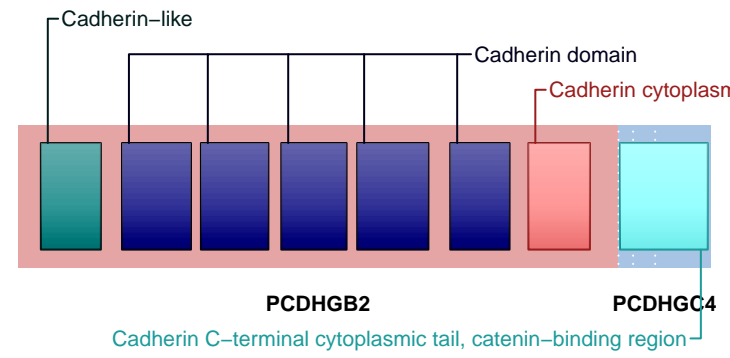


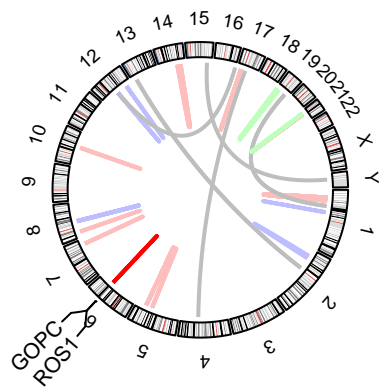
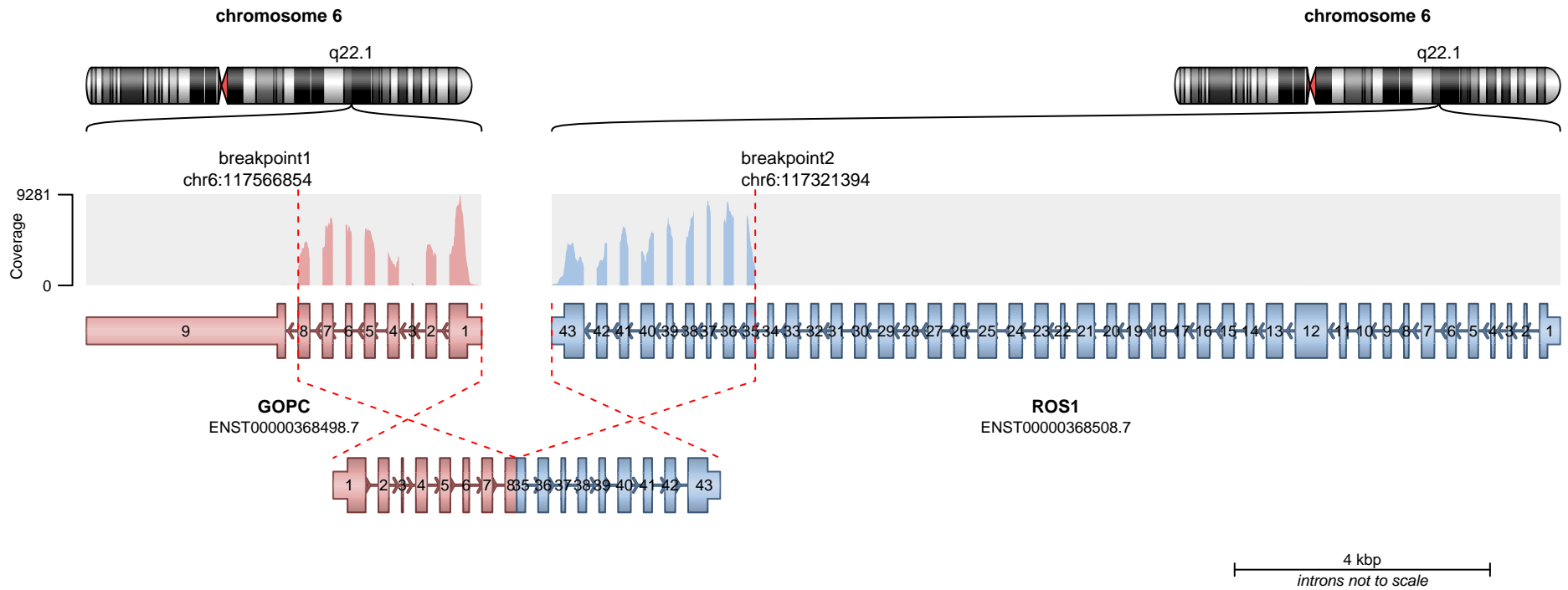
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



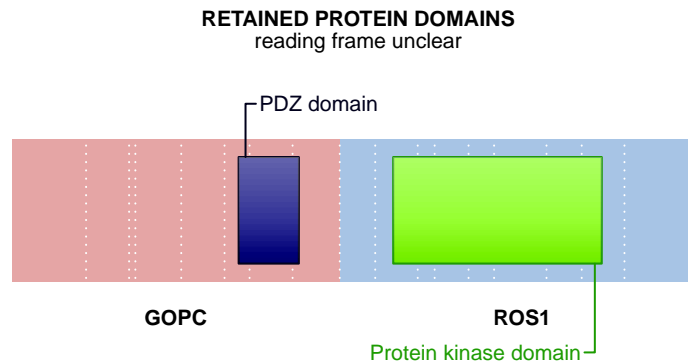
**SUPPORTING READ COUNT**

Split reads = 928  
Discordant mates = 8

— translocation    — deletion  
— duplication    — inversion

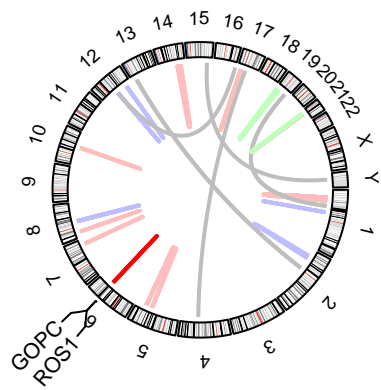
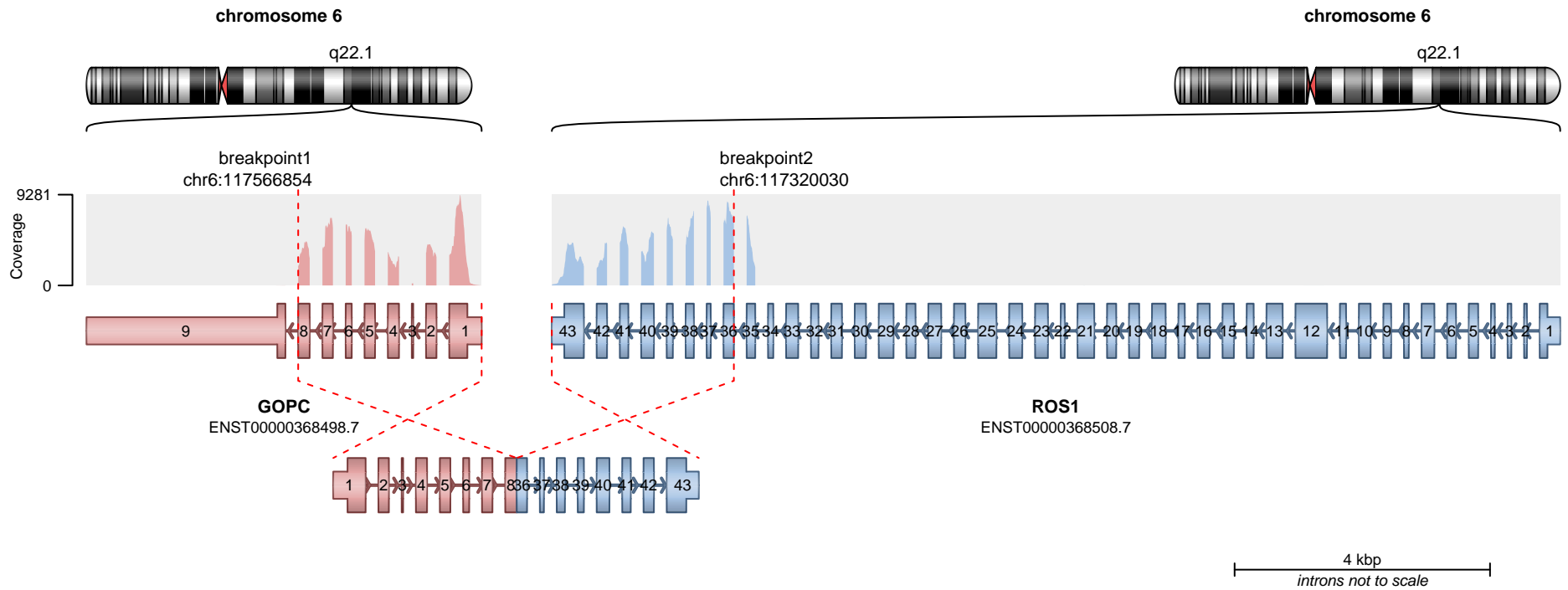


— translocation — deletion  
— duplication — inversion

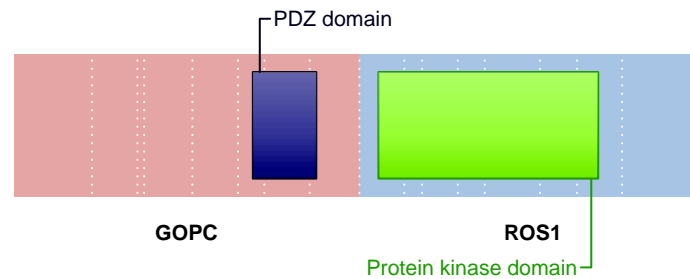


**SUPPORTING READ COUNT**

Split reads = 805  
Discordant mates = 9



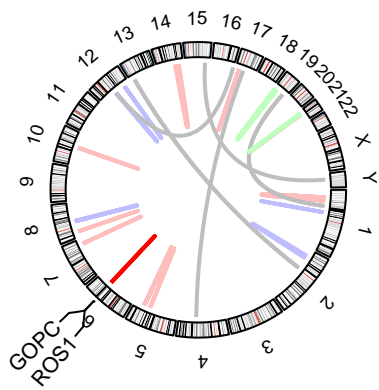
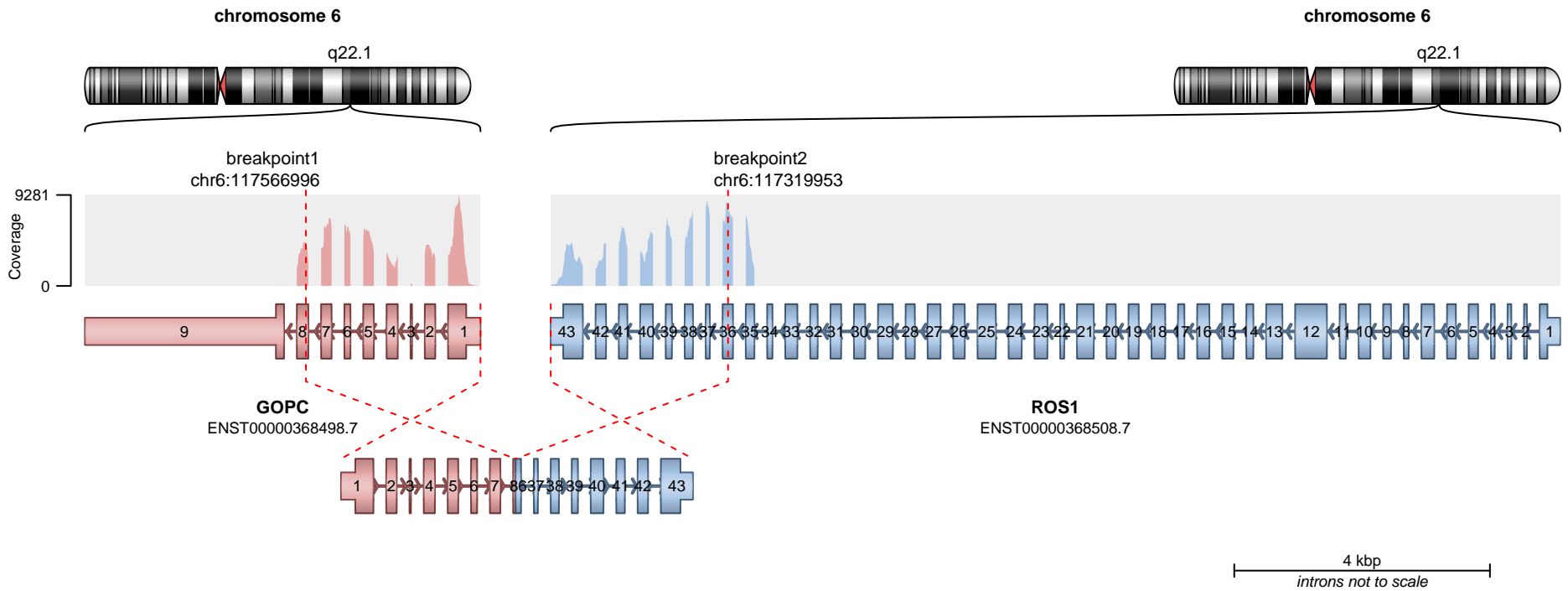
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



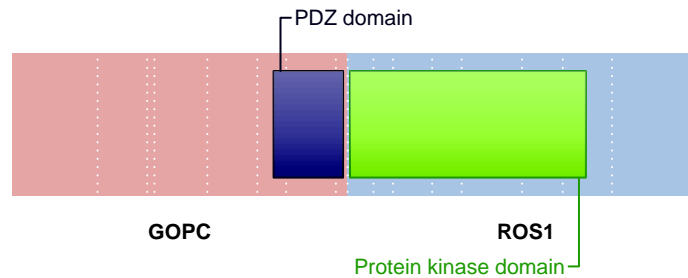
**SUPPORTING READ COUNT**

Split reads = 21  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



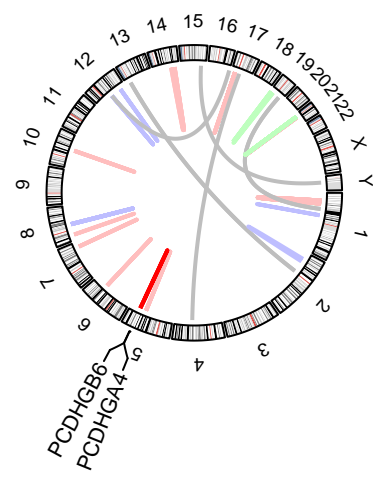
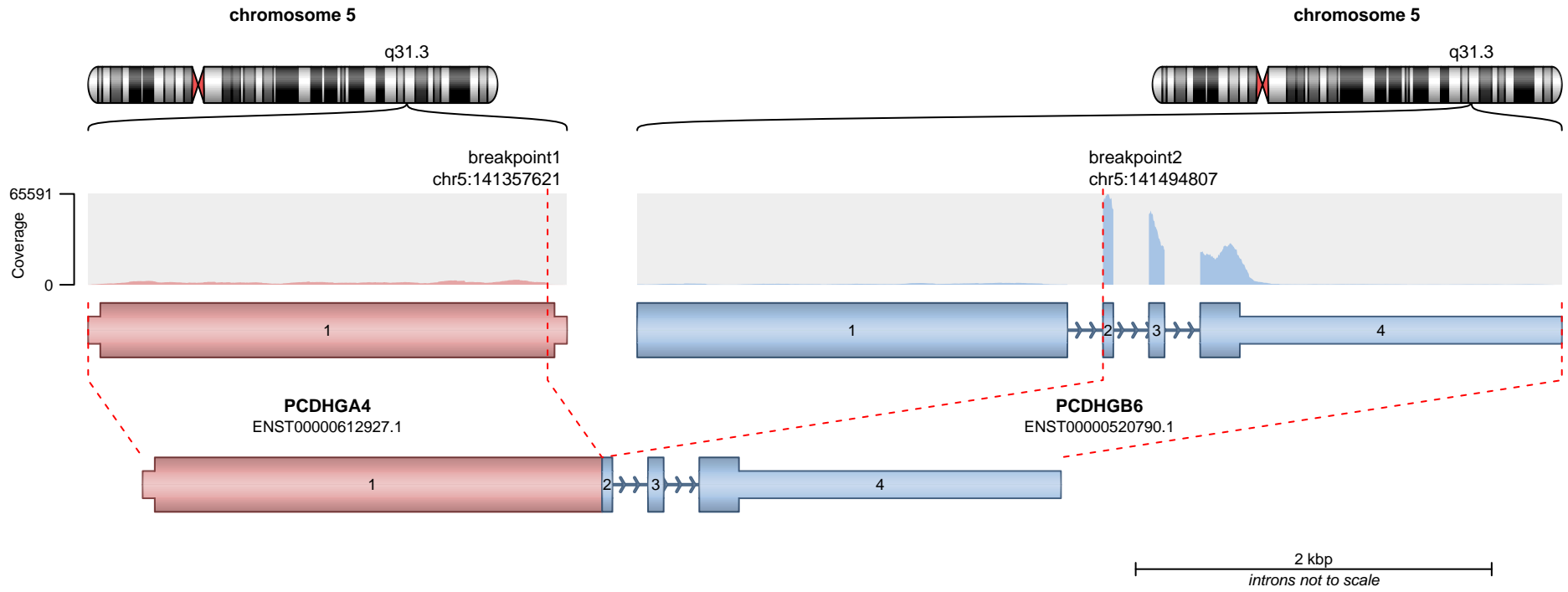
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

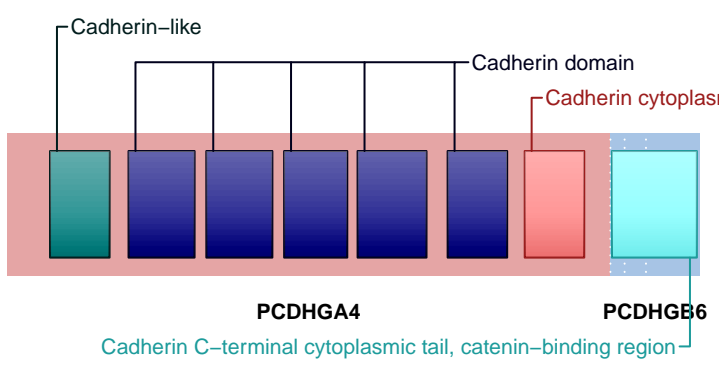
Split reads = 3  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



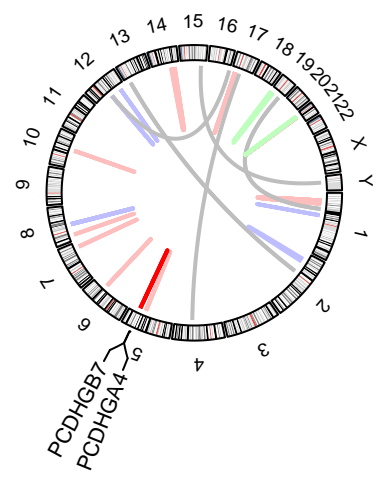
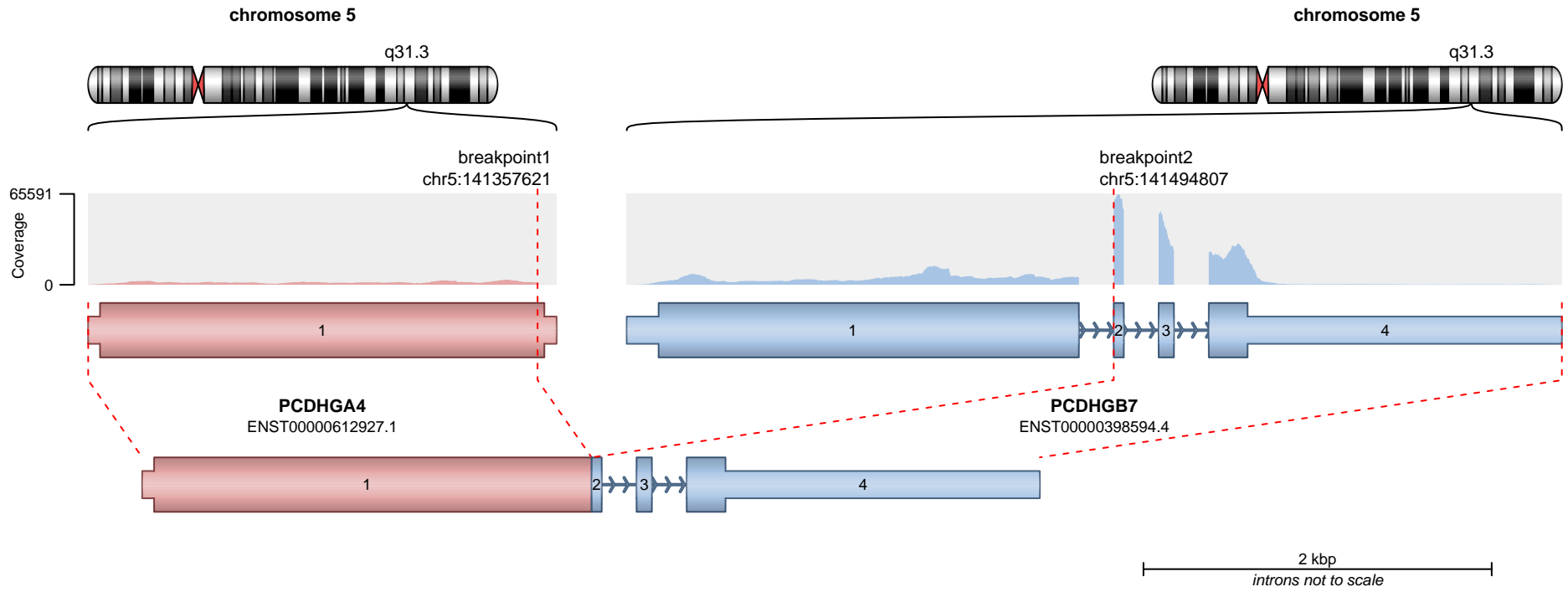
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



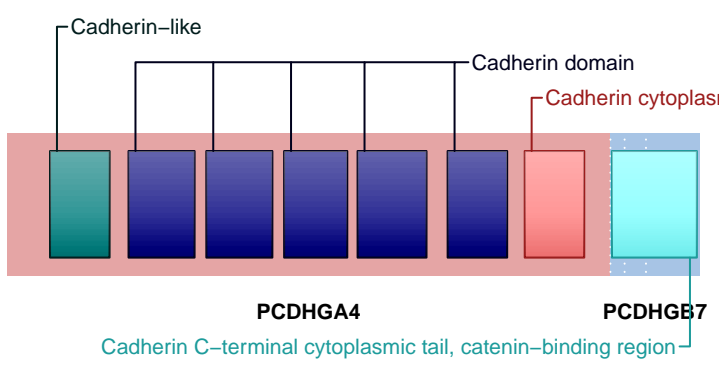
**SUPPORTING READ COUNT**

Split reads = 533  
Discordant mates = 6



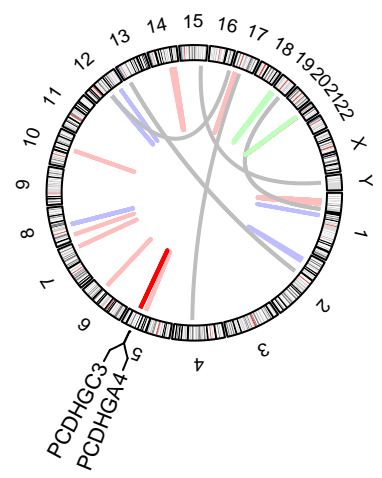
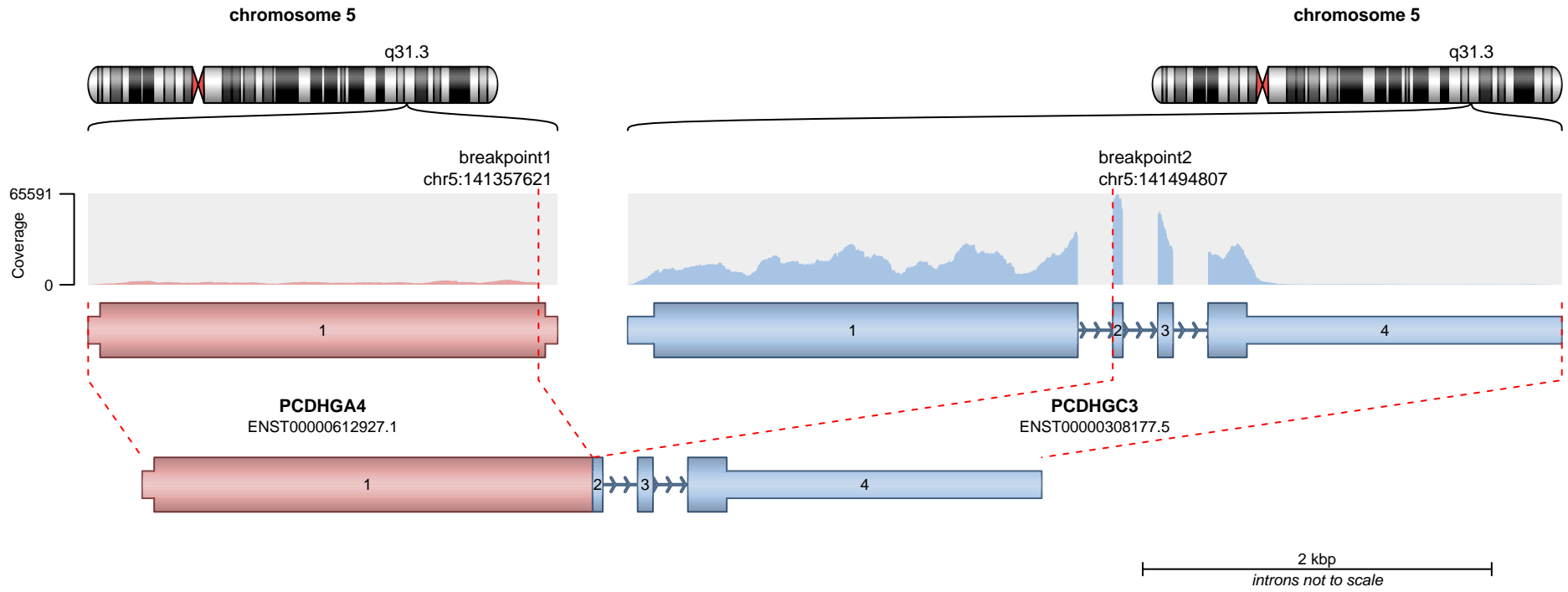
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



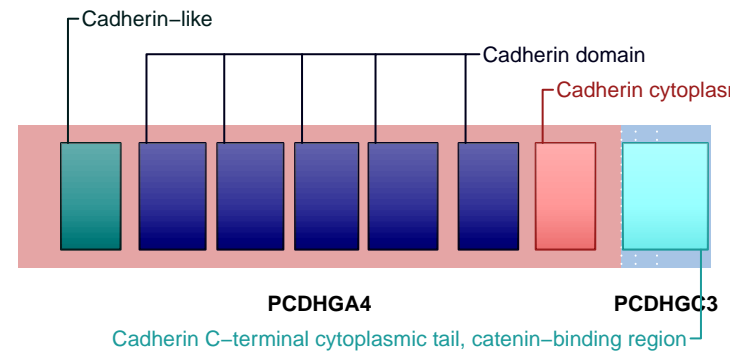
**SUPPORTING READ COUNT**

Split reads = 533  
Discordant mates = 6



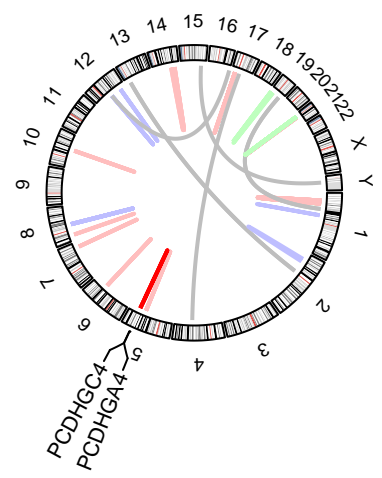
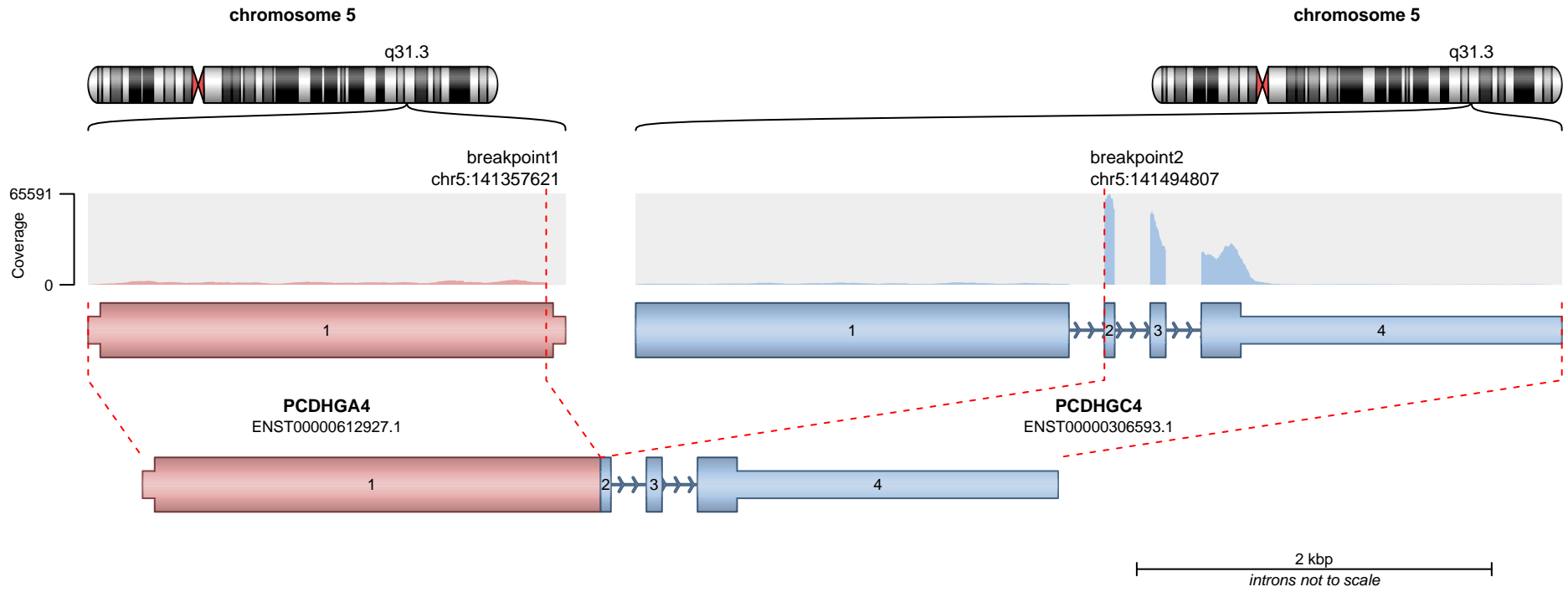
— translocation — deletion  
— duplication — inversion-like

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



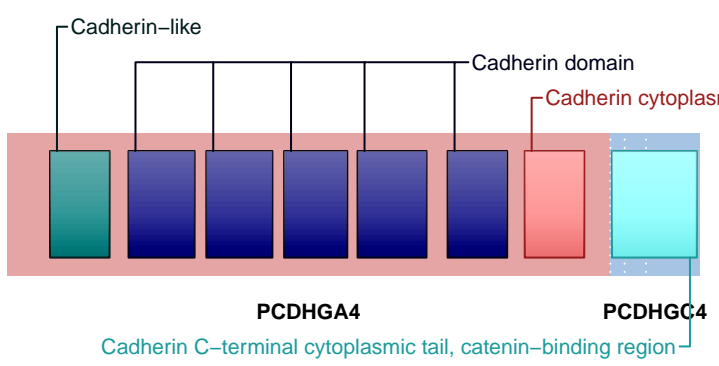
**SUPPORTING READ COUNT**

Split reads = 533  
Discordant mates = 6



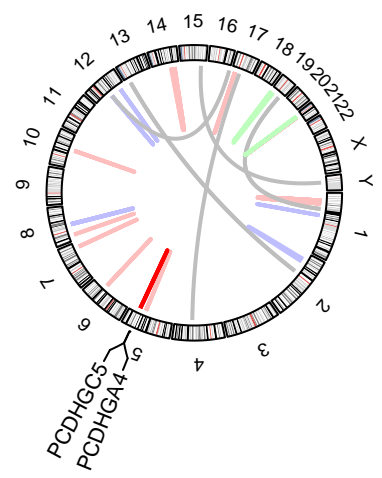
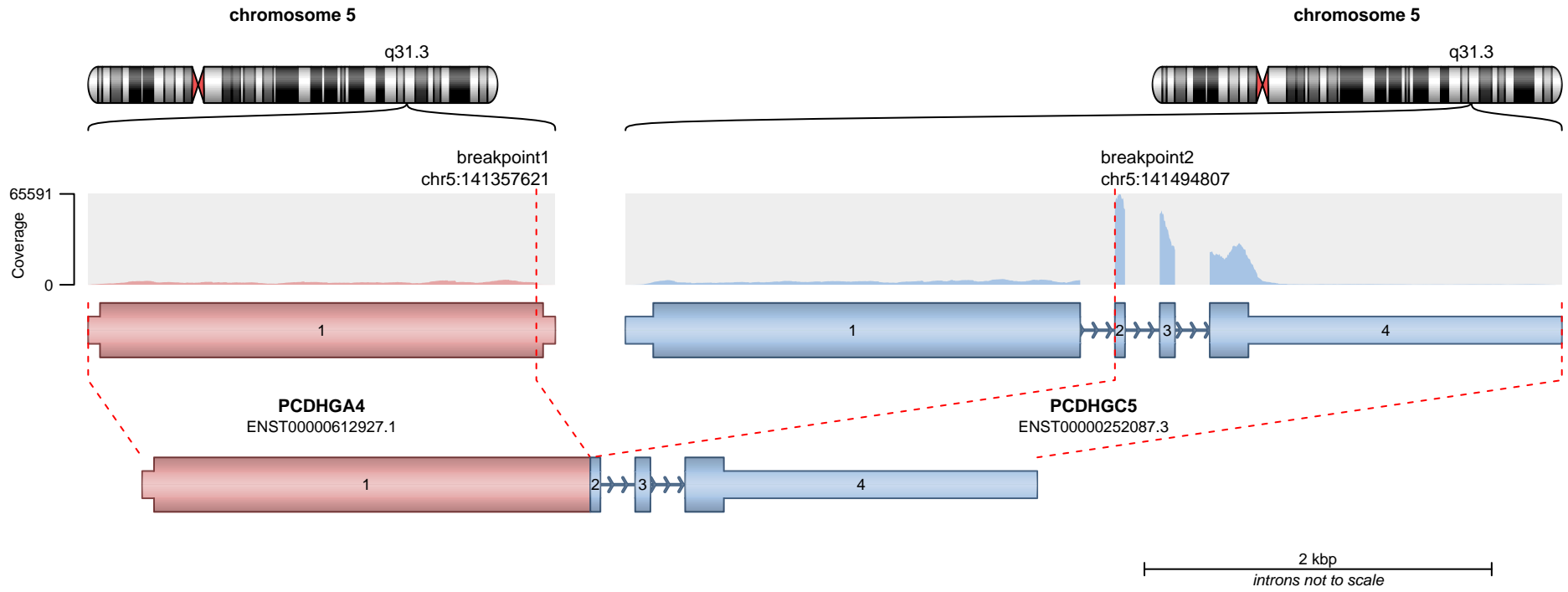
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



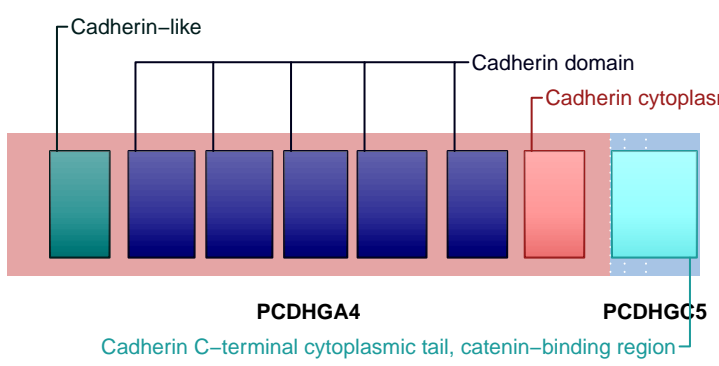
**SUPPORTING READ COUNT**

Split reads = 533  
Discordant mates = 6



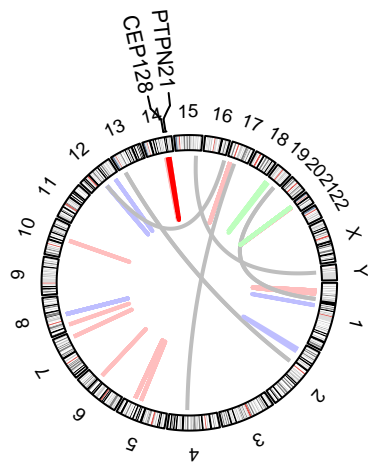
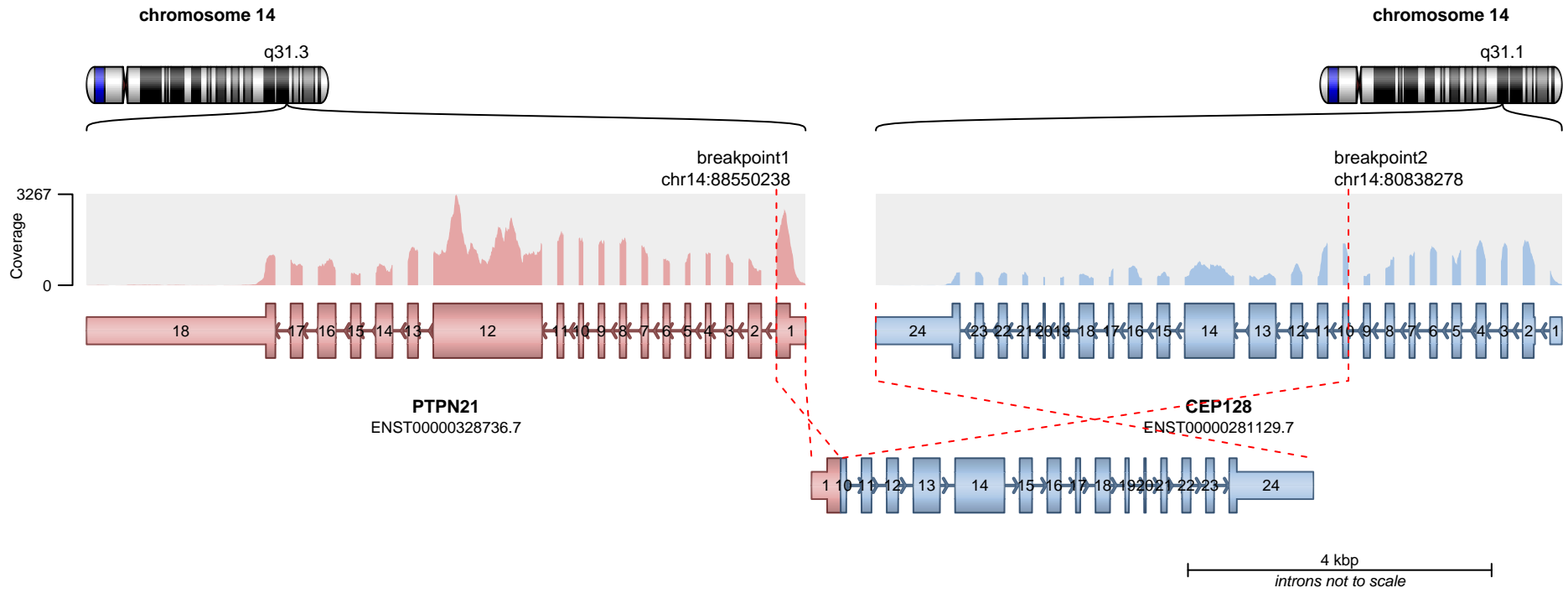
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear

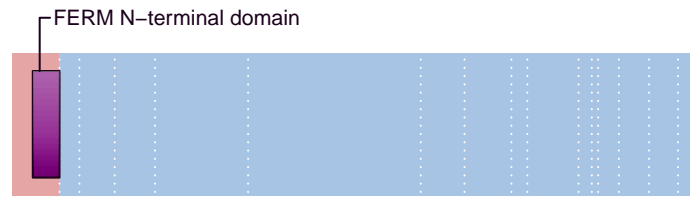


**SUPPORTING READ COUNT**

Split reads = 533  
Discordant mates = 6



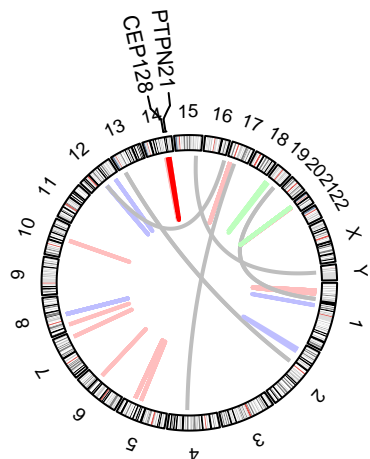
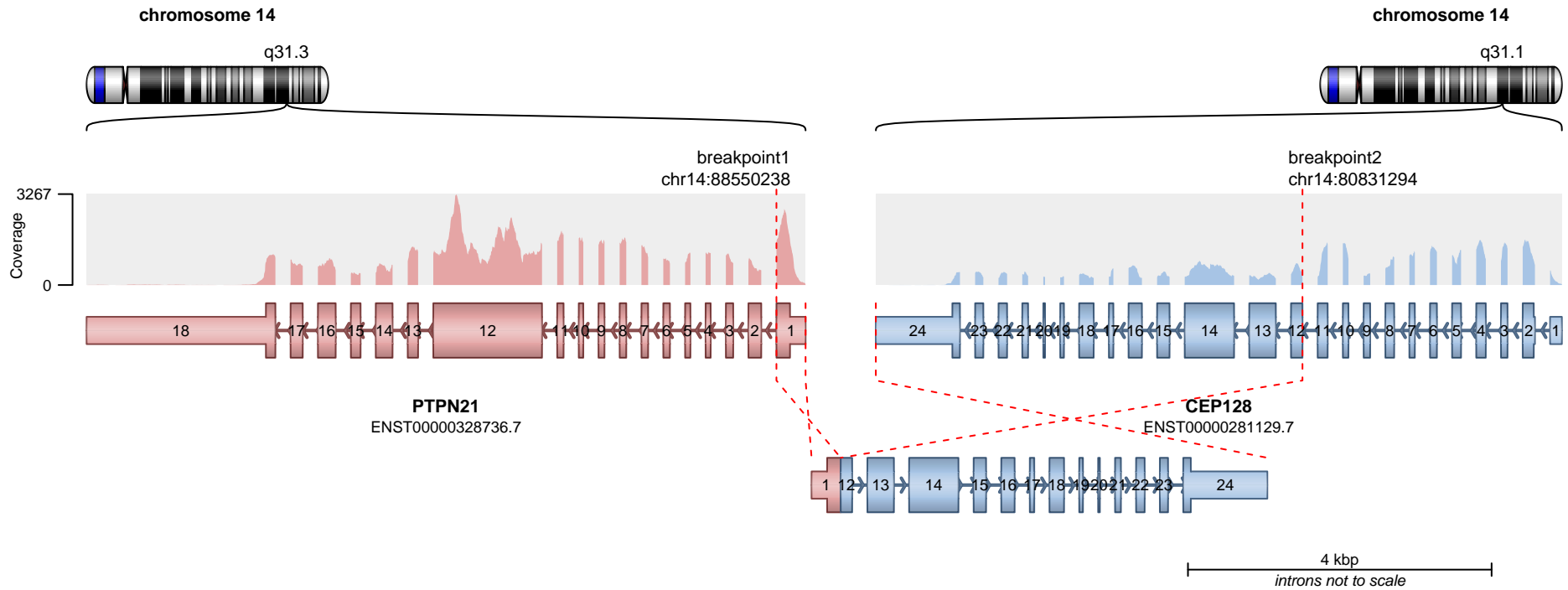
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



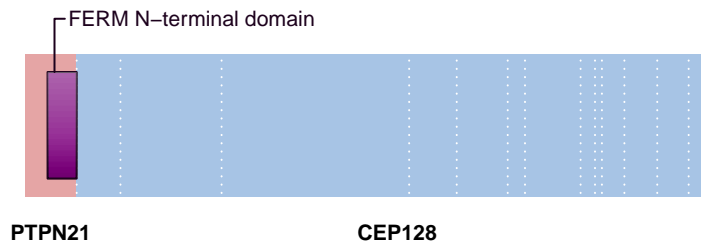
**SUPPORTING READ COUNT**

Split reads = 350  
Discordant mates = 13

- translocation
- duplication
- deletion
- inversion



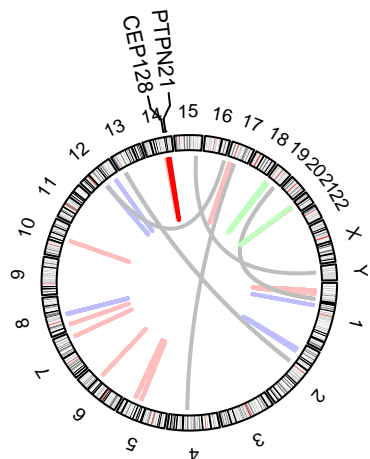
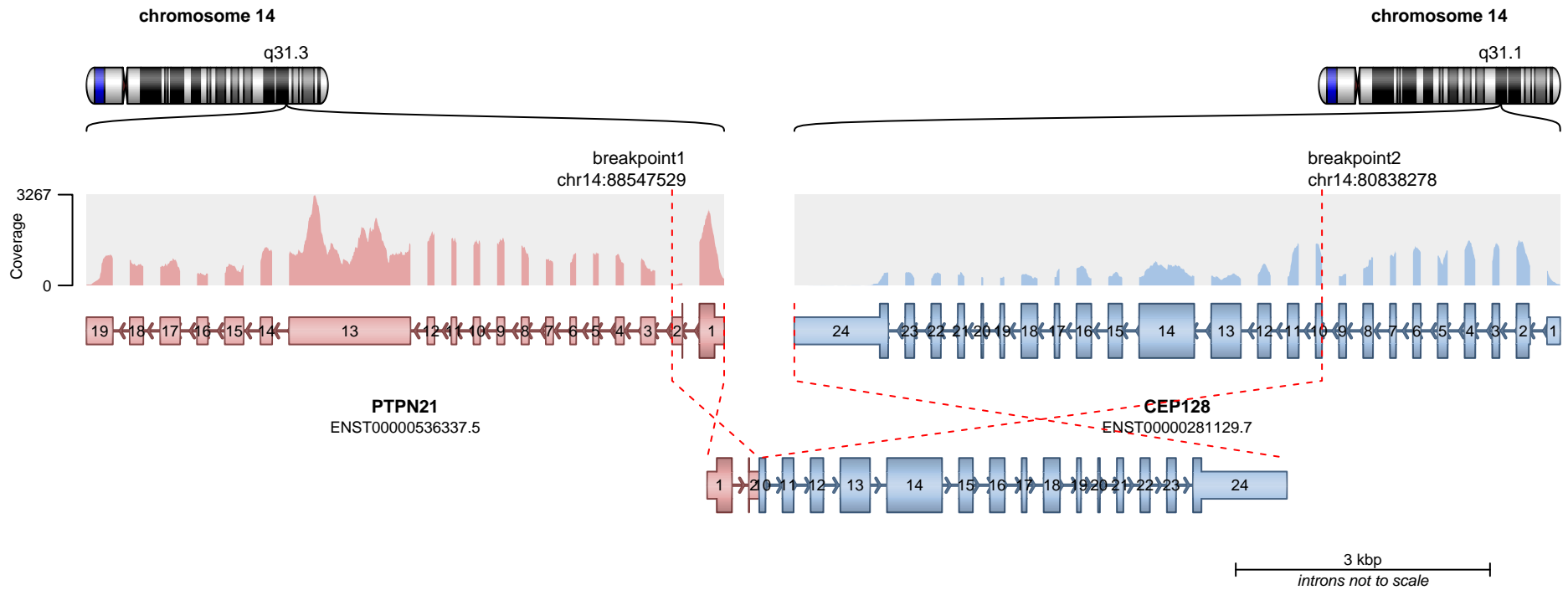
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



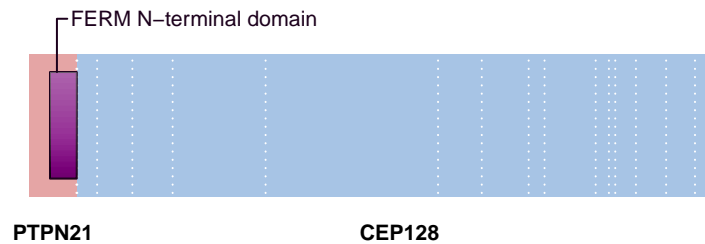
**SUPPORTING READ COUNT**

Split reads = 12  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



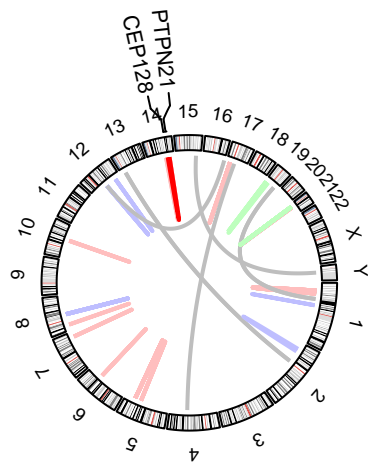
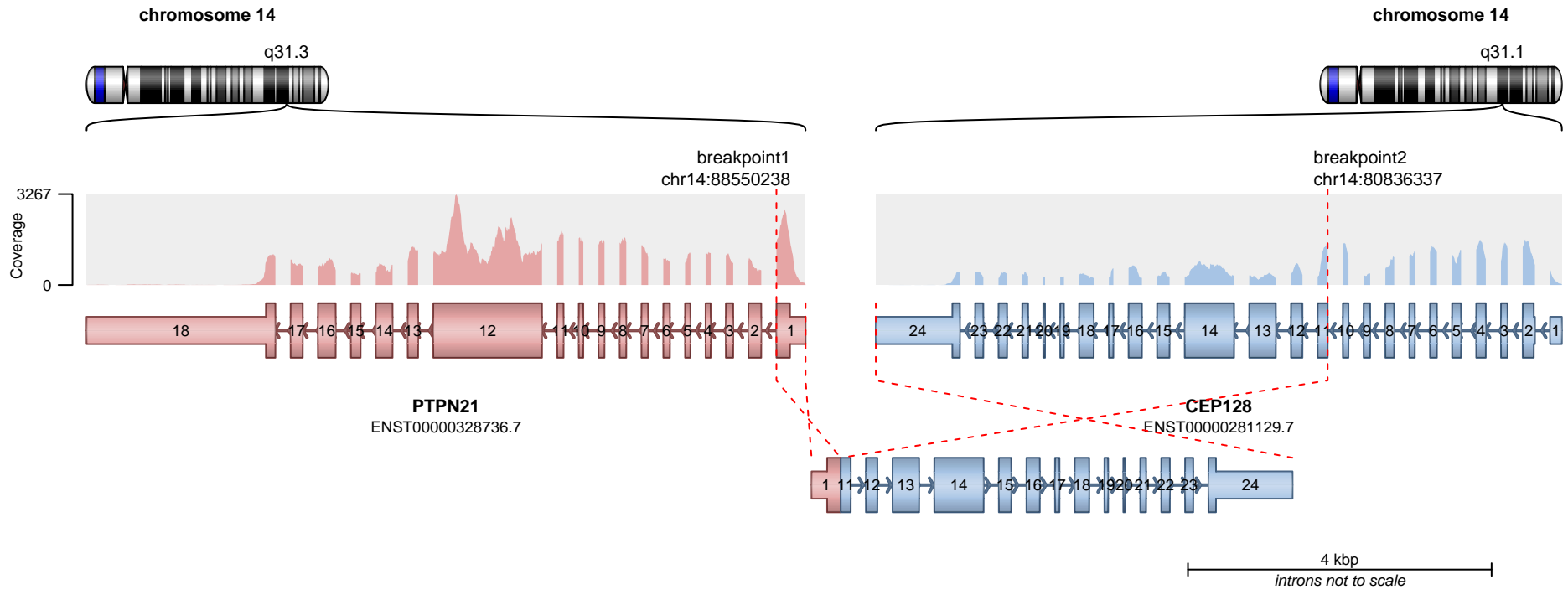
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



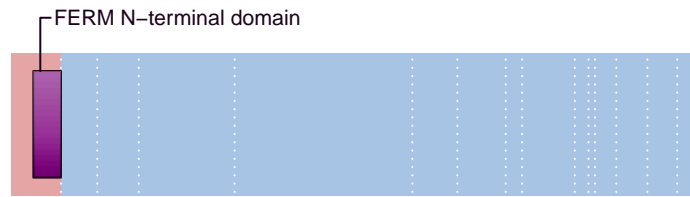
**SUPPORTING READ COUNT**

Split reads = 8  
Discordant mates = 14

— translocation — deletion  
— duplication — inversion



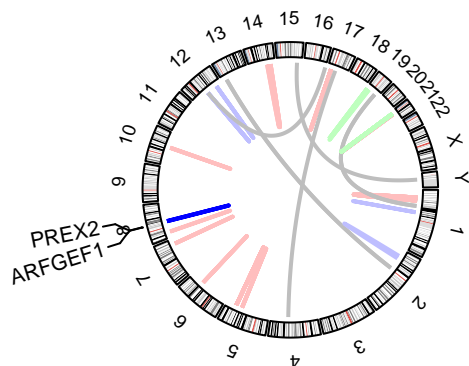
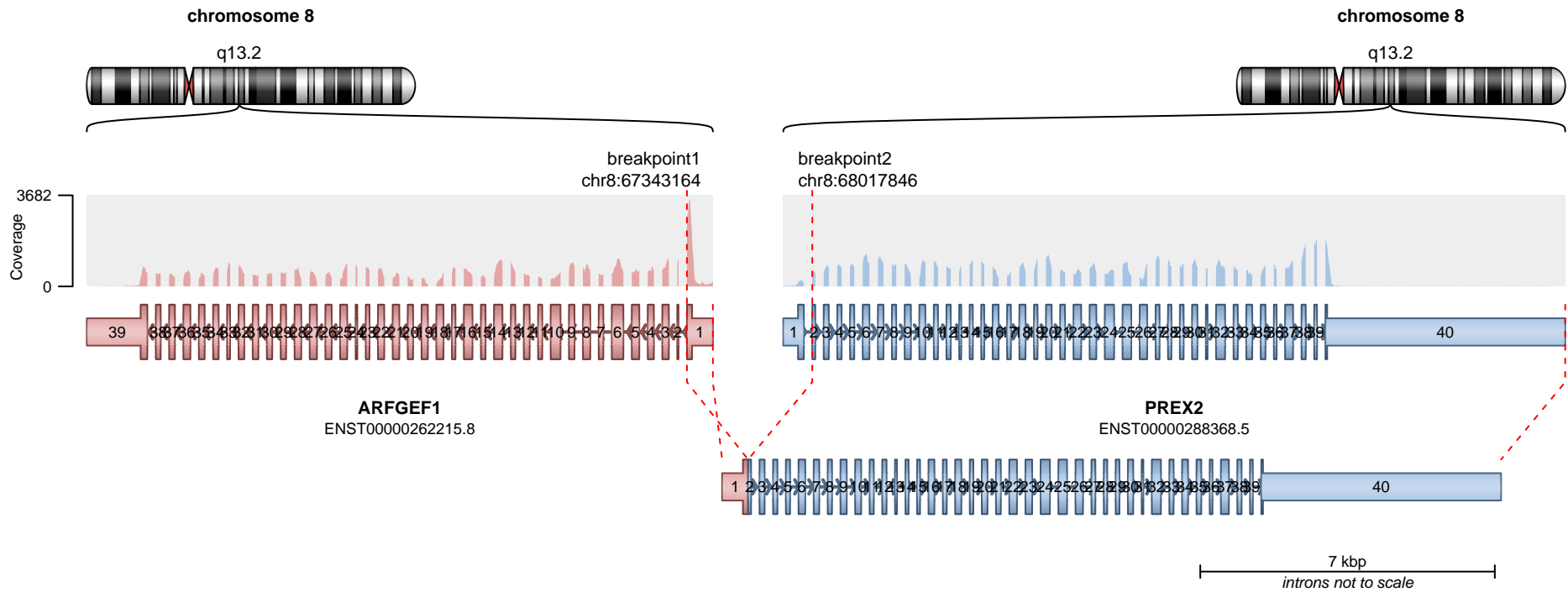
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



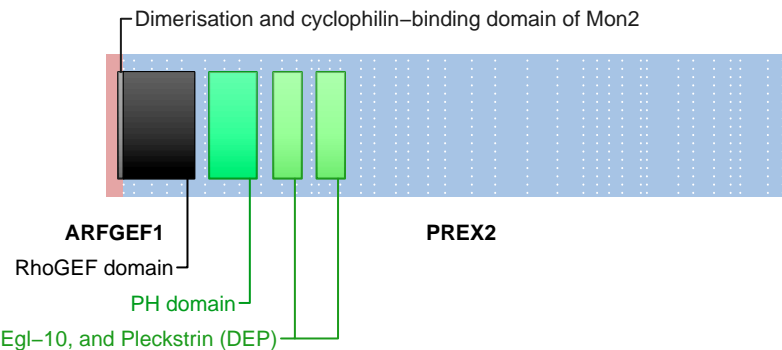
**SUPPORTING READ COUNT**

Split reads = 5  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



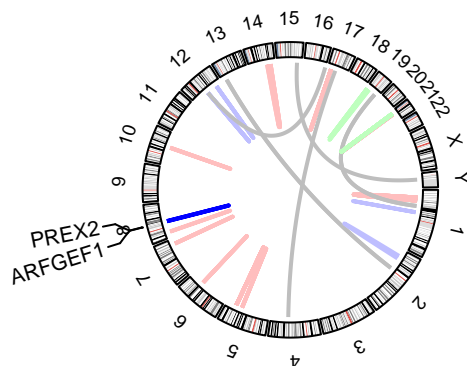
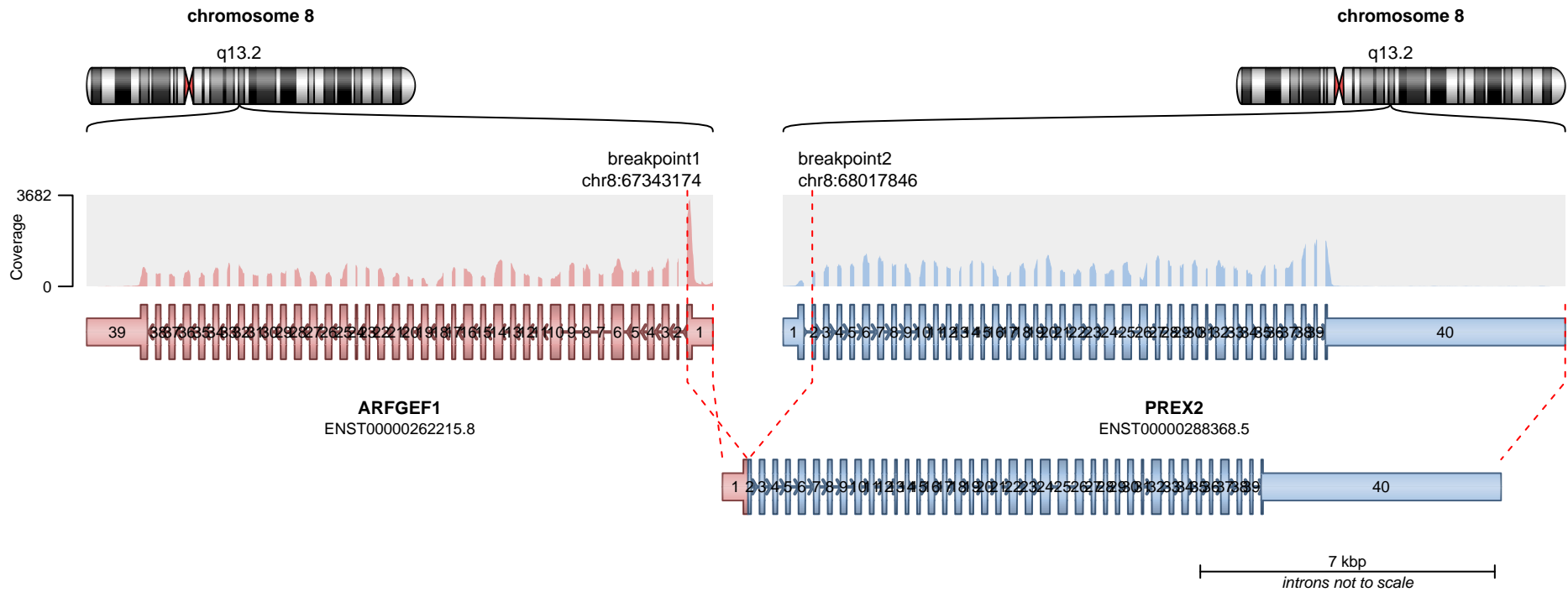
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



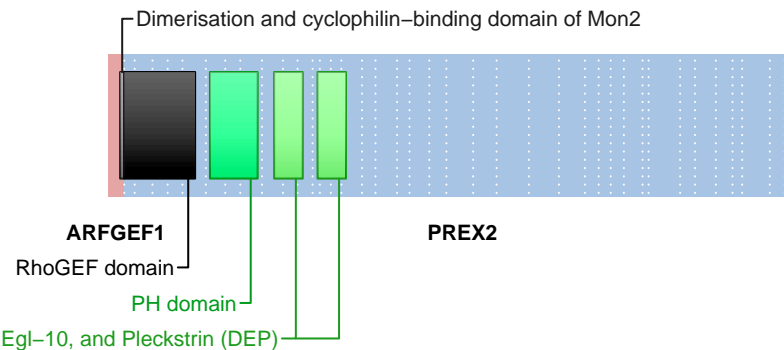
**SUPPORTING READ COUNT**

Split reads = 205  
Discordant mates = 3

- translocation
- duplication
- deletion
- inversion



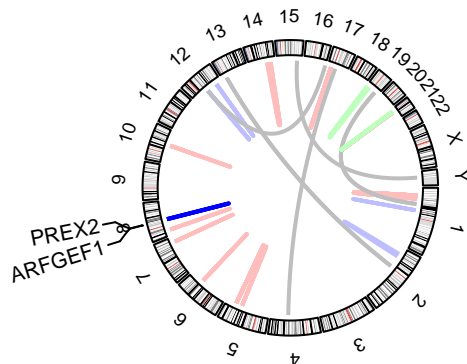
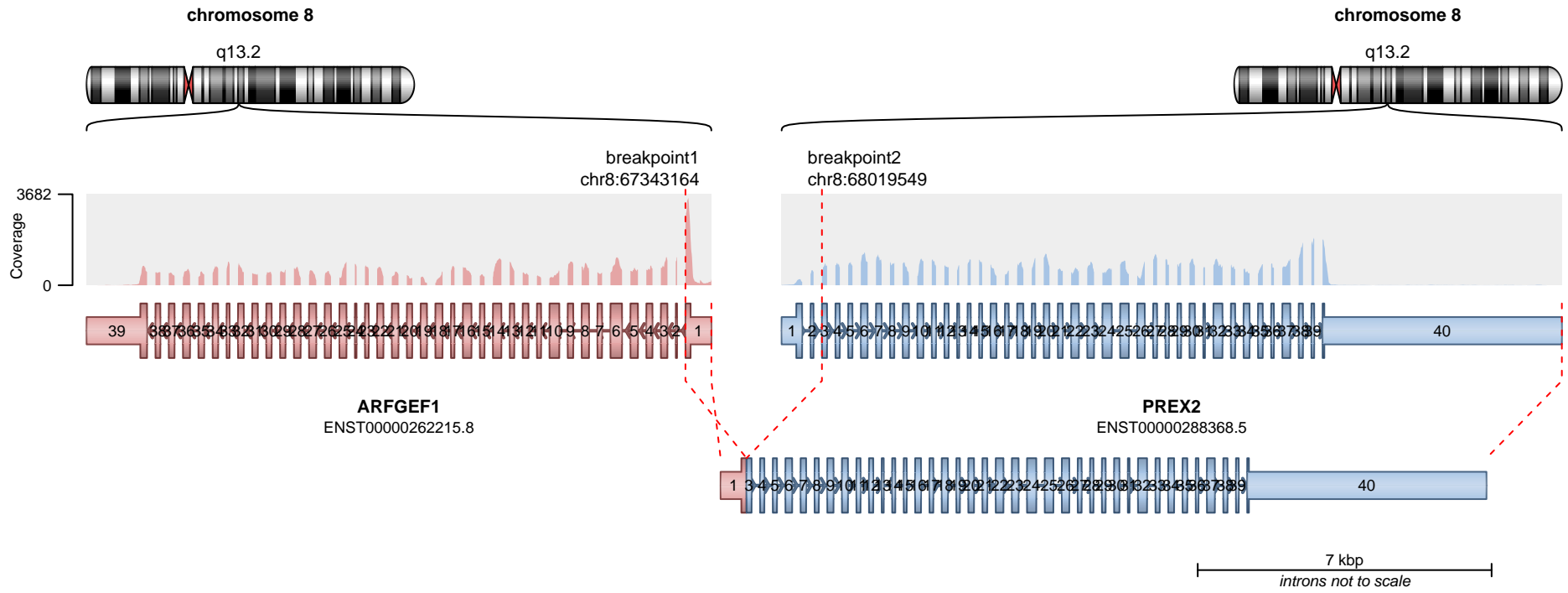
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



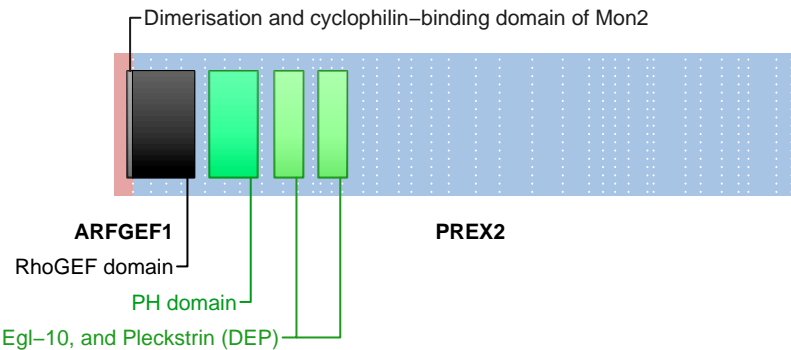
**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



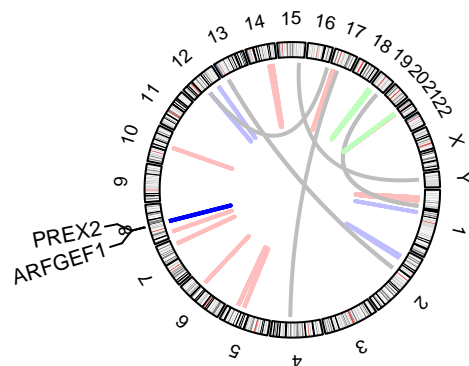
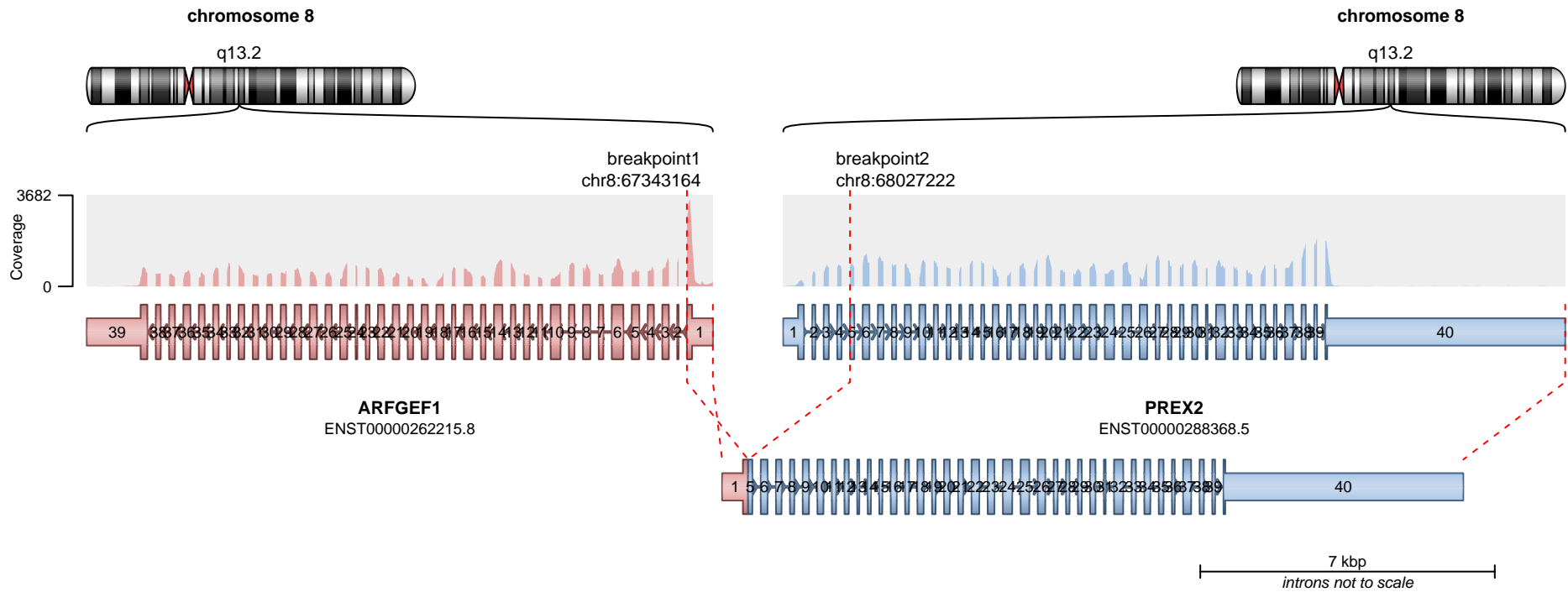
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



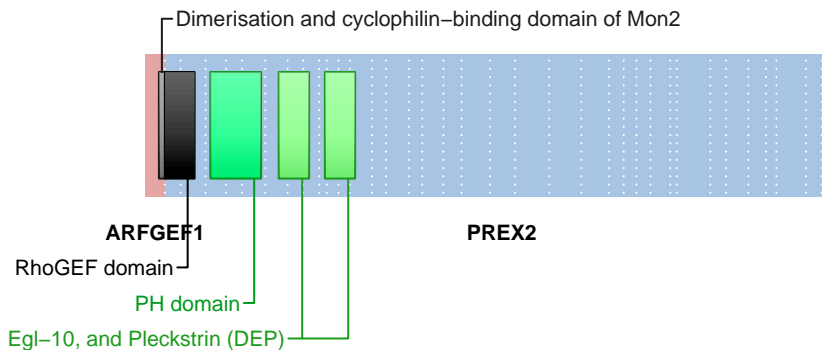
**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 3

- translocation
- duplication
- deletion
- inversion



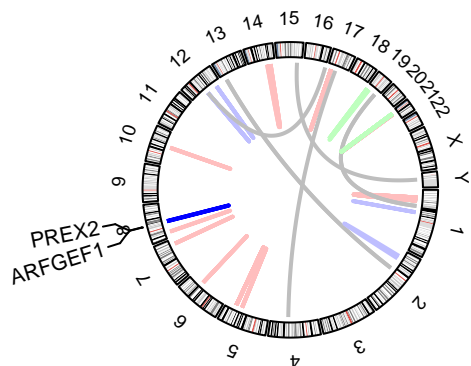
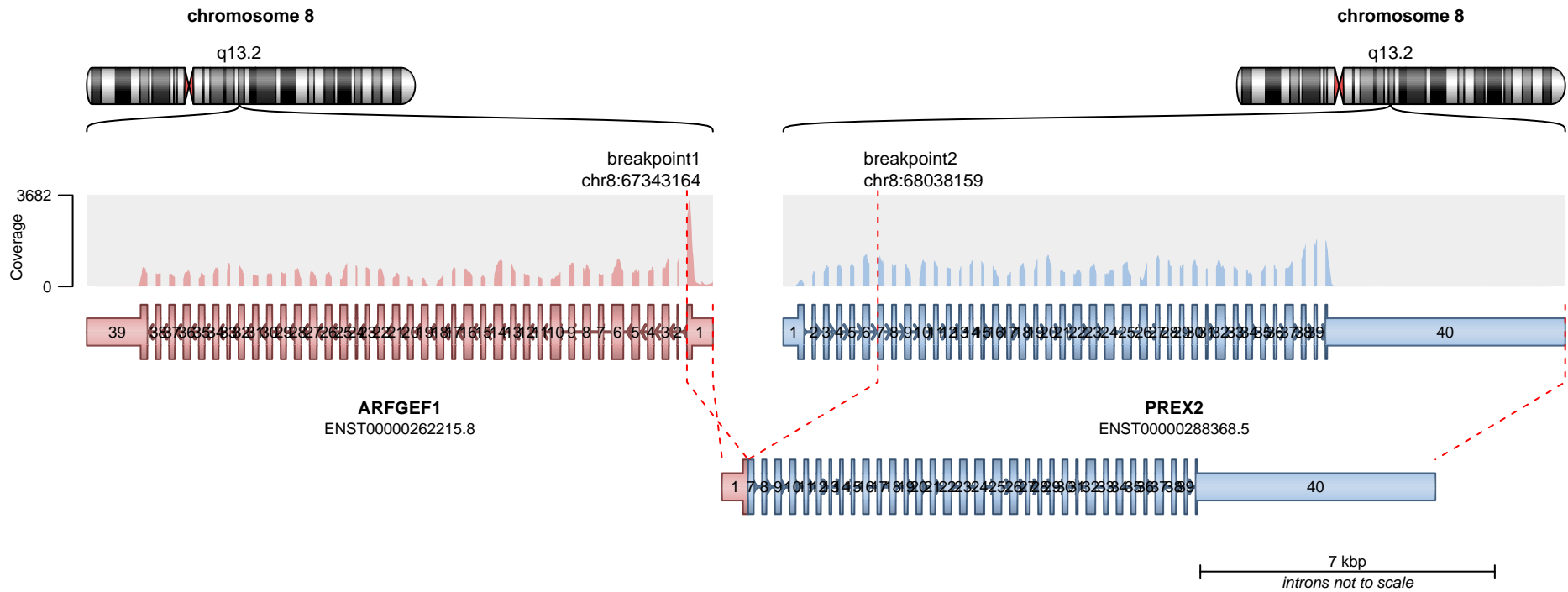
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



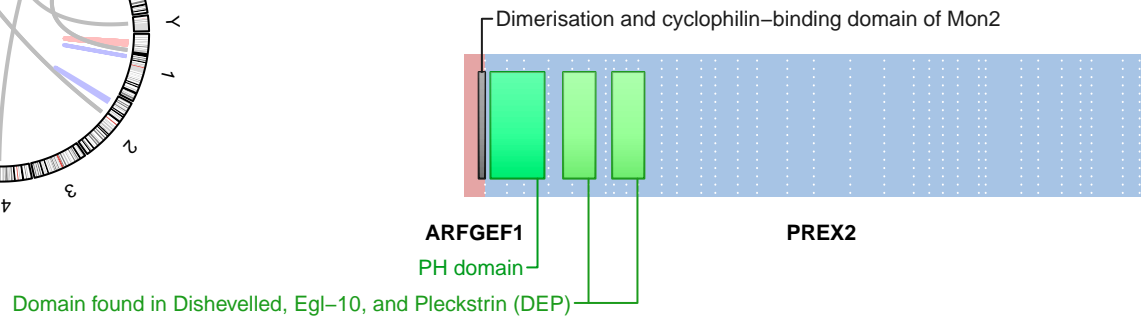
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



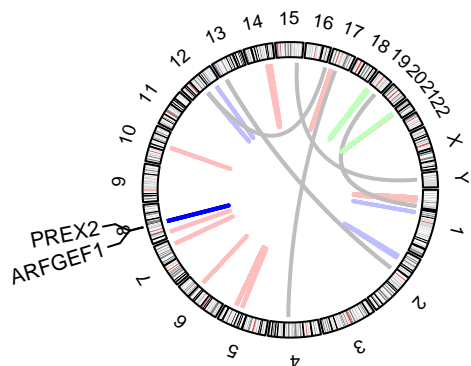
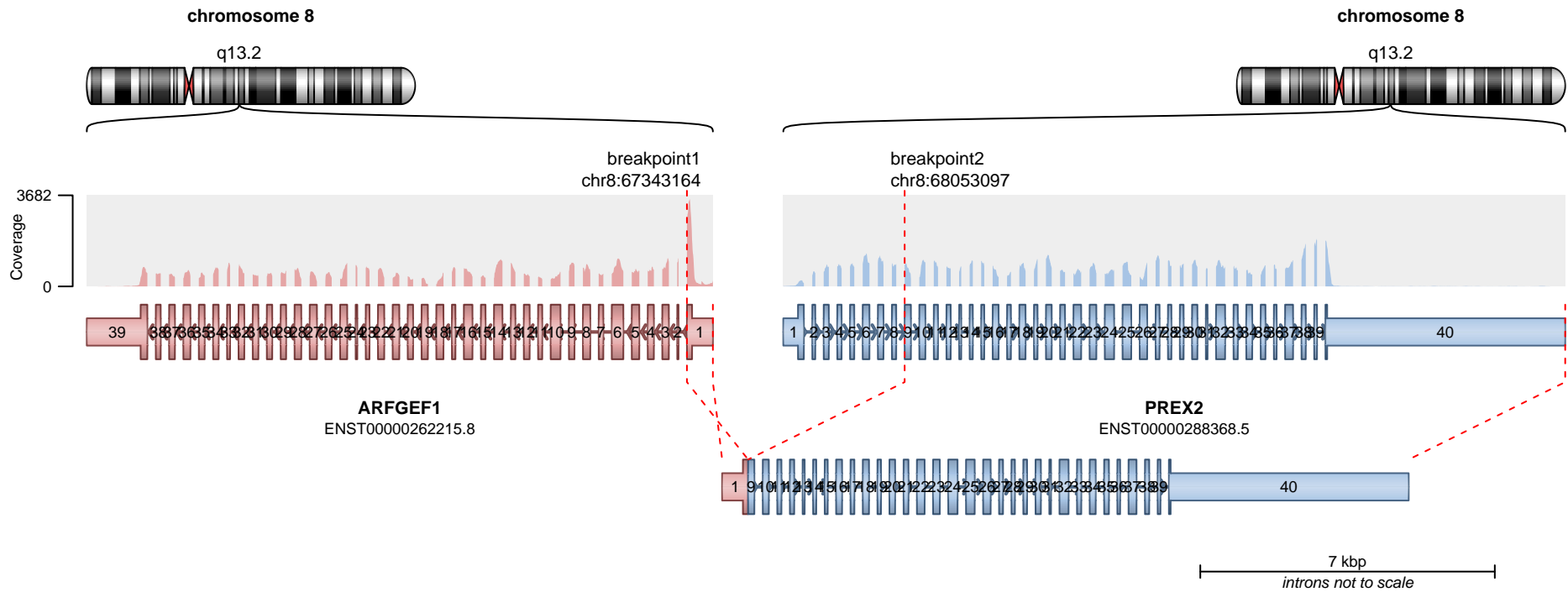
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



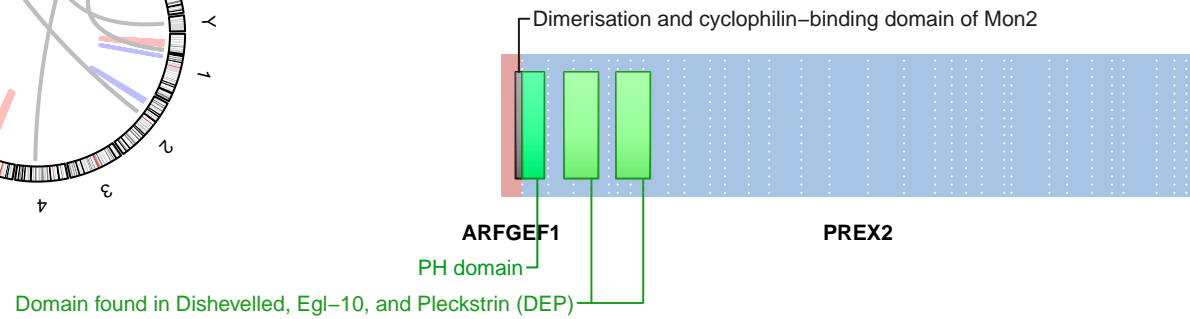
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



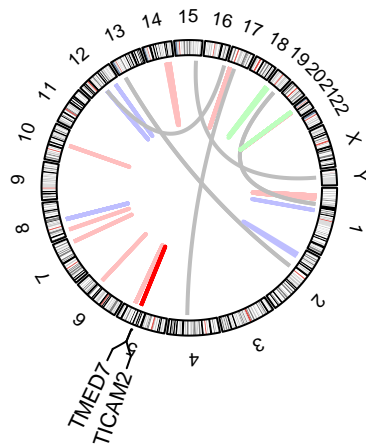
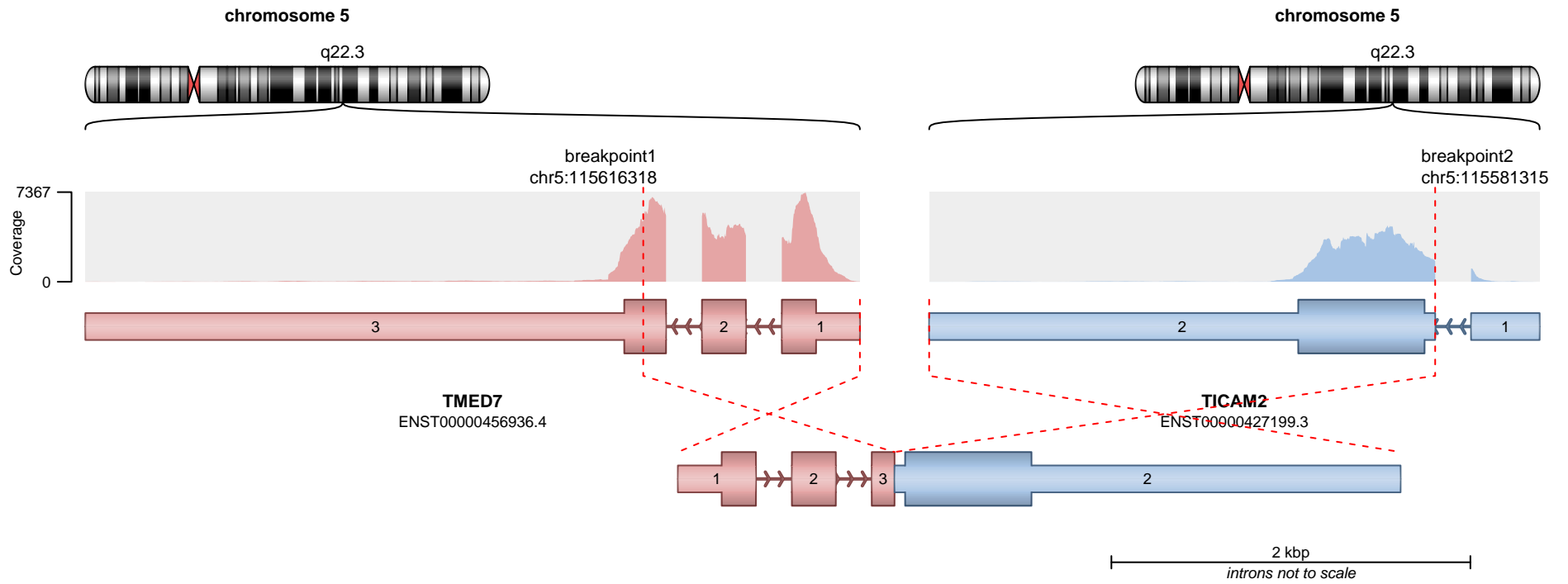
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



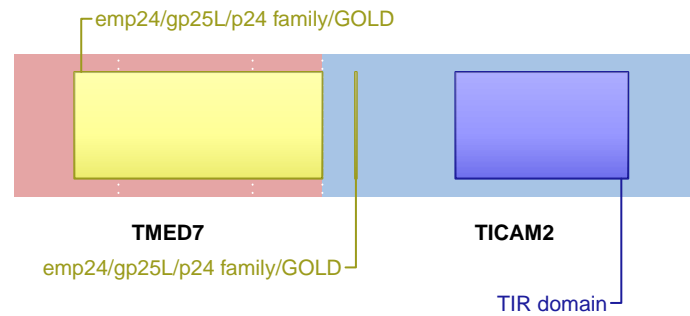
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



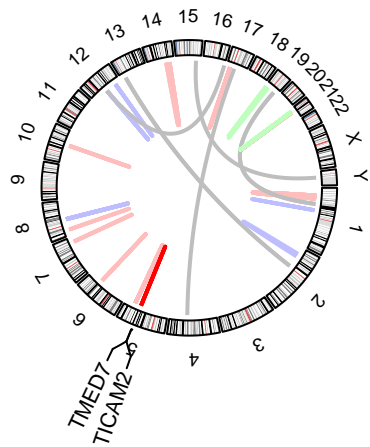
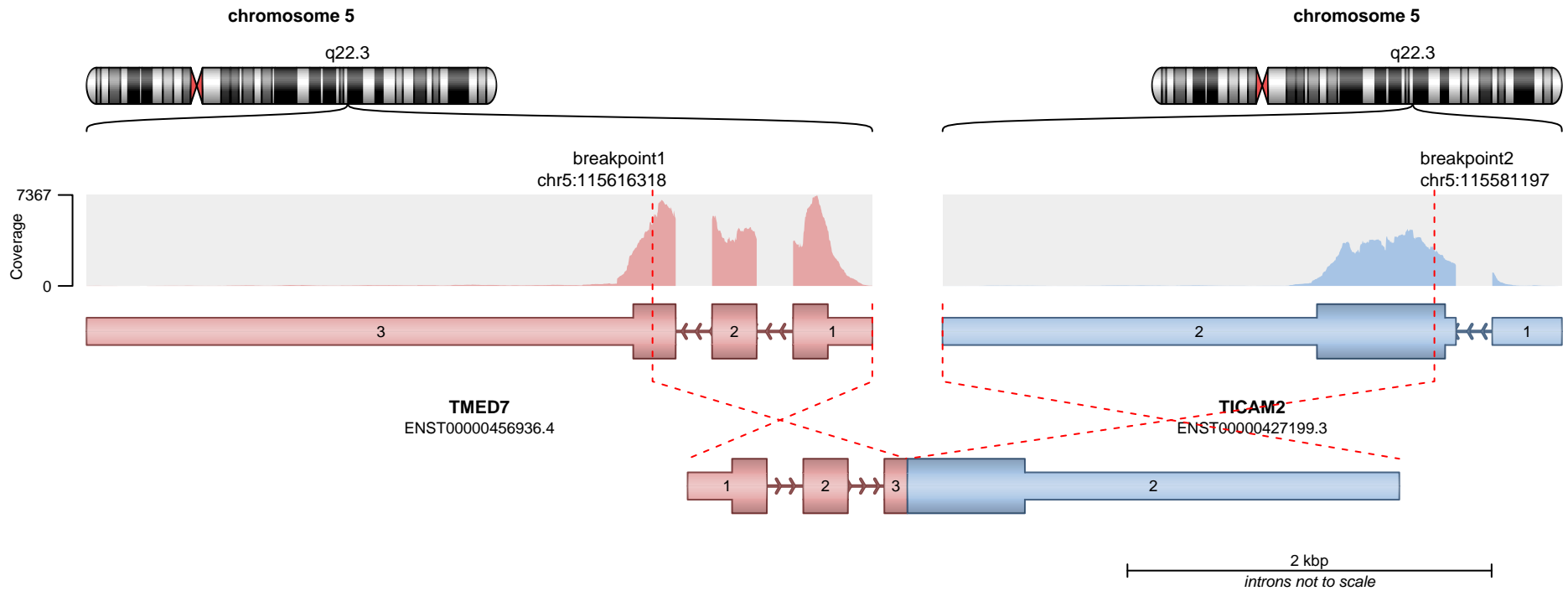
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



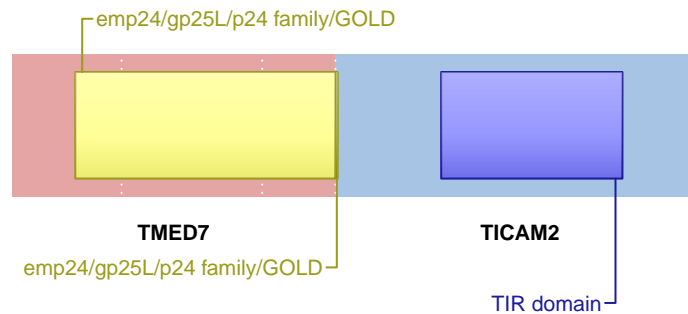
**SUPPORTING READ COUNT**

Split reads = 153  
Discordant mates = 9

— translocation — deletion  
— duplication — inversion



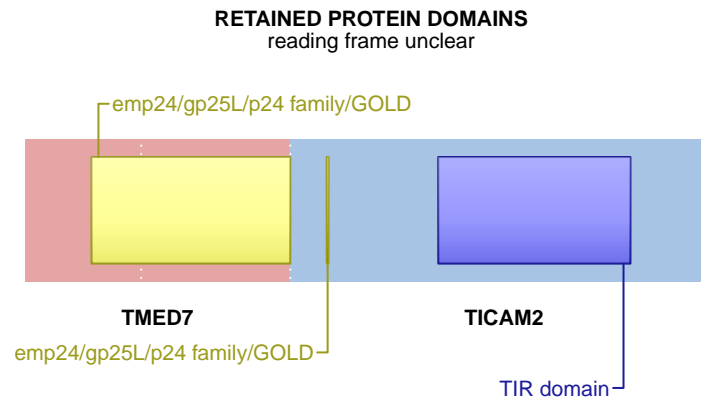
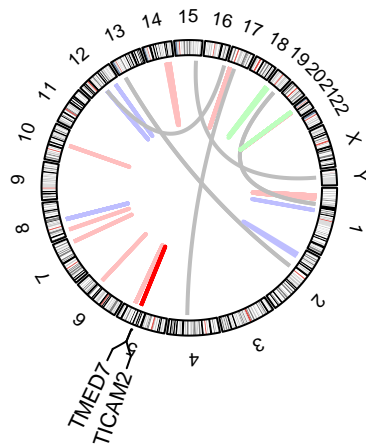
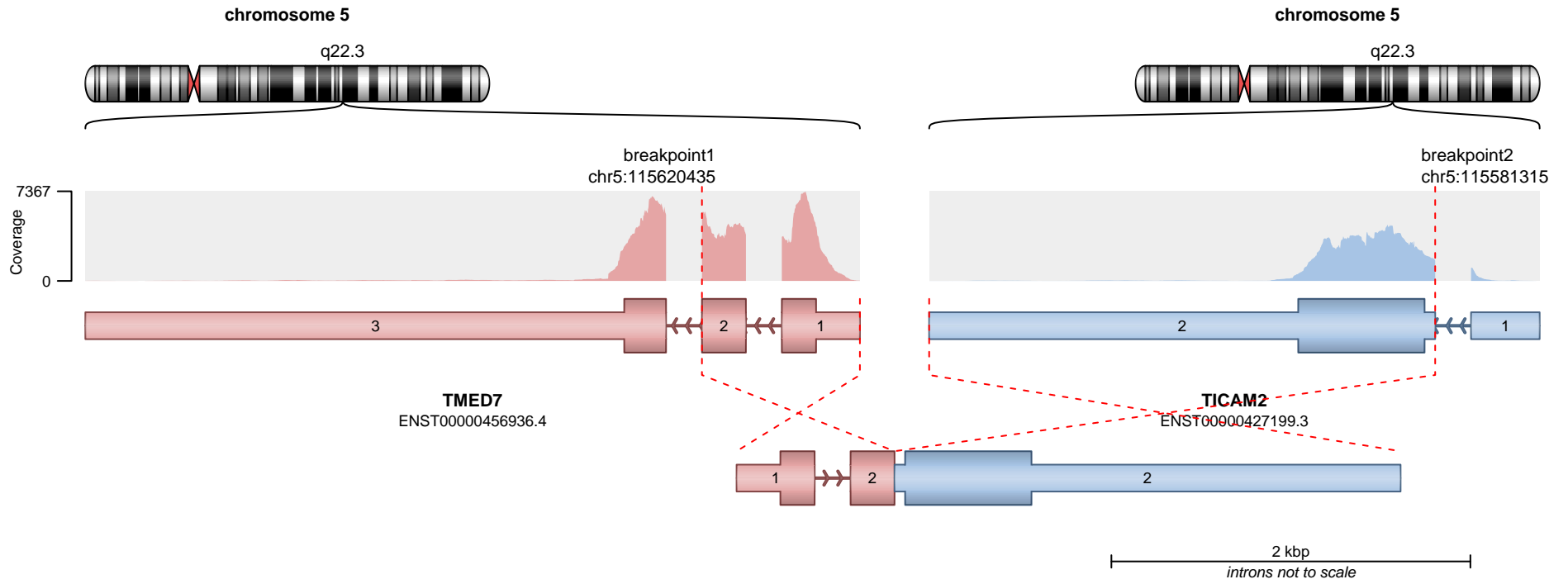
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 20  
Discordant mates = 1

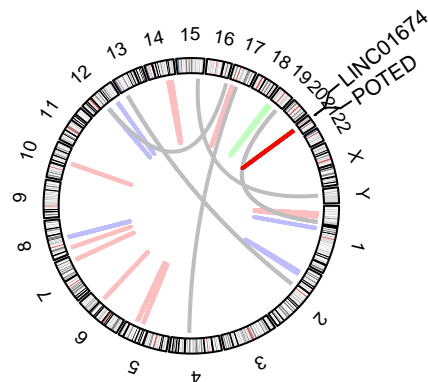
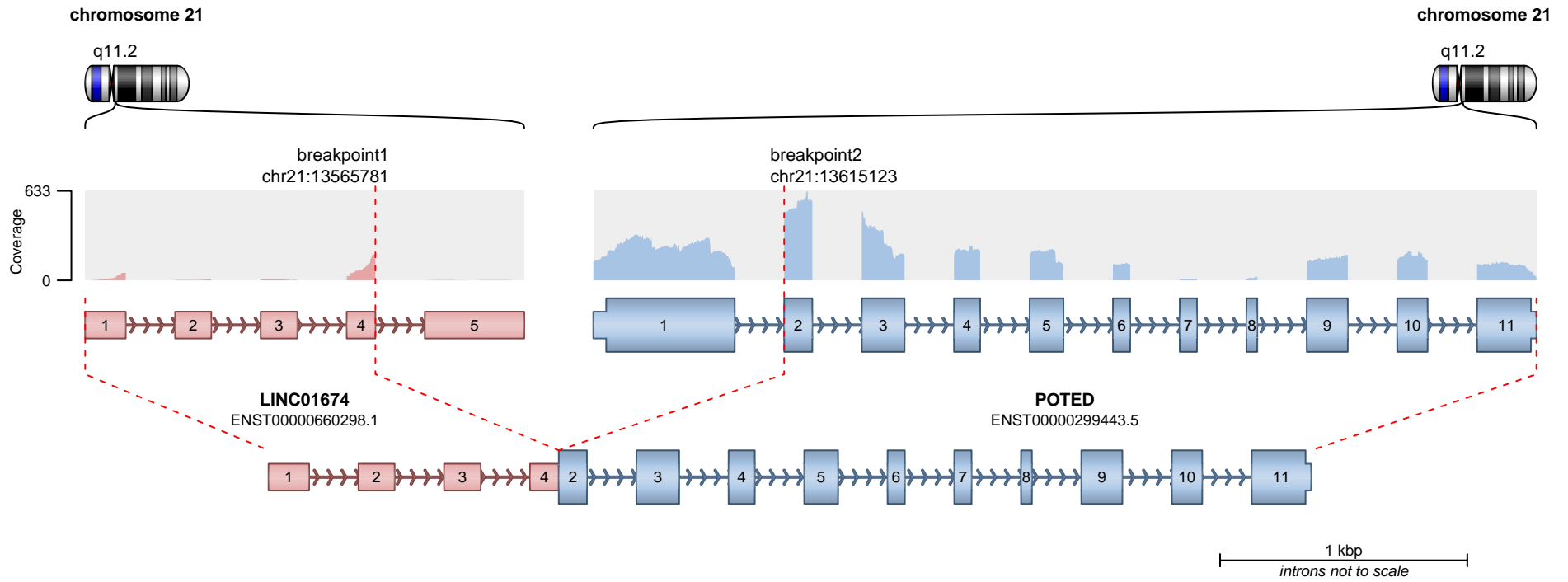
- translocation
- deletion
- duplication
- inversion



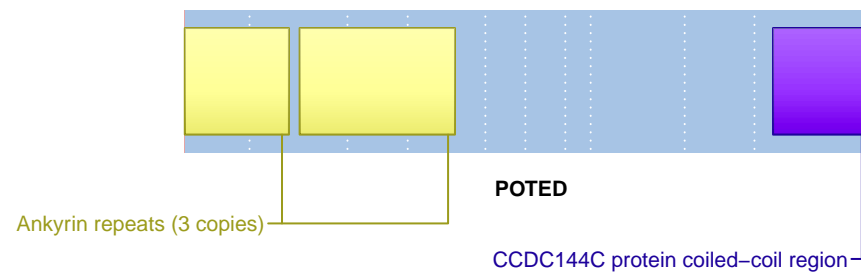
**SUPPORTING READ COUNT**

Split reads = 5  
Discordant mates = 1

— translocation    — deletion  
— duplication    — inversion



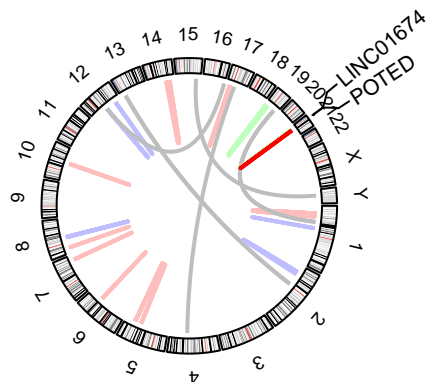
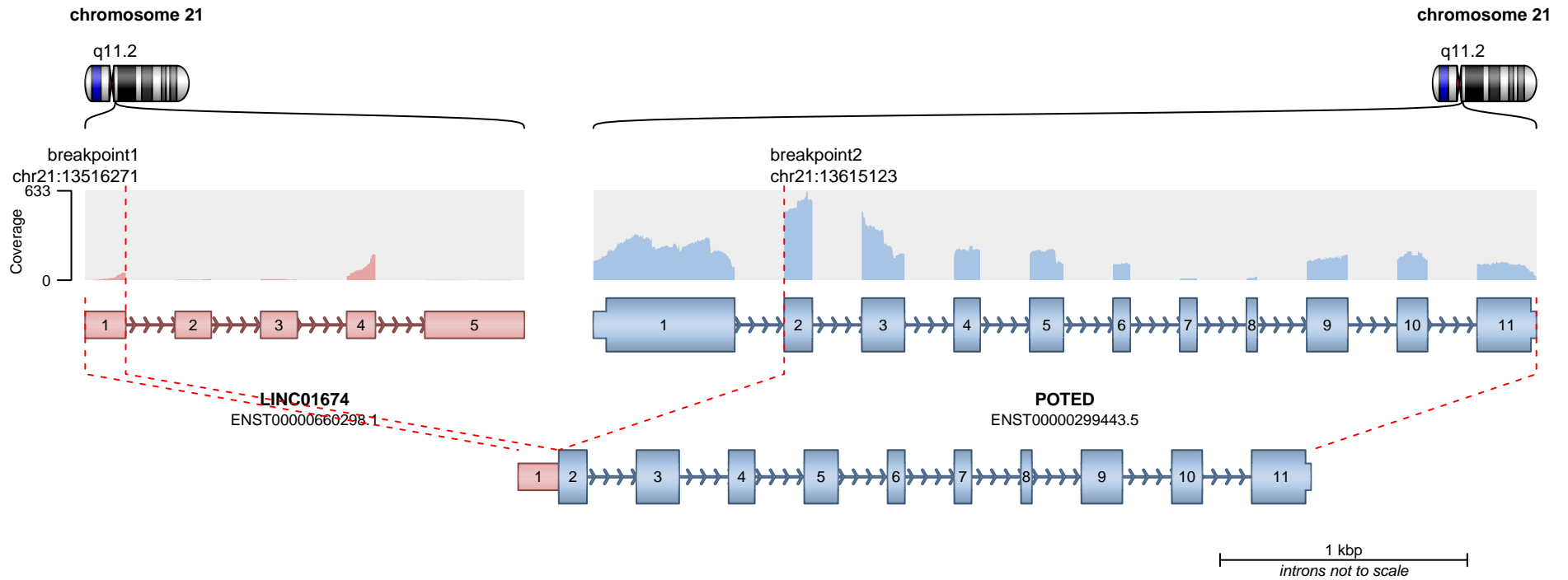
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



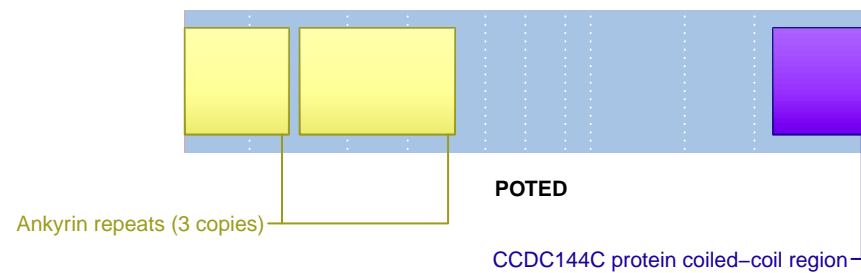
**SUPPORTING READ COUNT**

Split reads = 74  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



**RETAINED PROTEIN DOMAINS**  
reading frame unclear



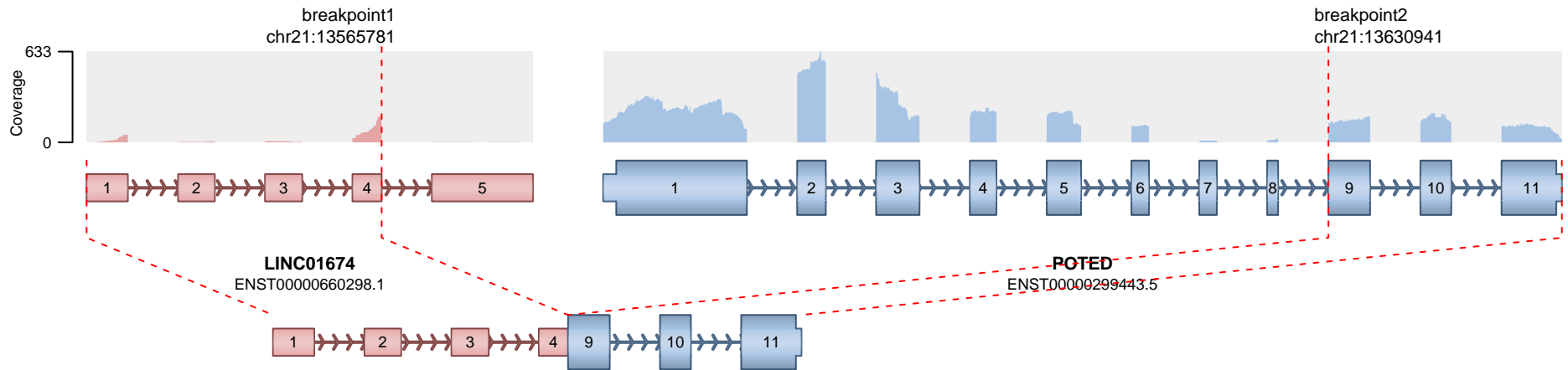
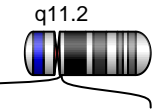
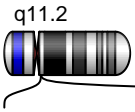
**SUPPORTING READ COUNT**

Split reads = 11  
Discordant mates = 0

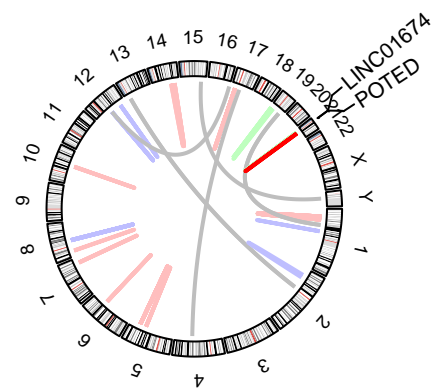
- translocation
- duplication
- deletion
- inversion

chromosome 21

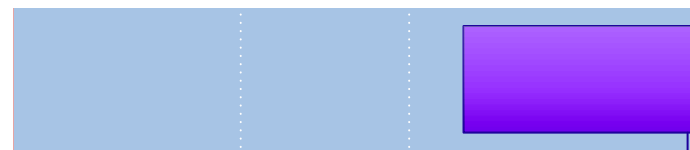
chromosome 21



1 kbp  
introns not to scale



RETAINED PROTEIN DOMAINS  
reading frame unclear

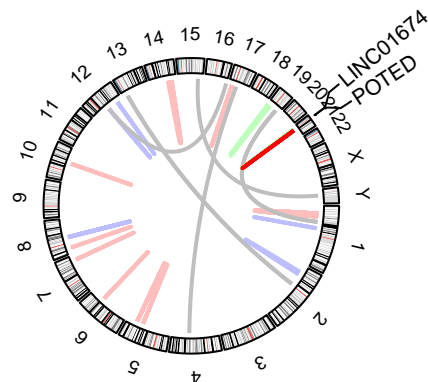
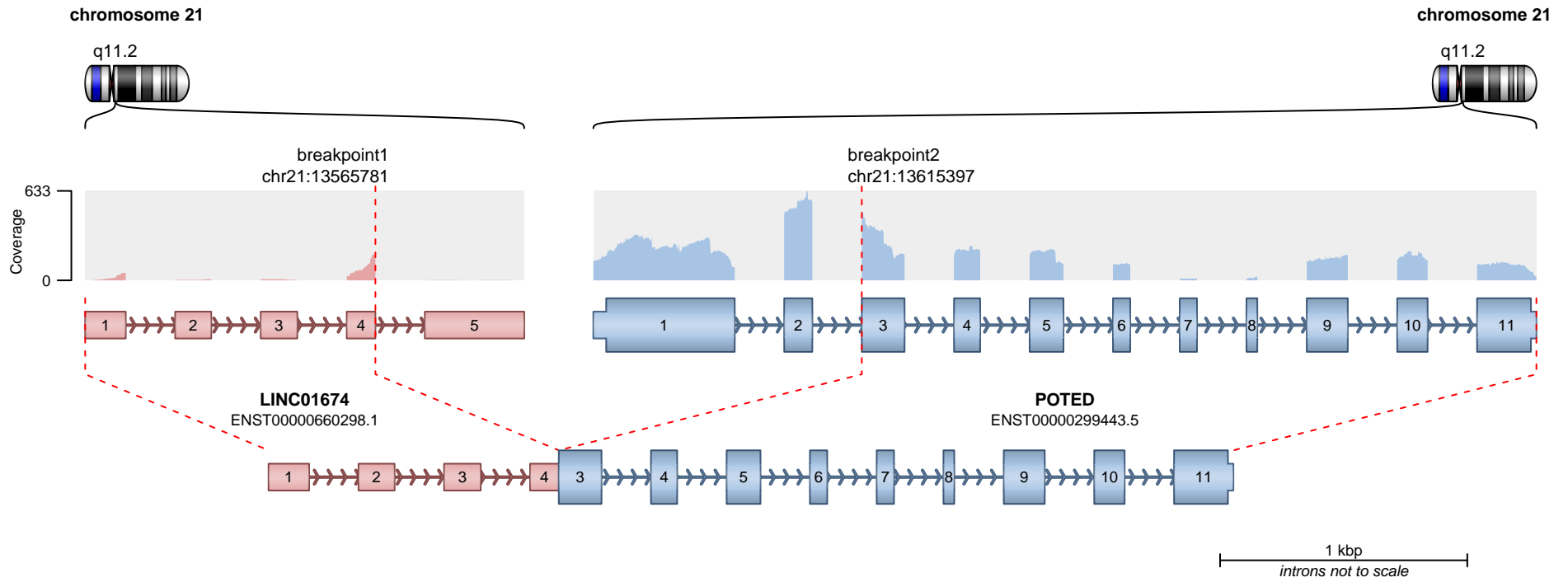


**POTES**  
CCDC144C protein coiled-coil region

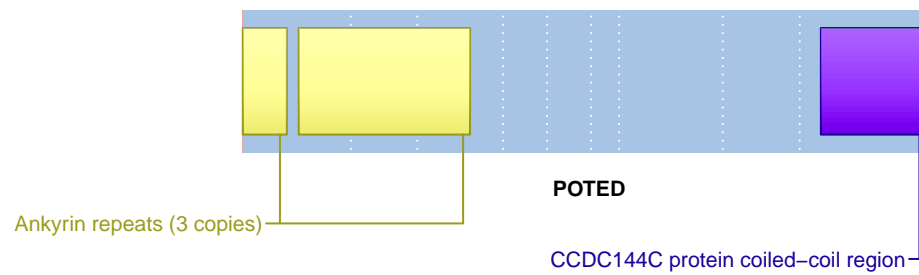
**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



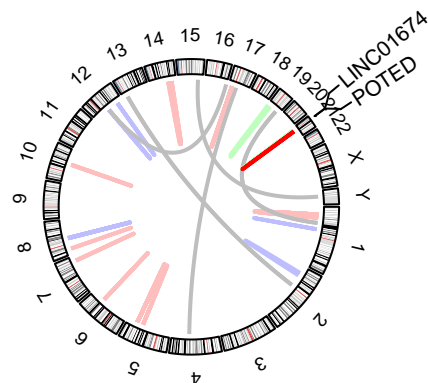
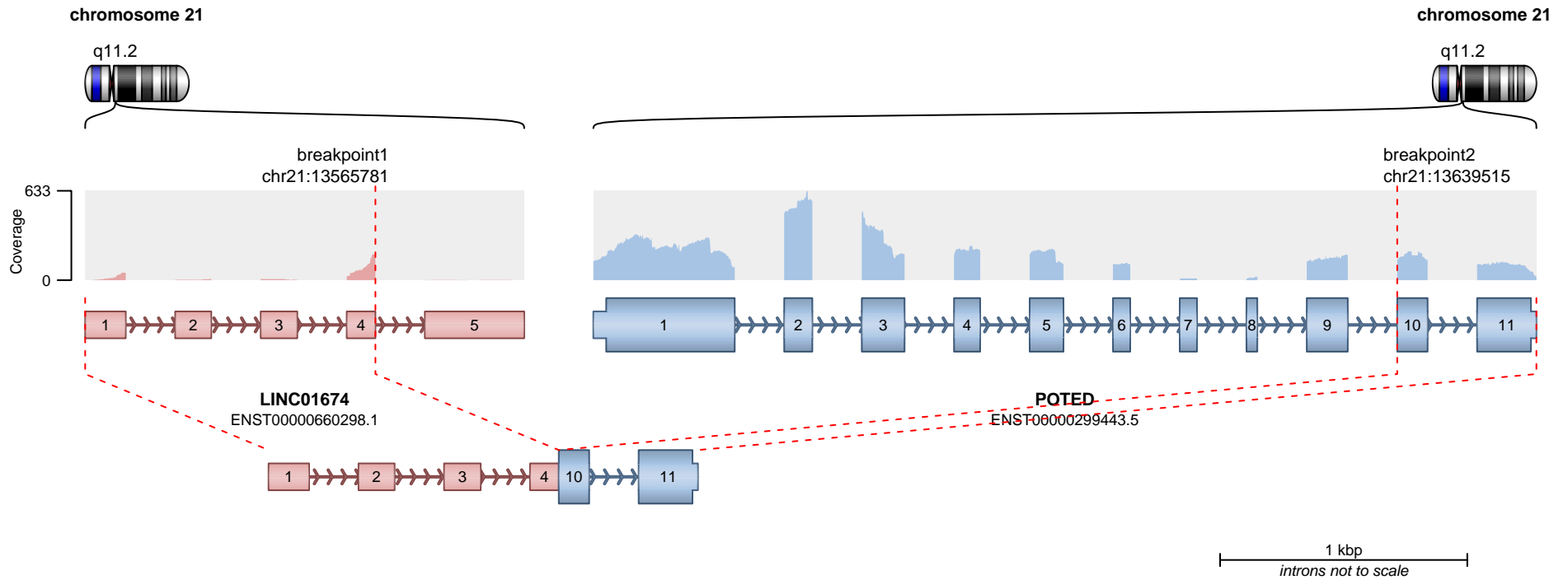
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



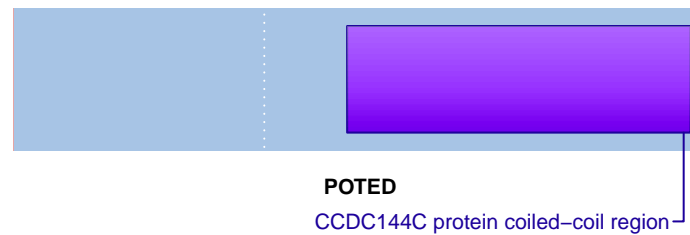
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



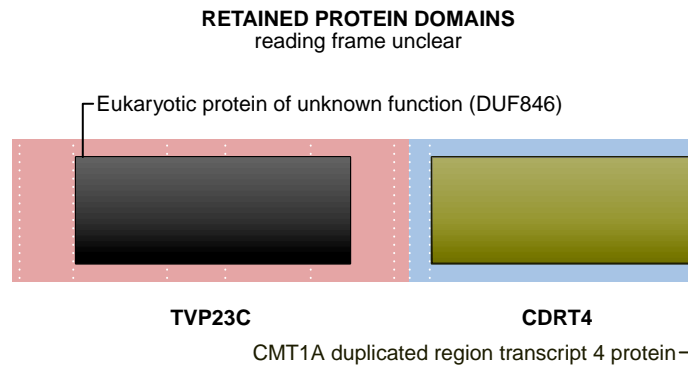
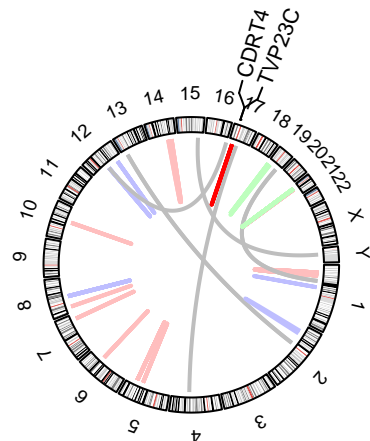
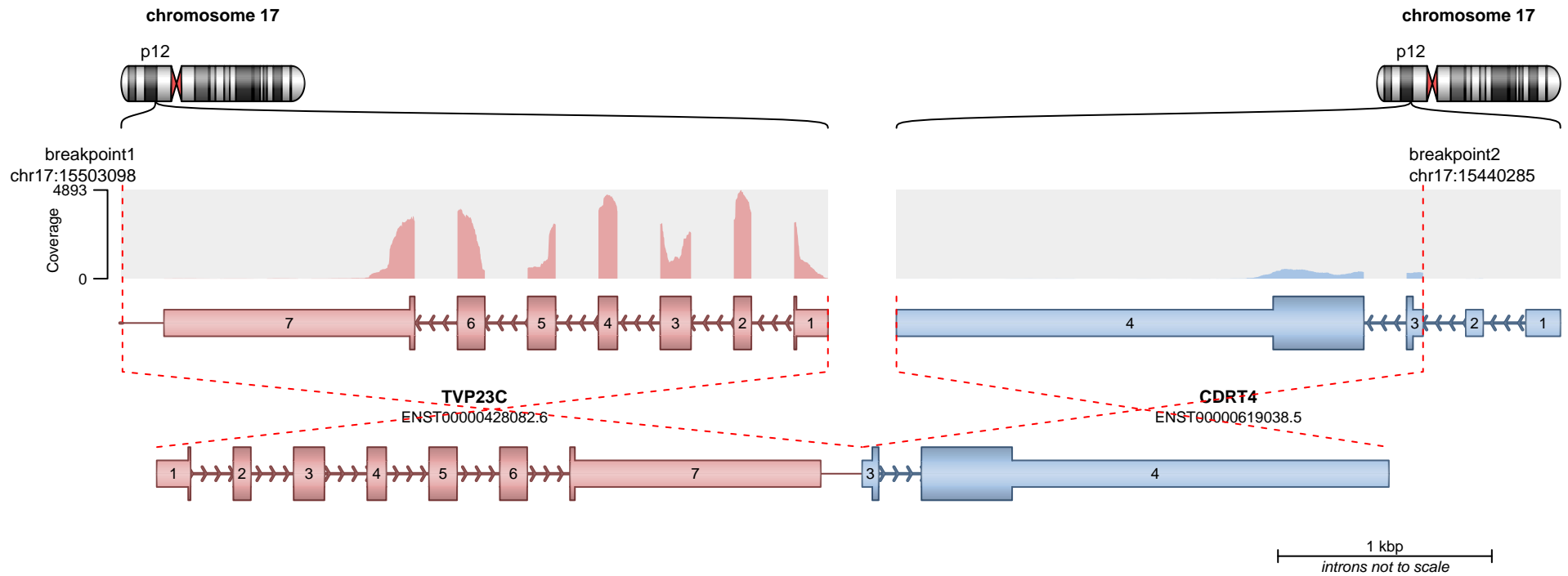
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

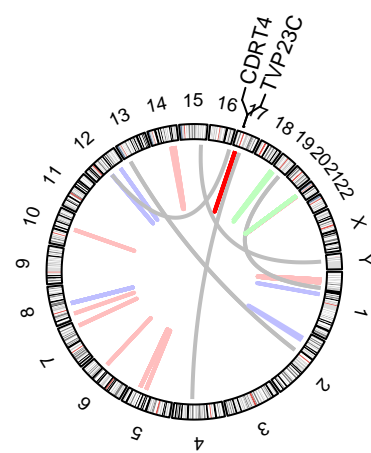
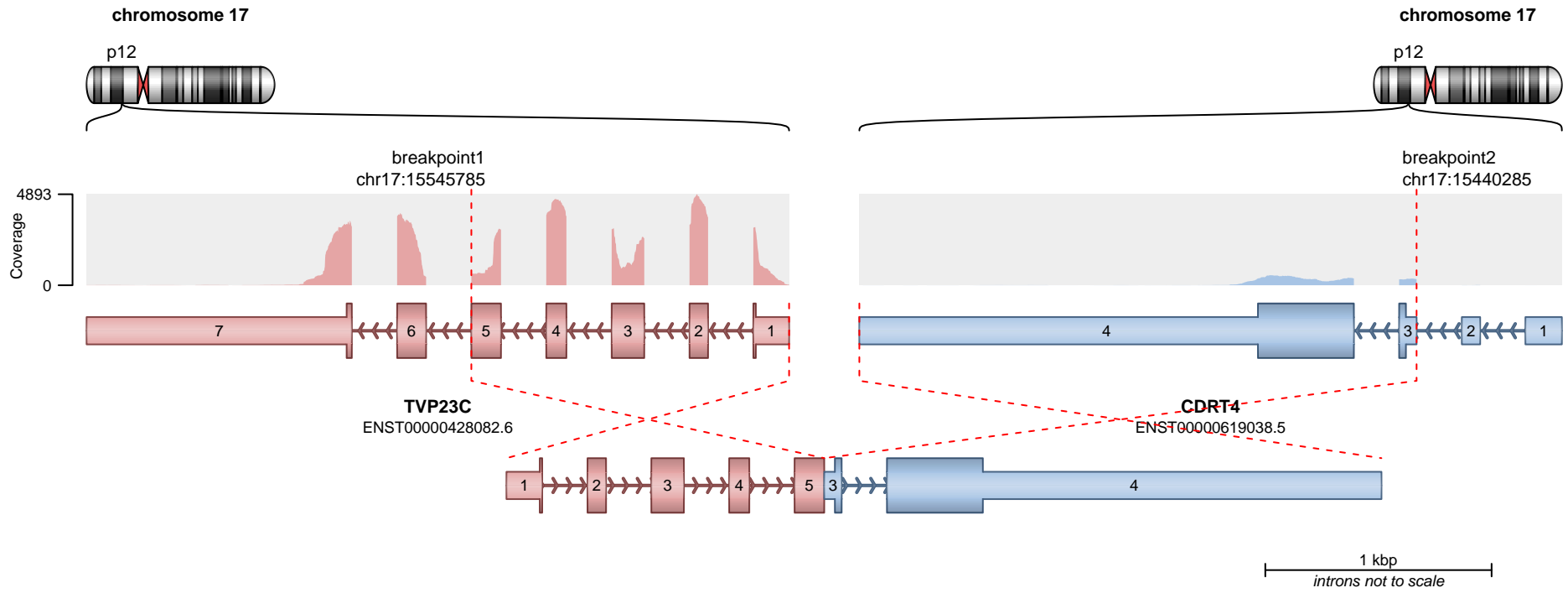
— translocation    — deletion  
— duplication    — inversion



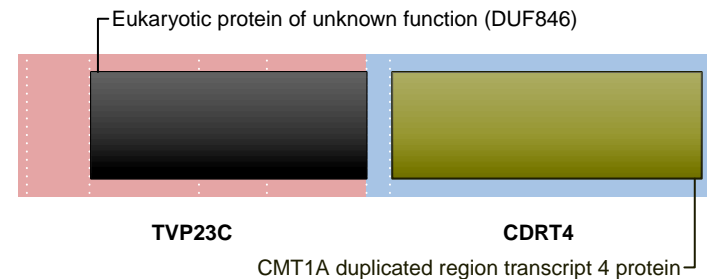
**SUPPORTING READ COUNT**

Split reads = 71  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



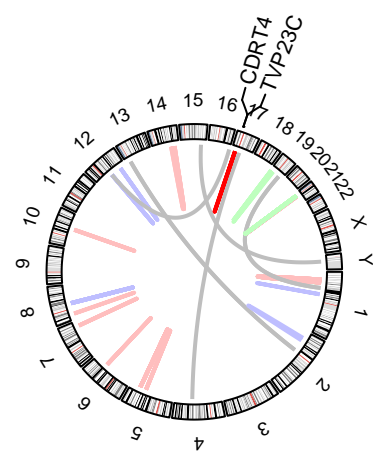
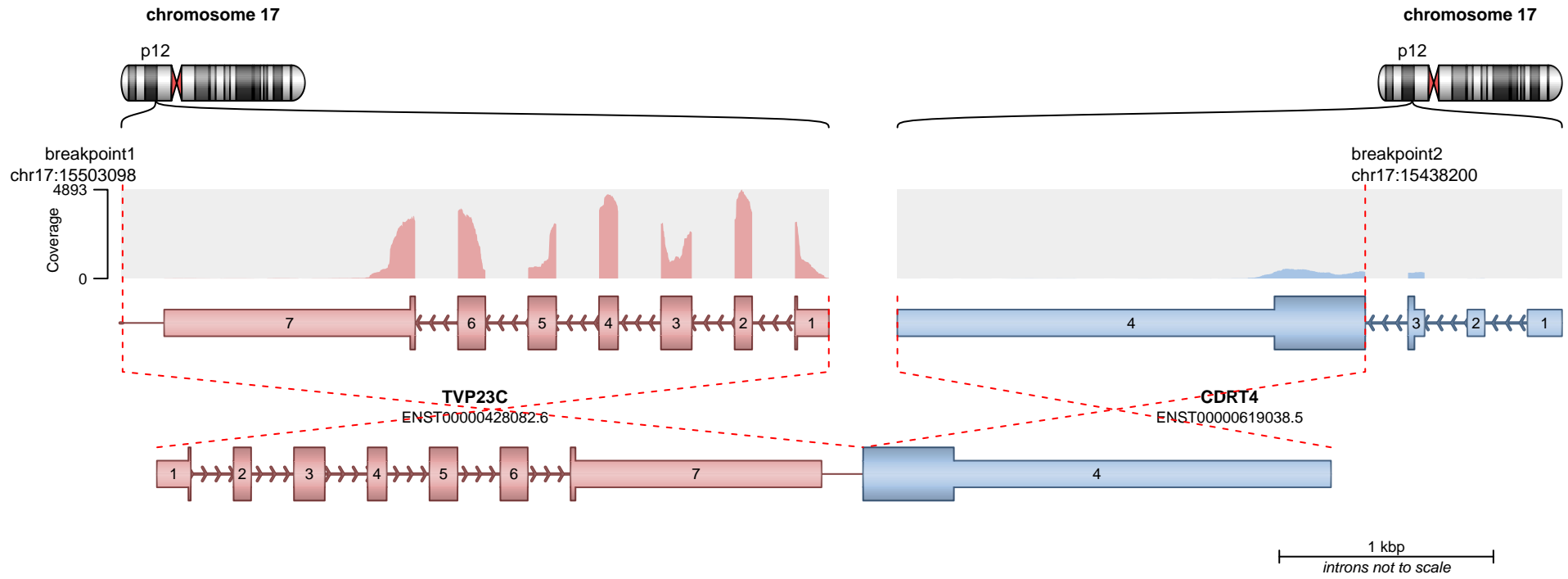
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



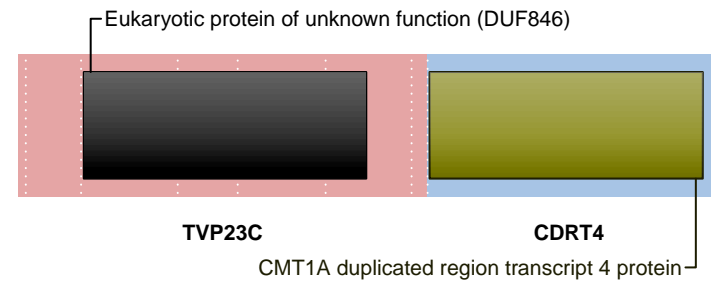
**SUPPORTING READ COUNT**

Split reads = 55  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



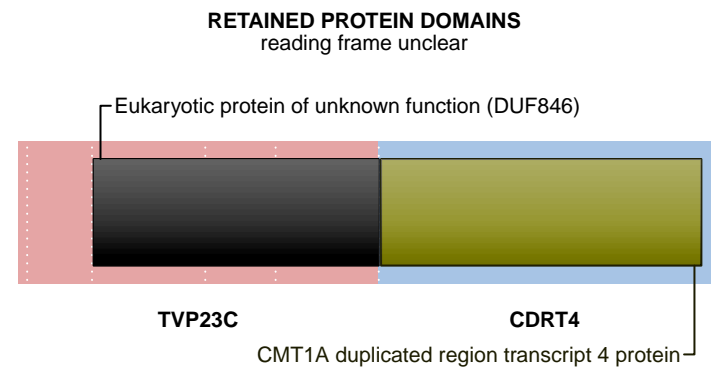
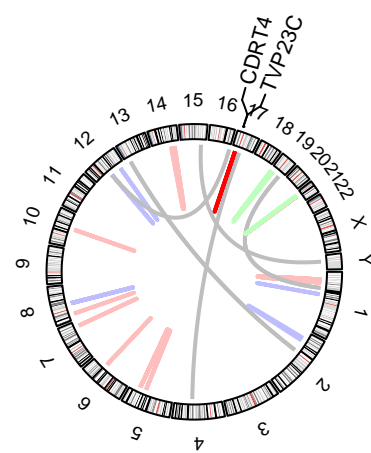
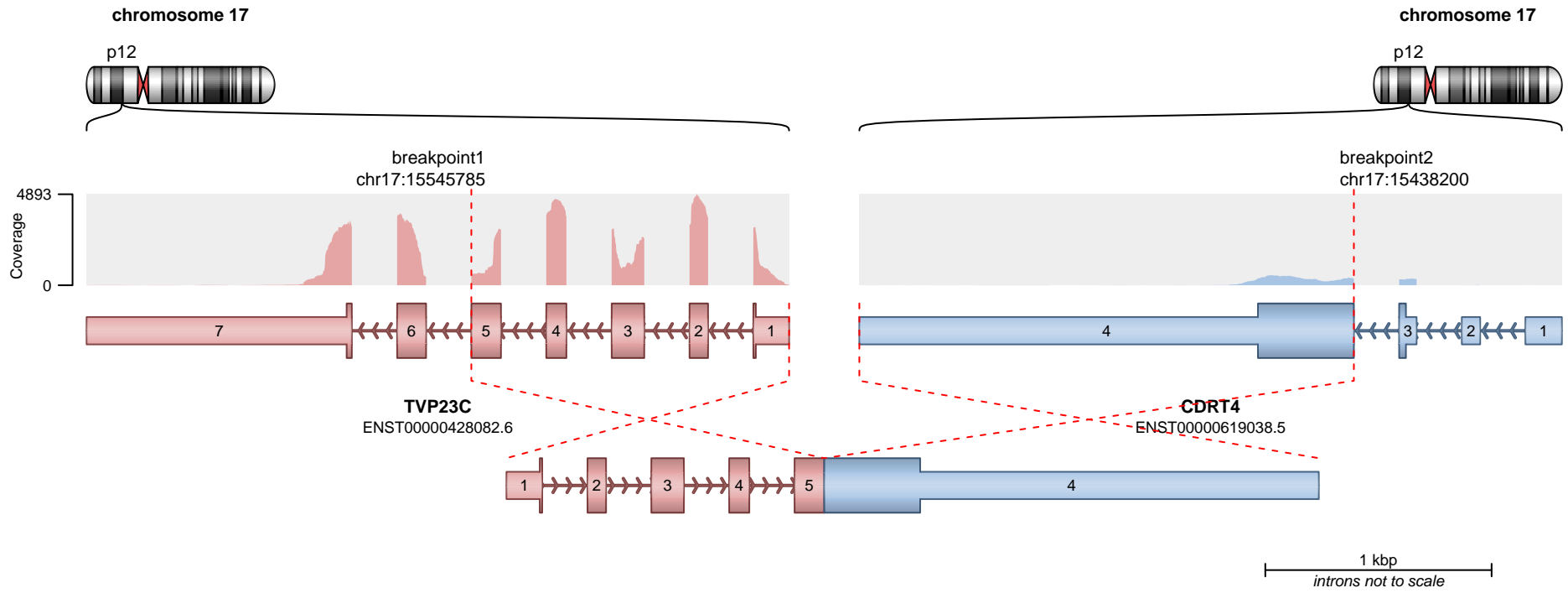
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 10  
Discordant mates = 0

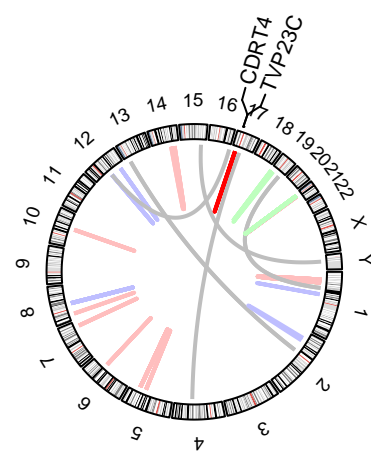
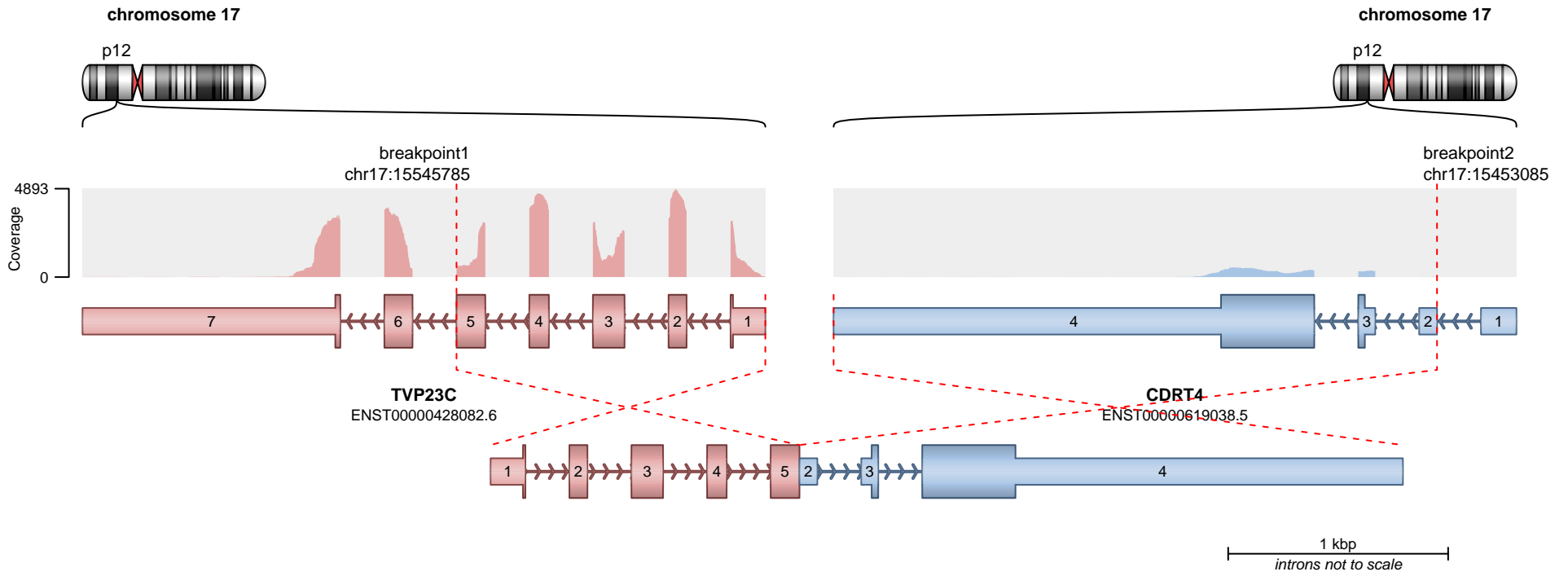
- translocation
- duplication
- deletion
- inversion



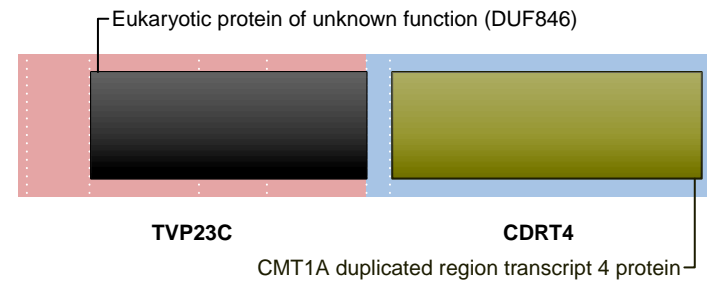
**SUPPORTING READ COUNT**

Split reads = 7  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



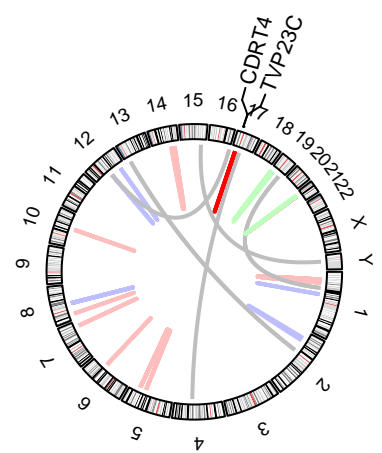
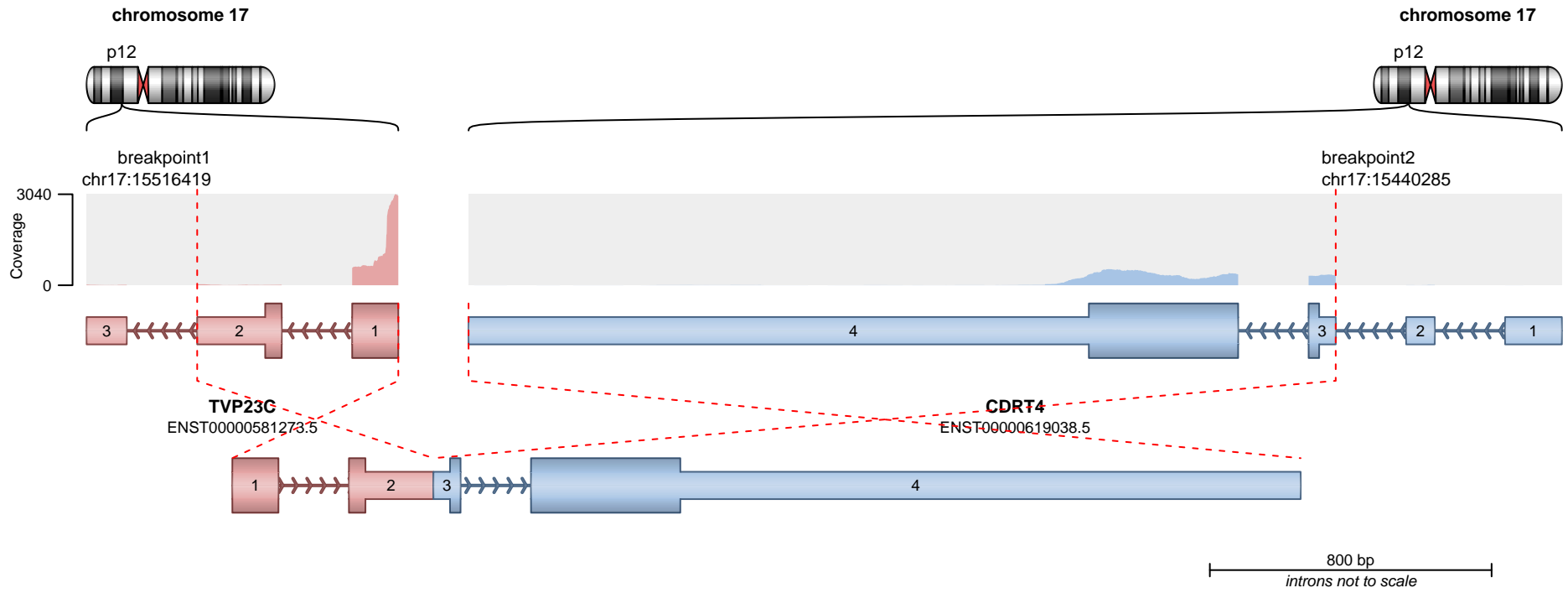
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



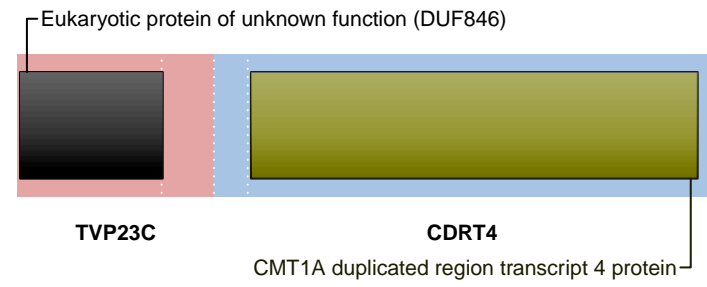
**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0

- translocation
- deletion
- duplication
- inversion



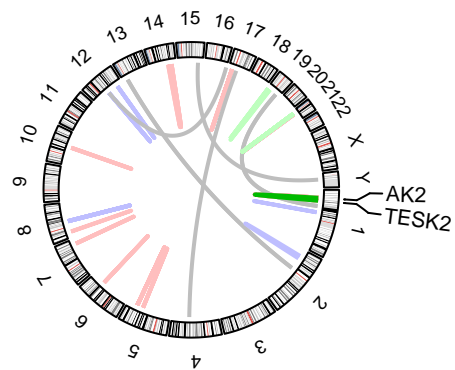
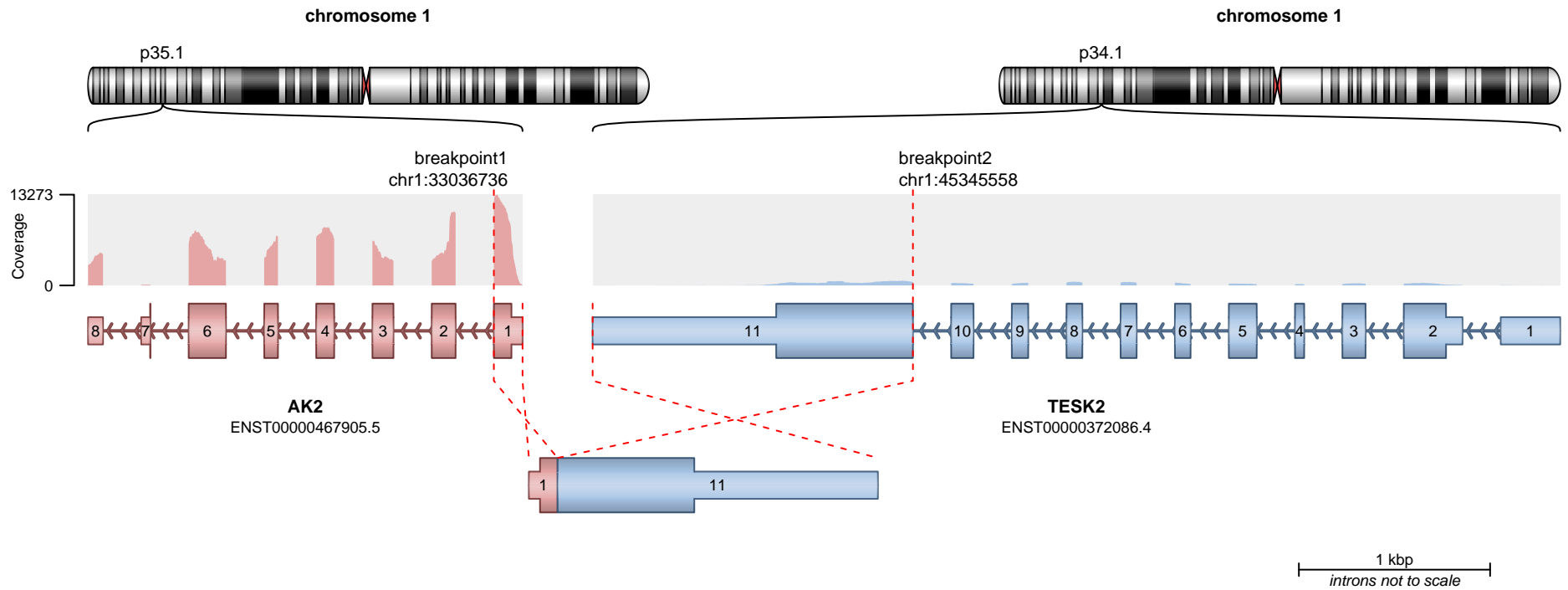
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



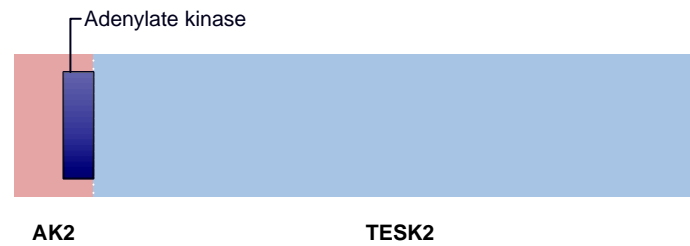
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



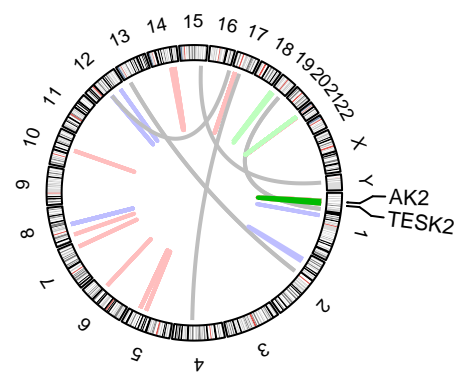
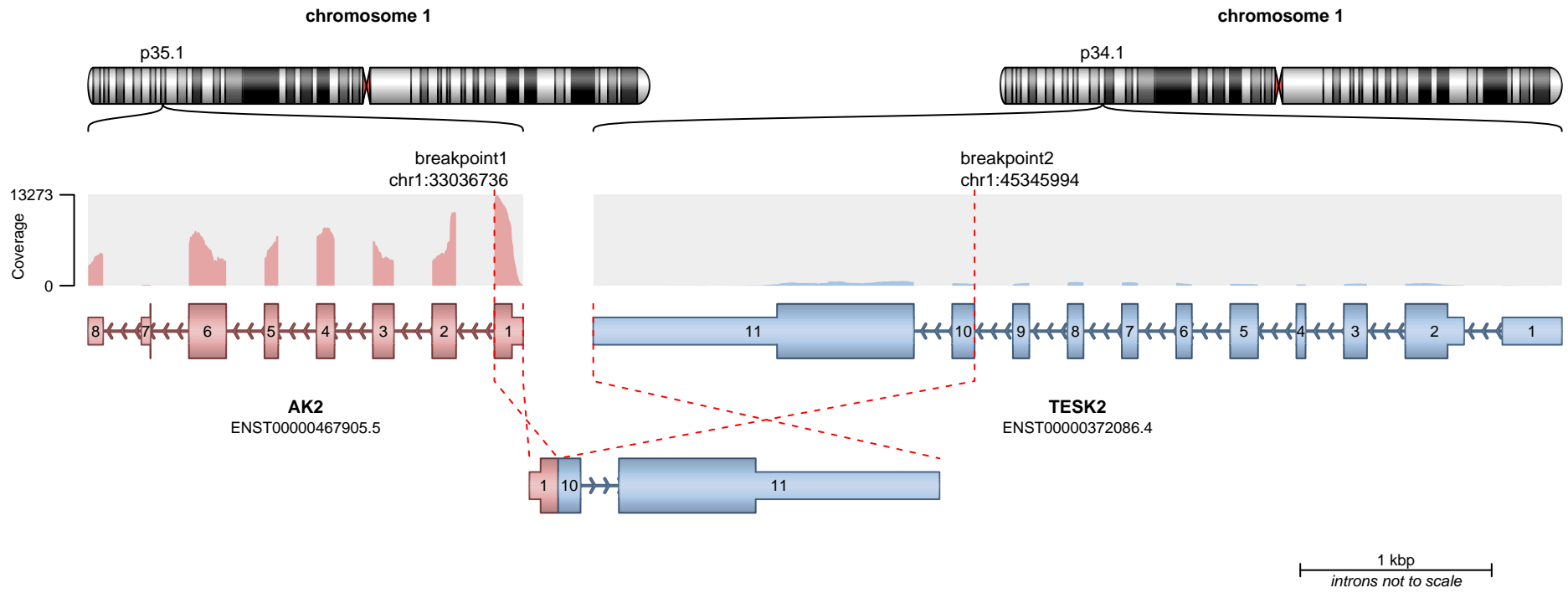
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



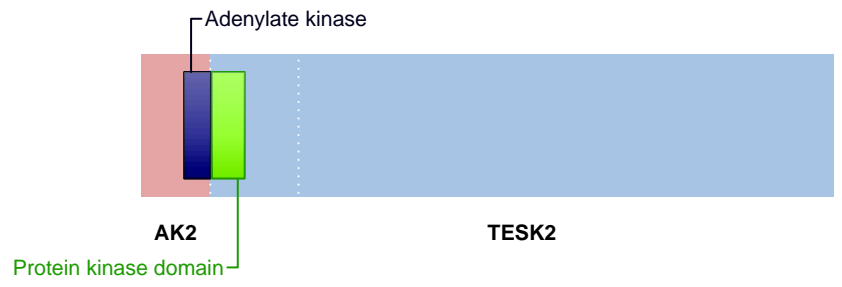
**SUPPORTING READ COUNT**

Split reads = 51  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



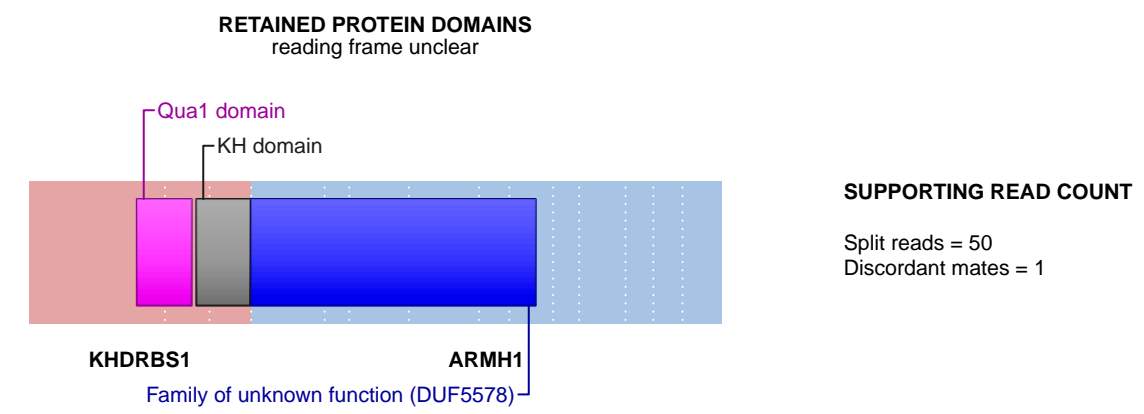
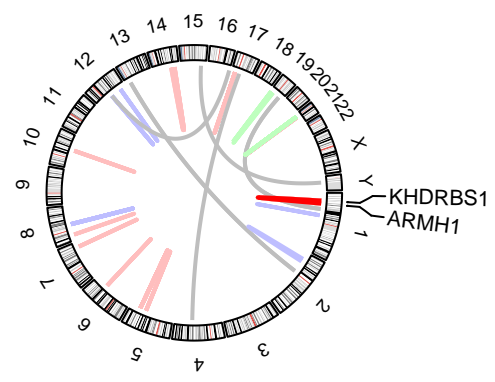
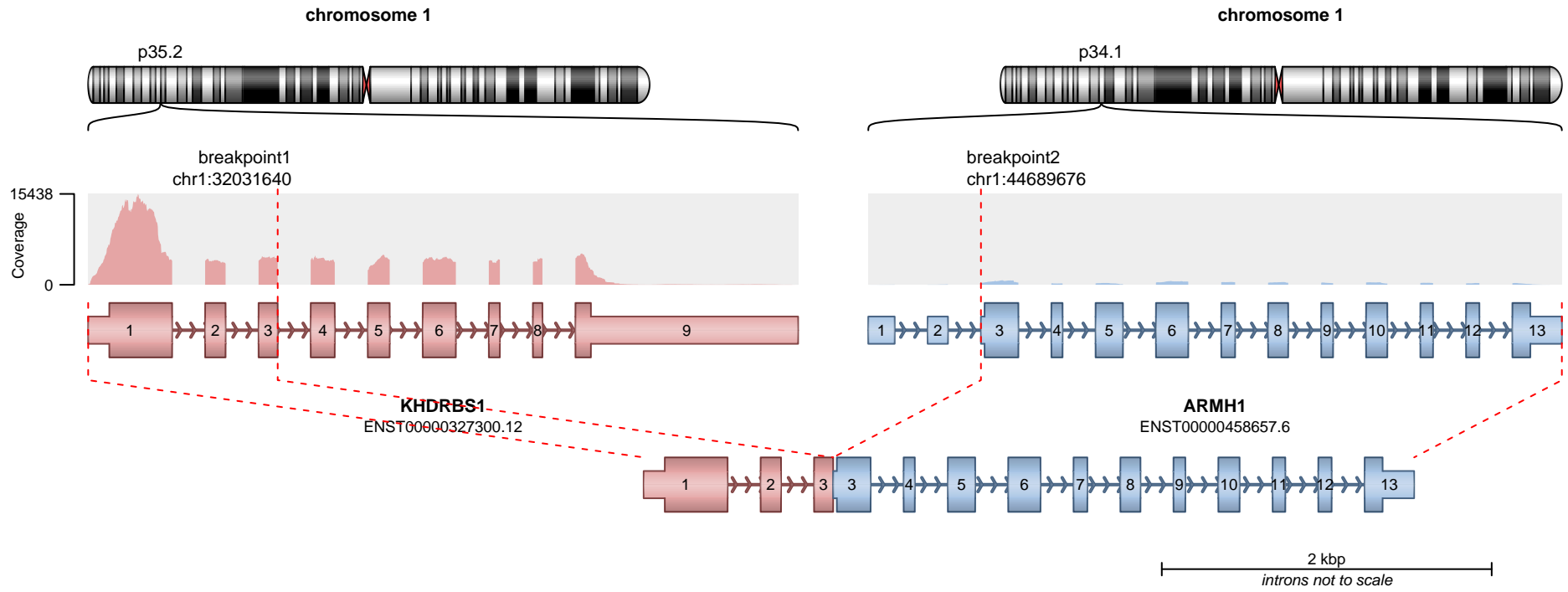
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



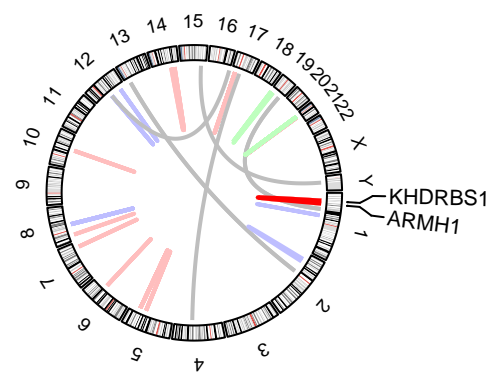
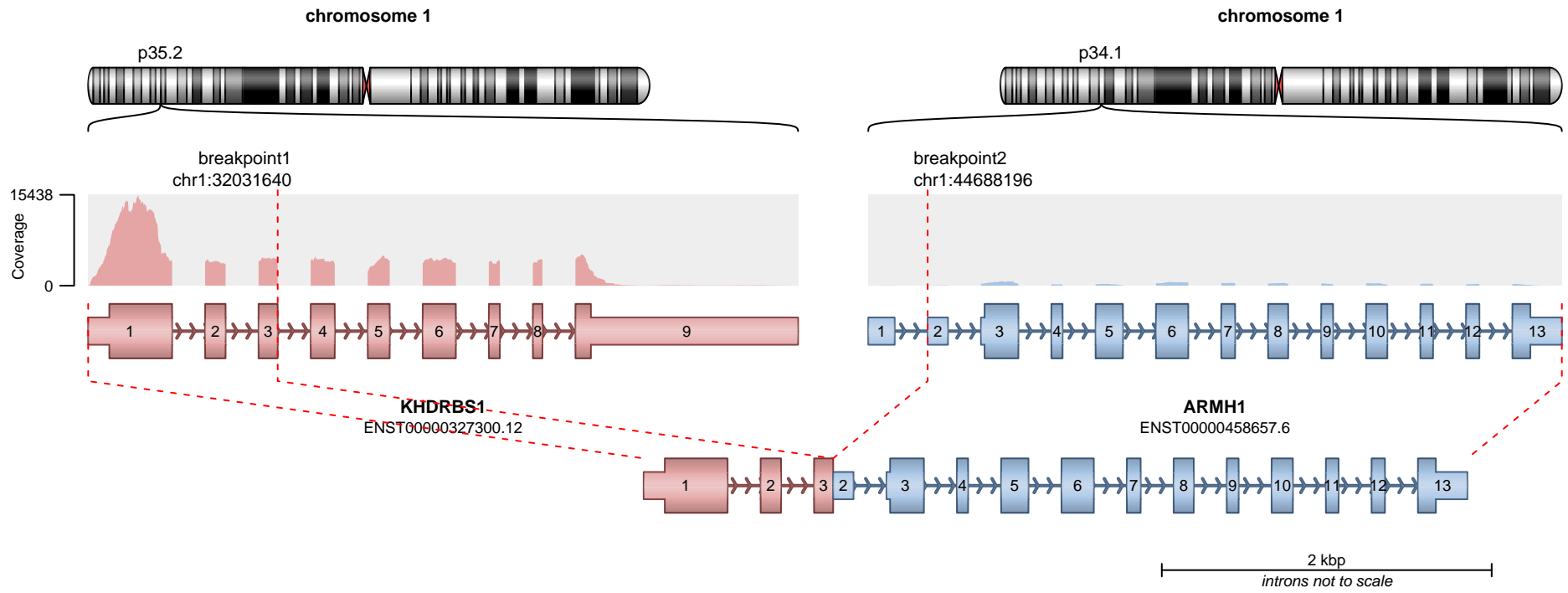
**SUPPORTING READ COUNT**

Split reads = 20  
Discordant mates = 0

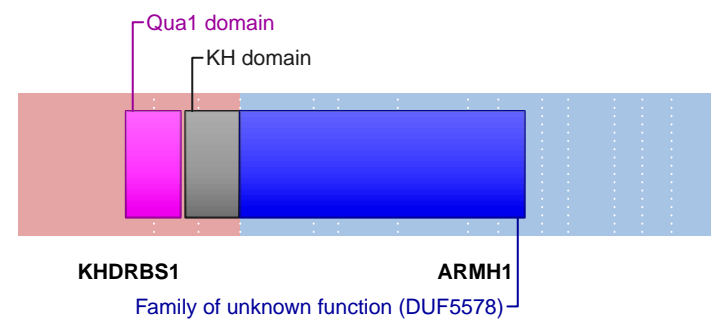
- translocation
- deletion
- duplication
- inversion



— translocation — deletion  
— duplication — inversion



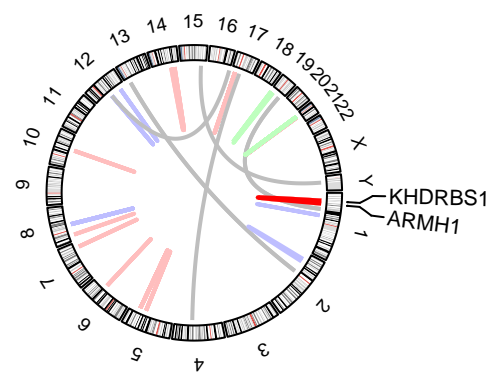
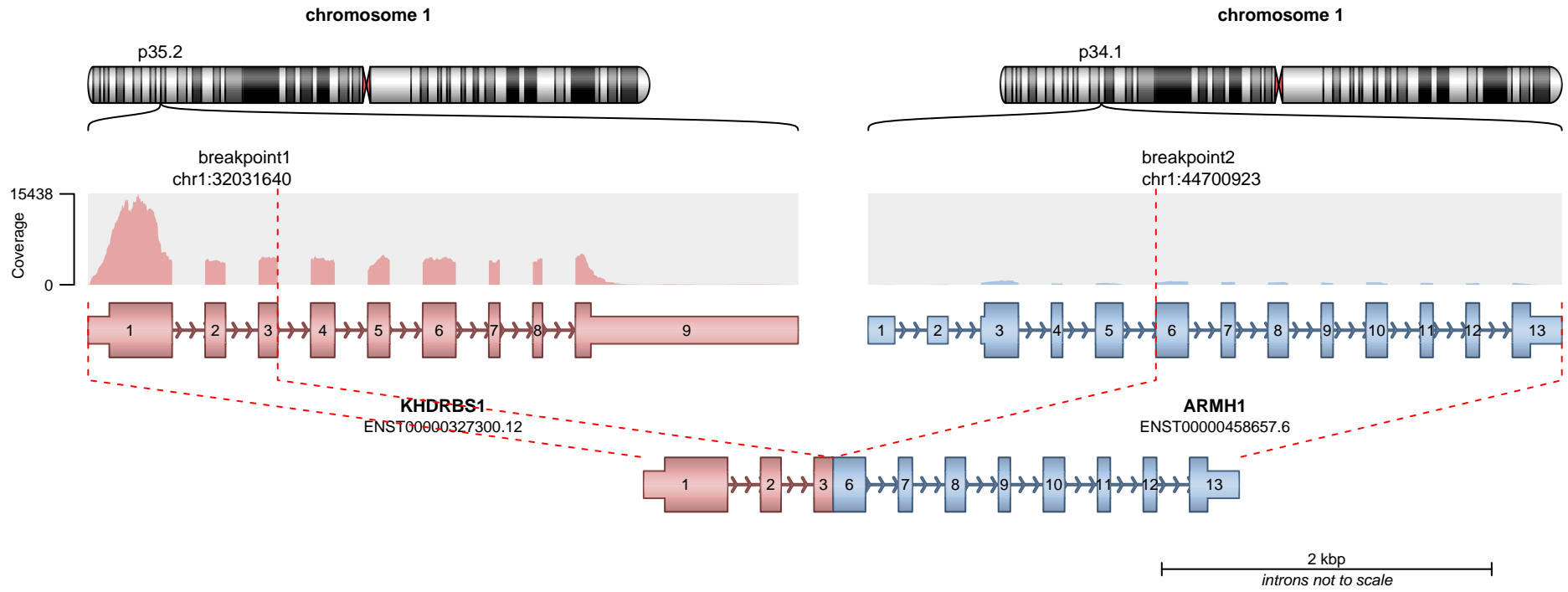
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



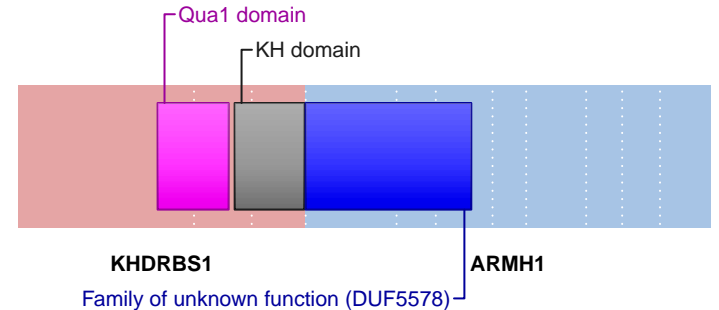
**SUPPORTING READ COUNT**

Split reads = 14  
Discordant mates = 2

- translocation
- duplication
- deletion
- inversion



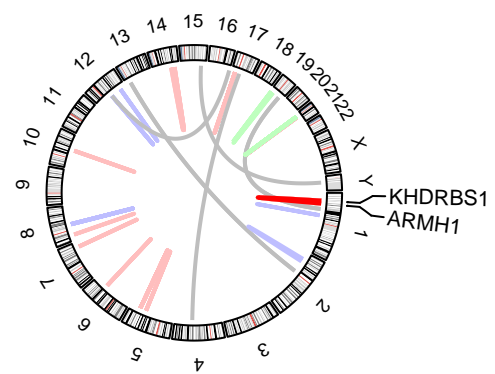
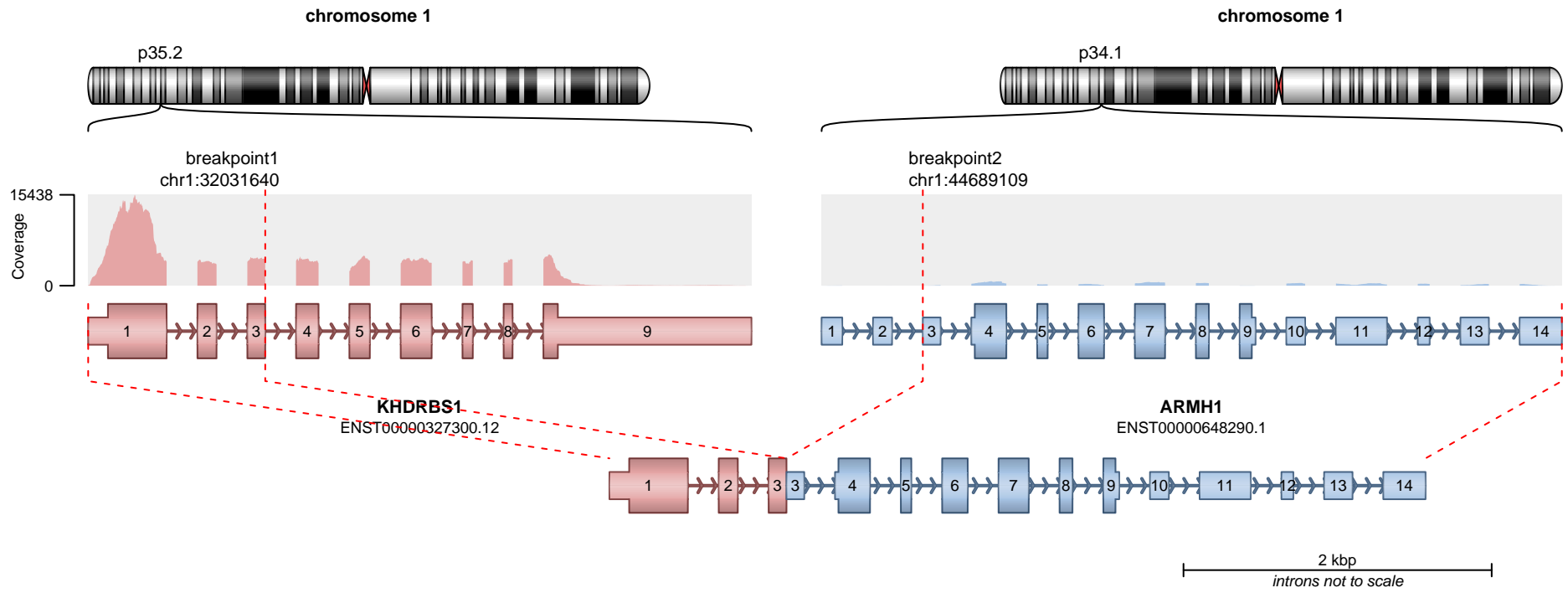
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



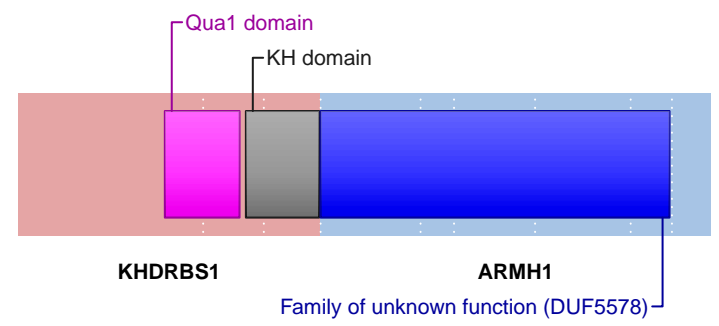
**SUPPORTING READ COUNT**

Split reads = 8  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



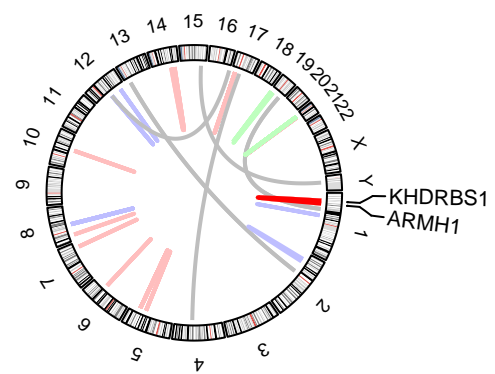
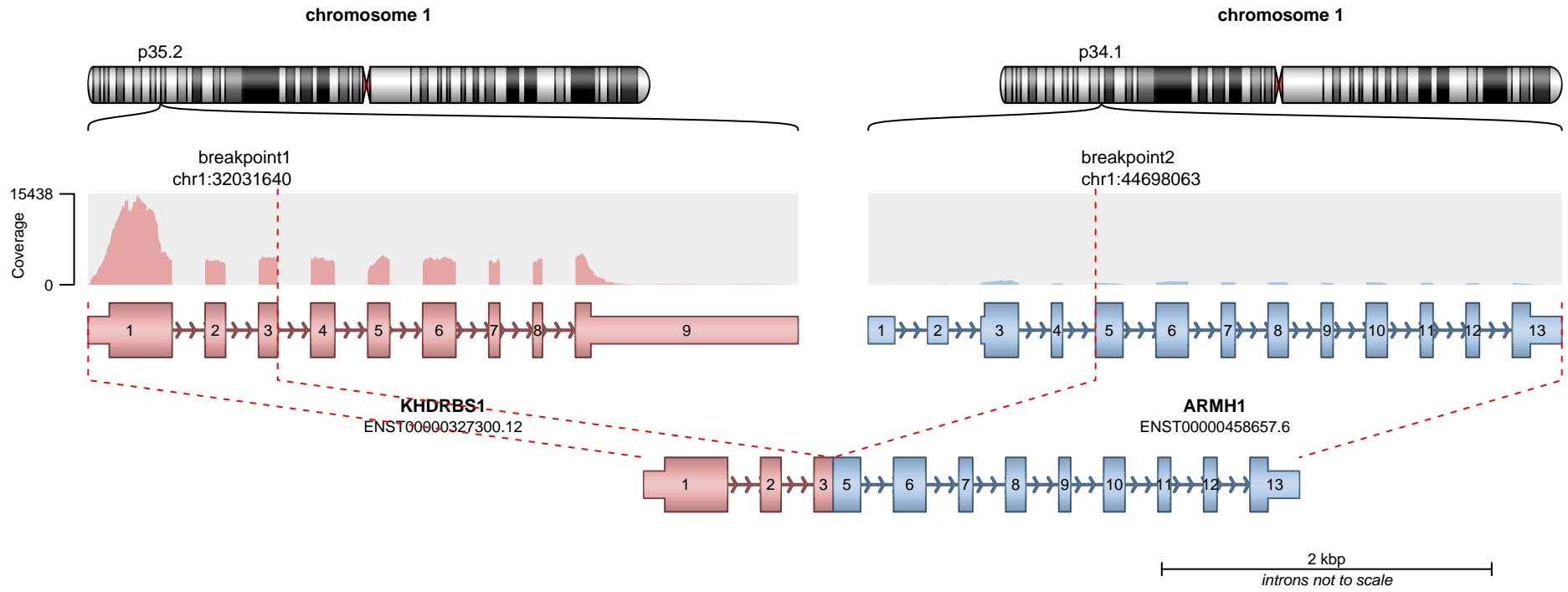
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



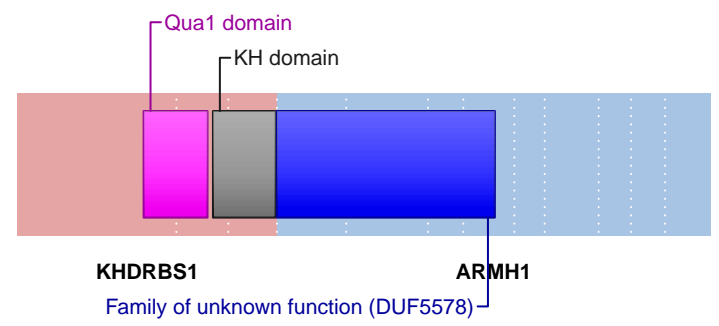
**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 2

- translocation
- duplication
- deletion
- inversion



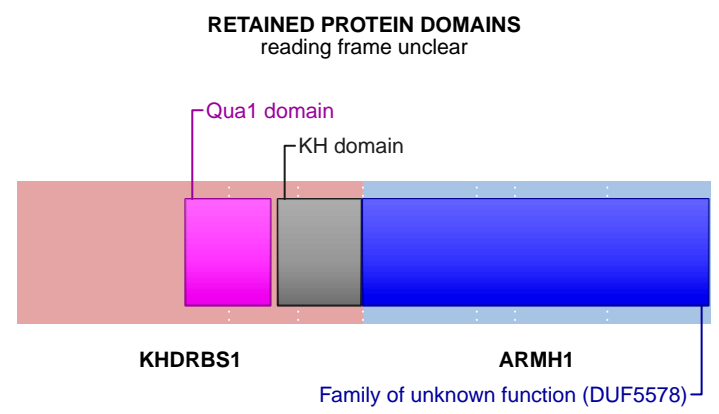
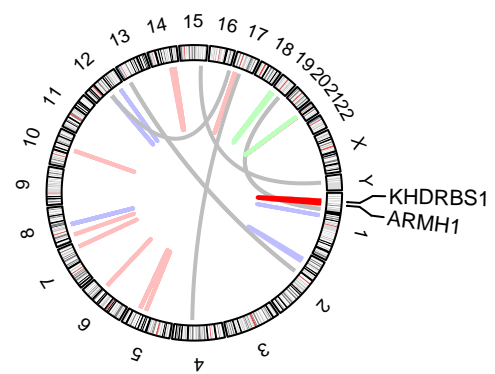
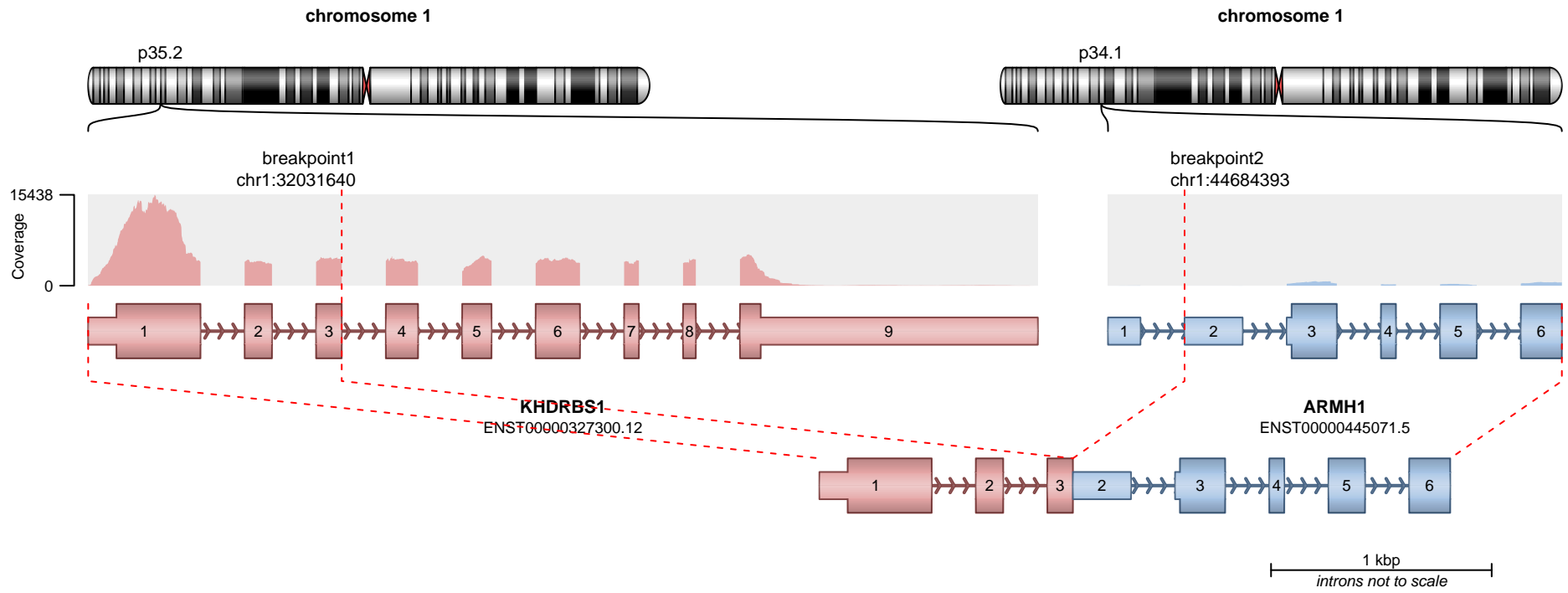
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0

- translocation
- deletion
- duplication
- inversion

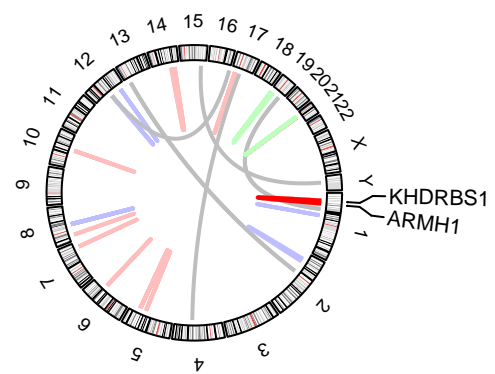
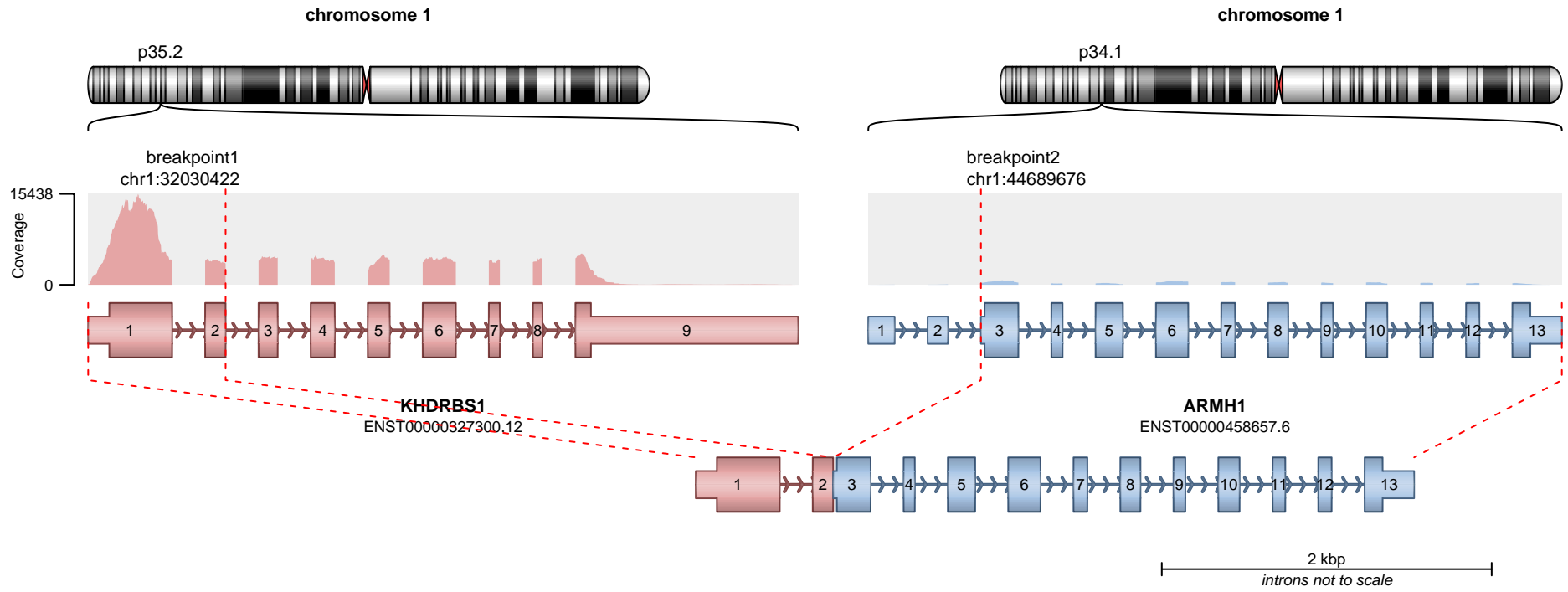


**SUPPORTING READ COUNT**

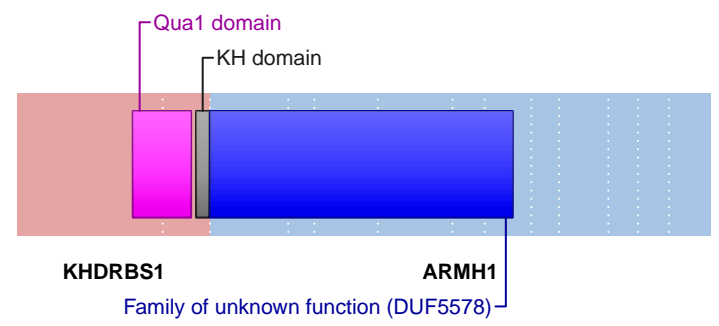
Split reads = 1

Discordant mates = 2

— translocation — deletion  
— duplication — inversion



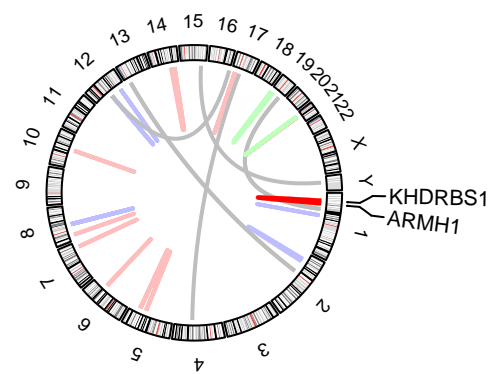
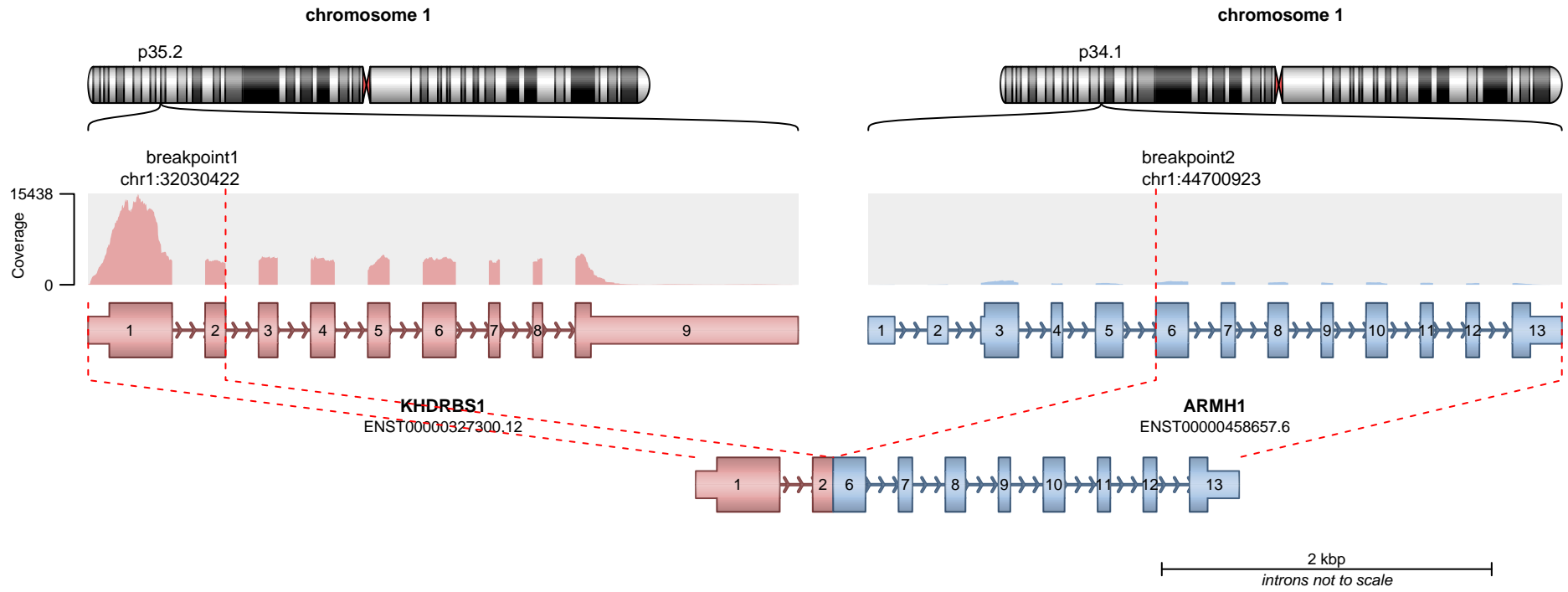
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



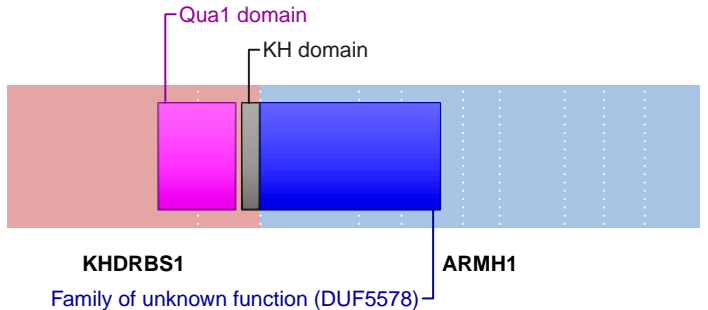
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



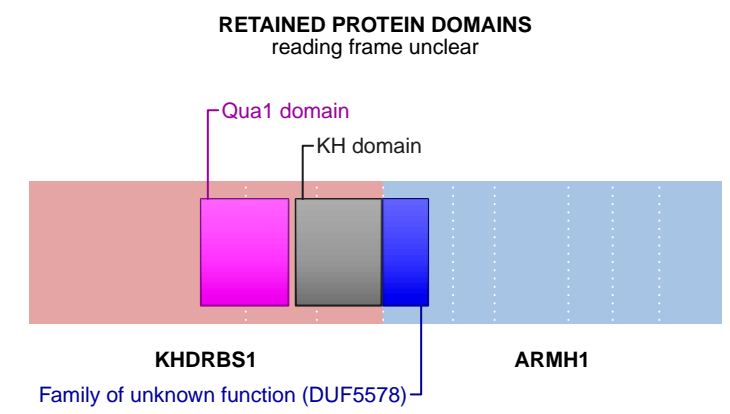
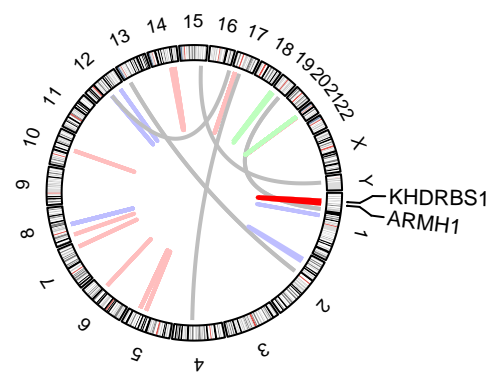
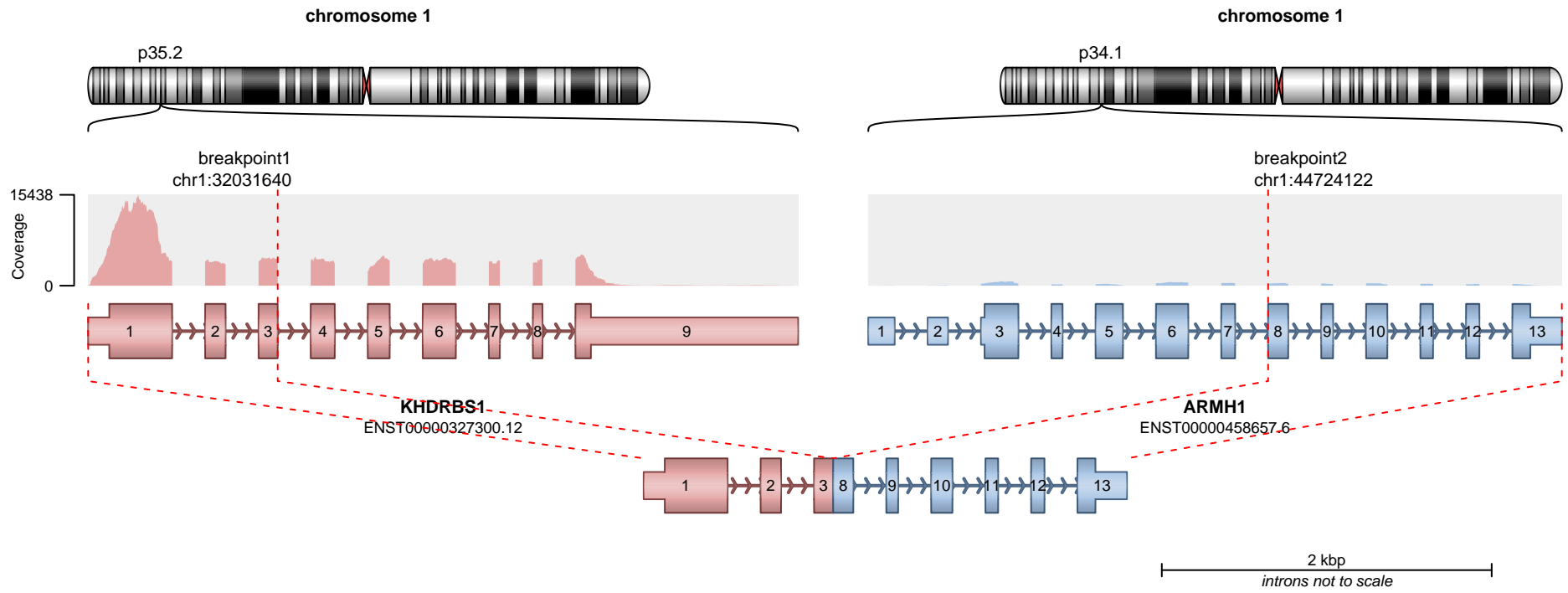
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

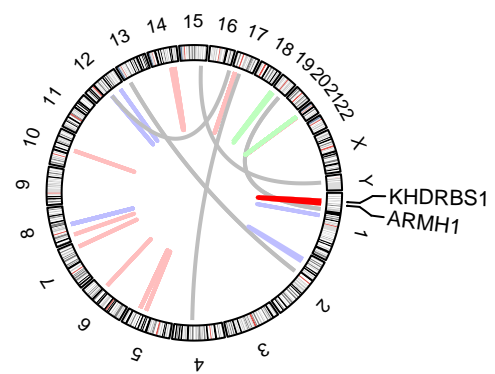
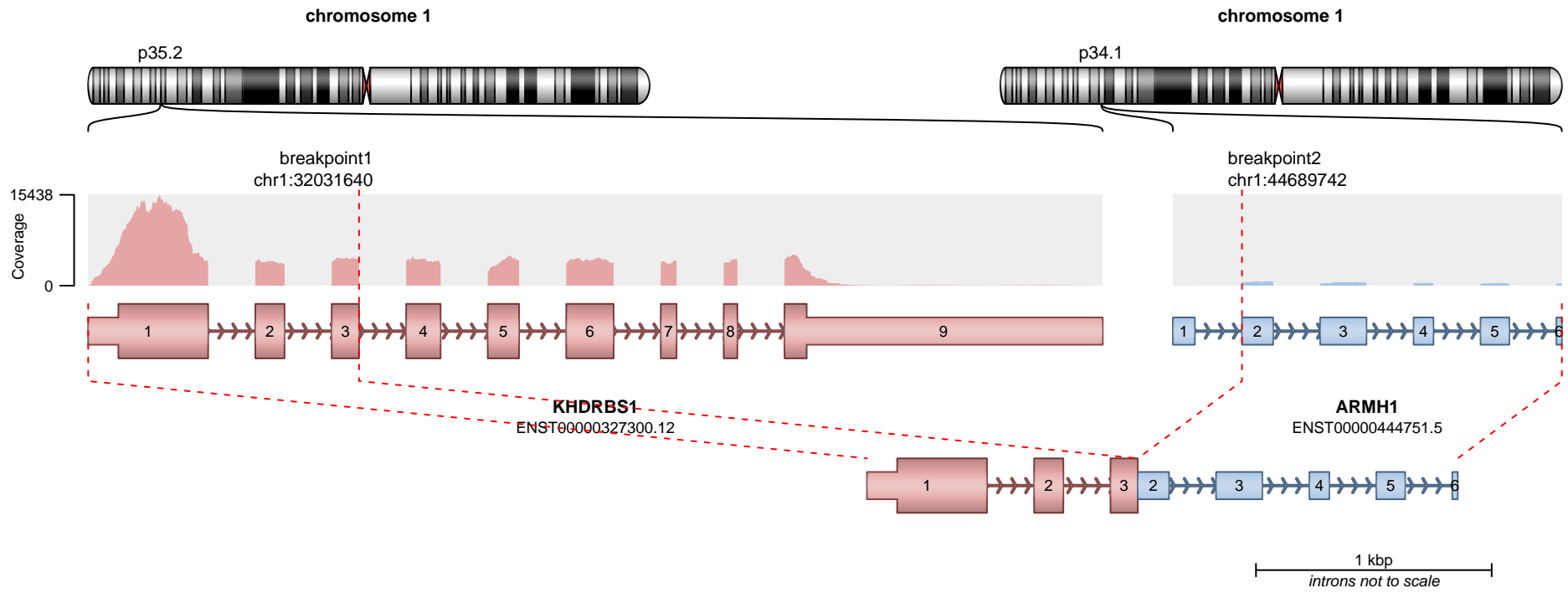
- translocation
- duplication
- deletion
- inversion



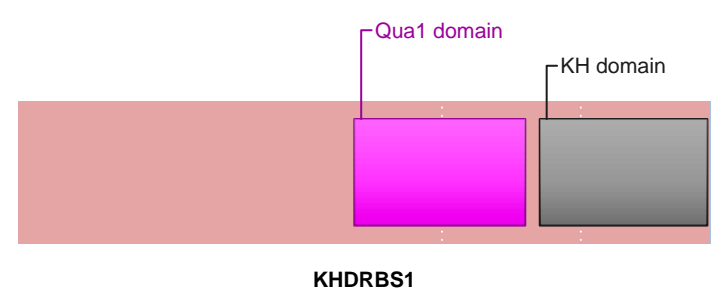
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



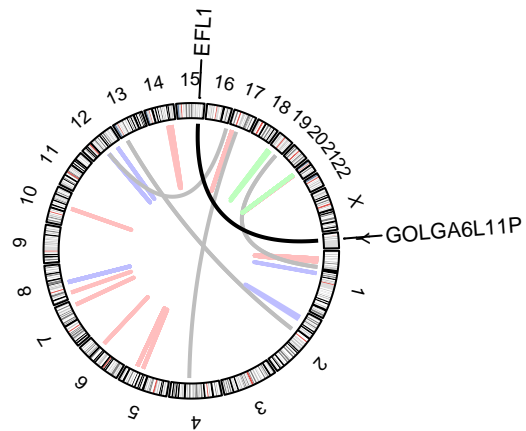
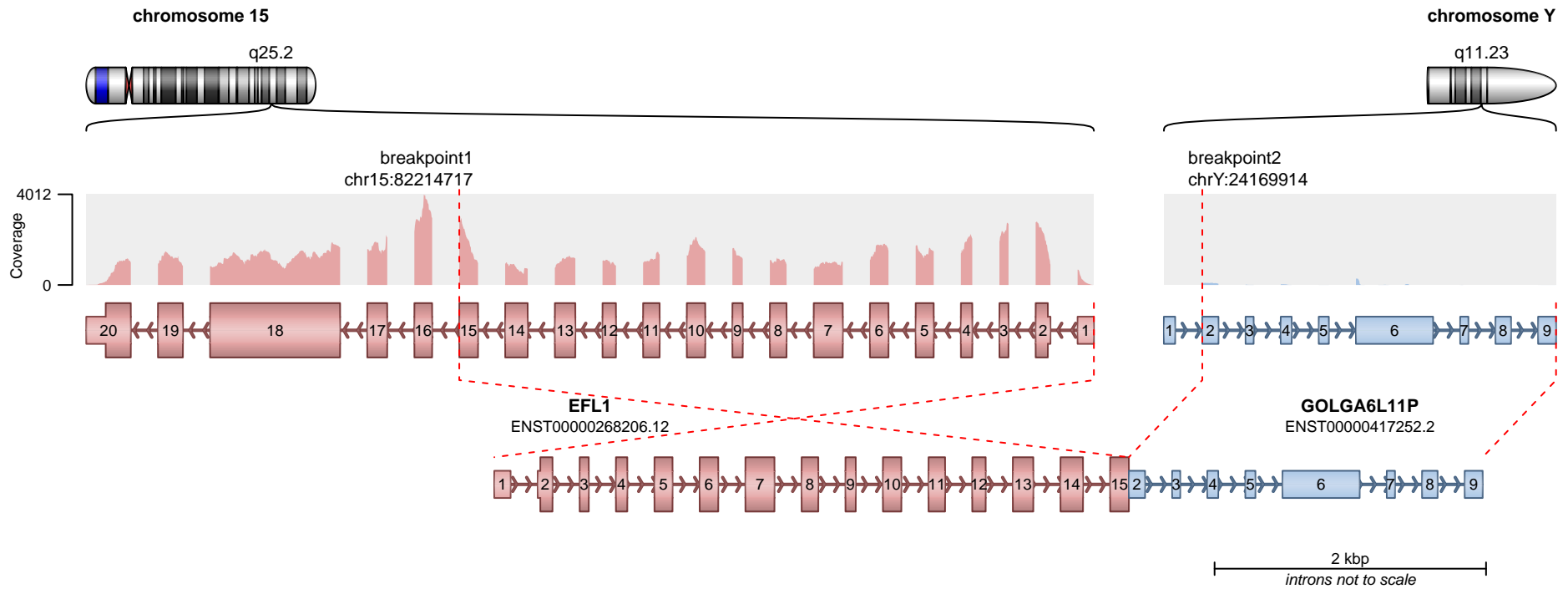
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



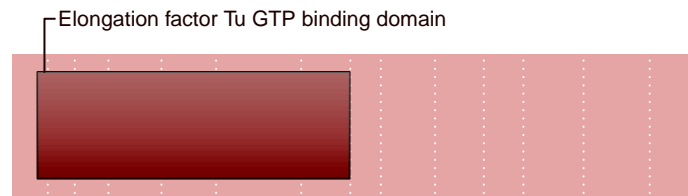
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



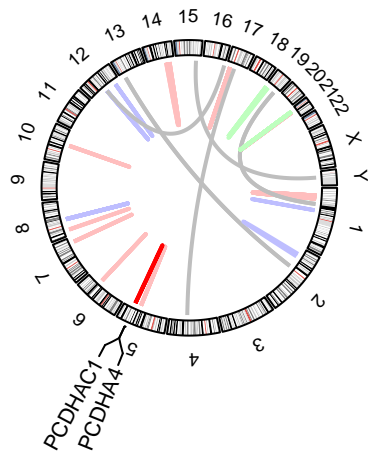
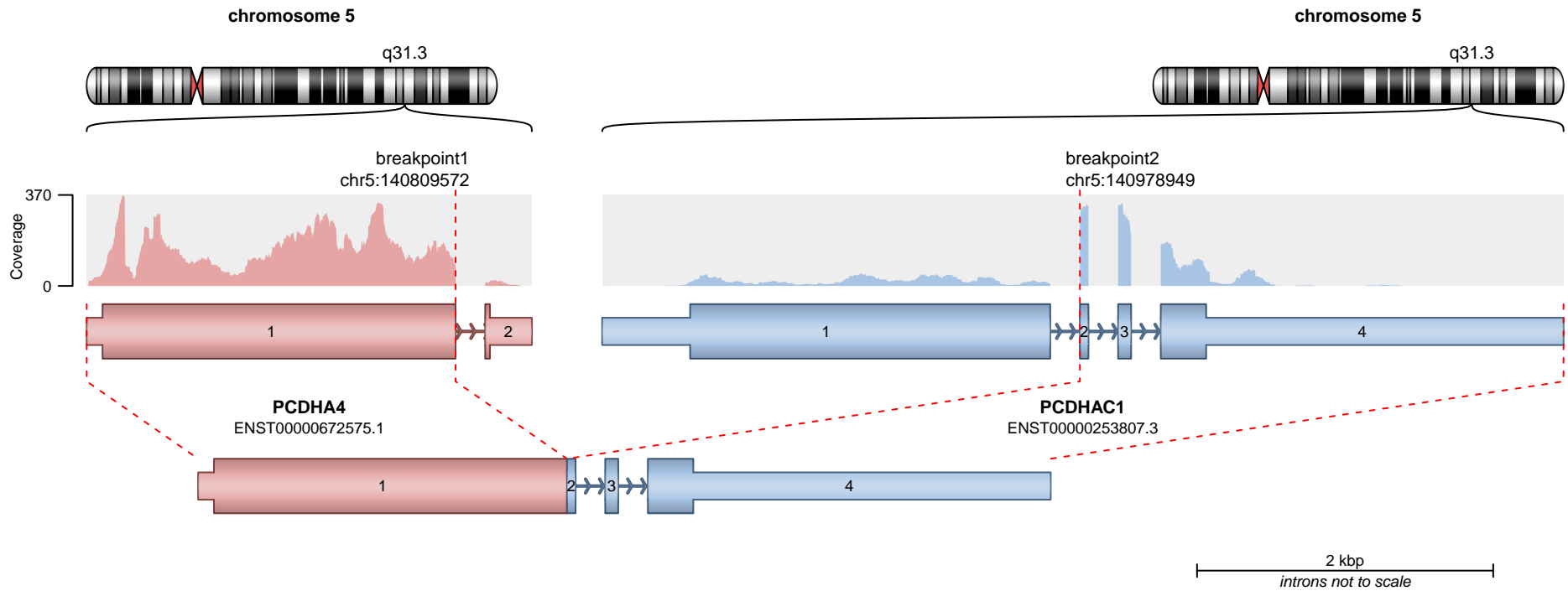
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



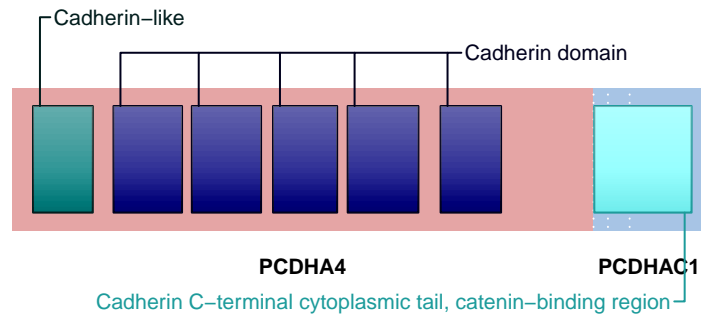
**SUPPORTING READ COUNT**

Split reads = 33  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



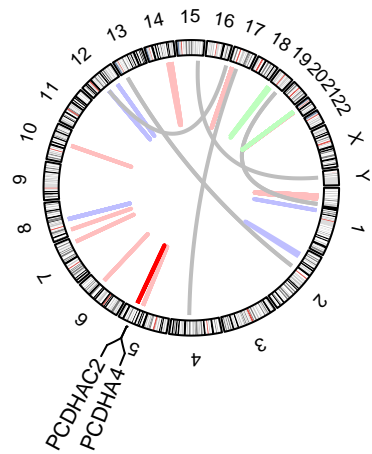
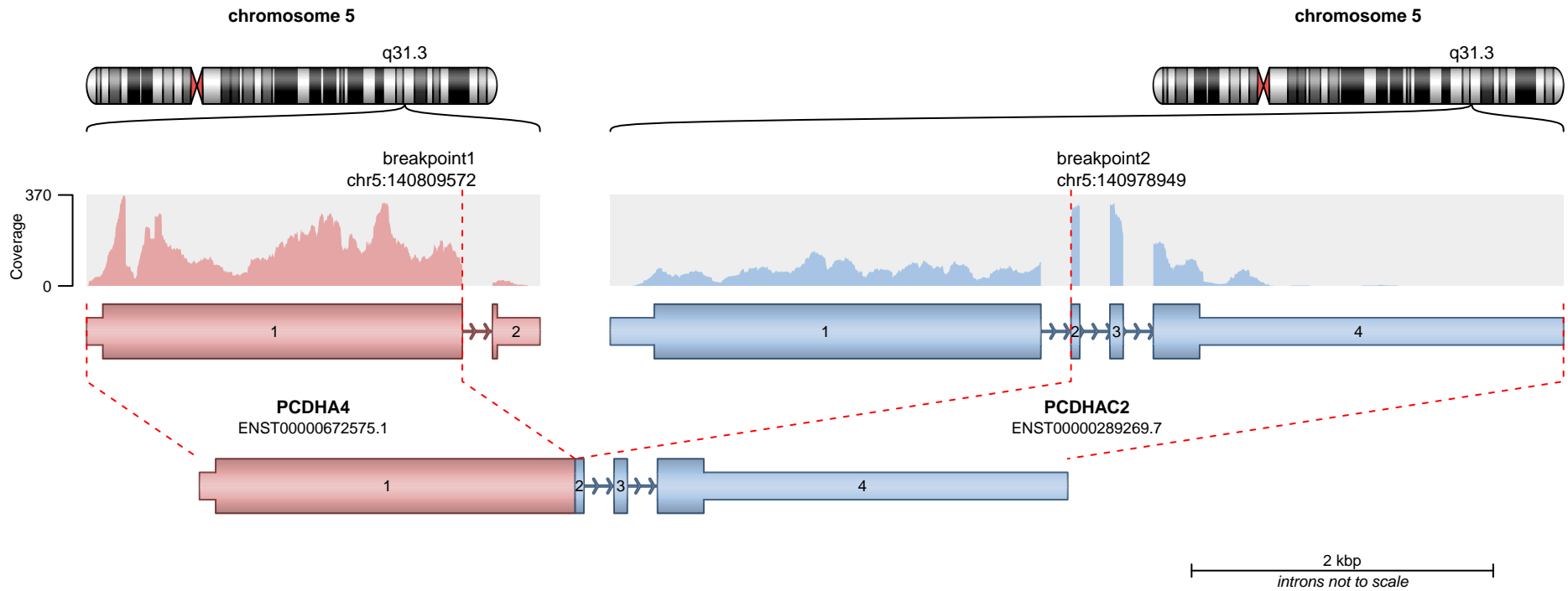
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



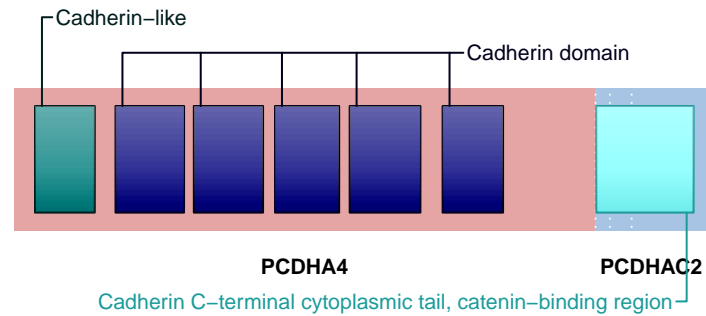
**SUPPORTING READ COUNT**

Split reads = 32  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



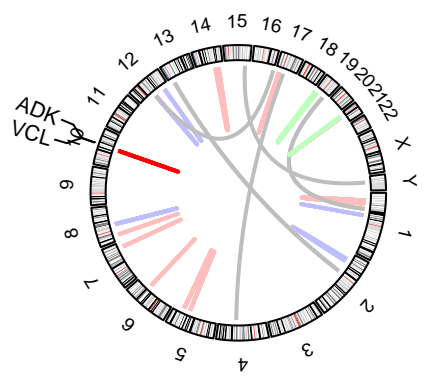
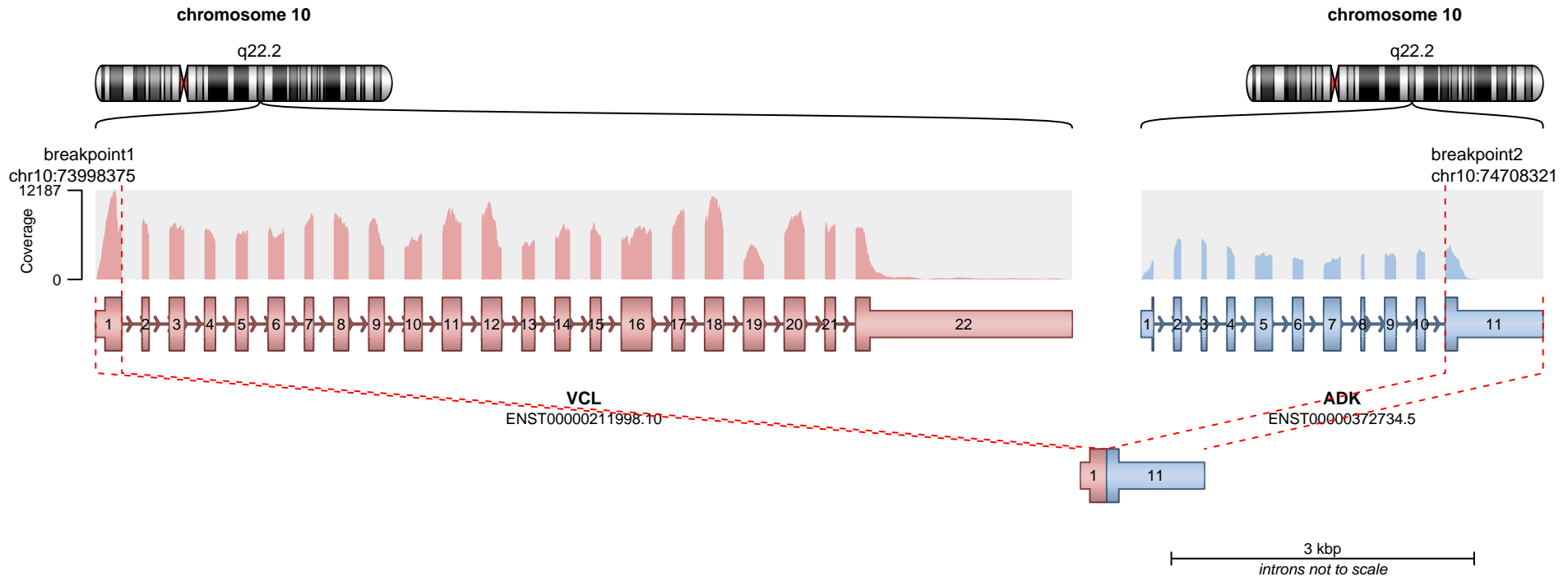
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



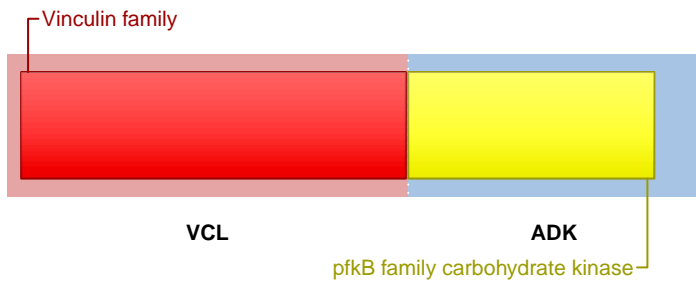
**SUPPORTING READ COUNT**

Split reads = 32  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



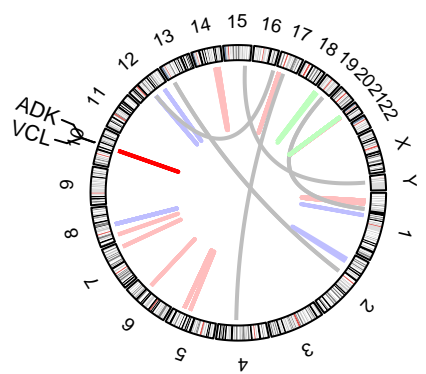
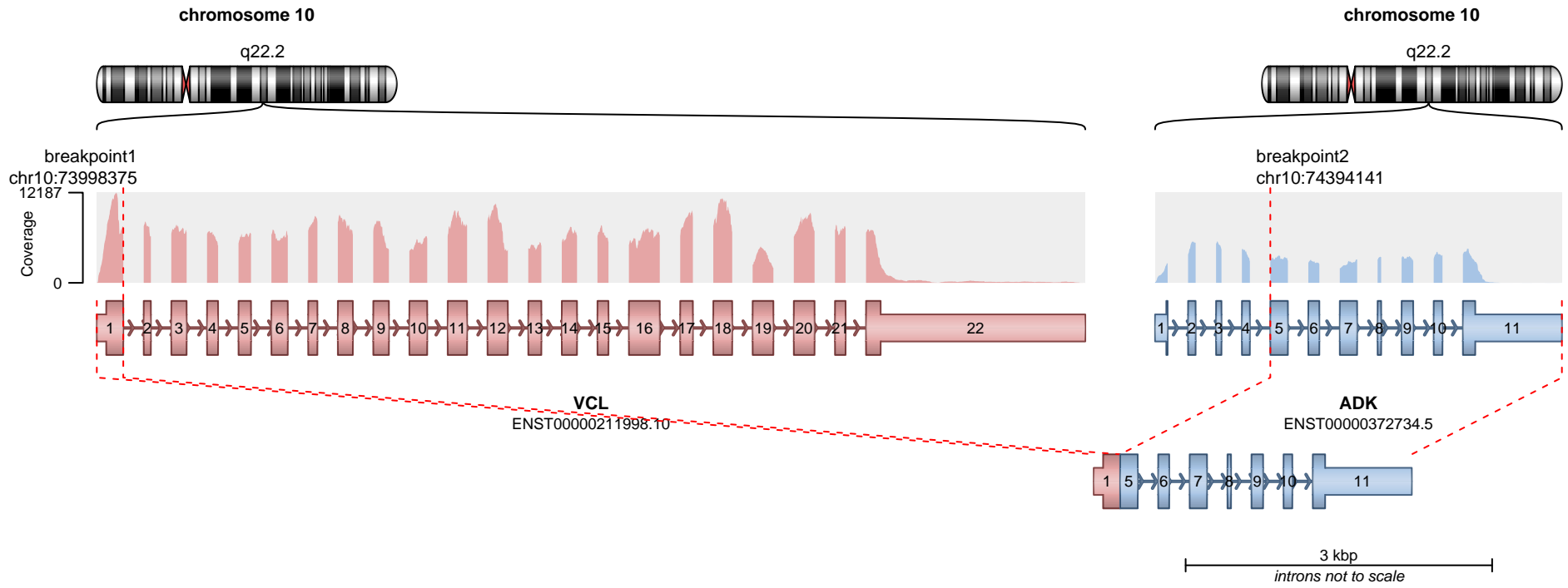
**RETAINED PROTEIN DOMAINS**  
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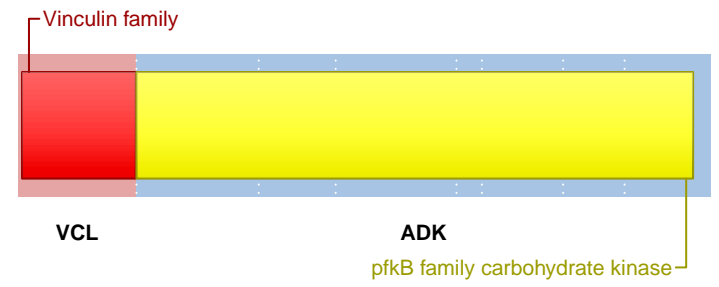
**SUPPORTING READ COUNT**

Split reads = 28  
Discordant mates = 1

— translocation — deletion  
— duplication — inversion



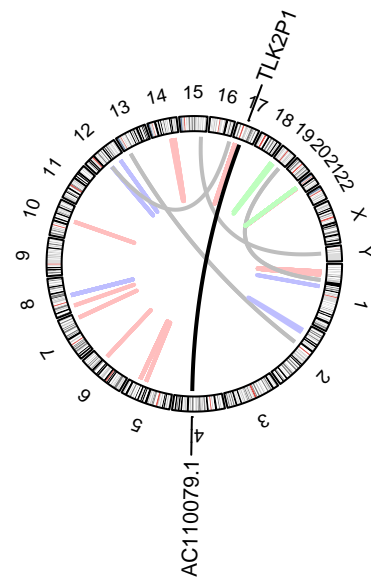
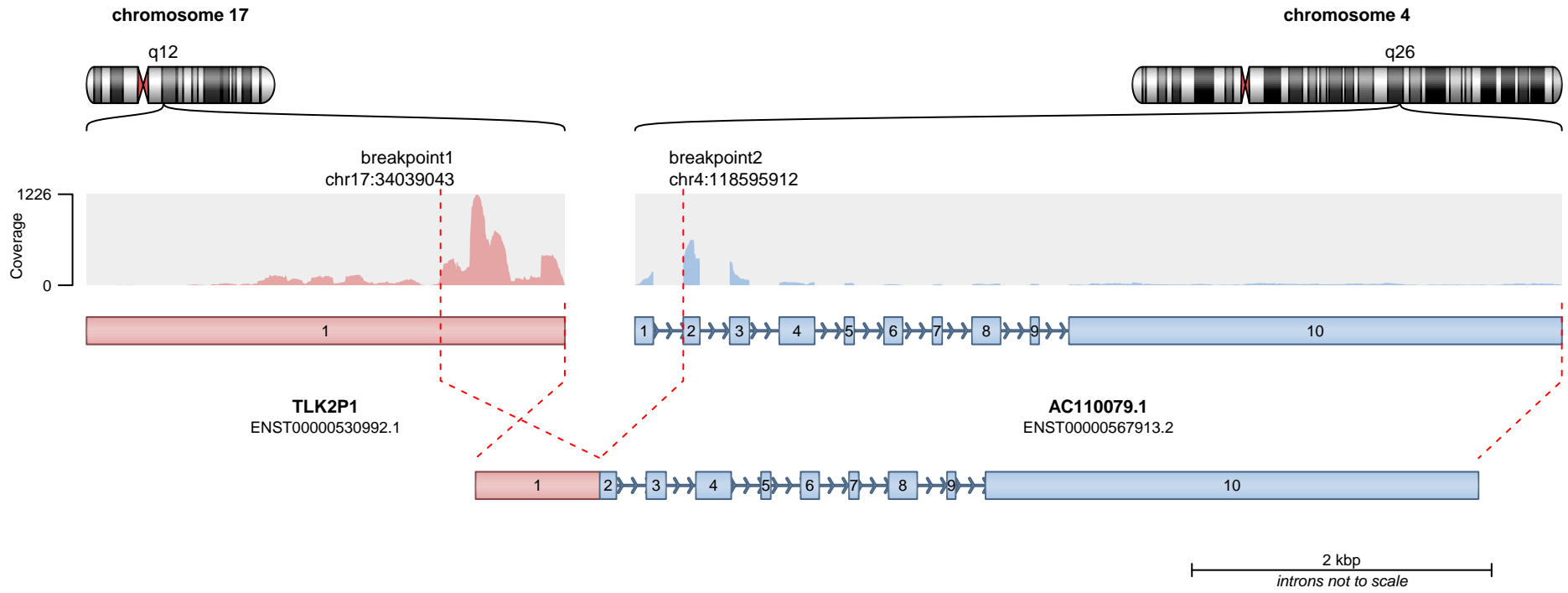
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion

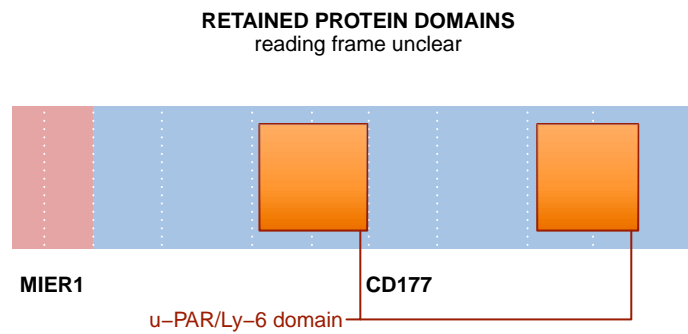
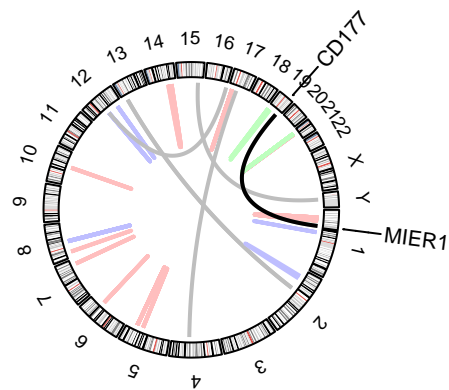
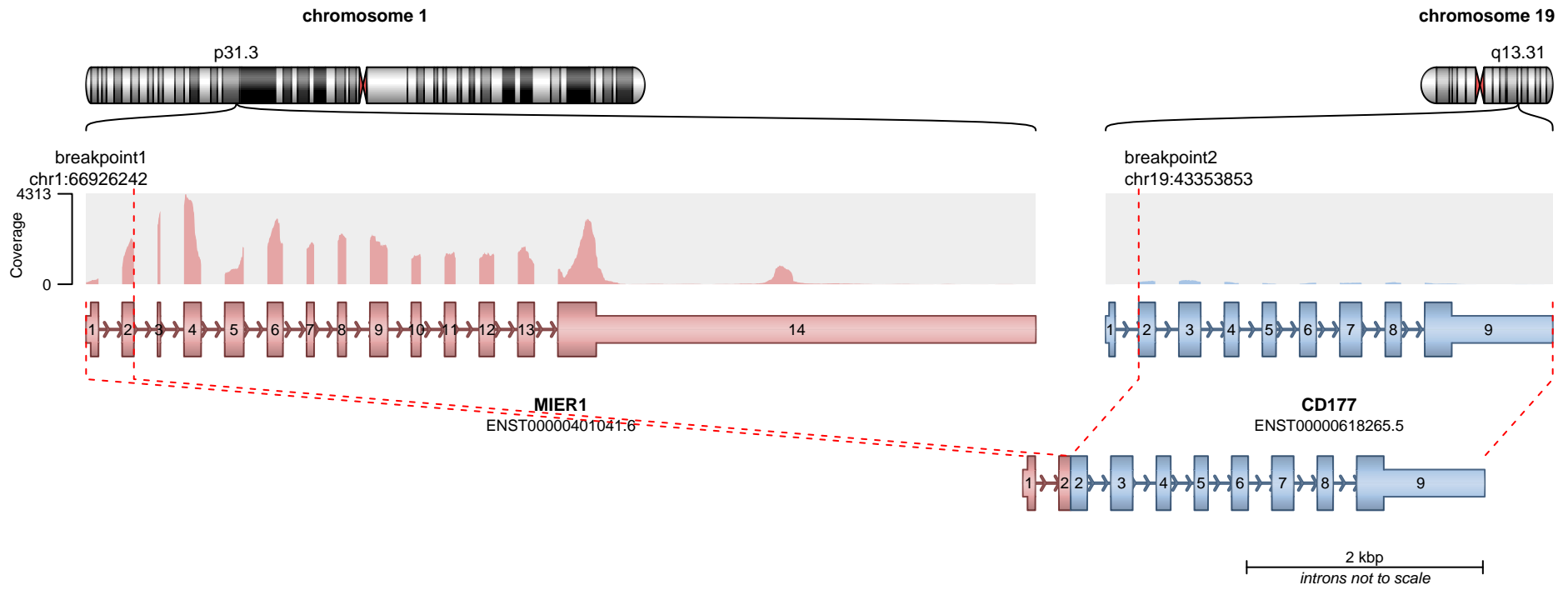


— translocation    — deletion  
 — duplication    — inversion

Genes are not protein-coding.

**SUPPORTING READ COUNT**

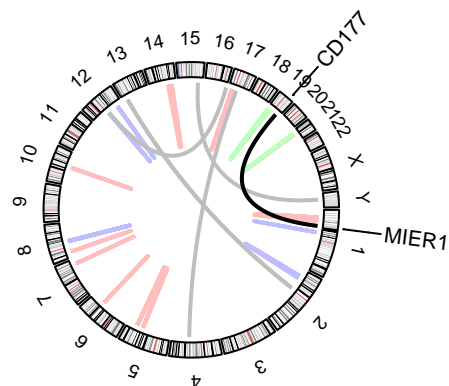
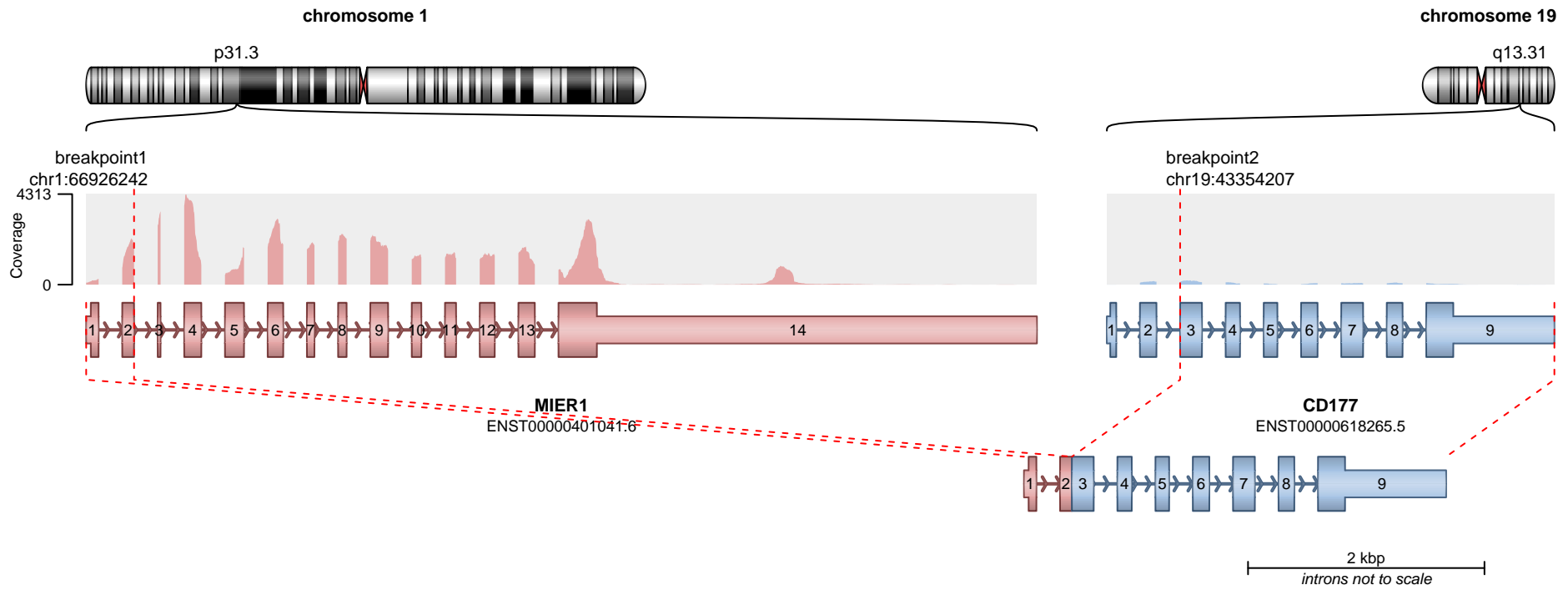
Split reads = 25  
 Discordant mates = 0



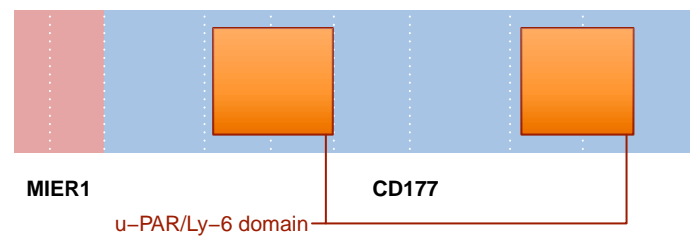
**SUPPORTING READ COUNT**

Split reads = 24  
Discordant mates = 1

— translocation — deletion  
— duplication — inversion



**RETAINED PROTEIN DOMAINS**  
reading frame unclear

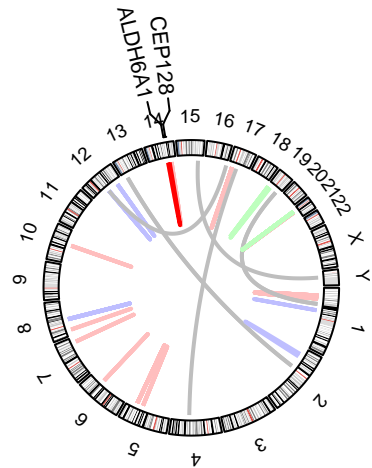
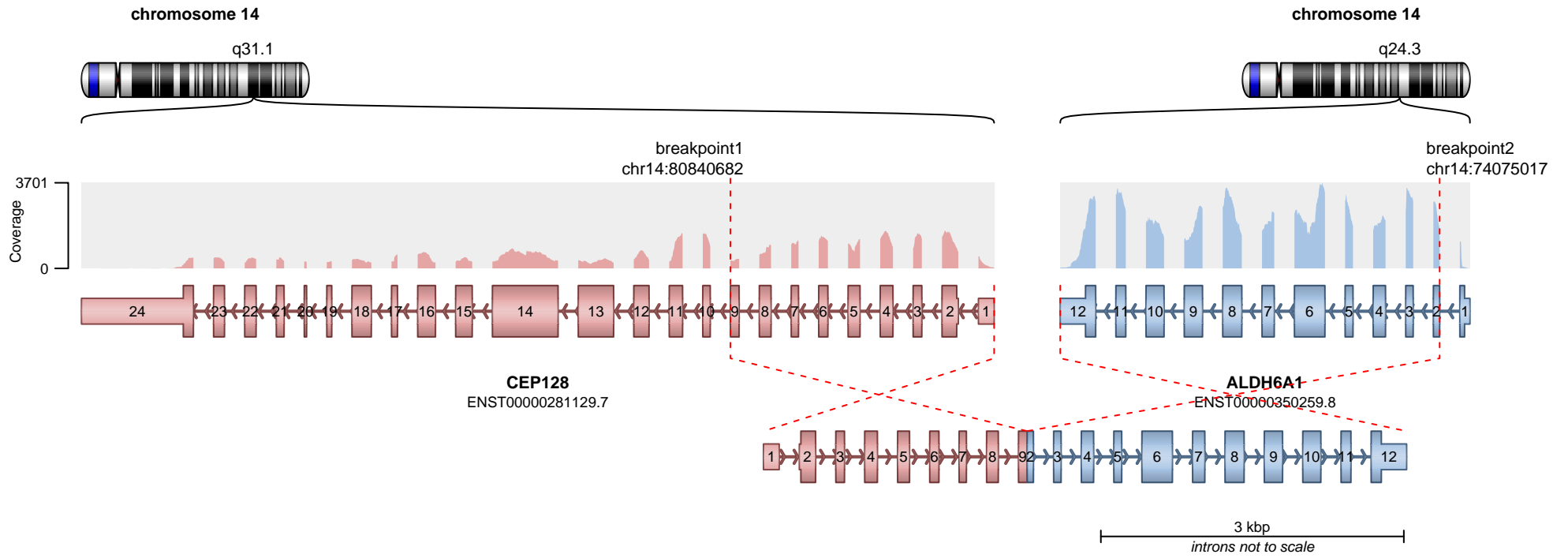


**SUPPORTING READ COUNT**

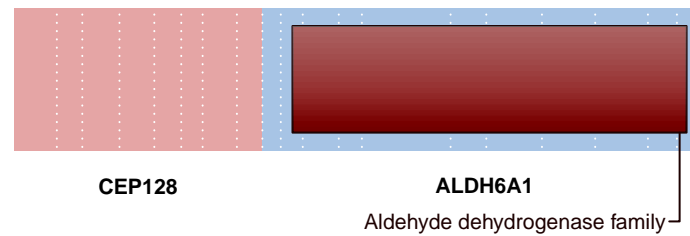
Split reads = 4  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion





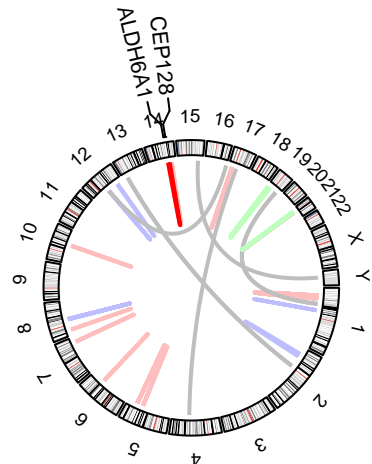
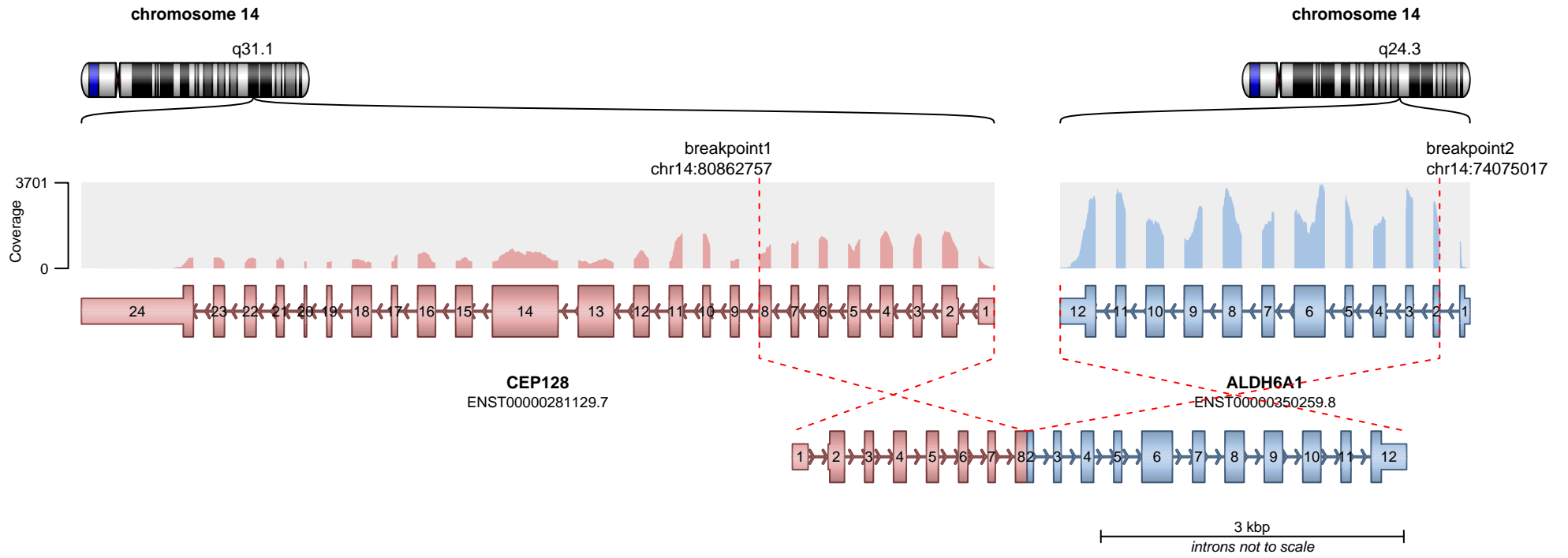
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



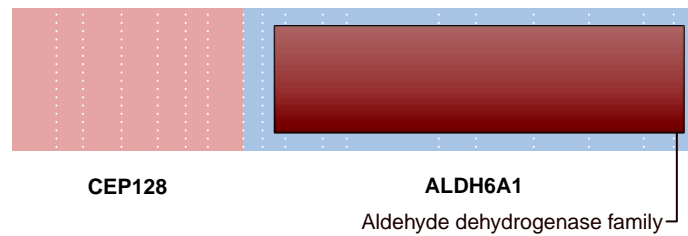
**SUPPORTING READ COUNT**

Split reads = 21  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



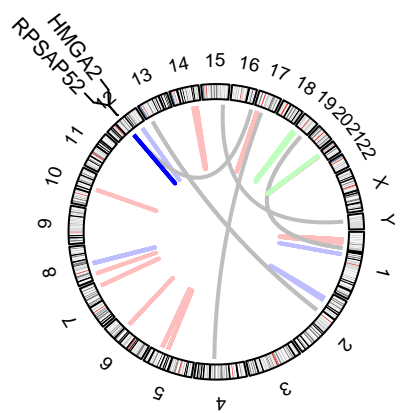
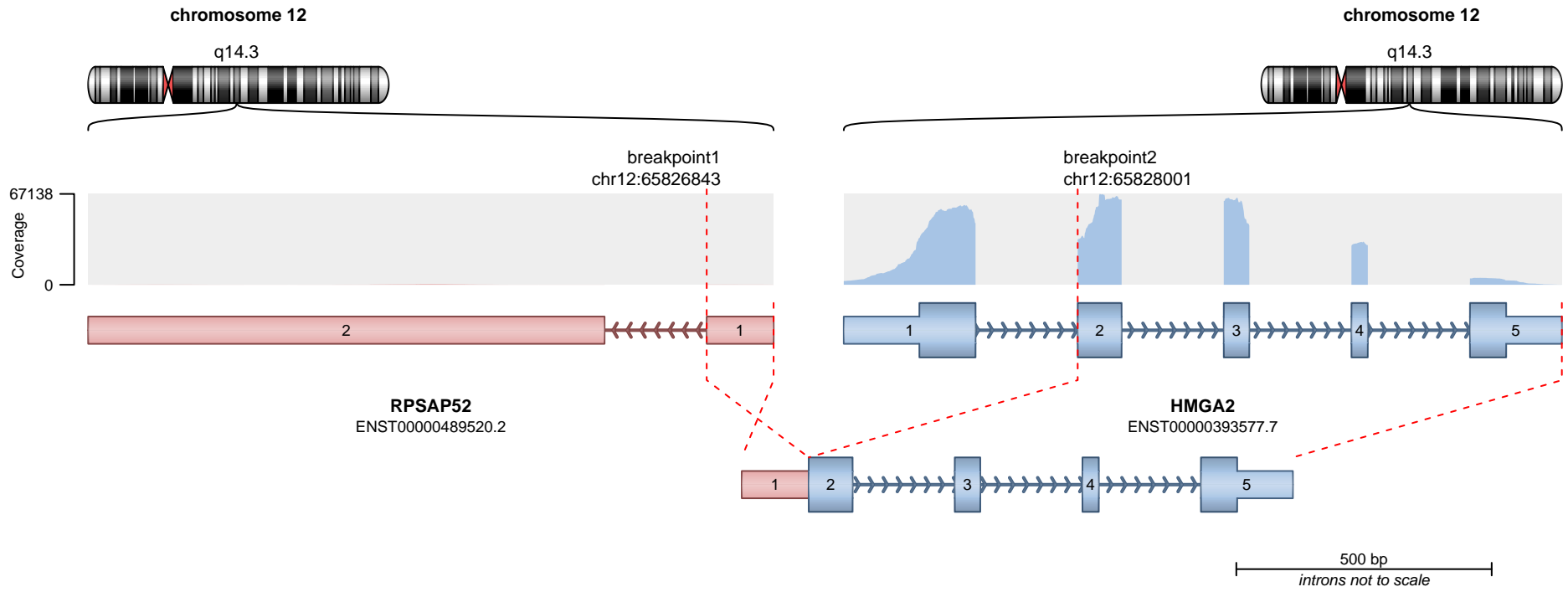
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



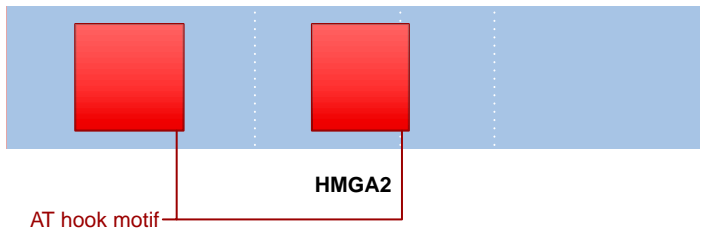
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



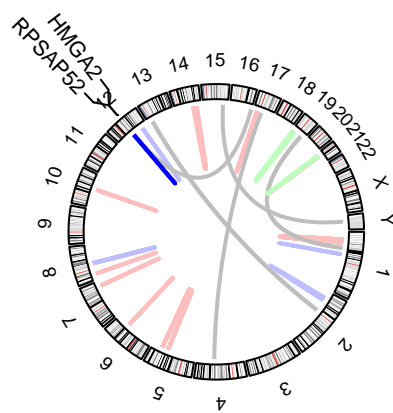
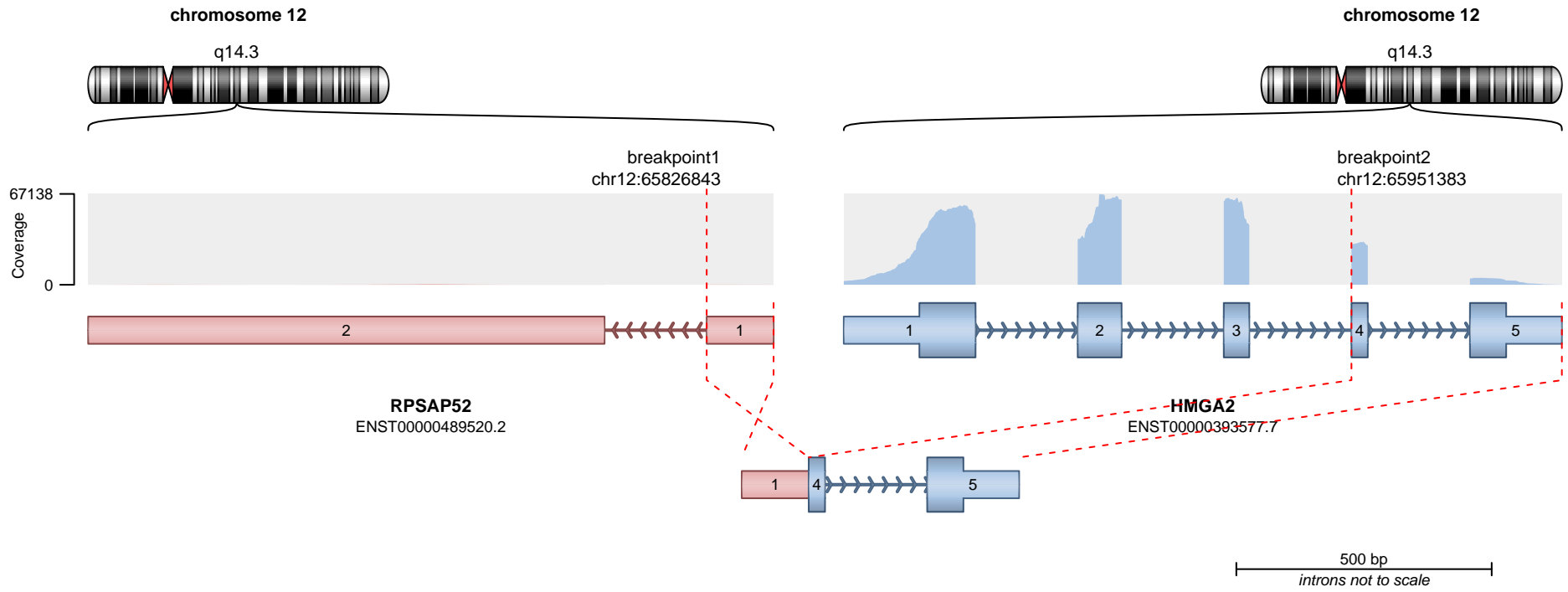
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



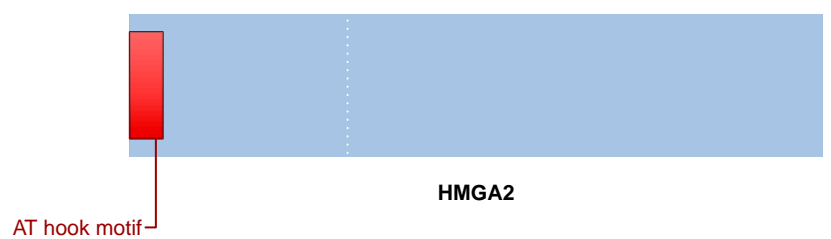
**SUPPORTING READ COUNT**

Split reads = 20  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



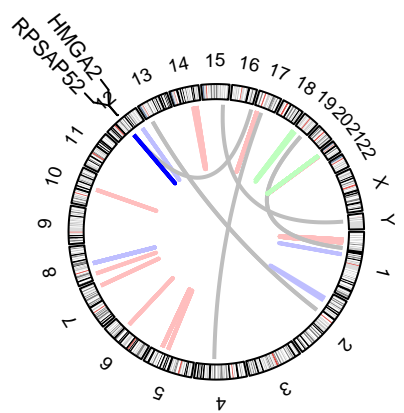
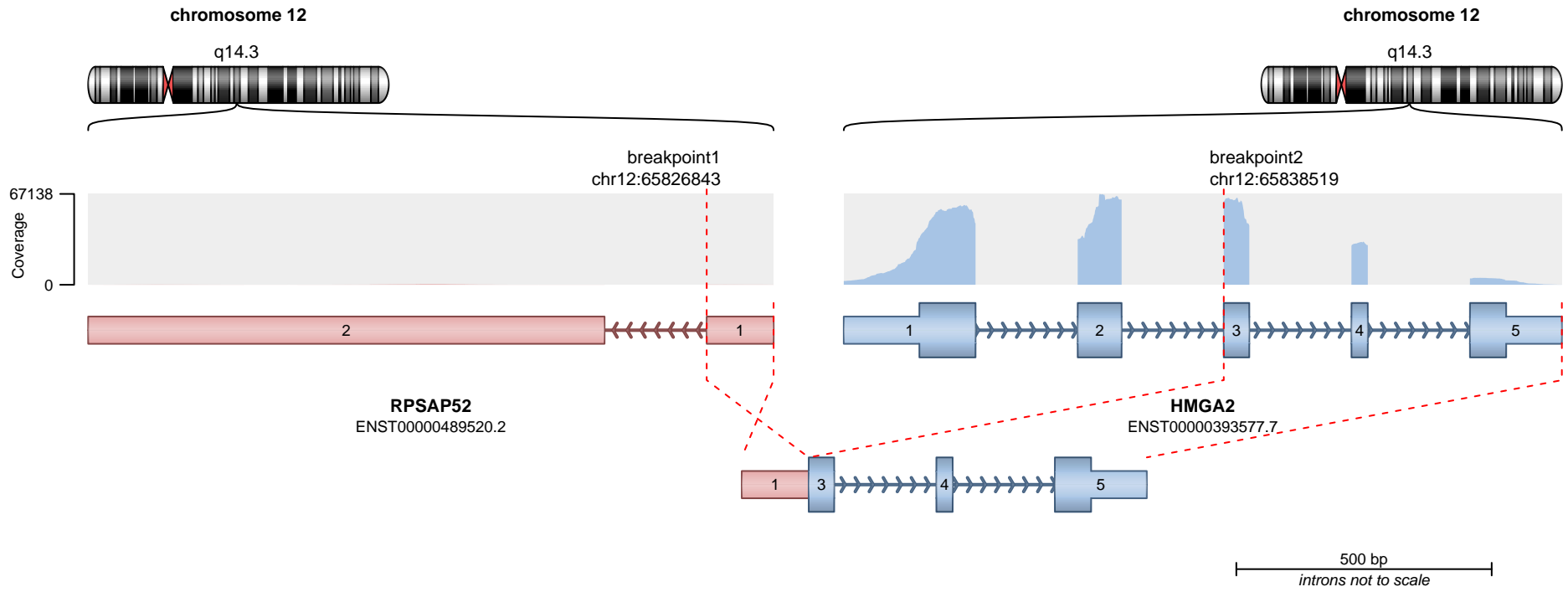
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



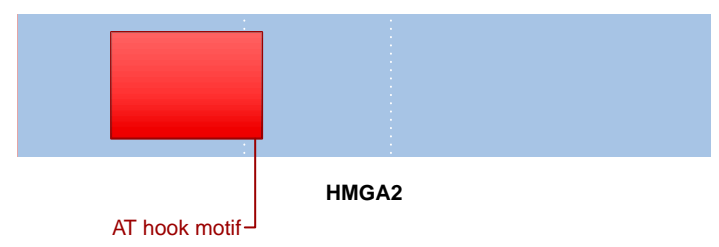
**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



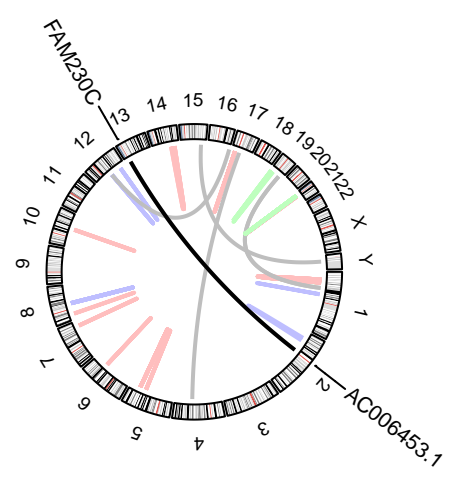
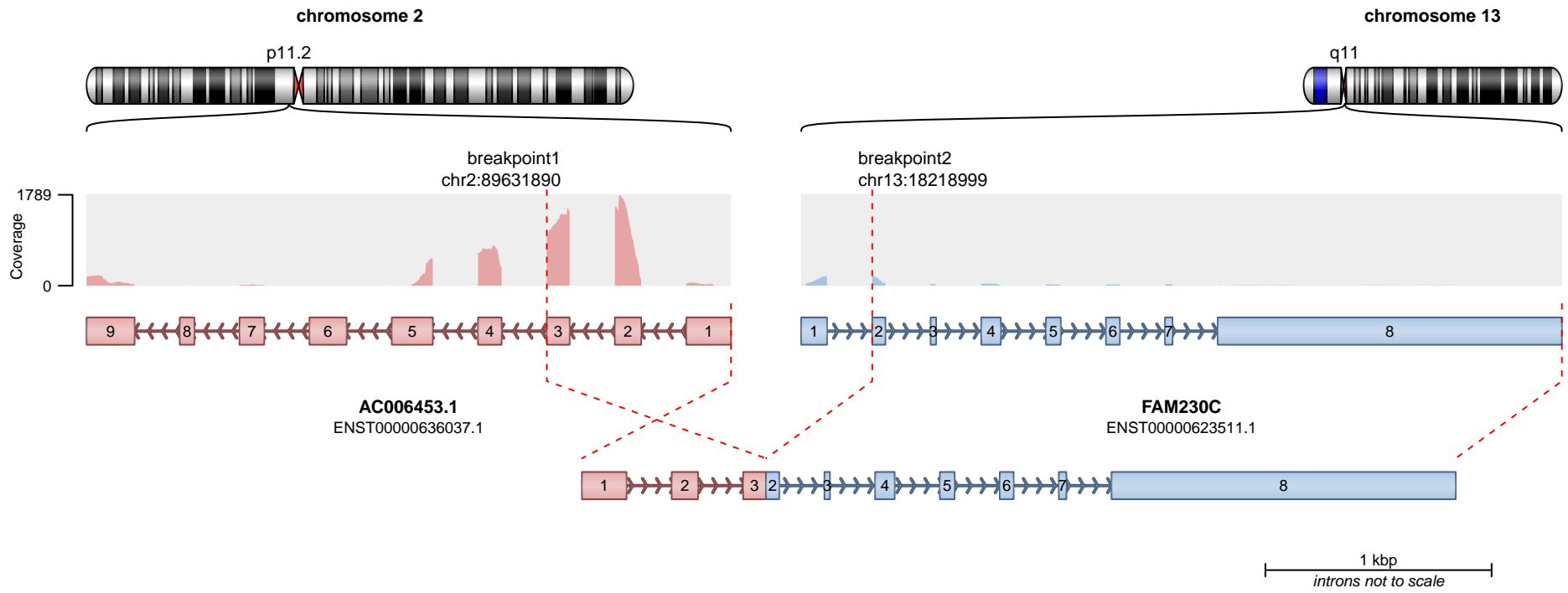
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion

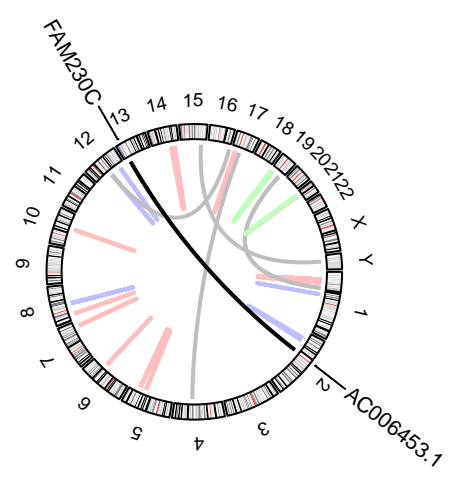
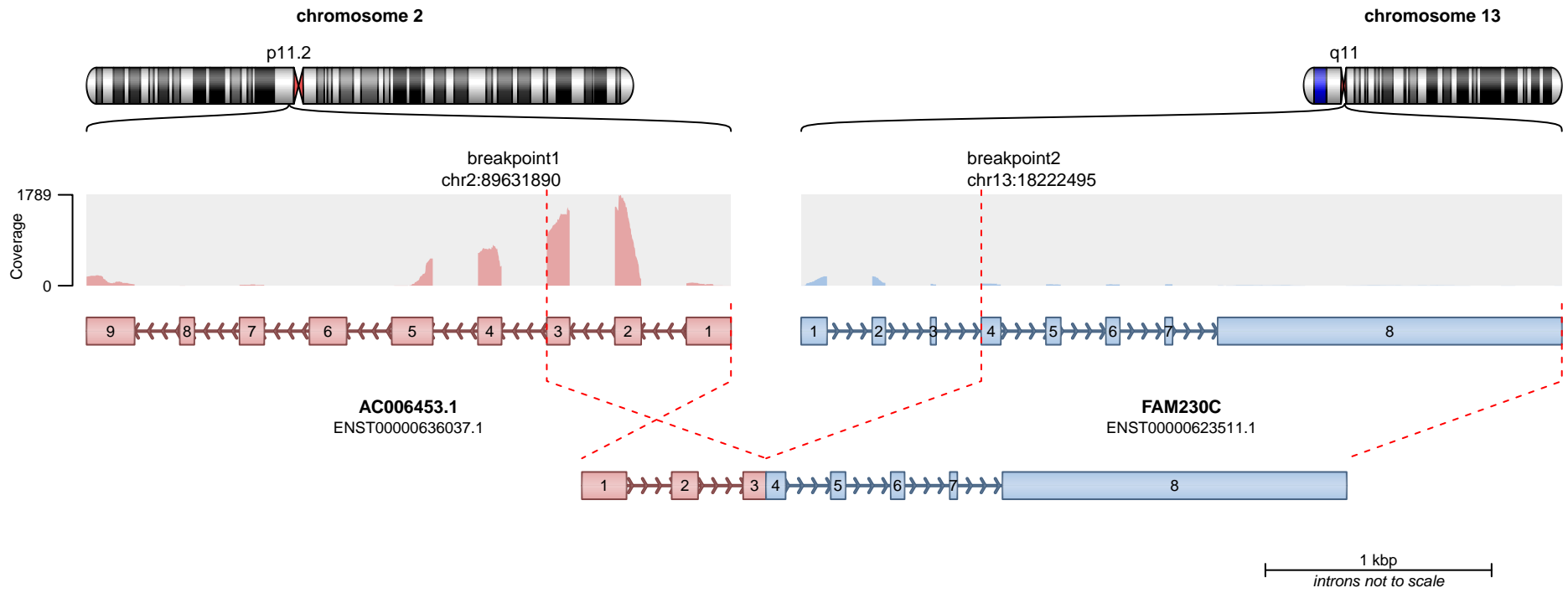


— translocation    — deletion  
— duplication    — inversion

Genes are not protein-coding.

**SUPPORTING READ COUNT**

Split reads = 18  
Discordant mates = 0

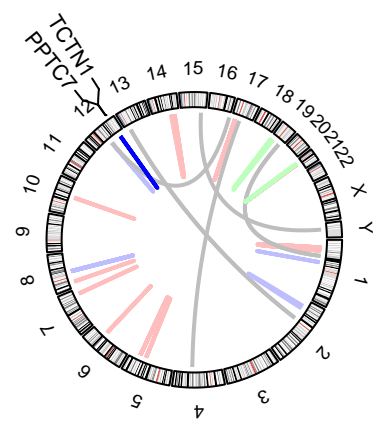
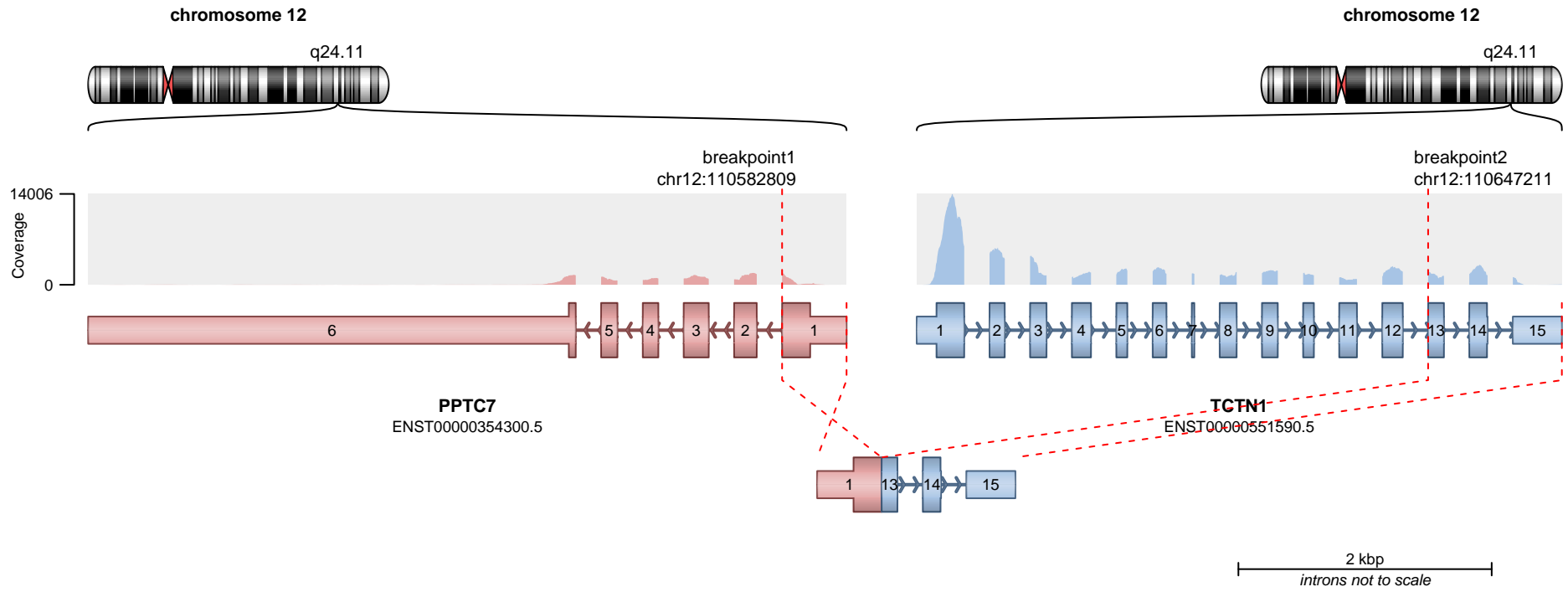


— translocation    — deletion  
— duplication    — inversion

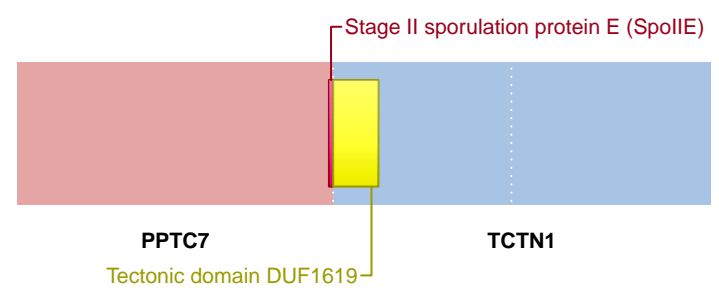
Genes are not protein-coding.

**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0



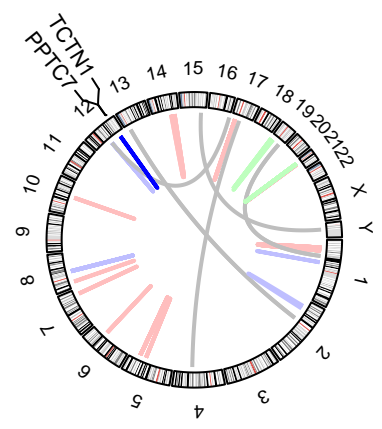
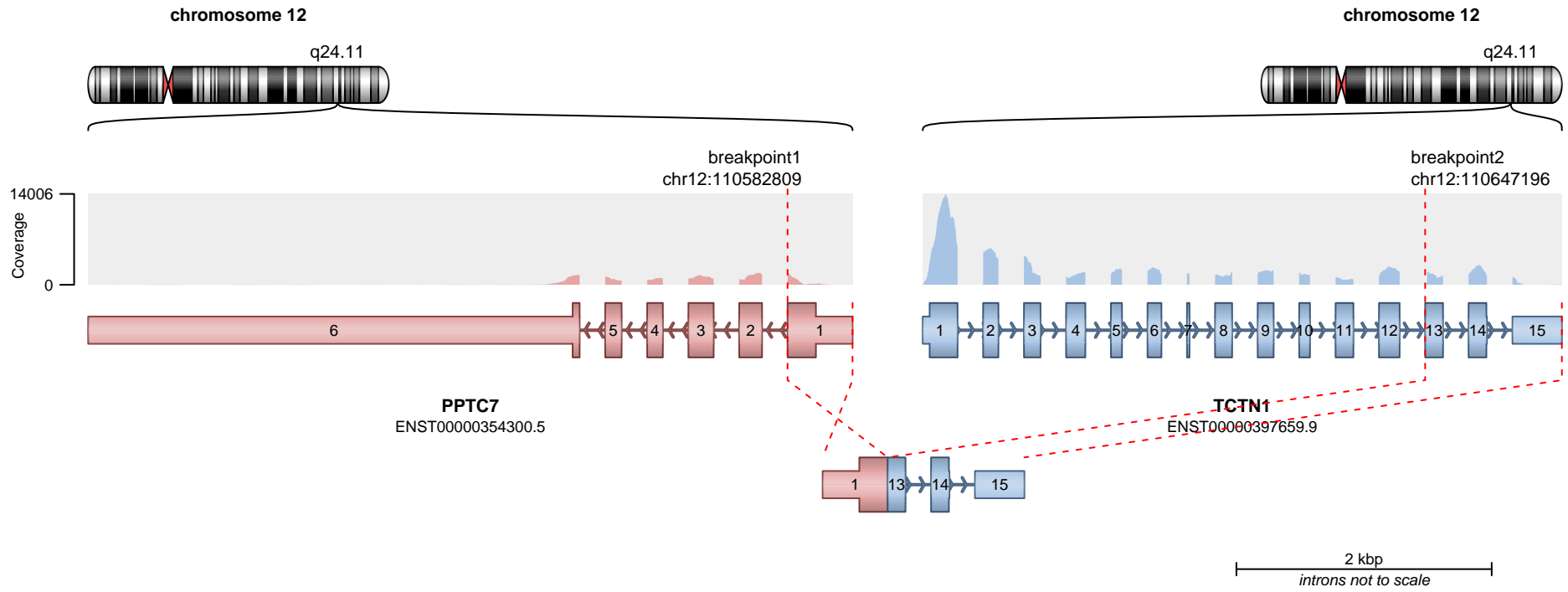
RETAINED PROTEIN DOMAINS  
reading frame unclear



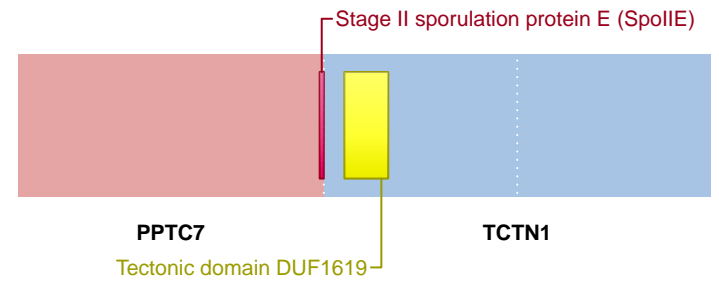
SUPPORTING READ COUNT

Split reads = 16  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



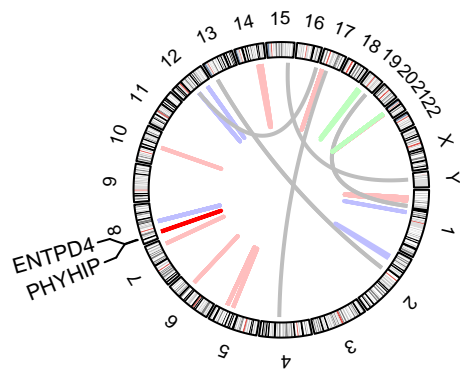
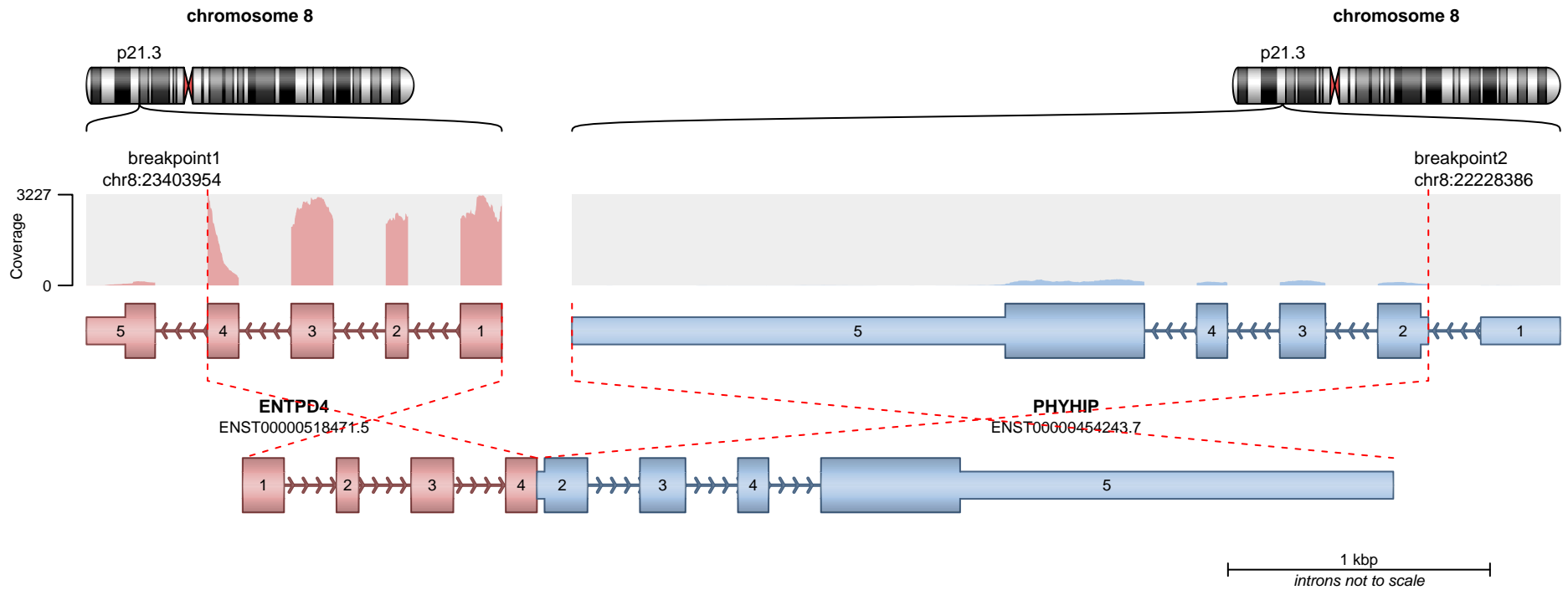
RETAINED PROTEIN DOMAINS  
reading frame unclear



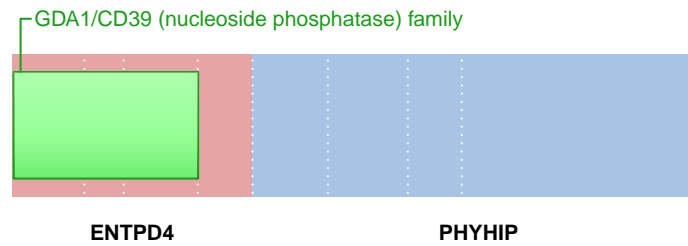
SUPPORTING READ COUNT

Split reads = 3  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



**RETAINED PROTEIN DOMAINS**  
reading frame unclear

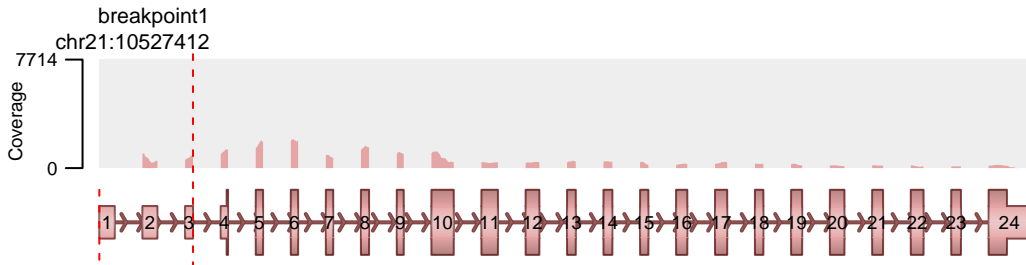


**SUPPORTING READ COUNT**

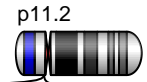
Split reads = 12  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion

chromosome 21

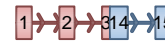


chromosome 21

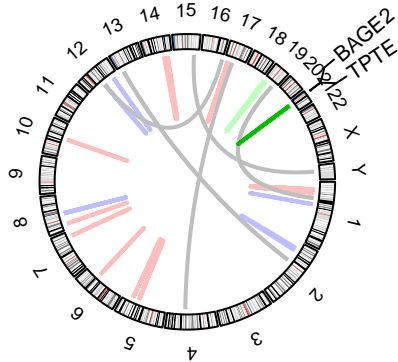


**TPTE**  
ENST00000618007.6

**BAGE2**  
ENST00000496773.1



2 kbp  
*introns not to scale*



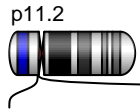
No coding regions retained in fusion transcript.

**SUPPORTING READ COUNT**

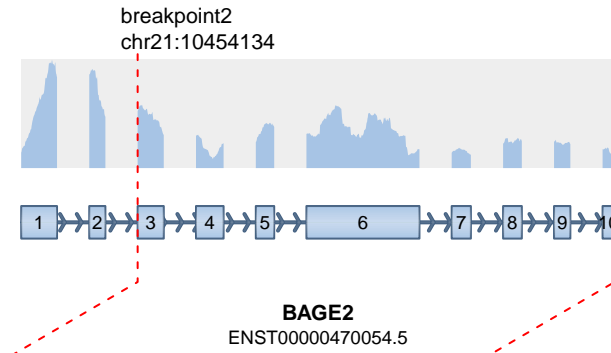
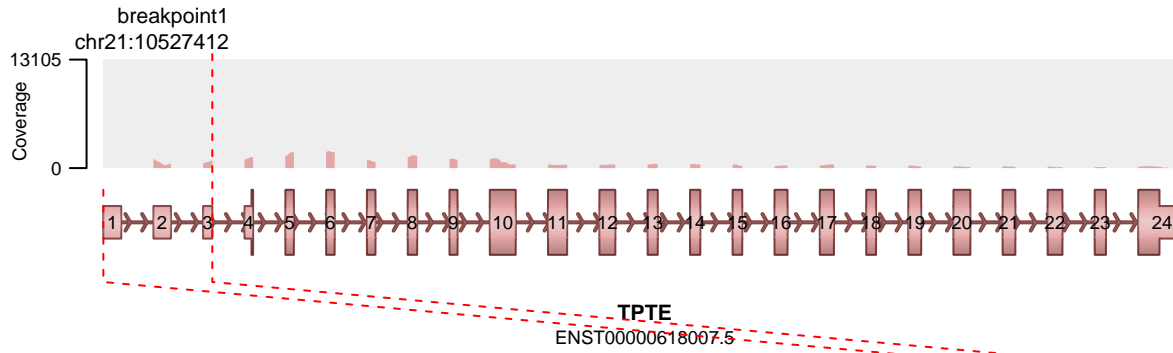
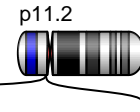
Split reads = 12  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion

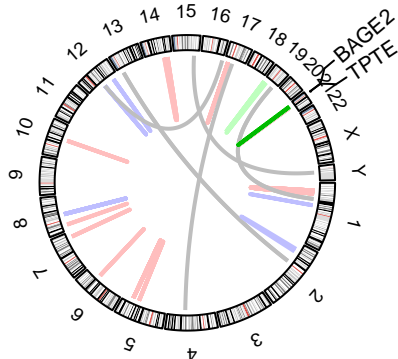
chromosome 21



chromosome 21



2 kbp  
introns not to scale



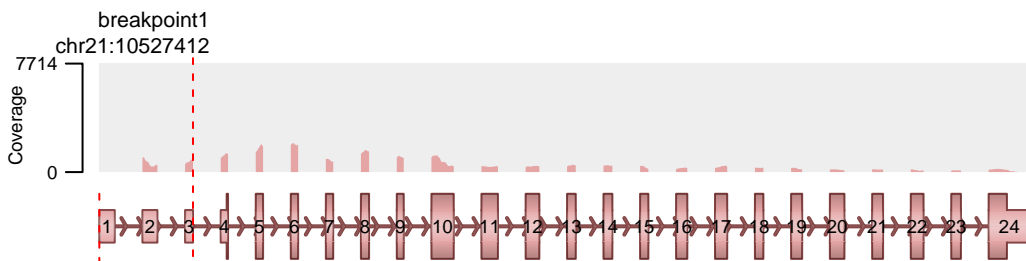
No coding regions retained in fusion transcript.

**SUPPORTING READ COUNT**

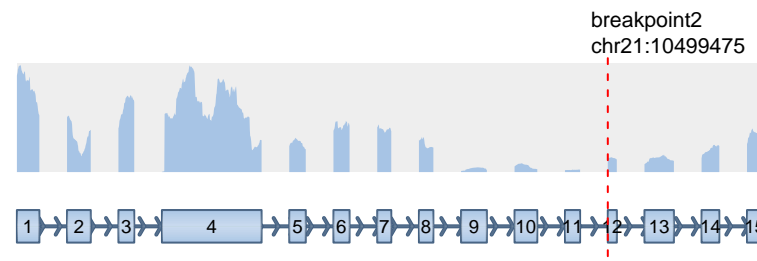
Split reads = 6  
Discordant mates = 1

— translocation    — deletion  
— duplication    — inversion

chromosome 21

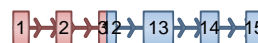


chromosome 21

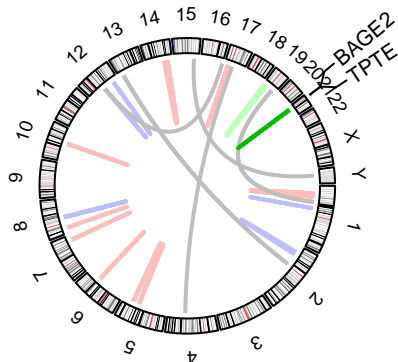


**TPTE**  
ENST00000618007.6

**BAGE2**  
ENST00000496773.1



2 kbp  
*introns not to scale*



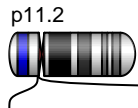
No coding regions retained in fusion transcript.

**SUPPORTING READ COUNT**

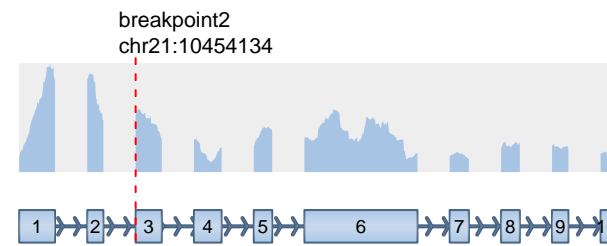
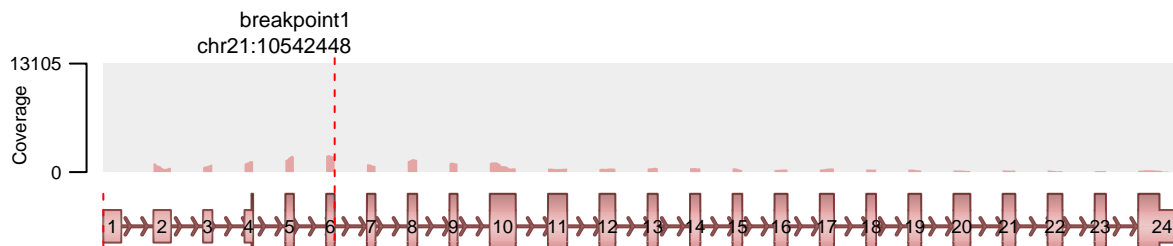
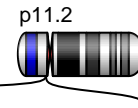
Split reads = 5  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion

chromosome 21

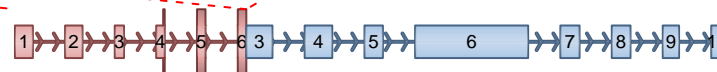


chromosome 21

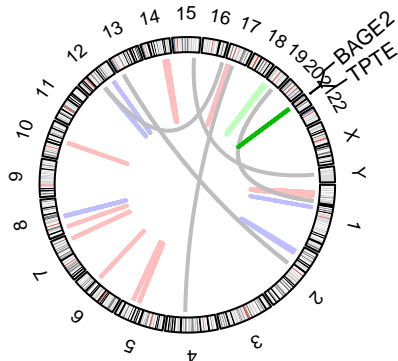


**TPTE**  
ENST00000618007.5

**BAGE2**  
ENST00000470054.5



2 kbp  
*introns not to scale*



No protein domains retained in fusion.

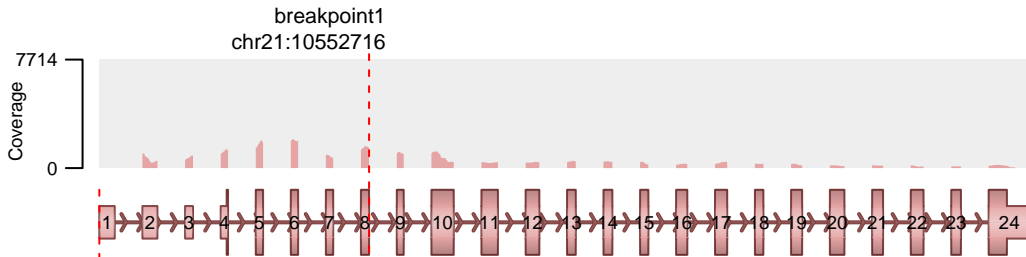
**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 1

— translocation    — deletion  
— duplication    — inversion

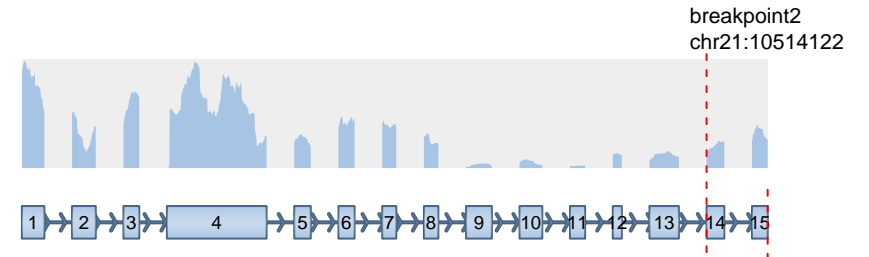
chromosome 21

p11.2



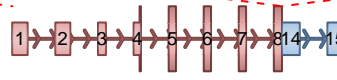
chromosome 21

p11.2

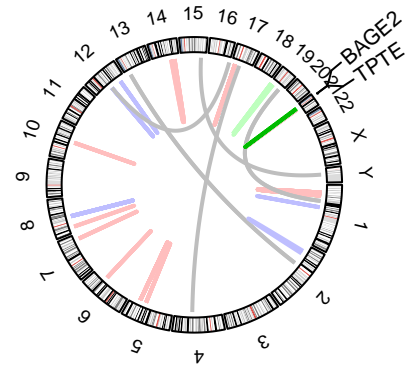


**TPTE**  
ENST00000618007.5

**BAGE2**  
ENST00000496773.1



2 kbp  
*introns not to scale*



No protein domains retained in fusion.

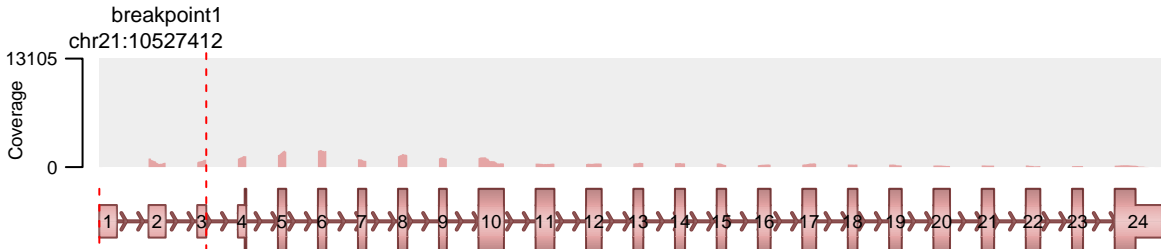
**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion

chromosome 21

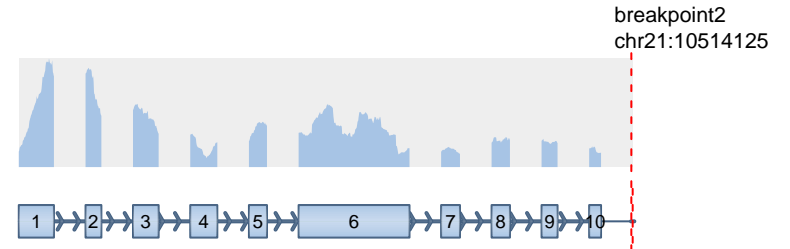
p11.2



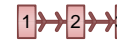
**TPTE**  
ENST00000618007.5

chromosome 21

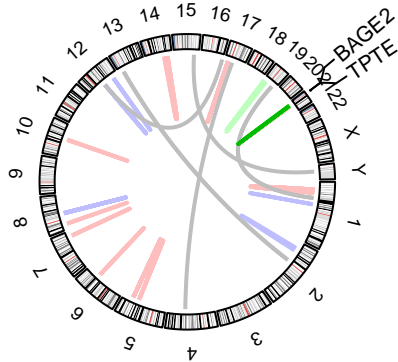
p11.2



**BAGE2**  
ENST00000470054.5



2 kbp  
*introns not to scale*



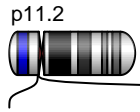
No coding regions retained in fusion transcript.

**SUPPORTING READ COUNT**

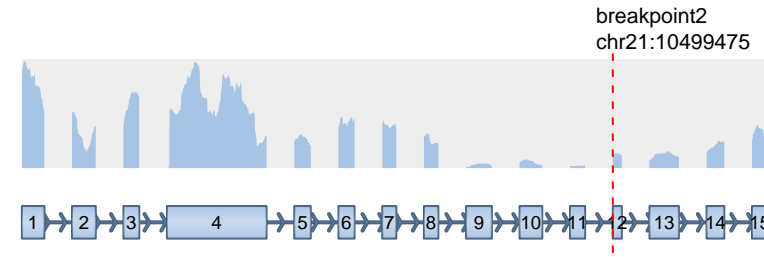
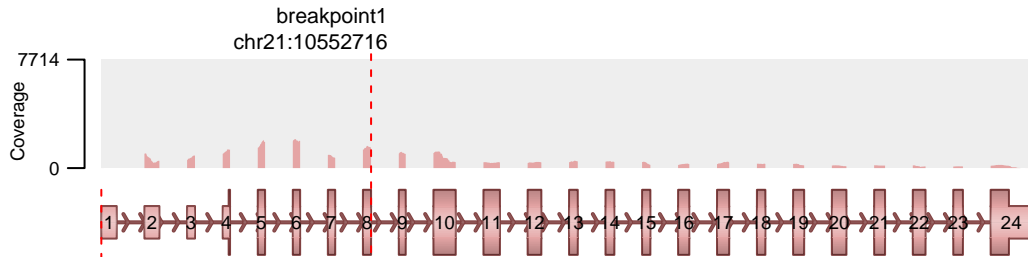
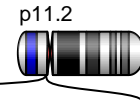
Split reads = 4  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion

chromosome 21

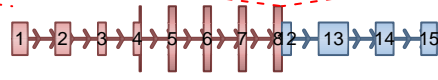


chromosome 21

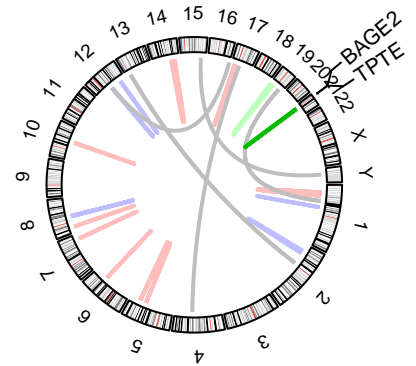


**TPTE**  
ENST00000618007.5

**BAGE2**  
ENST00000496773.1



2 kbp  
*introns not to scale*



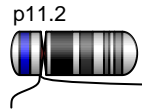
No protein domains retained in fusion.

**SUPPORTING READ COUNT**

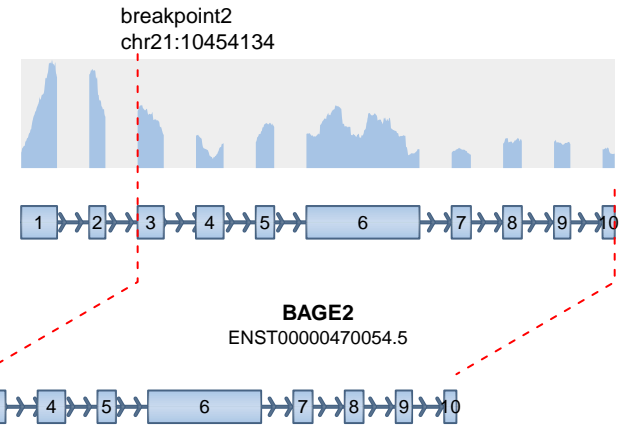
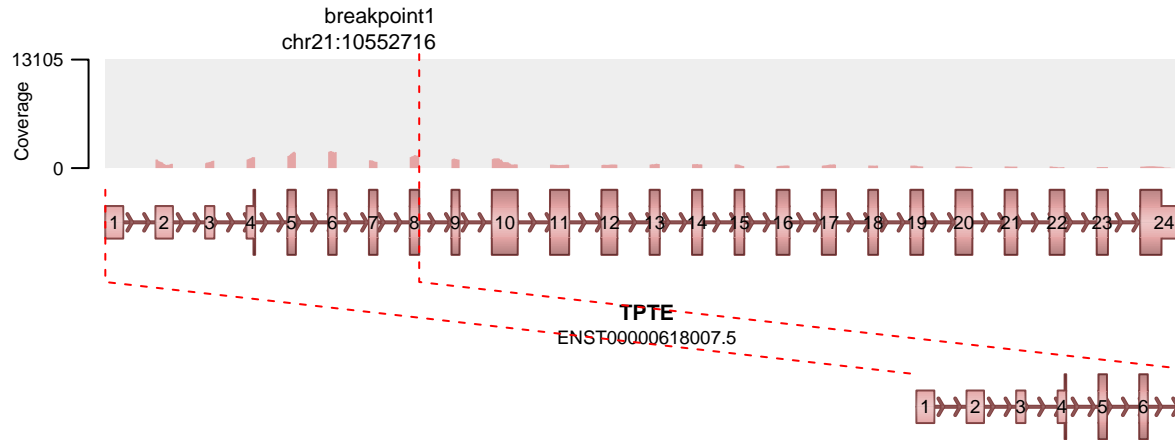
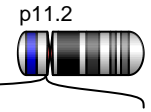
Split reads = 3  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion

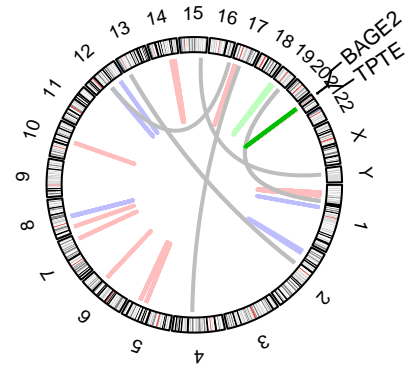
chromosome 21



chromosome 21



2 kbp  
introns not to scale



— translocation — deletion  
— duplication — inversion

No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 1

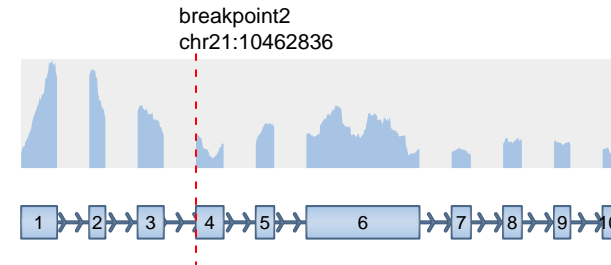
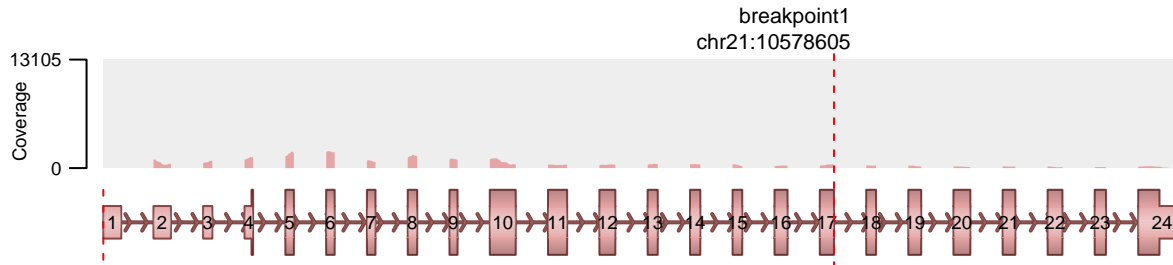
chromosome 21

p11.2



chromosome 21

p11.2

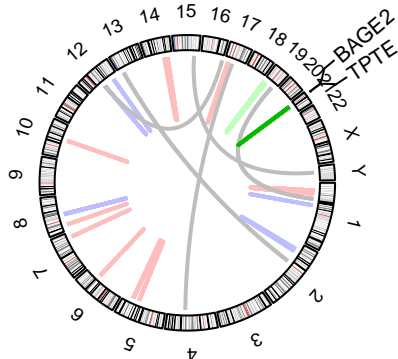


**TPTE**  
ENST00000618007.5

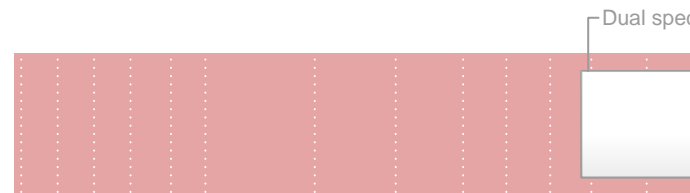
**BAGE2**  
ENST00000470054.5



2 kbp  
*introns not to scale*



**RETAINED PROTEIN DOMAINS**  
reading frame unclear



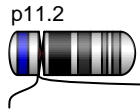
**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0

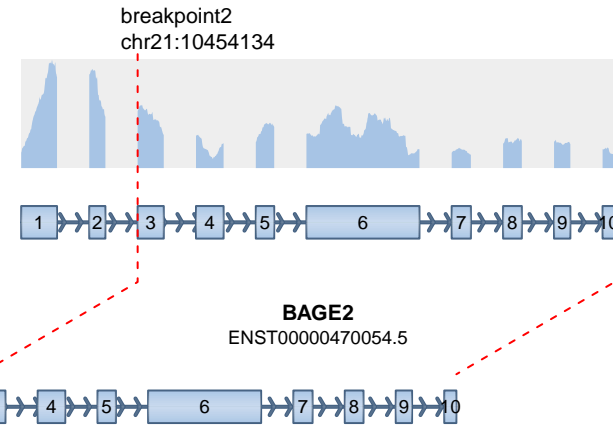
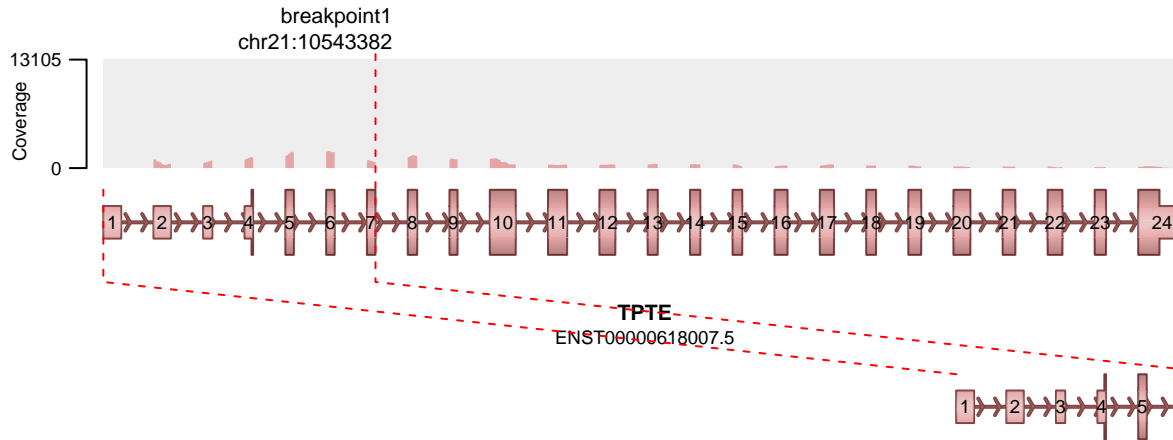
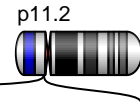
**TPTE**

— translocation    — deletion  
— duplication    — inversion

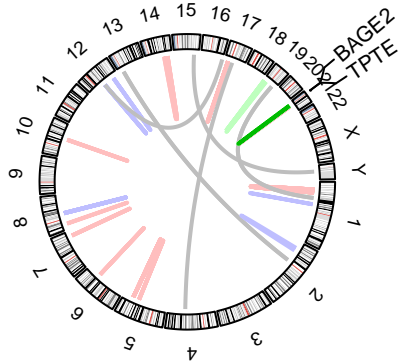
chromosome 21



chromosome 21



2 kbp  
introns not to scale



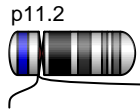
— translocation    — deletion  
— duplication    — inversion

No protein domains retained in fusion.

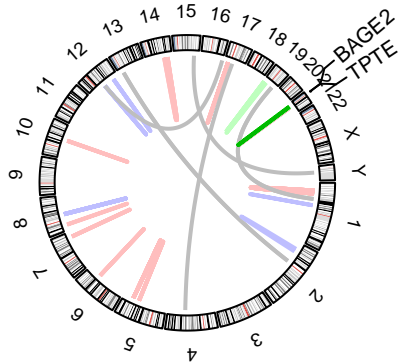
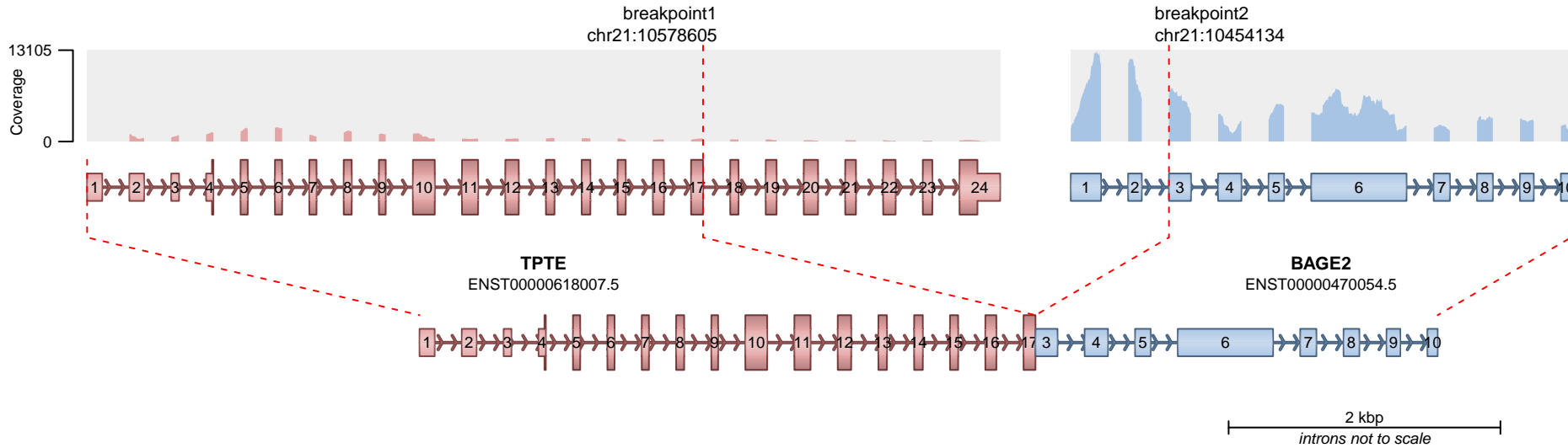
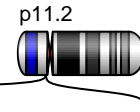
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 1

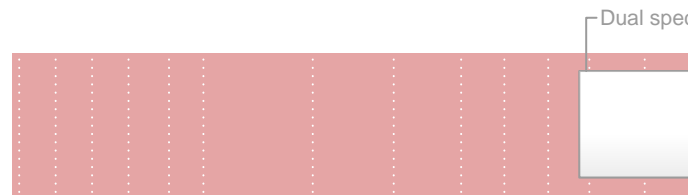
chromosome 21



chromosome 21



**RETAINED PROTEIN DOMAINS**  
reading frame unclear



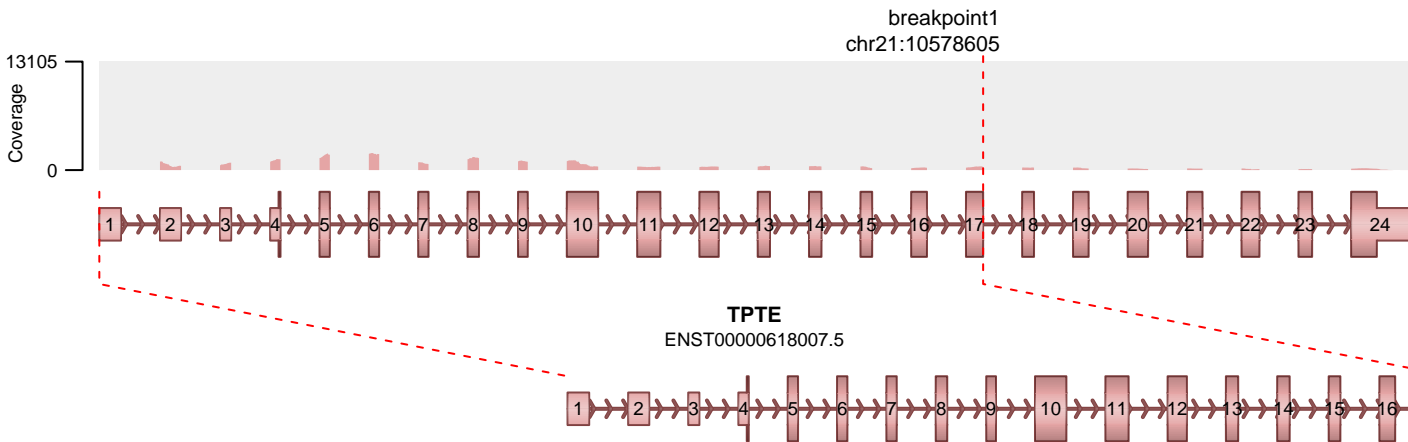
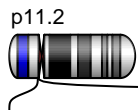
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 1

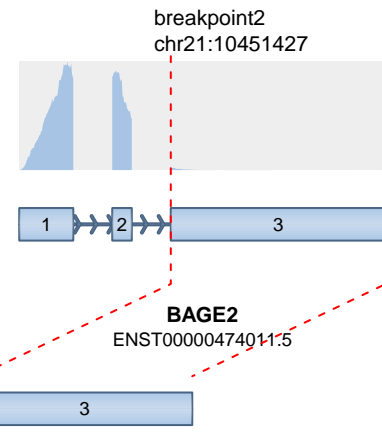
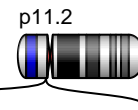
**TPTE**

— translocation    — deletion  
— duplication    — inversion

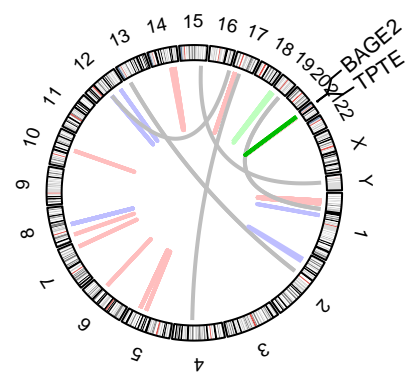
chromosome 21



chromosome 21

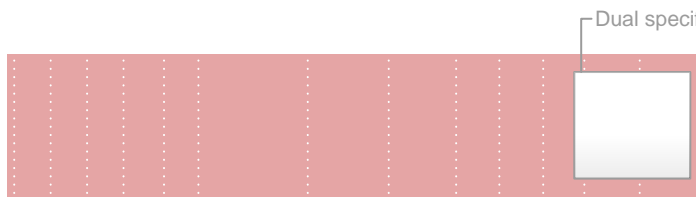


2 kbp  
introns not to scale



— translocation    — deletion  
— duplication    — inversion

RETAINED PROTEIN DOMAINS  
reading frame unclear



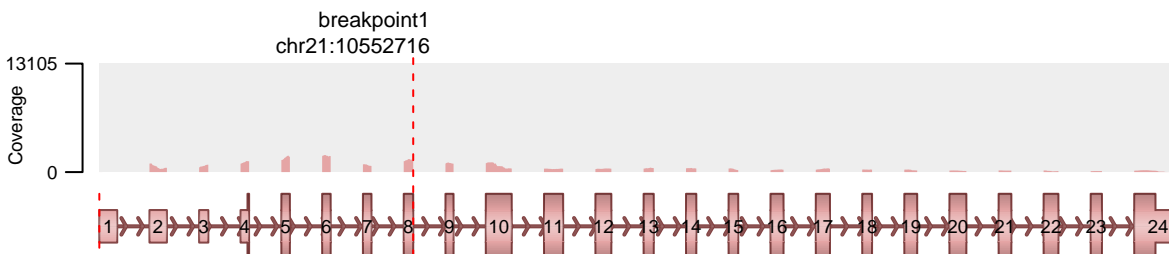
SUPPORTING READ COUNT

Split reads = 1  
Discordant mates = 1

TPTE

chromosome 21

p11.2

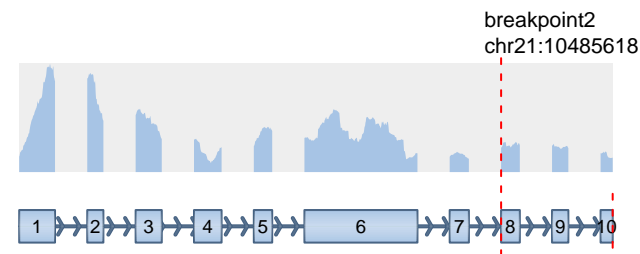


**TPTE**  
ENST00000618007.5



chromosome 21

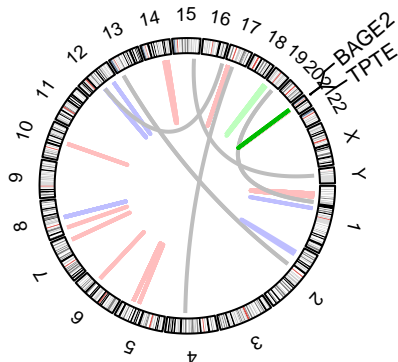
p11.2



**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

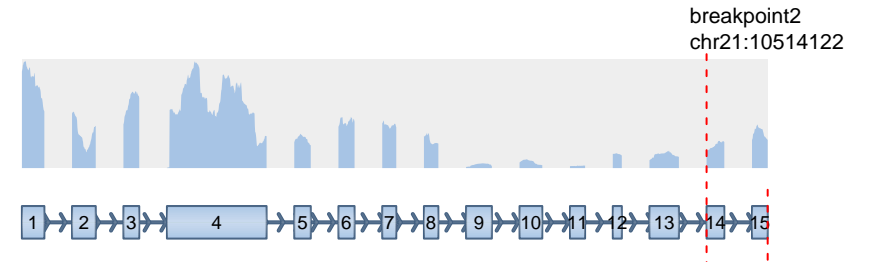
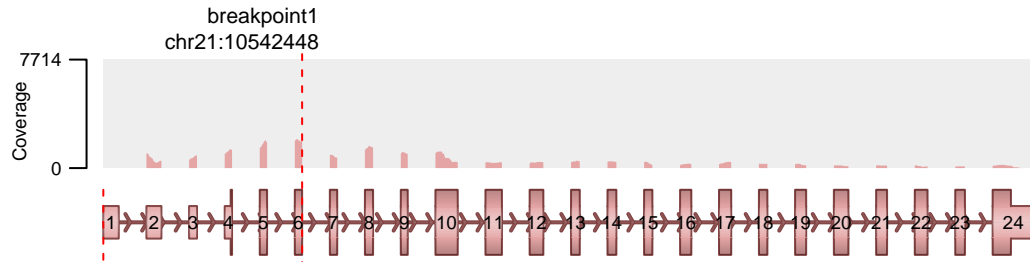
chromosome 21

p11.2



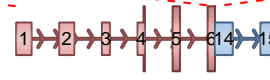
chromosome 21

p11.2

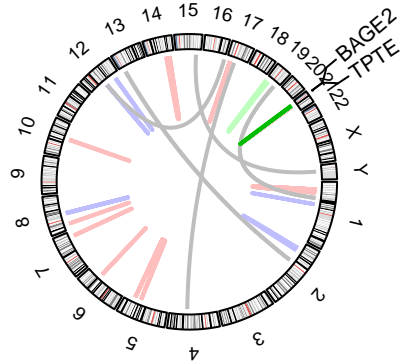


TPTE  
ENST00000618007.5

BAGE2  
ENST00000496773.1



2 kbp  
*introns not to scale*



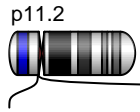
No protein domains retained in fusion.

**SUPPORTING READ COUNT**

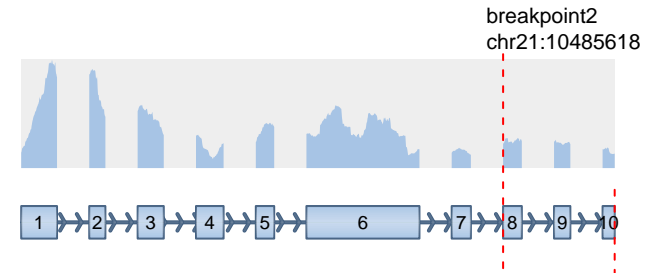
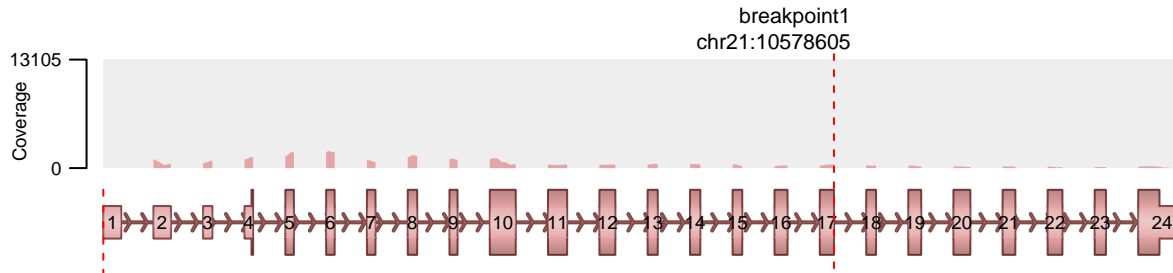
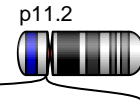
Split reads = 1  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion

chromosome 21

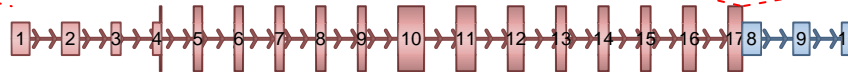


chromosome 21

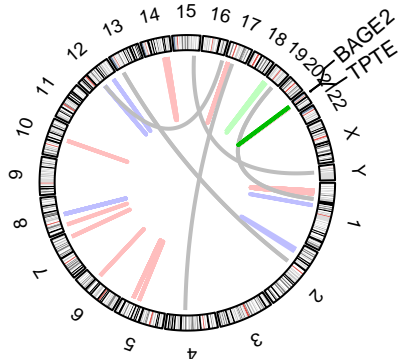


**TPTE**  
ENST00000618007.5

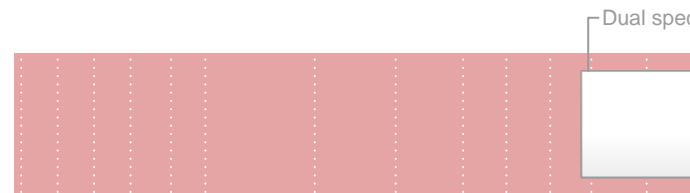
**BAGE2**  
ENST00000470054.5



2 kbp  
*introns not to scale*



**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

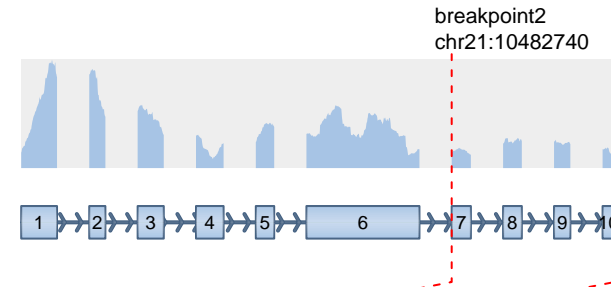
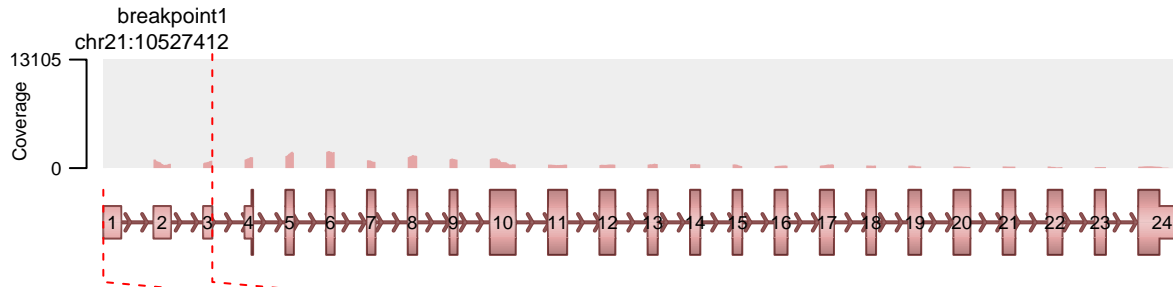
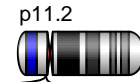
**TPTE**

— translocation    — deletion  
— duplication    — inversion

chromosome 21

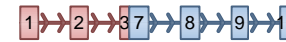


chromosome 21

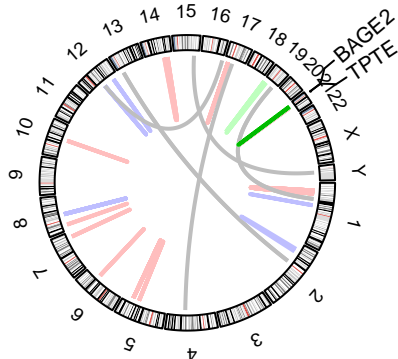


**TPTE**  
ENST00000618007.5

**BAGE2**  
ENST00000470054.5



2 kbp  
*introns not to scale*



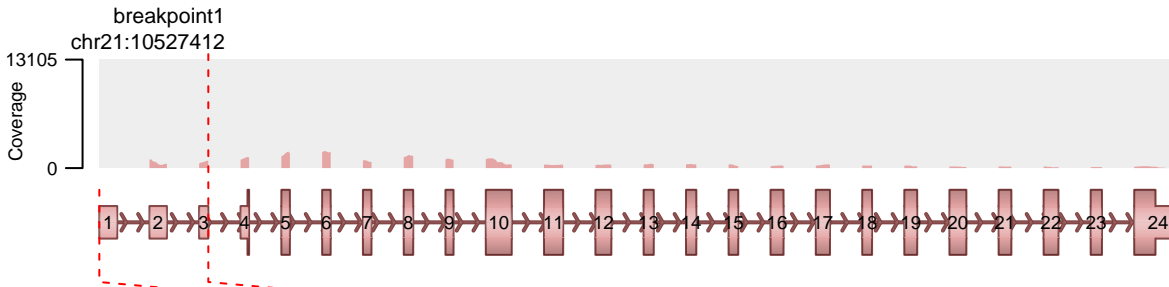
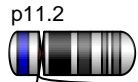
No coding regions retained in fusion transcript.

**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

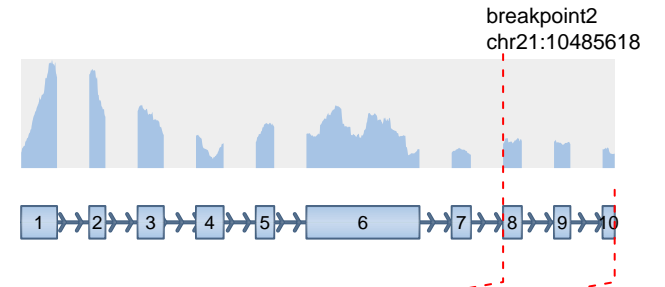
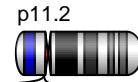
— translocation    — deletion  
— duplication    — inversion

chromosome 21

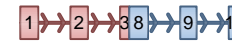


**TPTE**  
ENST00000618007.5

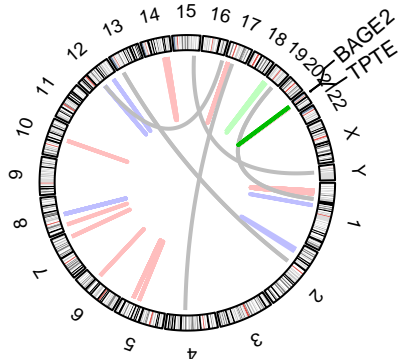
chromosome 21



**BAGE2**  
ENST00000470054.5



2 kbp  
*introns not to scale*

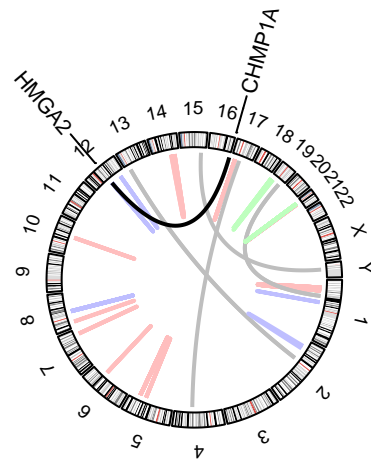
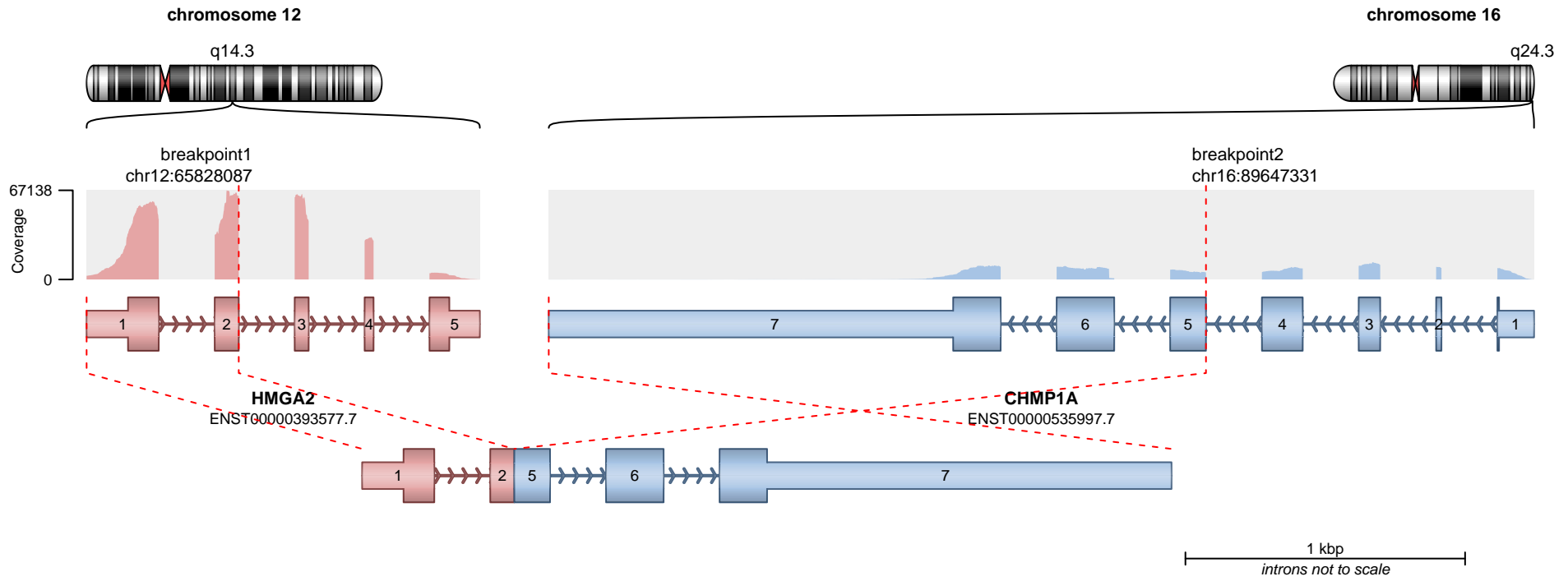


No coding regions retained in fusion transcript.

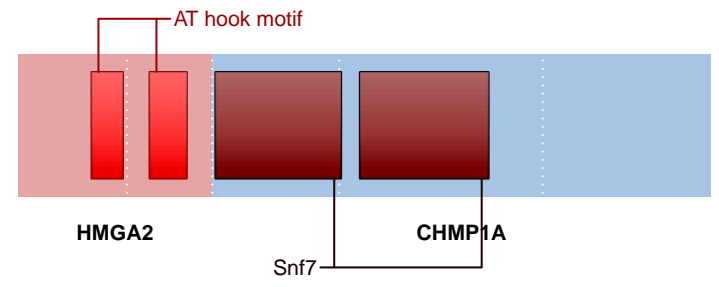
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 10  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

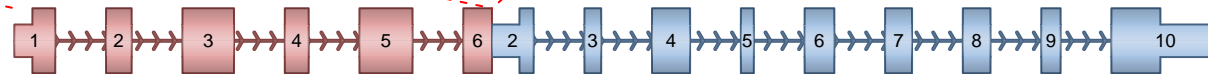
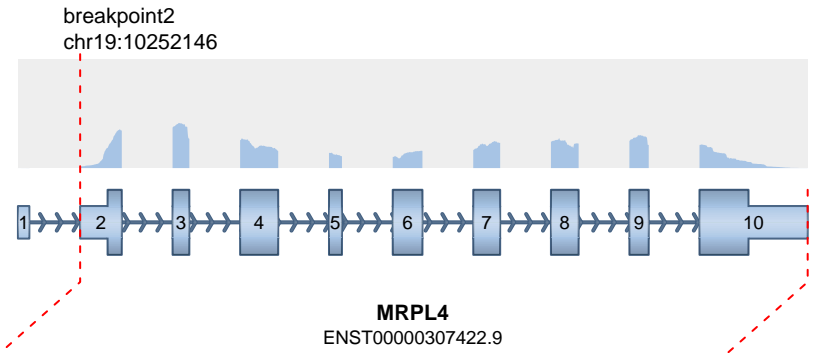
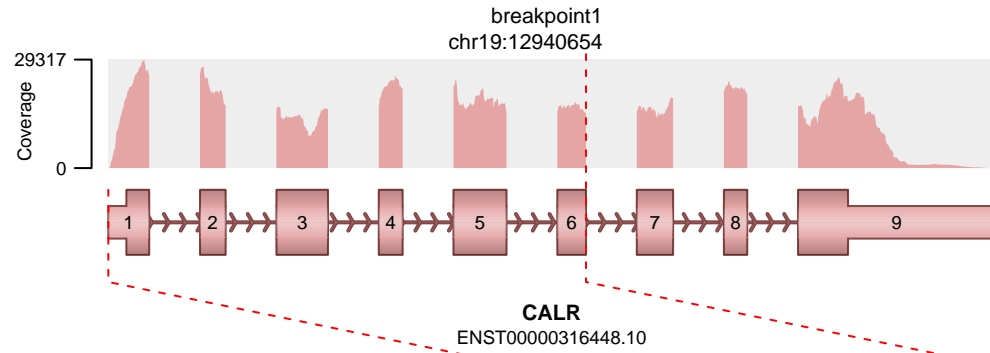
chromosome 19

p13.13

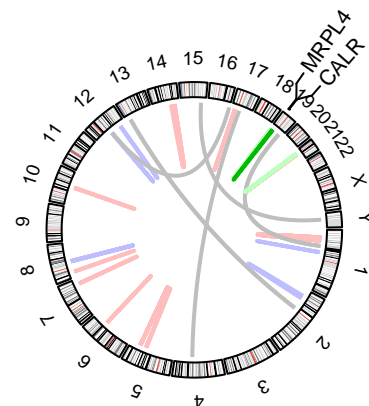


chromosome 19

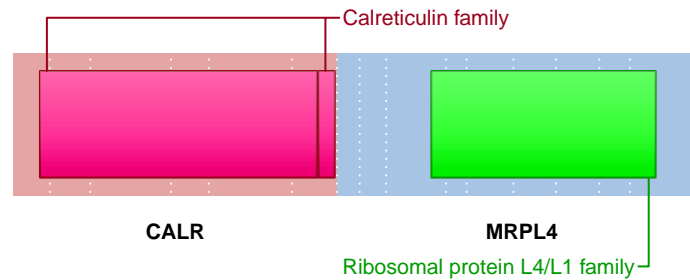
p13.2



1 kbp  
introns not to scale



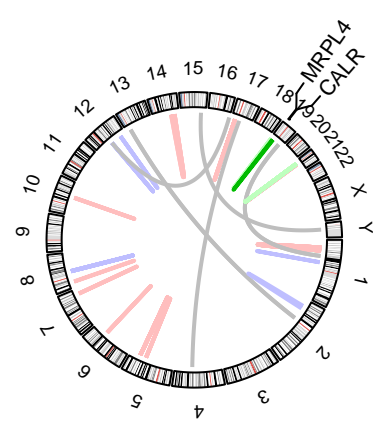
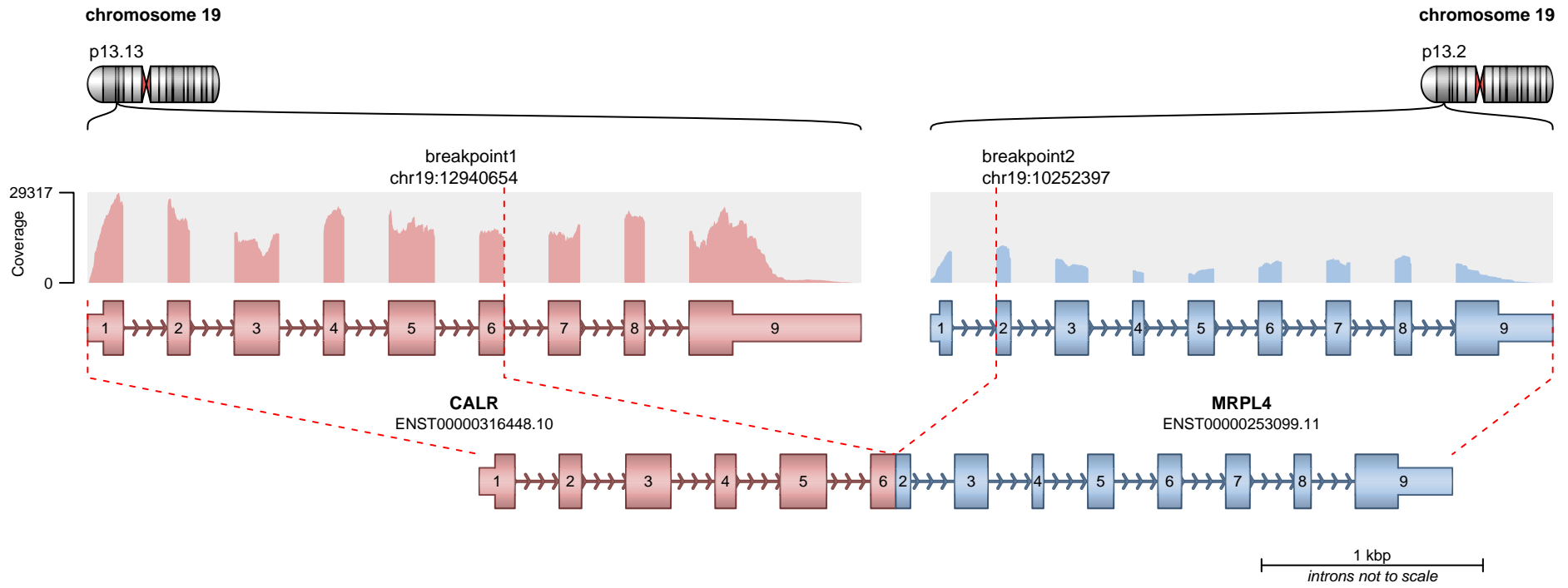
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



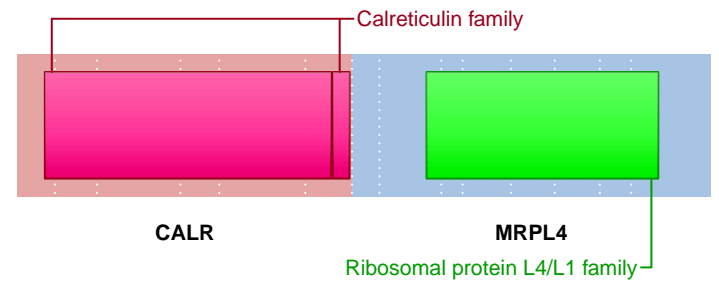
**SUPPORTING READ COUNT**

Split reads = 9  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



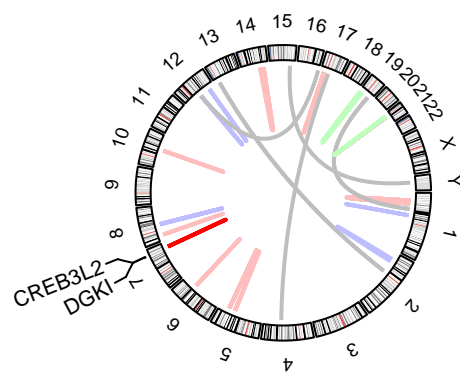
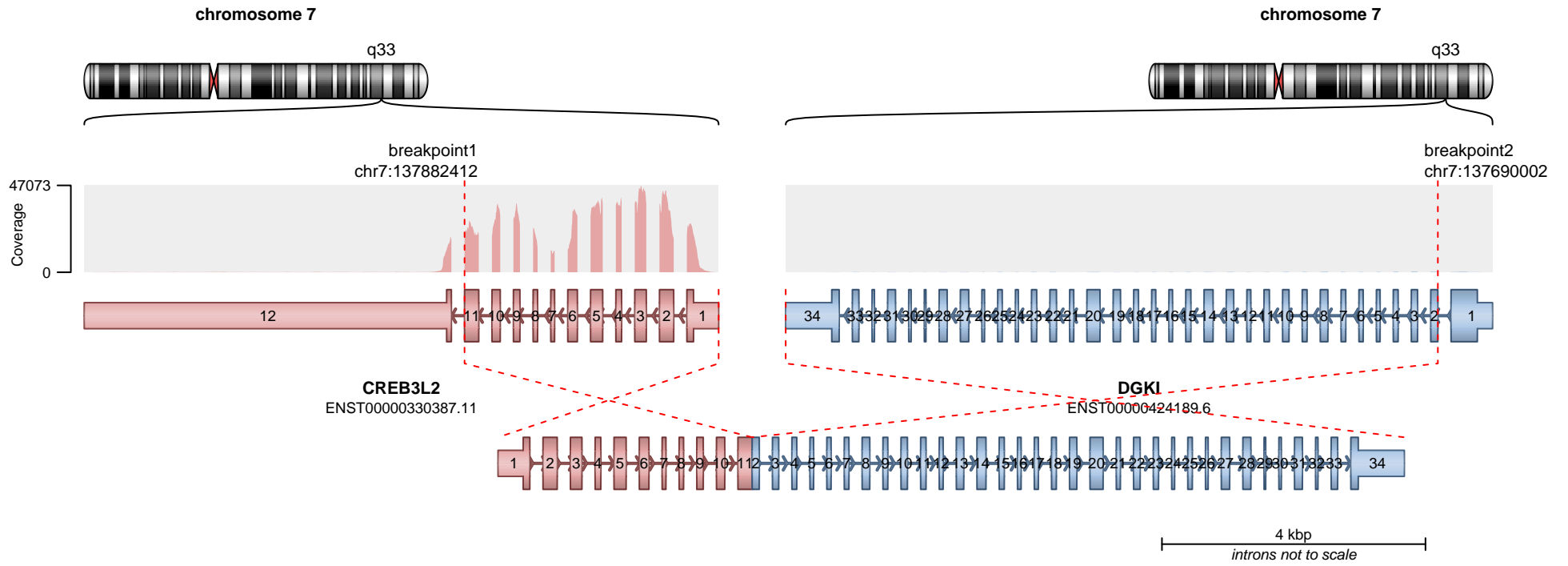
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

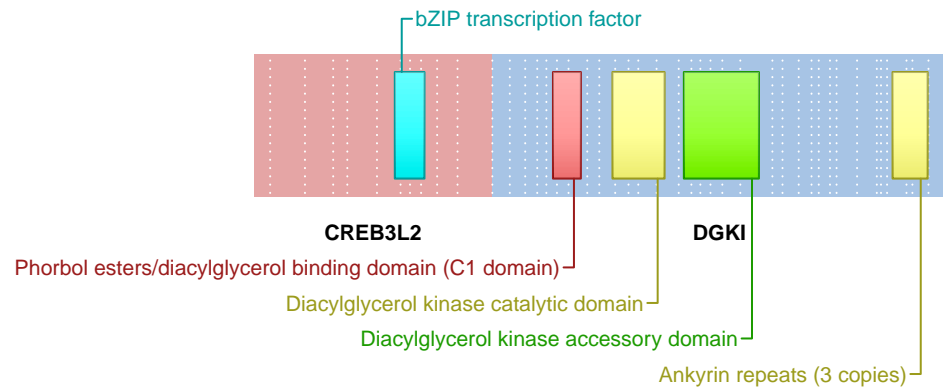
Split reads = 9  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



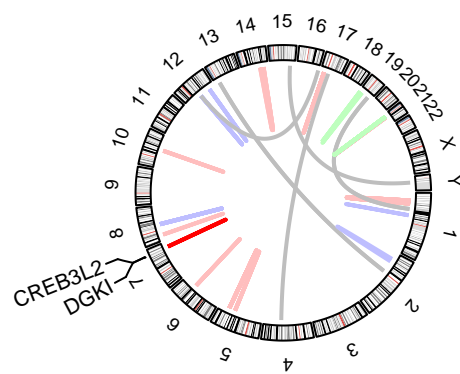
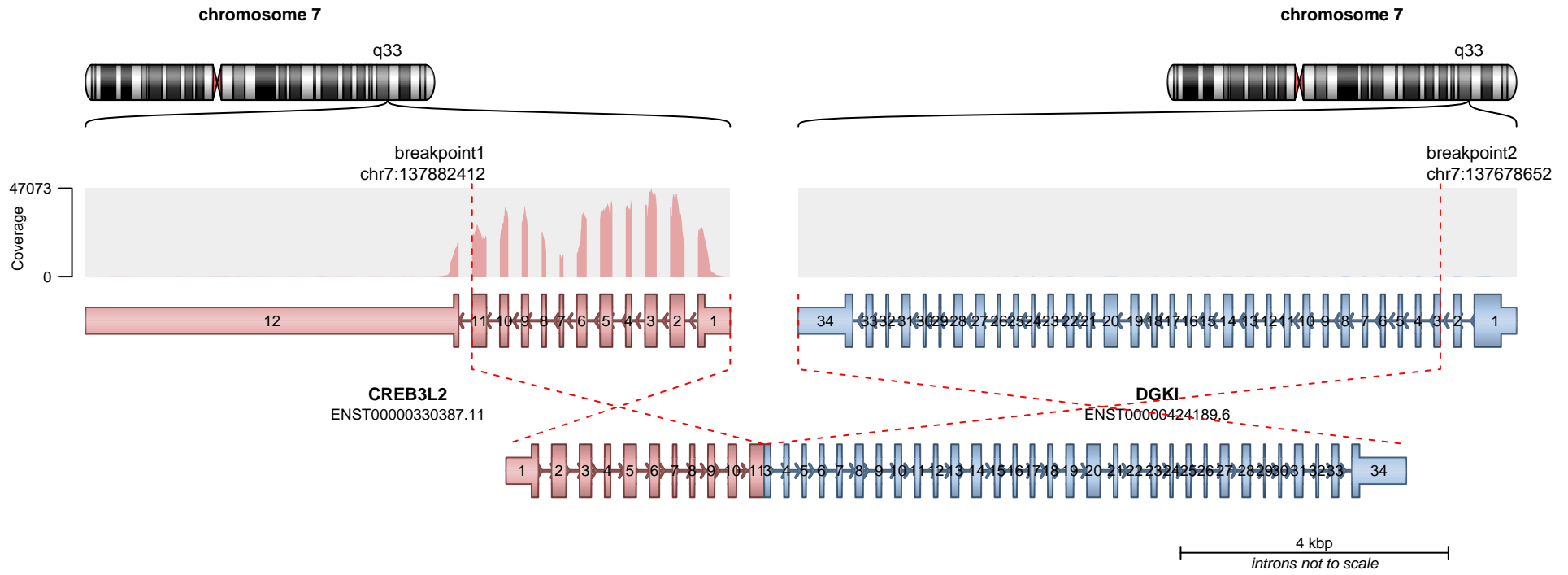
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



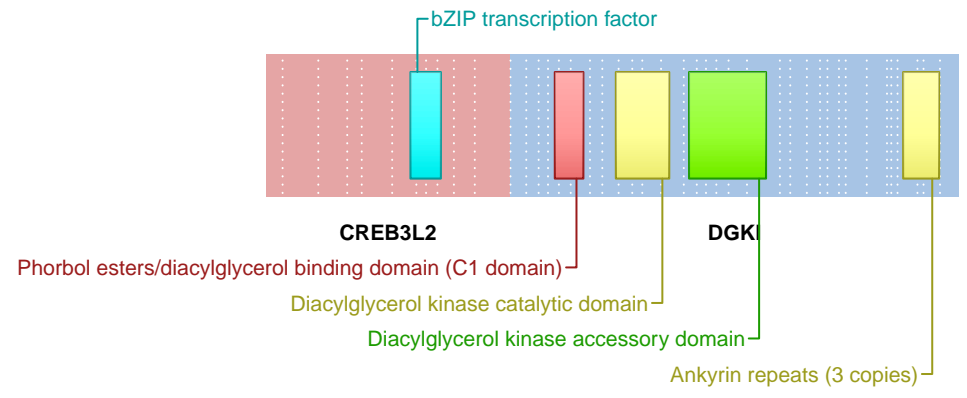
**SUPPORTING READ COUNT**

Split reads = 9  
Discordant mates = 0



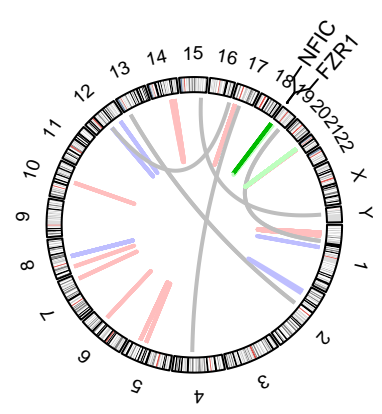
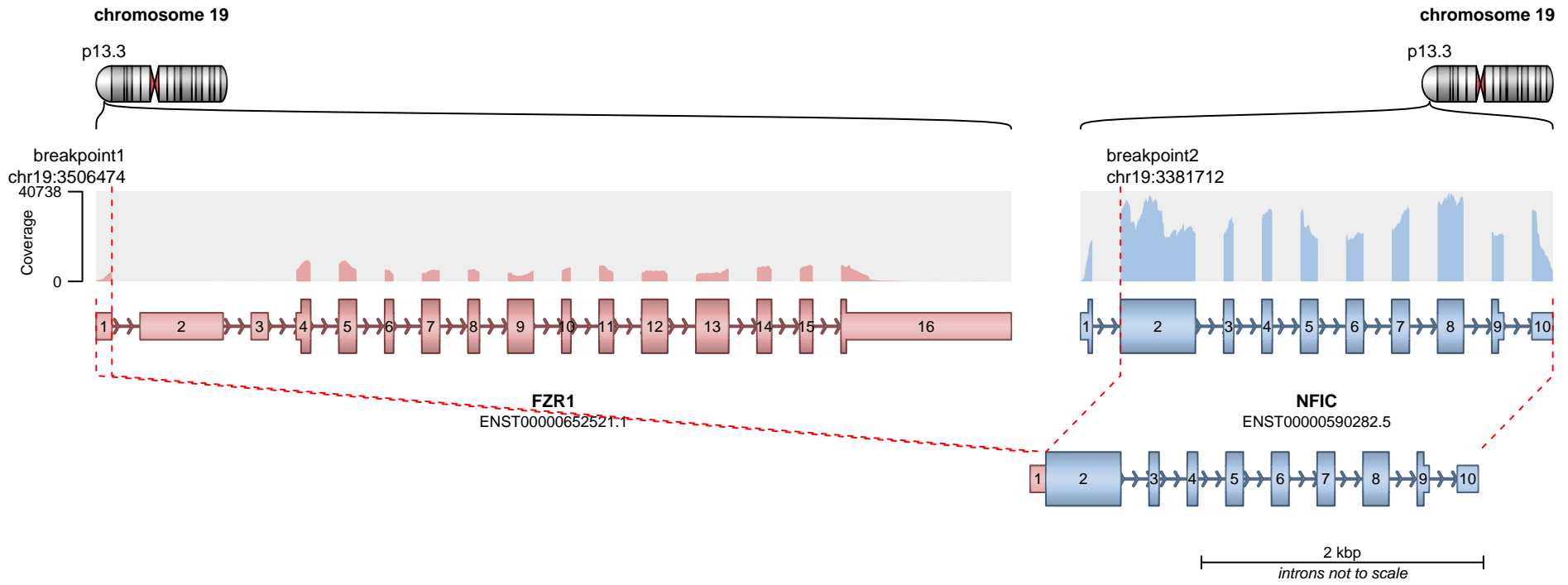
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear

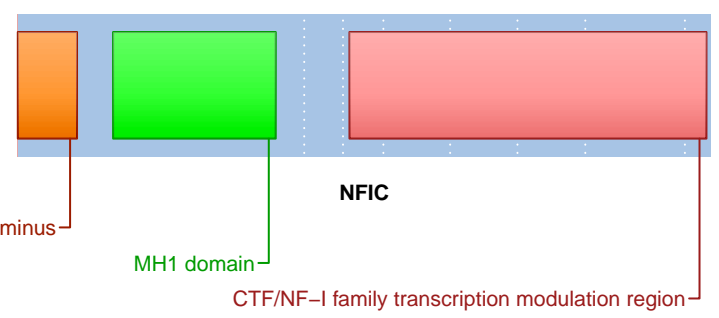


**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0



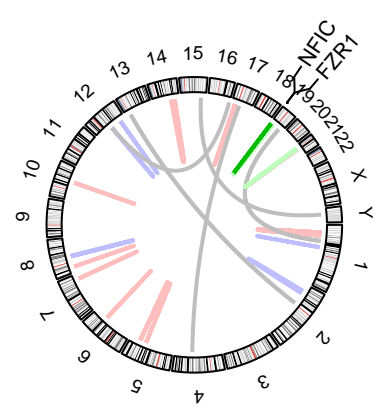
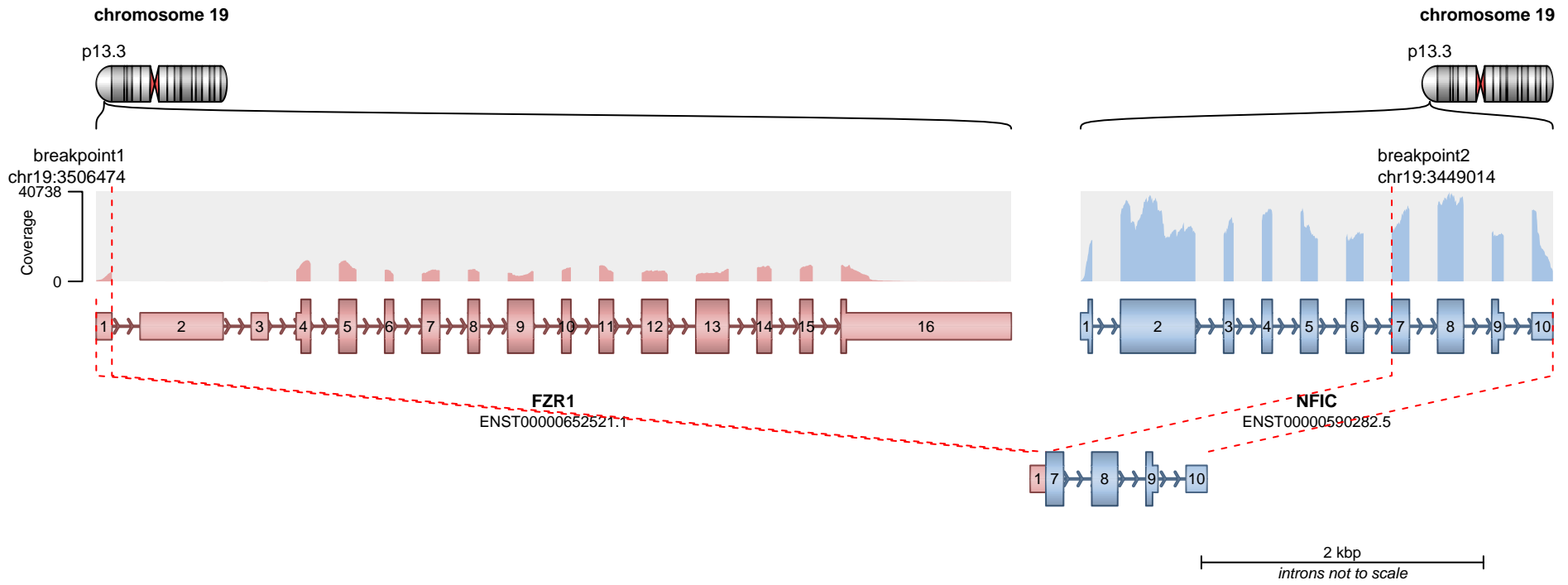
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



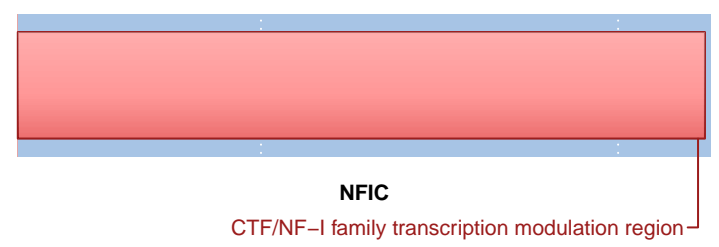
**SUPPORTING READ COUNT**

Split reads = 7  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



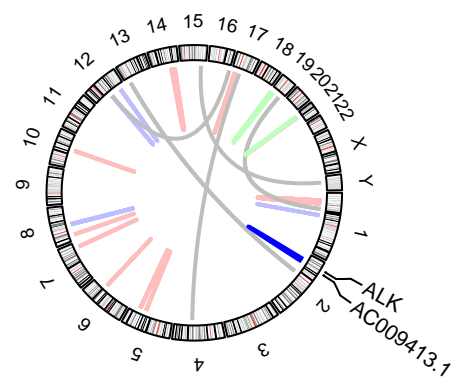
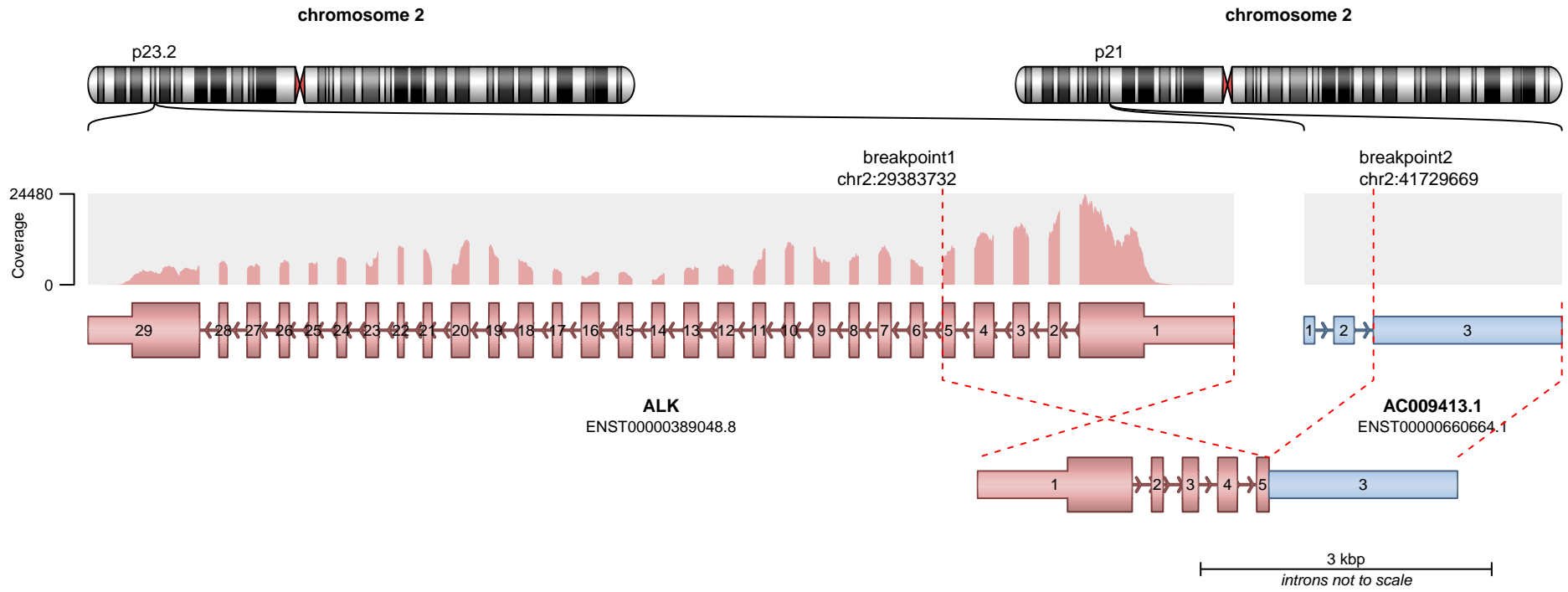
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



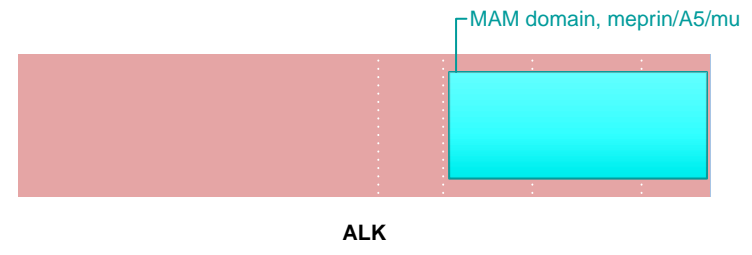
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion