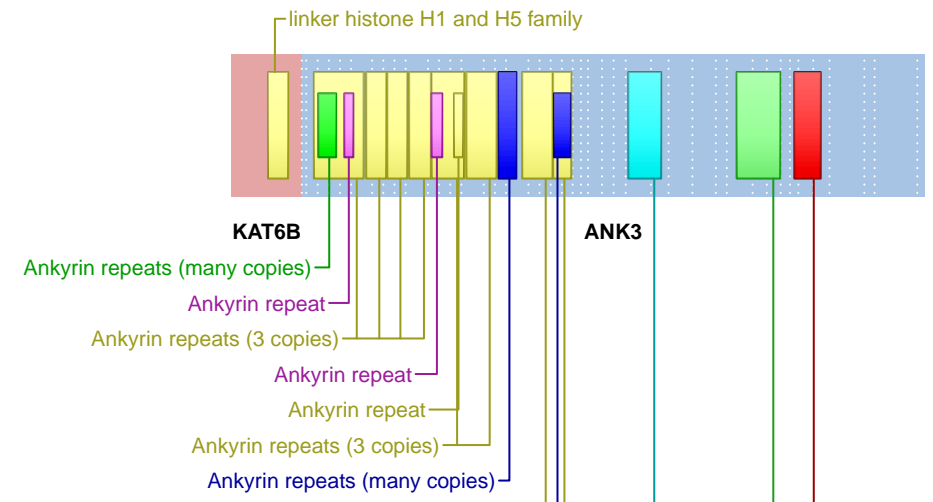


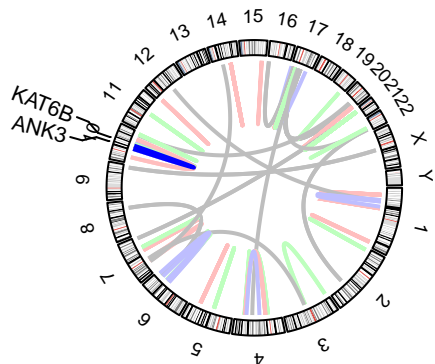
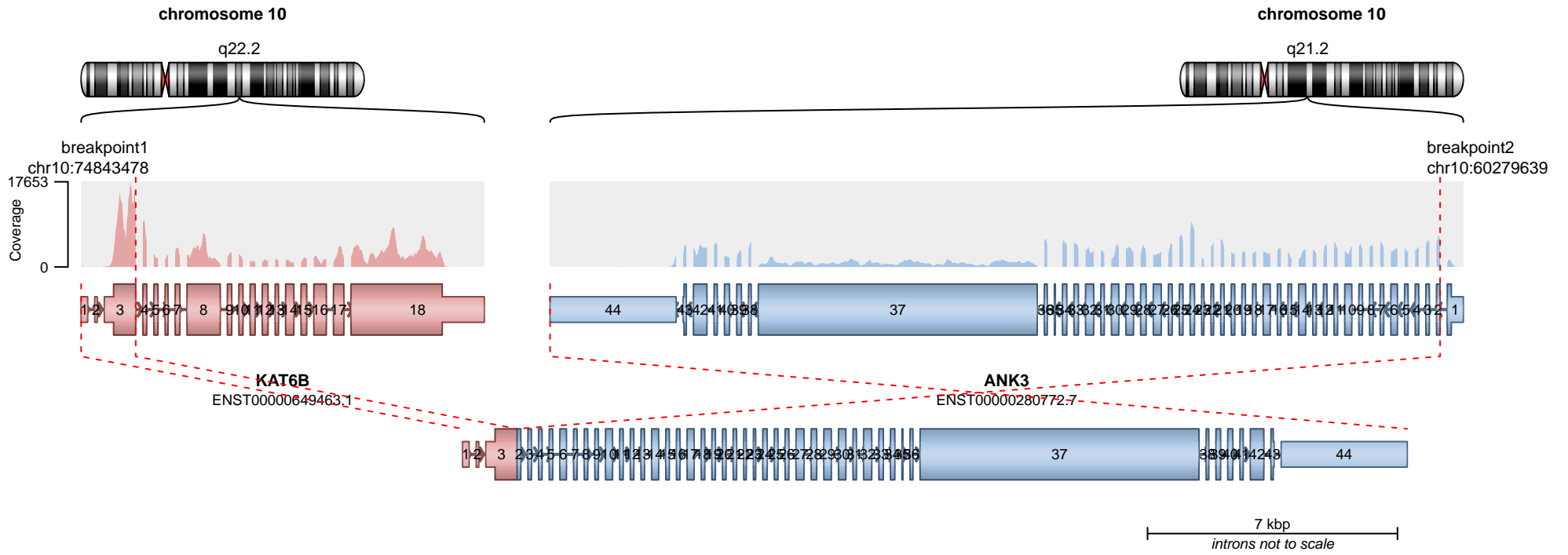
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



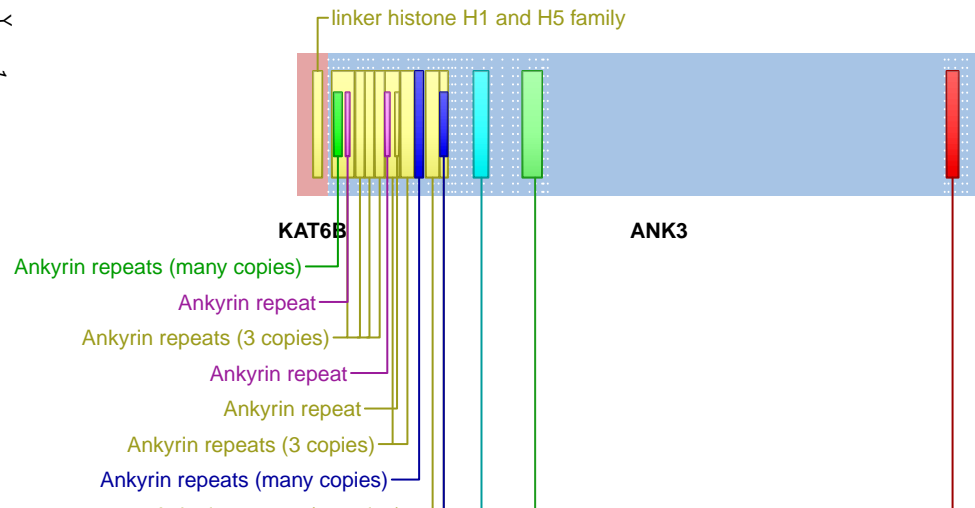
**SUPPORTING READ COUNT**

Split reads = 535  
Discordant mates = 2



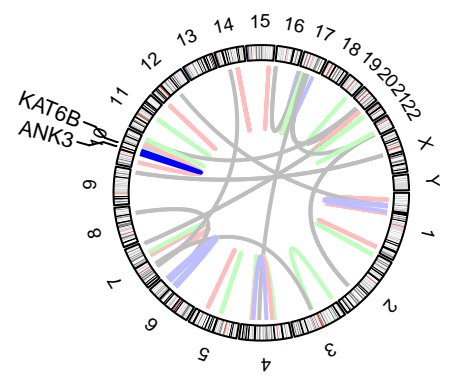
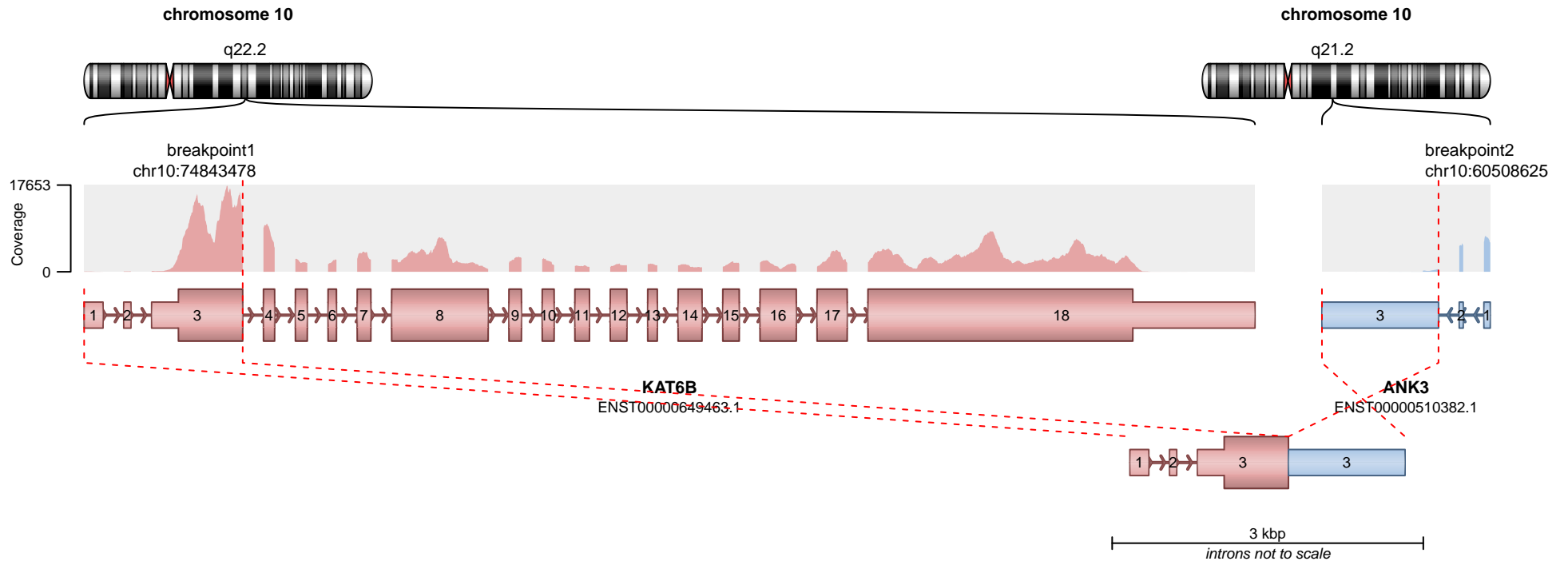
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear

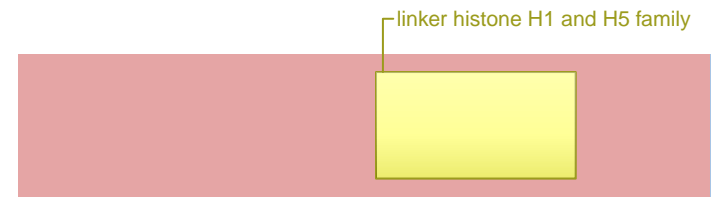


**SUPPORTING READ COUNT**

Split reads = 19  
Discordant mates = 1



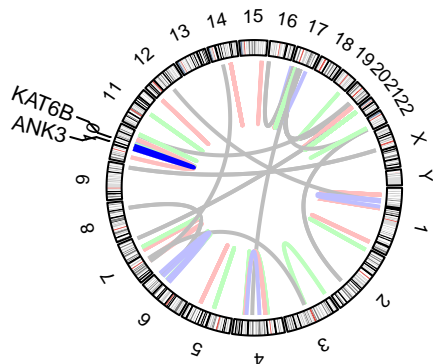
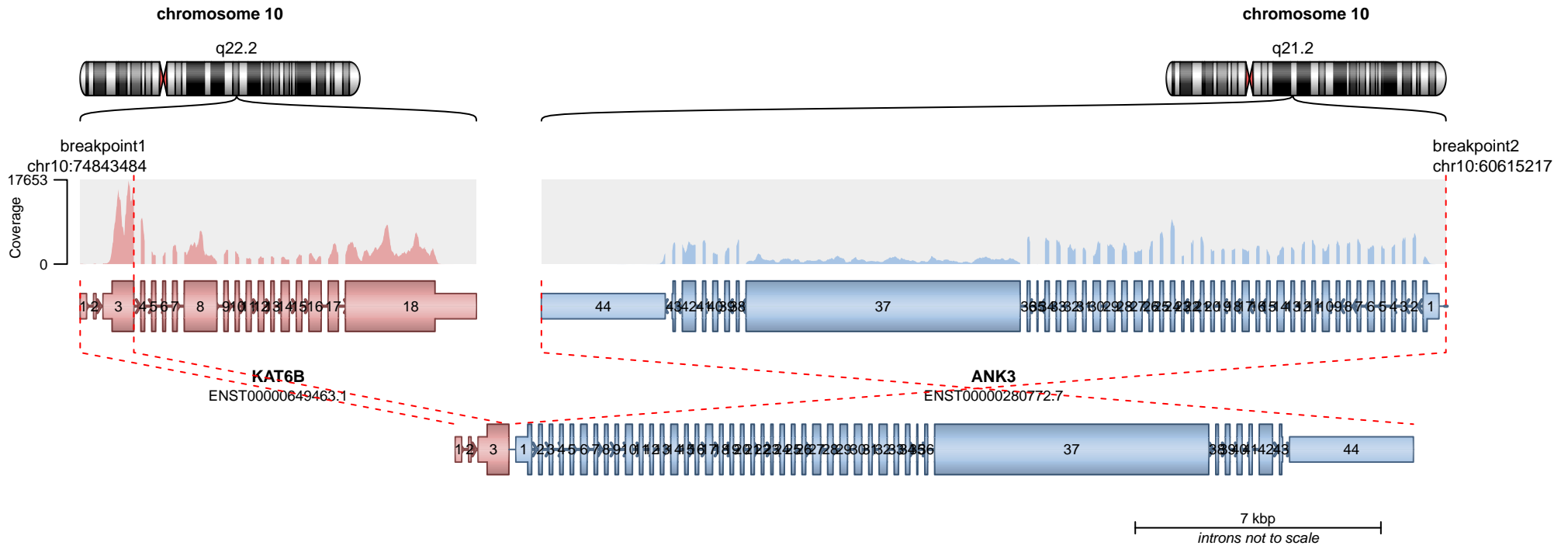
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

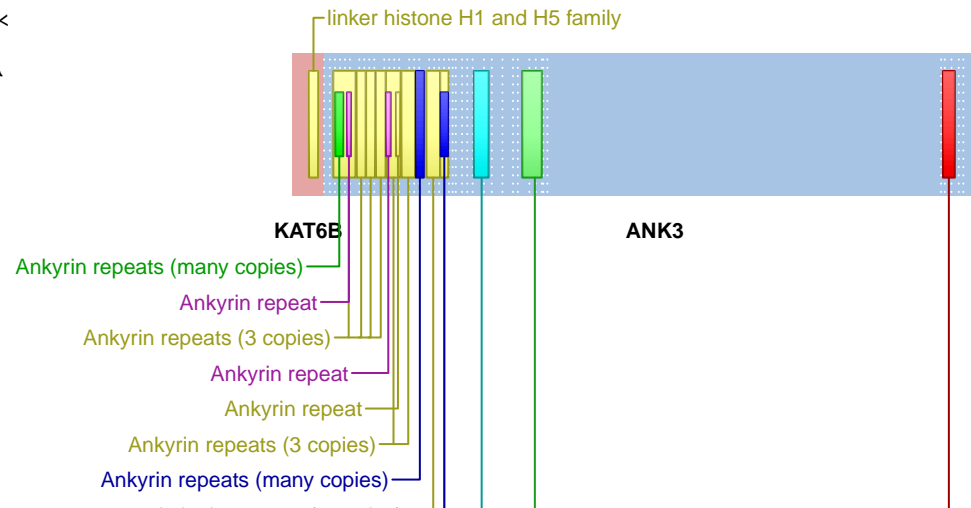
Split reads = 10  
Discordant mates = 1

— translocation    — deletion  
— duplication    — inversion



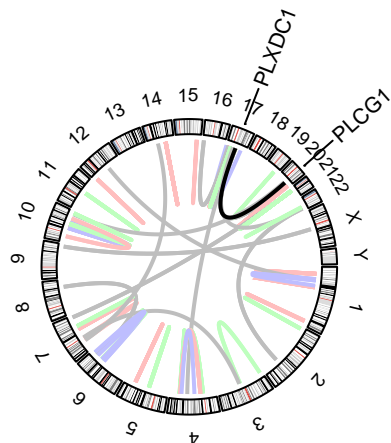
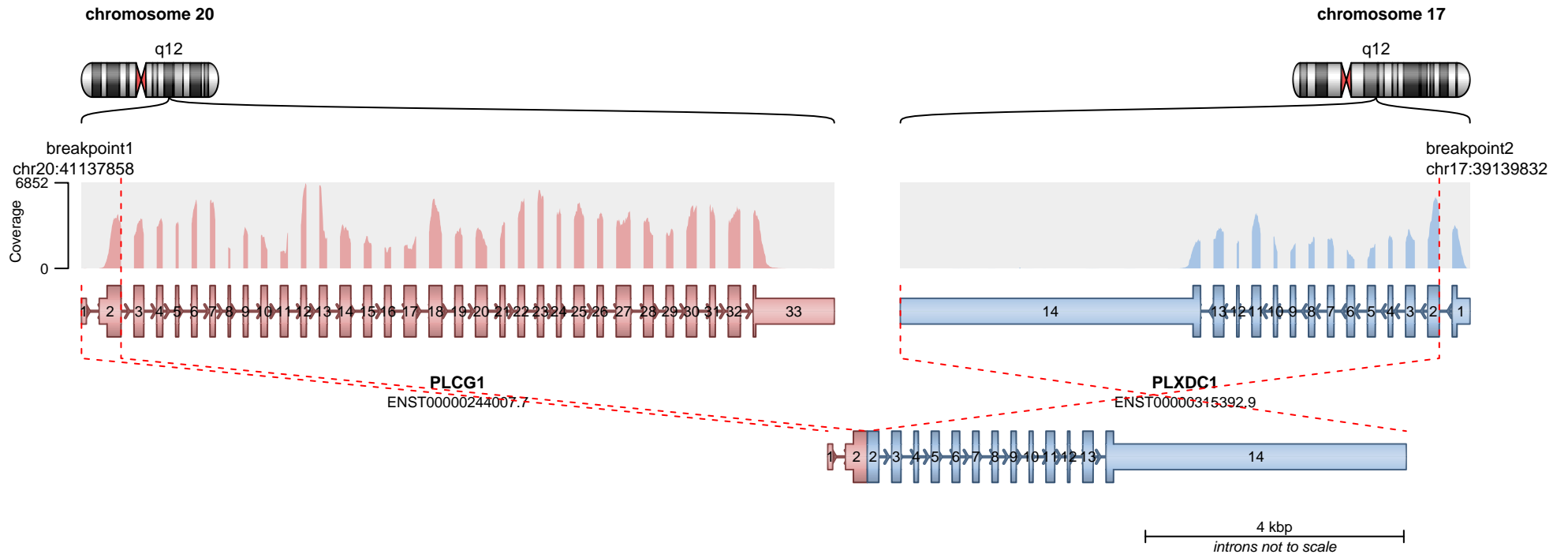
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear

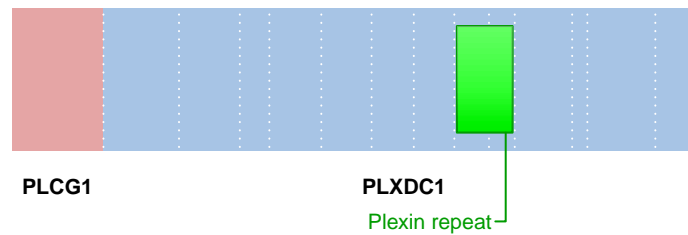


**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 2



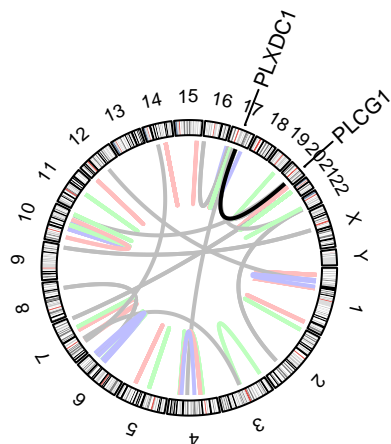
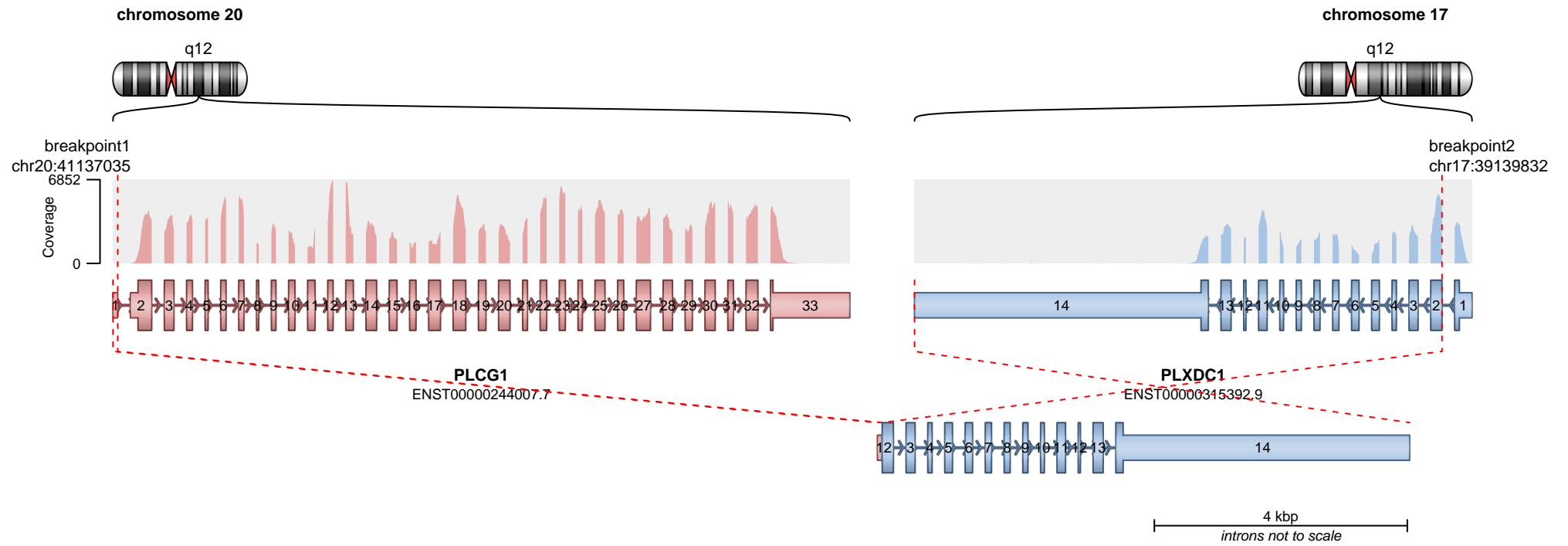
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



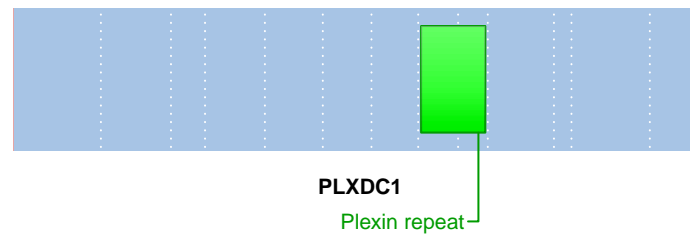
**SUPPORTING READ COUNT**

Split reads = 473  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



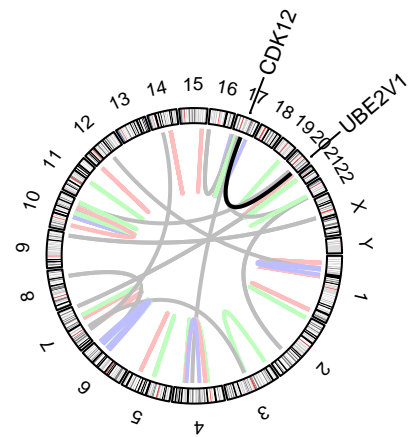
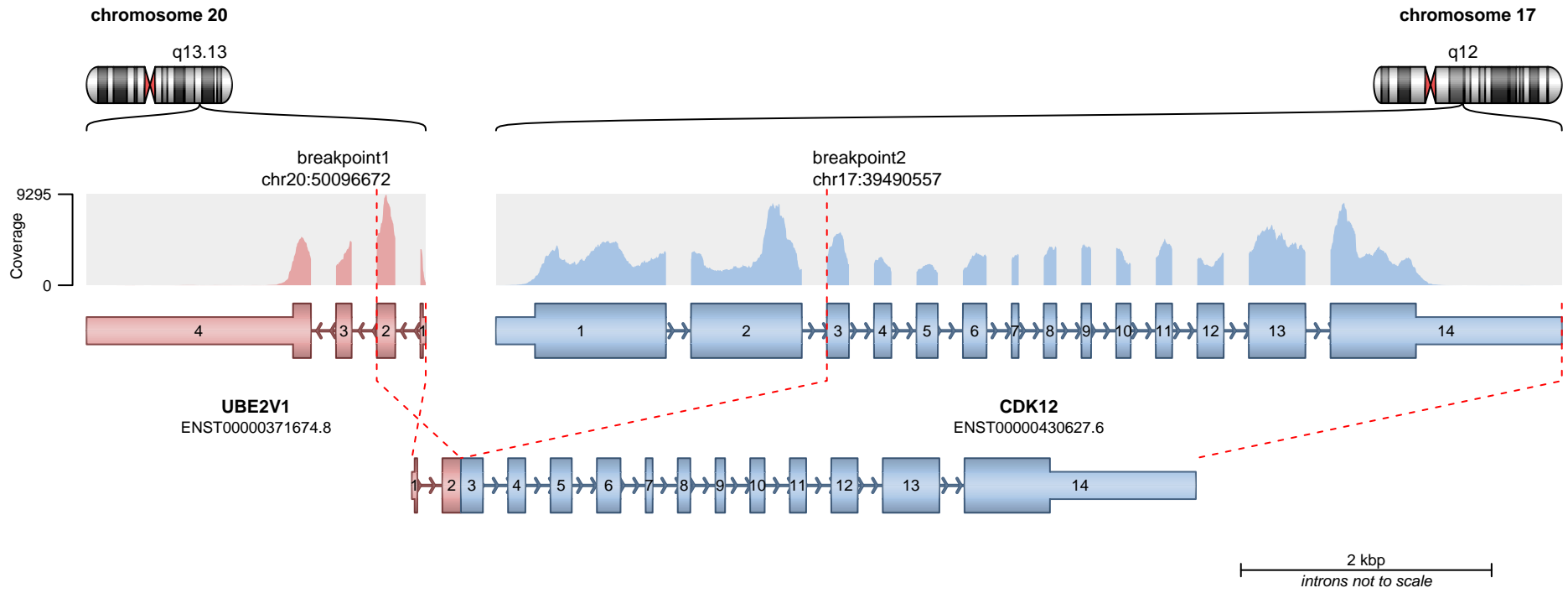
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



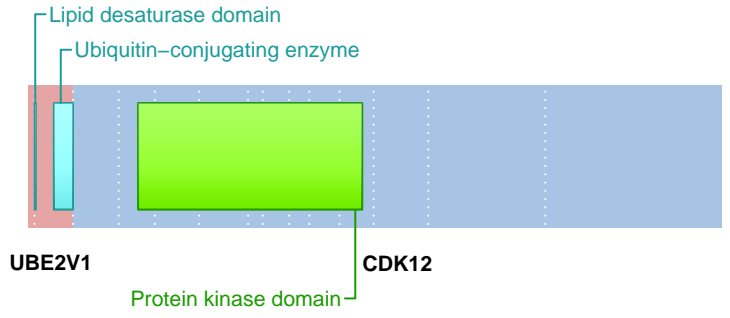
**SUPPORTING READ COUNT**

Split reads = 5  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



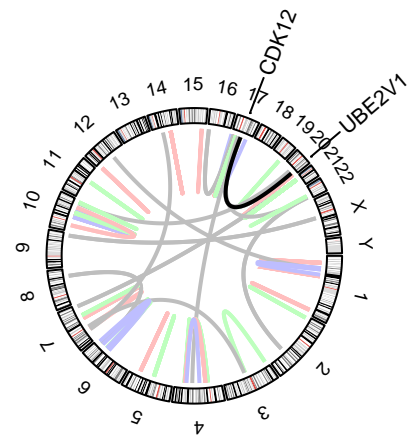
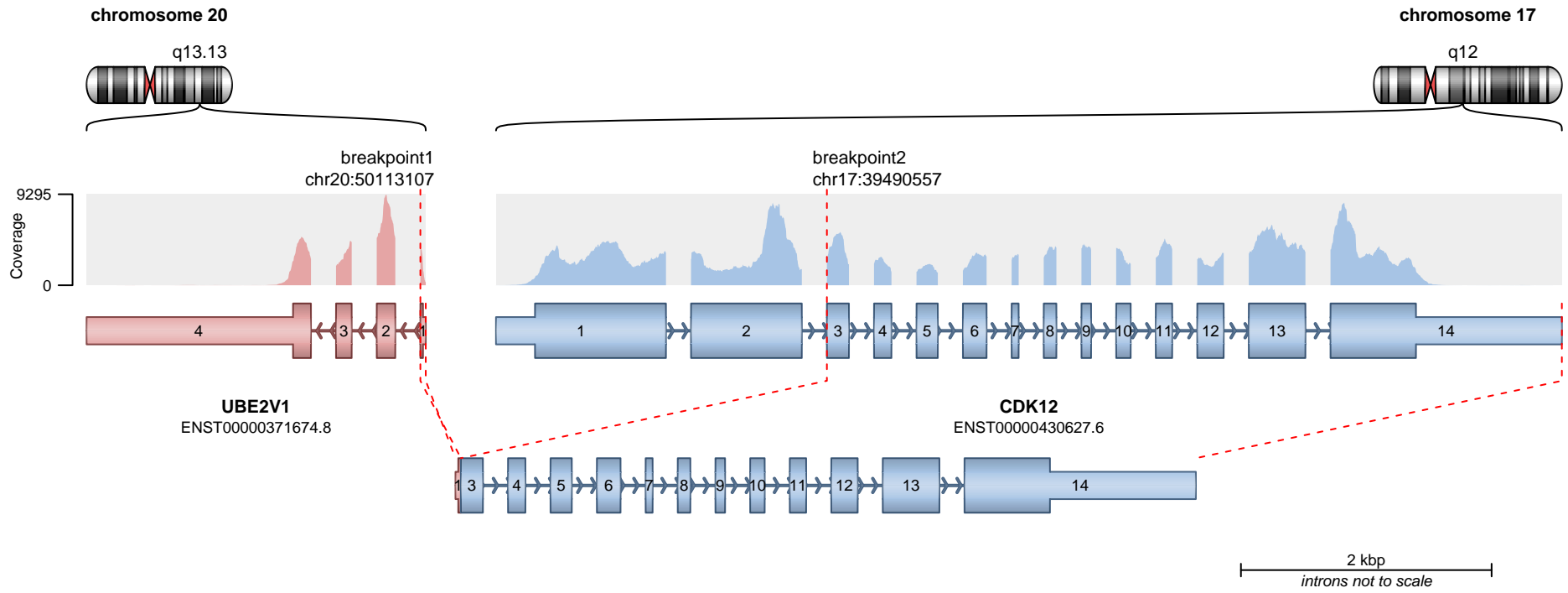
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



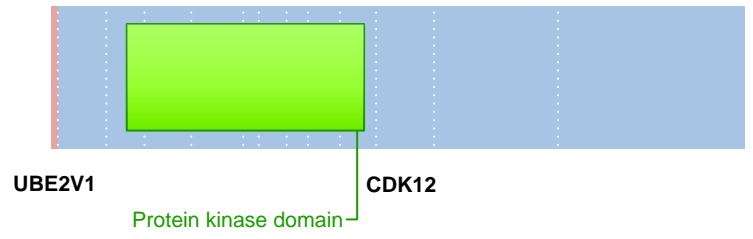
**SUPPORTING READ COUNT**

Split reads = 233  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



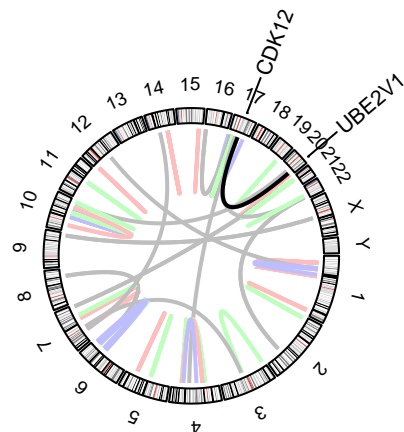
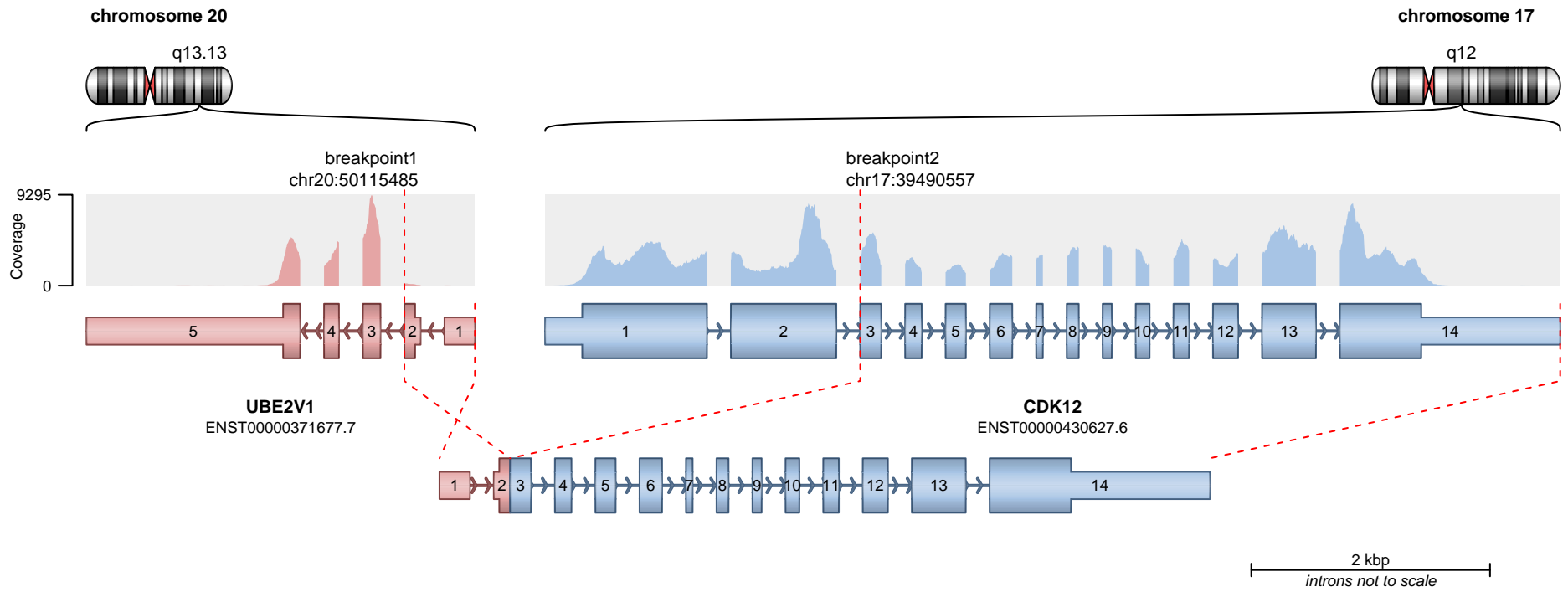
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



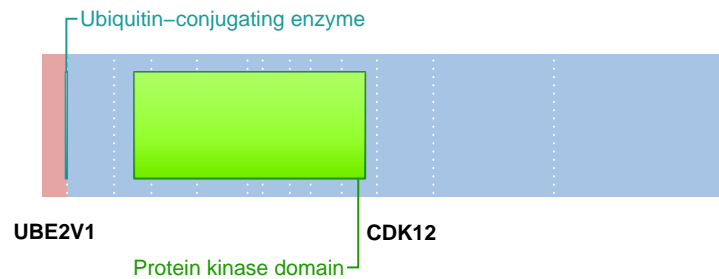
**SUPPORTING READ COUNT**

Split reads = 86  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



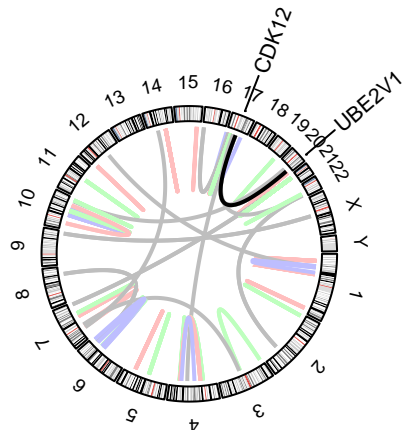
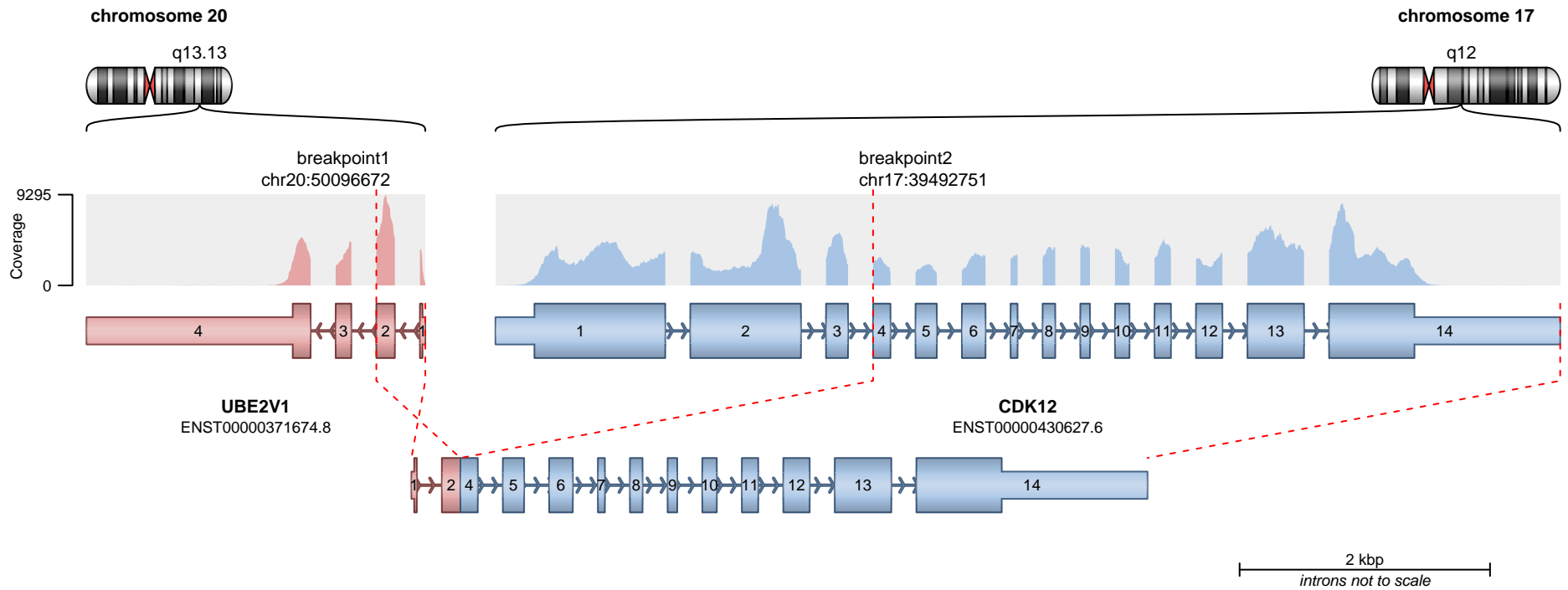
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



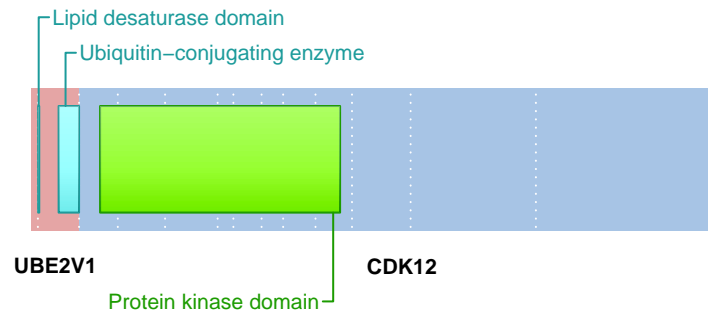
**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



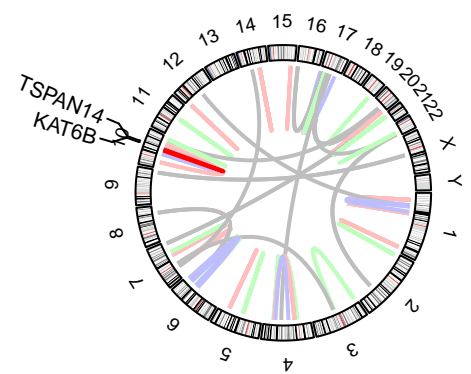
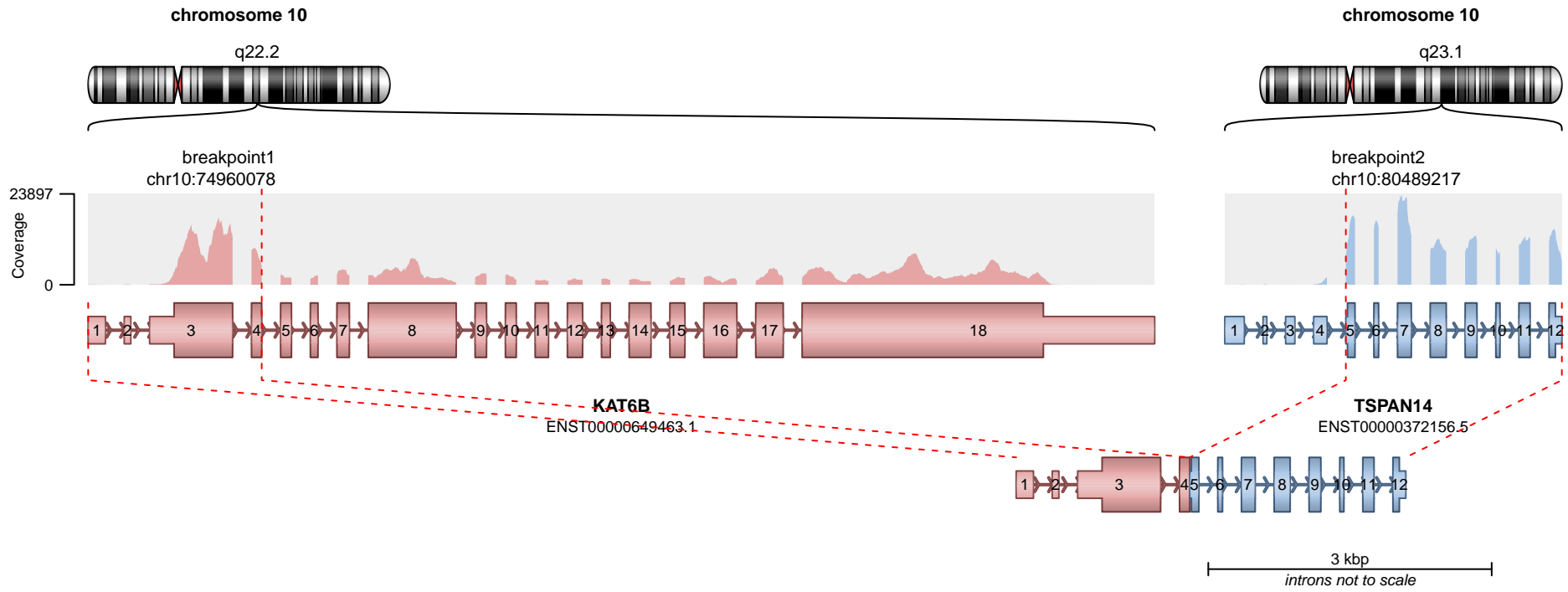
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



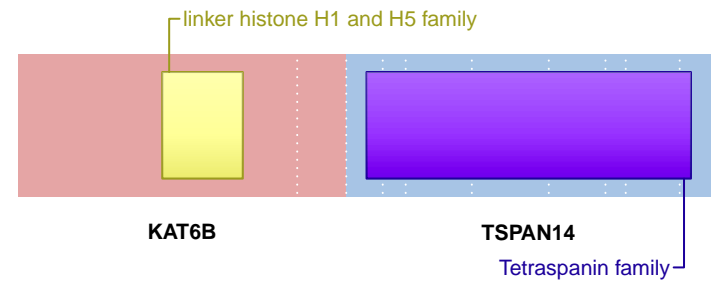
**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



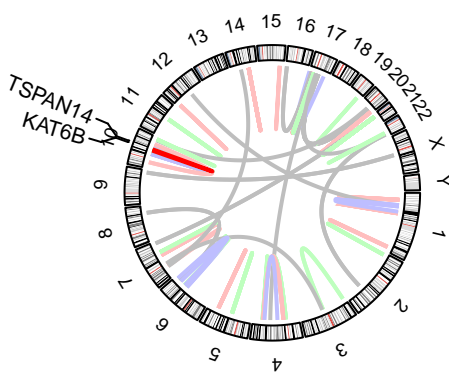
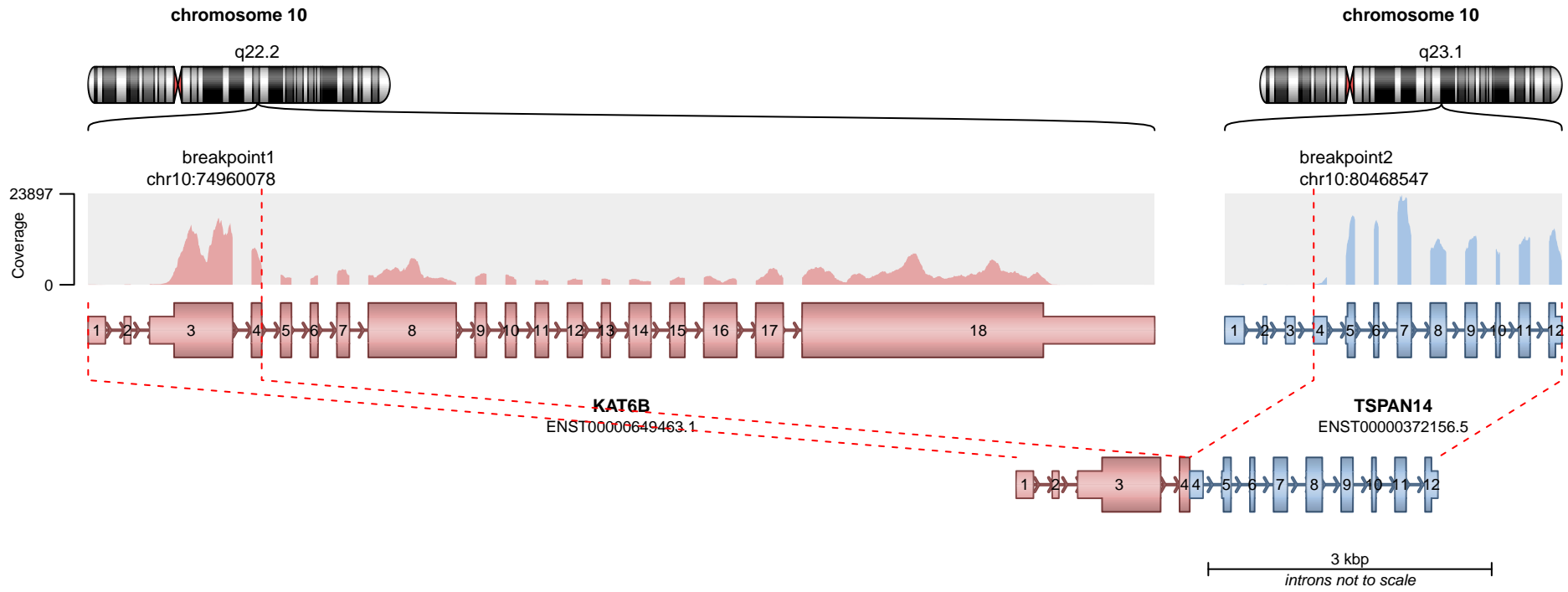
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



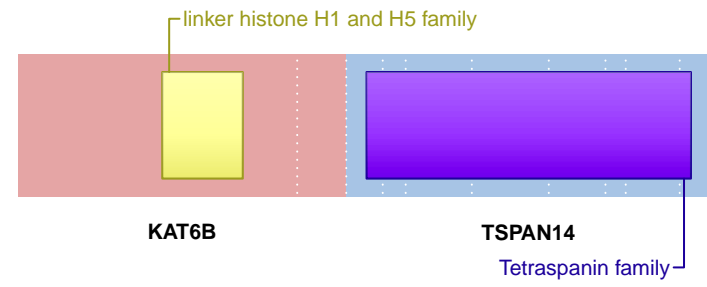
**SUPPORTING READ COUNT**

Split reads = 201  
Discordant mates = 2

— translocation    — deletion  
— duplication    — inversion



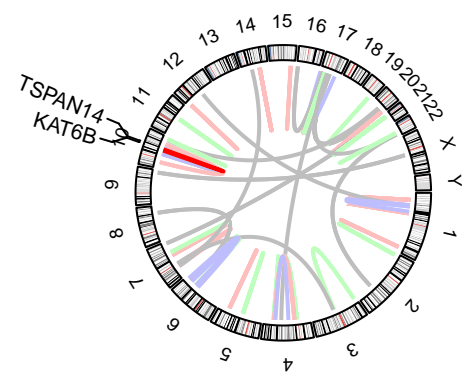
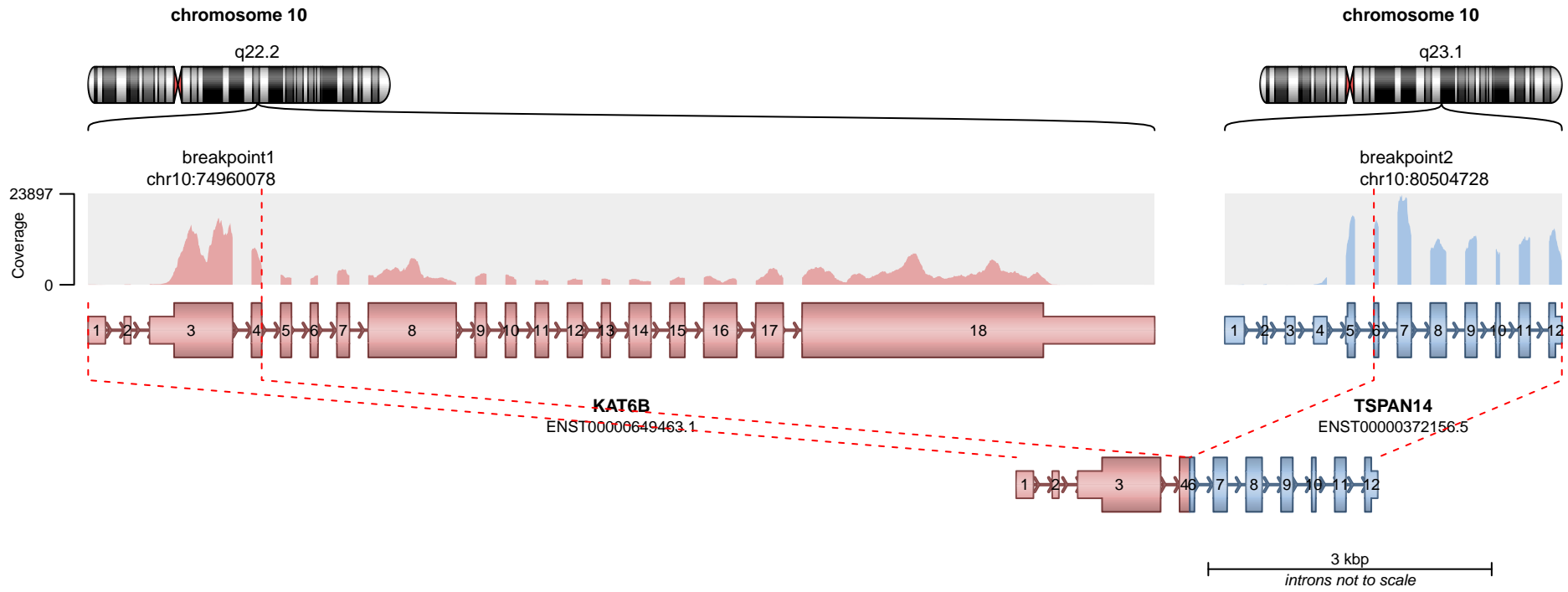
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



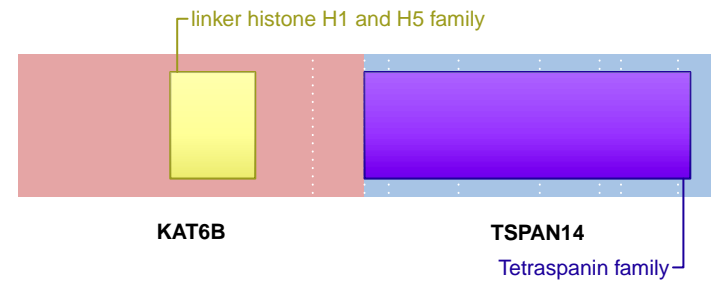
**SUPPORTING READ COUNT**

Split reads = 24  
Discordant mates = 2

- translocation
- duplication
- deletion
- inversion



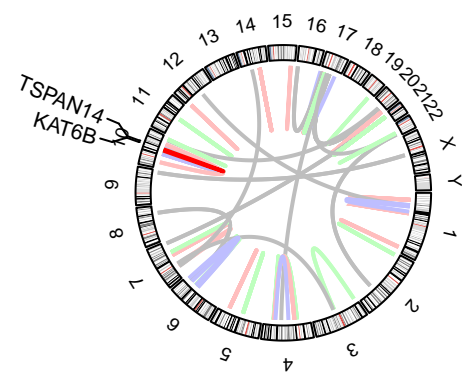
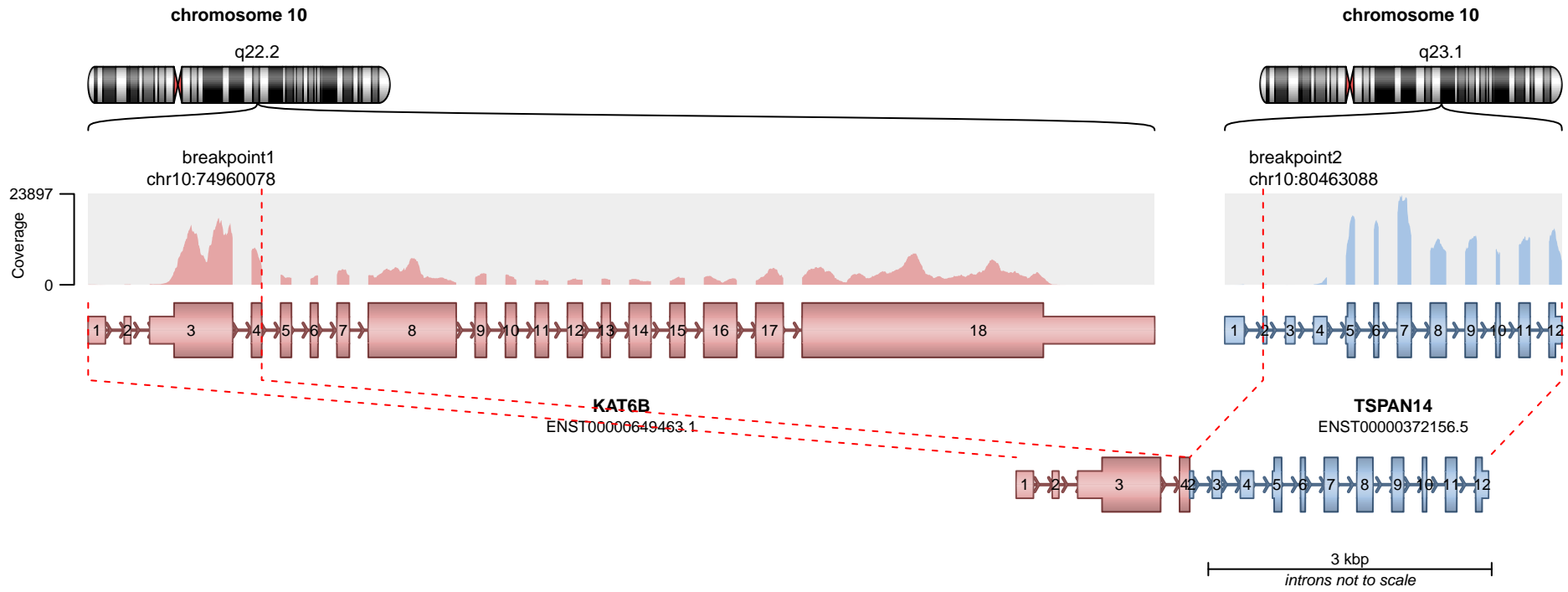
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



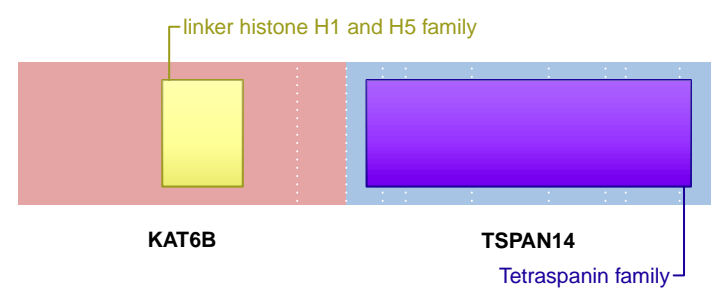
**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



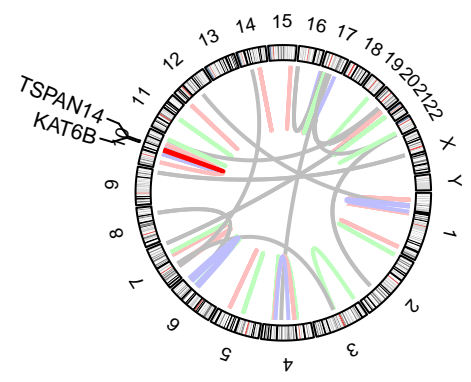
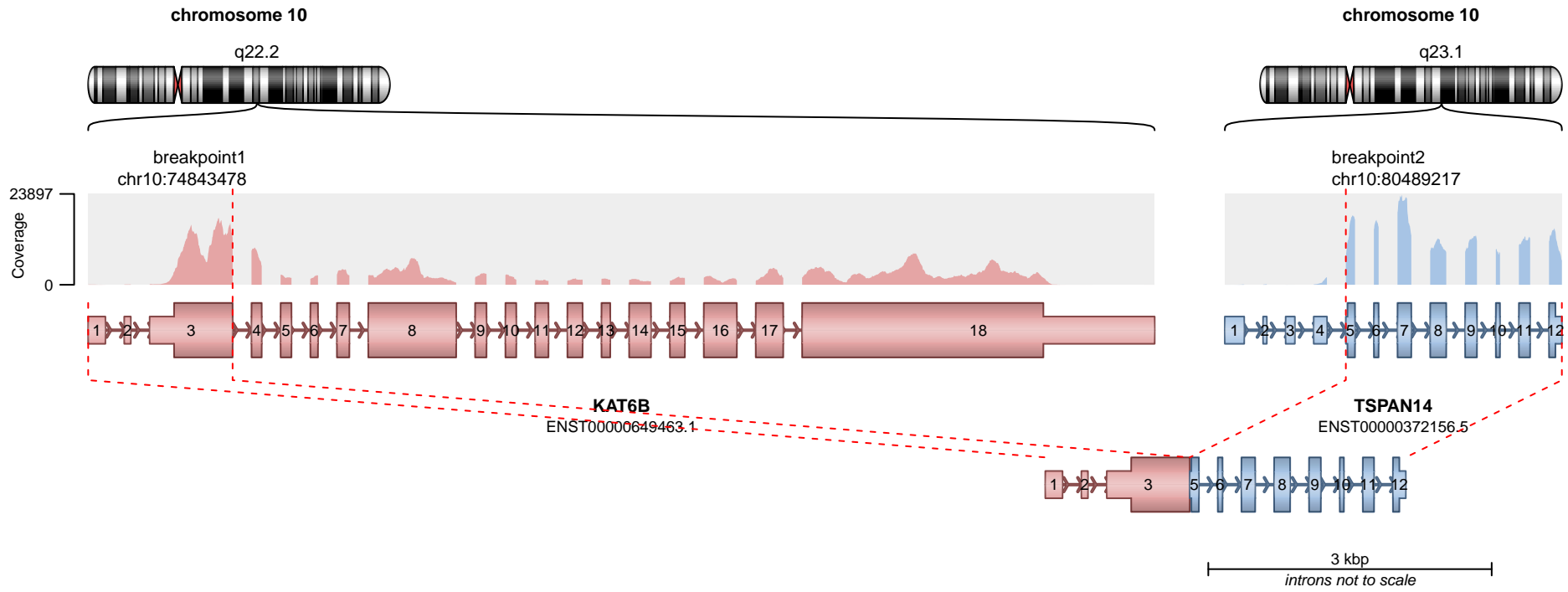
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



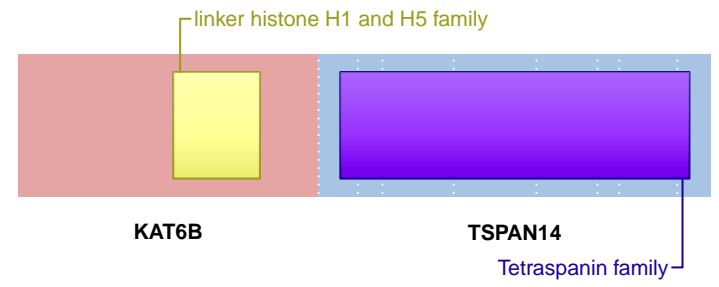
**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 2

- translocation
- duplication
- deletion
- inversion



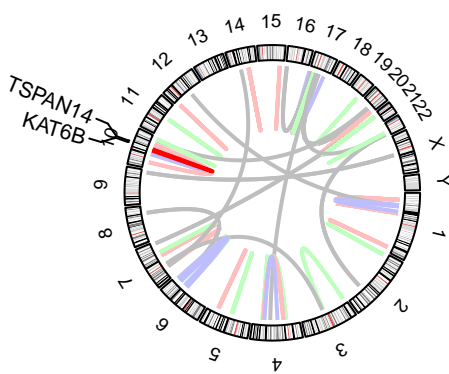
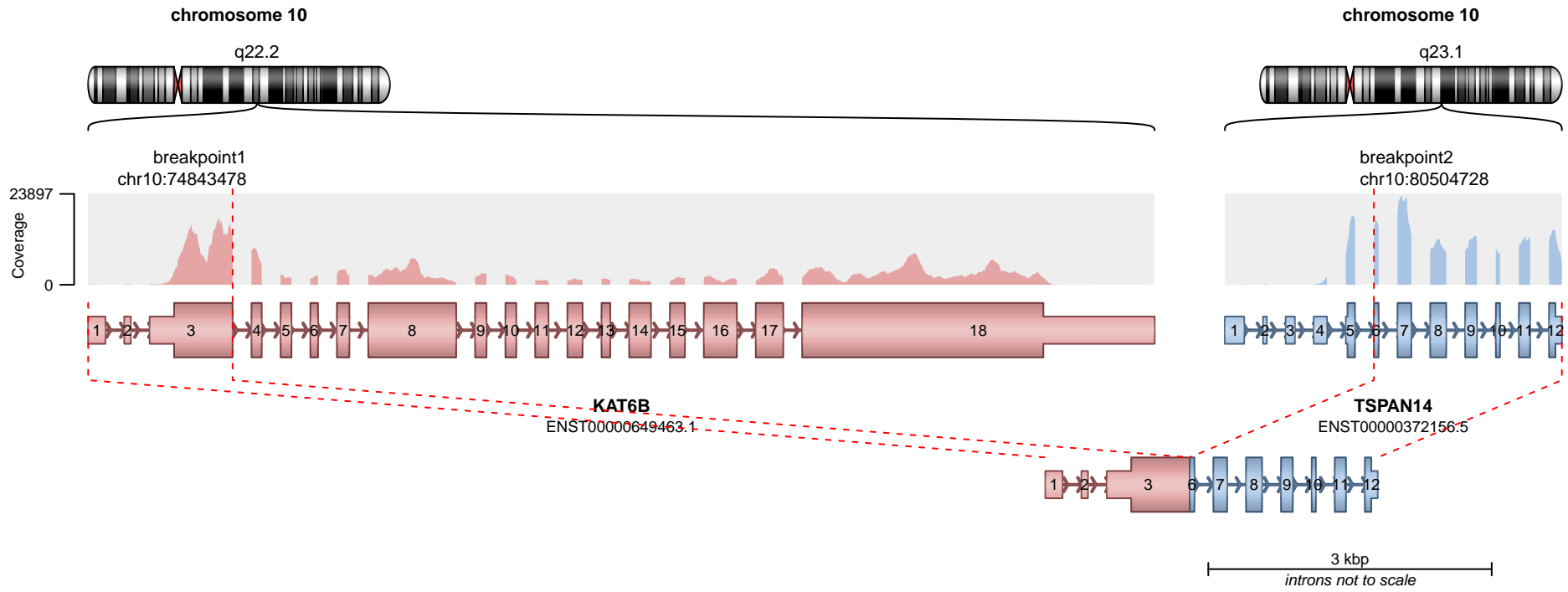
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



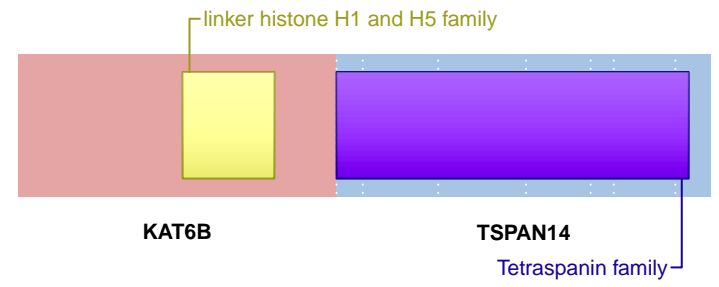
**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



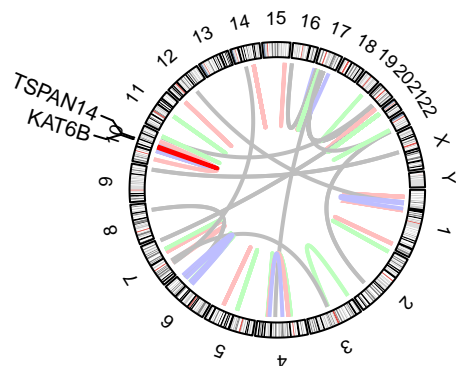
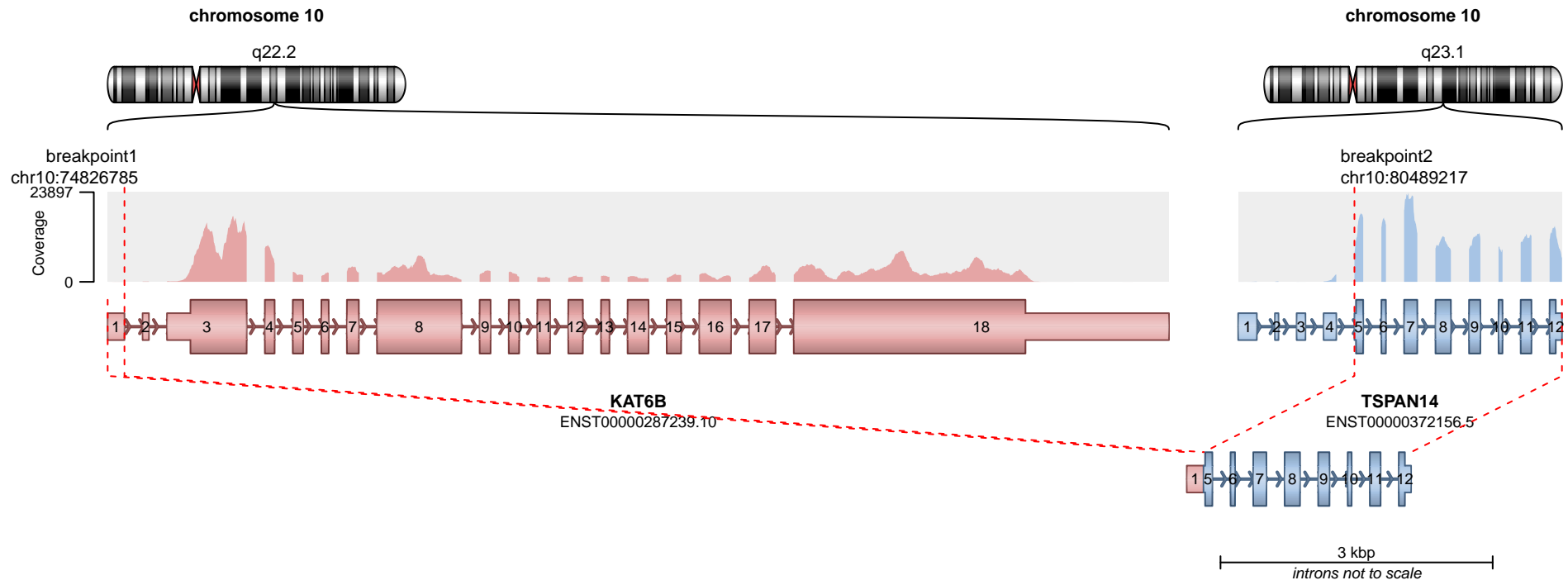
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



**RETAINED PROTEIN DOMAINS**  
reading frame unclear

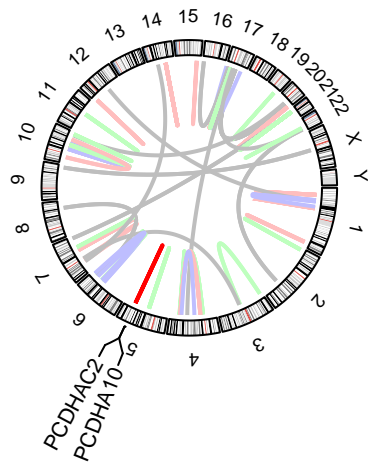
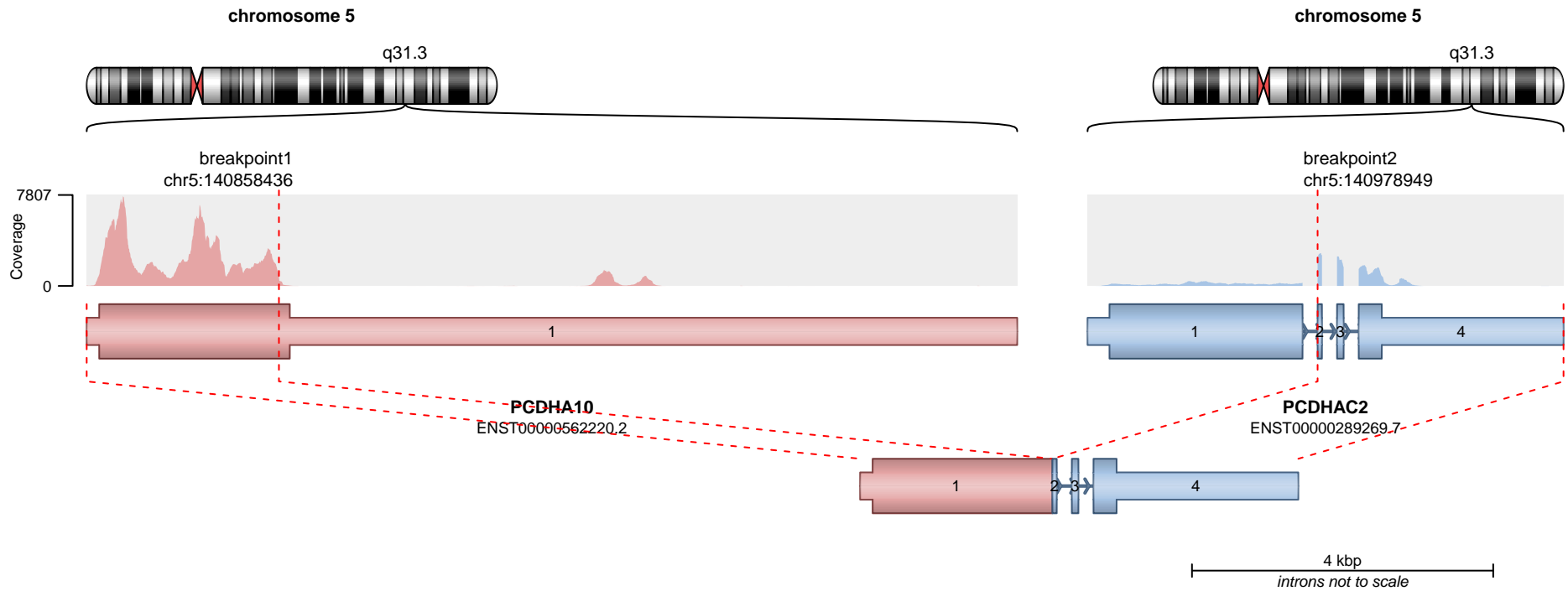


Tetraspanin family

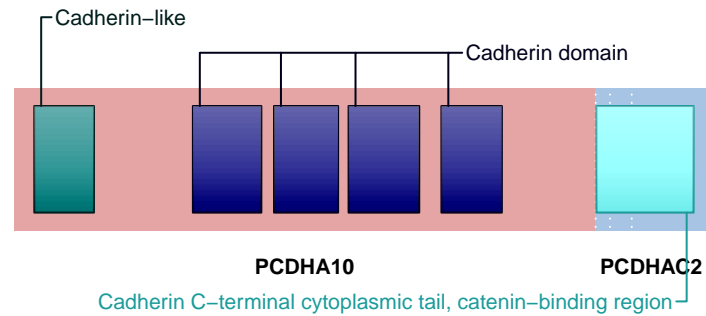
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



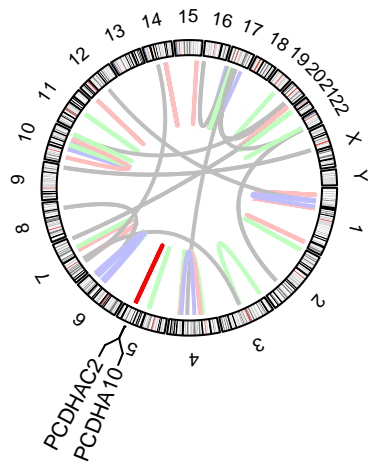
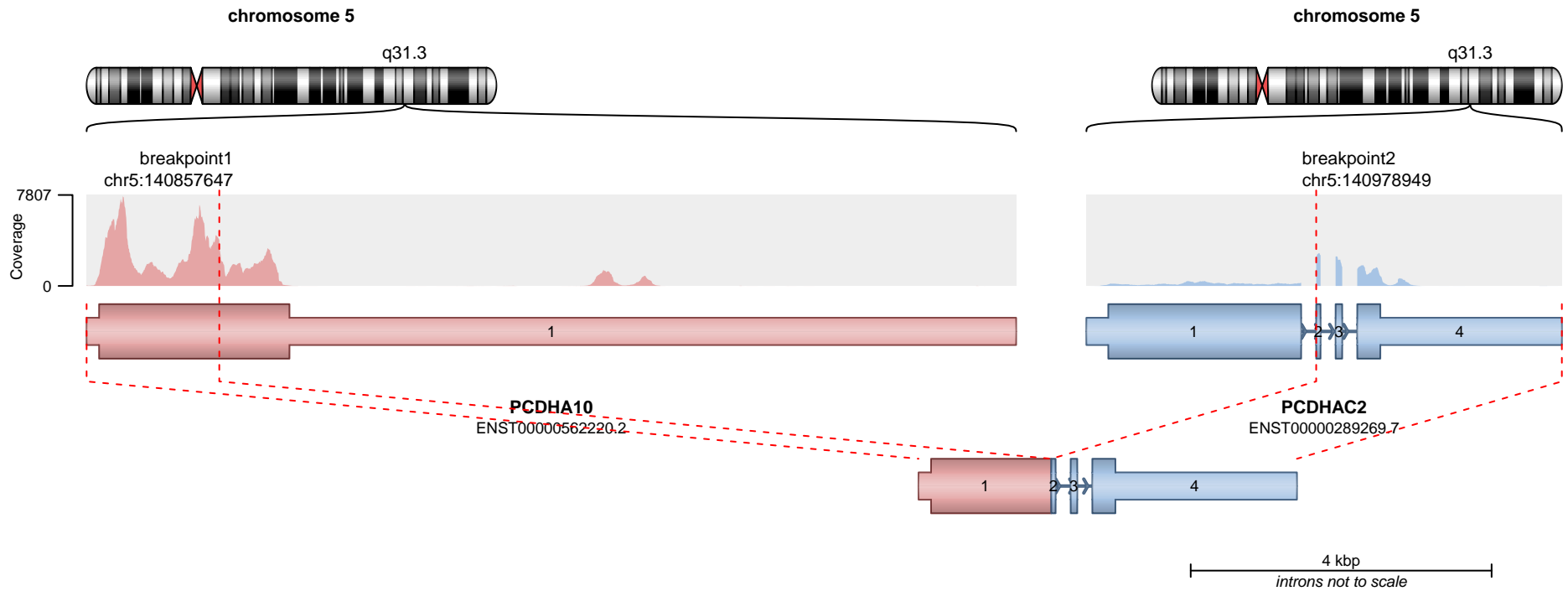
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



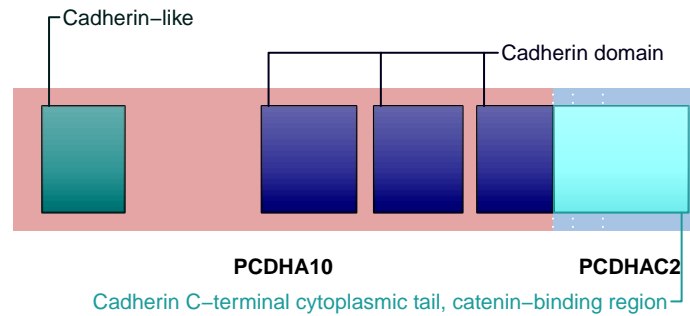
**SUPPORTING READ COUNT**

Split reads = 197  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



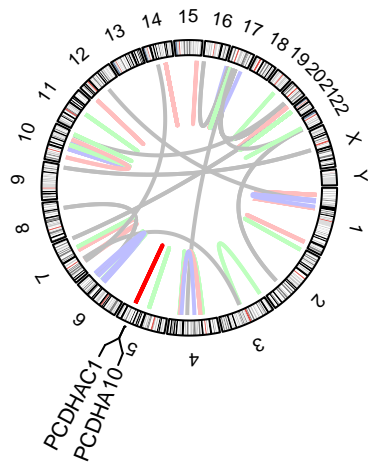
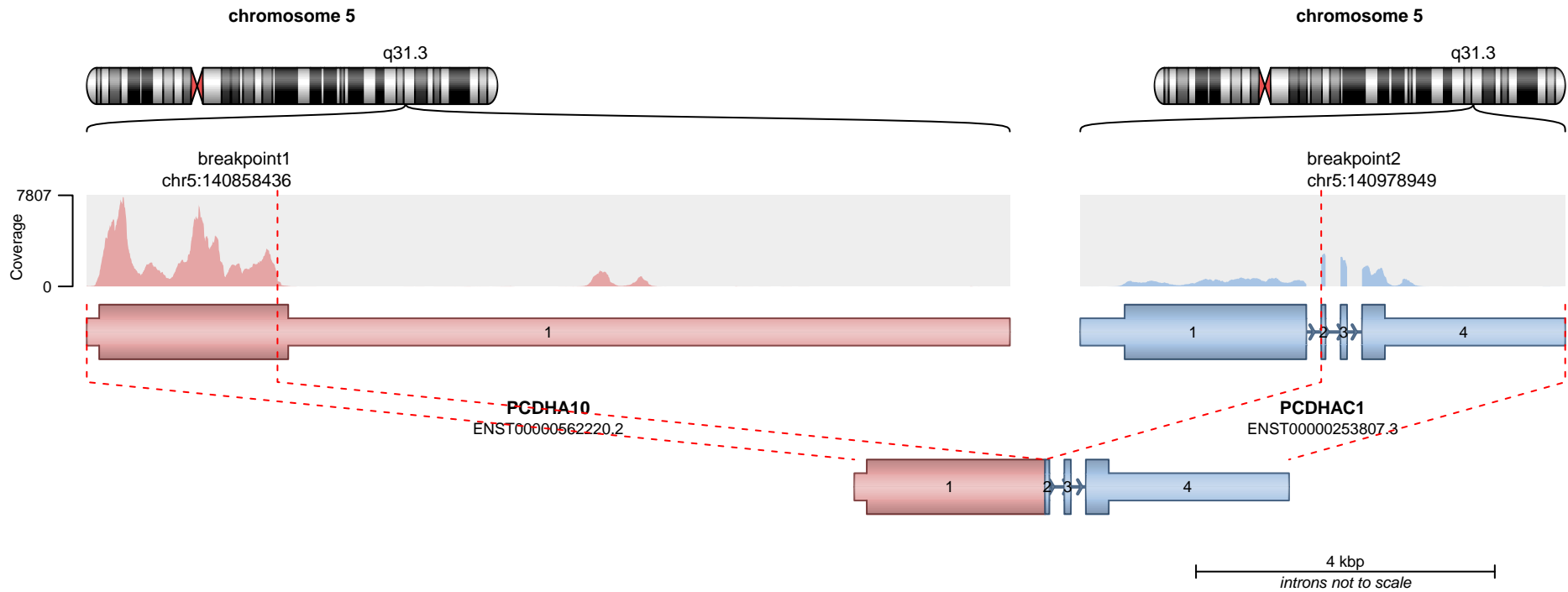
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



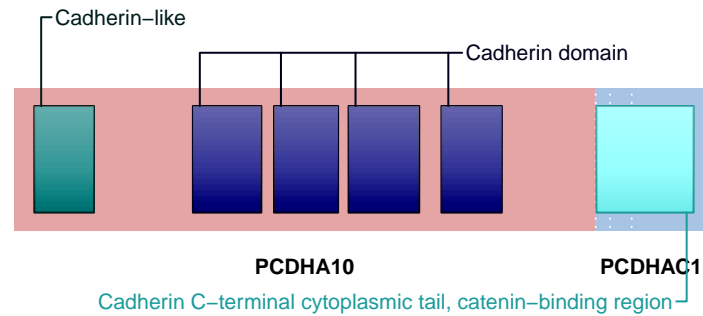
**SUPPORTING READ COUNT**

Split reads = 75  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



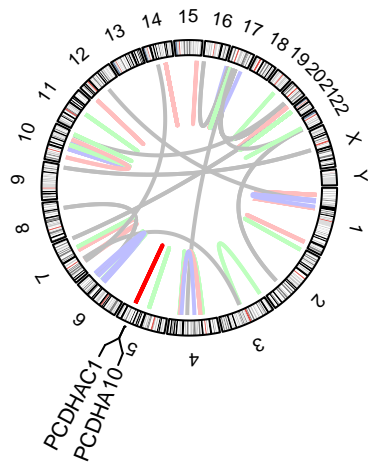
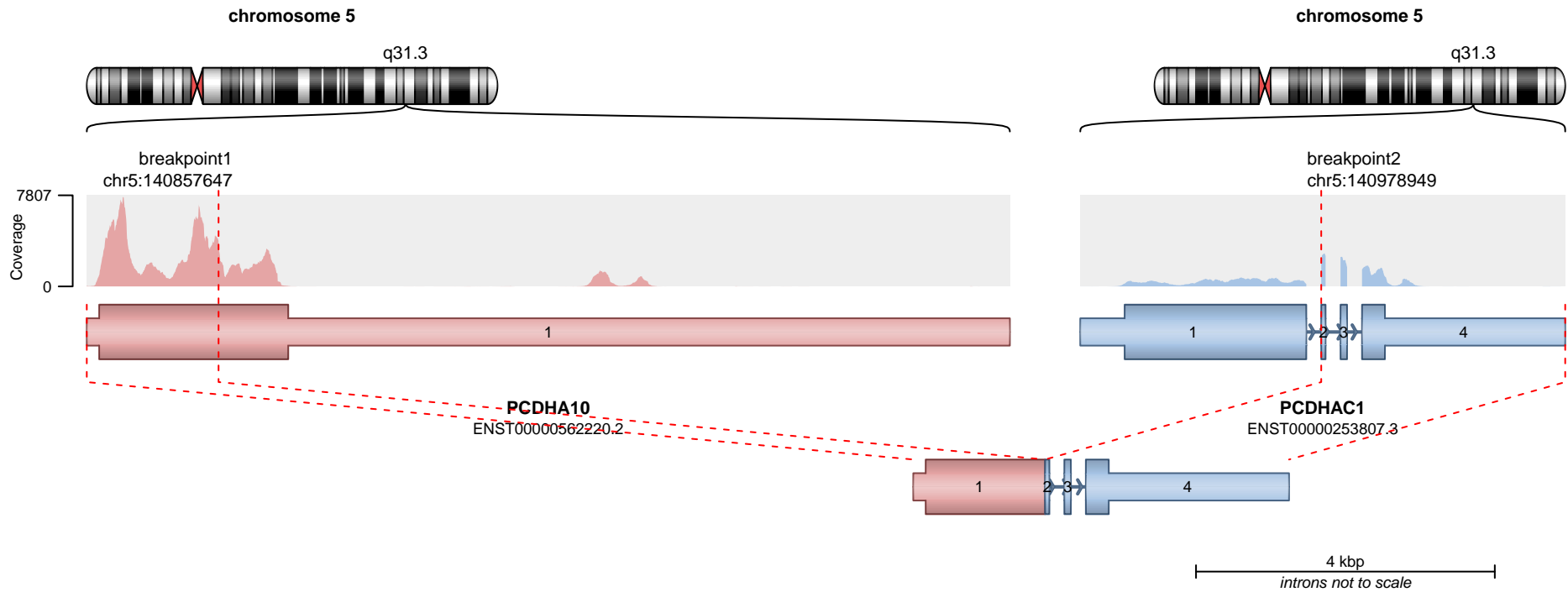
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



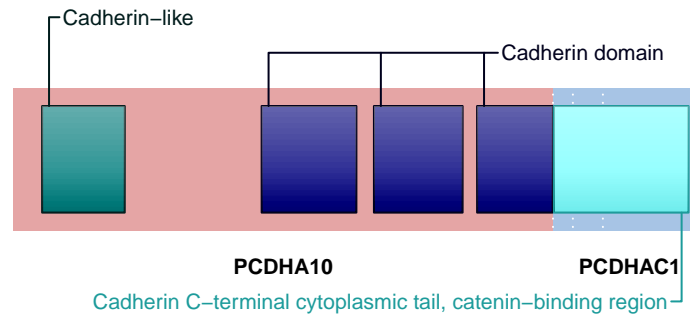
**SUPPORTING READ COUNT**

Split reads = 196  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



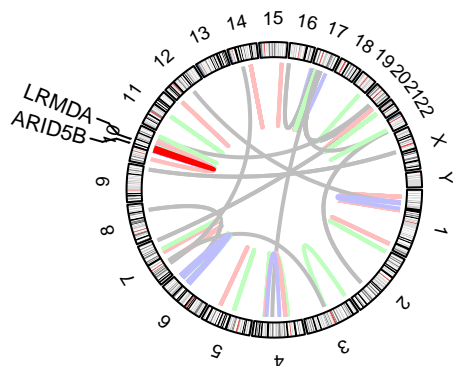
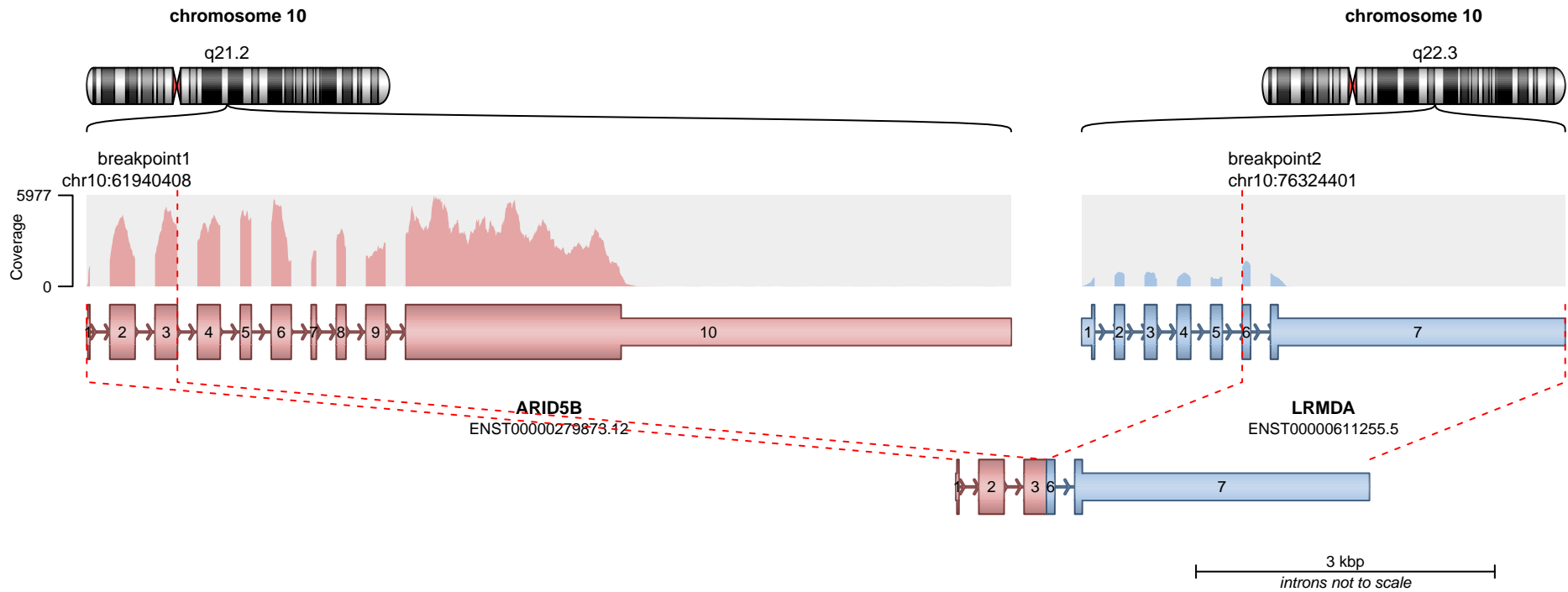
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 75  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

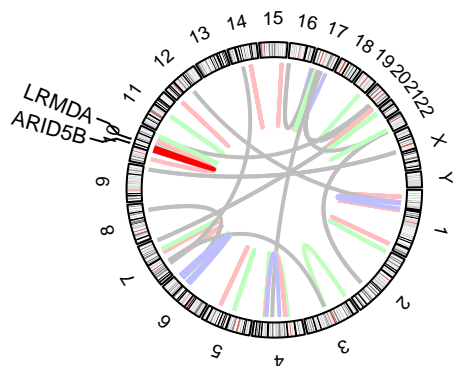
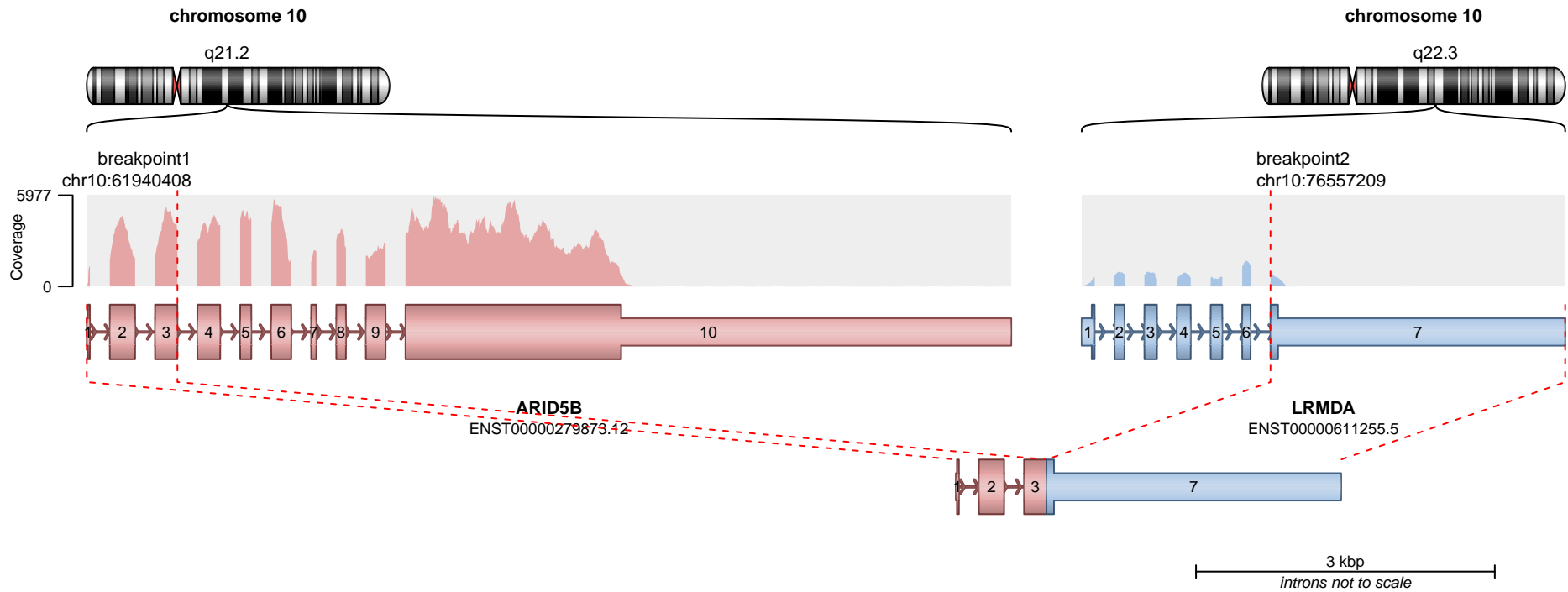


No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 188  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion

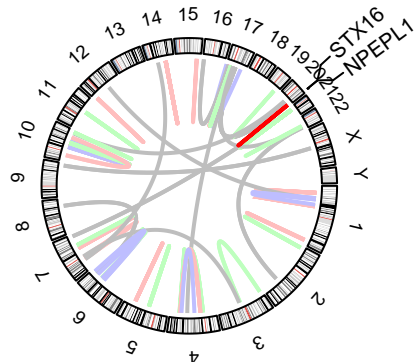
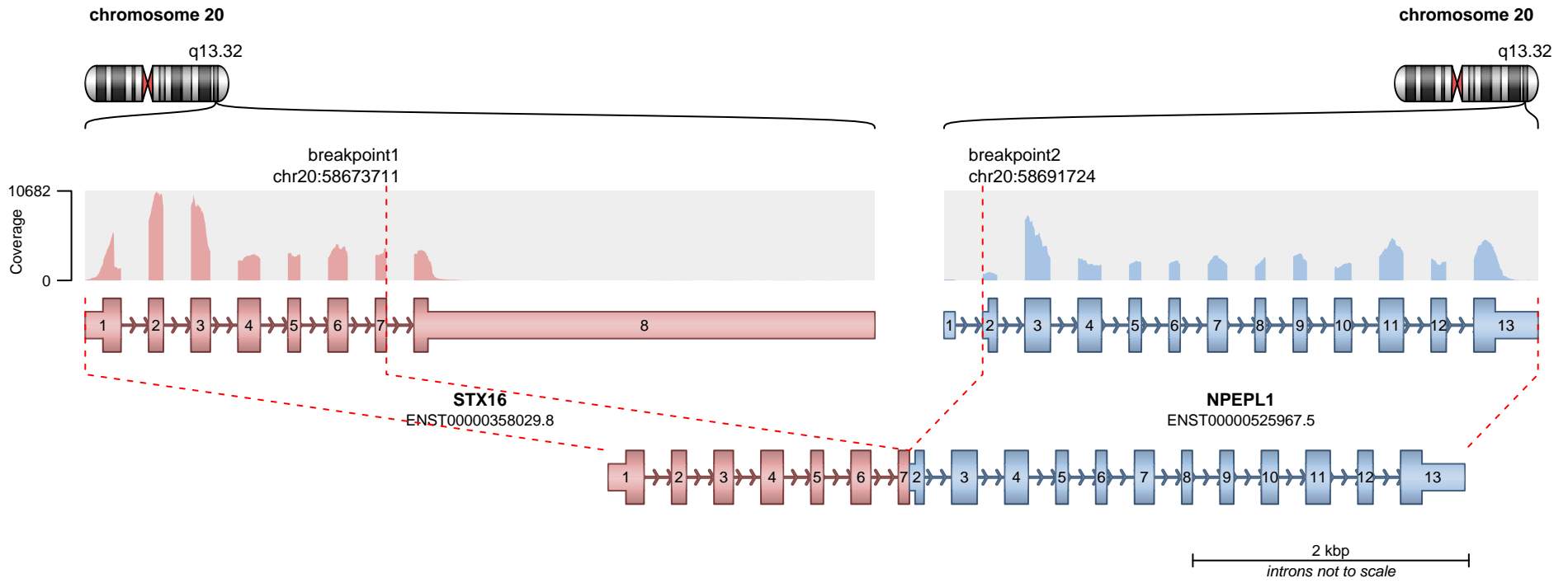


No protein domains retained in fusion.

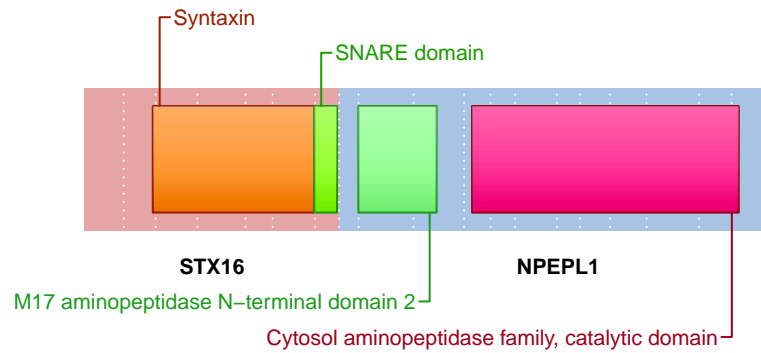
**SUPPORTING READ COUNT**

Split reads = 5  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



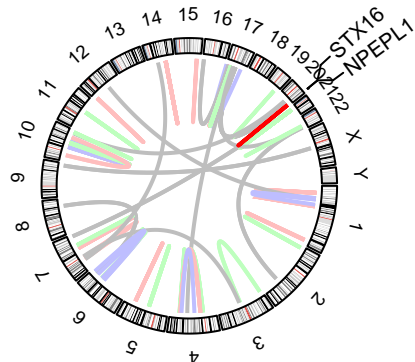
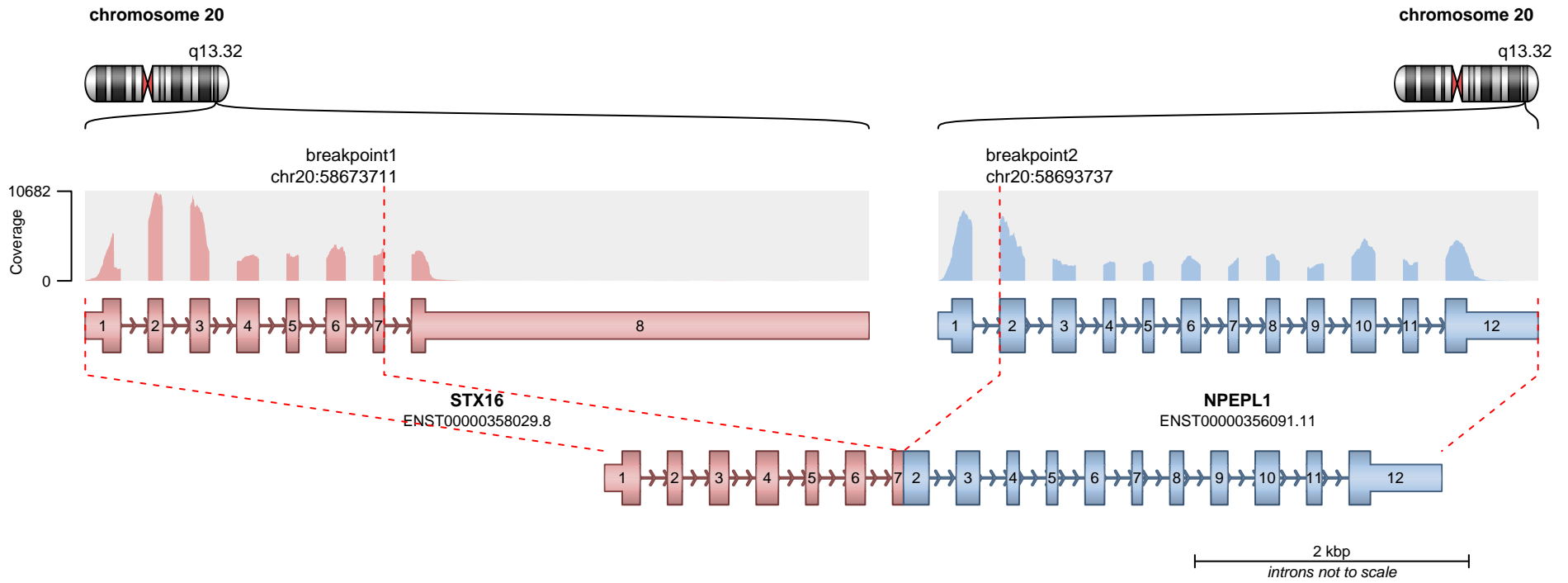
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



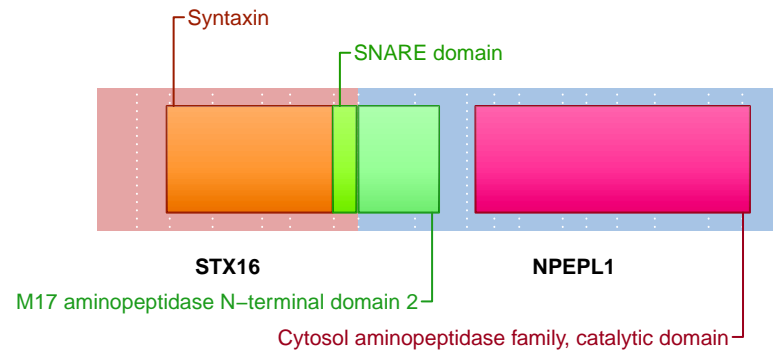
**SUPPORTING READ COUNT**

Split reads = 186  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



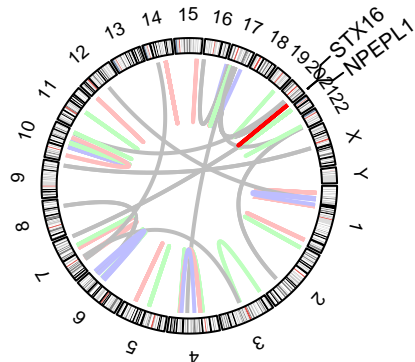
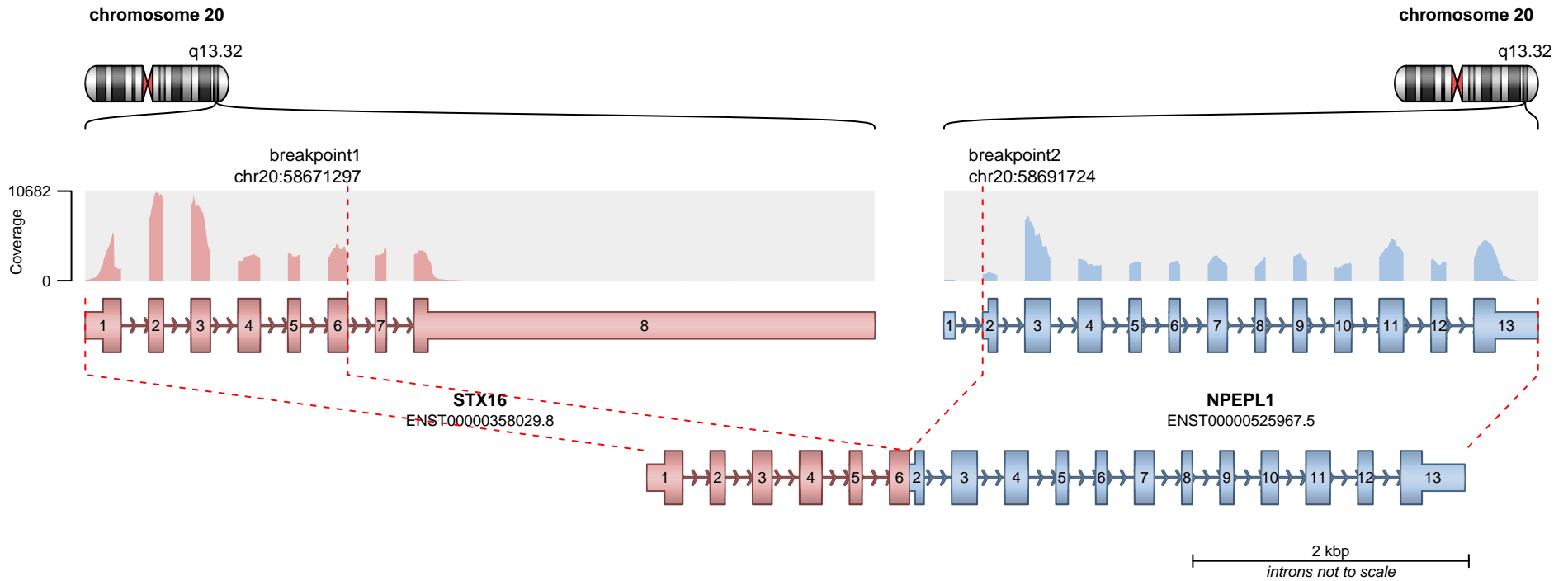
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



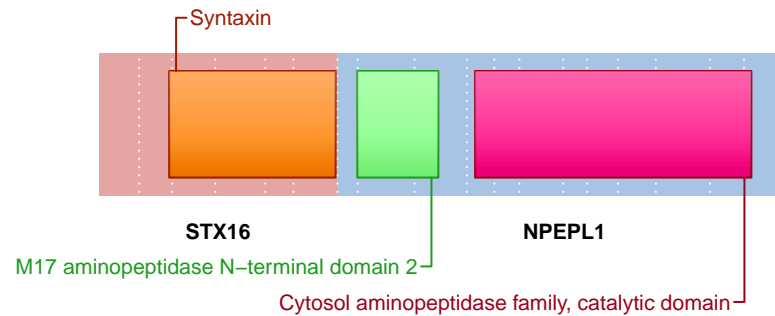
**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



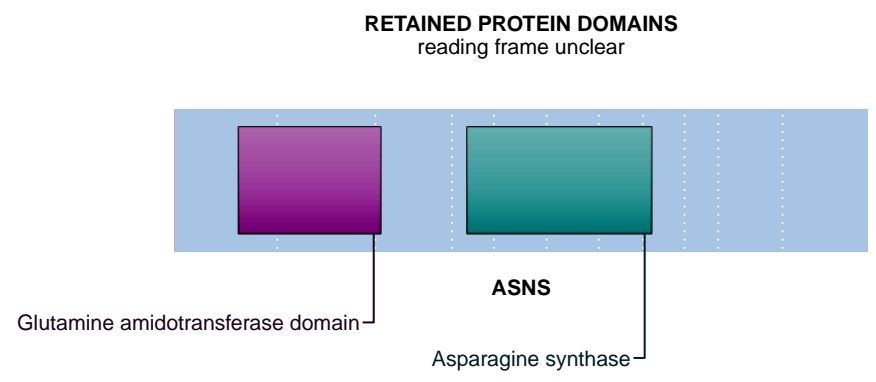
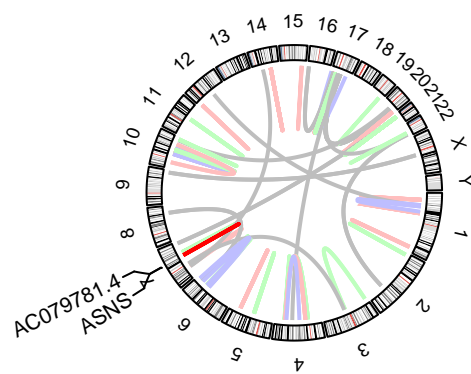
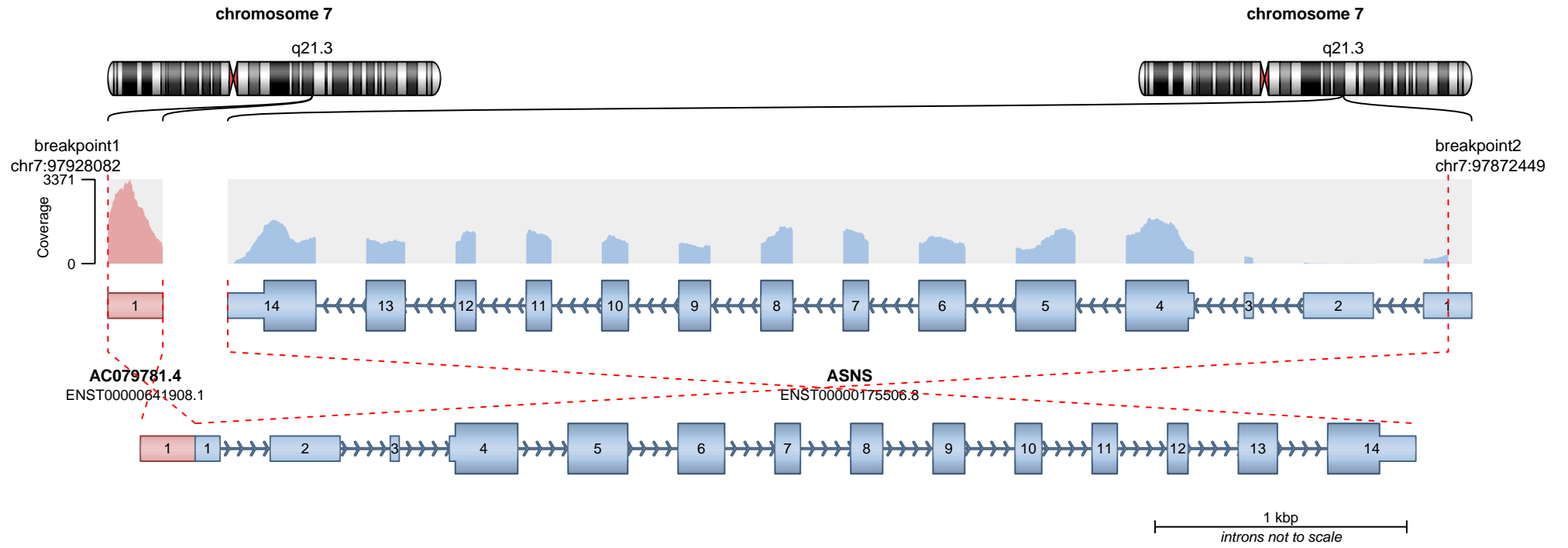
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0

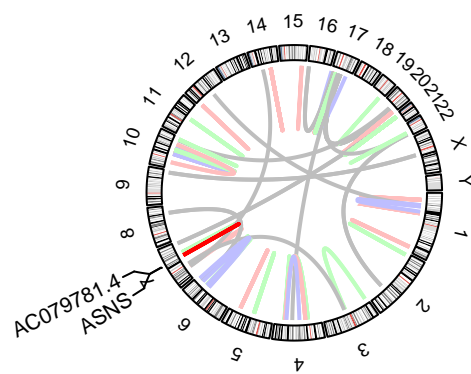
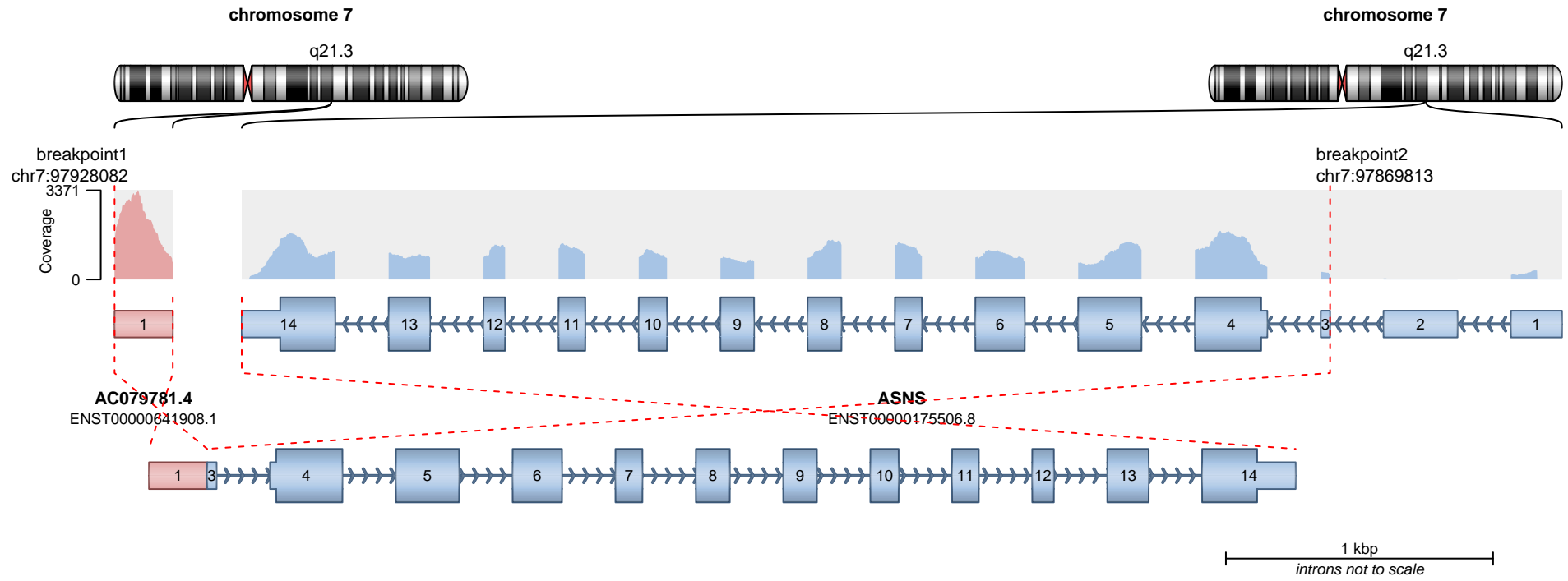
- translocation
- duplication
- deletion
- inversion



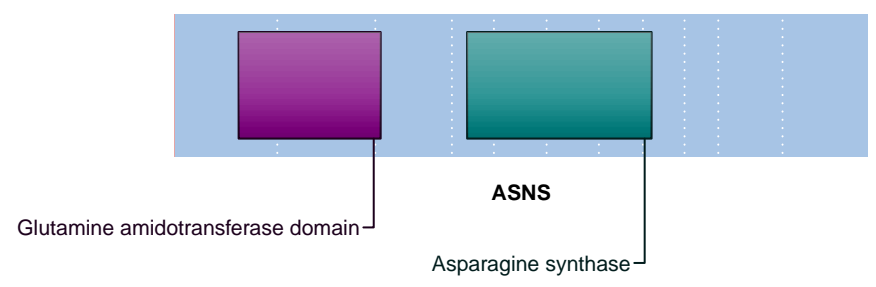
**SUPPORTING READ COUNT**

Split reads = 159  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



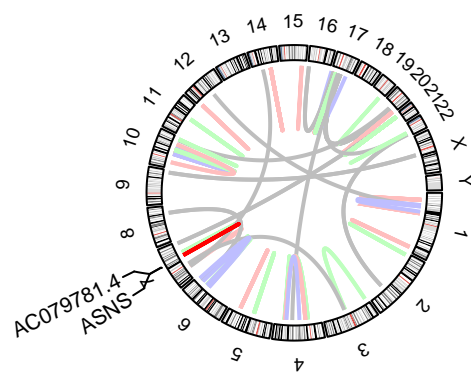
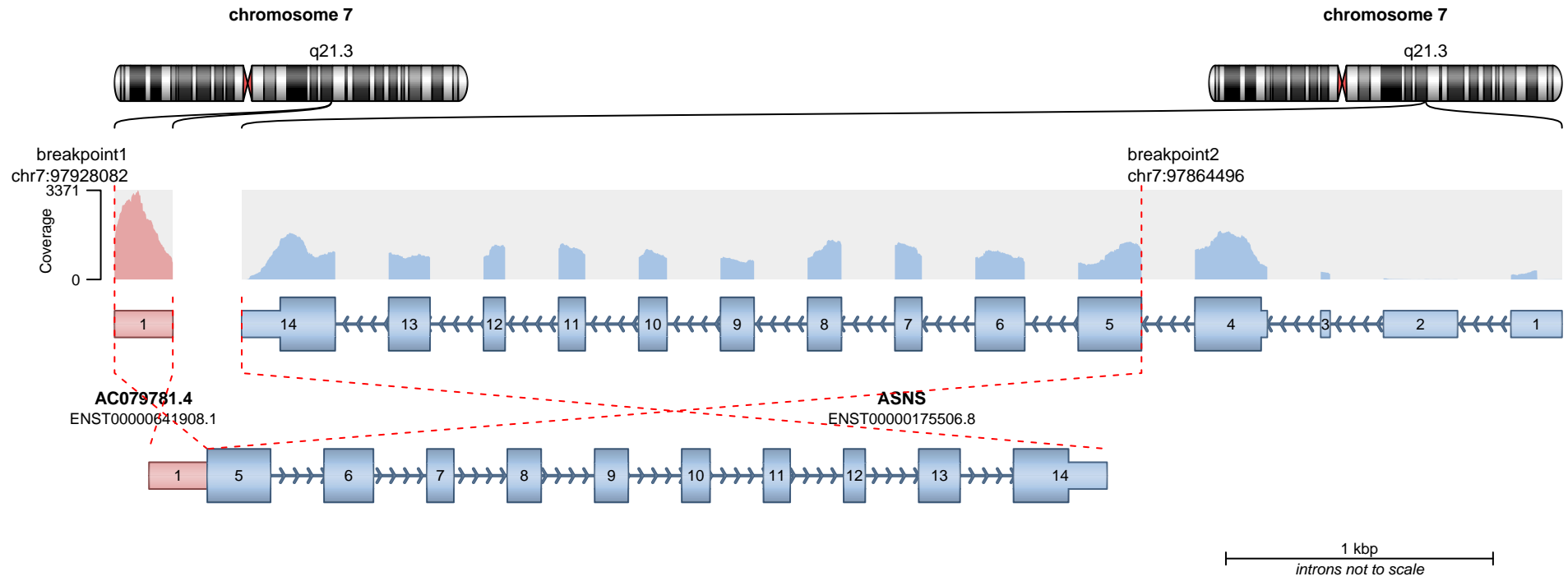
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



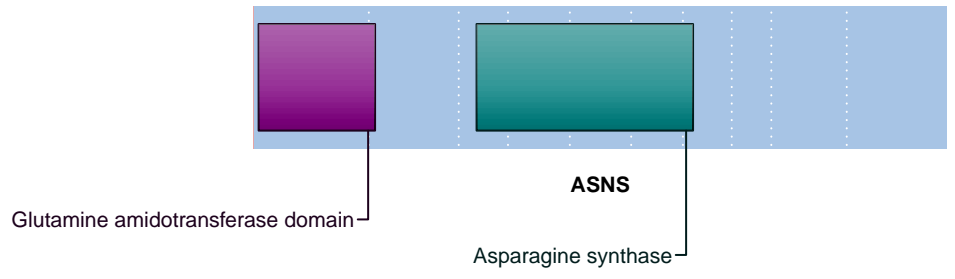
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



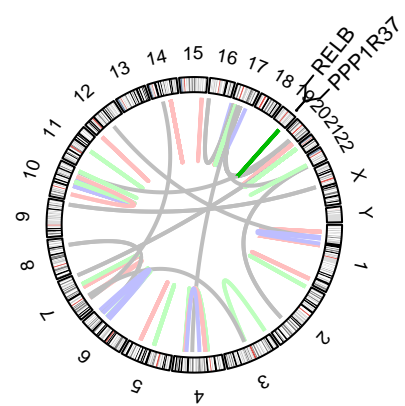
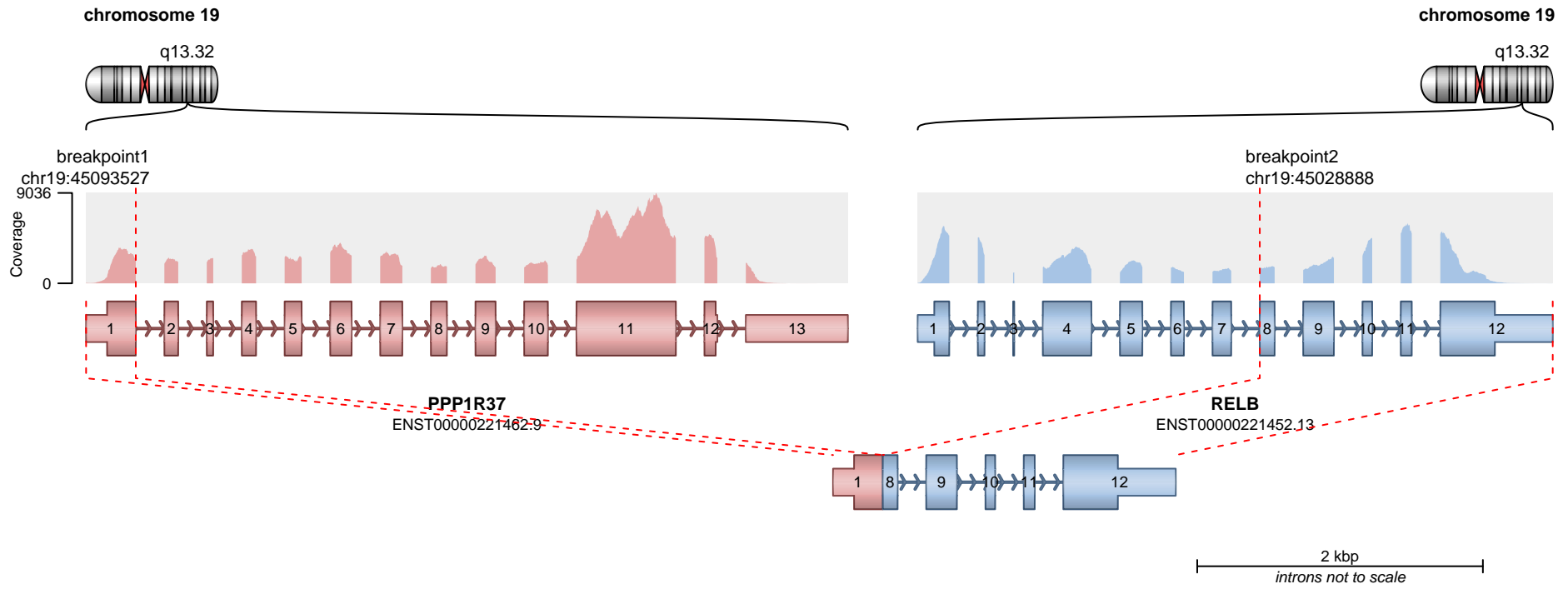
RETAINED PROTEIN DOMAINS  
reading frame unclear



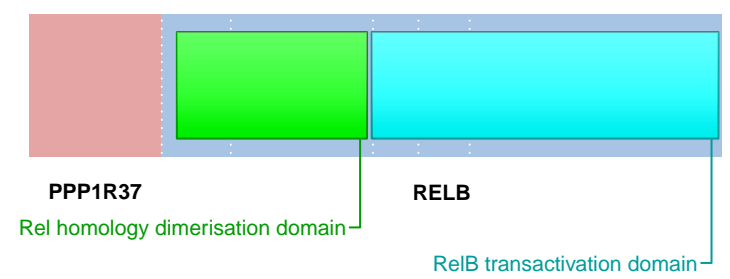
SUPPORTING READ COUNT

Split reads = 1  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



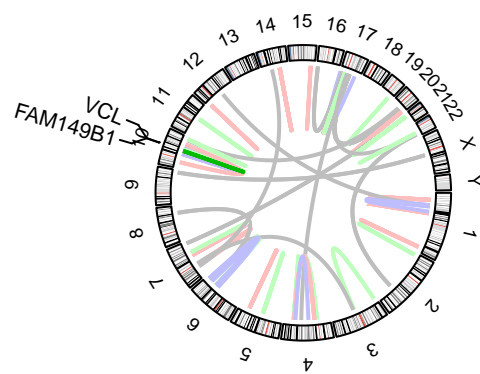
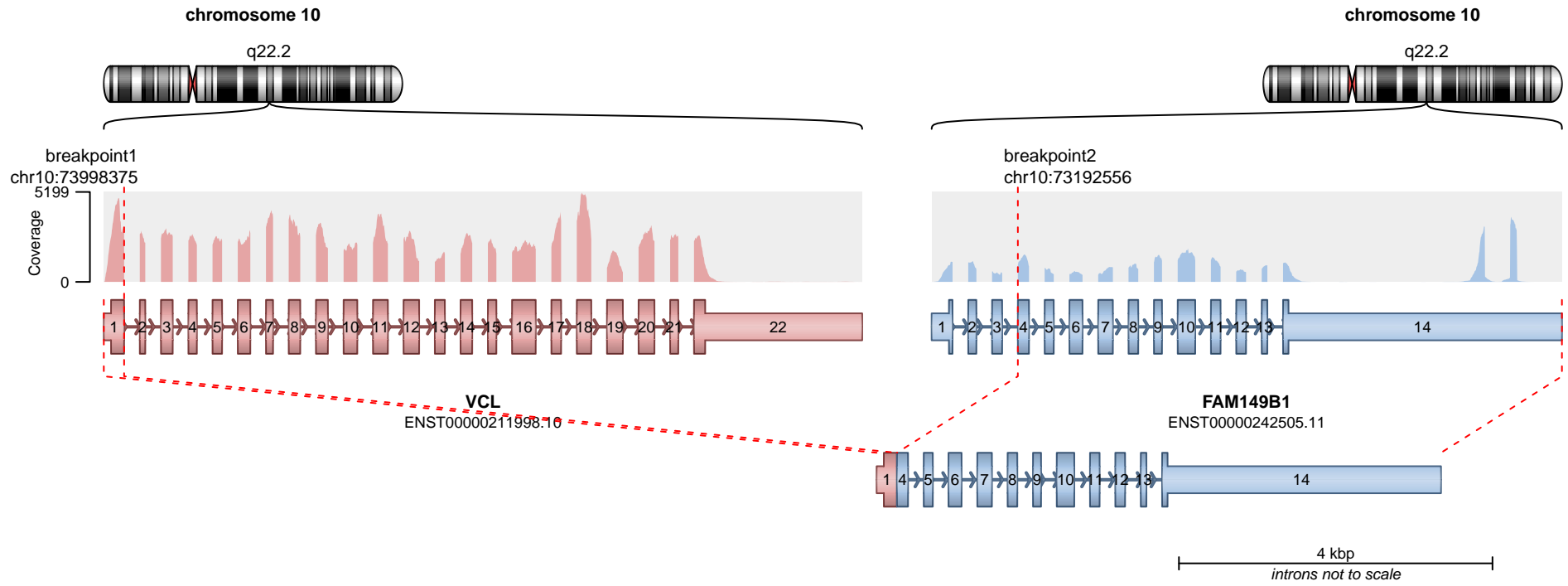
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



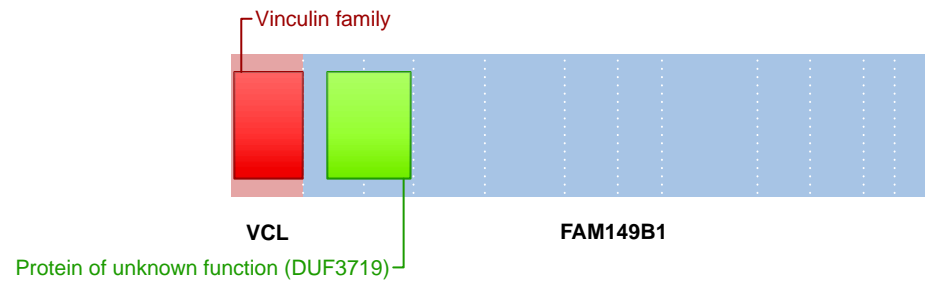
**SUPPORTING READ COUNT**

Split reads = 156  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



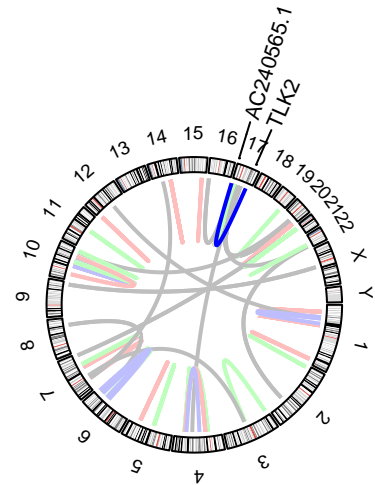
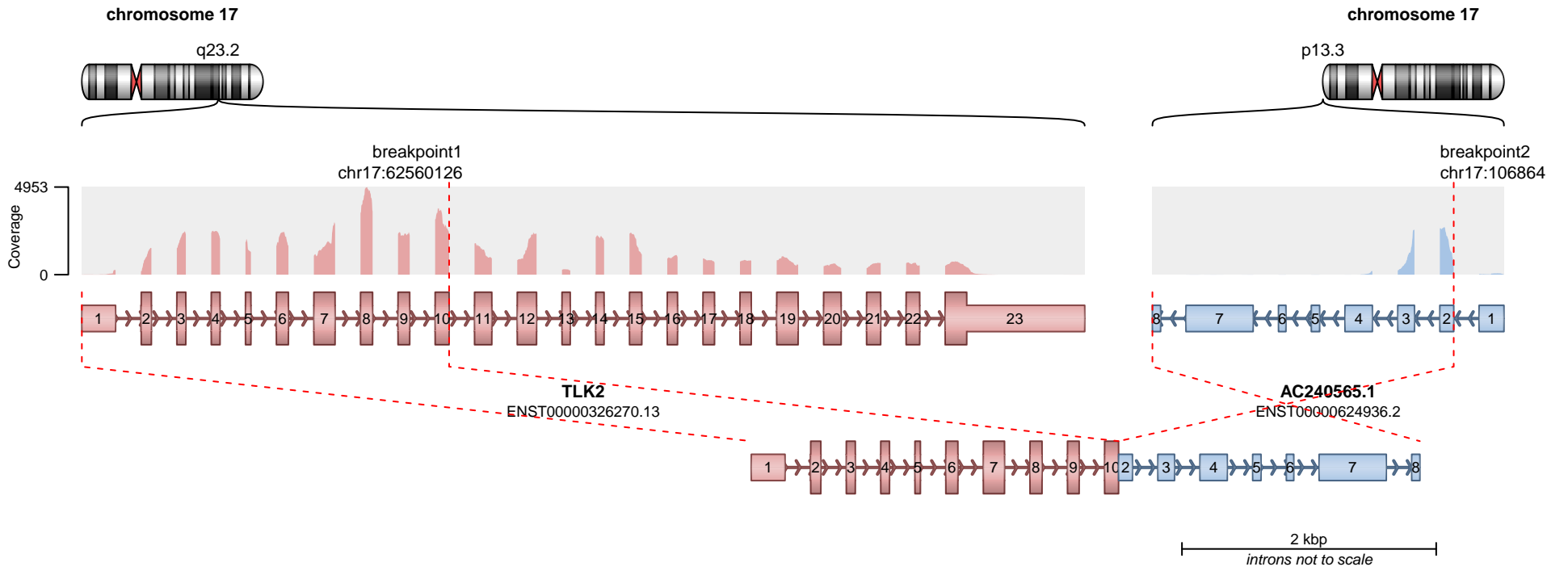
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 130  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion

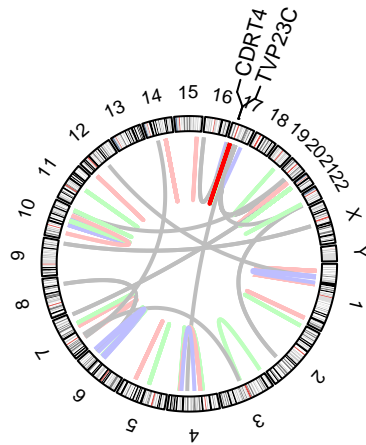
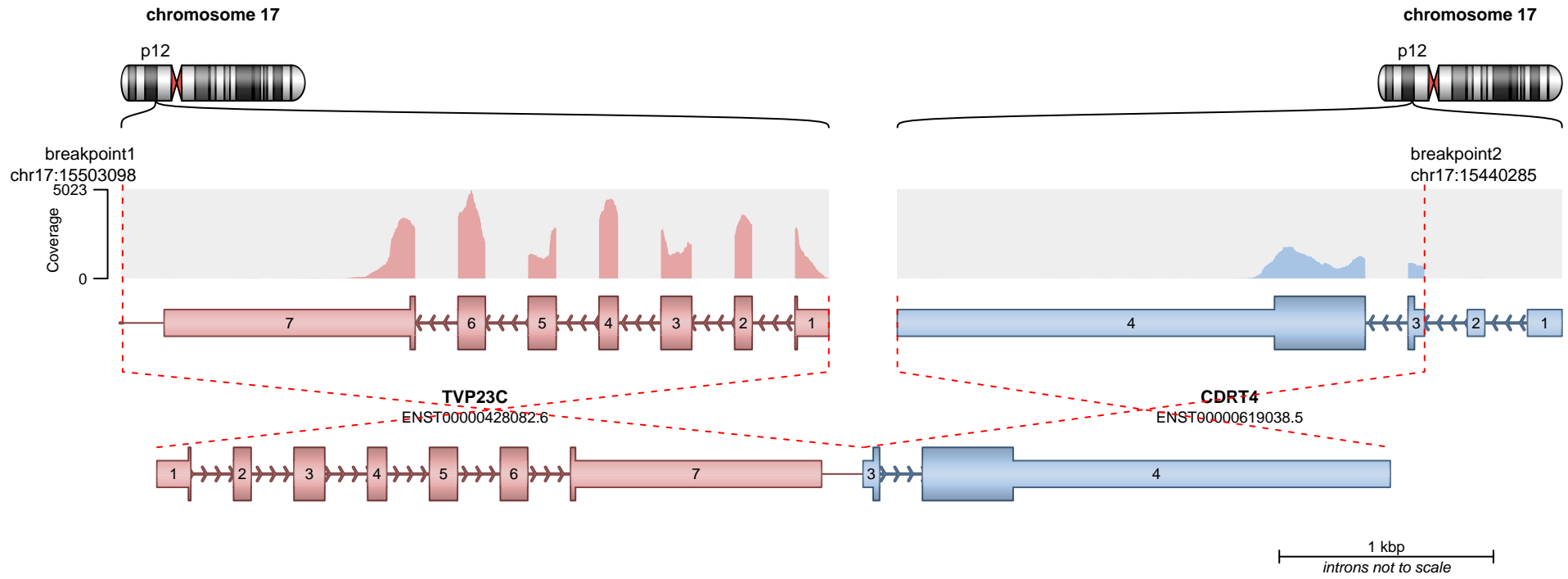


No protein domains retained in fusion.

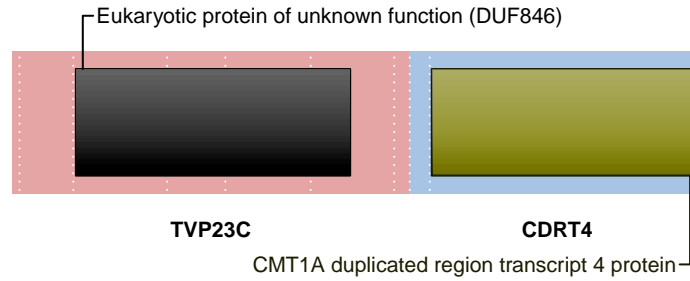
**SUPPORTING READ COUNT**

Split reads = 120  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



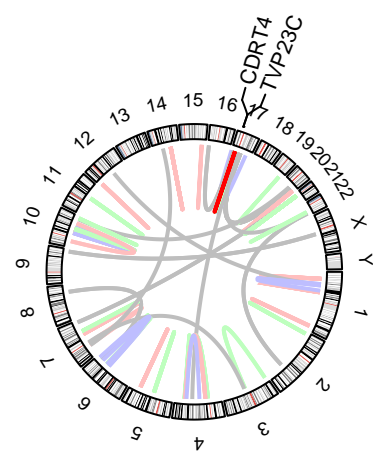
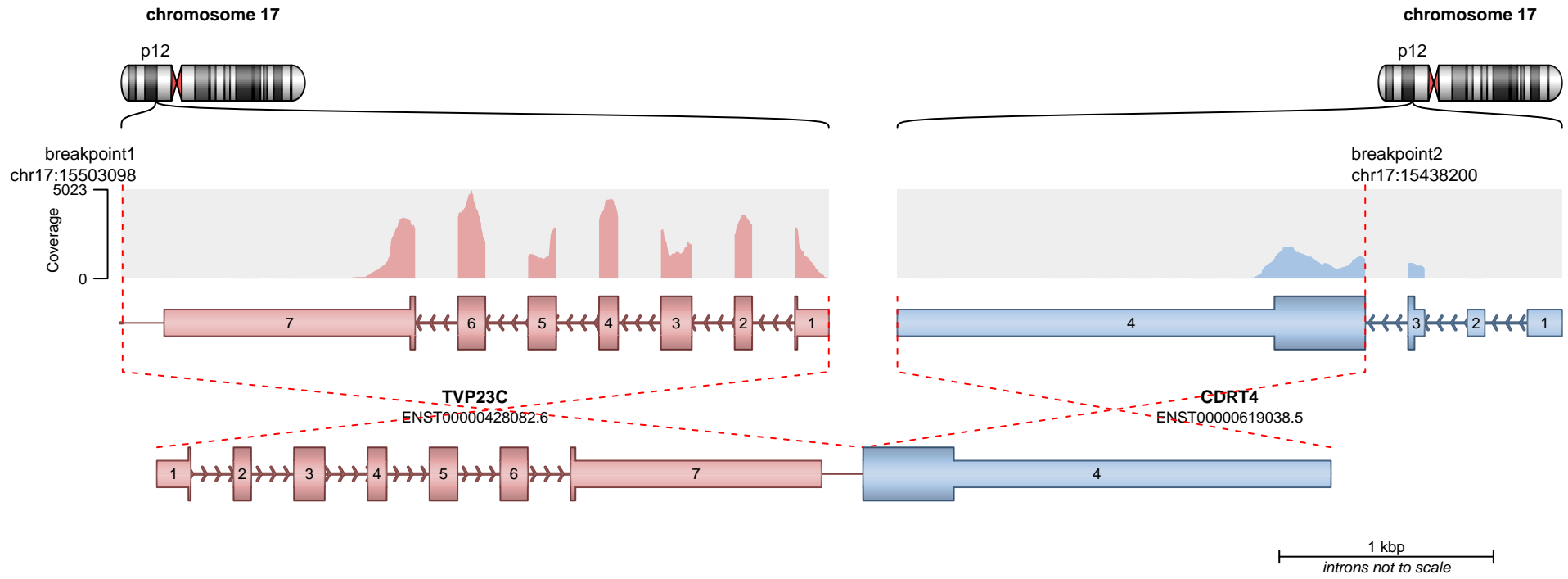
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



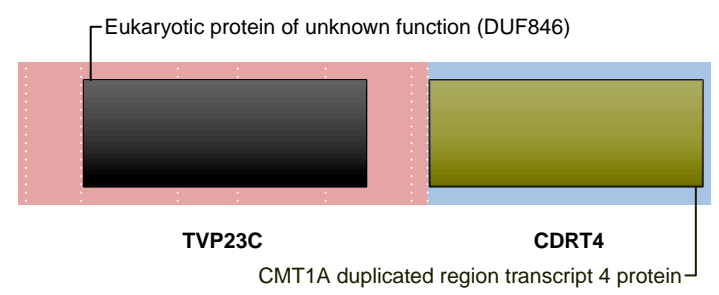
**SUPPORTING READ COUNT**

Split reads = 118  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



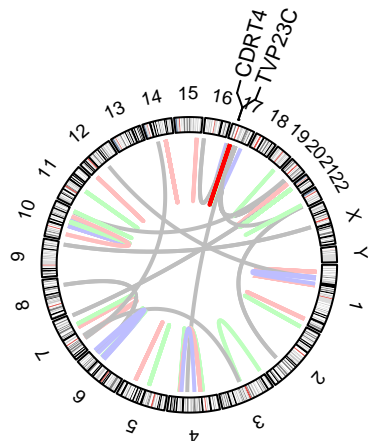
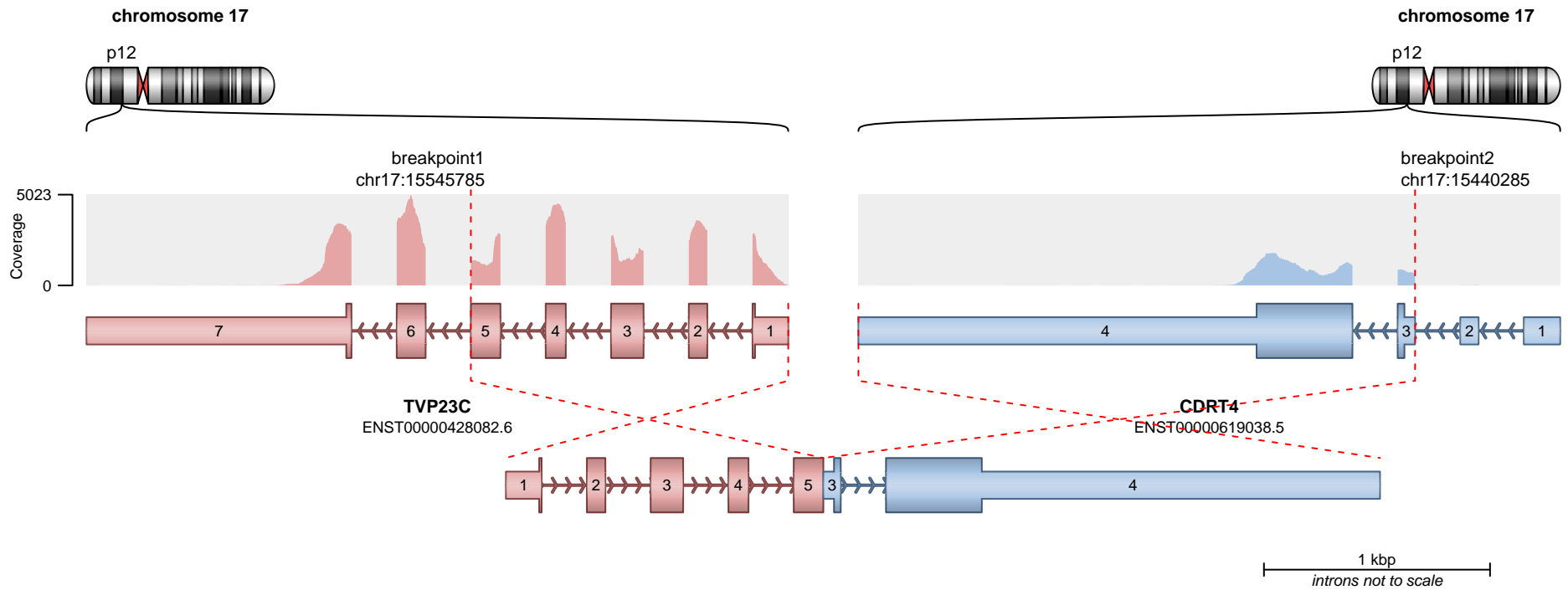
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



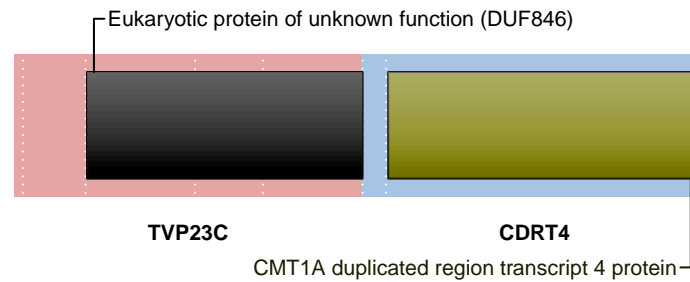
**SUPPORTING READ COUNT**

Split reads = 36  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



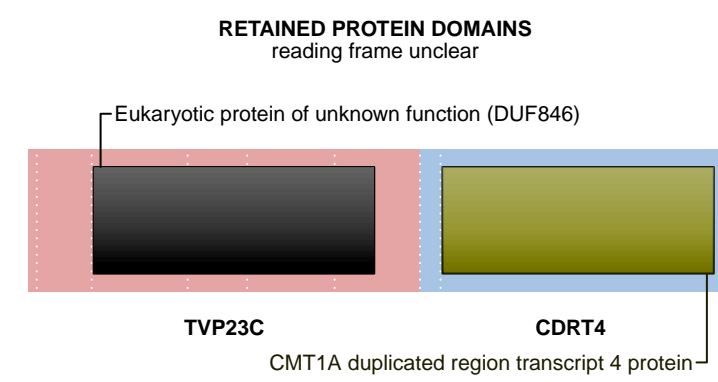
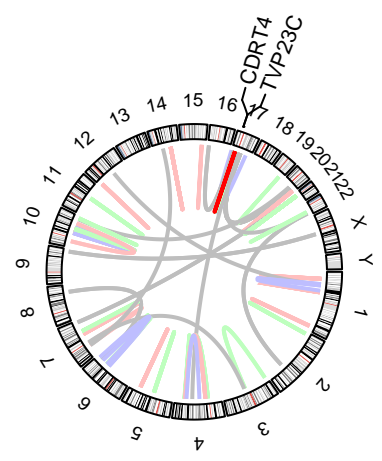
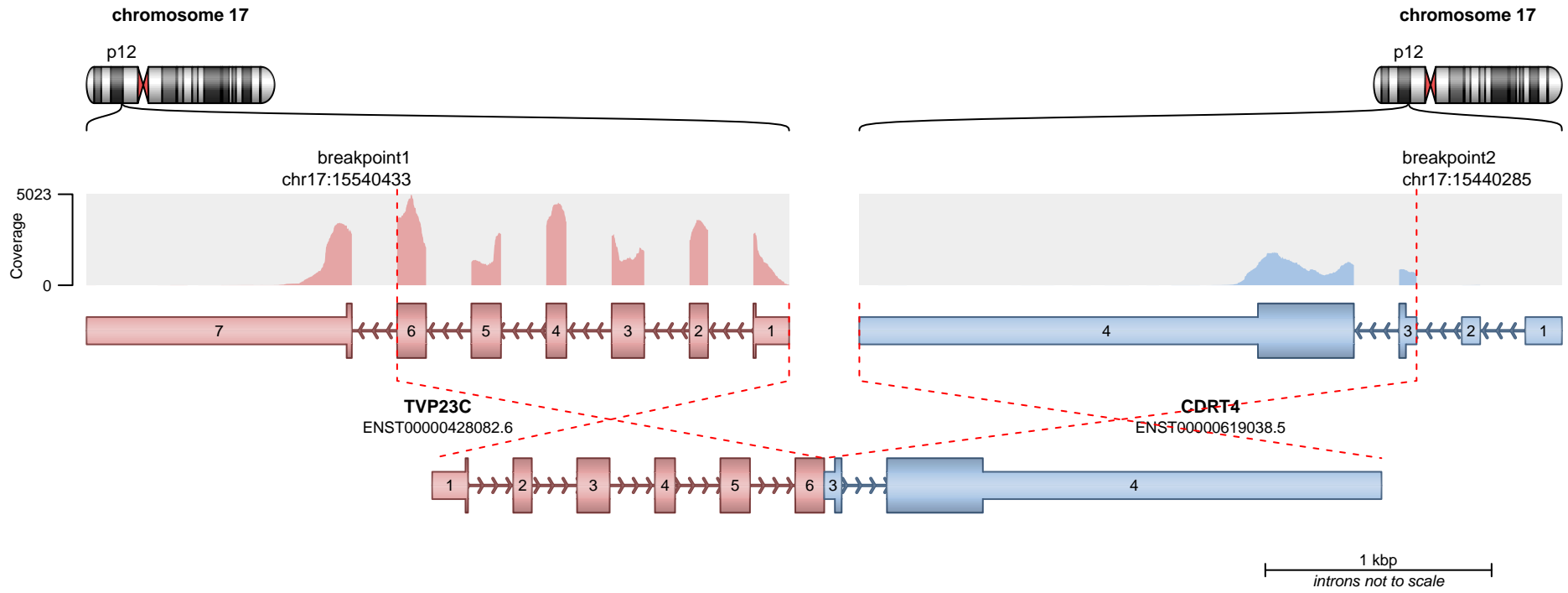
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 25  
Discordant mates = 0

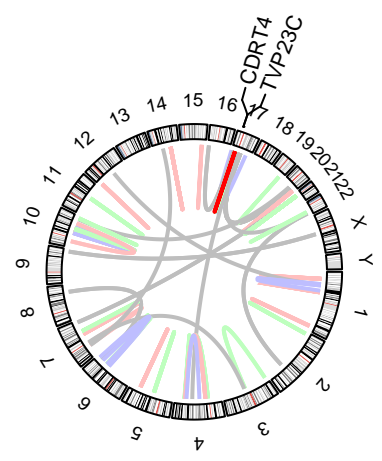
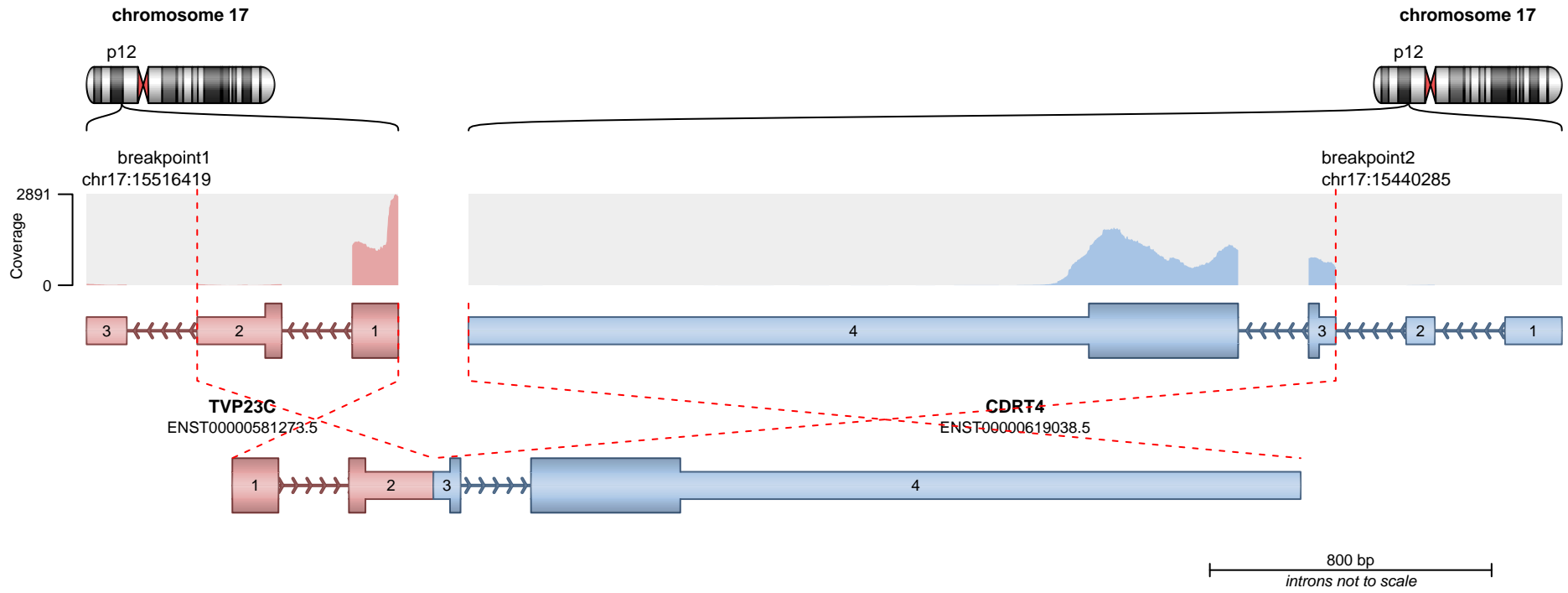
- translocation
- duplication
- deletion
- inversion



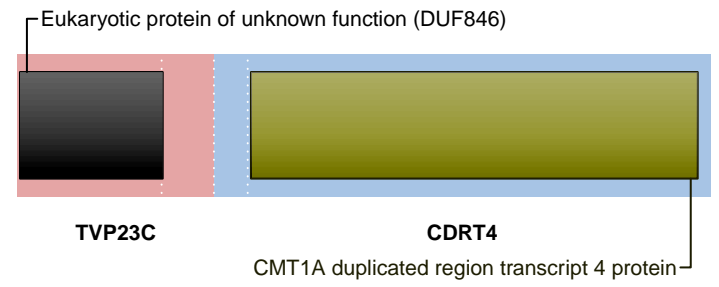
**SUPPORTING READ COUNT**

Split reads = 11  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



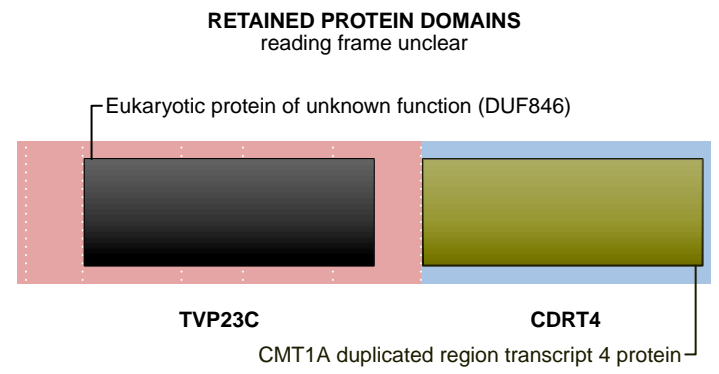
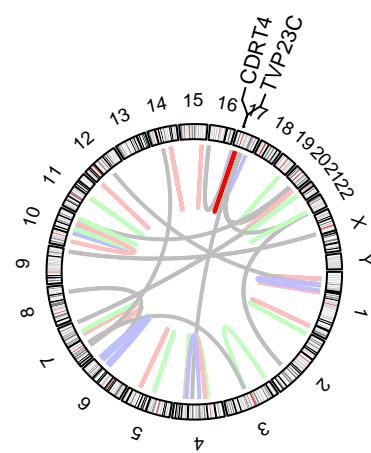
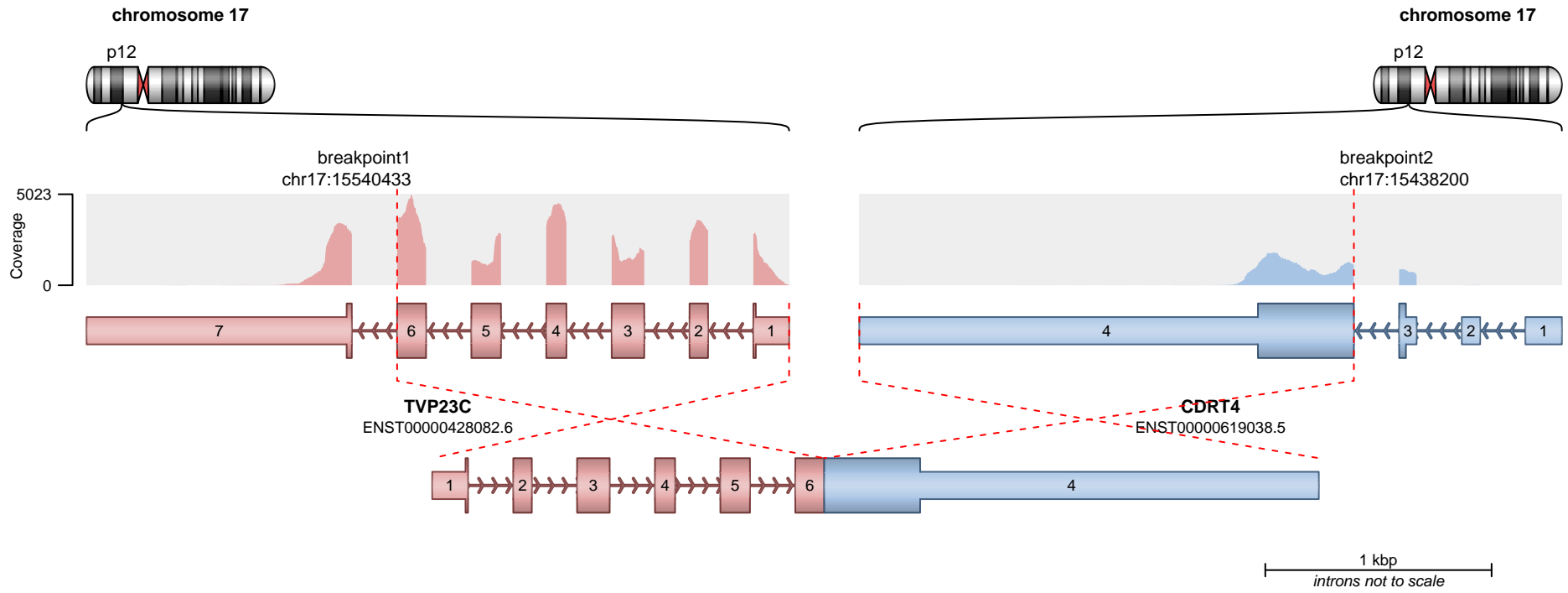
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 9  
Discordant mates = 0

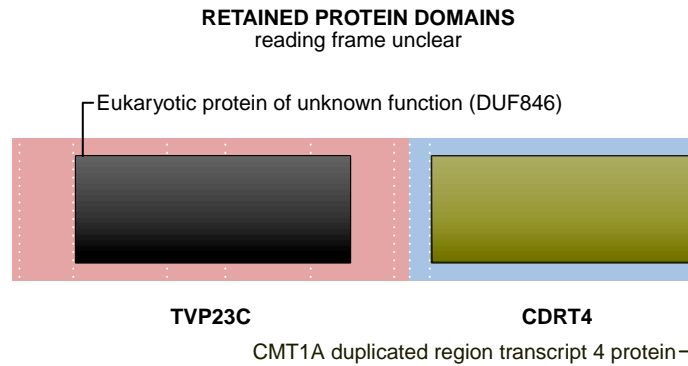
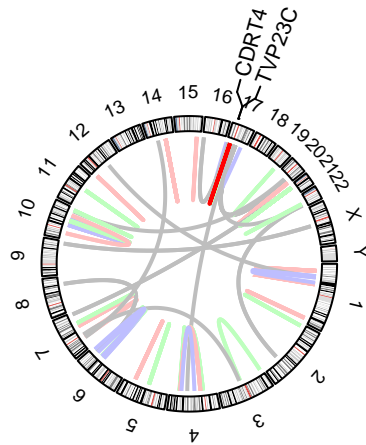
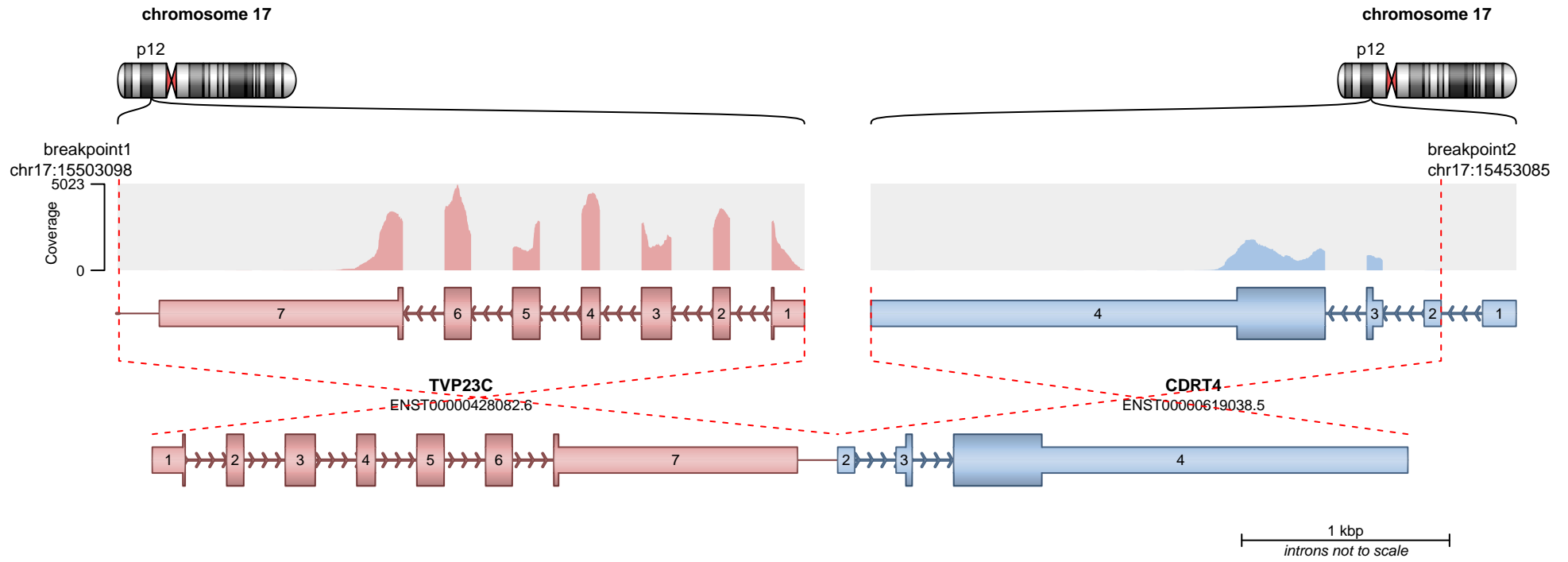
- translocation
- duplication
- deletion
- inversion



**SUPPORTING READ COUNT**

Split reads = 5  
Discordant mates = 0

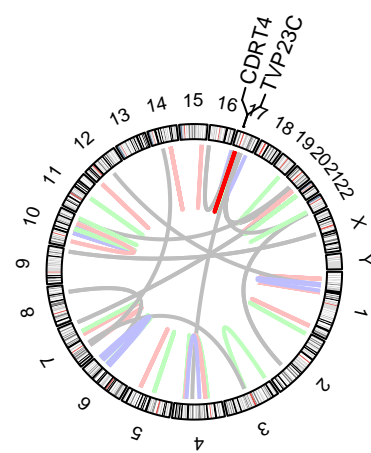
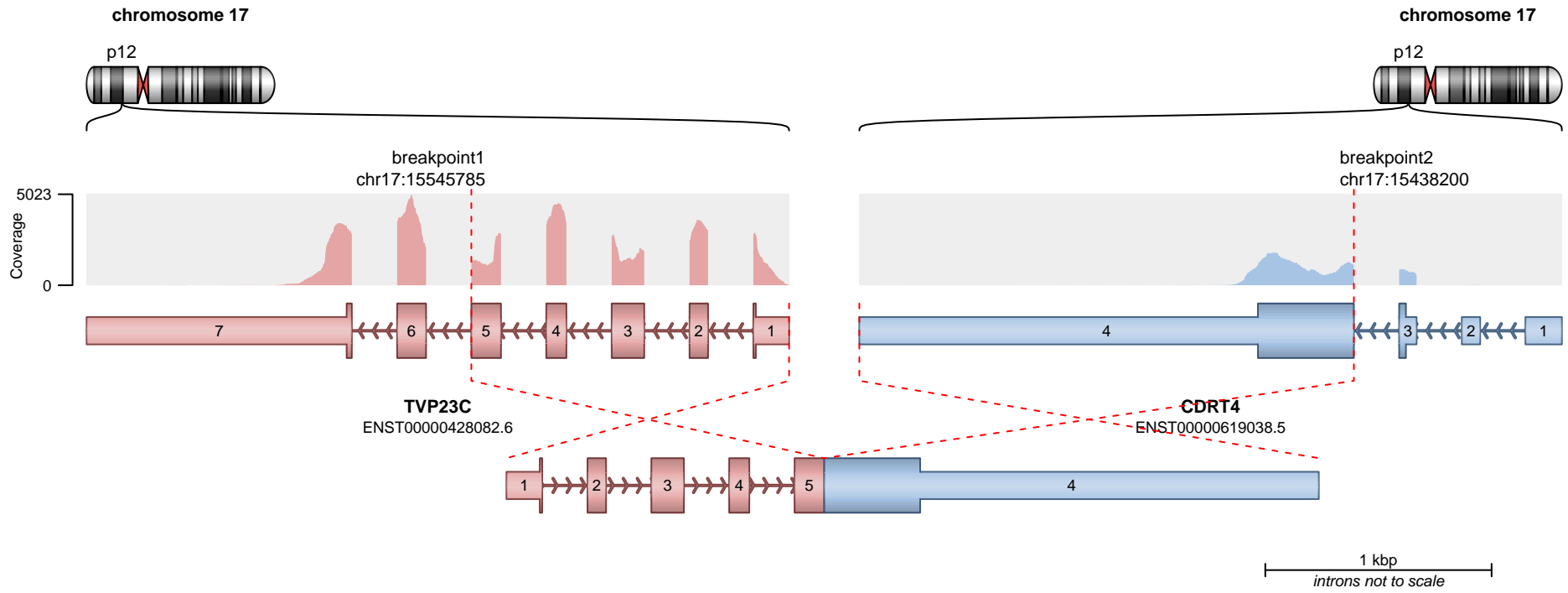
— translocation — deletion  
— duplication — inversion



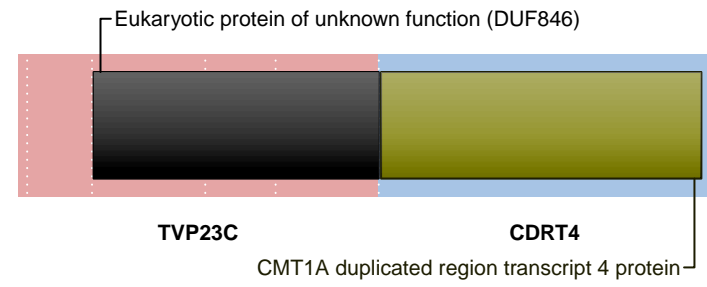
**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



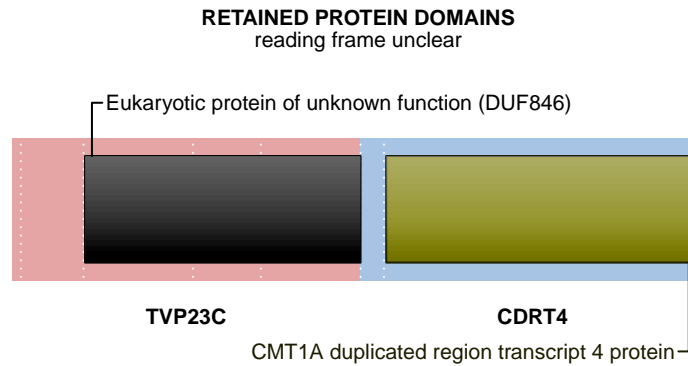
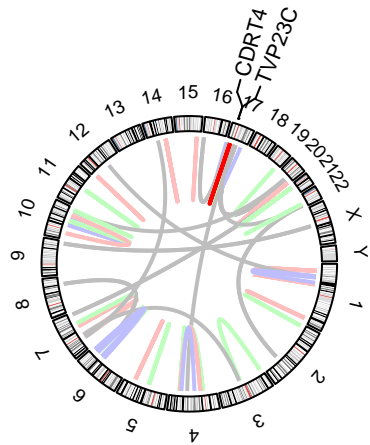
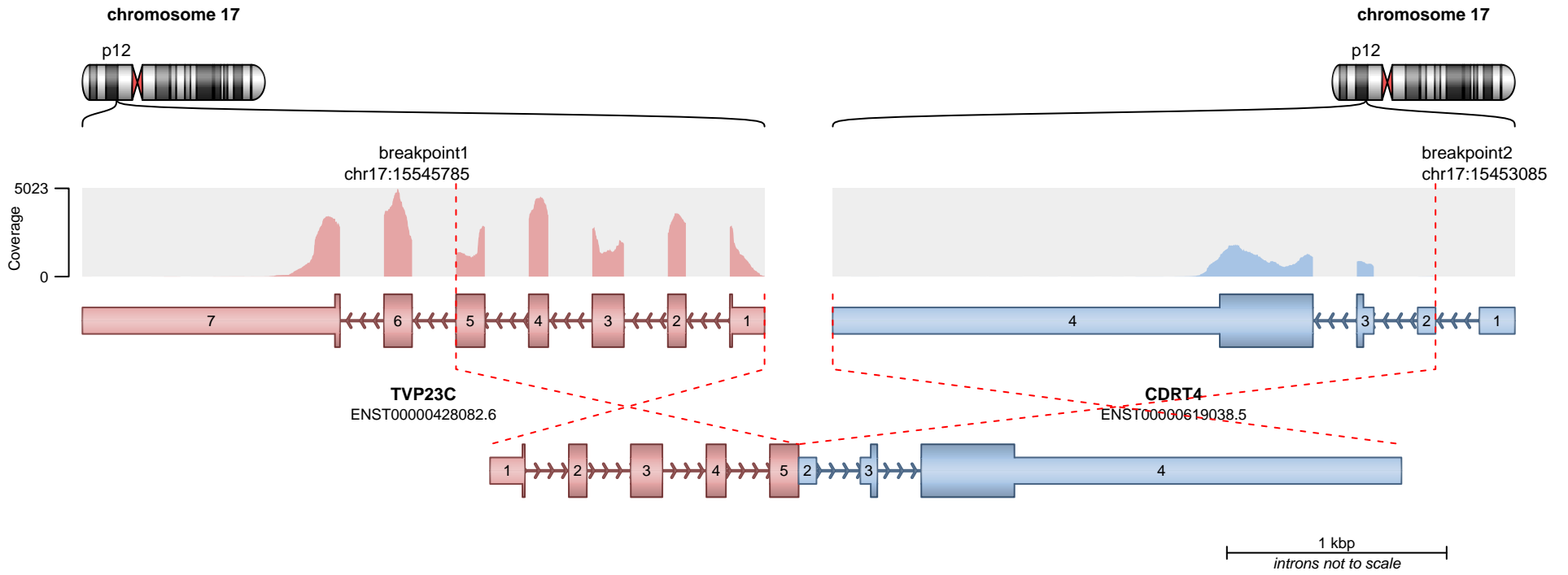
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0

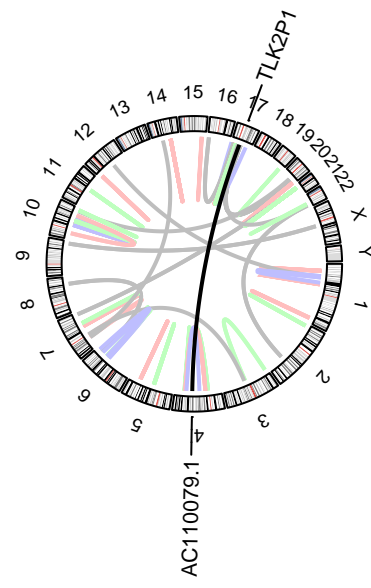
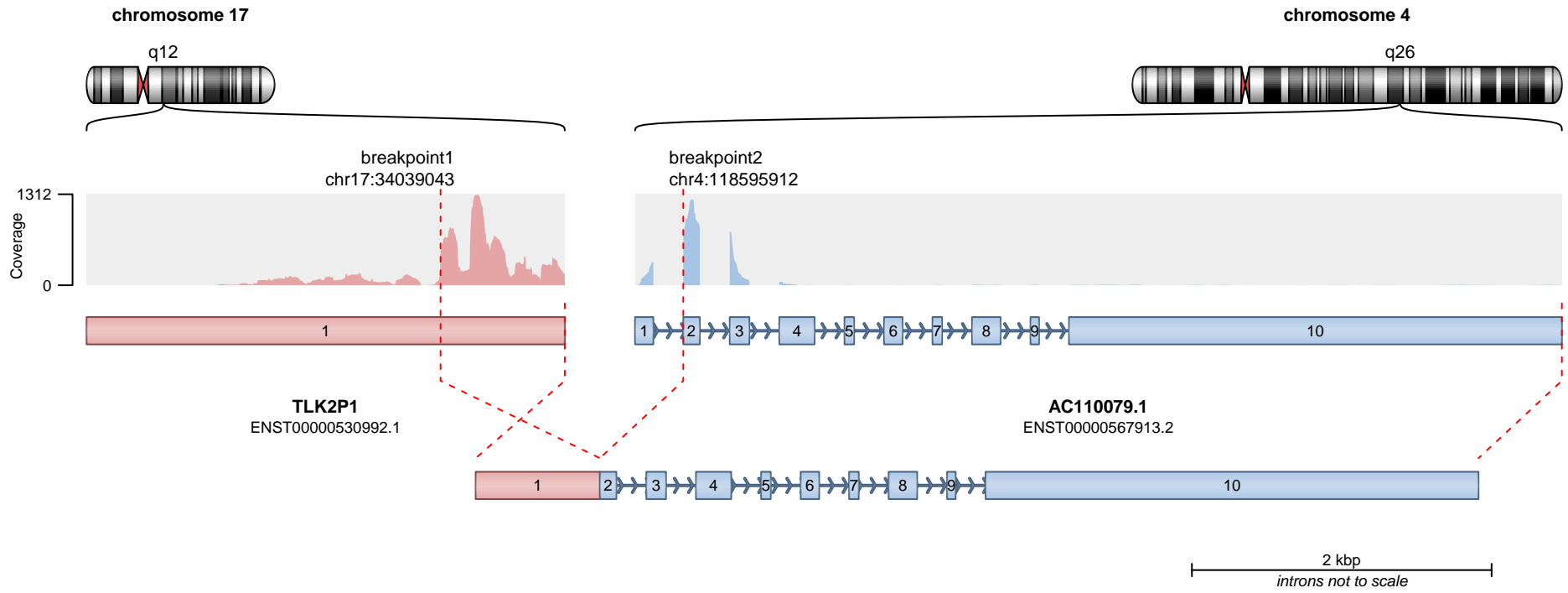
- translocation
- duplication
- deletion
- inversion



**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion

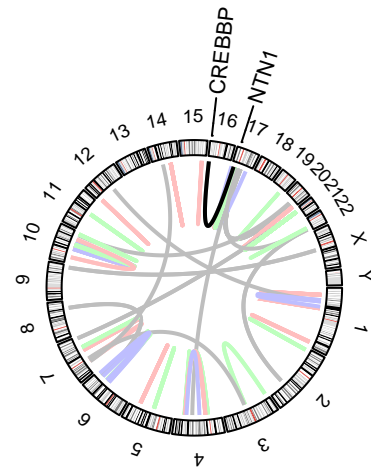
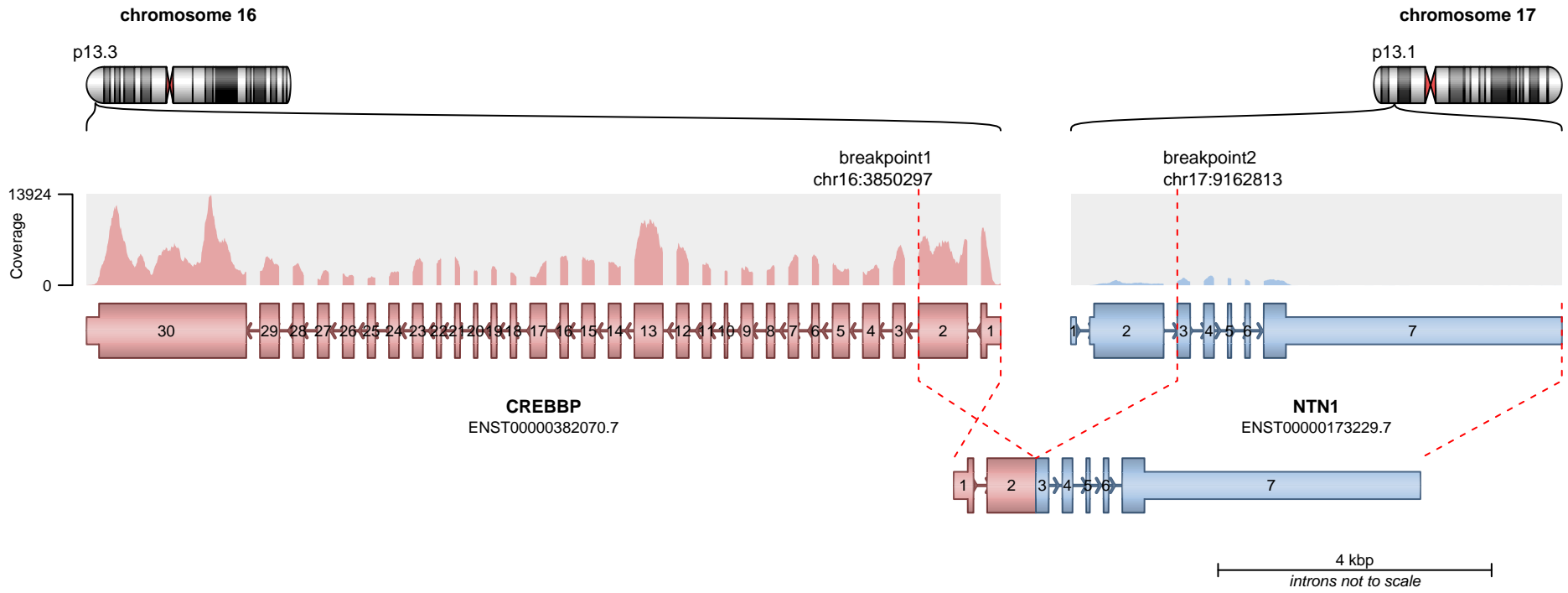


— translocation    — deletion  
 — duplication    — inversion

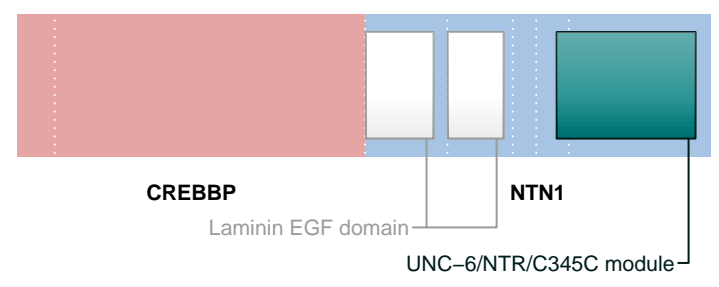
Genes are not protein-coding.

**SUPPORTING READ COUNT**

Split reads = 110  
 Discordant mates = 0



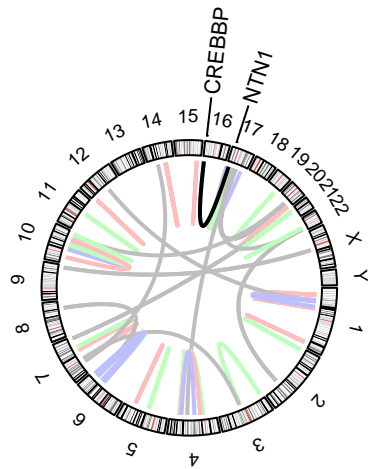
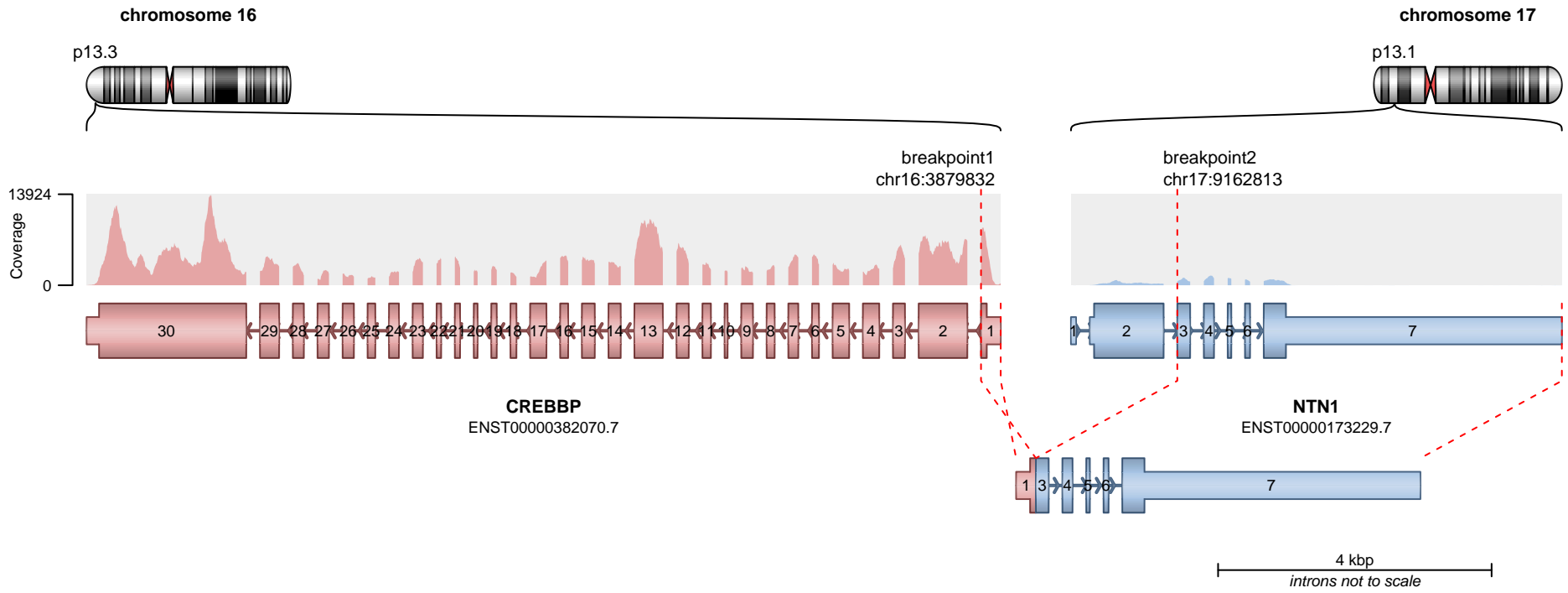
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



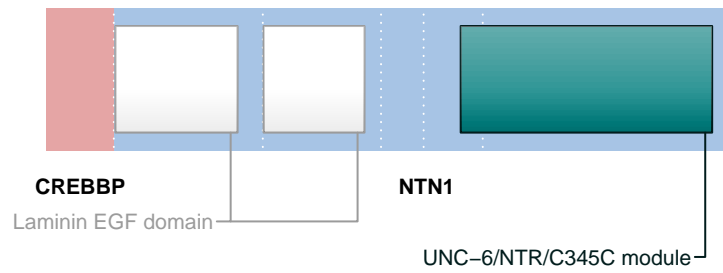
**SUPPORTING READ COUNT**

Split reads = 95  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



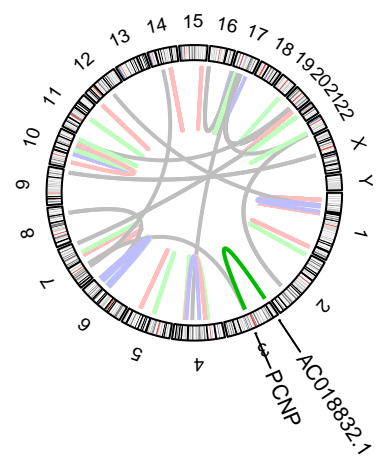
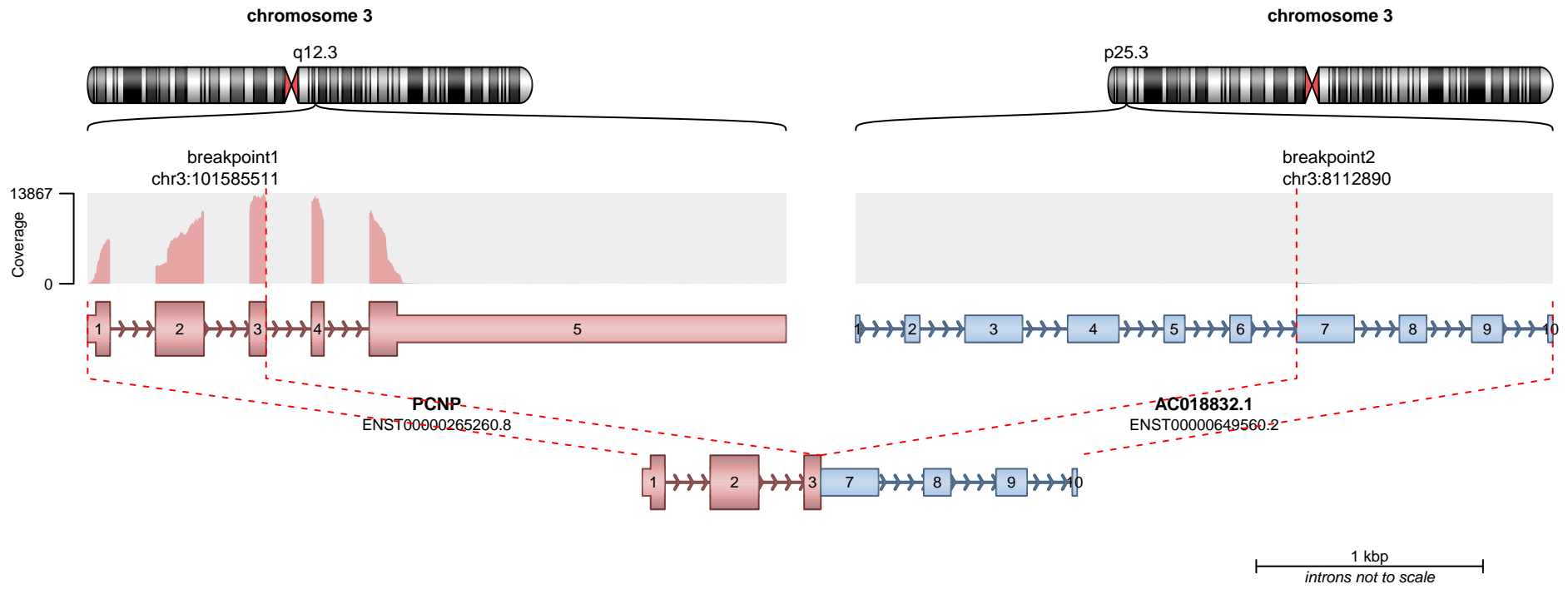
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



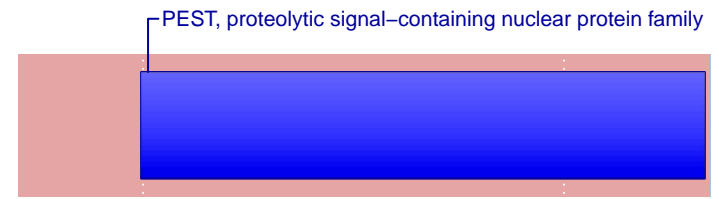
**SUPPORTING READ COUNT**

Split reads = 10  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



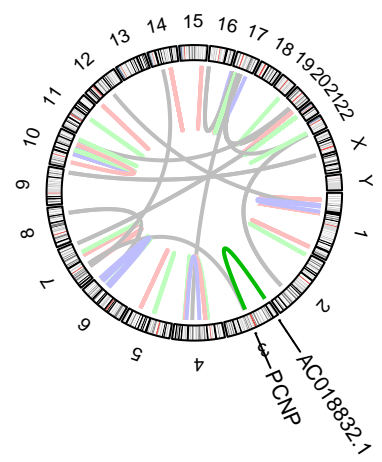
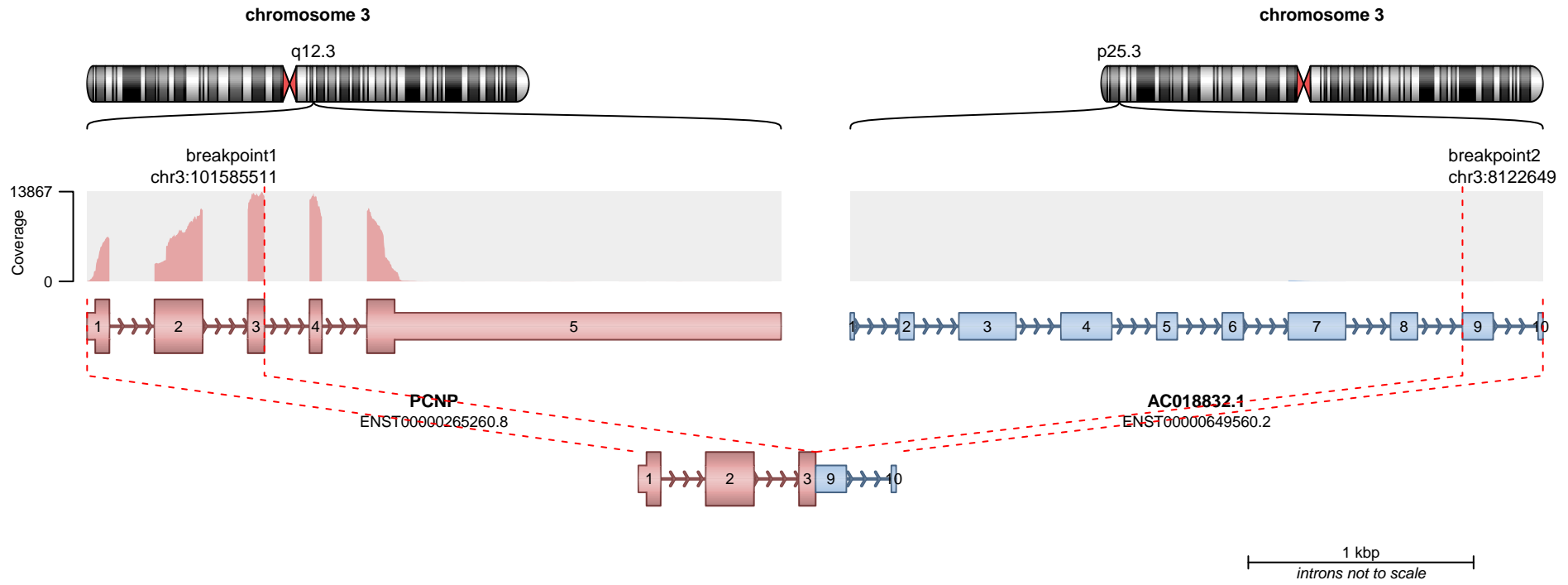
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



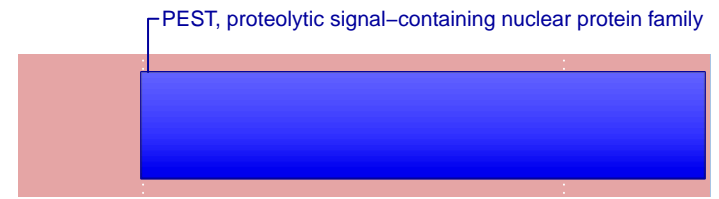
**SUPPORTING READ COUNT**

Split reads = 89  
Discordant mates = 3

- translocation
- duplication
- deletion
- inversion



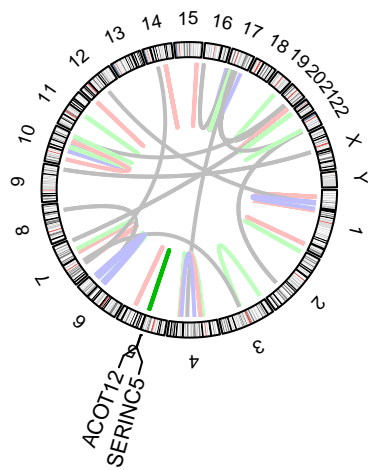
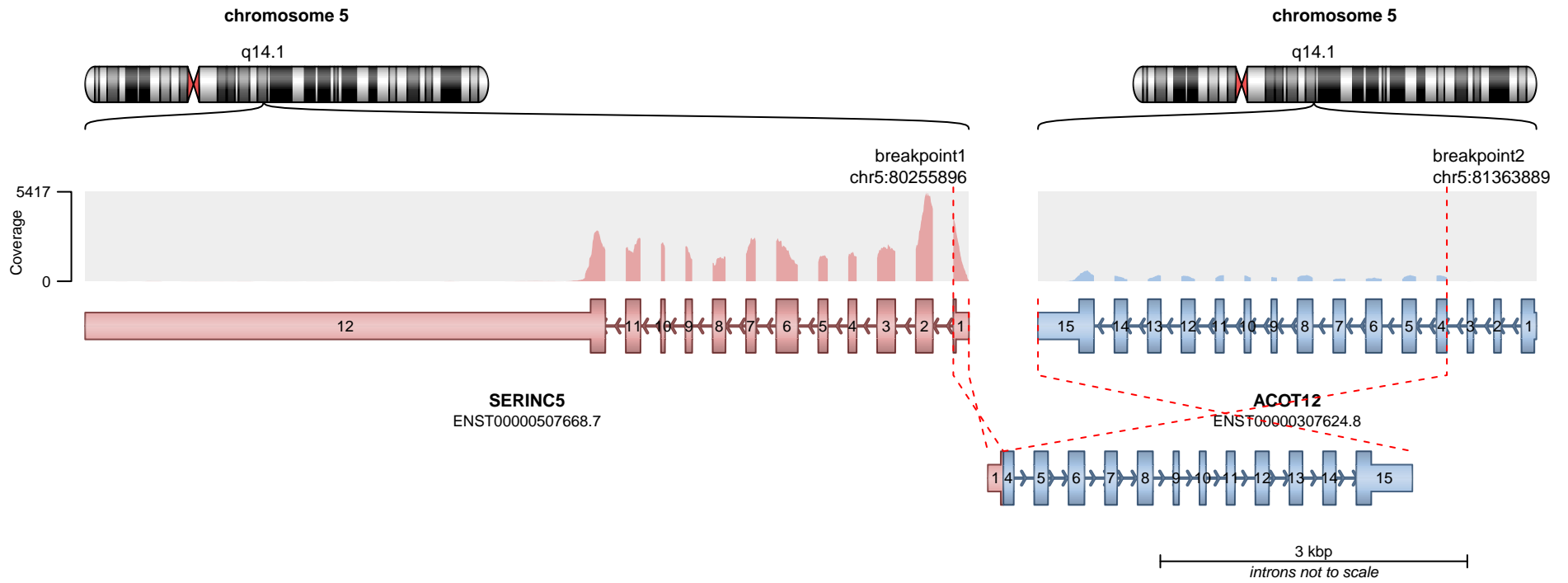
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

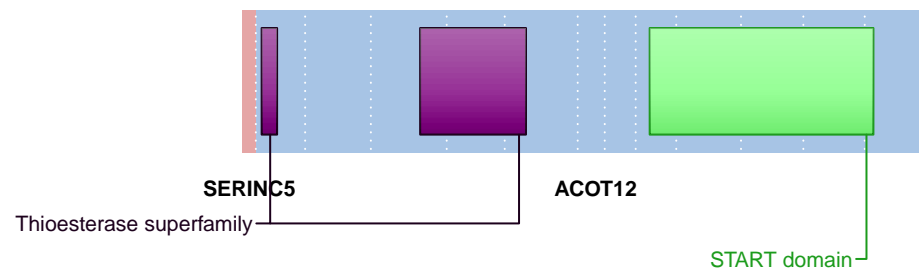
Split reads = 1  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



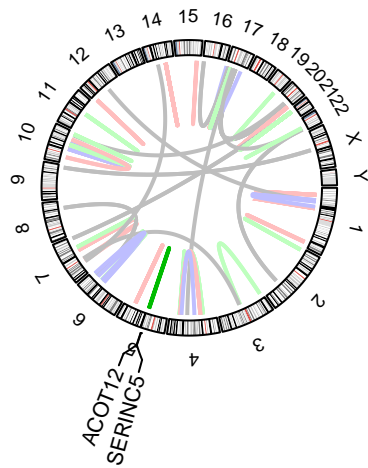
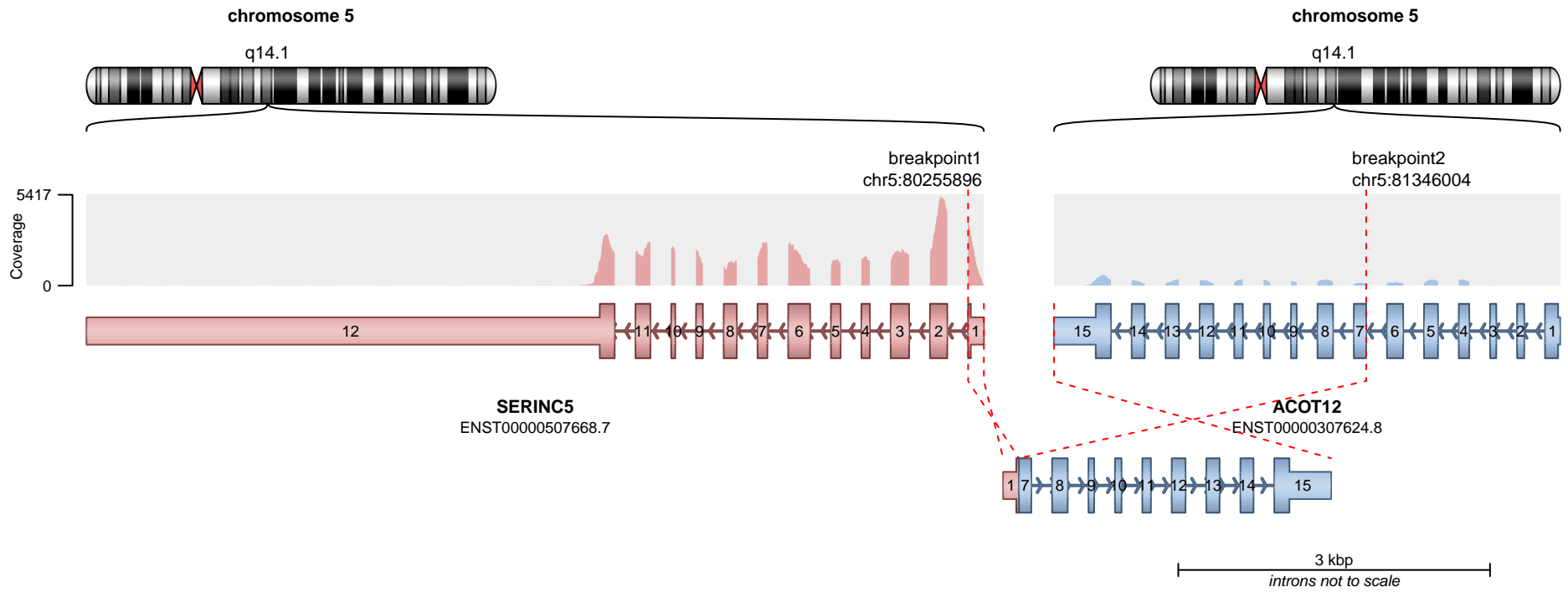
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear

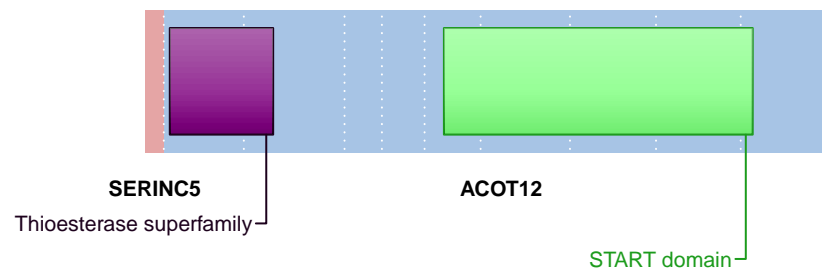


**SUPPORTING READ COUNT**

Split reads = 74  
Discordant mates = 0



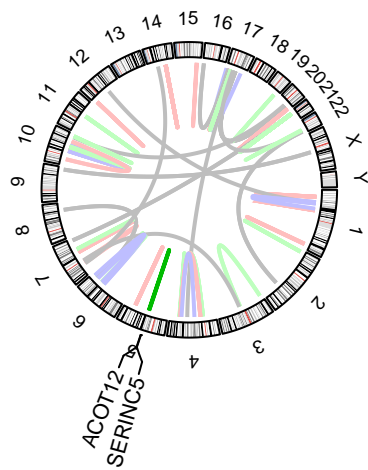
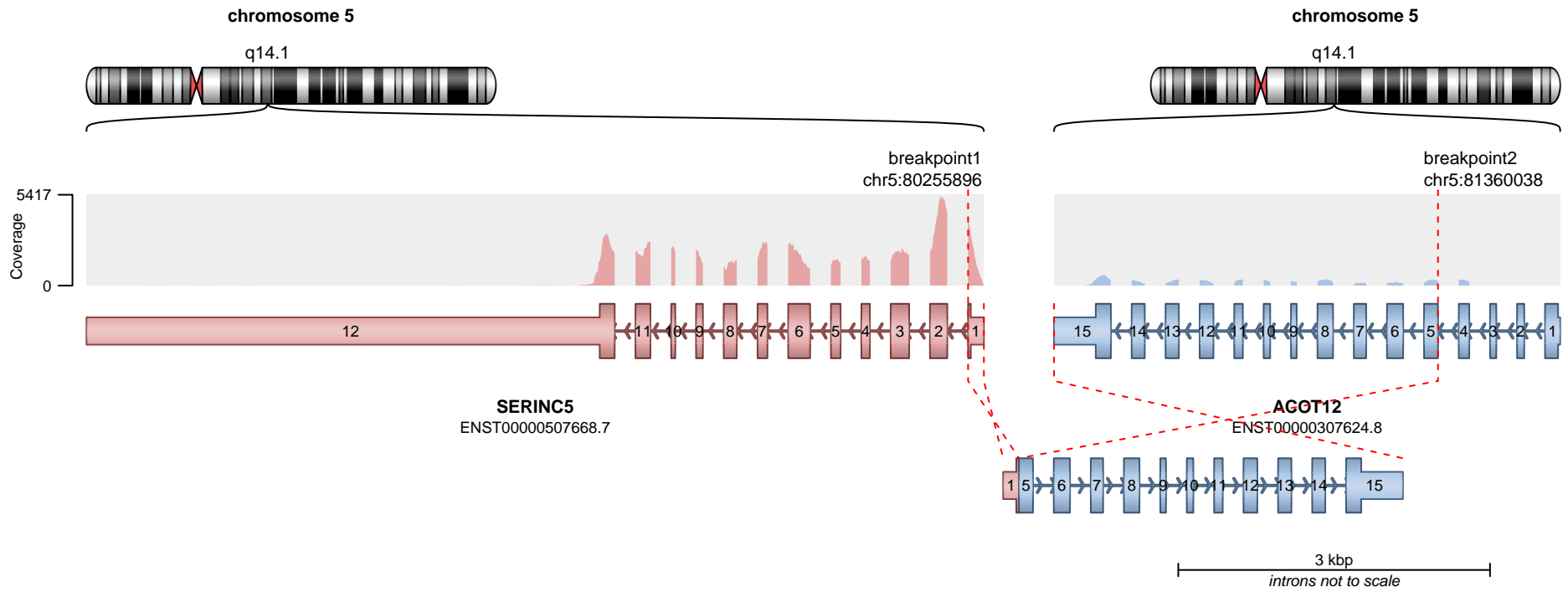
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

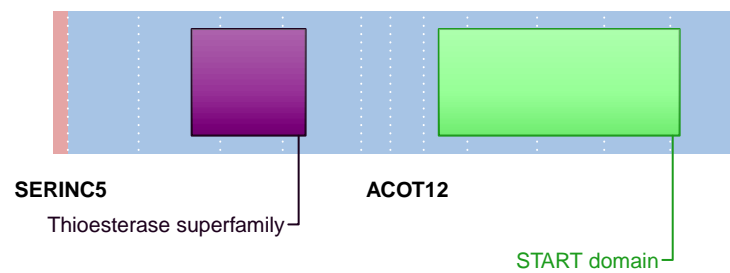
Split reads = 11  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



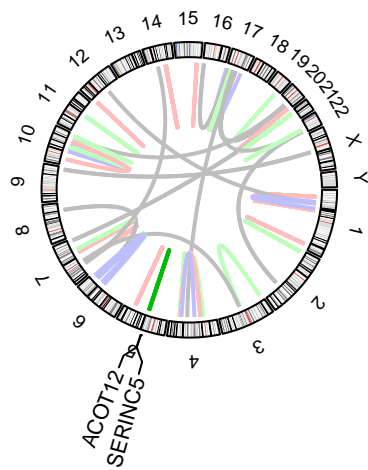
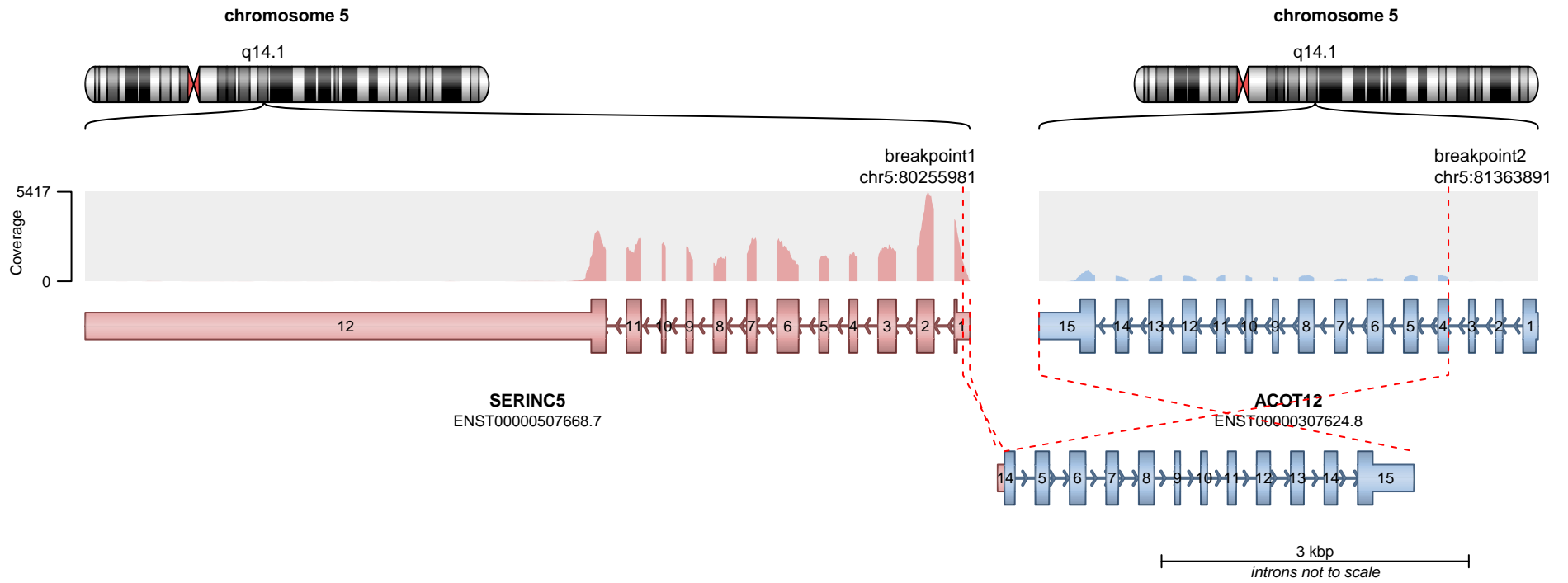
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



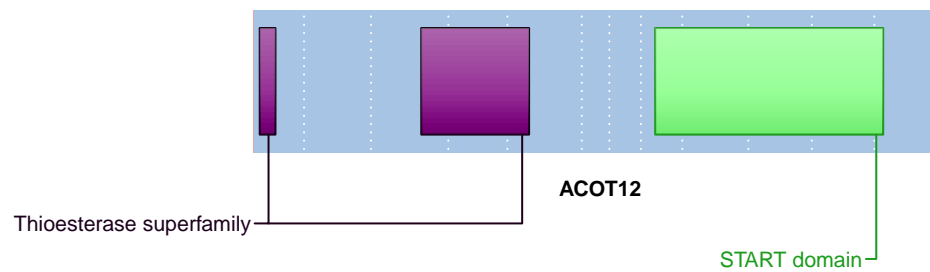
**SUPPORTING READ COUNT**

Split reads = 7  
Discordant mates = 0



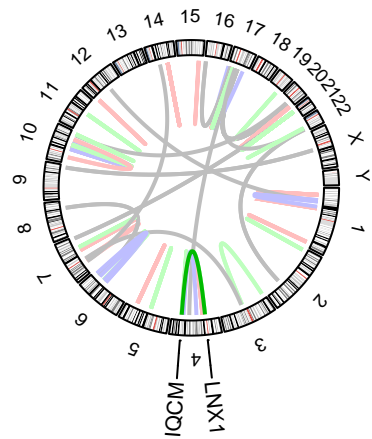
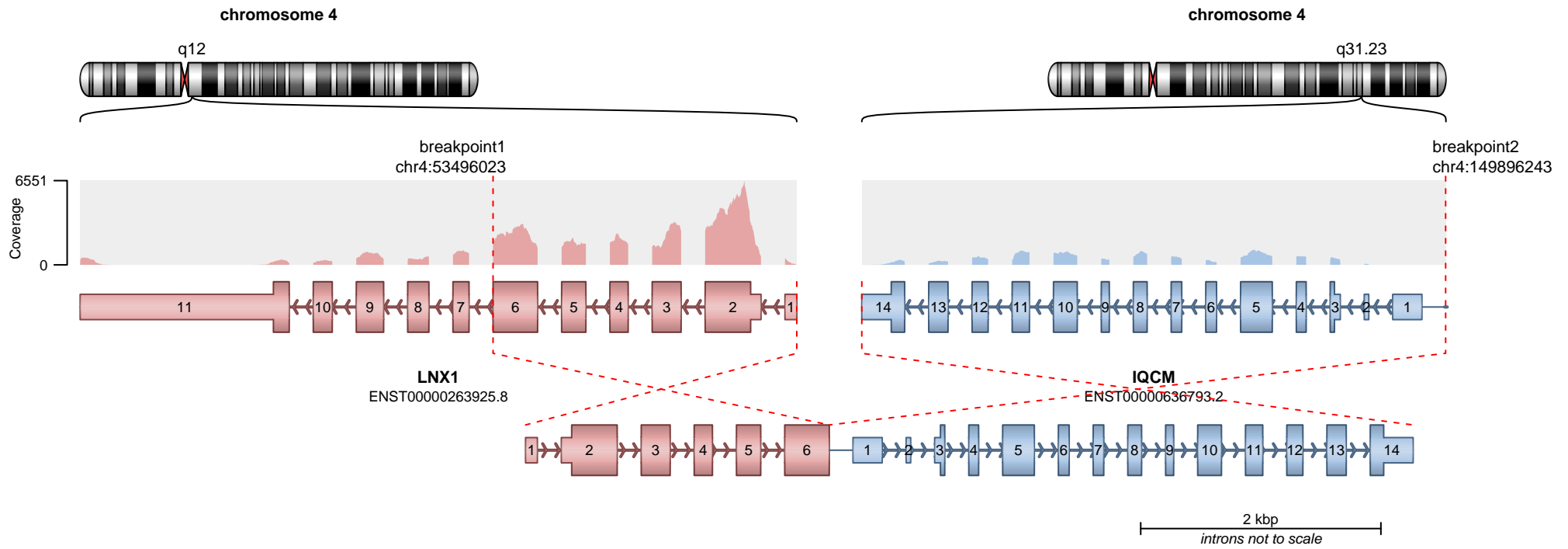
— translocation    — deletion  
— duplication    — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear

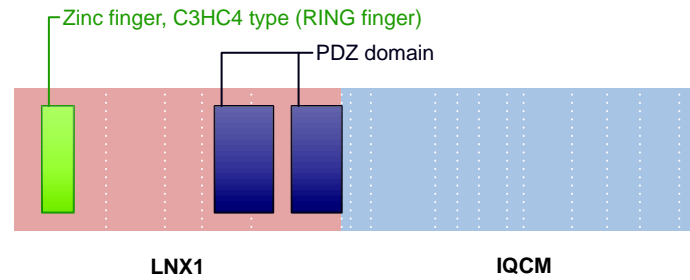


**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 0



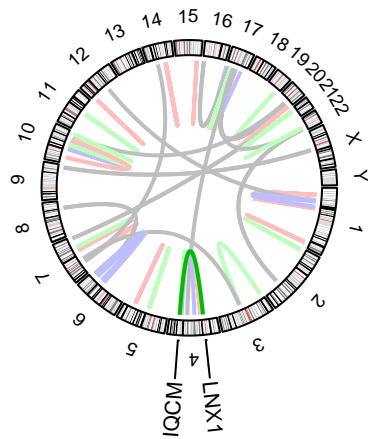
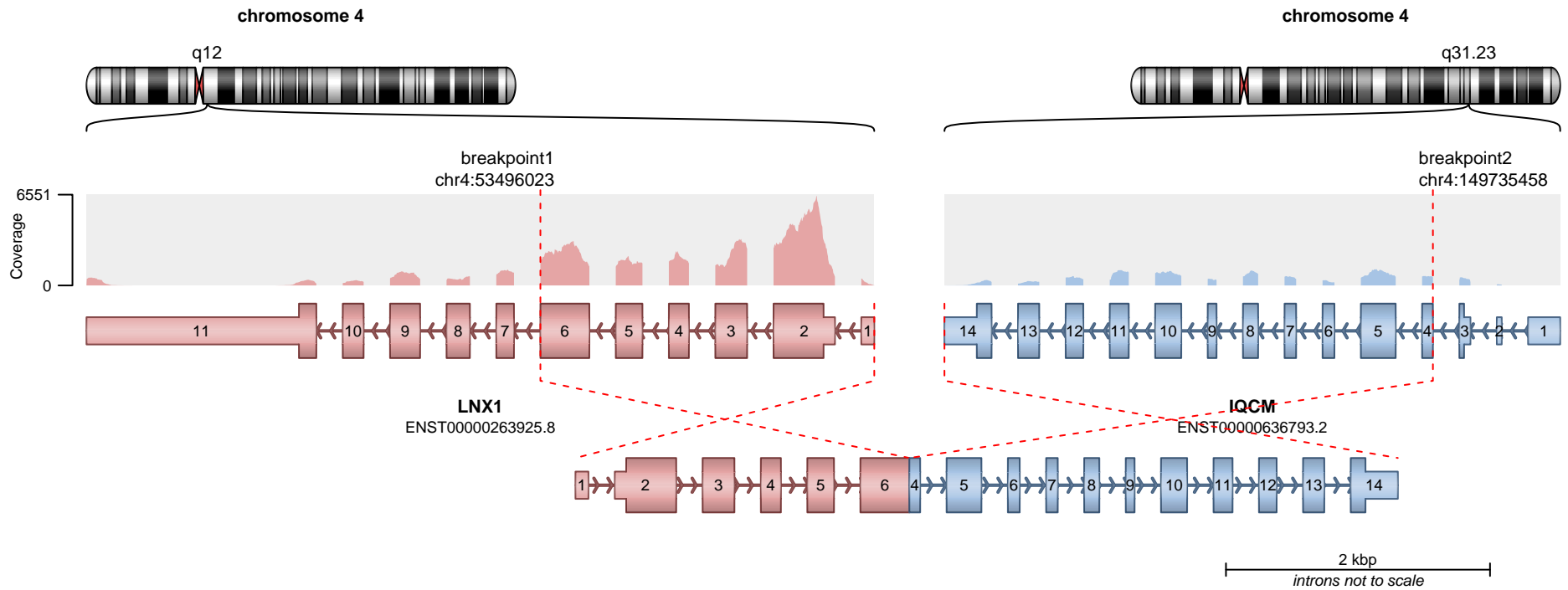
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



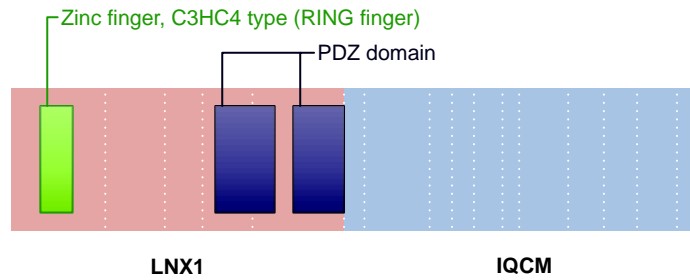
**SUPPORTING READ COUNT**

Split reads = 69  
Discordant mates = 2

— translocation    — deletion  
— duplication    — inversion



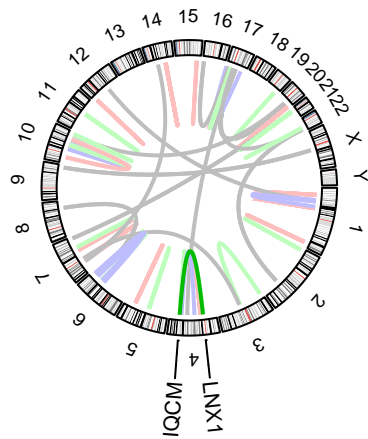
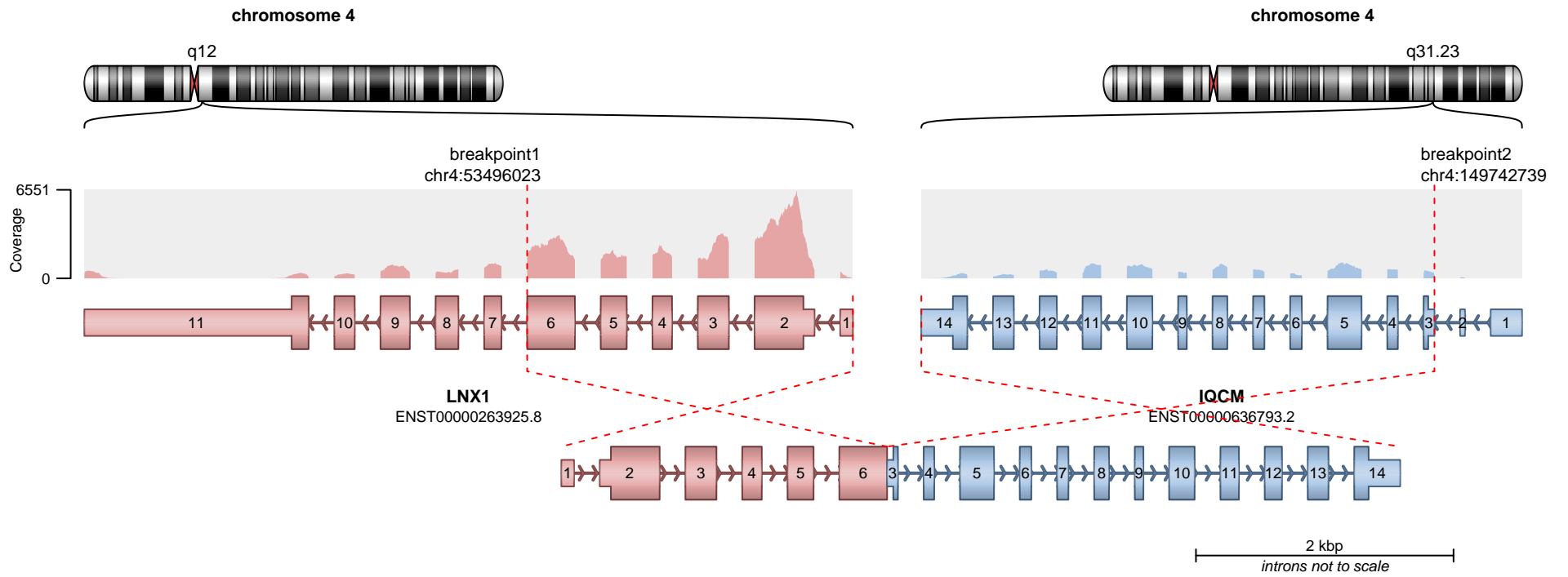
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



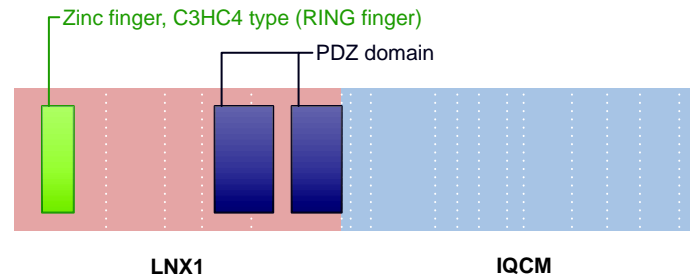
**SUPPORTING READ COUNT**

Split reads = 46  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



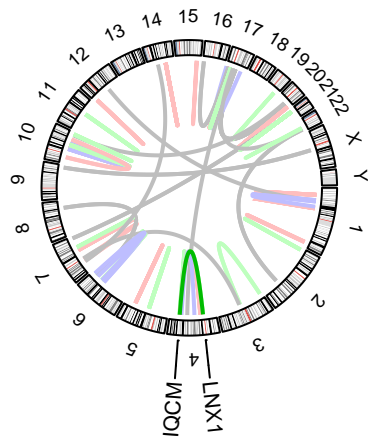
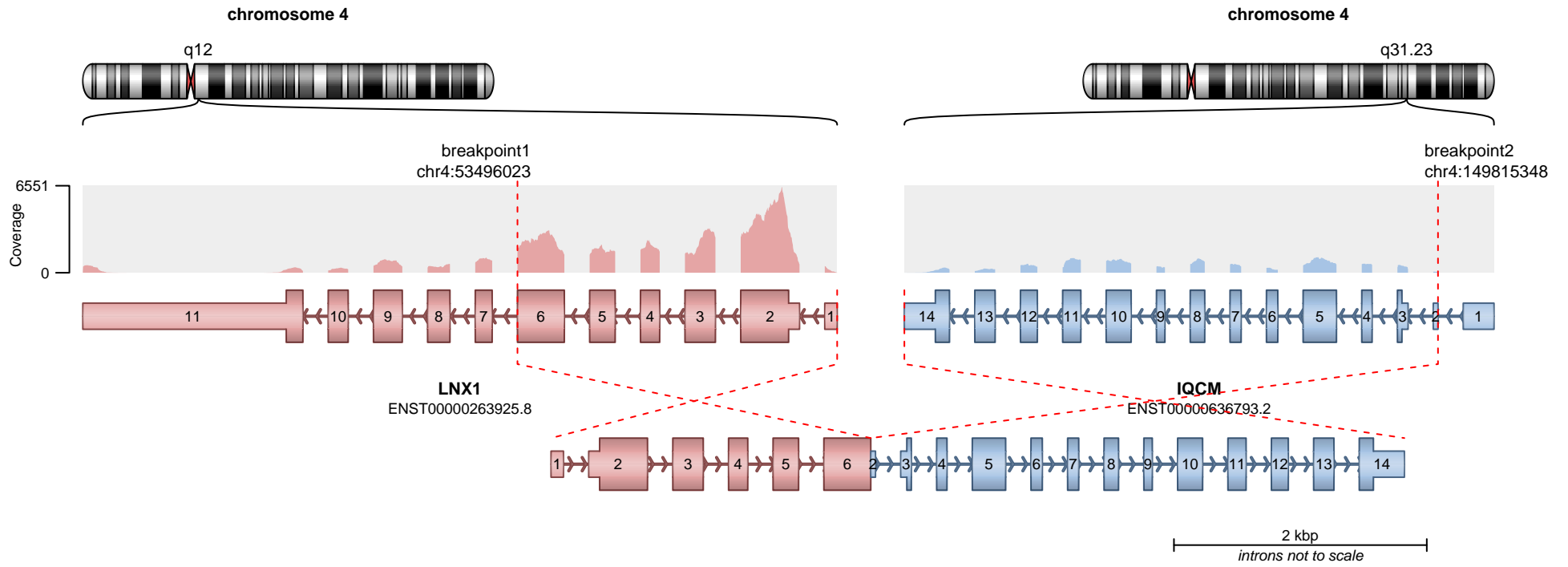
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



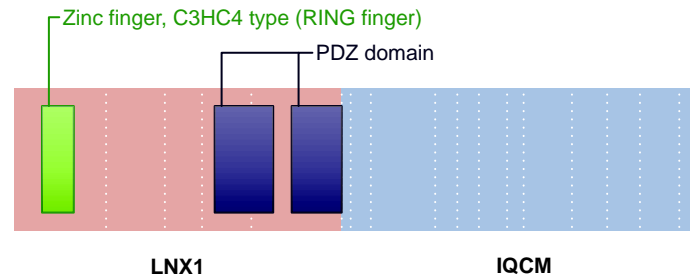
**SUPPORTING READ COUNT**

Split reads = 19  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



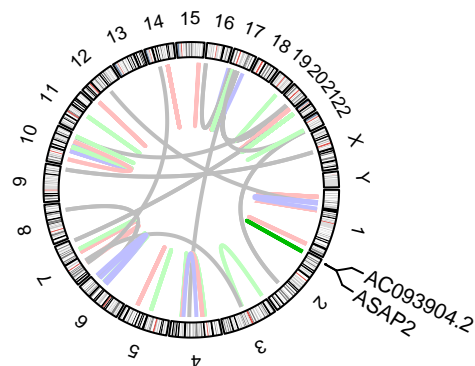
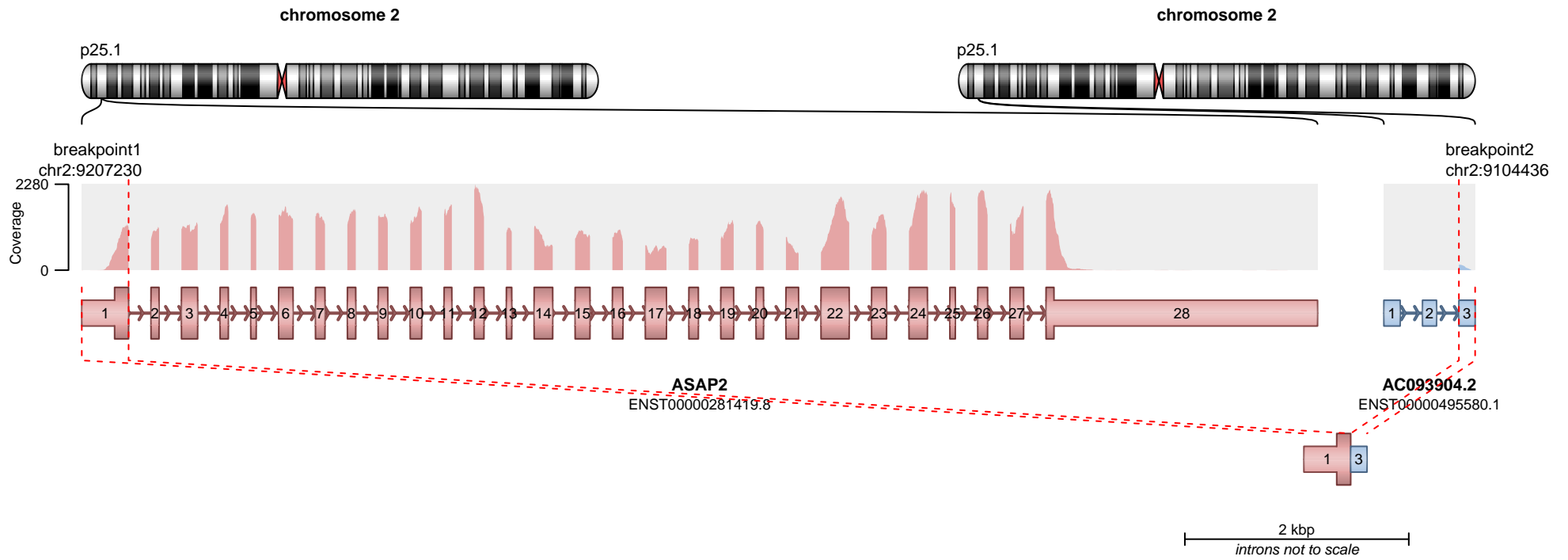
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



**RETAINED PROTEIN DOMAINS**  
reading frame unclear

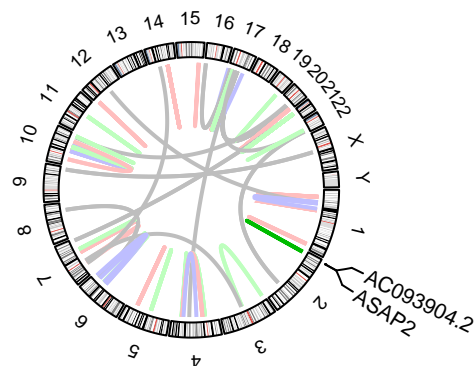
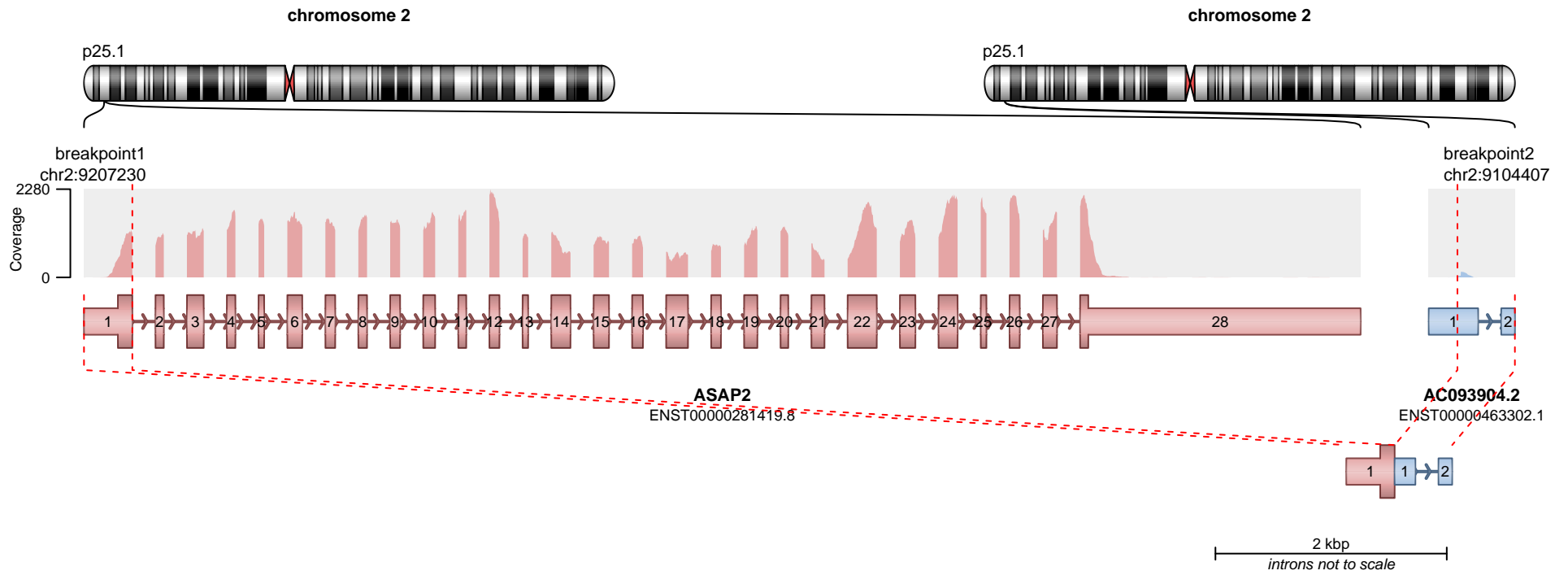


**ASAP2**

**SUPPORTING READ COUNT**

Split reads = 66  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



**RETAINED PROTEIN DOMAINS**  
reading frame unclear

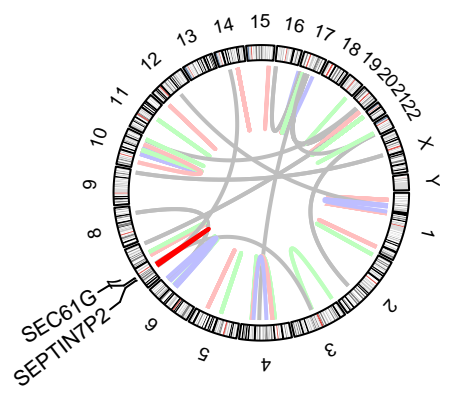
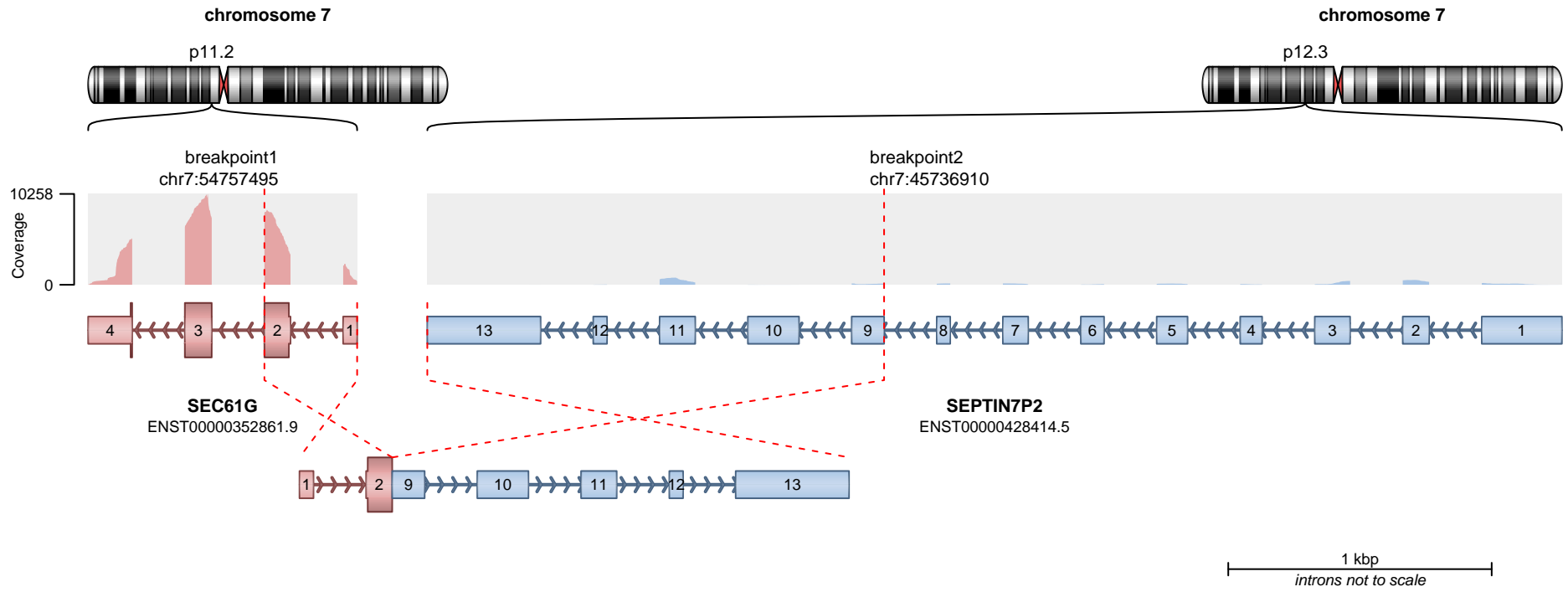


**ASAP2**

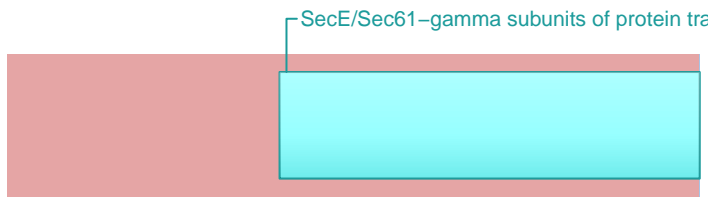
**SUPPORTING READ COUNT**

Split reads = 22  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



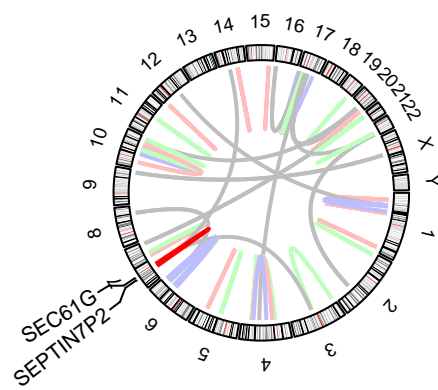
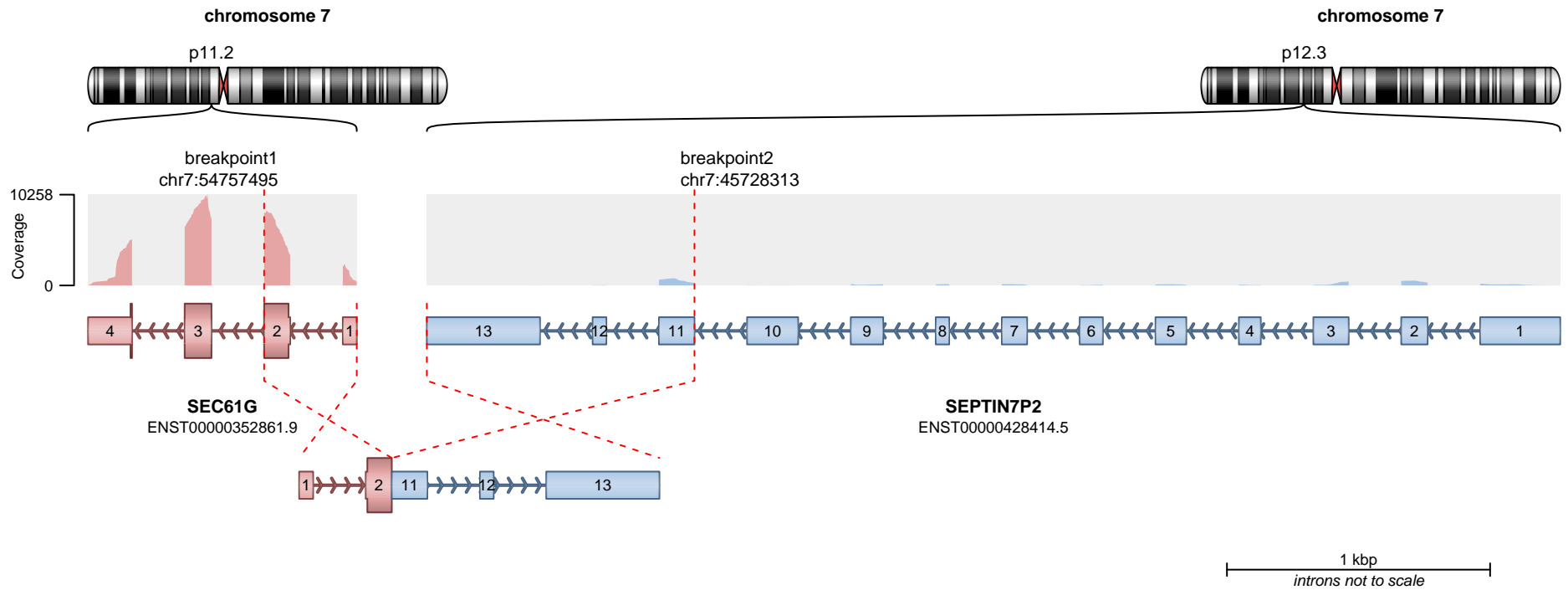
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



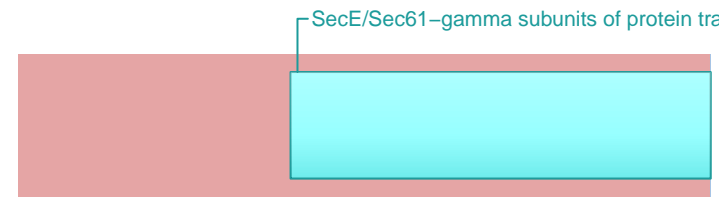
**SUPPORTING READ COUNT**

Split reads = 62  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



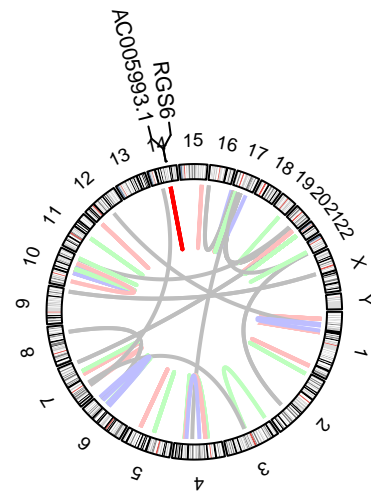
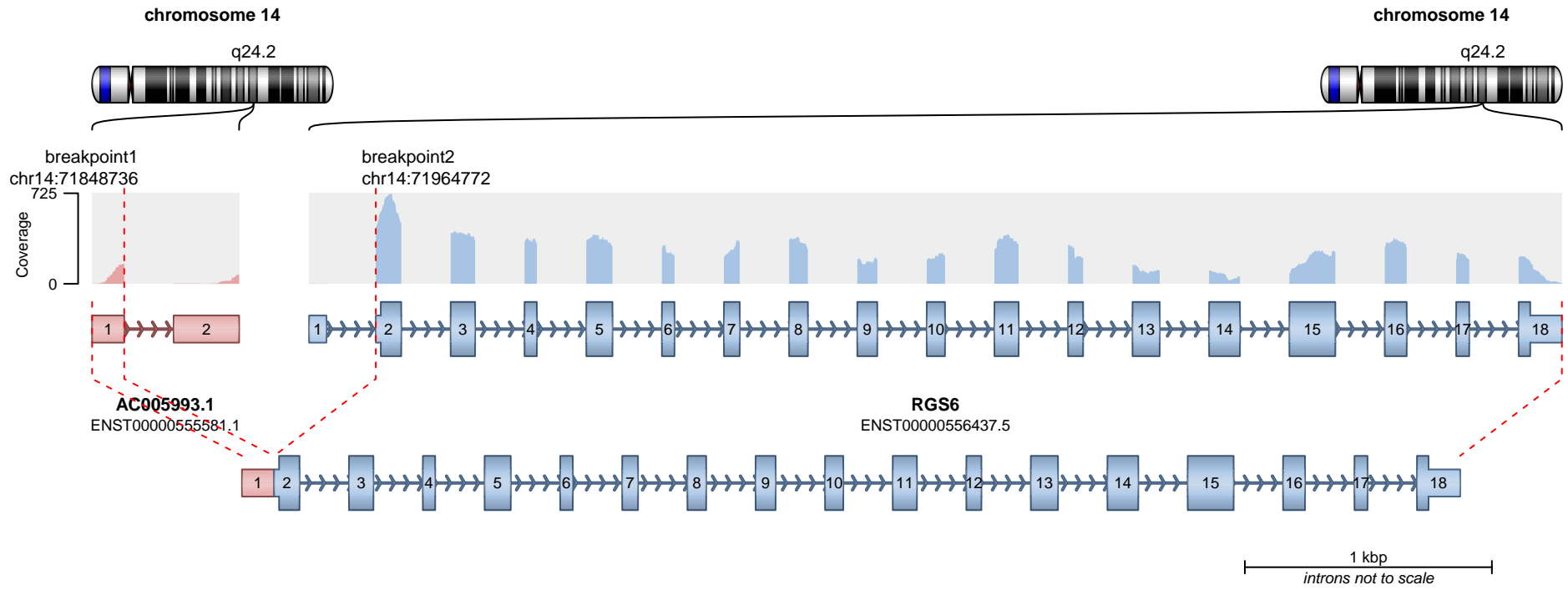
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



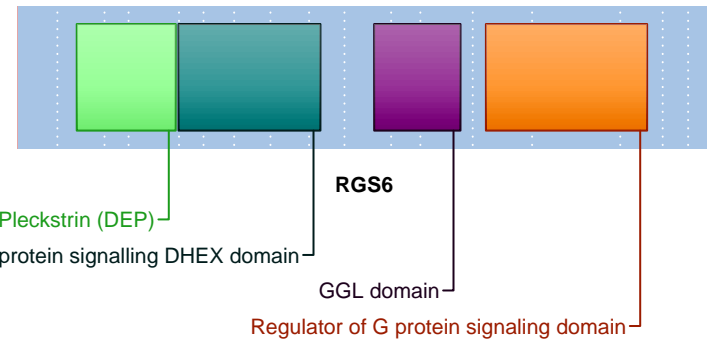
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



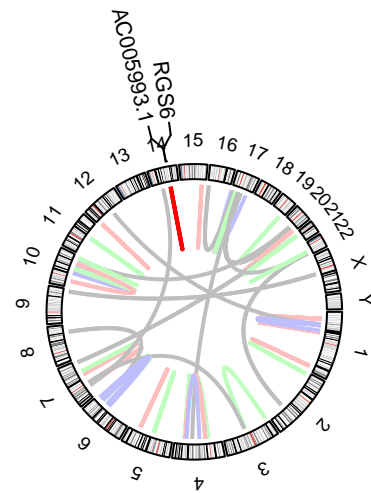
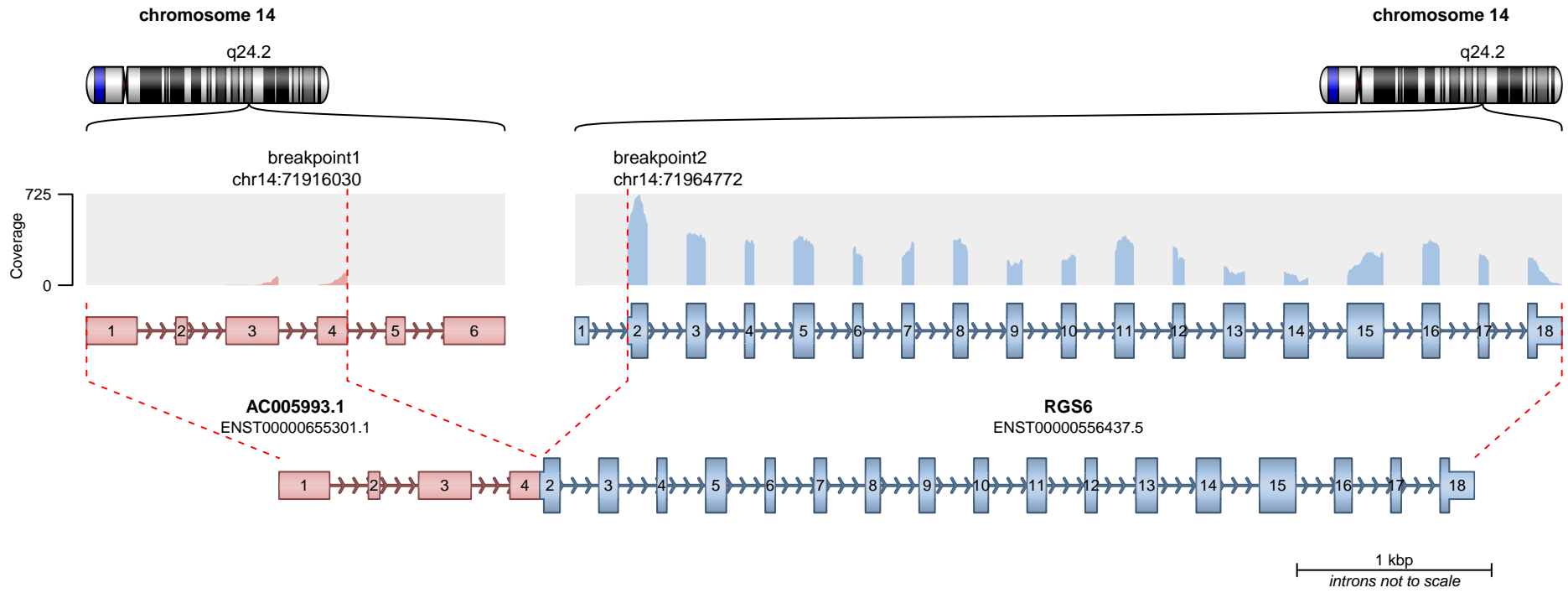
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



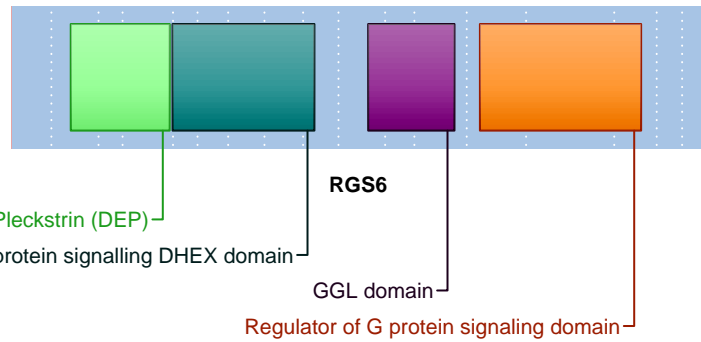
**SUPPORTING READ COUNT**

Split reads = 57  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



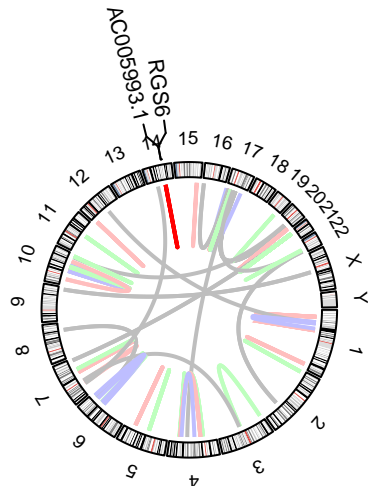
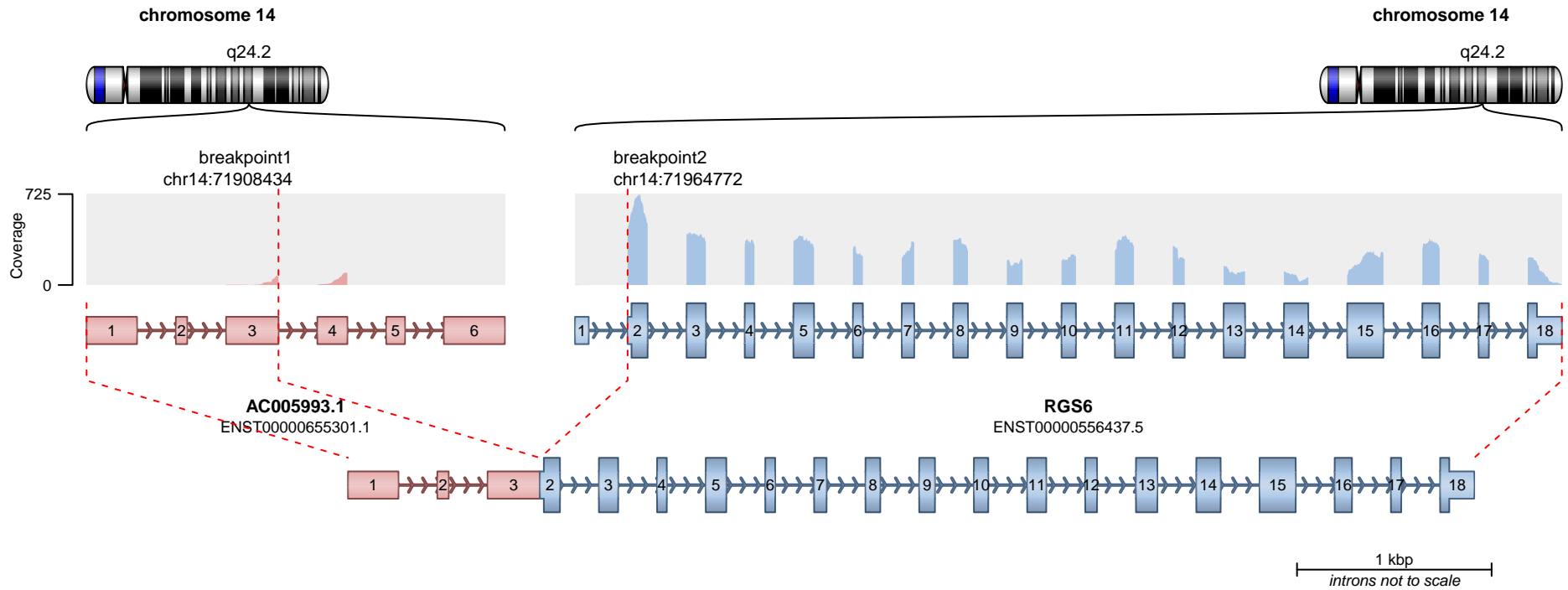
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



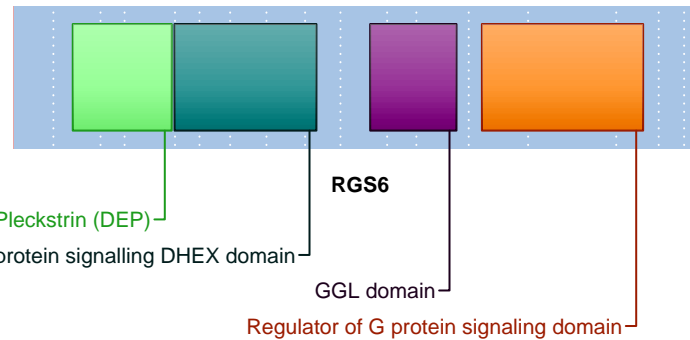
**SUPPORTING READ COUNT**

Split reads = 46  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



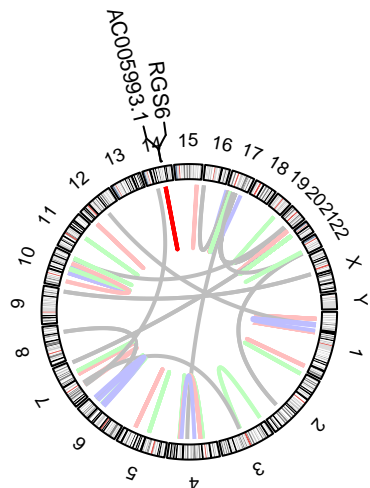
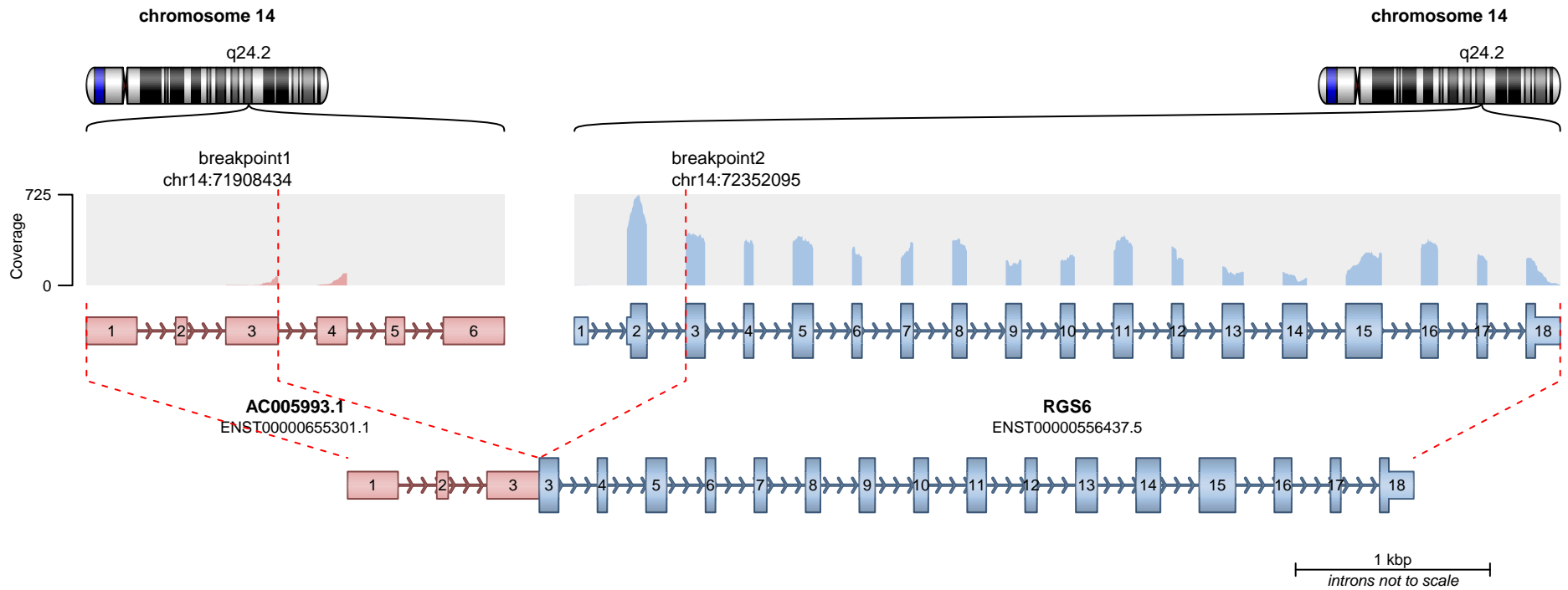
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



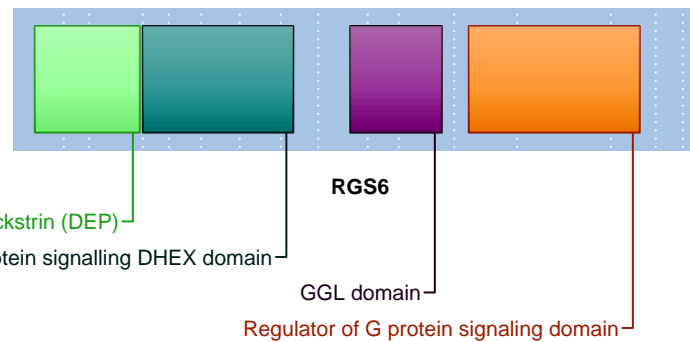
**SUPPORTING READ COUNT**

Split reads = 27  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



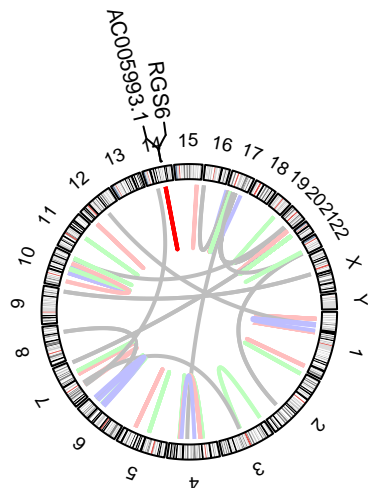
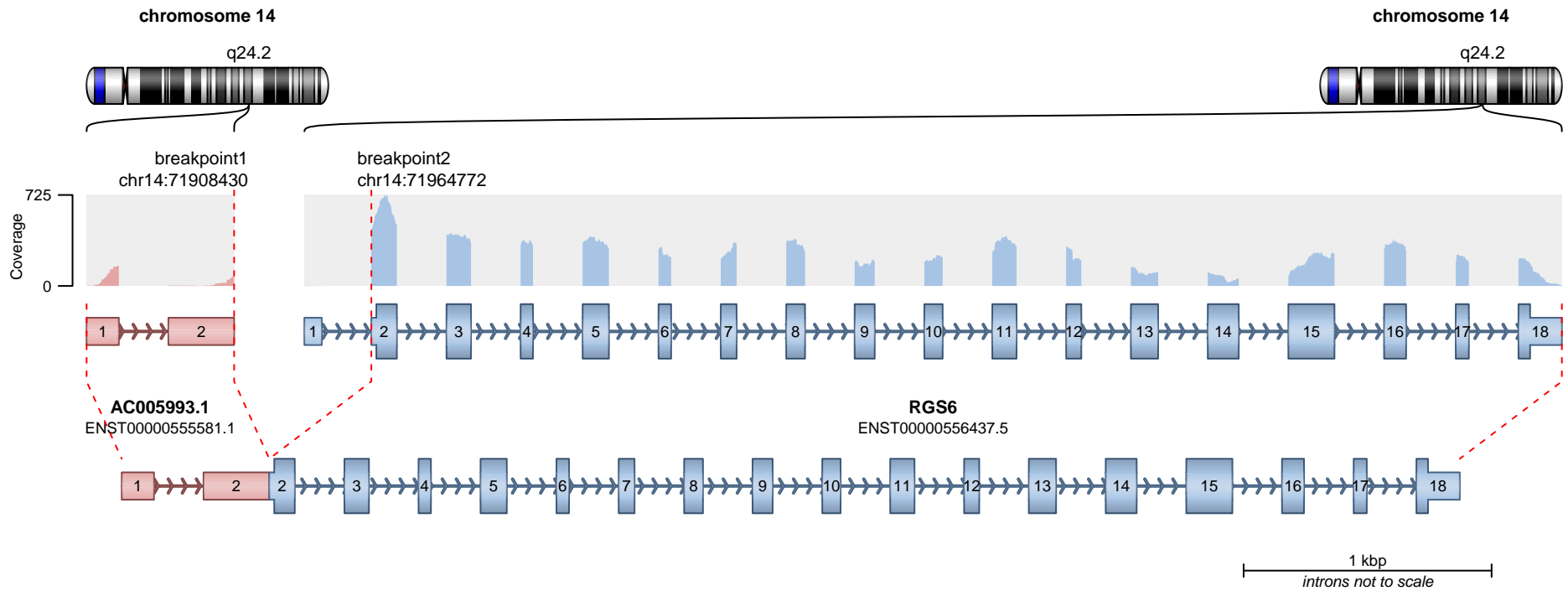
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



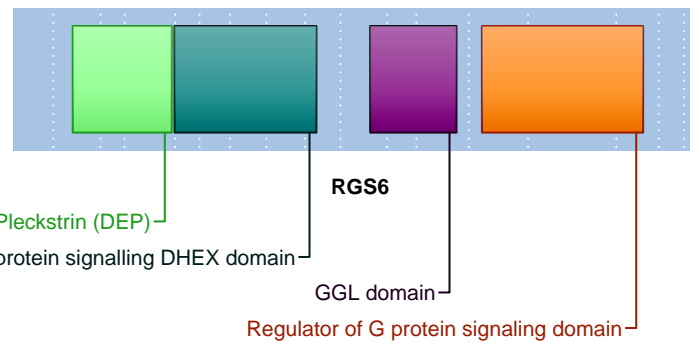
**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



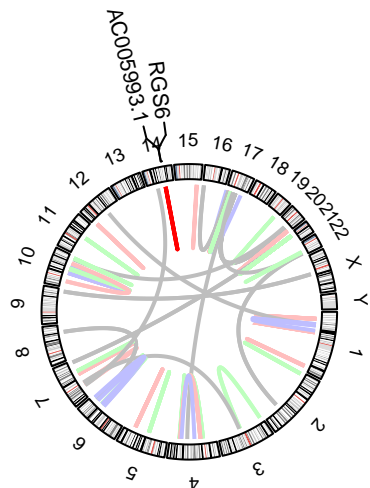
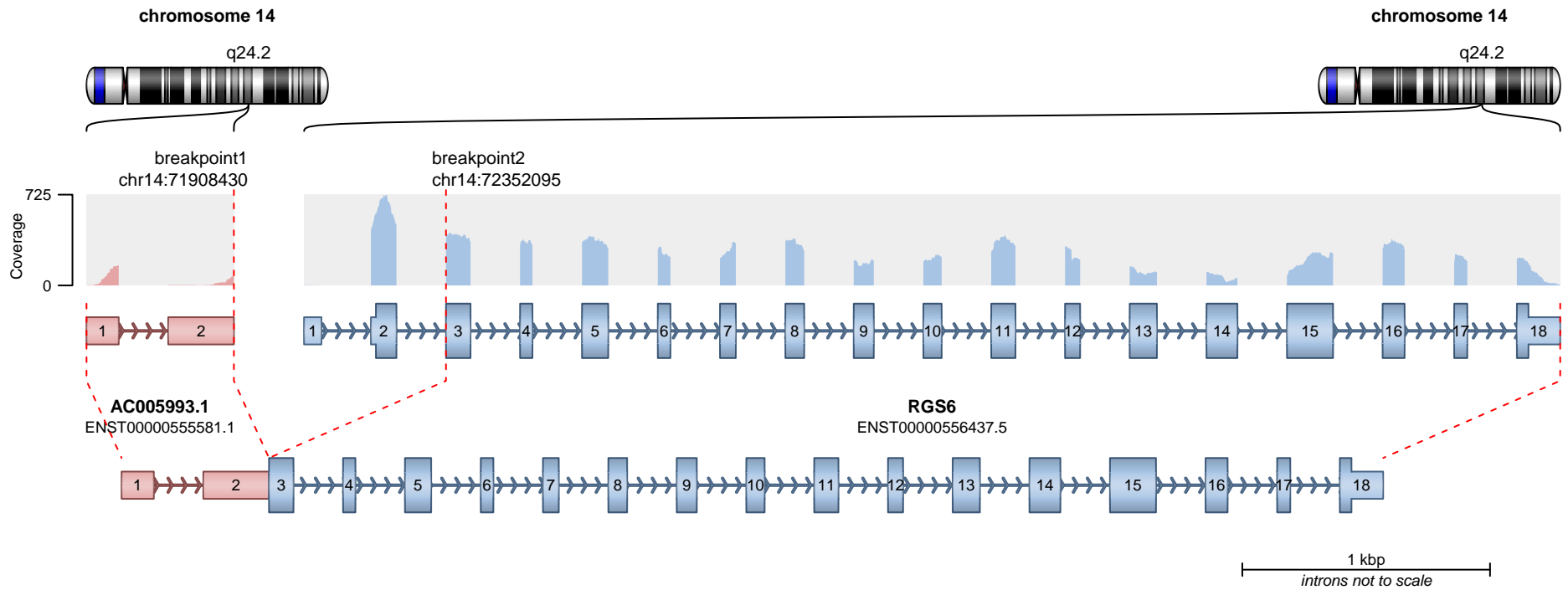
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



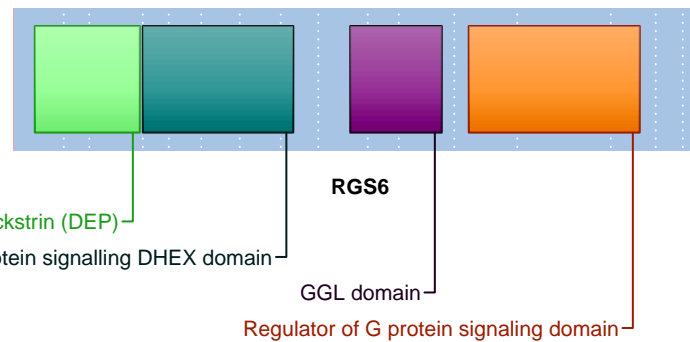
**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



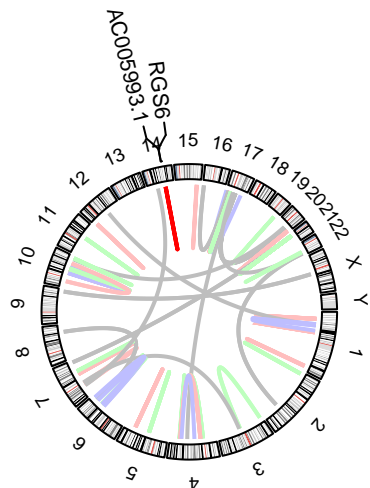
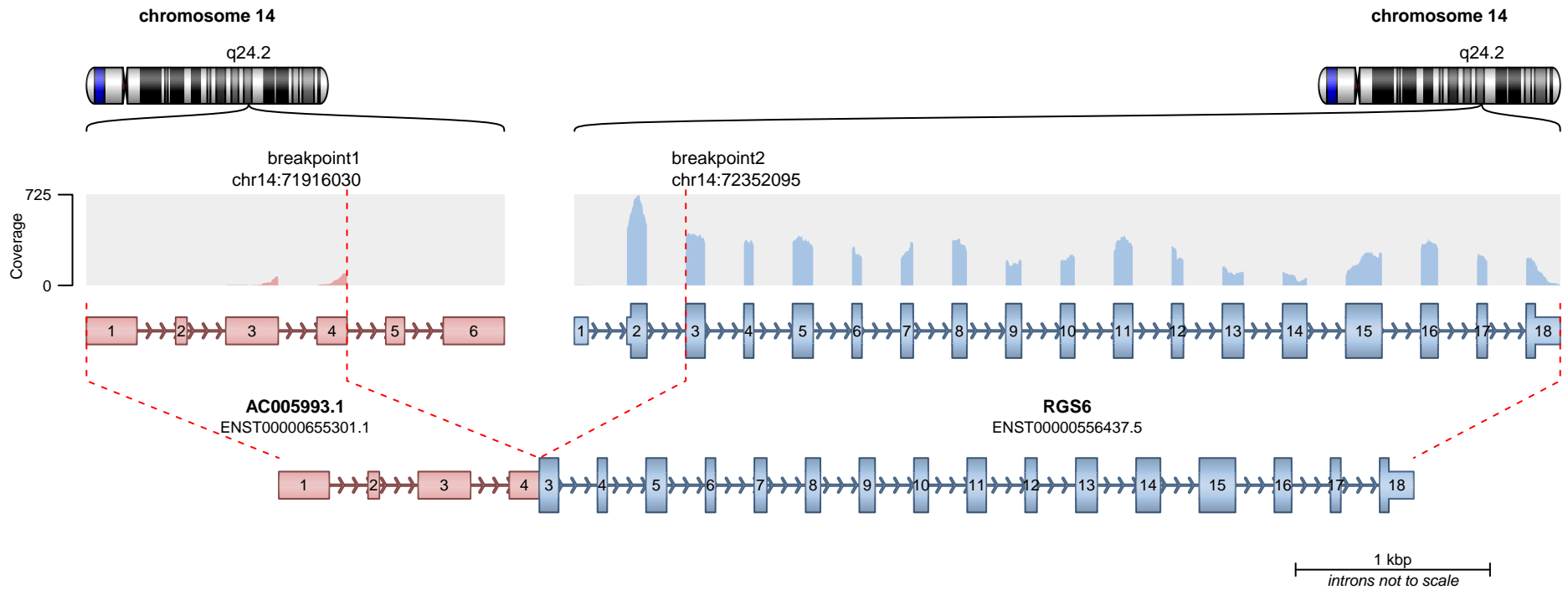
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



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

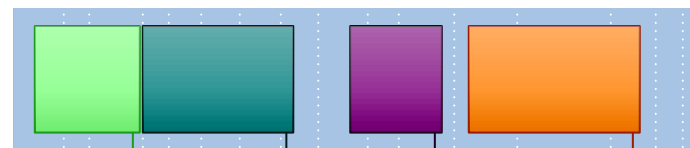
Regulator of G-protein signalling DHEX domain

RGS6

GGL domain

Regulator of G protein signaling domain

RETAINED PROTEIN DOMAINS  
reading frame unclear

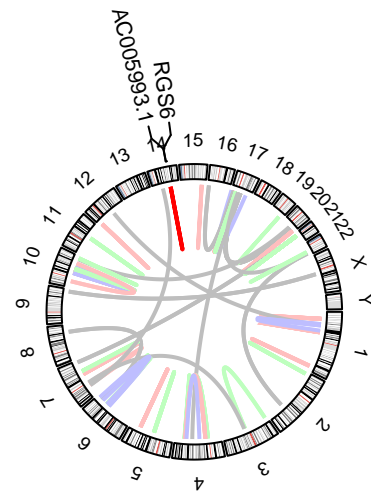
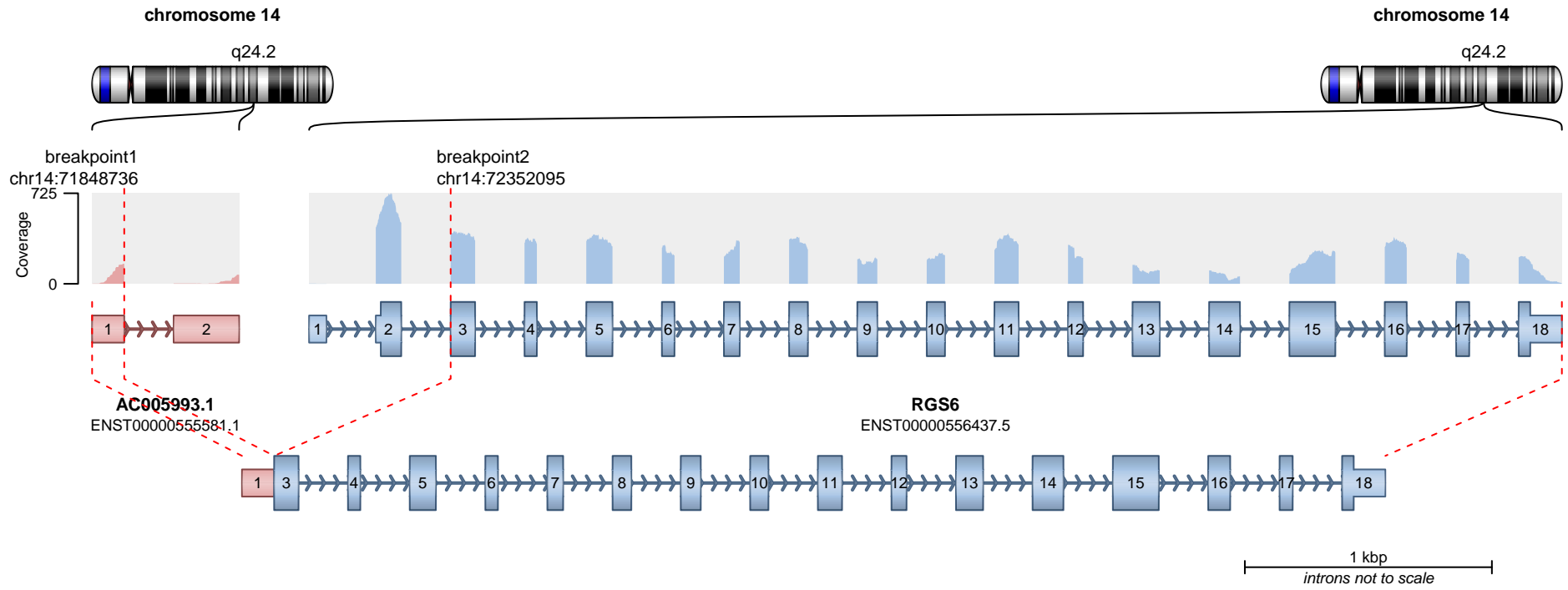


SUPPORTING READ COUNT

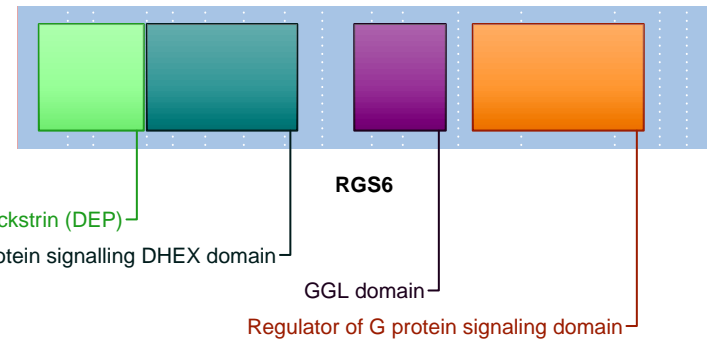
Split reads = 1

Discordant mates = 0

— translocation — deletion  
— duplication — inversion



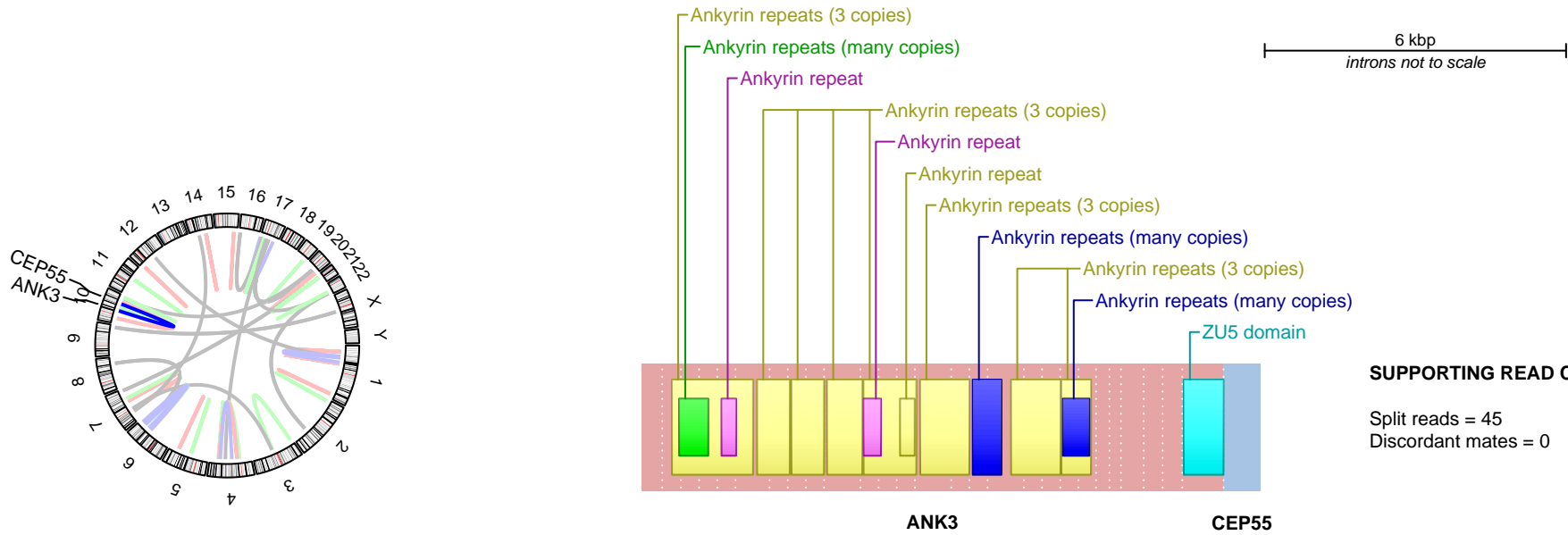
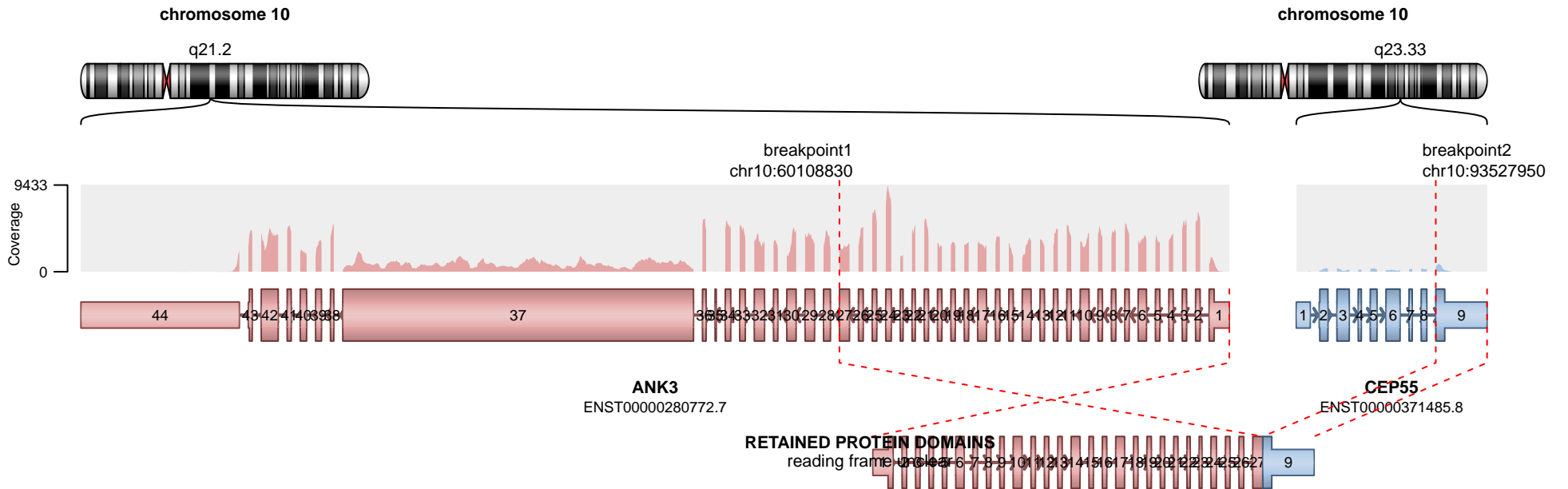
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



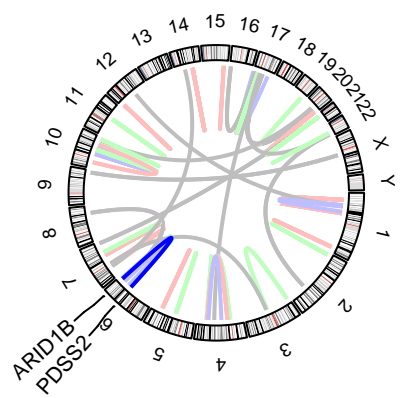
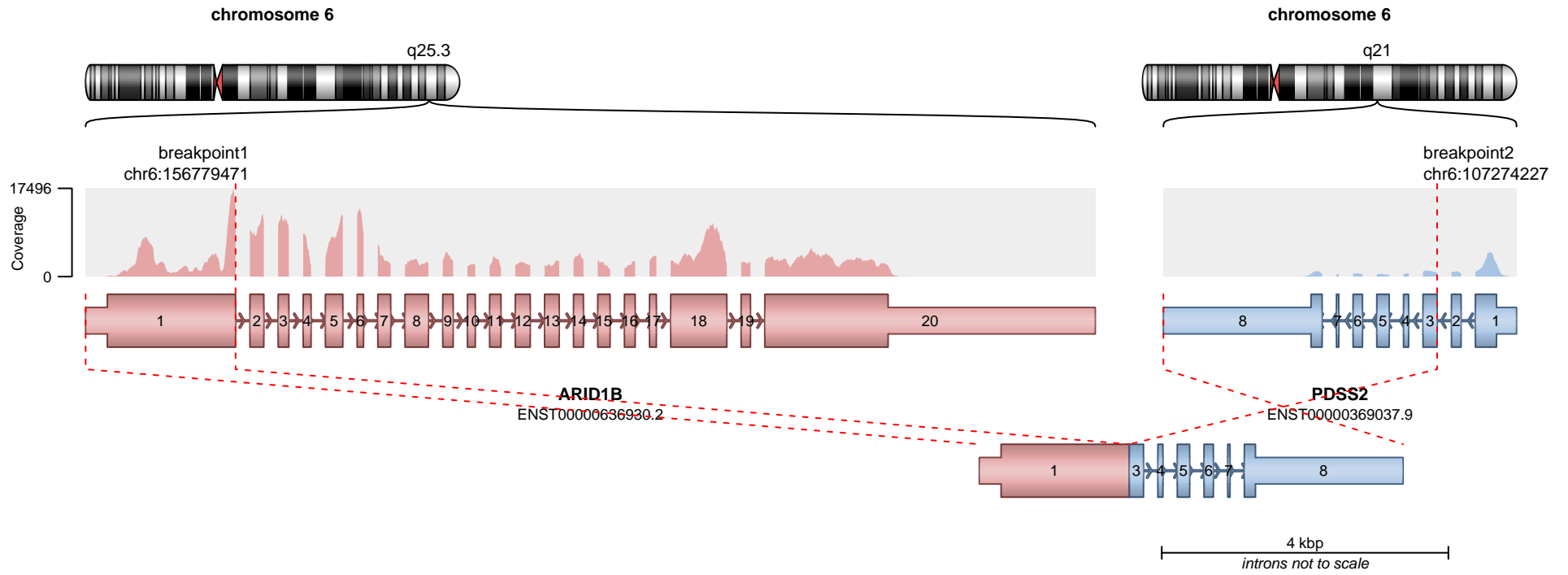
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

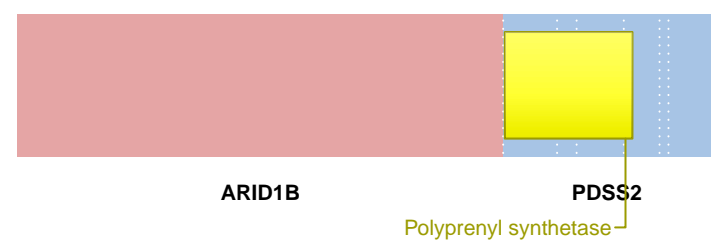
- translocation
- duplication
- deletion
- inversion



— translocation — deletion  
— duplication — inversion



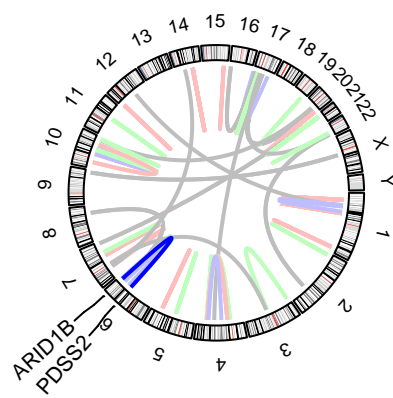
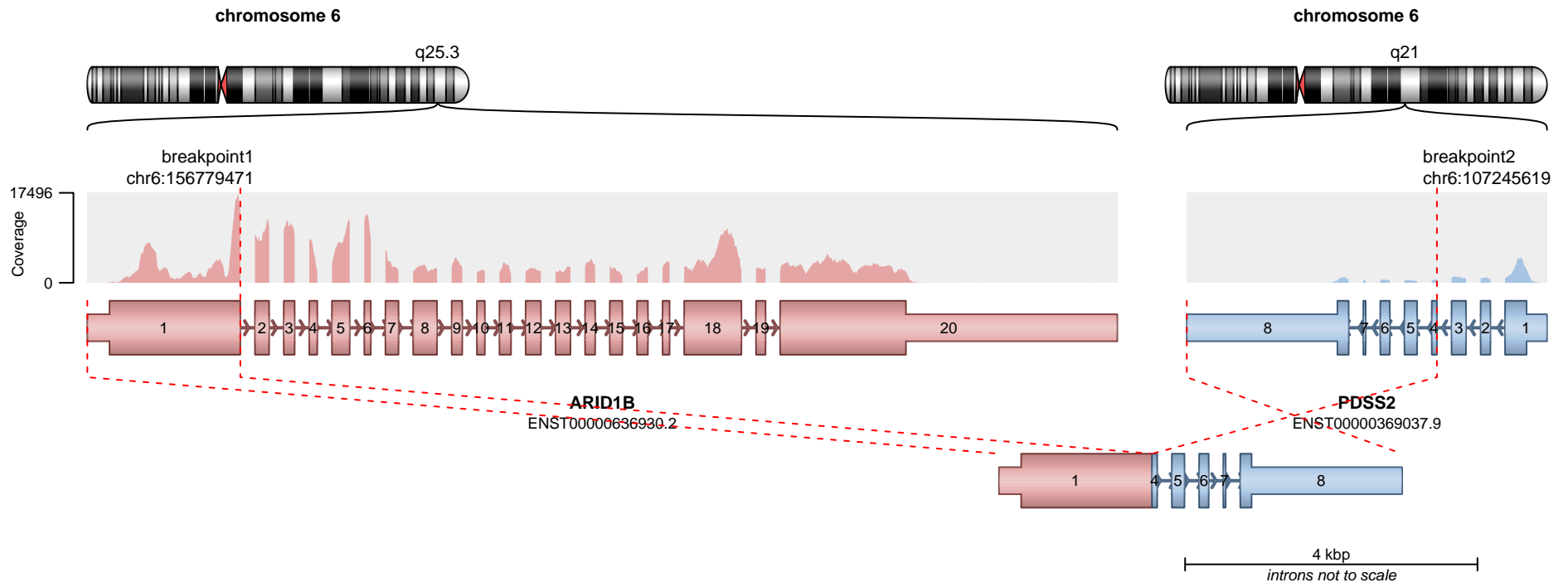
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



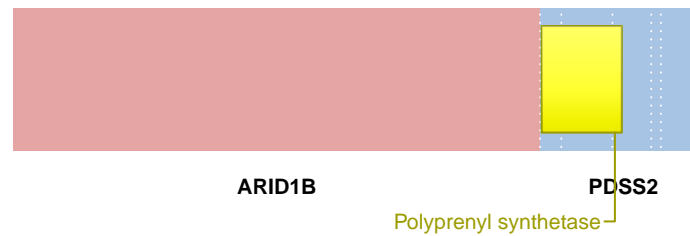
**SUPPORTING READ COUNT**

Split reads = 43  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



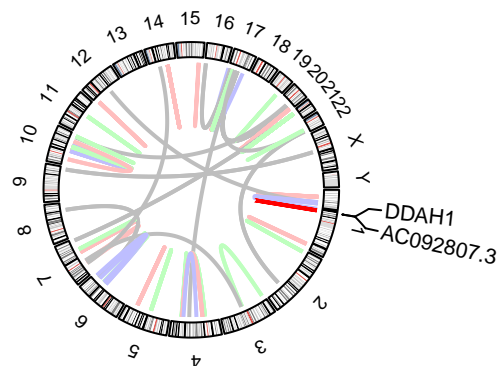
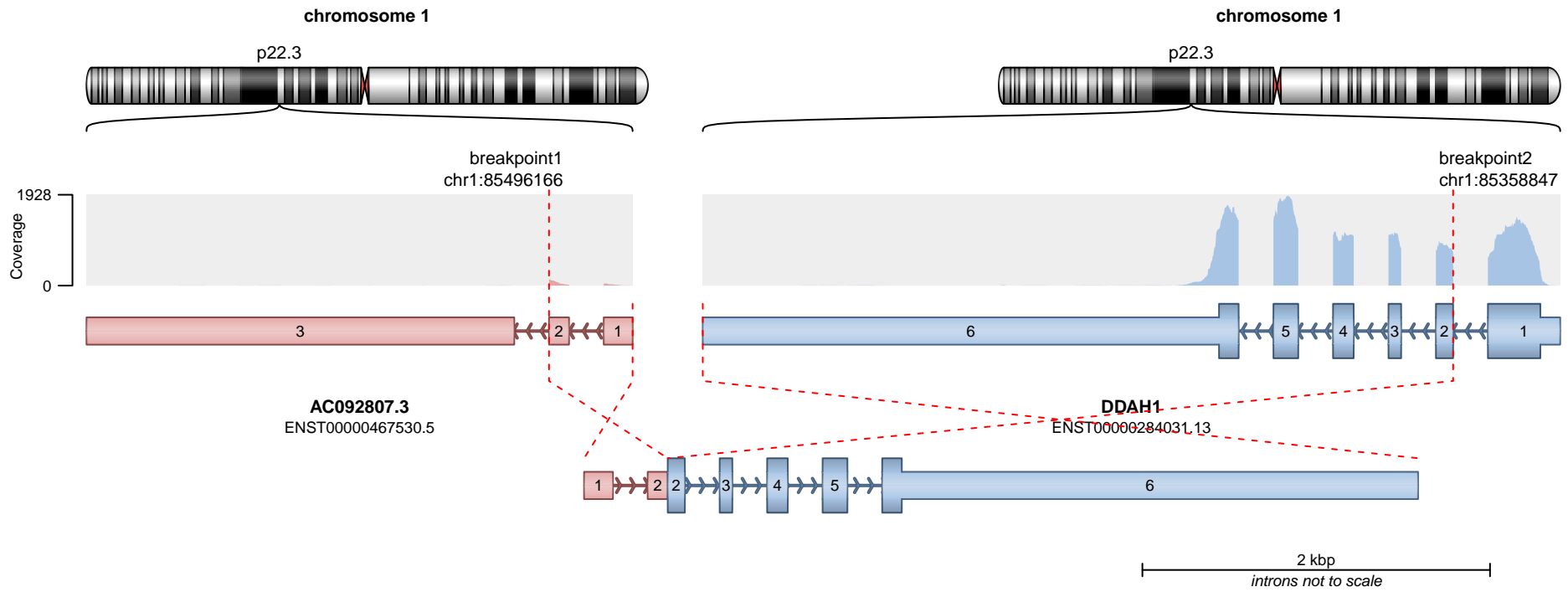
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



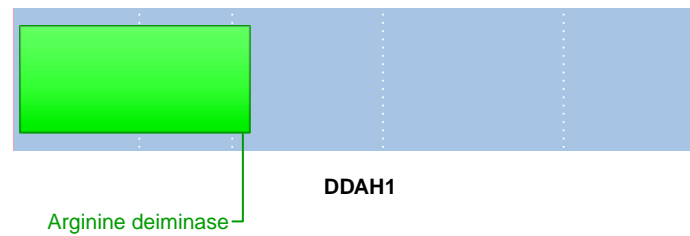
**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



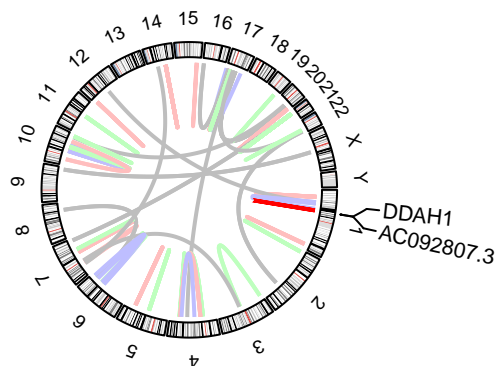
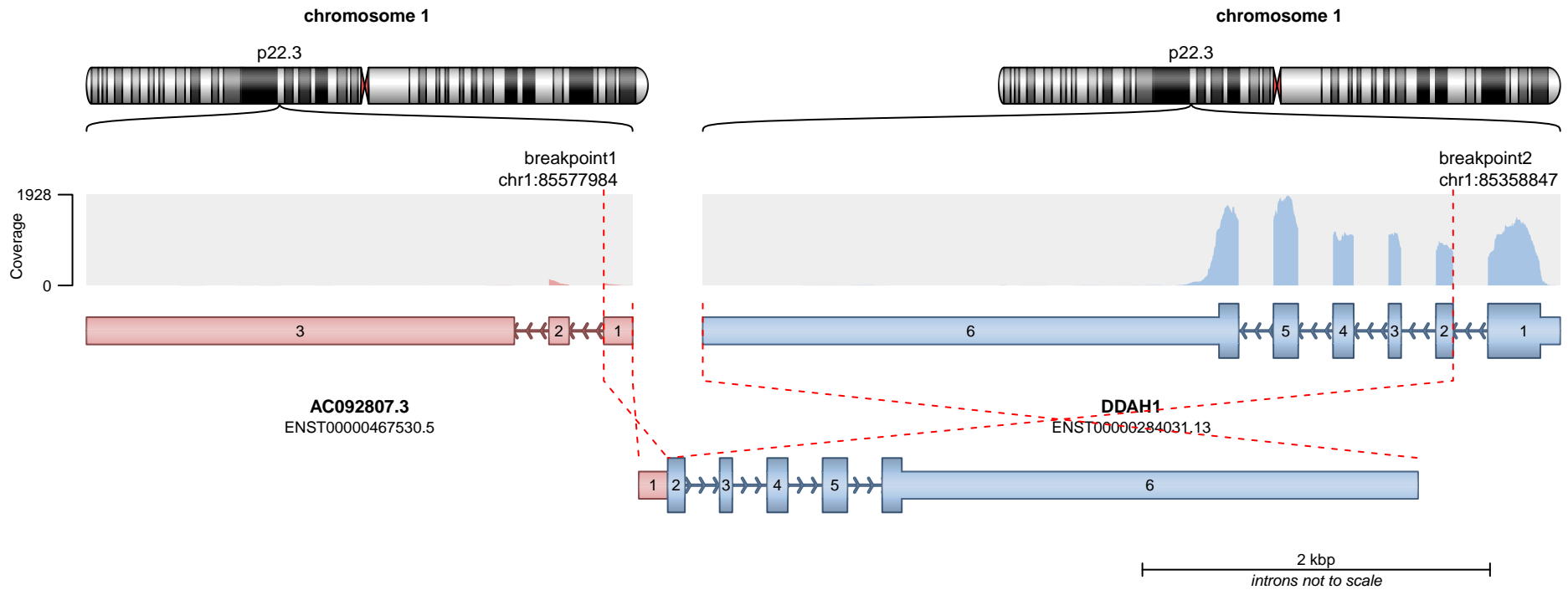
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



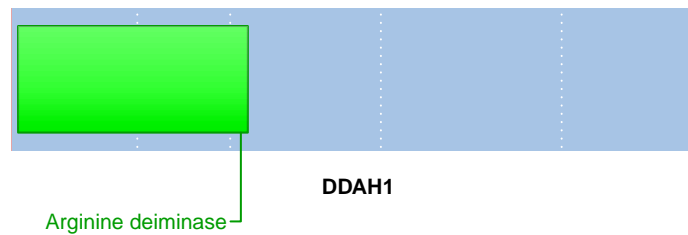
**SUPPORTING READ COUNT**

Split reads = 40  
Discordant mates = 1

— translocation — deletion  
— duplication — inversion



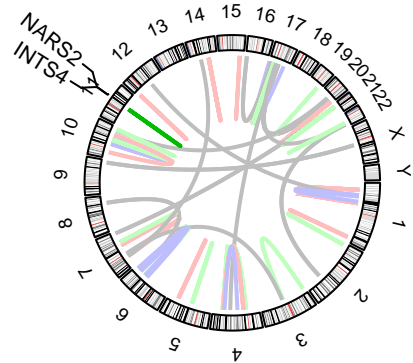
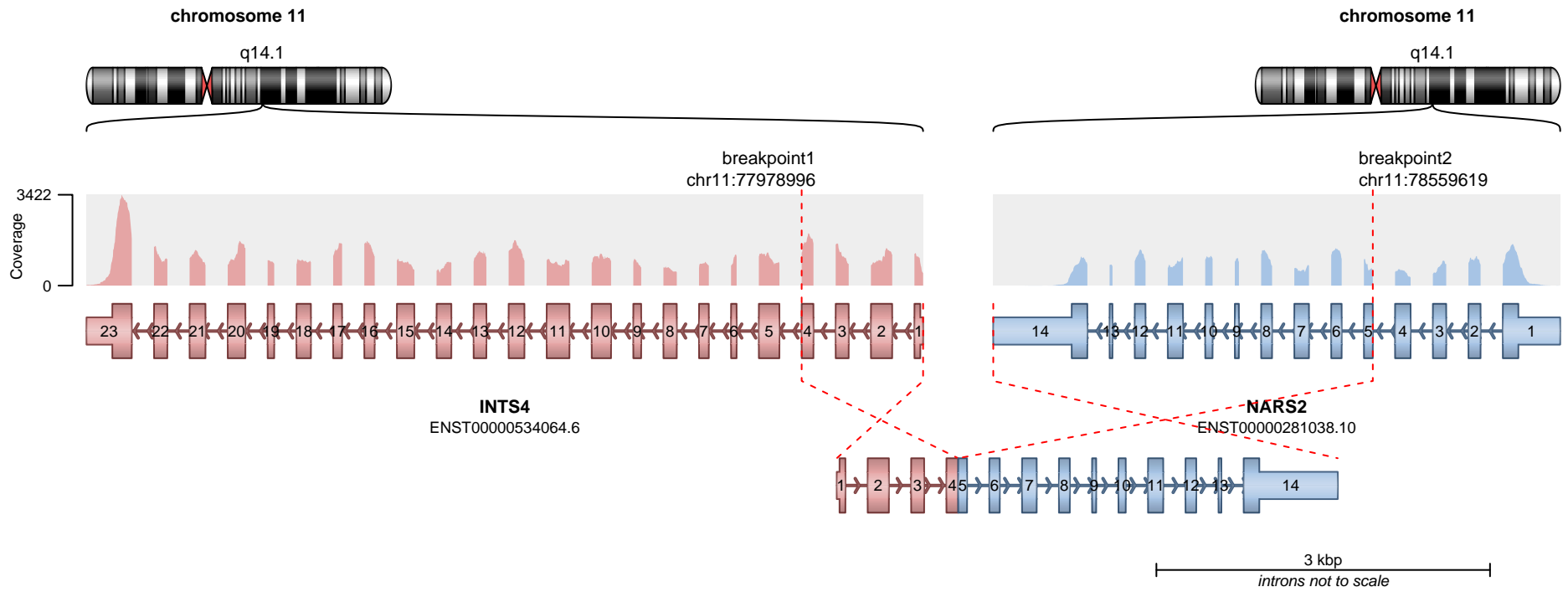
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



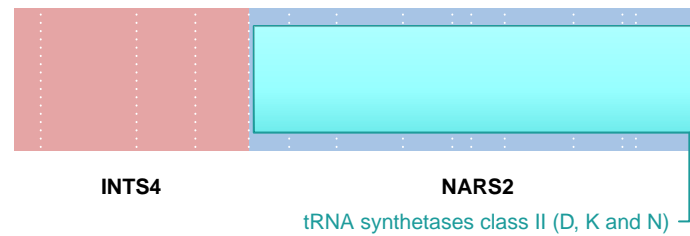
**SUPPORTING READ COUNT**

Split reads = 15  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



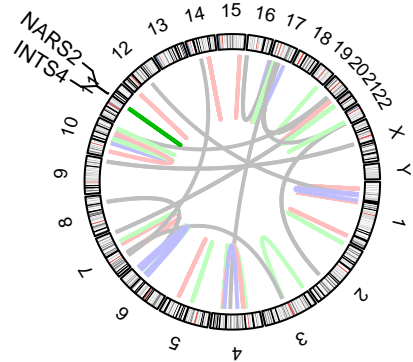
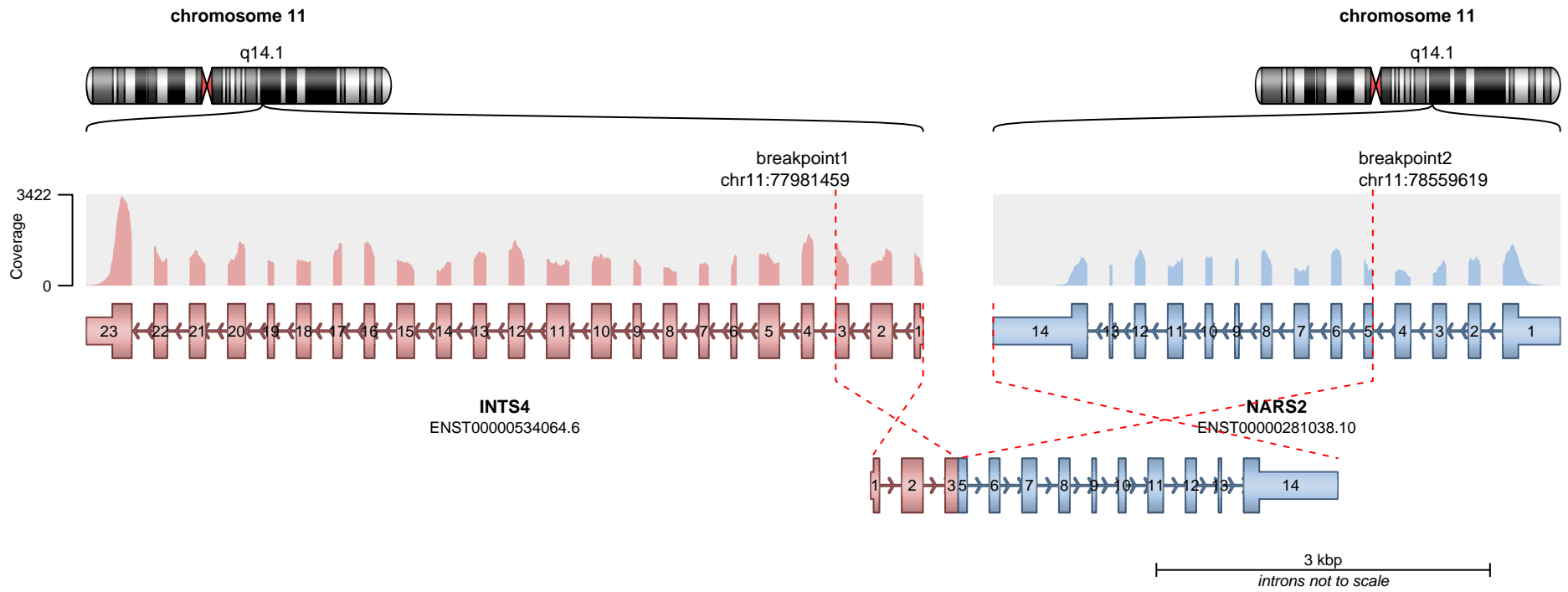
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



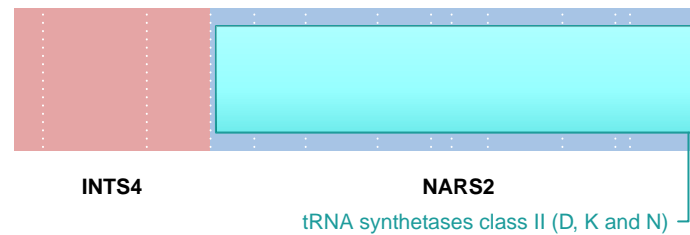
**SUPPORTING READ COUNT**

Split reads = 37  
Discordant mates = 1

— translocation    — deletion  
— duplication    — inversion



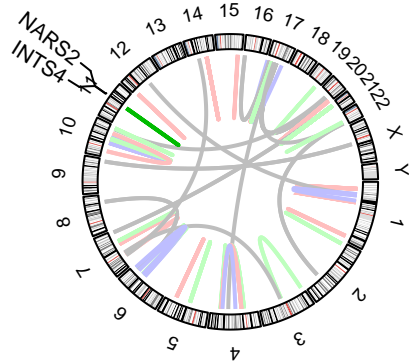
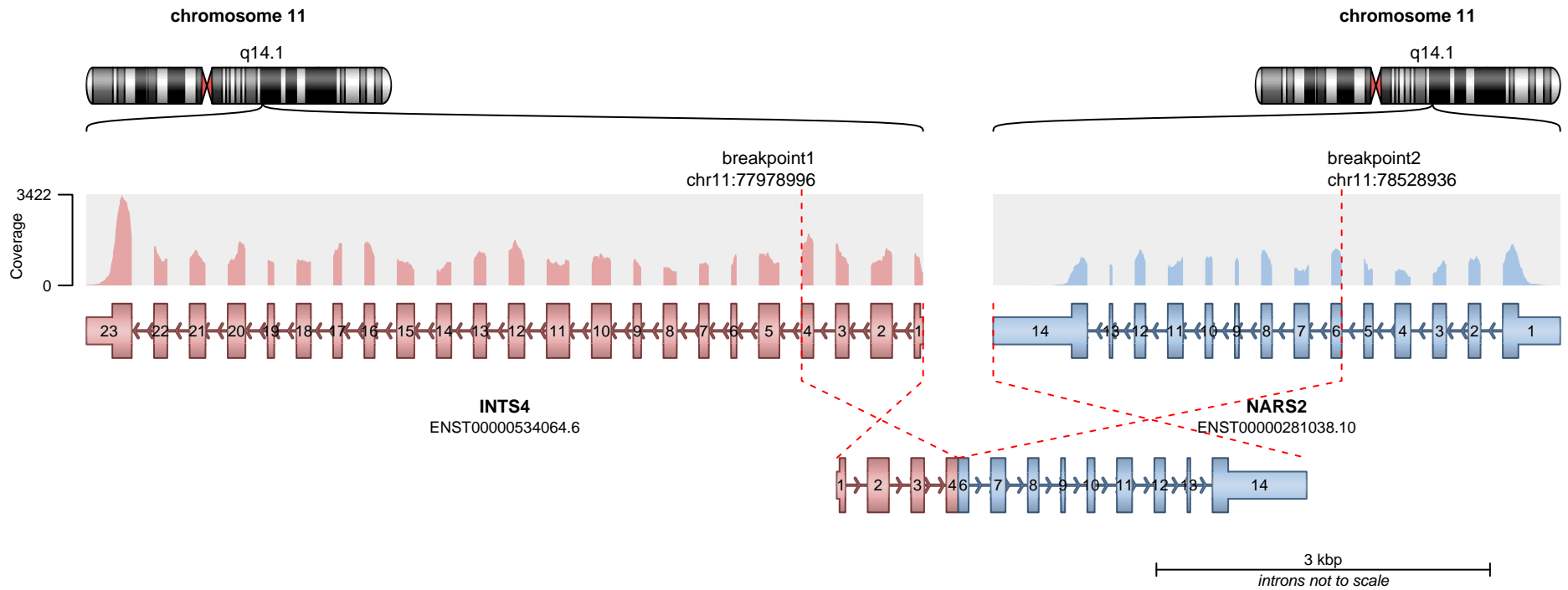
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



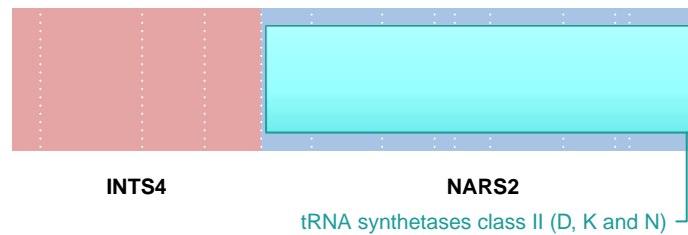
**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



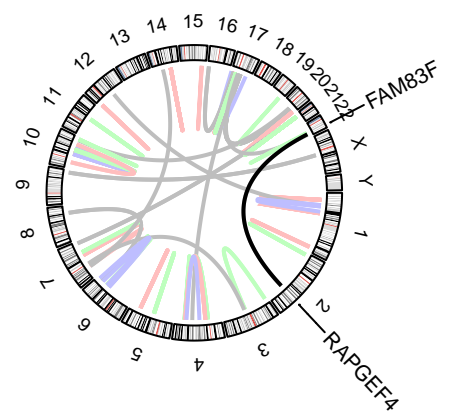
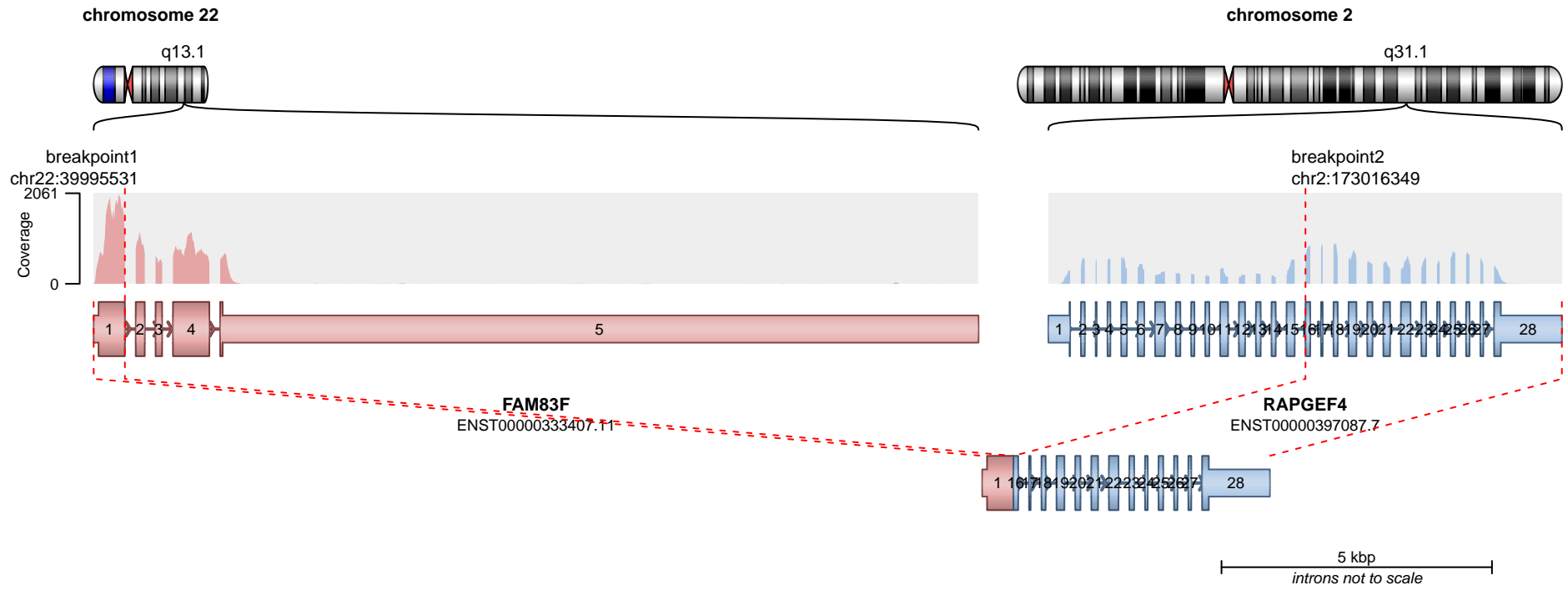
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



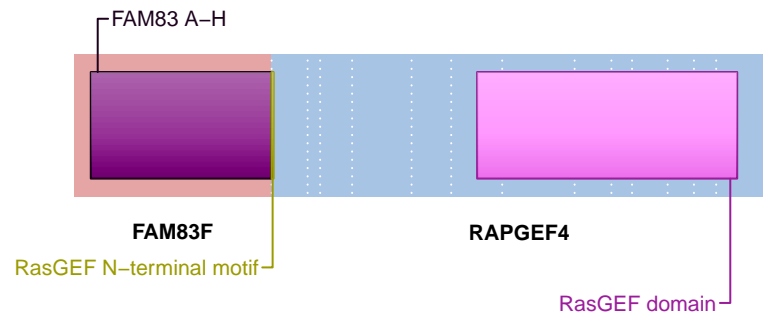
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



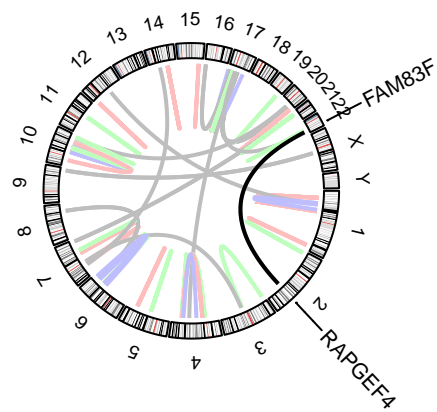
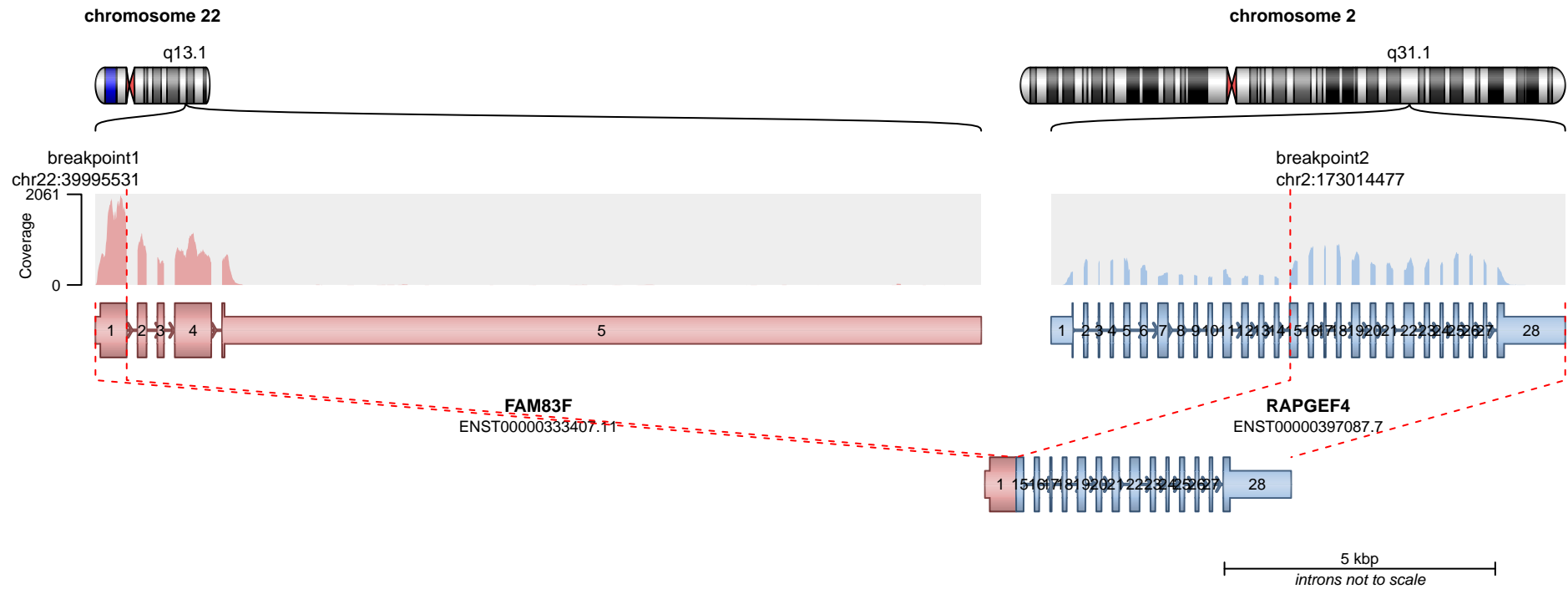
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



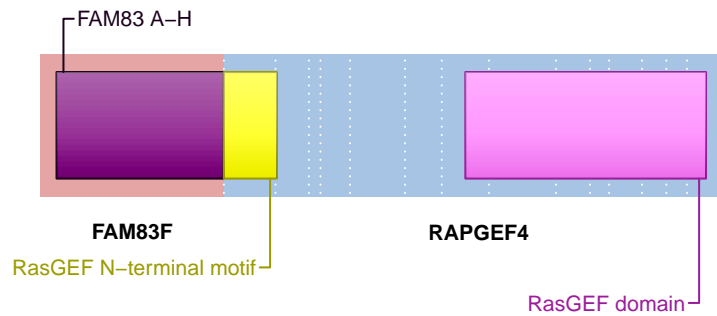
**SUPPORTING READ COUNT**

Split reads = 37  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



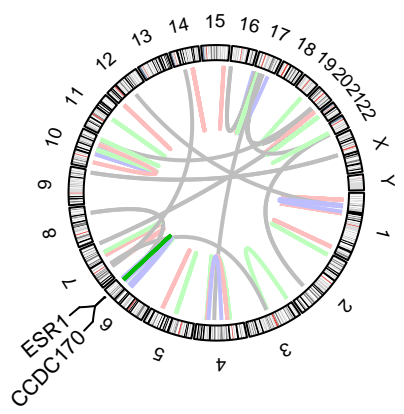
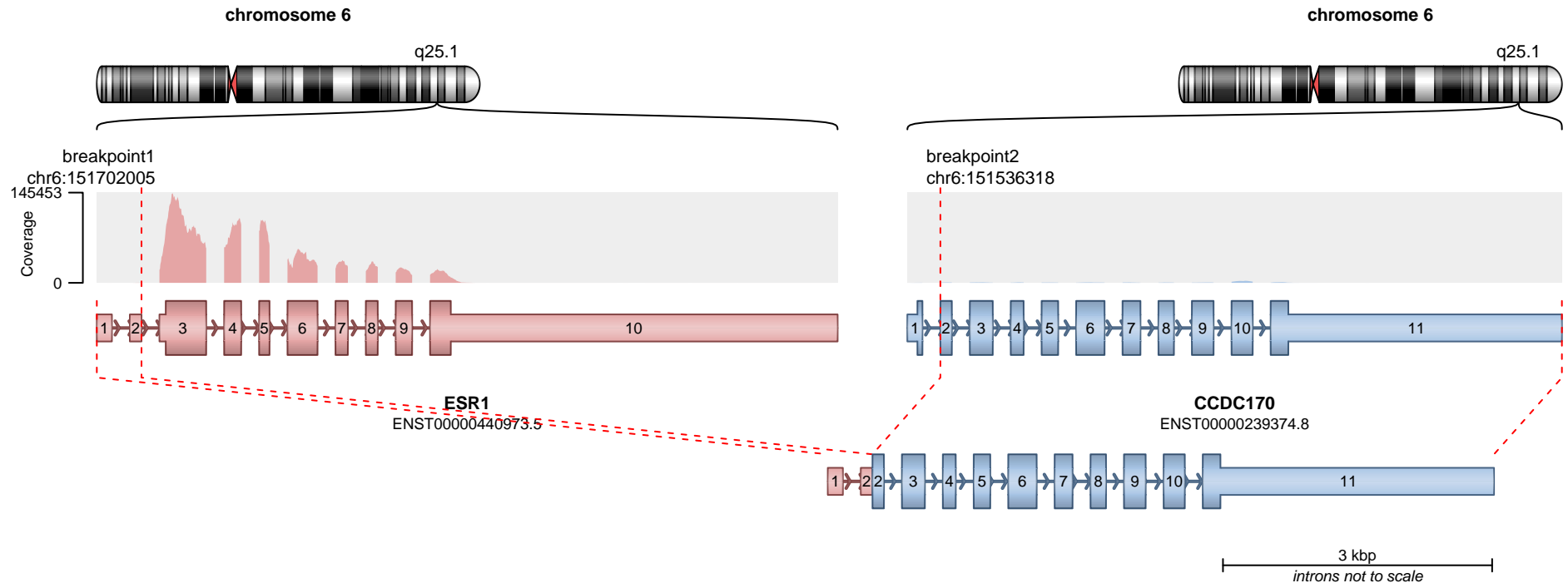
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 22  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

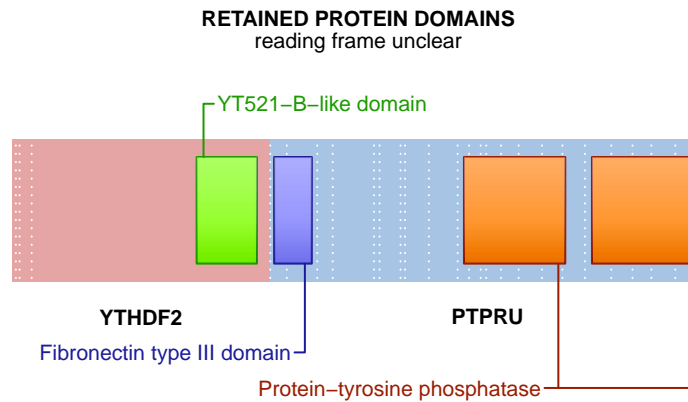
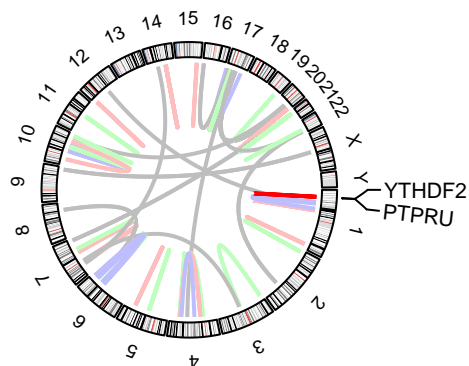
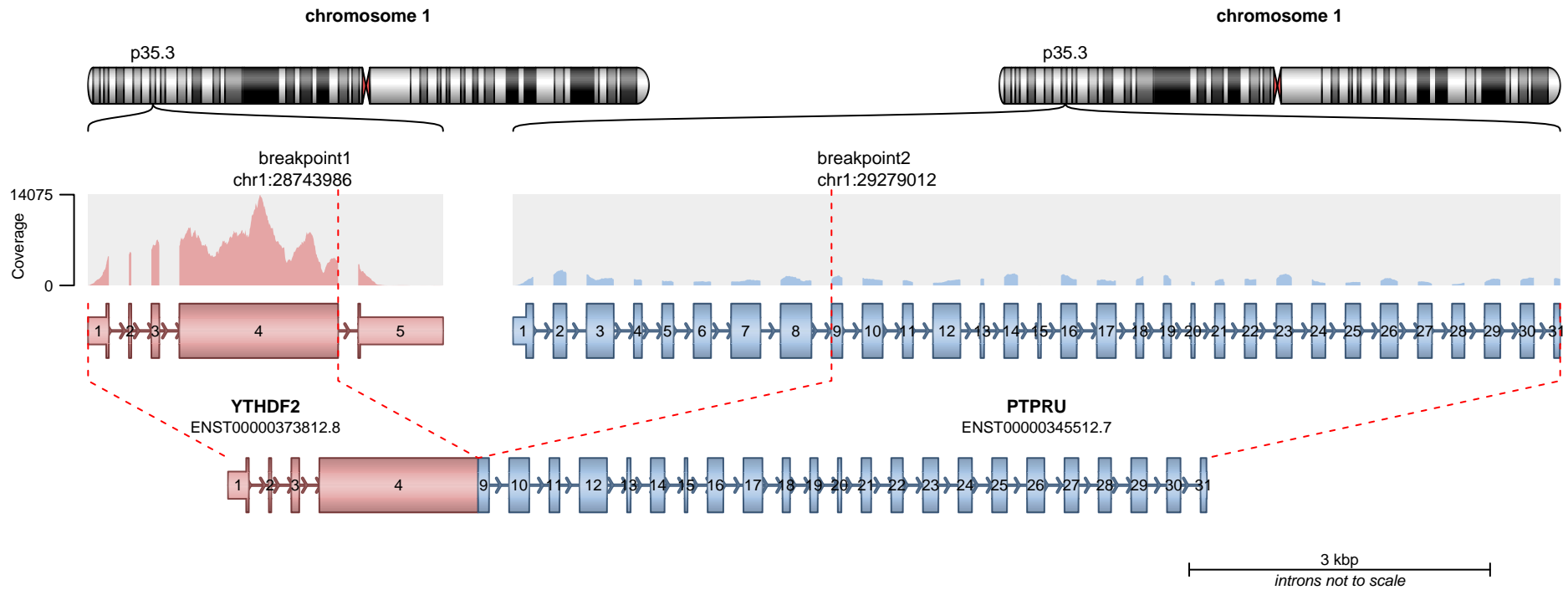


— translocation    — deletion  
— duplication    — inversion

No protein domains retained in fusion.

**SUPPORTING READ COUNT**

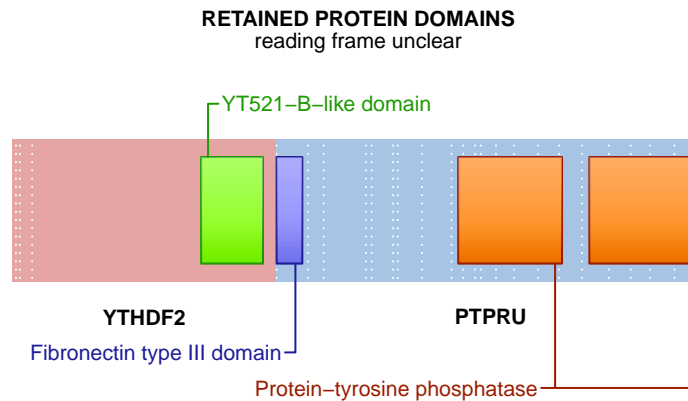
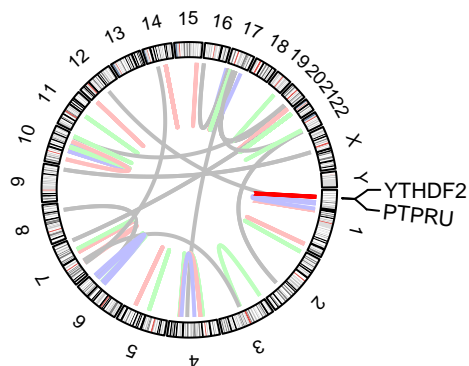
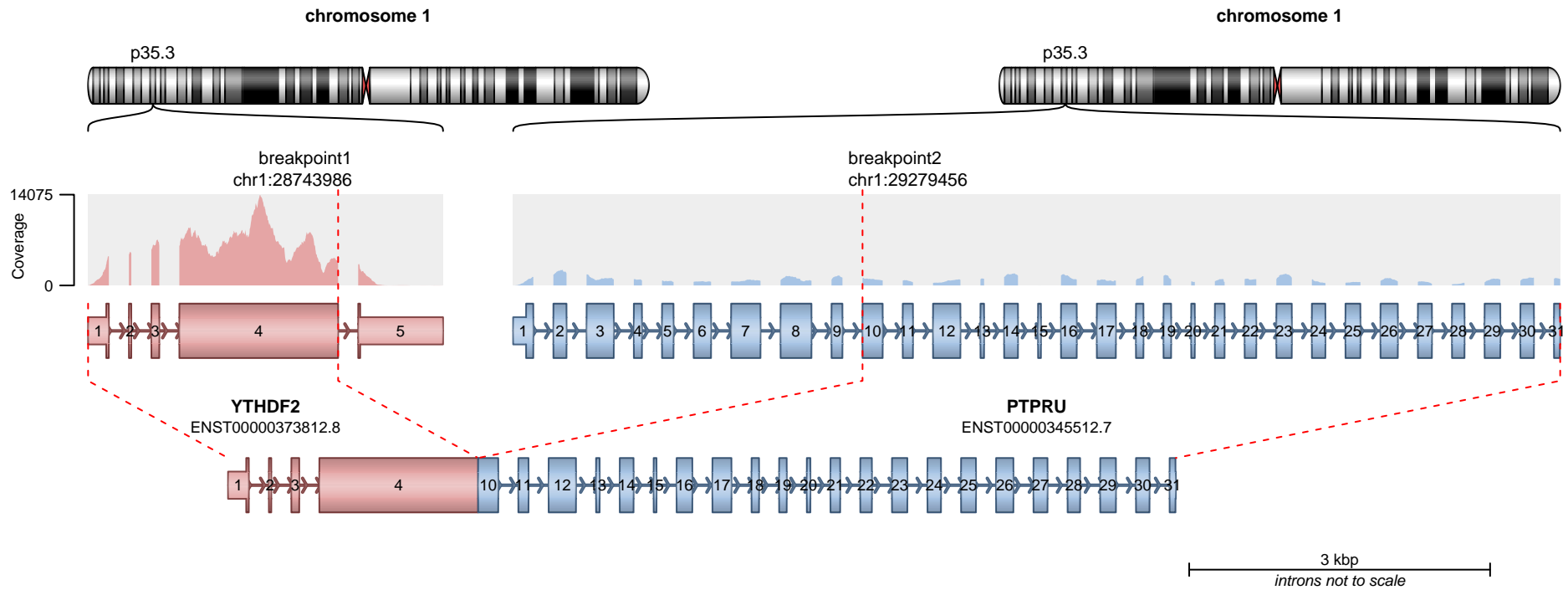
Split reads = 35  
Discordant mates = 2



**SUPPORTING READ COUNT**

Split reads = 31  
Discordant mates = 0

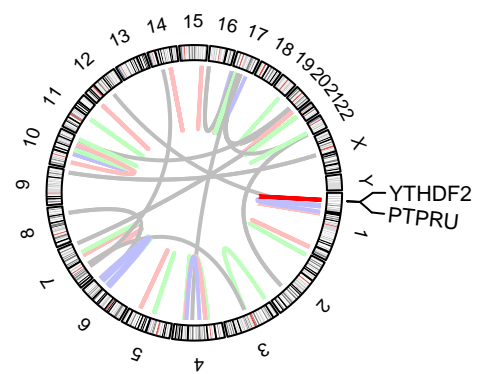
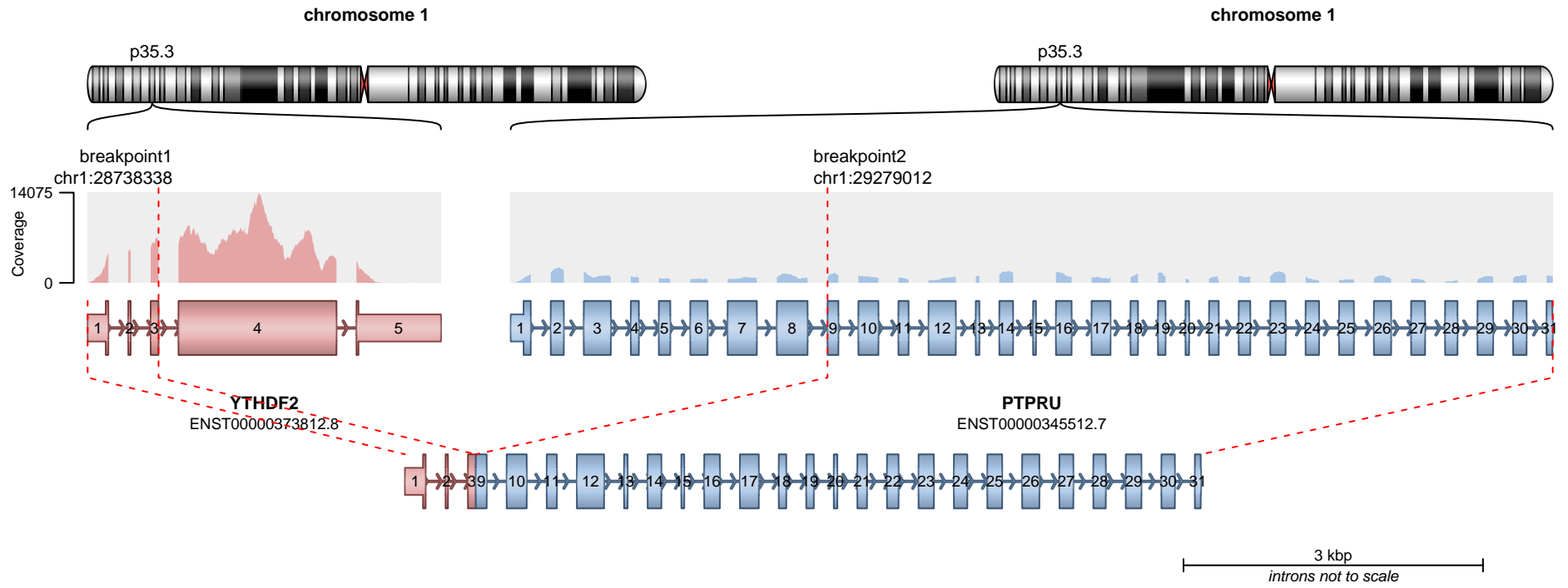
- translocation
- duplication
- deletion
- inversion



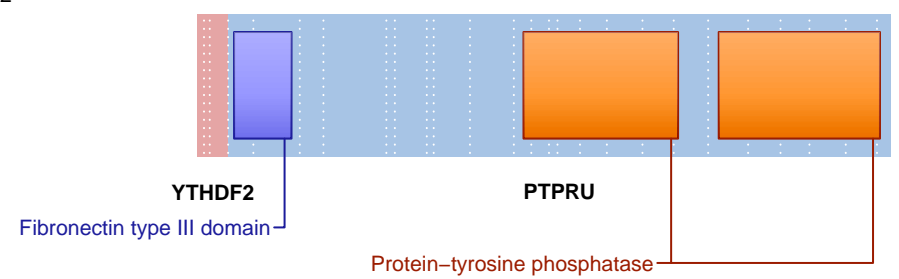
**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



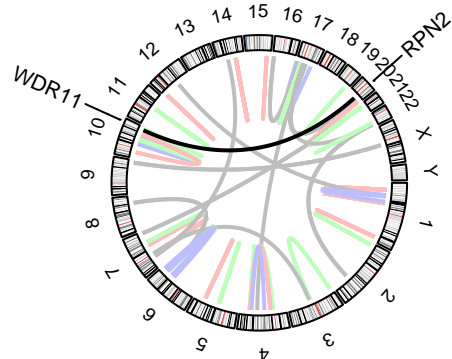
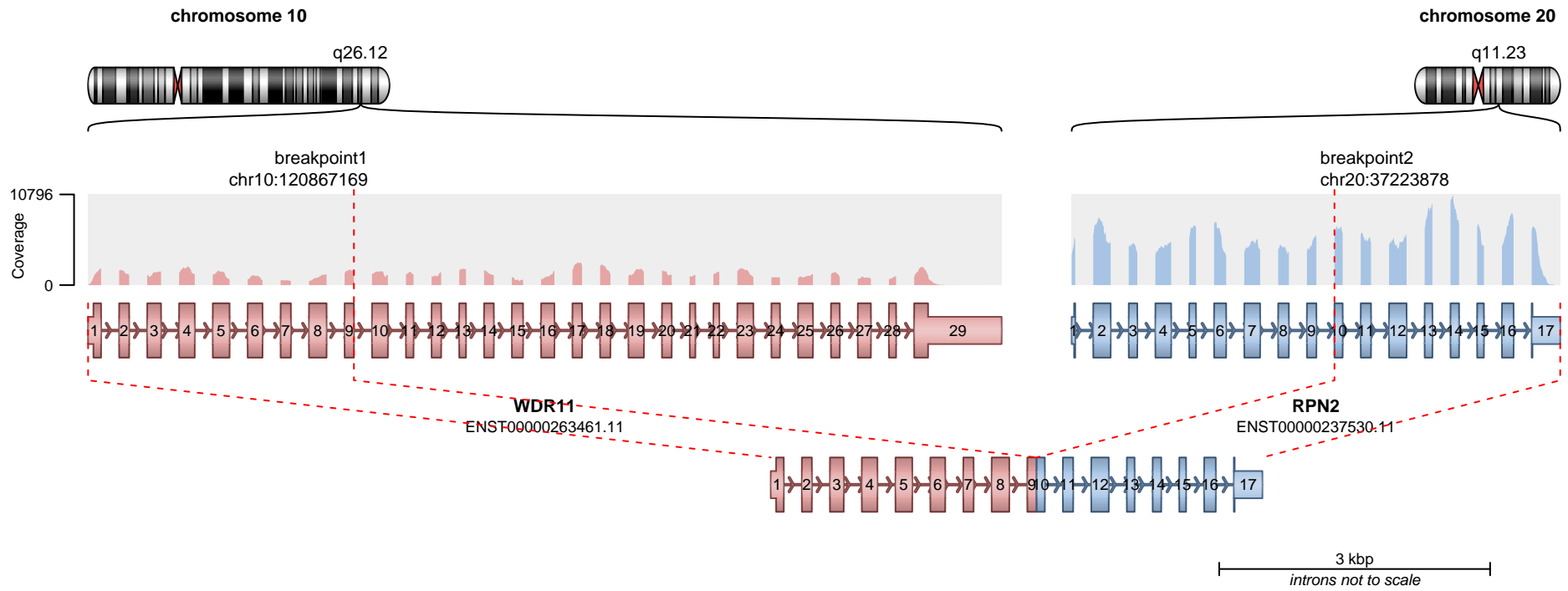
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



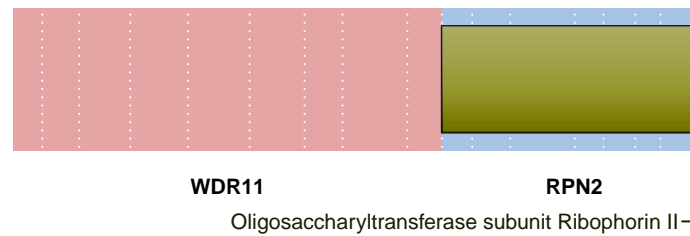
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



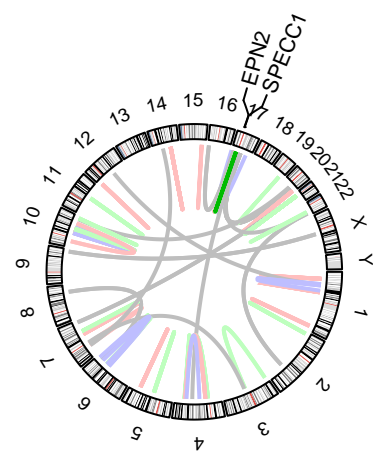
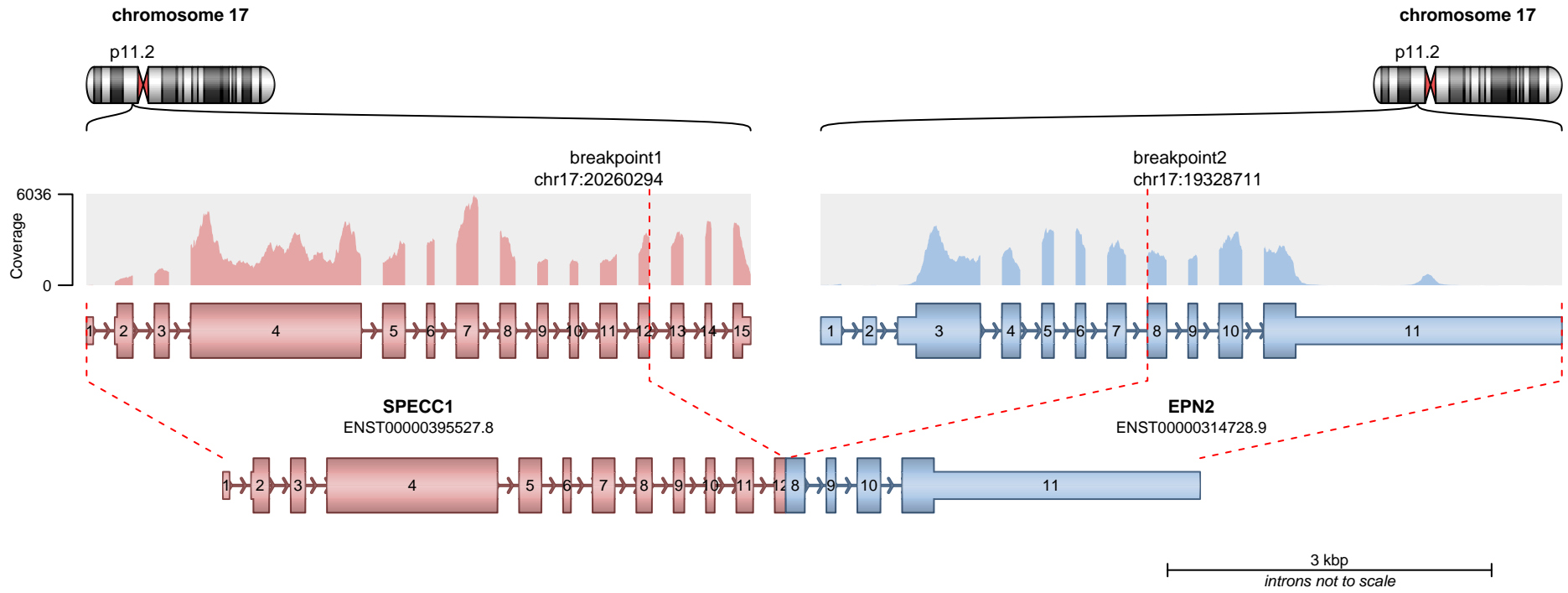
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



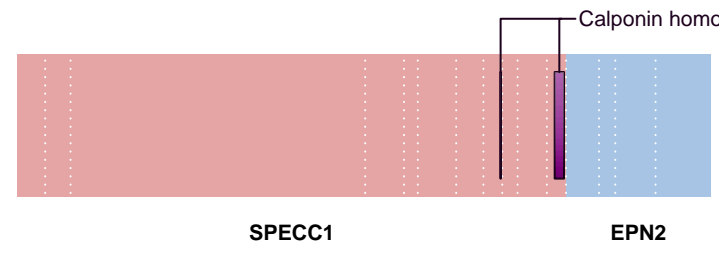
**SUPPORTING READ COUNT**

Split reads = 26  
Discordant mates = 1

— translocation — deletion  
— duplication — inversion



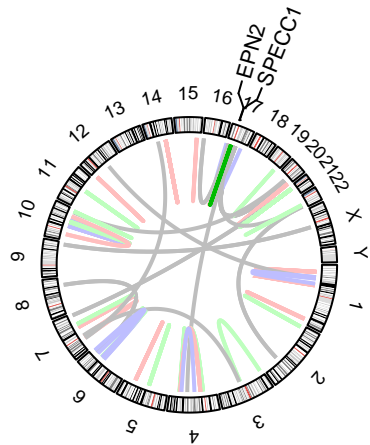
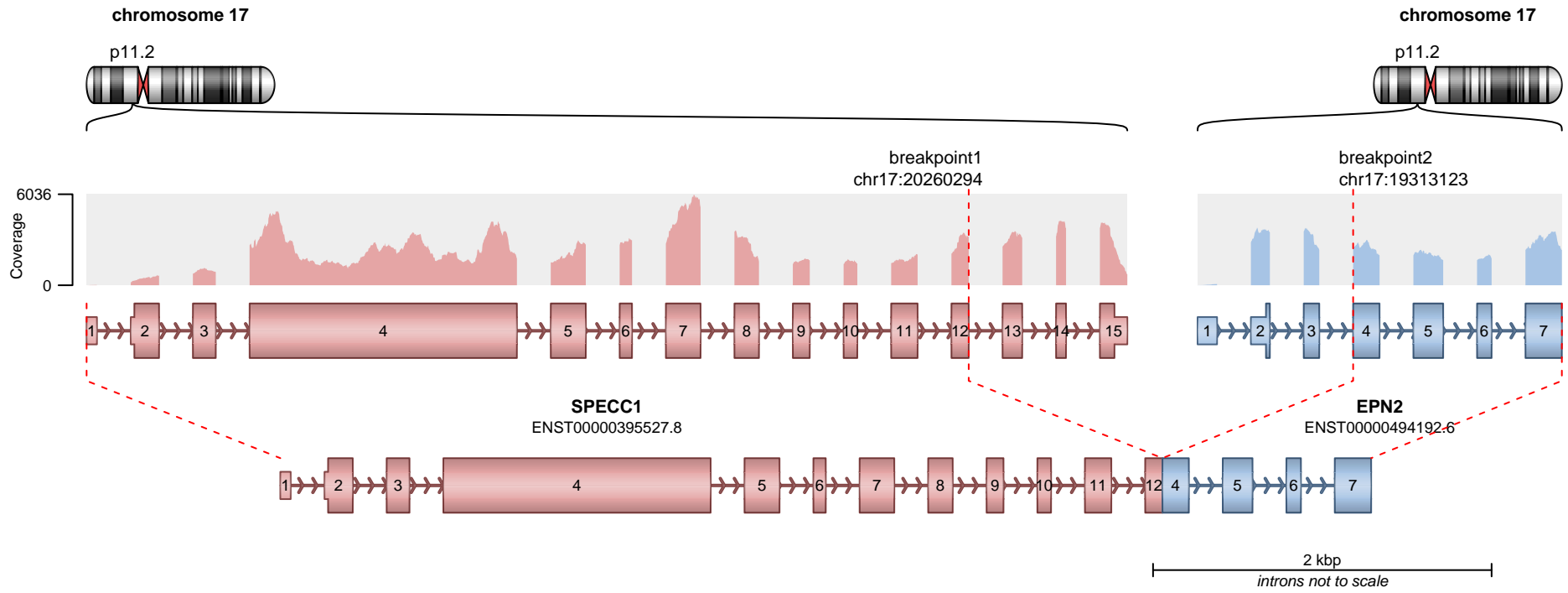
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



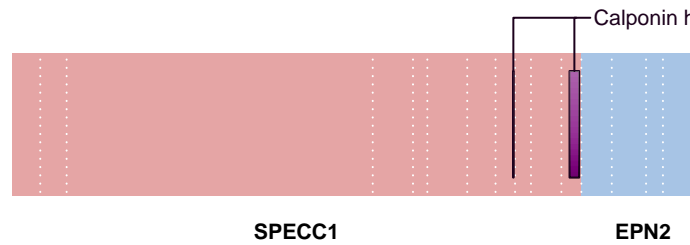
**SUPPORTING READ COUNT**

Split reads = 26  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



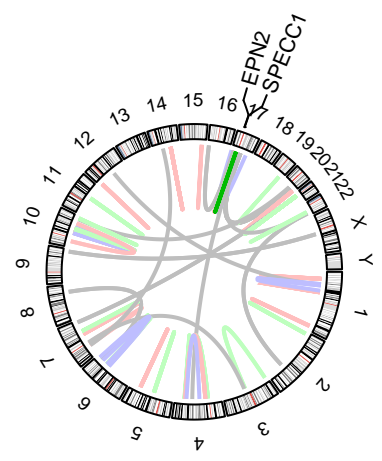
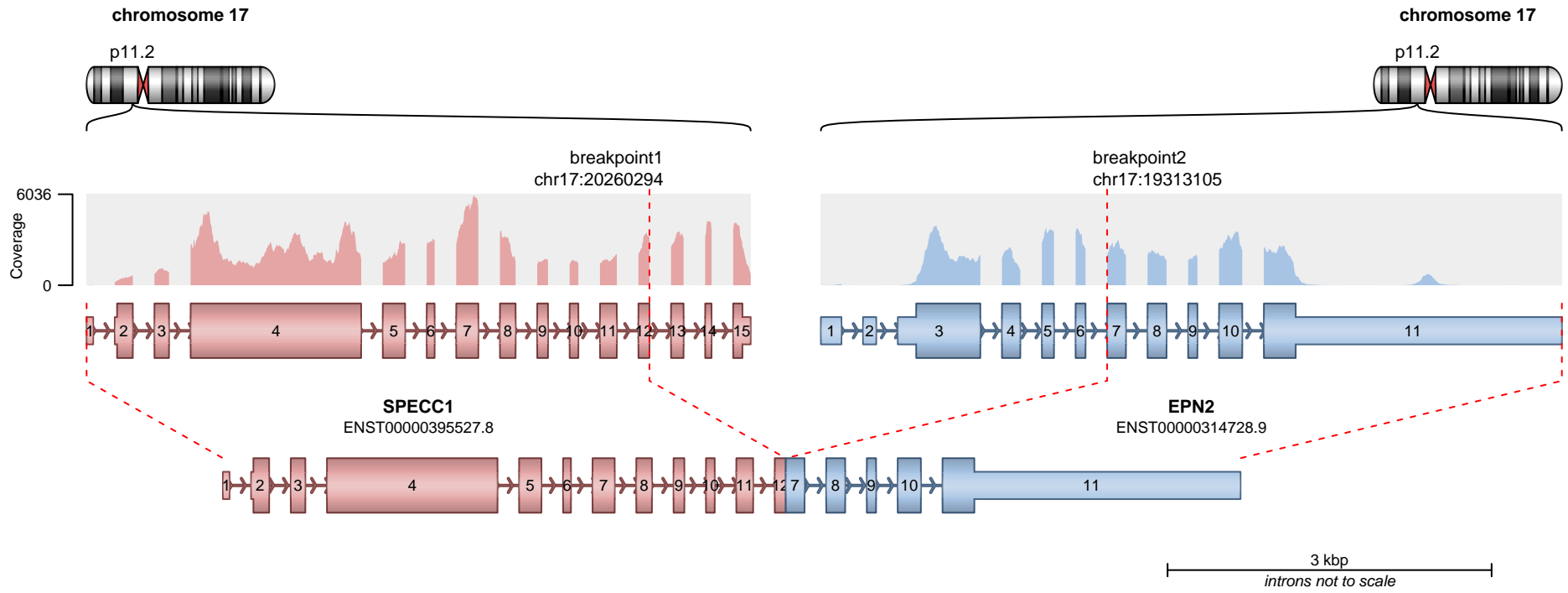
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



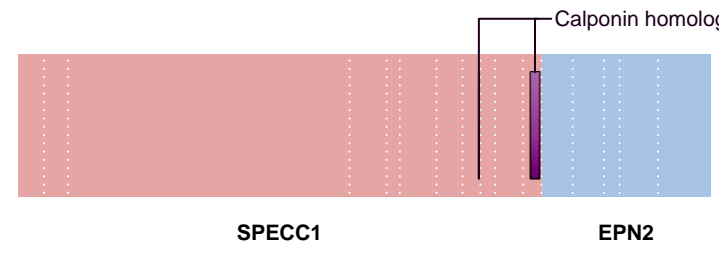
**SUPPORTING READ COUNT**

Split reads = 8  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



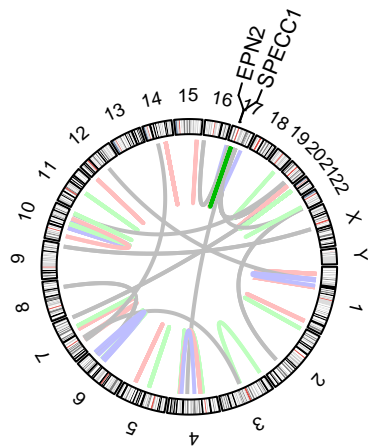
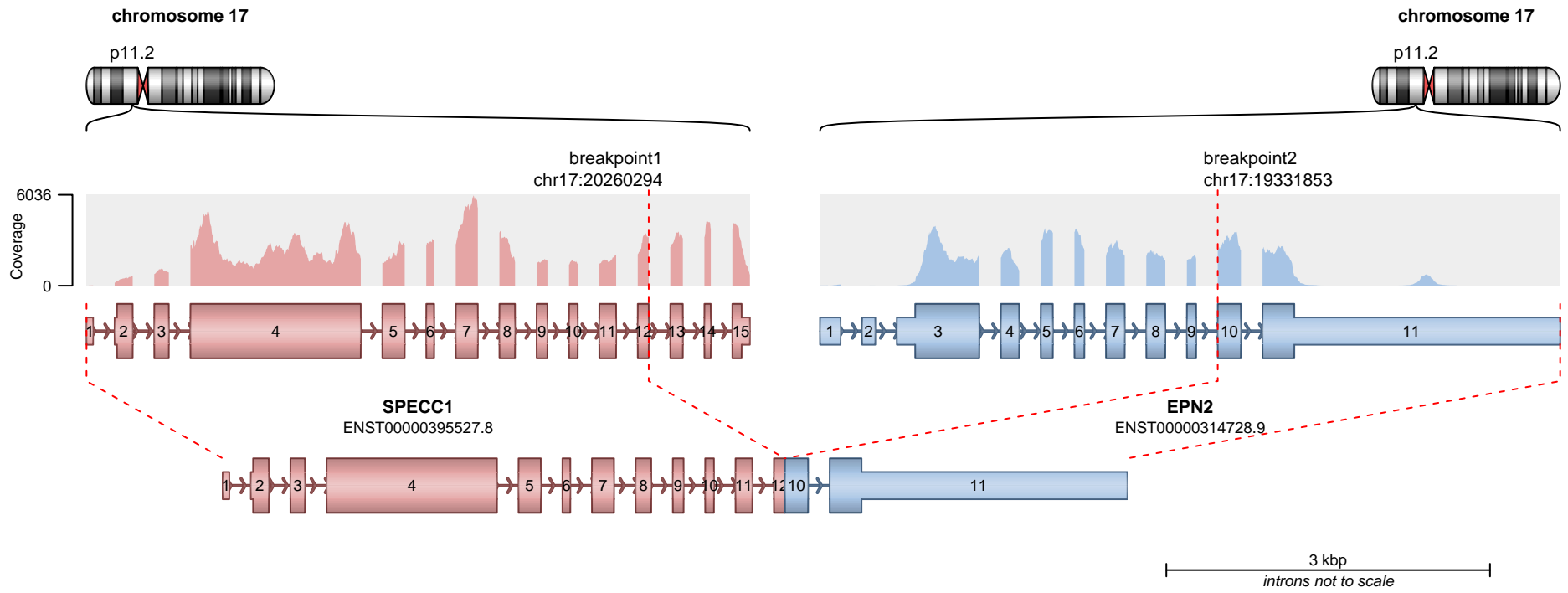
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



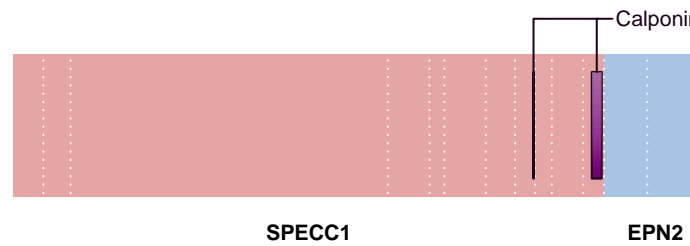
**SUPPORTING READ COUNT**

Split reads = 7  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



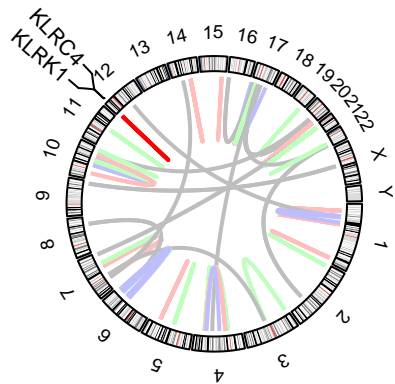
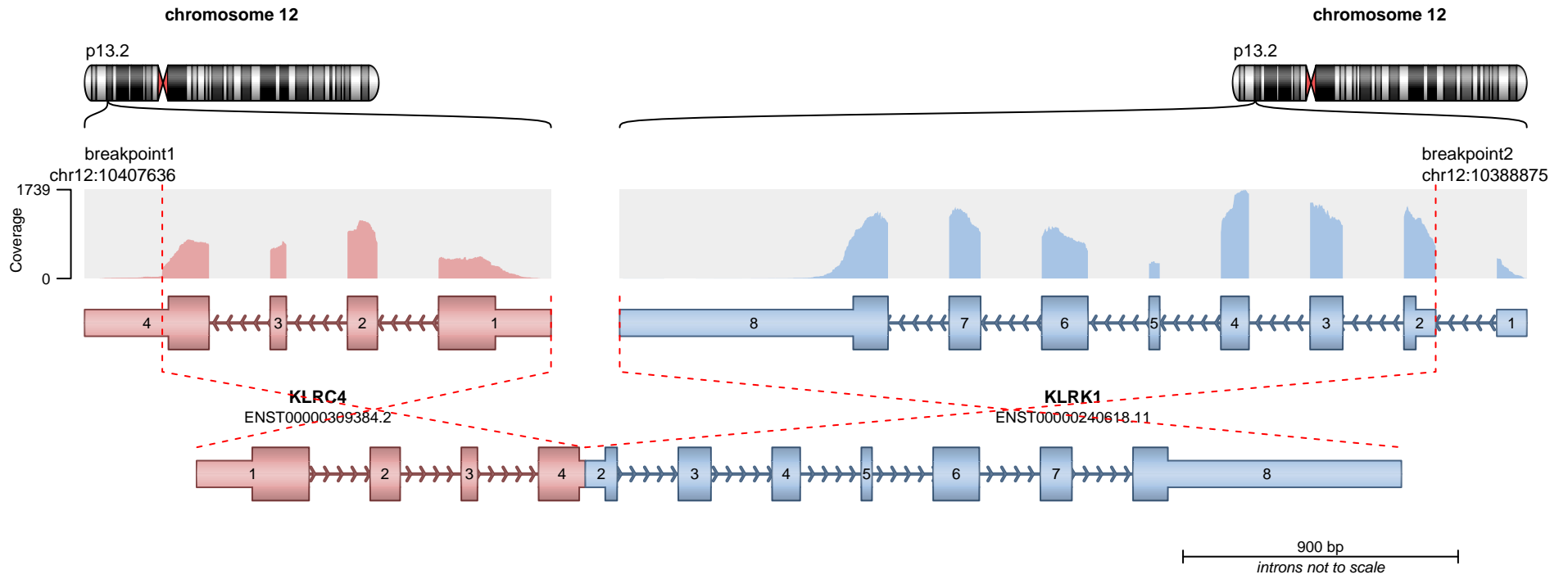
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



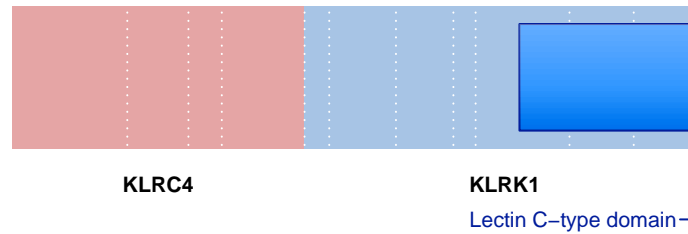
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



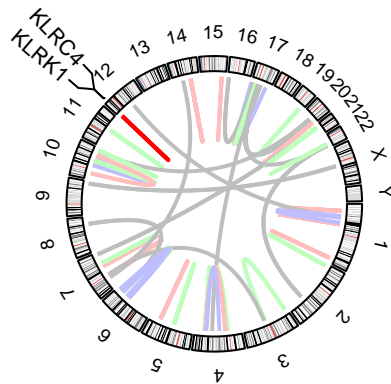
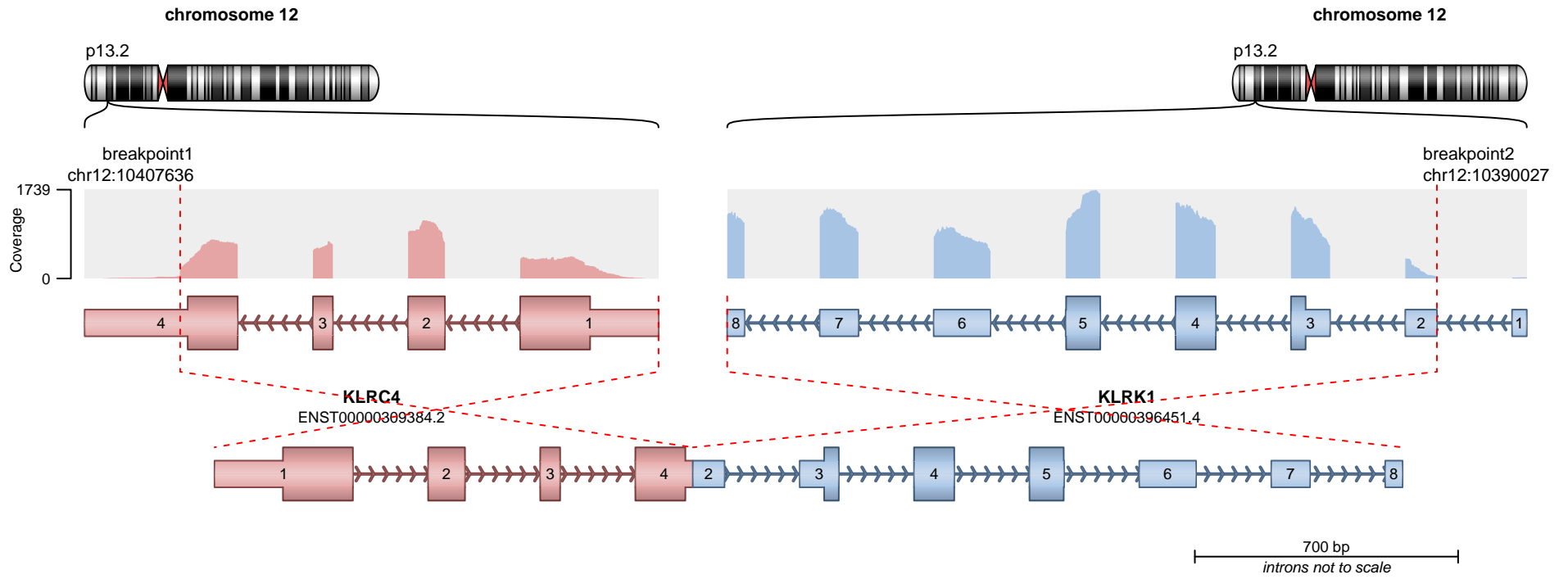
RETAINED PROTEIN DOMAINS  
reading frame unclear



SUPPORTING READ COUNT

Split reads = 25  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion

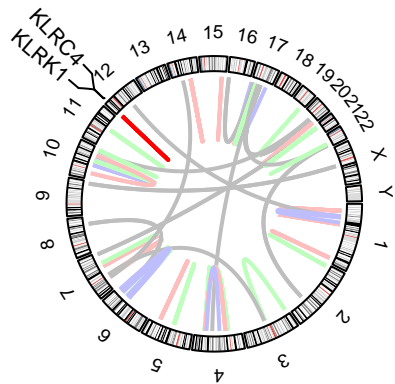
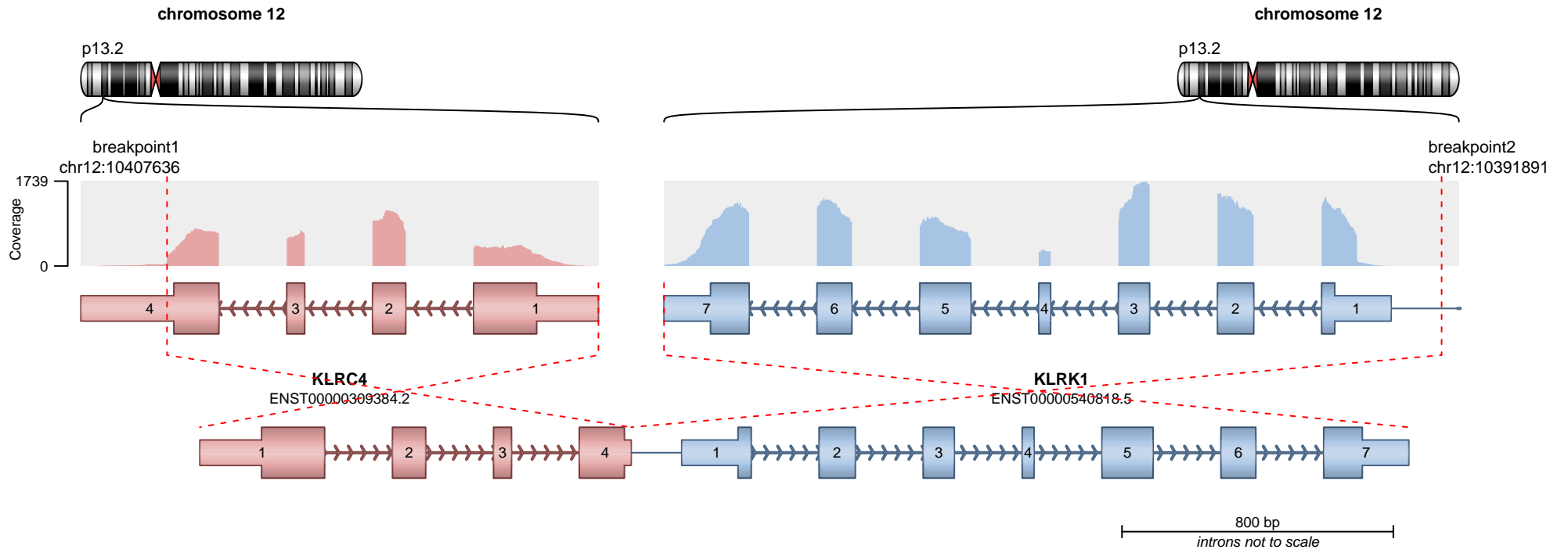


— translocation — deletion  
— duplication — inversion

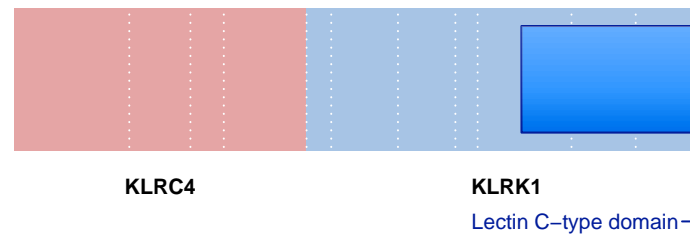
No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 0



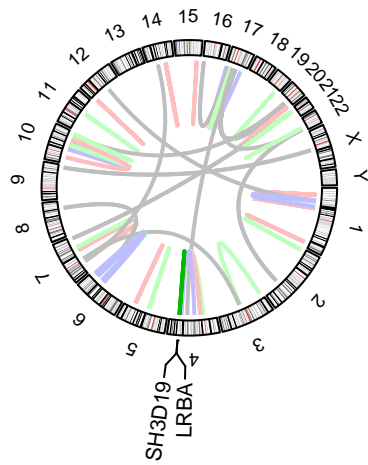
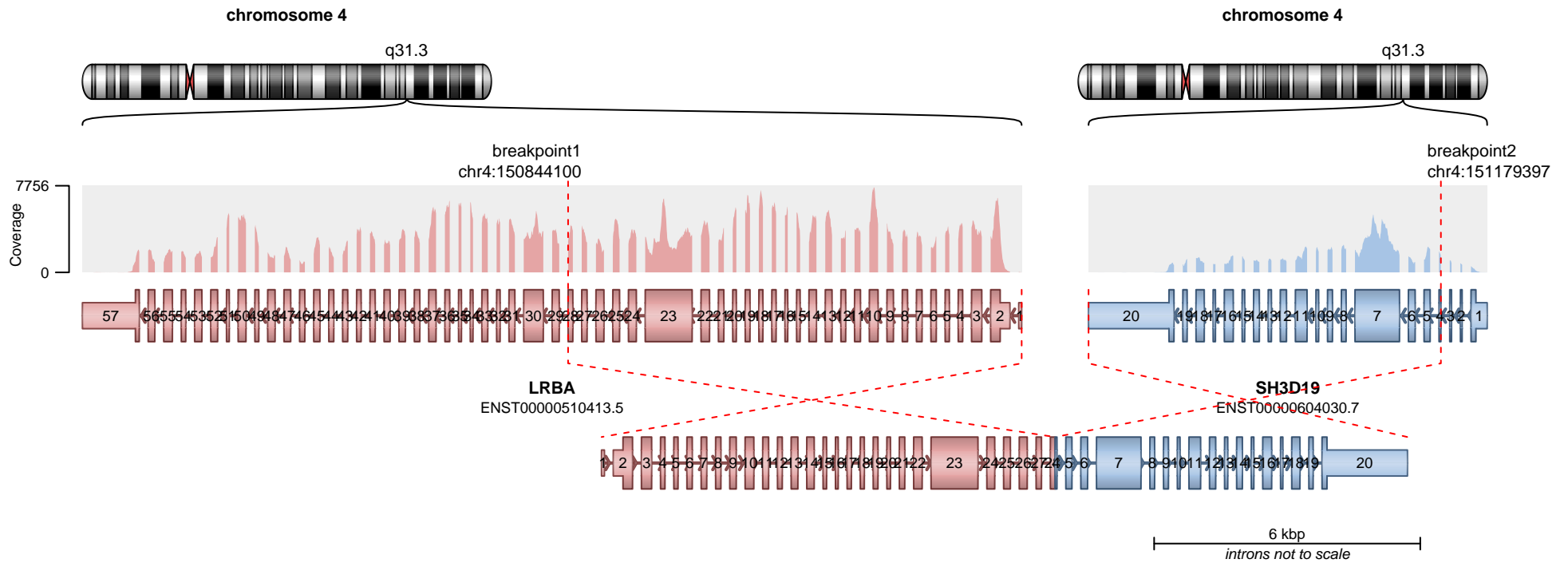
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

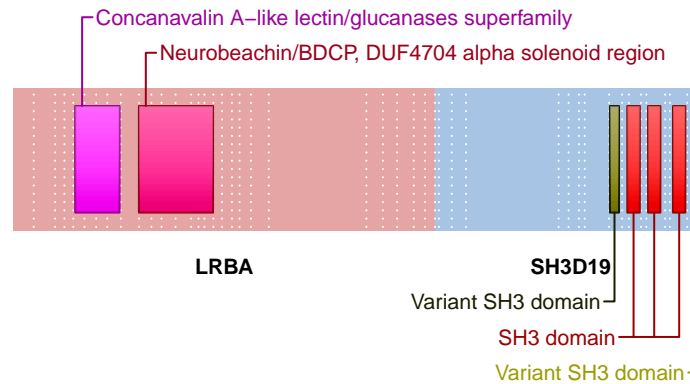
Split reads = 4  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



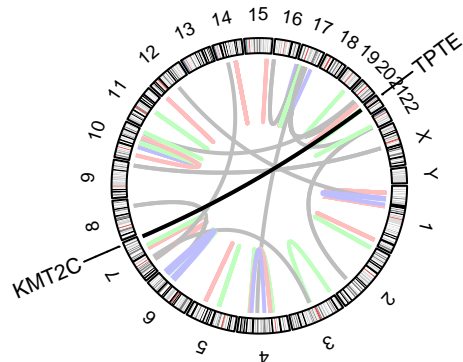
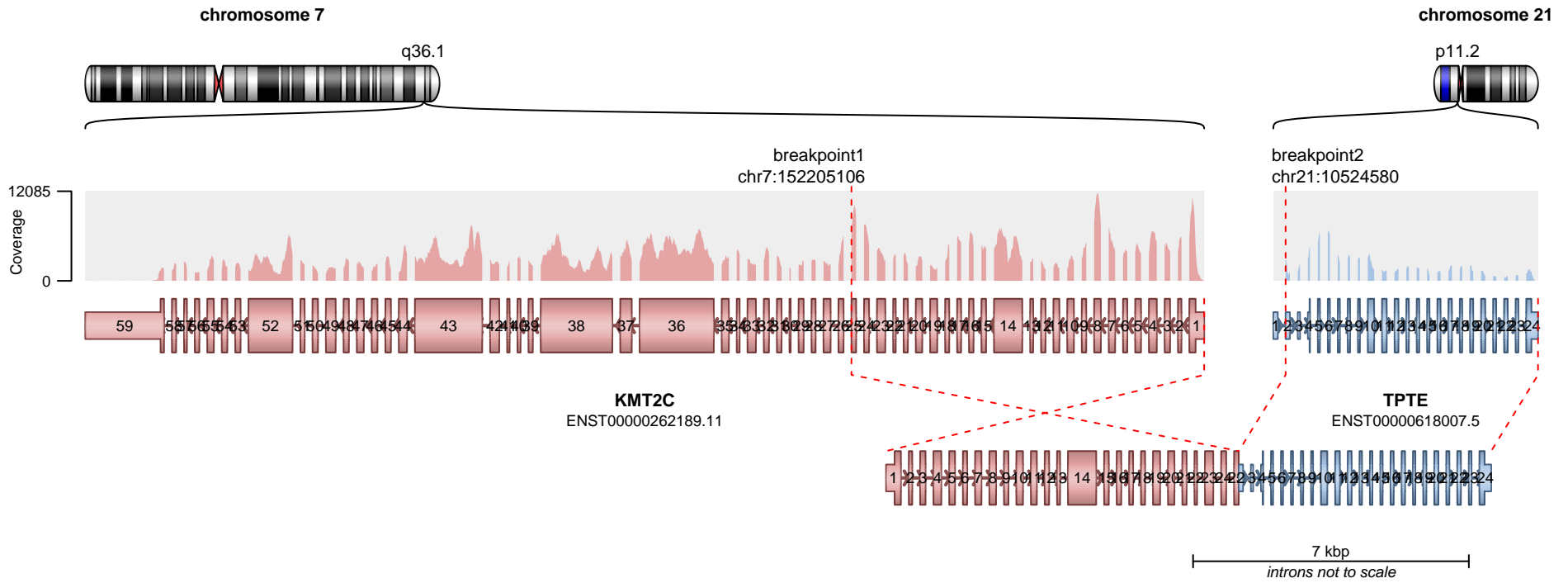
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear

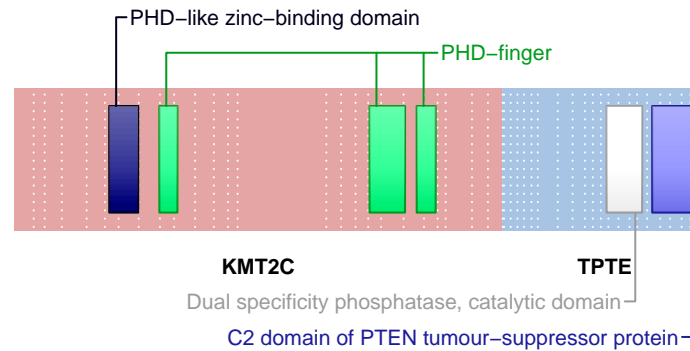


**SUPPORTING READ COUNT**

Split reads = 25  
Discordant mates = 0



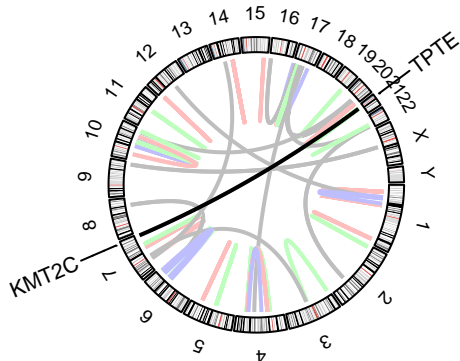
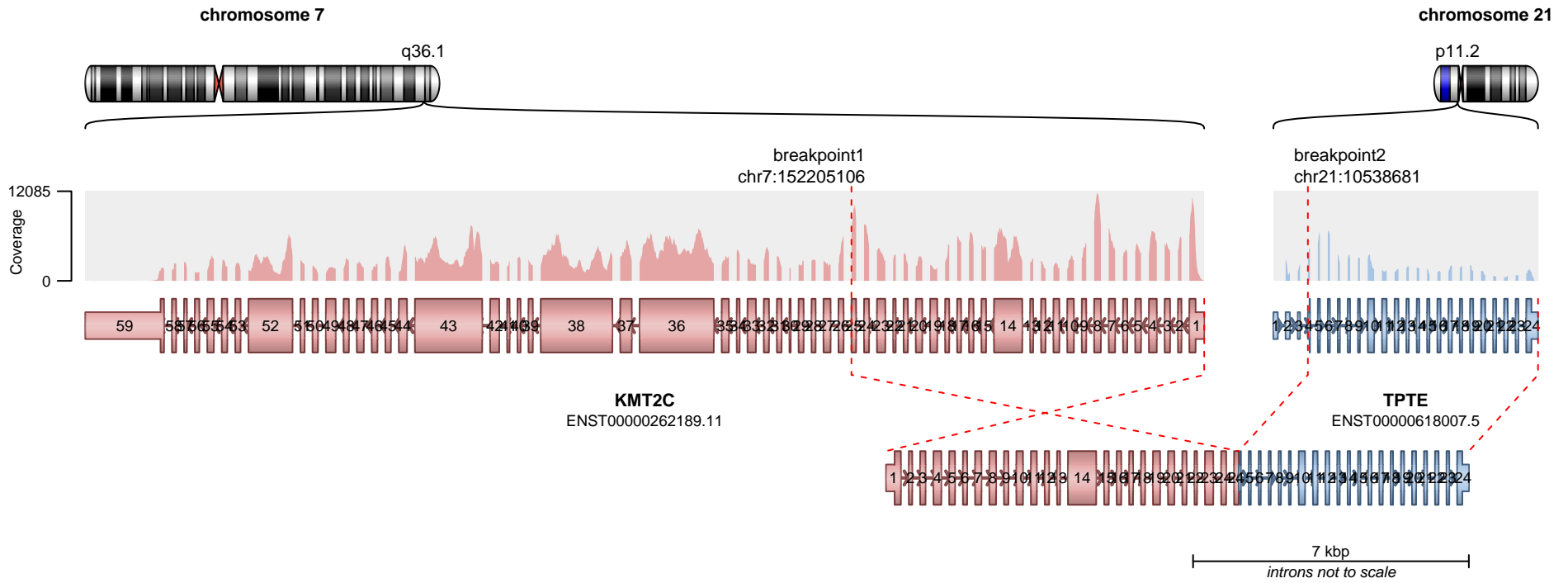
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



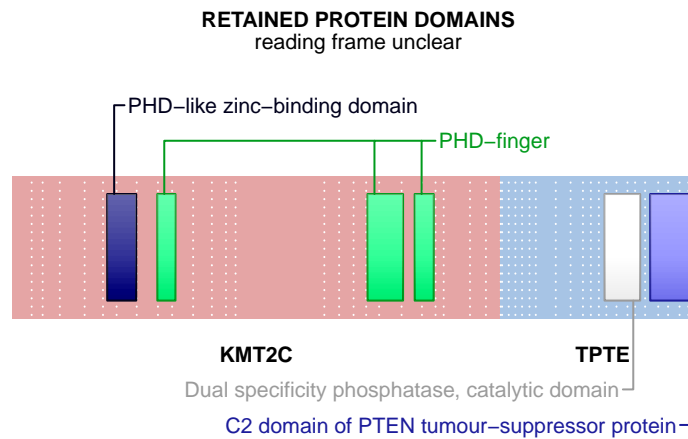
**SUPPORTING READ COUNT**

Split reads = 24  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion

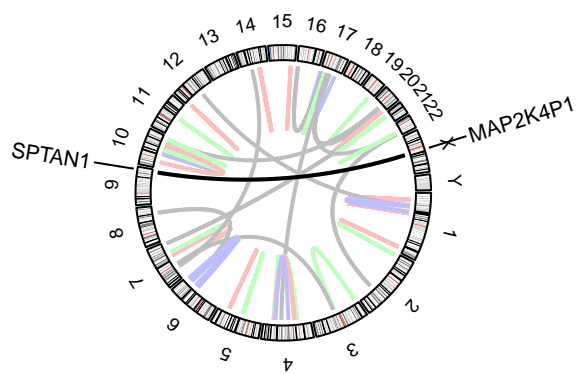
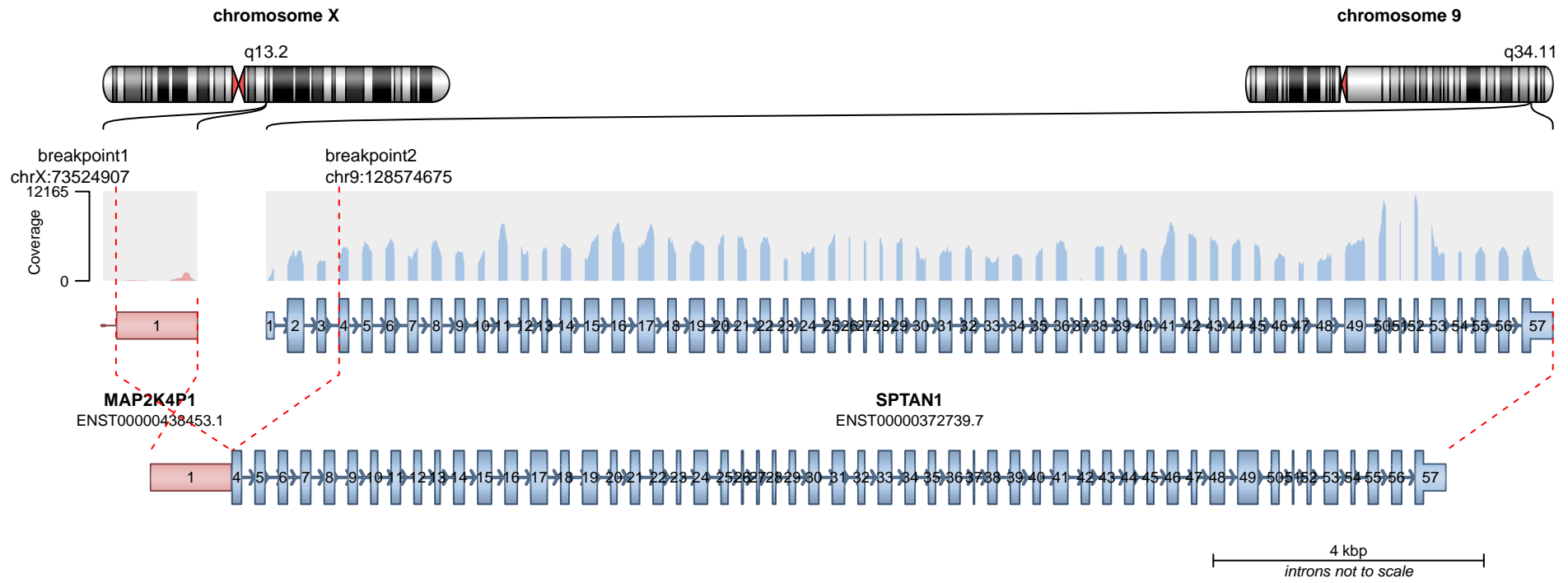


— translocation    — deletion  
— duplication    — inversion

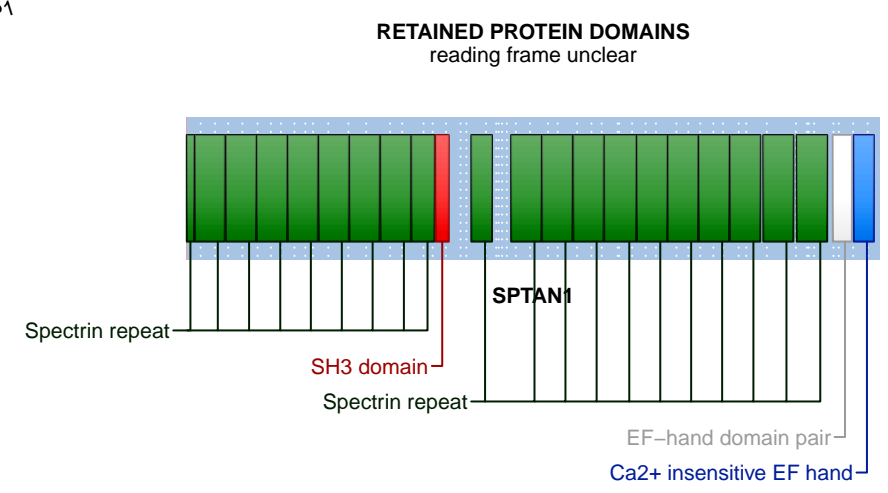


**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0

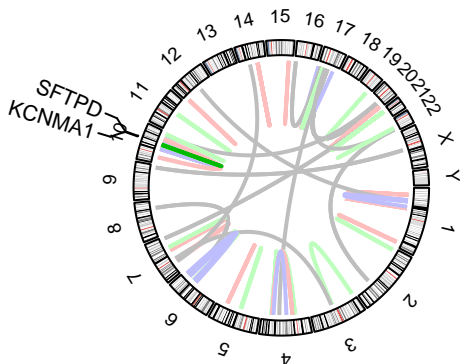
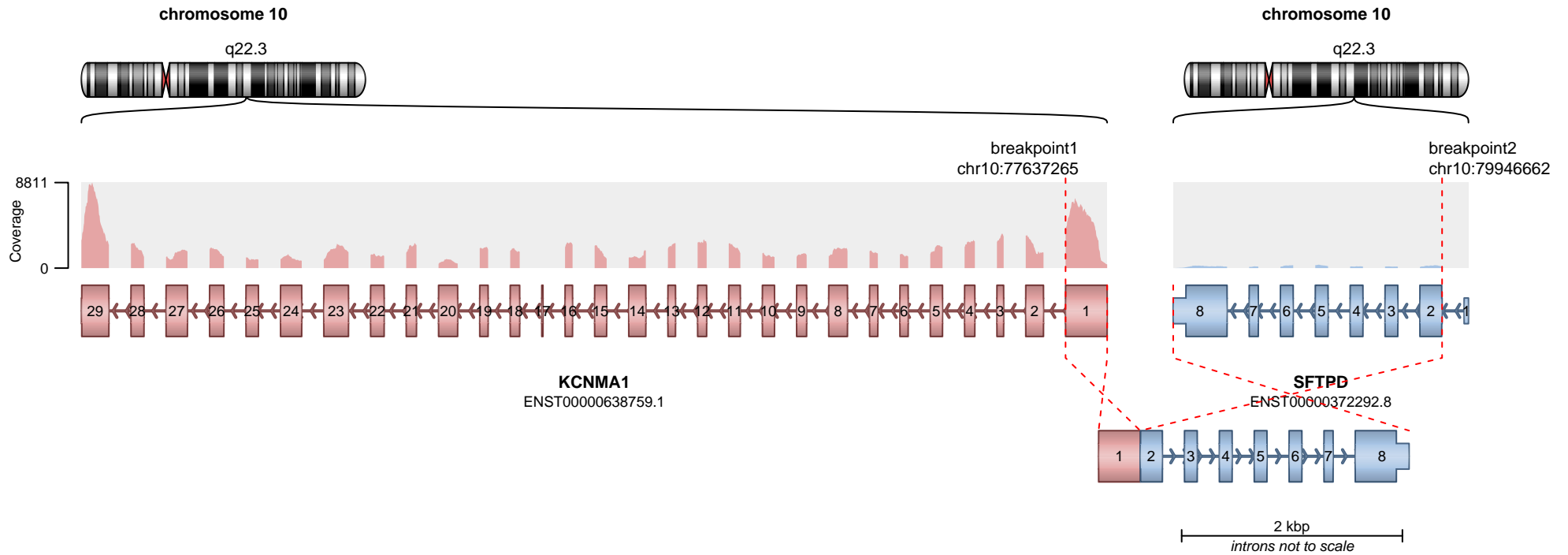


— translocation — deletion  
— duplication — inversion

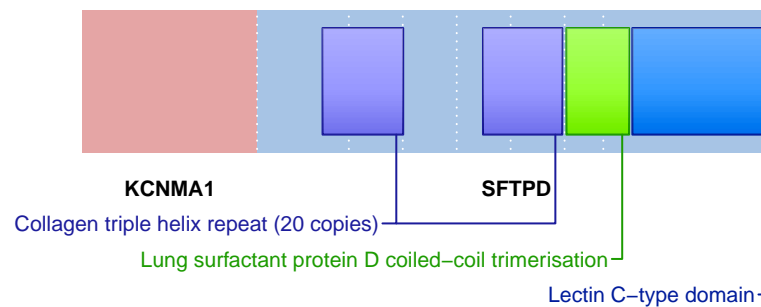


**SUPPORTING READ COUNT**

Split reads = 23  
 Discordant mates = 0



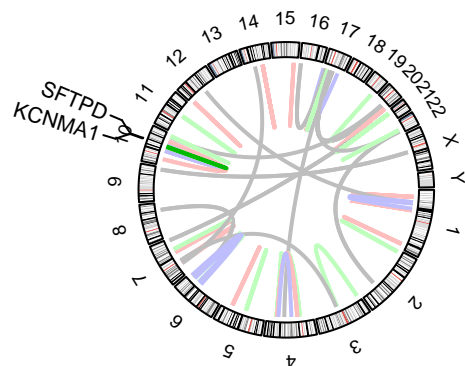
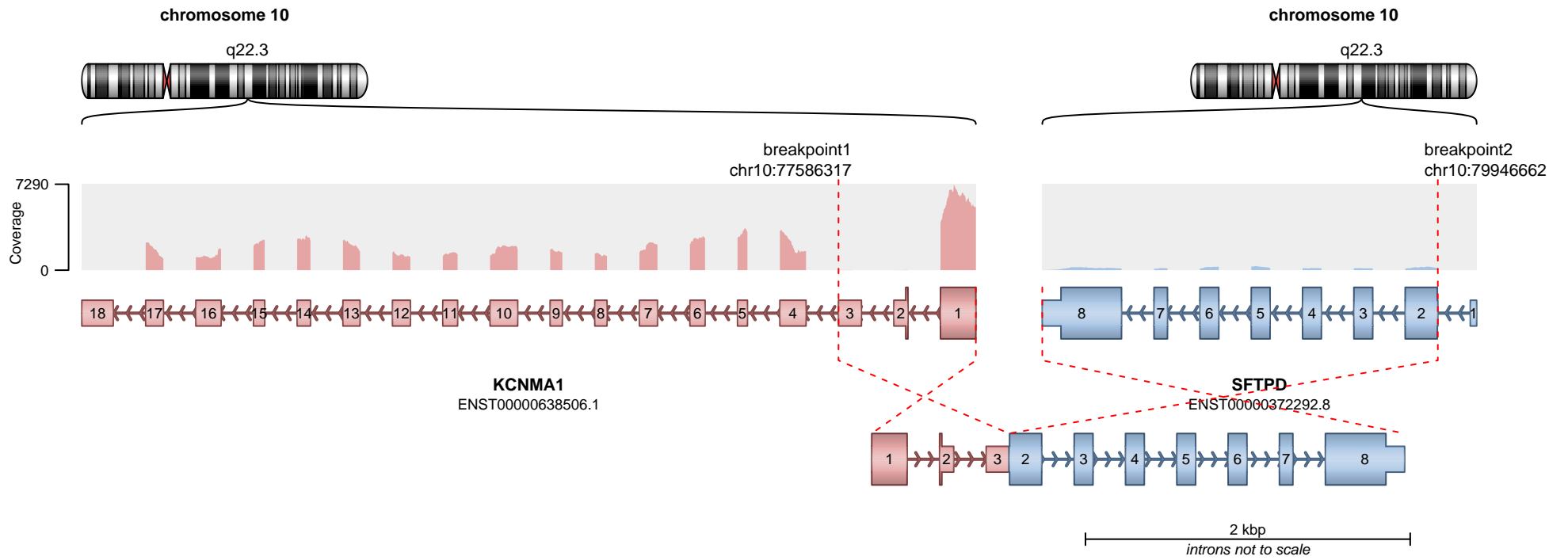
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



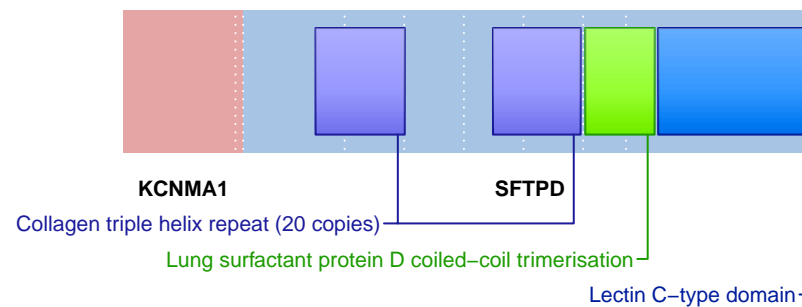
**SUPPORTING READ COUNT**

Split reads = 22  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



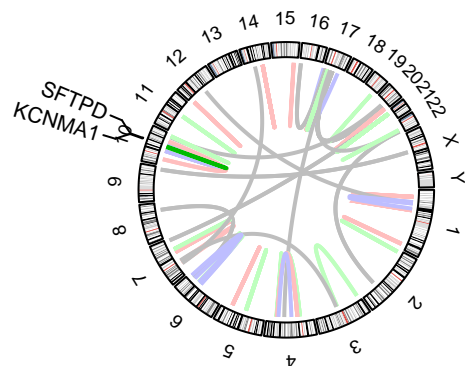
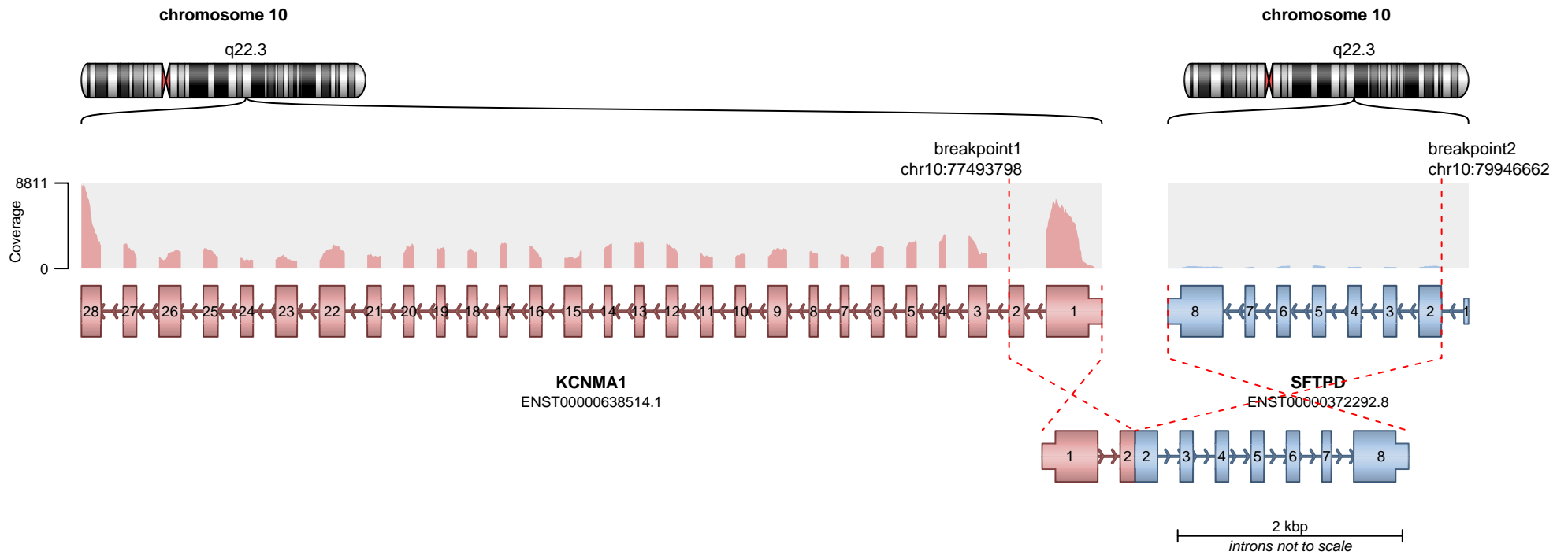
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



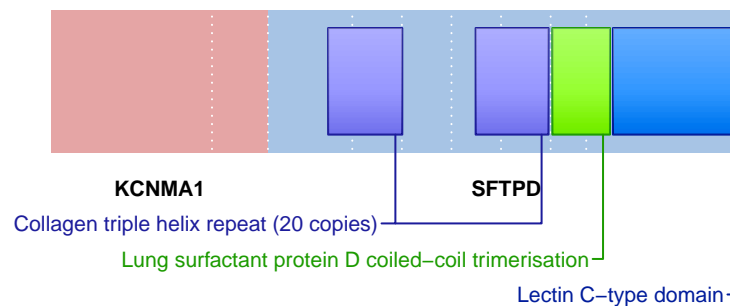
**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



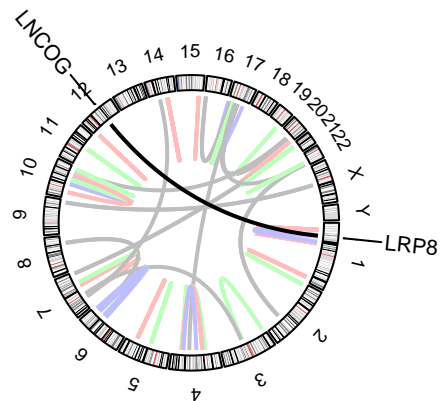
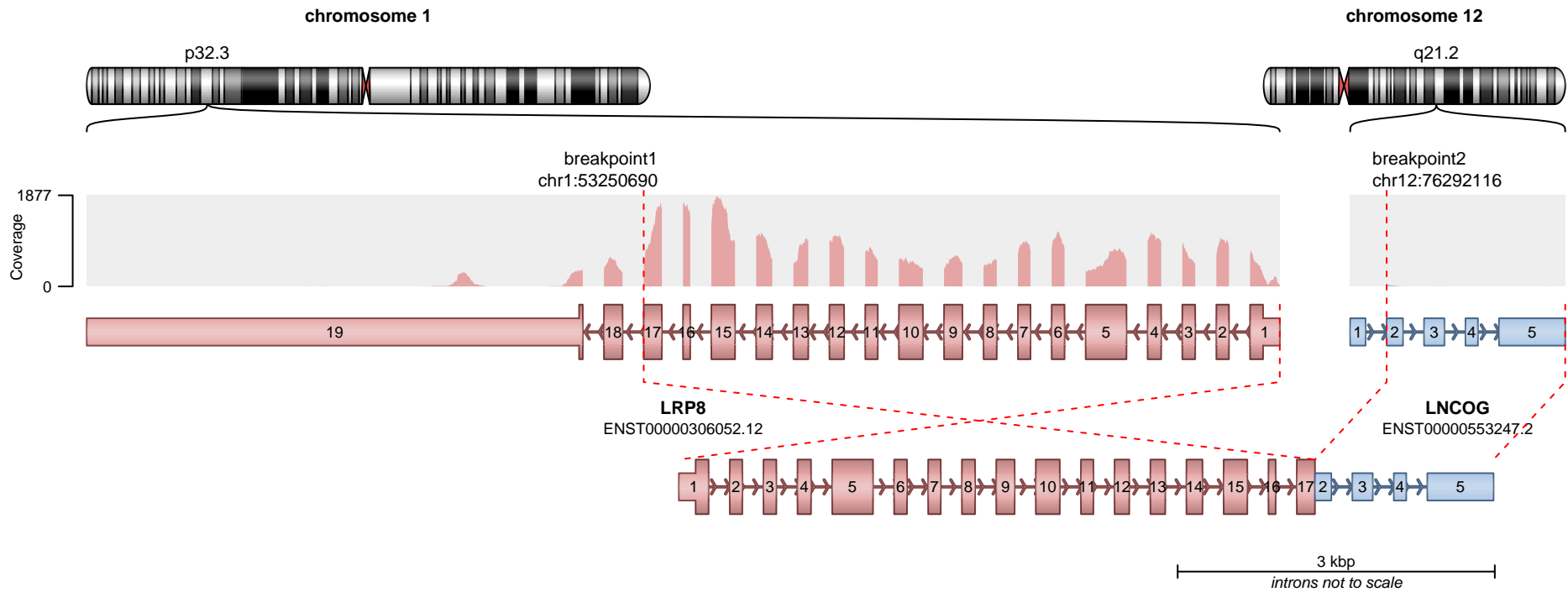
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



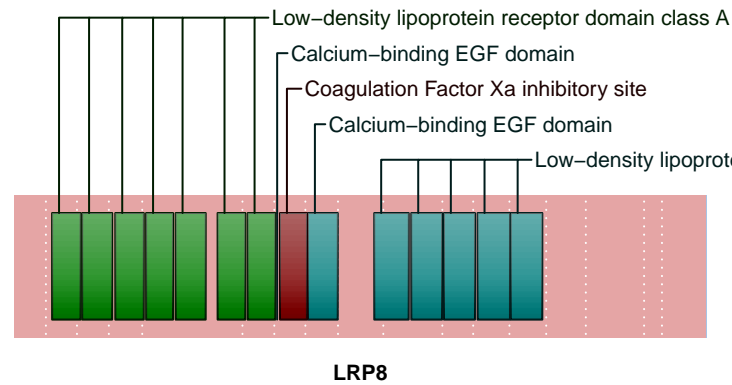
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



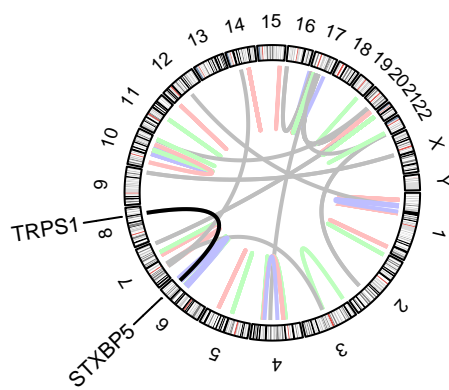
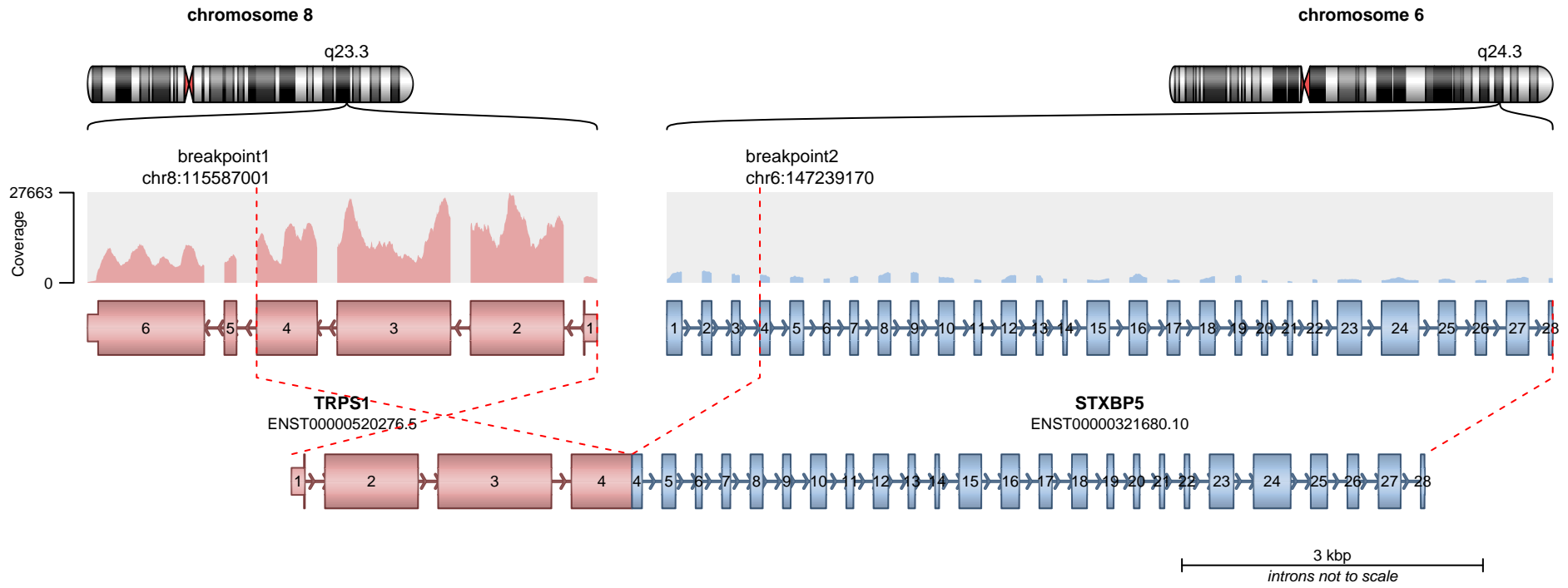
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

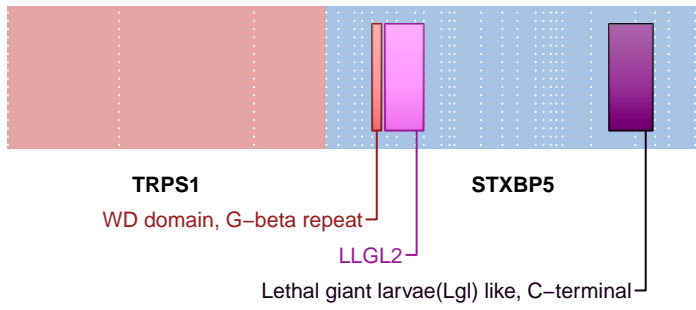
Split reads = 22  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



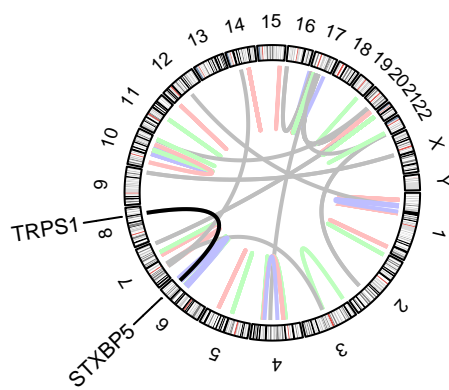
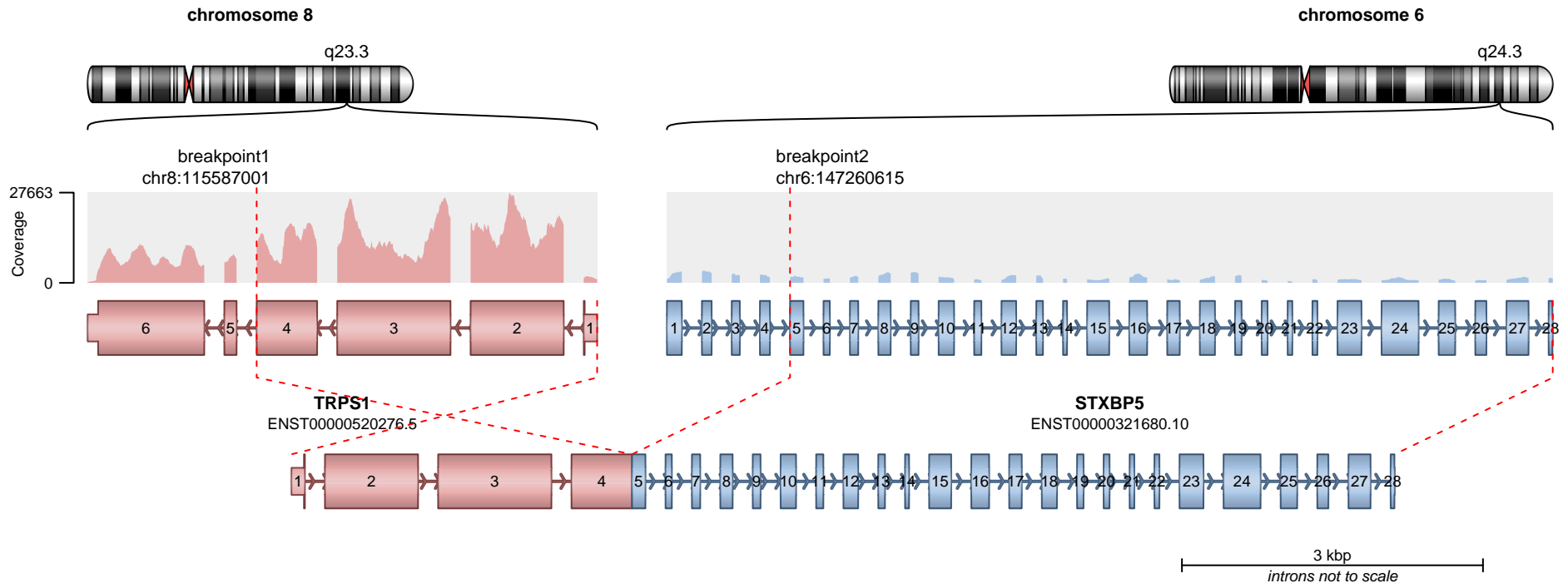
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



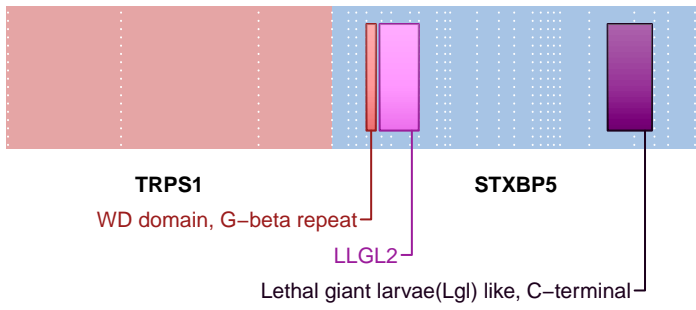
**SUPPORTING READ COUNT**

Split reads = 20  
Discordant mates = 1



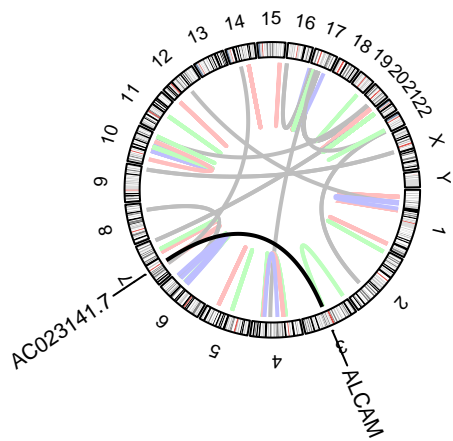
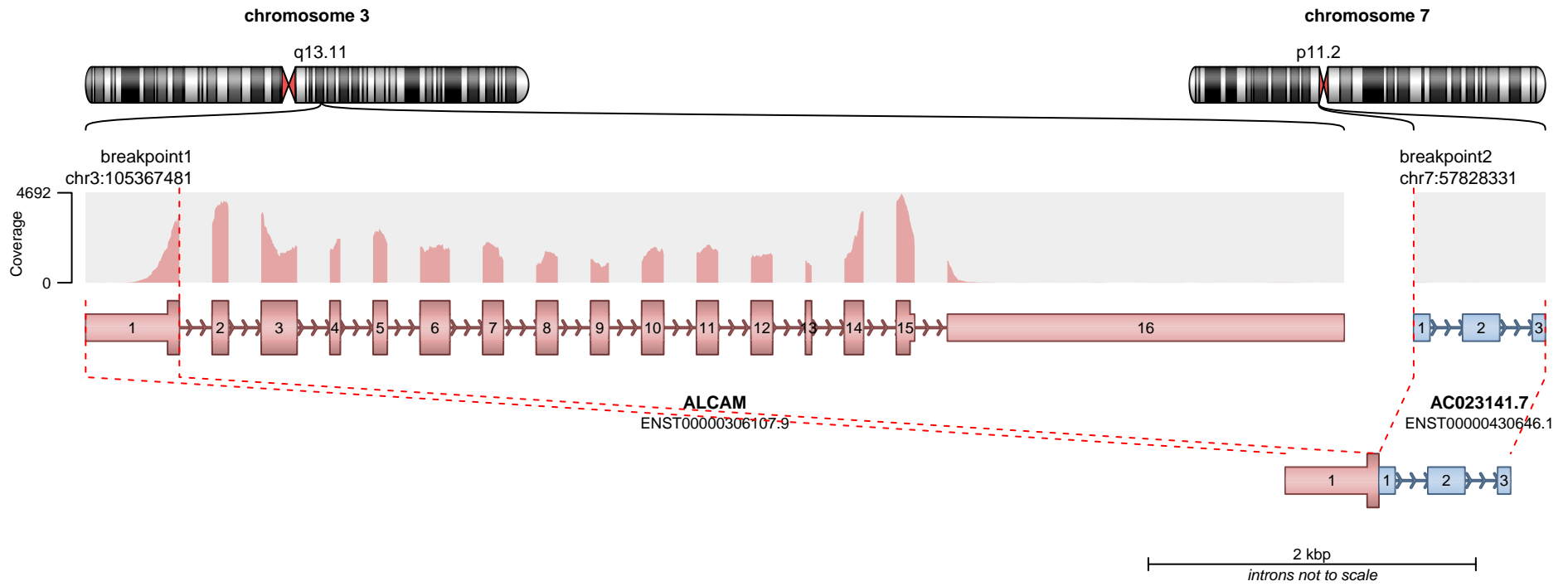
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 0

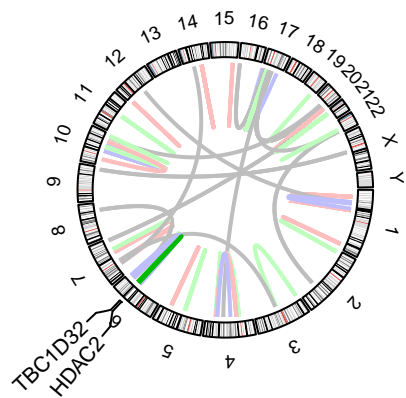
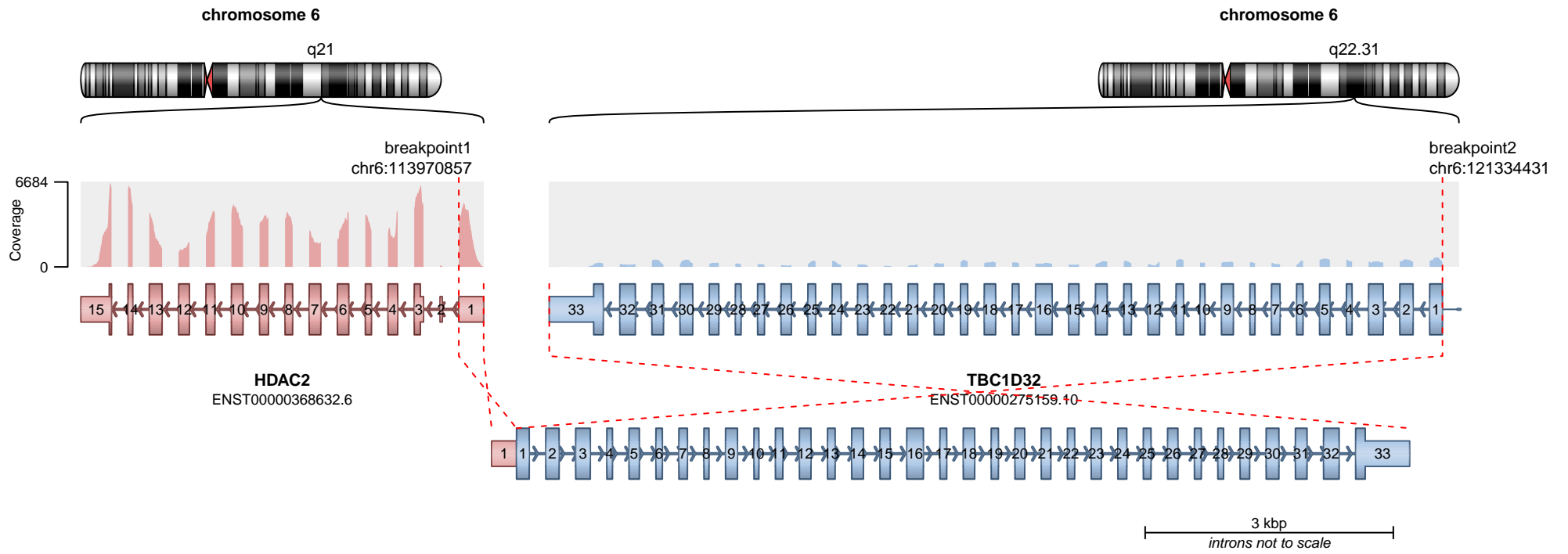


— translocation — deletion  
— duplication — inversion

No protein domains retained in fusion.

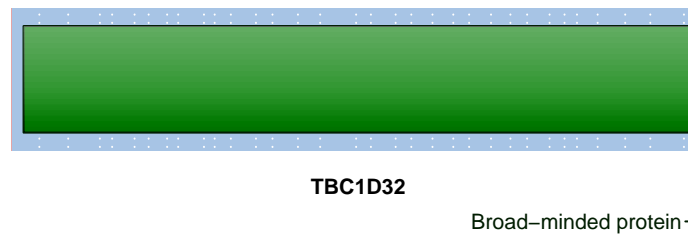
**SUPPORTING READ COUNT**

Split reads = 20  
Discordant mates = 0



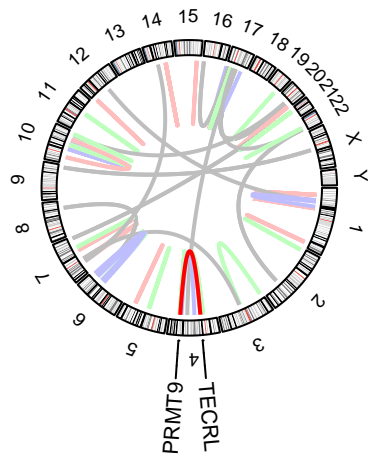
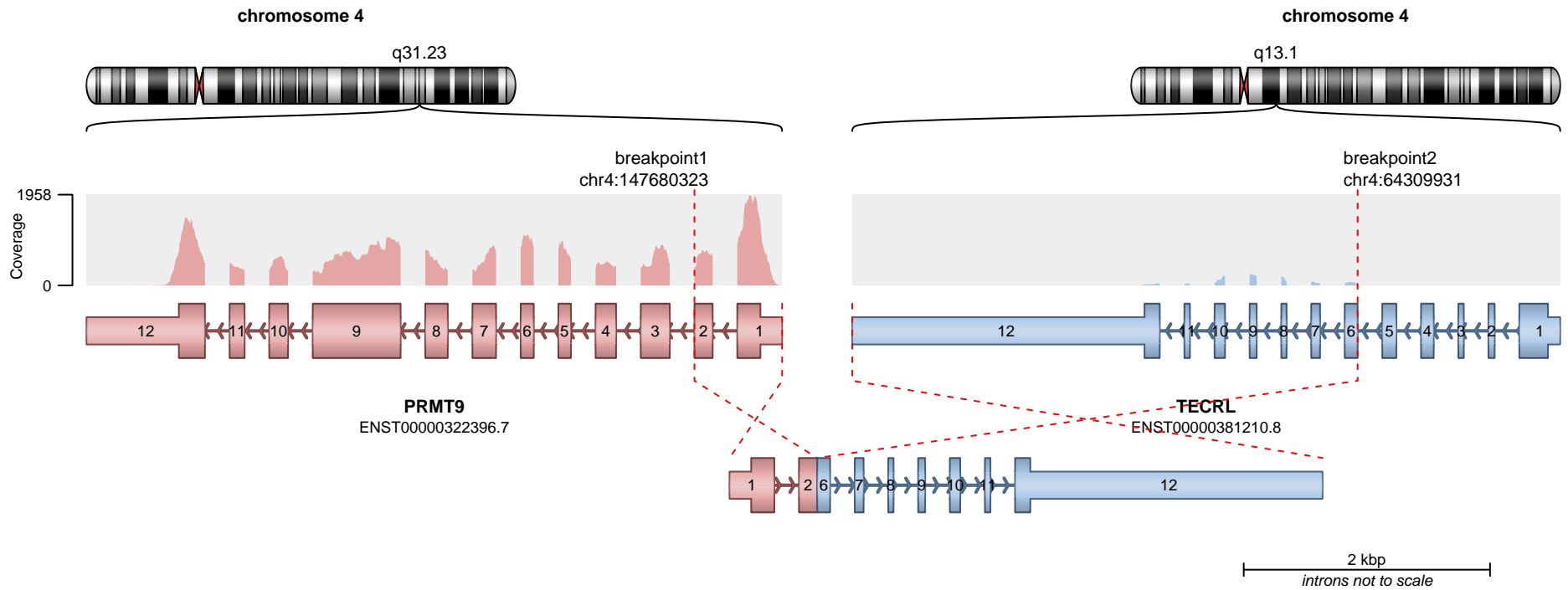
— translocation    — deletion  
— duplication    — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear

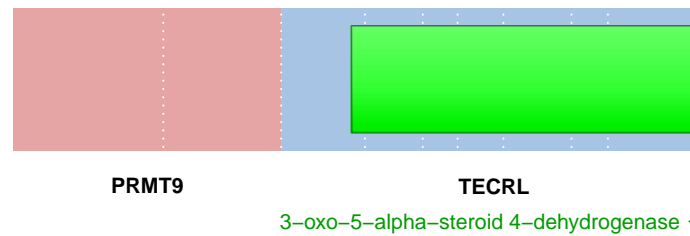


**SUPPORTING READ COUNT**

Split reads = 19  
Discordant mates = 0



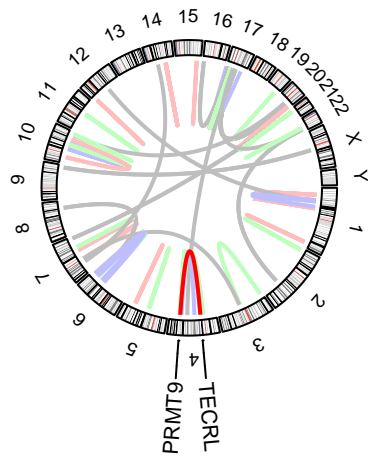
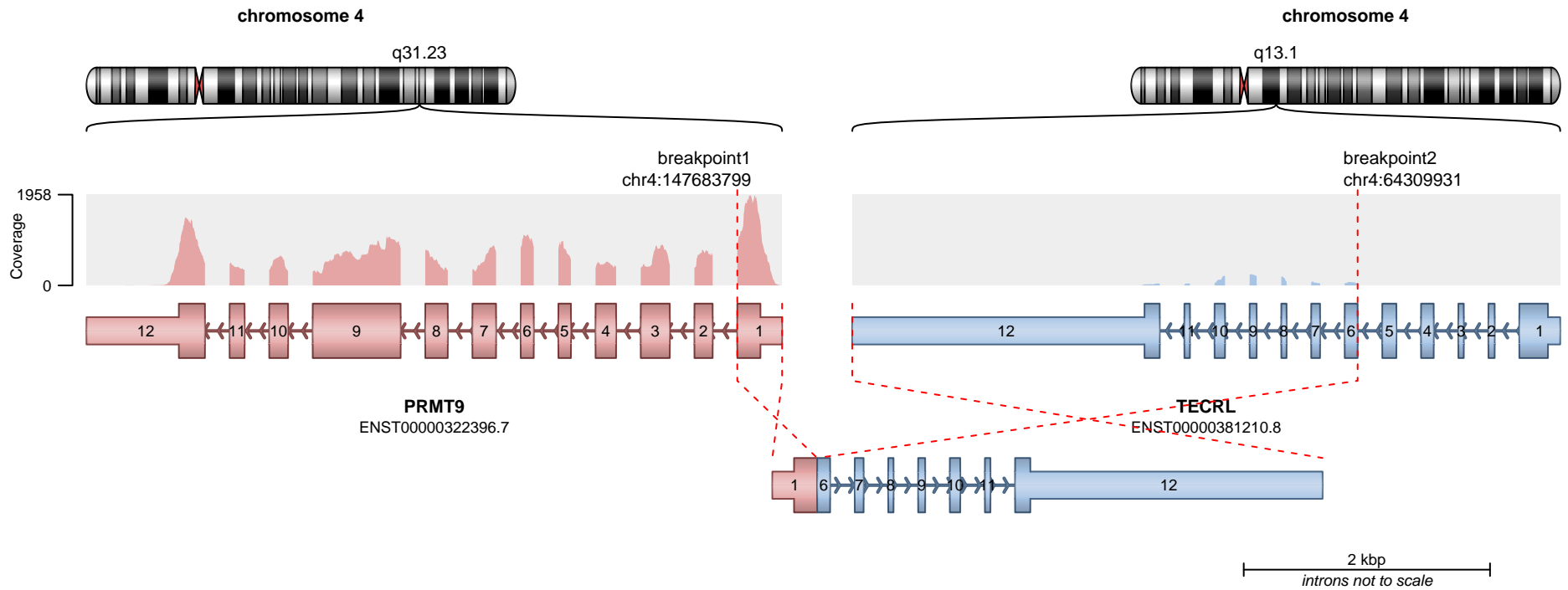
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



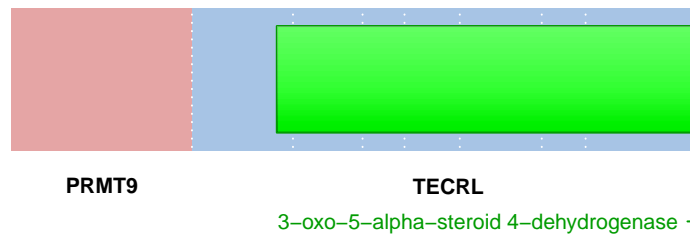
**SUPPORTING READ COUNT**

Split reads = 18  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



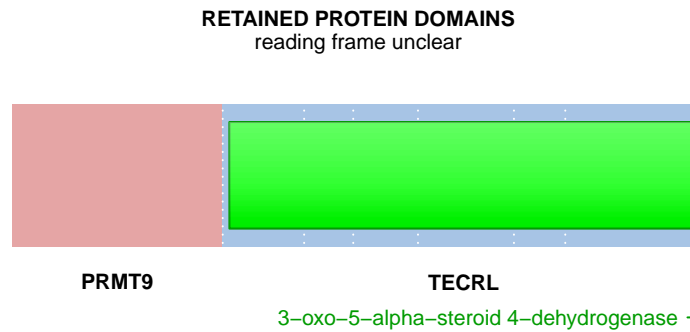
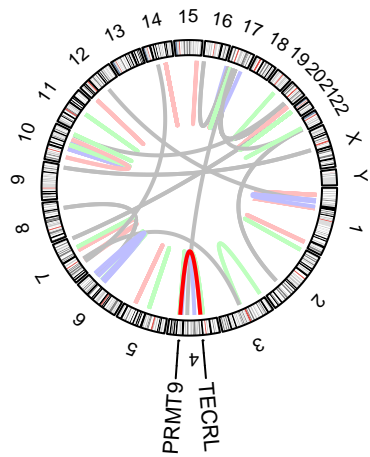
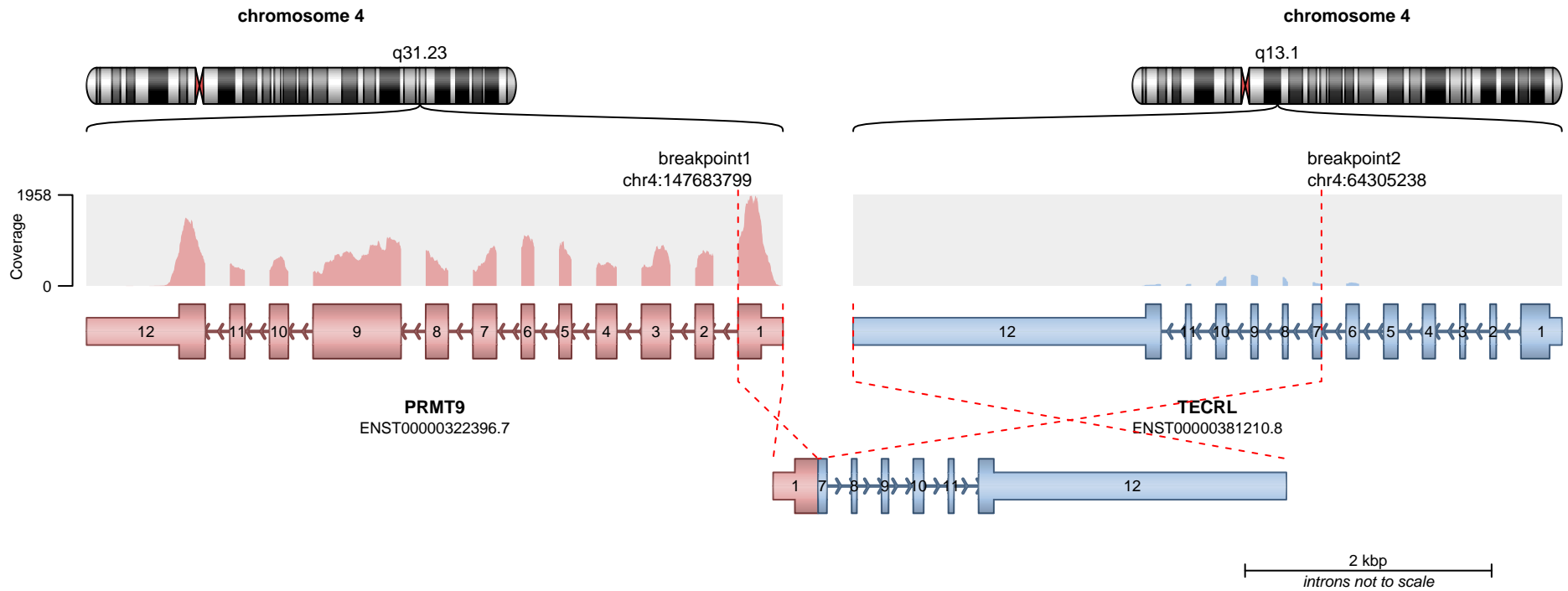
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 0

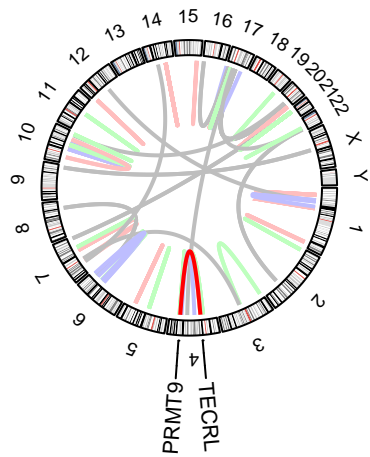
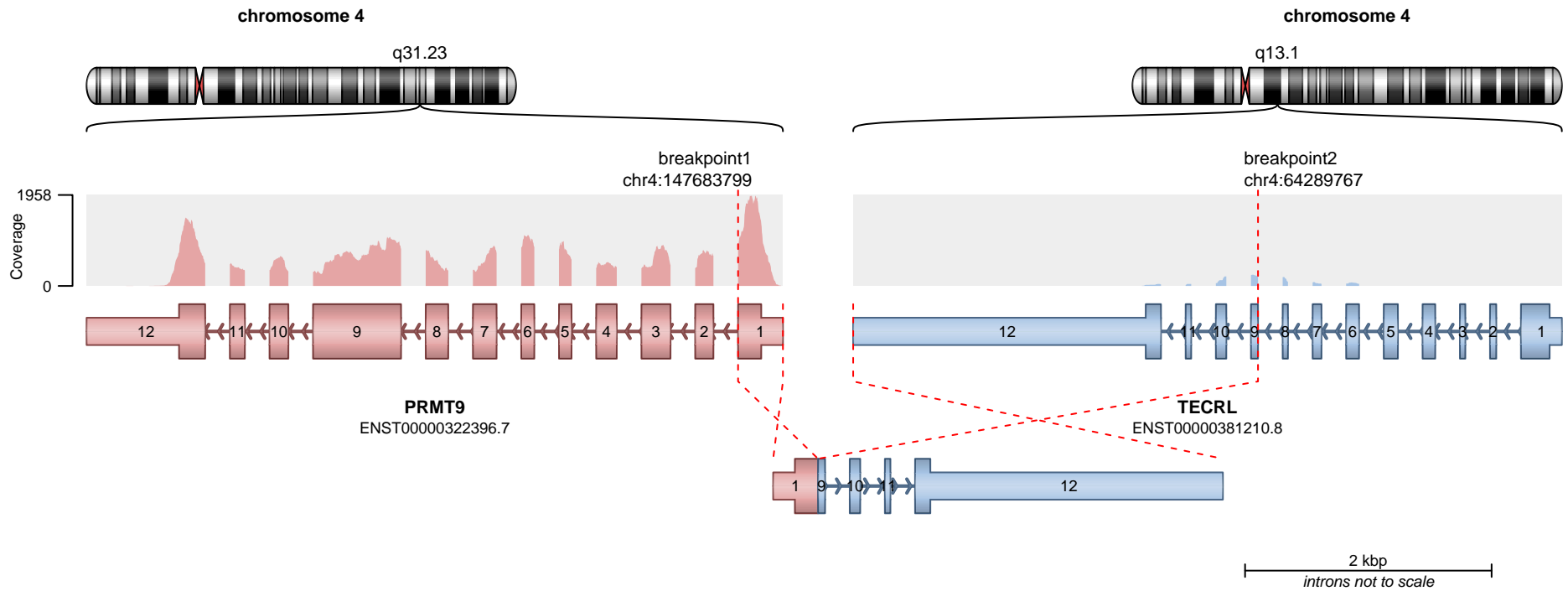
- translocation
- duplication
- deletion
- inversion



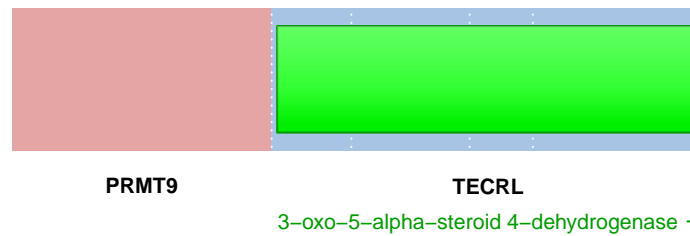
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



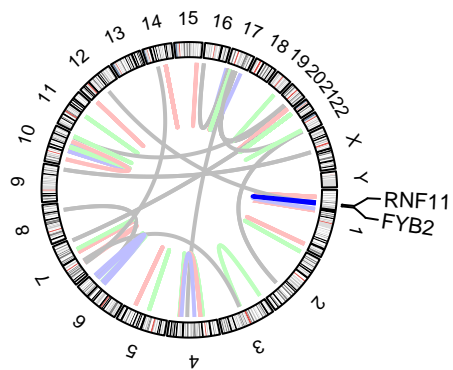
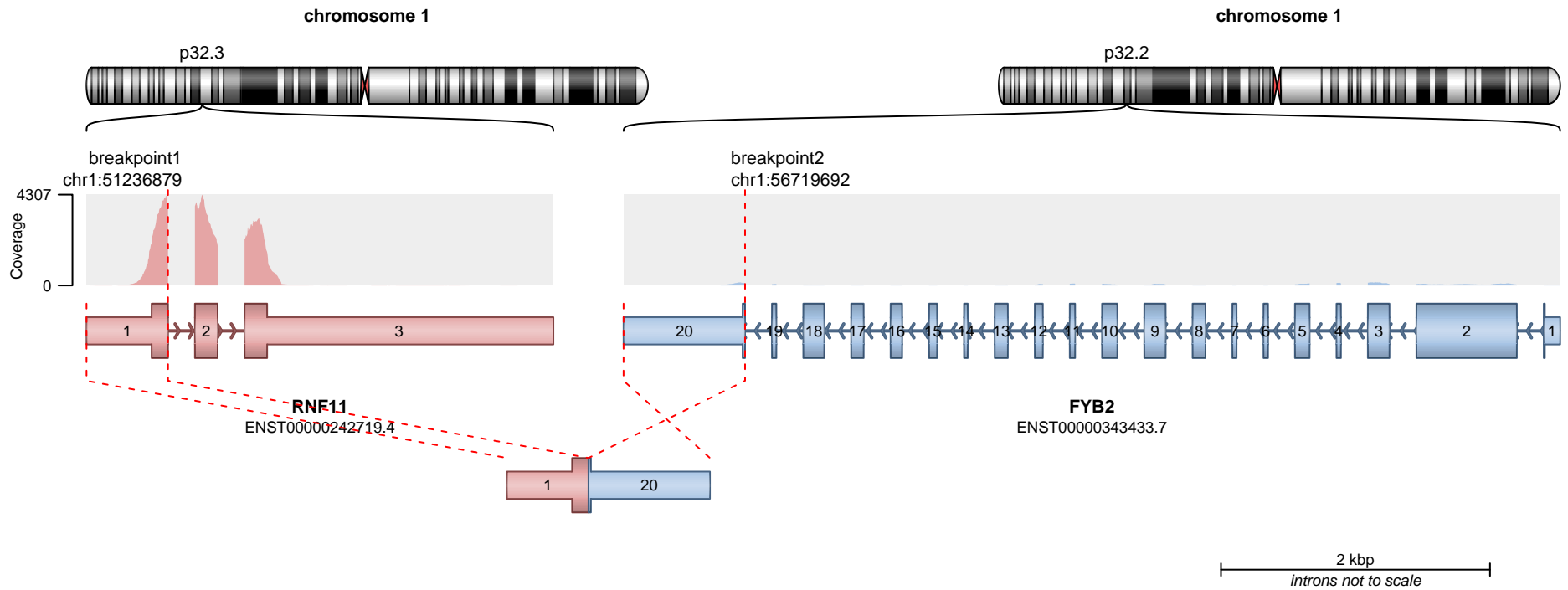
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

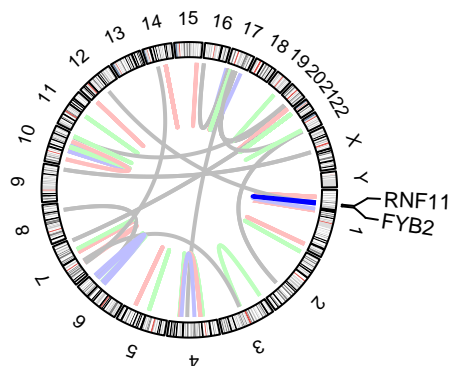
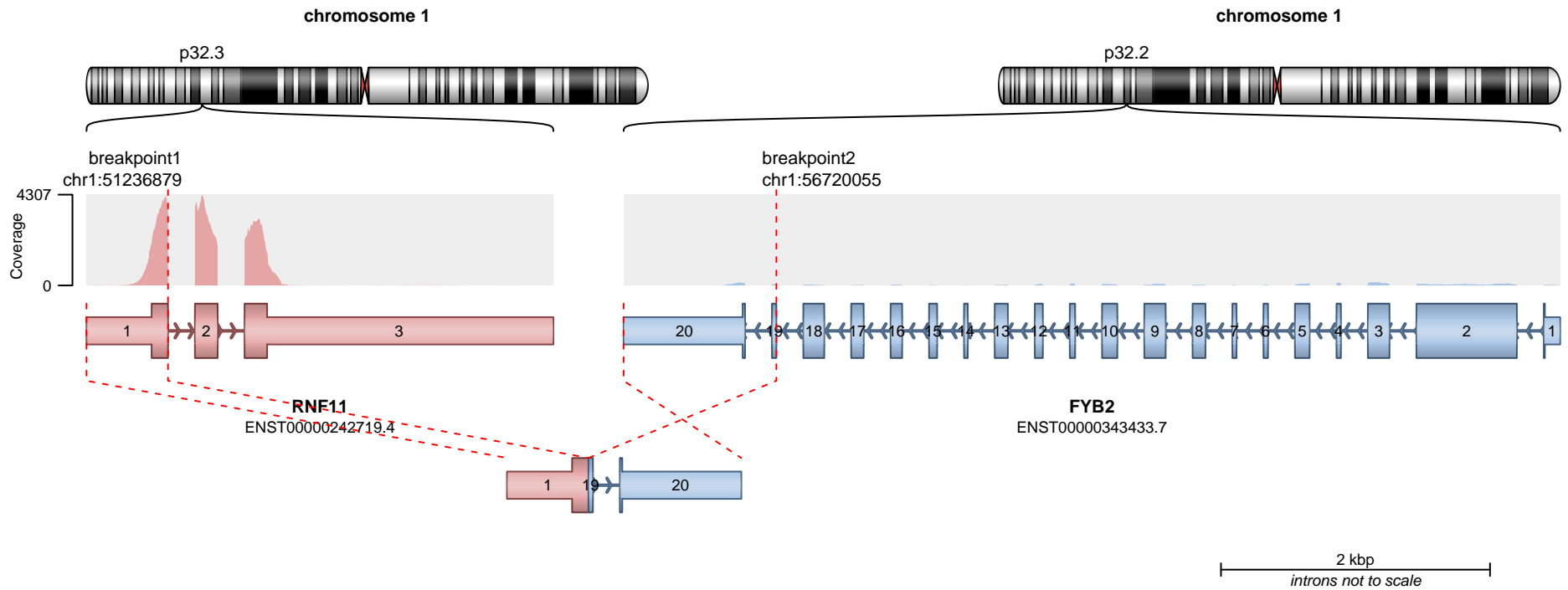


— translocation — deletion  
— duplication — inversion

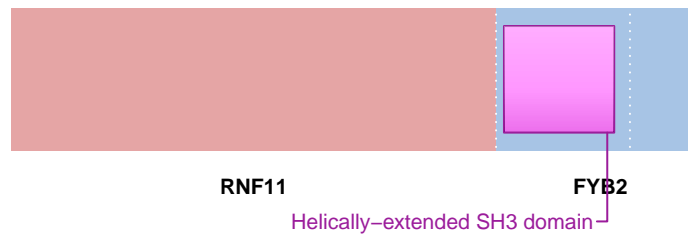
No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 18  
Discordant mates = 0



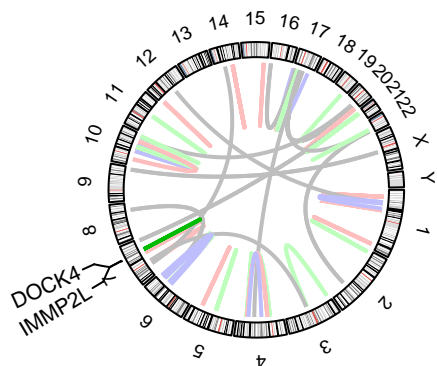
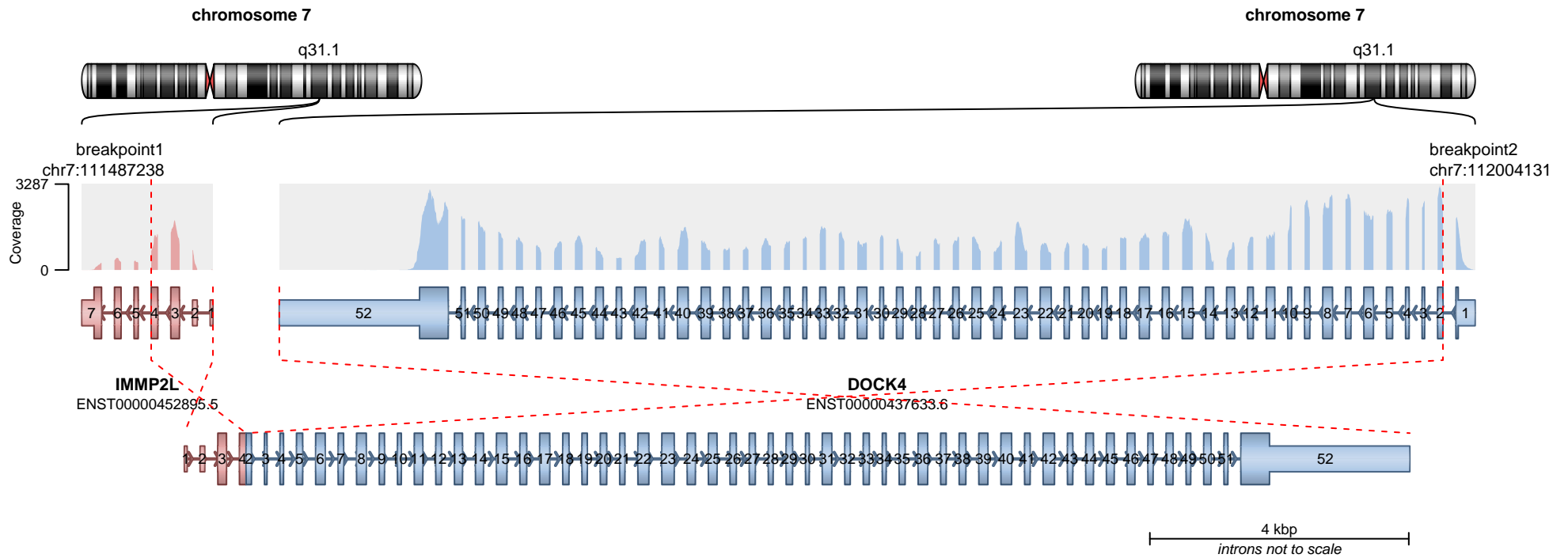
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



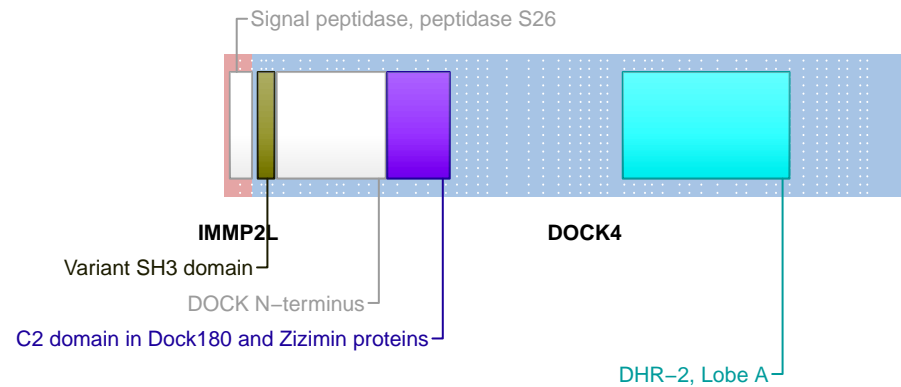
**SUPPORTING READ COUNT**

Split reads = 8  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



**RETAINED PROTEIN DOMAINS**  
reading frame unclear

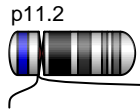


**SUPPORTING READ COUNT**

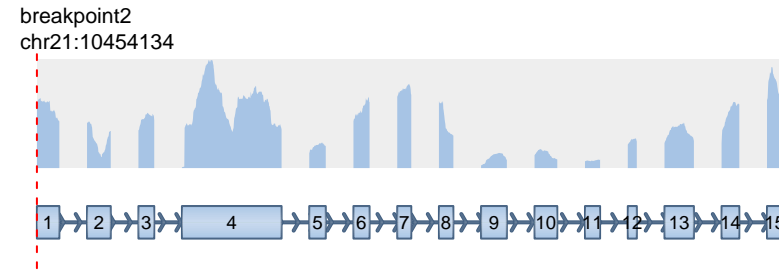
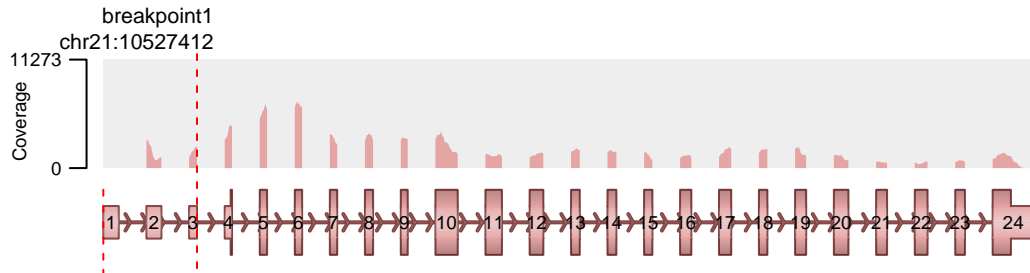
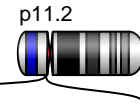
Split reads = 17  
Discordant mates = 1

— translocation — deletion  
— duplication — inversion

chromosome 21



chromosome 21

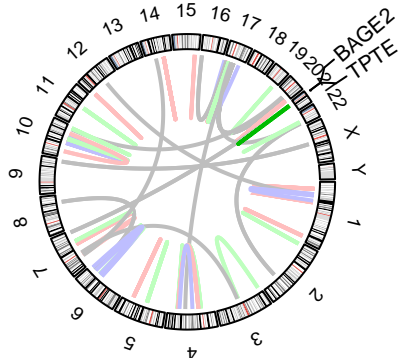


**TPTE**  
ENST00000618007.6

**BAGE2**  
ENST00000496773.1



2 kbp  
*introns not to scale*



— translocation    — deletion  
— duplication    — inversion

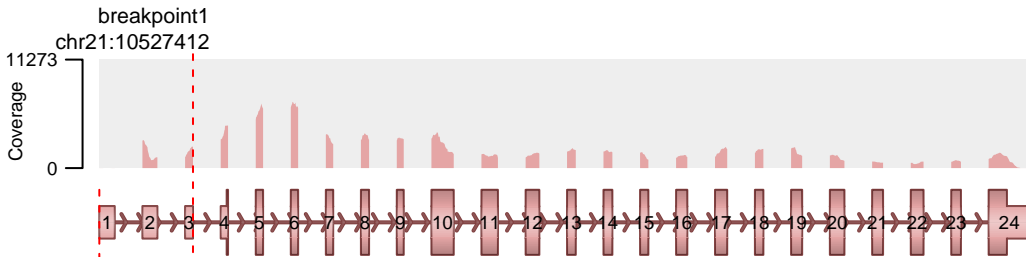
No coding regions retained in fusion transcript.

**SUPPORTING READ COUNT**

Split reads = 16  
Discordant mates = 1

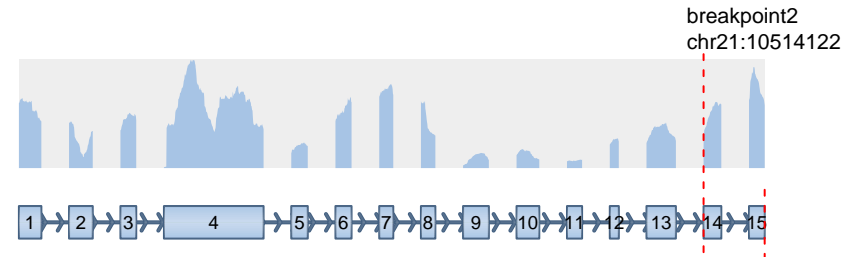
chromosome 21

p11.2



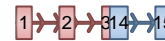
chromosome 21

p11.2

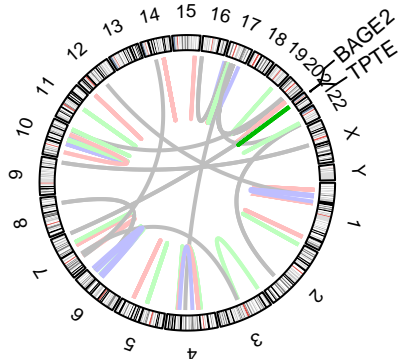


**TPTE**  
ENST00000618007.6

**BAGE2**  
ENST00000496773.1



2 kbp  
introns not to scale



No coding regions retained in fusion transcript.

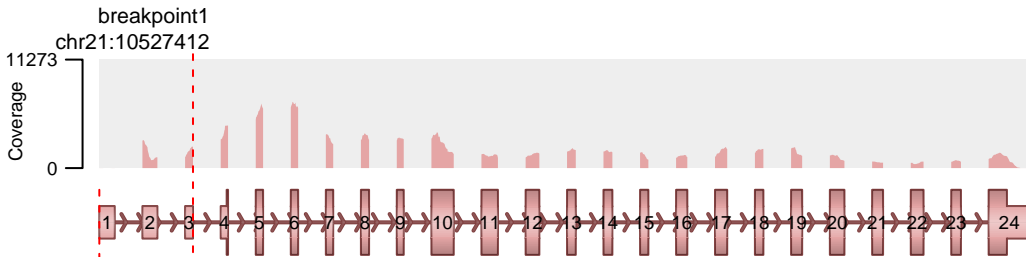
**SUPPORTING READ COUNT**

Split reads = 8  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion

chromosome 21

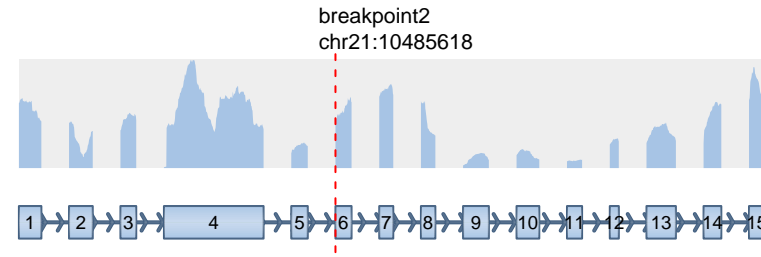
p11.2



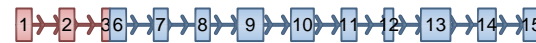
**TPTE**  
ENST00000618007.6

chromosome 21

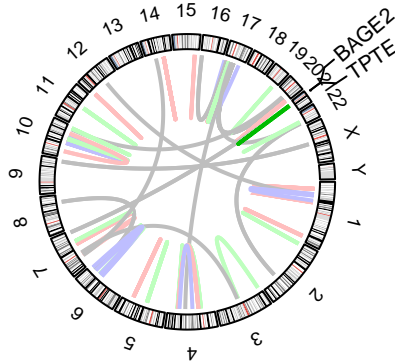
p11.2



**BAGE2**  
ENST00000496773.1



2 kbp  
*introns not to scale*



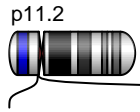
— translocation    — deletion  
— duplication    — inversion

No coding regions retained in fusion transcript.

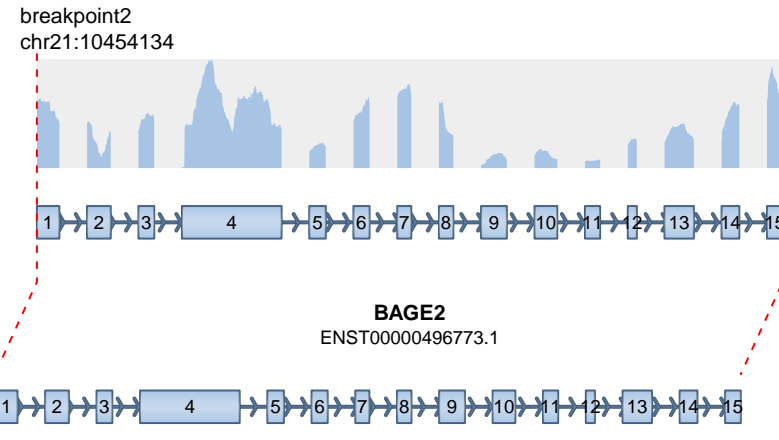
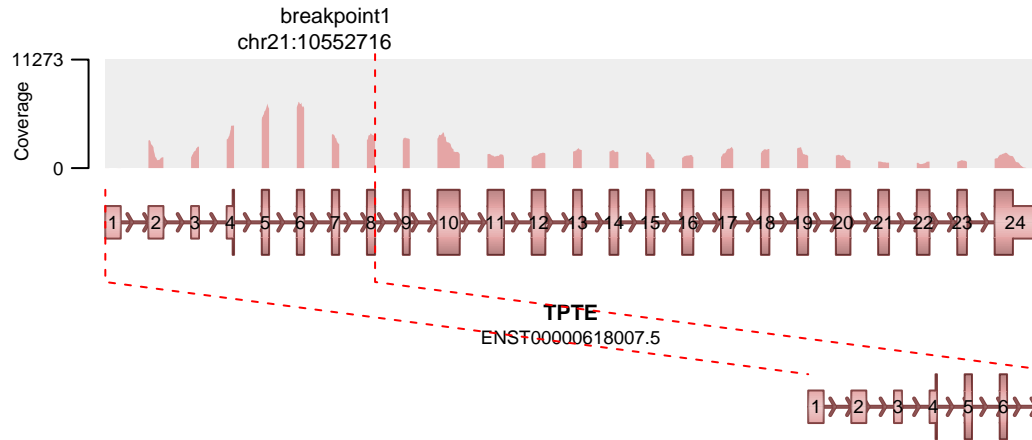
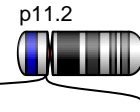
**SUPPORTING READ COUNT**

Split reads = 6  
Discordant mates = 0

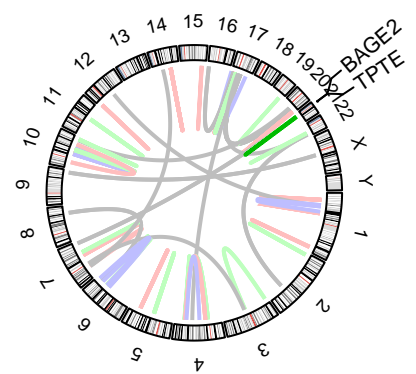
chromosome 21



chromosome 21



2 kbp  
introns not to scale



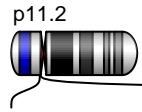
— translocation    — deletion  
— duplication    — inversion

No protein domains retained in fusion.

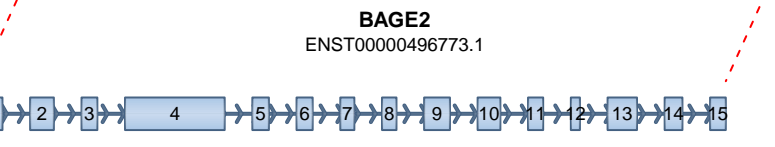
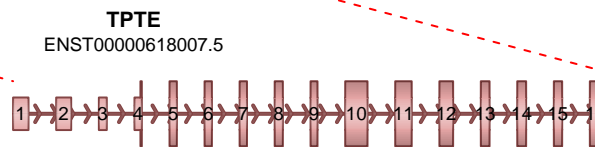
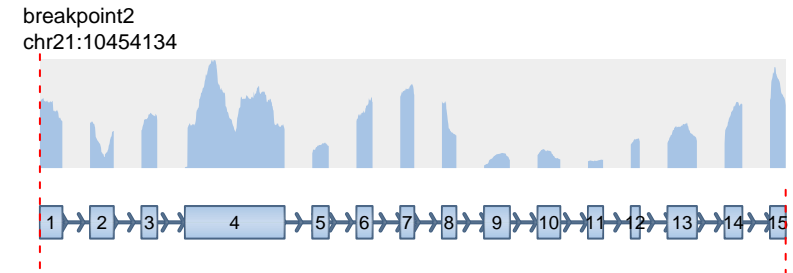
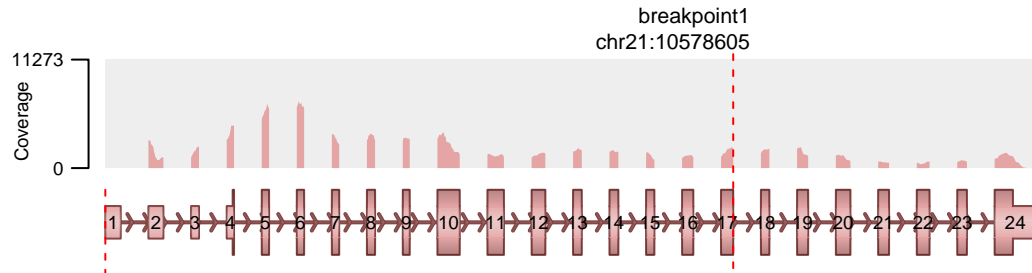
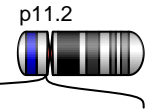
**SUPPORTING READ COUNT**

Split reads = 5  
Discordant mates = 1

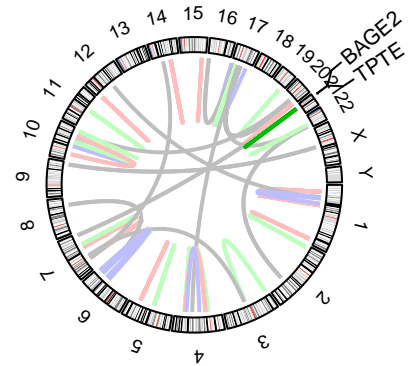
chromosome 21



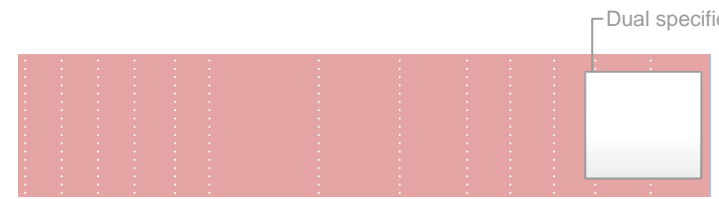
chromosome 21



2 kbp  
introns not to scale



**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 1

**TPTE**

- translocation
- duplication
- deletion
- inversion

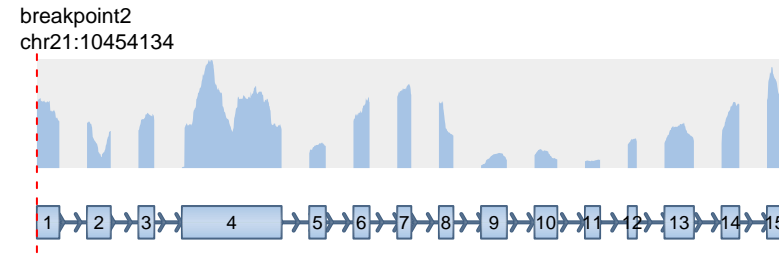
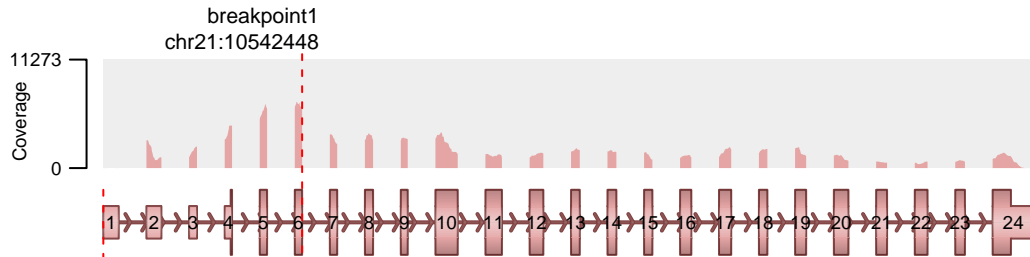
chromosome 21

p11.2



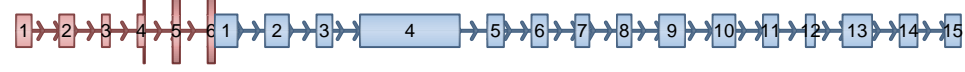
chromosome 21

p11.2

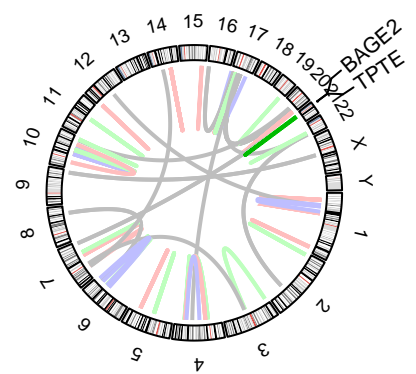


**TPTE**  
ENST00000618007.5

**BAGE2**  
ENST00000496773.1



2 kbp  
*introns not to scale*



— translocation    — deletion  
— duplication    — inversion

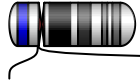
No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 1

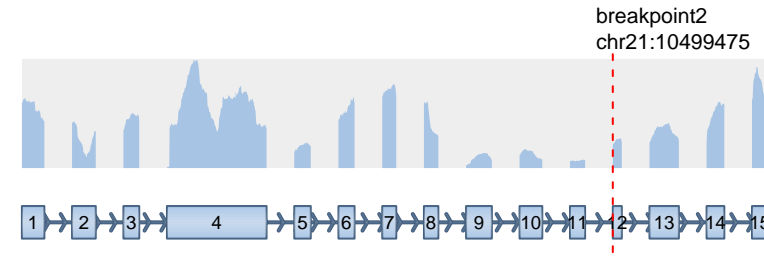
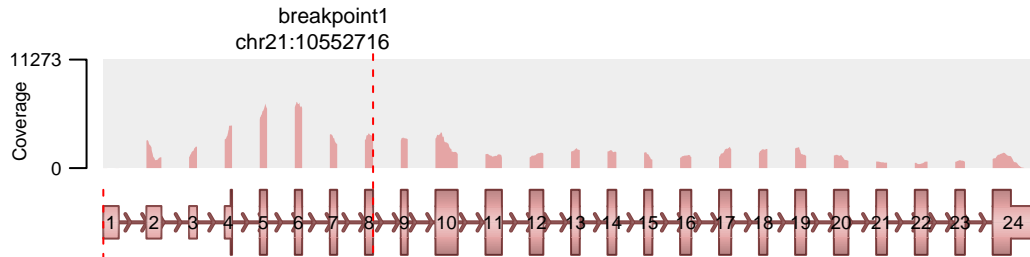
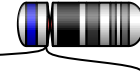
chromosome 21

p11.2



chromosome 21

p11.2

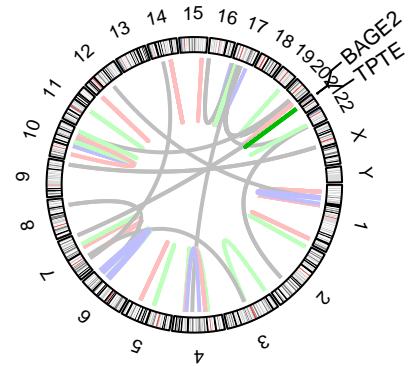


**TPTE**  
ENST00000618007.5

**BAGE2**  
ENST00000496773.1



2 kbp  
introns not to scale



No protein domains retained in fusion.

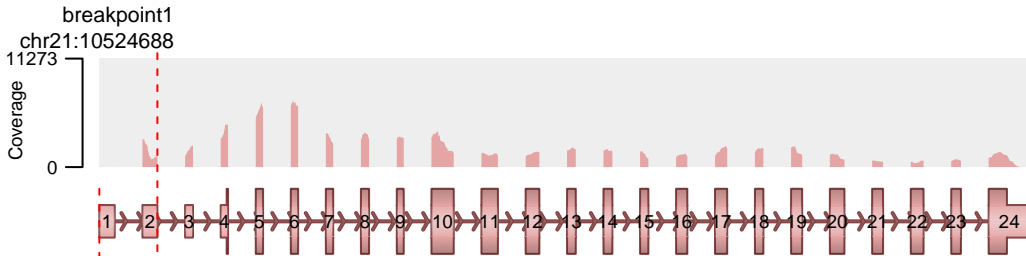
**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion

chromosome 21

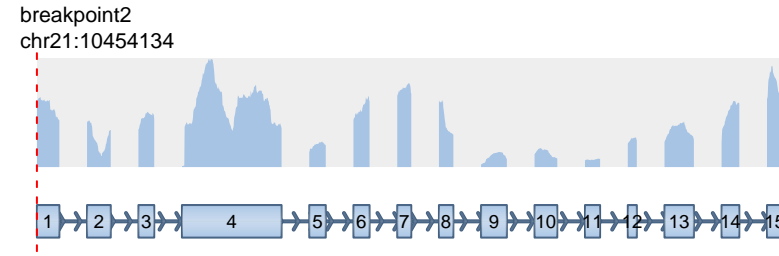
p11.2



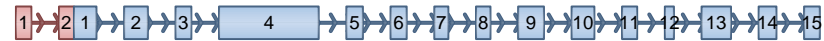
**TPTE**  
ENST00000618007.5

chromosome 21

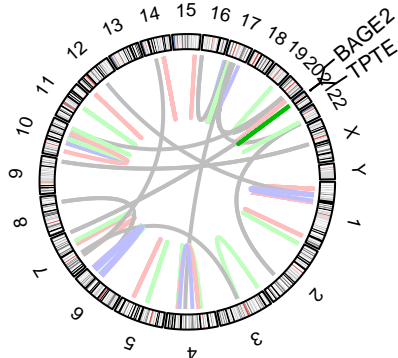
p11.2



**BAGE2**  
ENST00000496773.1



2 kbp  
*introns not to scale*



— translocation    — deletion  
— duplication    — inversion

No coding regions retained in fusion transcript.

**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0

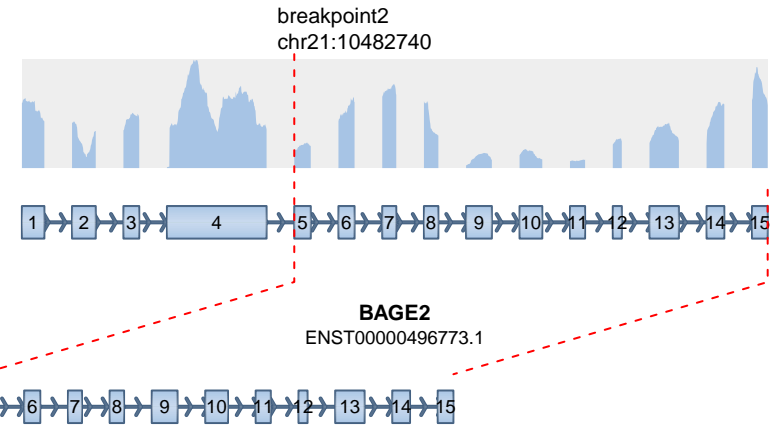
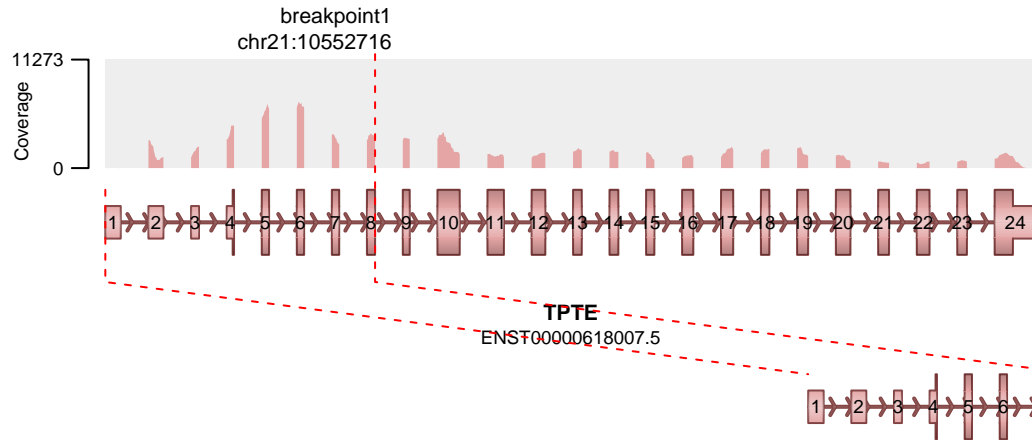
chromosome 21

p11.2

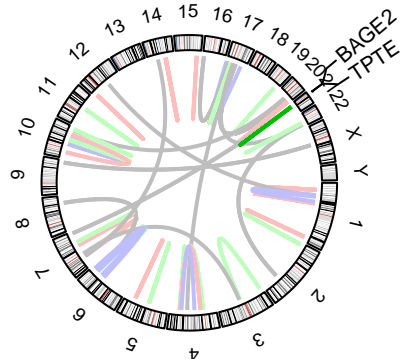


chromosome 21

p11.2



2 kbp  
introns not to scale



No protein domains retained in fusion.

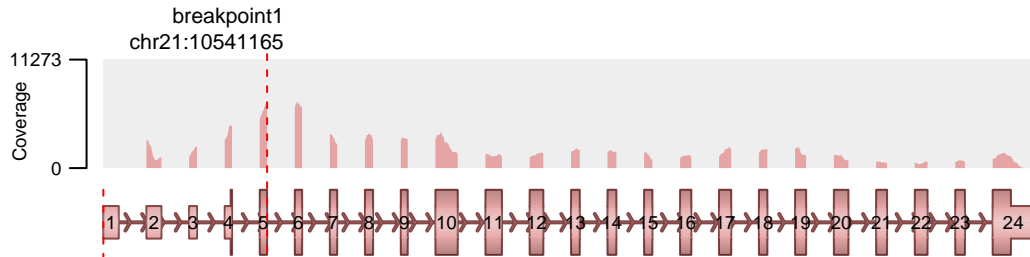
**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion

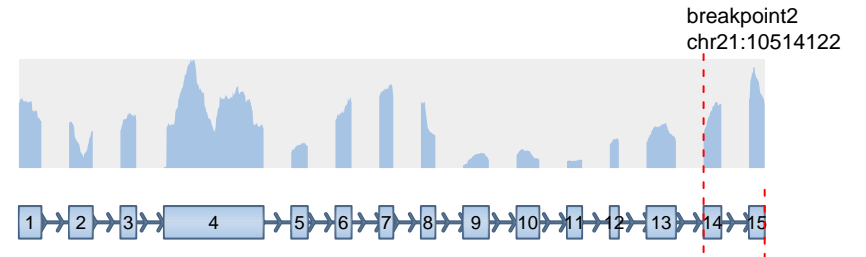
chromosome 21

p11.2



chromosome 21

p11.2

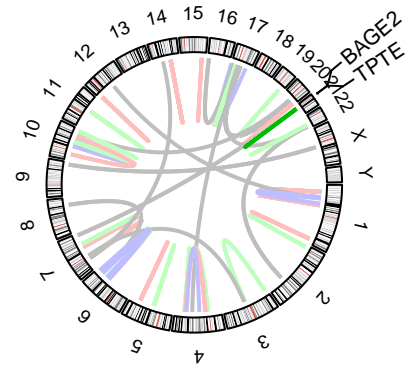


TPTE  
ENST00000618007.5

BAGE2  
ENST00000496773.1



2 kbp  
introns not to scale



— translocation    — deletion  
— duplication    — inversion

No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0

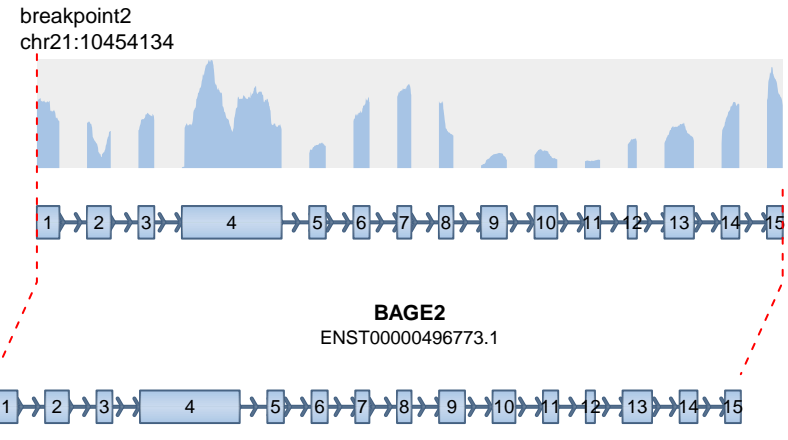
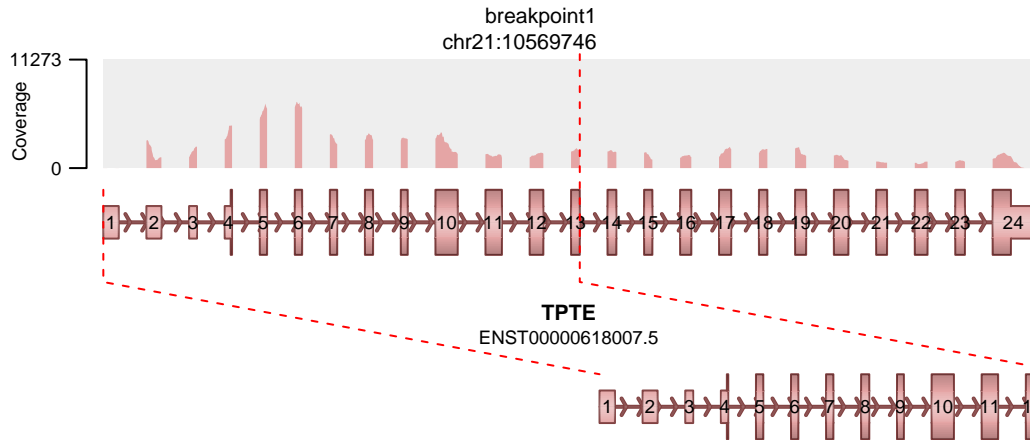
chromosome 21

p11.2

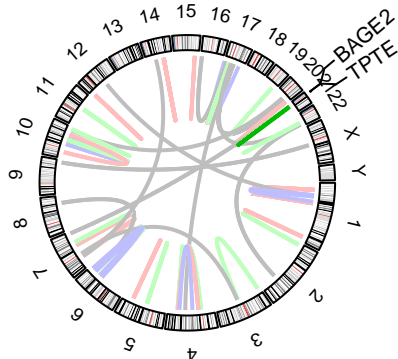


chromosome 21

p11.2



2 kbp  
introns not to scale



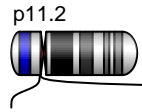
— translocation    — deletion  
— duplication    — inversion

No protein domains retained in fusion.

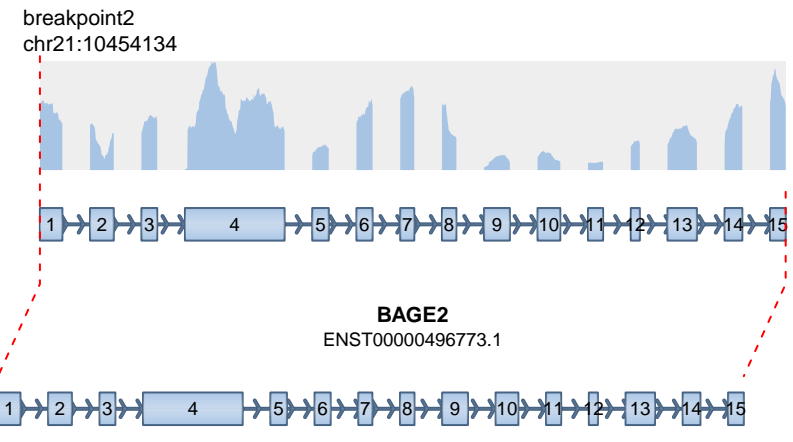
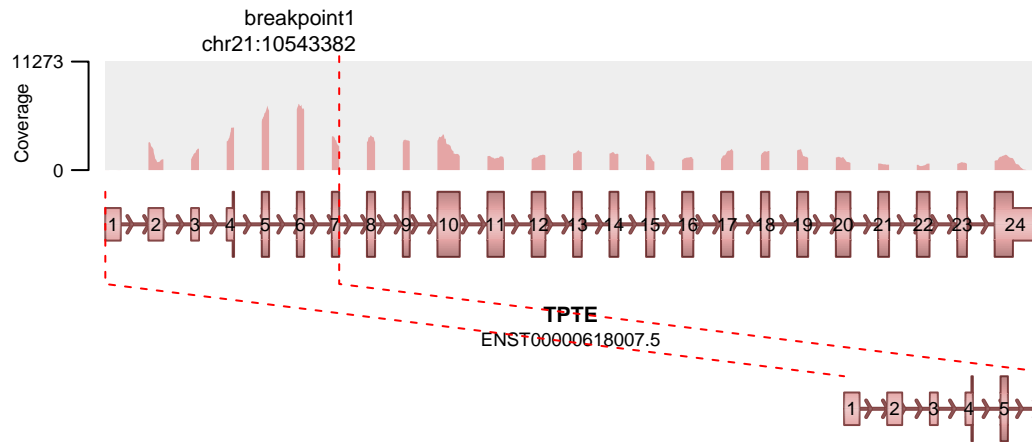
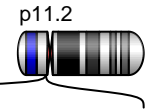
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 1

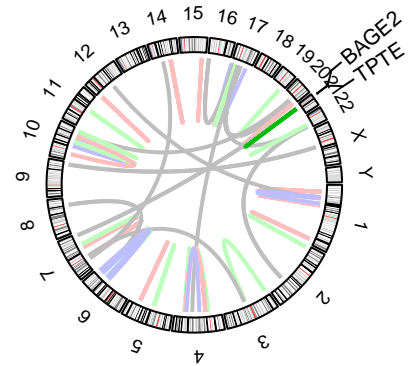
chromosome 21



chromosome 21



2 kbp  
introns not to scale



— translocation    — deletion  
— duplication    — inversion

No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 1

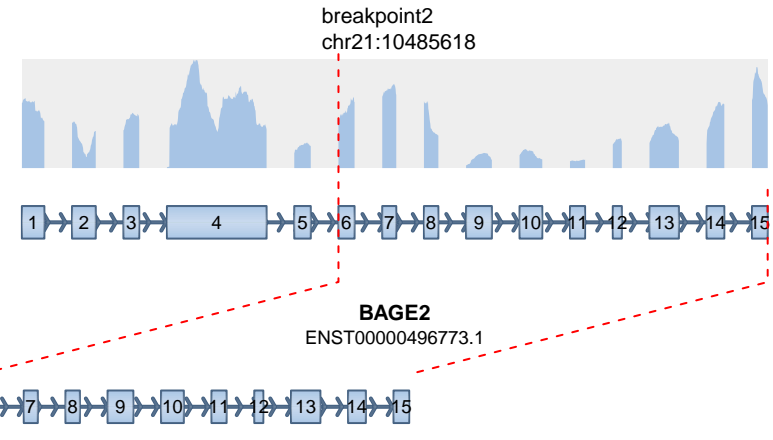
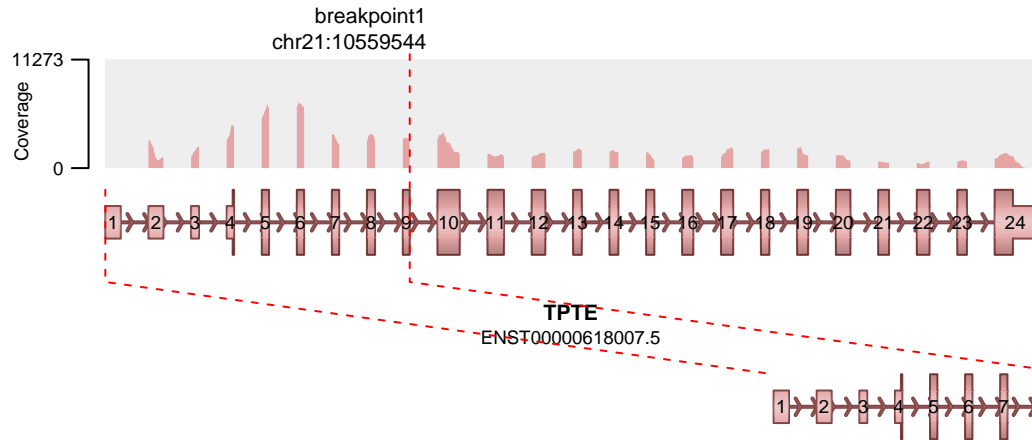
chromosome 21

p11.2

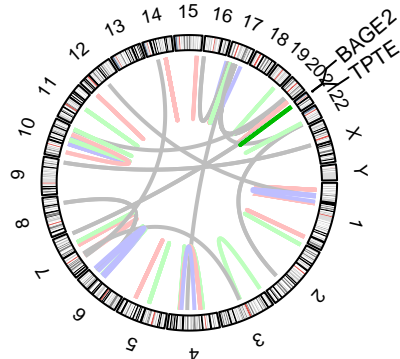


chromosome 21

p11.2



2 kbp  
introns not to scale



— translocation    — deletion  
— duplication    — inversion

No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

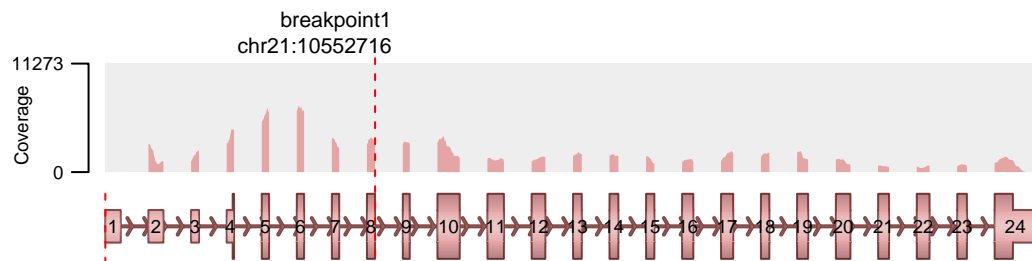
chromosome 21

p11.2



chromosome 21

p11.2

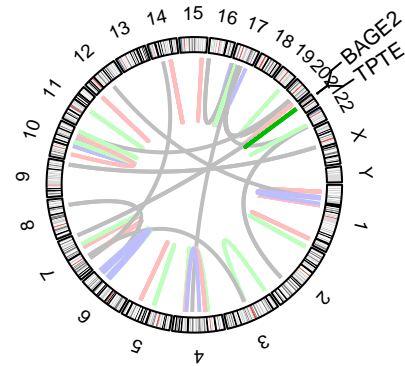


**TPTE**  
ENST00000618007.5

**BAGE2**  
ENST00000496773.1



2 kbp  
*introns not to scale*



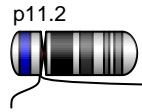
No protein domains retained in fusion.

**SUPPORTING READ COUNT**

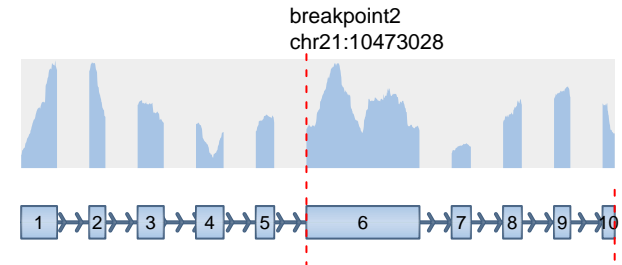
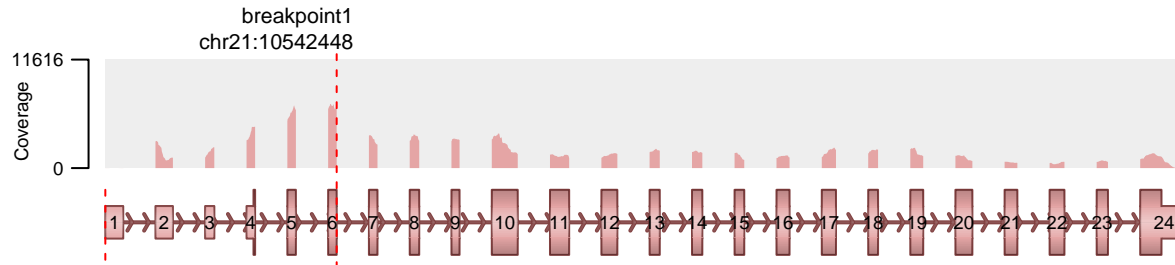
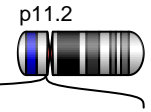
Split reads = 1  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

chromosome 21



chromosome 21

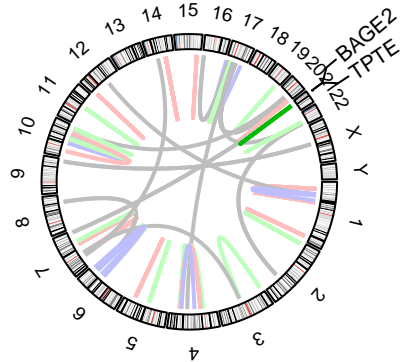


**TPTE**  
ENST00000618007.5

**BAGE2**  
ENST00000470054.5



2 kbp  
*introns not to scale*



No protein domains retained in fusion.

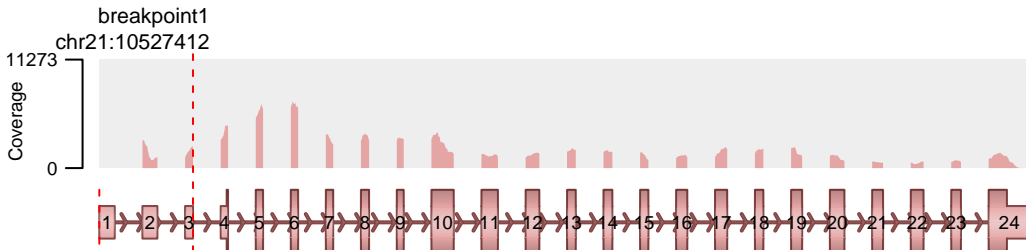
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion

chromosome 21

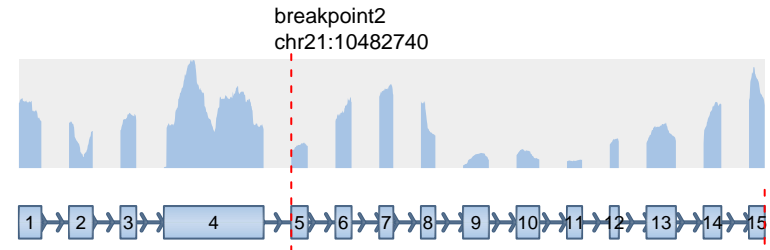
p11.2



**TPTE**  
ENST00000618007.6

chromosome 21

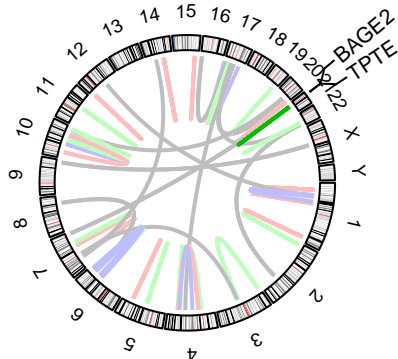
p11.2



**BAGE2**  
ENST00000496773.1



2 kbp  
*introns not to scale*



— translocation    — deletion  
— duplication    — inversion

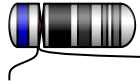
No coding regions retained in fusion transcript.

**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

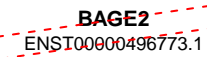
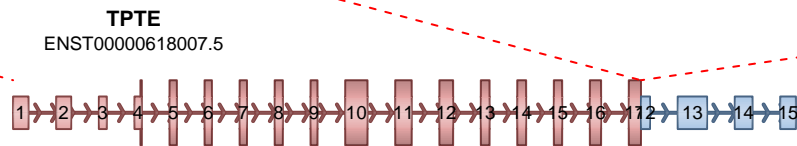
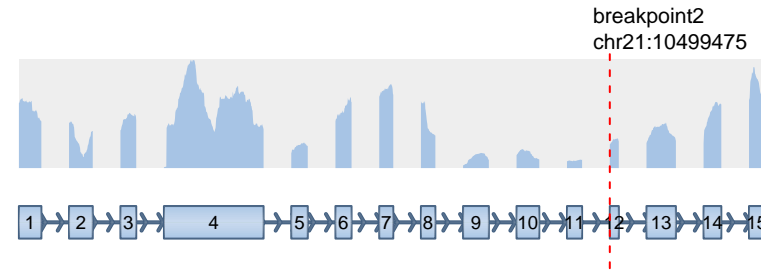
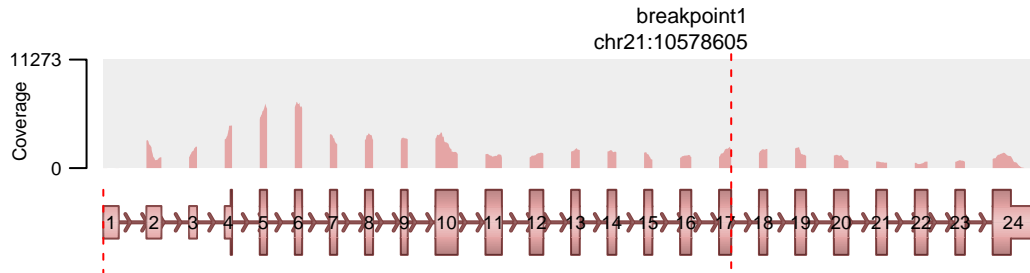
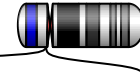
chromosome 21

p11.2

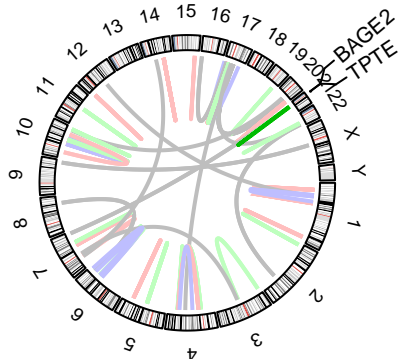


chromosome 21

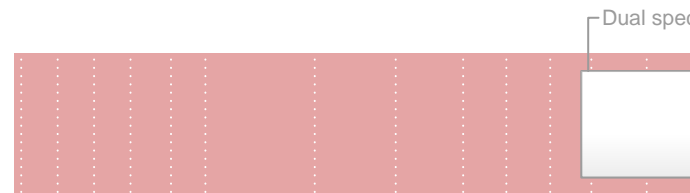
p11.2



2 kbp  
introns not to scale



**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

**TPTE**

— translocation    — deletion  
— duplication    — inversion

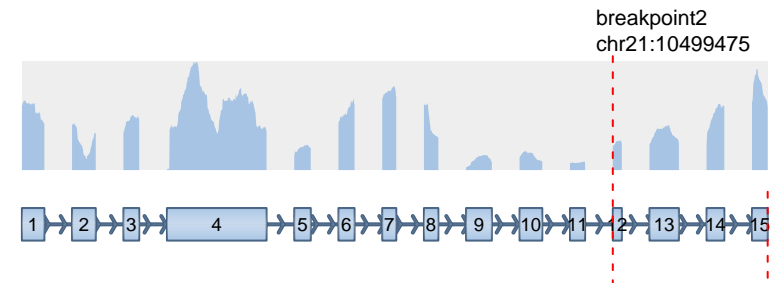
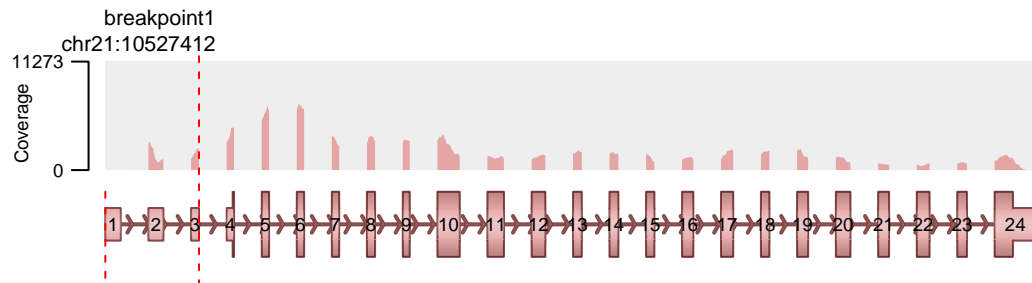
chromosome 21

p11.2



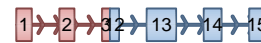
chromosome 21

p11.2

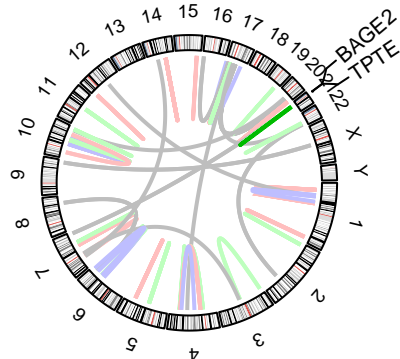


**TPTE**  
ENST00000618007.6

**BAGE2**  
ENST00000496773.1



2 kbp  
*introns not to scale*



No coding regions retained in fusion transcript.

**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion

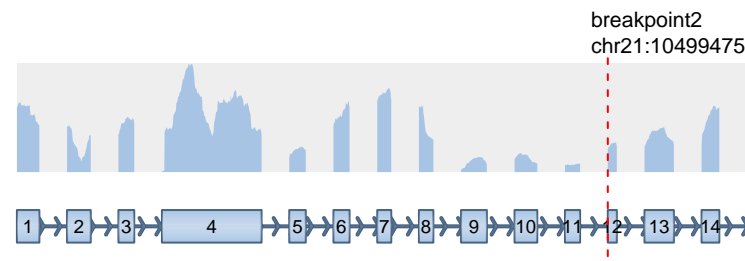
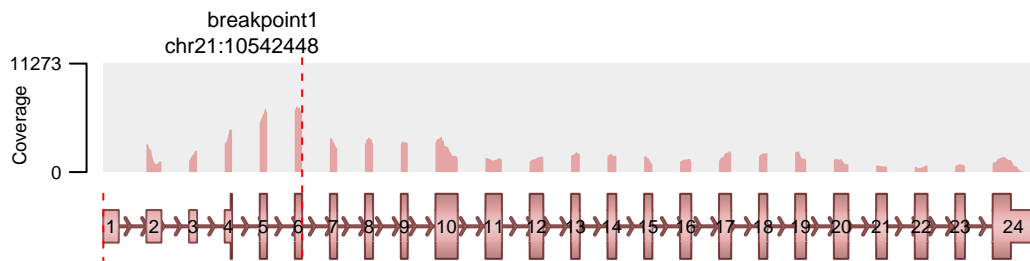
chromosome 21

p11.2



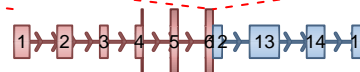
chromosome 21

p11.2

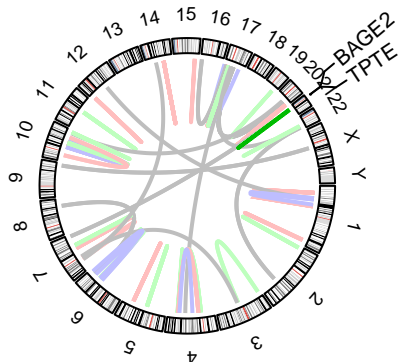


**TPTE**  
ENST00000618007.5

**BAGE2**  
ENST00000496773.1



2 kbp  
*introns not to scale*

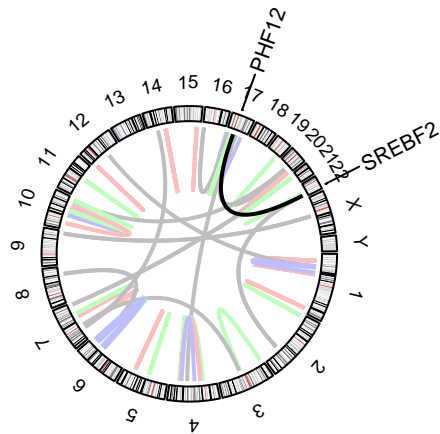
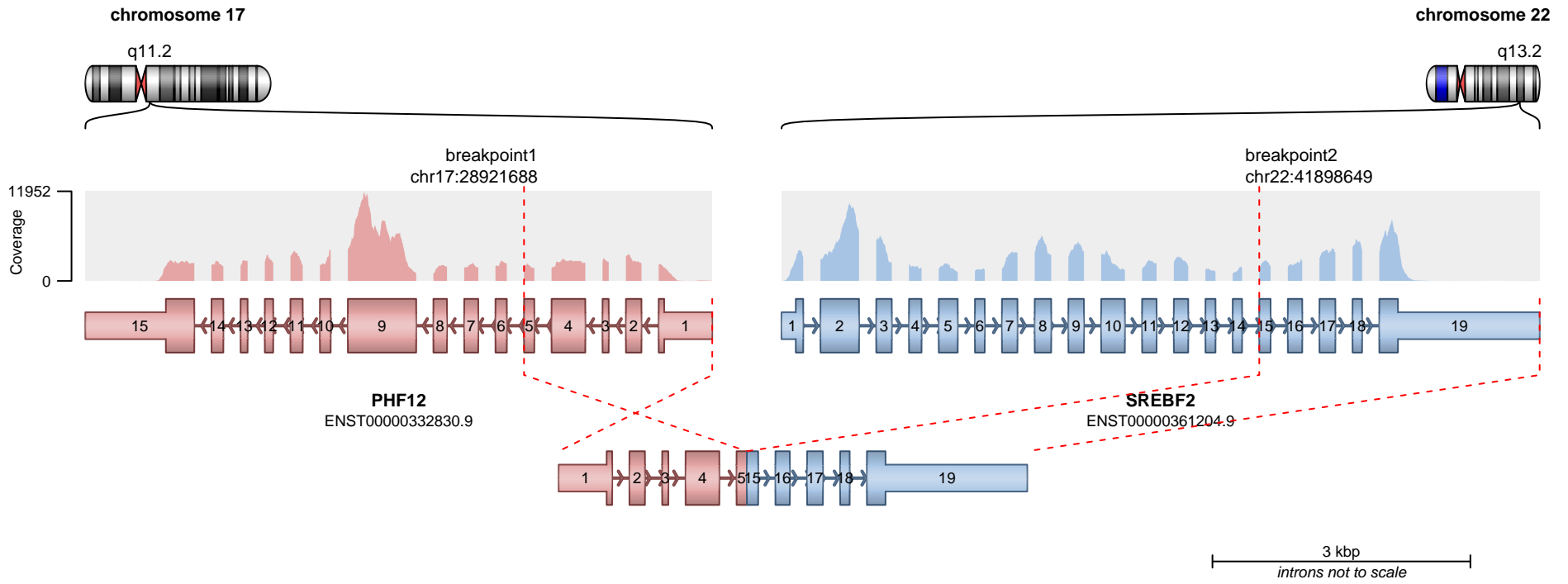


No protein domains retained in fusion.

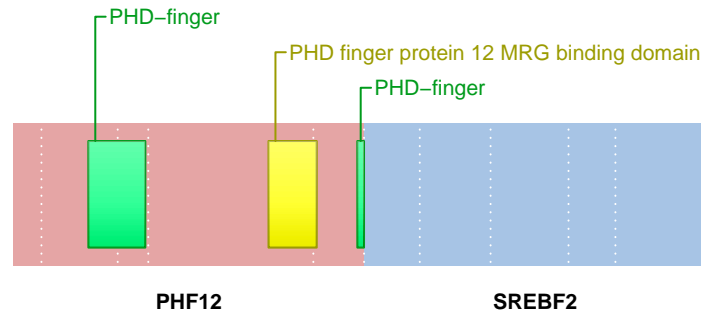
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



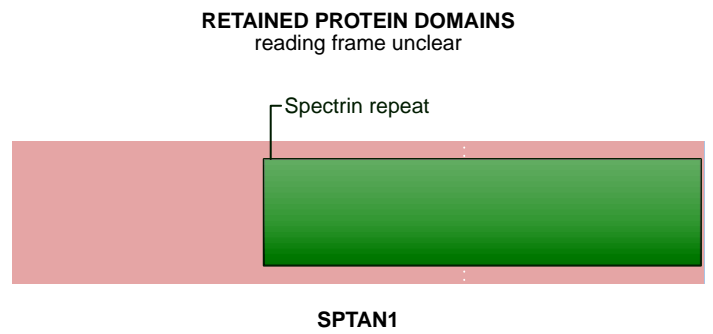
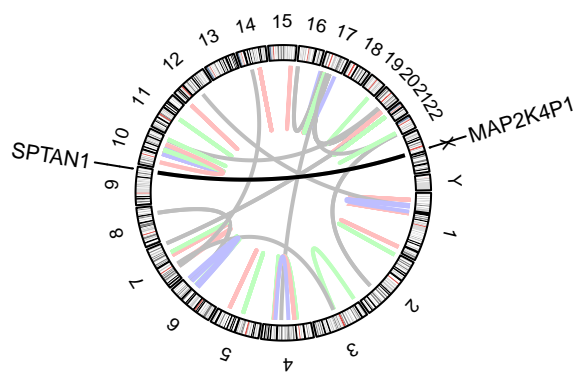
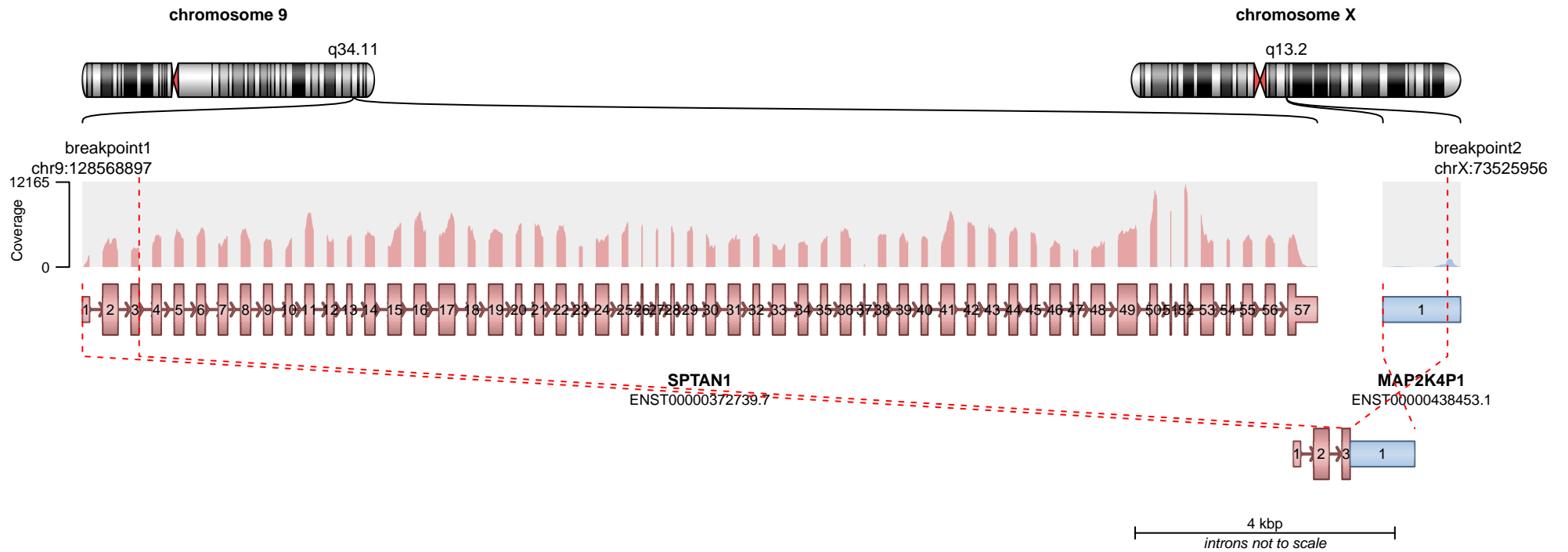
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 16  
Discordant mates = 0

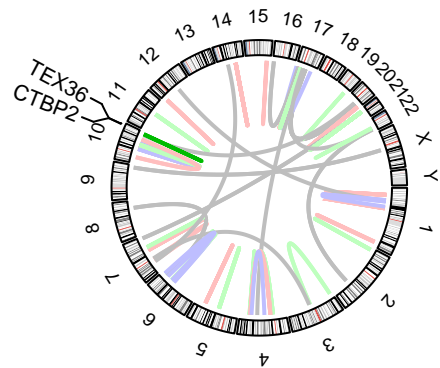
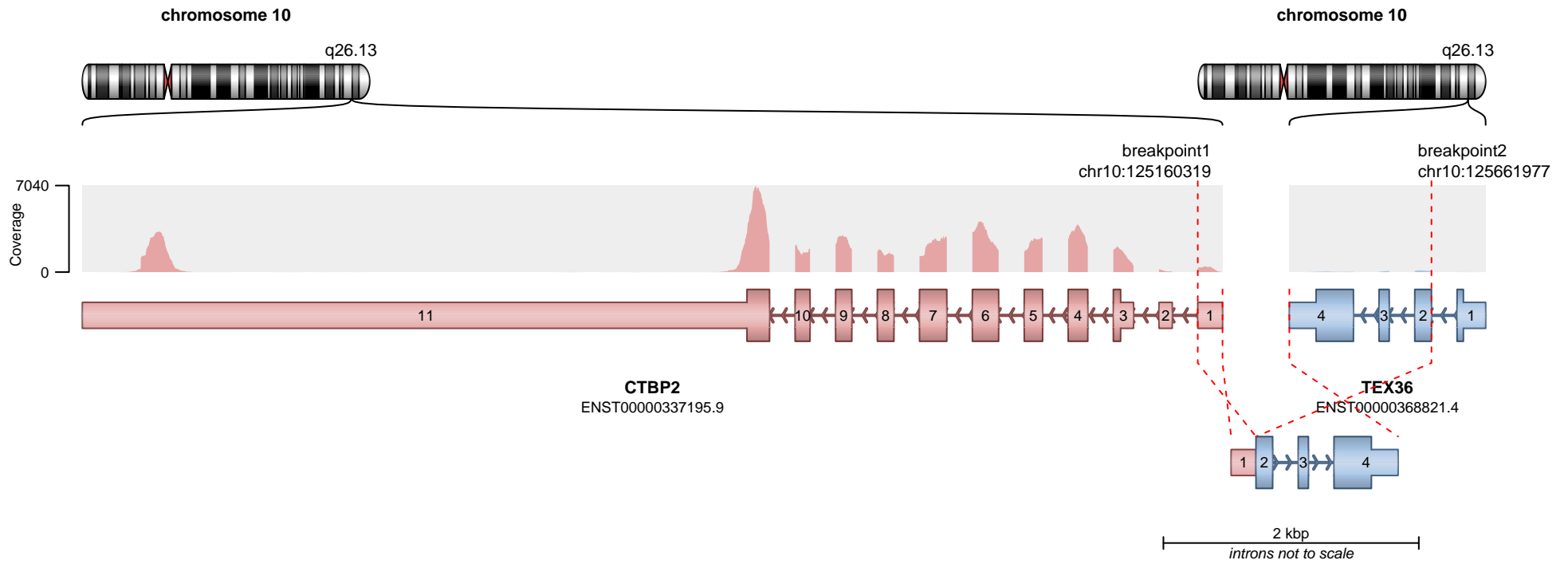
- translocation
- duplication
- deletion
- inversion



**SUPPORTING READ COUNT**

Split reads = 16  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



**RETAINED PROTEIN DOMAINS**  
reading frame unclear



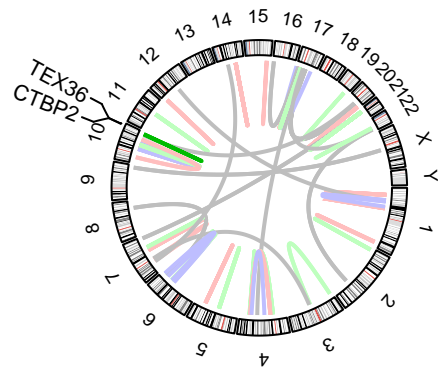
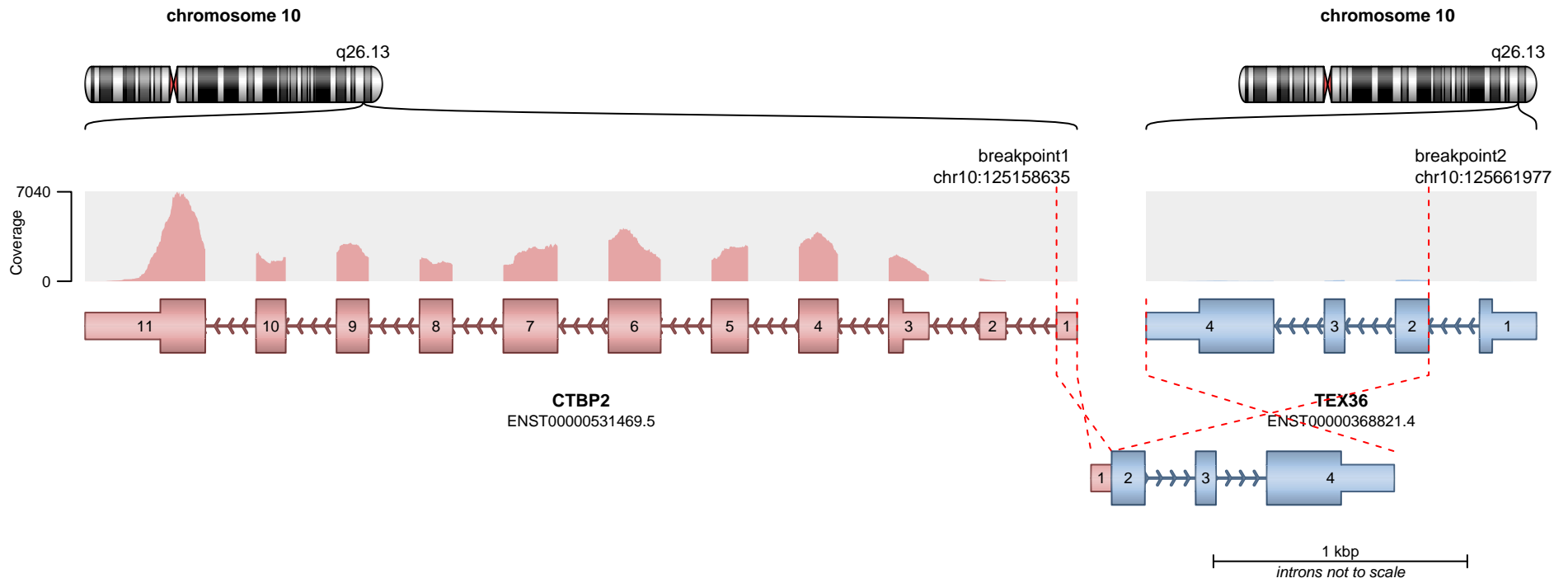
**TEX36**

Domain of unknown function with conserved HDNR motif

**SUPPORTING READ COUNT**

Split reads = 15  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



**RETAINED PROTEIN DOMAINS**  
reading frame unclear

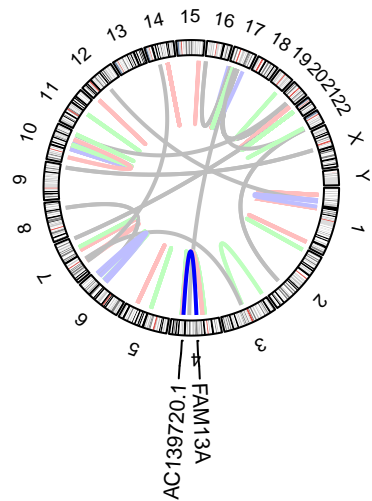
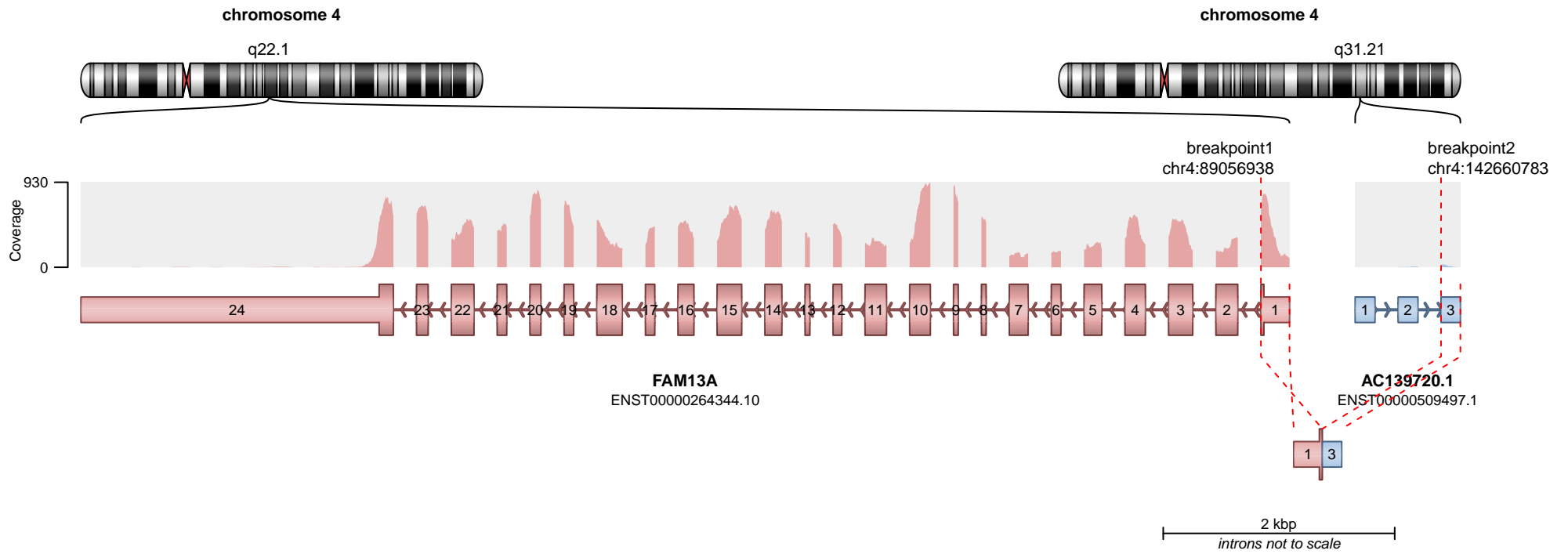


**TEX36**

Domain of unknown function with conserved HDNR motif

**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

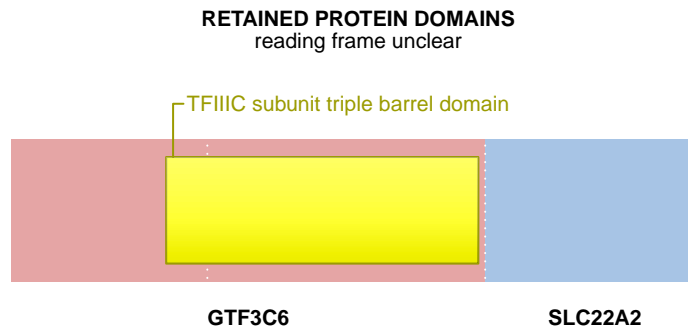
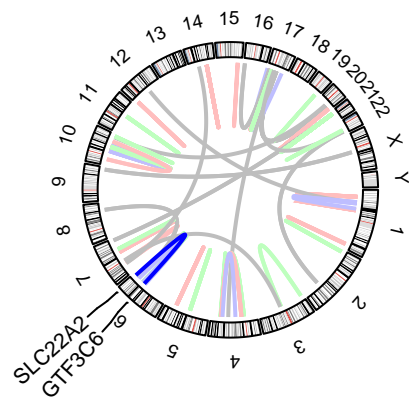
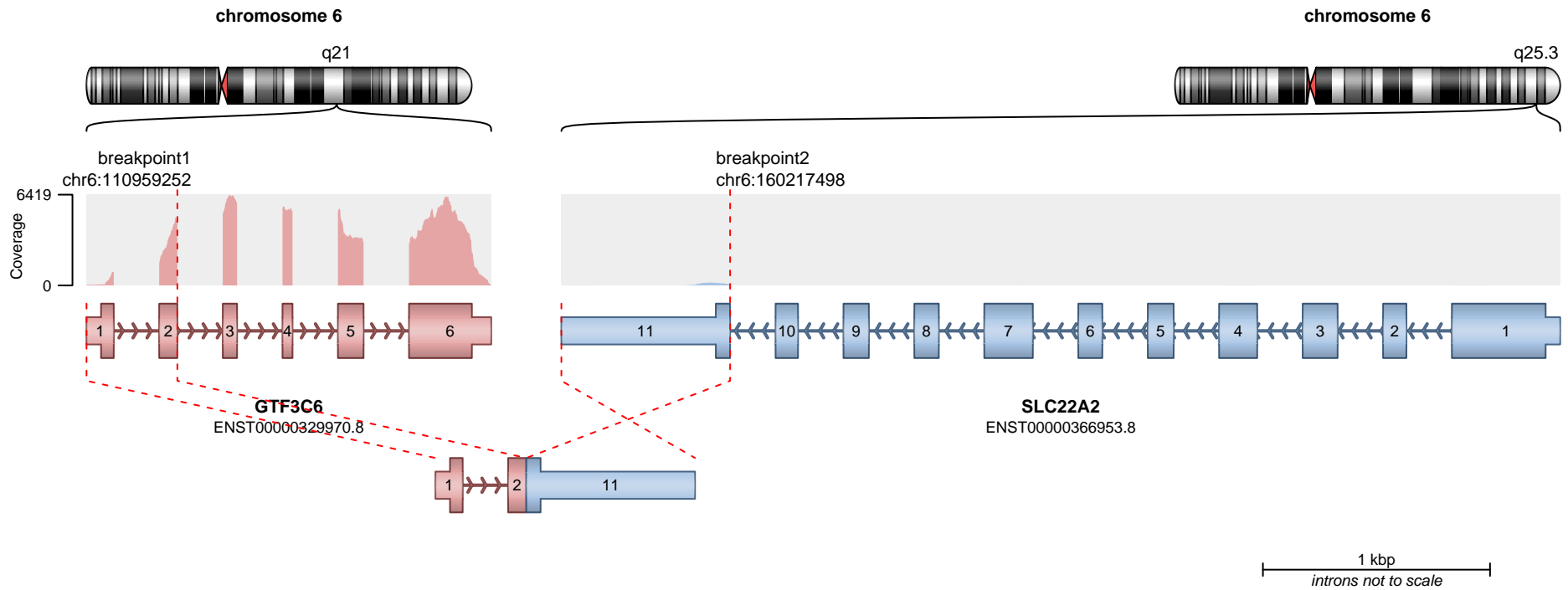


— translocation — deletion  
— duplication — inversion

No protein domains retained in fusion.

**SUPPORTING READ COUNT**

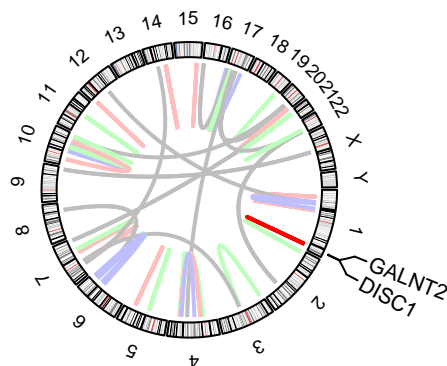
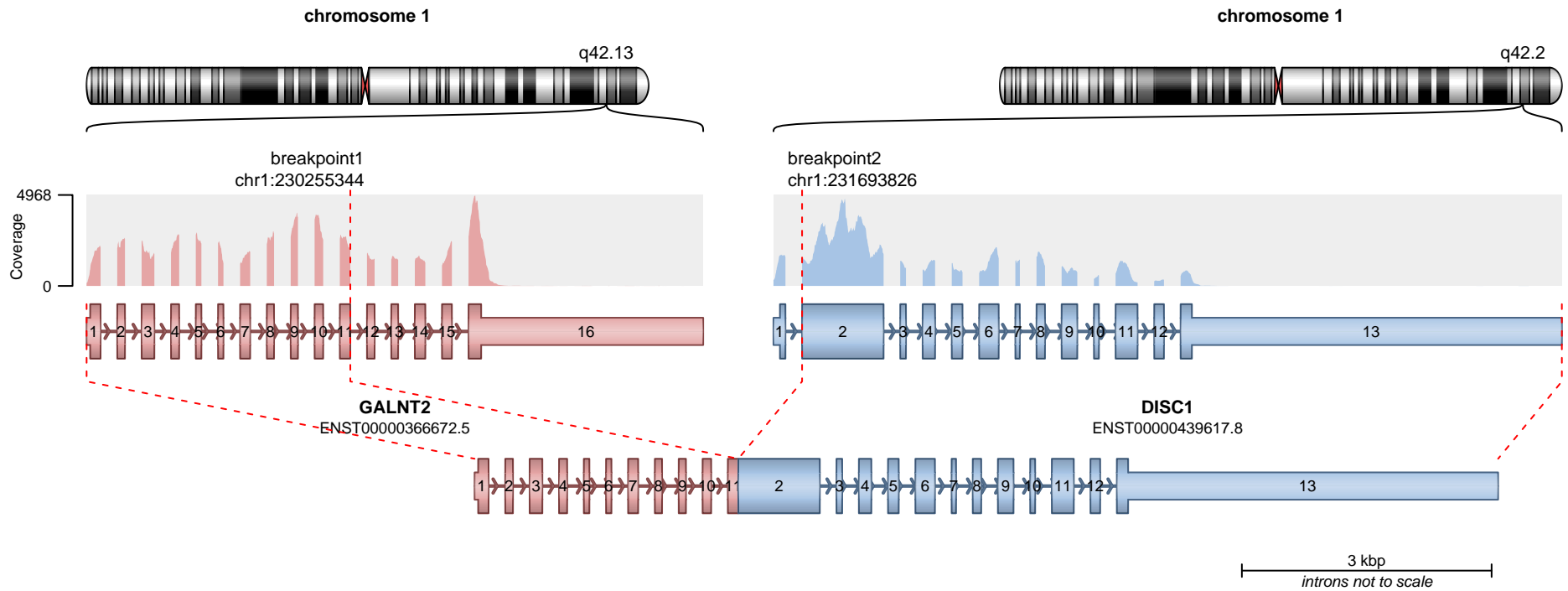
Split reads = 15  
Discordant mates = 0



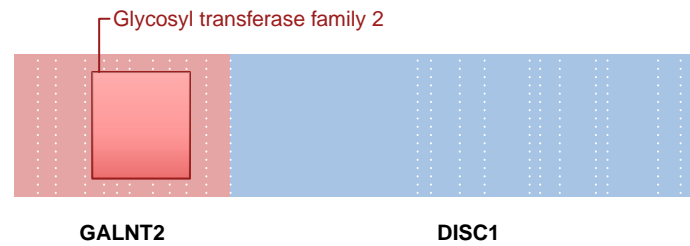
**SUPPORTING READ COUNT**

Split reads = 13  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



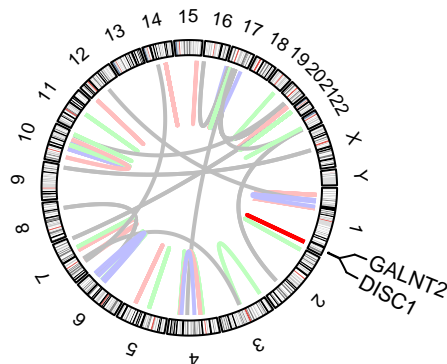
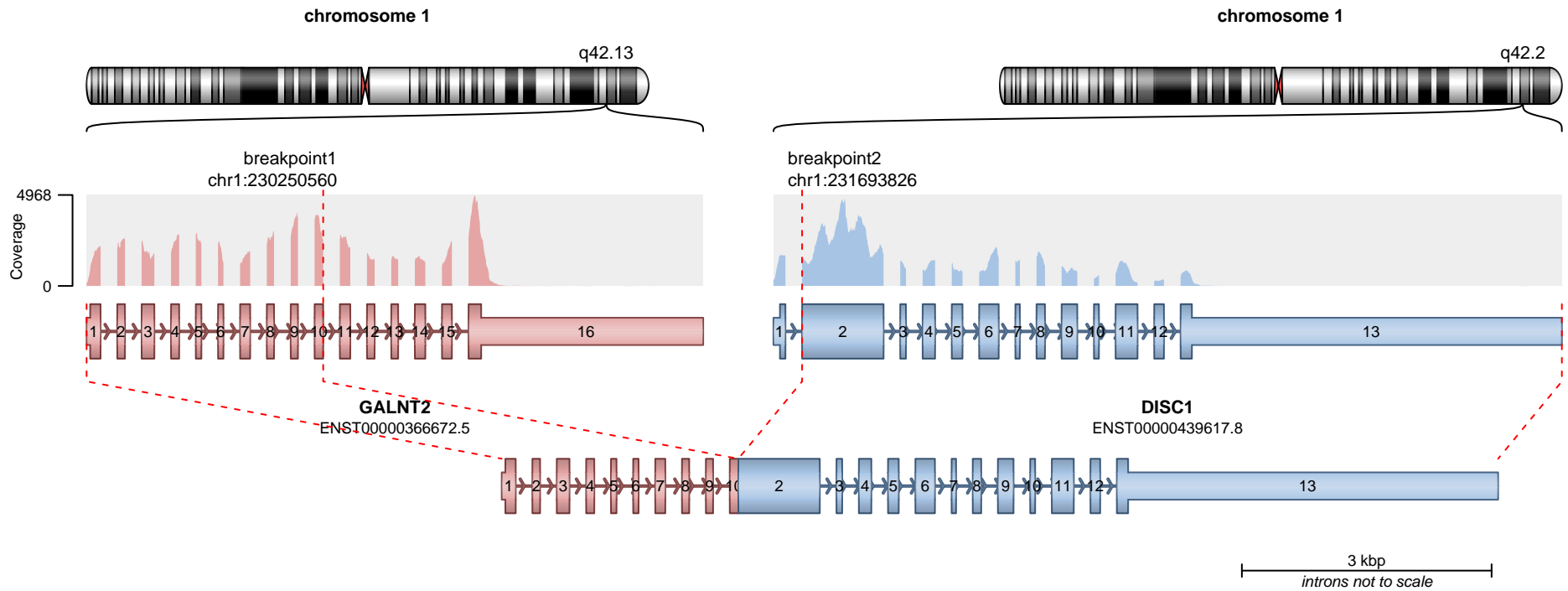
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 12  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



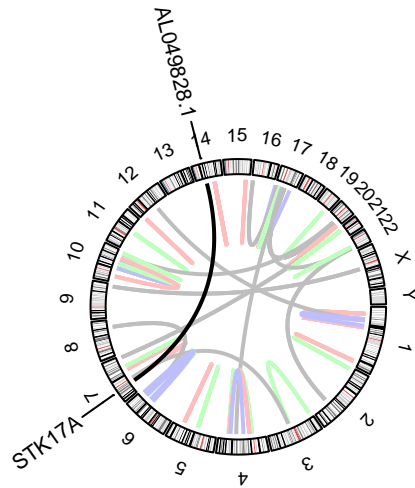
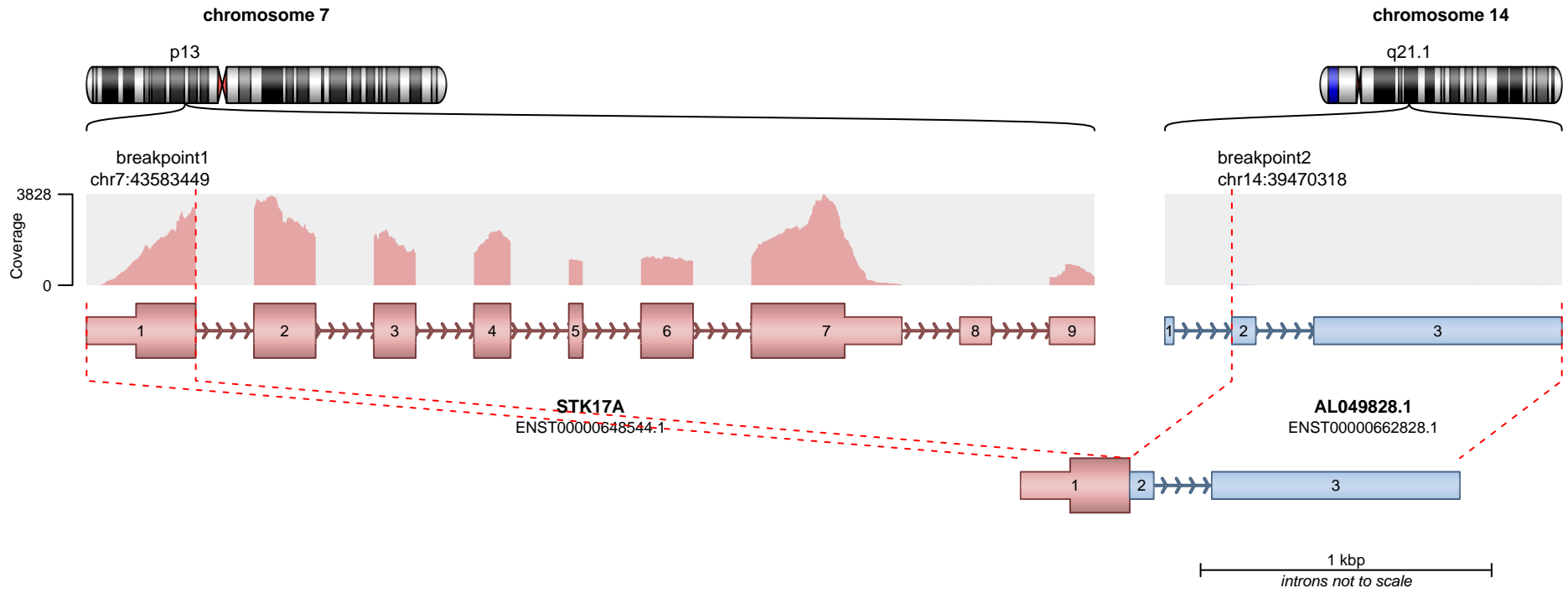
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



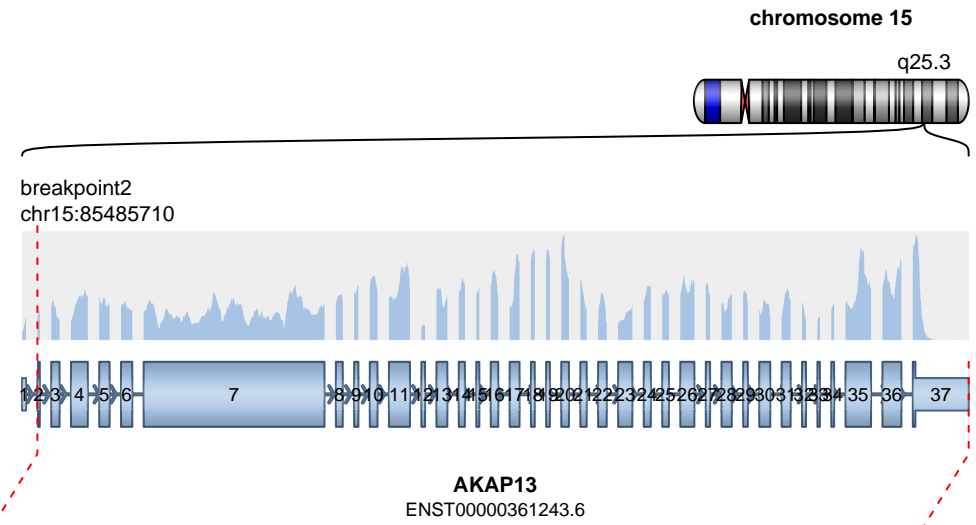
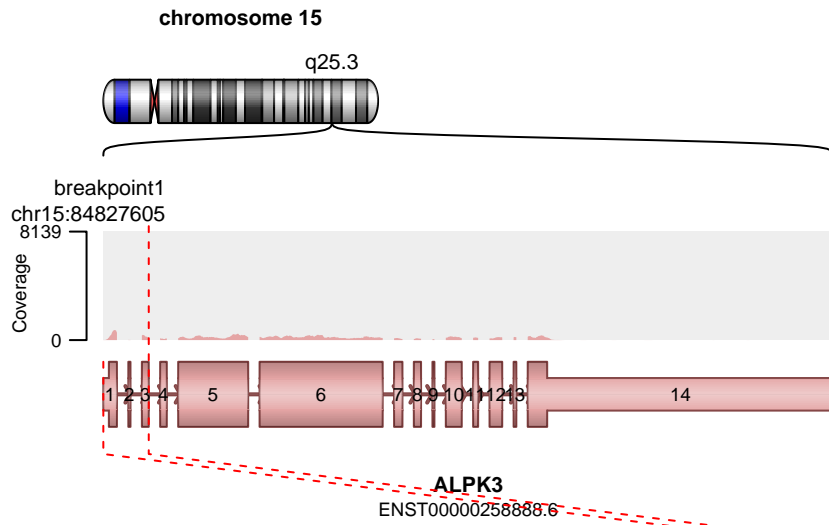
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



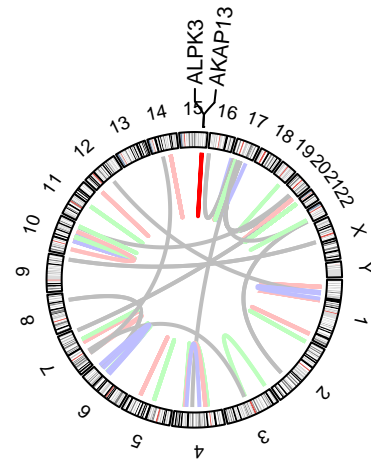
**SUPPORTING READ COUNT**

Split reads = 12  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion

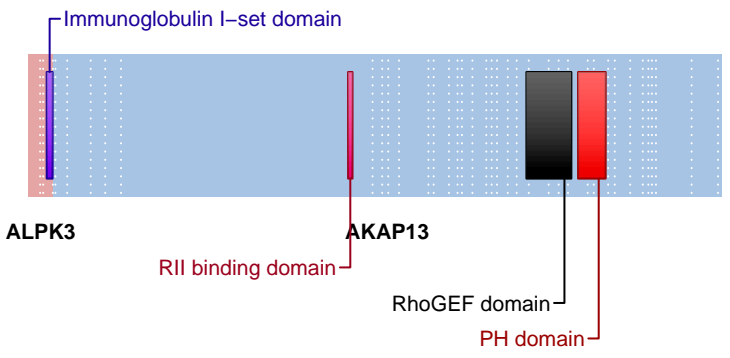


6 kbp  
introns not to scale



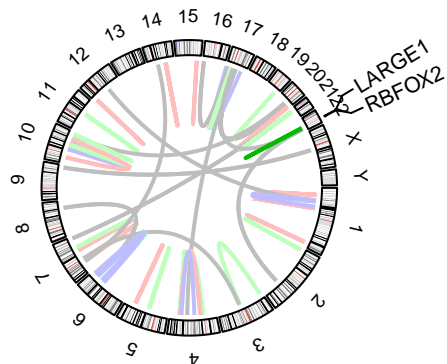
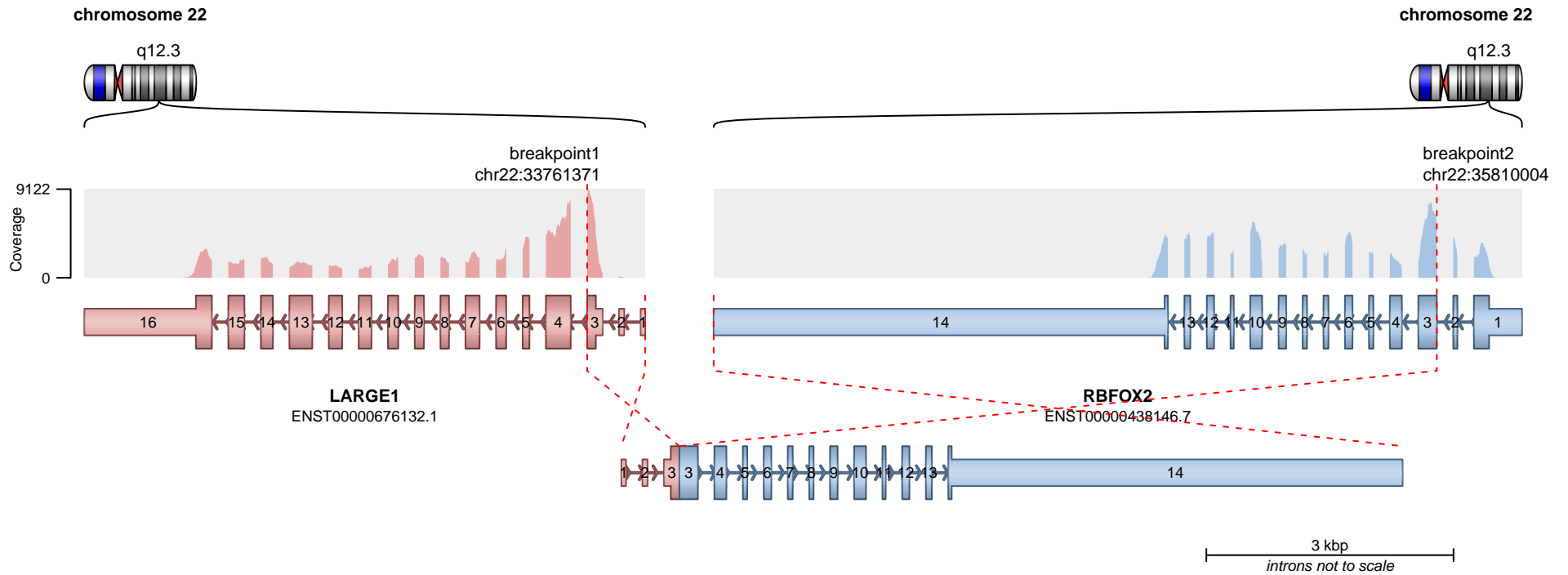
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear

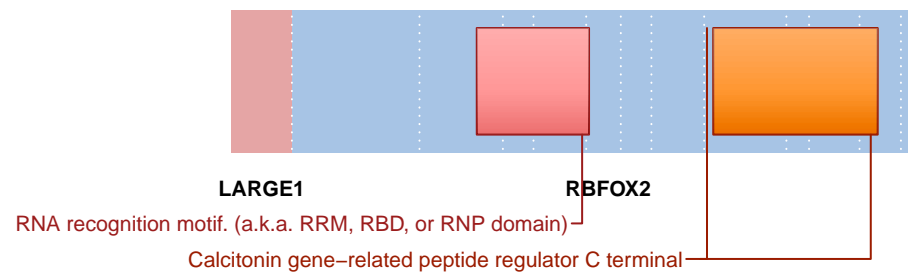


**SUPPORTING READ COUNT**

Split reads = 10  
Discordant mates = 0



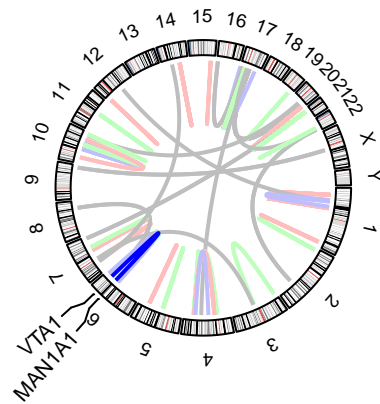
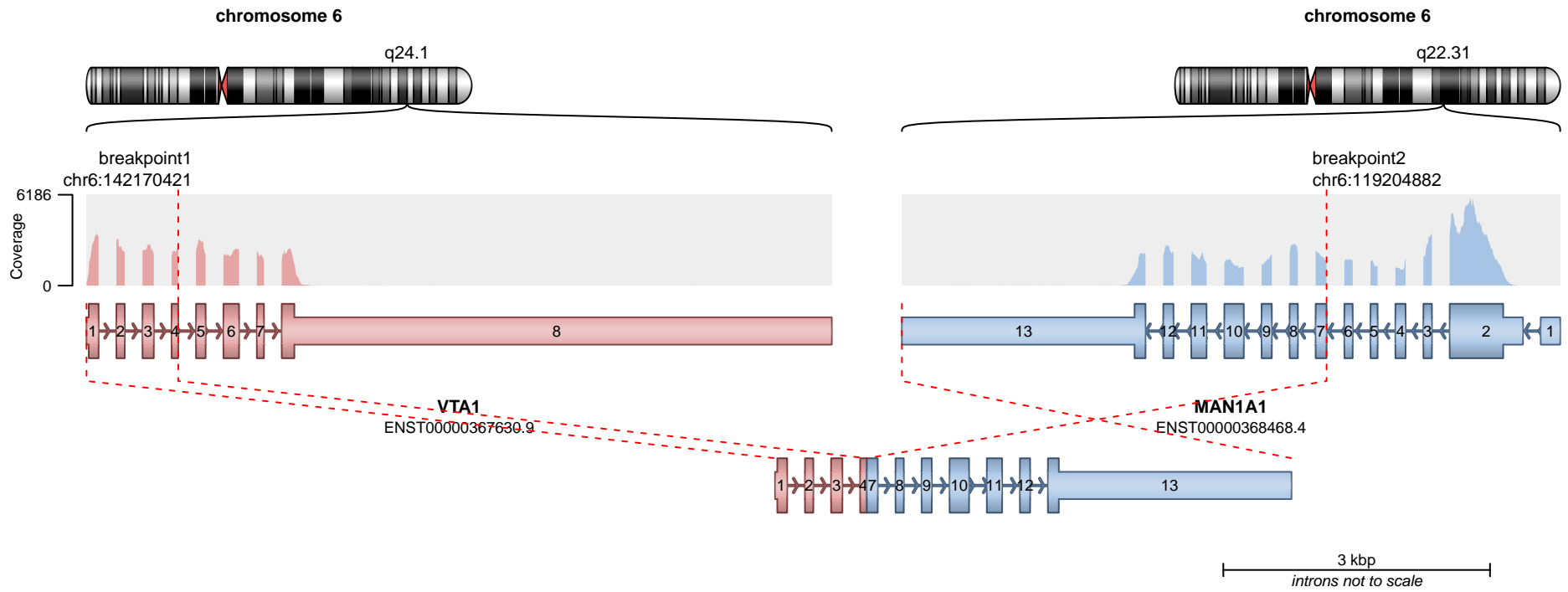
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



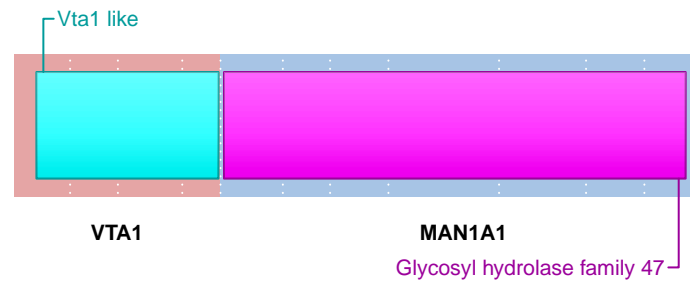
**SUPPORTING READ COUNT**

Split reads = 10  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



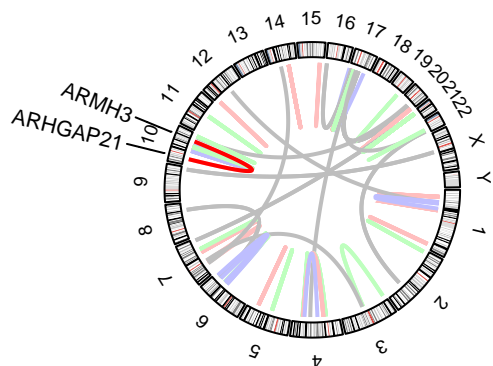
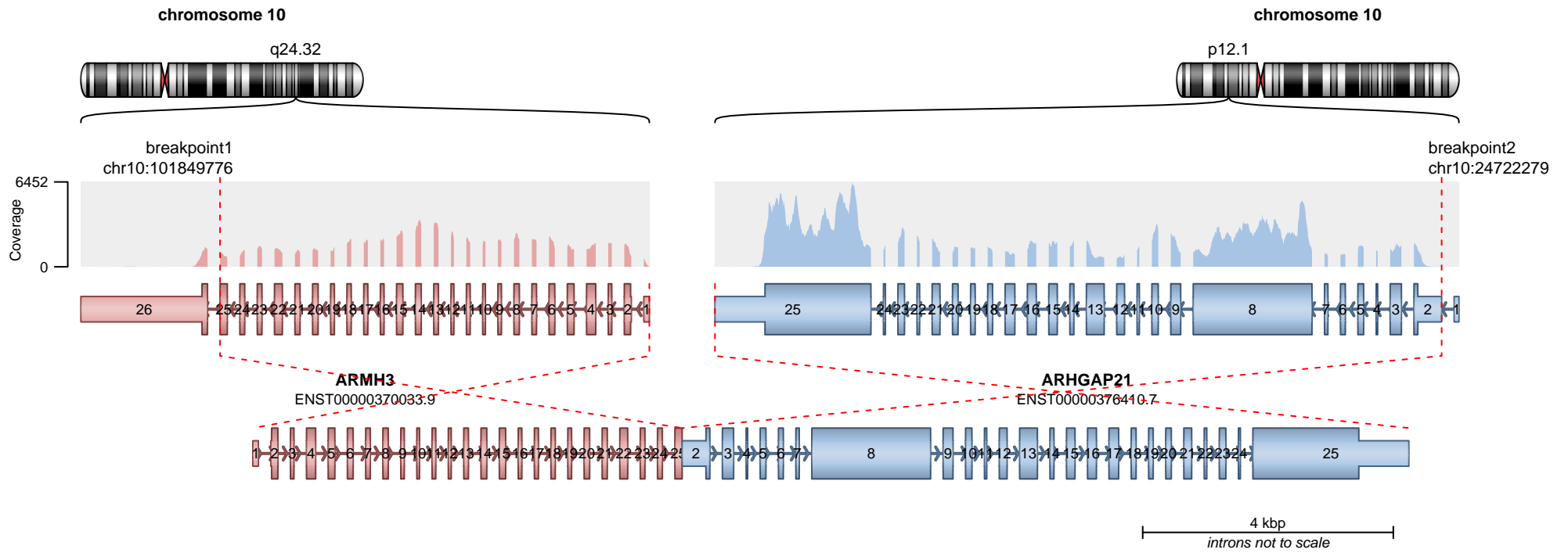
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



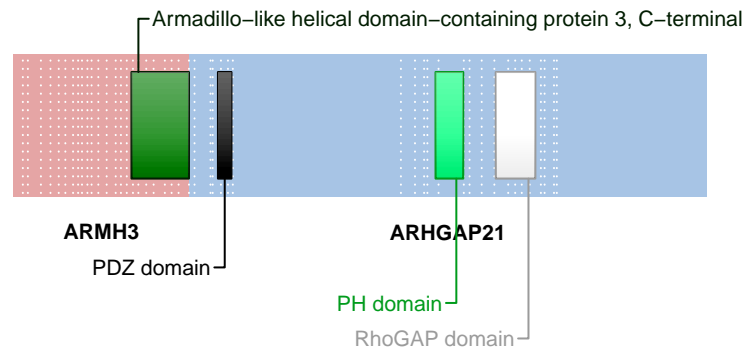
**SUPPORTING READ COUNT**

Split reads = 9  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



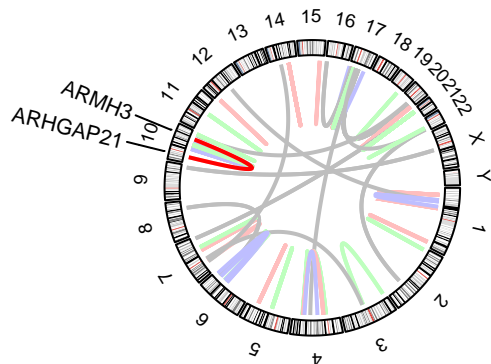
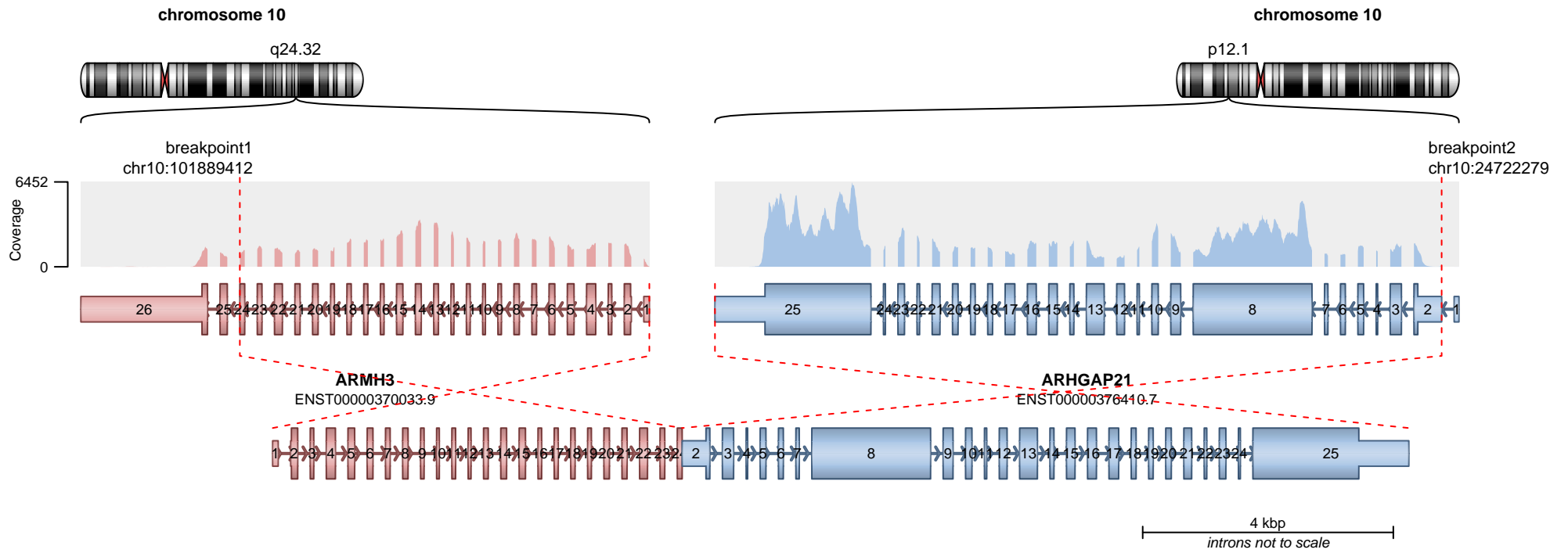
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



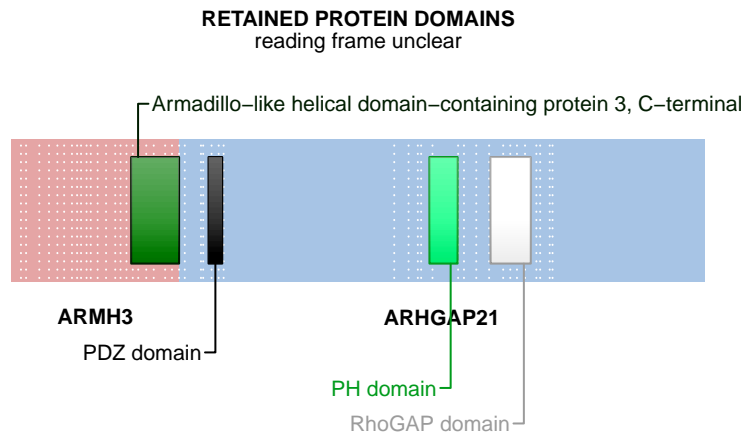
**SUPPORTING READ COUNT**

Split reads = 8  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

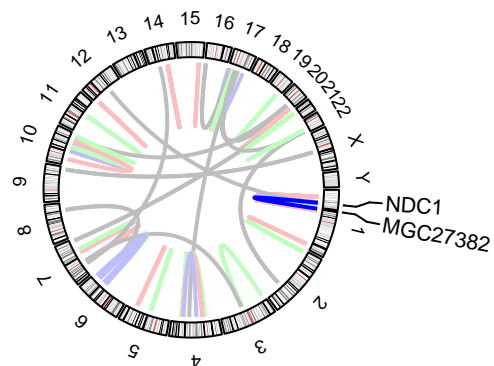
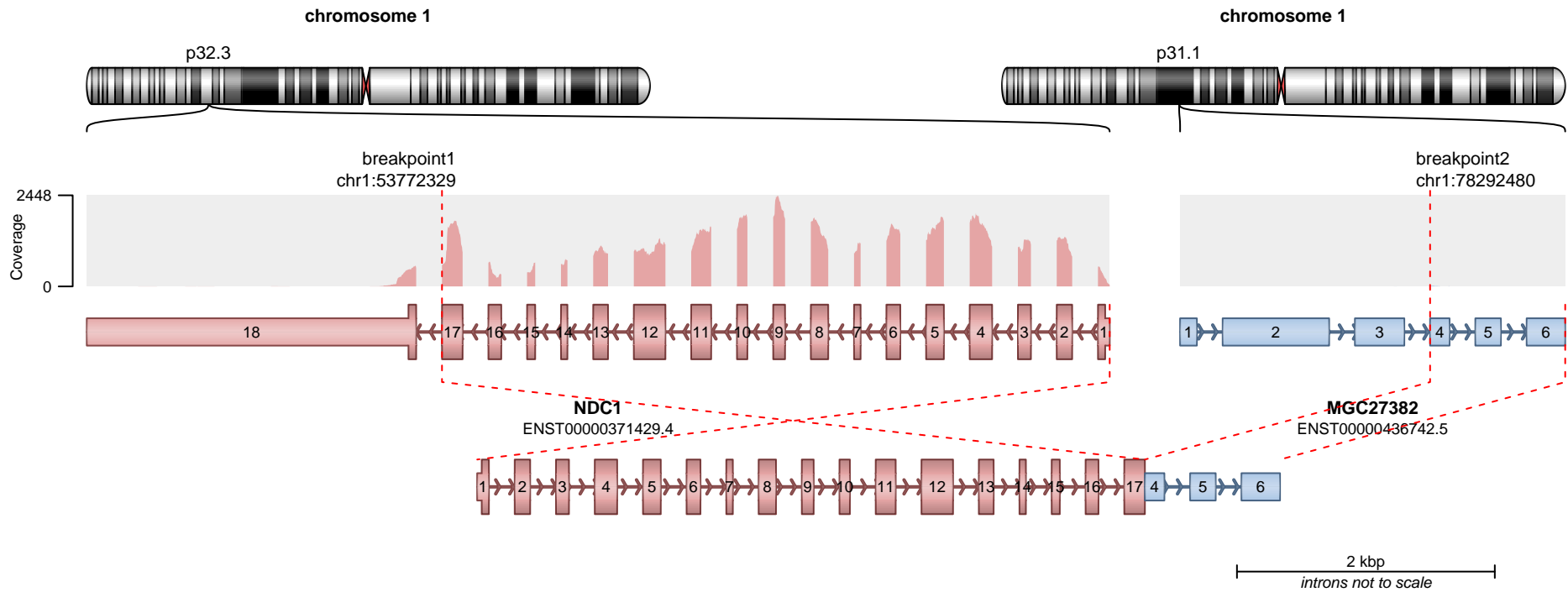


— translocation — deletion  
— duplication — inversion

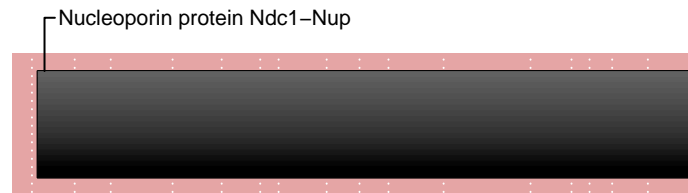


**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 0



**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**NDC1**

**SUPPORTING READ COUNT**

Split reads = 8  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion