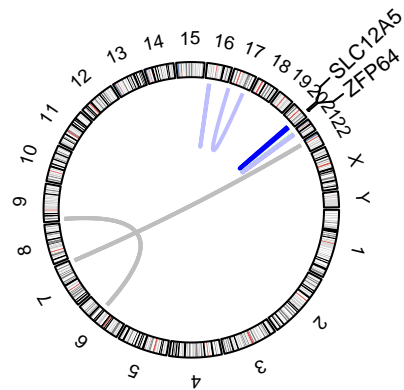
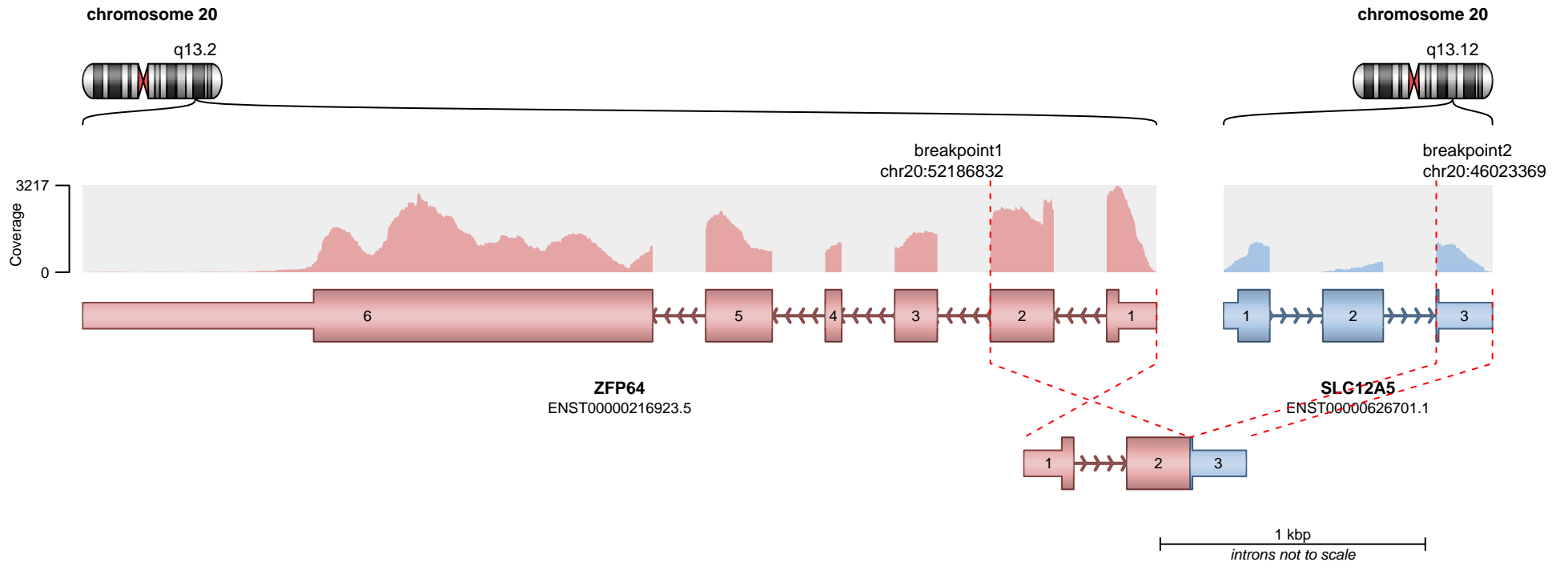


— translocation    — deletion  
— duplication    — inversion

No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 85  
Discordant mates = 0

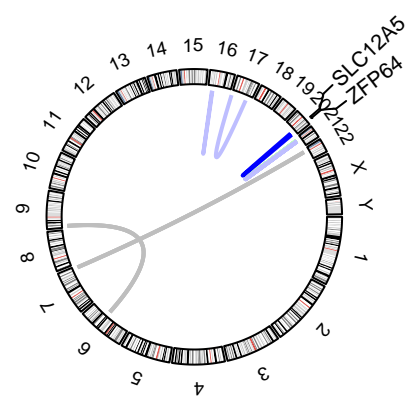
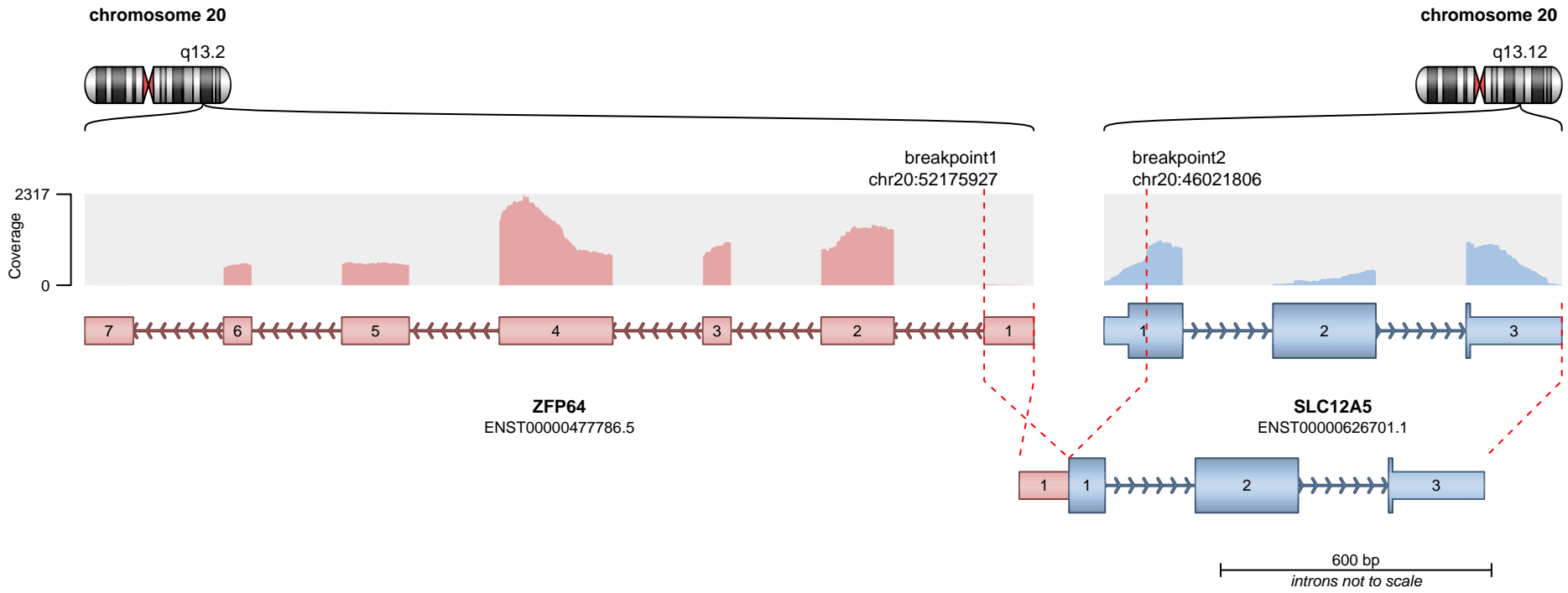


— translocation — deletion  
— duplication — inversion

No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 18  
Discordant mates = 0

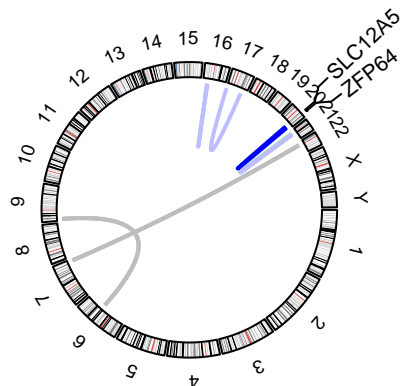
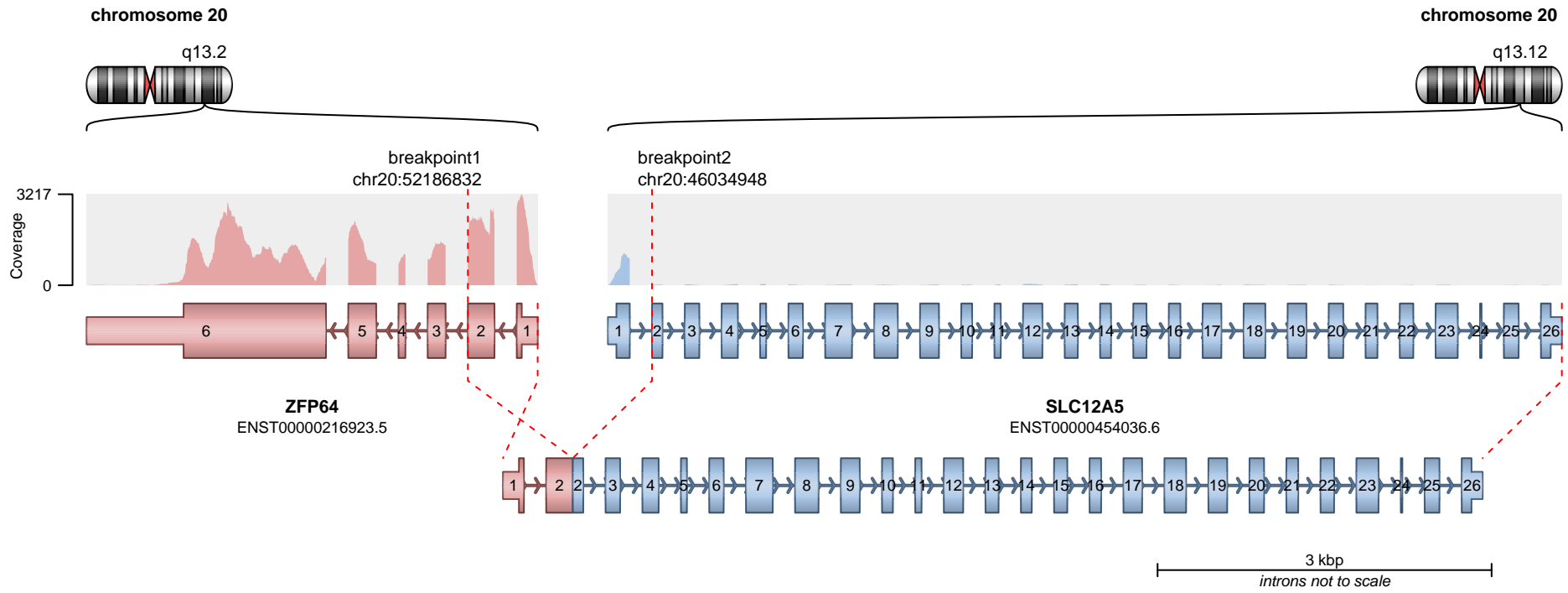


— translocation    — deletion  
— duplication    — inversion

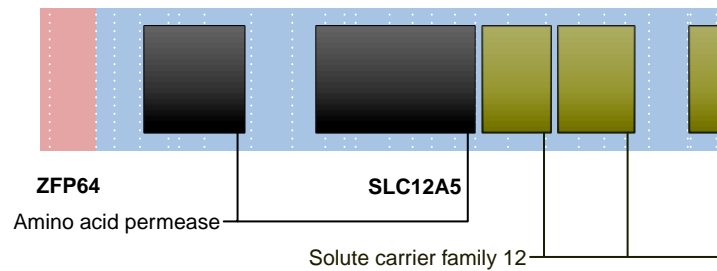
No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 9  
Discordant mates = 0



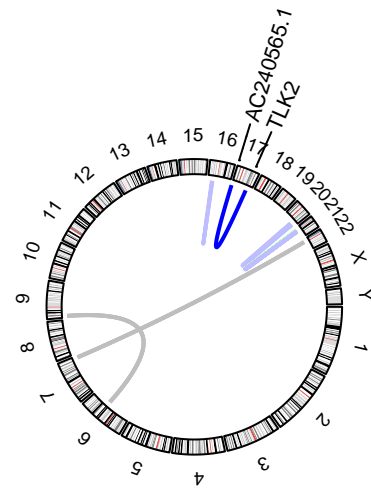
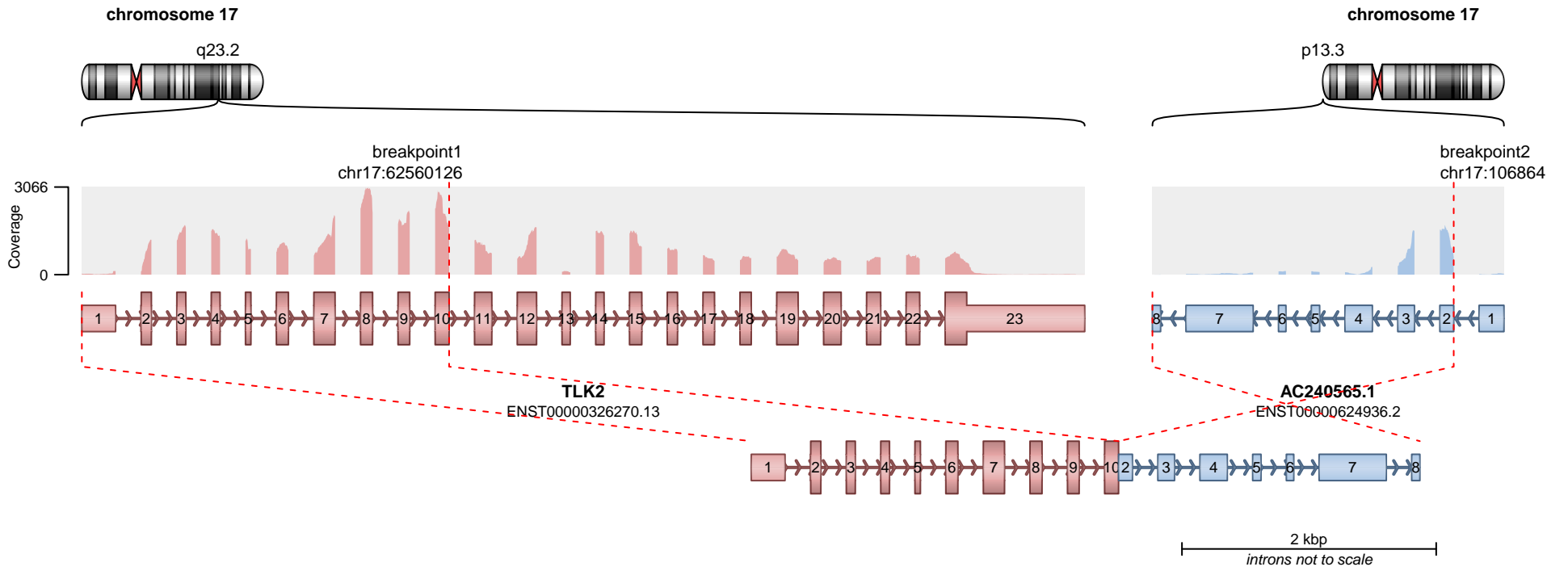
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 7  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

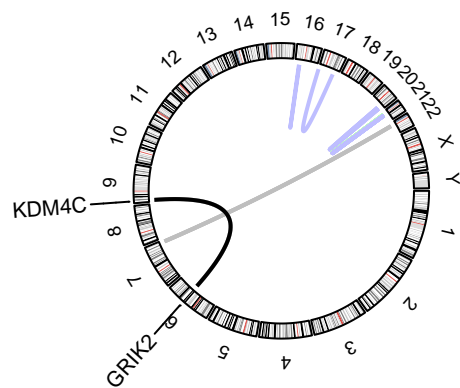
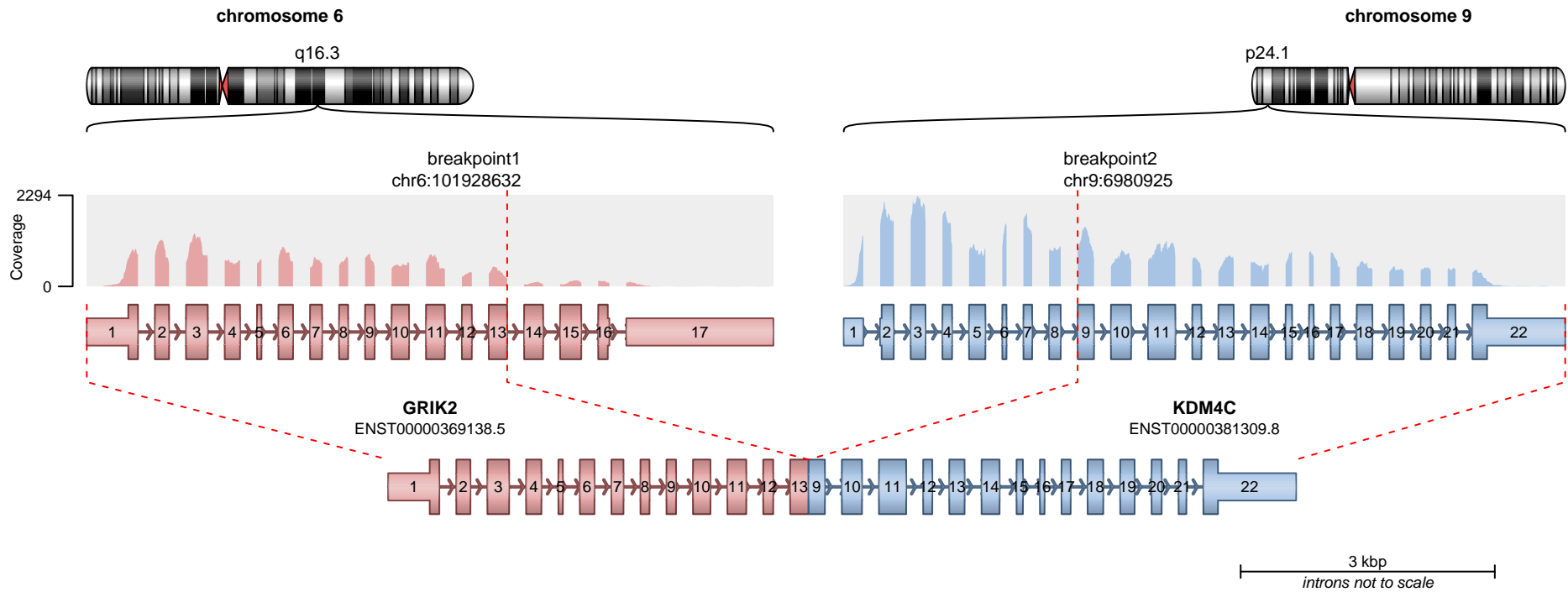


— translocation    — deletion  
— duplication    — inversion

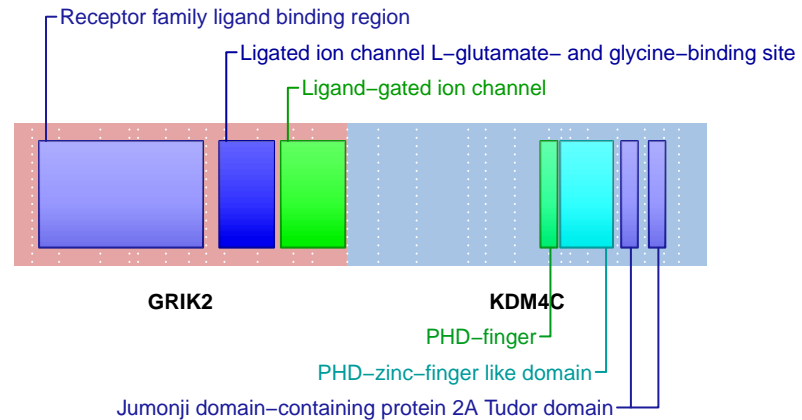
No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 81  
 Discordant mates = 0



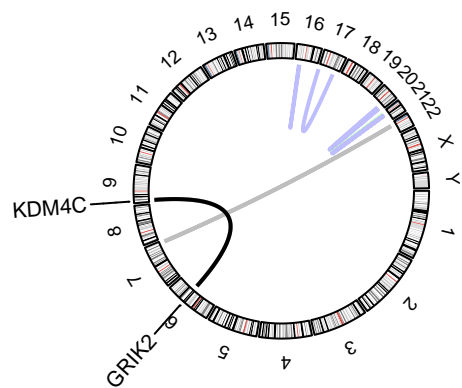
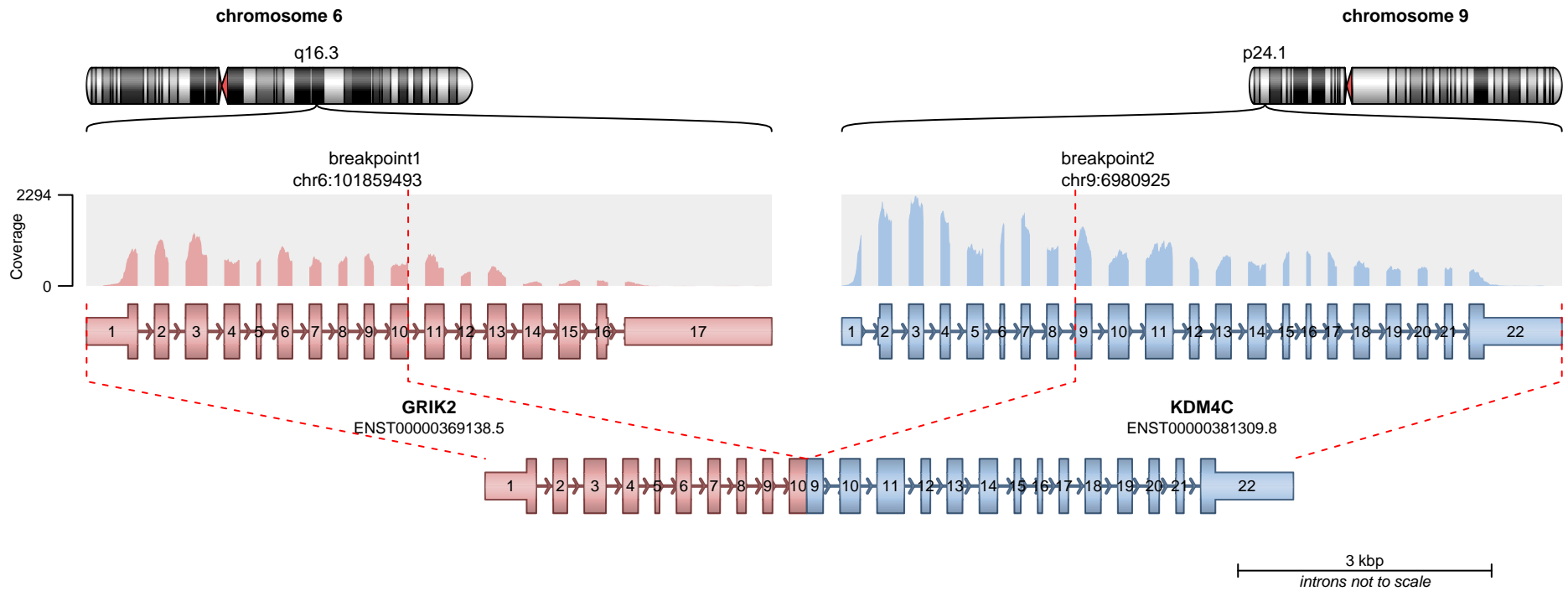
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



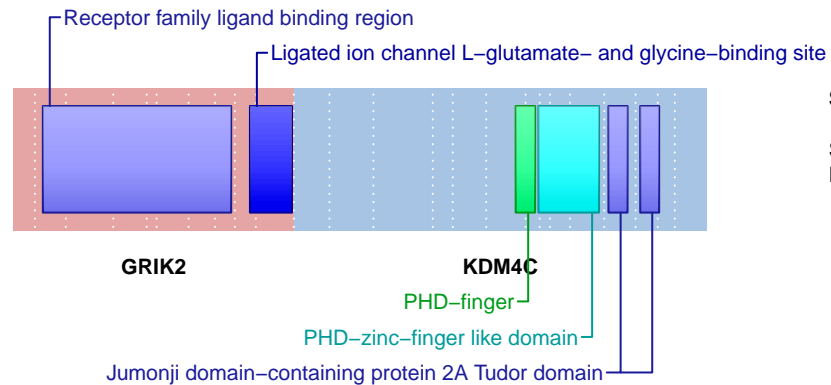
**SUPPORTING READ COUNT**

Split reads = 70  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



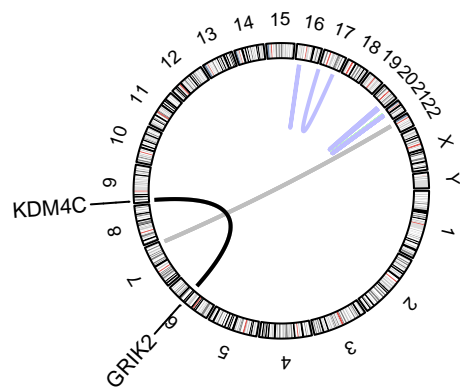
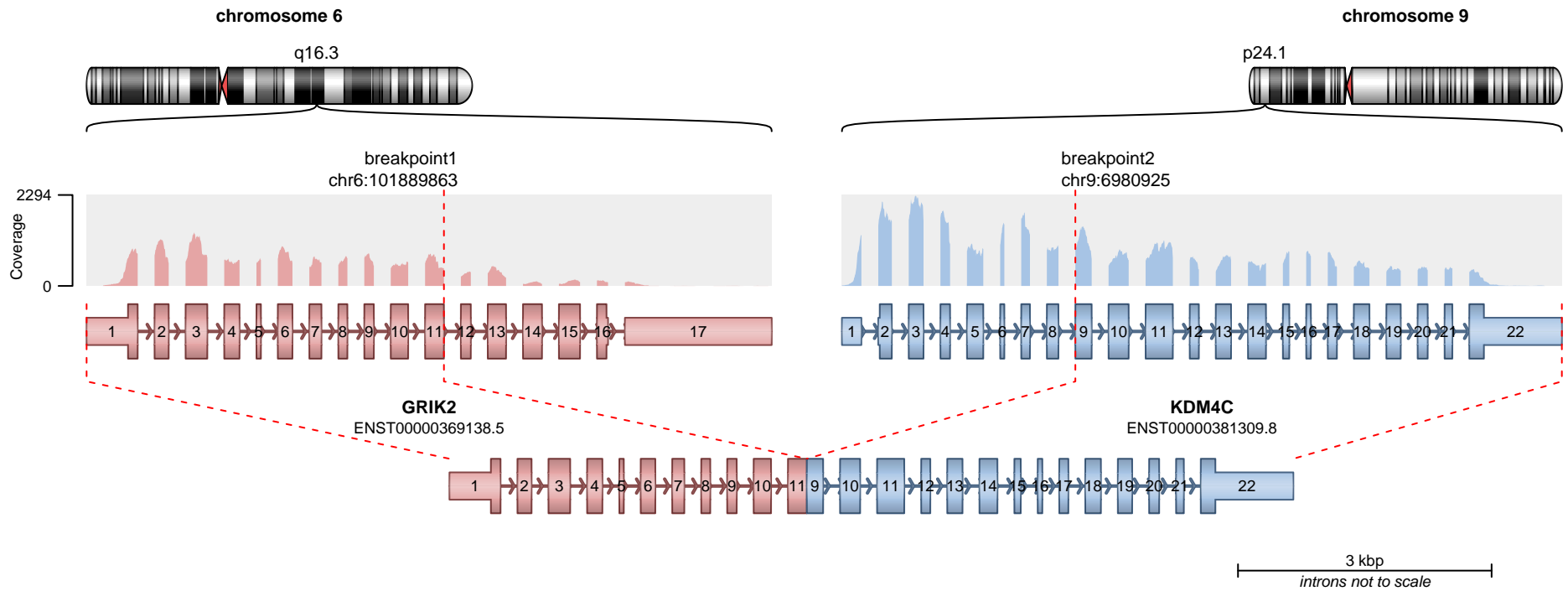
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



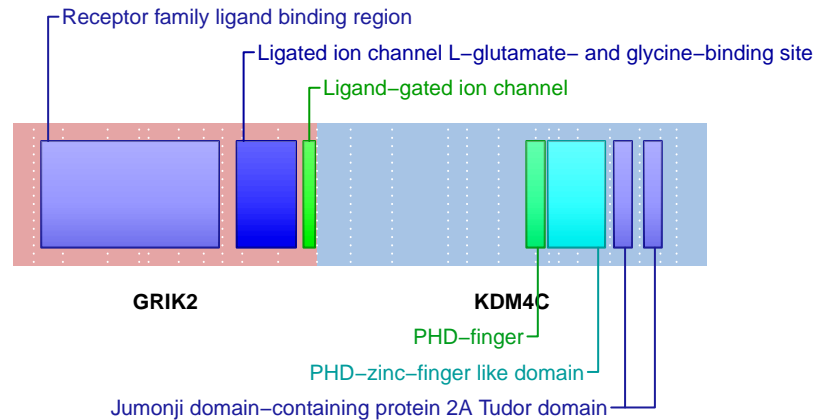
**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



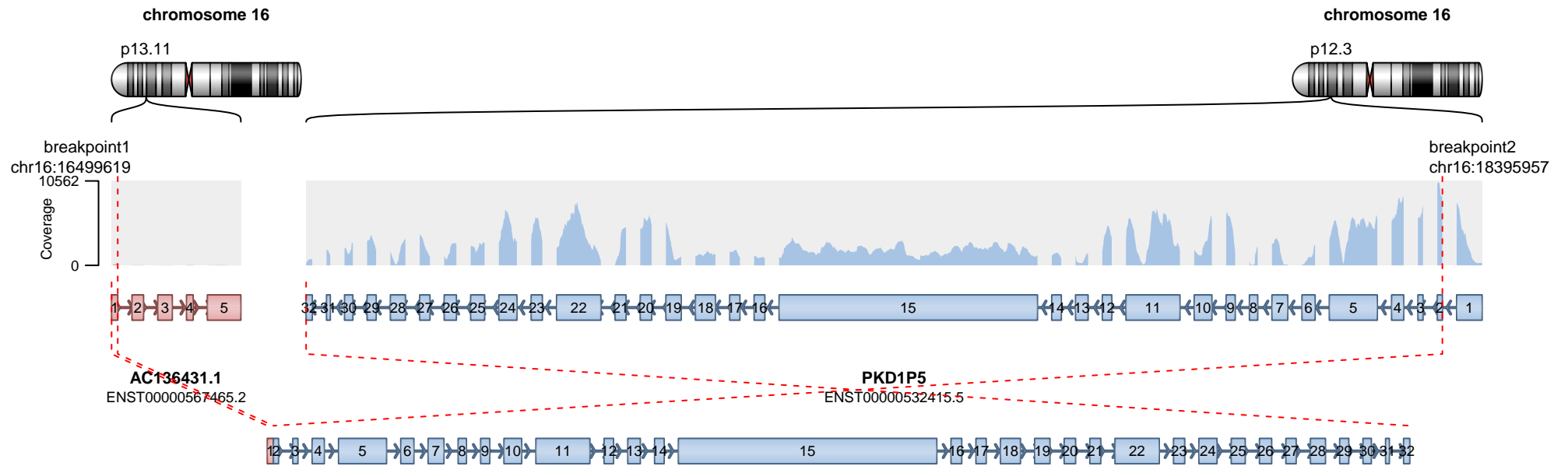
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



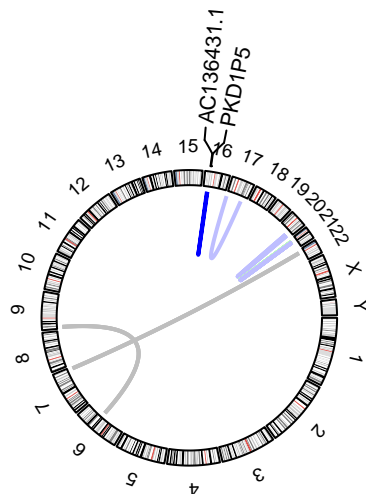
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



4 kbp  
introns not to scale

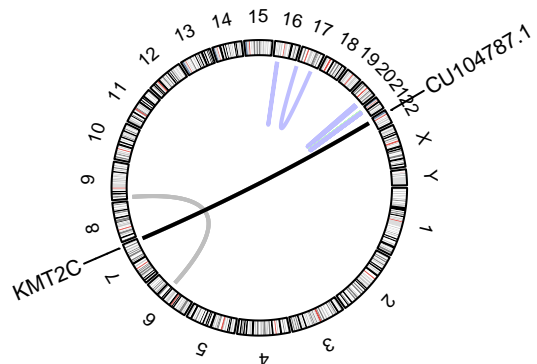
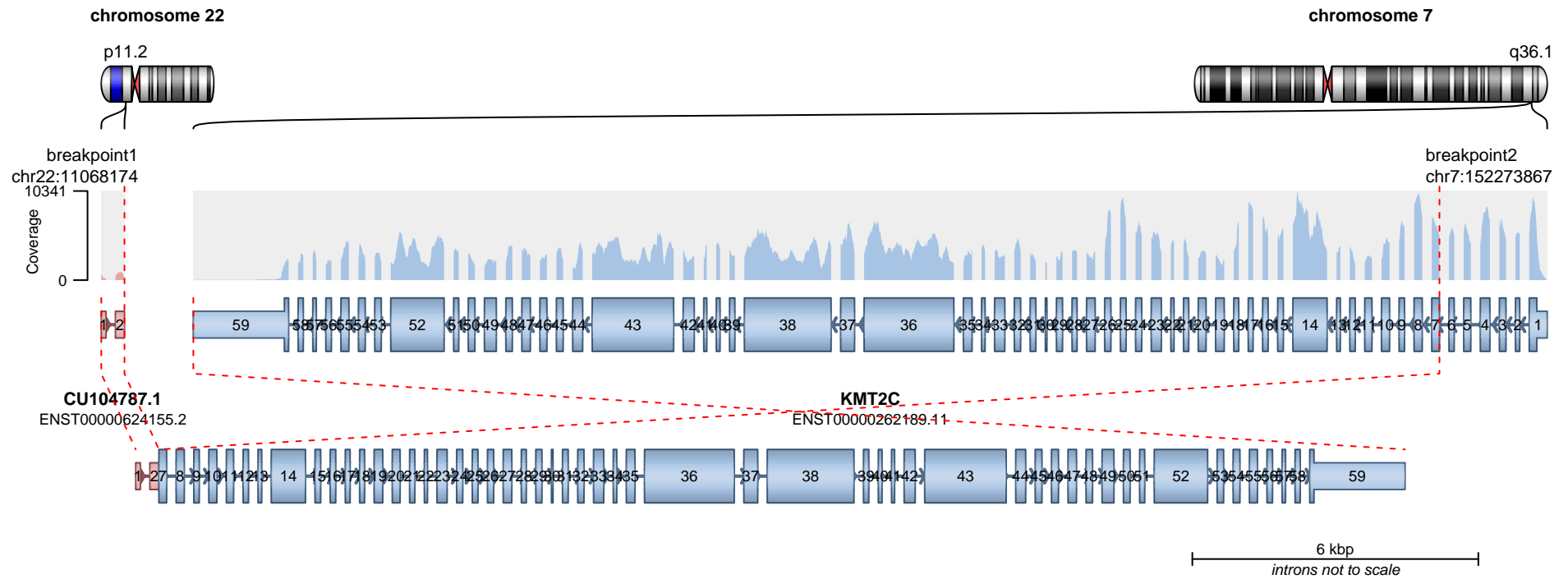


Genes are not protein-coding.

**SUPPORTING READ COUNT**

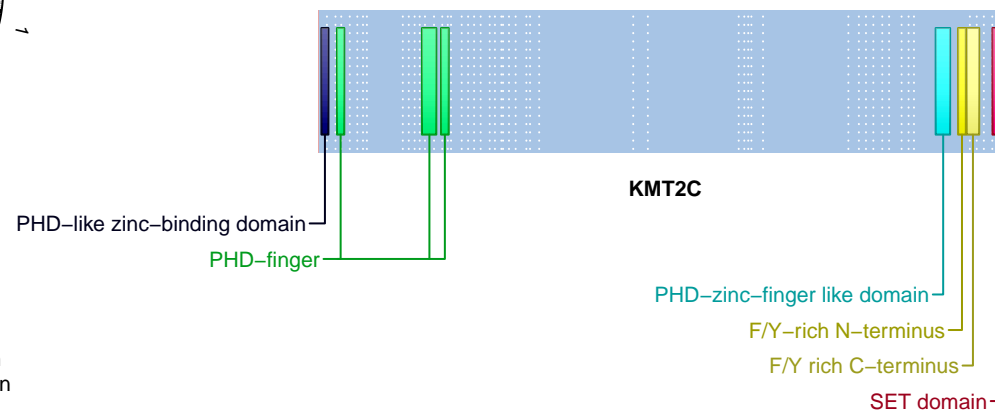
Split reads = 66  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



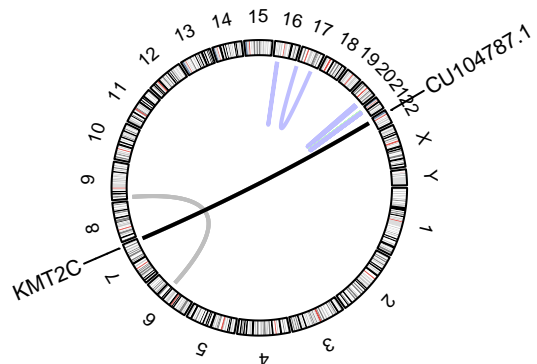
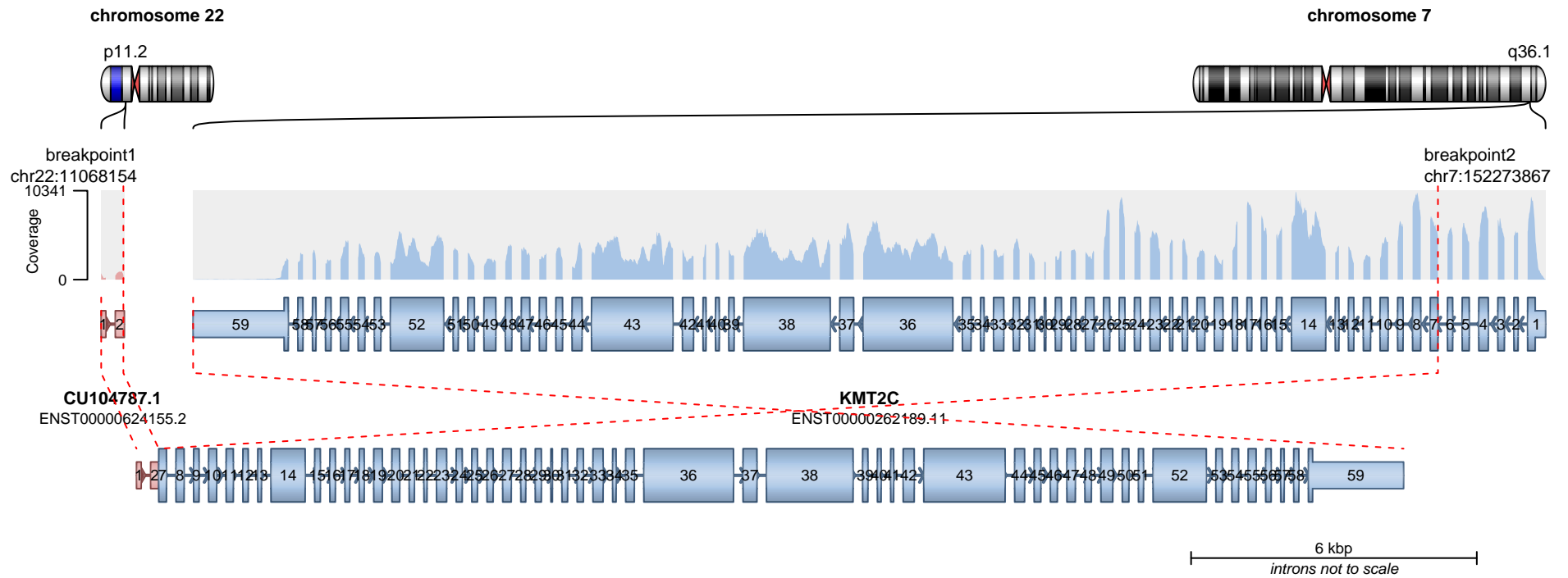
- translocation
- duplication
- deletion
- inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



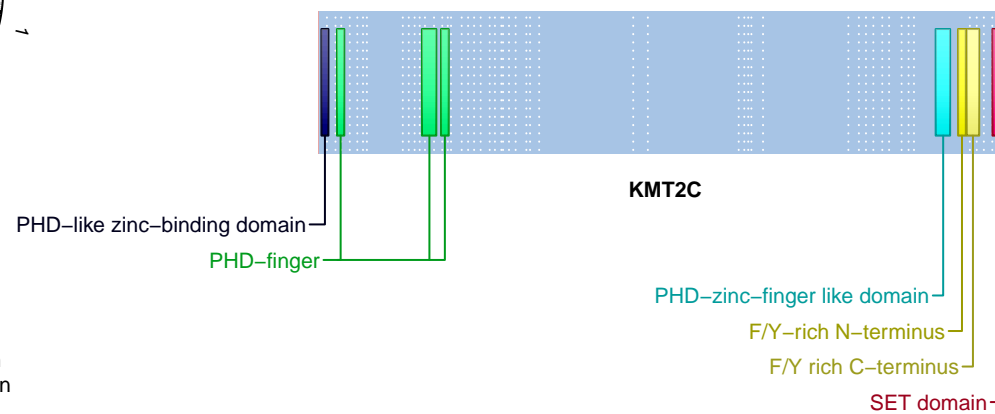
**SUPPORTING READ COUNT**

Split reads = 42  
Discordant mates = 1



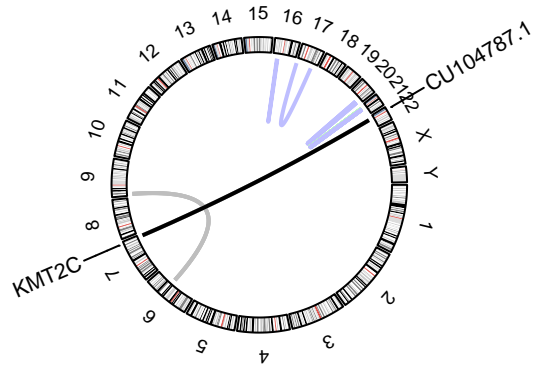
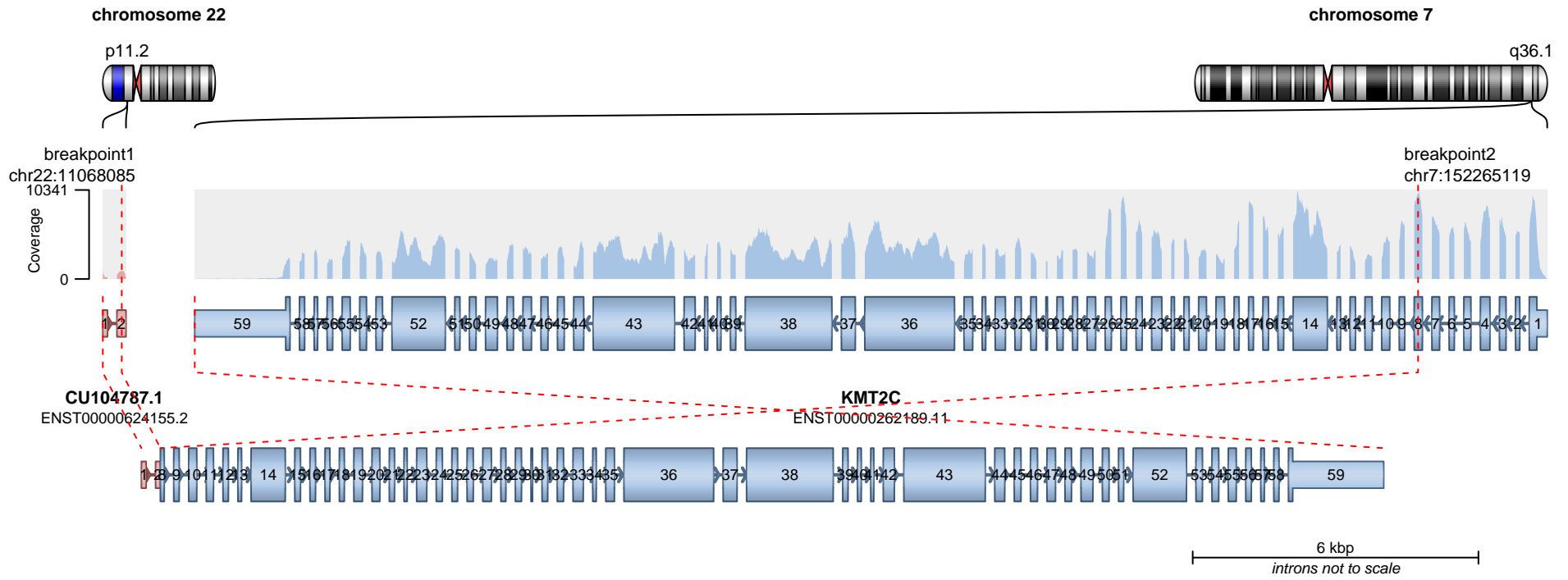
- translocation
- duplication
- deletion
- inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



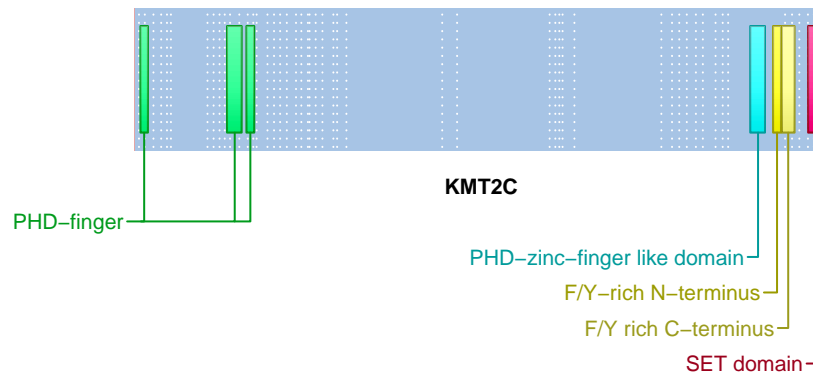
**SUPPORTING READ COUNT**

Split reads = 24  
Discordant mates = 1



— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear

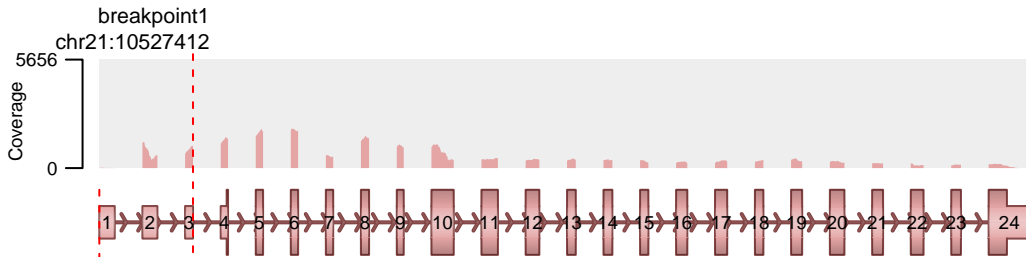


**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 0

chromosome 21

p11.2



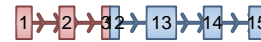
chromosome 21

p11.2

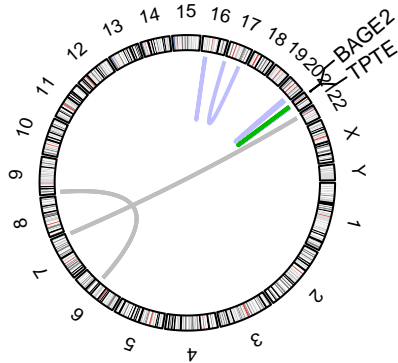


**TPTE**  
ENST00000618007.6

**BAGE2**  
ENST00000496773.1



2 kbp  
introns not to scale

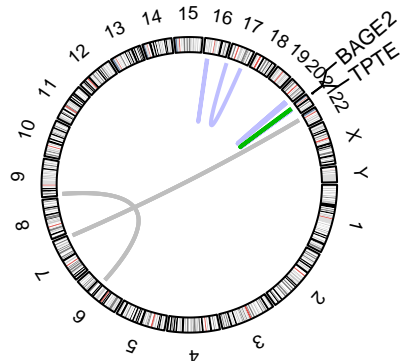
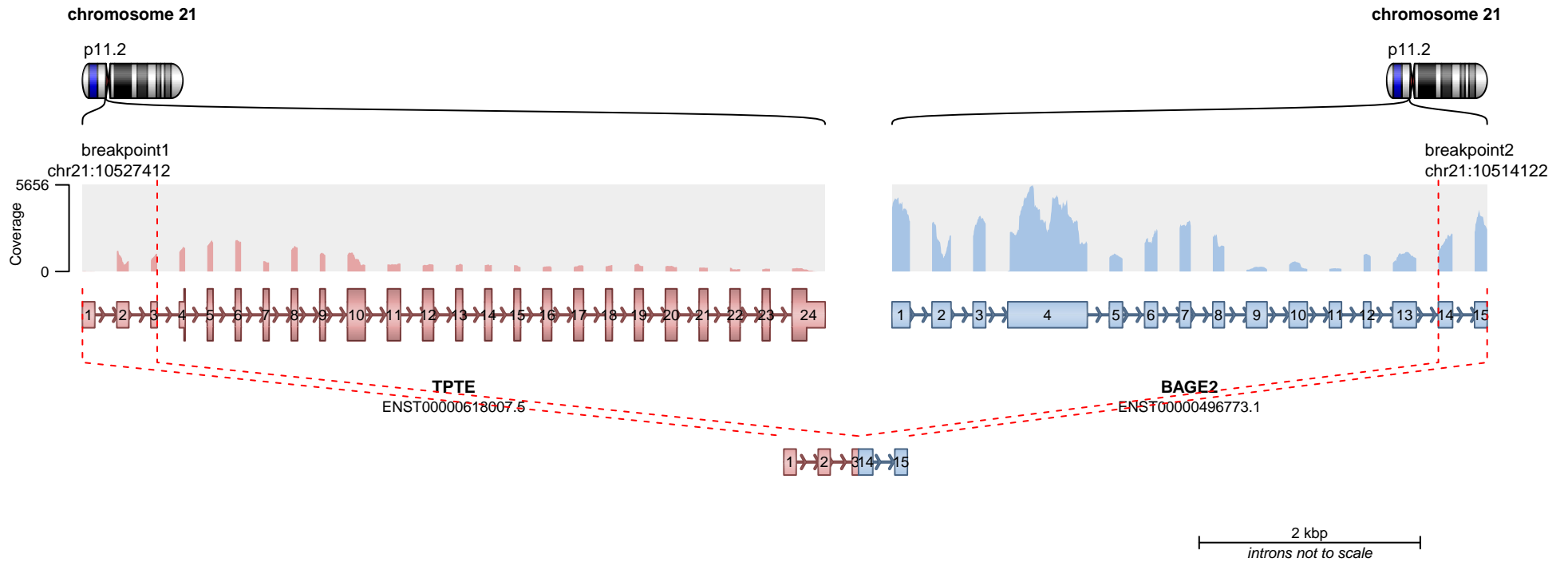


No coding regions retained in fusion transcript.

**SUPPORTING READ COUNT**

Split reads = 17  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



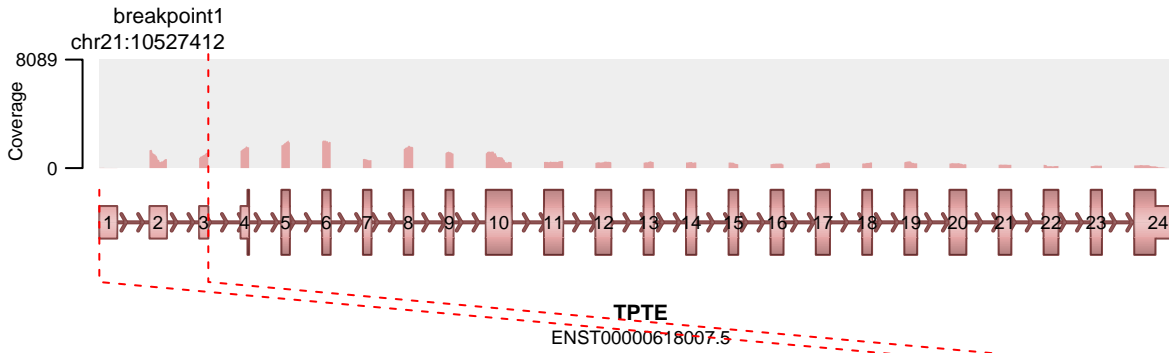
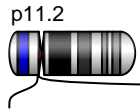
No coding regions retained in fusion transcript.

**SUPPORTING READ COUNT**

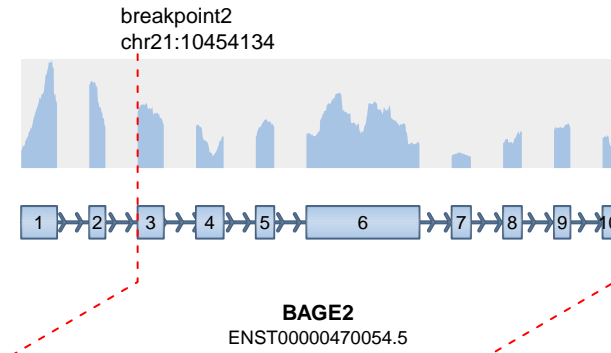
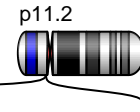
Split reads = 17  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion

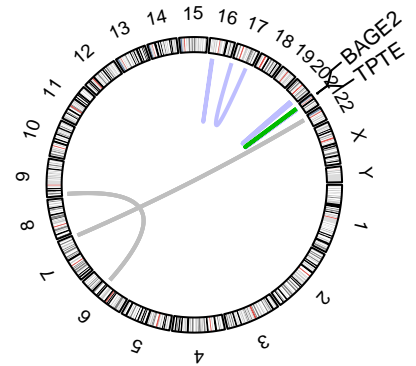
chromosome 21



chromosome 21



2 kbp  
introns not to scale



No coding regions retained in fusion transcript.

**SUPPORTING READ COUNT**

Split reads = 9  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion

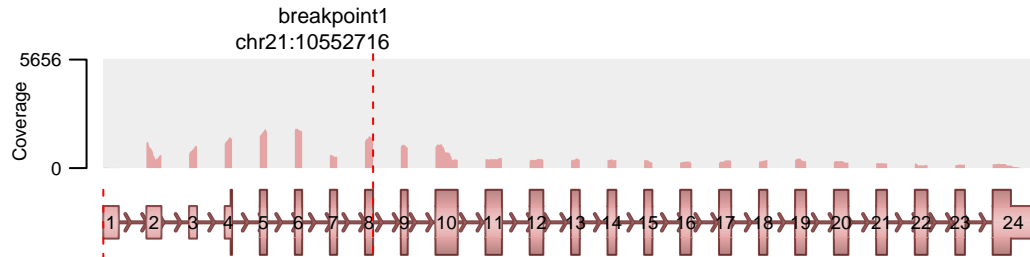
chromosome 21

p11.2



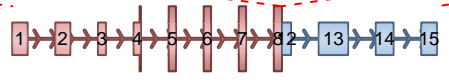
chromosome 21

p11.2

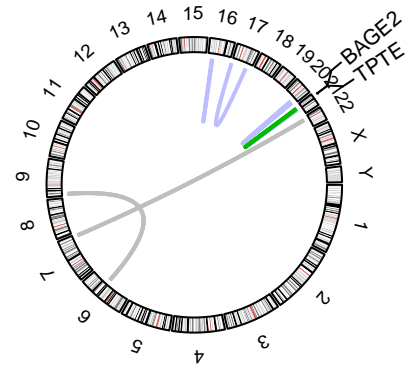


**TPTE**  
ENST00000618007.5

**BAGE2**  
ENST00000496773.1



2 kbp  
*introns not to scale*



No protein domains retained in fusion.

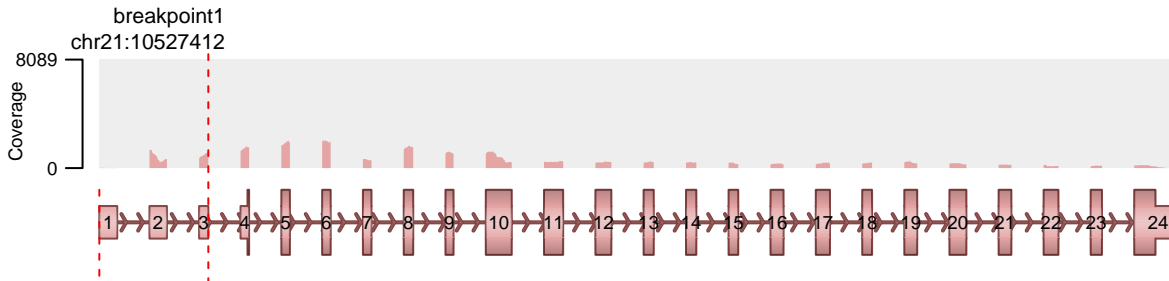
**SUPPORTING READ COUNT**

Split reads = 6  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

chromosome 21

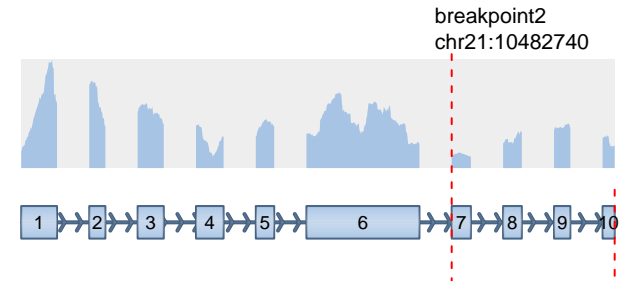
p11.2



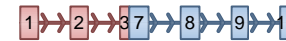
**TPTE**  
ENST00000618007.5

chromosome 21

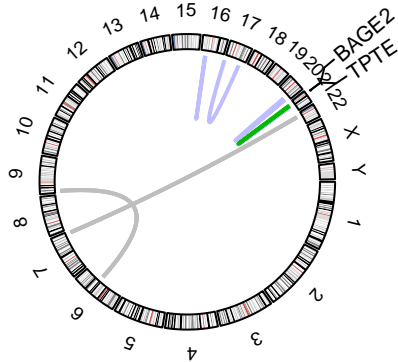
p11.2



**BAGE2**  
ENST00000470054.5



2 kbp  
*introns not to scale*



No coding regions retained in fusion transcript.

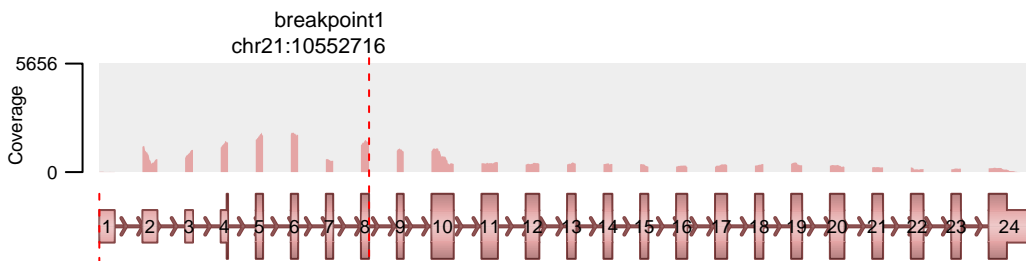
**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion

chromosome 21

p11.2

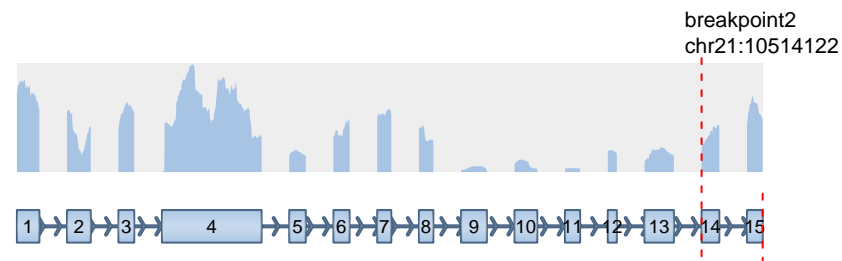


**TPTE**

ENST00000618007.5

chromosome 21

p11.2

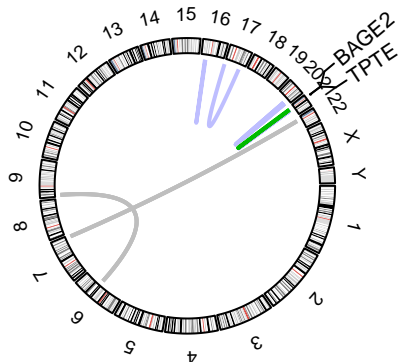


**BAGE2**

ENST00000496773.1



2 kbp  
introns not to scale



No protein domains retained in fusion.

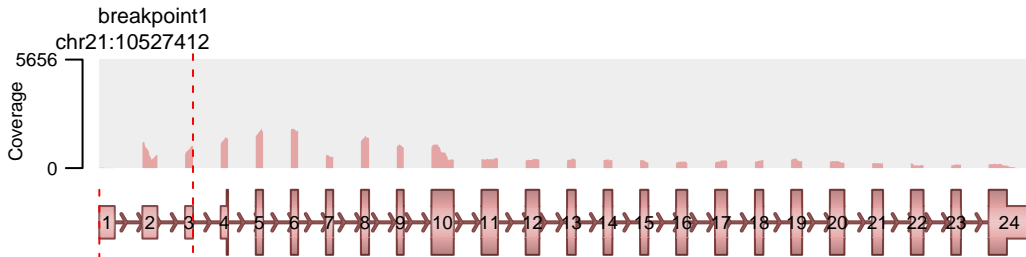
**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion

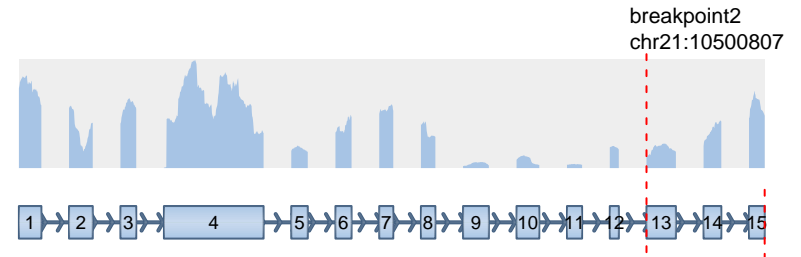
chromosome 21

p11.2



chromosome 21

p11.2

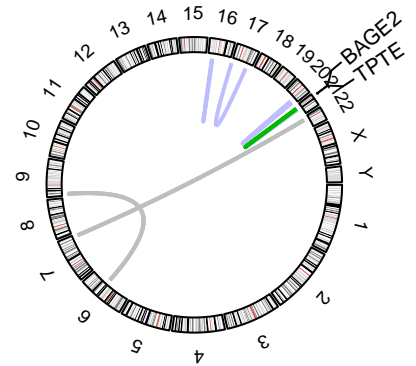


**TPTE**  
ENST00000618007.6

**BAGE2**  
ENST00000496773.1



2 kbp  
introns not to scale



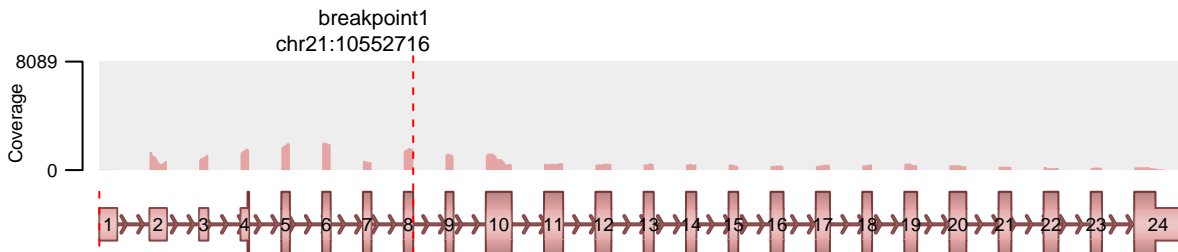
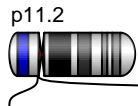
No coding regions retained in fusion transcript.

**SUPPORTING READ COUNT**

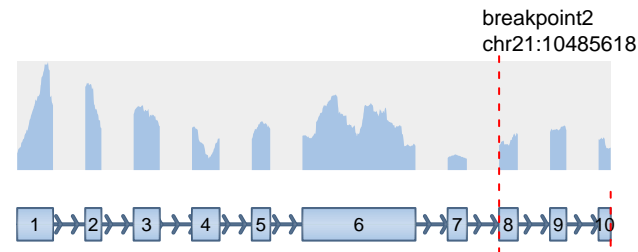
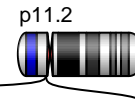
Split reads = 2  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

chromosome 21



chromosome 21

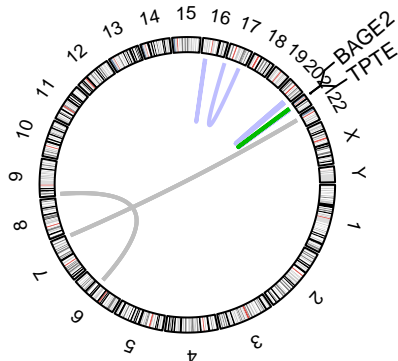


**TPTE**  
ENST00000618007.5

**BAGE2**  
ENST00000470054.5



2 kbp  
introns not to scale



— translocation    — deletion  
— duplication    — inversion

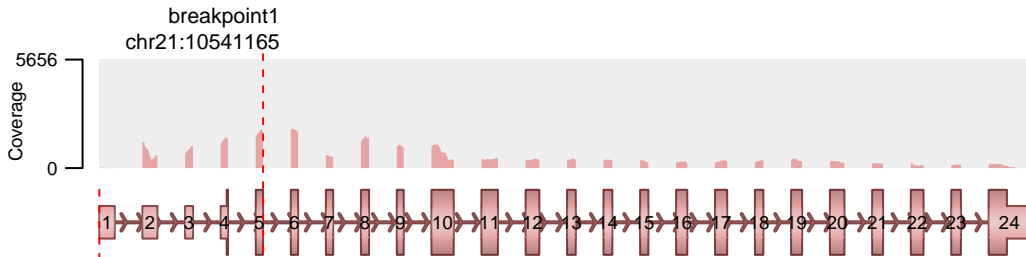
No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0

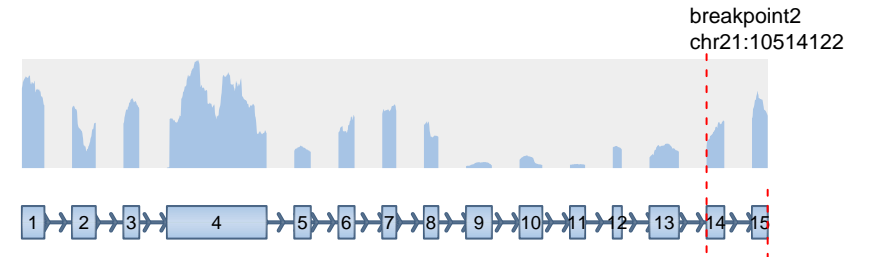
chromosome 21

p11.2



chromosome 21

p11.2

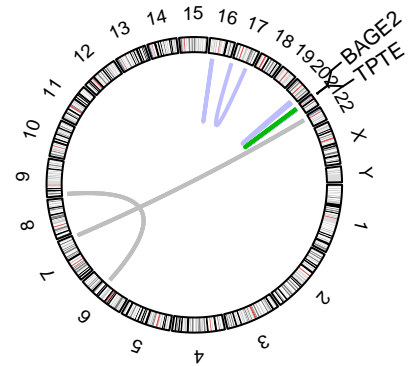


**TPTE**  
ENST00000618007.5

**BAGE2**  
ENST00000496773.1



2 kbp  
introns not to scale



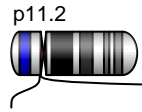
No protein domains retained in fusion.

**SUPPORTING READ COUNT**

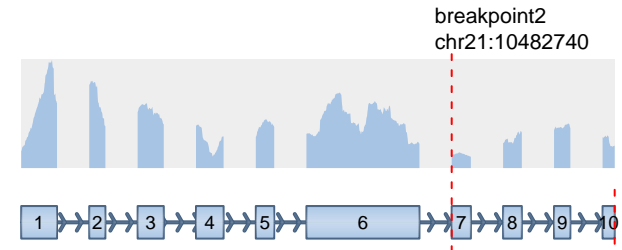
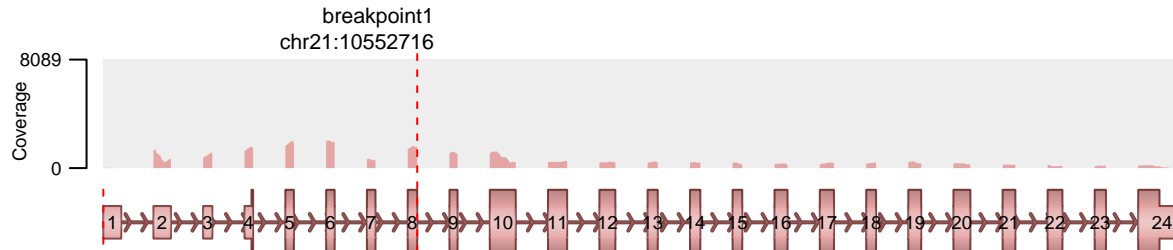
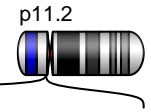
Split reads = 2  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

chromosome 21



chromosome 21

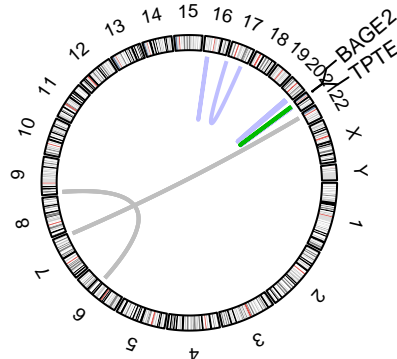


**TPTE**  
ENST00000618007.5

**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

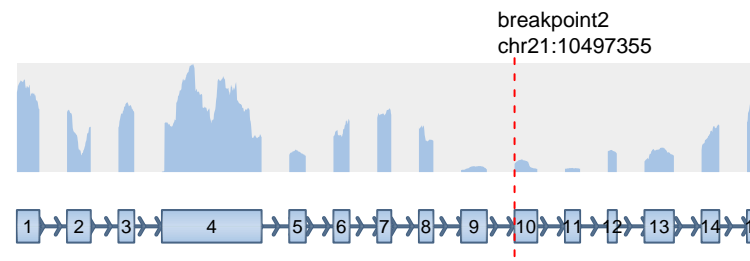
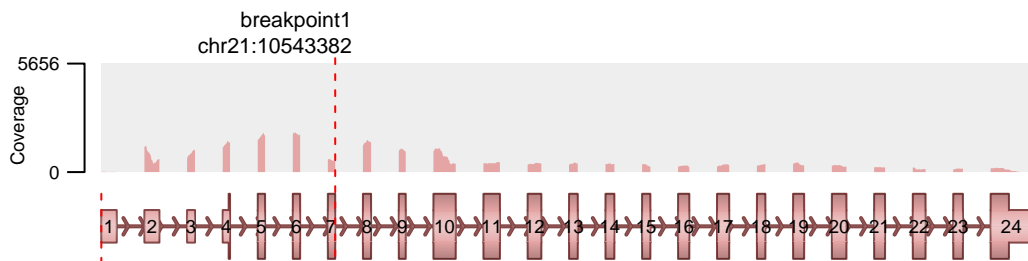
chromosome 21

p11.2



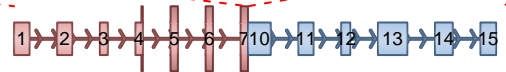
chromosome 21

p11.2

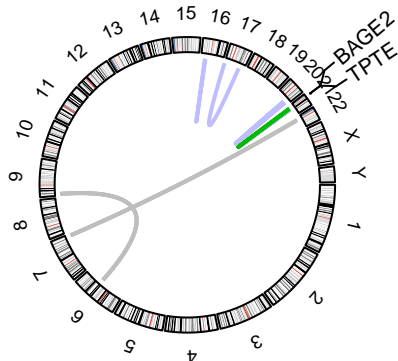


**TPTE**  
ENST00000618007.5

**BAGE2**  
ENST00000496773.1



2 kbp  
*introns not to scale*



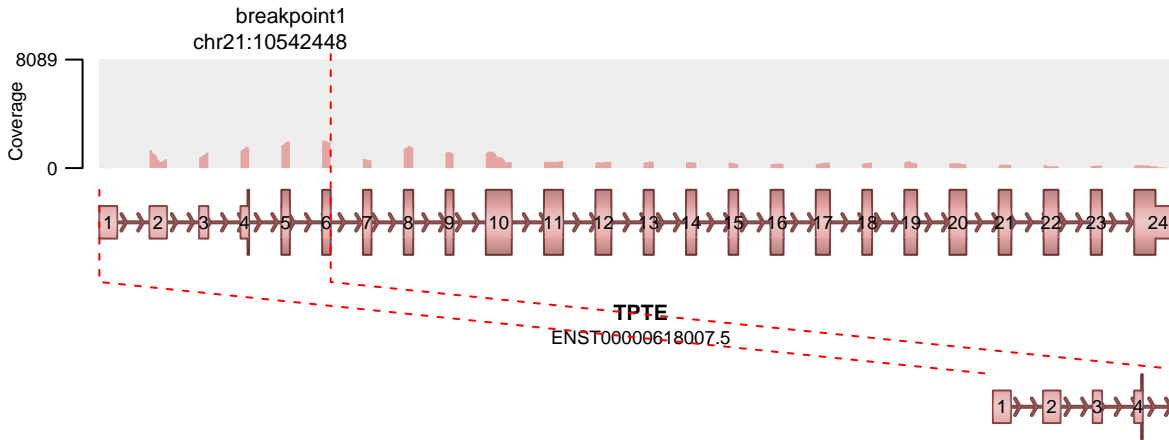
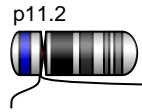
No protein domains retained in fusion.

**SUPPORTING READ COUNT**

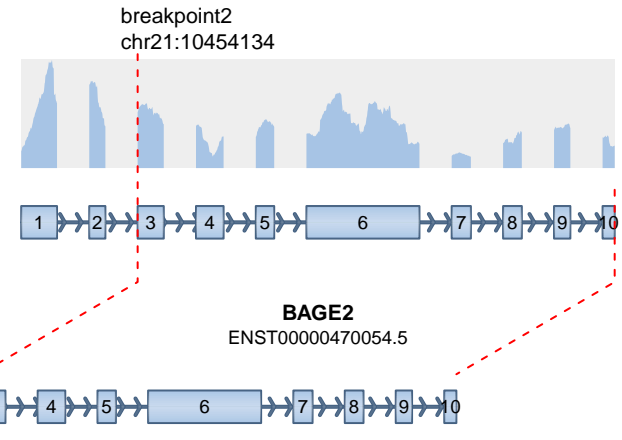
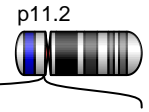
Split reads = 1  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

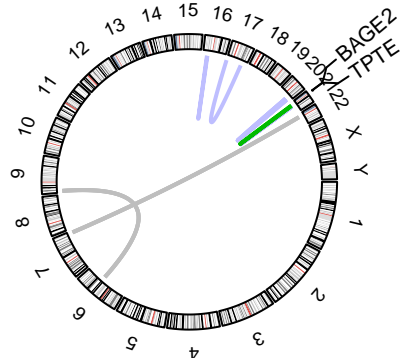
chromosome 21



chromosome 21



2 kbp  
introns not to scale

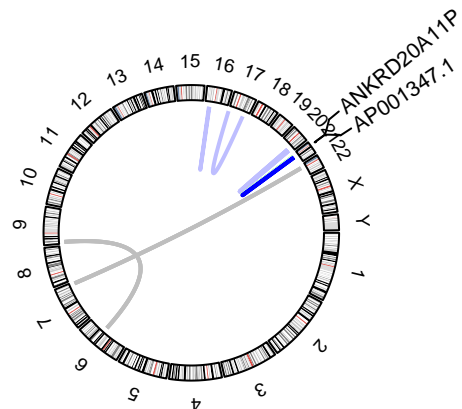
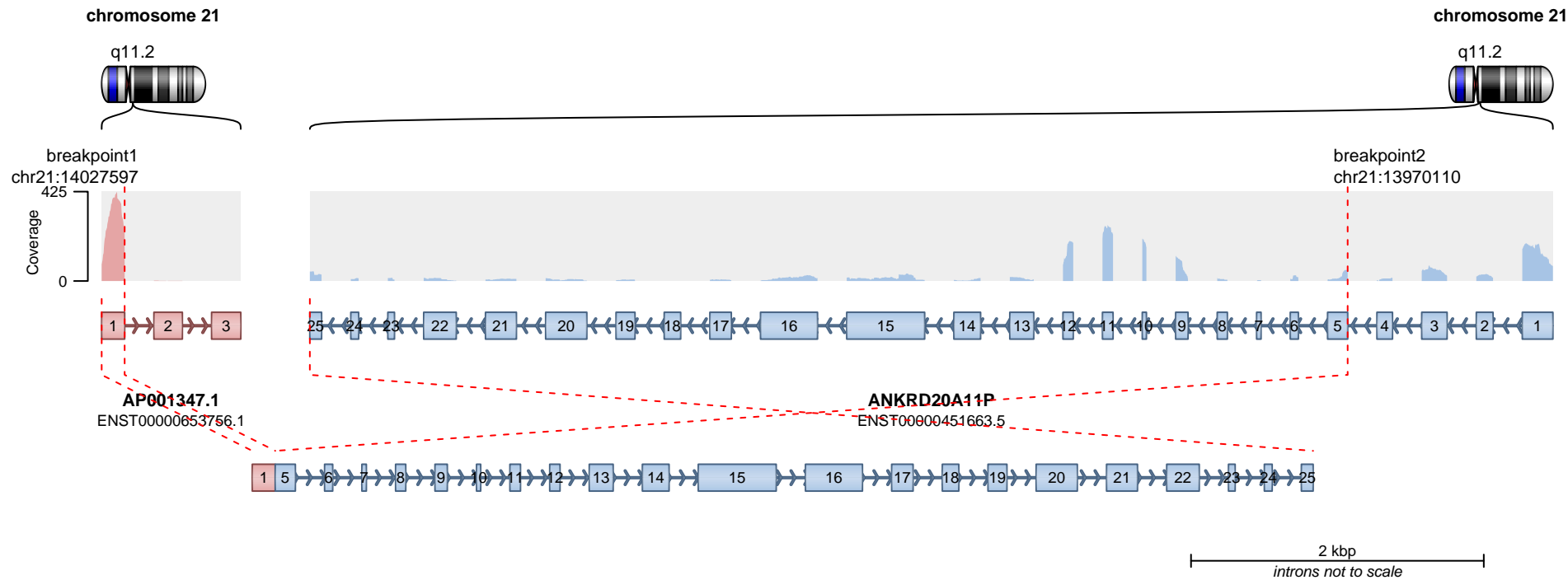


— translocation    — deletion  
— duplication    — inversion

No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

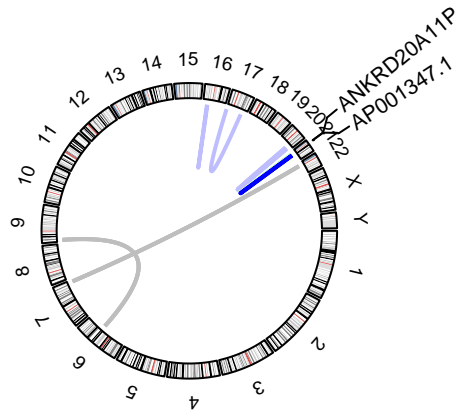
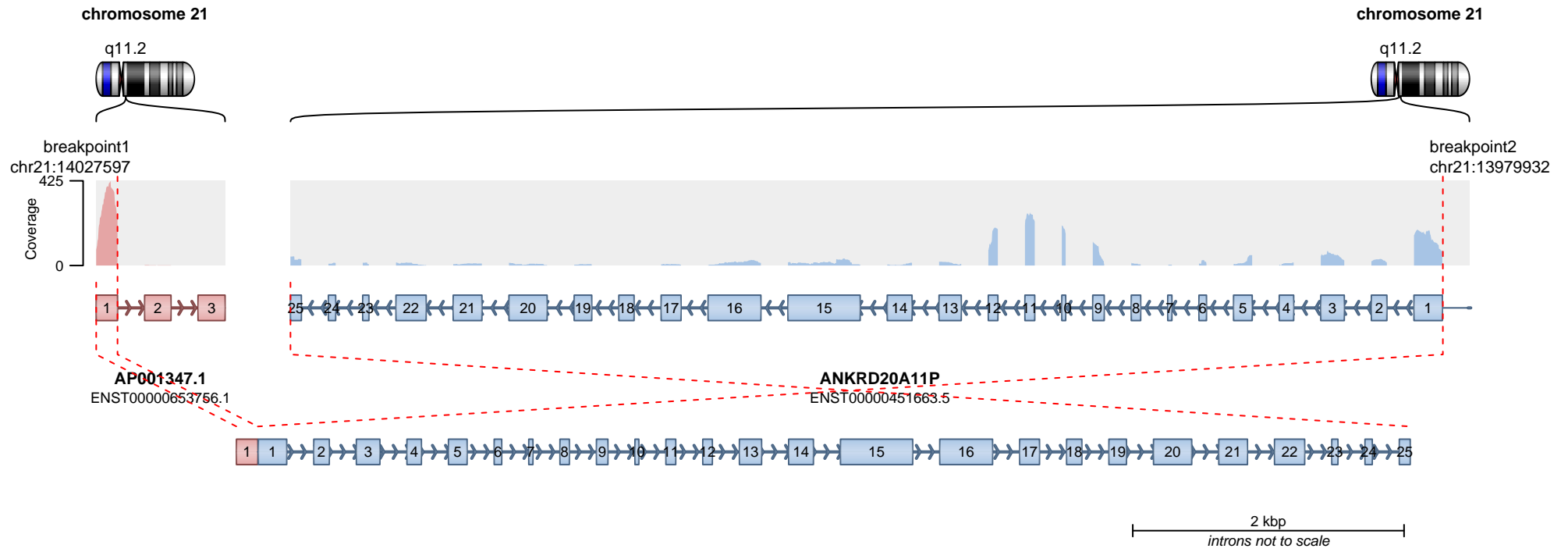


Genes are not protein-coding.

**SUPPORTING READ COUNT**

Split reads = 7  
Discordant mates = 1

— translocation    — deletion  
— duplication    — inversion

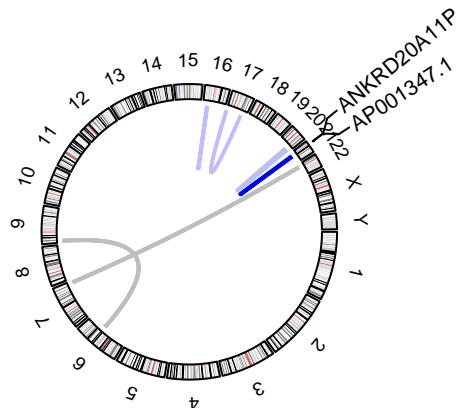
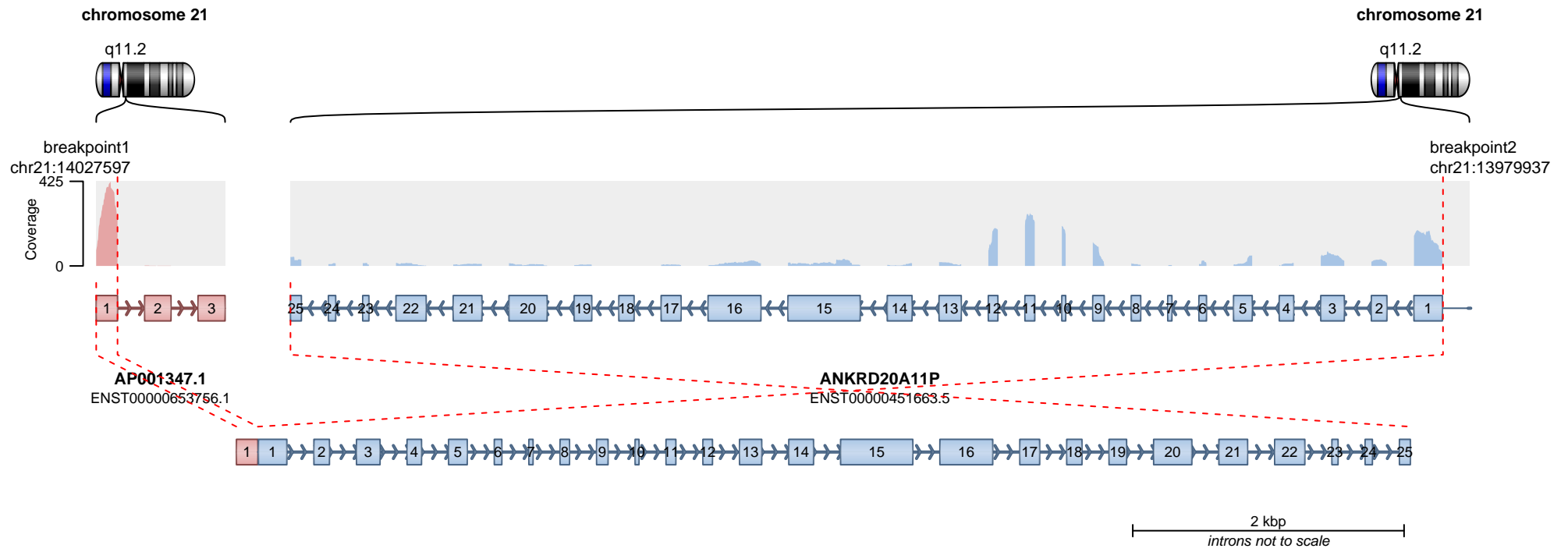


Genes are not protein-coding.

**SUPPORTING READ COUNT**

Split reads = 6  
Discordant mates = 2

- translocation
- duplication
- deletion
- inversion

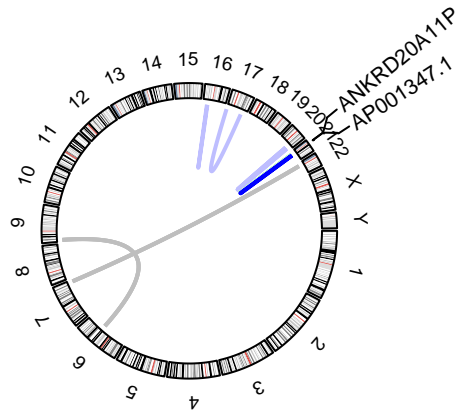
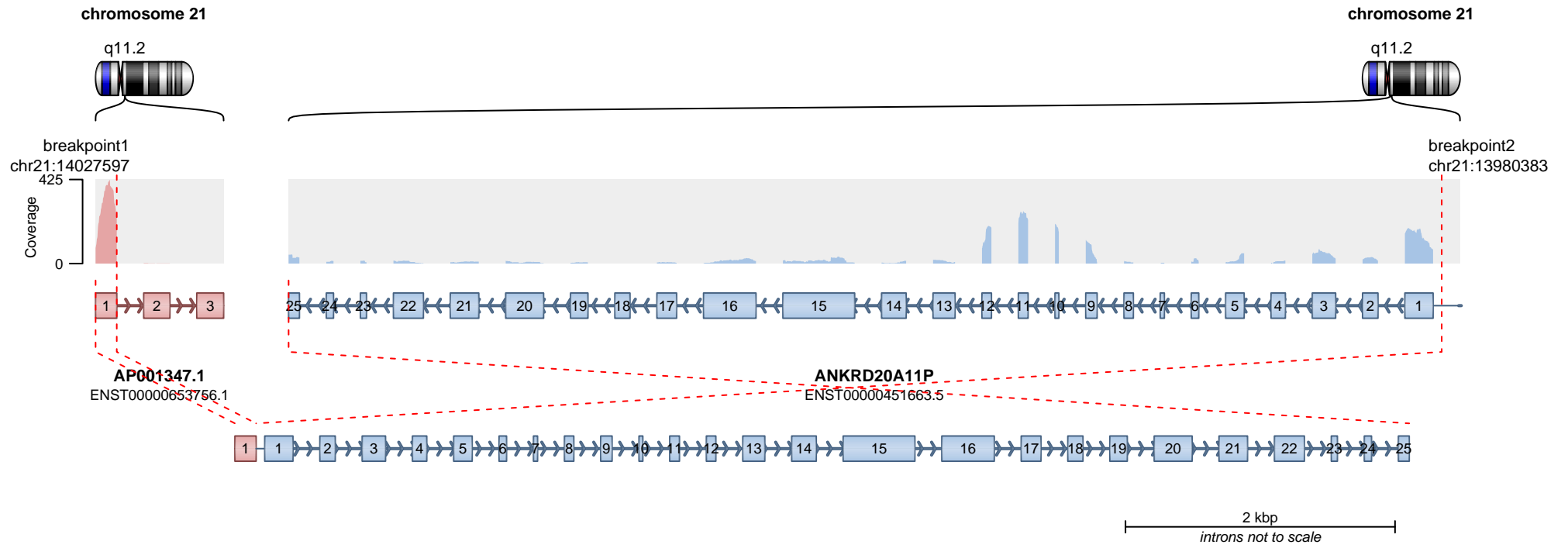


Genes are not protein-coding.

**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 2

- translocation
- duplication
- deletion
- inversion

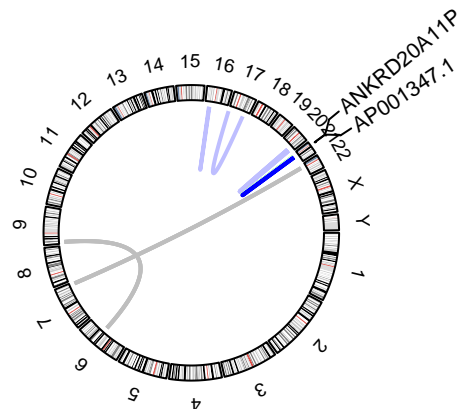
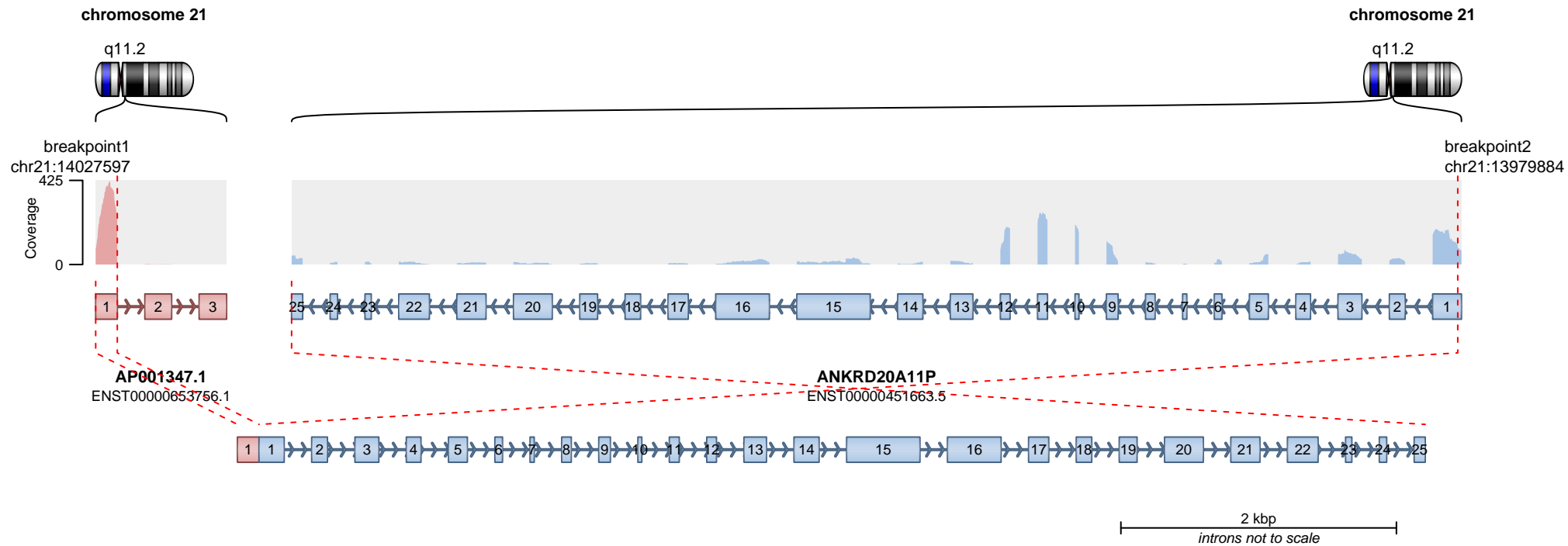


Genes are not protein-coding.

**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 2

— translocation — deletion  
— duplication — inversion

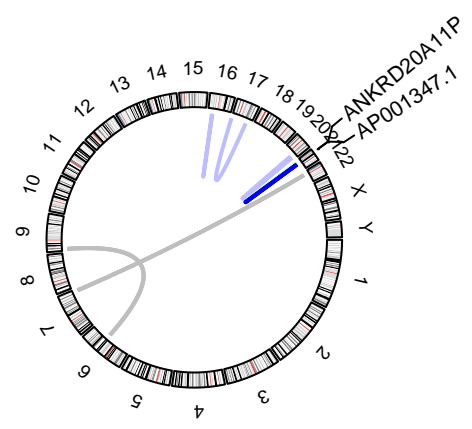
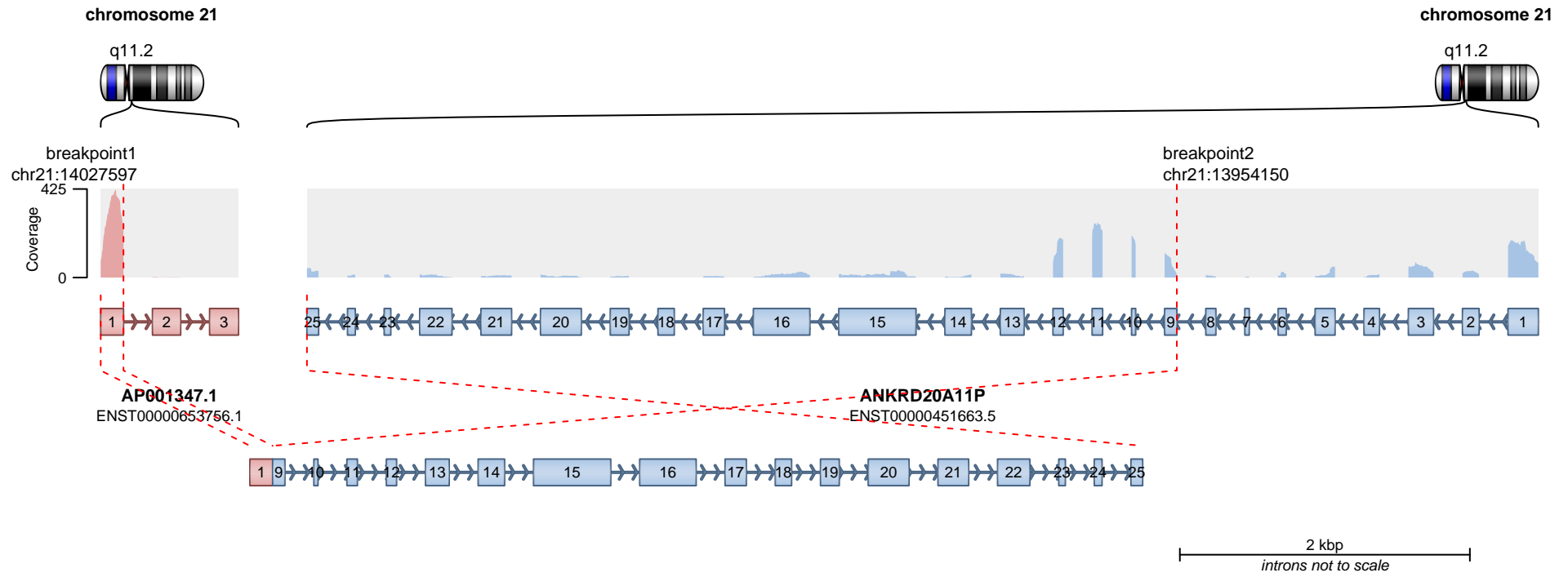


Genes are not protein-coding.

**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 1

— translocation    — deletion  
— duplication    — inversion



Genes are not protein-coding.

**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion