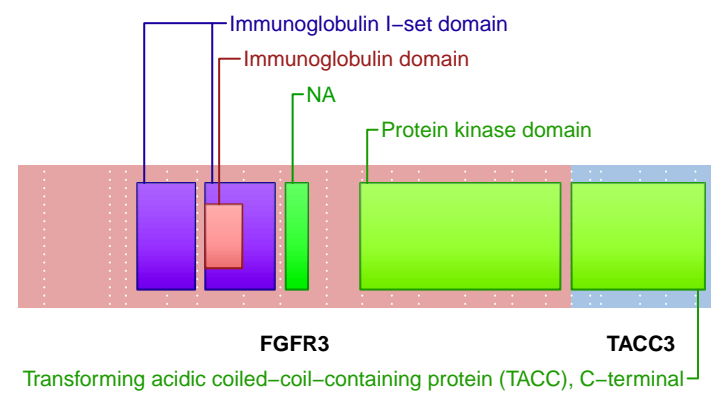


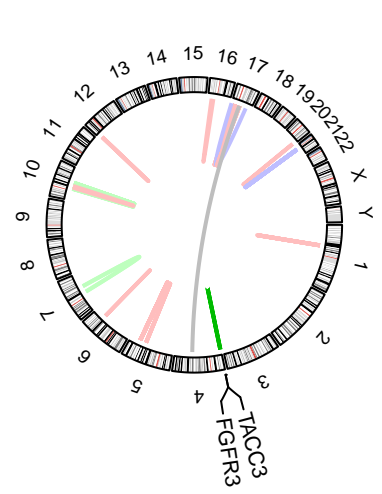
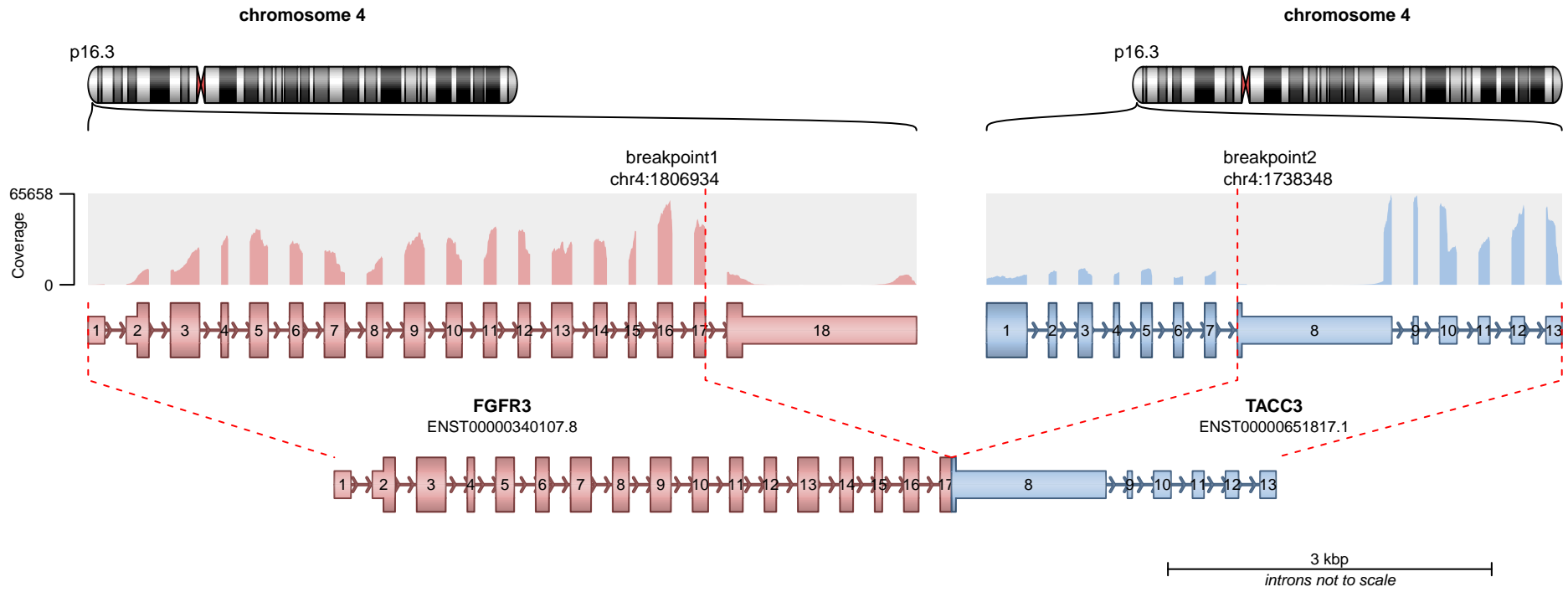
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



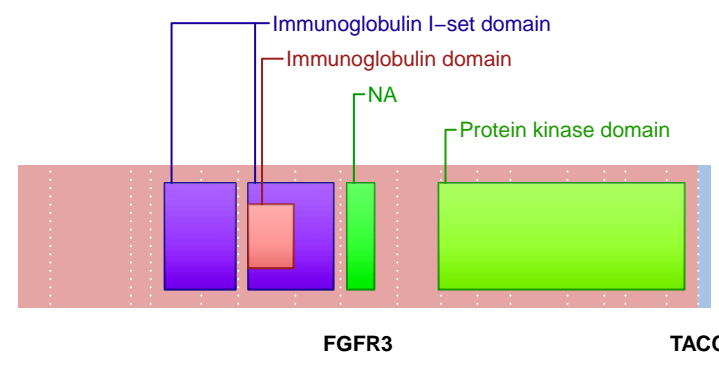
**SUPPORTING READ COUNT**

Split reads = 11036  
Discordant mates = 305

- translocation
- duplication
- deletion
- inversion



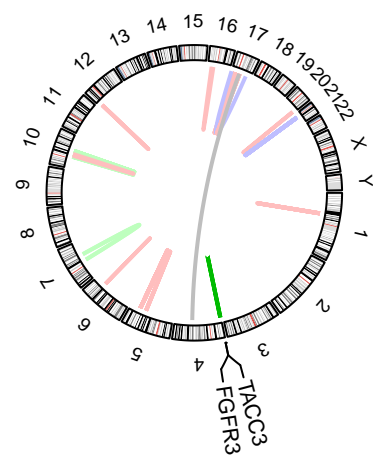
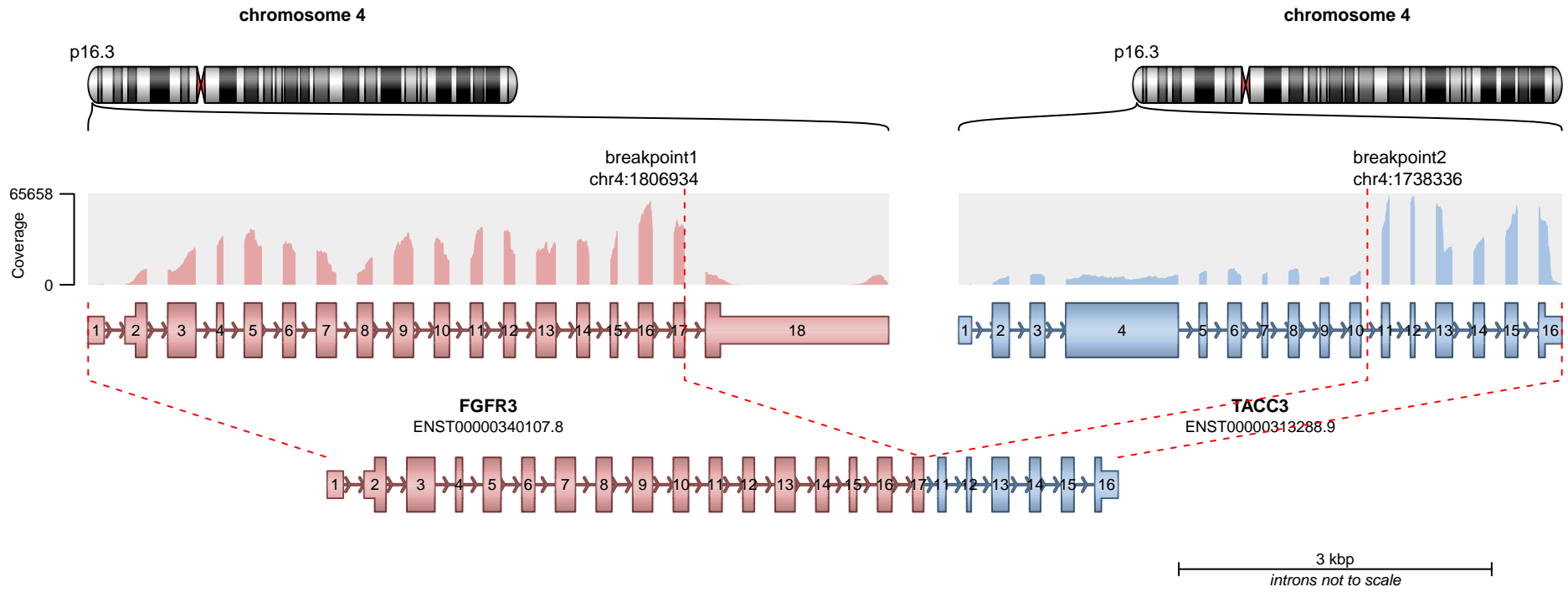
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



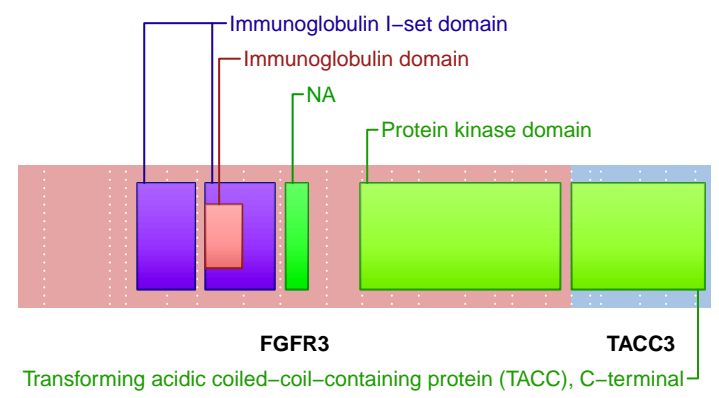
**SUPPORTING READ COUNT**

Split reads = 138  
Discordant mates = 308

- translocation
- duplication
- deletion
- inversion



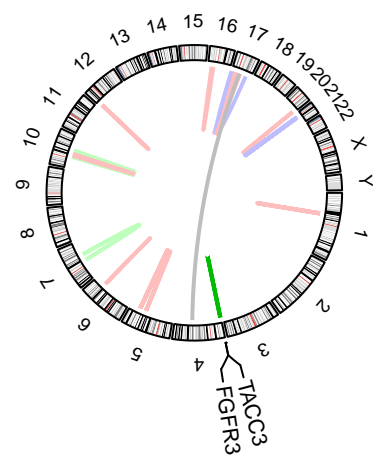
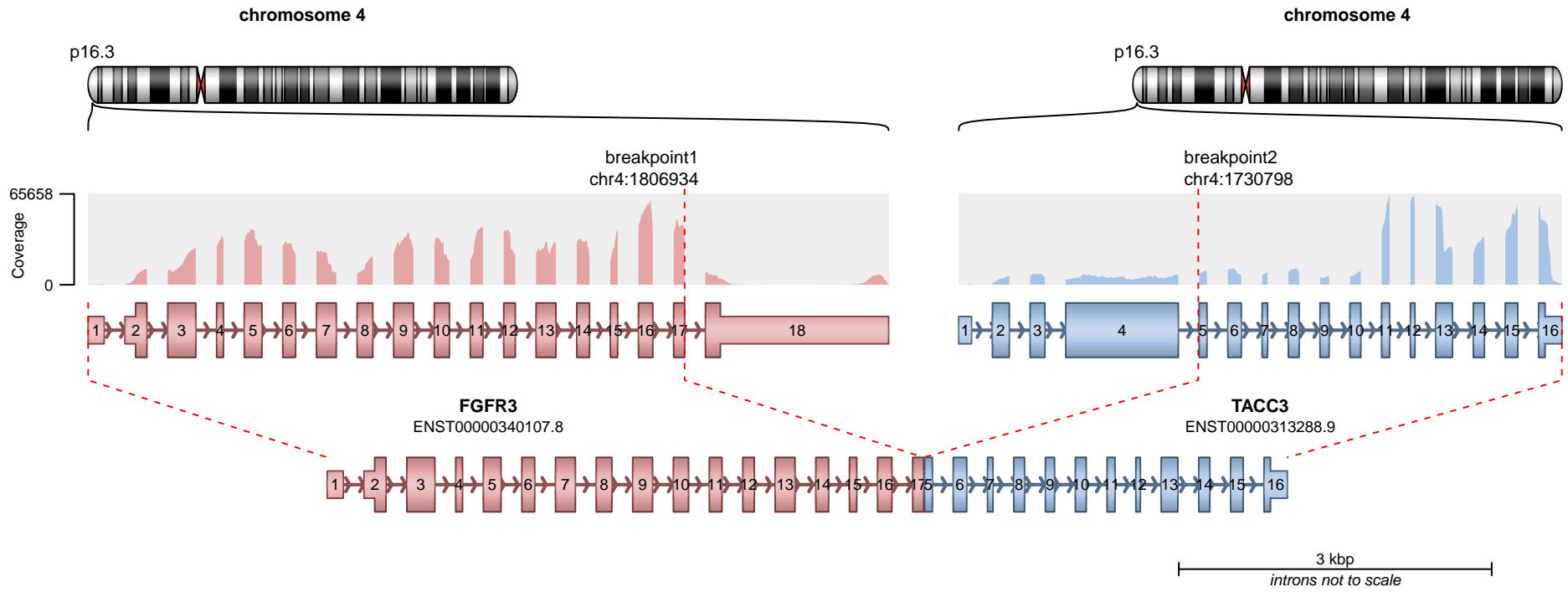
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



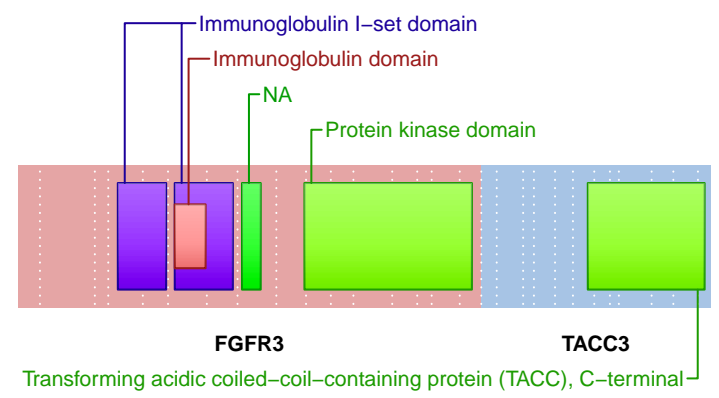
**SUPPORTING READ COUNT**

Split reads = 8  
Discordant mates = 308

- translocation
- duplication
- deletion
- inversion



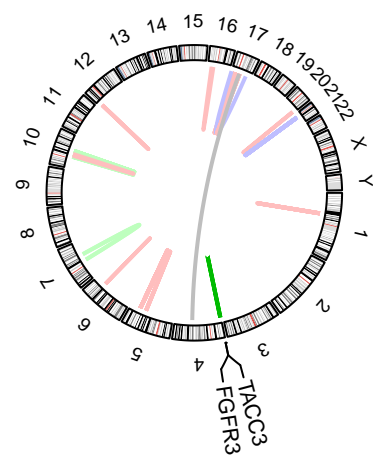
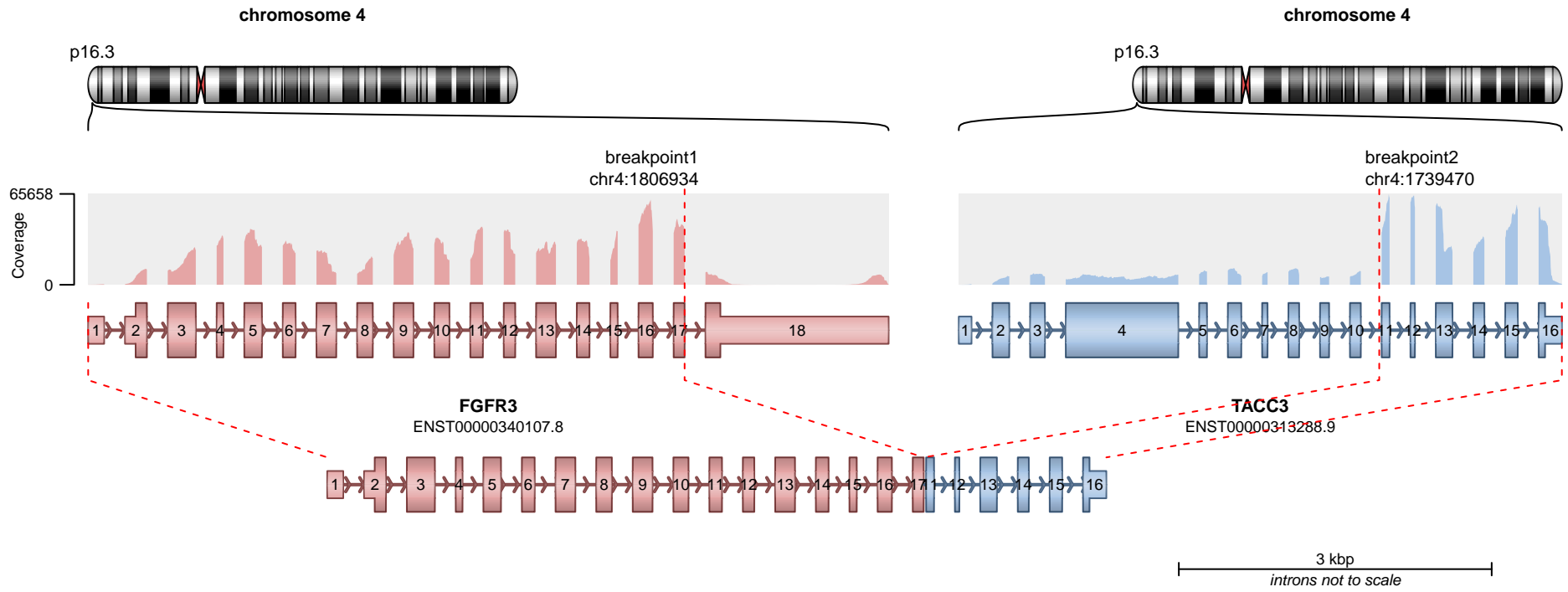
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



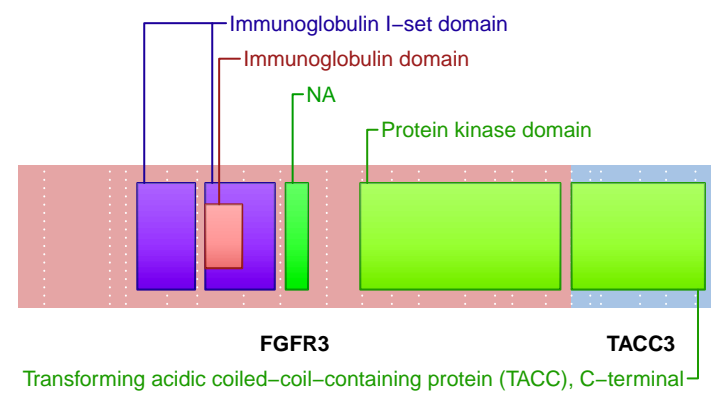
**SUPPORTING READ COUNT**

Split reads = 7  
Discordant mates = 308

- translocation
- duplication
- deletion
- inversion



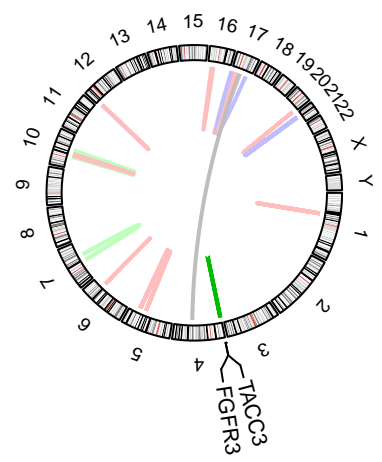
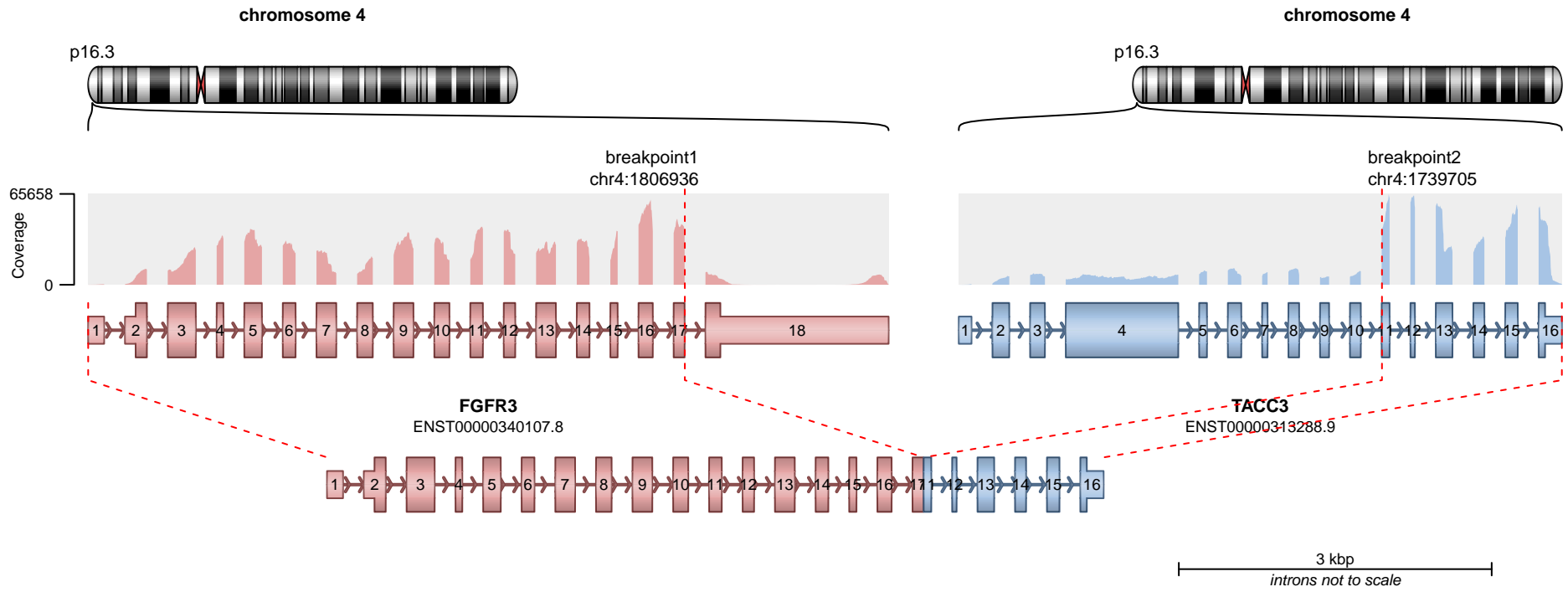
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



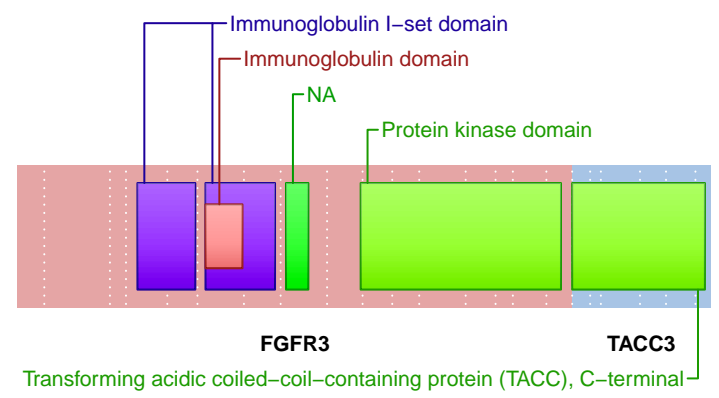
**SUPPORTING READ COUNT**

Split reads = 5  
Discordant mates = 305

- translocation
- duplication
- deletion
- inversion

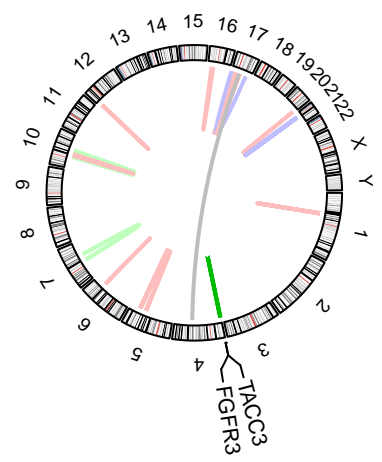
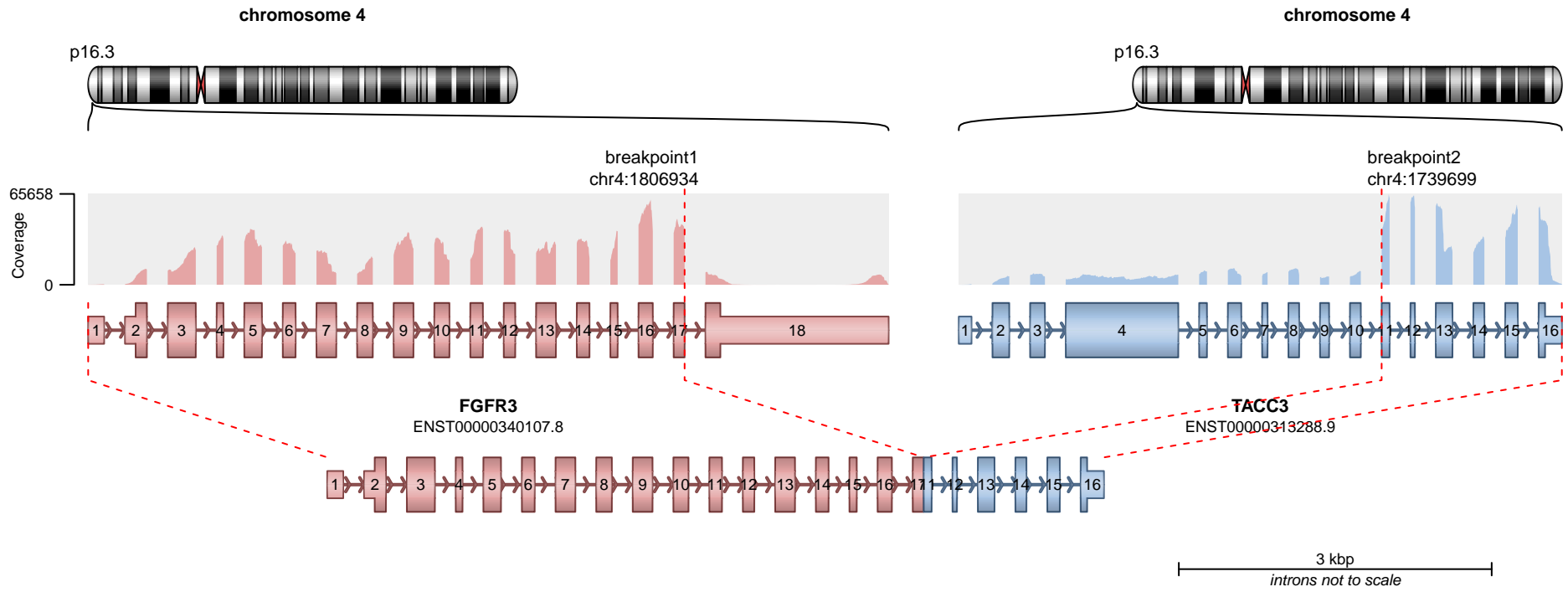


**RETAINED PROTEIN DOMAINS**  
reading frame unclear

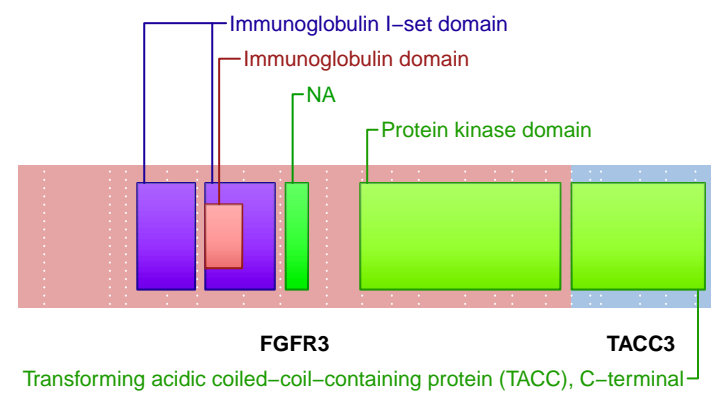


**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 305



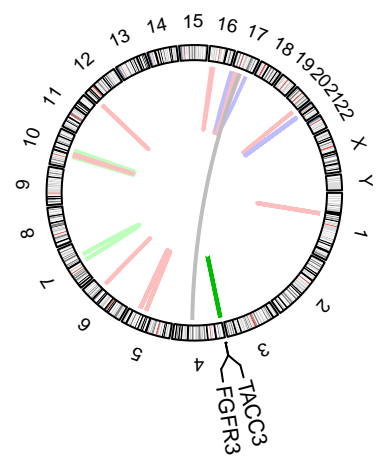
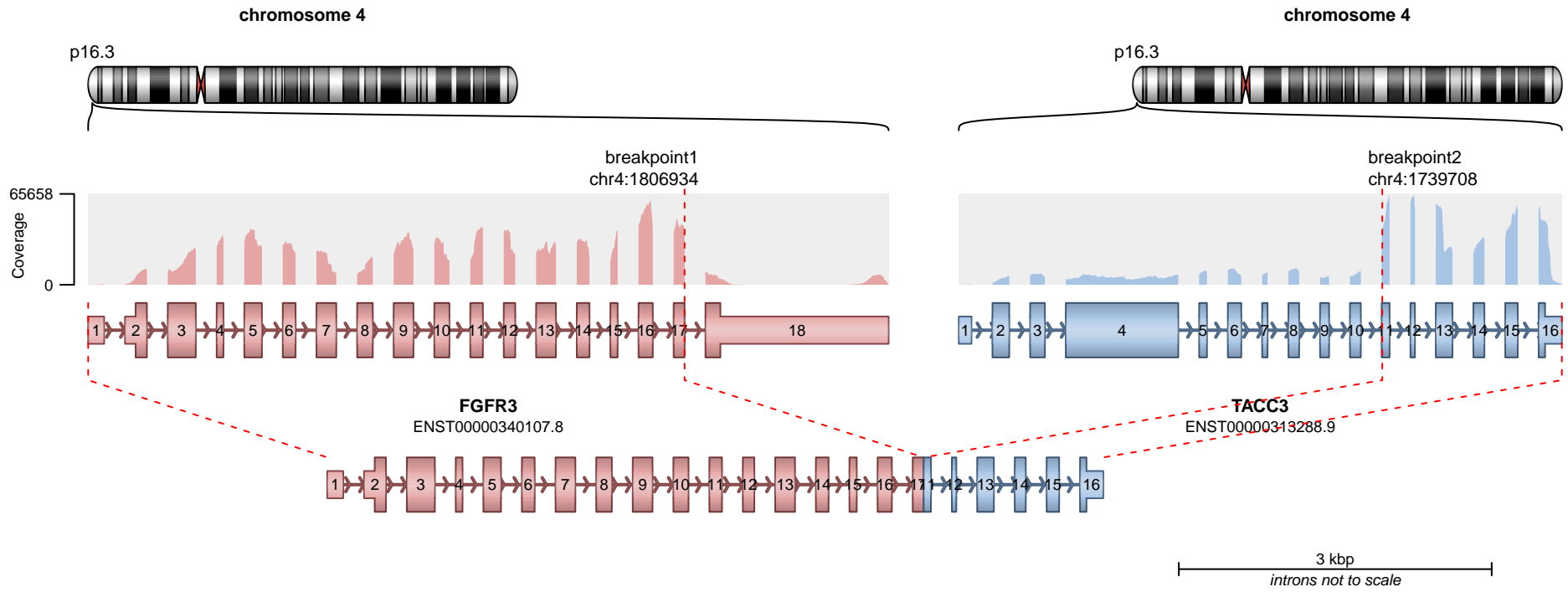
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



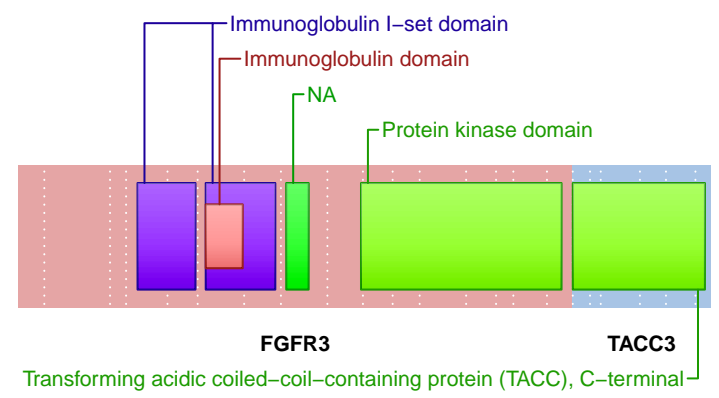
**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 305

- translocation
- duplication
- deletion
- inversion



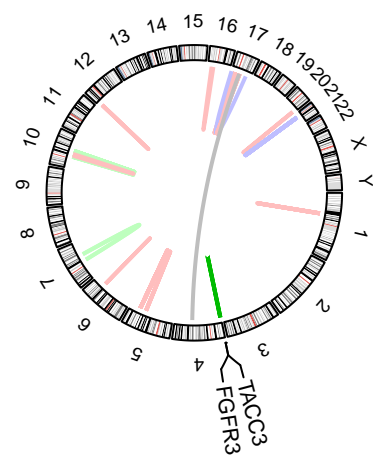
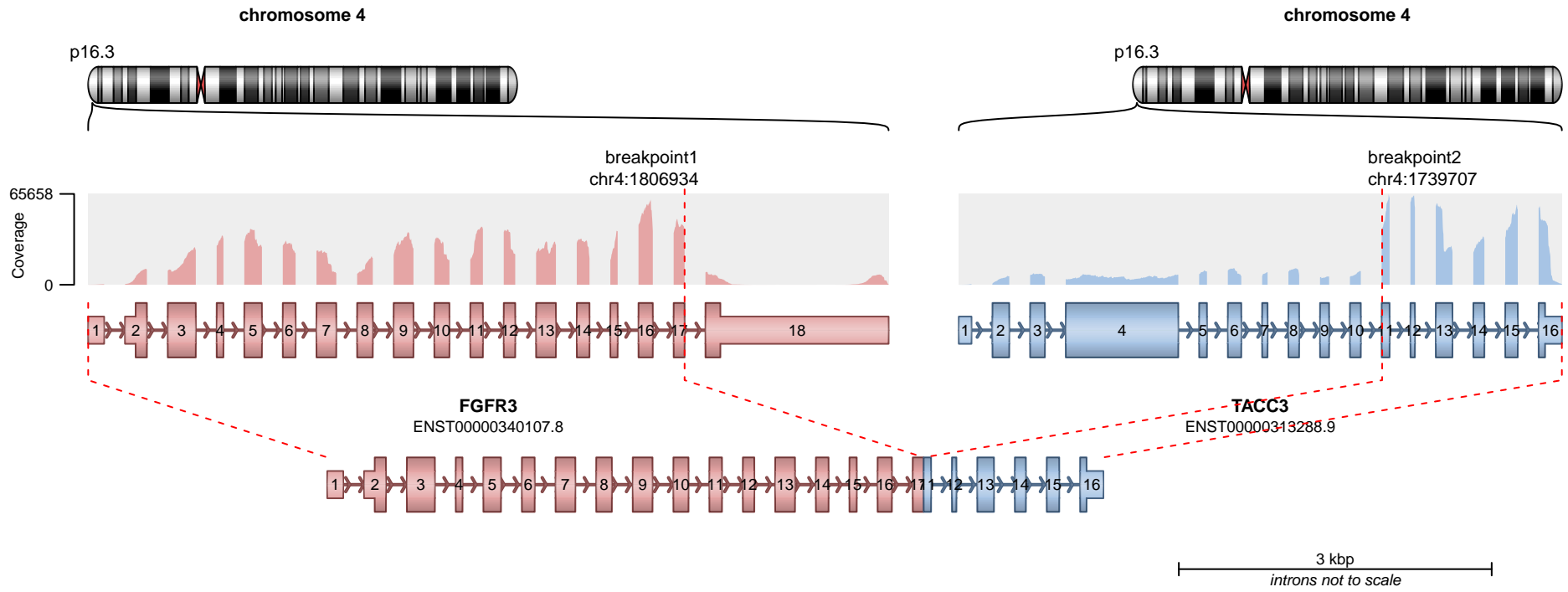
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



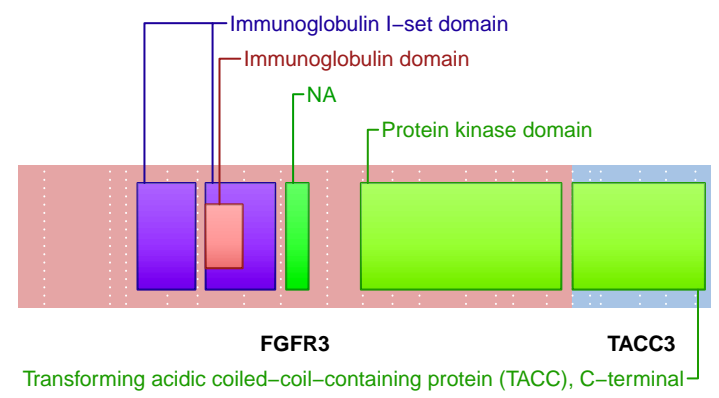
**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 294

- translocation
- duplication
- deletion
- inversion



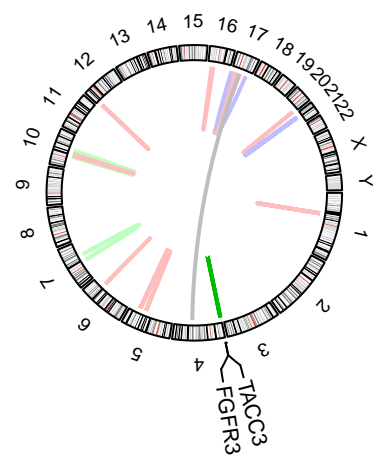
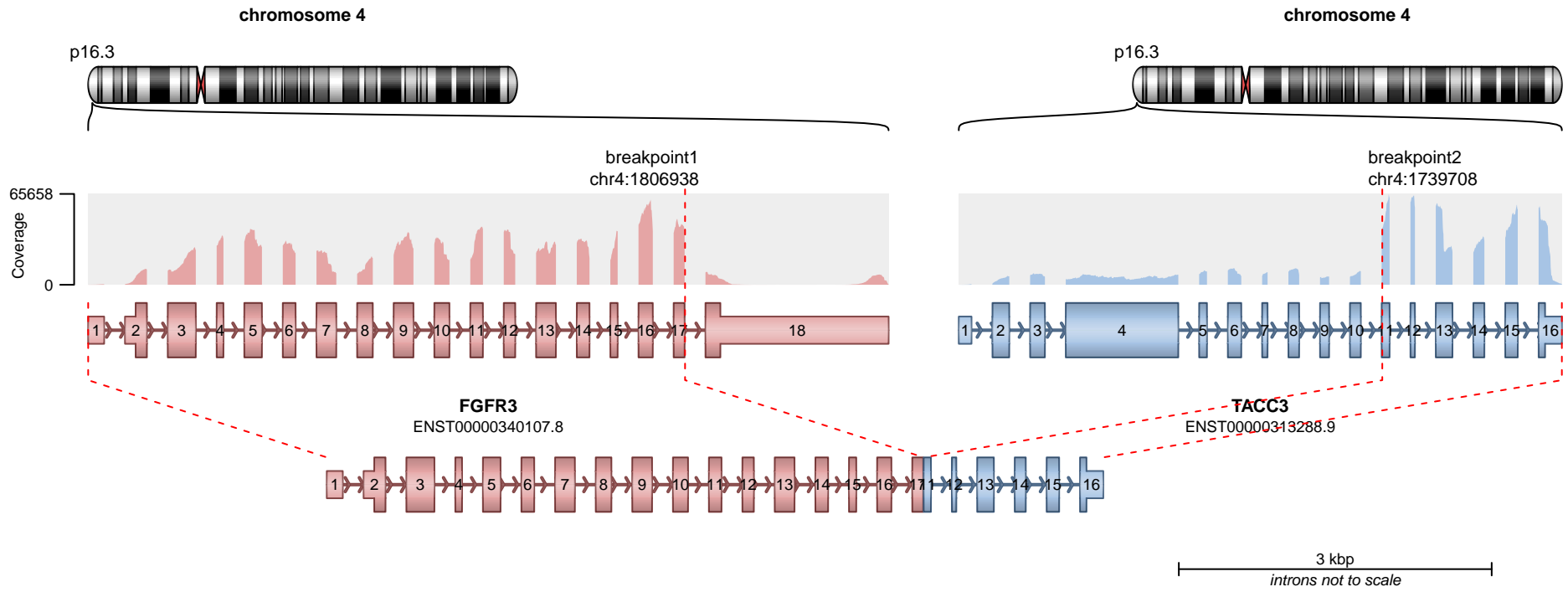
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



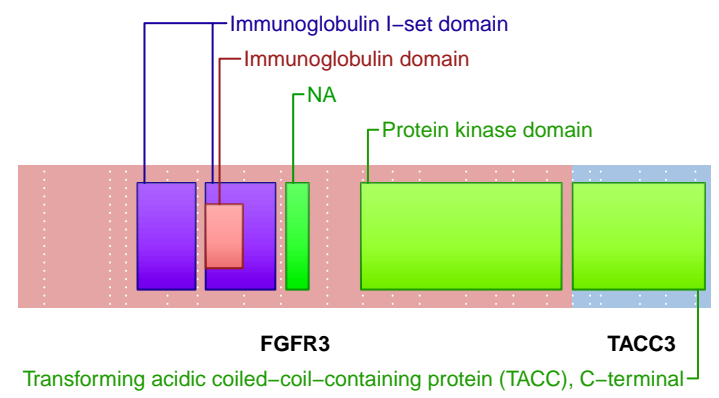
**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 295

- translocation
- duplication
- deletion
- inversion



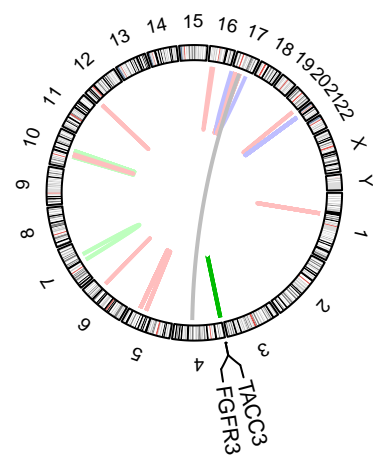
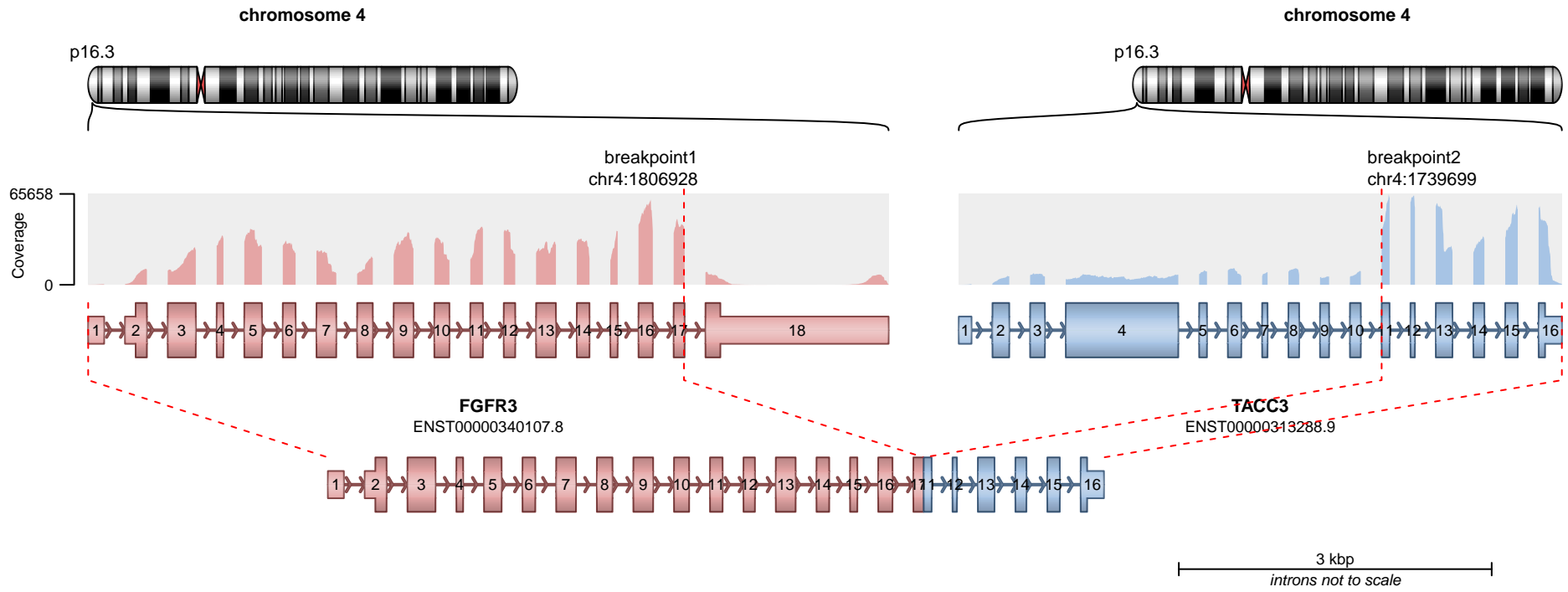
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



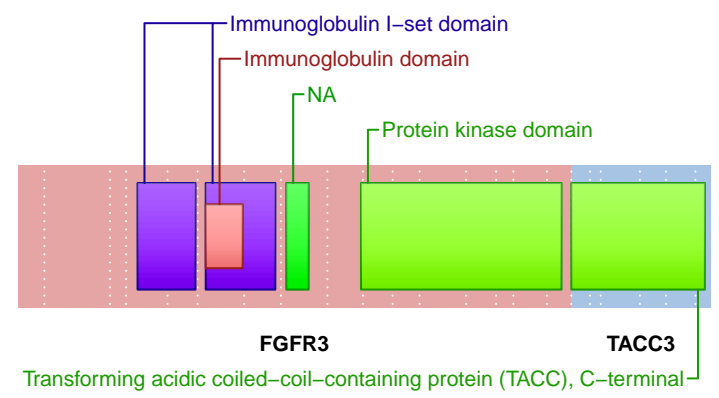
**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 294

- translocation
- duplication
- deletion
- inversion



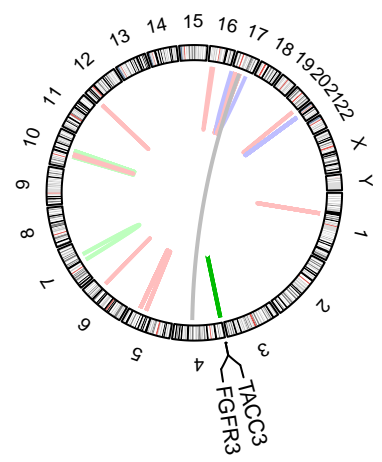
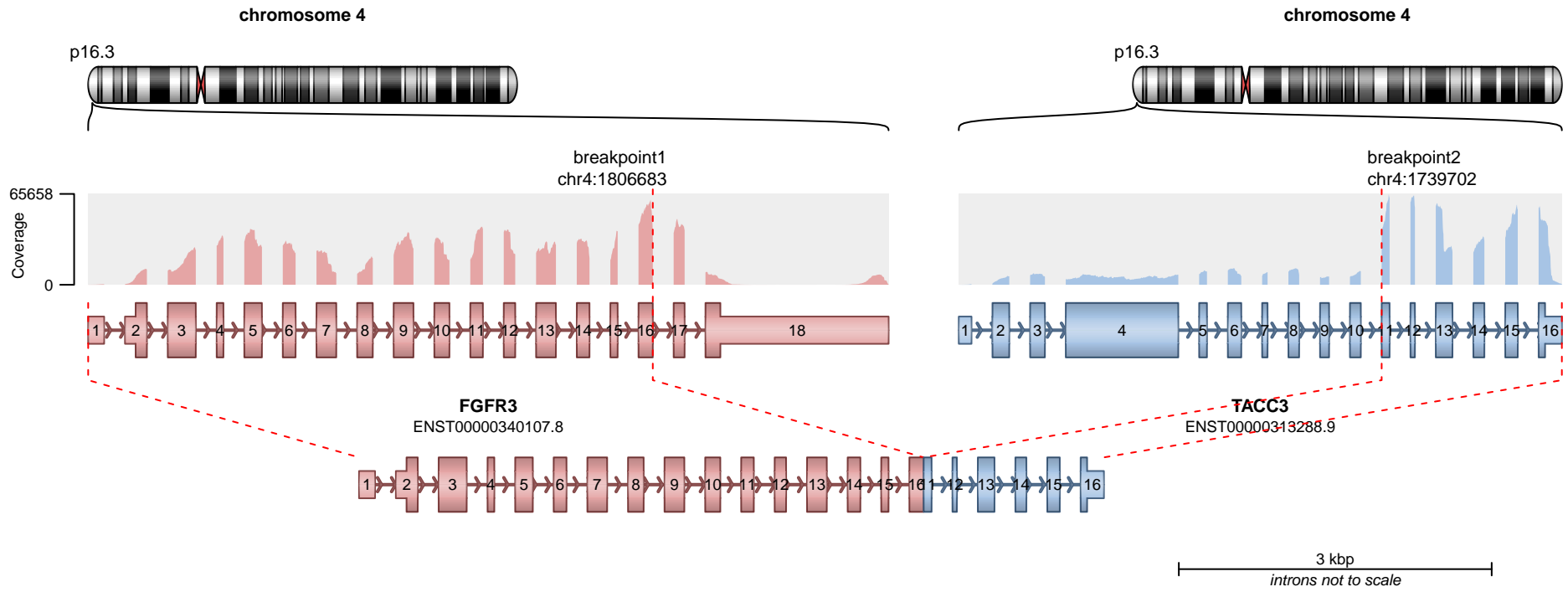
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



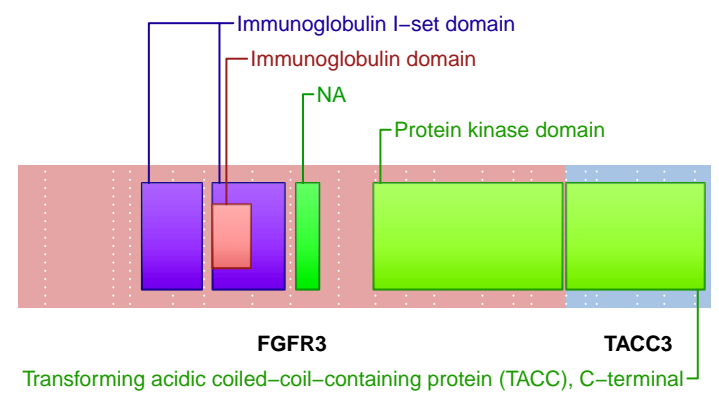
**SUPPORTING READ COUNT**

Split reads = 8  
Discordant mates = 237

- translocation
- duplication
- deletion
- inversion



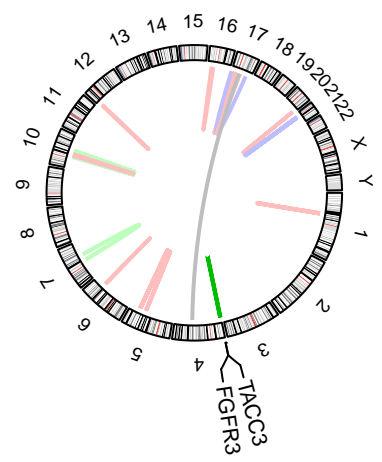
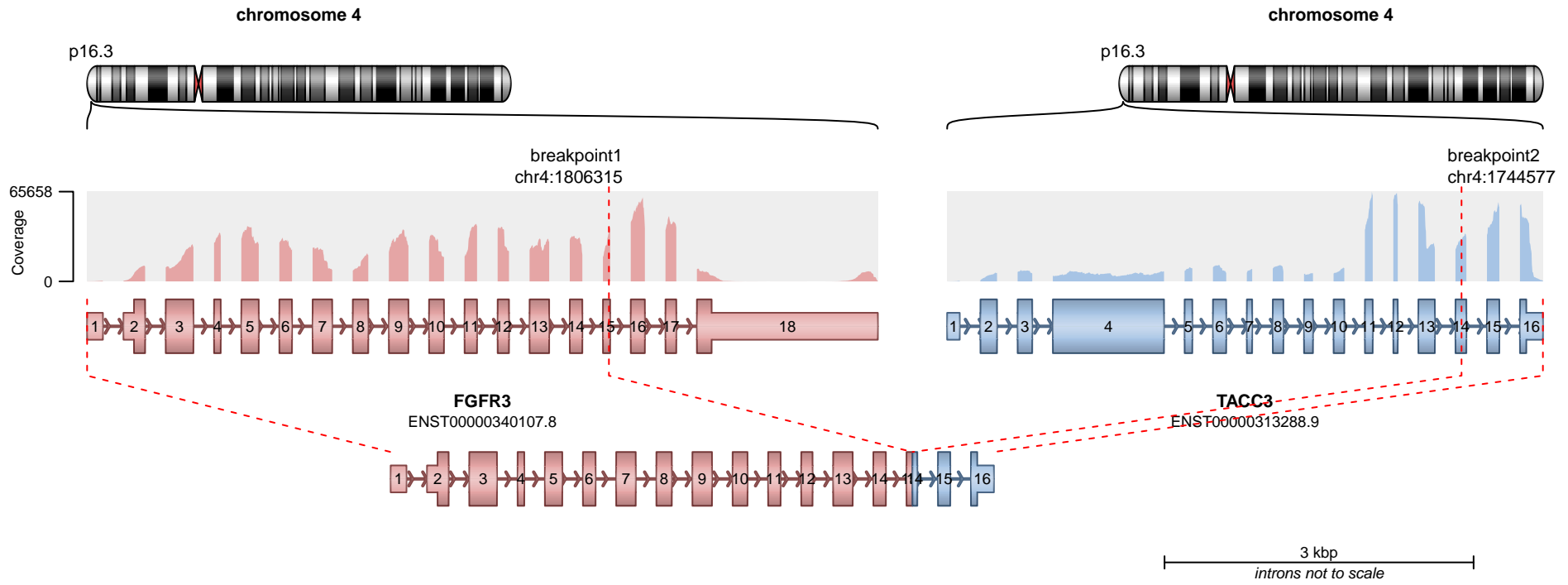
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



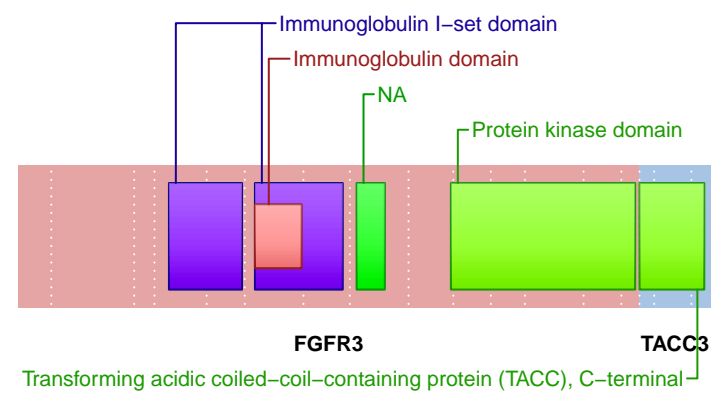
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 32

- translocation
- duplication
- deletion
- inversion



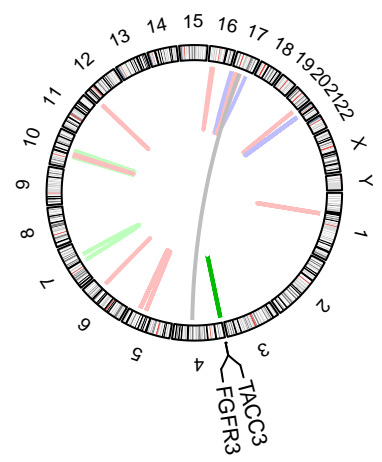
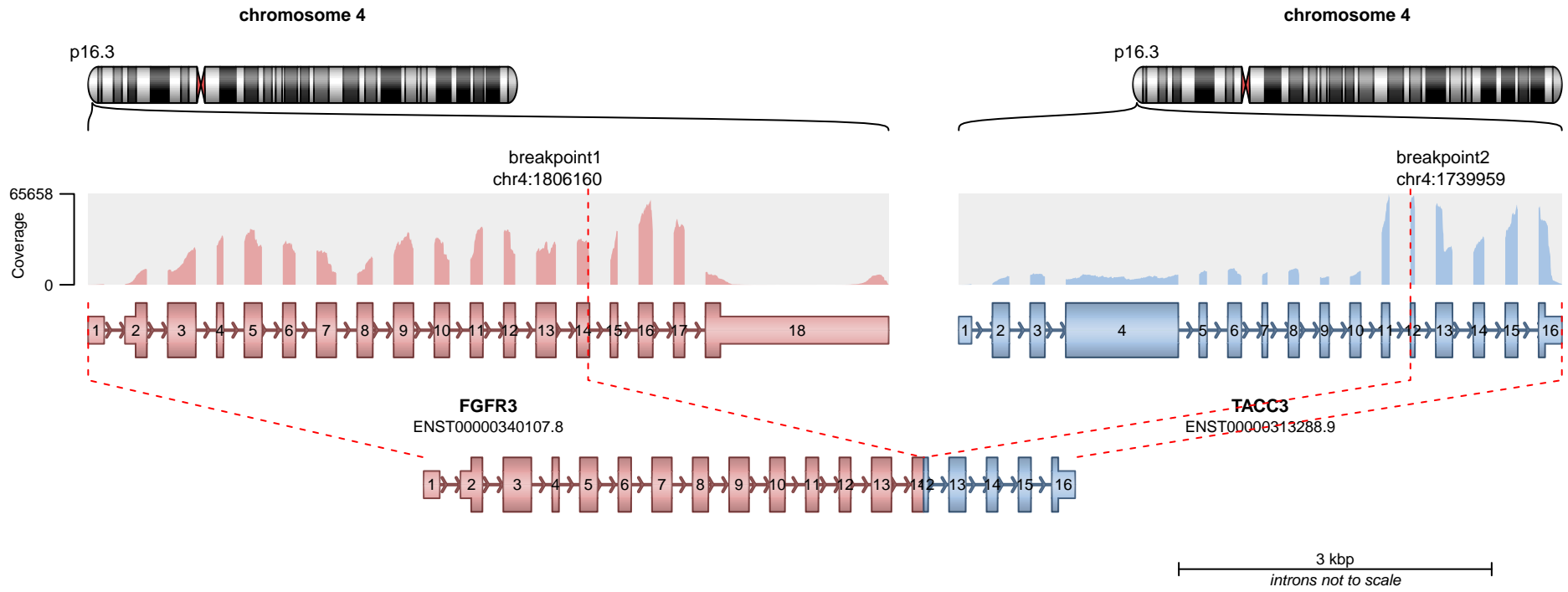
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



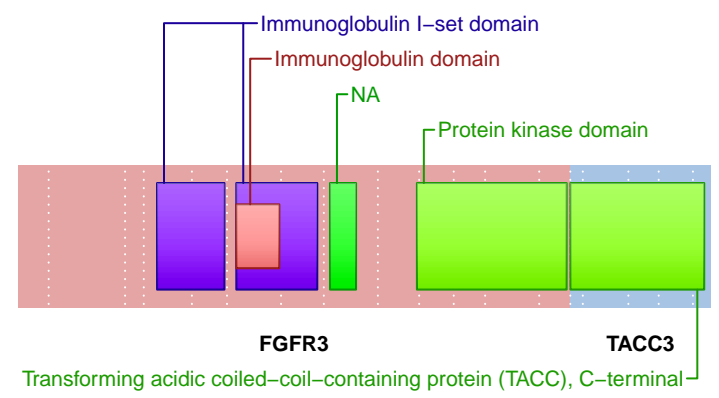
**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



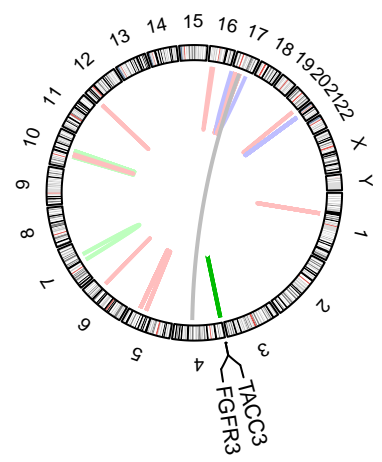
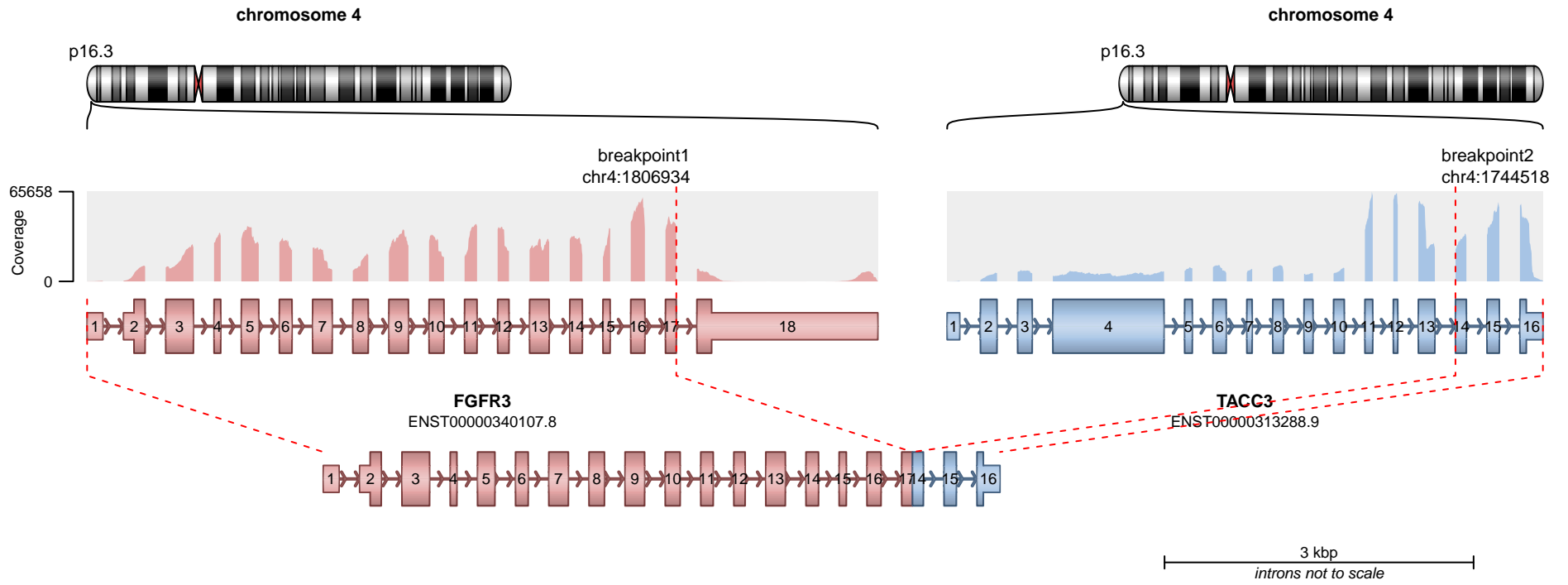
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



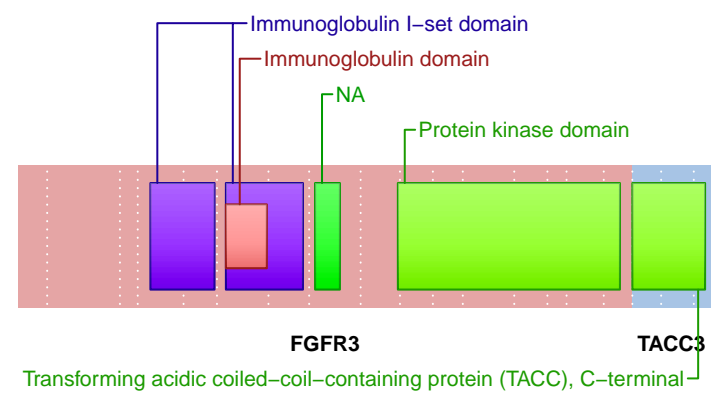
**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



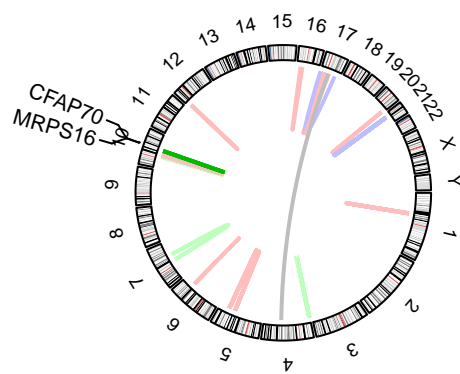
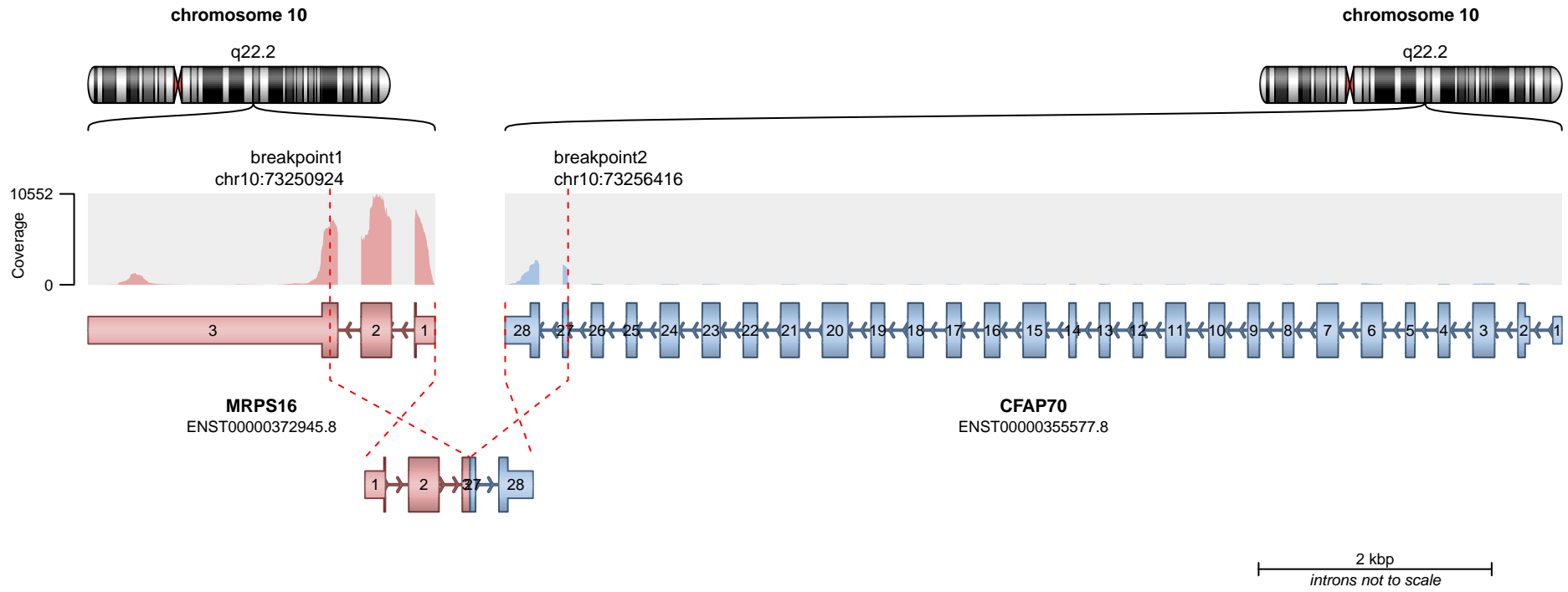
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



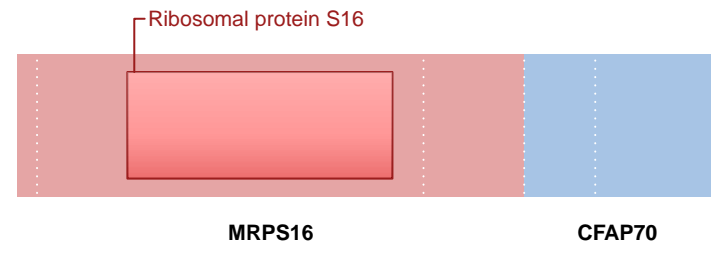
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



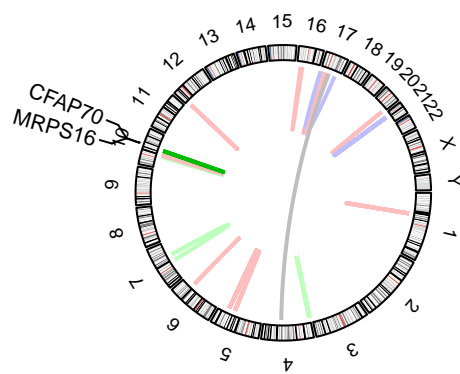
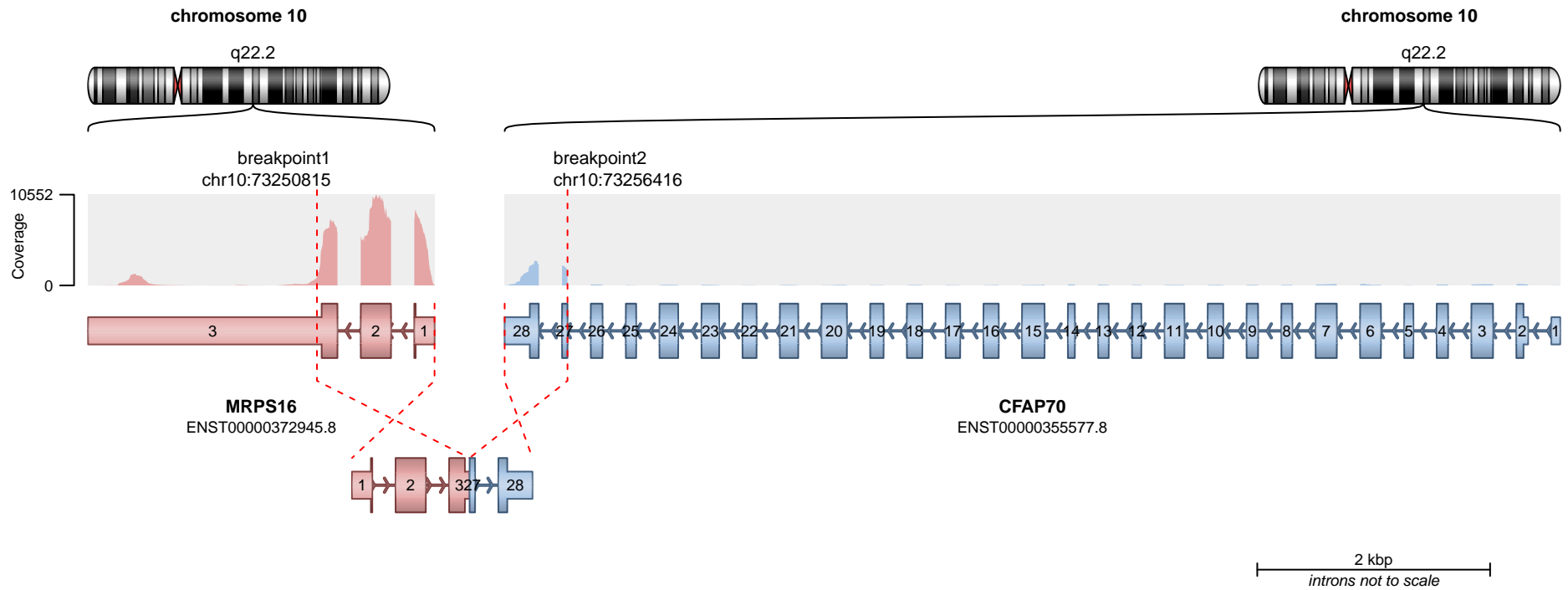
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



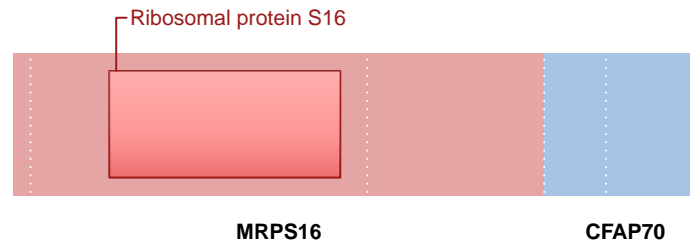
**SUPPORTING READ COUNT**

Split reads = 408  
Discordant mates = 11

- translocation
- duplication
- deletion
- inversion



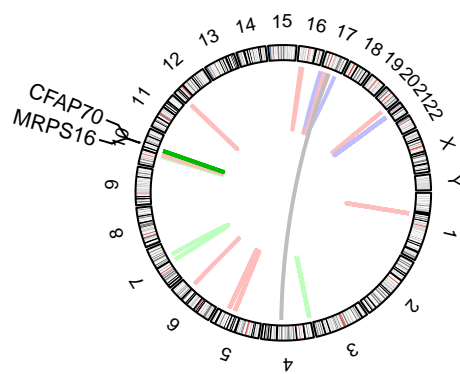
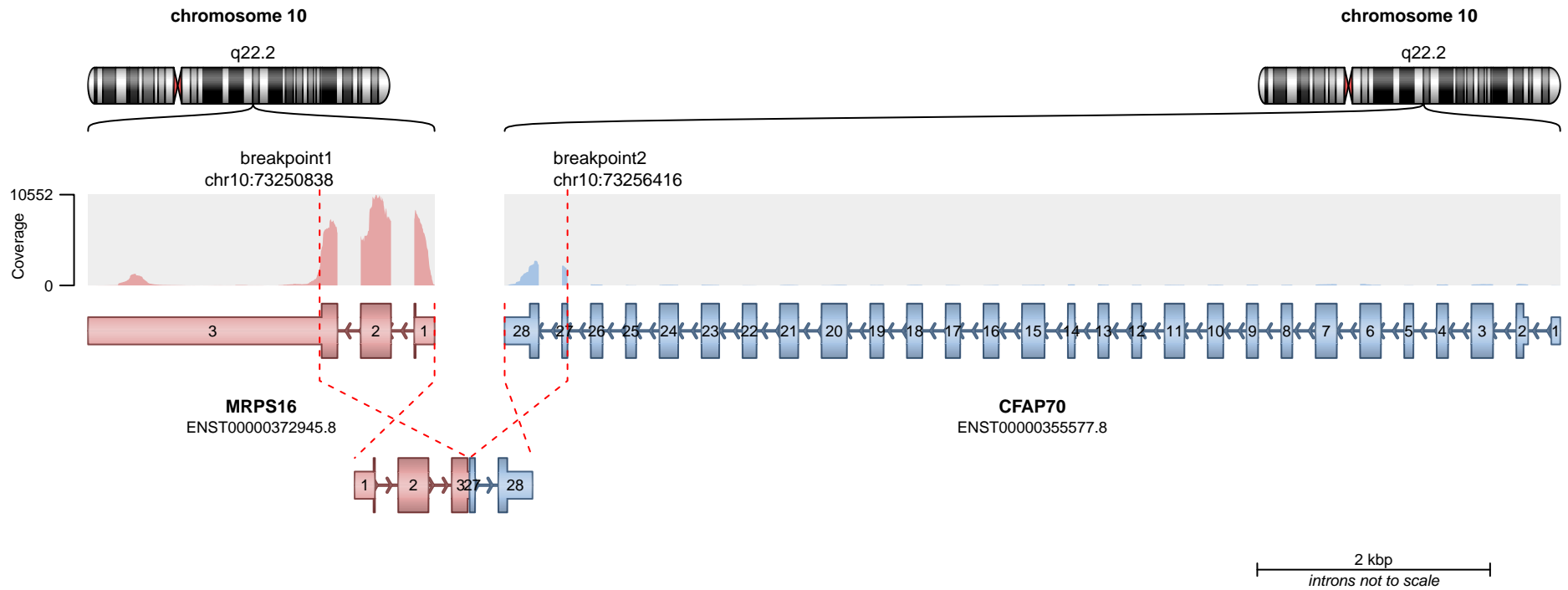
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



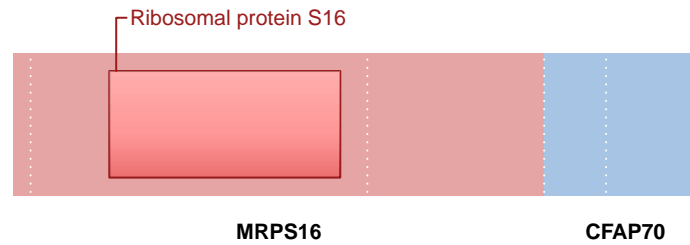
**SUPPORTING READ COUNT**

Split reads = 188  
Discordant mates = 23

- translocation
- duplication
- deletion
- inversion



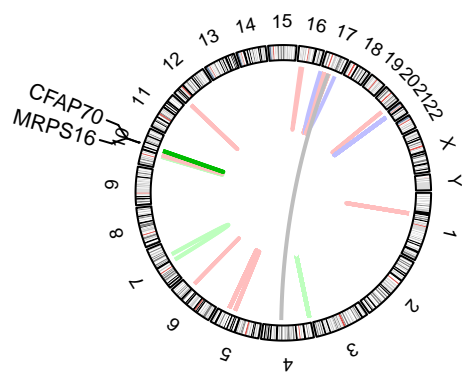
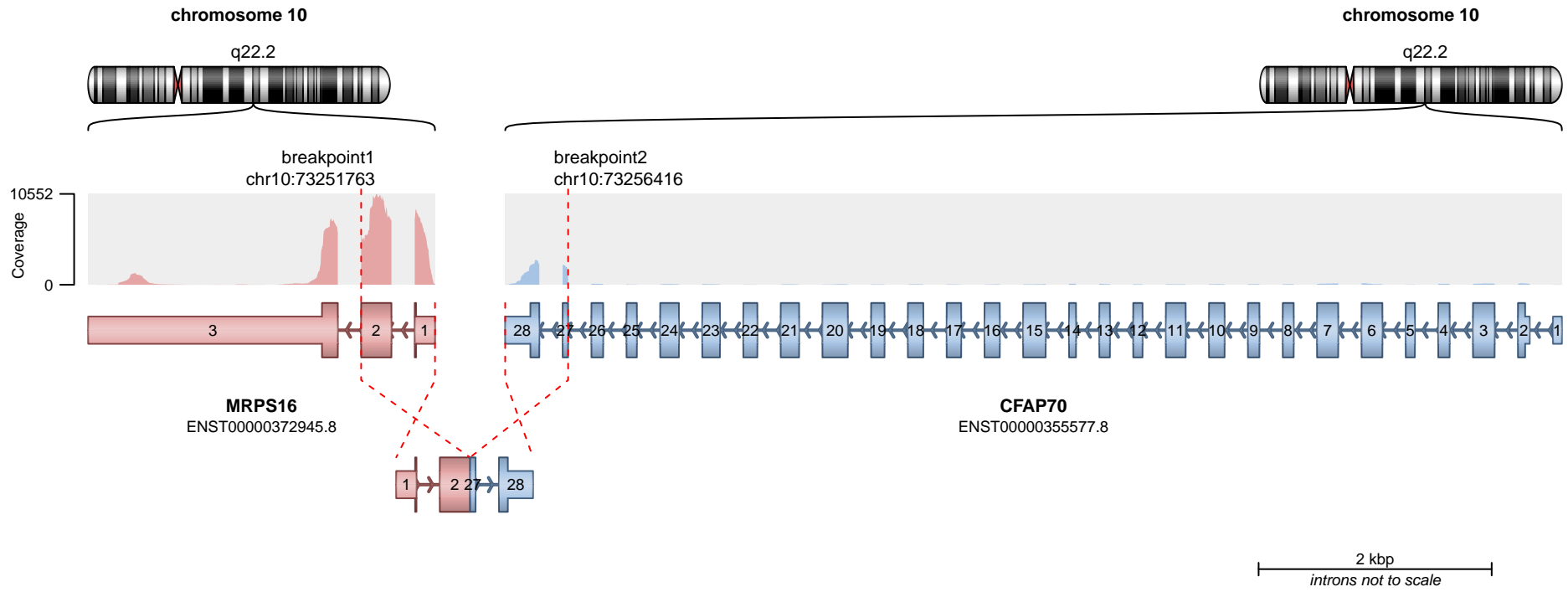
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



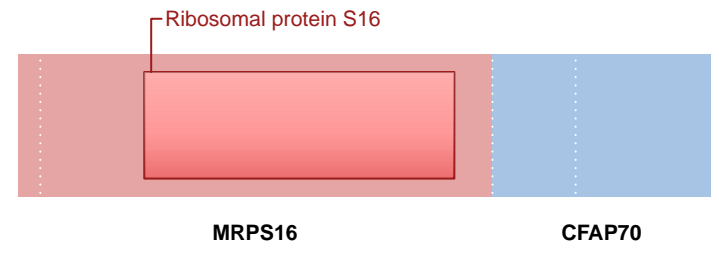
**SUPPORTING READ COUNT**

Split reads = 126  
Discordant mates = 21

— translocation    — deletion  
— duplication    — inversion



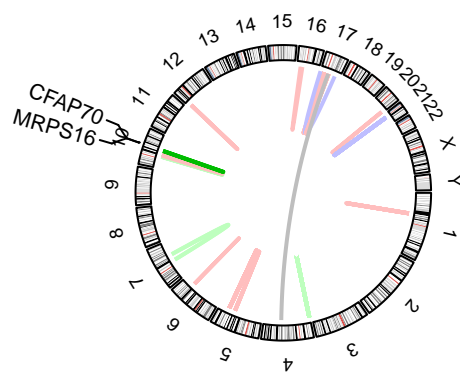
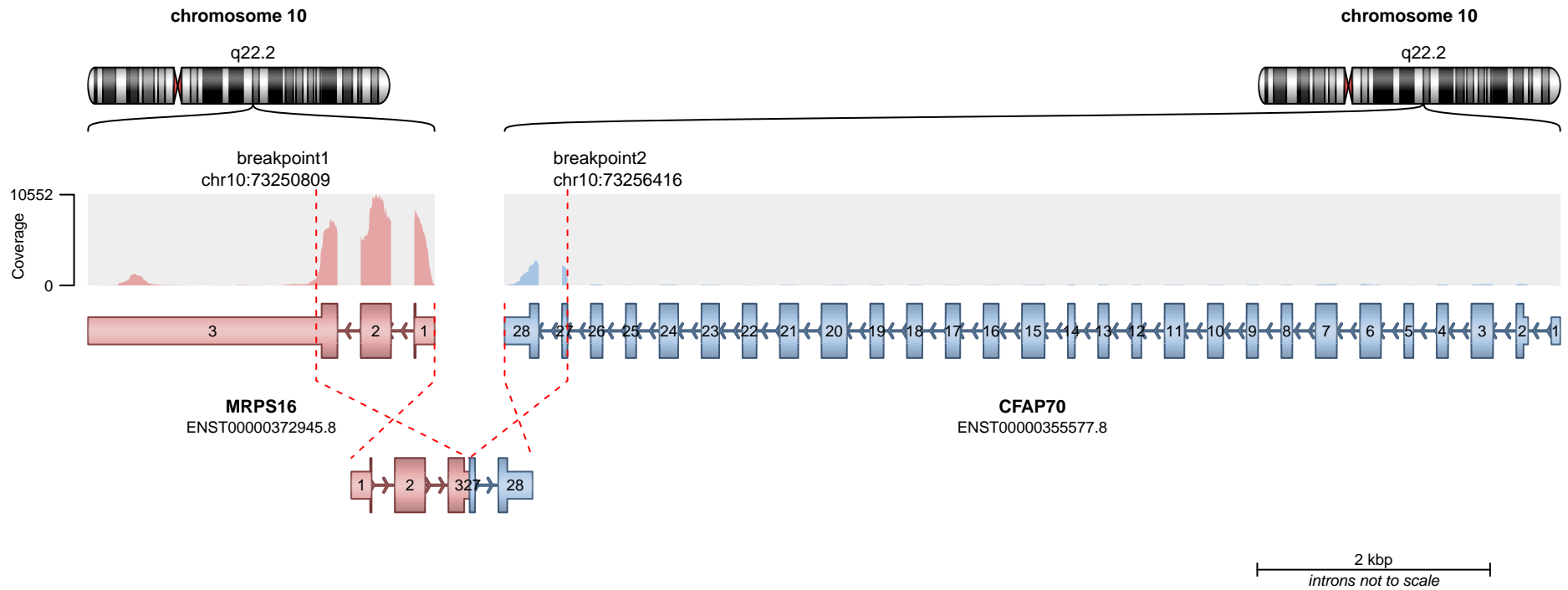
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



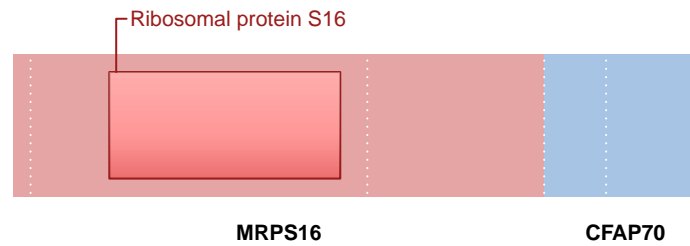
**SUPPORTING READ COUNT**

Split reads = 60  
Discordant mates = 4

- translocation
- duplication
- deletion
- inversion



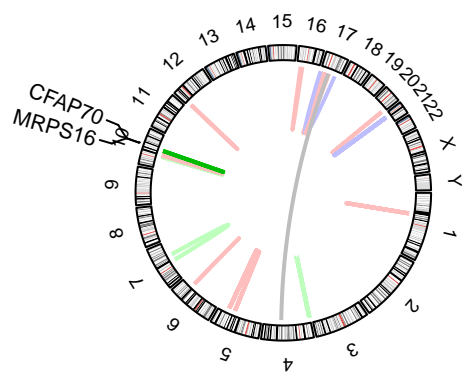
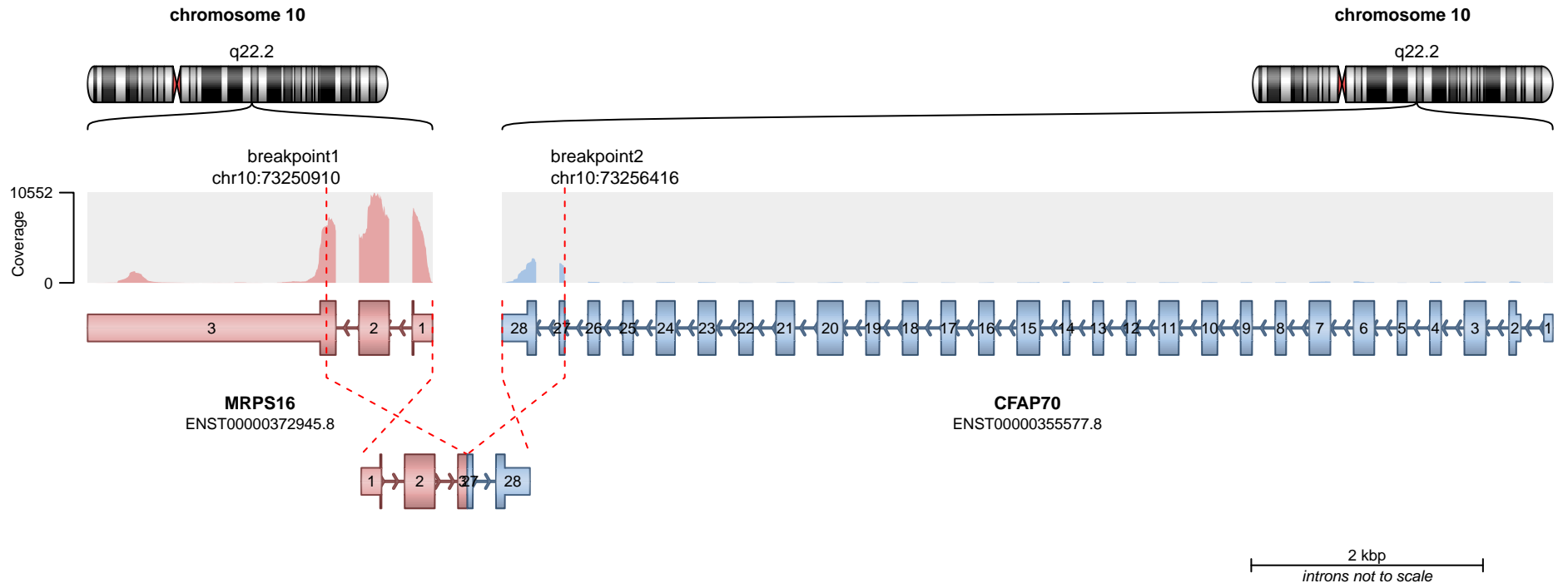
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



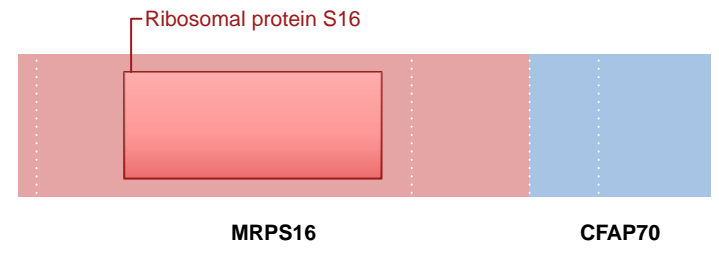
**SUPPORTING READ COUNT**

Split reads = 29  
Discordant mates = 23

- translocation
- duplication
- deletion
- inversion



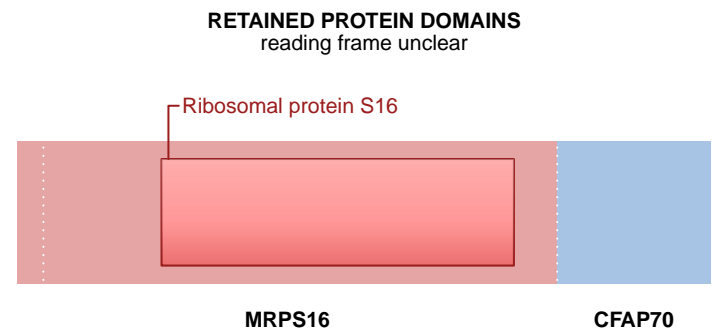
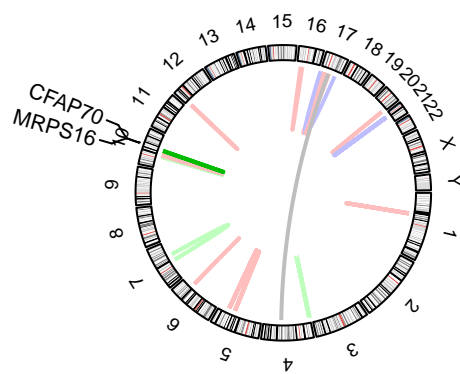
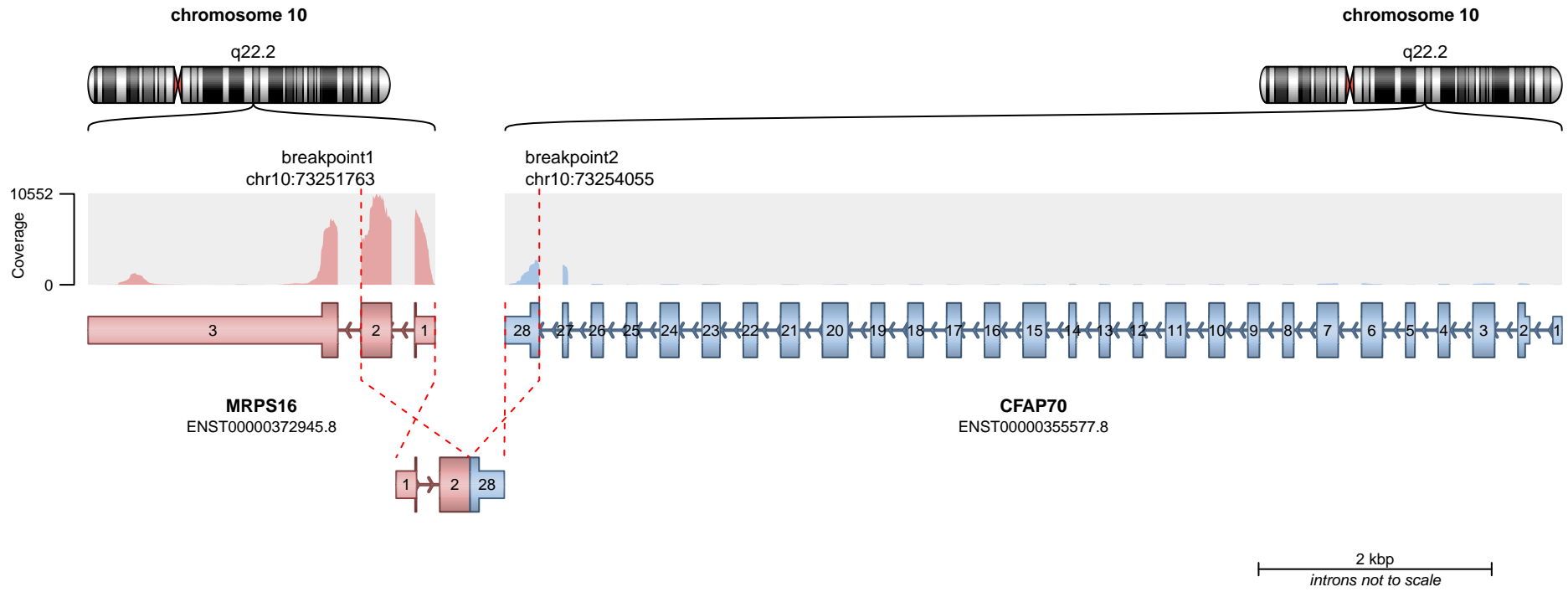
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 7  
Discordant mates = 12

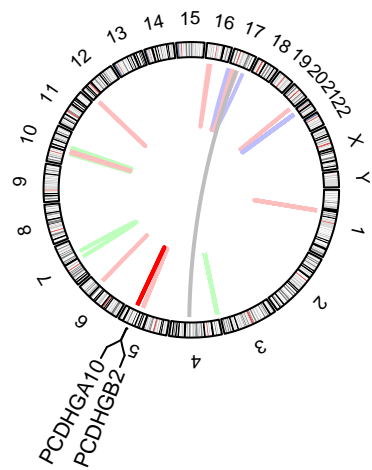
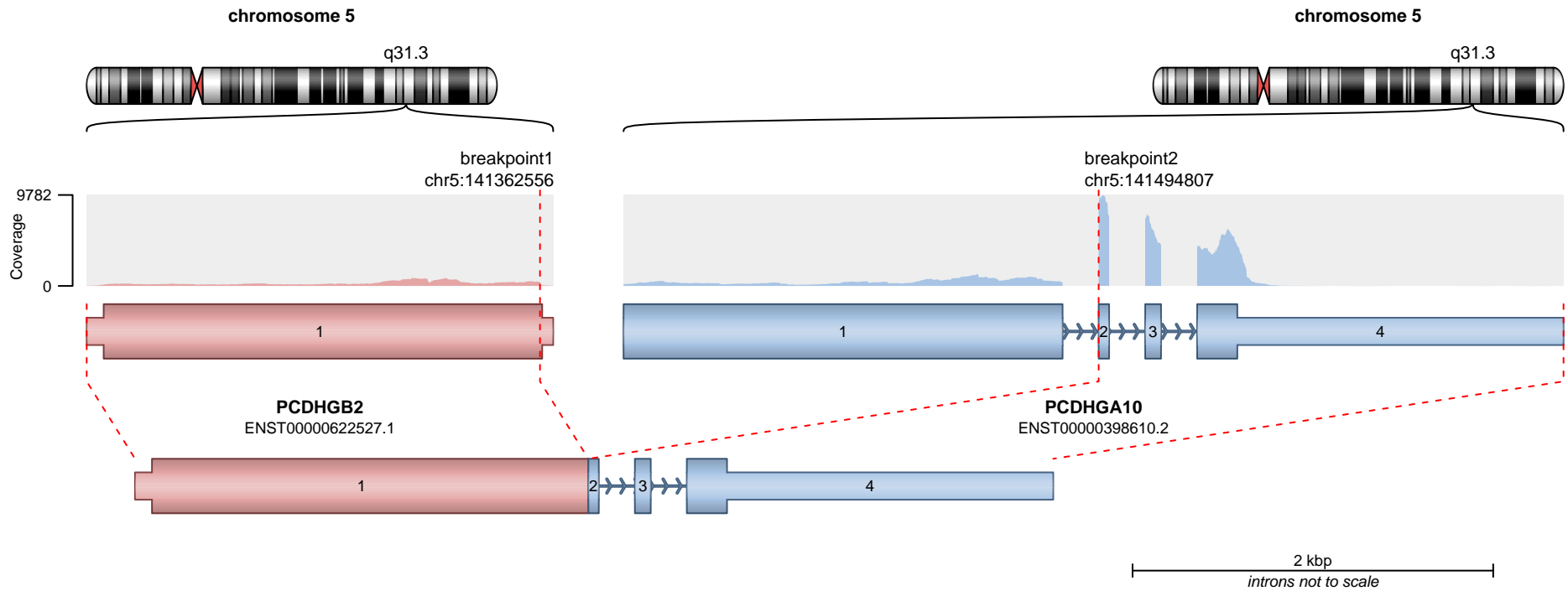
- translocation
- duplication
- deletion
- inversion



**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 4

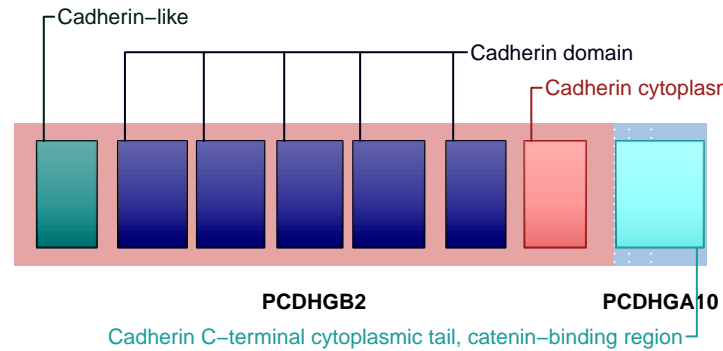
translocation (grey line) deletion (red line)  
duplication (green line) inversion (blue line)



— translocation — deletion  
— duplication — inversion

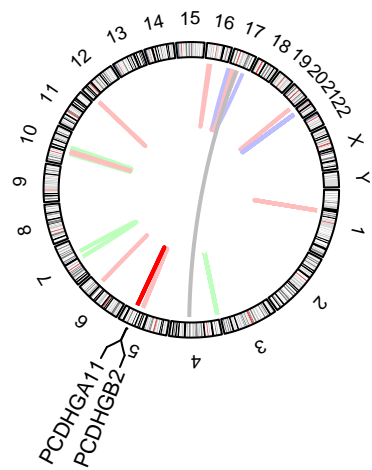
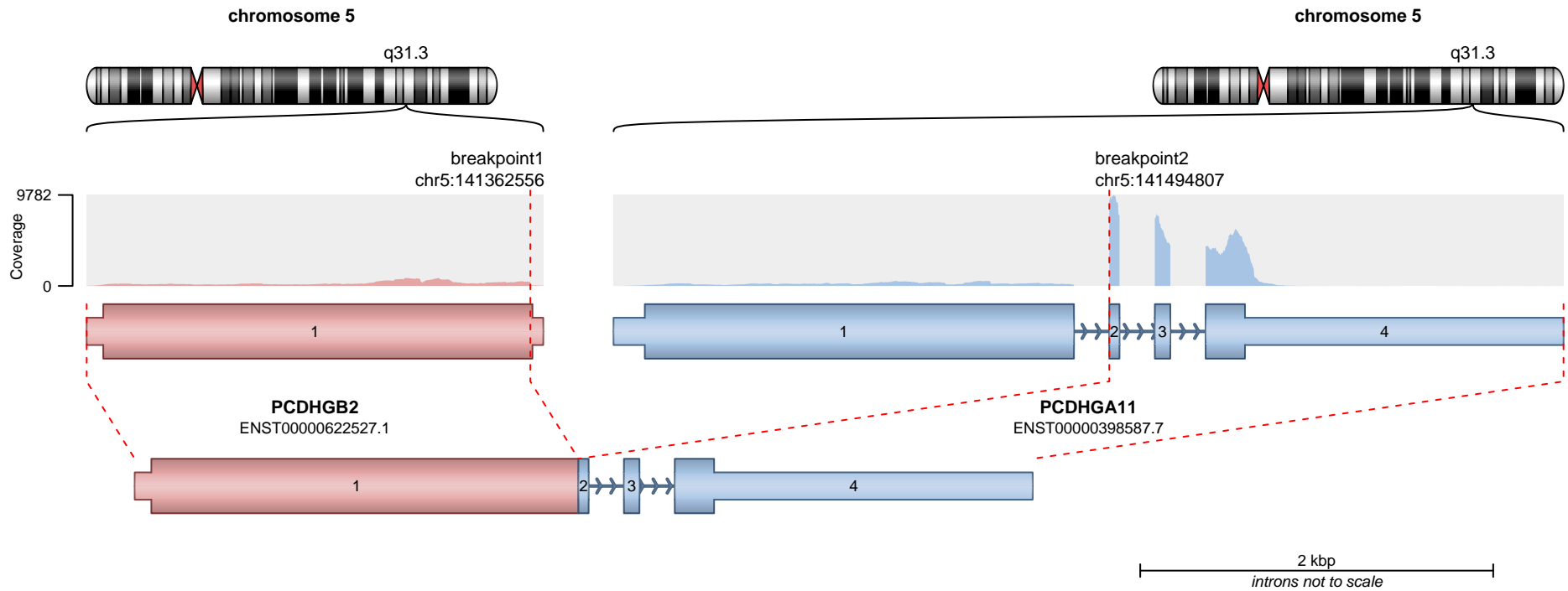
### RETAINED PROTEIN DOMAINS

reading frame unclear



### SUPPORTING READ COUNT

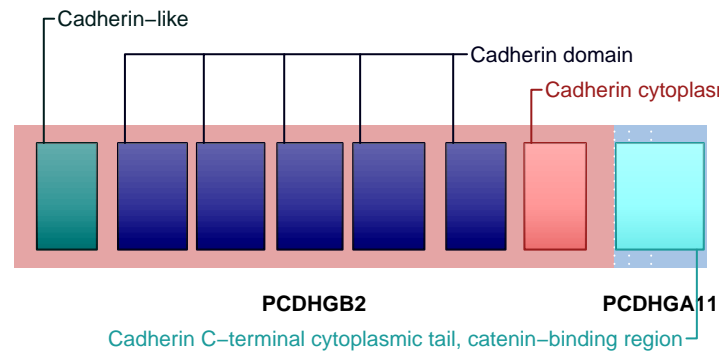
Split reads = 154  
Discordant mates = 0



— translocation — deletion  
— duplication — inversion

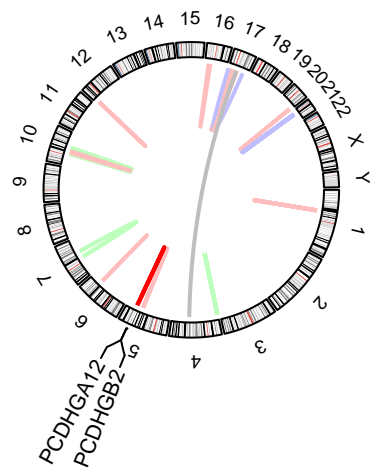
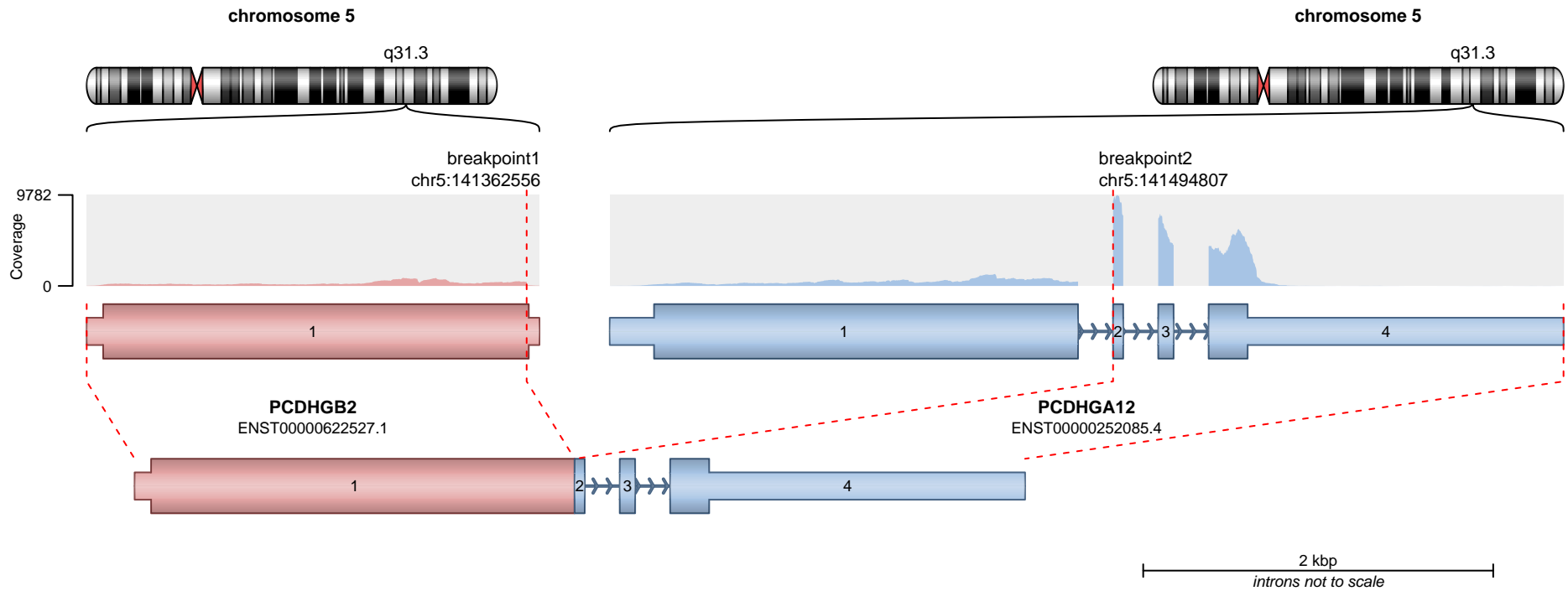
### RETAINED PROTEIN DOMAINS

reading frame unclear



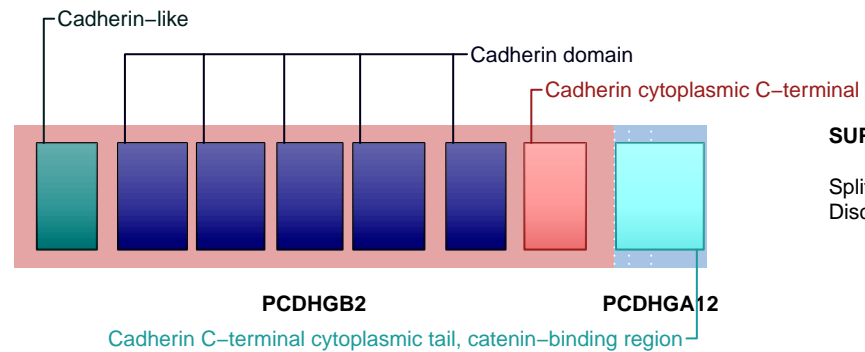
### SUPPORTING READ COUNT

Split reads = 154  
Discordant mates = 0



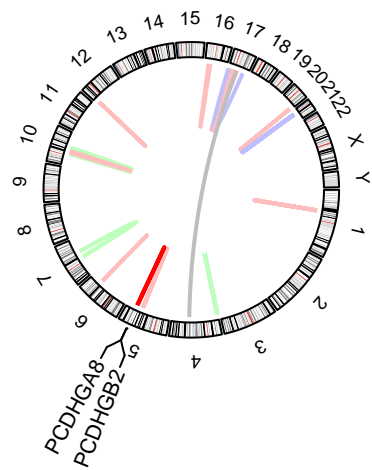
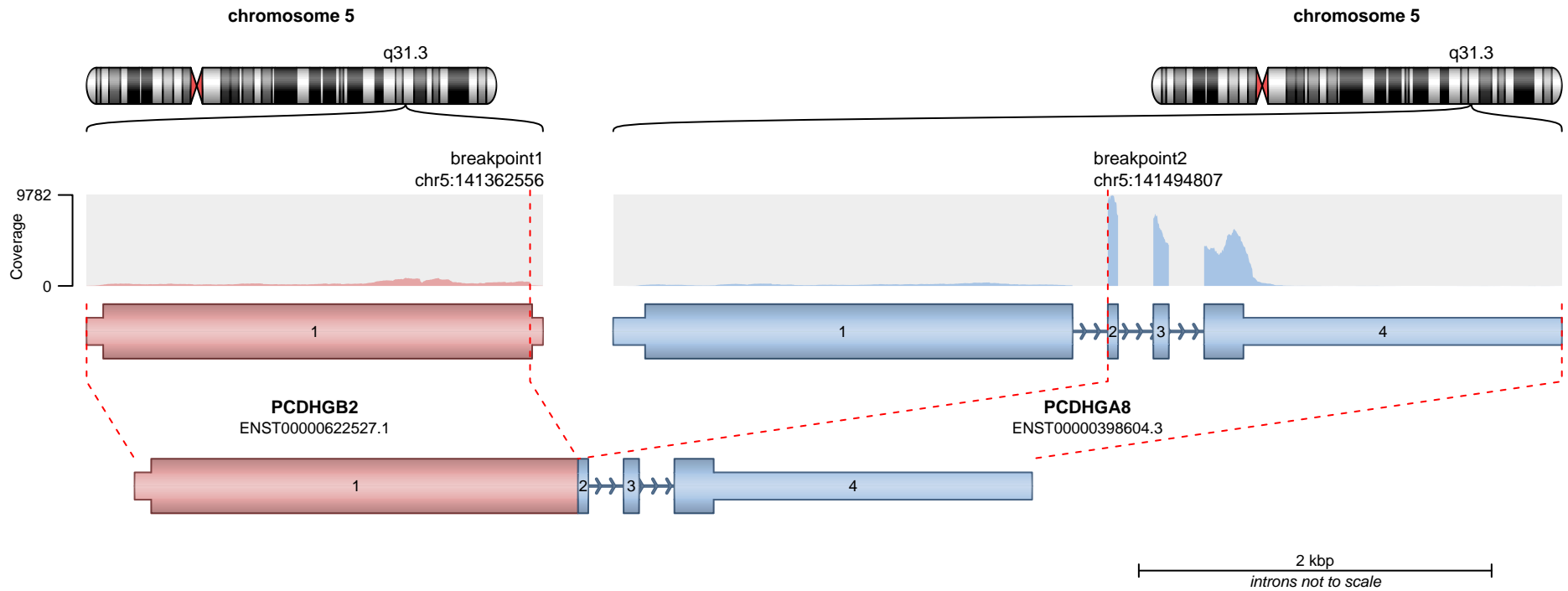
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

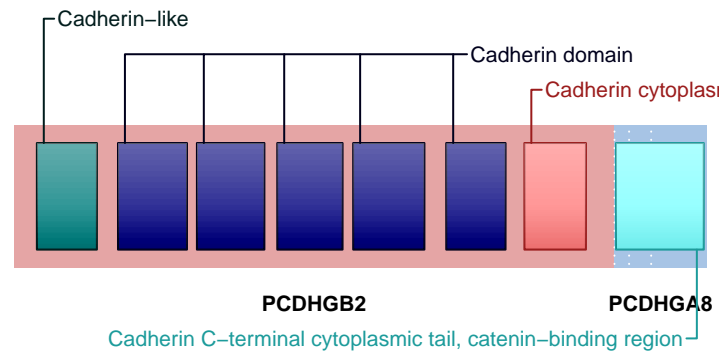
Split reads = 154  
Discordant mates = 0



— translocation — deletion  
— duplication — inversion

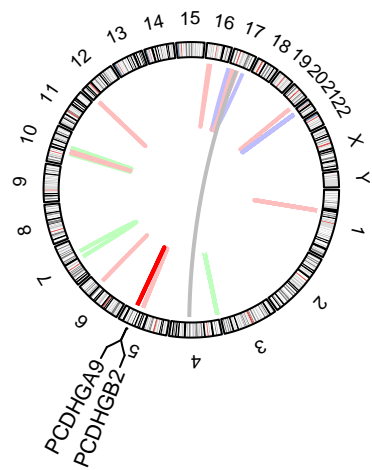
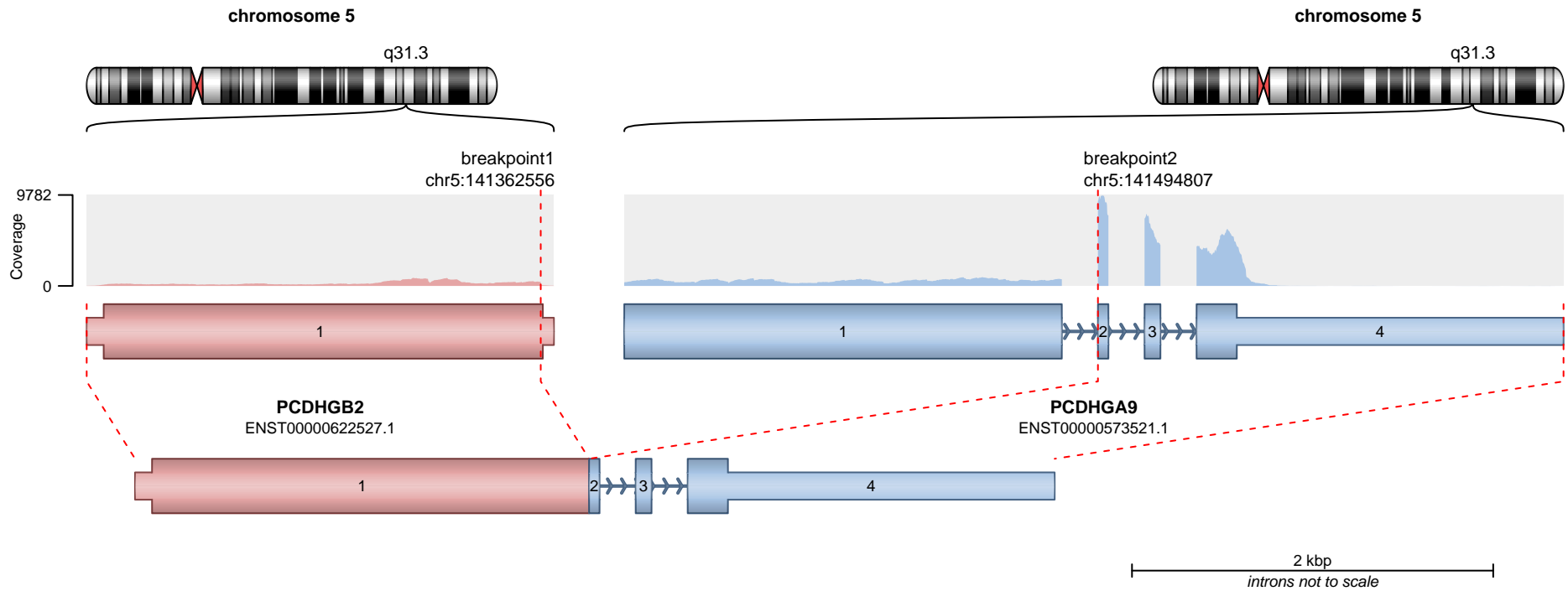
### RETAINED PROTEIN DOMAINS

reading frame unclear



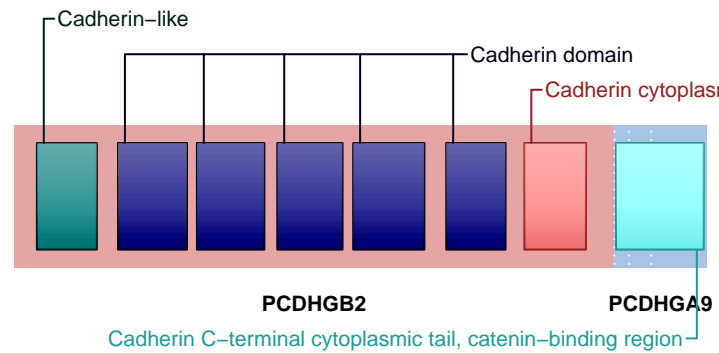
### SUPPORTING READ COUNT

Split reads = 154  
Discordant mates = 0



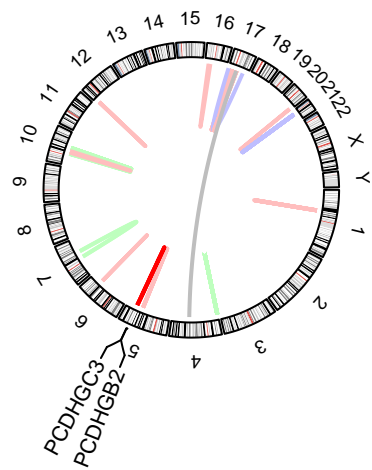
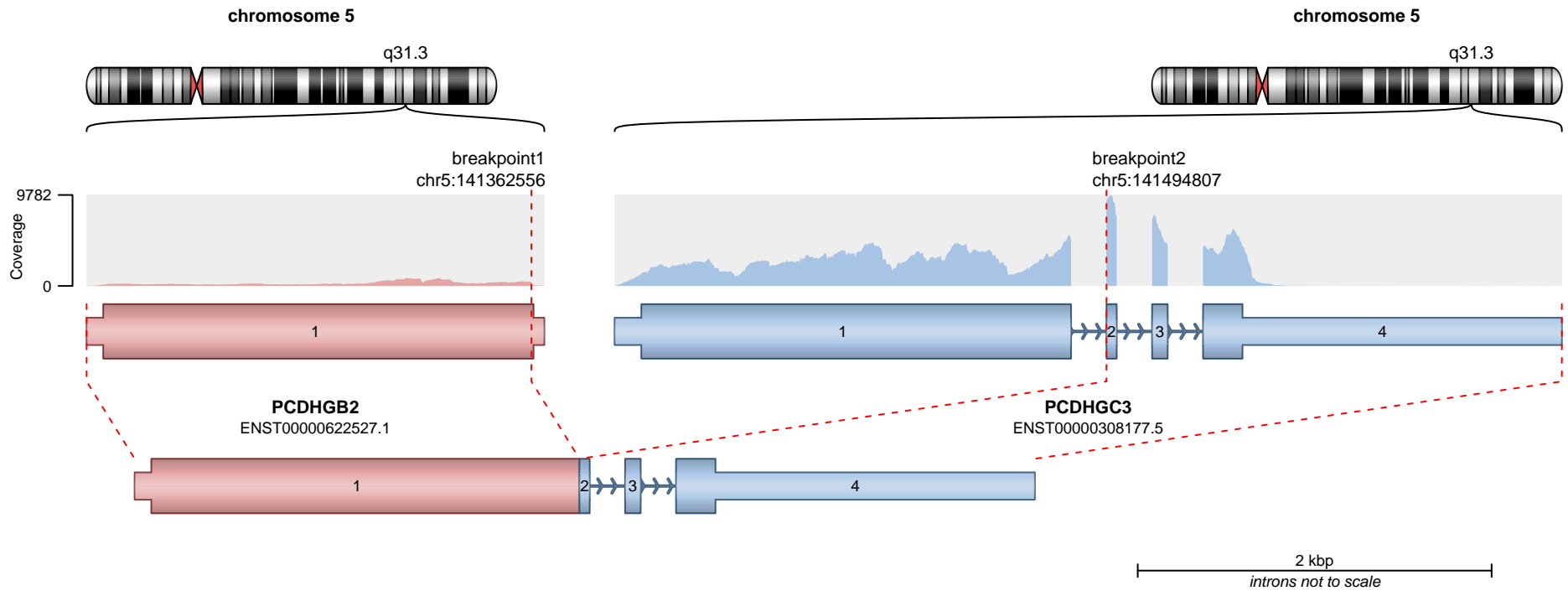
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



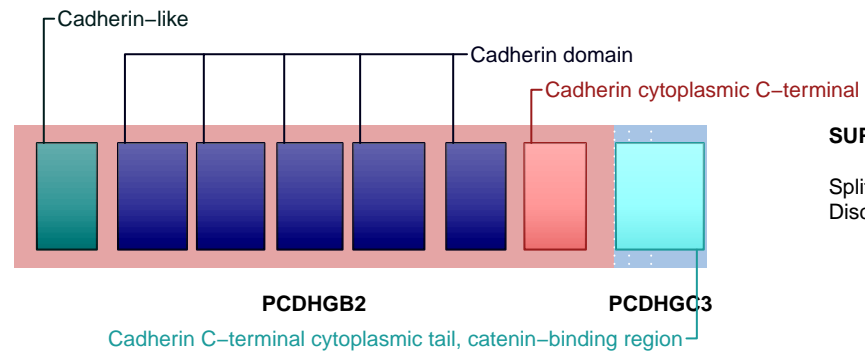
**SUPPORTING READ COUNT**

Split reads = 154  
Discordant mates = 0



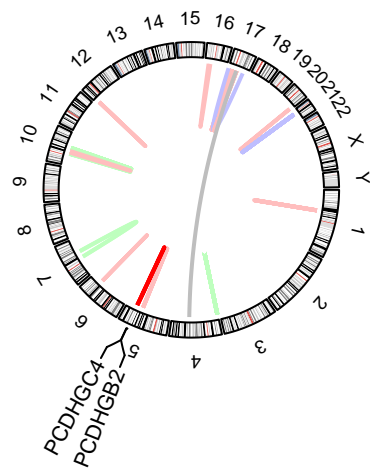
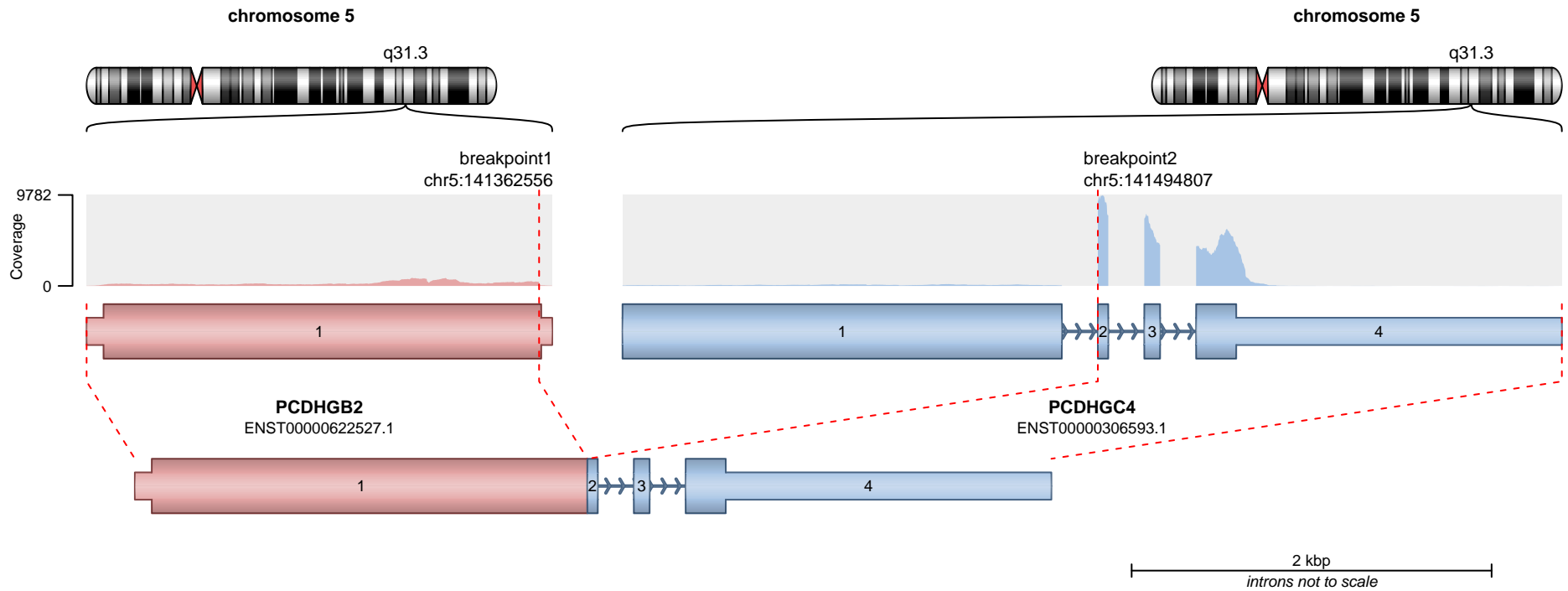
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



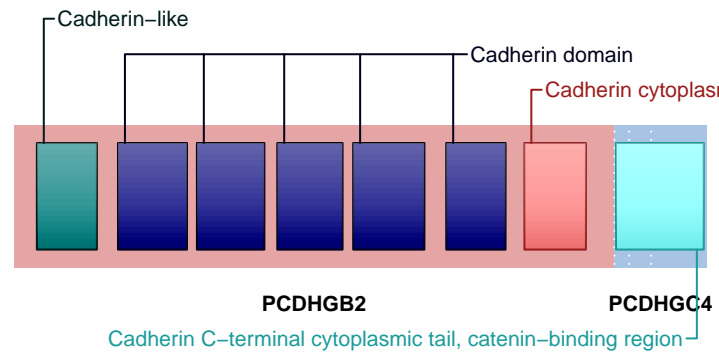
**SUPPORTING READ COUNT**

Split reads = 154  
Discordant mates = 0



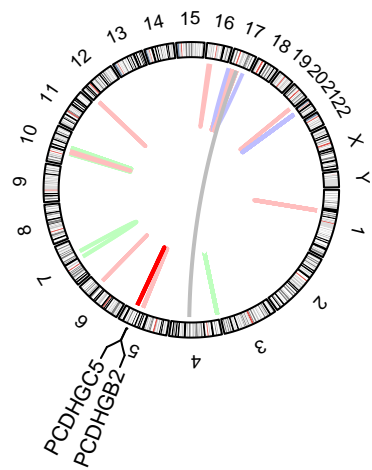
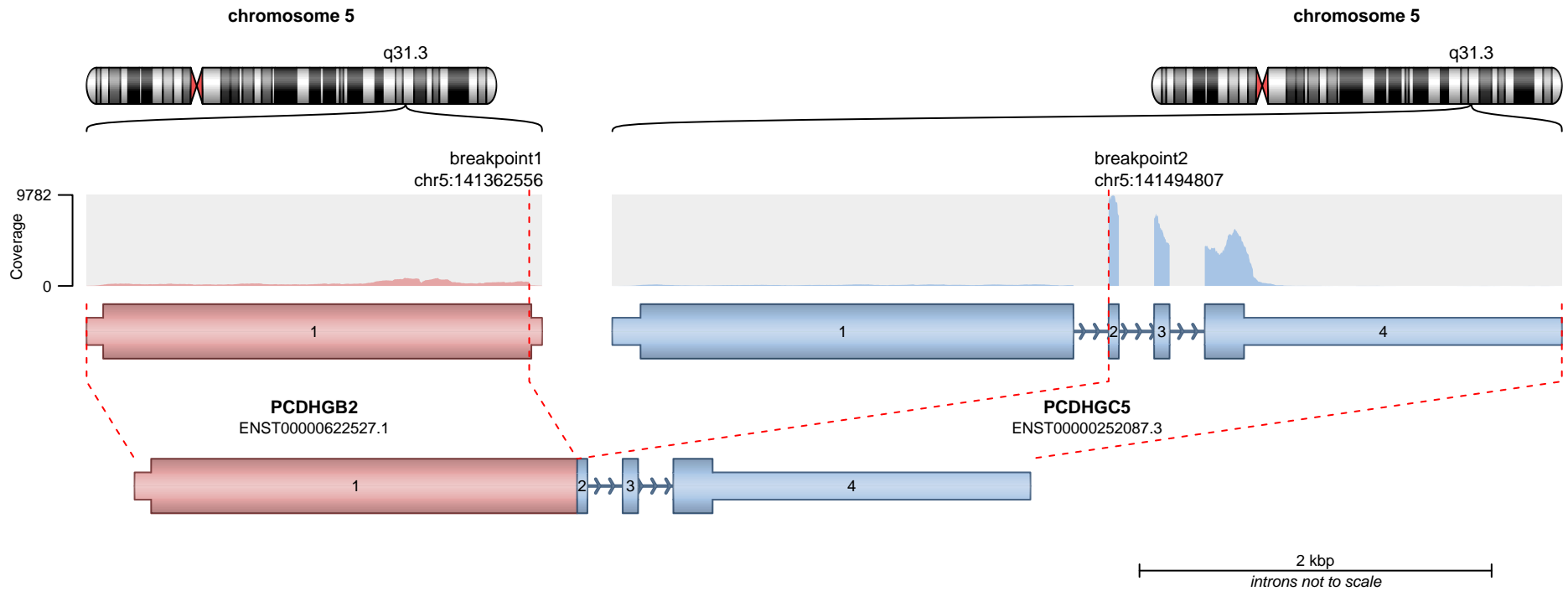
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



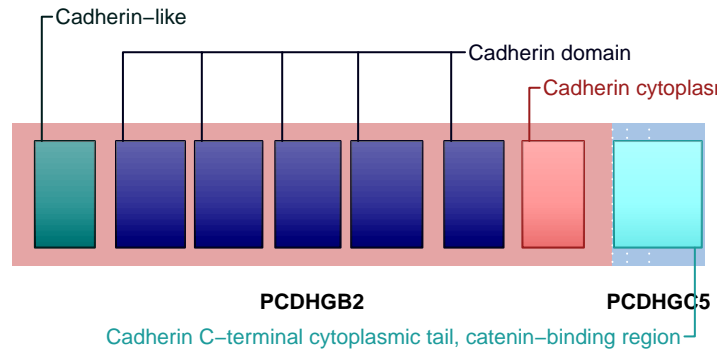
**SUPPORTING READ COUNT**

Split reads = 154  
Discordant mates = 0



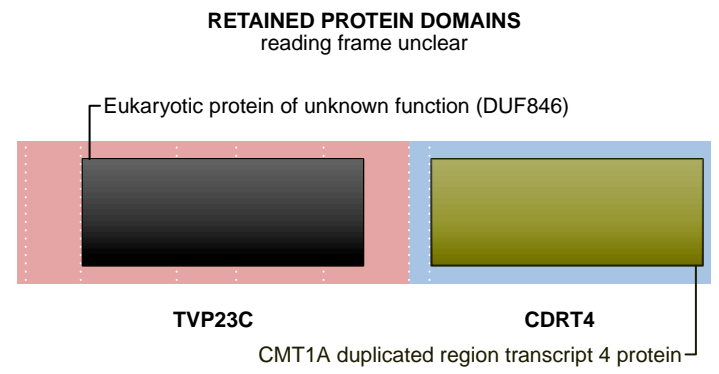
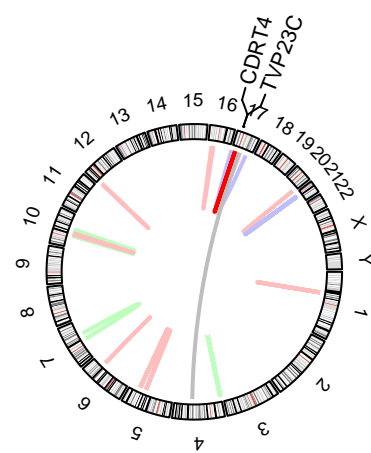
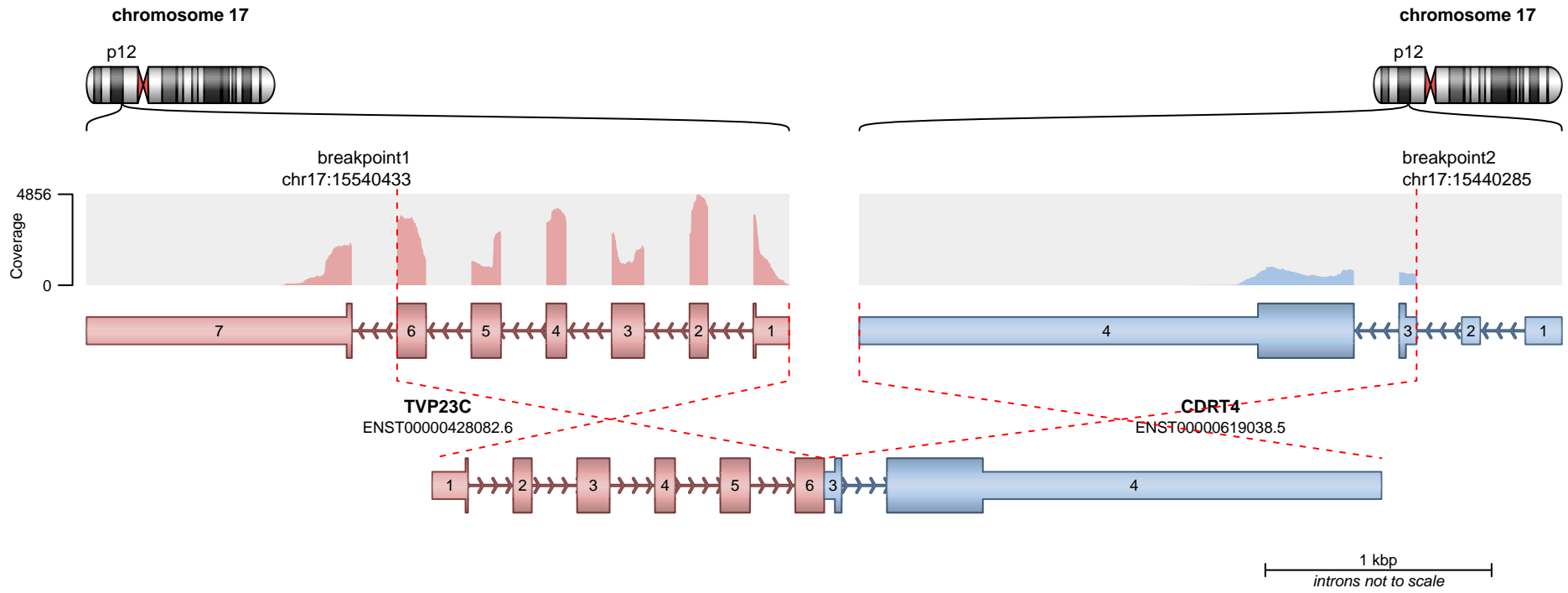
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

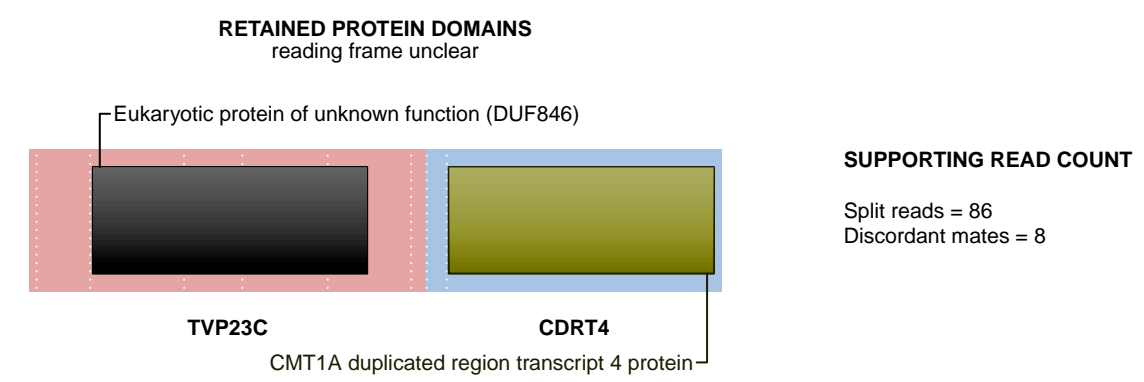
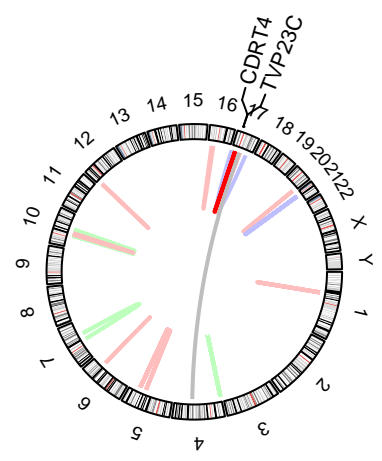
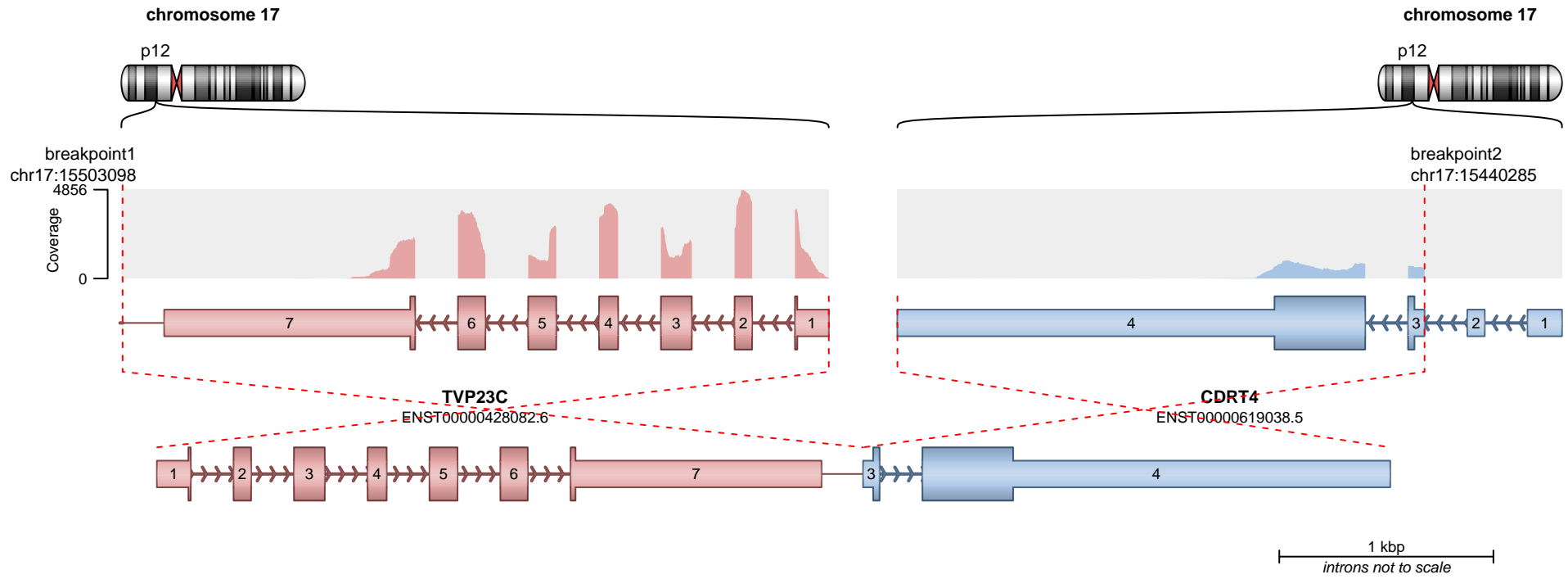
Split reads = 154  
Discordant mates = 0



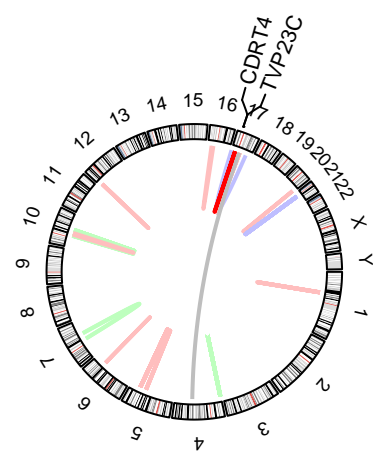
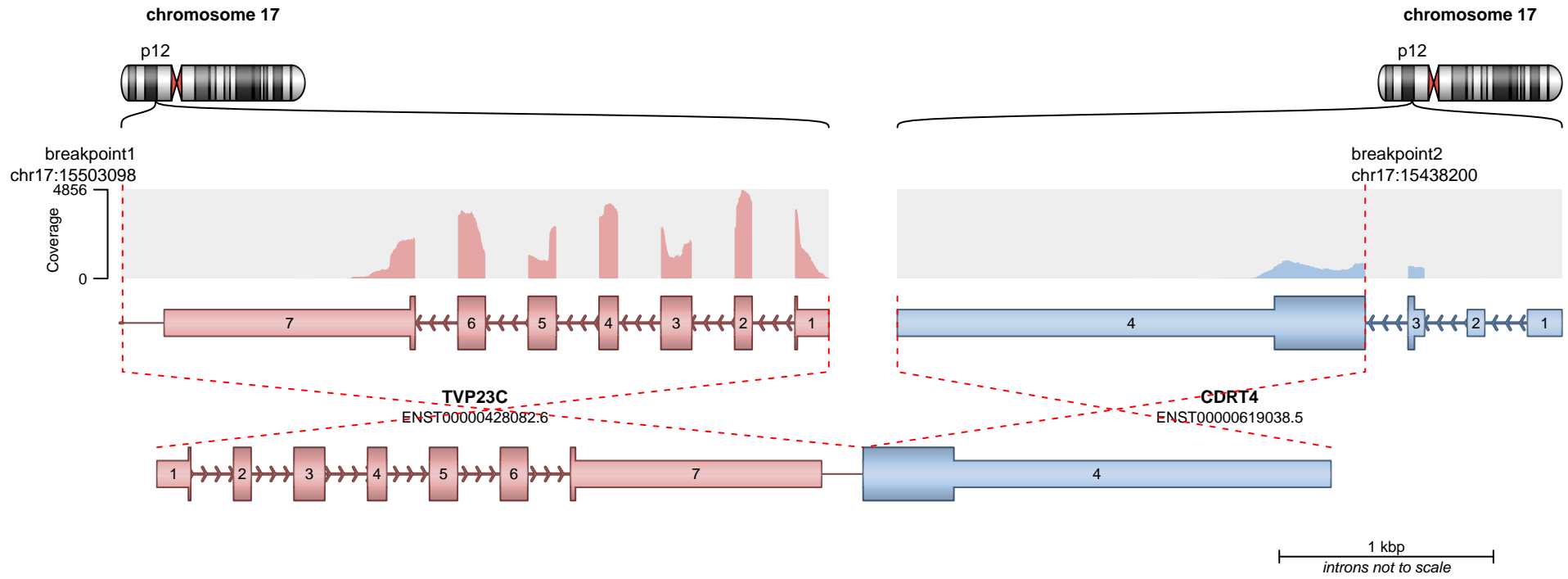
**SUPPORTING READ COUNT**

Split reads = 125  
Discordant mates = 2

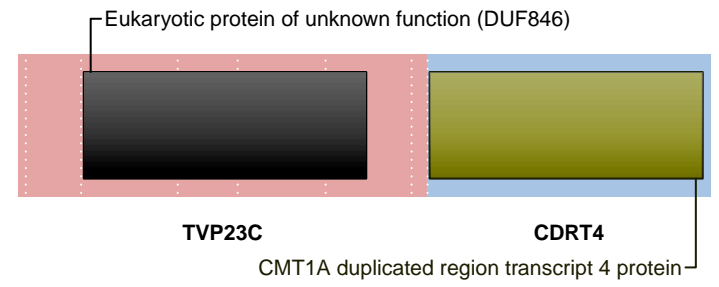
— translocation — deletion  
— duplication — inversion



— translocation    — deletion  
— duplication    — inversion



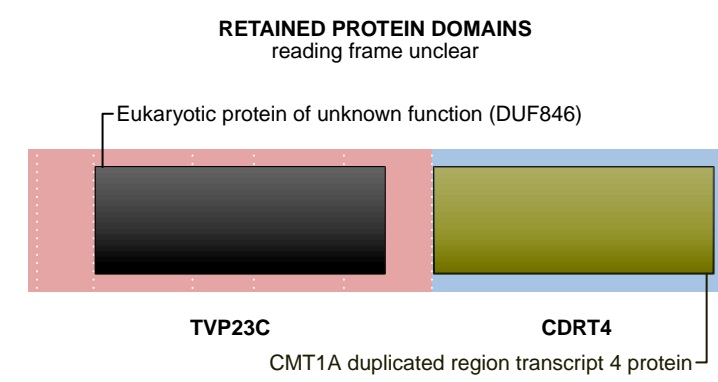
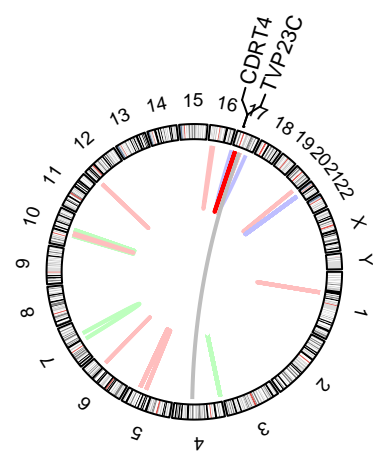
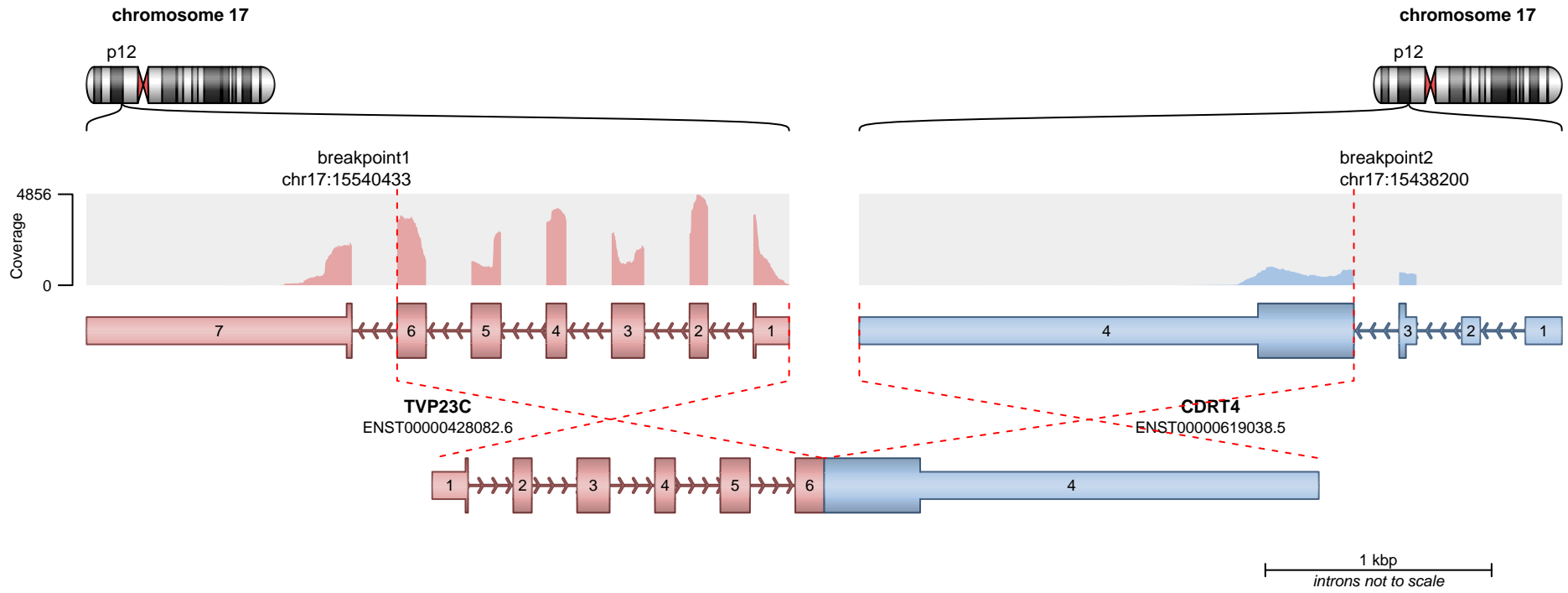
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 17  
Discordant mates = 2

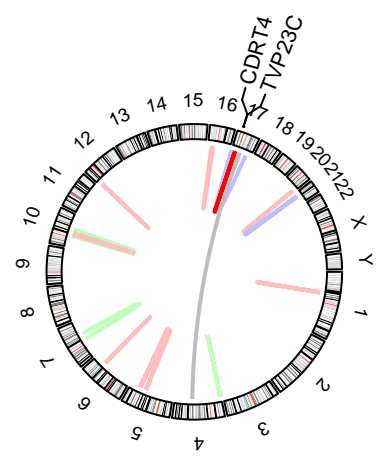
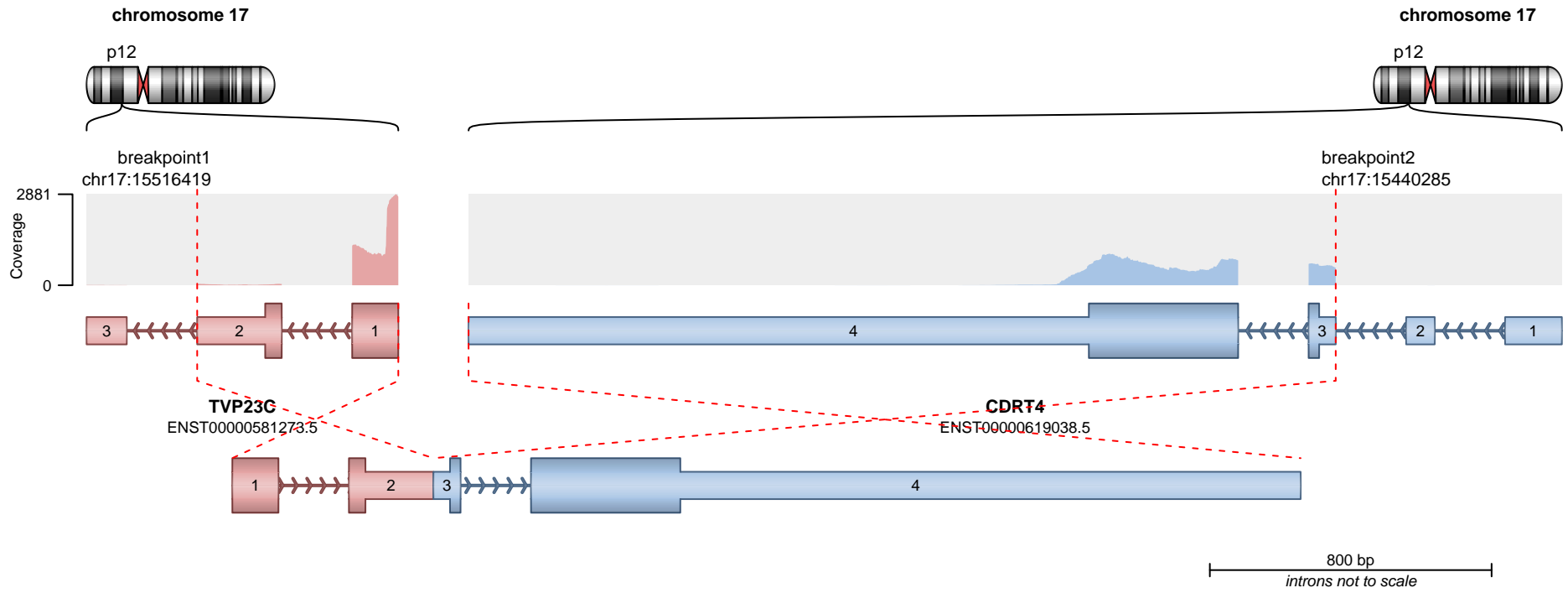
- translocation
- duplication
- deletion
- inversion



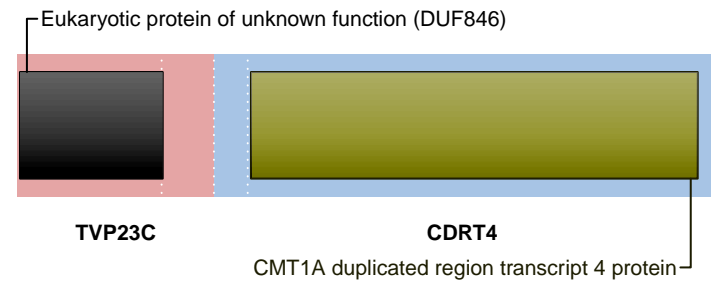
**SUPPORTING READ COUNT**

Split reads = 16  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



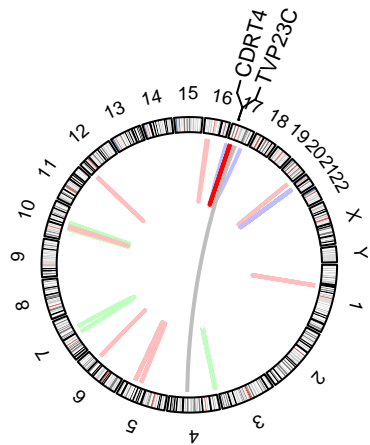
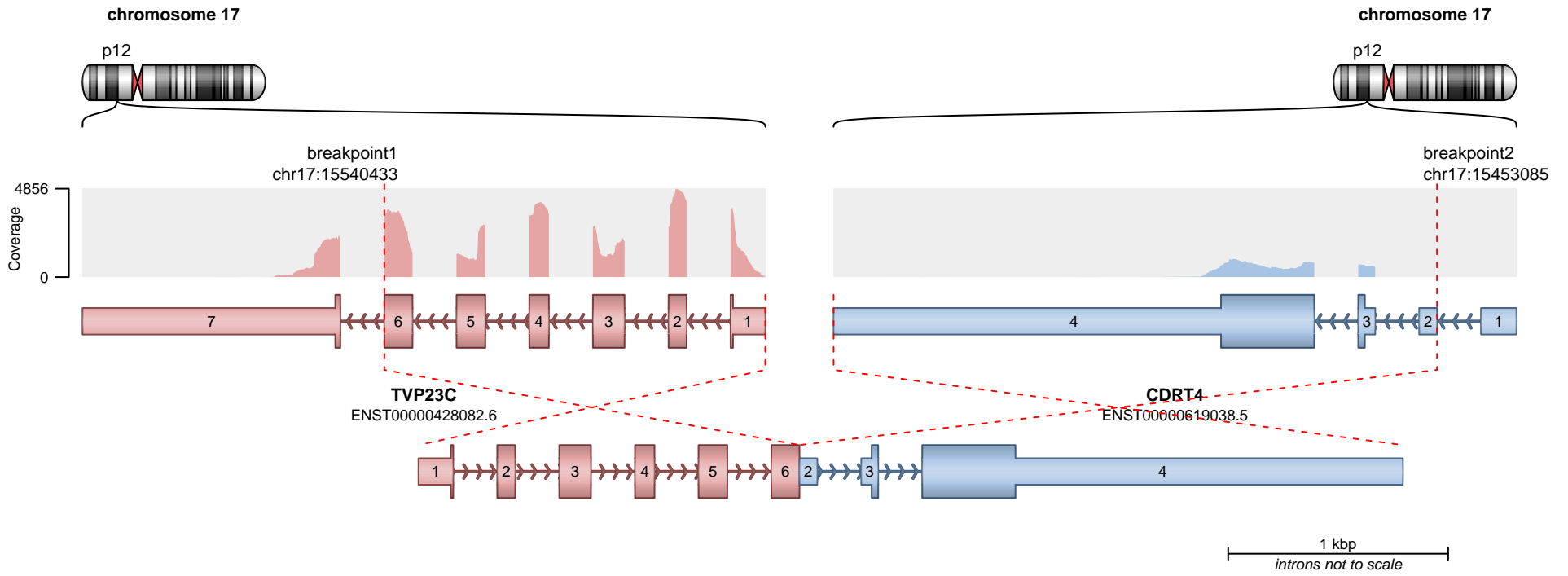
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



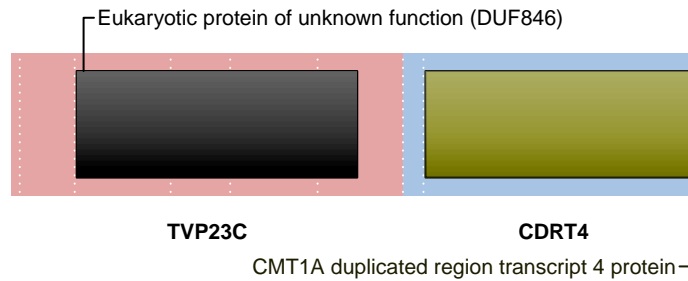
**SUPPORTING READ COUNT**

Split reads = 12  
Discordant mates = 2

- translocation
- duplication
- deletion
- inversion



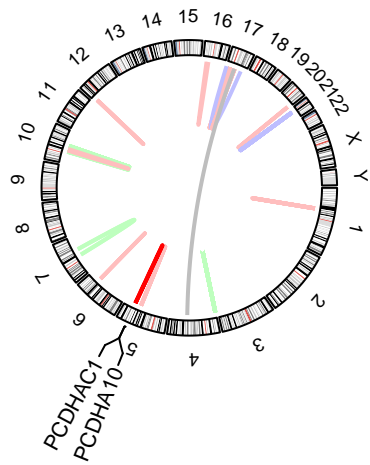
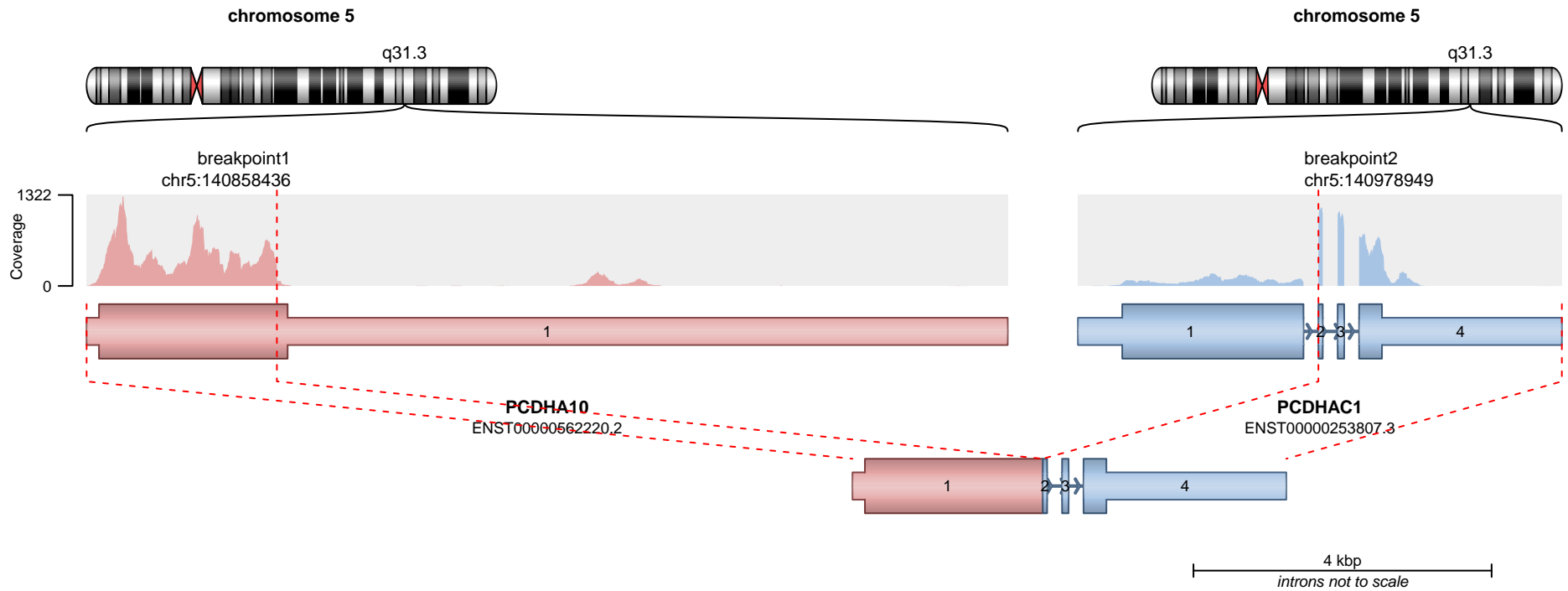
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



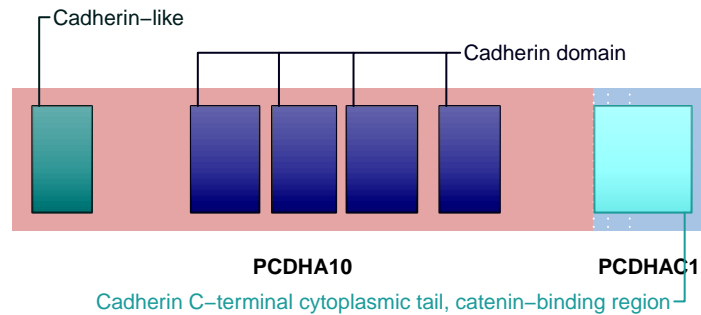
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 2

— translocation — deletion  
— duplication — inversion



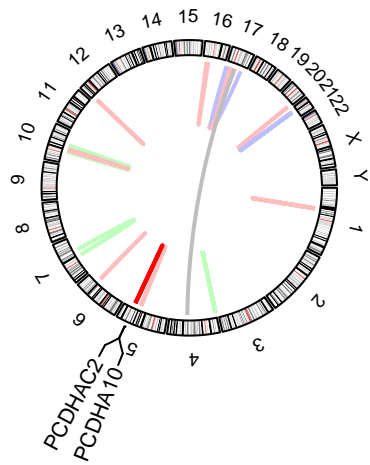
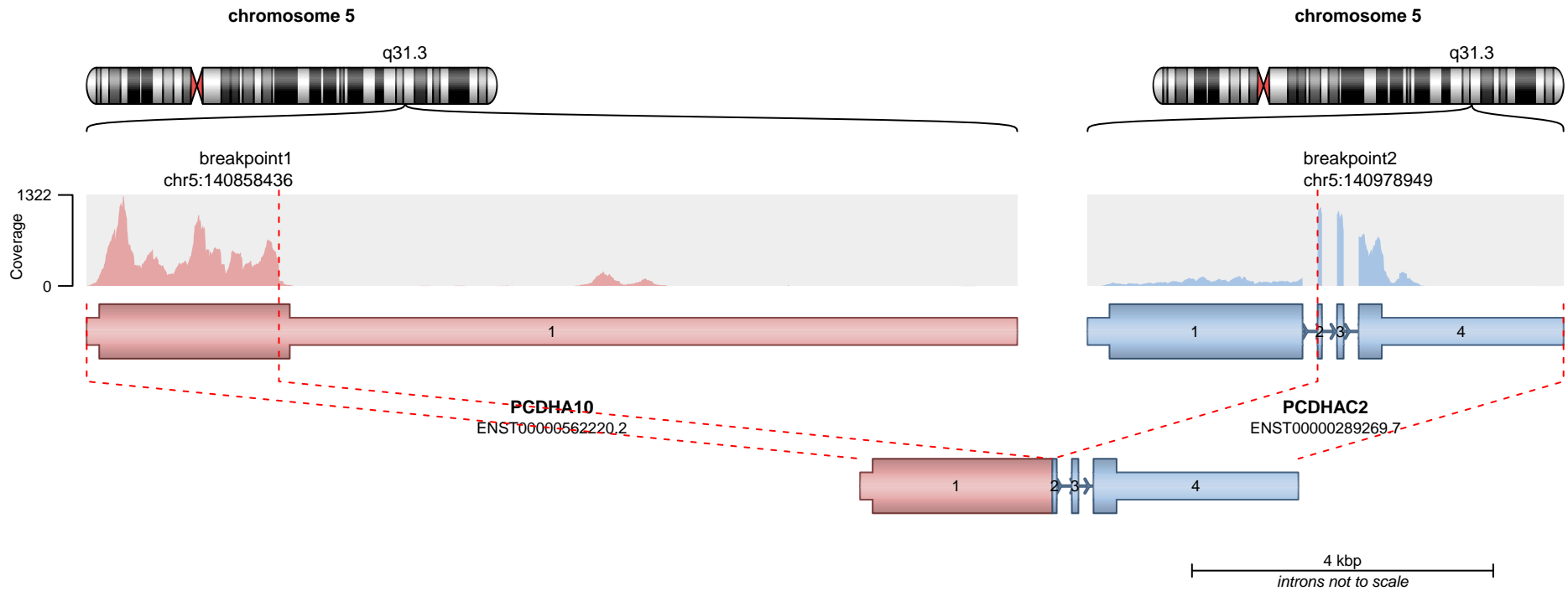
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



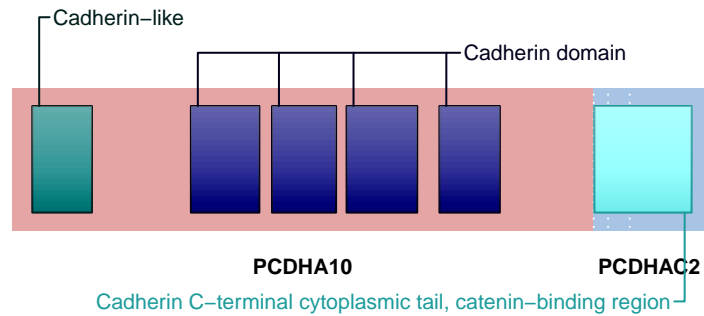
**SUPPORTING READ COUNT**

Split reads = 109  
Discordant mates = 6

- translocation
- duplication
- deletion
- inversion



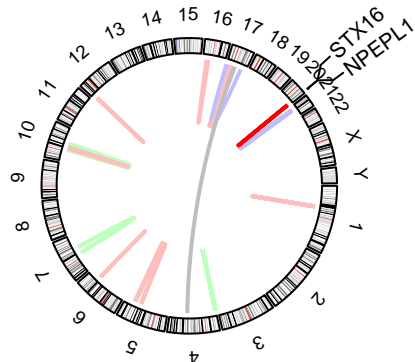
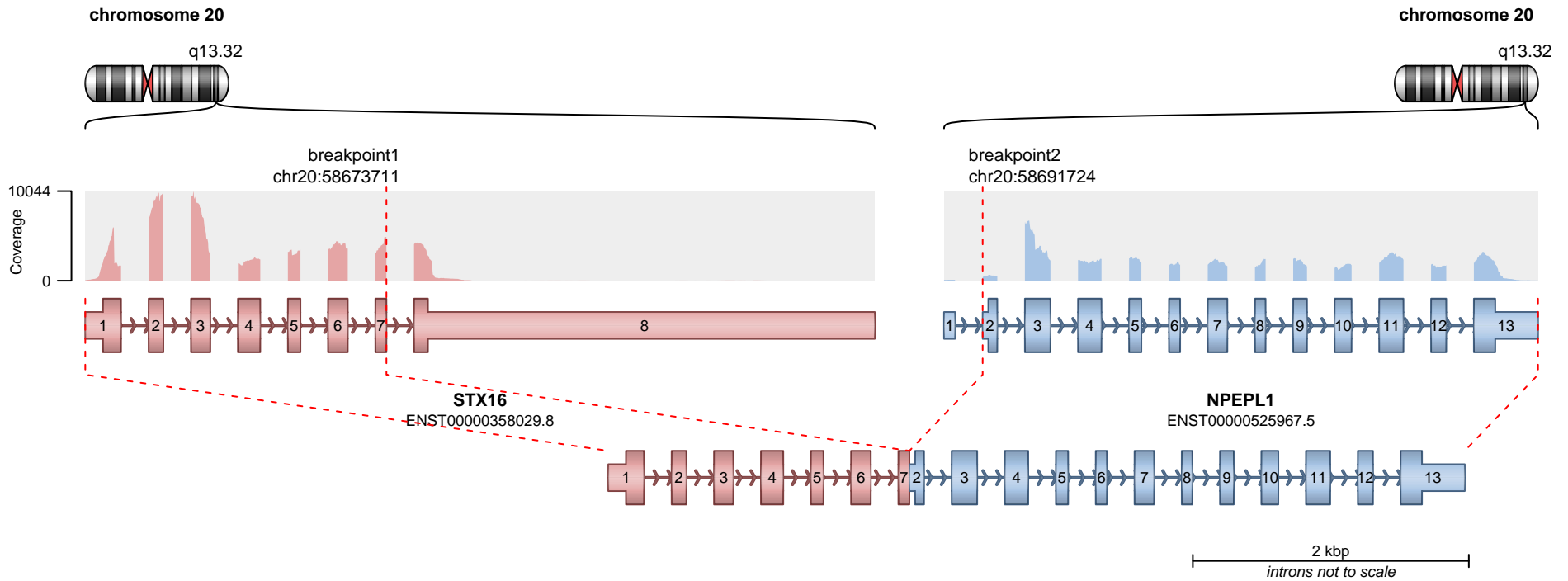
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



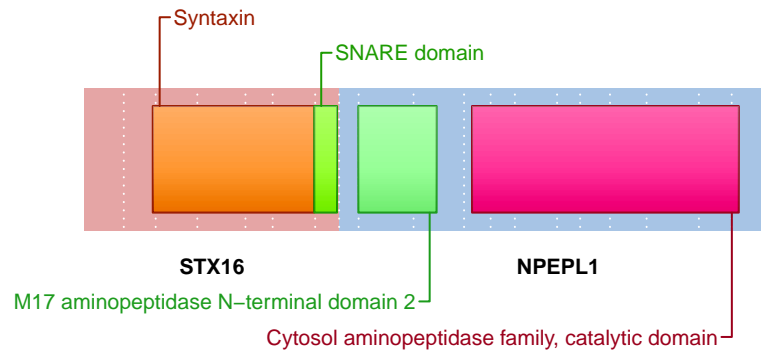
**SUPPORTING READ COUNT**

Split reads = 109  
Discordant mates = 6

— translocation — deletion  
— duplication — inversion



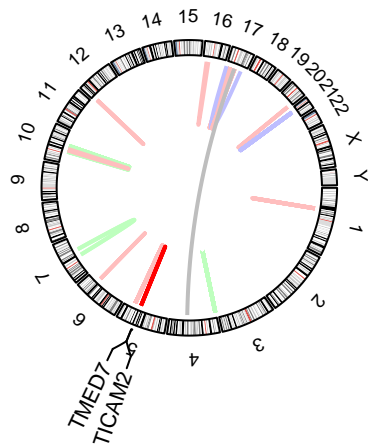
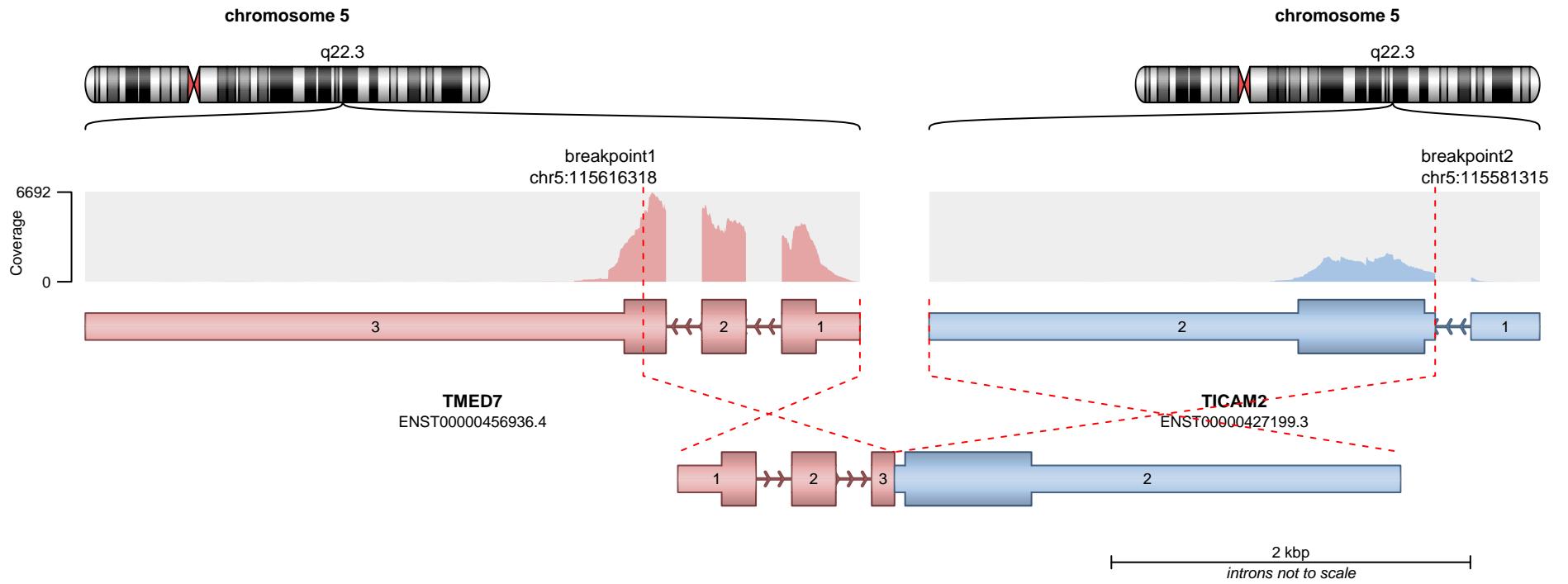
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



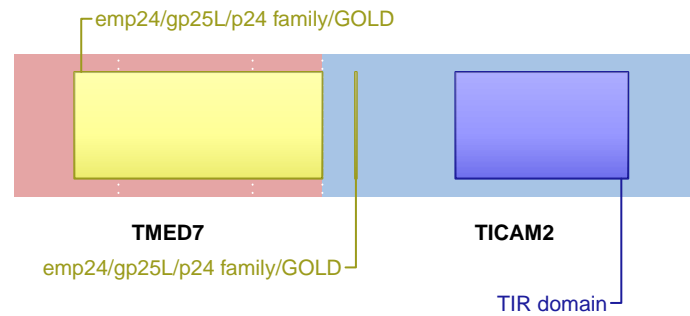
**SUPPORTING READ COUNT**

Split reads = 98  
Discordant mates = 7

- translocation
- duplication
- deletion
- inversion



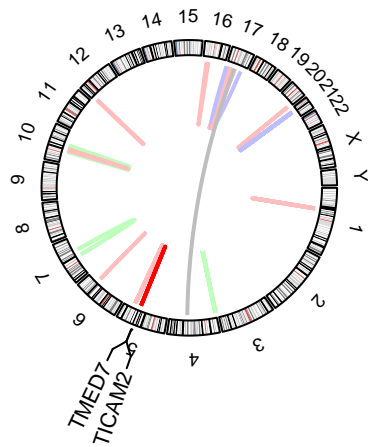
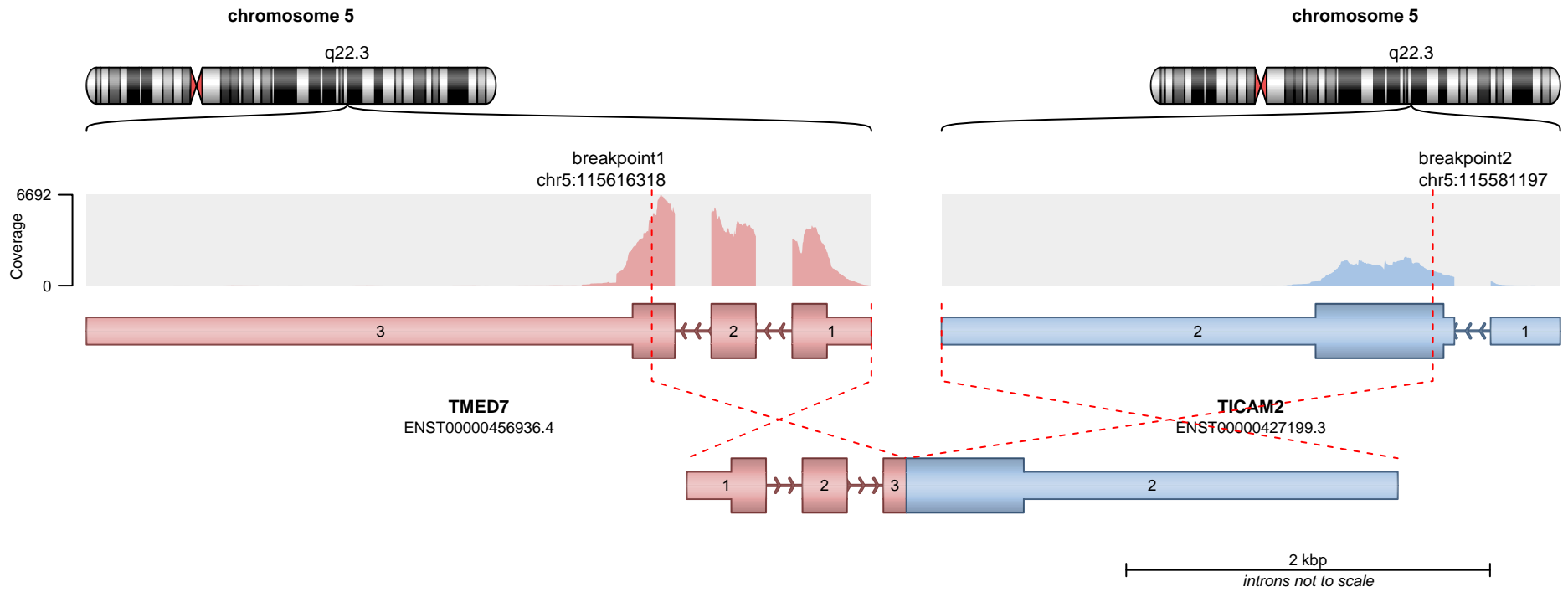
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



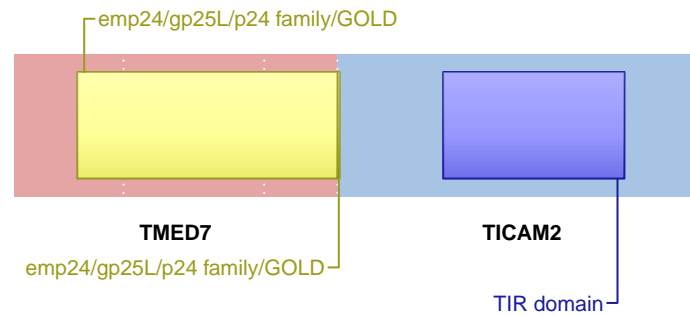
**SUPPORTING READ COUNT**

Split reads = 91  
Discordant mates = 12

— translocation    — deletion  
— duplication    — inversion



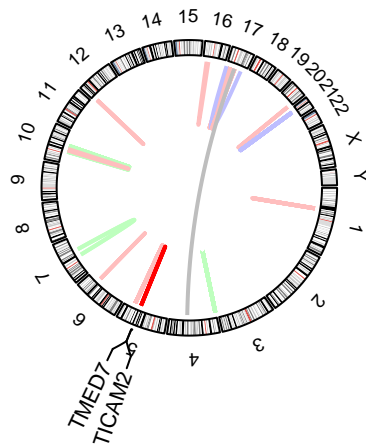
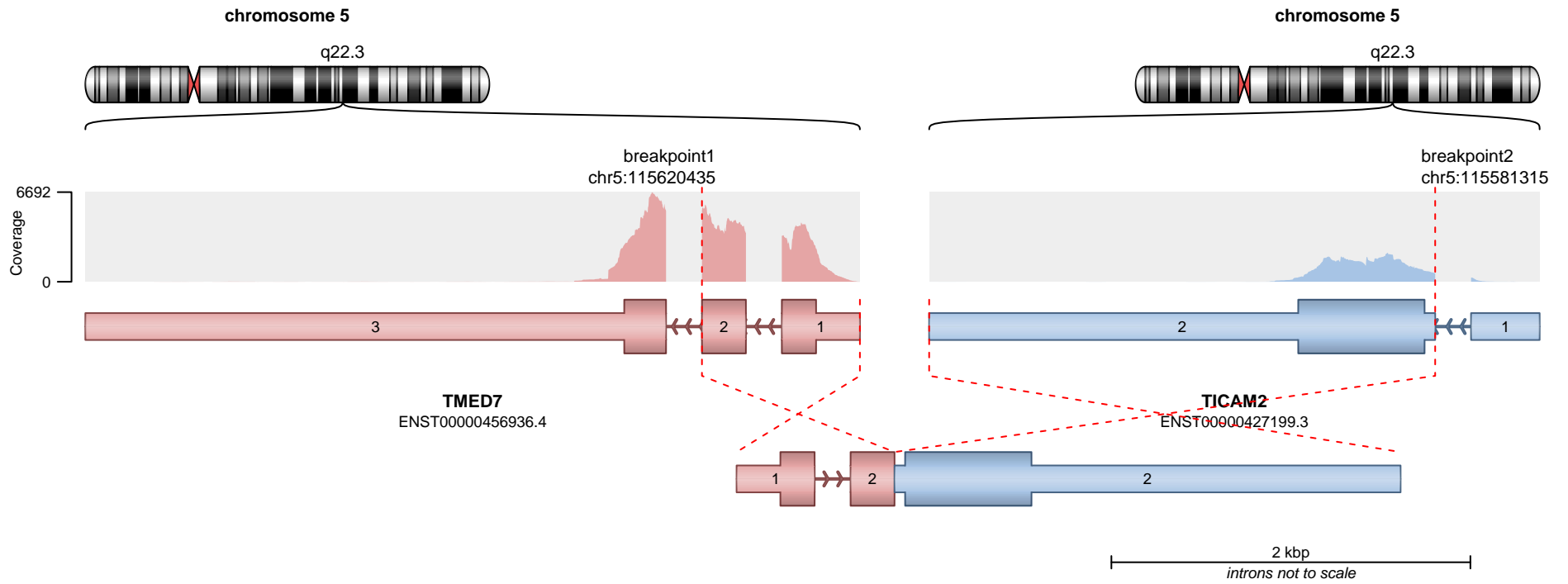
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



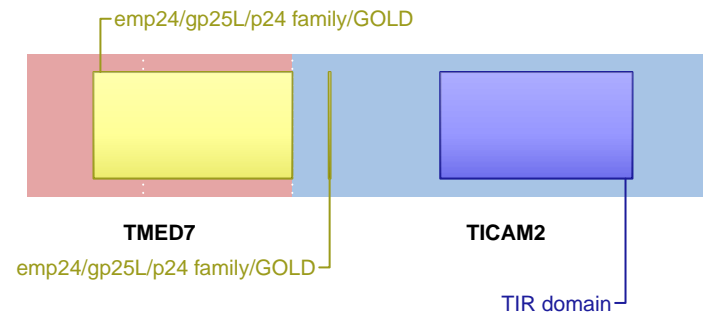
**SUPPORTING READ COUNT**

Split reads = 16  
Discordant mates = 4

— translocation    — deletion  
— duplication    — inversion



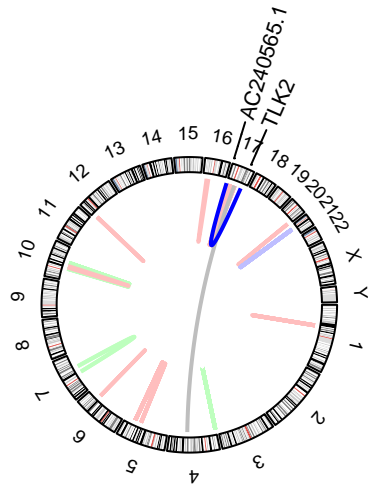
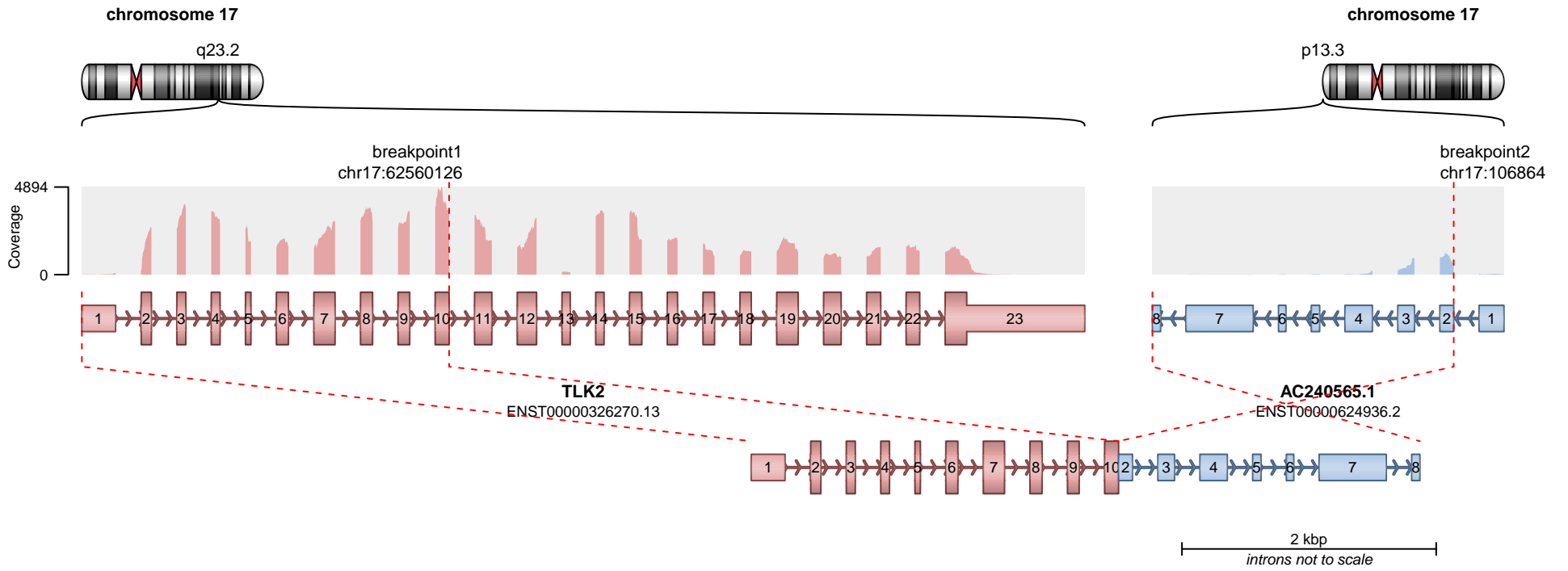
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 8  
Discordant mates = 1

— translocation    — deletion  
— duplication    — inversion

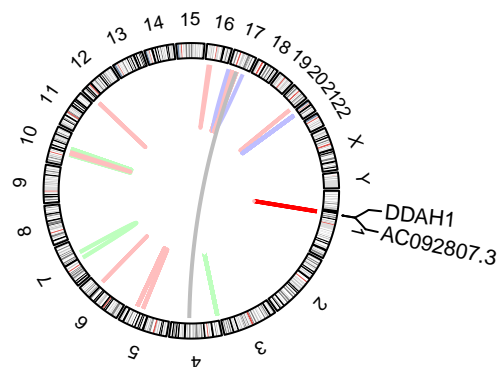
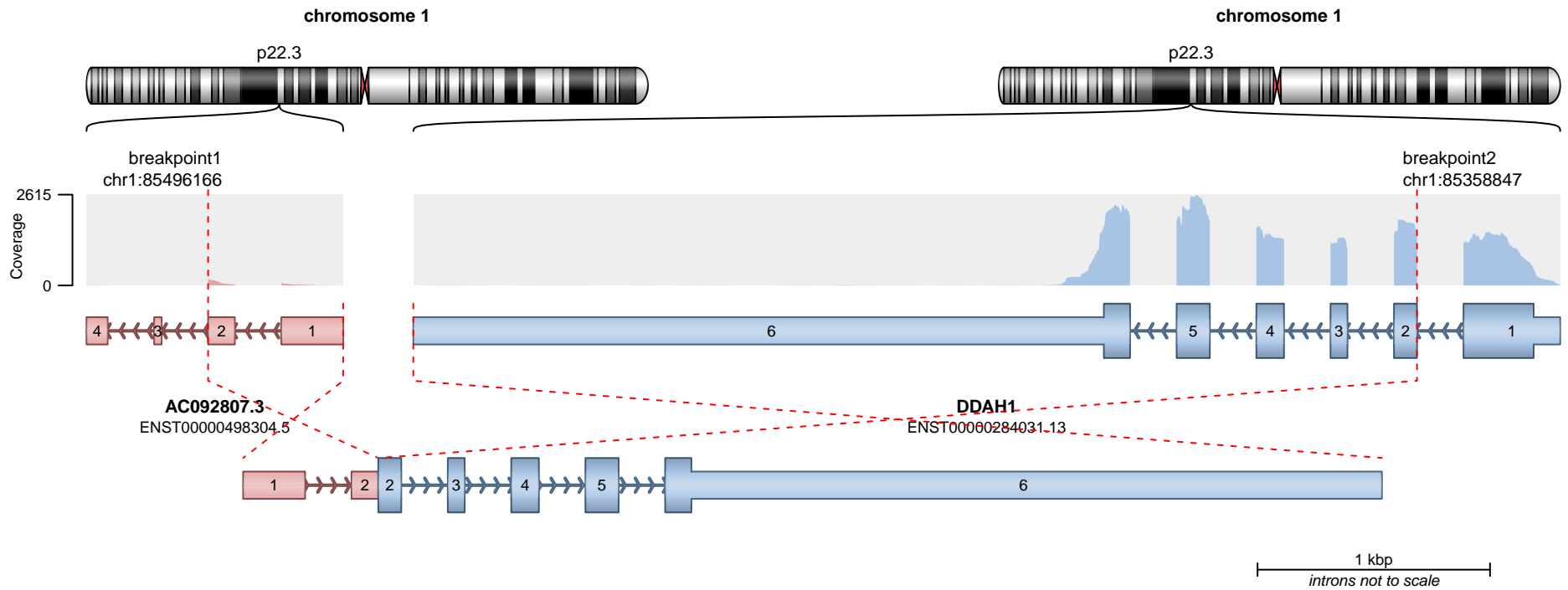


No protein domains retained in fusion.

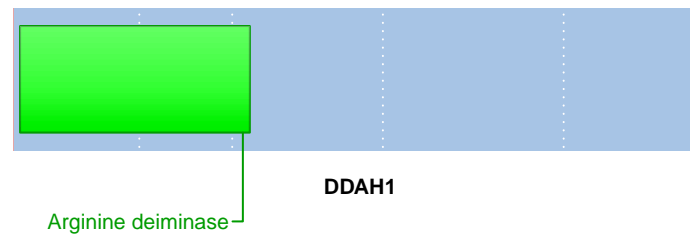
**SUPPORTING READ COUNT**

Split reads = 87  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



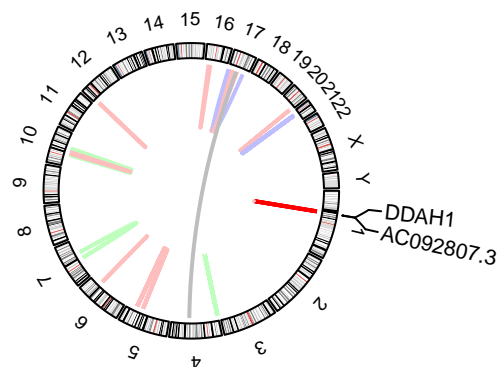
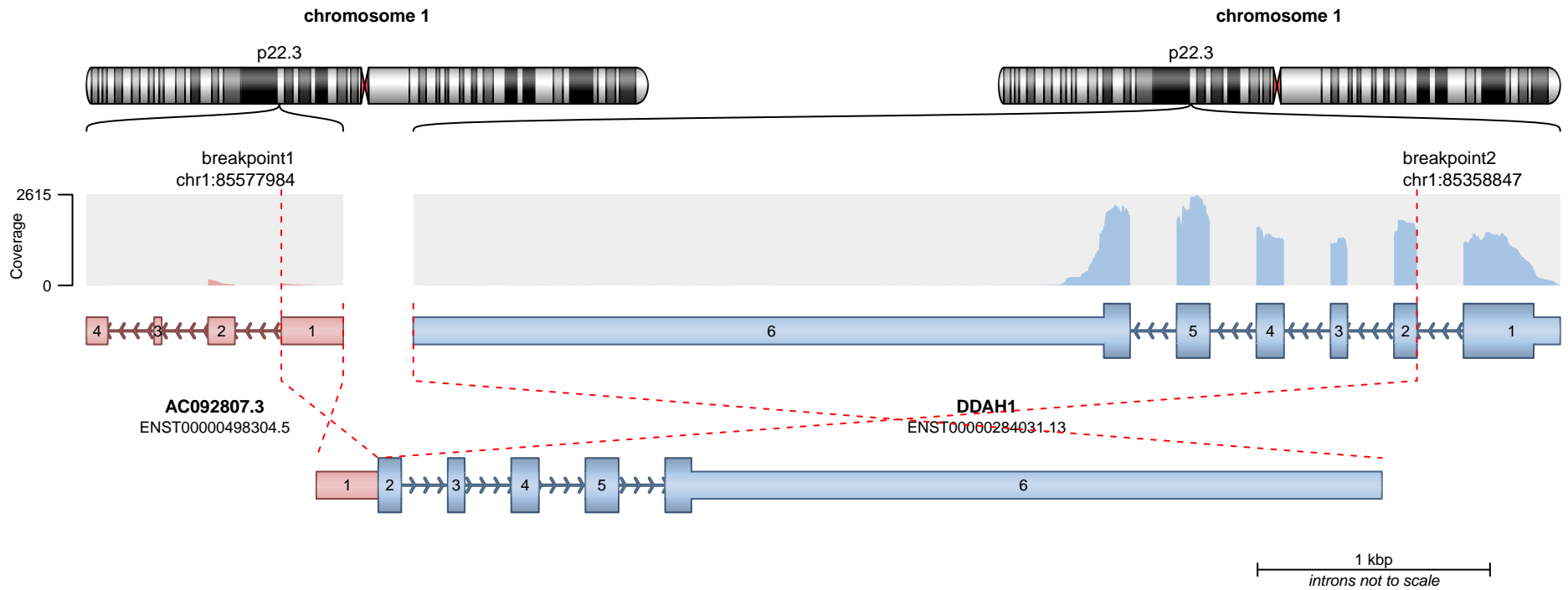
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



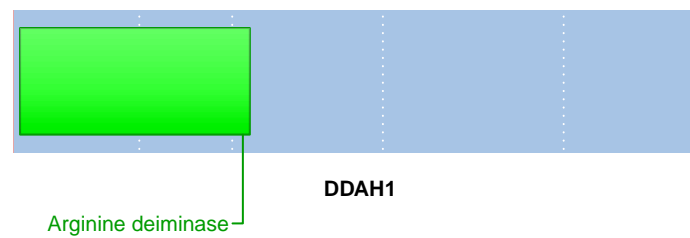
**SUPPORTING READ COUNT**

Split reads = 75  
Discordant mates = 7

— translocation    — deletion  
— duplication    — inversion



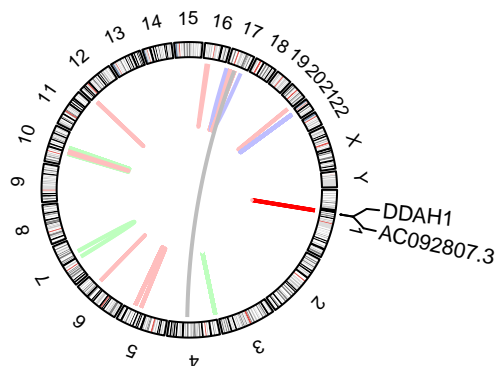
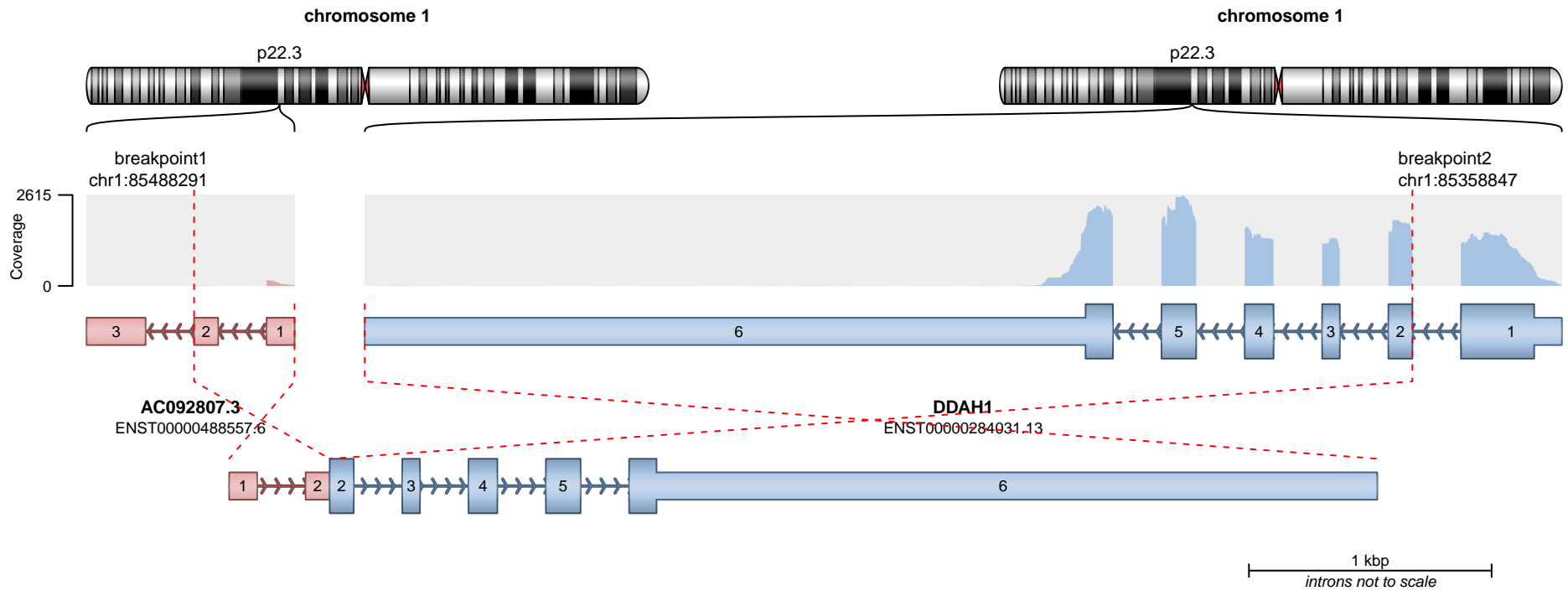
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



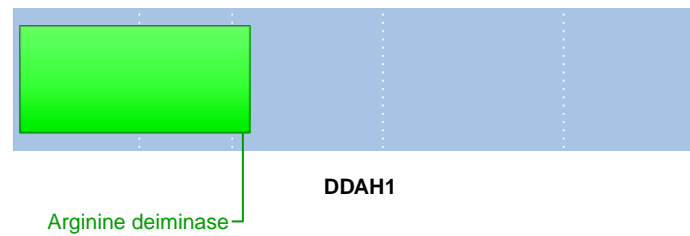
**SUPPORTING READ COUNT**

Split reads = 25  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



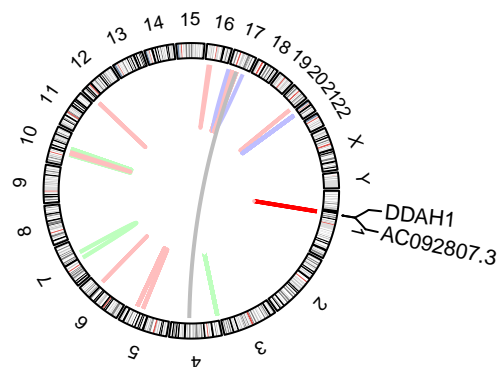
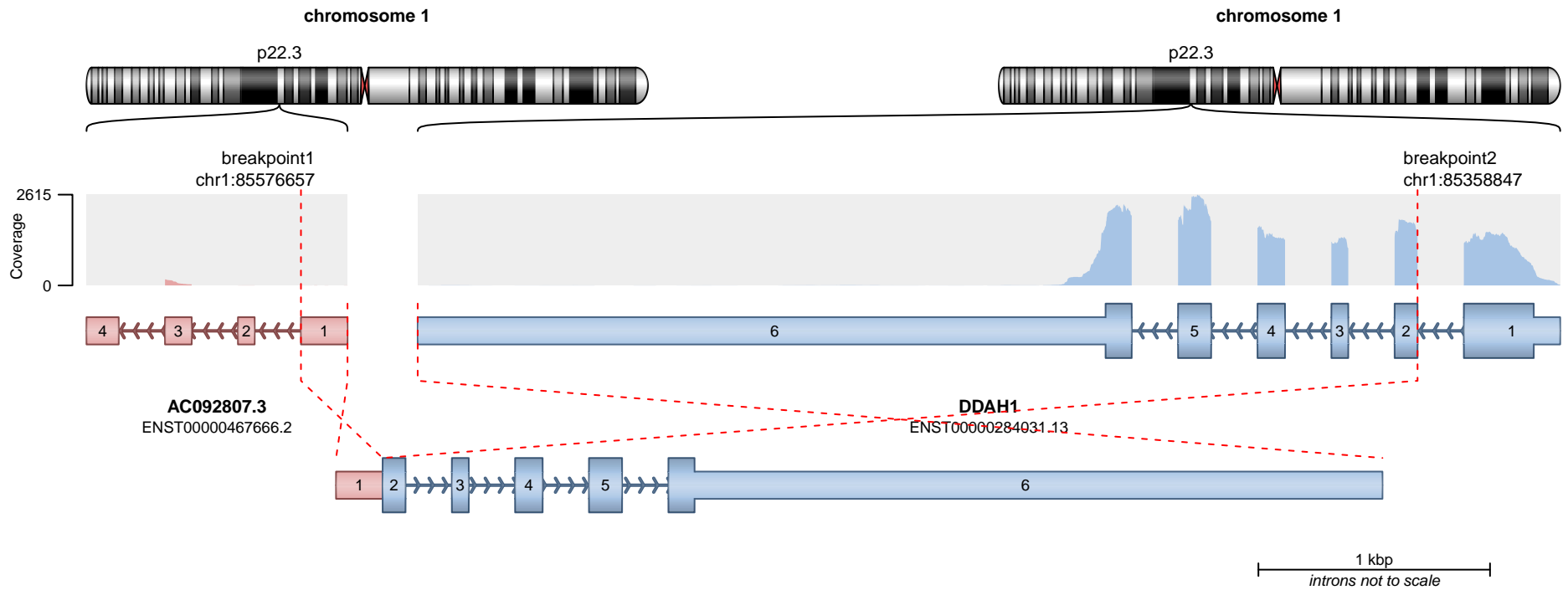
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



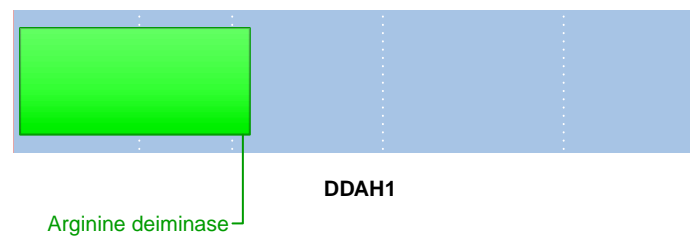
**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 7

- translocation
- duplication
- deletion
- inversion



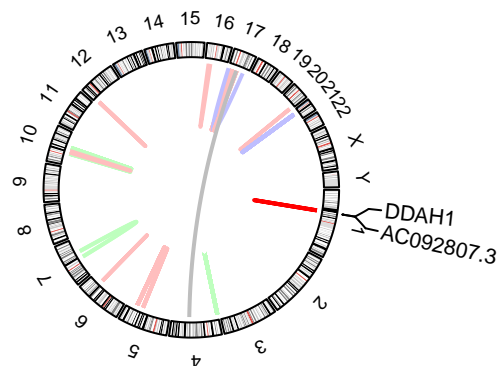
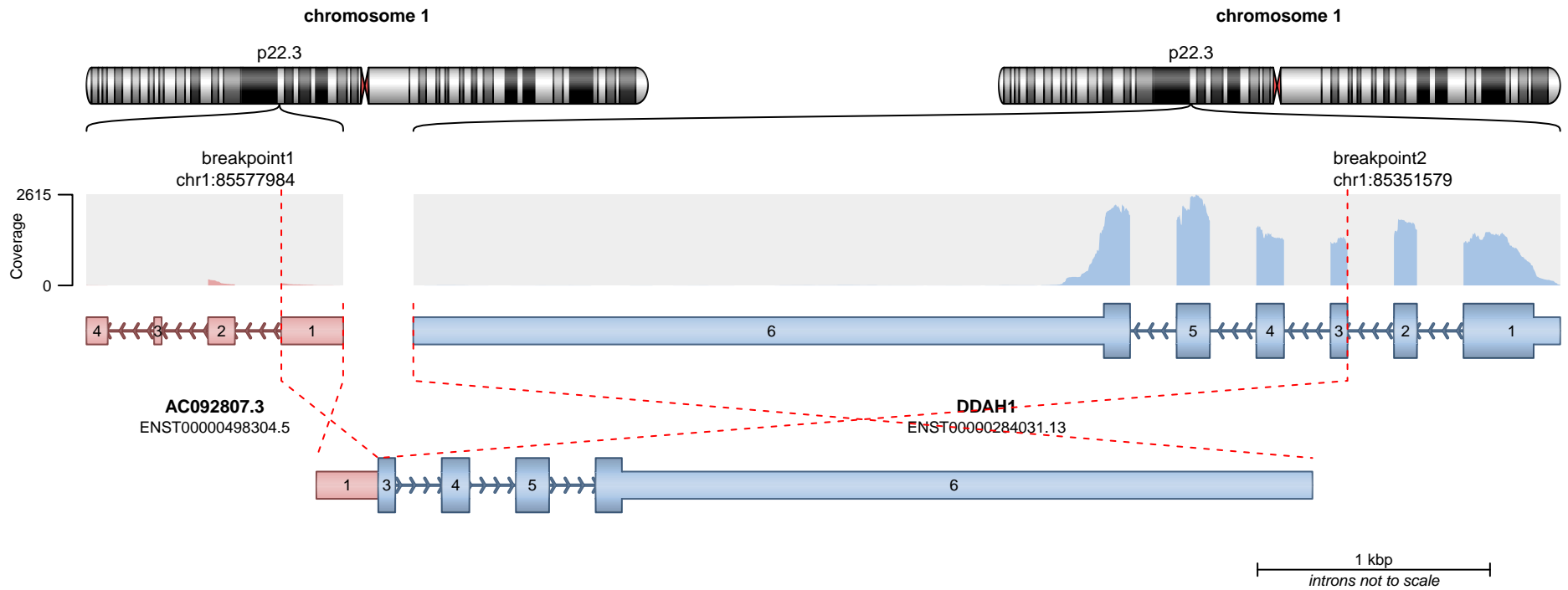
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



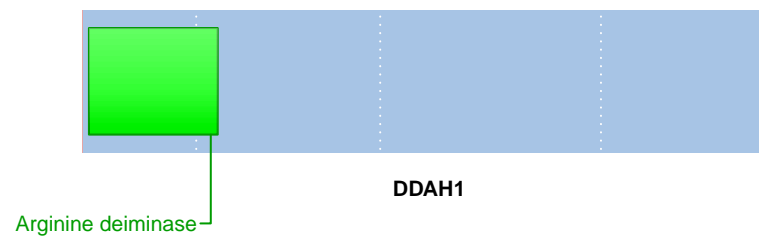
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



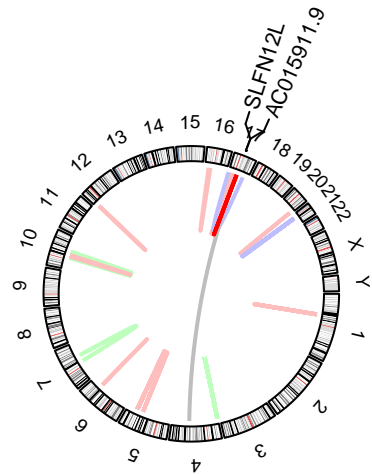
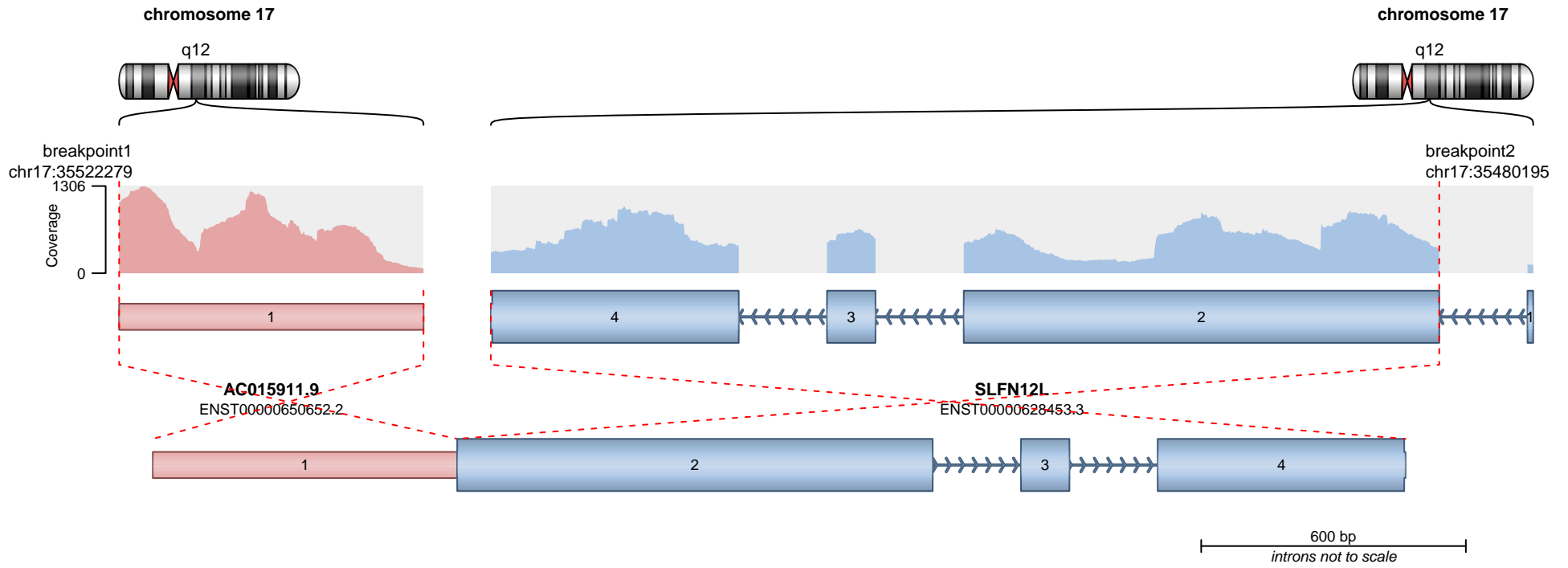
RETAINED PROTEIN DOMAINS  
reading frame unclear



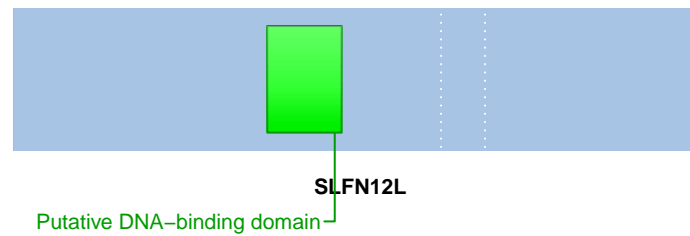
SUPPORTING READ COUNT

Split reads = 1  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



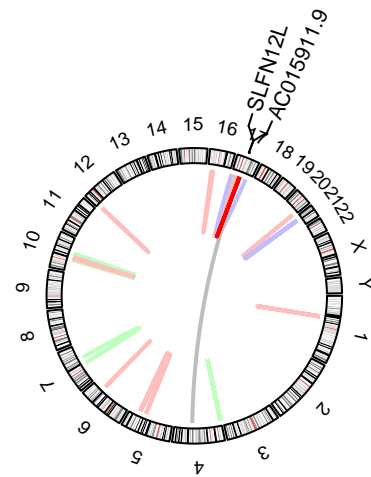
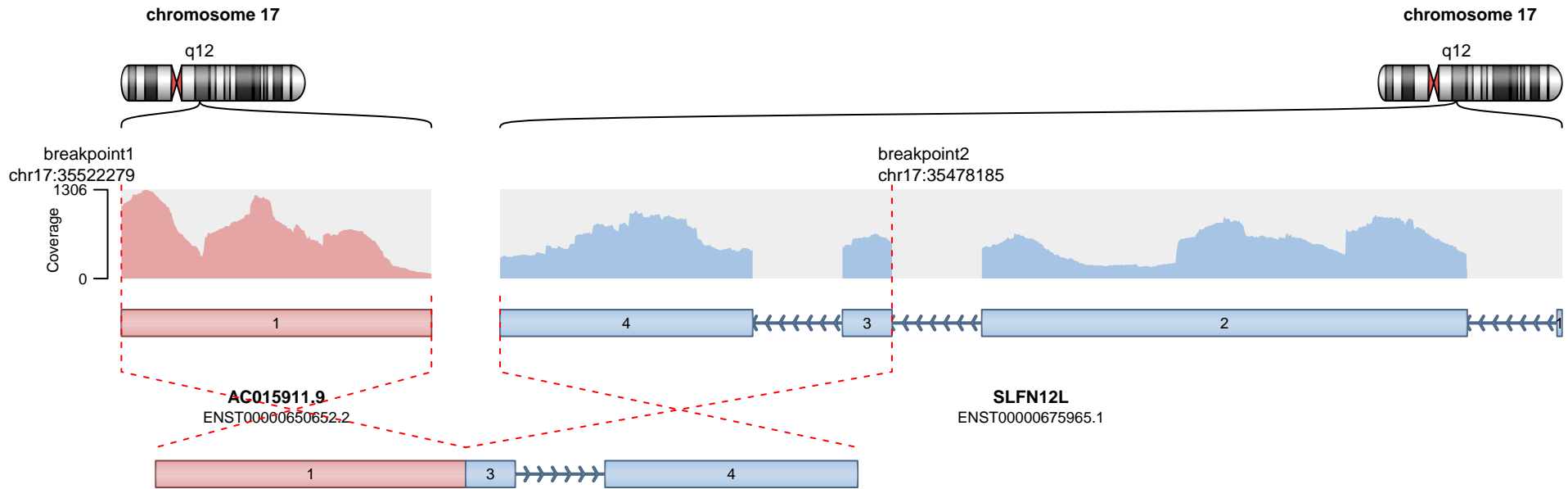
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 59  
Discordant mates = 14

— translocation    — deletion  
— duplication    — inversion

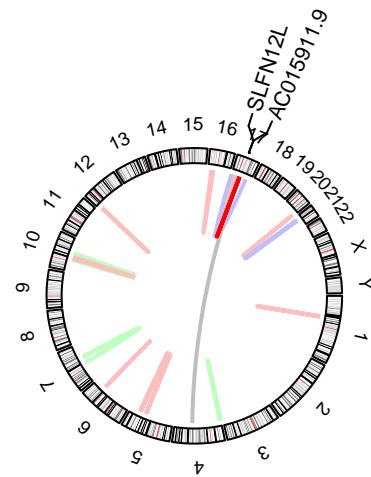
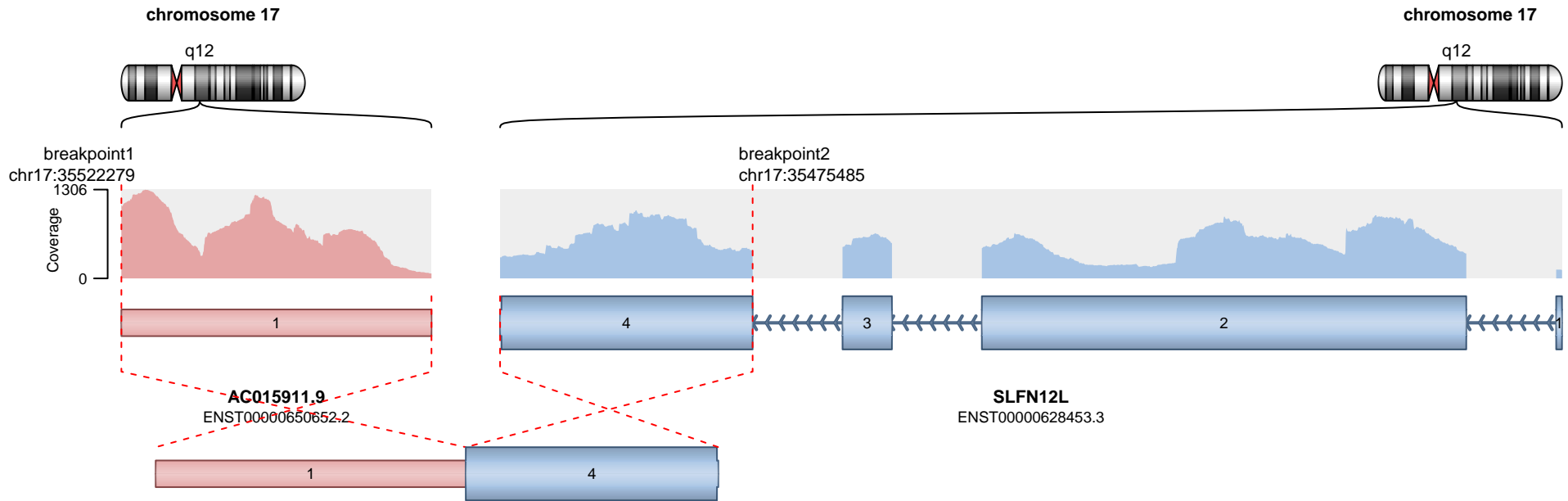


— translocation    — deletion  
— duplication    — inversion

Genes are not protein-coding.

**SUPPORTING READ COUNT**

Split reads = 28  
Discordant mates = 2

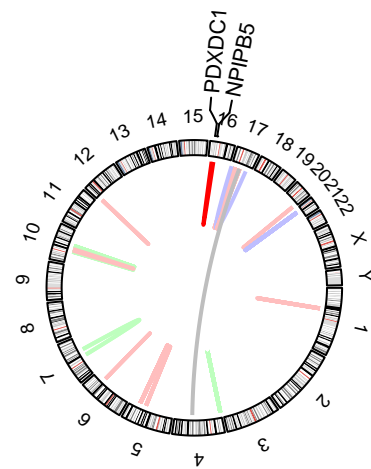
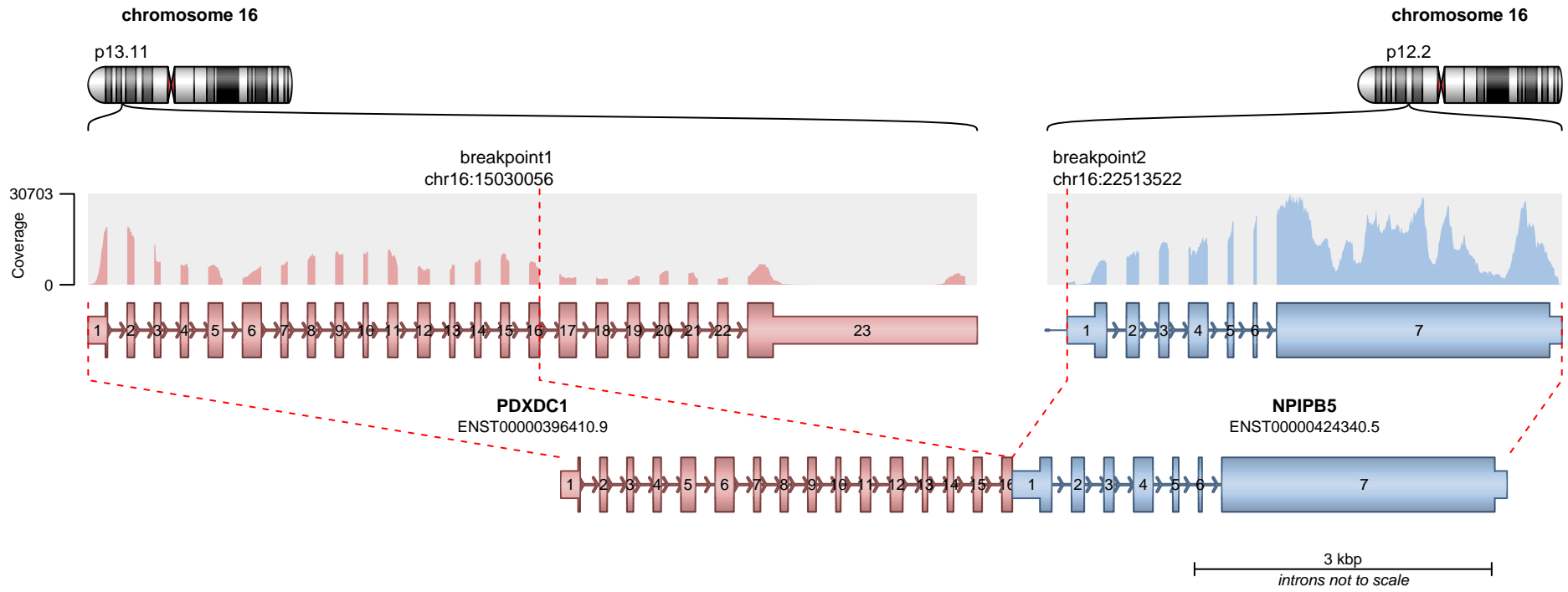


— translocation    — deletion  
— duplication    — inversion

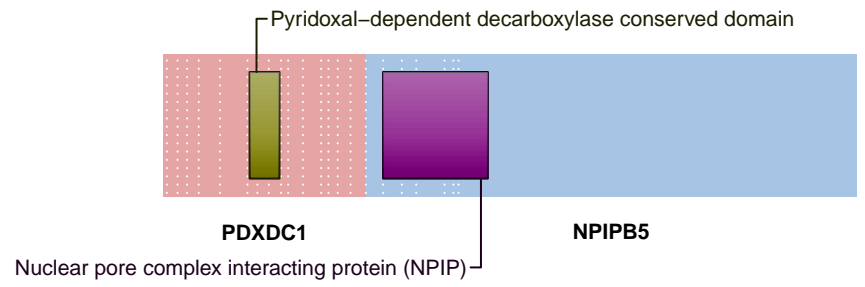
No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 6  
Discordant mates = 1



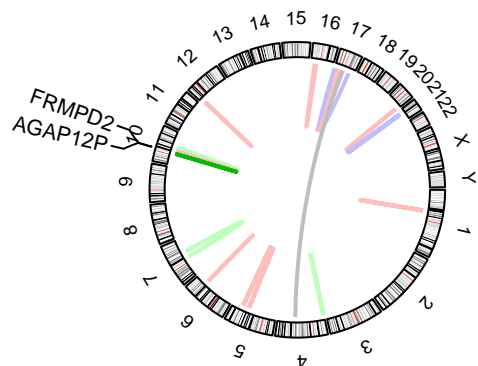
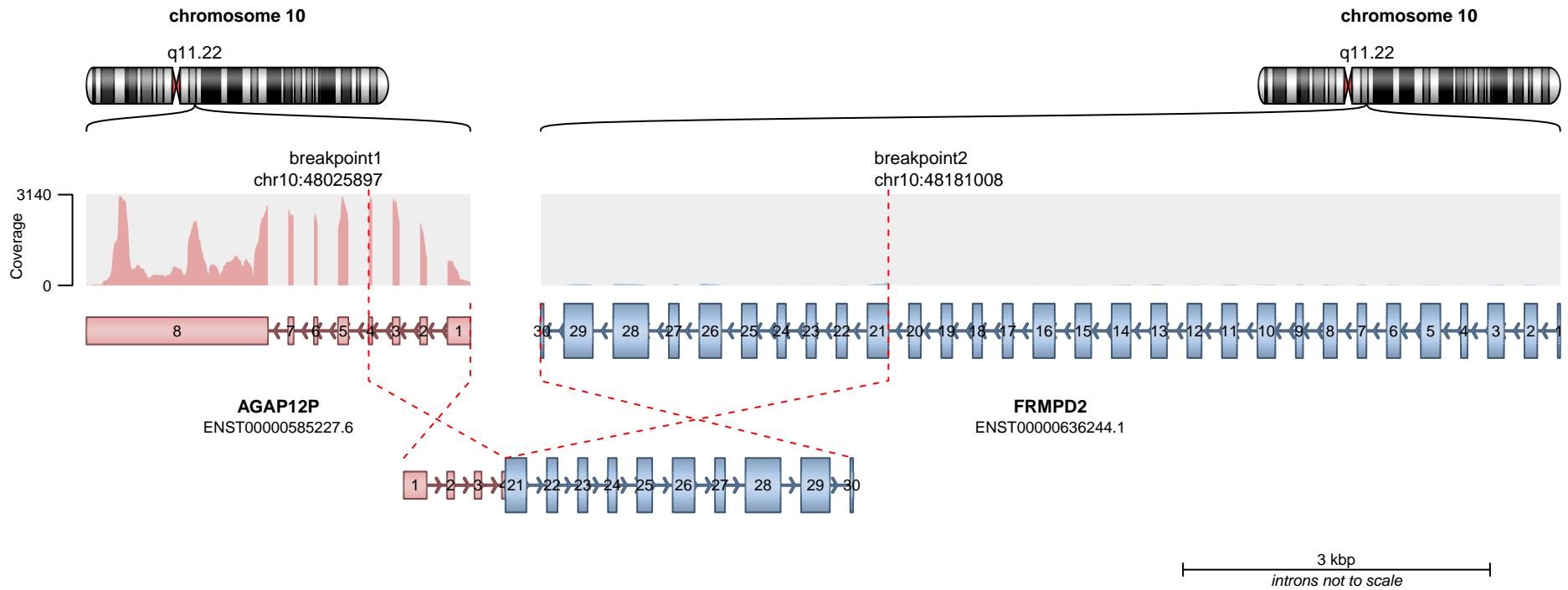
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



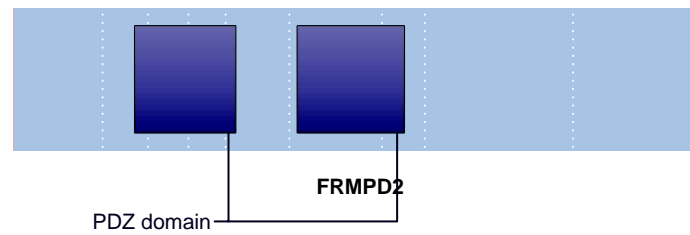
**SUPPORTING READ COUNT**

Split reads = 54  
Discordant mates = 18

- translocation
- duplication
- deletion
- inversion



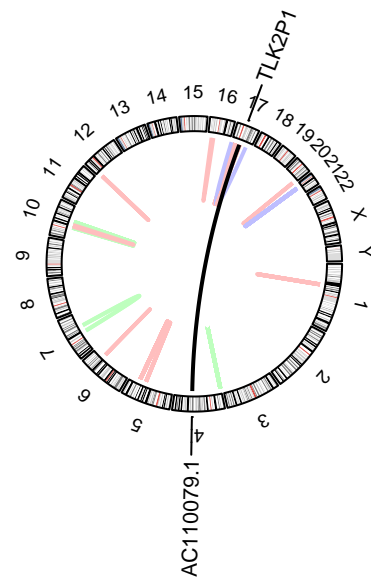
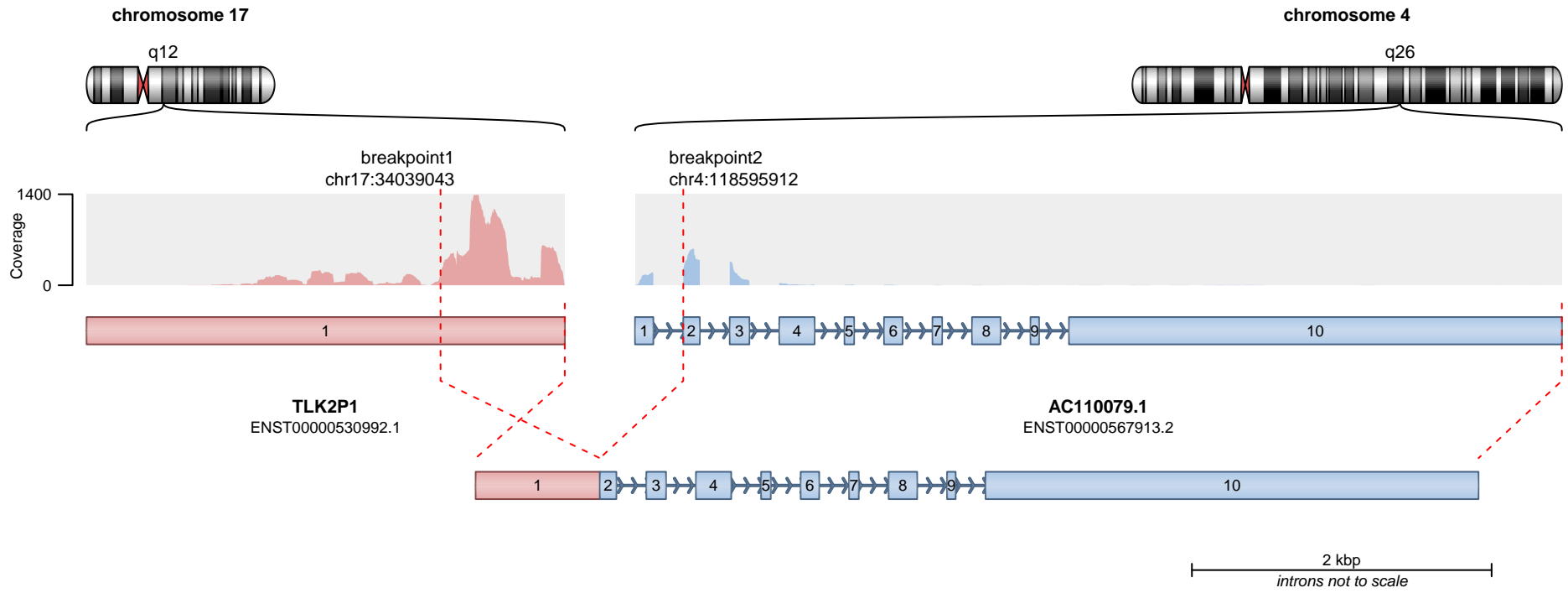
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 43  
Discordant mates = 2

— translocation    — deletion  
— duplication    — inversion

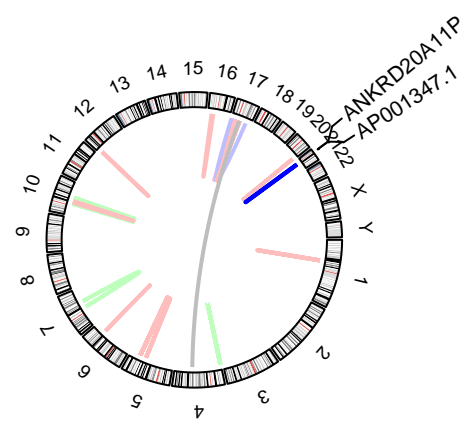
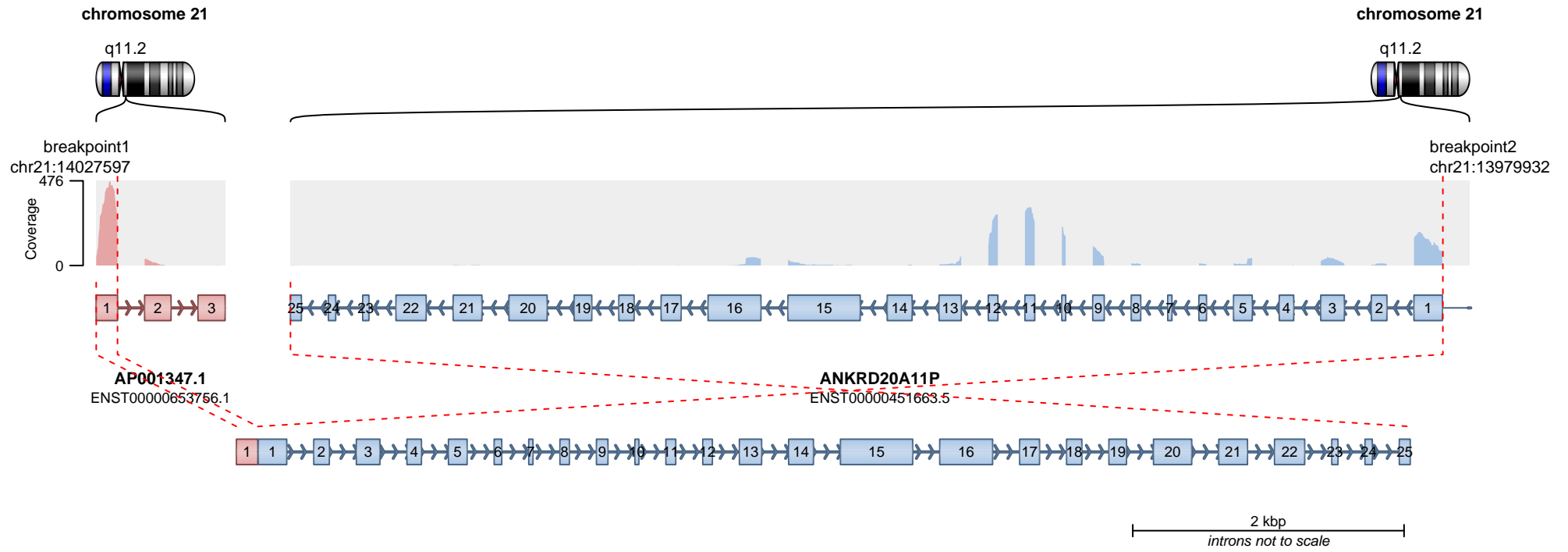


— translocation    — deletion  
 — duplication    — inversion

Genes are not protein-coding.

**SUPPORTING READ COUNT**

Split reads = 28  
Discordant mates = 0

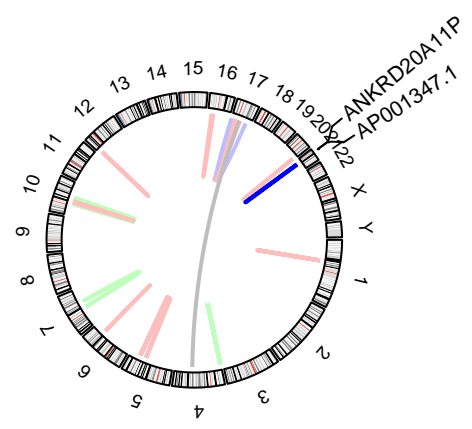
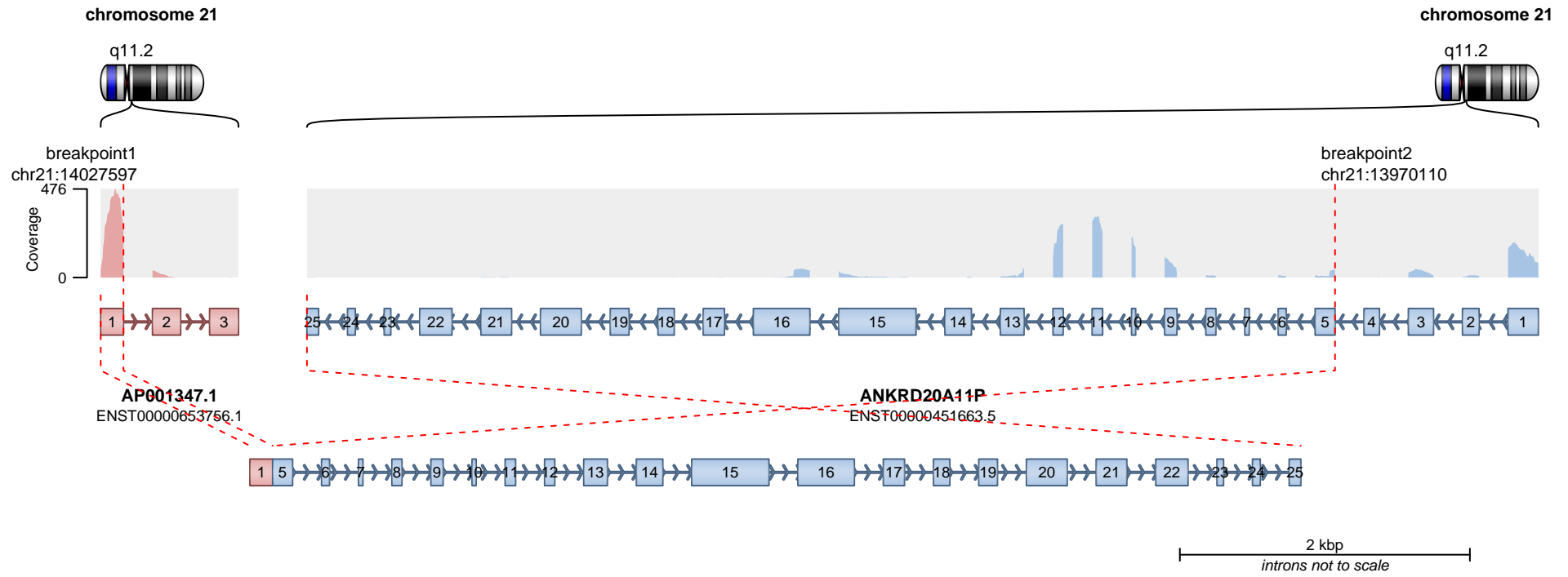


Genes are not protein-coding.

**SUPPORTING READ COUNT**

Split reads = 18  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion

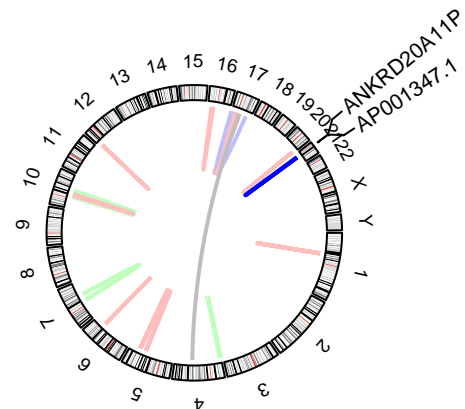
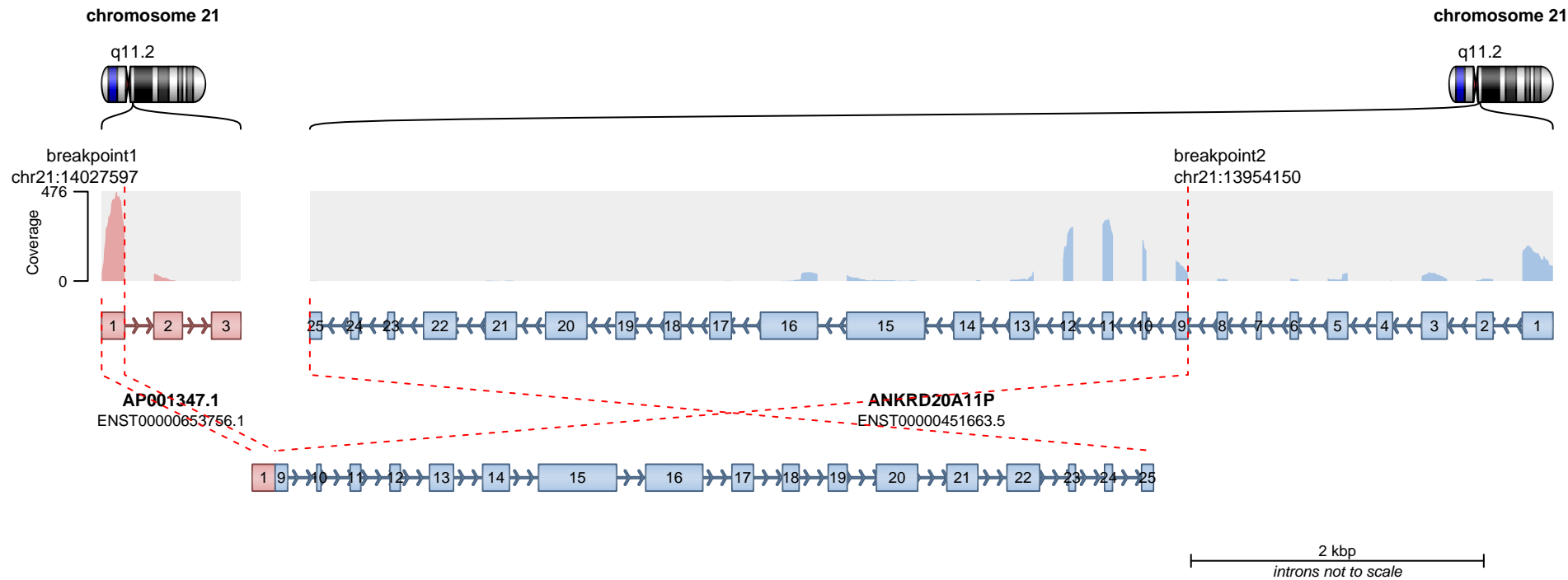


Genes are not protein-coding.

**SUPPORTING READ COUNT**

Split reads = 14  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion

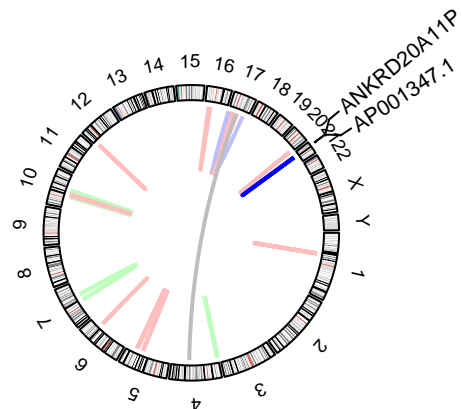
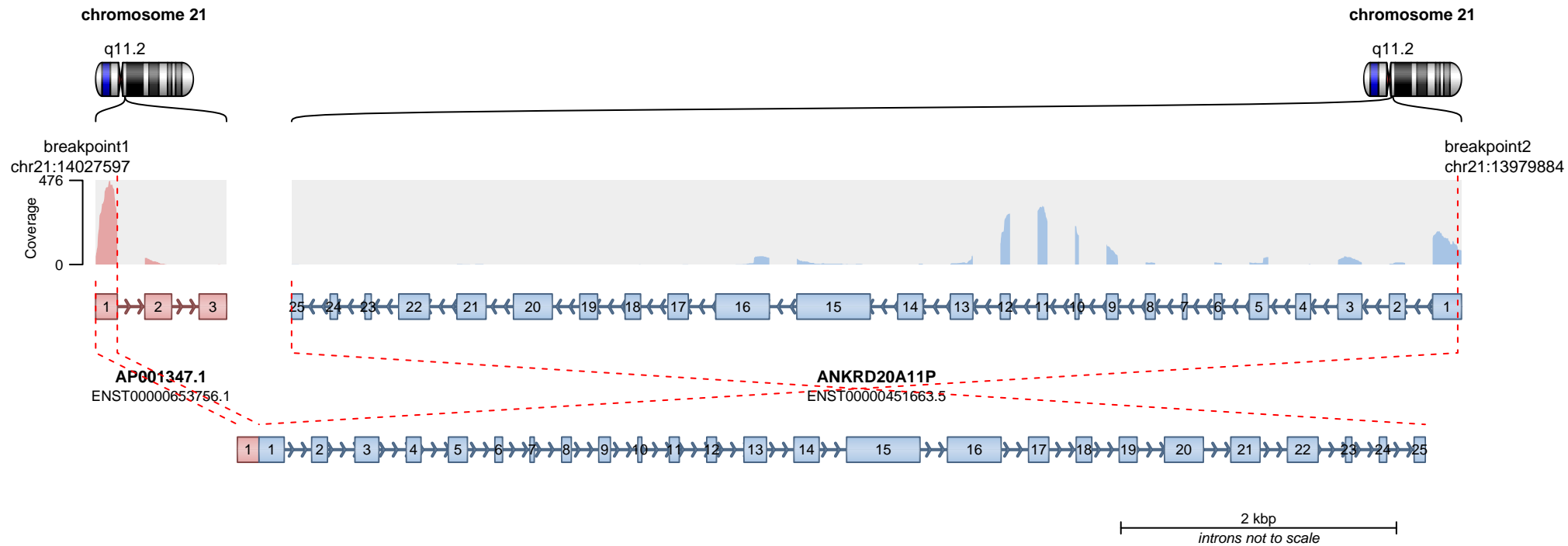


— translocation    — deletion  
— duplication      — inversion

Genes are not protein-coding.

**SUPPORTING READ COUNT**

Split reads = 10  
Discordant mates = 1

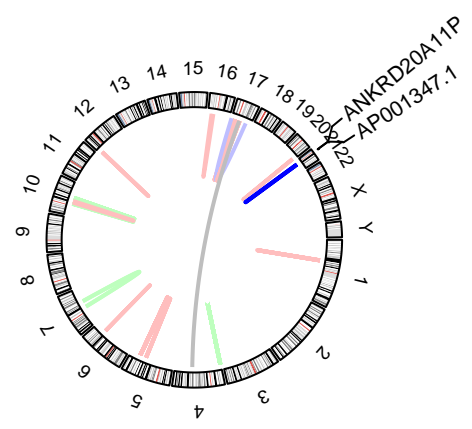
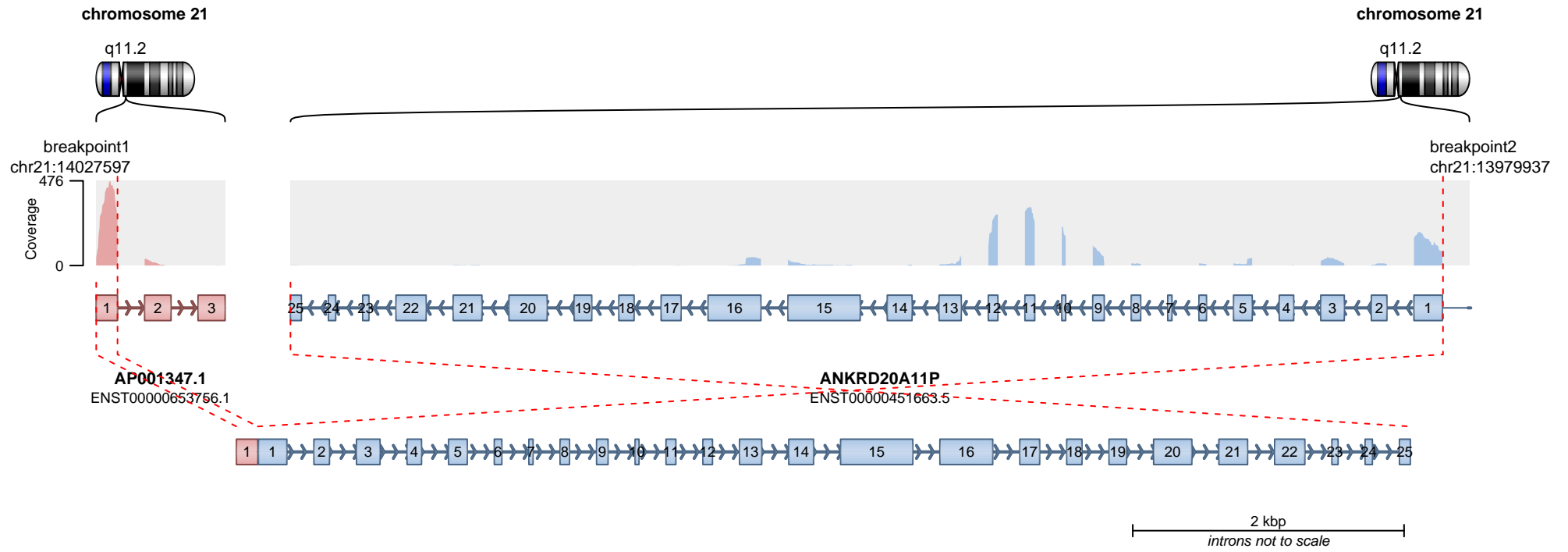


Genes are not protein-coding.

**SUPPORTING READ COUNT**

Split reads = 7  
Discordant mates = 1

— translocation    — deletion  
— duplication    — inversion

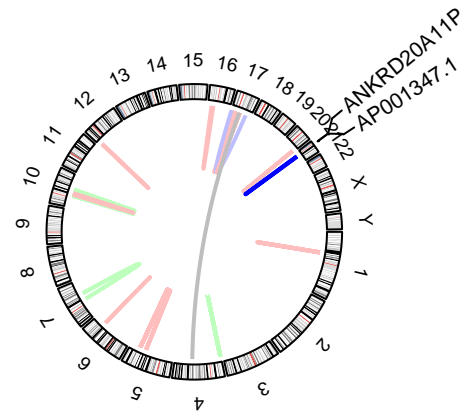
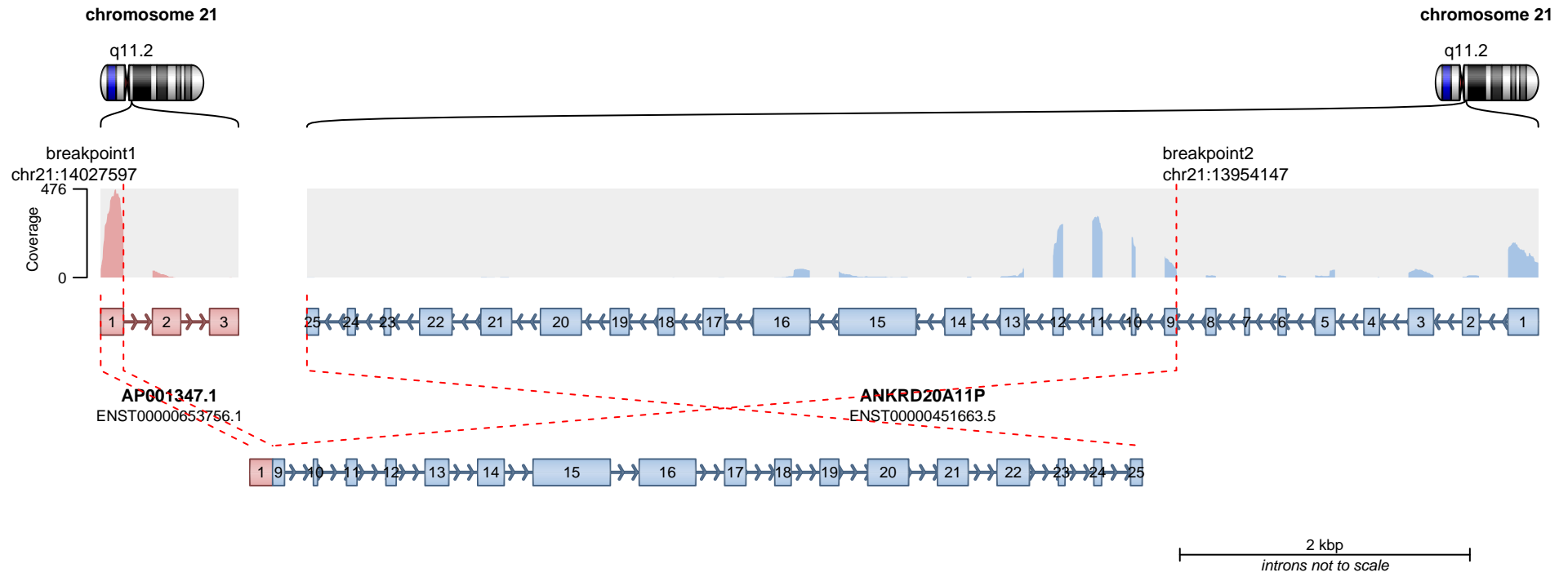


Genes are not protein-coding.

**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion

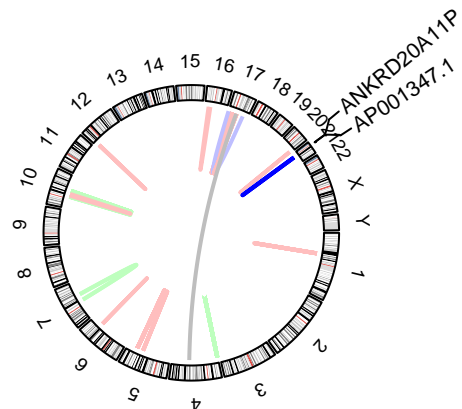
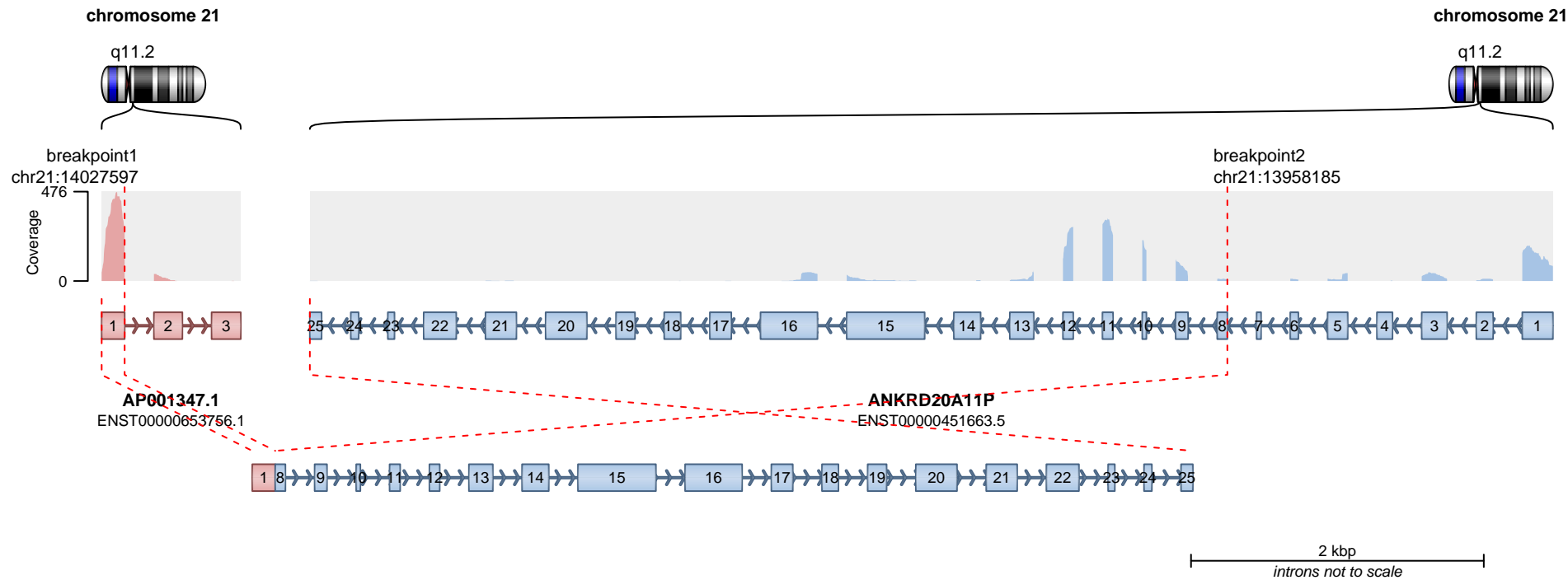


— translocation    — deletion  
— duplication      — inversion

Genes are not protein-coding.

**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 1



Genes are not protein-coding.

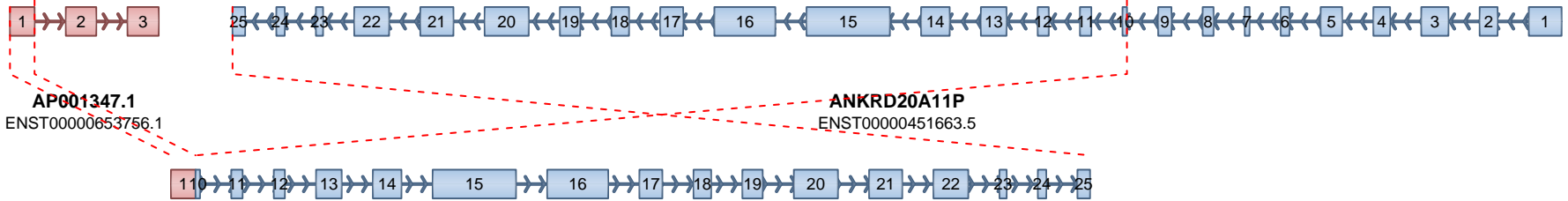
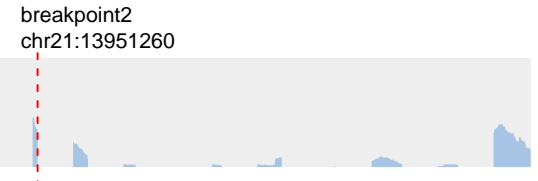
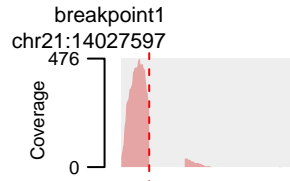
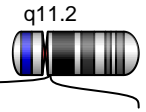
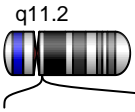
**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 1

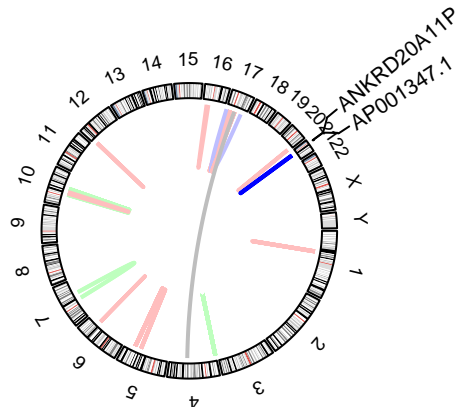
— translocation    — deletion  
— duplication    — inversion

chromosome 21

chromosome 21



2 kbp  
*introns not to scale*

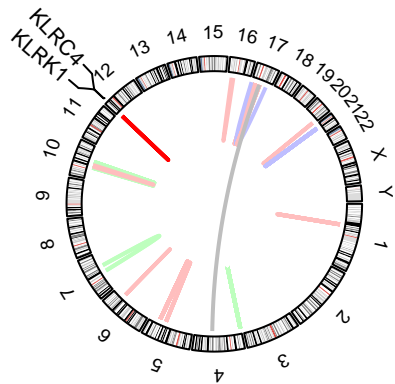
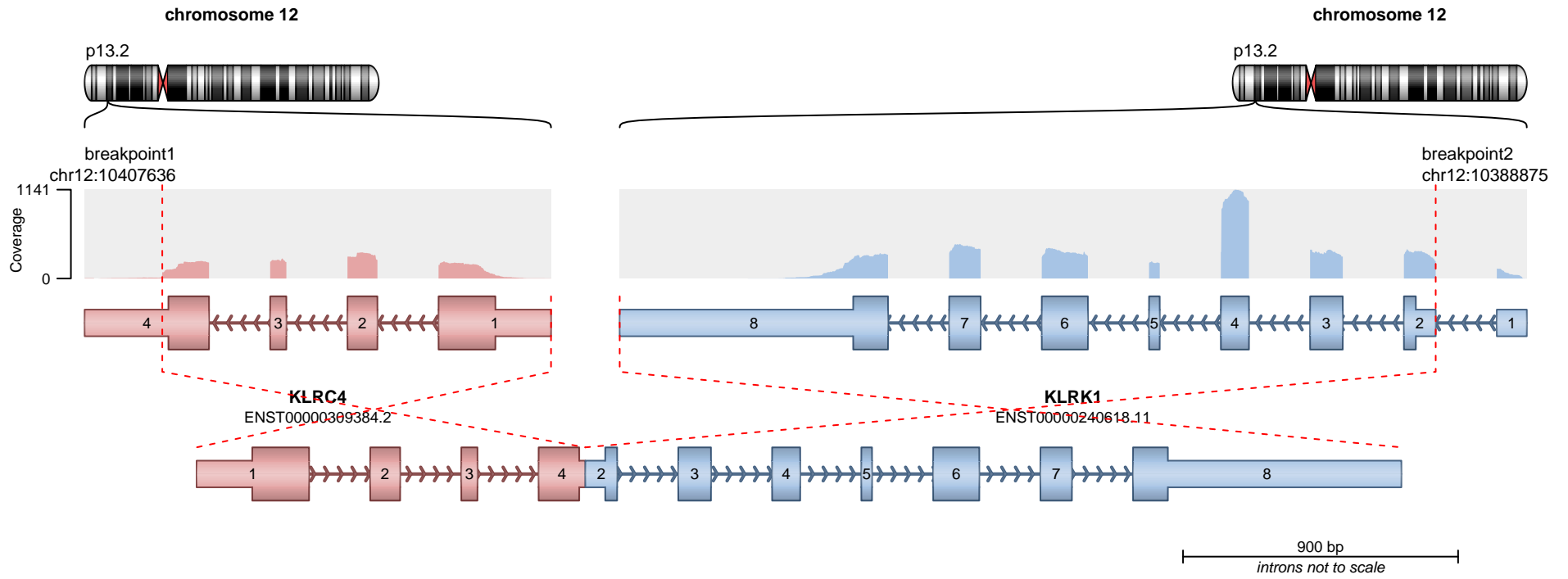


— translocation — deletion  
— duplication — inversion

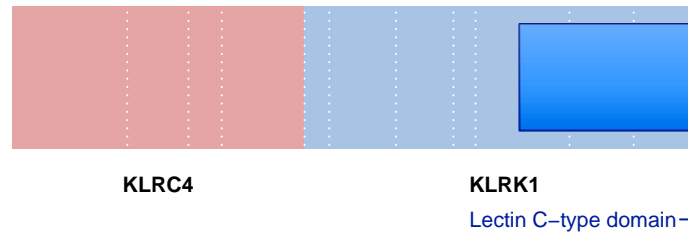
Genes are not protein-coding.

**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0



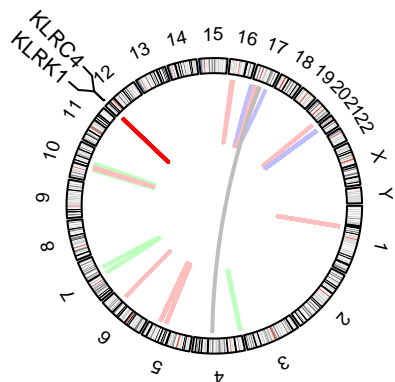
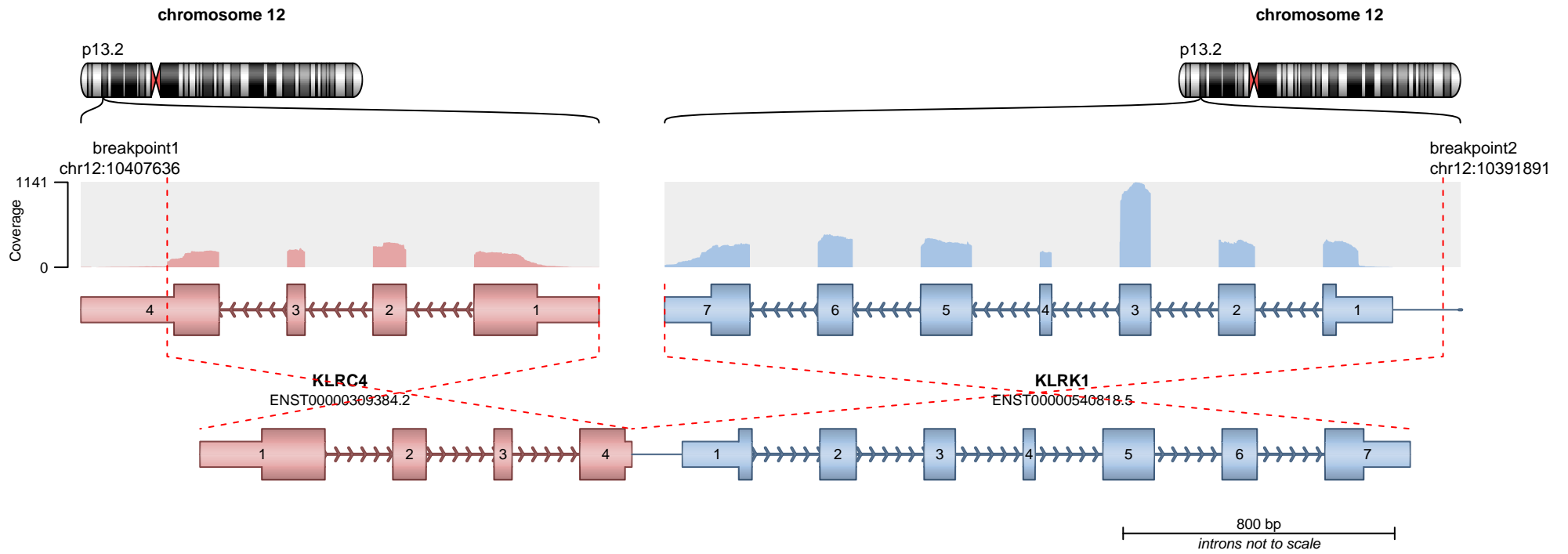
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



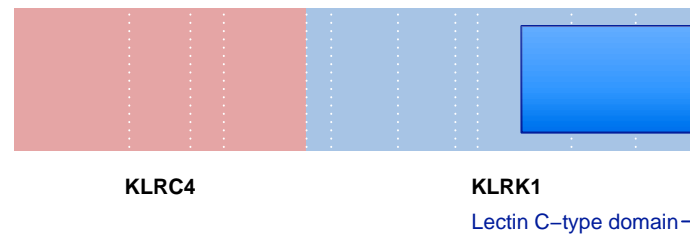
**SUPPORTING READ COUNT**

Split reads = 15  
Discordant mates = 3

— translocation — deletion  
— duplication — inversion



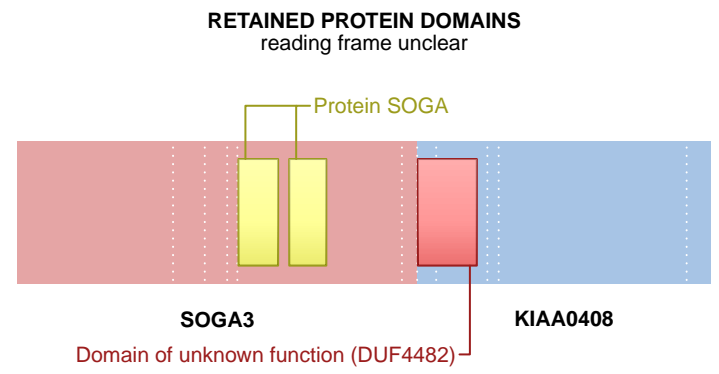
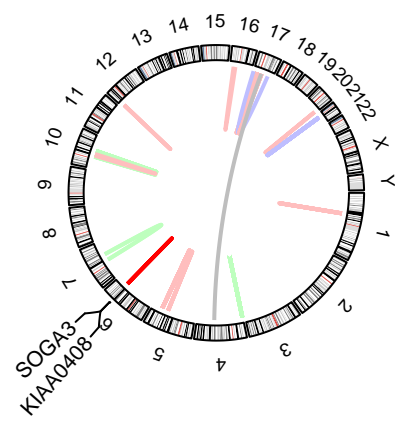
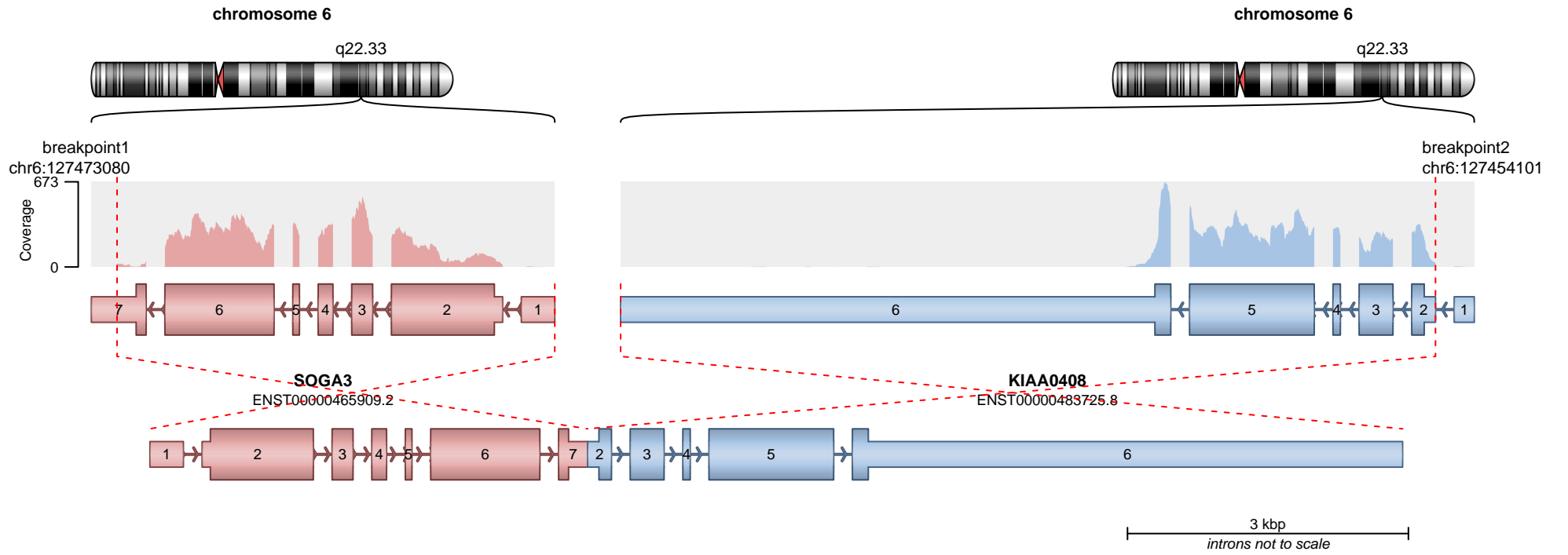
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 3

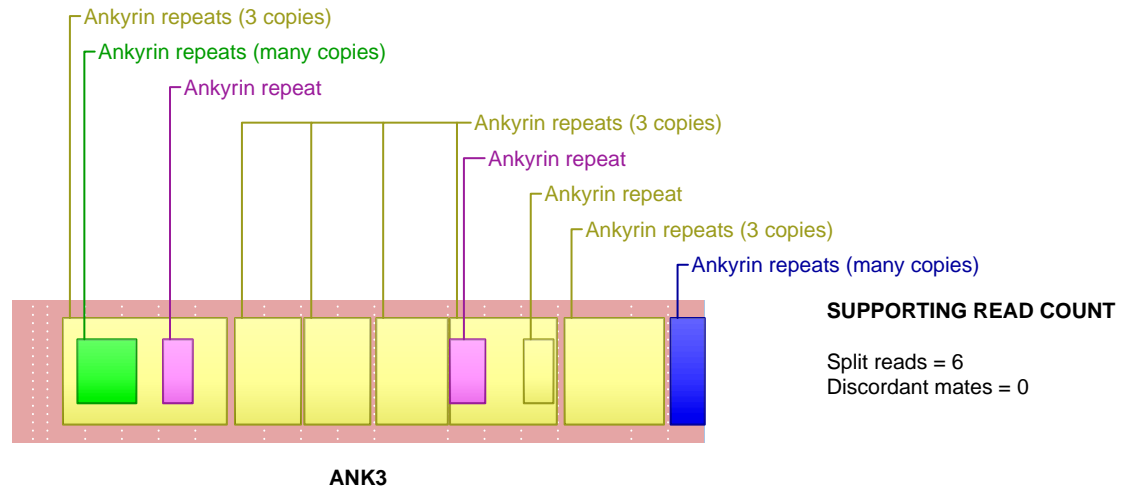
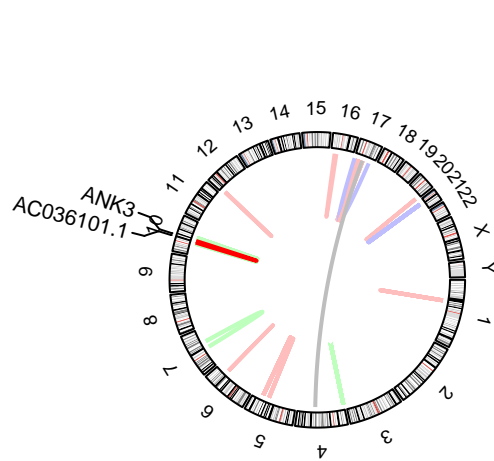
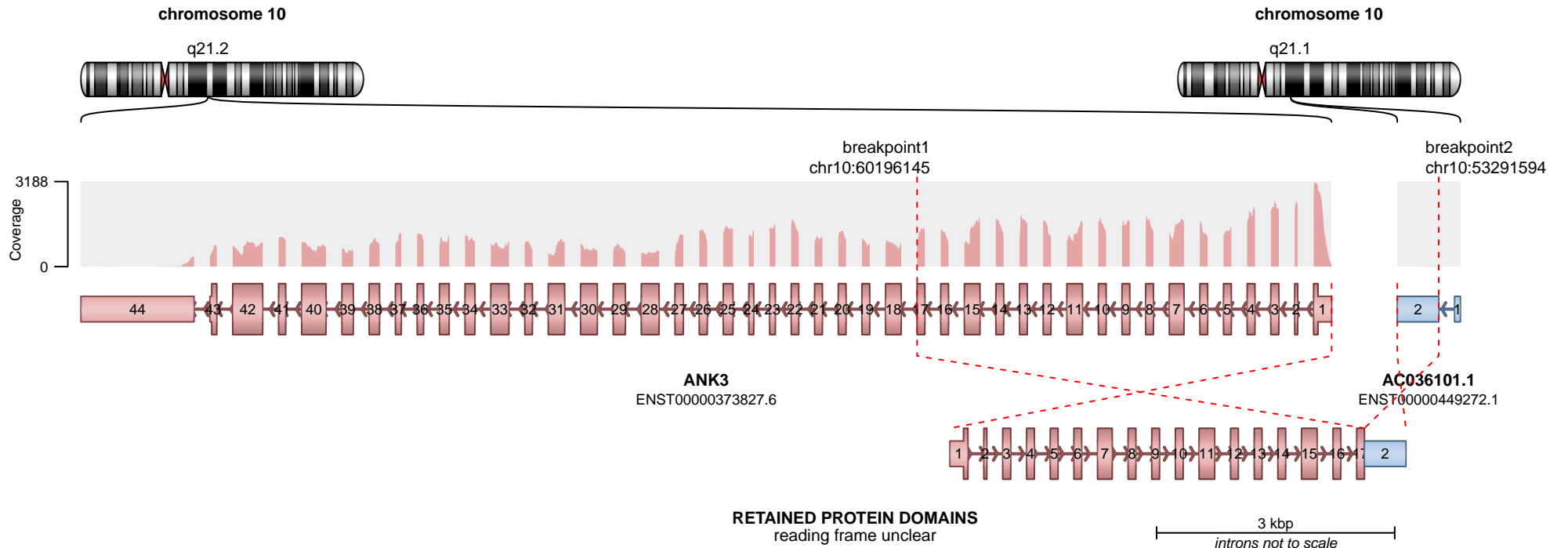
— translocation — deletion  
— duplication — inversion



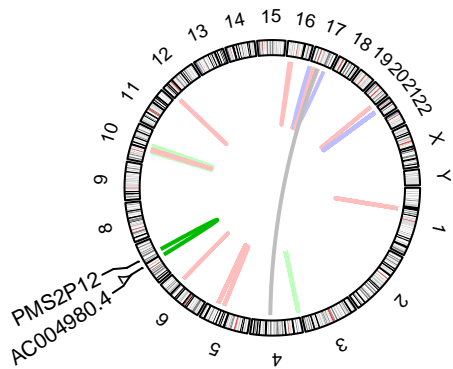
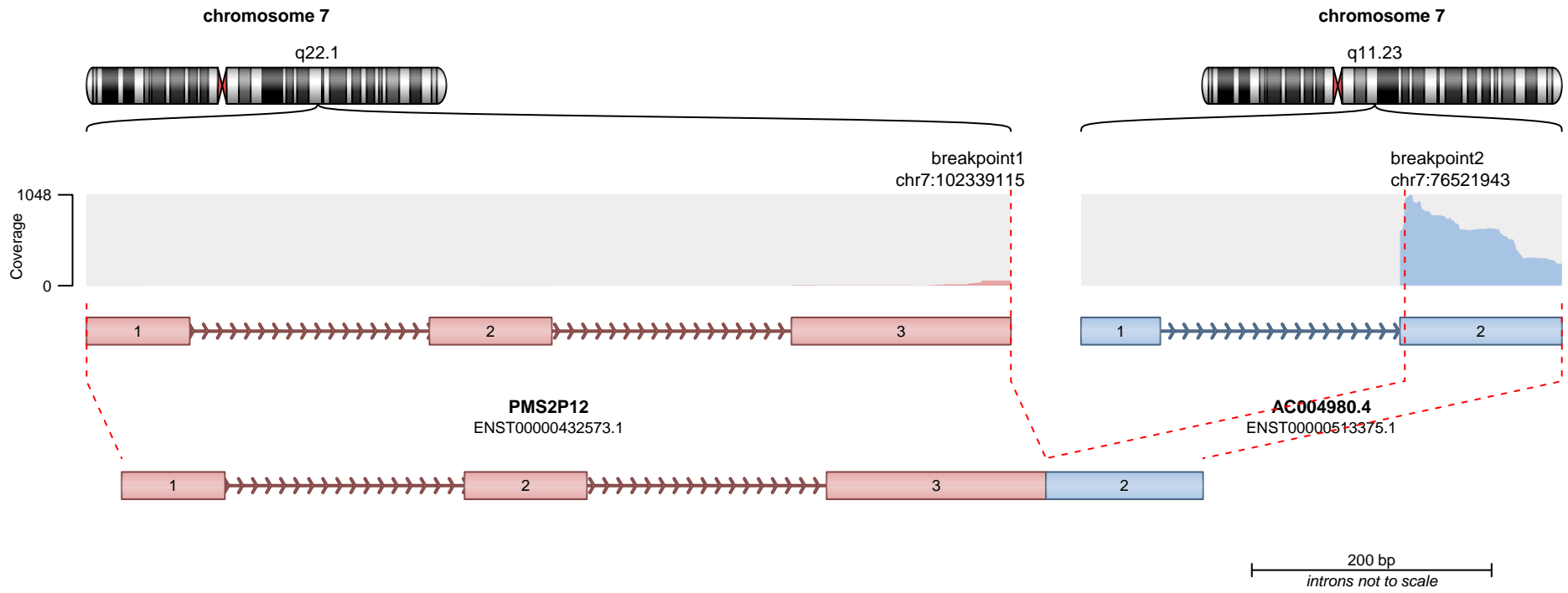
**SUPPORTING READ COUNT**

Split reads = 14  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



— translocation    — deletion  
— duplication    — inversion

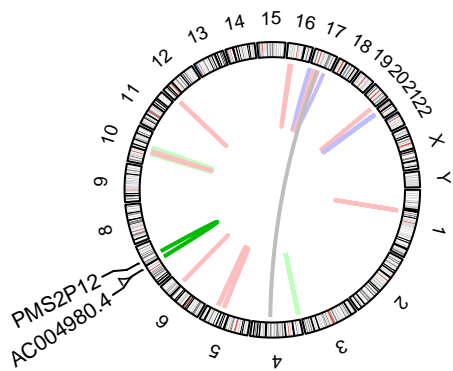
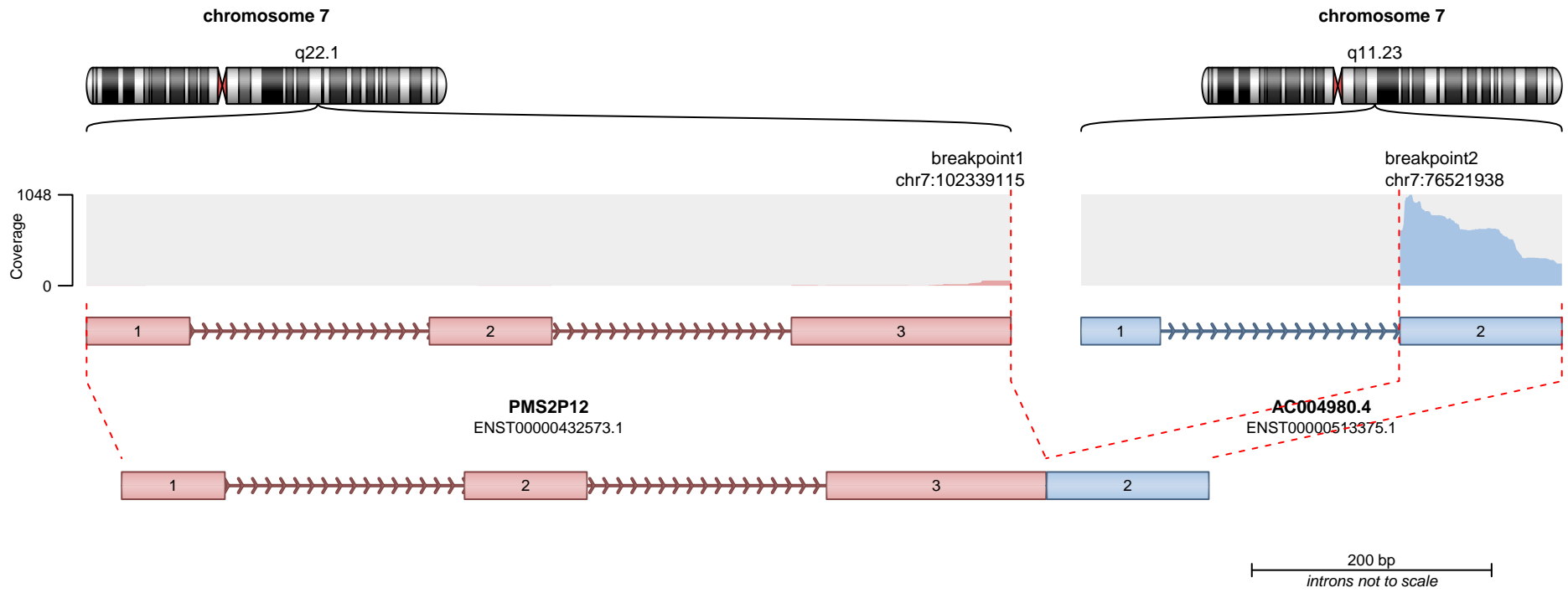


— translocation — deletion  
— duplication — inversion

Genes are not protein-coding.

**SUPPORTING READ COUNT**

Split reads = 5  
Discordant mates = 0



— translocation — deletion  
— duplication — inversion

Genes are not protein-coding.

**SUPPORTING READ COUNT**

Split reads = 5  
Discordant mates = 0