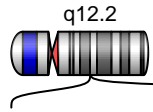
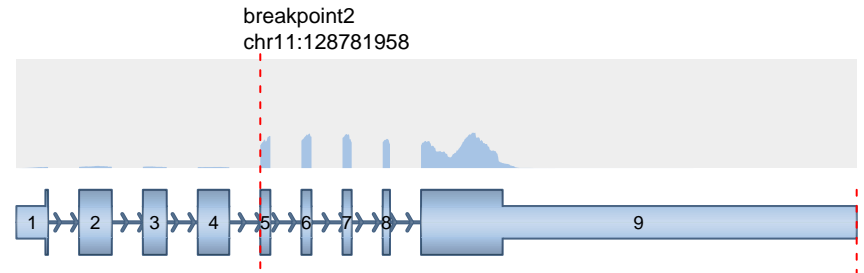
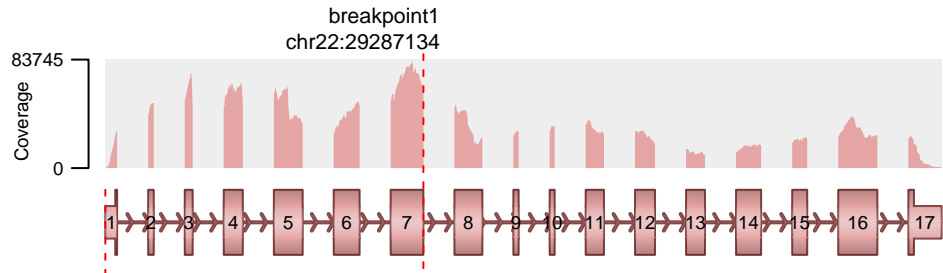


chromosome 22

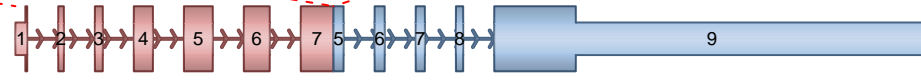


chromosome 11

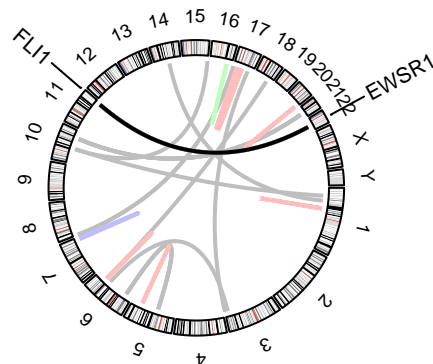


**EWSR1**  
ENST00000406548.5

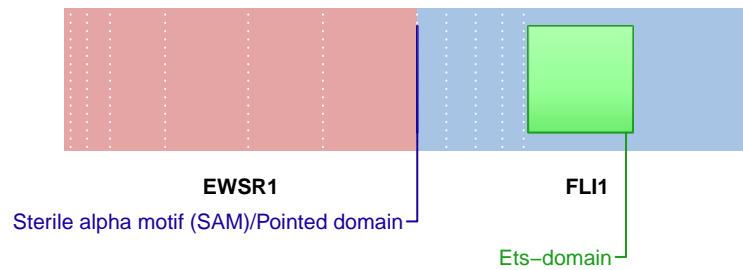
**FLI1**  
ENST00000527786.7



2 kbp  
*introns not to scale*



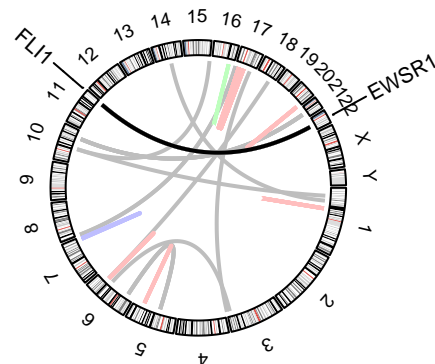
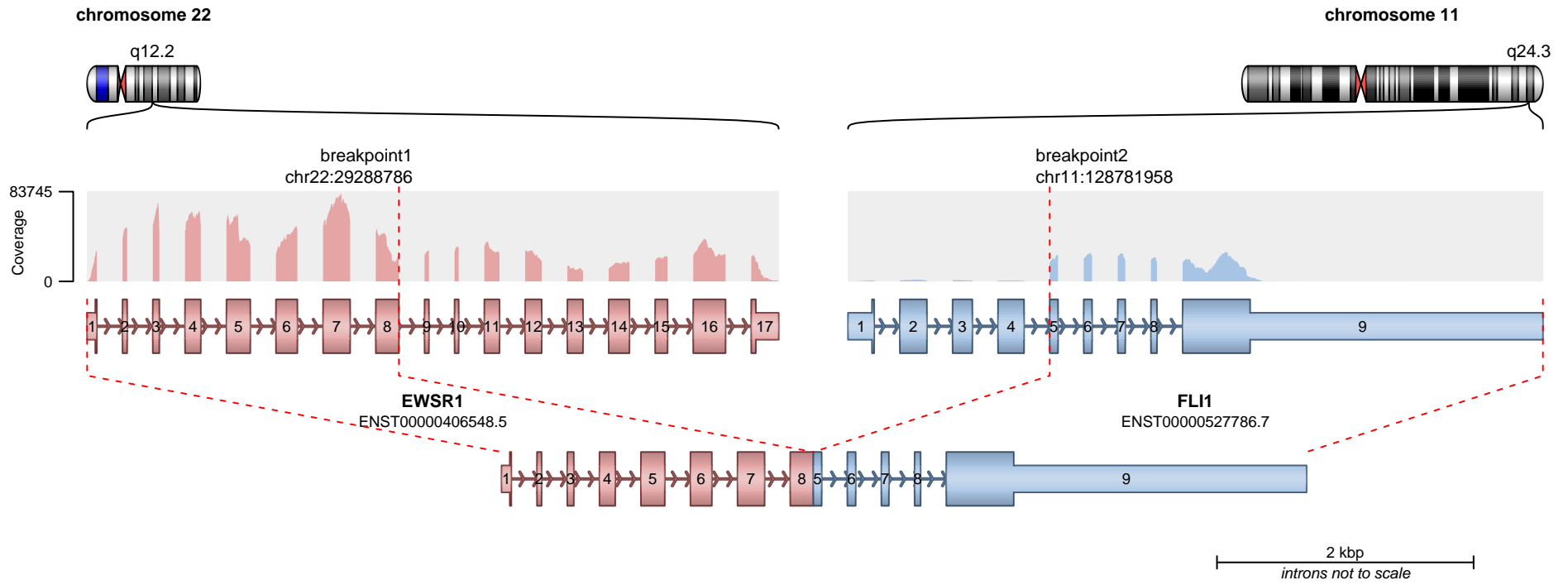
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



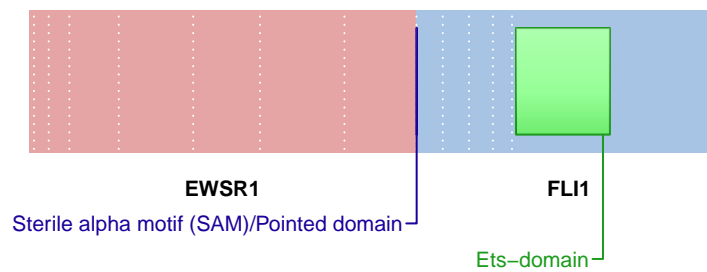
**SUPPORTING READ COUNT**

Split reads = 5207  
Discordant mates = 9

— translocation    — deletion  
— duplication    — inversion



**RETAINED PROTEIN DOMAINS**  
reading frame unclear

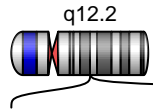


**SUPPORTING READ COUNT**

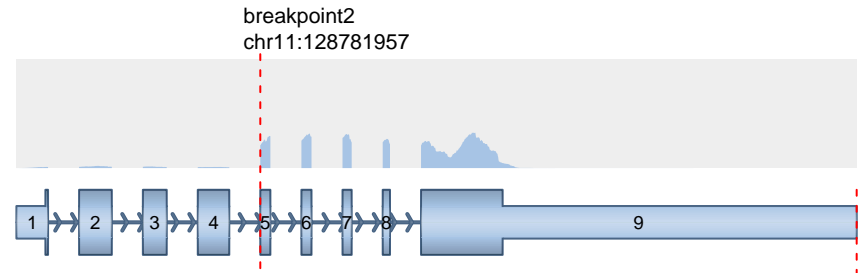
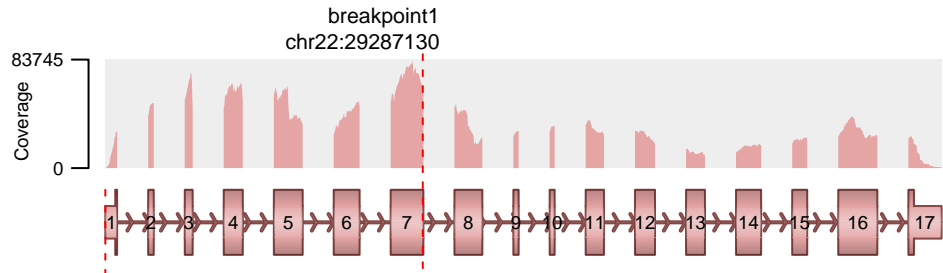
Split reads = 480  
Discordant mates = 12

- translocation
- duplication
- deletion
- inversion

chromosome 22

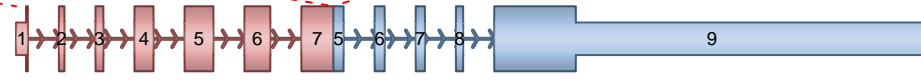


chromosome 11

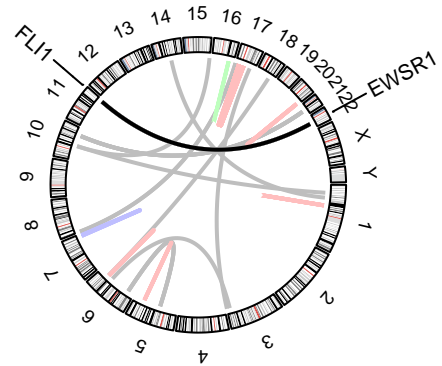


**EWSR1**  
ENST00000406548.5

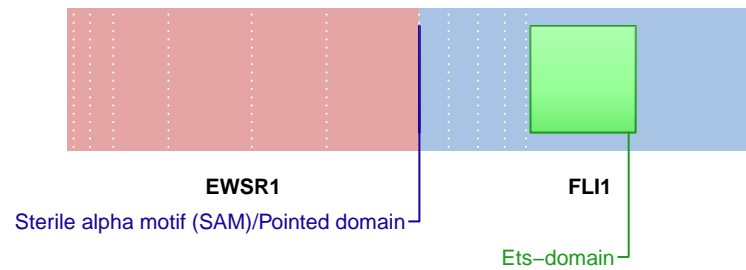
**FLI1**  
ENST00000527786.7



2 kbp  
*introns not to scale*



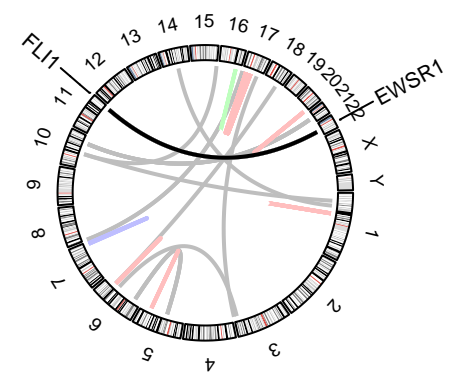
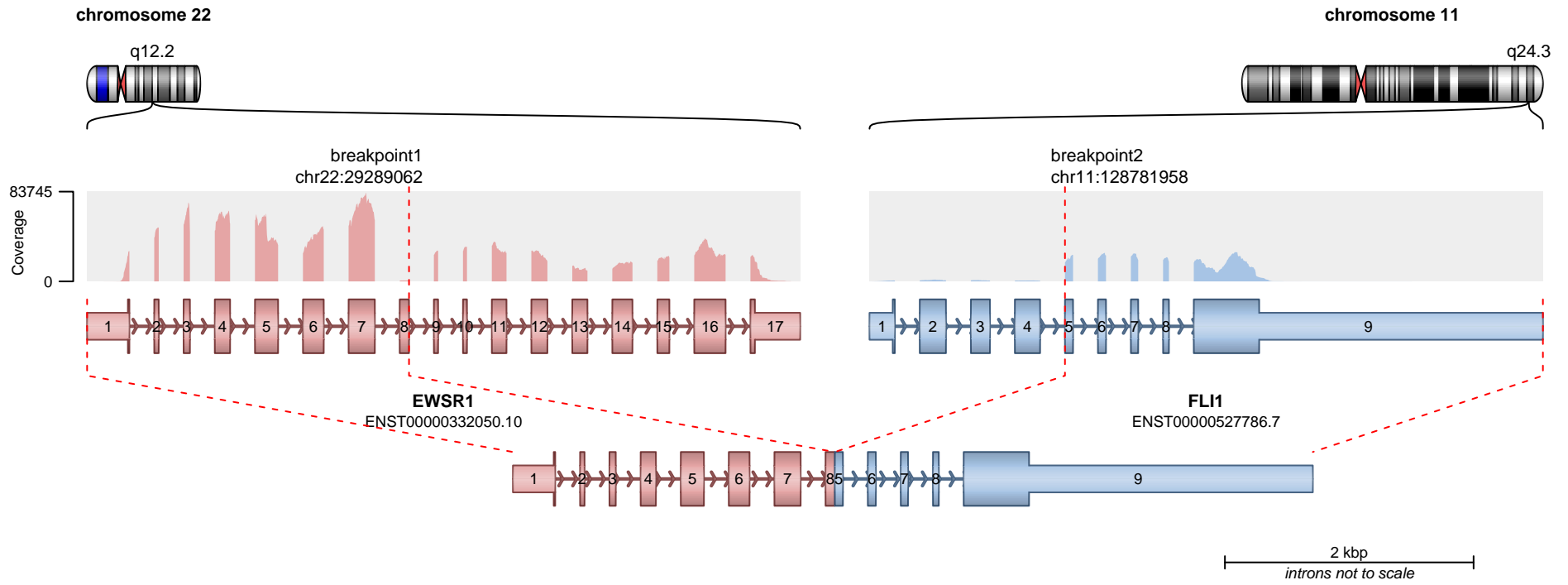
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



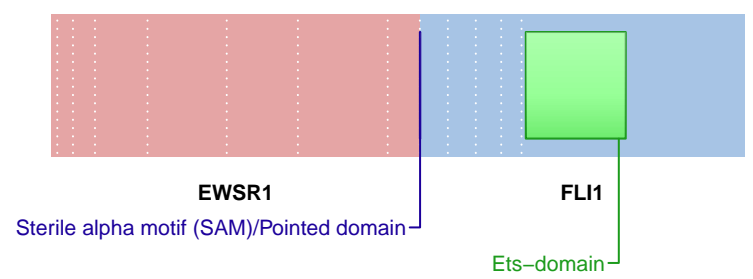
**SUPPORTING READ COUNT**

Split reads = 7  
Discordant mates = 8

— translocation    — deletion  
— duplication    — inversion



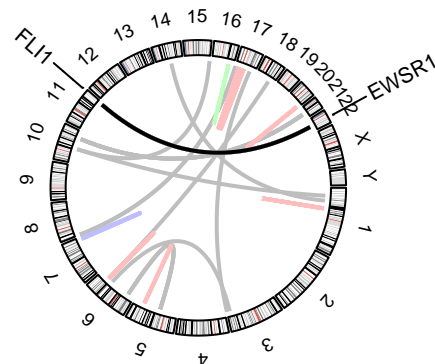
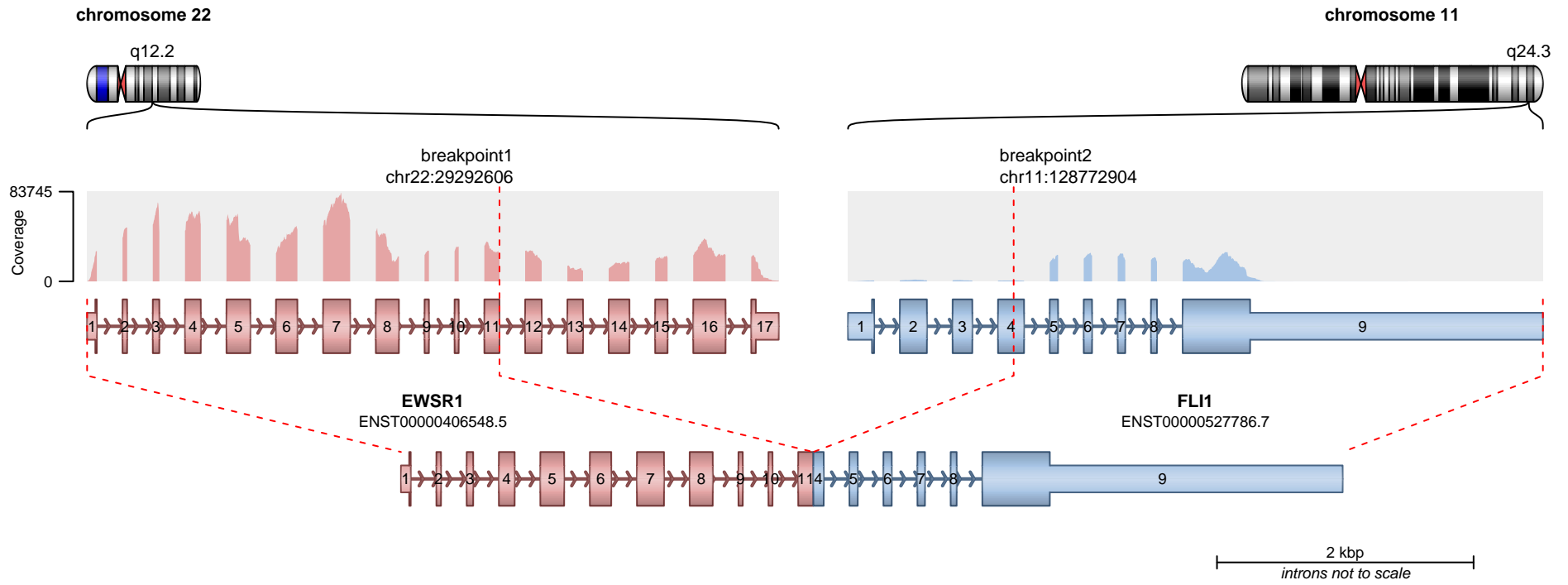
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



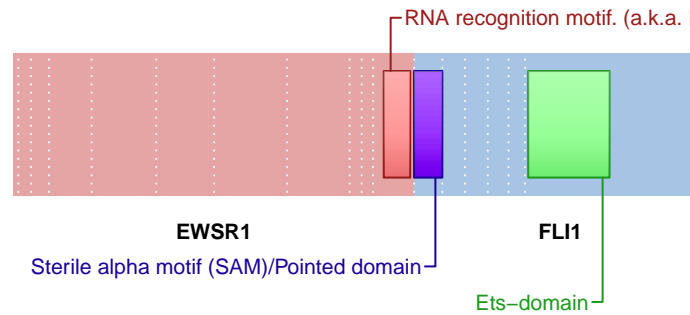
**SUPPORTING READ COUNT**

Split reads = 5  
Discordant mates = 12

- translocation
- duplication
- deletion
- inversion



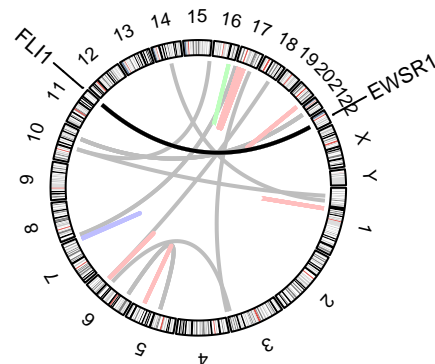
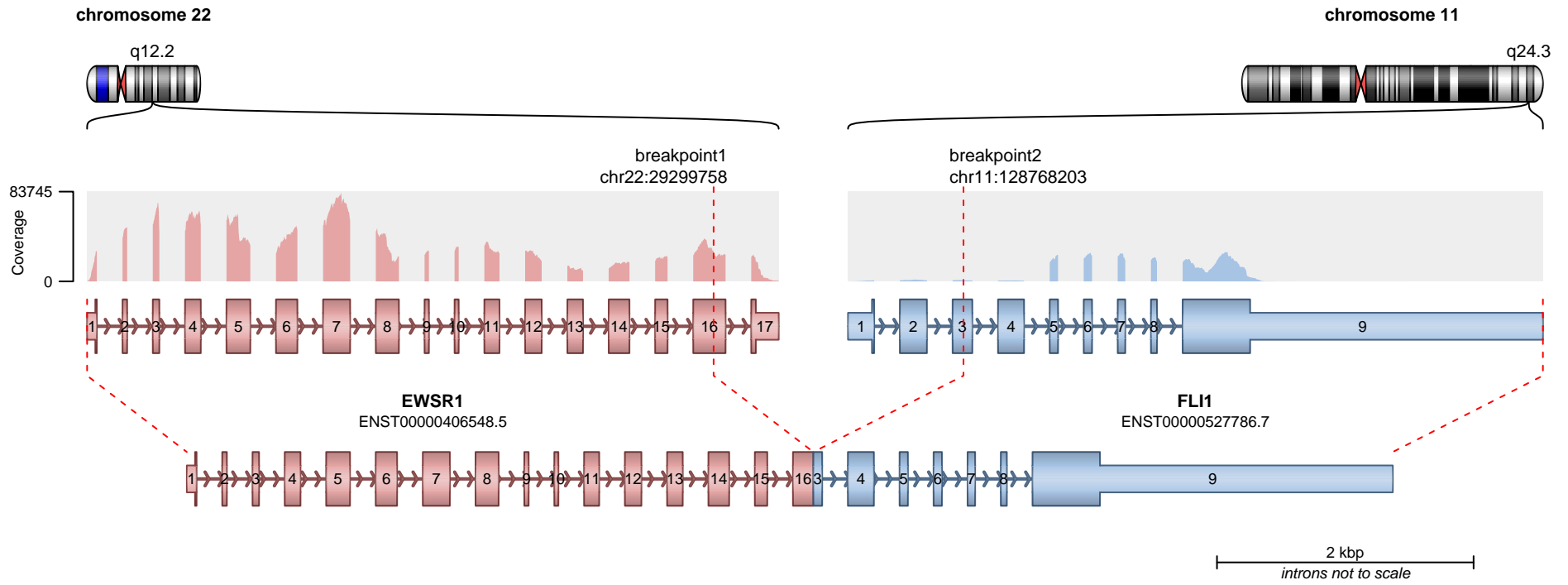
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



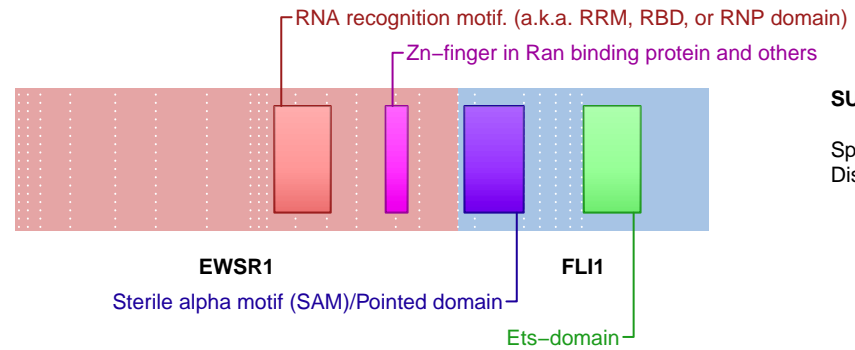
**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 12

- translocation
- duplication
- deletion
- inversion



**RETAINED PROTEIN DOMAINS**  
reading frame unclear

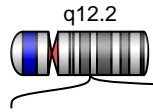


**SUPPORTING READ COUNT**

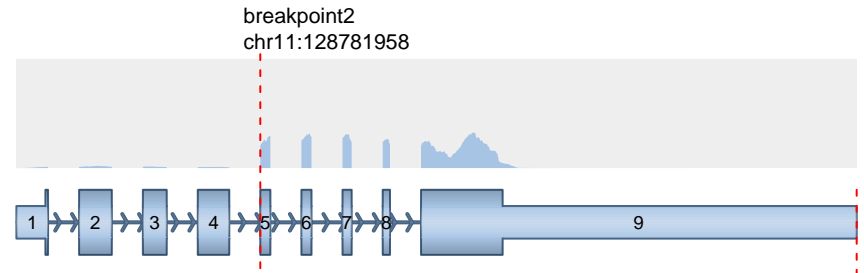
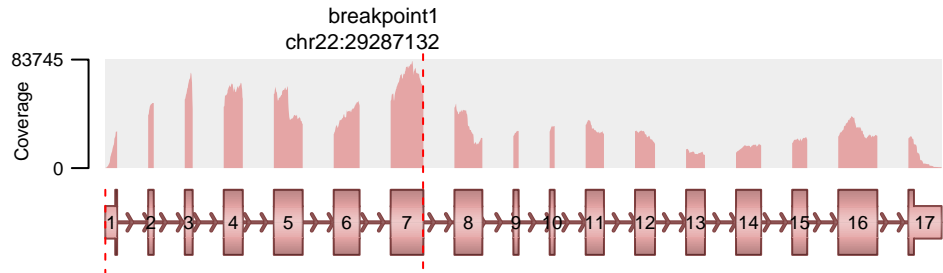
Split reads = 3  
Discordant mates = 12

- translocation
- deletion
- duplication
- inversion

chromosome 22

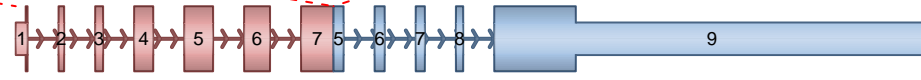


chromosome 11

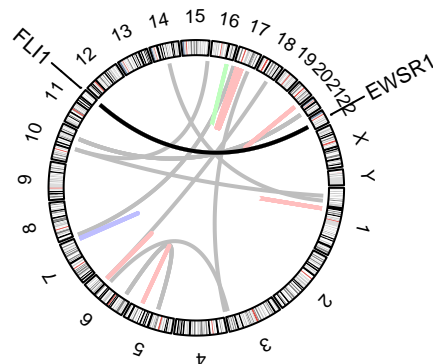


**EWSR1**  
ENST00000406548.5

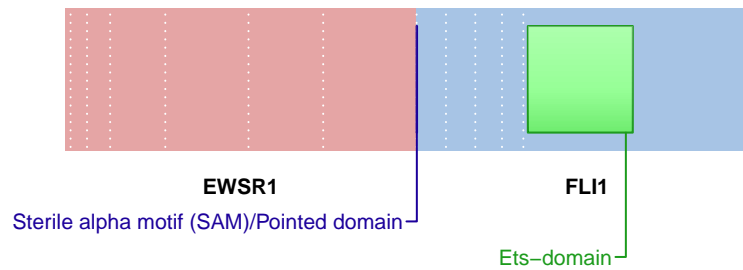
**FLI1**  
ENST00000527786.7



2 kbp  
*introns not to scale*



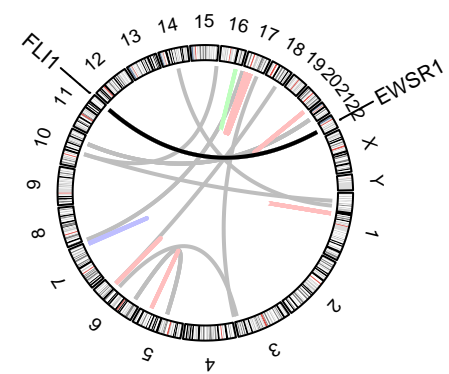
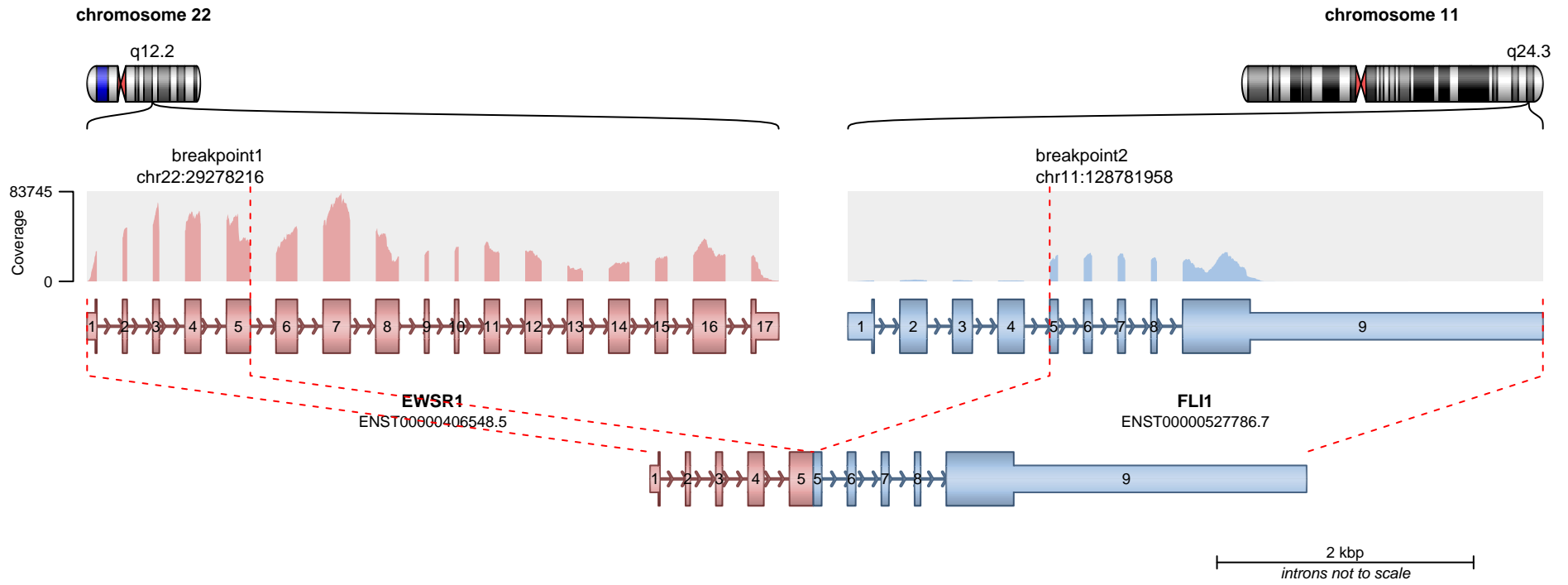
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



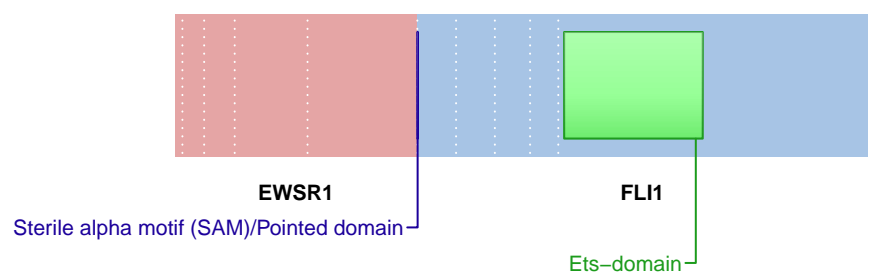
**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 9

— translocation    — deletion  
— duplication    — inversion



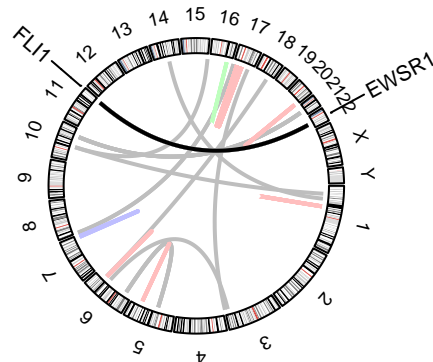
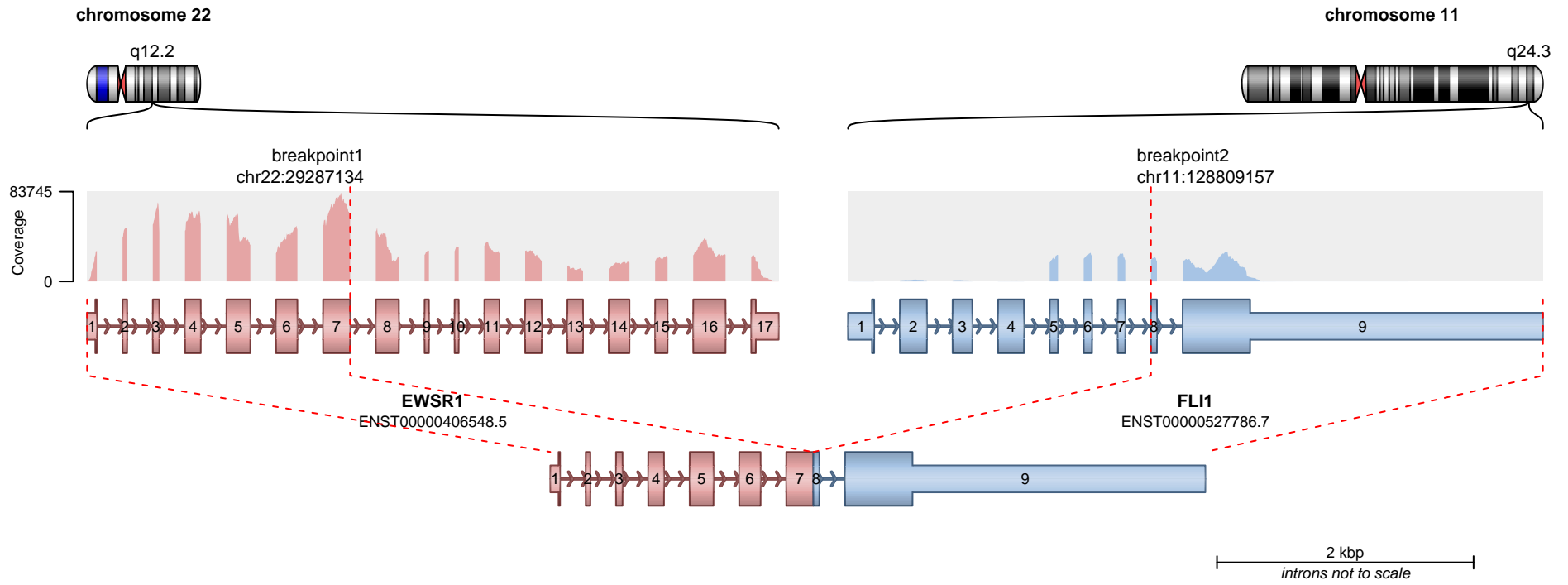
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



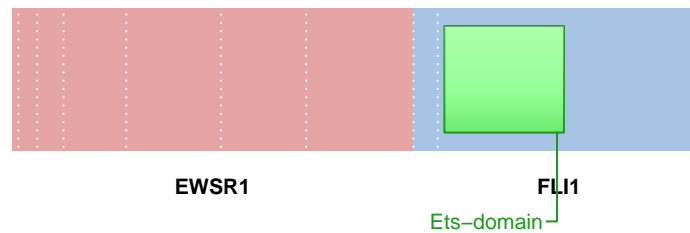
**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



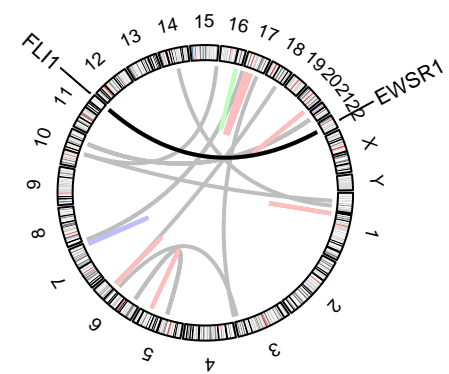
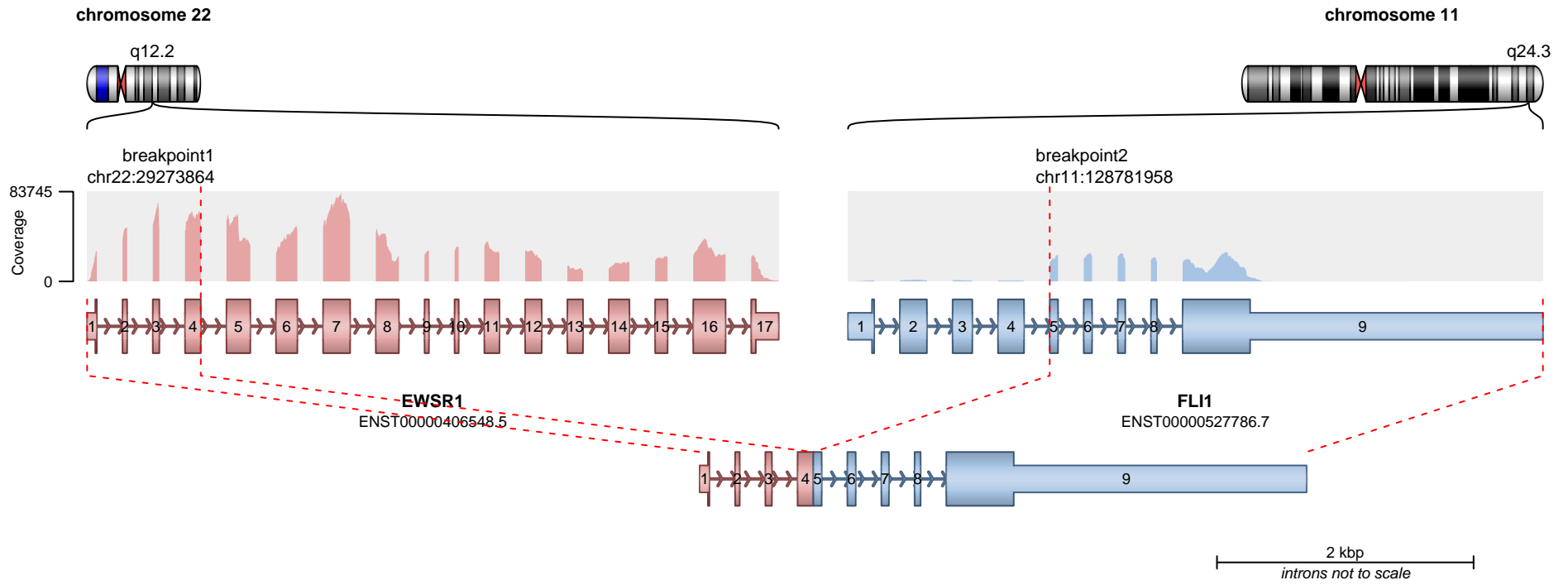
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



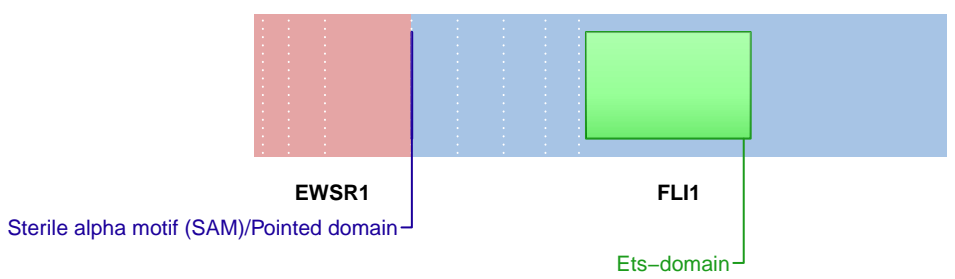
**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



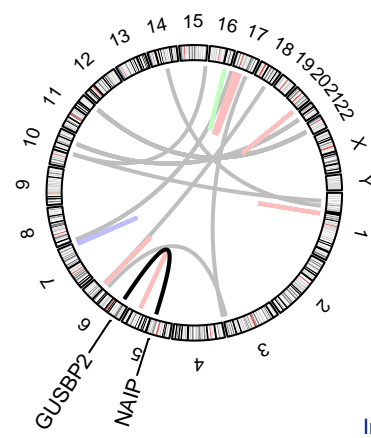
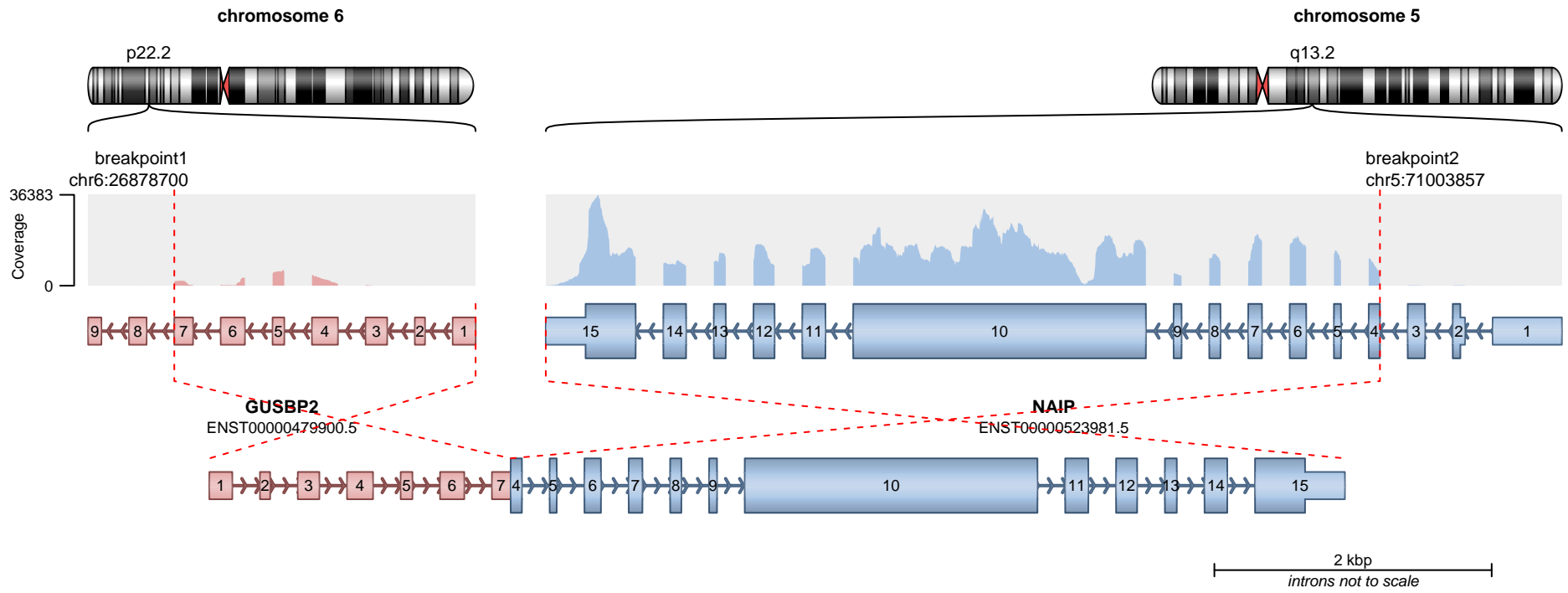
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

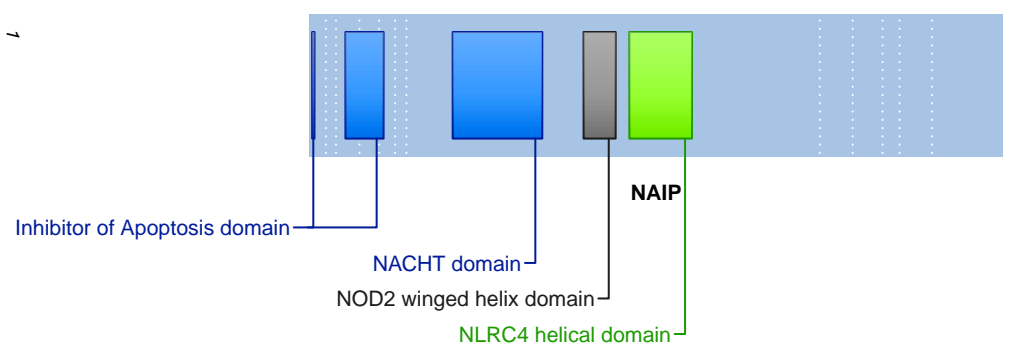
Split reads = 1  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



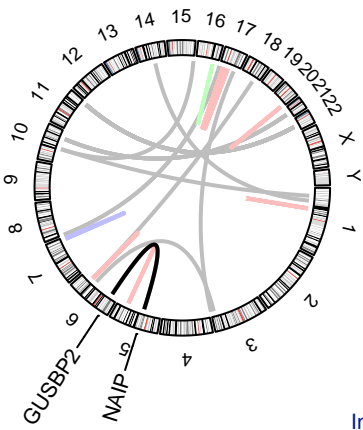
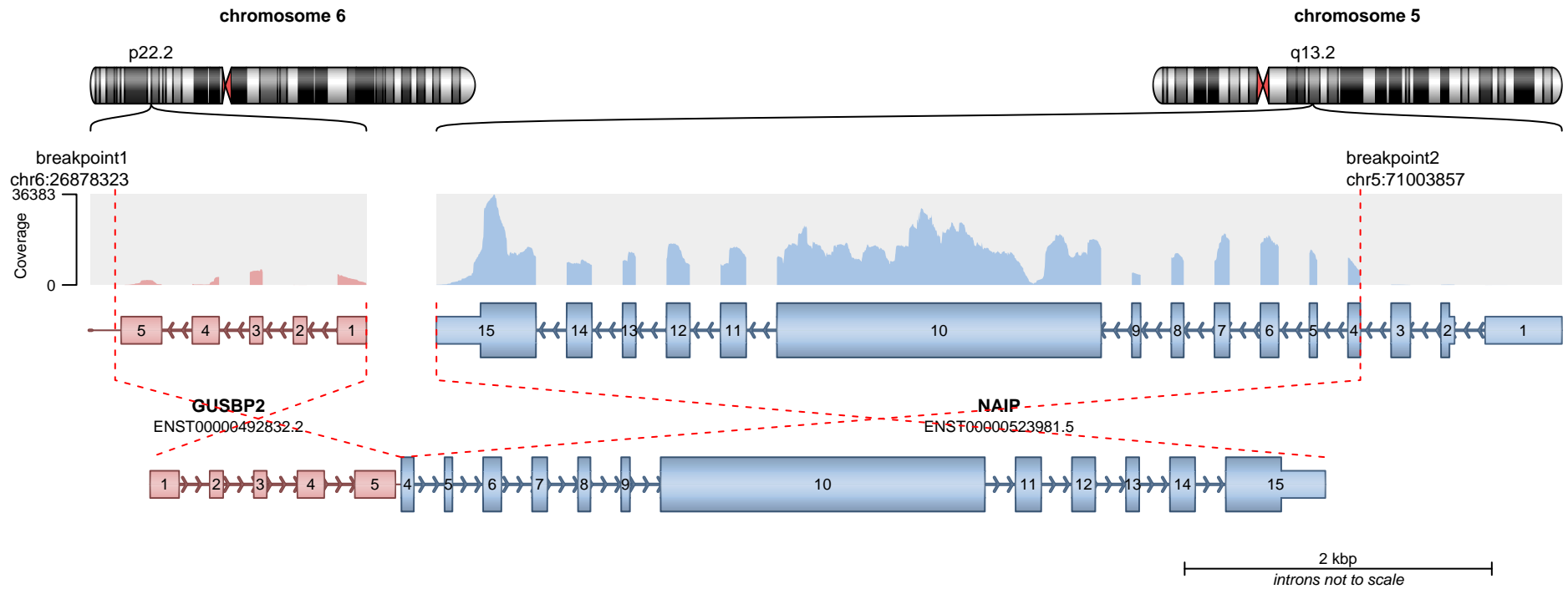
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



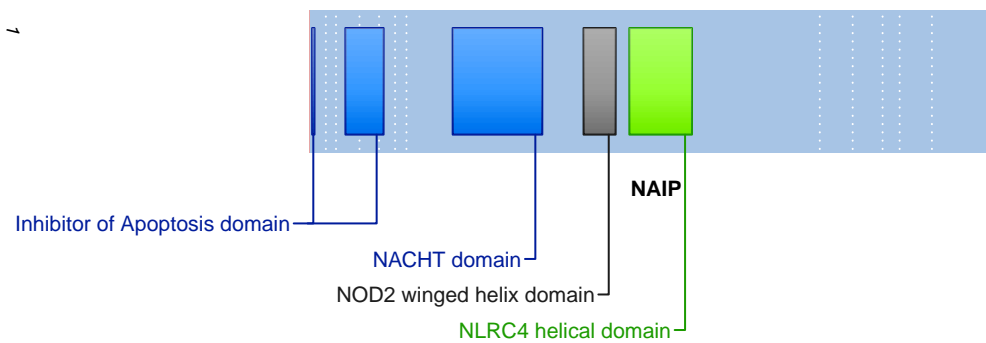
**SUPPORTING READ COUNT**

Split reads = 635  
Discordant mates = 1



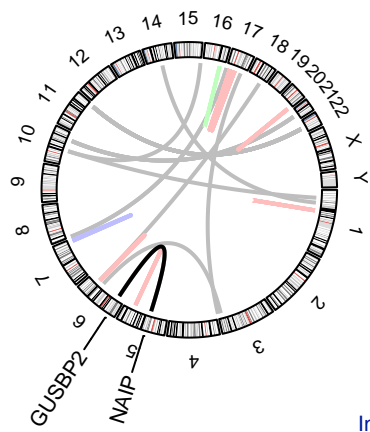
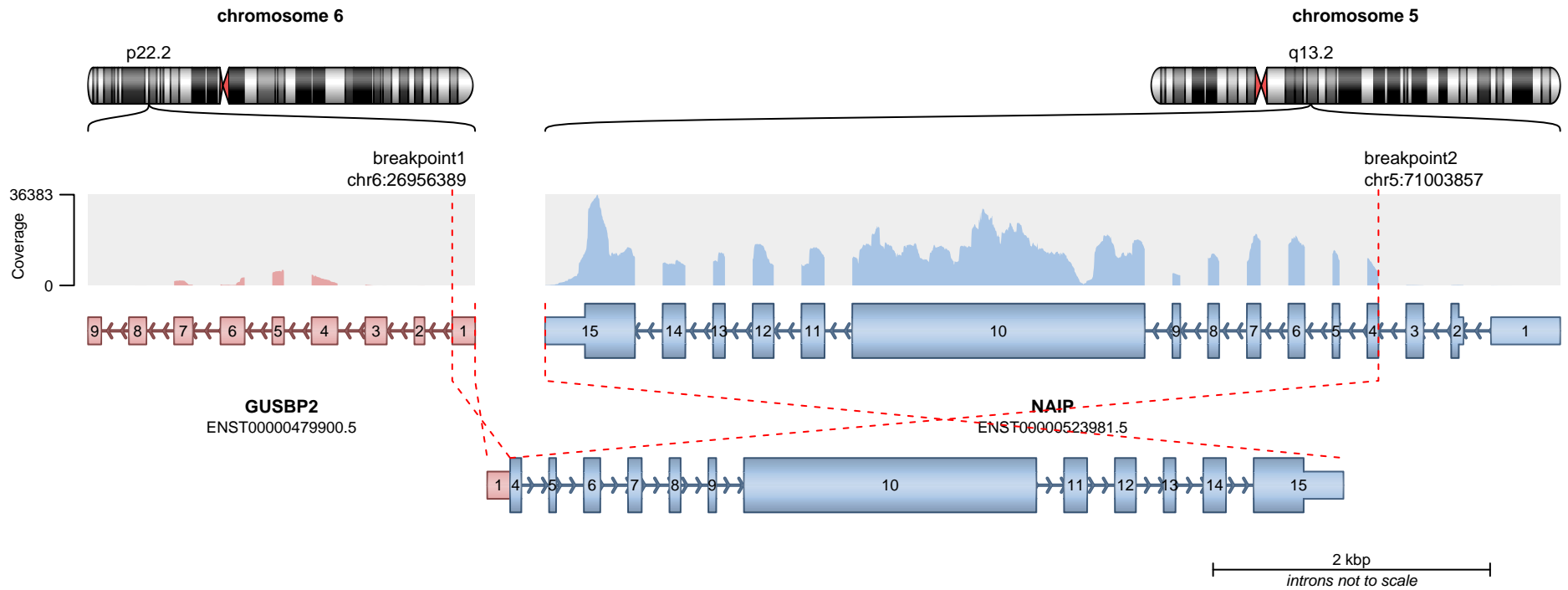
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



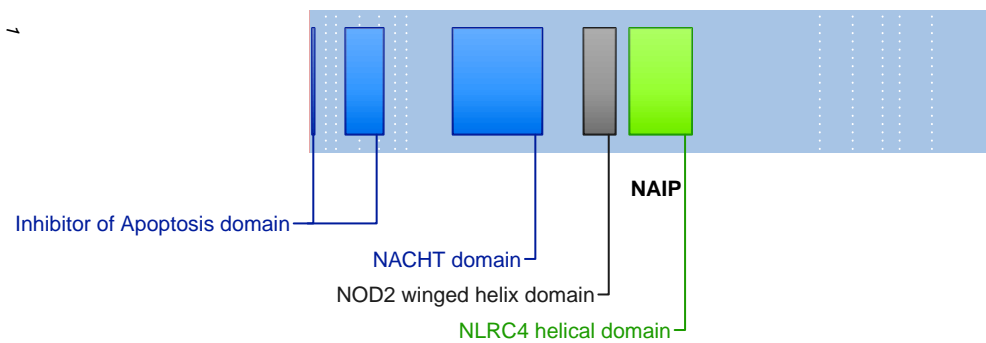
**SUPPORTING READ COUNT**

Split reads = 225  
Discordant mates = 1



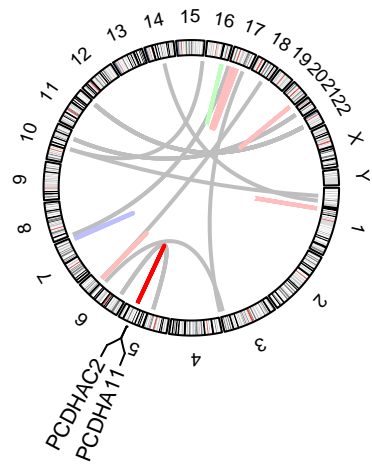
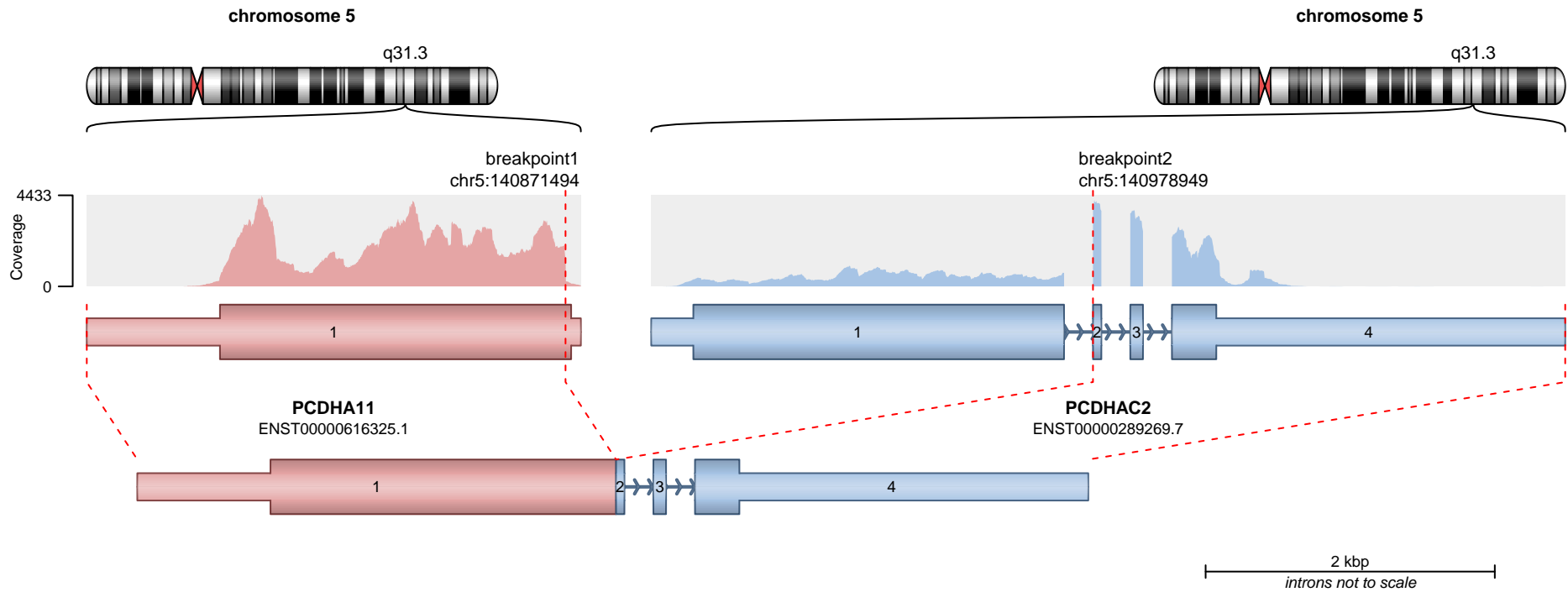
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



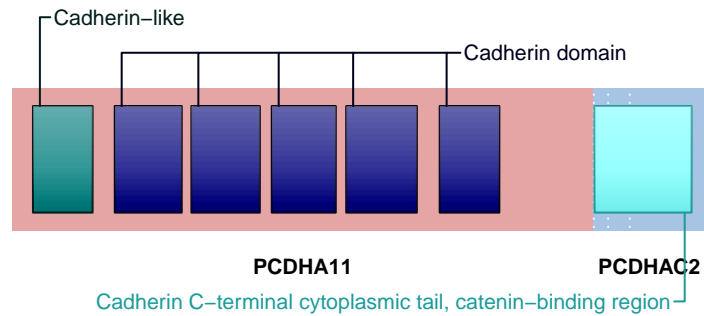
**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0



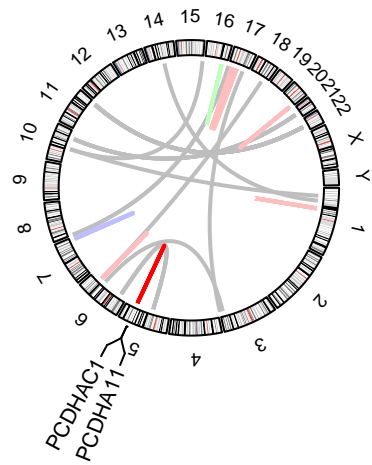
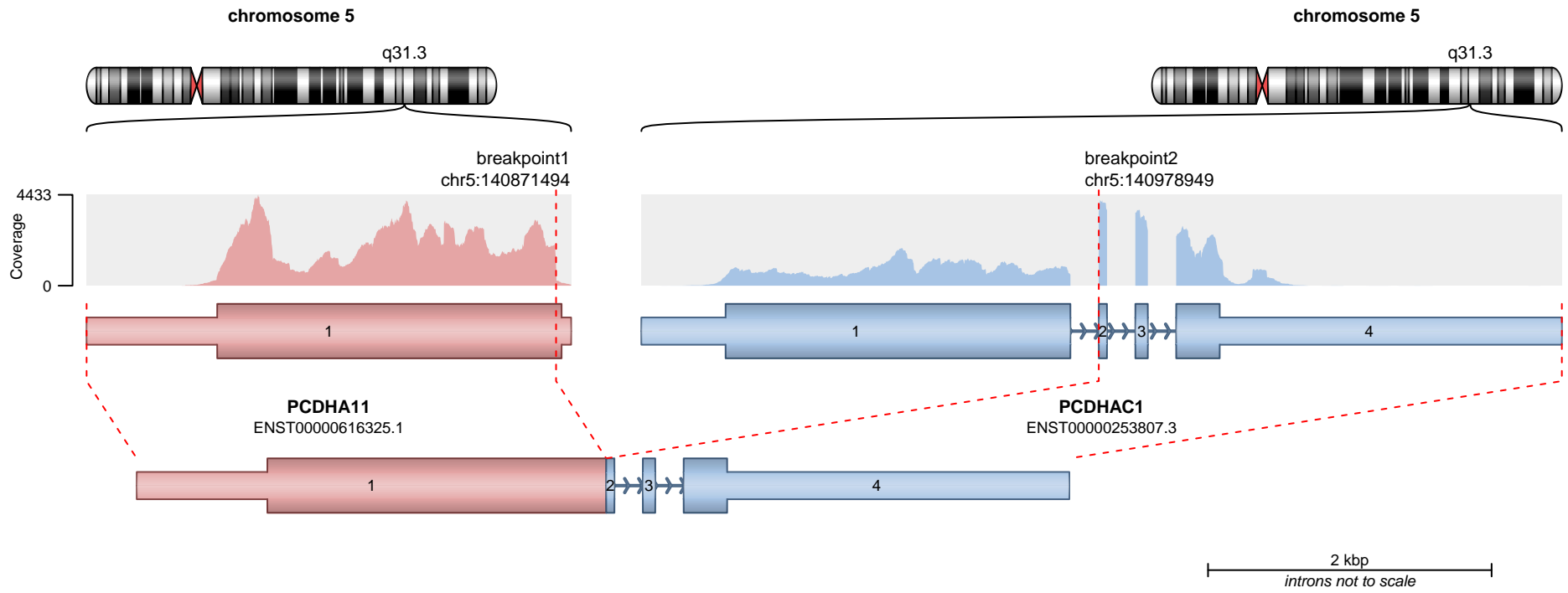
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



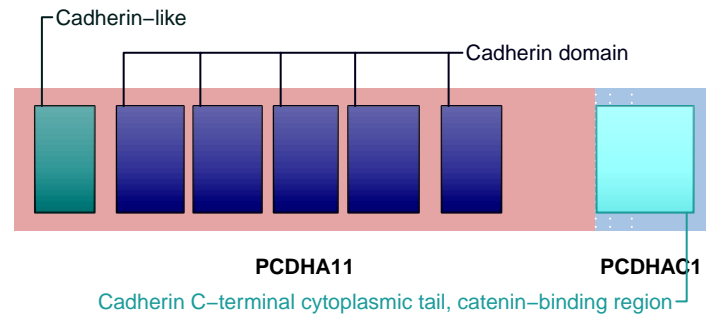
**SUPPORTING READ COUNT**

Split reads = 358  
Discordant mates = 4



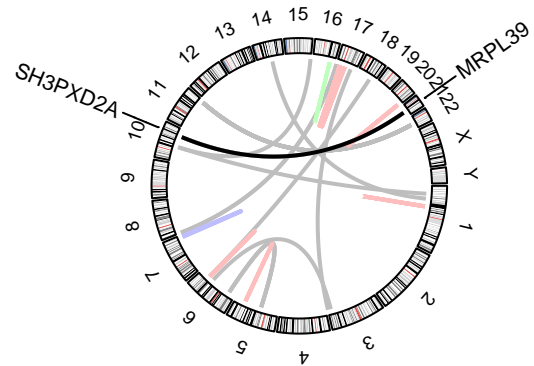
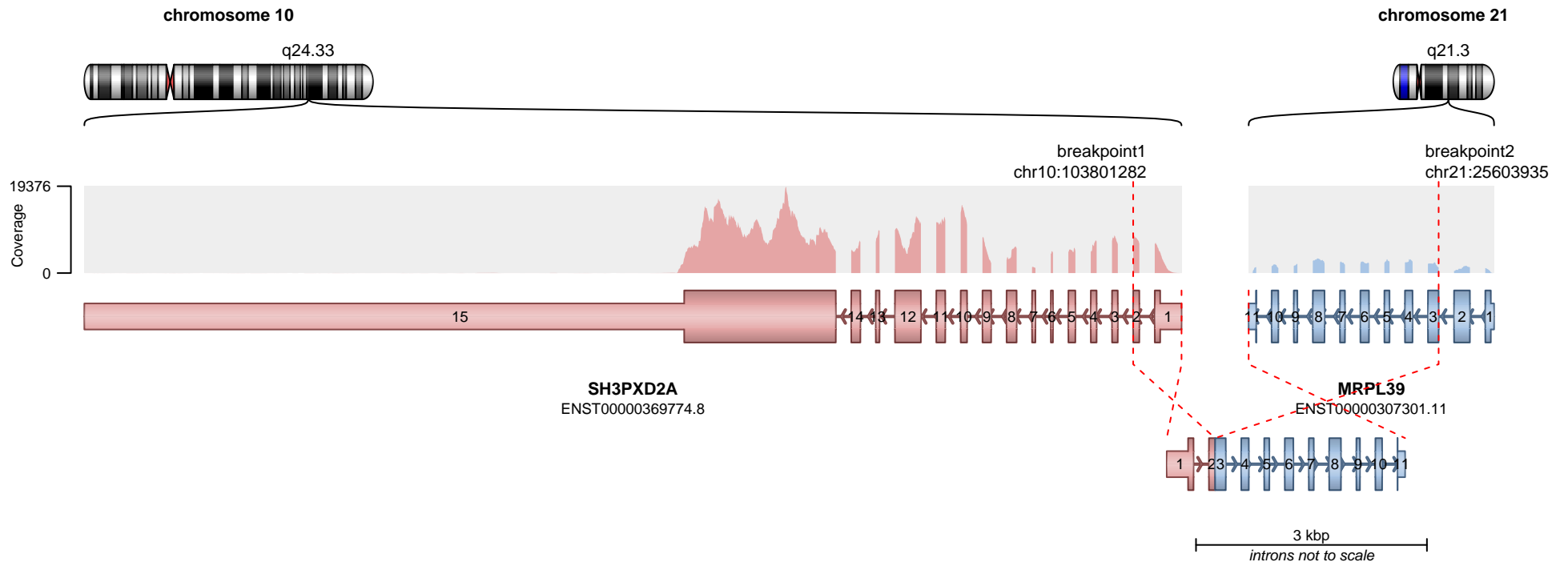
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear

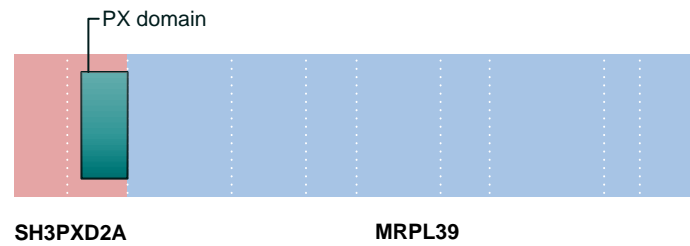


**SUPPORTING READ COUNT**

Split reads = 357  
Discordant mates = 4



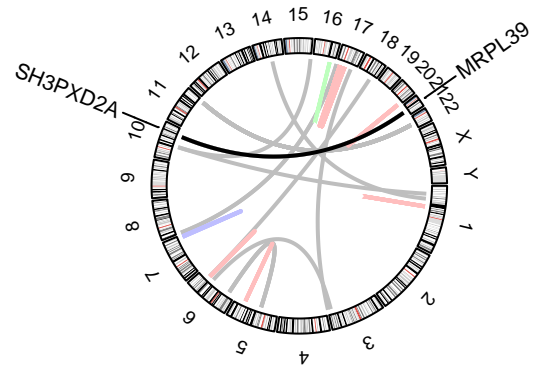
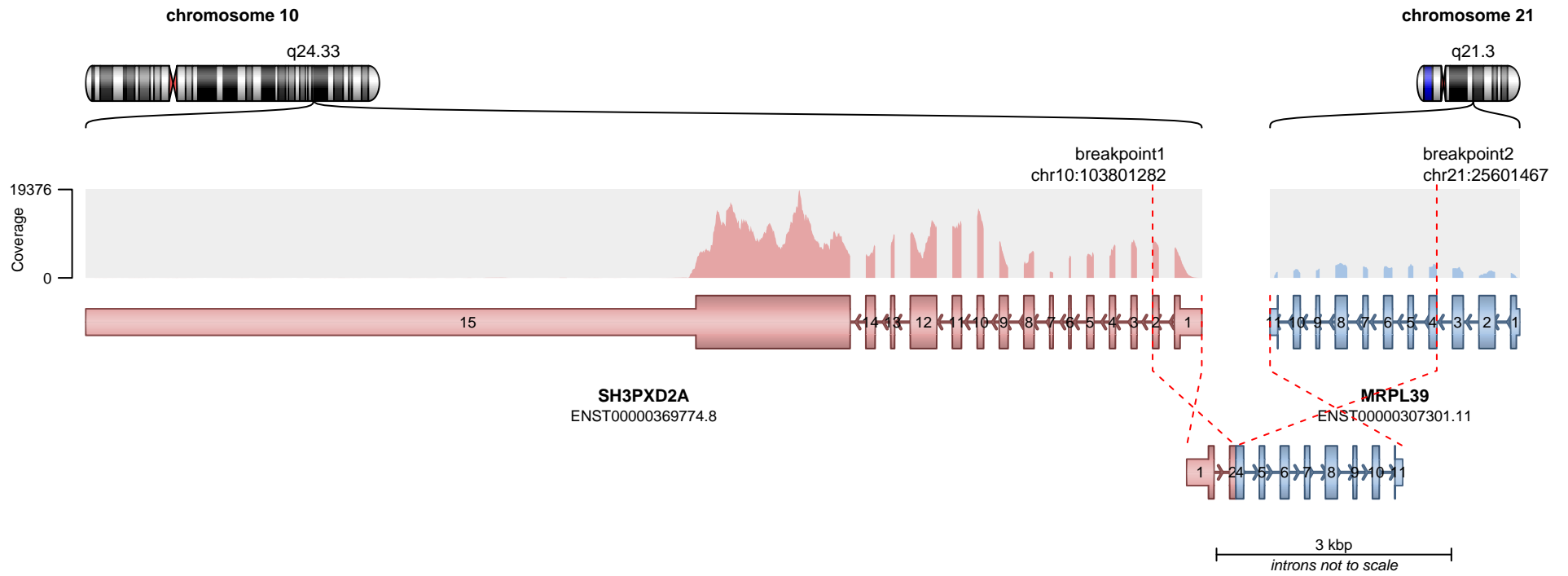
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



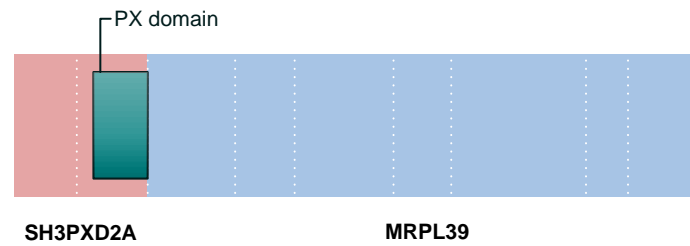
**SUPPORTING READ COUNT**

Split reads = 286  
Discordant mates = 19

— translocation    — deletion  
— duplication    — inversion



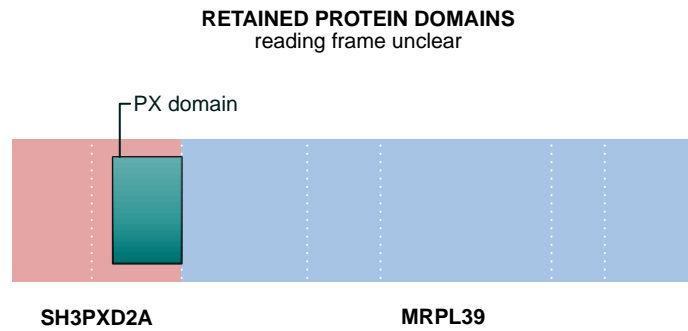
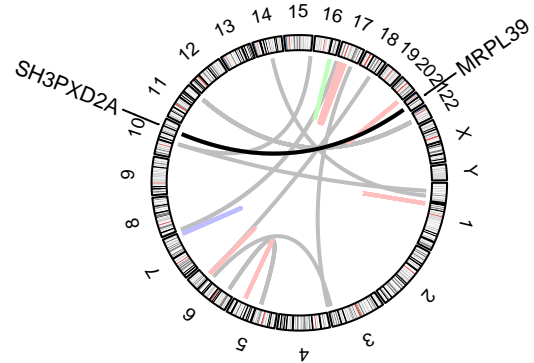
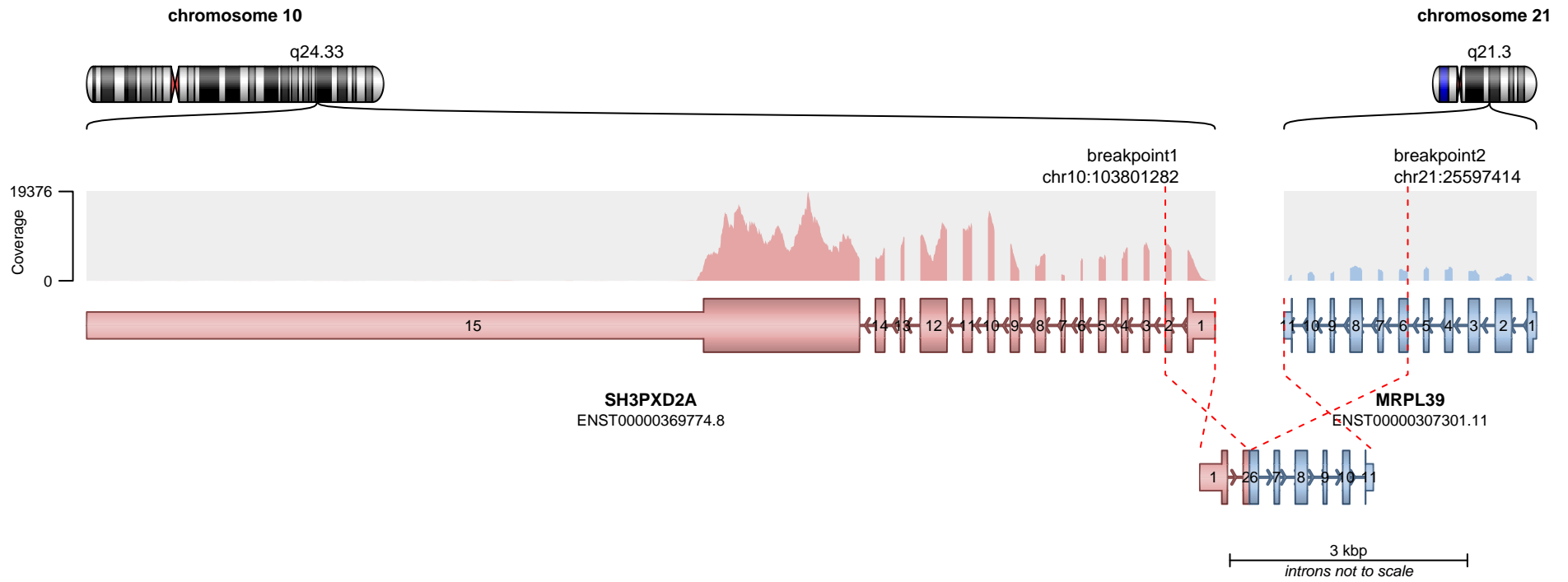
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 282  
Discordant mates = 7

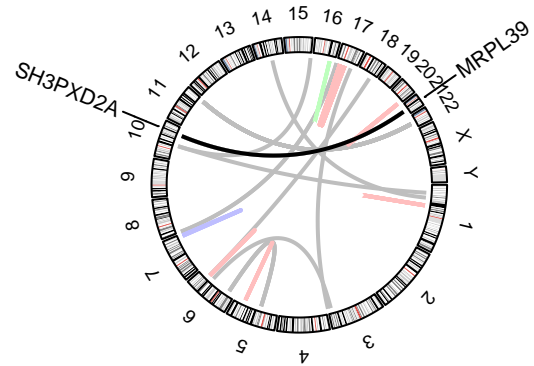
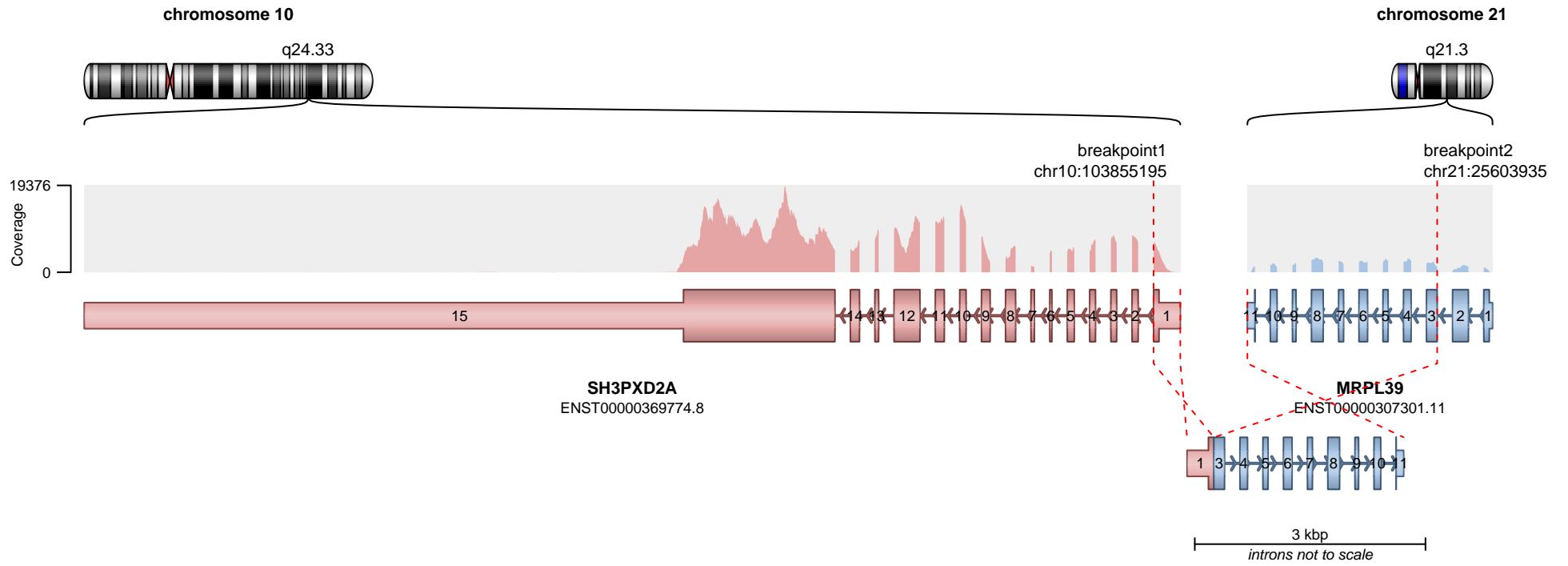
— translocation    — deletion  
— duplication    — inversion



**SUPPORTING READ COUNT**

Split reads = 16  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion

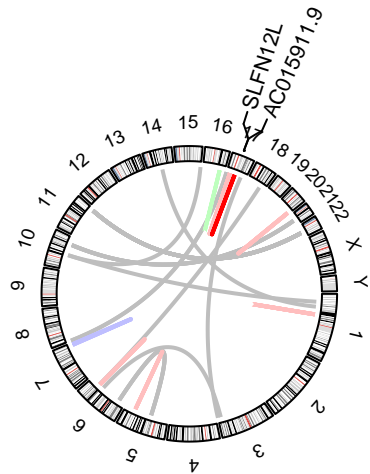
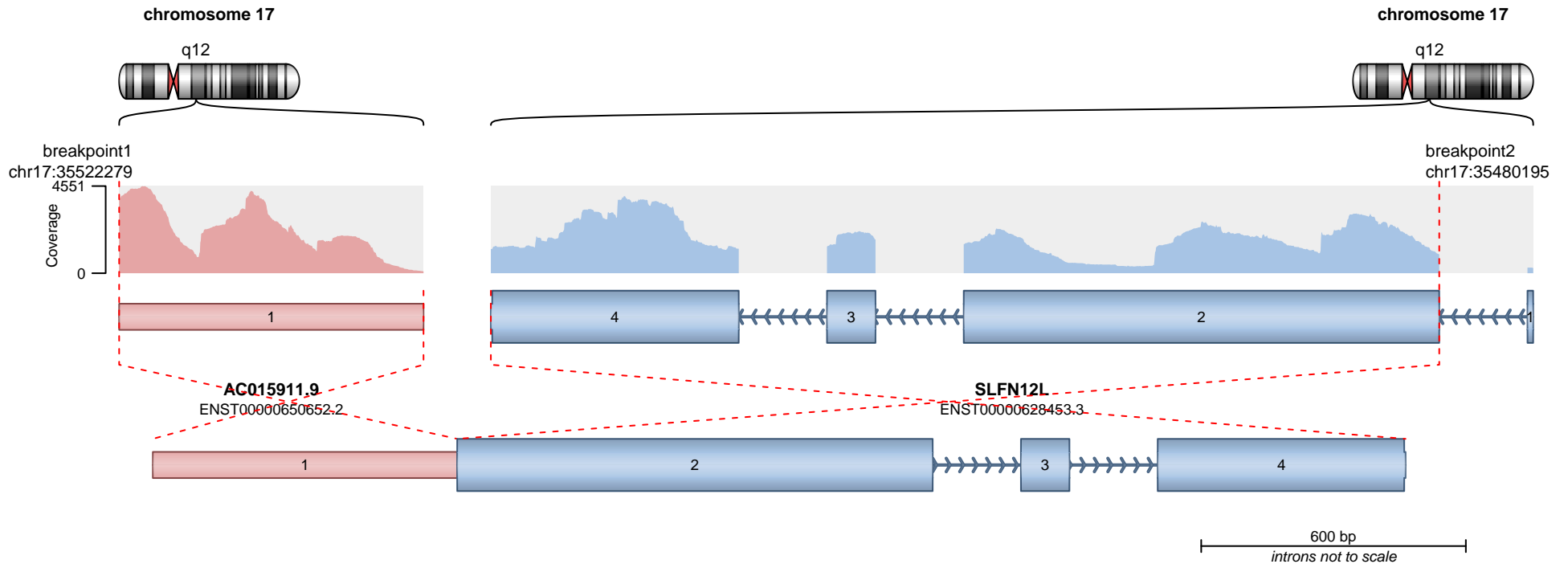


— translocation    — deletion  
— duplication    — inversion

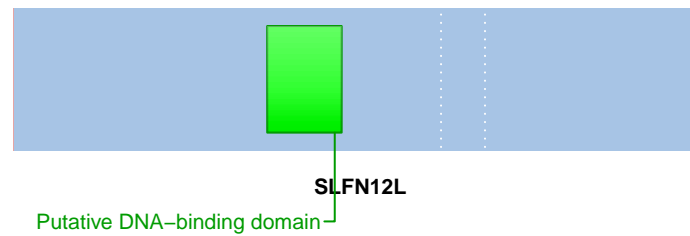
No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 4



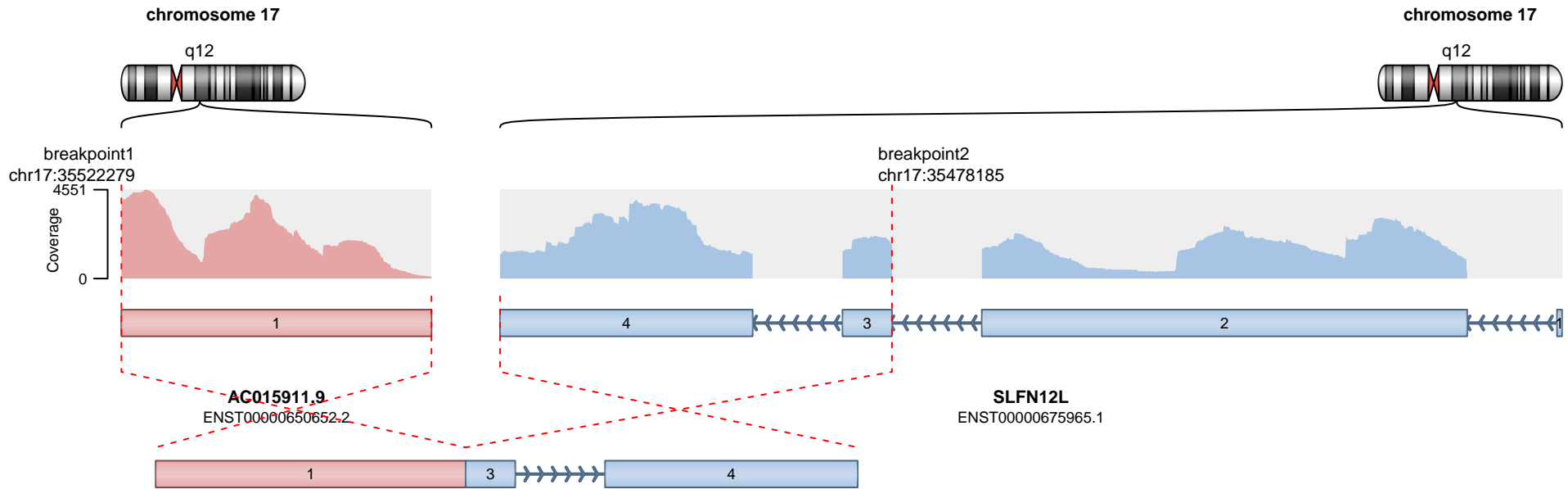
RETAINED PROTEIN DOMAINS  
reading frame unclear



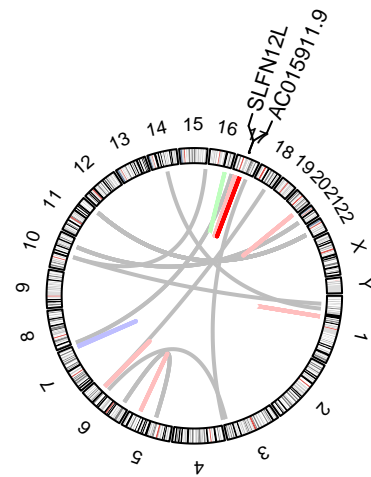
SUPPORTING READ COUNT

Split reads = 216  
Discordant mates = 19

— translocation — deletion  
— duplication — inversion



600 bp  
introns not to scale

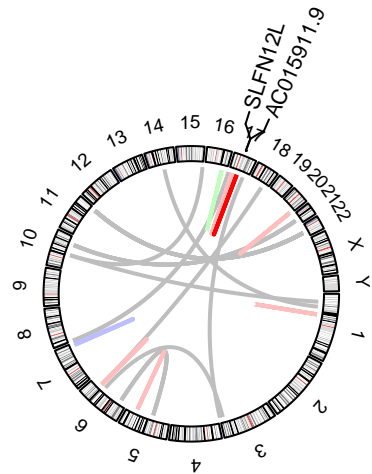
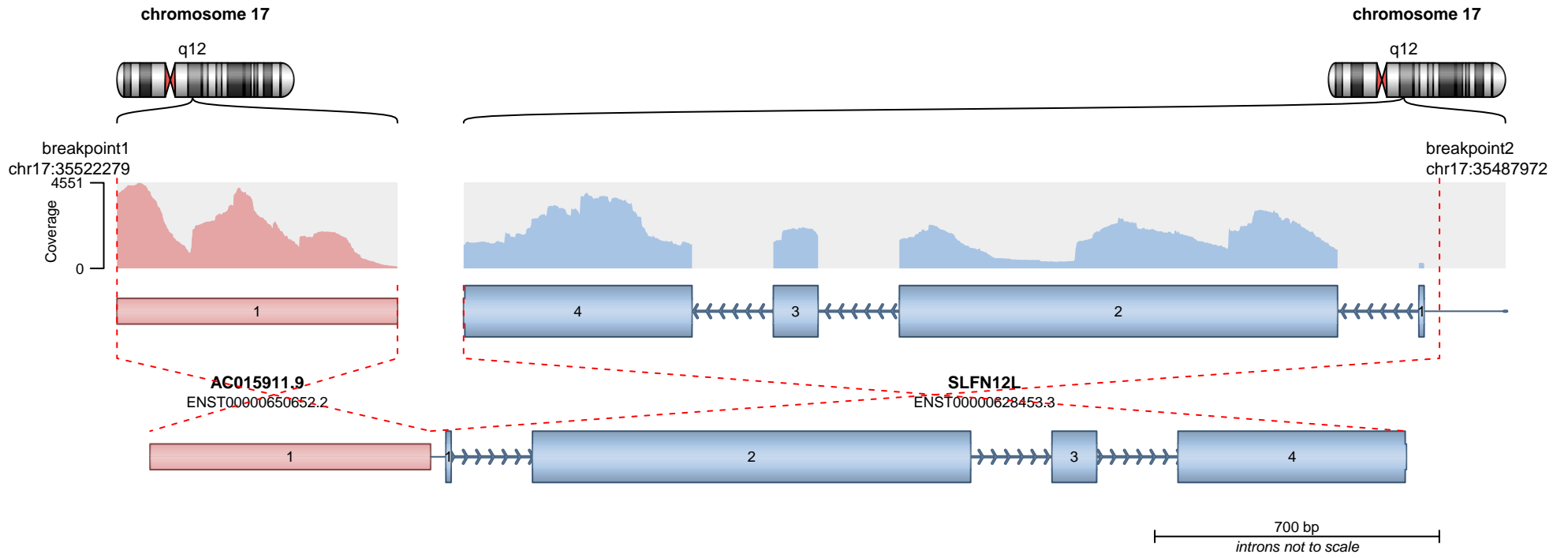


— translocation    — deletion  
— duplication    — inversion

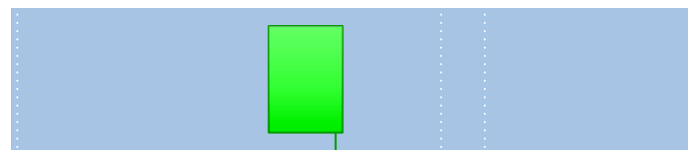
Genes are not protein-coding.

**SUPPORTING READ COUNT**

Split reads = 72  
Discordant mates = 3



**RETAINED PROTEIN DOMAINS**  
reading frame unclear

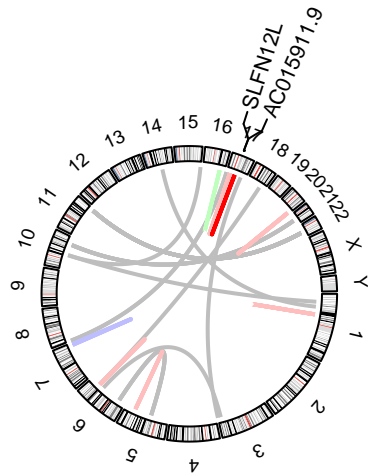
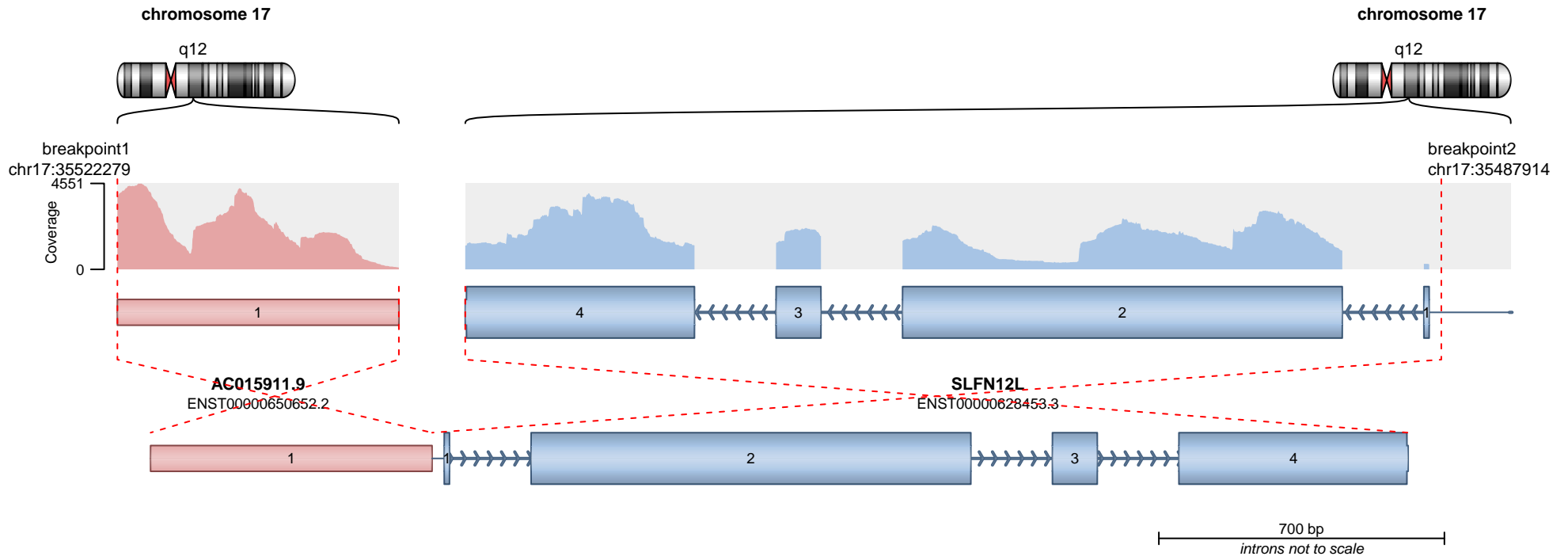


SLFN12L

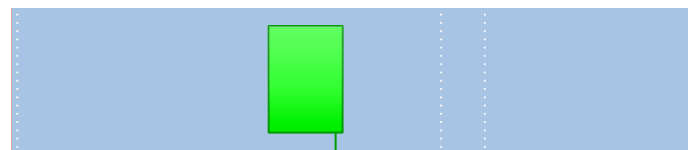
**SUPPORTING READ COUNT**

Split reads = 8  
Discordant mates = 19

— translocation    — deletion  
— duplication    — inversion



**RETAINED PROTEIN DOMAINS**  
reading frame unclear

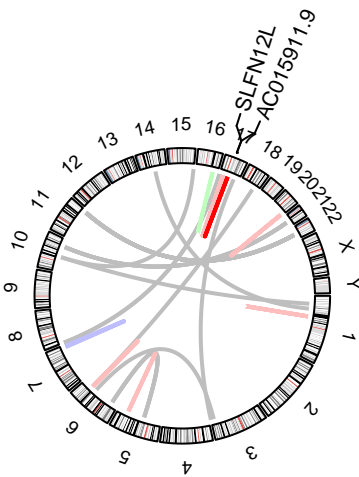
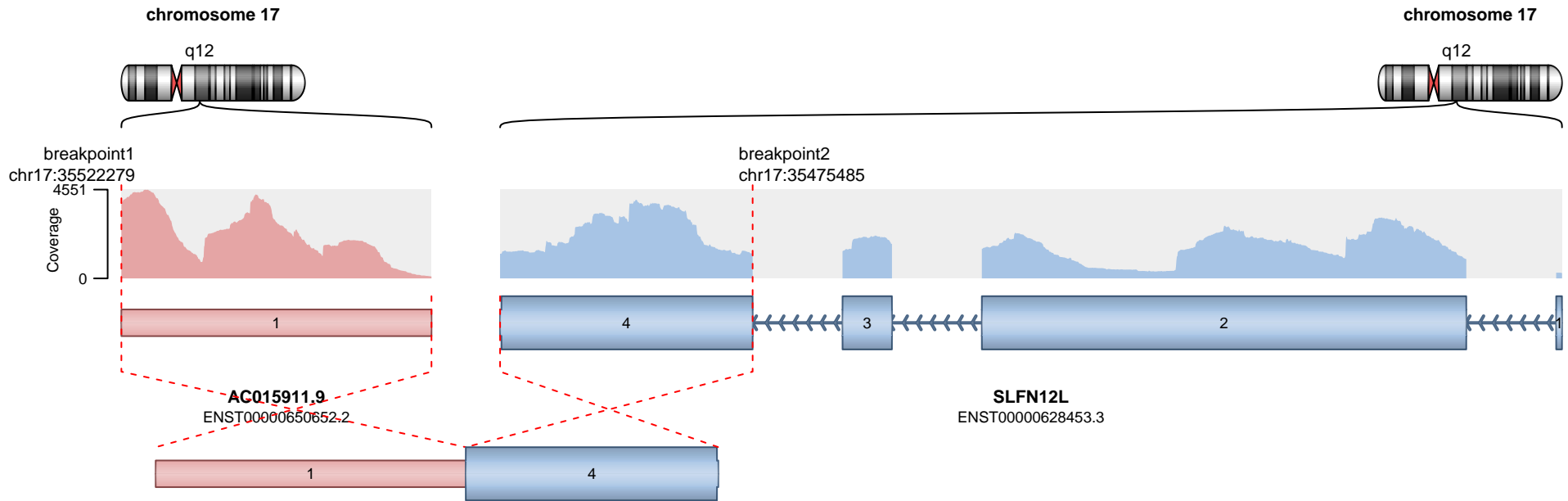


Putative DNA-binding domain

**SUPPORTING READ COUNT**

Split reads = 5  
Discordant mates = 19

— translocation    — deletion  
— duplication    — inversion

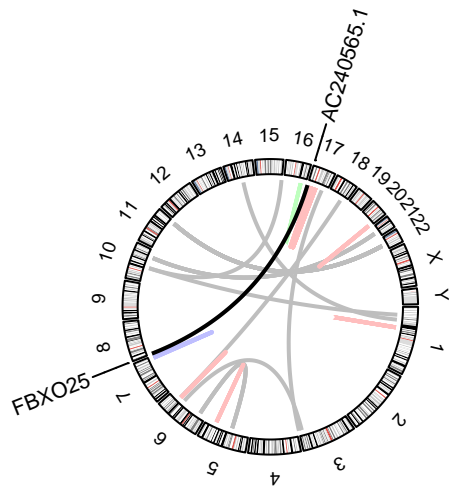
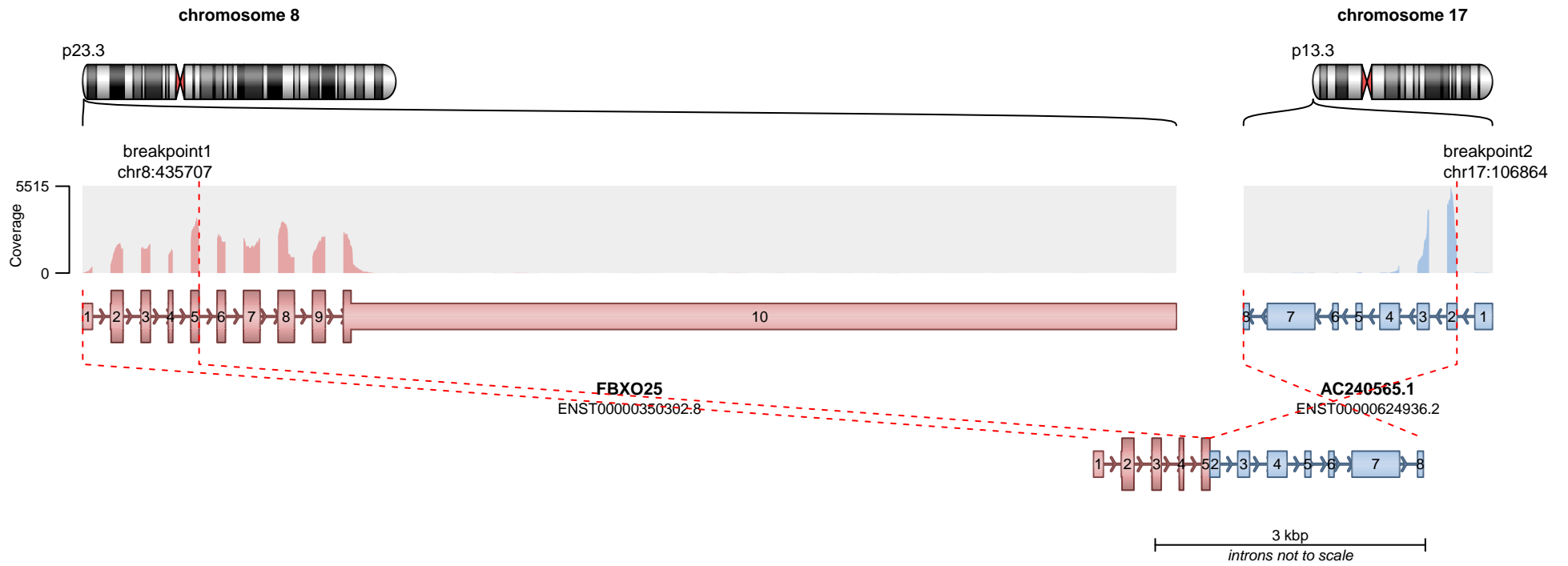


— translocation    — deletion  
— duplication    — inversion

No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

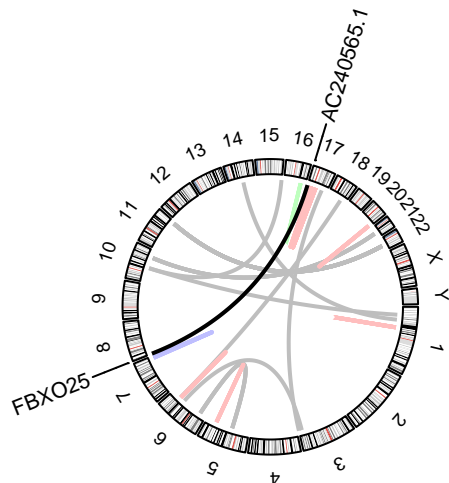
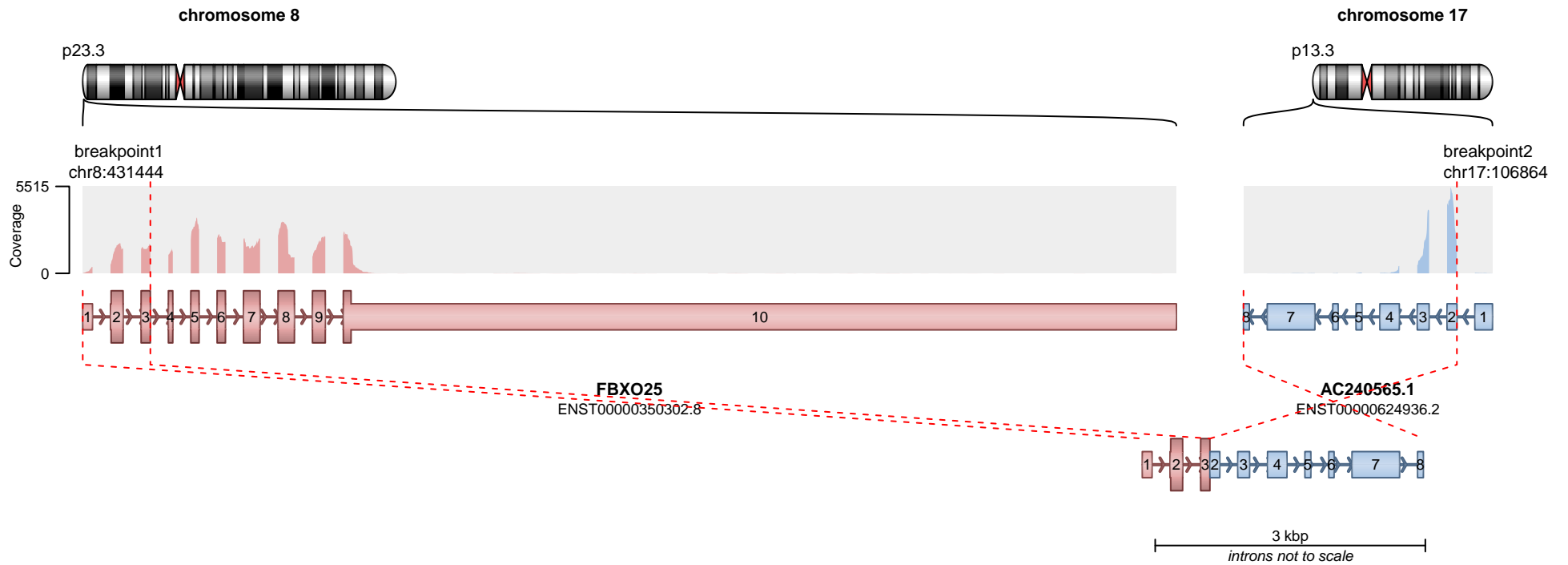


— translocation — deletion  
— duplication — inversion

No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 211  
Discordant mates = 0

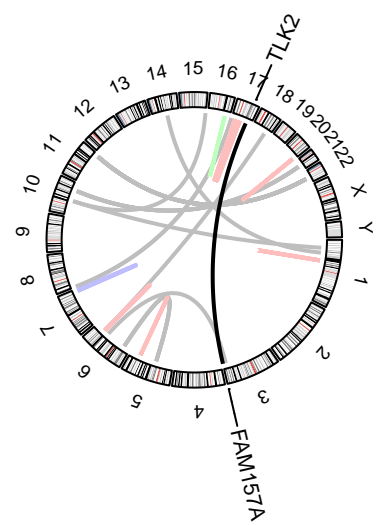
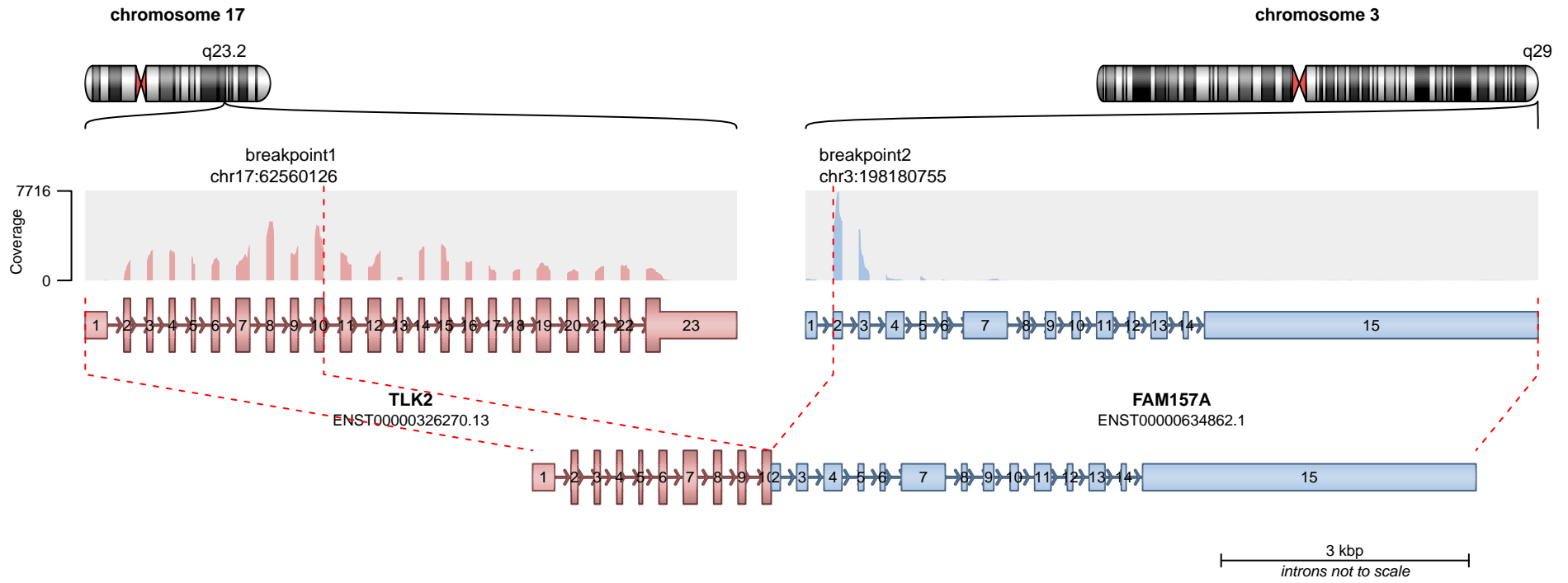


No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion

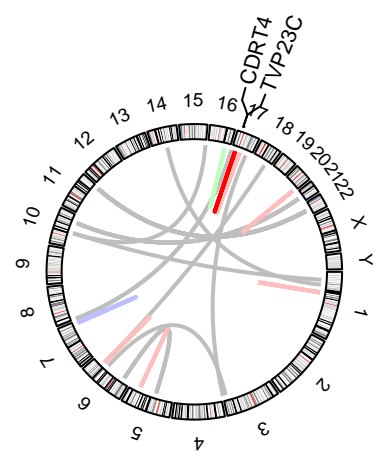
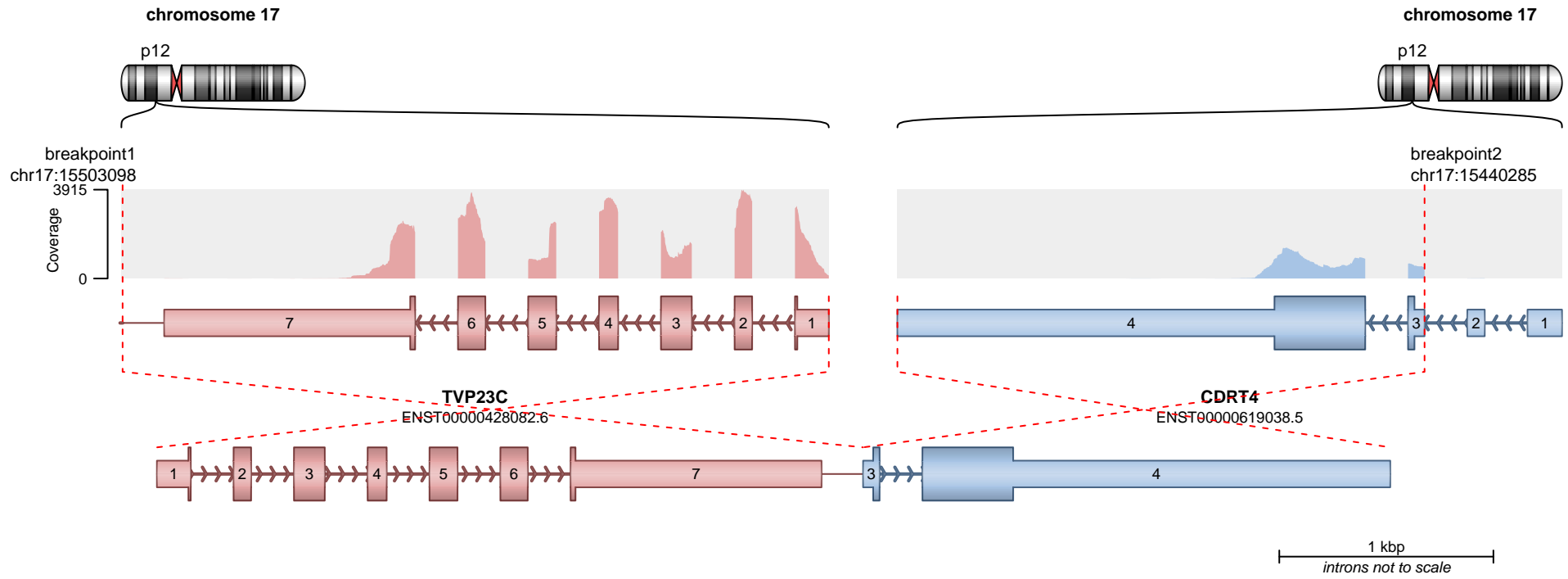


— translocation    — deletion  
— duplication    — inversion

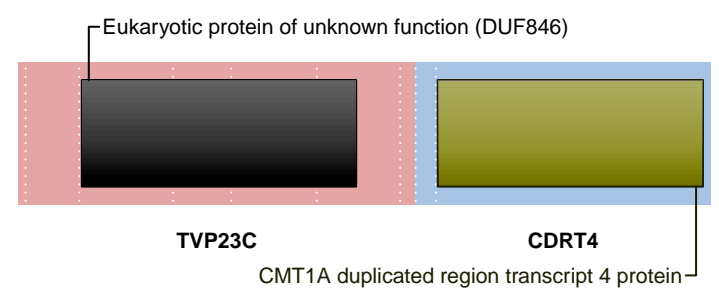
No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 109  
Discordant mates = 1



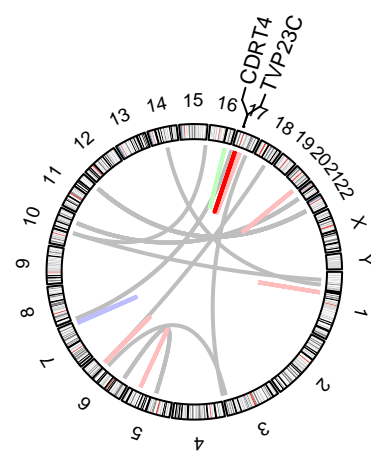
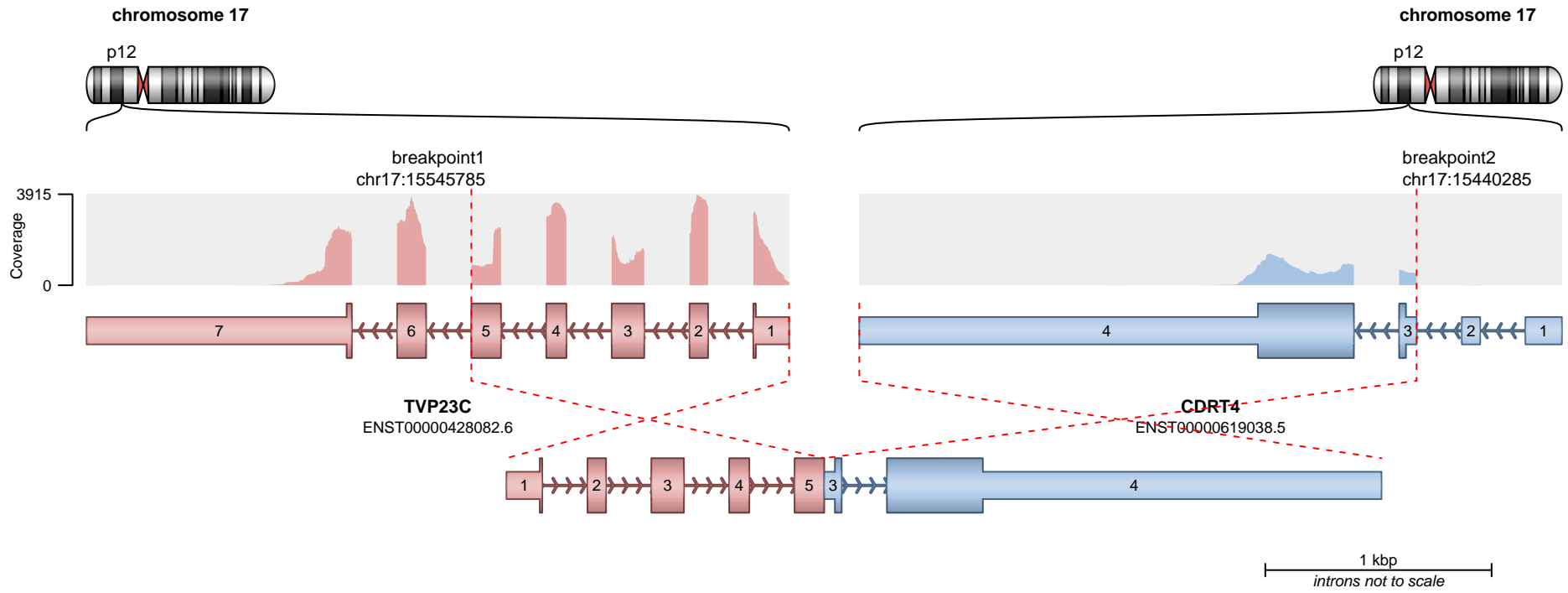
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



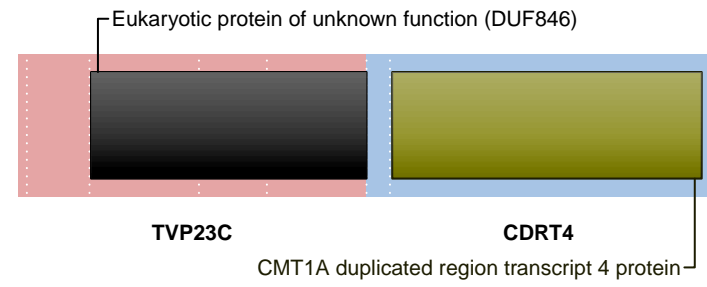
**SUPPORTING READ COUNT**

Split reads = 98  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



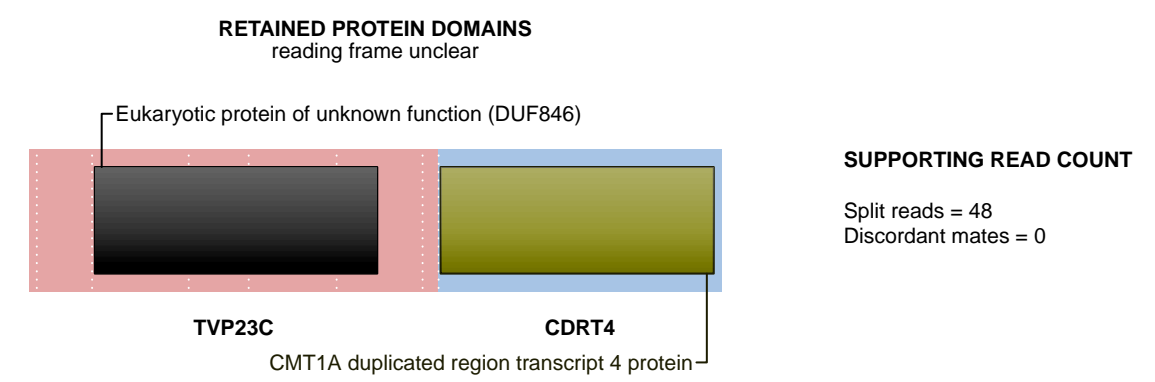
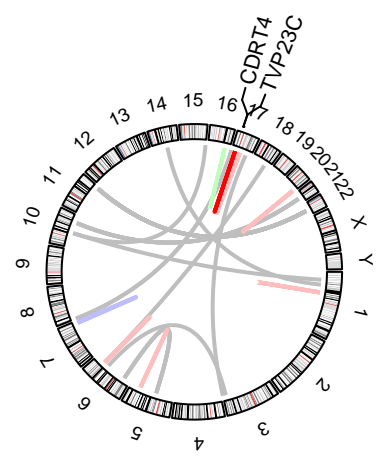
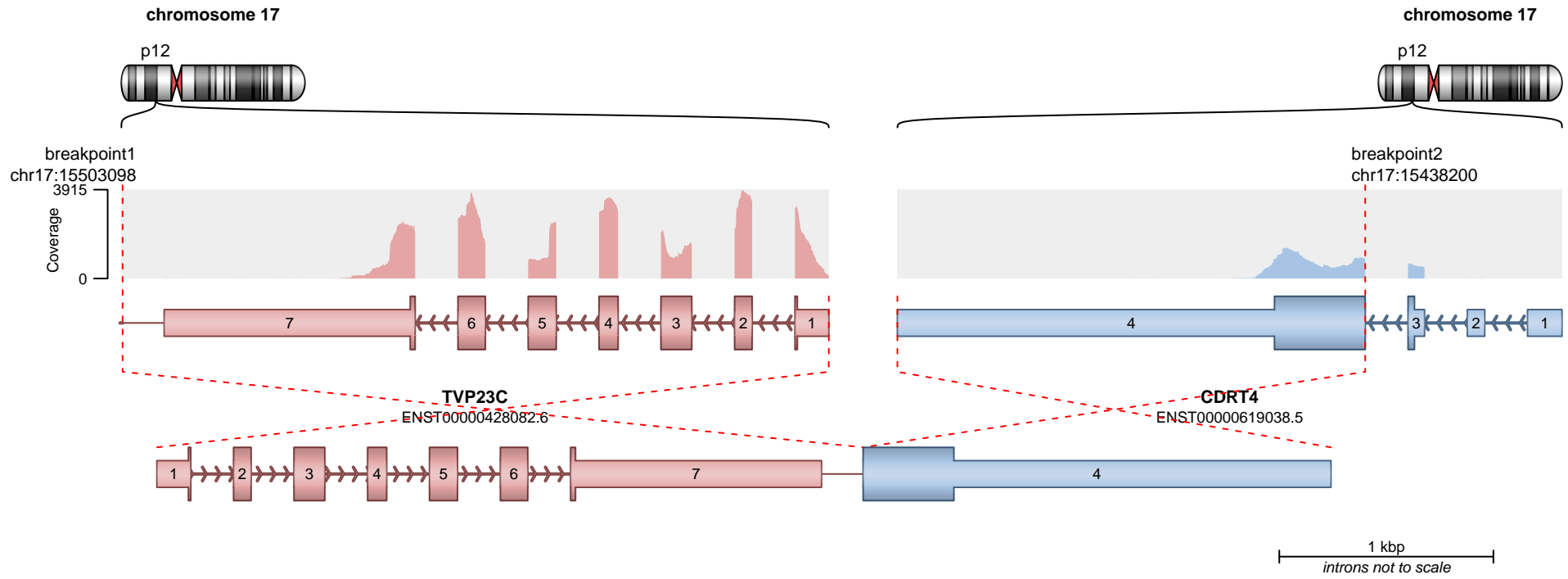
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



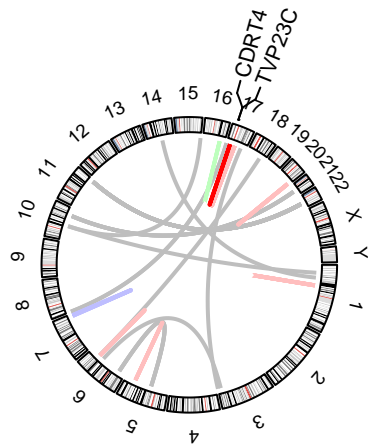
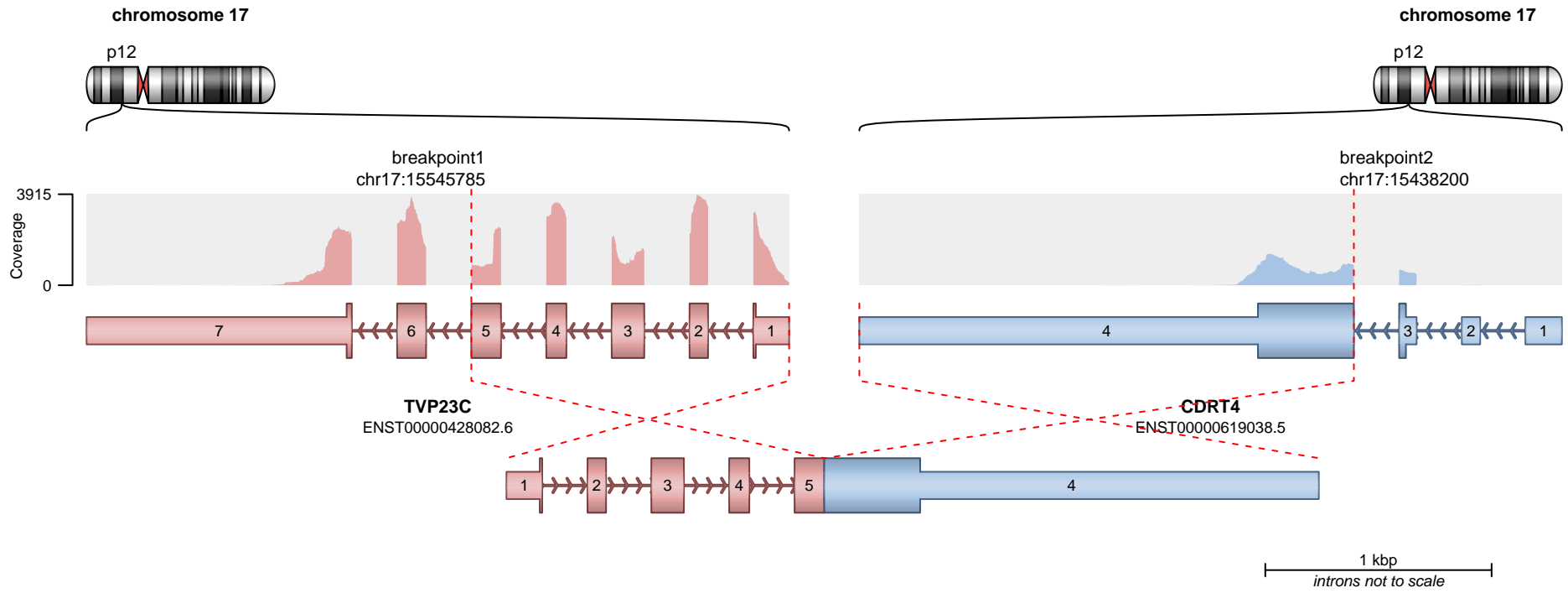
**SUPPORTING READ COUNT**

Split reads = 58  
Discordant mates = 1

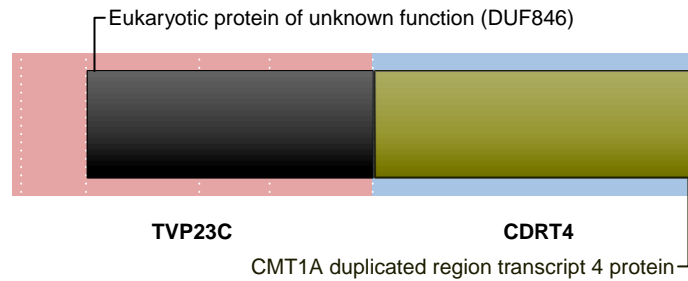
- translocation
- duplication
- deletion
- inversion



— translocation — deletion  
— duplication — inversion



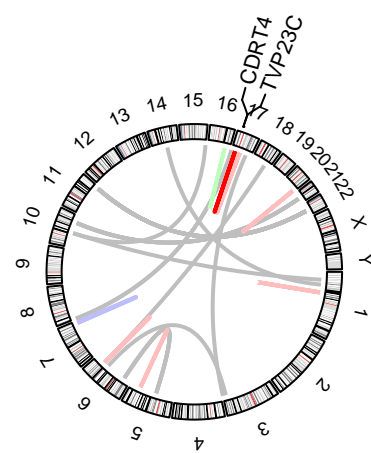
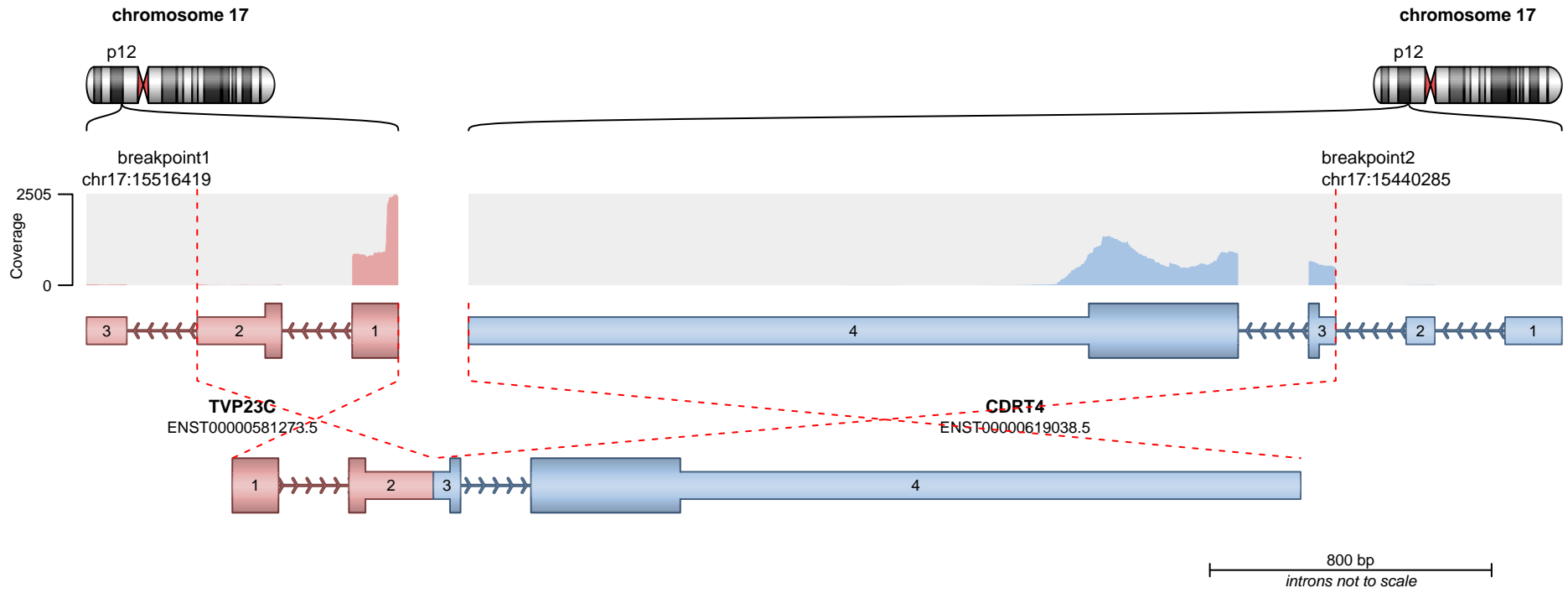
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



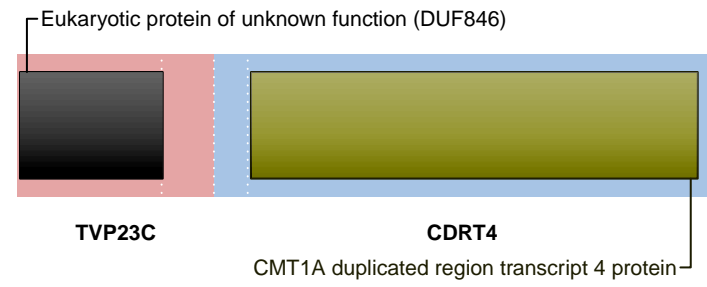
**SUPPORTING READ COUNT**

Split reads = 17  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



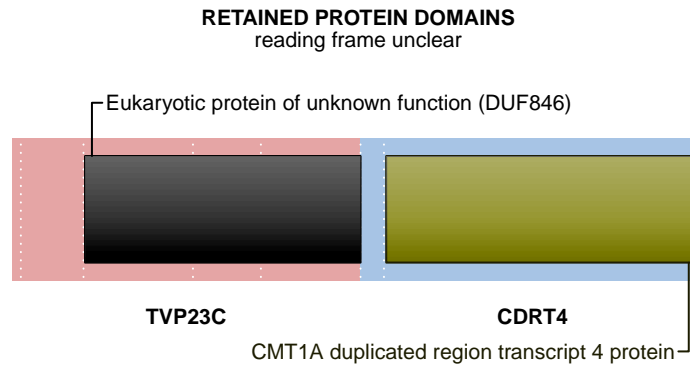
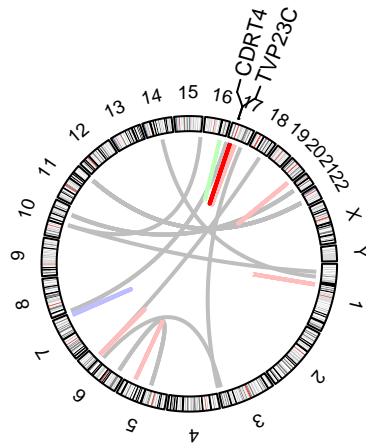
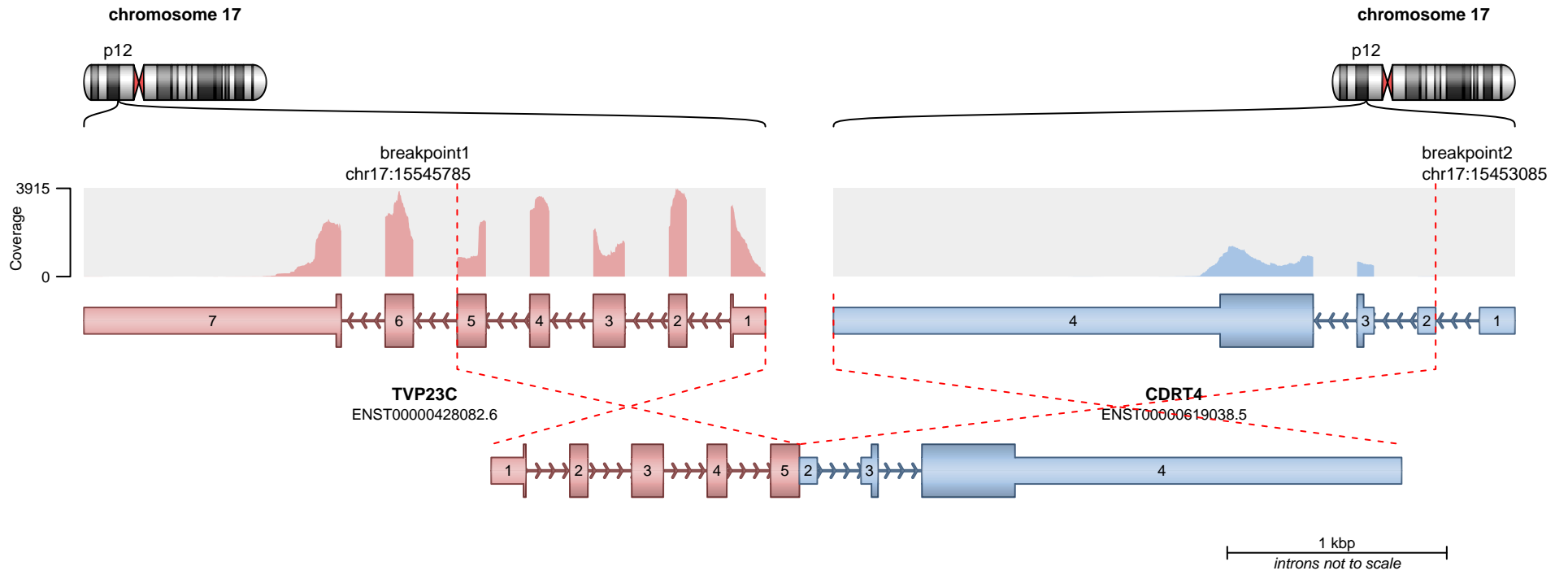
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 6  
Discordant mates = 1

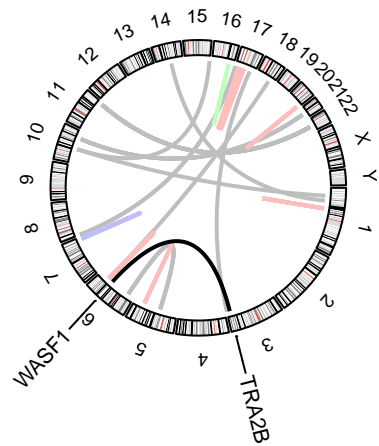
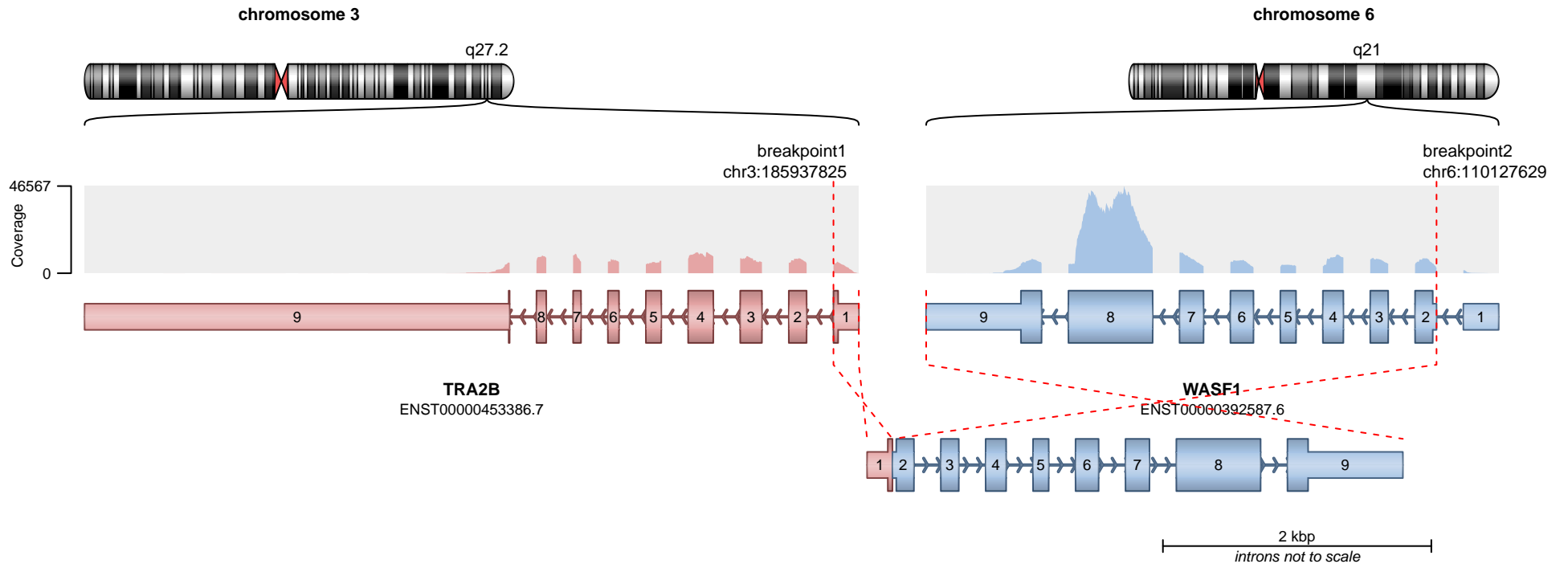
- translocation
- duplication
- deletion
- inversion



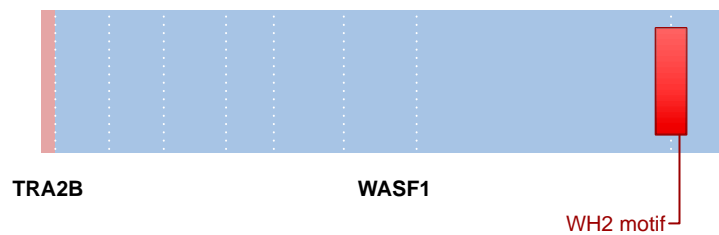
**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 1

— translocation — deletion  
— duplication — inversion



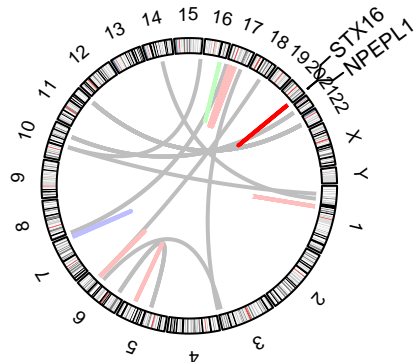
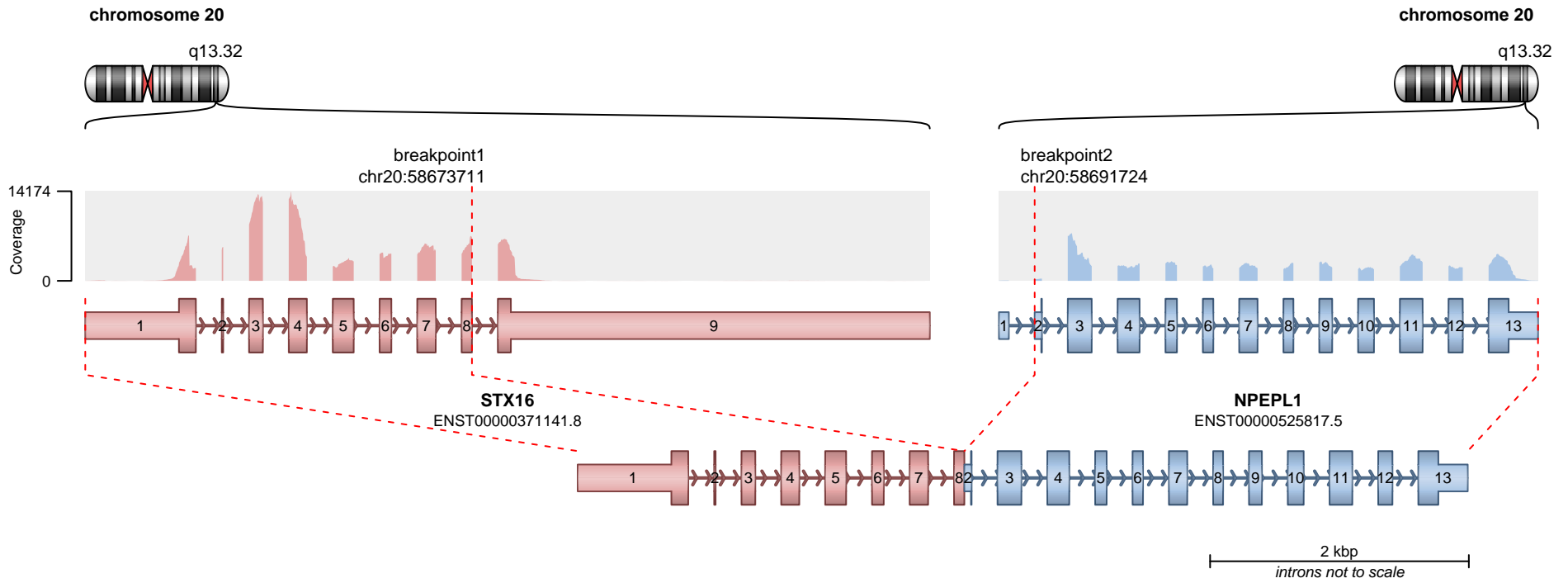
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



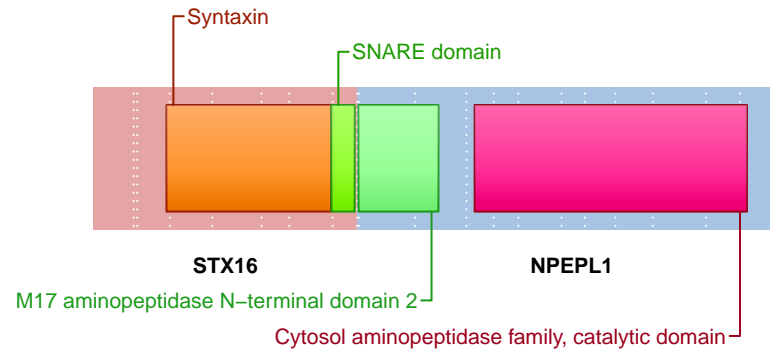
**SUPPORTING READ COUNT**

Split reads = 94  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



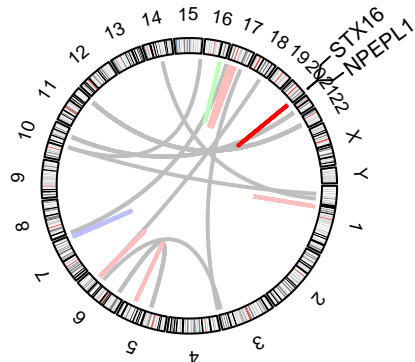
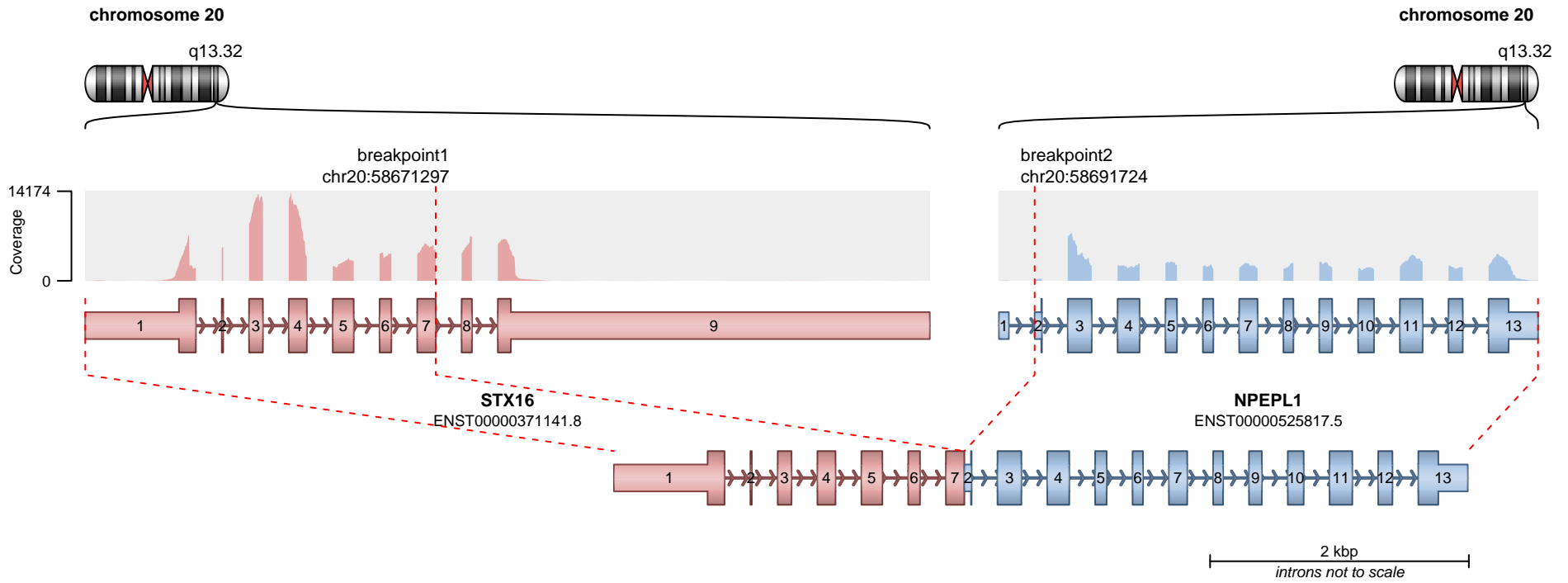
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



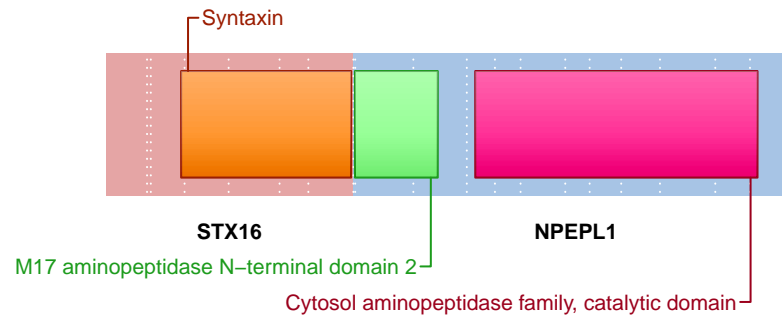
**SUPPORTING READ COUNT**

Split reads = 76  
Discordant mates = 2

- translocation
- duplication
- deletion
- inversion



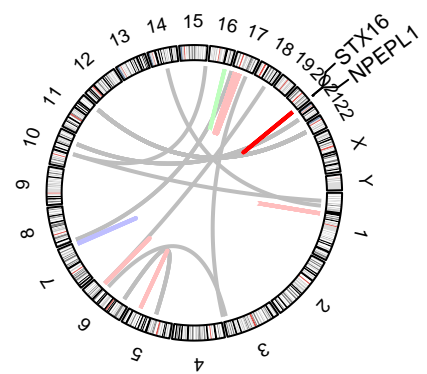
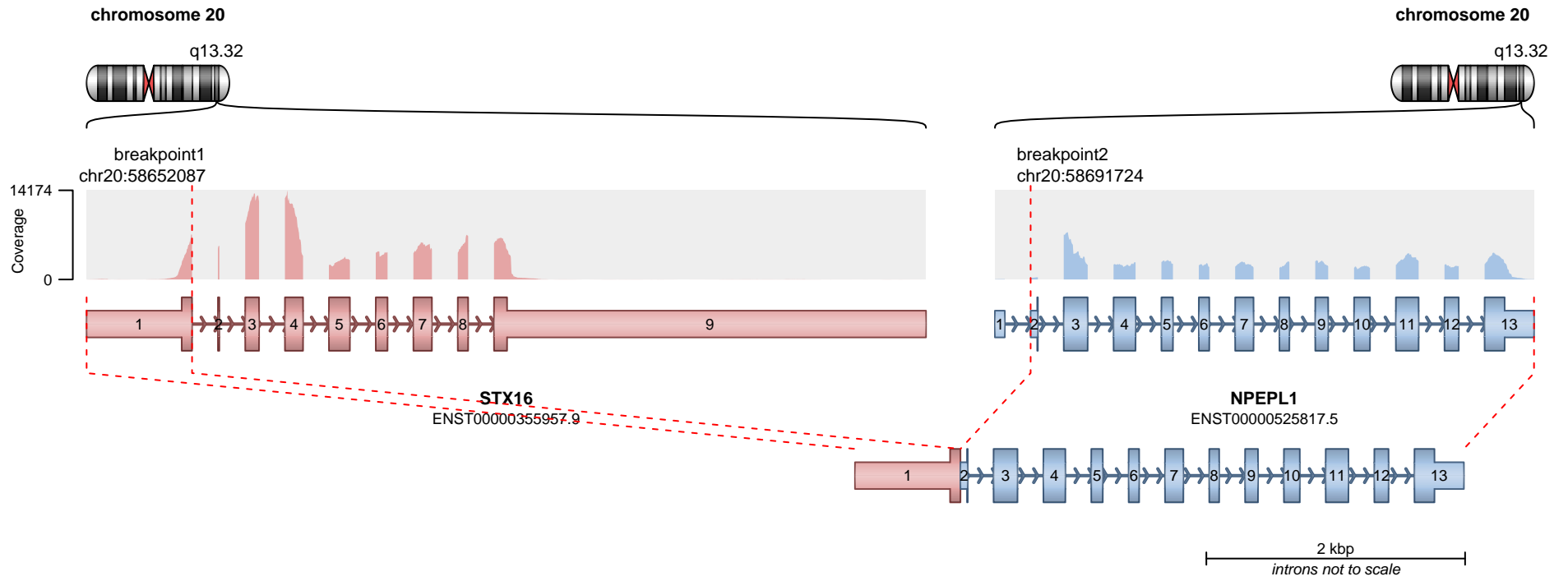
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



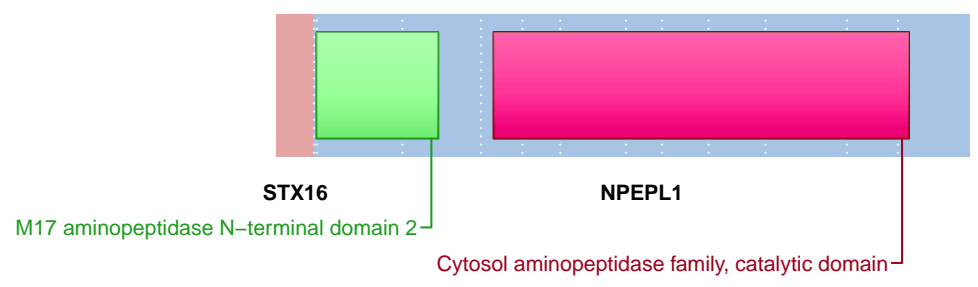
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



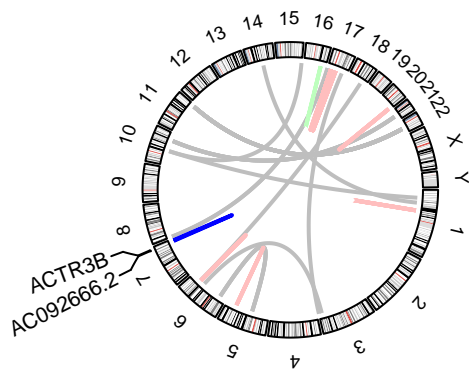
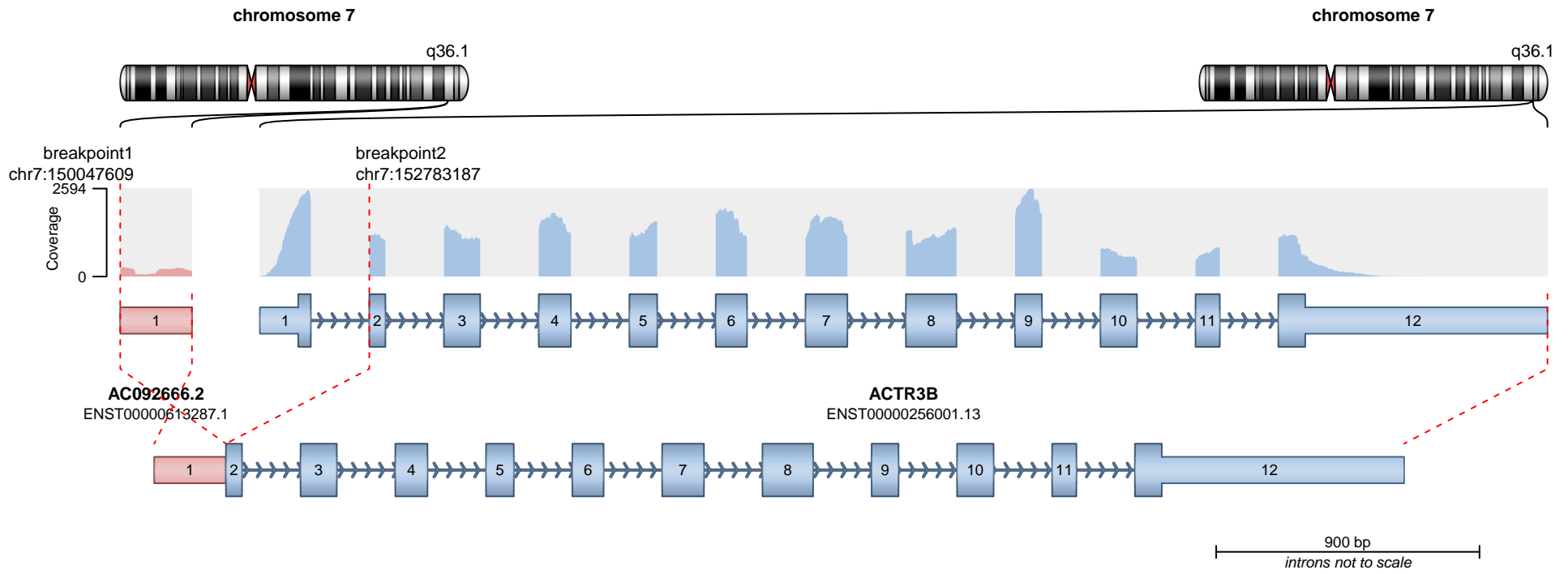
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

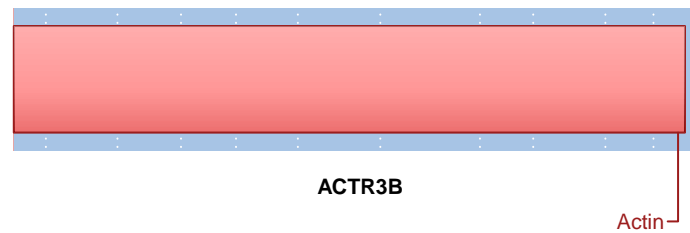
Split reads = 1  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



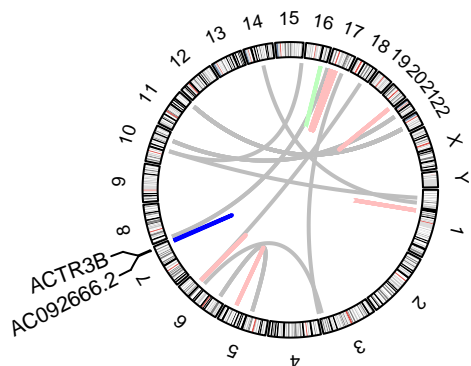
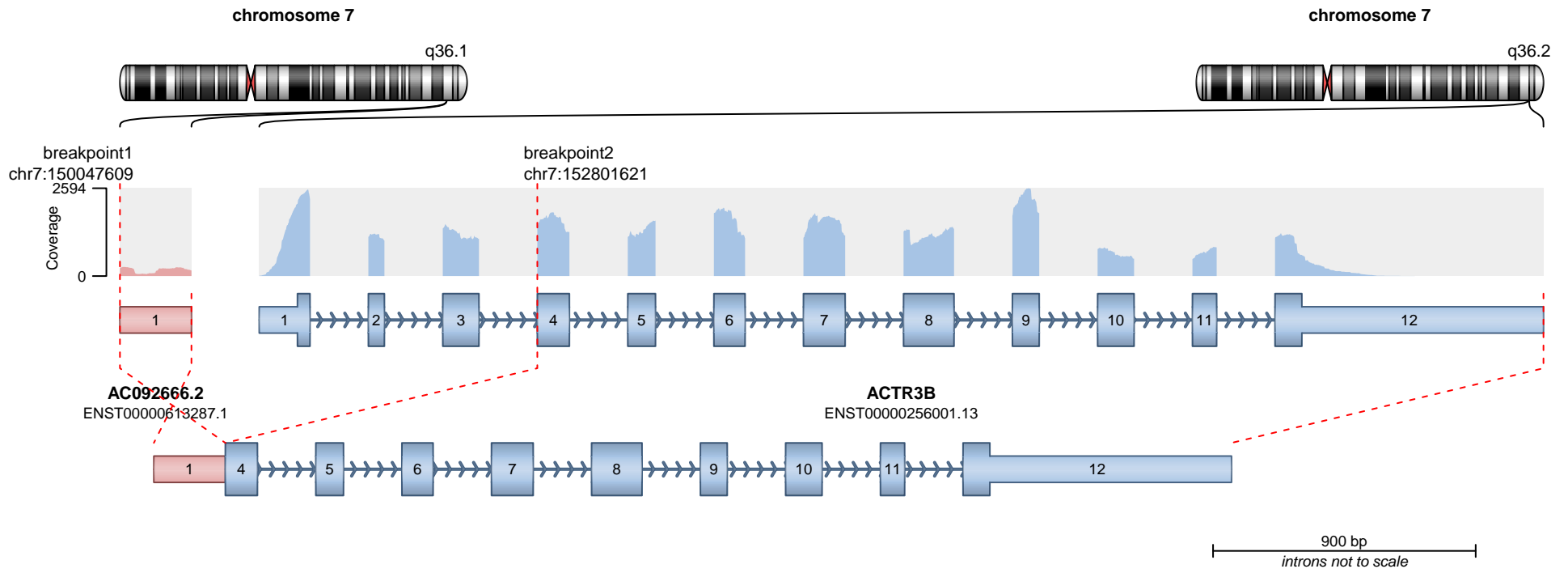
— translocation — deletion  
— duplication — inversion

RETAINED PROTEIN DOMAINS  
reading frame unclear



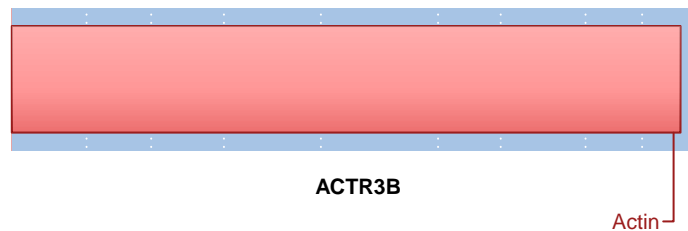
SUPPORTING READ COUNT

Split reads = 64  
Discordant mates = 0



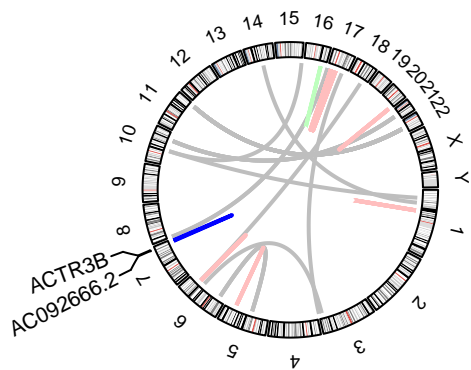
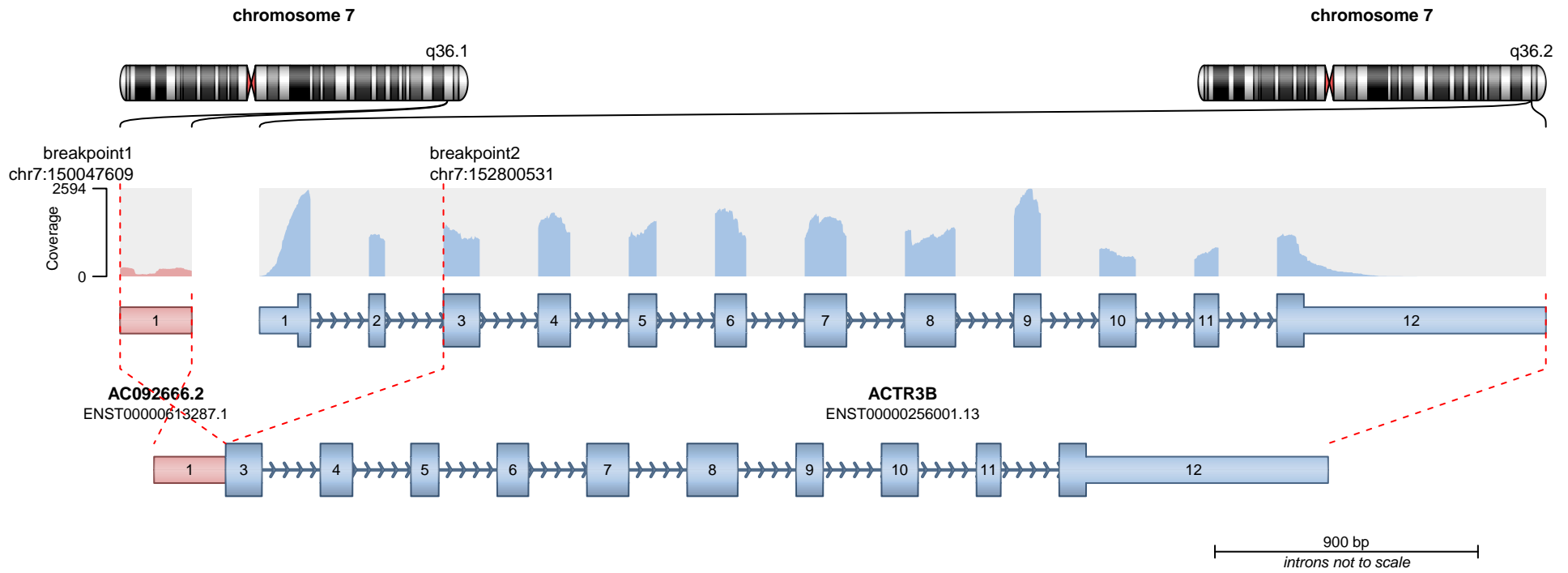
— translocation — deletion  
— duplication — inversion

RETAINED PROTEIN DOMAINS  
reading frame unclear

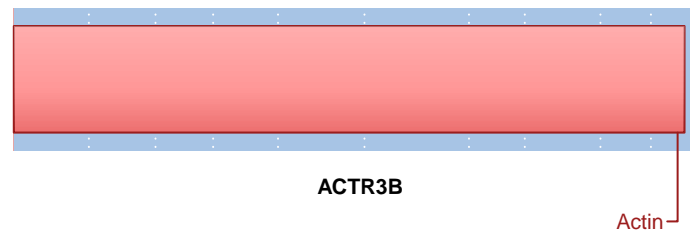


SUPPORTING READ COUNT

Split reads = 28  
Discordant mates = 0



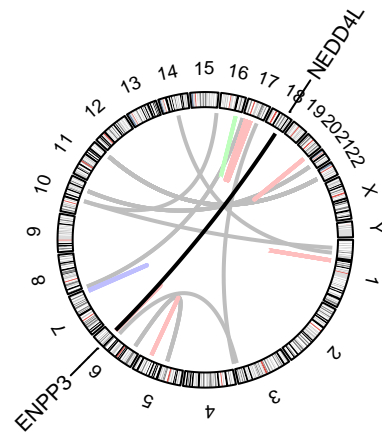
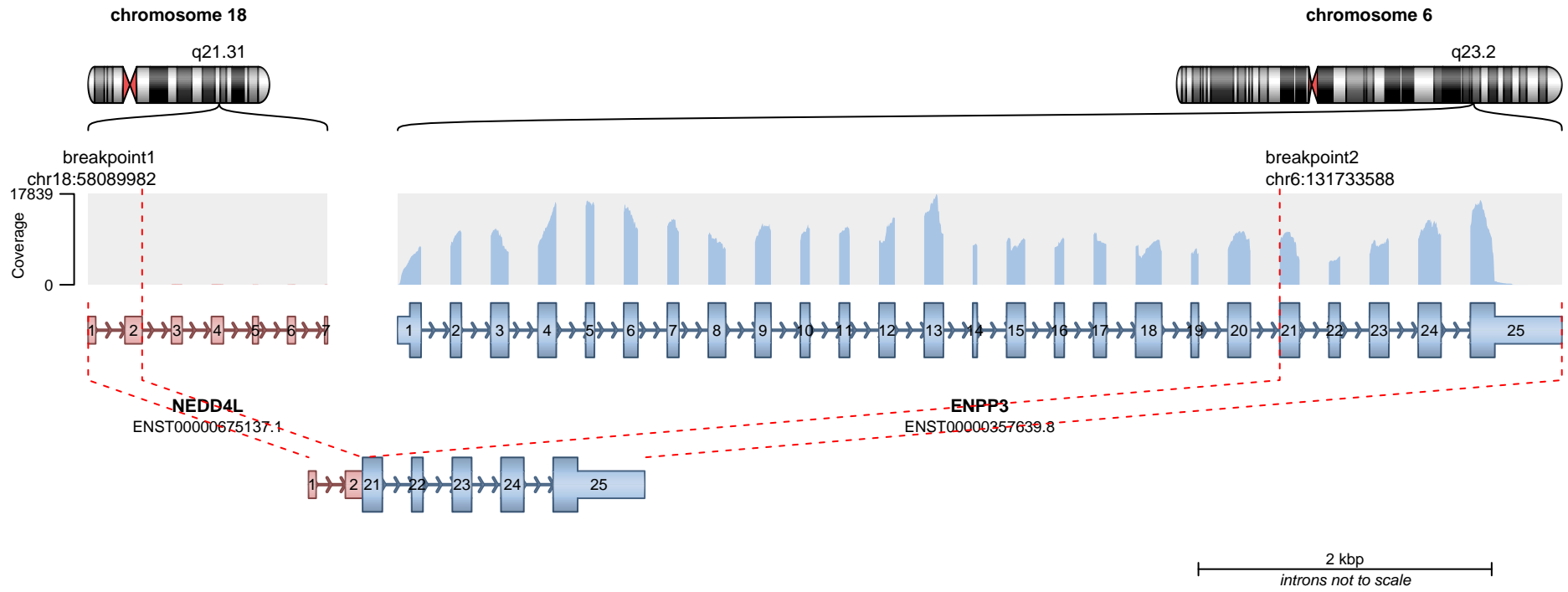
RETAINED PROTEIN DOMAINS  
reading frame unclear



SUPPORTING READ COUNT

Split reads = 5  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



**RETAINED PROTEIN DOMAINS**  
reading frame unclear

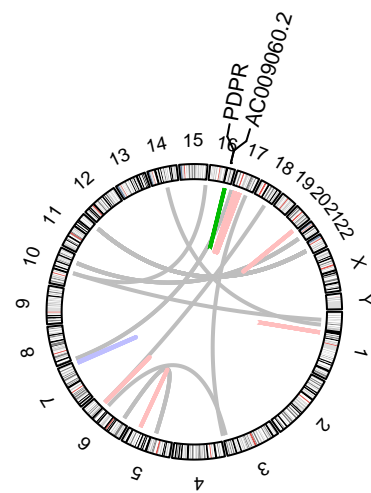
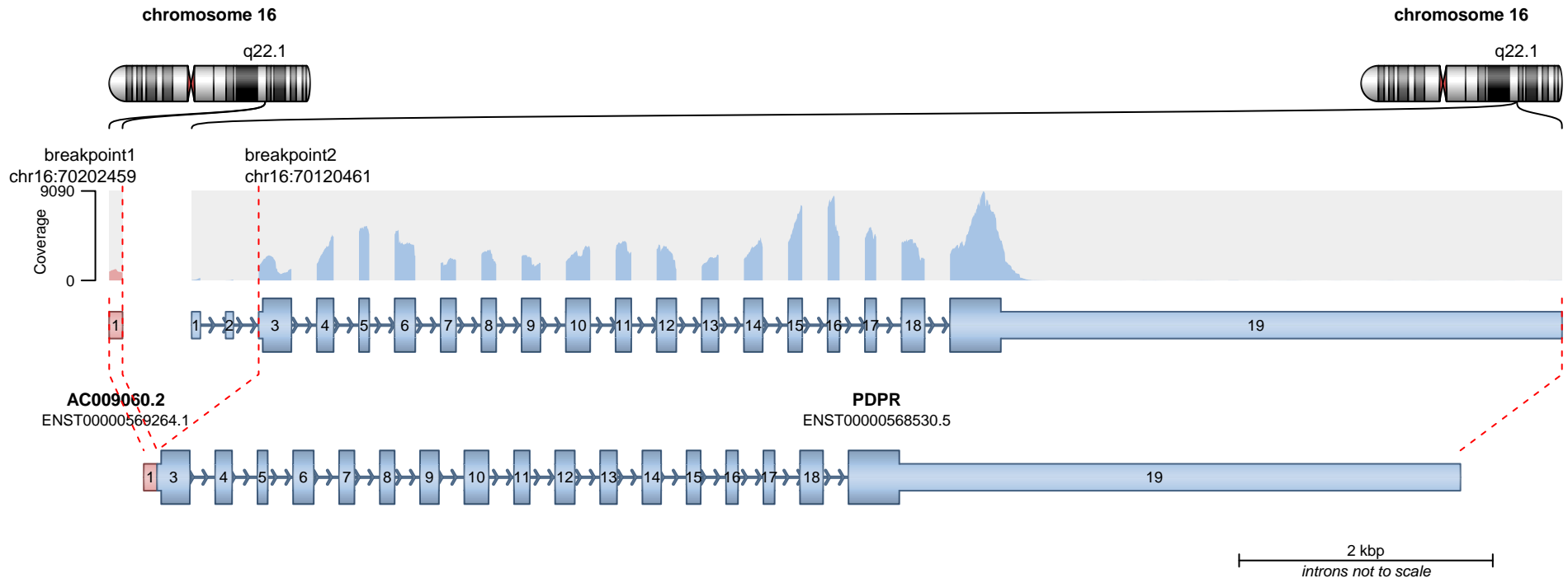


**ENPP3**  
DNA/RNA non-specific endonuclease

**SUPPORTING READ COUNT**

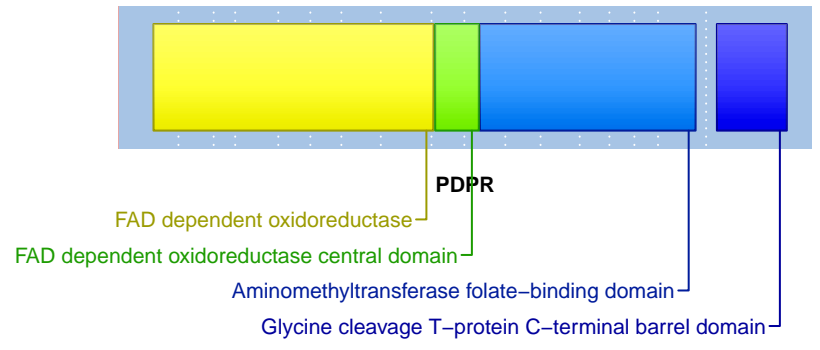
Split reads = 43  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



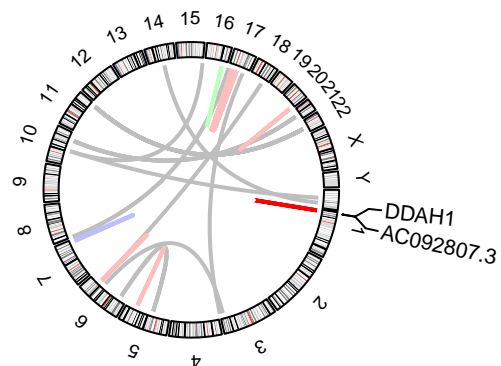
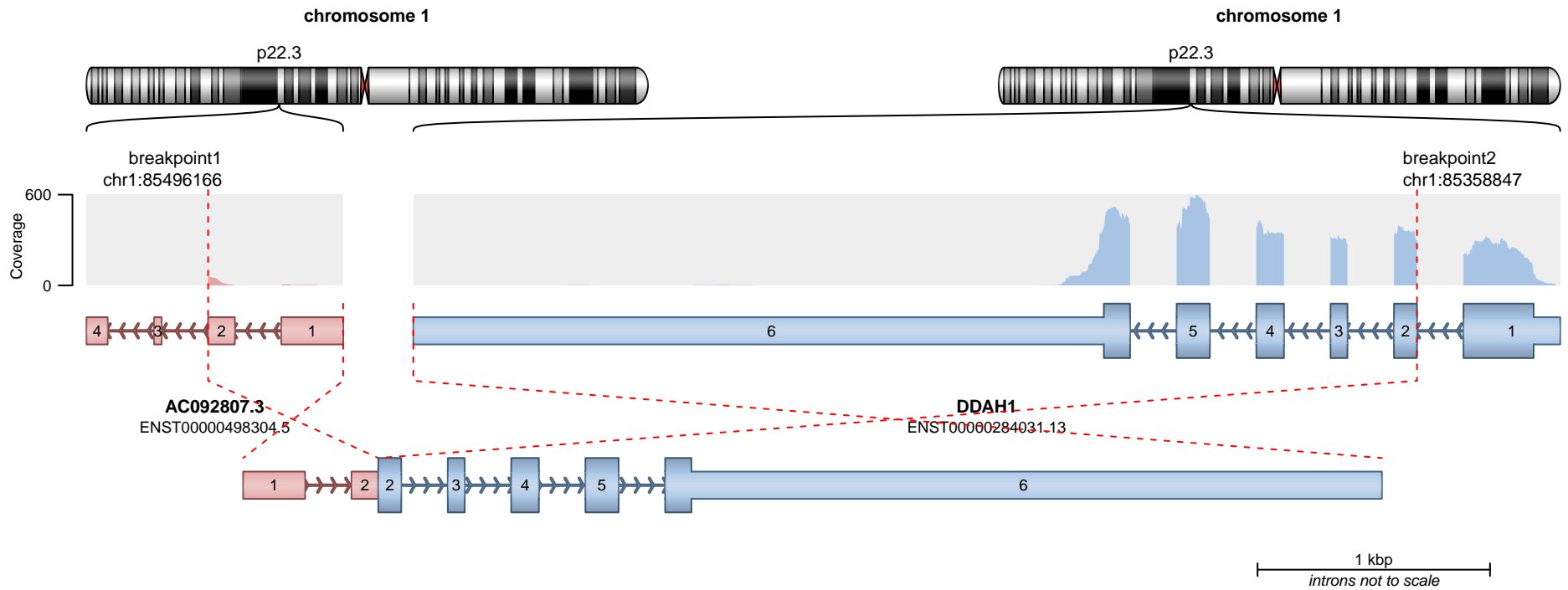
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear

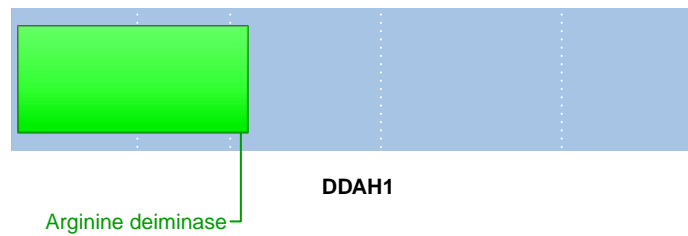


**SUPPORTING READ COUNT**

Split reads = 31  
Discordant mates = 0



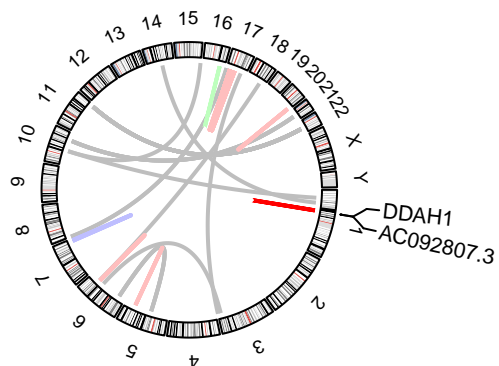
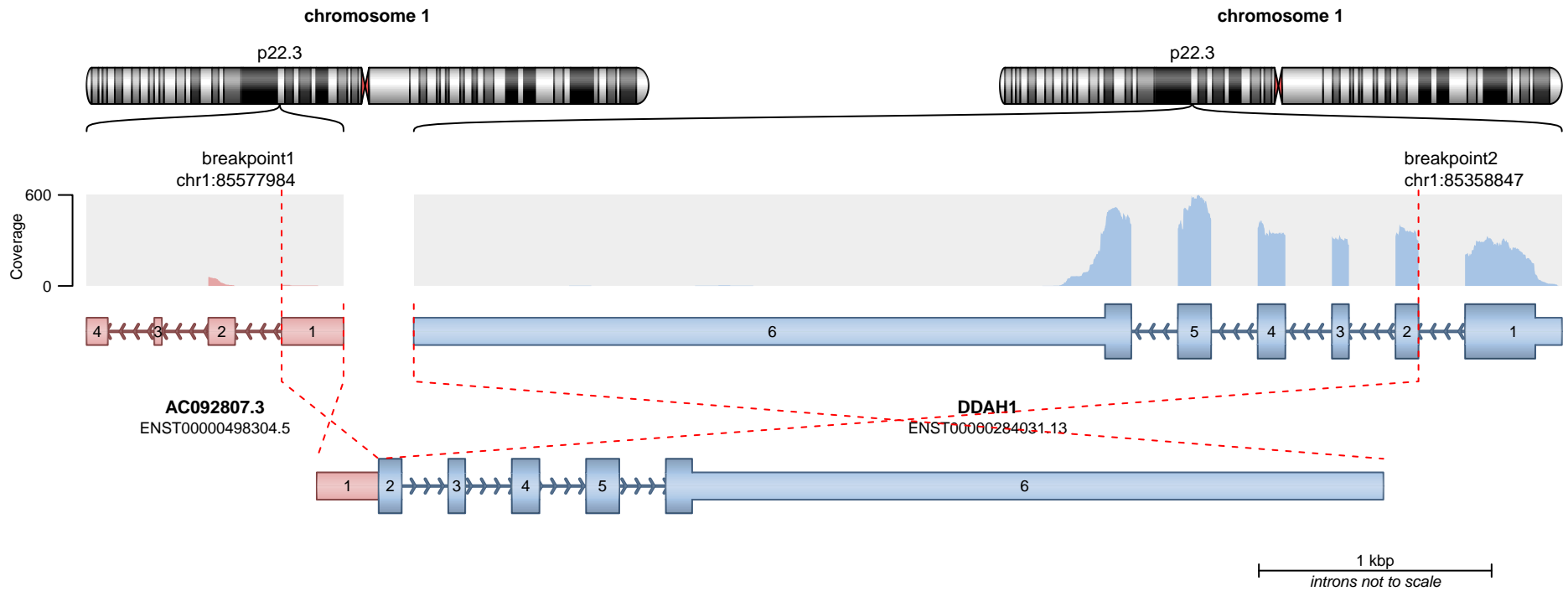
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



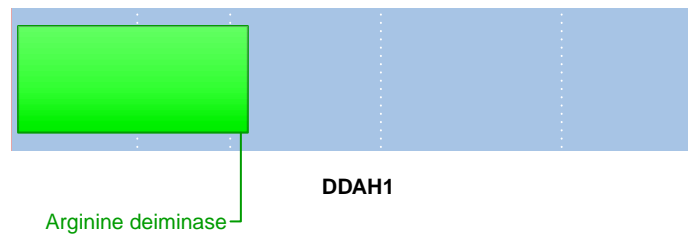
**SUPPORTING READ COUNT**

Split reads = 20  
Discordant mates = 3

- translocation
- duplication
- deletion
- inversion



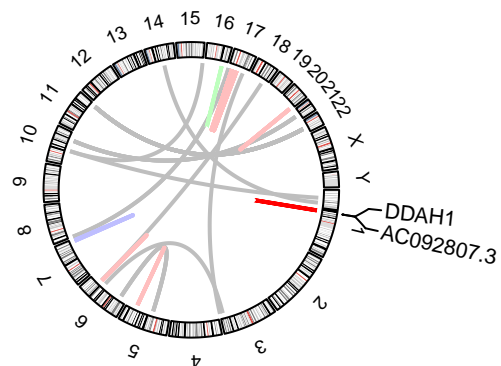
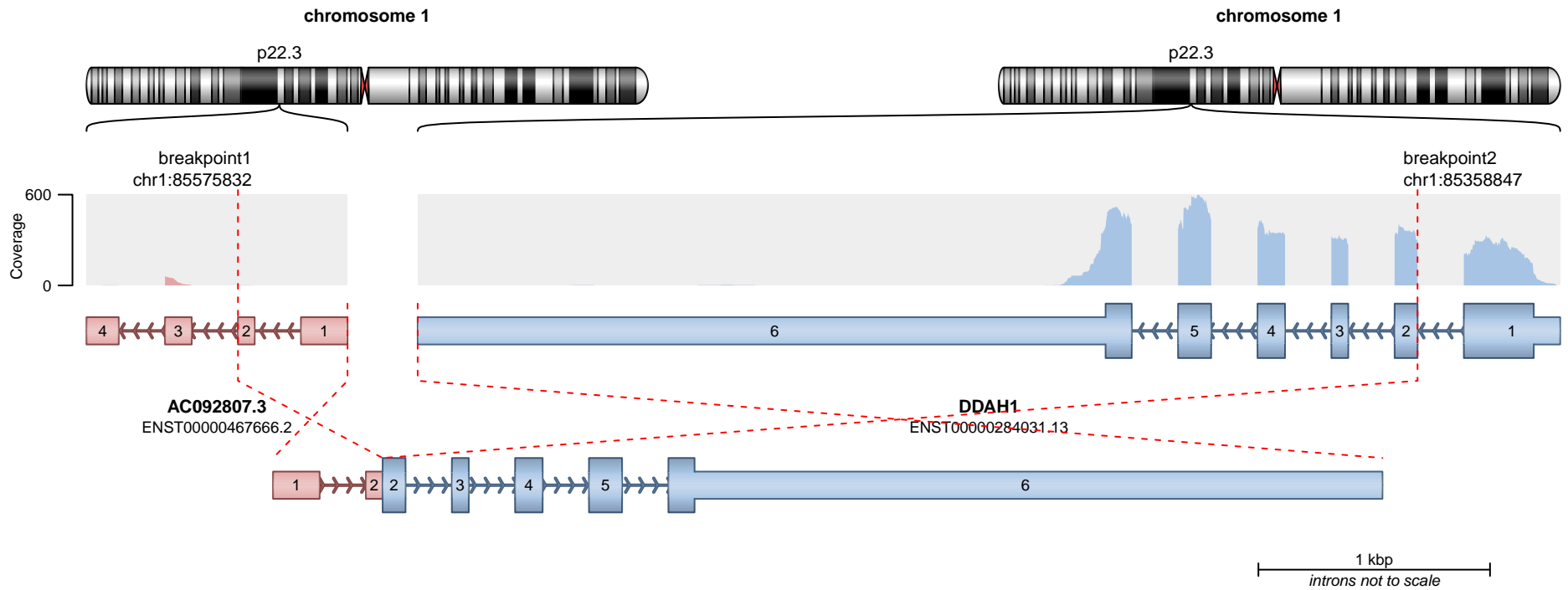
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



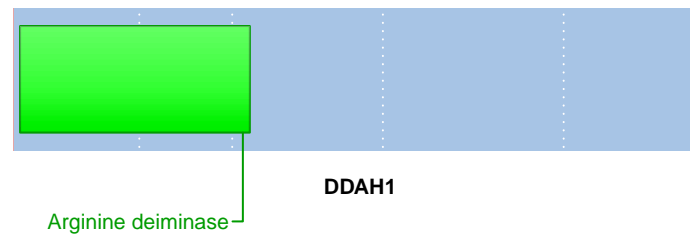
**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



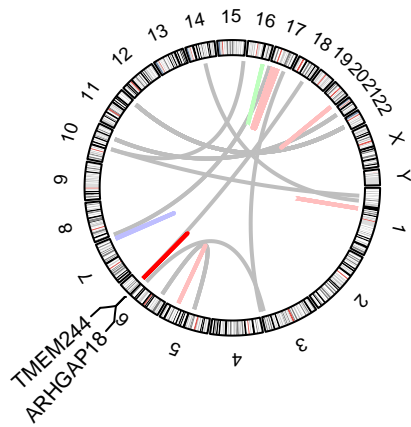
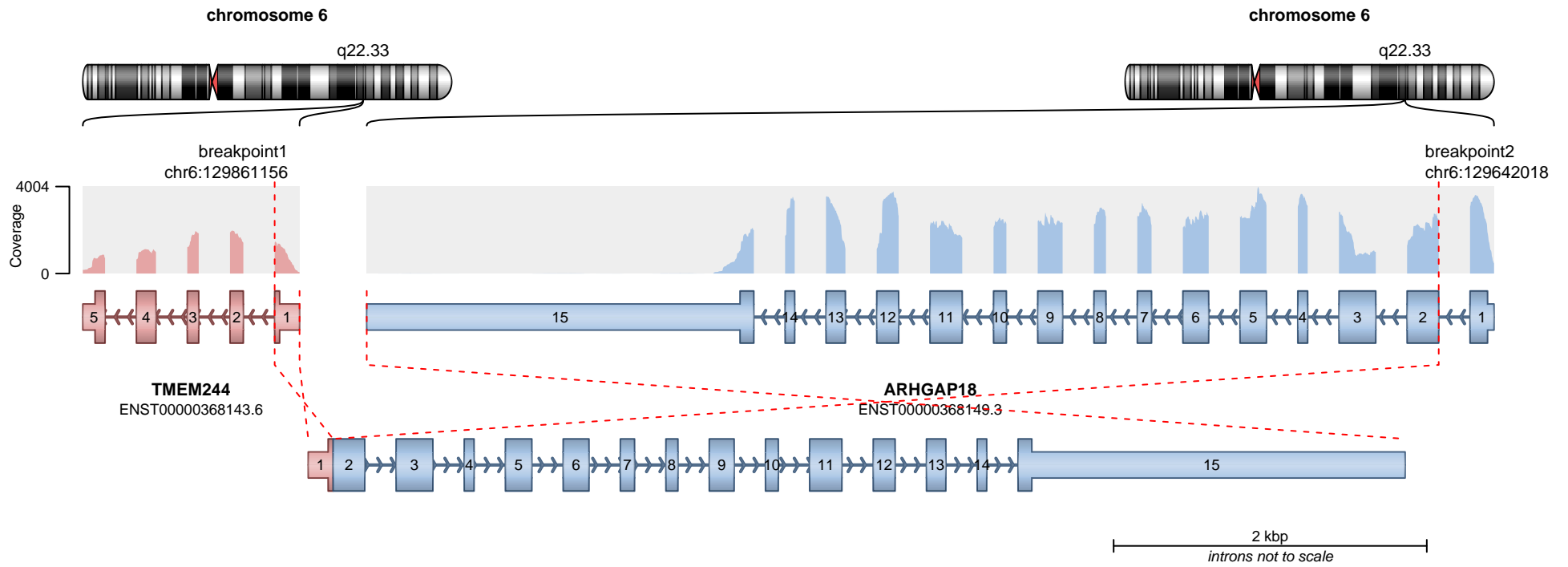
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



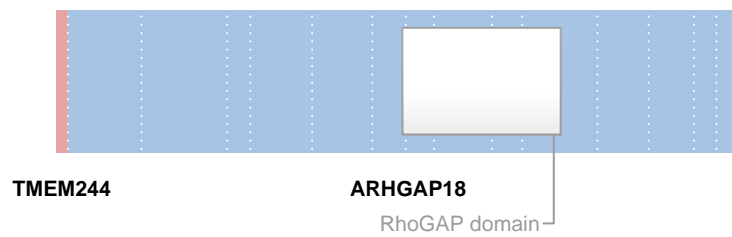
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



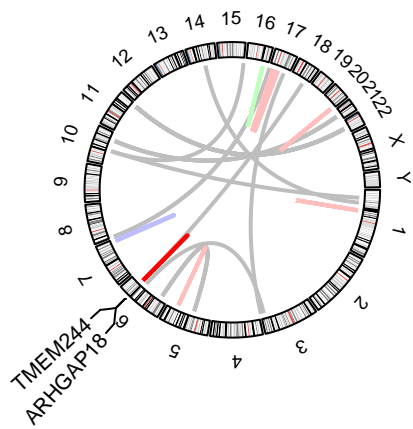
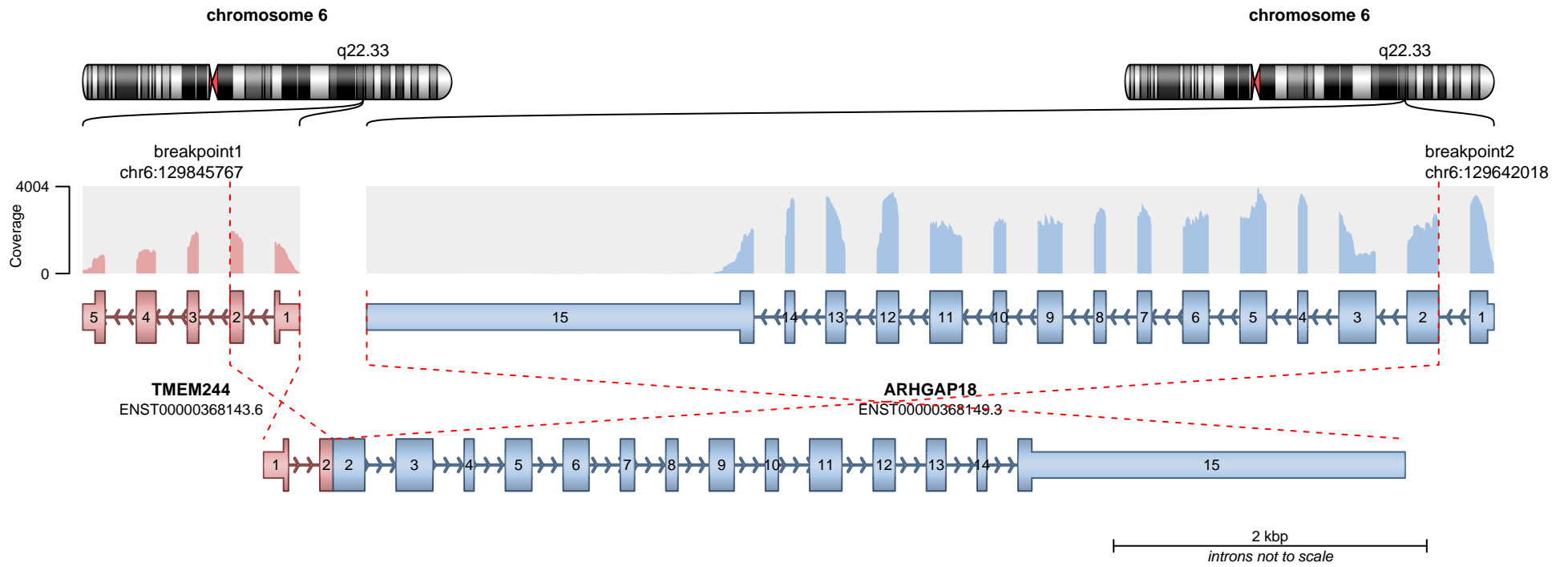
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



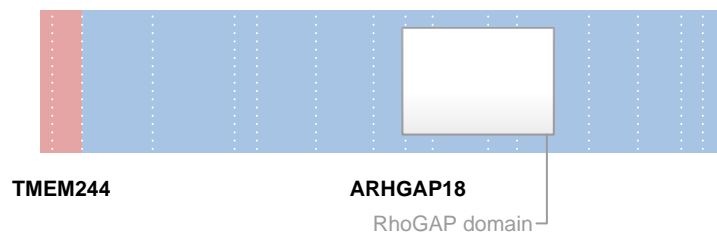
**SUPPORTING READ COUNT**

Split reads = 17  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



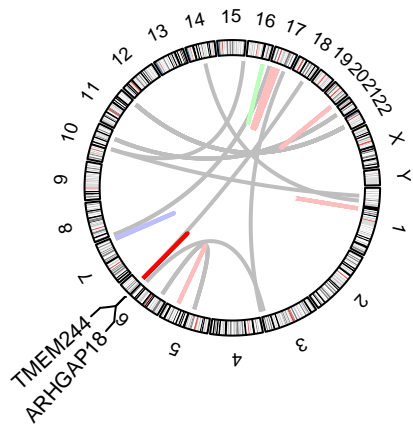
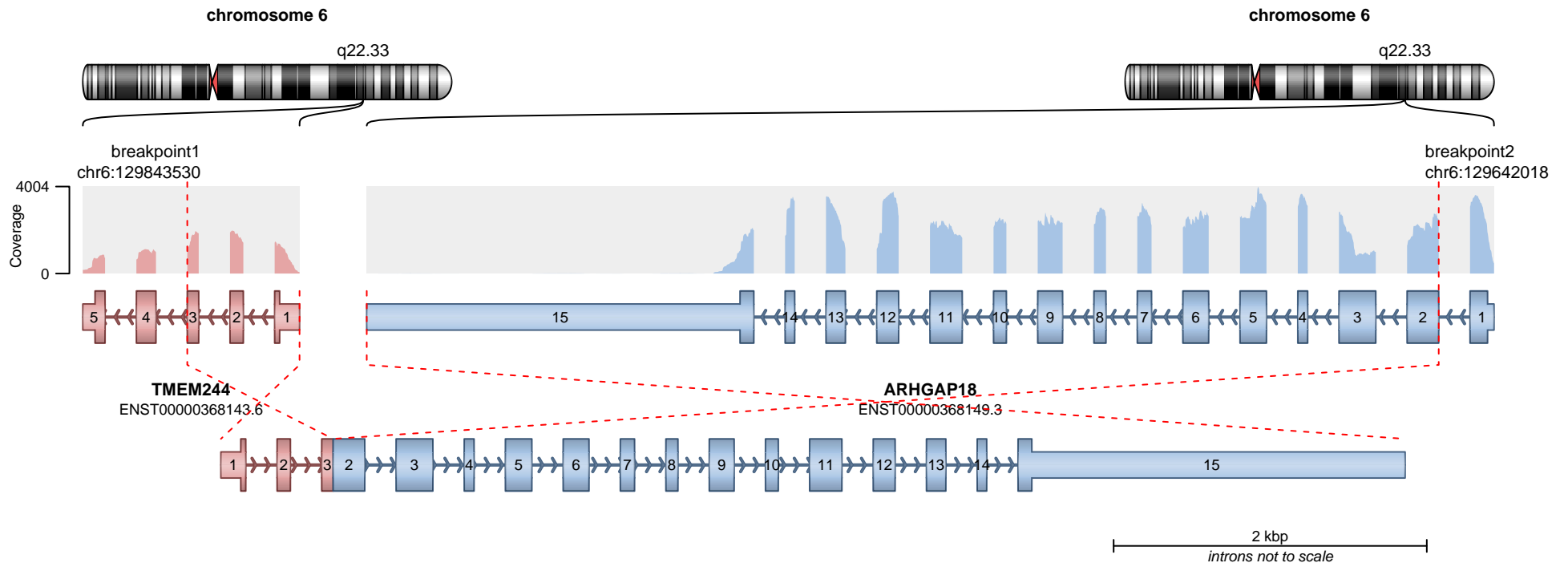
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



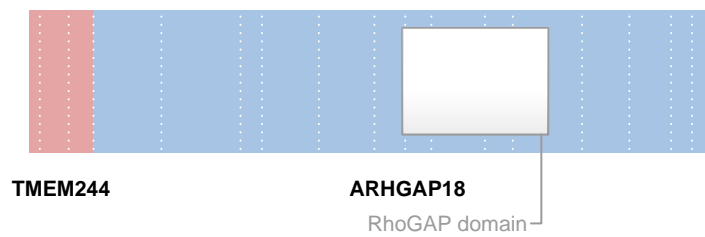
**SUPPORTING READ COUNT**

Split reads = 5  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



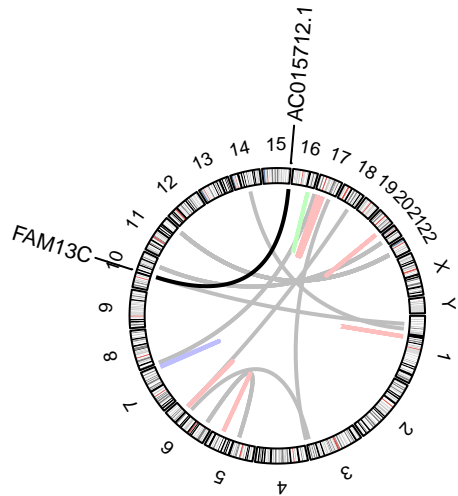
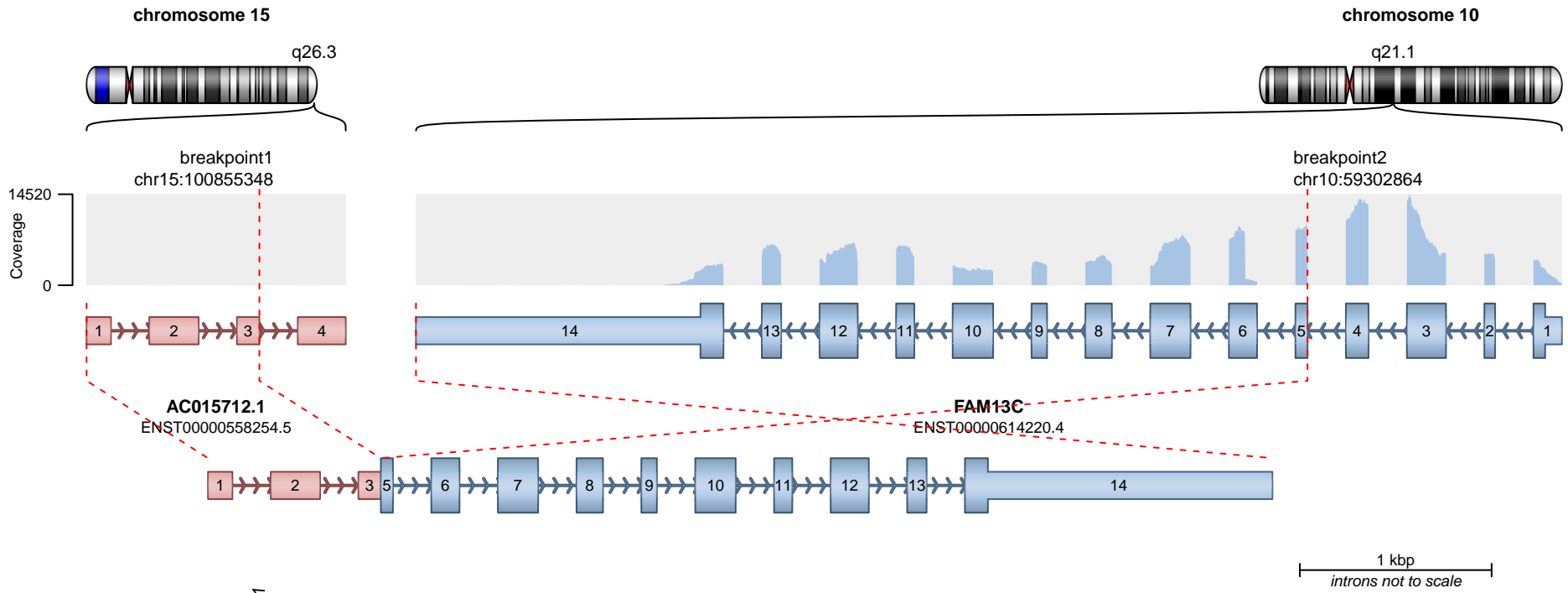
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

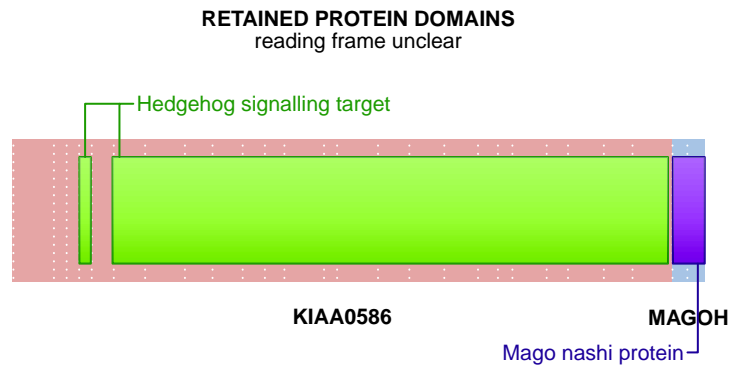
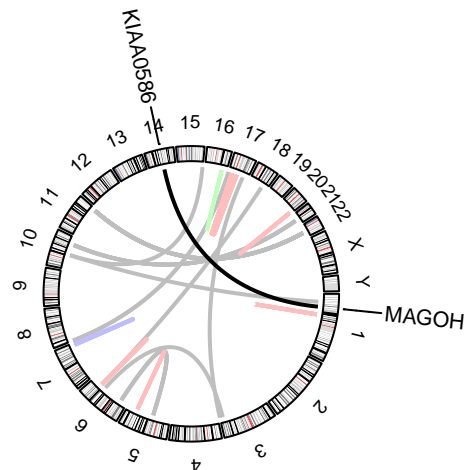
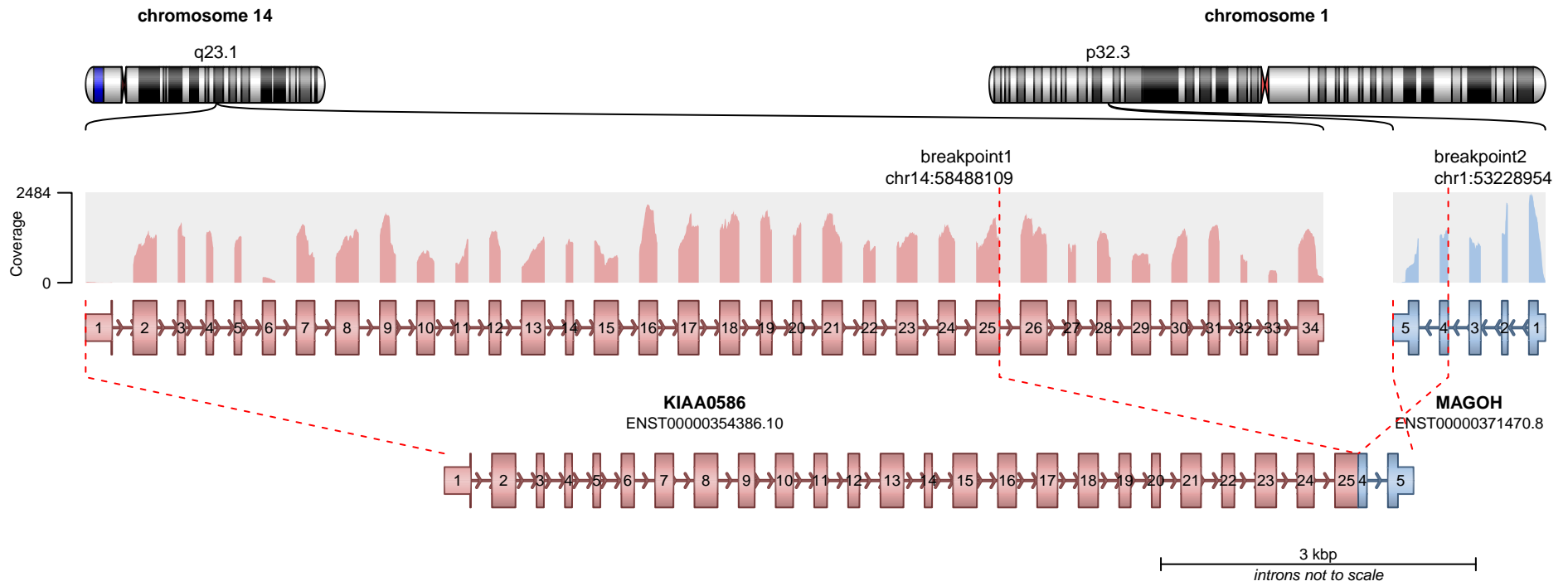


— translocation    — deletion  
 — duplication    — inversion

No protein domains retained in fusion.

**SUPPORTING READ COUNT**

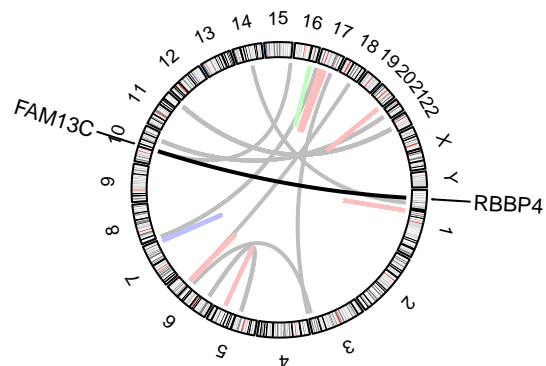
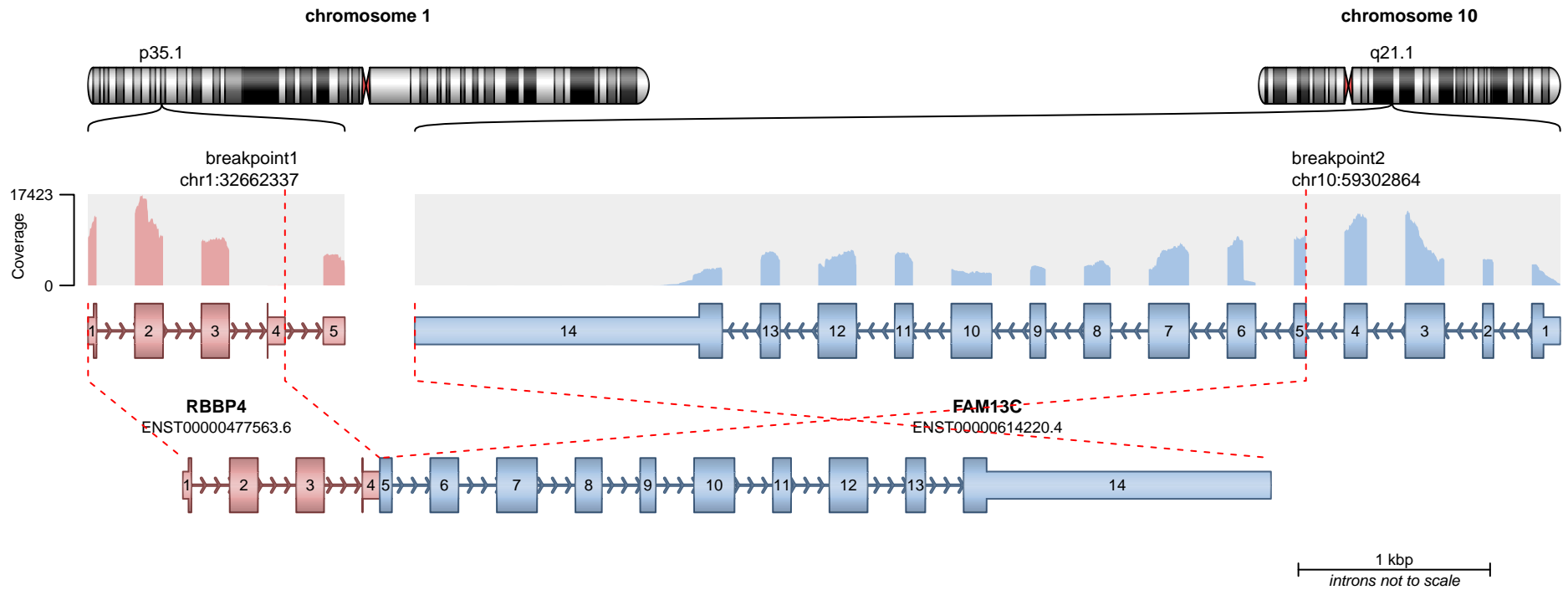
Split reads = 11  
 Discordant mates = 0



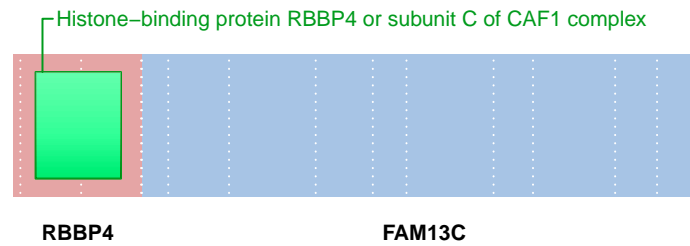
**SUPPORTING READ COUNT**

Split reads = 11  
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