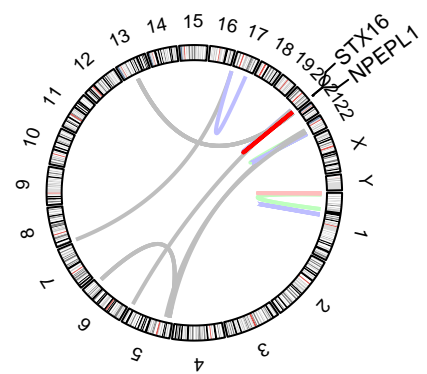
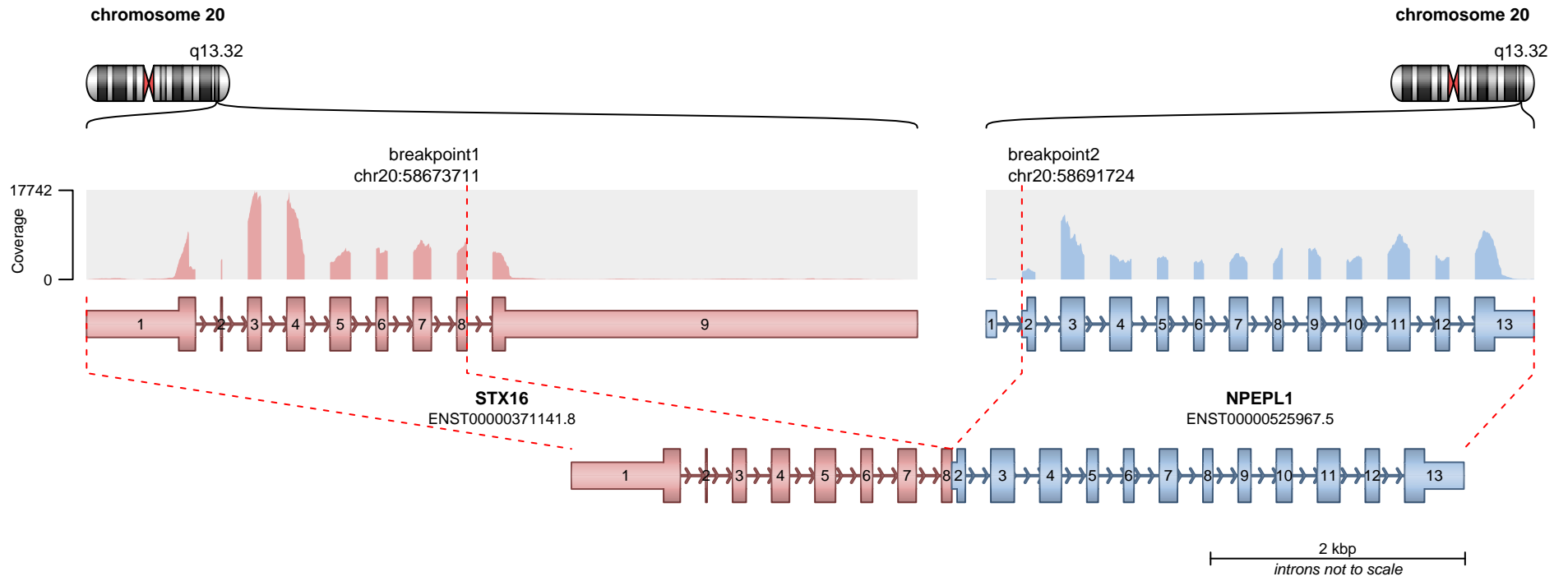


No protein domains retained in fusion.

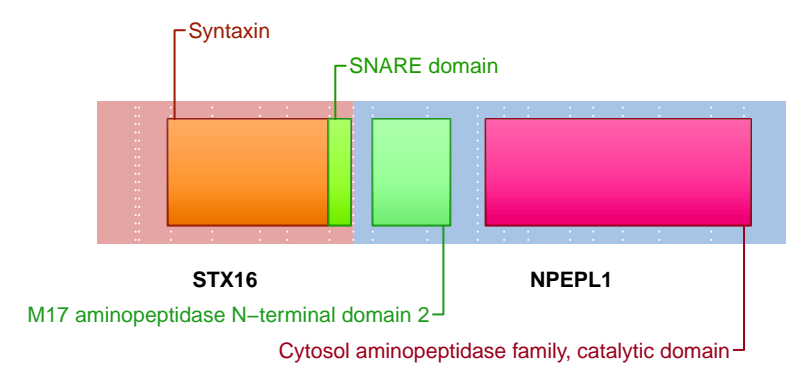
**SUPPORTING READ COUNT**

Split reads = 464  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



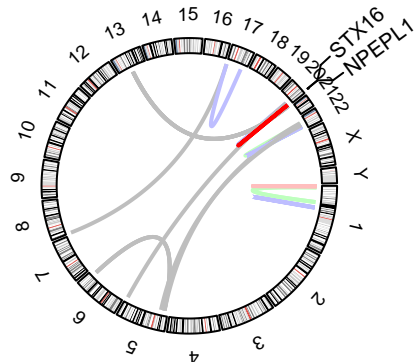
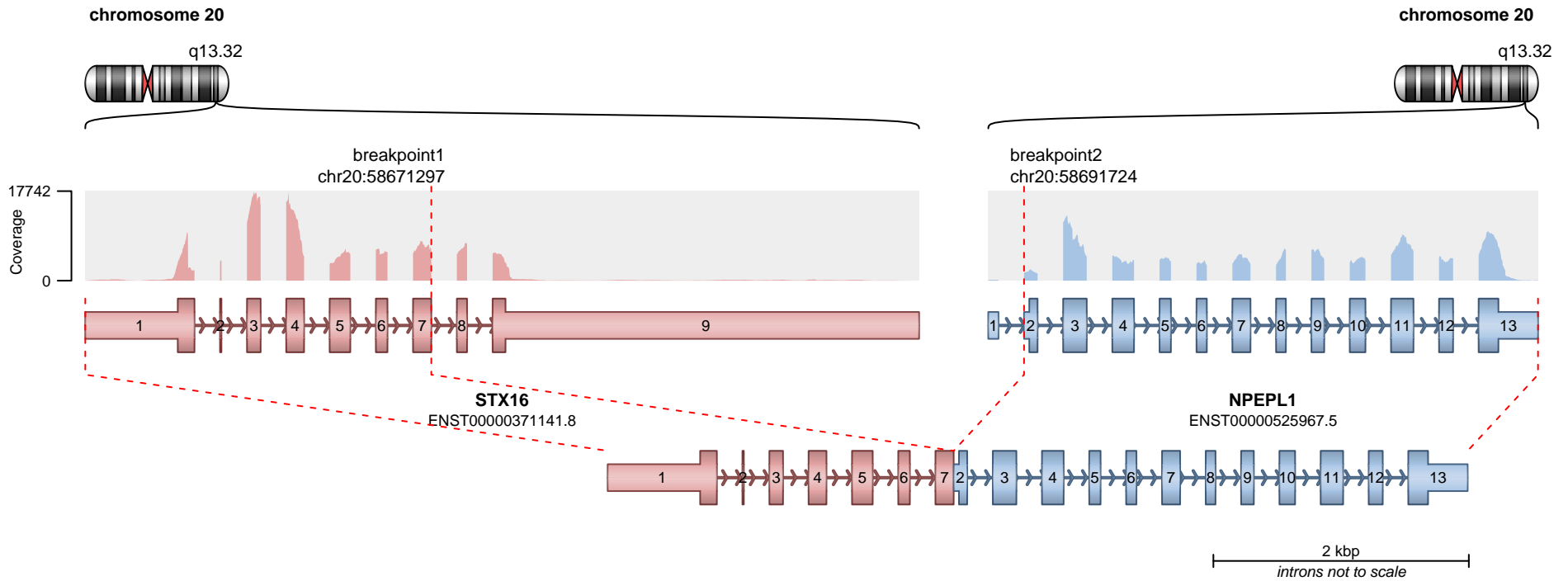
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



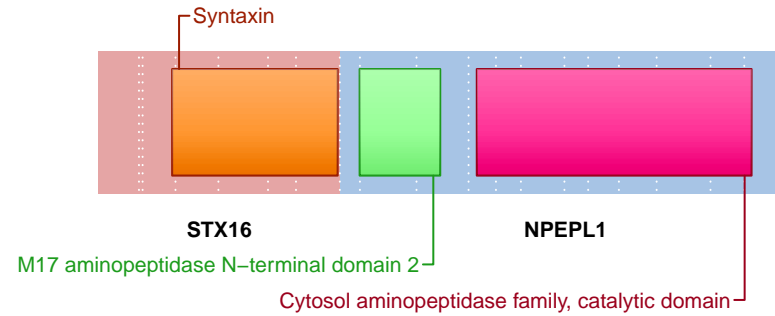
**SUPPORTING READ COUNT**

Split reads = 414  
Discordant mates = 4

- translocation
- duplication
- deletion
- inversion



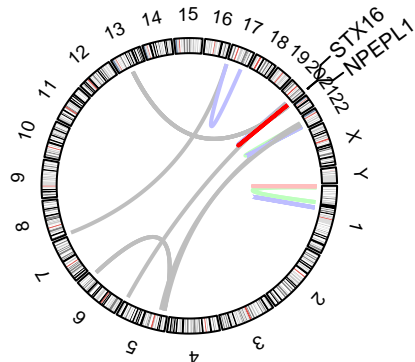
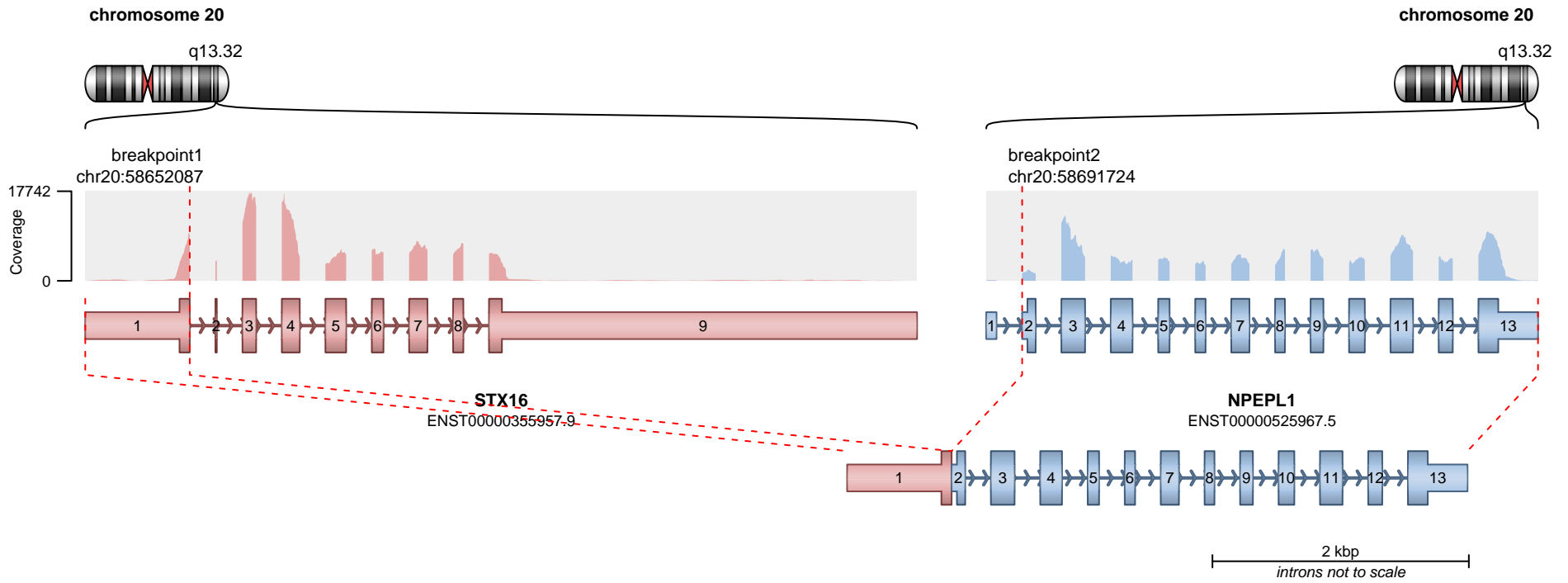
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



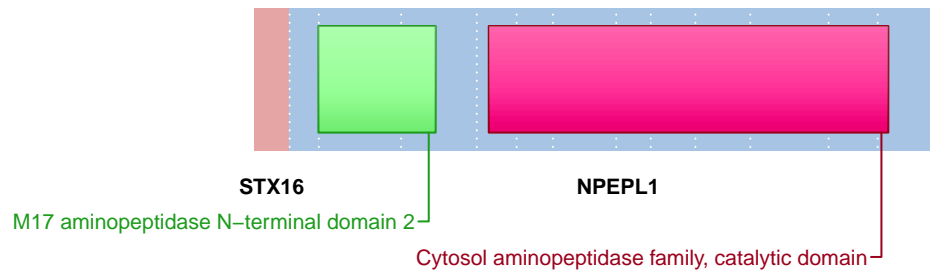
**SUPPORTING READ COUNT**

Split reads = 9  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



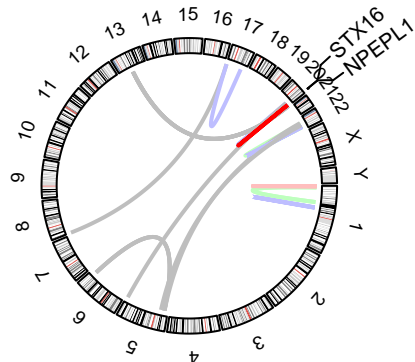
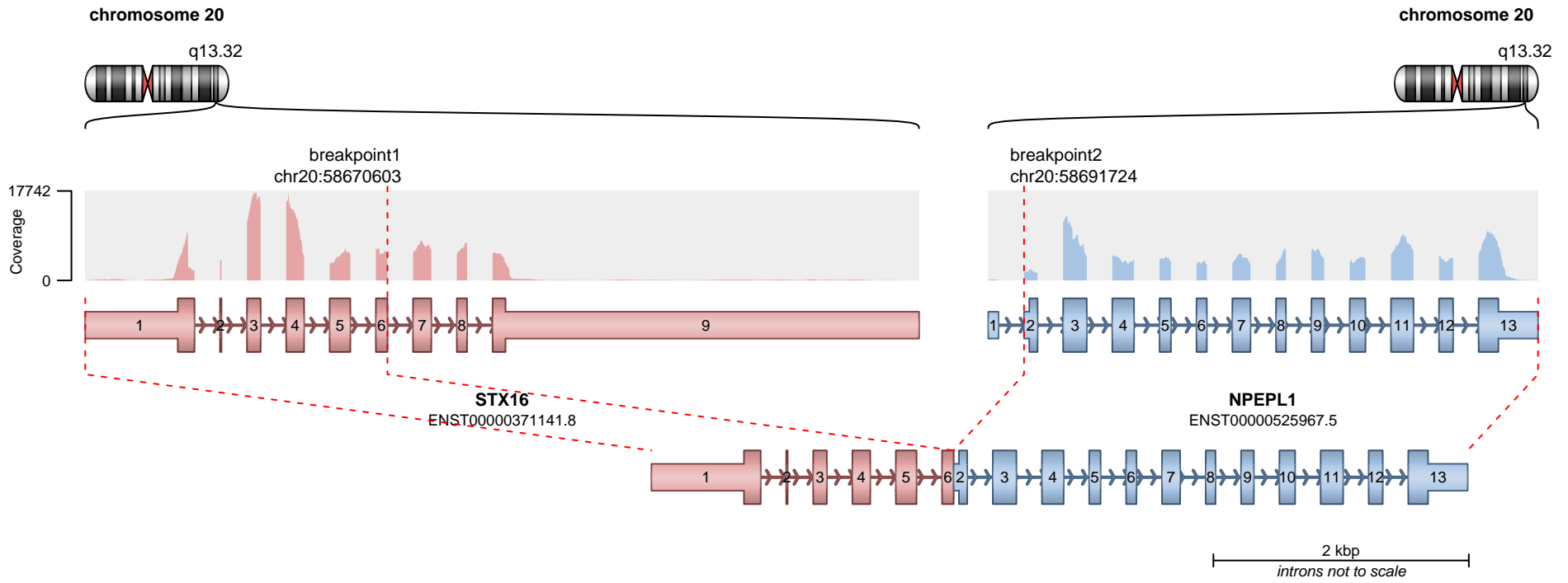
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



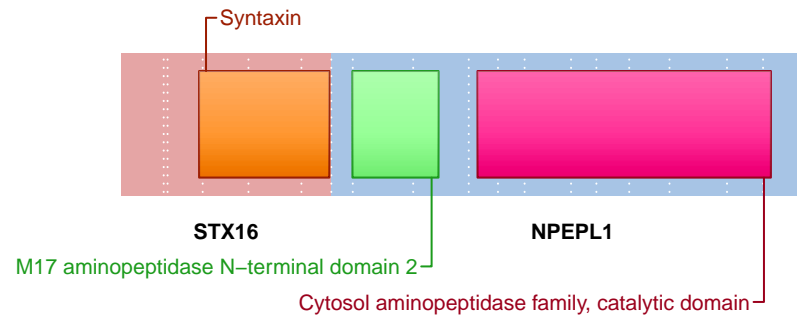
**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



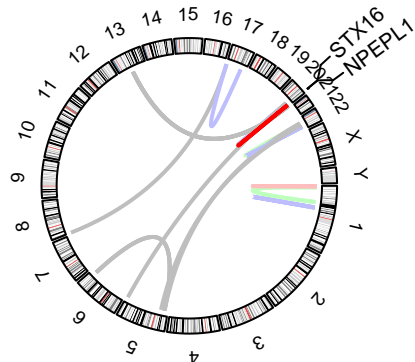
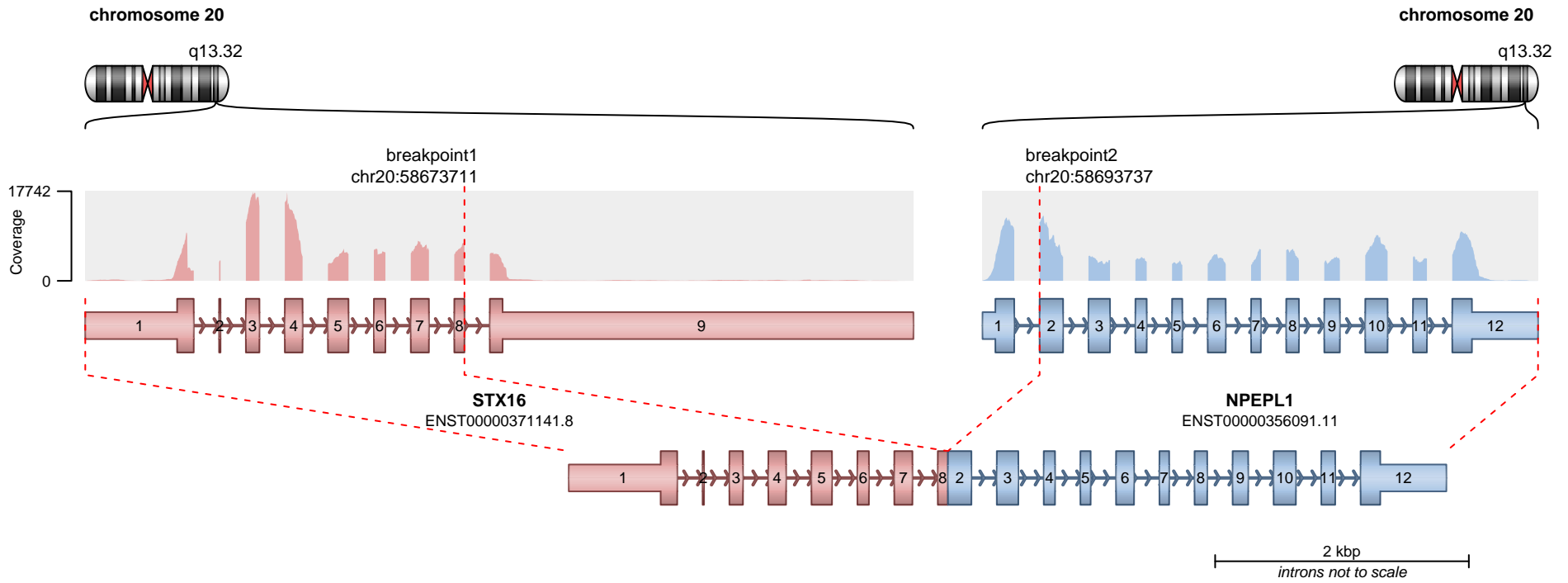
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



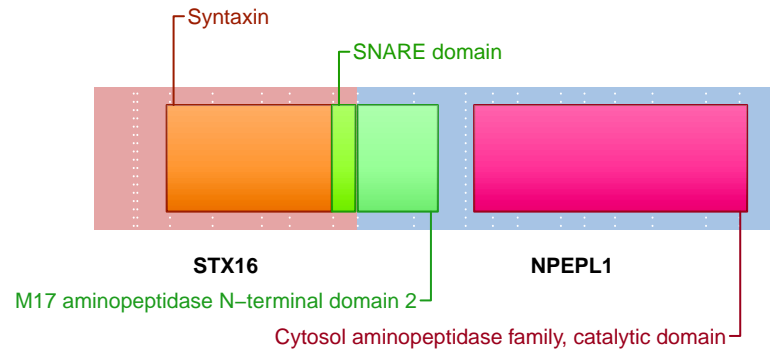
**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



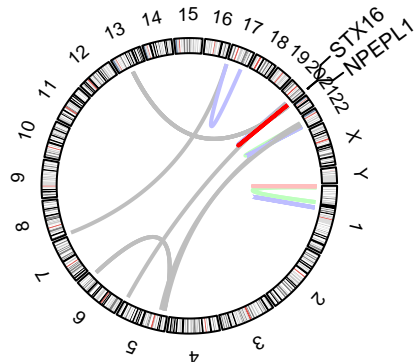
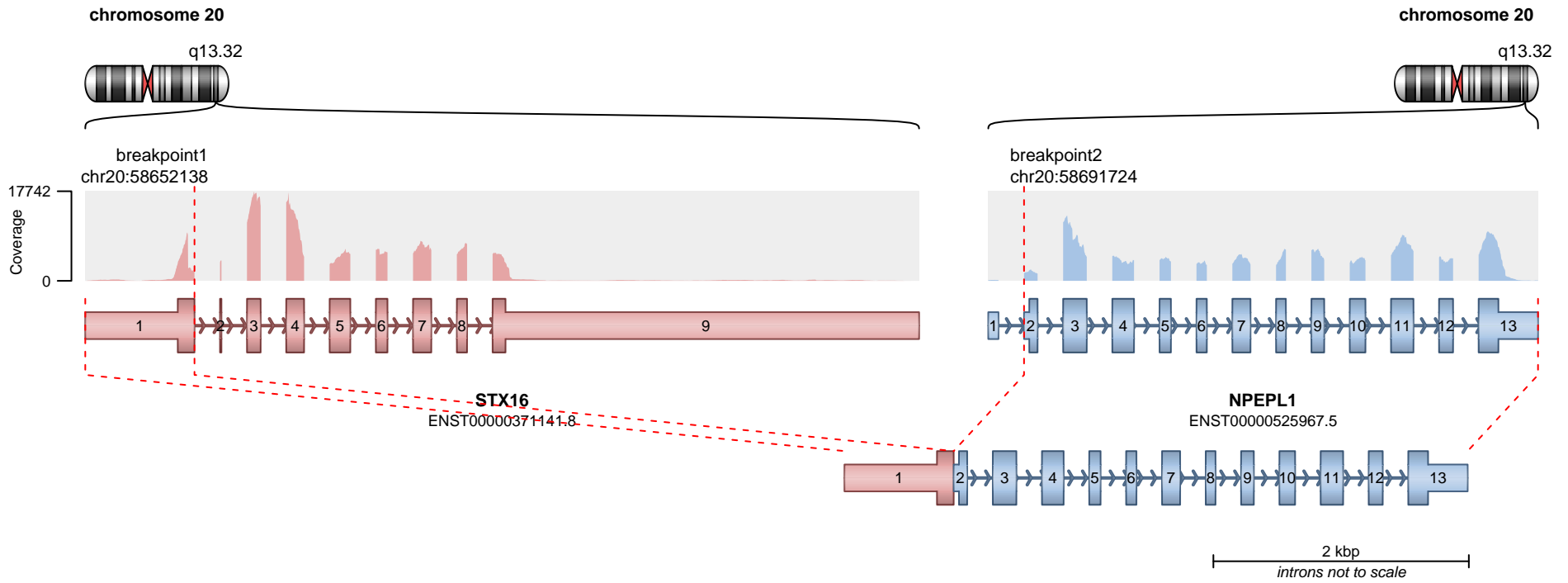
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



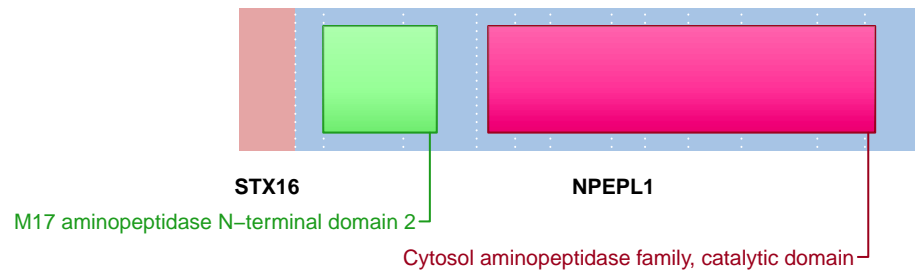
**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



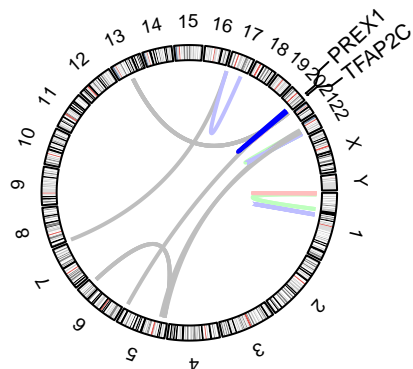
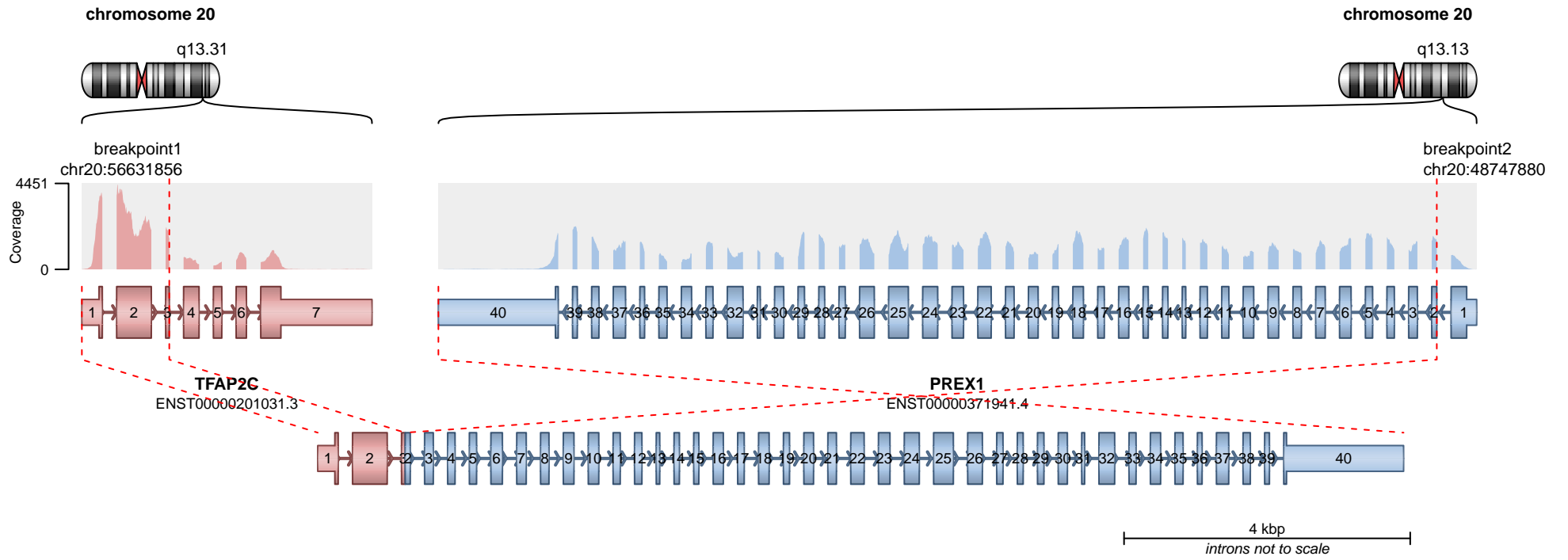
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



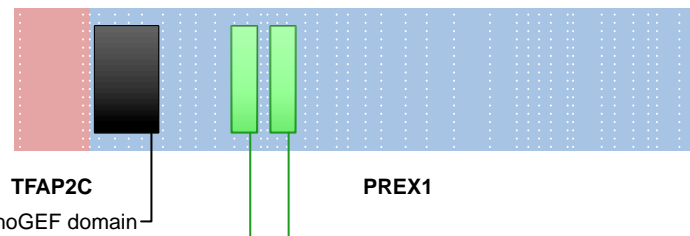
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



**RETAINED PROTEIN DOMAINS**  
reading frame unclear

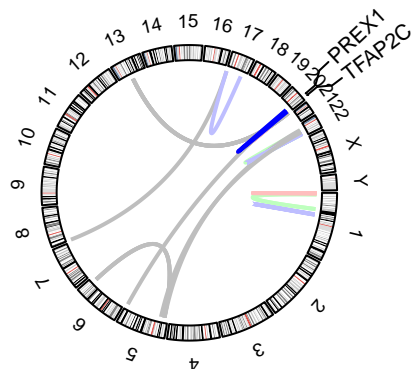
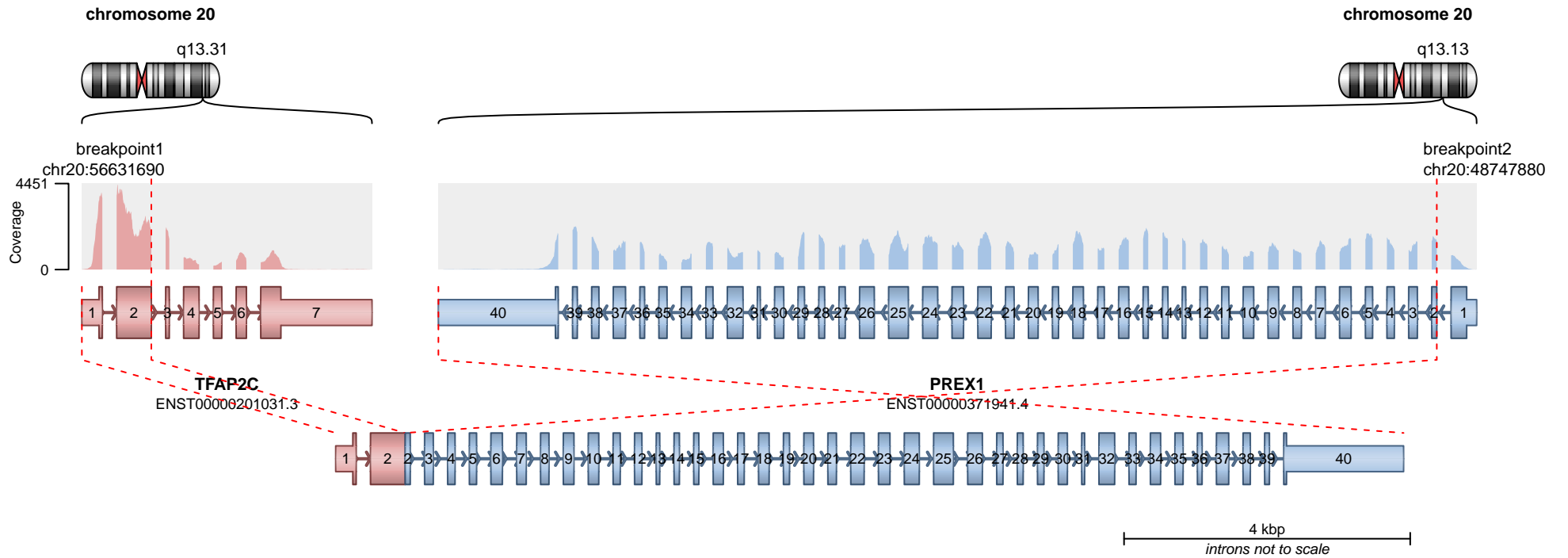


**SUPPORTING READ COUNT**

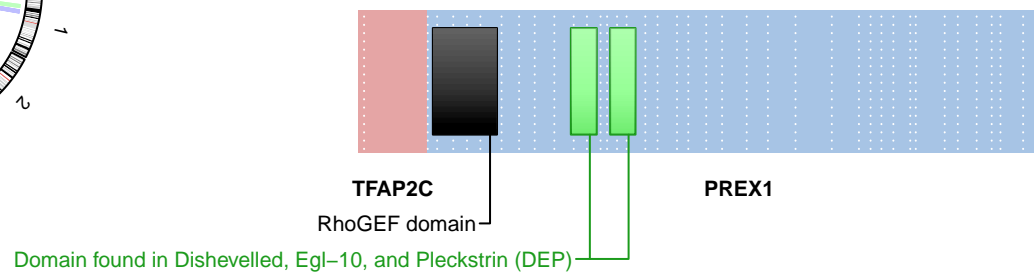
Split reads = 398  
Discordant mates = 2

Domain found in Dishevelled, Egl-10, and Pleckstrin (DEP)

- translocation
- duplication
- deletion
- inversion



**RETAINED PROTEIN DOMAINS**  
reading frame unclear

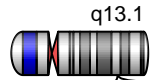


**SUPPORTING READ COUNT**

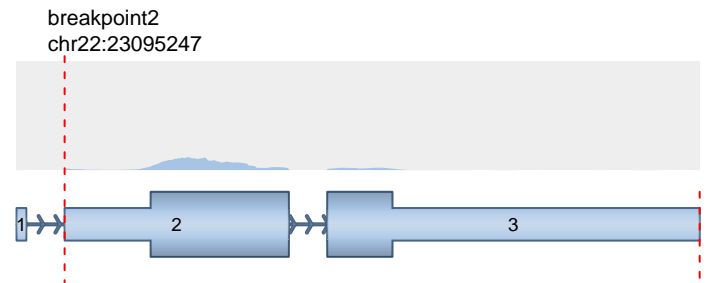
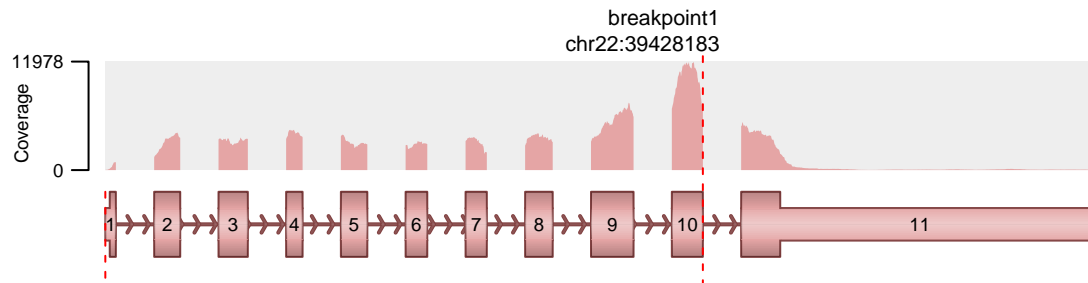
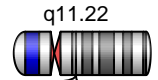
Split reads = 7  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

chromosome 22

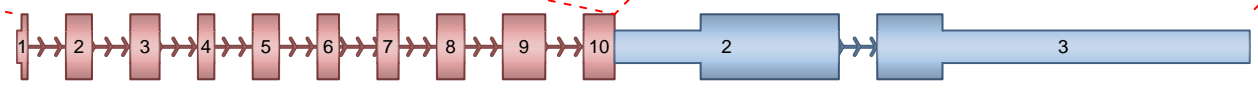


chromosome 22

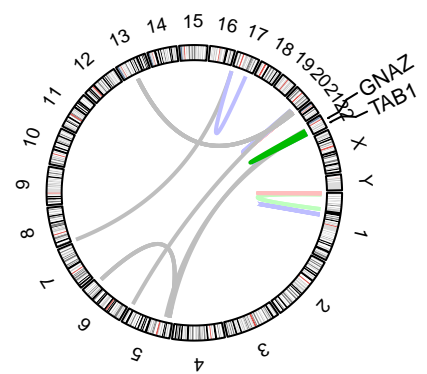


**TAB1**  
ENST00000216160.11

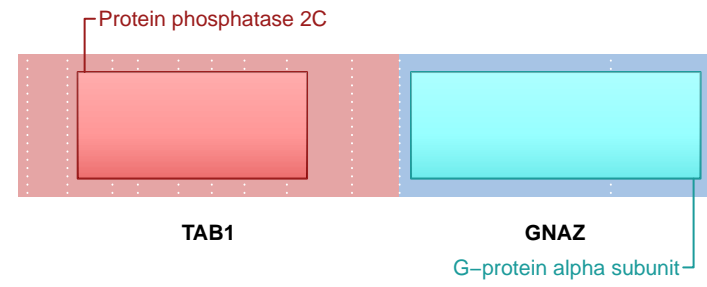
**GNAZ**  
ENST00000615612.2



2 kbp  
*introns not to scale*



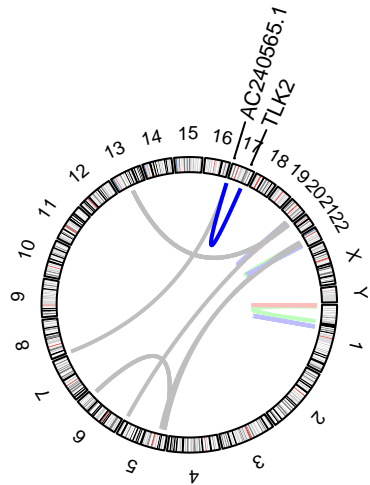
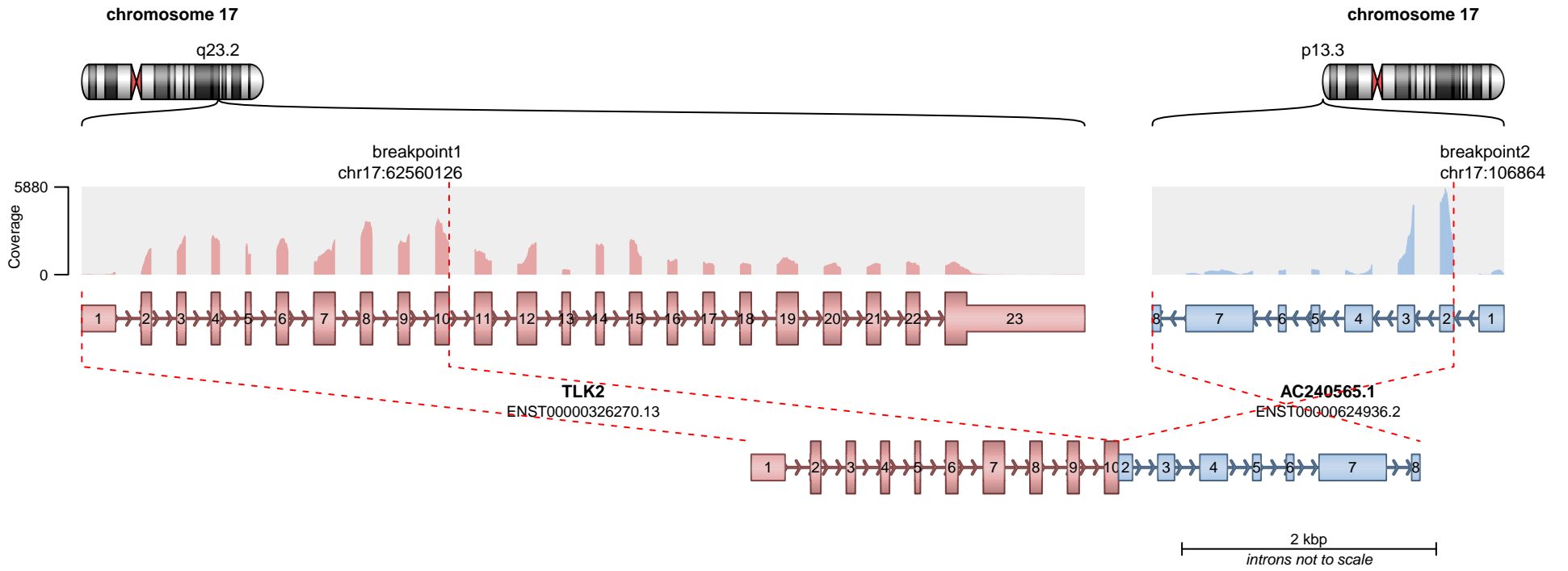
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 102  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

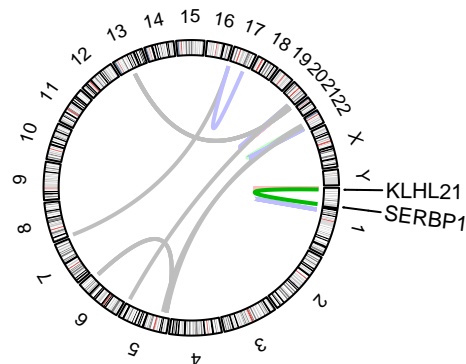
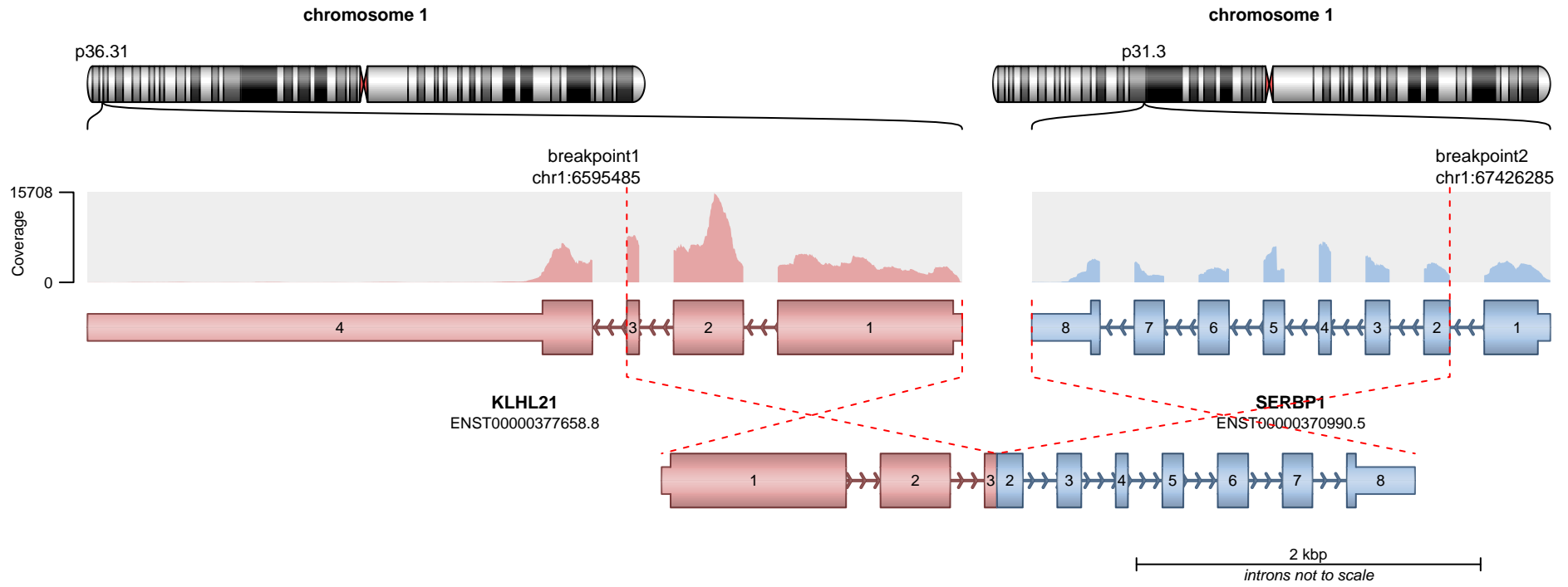


No protein domains retained in fusion.

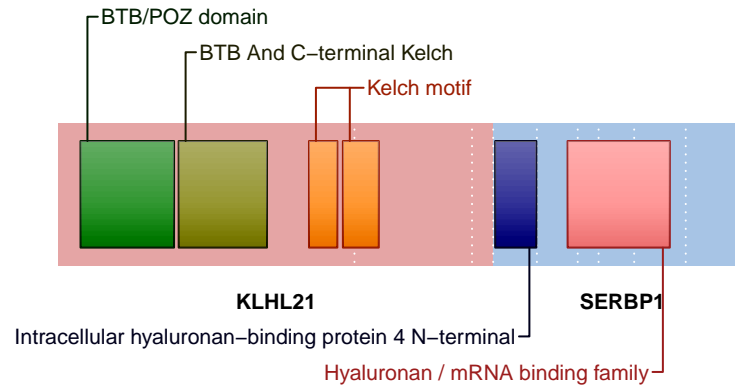
**SUPPORTING READ COUNT**

Split reads = 65  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



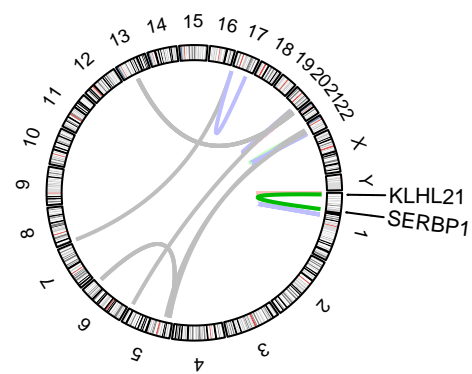
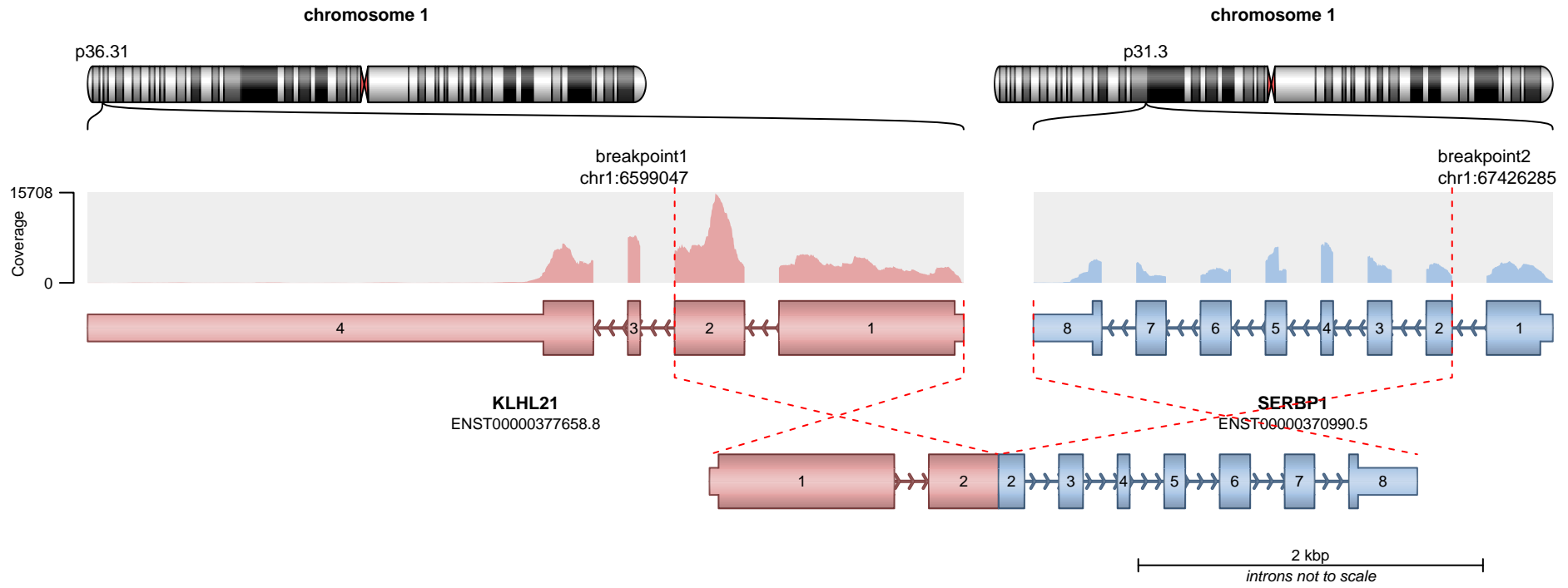
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



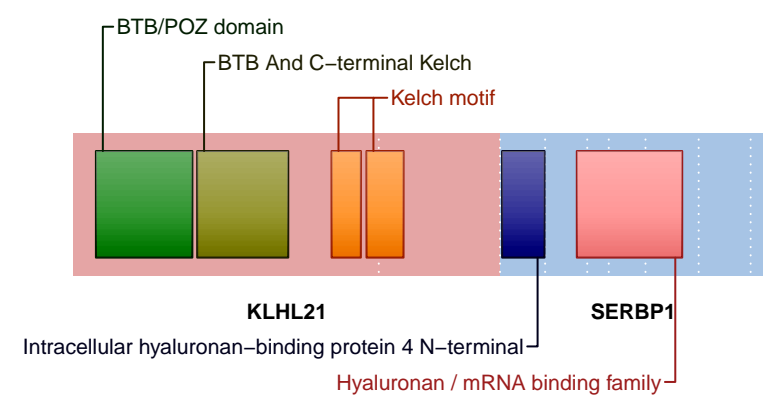
**SUPPORTING READ COUNT**

Split reads = 58  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



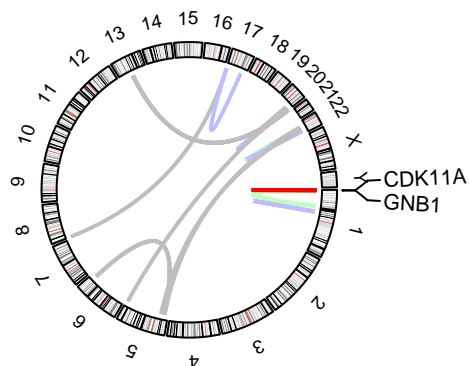
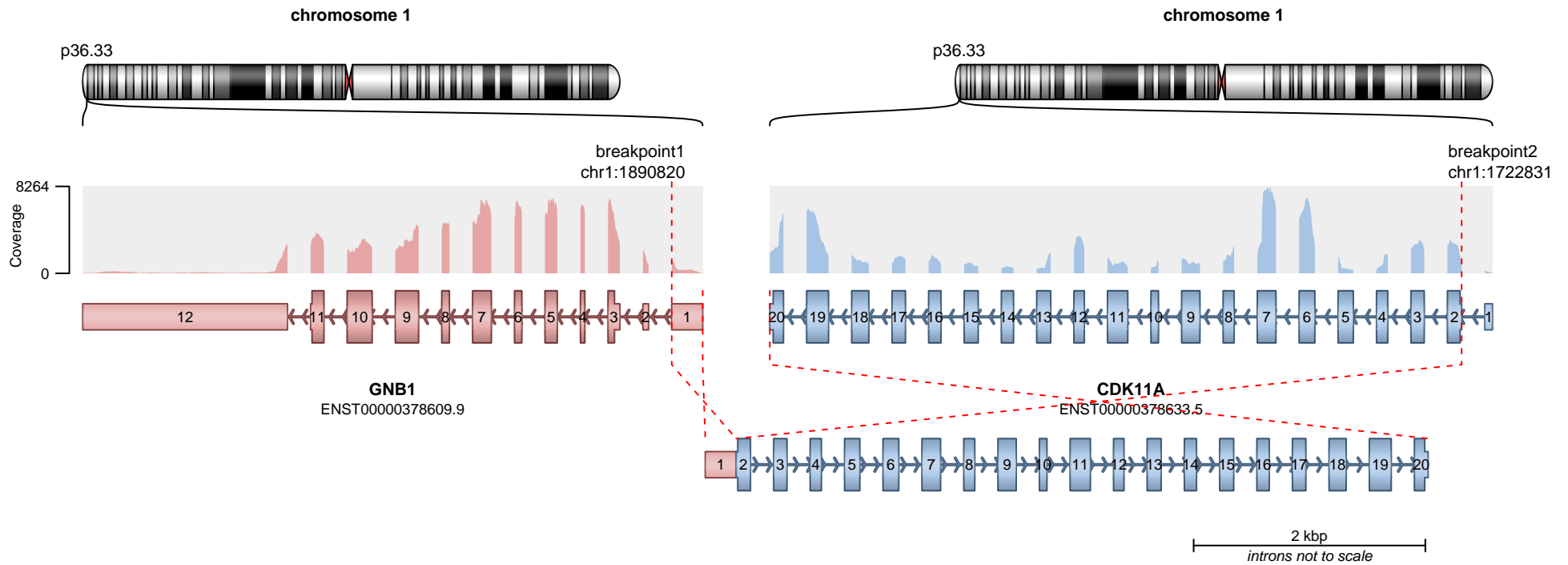
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



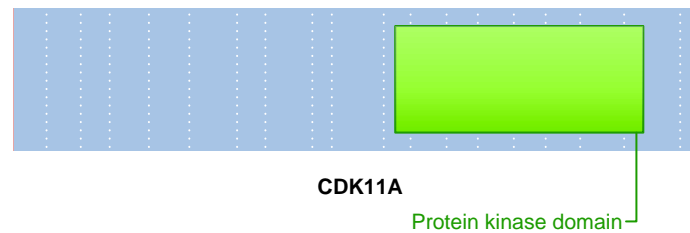
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



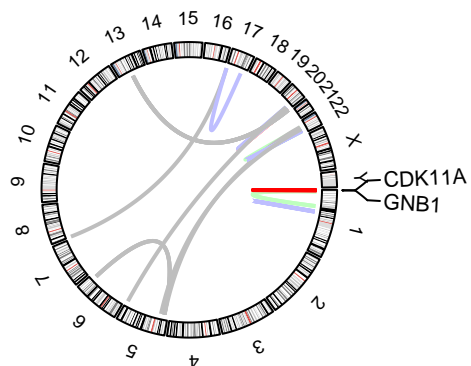
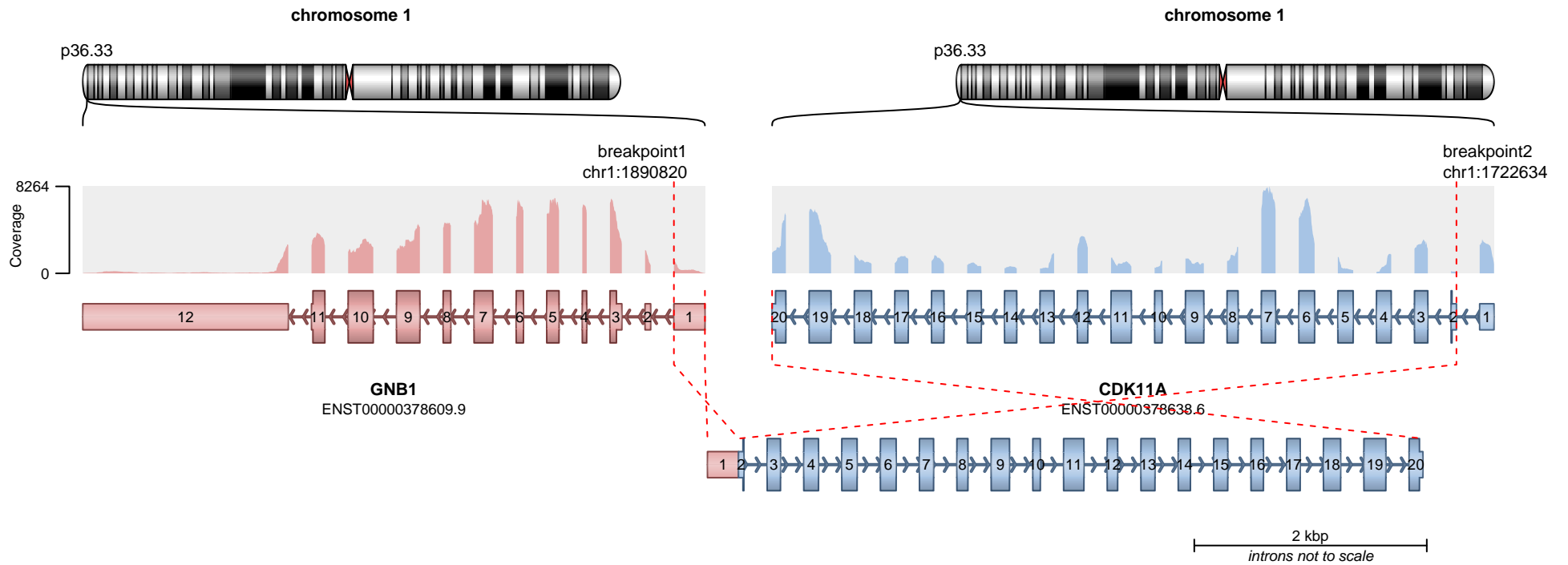
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



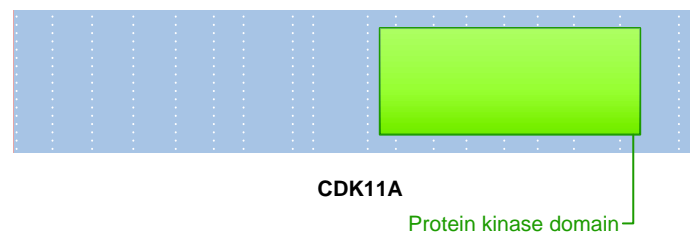
**SUPPORTING READ COUNT**

Split reads = 51  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



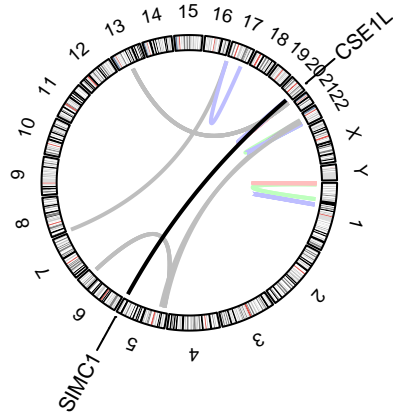
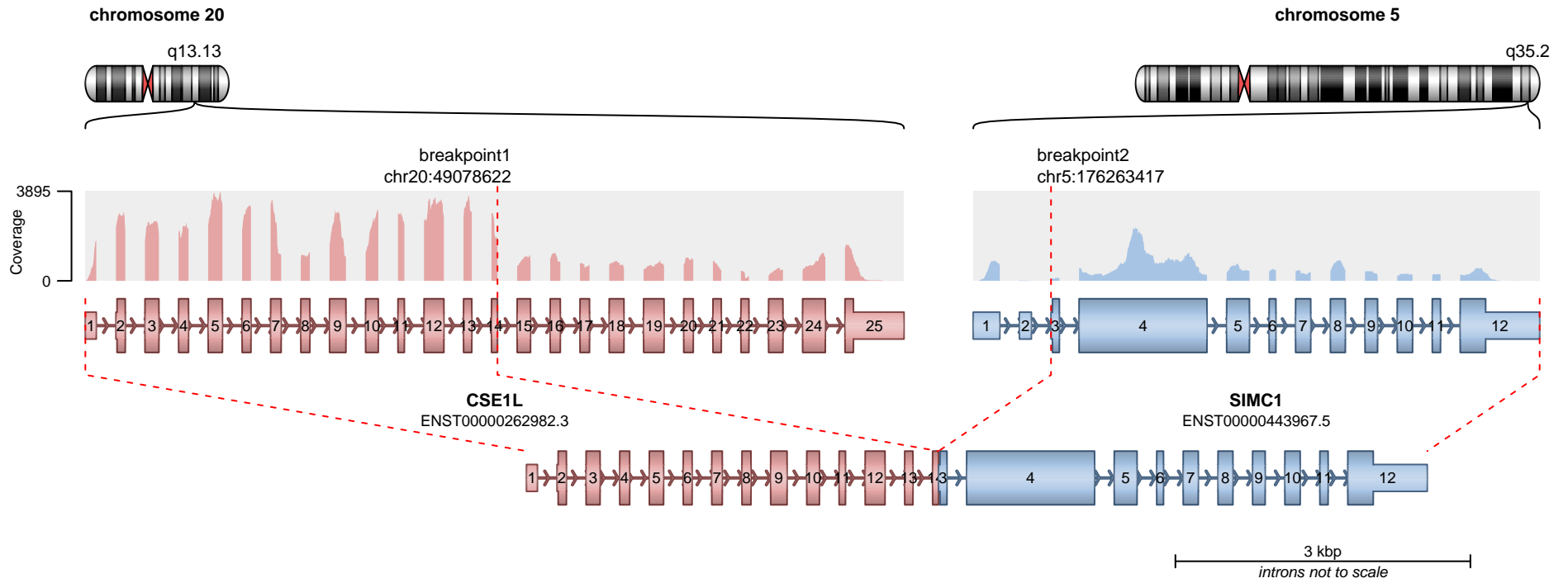
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



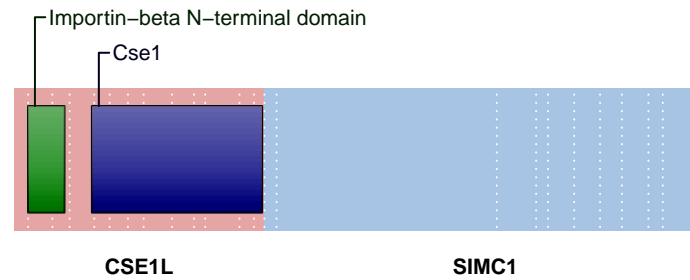
**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



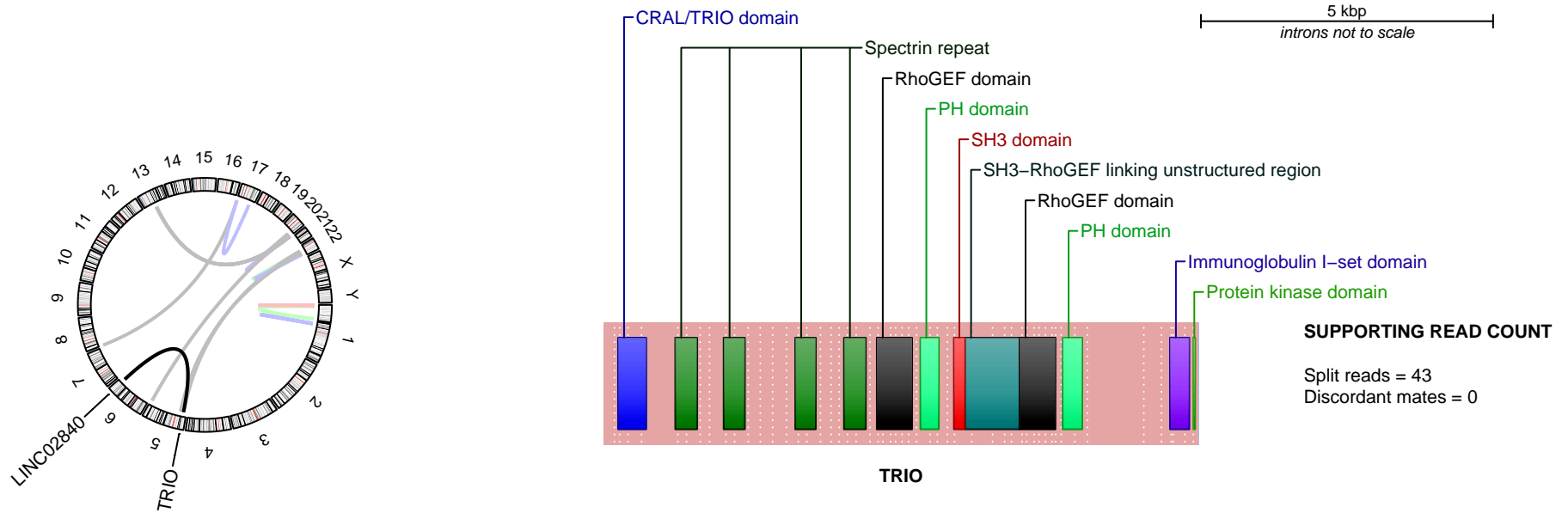
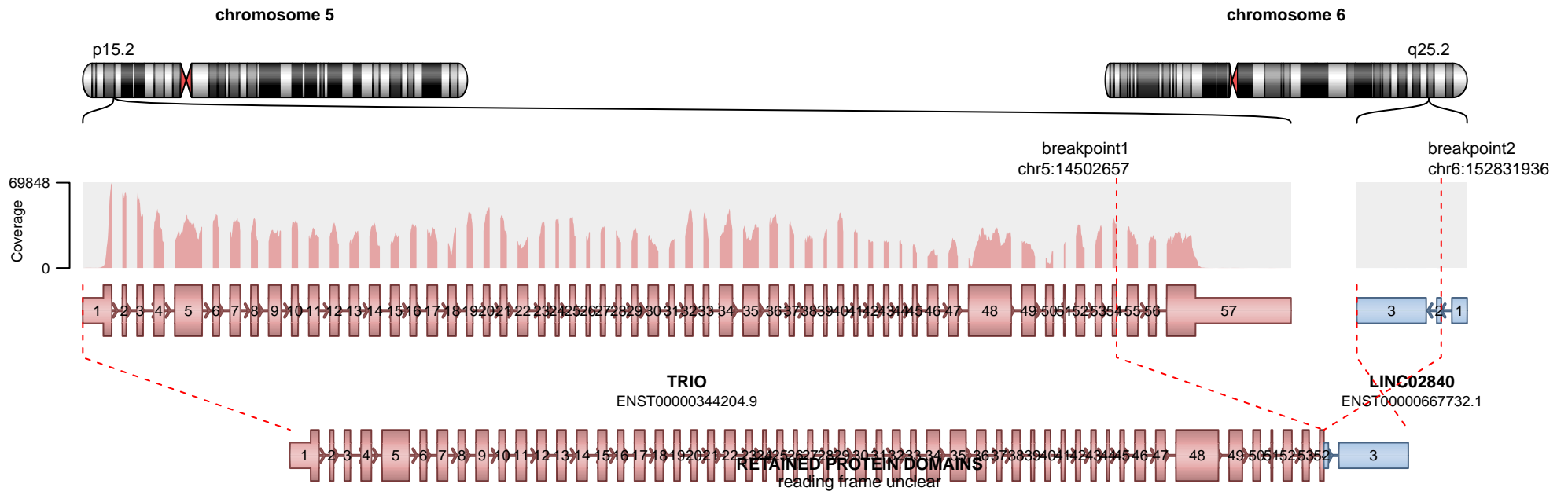
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



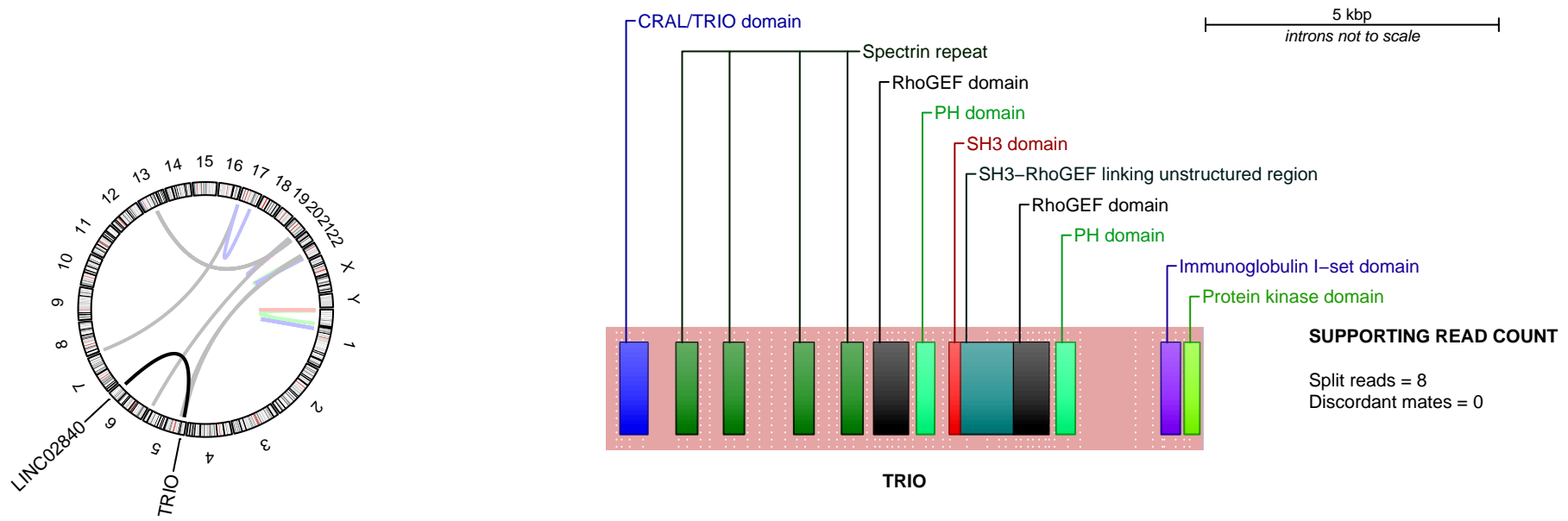
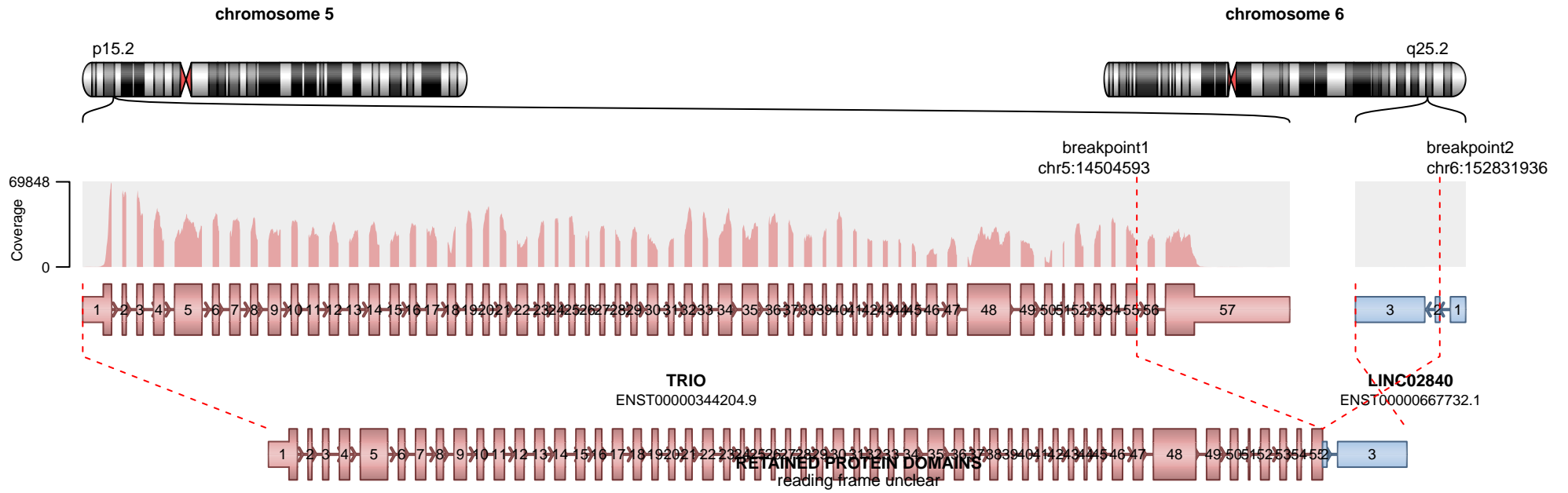
**SUPPORTING READ COUNT**

Split reads = 43  
Discordant mates = 0

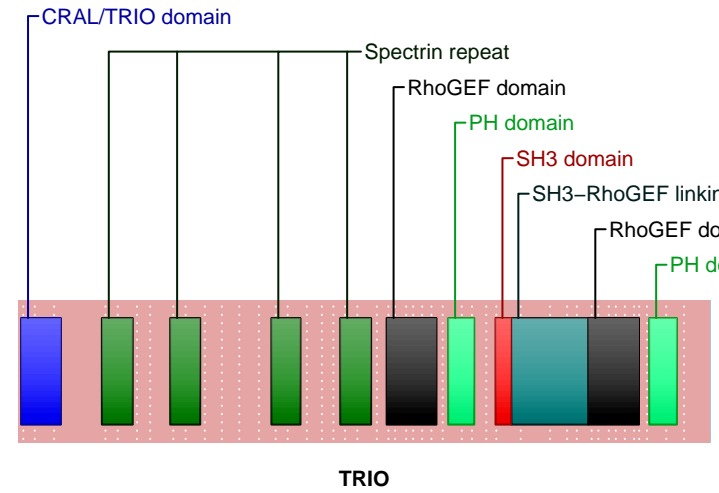
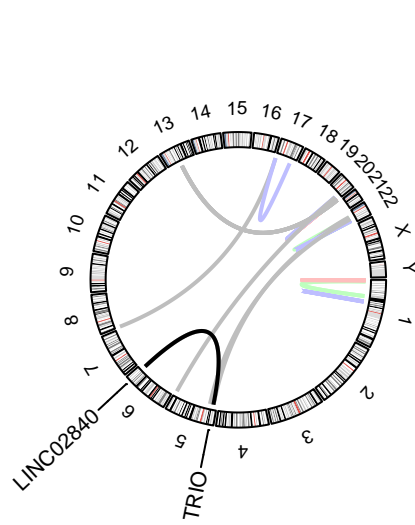
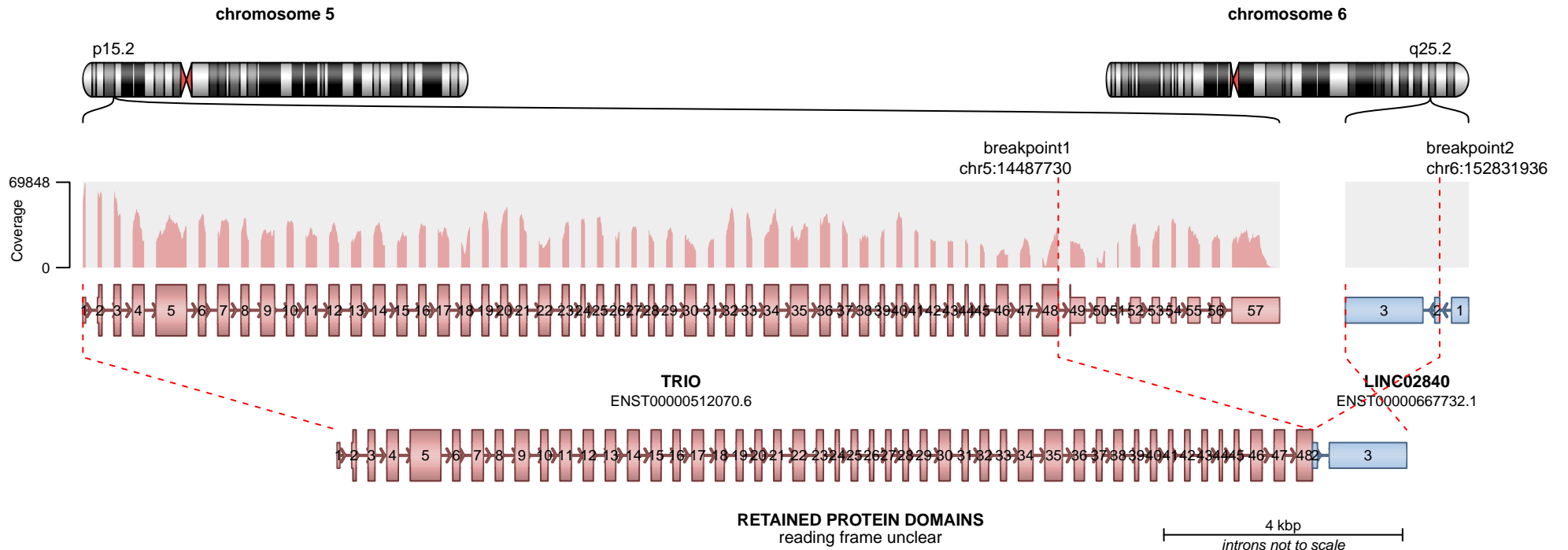
- translocation
- duplication
- deletion
- inversion



— translocation — deletion  
— duplication — inversion



— translocation — deletion  
— duplication — inversion



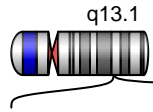
**SUPPORTING READ COUNT**

Split reads = 4

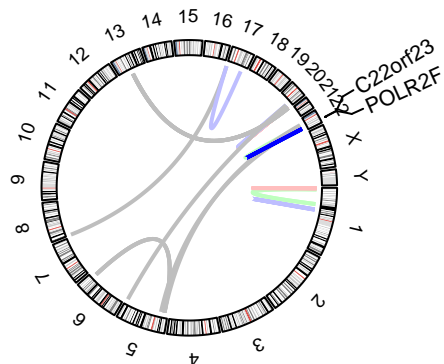
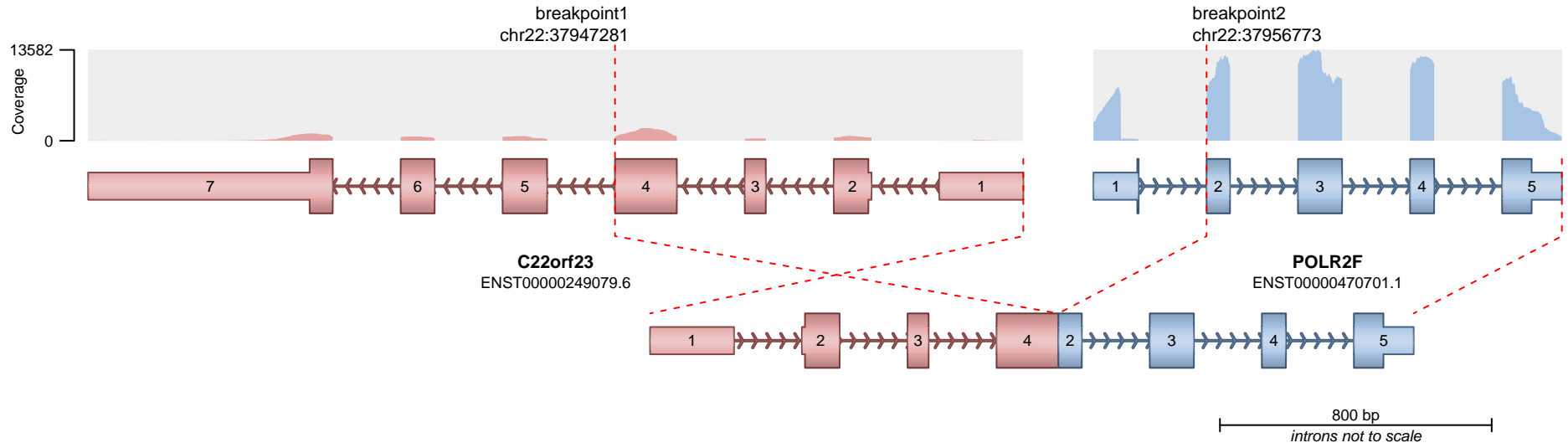
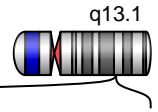
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion

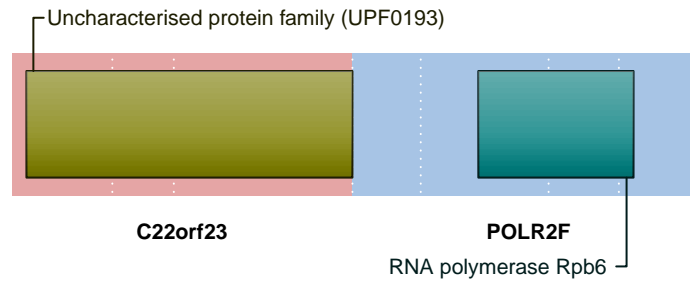
chromosome 22



chromosome 22



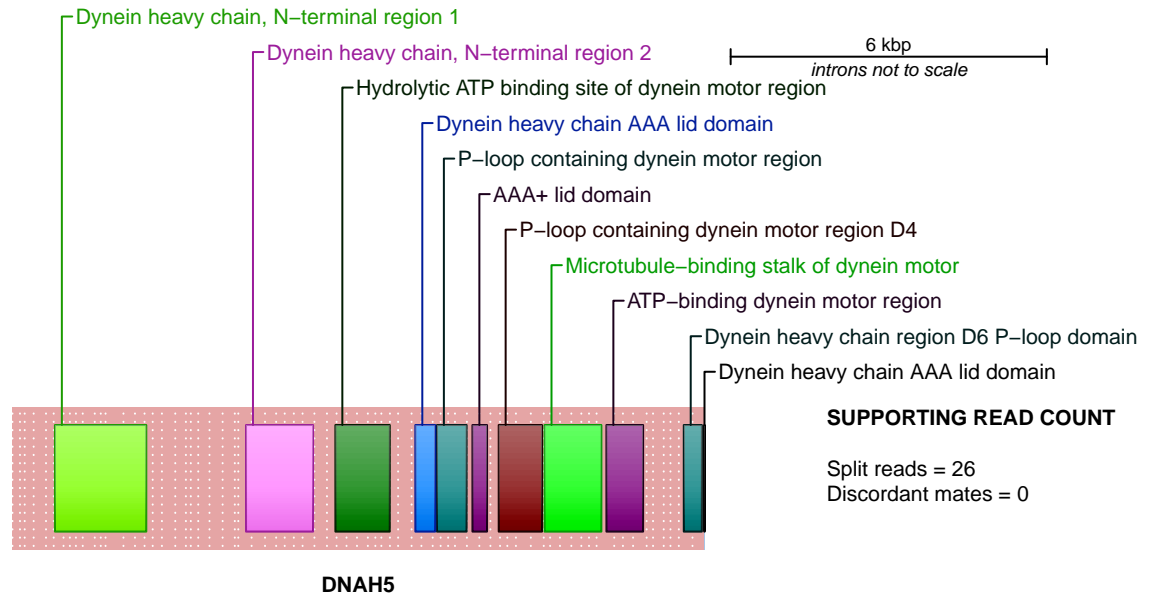
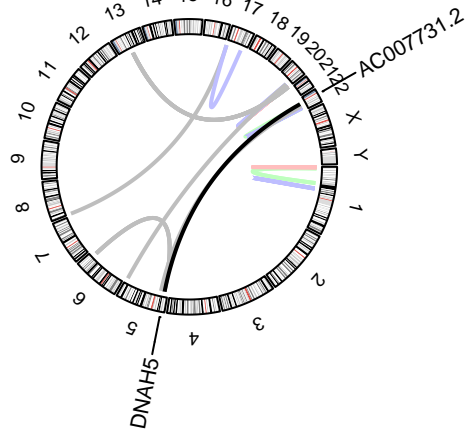
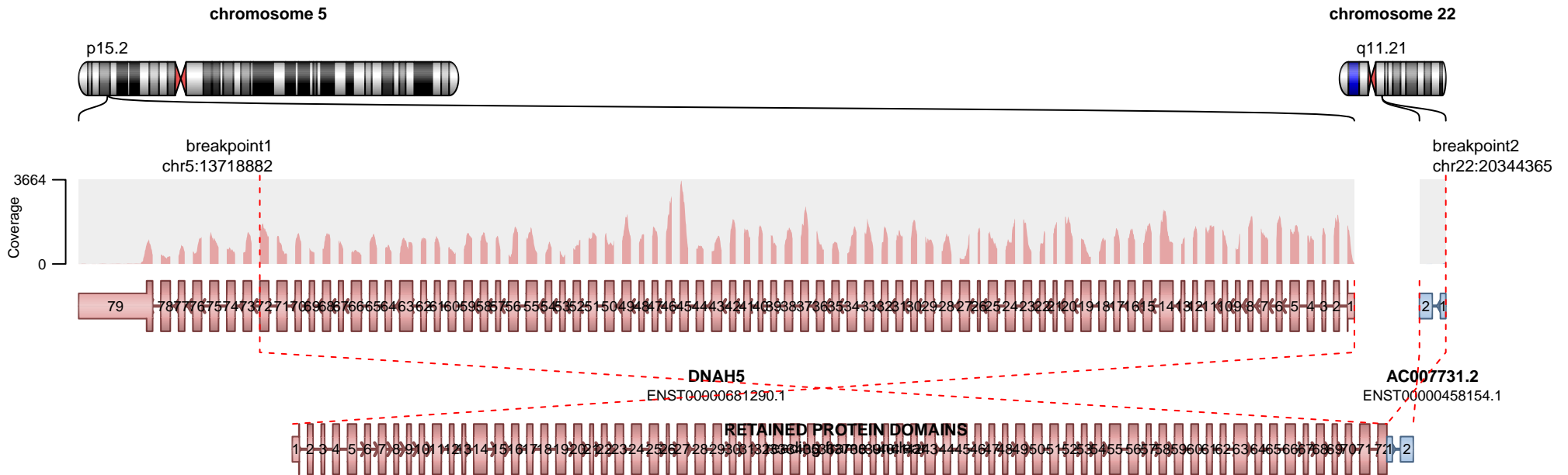
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



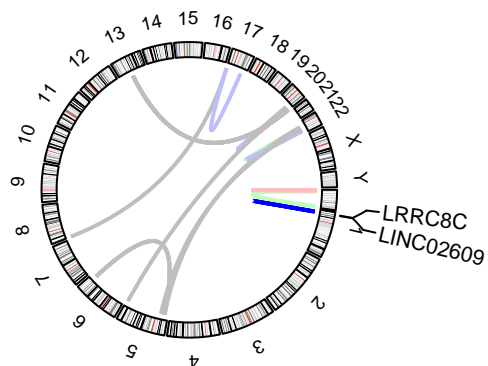
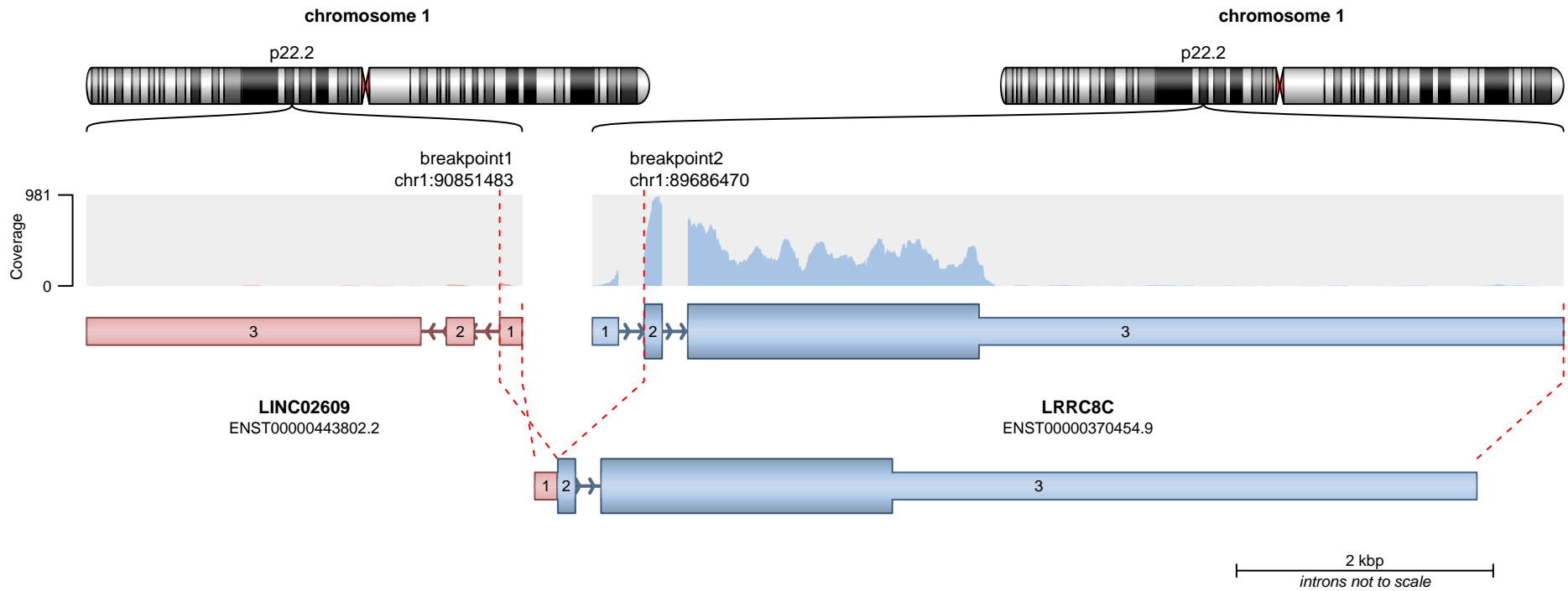
**SUPPORTING READ COUNT**

Split reads = 26  
Discordant mates = 0

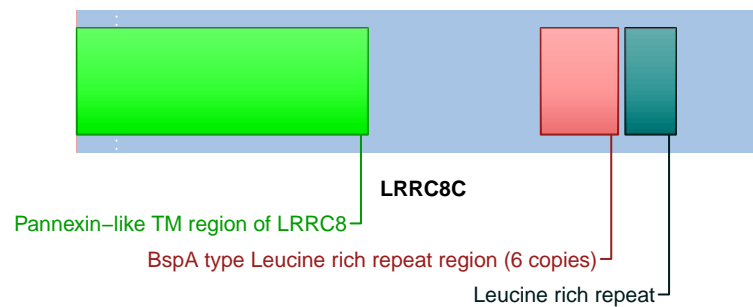
- translocation
- duplication
- deletion
- inversion



— translocation — deletion  
— duplication — inversion



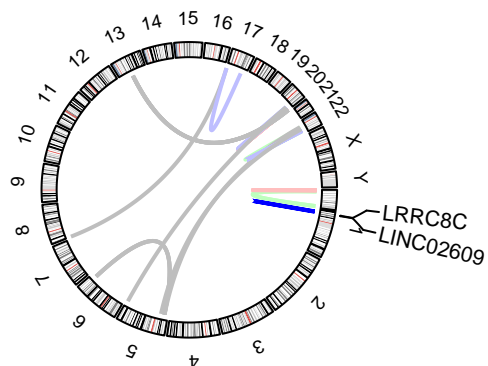
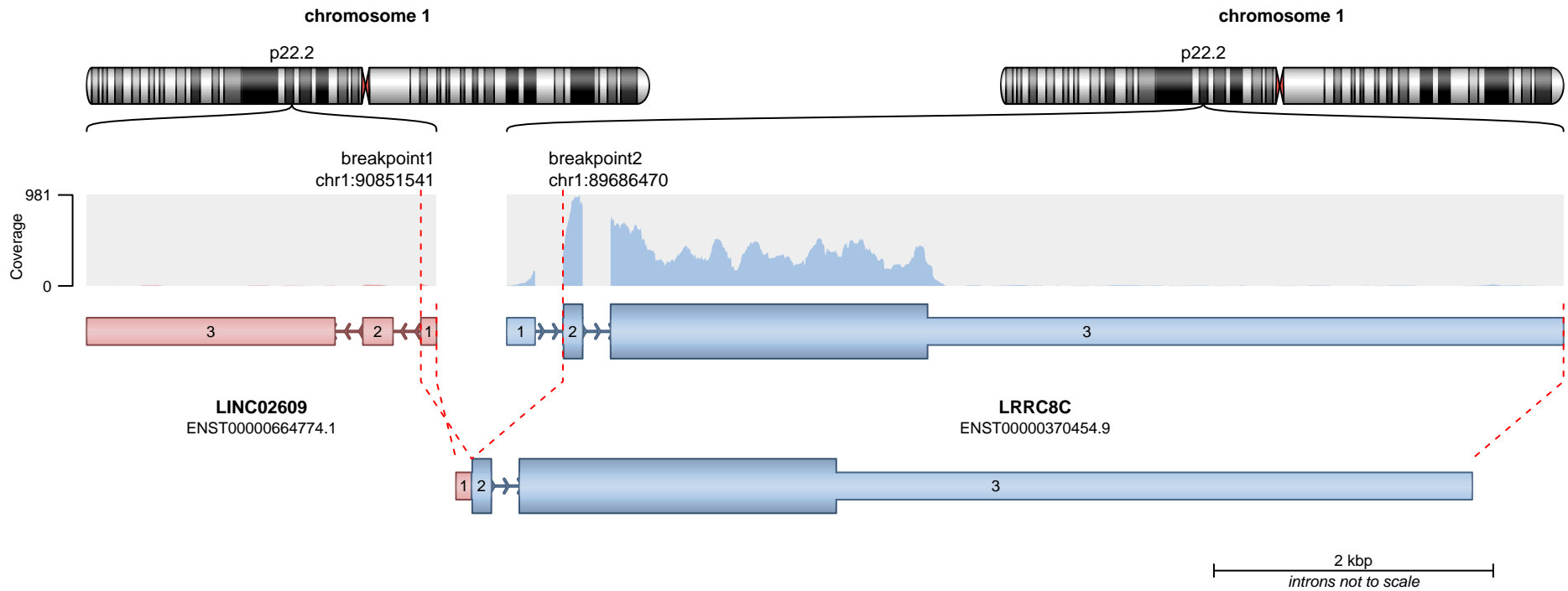
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



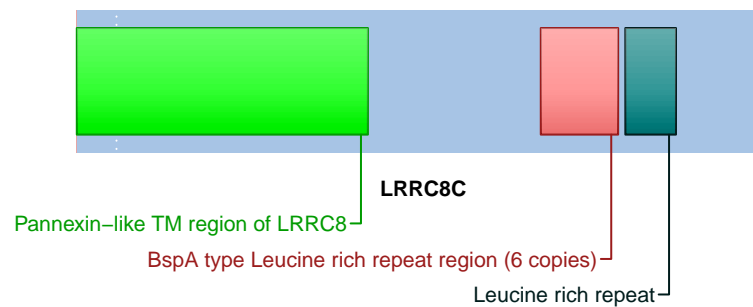
**SUPPORTING READ COUNT**

Split reads = 23  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



**RETAINED PROTEIN DOMAINS**  
reading frame unclear

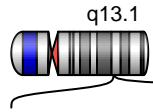


**SUPPORTING READ COUNT**

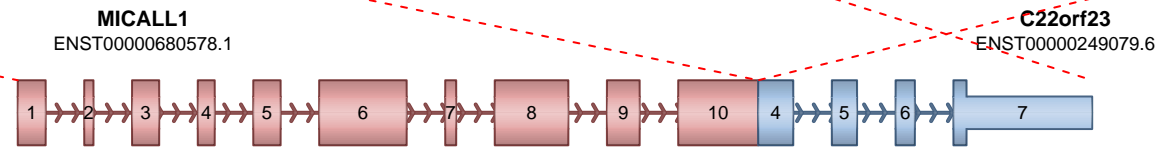
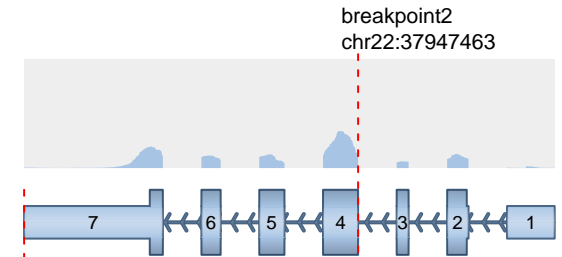
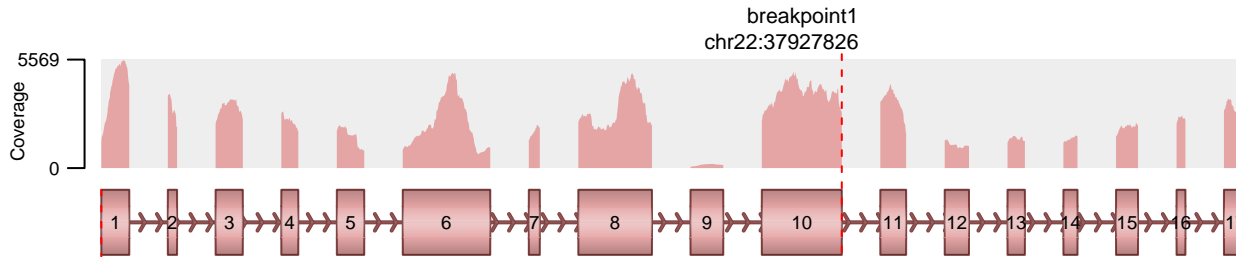
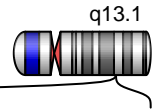
Split reads = 2  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion

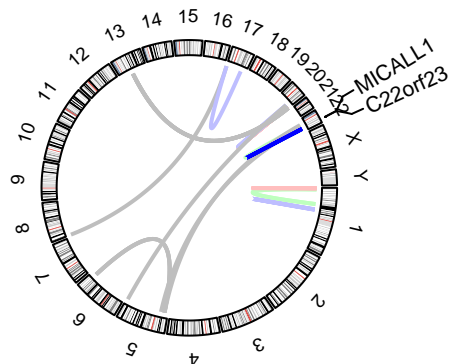
chromosome 22



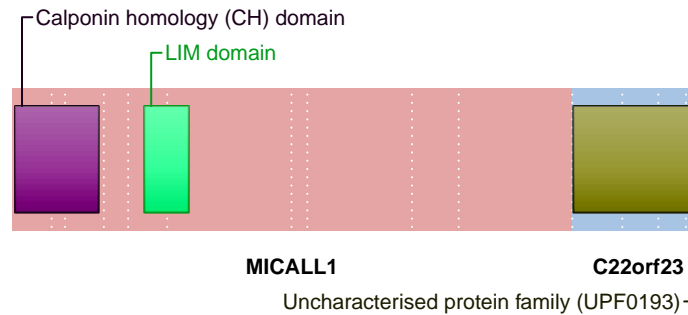
chromosome 22



2 kbp  
introns not to scale



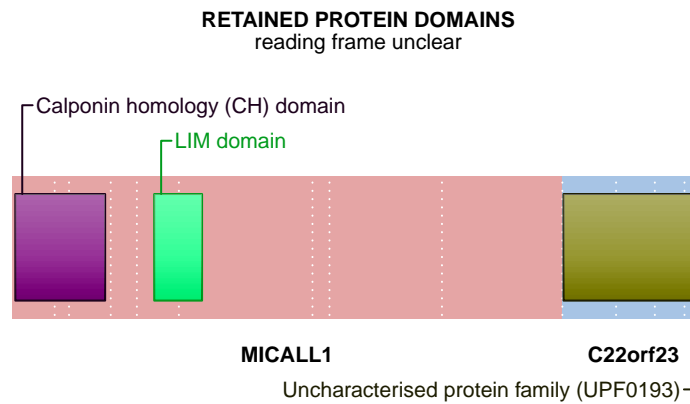
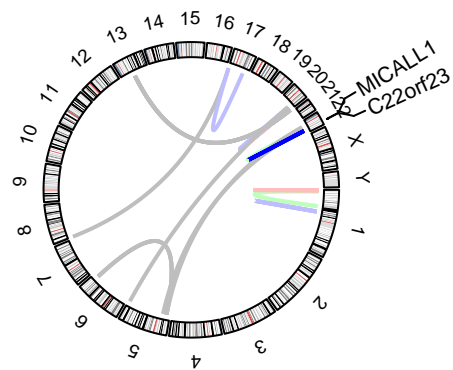
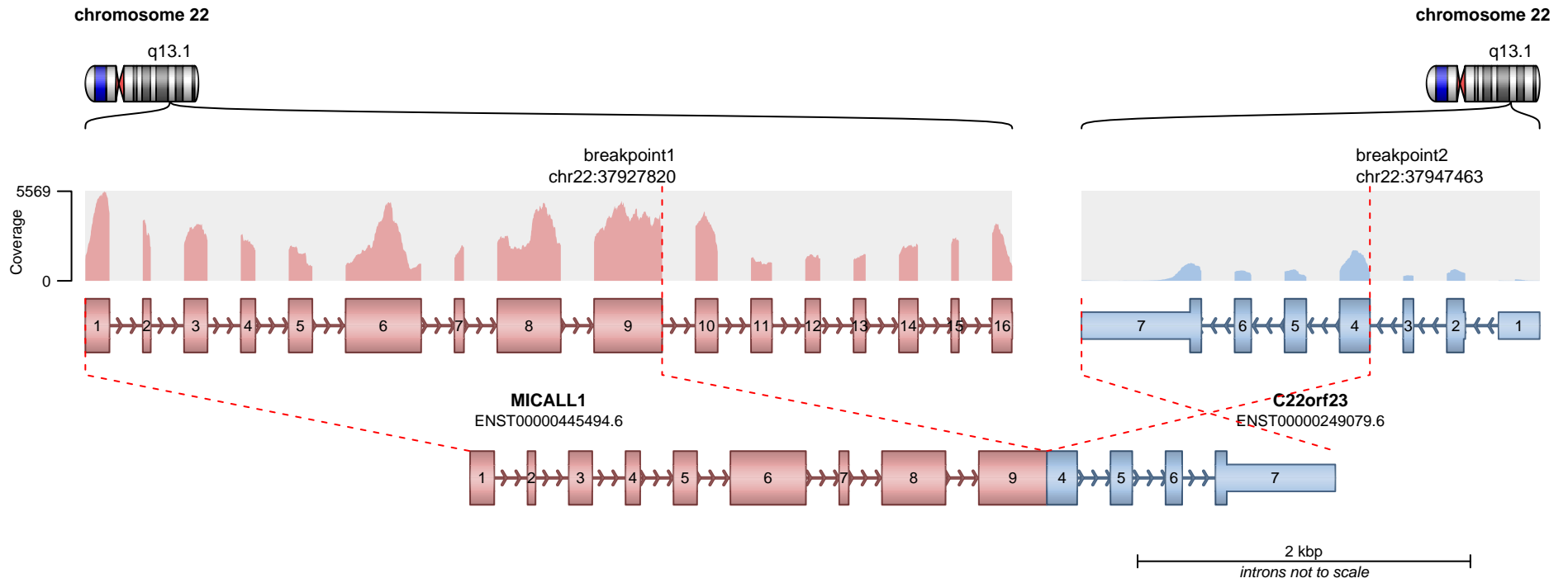
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 20  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



**SUPPORTING READ COUNT**

Split reads = 5  
Discordant mates = 0

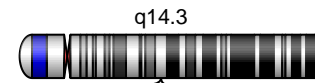
— translocation    — deletion  
— duplication    — inversion

chromosome 20

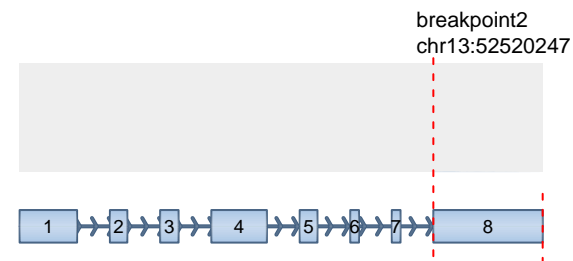
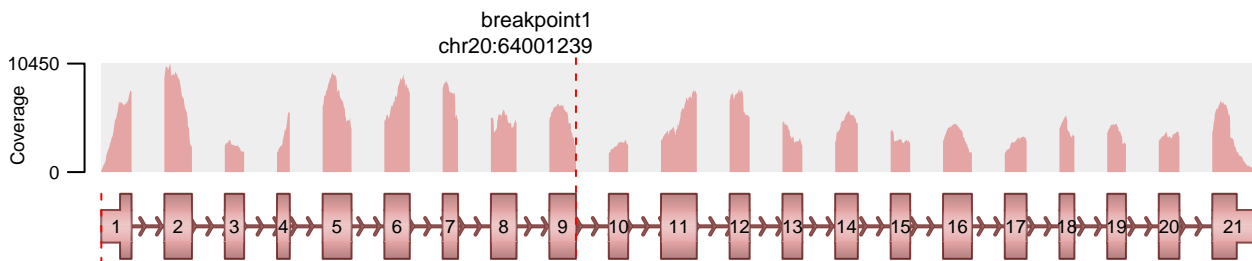


q13.33

chromosome 13

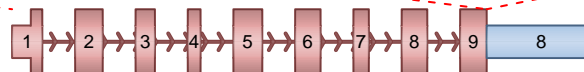


q14.3

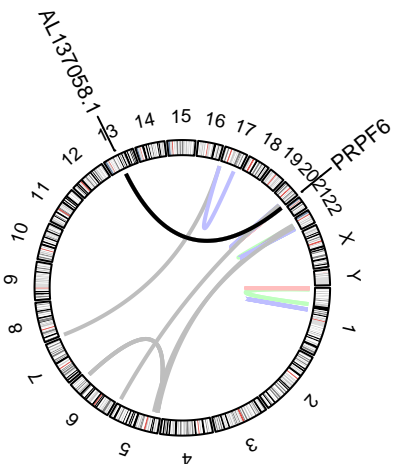


**PRPF6**  
ENST00000266079.5

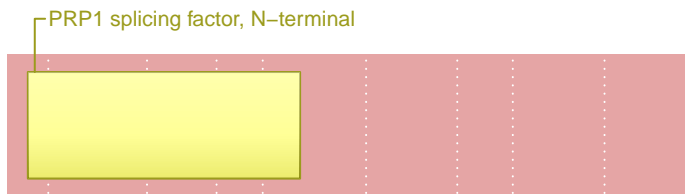
**AL137058.1**  
ENST00000418237.6



2 kbp  
introns not to scale



**RETAINED PROTEIN DOMAINS**  
reading frame unclear

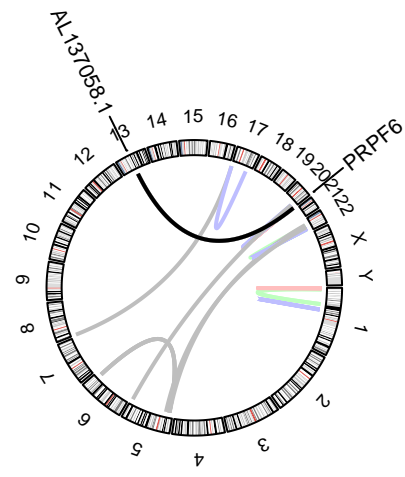
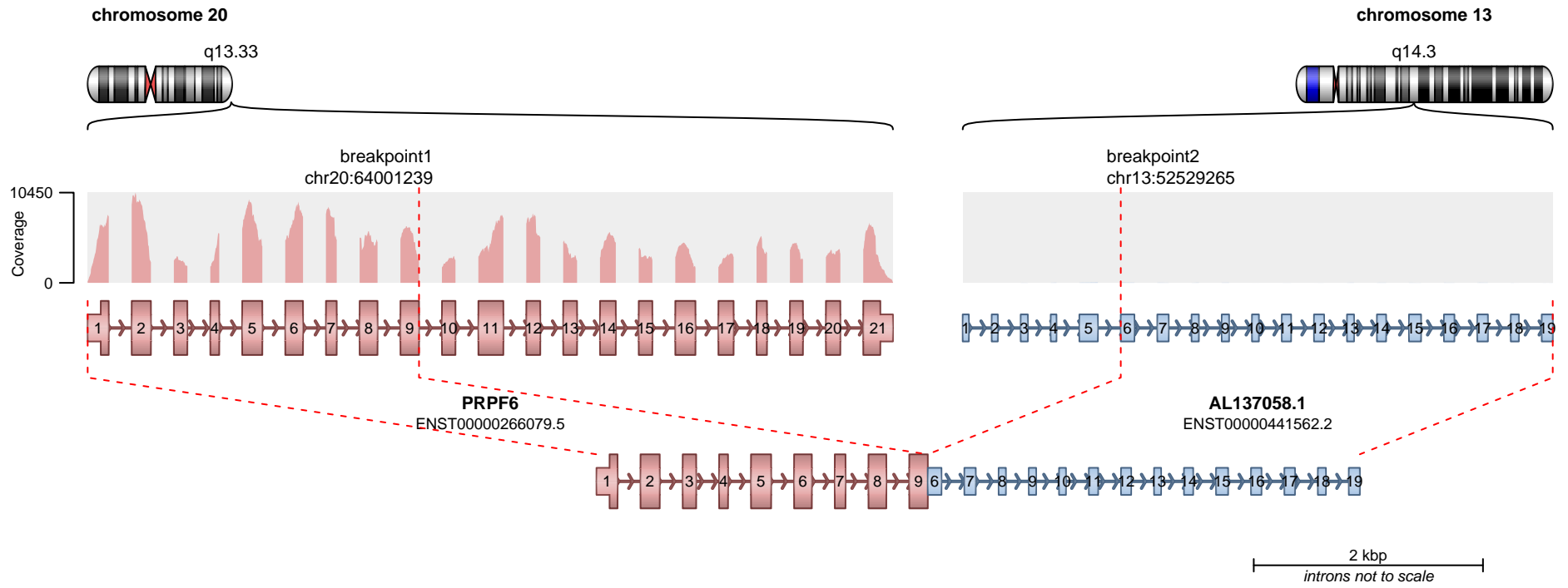


**PRPF6**

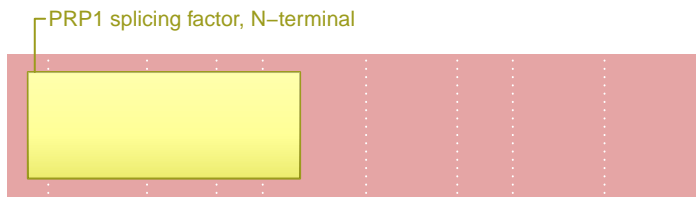
**SUPPORTING READ COUNT**

Split reads = 15  
Discordant mates = 1

— translocation    — deletion  
— duplication    — inversion



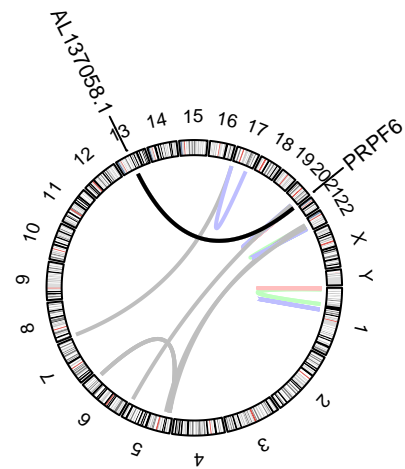
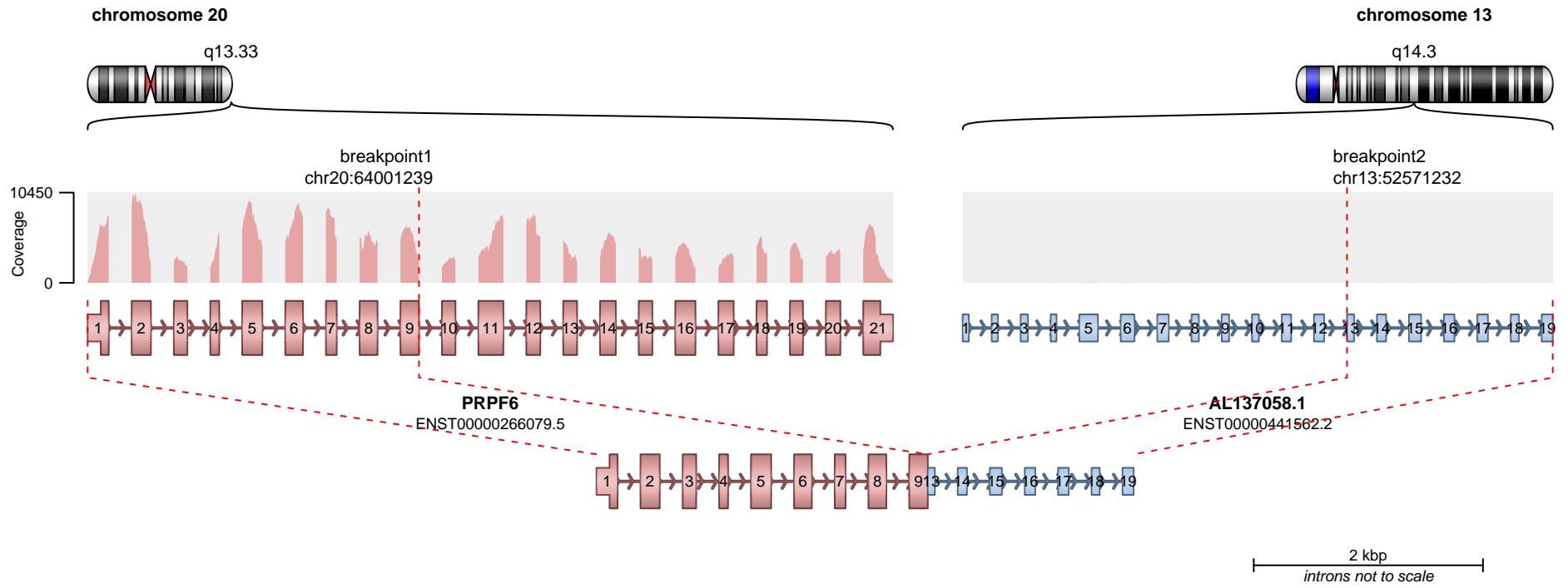
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



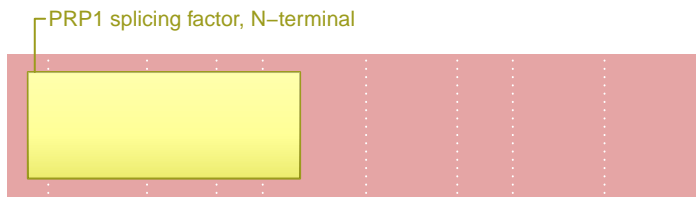
**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

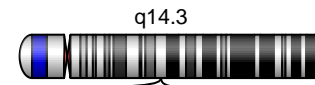
- translocation
- duplication
- deletion
- inversion

chromosome 20

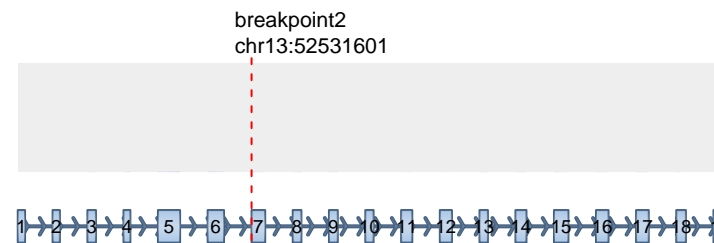
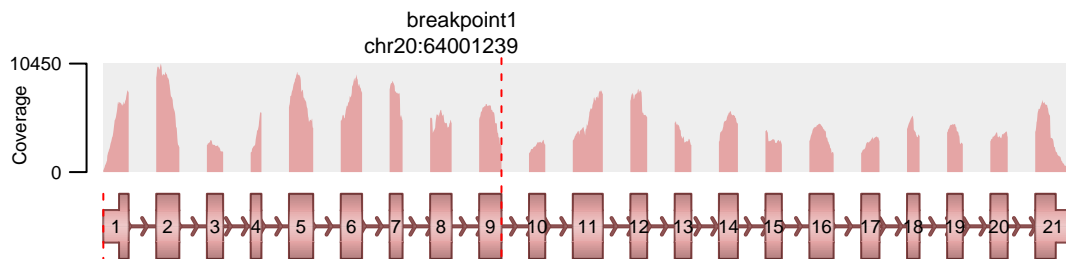


q13.33

chromosome 13

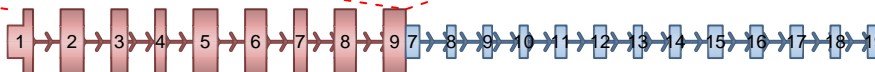


q14.3

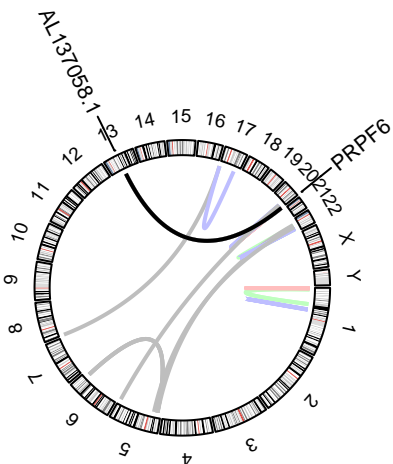


**PRPF6**  
ENST00000266079.5

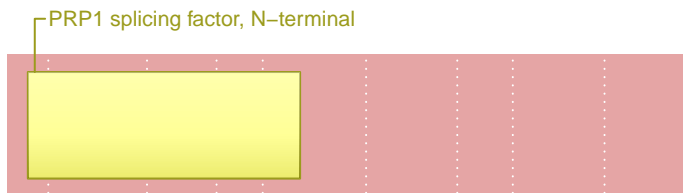
**AL137058.1**  
ENST00000441562.2



2 kbp  
introns not to scale



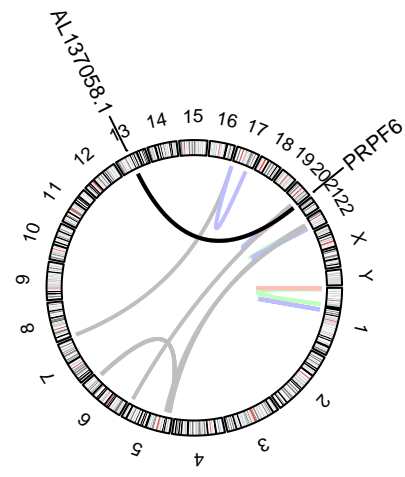
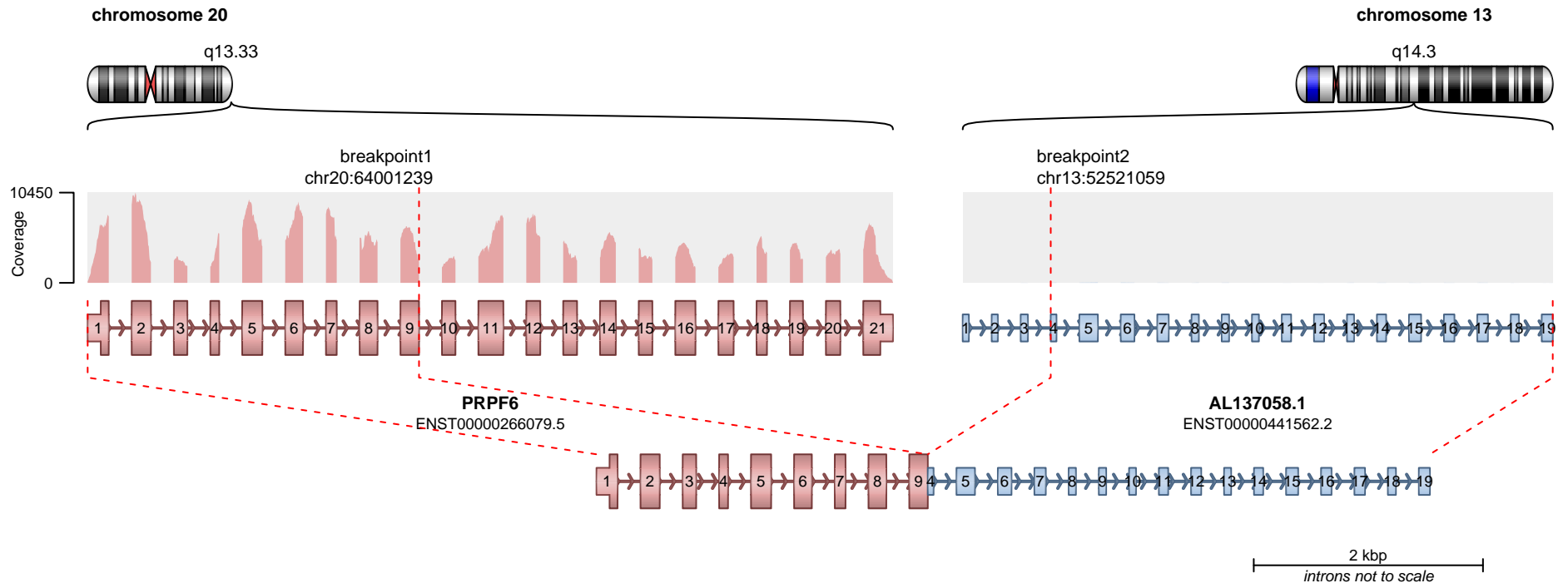
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



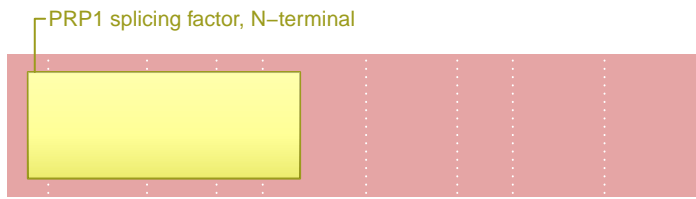
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



**RETAINED PROTEIN DOMAINS**  
reading frame unclear

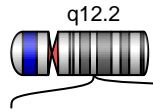


**SUPPORTING READ COUNT**

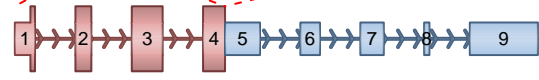
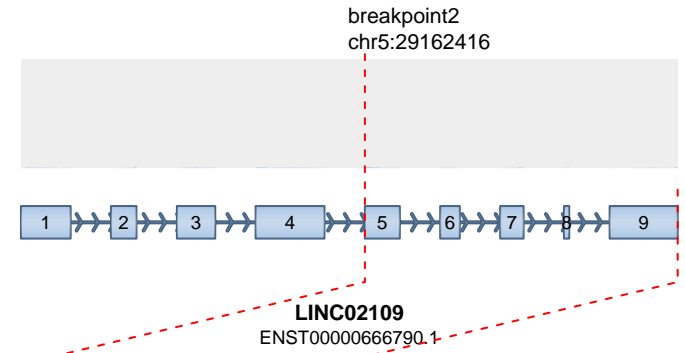
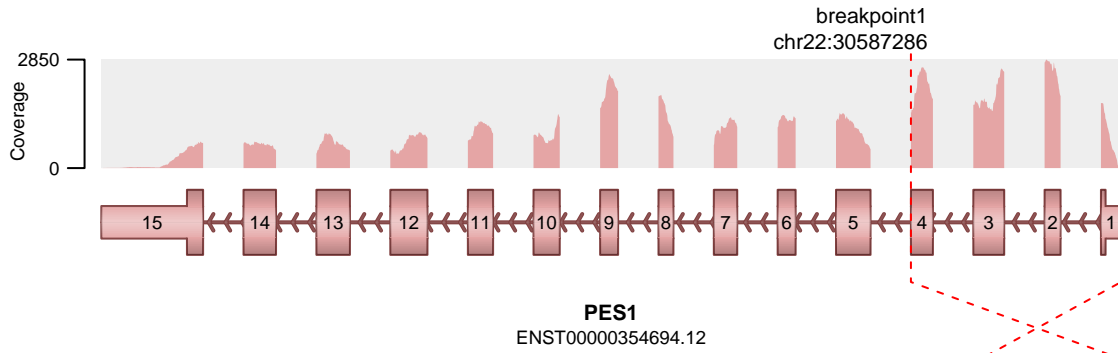
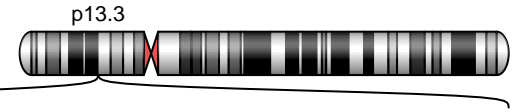
Split reads = 1  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

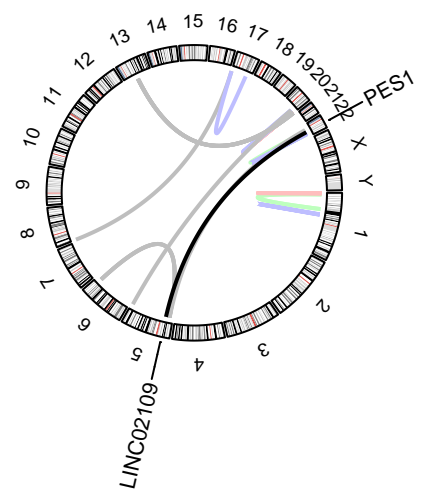
chromosome 22



chromosome 5

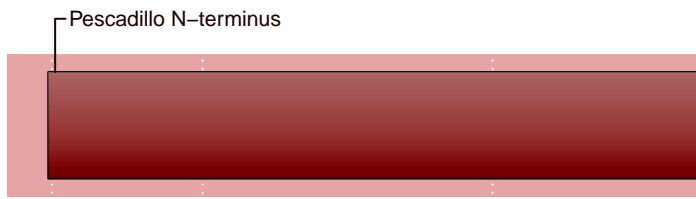


2 kbp  
introns not to scale



— translocation    — deletion  
— duplication    — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 15  
Discordant mates = 0