

# Time-In-Culture Analysis

June 28, 2017

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## 1 Intro

More stream-of-consciousness analysis, focused (euphemistically speaking) on Time-In-Culture effects, especially hemizygosity.

## 2 Preliminaries

Load utility R code; do setup:

```
source('.../.../.../R/wlr.R') # load util code; path relative this folder or sibling in scripts/larrys

## Running as: ruzzo @ ruzzo.local; SVN Id, I miss you. $Id: wlr.R 2017-06-26 or later $

setup.my.wd('tic')          # set working dir; UPDATE if this file moves, or if COPY/PASTE to new file
setup.my.knitr('figs-knitr/')
my.figs.dir <- 'figs-mine/'
generic.setup(my.figs.dir)      # Create figs dir etc., if needed.
# some more params for knitr
if(exists('opts_knit')){ 
  # If knitr is loaded, set some of its options.
  # (Skip if not loaded, e.g., when playing in Rstudio.)
  opts_chunk$set(fig.align='center',fig.show='hold',fig.pos='tp')
  opts_knit$set(eval.after='fig.cap') ## so fig caption can be built using values from the code
  # opts_knit$set(width=1350) # width=85 in setup.my.knitr; do we want to override it?
}
```

```
# from svntssh://cegl.ocean.washington.edu/var/svn/7_strains/trunk/code/snpNB/data
# load('...../data/des.rda')
```

### 3 CNVnator Analysis

Load Chris' CNVnator output file. The 4 paths below are (1) Larry's old path within the svn tree; (2) newer one within git tree; (3) the same, but relative to current dir; and (4) local dir. I decided to put a symlink in the local dir with that name, linked to the real file via path3; I think this will make it more obvious what to change should we ever reorganize the tree.

```
getwd() ## just to be sure it's set correctly

# [1] "/Users/ruzzo/Documents/g/projects/thaps/Thaps_7_strains/code/snpNB/scripts/larrys/tic"

#cnv.path1 <- '/Users/ruzzo/Documents/s/papers/Thaps/chris/cnv.txt'
#cnv.path2 <- '/Users/ruzzo/Documents/g/projects/thaps/Thaps_7_strains/code/snpNB/data/cnv.txt'
#cnv.path3 <- ' ../../data/cnv.txt'
cnv.path <- 'cnv.txt' ## should be a symlink in tic directory to the CNVnator output
cnv <- read.delim(cnv.path)
```

Check for/correct oddities:

```
str(cnv)

# 'data.frame': 2380 obs. of  9 variables:
# $ strain    : Factor w/ 7 levels "IT","tp1007",...: 3 3 3 3 3 3 3 3 3 ...
# $ chr        : Factor w/ 65 levels "BD1_7","BD10_65",...: 38 38 38 38 38 38 38 38 38 ...
# $ start      : int  10601 112001 215001 358901 536501 554801 673401 781801 806901 853201 ...
# $ end        : int  13500 116500 221100 370300 538600 559300 685000 787400 811100 855600 ...
# $ length     : int  2900 4500 6100 11400 2100 4500 11600 5600 4200 2400 ...
# $ filtered   : Factor w/ 2 levels "False","True": 1 1 1 2 1 1 1 1 1 ...
# $ type       : Factor w/ 1 level "CNVnator": 1 1 1 1 1 1 1 1 ...
# $ cov_ratio: num  0.63738 1.54893 1.65381 0.00204 0.68486 ...
# $ dup_frac  : num  0.41188 0.00908 0.01178 0.97997 0.0211 ...

cnv[c(1:4,2378:2380),]

#      strain      chr  start    end length filtered      type cov_ratio dup_frac
# 1    tp1012    Chrl 10601  13500    2900    False CNVnator 0.63738000 0.41187900
# 2    tp1012    Chrl 112001 116500    4500    False CNVnator 1.54893000 0.00907677
# 3    tp1012    Chrl 215001 221100    6100    False CNVnator 1.65381000 0.01178470
# 4    tp1012    Chrl 358901 370300   11400     True CNVnator 0.00204431 0.97997300
# 2378 tp1335 BD36_69   6201  11900    5700    False CNVnator 4.86642000 0.94409000
# 2379 tp1335 BD36_69  12001  17900    5900    False CNVnator 1.16742000 0.85396800
# 2380 tp1335 BD37_91      1  13900   13900     True CNVnator 0.67417500 0.53919900

cnv$filtered <- cnv$filtered == 'True'      ## convert factor to Bool
all(cnv$length == (cnv$end-cnv$start+1)) ## start/end/length as expected

# [1] TRUE

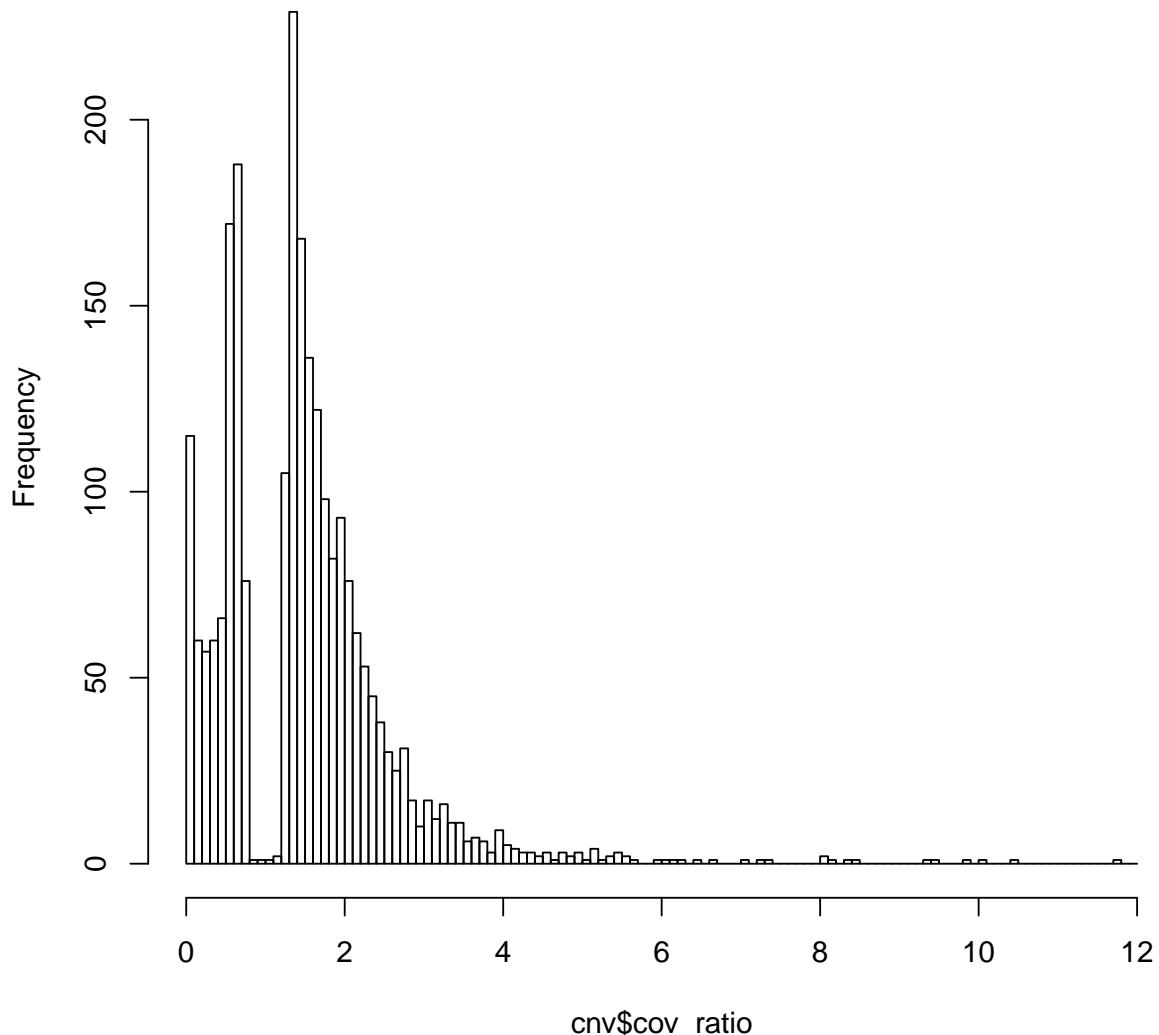
for(i in 1:9){
  if(any(is.na(cnv[,i]))){
    cat('NA in column',i,'\\n')
  }
}
strain.names <- c(paste('tp10',c('07','12:15'),sep=''), 'IT', 'tp1335') # old-school names; IT = 3367
rbind(sort(strain.names),levels(cnv$strain))

#      [,1] [,2]      [,3]      [,4]      [,5]      [,6]      [,7]
# [1,] "IT" "tp1007" "tp1012" "tp1013" "tp1014" "tp1015" "tp1335"
# [2,] "IT" "tp1007" "tp1012" "tp1013" "tp1014" "tp1015" "tp1335"
```

Some simple descriptive statistics. Cov ratios near 1 are expected, not called, but lots of stuff below 0.8 and above 1.2:

```
hist(cnv$cov_ratio, breaks=0:120/10)
```

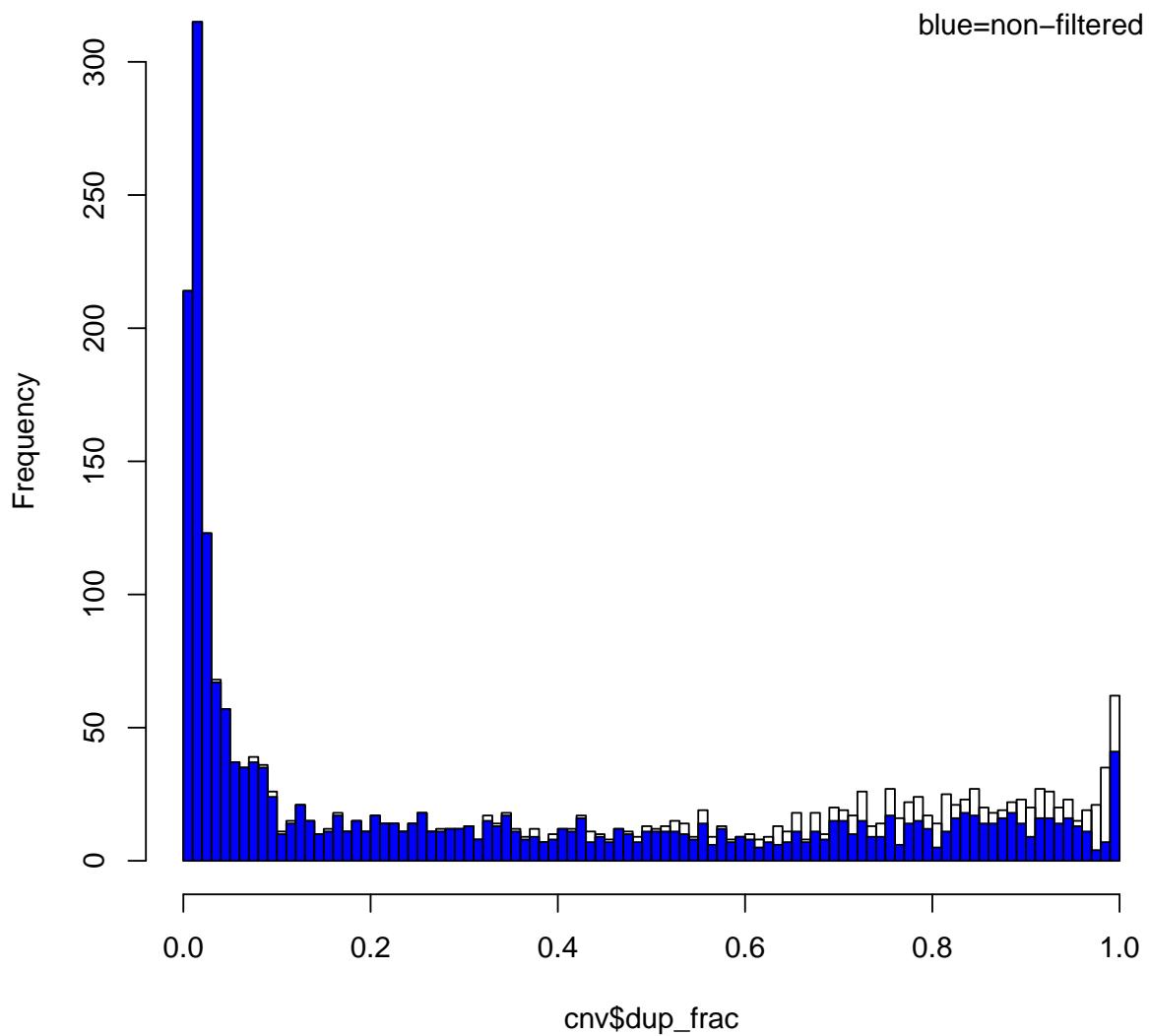
Histogram of cnv\$cov\_ratio



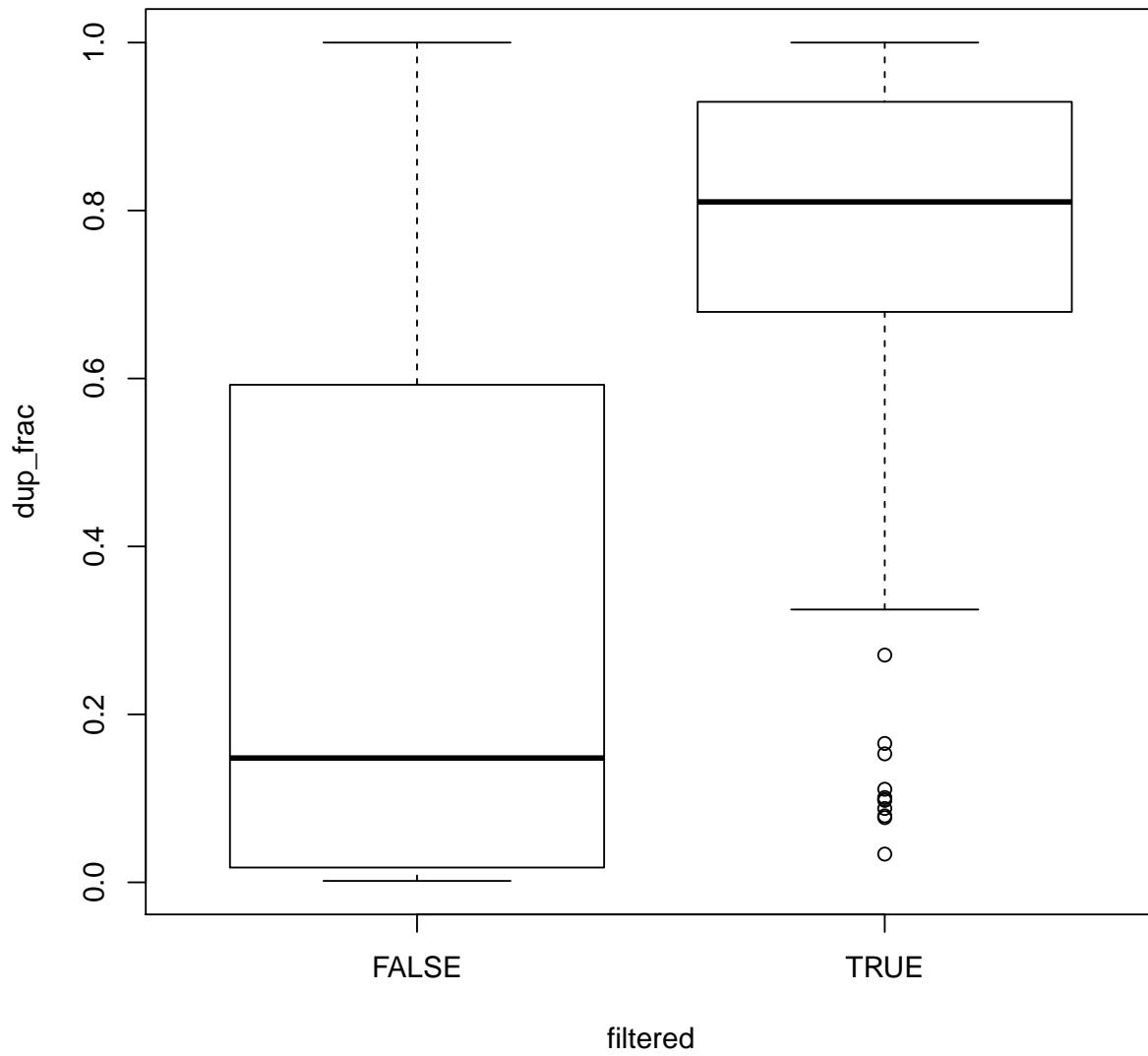
What does "Filtered" column mean? It correlates to dup\_frac, but loosely:

```
hist(cnv$dup_frac, breaks=0:100/100)
hist(cnv$dup_frac[!cnv$filtered], breaks=0:100/100, col='blue', add=T)
legend('topright', legend='blue=non-filtered', bty='n')
```

### Histogram of cnv\$dup\_frac



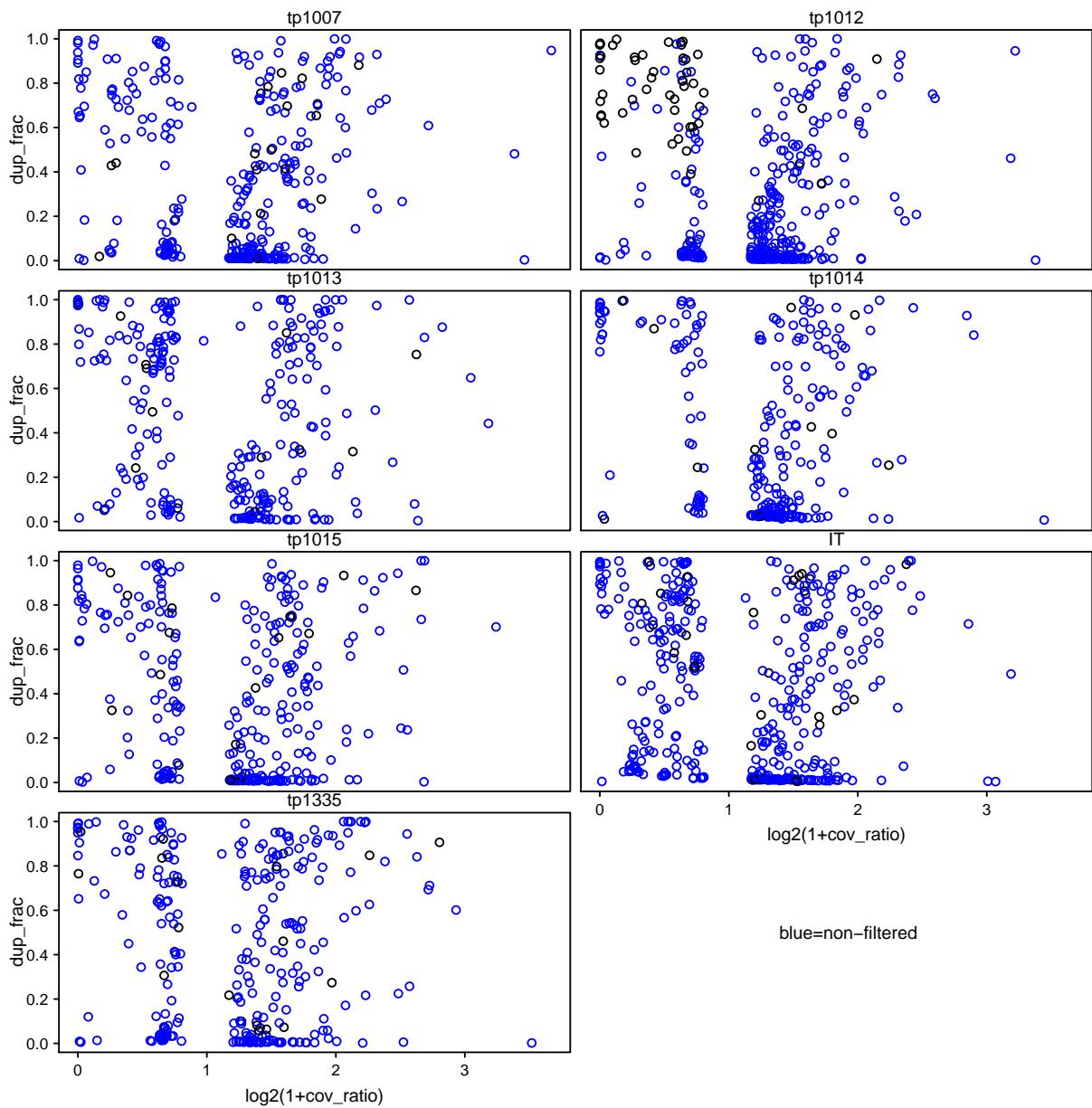
```
boxplot(dup_frac ~ filtered, data=cnv, ylab='dup_frac', xlab='filtered')
```



```

library(compactr)
opar <- par(mfrow=c(4,2), mar=c(0,0,1,.5), oma=c(3,4,1,0))
thexlim <- log2(1+range(cnv$cov_ratio))
for(st in strain.names){
  eplot(xlim=thexlim, xlab='log2(1+cov_ratio)', ylim=c(0,1), ylab='dup_frac', main=st)
  points(dup_frac[strain==st] ~ log2(1+cov_ratio[strain==st]), data=cnv, col=ifelse(filtered, 'black', 'blue'))
  if(st=='IT') {addxaxis()}
}
plot(0,0,type='n',axes=F,frame.plot=F,xlab='',ylab='')
legend('center',legend='blue=non-filtered', bty='n')
par(opar)

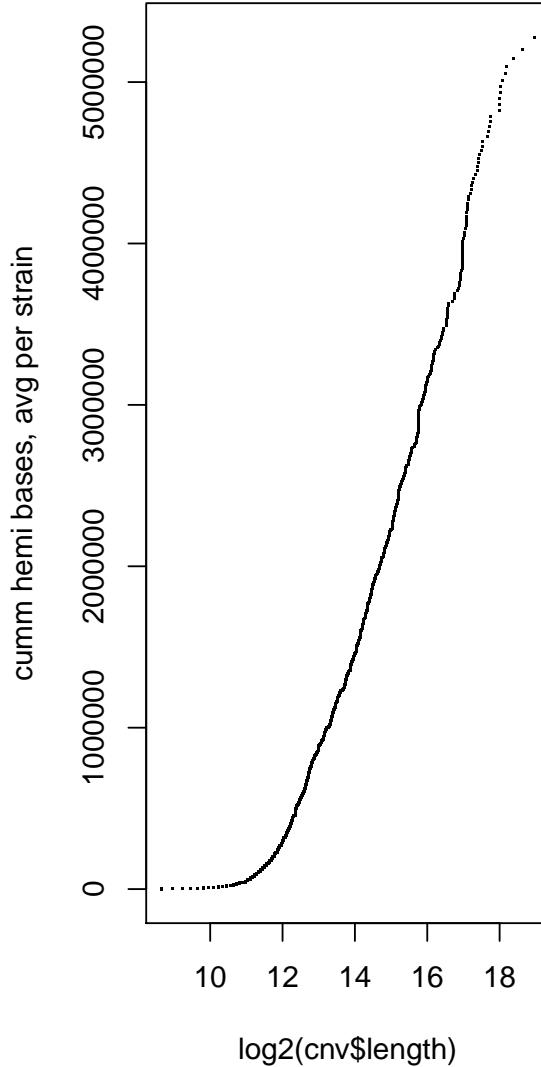
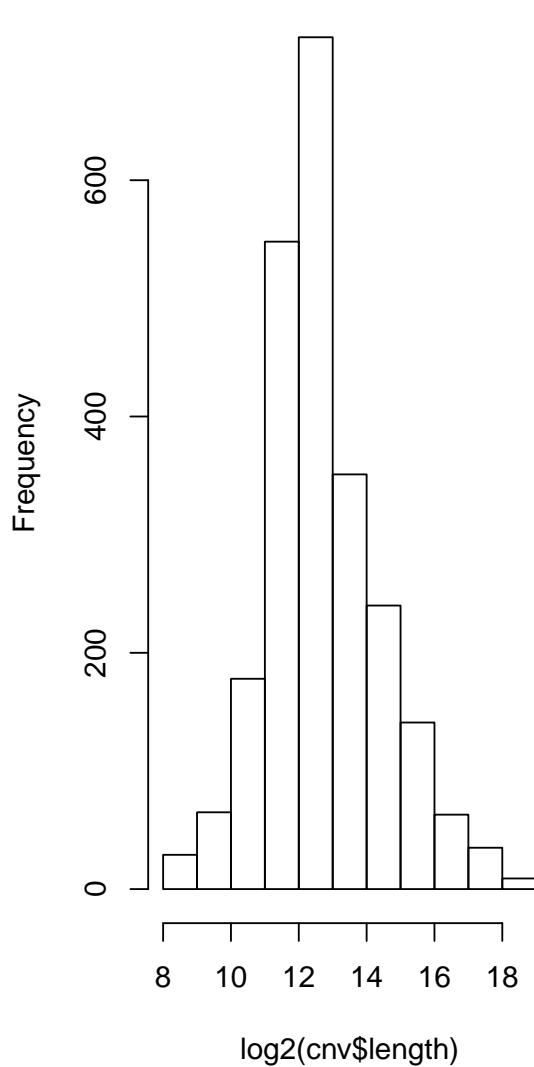
```



Most “events” are shorter than 5-10k, but the few big events cover most of the deleted bases.

```
opar <- par(mfrow=c(1, 2))
hist(log2(cnv$length))
sl <- sort(cnv$length)
plot(log2(sl), cumsum(sl)/7, xlab='log2(cnv$length)', ylab='cumm hemi bases, avg per strain', pch='.')
par(opar)
```

### Histogram of log2(cnv\$length)



## 4 Recreating the Time-In-Culture Plot

Per Chris' 10/3/2014 email, Michaela made the original TIC graph based on filtered = False,  $0.3 < \text{cov\_ratio} < 0.8$ , only on chromosomes. (gawk 1-liner broken over 3 for print purposes.)

```
gawk 'NR > 1 && $7 == "CNVnator" && $6 == "False" && $8 > .3 && $8 < .7 && \
substr($2,1,3) == "Chr" {x[$1] += $5} END \
{for (strain in x) {print strain " " x[strain]}}' cnv.txt
```

```
tp1012 1619100
tp1013 1374400
tp1014 495100
tp1015 935600
tp1007 1595600
tp1335 1428700
```

Can we reproduce that? For each strain, count number and total length of non-filtered regions on Chr's with coverage ratio in 10 equal bins from 0.0 to 1.0.

```

any(cnv$cov_ratio==1.0) ## FALSE
# [1] FALSE

any(cnv$cov_ratio==0.9) ## FALSE
# [1] FALSE

any(cnv$cov_ratio==0.8) ## FALSE
# [1] FALSE

any(cnv$cov_ratio==0.7) ## FALSE
# [1] FALSE

any(cnv$cov_ratio==0.3) ## FALSE
# [1] FALSE

sum(cnv$cov_ratio==0.0) ## 26, but only 1 not filtered, chromosomal:
# [1] 26

cnv[cnv$cov_ratio==0.0 & !cnv$filtered & substr(cnv$chr,1,3)=='Chr',]
#      strain      chr start   end length filtered      type cov_ratio dup_frac
# 248 tp1012 Chr11a 42601 44200   1600     FALSE CNVnator          0 0.0124481

# how many satisfy filtering criteria??
sum(!cnv$filtered) ## [1] 2020

# [1] 2020

sum(substr(as.character(cnv$chr),1,3) == 'Chr') ## [1] 1956
# [1] 1956

sum(cnv$cov_ratio <= 1.0) ## [1] 796
# [1] 796

sum(!cnv$filtered & substr(as.character(cnv$chr),1,3) == 'Chr' & cnv$cov_ratio <= 1.0) ## [1] 412
# [1] 412

pick <- !cnv$filtered & substr(as.character(cnv$chr),1,3) == 'Chr' & cnv$cov_ratio <= 1.0
cov.intervals <- paste('(', seq(0.0, 0.9, 0.1), ',', seq(0.1, 1.0, 0.1), ')', sep='')
low.length <- matrix(0,10,7,dimnames=list(cov.intervals, strain.names))
low.counts <- matrix(0,10,7,dimnames=list(cov.intervals, strain.names))
#pack <- logical(nrow(cnv))
for(i in 1:nrow(cnv)){
  if(!cnv$filtered[i] && substr(as.character(cnv$chr[i]),1,3) == 'Chr' && cnv$cov_ratio[i] <= 1.0){
    #pack[i] <- T
    rat <- ceiling(cnv$cov_ratio[i] * 10)
    st <- as.character(cnv$strain[i])
    low.counts[rat,st] <- low.counts[rat,st] + 1
    low.length[rat,st] <- low.length[rat,st] + cnv$length[i]
  }
}
# pick == pack & 412 entries, but one of them has zero ratio, so excluded from counts
low.counts.37 <- colSums(low.counts[4:7,]) ; low.counts.37

# tp1007 tp1012 tp1013 tp1014 tp1015      IT tp1335
#      34       47      50      11      27       68      34

```

```

low.length.37 <- colSums(low.length[4:7,]) ; low.length.37

# tp1007 tp1012 tp1013 tp1014 tp1015      IT tp1335
# 1595600 1619100 1374400 495100 935600 269900 1428700

# lengths match Chris' email (excluding IT, which he didn't report)
# tp1007 tp1012 tp1013 tp1014 tp1015      IT tp1335
# 1595600 1619100 1374400 495100 935600 269900 1428700
low.counts.38 <- colSums(low.counts[4:8,]) ; low.counts.38

# tp1007 tp1012 tp1013 tp1014 tp1015      IT tp1335
# 40     60     53     24     34     77     38

low.length.38 <- colSums(low.length[4:8,]) ; low.length.38

# tp1007 tp1012 tp1013 tp1014 tp1015      IT tp1335
# 1672500 1781500 1399400 1313700 988400 336500 1453000

low.length.all <- colSums(low.length) ; low.length.all

# tp1007 tp1012 tp1013 tp1014 tp1015      IT tp1335
# 1708500 1813000 1432300 1342200 1007100 426600 1468300

cbind(low.length, low.counts)

#          tp1007 tp1012 tp1013 tp1014 tp1015      IT tp1335 tp1007 tp1012 tp1013 tp1014 tp1015
# (0,0.1]   28300 26500 11800 28500 14700 33000 14800    4     3     1     4     3
# (0.1,0.2]  5400 3500 6400 0 2800 26600 500    7     4     7     0     4
# (0.2,0.3]  2300 1500 14700 0 1200 30500 0     3     2     3     0     1
# (0.3,0.4]  3300 3200 39100 0 20200 29500 500    1     1     12    0     4
# (0.4,0.5]  5500 8800 36800 0 1800 57500 2900   2     1     9     0     1
# (0.5,0.6] 217500 451100 241800 0 405700 131900 1053400 8     16    11     0    10
# (0.6,0.7] 1369300 1156000 1056700 495100 507900 51000 371900 23    29    18    11    12
# (0.7,0.8]  76900 162400 25000 818600 52800 66600 24300 6     13    3     13    7
# (0.8,0.9]    0     0     0     0     0     0     0     0     0     0     0     0
# (0.9,1]     0     0     0     0     0     0     0     0     0     0     0     0
#          IT tp1335
# (0,0.1]   3     3
# (0.1,0.2] 14    1
# (0.2,0.3] 18    0
# (0.3,0.4] 13    1
# (0.4,0.5] 23    3
# (0.5,0.6] 22    17
# (0.6,0.7] 10    13
# (0.7,0.8]  9    4
# (0.8,0.9]  0    0
# (0.9,1]    0    0

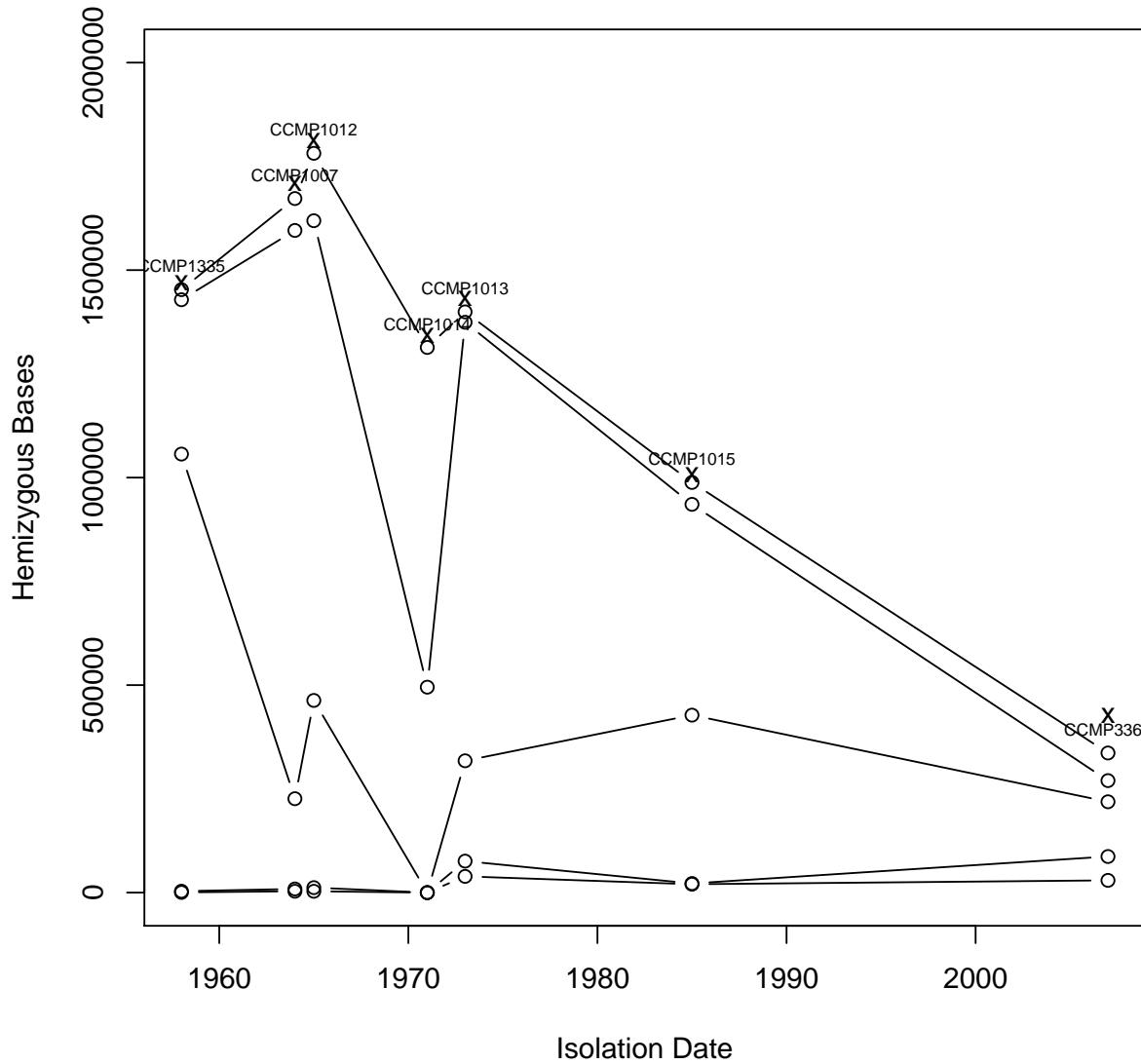
```

Nothing was called between 0.8 and 1.0, presumably CNVnator parameters. Total in the range between 0.3 and 0.7 matches the numbers in Chris' email. Total in all ranges matches, too, except for 1012, which has one region of ratio zero, that wasn't counted above (my first bin is (0.0, 0.1]). Below we plot total versus date placed in culture. The 5 lines are totals in the (.3, .4], (.3,.5], ..., (.3,.8] windows, just to see how each bin contributes to the total. The clear message, as is also obvious from the length table printed above, is that the .5 to .8 range is where most of the action is.

```

dates <- unlist(lapply(1:7, function(st){as.integer(st.loc(st,id=F,loc=F,date=T))})
perm <- order(dates)
plot(0,0,type='n', xlim=range(dates), ylim=c(0,2e6), xlab='Isolation Date', ylab='Hemizygous Bases')
lines(dates[perm], low.length[4,perm],type='b')
for(i in 5:8){
  lines(dates[perm], colSums(low.length[4:i,perm]),type='b')
}
ids <- unlist(lapply(1:7, function(st){st.loc(st,id=T,loc=F,date=F)}))
text(dates, low.length.38, labels=ids,cex=.6, pos=3)
points(dates,low.length.all,pch='x') # showing "all" changes little

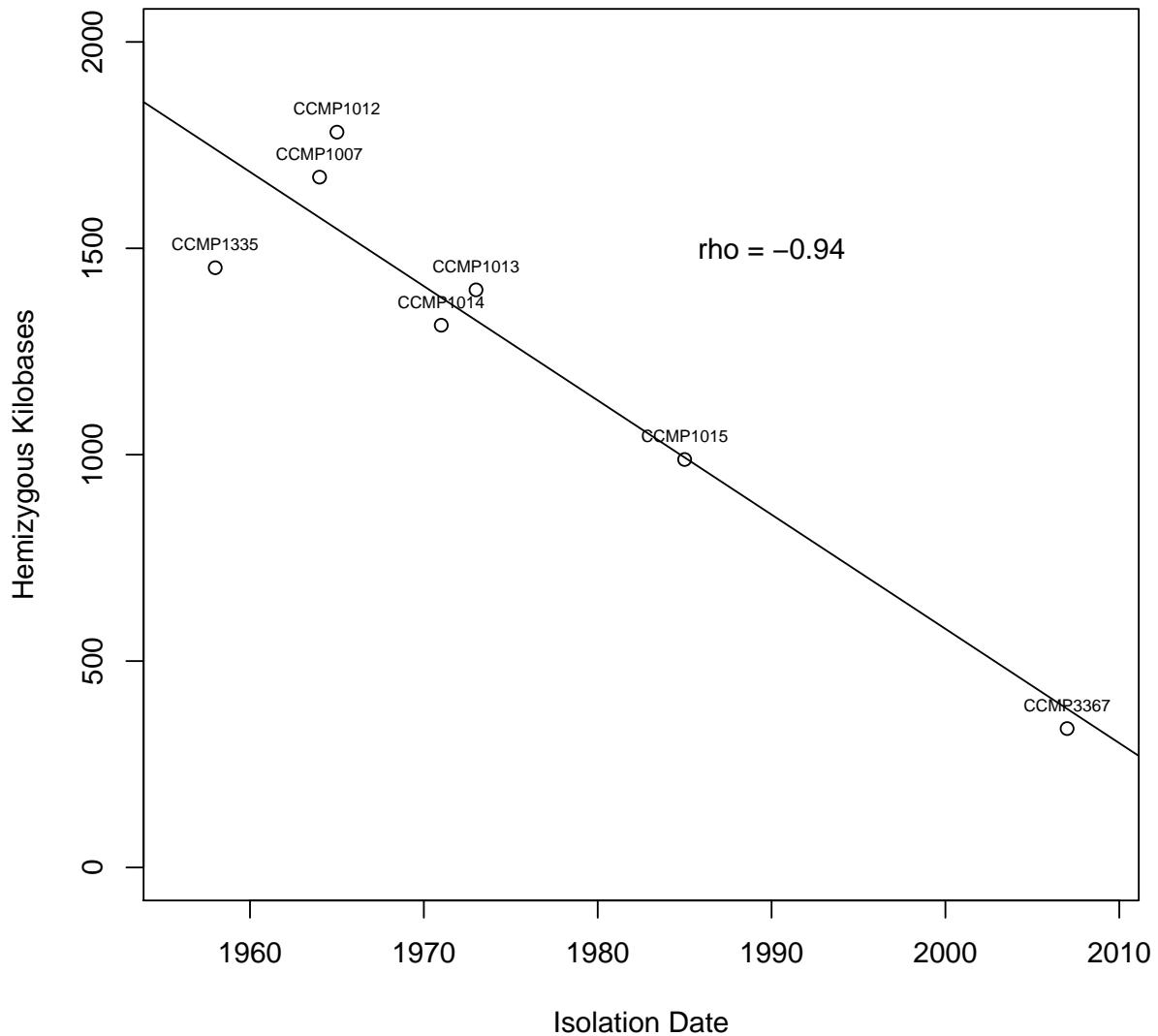
```



The graph Michaela made is most similar to the last (highest) of these, but her Y scale is a bit larger, perhaps due to inclusion of “non-Chr” and/or “filtered” calls. I like the above graph better, it seems a bit more conservative, while still showing the interesting trend.

For the paper supplement, I’d just show the .3–.8 points, plus a trend line.

```
plot(dates, low.length.38/1000, type='p', xlim=range(dates)+c(-2,2), ylim=c(0,2e6/1000),
      xlab='Isolation Date', ylab='Hemizygous Kilobases')
text(dates, low.length.38/1000, labels=ids, cex=.6, pos=3)
abline(lm(low.length.38/1000 ~ dates)$coefficients)
text(1990, 1.5e6/1000, paste('rho =', format(cor(low.length.38, dates), digits=2)))
```



Make the same plot for any coverage slice, optionally with fancy legend:

```
tic <- function(lo=0.3, hi=0.8,
                 cnv.tbl=cnv, thedates=dates, theids=ids,           # coverage thresholds
                 theylim=NULL,                                         # stuff computed above
                 fancy=FALSE, legcex=0.7)                            # y axis limits
{
  opar <- par(no.readonly=TRUE); on.exit(par(opar))
  pick <- !cnv.tbl$filtered & substr(as.character(cnv.tbl$chr),1,3) == 'Chr' &
    lo <= cnv.tbl$cov_ratio & cnv.tbl$cov_ratio <= hi
  lengths <- matrix(NA,7,1,dimnames=list(rep('',7)))
  for(st in 1:nlevels(cnv.tbl$strain)){
    st.fact <- levels(cnv.tbl$strain)[st]
    rownames(lengths)[st] <- st.fact
    lengths[st] <- sum(cnv.tbl$length[pick & cnv.tbl$strain==st.fact])
  }
  lengths <- lengths[c(2:6,1,7),] # reorder
  if(is.null(theylim)){theylim <- range(lengths)/1000}
```

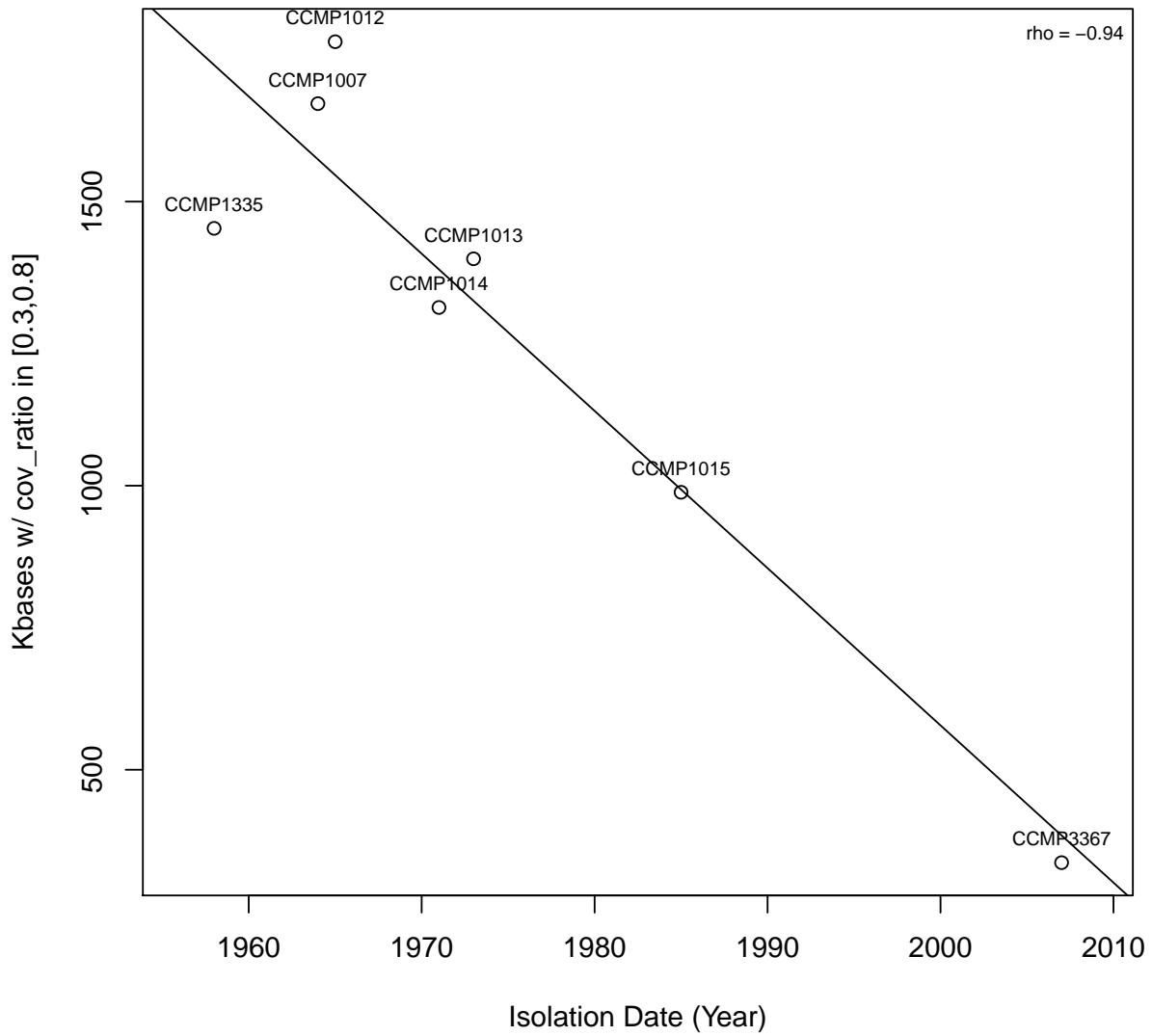
```

plot(thedates, lengths/1000, type='p',
      xlim=range(thedates)+c(-2,2),
      ylim=theylim,
      xlab='Isolation Date (Year)',
      ylab=ifelse(fancy, 'Estimated Hemizygous Deletion (Kilobases)',
                  paste('Kbases w/ cov_ratio in [', lo, ',', hi, ']', sep=''))
      ),
      pch=ifelse(fancy, 19, 1)
)
if(fancy){
  theids <- st.locs(1:7,id=F,loc=F,locabbrv=T,date=F)
}
text(thedates, lengths/1000, cex=legcex, pos=ifelse(fancy, 2, 3), labels=theids)
abline(lm(lengths/1000 ~ thedates)$coefficients)
legend(ifelse(fancy, 'bottomleft', 'topright'),
       legend=paste('rho =', format(cor(lengths/1000 , thedates), digits=2)),
       bty='n', cex=legcex)
if(fancy){
  thelocs <- st.locs(1:7,id=F,loc=T,locabbrv=F,date=F)
  thelocdate <- paste( ' - ', thelocs, ' (', thedates, ')', sep='')
  # getting legend to align nicely using non-monospaced font is a bit fussy.
  # Use "text()" to place strain "loc abbrev" (theids) separately from
  # " - full.loc (dates)" (thelocdate) so that I can control x-position.
  # Put legend at upper right. Several arbitrary constants below (lines marked **)
  # reflect empirical fiddling to make it look nice: top @ 25Kb below max y,
  # right edge @ 2009, 1.5x line spacing, rectangle margin
  widest.locdate <- max(strwidth(thelocdate, cex=legcex)) # widest location/date
  widest.abbrv <- max(strwidth(theids, cex=legcex)) # widest loc abbreviation
  height <- max(strheight(thelocdate, cex=legcex)) # text height
  yby <- height * 1.5 # ** line spacing
  # maxy <- max(lengths)/1000 - 25 # ** top just below highest point
  maxy <- theylim[2] - height - 25 # ** top just below y axis limit
  ys <- seq(from=maxy, by=-yby, length.out=7) # y-coords for each line
  x2 <- 2009 - widest.locdate # ** right edge @ 2009
  x1 <- x2 - widest.abbrv
  rect(x1-1.0, maxy-7.2*yby, 2009+1.0, maxy+1.2*yby) # ** inflate rectangle slightly
  text(x1, ys, cex=legcex, adj=0, labels=theids[order(dates)])
  text(x2, ys, cex=legcex, adj=0, labels=thelocdate[order(dates)])
}
return(lengths)
}

tic() # debug test: duplicate graph above?

# tp1007  tp1012  tp1013  tp1014  tp1015      IT  tp1335
# 1672500 1781500 1399400 1313700  988400   336500 1453000

```



```

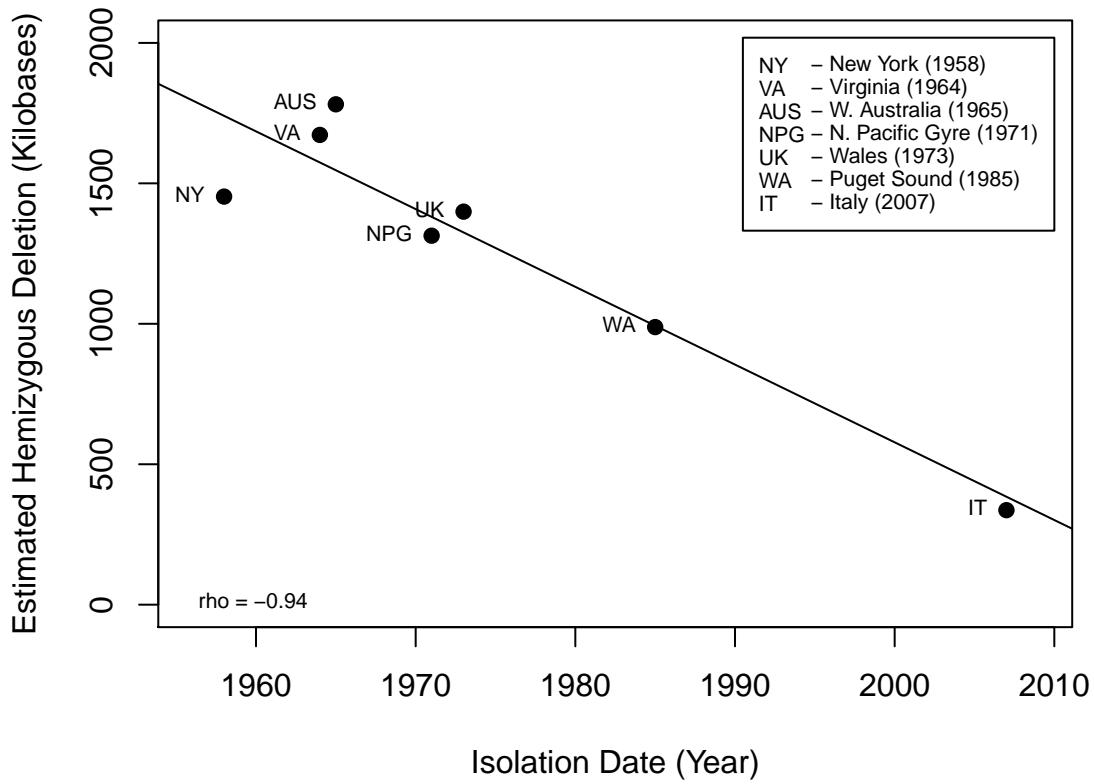
fig.S4.path <- paste(my.figs.dir, 'FigS4-hemizygosity.pdf', sep='')
pdf(fig.S4.path, height=5, width=6)
tic(fancy=TRUE, theylim=c(0, 2e6/1000)) # fancy version for paper (Supp Fig S4).

# tp1007 tp1012 tp1013 tp1014 tp1015      IT tp1335
# 1672500 1781500 1399400 1313700  988400   336500 1453000

dev.off()

# pdf
# 2

```

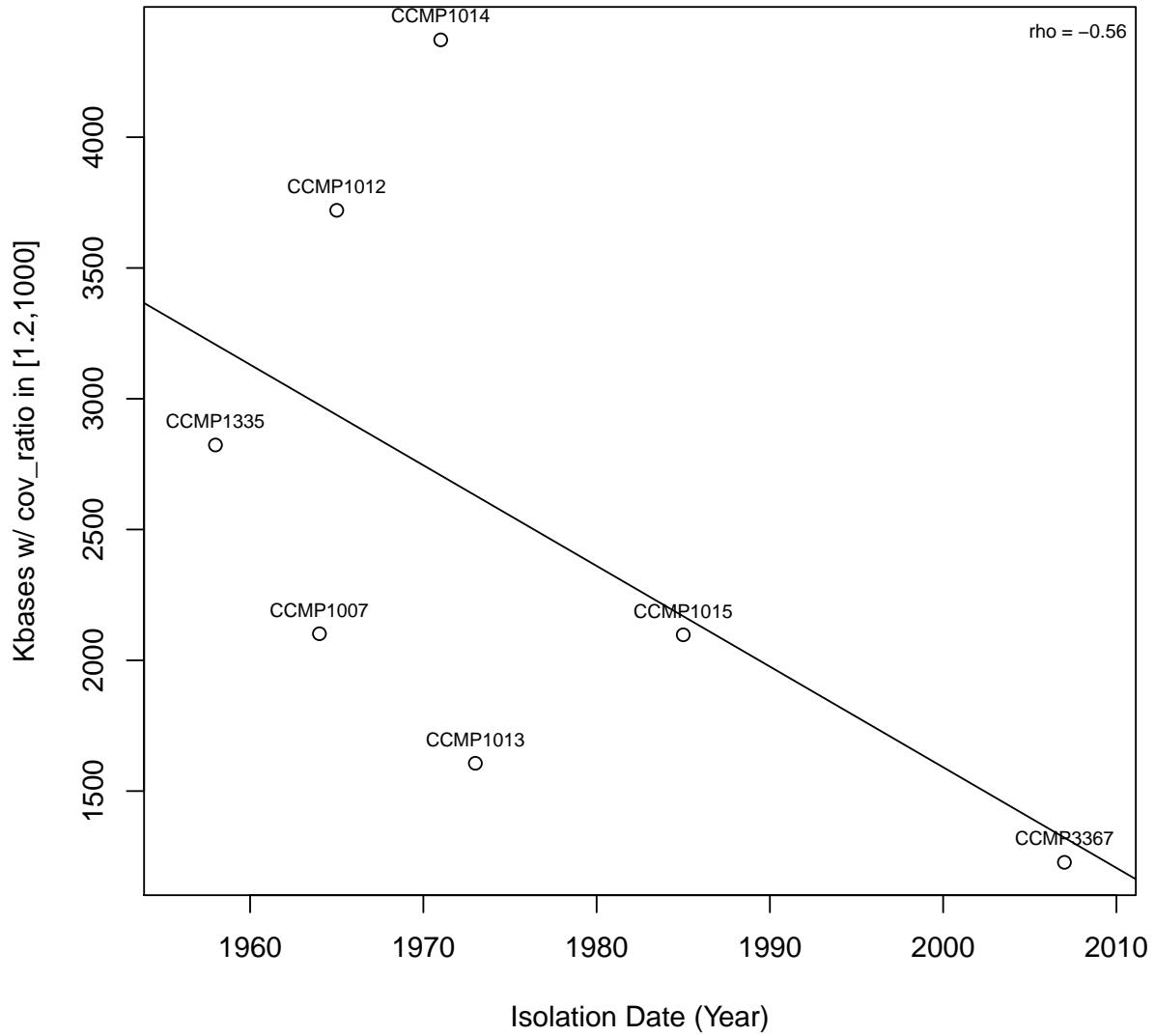


## 5 Time-In-Culture for Above-Average Coverages

```
max(cnv$cov_ratio)
# [1] 11.7308
```

Time-in-culture also correlates with coverage above 1:

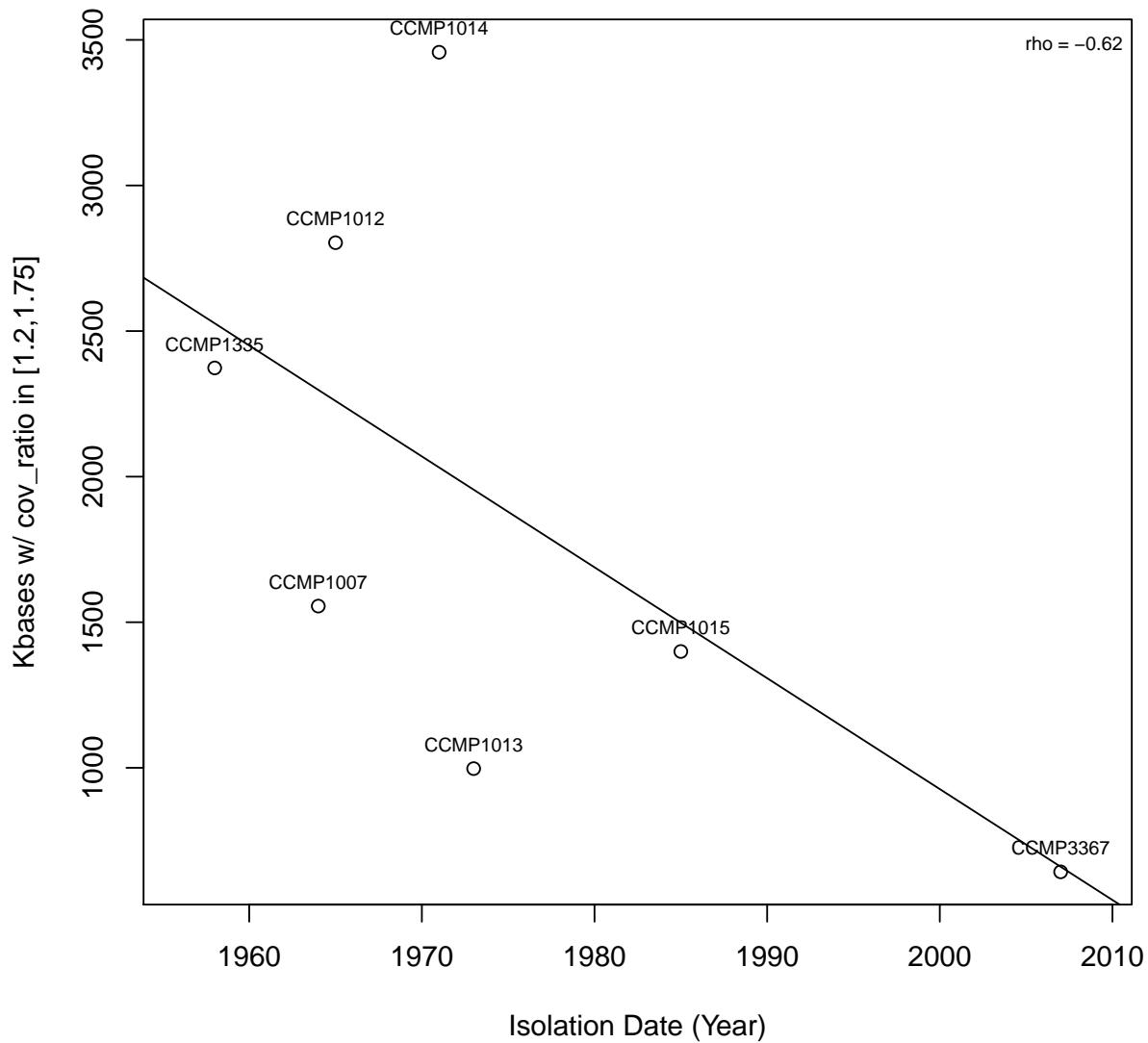
```
tic(1.2,1000)
# tp1007 tp1012 tp1013 tp1014 tp1015      IT tp1335
# 2101600 3720500 1606400 4372200 2097500 1227700 2823200
```



And with possible trisomies:

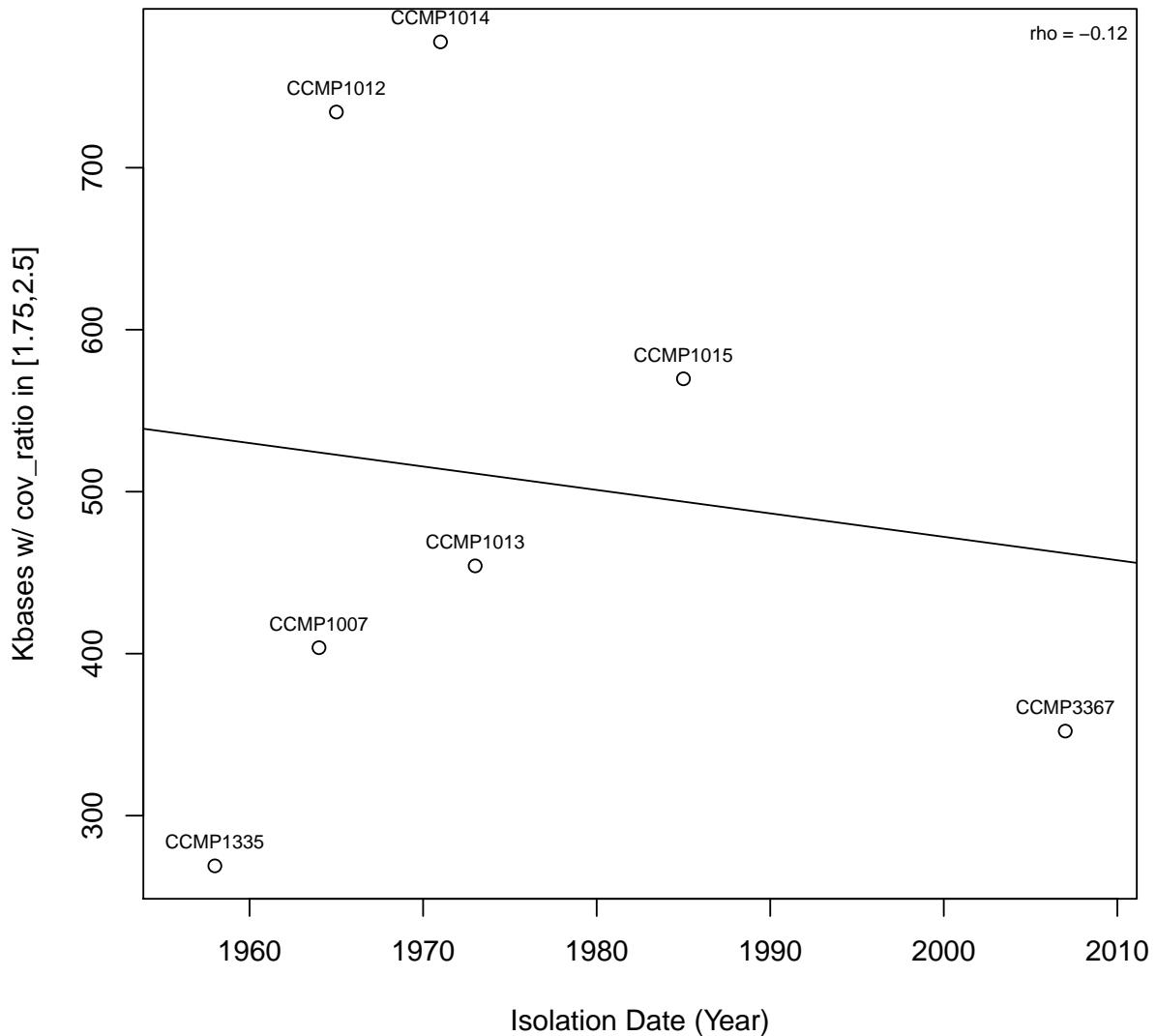
```
tic(1.2, 1.75)

# tp1007 tp1012 tp1013 tp1014 tp1015      IT tp1335
# 1555500 2803600 997300 3457700 1399600  642800 2373400
```



But only weakly with duplications:

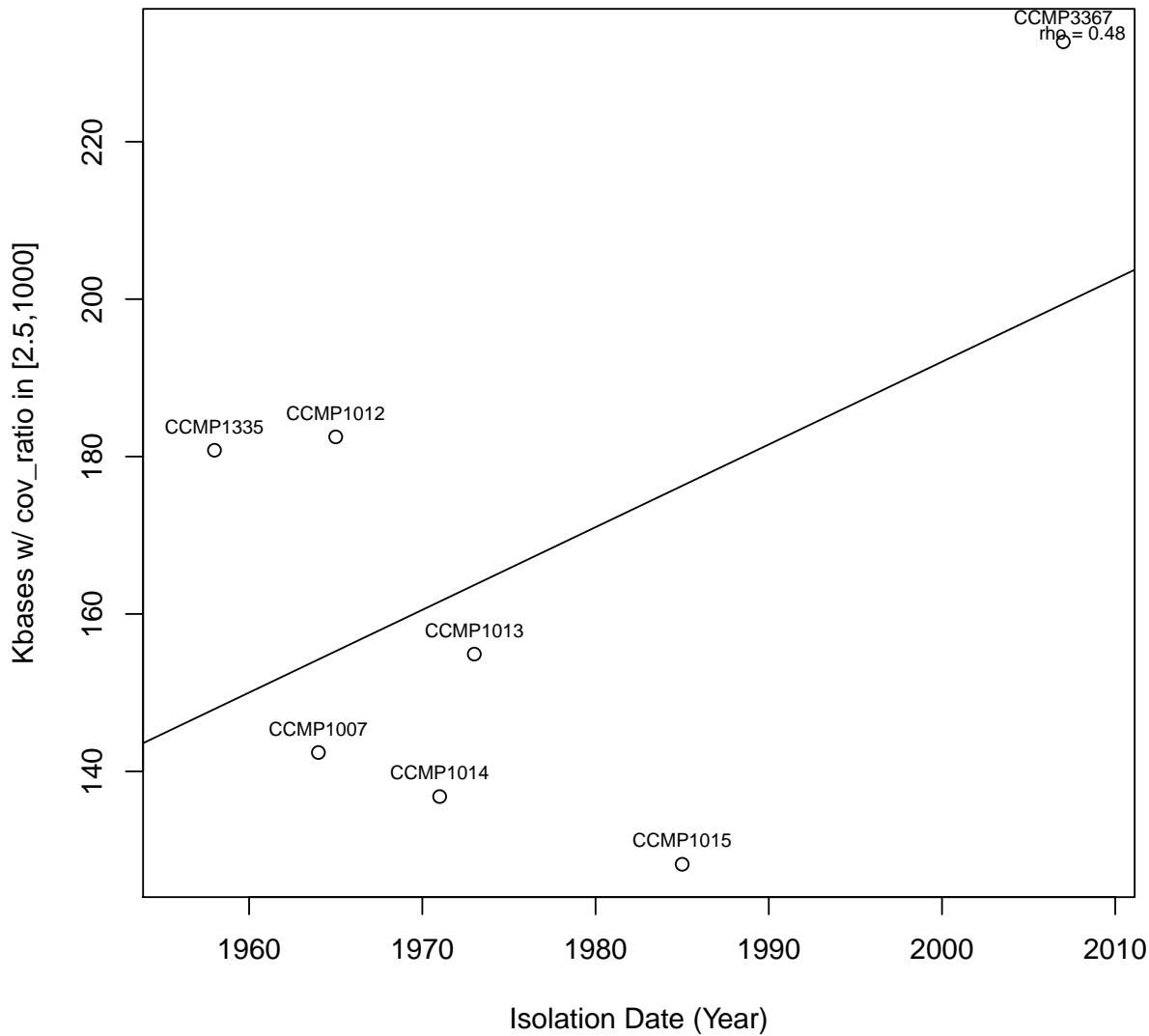
```
tic(1.75, 2.5)
# tp1007 tp1012 tp1013 tp1014 tp1015      IT tp1335
# 403700 734400 454200 777700 569700 352200 269000
```



And not with triplications (or higher), as the totals get smaller/noisier, (although there is a distinct trend if Italy were excluded):

```
tic(2.5, 1000)

# tp1007 tp1012 tp1013 tp1014 tp1015      IT tp1335
# 142400 182500 154900 136800 128200 232700 180800
```



## 6 Shared/Private Hemizygosity

A quick eyeball at shared/private

```

cnvp <- cnv[pick,]
pi <- order(cnvp$chr,cnvp$start,cnvp$length,cnvp$strain)
cnvv <- cnvp[pi,]
cnvv

#      strain      chr    start      end length filtered      type cov_ratio dup_frac
# 1669      IT     Chr1       1   25200   25200     FALSE CNVnator 0.722468000 0.69837600
# 1 tp1012     Chr1  10601   13500   2900     FALSE CNVnator 0.637380000 0.41187900
# 1366 tp1015     Chr1  10601   14400   3800     FALSE CNVnator 0.706210000 0.45966200
# 508  tp1013     Chr1  16601   25200   8600     FALSE CNVnator 0.636063000 0.68046000
# 1670      IT     Chr1  67901   70700   2800     FALSE CNVnator 0.501551000 0.20650300
# 1671      IT     Chr1  80601   82300   1700     FALSE CNVnator 0.223819000 0.04930390

```

|        |        |        |         |         |        |       |          |             |            |
|--------|--------|--------|---------|---------|--------|-------|----------|-------------|------------|
| # 2089 | tp1335 | Chr1   | 90501   | 91800   | 1300   | FALSE | CNVnator | 0.488495000 | 0.00997009 |
| # 509  | tp1013 | Chr1   | 106601  | 108600  | 2000   | FALSE | CNVnator | 0.555534000 | 0.70172500 |
| # 5    | tp1012 | Chr1   | 536501  | 538600  | 2100   | FALSE | CNVnator | 0.684861000 | 0.02109840 |
| # 1676 | IT     | Chr1   | 538801  | 543200  | 4400   | FALSE | CNVnator | 0.704481000 | 0.16905200 |
| # 2093 | tp1335 | Chr1   | 1222401 | 1224900 | 2500   | FALSE | CNVnator | 0.599521000 | 0.13329200 |
| # 1679 | IT     | Chr1   | 1222501 | 1224400 | 1900   | FALSE | CNVnator | 0.248841000 | 0.09708220 |
| # 512  | tp1013 | Chr1   | 1222601 | 1224700 | 2100   | FALSE | CNVnator | 0.378575000 | 0.18979700 |
| # 514  | tp1013 | Chr1   | 1865001 | 1865600 | 600    | FALSE | CNVnator | 0.111020000 | 0.07031250 |
| # 24   | tp1012 | Chr1   | 2464001 | 2465000 | 1000   | FALSE | CNVnator | 0.283469000 | 0.02288490 |
| # 1053 | tp1007 | Chr1   | 2464101 | 2464700 | 600    | FALSE | CNVnator | 0.199091000 | 0.03571430 |
| # 1375 | tp1015 | Chr1   | 2521201 | 2525500 | 4300   | FALSE | CNVnator | 0.546392000 | 0.02256380 |
| # 1687 | IT     | Chr1   | 2545801 | 2551100 | 5300   | FALSE | CNVnator | 0.653475000 | 0.39250500 |
| # 1061 | tp1007 | Chr1   | 3042101 | 3042600 | 500    | FALSE | CNVnator | 0.188780000 | 0.52830200 |
| # 31   | tp1012 | Chr1   | 3042101 | 3042600 | 500    | FALSE | CNVnator | 0.249870000 | 0.33256000 |
| # 1382 | tp1015 | Chr1   | 3042101 | 3042600 | 500    | FALSE | CNVnator | 0.187651000 | 0.37586700 |
| # 2105 | tp1335 | Chr1   | 3042101 | 3042600 | 500    | FALSE | CNVnator | 0.313598000 | 0.44981100 |
| # 597  | tp1013 | Chr10  | 12301   | 20100   | 7800   | FALSE | CNVnator | 0.639332000 | 0.94901100 |
| # 1826 | IT     | Chr10  | 12301   | 28500   | 16200  | FALSE | CNVnator | 0.526721000 | 0.82503700 |
| # 1828 | IT     | Chr10  | 103801  | 104500  | 700    | FALSE | CNVnator | 0.453978000 | 0.74776100 |
| # 1831 | IT     | Chr10  | 215601  | 218300  | 2700   | FALSE | CNVnator | 0.520260000 | 0.69291000 |
| # 602  | tp1013 | Chr10  | 215601  | 218300  | 2700   | FALSE | CNVnator | 0.446037000 | 0.69061400 |
| # 1171 | tp1007 | Chr10  | 812601  | 814700  | 2100   | FALSE | CNVnator | 0.737270000 | 0.01840490 |
| # 1835 | IT     | Chr10  | 915301  | 915800  | 500    | FALSE | CNVnator | 0.262656000 | 0.03667140 |
| # 608  | tp1013 | Chr11a | 1       | 5200    | 5200   | FALSE | CNVnator | 0.498237000 | 0.66891100 |
| # 1174 | tp1007 | Chr11a | 1001    | 1800    | 800    | FALSE | CNVnator | 0.204382000 | 0.77297300 |
| # 245  | tp1012 | Chr11a | 1001    | 1800    | 800    | FALSE | CNVnator | 0.183318000 | 0.80642000 |
| # 1499 | tp1015 | Chr11a | 1001    | 1800    | 800    | FALSE | CNVnator | 0.157815000 | 0.75340600 |
| # 247  | tp1012 | Chr11a | 12101   | 20900   | 8800   | FALSE | CNVnator | 0.417926000 | 0.85631200 |
| # 1839 | IT     | Chr11a | 12101   | 21100   | 9000   | FALSE | CNVnator | 0.434211000 | 0.84901600 |
| # 1176 | tp1007 | Chr11a | 12101   | 22300   | 10200  | FALSE | CNVnator | 0.554710000 | 0.84839400 |
| # 1501 | tp1015 | Chr11a | 12101   | 22300   | 10200  | FALSE | CNVnator | 0.387820000 | 0.83772200 |
| # 609  | tp1013 | Chr11a | 12101   | 58500   | 46400  | FALSE | CNVnator | 0.572295000 | 0.25616000 |
| # 1840 | IT     | Chr11a | 40901   | 45300   | 4400   | FALSE | CNVnator | 0.305445000 | 0.14415300 |
| # 1178 | tp1007 | Chr11a | 42501   | 44200   | 1700   | FALSE | CNVnator | 0.036484300 | 0.18320600 |
| # 886  | tp1014 | Chr11a | 42501   | 44300   | 1800   | FALSE | CNVnator | 0.055698900 | 0.20939300 |
| # 2203 | tp1335 | Chr11a | 42501   | 44300   | 1800   | FALSE | CNVnator | 0.057603600 | 0.12004700 |
| # 248  | tp1012 | Chr11a | 42601   | 44200   | 1600   | FALSE | CNVnator | 0.000000000 | 0.01244810 |
| # 1502 | tp1015 | Chr11a | 42601   | 44300   | 1700   | FALSE | CNVnator | 0.050497400 | 0.02290080 |
| # 1841 | IT     | Chr11a | 50501   | 58500   | 8000   | FALSE | CNVnator | 0.329241000 | 0.64361100 |
| # 610  | tp1013 | Chr11a | 65801   | 253100  | 187300 | FALSE | CNVnator | 0.622153000 | 0.04132020 |
| # 2204 | tp1335 | Chr11a | 148601  | 155200  | 6600   | FALSE | CNVnator | 0.688274000 | 0.41081400 |
| # 1844 | IT     | Chr11a | 150001  | 150800  | 800    | FALSE | CNVnator | 0.106640000 | 0.82812500 |
| # 1845 | IT     | Chr11a | 239301  | 240300  | 1000   | FALSE | CNVnator | 0.196624000 | 0.06914890 |
| # 611  | tp1013 | Chr11a | 254001  | 376100  | 122100 | FALSE | CNVnator | 0.601833000 | 0.04203160 |
| # 1846 | IT     | Chr11a | 328401  | 329400  | 1000   | FALSE | CNVnator | 0.234785000 | 0.04699250 |
| # 1179 | tp1007 | Chr11a | 328401  | 329400  | 1000   | FALSE | CNVnator | 0.213642000 | 0.07824430 |
| # 1503 | tp1015 | Chr11a | 328401  | 329400  | 1000   | FALSE | CNVnator | 0.188550000 | 0.05905510 |
| # 252  | tp1012 | Chr11a | 328501  | 329400  | 900    | FALSE | CNVnator | 0.137136000 | 0.08163270 |
| # 254  | tp1012 | Chr11a | 564201  | 570700  | 6500   | FALSE | CNVnator | 0.690573000 | 0.01360890 |
| # 889  | tp1014 | Chr11a | 738701  | 741600  | 2900   | FALSE | CNVnator | 0.721143000 | 0.47542900 |
| # 1181 | tp1007 | Chr11b | 1       | 3300    | 3300   | FALSE | CNVnator | 0.598547000 | 0.86469000 |
| # 1849 | IT     | Chr11b | 1       | 11900   | 11900  | FALSE | CNVnator | 0.508679000 | 0.69147400 |
| # 613  | tp1013 | Chr11b | 1       | 11900   | 11900  | FALSE | CNVnator | 0.506334000 | 0.68591100 |
| # 1184 | tp1007 | Chr12  | 6401    | 7600    | 1200   | FALSE | CNVnator | 0.031889200 | 0.00171233 |
| # 258  | tp1012 | Chr12  | 6401    | 7600    | 1200   | FALSE | CNVnator | 0.031739900 | 0.00325468 |
| # 892  | tp1014 | Chr12  | 6401    | 7600    | 1200   | FALSE | CNVnator | 0.024373500 | 0.01138210 |
| # 1508 | tp1015 | Chr12  | 6401    | 7600    | 1200   | FALSE | CNVnator | 0.024512100 | 0.00226757 |
| # 2208 | tp1335 | Chr12  | 6401    | 7600    | 1200   | FALSE | CNVnator | 0.015853200 | 0.00584226 |
| # 1509 | tp1015 | Chr12  | 8601    | 10000   | 1400   | FALSE | CNVnator | 0.562602000 | 0.87140300 |
| # 1855 | IT     | Chr12  | 93901   | 94300   | 400    | FALSE | CNVnator | 0.172570000 | 0.70017600 |
| # 1856 | IT     | Chr12  | 145001  | 148300  | 3300   | FALSE | CNVnator | 0.485841000 | 0.55902800 |
| # 1189 | tp1007 | Chr12  | 145001  | 148300  | 3300   | FALSE | CNVnator | 0.406828000 | 0.58149900 |
| # 2211 | tp1335 | Chr12  | 145001  | 149100  | 4100   | FALSE | CNVnator | 0.712069000 | 0.34550600 |
| # 895  | tp1014 | Chr12  | 145101  | 146200  | 1100   | FALSE | CNVnator | 0.643307000 | 0.34694800 |
| # 263  | tp1012 | Chr12  | 145101  | 148300  | 3200   | FALSE | CNVnator | 0.361142000 | 0.68381000 |
| # 1512 | tp1015 | Chr12  | 145101  | 148400  | 3300   | FALSE | CNVnator | 0.700742000 | 0.31829000 |
| # 267  | tp1012 | Chr12  | 217401  | 243900  | 26500  | FALSE | CNVnator | 0.678484000 | 0.02256290 |

|        |        |        |         |         |        |       |          |             |            |
|--------|--------|--------|---------|---------|--------|-------|----------|-------------|------------|
| # 1191 | tp1007 | Chr12  | 217401  | 244700  | 27300  | FALSE | CNVnator | 0.681074000 | 0.02712150 |
| # 1193 | tp1007 | Chr12  | 549001  | 551800  | 2800   | FALSE | CNVnator | 0.657839000 | 0.03097350 |
| # 2214 | tp1335 | Chr12  | 549001  | 552400  | 3400   | FALSE | CNVnator | 0.651156000 | 0.03264640 |
| # 272  | tp1012 | Chr12  | 549301  | 551800  | 2500   | FALSE | CNVnator | 0.579238000 | 0.02475730 |
| # 274  | tp1012 | Chr12  | 630301  | 636900  | 6600   | FALSE | CNVnator | 0.701986000 | 0.53518600 |
| # 622  | tp1013 | Chr12  | 680601  | 684100  | 3500   | FALSE | CNVnator | 0.568825000 | 0.72859500 |
| # 2218 | tp1335 | Chr12  | 680801  | 681600  | 800    | FALSE | CNVnator | 0.404811000 | 0.34371600 |
| # 1862 | IT     | Chr12  | 682601  | 684000  | 1400   | FALSE | CNVnator | 0.330565000 | 0.71039200 |
| # 625  | tp1013 | Chr12  | 727701  | 733500  | 5800   | FALSE | CNVnator | 0.296146000 | 0.19127400 |
| # 1865 | IT     | Chr12  | 728201  | 733500  | 5300   | FALSE | CNVnator | 0.276183000 | 0.27084500 |
| # 1866 | IT     | Chr12  | 744801  | 746700  | 1900   | FALSE | CNVnator | 0.435357000 | 0.13375400 |
| # 1867 | IT     | Chr12  | 870501  | 871400  | 900    | FALSE | CNVnator | 0.512929000 | 0.03467060 |
| # 628  | tp1013 | Chr12  | 1088601 | 1093900 | 5300   | FALSE | CNVnator | 0.708079000 | 0.06060300 |
| # 630  | tp1013 | Chr12  | 1118501 | 1124700 | 6200   | FALSE | CNVnator | 0.576839000 | 0.97147600 |
| # 1872 | IT     | Chr13  | 12101   | 17800   | 5700   | FALSE | CNVnator | 0.567094000 | 0.86300400 |
| # 1876 | IT     | Chr13  | 101901  | 103500  | 1600   | FALSE | CNVnator | 0.510143000 | 0.07302490 |
| # 1881 | IT     | Chr13  | 550201  | 551600  | 1400   | FALSE | CNVnator | 0.422201000 | 0.03243700 |
| # 637  | tp1013 | Chr13  | 660701  | 810700  | 150000 | FALSE | CNVnator | 0.615854000 | 0.07222820 |
| # 638  | tp1013 | Chr13  | 811801  | 991800  | 180000 | FALSE | CNVnator | 0.640233000 | 0.05413770 |
| # 1884 | IT     | Chr13  | 952101  | 956400  | 4300   | FALSE | CNVnator | 0.178057000 | 0.08043340 |
| # 639  | tp1013 | Chr13  | 1007701 | 1009000 | 1300   | FALSE | CNVnator | 0.416506000 | 0.53364000 |
| # 1218 | tp1007 | Chr14  | 640401  | 918000  | 277600 | FALSE | CNVnator | 0.608837000 | 0.04647710 |
| # 312  | tp1012 | Chr14  | 640601  | 773600  | 133000 | FALSE | CNVnator | 0.607432000 | 0.04016810 |
| # 313  | tp1012 | Chr14  | 777001  | 918000  | 141000 | FALSE | CNVnator | 0.595579000 | 0.04477800 |
| # 1892 | IT     | Chr14  | 900701  | 902400  | 1700   | FALSE | CNVnator | 0.590286000 | 0.66378400 |
| # 1219 | tp1007 | Chr14  | 920901  | 954800  | 33900  | FALSE | CNVnator | 0.581991000 | 0.08302350 |
| # 314  | tp1012 | Chr14  | 920901  | 954800  | 33900  | FALSE | CNVnator | 0.600277000 | 0.07165340 |
| # 1220 | tp1007 | Chr14  | 959901  | 994100  | 34200  | FALSE | CNVnator | 0.679309000 | 0.17957700 |
| # 1542 | tp1015 | Chr14  | 988101  | 994100  | 6000   | FALSE | CNVnator | 0.700485000 | 0.35190100 |
| # 2241 | tp1335 | Chr14  | 988101  | 994100  | 6000   | FALSE | CNVnator | 0.680615000 | 0.41375300 |
| # 1893 | IT     | Chr14  | 988701  | 993400  | 4700   | FALSE | CNVnator | 0.543516000 | 0.46760200 |
| # 1895 | IT     | Chr15  | 15101   | 17200   | 2100   | FALSE | CNVnator | 0.266991000 | 0.13812900 |
| # 1896 | IT     | Chr15  | 21201   | 21900   | 700    | FALSE | CNVnator | 0.231256000 | 0.77757700 |
| # 1898 | IT     | Chr15  | 63601   | 67500   | 3900   | FALSE | CNVnator | 0.581098000 | 0.72620900 |
| # 925  | tp1014 | Chr15  | 244201  | 246700  | 2500   | FALSE | CNVnator | 0.628294000 | 0.46420800 |
| # 1546 | tp1015 | Chr15  | 244601  | 246600  | 2000   | FALSE | CNVnator | 0.625186000 | 0.33766500 |
| # 1902 | IT     | Chr15  | 244601  | 246800  | 2200   | FALSE | CNVnator | 0.410410000 | 0.51271900 |
| # 645  | tp1013 | Chr15  | 244901  | 246700  | 1800   | FALSE | CNVnator | 0.433951000 | 0.59406100 |
| # 1225 | tp1007 | Chr15  | 245401  | 246600  | 1200   | FALSE | CNVnator | 0.598064000 | 0.56563900 |
| # 926  | tp1014 | Chr15  | 250801  | 262700  | 11900  | FALSE | CNVnator | 0.015139900 | 0.02658230 |
| # 1903 | IT     | Chr15  | 250901  | 262700  | 11800  | FALSE | CNVnator | 0.011022600 | 0.00471698 |
| # 1226 | tp1007 | Chr15  | 250901  | 262700  | 11800  | FALSE | CNVnator | 0.007738550 | 0.00920245 |
| # 646  | tp1013 | Chr15  | 250901  | 262700  | 11800  | FALSE | CNVnator | 0.006898370 | 0.01724140 |
| # 1547 | tp1015 | Chr15  | 250901  | 262700  | 11800  | FALSE | CNVnator | 0.008342290 | 0.00707965 |
| # 2245 | tp1335 | Chr15  | 250901  | 262700  | 11800  | FALSE | CNVnator | 0.008875390 | 0.00931677 |
| # 320  | tp1012 | Chr15  | 251001  | 262700  | 11700  | FALSE | CNVnator | 0.002593220 | 0.01626020 |
| # 1905 | IT     | Chr15  | 434901  | 437100  | 2200   | FALSE | CNVnator | 0.559315000 | 0.50345100 |
| # 2248 | tp1335 | Chr15  | 440601  | 442300  | 1700   | FALSE | CNVnator | 0.654304000 | 0.34205300 |
| # 649  | tp1013 | Chr15  | 451101  | 480900  | 29800  | FALSE | CNVnator | 0.626101000 | 0.03044200 |
| # 1908 | IT     | Chr15  | 569601  | 571600  | 2000   | FALSE | CNVnator | 0.598326000 | 0.09875460 |
| # 1909 | IT     | Chr15  | 619601  | 622600  | 3000   | FALSE | CNVnator | 0.675473000 | 0.05231230 |
| # 650  | tp1013 | Chr15  | 620601  | 622400  | 1800   | FALSE | CNVnator | 0.579476000 | 0.07424140 |
| # 1230 | tp1007 | Chr16a | 1       | 26700   | 26700  | FALSE | CNVnator | 0.659122000 | 0.08465140 |
| # 331  | tp1012 | Chr16a | 1       | 26700   | 26700  | FALSE | CNVnator | 0.637869000 | 0.08574790 |
| # 1550 | tp1015 | Chr16a | 101     | 1200    | 1100   | FALSE | CNVnator | 0.317346000 | 0.12708000 |
| # 334  | tp1012 | Chr16a | 47901   | 193300  | 145400 | FALSE | CNVnator | 0.671398000 | 0.03840930 |
| # 1232 | tp1007 | Chr16a | 65201   | 193000  | 127800 | FALSE | CNVnator | 0.619381000 | 0.04438160 |
| # 2254 | tp1335 | Chr16a | 248801  | 260000  | 11200  | FALSE | CNVnator | 0.735075000 | 0.40391200 |
| # 1553 | tp1015 | Chr16a | 248801  | 263100  | 14300  | FALSE | CNVnator | 0.728005000 | 0.23195700 |
| # 656  | tp1013 | Chr16a | 425401  | 432800  | 7400   | FALSE | CNVnator | 0.228692000 | 0.13027400 |
| # 1916 | IT     | Chr16a | 425801  | 433200  | 7400   | FALSE | CNVnator | 0.189131000 | 0.11917300 |
| # 657  | tp1013 | Chr16a | 443601  | 448500  | 4900   | FALSE | CNVnator | 0.481625000 | 0.08463430 |
| # 1917 | IT     | Chr16a | 446101  | 450500  | 4400   | FALSE | CNVnator | 0.638432000 | 0.07684990 |
| # 1918 | IT     | Chr16b | 96701   | 97400   | 700    | FALSE | CNVnator | 0.410839000 | 0.02878290 |
| # 1920 | IT     | Chr16b | 134701  | 147000  | 12300  | FALSE | CNVnator | 0.605966000 | 0.42431700 |
| # 346  | tp1012 | Chr16b | 138501  | 146600  | 8100   | FALSE | CNVnator | 0.673159000 | 0.55057300 |
| # 1556 | tp1015 | Chr16b | 138501  | 146600  | 8100   | FALSE | CNVnator | 0.665662000 | 0.52682700 |

|        |        |           |         |         |        |       |          |             |            |
|--------|--------|-----------|---------|---------|--------|-------|----------|-------------|------------|
| # 1923 | IT     | Chr17     | 45101   | 47000   | 1900   | FALSE | CNVnator | 0.535006000 | 0.36416700 |
| # 660  | tp1013 | Chr17     | 496401  | 499300  | 2900   | FALSE | CNVnator | 0.365310000 | 0.29959100 |
| # 1925 | IT     | Chr17     | 496401  | 499500  | 3100   | FALSE | CNVnator | 0.368494000 | 0.26301700 |
| # 663  | tp1013 | Chr18     | 1       | 500     | 500    | FALSE | CNVnator | 0.147840000 | 0.98798800 |
| # 1932 | IT     | Chr18     | 214201  | 215600  | 1400   | FALSE | CNVnator | 0.375745000 | 0.67514100 |
| # 1933 | IT     | Chr18     | 266201  | 267800  | 1600   | FALSE | CNVnator | 0.292130000 | 0.75044000 |
| # 667  | tp1013 | Chr18     | 306001  | 308800  | 2800   | FALSE | CNVnator | 0.187496000 | 0.07872880 |
| # 1935 | IT     | Chr18     | 532901  | 533800  | 900    | FALSE | CNVnator | 0.417276000 | 0.04513670 |
| # 1249 | tp1007 | Chr19a_19 | 1       | 2200    | 2200   | FALSE | CNVnator | 0.428953000 | 0.87500000 |
| # 1568 | tp1015 | Chr19a_19 | 1       | 13600   | 13600  | FALSE | CNVnator | 0.570280000 | 0.95649500 |
| # 672  | tp1013 | Chr19a_19 | 1       | 15700   | 15700  | FALSE | CNVnator | 0.613539000 | 0.95281800 |
| # 1938 | IT     | Chr19a_19 | 1       | 17700   | 17700  | FALSE | CNVnator | 0.507769000 | 0.94537700 |
| # 1251 | tp1007 | Chr19a_19 | 51401   | 168300  | 116900 | FALSE | CNVnator | 0.609581000 | 0.12852200 |
| # 369  | tp1012 | Chr19a_19 | 52301   | 171800  | 119500 | FALSE | CNVnator | 0.624911000 | 0.11855100 |
| # 950  | tp1014 | Chr19a_19 | 57501   | 277600  | 220100 | FALSE | CNVnator | 0.704901000 | 0.11884800 |
| # 2267 | tp1335 | Chr19a_19 | 62201   | 277800  | 215600 | FALSE | CNVnator | 0.587722000 | 0.07445520 |
| # 1570 | tp1015 | Chr19a_19 | 64101   | 277600  | 213500 | FALSE | CNVnator | 0.618078000 | 0.05370360 |
| # 1253 | tp1007 | Chr19a_19 | 276401  | 277600  | 1200   | FALSE | CNVnator | 0.190192000 | 0.03952900 |
| # 372  | tp1012 | Chr19a_19 | 276401  | 277600  | 1200   | FALSE | CNVnator | 0.144819000 | 0.04835320 |
| # 374  | tp1012 | Chr19a_19 | 281001  | 303300  | 22300  | FALSE | CNVnator | 0.550593000 | 0.03705670 |
| # 1255 | tp1007 | Chr19a_19 | 281101  | 303500  | 22400  | FALSE | CNVnator | 0.556496000 | 0.04356760 |
| # 2269 | tp1335 | Chr19a_19 | 281201  | 419000  | 137800 | FALSE | CNVnator | 0.550752000 | 0.02982230 |
| # 952  | tp1014 | Chr19a_19 | 281201  | 447600  | 166400 | FALSE | CNVnator | 0.704256000 | 0.06875420 |
| # 1572 | tp1015 | Chr19a_19 | 301401  | 303500  | 2100   | FALSE | CNVnator | 0.637889000 | 0.03539060 |
| # 1256 | tp1007 | Chr19a_19 | 309301  | 419200  | 109900 | FALSE | CNVnator | 0.604391000 | 0.03809330 |
| # 375  | tp1012 | Chr19a_19 | 309301  | 447600  | 138300 | FALSE | CNVnator | 0.603847000 | 0.03567760 |
| # 1941 | IT     | Chr19a_19 | 355001  | 356000  | 1000   | FALSE | CNVnator | 0.135931000 | 0.04867260 |
| # 1257 | tp1007 | Chr19a_19 | 420701  | 447500  | 26800  | FALSE | CNVnator | 0.601743000 | 0.03493850 |
| # 2270 | tp1335 | Chr19a_19 | 421001  | 447600  | 26600  | FALSE | CNVnator | 0.567876000 | 0.02296370 |
| # 1258 | tp1007 | Chr19a_19 | 451501  | 474600  | 23100  | FALSE | CNVnator | 0.658834000 | 0.05328300 |
| # 376  | tp1012 | Chr19a_19 | 451501  | 474600  | 23100  | FALSE | CNVnator | 0.689868000 | 0.04240480 |
| # 2272 | tp1335 | Chr19a_19 | 451501  | 474600  | 23100  | FALSE | CNVnator | 0.611366000 | 0.05751660 |
| # 954  | tp1014 | Chr19a_19 | 451601  | 474600  | 23000  | FALSE | CNVnator | 0.717257000 | 0.07109100 |
| # 1944 | IT     | Chr19a_19 | 477201  | 478900  | 1700   | FALSE | CNVnator | 0.491307000 | 0.58500400 |
| # 1260 | tp1007 | Chr19a_19 | 477201  | 548600  | 71400  | FALSE | CNVnator | 0.647829000 | 0.08028780 |
| # 378  | tp1012 | Chr19a_19 | 477201  | 548600  | 71400  | FALSE | CNVnator | 0.651697000 | 0.06597580 |
| # 956  | tp1014 | Chr19a_19 | 477201  | 548600  | 71400  | FALSE | CNVnator | 0.741519000 | 0.10175400 |
| # 676  | tp1013 | Chr19a_19 | 477301  | 478900  | 1600   | FALSE | CNVnator | 0.345092000 | 0.73324400 |
| # 2274 | tp1335 | Chr19a_19 | 479301  | 549200  | 69900  | FALSE | CNVnator | 0.610449000 | 0.05697390 |
| # 2276 | tp1335 | Chr19a_19 | 553501  | 585900  | 32400  | FALSE | CNVnator | 0.613418000 | 0.03374400 |
| # 1261 | tp1007 | Chr19a_19 | 554701  | 585900  | 31200  | FALSE | CNVnator | 0.672632000 | 0.03063070 |
| # 379  | tp1012 | Chr19a_19 | 554701  | 585900  | 31200  | FALSE | CNVnator | 0.707511000 | 0.02431850 |
| # 383  | tp1012 | Chr19b_31 | 96401   | 151700  | 55300  | FALSE | CNVnator | 0.598133000 | 0.02931950 |
| # 1263 | tp1007 | Chr19b_31 | 96601   | 151700  | 55100  | FALSE | CNVnator | 0.605423000 | 0.03456630 |
| # 1266 | tp1007 | Chr19c_29 | 17701   | 18600   | 900    | FALSE | CNVnator | 0.197089000 | 0.42897300 |
| # 1955 | IT     | Chr19c_29 | 74801   | 75400   | 600    | FALSE | CNVnator | 0.177943000 | 0.05803570 |
| # 1267 | tp1007 | Chr19c_29 | 74801   | 75400   | 600    | FALSE | CNVnator | 0.122288000 | 0.01912050 |
| # 387  | tp1012 | Chr19c_29 | 74801   | 75400   | 600    | FALSE | CNVnator | 0.118095000 | 0.02979740 |
| # 1268 | tp1007 | Chr19c_29 | 117701  | 203100  | 85400  | FALSE | CNVnator | 0.612598000 | 0.05561360 |
| # 388  | tp1012 | Chr19c_29 | 117701  | 215200  | 97500  | FALSE | CNVnator | 0.640018000 | 0.04365630 |
| # 961  | tp1014 | Chr19c_29 | 212101  | 216500  | 4400   | FALSE | CNVnator | 0.713864000 | 0.10809300 |
| # 520  | tp1013 | Chr2      | 1       | 400     | 400    | FALSE | CNVnator | 0.124843000 | 1.00000000 |
| # 1695 | IT     | Chr2      | 13901   | 15800   | 1900   | FALSE | CNVnator | 0.291698000 | 0.99228000 |
| # 1697 | IT     | Chr2      | 268801  | 279000  | 10200  | FALSE | CNVnator | 0.746898000 | 0.02374270 |
| # 1698 | IT     | Chr2      | 289201  | 293700  | 4500   | FALSE | CNVnator | 0.651090000 | 0.02153150 |
| # 1699 | IT     | Chr2      | 425901  | 434000  | 8100   | FALSE | CNVnator | 0.551524000 | 0.67650600 |
| # 522  | tp1013 | Chr2      | 426101  | 434100  | 8000   | FALSE | CNVnator | 0.561741000 | 0.71823900 |
| # 1064 | tp1007 | Chr2      | 468301  | 475600  | 7300   | FALSE | CNVnator | 0.715221000 | 0.23493800 |
| # 523  | tp1013 | Chr2      | 472801  | 475000  | 2200   | FALSE | CNVnator | 0.351087000 | 0.54451500 |
| # 1700 | IT     | Chr2      | 472801  | 475700  | 2900   | FALSE | CNVnator | 0.429586000 | 0.33506400 |
| # 790  | tp1014 | Chr2      | 667701  | 675200  | 7500   | FALSE | CNVnator | 0.720331000 | 0.89382300 |
| # 1065 | tp1007 | Chr2      | 667901  | 676500  | 8600   | FALSE | CNVnator | 0.713789000 | 0.61413300 |
| # 41   | tp1012 | Chr2      | 667901  | 676500  | 8600   | FALSE | CNVnator | 0.665539000 | 0.57918400 |
| # 1384 | tp1015 | Chr2      | 668501  | 676500  | 8000   | FALSE | CNVnator | 0.699609000 | 0.57970800 |
| # 1702 | IT     | Chr2      | 1082201 | 1084000 | 1800   | FALSE | CNVnator | 0.371998000 | 0.22044000 |
| # 524  | tp1013 | Chr2      | 1082201 | 1084000 | 1800   | FALSE | CNVnator | 0.398112000 | 0.16147500 |
| # 525  | tp1013 | Chr2      | 1462801 | 1465100 | 2300   | FALSE | CNVnator | 0.642293000 | 0.09843810 |

|        |        |       |         |         |        |       |          |             |            |
|--------|--------|-------|---------|---------|--------|-------|----------|-------------|------------|
| # 47   | tp1012 | Chr2  | 1615301 | 1621100 | 5800   | FALSE | CNVnator | 0.721374000 | 0.02537740 |
| # 50   | tp1012 | Chr2  | 1913801 | 1915800 | 2000   | FALSE | CNVnator | 0.526460000 | 0.60143300 |
| # 794  | tp1014 | Chr2  | 1913801 | 1915800 | 2000   | FALSE | CNVnator | 0.662122000 | 0.83930700 |
| # 1705 | IT     | Chr2  | 1913801 | 1915900 | 2100   | FALSE | CNVnator | 0.426123000 | 0.91774700 |
| # 527  | tp1013 | Chr2  | 1914101 | 1915300 | 1200   | FALSE | CNVnator | 0.343204000 | 0.88336400 |
| # 55   | tp1012 | Chr2  | 2139101 | 2143000 | 3900   | FALSE | CNVnator | 0.648747000 | 0.01630730 |
| # 797  | tp1014 | Chr2  | 2197001 | 2226700 | 29700  | FALSE | CNVnator | 0.660203000 | 0.04570830 |
| # 1071 | tp1007 | Chr2  | 2217301 | 2282900 | 65600  | FALSE | CNVnator | 0.590884000 | 0.02451360 |
| # 56   | tp1012 | Chr2  | 2217301 | 2282900 | 65600  | FALSE | CNVnator | 0.575951000 | 0.02003310 |
| # 1072 | tp1007 | Chr2  | 2293101 | 2330600 | 37500  | FALSE | CNVnator | 0.688328000 | 0.18568100 |
| # 58   | tp1012 | Chr2  | 2293101 | 2330600 | 37500  | FALSE | CNVnator | 0.661598000 | 0.17553100 |
| # 59   | tp1012 | Chr2  | 2347701 | 2444600 | 96900  | FALSE | CNVnator | 0.576283000 | 0.04497560 |
| # 1074 | tp1007 | Chr2  | 2348101 | 2446700 | 98600  | FALSE | CNVnator | 0.603629000 | 0.06496710 |
| # 2114 | tp1335 | Chr2  | 2399101 | 2444700 | 45600  | FALSE | CNVnator | 0.551821000 | 0.03854290 |
| # 1711 | IT     | Chr2  | 2447801 | 2448600 | 800    | FALSE | CNVnator | 0.422251000 | 0.83713000 |
| # 1075 | tp1007 | Chr2  | 2448101 | 2576700 | 128600 | FALSE | CNVnator | 0.616484000 | 0.03685140 |
| # 60   | tp1012 | Chr2  | 2448101 | 2576700 | 128600 | FALSE | CNVnator | 0.616946000 | 0.03196430 |
| # 2115 | tp1335 | Chr2  | 2448101 | 2576700 | 128600 | FALSE | CNVnator | 0.565107000 | 0.02947710 |
| # 1394 | tp1015 | Chr2  | 2555701 | 2576700 | 21000  | FALSE | CNVnator | 0.648062000 | 0.01758280 |
| # 1077 | tp1007 | Chr2  | 2582001 | 2635300 | 53300  | FALSE | CNVnator | 0.628802000 | 0.06580890 |
| # 62   | tp1012 | Chr2  | 2582001 | 2635300 | 53300  | FALSE | CNVnator | 0.636809000 | 0.05970500 |
| # 802  | tp1014 | Chr2  | 2582101 | 2635300 | 53200  | FALSE | CNVnator | 0.711183000 | 0.09182670 |
| # 1396 | tp1015 | Chr2  | 2582101 | 2635300 | 53200  | FALSE | CNVnator | 0.605916000 | 0.05057020 |
| # 2117 | tp1335 | Chr2  | 2582101 | 2635300 | 53200  | FALSE | CNVnator | 0.598177000 | 0.07068140 |
| # 1713 | IT     | Chr2  | 2594101 | 2597700 | 3600   | FALSE | CNVnator | 0.738147000 | 0.02106920 |
| # 1398 | tp1015 | Chr2  | 2638001 | 2665200 | 27200  | FALSE | CNVnator | 0.659745000 | 0.04780680 |
| # 64   | tp1012 | Chr2  | 2638101 | 2648900 | 10800  | FALSE | CNVnator | 0.722242000 | 0.02690250 |
| # 2119 | tp1335 | Chr2  | 2638101 | 2648900 | 10800  | FALSE | CNVnator | 0.603761000 | 0.02904900 |
| # 1079 | tp1007 | Chr2  | 2638101 | 2665200 | 27100  | FALSE | CNVnator | 0.702276000 | 0.05371110 |
| # 2120 | tp1335 | Chr2  | 2650901 | 2665200 | 14300  | FALSE | CNVnator | 0.624645000 | 0.07986680 |
| # 65   | tp1012 | Chr2  | 2651201 | 2665200 | 14000  | FALSE | CNVnator | 0.682161000 | 0.07609120 |
| # 805  | tp1014 | Chr2  | 2676901 | 2699600 | 22700  | FALSE | CNVnator | 0.748183000 | 0.24103400 |
| # 1081 | tp1007 | Chr2  | 2676901 | 2699800 | 22900  | FALSE | CNVnator | 0.717249000 | 0.21807500 |
| # 1400 | tp1015 | Chr2  | 2677001 | 2699300 | 22300  | FALSE | CNVnator | 0.666957000 | 0.18817200 |
| # 2122 | tp1335 | Chr2  | 2677001 | 2699800 | 22800  | FALSE | CNVnator | 0.654383000 | 0.19288800 |
| # 533  | tp1013 | Chr2  | 2706701 | 2707200 | 500    | FALSE | CNVnator | 0.165937000 | 0.72642800 |
| # 1580 | tp1015 | Chr20 | 1       | 1500    | 1500   | FALSE | CNVnator | 0.305420000 | 0.20285500 |
| # 1960 | IT     | Chr20 | 20501   | 23400   | 2900   | FALSE | CNVnator | 0.603338000 | 0.92766400 |
| # 683  | tp1013 | Chr20 | 23601   | 28600   | 5000   | FALSE | CNVnator | 0.628852000 | 0.94066200 |
| # 1961 | IT     | Chr20 | 24301   | 25500   | 1200   | FALSE | CNVnator | 0.407886000 | 0.99481900 |
| # 684  | tp1013 | Chr20 | 34401   | 35300   | 900    | FALSE | CNVnator | 0.158660000 | 0.05762080 |
| # 391  | tp1012 | Chr20 | 127101  | 130200  | 3100   | FALSE | CNVnator | 0.702686000 | 0.01306440 |
| # 685  | tp1013 | Chr20 | 128401  | 130400  | 2000   | FALSE | CNVnator | 0.481347000 | 0.02918420 |
| # 1962 | IT     | Chr20 | 128401  | 130600  | 2200   | FALSE | CNVnator | 0.430239000 | 0.03550640 |
| # 1966 | IT     | Chr20 | 405801  | 407600  | 1800   | FALSE | CNVnator | 0.377246000 | 0.66788500 |
| # 1970 | IT     | Chr20 | 469501  | 474100  | 4600   | FALSE | CNVnator | 0.747276000 | 0.02485460 |
| # 1971 | IT     | Chr20 | 486101  | 488500  | 2400   | FALSE | CNVnator | 0.478693000 | 0.68401300 |
| # 1277 | tp1007 | Chr20 | 486201  | 553200  | 67000  | FALSE | CNVnator | 0.568891000 | 0.16341100 |
| # 690  | tp1013 | Chr20 | 492401  | 500100  | 7700   | FALSE | CNVnator | 0.390255000 | 0.87323800 |
| # 1972 | IT     | Chr20 | 492501  | 500000  | 7500   | FALSE | CNVnator | 0.047177400 | 0.77975000 |
| # 691  | tp1013 | Chr20 | 532801  | 620200  | 87400  | FALSE | CNVnator | 0.653812000 | 0.07429660 |
| # 400  | tp1012 | Chr20 | 533301  | 553300  | 20000  | FALSE | CNVnator | 0.552848000 | 0.01987580 |
| # 2288 | tp1335 | Chr20 | 564401  | 591200  | 26800  | FALSE | CNVnator | 0.584050000 | 0.01598710 |
| # 1585 | tp1015 | Chr20 | 583101  | 591200  | 8100   | FALSE | CNVnator | 0.584864000 | 0.01883400 |
| # 1973 | IT     | Chr20 | 592001  | 594300  | 2300   | FALSE | CNVnator | 0.597471000 | 0.92497400 |
| # 1586 | tp1015 | Chr20 | 593901  | 722400  | 128500 | FALSE | CNVnator | 0.532435000 | 0.08194460 |
| # 2289 | tp1335 | Chr20 | 594201  | 620300  | 26100  | FALSE | CNVnator | 0.598959000 | 0.02773180 |
| # 1278 | tp1007 | Chr20 | 621601  | 635200  | 13600  | FALSE | CNVnator | 0.000778748 | 0.90507700 |
| # 401  | tp1012 | Chr20 | 621601  | 635200  | 13600  | FALSE | CNVnator | 0.001017640 | 0.92618100 |
| # 966  | tp1014 | Chr20 | 621601  | 635200  | 13600  | FALSE | CNVnator | 0.001089970 | 0.96774200 |
| # 1974 | IT     | Chr20 | 621601  | 635300  | 13700  | FALSE | CNVnator | 0.003916590 | 0.92067300 |
| # 2290 | tp1335 | Chr20 | 621601  | 728000  | 106400 | FALSE | CNVnator | 0.522981000 | 0.12207600 |
| # 692  | tp1013 | Chr20 | 621601  | 762600  | 141000 | FALSE | CNVnator | 0.584357000 | 0.08828350 |
| # 1975 | IT     | Chr20 | 651101  | 653100  | 2000   | FALSE | CNVnator | 0.543484000 | 0.99526600 |
| # 1976 | IT     | Chr20 | 720301  | 722400  | 2100   | FALSE | CNVnator | 0.495901000 | 0.82358700 |
| # 1279 | tp1007 | Chr20 | 720501  | 722500  | 2000   | FALSE | CNVnator | 0.608568000 | 0.60139900 |
| # 403  | tp1012 | Chr20 | 720501  | 723200  | 2700   | FALSE | CNVnator | 0.682179000 | 0.65858600 |

|        |        |       |         |         |        |       |          |             |            |
|--------|--------|-------|---------|---------|--------|-------|----------|-------------|------------|
| # 2291 | tp1335 | Chr20 | 729801  | 743100  | 13300  | FALSE | CNVnator | 0.585015000 | 0.02043980 |
| # 1587 | tp1015 | Chr20 | 729801  | 762500  | 32700  | FALSE | CNVnator | 0.550001000 | 0.03095000 |
| # 2292 | tp1335 | Chr20 | 744601  | 766000  | 21400  | FALSE | CNVnator | 0.668735000 | 0.03355920 |
| # 1281 | tp1007 | Chr20 | 748601  | 762500  | 13900  | FALSE | CNVnator | 0.558705000 | 0.03440030 |
| # 405  | tp1012 | Chr20 | 748601  | 762600  | 14000  | FALSE | CNVnator | 0.552471000 | 0.02980800 |
| # 1979 | IT     | Chr20 | 759501  | 762500  | 3000   | FALSE | CNVnator | 0.199287000 | 0.14906600 |
| # 1981 | IT     | Chr20 | 769801  | 770700  | 900    | FALSE | CNVnator | 0.411868000 | 0.63964000 |
| # 1589 | tp1015 | Chr20 | 776901  | 794800  | 17900  | FALSE | CNVnator | 0.719116000 | 0.07834050 |
| # 1984 | IT     | Chr22 | 87301   | 89500   | 2200   | FALSE | CNVnator | 0.258202000 | 0.20347100 |
| # 695  | tp1013 | Chr22 | 87301   | 96700   | 9400   | FALSE | CNVnator | 0.398384000 | 0.50485500 |
| # 1985 | IT     | Chr22 | 90101   | 90800   | 700    | FALSE | CNVnator | 0.409293000 | 0.68760800 |
| # 1986 | IT     | Chr22 | 93801   | 96700   | 2900   | FALSE | CNVnator | 0.255802000 | 0.41169000 |
| # 1992 | IT     | Chr22 | 231901  | 232400  | 500    | FALSE | CNVnator | 0.205742000 | 0.63655500 |
| # 700  | tp1013 | Chr22 | 248901  | 250500  | 1600   | FALSE | CNVnator | 0.420313000 | 0.19891700 |
| # 1994 | IT     | Chr22 | 249001  | 250400  | 1400   | FALSE | CNVnator | 0.384721000 | 0.37625100 |
| # 701  | tp1013 | Chr22 | 253101  | 267600  | 14500  | FALSE | CNVnator | 0.493564000 | 0.49461200 |
| # 1995 | IT     | Chr22 | 253101  | 270600  | 17500  | FALSE | CNVnator | 0.548667000 | 0.52338100 |
| # 704  | tp1013 | Chr22 | 662501  | 681400  | 18900  | FALSE | CNVnator | 0.690393000 | 0.83231500 |
| # 977  | tp1014 | Chr22 | 667401  | 672900  | 5500   | FALSE | CNVnator | 0.734189000 | 0.71108100 |
| # 419  | tp1012 | Chr22 | 667601  | 672800  | 5200   | FALSE | CNVnator | 0.744870000 | 0.67710200 |
| # 2002 | IT     | Chr22 | 748701  | 749500  | 800    | FALSE | CNVnator | 0.334189000 | 0.13508600 |
| # 1297 | tp1007 | Chr22 | 958701  | 959400  | 700    | FALSE | CNVnator | 0.183420000 | 0.04906540 |
| # 1301 | tp1007 | Chr23 | 1       | 8900    | 8900   | FALSE | CNVnator | 0.747616000 | 0.27762800 |
| # 426  | tp1012 | Chr23 | 1       | 9100    | 9100   | FALSE | CNVnator | 0.738877000 | 0.25208700 |
| # 2310 | tp1335 | Chr23 | 1       | 96000   | 96000  | FALSE | CNVnator | 0.572798000 | 0.04622430 |
| # 982  | tp1014 | Chr23 | 1       | 190200  | 190200 | FALSE | CNVnator | 0.693628000 | 0.06578740 |
| # 2007 | IT     | Chr23 | 305401  | 307700  | 2300   | FALSE | CNVnator | 0.736511000 | 0.02187600 |
| # 2008 | IT     | Chr23 | 341701  | 342300  | 600    | FALSE | CNVnator | 0.196845000 | 0.12607400 |
| # 711  | tp1013 | Chr23 | 444401  | 447900  | 3500   | FALSE | CNVnator | 0.529023000 | 0.40673400 |
| # 2012 | IT     | Chr24 | 10901   | 15100   | 4200   | FALSE | CNVnator | 0.427274000 | 0.57034200 |
| # 439  | tp1012 | Chr24 | 77901   | 79400   | 1500   | FALSE | CNVnator | 0.578579000 | 0.02585100 |
| # 2316 | tp1335 | Chr24 | 77901   | 79400   | 1500   | FALSE | CNVnator | 0.568258000 | 0.01343520 |
| # 2015 | IT     | Chr24 | 149801  | 150700  | 900    | FALSE | CNVnator | 0.168316000 | 0.04994800 |
| # 2016 | IT     | Chr24 | 173701  | 177800  | 4100   | FALSE | CNVnator | 0.508927000 | 0.21131000 |
| # 715  | tp1013 | Chr24 | 175501  | 177800  | 2300   | FALSE | CNVnator | 0.391339000 | 0.33712400 |
| # 717  | tp1013 | Chr24 | 281601  | 297400  | 15800  | FALSE | CNVnator | 0.695184000 | 0.82764800 |
| # 2018 | IT     | Chr24 | 281801  | 297400  | 15600  | FALSE | CNVnator | 0.582125000 | 0.87198800 |
| # 2125 | tp1335 | Chr3  | 6401    | 10900   | 4500   | FALSE | CNVnator | 0.722187000 | 0.11390400 |
| # 1718 | IT     | Chr3  | 10001   | 10900   | 900    | FALSE | CNVnator | 0.407626000 | 0.03470720 |
| # 536  | tp1013 | Chr3  | 10101   | 10800   | 700    | FALSE | CNVnator | 0.152805000 | 0.05070750 |
| # 2129 | tp1335 | Chr3  | 98801   | 99300   | 500    | FALSE | CNVnator | 0.108673000 | 0.01360540 |
| # 1720 | IT     | Chr3  | 100801  | 102300  | 1500   | FALSE | CNVnator | 0.400042000 | 0.79261700 |
| # 2132 | tp1335 | Chr3  | 425501  | 430000  | 4500   | FALSE | CNVnator | 0.745122000 | 0.01049240 |
| # 1408 | tp1015 | Chr3  | 426501  | 428200  | 1700   | FALSE | CNVnator | 0.571680000 | 0.01441340 |
| # 1090 | tp1007 | Chr3  | 426601  | 430000  | 3400   | FALSE | CNVnator | 0.665371000 | 0.01664660 |
| # 1724 | IT     | Chr3  | 902401  | 908200  | 5800   | FALSE | CNVnator | 0.691287000 | 0.13959200 |
| # 2134 | tp1335 | Chr3  | 1272601 | 1273400 | 800    | FALSE | CNVnator | 0.475389000 | 0.01285520 |
| # 540  | tp1013 | Chr3  | 1350301 | 1353700 | 3400   | FALSE | CNVnator | 0.642680000 | 0.28984300 |
| # 1727 | IT     | Chr3  | 1523201 | 1525200 | 2000   | FALSE | CNVnator | 0.212223000 | 0.06576630 |
| # 541  | tp1013 | Chr3  | 1667501 | 1670300 | 2800   | FALSE | CNVnator | 0.453185000 | 0.39464200 |
| # 1728 | IT     | Chr3  | 1669301 | 1670000 | 700    | FALSE | CNVnator | 0.189626000 | 0.26270000 |
| # 93   | tp1012 | Chr3  | 2220701 | 2225500 | 4800   | FALSE | CNVnator | 0.731834000 | 0.01553320 |
| # 1732 | IT     | Chr3  | 2373401 | 2383300 | 9900   | FALSE | CNVnator | 0.499923000 | 0.84057600 |
| # 543  | tp1013 | Chr3  | 2373401 | 2383600 | 10200  | FALSE | CNVnator | 0.544605000 | 0.80852300 |
| # 814  | tp1014 | Chr3  | 2373401 | 2383800 | 10400  | FALSE | CNVnator | 0.683433000 | 0.88617100 |
| # 96   | tp1012 | Chr3  | 2437801 | 2440100 | 2300   | FALSE | CNVnator | 0.556195000 | 0.81154000 |
| # 97   | tp1012 | Chr4  | 20501   | 88400   | 67900  | FALSE | CNVnator | 0.715057000 | 0.11733700 |
| # 1735 | IT     | Chr4  | 66701   | 67600   | 900    | FALSE | CNVnator | 0.386482000 | 0.57796400 |
| # 1737 | IT     | Chr4  | 408301  | 410500  | 2200   | FALSE | CNVnator | 0.663345000 | 0.08737860 |
| # 1738 | IT     | Chr4  | 477801  | 478600  | 800    | FALSE | CNVnator | 0.203286000 | 0.06728230 |
| # 1422 | tp1015 | Chr4  | 1566901 | 1572600 | 5700   | FALSE | CNVnator | 0.596592000 | 0.01885360 |
| # 1748 | IT     | Chr4  | 2109601 | 2110100 | 500    | FALSE | CNVnator | 0.216820000 | 0.06140350 |
| # 115  | tp1012 | Chr4  | 2170101 | 2175500 | 5400   | FALSE | CNVnator | 0.715822000 | 0.02893640 |
| # 549  | tp1013 | Chr4  | 2277001 | 2281900 | 4900   | FALSE | CNVnator | 0.687000000 | 0.99152600 |
| # 120  | tp1012 | Chr4  | 2399801 | 2402400 | 2600   | FALSE | CNVnator | 0.706984000 | 0.30433200 |
| # 122  | tp1012 | Chr5  | 138601  | 184600  | 46000  | FALSE | CNVnator | 0.606680000 | 0.02052890 |
| # 1107 | tp1007 | Chr5  | 346401  | 353000  | 6600   | FALSE | CNVnator | 0.603503000 | 0.02641470 |

|        |        |      |         |         |        |       |          |             |            |
|--------|--------|------|---------|---------|--------|-------|----------|-------------|------------|
| # 132  | tp1012 | Chr5 | 919701  | 926000  | 6300   | FALSE | CNVnator | 0.698900000 | 0.09626590 |
| # 1757 | IT     | Chr5 | 920501  | 924700  | 4200   | FALSE | CNVnator | 0.514922000 | 0.11638100 |
| # 1758 | IT     | Chr5 | 1323501 | 1330800 | 7300   | FALSE | CNVnator | 0.720049000 | 0.02023940 |
| # 1760 | IT     | Chr5 | 1967701 | 1971700 | 4000   | FALSE | CNVnator | 0.742413000 | 0.02076000 |
| # 2151 | tp1335 | Chr5 | 1976301 | 1977500 | 1200   | FALSE | CNVnator | 0.585662000 | 0.01479850 |
| # 1761 | IT     | Chr5 | 2049701 | 2053600 | 3900   | FALSE | CNVnator | 0.493041000 | 0.15337400 |
| # 1120 | tp1007 | Chr6 | 101     | 600     | 500    | FALSE | CNVnator | 0.227144000 | 0.72766000 |
| # 1437 | tp1015 | Chr6 | 101     | 600     | 500    | FALSE | CNVnator | 0.155082000 | 0.69519800 |
| # 151  | tp1012 | Chr6 | 3101    | 5600    | 2500   | FALSE | CNVnator | 0.632608000 | 0.85167000 |
| # 555  | tp1013 | Chr6 | 3201    | 5500    | 2300   | FALSE | CNVnator | 0.317654000 | 0.98897800 |
| # 1765 | IT     | Chr6 | 3301    | 5500    | 2200   | FALSE | CNVnator | 0.598299000 | 0.99423200 |
| # 2157 | tp1335 | Chr6 | 9601    | 165900  | 156300 | FALSE | CNVnator | 0.607829000 | 0.03904580 |
| # 831  | tp1014 | Chr6 | 28801   | 169100  | 140300 | FALSE | CNVnator | 0.708383000 | 0.08221160 |
| # 557  | tp1013 | Chr6 | 29001   | 168400  | 139400 | FALSE | CNVnator | 0.639700000 | 0.05357880 |
| # 1439 | tp1015 | Chr6 | 29901   | 165900  | 136000 | FALSE | CNVnator | 0.592855000 | 0.03557720 |
| # 1767 | IT     | Chr6 | 104901  | 105500  | 600    | FALSE | CNVnator | 0.185099000 | 0.05102040 |
| # 559  | tp1013 | Chr6 | 174401  | 181700  | 7300   | FALSE | CNVnator | 0.591648000 | 0.12956700 |
| # 153  | tp1012 | Chr6 | 174501  | 176600  | 2100   | FALSE | CNVnator | 0.588518000 | 0.35947000 |
| # 833  | tp1014 | Chr6 | 174501  | 268500  | 94000  | FALSE | CNVnator | 0.708520000 | 0.06678830 |
| # 1441 | tp1015 | Chr6 | 174501  | 268500  | 94000  | FALSE | CNVnator | 0.611032000 | 0.03649060 |
| # 2159 | tp1335 | Chr6 | 174501  | 268500  | 94000  | FALSE | CNVnator | 0.581503000 | 0.03645070 |
| # 1443 | tp1015 | Chr6 | 272601  | 346300  | 73700  | FALSE | CNVnator | 0.585876000 | 0.04559890 |
| # 2161 | tp1335 | Chr6 | 272601  | 346500  | 73900  | FALSE | CNVnator | 0.588544000 | 0.07020230 |
| # 835  | tp1014 | Chr6 | 272901  | 347000  | 74100  | FALSE | CNVnator | 0.685266000 | 0.08264270 |
| # 1771 | IT     | Chr6 | 660301  | 661300  | 1000   | FALSE | CNVnator | 0.388079000 | 0.54304200 |
| # 2164 | tp1335 | Chr6 | 771501  | 774700  | 3200   | FALSE | CNVnator | 0.692665000 | 0.40022400 |
| # 843  | tp1014 | Chr6 | 1011201 | 1018400 | 7200   | FALSE | CNVnator | 0.739117000 | 0.03886360 |
| # 565  | tp1013 | Chr6 | 1933901 | 2010600 | 76700  | FALSE | CNVnator | 0.645678000 | 0.04616130 |
| # 162  | tp1012 | Chr6 | 1939501 | 1942200 | 2700   | FALSE | CNVnator | 0.661940000 | 0.01608930 |
| # 1778 | IT     | Chr6 | 1940701 | 1942300 | 1600   | FALSE | CNVnator | 0.172942000 | 0.07818180 |
| # 1449 | tp1015 | Chr6 | 1997501 | 2010600 | 13100  | FALSE | CNVnator | 0.652542000 | 0.02202160 |
| # 566  | tp1013 | Chr6 | 2018601 | 2035100 | 16500  | FALSE | CNVnator | 0.714790000 | 0.08191350 |
| # 1781 | IT     | Chr6 | 2033201 | 2041700 | 8500   | FALSE | CNVnator | 0.663588000 | 0.55194400 |
| # 164  | tp1012 | Chr6 | 2033301 | 2038700 | 5400   | FALSE | CNVnator | 0.673856000 | 0.50351200 |
| # 1131 | tp1007 | Chr6 | 2035401 | 2038700 | 3300   | FALSE | CNVnator | 0.303760000 | 0.72290700 |
| # 1451 | tp1015 | Chr6 | 2060301 | 2061500 | 1200   | FALSE | CNVnator | 0.241682000 | 0.72440900 |
| # 1133 | tp1007 | Chr6 | 2060501 | 2061400 | 900    | FALSE | CNVnator | 0.156744000 | 0.58962300 |
| # 170  | tp1012 | Chr7 | 116801  | 134600  | 17800  | FALSE | CNVnator | 0.582632000 | 0.02730810 |
| # 1137 | tp1007 | Chr7 | 116801  | 136100  | 19300  | FALSE | CNVnator | 0.610343000 | 0.07486530 |
| # 1788 | IT     | Chr7 | 467701  | 472700  | 5000   | FALSE | CNVnator | 0.743444000 | 0.14726700 |
| # 1456 | tp1015 | Chr7 | 481401  | 484600  | 3200   | FALSE | CNVnator | 0.711443000 | 0.34281500 |
| # 176  | tp1012 | Chr7 | 481601  | 483600  | 2000   | FALSE | CNVnator | 0.623885000 | 0.57303400 |
| # 1789 | IT     | Chr7 | 481801  | 483500  | 1700   | FALSE | CNVnator | 0.387065000 | 0.85271900 |
| # 570  | tp1013 | Chr7 | 481801  | 483600  | 1800   | FALSE | CNVnator | 0.375032000 | 0.84210500 |
| # 178  | tp1012 | Chr7 | 755901  | 758200  | 2300   | FALSE | CNVnator | 0.700398000 | 0.01656250 |
| # 572  | tp1013 | Chr7 | 849501  | 852700  | 3200   | FALSE | CNVnator | 0.731700000 | 0.02088900 |
| # 181  | tp1012 | Chr7 | 1001801 | 1009400 | 7600   | FALSE | CNVnator | 0.734576000 | 0.01301310 |
| # 851  | tp1014 | Chr7 | 1522101 | 1546000 | 23900  | FALSE | CNVnator | 0.664058000 | 0.04608910 |
| # 1797 | IT     | Chr7 | 1785901 | 1788700 | 2800   | FALSE | CNVnator | 0.206303000 | 0.07206120 |
| # 583  | tp1013 | Chr8 | 115201  | 116800  | 1600   | FALSE | CNVnator | 0.639004000 | 0.65061500 |
| # 199  | tp1012 | Chr8 | 207801  | 211500  | 3700   | FALSE | CNVnator | 0.665493000 | 0.31443100 |
| # 1153 | tp1007 | Chr8 | 208001  | 211800  | 3800   | FALSE | CNVnator | 0.674562000 | 0.23607400 |
| # 203  | tp1012 | Chr8 | 606201  | 608100  | 1900   | FALSE | CNVnator | 0.565315000 | 0.02021510 |
| # 858  | tp1014 | Chr8 | 691701  | 831700  | 140000 | FALSE | CNVnator | 0.692858000 | 0.09906360 |
| # 859  | tp1014 | Chr8 | 846801  | 864200  | 17400  | FALSE | CNVnator | 0.613884000 | 0.06093480 |
| # 2185 | tp1335 | Chr8 | 869001  | 873300  | 4300   | FALSE | CNVnator | 0.558186000 | 0.35728700 |
| # 1805 | IT     | Chr8 | 869101  | 872800  | 3700   | FALSE | CNVnator | 0.122531000 | 0.45884400 |
| # 207  | tp1012 | Chr8 | 869101  | 872800  | 3700   | FALSE | CNVnator | 0.503915000 | 0.38638000 |
| # 1806 | IT     | Chr8 | 1005101 | 1006900 | 1800   | FALSE | CNVnator | 0.393993000 | 0.02948230 |
| # 209  | tp1012 | Chr8 | 1242601 | 1244800 | 2200   | FALSE | CNVnator | 0.588488000 | 0.35306600 |
| # 588  | tp1013 | Chr8 | 1242801 | 1244300 | 1500   | FALSE | CNVnator | 0.248387000 | 0.83768700 |
| # 1475 | tp1015 | Chr9 | 3901    | 5700    | 1800   | FALSE | CNVnator | 0.430504000 | 0.57271000 |
| # 593  | tp1013 | Chr9 | 391401  | 395200  | 3800   | FALSE | CNVnator | 0.338065000 | 0.41723900 |
| # 1814 | IT     | Chr9 | 392801  | 394400  | 1600   | FALSE | CNVnator | 0.230253000 | 0.23161000 |
| # 1816 | IT     | Chr9 | 463401  | 465500  | 2100   | FALSE | CNVnator | 0.653378000 | 0.01849750 |
| # 1481 | tp1015 | Chr9 | 776001  | 780300  | 4300   | FALSE | CNVnator | 0.723044000 | 0.01524730 |
| # 867  | tp1014 | Chr9 | 776401  | 780200  | 3800   | FALSE | CNVnator | 0.697923000 | 0.03773580 |

|        |        |      |         |         |       |       |          |             |            |
|--------|--------|------|---------|---------|-------|-------|----------|-------------|------------|
| # 220  | tp1012 | Chr9 | 776401  | 780300  | 3900  | FALSE | CNVnator | 0.696134000 | 0.01537680 |
| # 1824 | IT     | Chr9 | 1137601 | 1138100 | 500   | FALSE | CNVnator | 0.202686000 | 0.07518800 |
| # 1487 | tp1015 | Chr9 | 1139301 | 1182700 | 43400 | FALSE | CNVnator | 0.616833000 | 0.02305640 |
| # 1488 | tp1015 | Chr9 | 1183701 | 1191100 | 7400  | FALSE | CNVnator | 0.329386000 | 0.65346500 |

Load full tables.

```
full.tables.01.26.14 <- load.snp.tables(use.chrl.tables = FALSE, data.name='full.tables.01.26.14')

# Loading full tables from ../../data/ungit-data/full.tables.01.26.14.rda ...Loaded.
# ..00common/mycache/snp.tables.chrl.ungqfiltered.rda saved.

names(full.tables.01.26.14) <- c('1007','1012','1013','1014','1015','3367','1335')
full <- full.tables.01.26.14

# return table with chr names, start/end positions and lengths for all 66 chroms, scaffolds etc.
find.chromosome.boundaries <- function(full=full.tables.01.26.14){
  starts <- which(full[[1]]$pos==1)
  ends <- c(starts[-1]-1,nrow(full[[1]]))
  chromosome.table <- data.frame(chr=full[[1]]$chr[ends], start=starts, end=ends,
                                    len=full[[1]]$pos[ends],stringsAsFactors=F,
                                    row.names = as.character(full[[1]]$chr[ends]))
  return(chromosome.table)
}
cachet('chromosome.table', find.chromosome.boundaries())

# Loading... chromosome.table

# convert global index 1..32M into 'ChrX:offset' format.
g2chrloc <- function(x, chr.tab=chromosome.table){
  for(i in 1:nrow(chr.tab)){
    if(x <= chr.tab$end[i]){
      break
    }
  }
  return(paste(chr.tab$chr[i], x-chr.tab$start[i]+1, sep=':'))
}
# the reverse; x is numeric or 'digits' or list(chr,pos) or 'chr:pos'
chrloc2g <- function(x, chr.tab=chromosome.table){
  if(is.list(x)){
    return(chrloc2gi(x[[1]], x[[2]], chr.tab=chr.tab))
  }
  if(is.numeric(x)){
    return(x)
  }
  if(grepl('^\\d+$', x)){
    return(as.numeric(x))
  }
  if(grepl('^\\w*:\\d$', x)){
    split <- strsplit(x, ':')[[1]]
    return(chrloc2gi(split[1], split[2], chr.tab=chr.tab))
  }
  cat('Unrecognized chrloc format', x, '\n')
  return(NA)
}
chrloc2gi <- function(chr, loc, chr.tab=chromosome.table){
  row <- chr.tab[chr,]
  return(row$start+as.numeric(loc)-1)
}

#tests:
#chrloc2g('Chr1:1')
#chrloc2g('Chr2:1')
#chrloc2g('Chr2:10')
```

```

chrs <- grep('Chr', as.character(chromosome.table$chr))
chr.starts <- paste(as.character(chromosome.table$chr[chrs]), 1, sep=':')
chr.ends <- paste(as.character(chromosome.table$chr[chrs]), chromosome.table$len[chrs], sep=':')
cnvv.starts <- paste(as.character(cnvp$chr), cnvp$start, sep=':')
cnvv.ends <- paste(as.character(cnvp$chr), cnvp$end+1, sep=':')
breakpoints <- sort(unique(c(chr.starts, chr.ends, cnvv.starts, cnvv.ends)))
bkp.chr <- sub('.*!', '', breakpoints)
bkp.start <- as.integer(sub('.*:', '', breakpoints))
pi2 <- order(bkp.chr, bkp.start)
hemi.tab <- data.frame(chr=bkp.chr[pi2], start = bkp.start[pi2], end=0, length=0,
                        row.names=breakpoints[pi2],
                        matrix(nrow=length(pi2), ncol=7, dimnames=list(NULL, strain.names)),
                        stringsAsFactors=F)
hemi.tab$end <- c(hemi.tab$start[-1]-1, 0) # drop first, add zero at end
endz <- (hemi.tab$end == 0) # above puts zeros at last entry for each chr;
hemi.tab$end[endz] <- hemi.tab$start[endz]-1 # replace with start-1 (==> length 0 segment)
hemi.tab$length <- hemi.tab$end - hemi.tab$start + 1
# NOTE: chr ends are still sometimes funky in the table, since I put in the exact chr end, whereas
# CNVnator seems to round up to a multiple of 100, so the real end sometimes preceeds the end of a
# CNVnator block.
for(i in 1:nrow(cnvv)){
  #cat(i, ': ')
  j <- match(paste(cnvv$chr[i],cnvv$start[i], sep=':'), rownames(hemi.tab))
  if(is.na(j)){cat(i,'not found\n')}
  while(j <= nrow(hemi.tab) &&
        hemi.tab$chr[j] == as.character(cnvv$chr[i]) &&
        hemi.tab$start[j] <= cnvv$end[i]){
    #cat(j, ', ')
    hemi.tab[j,as.character(cnvv$strain[i])] <- cnvv$cov_ratio[i]
    j <- j+1
  }
  #cat('\n')
}

```

```

# variant of 'tobin' from shared-snps:
# convert (n x 7) NA/float matrix to n vector of 0-127
tobin <- function(x){
  bin <- integer(nrow(x)) # initialized to 0
  for(i in 1:7){
    bin <- bin*2 + as.integer(!is.na(x[,i]))
  }
  return(as.octmode(bin))
}

```

```

# leverage NA/non-NA in 7 strain columns to define shared-deletion pattern
hemi.tab$pattern <- tobin(hemi.tab[,strain.names])
# and count hemi- bases in each group
bp.by.pat <- data.frame(pattern=0:127, bp=0)
bp.by.pat$pattern <- as.octmode(bp.by.pat$pattern)
for(i in 1:nrow(hemi.tab)){
  bp.by.pat[1+hemi.tab$pattern[i], 2] <- bp.by.pat[1+hemi.tab$pattern[i], 2] + hemi.tab$length[i]
}
sum(bp.by.pat[-1,2]) # exclude undeleted (pattern 000)

# [1] 4251600

pi3 <- order(bp.by.pat[,2])
bp.by.pat[pi3,]

#      pattern      bp
# 8       007       0
# 11      012       0
# 12      013       0
# 13      014       0
# 16      017       0

```

|       |     |      |
|-------|-----|------|
| # 28  | 033 | 0    |
| # 29  | 034 | 0    |
| # 38  | 045 | 0    |
| # 40  | 047 | 0    |
| # 44  | 053 | 0    |
| # 47  | 056 | 0    |
| # 48  | 057 | 0    |
| # 52  | 063 | 0    |
| # 54  | 065 | 0    |
| # 56  | 067 | 0    |
| # 58  | 071 | 0    |
| # 60  | 073 | 0    |
| # 61  | 074 | 0    |
| # 63  | 076 | 0    |
| # 64  | 077 | 0    |
| # 71  | 106 | 0    |
| # 75  | 112 | 0    |
| # 76  | 113 | 0    |
| # 77  | 114 | 0    |
| # 79  | 116 | 0    |
| # 80  | 117 | 0    |
| # 82  | 121 | 0    |
| # 84  | 123 | 0    |
| # 86  | 125 | 0    |
| # 88  | 127 | 0    |
| # 89  | 130 | 0    |
| # 90  | 131 | 0    |
| # 91  | 132 | 0    |
| # 93  | 134 | 0    |
| # 94  | 135 | 0    |
| # 103 | 146 | 0    |
| # 111 | 156 | 0    |
| # 115 | 162 | 0    |
| # 116 | 163 | 0    |
| # 121 | 170 | 0    |
| # 122 | 171 | 0    |
| # 124 | 173 | 0    |
| # 125 | 174 | 0    |
| # 126 | 175 | 0    |
| # 127 | 176 | 0    |
| # 53  | 064 | 100  |
| # 68  | 103 | 100  |
| # 73  | 110 | 100  |
| # 92  | 133 | 100  |
| # 96  | 137 | 100  |
| # 107 | 152 | 100  |
| # 114 | 161 | 100  |
| # 4   | 003 | 300  |
| # 15  | 016 | 300  |
| # 37  | 044 | 300  |
| # 42  | 051 | 300  |
| # 74  | 111 | 300  |
| # 31  | 036 | 500  |
| # 100 | 143 | 500  |
| # 32  | 037 | 700  |
| # 81  | 120 | 700  |
| # 43  | 052 | 800  |
| # 50  | 061 | 800  |
| # 117 | 164 | 800  |
| # 7   | 006 | 900  |
| # 26  | 031 | 900  |
| # 108 | 153 | 1000 |
| # 59  | 072 | 1200 |
| # 85  | 124 | 1200 |
| # 95  | 136 | 1200 |
| # 34  | 041 | 1500 |
| # 123 | 172 | 1600 |

```

# 55      066    1700
# 62      075    2100
# 104     147    2100
# 24      027    2400
# 66      101    2400
# 101     144    2400
# 87      126    2500
# 49      060    2900
# 67      102    2900
# 25      030    3100
# 70      105    3200
# 20      023    3300
# 69      104    3400
# 46      055    3500
# 36      043    3700
# 45      054    3800
# 41      050    4600
# 72      107    4700
# 112     157    4700
# 120     167    4900
# 57      070    5200
# 35      042    5400
# 99      142    5600
# 109     154    6700
# 51      062    7300
# 119     166    9700
# 27      032    10000
# 118     165    10900
# 39      046    11000
# 23      026    11700
# 6       005    11800
# 83      122    13000
# 21      024    14600
# 105     150    15600
# 113     160    19900
# 78      115    22500
# 128     177    26900
# 18      021    30400
# 2       001    40100
# 102     145    46300
# 65      100    88700
# 5       004    89800
# 10      011    93100
# 19      022    121600
# 22      025    134300
# 30      035    140500
# 110     155    158100
# 3       002    162100
# 98      141    186400
# 33      040    197000
# 106     151    258500
# 14      015    264800
# 9       010    309300
# 97      140    798600
# 17      020    843400
# 1       000    27050421

```

Dump table to a file, if it doesn't exist:

```

options(width=120)
if(!file.exists('hemitab.txt')){
  # for some reason, this branch is failing on linux (hemitab.txt is created, 0 length, knitr dies)
  # but working on laptop.
  sink('hemitab.txt', type='output')
  print(hemi.tab,digits=2)
  sink()
} else {
  print(hemi.tab,digits=2)
}

```

| #               | chr    | start   | end     | length | tp1007  | tp1012 | tp1013 | tp1014 | tp1015 | IT     | tp1335 | pattern |
|-----------------|--------|---------|---------|--------|---------|--------|--------|--------|--------|--------|--------|---------|
| # Chr1:1        | Chr1   | 1       | 10600   | 10600  | NA      | NA     | NA     | NA     | NA     | 0.7225 | NA     | 002     |
| # Chr1:10601    | Chr1   | 10601   | 13500   | 2900   | NA      | 0.6374 | NA     | NA     | 0.7062 | 0.7225 | NA     | 046     |
| # Chr1:13501    | Chr1   | 13501   | 14400   | 900    | NA      | NA     | NA     | NA     | 0.7062 | 0.7225 | NA     | 006     |
| # Chr1:14401    | Chr1   | 14401   | 16600   | 2200   | NA      | NA     | NA     | NA     | NA     | 0.7225 | NA     | 002     |
| # Chr1:16601    | Chr1   | 16601   | 25200   | 8600   | NA      | NA     | 0.6361 | NA     | NA     | 0.7225 | NA     | 022     |
| # Chr1:25201    | Chr1   | 25201   | 67900   | 42700  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000     |
| # Chr1:67901    | Chr1   | 67901   | 70700   | 2800   | NA      | NA     | NA     | NA     | NA     | 0.5016 | NA     | 002     |
| # Chr1:70701    | Chr1   | 70701   | 80600   | 9900   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000     |
| # Chr1:80601    | Chr1   | 80601   | 82300   | 1700   | NA      | NA     | NA     | NA     | NA     | 0.2238 | NA     | 002     |
| # Chr1:82301    | Chr1   | 82301   | 90500   | 8200   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000     |
| # Chr1:90501    | Chr1   | 90501   | 91800   | 1300   | NA      | NA     | NA     | NA     | NA     | NA     | 0.4885 | 001     |
| # Chr1:91801    | Chr1   | 91801   | 106600  | 14800  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000     |
| # Chr1:106601   | Chr1   | 106601  | 108600  | 2000   | NA      | NA     | 0.5555 | NA     | NA     | NA     | NA     | 020     |
| # Chr1:108601   | Chr1   | 108601  | 536500  | 427900 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000     |
| # Chr1:536501   | Chr1   | 536501  | 538600  | 2100   | NA      | 0.6849 | NA     | NA     | NA     | NA     | NA     | 040     |
| # Chr1:538601   | Chr1   | 538601  | 538800  | 200    | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000     |
| # Chr1:538801   | Chr1   | 538801  | 543200  | 4400   | NA      | NA     | NA     | NA     | NA     | 0.7045 | NA     | 002     |
| # Chr1:543201   | Chr1   | 543201  | 1222400 | 679200 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000     |
| # Chr1:1222401  | Chr1   | 1222401 | 1222500 | 100    | NA      | NA     | NA     | NA     | NA     | NA     | 0.5995 | 001     |
| # Chr1:1222501  | Chr1   | 1222501 | 1222600 | 100    | NA      | NA     | NA     | NA     | NA     | 0.2488 | 0.5995 | 003     |
| # Chr1:1222601  | Chr1   | 1222601 | 1224400 | 1800   | NA      | NA     | 0.3786 | NA     | NA     | 0.2488 | 0.5995 | 023     |
| # Chr1:1224401  | Chr1   | 1224401 | 1224700 | 300    | NA      | NA     | 0.3786 | NA     | NA     | NA     | 0.5995 | 021     |
| # Chr1:1224701  | Chr1   | 1224701 | 1224900 | 200    | NA      | NA     | NA     | NA     | NA     | NA     | 0.5995 | 001     |
| # Chr1:1224901  | Chr1   | 1224901 | 1865000 | 640100 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000     |
| # Chr1:1865001  | Chr1   | 1865001 | 1865600 | 600    | NA      | NA     | 0.1110 | NA     | NA     | NA     | NA     | 020     |
| # Chr1:1865601  | Chr1   | 1865601 | 2464000 | 598400 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000     |
| # Chr1:2464001  | Chr1   | 2464001 | 2464100 | 100    | NA      | 0.2835 | NA     | NA     | NA     | NA     | NA     | 040     |
| # Chr1:2464101  | Chr1   | 2464101 | 2464700 | 600    | 0.19909 | 0.2835 | NA     | NA     | NA     | NA     | NA     | 140     |
| # Chr1:2464701  | Chr1   | 2464701 | 2465000 | 300    | NA      | 0.2835 | NA     | NA     | NA     | NA     | NA     | 040     |
| # Chr1:2465001  | Chr1   | 2465001 | 2521200 | 56200  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000     |
| # Chr1:2521201  | Chr1   | 2521201 | 2525500 | 4300   | NA      | NA     | NA     | NA     | NA     | 0.5464 | NA     | 004     |
| # Chr1:2525501  | Chr1   | 2525501 | 2545800 | 20300  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000     |
| # Chr1:2545801  | Chr1   | 2545801 | 2551100 | 5300   | NA      | NA     | NA     | NA     | NA     | 0.6535 | NA     | 002     |
| # Chr1:2551101  | Chr1   | 2551101 | 3042100 | 491000 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000     |
| # Chr1:3042101  | Chr1   | 3042101 | 3042584 | 484    | 0.18878 | 0.2499 | NA     | NA     | 0.1877 | NA     | 0.3136 | 145     |
| # Chr1:3042585  | Chr1   | 3042585 | 3042600 | 16     | 0.18878 | 0.2499 | NA     | NA     | 0.1877 | NA     | 0.3136 | 145     |
| # Chr1:3042601  | Chr1   | 3042601 | 3042600 | 0      | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000     |
| # Chr10:1       | Chr10  | 1       | 12300   | 12300  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000     |
| # Chr10:12301   | Chr10  | 12301   | 20100   | 7800   | NA      | NA     | 0.6393 | NA     | NA     | 0.5267 | NA     | 022     |
| # Chr10:20101   | Chr10  | 20101   | 28500   | 8400   | NA      | NA     | NA     | NA     | NA     | 0.5267 | NA     | 002     |
| # Chr10:28501   | Chr10  | 28501   | 103800  | 75300  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000     |
| # Chr10:103801  | Chr10  | 103801  | 104500  | 700    | NA      | NA     | NA     | NA     | NA     | 0.4540 | NA     | 002     |
| # Chr10:104501  | Chr10  | 104501  | 215600  | 111100 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000     |
| # Chr10:215601  | Chr10  | 215601  | 218300  | 2700   | NA      | NA     | 0.4460 | NA     | NA     | 0.5203 | NA     | 022     |
| # Chr10:218301  | Chr10  | 218301  | 812600  | 594300 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000     |
| # Chr10:812601  | Chr10  | 812601  | 814700  | 2100   | 0.73727 | NA     | NA     | NA     | NA     | NA     | NA     | 100     |
| # Chr10:814701  | Chr10  | 814701  | 915300  | 100600 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000     |
| # Chr10:915301  | Chr10  | 915301  | 915800  | 500    | NA      | NA     | NA     | NA     | NA     | 0.2627 | NA     | 002     |
| # Chr10:915801  | Chr10  | 915801  | 1105667 | 189867 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000     |
| # Chr10:1105668 | Chr10  | 1105668 | 1105667 | 0      | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000     |
| # Chr11a:1      | Chr11a | 1       | 1000    | 1000   | NA      | 0.4982 | NA     | NA     | NA     | NA     | NA     | 020     |
| # Chr11a:1001   | Chr11a | 1001    | 1800    | 800    | 0.20438 | 0.1833 | 0.4982 | NA     | 0.1578 | NA     | NA     | 164     |
| # Chr11a:1801   | Chr11a | 1801    | 5200    | 3400   | NA      | 0.4982 | NA     | NA     | NA     | NA     | NA     | 020     |
| # Chr11a:5201   | Chr11a | 5201    | 12100   | 6900   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000     |
| # Chr11a:12101  | Chr11a | 12101   | 20900   | 8800   | 0.55471 | 0.4179 | 0.5723 | NA     | 0.3878 | 0.4342 | NA     | 166     |
| # Chr11a:20901  | Chr11a | 20901   | 21100   | 200    | 0.55471 | NA     | 0.5723 | NA     | 0.3878 | 0.4342 | NA     | 126     |
| # Chr11a:21101  | Chr11a | 21101   | 22300   | 1200   | 0.55471 | NA     | 0.5723 | NA     | 0.3878 | NA     | NA     | 124     |
| # Chr11a:22301  | Chr11a | 22301   | 40900   | 18600  | NA      | NA     | 0.5723 | NA     | NA     | NA     | NA     | 020     |
| # Chr11a:40901  | Chr11a | 40901   | 42500   | 1600   | NA      | 0.5723 | NA     | NA     | 0.3054 | NA     | NA     | 022     |
| # Chr11a:42501  | Chr11a | 42501   | 42600   | 100    | 0.03648 | NA     | 0.5723 | 0.0557 | NA     | 0.3054 | 0.0576 | 133     |
| # Chr11a:42601  | Chr11a | 42601   | 44200   | 1600   | 0.03648 | 0.0000 | 0.5723 | 0.0557 | 0.0505 | 0.3054 | 0.0576 | 177     |
| # Chr11a:44201  | Chr11a | 44201   | 44300   | 100    | NA      | NA     | 0.5723 | 0.0557 | 0.0505 | 0.3054 | 0.0576 | 037     |
| # Chr11a:44301  | Chr11a | 44301   | 45300   | 1000   | NA      | NA     | 0.5723 | NA     | NA     | 0.3054 | NA     | 022     |
| # Chr11a:45301  | Chr11a | 45301   | 50500   | 5200   | NA      | NA     | 0.5723 | NA     | NA     | NA     | NA     | 020     |
| # Chr11a:50501  | Chr11a | 50501   | 58500   | 8000   | NA      | NA     | 0.5723 | NA     | NA     | 0.3292 | NA     | 022     |
| # Chr11a:58501  | Chr11a | 58501   | 65800   | 7300   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000     |
| # Chr11a:65801  | Chr11a | 65801   | 148600  | 82800  | NA      | NA     | 0.6222 | NA     | NA     | NA     | NA     | 020     |
| # Chr11a:148601 | Chr11a | 148601  | 150000  | 1400   | NA      | NA     | 0.6222 | NA     | NA     | NA     | 0.6883 | 021     |
| # Chr11a:150001 | Chr11a | 150001  | 150800  | 800    | NA      | NA     | 0.6222 | NA     | NA     | 0.1066 | 0.6883 | 023     |
| # Chr11a:150801 | Chr11a | 150801  | 155200  | 4400   | NA      | NA     | 0.6222 | NA     | NA     | NA     | 0.6883 | 021     |
| # Chr11a:155201 | Chr11a | 155201  | 239300  | 84100  | NA      | NA     | 0.6222 | NA     | NA     | NA     | NA     | 020     |
| # Chr11a:239301 | Chr11a | 239301  | 240300  | 1000   | NA      | NA     | 0.6222 | NA     | NA     | 0.1966 | NA     | 022     |
| # Chr11a:240301 | Chr11a | 240301  | 253100  | 12800  | NA      | NA     | 0.6222 | NA     | NA     | NA     | NA     | 020     |
| # Chr11a:253101 | Chr11a | 253101  | 254000  | 900    | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000     |
| # Chr11a:254001 | Chr11a | 254001  | 328400  | 74400  | NA      | NA     | 0.6018 | NA     | NA     | NA     | NA     | 020     |
| # Chr11a:328401 | Chr11a | 328401  | 328500  | 100    | 0.21364 | NA     | 0.6018 | NA     | 0.1885 | 0.2348 | NA     | 126     |
| # Chr11a:328501 | Chr11a | 328501  | 329400  | 900    | 0.21364 | 0.1371 | 0.6018 | NA     | 0.1885 | 0.2348 | NA     | 166     |
| # Chr11a:329401 | Chr11a | 329401  | 376100  | 46700  | NA      | NA     | 0.6018 | NA     | NA     | NA     | NA     | 020     |
| # Chr11a:376101 | Chr11a | 376101  | 564200  | 188100 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000     |

|                 |        |         |         |        |         |        |        |        |        |        |        |     |     |
|-----------------|--------|---------|---------|--------|---------|--------|--------|--------|--------|--------|--------|-----|-----|
| # Chr11a:564201 | Chr11a | 564201  | 570700  | 6500   | NA      | 0.6906 | NA     | NA     | NA     | NA     | NA     | NA  | 040 |
| # Chr11a:570701 | Chr11a | 570701  | 738700  | 168000 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr11a:738701 | Chr11a | 738701  | 741600  | 2900   | NA      | NA     | NA     | 0.7211 | NA     | NA     | NA     | NA  | 010 |
| # Chr11a:741601 | Chr11a | 741601  | 806141  | 64541  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr11a:806142 | Chr11a | 806142  | 806141  | 0      | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr11b:1      | Chr11b | 1       | 3300    | 3300   | 0.59855 | NA     | 0.5063 | NA     | NA     | 0.5087 | NA     | NA  | 122 |
| # Chr11b:3301   | Chr11b | 3301    | 11900   | 8600   | NA      | NA     | 0.5063 | NA     | NA     | 0.5087 | NA     | NA  | 022 |
| # Chr11b:11901  | Chr11b | 11901   | 82842   | 70942  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr11b:82843  | Chr11b | 82843   | 82842   | 0      | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr12:1       | Chr12  | 1       | 6400    | 6400   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr12:6401    | Chr12  | 6401    | 7600    | 1200   | 0.03189 | 0.0317 | NA     | 0.0244 | 0.0245 | NA     | 0.0159 | 155 |     |
| # Chr12:7601    | Chr12  | 7601    | 8600    | 1000   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr12:8601    | Chr12  | 8601    | 10000   | 1400   | NA      | NA     | NA     | 0.5626 | NA     | NA     | NA     | NA  | 004 |
| # Chr12:10001   | Chr12  | 10001   | 93900   | 83900  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr12:93901   | Chr12  | 93901   | 94300   | 400    | NA      | NA     | NA     | NA     | NA     | 0.1726 | NA     | NA  | 002 |
| # Chr12:94301   | Chr12  | 94301   | 145000  | 50700  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr12:145001  | Chr12  | 145001  | 145100  | 100    | 0.40683 | NA     | NA     | NA     | NA     | 0.4858 | 0.7121 | 103 |     |
| # Chr12:145101  | Chr12  | 145101  | 146200  | 1100   | 0.40683 | 0.3611 | NA     | 0.6433 | 0.7007 | 0.4858 | 0.7121 | 157 |     |
| # Chr12:146201  | Chr12  | 146201  | 148300  | 2100   | 0.40683 | 0.3611 | NA     | NA     | 0.7007 | 0.4858 | 0.7121 | 147 |     |
| # Chr12:148301  | Chr12  | 148301  | 148400  | 100    | NA      | NA     | NA     | 0.7007 | NA     | 0.7121 | NA     | 005 |     |
| # Chr12:148401  | Chr12  | 148401  | 149100  | 700    | NA      | NA     | NA     | NA     | NA     | NA     | 0.7121 | 001 |     |
| # Chr12:149101  | Chr12  | 149101  | 217400  | 68300  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr12:217401  | Chr12  | 217401  | 243900  | 26500  | 0.68107 | 0.6785 | NA     | NA     | NA     | NA     | NA     | NA  | 140 |
| # Chr12:243901  | Chr12  | 243901  | 244700  | 800    | 0.68107 | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 100 |
| # Chr12:244701  | Chr12  | 244701  | 549000  | 304300 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr12:549001  | Chr12  | 549001  | 549300  | 300    | 0.65784 | NA     | NA     | NA     | NA     | NA     | 0.6512 | 101 |     |
| # Chr12:549301  | Chr12  | 549301  | 551800  | 2500   | 0.65784 | 0.5792 | NA     | NA     | NA     | NA     | 0.6512 | 141 |     |
| # Chr12:551801  | Chr12  | 551801  | 552400  | 600    | NA      | NA     | NA     | NA     | NA     | NA     | 0.6512 | 001 |     |
| # Chr12:552401  | Chr12  | 552401  | 630300  | 77900  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr12:630301  | Chr12  | 630301  | 636900  | 6600   | NA      | 0.7020 | NA     | NA     | NA     | NA     | NA     | NA  | 040 |
| # Chr12:636901  | Chr12  | 636901  | 680600  | 43700  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr12:680601  | Chr12  | 680601  | 680800  | 200    | NA      | 0.5688 | NA     | NA     | NA     | NA     | NA     | NA  | 020 |
| # Chr12:680801  | Chr12  | 680801  | 681600  | 800    | NA      | 0.5688 | NA     | NA     | NA     | NA     | 0.4048 | 021 |     |
| # Chr12:681601  | Chr12  | 681601  | 682600  | 1000   | NA      | 0.5688 | NA     | NA     | NA     | NA     | NA     | NA  | 020 |
| # Chr12:682601  | Chr12  | 682601  | 684000  | 1400   | NA      | 0.5688 | NA     | NA     | 0.3306 | NA     | NA     | 022 |     |
| # Chr12:684001  | Chr12  | 684001  | 684100  | 100    | NA      | 0.5688 | NA     | NA     | NA     | NA     | NA     | NA  | 020 |
| # Chr12:684101  | Chr12  | 684101  | 727700  | 43600  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr12:727701  | Chr12  | 727701  | 728200  | 500    | NA      | 0.2961 | NA     | NA     | NA     | NA     | NA     | NA  | 020 |
| # Chr12:728201  | Chr12  | 728201  | 733500  | 5300   | NA      | 0.2961 | NA     | NA     | 0.2762 | NA     | NA     | 022 |     |
| # Chr12:733501  | Chr12  | 733501  | 744800  | 11300  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr12:744801  | Chr12  | 744801  | 746700  | 1900   | NA      | NA     | NA     | NA     | 0.4354 | NA     | NA     | 002 |     |
| # Chr12:746701  | Chr12  | 746701  | 870500  | 123800 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr12:870501  | Chr12  | 870501  | 871400  | 900    | NA      | NA     | NA     | NA     | 0.5129 | NA     | NA     | 002 |     |
| # Chr12:871401  | Chr12  | 871401  | 1088600 | 217200 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr12:1088601 | Chr12  | 1088601 | 1093900 | 5300   | NA      | 0.7081 | NA     | NA     | NA     | NA     | NA     | NA  | 020 |
| # Chr12:1093901 | Chr12  | 1093901 | 1118500 | 24600  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr12:1118501 | Chr12  | 1118501 | 1124700 | 6200   | NA      | 0.5768 | NA     | NA     | NA     | NA     | NA     | NA  | 020 |
| # Chr12:1124701 | Chr12  | 1124701 | 1128381 | 3681   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr12:1128382 | Chr12  | 1128382 | 1128381 | 0      | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr13:1       | Chr13  | 1       | 12100   | 12100  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr13:12101   | Chr13  | 12101   | 17800   | 5700   | NA      | NA     | NA     | 0.5671 | NA     | NA     | 002    |     |     |
| # Chr13:17801   | Chr13  | 17801   | 101900  | 84100  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr13:101901  | Chr13  | 101901  | 103500  | 1600   | NA      | NA     | NA     | 0.5101 | NA     | NA     | 002    |     |     |
| # Chr13:103501  | Chr13  | 103501  | 550200  | 446700 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr13:550201  | Chr13  | 550201  | 551600  | 1400   | NA      | NA     | NA     | 0.4222 | NA     | NA     | 002    |     |     |
| # Chr13:551601  | Chr13  | 551601  | 660700  | 109100 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr13:660701  | Chr13  | 660701  | 810700  | 150000 | NA      | 0.6159 | NA     | NA     | NA     | NA     | NA     | NA  | 020 |
| # Chr13:810701  | Chr13  | 810701  | 811800  | 1100   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr13:811801  | Chr13  | 811801  | 952100  | 140300 | NA      | 0.6402 | NA     | NA     | NA     | NA     | NA     | NA  | 020 |
| # Chr13:952101  | Chr13  | 952101  | 956400  | 4300   | NA      | 0.6402 | NA     | 0.1781 | NA     | NA     | 022    |     |     |
| # Chr13:956401  | Chr13  | 956401  | 991800  | 35400  | NA      | 0.6402 | NA     | NA     | NA     | NA     | NA     | 020 |     |
| # Chr13:991801  | Chr13  | 991801  | 1007700 | 15900  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr13:1007701 | Chr13  | 1007701 | 1009000 | 1300   | NA      | 0.4165 | NA     | NA     | NA     | NA     | NA     | NA  | 020 |
| # Chr13:1009001 | Chr13  | 1009001 | 1052195 | 43195  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr13:1052196 | Chr13  | 1052196 | 1052195 | 0      | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr14:1       | Chr14  | 1       | 640400  | 640400 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr14:640401  | Chr14  | 640401  | 640600  | 200    | 0.60884 | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 100 |
| # Chr14:640601  | Chr14  | 640601  | 773600  | 133000 | 0.60884 | 0.6074 | NA     | NA     | NA     | NA     | NA     | NA  | 140 |
| # Chr14:773601  | Chr14  | 773601  | 777000  | 3400   | 0.60884 | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 100 |
| # Chr14:777001  | Chr14  | 777001  | 900700  | 123700 | 0.60884 | 0.5956 | NA     | NA     | NA     | NA     | NA     | NA  | 140 |
| # Chr14:900701  | Chr14  | 900701  | 902400  | 1700   | 0.60884 | 0.5956 | NA     | NA     | 0.5903 | NA     | NA     | 142 |     |
| # Chr14:902401  | Chr14  | 902401  | 918000  | 15600  | 0.60884 | 0.5956 | NA     | NA     | NA     | NA     | NA     | NA  | 140 |
| # Chr14:918001  | Chr14  | 918001  | 920900  | 2900   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr14:920901  | Chr14  | 920901  | 954800  | 33900  | 0.58199 | 0.6003 | NA     | NA     | NA     | NA     | NA     | NA  | 140 |
| # Chr14:954801  | Chr14  | 954801  | 959900  | 5100   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr14:959901  | Chr14  | 959901  | 988100  | 28200  | 0.67931 | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 100 |
| # Chr14:988101  | Chr14  | 988101  | 988700  | 600    | 0.67931 | NA     | NA     | 0.7005 | NA     | 0.6806 | 105    |     |     |
| # Chr14:988701  | Chr14  | 988701  | 993400  | 4700   | 0.67931 | NA     | NA     | 0.7005 | 0.5435 | 0.6806 | 107    |     |     |
| # Chr14:993401  | Chr14  | 993401  | 994100  | 700    | 0.67931 | NA     | NA     | 0.7005 | NA     | 0.6806 | 105    |     |     |
| # Chr14:994101  | Chr14  | 994101  | 998642  | 4542   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |

|                  |           |        |        |        |         |        |        |        |        |        |        |     |     |
|------------------|-----------|--------|--------|--------|---------|--------|--------|--------|--------|--------|--------|-----|-----|
| # Chr14:998643   | Chr14     | 998643 | 998642 | 0      | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr15:1        | Chr15     | 1      | 15100  | 15100  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr15:15101    | Chr15     | 15101  | 17200  | 2100   | NA      | NA     | NA     | NA     | NA     | 0.2670 | NA     | NA  | 002 |
| # Chr15:17201    | Chr15     | 17201  | 21200  | 4000   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr15:21201    | Chr15     | 21201  | 21900  | 700    | NA      | NA     | NA     | NA     | NA     | 0.2313 | NA     | NA  | 002 |
| # Chr15:21901    | Chr15     | 21901  | 63600  | 41700  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr15:63601    | Chr15     | 63601  | 67500  | 3900   | NA      | NA     | NA     | NA     | NA     | 0.5811 | NA     | NA  | 002 |
| # Chr15:67501    | Chr15     | 67501  | 244200 | 176700 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr15:244201   | Chr15     | 244201 | 244600 | 400    | NA      | NA     | NA     | 0.6283 | NA     | NA     | NA     | NA  | 010 |
| # Chr15:244601   | Chr15     | 244601 | 244900 | 300    | NA      | NA     | NA     | 0.6283 | 0.6252 | 0.4104 | NA     | NA  | 016 |
| # Chr15:244901   | Chr15     | 244901 | 245400 | 500    | NA      | NA     | NA     | 0.4340 | 0.6283 | 0.6252 | 0.4104 | NA  | 036 |
| # Chr15:245401   | Chr15     | 245401 | 246600 | 1200   | 0.59806 | NA     | NA     | 0.4340 | 0.6283 | 0.6252 | 0.4104 | NA  | 136 |
| # Chr15:246601   | Chr15     | 246601 | 246700 | 100    | NA      | NA     | 0.4340 | 0.6283 | NA     | 0.4104 | NA     | NA  | 032 |
| # Chr15:246701   | Chr15     | 246701 | 246800 | 100    | NA      | NA     | NA     | NA     | NA     | 0.4104 | NA     | NA  | 002 |
| # Chr15:246801   | Chr15     | 246801 | 250800 | 4000   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr15:250801   | Chr15     | 250801 | 250900 | 100    | NA      | NA     | NA     | 0.0151 | NA     | NA     | NA     | NA  | 010 |
| # Chr15:250901   | Chr15     | 250901 | 251000 | 100    | 0.00774 | NA     | 0.0069 | 0.0151 | 0.0083 | 0.0110 | 0.0089 | 137 |     |
| # Chr15:251001   | Chr15     | 251001 | 262700 | 11700  | 0.00774 | 0.0026 | 0.0069 | 0.0151 | 0.0083 | 0.0110 | 0.0089 | 177 |     |
| # Chr15:262701   | Chr15     | 262701 | 434900 | 172200 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr15:434901   | Chr15     | 434901 | 437100 | 2200   | NA      | NA     | NA     | NA     | NA     | 0.5593 | NA     | NA  | 002 |
| # Chr15:437101   | Chr15     | 437101 | 440600 | 3500   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr15:440601   | Chr15     | 440601 | 442300 | 1700   | NA      | NA     | NA     | NA     | NA     | NA     | 0.6543 | 001 |     |
| # Chr15:442301   | Chr15     | 442301 | 451100 | 8800   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr15:451101   | Chr15     | 451101 | 480900 | 29800  | NA      | NA     | 0.6261 | NA     | NA     | NA     | NA     | NA  | 020 |
| # Chr15:480901   | Chr15     | 480901 | 569600 | 88700  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr15:569601   | Chr15     | 569601 | 571600 | 2000   | NA      | NA     | NA     | NA     | NA     | 0.5983 | NA     | 002 |     |
| # Chr15:571601   | Chr15     | 571601 | 619600 | 48000  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr15:619601   | Chr15     | 619601 | 620600 | 1000   | NA      | NA     | NA     | NA     | NA     | 0.6755 | NA     | 002 |     |
| # Chr15:620601   | Chr15     | 620601 | 622400 | 1800   | NA      | NA     | 0.5795 | NA     | NA     | 0.6755 | NA     | 022 |     |
| # Chr15:622401   | Chr15     | 622401 | 622600 | 200    | NA      | NA     | NA     | NA     | NA     | 0.6755 | NA     | 002 |     |
| # Chr15:622601   | Chr15     | 622601 | 931267 | 308667 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr15:931268   | Chr15     | 931268 | 931267 | 0      | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr16a:1       | Chr16a    | 1      | 100    | 100    | 0.65912 | 0.6379 | NA     | NA     | NA     | NA     | NA     | NA  | 140 |
| # Chr16a:101     | Chr16a    | 101    | 1200   | 1100   | 0.65912 | 0.6379 | NA     | NA     | 0.3173 | NA     | NA     | NA  | 144 |
| # Chr16a:1201    | Chr16a    | 1201   | 26700  | 25500  | 0.65912 | 0.6379 | NA     | NA     | NA     | NA     | NA     | NA  | 140 |
| # Chr16a:26701   | Chr16a    | 26701  | 47900  | 21200  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr16a:47901   | Chr16a    | 47901  | 65200  | 17300  | NA      | 0.6714 | NA     | NA     | NA     | NA     | NA     | NA  | 040 |
| # Chr16a:65201   | Chr16a    | 65201  | 193000 | 127800 | 0.61938 | 0.6714 | NA     | NA     | NA     | NA     | NA     | NA  | 140 |
| # Chr16a:193001  | Chr16a    | 193001 | 193300 | 300    | NA      | 0.6714 | NA     | NA     | NA     | NA     | NA     | NA  | 040 |
| # Chr16a:193301  | Chr16a    | 193301 | 248800 | 55500  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr16a:248801  | Chr16a    | 248801 | 260000 | 11200  | NA      | NA     | NA     | NA     | 0.7280 | NA     | 0.7351 | 005 |     |
| # Chr16a:260001  | Chr16a    | 260001 | 263100 | 3100   | NA      | NA     | NA     | NA     | 0.7280 | NA     | NA     | 004 |     |
| # Chr16a:263101  | Chr16a    | 263101 | 425400 | 162300 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr16a:425401  | Chr16a    | 425401 | 425800 | 400    | NA      | NA     | 0.2287 | NA     | NA     | NA     | NA     | NA  | 020 |
| # Chr16a:425801  | Chr16a    | 425801 | 432800 | 7000   | NA      | NA     | 0.2287 | NA     | NA     | 0.1891 | NA     | NA  | 022 |
| # Chr16a:432801  | Chr16a    | 432801 | 433200 | 400    | NA      | NA     | NA     | NA     | 0.1891 | NA     | NA     | 002 |     |
| # Chr16a:433201  | Chr16a    | 433201 | 443600 | 10400  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr16a:443601  | Chr16a    | 443601 | 446100 | 2500   | NA      | NA     | 0.4816 | NA     | NA     | NA     | NA     | NA  | 020 |
| # Chr16a:446101  | Chr16a    | 446101 | 448500 | 2400   | NA      | NA     | 0.4816 | NA     | NA     | 0.6384 | NA     | NA  | 022 |
| # Chr16a:448501  | Chr16a    | 448501 | 450500 | 2000   | NA      | NA     | NA     | NA     | NA     | 0.6384 | NA     | NA  | 002 |
| # Chr16a:450501  | Chr16a    | 450501 | 459775 | 9275   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr16a:459776  | Chr16a    | 459776 | 459775 | 0      | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr16b:1       | Chr16b    | 1      | 96700  | 96700  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr16b:96701   | Chr16b    | 96701  | 97400  | 700    | NA      | NA     | NA     | NA     | 0.4108 | NA     | NA     | 002 |     |
| # Chr16b:97401   | Chr16b    | 97401  | 134700 | 37300  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr16b:134701  | Chr16b    | 134701 | 138500 | 3800   | NA      | NA     | NA     | NA     | 0.6060 | NA     | NA     | 002 |     |
| # Chr16b:138501  | Chr16b    | 138501 | 146600 | 8100   | NA      | 0.6732 | NA     | NA     | 0.6657 | 0.6060 | NA     | NA  | 046 |
| # Chr16b:146601  | Chr16b    | 146601 | 147000 | 400    | NA      | NA     | NA     | NA     | 0.6060 | NA     | NA     | 002 |     |
| # Chr16b:147001  | Chr16b    | 147001 | 169375 | 22375  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr16b:169376  | Chr16b    | 169376 | 169375 | 0      | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr17:1        | Chr17     | 1      | 45100  | 45100  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr17:45101    | Chr17     | 45101  | 47000  | 1900   | NA      | NA     | NA     | NA     | 0.5350 | NA     | NA     | 002 |     |
| # Chr17:47001    | Chr17     | 47001  | 496400 | 449400 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr17:496401   | Chr17     | 496401 | 499300 | 2900   | NA      | NA     | 0.3653 | NA     | NA     | 0.3685 | NA     | NA  | 022 |
| # Chr17:499301   | Chr17     | 499301 | 499500 | 200    | NA      | NA     | NA     | NA     | NA     | 0.3685 | NA     | NA  | 002 |
| # Chr17:499501   | Chr17     | 499501 | 659923 | 160423 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr17:659924   | Chr17     | 659924 | 659923 | 0      | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr18:1        | Chr18     | 1      | 500    | 500    | NA      | NA     | 0.1478 | NA     | NA     | NA     | NA     | NA  | 020 |
| # Chr18:501      | Chr18     | 501    | 214200 | 213700 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr18:214201   | Chr18     | 214201 | 215600 | 1400   | NA      | NA     | NA     | NA     | 0.3757 | NA     | NA     | 002 |     |
| # Chr18:215601   | Chr18     | 215601 | 266200 | 50600  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr18:266201   | Chr18     | 266201 | 267800 | 1600   | NA      | NA     | NA     | NA     | 0.2921 | NA     | NA     | 002 |     |
| # Chr18:267801   | Chr18     | 267801 | 306000 | 38200  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr18:306001   | Chr18     | 306001 | 308800 | 2800   | NA      | NA     | 0.1875 | NA     | NA     | NA     | NA     | NA  | 020 |
| # Chr18:308801   | Chr18     | 308801 | 532900 | 224100 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr18:532901   | Chr18     | 532901 | 533800 | 900    | NA      | NA     | NA     | NA     | 0.4173 | NA     | NA     | 002 |     |
| # Chr18:533801   | Chr18     | 533801 | 827052 | 293252 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr18:827053   | Chr18     | 827053 | 827052 | 0      | NA      | NA     | NA     | NA     | NA     | NA     | NA     | NA  | 000 |
| # Chr19a_19:1    | Chr19a_19 | 1      | 2200   | 2200   | 0.42895 | NA     | 0.6135 | NA     | 0.5703 | 0.5078 | NA     | NA  | 126 |
| # Chr19a_19:2201 | Chr19a_19 | 2201   | 13600  | 11400  | NA      | NA     | 0.6135 | NA     | 0.5703 | 0.5078 | NA     | NA  | 026 |

|                    |           |         |         |        |         |        |        |        |        |        |        |     |
|--------------------|-----------|---------|---------|--------|---------|--------|--------|--------|--------|--------|--------|-----|
| # Chr19a_19:13601  | Chr19a_19 | 13601   | 15700   | 2100   | NA      | NA     | 0.6135 | NA     | NA     | 0.5078 | NA     | 022 |
| # Chr19a_19:15701  | Chr19a_19 | 15701   | 17700   | 2000   | NA      | NA     | NA     | NA     | NA     | 0.5078 | NA     | 002 |
| # Chr19a_19:17701  | Chr19a_19 | 17701   | 51400   | 33700  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr19a_19:51401  | Chr19a_19 | 51401   | 52300   | 900    | 0.60958 | NA     | NA     | NA     | NA     | NA     | NA     | 100 |
| # Chr19a_19:52301  | Chr19a_19 | 52301   | 57500   | 5200   | 0.60958 | 0.6249 | NA     | NA     | NA     | NA     | NA     | 140 |
| # Chr19a_19:57501  | Chr19a_19 | 57501   | 62200   | 4700   | 0.60958 | 0.6249 | NA     | 0.7049 | NA     | NA     | NA     | 150 |
| # Chr19a_19:62201  | Chr19a_19 | 62201   | 64100   | 1900   | 0.60958 | 0.6249 | NA     | 0.7049 | NA     | NA     | 0.5877 | 151 |
| # Chr19a_19:64101  | Chr19a_19 | 64101   | 168300  | 104200 | 0.60958 | 0.6249 | NA     | 0.7049 | 0.6181 | NA     | 0.5877 | 155 |
| # Chr19a_19:168301 | Chr19a_19 | 168301  | 171800  | 3500   | NA      | 0.6249 | NA     | 0.7049 | 0.6181 | NA     | 0.5877 | 055 |
| # Chr19a_19:171801 | Chr19a_19 | 171801  | 276400  | 104600 | NA      | NA     | NA     | 0.7049 | 0.6181 | NA     | 0.5877 | 015 |
| # Chr19a_19:276401 | Chr19a_19 | 276401  | 277600  | 1200   | 0.19019 | 0.1448 | NA     | 0.7049 | 0.6181 | NA     | 0.5877 | 155 |
| # Chr19a_19:277601 | Chr19a_19 | 277601  | 277800  | 200    | NA      | NA     | NA     | NA     | NA     | NA     | 0.5877 | 001 |
| # Chr19a_19:277801 | Chr19a_19 | 277801  | 281000  | 3200   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr19a_19:281001 | Chr19a_19 | 281001  | 281100  | 100    | NA      | 0.5506 | NA     | NA     | NA     | NA     | NA     | 040 |
| # Chr19a_19:281101 | Chr19a_19 | 281101  | 281200  | 100    | 0.55650 | 0.5506 | NA     | NA     | NA     | NA     | NA     | 140 |
| # Chr19a_19:281201 | Chr19a_19 | 281201  | 301400  | 20200  | 0.55650 | 0.5506 | NA     | 0.7043 | NA     | NA     | 0.5508 | 151 |
| # Chr19a_19:301401 | Chr19a_19 | 301401  | 303300  | 1900   | 0.55650 | 0.5506 | NA     | 0.7043 | 0.6379 | NA     | 0.5508 | 155 |
| # Chr19a_19:303301 | Chr19a_19 | 303301  | 303500  | 200    | 0.55650 | NA     | NA     | 0.7043 | 0.6379 | NA     | 0.5508 | 115 |
| # Chr19a_19:303501 | Chr19a_19 | 303501  | 309300  | 5800   | NA      | NA     | NA     | 0.7043 | NA     | NA     | 0.5508 | 011 |
| # Chr19a_19:309301 | Chr19a_19 | 309301  | 355000  | 45700  | 0.60439 | 0.6038 | NA     | 0.7043 | NA     | NA     | 0.5508 | 151 |
| # Chr19a_19:355001 | Chr19a_19 | 355001  | 356000  | 1000   | 0.60439 | 0.6038 | NA     | 0.7043 | NA     | 0.1359 | 0.5508 | 153 |
| # Chr19a_19:356001 | Chr19a_19 | 356001  | 419000  | 63000  | 0.60439 | 0.6038 | NA     | 0.7043 | NA     | NA     | 0.5508 | 151 |
| # Chr19a_19:419001 | Chr19a_19 | 419001  | 419200  | 200    | 0.60439 | 0.6038 | NA     | 0.7043 | NA     | NA     | NA     | 150 |
| # Chr19a_19:419201 | Chr19a_19 | 419201  | 420700  | 1500   | NA      | 0.6038 | NA     | 0.7043 | NA     | NA     | NA     | 050 |
| # Chr19a_19:420701 | Chr19a_19 | 420701  | 421000  | 300    | 0.60174 | 0.6038 | NA     | 0.7043 | NA     | NA     | NA     | 150 |
| # Chr19a_19:421001 | Chr19a_19 | 421001  | 447500  | 26500  | 0.60174 | 0.6038 | NA     | 0.7043 | NA     | NA     | 0.5679 | 151 |
| # Chr19a_19:447501 | Chr19a_19 | 447501  | 447600  | 100    | NA      | 0.6038 | NA     | 0.7043 | NA     | NA     | 0.5679 | 051 |
| # Chr19a_19:447601 | Chr19a_19 | 447601  | 451500  | 3900   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr19a_19:451501 | Chr19a_19 | 451501  | 451600  | 100    | 0.65883 | 0.6899 | NA     | NA     | NA     | NA     | 0.6114 | 141 |
| # Chr19a_19:451601 | Chr19a_19 | 451601  | 474600  | 23000  | 0.65883 | 0.6899 | NA     | 0.7173 | NA     | NA     | 0.6114 | 151 |
| # Chr19a_19:474601 | Chr19a_19 | 474601  | 477200  | 2600   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr19a_19:477201 | Chr19a_19 | 477201  | 477300  | 100    | 0.64783 | 0.6517 | NA     | 0.7415 | NA     | 0.4913 | NA     | 152 |
| # Chr19a_19:477301 | Chr19a_19 | 477301  | 478900  | 1600   | 0.64783 | 0.6517 | 0.3451 | 0.7415 | NA     | 0.4913 | NA     | 172 |
| # Chr19a_19:478901 | Chr19a_19 | 478901  | 479300  | 400    | 0.64783 | 0.6517 | NA     | 0.7415 | NA     | NA     | NA     | 150 |
| # Chr19a_19:479301 | Chr19a_19 | 479301  | 548600  | 69300  | 0.64783 | 0.6517 | NA     | 0.7415 | NA     | NA     | 0.6104 | 151 |
| # Chr19a_19:548601 | Chr19a_19 | 548601  | 549200  | 600    | NA      | NA     | NA     | NA     | NA     | NA     | 0.6104 | 001 |
| # Chr19a_19:549201 | Chr19a_19 | 549201  | 553500  | 4300   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr19a_19:553501 | Chr19a_19 | 553501  | 554700  | 1200   | NA      | NA     | NA     | NA     | NA     | NA     | 0.6134 | 001 |
| # Chr19a_19:554701 | Chr19a_19 | 554701  | 585900  | 31200  | 0.67263 | 0.7075 | NA     | NA     | NA     | NA     | 0.6134 | 141 |
| # Chr19a_19:585901 | Chr19a_19 | 585901  | 607238  | 21338  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr19a_19:607239 | Chr19a_19 | 607239  | 607238  | 0      | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr19b_31:1      | Chr19b_31 | 1       | 96400   | 96400  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr19b_31:96401  | Chr19b_31 | 96401   | 96600   | 200    | NA      | 0.5981 | NA     | NA     | NA     | NA     | NA     | 040 |
| # Chr19b_31:96601  | Chr19b_31 | 96601   | 151676  | 55076  | 0.60542 | 0.5981 | NA     | NA     | NA     | NA     | NA     | 140 |
| # Chr19b_31:151677 | Chr19b_31 | 151677  | 151700  | 24     | 0.60542 | 0.5981 | NA     | NA     | NA     | NA     | NA     | 140 |
| # Chr19b_31:151701 | Chr19b_31 | 151701  | 151700  | 0      | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr19c_29:1      | Chr19c_29 | 1       | 17700   | 17700  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr19c_29:17701  | Chr19c_29 | 17701   | 18600   | 900    | 0.19709 | NA     | NA     | NA     | NA     | NA     | NA     | 100 |
| # Chr19c_29:18601  | Chr19c_29 | 18601   | 74800   | 56200  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr19c_29:74801  | Chr19c_29 | 74801   | 75400   | 600    | 0.12229 | 0.1181 | NA     | NA     | NA     | 0.1779 | NA     | 142 |
| # Chr19c_29:75401  | Chr19c_29 | 75401   | 117700  | 42300  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr19c_29:117701 | Chr19c_29 | 117701  | 203100  | 85400  | 0.61260 | 0.6400 | NA     | NA     | NA     | NA     | NA     | 140 |
| # Chr19c_29:203101 | Chr19c_29 | 203101  | 212100  | 9000   | NA      | 0.6400 | NA     | NA     | NA     | NA     | NA     | 040 |
| # Chr19c_29:212101 | Chr19c_29 | 212101  | 215200  | 3100   | NA      | 0.6400 | NA     | 0.7139 | NA     | NA     | NA     | 050 |
| # Chr19c_29:215201 | Chr19c_29 | 215201  | 216500  | 1300   | NA      | NA     | NA     | 0.7139 | NA     | NA     | NA     | 010 |
| # Chr19c_29:216501 | Chr19c_29 | 216501  | 291193  | 74693  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr19c_29:291194 | Chr19c_29 | 291194  | 291193  | 0      | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr2:1           | Chr2      | 1       | 400     | 400    | NA      | NA     | 0.1248 | NA     | NA     | NA     | NA     | 020 |
| # Chr2:401         | Chr2      | 401     | 13900   | 13500  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr2:13901       | Chr2      | 13901   | 15800   | 1900   | NA      | NA     | NA     | NA     | NA     | 0.2917 | NA     | 002 |
| # Chr2:15801       | Chr2      | 15801   | 268800  | 253000 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr2:268801      | Chr2      | 268801  | 279000  | 10200  | NA      | NA     | NA     | NA     | 0.7469 | NA     | 002    |     |
| # Chr2:279001      | Chr2      | 279001  | 289200  | 10200  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr2:289201      | Chr2      | 289201  | 293700  | 4500   | NA      | NA     | NA     | NA     | NA     | 0.6511 | NA     | 002 |
| # Chr2:293701      | Chr2      | 293701  | 425900  | 132200 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr2:425901      | Chr2      | 425901  | 426100  | 200    | NA      | NA     | NA     | NA     | 0.5515 | NA     | 002    |     |
| # Chr2:426101      | Chr2      | 426101  | 434000  | 7900   | NA      | NA     | 0.5617 | NA     | NA     | 0.5515 | NA     | 022 |
| # Chr2:434001      | Chr2      | 434001  | 434100  | 100    | NA      | NA     | 0.5617 | NA     | NA     | NA     | NA     | 020 |
| # Chr2:434101      | Chr2      | 434101  | 468300  | 34200  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr2:468301      | Chr2      | 468301  | 472800  | 4500   | 0.71522 | NA     | NA     | NA     | NA     | NA     | NA     | 100 |
| # Chr2:472801      | Chr2      | 472801  | 475000  | 2200   | 0.71522 | NA     | 0.3511 | NA     | NA     | 0.4296 | NA     | 122 |
| # Chr2:475001      | Chr2      | 475001  | 475600  | 600    | 0.71522 | NA     | NA     | NA     | 0.4296 | NA     | 102    |     |
| # Chr2:475601      | Chr2      | 475601  | 475700  | 100    | NA      | NA     | NA     | NA     | 0.4296 | NA     | 002    |     |
| # Chr2:475701      | Chr2      | 475701  | 667700  | 192000 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr2:667701      | Chr2      | 667701  | 667900  | 200    | NA      | NA     | NA     | 0.7203 | NA     | NA     | NA     | 010 |
| # Chr2:667901      | Chr2      | 667901  | 668500  | 600    | 0.71379 | 0.6655 | NA     | 0.7203 | NA     | NA     | NA     | 150 |
| # Chr2:668501      | Chr2      | 668501  | 675200  | 6700   | 0.71379 | 0.6655 | NA     | 0.7203 | 0.6996 | NA     | NA     | 154 |
| # Chr2:675201      | Chr2      | 675201  | 676500  | 1300   | 0.71379 | 0.6655 | NA     | NA     | 0.6996 | NA     | NA     | 144 |
| # Chr2:676501      | Chr2      | 676501  | 1082200 | 405700 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr2:1082201     | Chr2      | 1082201 | 1084000 | 1800   | NA      | NA     | 0.3981 | NA     | NA     | 0.3720 | NA     | 022 |

|                |       |         |         |        |         |        |        |        |        |        |        |     |
|----------------|-------|---------|---------|--------|---------|--------|--------|--------|--------|--------|--------|-----|
| # Chr2:1084001 | Chr2  | 1084001 | 1462800 | 378800 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr2:1462801 | Chr2  | 1462801 | 1465100 | 2300   | NA      | NA     | 0.6423 | NA     | NA     | NA     | NA     | 020 |
| # Chr2:1465101 | Chr2  | 1465101 | 1615300 | 150200 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr2:1615301 | Chr2  | 1615301 | 1621100 | 5800   | NA      | 0.7214 | NA     | NA     | NA     | NA     | NA     | 040 |
| # Chr2:1621101 | Chr2  | 1621101 | 1913800 | 292700 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr2:1913801 | Chr2  | 1913801 | 1914100 | 300    | NA      | 0.5265 | NA     | 0.6621 | NA     | 0.4261 | NA     | 052 |
| # Chr2:1914101 | Chr2  | 1914101 | 1915300 | 1200   | NA      | 0.5265 | 0.3432 | 0.6621 | NA     | 0.4261 | NA     | 072 |
| # Chr2:1915301 | Chr2  | 1915301 | 1915800 | 500    | NA      | 0.5265 | NA     | 0.6621 | NA     | 0.4261 | NA     | 052 |
| # Chr2:1915801 | Chr2  | 1915801 | 1915900 | 100    | NA      | NA     | NA     | NA     | NA     | 0.4261 | NA     | 002 |
| # Chr2:1915901 | Chr2  | 1915901 | 2139100 | 223200 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr2:2139101 | Chr2  | 2139101 | 2143000 | 3900   | NA      | 0.6487 | NA     | NA     | NA     | NA     | NA     | 040 |
| # Chr2:2143001 | Chr2  | 2143001 | 2197000 | 54000  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr2:2197001 | Chr2  | 2197001 | 2217300 | 20300  | NA      | NA     | NA     | 0.6602 | NA     | NA     | NA     | 010 |
| # Chr2:2217301 | Chr2  | 2217301 | 2226700 | 9400   | 0.59088 | 0.5760 | NA     | 0.6602 | NA     | NA     | NA     | 150 |
| # Chr2:2226701 | Chr2  | 2226701 | 2282900 | 56200  | 0.59088 | 0.5760 | NA     | NA     | NA     | NA     | NA     | 140 |
| # Chr2:2282901 | Chr2  | 2282901 | 2293100 | 10200  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr2:2293101 | Chr2  | 2293101 | 2330600 | 37500  | 0.68833 | 0.6616 | NA     | NA     | NA     | NA     | NA     | 140 |
| # Chr2:2330601 | Chr2  | 2330601 | 2347700 | 17100  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr2:2347701 | Chr2  | 2347701 | 2348100 | 400    | NA      | 0.5763 | NA     | NA     | NA     | NA     | NA     | 040 |
| # Chr2:2348101 | Chr2  | 2348101 | 2399100 | 51000  | 0.60363 | 0.5763 | NA     | NA     | NA     | NA     | NA     | 140 |
| # Chr2:2399101 | Chr2  | 2399101 | 2444600 | 45500  | 0.60363 | 0.5763 | NA     | NA     | NA     | 0.5518 | 141    |     |
| # Chr2:2444601 | Chr2  | 2444601 | 2444700 | 100    | 0.60363 | NA     | NA     | NA     | NA     | NA     | 0.5518 | 101 |
| # Chr2:2444701 | Chr2  | 2444701 | 2446700 | 2000   | 0.60363 | NA     | NA     | NA     | NA     | NA     | NA     | 100 |
| # Chr2:2446701 | Chr2  | 2446701 | 2447800 | 1100   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr2:2447801 | Chr2  | 2447801 | 2448100 | 300    | NA      | NA     | NA     | NA     | 0.4223 | NA     | 002    |     |
| # Chr2:2448101 | Chr2  | 2448101 | 2448600 | 500    | 0.61648 | 0.6169 | NA     | NA     | NA     | 0.4223 | 0.5651 | 143 |
| # Chr2:2448601 | Chr2  | 2448601 | 2555700 | 107100 | 0.61648 | 0.6169 | NA     | NA     | NA     | NA     | 0.5651 | 141 |
| # Chr2:2555701 | Chr2  | 2555701 | 2576700 | 21000  | 0.61648 | 0.6169 | NA     | NA     | 0.6481 | NA     | 0.5651 | 145 |
| # Chr2:2576701 | Chr2  | 2576701 | 2582000 | 5300   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr2:2582001 | Chr2  | 2582001 | 2582100 | 100    | 0.62880 | 0.6368 | NA     | NA     | NA     | NA     | NA     | 140 |
| # Chr2:2582101 | Chr2  | 2582101 | 2594100 | 12000  | 0.62880 | 0.6368 | NA     | 0.7112 | 0.6059 | NA     | 0.5982 | 155 |
| # Chr2:2594101 | Chr2  | 2594101 | 2597700 | 3600   | 0.62880 | 0.6368 | NA     | 0.7112 | 0.6059 | 0.7381 | 0.5982 | 157 |
| # Chr2:2597701 | Chr2  | 2597701 | 2635300 | 37600  | 0.62880 | 0.6368 | NA     | 0.7112 | 0.6059 | NA     | 0.5982 | 155 |
| # Chr2:2635301 | Chr2  | 2635301 | 2638000 | 2700   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr2:2638001 | Chr2  | 2638001 | 2638100 | 100    | NA      | NA     | NA     | NA     | 0.6597 | NA     | NA     | 004 |
| # Chr2:2638101 | Chr2  | 2638101 | 2648900 | 10800  | 0.70228 | 0.7222 | NA     | NA     | 0.6597 | NA     | 0.6038 | 145 |
| # Chr2:2648901 | Chr2  | 2648901 | 2650900 | 2000   | 0.70228 | NA     | NA     | NA     | 0.6597 | NA     | NA     | 104 |
| # Chr2:2650901 | Chr2  | 2650901 | 2651200 | 300    | 0.70228 | NA     | NA     | NA     | 0.6597 | NA     | 0.6246 | 105 |
| # Chr2:2651201 | Chr2  | 2651201 | 2665200 | 14000  | 0.70228 | 0.6822 | NA     | NA     | 0.6597 | NA     | 0.6246 | 145 |
| # Chr2:2665201 | Chr2  | 2665201 | 2676900 | 11700  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr2:2676901 | Chr2  | 2676901 | 2677000 | 100    | 0.71725 | NA     | NA     | 0.7482 | NA     | NA     | NA     | 110 |
| # Chr2:2677001 | Chr2  | 2677001 | 2699300 | 22300  | 0.71725 | NA     | NA     | 0.7482 | 0.6670 | NA     | 0.6544 | 115 |
| # Chr2:2699301 | Chr2  | 2699301 | 2699600 | 300    | 0.71725 | NA     | NA     | 0.7482 | NA     | NA     | 0.6544 | 111 |
| # Chr2:2699601 | Chr2  | 2699601 | 2699800 | 200    | 0.71725 | NA     | NA     | NA     | NA     | NA     | 0.6544 | 101 |
| # Chr2:2699801 | Chr2  | 2699801 | 2706700 | 6900   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr2:2706701 | Chr2  | 2706701 | 2707194 | 494    | NA      | NA     | 0.1659 | NA     | NA     | NA     | NA     | 020 |
| # Chr2:2707195 | Chr2  | 2707195 | 2707200 | 6      | NA      | NA     | 0.1659 | NA     | NA     | NA     | NA     | 020 |
| # Chr2:2707201 | Chr2  | 2707201 | 2707200 | 0      | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr20:1      | Chr20 | 1       | 1500    | 1500   | NA      | NA     | NA     | NA     | 0.3054 | NA     | NA     | 004 |
| # Chr20:1501   | Chr20 | 1501    | 20500   | 19000  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr20:20501  | Chr20 | 20501   | 23400   | 2900   | NA      | NA     | NA     | NA     | 0.6033 | NA     | 002    |     |
| # Chr20:23401  | Chr20 | 23401   | 23600   | 200    | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr20:23601  | Chr20 | 23601   | 24300   | 700    | NA      | NA     | 0.6289 | NA     | NA     | NA     | NA     | 020 |
| # Chr20:24301  | Chr20 | 24301   | 25500   | 1200   | NA      | NA     | 0.6289 | NA     | NA     | 0.4079 | NA     | 022 |
| # Chr20:25501  | Chr20 | 25501   | 28600   | 3100   | NA      | NA     | 0.6289 | NA     | NA     | NA     | NA     | 020 |
| # Chr20:28601  | Chr20 | 28601   | 34400   | 5800   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr20:34401  | Chr20 | 34401   | 35300   | 900    | NA      | NA     | 0.1587 | NA     | NA     | NA     | NA     | 020 |
| # Chr20:35301  | Chr20 | 35301   | 127100  | 91800  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr20:127101 | Chr20 | 127101  | 128400  | 1300   | NA      | 0.7027 | NA     | NA     | NA     | NA     | NA     | 040 |
| # Chr20:128401 | Chr20 | 128401  | 130200  | 1800   | NA      | 0.7027 | 0.4813 | NA     | NA     | 0.4302 | NA     | 062 |
| # Chr20:130201 | Chr20 | 130201  | 130400  | 200    | NA      | 0.4813 | NA     | NA     | 0.4302 | NA     | 022    |     |
| # Chr20:130401 | Chr20 | 130401  | 130600  | 200    | NA      | NA     | NA     | NA     | 0.4302 | NA     | 002    |     |
| # Chr20:130601 | Chr20 | 130601  | 405800  | 275200 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr20:405801 | Chr20 | 405801  | 407600  | 1800   | NA      | NA     | NA     | NA     | 0.3772 | NA     | 002    |     |
| # Chr20:407601 | Chr20 | 407601  | 469500  | 61900  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr20:469501 | Chr20 | 469501  | 474100  | 4600   | NA      | NA     | NA     | NA     | 0.7473 | NA     | 002    |     |
| # Chr20:474101 | Chr20 | 474101  | 486100  | 12000  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr20:486101 | Chr20 | 486101  | 486200  | 100    | NA      | NA     | NA     | NA     | 0.4787 | NA     | 002    |     |
| # Chr20:486201 | Chr20 | 486201  | 488500  | 2300   | 0.56889 | NA     | NA     | NA     | 0.4787 | NA     | 102    |     |
| # Chr20:488501 | Chr20 | 488501  | 492400  | 3900   | 0.56889 | NA     | NA     | NA     | 0.4787 | NA     | 100    |     |
| # Chr20:492401 | Chr20 | 492401  | 492500  | 100    | 0.56889 | NA     | 0.3903 | NA     | NA     | NA     | NA     | 120 |
| # Chr20:492501 | Chr20 | 492501  | 500000  | 7500   | 0.56889 | NA     | 0.3903 | NA     | NA     | 0.0472 | NA     | 122 |
| # Chr20:500001 | Chr20 | 500001  | 500100  | 100    | 0.56889 | NA     | 0.3903 | NA     | NA     | NA     | NA     | 120 |
| # Chr20:500101 | Chr20 | 500101  | 532800  | 32700  | 0.56889 | NA     | NA     | NA     | NA     | NA     | NA     | 100 |
| # Chr20:532801 | Chr20 | 532801  | 533300  | 500    | 0.56889 | NA     | 0.6538 | NA     | NA     | NA     | NA     | 120 |
| # Chr20:533301 | Chr20 | 533301  | 553200  | 19900  | 0.56889 | 0.5528 | 0.6538 | NA     | NA     | NA     | NA     | 160 |
| # Chr20:553201 | Chr20 | 553201  | 553300  | 100    | NA      | 0.5528 | 0.6538 | NA     | NA     | NA     | NA     | 060 |
| # Chr20:553301 | Chr20 | 553301  | 564400  | 11100  | NA      | NA     | 0.6538 | NA     | NA     | NA     | NA     | 020 |
| # Chr20:564401 | Chr20 | 564401  | 583100  | 18700  | NA      | NA     | 0.6538 | NA     | NA     | NA     | 0.5840 | 021 |
| # Chr20:583101 | Chr20 | 583101  | 591200  | 8100   | NA      | NA     | 0.6538 | NA     | 0.5849 | NA     | 0.5840 | 025 |

|                 |       |         |         |        |         |        |        |        |        |        |        |     |
|-----------------|-------|---------|---------|--------|---------|--------|--------|--------|--------|--------|--------|-----|
| # Chr20:591201  | Chr20 | 591201  | 592000  | 800    | NA      | NA     | 0.6538 | NA     | NA     | NA     | NA     | 020 |
| # Chr20:592001  | Chr20 | 592001  | 593900  | 1900   | NA      | NA     | 0.6538 | NA     | NA     | 0.5975 | NA     | 022 |
| # Chr20:593901  | Chr20 | 593901  | 594200  | 300    | NA      | NA     | 0.6538 | NA     | 0.5324 | 0.5975 | NA     | 026 |
| # Chr20:594201  | Chr20 | 594201  | 594300  | 100    | NA      | NA     | 0.6538 | NA     | 0.5324 | 0.5975 | 0.5990 | 027 |
| # Chr20:594301  | Chr20 | 594301  | 620200  | 25900  | NA      | NA     | 0.6538 | NA     | 0.5324 | NA     | 0.5990 | 025 |
| # Chr20:620201  | Chr20 | 620201  | 620300  | 100    | NA      | NA     | NA     | NA     | 0.5324 | NA     | 0.5990 | 005 |
| # Chr20:620301  | Chr20 | 620301  | 621600  | 1300   | NA      | NA     | NA     | NA     | 0.5324 | NA     | NA     | 004 |
| # Chr20:621601  | Chr20 | 621601  | 635200  | 13600  | 0.00078 | 0.0010 | 0.5844 | 0.0011 | 0.5324 | 0.0039 | 0.5230 | 177 |
| # Chr20:635201  | Chr20 | 635201  | 635300  | 100    | NA      | NA     | 0.5844 | NA     | 0.5324 | 0.0039 | 0.5230 | 027 |
| # Chr20:635301  | Chr20 | 635301  | 651100  | 15800  | NA      | NA     | 0.5844 | NA     | 0.5324 | NA     | 0.5230 | 025 |
| # Chr20:651101  | Chr20 | 651101  | 653100  | 2000   | NA      | NA     | 0.5844 | NA     | 0.5324 | 0.5435 | 0.5230 | 027 |
| # Chr20:653101  | Chr20 | 653101  | 720300  | 67200  | NA      | NA     | 0.5844 | NA     | 0.5324 | NA     | 0.5230 | 025 |
| # Chr20:720301  | Chr20 | 720301  | 720500  | 200    | NA      | NA     | 0.5844 | NA     | 0.5324 | 0.4959 | 0.5230 | 027 |
| # Chr20:720501  | Chr20 | 720501  | 722400  | 1900   | 0.60857 | 0.6822 | 0.5844 | NA     | 0.5324 | 0.4959 | 0.5230 | 167 |
| # Chr20:722401  | Chr20 | 722401  | 722500  | 100    | 0.60857 | 0.6822 | 0.5844 | NA     | NA     | NA     | 0.5230 | 161 |
| # Chr20:722501  | Chr20 | 722501  | 723200  | 700    | NA      | 0.6822 | 0.5844 | NA     | NA     | NA     | 0.5230 | 061 |
| # Chr20:723201  | Chr20 | 723201  | 728000  | 4800   | NA      | NA     | 0.5844 | NA     | NA     | NA     | 0.5230 | 021 |
| # Chr20:728001  | Chr20 | 728001  | 729800  | 1800   | NA      | NA     | 0.5844 | NA     | NA     | NA     | NA     | 020 |
| # Chr20:729801  | Chr20 | 729801  | 743100  | 13300  | NA      | NA     | 0.5844 | NA     | 0.5500 | NA     | 0.5850 | 025 |
| # Chr20:743101  | Chr20 | 743101  | 744600  | 1500   | NA      | NA     | 0.5844 | NA     | 0.5500 | NA     | NA     | 024 |
| # Chr20:744601  | Chr20 | 744601  | 748600  | 4000   | NA      | NA     | 0.5844 | NA     | 0.5500 | NA     | 0.6687 | 025 |
| # Chr20:748601  | Chr20 | 748601  | 759500  | 10900  | 0.55871 | 0.5525 | 0.5844 | NA     | 0.5500 | NA     | 0.6687 | 165 |
| # Chr20:759501  | Chr20 | 759501  | 762500  | 3000   | 0.55871 | 0.5525 | 0.5844 | NA     | 0.5500 | 0.1993 | 0.6687 | 167 |
| # Chr20:762501  | Chr20 | 762501  | 762600  | 100    | NA      | 0.5525 | 0.5844 | NA     | NA     | NA     | 0.6687 | 061 |
| # Chr20:762601  | Chr20 | 762601  | 766000  | 3400   | NA      | NA     | NA     | NA     | NA     | NA     | 0.6687 | 001 |
| # Chr20:766001  | Chr20 | 766001  | 769800  | 3800   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr20:769801  | Chr20 | 769801  | 770700  | 900    | NA      | NA     | NA     | NA     | NA     | 0.4119 | NA     | 002 |
| # Chr20:770701  | Chr20 | 770701  | 776900  | 6200   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr20:776901  | Chr20 | 776901  | 794800  | 17900  | NA      | NA     | NA     | NA     | 0.7191 | NA     | NA     | 004 |
| # Chr20:794801  | Chr20 | 794801  | 800233  | 5433   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr20:800234  | Chr20 | 800234  | 800233  | 0      | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr22:1       | Chr22 | 1       | 87300   | 87300  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr22:87301   | Chr22 | 87301   | 89500   | 2200   | NA      | NA     | 0.3984 | NA     | NA     | 0.2582 | NA     | 022 |
| # Chr22:89501   | Chr22 | 89501   | 90100   | 600    | NA      | NA     | 0.3984 | NA     | NA     | NA     | NA     | 020 |
| # Chr22:90101   | Chr22 | 90101   | 90800   | 700    | NA      | NA     | 0.3984 | NA     | NA     | 0.4093 | NA     | 022 |
| # Chr22:90801   | Chr22 | 90801   | 93800   | 3000   | NA      | NA     | 0.3984 | NA     | NA     | NA     | NA     | 020 |
| # Chr22:93801   | Chr22 | 93801   | 96700   | 2900   | NA      | NA     | 0.3984 | NA     | NA     | 0.2558 | NA     | 022 |
| # Chr22:96701   | Chr22 | 96701   | 231900  | 135200 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr22:231901  | Chr22 | 231901  | 232400  | 500    | NA      | NA     | NA     | NA     | NA     | 0.2057 | NA     | 002 |
| # Chr22:232401  | Chr22 | 232401  | 248900  | 16500  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr22:248901  | Chr22 | 248901  | 249000  | 100    | NA      | NA     | 0.4203 | NA     | NA     | NA     | NA     | 020 |
| # Chr22:249001  | Chr22 | 249001  | 250400  | 1400   | NA      | NA     | 0.4203 | NA     | NA     | 0.3847 | NA     | 022 |
| # Chr22:250401  | Chr22 | 250401  | 250500  | 100    | NA      | NA     | 0.4203 | NA     | NA     | NA     | NA     | 020 |
| # Chr22:250501  | Chr22 | 250501  | 253100  | 2600   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr22:253101  | Chr22 | 253101  | 267600  | 14500  | NA      | NA     | 0.4936 | NA     | NA     | 0.5487 | NA     | 022 |
| # Chr22:267601  | Chr22 | 267601  | 270600  | 3000   | NA      | NA     | NA     | NA     | NA     | 0.5487 | NA     | 002 |
| # Chr22:270601  | Chr22 | 270601  | 662500  | 391900 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr22:662501  | Chr22 | 662501  | 667400  | 4900   | NA      | NA     | 0.6904 | NA     | NA     | NA     | NA     | 020 |
| # Chr22:667401  | Chr22 | 667401  | 667600  | 200    | NA      | NA     | 0.6904 | 0.7342 | NA     | NA     | NA     | 030 |
| # Chr22:667601  | Chr22 | 667601  | 672800  | 5200   | NA      | 0.7449 | 0.6904 | 0.7342 | NA     | NA     | NA     | 070 |
| # Chr22:672801  | Chr22 | 672801  | 672900  | 100    | NA      | NA     | 0.6904 | 0.7342 | NA     | NA     | NA     | 030 |
| # Chr22:672901  | Chr22 | 672901  | 681400  | 8500   | NA      | NA     | 0.6904 | NA     | NA     | NA     | NA     | 020 |
| # Chr22:681401  | Chr22 | 681401  | 748700  | 67300  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr22:748701  | Chr22 | 748701  | 749500  | 800    | NA      | NA     | NA     | NA     | NA     | 0.3342 | NA     | 002 |
| # Chr22:749501  | Chr22 | 749501  | 958700  | 209200 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr22:958701  | Chr22 | 958701  | 959400  | 700    | 0.18342 | NA     | NA     | NA     | NA     | NA     | NA     | 100 |
| # Chr22:959401  | Chr22 | 959401  | 1057564 | 98164  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr22:1057565 | Chr22 | 1057565 | 1057564 | 0      | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr23:1       | Chr23 | 1       | 8900    | 8900   | 0.74762 | 0.7389 | NA     | 0.6936 | NA     | NA     | 0.5728 | 151 |
| # Chr23:8901    | Chr23 | 8901    | 9100    | 200    | NA      | 0.7389 | NA     | 0.6936 | NA     | NA     | 0.5728 | 051 |
| # Chr23:9101    | Chr23 | 9101    | 96000   | 86900  | NA      | NA     | NA     | 0.6936 | NA     | NA     | 0.5728 | 011 |
| # Chr23:96001   | Chr23 | 96001   | 190200  | 94200  | NA      | NA     | NA     | 0.6936 | NA     | NA     | NA     | 010 |
| # Chr23:190201  | Chr23 | 190201  | 305400  | 115200 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr23:305401  | Chr23 | 305401  | 307700  | 2300   | NA      | NA     | NA     | NA     | NA     | 0.7365 | NA     | 002 |
| # Chr23:307701  | Chr23 | 307701  | 341700  | 34000  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr23:341701  | Chr23 | 341701  | 342300  | 600    | NA      | NA     | NA     | NA     | NA     | 0.1968 | NA     | 002 |
| # Chr23:342301  | Chr23 | 342301  | 444400  | 102100 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr23:444401  | Chr23 | 444401  | 447900  | 3500   | NA      | NA     | 0.5290 | NA     | NA     | NA     | NA     | 020 |
| # Chr23:447901  | Chr23 | 447901  | 454953  | 7053   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr23:454954  | Chr23 | 454954  | 454953  | 0      | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr24:1       | Chr24 | 1       | 10900   | 10900  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr24:10901   | Chr24 | 10901   | 15100   | 4200   | NA      | NA     | NA     | NA     | NA     | 0.4273 | NA     | 002 |
| # Chr24:15101   | Chr24 | 15101   | 77900   | 62800  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr24:77901   | Chr24 | 77901   | 79400   | 1500   | NA      | 0.5786 | NA     | NA     | NA     | NA     | 0.5683 | 041 |
| # Chr24:79401   | Chr24 | 79401   | 149800  | 70400  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr24:149801  | Chr24 | 149801  | 150700  | 900    | NA      | NA     | NA     | NA     | NA     | 0.1683 | NA     | 002 |
| # Chr24:150701  | Chr24 | 150701  | 173700  | 23000  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr24:173701  | Chr24 | 173701  | 175500  | 1800   | NA      | NA     | NA     | NA     | NA     | 0.5089 | NA     | 002 |
| # Chr24:175501  | Chr24 | 175501  | 177800  | 2300   | NA      | NA     | 0.3913 | NA     | NA     | 0.5089 | NA     | 022 |
| # Chr24:177801  | Chr24 | 177801  | 281600  | 103800 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000 |

|                |       |         |         |         |         |        |        |        |        |        |        |        |
|----------------|-------|---------|---------|---------|---------|--------|--------|--------|--------|--------|--------|--------|
| # Chr24:281601 | Chr24 | 281601  | 281800  | 200     | NA      | NA     | 0.6952 | NA     | NA     | NA     | NA     | 020    |
| # Chr24:281801 | Chr24 | 281801  | 297348  | 15548   | NA      | NA     | 0.6952 | NA     | NA     | 0.5821 | NA     | 022    |
| # Chr24:297349 | Chr24 | 297349  | 297400  | 52      | NA      | NA     | 0.6952 | NA     | NA     | 0.5821 | NA     | 022    |
| # Chr24:297401 | Chr24 | 297401  | 297400  | 0       | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr3:1       | Chr3  | 1       | 6400    | 6400    | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr3:6401    | Chr3  | 6401    | 10000   | 3600    | NA      | NA     | NA     | NA     | NA     | NA     | 0.7222 | 001    |
| # Chr3:10001   | Chr3  | 10001   | 10100   | 100     | NA      | NA     | NA     | NA     | NA     | 0.4076 | 0.7222 | 003    |
| # Chr3:10101   | Chr3  | 10101   | 10800   | 700     | NA      | NA     | 0.1528 | NA     | NA     | 0.4076 | 0.7222 | 023    |
| # Chr3:10801   | Chr3  | 10801   | 10900   | 100     | NA      | NA     | NA     | NA     | NA     | 0.4076 | 0.7222 | 003    |
| # Chr3:10901   | Chr3  | 10901   | 98800   | 87900   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr3:98801   | Chr3  | 98801   | 99300   | 500     | NA      | NA     | NA     | NA     | NA     | NA     | 0.1087 | 001    |
| # Chr3:99301   | Chr3  | 99301   | 100800  | 1500    | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr3:100801  | Chr3  | 100801  | 102300  | 1500    | NA      | NA     | NA     | NA     | NA     | 0.4000 | NA     | 002    |
| # Chr3:102301  | Chr3  | 102301  | 425500  | 323200  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr3:425501  | Chr3  | 425501  | 426500  | 1000    | NA      | NA     | NA     | NA     | NA     | NA     | 0.7451 | 001    |
| # Chr3:426501  | Chr3  | 426501  | 426600  | 100     | NA      | NA     | NA     | NA     | NA     | 0.5717 | NA     | 0.7451 |
| # Chr3:426601  | Chr3  | 426601  | 428200  | 1600    | 0.66537 | NA     | NA     | NA     | NA     | 0.5717 | NA     | 0.7451 |
| # Chr3:428201  | Chr3  | 428201  | 430000  | 1800    | 0.66537 | NA     | NA     | NA     | NA     | NA     | 0.7451 | 101    |
| # Chr3:430001  | Chr3  | 430001  | 902400  | 472400  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr3:902401  | Chr3  | 902401  | 908200  | 5800    | NA      | NA     | NA     | NA     | NA     | 0.6913 | NA     | 002    |
| # Chr3:908201  | Chr3  | 908201  | 1272600 | 364400  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr3:1272601 | Chr3  | 1272601 | 1273400 | 800     | NA      | NA     | NA     | NA     | NA     | NA     | 0.4754 | 001    |
| # Chr3:1273401 | Chr3  | 1273401 | 1350300 | 76900   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr3:1350301 | Chr3  | 1350301 | 1353700 | 3400    | NA      | NA     | 0.6427 | NA     | NA     | NA     | NA     | 020    |
| # Chr3:1353701 | Chr3  | 1353701 | 1523200 | 169500  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr3:1523201 | Chr3  | 1523201 | 1525200 | 2000    | NA      | NA     | NA     | NA     | NA     | 0.2122 | NA     | 002    |
| # Chr3:1525201 | Chr3  | 1525201 | 1667500 | 142300  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr3:1667501 | Chr3  | 1667501 | 1669300 | 1800    | NA      | NA     | 0.4532 | NA     | NA     | NA     | NA     | 020    |
| # Chr3:1669301 | Chr3  | 1669301 | 1670000 | 700     | NA      | NA     | 0.4532 | NA     | NA     | 0.1896 | NA     | 022    |
| # Chr3:1670001 | Chr3  | 1670001 | 1670300 | 300     | NA      | NA     | 0.4532 | NA     | NA     | NA     | NA     | 020    |
| # Chr3:1670301 | Chr3  | 1670301 | 2220700 | 550400  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr3:2220701 | Chr3  | 2220701 | 2225500 | 4800    | NA      | 0.7318 | NA     | NA     | NA     | NA     | NA     | 040    |
| # Chr3:2225501 | Chr3  | 2225501 | 2373400 | 147900  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr3:2373401 | Chr3  | 2373401 | 2383300 | 9900    | NA      | NA     | 0.5446 | 0.6834 | NA     | 0.4999 | NA     | 032    |
| # Chr3:2383301 | Chr3  | 2383301 | 2383600 | 300     | NA      | NA     | 0.5446 | 0.6834 | NA     | NA     | NA     | 030    |
| # Chr3:2383601 | Chr3  | 2383601 | 2383800 | 200     | NA      | NA     | 0.6834 | NA     | NA     | NA     | NA     | 010    |
| # Chr3:2383801 | Chr3  | 2383801 | 2437800 | 54000   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr3:2437801 | Chr3  | 2437801 | 2440051 | 2251    | NA      | 0.5562 | NA     | NA     | NA     | NA     | NA     | 040    |
| # Chr3:2440052 | Chr3  | 2440052 | 2440100 | 49      | NA      | 0.5562 | NA     | NA     | NA     | NA     | NA     | 040    |
| # Chr3:2440101 | Chr3  | 2440101 | 2440100 | 0       | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr4:1       | Chr4  | 1       | 20500   | 20500   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr4:20501   | Chr4  | 20501   | 66700   | 46200   | NA      | 0.7151 | NA     | NA     | NA     | NA     | NA     | 040    |
| # Chr4:66701   | Chr4  | 66701   | 67600   | 900     | NA      | 0.7151 | NA     | NA     | NA     | 0.3865 | NA     | 042    |
| # Chr4:67601   | Chr4  | 67601   | 88400   | 20800   | NA      | 0.7151 | NA     | NA     | NA     | NA     | NA     | 040    |
| # Chr4:88401   | Chr4  | 88401   | 408300  | 319900  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr4:408301  | Chr4  | 408301  | 410500  | 2200    | NA      | NA     | NA     | NA     | NA     | 0.6633 | NA     | 002    |
| # Chr4:410501  | Chr4  | 410501  | 477800  | 67300   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr4:477801  | Chr4  | 477801  | 478600  | 800     | NA      | NA     | NA     | NA     | NA     | 0.2033 | NA     | 002    |
| # Chr4:478601  | Chr4  | 478601  | 1566900 | 1088300 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr4:1566901 | Chr4  | 1566901 | 1572600 | 5700    | NA      | NA     | NA     | NA     | 0.5966 | NA     | NA     | 004    |
| # Chr4:1572601 | Chr4  | 1572601 | 2109600 | 537000  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr4:2109601 | Chr4  | 2109601 | 2110100 | 500     | NA      | NA     | NA     | NA     | NA     | 0.2168 | NA     | 002    |
| # Chr4:2110101 | Chr4  | 2110101 | 2170100 | 60000   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr4:2170101 | Chr4  | 2170101 | 2175500 | 5400    | NA      | 0.7158 | NA     | NA     | NA     | NA     | NA     | 040    |
| # Chr4:2175501 | Chr4  | 2175501 | 2277000 | 101500  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr4:2277001 | Chr4  | 2277001 | 2281900 | 4900    | NA      | NA     | 0.6870 | NA     | NA     | NA     | NA     | 020    |
| # Chr4:2281901 | Chr4  | 2281901 | 2399800 | 117900  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr4:2399801 | Chr4  | 2399801 | 2402322 | 2522    | NA      | 0.7070 | NA     | NA     | NA     | NA     | NA     | 040    |
| # Chr4:2402323 | Chr4  | 2402323 | 2402400 | 78      | NA      | 0.7070 | NA     | NA     | NA     | NA     | NA     | 040    |
| # Chr4:2402401 | Chr4  | 2402401 | 2402400 | 0       | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr5:1       | Chr5  | 1       | 138600  | 138600  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr5:138601  | Chr5  | 138601  | 184600  | 46000   | NA      | 0.6067 | NA     | NA     | NA     | NA     | NA     | 040    |
| # Chr5:184601  | Chr5  | 184601  | 346400  | 161800  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr5:346401  | Chr5  | 346401  | 353000  | 6600    | 0.60350 | NA     | NA     | NA     | NA     | NA     | NA     | 100    |
| # Chr5:353001  | Chr5  | 353001  | 919700  | 566700  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr5:919701  | Chr5  | 919701  | 920500  | 800     | NA      | 0.6989 | NA     | NA     | NA     | NA     | NA     | 040    |
| # Chr5:920501  | Chr5  | 920501  | 924700  | 4200    | NA      | 0.6989 | NA     | NA     | NA     | 0.5149 | NA     | 042    |
| # Chr5:924701  | Chr5  | 924701  | 926000  | 1300    | NA      | 0.6989 | NA     | NA     | NA     | NA     | NA     | 040    |
| # Chr5:926001  | Chr5  | 926001  | 1323500 | 397500  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr5:1323501 | Chr5  | 1323501 | 1330800 | 7300    | NA      | NA     | NA     | NA     | NA     | 0.7200 | NA     | 002    |
| # Chr5:1330801 | Chr5  | 1330801 | 1967700 | 636900  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr5:1967701 | Chr5  | 1967701 | 1971700 | 4000    | NA      | NA     | NA     | NA     | 0.7424 | NA     | 002    |        |
| # Chr5:1971701 | Chr5  | 1971701 | 1976300 | 4600    | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr5:1976301 | Chr5  | 1976301 | 1977500 | 1200    | NA      | NA     | NA     | NA     | NA     | 0.5857 | 001    |        |
| # Chr5:1977501 | Chr5  | 1977501 | 2049700 | 72200   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr5:2049701 | Chr5  | 2049701 | 2053600 | 3900    | NA      | NA     | NA     | NA     | NA     | 0.4930 | NA     | 002    |
| # Chr5:2053601 | Chr5  | 2053601 | 2305971 | 252371  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr5:2305972 | Chr5  | 2305972 | 2305971 | 0       | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr6:1       | Chr6  | 1       | 100     | 100     | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr6:101     | Chr6  | 101     | 600     | 500     | 0.22714 | NA     | NA     | NA     | 0.1551 | NA     | NA     | 104    |

|                |      |         |         |        |         |        |        |        |        |        |        |        |
|----------------|------|---------|---------|--------|---------|--------|--------|--------|--------|--------|--------|--------|
| # Chr6:601     | Chr6 | 601     | 3100    | 2500   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr6:3101    | Chr6 | 3101    | 3200    | 100    | NA      | 0.6326 | NA     | NA     | NA     | NA     | NA     | 040    |
| # Chr6:3201    | Chr6 | 3201    | 3300    | 100    | NA      | 0.6326 | 0.3177 | NA     | NA     | NA     | NA     | 060    |
| # Chr6:3301    | Chr6 | 3301    | 5500    | 2200   | NA      | 0.6326 | 0.3177 | NA     | NA     | 0.5983 | NA     | 062    |
| # Chr6:5501    | Chr6 | 5501    | 5600    | 100    | NA      | 0.6326 | NA     | NA     | NA     | NA     | NA     | 040    |
| # Chr6:5601    | Chr6 | 5601    | 9600    | 4000   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr6:9601    | Chr6 | 9601    | 28800   | 19200  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 0.6078 |
| # Chr6:28801   | Chr6 | 28801   | 29000   | 200    | NA      | NA     | 0.7084 | NA     | NA     | NA     | NA     | 0.6078 |
| # Chr6:29001   | Chr6 | 29001   | 29900   | 900    | NA      | NA     | 0.6397 | 0.7084 | NA     | NA     | 0.6078 | 031    |
| # Chr6:29901   | Chr6 | 29901   | 104900  | 75000  | NA      | NA     | 0.6397 | 0.7084 | 0.5929 | NA     | 0.6078 | 035    |
| # Chr6:104901  | Chr6 | 104901  | 105500  | 600    | NA      | NA     | 0.6397 | 0.7084 | 0.5929 | 0.1851 | 0.6078 | 037    |
| # Chr6:105501  | Chr6 | 105501  | 165900  | 60400  | NA      | NA     | 0.6397 | 0.7084 | 0.5929 | NA     | 0.6078 | 035    |
| # Chr6:165901  | Chr6 | 165901  | 168400  | 2500   | NA      | NA     | 0.6397 | 0.7084 | NA     | NA     | NA     | 030    |
| # Chr6:168401  | Chr6 | 168401  | 169100  | 700    | NA      | NA     | 0.7084 | NA     | NA     | NA     | NA     | 010    |
| # Chr6:169101  | Chr6 | 169101  | 174400  | 5300   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr6:174401  | Chr6 | 174401  | 174500  | 100    | NA      | NA     | 0.5916 | NA     | NA     | NA     | NA     | 020    |
| # Chr6:174501  | Chr6 | 174501  | 176600  | 2100   | NA      | 0.5885 | 0.5916 | 0.7085 | 0.6110 | NA     | 0.5815 | 075    |
| # Chr6:176601  | Chr6 | 176601  | 181700  | 5100   | NA      | NA     | 0.5916 | 0.7085 | 0.6110 | NA     | 0.5815 | 035    |
| # Chr6:181701  | Chr6 | 181701  | 268500  | 86800  | NA      | NA     | 0.7085 | 0.6110 | NA     | 0.5815 | 015    |        |
| # Chr6:268501  | Chr6 | 268501  | 272600  | 4100   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr6:272601  | Chr6 | 272601  | 272900  | 300    | NA      | NA     | NA     | NA     | 0.5859 | NA     | 0.5885 | 005    |
| # Chr6:272901  | Chr6 | 272901  | 346300  | 73400  | NA      | NA     | NA     | NA     | 0.6853 | 0.5859 | NA     | 0.5885 |
| # Chr6:346301  | Chr6 | 346301  | 346500  | 200    | NA      | NA     | 0.6853 | NA     | NA     | 0.5885 | 011    |        |
| # Chr6:346501  | Chr6 | 346501  | 347000  | 500    | NA      | NA     | 0.6853 | NA     | NA     | NA     | NA     | 010    |
| # Chr6:347001  | Chr6 | 347001  | 660300  | 313300 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr6:660301  | Chr6 | 660301  | 661300  | 1000   | NA      | NA     | NA     | NA     | NA     | 0.3881 | NA     | 002    |
| # Chr6:661301  | Chr6 | 661301  | 771500  | 110200 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr6:771501  | Chr6 | 771501  | 774700  | 3200   | NA      | NA     | NA     | NA     | NA     | NA     | 0.6927 | 001    |
| # Chr6:774701  | Chr6 | 774701  | 1011200 | 236500 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr6:1011201 | Chr6 | 1011201 | 1018400 | 7200   | NA      | NA     | NA     | 0.7391 | NA     | NA     | NA     | 010    |
| # Chr6:1018401 | Chr6 | 1018401 | 1933900 | 915500 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr6:1933901 | Chr6 | 1933901 | 1939500 | 5600   | NA      | NA     | 0.6457 | NA     | NA     | NA     | NA     | 020    |
| # Chr6:1939501 | Chr6 | 1939501 | 1940700 | 1200   | NA      | 0.6619 | 0.6457 | NA     | NA     | NA     | NA     | 060    |
| # Chr6:1940701 | Chr6 | 1940701 | 1942200 | 1500   | NA      | 0.6619 | 0.6457 | NA     | NA     | 0.1729 | NA     | 062    |
| # Chr6:1942201 | Chr6 | 1942201 | 1942300 | 100    | NA      | NA     | 0.6457 | NA     | NA     | 0.1729 | NA     | 022    |
| # Chr6:1942301 | Chr6 | 1942301 | 1997500 | 55200  | NA      | NA     | 0.6457 | NA     | NA     | NA     | NA     | 020    |
| # Chr6:1997501 | Chr6 | 1997501 | 2010600 | 13100  | NA      | NA     | 0.6457 | NA     | 0.6525 | NA     | NA     | 024    |
| # Chr6:2010601 | Chr6 | 2010601 | 2018600 | 8000   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr6:2018601 | Chr6 | 2018601 | 2033200 | 14600  | NA      | NA     | 0.7148 | NA     | NA     | NA     | NA     | 020    |
| # Chr6:2033201 | Chr6 | 2033201 | 2033300 | 100    | NA      | NA     | 0.7148 | NA     | NA     | 0.6636 | NA     | 022    |
| # Chr6:2033301 | Chr6 | 2033301 | 2035100 | 1800   | NA      | 0.6739 | 0.7148 | NA     | NA     | 0.6636 | NA     | 062    |
| # Chr6:2035101 | Chr6 | 2035101 | 2035400 | 300    | NA      | 0.6739 | NA     | NA     | NA     | 0.6636 | NA     | 042    |
| # Chr6:2035401 | Chr6 | 2035401 | 2038700 | 3300   | 0.30376 | 0.6739 | NA     | NA     | NA     | 0.6636 | NA     | 142    |
| # Chr6:2038701 | Chr6 | 2038701 | 2041700 | 3000   | NA      | NA     | NA     | NA     | NA     | 0.6636 | NA     | 002    |
| # Chr6:2041701 | Chr6 | 2041701 | 2060300 | 18600  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr6:2060301 | Chr6 | 2060301 | 2060500 | 200    | NA      | NA     | NA     | NA     | 0.2417 | NA     | NA     | 004    |
| # Chr6:2060501 | Chr6 | 2060501 | 2061400 | 900    | 0.15674 | NA     | NA     | NA     | 0.2417 | NA     | NA     | 104    |
| # Chr6:2061401 | Chr6 | 2061401 | 2061500 | 100    | NA      | NA     | NA     | NA     | 0.2417 | NA     | NA     | 004    |
| # Chr6:2061501 | Chr6 | 2061501 | 2071479 | 9979   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr6:2071480 | Chr6 | 2071480 | 2071479 | 0      | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr7:1       | Chr7 | 1       | 116800  | 116800 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr7:116801  | Chr7 | 116801  | 134600  | 17800  | 0.61034 | 0.5826 | NA     | NA     | NA     | NA     | NA     | 140    |
| # Chr7:134601  | Chr7 | 134601  | 136100  | 1500   | 0.61034 | NA     | NA     | NA     | NA     | NA     | NA     | 100    |
| # Chr7:136101  | Chr7 | 136101  | 467700  | 331600 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr7:467701  | Chr7 | 467701  | 472700  | 5000   | NA      | NA     | NA     | NA     | 0.7434 | NA     | NA     | 002    |
| # Chr7:472701  | Chr7 | 472701  | 481400  | 8700   | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr7:481401  | Chr7 | 481401  | 481600  | 200    | NA      | NA     | NA     | NA     | 0.7114 | NA     | NA     | 004    |
| # Chr7:481601  | Chr7 | 481601  | 481800  | 200    | NA      | 0.6239 | NA     | NA     | 0.7114 | NA     | NA     | 044    |
| # Chr7:481801  | Chr7 | 481801  | 483500  | 1700   | NA      | 0.6239 | 0.3750 | NA     | 0.7114 | 0.3871 | NA     | 066    |
| # Chr7:483501  | Chr7 | 483501  | 483600  | 100    | NA      | 0.6239 | 0.3750 | NA     | 0.7114 | NA     | NA     | 064    |
| # Chr7:484601  | Chr7 | 484601  | 484600  | 1000   | NA      | NA     | NA     | NA     | 0.7114 | NA     | NA     | 004    |
| # Chr7:484601  | Chr7 | 484601  | 755900  | 271300 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr7:755901  | Chr7 | 755901  | 758200  | 2300   | NA      | 0.7004 | NA     | NA     | NA     | NA     | NA     | 040    |
| # Chr7:758201  | Chr7 | 758201  | 849500  | 91300  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr7:849501  | Chr7 | 849501  | 852700  | 3200   | NA      | NA     | 0.7317 | NA     | NA     | NA     | NA     | 020    |
| # Chr7:852701  | Chr7 | 852701  | 1001800 | 149100 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr7:1001801 | Chr7 | 1001801 | 1009400 | 7600   | NA      | 0.7346 | NA     | NA     | NA     | NA     | NA     | 040    |
| # Chr7:1009401 | Chr7 | 1009401 | 1522100 | 512700 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr7:1522101 | Chr7 | 1522101 | 1546000 | 23900  | NA      | NA     | NA     | 0.6641 | NA     | NA     | NA     | 010    |
| # Chr7:1546001 | Chr7 | 1546001 | 1785900 | 239900 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr7:1785901 | Chr7 | 1785901 | 1788700 | 2800   | NA      | NA     | NA     | NA     | NA     | 0.2063 | NA     | 002    |
| # Chr7:1788701 | Chr7 | 1788701 | 1992433 | 203733 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr7:1992434 | Chr7 | 1992434 | 1992433 | 0      | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr8:1       | Chr8 | 1       | 115200  | 115200 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr8:115201  | Chr8 | 115201  | 116800  | 1600   | NA      | NA     | 0.6390 | NA     | NA     | NA     | NA     | 020    |
| # Chr8:116801  | Chr8 | 116801  | 207800  | 91000  | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |
| # Chr8:207801  | Chr8 | 207801  | 208000  | 200    | NA      | 0.6655 | NA     | NA     | NA     | NA     | NA     | 040    |
| # Chr8:208001  | Chr8 | 208001  | 211500  | 3500   | 0.67456 | 0.6655 | NA     | NA     | NA     | NA     | NA     | 140    |
| # Chr8:211501  | Chr8 | 211501  | 211800  | 300    | 0.67456 | NA     | NA     | NA     | NA     | NA     | NA     | 100    |
| # Chr8:211801  | Chr8 | 211801  | 606200  | 394400 | NA      | NA     | NA     | NA     | NA     | NA     | NA     | 000    |

|                |      |         |         |        |    |        |        |        |        |        |        |     |
|----------------|------|---------|---------|--------|----|--------|--------|--------|--------|--------|--------|-----|
| # Chr8:606201  | Chr8 | 606201  | 608100  | 1900   | NA | 0.5653 | NA     | NA     | NA     | NA     | NA     | 040 |
| # Chr8:608101  | Chr8 | 608101  | 691700  | 83600  | NA | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr8:691701  | Chr8 | 691701  | 831700  | 140000 | NA | NA     | NA     | 0.6929 | NA     | NA     | NA     | 010 |
| # Chr8:831701  | Chr8 | 831701  | 846800  | 15100  | NA | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr8:846801  | Chr8 | 846801  | 864200  | 17400  | NA | NA     | NA     | 0.6139 | NA     | NA     | NA     | 010 |
| # Chr8:864201  | Chr8 | 864201  | 869000  | 4800   | NA | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr8:869001  | Chr8 | 869001  | 869100  | 100    | NA | NA     | NA     | NA     | NA     | NA     | 0.5582 | 001 |
| # Chr8:869101  | Chr8 | 869101  | 872800  | 3700   | NA | 0.5039 | NA     | NA     | NA     | 0.1225 | 0.5582 | 043 |
| # Chr8:872801  | Chr8 | 872801  | 873300  | 500    | NA | NA     | NA     | NA     | NA     | NA     | 0.5582 | 001 |
| # Chr8:873301  | Chr8 | 873301  | 1005100 | 131800 | NA | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr8:1005101 | Chr8 | 1005101 | 1006900 | 1800   | NA | NA     | NA     | NA     | NA     | 0.3940 | NA     | 002 |
| # Chr8:1006901 | Chr8 | 1006901 | 1242600 | 235700 | NA | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr8:1242601 | Chr8 | 1242601 | 1242800 | 200    | NA | 0.5885 | NA     | NA     | NA     | NA     | NA     | 040 |
| # Chr8:1242801 | Chr8 | 1242801 | 1244300 | 1500   | NA | 0.5885 | 0.2484 | NA     | NA     | NA     | NA     | 060 |
| # Chr8:1244301 | Chr8 | 1244301 | 1244800 | 500    | NA | 0.5885 | NA     | NA     | NA     | NA     | NA     | 040 |
| # Chr8:1244801 | Chr8 | 1244801 | 1267197 | 22397  | NA | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr8:1267198 | Chr8 | 1267198 | 1267197 | 0      | NA | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr9:1       | Chr9 | 1       | 3900    | 3900   | NA | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr9:3901    | Chr9 | 3901    | 5700    | 1800   | NA | NA     | NA     | NA     | 0.4305 | NA     | NA     | 004 |
| # Chr9:5701    | Chr9 | 5701    | 391400  | 385700 | NA | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr9:391401  | Chr9 | 391401  | 392800  | 1400   | NA | NA     | 0.3381 | NA     | NA     | NA     | NA     | 020 |
| # Chr9:392801  | Chr9 | 392801  | 394400  | 1600   | NA | NA     | 0.3381 | NA     | NA     | 0.2303 | NA     | 022 |
| # Chr9:394401  | Chr9 | 394401  | 395200  | 800    | NA | NA     | 0.3381 | NA     | NA     | NA     | NA     | 020 |
| # Chr9:395201  | Chr9 | 395201  | 463400  | 68200  | NA | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr9:463401  | Chr9 | 463401  | 465500  | 2100   | NA | NA     | NA     | NA     | 0.6534 | NA     | 002    |     |
| # Chr9:465501  | Chr9 | 465501  | 776000  | 310500 | NA | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr9:776001  | Chr9 | 776001  | 776400  | 400    | NA | NA     | NA     | NA     | 0.7230 | NA     | NA     | 004 |
| # Chr9:776401  | Chr9 | 776401  | 780200  | 3800   | NA | 0.6961 | NA     | 0.6979 | 0.7230 | NA     | NA     | 054 |
| # Chr9:780201  | Chr9 | 780201  | 780300  | 100    | NA | 0.6961 | NA     | NA     | 0.7230 | NA     | NA     | 044 |
| # Chr9:780301  | Chr9 | 780301  | 1137600 | 357300 | NA | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr9:1137601 | Chr9 | 1137601 | 1138100 | 500    | NA | NA     | NA     | NA     | 0.2027 | NA     | 002    |     |
| # Chr9:1138101 | Chr9 | 1138101 | 1139300 | 1200   | NA | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr9:1139301 | Chr9 | 1139301 | 1182700 | 43400  | NA | NA     | NA     | NA     | 0.6168 | NA     | NA     | 004 |
| # Chr9:1182701 | Chr9 | 1182701 | 1183700 | 1000   | NA | NA     | NA     | NA     | NA     | NA     | NA     | 000 |
| # Chr9:1183701 | Chr9 | 1183701 | 1191059 | 7359   | NA | NA     | NA     | NA     | 0.3294 | NA     | NA     | 004 |
| # Chr9:1191060 | Chr9 | 1191060 | 1191100 | 41     | NA | NA     | NA     | NA     | 0.3294 | NA     | NA     | 004 |
| # Chr9:1191101 | Chr9 | 1191101 | 1191100 | 0      | NA | NA     | NA     | NA     | NA     | NA     | NA     | 000 |

A few examples. There are few hemi regions shared by all 7; one of them is this segment on chr15, which is below 2% of average coverage in *all seven*, suggesting an assembly error in 1335. (The in/exclusion of the previous 200bp may just be vagaries of CNVnators binning choices.) There are some other regions that look similar.

|  |         |        |        |        |            |            |            |           |            |           |            |
|--|---------|--------|--------|--------|------------|------------|------------|-----------|------------|-----------|------------|
| show.hemi <- function(chr.pos,krows){  |         |        |        |        |            |            |            |           |            |           |            |
| j <- match(chr.pos,rownames(hemi.tab)) |         |        |        |        |            |            |            |           |            |           |            |
| hemi.tab[j:(j+krows-1),]               |         |        |        |        |            |            |            |           |            |           |            |
| }                                      |         |        |        |        |            |            |            |           |            |           |            |
| show.hemi('Chr15:246801',5)            |         |        |        |        |            |            |            |           |            |           |            |
| #                                      | chr     | start  | end    | length | tp1007     | tp1012     | tp1013     | tp1014    | tp1015     | IT        | tp1335     |
| # Chr15:246801                         | Chr15   | 246801 | 250800 | 4000   | NA         | NA         | NA         | NA        | NA         | NA        | NA         |
| # Chr15:250801                         | Chr15   | 250801 | 250900 | 100    | NA         | NA         | NA         | 0.0151399 | NA         | NA        | NA         |
| # Chr15:250901                         | Chr15   | 250901 | 251000 | 100    | 0.00773855 | NA         | 0.00689837 | 0.0151399 | 0.00834229 | 0.0110226 | 0.00887539 |
| # Chr15:251001                         | Chr15   | 251001 | 262700 | 11700  | 0.00773855 | 0.00259322 | 0.00689837 | 0.0151399 | 0.00834229 | 0.0110226 | 0.00887539 |
| # Chr15:262701                         | Chr15   | 262701 | 434900 | 172200 | NA         | NA         | NA         | NA        | NA         | NA        | NA         |
| #                                      | pattern |        |        |        |            |            |            |           |            |           |            |
| # Chr15:246801                         |         | 000    |        |        |            |            |            |           |            |           |            |
| # Chr15:250801                         |         | 010    |        |        |            |            |            |           |            |           |            |
| # Chr15:250901                         |         | 137    |        |        |            |            |            |           |            |           |            |
| # Chr15:251001                         |         | 177    |        |        |            |            |            |           |            |           |            |
| # Chr15:262701                         |         | 000    |        |        |            |            |            |           |            |           |            |

I often see (mostly) “nested” patterns, like the one below: a large loss in 1335, a shorter but largely overlapping loss in 1014, shorter still in 1013, shorter still in 1015, and a very short one in IT. Shared ancestry may explain some of the shared deletion, but it seems likely that “fragile sites” (e.g., perhaps repetitive DNA) in this region of the genome (or just luck) have allowed independent expansions around the shared deletions in the different cultures.

|                           |      |        |        |        |        |        |        |          |          |          |          |         |
|---------------------------|------|--------|--------|--------|--------|--------|--------|----------|----------|----------|----------|---------|
| show.hemi('Chr6:5601',10) |      |        |        |        |        |        |        |          |          |          |          |         |
| #                         | chr  | start  | end    | length | tp1007 | tp1012 | tp1013 | tp1014   | tp1015   | IT       | tp1335   | pattern |
| # Chr6:5601               | Chr6 | 5601   | 9600   | 4000   | NA     | NA     | NA     | NA       | NA       | NA       | NA       | 00      |
| # Chr6:9601               | Chr6 | 9601   | 28800  | 19200  | NA     | NA     | NA     | NA       | NA       | NA       | 0.607829 | 01      |
| # Chr6:28801              | Chr6 | 28801  | 29000  | 200    | NA     | NA     | NA     | 0.708383 | NA       | NA       | 0.607829 | 11      |
| # Chr6:29001              | Chr6 | 29001  | 29900  | 900    | NA     | NA     | 0.6397 | 0.708383 | NA       | NA       | 0.607829 | 31      |
| # Chr6:29901              | Chr6 | 29901  | 104900 | 75000  | NA     | NA     | 0.6397 | 0.708383 | 0.592855 | NA       | 0.607829 | 35      |
| # Chr6:104901             | Chr6 | 104901 | 105500 | 600    | NA     | NA     | 0.6397 | 0.708383 | 0.592855 | 0.185099 | 0.607829 | 37      |

|               |      |        |        |       |    |    |        |          |          |    |          |    |
|---------------|------|--------|--------|-------|----|----|--------|----------|----------|----|----------|----|
| # Chr6:105501 | Chr6 | 105501 | 165900 | 60400 | NA | NA | 0.6397 | 0.708383 | 0.592855 | NA | 0.607829 | 35 |
| # Chr6:165901 | Chr6 | 165901 | 168400 | 2500  | NA | NA | 0.6397 | 0.708383 | NA       | NA | NA       | 30 |
| # Chr6:168401 | Chr6 | 168401 | 169100 | 700   | NA | NA | NA     | 0.708383 | NA       | NA | NA       | 10 |
| # Chr6:169101 | Chr6 | 169101 | 174400 | 5300  | NA | NA | NA     | NA       | NA       | NA | NA       | 00 |

From shared-snps:

```
tobitvec <- function(x) {
  bitvec <- integer(7)
  for(i in 7:1){
    bitvec[i] <- x %% 2
    x <- x %/% 2
  }
  return(bitvec)
}

flg <- function(x){
  return(ifelse(x==1, 'X', ''))
}

pat.summary <- function(listOfTbls){
  mydf <- data.frame(pat=0:127, sharedBy=NA,
                      tp1007='', tp1012='', tp1013='', tp1014='', tp1015='', tp3367='', tp1335='',
                      count1=NA, count2=NA, count3=NA, stringsAsFactors=F)

  for(i in 1:128){
    bvec <- tobitvec(i-1)
    mydf[i, 'sharedBy']=sum(bvec)
    mydf[i, 'tp1007']=flg(bvec[1])
    mydf[i, 'tp1012']=flg(bvec[2])
    mydf[i, 'tp1013']=flg(bvec[3])
    mydf[i, 'tp1014']=flg(bvec[4])
    mydf[i, 'tp1015']=flg(bvec[5])
    mydf[i, 'tp3367']=flg(bvec[6])
    mydf[i, 'tp1335']=flg(bvec[7])
  }

  for(i in 1:length(listOfTbls)){
    tbl <- listOfTbls[[i]]
    if(!is.null(tbl)){
      mydf[,9+i] <- tbl[,2] ## count1/2/3 are columns 10/11/12 in mydf
      #for(j in 1:length(tbl)){
      #  k <- as.integer(rownames(tbl)[j]);
      #  mydf[k+1,9+i] <- tbl[j] ## count1/2/3 are columns 10/11/12
      #}
    }
  }

  mydf$pat <-as.octmode(mydf$pat) # display bit pattern in octal
  return(mydf)
}

pat.summaries <- pat.summary(list(NULL, bp.by.pat, NULL))
```

```
# Show a subset of pat.summaries, optionally with totals of count_i in last row, and optionally
# aggregating low-count rows as ``Other''
#
#   sharedBy=c(2,4) selects SNPs shared by 2 or 4 strains,
#   subset=as.octmode('35') select those with sharing pattern a subset (optionally proper) of this
#   split=as.octmode('14') additionally restricts to patterns stradling split/subset minus split
#   c2.thresh=42 suppresses printout of rows with count2 < 42
showgroup <- function(p.summ=pat.summaries, sharedBy=0:7, subset=127, split=NULL, proper.subset=F,
                      total=T, c2.thresh=0, thirteenth=F){
  # pick just those bit patterns that are subsets of 'subset'
  pick <- bitwAnd(0:127, bitwNot(subset))==0
  if(proper.subset){
    pick[subset+1] <- F
  }
  if(total){
```

```

}
if(!is.null(split)){ # AND that straddle left/right subtrees
  cosplit <- bitwAnd(subset,bitwNot(split))
  pick <- pick & bitwAnd(0:127,split)!=0 & bitwAnd(0:127,cosplit)!=0
}
# and have desired shareBy counts
pick <- pick & (p.summ$sharedBy %in% sharedBy)
pick.low <- pick & (p.summ$count2 < c2.thresh)
show <- p.summ[pick & !pick.low,]
# rename columns just to narrow the printouts
colnames(show) <- c('Pat','ShrBy','1007', '1012', '1013', '1014', '1015', '3367', '1335',
  'count1', 'count2', 'count3')
show[,1] <- format(show[,1]) # convert octal col to char so can override in last row(2)
nlow <- sum(pick.low)
if(nlow > 0){
  n <- nrow(show)+1
  lows <- apply(p.summ[pick.low,10:12],2,sum)
  show[n,10:12] <- lows
  show[n,1:9] <- ''
  row.names(show)[n] <- 'Other'
  if(thirteenth){
    # do this: add 13th col just to hold this comment:
    show <- cbind(show, '=' , stringsAsFactors=F)
    show[n,13] <- paste('(', nlow, 'rows w/ c2 <', c2.thresh, ')')
  } else {
    ## or this (looks a bit funky, but fits across page without line-wrap):
    show[n,1:8] <-c('(', nlow, 'rows', 'w/', 'c2', '<', c2.thresh, ')')
  }
}
if(total){
  n <- nrow(show)+1
  tots <- apply(show[,10:12],2,sum)
  show[n,10:12] <- tots
  show[n,1:9] <- ''
  row.names(show)[n] <- 'Total'
  if(ncol(show)==13){show[n,13]<-''}
}
return(show)
}

```

analysis akin to shared-snps:

```

showgroup(sharedBy=0)

#      Pat ShrBy 1007 1012 1013 1014 1015 3367 1335 count1  count2 count3
# 1      0      0                               NA 27050421      NA
# Total                           NA 27050421      NA

showgroup(sharedBy=1)

#      Pat ShrBy 1007 1012 1013 1014 1015 3367 1335 count1  count2 count3
# 2      001      1                               X  NA 40100      NA
# 3      002      1                               X  NA 162100     NA
# 5      004      1                               X  NA 89800      NA
# 9      010      1                               X  NA 309300     NA
# 17     020      1                               X  NA 843400     NA
# 33     040      1                               X  NA 197000     NA
# 65     100      1      X  NA 88700      NA
# Total                           NA 1730400     NA

showgroup(sharedBy=2, c2.thresh=15000)

#      Pat ShrBy 1007 1012 1013 1014 1015 3367 1335 count1  count2 count3
# 10     011      2                               X  X  NA 93100      NA
# 18     021      2                               X  X  NA 30400      NA
# 19     022      2                               X  X  NA 121600     NA
# 97     140      2      X  X  NA 798600     NA
# Other   (      17 rows  w/  c2  < 15000  )  NA 54900      NA
# Total                           NA 1098600     NA

```

```

showgroup(sharedBy=3, c2.thresh=15000)

#      Pat ShrBy 1007 1012 1013 1014  1015 3367 1335 count1 count2 count3
# 14    015     3           X     X     X NA 264800   NA
# 22    025     3           X     X     X NA 134300   NA
# 98    141     3     X   X           X NA 186400   NA
# 105   150     3     X   X           X NA 15600    NA
# 113   160     3     X   X   X       NA 19900    NA
# Other ( 30 rows w/ c2 < 15000 ) NA 85000    NA
# Total                           NA 706000   NA

showgroup(sharedBy=4, c2.thresh=15000)

#      Pat ShrBy 1007 1012 1013 1014  1015 3367 1335 count1 count2 count3
# 30    035     4           X     X     X NA 140500   NA
# 78    115     4     X           X     X NA 22500    NA
# 102   145     4     X   X           X NA 46300    NA
# 106   151     4     X   X           X NA 258500   NA
# Other ( 31 rows w/ c2 < 15000 ) NA 24700    NA
# Total                           NA 492500   NA

showgroup(sharedBy=5, c2.thresh=15000)

#      Pat ShrBy 1007 1012 1013 1014  1015 3367 1335 count1 count2 count3
# 110   155     5     X   X           X     X     X NA 158100   NA
# Other ( 20 rows w/ c2 < 15000 ) NA 29400    NA
# Total                           NA 187500   NA

showgroup(sharedBy=6, c2.thresh=15000)

#      Pat ShrBy 1007 1012 1013 1014  1015 3367 1335 count1 count2 count3
# Other ( 7 rows w/ c2 < 15000 ) NA 9700    NA
# Total                           NA 9700    NA

showgroup(sharedBy=7, c2.thresh=15000)

#      Pat ShrBy 1007 1012 1013 1014  1015 3367 1335 count1 count2 count3
# 128   177     7     X   X   X     X     X     X NA 26900    NA
# Total                           NA 26900   NA

```

This data does not seem to follow the snp tree, nor do private deletions show a t-i-c trend.

Another tack: look at Cov % vs strain.

```

library(compactr)

plt.hemi <- function(bins = 50, logy=F, debug=F){
  opar <- par(mfrow=c(4,2),mar=c(0,0,1,.5),oma=c(3,4,1,0)); on.exit(par(opar))
  bin.upper <- (1:bins)/bins
  bin.range <- c('[0]', paste('(', c(0,bin.upper[-bins]), ', ', bin.upper, ')', sep=''))
  hh <- matrix(0, bins+1, 7, dimnames=list(bin.range, strain.names))
  for(i in 1:nrow(hemi.tab)){
    for(j in 1:7){
      if(!is.na(hemi.tab[i,j+4])){
        hh[1+ceiling(bins*hemi.tab[i,j+4]),j] <-
          hh[1+ceiling(bins*hemi.tab[i,j+4]),j] + hemi.tab$length[i]
      }
    }
    #print(hh);print(logy)
    for(i in 1:7){
      if(floor(i/2)*2 < i){
        ymx <- max(hh[,unique(c(i,min(7,i+1)))])
      }
      eplot(xlim=c(0,1), ylim=c(0,ifelse(logy,log2(ymx),ymx)),main=st.loc(i,date=T))
      xx <- c(0,1/(2*bins)+seq(from=0, by=1/bins,length.out=bins))
      yy <- hh[,i]
      if(logy){

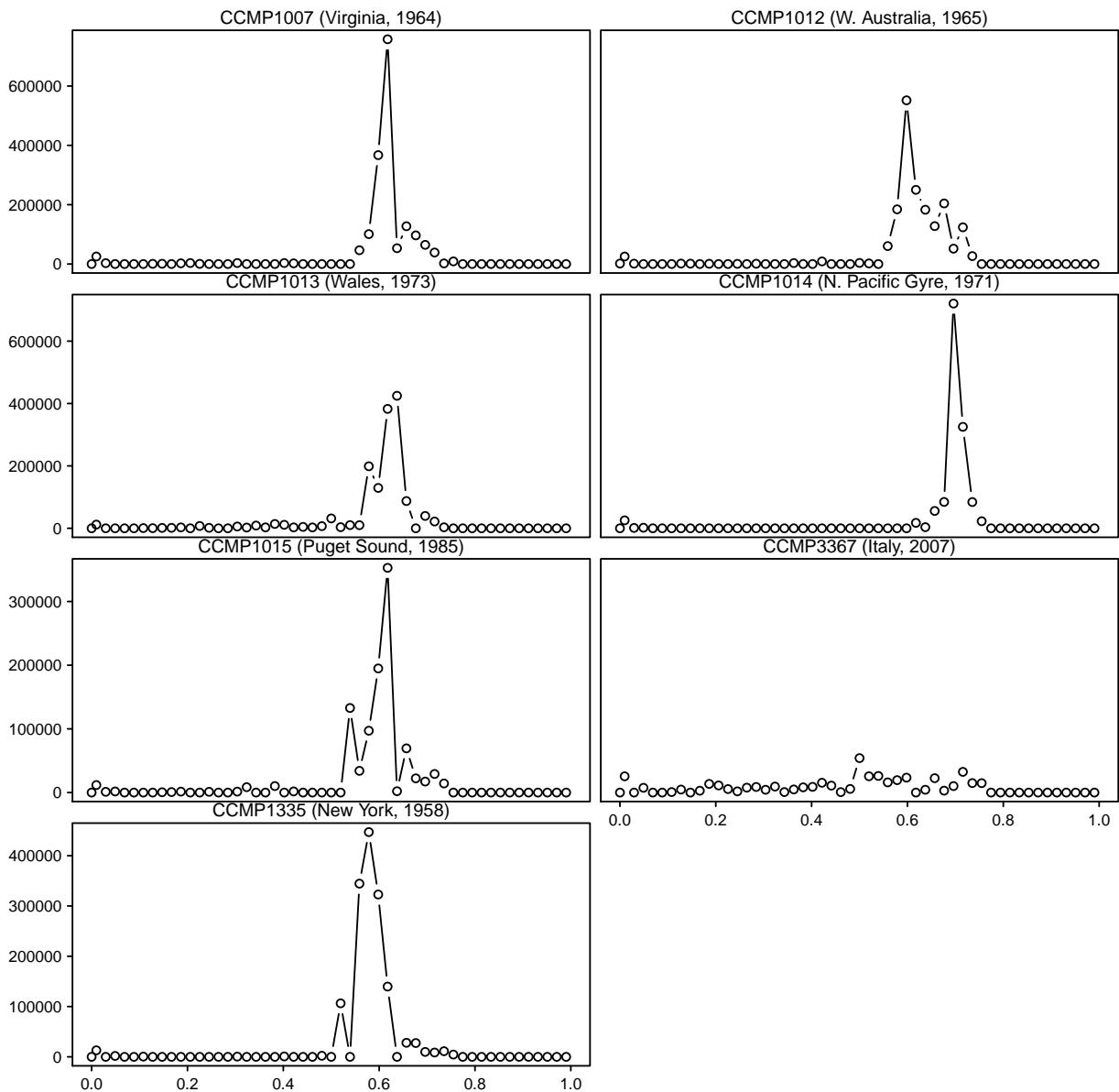
```

```

        yy <- log2(1+yy)
    }
    points(xx, yy, type='b')
    if(i==6){addxaxis()}
}
if(debug){return(rbind(hh,Tot=colSums(hh)))}
}
plt.hemi(bins=51,debug=T)

#
# tp1007 tp1012 tp1013 tp1014 tp1015 IT tp1335
# [0]      0   1600     0     0     0     0     0     0
# (0, 0.0196078431372549] 25400  25300  11800  25500  11800  25500  13000
# (0.0196078431372549, 0.0392156862745098] 2900   1200     0   1200   1200     0     0
# (0.0392156862745098, 0.0588235294117647] 0       0     0   1800   1700   7500   1800
# (0.0588235294117647, 0.0784313725490196] 0       0     0     0     0     0     0
# (0.0784313725490196, 0.0980392156862745] 0       0     0     0     0     0     0
# (0.0980392156862745, 0.117647058823529] 0       0     600     0     0     800   500
# (0.117647058823529, 0.137254901960784] 600    1500   400     0     0   4700     0
# (0.137254901960784, 0.156862745098039] 900    1200   1200     0   500     0     0
# (0.156862745098039, 0.176470588235294] 0       0   1400     0   800   2900     0
# (0.176470588235294, 0.196078431372549] 2400   800    2800     0   1500   13600     0
# (0.196078431372549, 0.215686274509804] 3300   0       0     0     0   11200     0
# (0.215686274509804, 0.235294117647059] 500    0       7400     0     0   5500     0
# (0.235294117647059, 0.254901960784314] 0       500   1500     0   1200   1900     0
# (0.254901960784314, 0.274509803921569] 0       0       0     0     0   7700     0
# (0.274509803921569, 0.294117647058824] 0       1000     0     0     0   8800     0
# (0.294117647058824, 0.313725490196078] 3300   0       5800     0   1500   4400   500
# (0.313725490196078, 0.333333333333333] 0       0   2300     0   8500   9400     0
# (0.333333333333333, 0.352941176470588] 0       0   8800     0     0   800     0
# (0.352941176470588, 0.372549019607843] 0       3200   2900     0     0   4900     0
# (0.372549019607843, 0.392156862745098] 0       0   13900     0   10200   8200     0
# (0.392156862745098, 0.411764705882353] 3300   0   11200     0     0   9000   800
# (0.411764705882353, 0.431372549019608] 2200   8800   2900     0   1800   15400     0
# (0.431372549019608, 0.450980392156863] 0       0   4500     0     0   10900     0
# (0.450980392156863, 0.470588235294118] 0       0   2800     0     0   700     0
# (0.470588235294118, 0.490196078431373] 0       0   6900     0     0   5700   2100
# (0.490196078431373, 0.509803921568627] 0       3700   31600     0     0   54100     0
# (0.509803921568627, 0.529411764705882] 0       2000   3500     0     0   25600   106400
# (0.529411764705882, 0.549019607843137] 0       0   10200     0   132800   26100     0
# (0.549019607843137, 0.568627450980392] 46500  60500  10000     0   34100   16000   344400
# (0.568627450980392, 0.588235294117647] 100900 184300  198900     0   97100   19500   446900
# (0.588235294117647, 0.607843137254902] 367100 551800  129400     0   194900   23400   322800
# (0.607843137254902, 0.627450980392157] 757600 250100  382800  17400   352900     0   139700
# (0.627450980392157, 0.647058823529412] 53300  182900  424800  3600   2100   4400     0
# (0.647058823529412, 0.666666666666667] 127400 127800  87400   55600   69400   22600   27900
# (0.666666666666667, 0.686274509803922] 96500  204200     0   84500   22300   3000   27400
# (0.686274509803922, 0.705882352941177] 64600  51800   39600   720500   17300   10200   9800
# (0.705882352941177, 0.725490196078431] 38800 123700  21800   325300   29200   32500   8600
# (0.725490196078431, 0.745098039215686] 2100   26700   3200   84100   14300   14900   11200
# (0.745098039215686, 0.764705882352941] 8900   0       0   22700     0   14800   4500
# (0.764705882352941, 0.784313725490196] 0       0       0     0     0     0     0
# (0.784313725490196, 0.803921568627451] 0       0       0     0     0     0     0
# (0.803921568627451, 0.823529411764706] 0       0       0     0     0     0     0
# (0.823529411764706, 0.843137254901961] 0       0       0     0     0     0     0
# (0.843137254901961, 0.862745098039216] 0       0       0     0     0     0     0
# (0.862745098039216, 0.882352941176471] 0       0       0     0     0     0     0
# (0.882352941176471, 0.901960784313726] 0       0       0     0     0     0     0
# (0.901960784313726, 0.92156862745098] 0       0       0     0     0     0     0
# (0.92156862745098, 0.941176470588235] 0       0       0     0     0     0     0
# (0.941176470588235, 0.96078431372549] 0       0       0     0     0     0     0
# (0.96078431372549, 0.980392156862745] 0       0       0     0     0     0     0
# (0.980392156862745, 1] 0       0       0     0     0     0     0
# Tot          1708500 1814600 1432300 1342200 1007100 426600 1468300

```



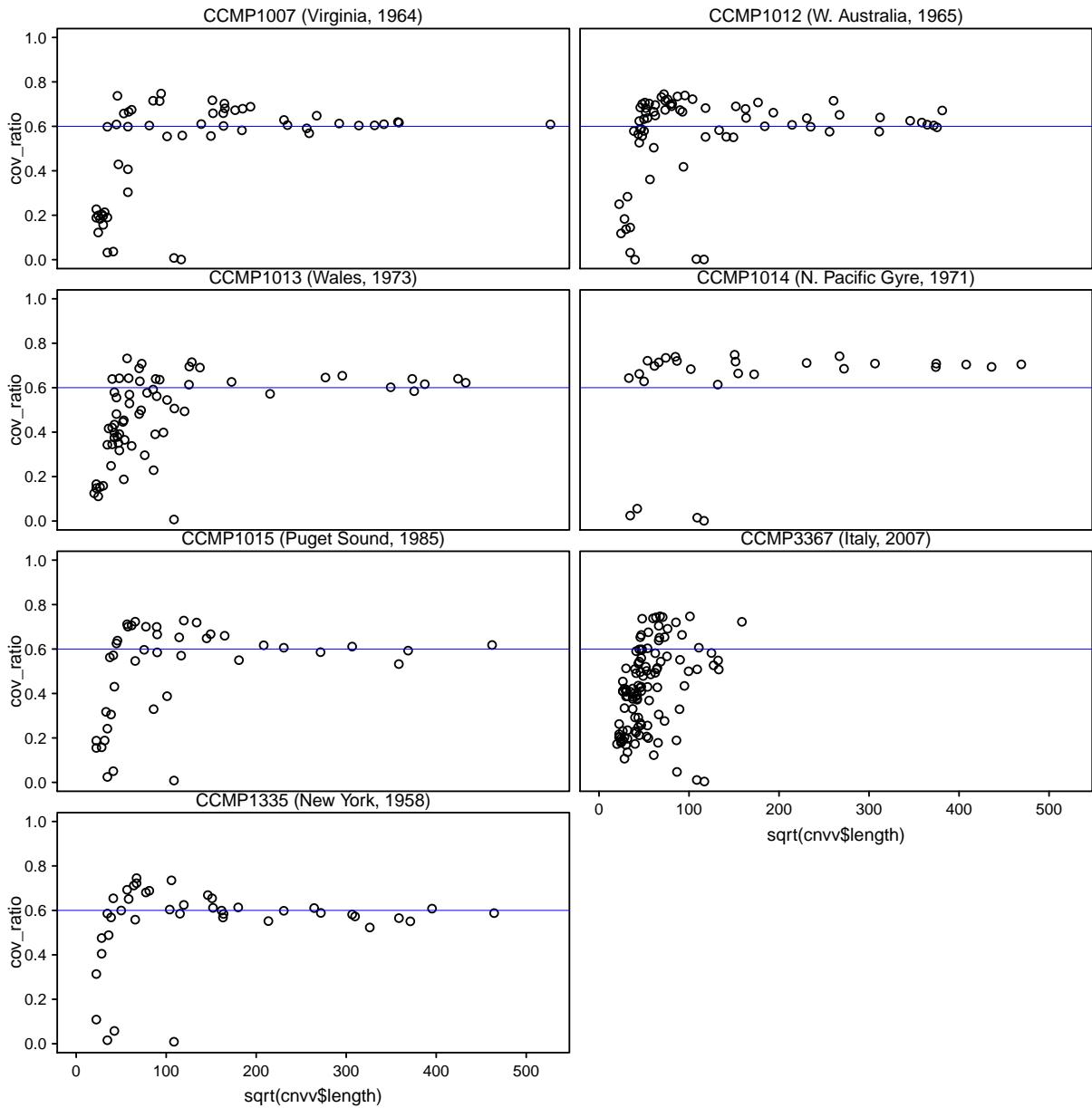
Observations: T-i-c is roughly reflected in peak heights, with Italy being most extreme. NY mode is  $\approx 0.59$ , 1007, 1012 and 1015 at  $\approx 0.61$ , 1013 at  $\approx 0.63$ , gyre at  $\approx 0.71$  (and Italy has no clear peak). If these are really hemizygous deletions, why are they not at 0.5? Some regions may simply be at the low end of normal fluctuation in coverage, not deletions at all. Additionally, discrete bin boundaries used by CNVnator may tend to include extraneous stuff at the ends of each interval. Both effects should be reduced for longer regions; is there a length trend?

```
plt.hemi.frac.by.len <- function(logx=F, sqrtx=T){
  opar <- par(mfrow=c(4,2), mar=c(0,0,1,.5), oma=c(3,4,1,0)); on.exit(par(opar))
  xmx <- max(cnvv$length)
  for(i in 1:7){
    pick <- as.character(cnvv$strain) == strain.names[i]
    x <- cnvv$length[pick]
    xlm <- xmx
    xlb <- 'cnvv$length'
    if(logx) {
      x <- log2(x)
      xlm <- log2(xmx)
    }
    plot(x, xlab=xlb, ylab='Count', main=paste(strain.names[i], '(', year[i], ')'),
         xaxt='top', xaxs='log', yaxt='right', yaxs='log', log='xy')
    points(x, type='o', pch=1)
    lines(x, type='l')
  }
}
```

```

    xlб <- 'log2(cnvv$length)'
} else if(sqrtx){
  x <- sqrt(x)
  xlм <- sqrt(xmx)
  xlб <- 'sqrt(cnvv$length)'
}
eplot(ylim=c(0,1), xlim=c(0,xlm), xlab=xlб, ylab='cov_ratio',main=st.loc(i,date=T) )
points(x, cnvv$cov_ratio[pick])
abline(h=0.6,lwd=0.5,col='blue')
if(i==6){addxaxis()}
}
}
plt.hemi.frac.by.len()

```



I'd say, no. Coverage ratio is variable below 10k, but flat near 0.6 above that. (A bit higher in Gyre, again either a symptom of increased noise or increased diversity in Gyre.) Another possibility is that, just as coverage is low across SNPs due to a mapping bias against non-reference positions, there is a counter-trend *towards* accepting erroneous

reads that happen to *match* the reference. I suppose it is possible that this has inflated the ratio to 0.6 (or a bit more in Gyre, if it is noisier). This one would imply a rather startling rate of erroneous reads: If the number of “correct” reads across a diploid section averages  $x$ , and some additional fraction  $\epsilon x$  of erroneous reads map there too, then

$$\frac{x/2 + \epsilon x}{x + \epsilon x} = 0.6,$$

implying  $\epsilon = 1/4$ .

Another possibility is that stochasticity contributes: fluctuation around average read count of 0.5 can’t fall below zero, but can rise above 1.0, which might tend to inflate the observed average. Additionally, duplicated or non-hemi regions embedded in/sandwiched between two long hemi regions might, if short, not be properly split by CNVnator, inflating the average. Another contributor is that a significant proportion of hemizygosity will lower the genomic coverage average against which cov\_ratio is measured. (This effect should be strongest on the older strains, where deletion appears most widespread, but I don’t see an obvious trend in that direction. Although we didn’t look, I wouldn’t be surprised to see duplications increasing with age, too, which would partially offset this effect. UPDATE: I did take a quick look; 1.5x and 2x appear to increase with age, and there’s a lot around 1.5x but relatively little at 2x or above, e.g. an average of about 0.5 Mb between 1.7x and 2.3x, vs at least twice that in hemizygous regions.)

Big NY deletions:

```
pick <- cnvv$strain == 'tp1335' & cnvv$length > 40000
sum(pick)

# [1] 11

pi.length <- order(cnvv$length)
cnvv[pi.length,][pick[pi.length],]

#      strain      chr    start      end length filtered      type cov_ratio dup_frac
# 2114 tp1335 Chr2 2399101 2444700 45600 FALSE CNVnator 0.551821 0.0385429
# 2117 tp1335 Chr2 2582101 2635300 53200 FALSE CNVnator 0.598177 0.0706814
# 2274 tp1335 Chr19a_19 479301 549200 69900 FALSE CNVnator 0.610449 0.0569739
# 2161 tp1335 Chr6 272601 346500 73900 FALSE CNVnator 0.588544 0.0702023
# 2159 tp1335 Chr6 174501 268500 94000 FALSE CNVnator 0.581503 0.0364507
# 2310 tp1335 Chr23 1 96000 96000 FALSE CNVnator 0.572798 0.0462243
# 2290 tp1335 Chr20 621601 728000 106400 FALSE CNVnator 0.522981 0.1220760
# 2115 tp1335 Chr2 2448101 2576700 128600 FALSE CNVnator 0.565107 0.0294771
# 2269 tp1335 Chr19a_19 281201 419000 137800 FALSE CNVnator 0.550752 0.0298223
# 2157 tp1335 Chr6 9601 165900 156300 FALSE CNVnator 0.607829 0.0390458
# 2267 tp1335 Chr19a_19 62201 277800 215600 FALSE CNVnator 0.587722 0.0744552
```

## 7 Examples

Looking at some examples:

```
# look up a coord in hemi table
hemi.row <- function(coord,h.t=hemi.tab){
  r <- match(coord,rownames(h.t))
  if(is.na(r)){
    }
  }
# rows = range of row indices e.g. 18:24, or pair of row names c('Chr10:104501','Chr10:104501')
# alt.win is start if first to end of 2nd; print tab for a row earlier to row later
hemi.chunk <- function(rows,strains=c(7,1:6),margin=1000,ymax=250, h.t=hemi.tab){
  if(length(strains)>1){
    opar <- par(ask=T); on.exit(par(opar))
  }
  if(is.numeric(rows)){
    j <- min(rows)
    k <- max(rows)
  } else {
```

```

j <- match(rows[1], rownames(h.t))
k <- match(rows[length(rows)], rownames(h.t))
cat('Rows', j, ':', k, '\n')
}
print(h.t[max(1, j-1):min(nrow(h.t), k+1), ], digits=3)
start <- chrloc2g(list(h.t$chr[j], h.t$start[j]))
end <- chrloc2g(list(h.t$chr[k], h.t$end[k]))
for(i in strains){
  #cat('x=', (start+end)/2, 'width=', (end-start)/2+margin, '\n')
  seechunk(i, ceiling((start+end)/2), width=ceiling((end-start)/2)+margin,
            alt.win=c(start, end), ymax=ymax)
}
}

```

Start with big NY deletions. The first is about 45k long. As expected for a hemizygous region, it is essentially SNP-free in NY (there are 2 or 3 called SNPs, all with very low non-reference read counts). An even longer region is deleted in 1007 and 1012, and each has about 5 called SNPs with substantial nonreference counts (possibly at shared positions), plus 2–3 others with low counts. In other words, all 3 strains appear to be hemizygous here, and to share the same haplotype, give or take a handful of nucleotides. 1014 and 1015 have normal coverage, but few SNPs (4–7)—essentially homozygous for the NY haplotype. Italy and Wales have normal coverage and many SNPs, although the Italy’s SNPs are somewhat patchy. Italian and Welsh SNPs have a complex sharing pattern, with a majority of Wales below 0.5 nonref frac, and IT the opposite; many of the high nonref frac are shared, but many of all frequencies are private to each strain (see pairs plot below).

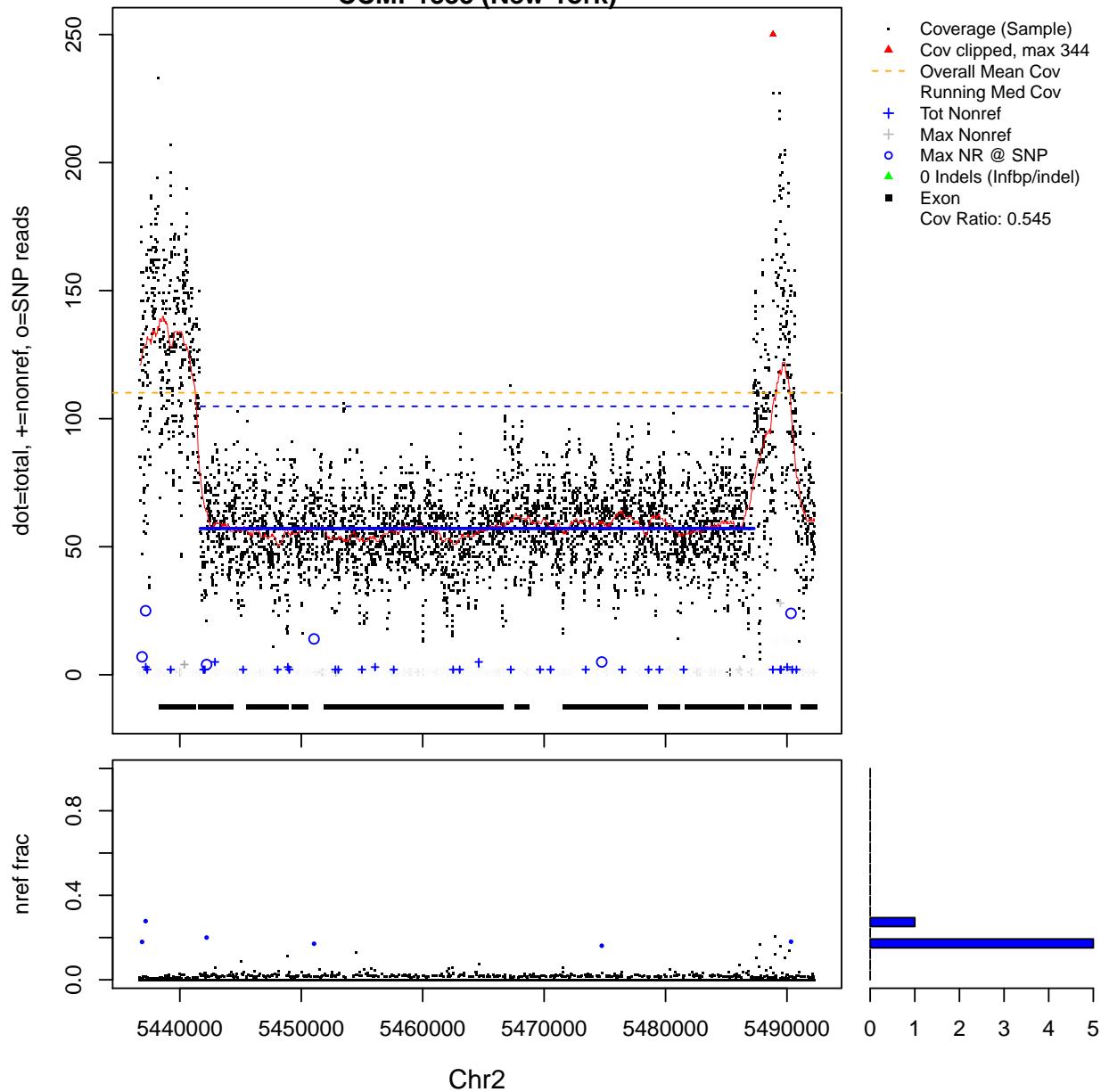
```

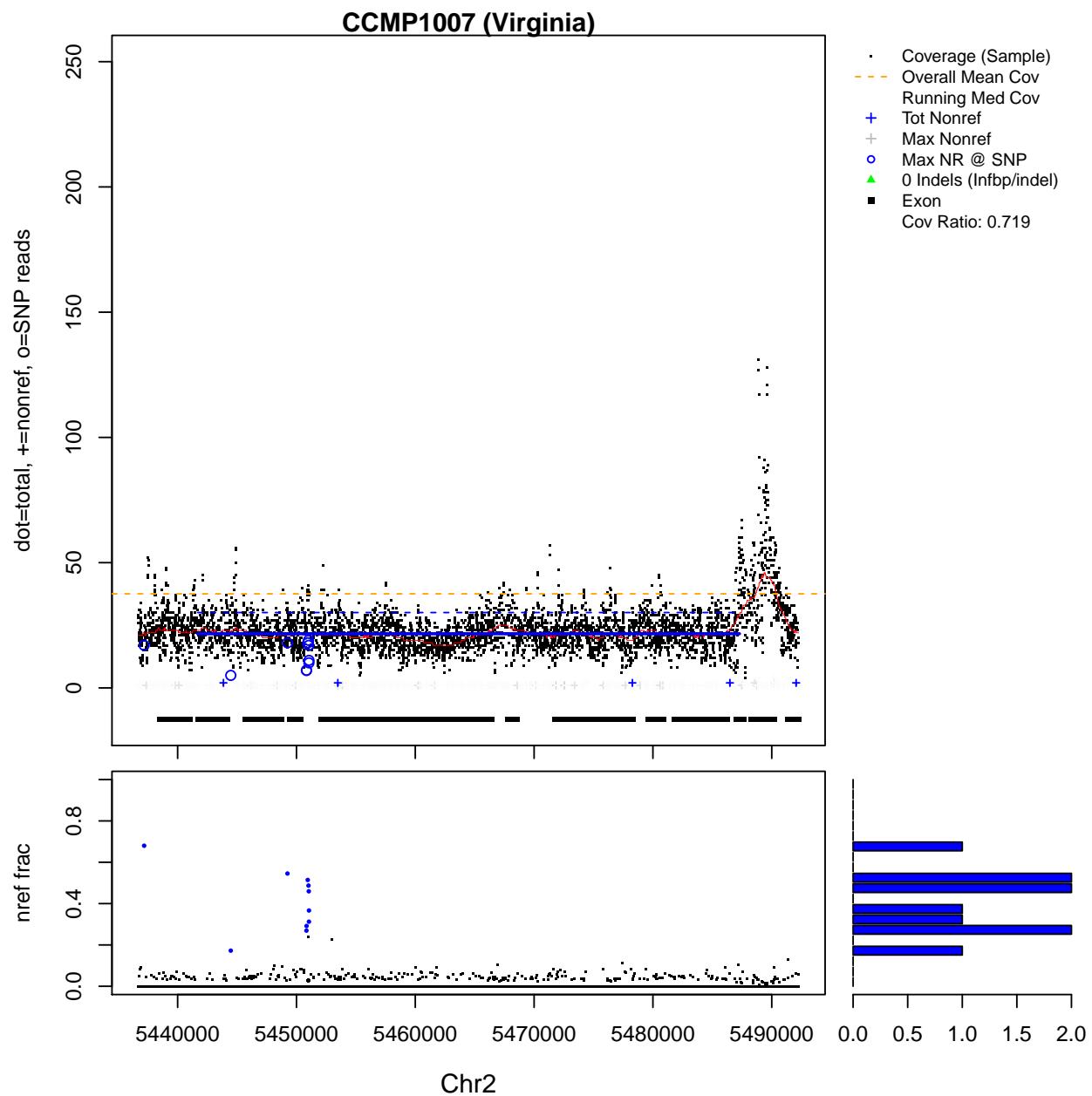
hemi.chunk(c('Chr2:2399101', 'Chr2:2444601'), margin=5000)

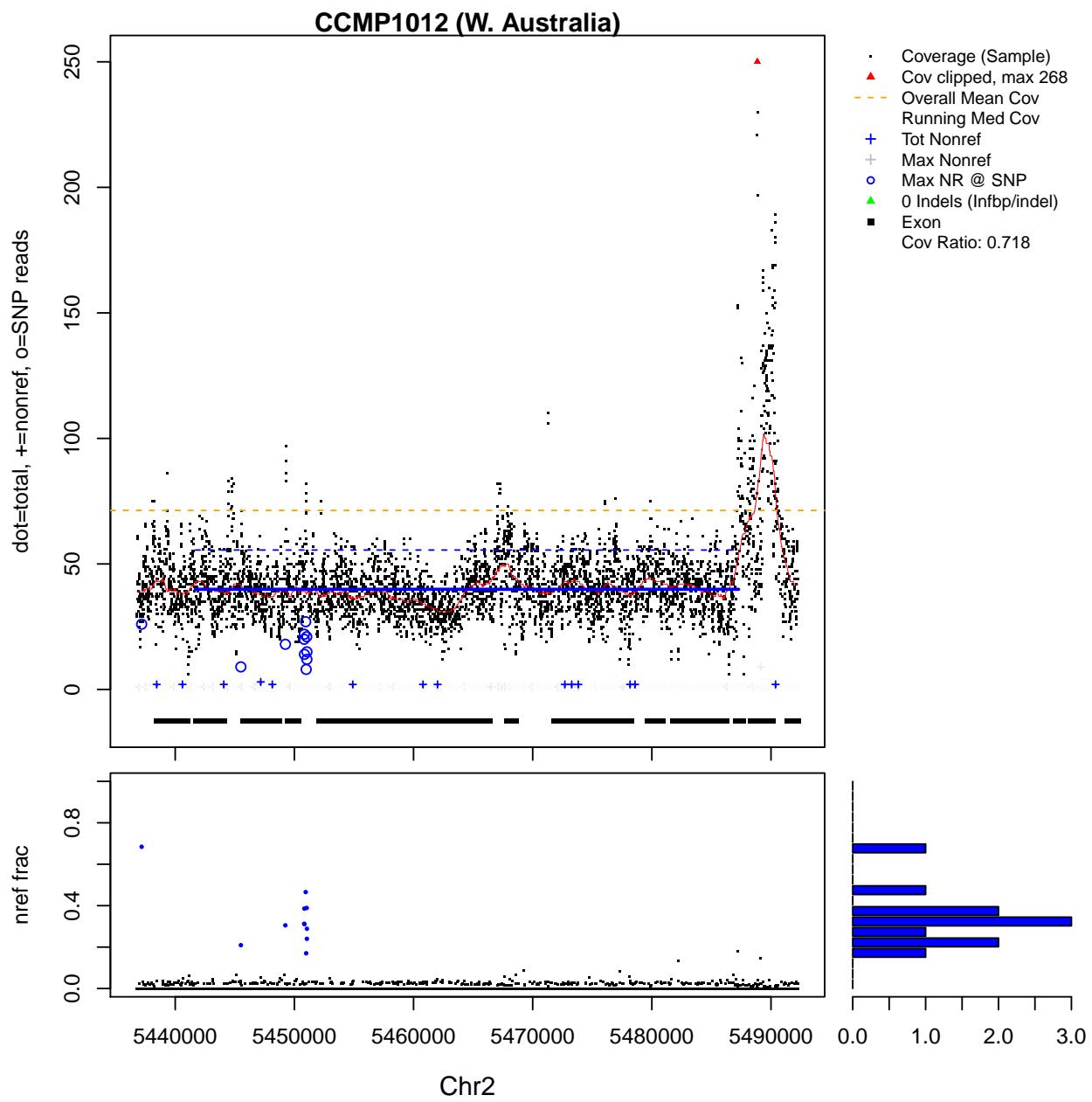
# Rows 340 : 341
#          chr    start      end length tp1007 tp1012 tp1013 tp1014 tp1015 IT tp1335 pattern
# Chr2:2348101 Chr2 2348101 2399100  51000  0.604  0.576     NA     NA     NA NA     NA     140
# Chr2:2399101 Chr2 2399101 2444600  45500  0.604  0.576     NA     NA     NA NA  0.552     141
# Chr2:2444601 Chr2 2444601 2444700     100  0.604     NA     NA     NA NA  0.552     101
# Chr2:2444701 Chr2 2444701 2446700   2000  0.604     NA     NA     NA NA     NA     100

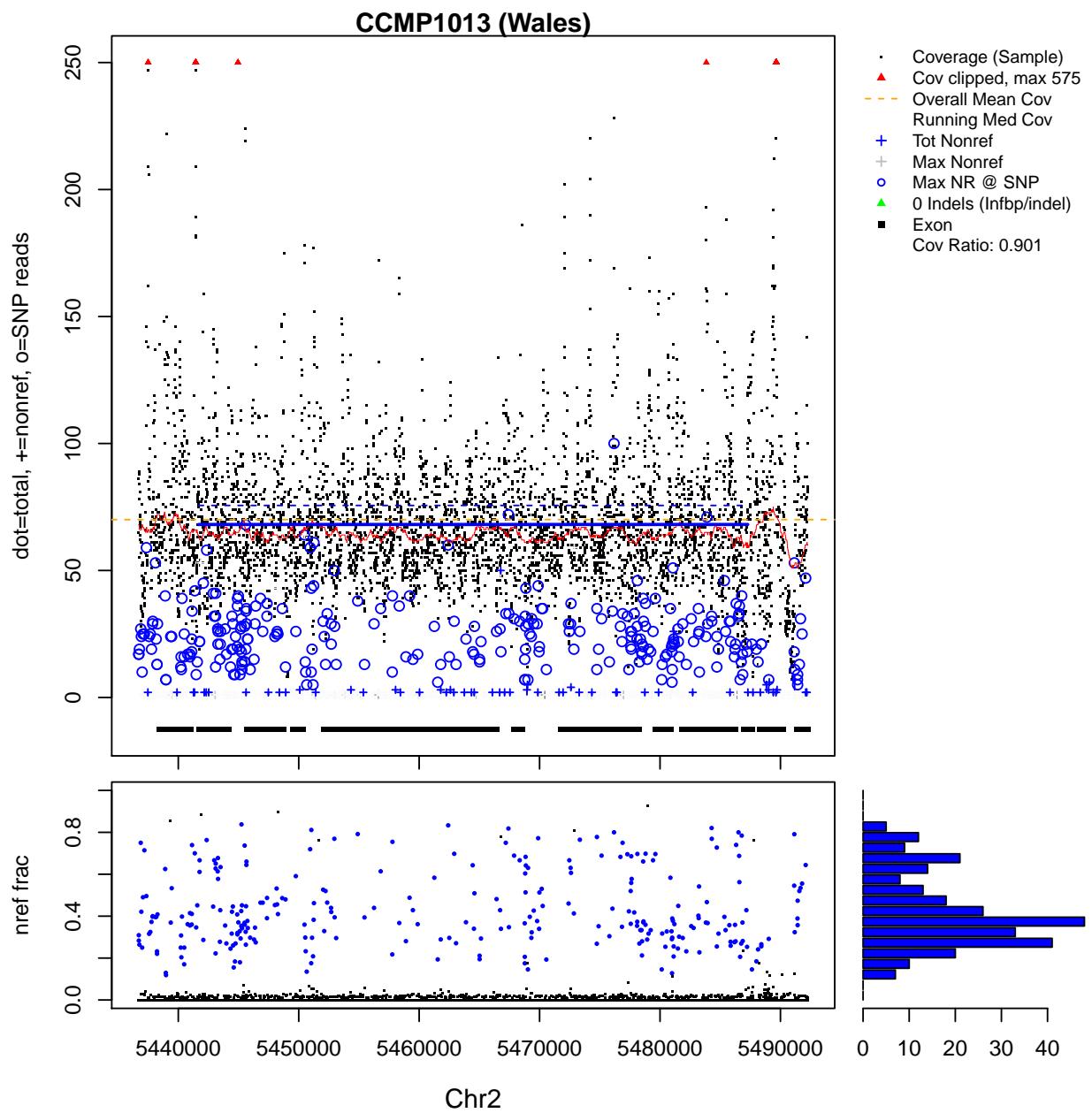
```

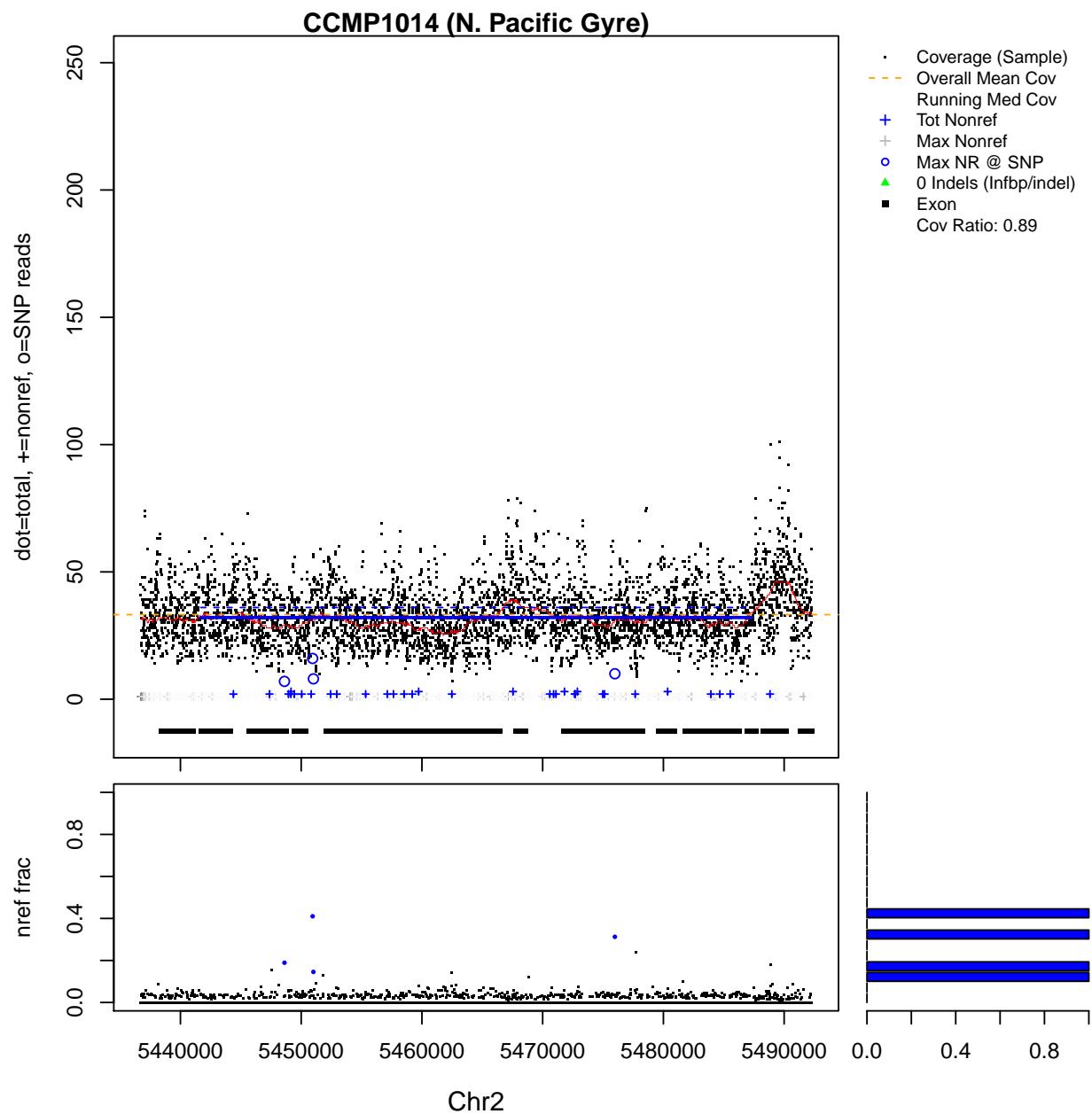
### CCMP1335 (New York)

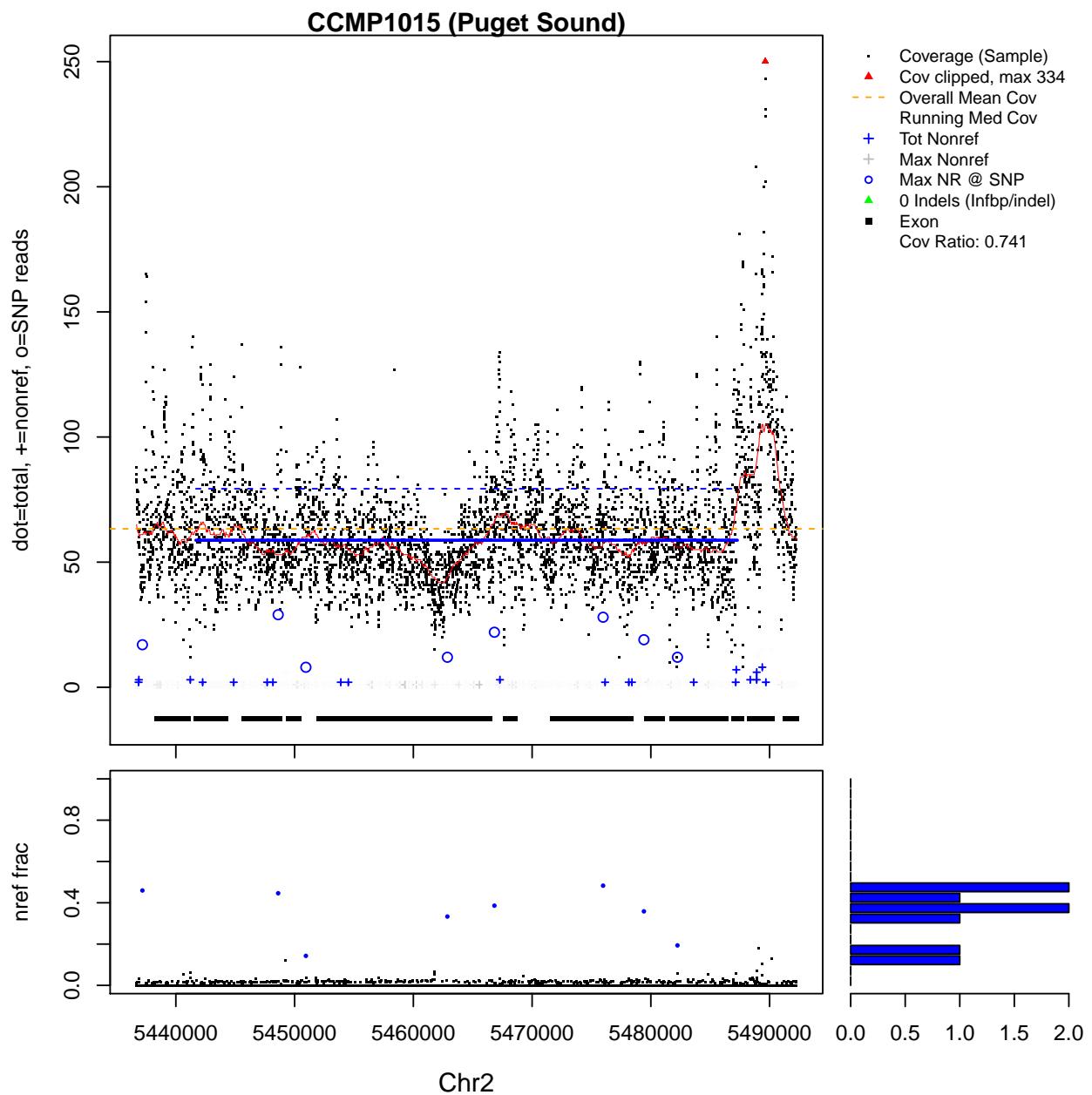


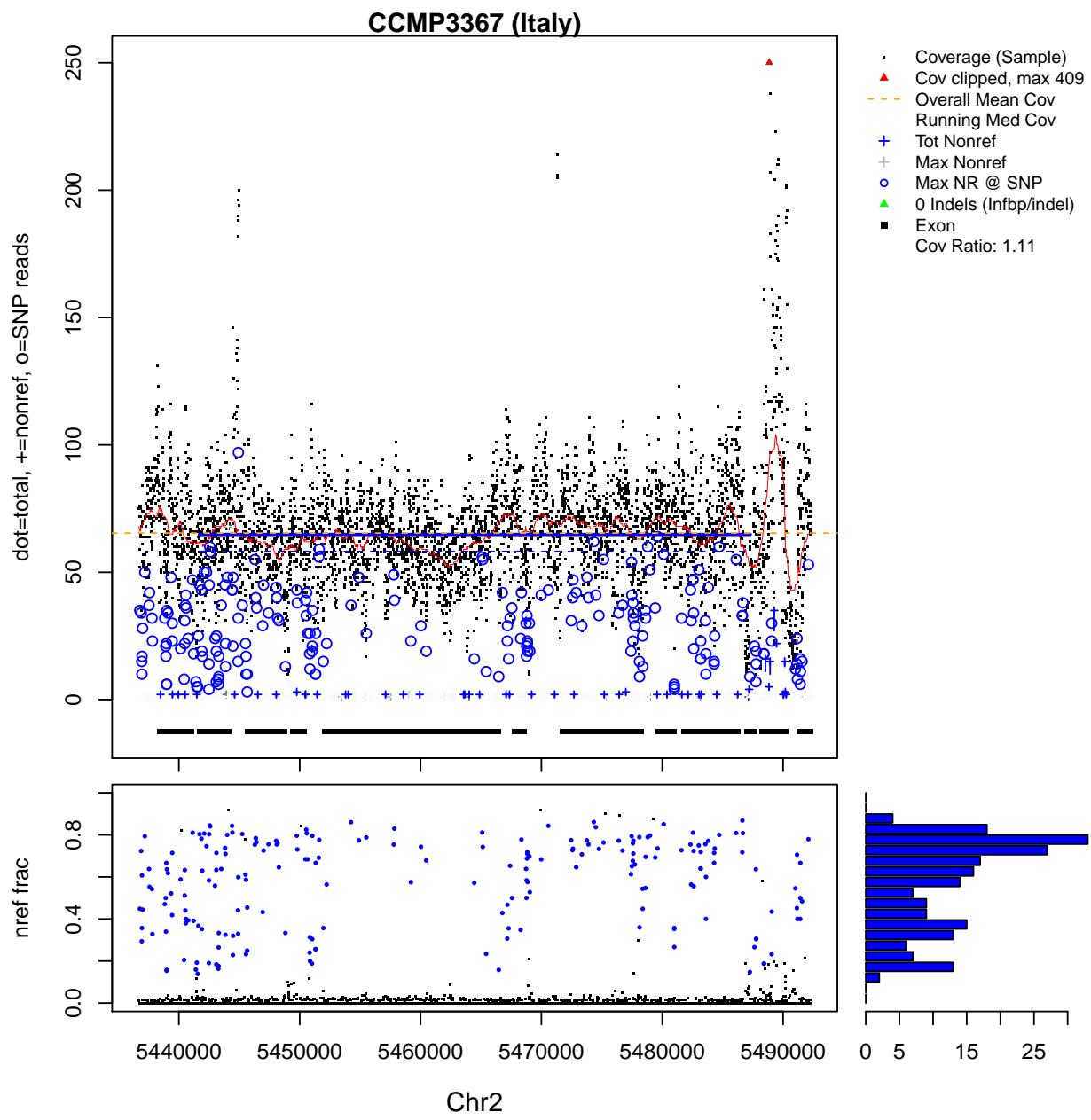






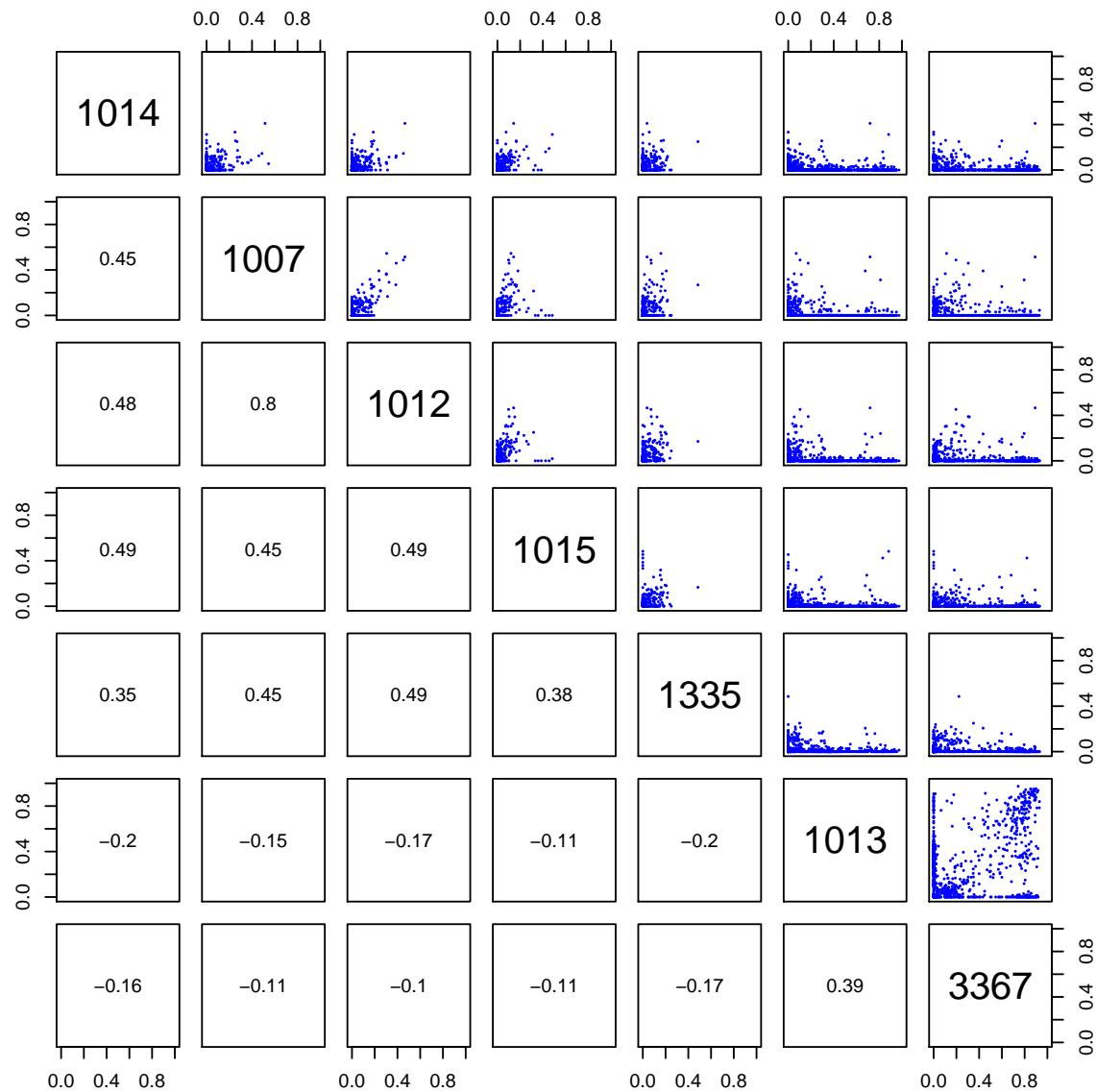






pairs plot of same region:

```
nrf.pairs(mask=seg.mask(5440000, 5500000))
```

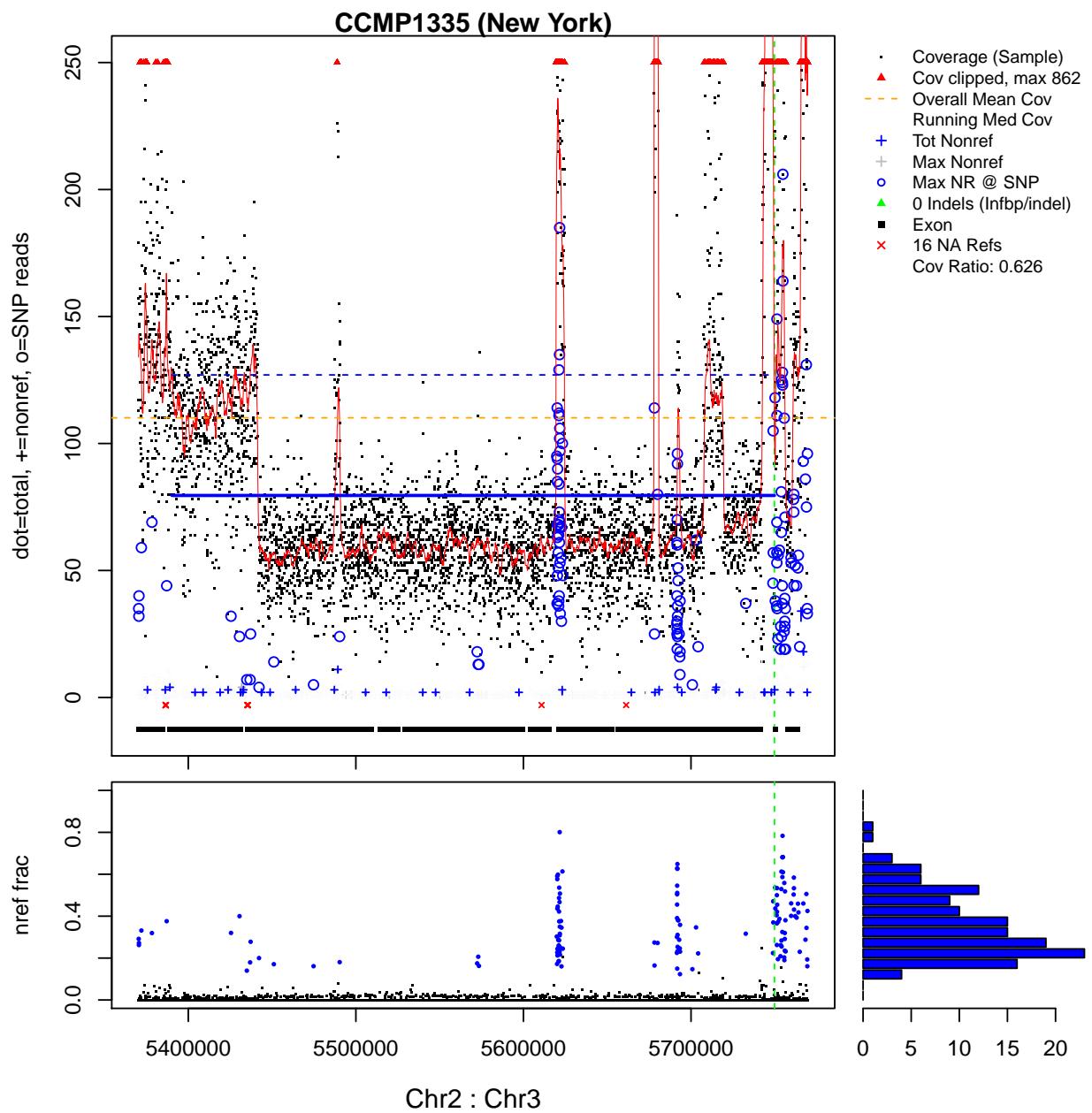


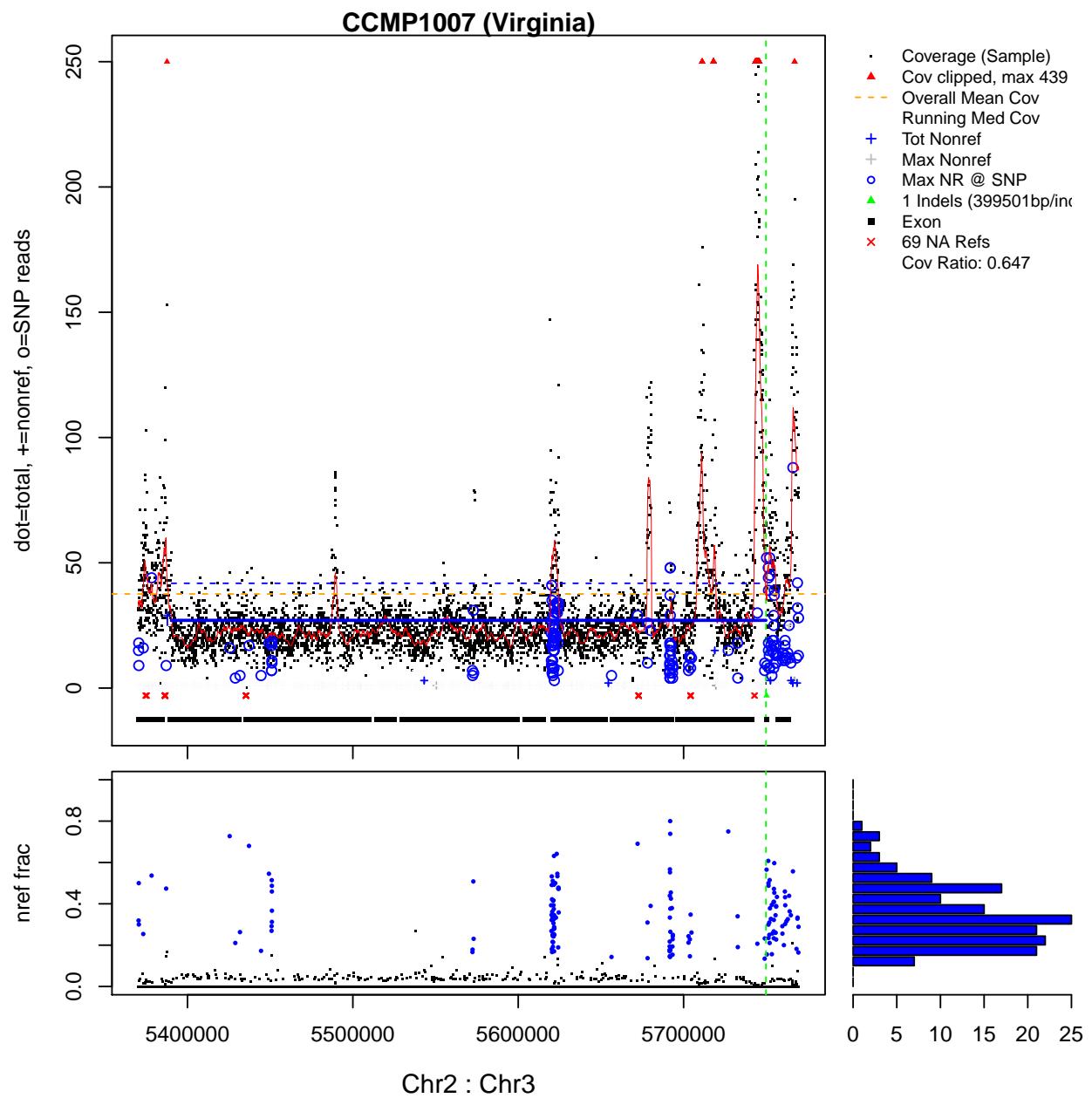
Extending that, we see that, with a few relatively short interruptions (perhaps duplicated regions), the NY deletion essentially runs to the end of Chr2, although not consistently called by CNVnator, and the described pattern above applies to the whole region ( $\approx 400K$ ), *except*, 1014 and 1015 share a region of about 100k that is very SNPy.

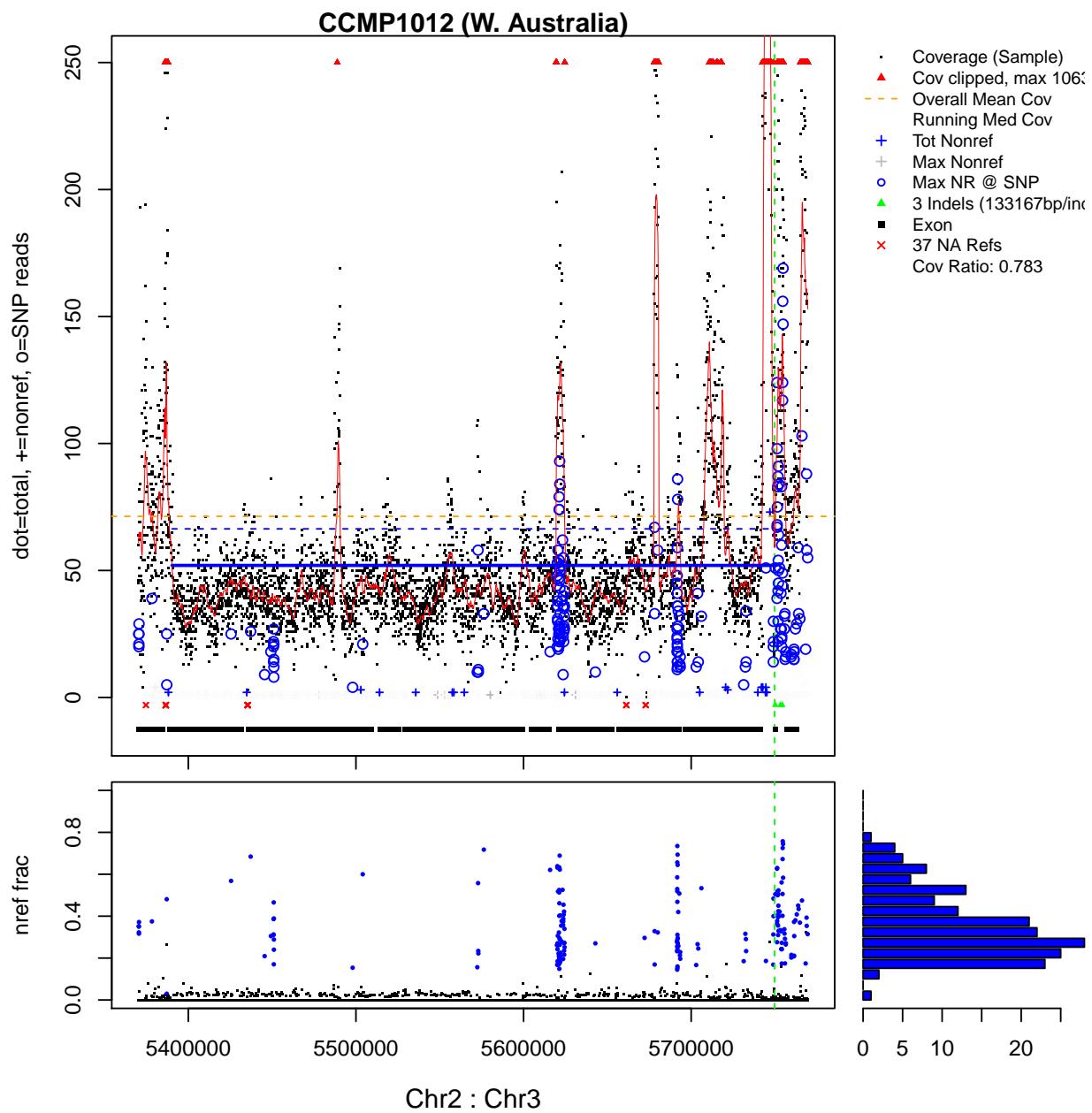
```
hemi.chunk(338:366, margin=20000)
```

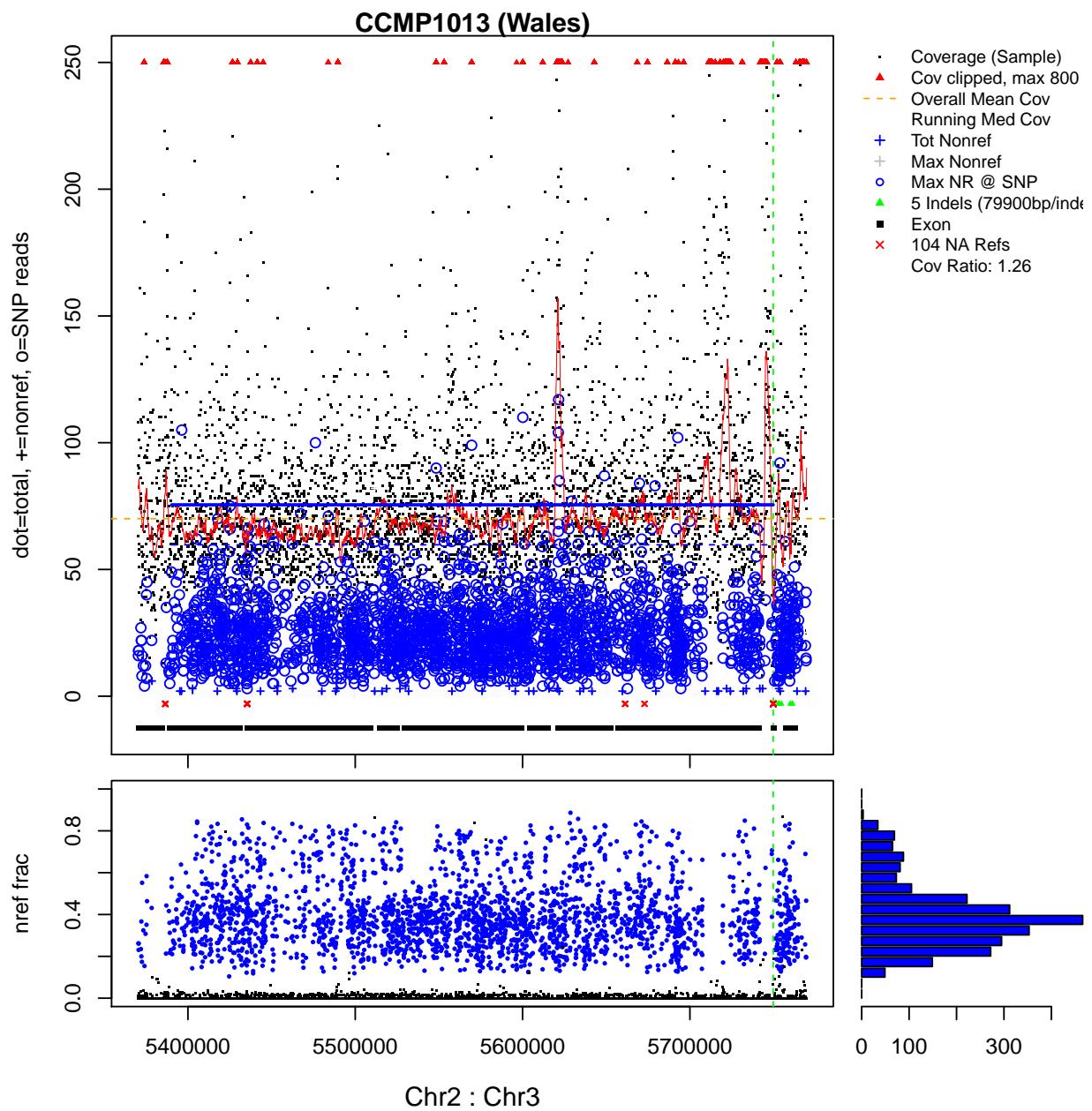
|   | chr          | start | end     | length  | tp1007 | tp1012 | tp1013 | tp1014 | tp1015 | IT    | tp1335 | pattern |     |
|---|--------------|-------|---------|---------|--------|--------|--------|--------|--------|-------|--------|---------|-----|
| # | Chr2:2330601 | Chr2  | 2330601 | 2347700 | 17100  | NA     | NA     | NA     | NA     | NA    | NA     | NA      | 000 |
| # | Chr2:2347701 | Chr2  | 2347701 | 2348100 | 400    | NA     | 0.576  | NA     | NA     | NA    | NA     | NA      | 040 |
| # | Chr2:2348101 | Chr2  | 2348101 | 2399100 | 51000  | 0.604  | 0.576  | NA     | NA     | NA    | NA     | NA      | 140 |
| # | Chr2:2399101 | Chr2  | 2399101 | 2444600 | 45500  | 0.604  | 0.576  | NA     | NA     | NA    | NA     | 0.552   | 141 |
| # | Chr2:2444601 | Chr2  | 2444601 | 2444700 | 100    | 0.604  | NA     | NA     | NA     | NA    | NA     | 0.552   | 101 |
| # | Chr2:2444701 | Chr2  | 2444701 | 2446700 | 2000   | 0.604  | NA     | NA     | NA     | NA    | NA     | NA      | 100 |
| # | Chr2:2446701 | Chr2  | 2446701 | 2447800 | 1100   | NA     | NA     | NA     | NA     | NA    | NA     | NA      | 000 |
| # | Chr2:2447801 | Chr2  | 2447801 | 2448100 | 300    | NA     | NA     | NA     | NA     | NA    | 0.422  | NA      | 002 |
| # | Chr2:2448101 | Chr2  | 2448101 | 2448600 | 500    | 0.616  | 0.617  | NA     | NA     | NA    | 0.422  | 0.565   | 143 |
| # | Chr2:2448601 | Chr2  | 2448601 | 2555700 | 107100 | 0.616  | 0.617  | NA     | NA     | NA    | NA     | 0.565   | 141 |
| # | Chr2:2555701 | Chr2  | 2555701 | 2576700 | 21000  | 0.616  | 0.617  | NA     | NA     | 0.648 | NA     | 0.565   | 145 |

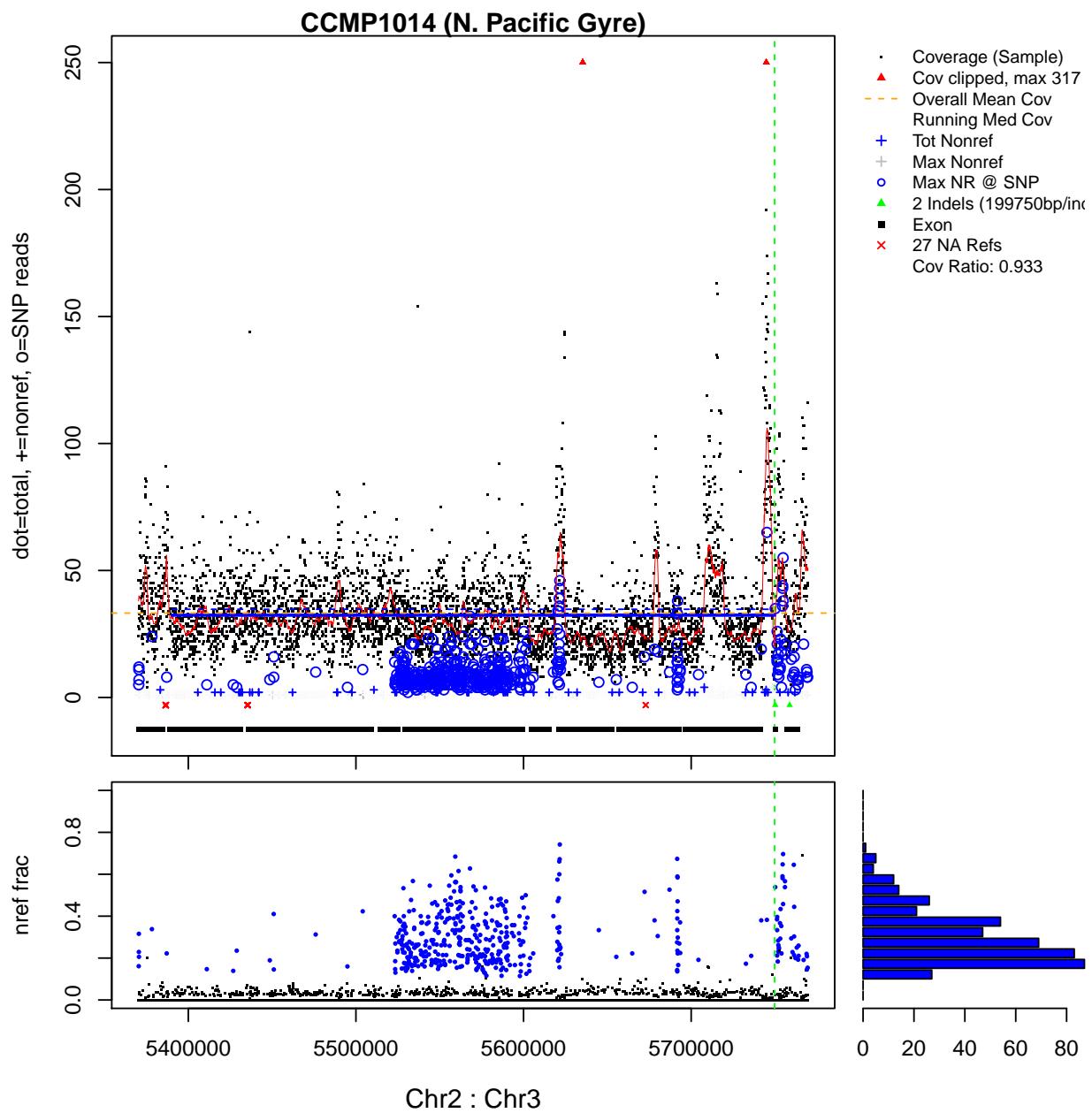
|                |      |         |         |       |       |       |       |       |       |       |       |     |     |
|----------------|------|---------|---------|-------|-------|-------|-------|-------|-------|-------|-------|-----|-----|
| # Chr2:2576701 | Chr2 | 2576701 | 2582000 | 5300  | NA    | NA  | 000 |
| # Chr2:2582001 | Chr2 | 2582001 | 2582100 | 100   | 0.629 | 0.637 | NA    | NA    | NA    | NA    | NA    | NA  | 140 |
| # Chr2:2582101 | Chr2 | 2582101 | 2594100 | 12000 | 0.629 | 0.637 | NA    | 0.711 | 0.606 | NA    | 0.598 | 155 |     |
| # Chr2:2594101 | Chr2 | 2594101 | 2597700 | 3600  | 0.629 | 0.637 | NA    | 0.711 | 0.606 | 0.738 | 0.598 | 157 |     |
| # Chr2:2597701 | Chr2 | 2597701 | 2635300 | 37600 | 0.629 | 0.637 | NA    | 0.711 | 0.606 | NA    | 0.598 | 155 |     |
| # Chr2:2635301 | Chr2 | 2635301 | 2638000 | 2700  | NA    | NA  | 000 |
| # Chr2:2638001 | Chr2 | 2638001 | 2638100 | 100   | NA    | NA    | NA    | NA    | 0.660 | NA    | NA    | NA  | 004 |
| # Chr2:2638101 | Chr2 | 2638101 | 2648900 | 10800 | 0.702 | 0.722 | NA    | NA    | 0.660 | NA    | 0.604 | 145 |     |
| # Chr2:2648901 | Chr2 | 2648901 | 2650900 | 2000  | 0.702 | NA    | NA    | NA    | 0.660 | NA    | NA    | NA  | 104 |
| # Chr2:2650901 | Chr2 | 2650901 | 2651200 | 300   | 0.702 | NA    | NA    | NA    | 0.660 | NA    | 0.625 | 105 |     |
| # Chr2:2651201 | Chr2 | 2651201 | 2665200 | 14000 | 0.702 | 0.682 | NA    | NA    | 0.660 | NA    | 0.625 | 145 |     |
| # Chr2:2665201 | Chr2 | 2665201 | 2676900 | 11700 | NA    | NA  | 000 |
| # Chr2:2676901 | Chr2 | 2676901 | 2677000 | 100   | 0.717 | NA    | NA    | 0.748 | NA    | NA    | NA    | NA  | 110 |
| # Chr2:2677001 | Chr2 | 2677001 | 2699300 | 22300 | 0.717 | NA    | NA    | 0.748 | 0.667 | NA    | 0.654 | 115 |     |
| # Chr2:2699301 | Chr2 | 2699301 | 2699600 | 300   | 0.717 | NA    | NA    | 0.748 | NA    | NA    | 0.654 | 111 |     |
| # Chr2:2699601 | Chr2 | 2699601 | 2699800 | 200   | 0.717 | NA    | NA    | NA    | NA    | NA    | 0.654 | 101 |     |
| # Chr2:2699801 | Chr2 | 2699801 | 2706700 | 6900  | NA    | NA  | 000 |
| # Chr2:2706701 | Chr2 | 2706701 | 2707194 | 494   | NA    | NA    | 0.166 | NA    | NA    | NA    | NA    | NA  | 020 |
| # Chr2:2707195 | Chr2 | 2707195 | 2707200 | 6     | NA    | NA    | 0.166 | NA    | NA    | NA    | NA    | NA  | 020 |
| # Chr2:2707201 | Chr2 | 2707201 | 2707200 | 0     | NA    | NA  | 000 |

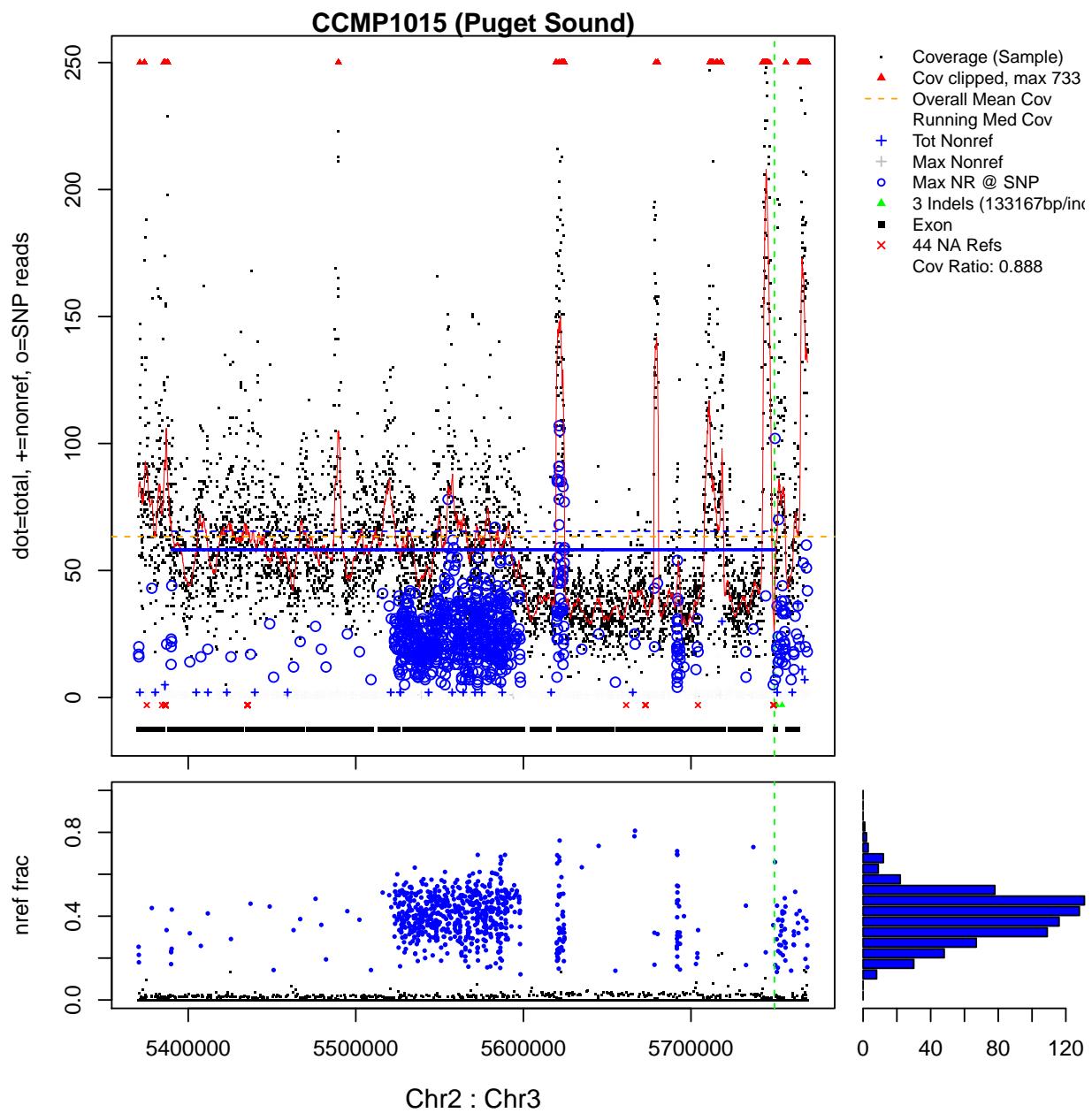


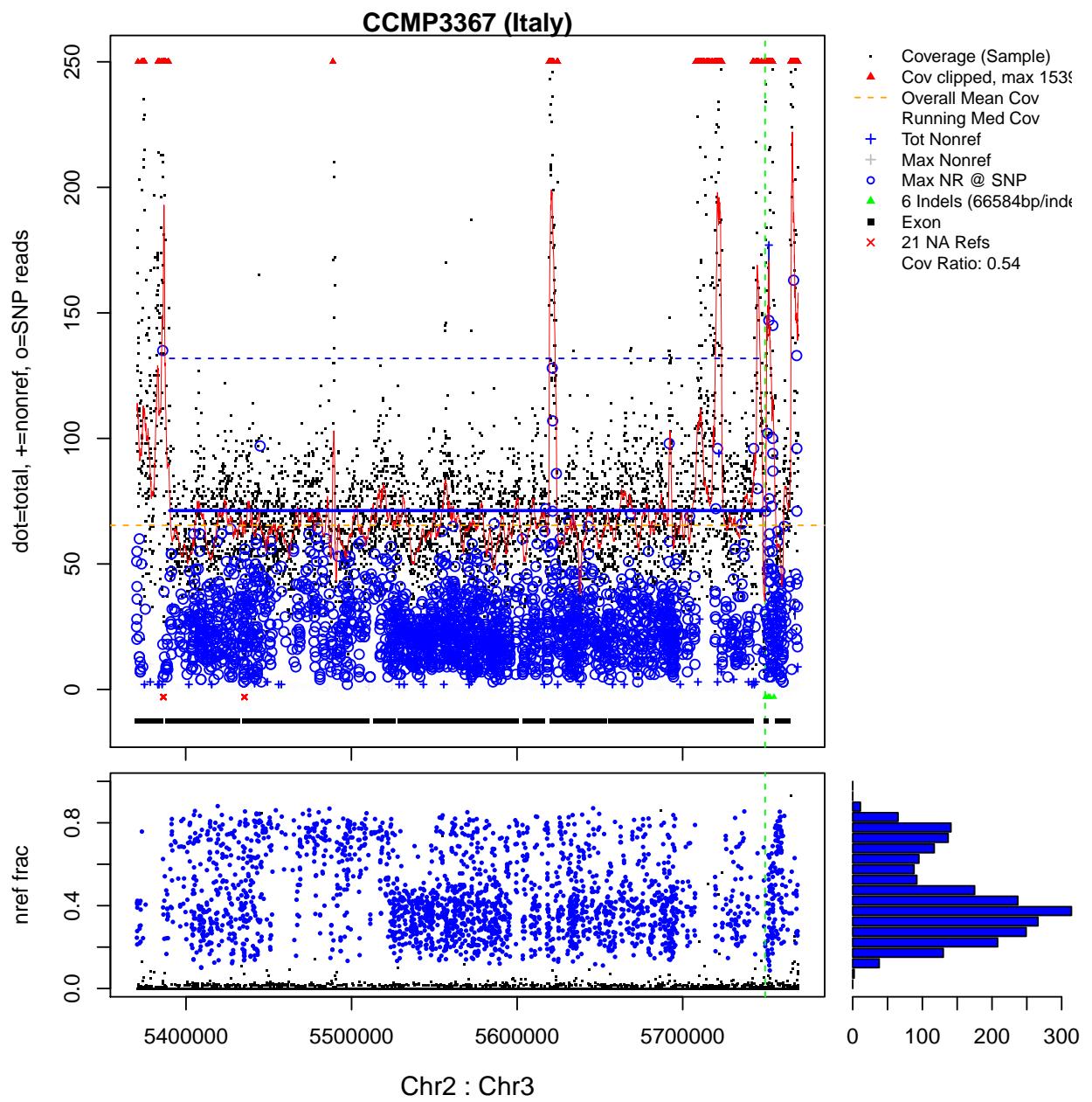


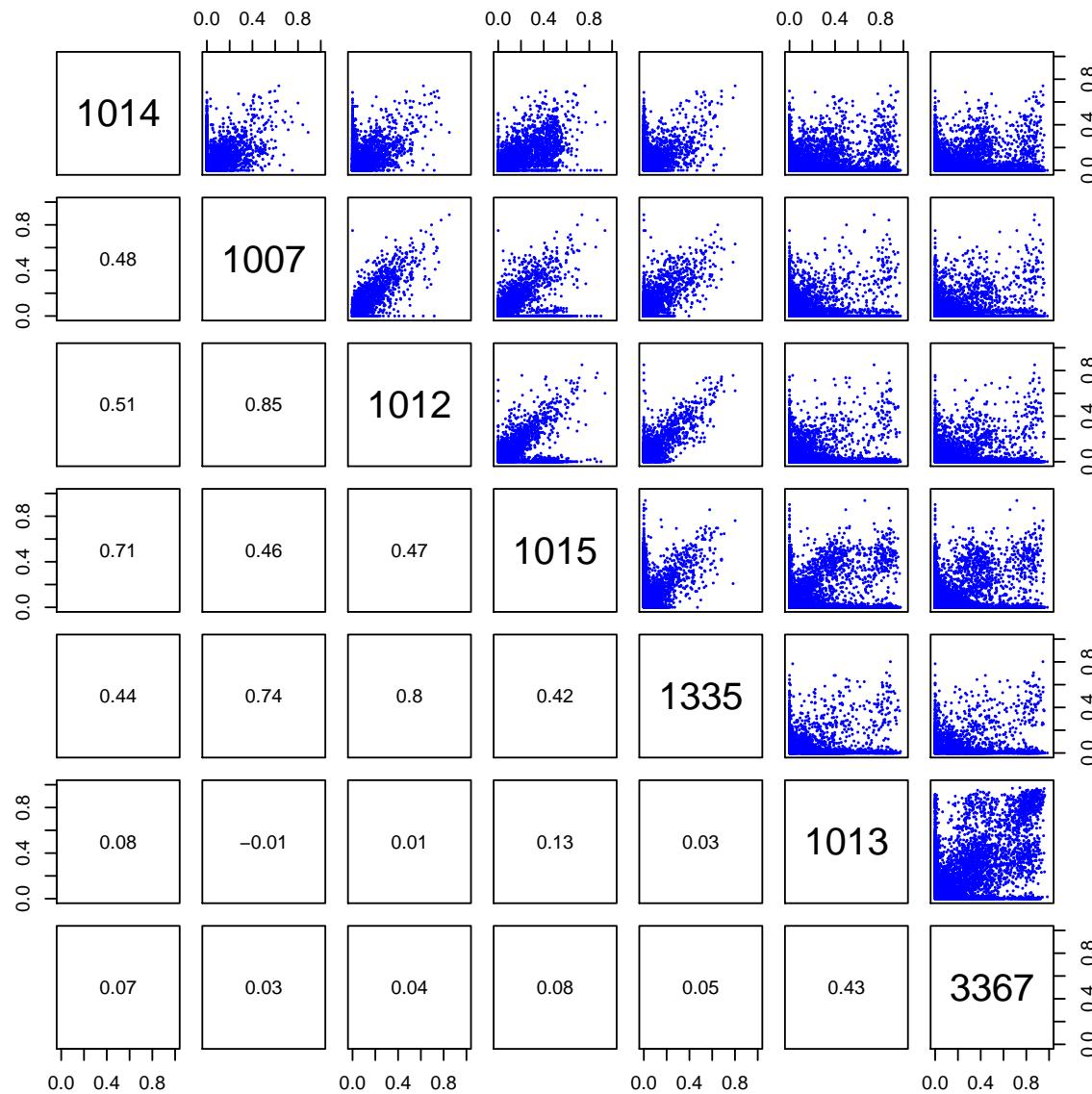










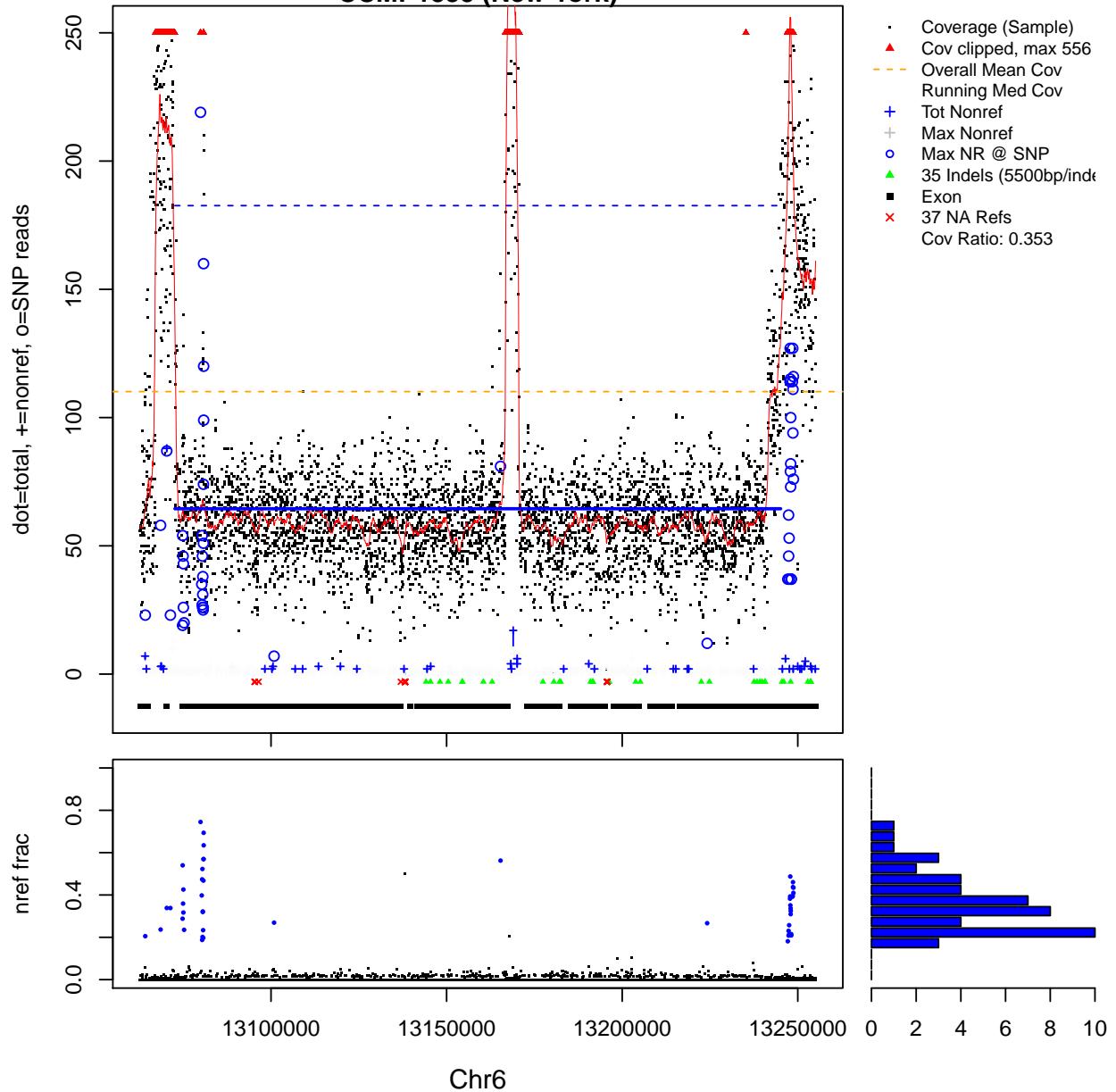


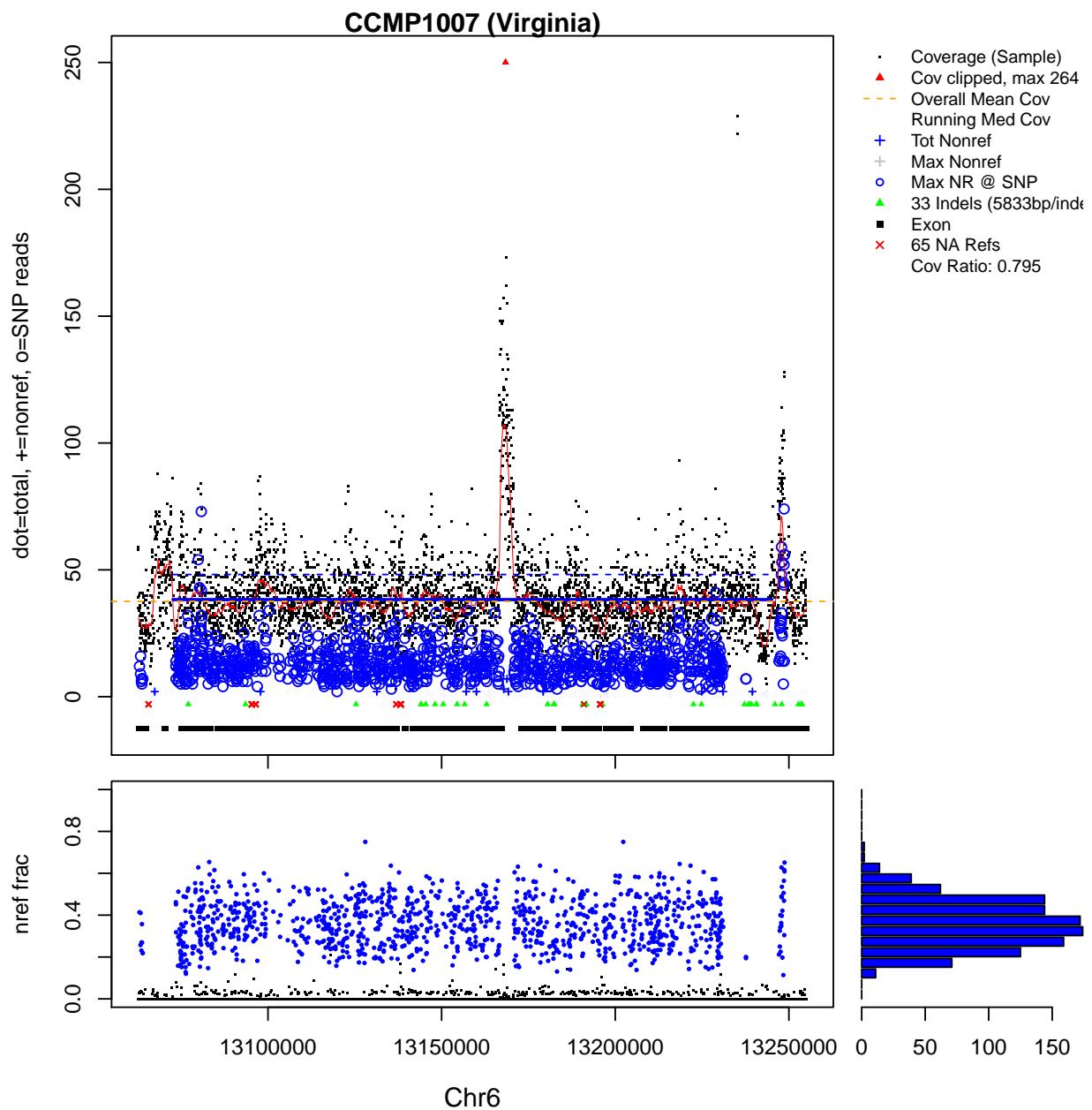
Another big NY chunk. VA: undel, snpy; AU: maybe del, snpy; Wales: undel, snpy (but maybe low nonref); Gyre: maybe del, few snps; 1015: del, few snps; IT: undel, snpy (but low); NY del, few snps. I.e., NY, 1015 are hemi; gyre is homo-ref, others seem het.

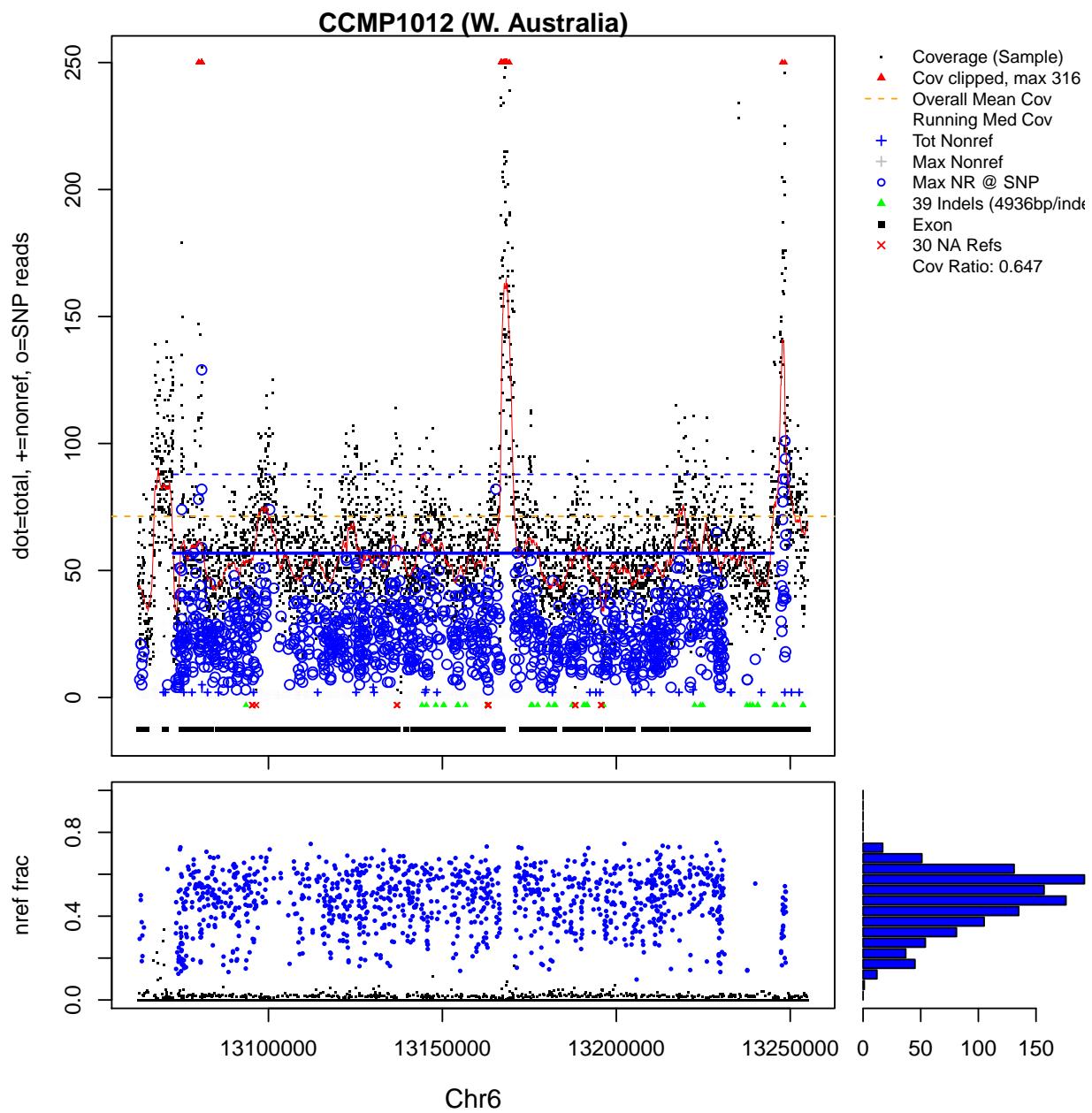
```
hemi.chunk(c('Chr6:174501', 'Chr6:346501'), margin=10000)
```

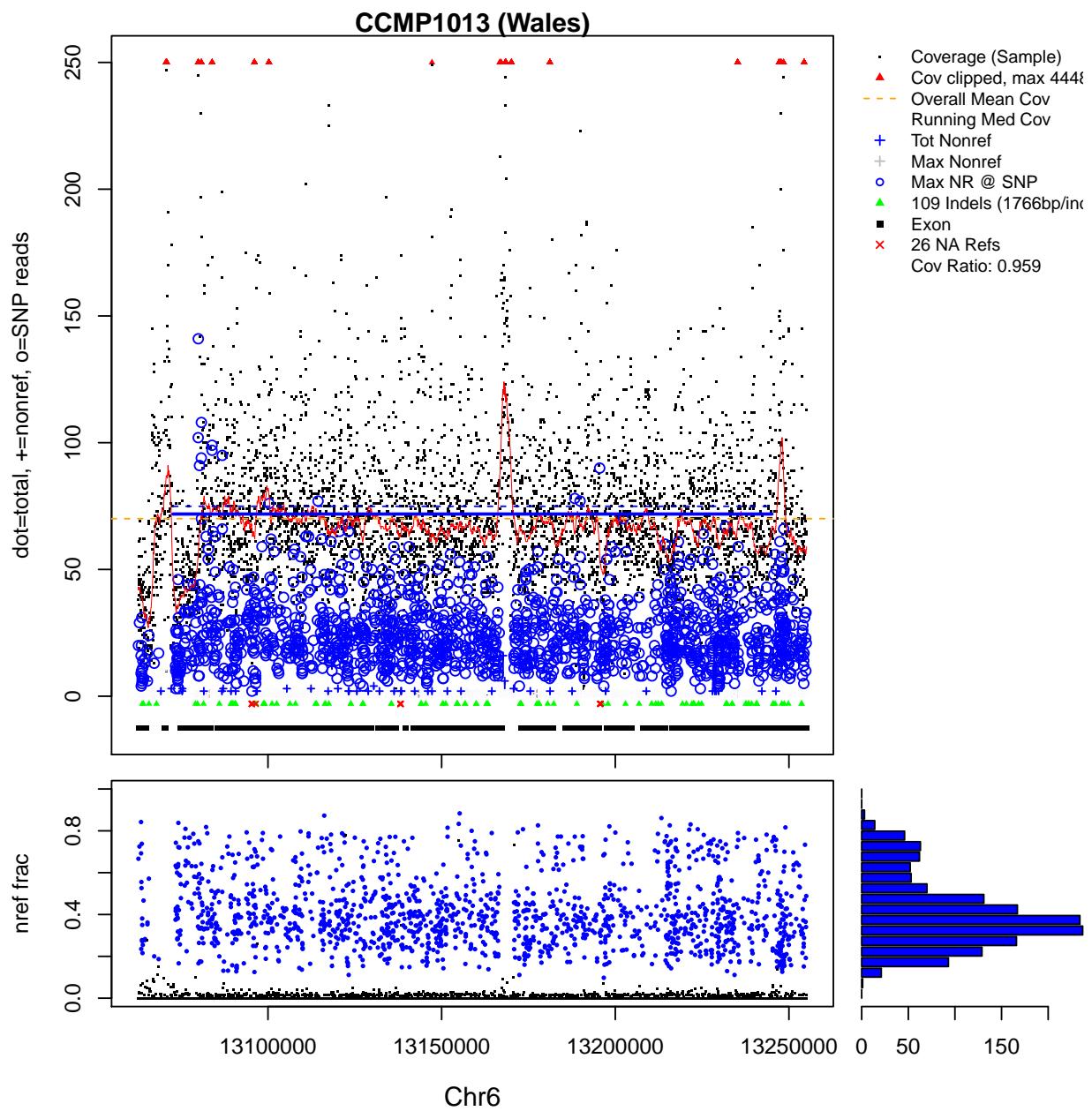
```
# Rows 576 : 583
#          chr start   end length tp1007 tp1012 tp1013 tp1014 tp1015 IT tp1335 pattern
# Chr6:174401 Chr6 174401 174500    100     NA     NA  0.592     NA     NA NA NA     NA      20
# Chr6:174501 Chr6 174501 176600   2100     NA  0.589  0.592  0.709  0.611 NA 0.582    75
# Chr6:176601 Chr6 176601 181700   5100     NA     NA  0.592  0.709  0.611 NA 0.582    35
# Chr6:181701 Chr6 181701 268500  86800     NA     NA     NA  0.709  0.611 NA 0.582    15
# Chr6:268501 Chr6 268501 272600   4100     NA     NA     NA     NA NA NA     NA      00
# Chr6:272601 Chr6 272601 272900    300     NA     NA     NA     NA 0.586 NA 0.589    05
# Chr6:272901 Chr6 272901 346300  73400     NA     NA     NA  0.685  0.586 NA 0.589    15
# Chr6:346301 Chr6 346301 346500    200     NA     NA     NA  0.685     NA NA 0.589    11
# Chr6:346501 Chr6 346501 347000    500     NA     NA     NA  0.685     NA NA     NA      10
# Chr6:347001 Chr6 347001 660300 313300     NA     NA     NA     NA NA NA     NA      00
```

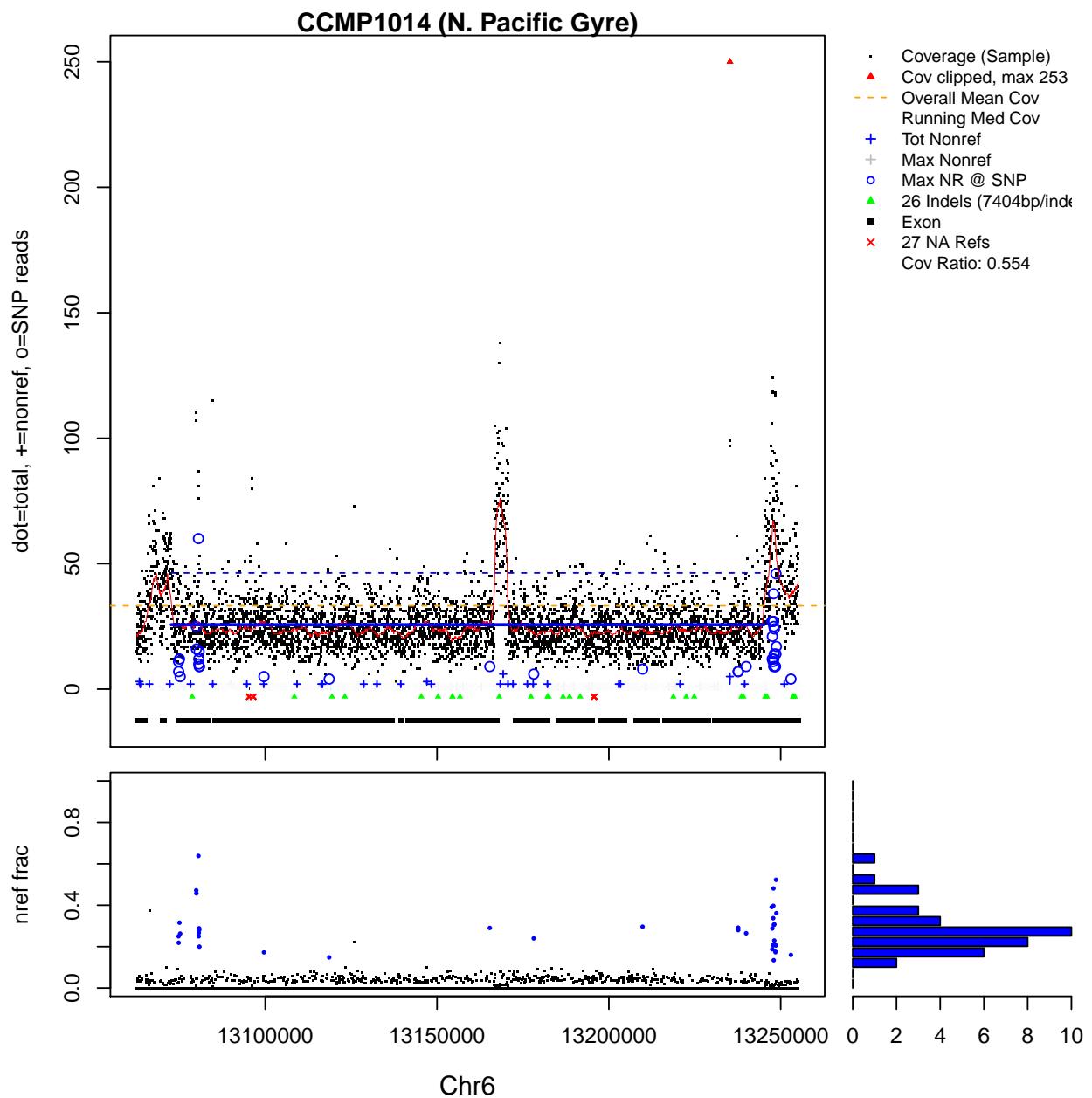
### CCMP1335 (New York)

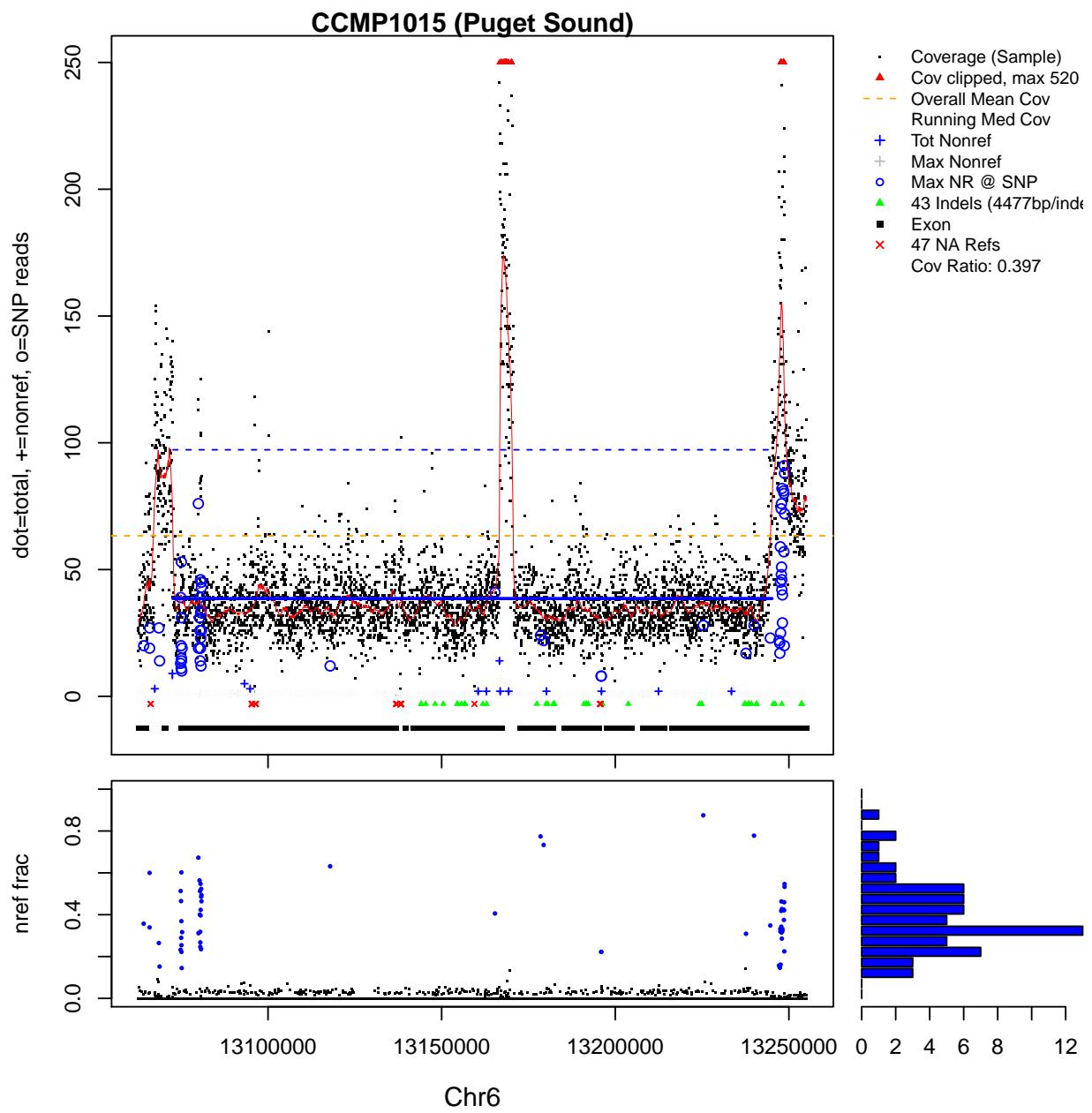


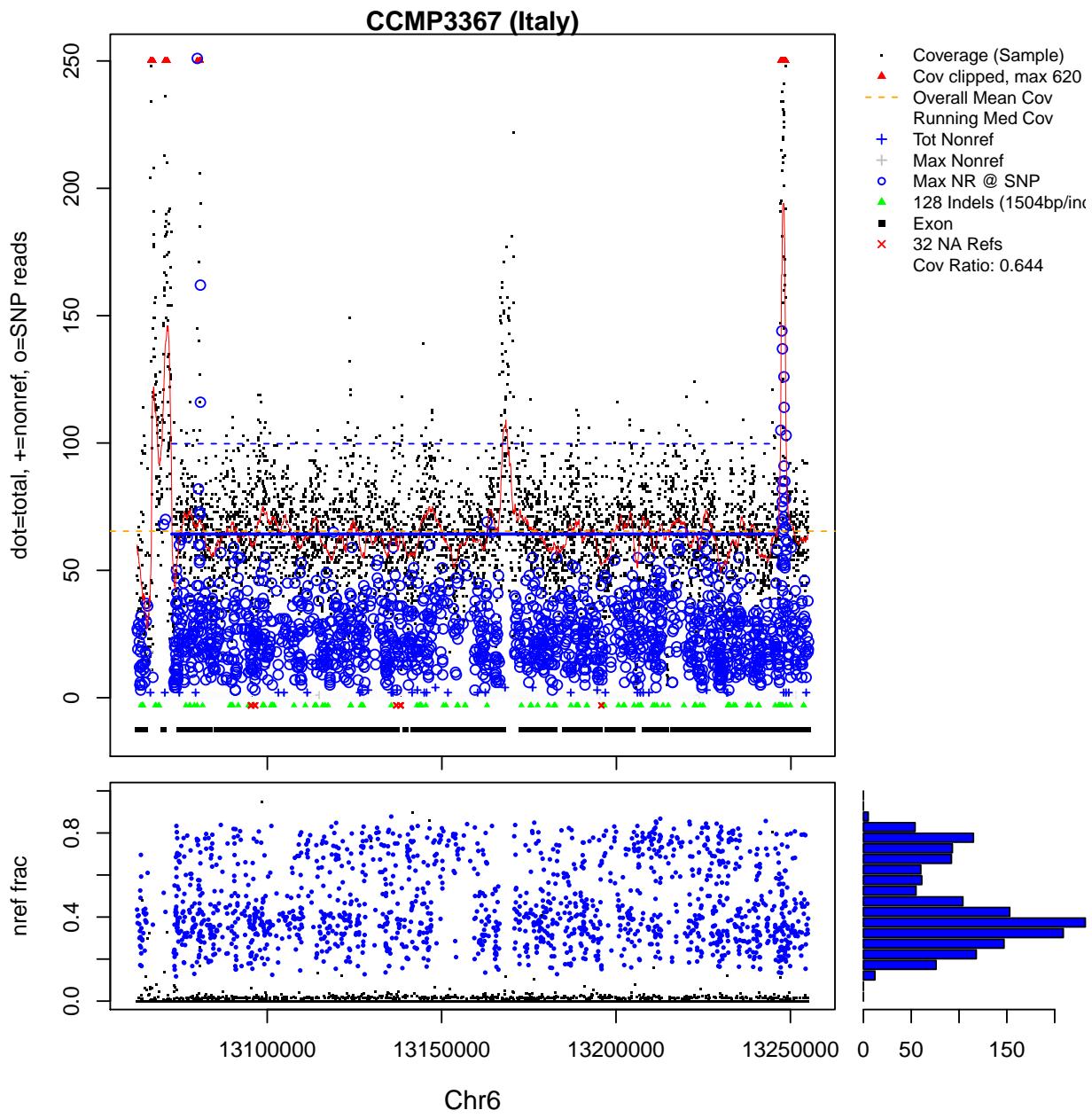












Are IT/Wales low nonref? not really:

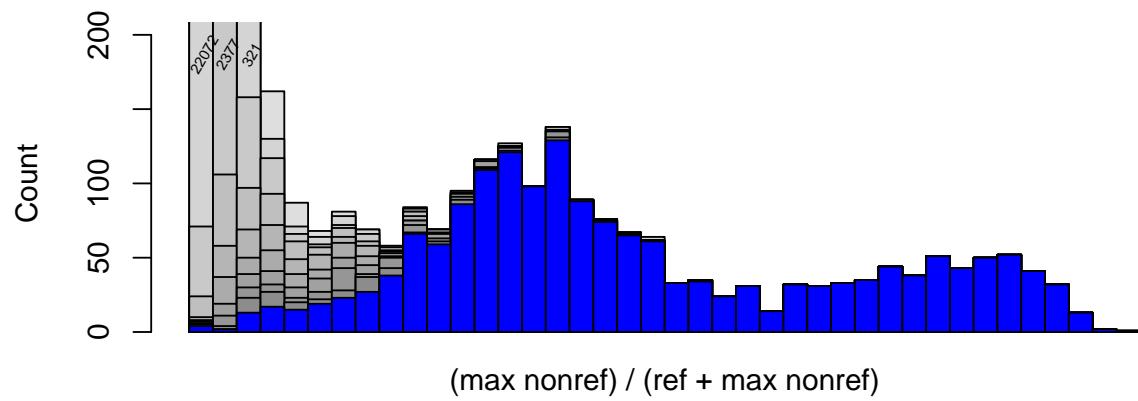
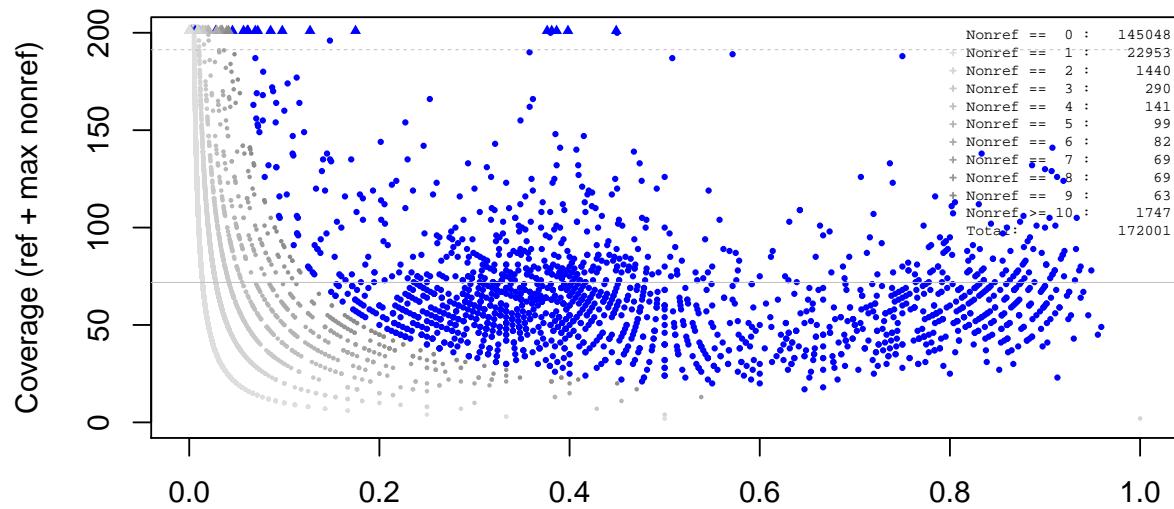
```
show.allele.scatter(3, seg.mask(chrloc2g('Chr6:174501'), chrloc2g('Chr6:346501')))
```

```
#      [,1]   [,2]   [,3]   [,4]   [,5]   [,6]   [,7]   [,8]   [,9]   [,10]  [,11]
# [1,] "blue" "nm3"  "nm3x" "nm3hi" "red"  "black" "green" "orange" "orngchi" "nzgrey" "grey"
# [2,] "1747" "1236" NA     "0"    NA     NA     NA     NA     NA     NA     NA
```

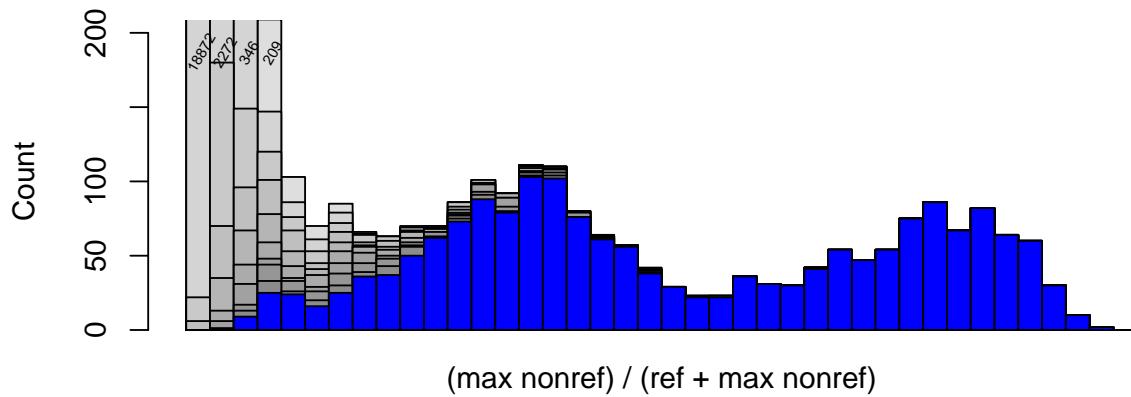
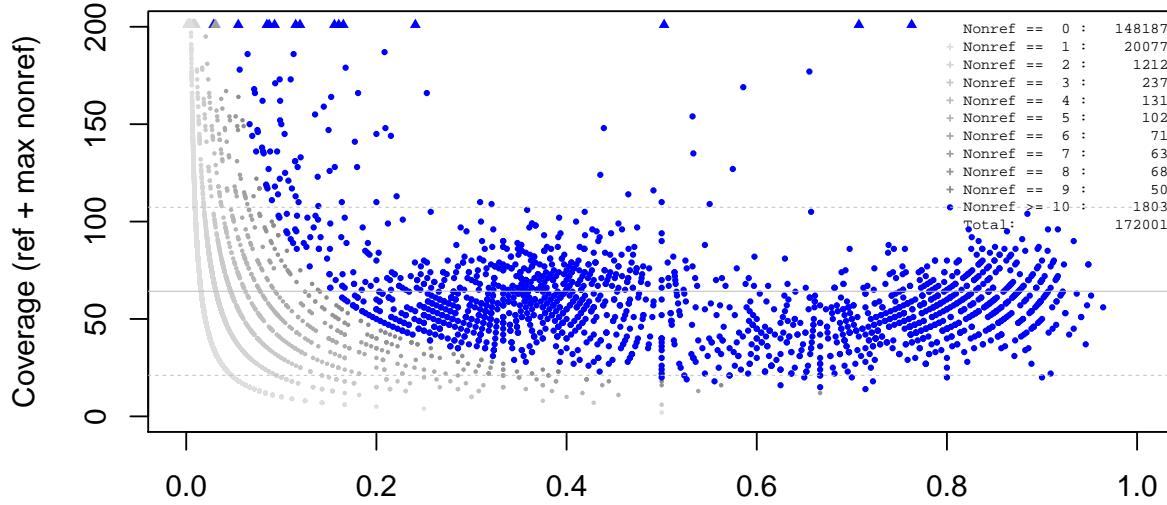
```
show.allele.scatter(6, seg.mask(chrloc2g('Chr6:174501'), chrloc2g('Chr6:346501')))
```

```
#      [,1]   [,2]   [,3]   [,4]   [,5]   [,6]   [,7]   [,8]   [,9]   [,10]  [,11]
# [1,] "blue" "nm3"  "nm3x" "nm3hi" "red"  "black" "green" "orange" "orngchi" "nzgrey" "grey"
# [2,] "1803" "1070" NA     "0"    NA     NA     NA     NA     NA     NA     NA
```

## CCMP1013 (Wales)



## CCMP3367 (Italy)

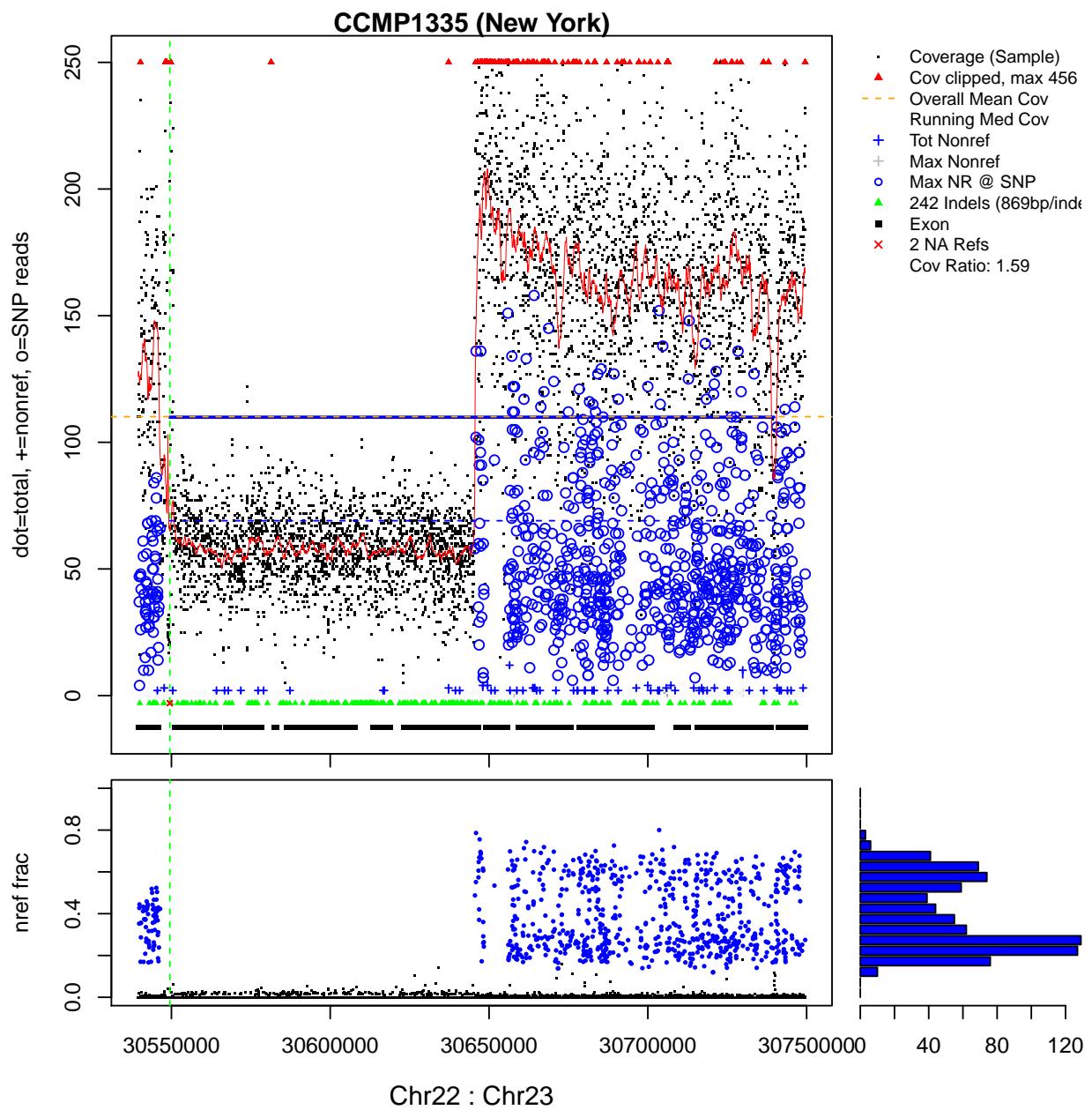


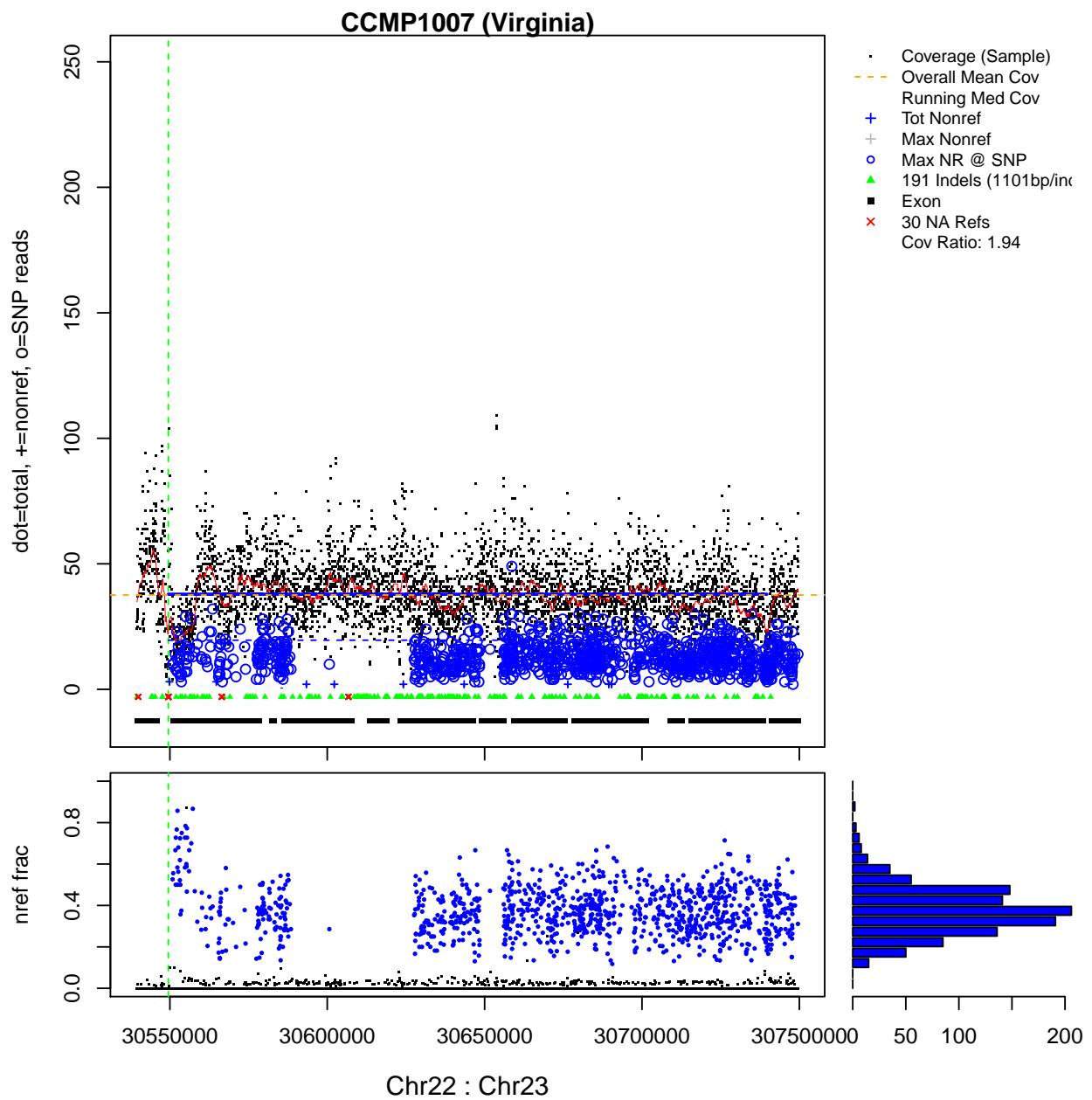
Another NY chunk: 1st 96k of chr23. VA: undel, snpy, except for about 20k. AUS: ditto, 1015: ditto. 1014: del, snpy except same 20k. IT/wales: undel, snpy all over. NY: 96k del,.snp-free, followed by 100K @ 1.5x.

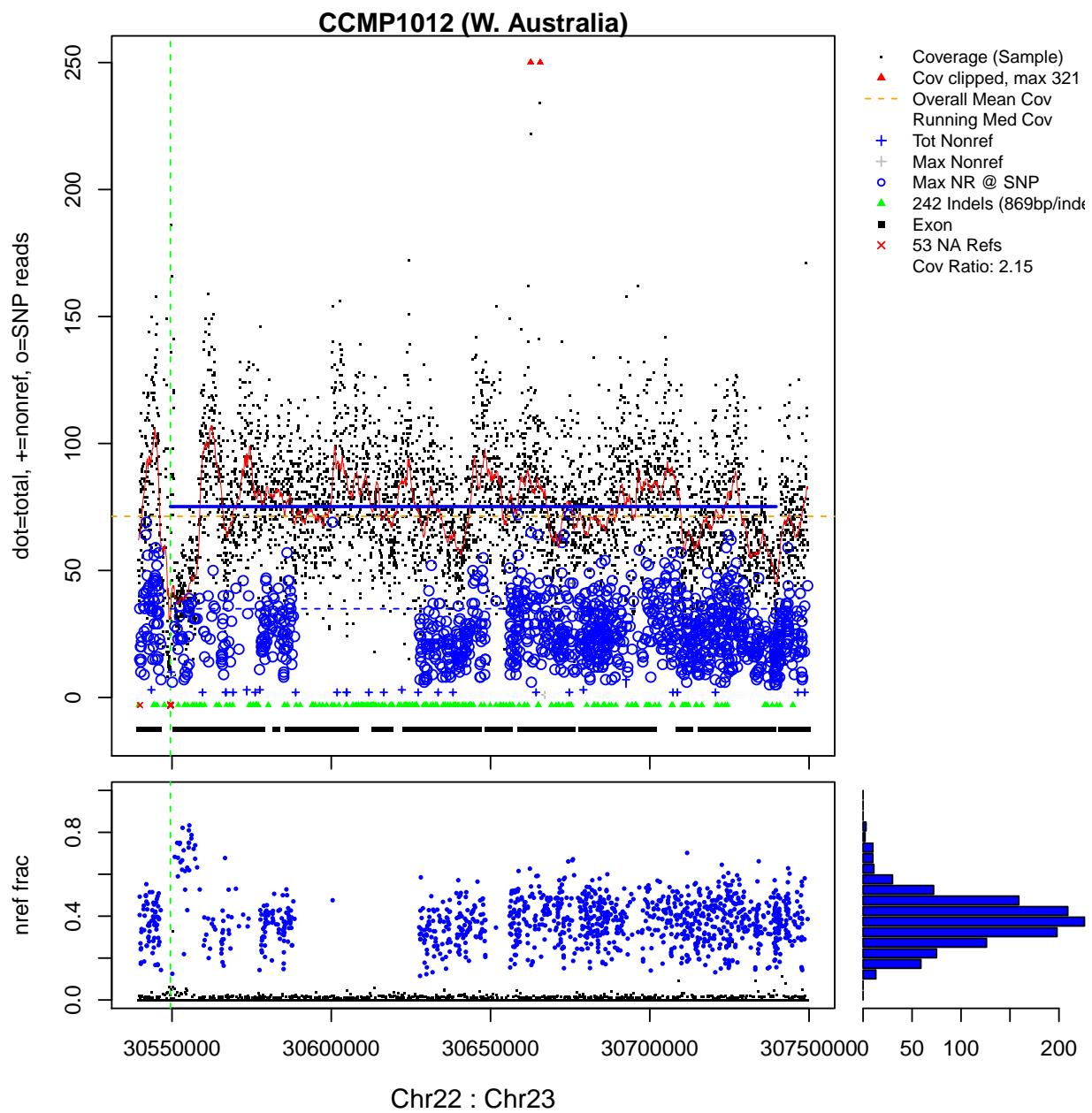
Especially interesting: Approx 10k at left tip in 1007+1012 is hemizygous, but nonref frac near 0.7.

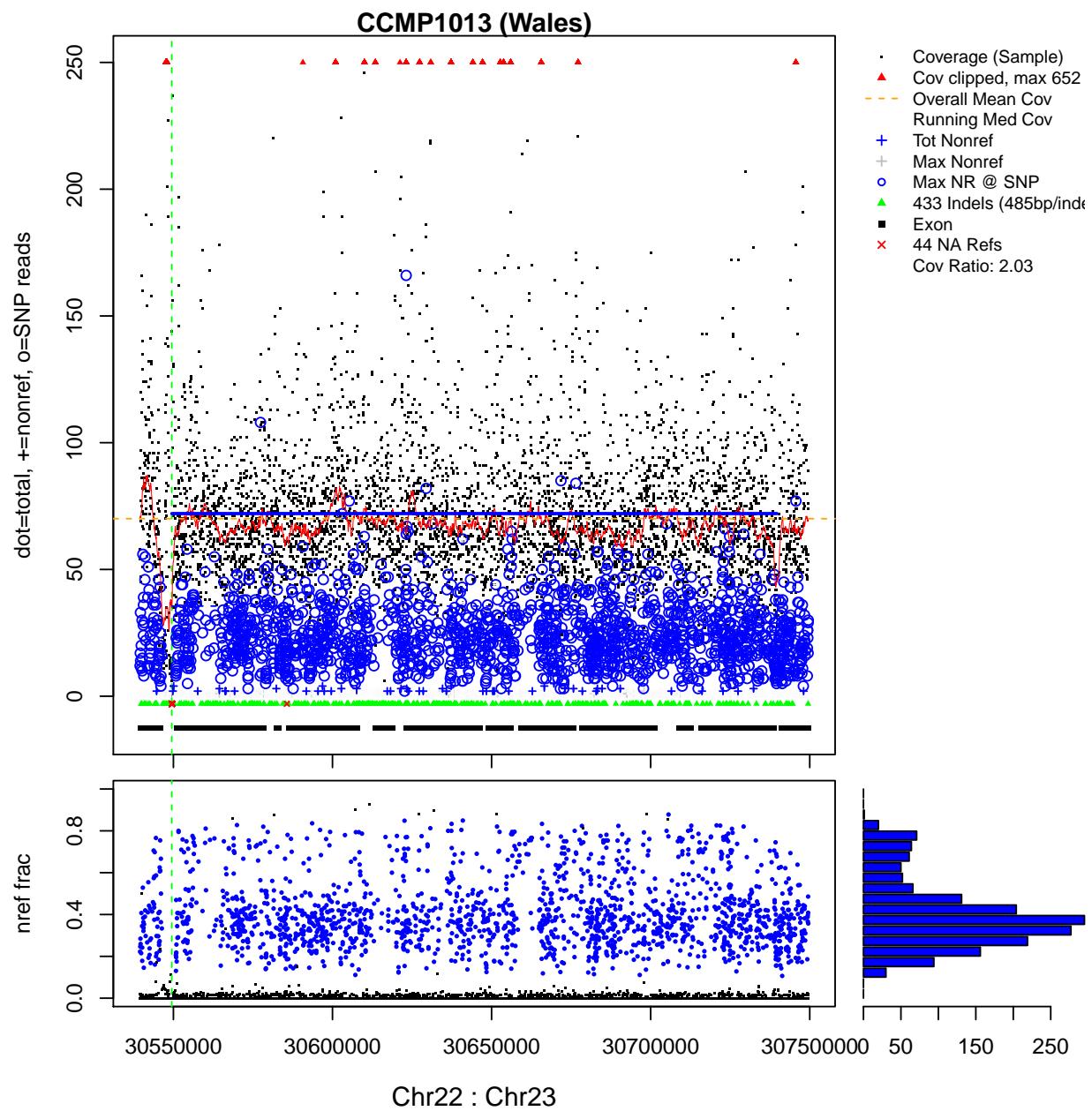
```
hemi.chunk(c('Chr23:1', 'Chr23:96001'), margin=10000)
```

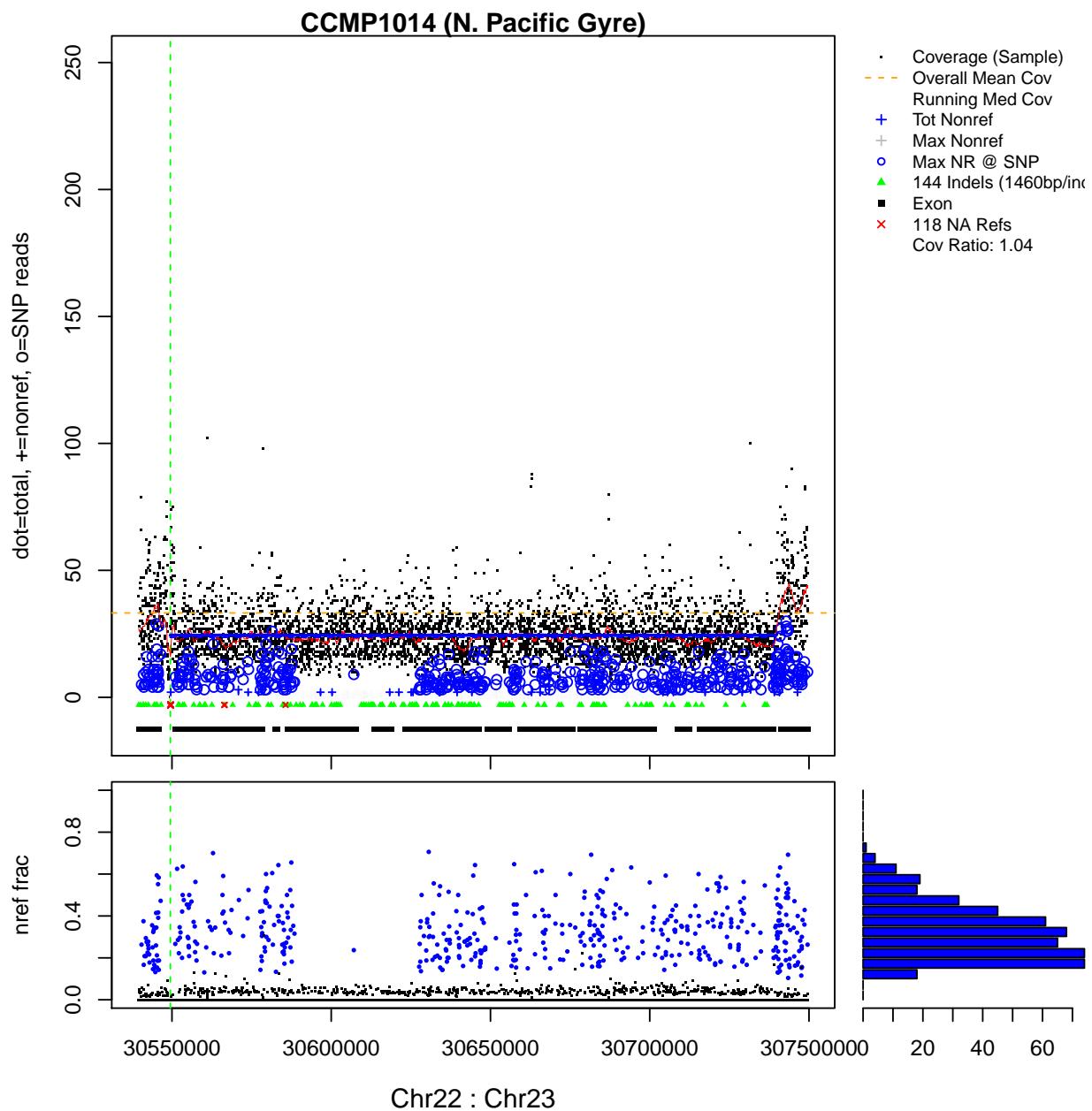
```
# Rows 458 : 461
#           chr   start     end length tp1007 tp1012 tp1013 tp1014 tp1015 IT tp1335 pattern
# Chr22:1057565 Chr22 1057565 1057564      0     NA     NA     NA     NA     NA NA NA     NA 000
# Chr23:1         Chr23      1    8900     8900  0.748  0.739     NA  0.694     NA NA 0.573 151
# Chr23:8901      Chr23    8901     9100     200     NA  0.739     NA  0.694     NA NA 0.573 051
# Chr23:9101      Chr23    9101    96000    86900     NA     NA  0.694     NA NA 0.573 011
# Chr23:96001     Chr23   96001   190200    94200     NA     NA  0.694     NA NA     NA 010
# Chr23:190201    Chr23  190201   305400   115200     NA     NA     NA     NA NA NA     NA 000
```

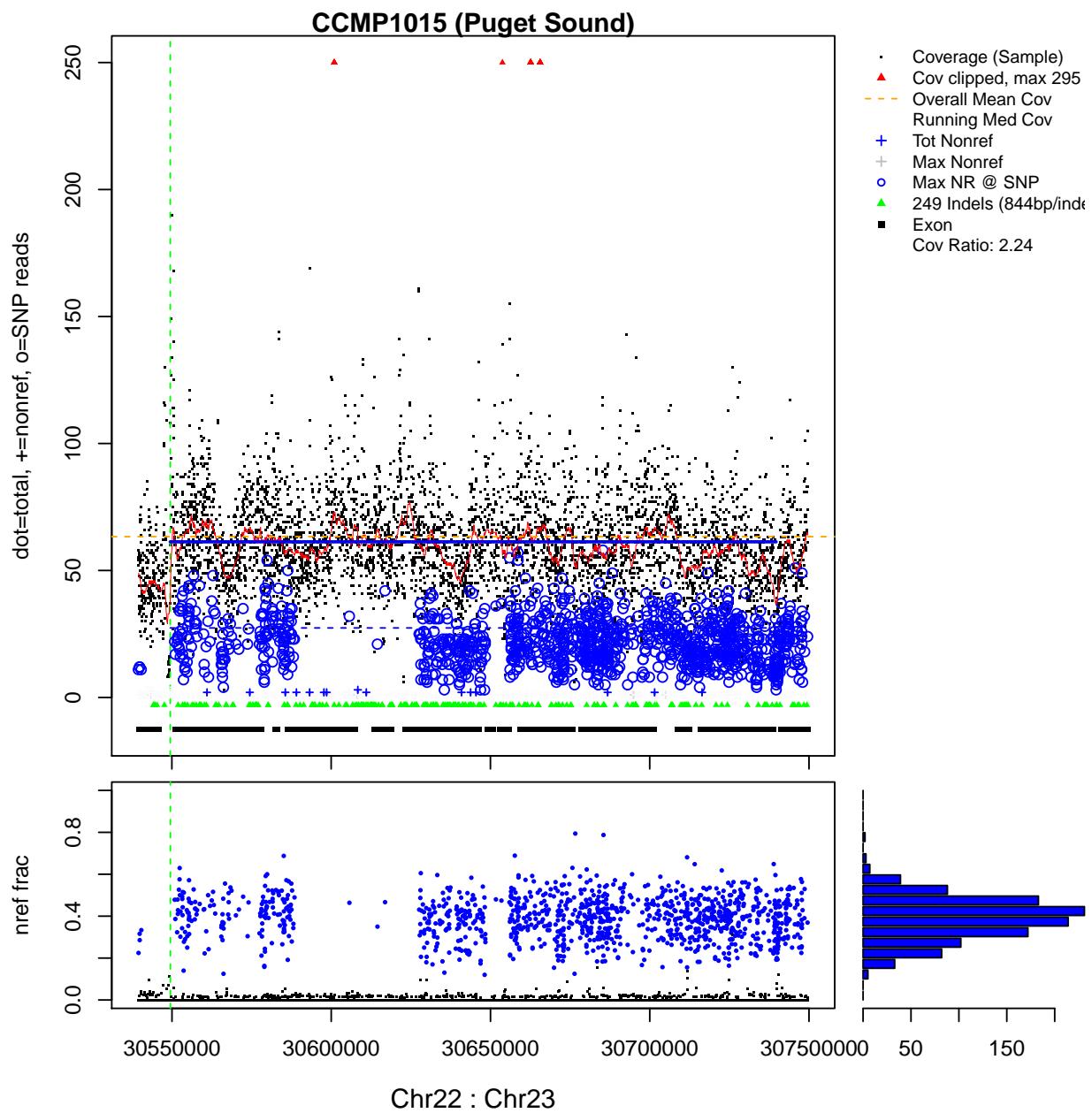


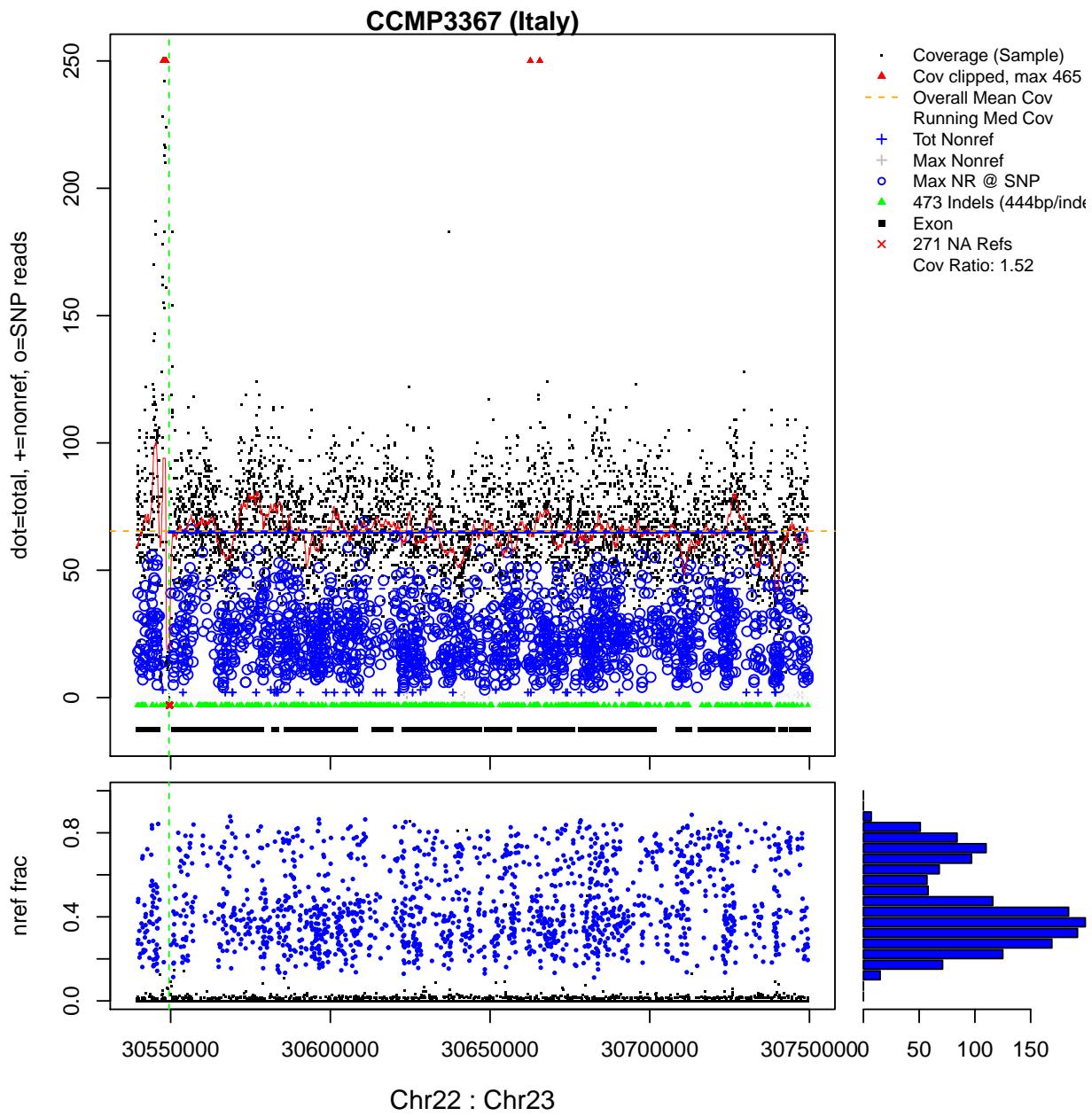












Great snap of locality in nonref frac in NY: left 96k of chr23 is hemi, snpless; rest is 1.5x, and snp-frac is bi-modal at about 1/3 , 2/3, *except* for a 50k chunk near the middle, which is only 1/3. 1007,1012, 1015: normal coverage , 50K LOH 1013/IT: normal coverage, snpy, usual bimodal pattern, heavier on 0.4. Gyre has 200K region at .7 coverage, with the same 50K LOH. SNP density is lower than 1015, say (as usual) , but appears unimodal, despite *elevated* coverage on the other 250K.

```
hemi.chunk(c('Chr23:1', 'Chr23:454954'), 7, margin=1000)
```

```
# Rows 458 : 469
#           chr   start     end length tp1007 tp1012 tp1013 tp1014 tp1015      IT tp1335 pattern
# Chr22:1057565 Chr22 1057565 1057564     0    NA    NA    NA    NA    NA    NA    NA    NA    000
# Chr23:1        Chr23      1     8900    8900  0.748  0.739  NA  0.694  NA    NA  0.573  151
# Chr23:8901     Chr23    8901    9100    200    NA  0.739  NA  0.694  NA    NA  0.573  051
# Chr23:9101     Chr23    9101   96000   86900    NA    NA  0.694  NA    NA  0.573  011
# Chr23:96001    Chr23   96001   190200   94200    NA    NA  0.694  NA    NA    NA    NA  010
# Chr23:190201   Chr23  190201   305400  115200    NA    NA    NA    NA    NA    NA    NA  000
# Chr23:305401   Chr23  305401   307700   2300    NA    NA    NA    NA  0.737  NA  002
```

```

# Chr23:307701 Chr23 307701 341700 34000 NA NA NA NA NA NA NA NA 000
# Chr23:341701 Chr23 341701 342300 600 NA NA NA NA NA NA 0.197 NA 002
# Chr23:342301 Chr23 342301 444400 102100 NA NA NA NA NA NA NA NA 000
# Chr23:444401 Chr23 444401 447900 3500 NA NA NA 0.529 NA NA NA NA 020
# Chr23:447901 Chr23 447901 454953 7053 NA NA NA NA NA NA NA NA 000
# Chr23:454954 Chr23 454954 454953 0 NA NA NA NA NA NA NA NA 000
# Chr24:1 Chr24 1 10900 10900 NA NA NA NA NA NA NA NA 000

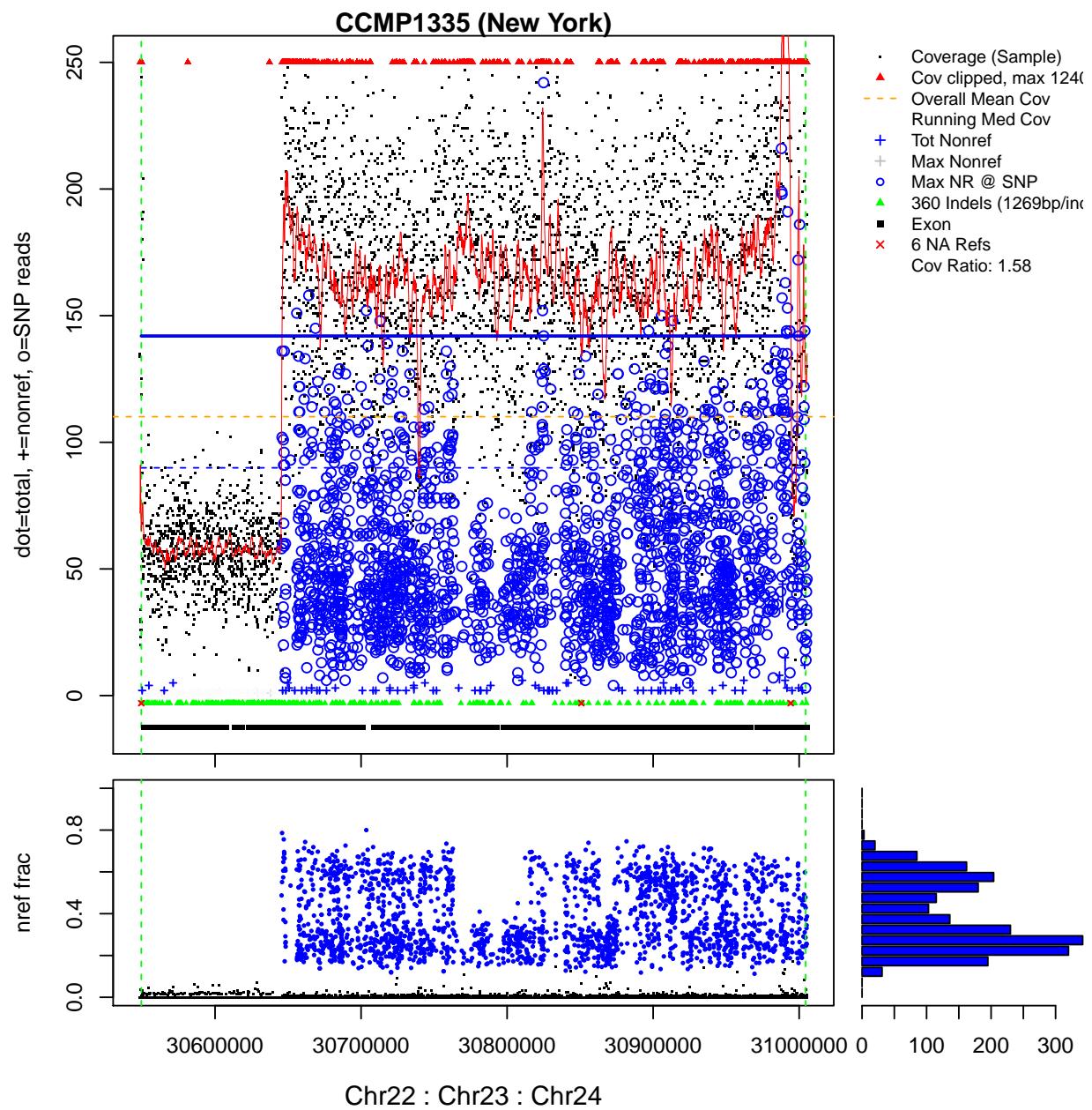


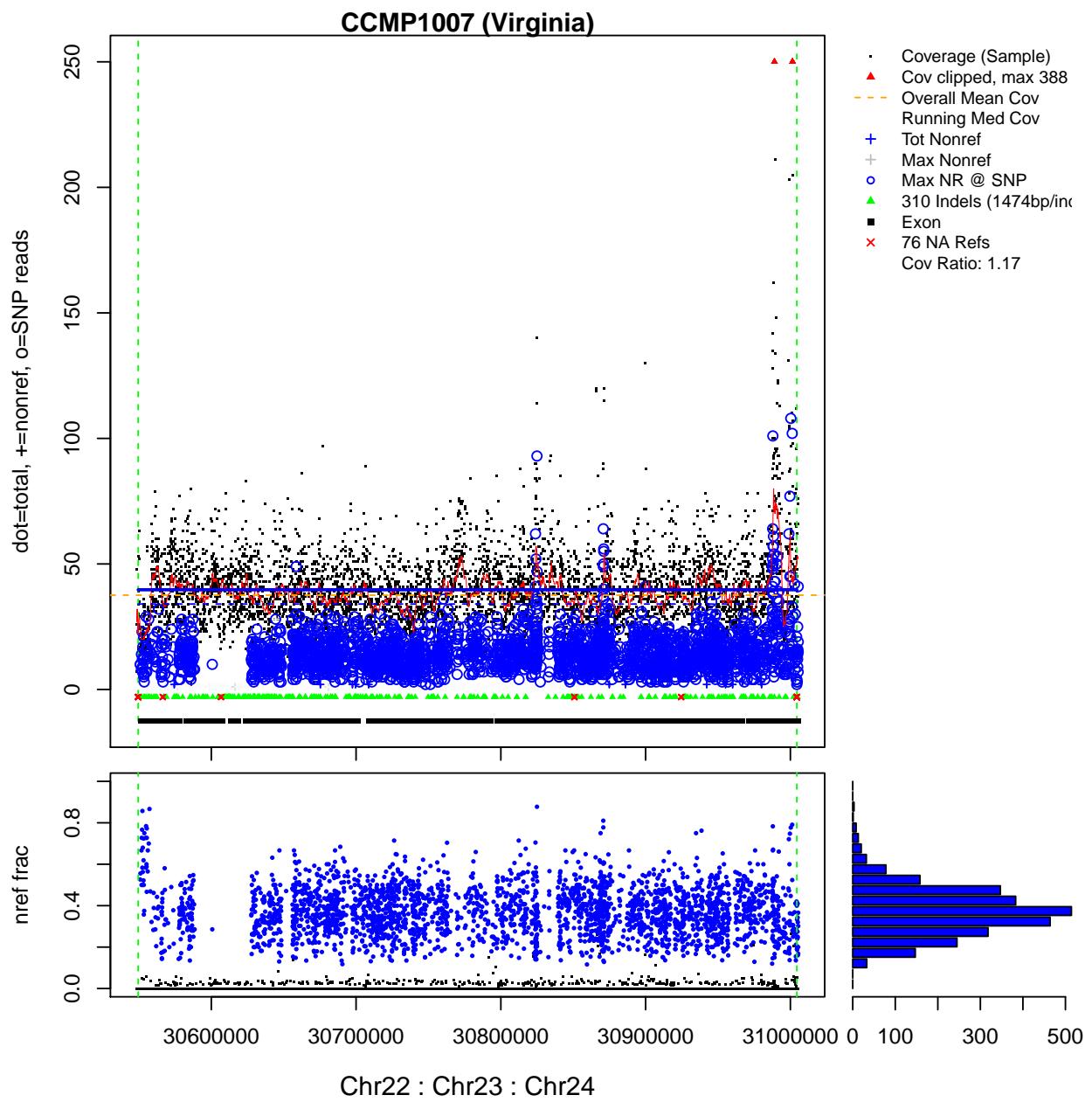
### hemi.chunk(c('Chr23:1','Chr23:454954'),1:6,margin=1000)

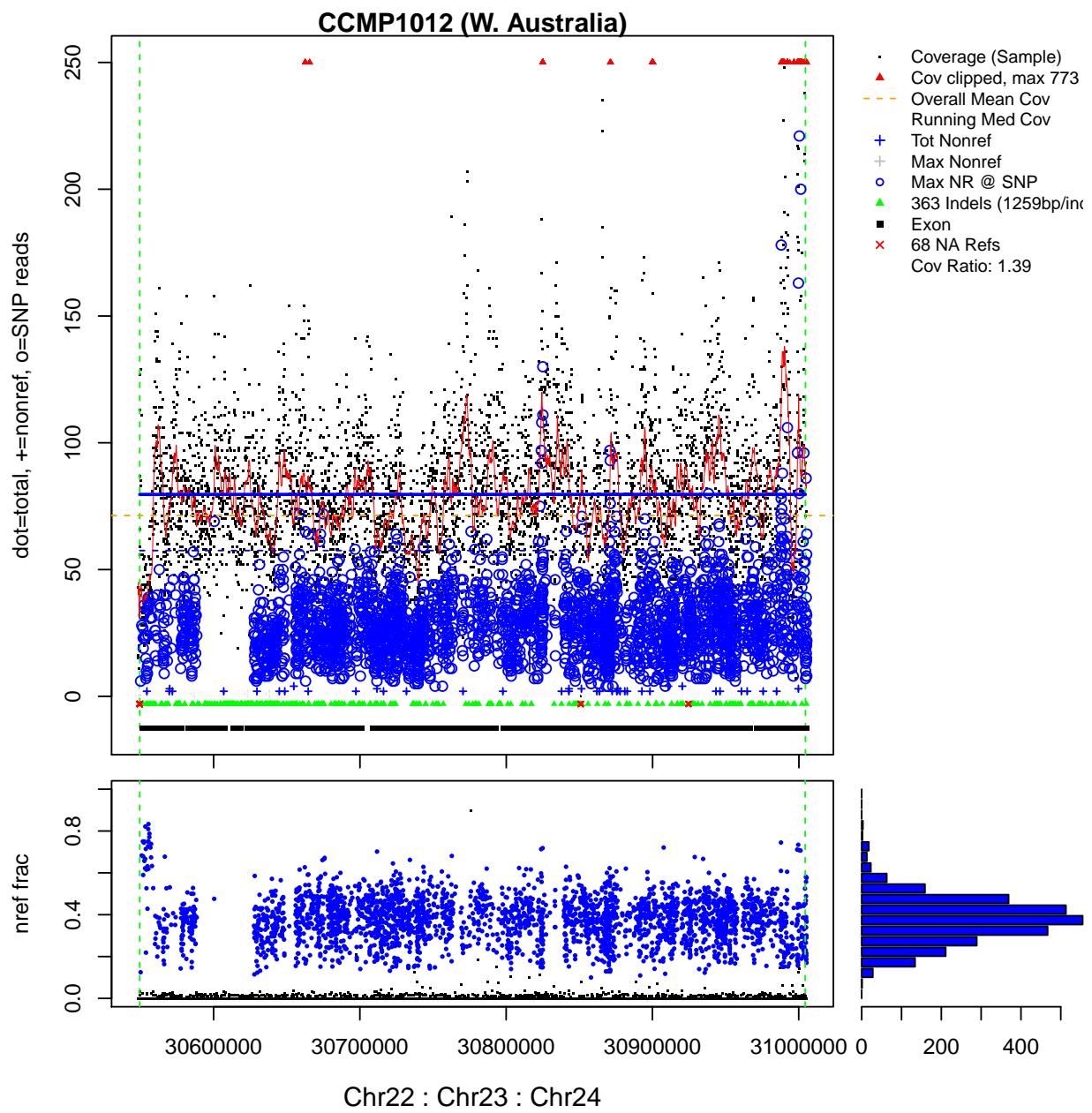


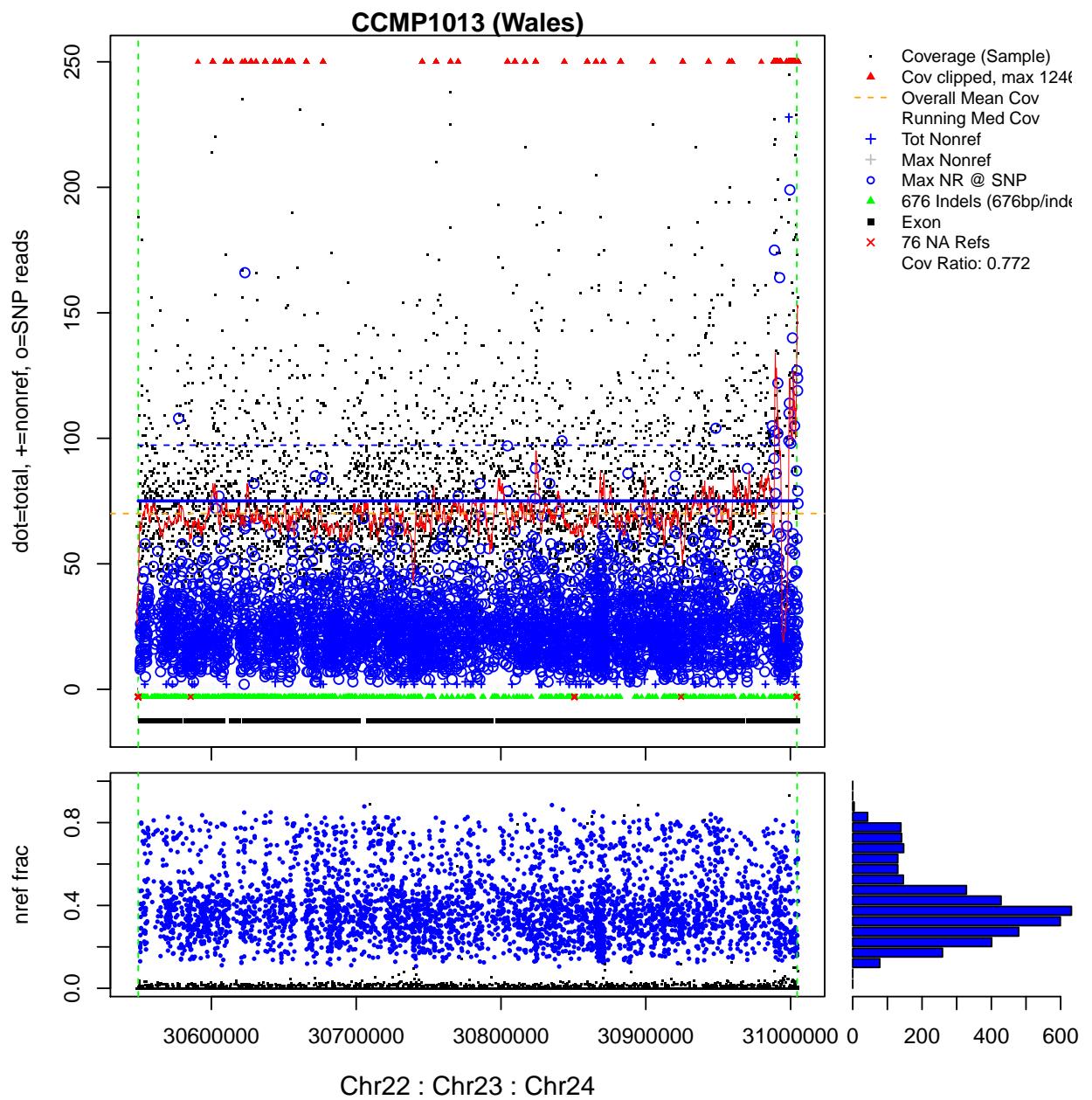
# Rows 458 : 469
#          chr start      end length tp1007 tp1012 tp1013 tp1014 tp1015 IT tp1335 pattern
# Chr22:1057565 Chr22 1057565 1057564 0 NA NA NA NA NA NA NA NA 000
# Chr23:1 Chr23 1 8900 8900 0.748 0.739 NA 0.694 NA NA 0.573 151
# Chr23:8901 Chr23 8901 9100 200 NA 0.739 NA 0.694 NA NA 0.573 051
# Chr23:9101 Chr23 9101 96000 86900 NA NA NA 0.694 NA NA 0.573 011
# Chr23:96001 Chr23 96001 190200 94200 NA NA NA 0.694 NA NA NA 010
# Chr23:190201 Chr23 190201 305400 115200 NA NA NA NA NA NA NA 000
# Chr23:305401 Chr23 305401 307700 2300 NA NA NA NA NA 0.737 NA 002
# Chr23:307701 Chr23 307701 341700 34000 NA NA NA NA NA NA NA 000
# Chr23:341701 Chr23 341701 342300 600 NA NA NA NA NA 0.197 NA 002
# Chr23:342301 Chr23 342301 444400 102100 NA NA NA NA NA NA NA 000
# Chr23:444401 Chr23 444401 447900 3500 NA NA NA 0.529 NA NA NA NA 020
# Chr23:447901 Chr23 447901 454953 7053 NA NA NA NA NA NA NA NA 000
# Chr23:454954 Chr23 454954 454953 0 NA NA NA NA NA NA NA NA 000
# Chr24:1 Chr24 1 10900 10900 NA NA NA NA NA NA NA NA 000

```

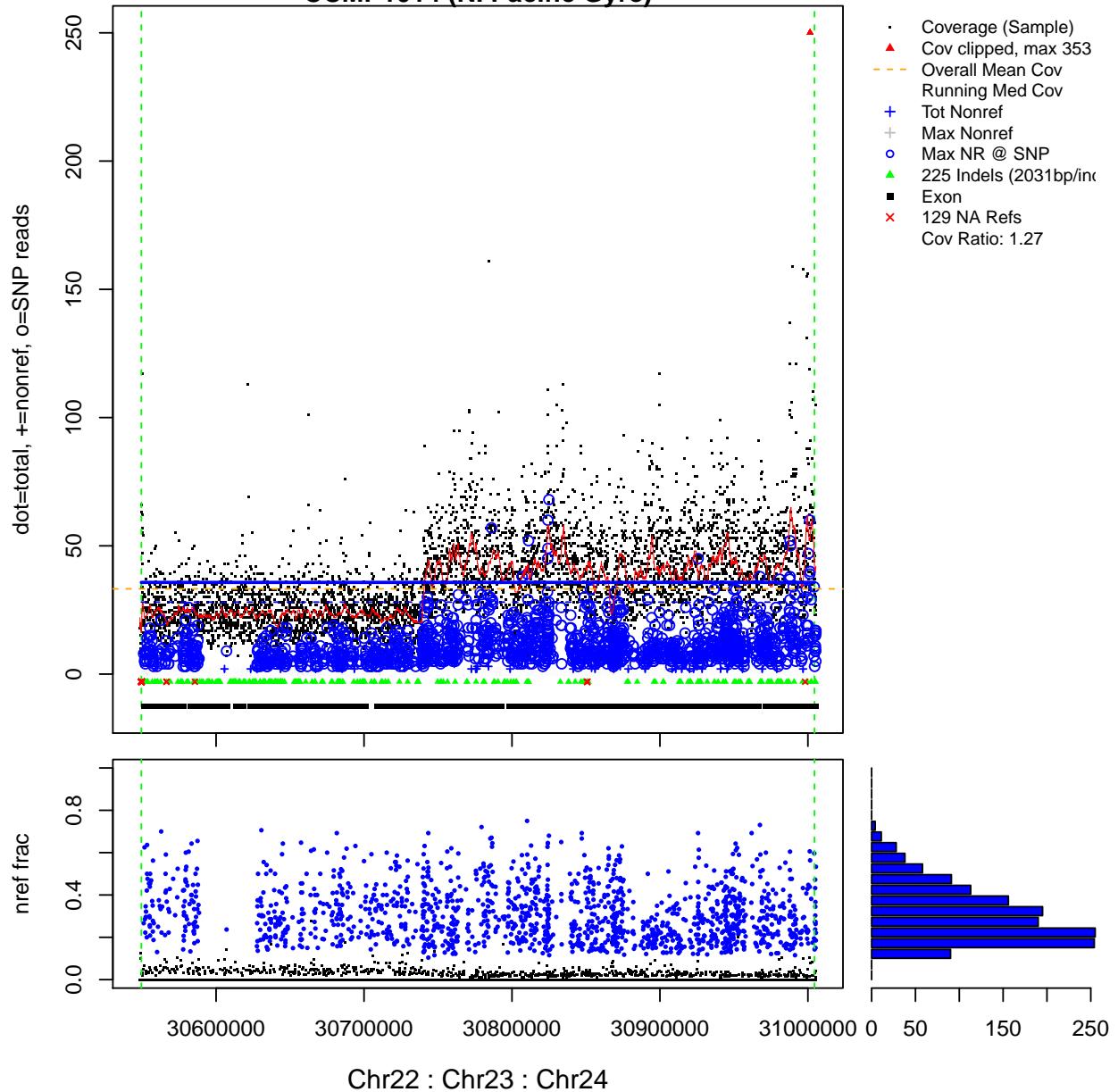


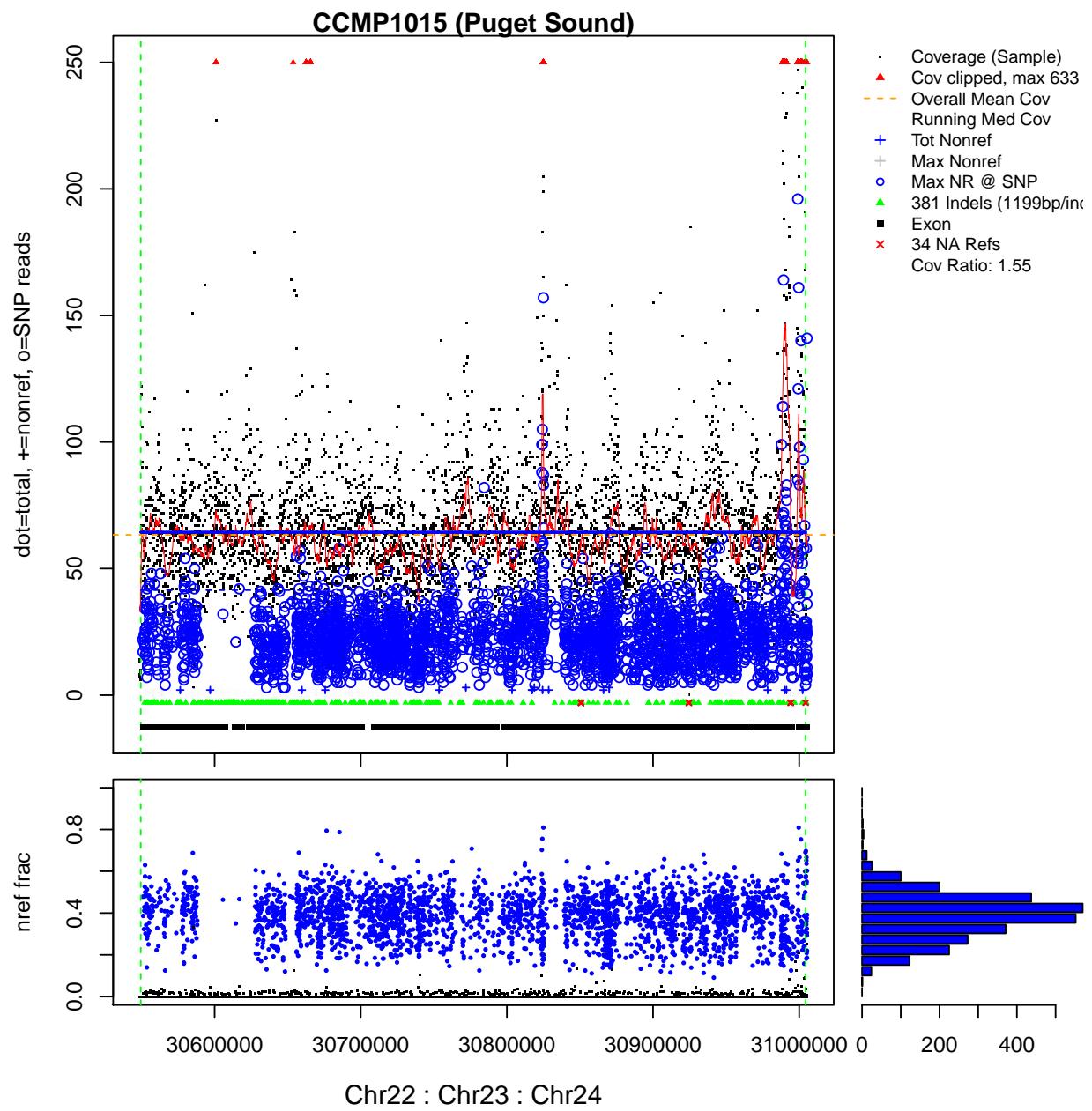


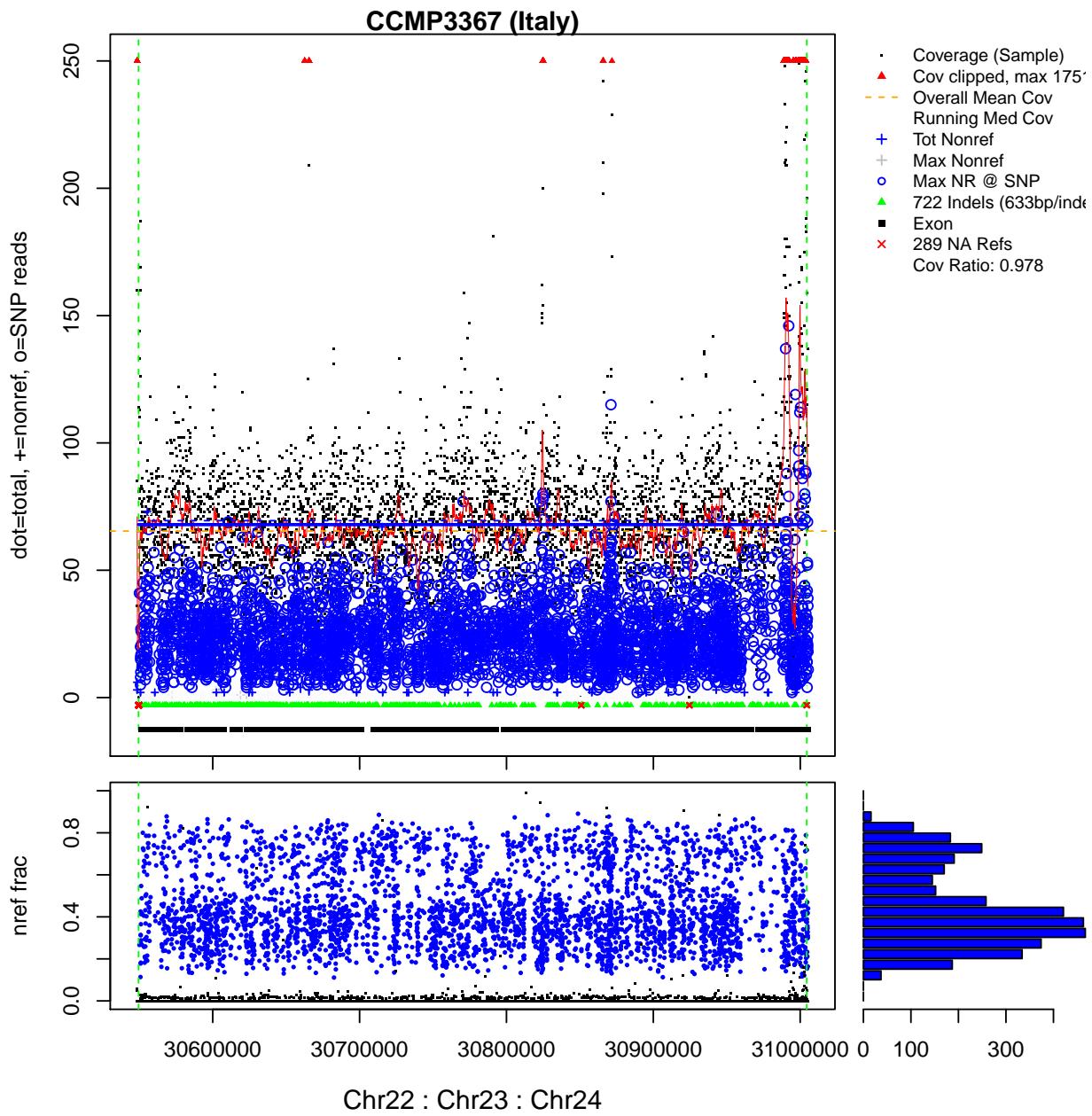




### CCMP1014 (N. Pacific Gyre)







Other possible trisomies? 23 segments longer than 100k:

```

trisome <- 1.3 <= cnv$cov_ratio & cnv$cov_ratio <= 1.7
sum(trisome)    ## [1] 655
# [1] 655

tripi <- order(cnv$length[trisome], decreasing=T)
cnv[trisome,][tripi[1:25],]

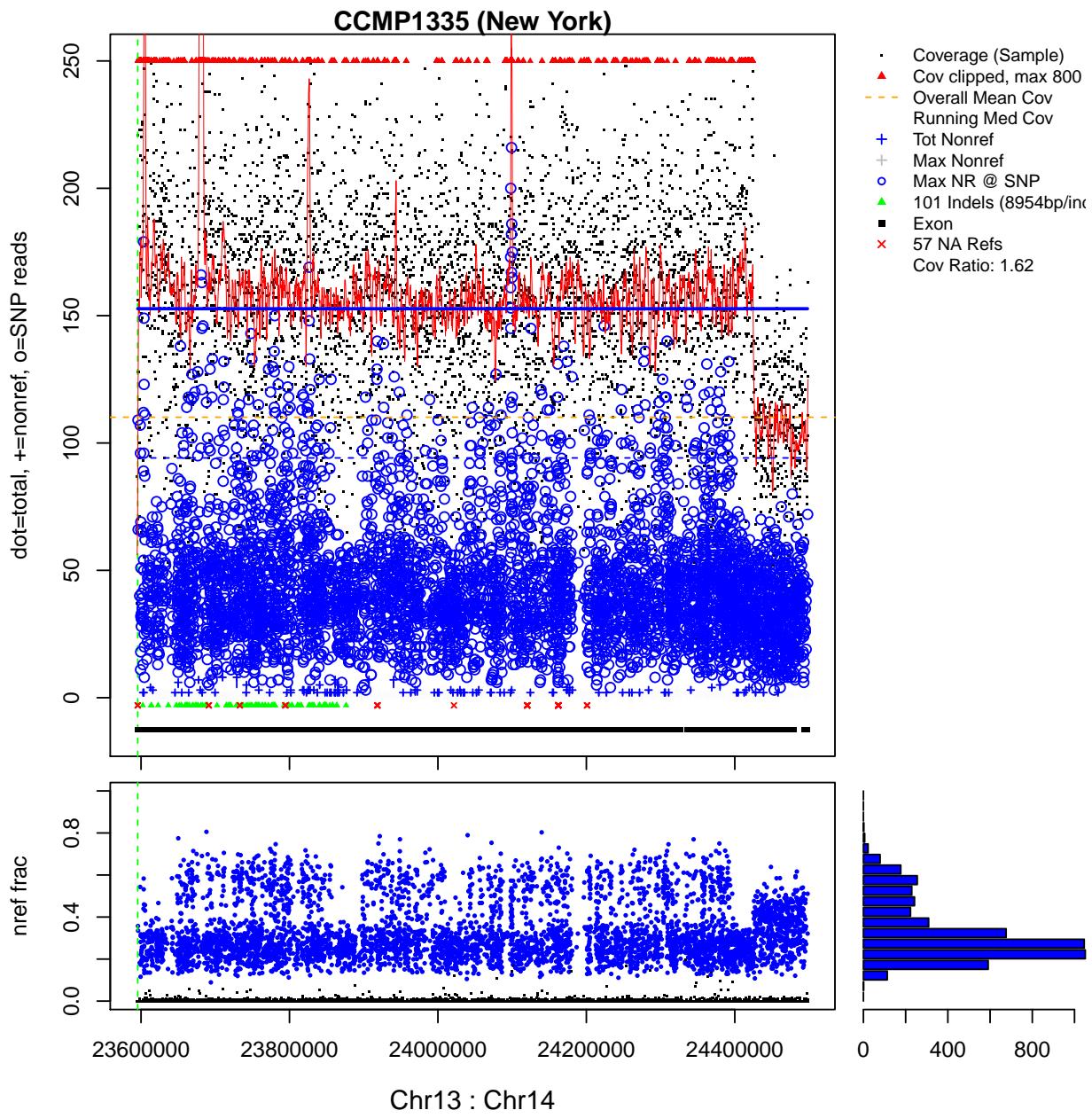
#      strain      chr     start      end length filtered      type cov_ratio dup_frac
# 2238 tp1335   Chr14    57701  566500  508800 FALSE CNVnator  1.52069 0.0295811
# 874  tp1014   Chr10   260101  602100  342000 FALSE CNVnator  1.46552 0.0288144
# 1473 tp1015   Chr8    967701 1267200 299500 FALSE CNVnator  1.56302 0.0838569
# 861  tp1014   Chr8    947001 1242800 295800 FALSE CNVnator  1.69376 0.0498832
# 2162 tp1335   Chr6    346501  615100  268600 FALSE CNVnator  1.48366 0.0116308
# 1444 tp1015   Chr6    346301  610700  264400 FALSE CNVnator  1.47470 0.0148579
# 2239 tp1335   Chr14   566701  829300  262600 FALSE CNVnator  1.51717 0.0154430

```

|        |        |           |         |         |        |       |          |         |           |
|--------|--------|-----------|---------|---------|--------|-------|----------|---------|-----------|
| # 2186 | tp1335 | Chr8      | 1005101 | 1267200 | 262100 | FALSE | CNVnator | 1.60923 | 0.0968873 |
| # 873  | tp1014 | Chr10     | 28501   | 246900  | 218400 | FALSE | CNVnator | 1.57852 | 0.1519620 |
| # 668  | tp1013 | Chr18     | 309801  | 518300  | 208500 | FALSE | CNVnator | 1.52974 | 0.0244539 |
| # 960  | tp1014 | Chr19c_29 | 4901    | 180800  | 175900 | TRUE  | CNVnator | 1.51288 | 0.0792422 |
| # 2311 | tp1335 | Chr23     | 96001   | 271800  | 175800 | FALSE | CNVnator | 1.61818 | 0.0813743 |
| # 2312 | tp1335 | Chr23     | 272001  | 445100  | 173100 | FALSE | CNVnator | 1.64695 | 0.0570672 |
| # 945  | tp1014 | Chr18     | 374401  | 547300  | 172900 | FALSE | CNVnator | 1.38503 | 0.0378534 |
| # 669  | tp1013 | Chr18     | 519801  | 674100  | 154300 | FALSE | CNVnator | 1.53579 | 0.0275490 |
| # 958  | tp1014 | Chr19b_31 | 1       | 151700  | 151700 | FALSE | CNVnator | 1.40821 | 0.0380134 |
| # 1273 | tp1007 | Chr20     | 263301  | 408900  | 145600 | FALSE | CNVnator | 1.69331 | 0.1602950 |
| # 877  | tp1014 | Chr10     | 681001  | 810000  | 129000 | FALSE | CNVnator | 1.41920 | 0.0501984 |
| # 941  | tp1014 | Chr18     | 5701    | 133700  | 128000 | FALSE | CNVnator | 1.63863 | 0.0535742 |
| # 1214 | tp1007 | Chr14     | 57601   | 182600  | 125000 | FALSE | CNVnator | 1.68366 | 0.0961556 |
| # 986  | tp1014 | Chr23     | 332901  | 455000  | 122100 | FALSE | CNVnator | 1.65306 | 0.1235470 |
| # 1223 | tp1007 | Chr15     | 86201   | 197400  | 111200 | FALSE | CNVnator | 1.54600 | 0.0547763 |
| # 944  | tp1014 | Chr18     | 256801  | 366300  | 109500 | FALSE | CNVnator | 1.47736 | 0.0533481 |
| # 807  | tp1014 | Chr3      | 1       | 98300   | 98300  | FALSE | CNVnator | 1.33840 | 0.1953450 |
| # 991  | tp1014 | Chr24     | 200101  | 297400  | 97300  | FALSE | CNVnator | 1.63994 | 0.2968230 |

```
#hemi.chunk(c('Chr14:1', 'Chr14:829301'), 7, margin=1000)
hemi.chunk(c('Chr14:1', 'Chr14:900701'), 7, margin=1000)
```

| # Rows 145 : 150 |       |         |         |        |        |        |        |        |        |      |        |         |
|------------------|-------|---------|---------|--------|--------|--------|--------|--------|--------|------|--------|---------|
| #                | chr   | start   | end     | length | tp1007 | tp1012 | tp1013 | tp1014 | tp1015 | IT   | tp1335 | pattern |
| # Chr13:1052196  | Chr13 | 1052196 | 1052195 | 0      | NA     | NA     | NA     | NA     | NA     | NA   | NA     | 000     |
| # Chr14:1        | Chr14 | 1       | 640400  | 640400 | NA     | NA     | NA     | NA     | NA     | NA   | NA     | 000     |
| # Chr14:640401   | Chr14 | 640401  | 640600  | 200    | 0.609  | NA     | NA     | NA     | NA     | NA   | NA     | 100     |
| # Chr14:640601   | Chr14 | 640601  | 773600  | 133000 | 0.609  | 0.607  | NA     | NA     | NA     | NA   | NA     | 140     |
| # Chr14:773601   | Chr14 | 773601  | 777000  | 3400   | 0.609  | NA     | NA     | NA     | NA     | NA   | NA     | 100     |
| # Chr14:777001   | Chr14 | 777001  | 900700  | 123700 | 0.609  | 0.596  | NA     | NA     | NA     | NA   | NA     | 140     |
| # Chr14:900701   | Chr14 | 900701  | 902400  | 1700   | 0.609  | 0.596  | NA     | NA     | NA     | 0.59 | NA     | 142     |
| # Chr14:902401   | Chr14 | 902401  | 918000  | 15600  | 0.609  | 0.596  | NA     | NA     | NA     | NA   | NA     | 140     |



```

indel.counts <- unlist(lapply(full, function(x){sum(x$indel)})); indel.counts

#   1007   1012   1013   1014   1015   3367   1335
#  7186   8160  15149   5700   8363  15728   7633

sum(full[[7]]$indel[chrlc2g('Chr14:1')+(1:3e5)])

# [1] 101

indel.counts[7]/nrow(full[[7]]) * 3e5

#      1335
# 70.22078

sum(full[[7]]$indel[chrlc2g('Chr14:1')+(3e5:1e6)])

# [1] 0

```

```

indel.counts[7]/nrow(full[[7]]) * 7e5
#      1335
# 163.8485

```

Answer: yes, a bit odd, but *lack* if indels in the rest of chr2 is odder.

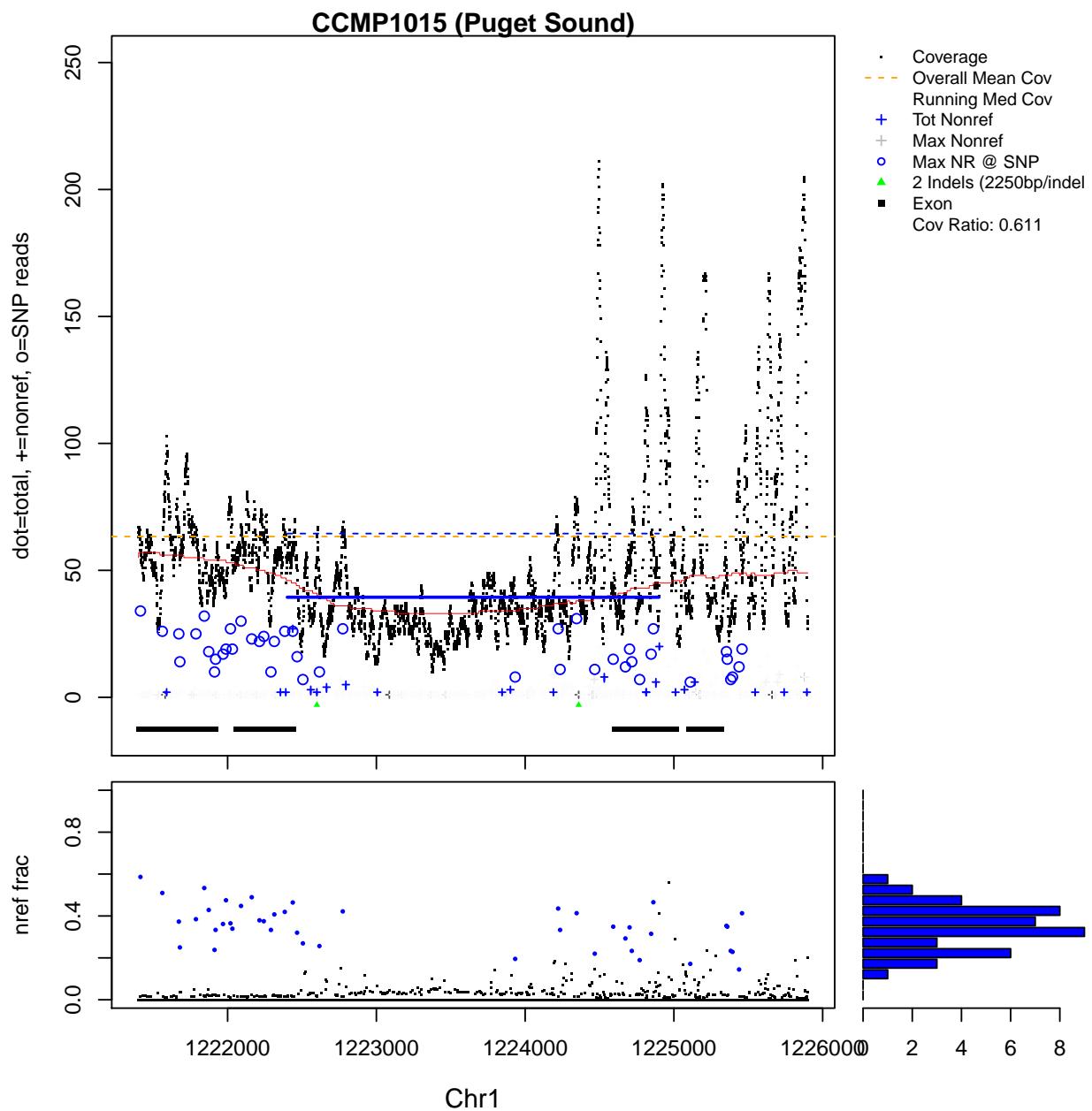
More 1335 deletions:

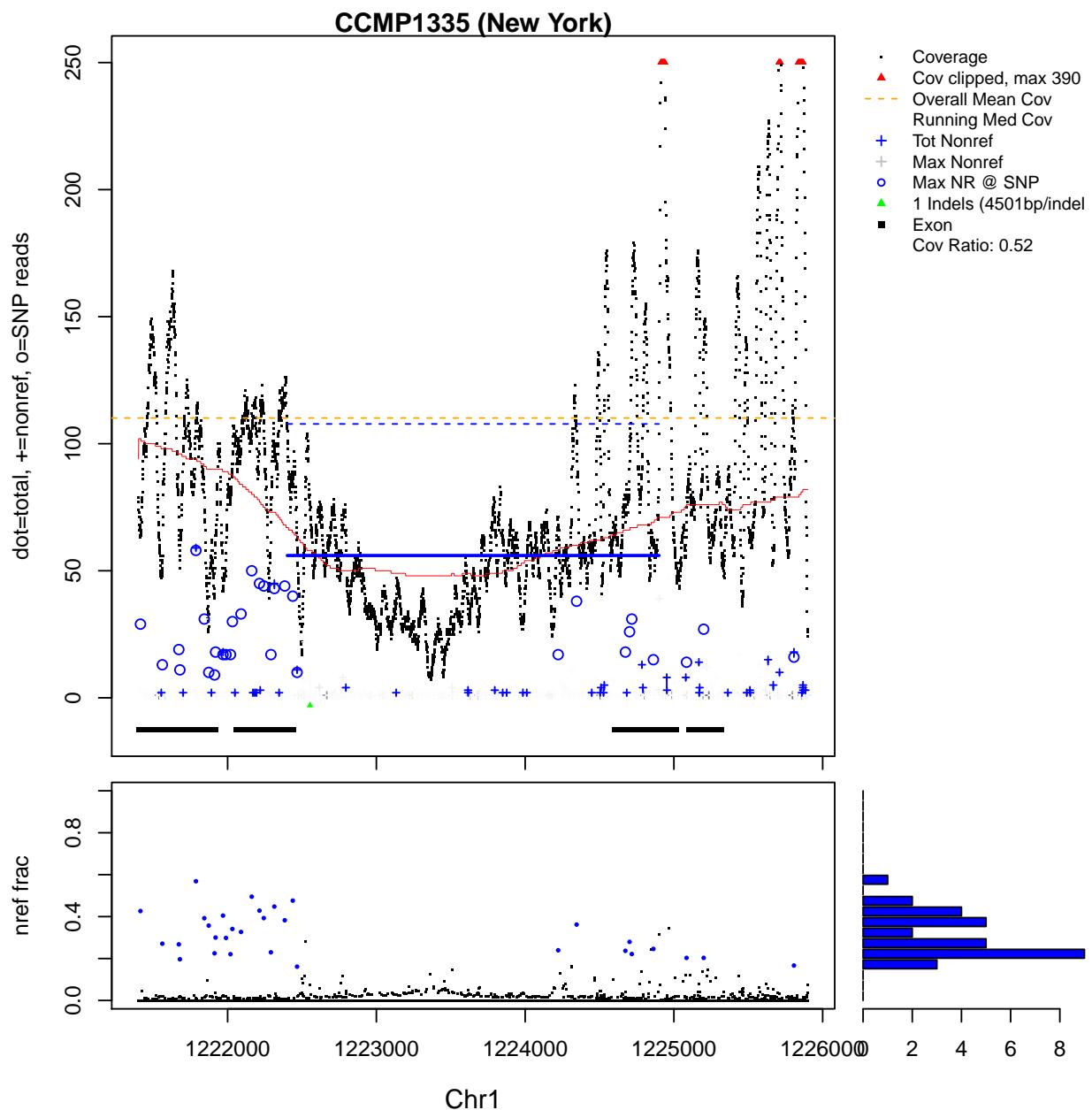
```

hemi.chunk(19:23, c(5, 7))

#           chr     start     end length tp1007 tp1012 tp1013 tp1014 tp1015      IT tp1335 pattern
# Chr1:543201 Chr1 543201 1222400 679200     NA     NA     NA     NA     NA     NA     NA     NA     00
# Chr1:1222401 Chr1 1222401 1222500    100     NA     NA     NA     NA     NA     NA     NA     0.6    01
# Chr1:1222501 Chr1 1222501 1222600    100     NA     NA     NA     NA     NA     NA     0.249   0.6    03
# Chr1:1222601 Chr1 1222601 1224400   1800     NA     NA    0.379    NA     NA     0.249   0.6    23
# Chr1:1224401 Chr1 1224401 1224700    300     NA     NA    0.379    NA     NA     NA     0.6    21
# Chr1:1224701 Chr1 1224701 1224900    200     NA     NA     NA     NA     NA     NA     0.6    01
# Chr1:1224901 Chr1 1224901 1865000 640100     NA     NA     NA     NA     NA     NA     NA     00

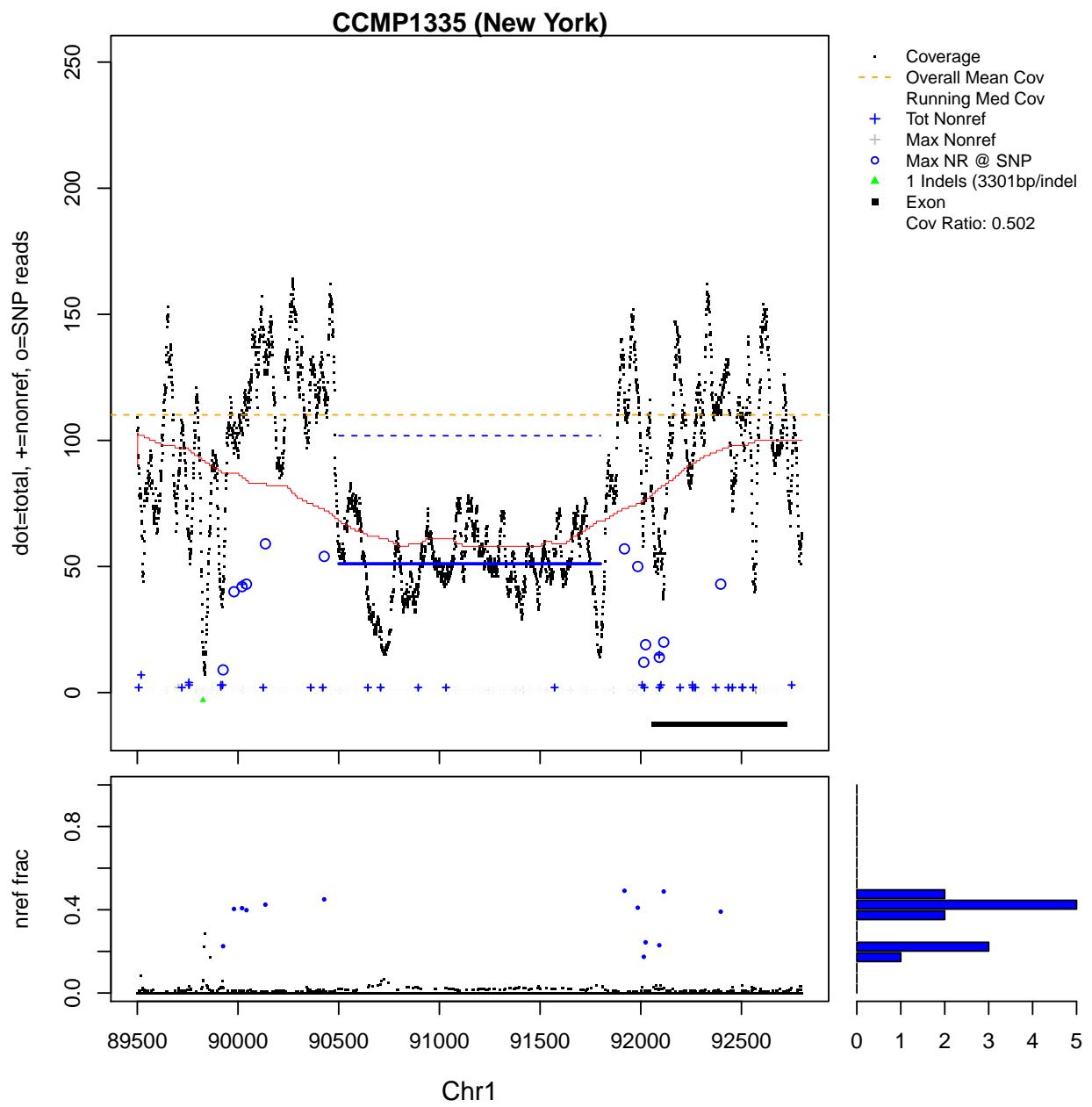
```



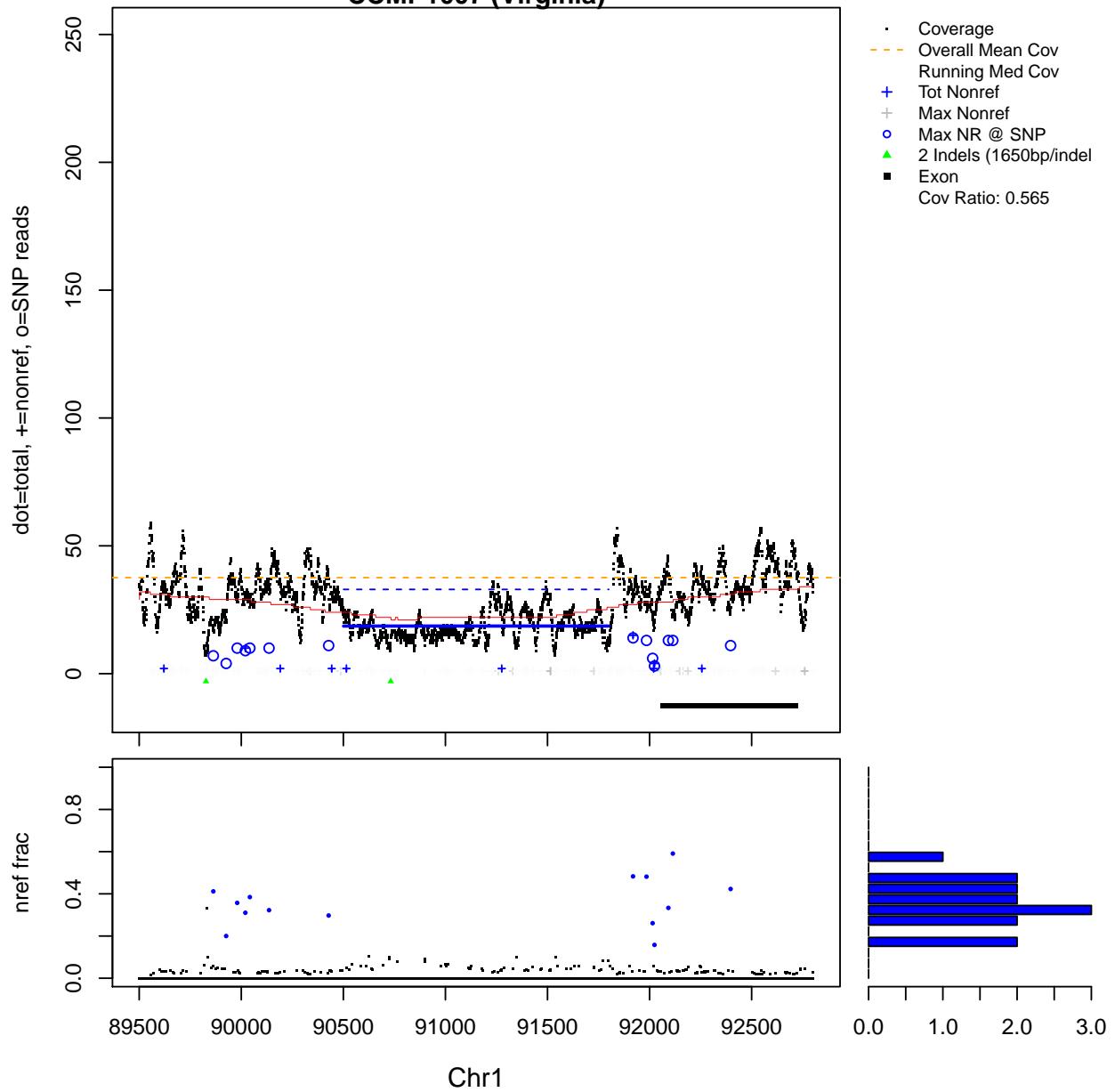


**hemi.chunk(11)**

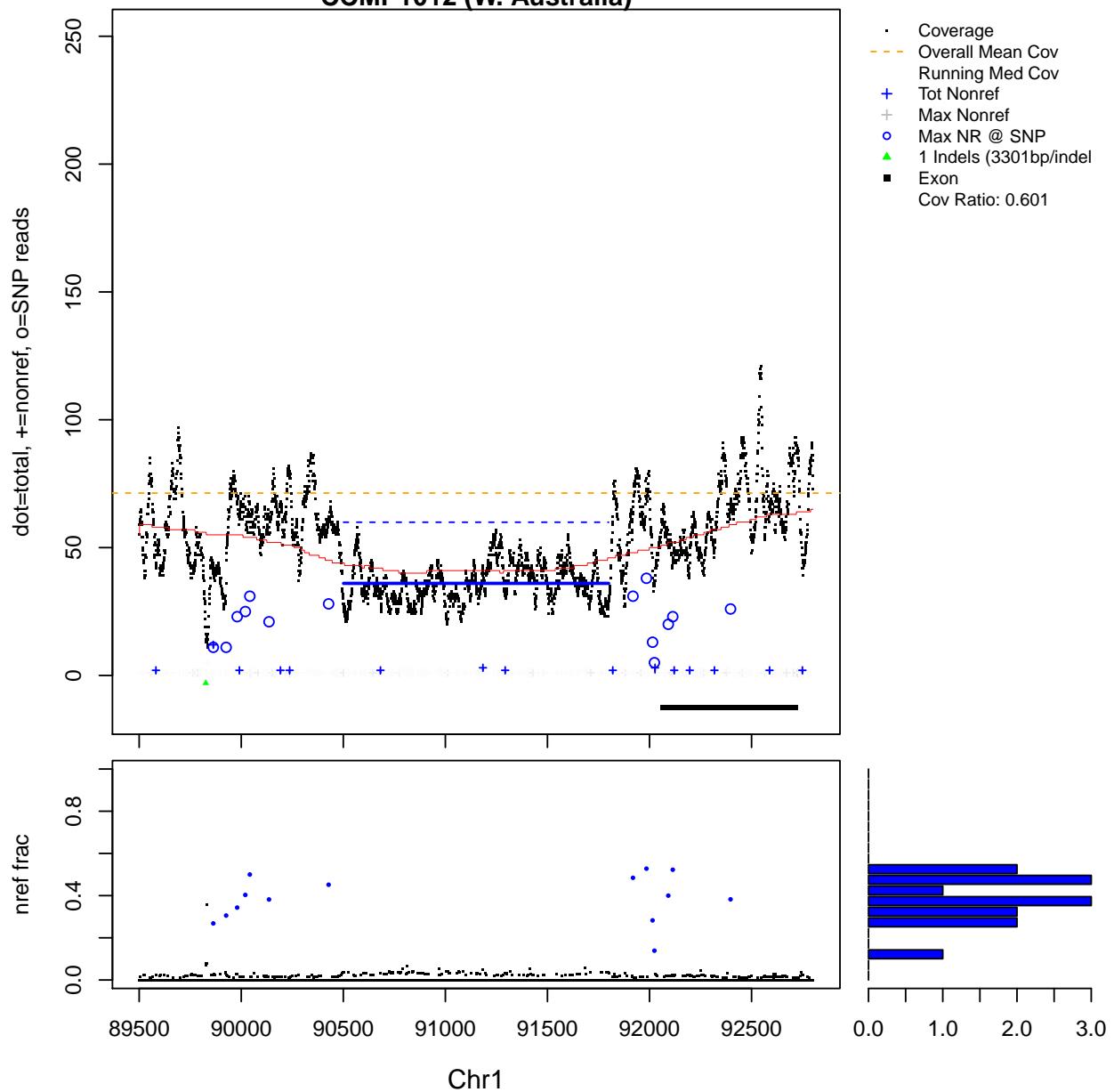
| # | chr        | start | end   | length | tp1007 | tp1012 | tp1013 | tp1014 | tp1015 | IT | tp1335 | pattern |   |
|---|------------|-------|-------|--------|--------|--------|--------|--------|--------|----|--------|---------|---|
| # | Chr1:82301 | Chr1  | 82301 | 90500  | 8200   | NA     | NA     | NA     | NA     | NA | NA     | NA      | 0 |
| # | Chr1:90501 | Chr1  | 90501 | 91800  | 1300   | NA     | NA     | NA     | NA     | NA | NA     | 0.488   | 1 |
| # | Chr1:91801 | Chr1  | 91801 | 106600 | 14800  | NA     | NA     | NA     | NA     | NA | NA     | NA      | 0 |



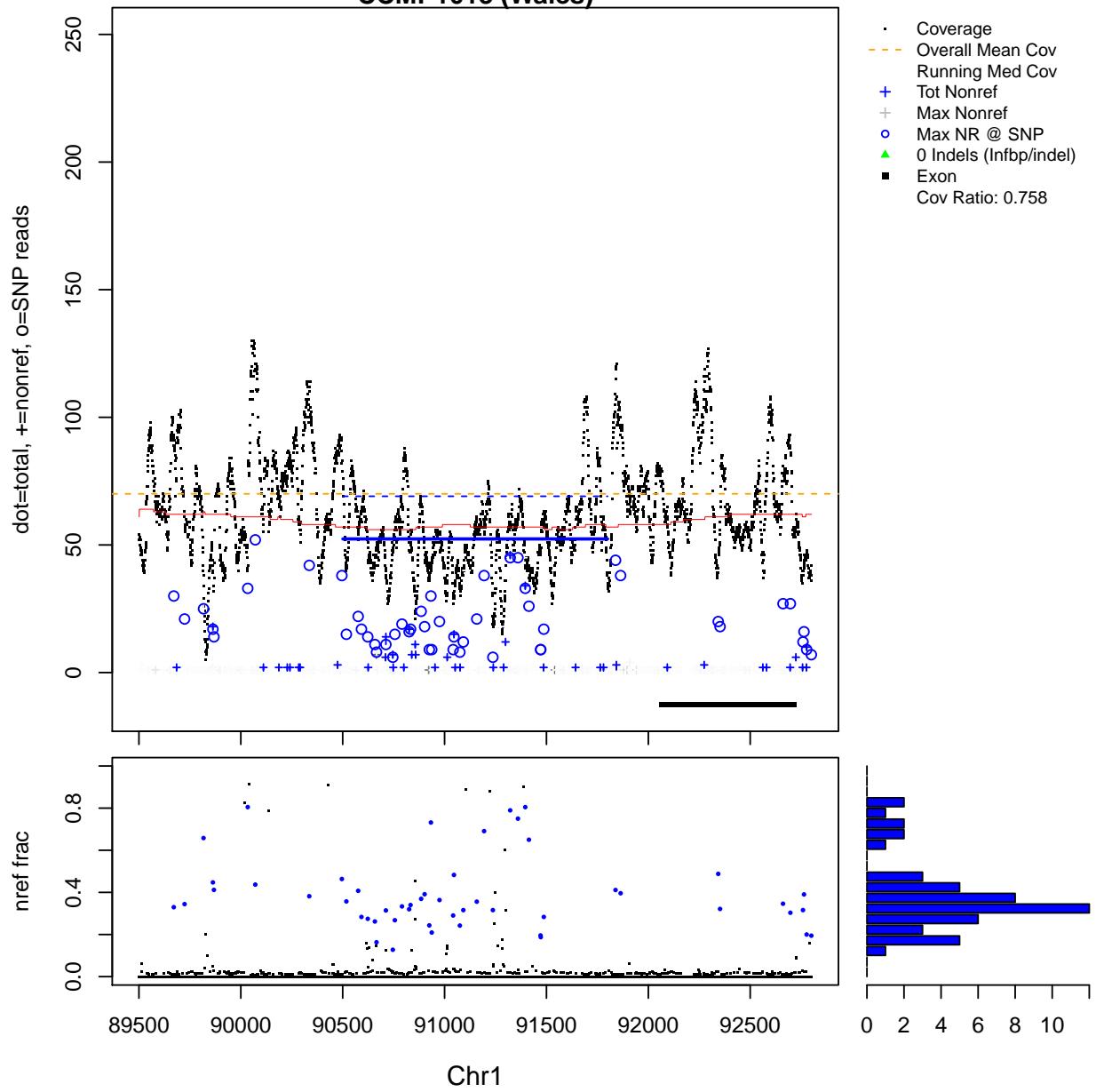
### CCMP1007 (Virginia)



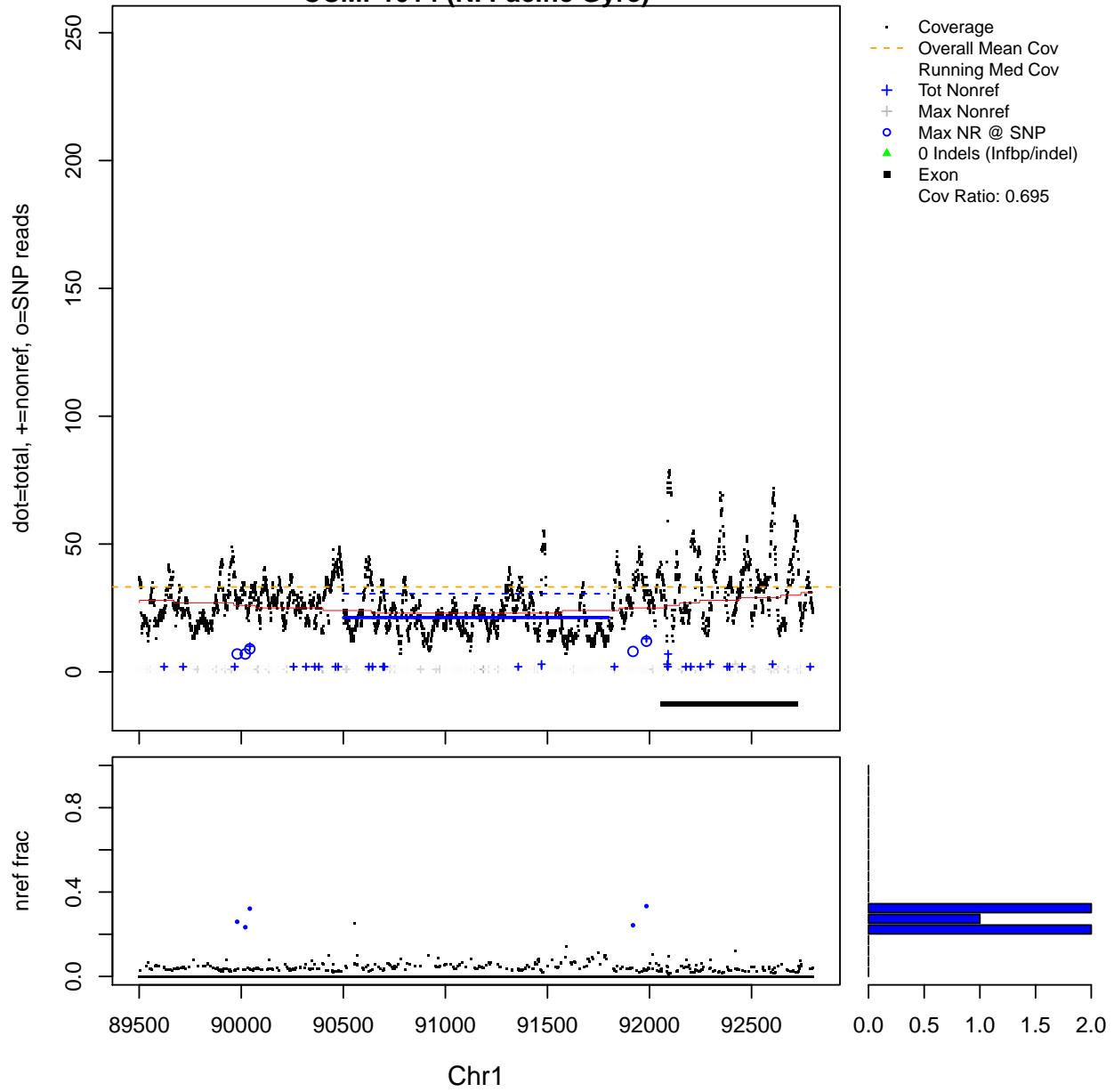
### CCMP1012 (W. Australia)

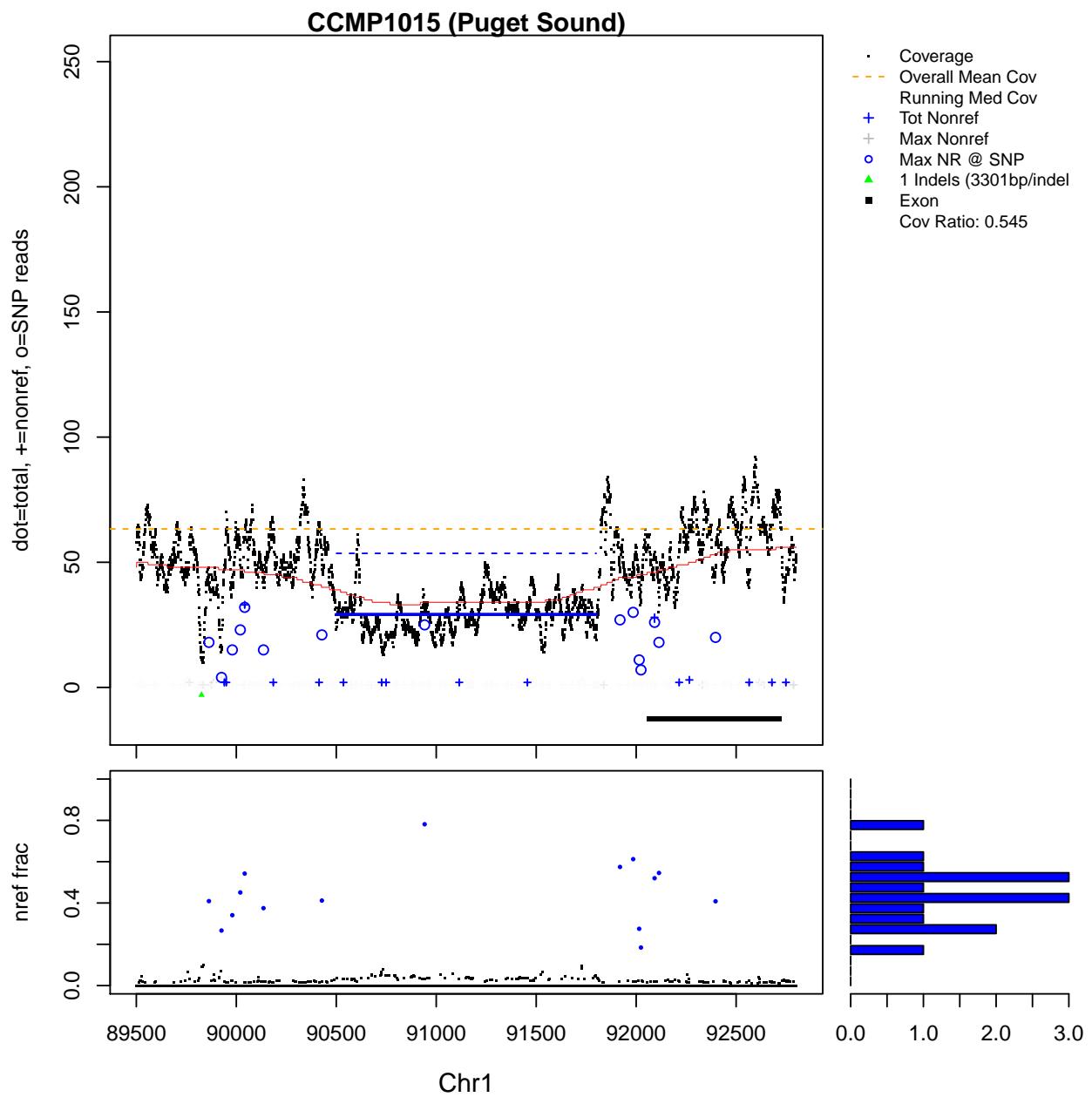


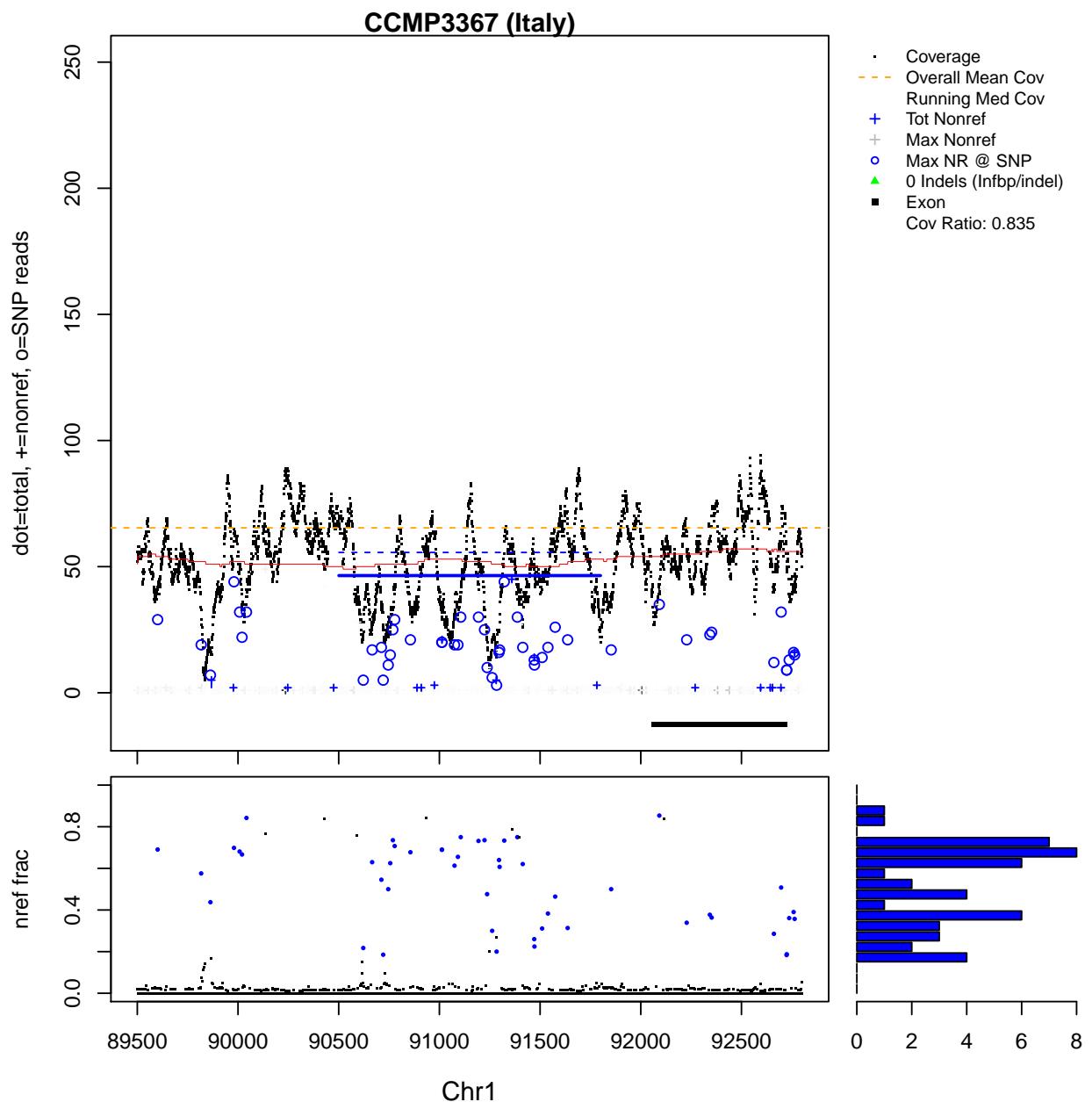
### CCMP1013 (Wales)



### CCMP1014 (N. Pacific Gyre)

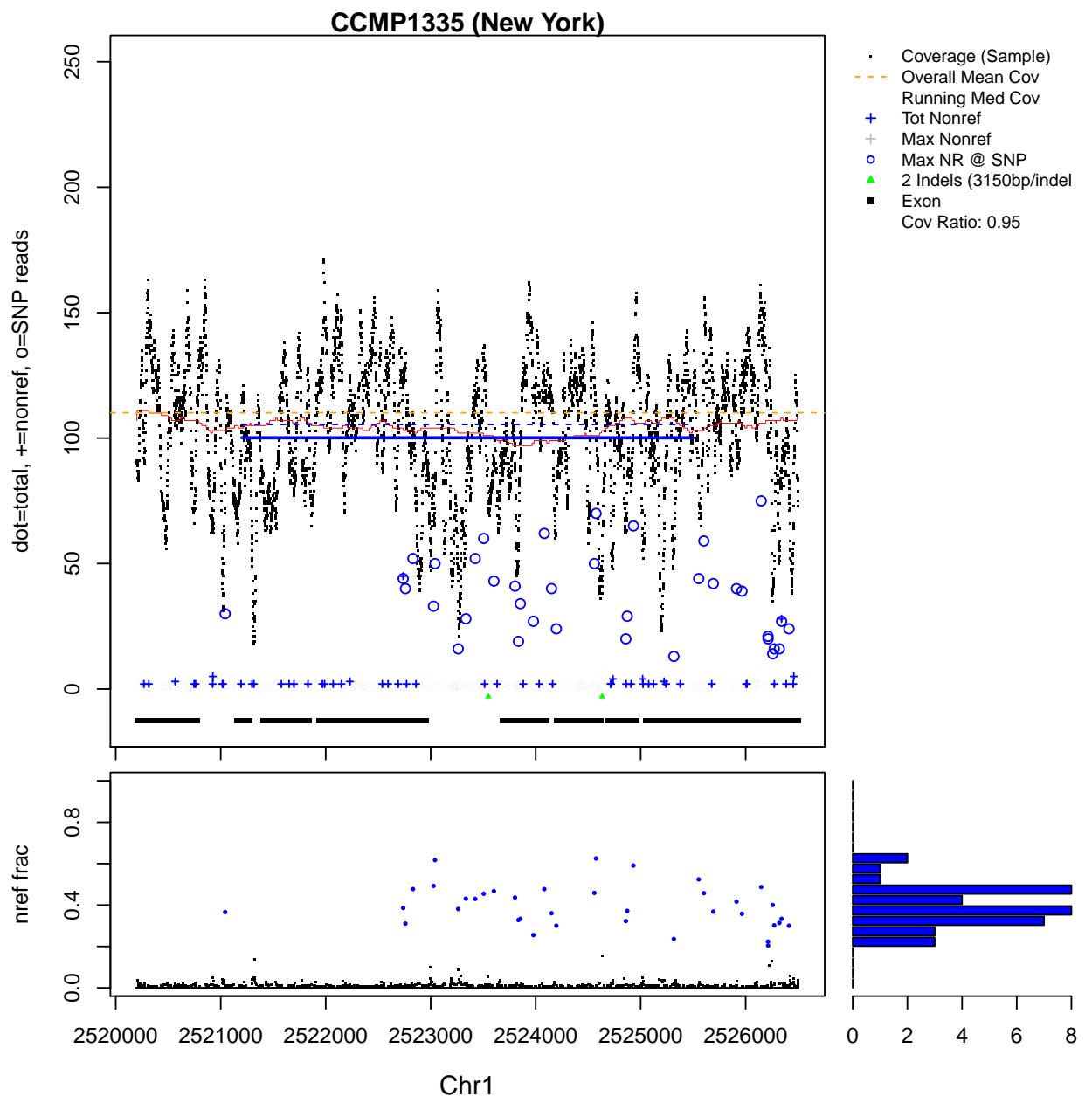






```
hemi.chunk('Chr1:2521201', 7)
```

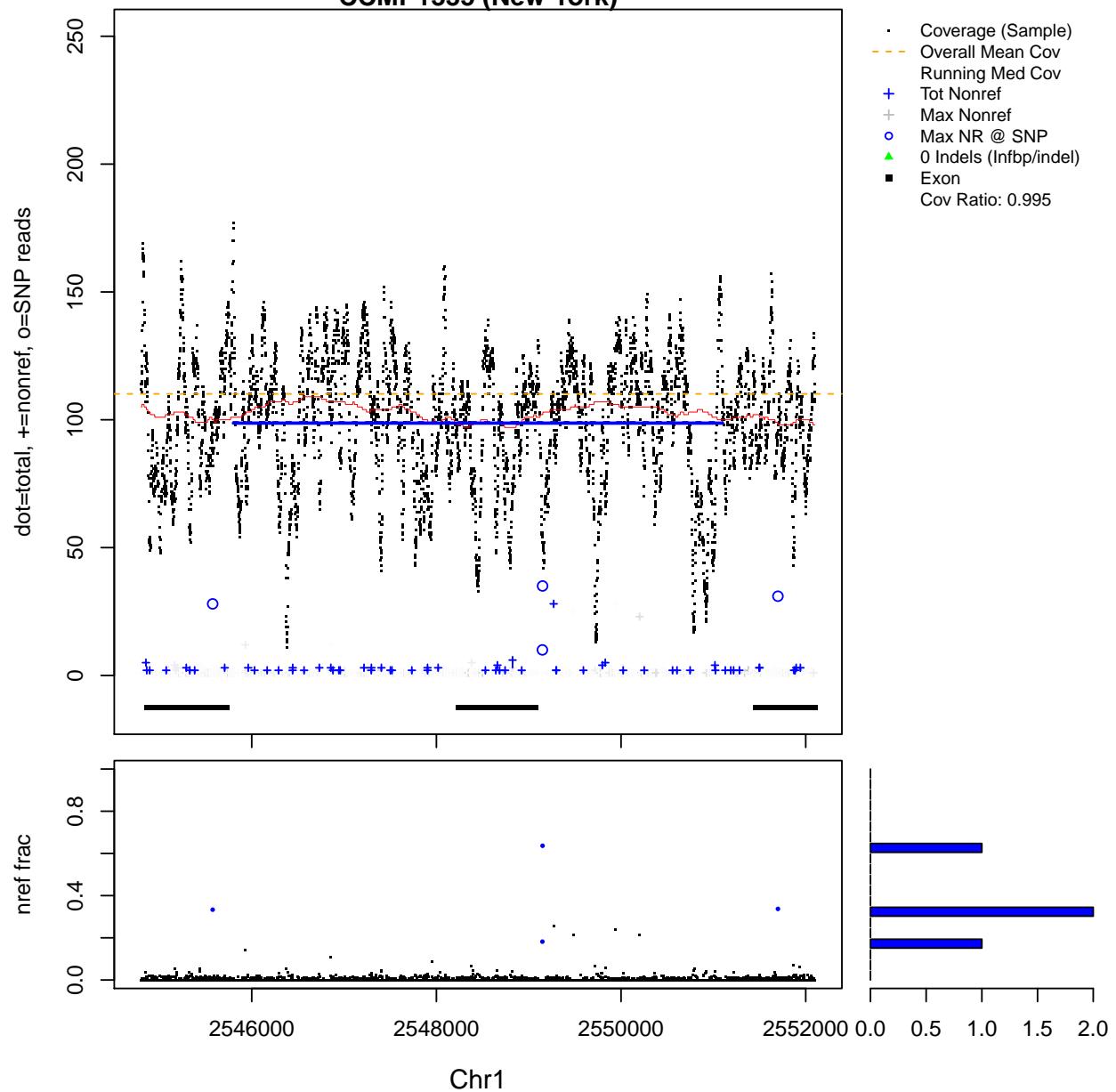
```
# Rows 31 : 31
#           chr    start      end length tp1007 tp1012 tp1013 tp1014 tp1015 IT tp1335 pattern
# Chr1:2465001 Chr1 2465001 2521200  56200     NA     NA     NA     NA     NA NA     NA     NA     0
# Chr1:2521201 Chr1 2521201 2525500   4300     NA     NA     NA     NA  0.546 NA     NA     NA     4
# Chr1:2525501 Chr1 2525501 2545800  20300     NA     NA     NA     NA     NA NA     NA     NA     0
```

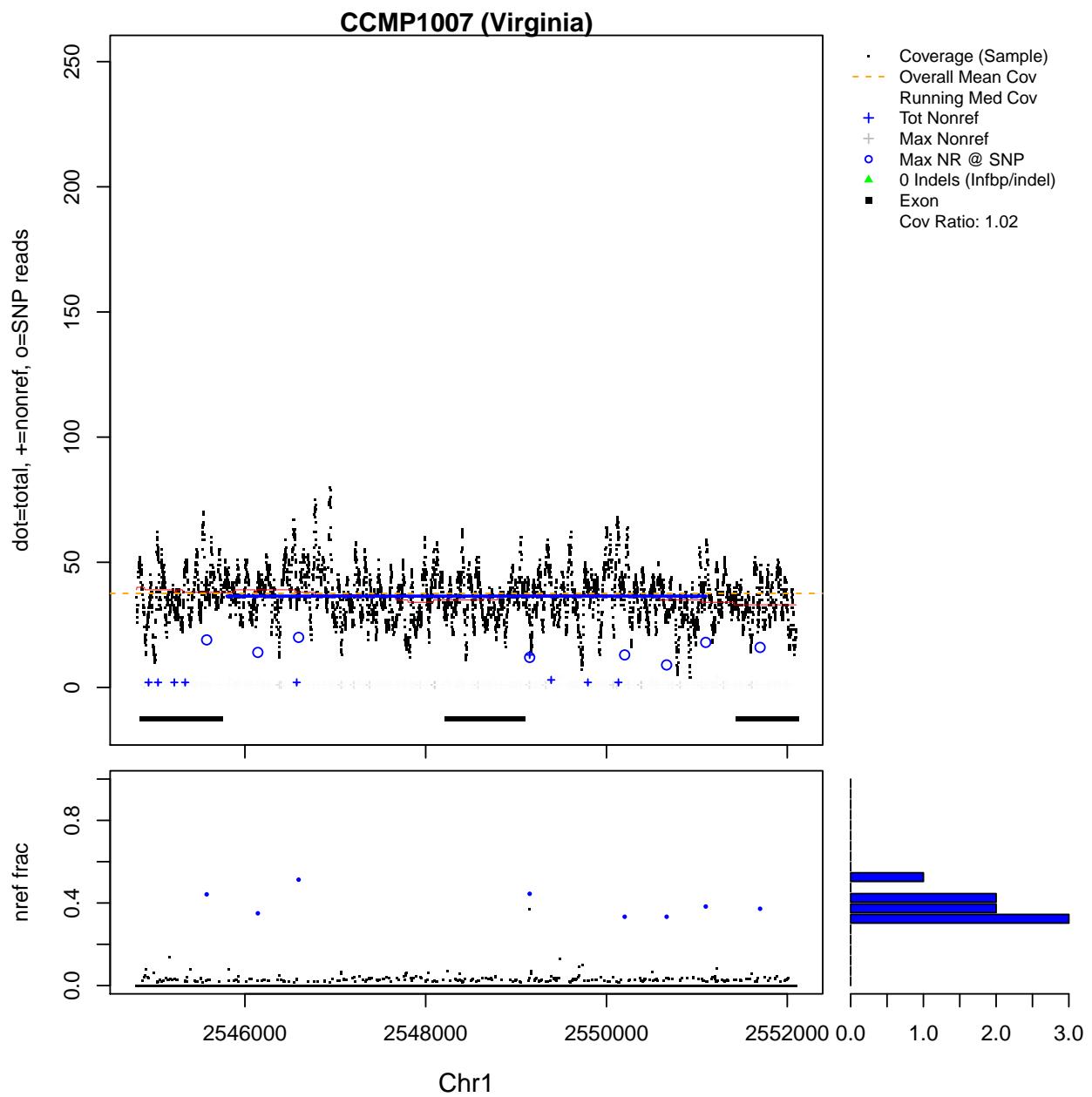


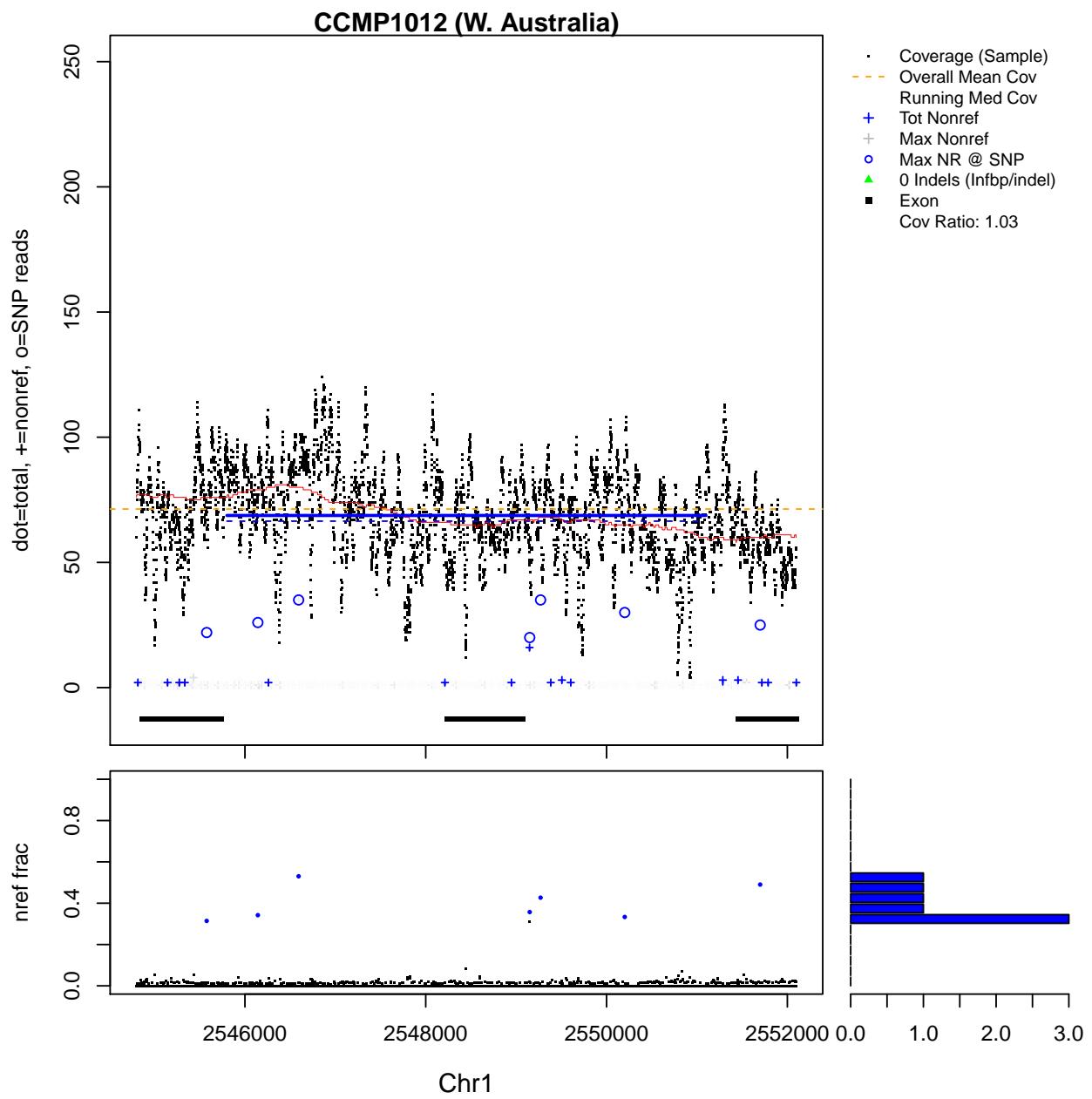
**hemi.chunk (33)**

| # | chr          | start | end     | length  | tp1007 | tp1012 | tp1013 | tp1014 | tp1015 | IT | tp1335 | pattern |   |
|---|--------------|-------|---------|---------|--------|--------|--------|--------|--------|----|--------|---------|---|
| # | Chr1:2525501 | Chr1  | 2525501 | 2545800 | 20300  | NA     | NA     | NA     | NA     | NA | NA     | NA      | 0 |
| # | Chr1:2545801 | Chr1  | 2545801 | 2551100 | 5300   | NA     | NA     | NA     | NA     | NA | 0.653  | NA      | 2 |
| # | Chr1:2551101 | Chr1  | 2551101 | 3042100 | 491000 | NA     | NA     | NA     | NA     | NA | NA     | NA      | 0 |

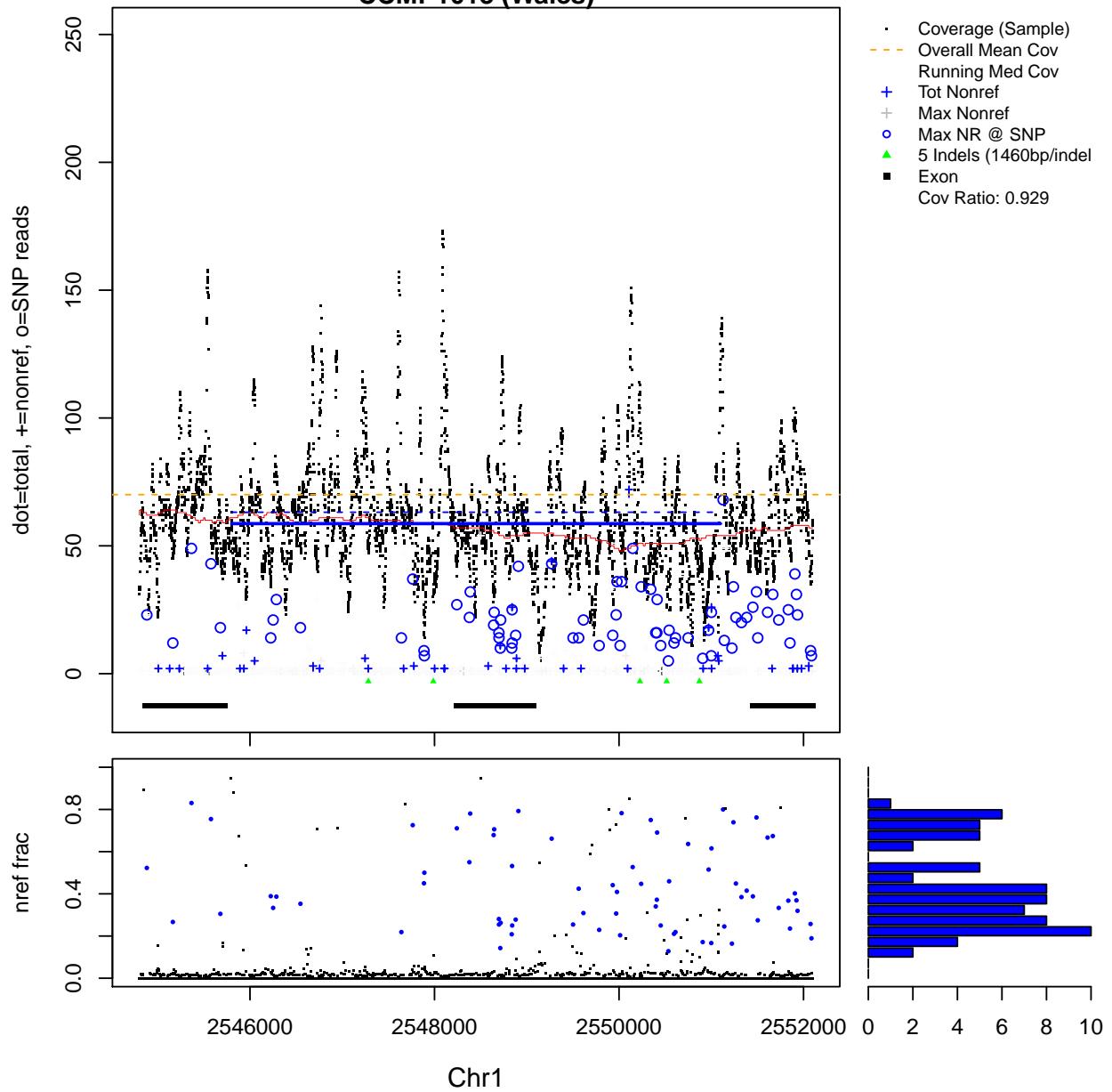
### CCMP1335 (New York)

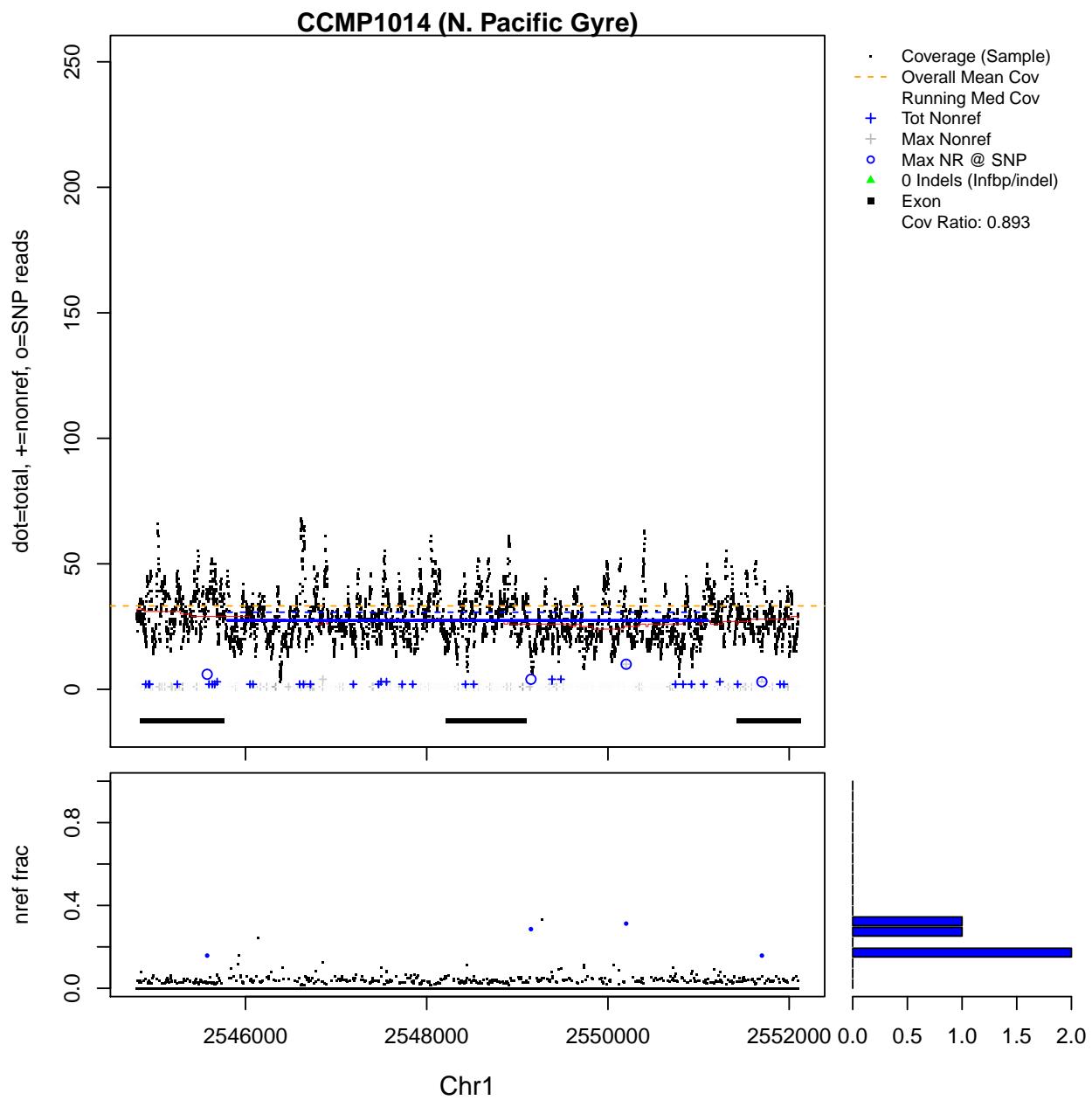


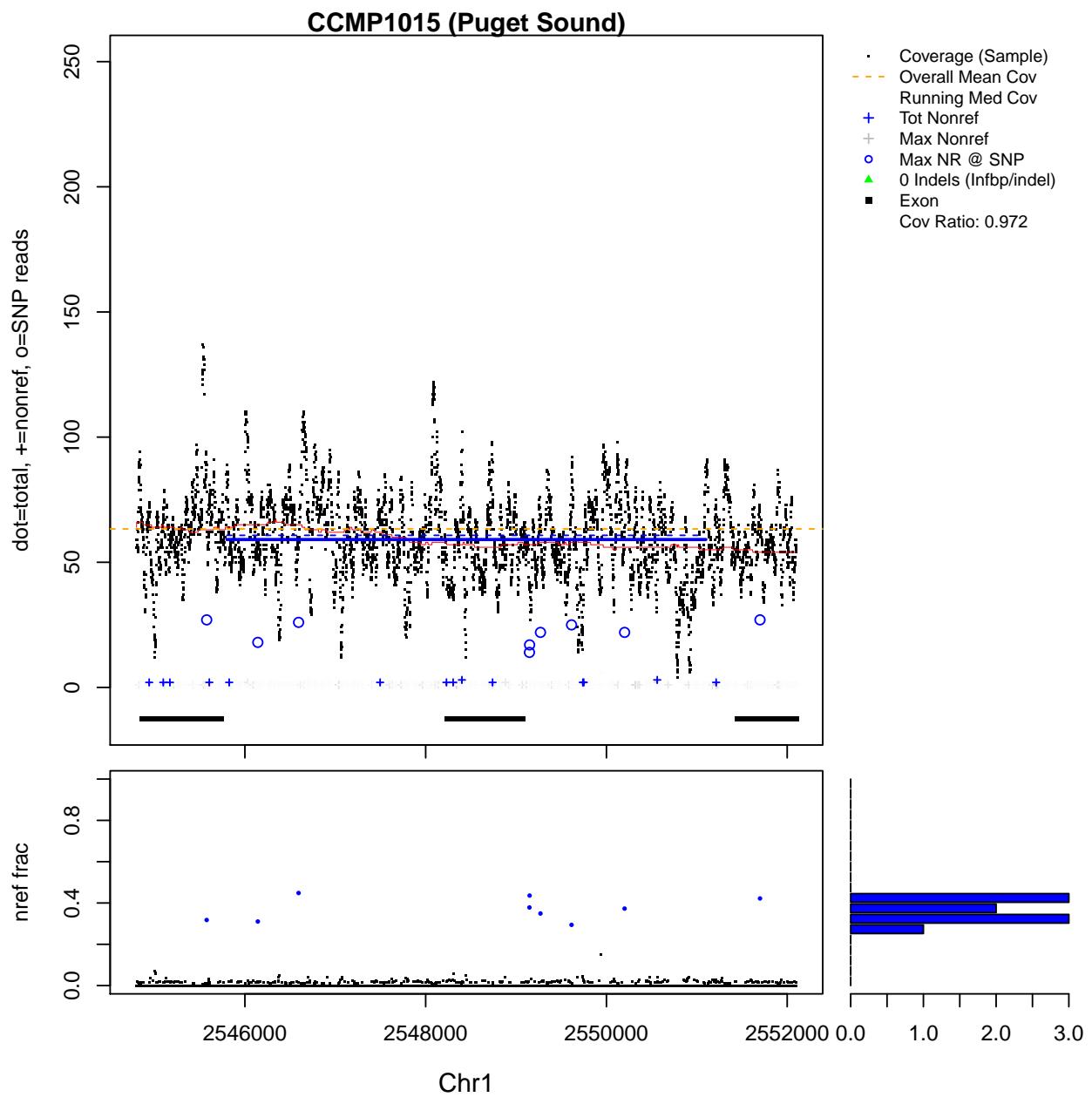


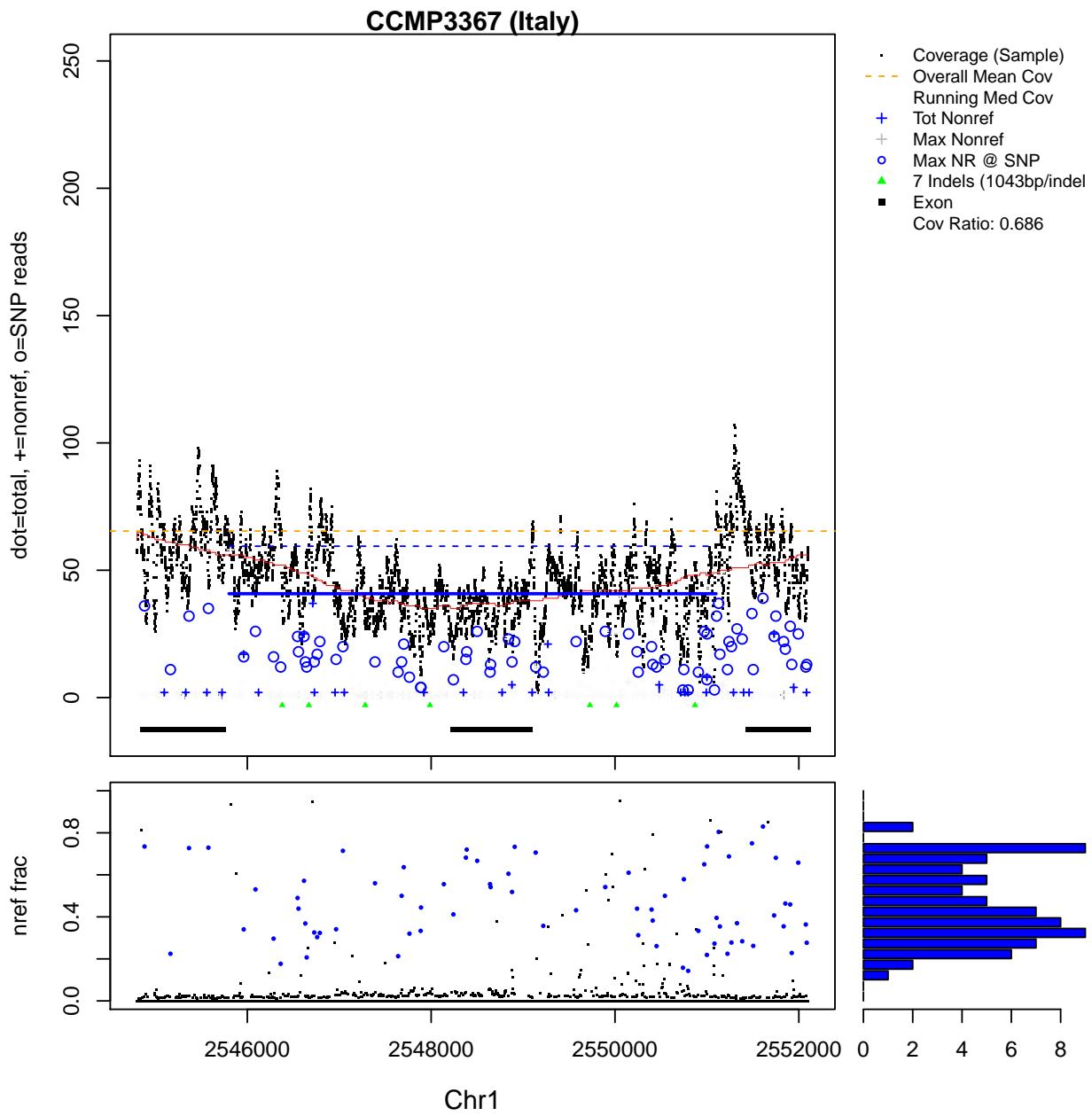


### CCMP1013 (Wales)







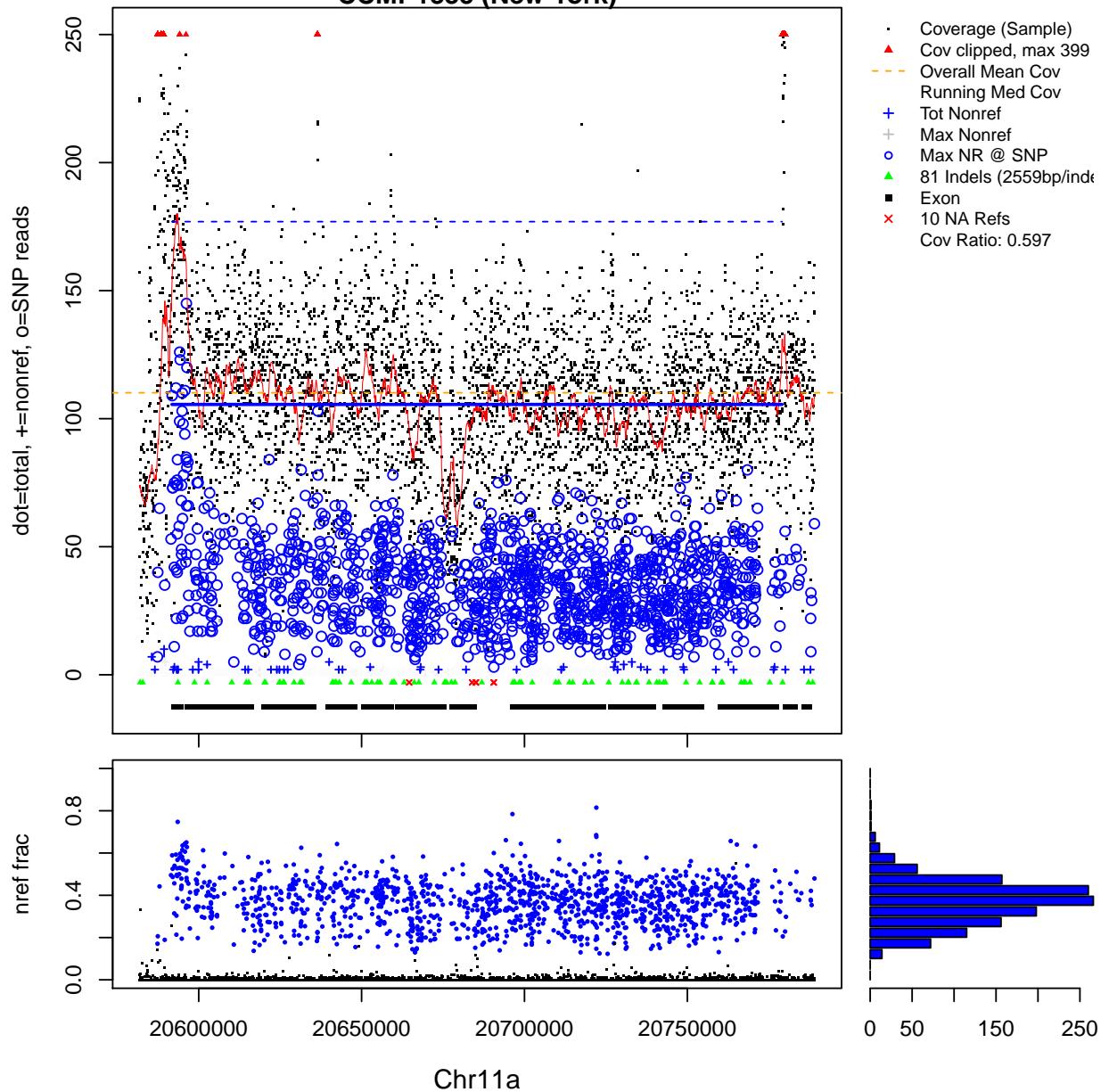


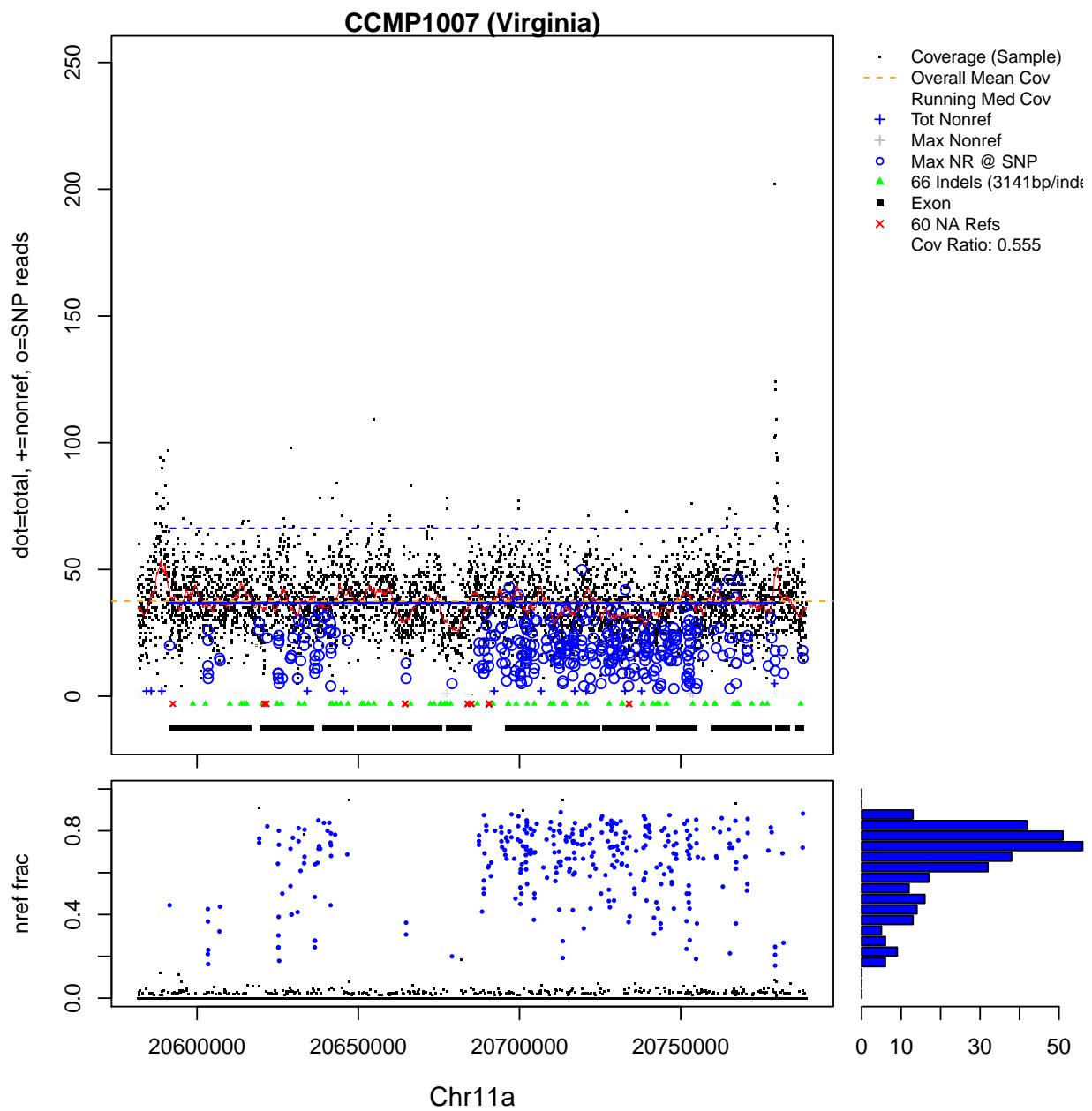
Below is another case where IT/Wales seem to be SNPy, but consistently below 50% nonref. Wales deletion; others not. Gyre also snpy but low nonref frac.

```
hemi.chunk(c('Chr11a:65801', 'Chr11a:240301'), margin=10000)
```

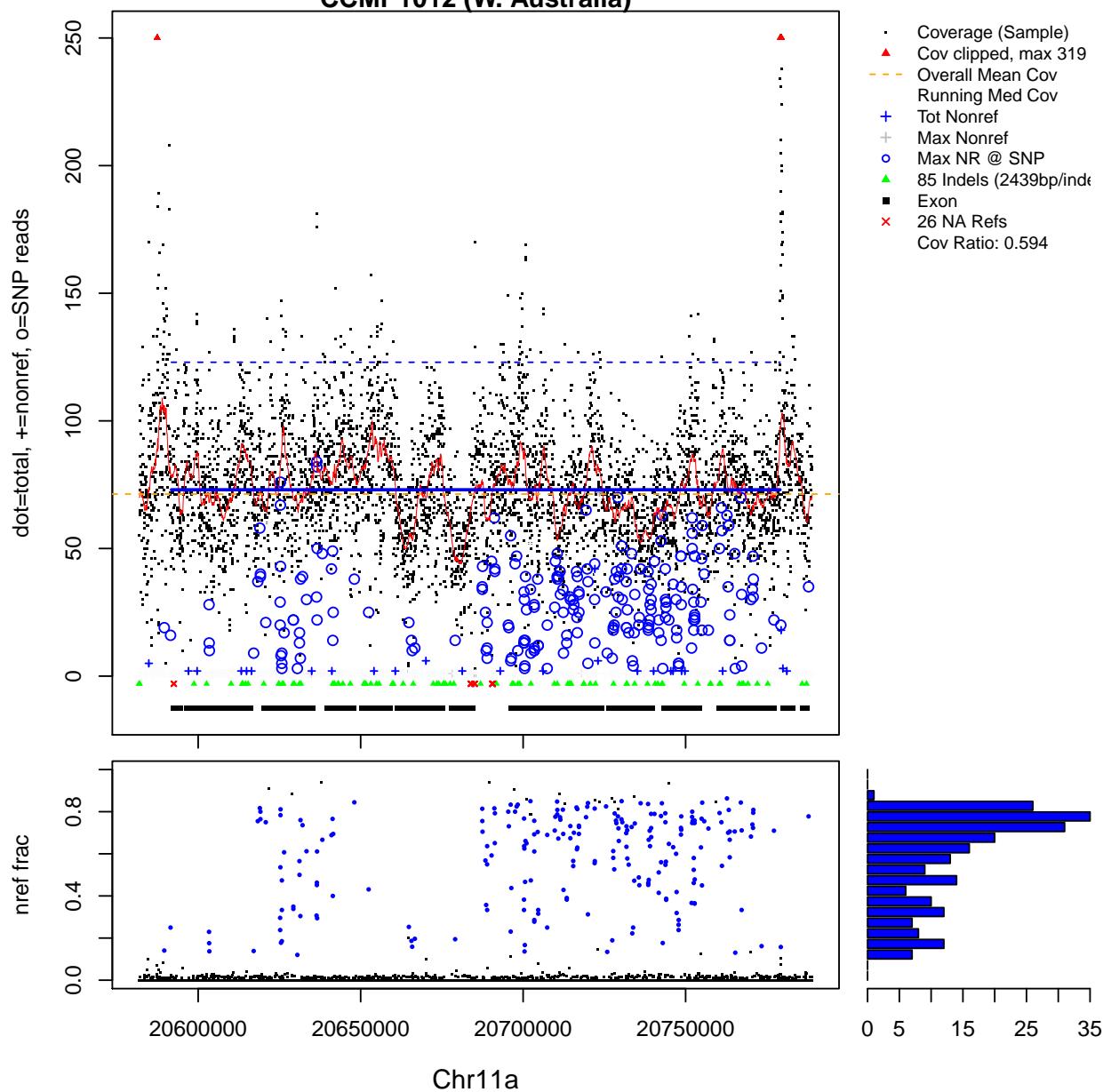
```
# Rows 67 : 73
#           chr   start     end length tp1007 tp1012 tp1013 tp1014 tp1015      IT tp1335 pattern
# Chr11a:58501 Chr11a  58501   65800    7300    NA     NA     NA     NA     NA     NA     NA     00
# Chr11a:65801 Chr11a  65801  148600   82800    NA     NA  0.622    NA     NA     NA     NA     20
# Chr11a:148601 Chr11a 148601 150000   1400    NA     NA  0.622    NA     NA     NA  0.688    21
# Chr11a:150001 Chr11a 150001 150800    800    NA     NA  0.622    NA     NA  0.107  0.688    23
# Chr11a:150801 Chr11a 150801 155200   4400    NA     NA  0.622    NA     NA     NA  0.688    21
# Chr11a:155201 Chr11a 155201 239300   84100    NA     NA  0.622    NA     NA     NA     NA     20
# Chr11a:239301 Chr11a 239301 240300   1000    NA     NA  0.622    NA     NA  0.197    NA     22
# Chr11a:240301 Chr11a 240301 253100   12800    NA     NA  0.622    NA     NA     NA     NA     20
# Chr11a:253101 Chr11a 253101 254000    900    NA     NA     NA     NA     NA     NA     NA     00
```

### CCMP1335 (New York)

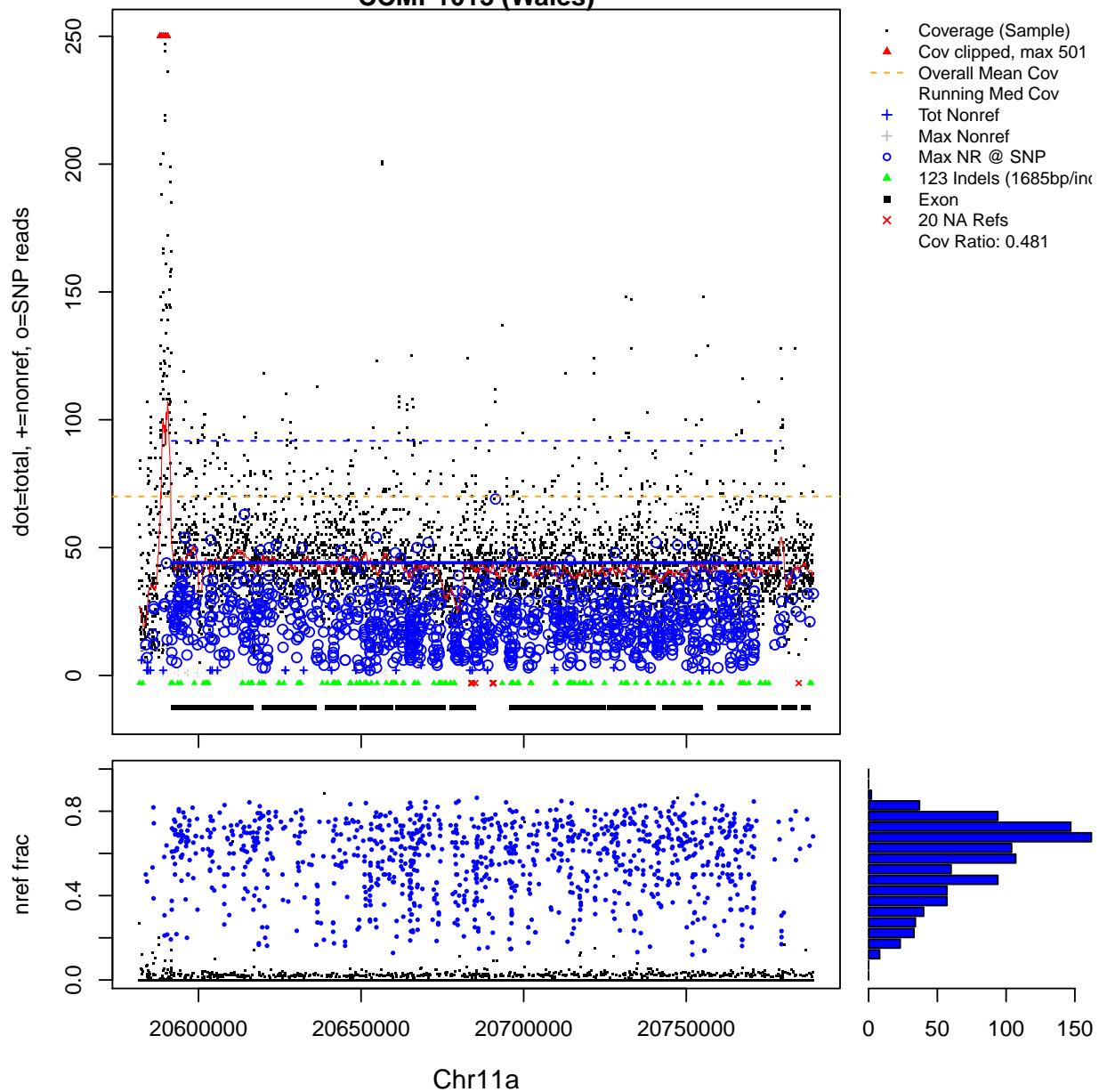


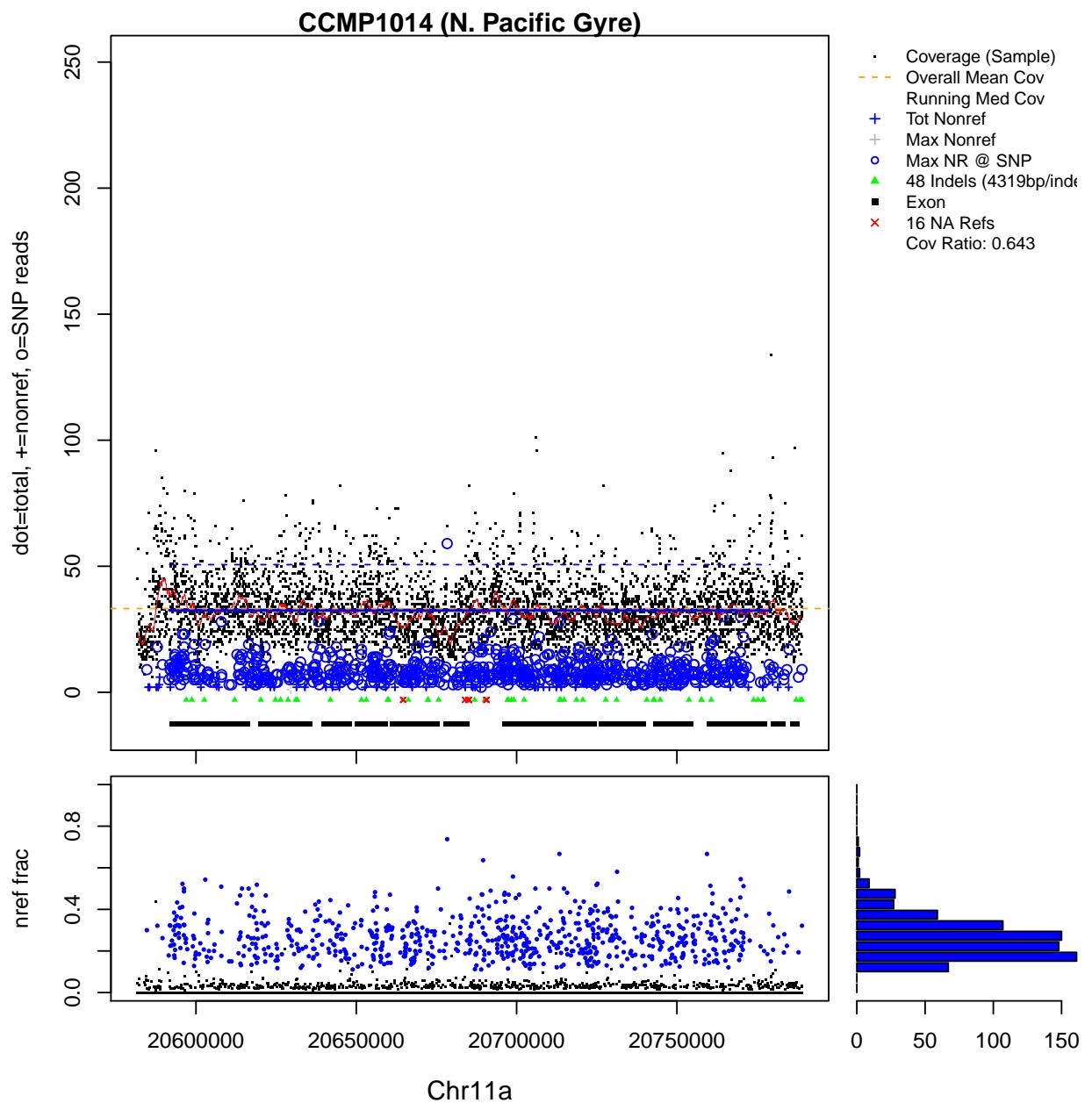


### CCMP1012 (W. Australia)

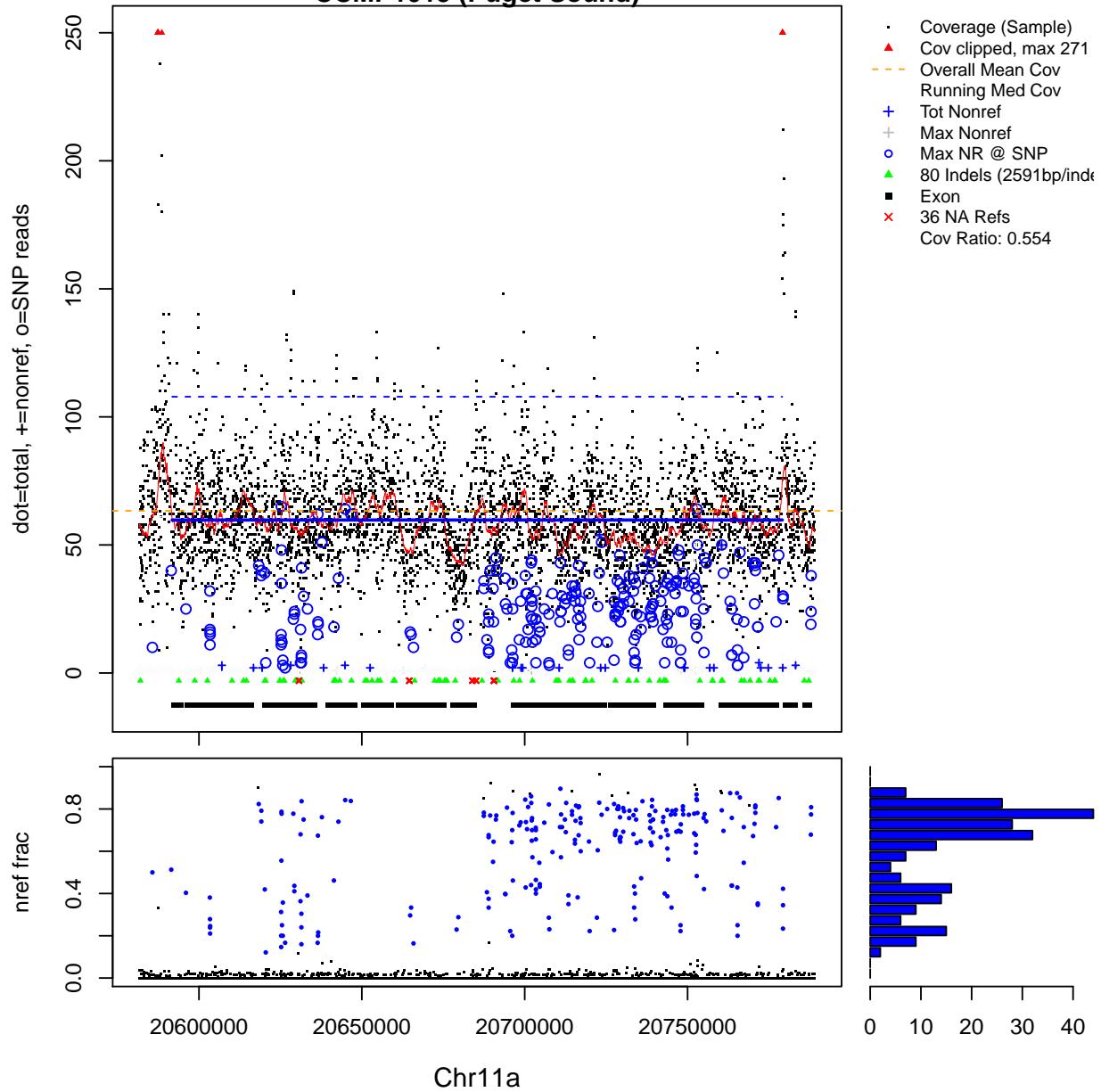


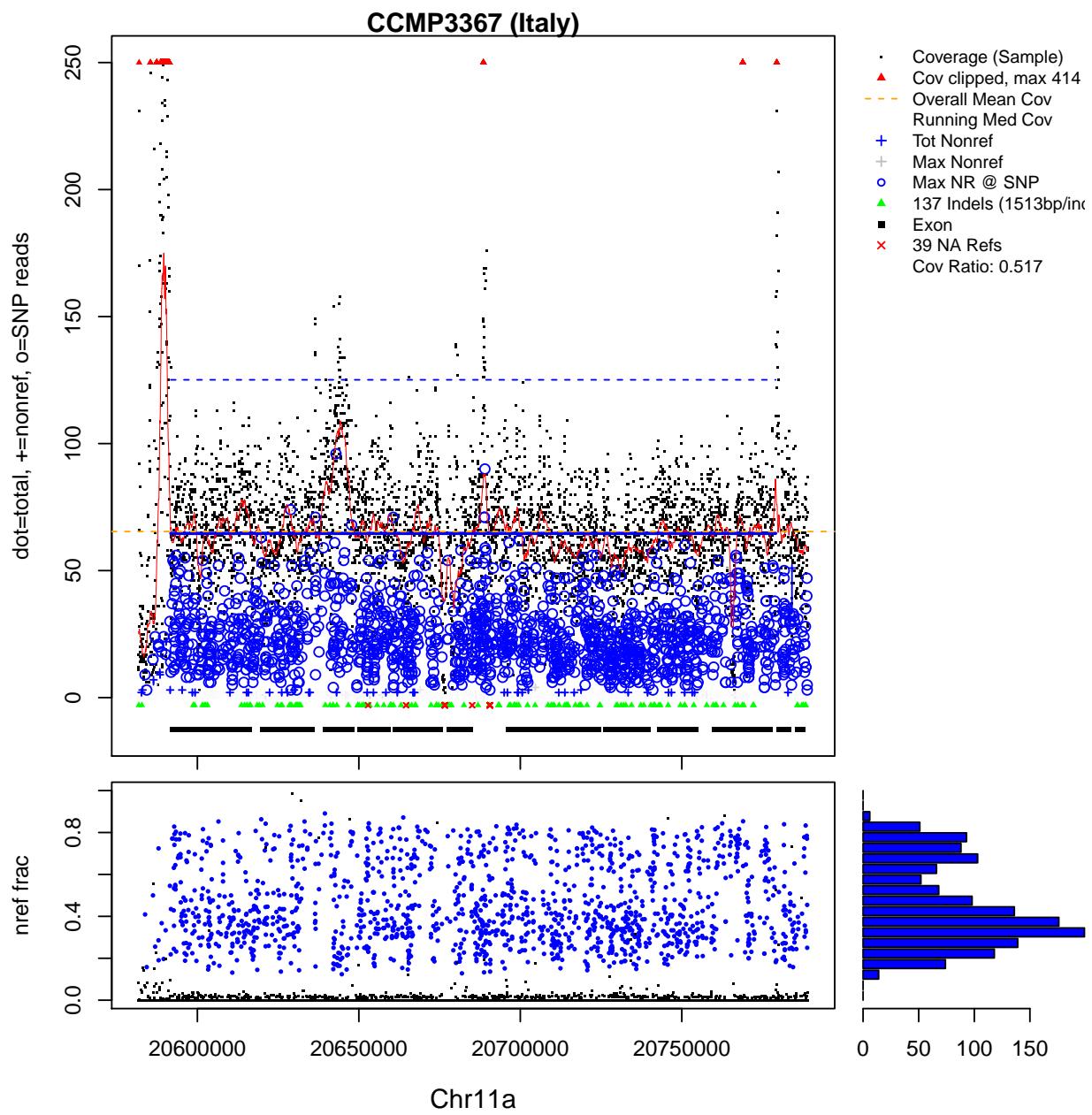
### CCMP1013 (Wales)





### CCMP1015 (Puget Sound)

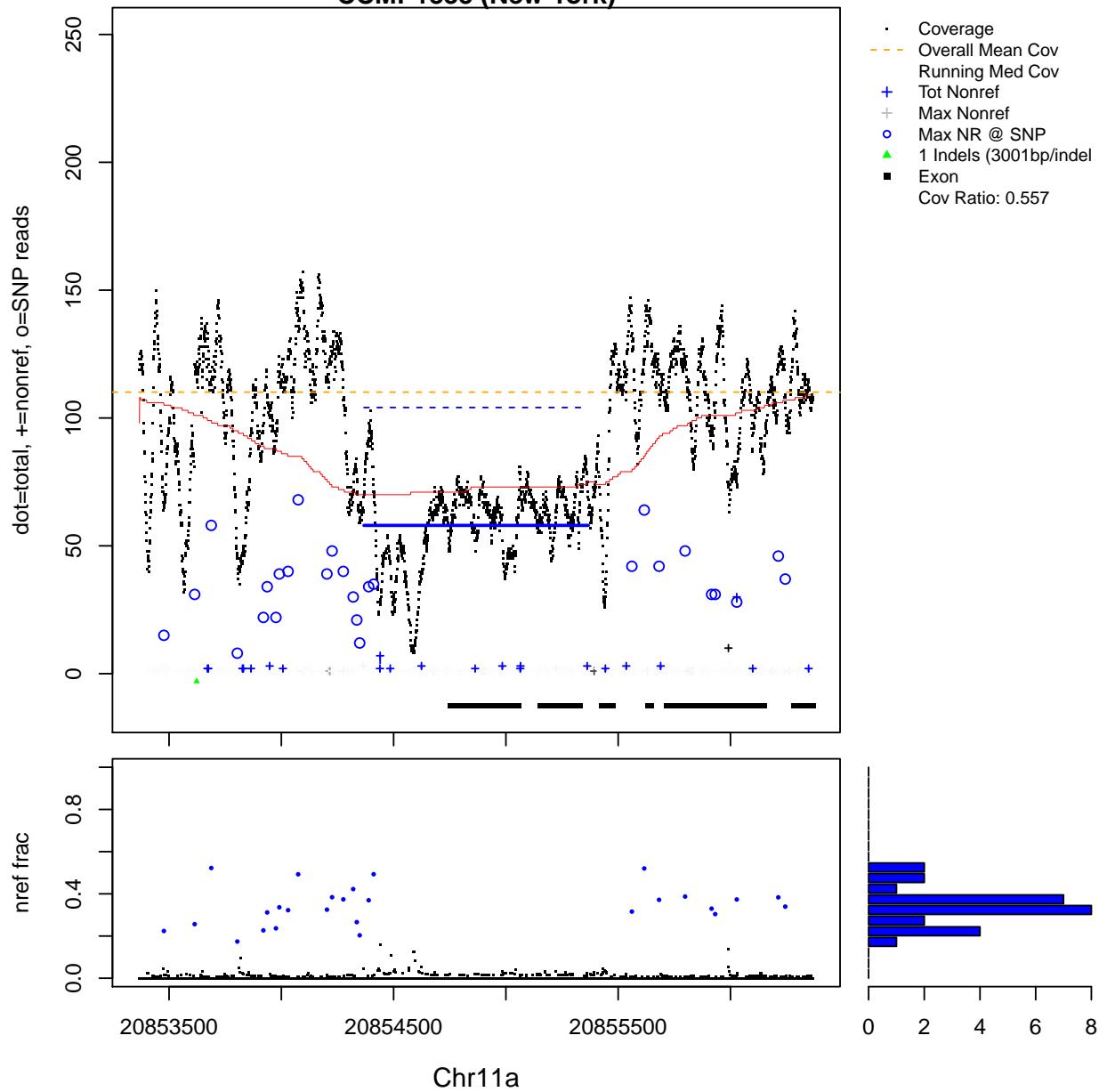


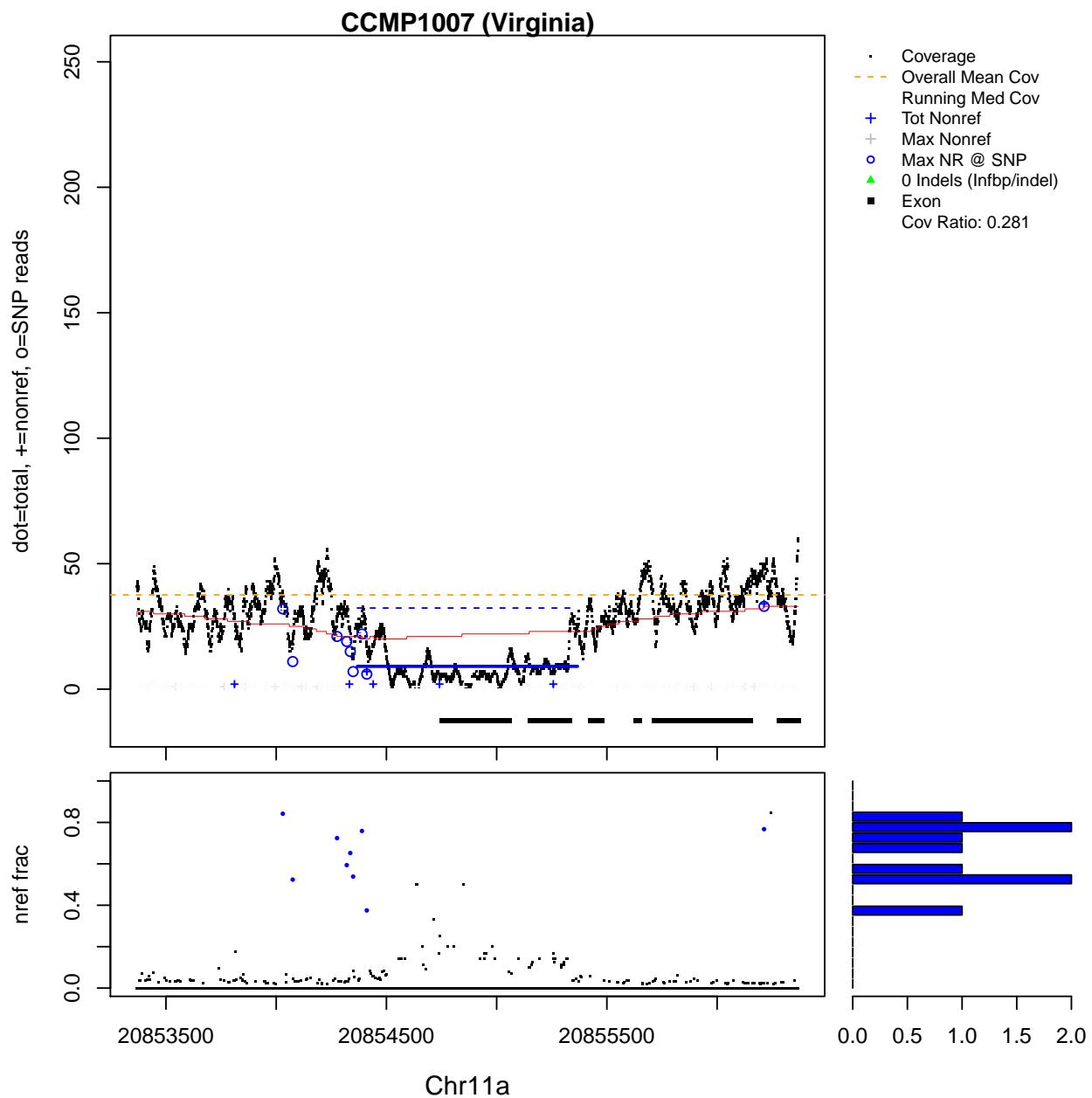


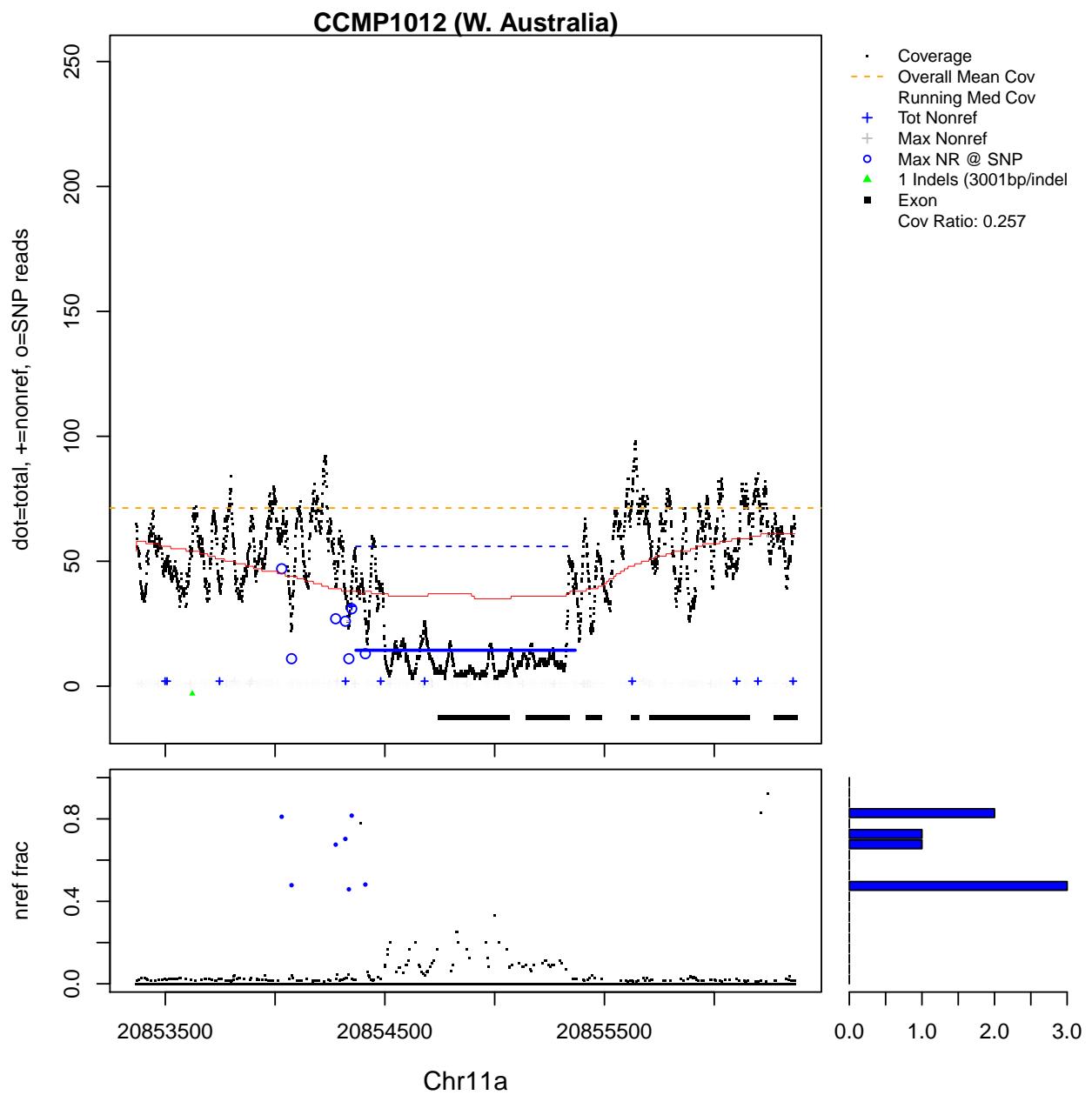
```
hemi.chunk(76:77)

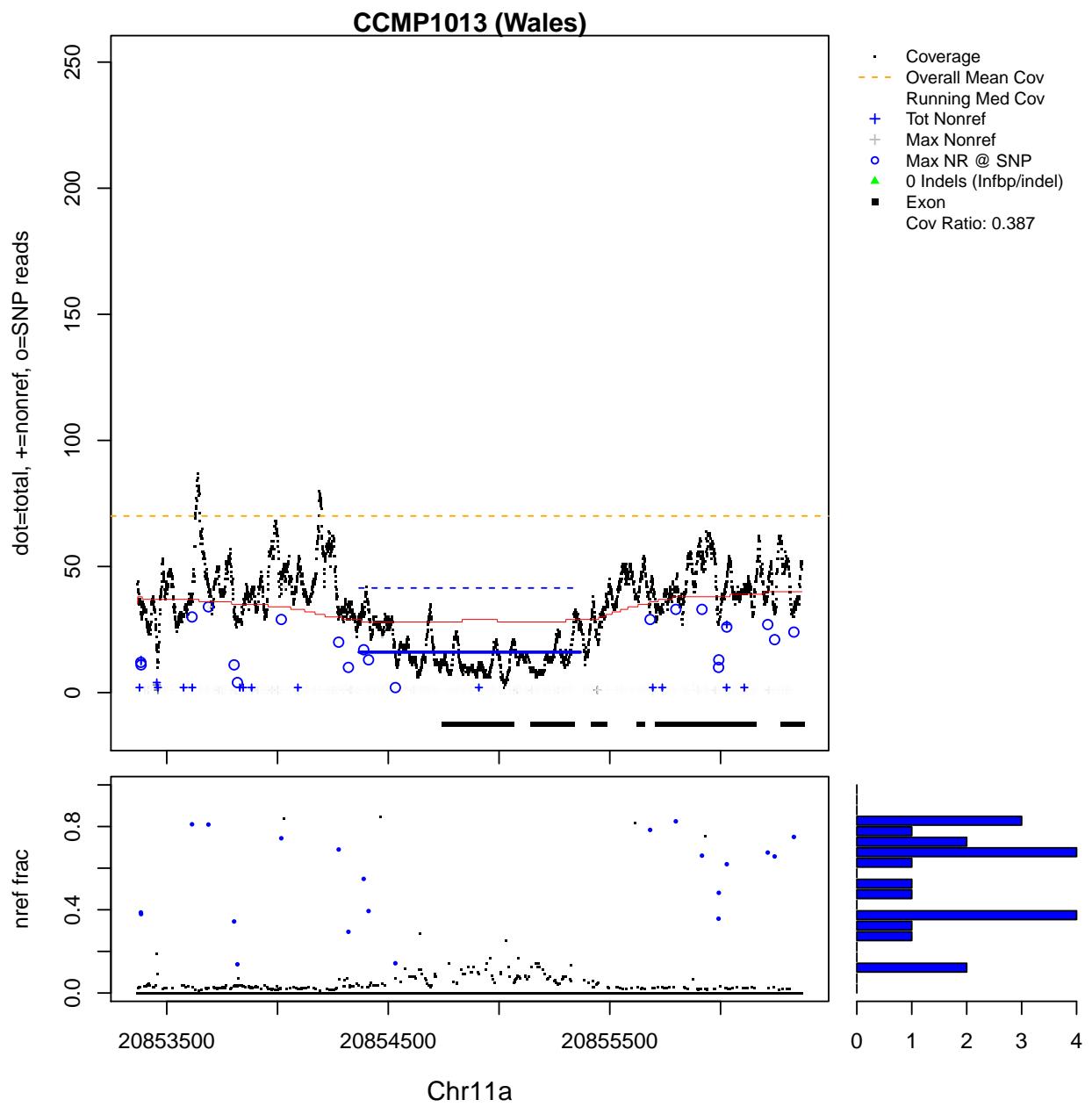
#          chr  start    end length tp1007 tp1012 tp1013 tp1014 tp1015      IT tp1335 pattern
# Chr11a:254001 Chr11a 254001 328400   74400     NA     NA  0.602     NA     NA     NA     NA     020
# Chr11a:328401 Chr11a 328401 328500     100  0.214     NA  0.602     NA  0.189  0.235     NA     126
# Chr11a:328501 Chr11a 328501 329400    900  0.214  0.137  0.602     NA  0.189  0.235     NA     166
# Chr11a:329401 Chr11a 329401 376100   46700     NA     NA  0.602     NA     NA     NA     NA     020
```

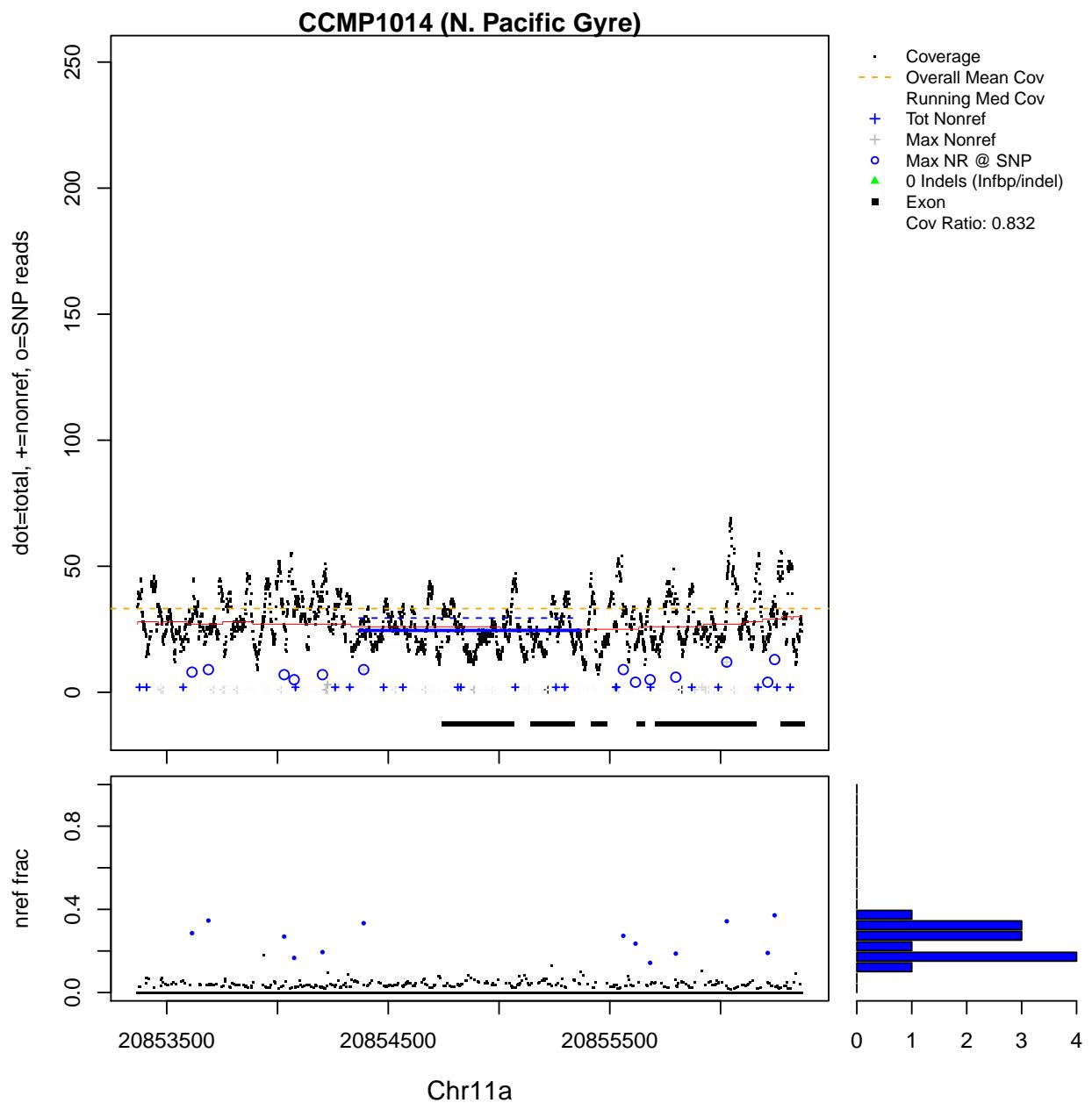
### CCMP1335 (New York)

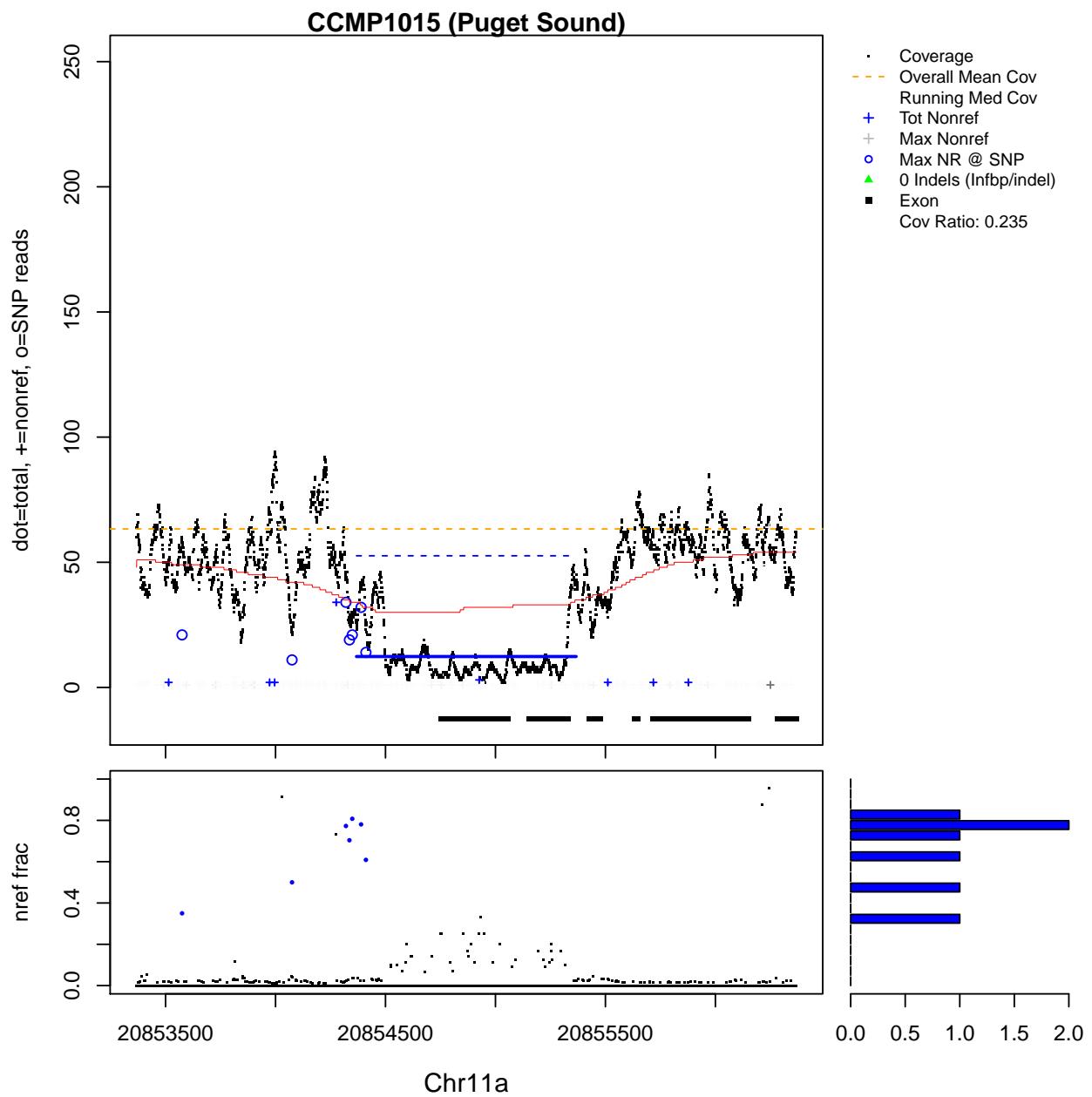


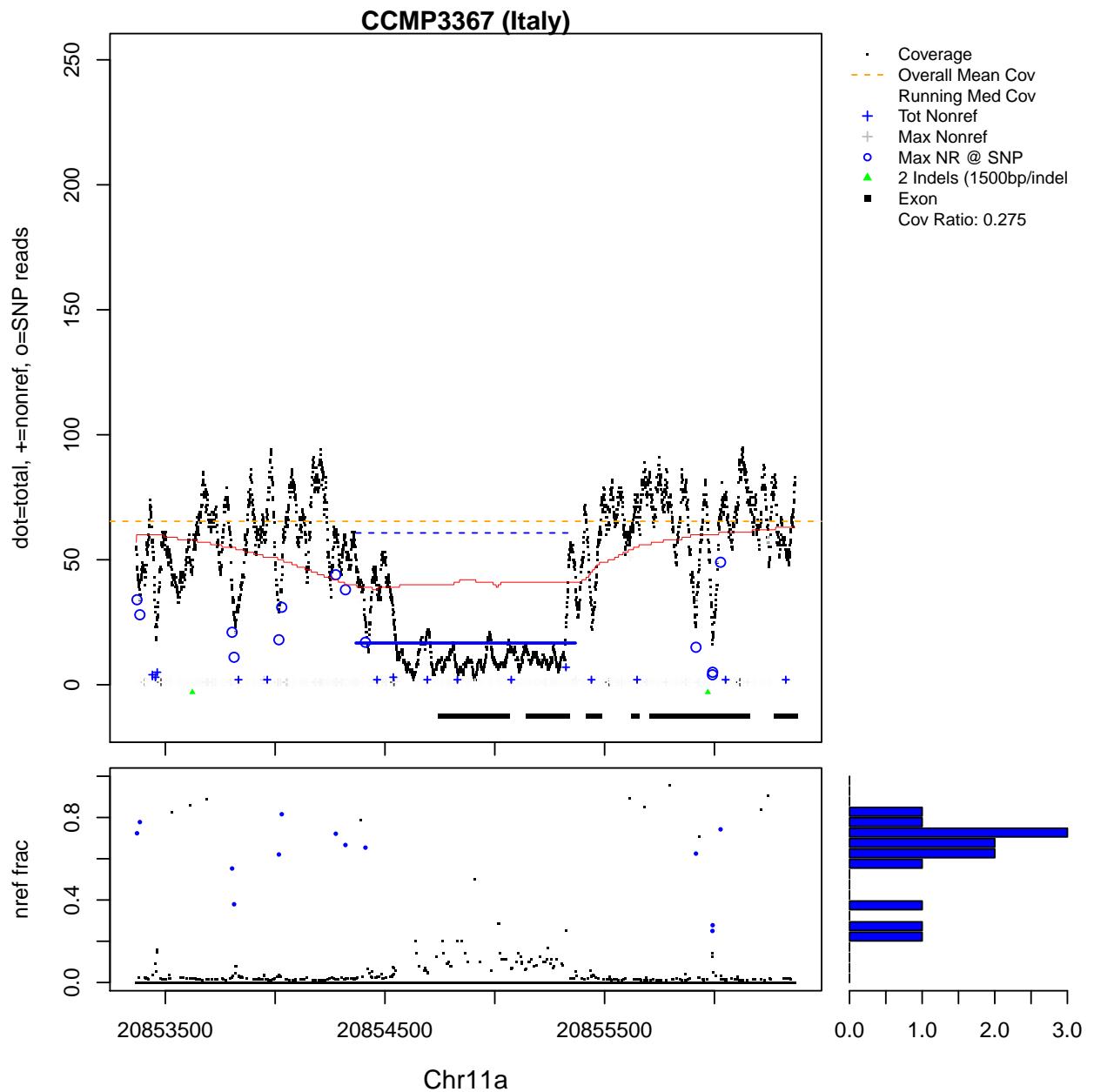








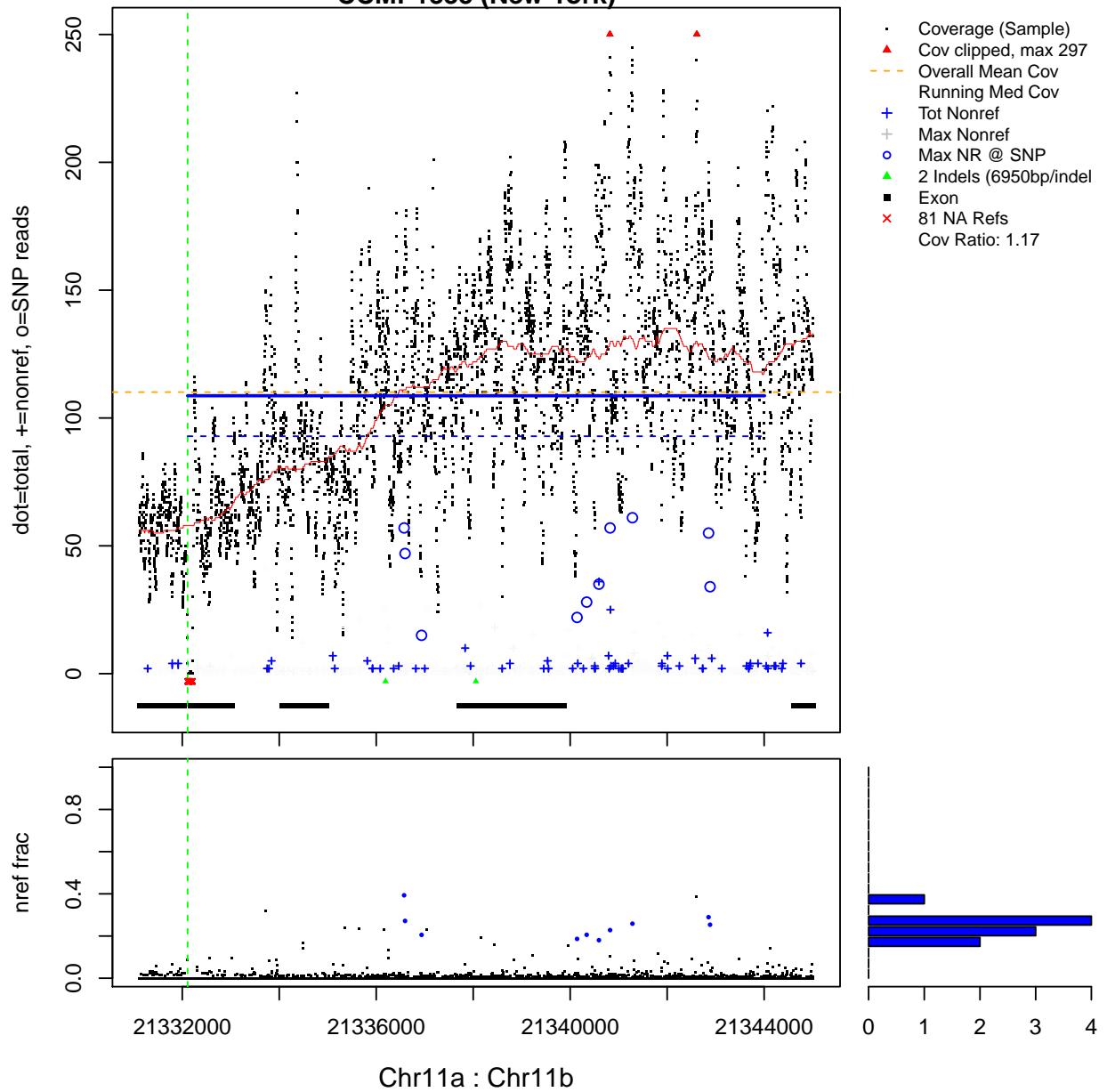




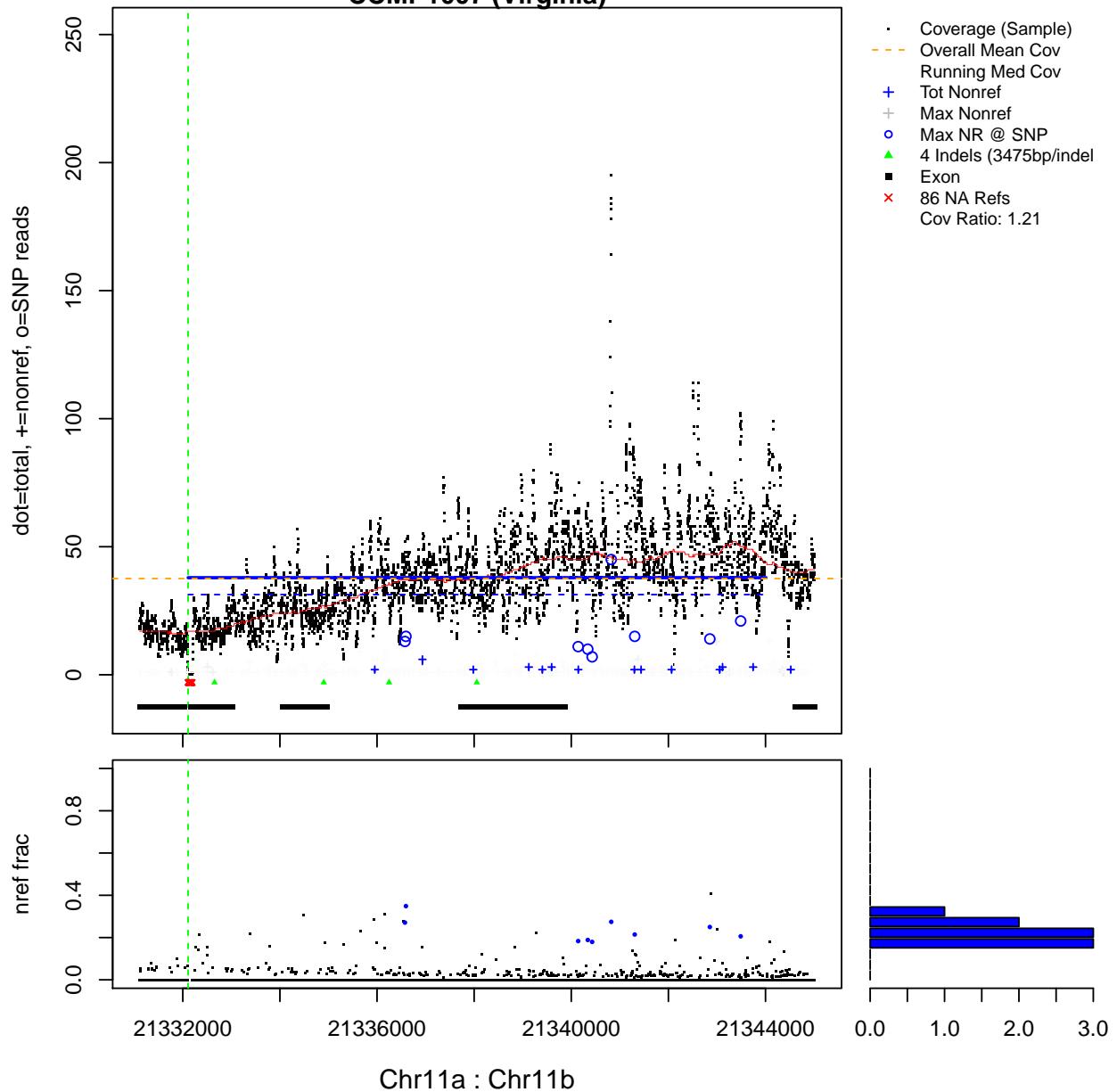
```
hemi.chunk(c('Chr11b:1', 'Chr11b:3301')) # weirdness at 11b teleomere
```

```
# Rows 85 : 86
#           chr  start     end length tp1007 tp1012 tp1013 tp1014 tp1015      IT tp1335 pattern
# Chr11a:806142 Chr11a 806142 806141      0     NA     NA     NA     NA     NA     NA     NA     NA     000
# Chr11b:1       Chr11b      1   3300    3300  0.599     NA  0.506     NA     NA  0.509     NA     122
# Chr11b:3301    Chr11b   3301  11900    8600     NA     NA  0.506     NA     NA  0.509     NA     022
# Chr11b:11901   Chr11b  11901  82842   70942     NA     NA     NA     NA     NA     NA     NA     000
```

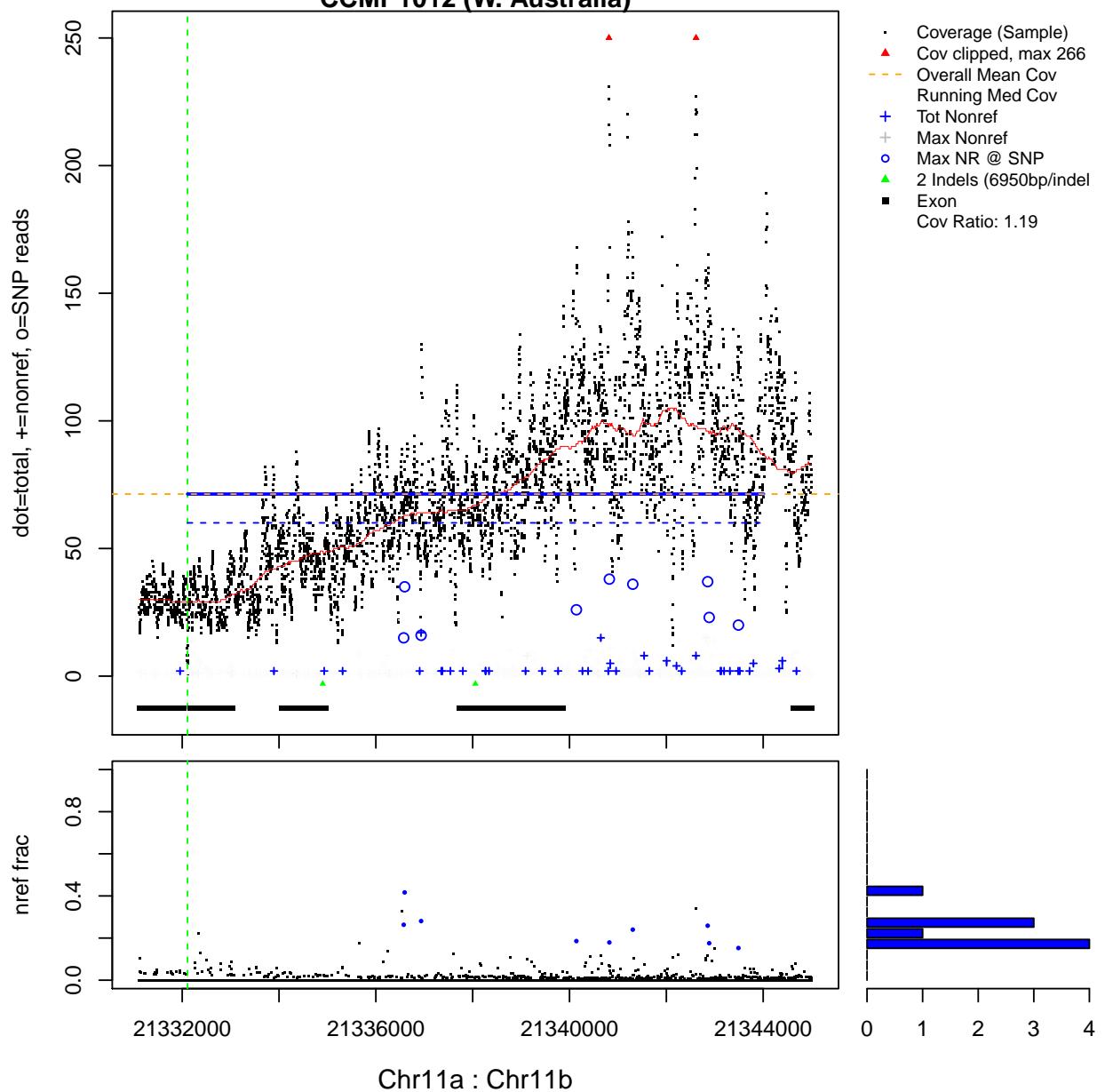
### CCMP1335 (New York)



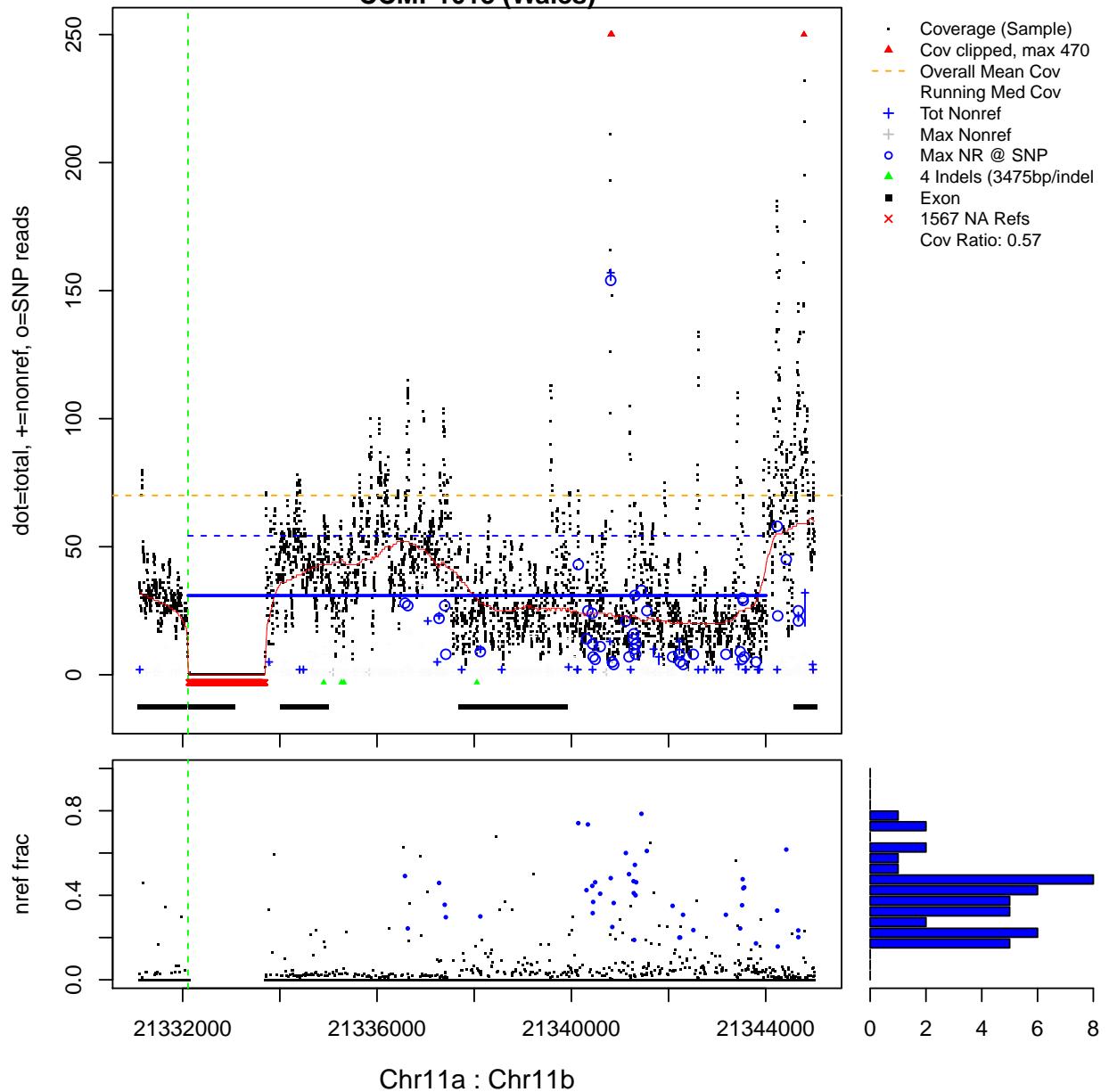
### CCMP1007 (Virginia)



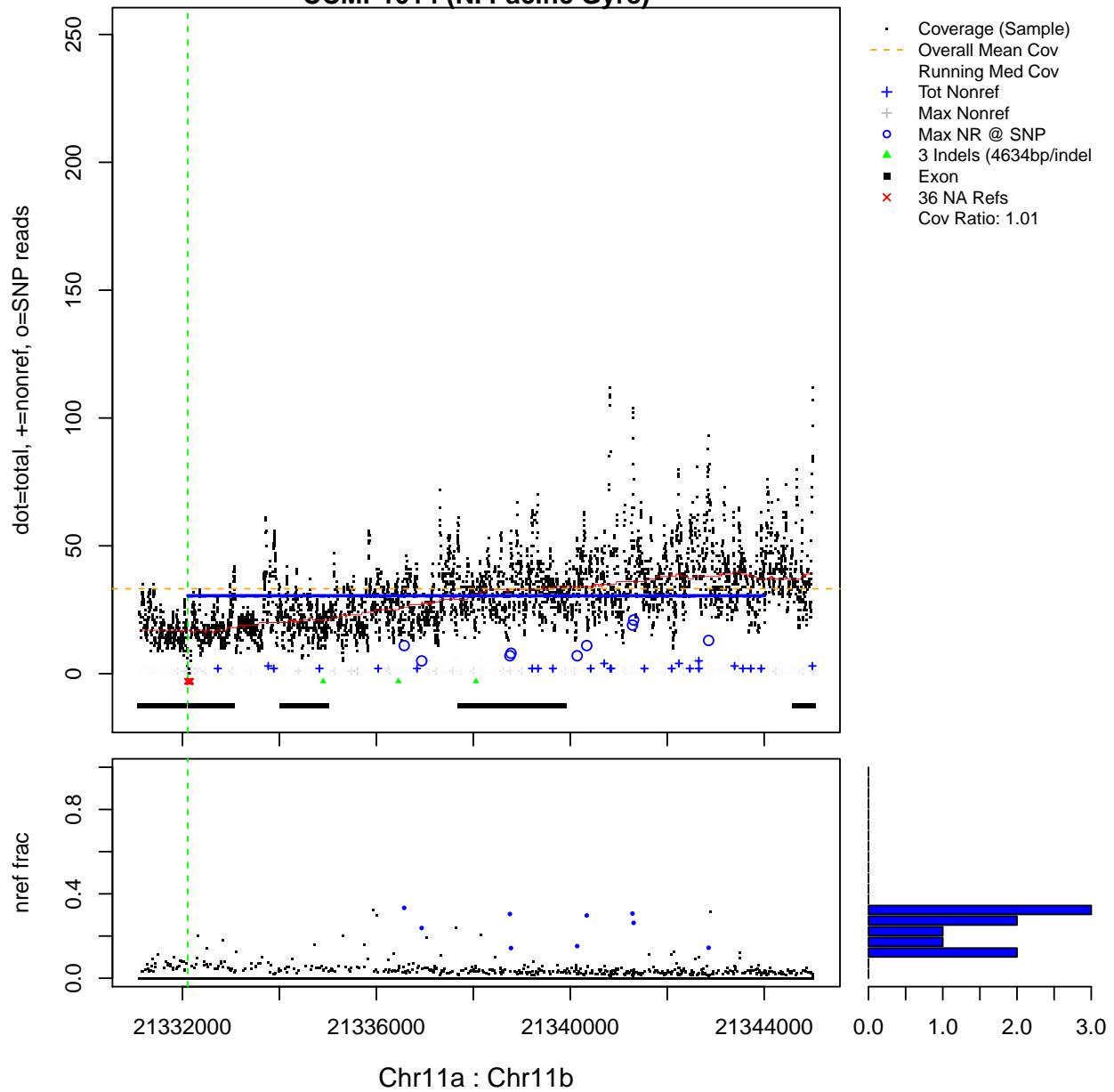
### CCMP1012 (W. Australia)



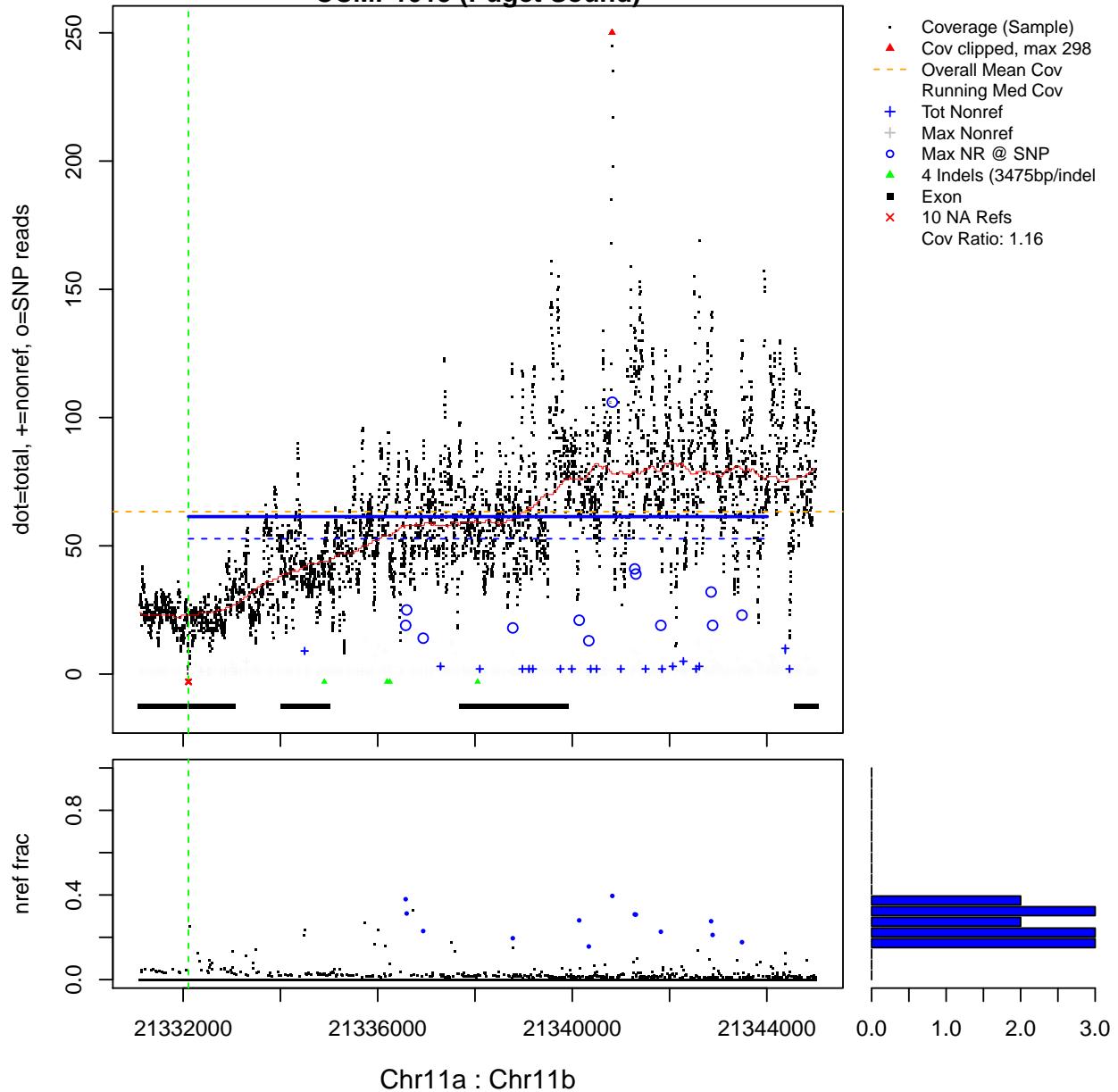
### CCMP1013 (Wales)

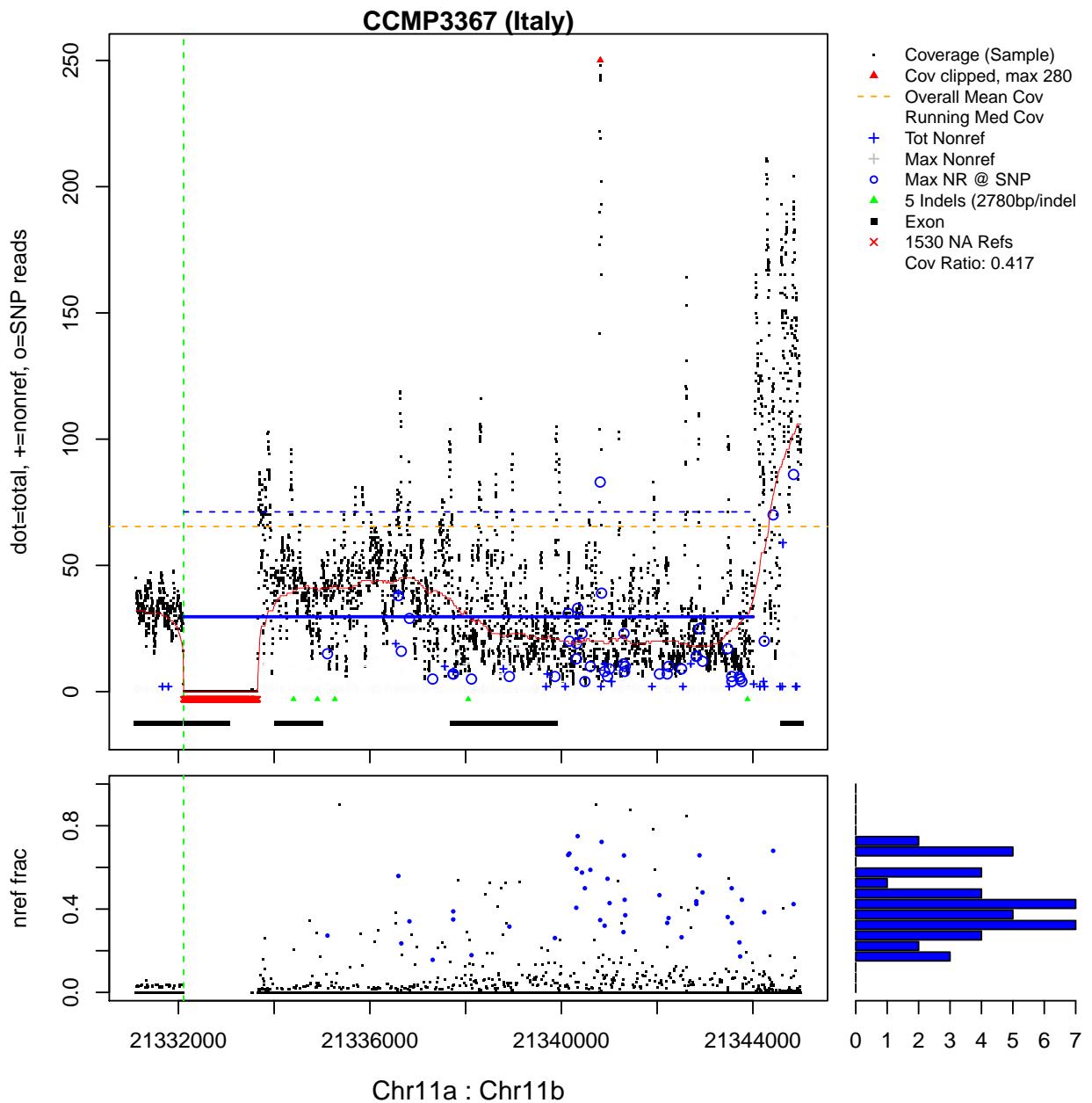


### CCMP1014 (N. Pacific Gyre)



### CCMP1015 (Puget Sound)

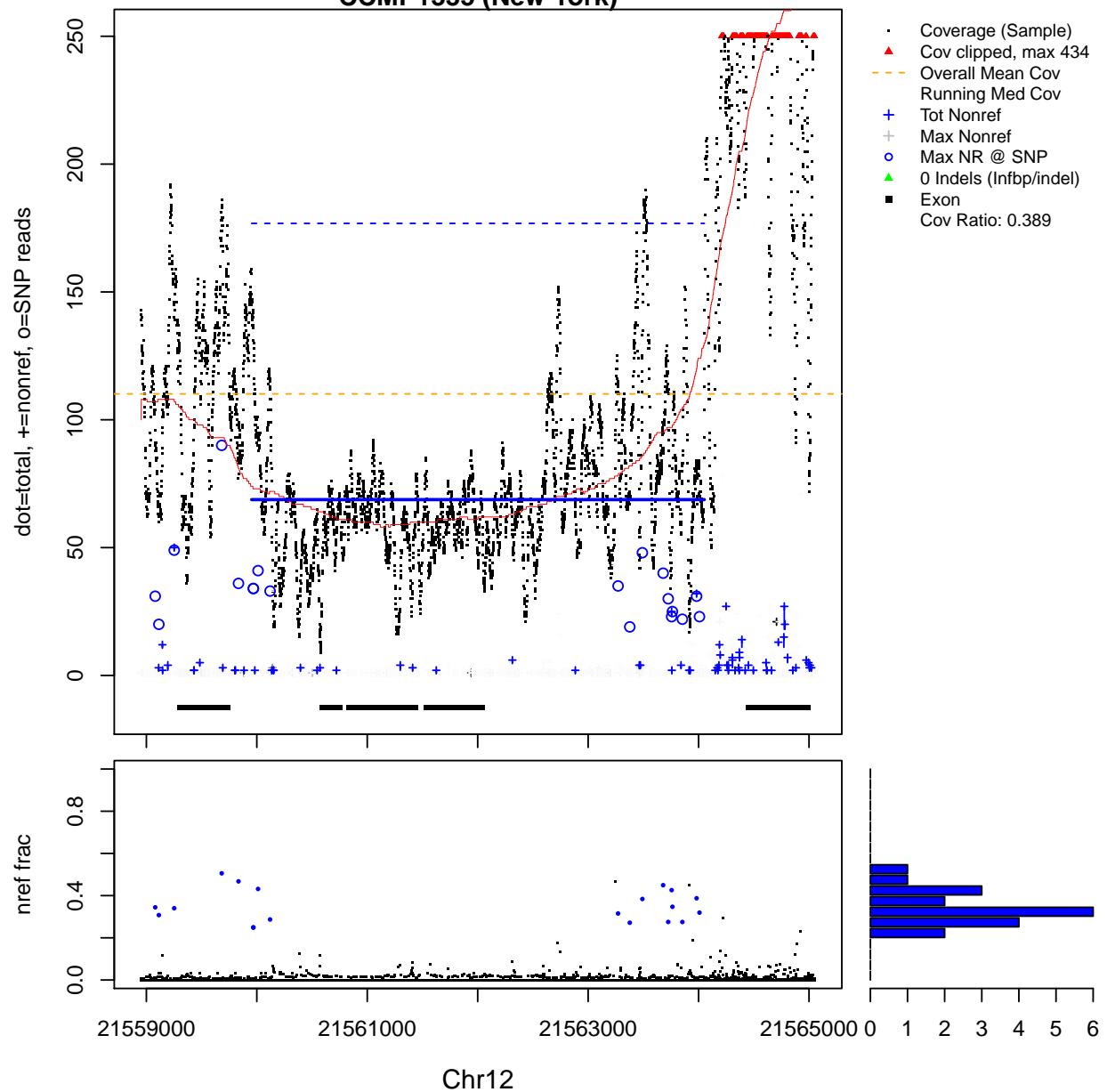


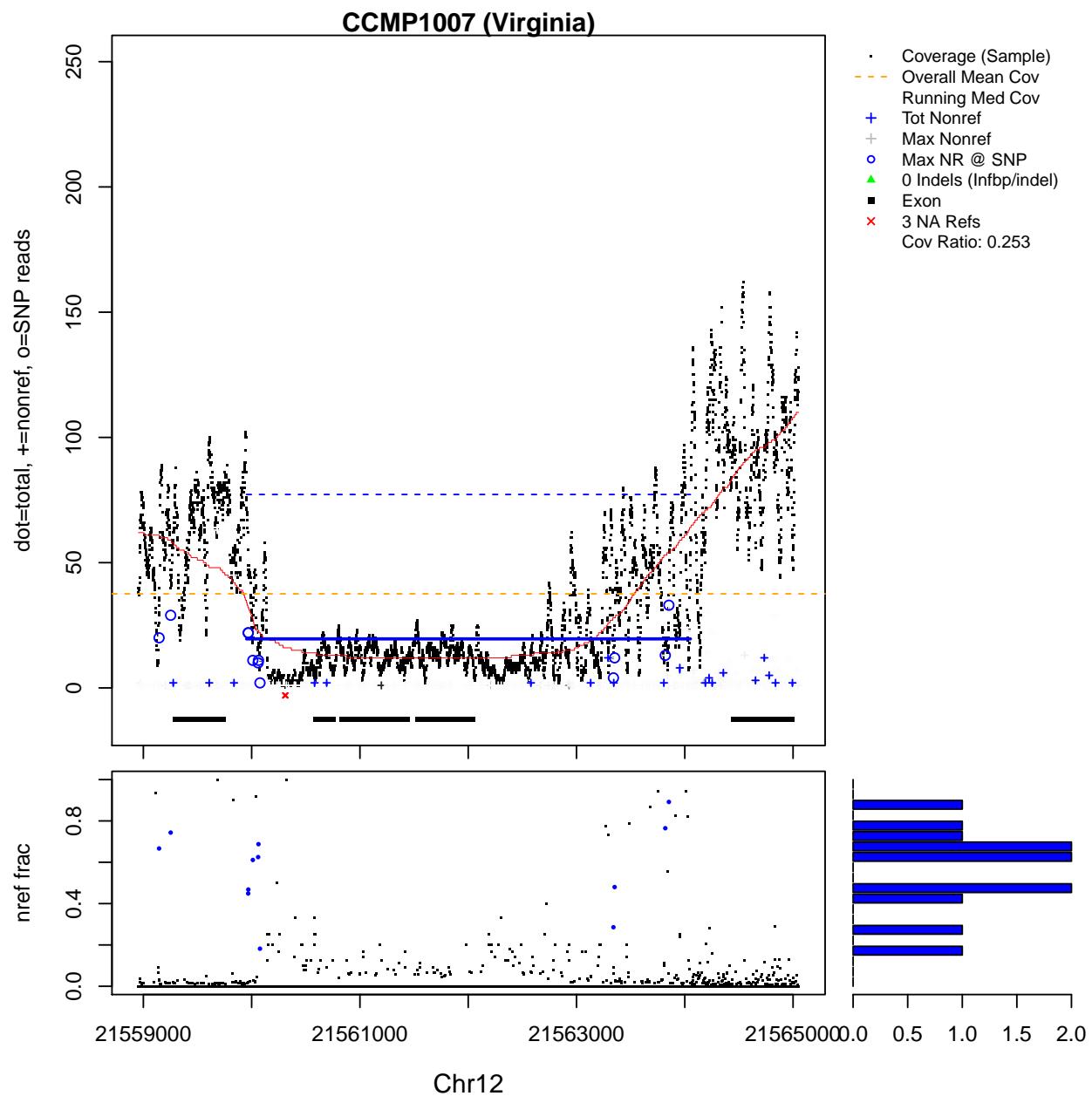


```
hemi.chunk(c('Chr12:145001', 'Chr12:148401')) # last 7-800 in NY is higher & snpy, rest ok
```

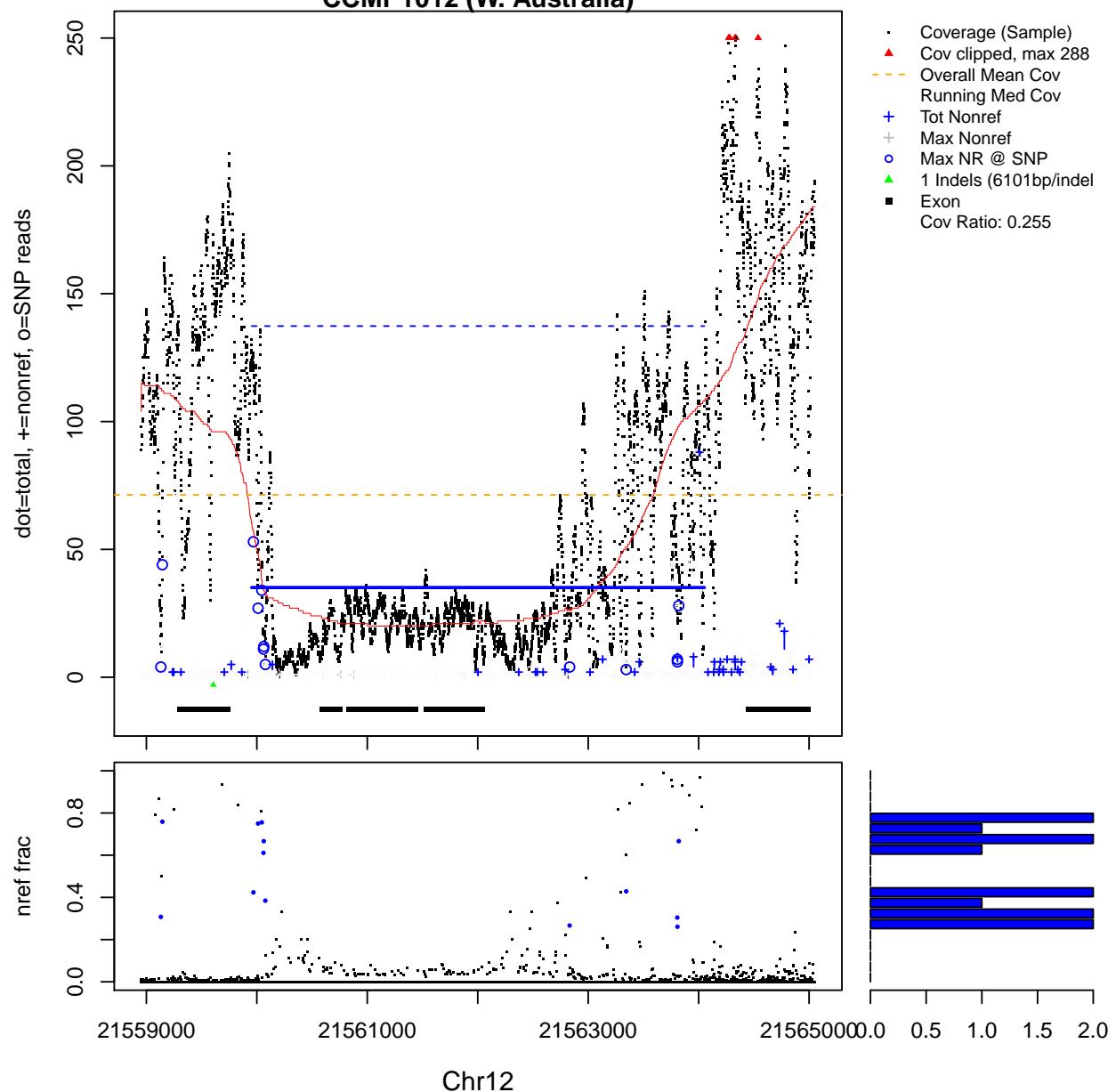
```
# Rows 96 : 100
#           chr start      end length tp1007 tp1012 tp1013 tp1014 tp1015      IT tp1335 pattern
# Chr12:94301 Chr12 94301 145000    50700     NA     NA     NA     NA     NA     NA     NA     NA     000
# Chr12:145001 Chr12 145001 145100    100  0.407     NA     NA     NA     NA     NA  0.486  0.712    103
# Chr12:145101 Chr12 145101 146200   1100  0.407  0.361     NA     NA  0.643  0.701  0.486  0.712    157
# Chr12:146201 Chr12 146201 148300   2100  0.407  0.361     NA     NA  0.701  0.486  0.712    147
# Chr12:148301 Chr12 148301 148400    100     NA     NA     NA     NA  0.701     NA  0.712    005
# Chr12:148401 Chr12 148401 149100    700     NA     NA     NA     NA     NA     NA  0.712    001
# Chr12:149101 Chr12 149101 217400   68300     NA     NA     NA     NA     NA     NA     NA     000
```

### CCMP1335 (New York)

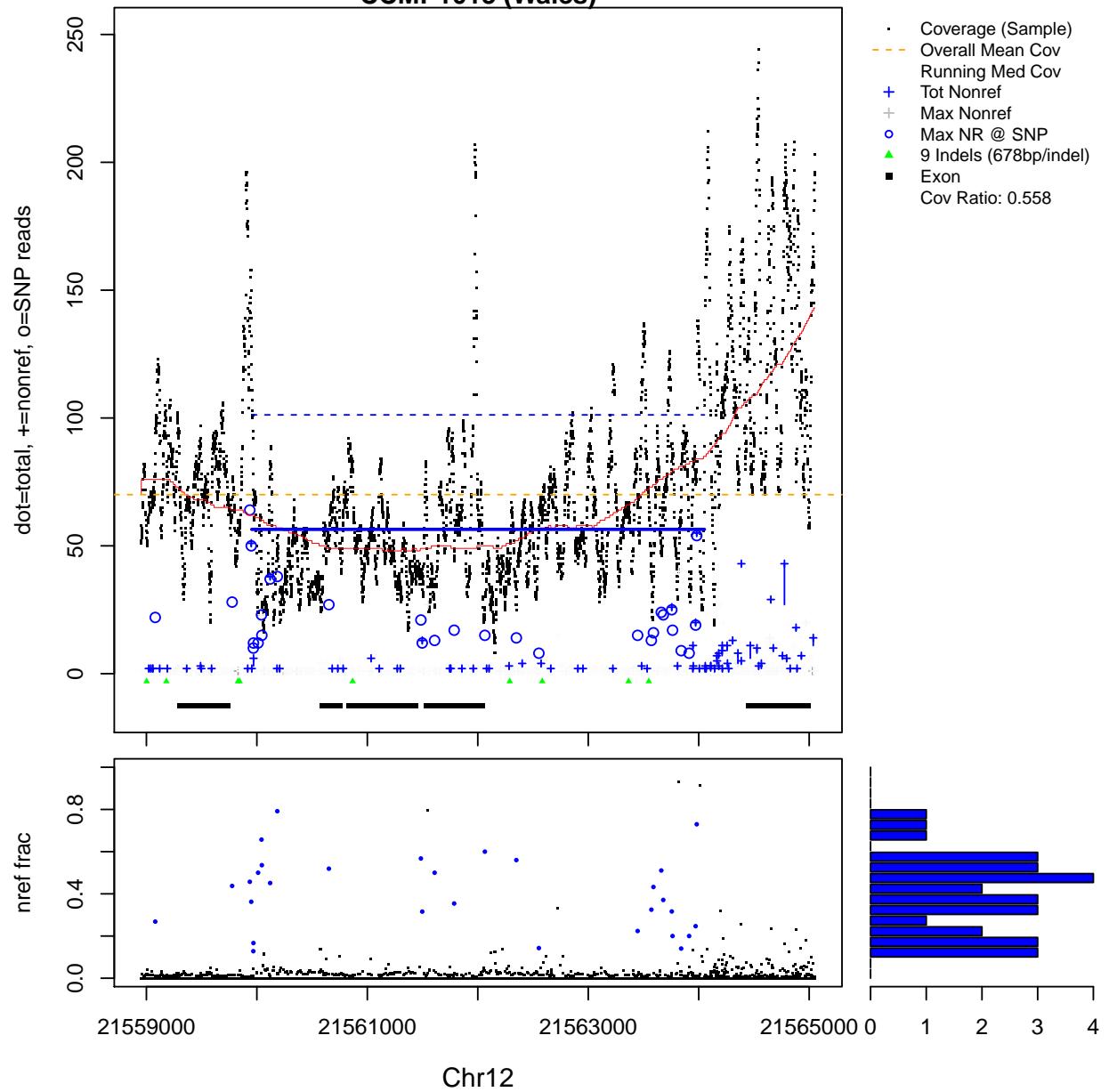


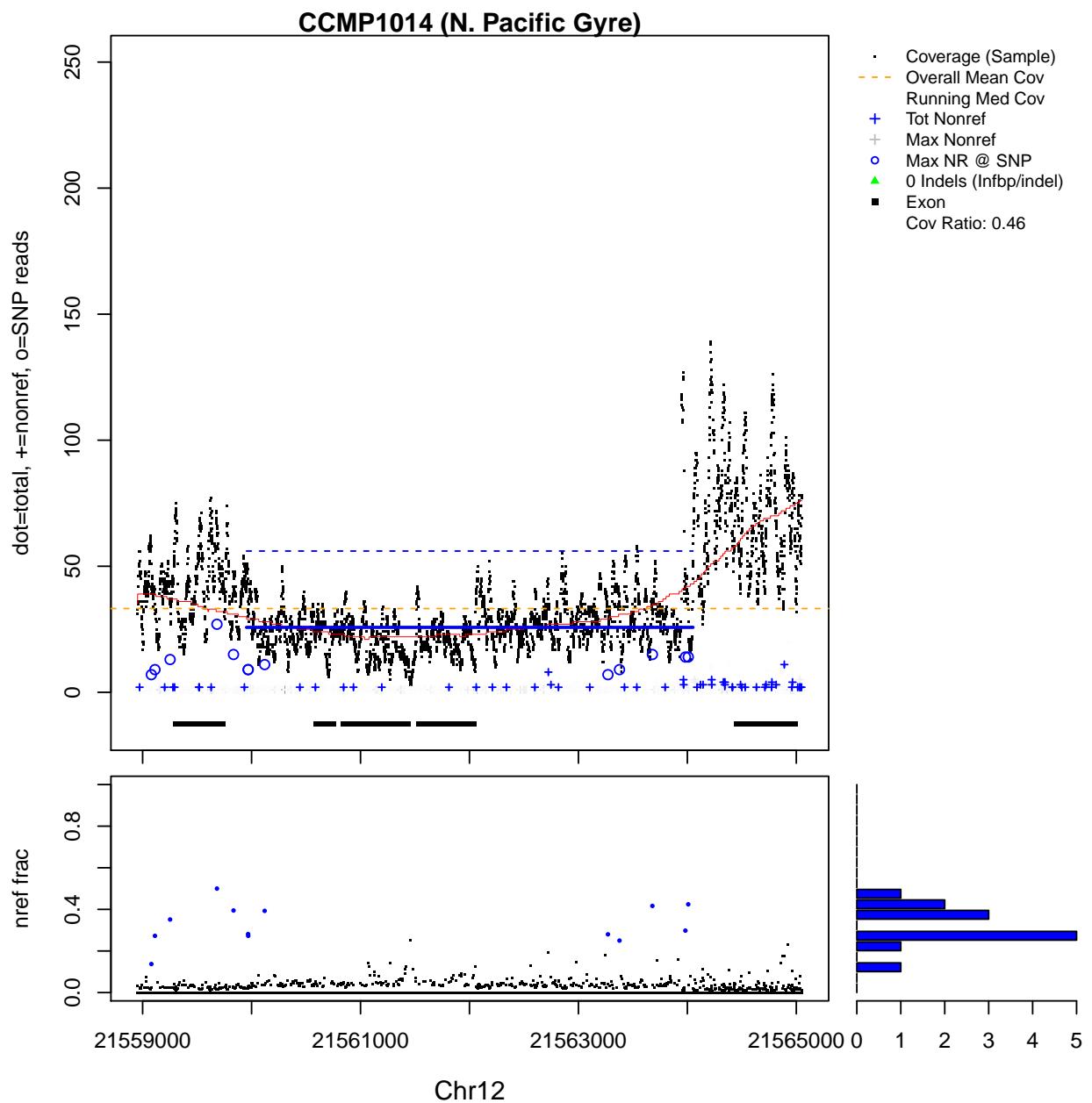


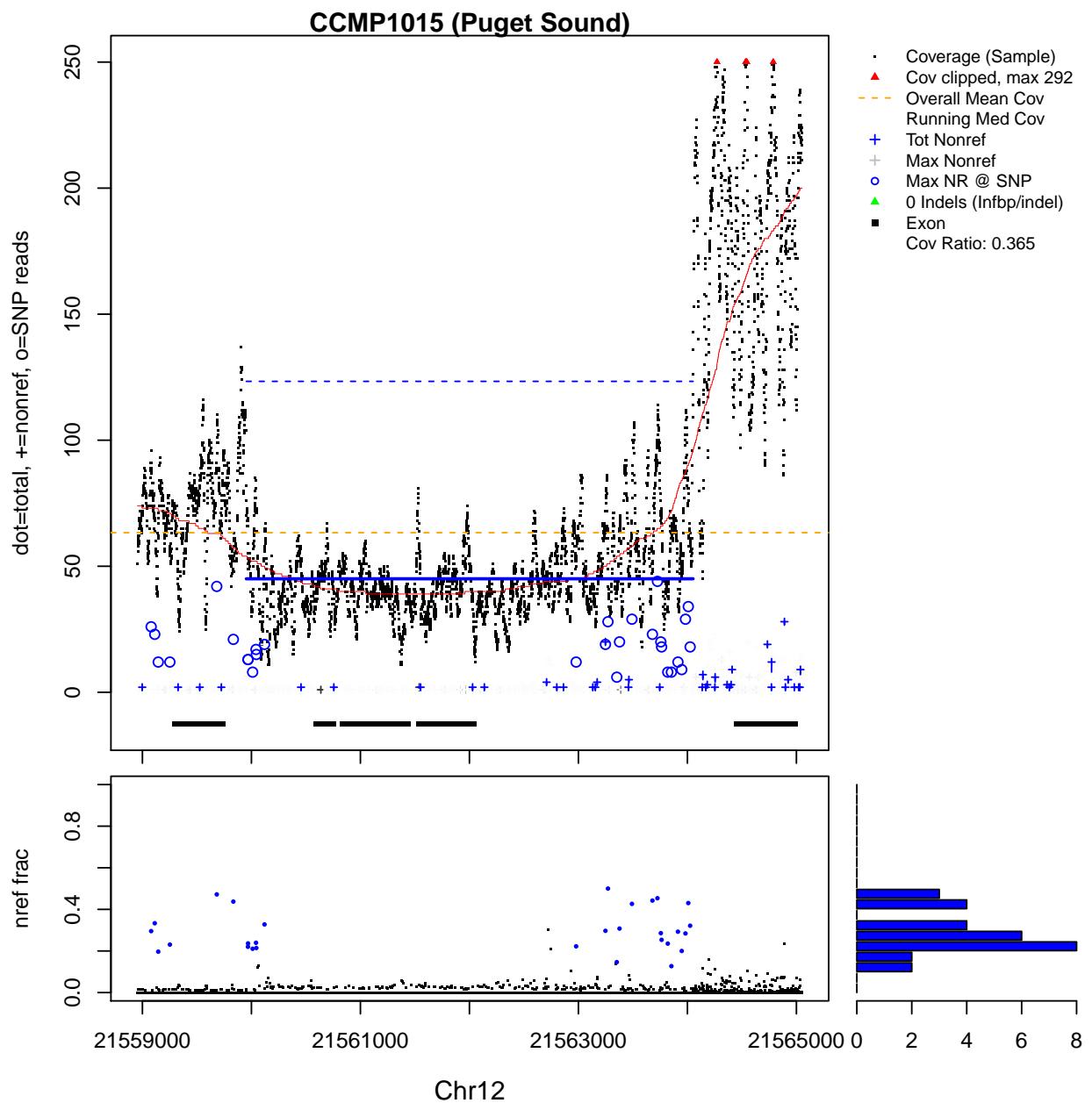
### CCMP1012 (W. Australia)

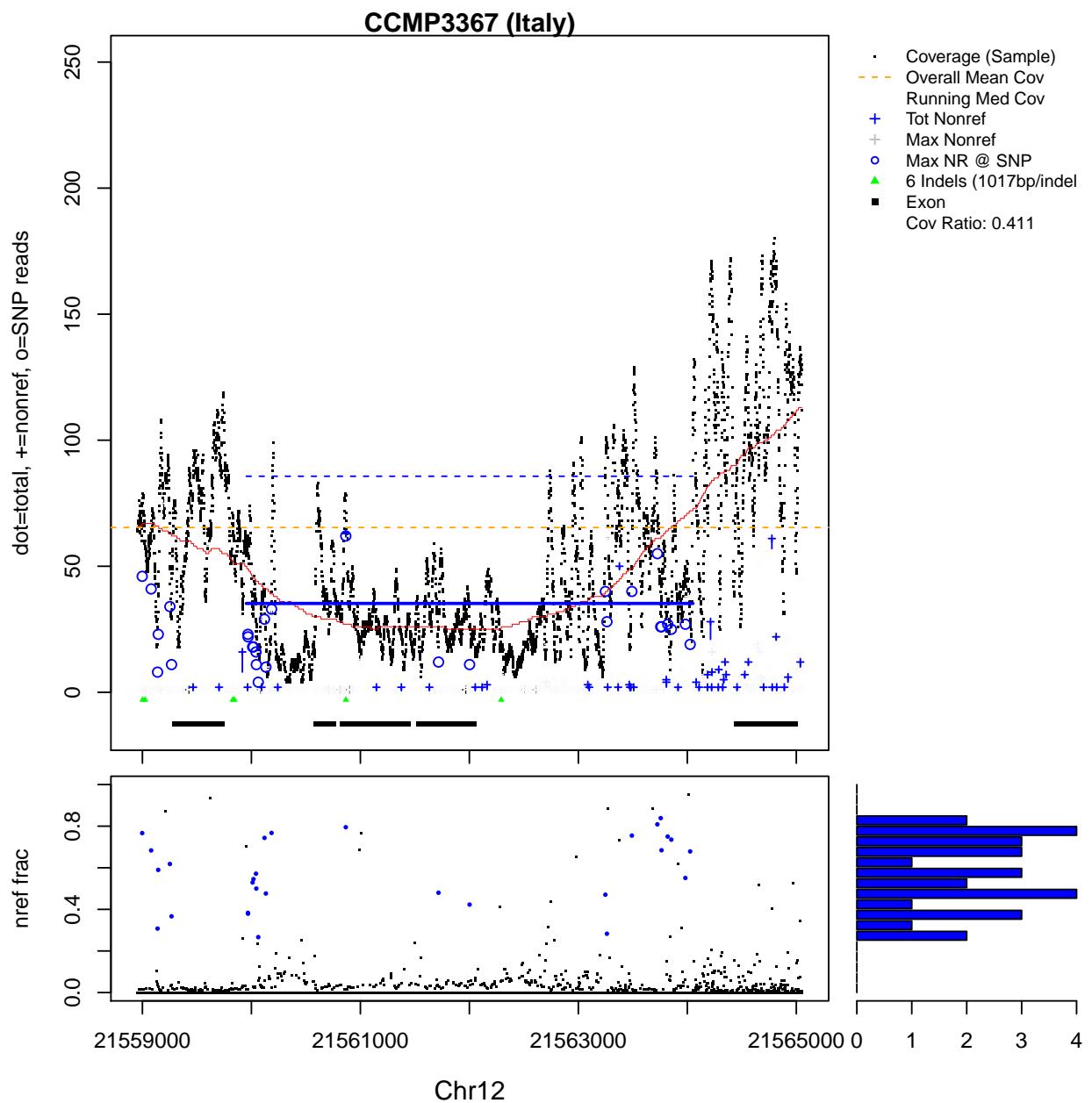


### CCMP1013 (Wales)





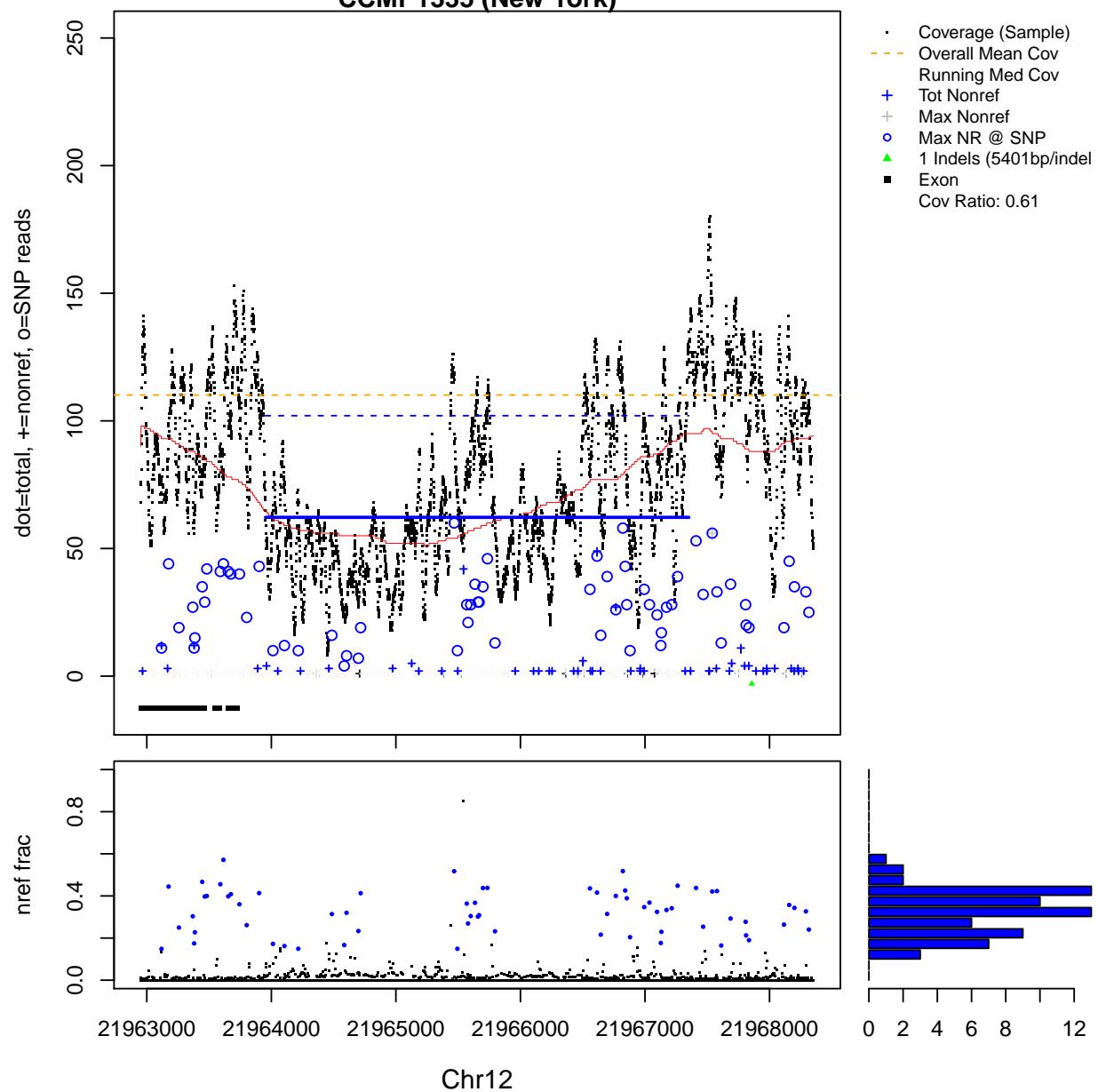


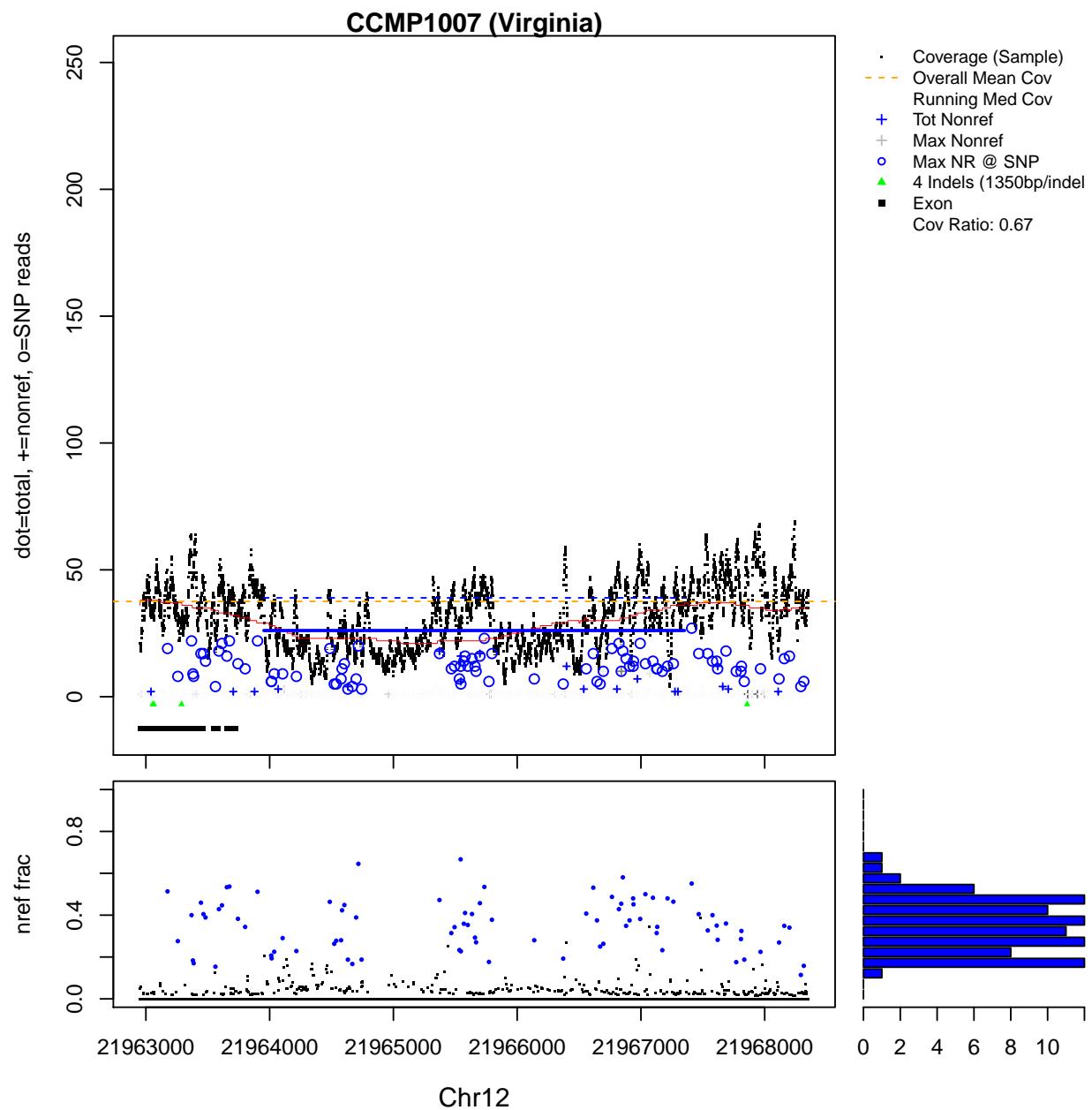


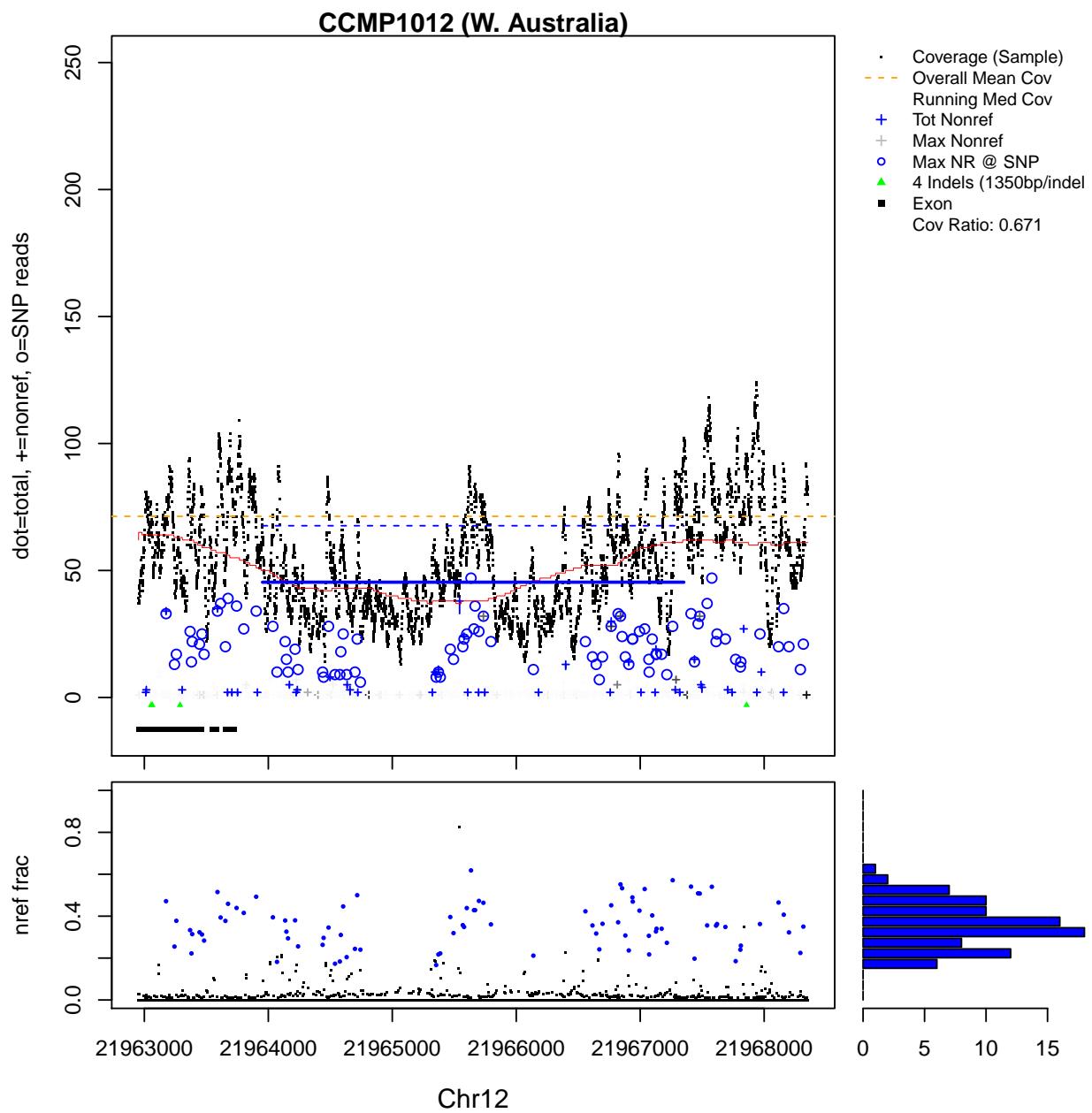
```
hemi.chunk(c('Chr12:549001', 'Chr12:551801')) # snpy all 7
```

```
# Rows 105 : 107
#          chr start      end length tp1007 tp1012 tp1013 tp1014 tp1015 IT tp1335 pattern
# Chr12:244701 Chr12 244701 549000 304300     NA     NA     NA     NA     NA NA NA     NA 000
# Chr12:549001 Chr12 549001 549300    300 0.658     NA     NA     NA     NA     NA NA NA 0.651 101
# Chr12:549301 Chr12 549301 551800   2500 0.658 0.579     NA     NA     NA     NA     NA NA NA 0.651 141
# Chr12:551801 Chr12 551801 552400    600     NA     NA     NA     NA     NA NA NA 0.651 001
# Chr12:552401 Chr12 552401 630300  77900     NA     NA     NA     NA     NA NA NA     NA 000
```

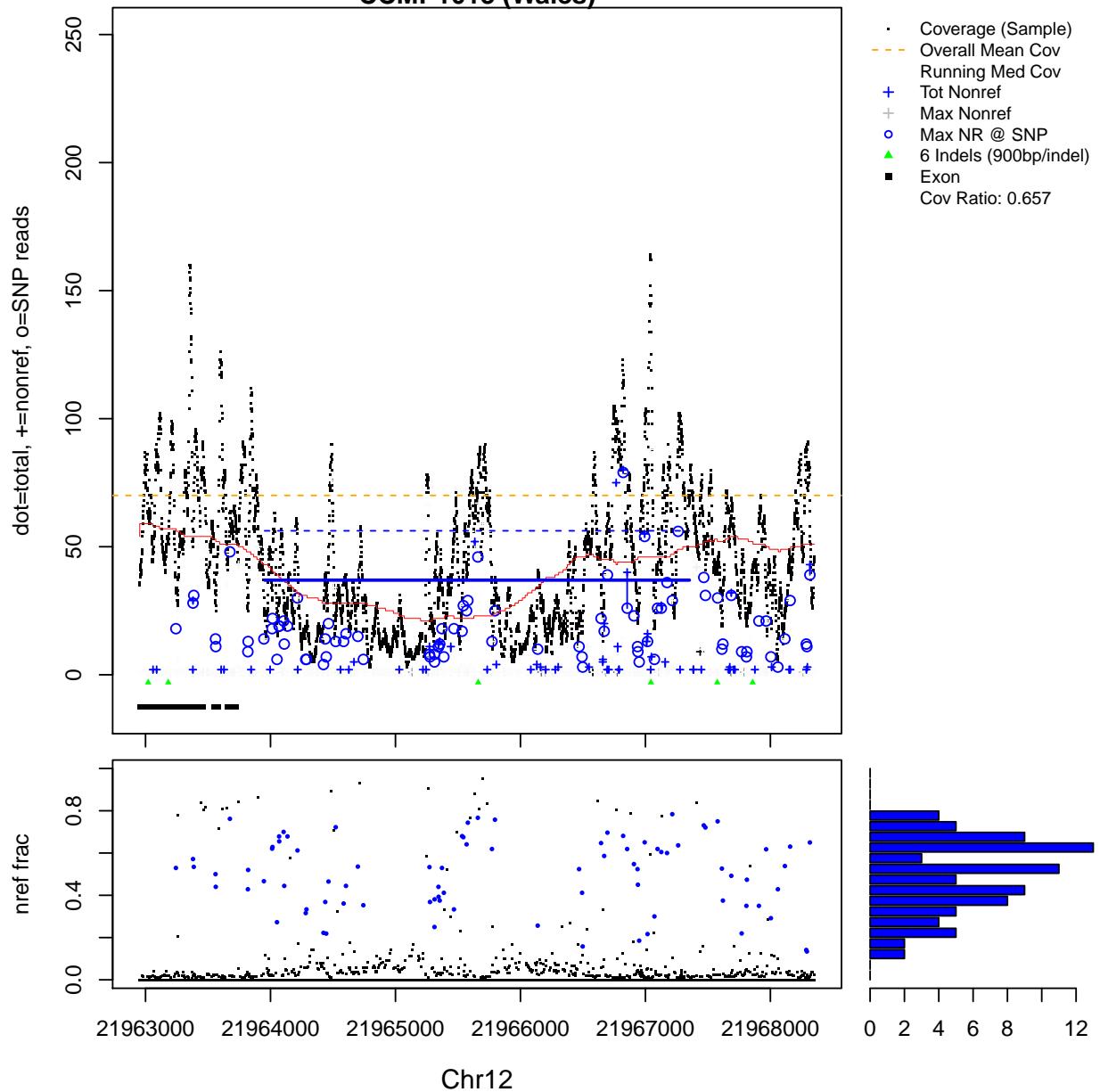
### CCMP1335 (New York)

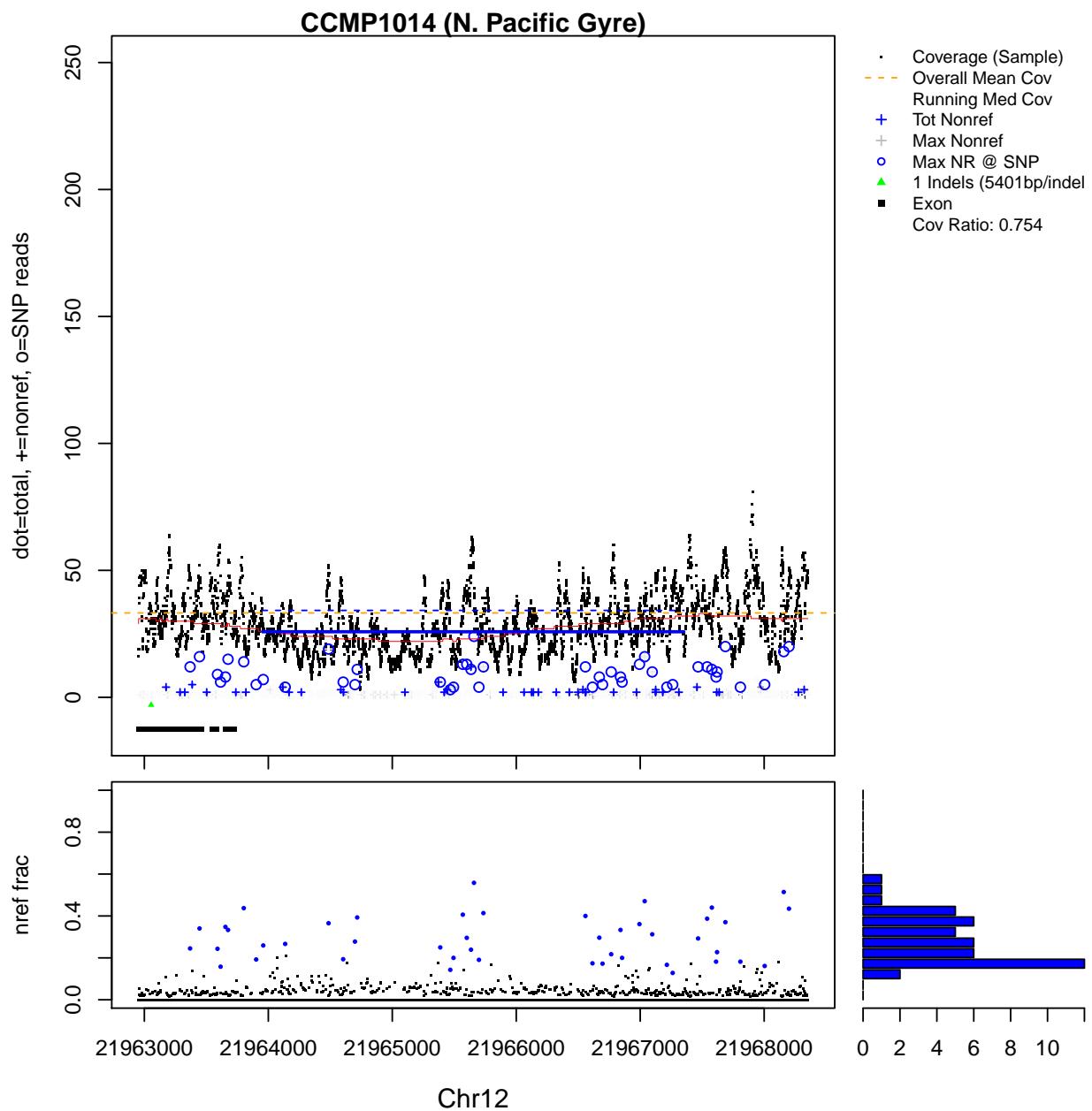


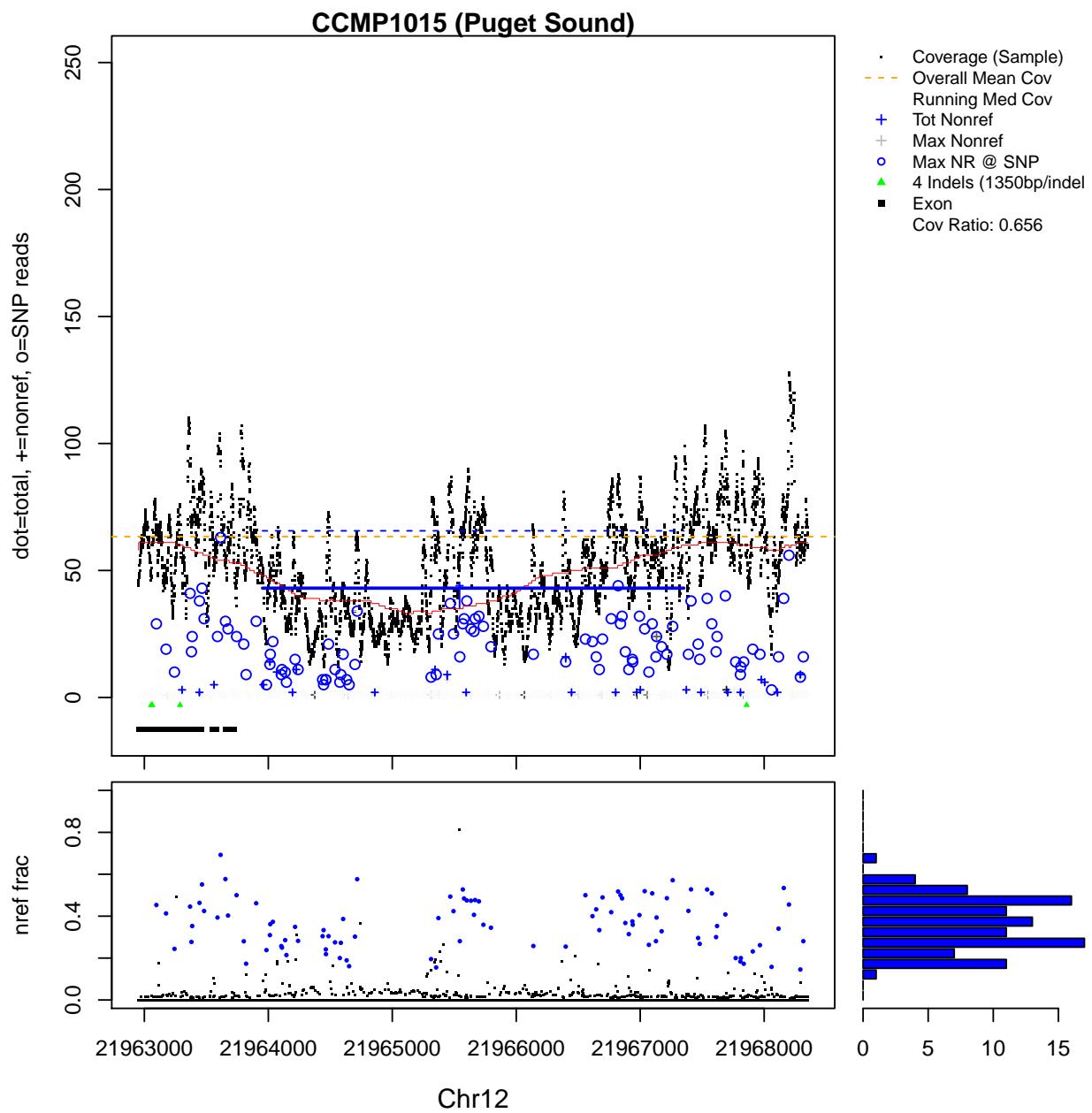


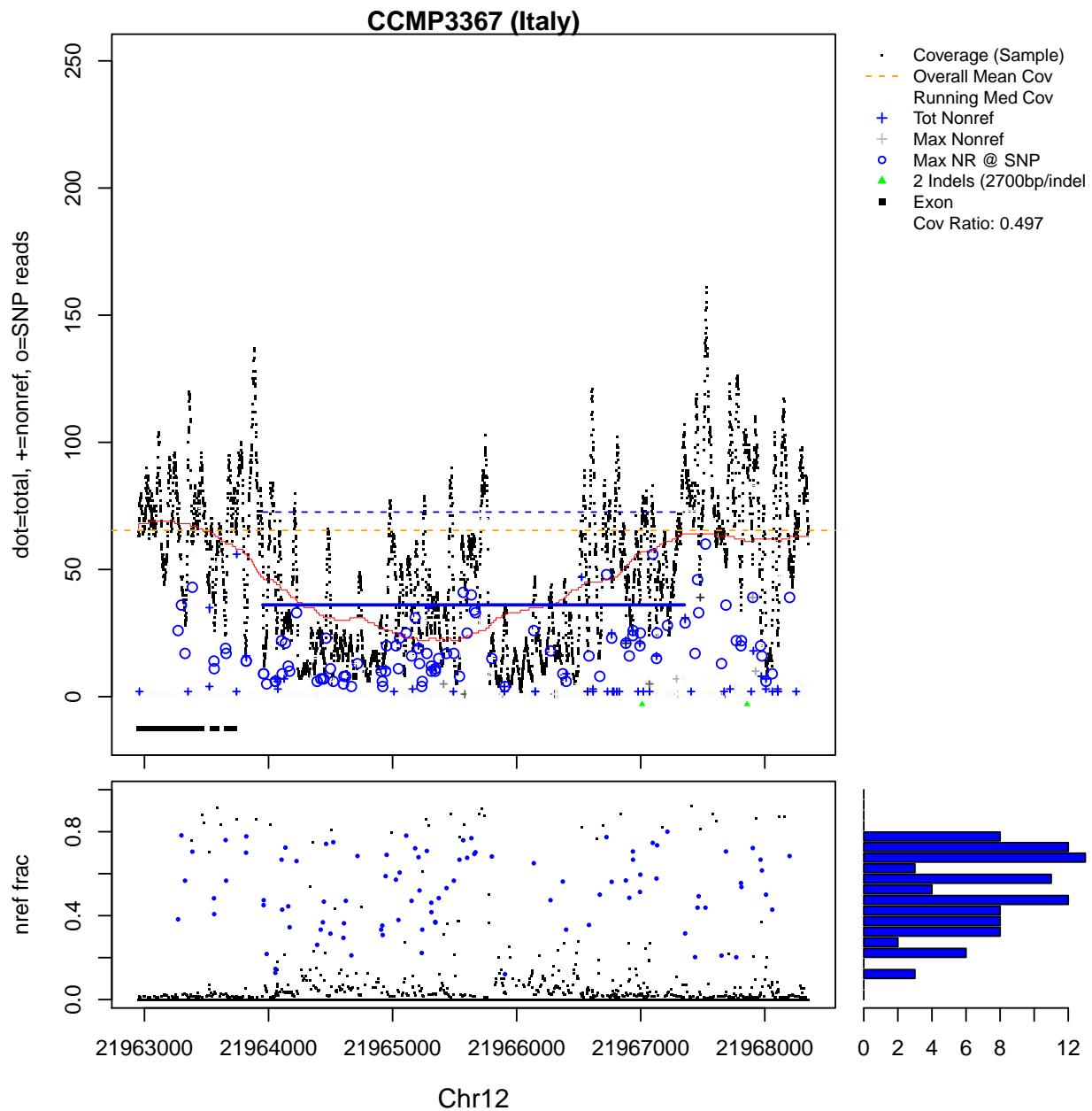


### CCMP1013 (Wales)





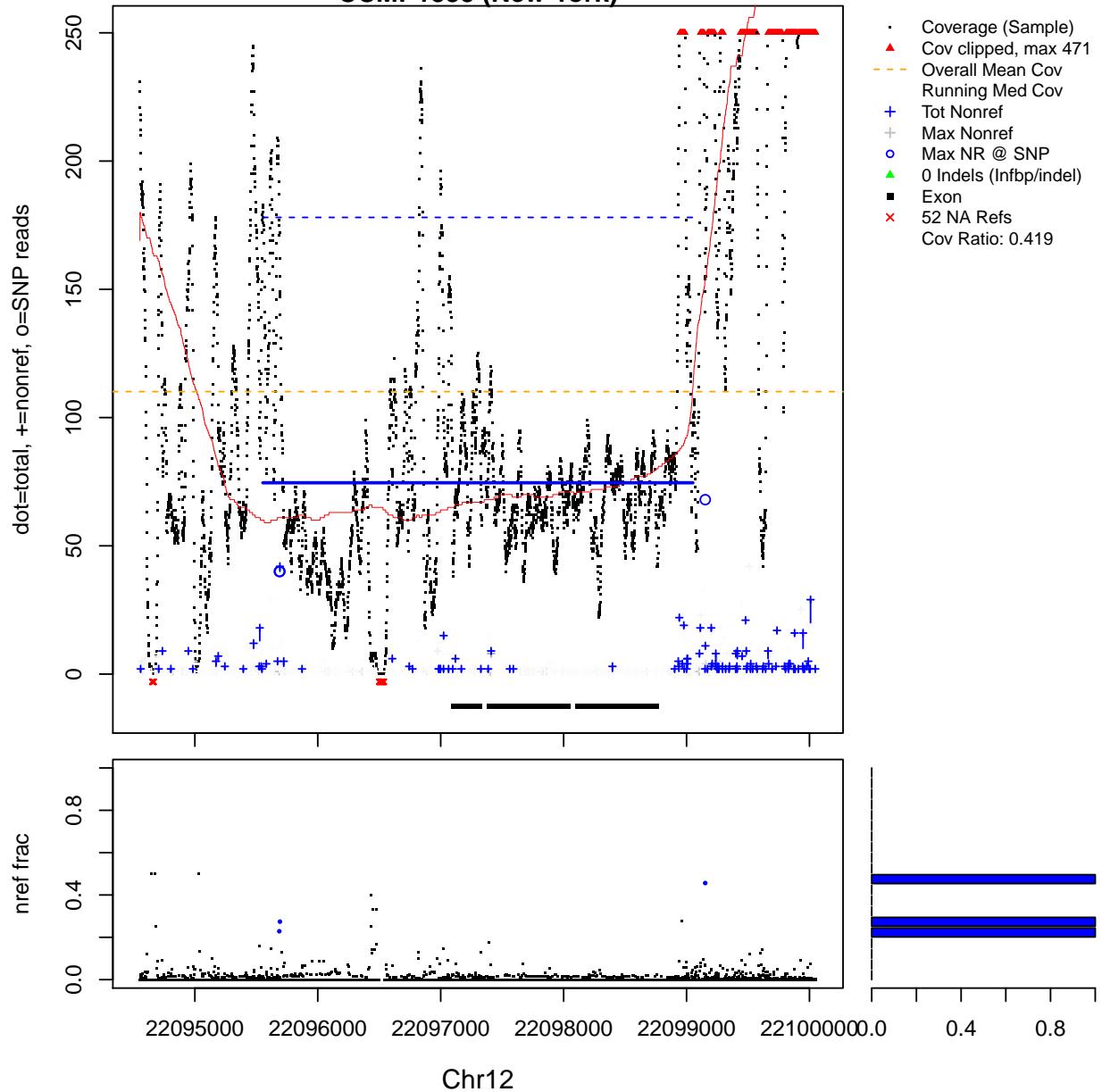




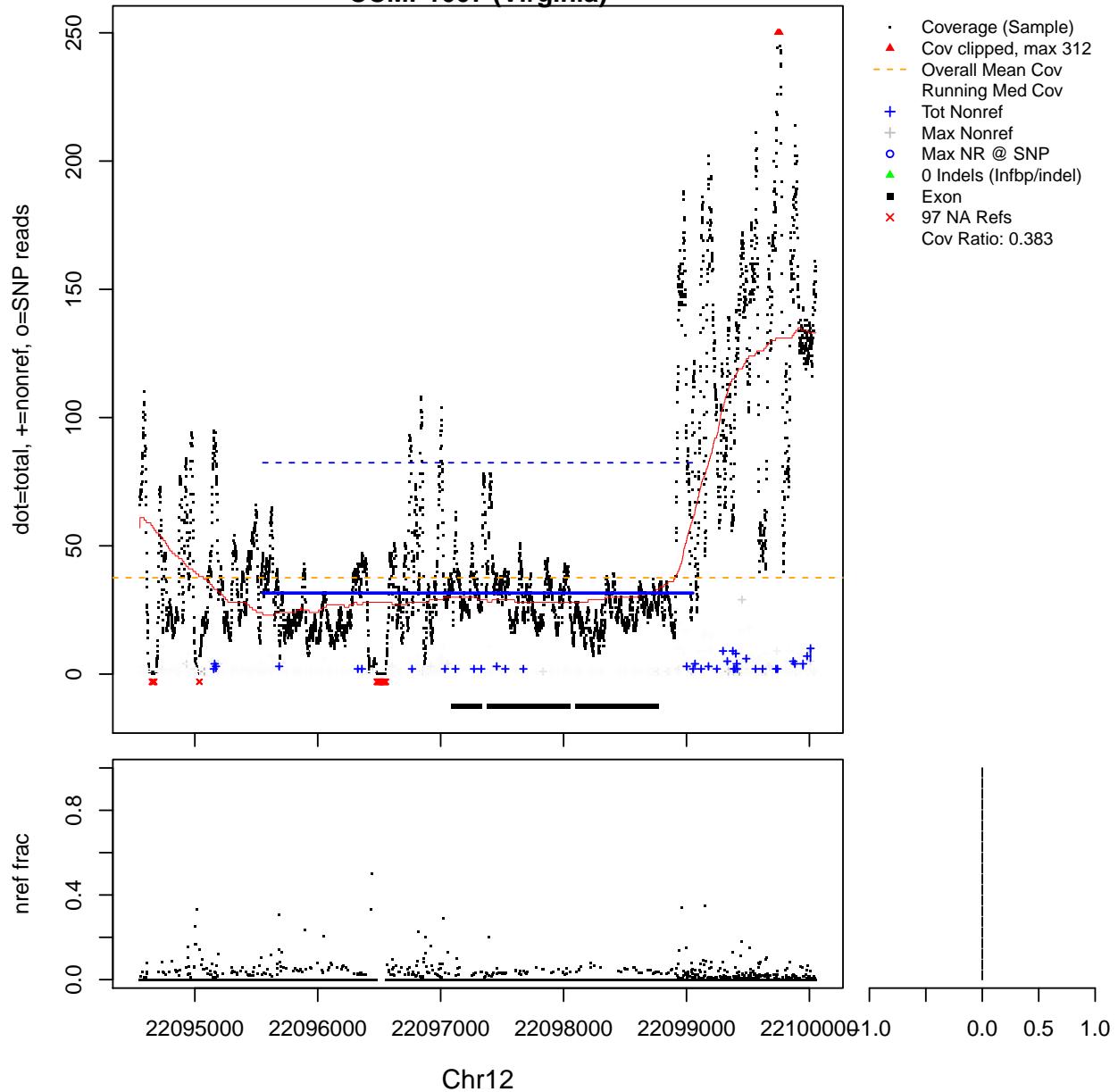
```
# 07,12,14:No; 15: maybe; 13:1st half snpy, 2nd not & exonic, IT yes, no snps, NY yes
hemi.chunk(c('Chr12:680601','Chr12:684001'))
```

```
# Rows 111 : 115
#          chr start    end length tp1007 tp1012 tp1013 tp1014 tp1015      IT tp1335 pattern
# Chr12:636901 Chr12 636901 680600   43700     NA     NA     NA     NA     NA     NA     NA     NA     00
# Chr12:680601 Chr12 680601 680800     200     NA     NA  0.569     NA     NA     NA     NA     NA     20
# Chr12:680801 Chr12 680801 681600    800     NA     NA  0.569     NA     NA     NA     NA  0.405     21
# Chr12:681601 Chr12 681601 682600   1000     NA     NA  0.569     NA     NA     NA     NA     NA     20
# Chr12:682601 Chr12 682601 684000   1400     NA     NA  0.569     NA     NA  0.331     NA     22
# Chr12:684001 Chr12 684001 684100     100     NA     NA  0.569     NA     NA     NA     NA     NA     20
# Chr12:684101 Chr12 684101 727700   43600     NA     NA     NA     NA     NA     NA     NA     NA     00
```

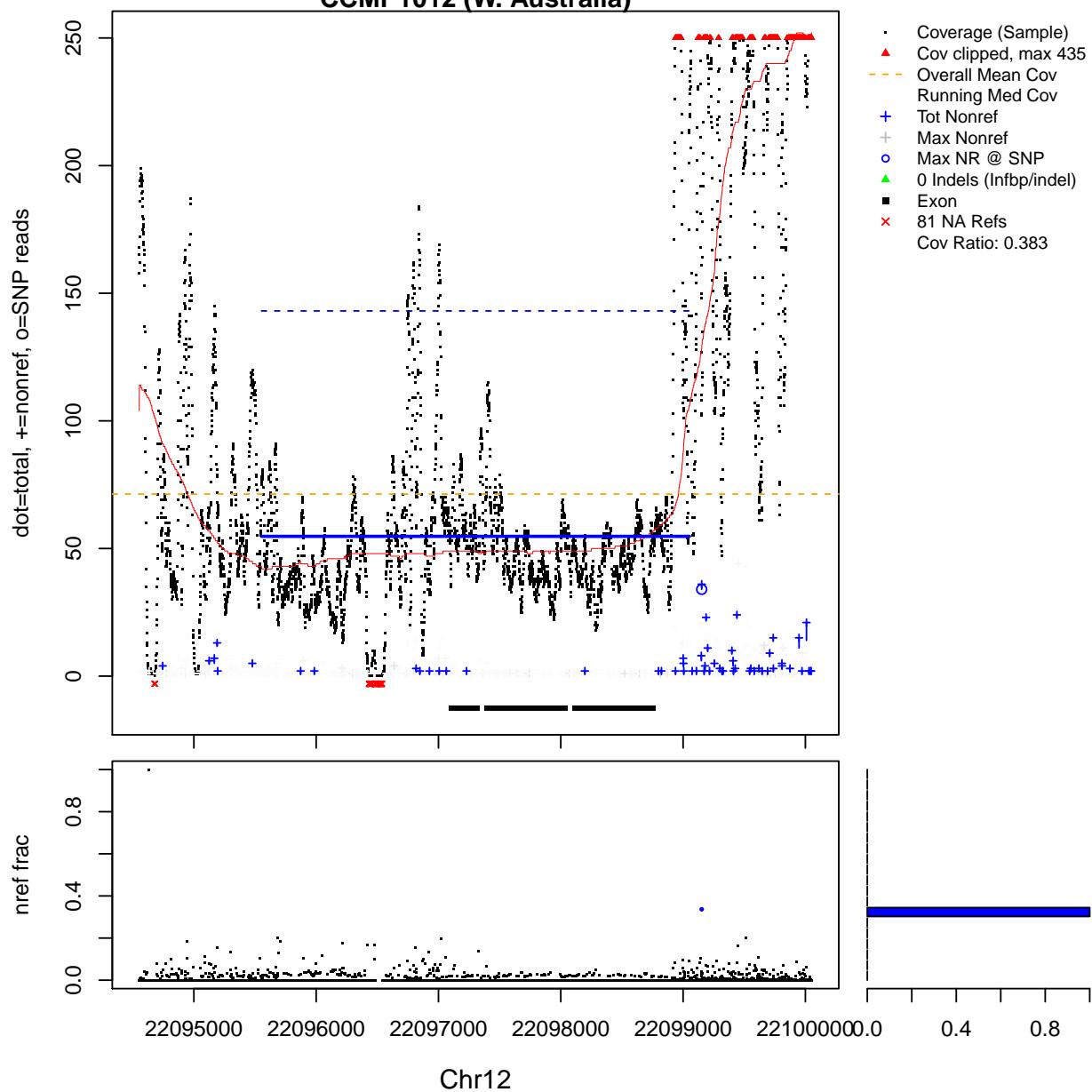
### CCMP1335 (New York)



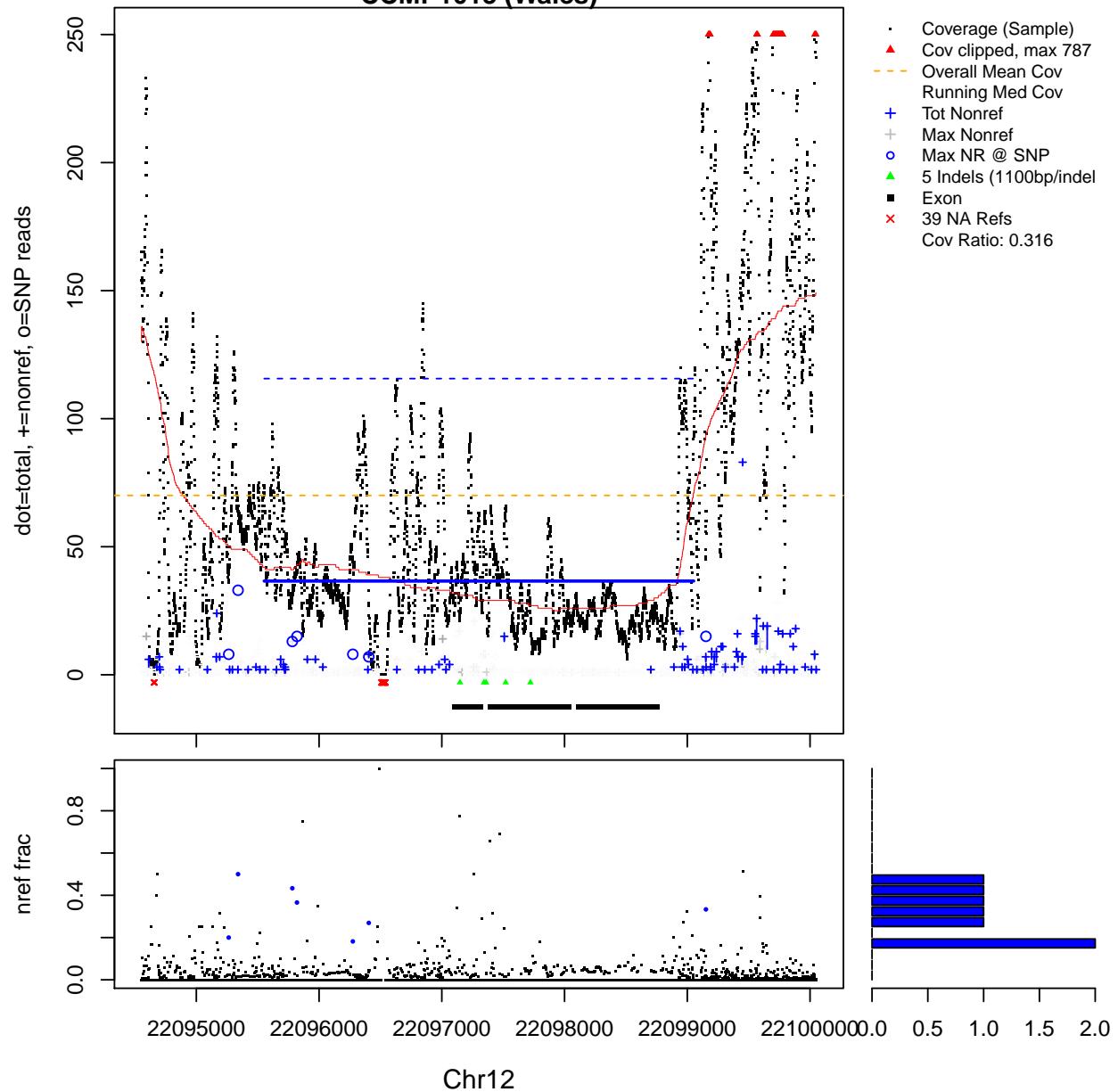
### CCMP1007 (Virginia)

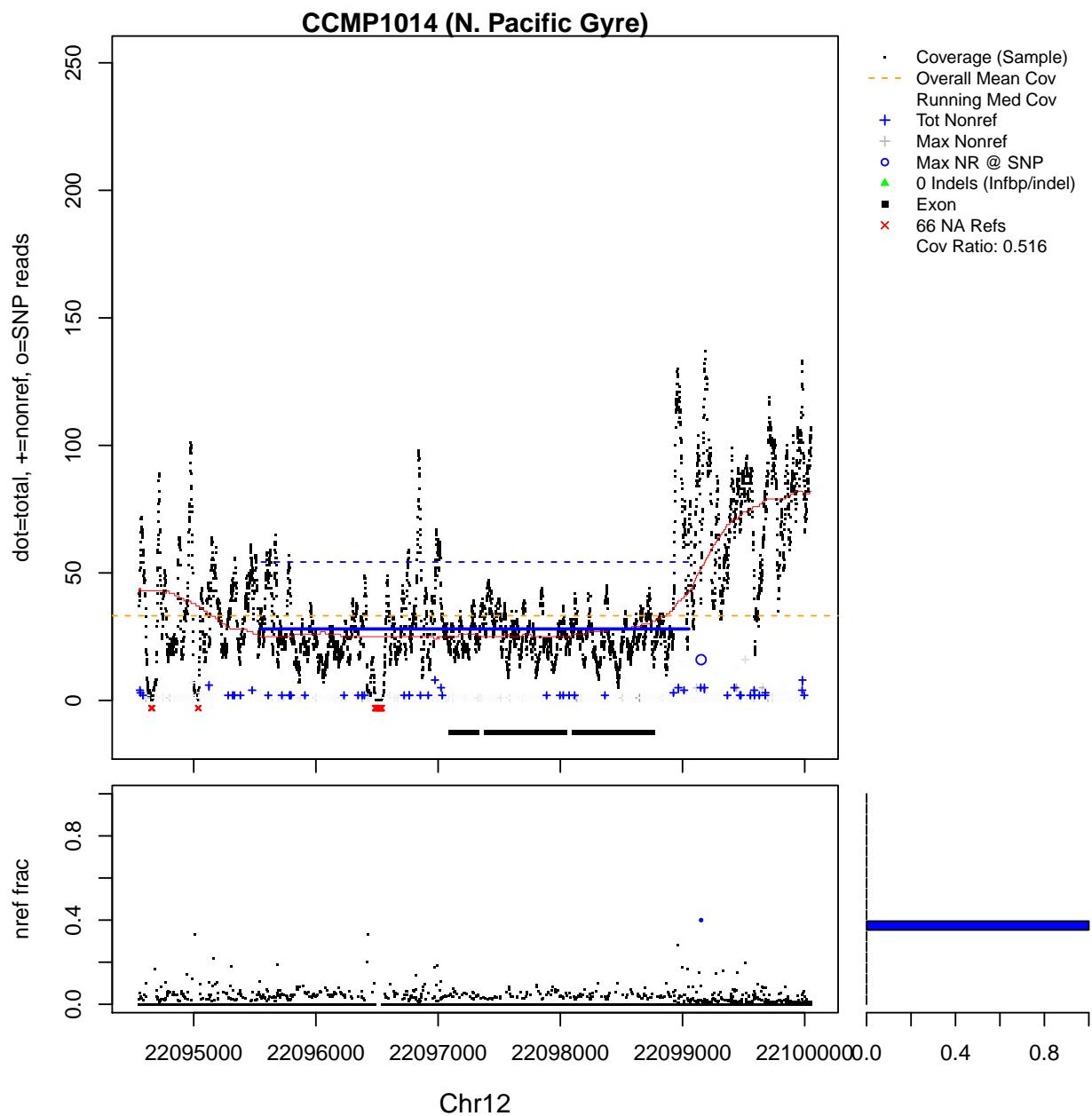


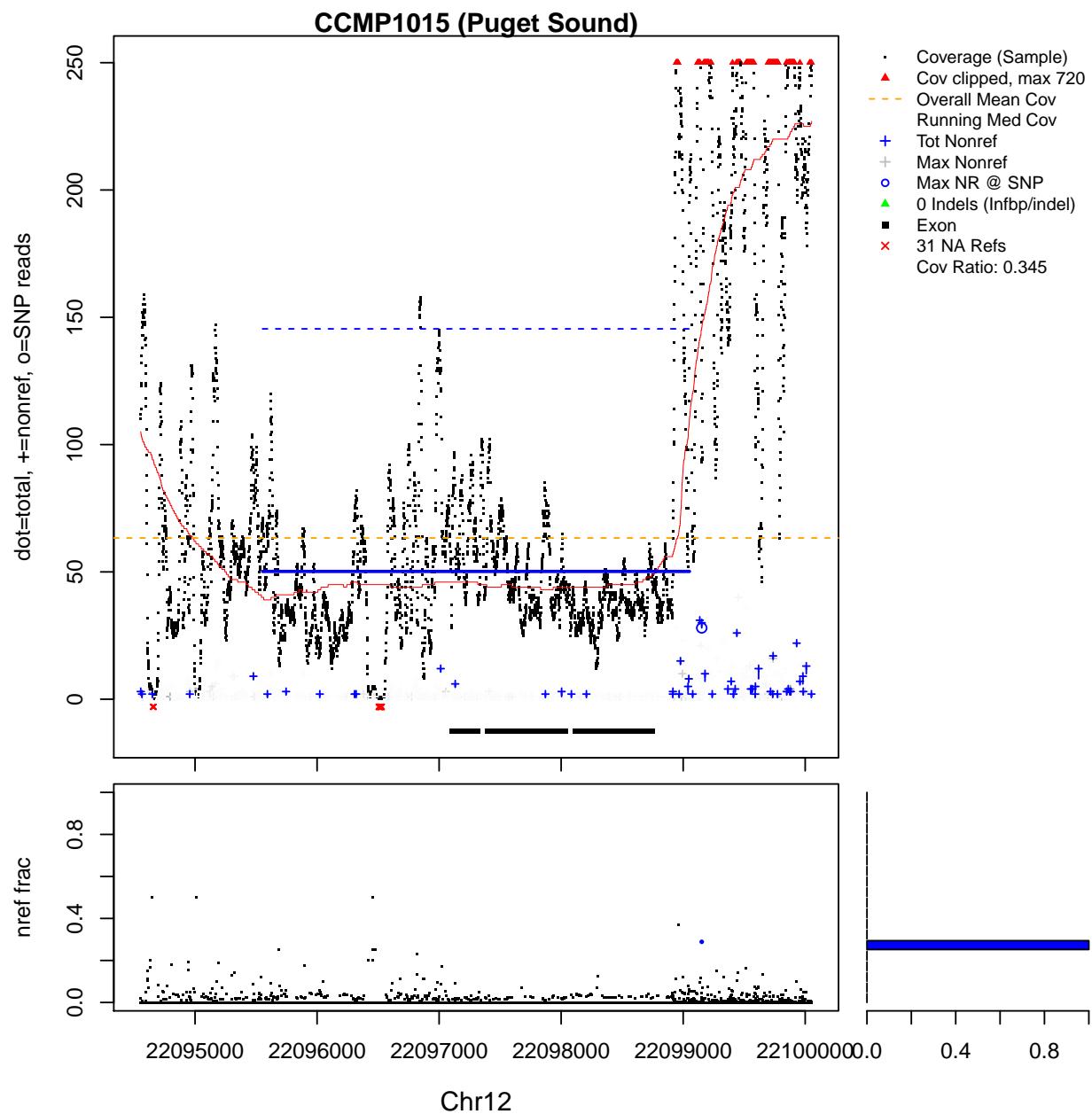
### CCMP1012 (W. Australia)

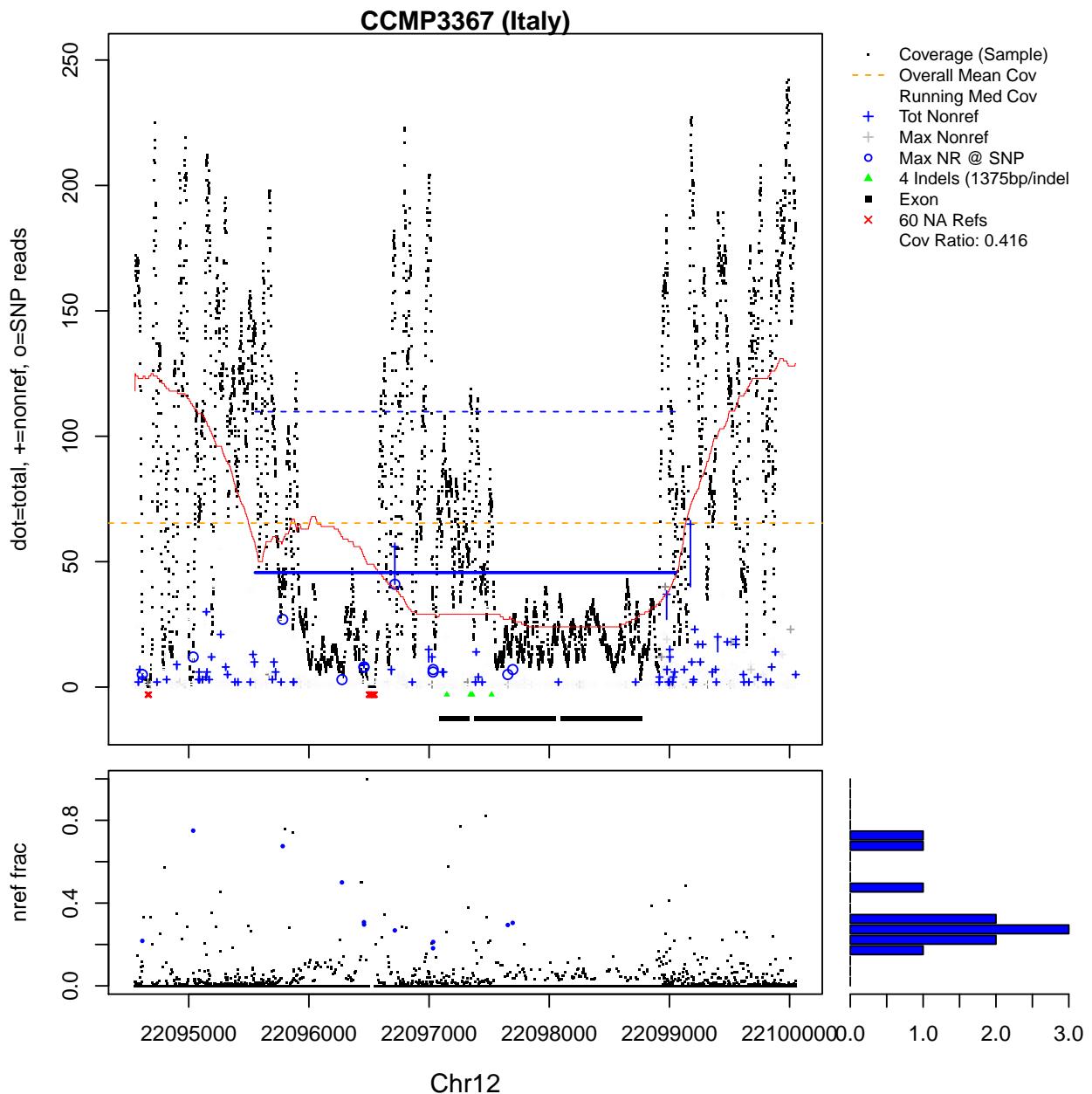


### CCMP1013 (Wales)









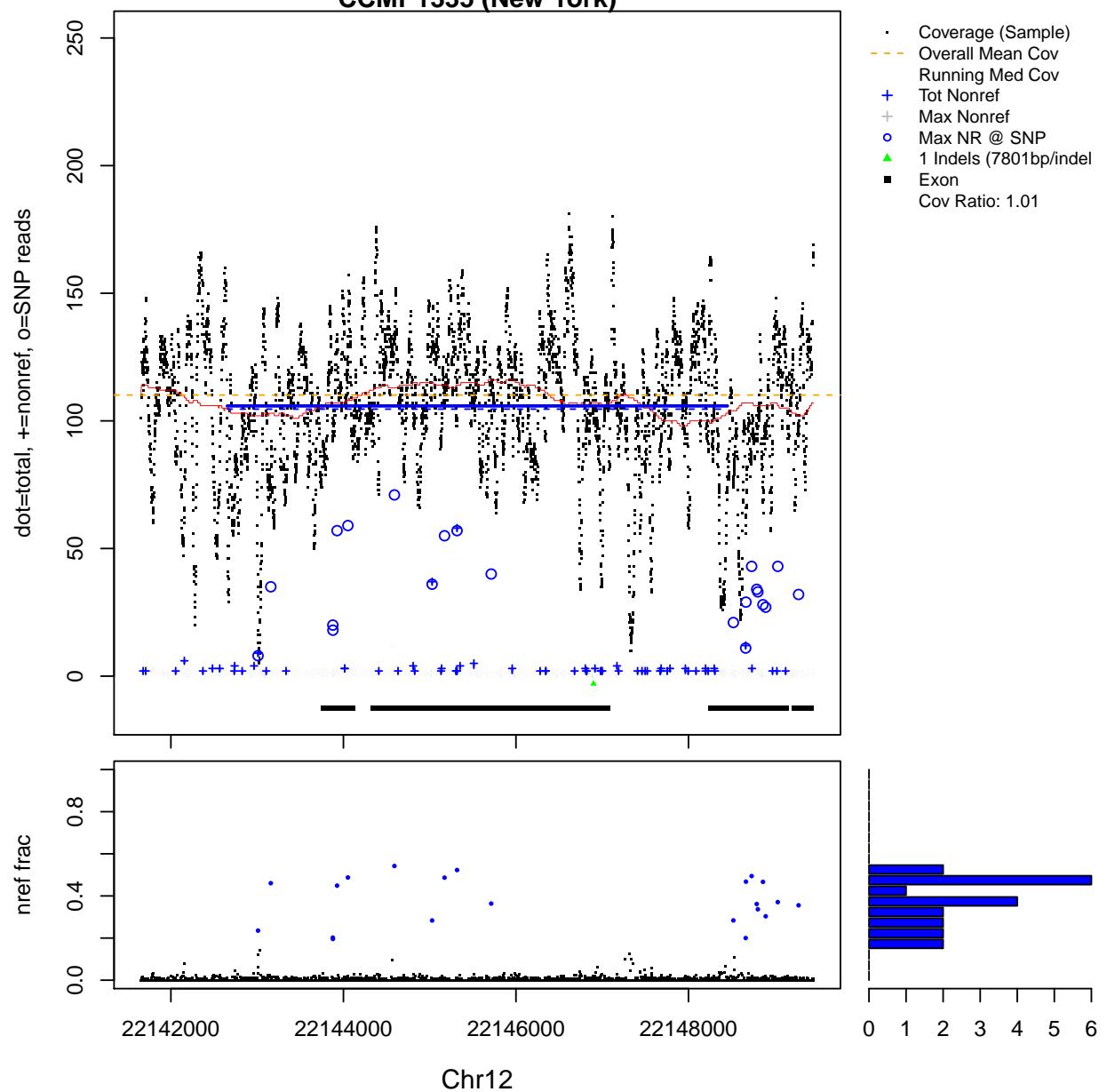
### Chr12

Below is surprising: NY is NOT hemi, and IS SNPy, but IT/Wales both hemi and *match ref* there, on a region of 4K or longer. I.e., we expect ref to be a mosaic of the 2 haplotypes present, (just majority vote?) but this suggests that ref captures haplotype on a scale of several KB. Longer Sanger reads (and mate pairs?) in assembly may have created this.

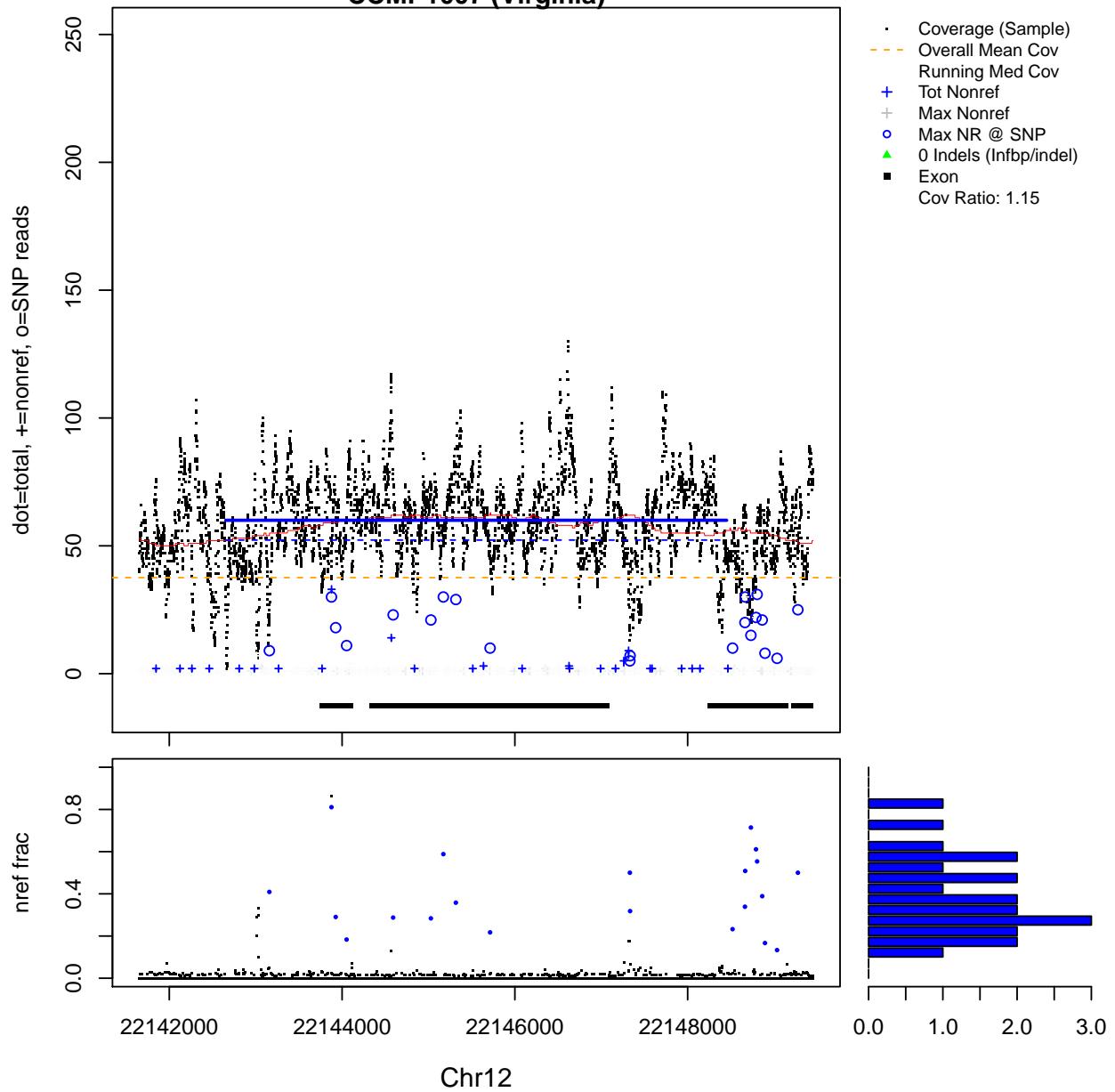
```
hemi.chunk(117:118) # it/wates: yes, snpless; others no
```

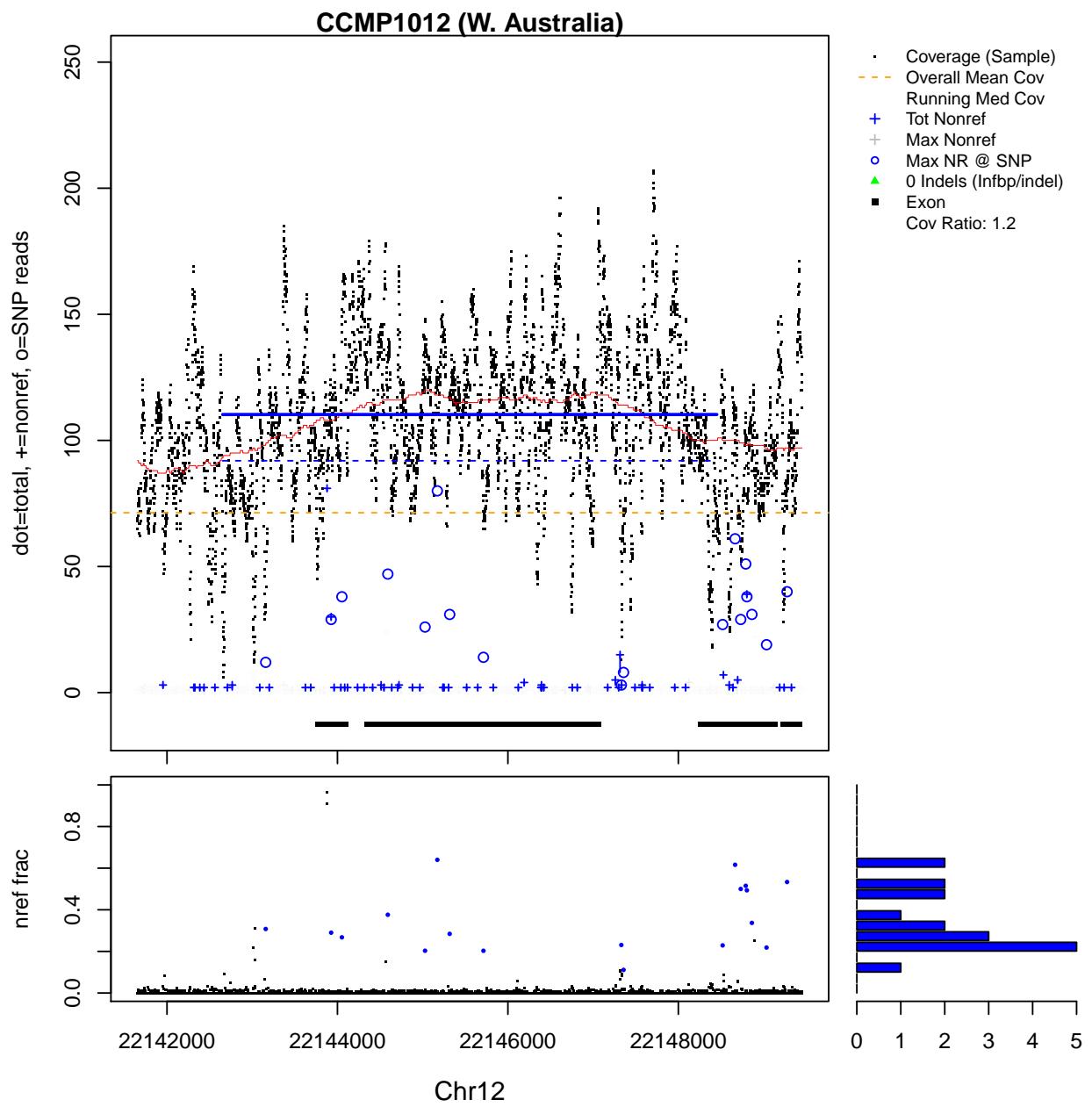
| # | chr          | start | end    | length | tp1007 | tp1012 | tp1013 | tp1014 | tp1015 | IT | tp1335 | pattern |    |
|---|--------------|-------|--------|--------|--------|--------|--------|--------|--------|----|--------|---------|----|
| # | Chr12:684101 | Chr12 | 684101 | 727700 | 43600  | NA     | NA     | NA     | NA     | NA | NA     | NA      | 00 |
| # | Chr12:727701 | Chr12 | 727701 | 728200 | 500    | NA     | NA     | 0.296  | NA     | NA | NA     | NA      | 20 |
| # | Chr12:728201 | Chr12 | 728201 | 733500 | 5300   | NA     | NA     | 0.296  | NA     | NA | 0.276  | NA      | 22 |
| # | Chr12:733501 | Chr12 | 733501 | 744800 | 11300  | NA     | NA     | NA     | NA     | NA | NA     | NA      | 00 |

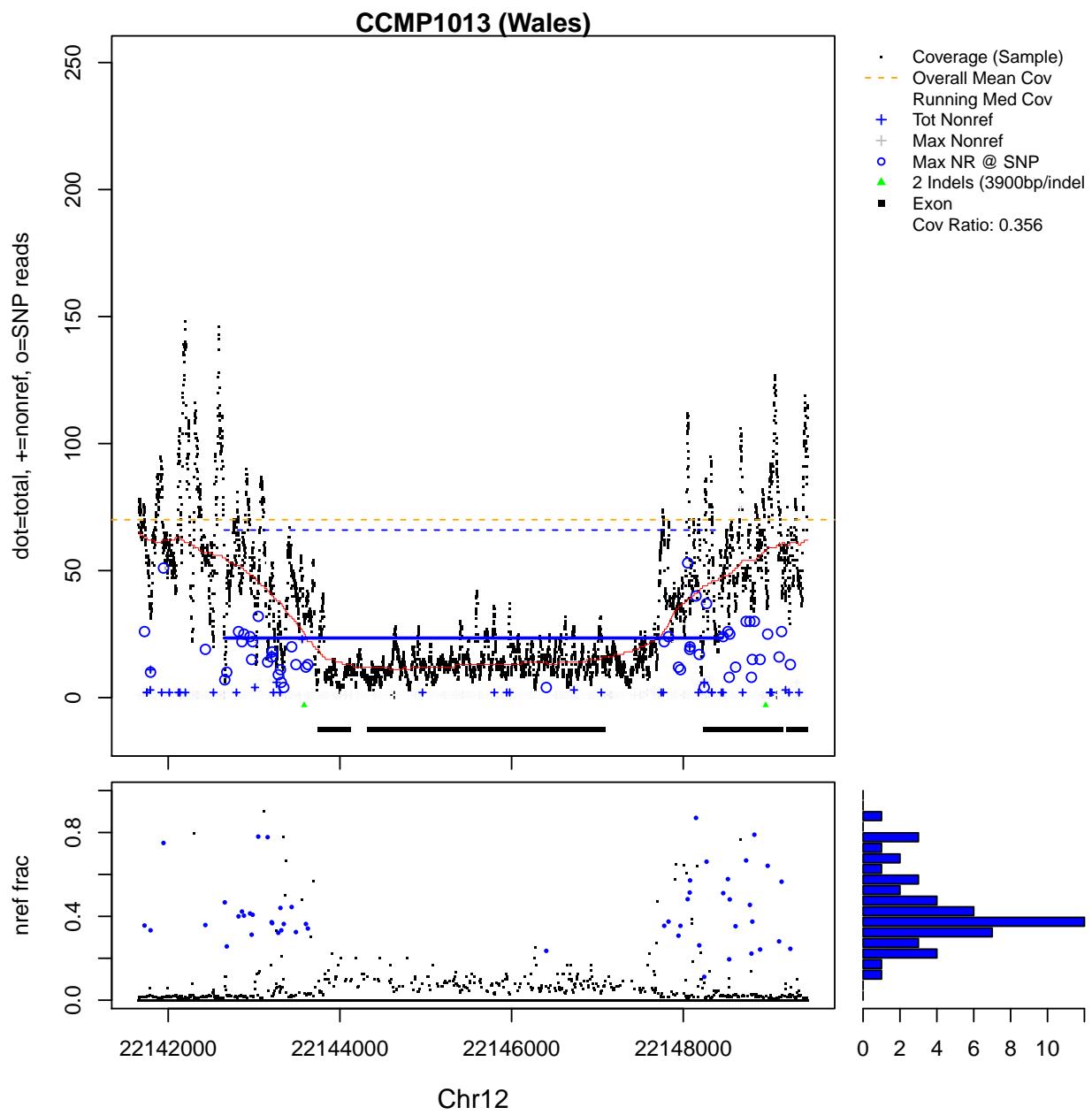
### CCMP1335 (New York)



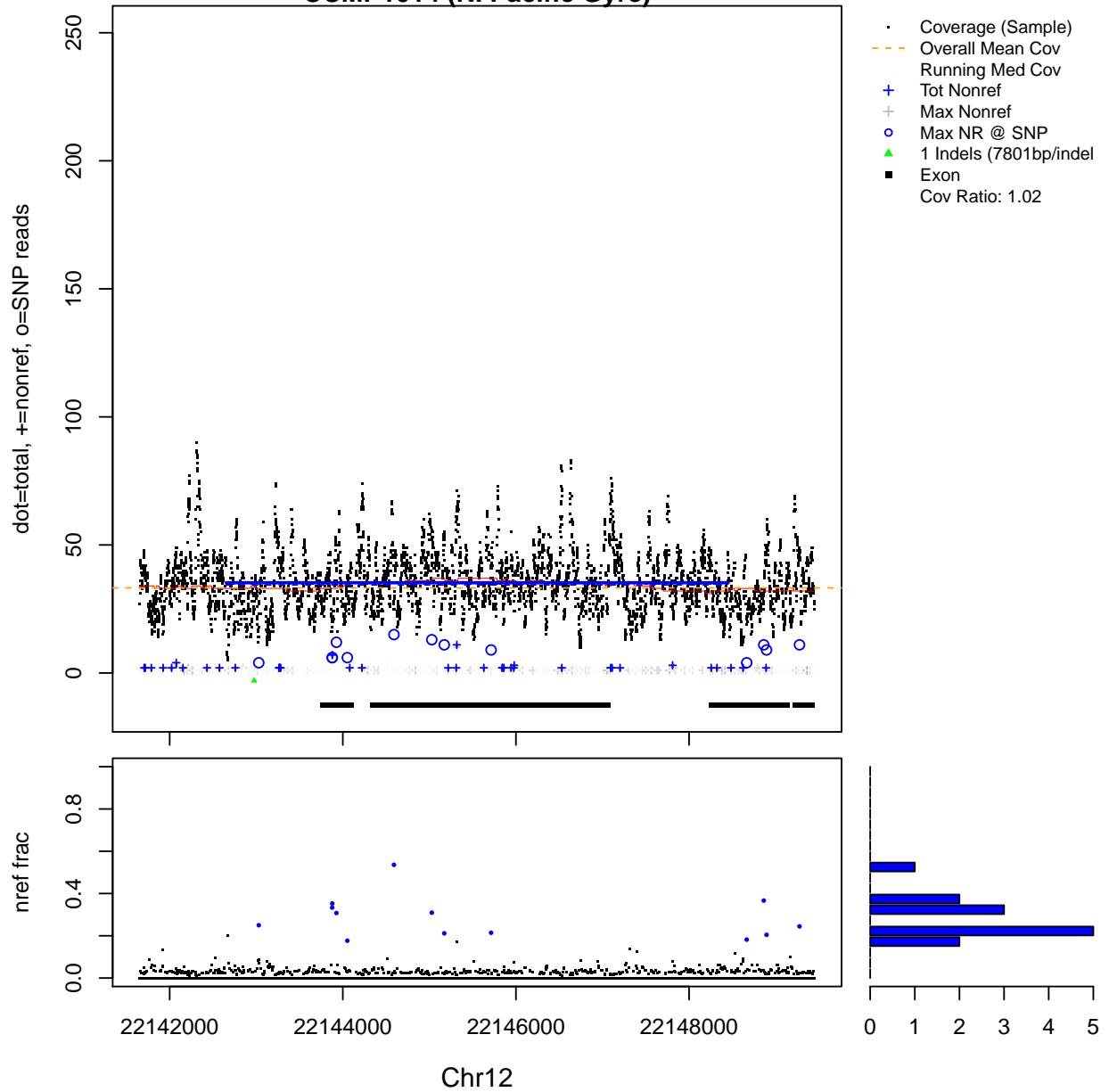
### CCMP1007 (Virginia)

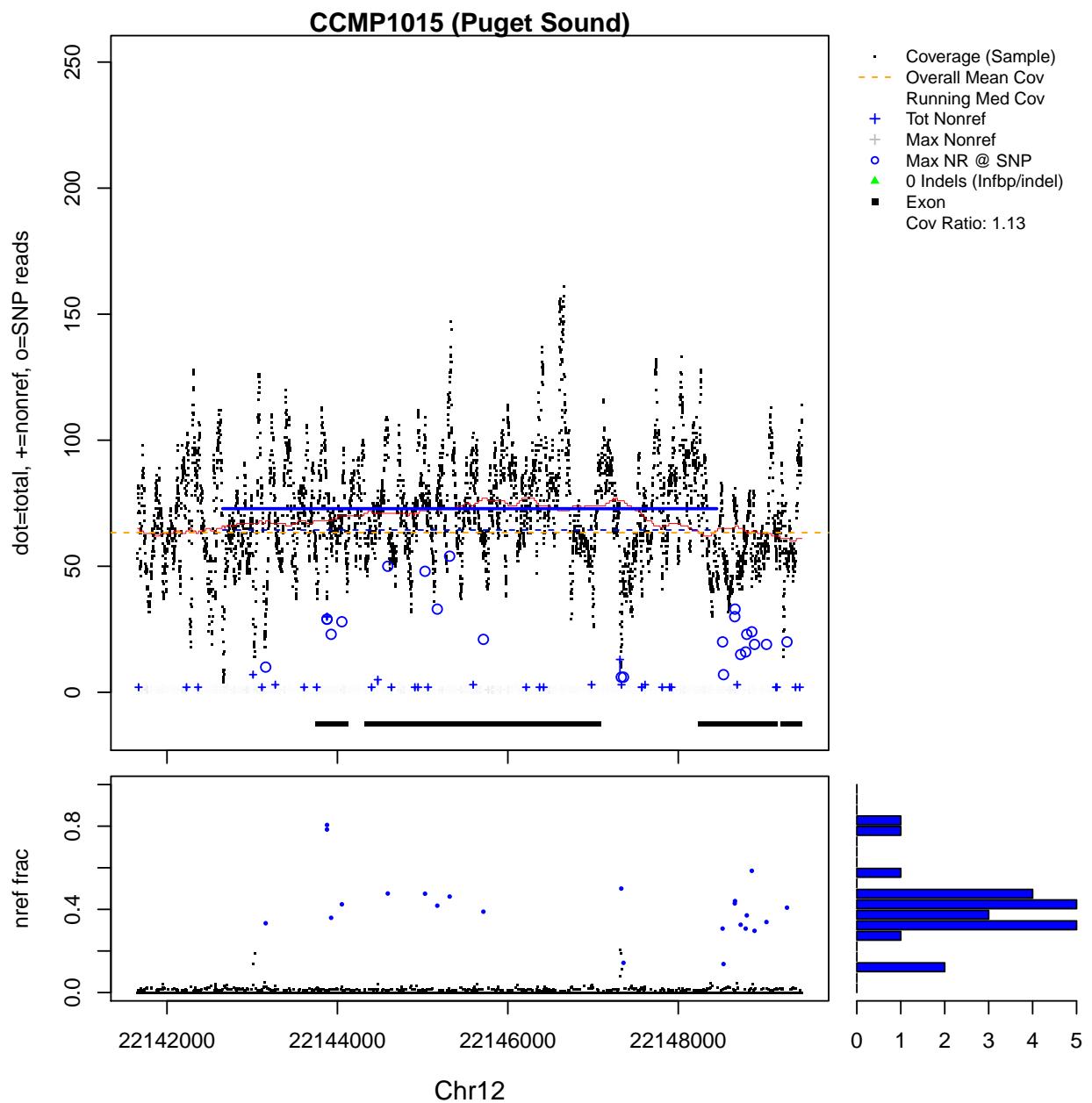


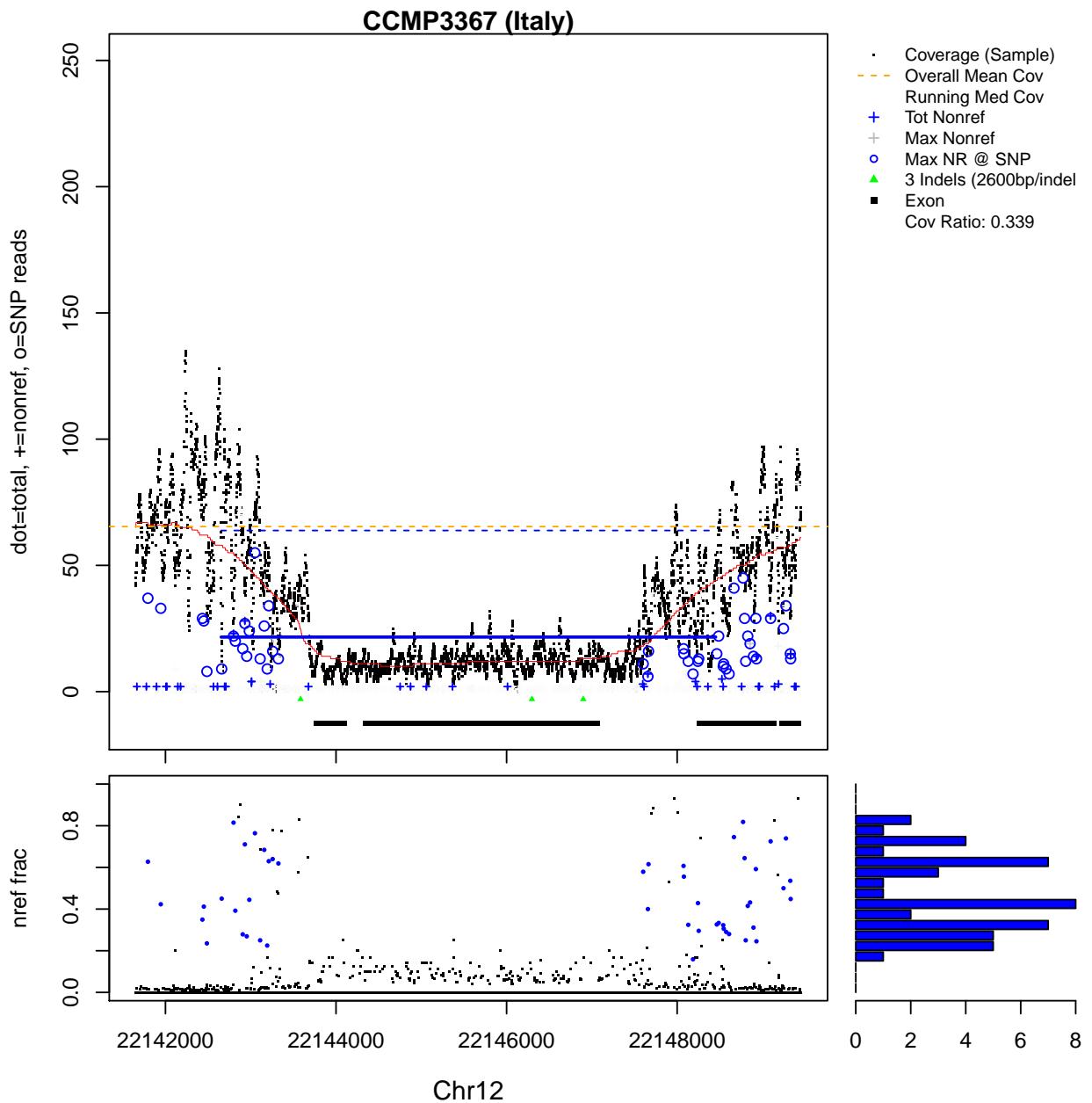




### CCMP1014 (N. Pacific Gyre)







```

hemi.chunk(c('Chr15:250801', 'Chr15:251001')) # missing x 7; nonzero cov_ratio only due to edge effects

# Rows 175 : 177
#          chr start   end length tp1007 tp1012 tp1013 tp1014 tp1015 IT tp1335 pattern
# Chr15:246801 Chr15 246801 250800    4000     NA     NA     NA     NA     NA NA NA 000
# Chr15:250801 Chr15 250801 250900     100     NA     NA     NA 0.0151     NA NA NA 010
# Chr15:250901 Chr15 250901 251000     100 0.00774     NA 0.0069 0.0151 0.00834 0.011 0.00888 137
# Chr15:251001 Chr15 251001 262700 11700 0.00774 0.00259 0.0069 0.0151 0.00834 0.011 0.00888 177
# Chr15:262701 Chr15 262701 434900 172200     NA     NA     NA     NA     NA NA NA 000

# ref seq undefined in this interval:
full[[1]][24845134+1:10,]

#          chr pos snp   Chr   Pos Ref Cov a g c t n .match exon indel
# 24845135 Chr15 250962   0 Chr15 250962   A 11 0 0 0 0 0      11 FALSE FALSE
# 24845136 Chr15 250963   0 Chr15 250963   C  9 0 0 0 0 0      9 FALSE FALSE
# 24845137 Chr15 250964   0 Chr15 250964   N  7 3 0 1 3 0      0 FALSE FALSE
# 24845138 Chr15 250965   0 Chr15 250965   N  5 0 0 5 0 0      0 FALSE FALSE

```

```

# 24845139 Chr15 250966 0 Chr15 250966 N 3 0 3 0 0 0 0 FALSE FALSE
# 24845140 Chr15 250967 0 Chr15 250967 N 2 0 2 0 0 0 0 FALSE FALSE
# 24845141 Chr15 250968 0 Chr15 250968 N 1 0 1 0 0 0 0 FALSE FALSE
# 24845142 Chr15 250969 0 Chr15 250969 N 1 0 1 0 0 0 0 FALSE FALSE
# 24845143 Chr15 250970 0 <NA> NA <NA> 0 0 0 0 0 0 0 FALSE FALSE
# 24845144 Chr15 250971 0 <NA> NA <NA> 0 0 0 0 0 0 0 FALSE FALSE

full[[1]][24845134+1:20+11665,]

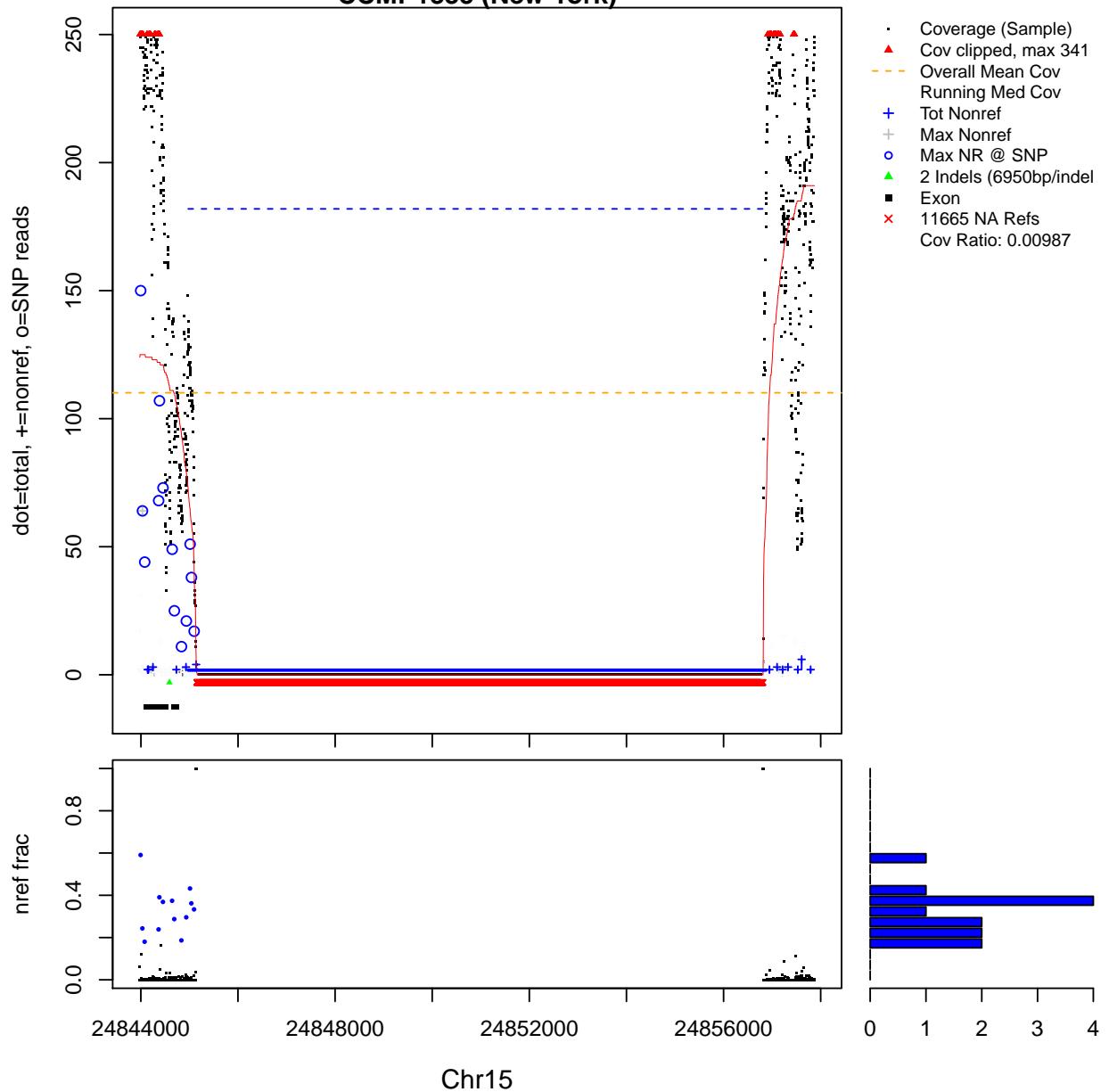
#      chr    pos  snp   Chr    Pos  Ref Cov a g c t n .match exon indel
# 24856800 Chr15 262627 0 <NA> NA <NA> 0 0 0 0 0 0 0 FALSE FALSE
# 24856801 Chr15 262628 0 <NA> NA <NA> 0 0 0 0 0 0 0 FALSE FALSE
# 24856802 Chr15 262629 0 <NA> NA <NA> 0 0 0 0 0 0 0 FALSE FALSE
# 24856803 Chr15 262630 0 <NA> NA <NA> 0 0 0 0 0 0 0 FALSE FALSE
# 24856804 Chr15 262631 0 <NA> NA <NA> 0 0 0 0 0 0 0 FALSE FALSE
# 24856805 Chr15 262632 0 <NA> NA <NA> 0 0 0 0 0 0 0 FALSE FALSE
# 24856806 Chr15 262633 0 Chr15 262633 N 1 0 0 0 1 0 0 FALSE FALSE
# 24856807 Chr15 262634 0 Chr15 262634 N 1 0 0 1 0 0 0 FALSE FALSE
# 24856808 Chr15 262635 0 Chr15 262635 N 2 2 0 0 0 0 0 FALSE FALSE
# 24856809 Chr15 262636 0 Chr15 262636 N 2 0 0 0 2 0 0 FALSE FALSE
# 24856810 Chr15 262637 0 Chr15 262637 N 4 0 4 0 0 0 0 FALSE FALSE
# 24856811 Chr15 262638 0 Chr15 262638 N 5 5 0 0 0 0 0 FALSE FALSE
# 24856812 Chr15 262639 0 Chr15 262639 N 5 5 0 0 0 0 0 FALSE FALSE
# 24856813 Chr15 262640 0 Chr15 262640 N 5 0 0 0 5 0 0 FALSE FALSE
# 24856814 Chr15 262641 0 Chr15 262641 N 6 0 0 0 6 0 0 FALSE FALSE
# 24856815 Chr15 262642 0 Chr15 262642 N 7 0 0 0 7 0 0 FALSE FALSE
# 24856816 Chr15 262643 0 Chr15 262643 G 8 0 0 0 0 0 8 FALSE FALSE
# 24856817 Chr15 262644 0 Chr15 262644 G 8 0 0 0 0 0 8 FALSE FALSE
# 24856818 Chr15 262645 0 Chr15 262645 T 8 0 0 0 0 0 8 FALSE FALSE
# 24856819 Chr15 262646 0 Chr15 262646 A 8 0 1 0 0 0 7 FALSE FALSE

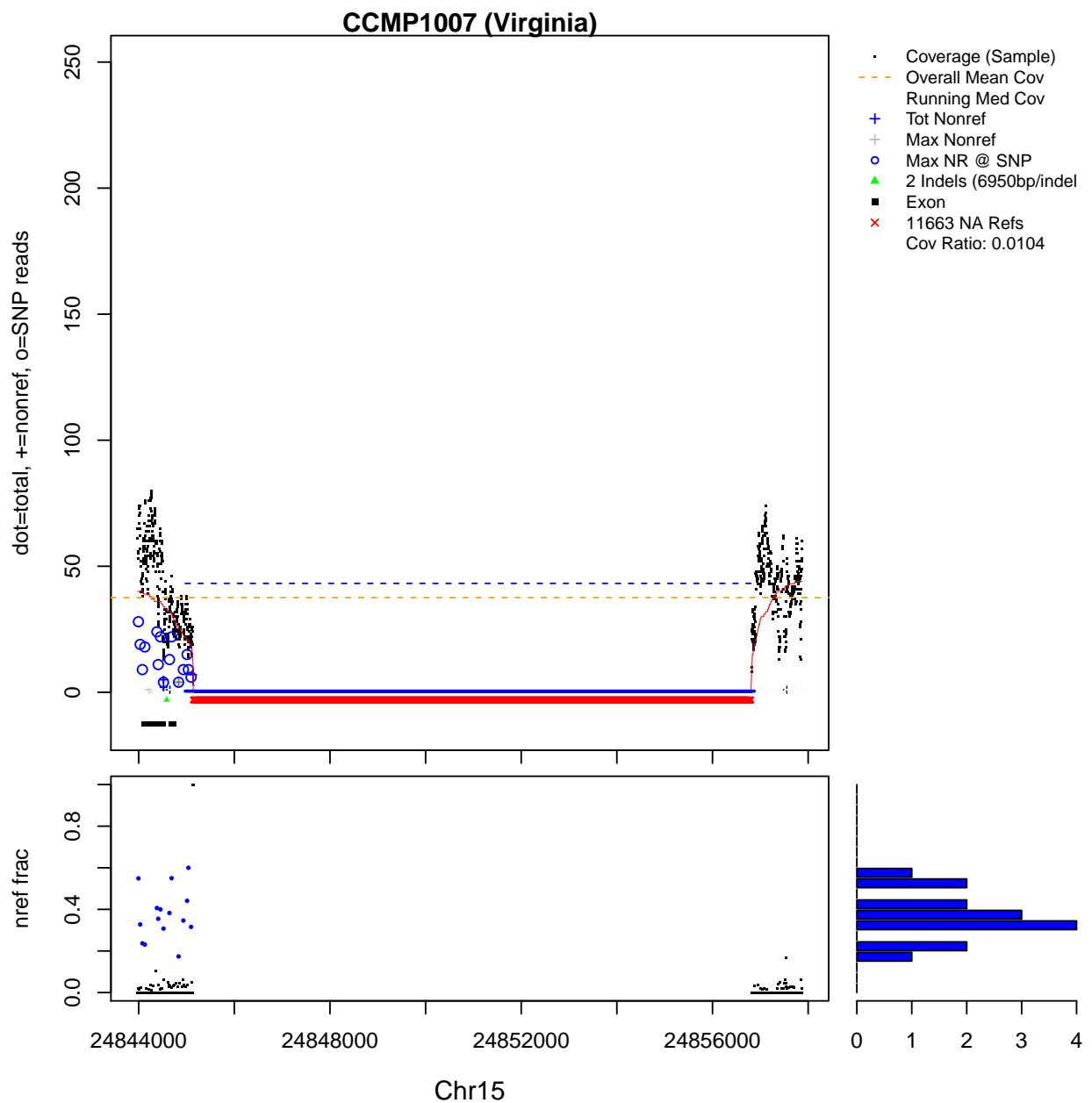
all(is.na(full[[1]]$Ref[(24845134+9):(24845134+6+11665)]))

# [1] TRUE

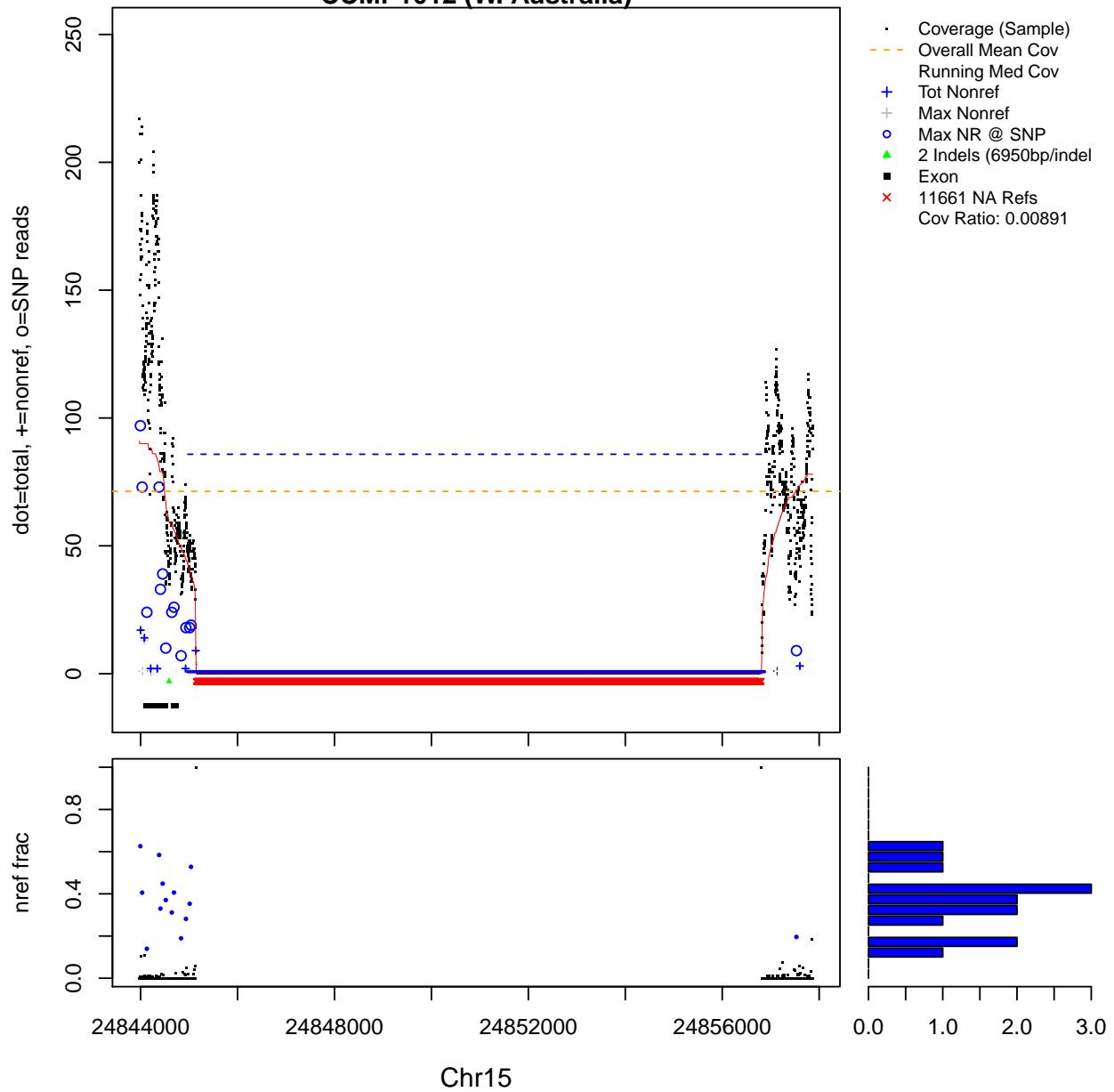
```

### CCMP1335 (New York)

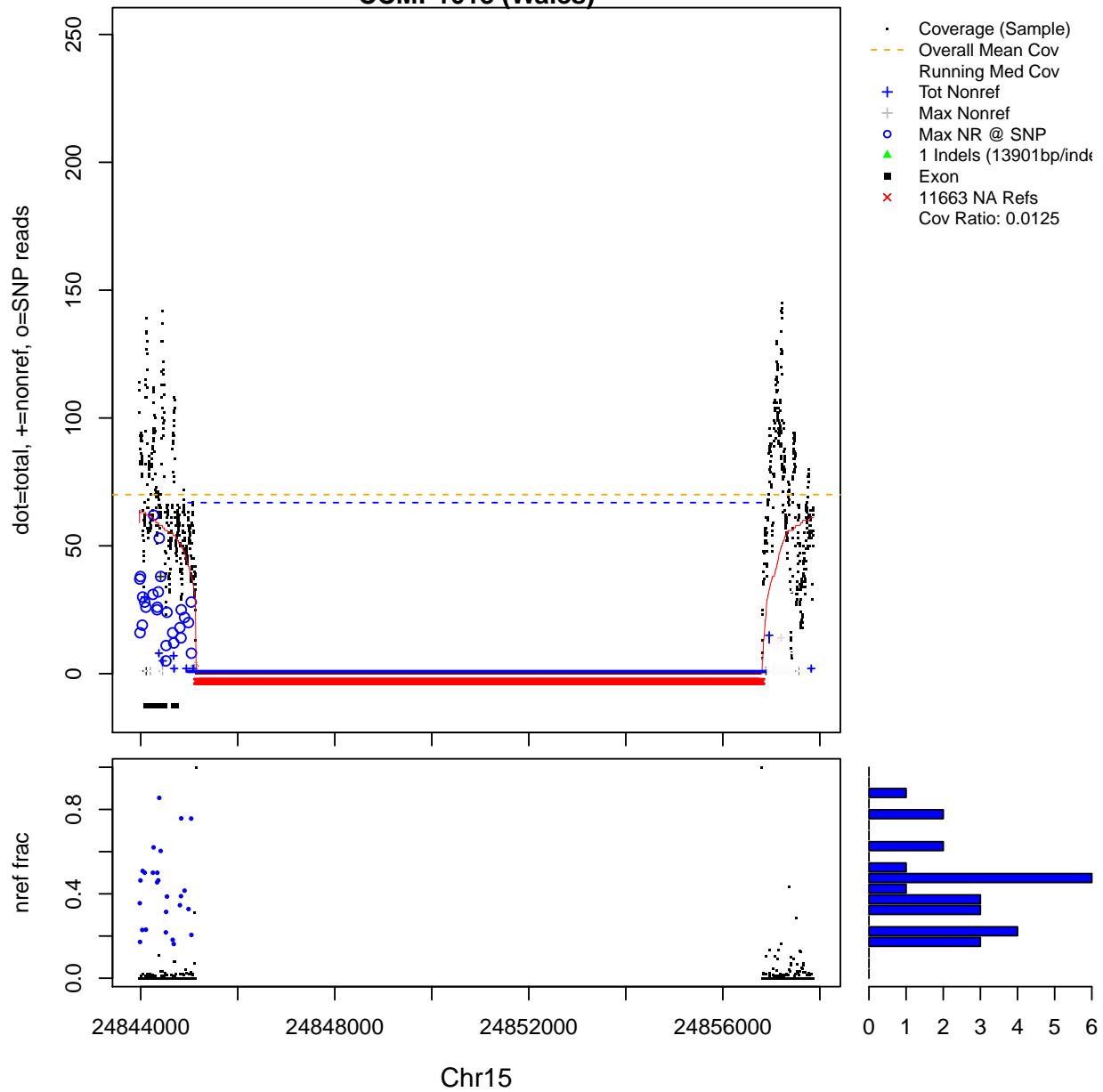


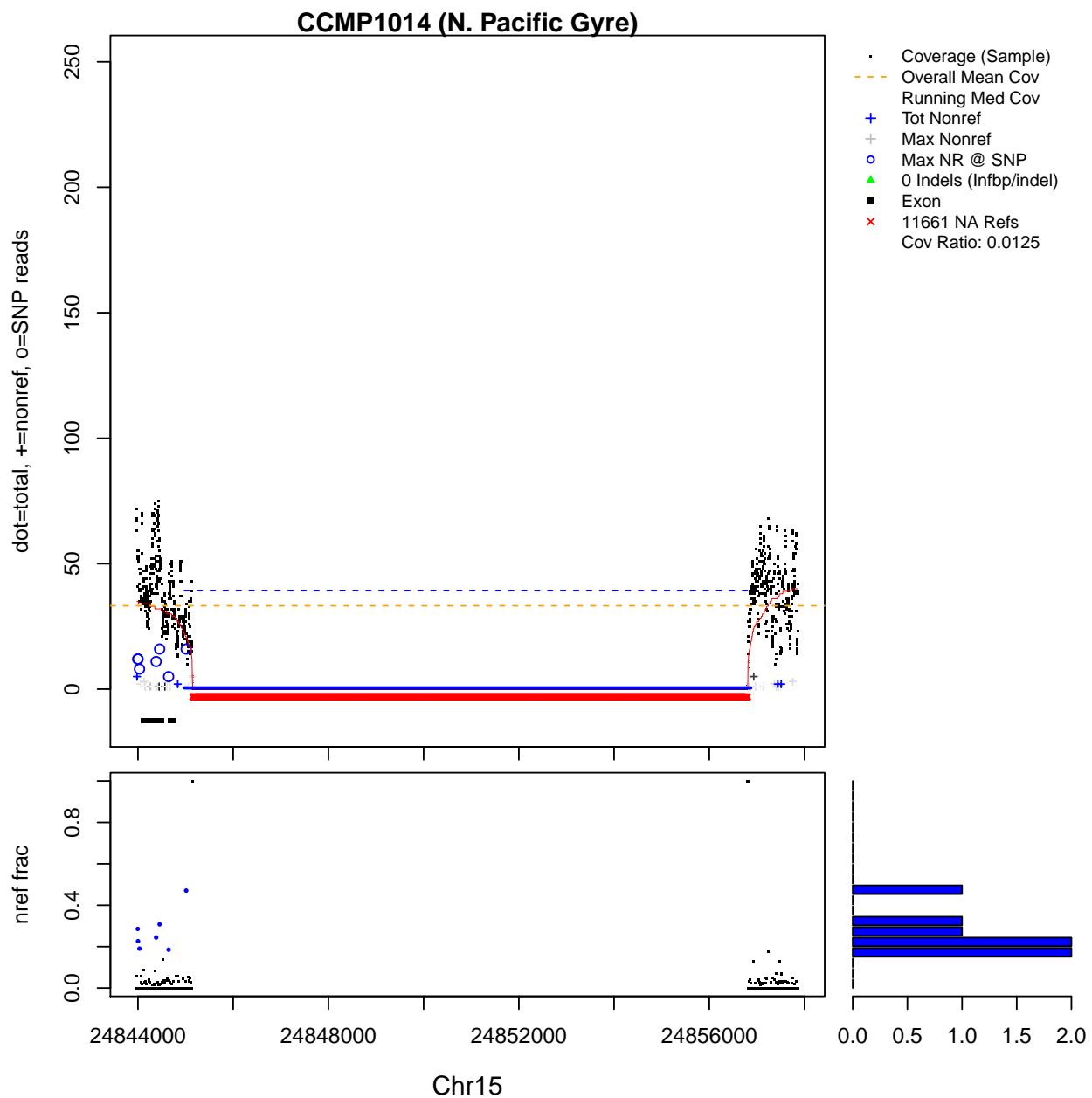


### CCMP1012 (W. Australia)

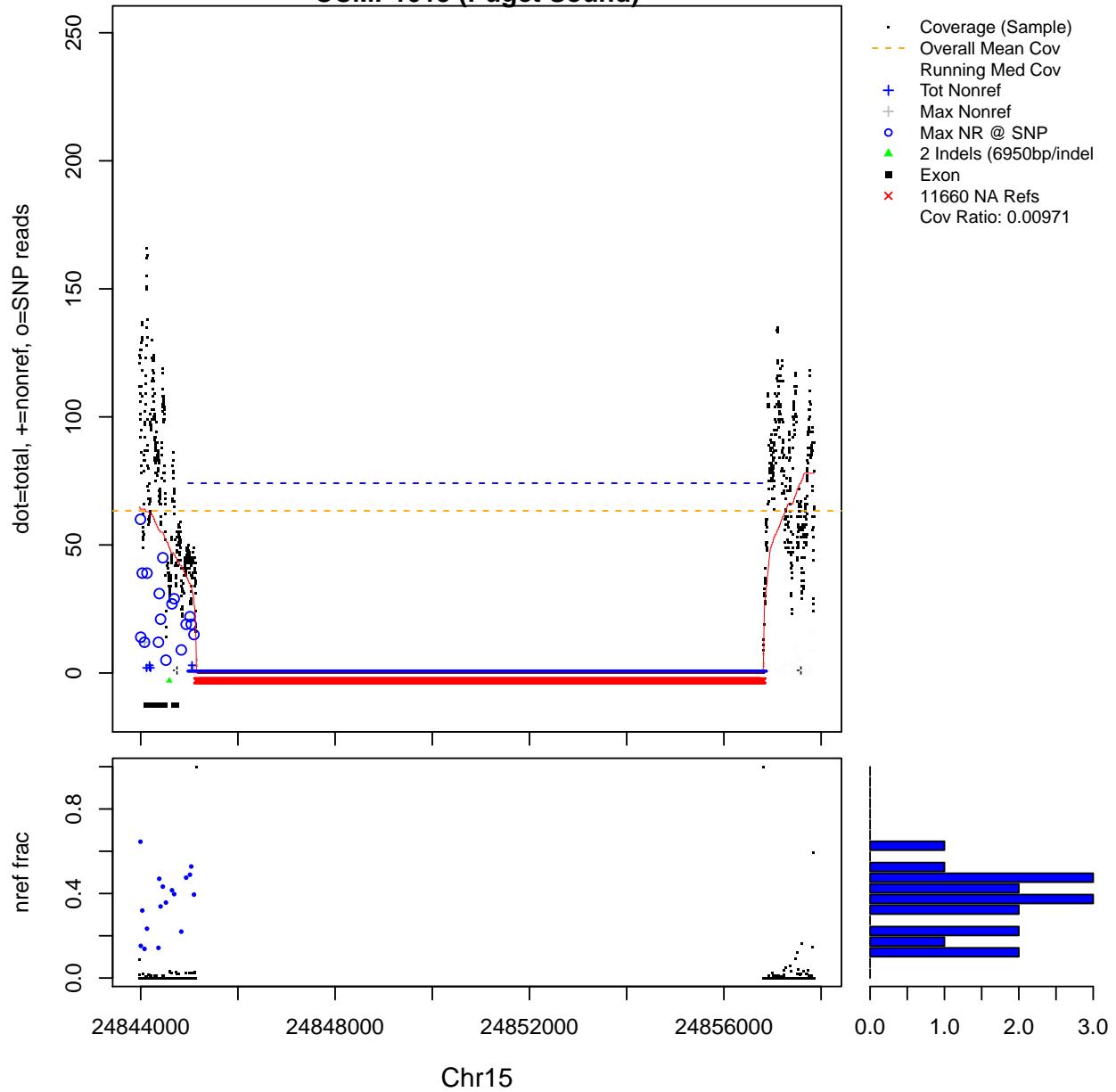


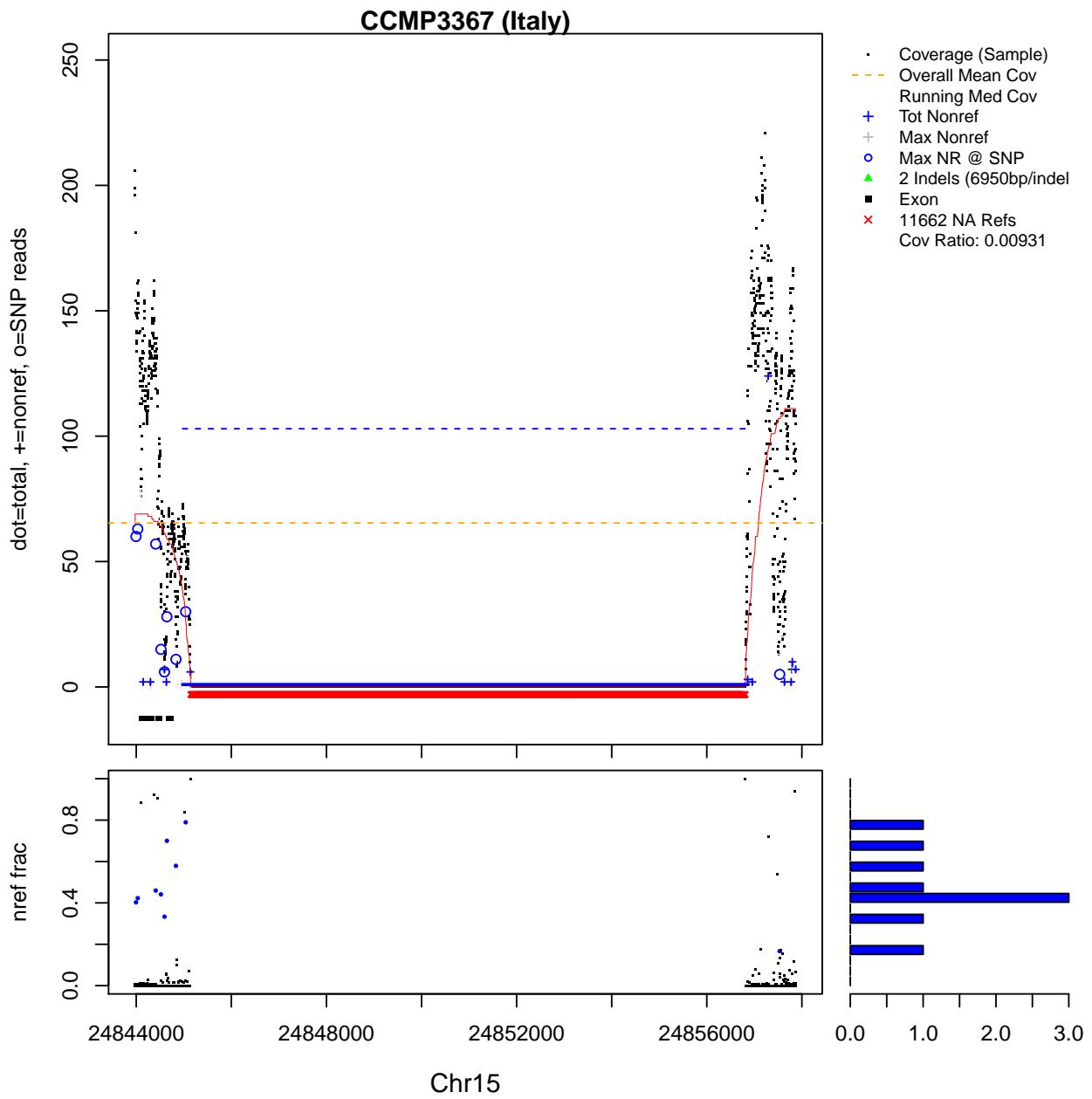
### CCMP1013 (Wales)





### CCMP1015 (Puget Sound)





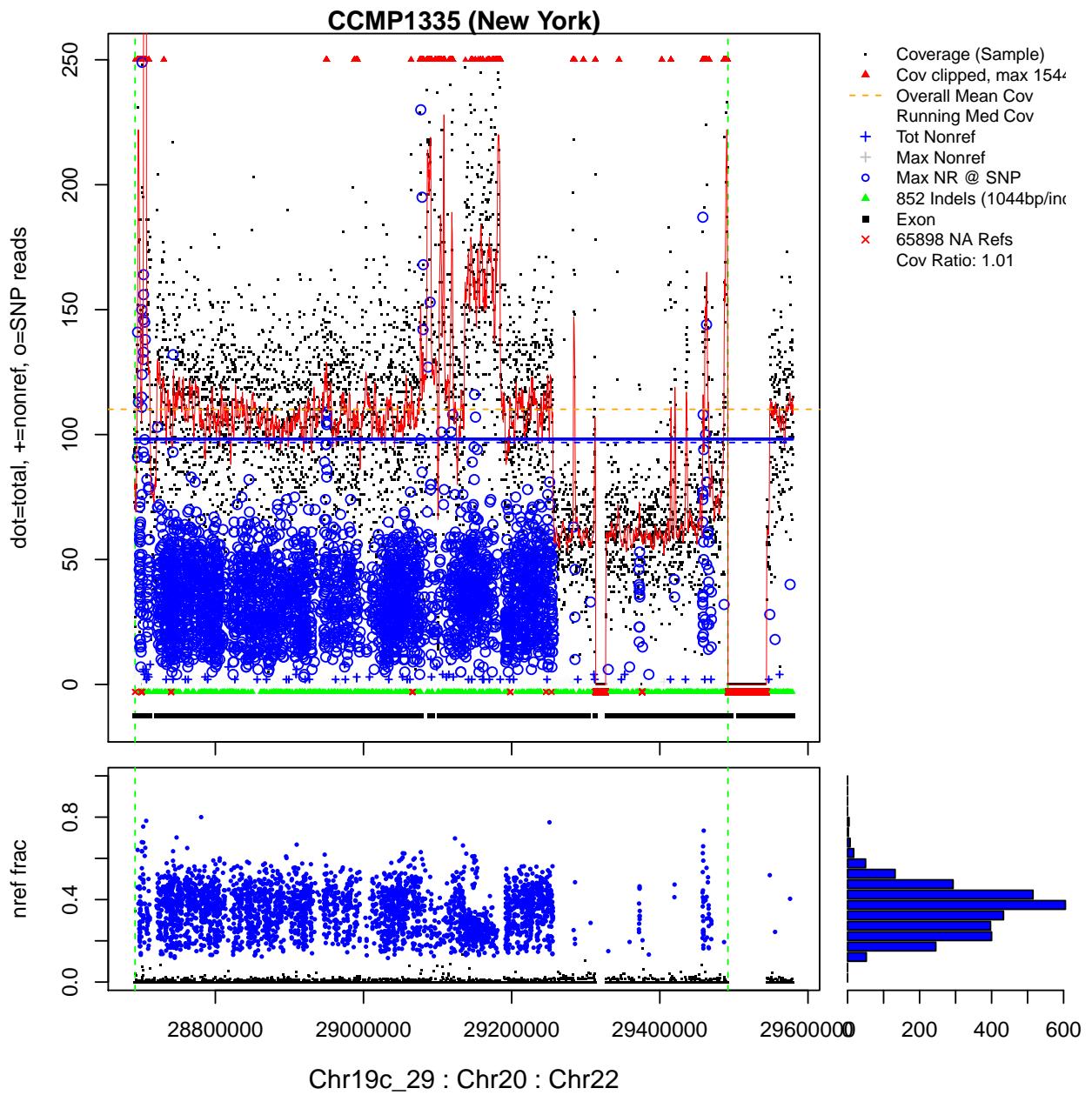
```

hemi.chunk(c('Chr20:1', 'Chr22:1'), 7, margin=1000)

# Rows 368 : 431
#          chr start     end length tp1007 tp1012 tp1013 tp1014 tp1015      IT tp1335 pattern
# Chr2:2707201 Chr2 2707201 2707200     0     NA     NA     NA     NA     NA     NA     NA     NA     000
# Chr20:1       Chr20      1    1500    1500     NA     NA     NA     NA     0.305    NA     NA     004
# Chr20:1501   Chr20    1501    20500   19000     NA     NA     NA     NA     NA     NA     NA     NA     000
# Chr20:20501   Chr20   20501    23400   2900     NA     NA     NA     NA     0.60334   NA     NA     002
# Chr20:23401   Chr20   23401    23600    200     NA     NA     NA     NA     NA     NA     NA     NA     000
# Chr20:23601   Chr20   23601    24300    700     NA     NA     0.629    NA     NA     NA     NA     020
# Chr20:24301   Chr20   24301    25500   1200     NA     NA     0.629    NA     NA     0.40789   NA     022
# Chr20:25501   Chr20   25501    28600   3100     NA     NA     0.629    NA     NA     NA     NA     020
# Chr20:28601   Chr20   28601    34400   5800     NA     NA     NA     NA     NA     NA     NA     NA     000
# Chr20:34401   Chr20   34401    35300    900     NA     NA     0.159    NA     NA     NA     NA     020
# Chr20:35301   Chr20   35301   127100   91800     NA     NA     NA     NA     NA     NA     NA     NA     000
# Chr20:127101  Chr20  127101   128400   1300     NA     0.70269   NA     NA     NA     NA     NA     040
# Chr20:128401  Chr20  128401   130200   1800     NA     0.70269   0.481    NA     NA     0.43024   NA     062
# Chr20:130201  Chr20  130201   130400    200     NA     NA     0.481    NA     NA     0.43024   NA     022

```

|                |       |        |        |        |          |         |       |         |       |         |       |     |
|----------------|-------|--------|--------|--------|----------|---------|-------|---------|-------|---------|-------|-----|
| # Chr20:130401 | Chr20 | 130401 | 130600 | 200    | NA       | NA      | NA    | NA      | NA    | 0.43024 | NA    | 002 |
| # Chr20:130601 | Chr20 | 130601 | 405800 | 275200 | NA       | NA      | NA    | NA      | NA    | NA      | NA    | 000 |
| # Chr20:405801 | Chr20 | 405801 | 407600 | 1800   | NA       | NA      | NA    | NA      | NA    | 0.37725 | NA    | 002 |
| # Chr20:407601 | Chr20 | 407601 | 469500 | 61900  | NA       | NA      | NA    | NA      | NA    | NA      | NA    | 000 |
| # Chr20:469501 | Chr20 | 469501 | 474100 | 4600   | NA       | NA      | NA    | NA      | NA    | 0.74728 | NA    | 002 |
| # Chr20:474101 | Chr20 | 474101 | 486100 | 12000  | NA       | NA      | NA    | NA      | NA    | NA      | NA    | 000 |
| # Chr20:486101 | Chr20 | 486101 | 486200 | 100    | NA       | NA      | NA    | NA      | NA    | 0.47869 | NA    | 002 |
| # Chr20:486201 | Chr20 | 486201 | 488500 | 2300   | 0.568891 | NA      | NA    | NA      | NA    | 0.47869 | NA    | 102 |
| # Chr20:488501 | Chr20 | 488501 | 492400 | 3900   | 0.568891 | NA      | NA    | NA      | NA    | NA      | NA    | 100 |
| # Chr20:492401 | Chr20 | 492401 | 492500 | 100    | 0.568891 | NA      | 0.390 | NA      | NA    | NA      | NA    | 120 |
| # Chr20:492501 | Chr20 | 492501 | 500000 | 7500   | 0.568891 | NA      | 0.390 | NA      | NA    | 0.04718 | NA    | 122 |
| # Chr20:500001 | Chr20 | 500001 | 500100 | 100    | 0.568891 | NA      | 0.390 | NA      | NA    | NA      | NA    | 120 |
| # Chr20:500101 | Chr20 | 500101 | 532800 | 32700  | 0.568891 | NA      | NA    | NA      | NA    | NA      | NA    | 100 |
| # Chr20:532801 | Chr20 | 532801 | 533300 | 500    | 0.568891 | NA      | 0.654 | NA      | NA    | NA      | NA    | 120 |
| # Chr20:533301 | Chr20 | 533301 | 553200 | 19900  | 0.568891 | 0.55285 | 0.654 | NA      | NA    | NA      | NA    | 160 |
| # Chr20:553201 | Chr20 | 553201 | 553300 | 100    | NA       | 0.55285 | 0.654 | NA      | NA    | NA      | NA    | 060 |
| # Chr20:553301 | Chr20 | 553301 | 564400 | 11100  | NA       | NA      | 0.654 | NA      | NA    | NA      | NA    | 020 |
| # Chr20:564401 | Chr20 | 564401 | 583100 | 18700  | NA       | NA      | 0.654 | NA      | NA    | 0.584   | NA    | 021 |
| # Chr20:583101 | Chr20 | 583101 | 591200 | 8100   | NA       | NA      | 0.654 | NA      | 0.585 | NA      | 0.584 | 025 |
| # Chr20:591201 | Chr20 | 591201 | 592000 | 800    | NA       | NA      | 0.654 | NA      | NA    | NA      | NA    | 020 |
| # Chr20:592001 | Chr20 | 592001 | 593900 | 1900   | NA       | NA      | 0.654 | NA      | NA    | 0.59747 | NA    | 022 |
| # Chr20:593901 | Chr20 | 593901 | 594200 | 300    | NA       | NA      | 0.654 | NA      | 0.532 | 0.59747 | NA    | 026 |
| # Chr20:594201 | Chr20 | 594201 | 594300 | 100    | NA       | NA      | 0.654 | NA      | 0.532 | 0.59747 | 0.599 | 027 |
| # Chr20:594301 | Chr20 | 594301 | 620200 | 25900  | NA       | NA      | 0.654 | NA      | 0.532 | NA      | 0.599 | 025 |
| # Chr20:620201 | Chr20 | 620201 | 620300 | 100    | NA       | NA      | NA    | NA      | 0.532 | NA      | 0.599 | 005 |
| # Chr20:620301 | Chr20 | 620301 | 621600 | 1300   | NA       | NA      | NA    | NA      | 0.532 | NA      | NA    | 004 |
| # Chr20:621601 | Chr20 | 621601 | 635200 | 13600  | 0.000779 | 0.00102 | 0.584 | 0.00109 | 0.532 | 0.00392 | 0.523 | 177 |
| # Chr20:635201 | Chr20 | 635201 | 635300 | 100    | NA       | NA      | 0.584 | NA      | 0.532 | 0.00392 | 0.523 | 027 |
| # Chr20:635301 | Chr20 | 635301 | 651100 | 15800  | NA       | NA      | 0.584 | NA      | 0.532 | NA      | 0.523 | 025 |
| # Chr20:651101 | Chr20 | 651101 | 653100 | 2000   | NA       | NA      | 0.584 | NA      | 0.532 | 0.54348 | 0.523 | 027 |
| # Chr20:653101 | Chr20 | 653101 | 720300 | 67200  | NA       | NA      | 0.584 | NA      | 0.532 | NA      | 0.523 | 025 |
| # Chr20:720301 | Chr20 | 720301 | 720500 | 200    | NA       | NA      | 0.584 | NA      | 0.532 | 0.49590 | 0.523 | 027 |
| # Chr20:720501 | Chr20 | 720501 | 722400 | 1900   | 0.608568 | 0.68218 | 0.584 | NA      | 0.532 | 0.49590 | 0.523 | 167 |
| # Chr20:722401 | Chr20 | 722401 | 722500 | 100    | 0.608568 | 0.68218 | 0.584 | NA      | NA    | NA      | 0.523 | 161 |
| # Chr20:722501 | Chr20 | 722501 | 723200 | 700    | NA       | 0.68218 | 0.584 | NA      | NA    | NA      | 0.523 | 061 |
| # Chr20:723201 | Chr20 | 723201 | 728000 | 4800   | NA       | NA      | 0.584 | NA      | NA    | NA      | 0.523 | 021 |
| # Chr20:728001 | Chr20 | 728001 | 729800 | 1800   | NA       | NA      | 0.584 | NA      | NA    | NA      | NA    | 020 |
| # Chr20:729801 | Chr20 | 729801 | 743100 | 13300  | NA       | NA      | 0.584 | NA      | 0.550 | NA      | 0.585 | 025 |
| # Chr20:743101 | Chr20 | 743101 | 744600 | 1500   | NA       | NA      | 0.584 | NA      | 0.550 | NA      | NA    | 024 |
| # Chr20:744601 | Chr20 | 744601 | 748600 | 4000   | NA       | NA      | 0.584 | NA      | 0.550 | NA      | 0.669 | 025 |
| # Chr20:748601 | Chr20 | 748601 | 759500 | 10900  | 0.558705 | 0.55247 | 0.584 | NA      | 0.550 | NA      | 0.669 | 165 |
| # Chr20:759501 | Chr20 | 759501 | 762500 | 3000   | 0.558705 | 0.55247 | 0.584 | NA      | 0.550 | 0.19929 | 0.669 | 167 |
| # Chr20:762501 | Chr20 | 762501 | 762600 | 100    | NA       | 0.55247 | 0.584 | NA      | NA    | NA      | 0.669 | 061 |
| # Chr20:762601 | Chr20 | 762601 | 766000 | 3400   | NA       | NA      | NA    | NA      | NA    | NA      | 0.669 | 001 |
| # Chr20:766001 | Chr20 | 766001 | 769800 | 3800   | NA       | NA      | NA    | NA      | NA    | NA      | NA    | 000 |
| # Chr20:769801 | Chr20 | 769801 | 770700 | 900    | NA       | NA      | NA    | NA      | NA    | 0.41187 | NA    | 002 |
| # Chr20:770701 | Chr20 | 770701 | 776900 | 6200   | NA       | NA      | NA    | NA      | NA    | NA      | NA    | 000 |
| # Chr20:776901 | Chr20 | 776901 | 794800 | 17900  | NA       | NA      | NA    | NA      | 0.719 | NA      | NA    | 004 |
| # Chr20:794801 | Chr20 | 794801 | 800233 | 5433   | NA       | NA      | NA    | NA      | NA    | NA      | NA    | 000 |
| # Chr20:800234 | Chr20 | 800234 | 800233 | 0      | NA       | NA      | NA    | NA      | NA    | NA      | NA    | 000 |
| # Chr22:1      | Chr22 | 1      | 87300  | 87300  | NA       | NA      | NA    | NA      | NA    | NA      | NA    | 000 |
| # Chr22:87301  | Chr22 | 87301  | 89500  | 2200   | NA       | NA      | 0.398 | NA      | NA    | 0.25820 | NA    | 022 |



```
chr20x7.filenames <- paste(my.figs.dir, 'chr20x7-%02d.pdf', sep=' ')
pdf(file=chr20x7.filenames, onefile=FALSE, width=11, height=8.5)
hemi.chunk(390:430, margin=1000, ymax=150)
```

|   | chr          | start | end    | length | tp1007 | tp1012   | tp1013  | tp1014 | tp1015 | IT    | tp1335  | pattern |     |
|---|--------------|-------|--------|--------|--------|----------|---------|--------|--------|-------|---------|---------|-----|
| # | Chr20:488501 | Chr20 | 488501 | 492400 | 3900   | 0.568891 | NA      | NA     | NA     | NA    | NA      | NA      | 100 |
| # | Chr20:492401 | Chr20 | 492401 | 492500 | 100    | 0.568891 | NA      | 0.390  | NA     | NA    | NA      | NA      | 120 |
| # | Chr20:492501 | Chr20 | 492501 | 500000 | 7500   | 0.568891 | NA      | 0.390  | NA     | NA    | 0.04718 | NA      | 122 |
| # | Chr20:500001 | Chr20 | 500001 | 500100 | 100    | 0.568891 | NA      | 0.390  | NA     | NA    | NA      | NA      | 120 |
| # | Chr20:500101 | Chr20 | 500101 | 532800 | 32700  | 0.568891 | NA      | NA     | NA     | NA    | NA      | NA      | 100 |
| # | Chr20:532801 | Chr20 | 532801 | 533300 | 500    | 0.568891 | NA      | 0.654  | NA     | NA    | NA      | NA      | 120 |
| # | Chr20:533301 | Chr20 | 533301 | 553200 | 19900  | 0.568891 | 0.55285 | 0.654  | NA     | NA    | NA      | NA      | 160 |
| # | Chr20:553201 | Chr20 | 553201 | 553300 | 100    | NA       | 0.55285 | 0.654  | NA     | NA    | NA      | NA      | 060 |
| # | Chr20:553301 | Chr20 | 553301 | 564400 | 11100  | NA       | NA      | 0.654  | NA     | NA    | NA      | NA      | 020 |
| # | Chr20:564401 | Chr20 | 564401 | 583100 | 18700  | NA       | NA      | 0.654  | NA     | NA    | NA      | 0.584   | 021 |
| # | Chr20:583101 | Chr20 | 583101 | 591200 | 8100   | NA       | NA      | 0.654  | NA     | 0.585 | NA      | 0.584   | 025 |
| # | Chr20:591201 | Chr20 | 591201 | 592000 | 800    | NA       | NA      | 0.654  | NA     | NA    | NA      | NA      | 020 |
| # | Chr20:592001 | Chr20 | 592001 | 593900 | 1900   | NA       | NA      | 0.654  | NA     | NA    | 0.59747 | NA      | 022 |

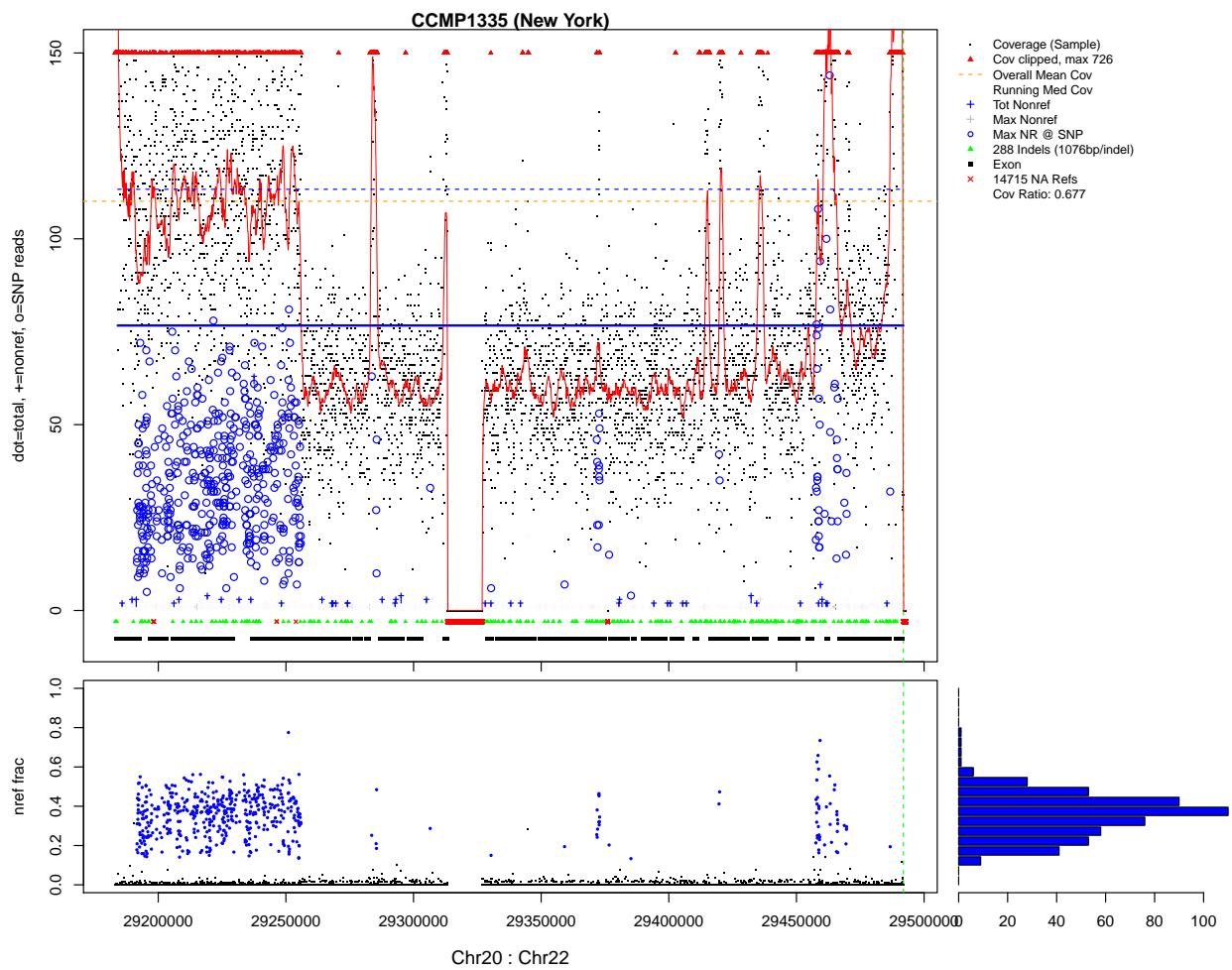
```

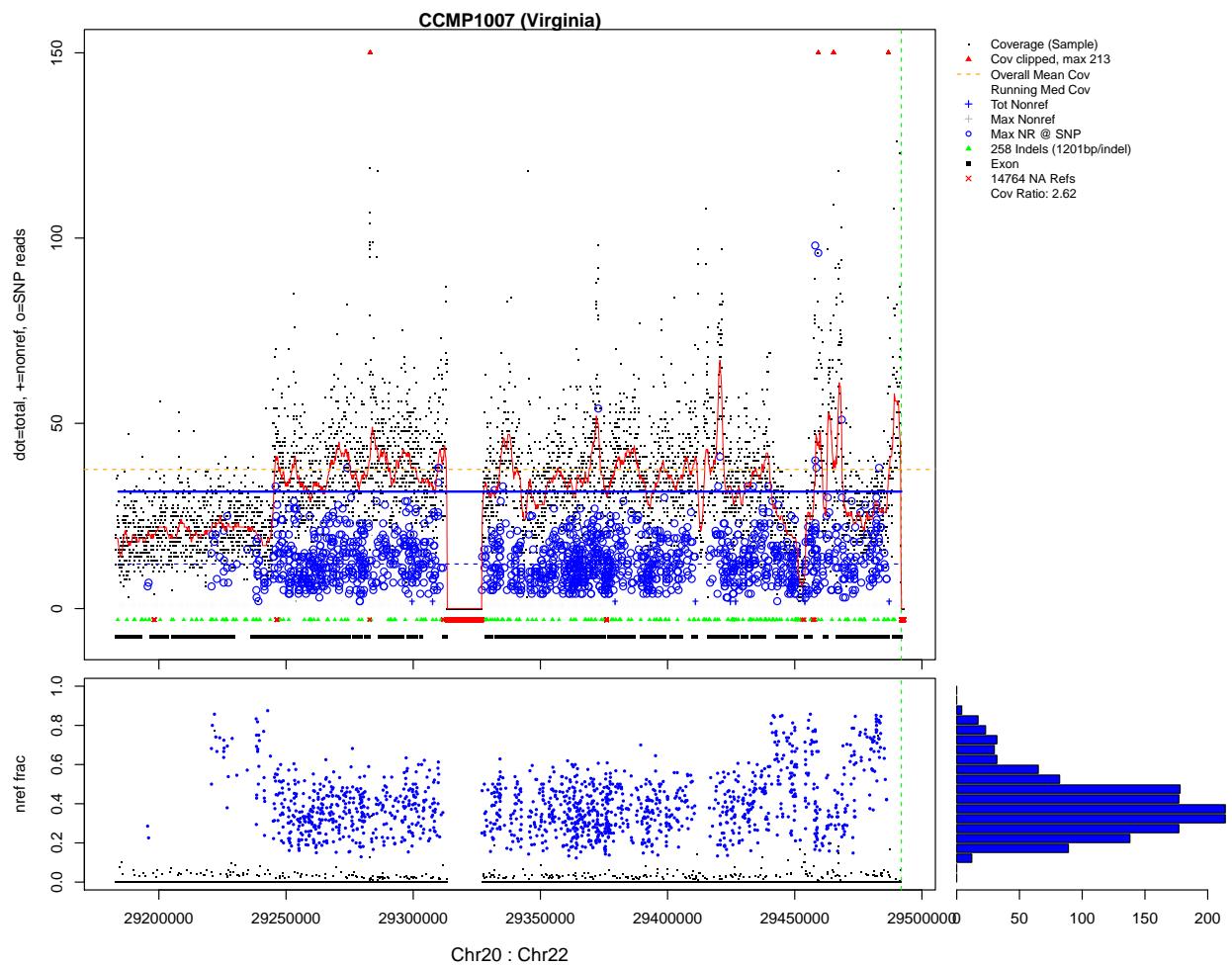
# Chr20:593901 Chr20 593901 594200 300 NA NA 0.654 NA 0.532 0.59747 NA 026
# Chr20:594201 Chr20 594201 594300 100 NA NA 0.654 NA 0.532 0.59747 0.599 027
# Chr20:594301 Chr20 594301 620200 25900 NA NA 0.654 NA 0.532 NA 0.599 025
# Chr20:620201 Chr20 620201 620300 100 NA NA NA NA 0.532 NA 0.599 005
# Chr20:620301 Chr20 620301 621600 1300 NA NA NA NA 0.532 NA NA 004
# Chr20:621601 Chr20 621601 635200 13600 0.000779 0.00102 0.584 0.00109 0.532 0.00392 0.523 177
# Chr20:635201 Chr20 635201 635300 100 NA NA 0.584 NA 0.532 0.00392 0.523 027
# Chr20:635301 Chr20 635301 651100 15800 NA NA 0.584 NA 0.532 NA 0.523 025
# Chr20:651101 Chr20 651101 653100 2000 NA NA 0.584 NA 0.532 0.54348 0.523 027
# Chr20:653101 Chr20 653101 720300 67200 NA NA 0.584 NA 0.532 NA 0.523 025
# Chr20:720301 Chr20 720301 720500 200 NA NA 0.584 NA 0.532 0.49590 0.523 027
# Chr20:720501 Chr20 720501 722400 1900 0.608568 0.68218 0.584 NA 0.532 0.49590 0.523 167
# Chr20:722401 Chr20 722401 722500 100 0.608568 0.68218 0.584 NA NA NA 0.523 161
# Chr20:722501 Chr20 722501 723200 700 NA 0.68218 0.584 NA NA NA 0.523 061
# Chr20:723201 Chr20 723201 728000 4800 NA NA 0.584 NA NA NA 0.523 021
# Chr20:728001 Chr20 728001 729800 1800 NA NA 0.584 NA NA NA NA 020
# Chr20:729801 Chr20 729801 743100 13300 NA NA 0.584 NA 0.550 NA 0.585 025
# Chr20:743101 Chr20 743101 744600 1500 NA NA 0.584 NA 0.550 NA NA 024
# Chr20:744601 Chr20 744601 748600 4000 NA NA 0.584 NA 0.550 NA 0.669 025
# Chr20:748601 Chr20 748601 759500 10900 0.558705 0.55247 0.584 NA 0.550 NA 0.669 165
# Chr20:759501 Chr20 759501 762500 3000 0.558705 0.55247 0.584 NA 0.550 0.19929 0.669 167
# Chr20:762501 Chr20 762501 762600 100 NA 0.55247 0.584 NA NA NA 0.669 061
# Chr20:762601 Chr20 762601 766000 3400 NA NA NA NA NA NA 0.669 001
# Chr20:766001 Chr20 766001 769800 3800 NA NA NA NA NA NA NA 000
# Chr20:769801 Chr20 769801 770700 900 NA NA NA NA NA 0.41187 NA 002
# Chr20:770701 Chr20 770701 776900 6200 NA NA NA NA NA NA NA 000
# Chr20:776901 Chr20 776901 794800 17900 NA NA NA NA 0.719 NA NA 004
# Chr20:794801 Chr20 794801 800233 5433 NA NA NA NA NA NA NA 000
# Chr20:800234 Chr20 800234 800233 0 NA NA NA NA NA NA NA 000
# Chr22:1 Chr22 1 87300 87300 NA NA NA NA NA NA NA 000

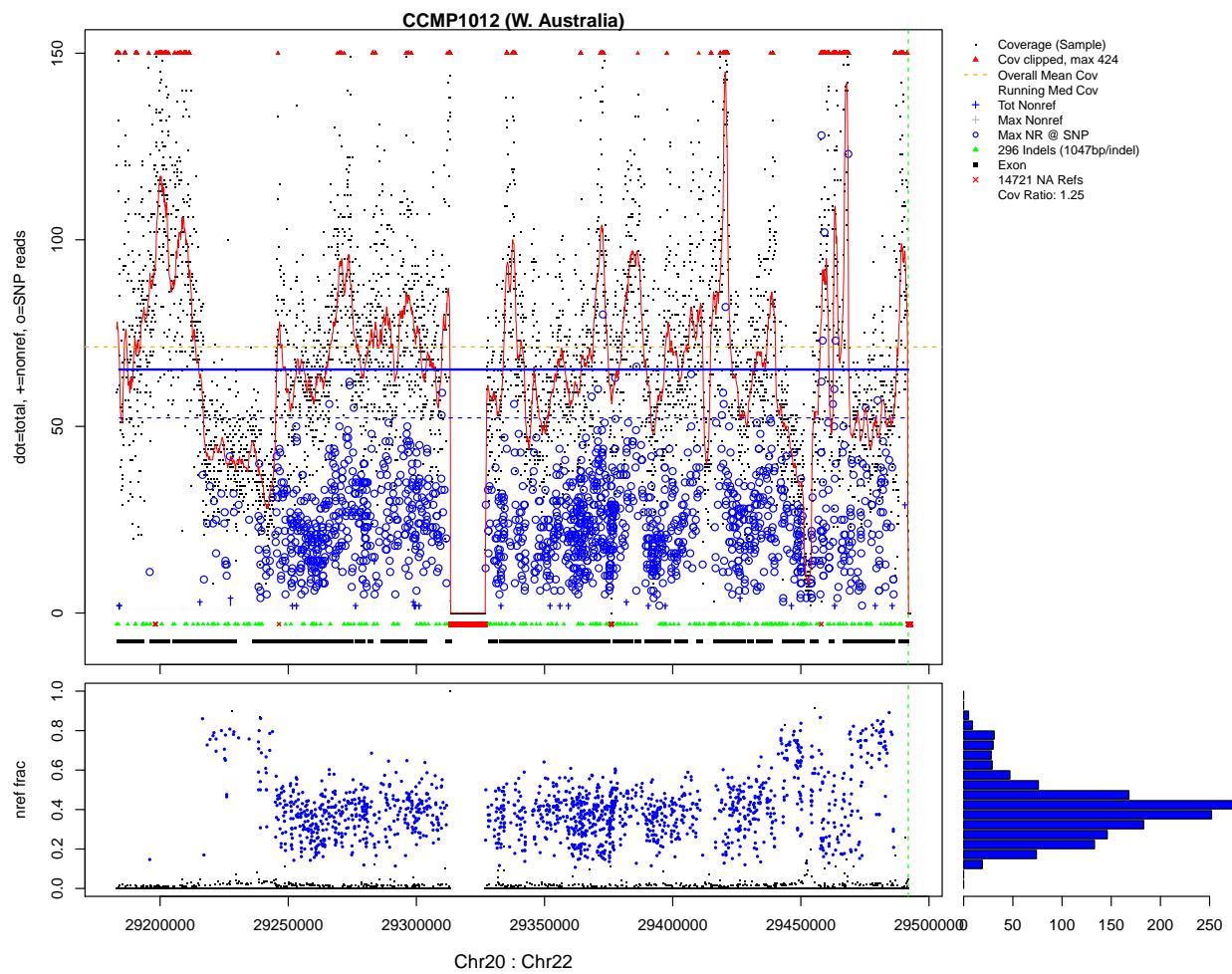
dev.off()

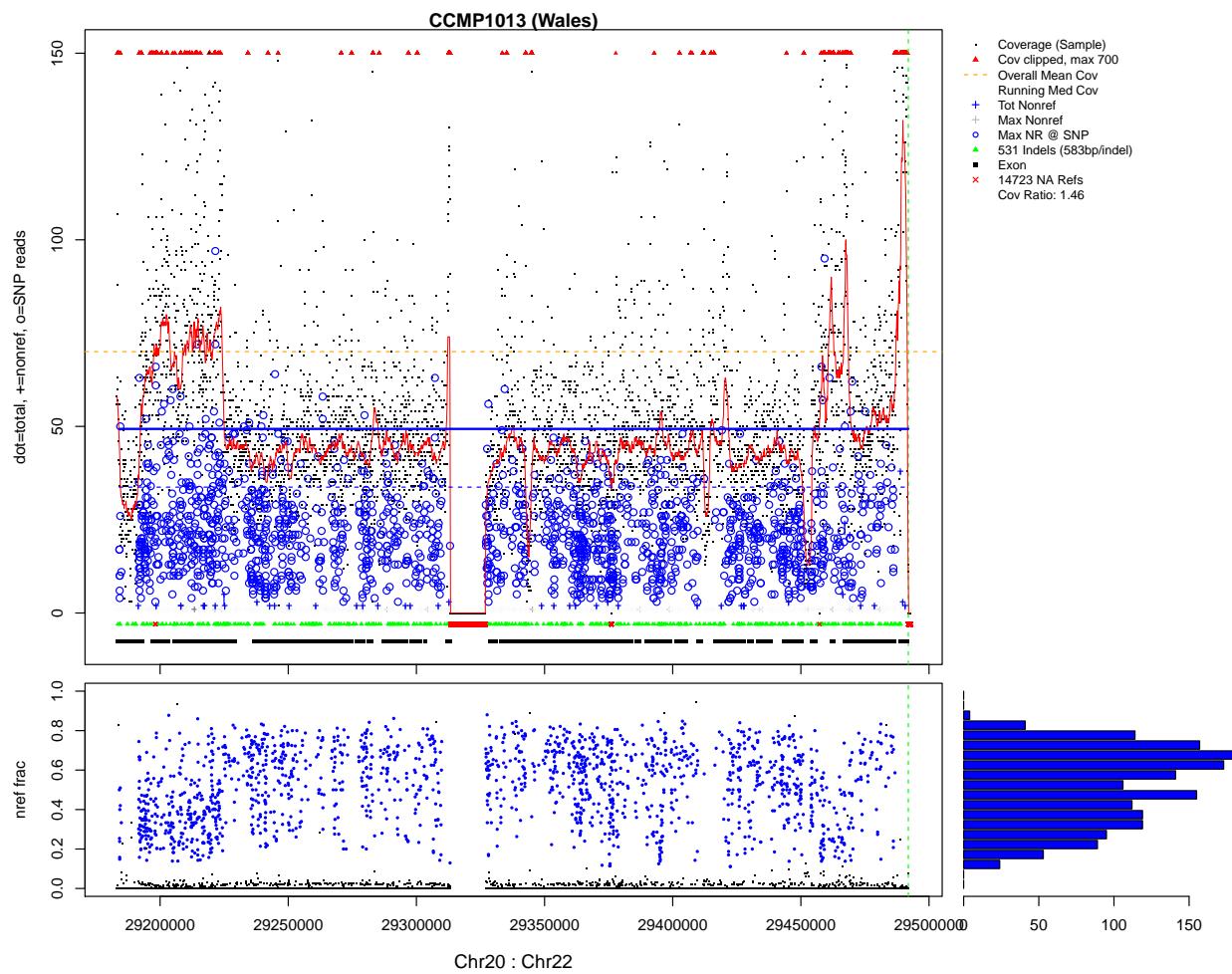
# pdf
# 2

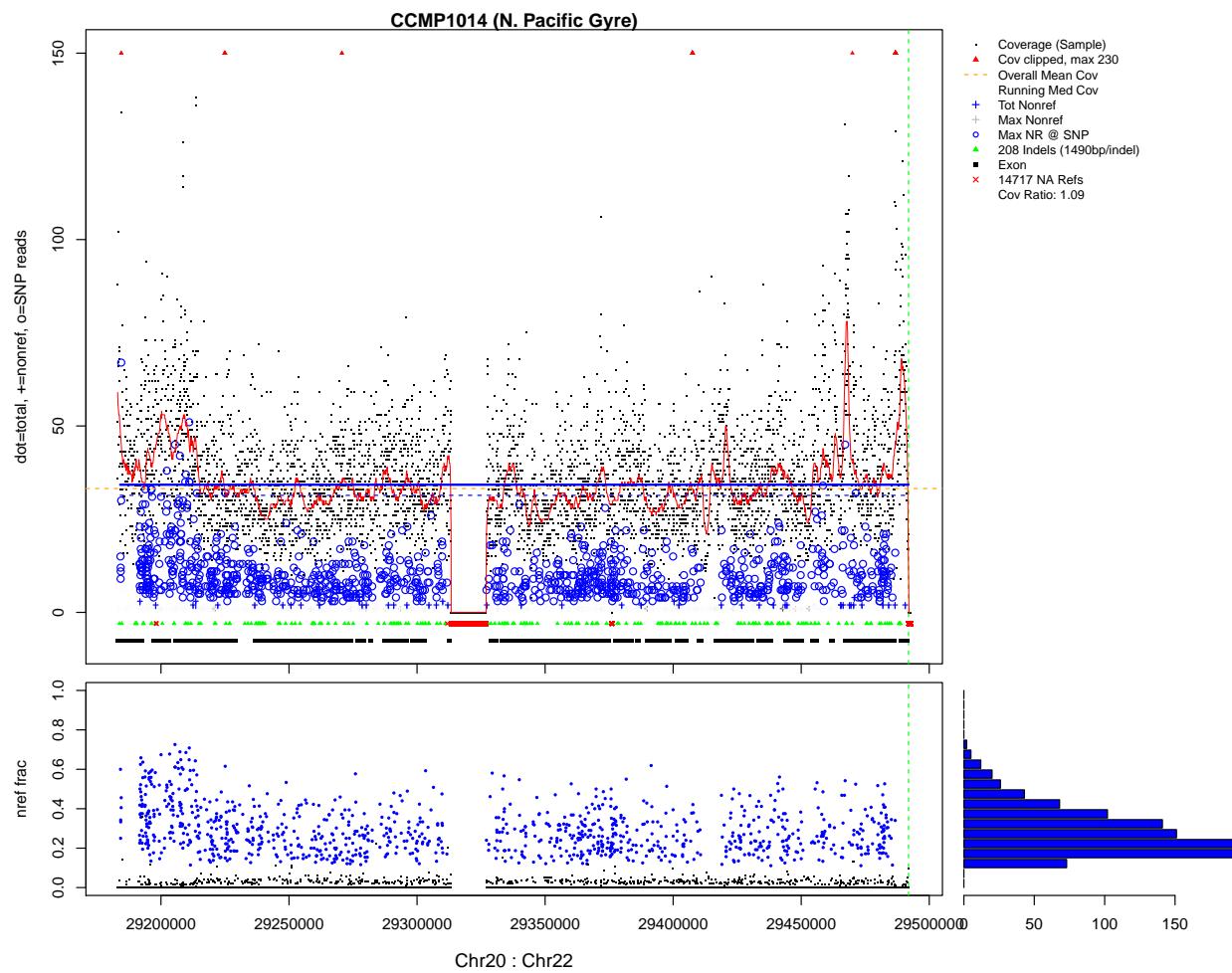
```

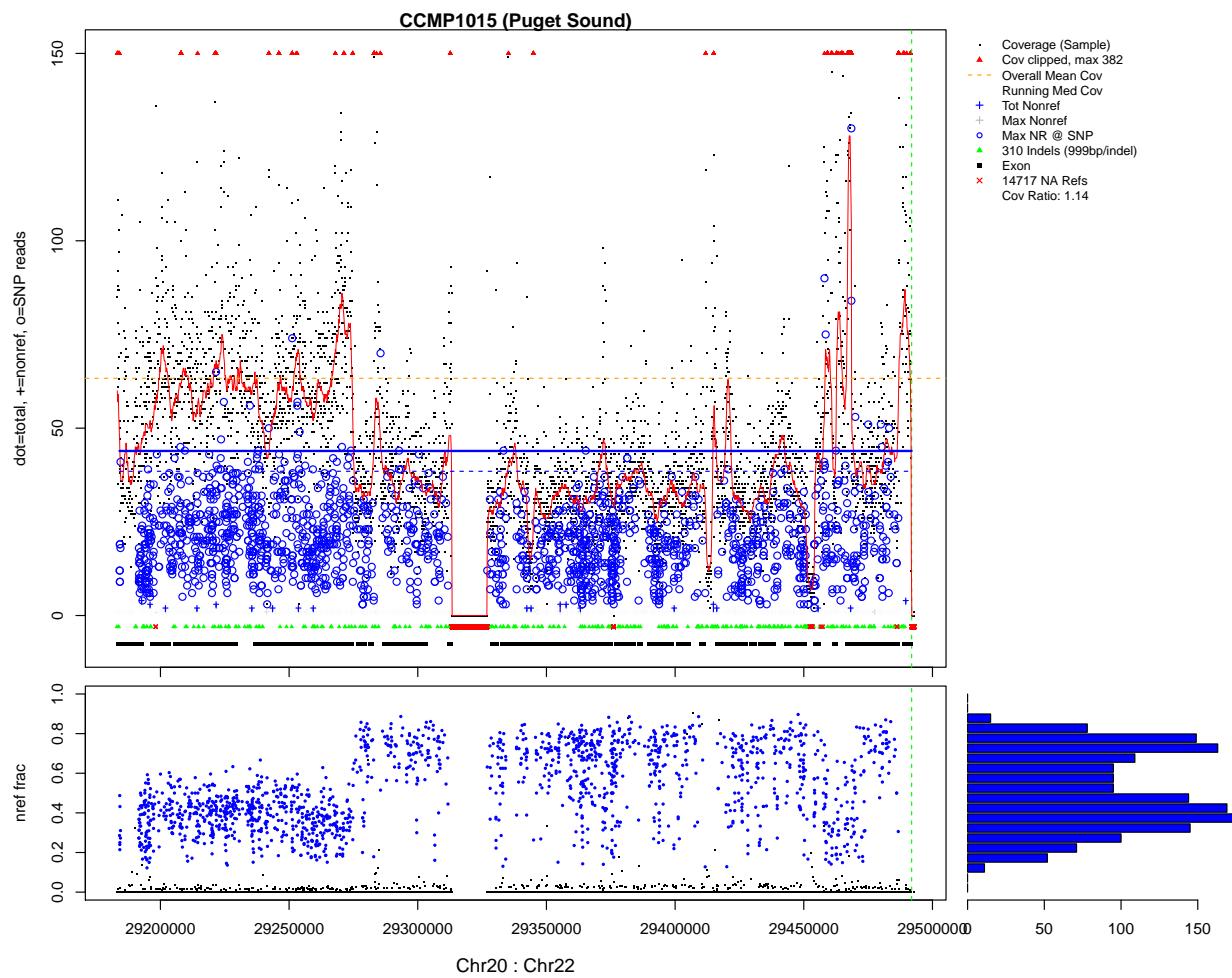


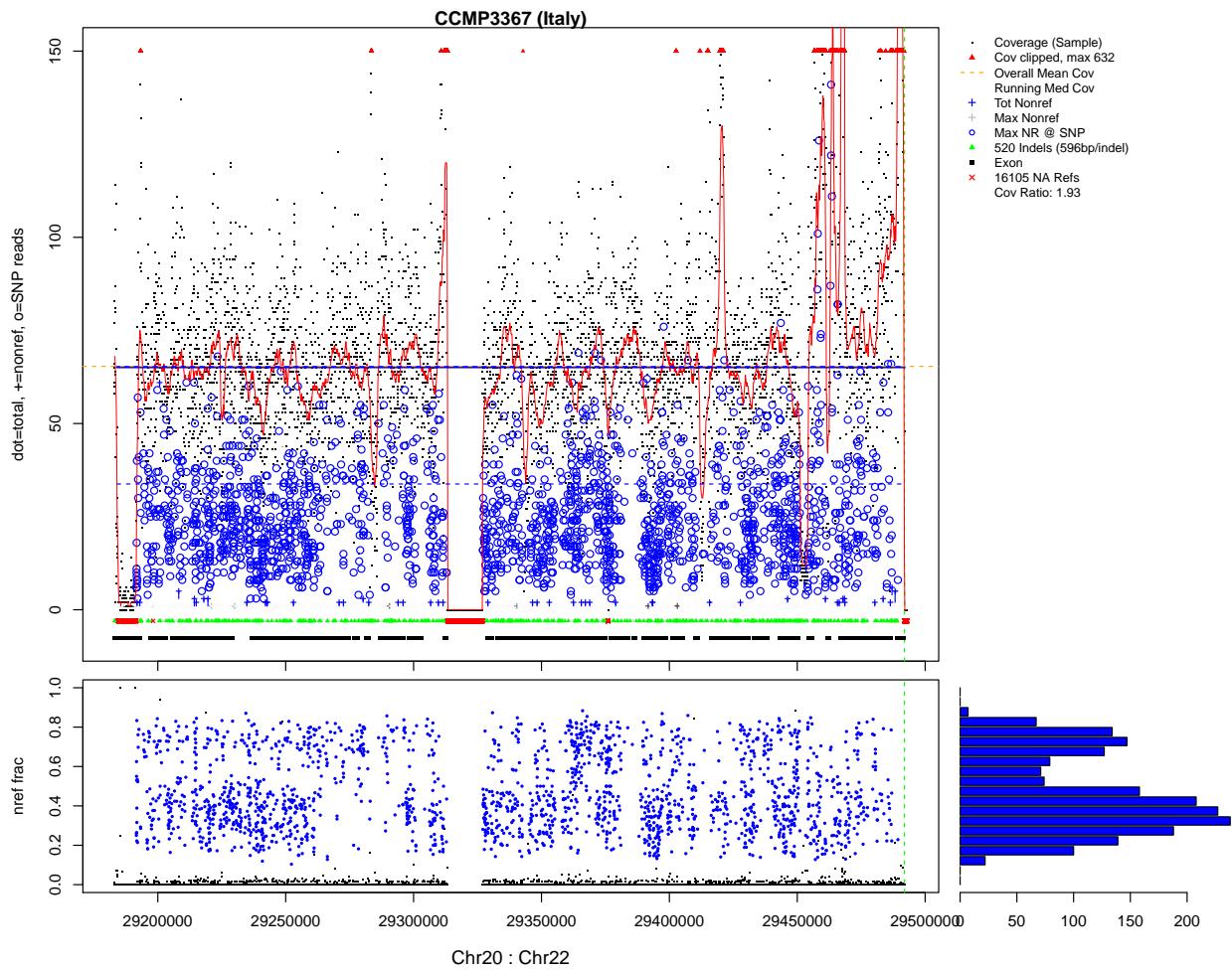












## 8 Unshared hemi regions

Tony's initial look at this.

```
# hemizygosity numbers from tony's email 10/2/2014
#          tp1007  tp1012  tp1013  tp1014  tp1015      IT  tp1335
hemi.total.bp <- c(4471700, 6318900, 3535400, 6274400, 3637700, 2130100, 4843600)

#          tp1007  tp1012  tp1013  tp1014  tp1015      IT  tp1335
hemi.unique.bp <- c(42800, 822600, 82500, 185100, 53200, 207600, 19800)

#          tp1007  tp1012  tp1013  tp1014  tp1015      IT  tp1335
hemi.unique.events <- c(9,    113,     15,     18,    10,    64,   10)

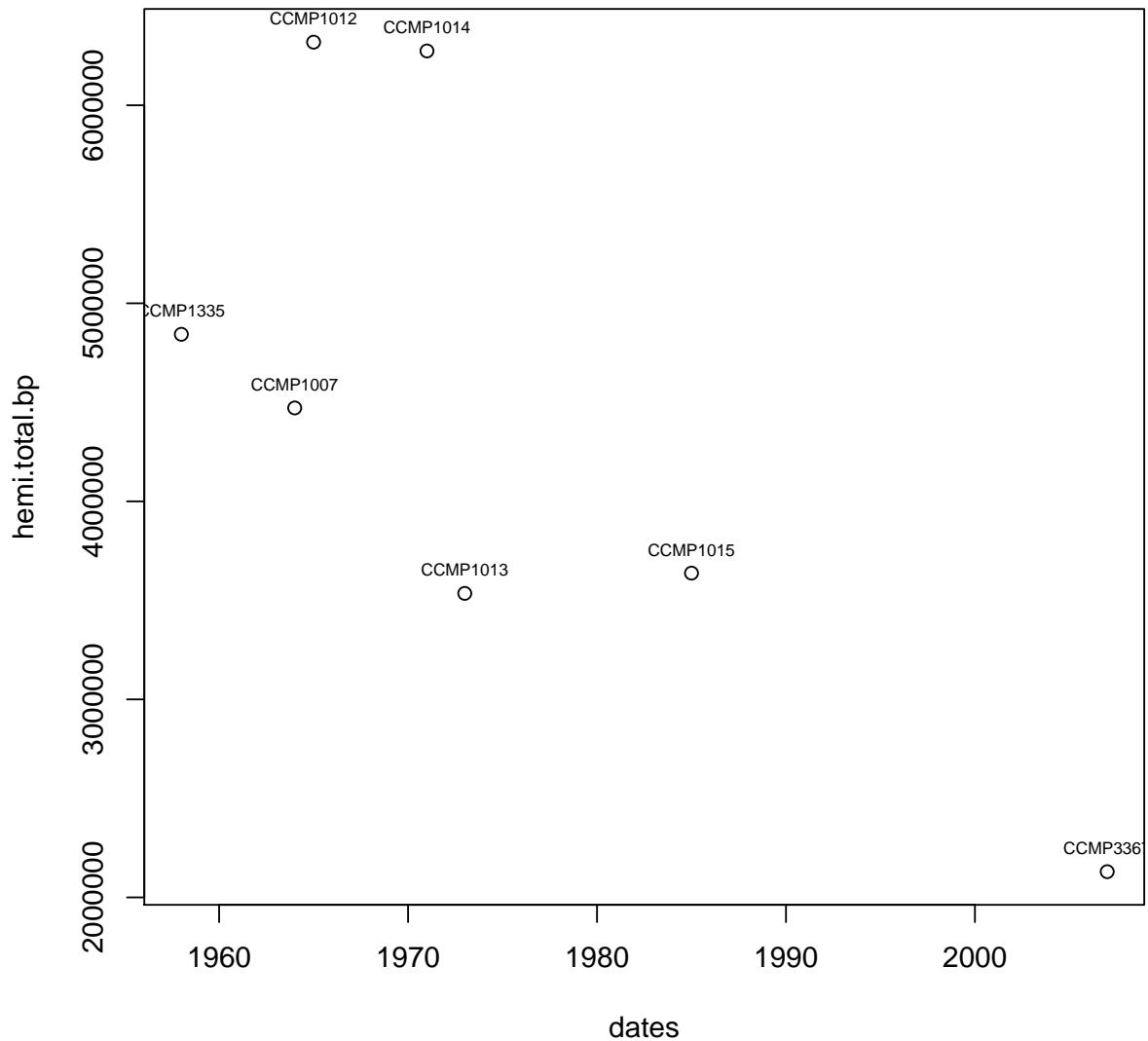
hemi.unique.bp/hemi.unique.events

# [1] 4755.556 7279.646 5500.000 10283.333 5320.000 3243.750 1980.000

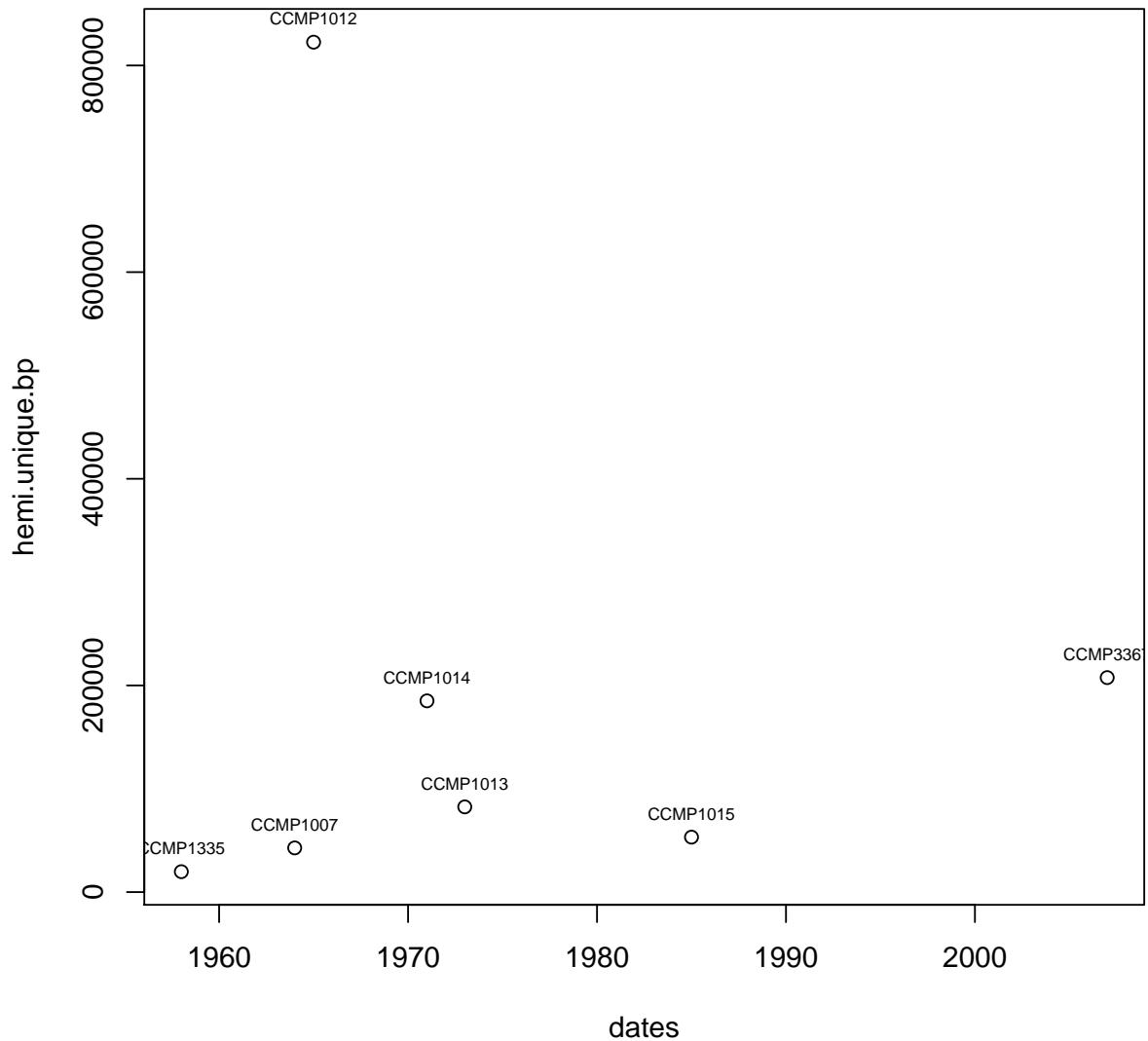
dates <- unlist(lapply(1:7,function(st){as.integer(st.loc(st,id=F,loc=F,date=T))})) 

ids <- unlist(lapply(1:7,function(st){st.loc(st,id=T,loc=F,date=F)}))

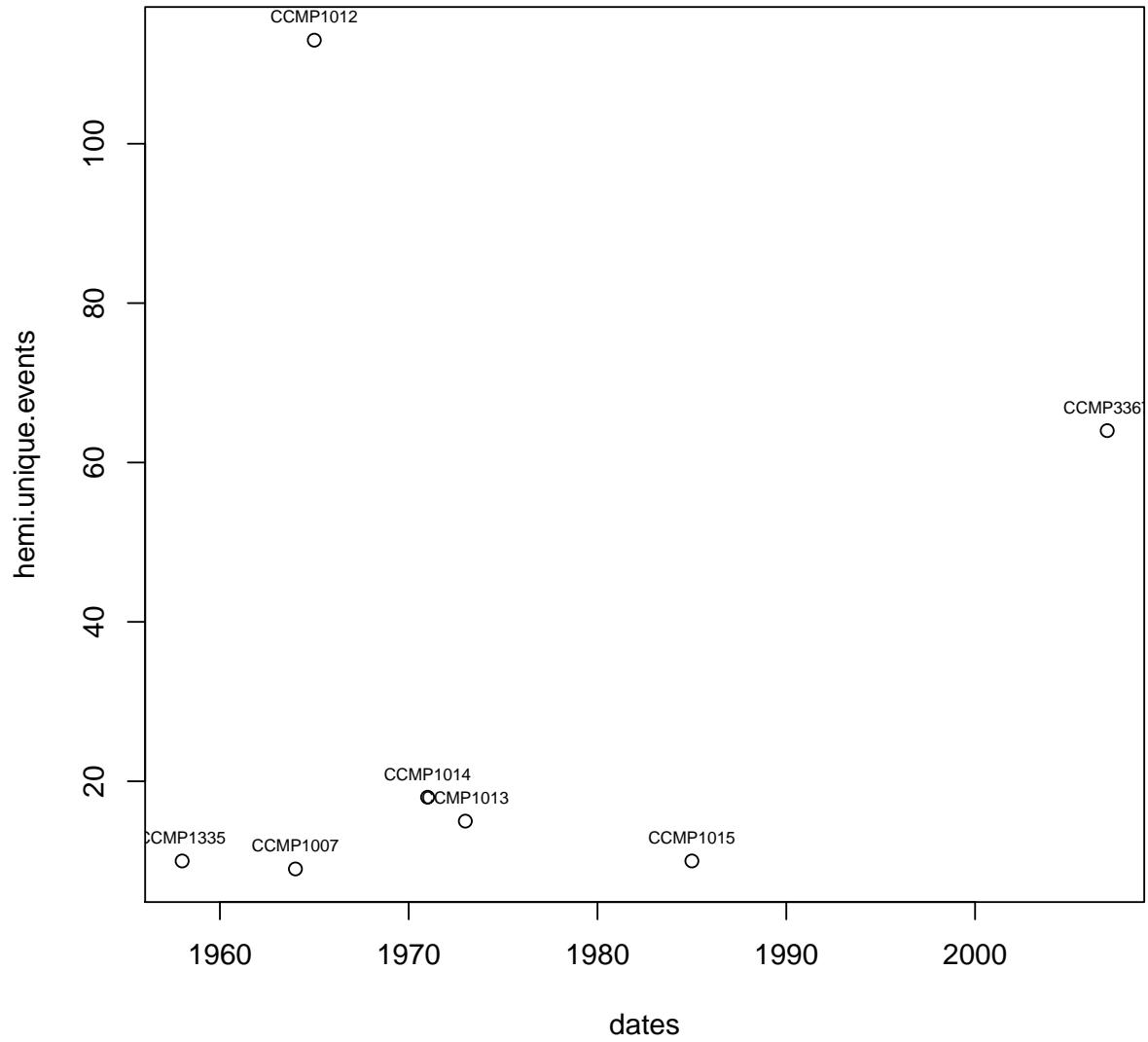
plot(dates,hemi.total.bp)
text(dates,hemi.total.bp,labels=ids,cex=.6,pos=3)
```



```
plot(dates,hemi.unique.bp)
text(dates,hemi.unique.bp,labels=ids,cex=.6,pos=3)
```



```
plot(dates,hemi.unique.events)
text(dates,hemi.unique.events,labels=ids,cex=.6,pos=3)
```



SVN ID I miss you Id: tic.rnw 2017-06-28 or later ruzzo