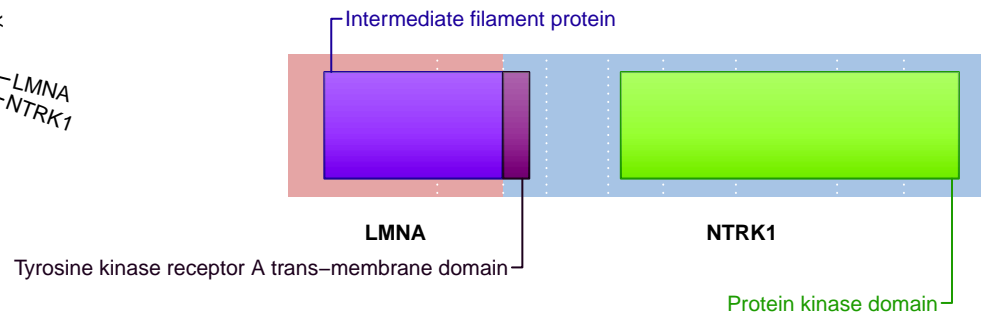


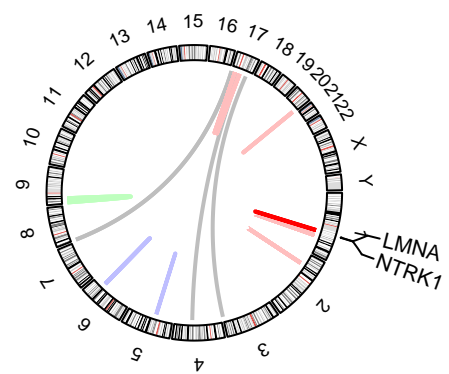
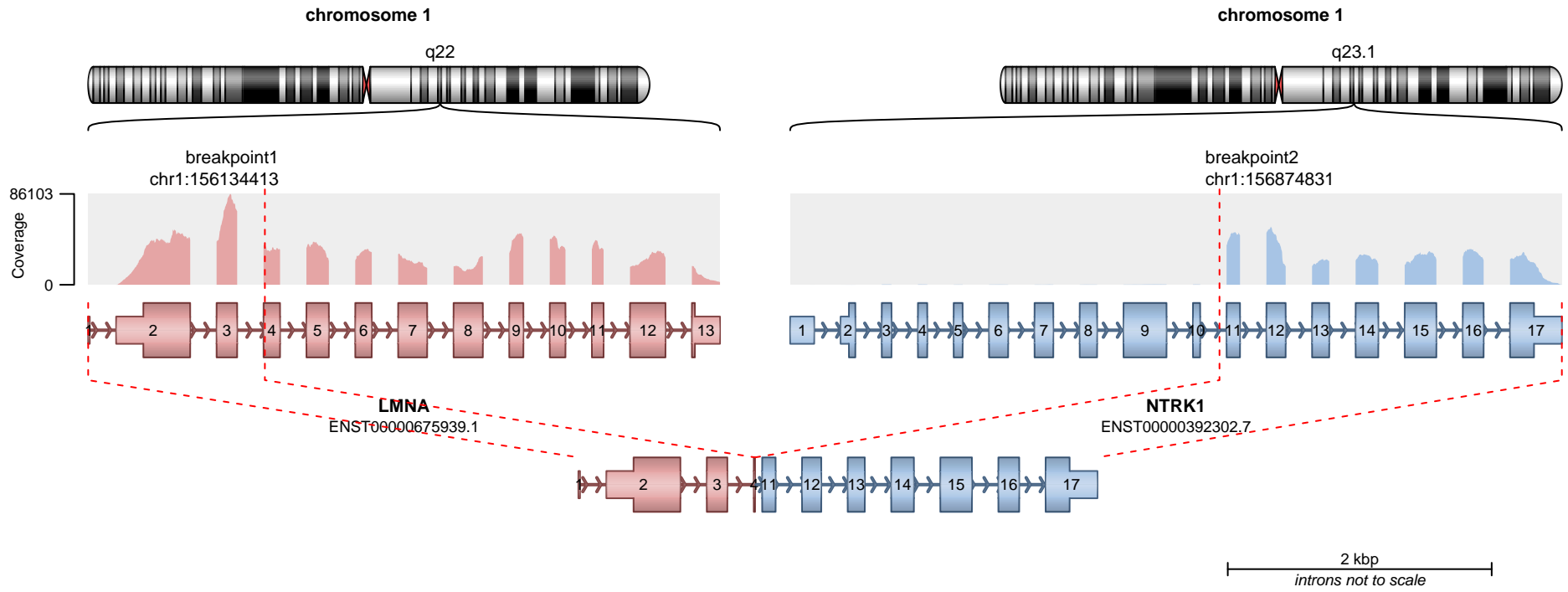
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



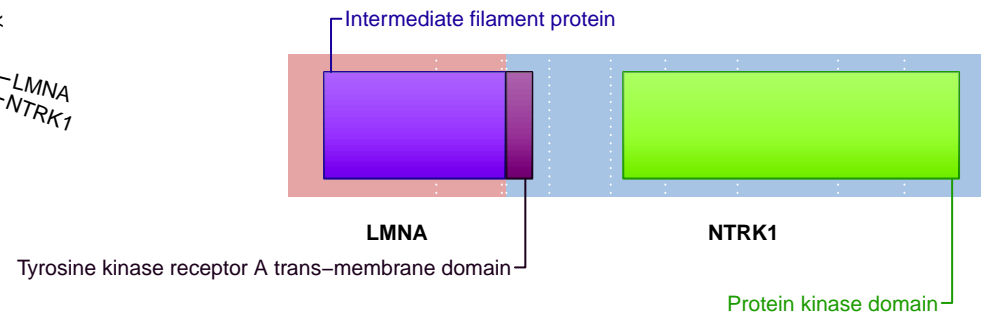
**SUPPORTING READ COUNT**

Split reads = 8367  
Discordant mates = 127

- translocation
- duplication
- deletion
- inversion



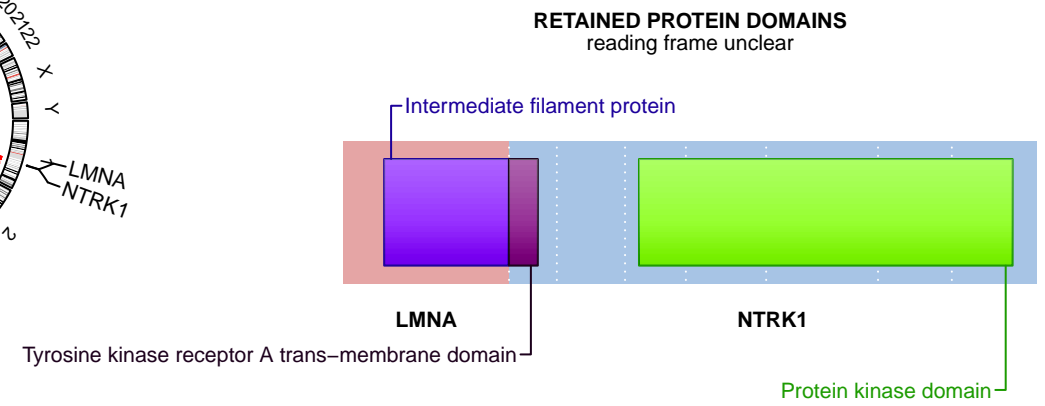
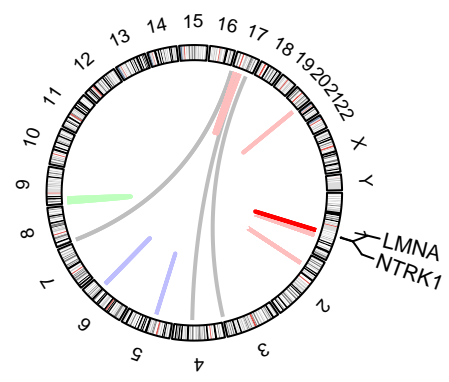
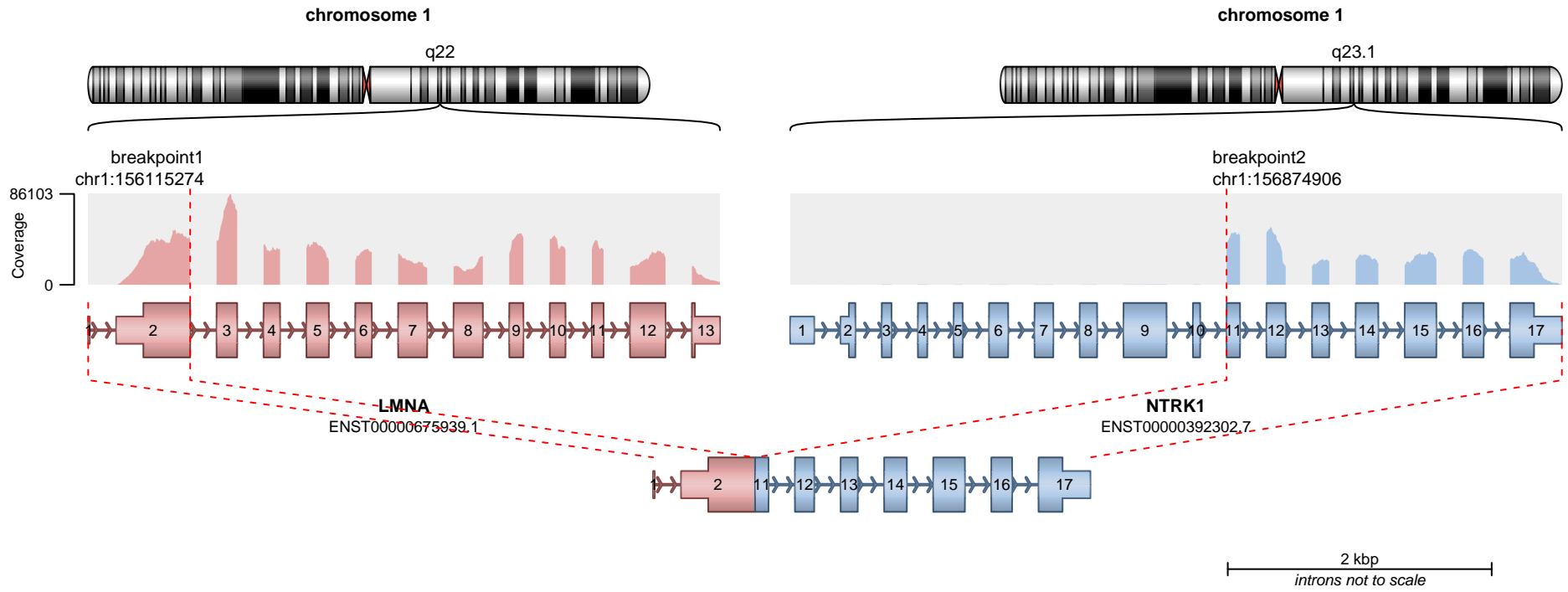
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 128  
Discordant mates = 128

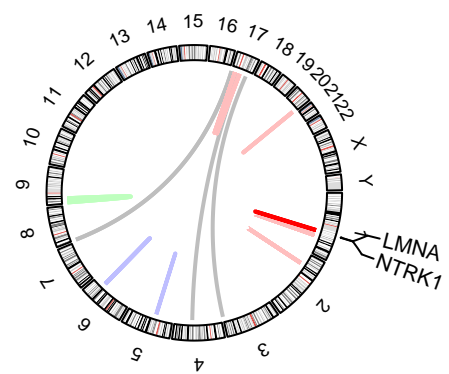
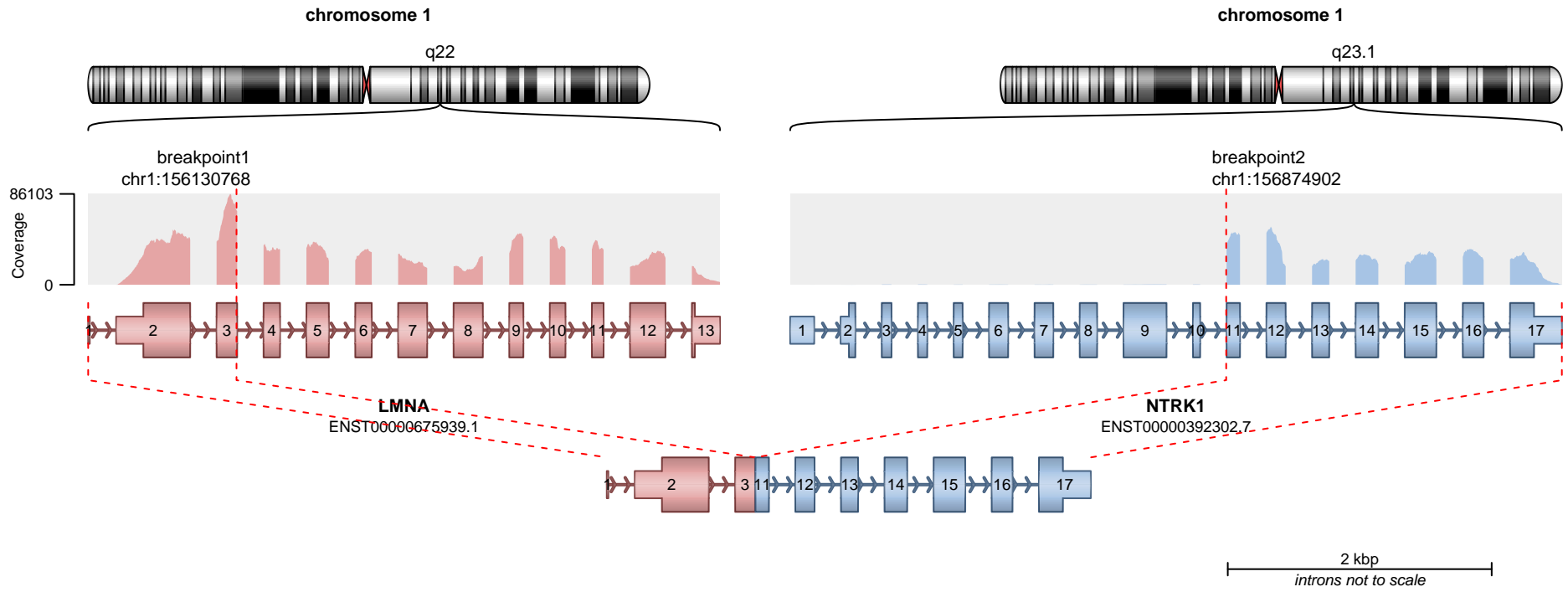
- translocation
- duplication
- deletion
- inversion



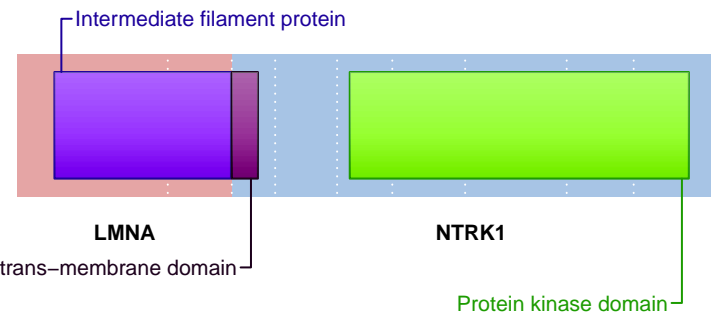
**SUPPORTING READ COUNT**

Split reads = 108  
Discordant mates = 6

— translocation — deletion  
— duplication — inversion



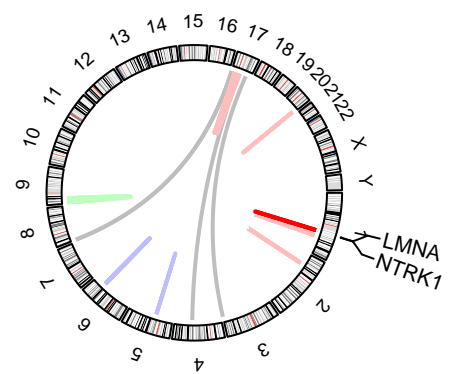
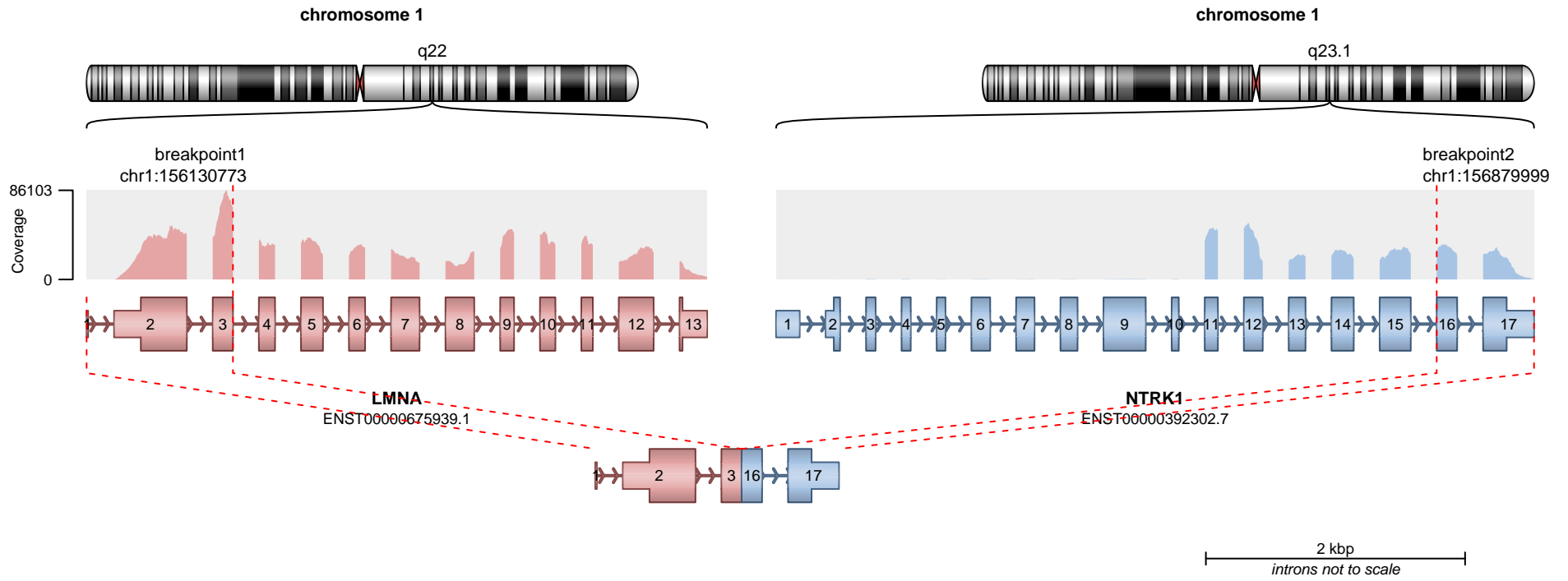
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



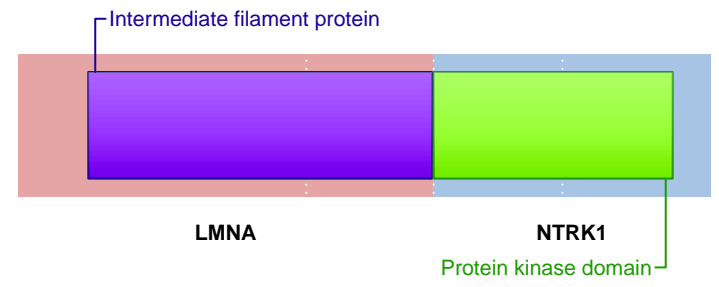
**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 80

- translocation
- duplication
- deletion
- inversion



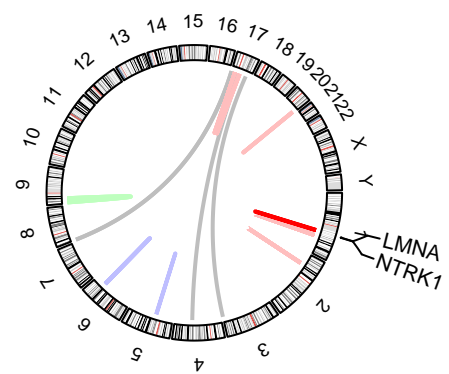
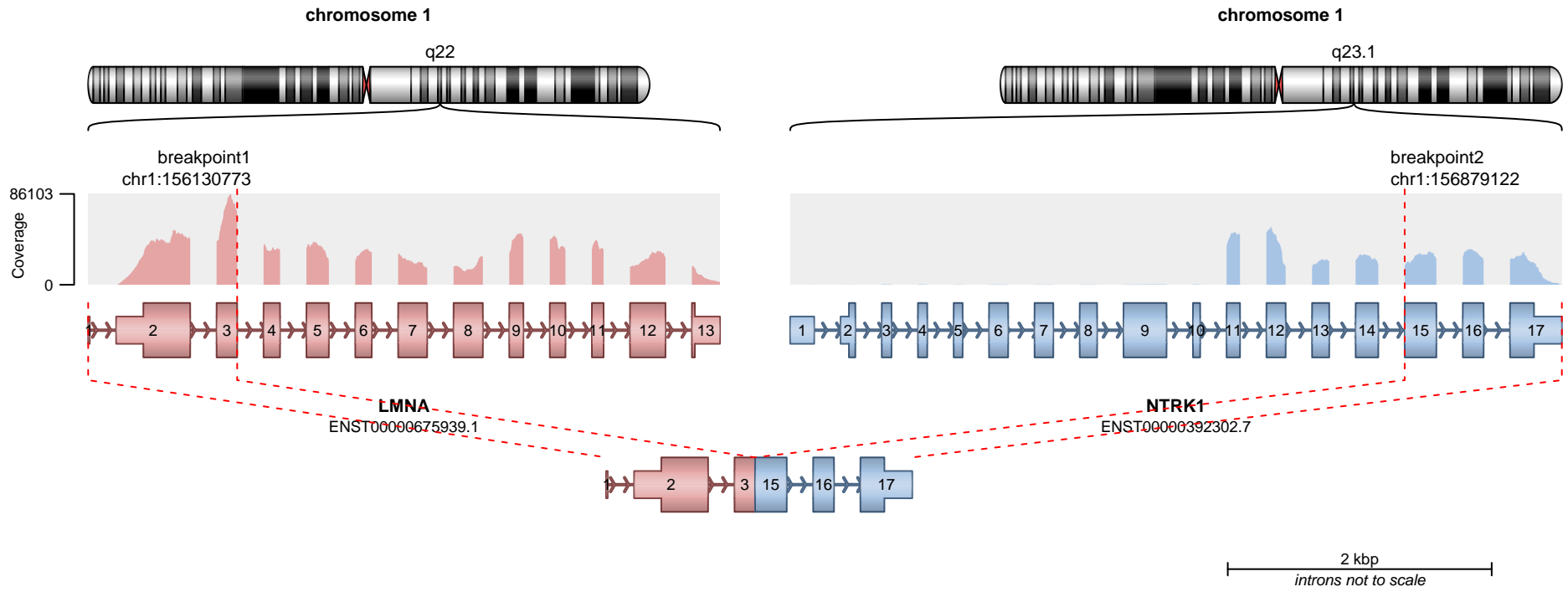
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



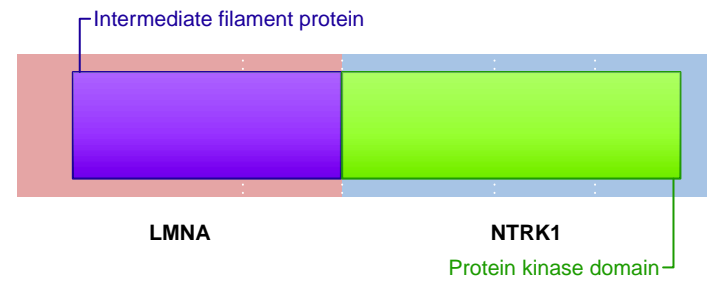
**SUPPORTING READ COUNT**

Split reads = 13  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



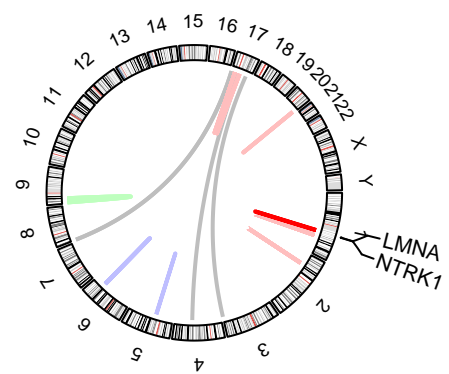
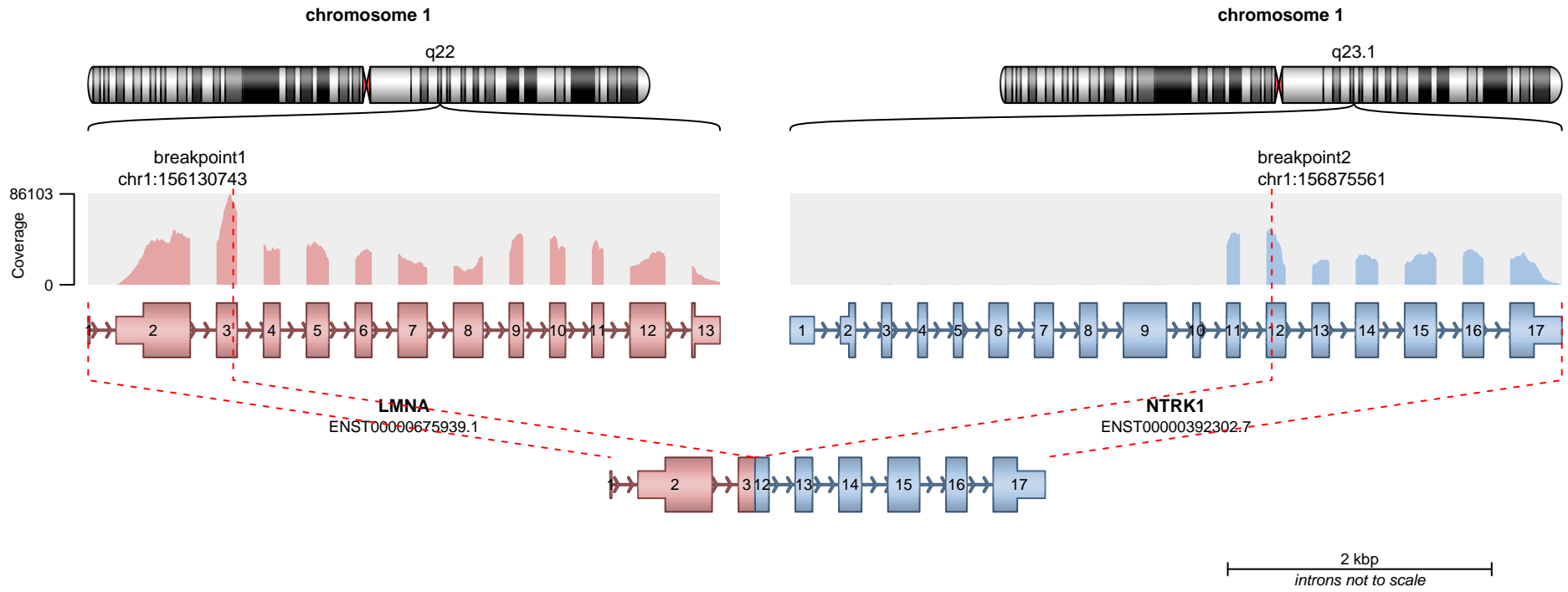
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



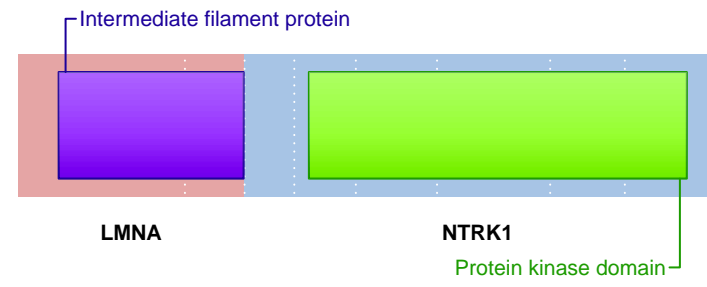
**SUPPORTING READ COUNT**

Split reads = 5  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



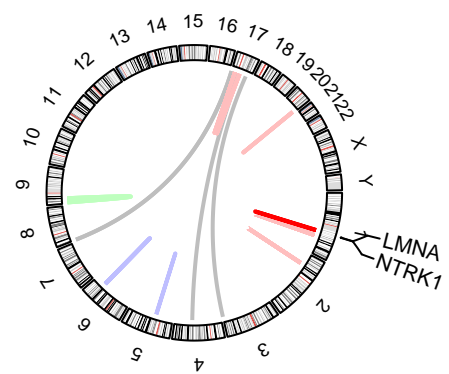
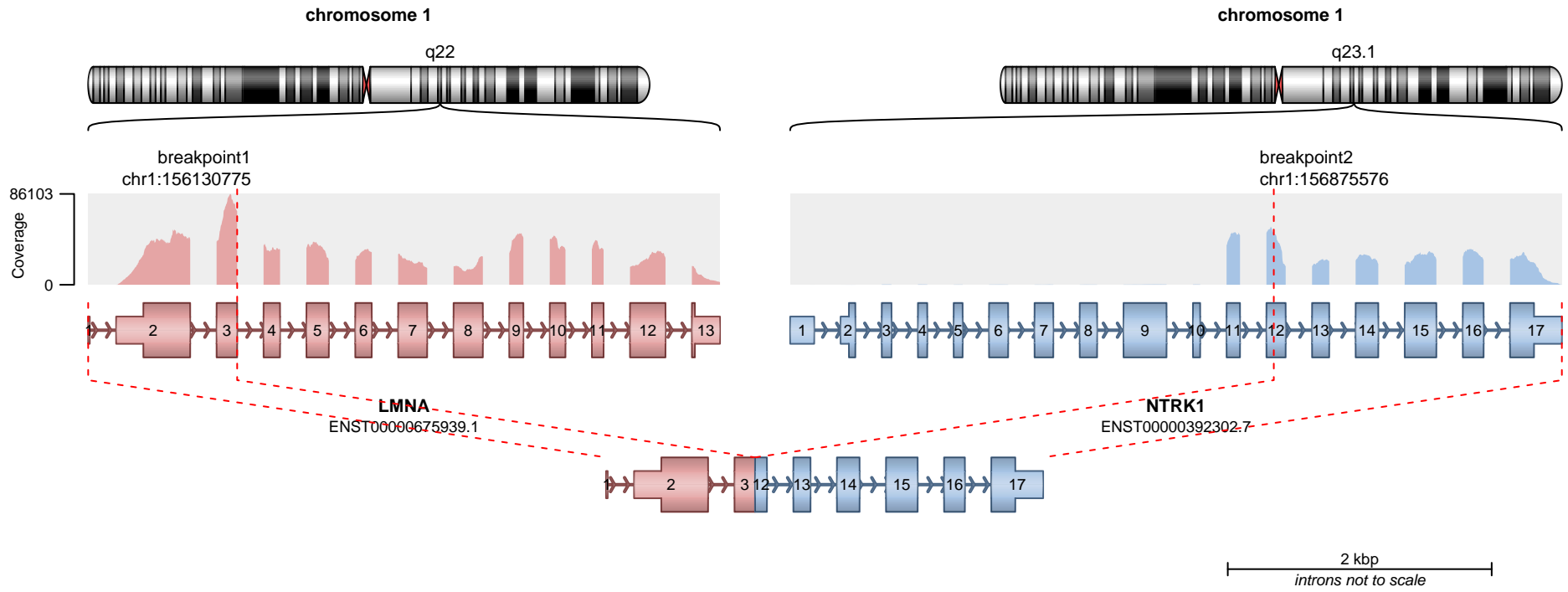
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



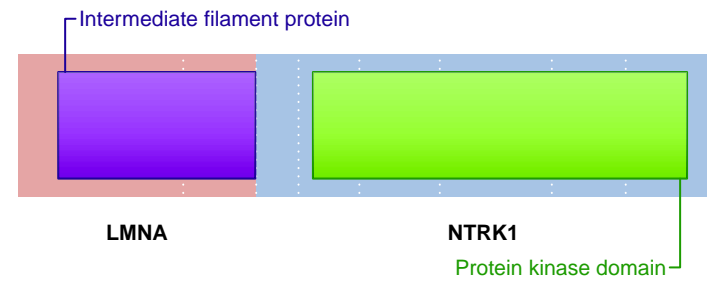
**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



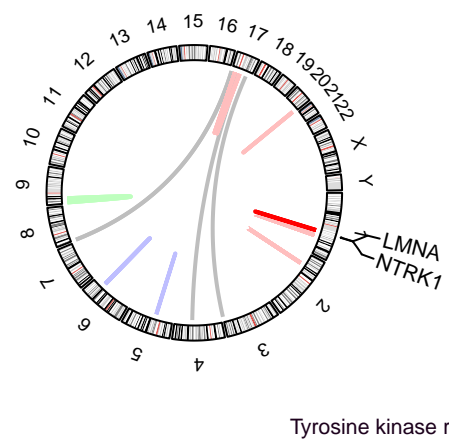
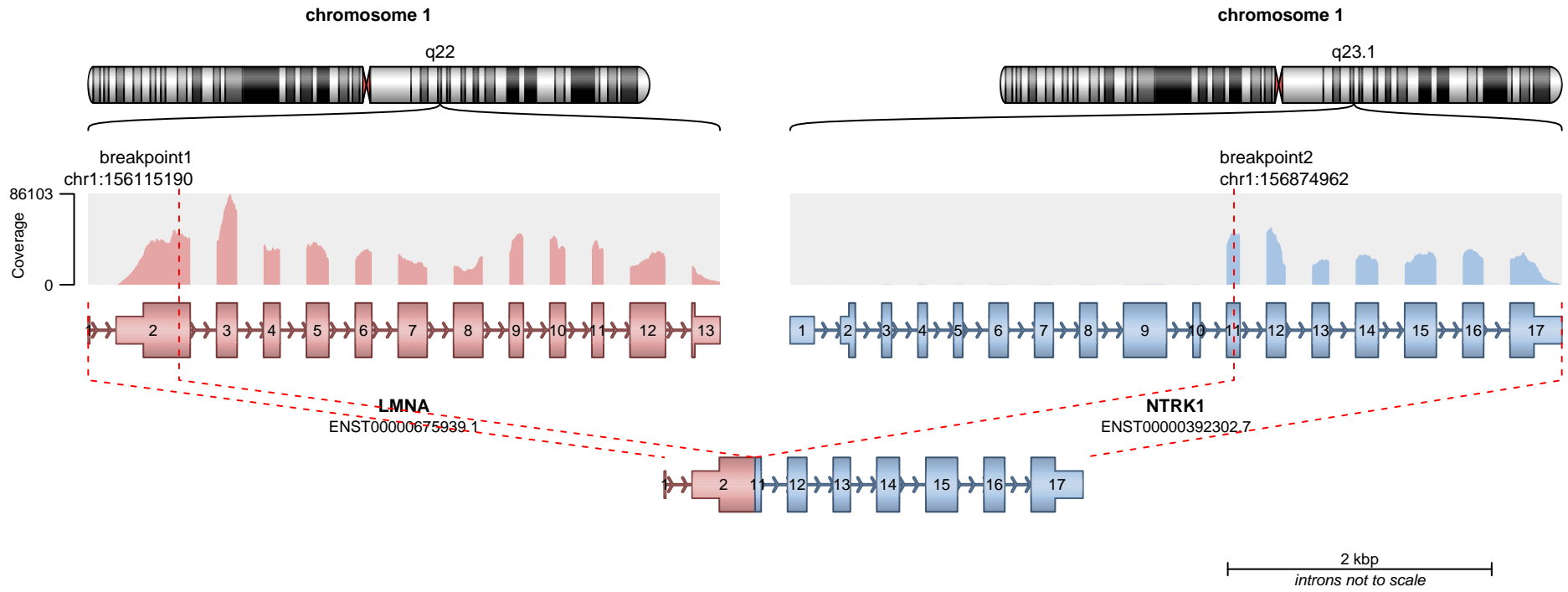
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



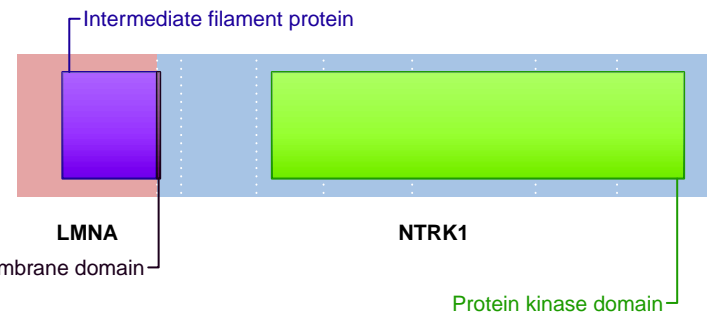
**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



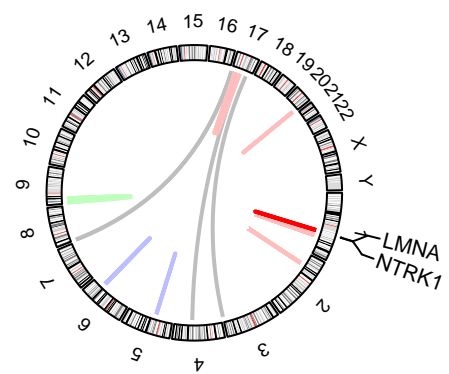
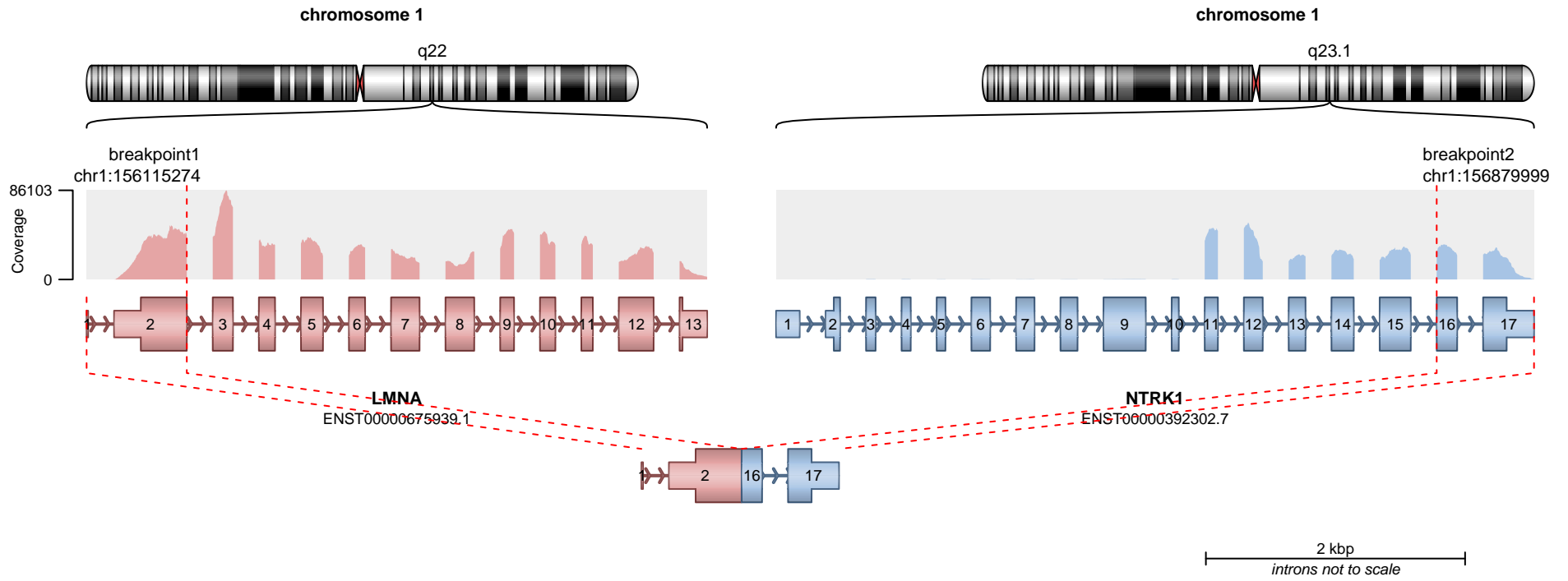
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



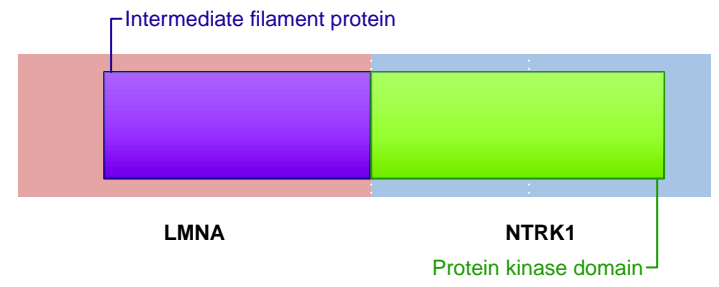
**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



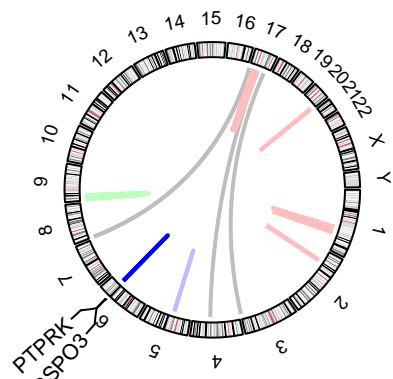
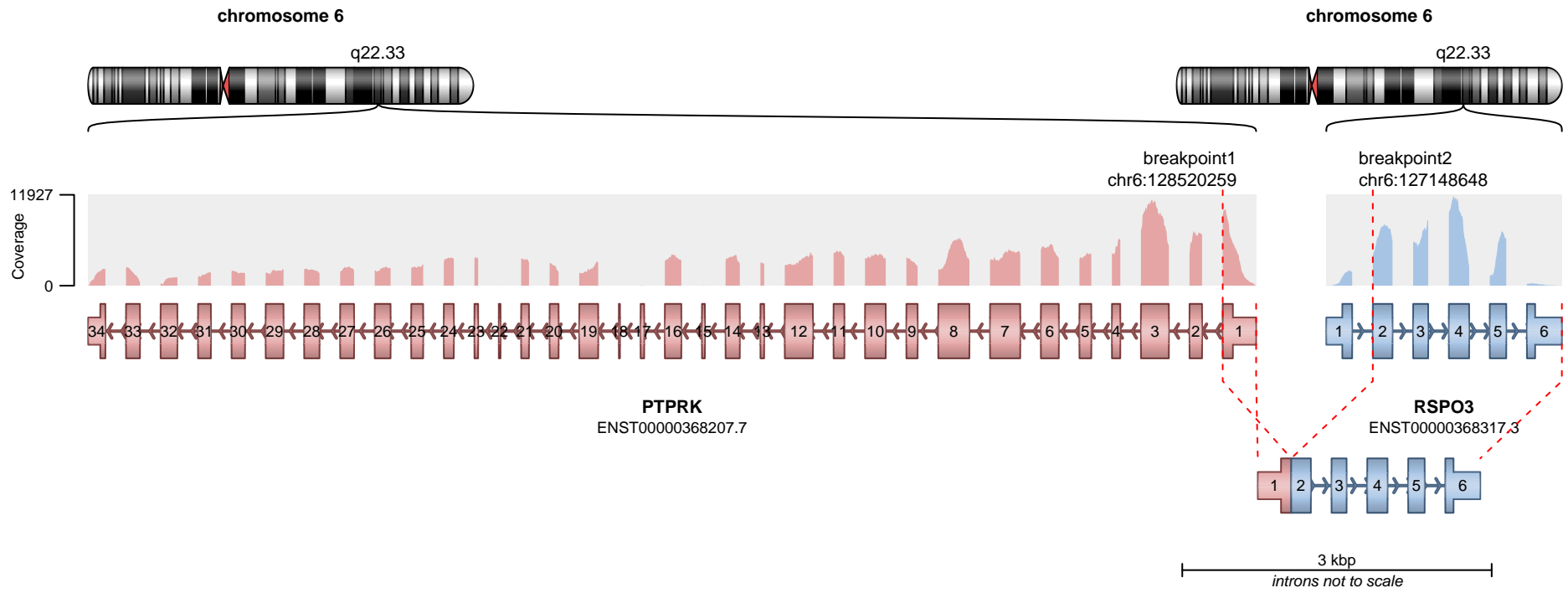
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

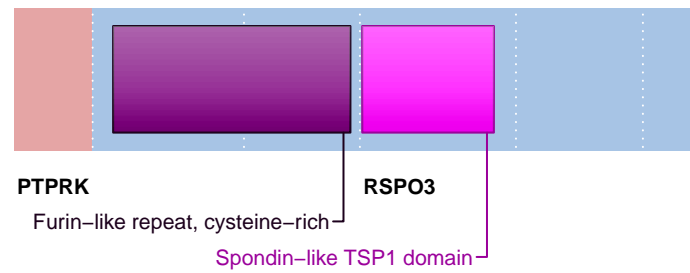
Split reads = 1  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



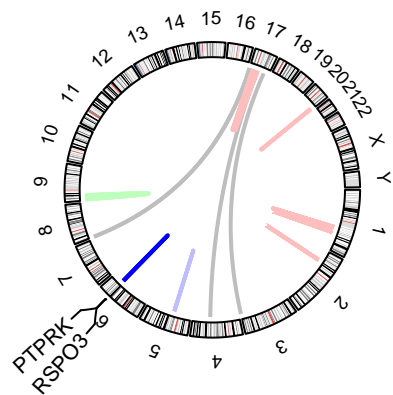
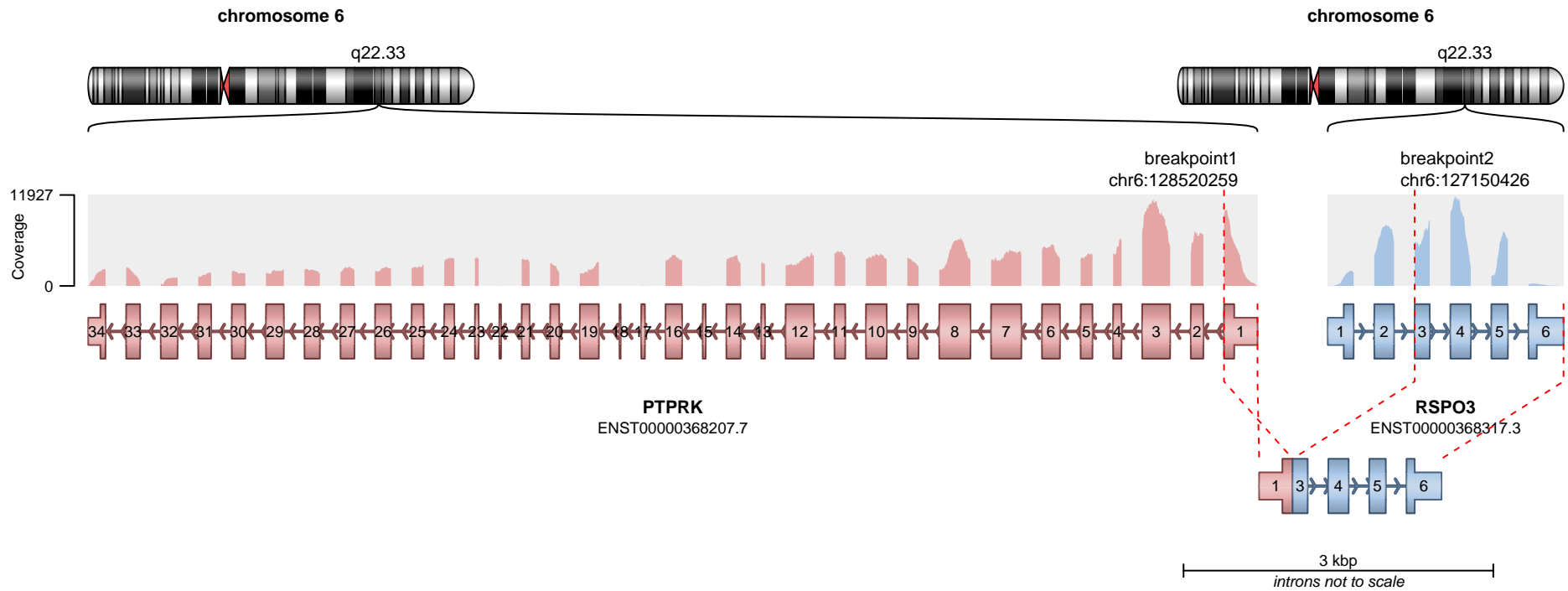
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear

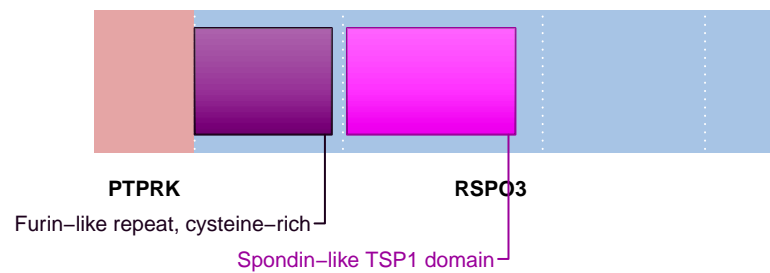


**SUPPORTING READ COUNT**

Split reads = 760  
Discordant mates = 15



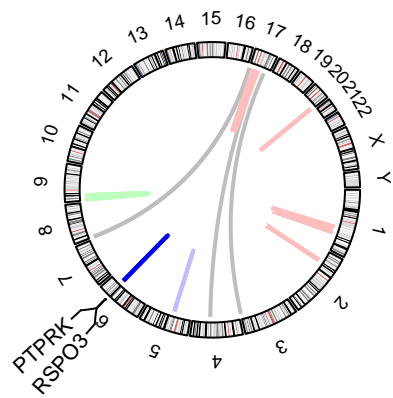
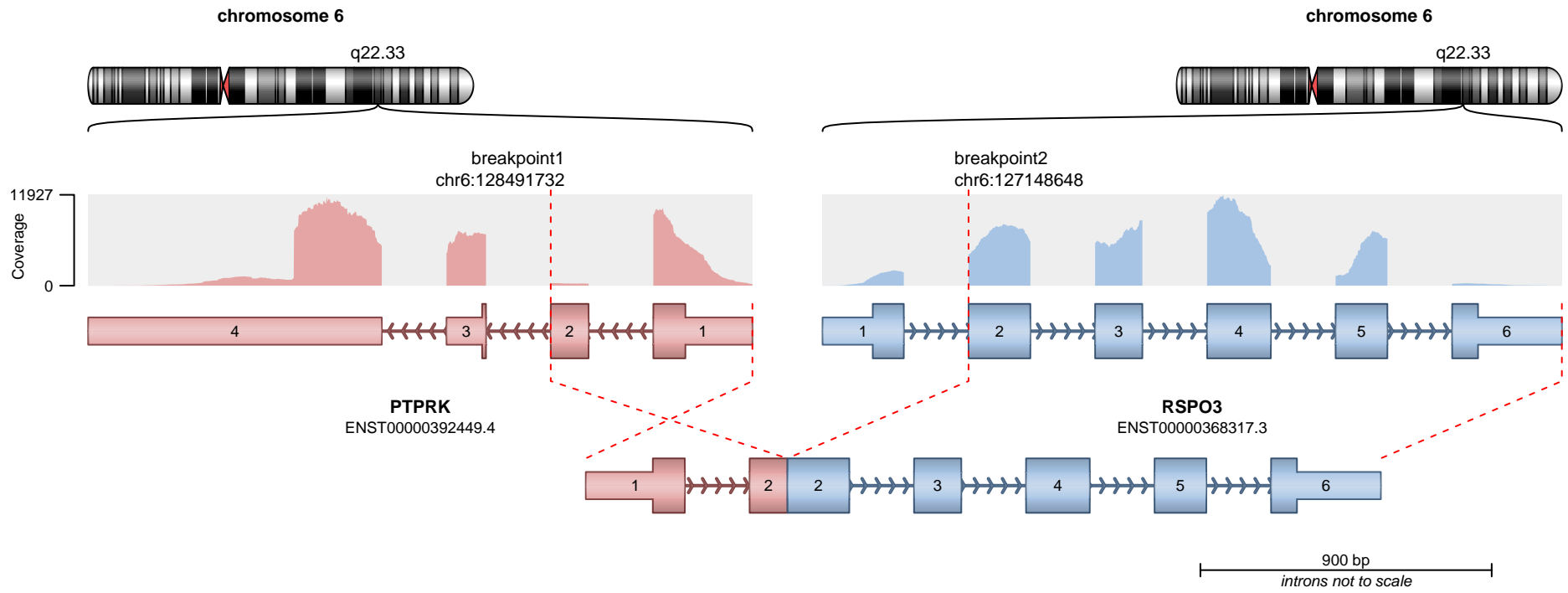
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



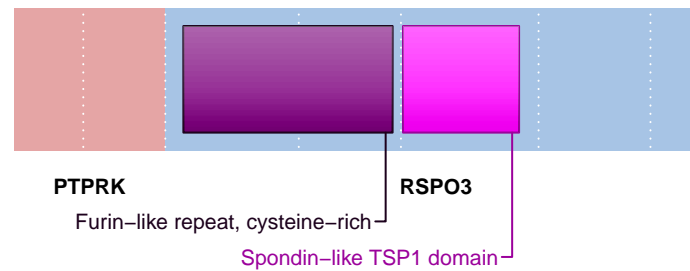
**SUPPORTING READ COUNT**

Split reads = 10  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



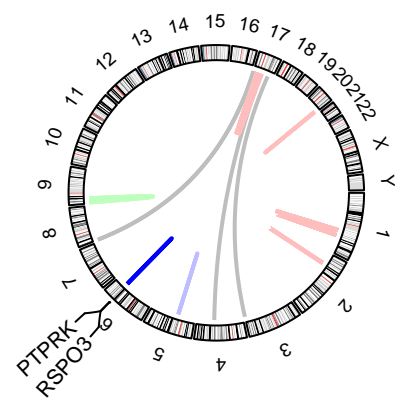
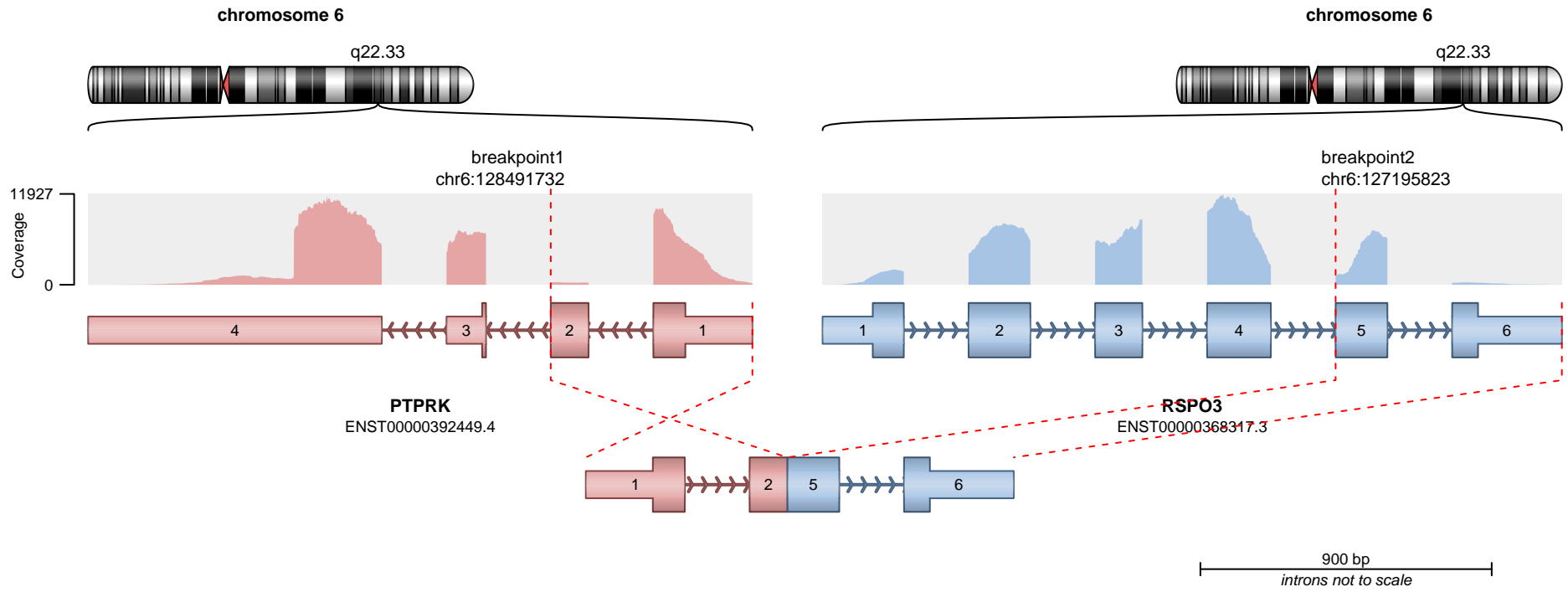
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 5  
Discordant mates = 15

- translocation
- duplication
- deletion
- inversion

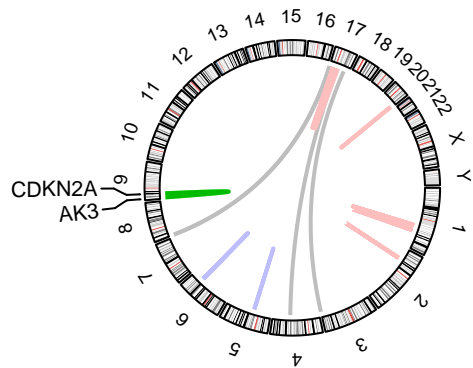
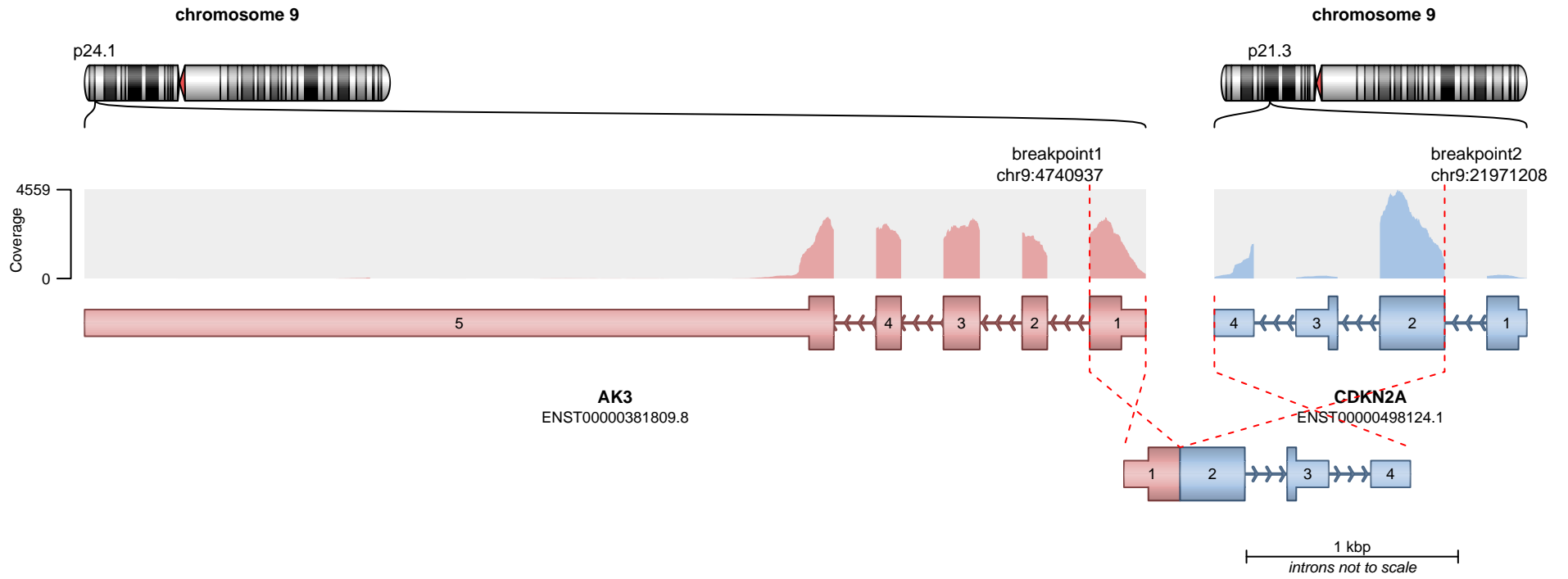


— translocation — deletion  
— duplication — inversion

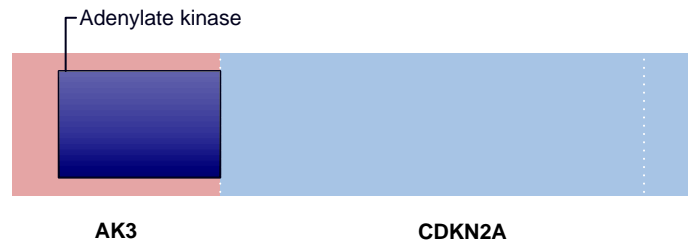
No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0



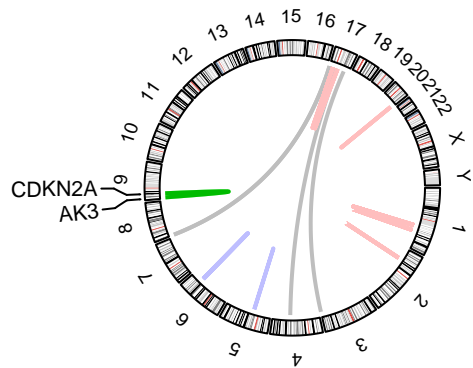
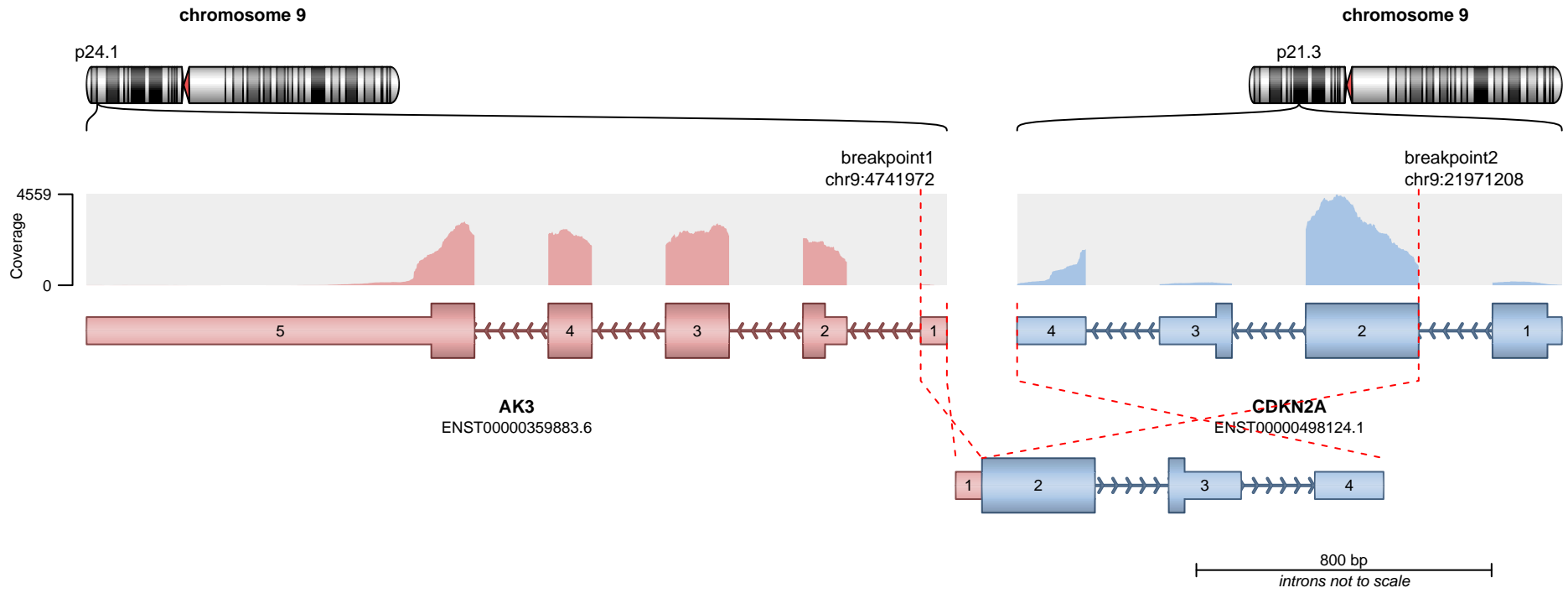
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 194  
Discordant mates = 5

— translocation — deletion  
— duplication — inversion

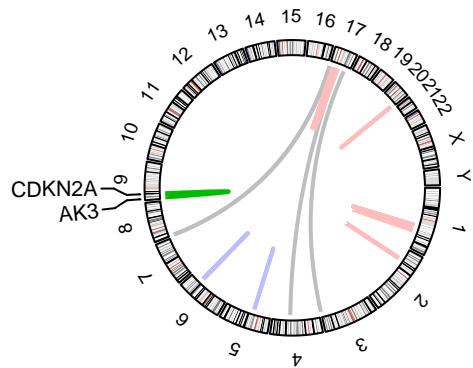
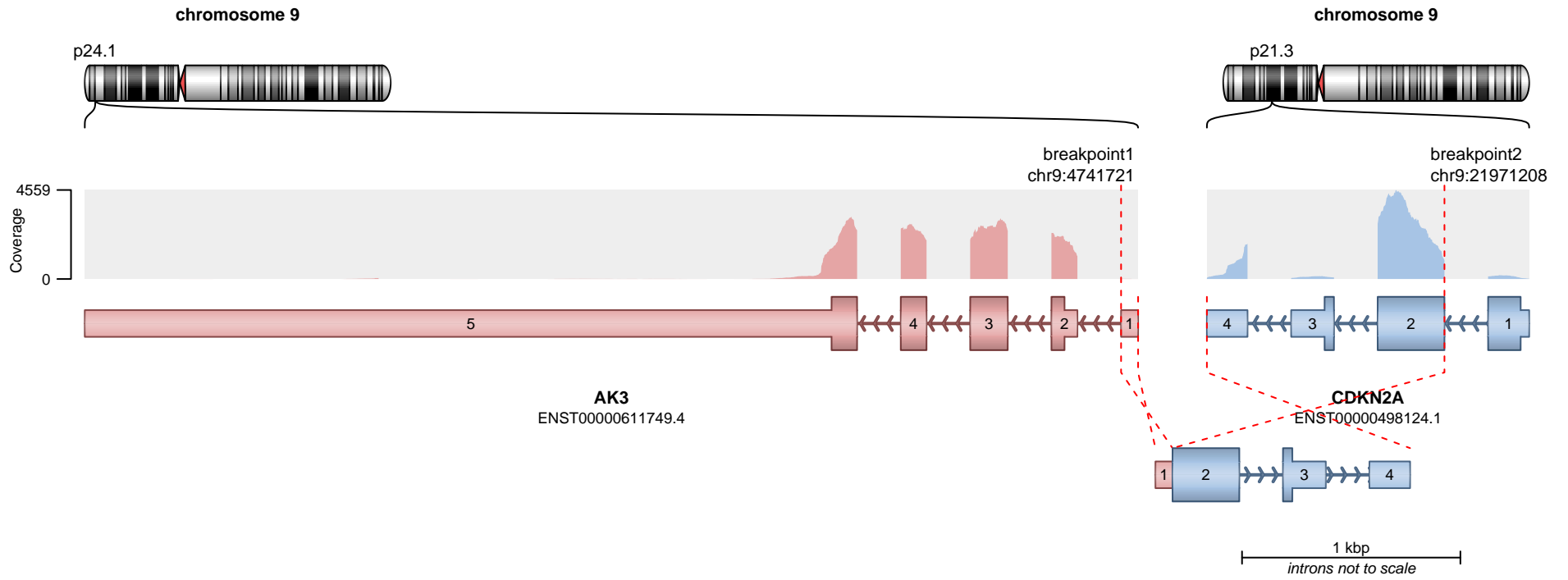


No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 12  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion

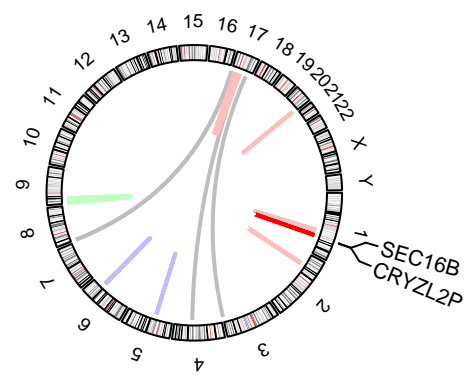
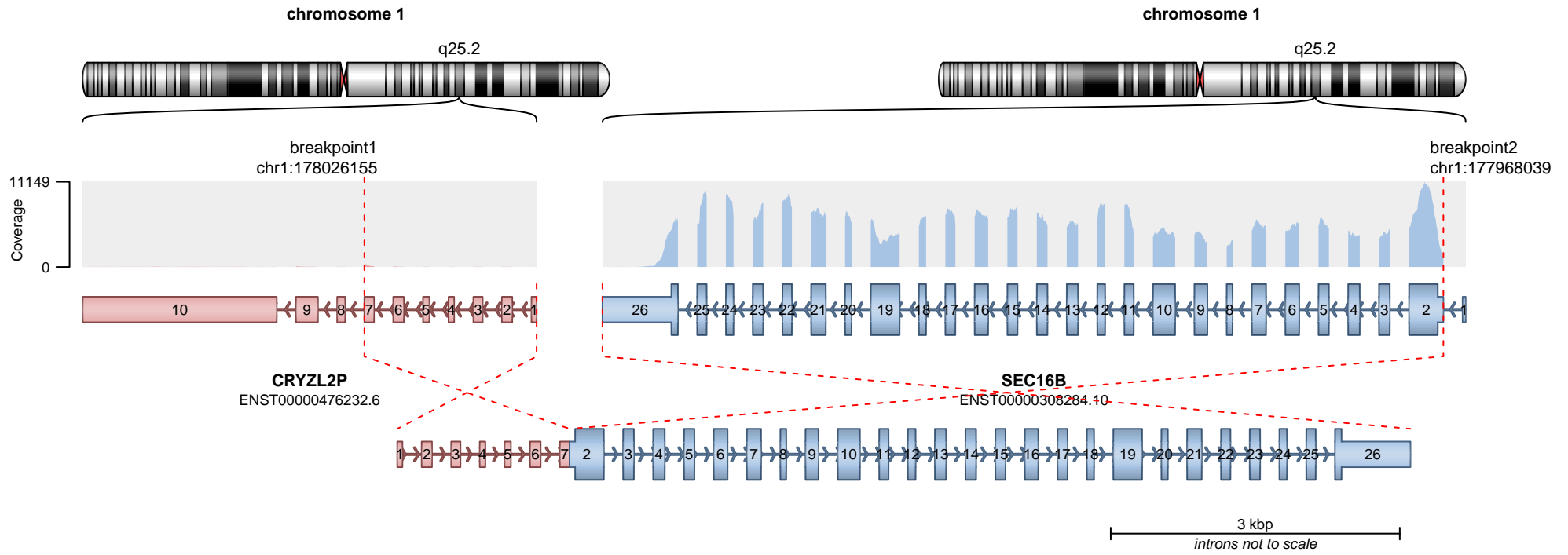


— translocation    — deletion  
— duplication    — inversion

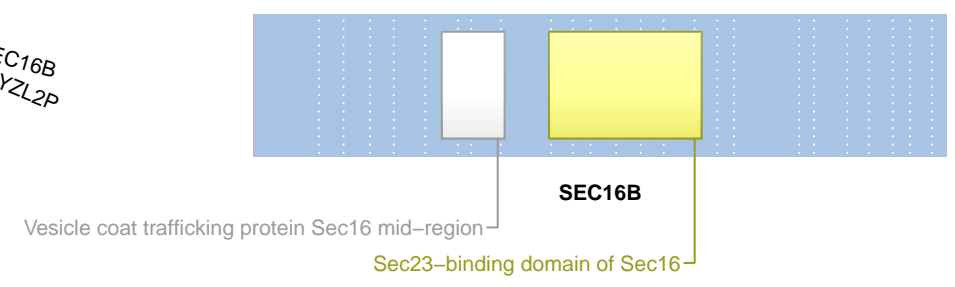
No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 5  
Discordant mates = 0



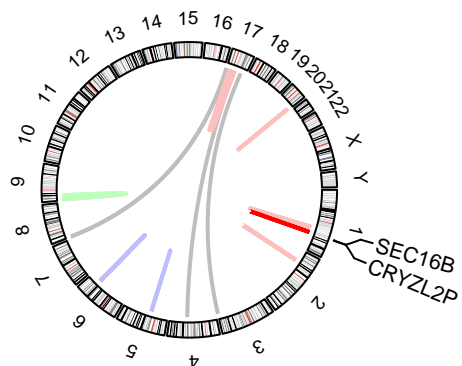
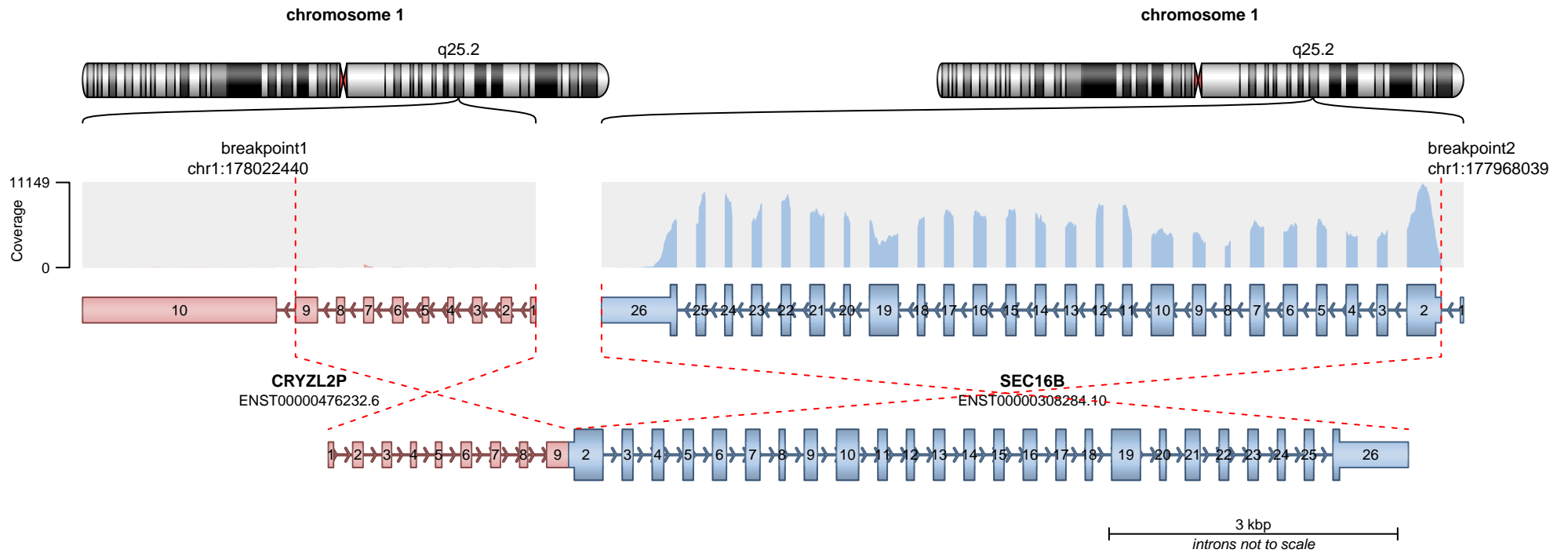
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 191  
Discordant mates = 11

- translocation
- duplication
- deletion
- inversion



**RETAINED PROTEIN DOMAINS**  
reading frame unclear



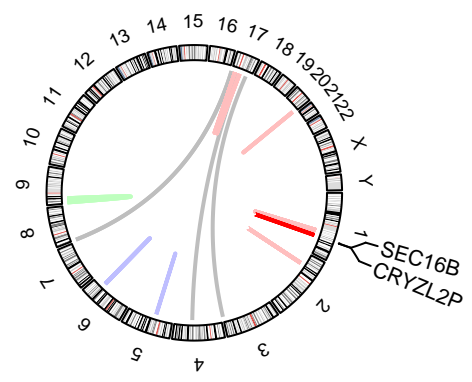
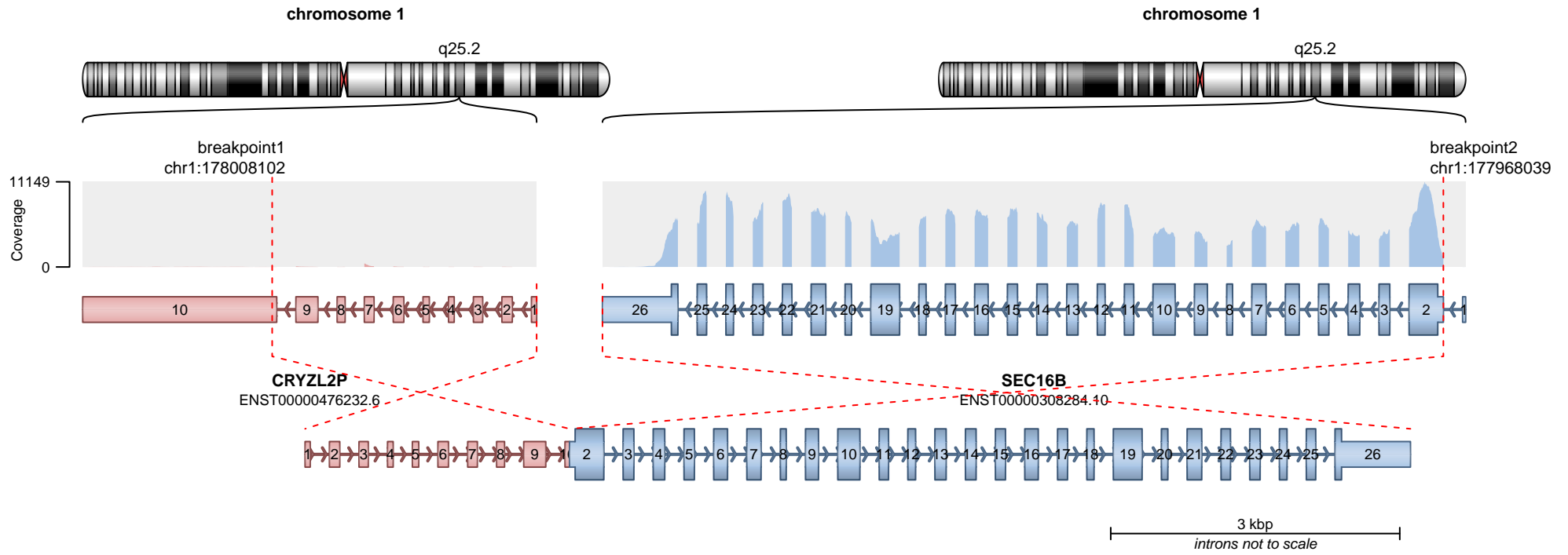
**SUPPORTING READ COUNT**

Split reads = 37  
Discordant mates = 13

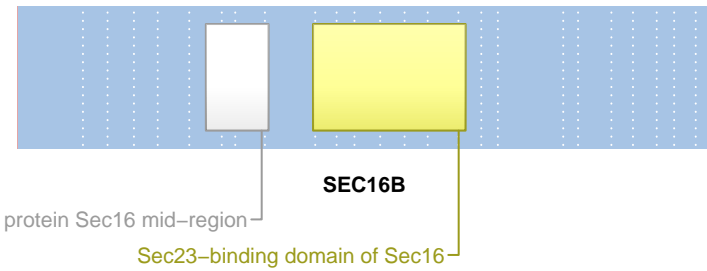
- translocation
- duplication
- deletion
- inversion

Vesicle coat trafficking protein Sec16 mid-region

Sec23-binding domain of Sec16



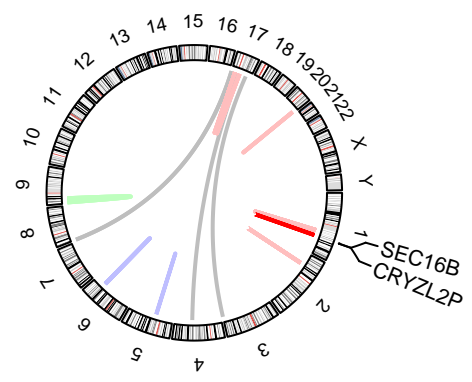
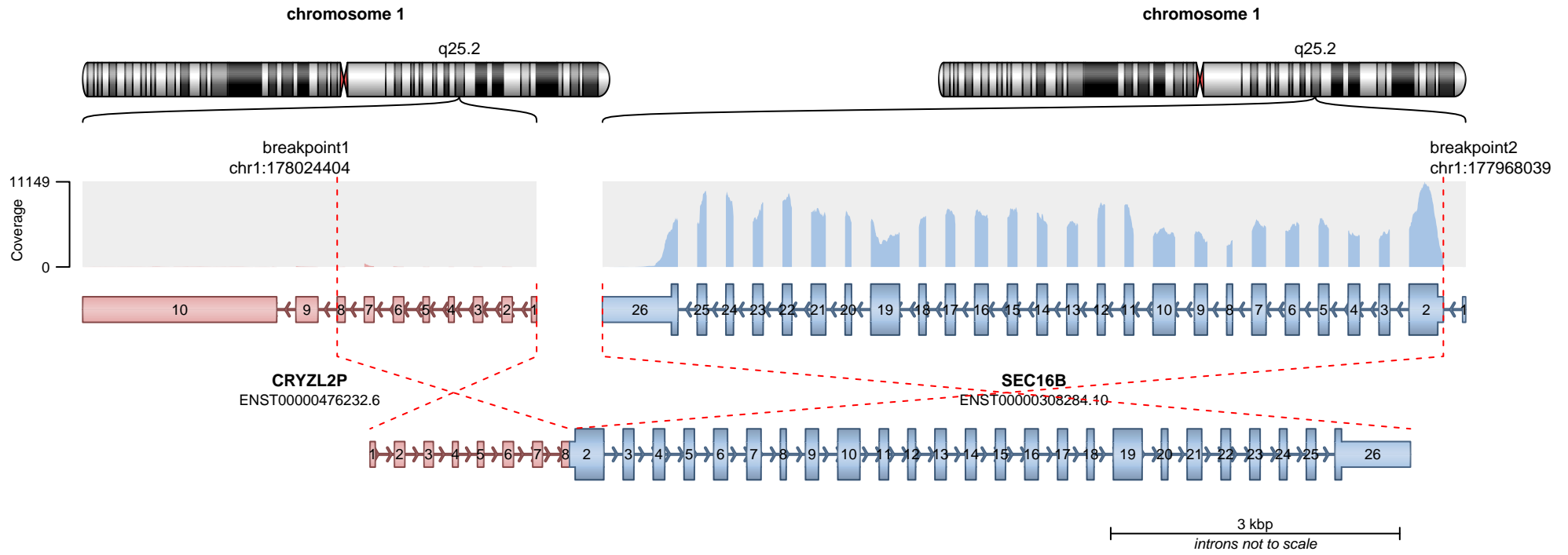
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



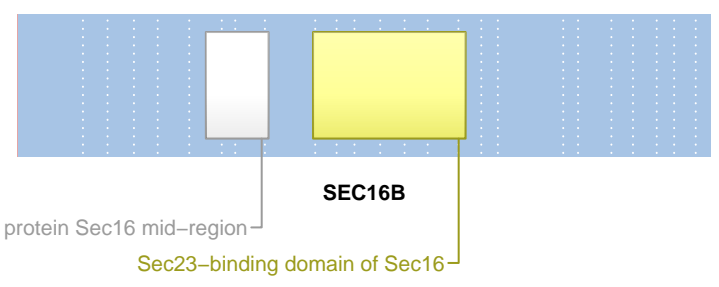
**SUPPORTING READ COUNT**

Split reads = 8  
Discordant mates = 13

- translocation
- duplication
- deletion
- inversion



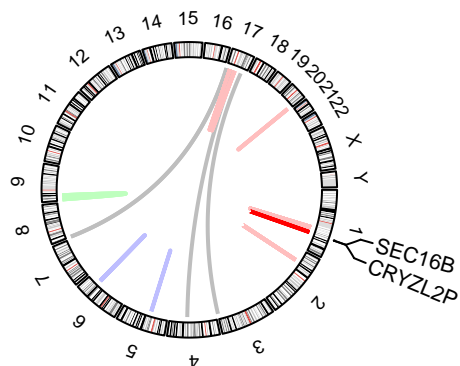
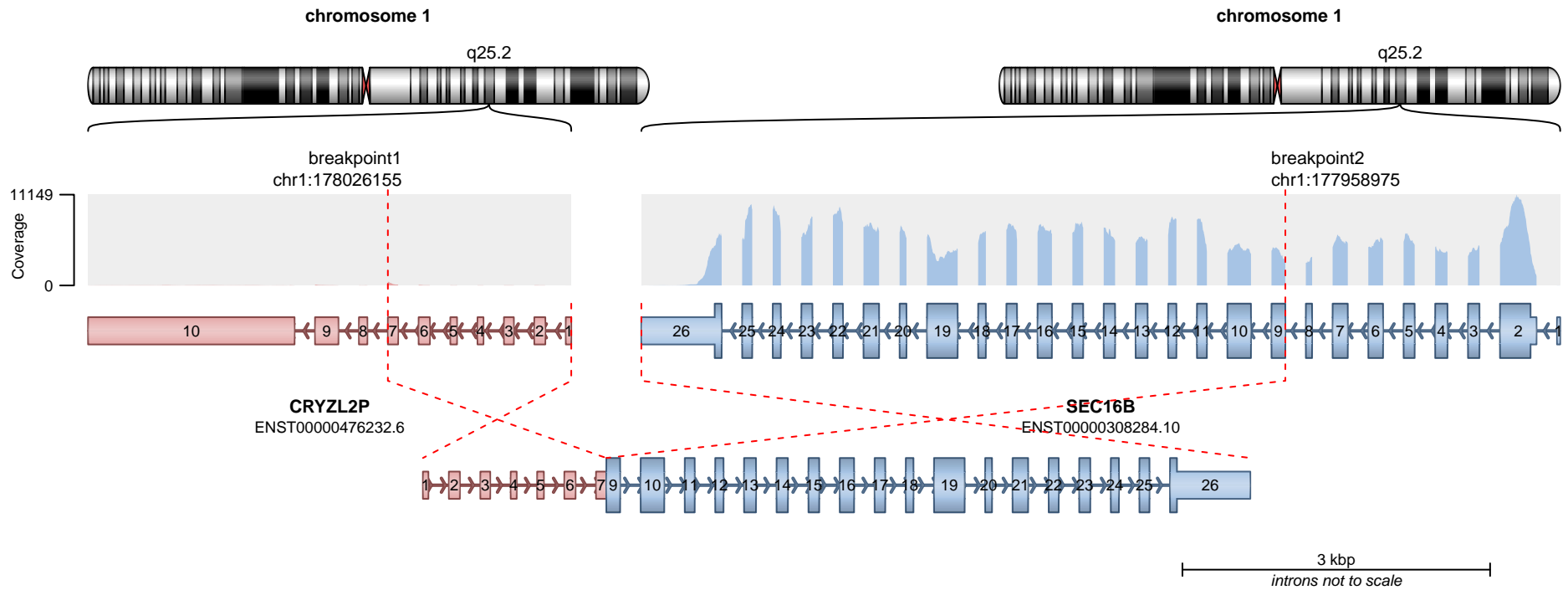
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

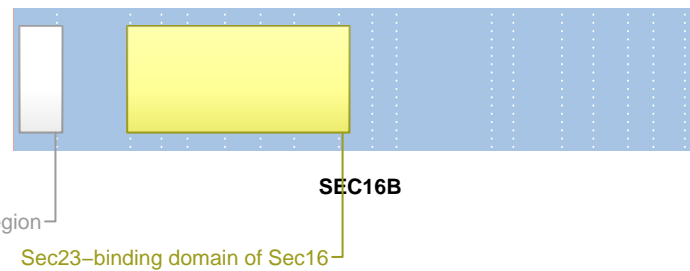
Split reads = 3  
Discordant mates = 11

- translocation
- duplication
- deletion
- inversion



Vesicle coat trafficking protein Sec16 mid-region

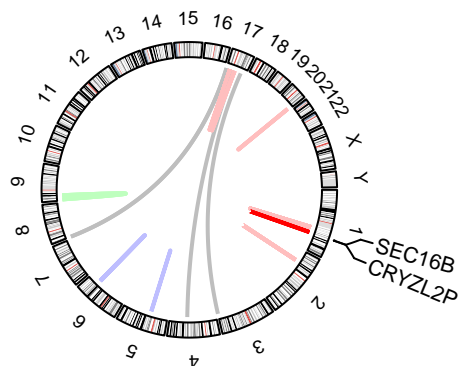
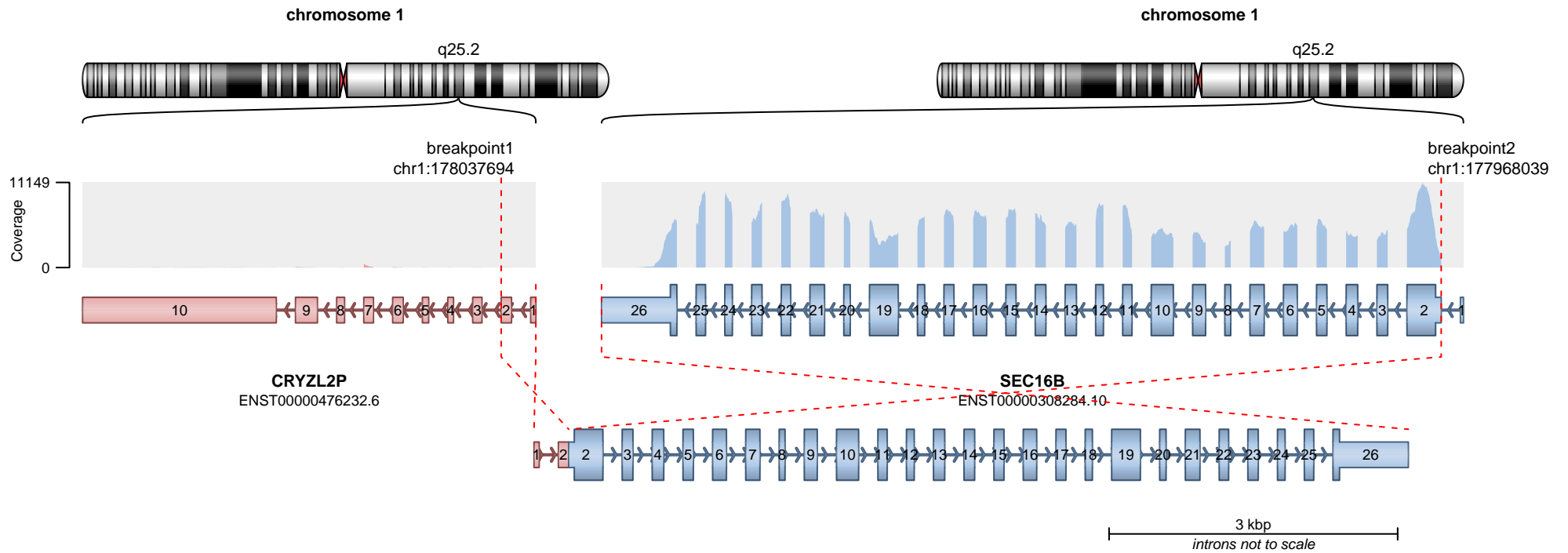
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



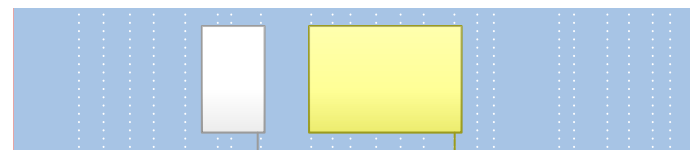
**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



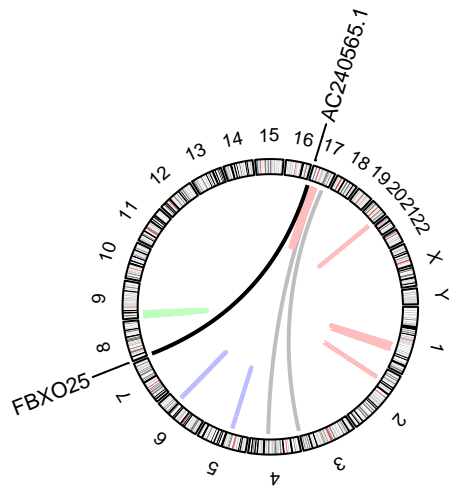
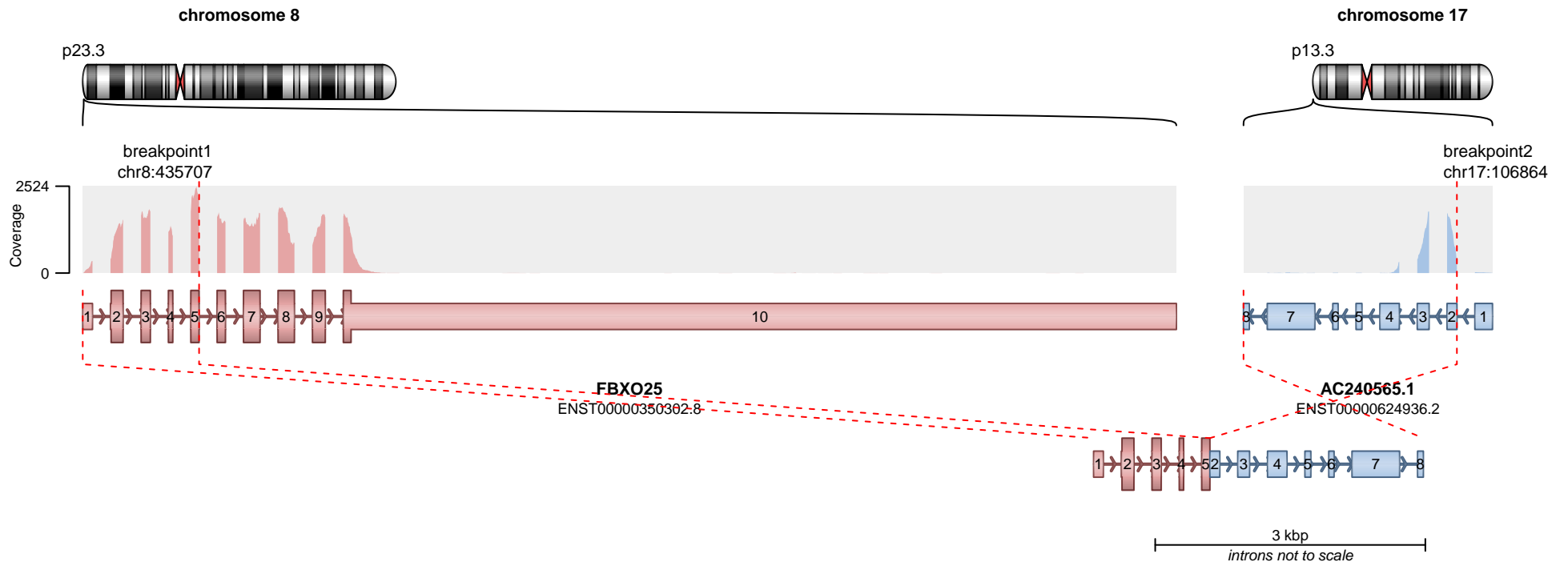
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

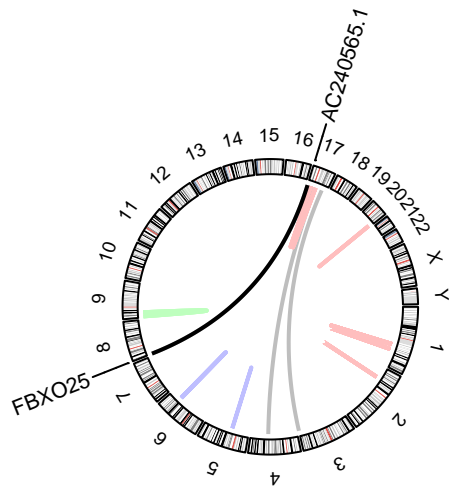
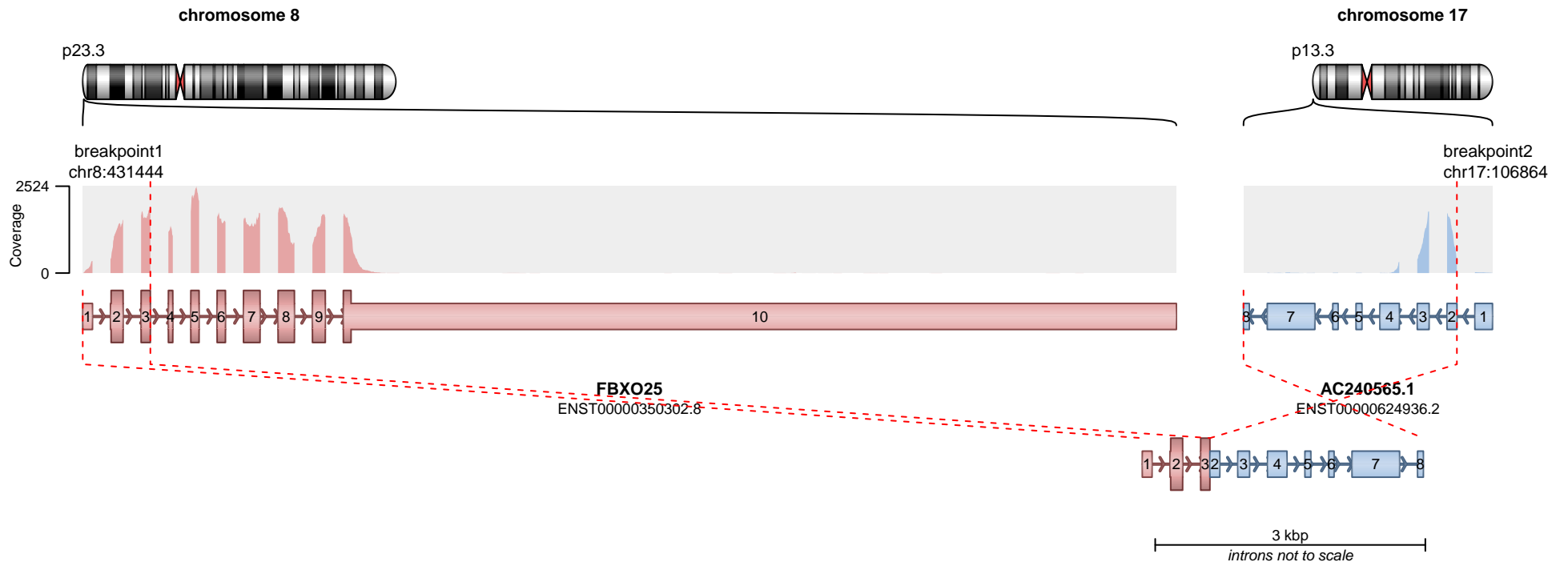


No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 146  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion

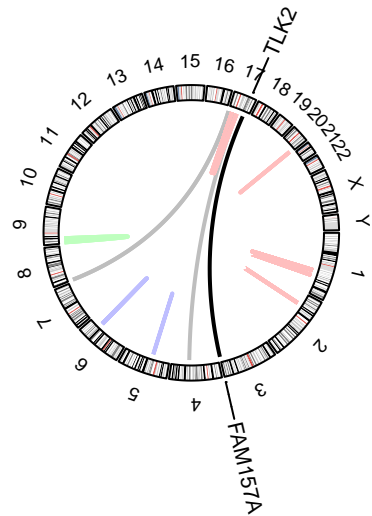
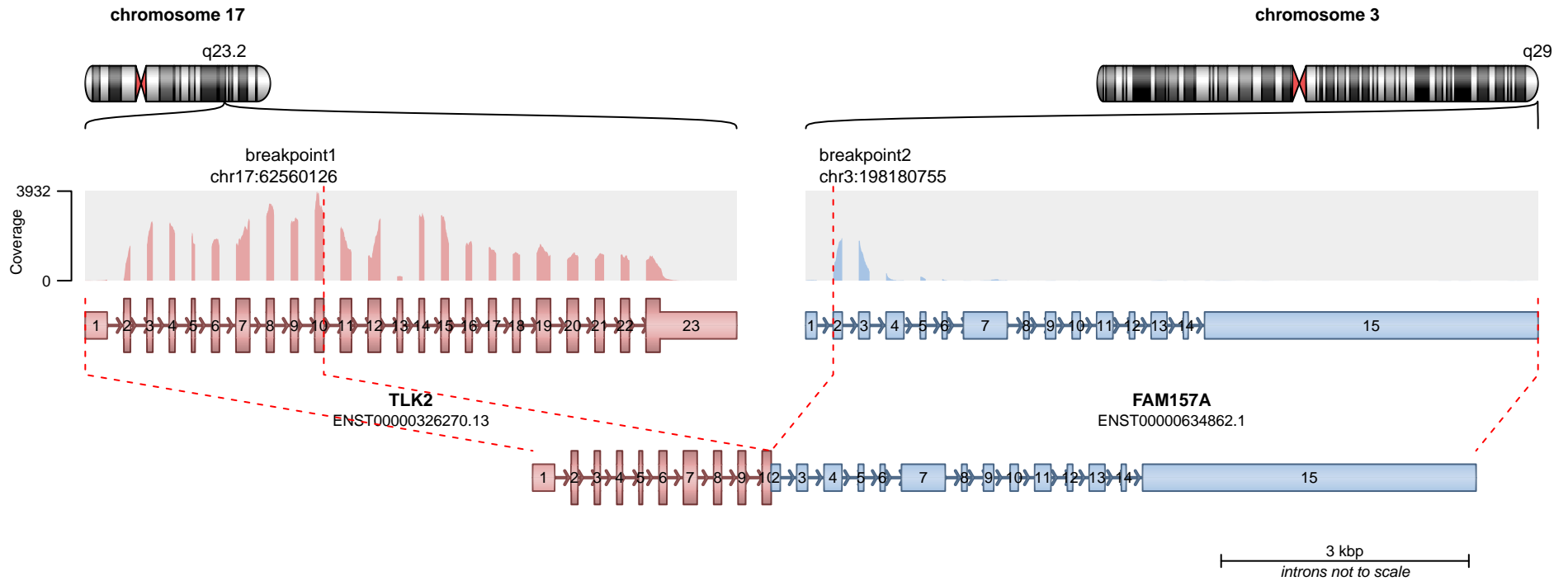


No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion

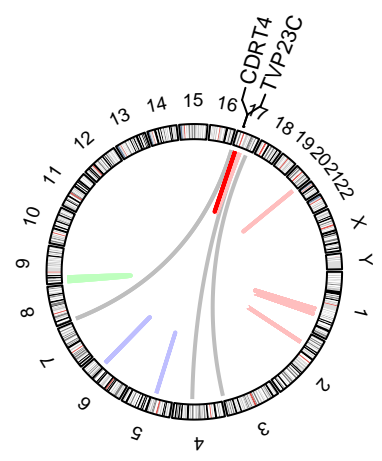
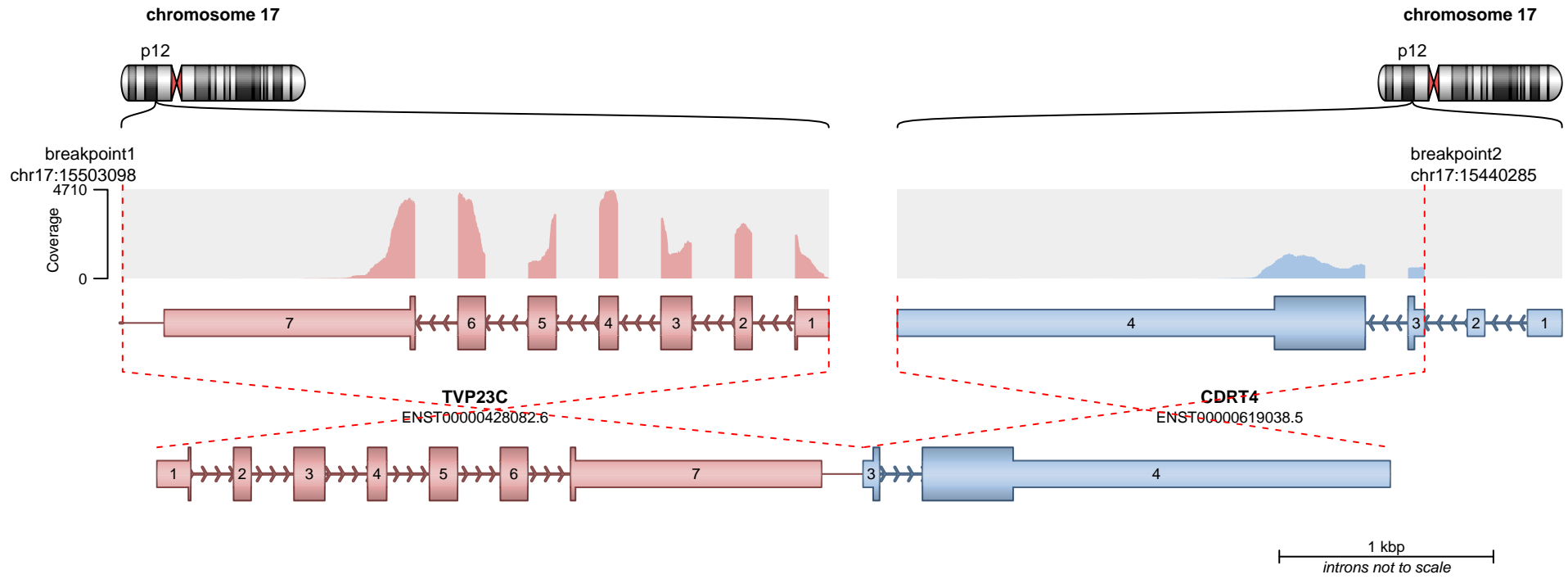


— translocation    — deletion  
— duplication    — inversion

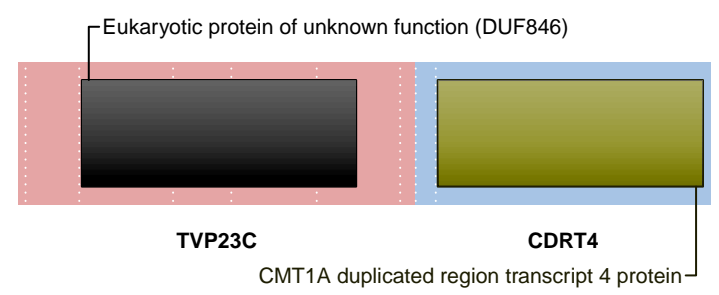
No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 136  
Discordant mates = 0



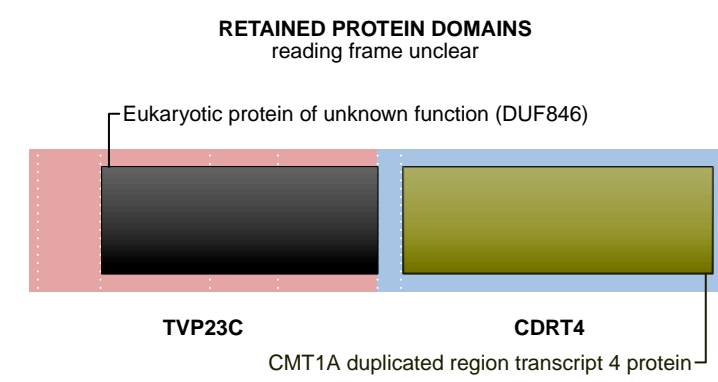
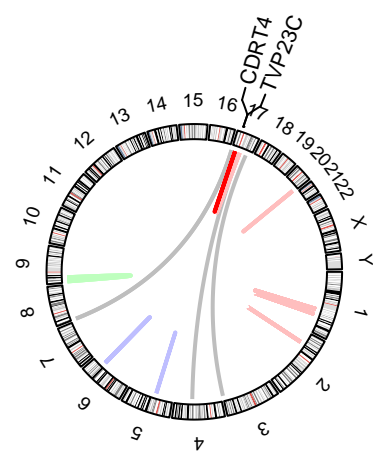
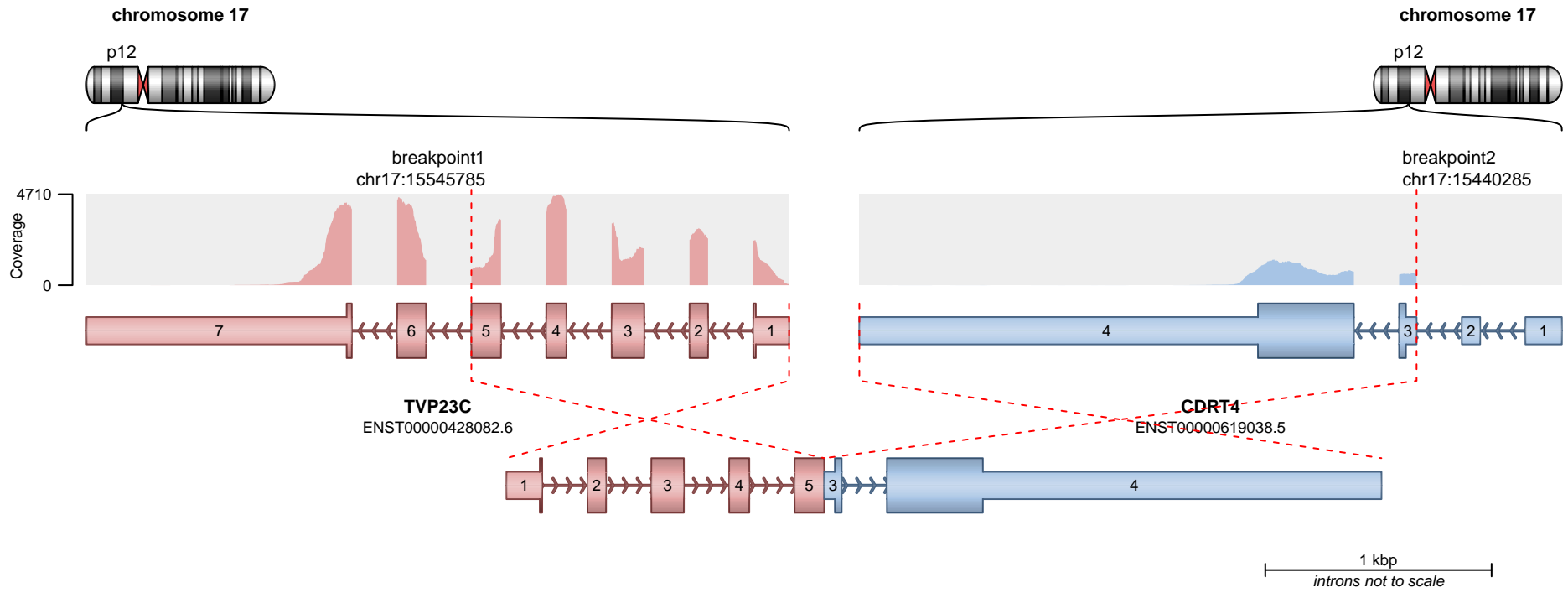
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 114  
Discordant mates = 4

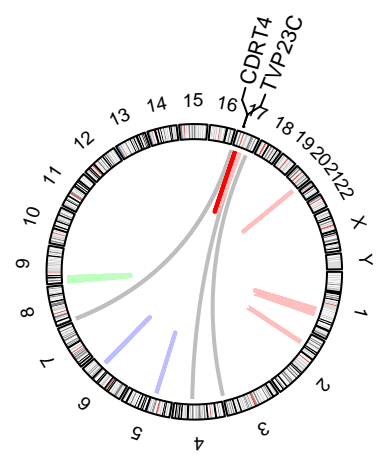
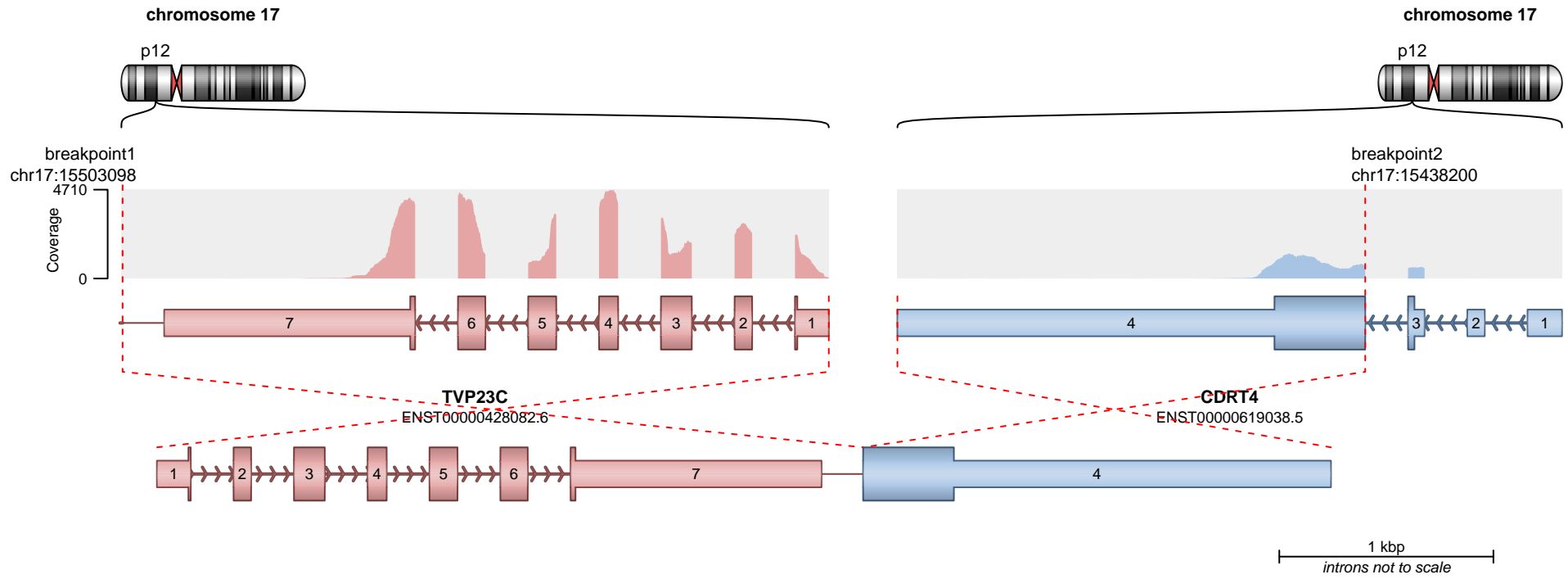
- translocation
- duplication
- deletion
- inversion



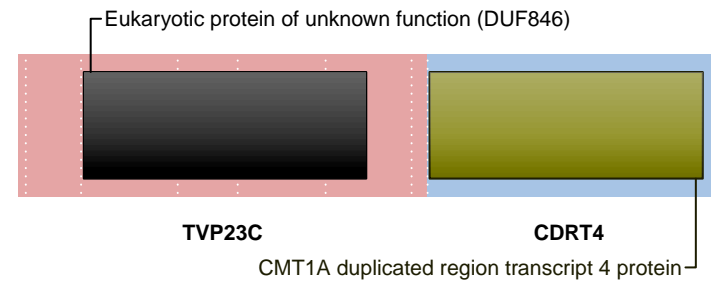
**SUPPORTING READ COUNT**

Split reads = 45  
Discordant mates = 2

— translocation — deletion  
— duplication — inversion



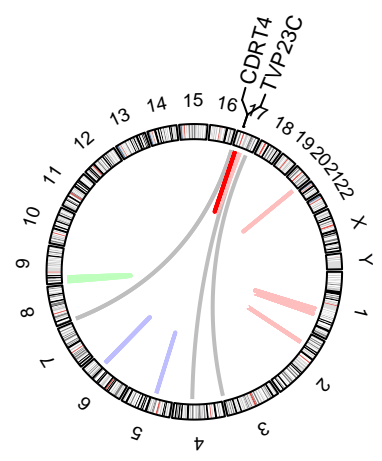
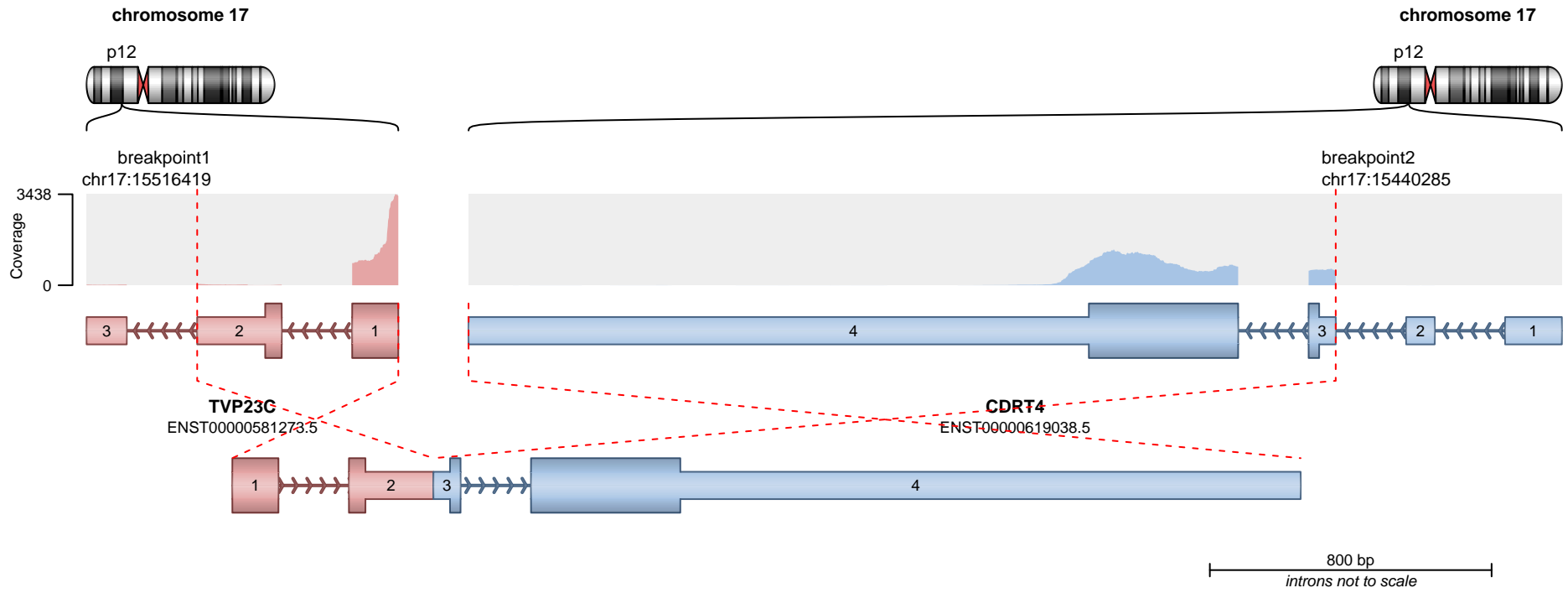
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



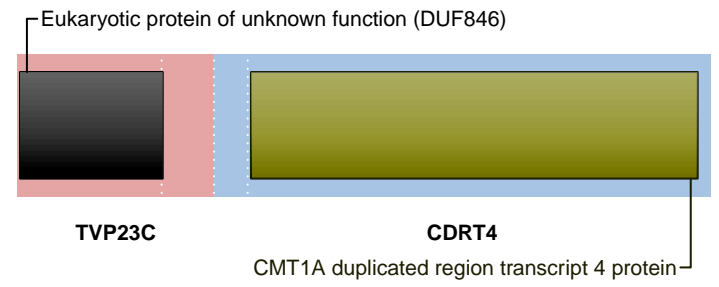
**SUPPORTING READ COUNT**

Split reads = 27  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



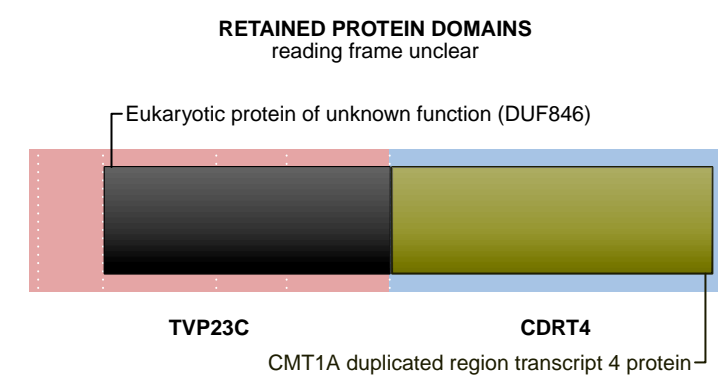
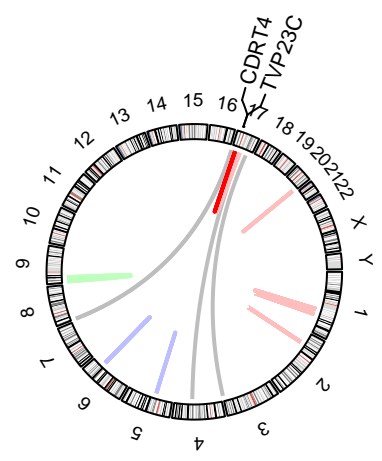
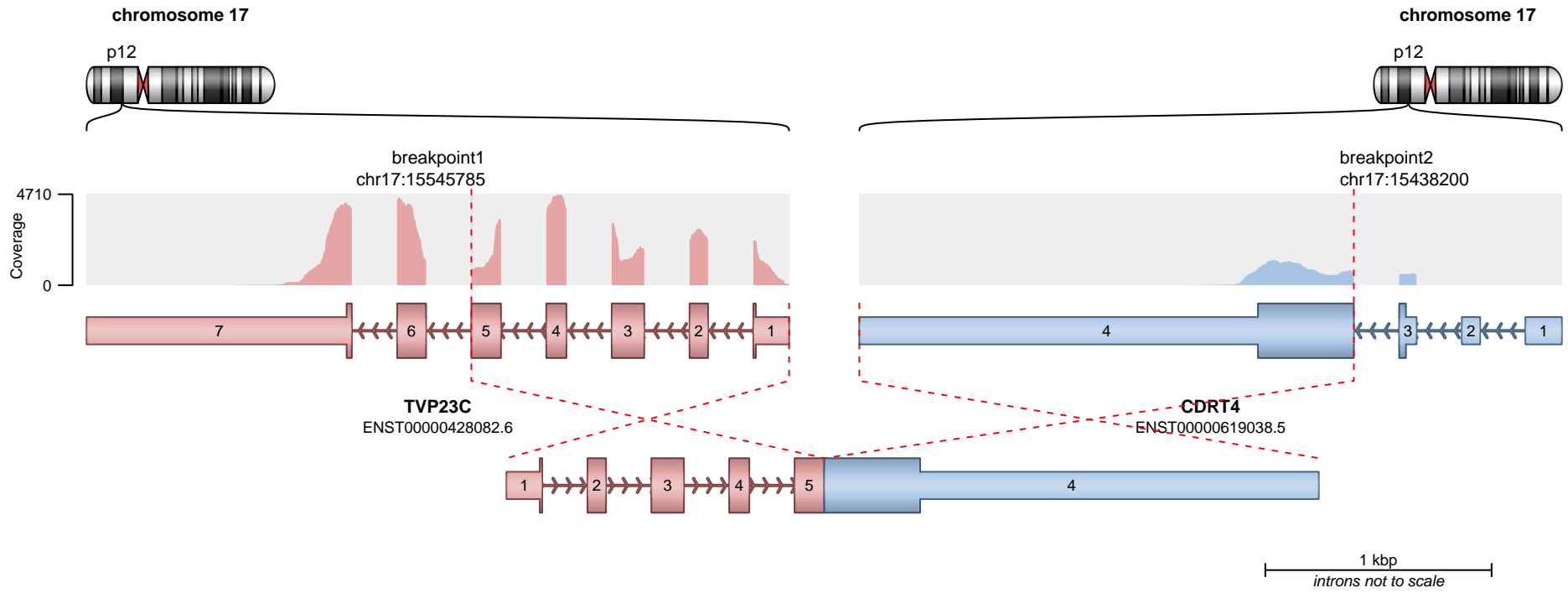
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 11  
Discordant mates = 2

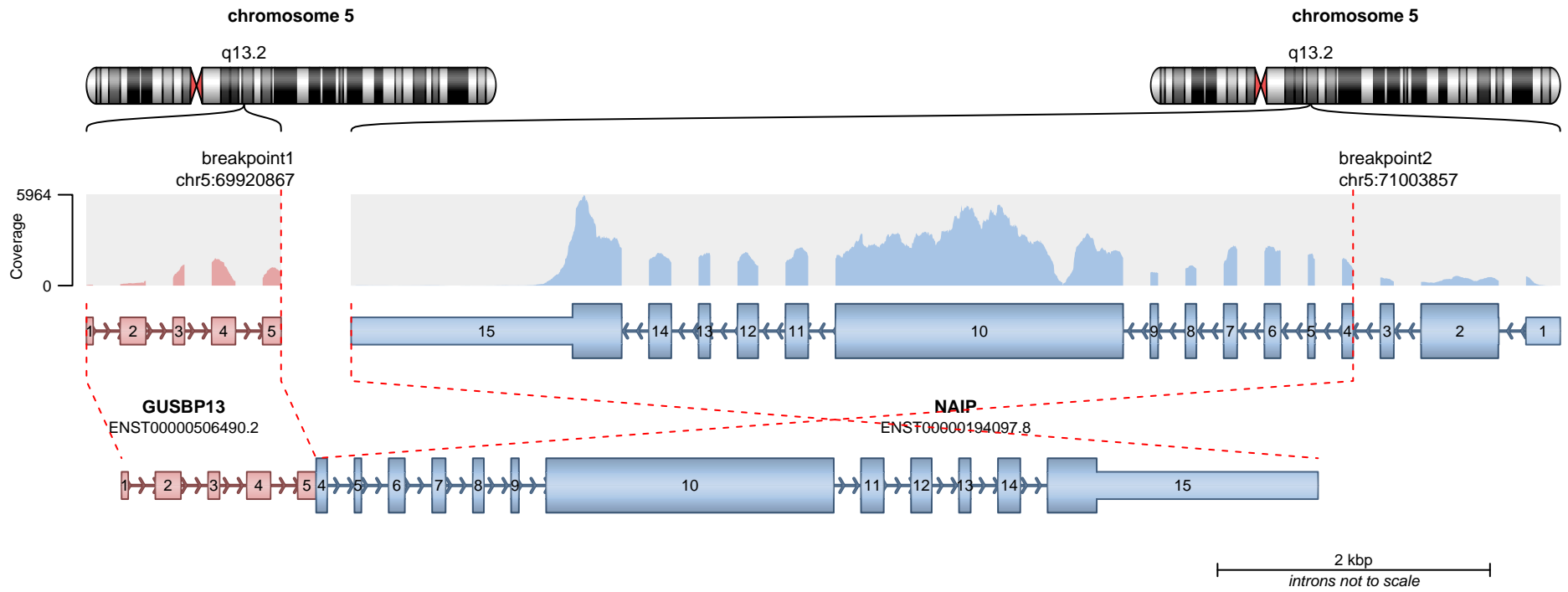
- translocation
- duplication
- deletion
- inversion



**SUPPORTING READ COUNT**

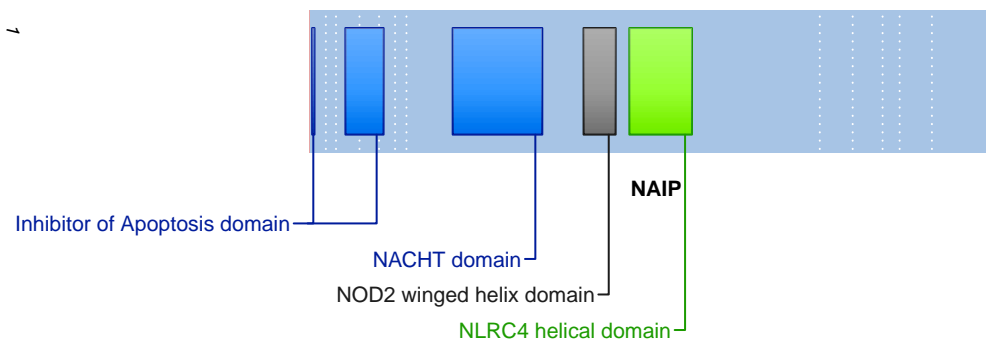
Split reads = 10  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



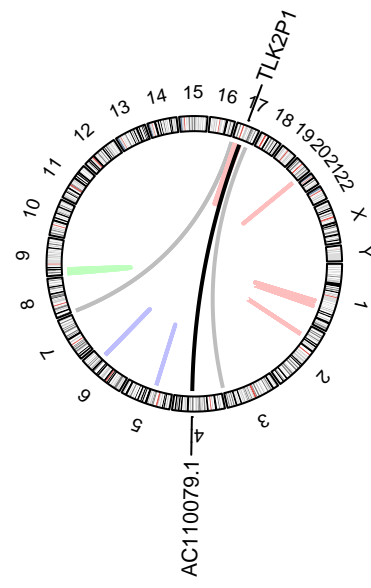
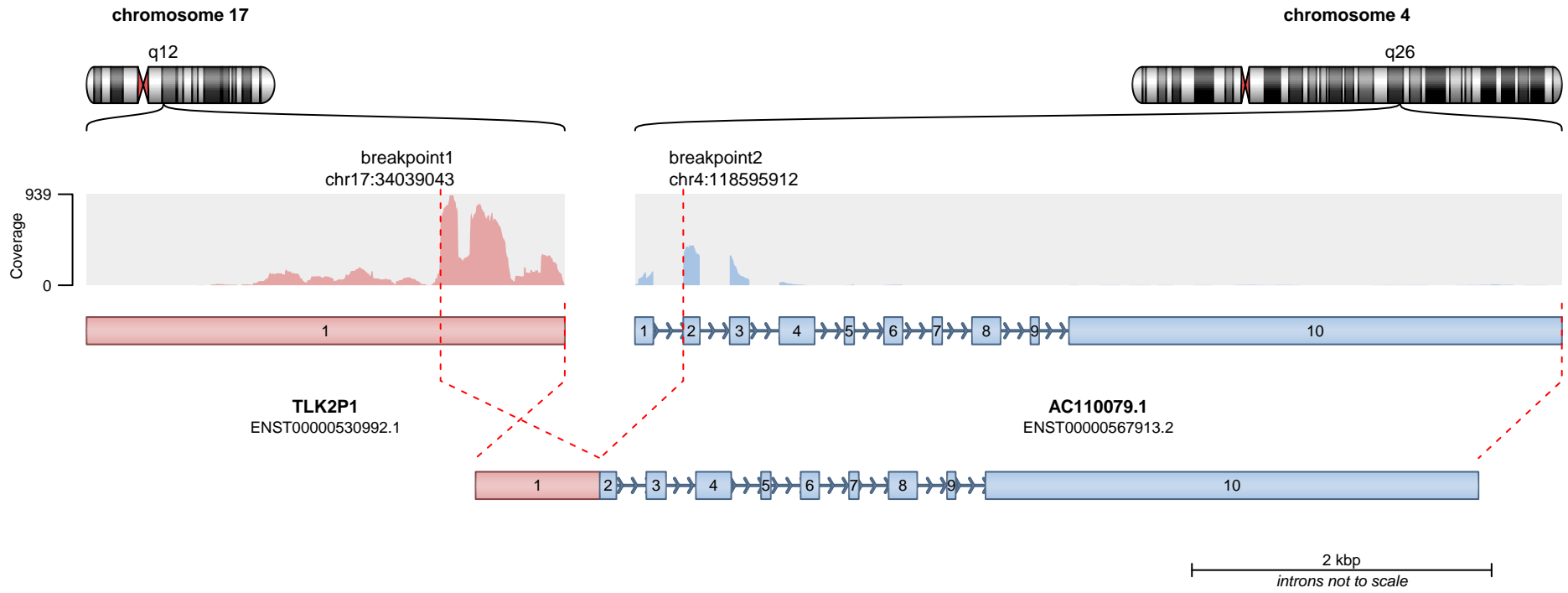
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 99  
Discordant mates = 1

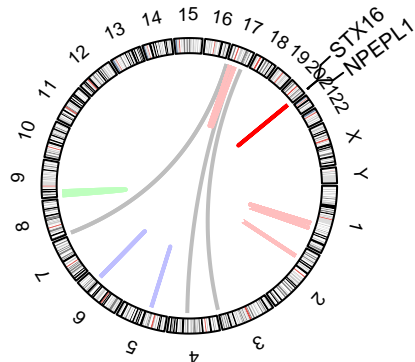
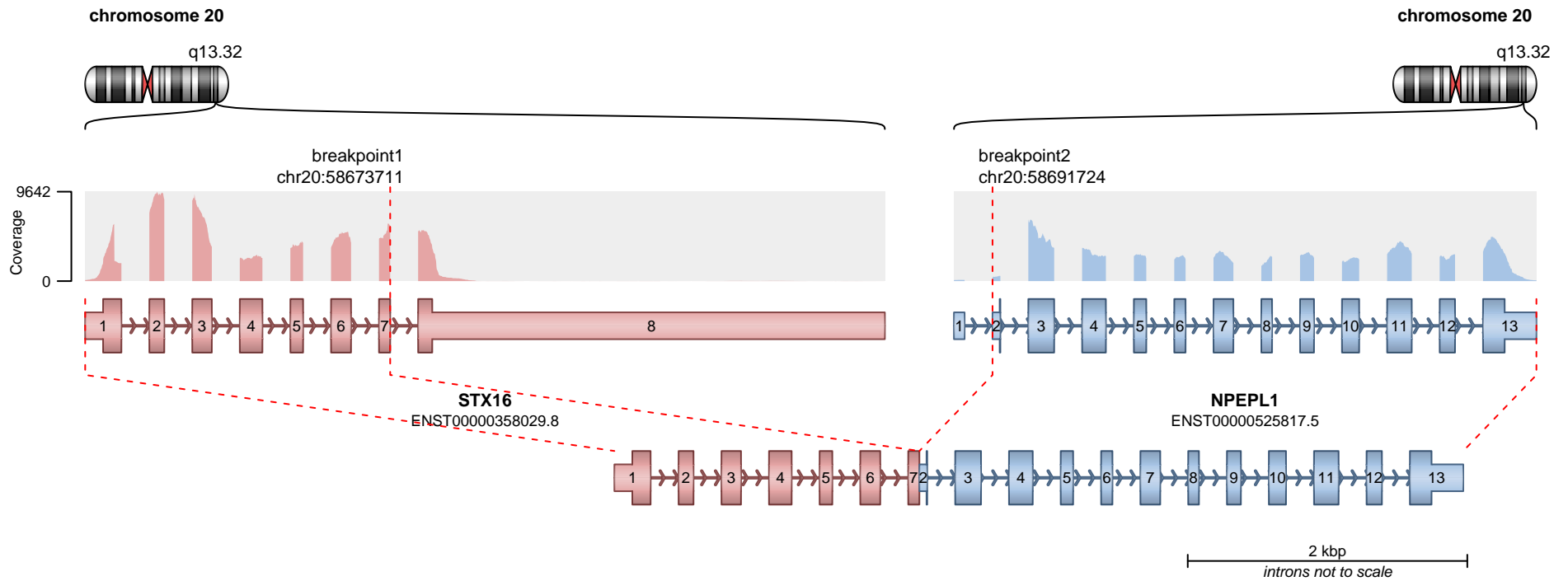


— translocation    — deletion  
 — duplication    — inversion

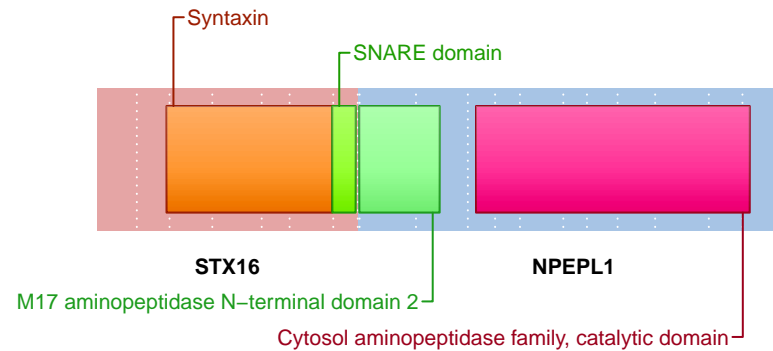
Genes are not protein-coding.

**SUPPORTING READ COUNT**

Split reads = 89  
Discordant mates = 0



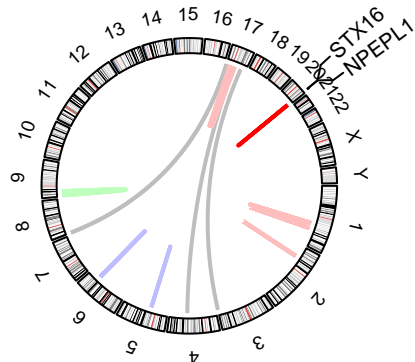
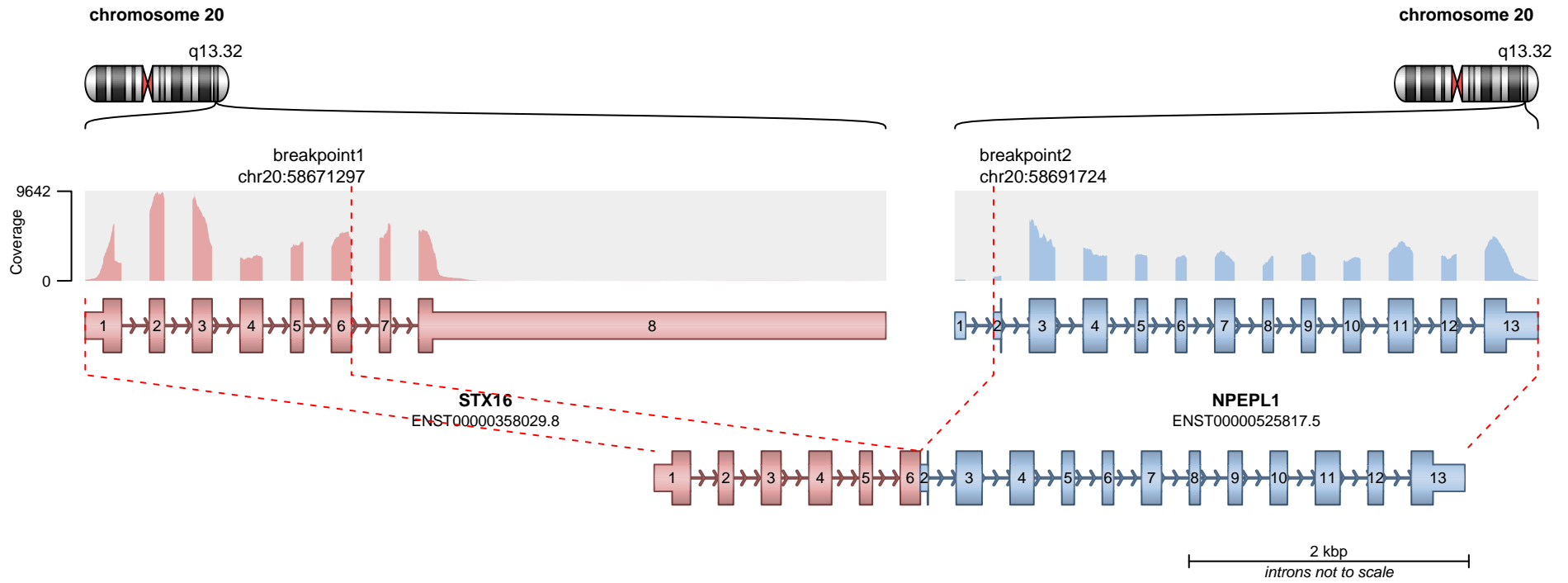
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



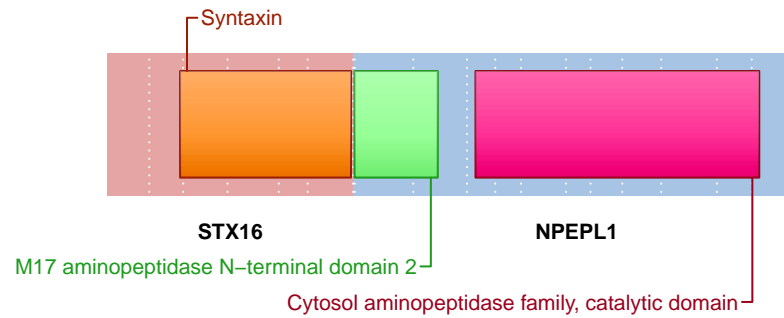
**SUPPORTING READ COUNT**

Split reads = 85  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



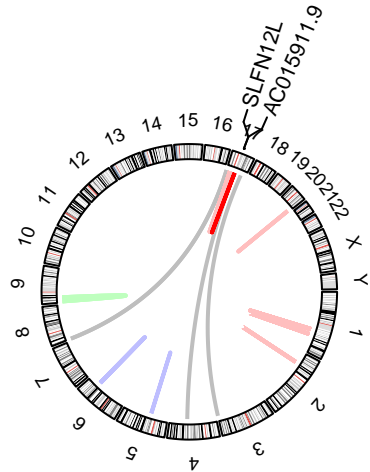
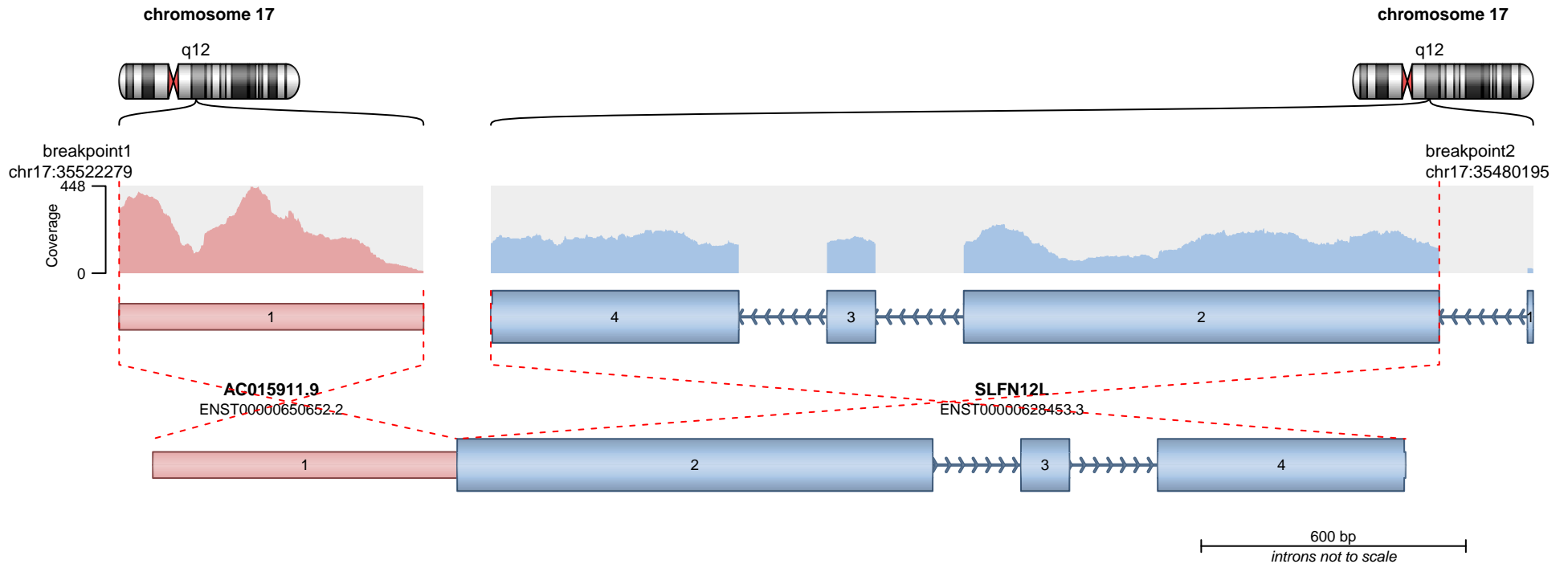
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



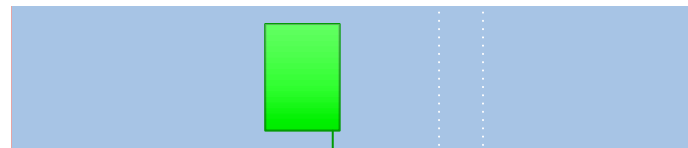
**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



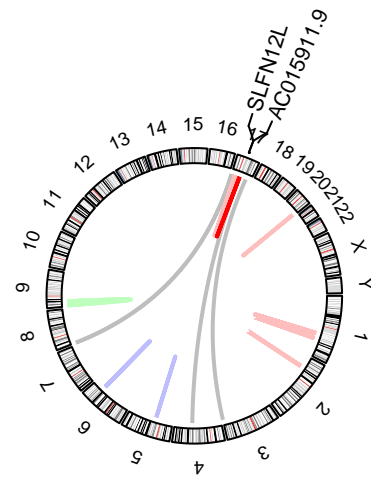
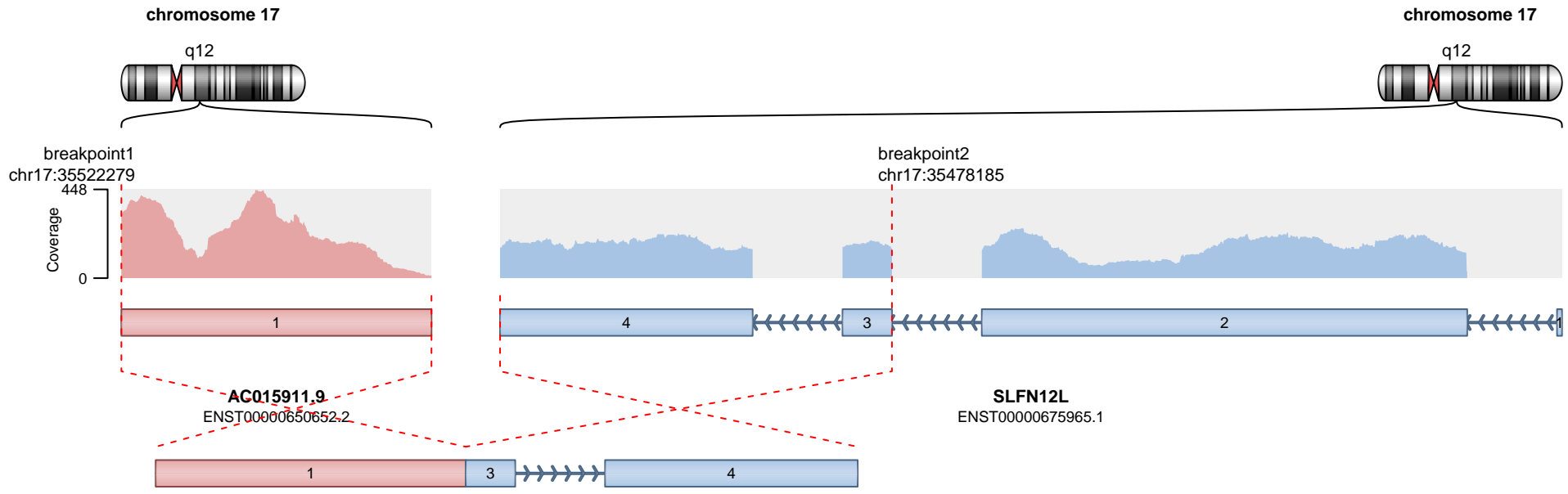
RETAINED PROTEIN DOMAINS  
reading frame unclear



SUPPORTING READ COUNT

Split reads = 28  
Discordant mates = 3

— translocation — deletion  
— duplication — inversion

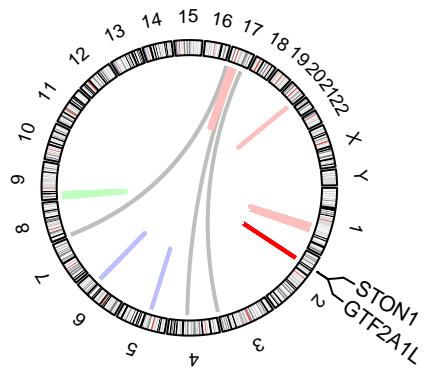
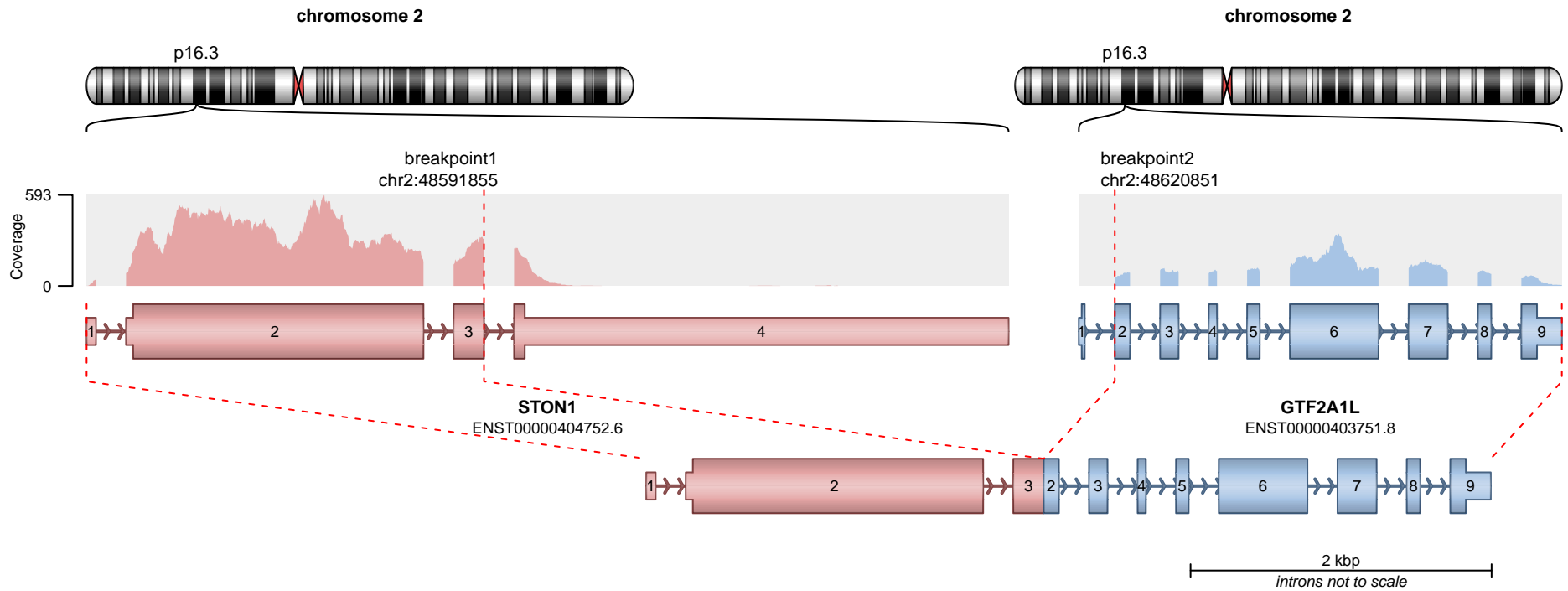


— translocation    — deletion  
— duplication    — inversion

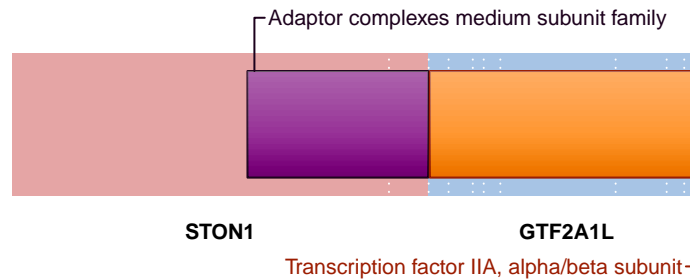
Genes are not protein-coding.

**SUPPORTING READ COUNT**

Split reads = 6  
Discordant mates = 0



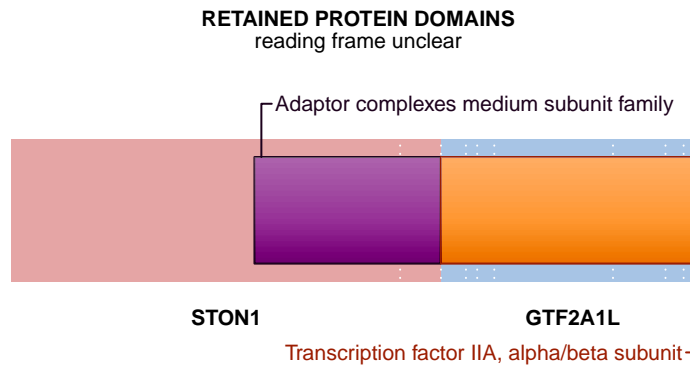
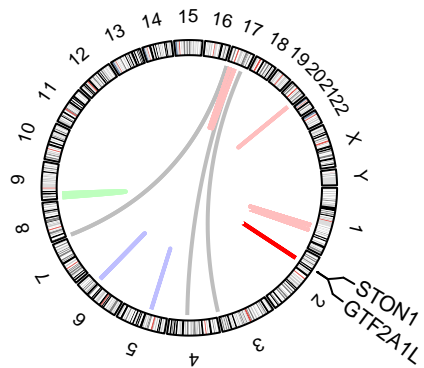
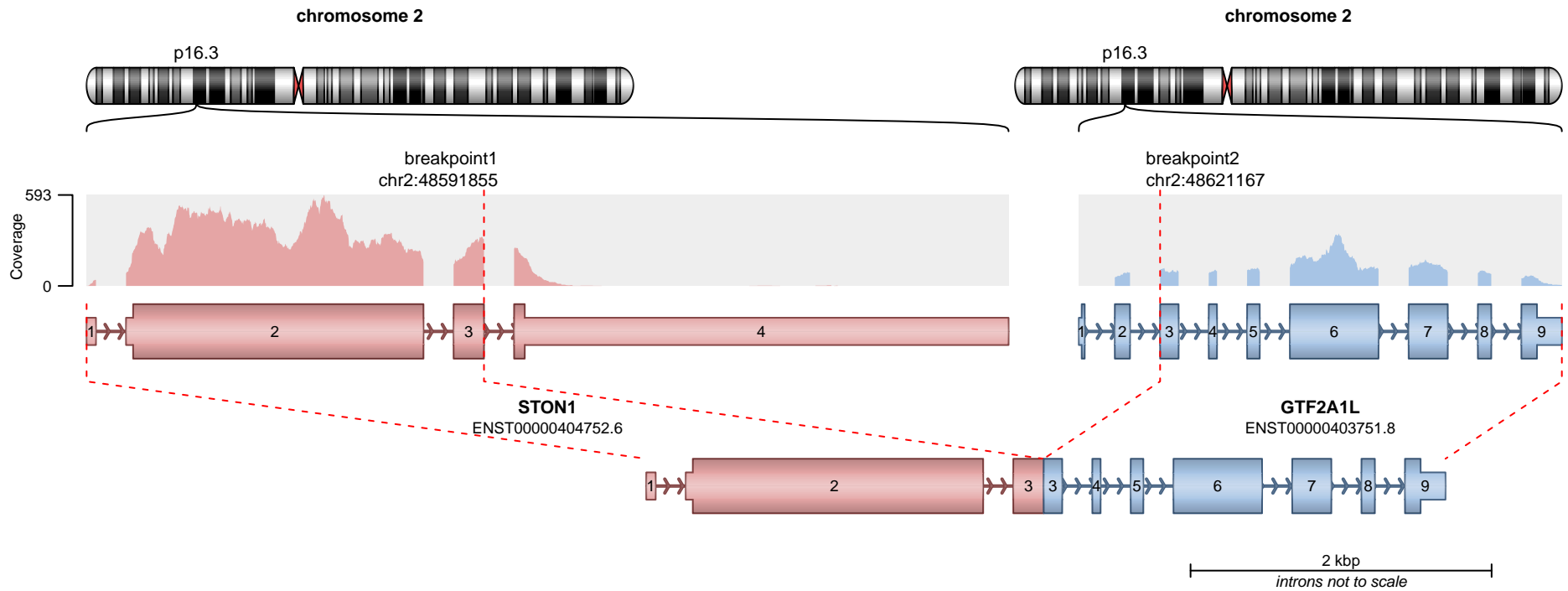
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 16  
Discordant mates = 2

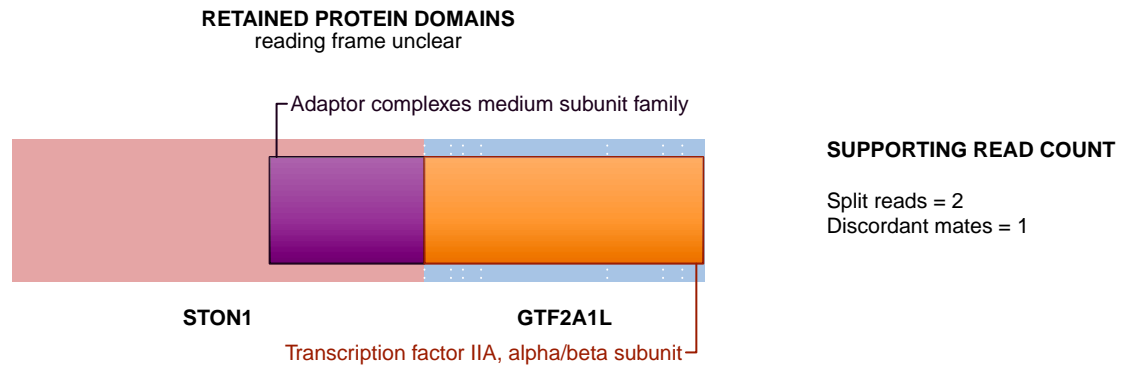
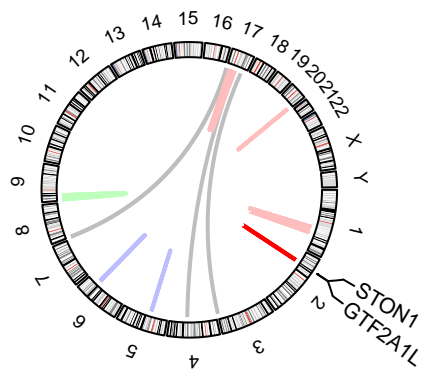
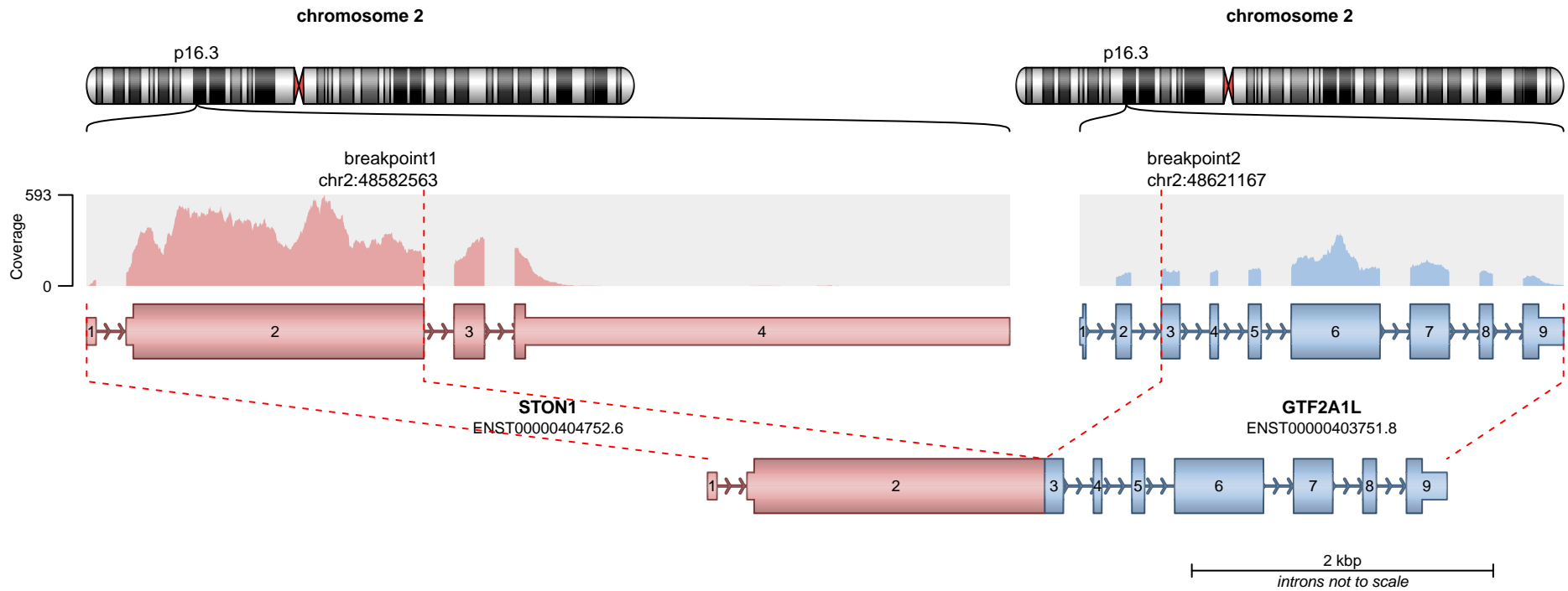
- translocation
- duplication
- deletion
- inversion



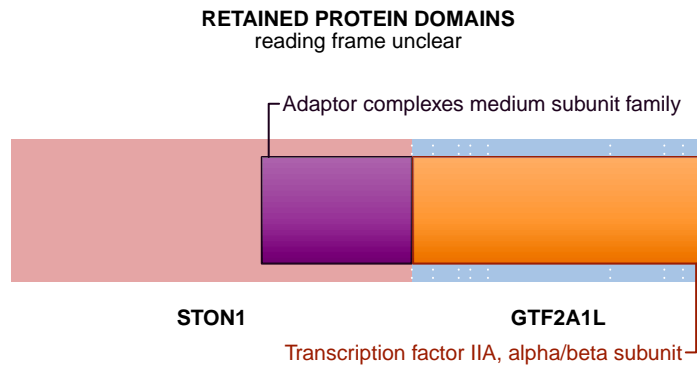
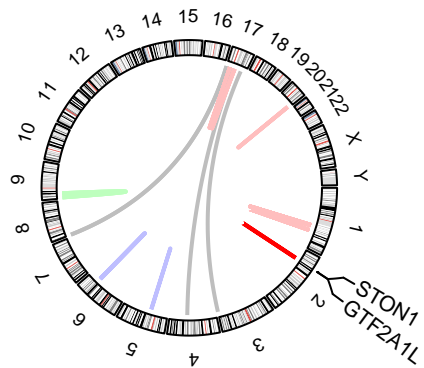
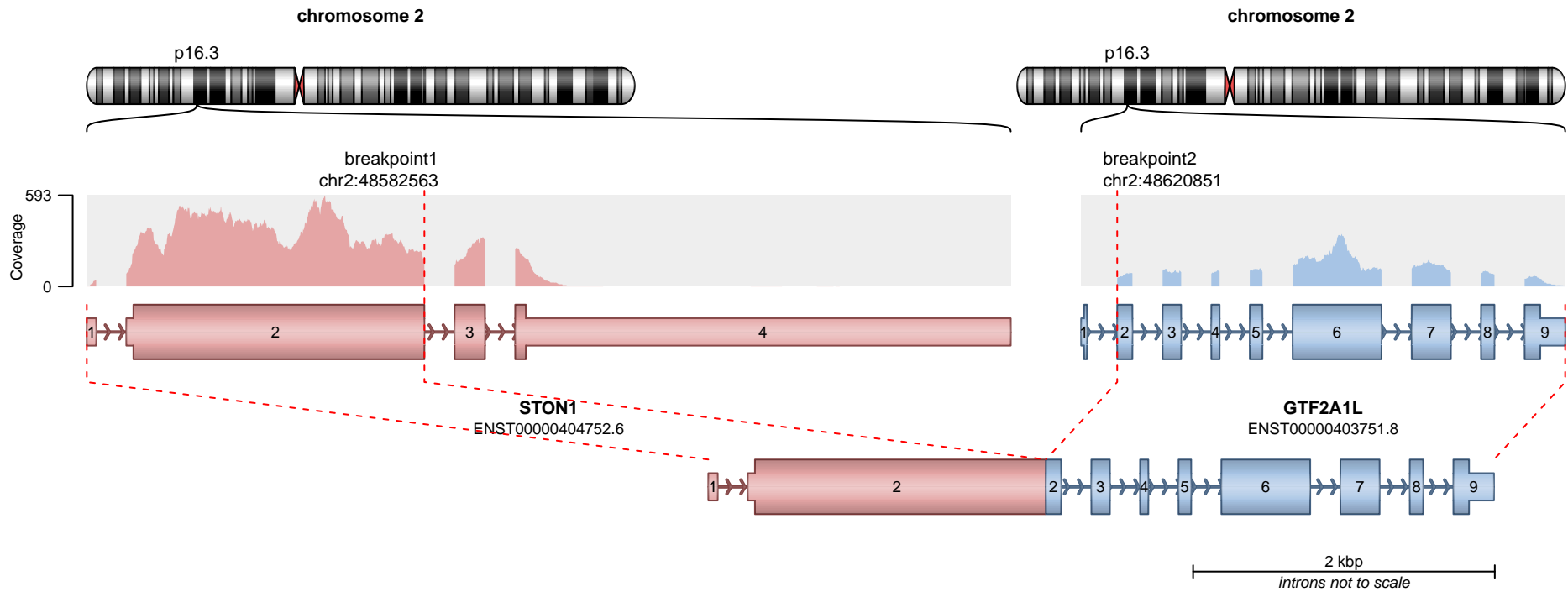
**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 2

- translocation
- duplication
- deletion
- inversion



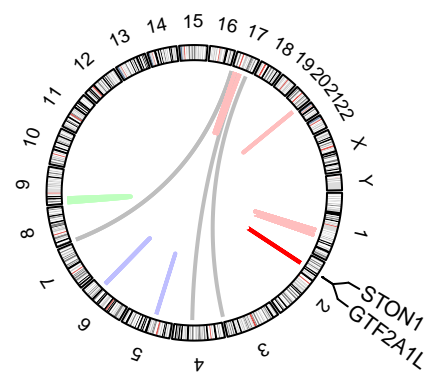
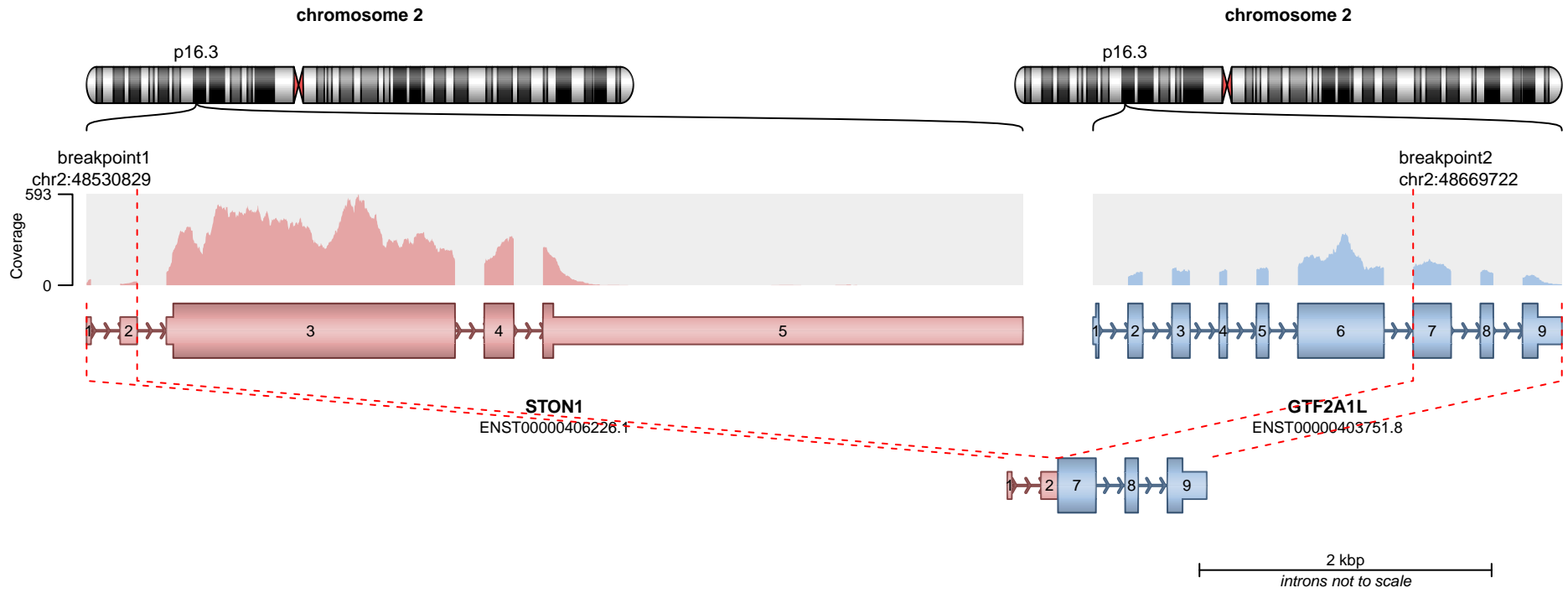
— translocation — deletion  
— duplication — inversion



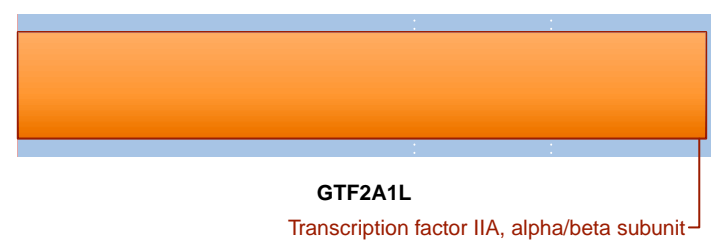
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion