BIO392-cnv-freq

Michelle

2022-09-28

Step 1: Install package

```
if (!require(devtools)){ install.packages('devtools')
}
```

```
## Loading required package: devtools
```

```
## Loading required package: usethis
```

```
 if (!require(pgxRpi)){ devtools::install_github('progenetix/pgxRpi')
}
```

```
## Loading required package: pgxRpi
```

```
library(pgxRpi)
```

Step2: Search esophageal adenocarcinoma NCIt code

Step3: Access the CNV frequency data from samples with esophageal adenocarcinoma

```
 freq <- pgxLoader(type='frequency', output='pgxseg',filters='NCIT:C9245', codematches=T)
```

The retreived data is an object contaning two slots `meta` and `data`.

The `meta` slot looks like this:

```
freq$meta
```

```
##         code                      label sample_count
## 1 NCIT:C9245 Invasive Breast Carcinoma         3796
## 2      total                                   3796
```

The `data` slot includes two matrices.

```
names(freq$data)
```

```
## [1] "NCIT:C9245" "total"
```

The frequency matrix looks like this

```
head(freq$data$`NCIT:C4025`)
```

```
## NULL
```

Dimension of this matrix

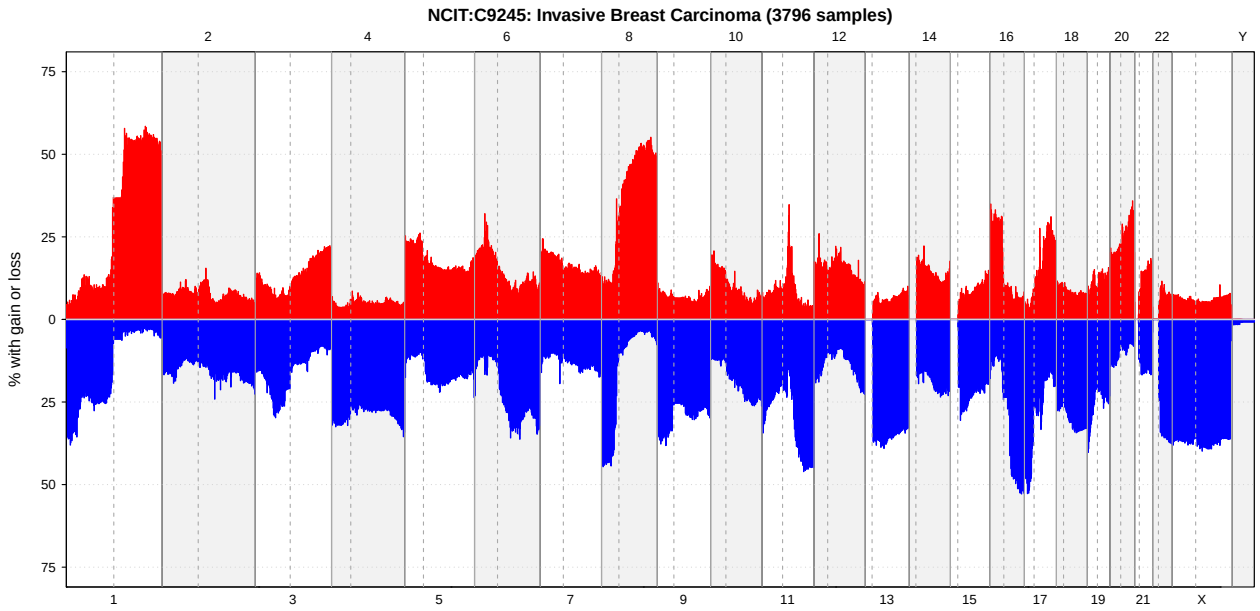
```
dim(freq$data$`NCIT:C4025`)
```

```
## NULL
```

Step4: Visualize data

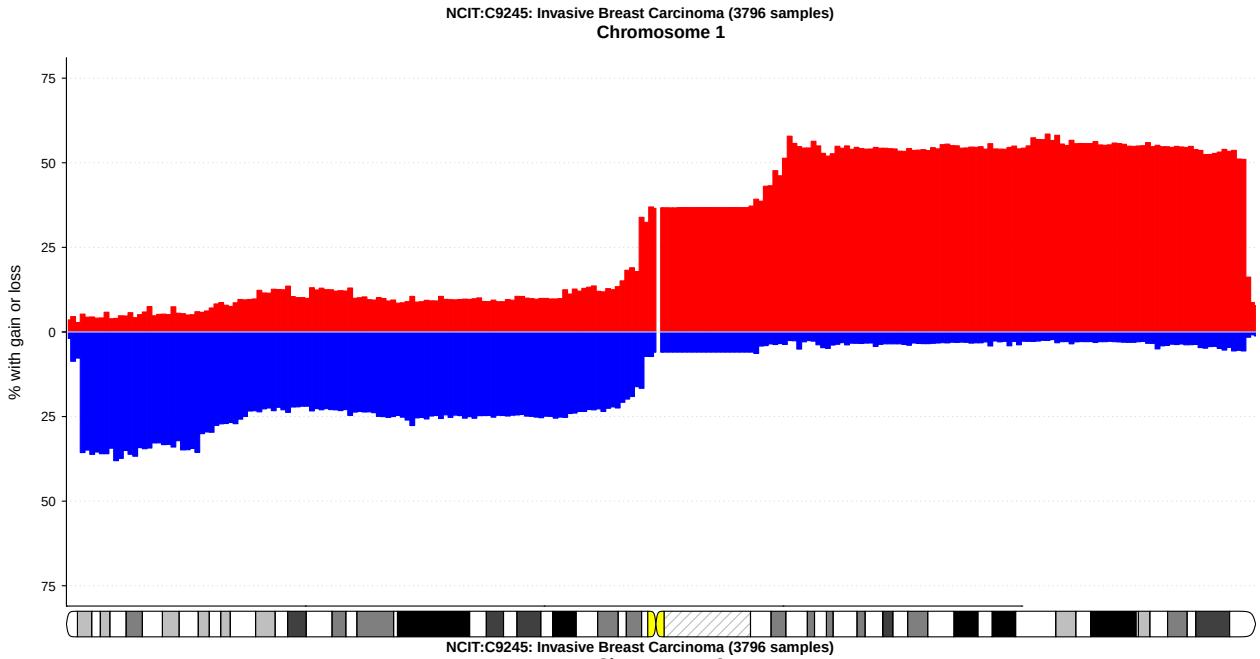
By genome

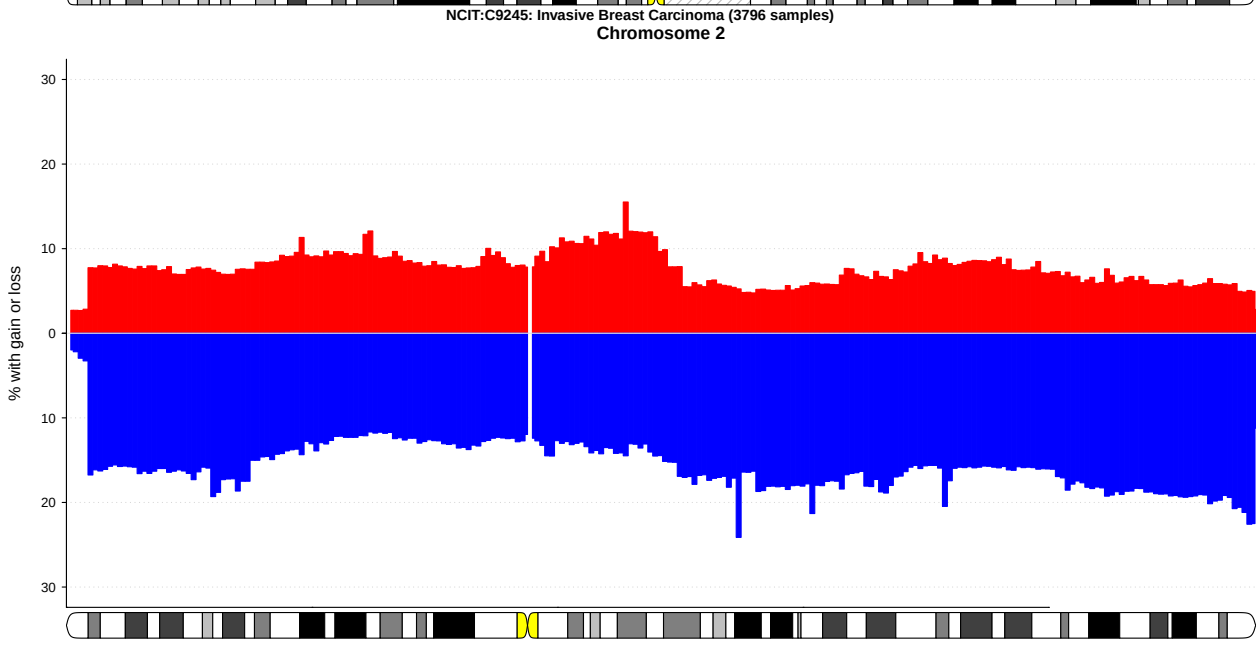
```
pgxFreqplot(freq)
```

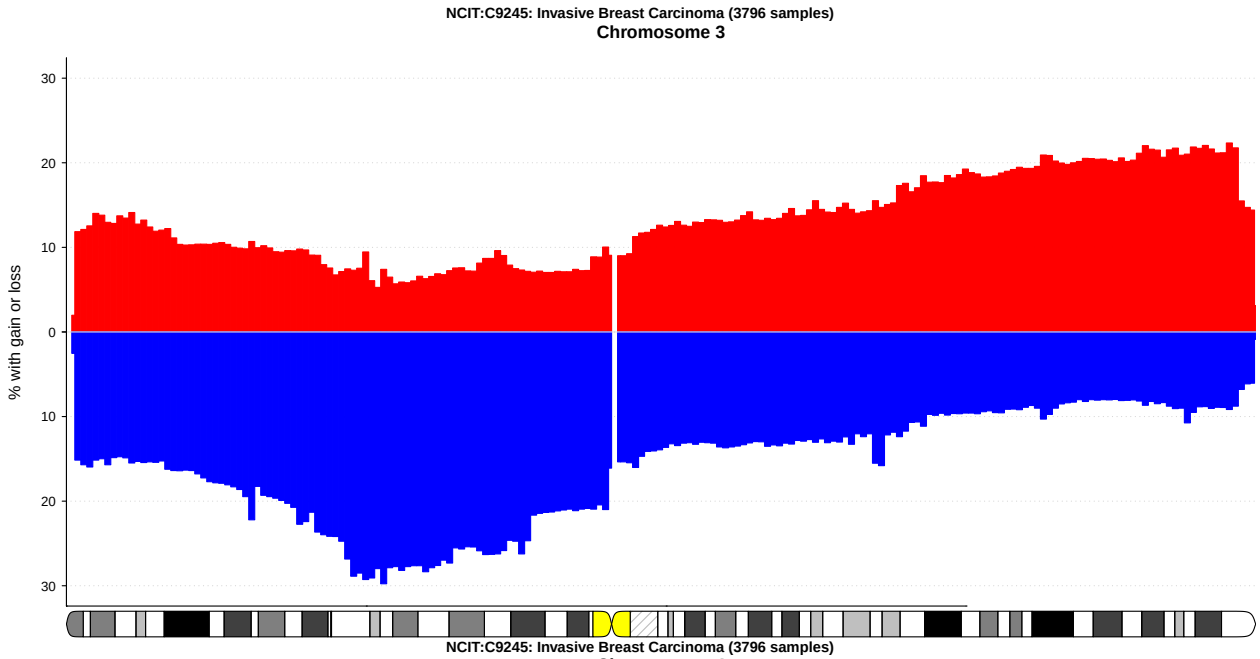


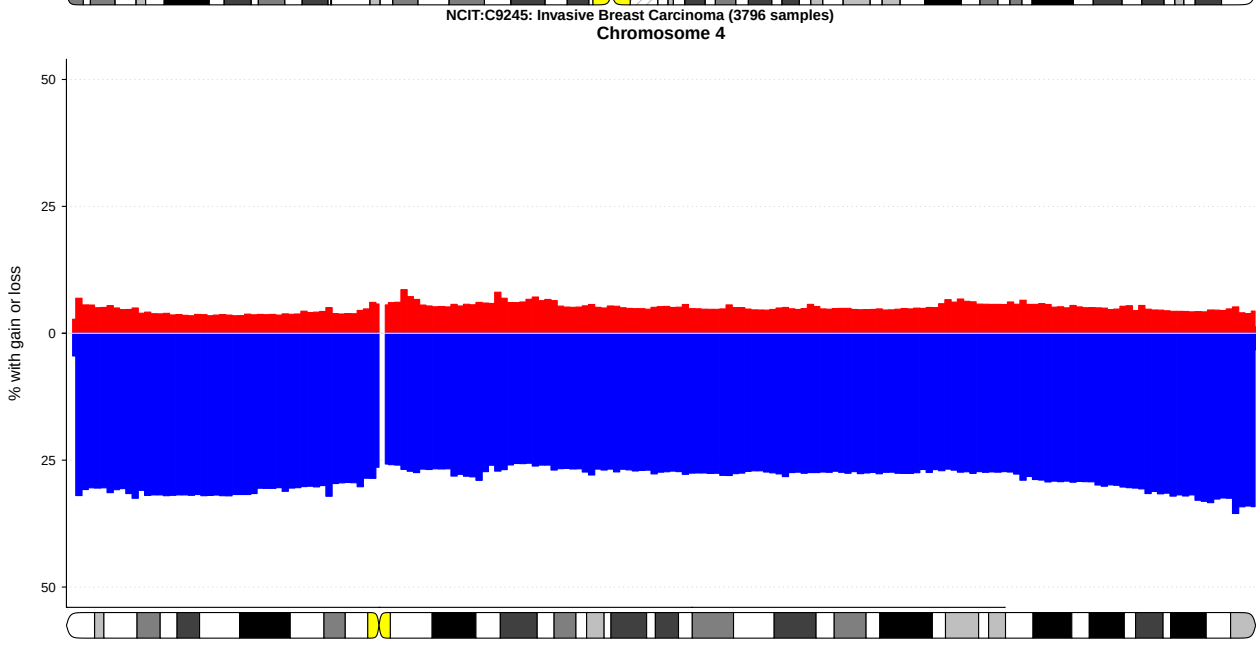
By chromosome

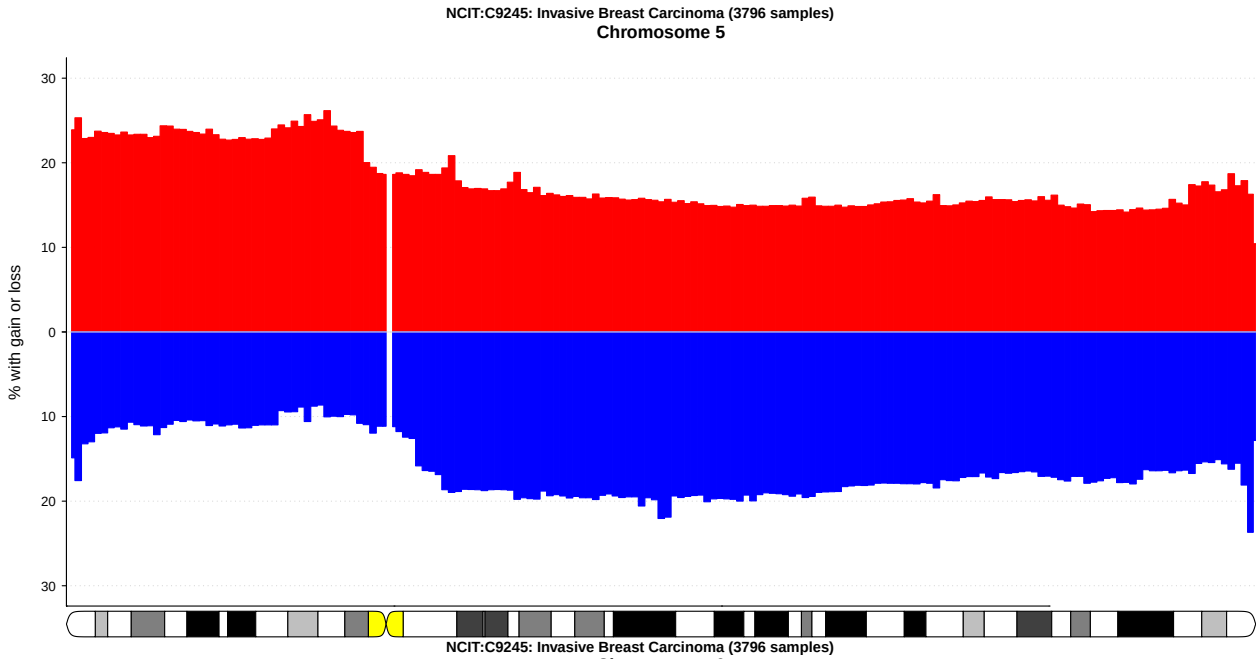
```
for (x in 1:22){
pgxFreqplot(freq,chrom = x)
}
```

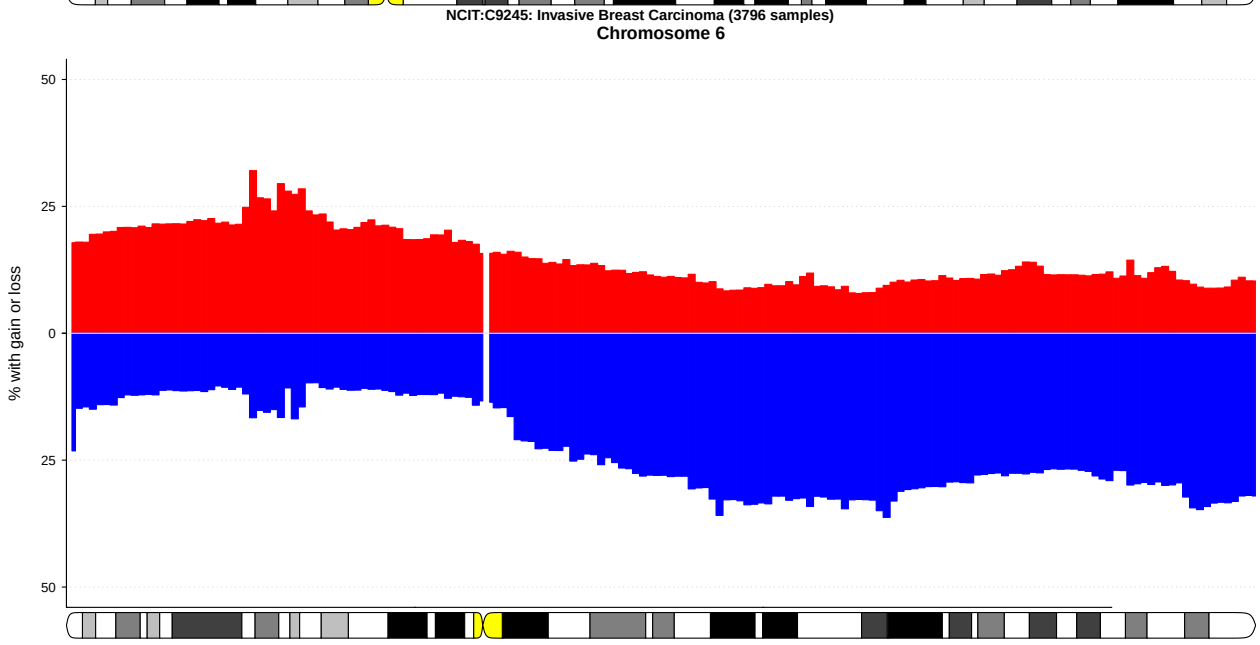

NCIT:C9245: Invasive Breast Carcinoma (3796 samples)
Chromosome 1
% with gain or loss
75
50
25
0
25
50
75

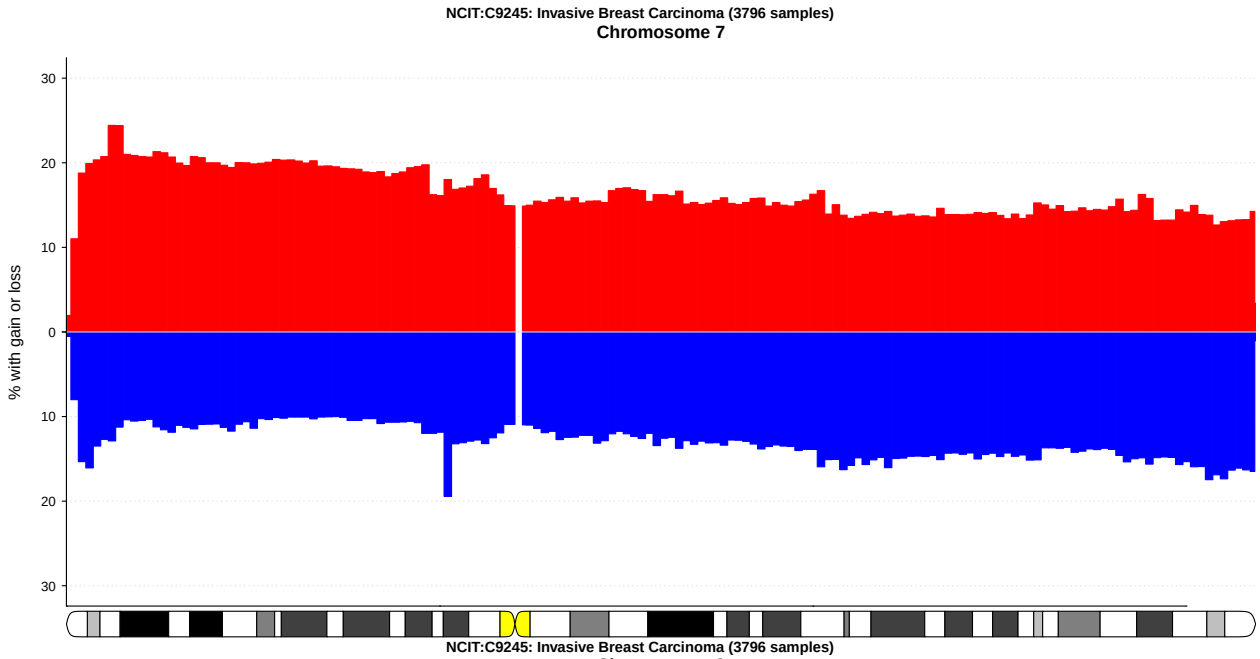

NCIT:C9245: Invasive Breast Carcinoma (3796 samples)
Chromosome 2
% with gain or loss
30
20
10
0
10
20
30

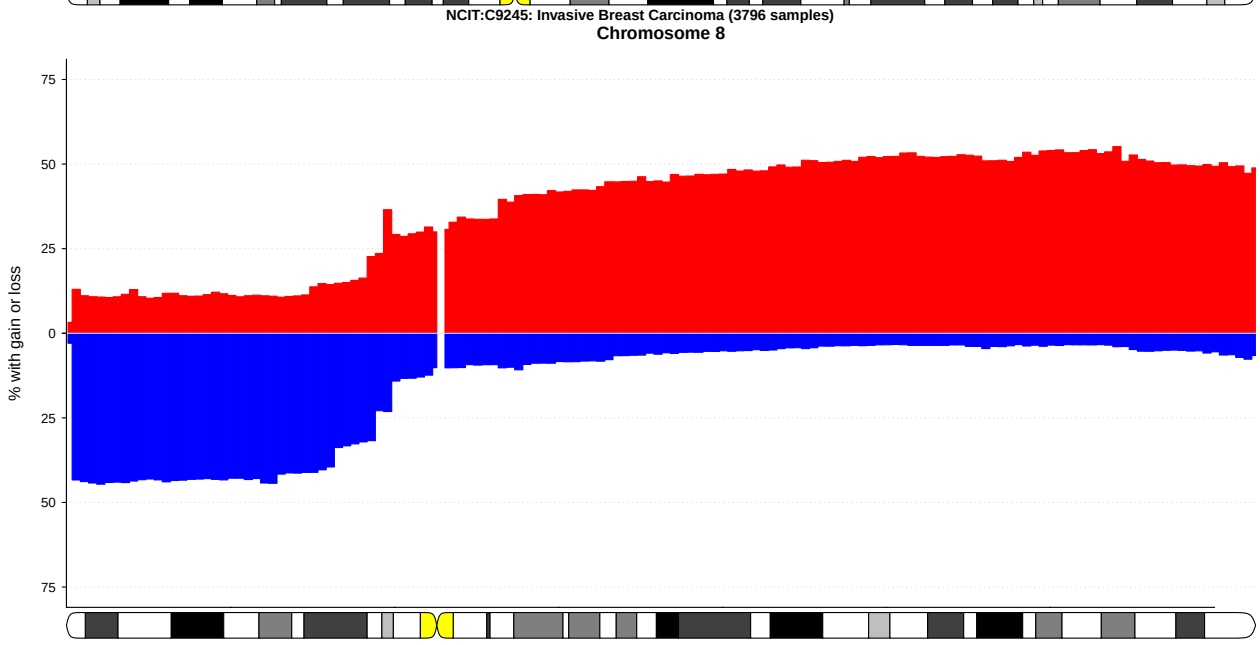

NCIT:C9245: Invasive Breast Carcinoma (3796 samples)
Chromosome 3
% with gain or loss
30
20
10
0
10
20
30

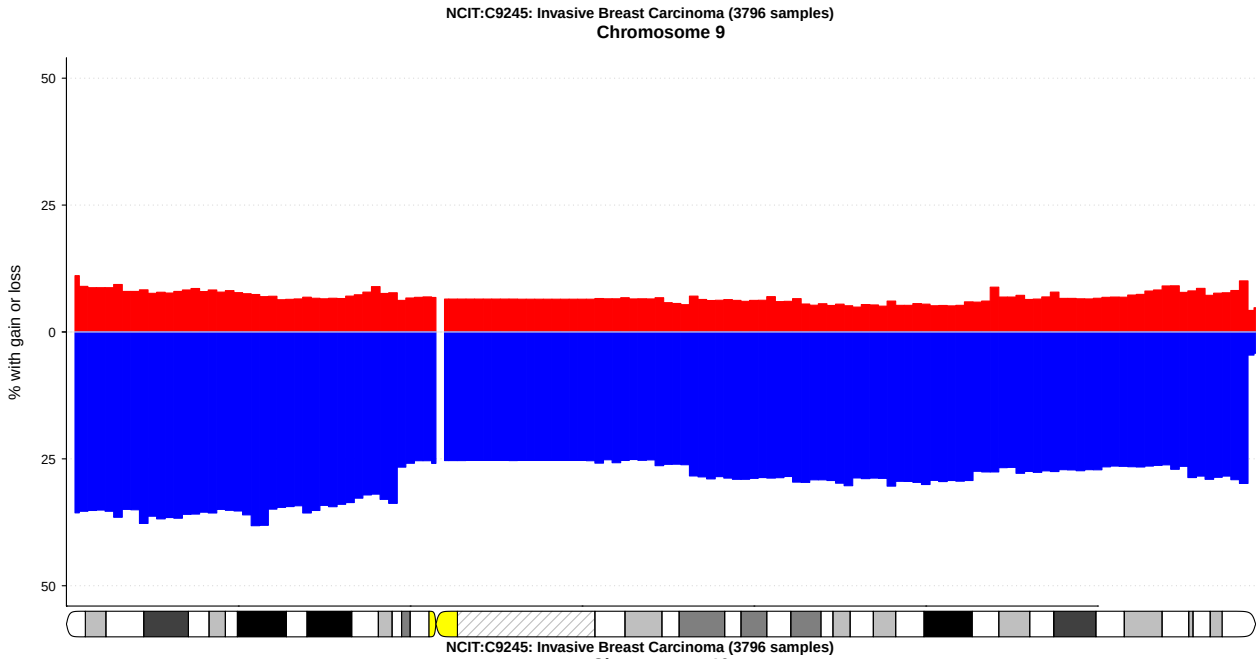

NCIT:C9245: Invasive Breast Carcinoma (3796 samples)
Chromosome 4
% with gain or loss
50
25
0
25
50

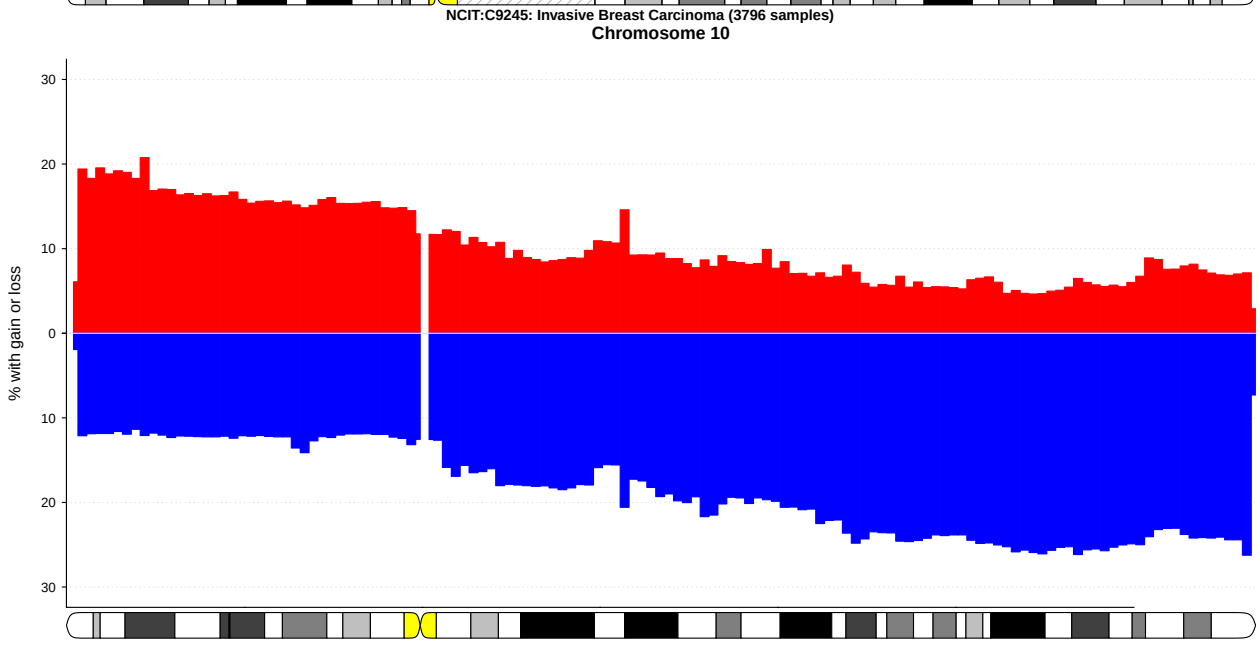

NCIT:C9245: Invasive Breast Carcinoma (3796 samples)
Chromosome 5
% with gain or loss
30
20
10
0
10
20
30

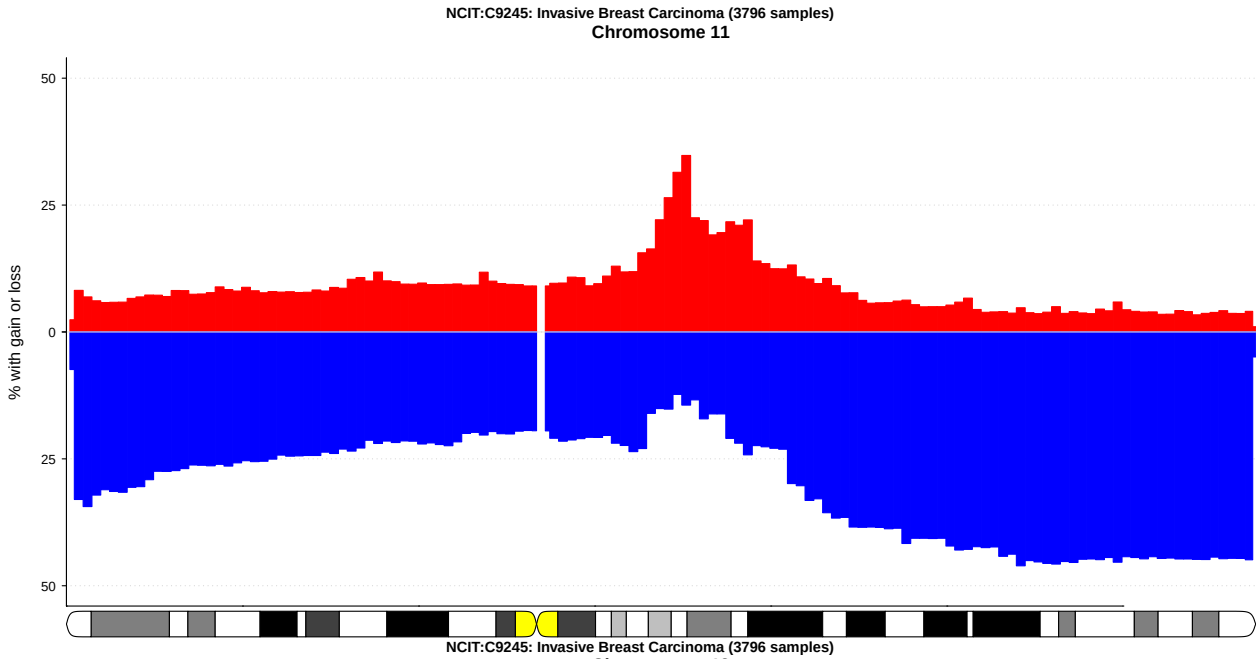

NCIT:C9245: Invasive Breast Carcinoma (3796 samples)
Chromosome 6
% with gain or loss
50
25
0
25
50

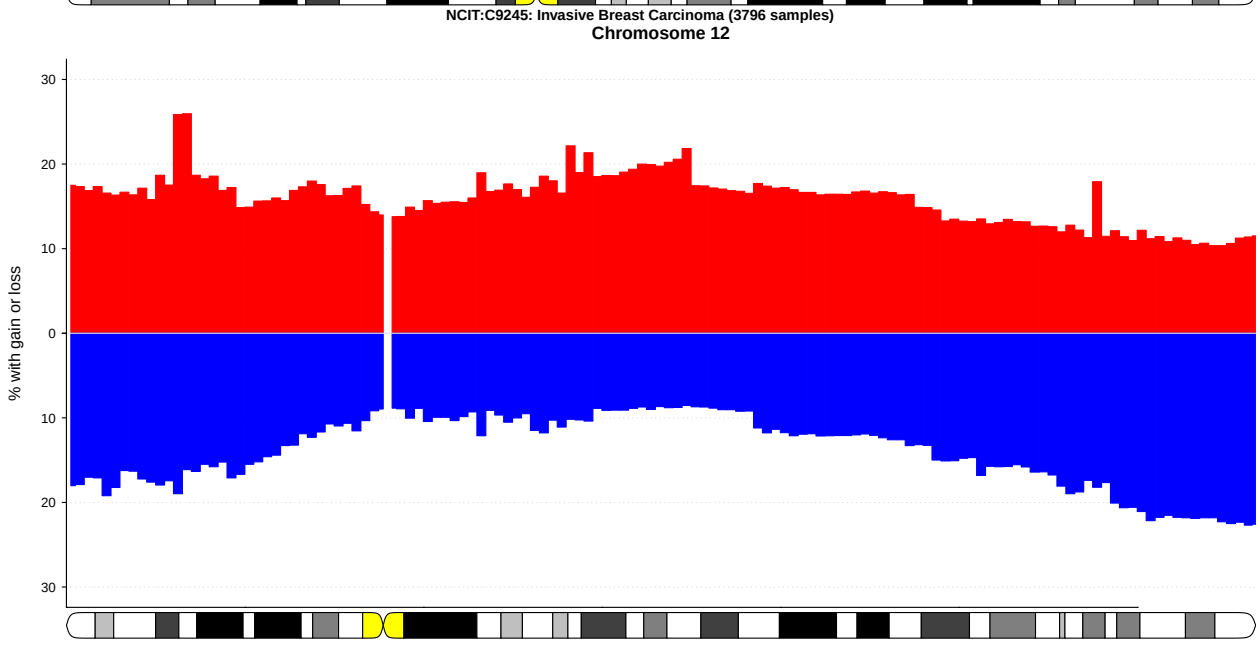

NCIT:C9245: Invasive Breast Carcinoma (3796 samples)
Chromosome 7
% with gain or loss
30
20
10
0
10
20
30

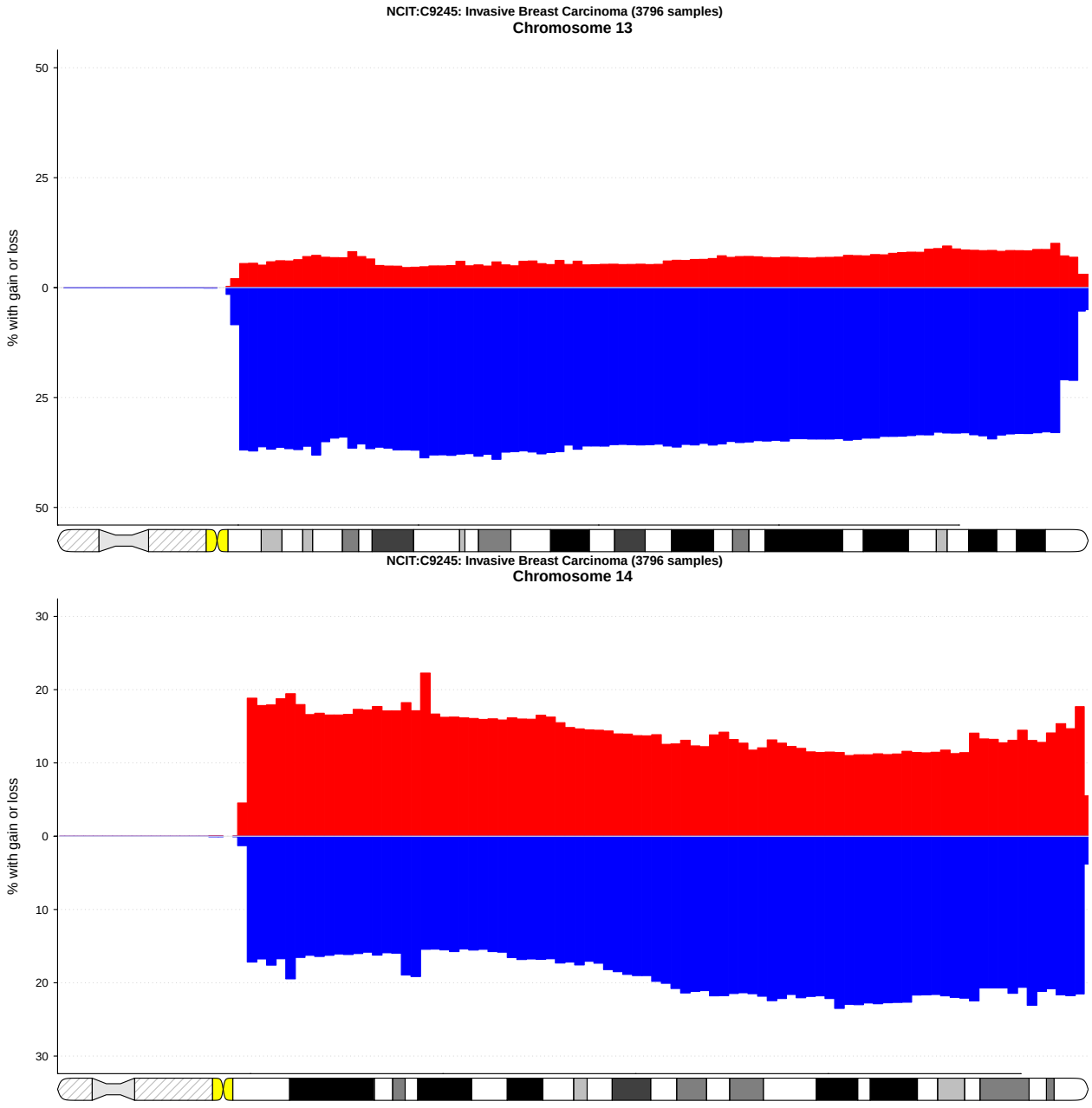

NCIT:C9245: Invasive Breast Carcinoma (3796 samples)
Chromosome 8
% with gain or loss
75
50
25
0
25
50
75

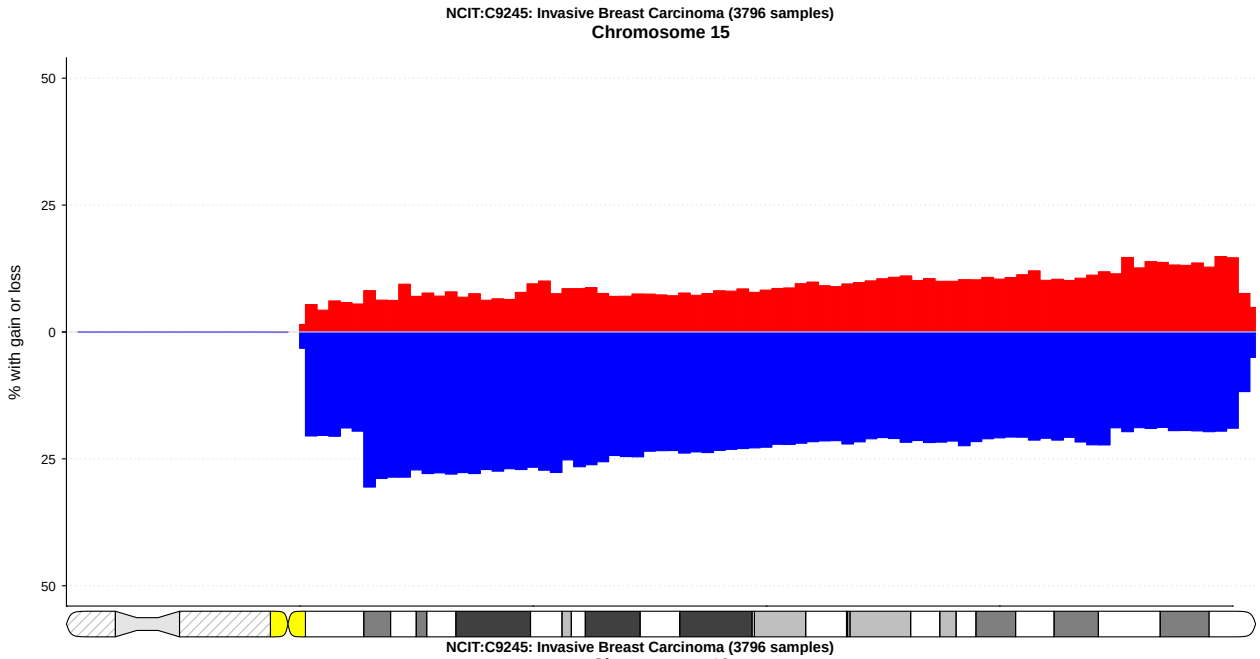

NCIT:C9245: Invasive Breast Carcinoma (3796 samples)
Chromosome 9
% with gain or loss
50
25
0
25
50

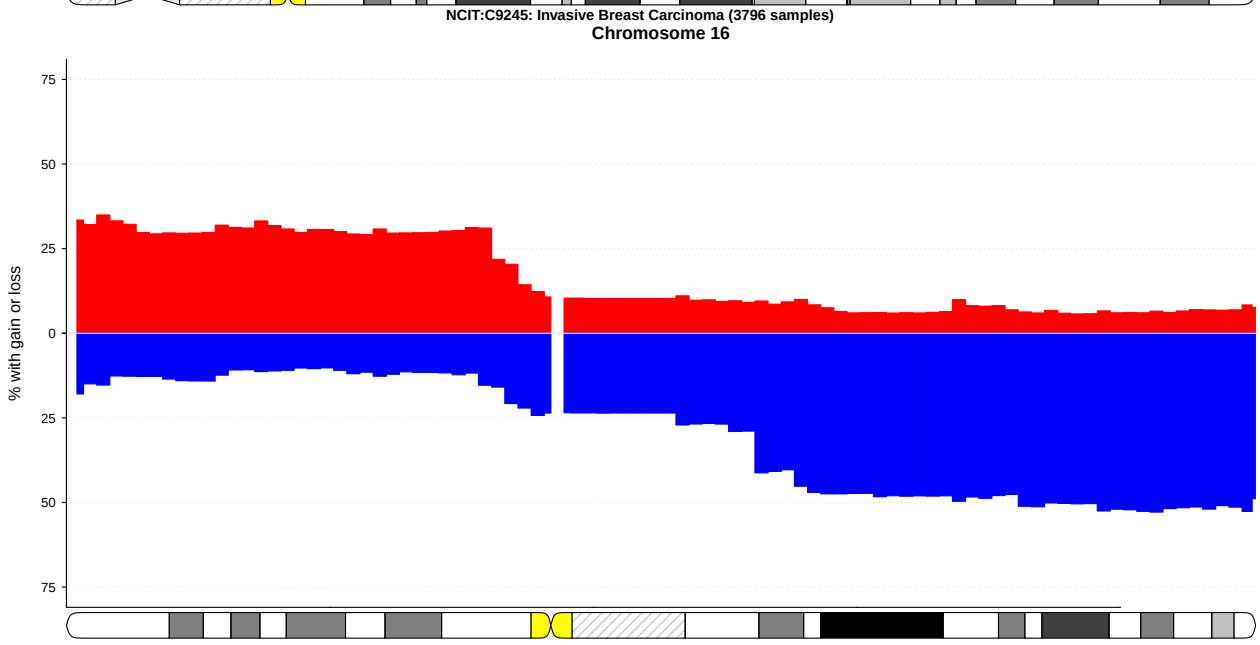

NCIT:C9245: Invasive Breast Carcinoma (3796 samples)
Chromosome 10
% with gain or loss
30
20
10
0
10
20
30

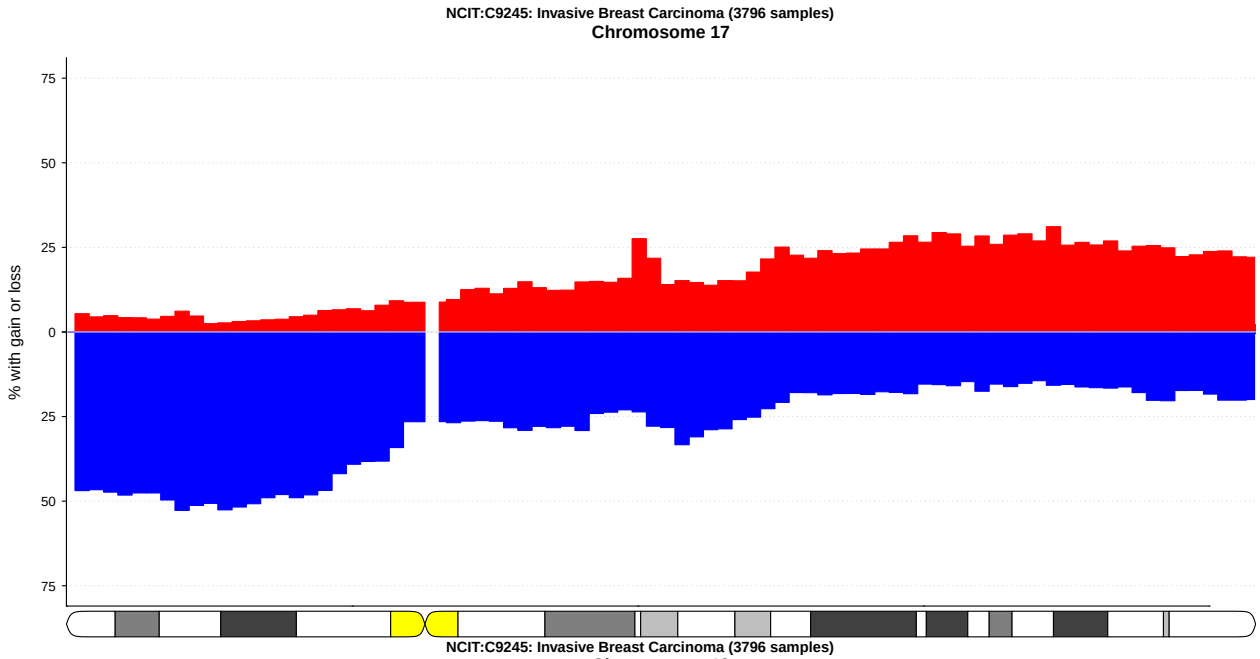

NCIT:C9245: Invasive Breast Carcinoma (3796 samples)
Chromosome 11
% with gain or loss
50
25
0
25
50

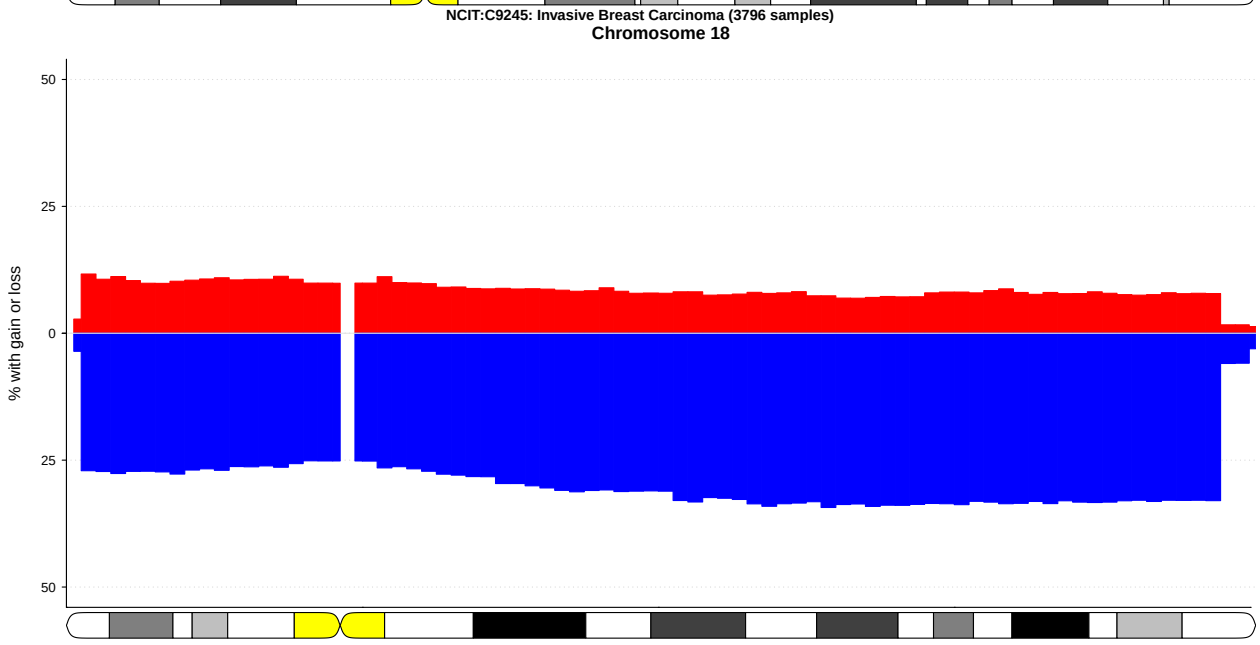

NCIT:C9245: Invasive Breast Carcinoma (3796 samples)
Chromosome 12
% with gain or loss
30
20
10
0
10
20
30

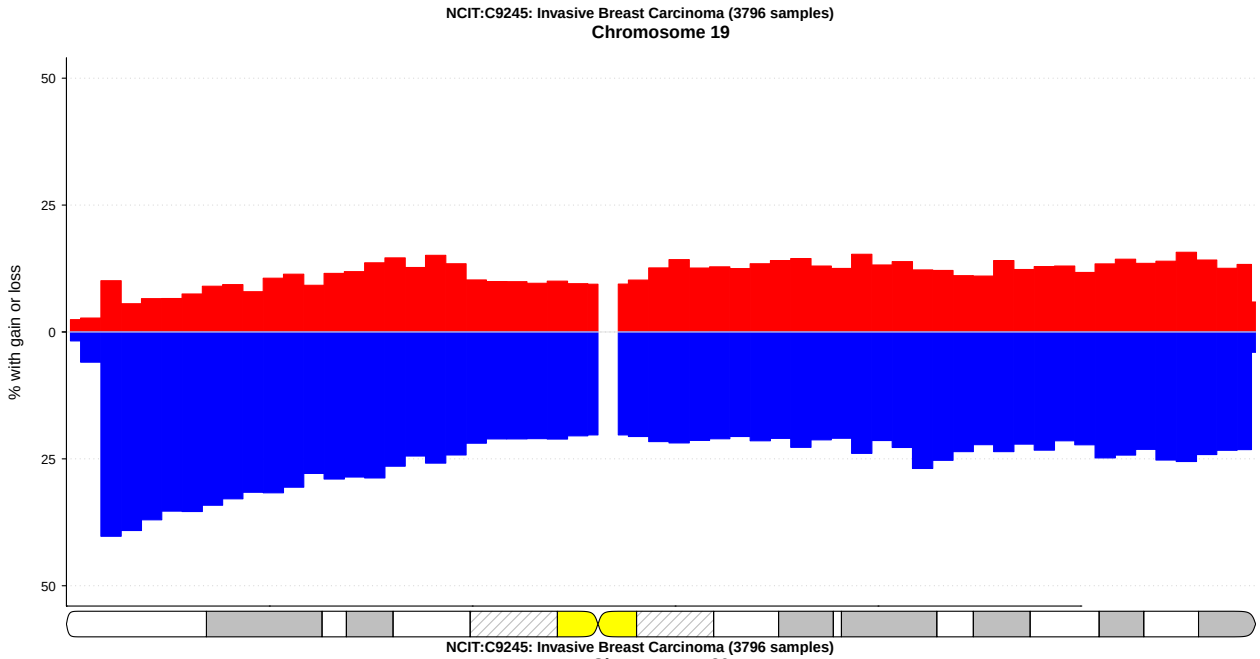

NCIT:C9245: Invasive Breast Carcinoma (3796 samples)
Chromosome 13
% with gain or loss
50
25
0
25
50
NCIT:C9245: Invasive Breast Carcinoma (3796 samples)
Chromosome 14
% with gain or loss
30
20
10
0
10
20
30

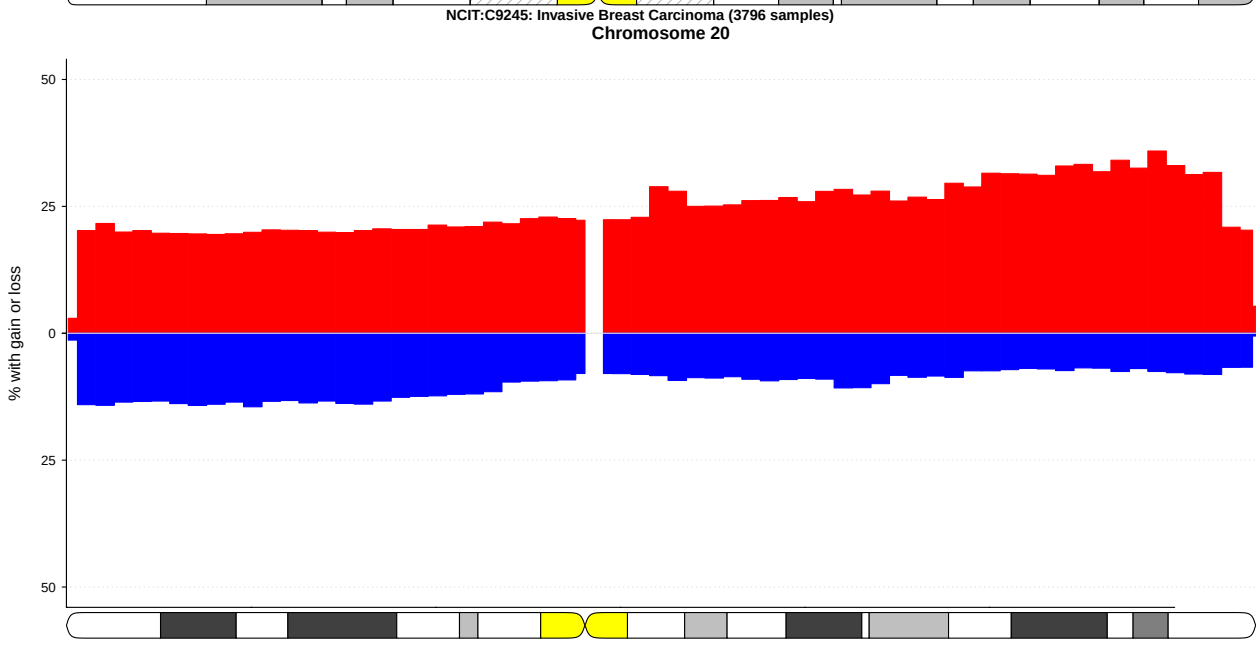

NCIT:C9245: Invasive Breast Carcinoma (3796 samples)
Chromosome 15
% with gain or loss
50
25
0
25
50

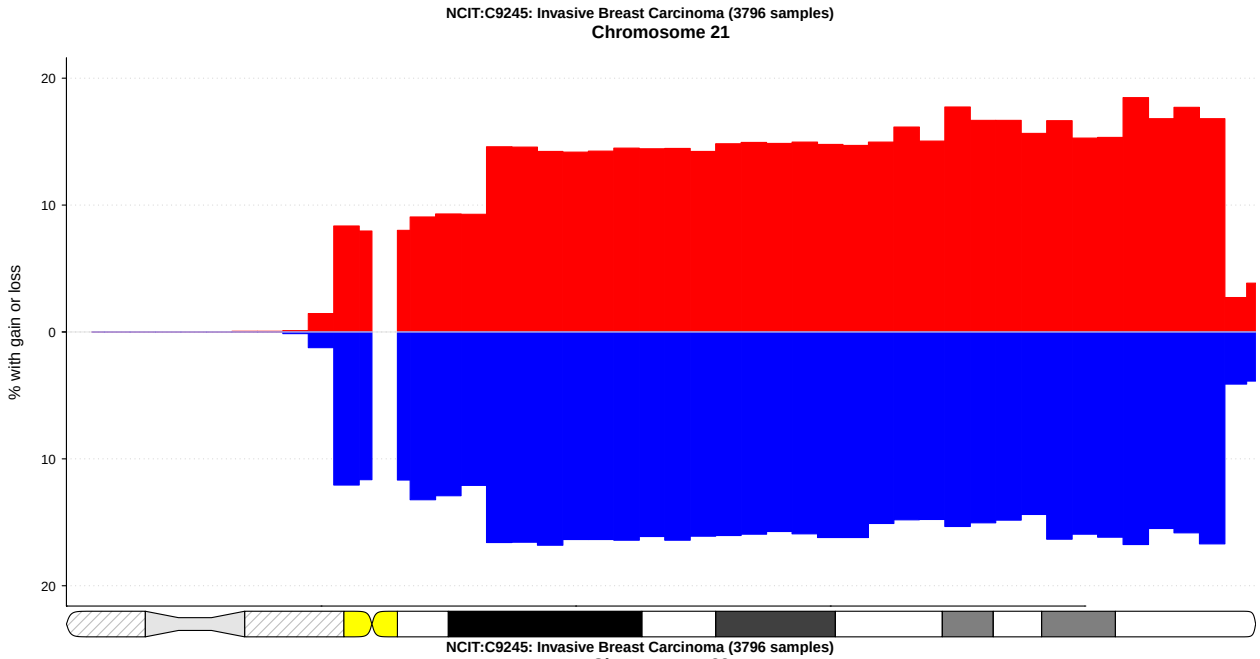

NCIT:C9245: Invasive Breast Carcinoma (3796 samples)
Chromosome 16
% with gain or loss
75
50
25
0
25
50
75

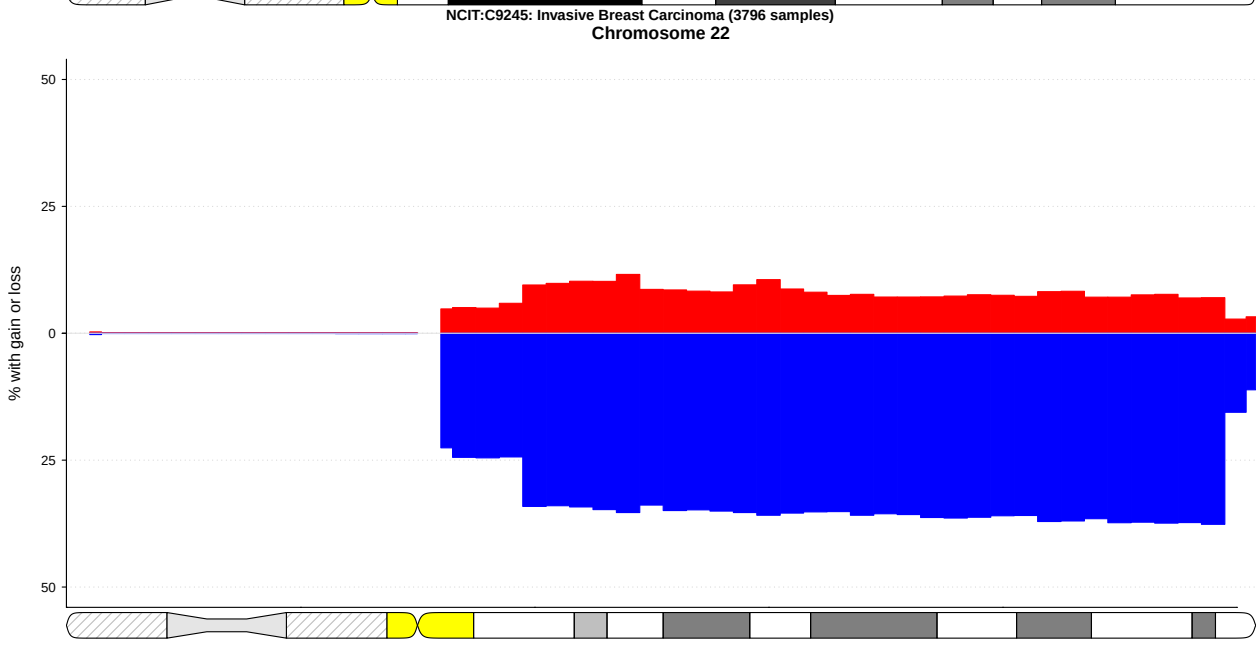

NCIT:C9245: Invasive Breast Carcinoma (3796 samples)
Chromosome 17
% with gain or loss
75
50
25
0
25
50
75


NCIT:C9245: Invasive Breast Carcinoma (3796 samples)
Chromosome 18
% with gain or loss
50
25
0
25
50


NCIT:C9245: Invasive Breast Carcinoma (3796 samples)
Chromosome 19
% with gain or loss
50
25
0
25
50


NCIT:C9245: Invasive Breast Carcinoma (3796 samples)
Chromosome 20
% with gain or loss
50
25
0
25
50





Step5: Analyse the data

According the plot, we can see frequent gains on chromosome 1q, 3q, 5p, 8q, 16p, 20q and frequent losses on chromosome 1p, 3p, 8p, 10q, 11q, 16q, 17p, 19p

There is literature where the findings are consistent with 1q,5q,16p,20q-gain and 11q,16q-loss.