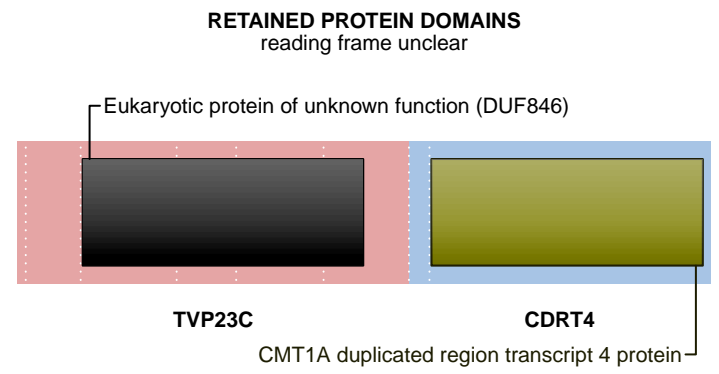
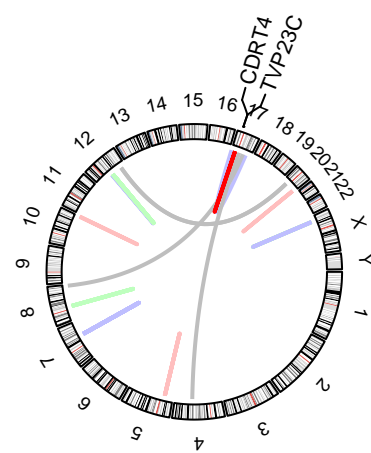
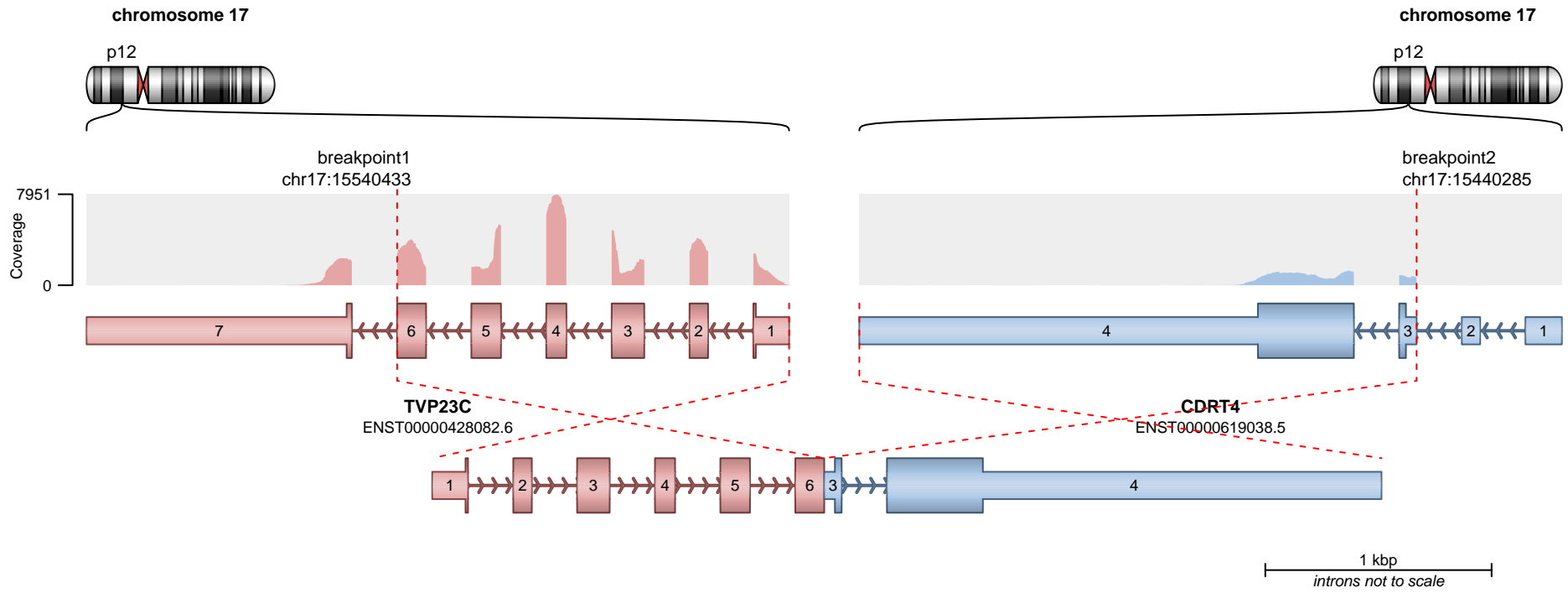


**SUPPORTING READ COUNT**

Split reads = 116  
Discordant mates = 1

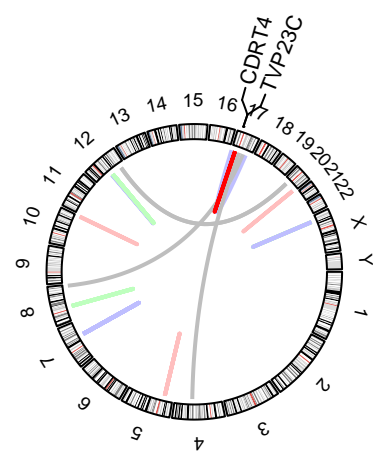
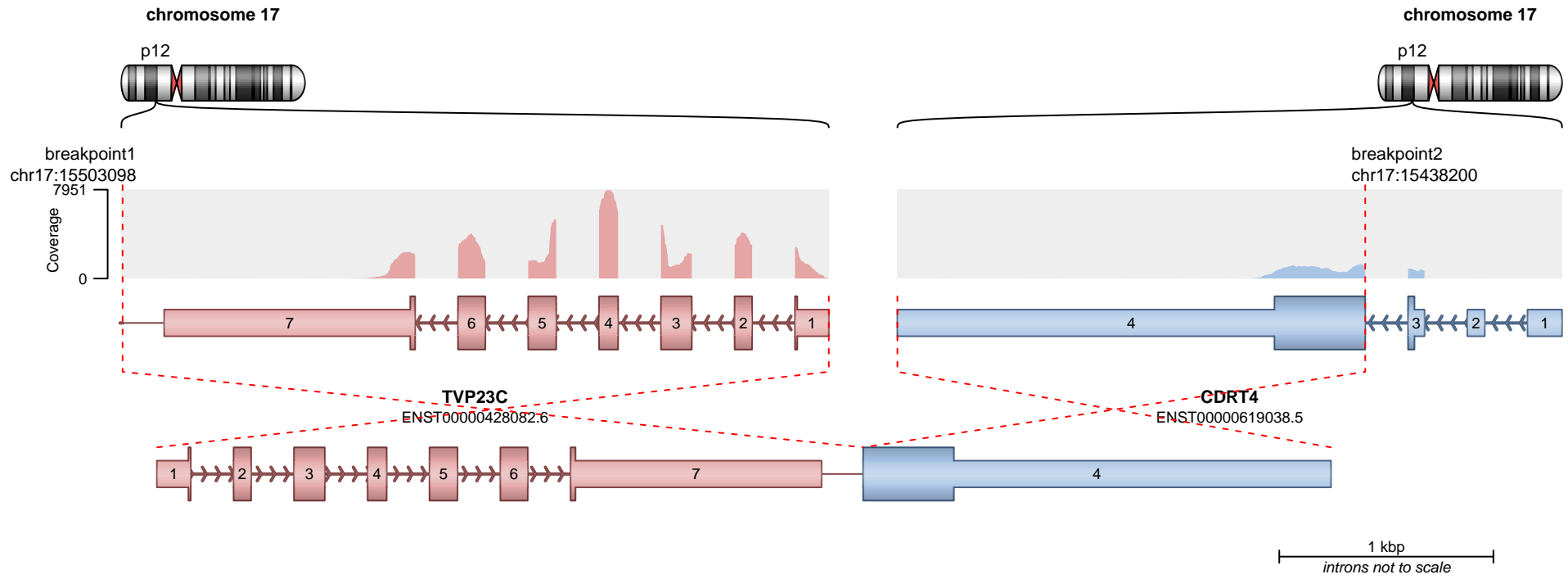
— translocation — deletion  
— duplication — inversion



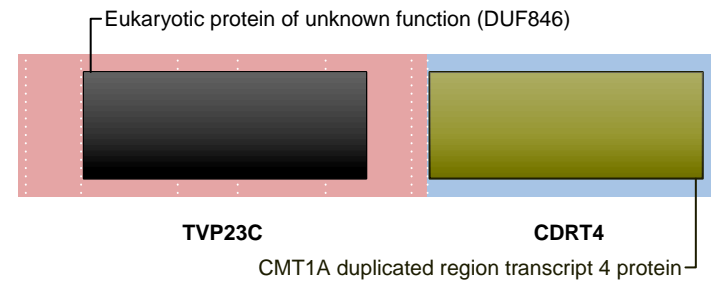
**SUPPORTING READ COUNT**

Split reads = 55  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



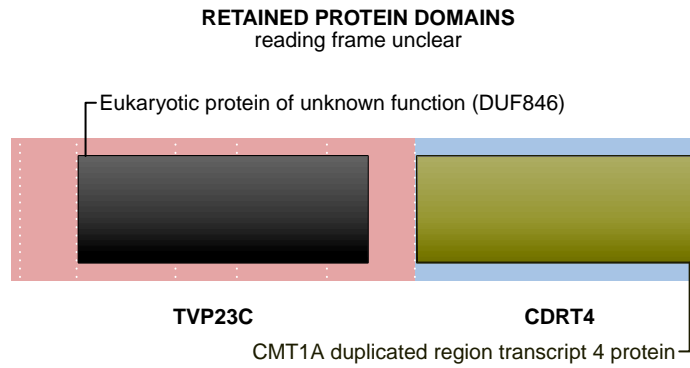
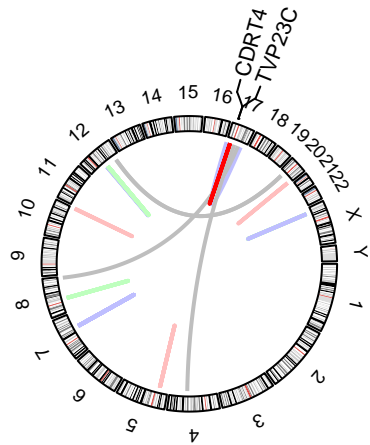
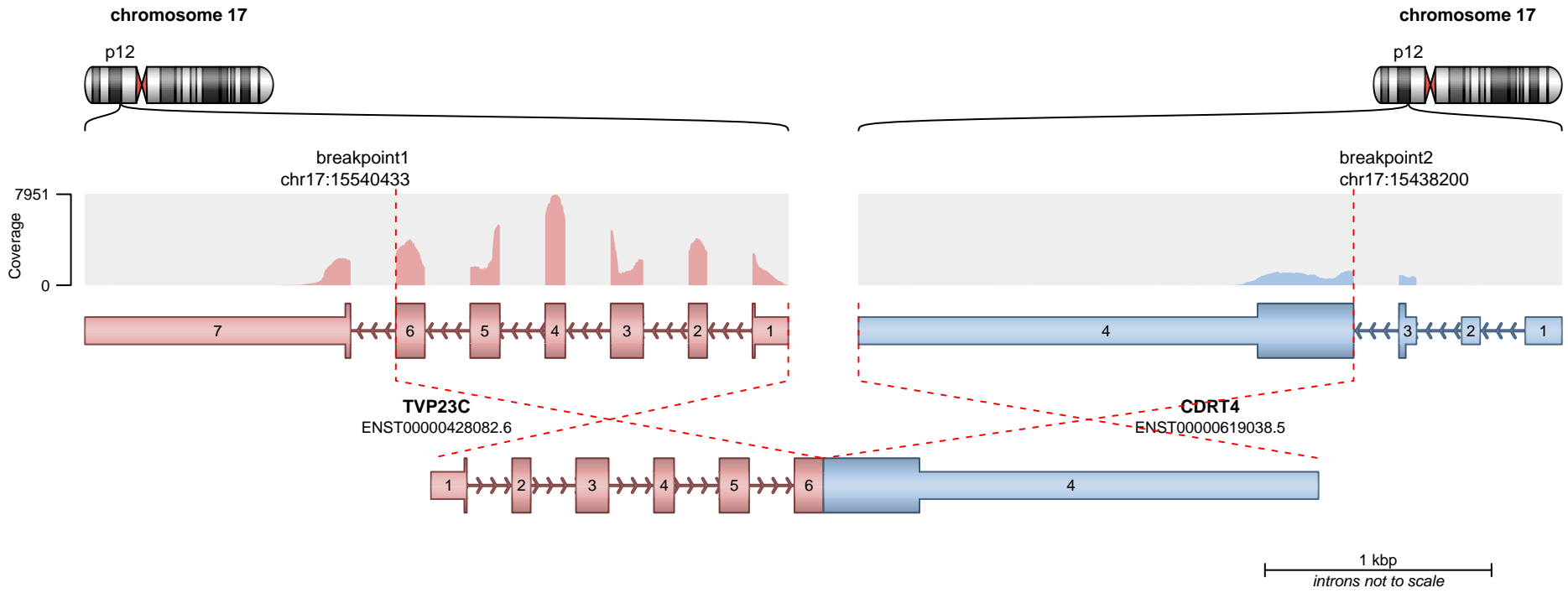
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 42  
Discordant mates = 0

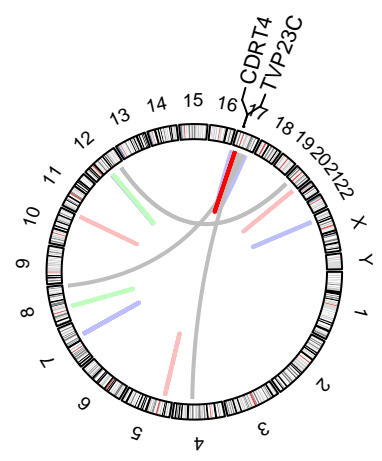
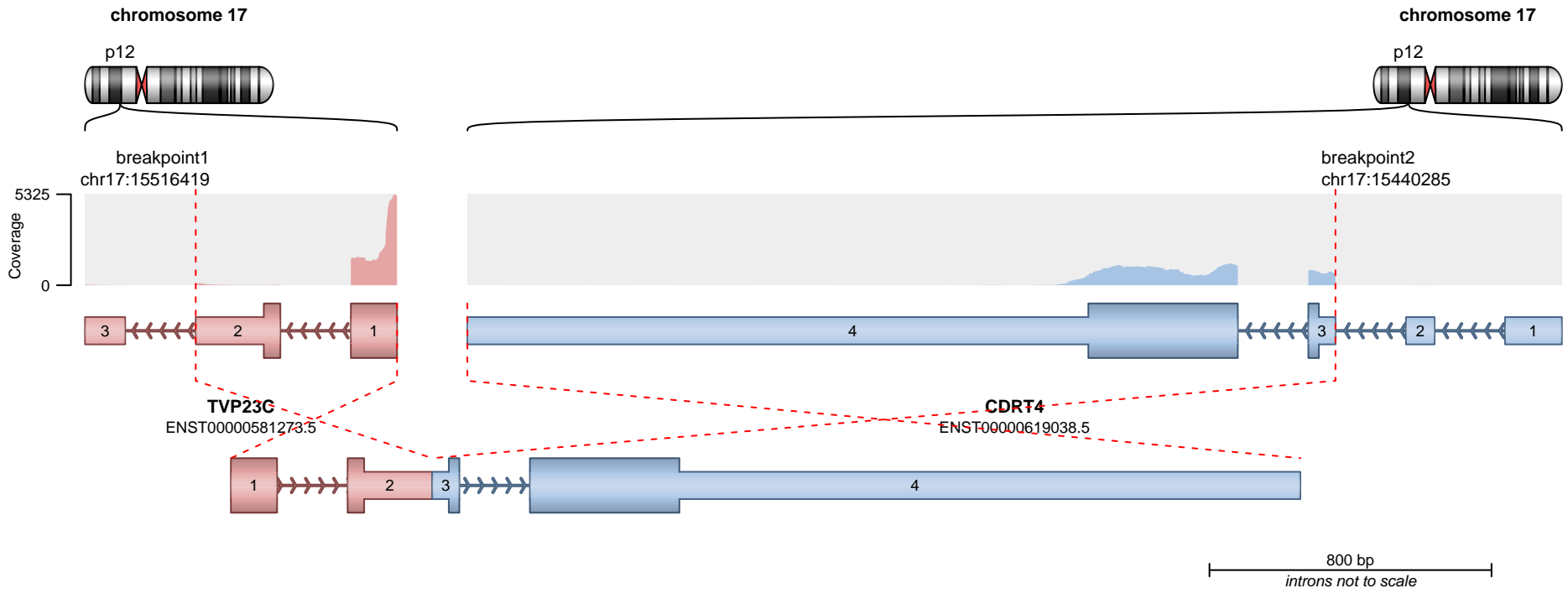
- translocation
- duplication
- deletion
- inversion



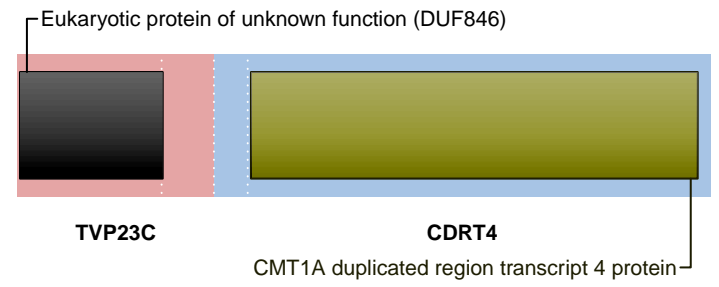
**SUPPORTING READ COUNT**

Split reads = 11  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



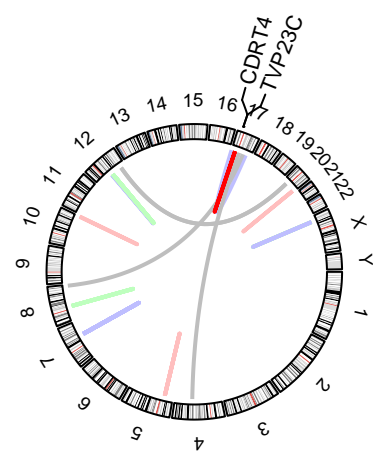
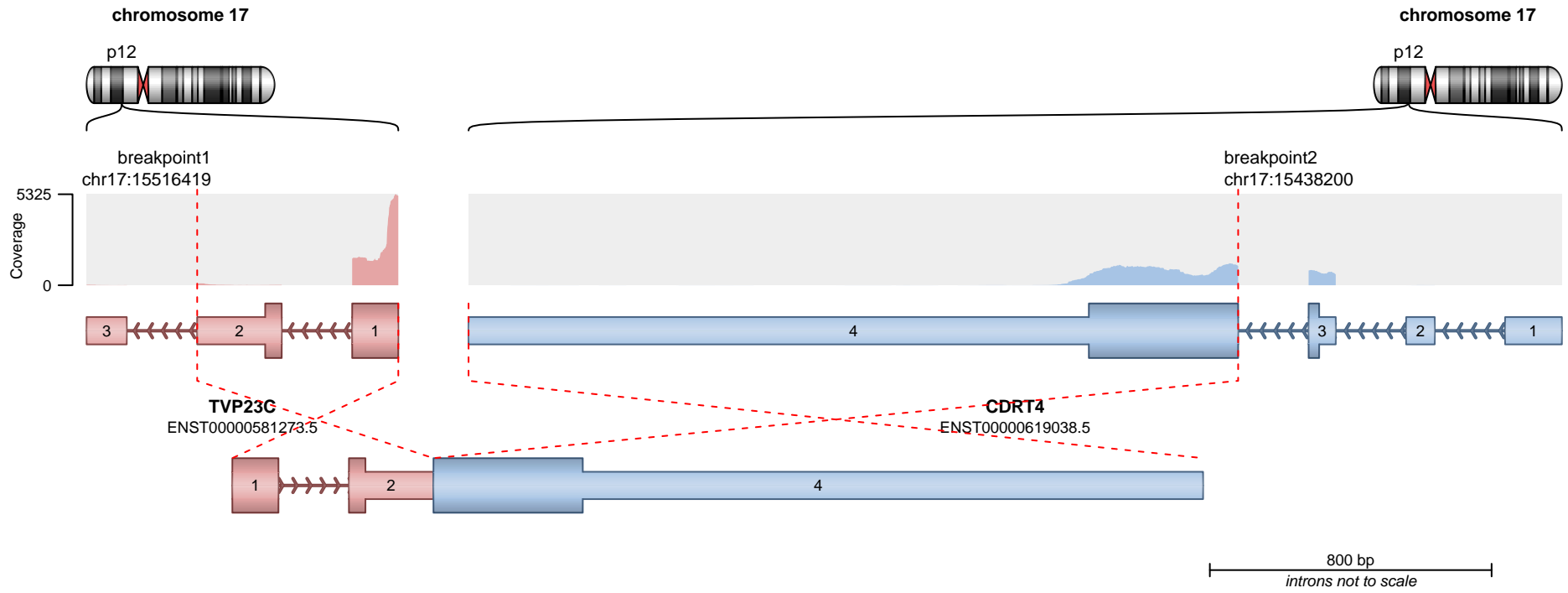
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



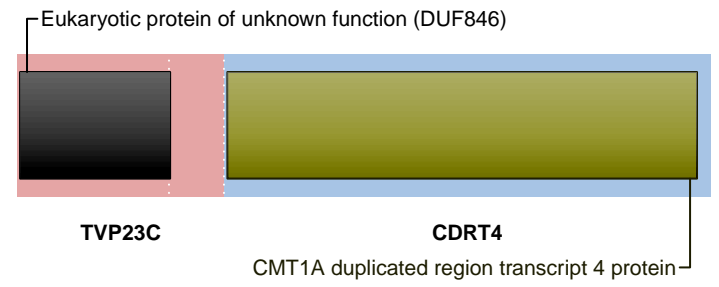
**SUPPORTING READ COUNT**

Split reads = 6  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



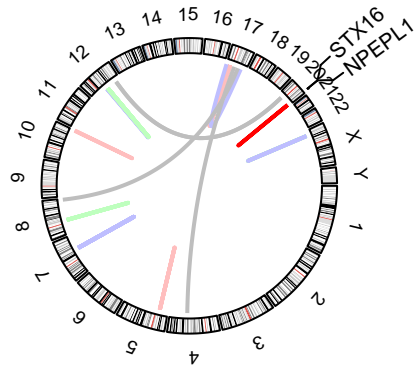
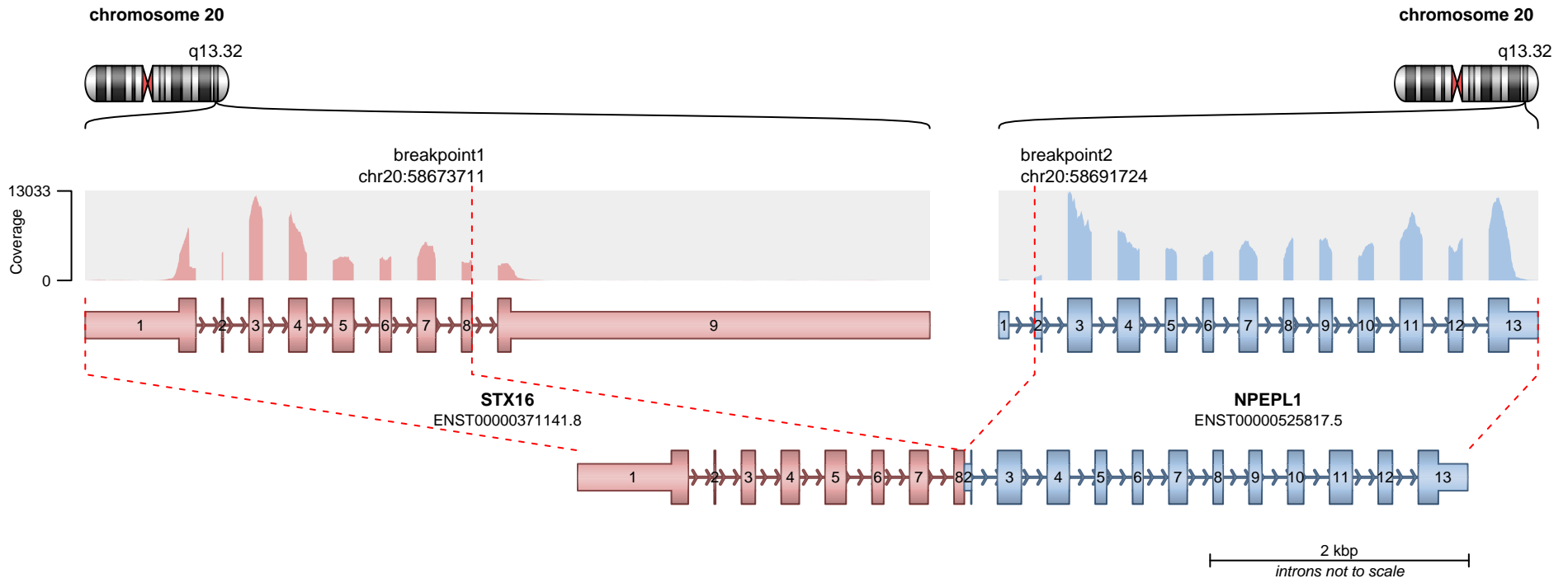
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



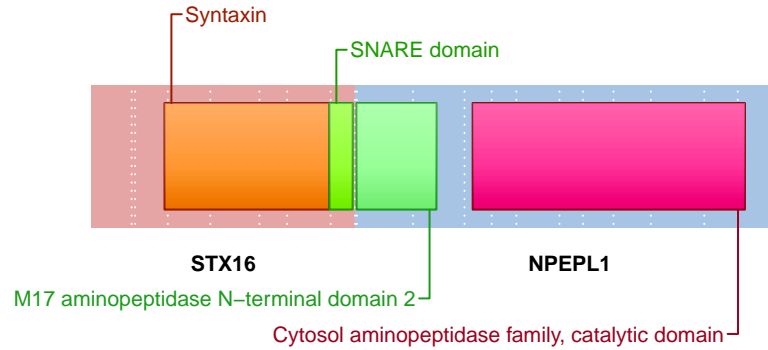
**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



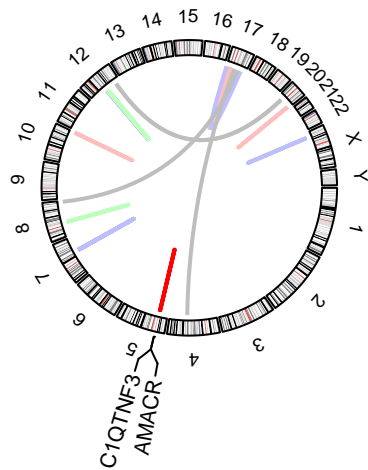
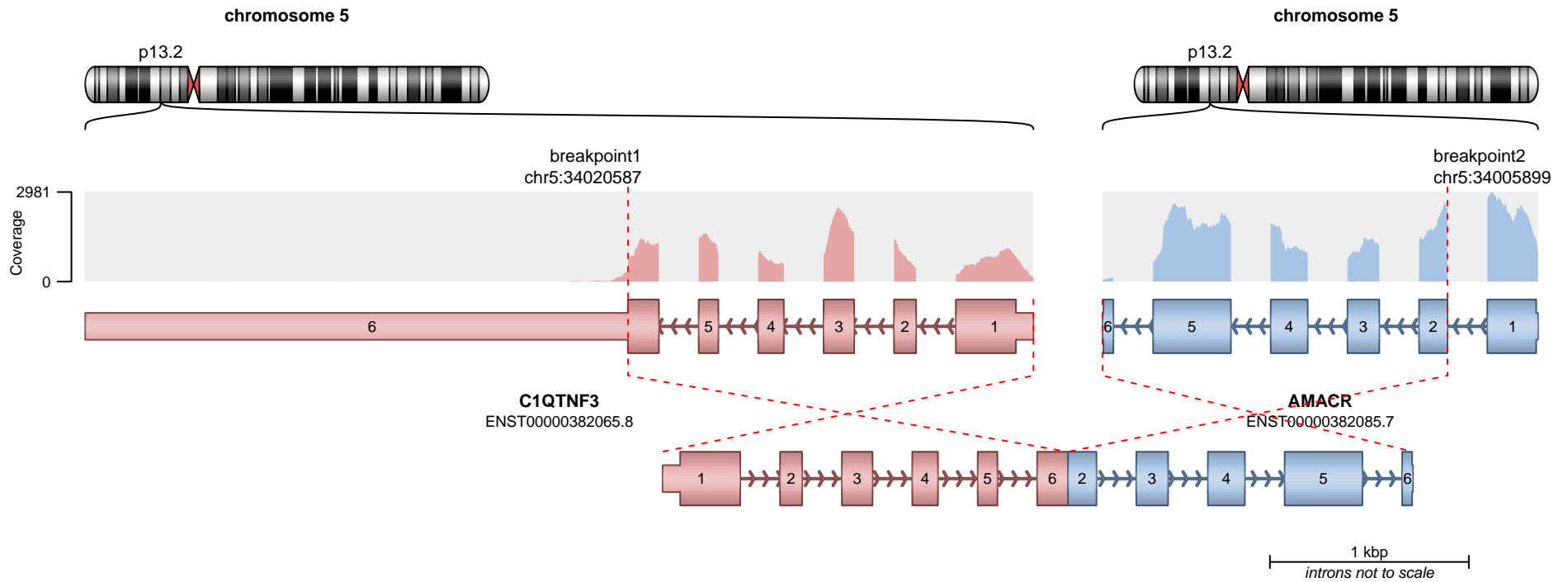
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



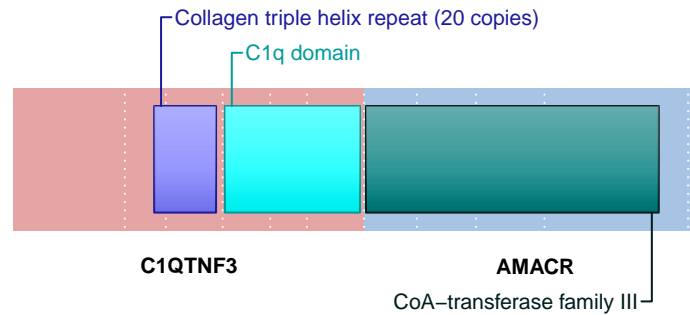
**SUPPORTING READ COUNT**

Split reads = 103  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



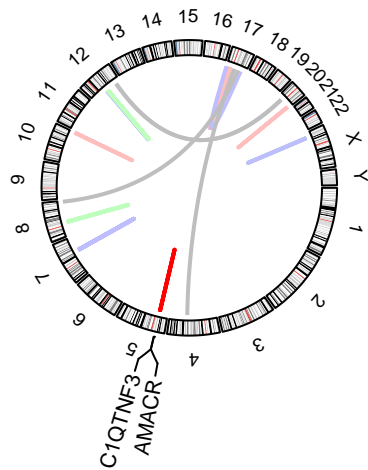
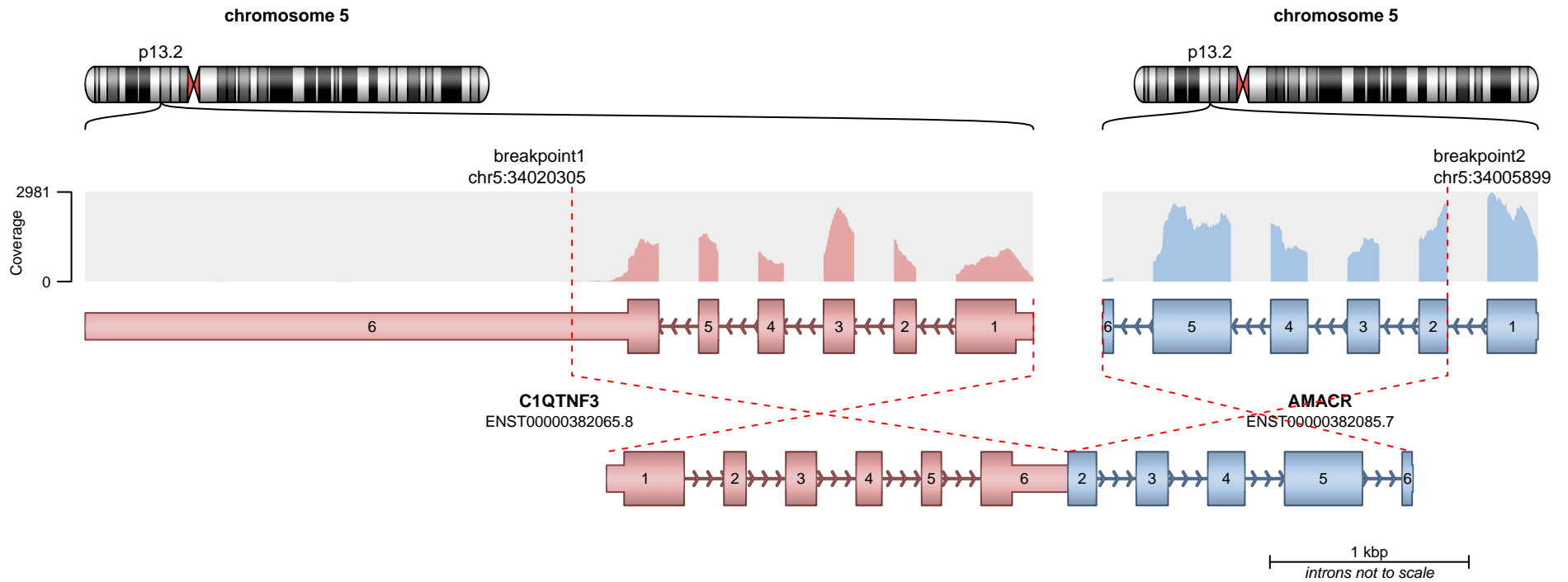
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



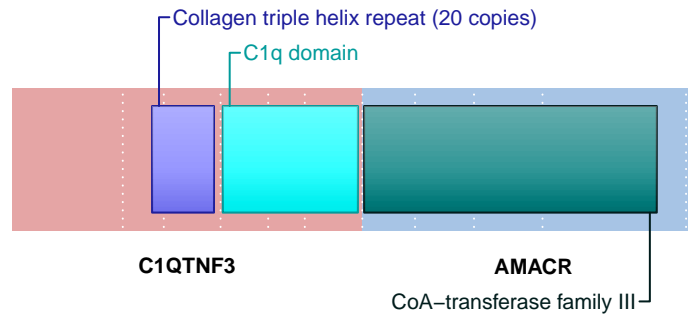
**SUPPORTING READ COUNT**

Split reads = 99  
Discordant mates = 2

— translocation    — deletion  
— duplication    — inversion



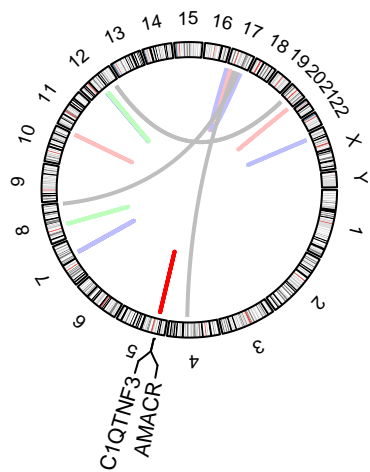
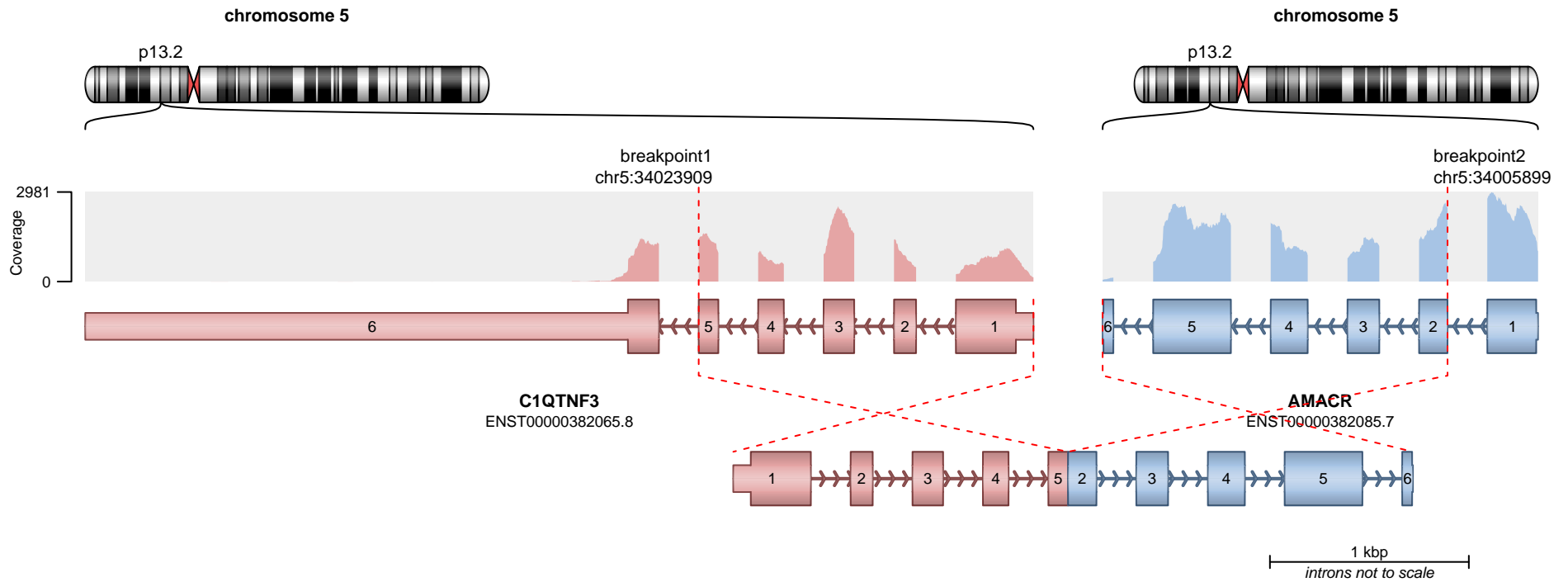
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



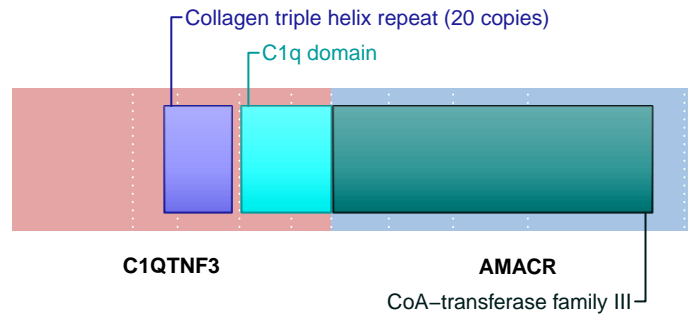
**SUPPORTING READ COUNT**

Split reads = 6  
Discordant mates = 2

— translocation    — deletion  
— duplication    — inversion



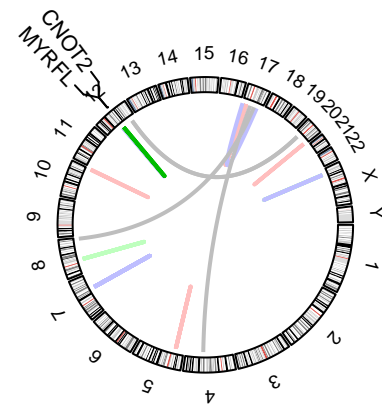
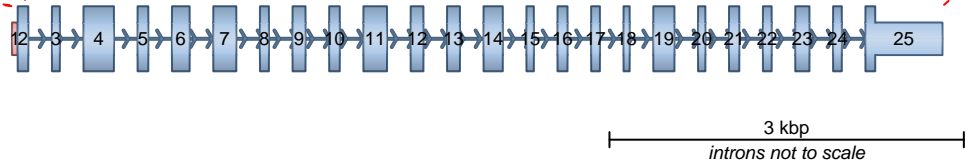
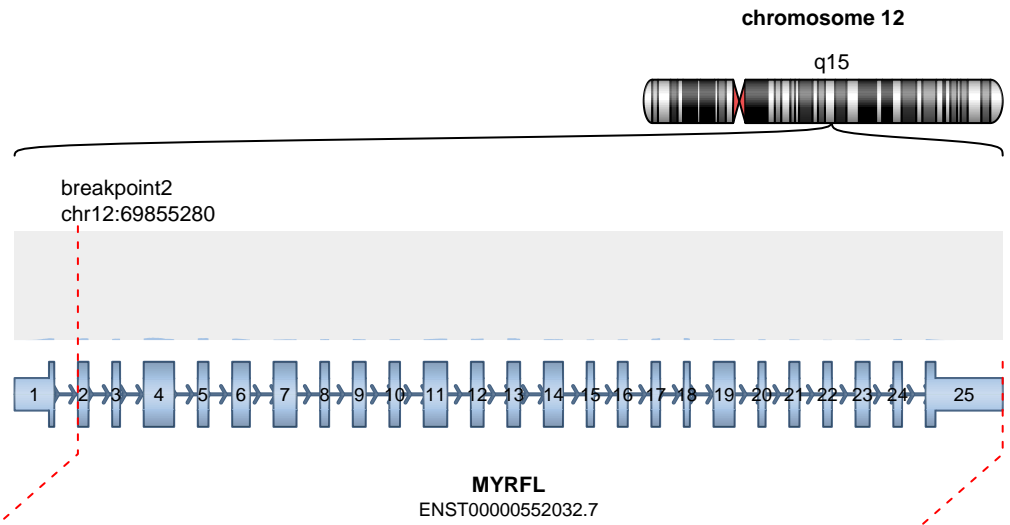
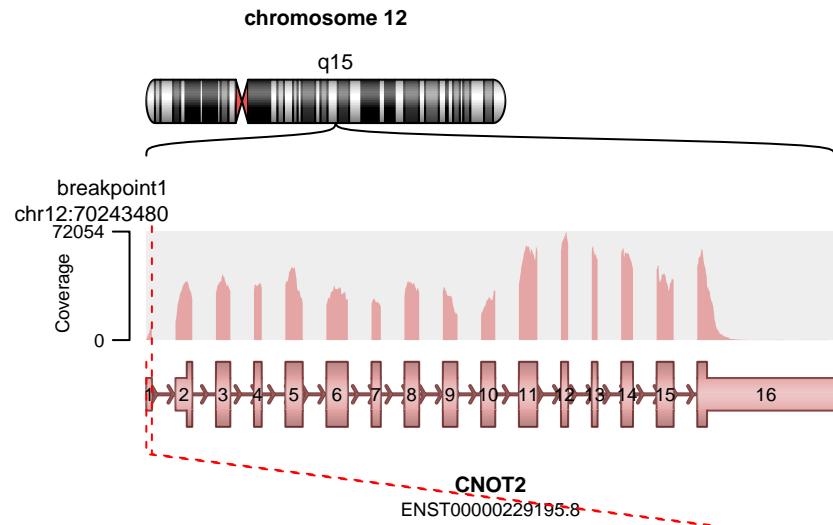
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

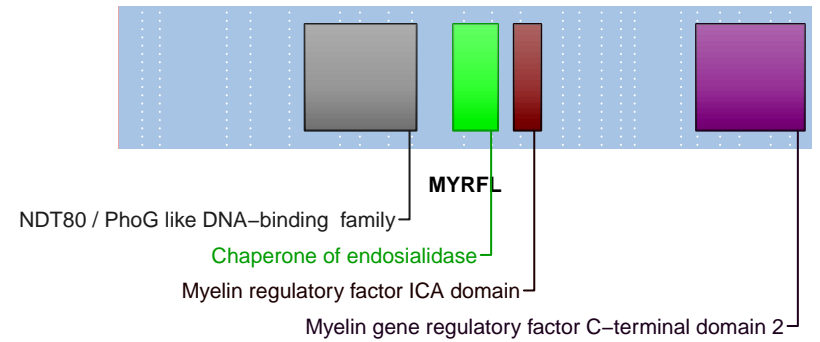
Split reads = 2  
Discordant mates = 1

— translocation    — deletion  
— duplication    — inversion



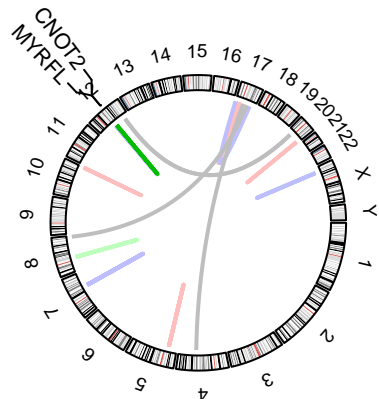
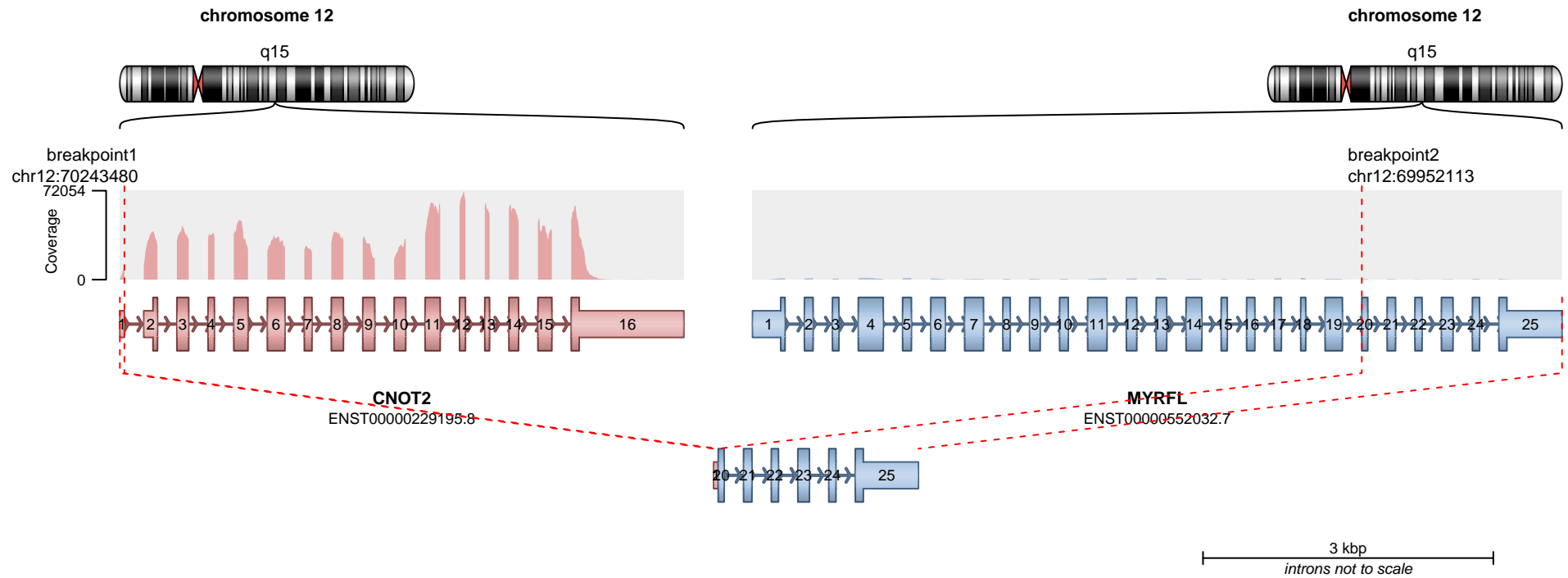
— translocation    — deletion  
— duplication    — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 76  
Discordant mates = 0



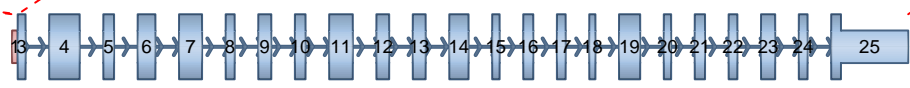
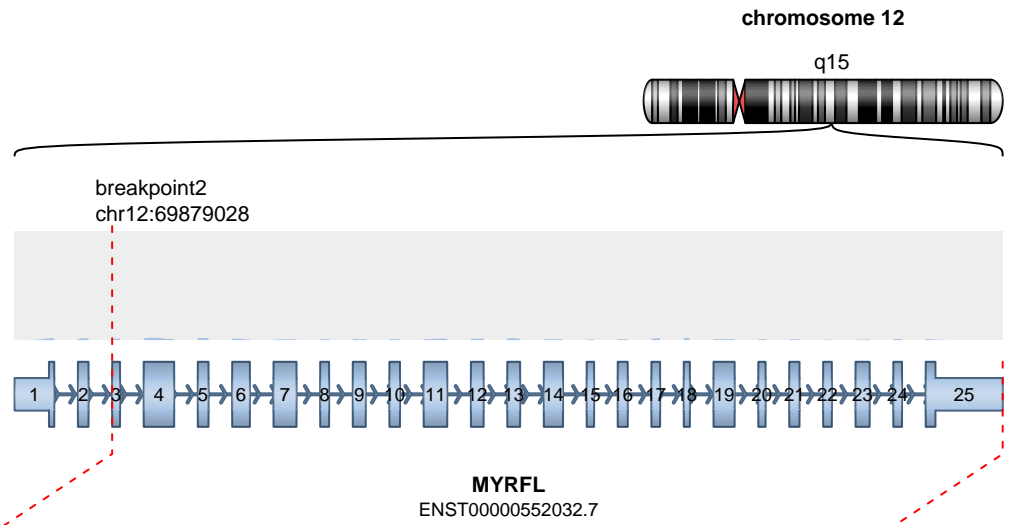
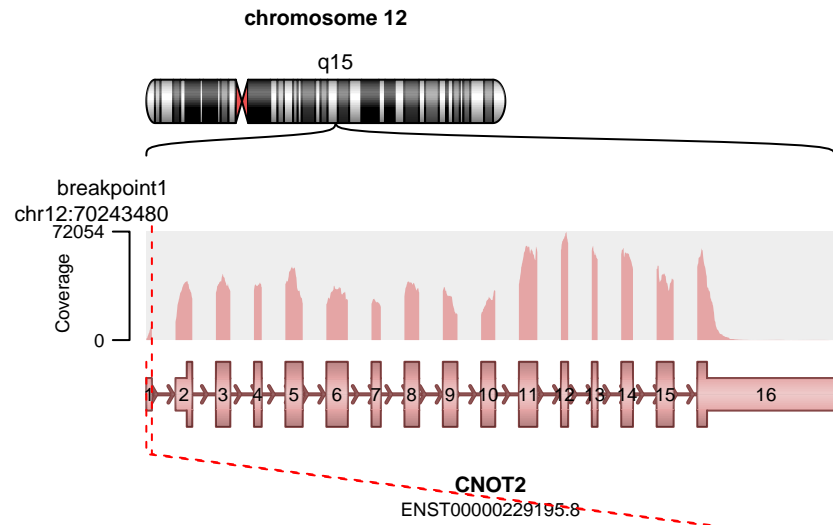
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear

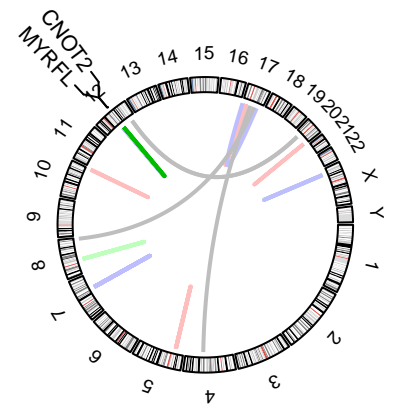


**SUPPORTING READ COUNT**

Split reads = 7  
Discordant mates = 0

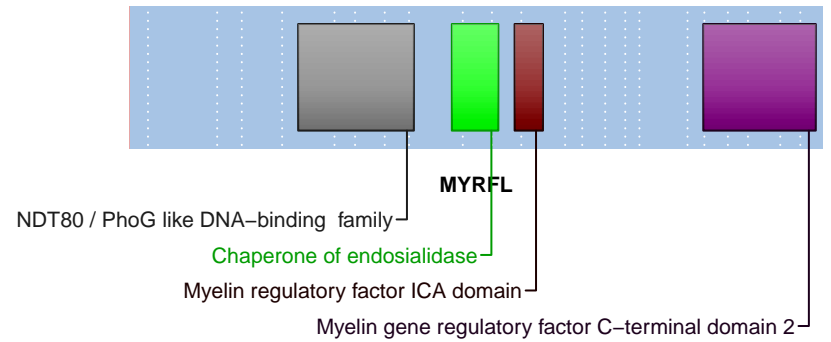


3 kbp  
*introns not to scale*



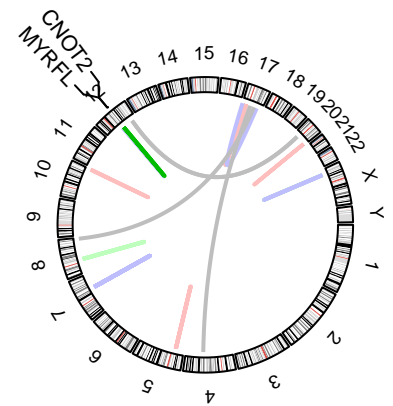
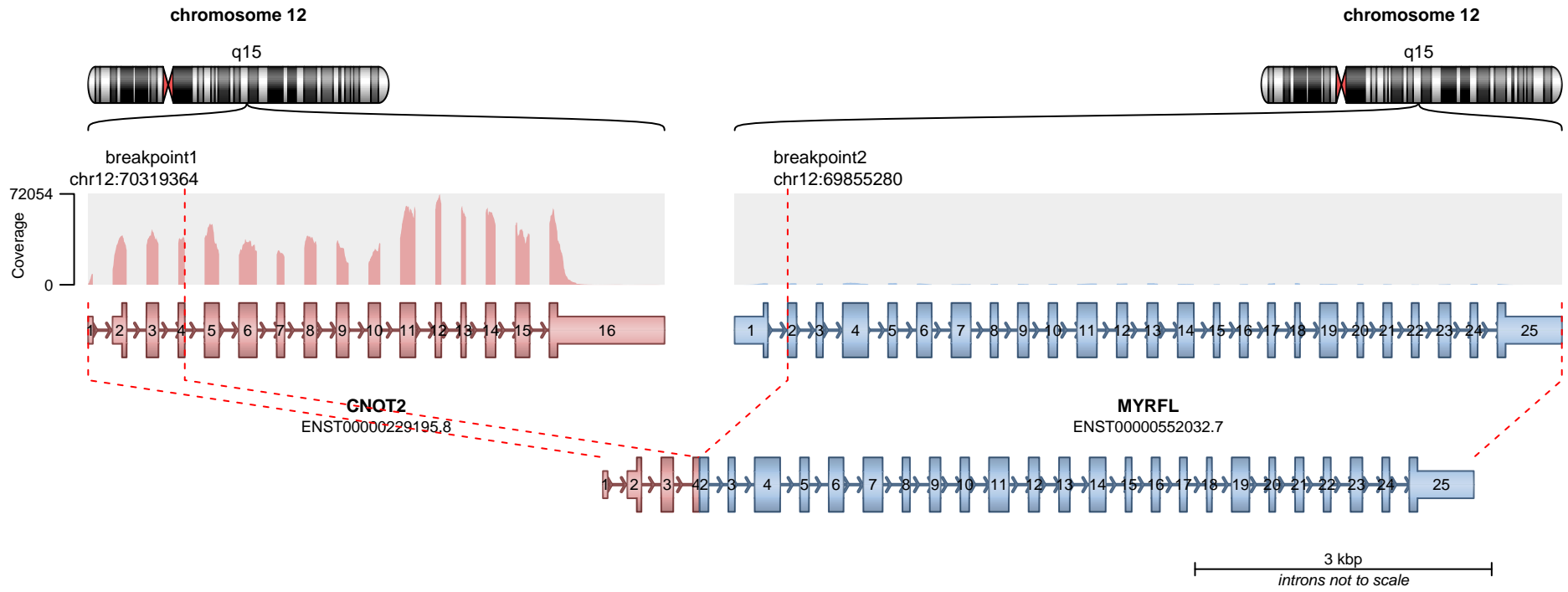
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear

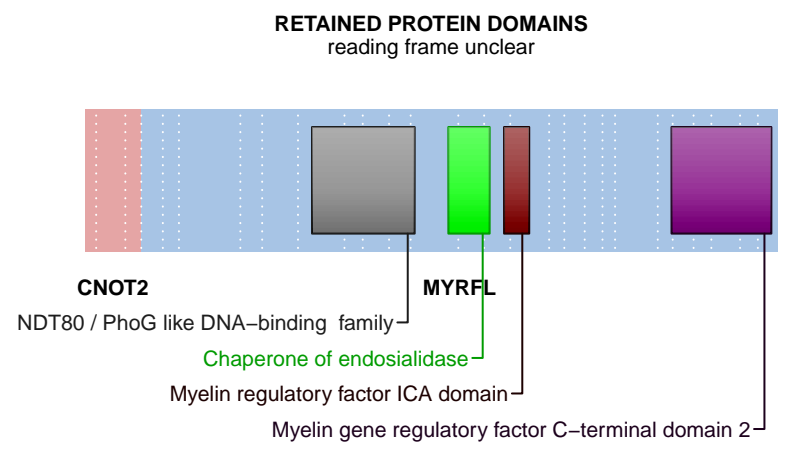


**SUPPORTING READ COUNT**

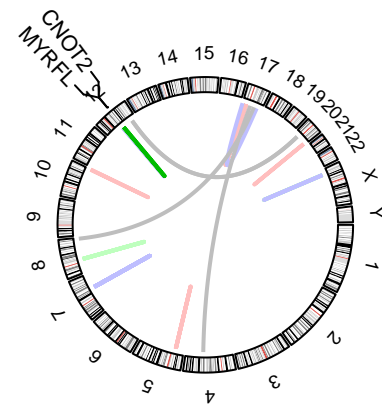
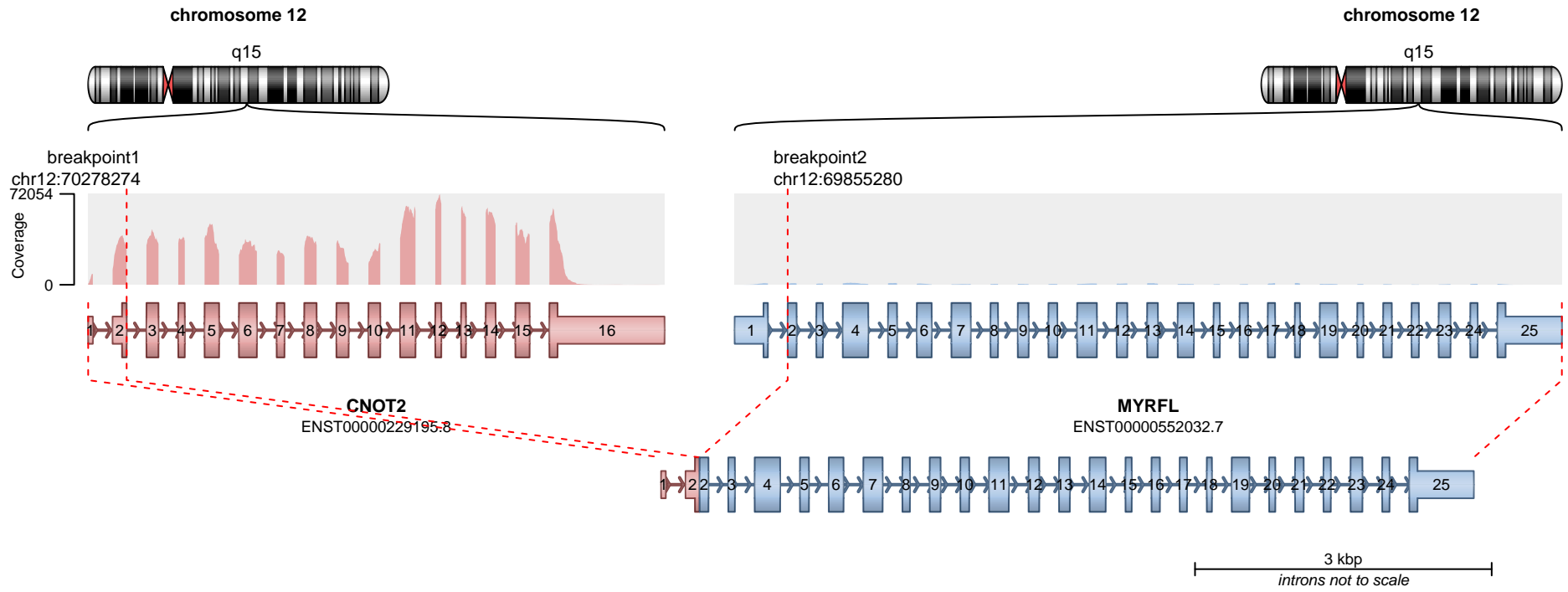
Split reads = 2  
Discordant mates = 0



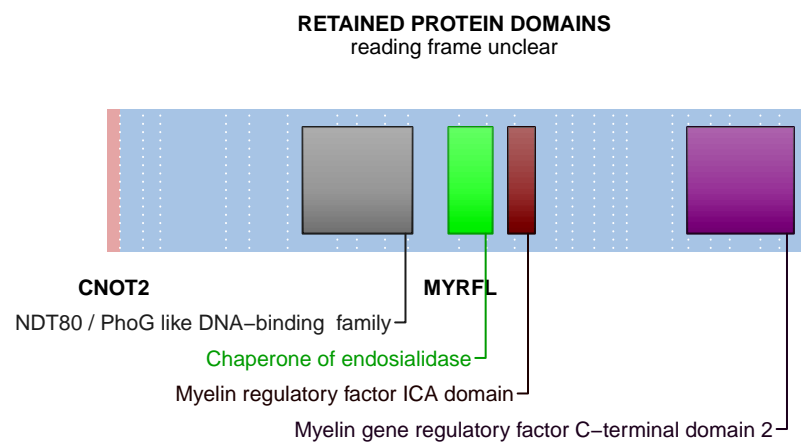
— translocation — deletion  
— duplication — inversion



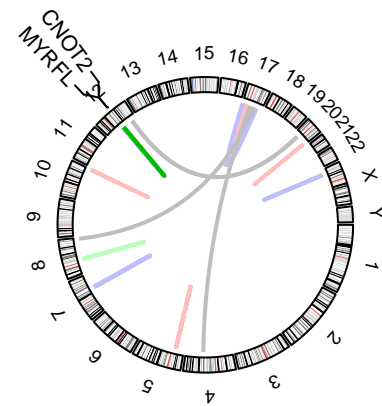
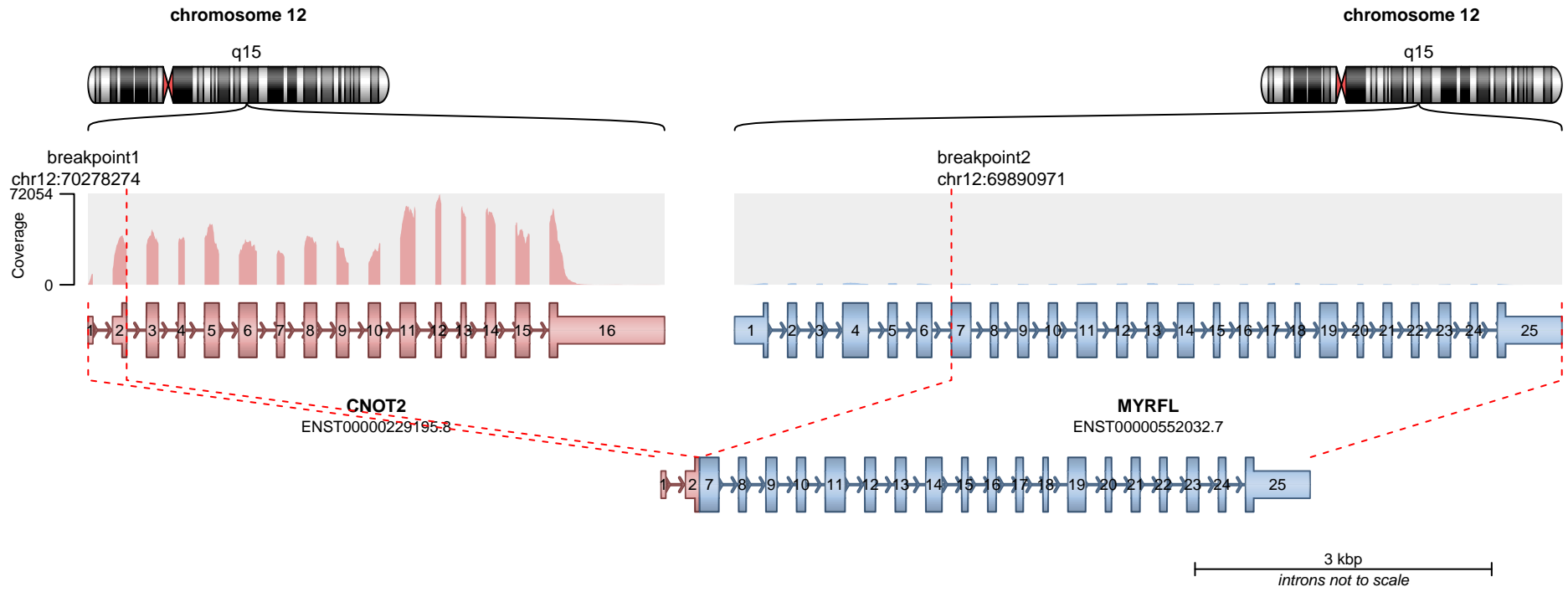
**SUPPORTING READ COUNT**  
Split reads = 2  
Discordant mates = 0



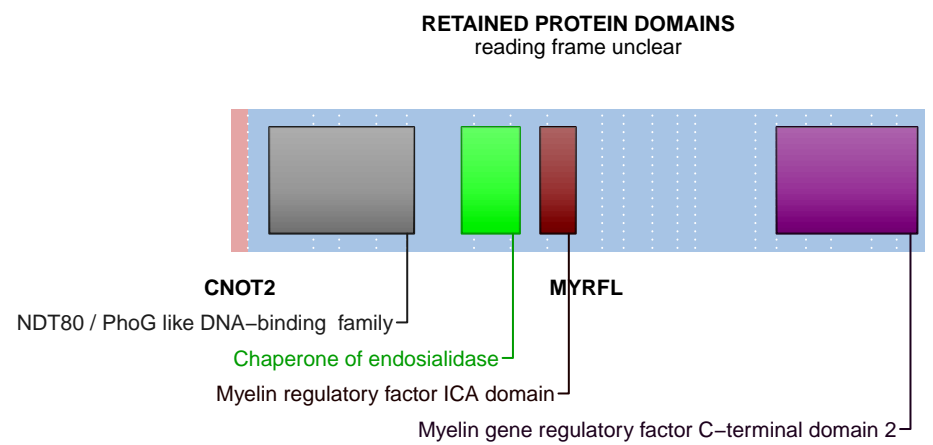
— translocation    — deletion  
— duplication    — inversion



**SUPPORTING READ COUNT**  
Split reads = 2  
Discordant mates = 0

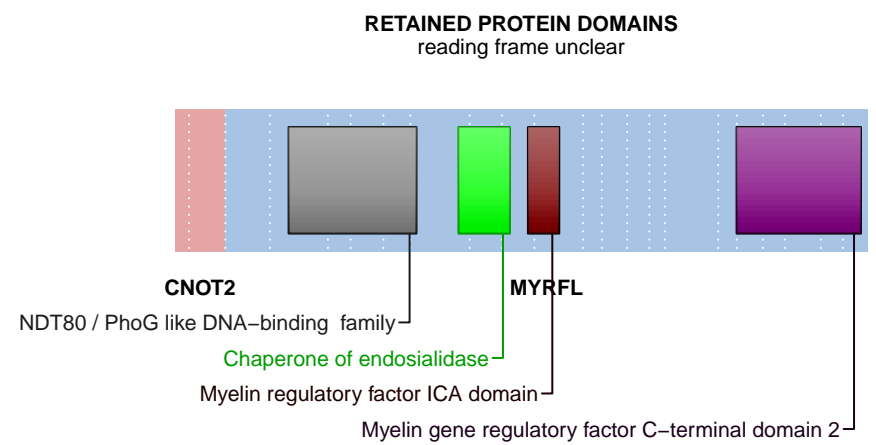
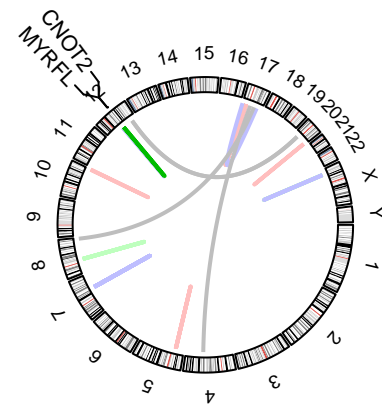
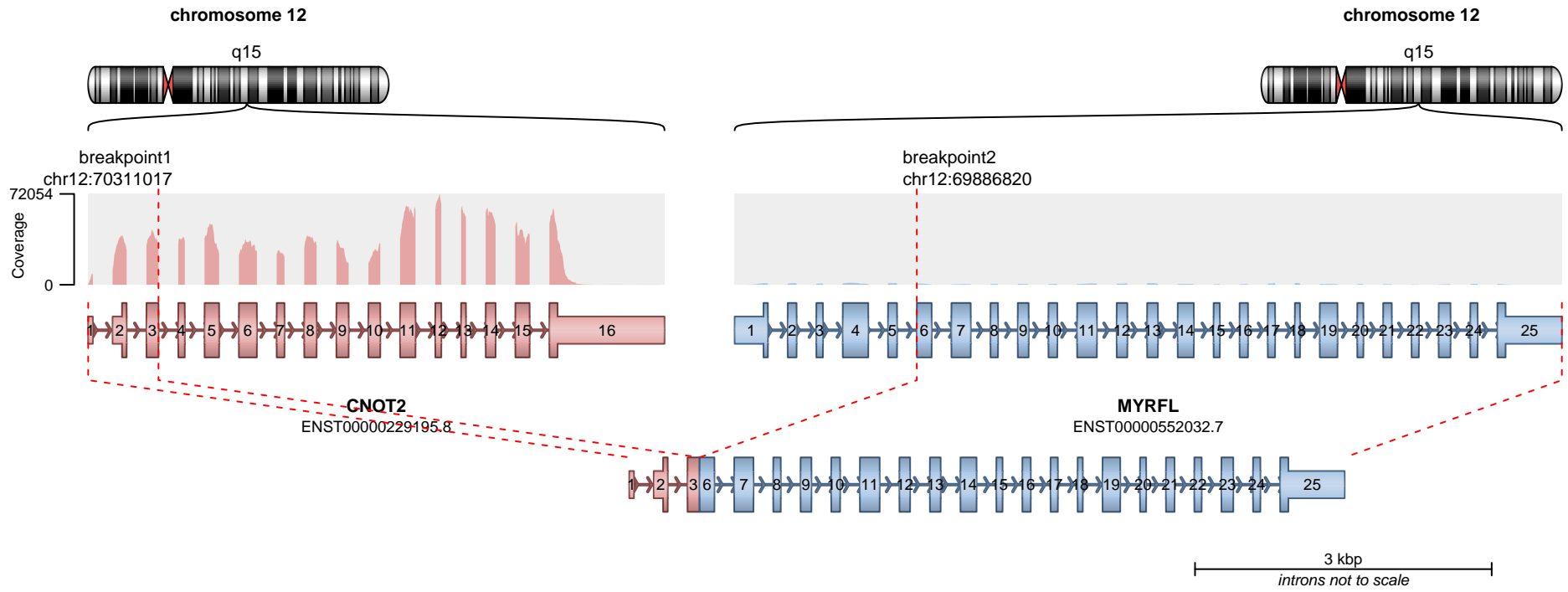


— translocation — deletion  
— duplication — inversion



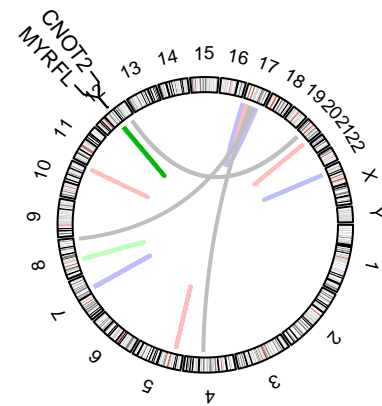
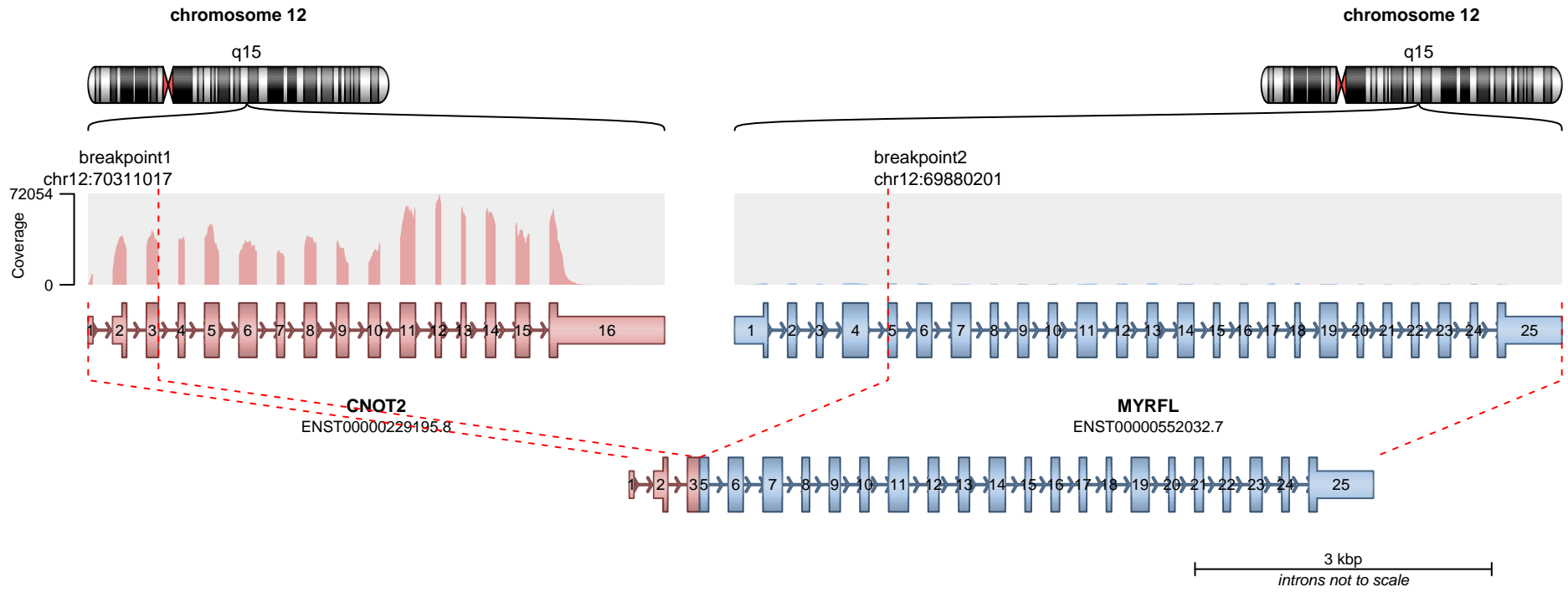
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

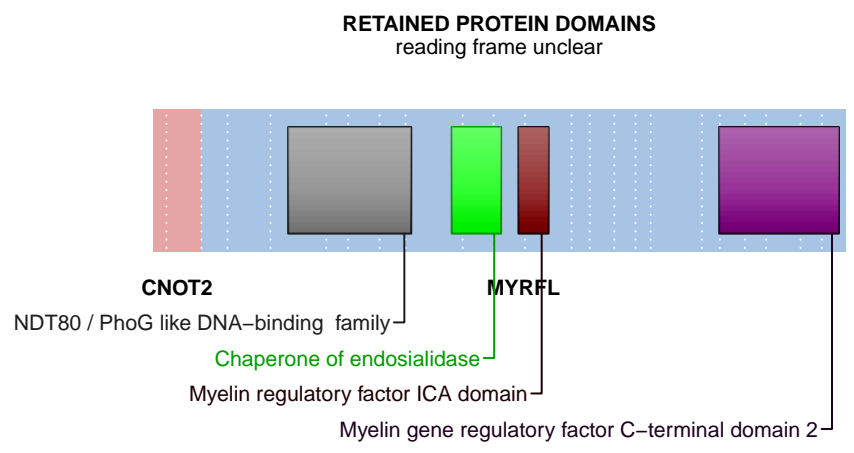


**SUPPORTING READ COUNT**

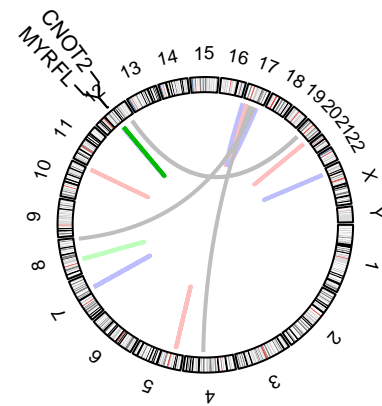
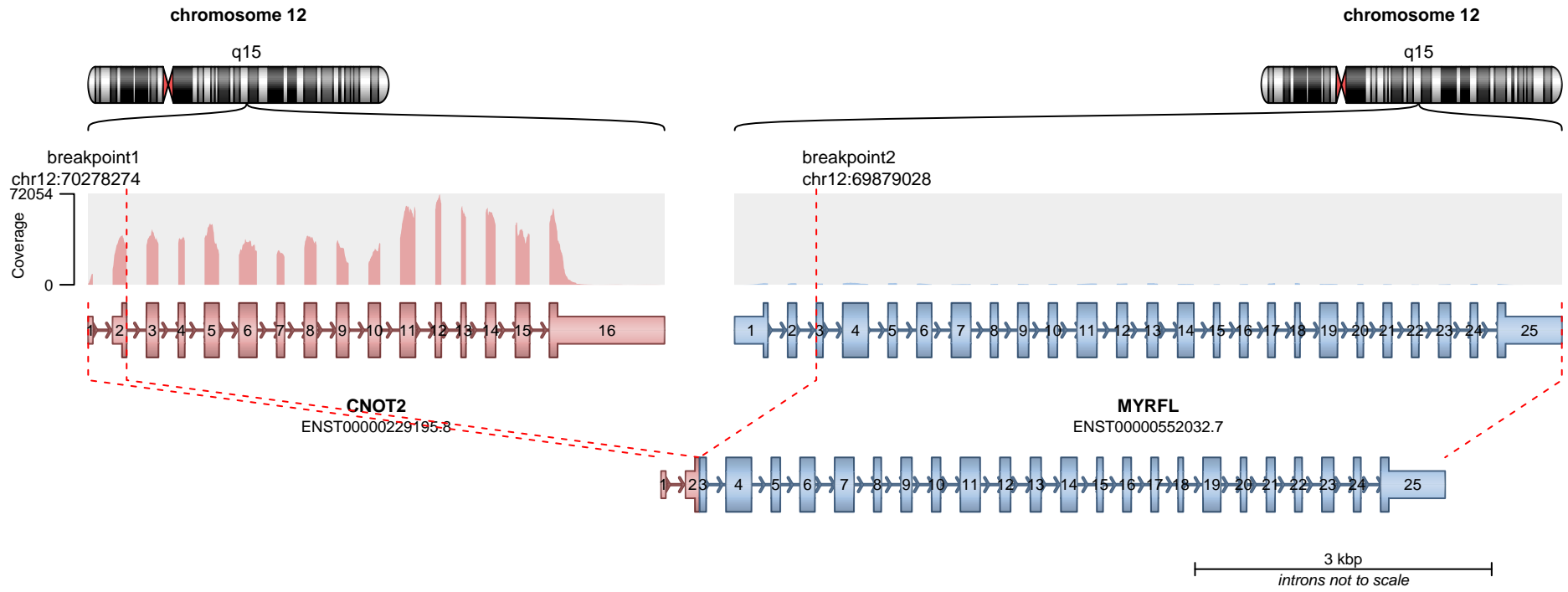
Split reads = 1  
Discordant mates = 0



— translocation — deletion  
— duplication — inversion

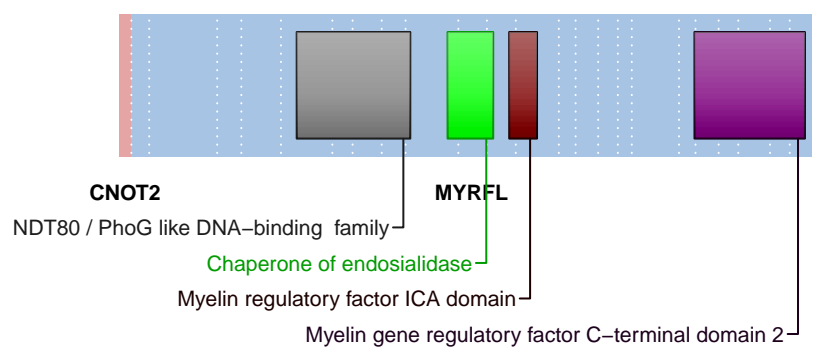


**SUPPORTING READ COUNT**  
Split reads = 1  
Discordant mates = 0



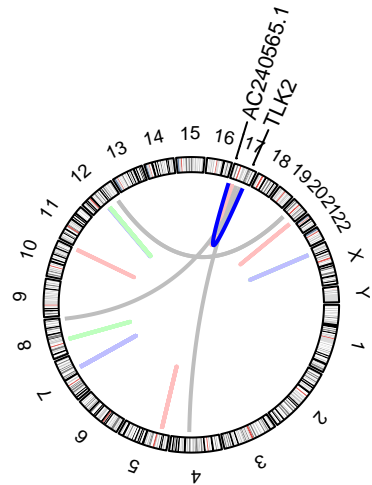
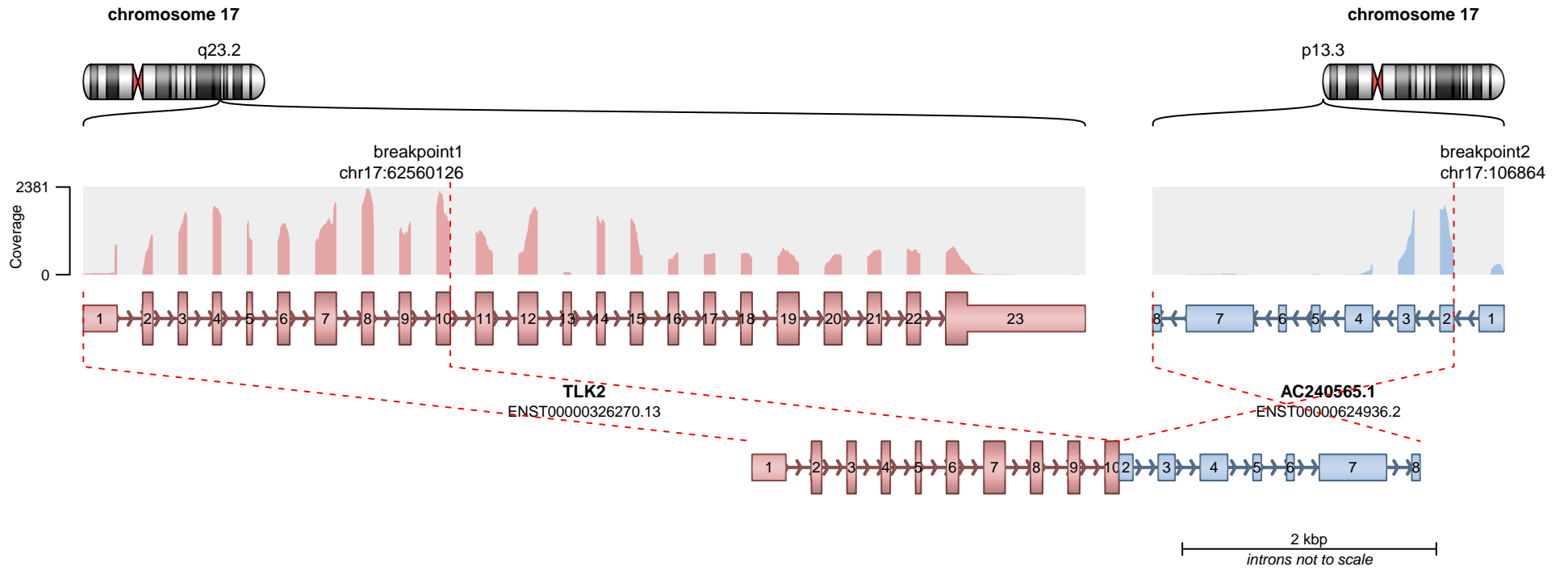
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

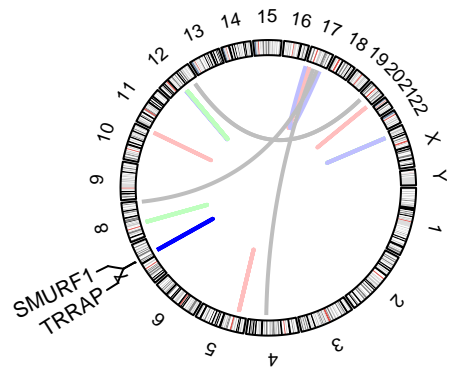
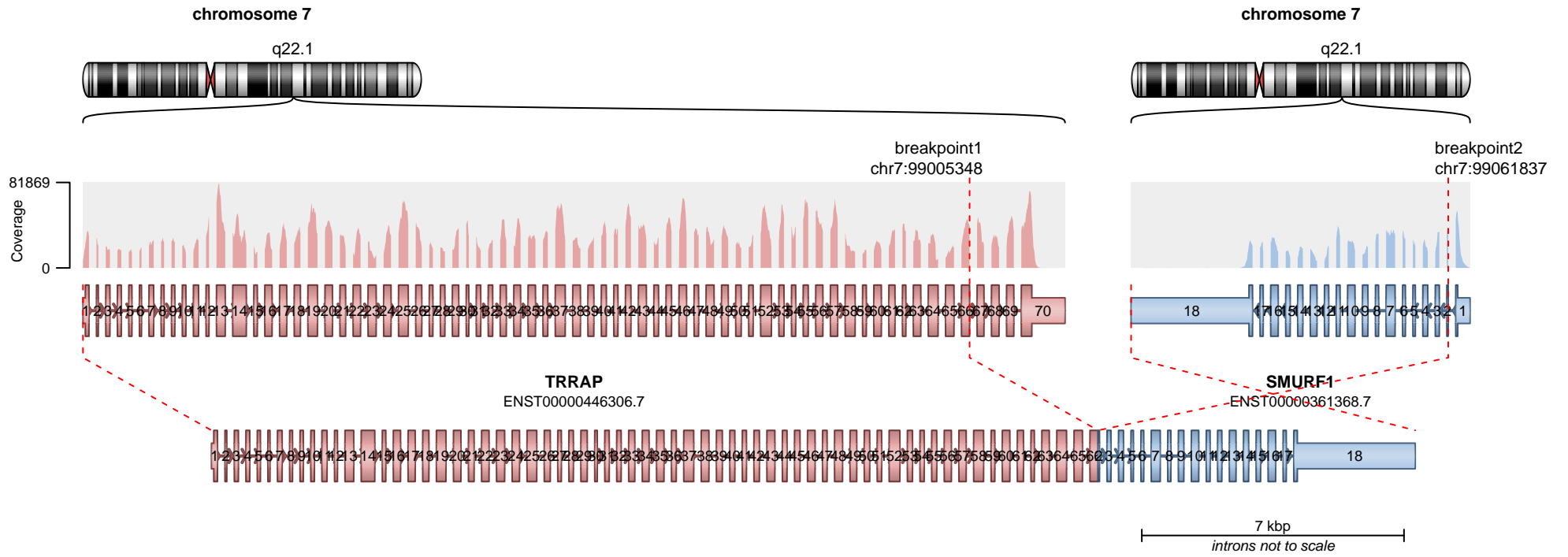


— translocation — deletion  
— duplication — inversion

No protein domains retained in fusion.

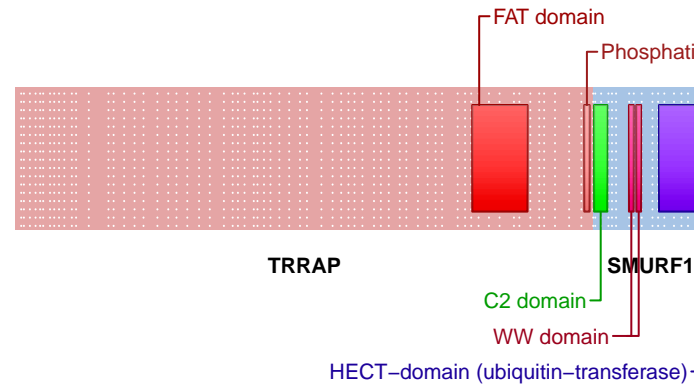
**SUPPORTING READ COUNT**

Split reads = 74  
Discordant mates = 0



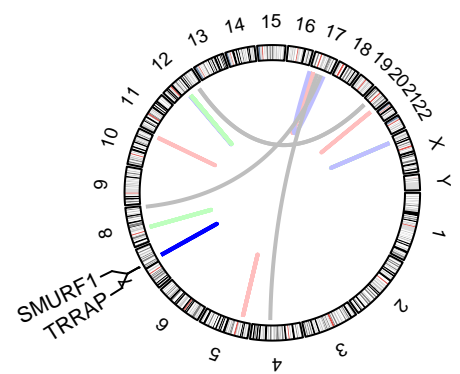
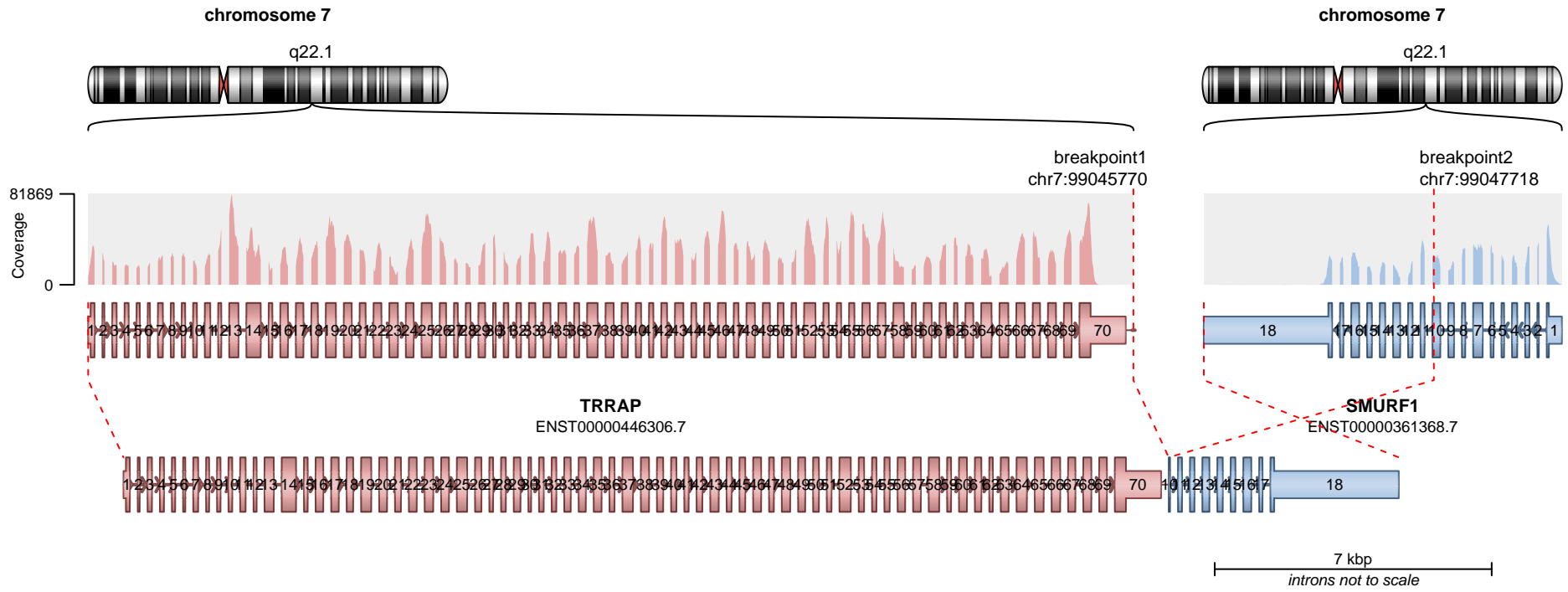
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear

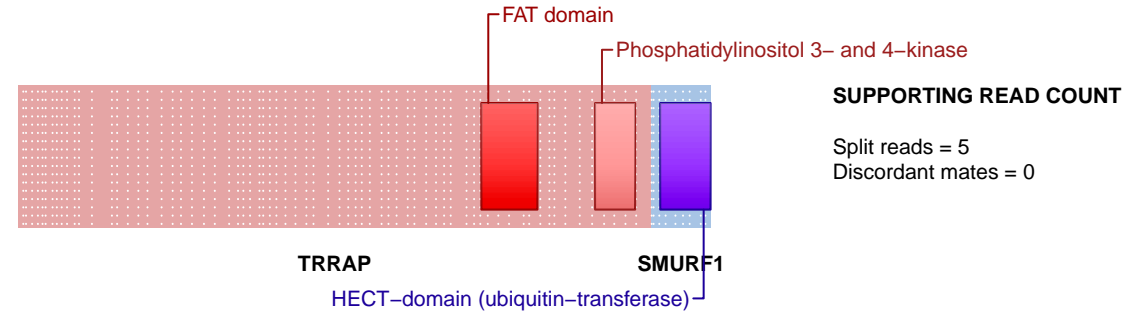


**SUPPORTING READ COUNT**

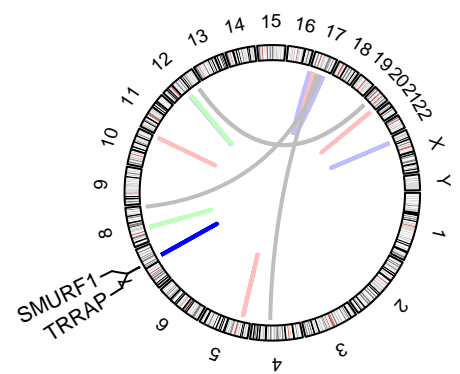
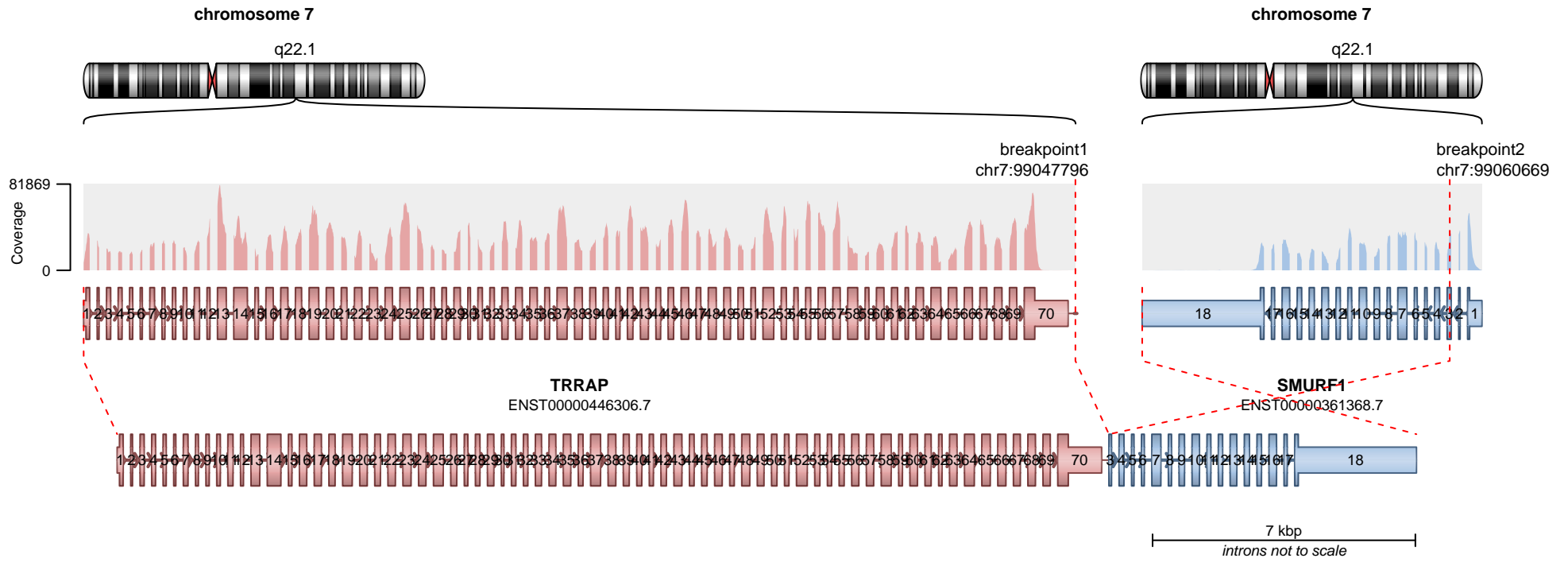
Split reads = 63  
Discordant mates = 0



**RETAINED PROTEIN DOMAINS**  
reading frame unclear

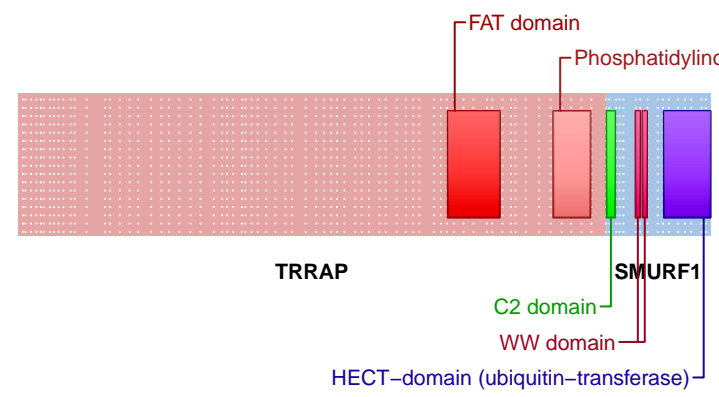


- translocation
- duplication
- deletion
- inversion



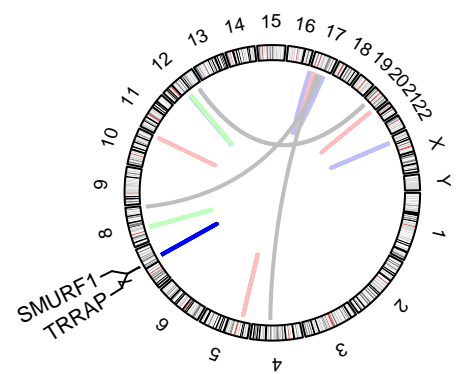
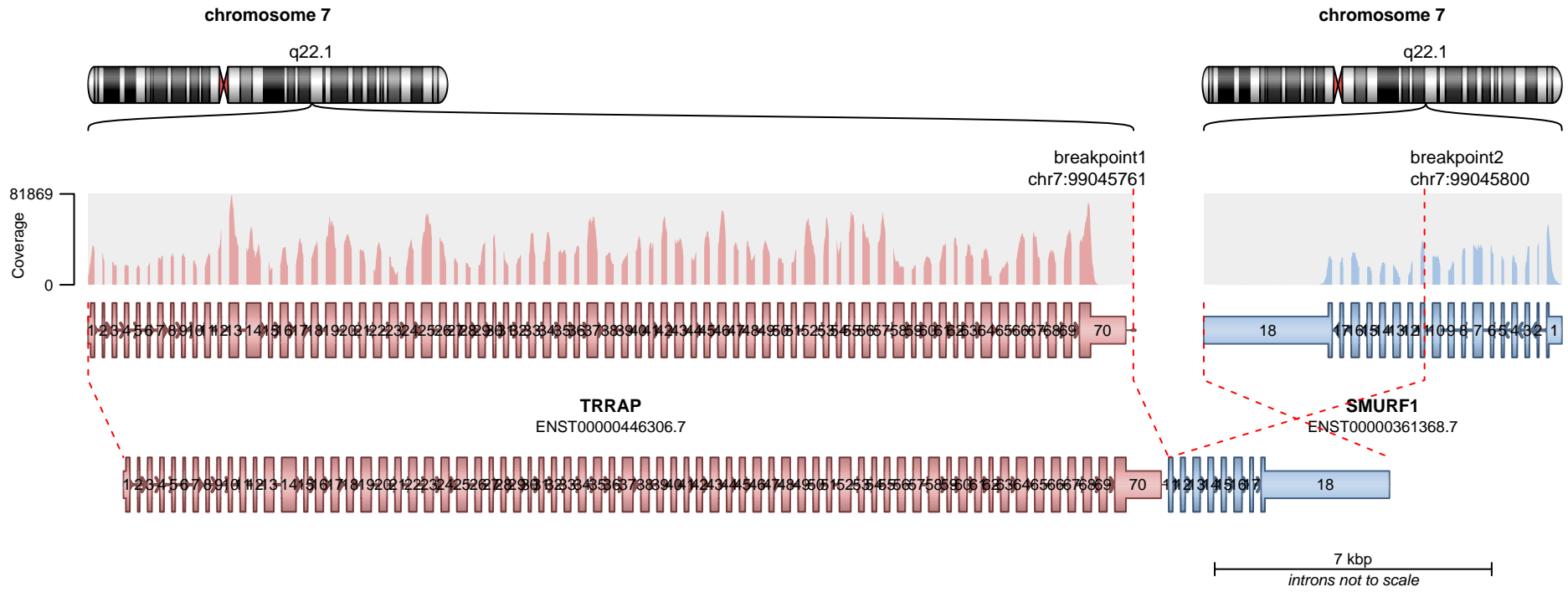
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear

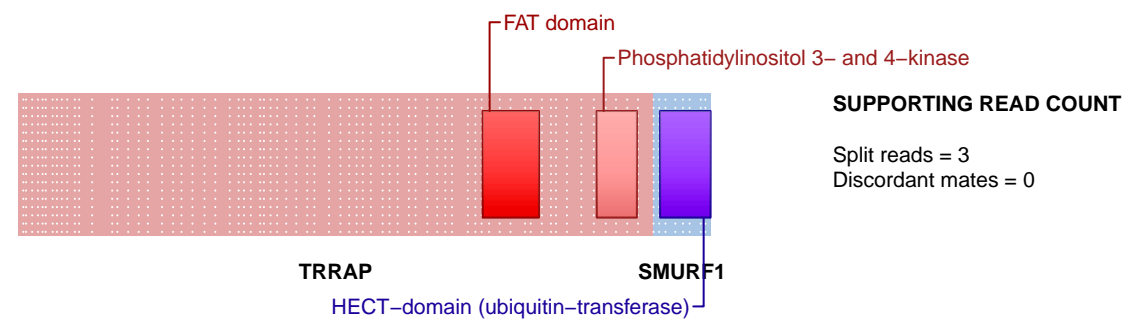


**SUPPORTING READ COUNT**

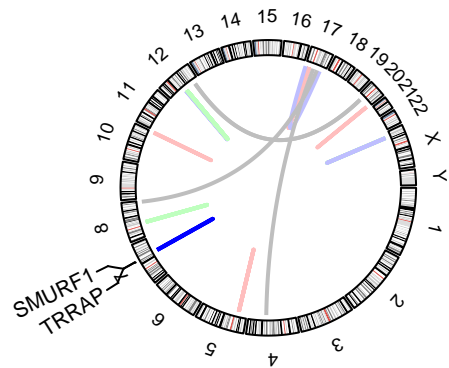
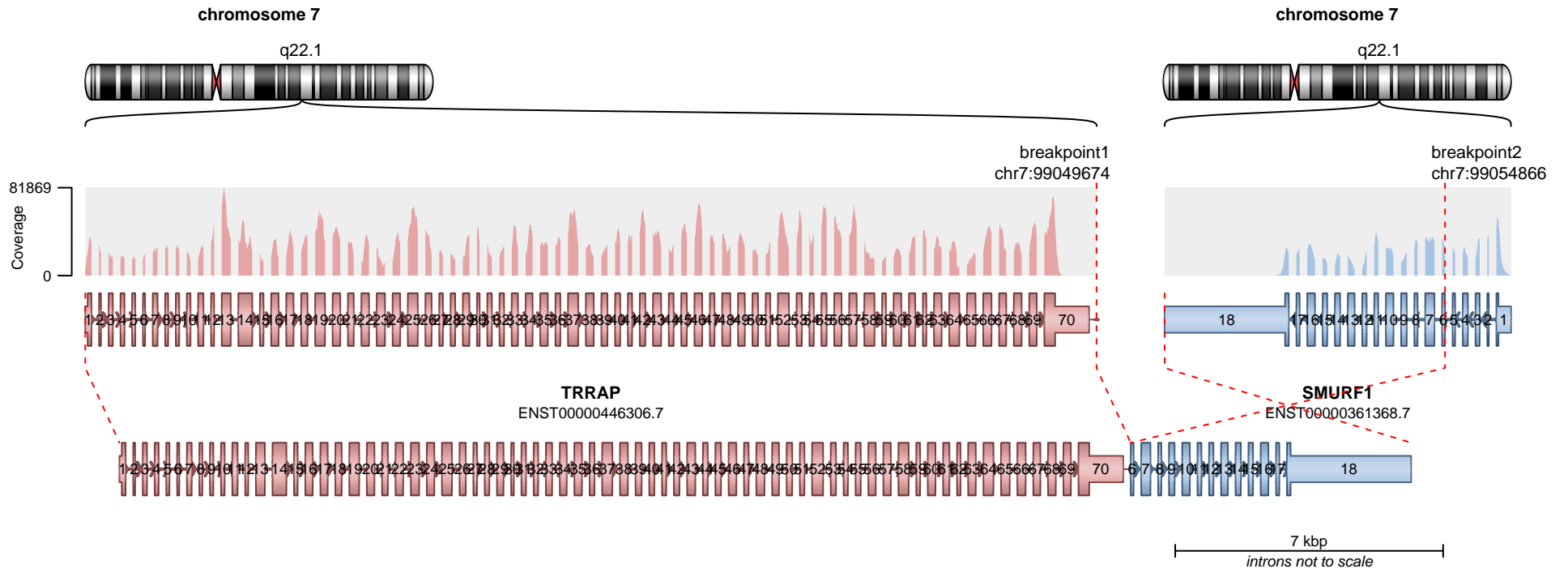
Split reads = 3  
Discordant mates = 0



**RETAINED PROTEIN DOMAINS**  
reading frame unclear

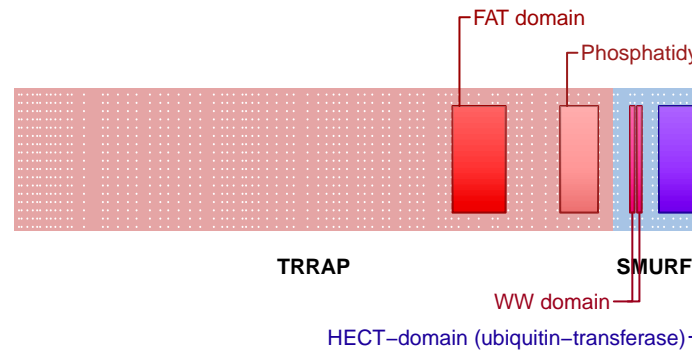


- translocation
- duplication
- deletion
- inversion



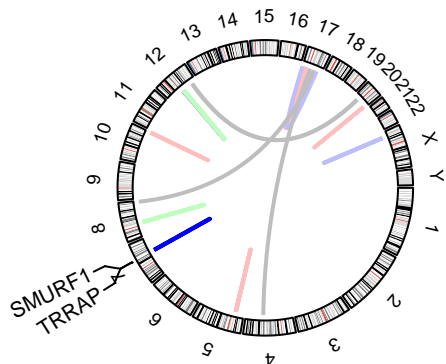
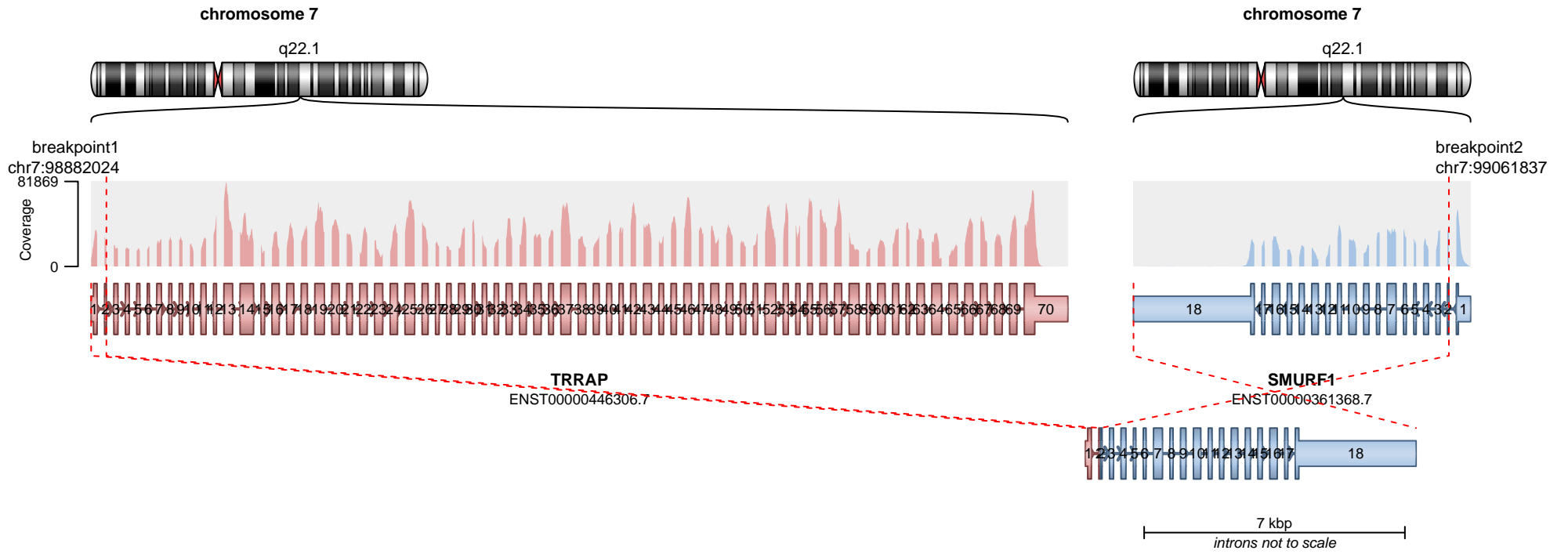
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear

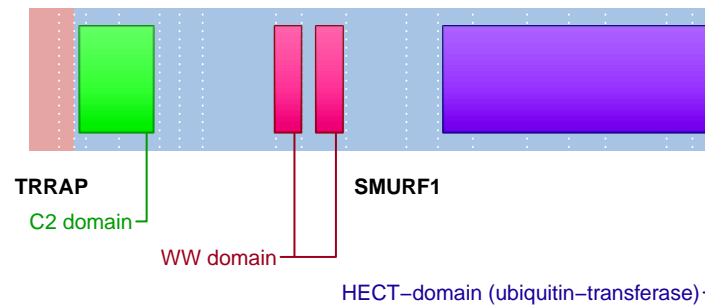


**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 0



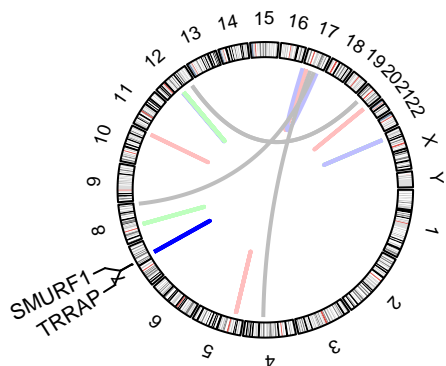
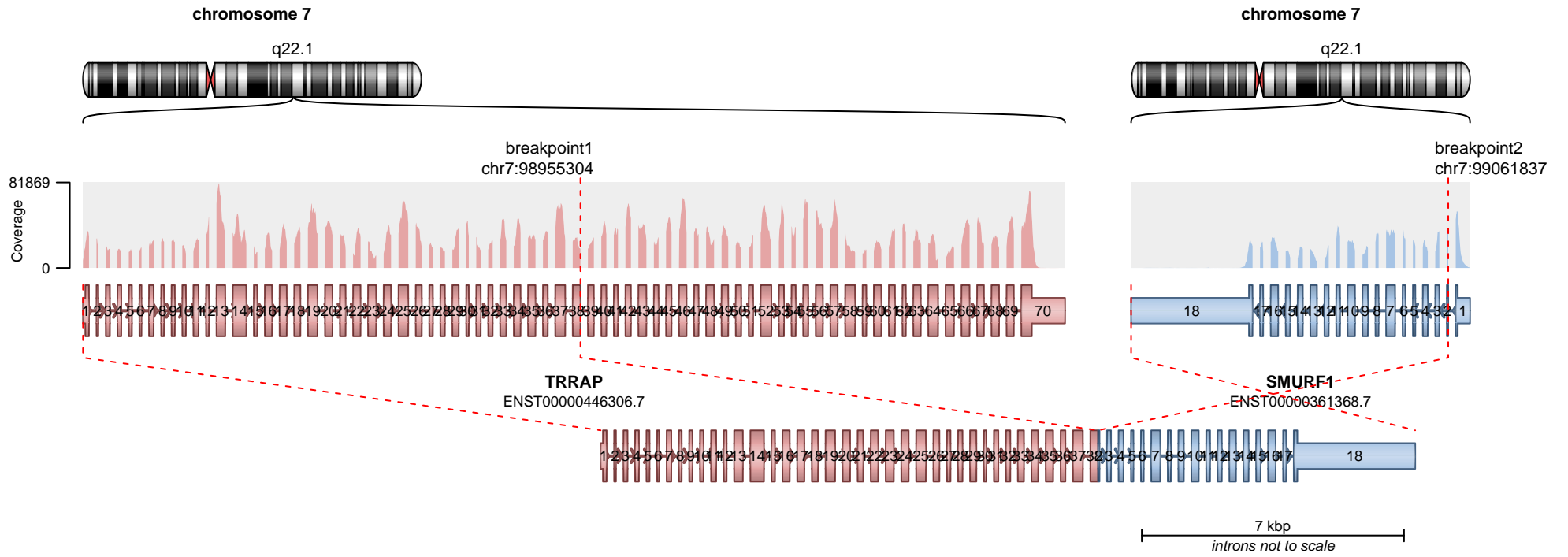
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

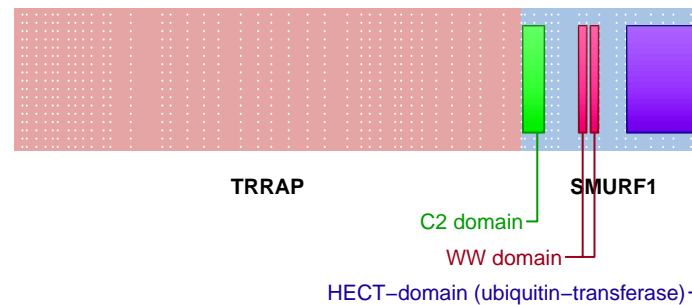
Split reads = 1  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



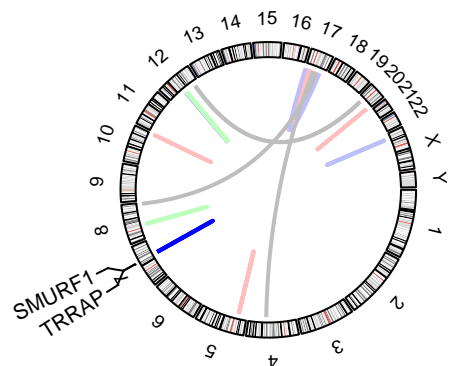
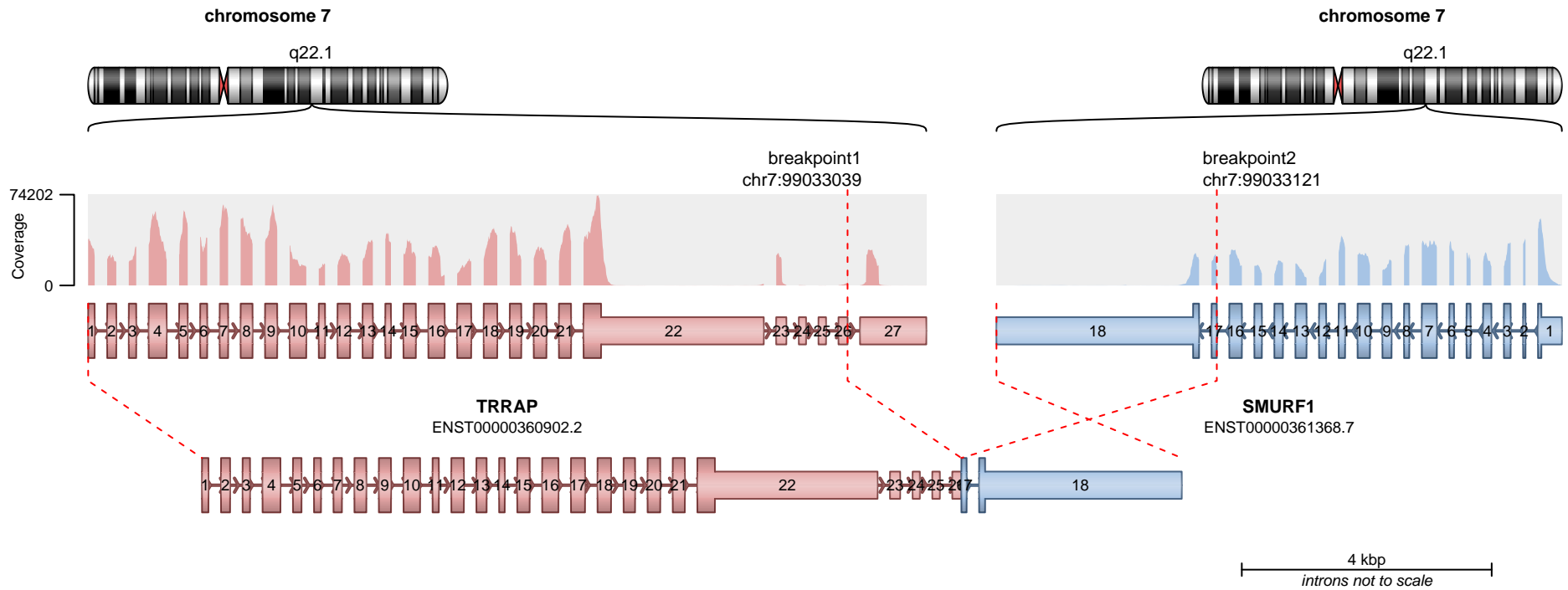
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear

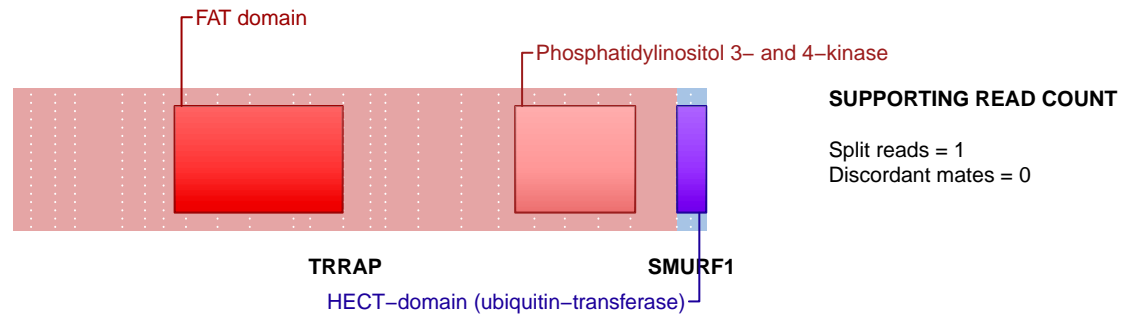


**SUPPORTING READ COUNT**

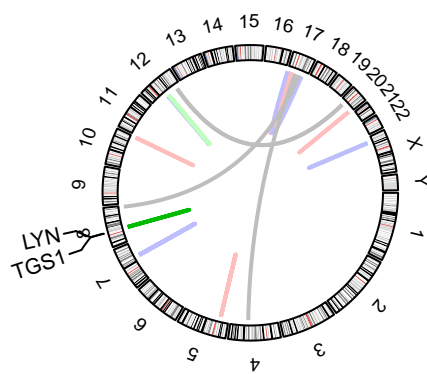
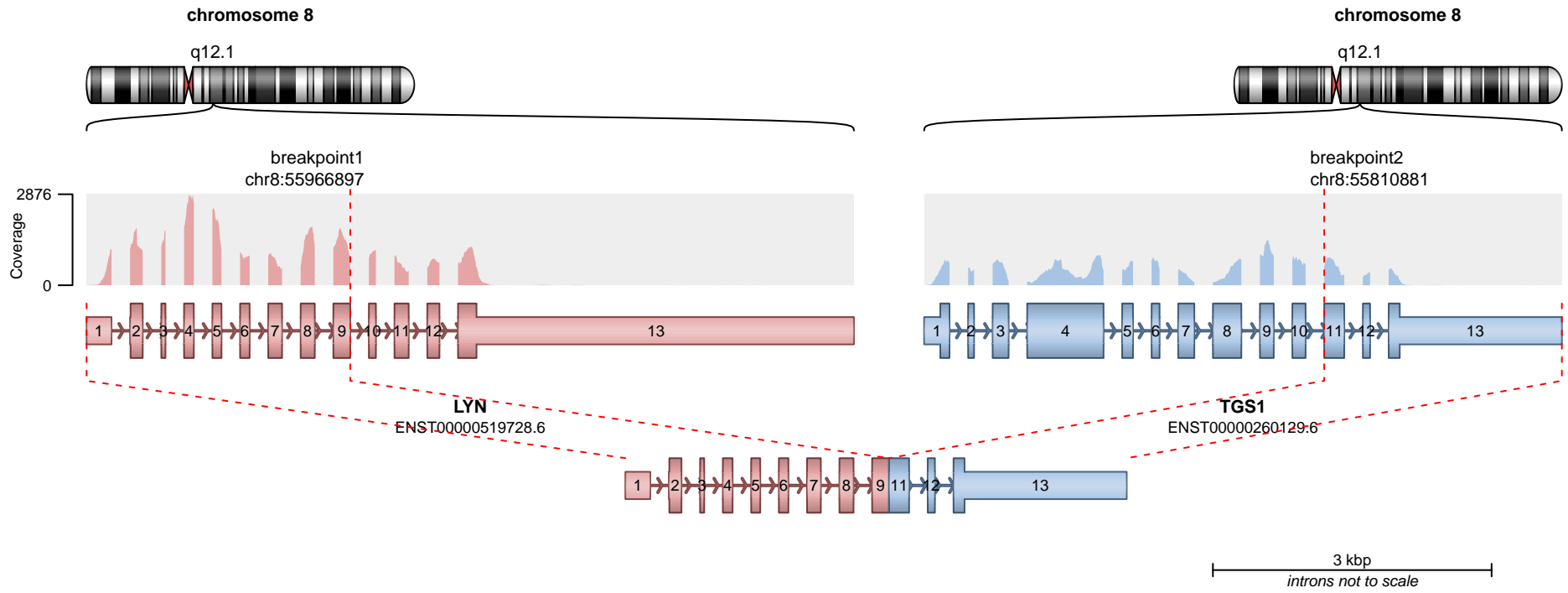
Split reads = 1  
Discordant mates = 0



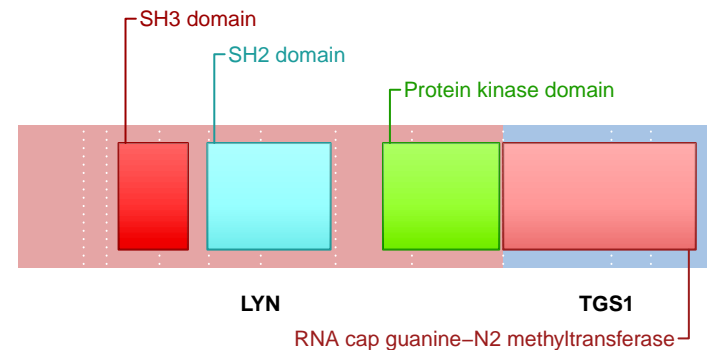
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



- translocation
- duplication
- deletion
- inversion



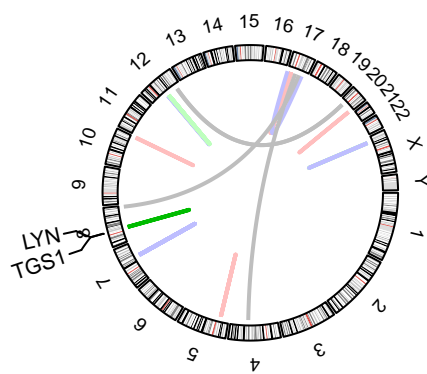
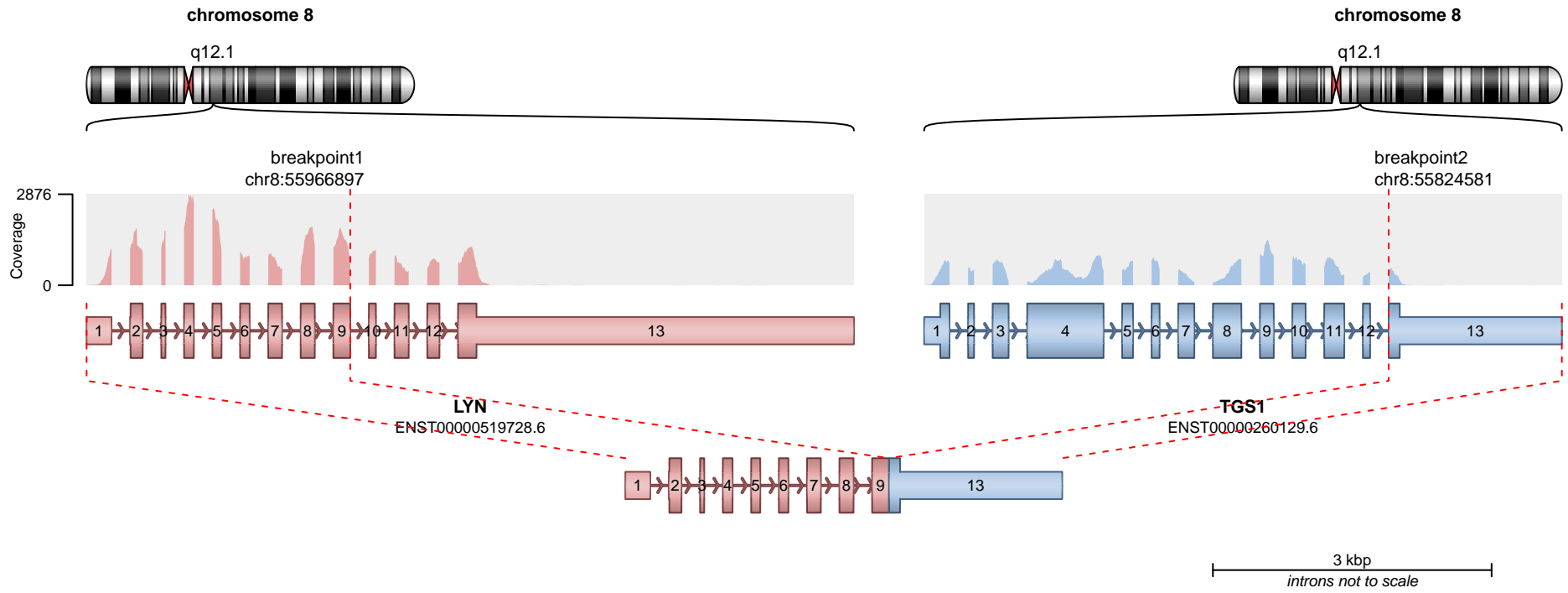
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



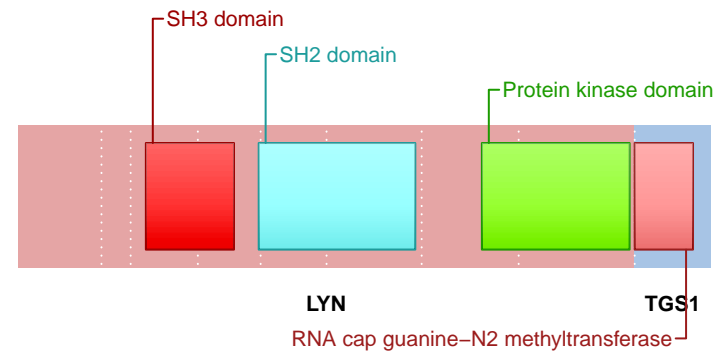
**SUPPORTING READ COUNT**

Split reads = 50  
Discordant mates = 2

- translocation
- duplication
- deletion
- inversion



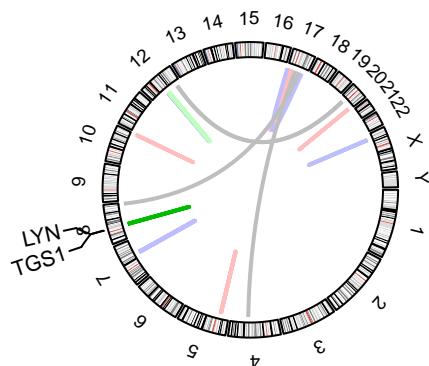
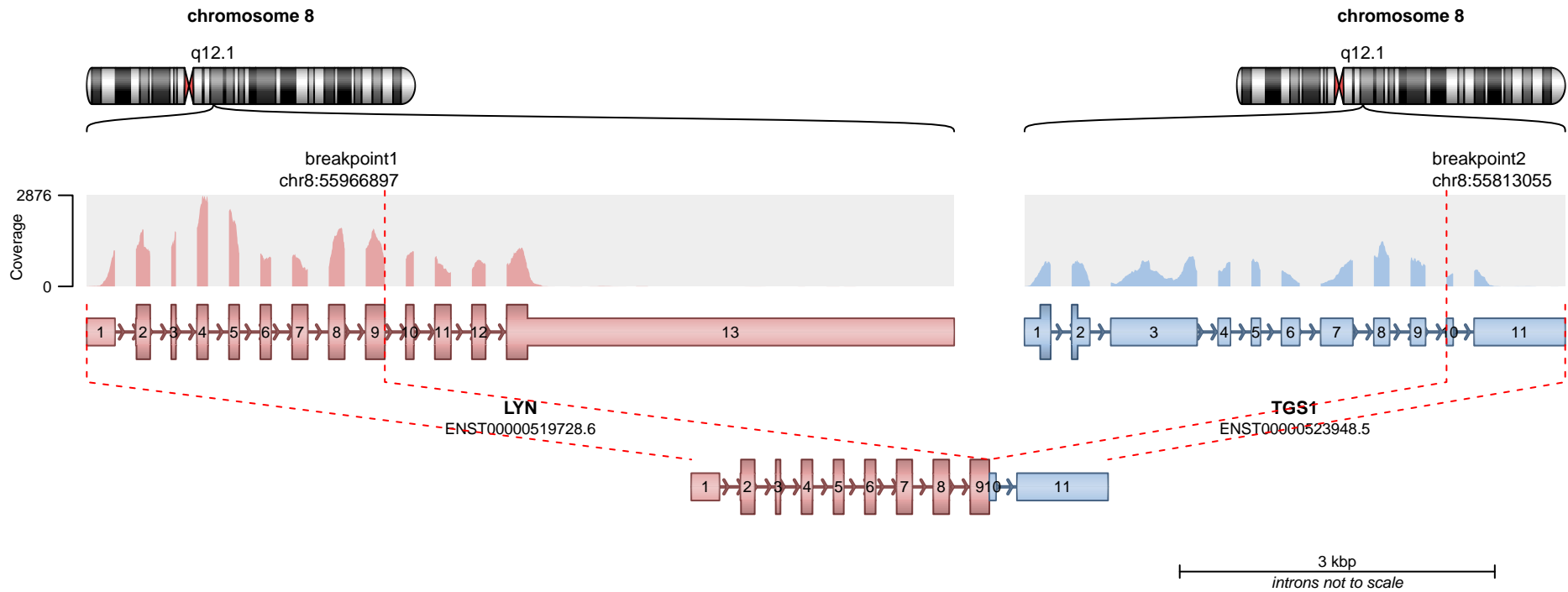
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



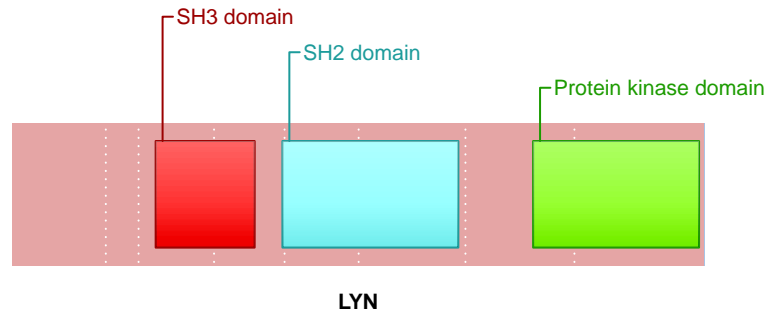
**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



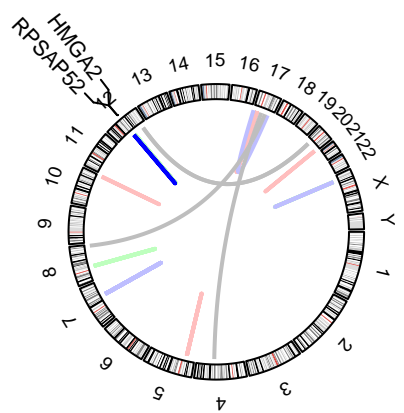
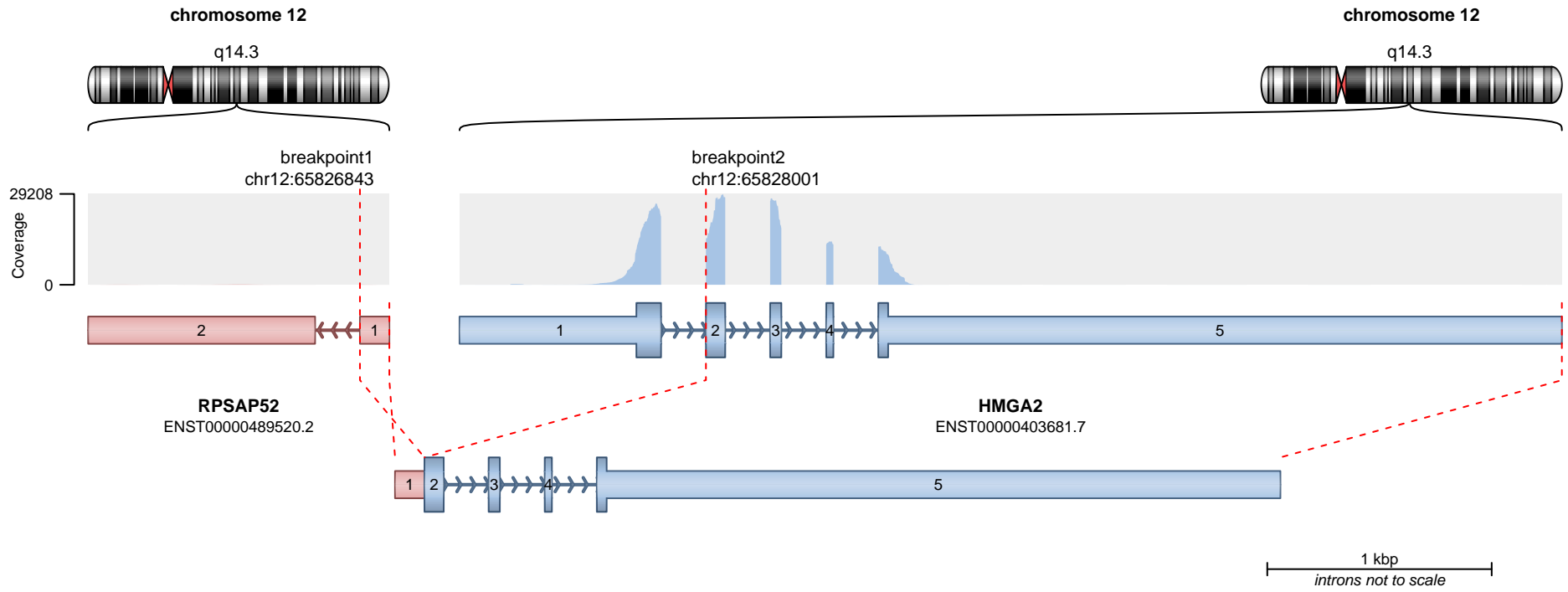
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



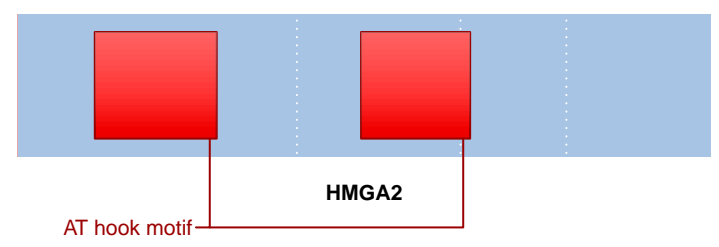
**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



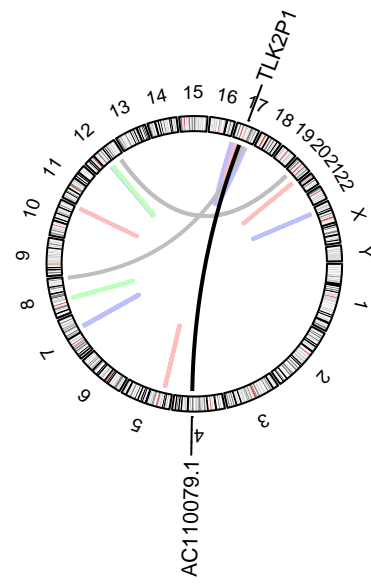
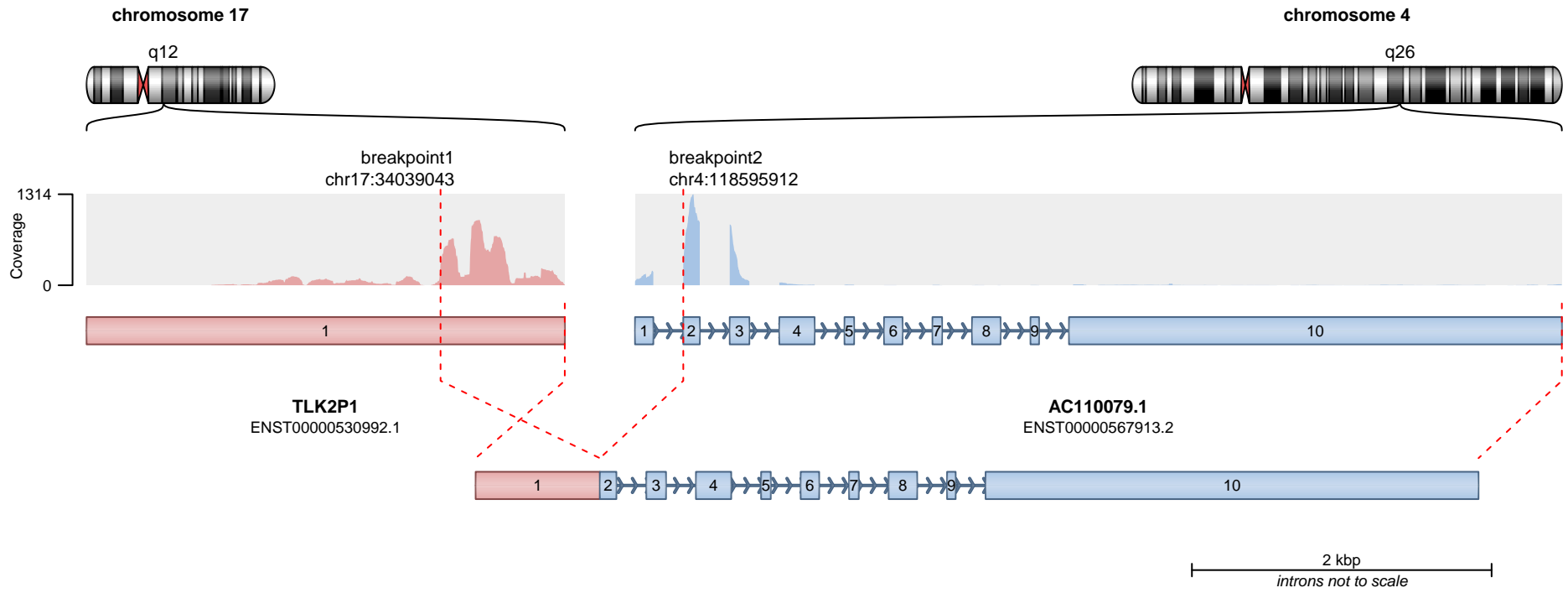
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 44  
Discordant mates = 0

— translocation    — deletion  
— duplication      — inversion

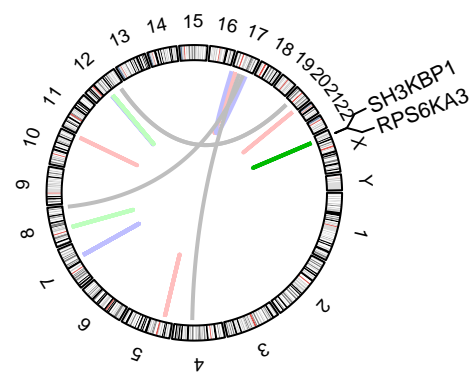
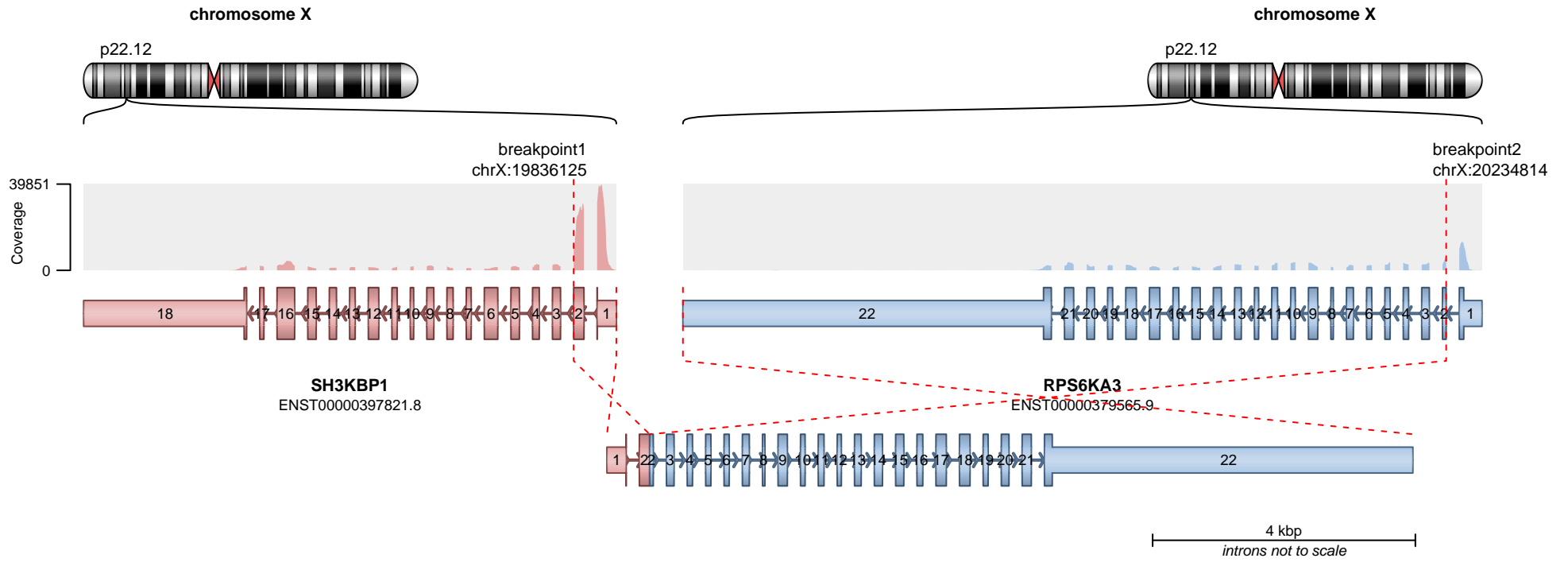


— translocation    — deletion  
 — duplication    — inversion

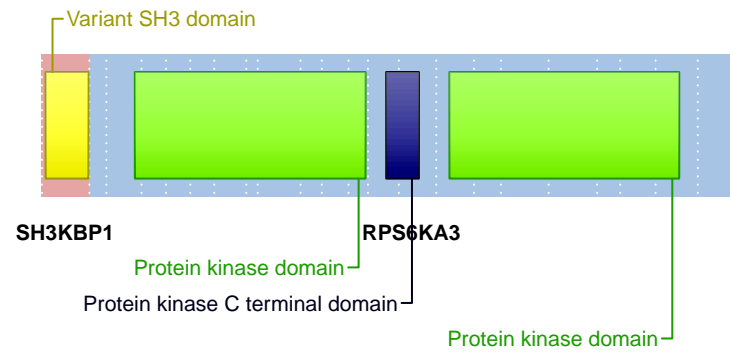
Genes are not protein-coding.

**SUPPORTING READ COUNT**

Split reads = 41  
 Discordant mates = 0



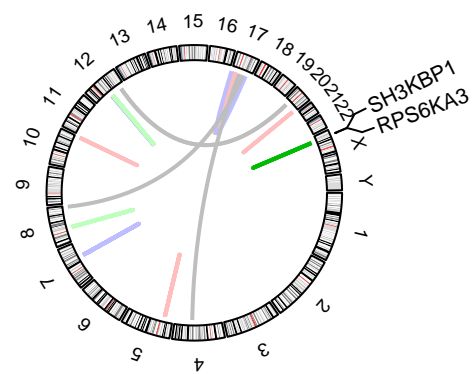
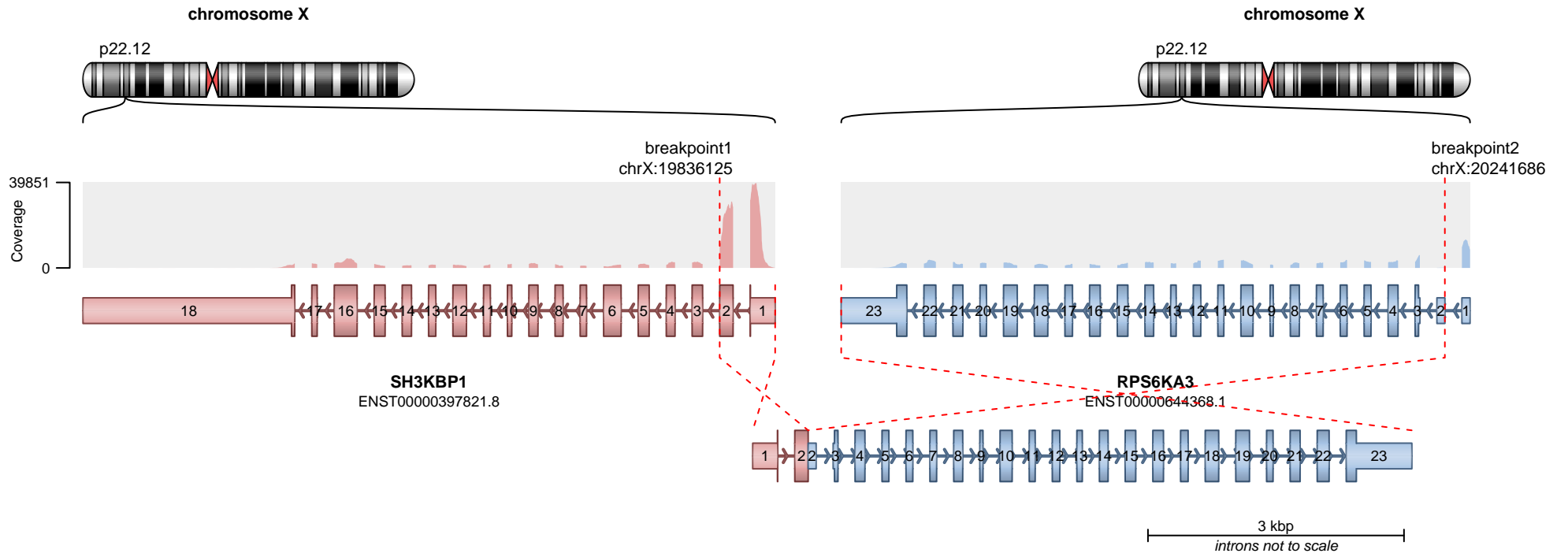
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



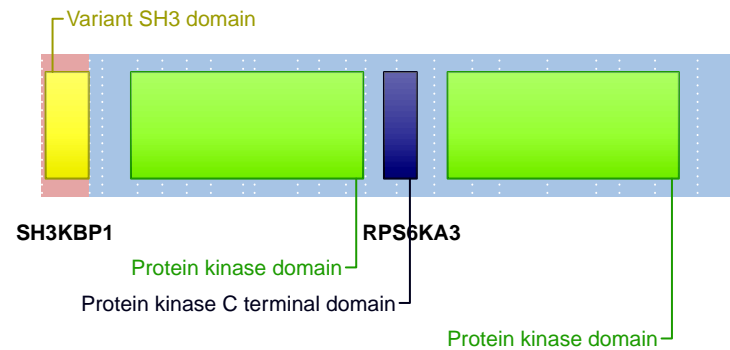
**SUPPORTING READ COUNT**

Split reads = 25  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



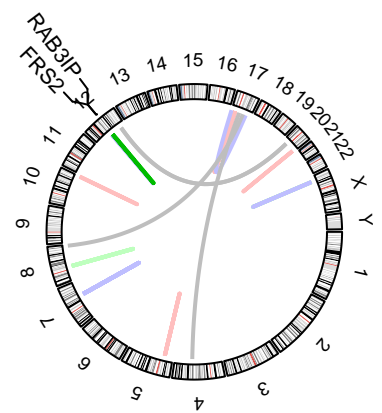
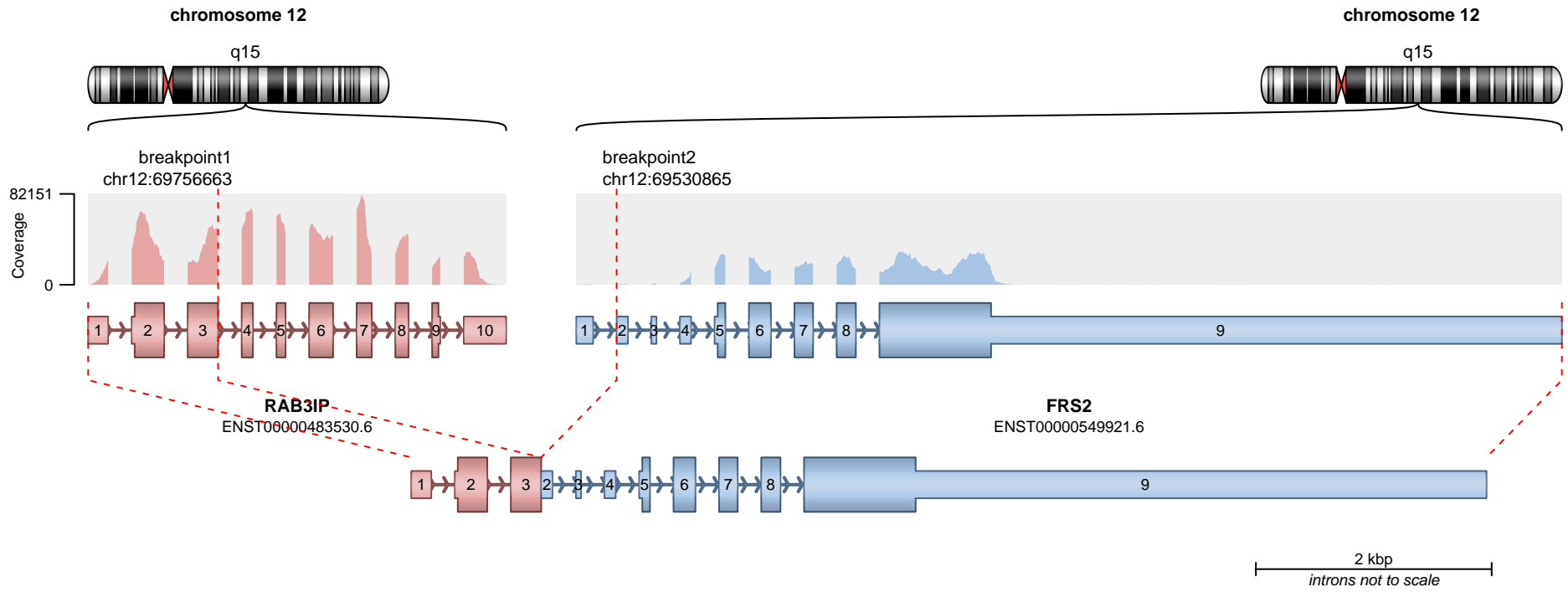
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

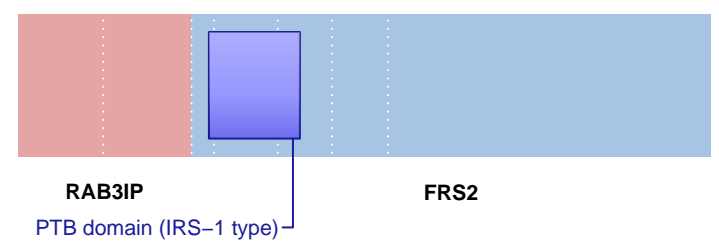
Split reads = 1  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



— translocation    — deletion  
— duplication    — inversion

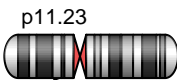
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



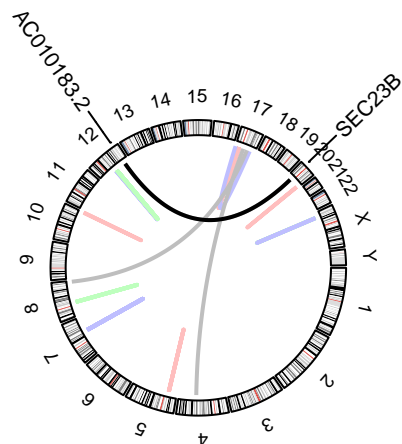
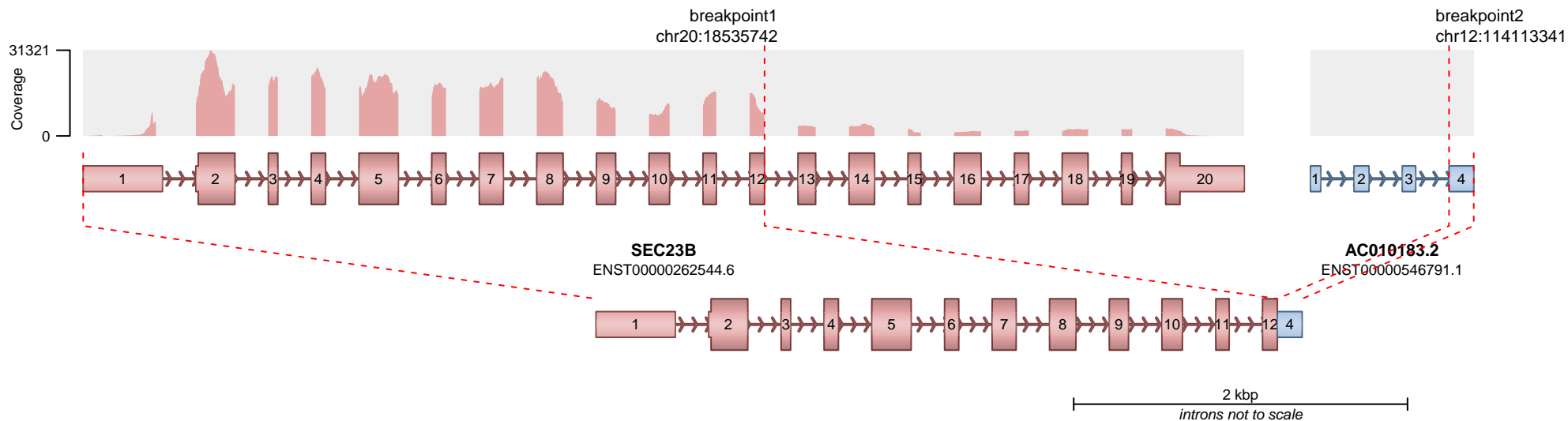
**SUPPORTING READ COUNT**

Split reads = 23  
Discordant mates = 2

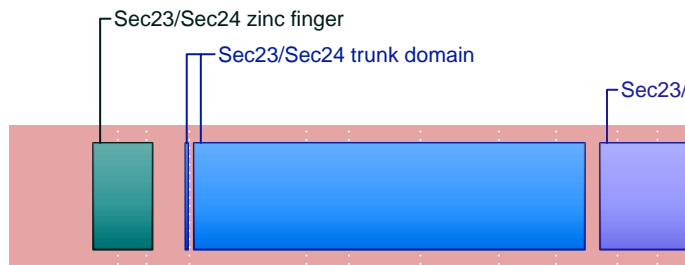
chromosome 20



chromosome 12



**RETAINED PROTEIN DOMAINS**  
reading frame unclear



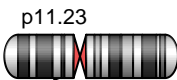
**SUPPORTING READ COUNT**

Split reads = 11  
Discordant mates = 0

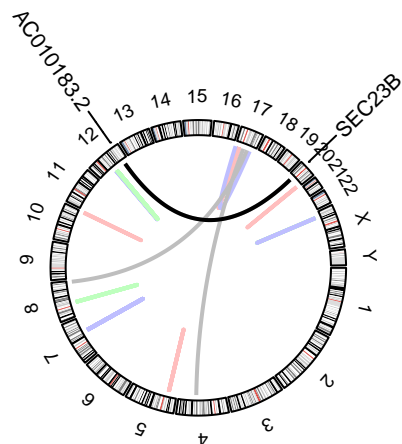
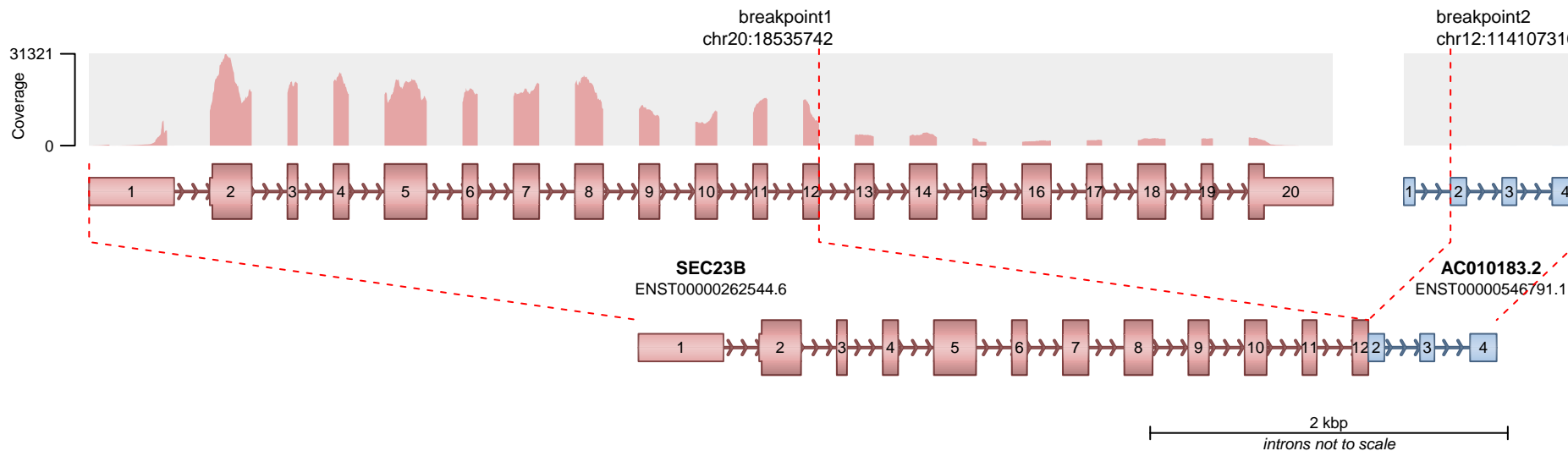
**SEC23B**

— translocation    — deletion  
— duplication    — inversion

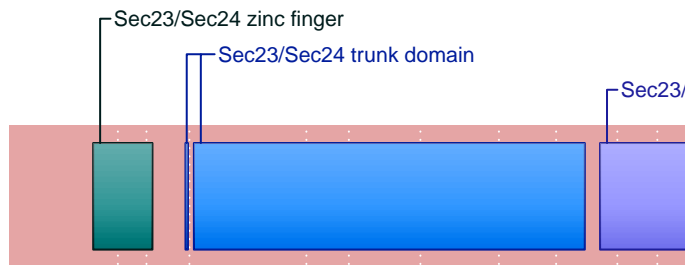
chromosome 20



chromosome 12



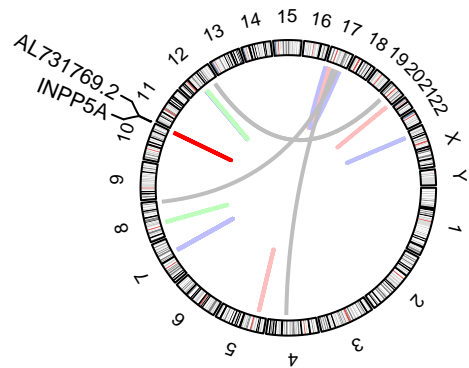
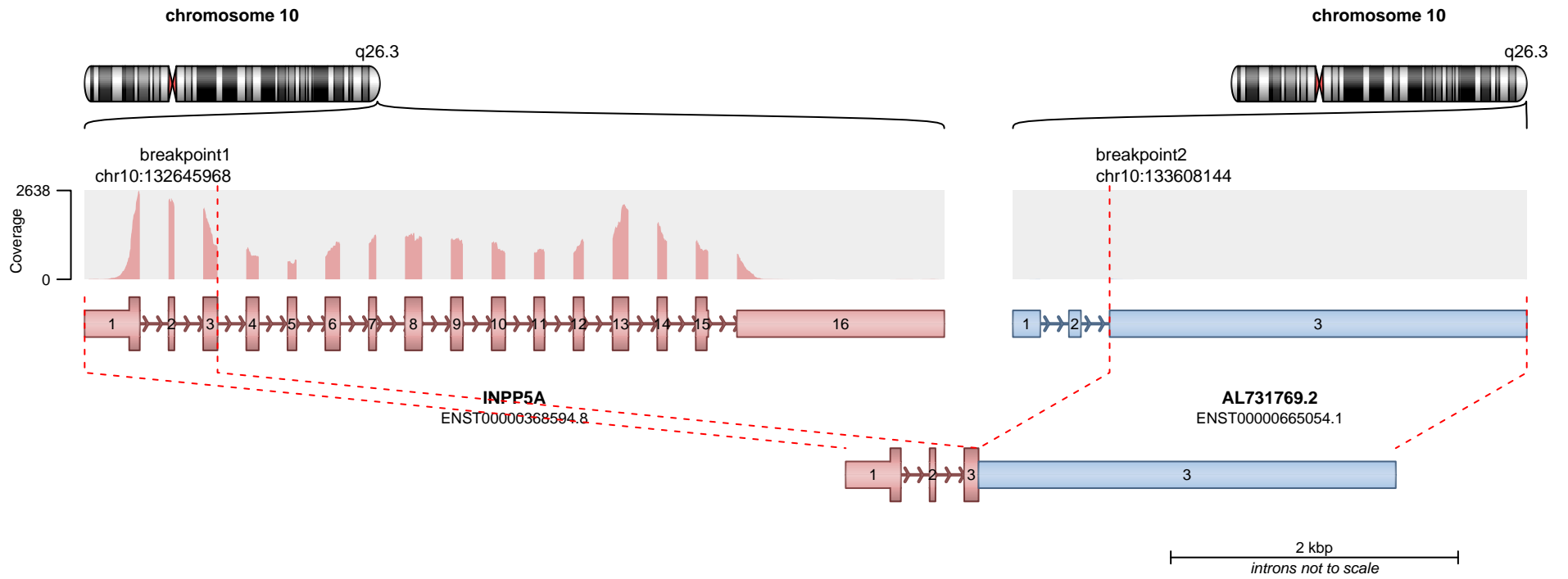
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



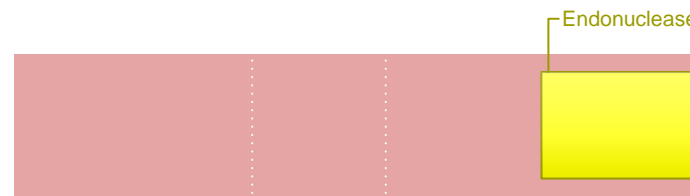
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



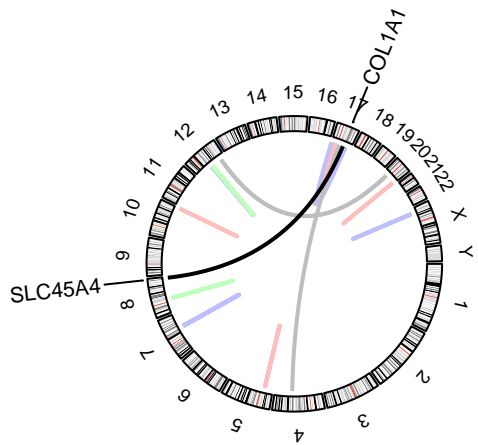
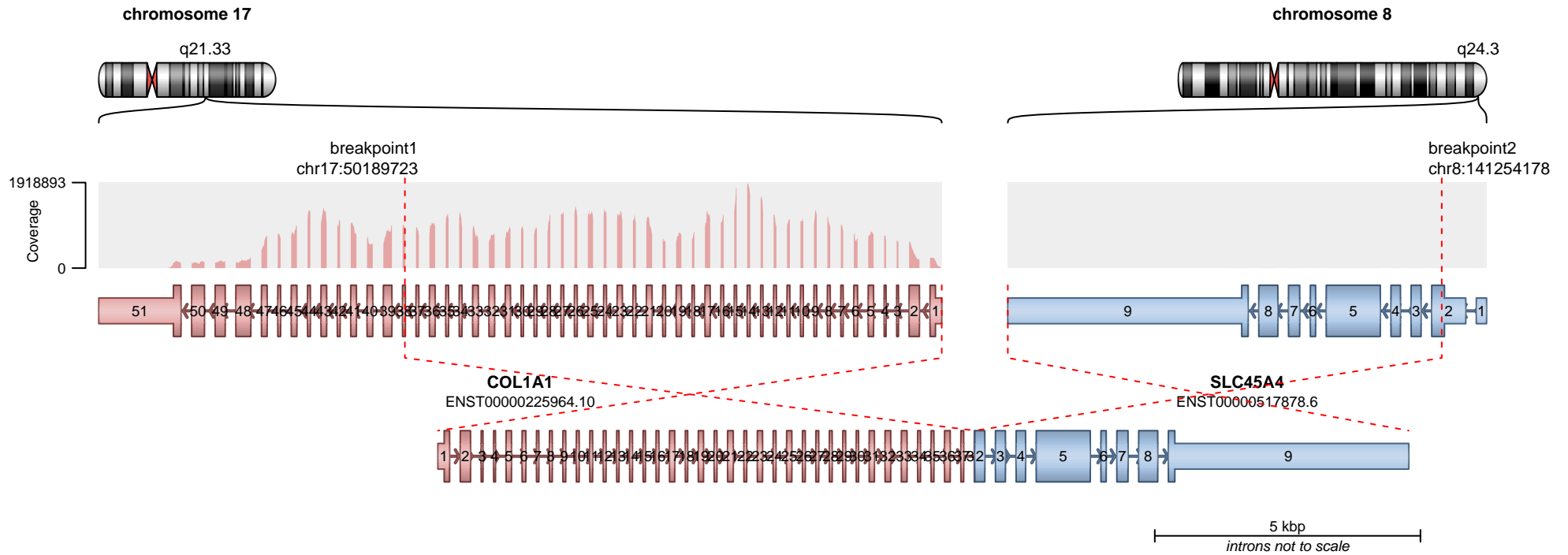
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



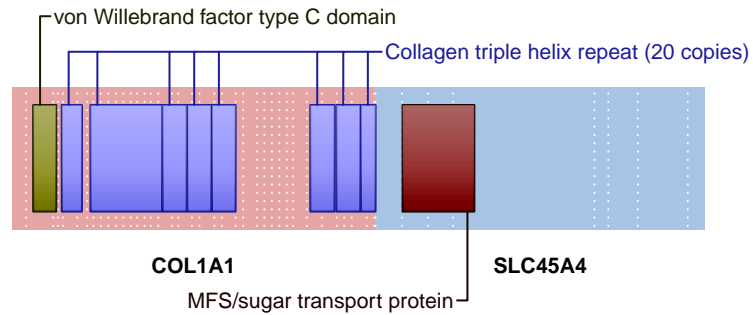
**SUPPORTING READ COUNT**

Split reads = 10  
Discordant mates = 1

— translocation    — deletion  
— duplication    — inversion



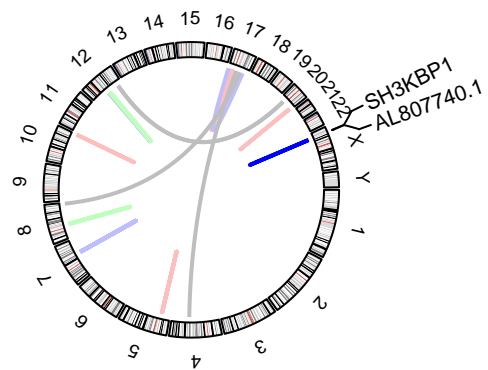
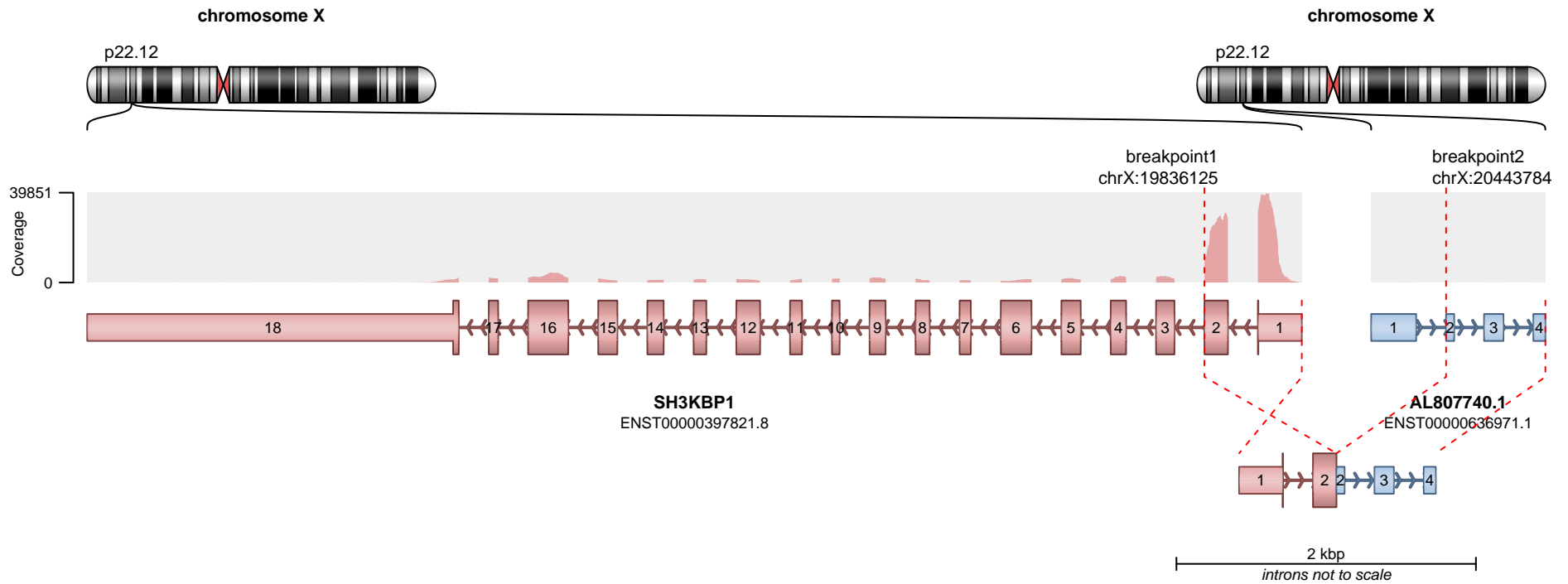
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



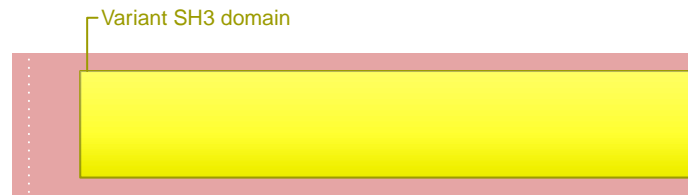
**SUPPORTING READ COUNT**

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
- deletion
- duplication
- inversion