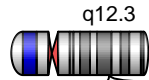
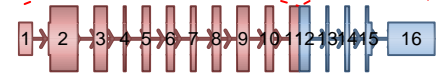
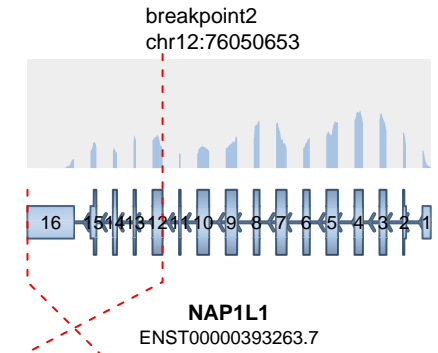
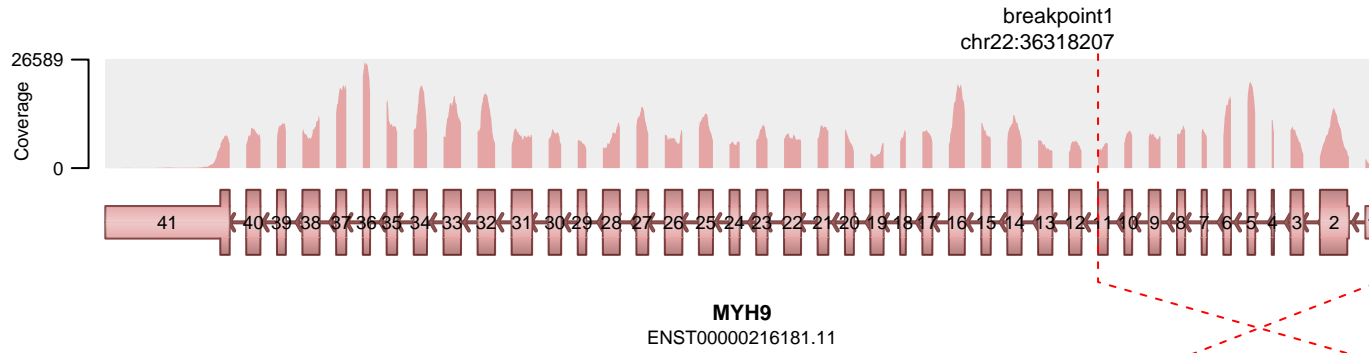


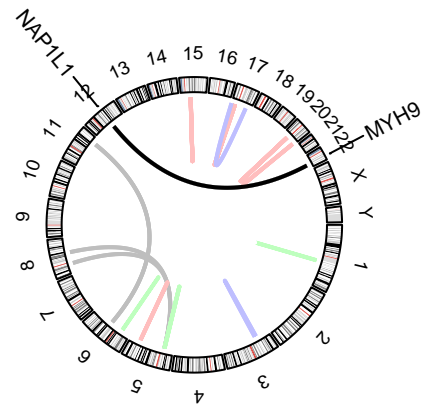
chromosome 22



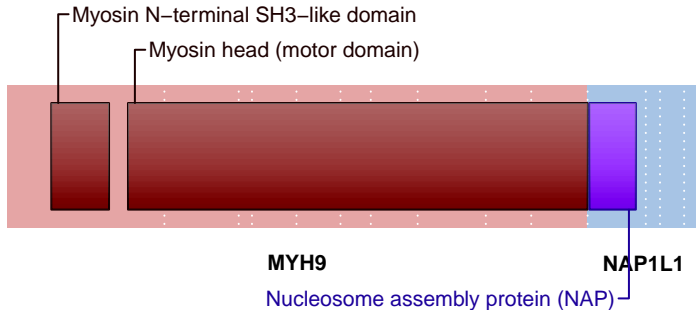
chromosome 12



4 kbp  
introns not to scale



**RETAINED PROTEIN DOMAINS**  
reading frame unclear

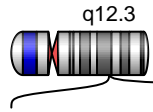


**SUPPORTING READ COUNT**

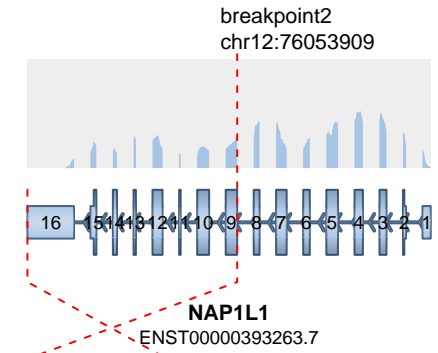
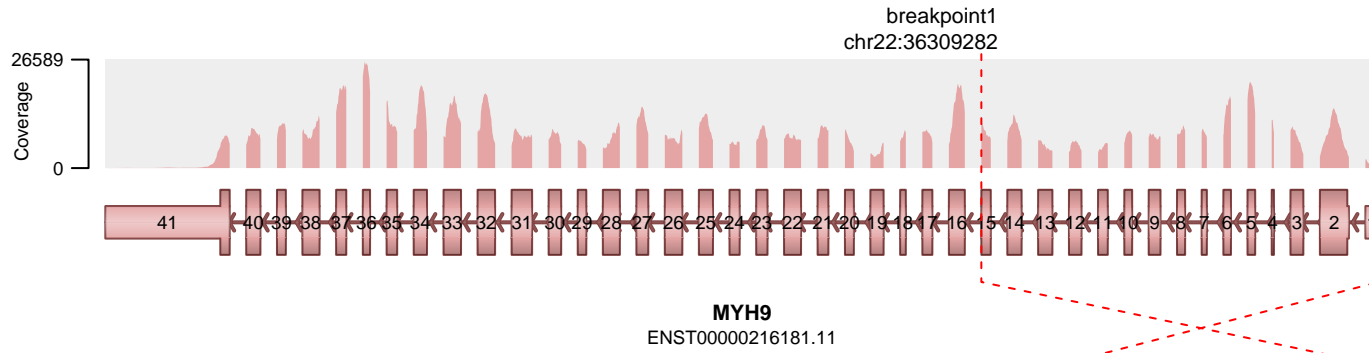
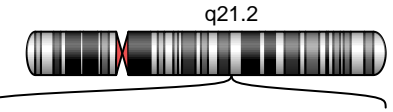
Split reads = 323  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion

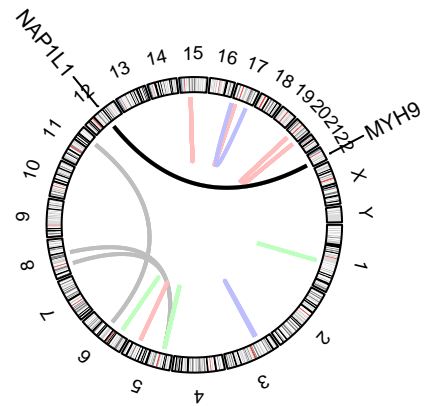
chromosome 22



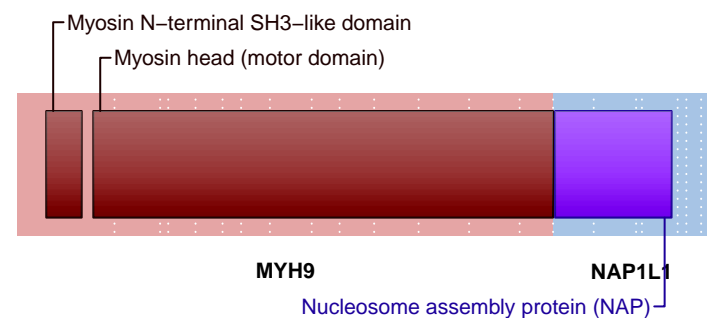
chromosome 12



4 kbp  
introns not to scale



**RETAINED PROTEIN DOMAINS**  
reading frame unclear

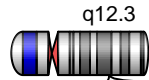


**SUPPORTING READ COUNT**

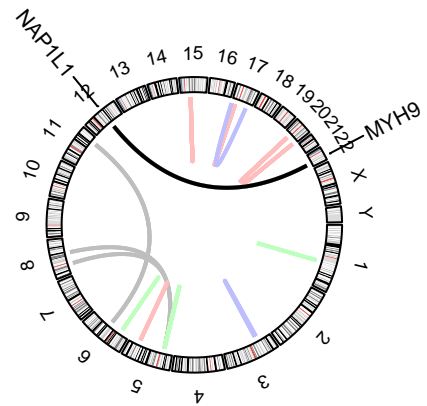
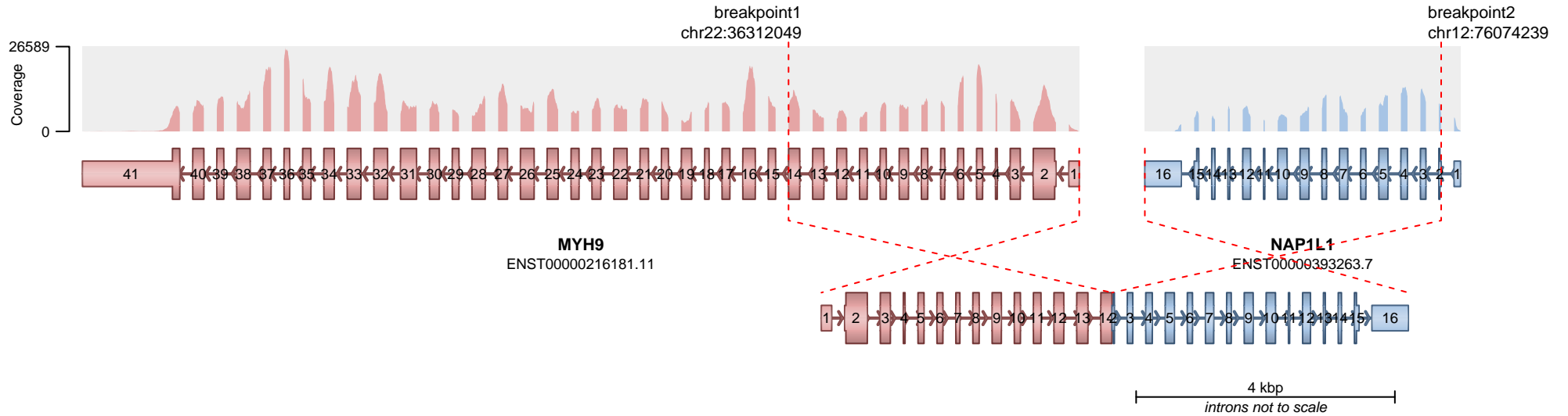
Split reads = 1  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion

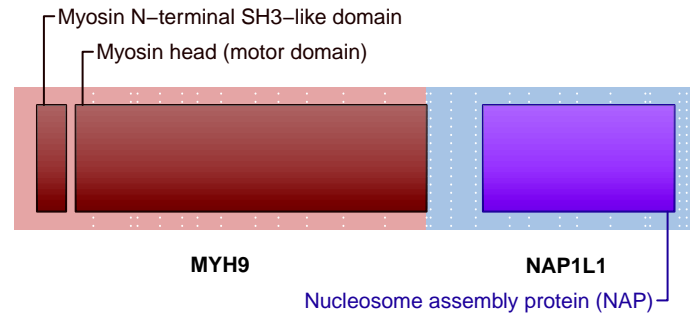
chromosome 22



chromosome 12



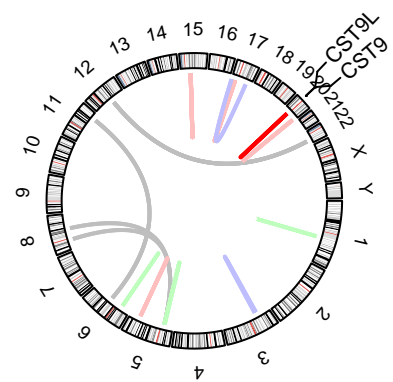
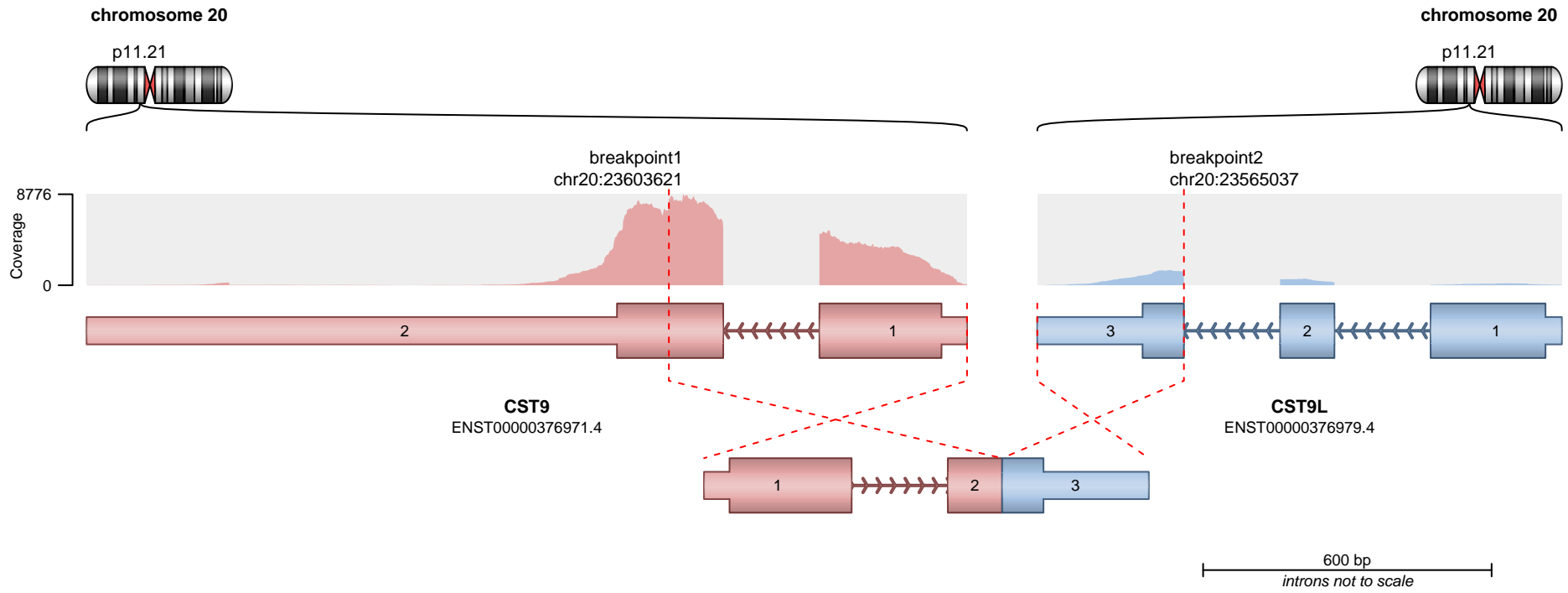
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



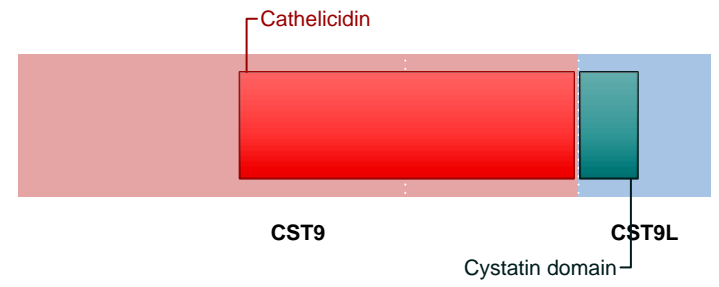
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



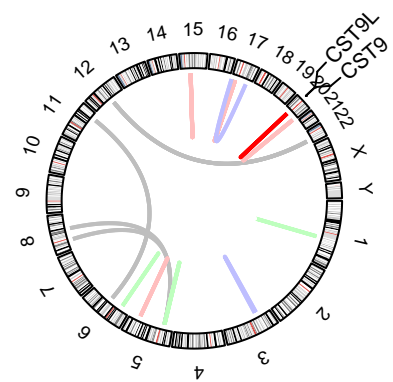
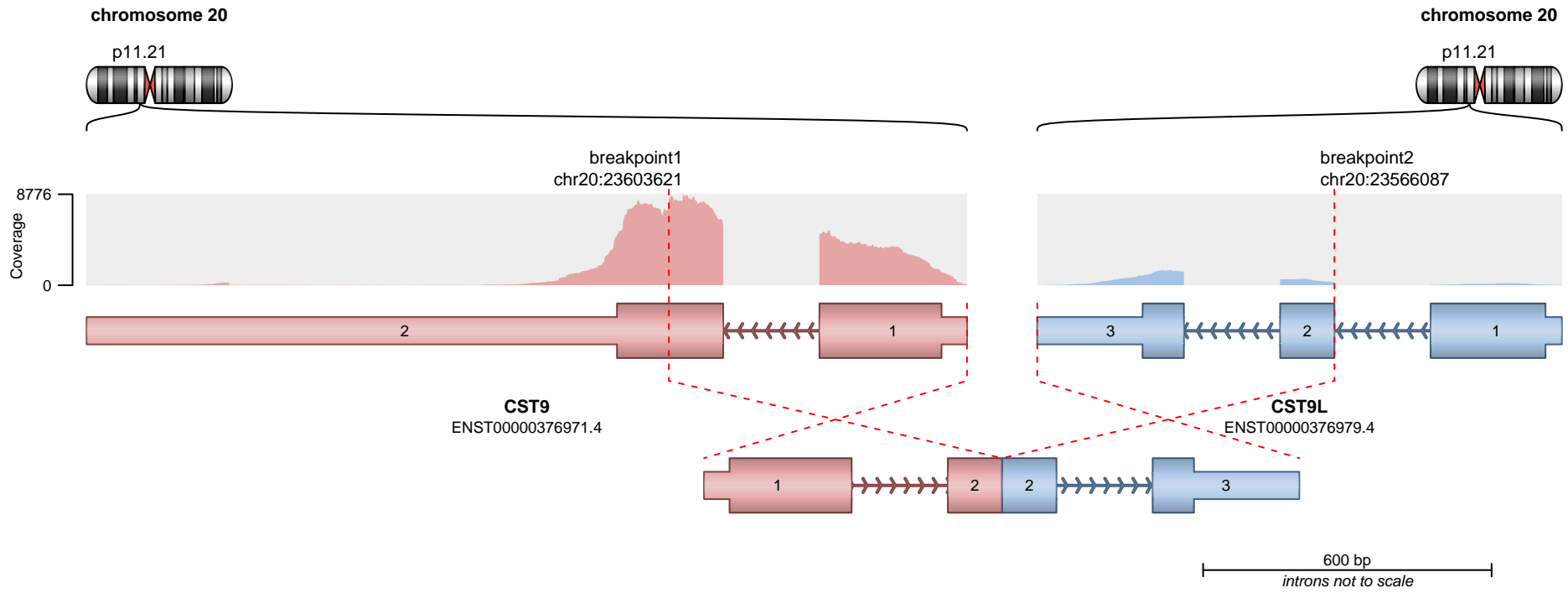
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



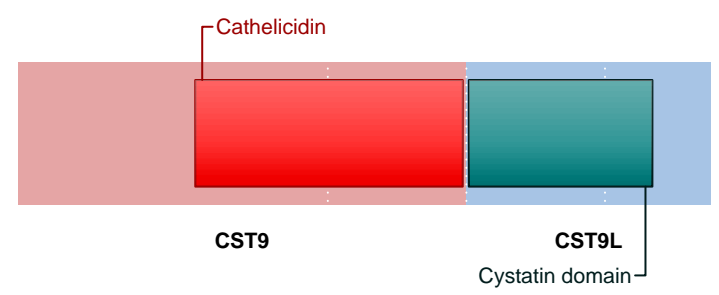
**SUPPORTING READ COUNT**

Split reads = 198  
Discordant mates = 1

- translocation
- deletion
- duplication
- inversion



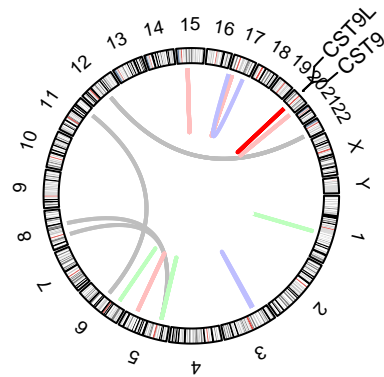
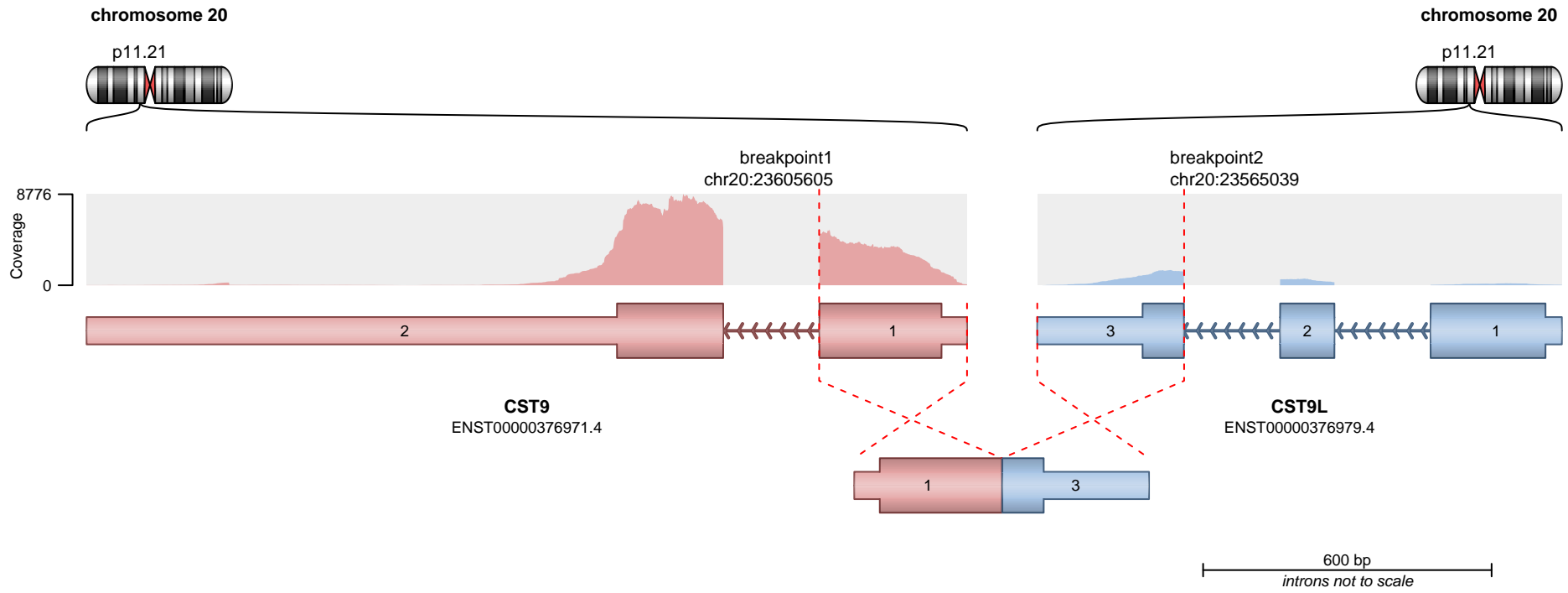
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

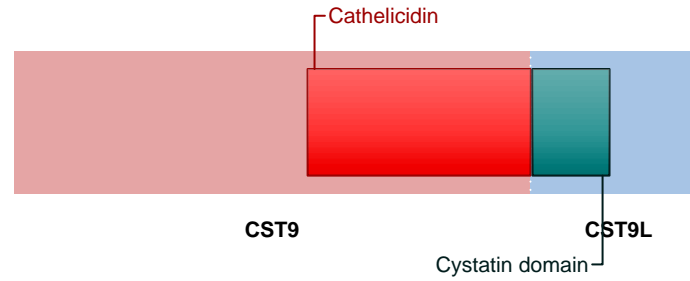
Split reads = 36  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



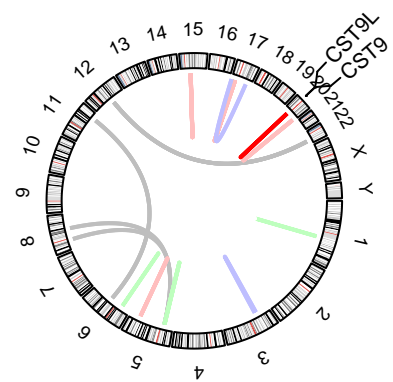
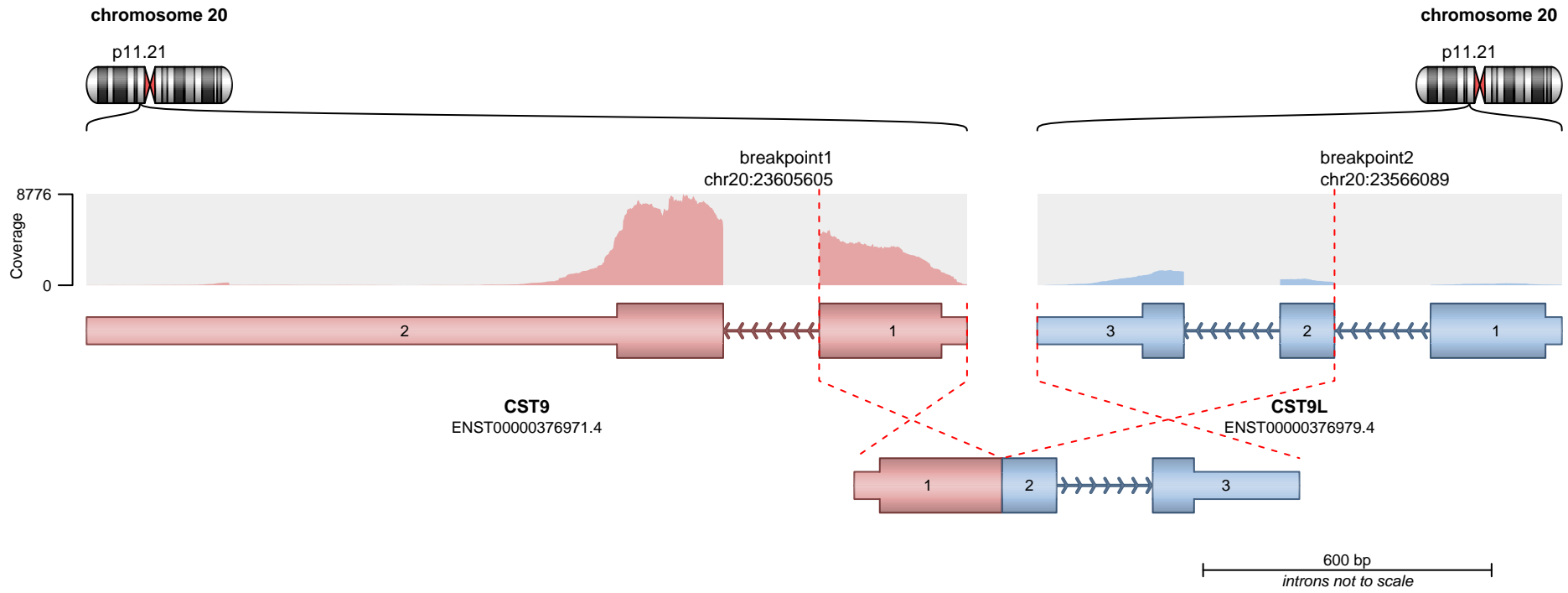
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear

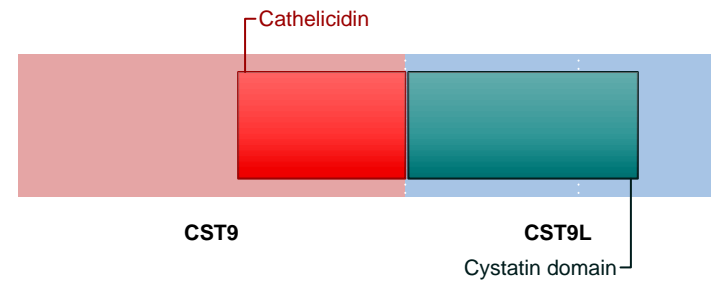


**SUPPORTING READ COUNT**

Split reads = 30  
Discordant mates = 0



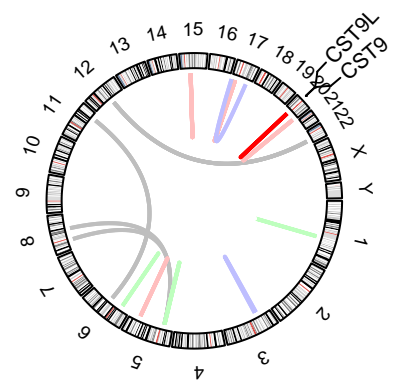
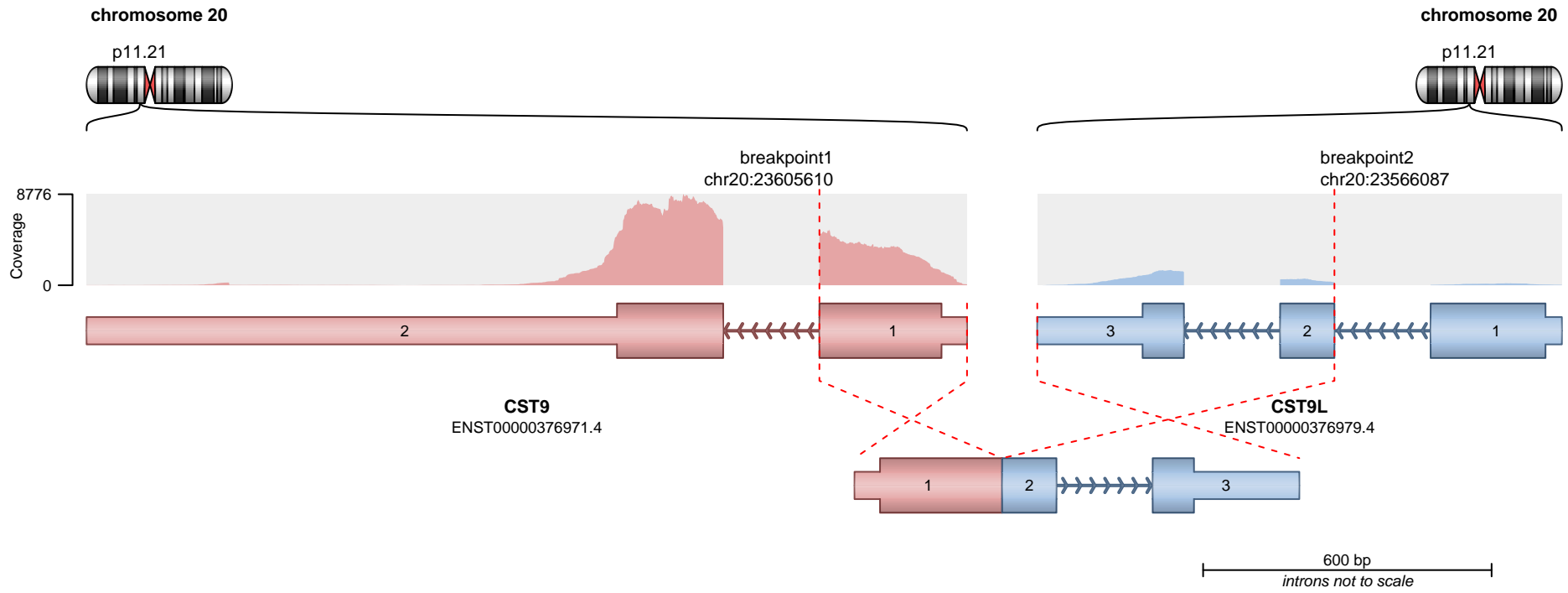
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



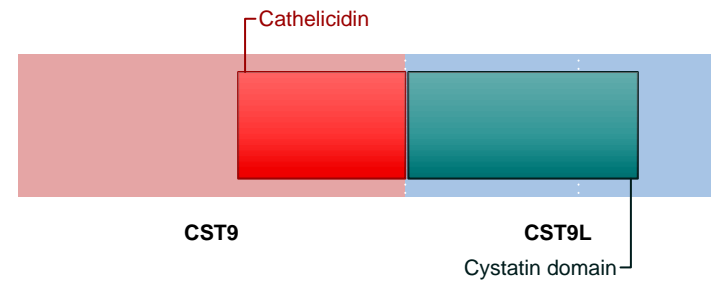
**SUPPORTING READ COUNT**

Split reads = 26  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



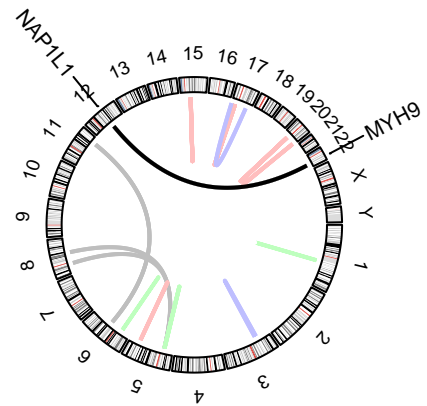
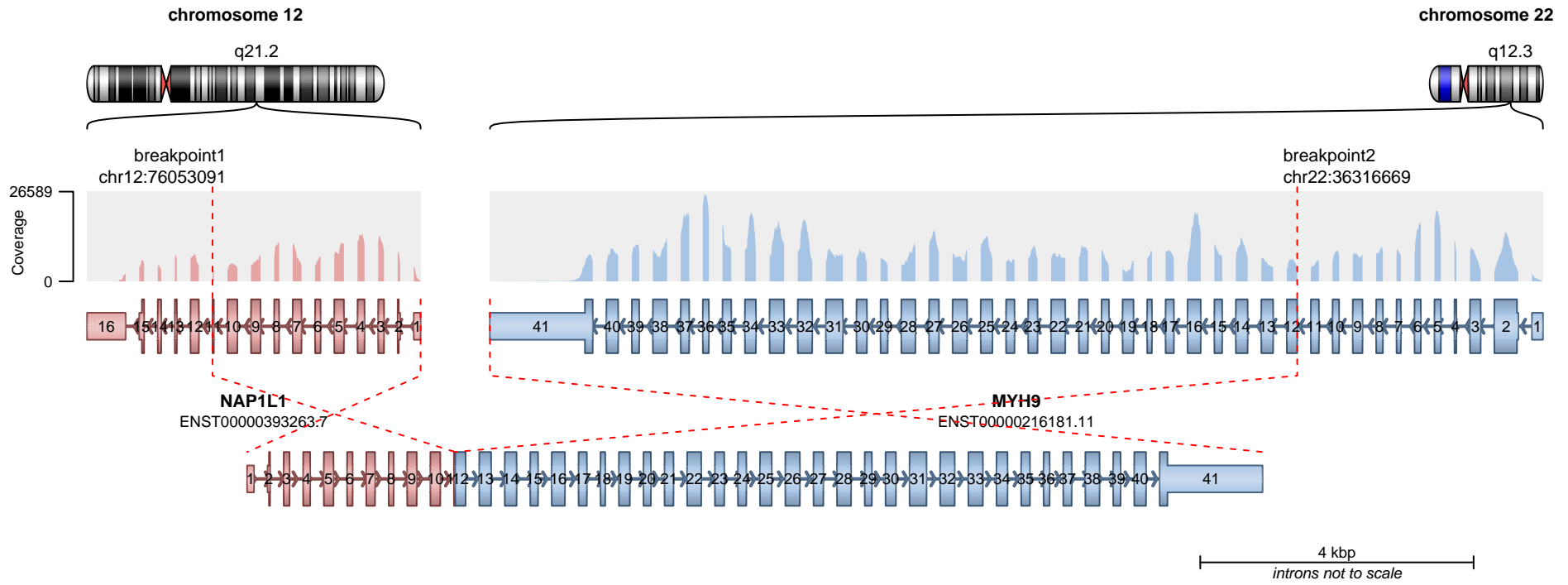
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



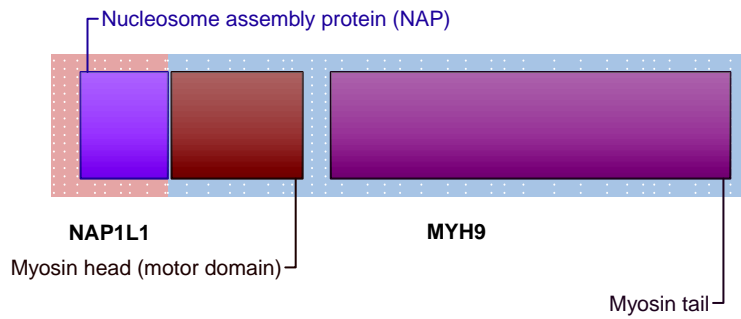
**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



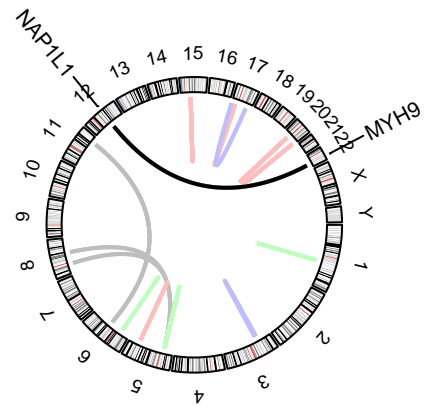
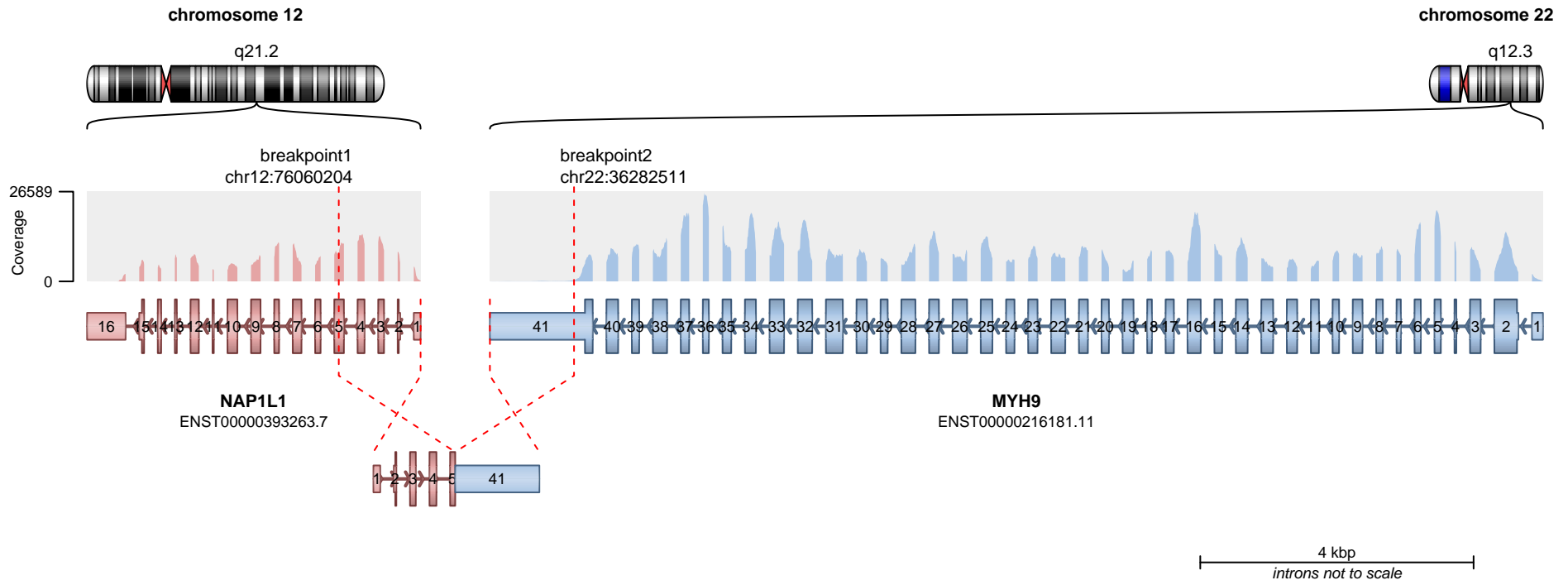
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 154  
Discordant mates = 3

- translocation
- duplication
- deletion
- inversion



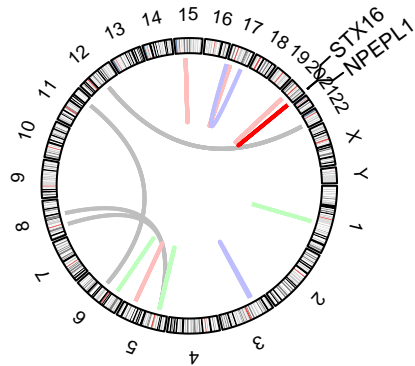
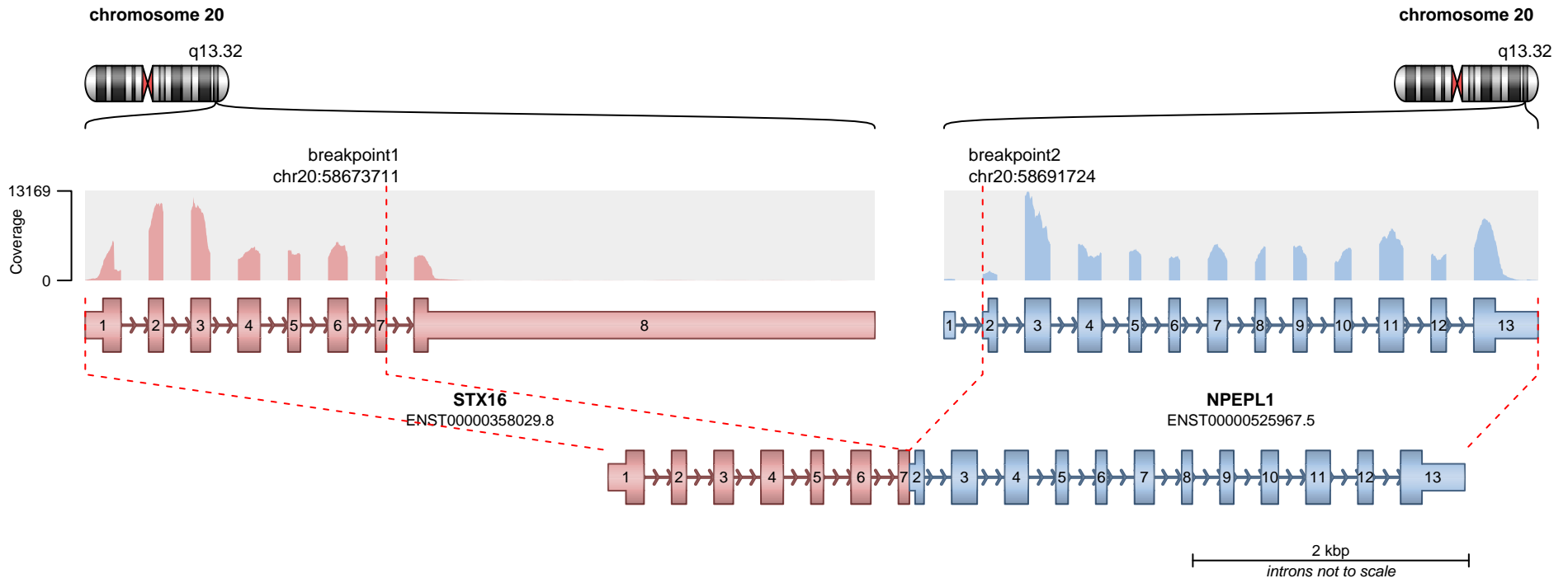
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



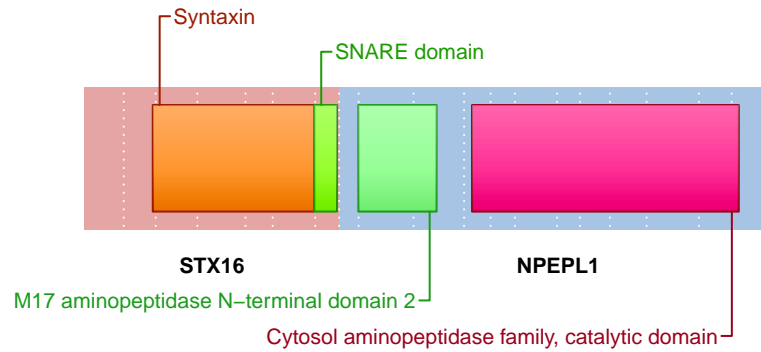
**SUPPORTING READ COUNT**

Split reads = 6  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



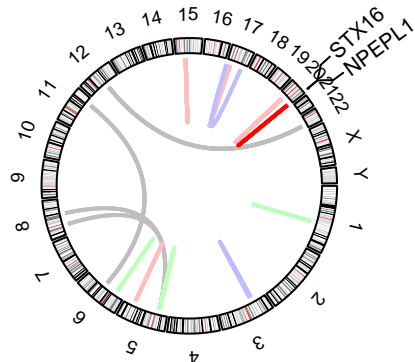
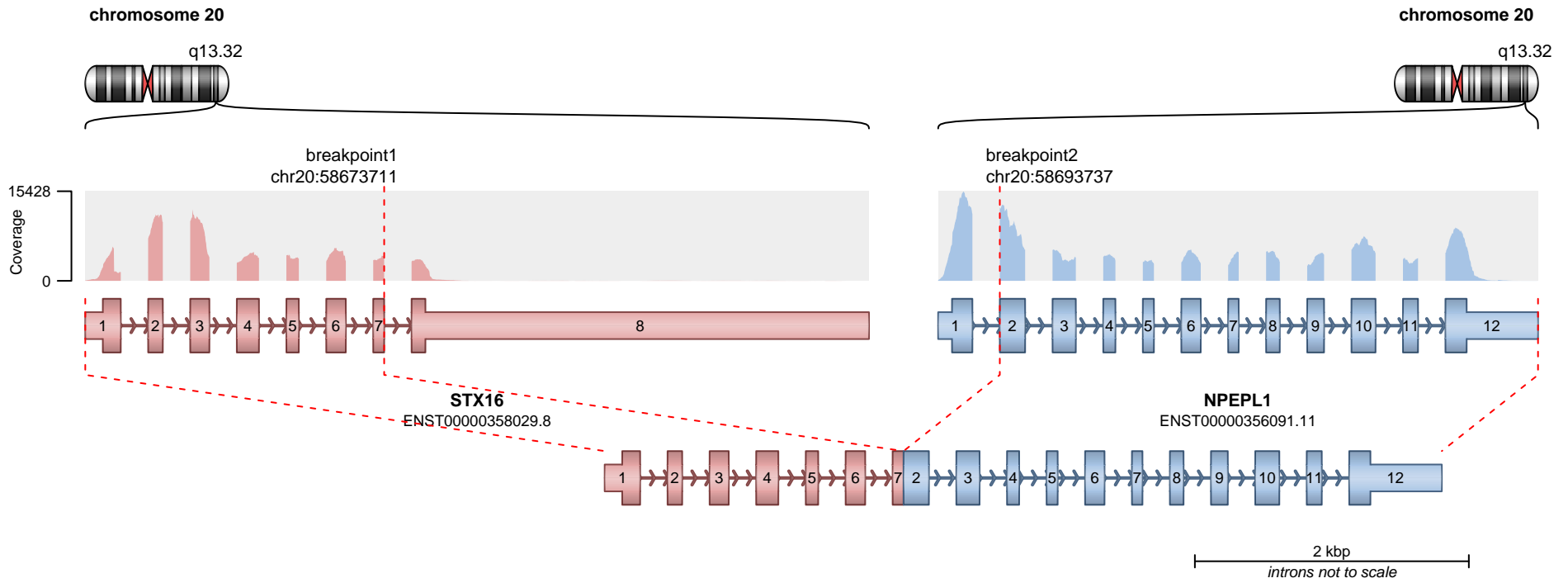
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



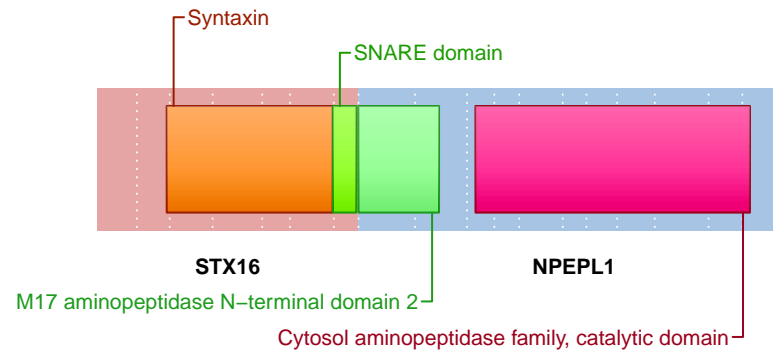
**SUPPORTING READ COUNT**

Split reads = 152  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



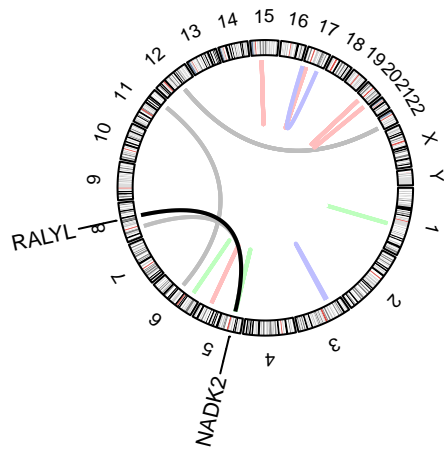
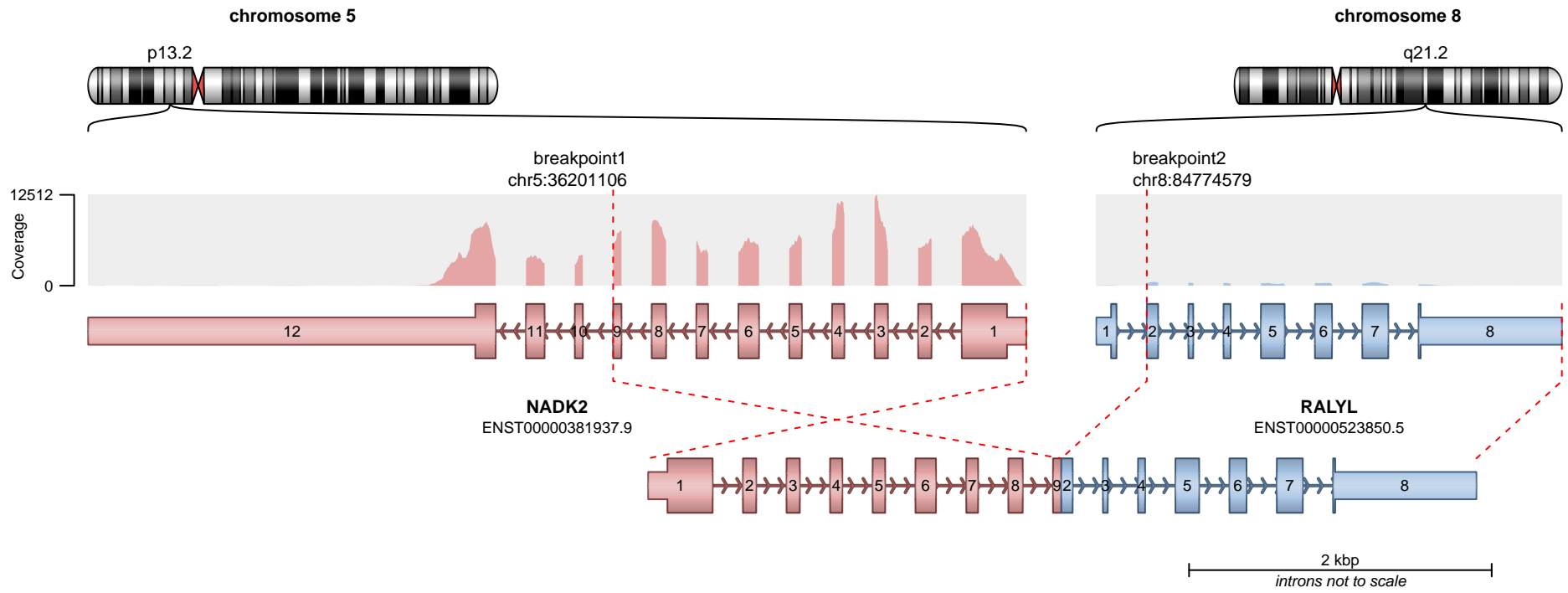
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



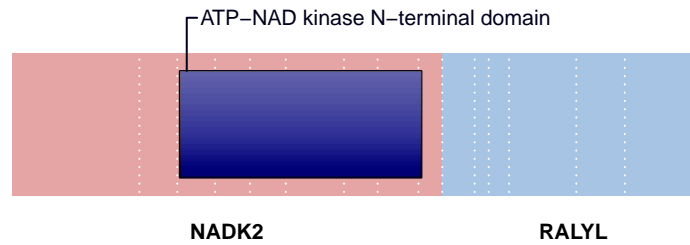
**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



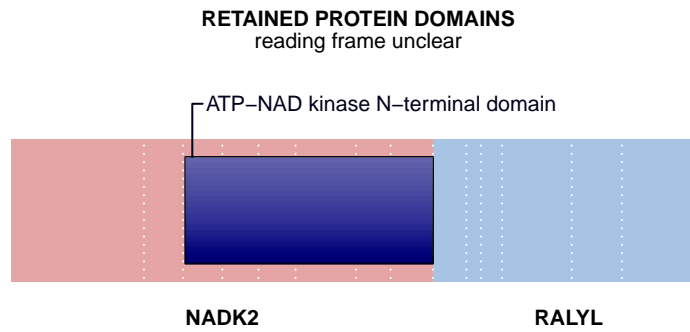
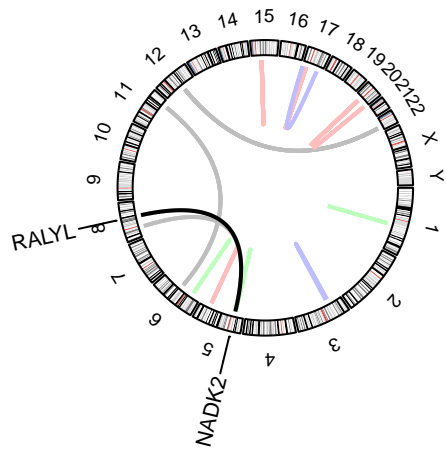
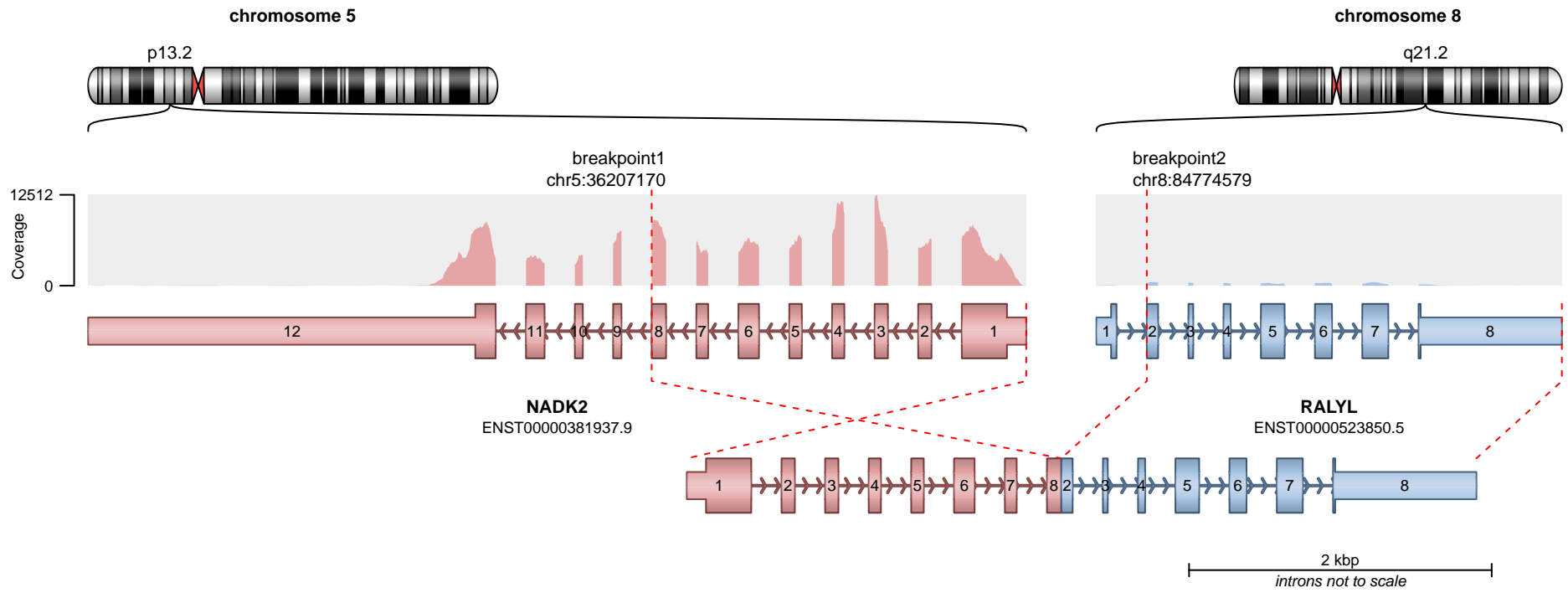
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 129  
Discordant mates = 0

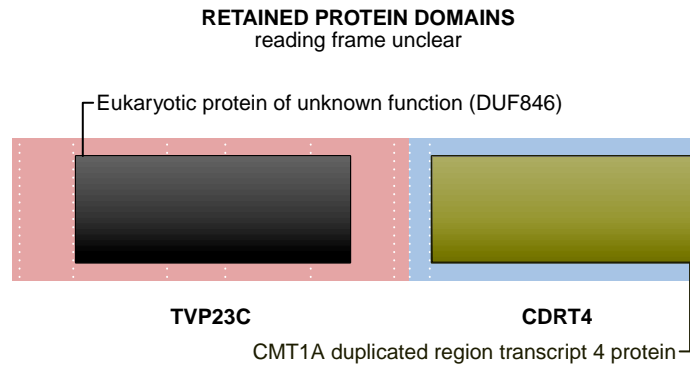
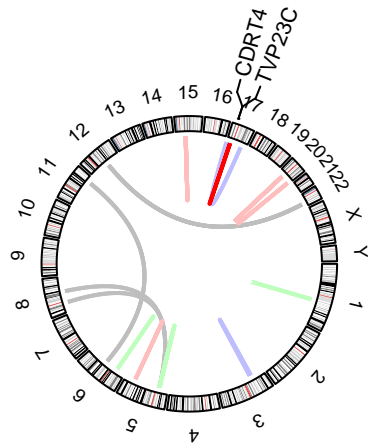
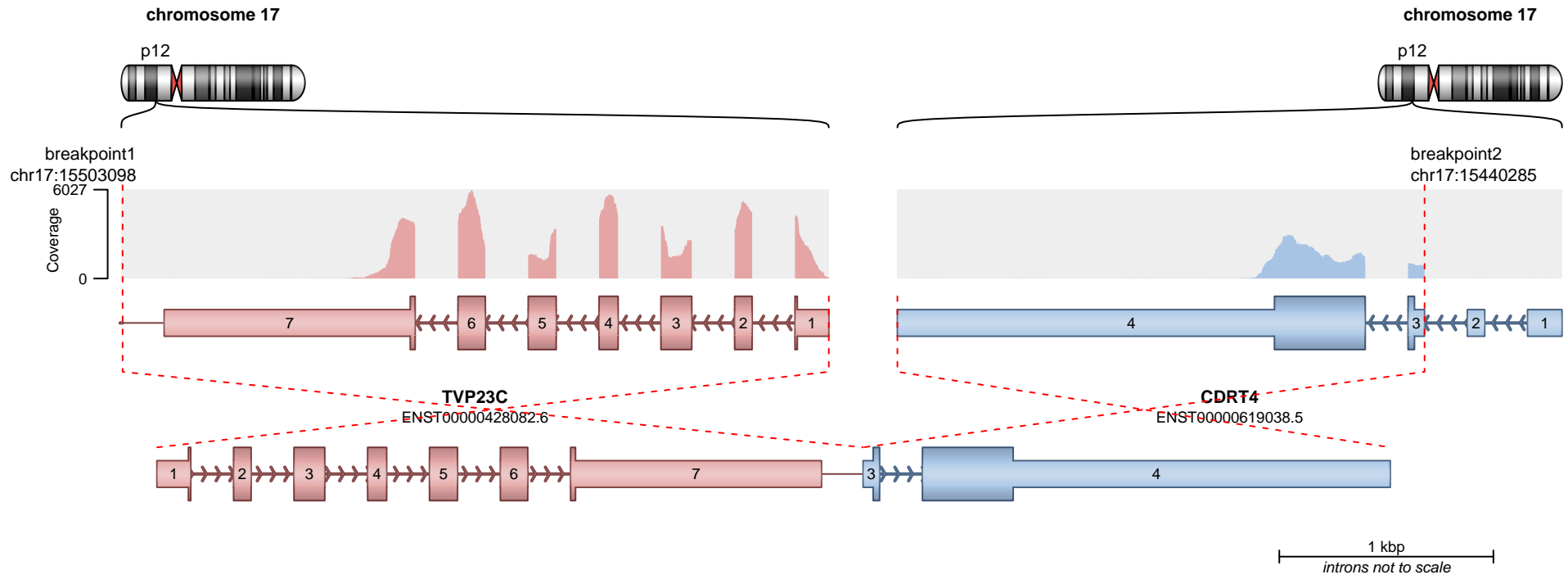
- translocation
- duplication
- deletion
- inversion



**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

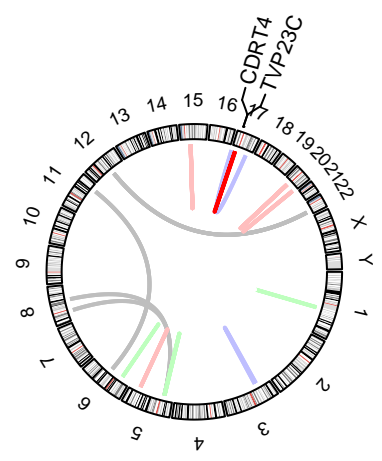
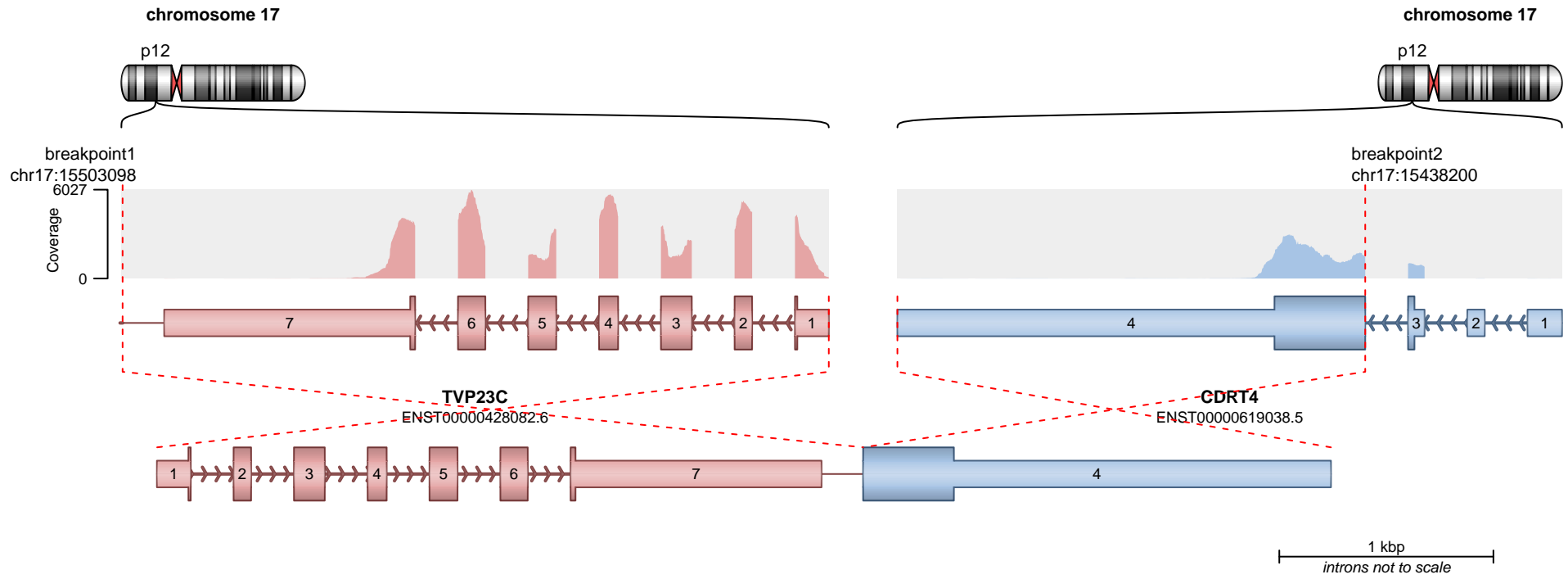
- translocation
- duplication
- deletion
- inversion



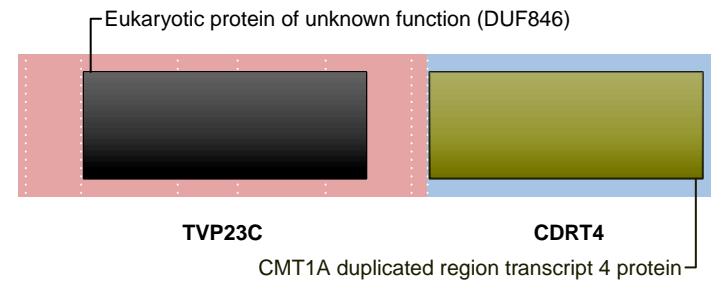
**SUPPORTING READ COUNT**

Split reads = 121  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



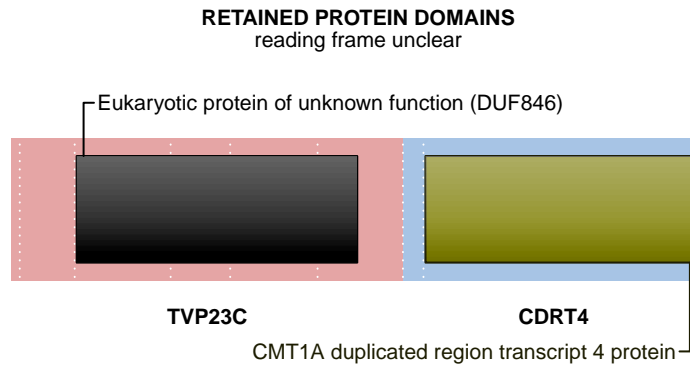
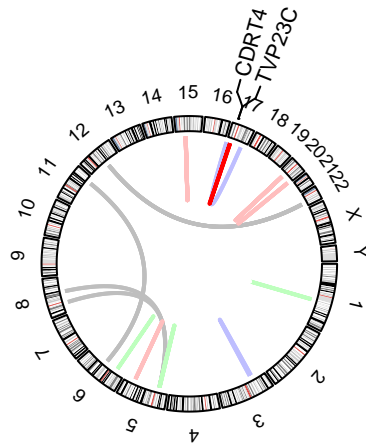
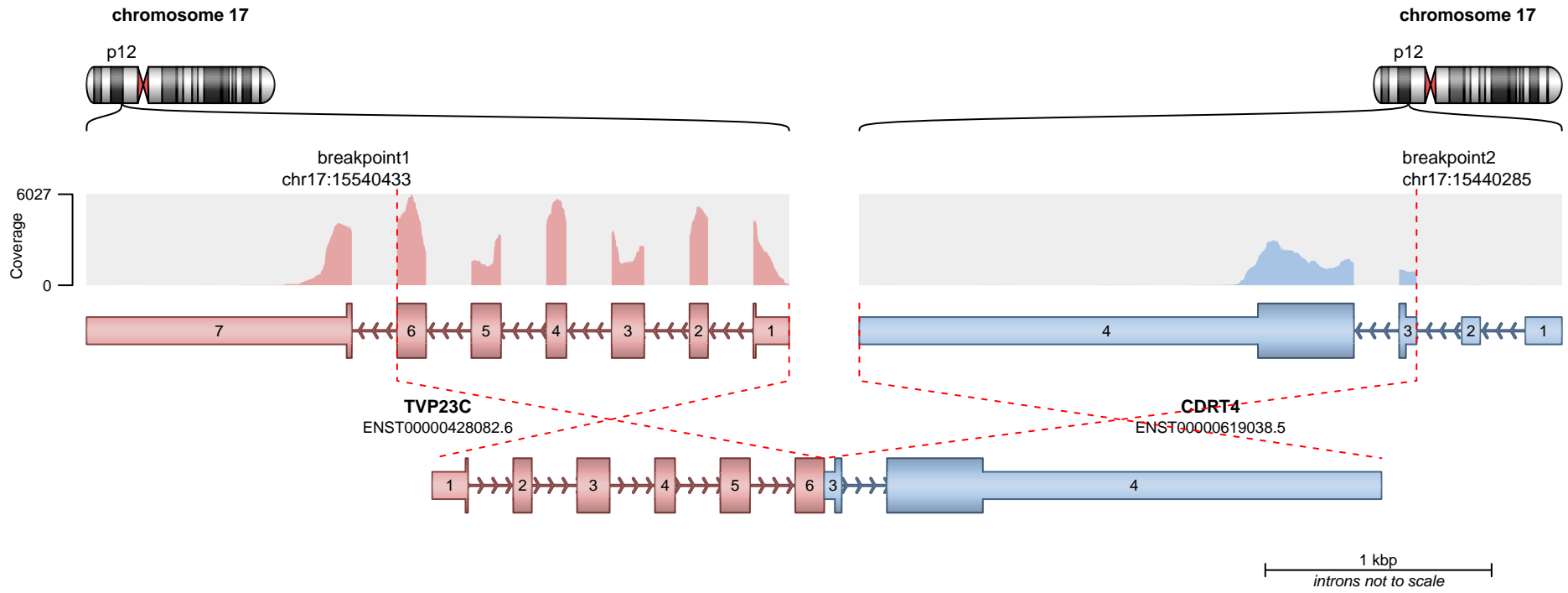
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 79  
Discordant mates = 0

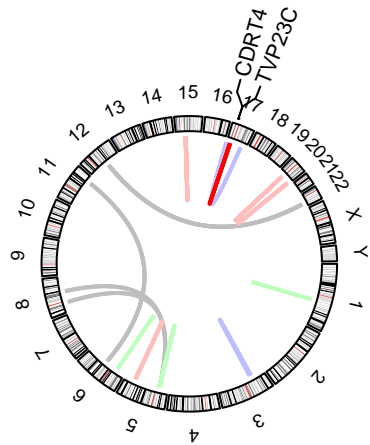
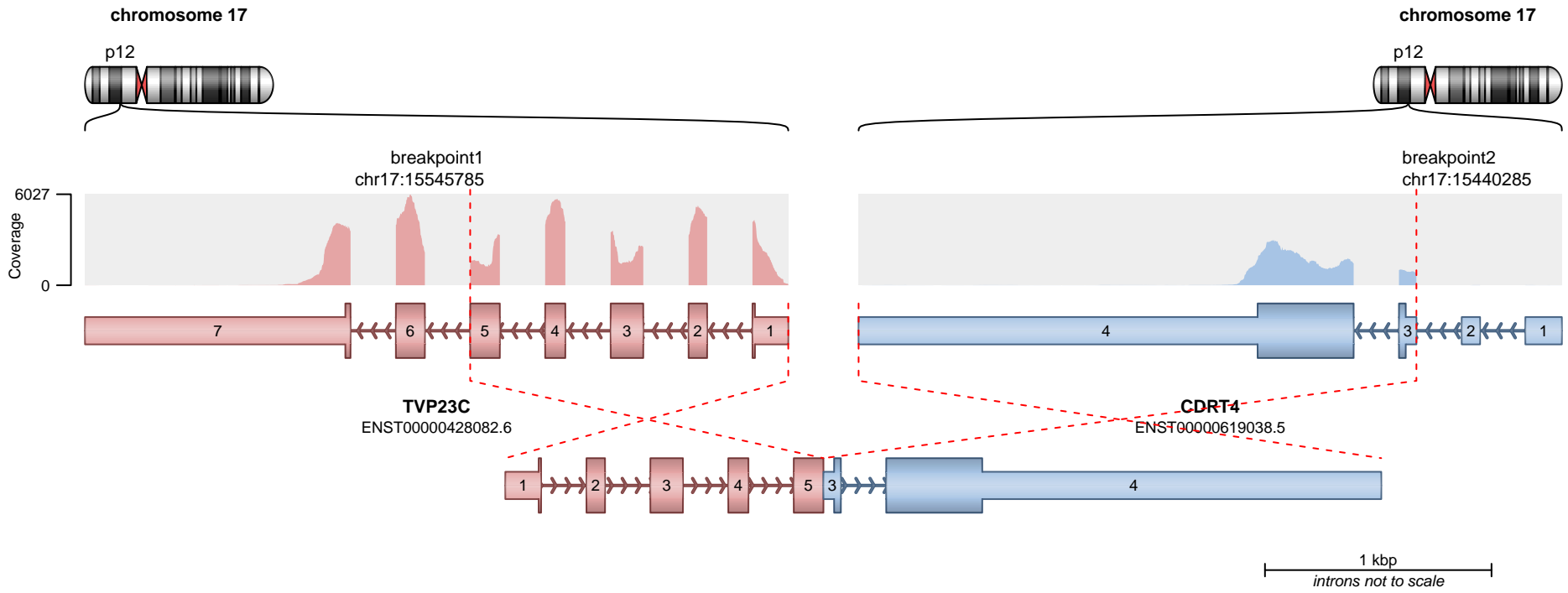
- translocation
- duplication
- deletion
- inversion



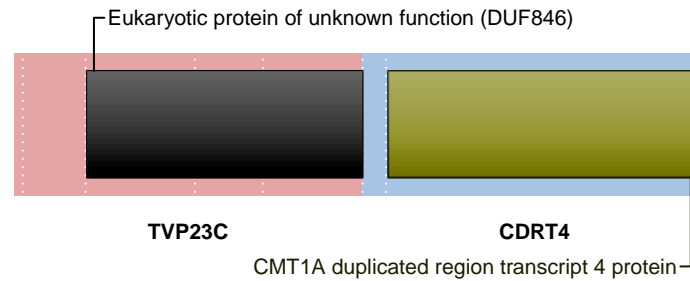
**SUPPORTING READ COUNT**

Split reads = 30  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



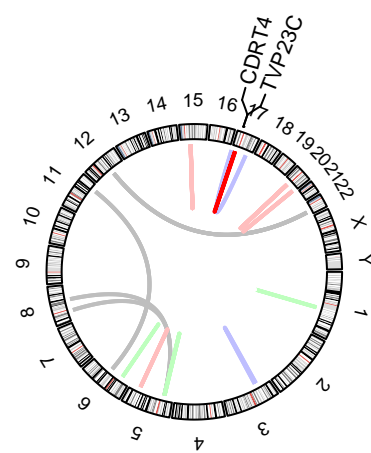
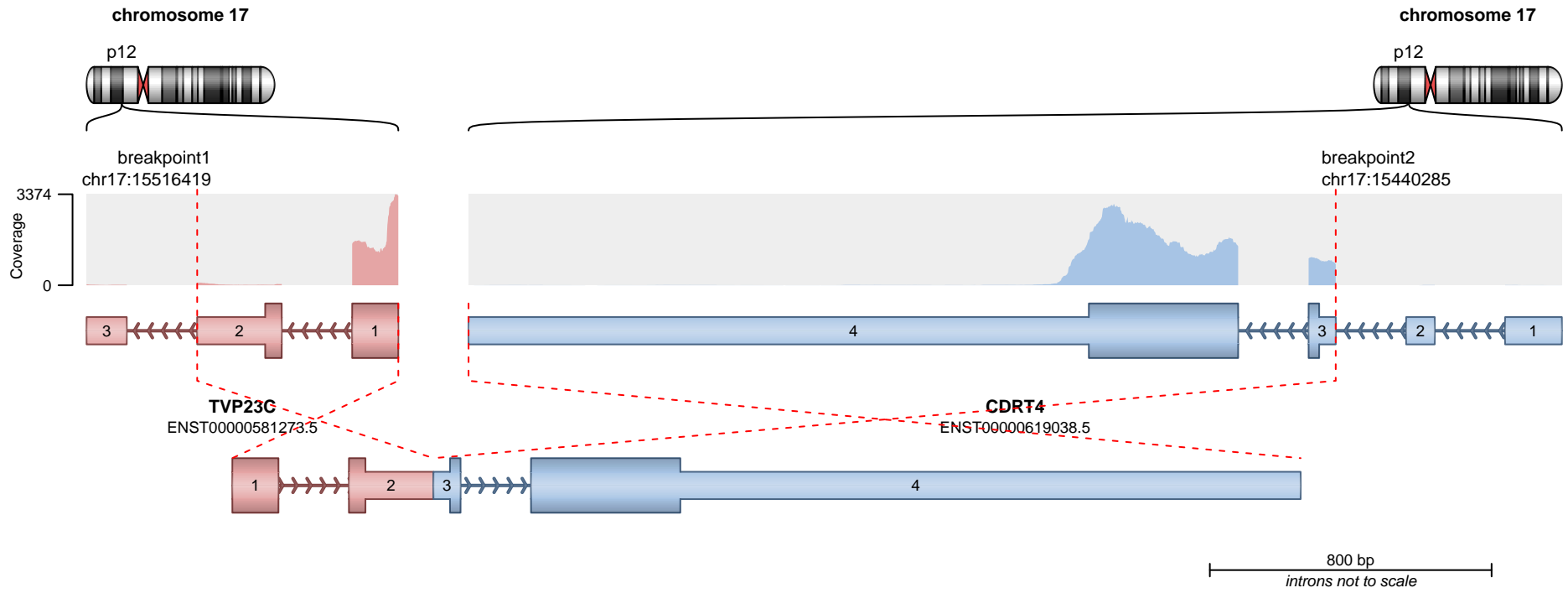
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



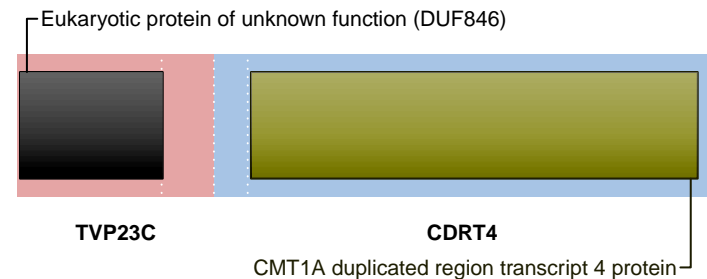
**SUPPORTING READ COUNT**

Split reads = 17  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



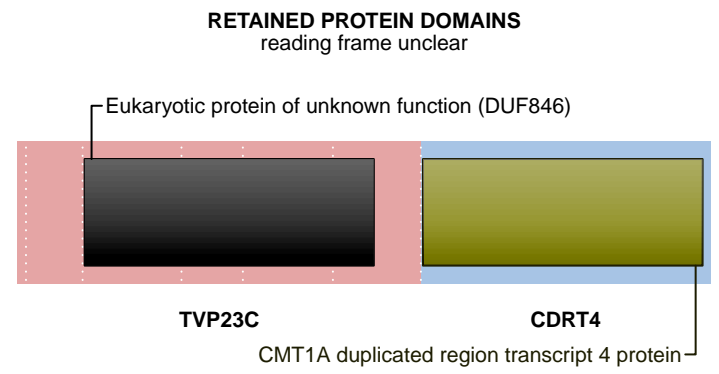
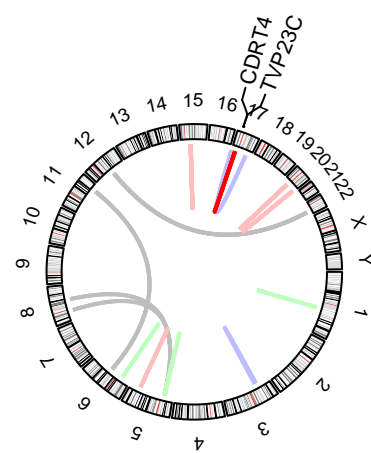
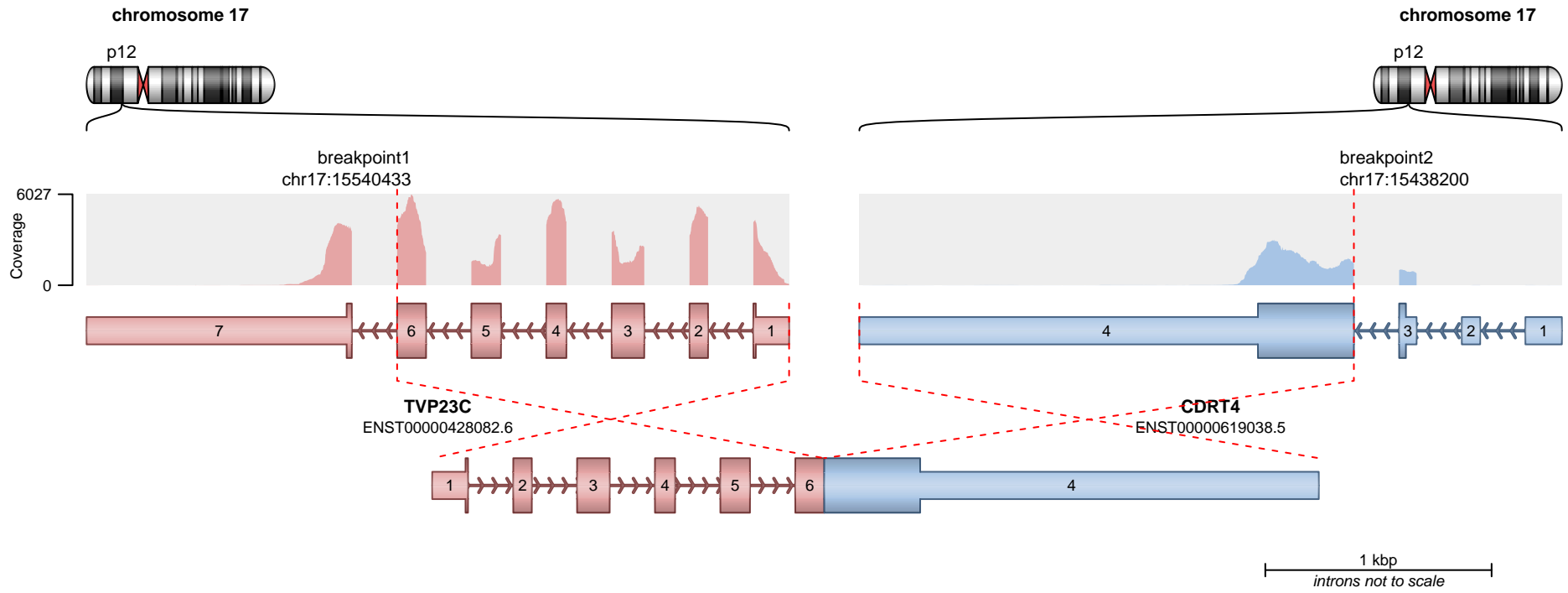
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 11  
Discordant mates = 0

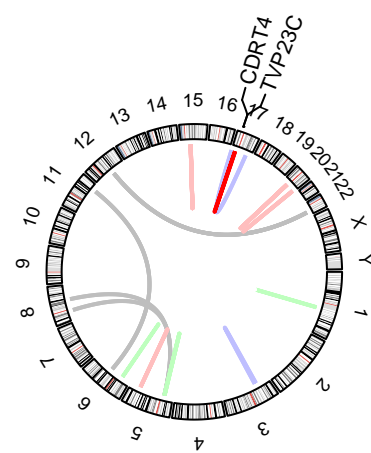
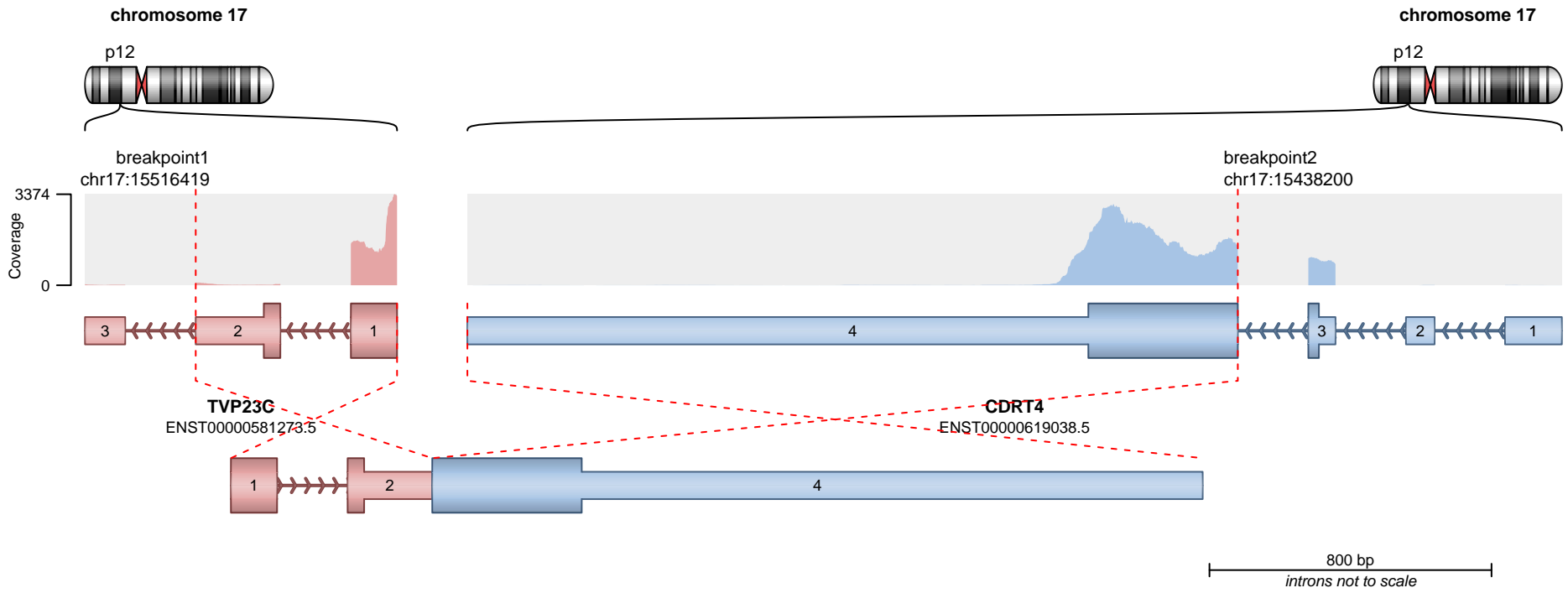
— translocation — deletion  
— duplication — inversion



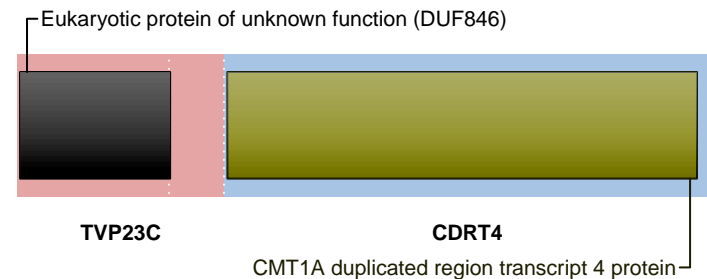
**SUPPORTING READ COUNT**

Split reads = 8  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



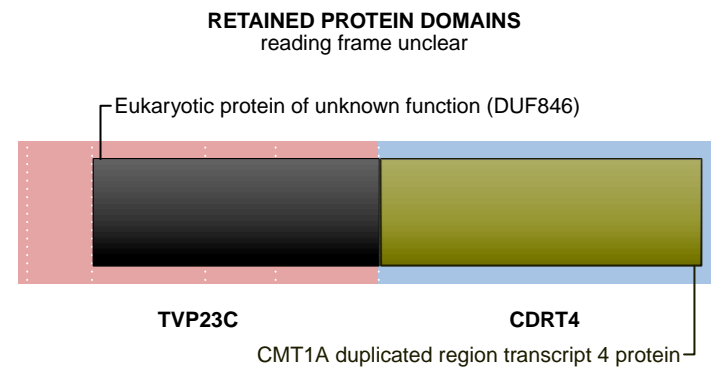
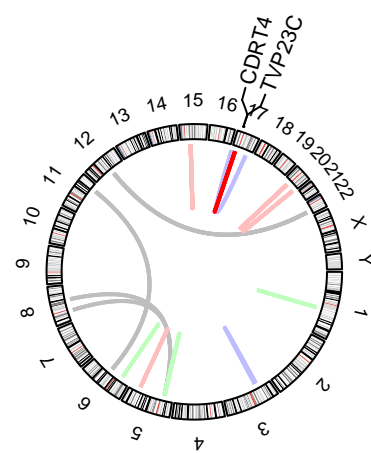
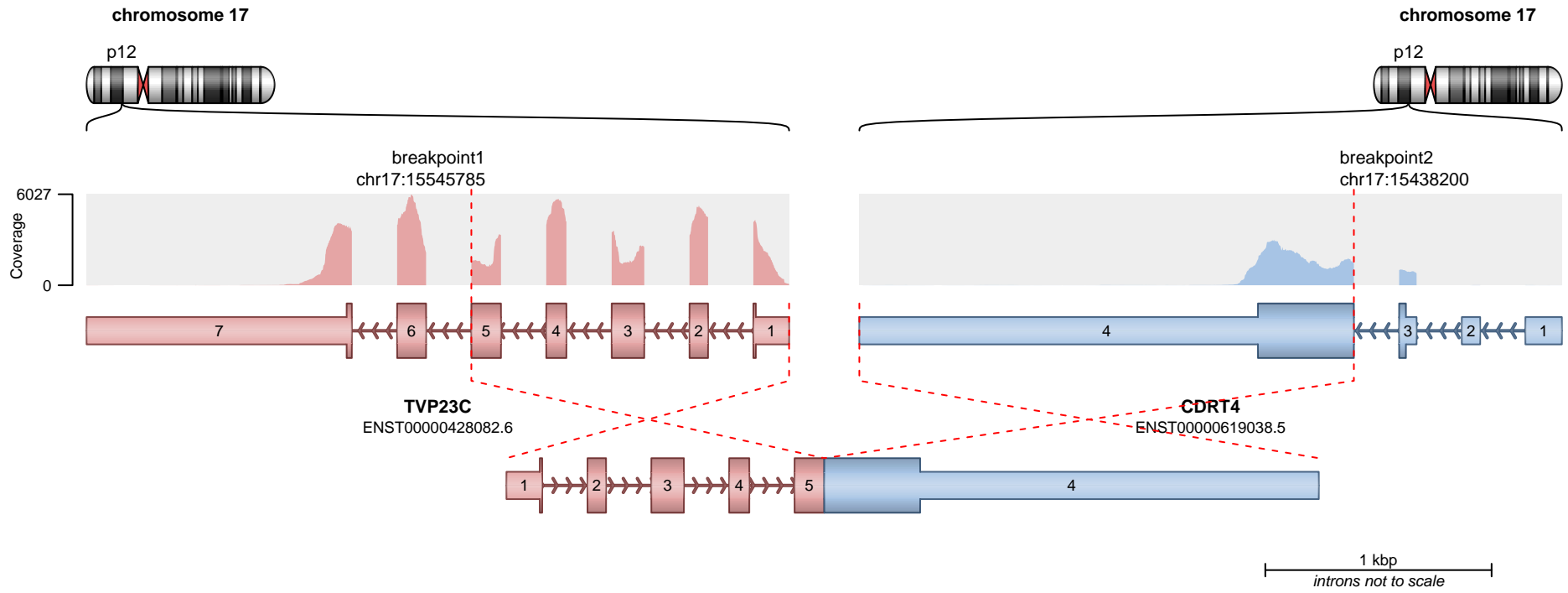
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 5  
Discordant mates = 0

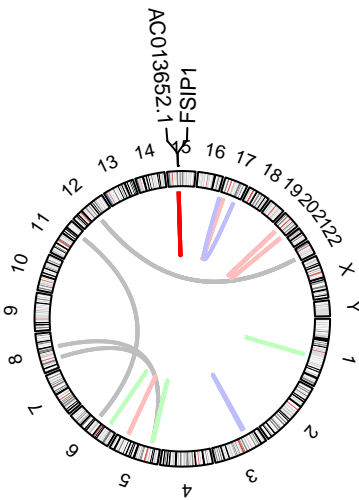
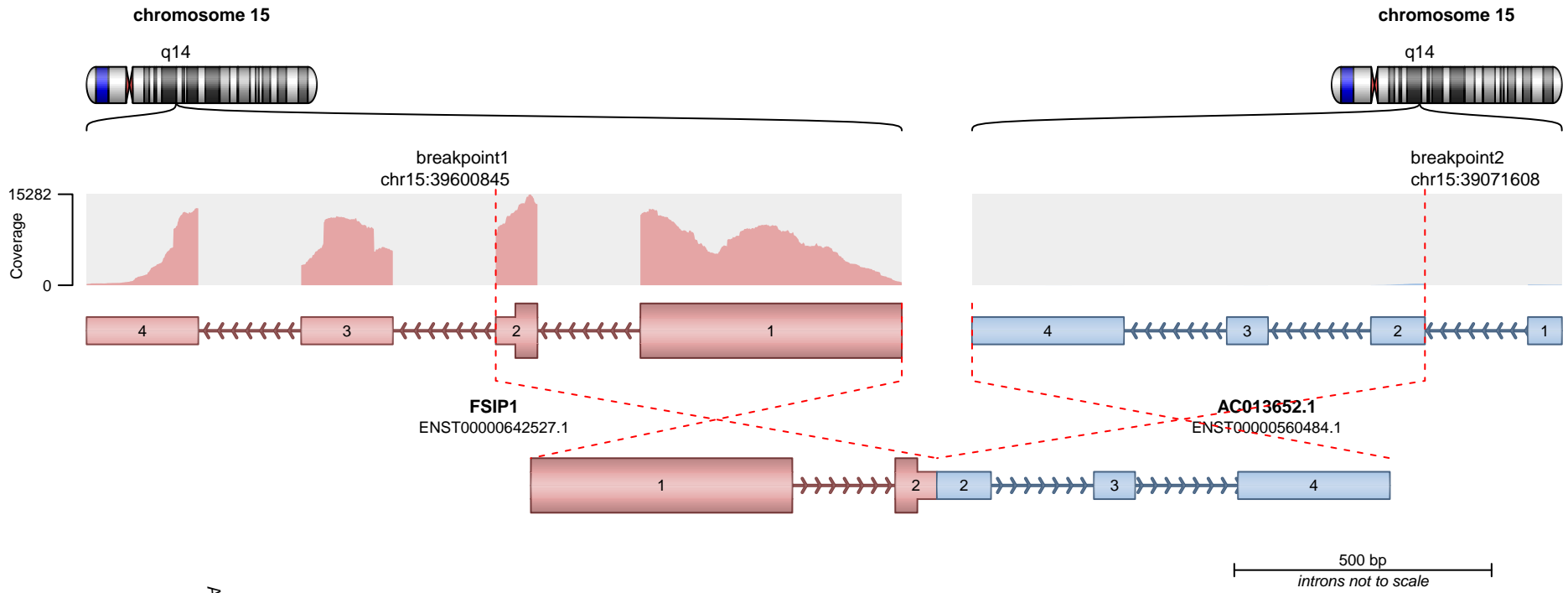
- translocation
- duplication
- deletion
- inversion



**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion

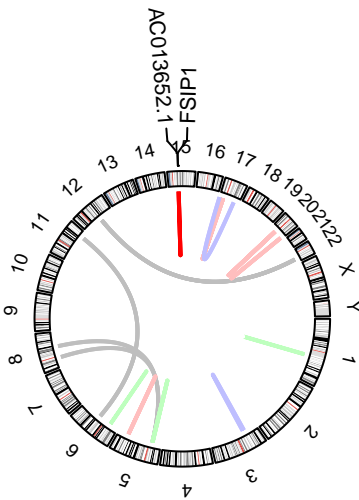
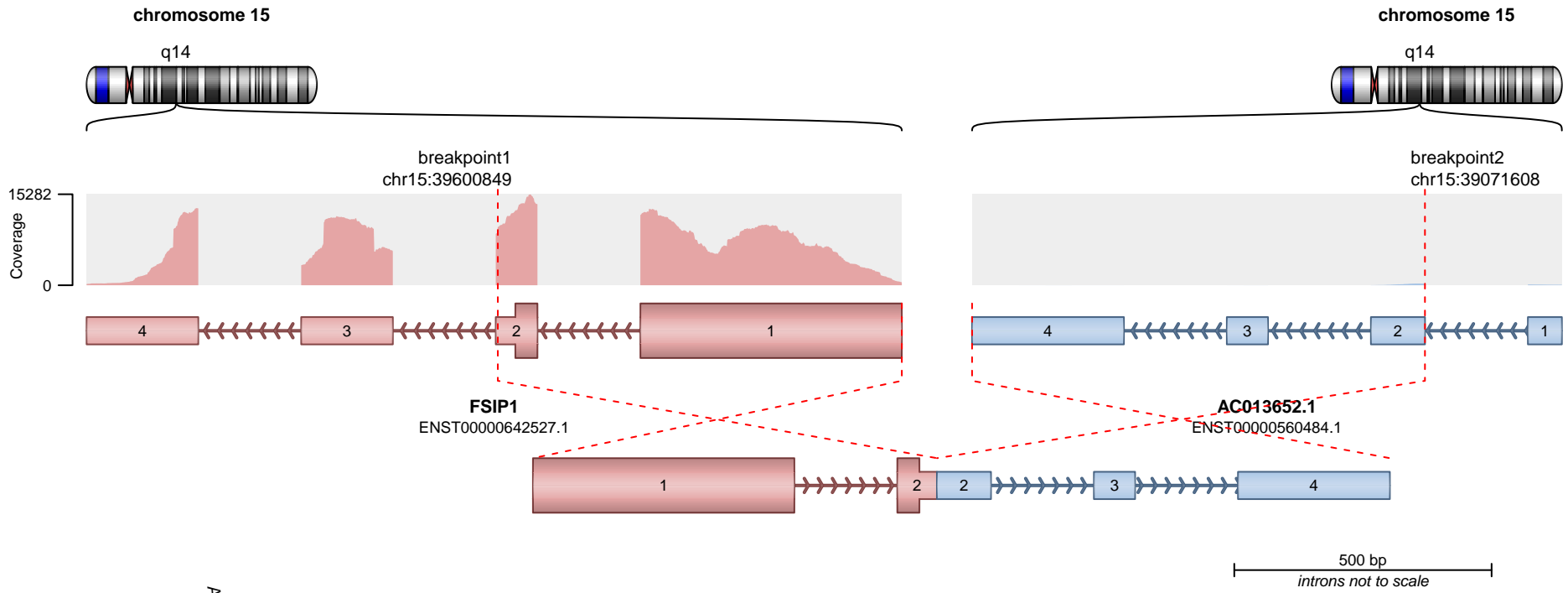


— translocation    — deletion  
— duplication    — inversion

No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 109  
Discordant mates = 1

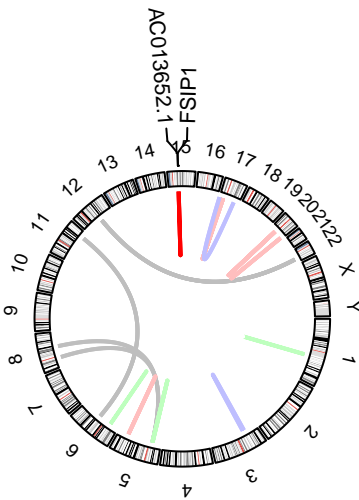
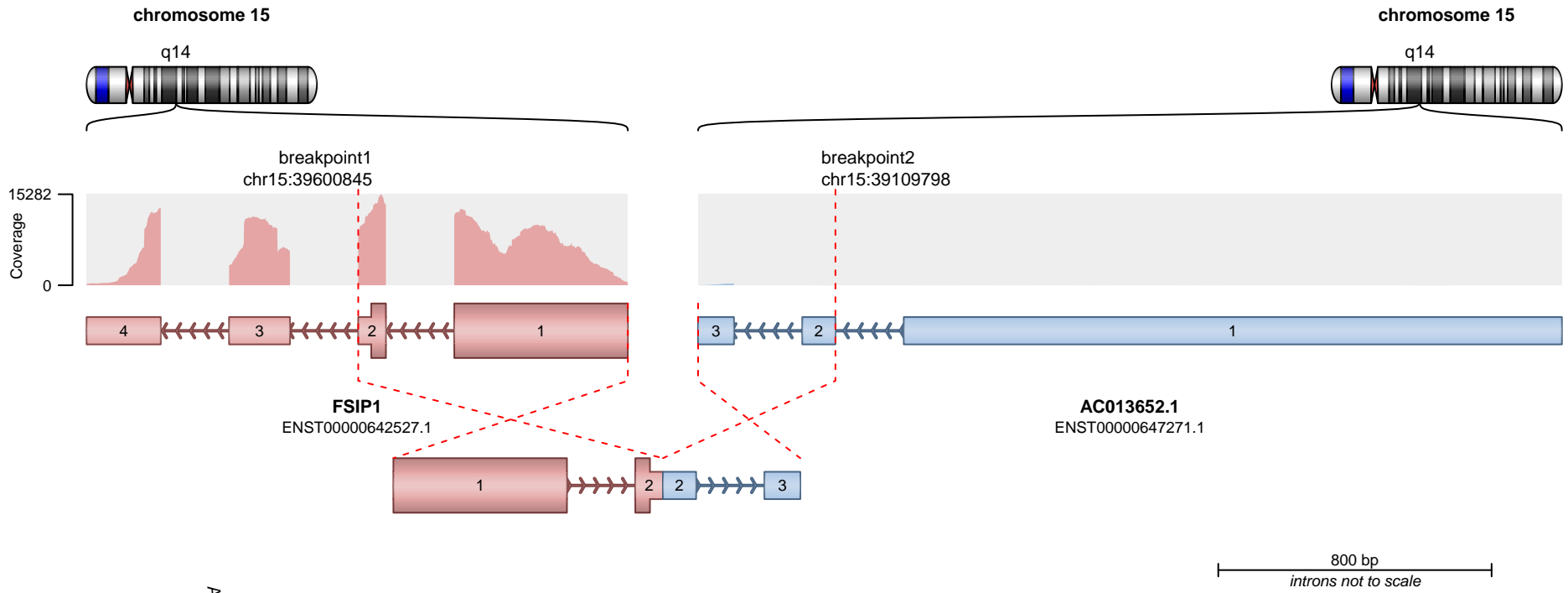


No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 15  
Discordant mates = 1

— translocation    — deletion  
— duplication    — inversion

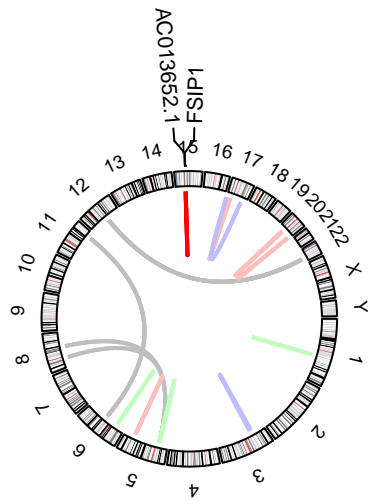
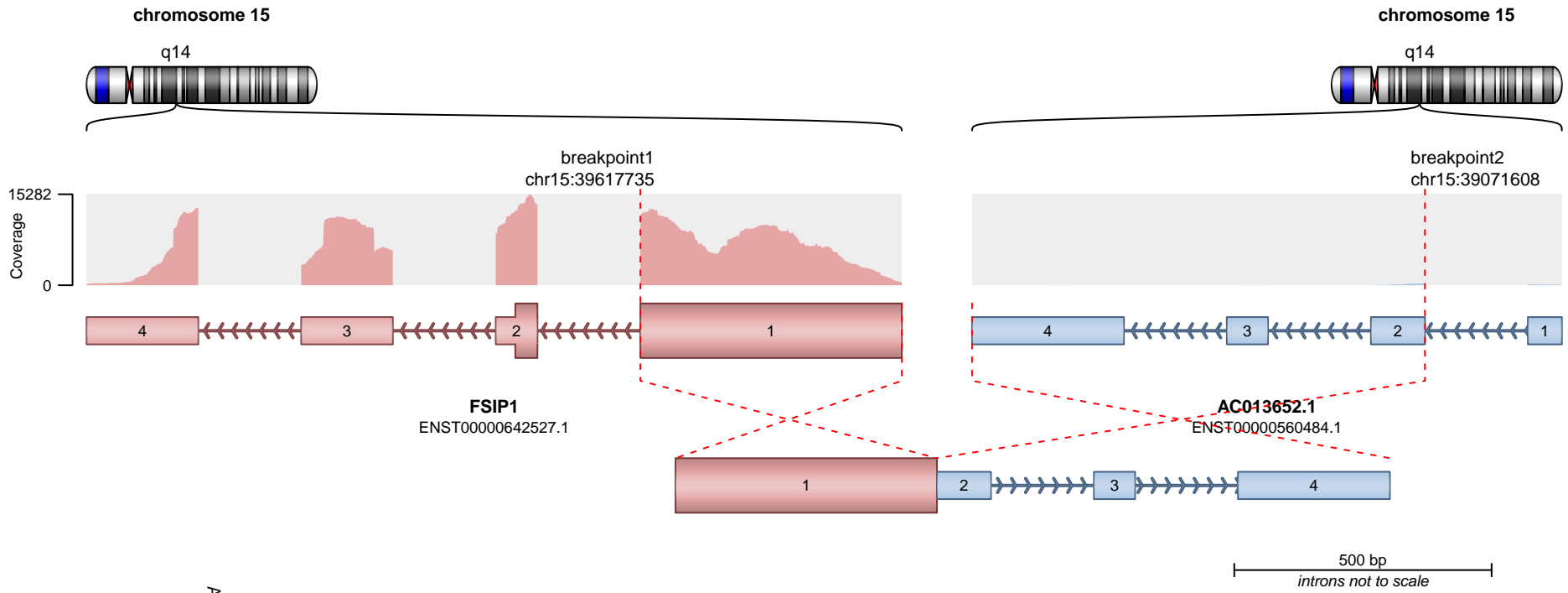


— translocation    — deletion  
— duplication    — inversion

No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 6  
Discordant mates = 1

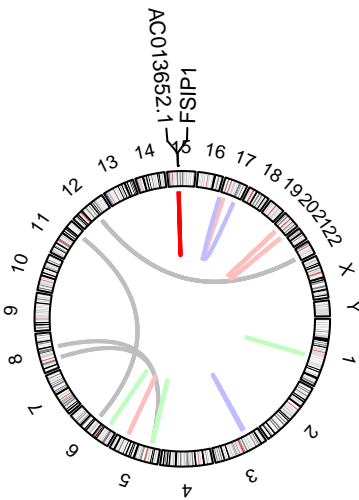
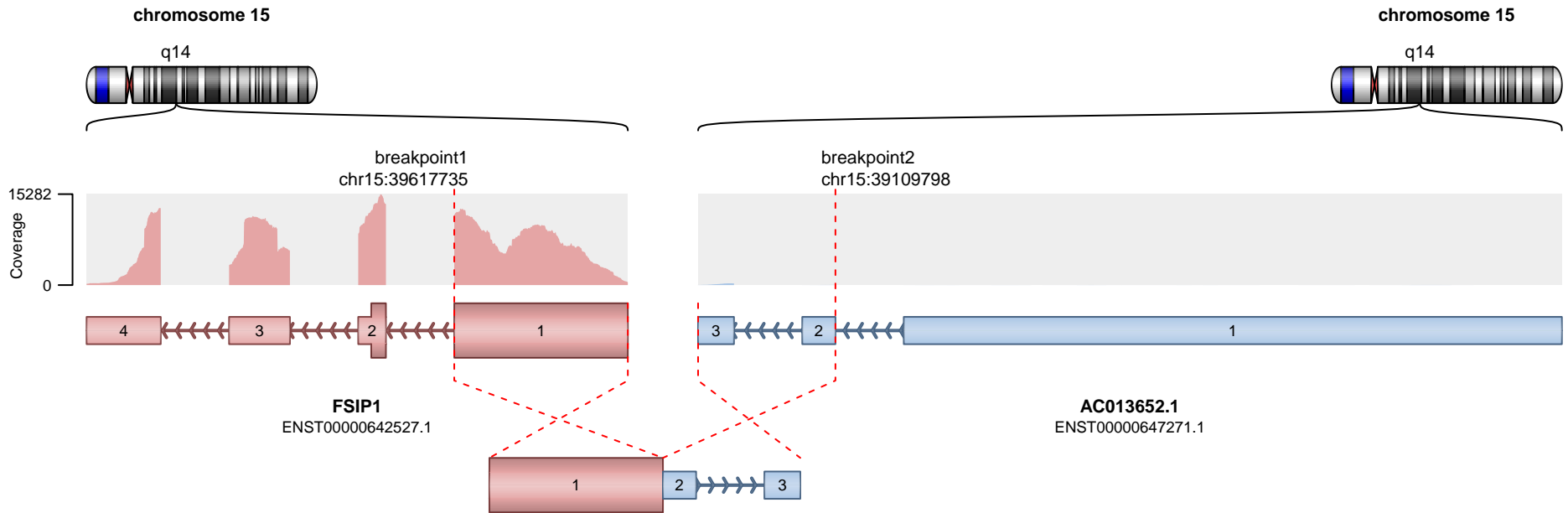


— translocation — deletion  
— duplication — inversion

No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 5  
Discordant mates = 0

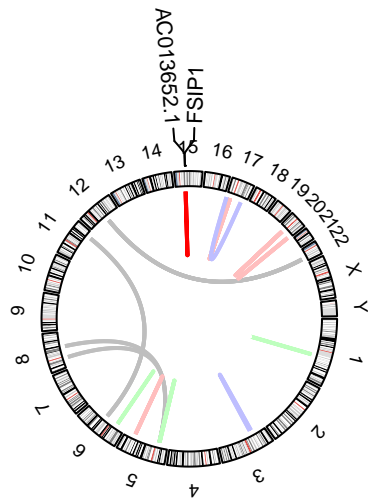
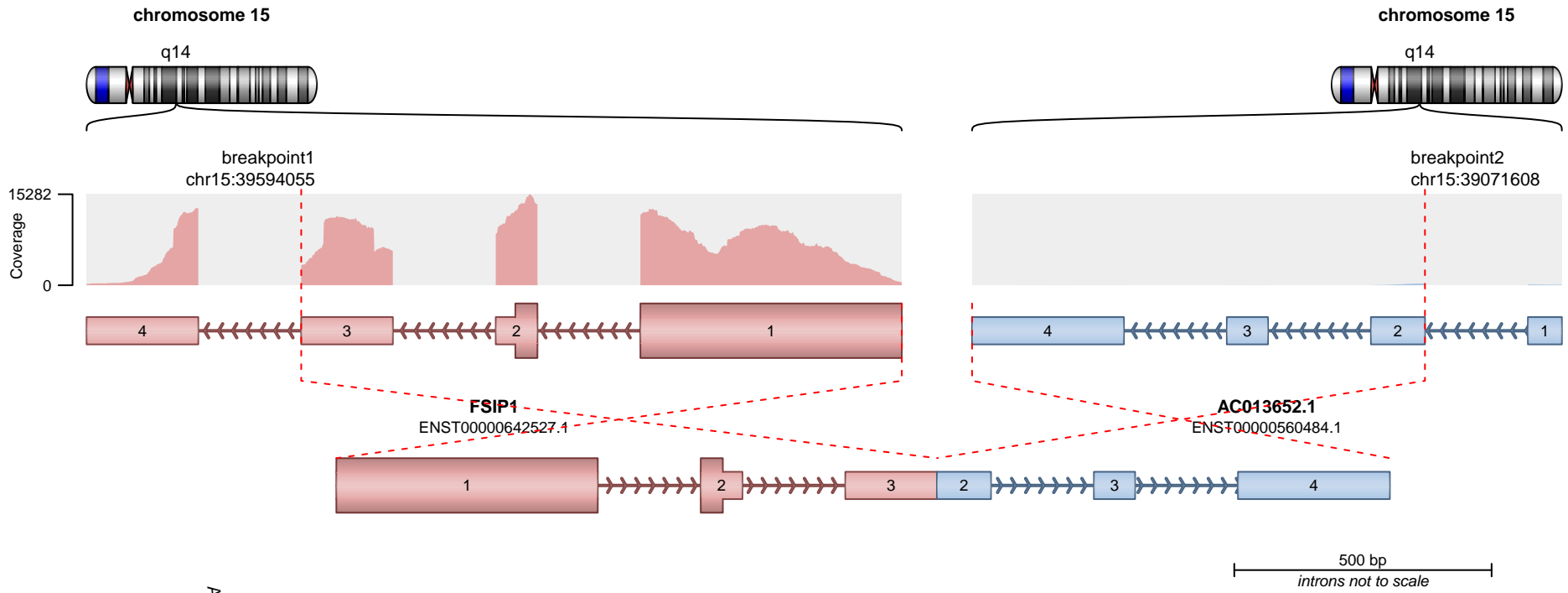


— translocation    — deletion  
— duplication    — inversion

No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 0

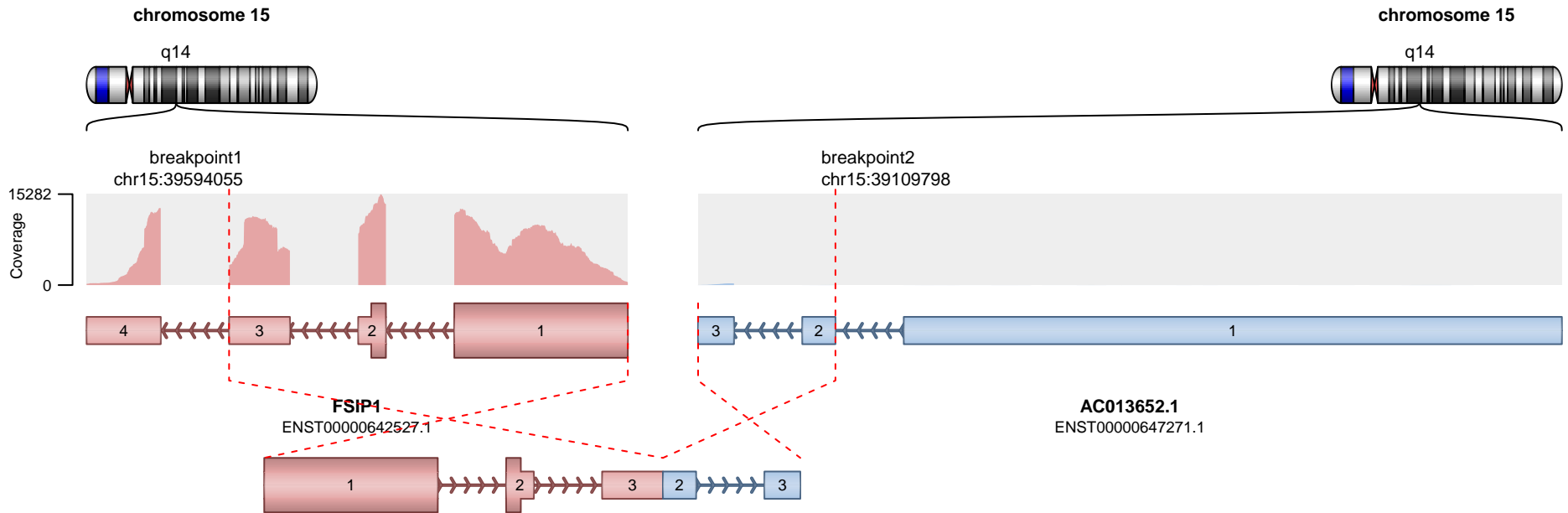


— translocation    — deletion  
— duplication    — inversion

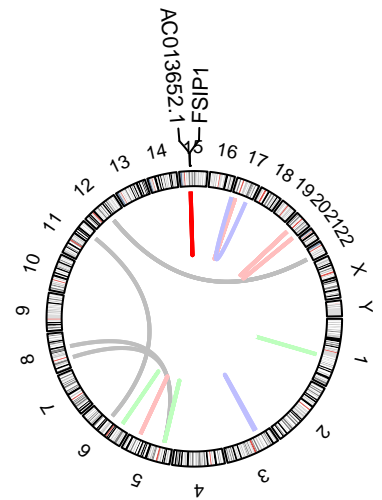
No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 1



800 bp  
*introns not to scale*

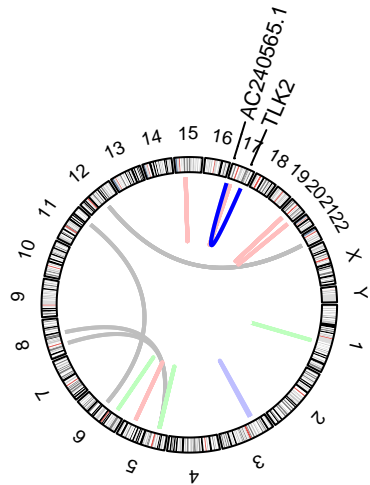
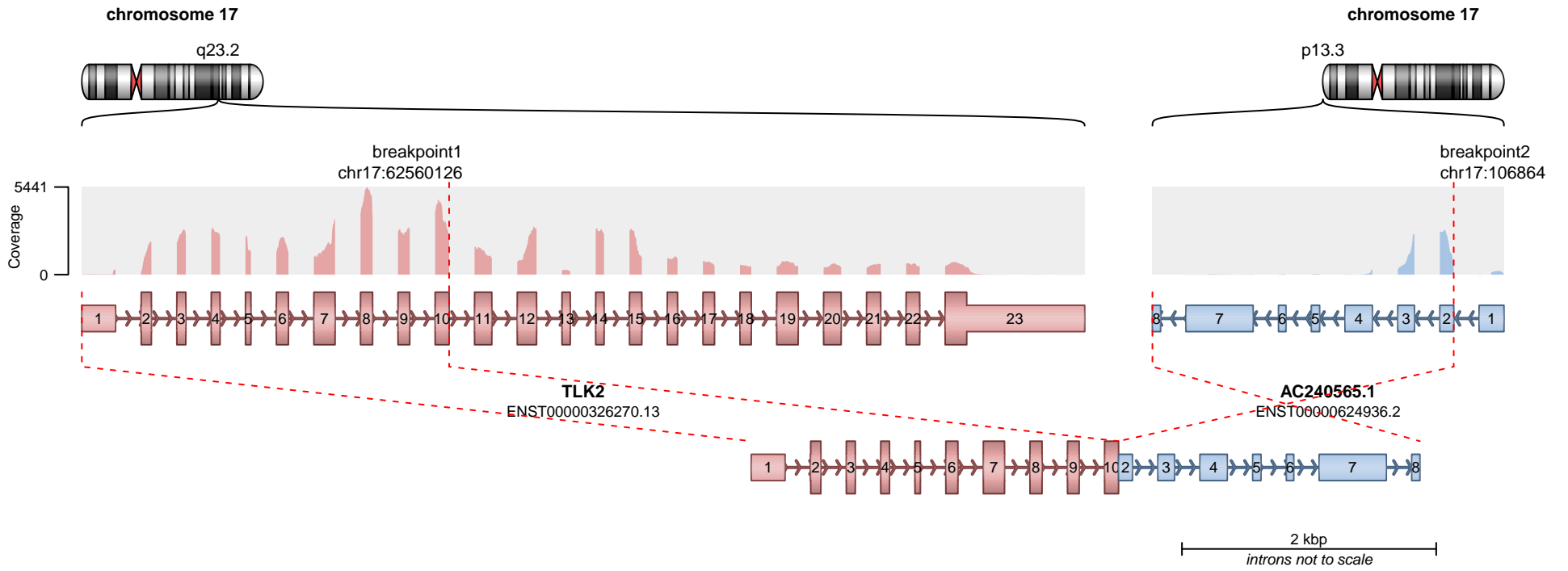


— translocation    — deletion  
— duplication    — inversion

No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 1

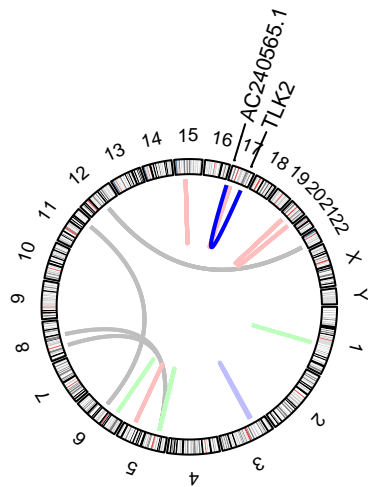
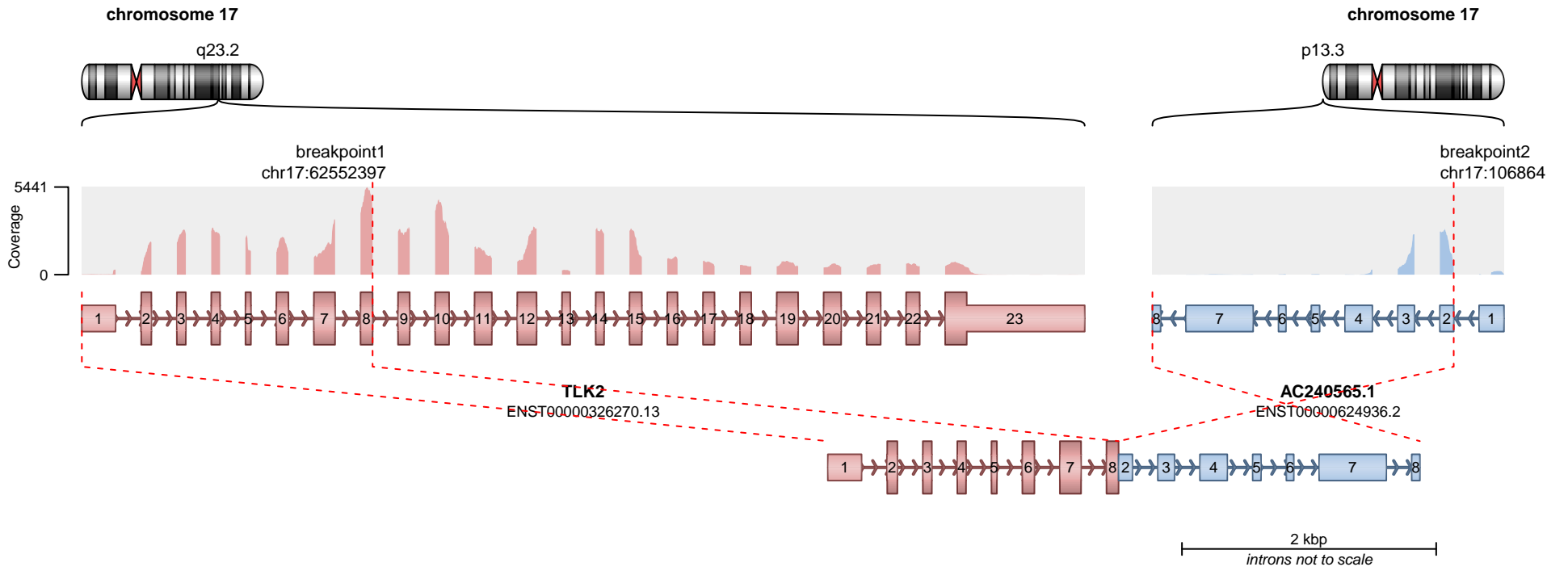


— translocation    — deletion  
— duplication    — inversion

No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 94  
Discordant mates = 0

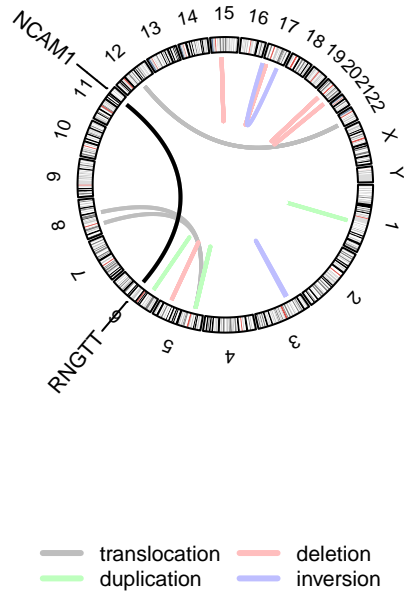
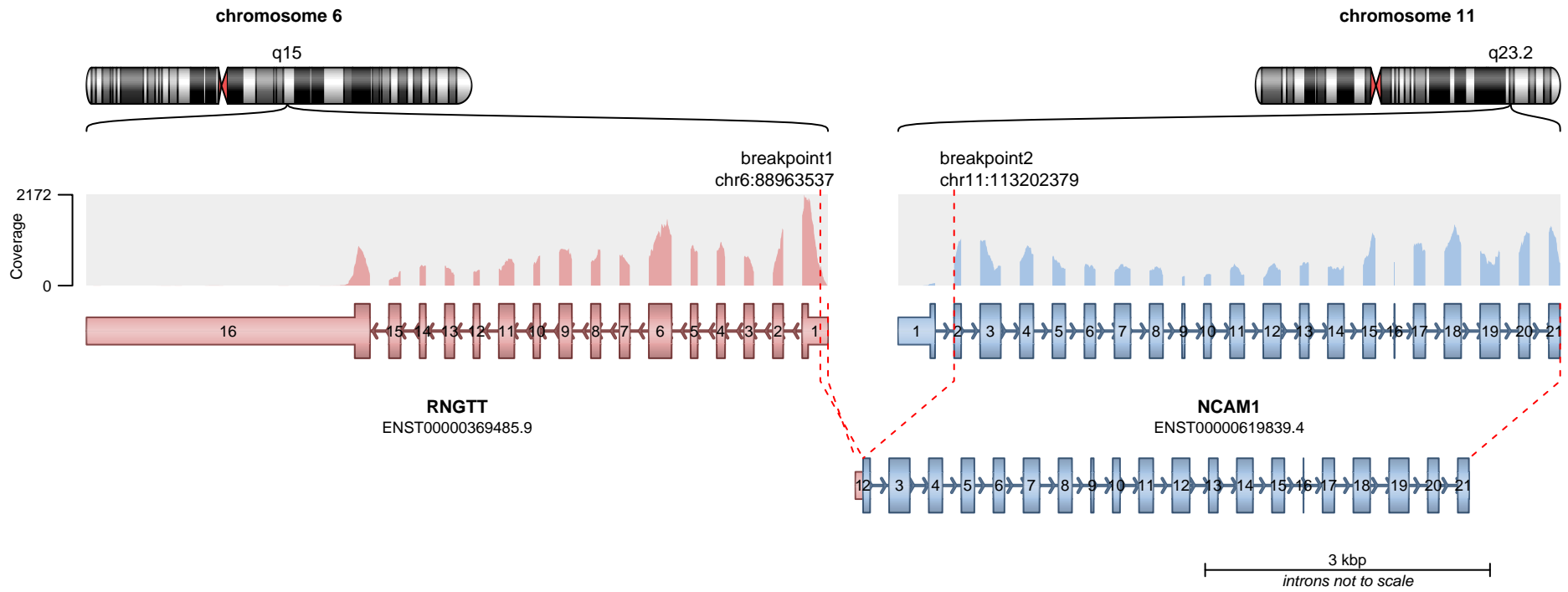


— translocation    — deletion  
— duplication    — inversion

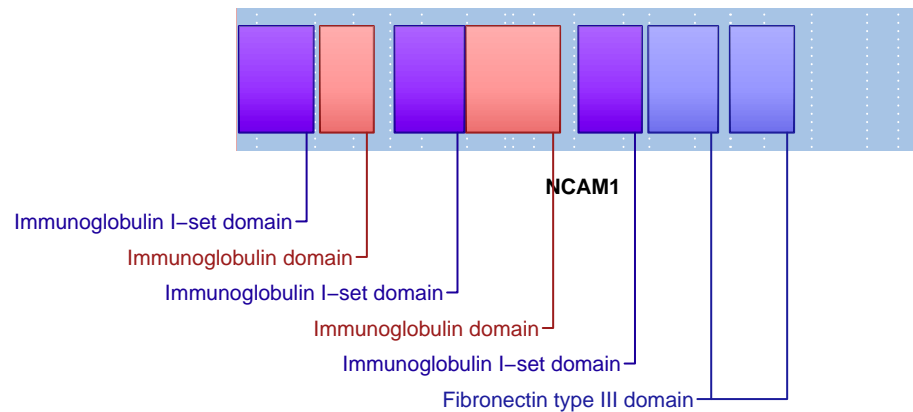
No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 0

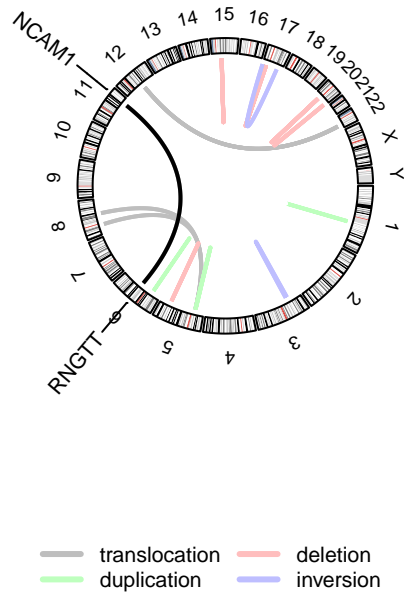
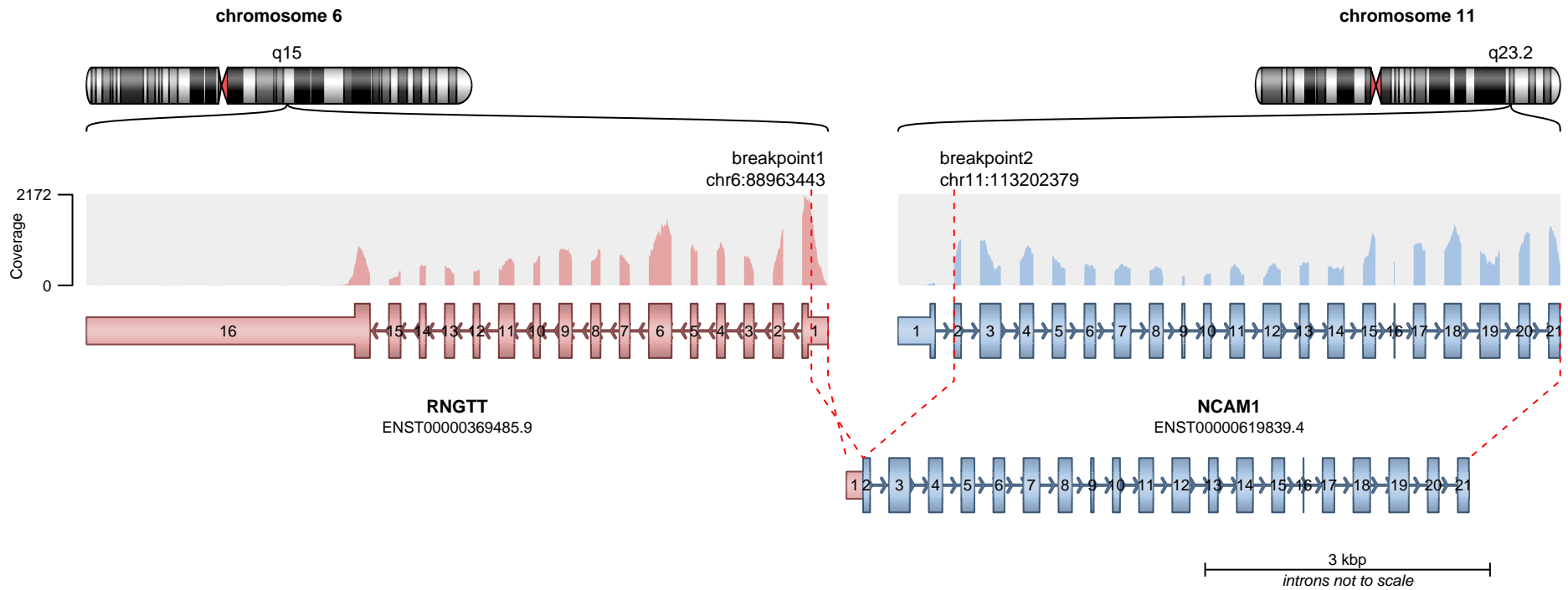


**RETAINED PROTEIN DOMAINS**  
reading frame unclear

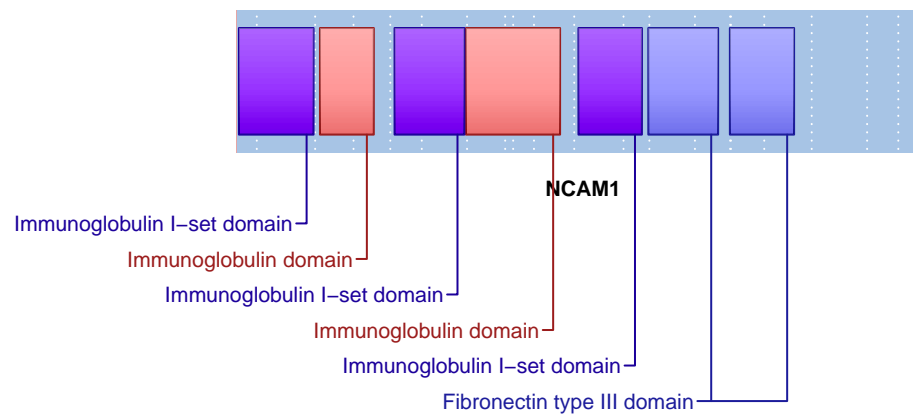


**SUPPORTING READ COUNT**

Split reads = 53  
Discordant mates = 0

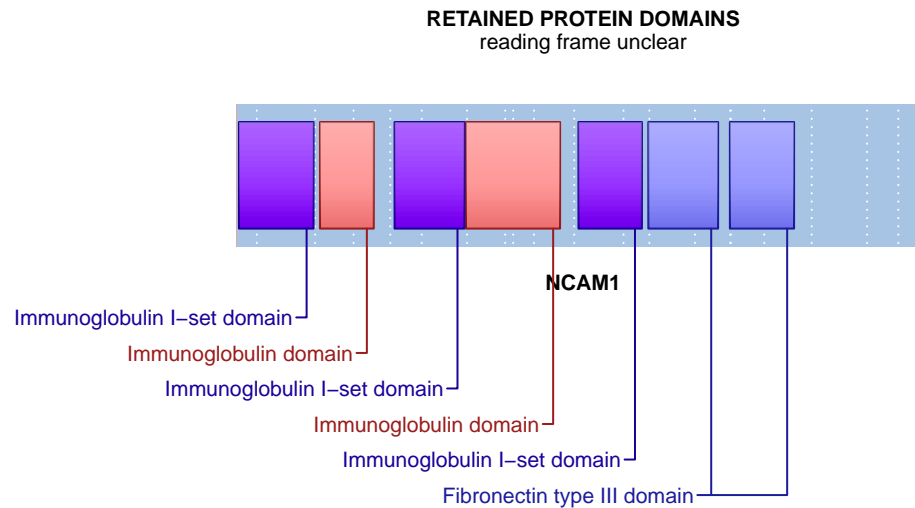
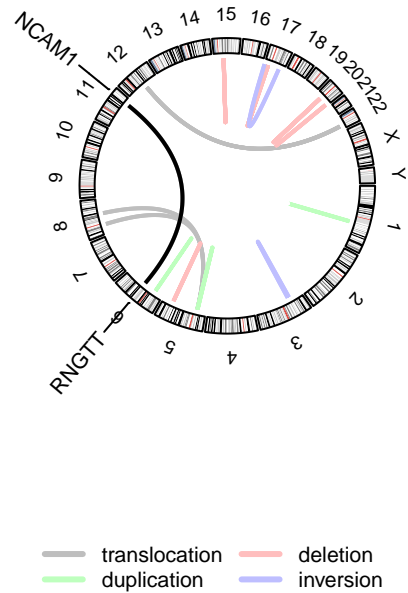
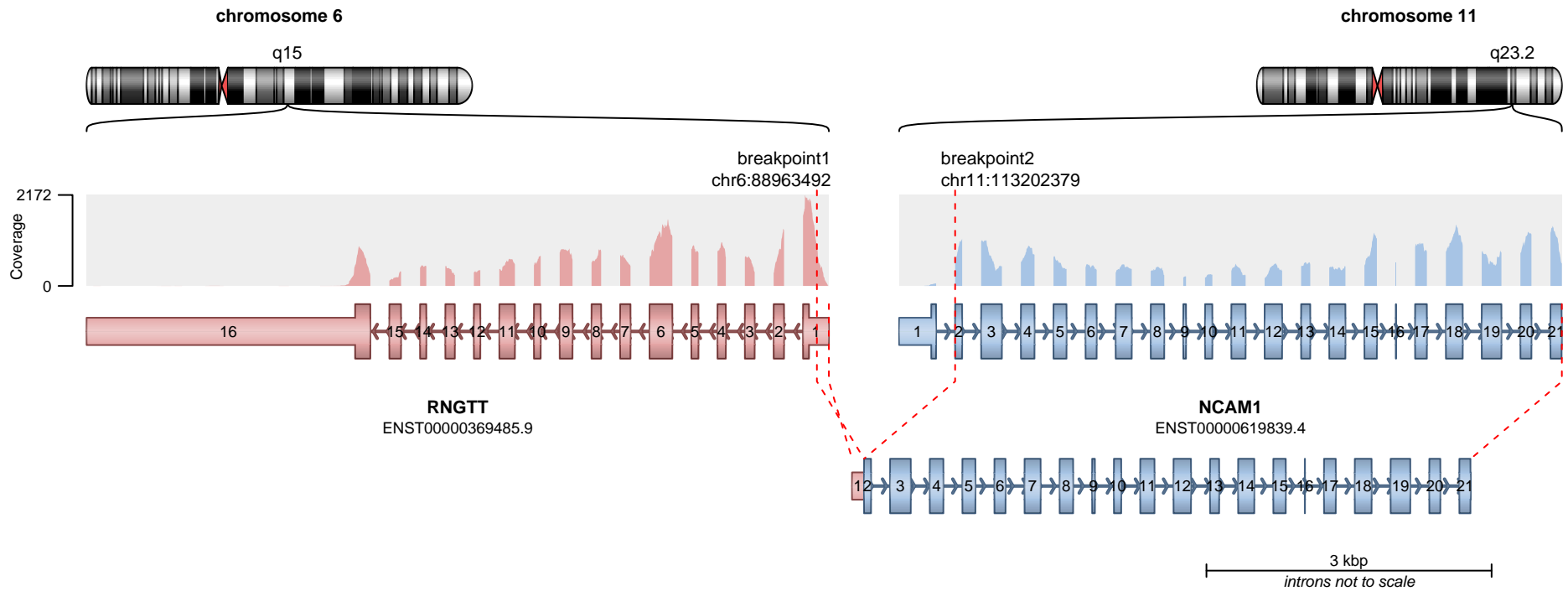


**RETAINED PROTEIN DOMAINS**  
reading frame unclear

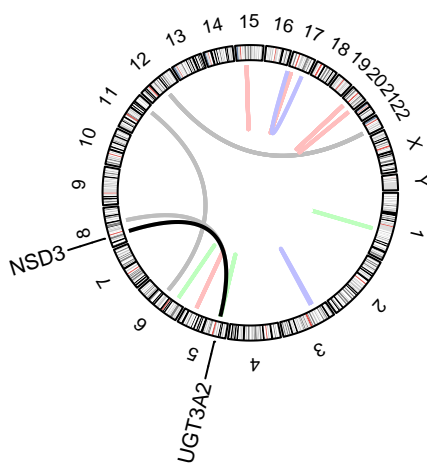
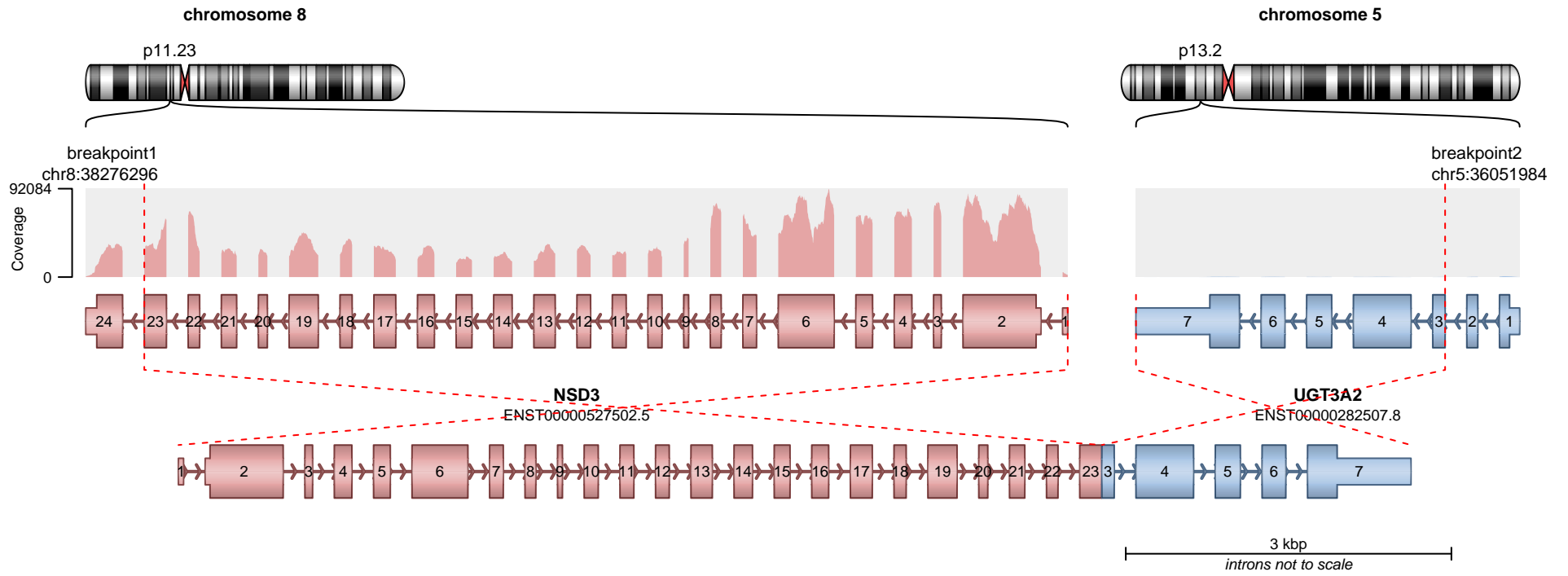


**SUPPORTING READ COUNT**

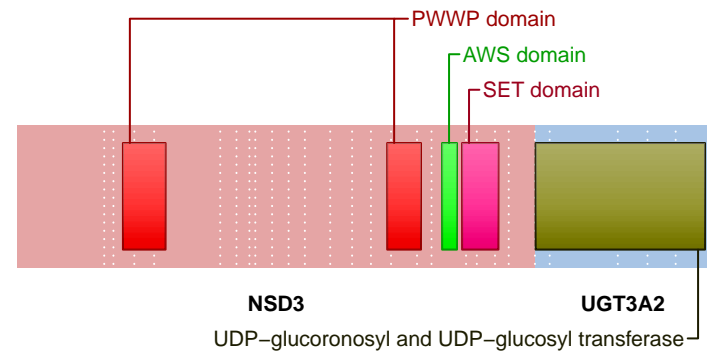
Split reads = 49  
Discordant mates = 0



**SUPPORTING READ COUNT**  
Split reads = 14  
Discordant mates = 0



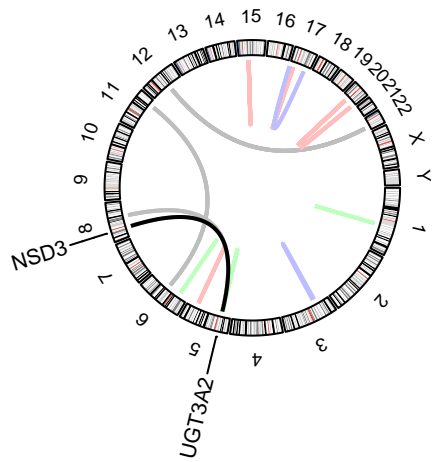
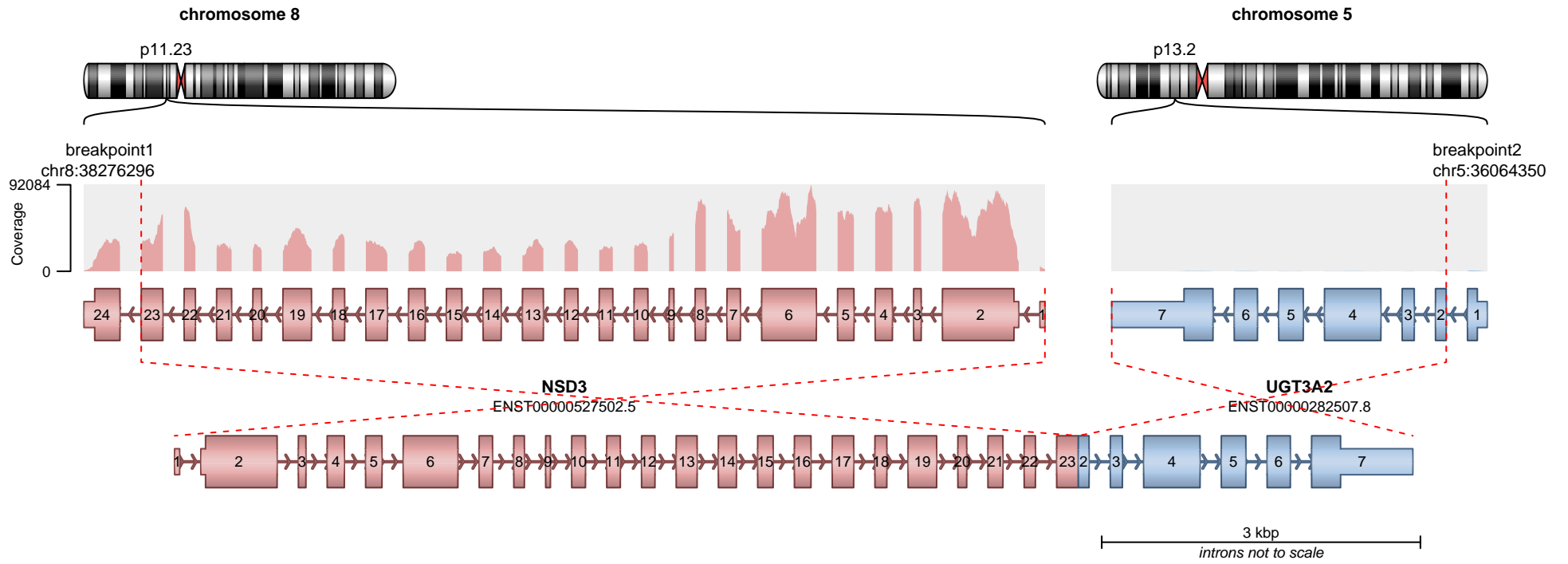
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



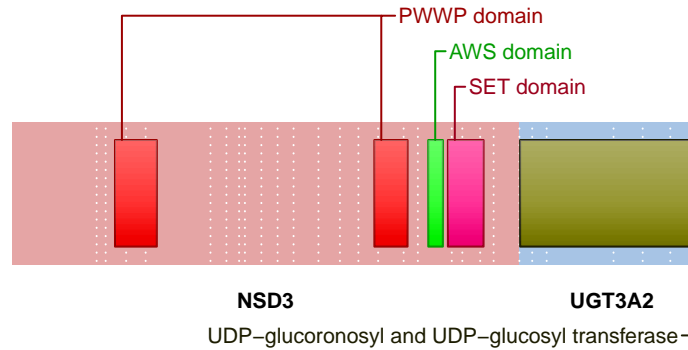
**SUPPORTING READ COUNT**

Split reads = 44  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



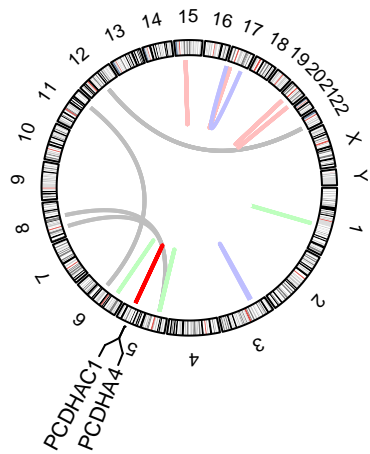
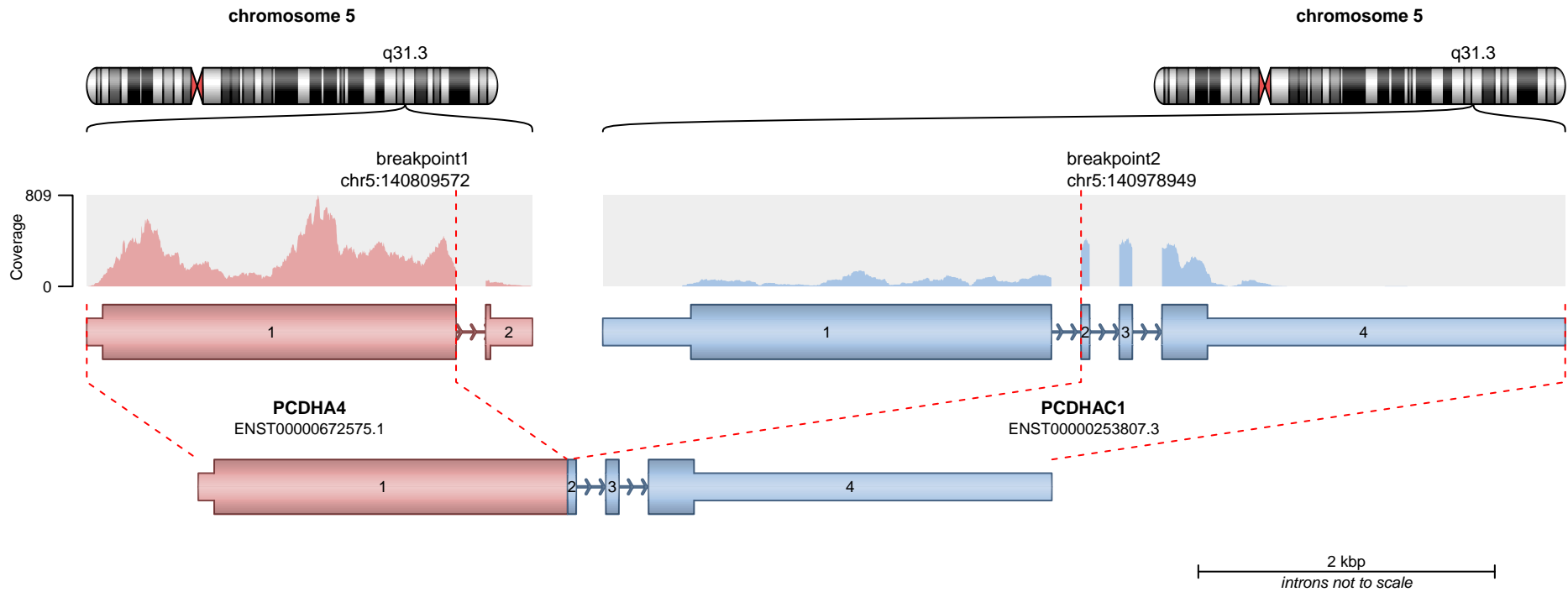
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



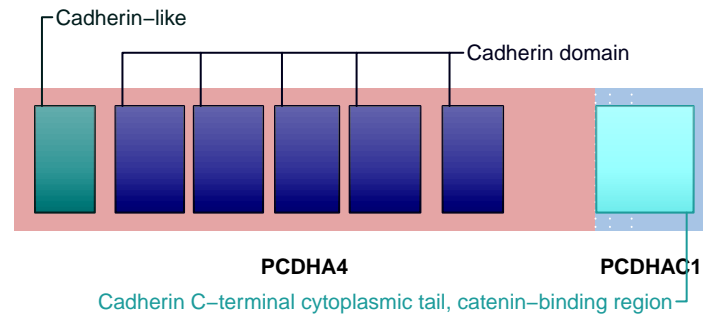
**SUPPORTING READ COUNT**

Split reads = 20  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



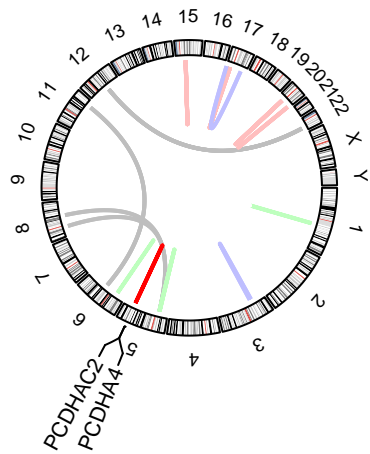
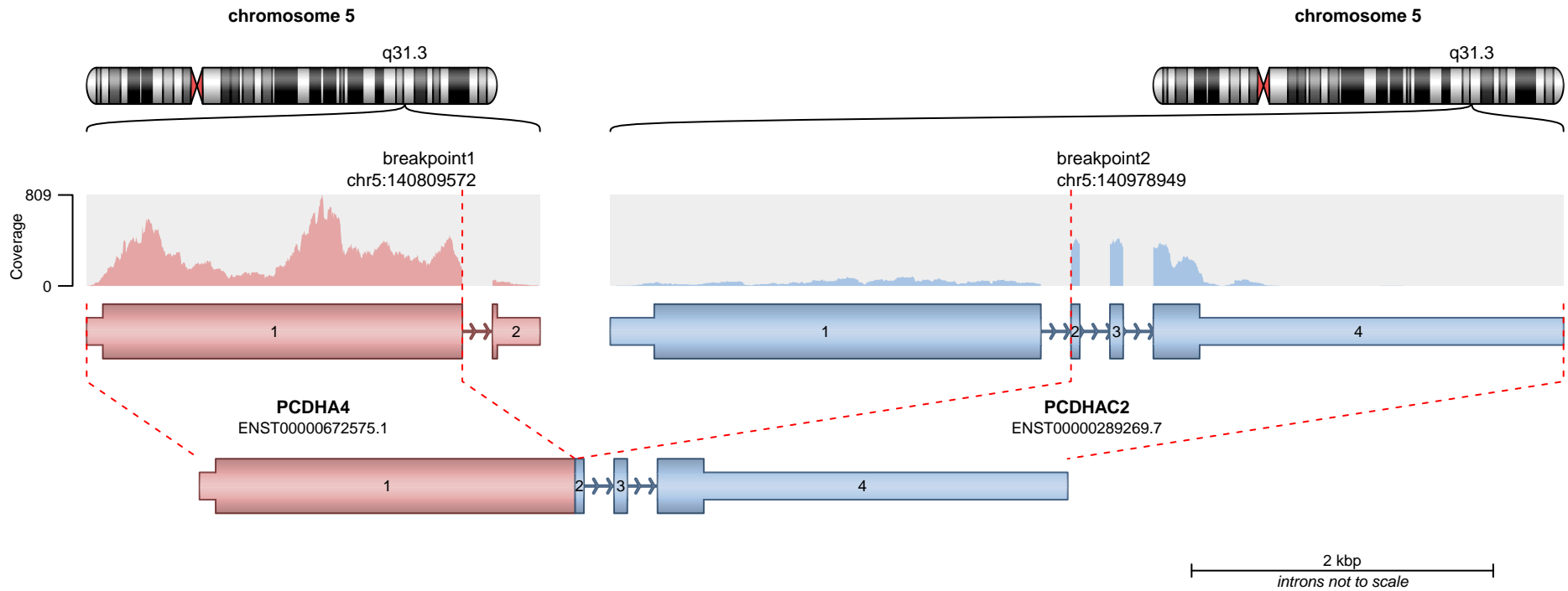
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



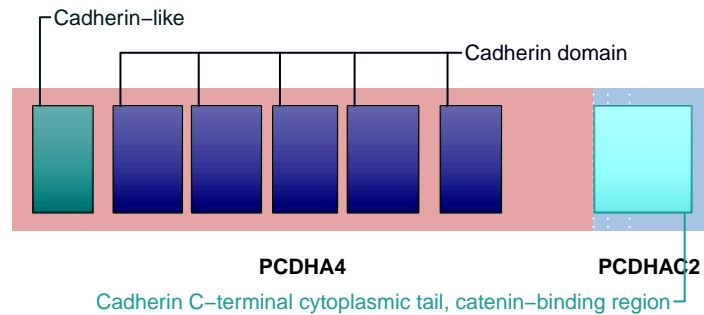
**SUPPORTING READ COUNT**

Split reads = 35  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



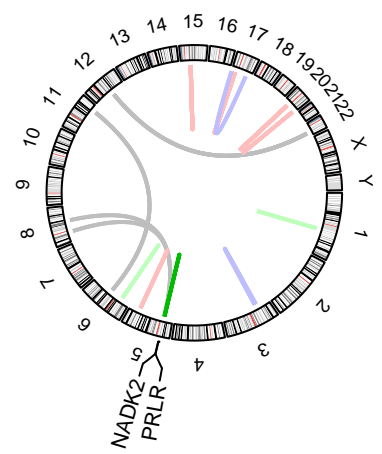
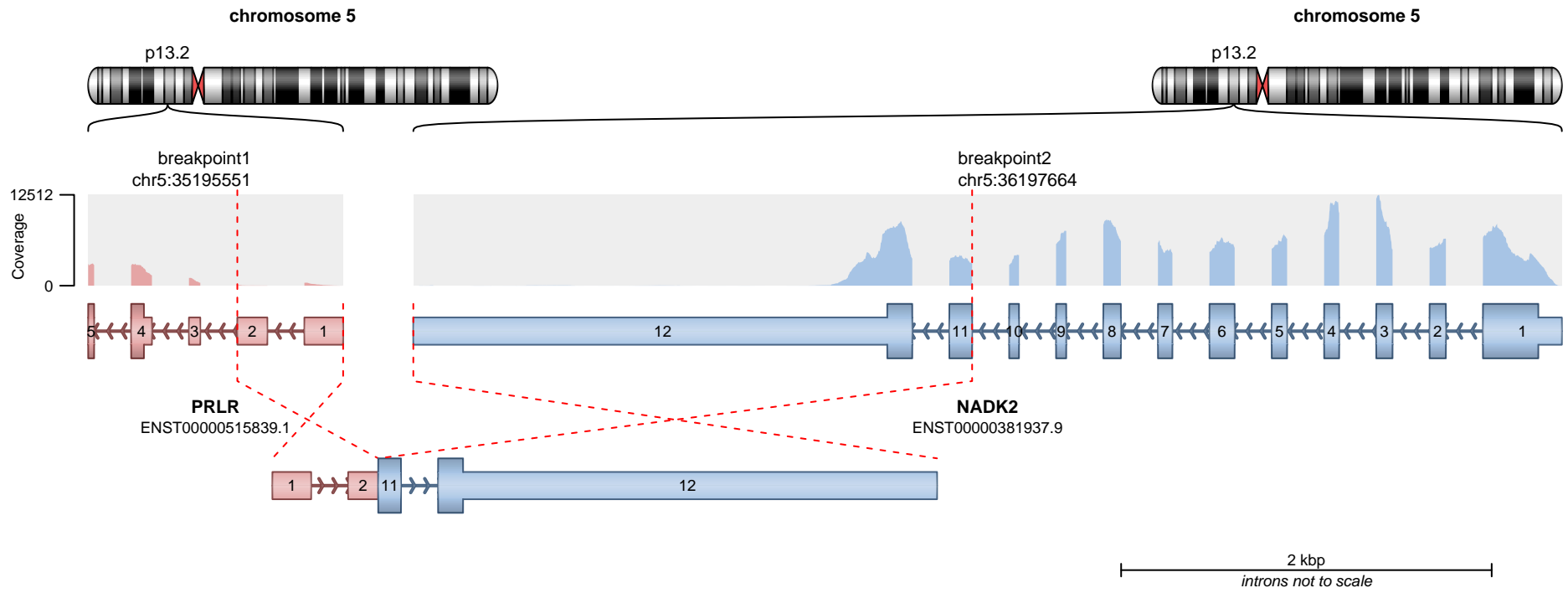
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 35  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion

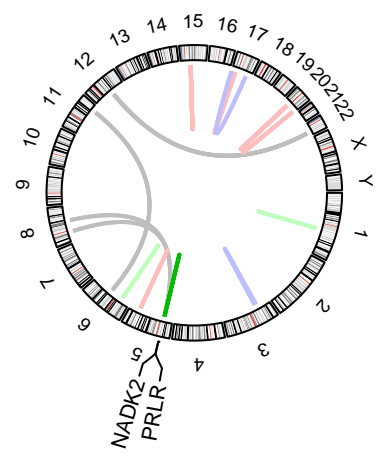
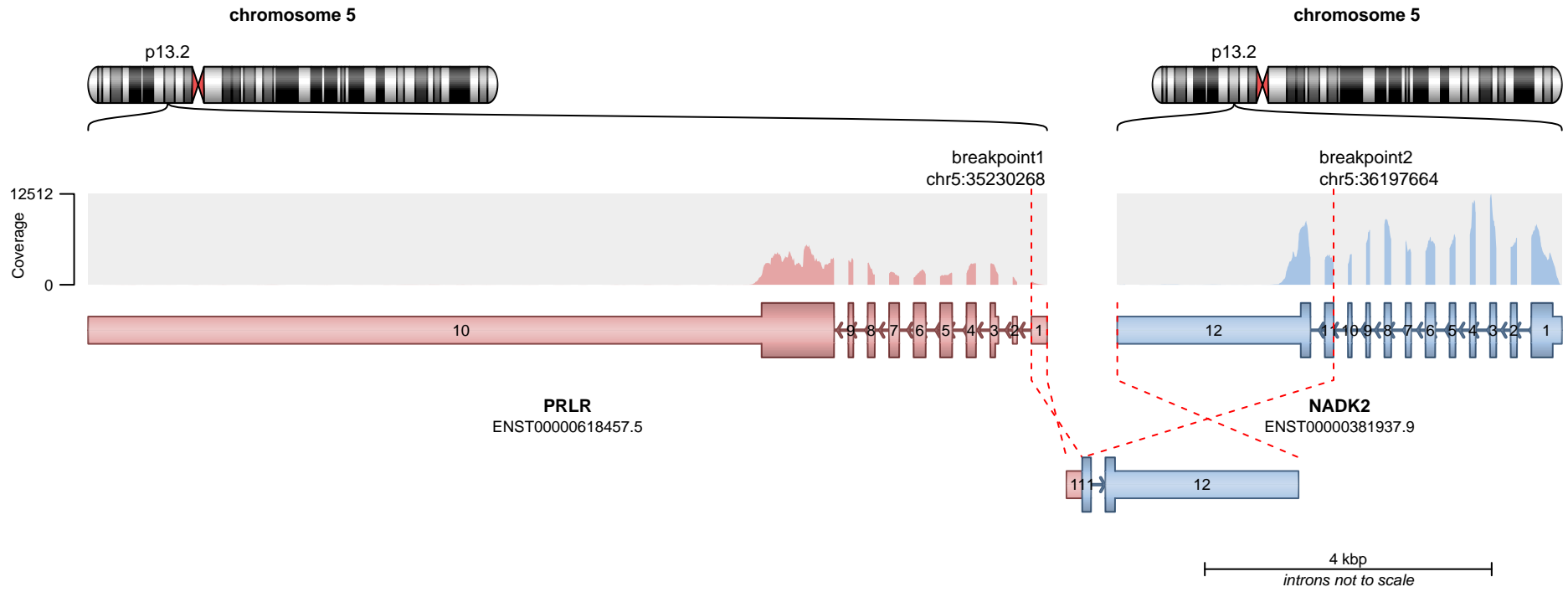


— translocation    — deletion  
 — duplication    — inversion

No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 34  
 Discordant mates = 0

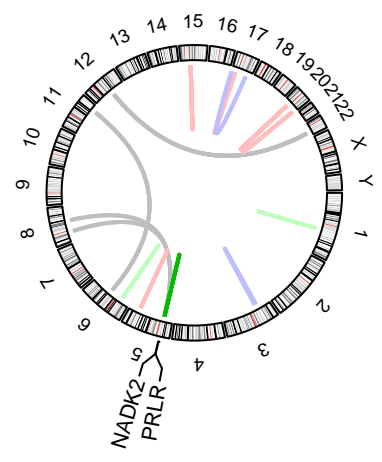
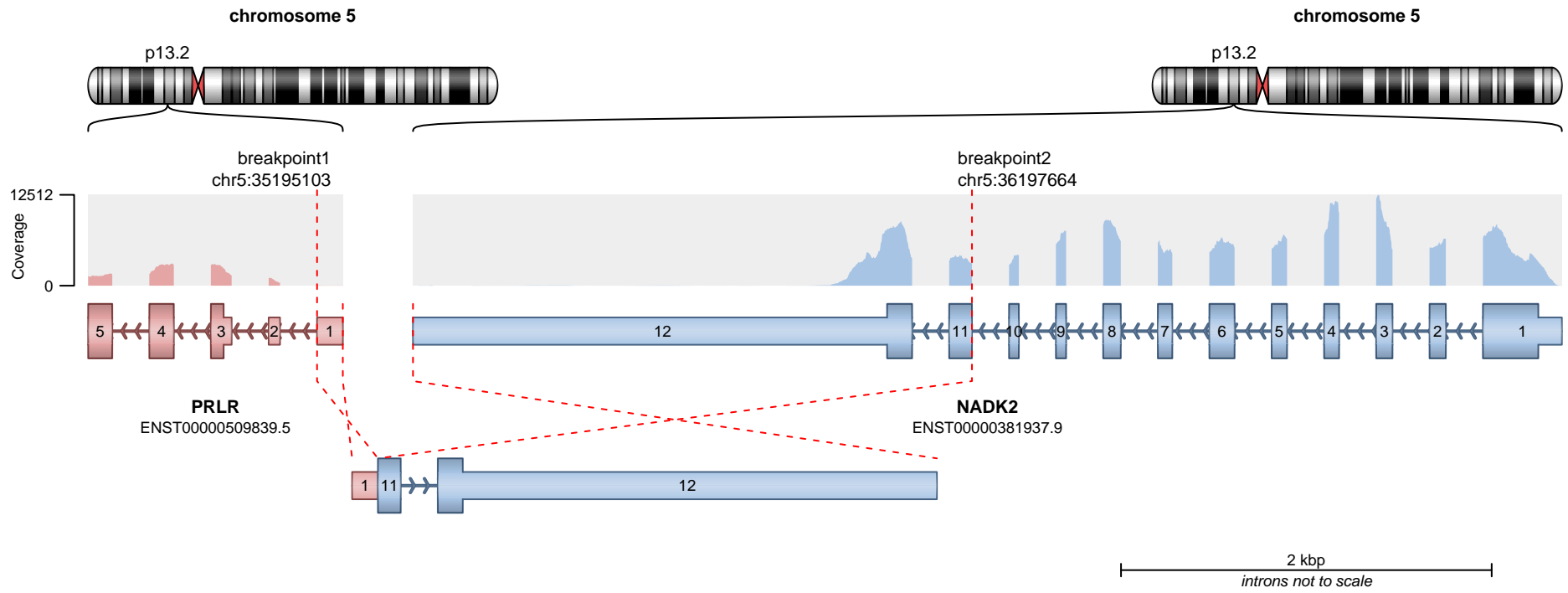


— translocation — deletion  
— duplication — inversion

No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 32  
Discordant mates = 0

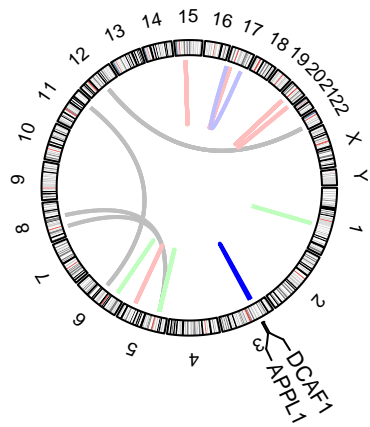
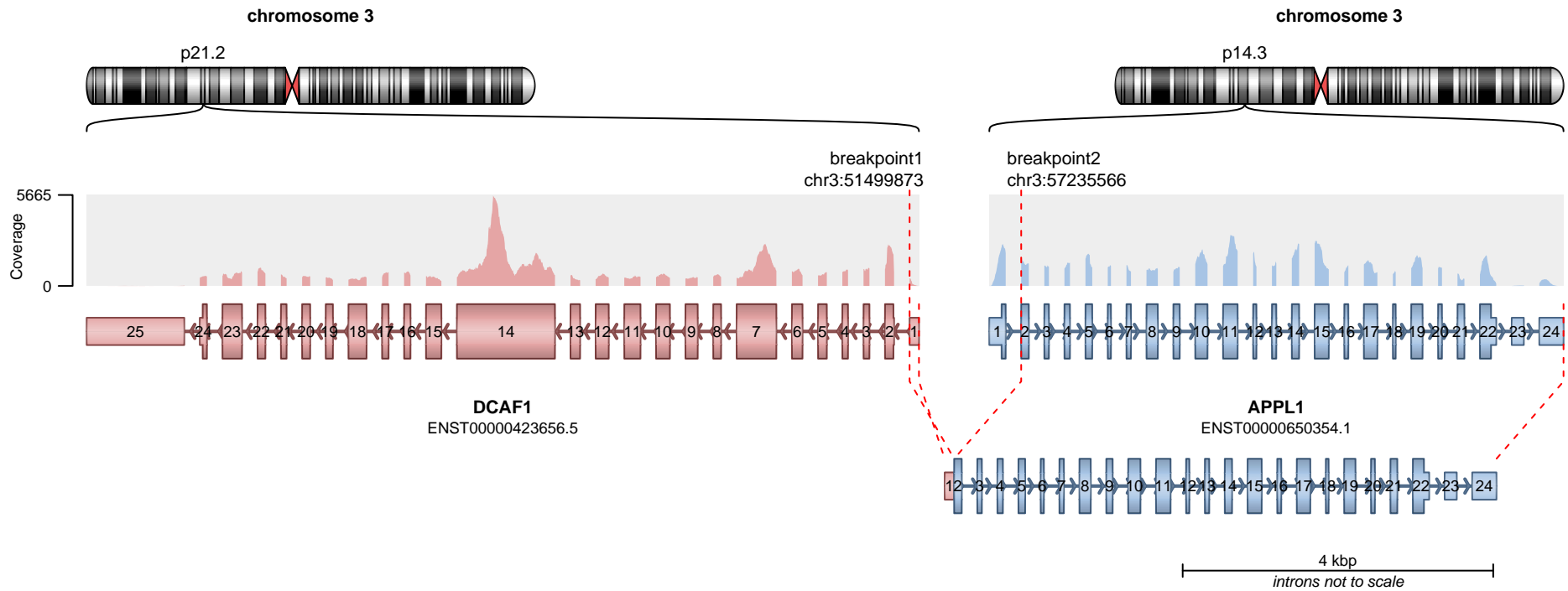


— translocation    — deletion  
— duplication    — inversion

No protein domains retained in fusion.

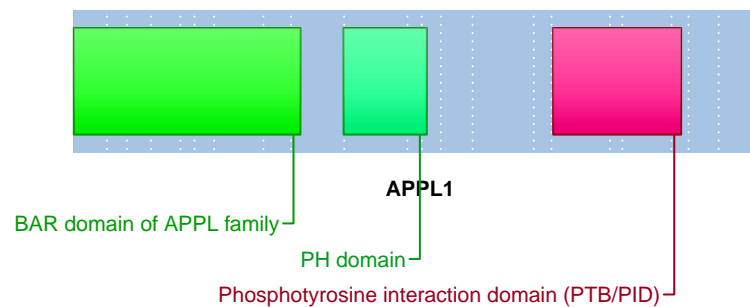
**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0



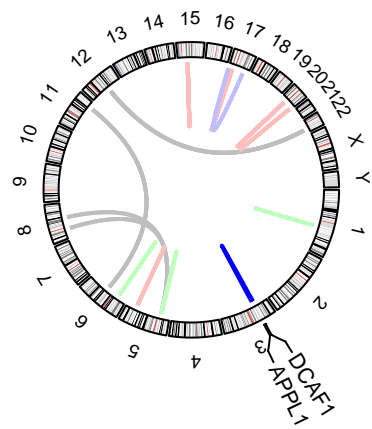
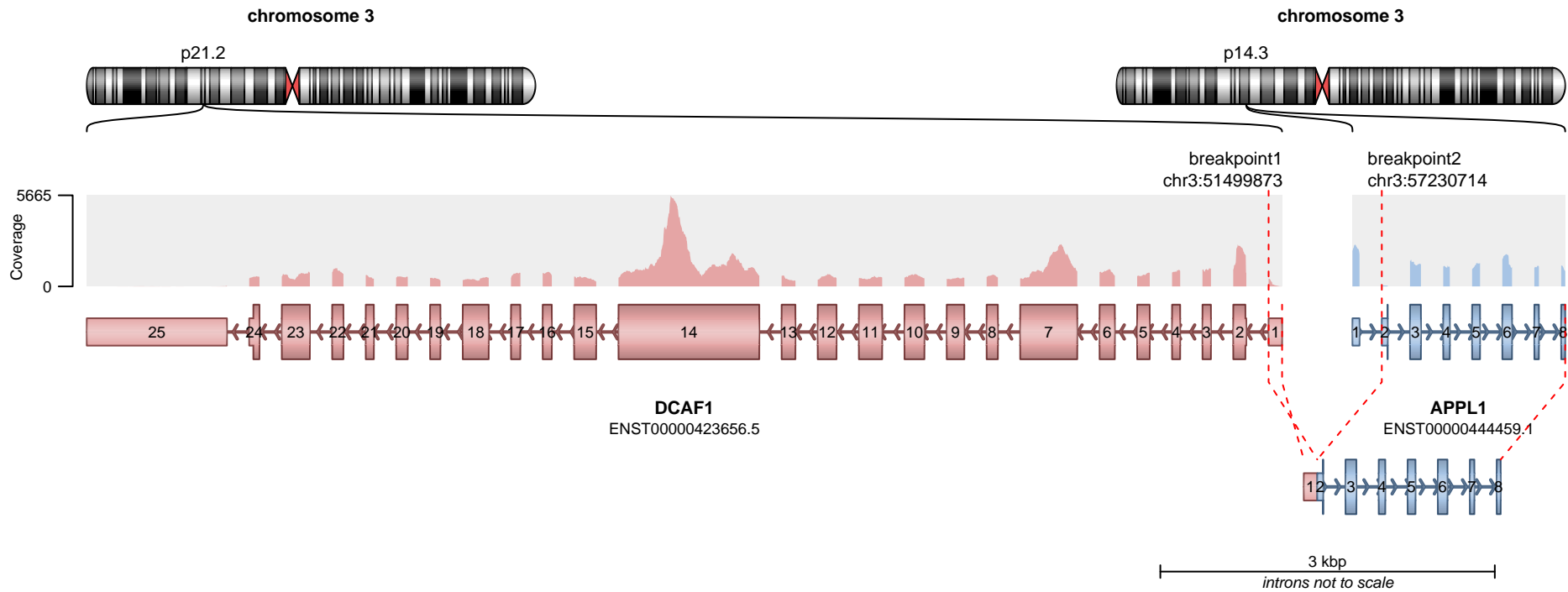
— translocation    — deletion  
— duplication    — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear

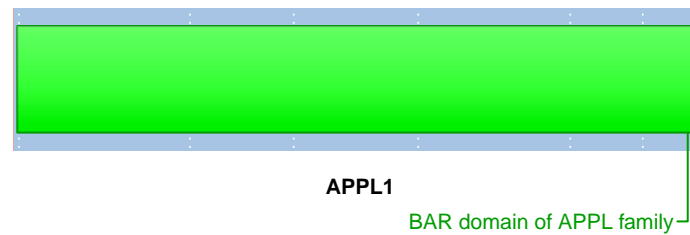


**SUPPORTING READ COUNT**

Split reads = 21  
Discordant mates = 0



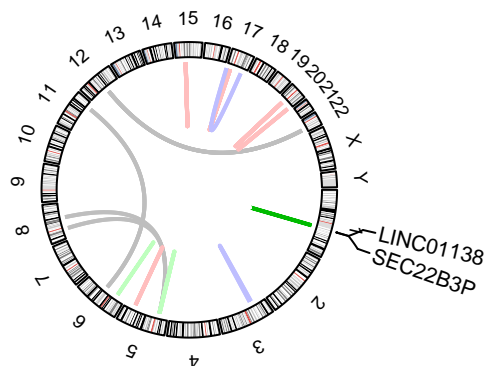
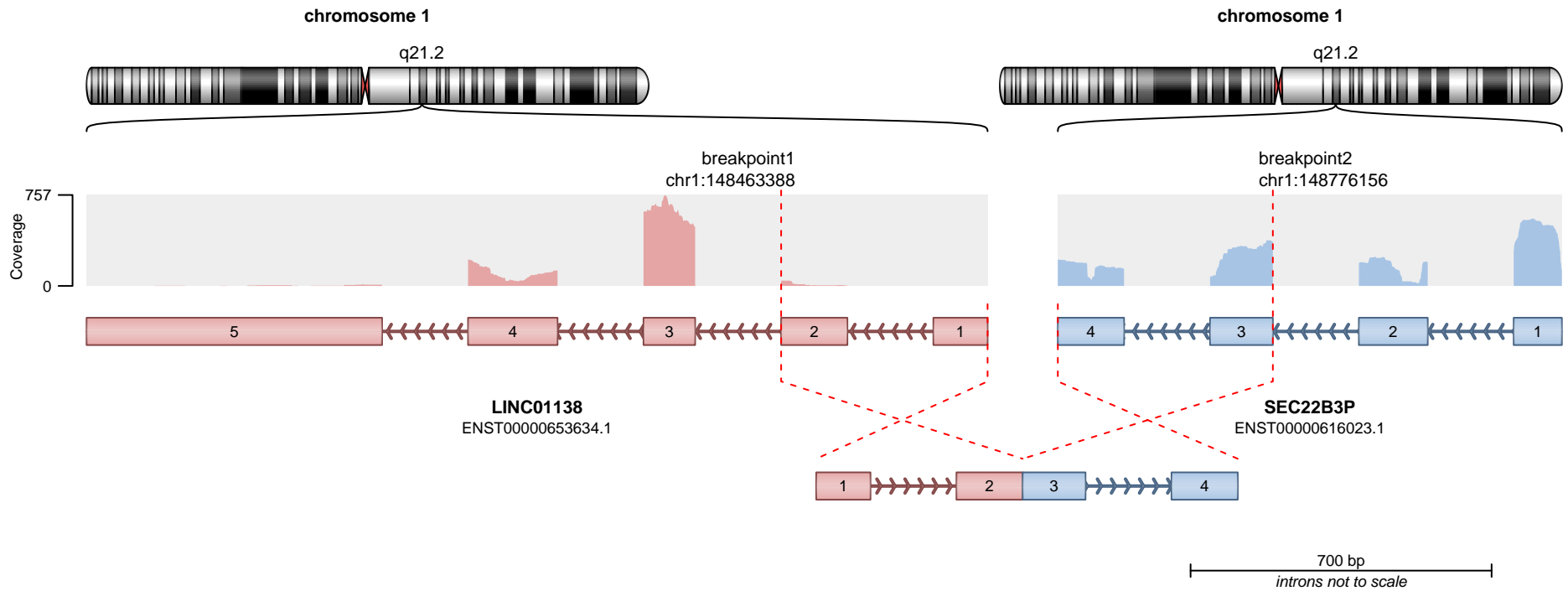
RETAINED PROTEIN DOMAINS  
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion

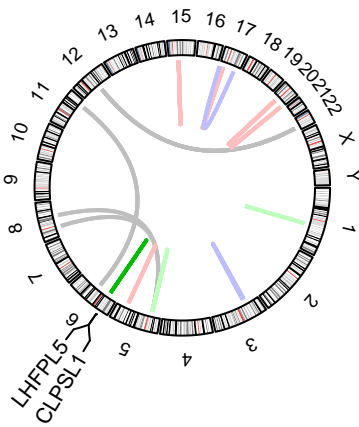
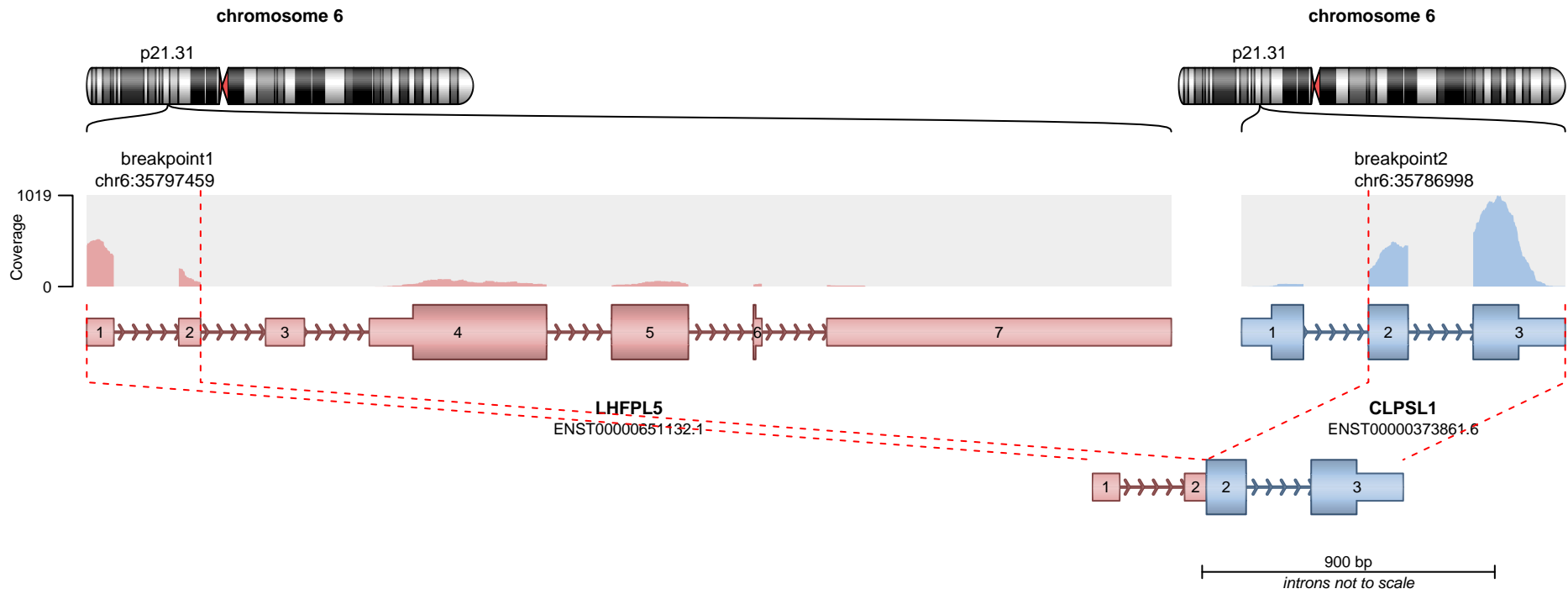


— translocation    — deletion  
 — duplication    — inversion

Genes are not protein-coding.

**SUPPORTING READ COUNT**

Split reads = 14  
 Discordant mates = 0



— translocation    — deletion  
— duplication    — inversion

No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 12  
Discordant mates = 0