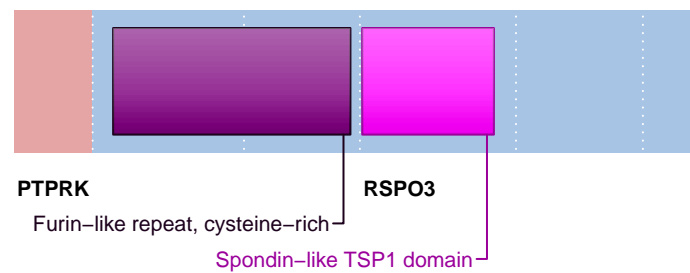


— translocation — deletion  
— duplication — inversion

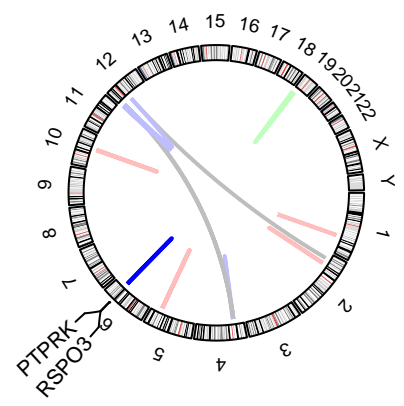
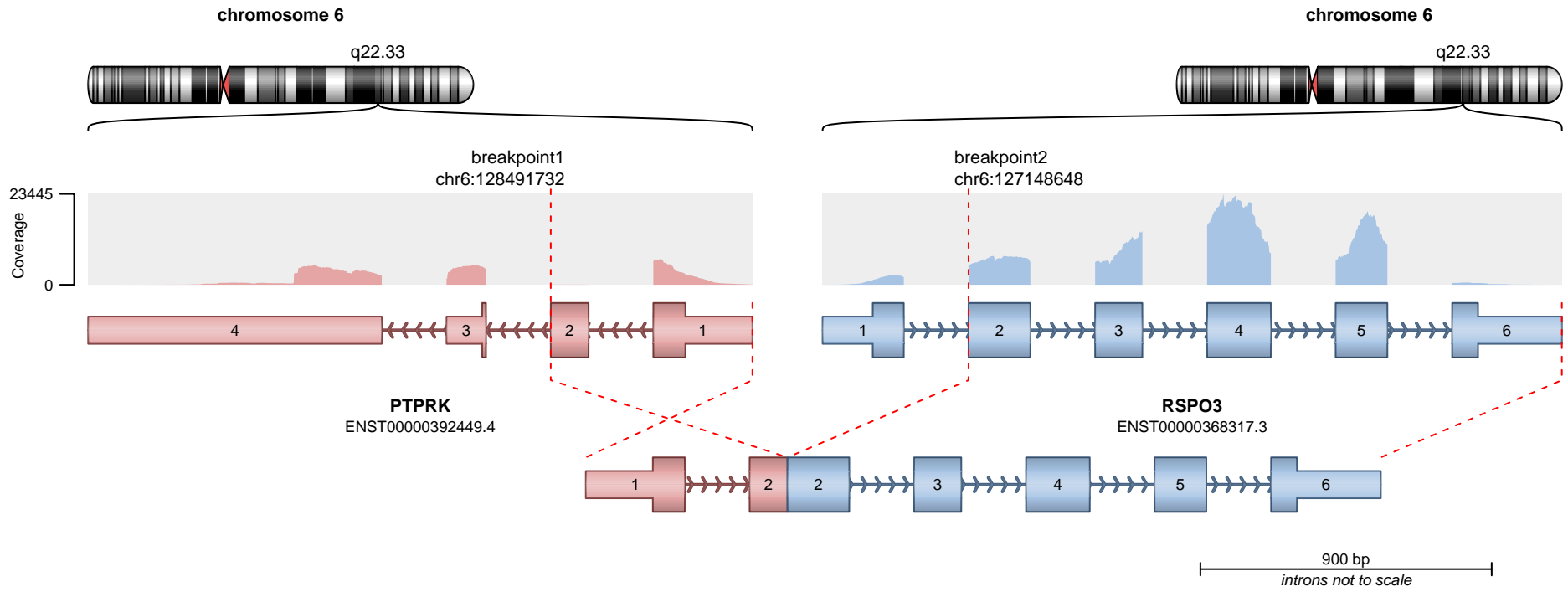
### RETAINED PROTEIN DOMAINS

reading frame unclear

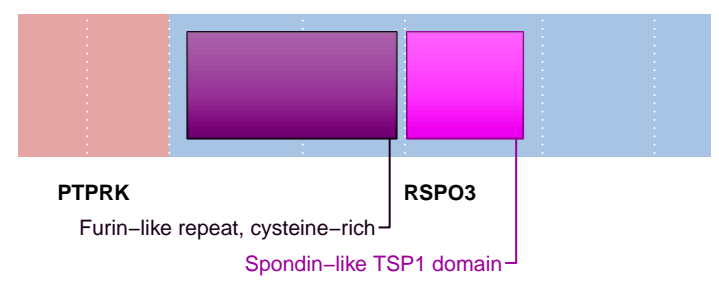


### SUPPORTING READ COUNT

Split reads = 1449  
Discordant mates = 7



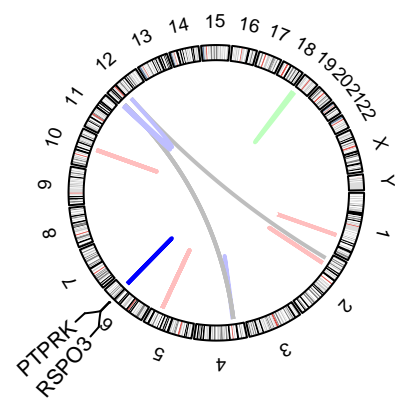
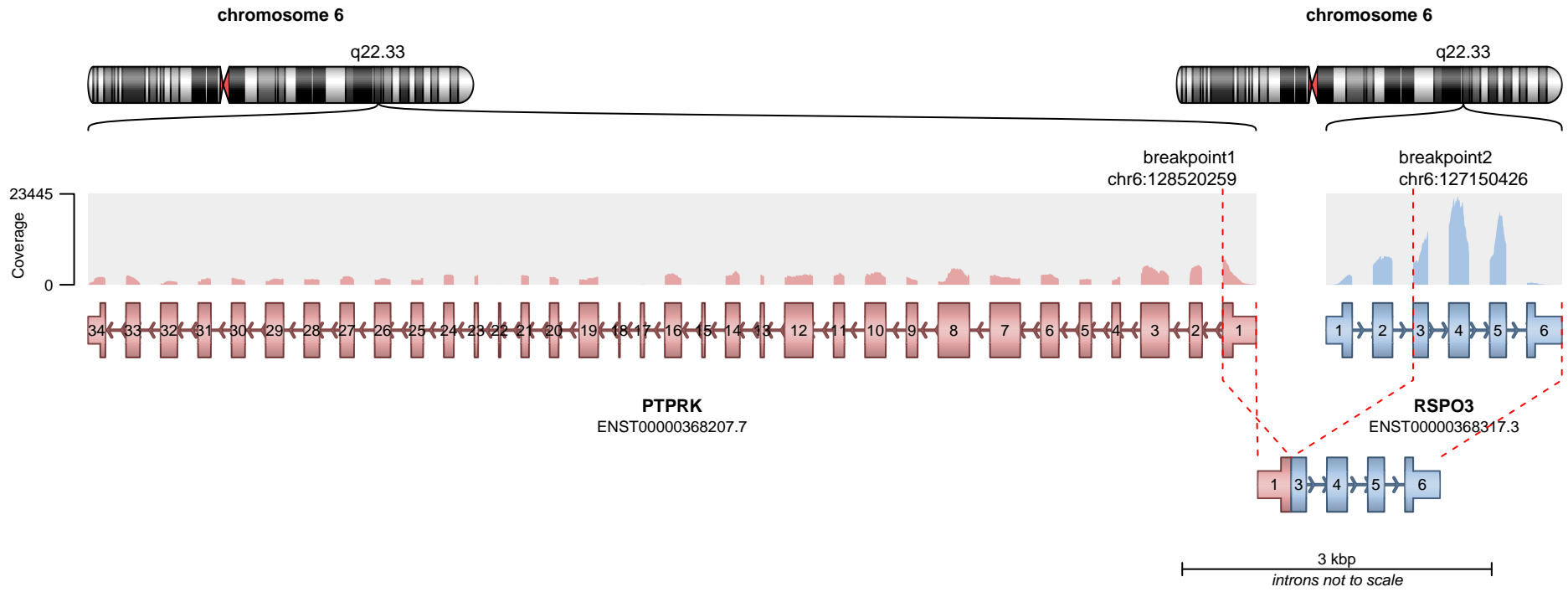
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

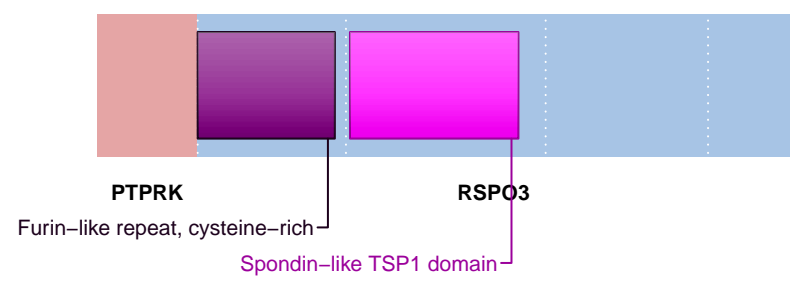
Split reads = 4  
Discordant mates = 7

- translocation
- duplication
- deletion
- inversion



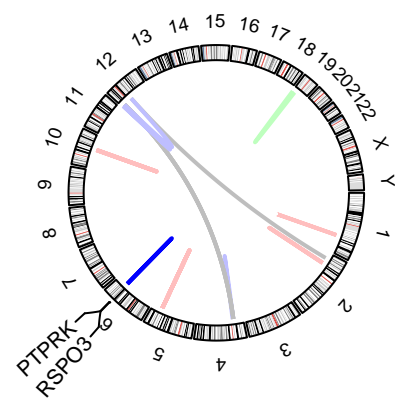
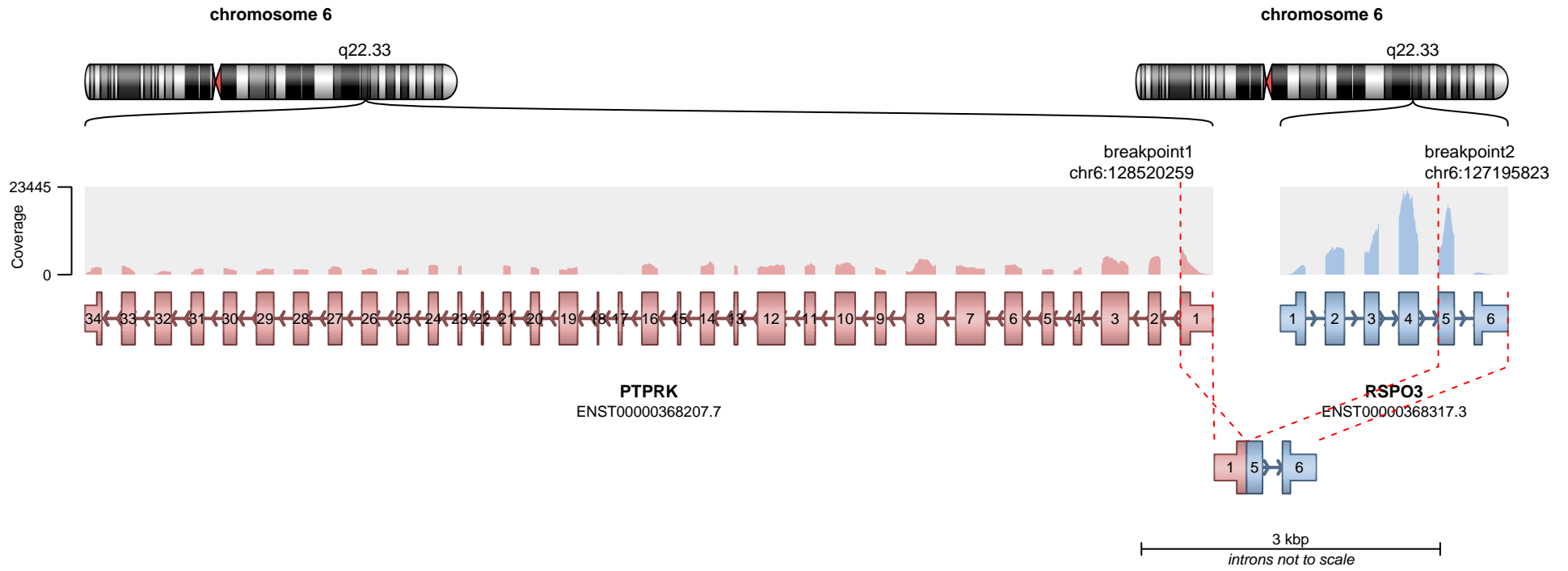
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 5  
Discordant mates = 1

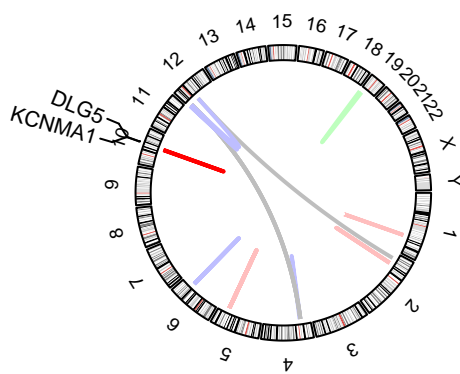
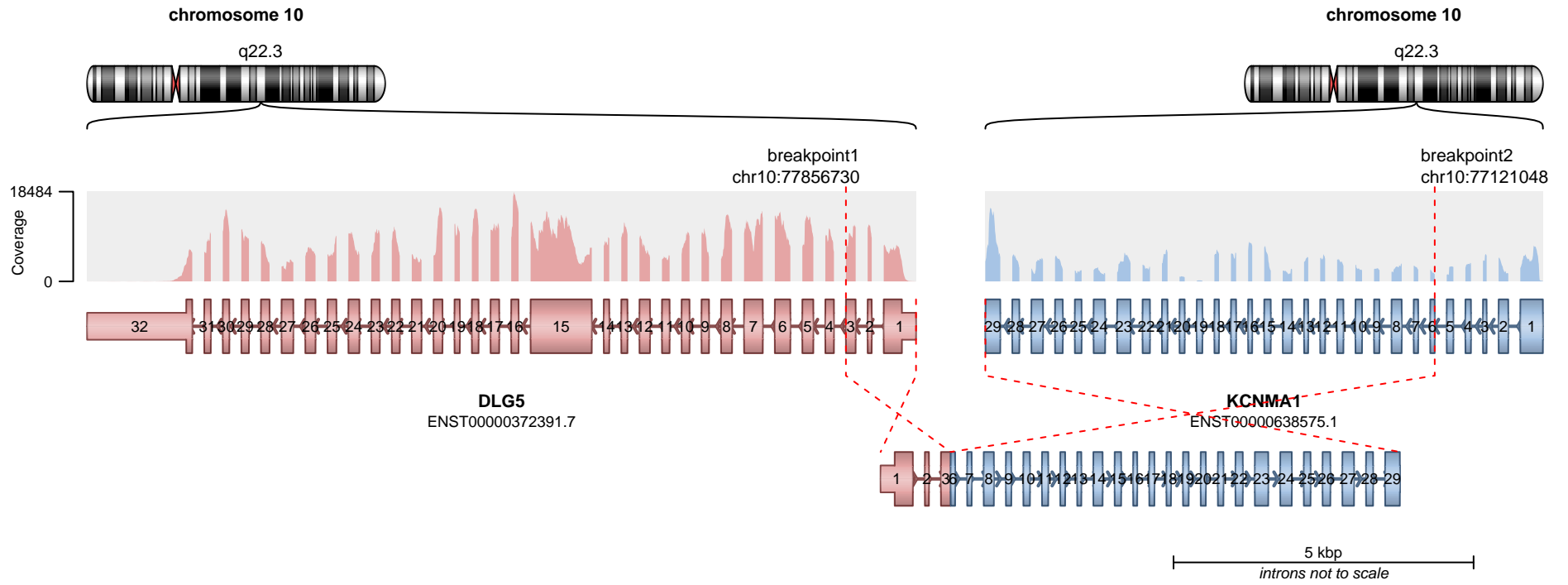


— translocation    — deletion  
— duplication    — inversion

No protein domains retained in fusion.

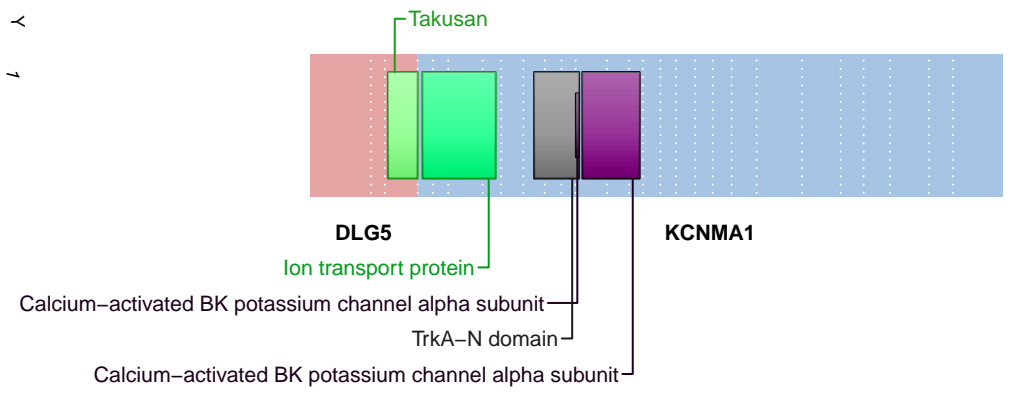
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0



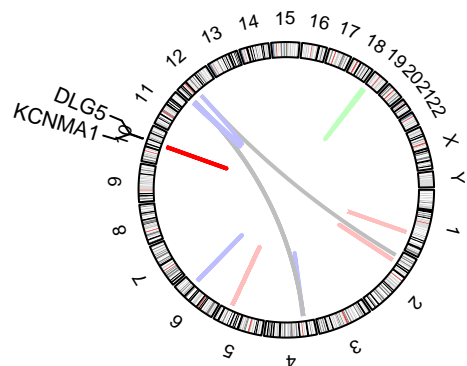
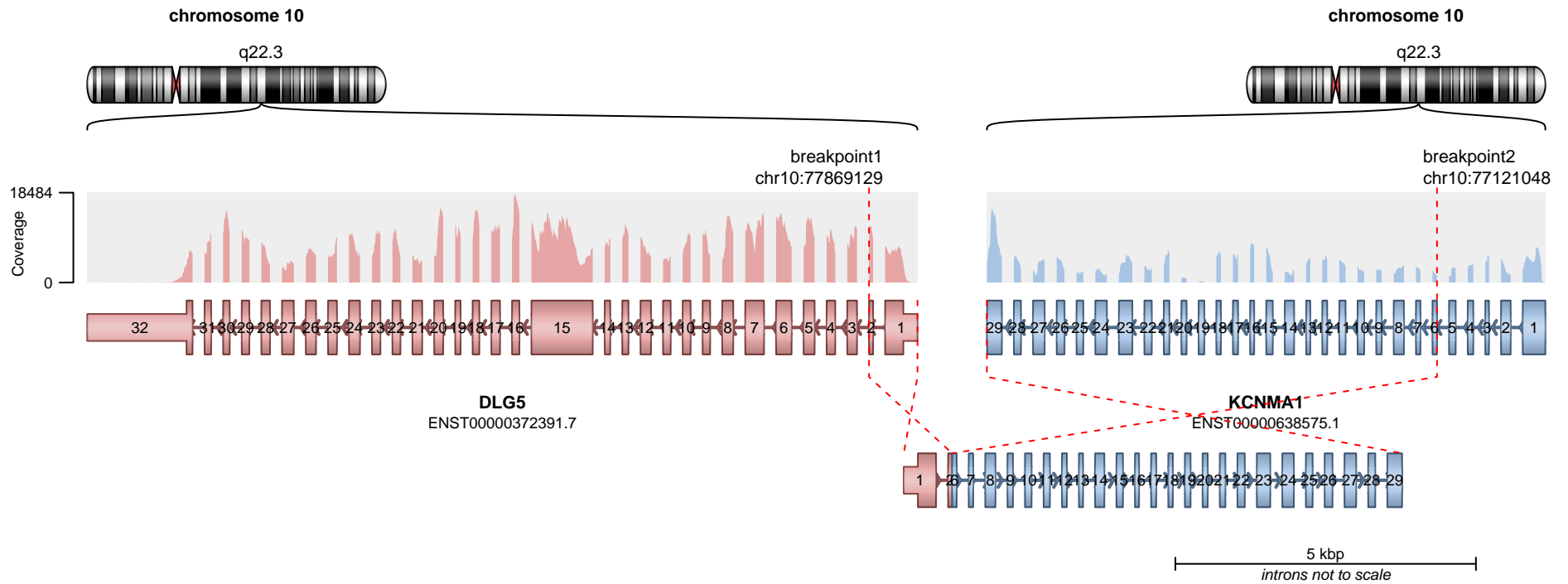
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



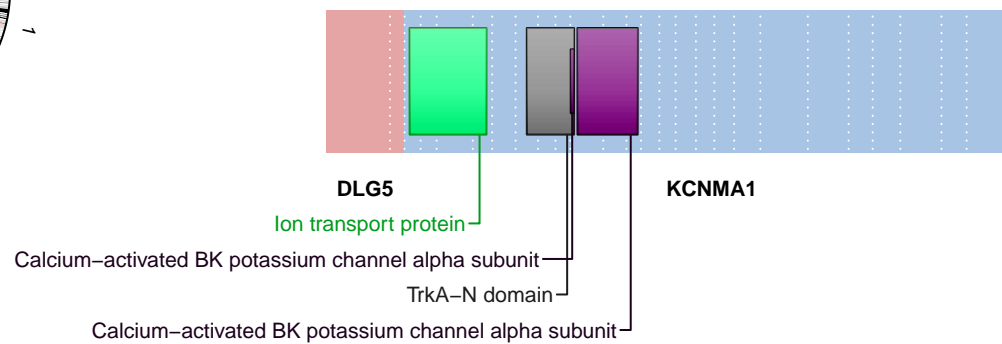
**SUPPORTING READ COUNT**

Split reads = 109  
Discordant mates = 10



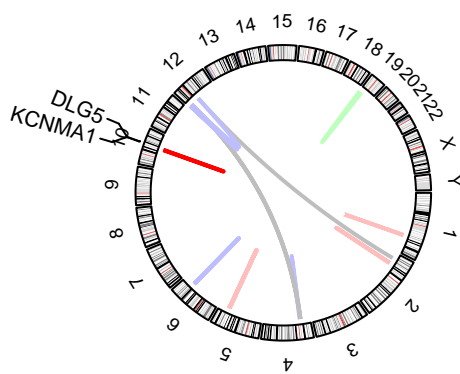
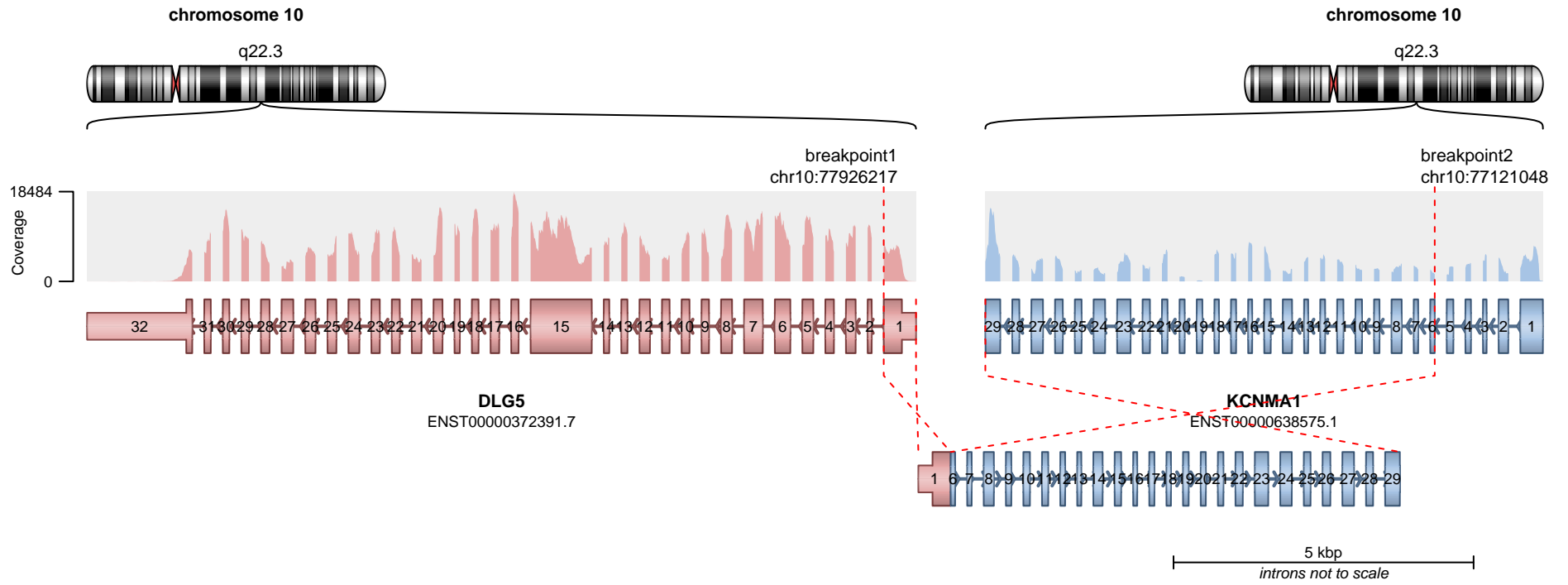
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



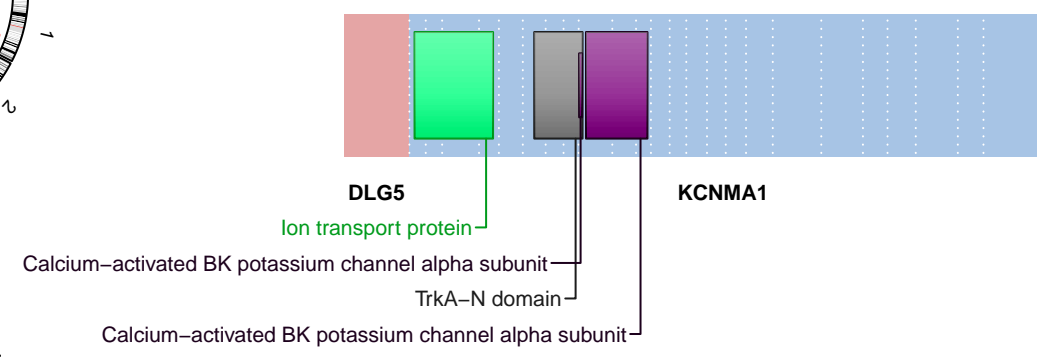
**SUPPORTING READ COUNT**

Split reads = 15  
Discordant mates = 1



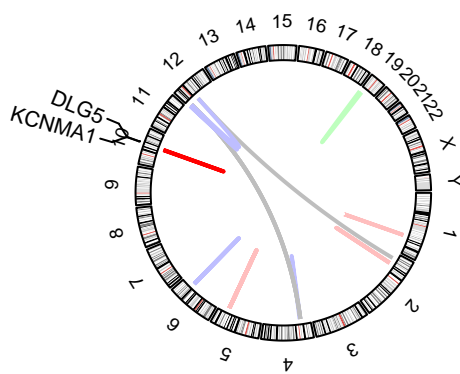
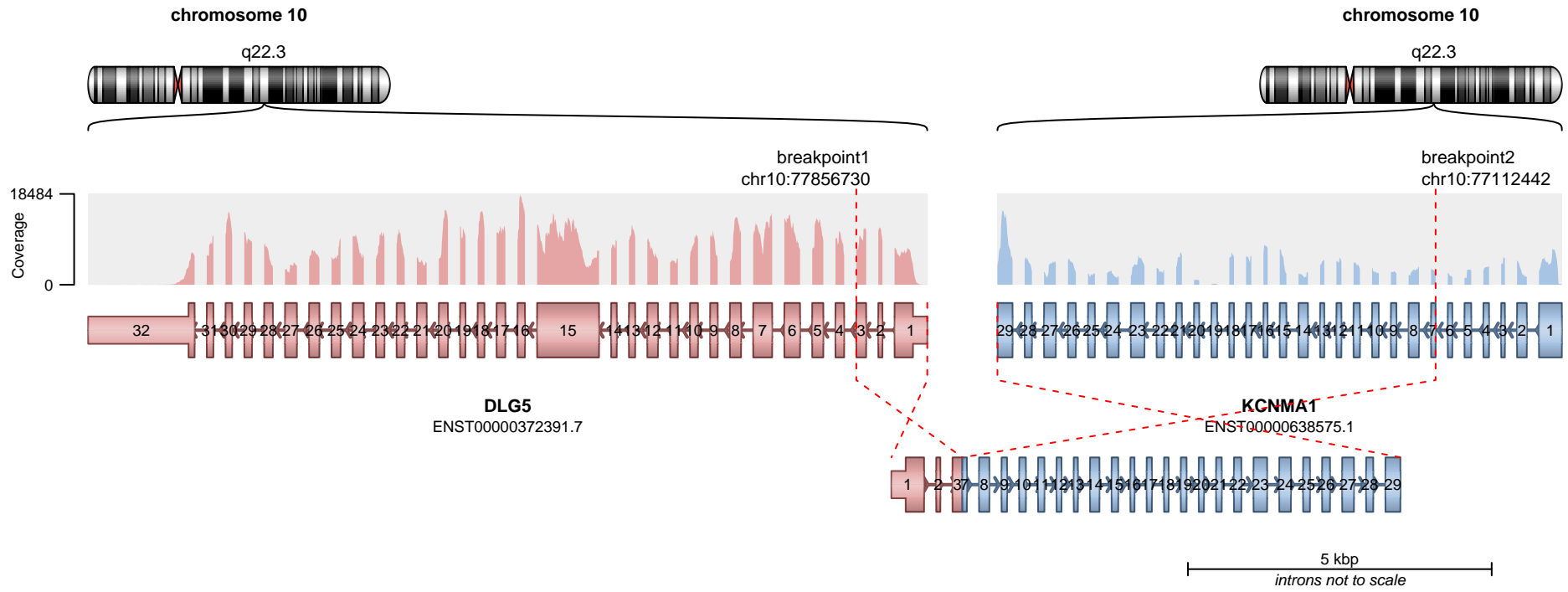
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



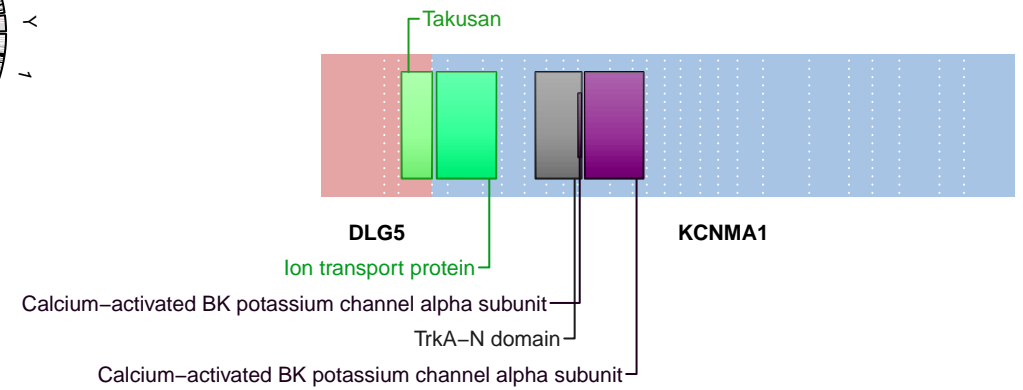
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0



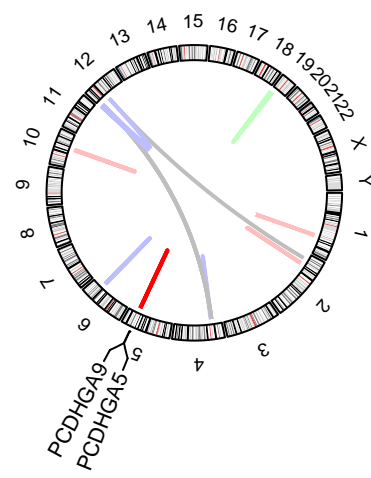
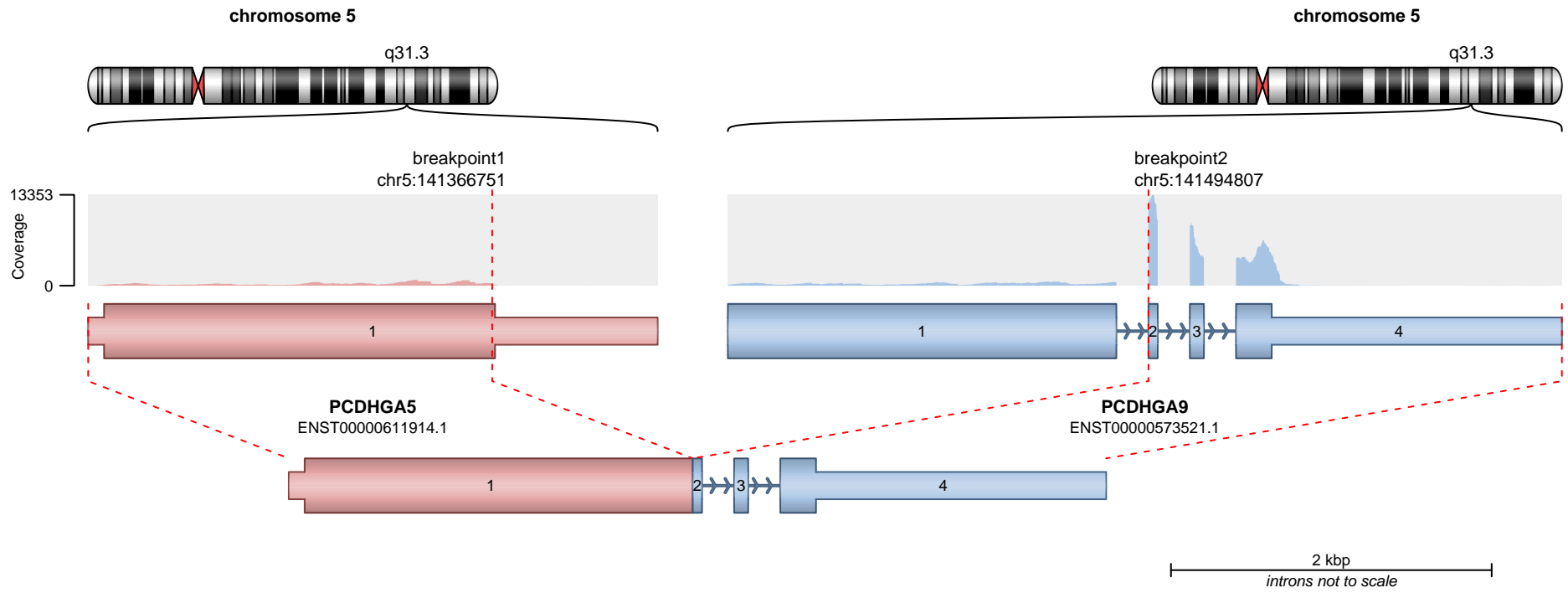
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear

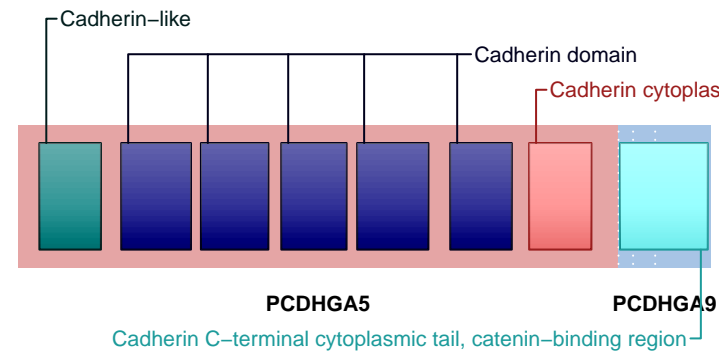


**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0



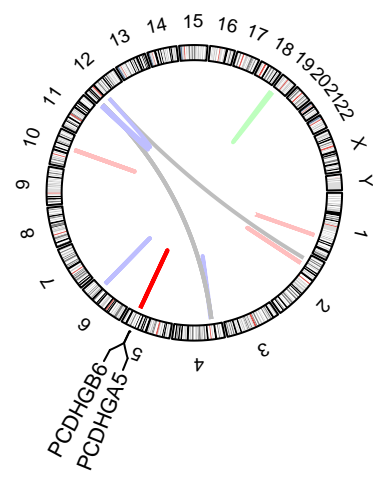
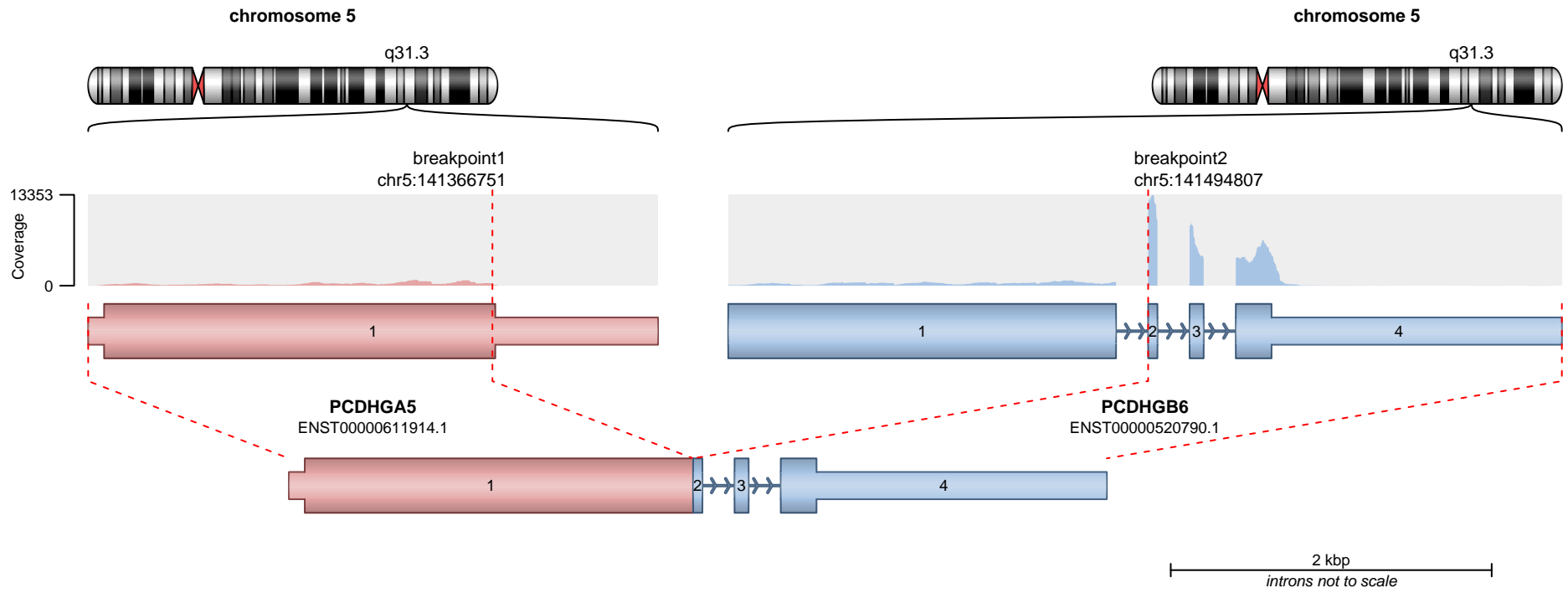
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

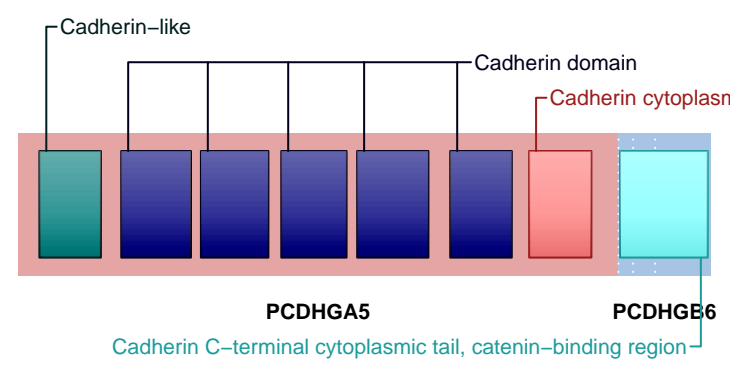
Split reads = 89  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



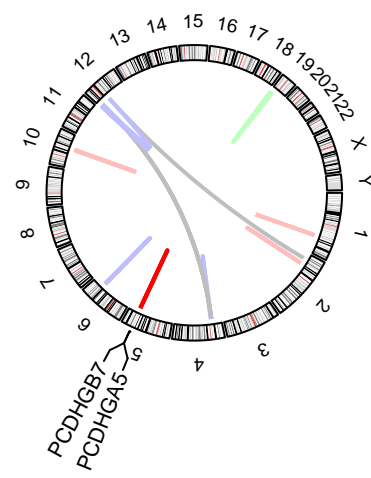
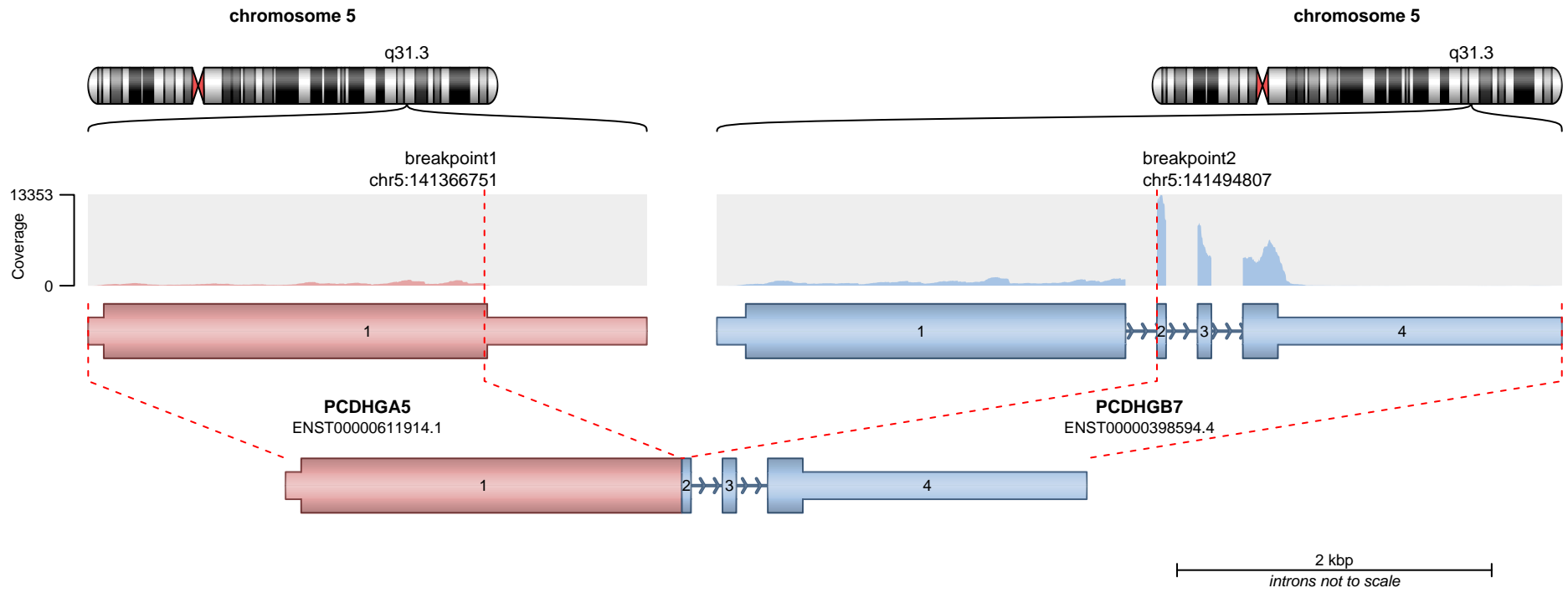
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



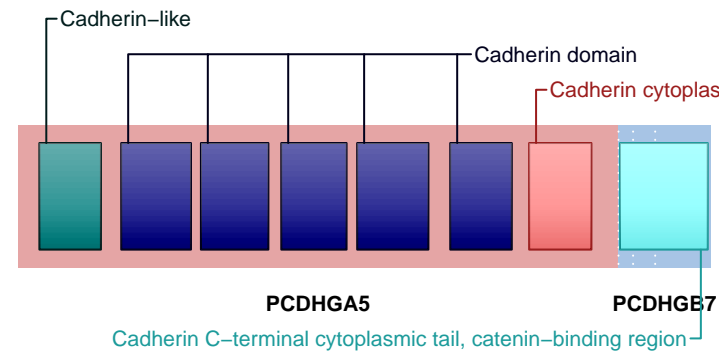
**SUPPORTING READ COUNT**

Split reads = 89  
Discordant mates = 0



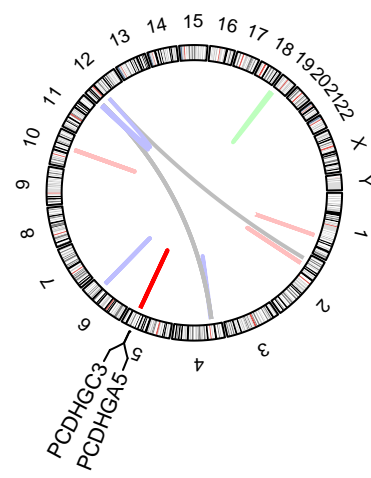
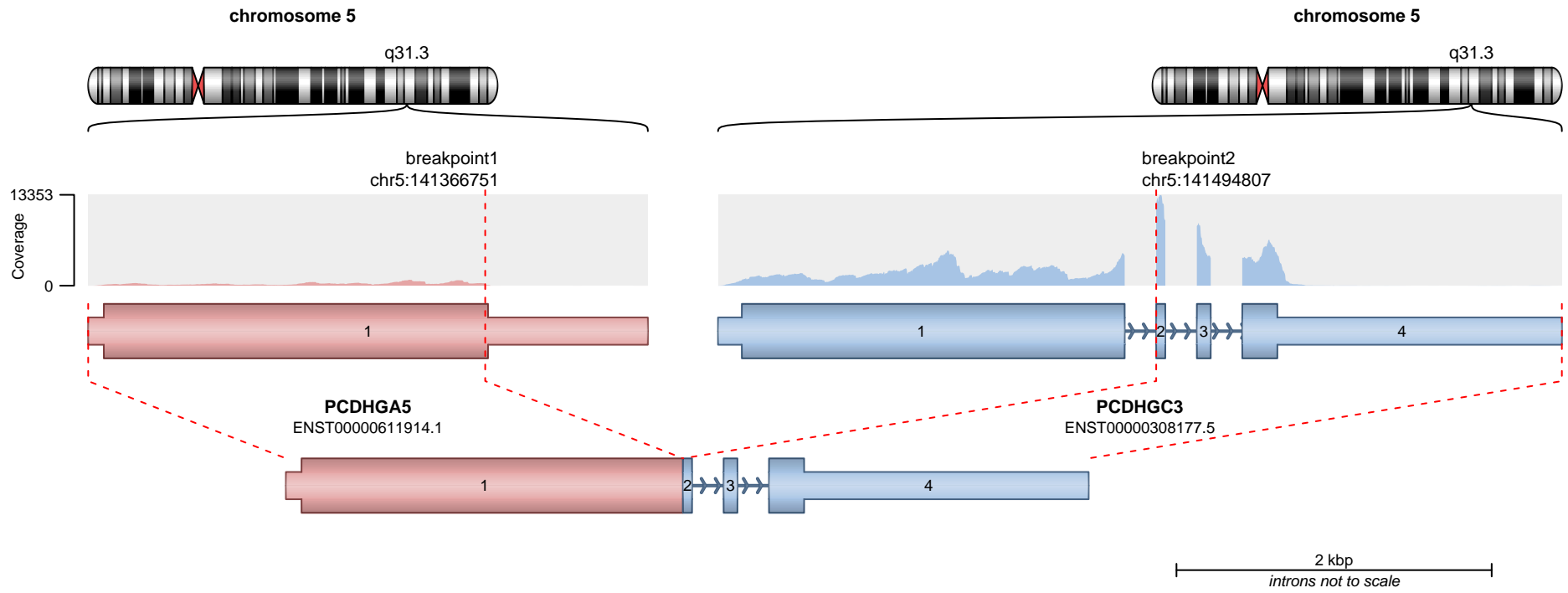
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



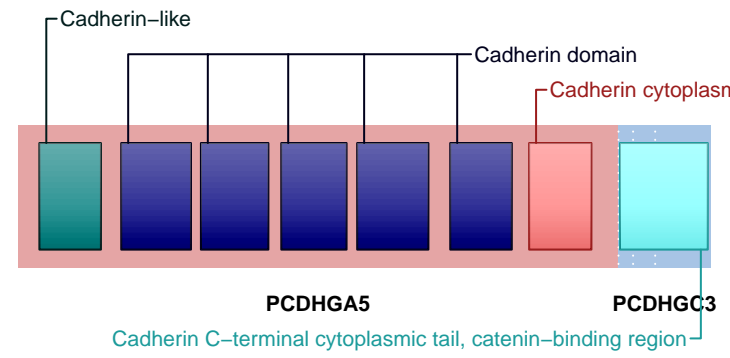
**SUPPORTING READ COUNT**

Split reads = 89  
Discordant mates = 0



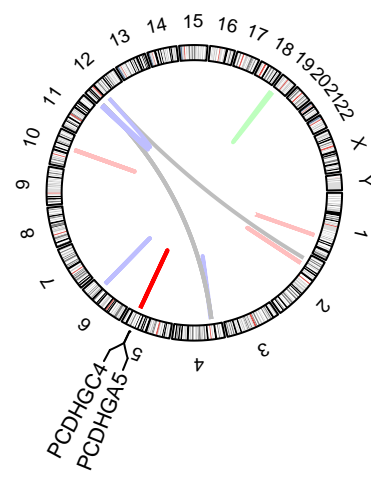
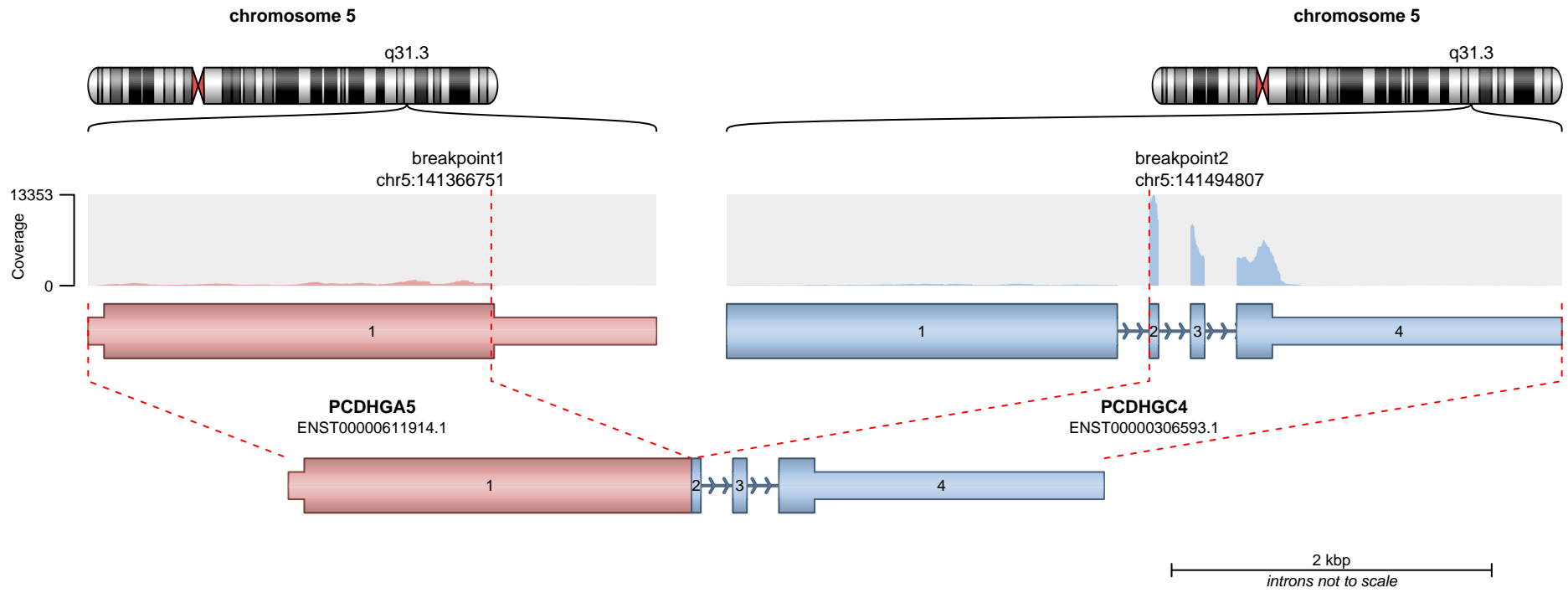
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear

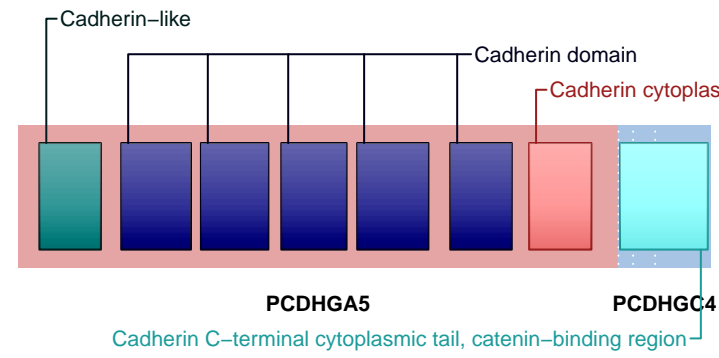


**SUPPORTING READ COUNT**

Split reads = 89  
Discordant mates = 0



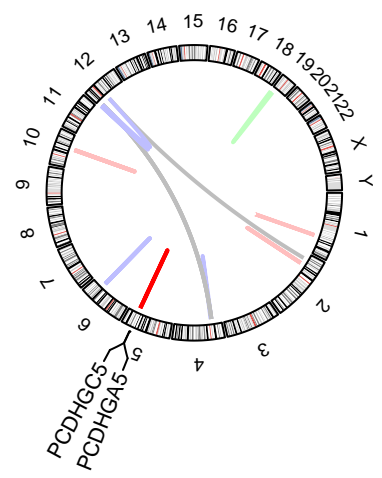
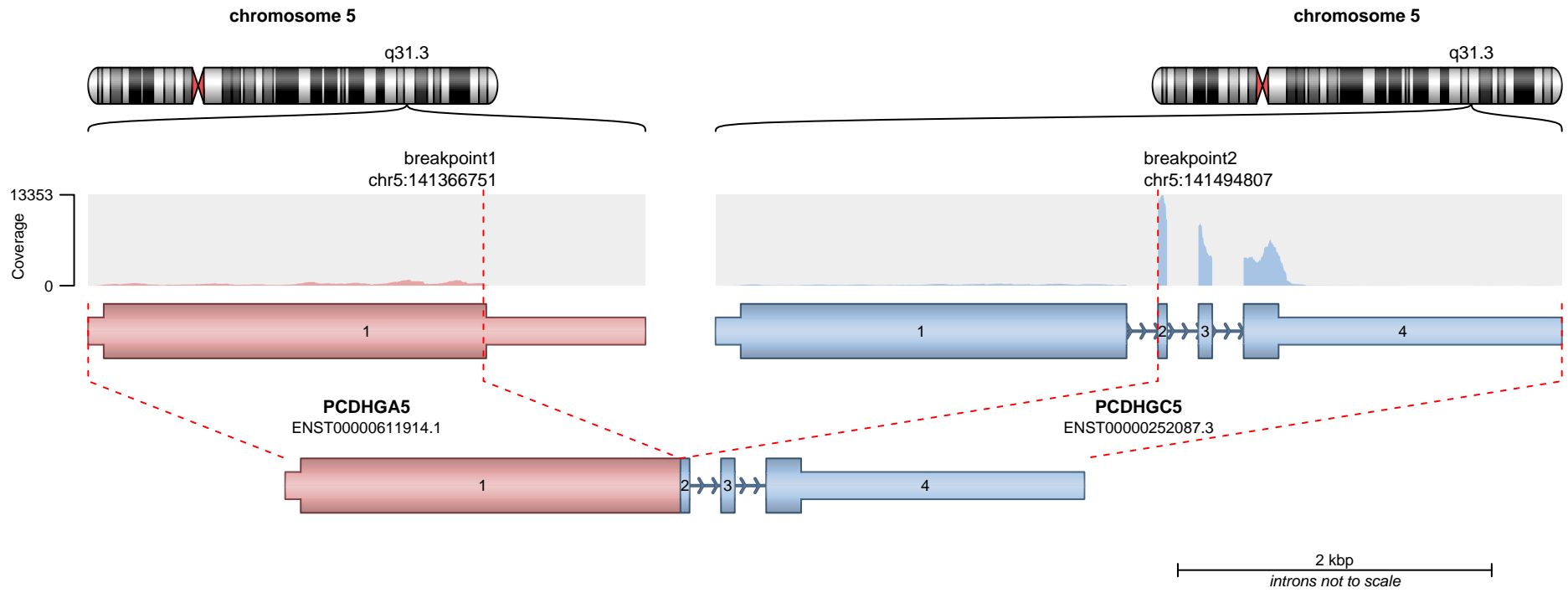
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

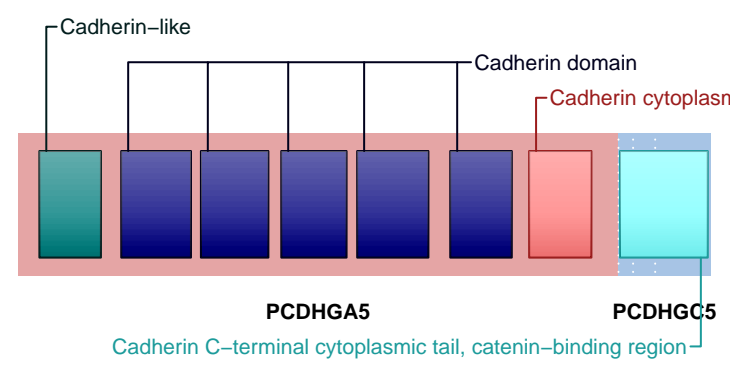
Split reads = 89  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



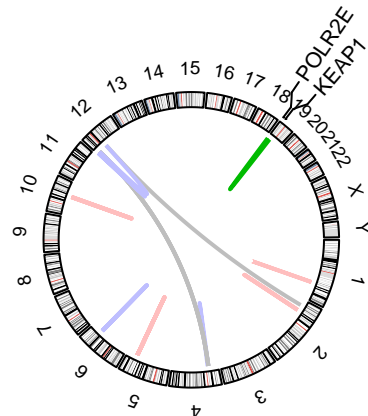
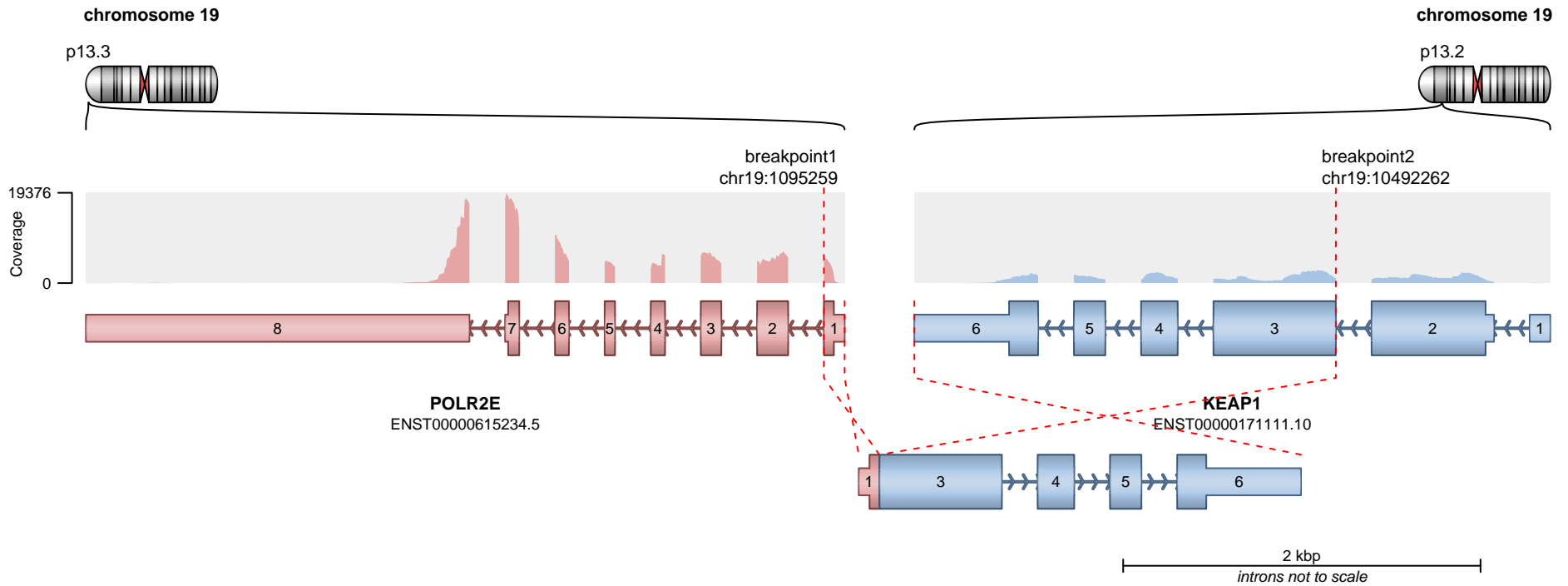
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear

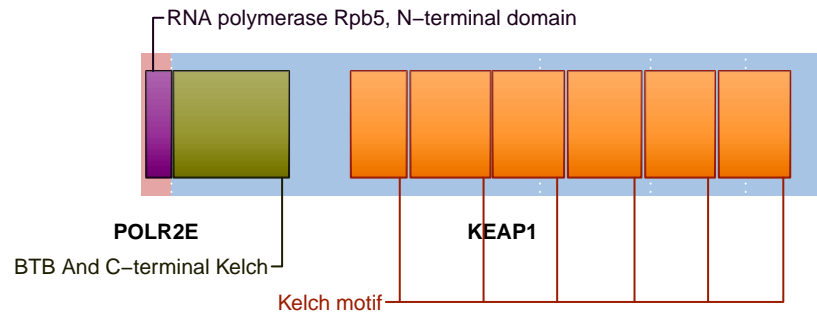


**SUPPORTING READ COUNT**

Split reads = 89  
Discordant mates = 0



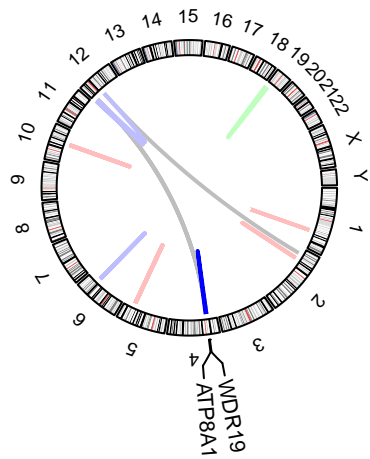
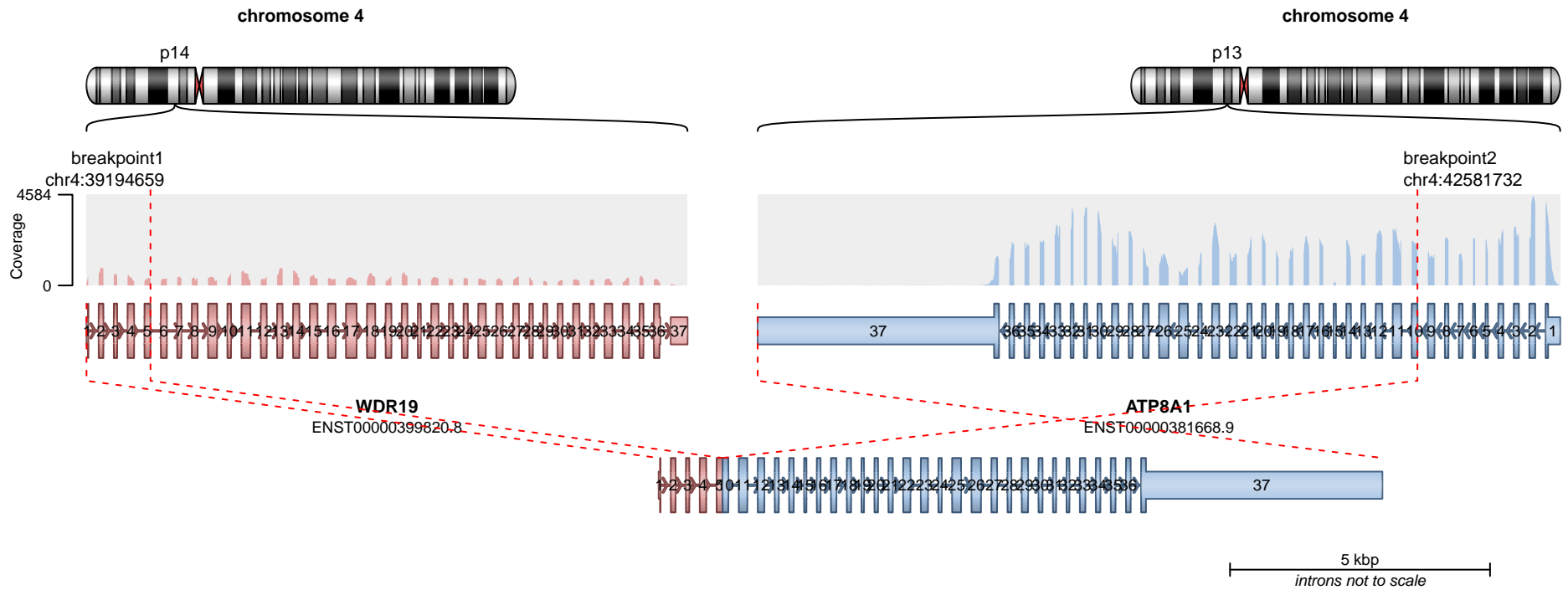
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



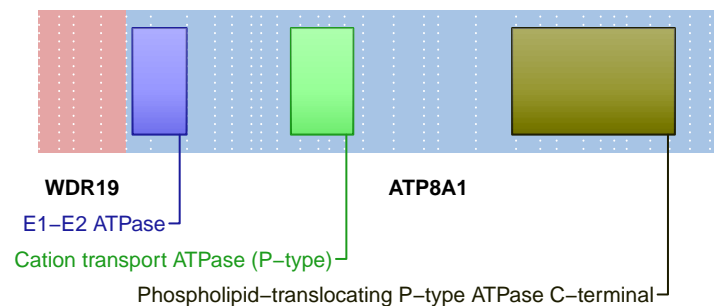
**SUPPORTING READ COUNT**

Split reads = 76  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



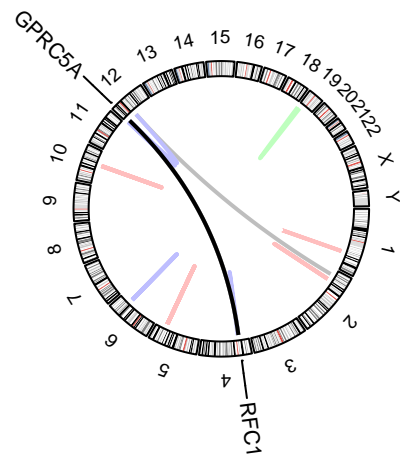
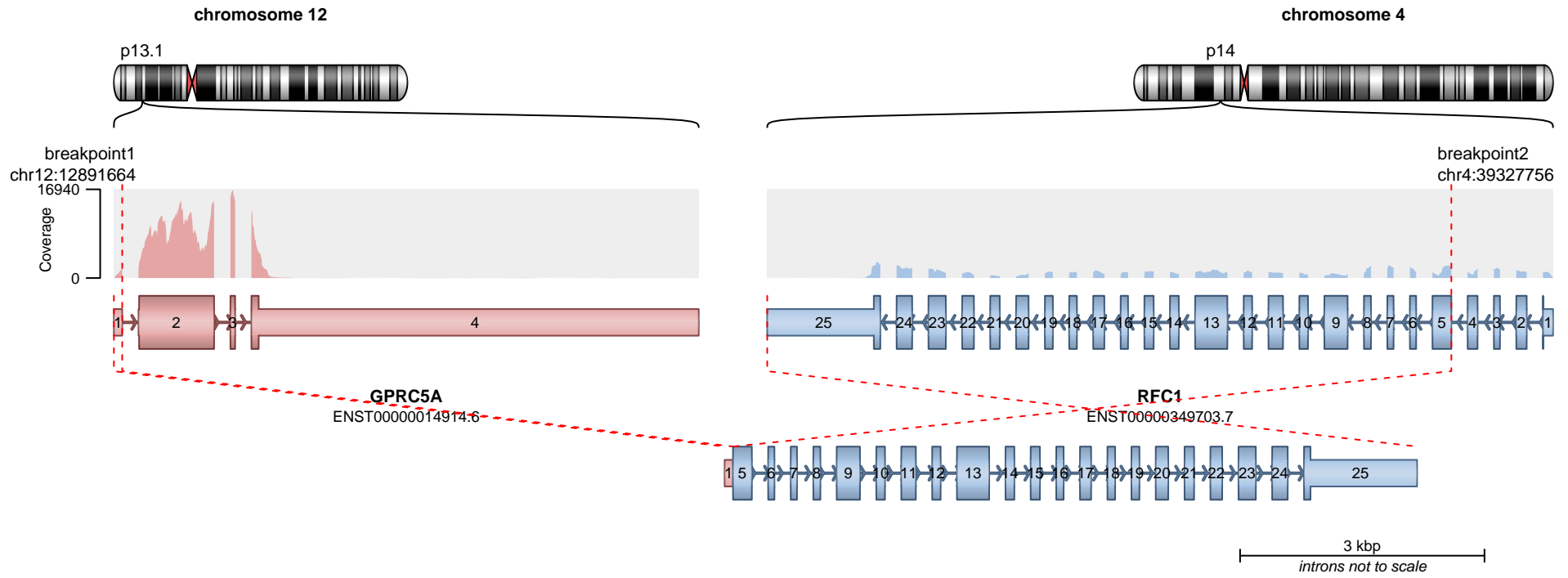
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

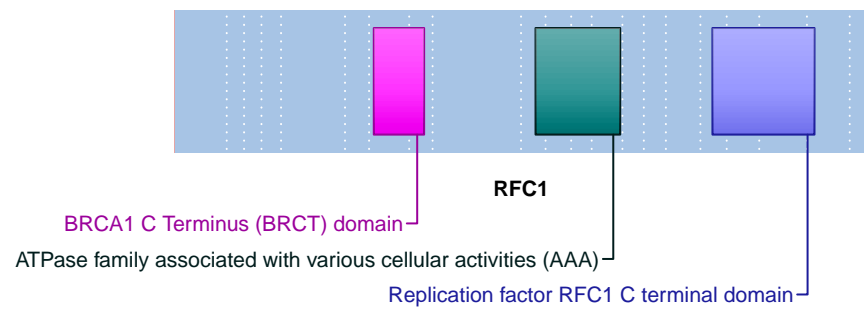
Split reads = 76  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



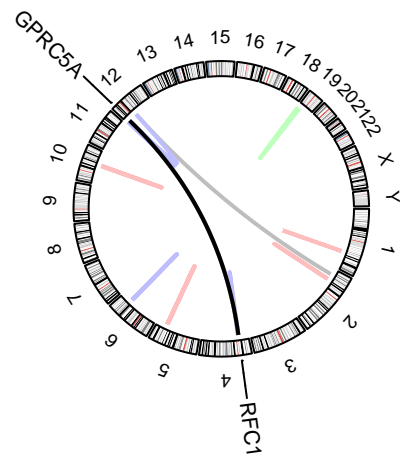
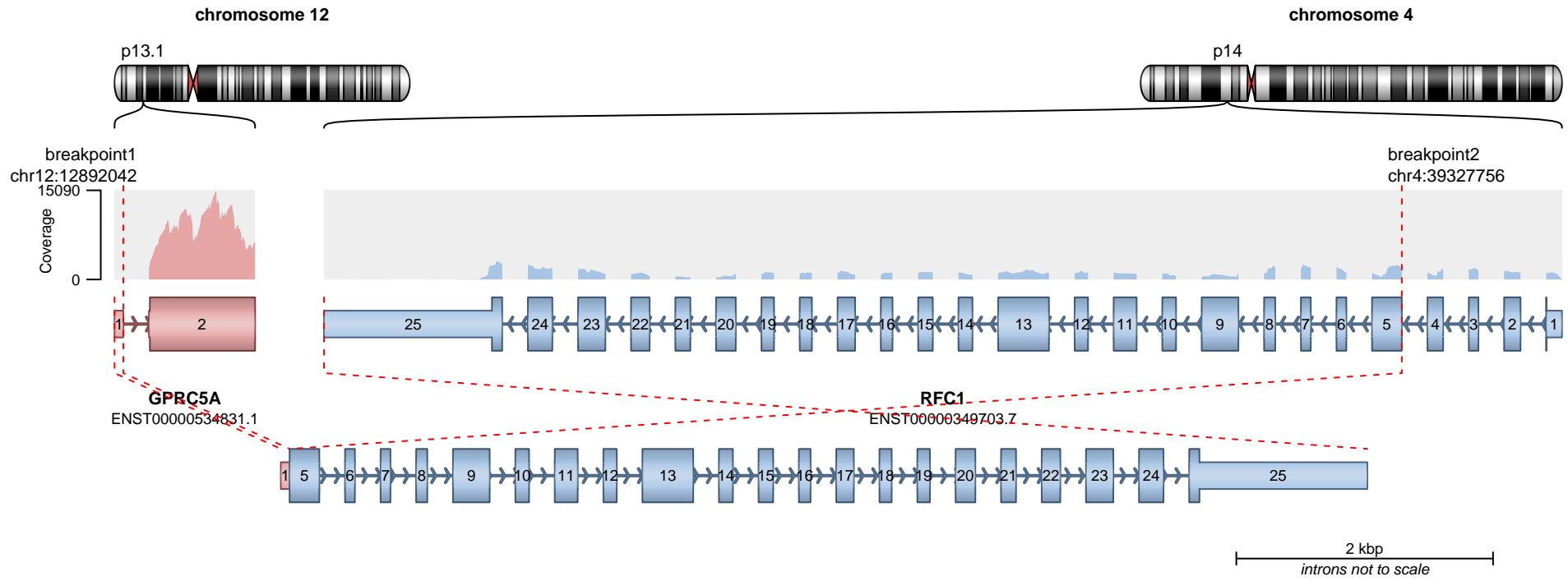
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



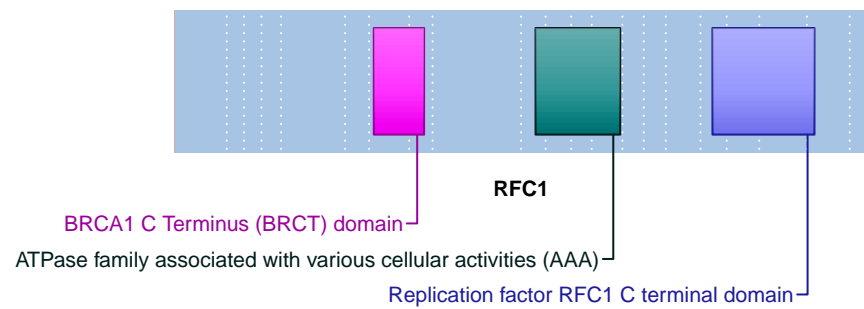
**SUPPORTING READ COUNT**

Split reads = 56  
Discordant mates = 0



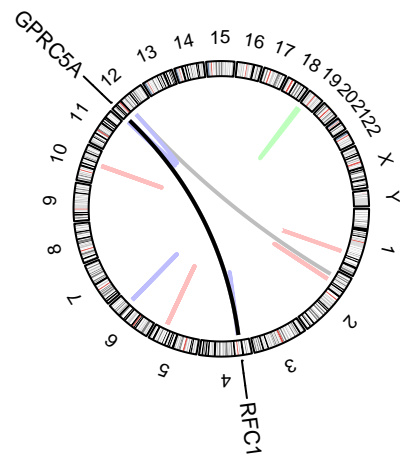
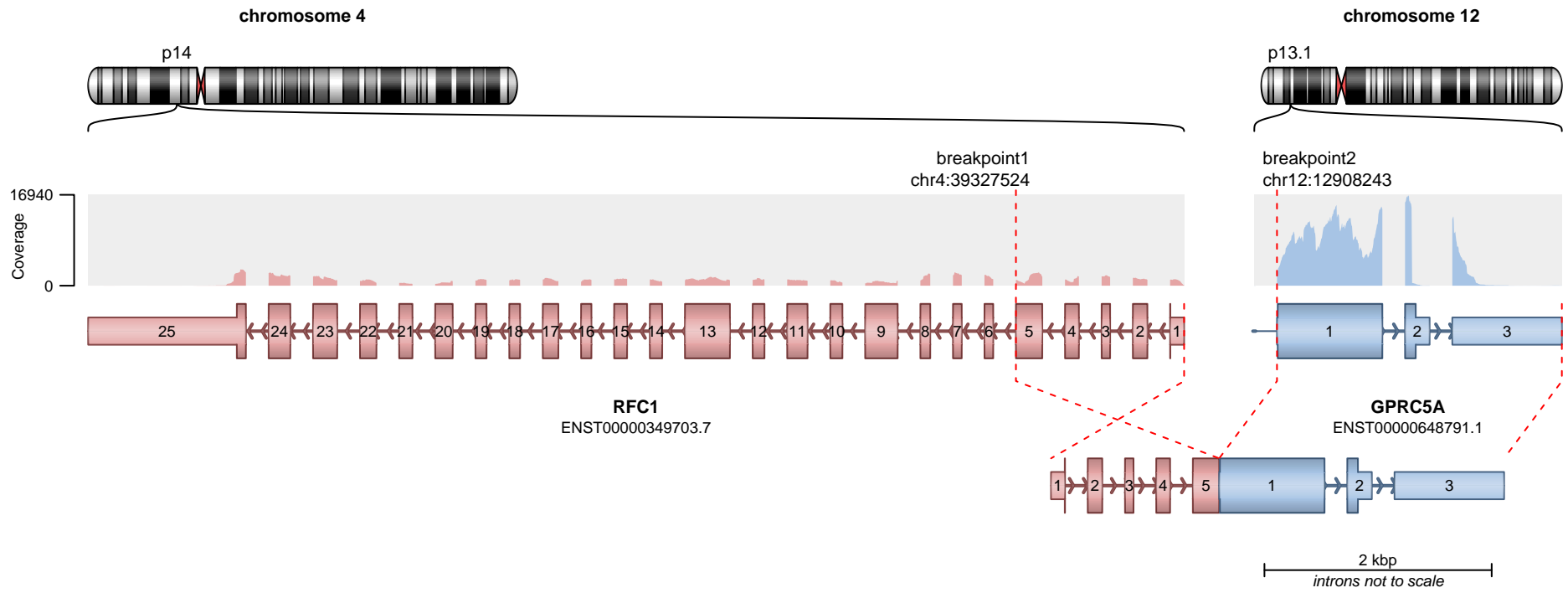
- translocation
- duplication
- deletion
- inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0



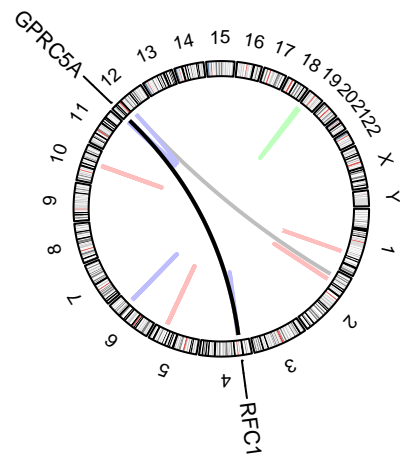
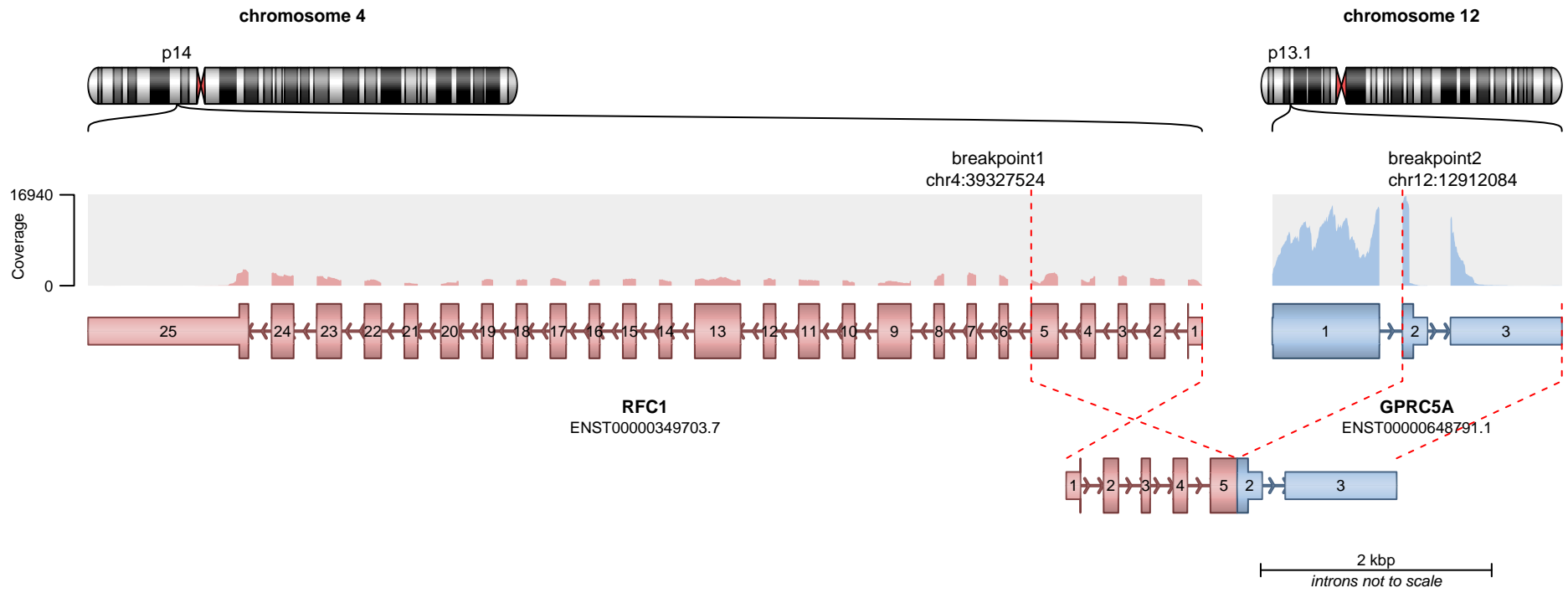
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 48  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion

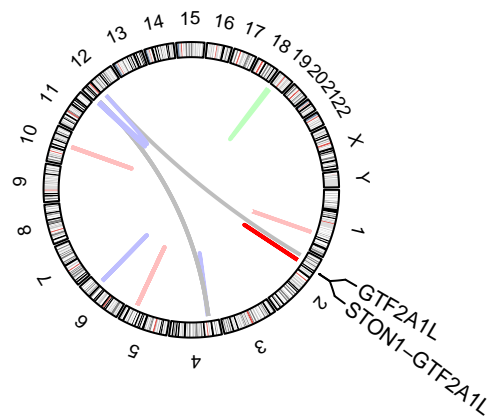
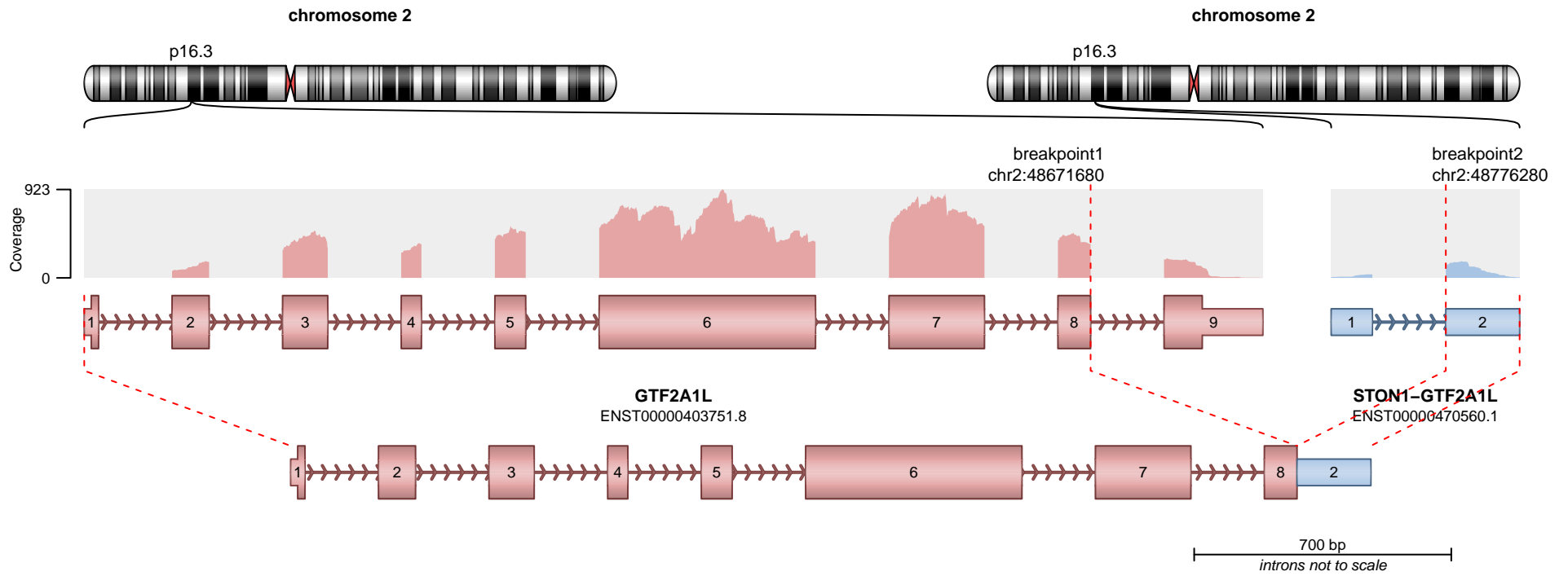


— translocation    — deletion  
— duplication    — inversion

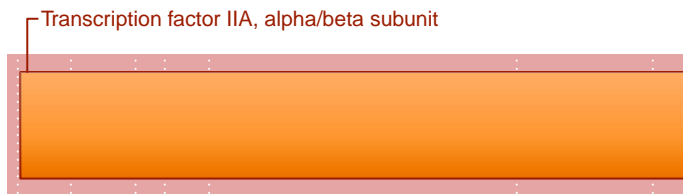
No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0



**RETAINED PROTEIN DOMAINS**  
reading frame unclear

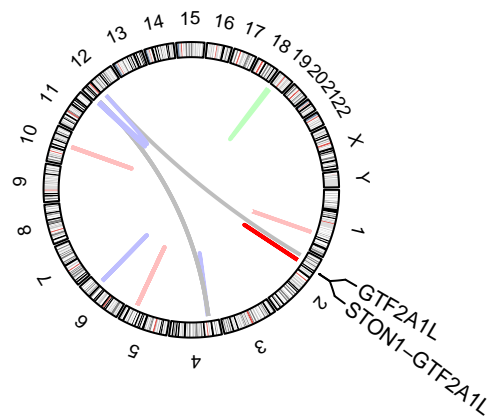
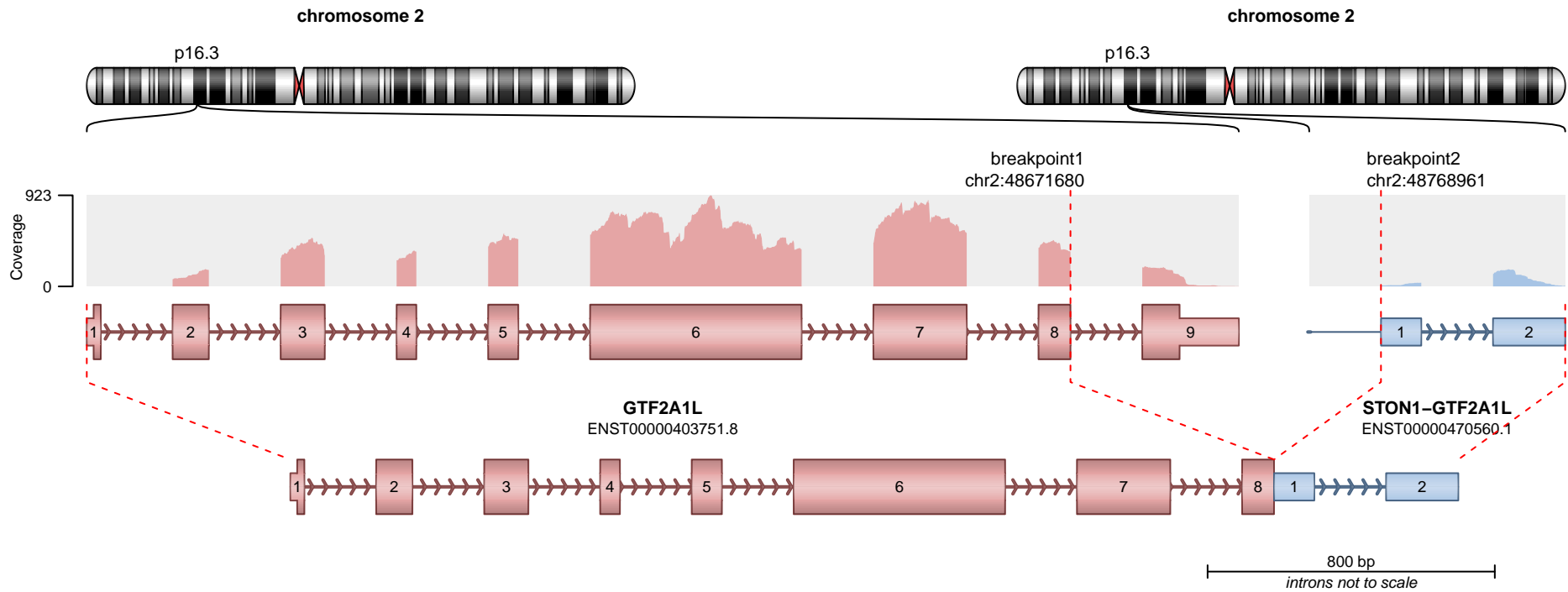


**GTF2A1L**

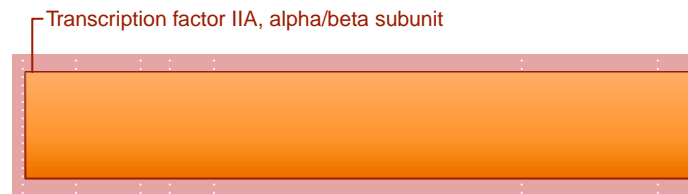
**SUPPORTING READ COUNT**

Split reads = 20  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



**RETAINED PROTEIN DOMAINS**  
reading frame unclear

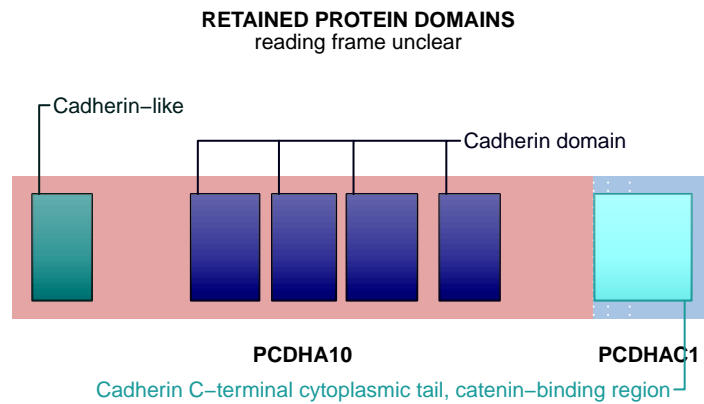
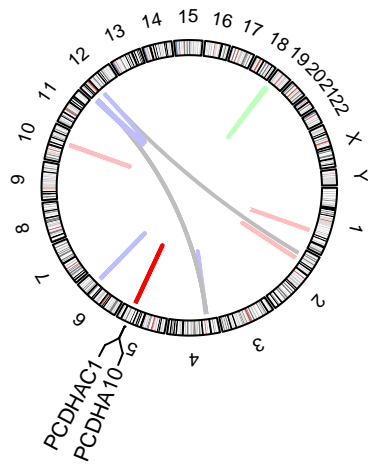
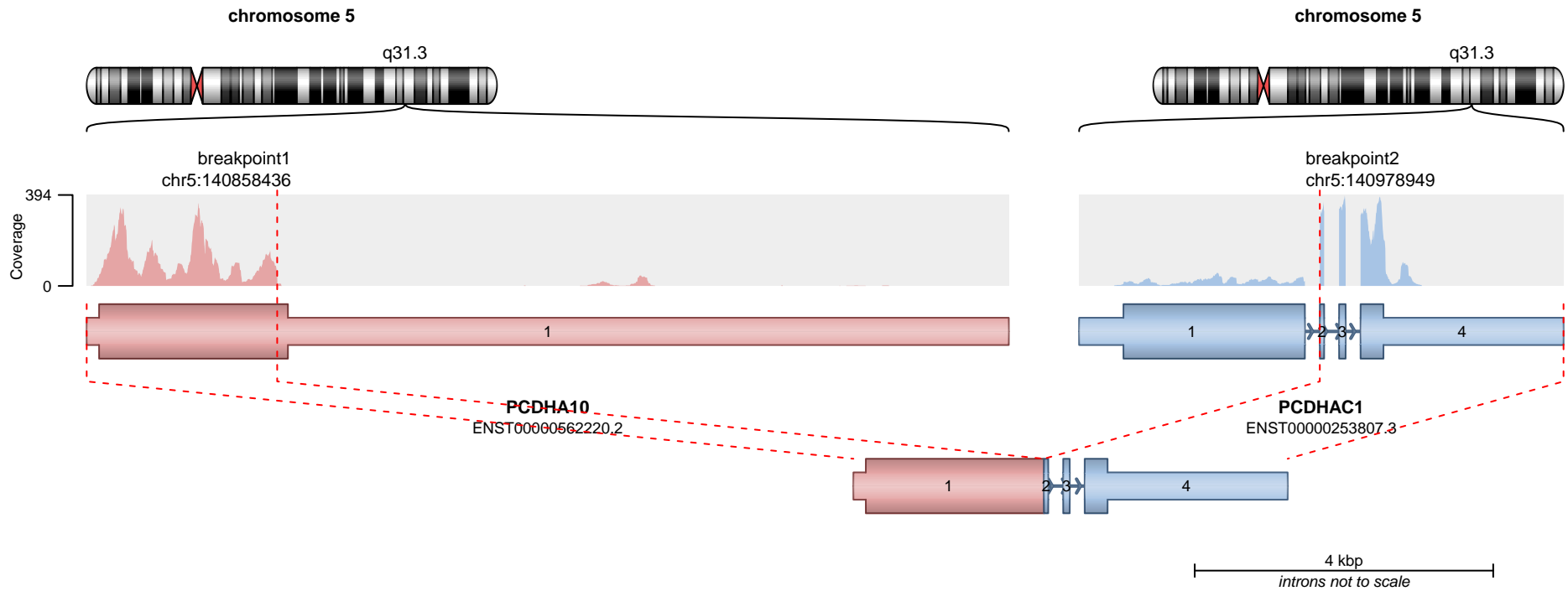


GTF2A1L

**SUPPORTING READ COUNT**

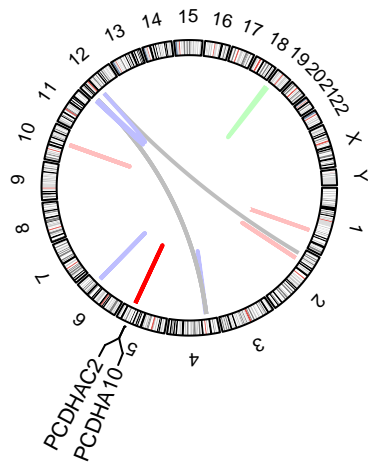
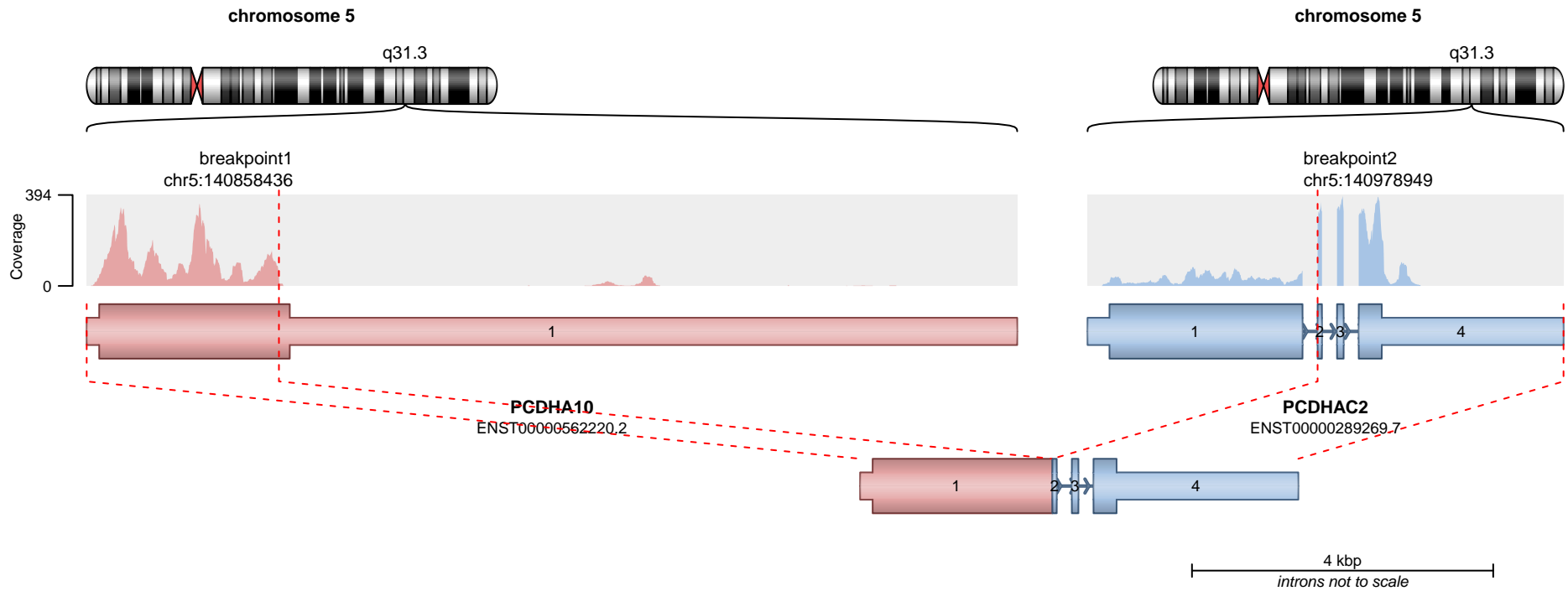
Split reads = 3  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

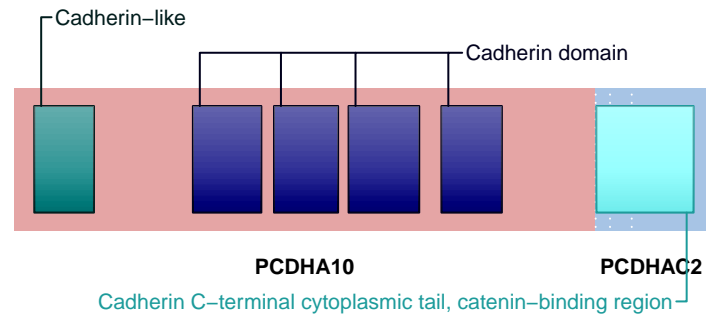


**SUPPORTING READ COUNT**

Split reads = 20  
Discordant mates = 0



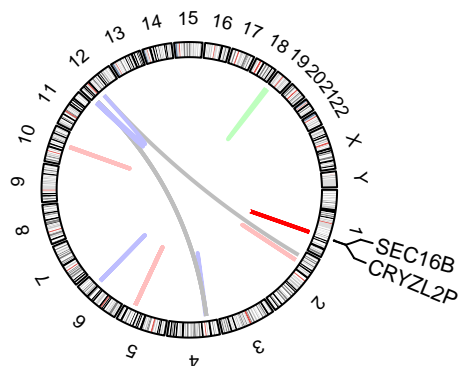
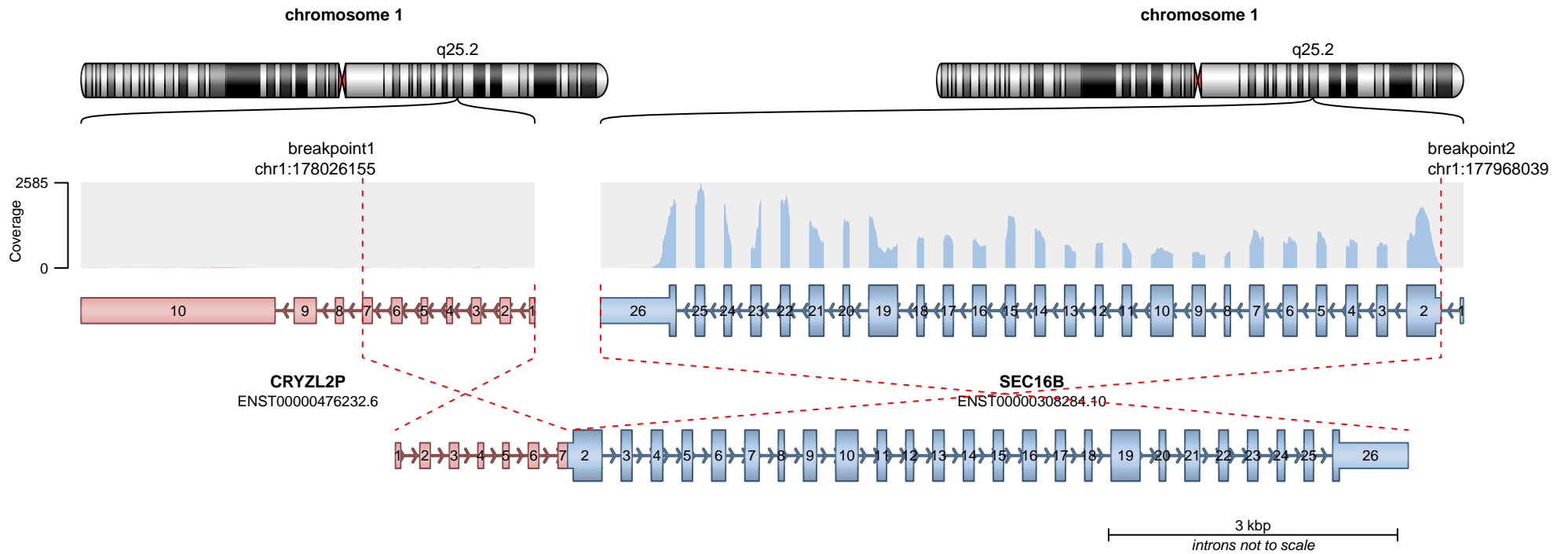
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



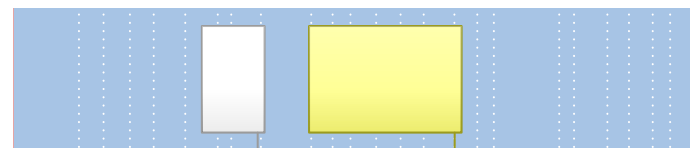
**SUPPORTING READ COUNT**

Split reads = 20  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



**RETAINED PROTEIN DOMAINS**  
reading frame unclear

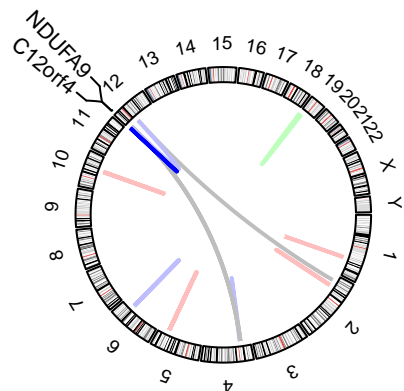
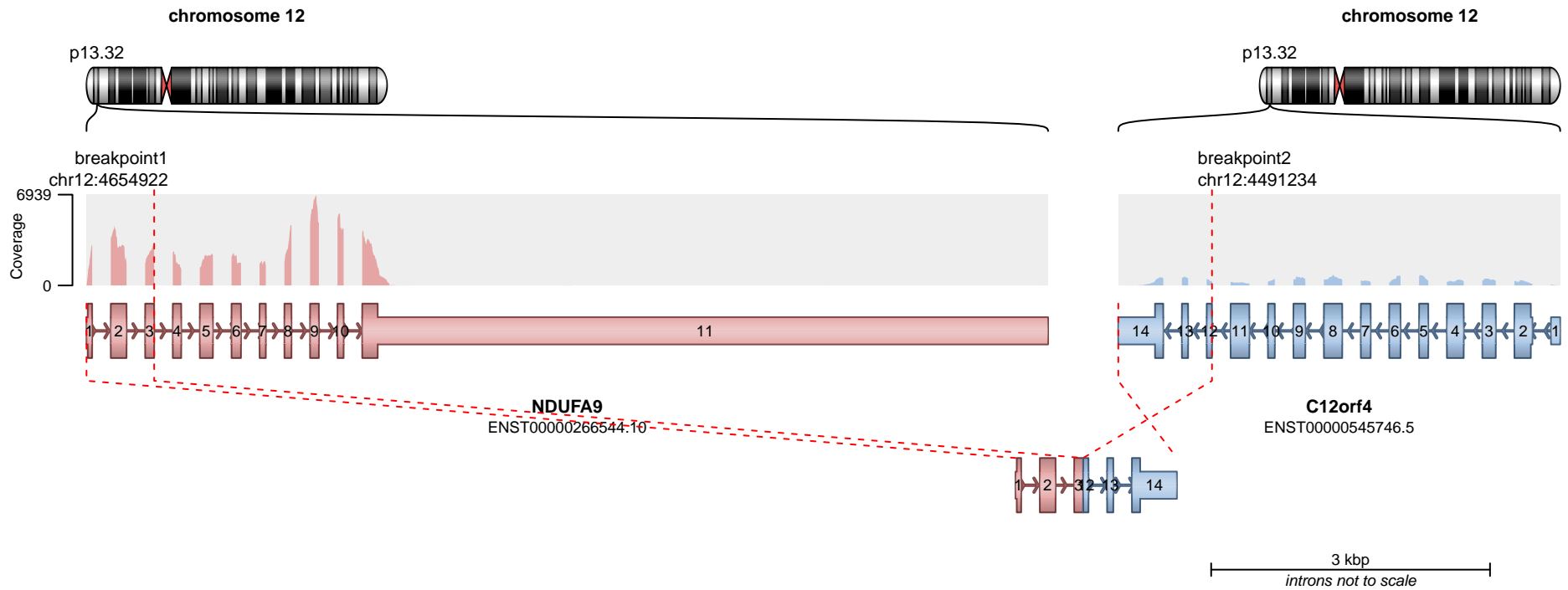


**SUPPORTING READ COUNT**

Split reads = 16  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion





**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 13  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion

