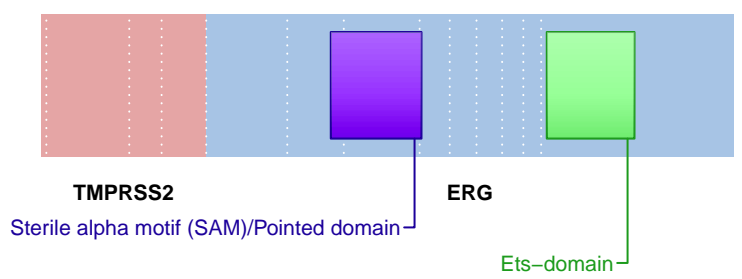


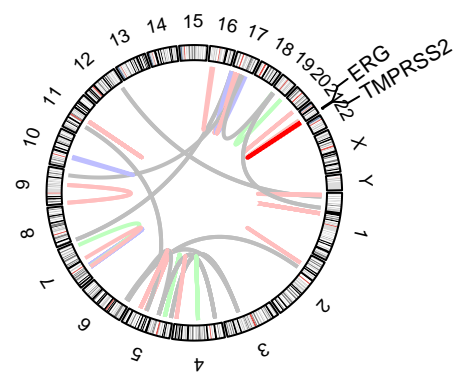
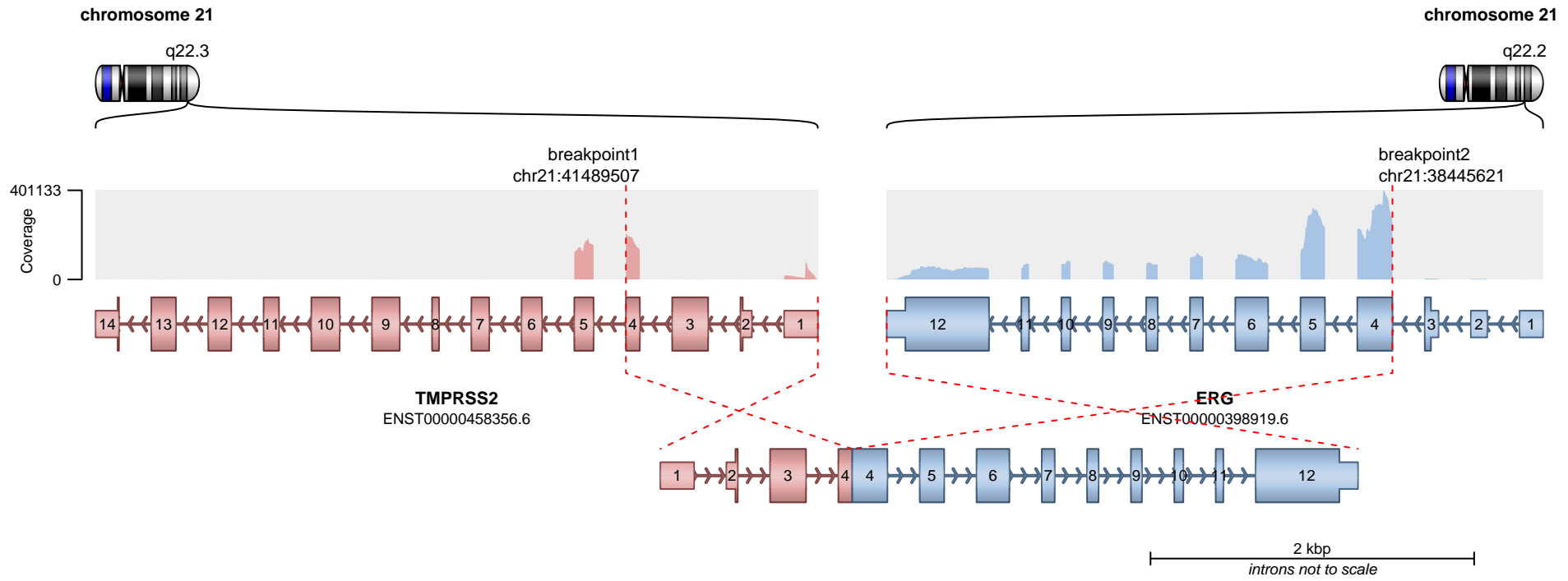
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



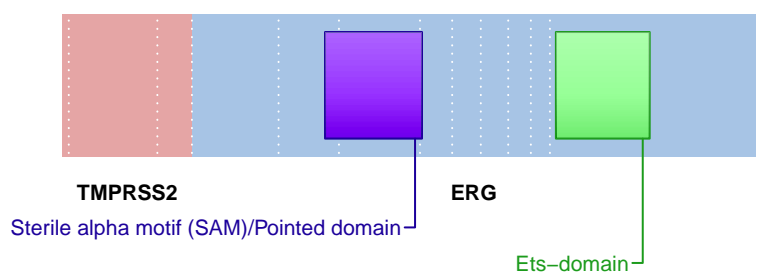
**SUPPORTING READ COUNT**

Split reads = 61238  
Discordant mates = 303

- translocation
- duplication
- deletion
- inversion



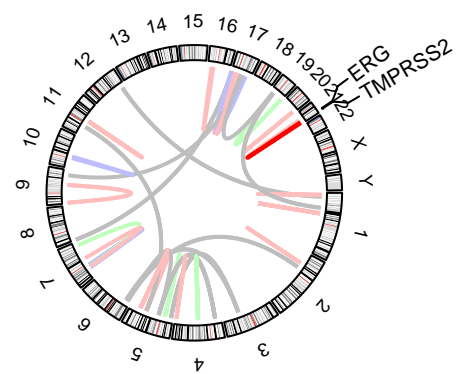
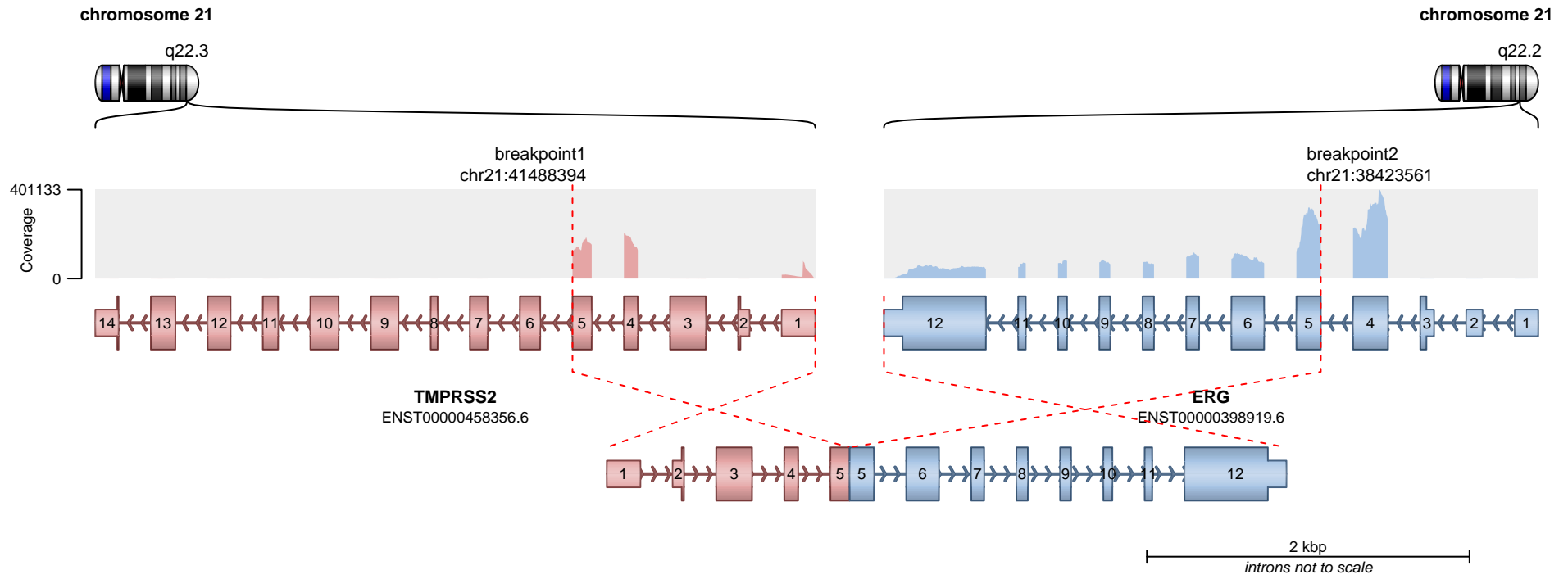
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



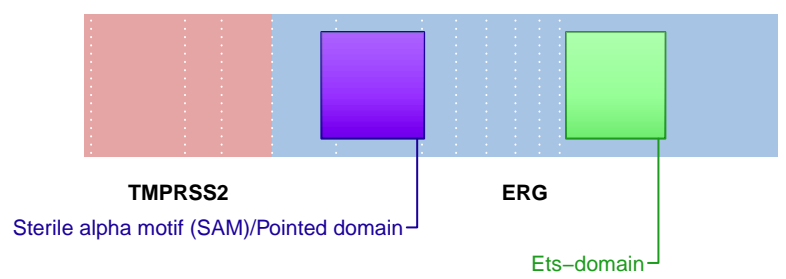
**SUPPORTING READ COUNT**

Split reads = 18206  
Discordant mates = 40

- translocation
- duplication
- deletion
- inversion



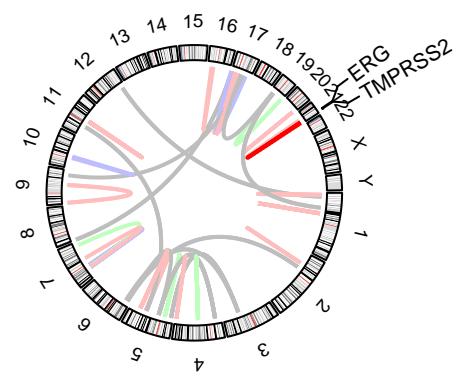
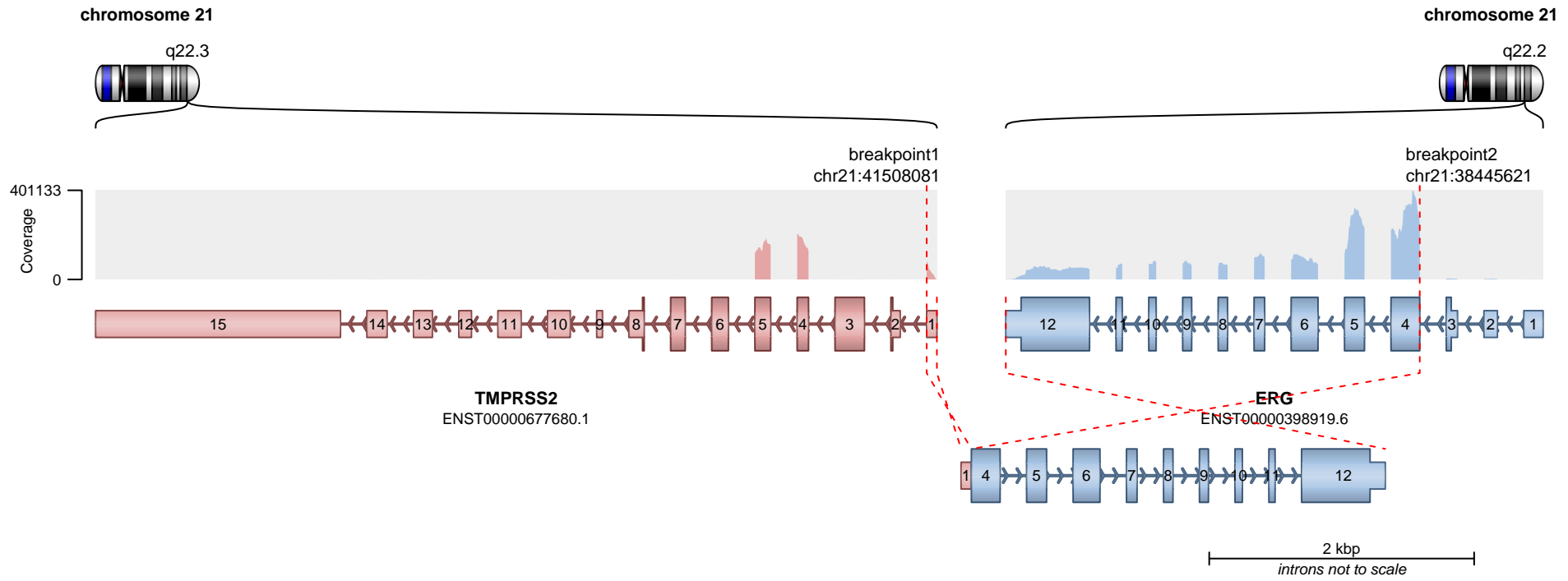
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



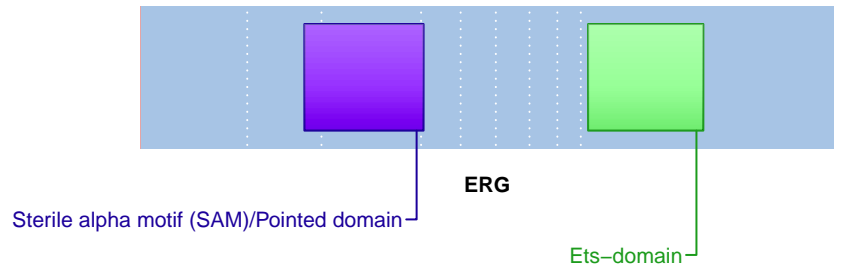
**SUPPORTING READ COUNT**

Split reads = 501  
Discordant mates = 10

- translocation
- duplication
- deletion
- inversion



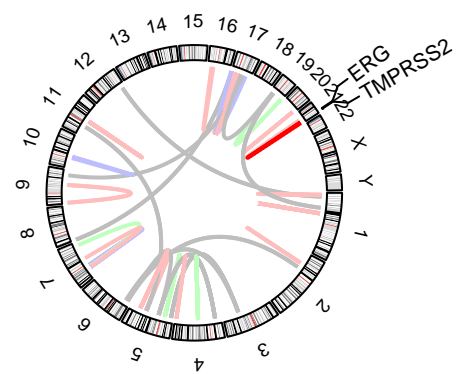
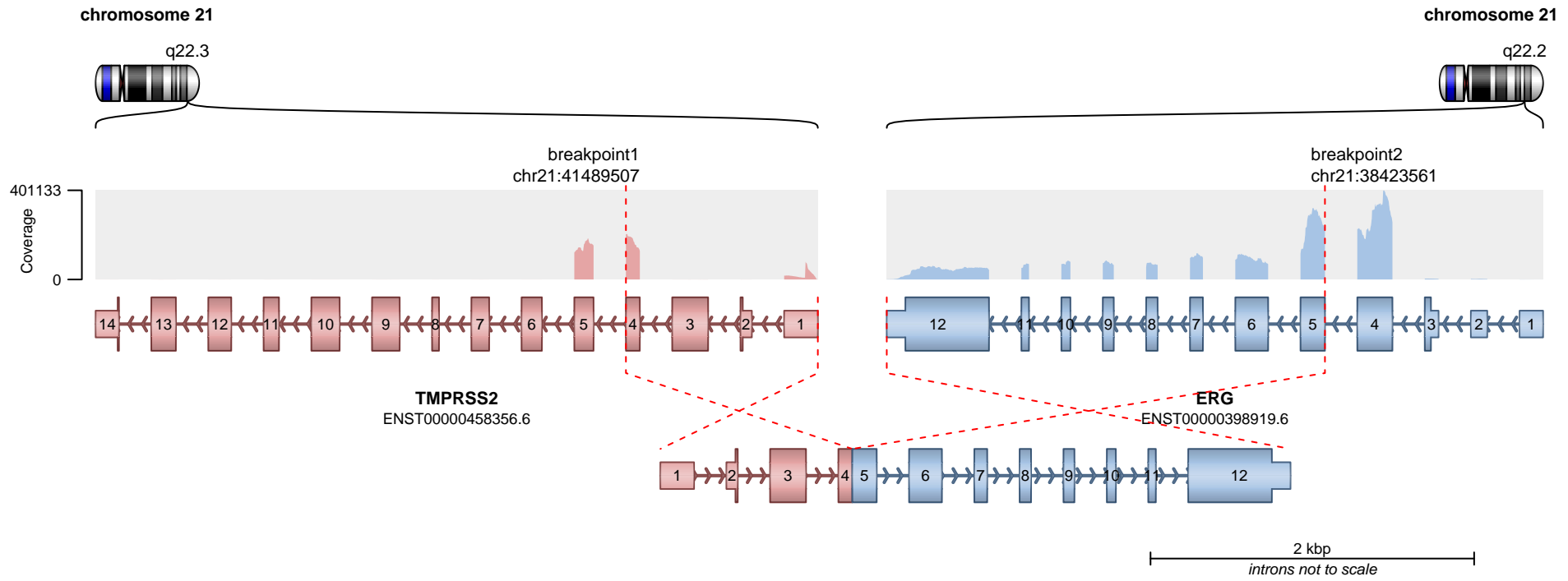
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



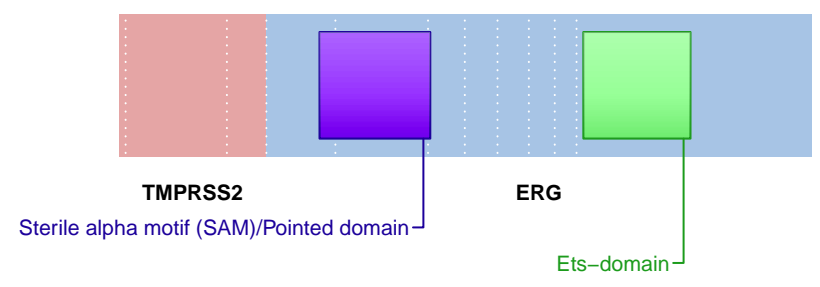
**SUPPORTING READ COUNT**

Split reads = 345  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



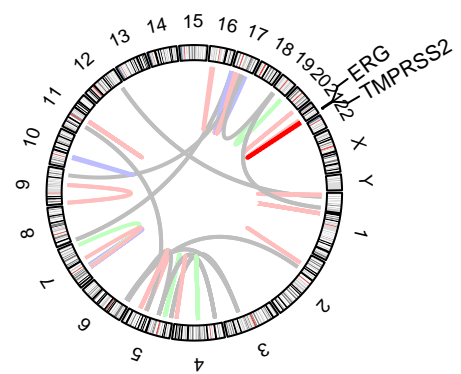
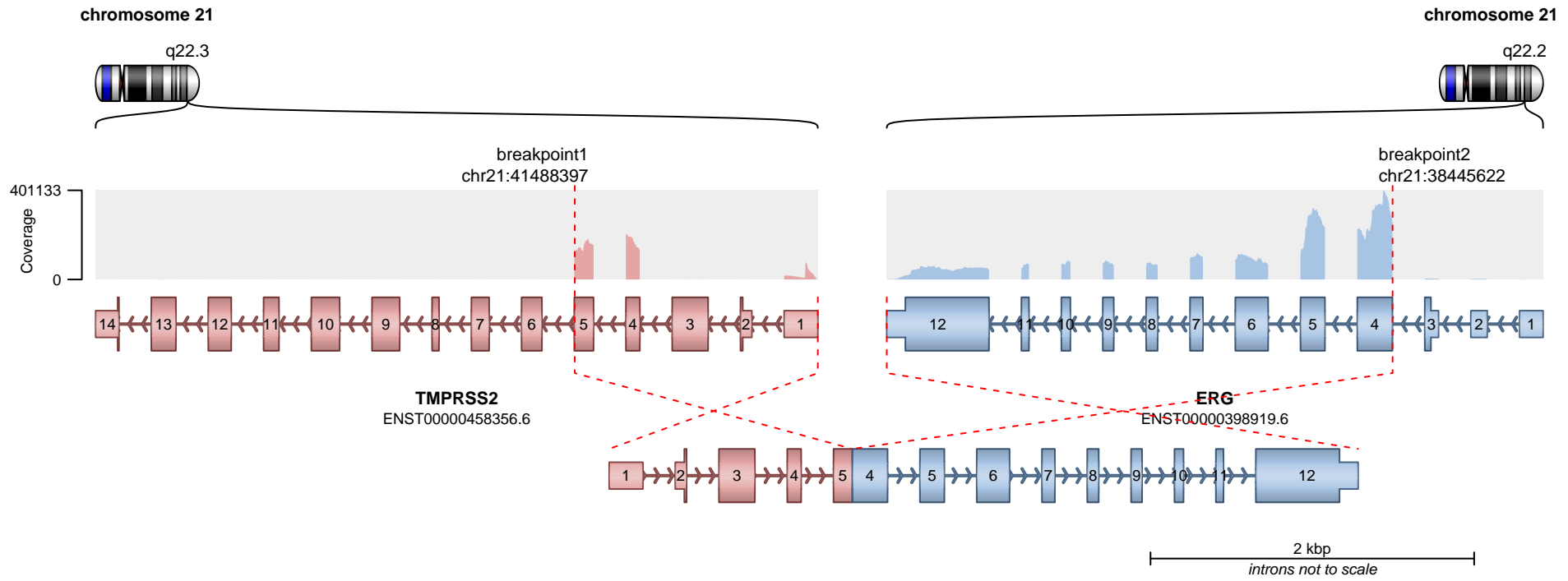
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



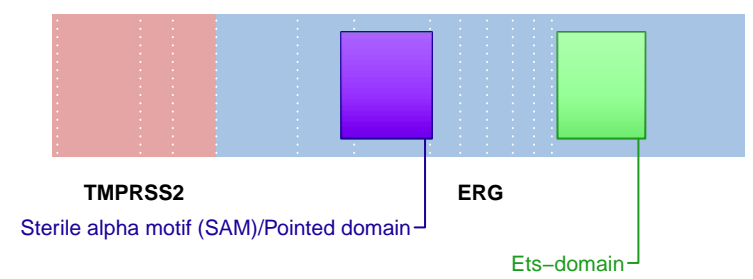
**SUPPORTING READ COUNT**

Split reads = 235  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



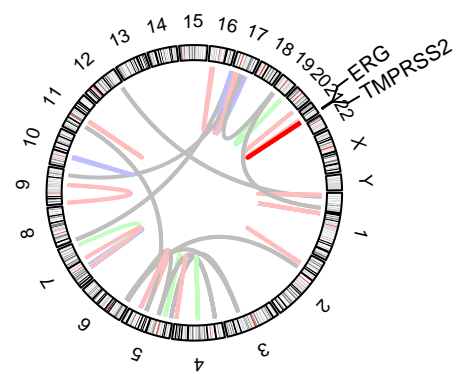
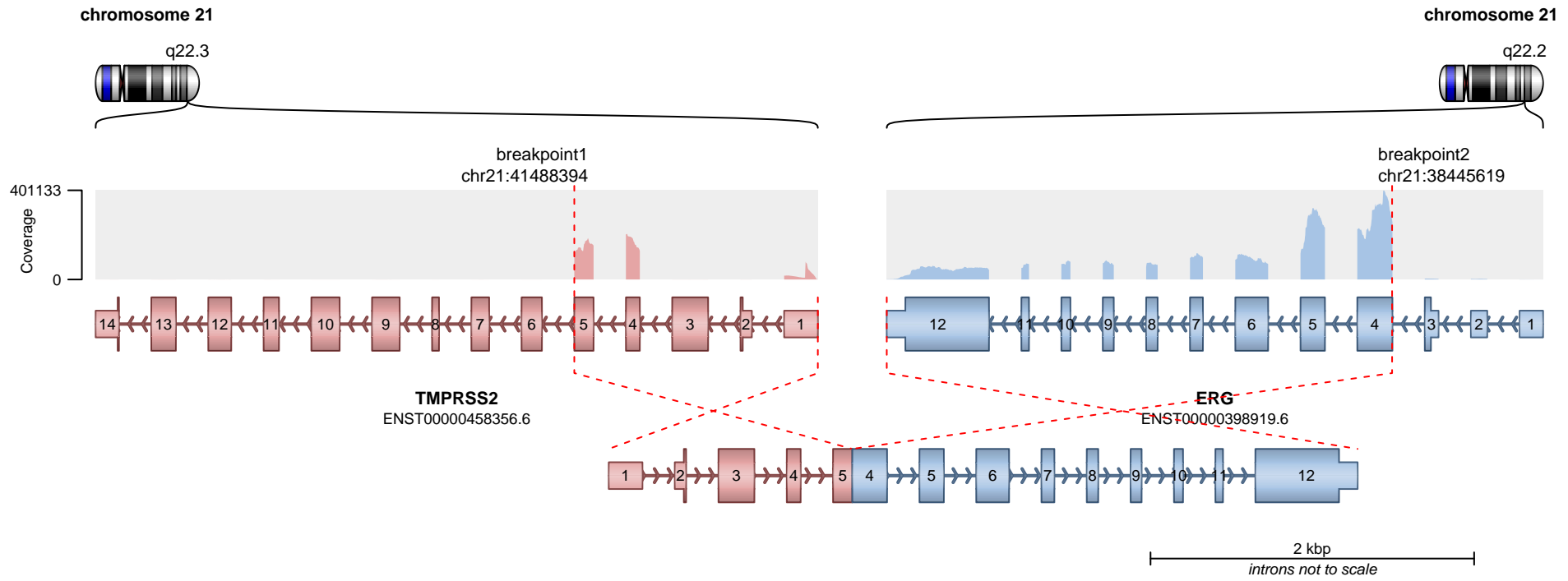
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



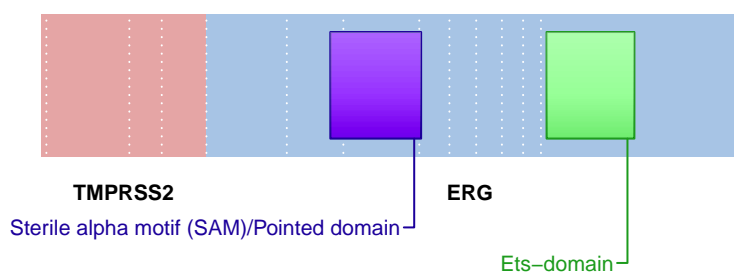
**SUPPORTING READ COUNT**

Split reads = 9  
Discordant mates = 303

- translocation
- duplication
- deletion
- inversion



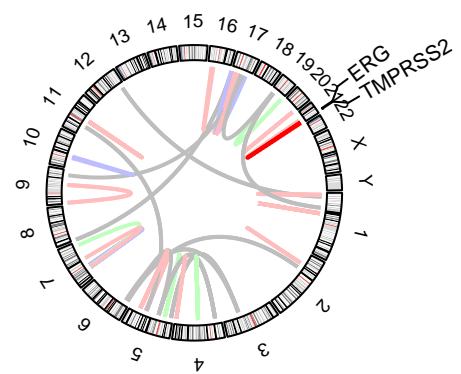
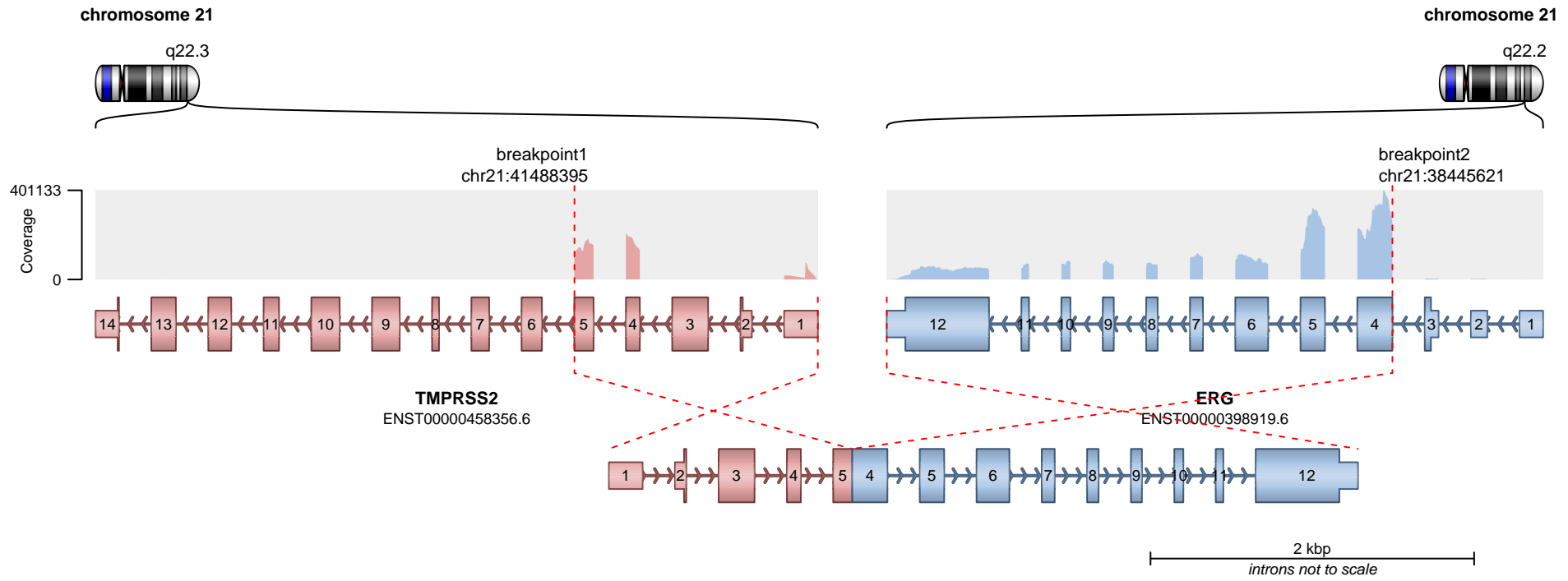
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



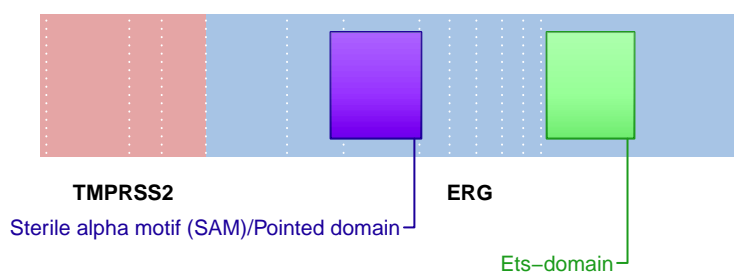
**SUPPORTING READ COUNT**

Split reads = 7  
Discordant mates = 303

- translocation
- duplication
- deletion
- inversion



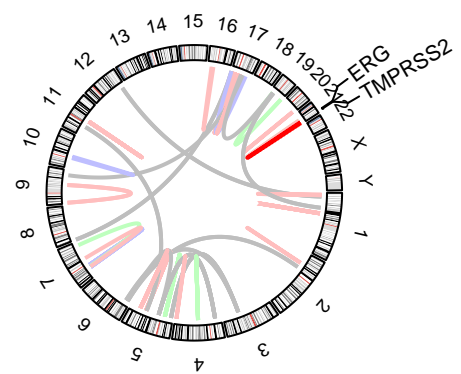
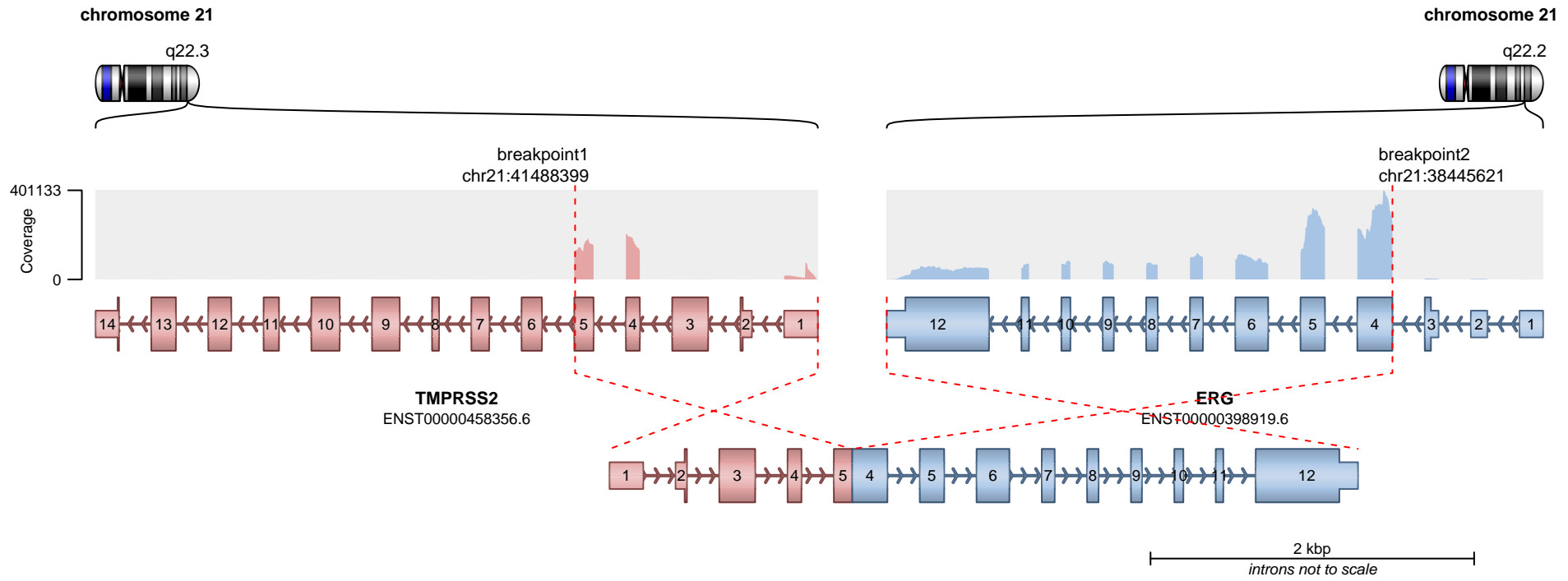
**RETAINED PROTEIN DOMAINS**  
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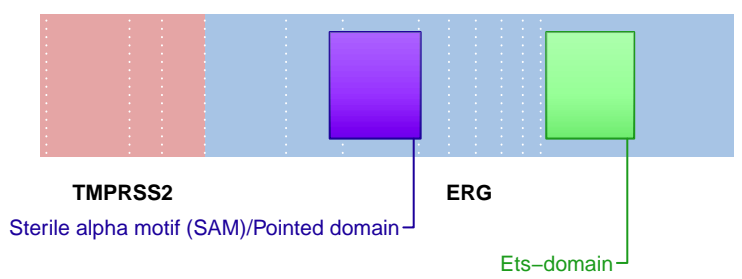
**SUPPORTING READ COUNT**

Split reads = 7  
Discordant mates = 303

- translocation
- duplication
- deletion
- inversion



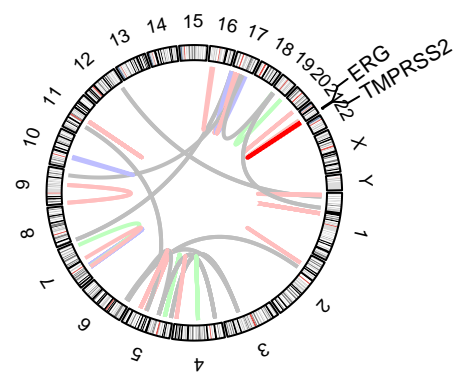
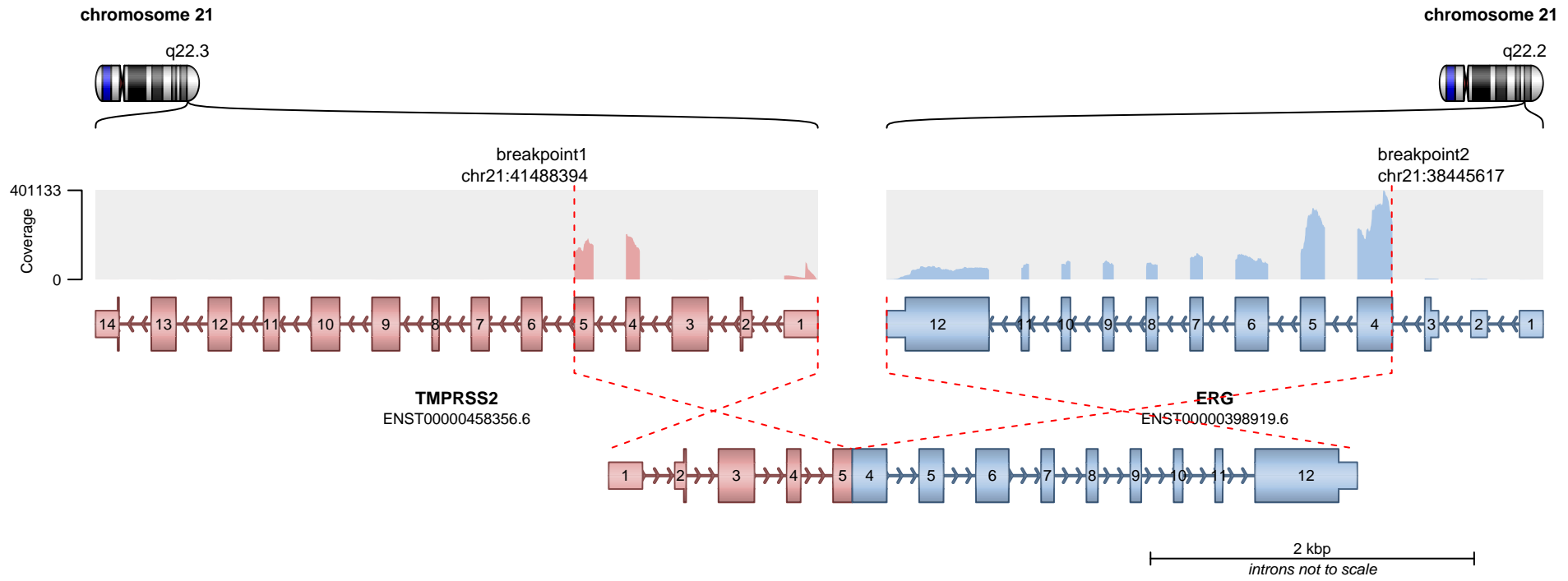
**RETAINED PROTEIN DOMAINS**  
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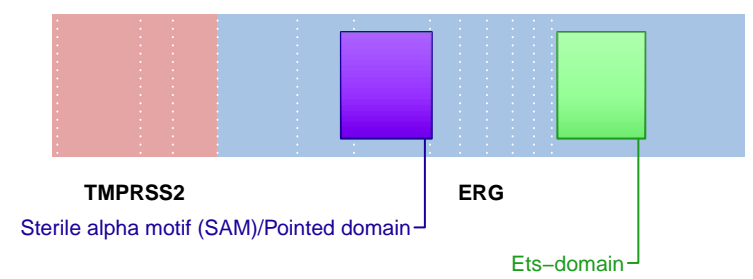
**SUPPORTING READ COUNT**

Split reads = 12  
Discordant mates = 283

- translocation
- duplication
- deletion
- inversion



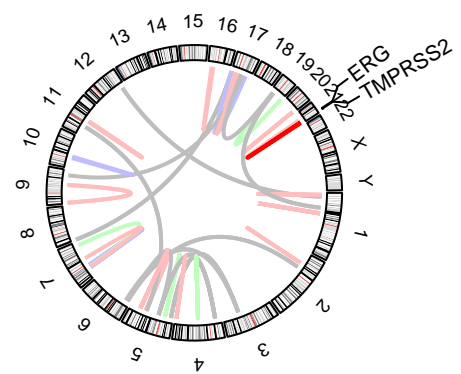
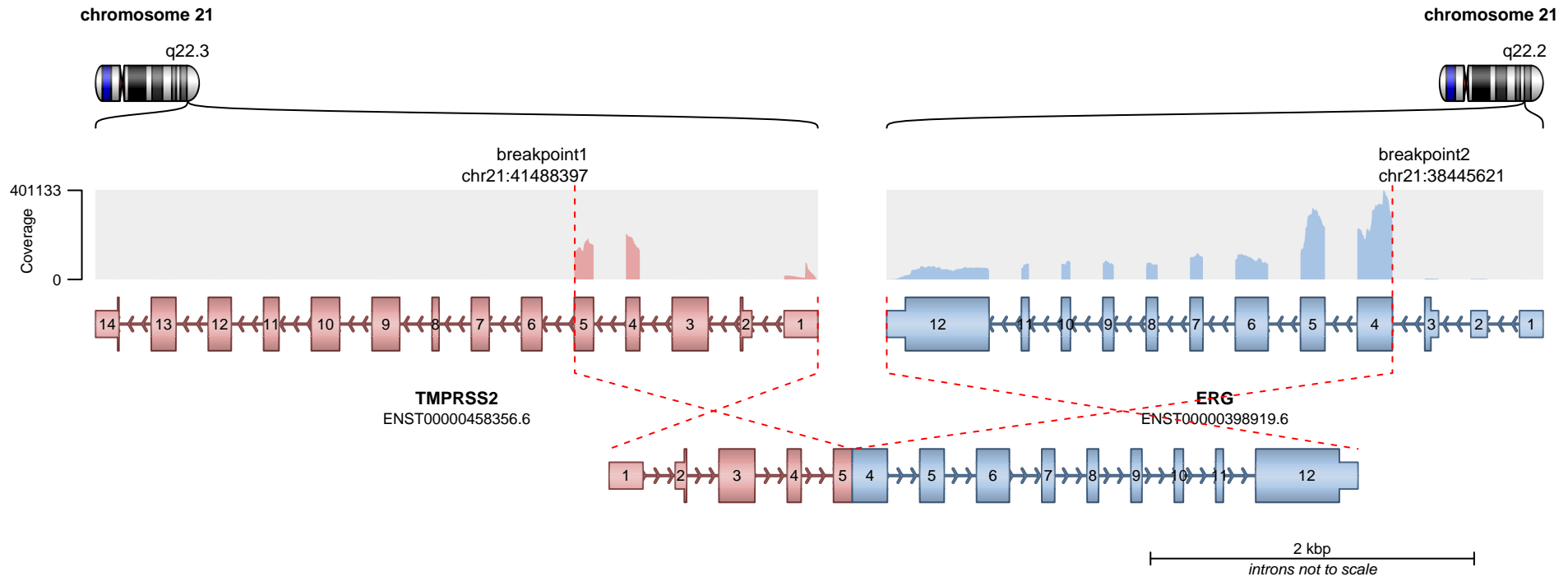
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



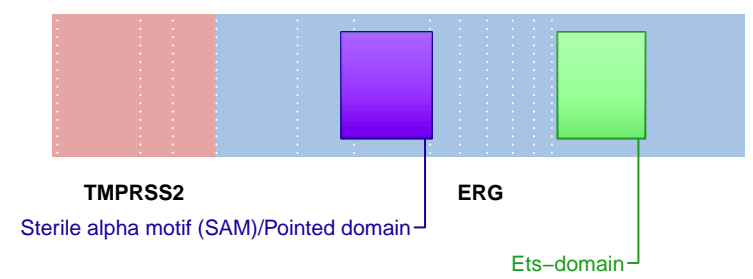
**SUPPORTING READ COUNT**

Split reads = 12  
Discordant mates = 273

- translocation
- duplication
- deletion
- inversion



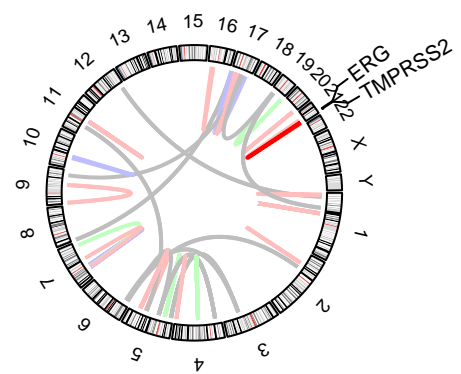
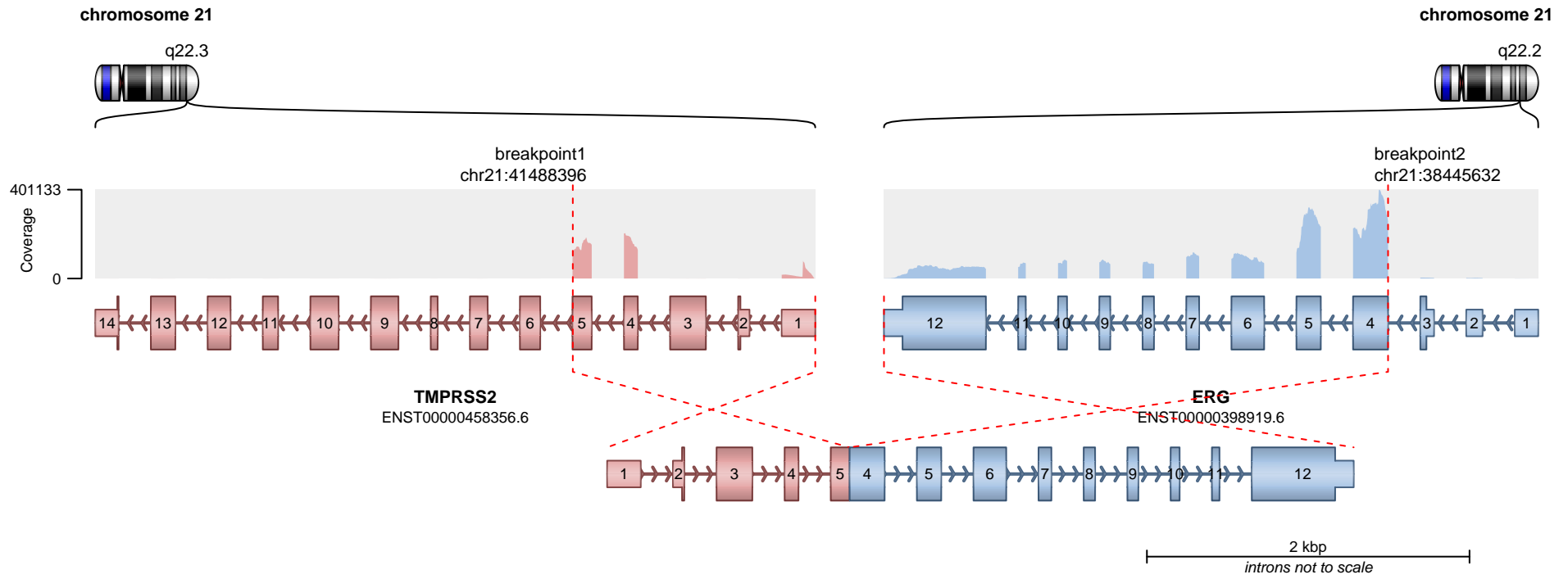
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



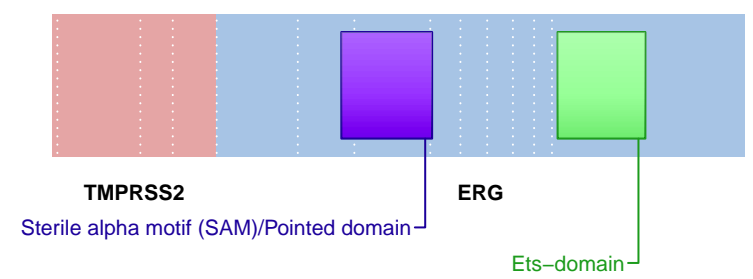
**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 303

- translocation
- duplication
- deletion
- inversion



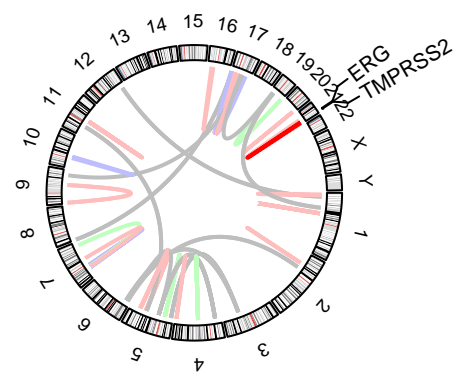
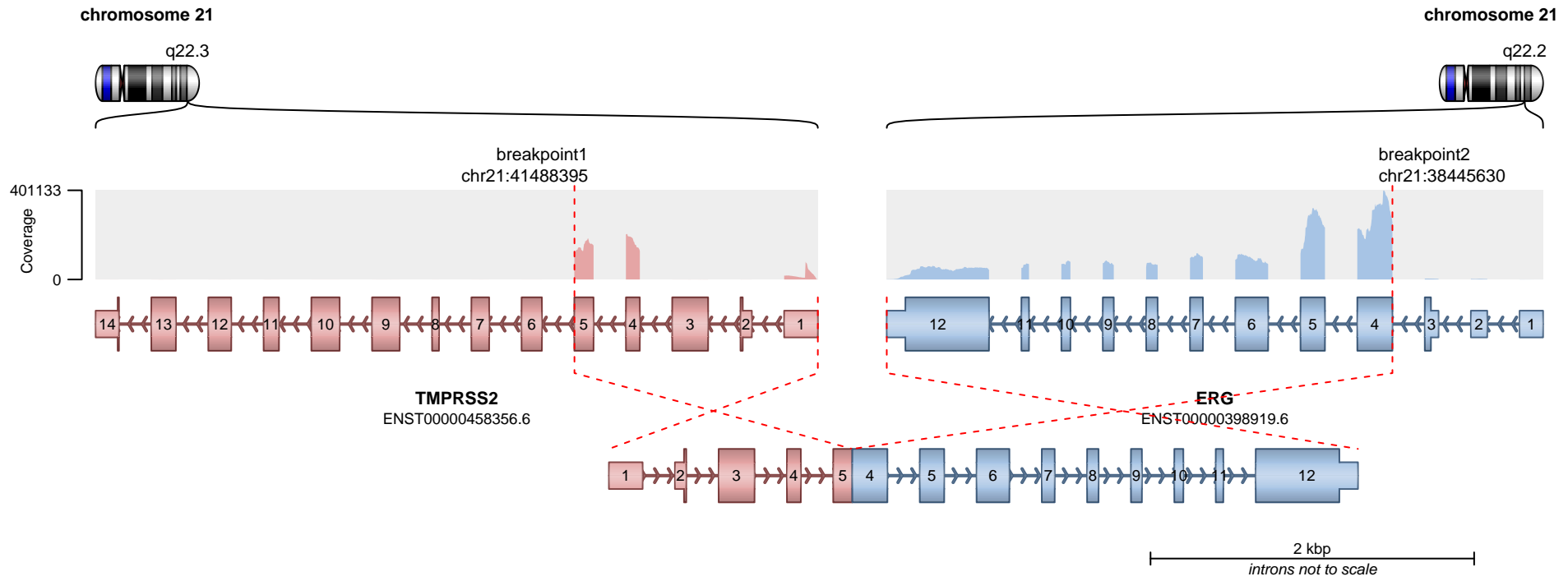
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



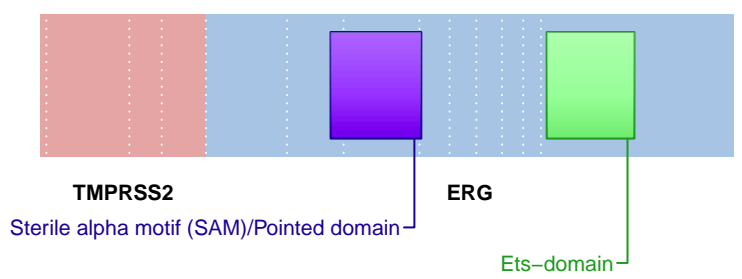
**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 303

- translocation
- duplication
- deletion
- inversion



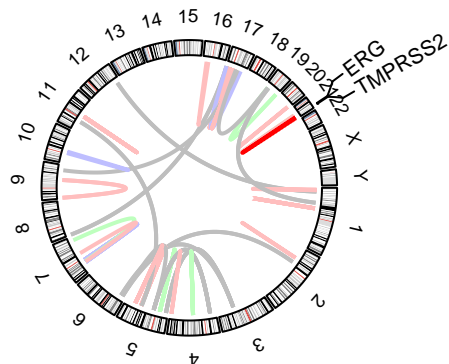
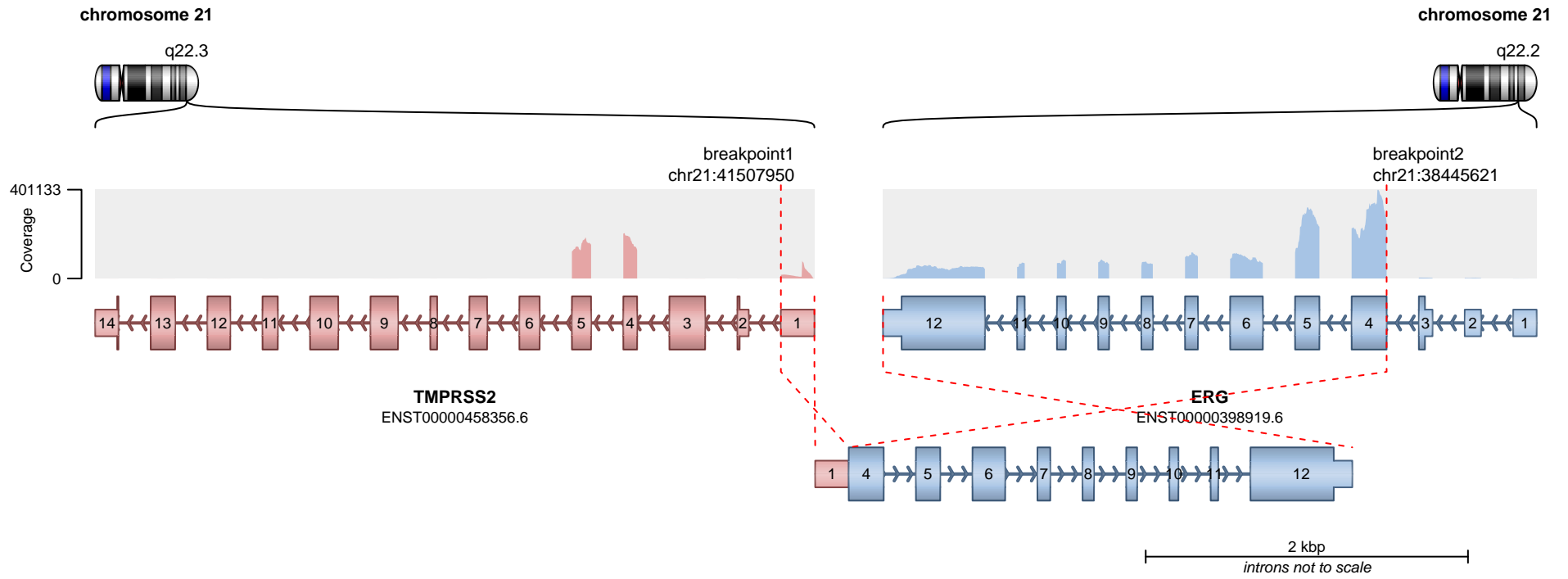
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



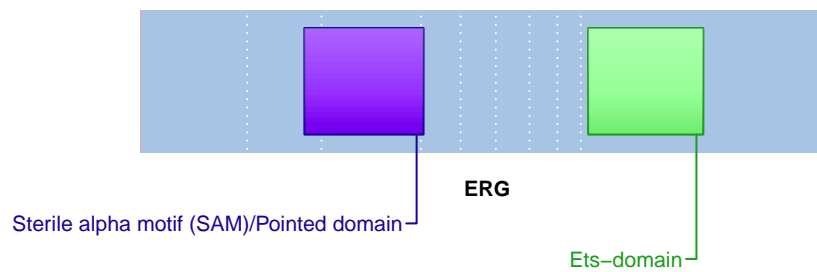
**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 303

- translocation
- duplication
- deletion
- inversion



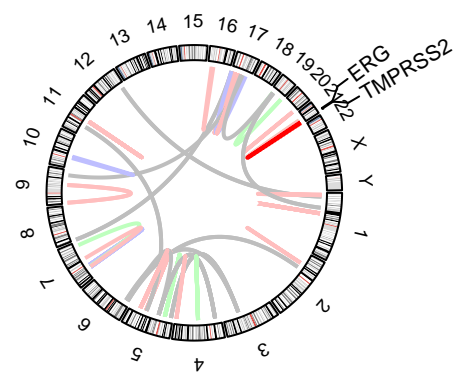
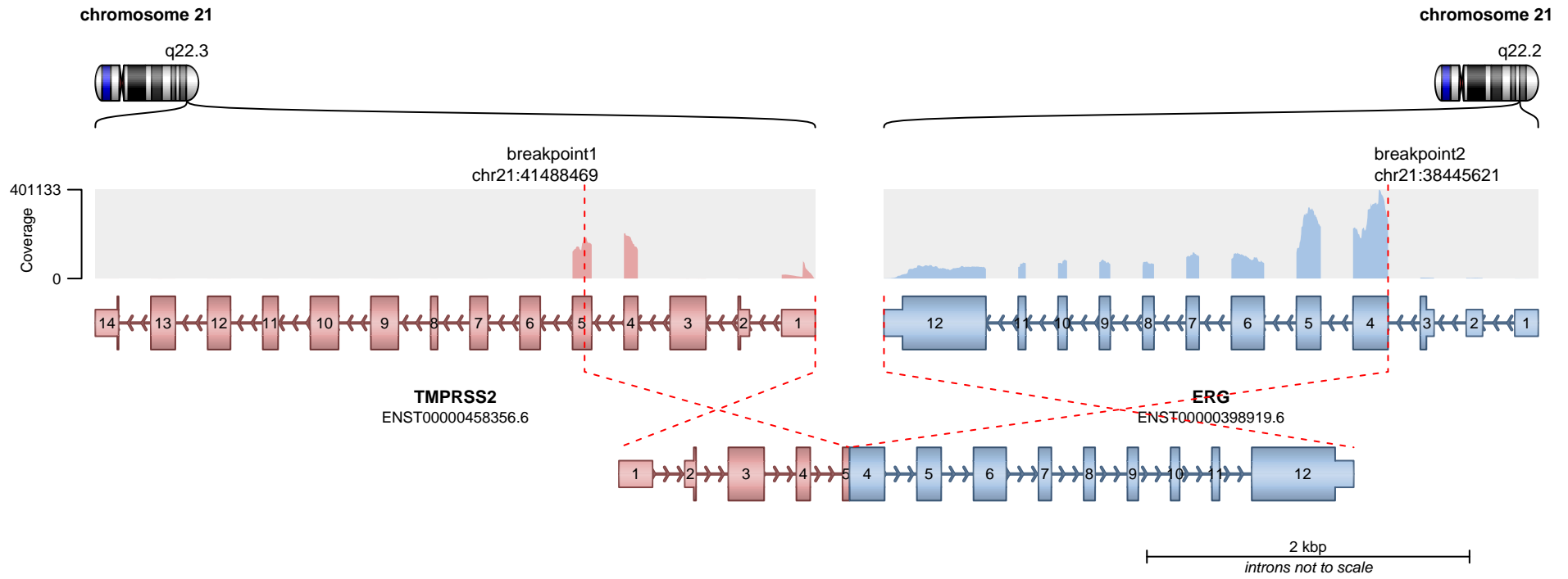
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



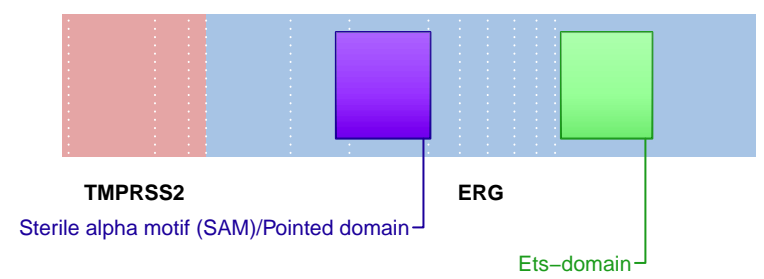
**SUPPORTING READ COUNT**

Split reads = 63  
Discordant mates = 2

- translocation
- duplication
- deletion
- inversion



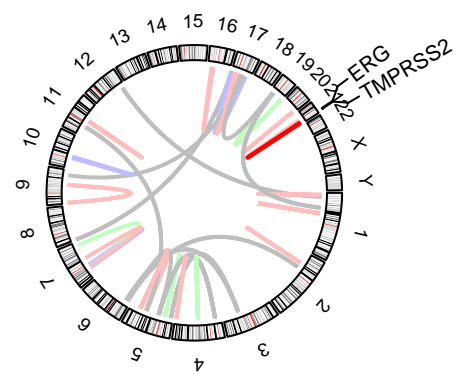
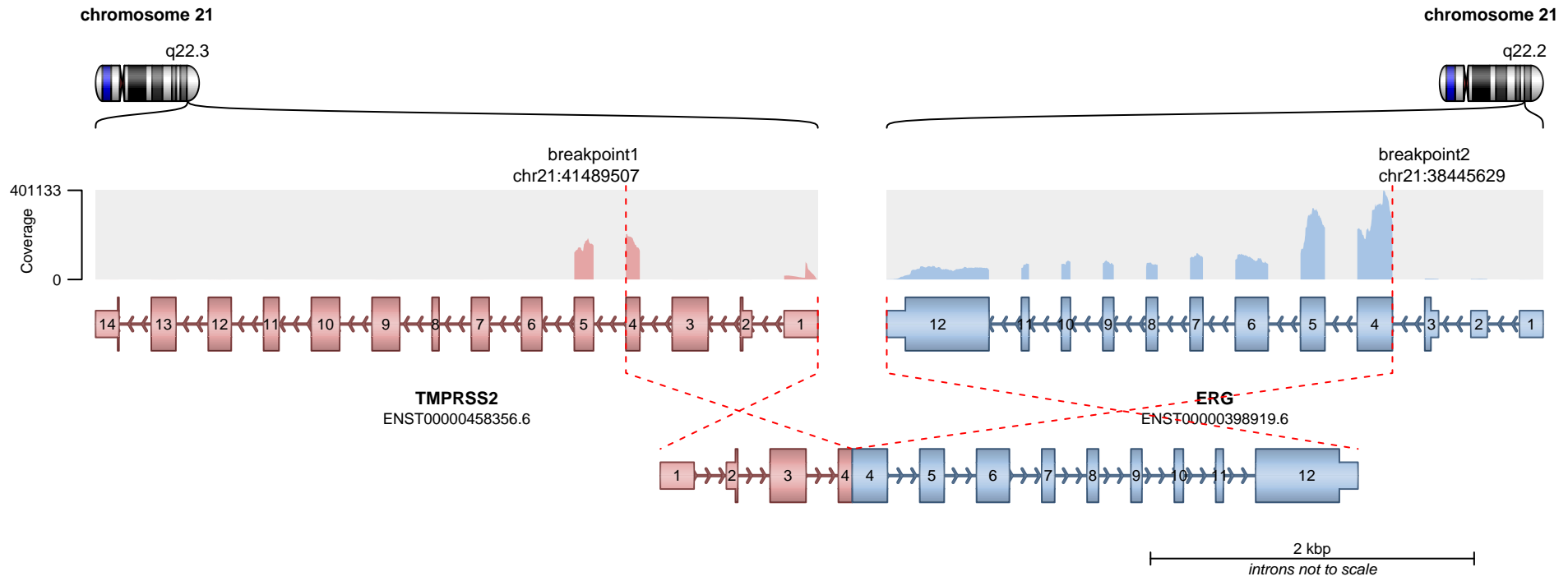
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



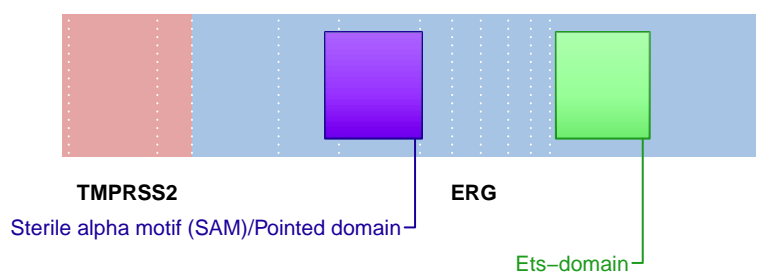
**SUPPORTING READ COUNT**

Split reads = 23  
Discordant mates = 77

- translocation
- duplication
- deletion
- inversion



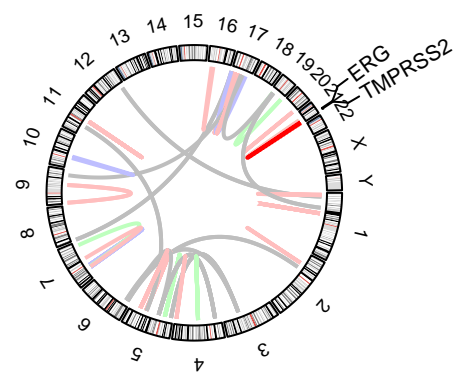
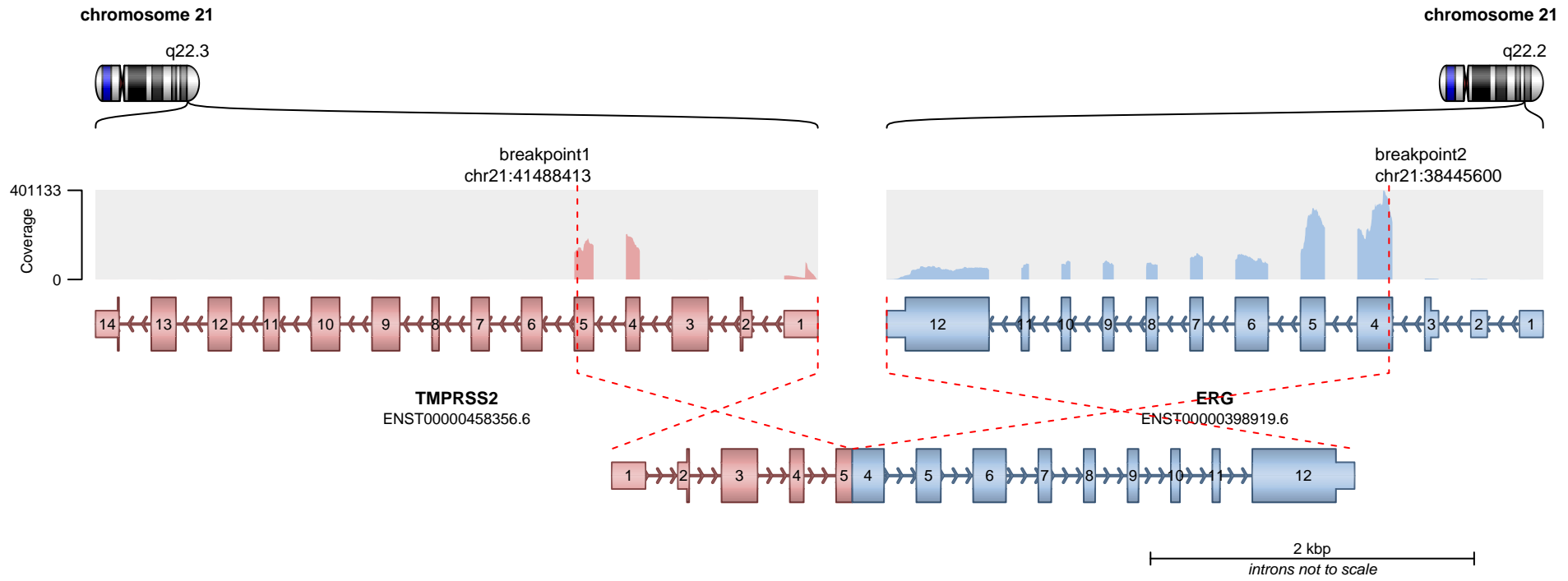
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



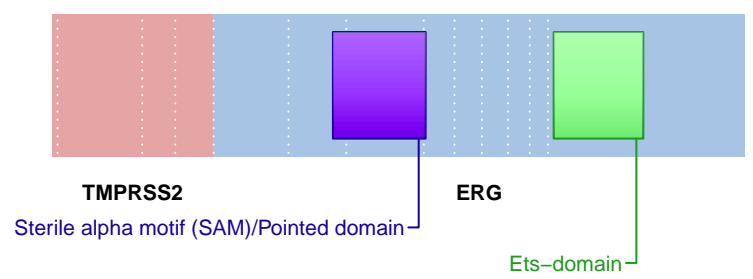
**SUPPORTING READ COUNT**

Split reads = 28  
Discordant mates = 40

- translocation
- duplication
- deletion
- inversion



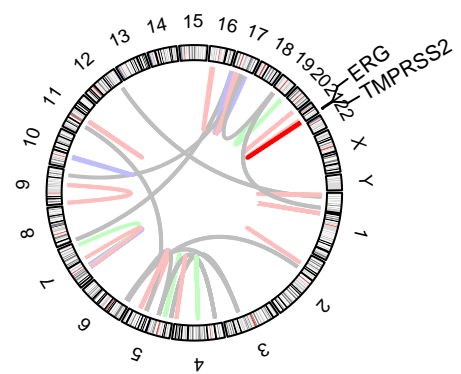
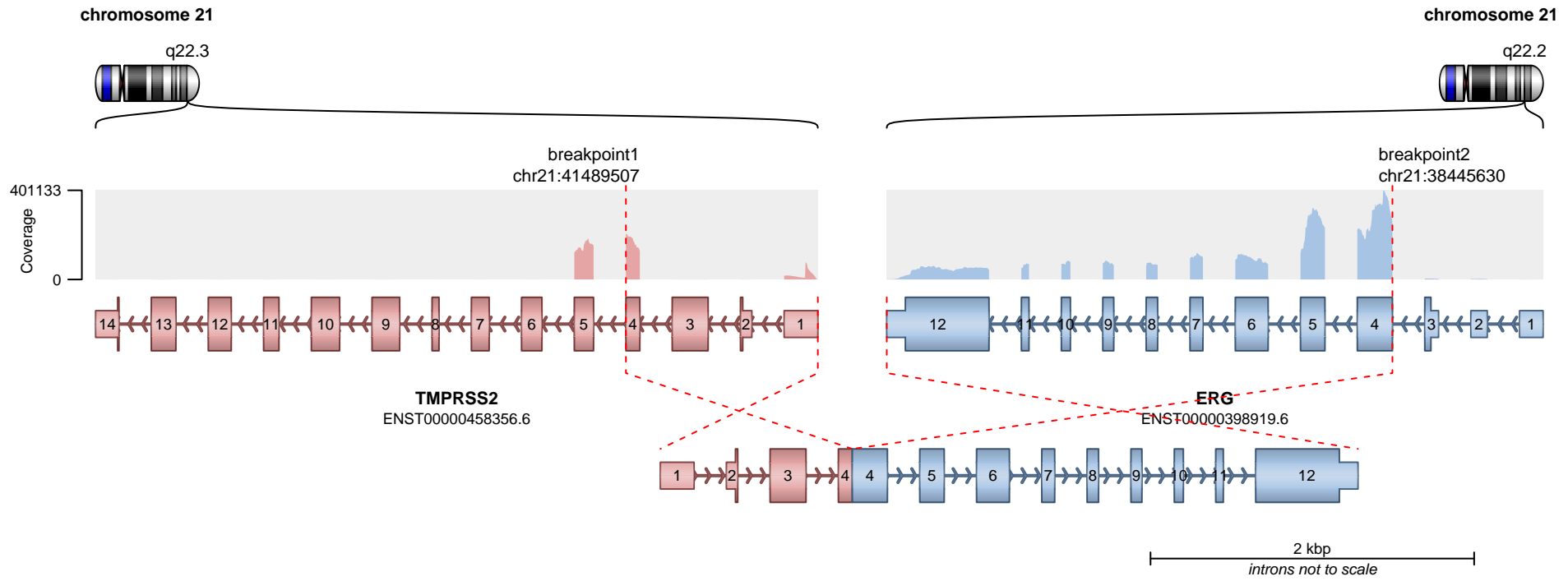
**RETAINED PROTEIN DOMAINS**  
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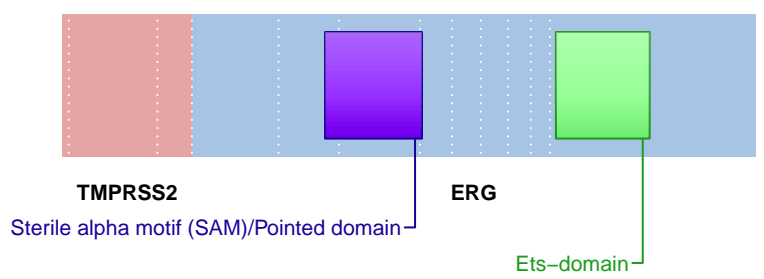
**SUPPORTING READ COUNT**

Split reads = 6  
Discordant mates = 108

- translocation
- duplication
- deletion
- inversion



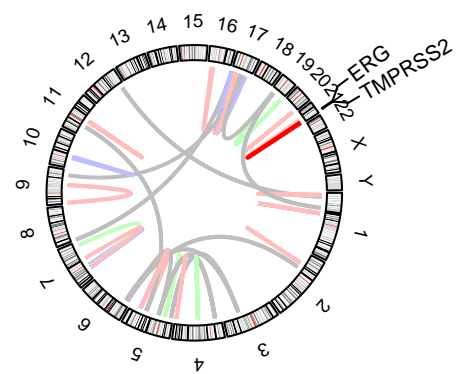
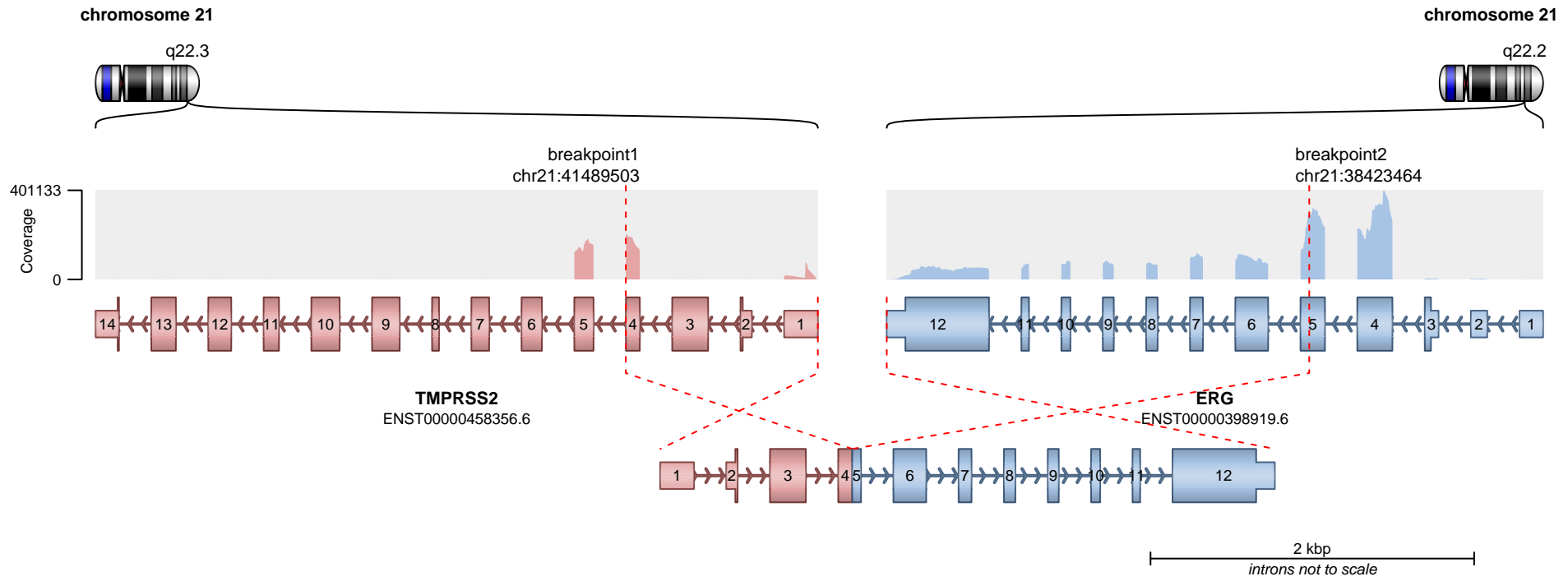
**RETAINED PROTEIN DOMAINS**  
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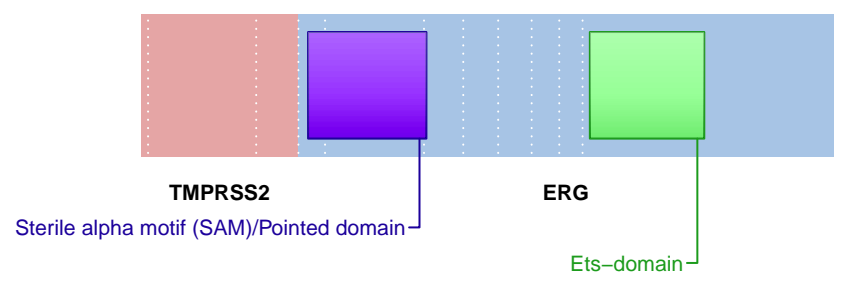
**SUPPORTING READ COUNT**

Split reads = 12  
Discordant mates = 40

- translocation
- duplication
- deletion
- inversion



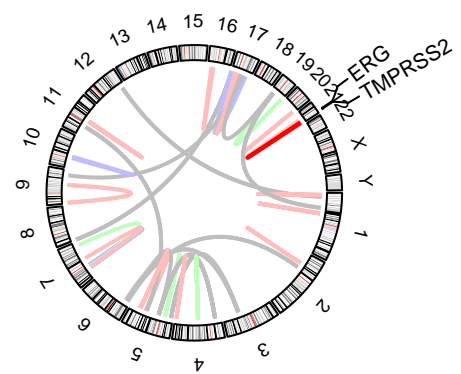
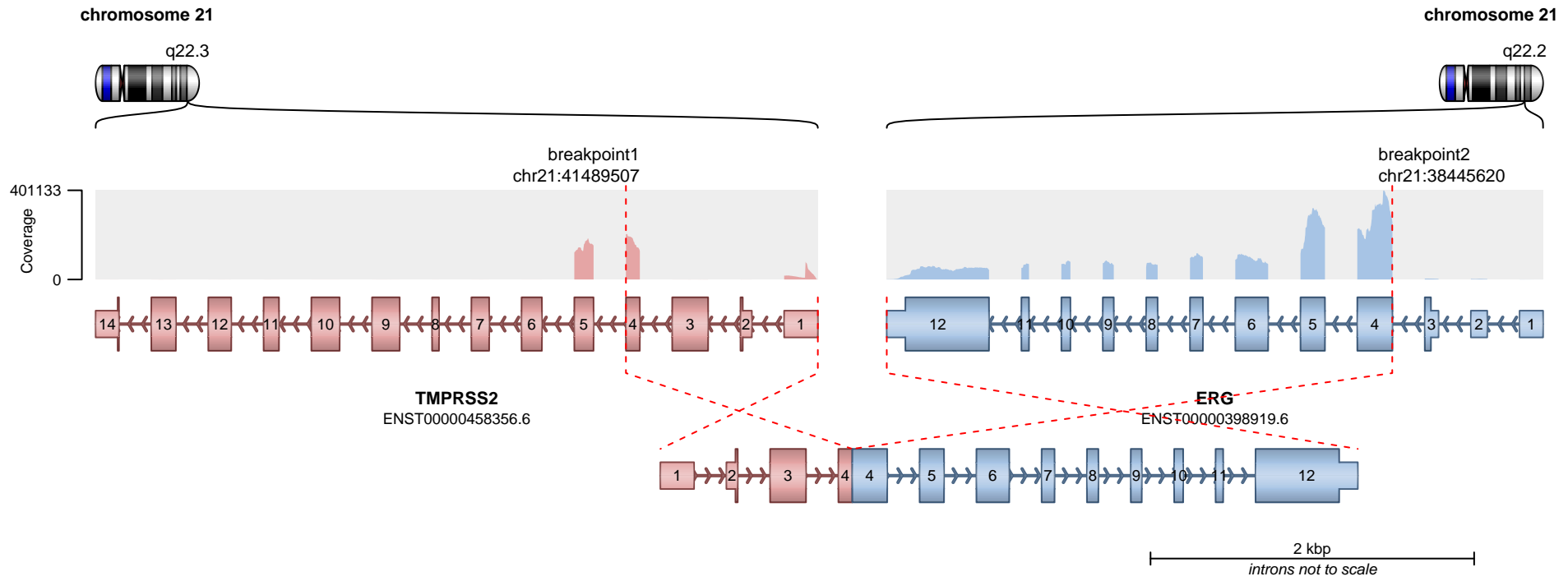
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



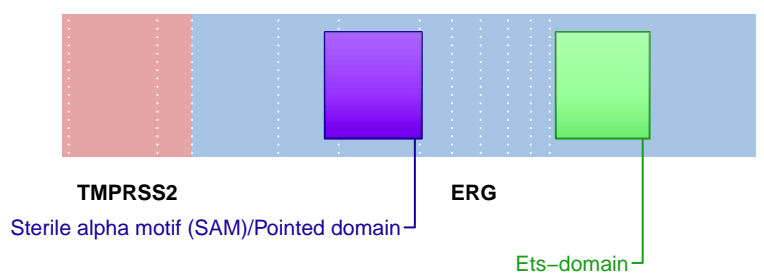
**SUPPORTING READ COUNT**

Split reads = 14  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



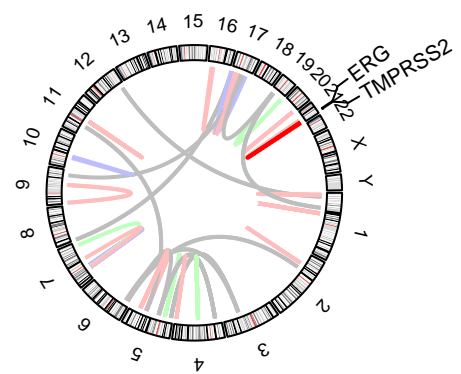
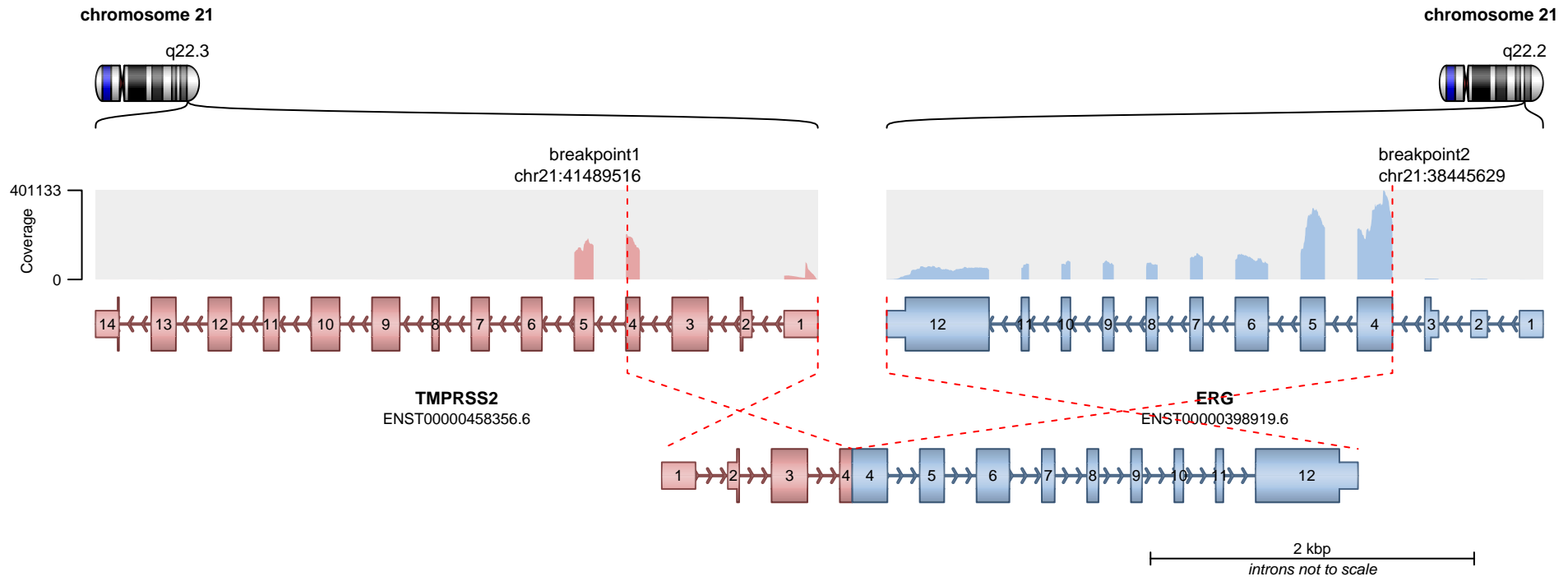
**RETAINED PROTEIN DOMAINS**  
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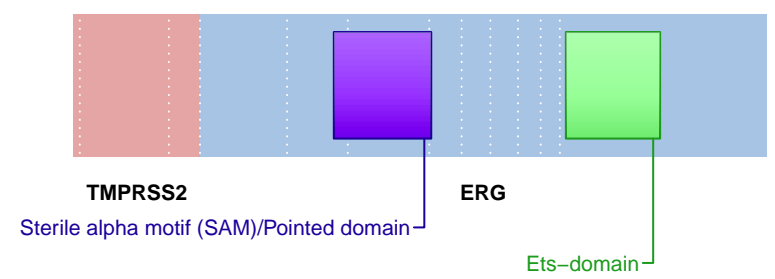
**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 40

- translocation
- duplication
- deletion
- inversion



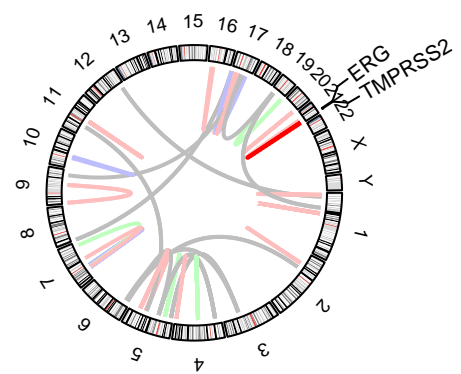
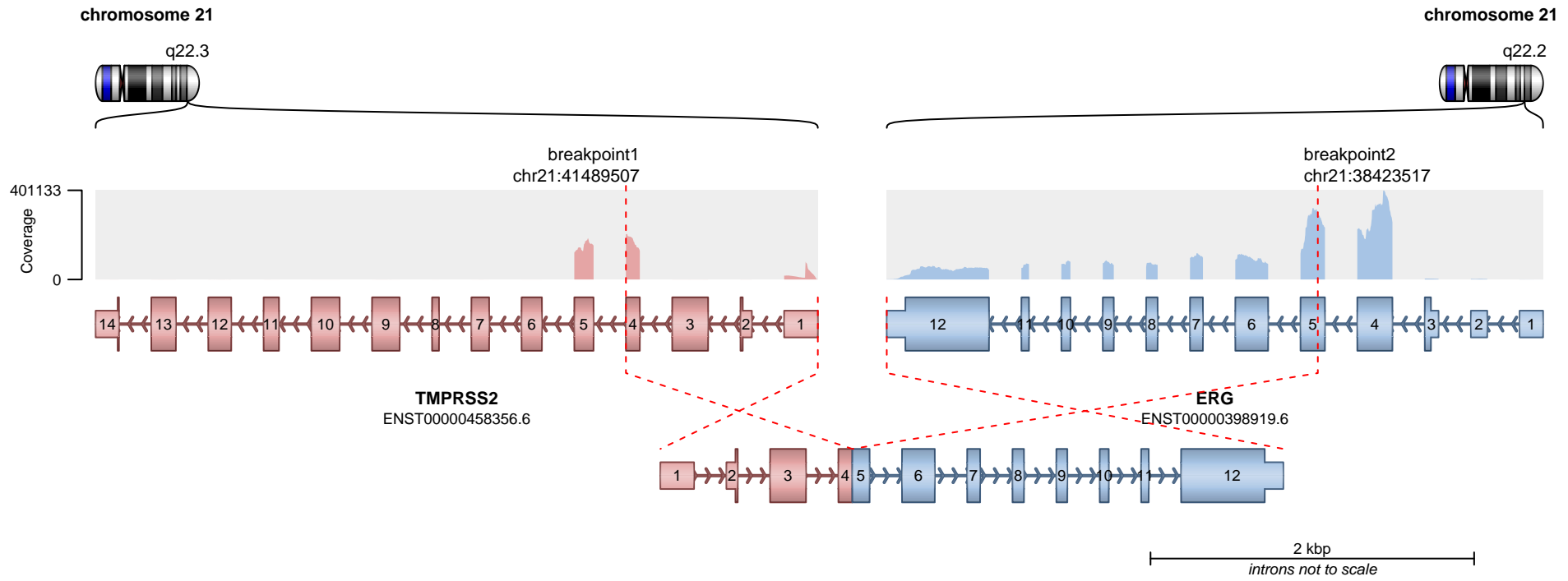
**RETAINED PROTEIN DOMAINS**  
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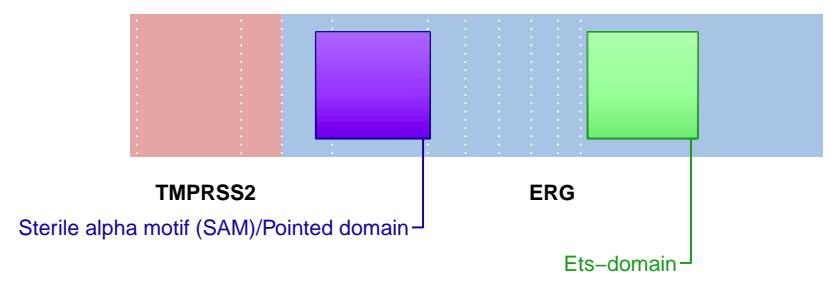
**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 22

- translocation
- duplication
- deletion
- inversion



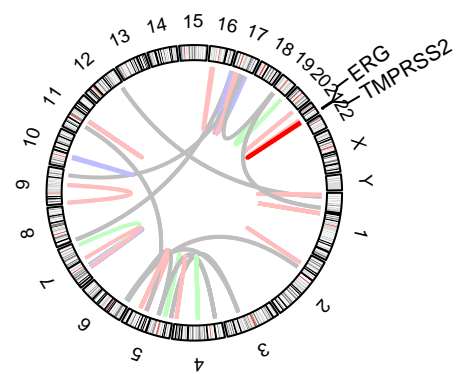
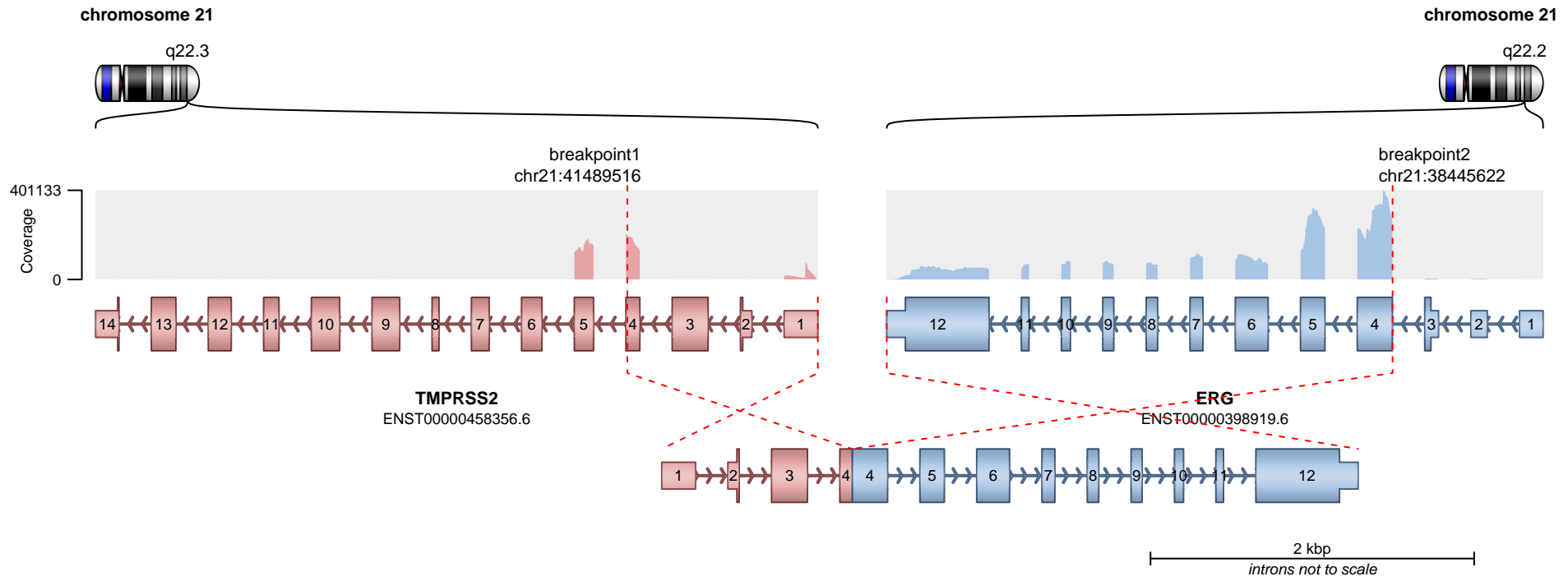
**RETAINED PROTEIN DOMAINS**  
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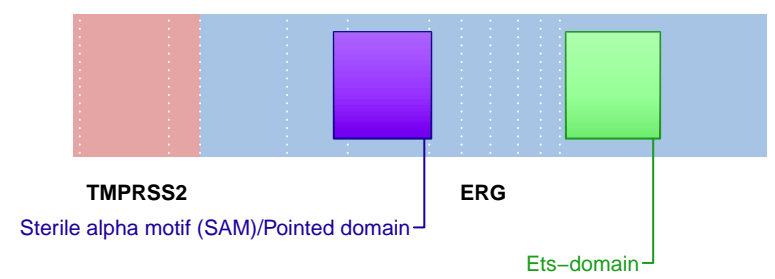
**SUPPORTING READ COUNT**

Split reads = 9  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



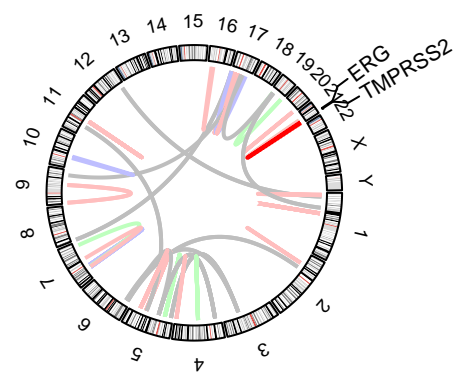
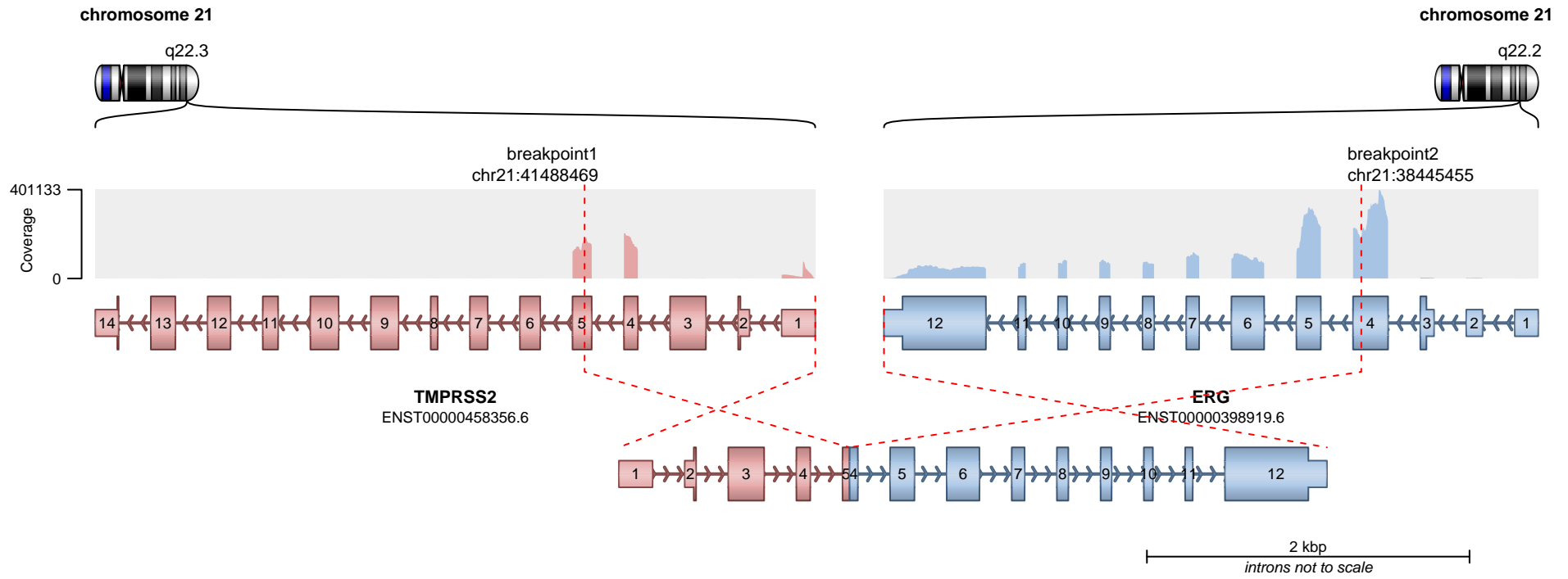
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



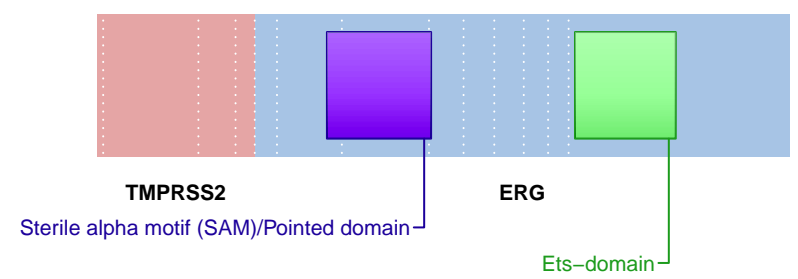
**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 22

- translocation
- duplication
- deletion
- inversion



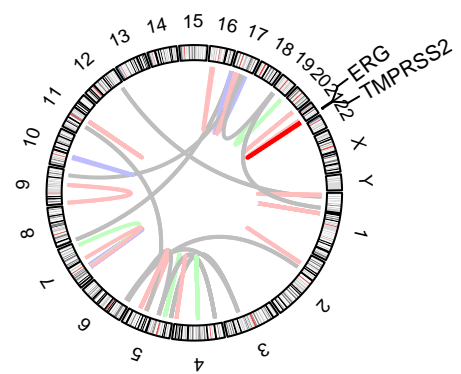
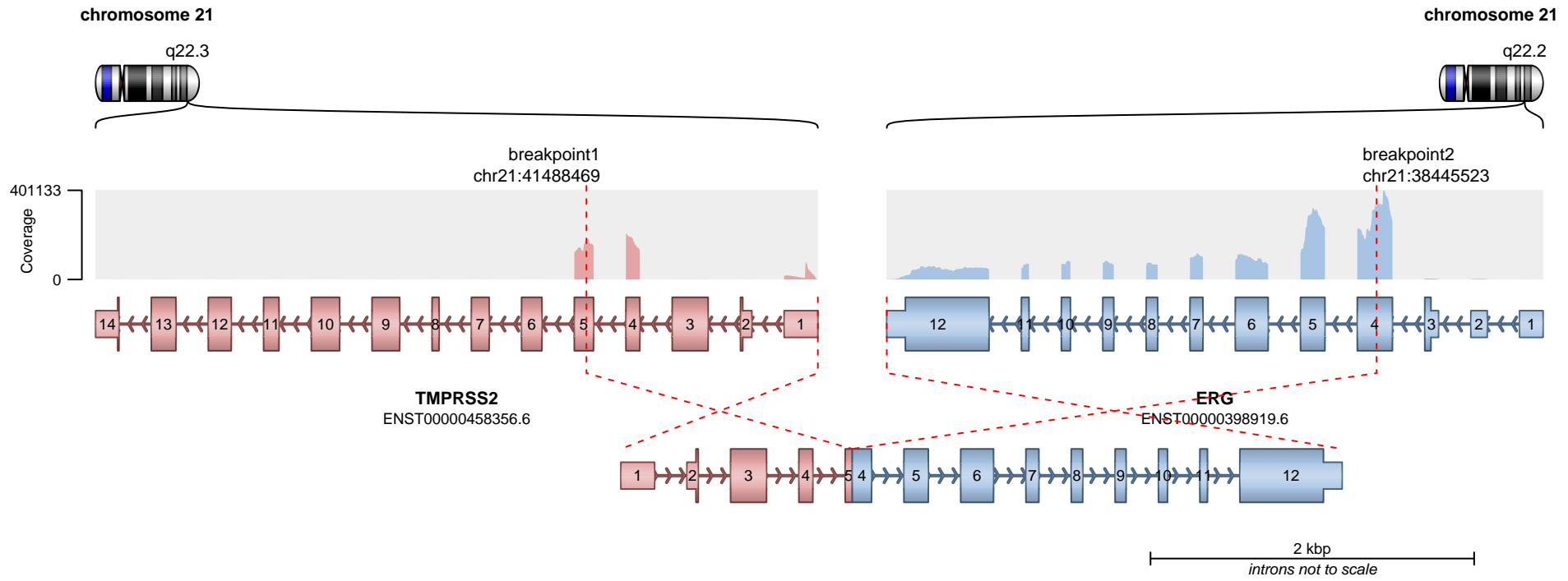
**RETAINED PROTEIN DOMAINS**  
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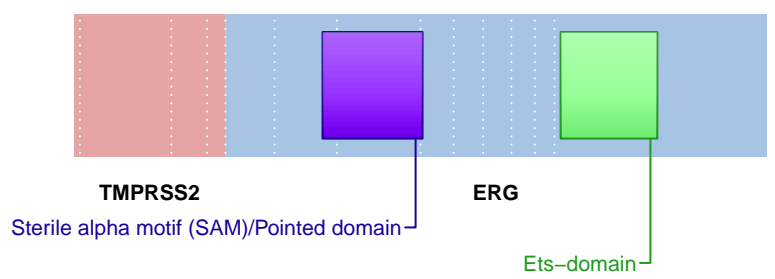
**SUPPORTING READ COUNT**

Split reads = 6  
Discordant mates = 9

- translocation
- duplication
- deletion
- inversion



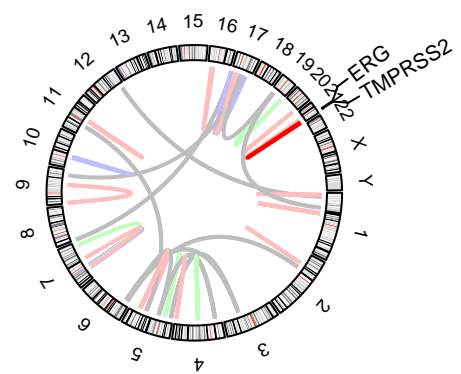
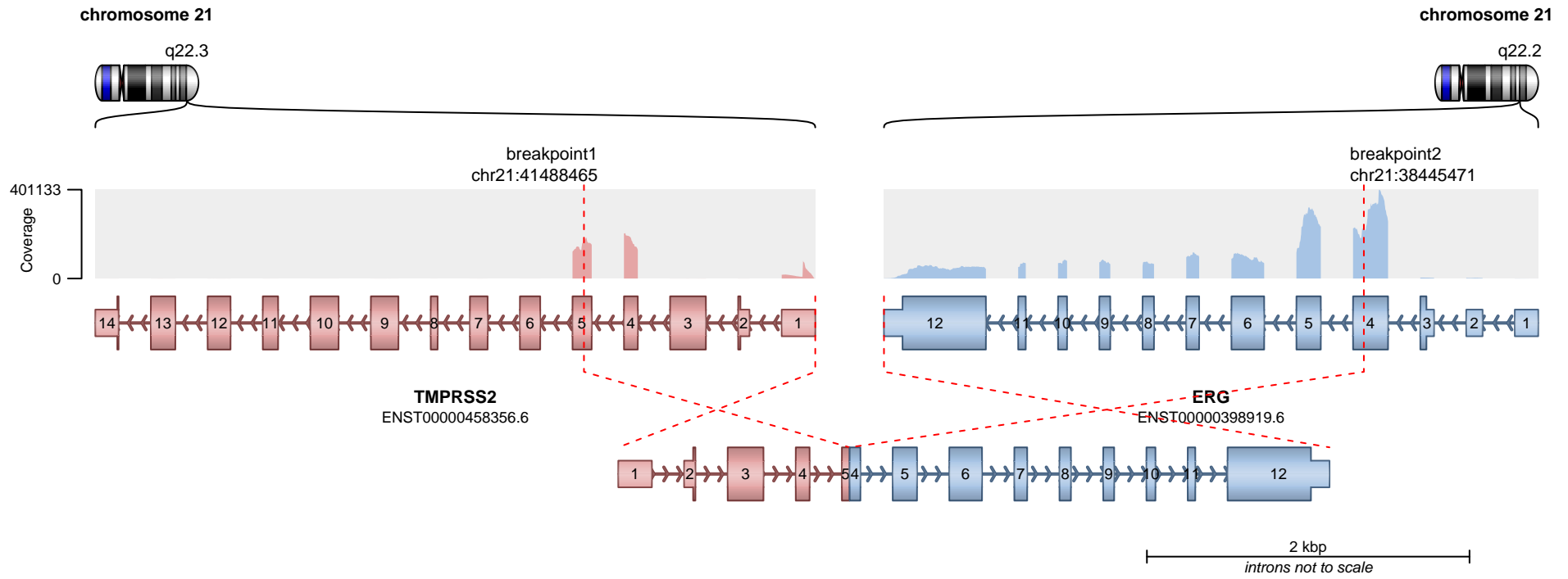
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



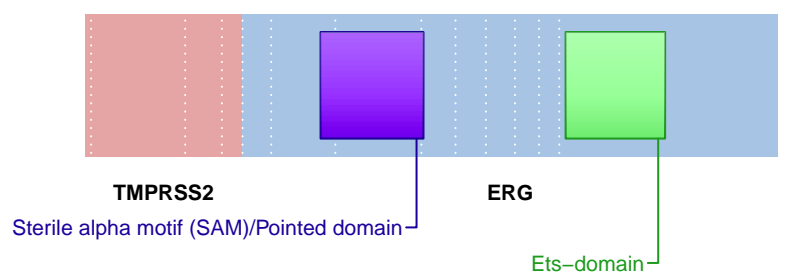
**SUPPORTING READ COUNT**

Split reads = 5  
Discordant mates = 10

- translocation
- duplication
- deletion
- inversion



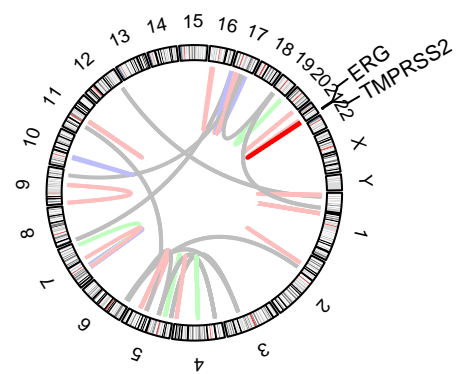
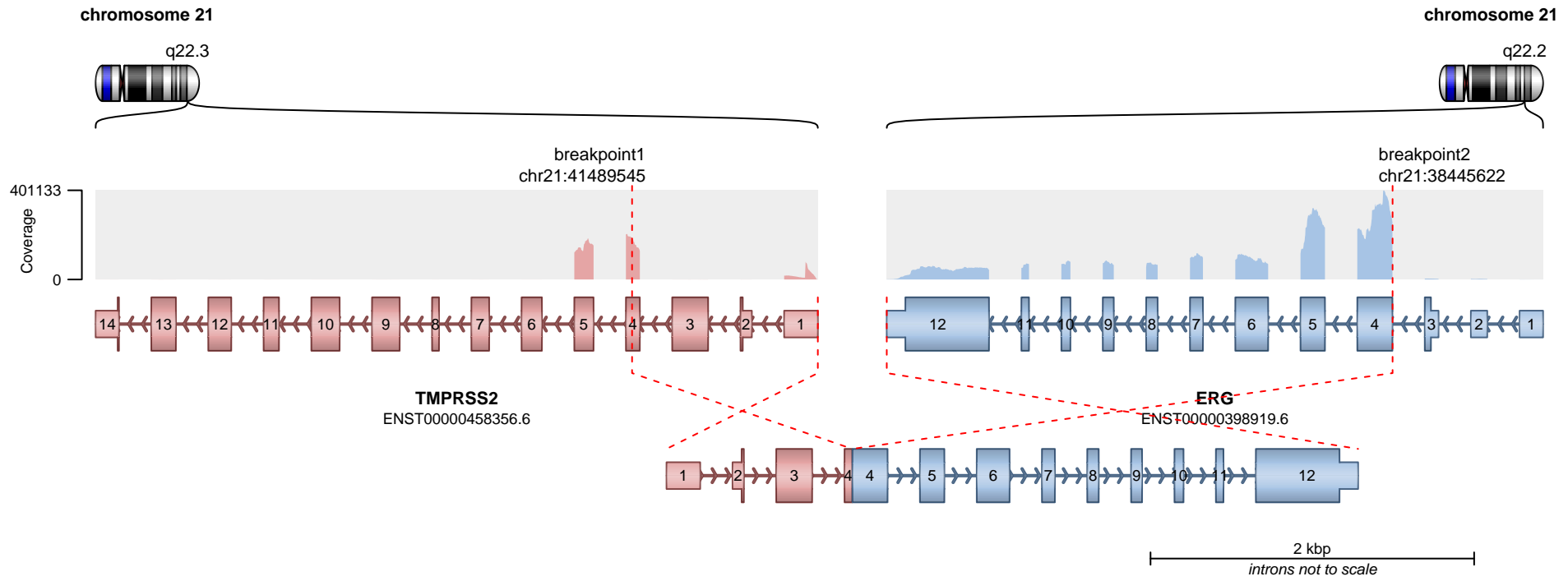
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



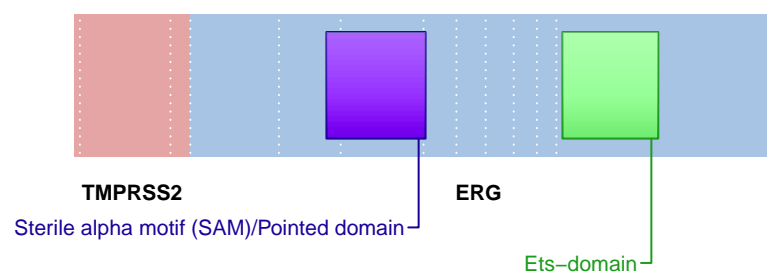
**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 13

- translocation
- duplication
- deletion
- inversion



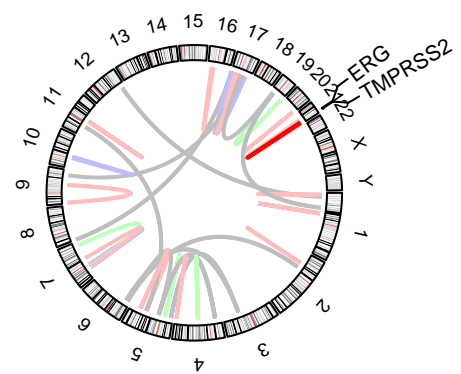
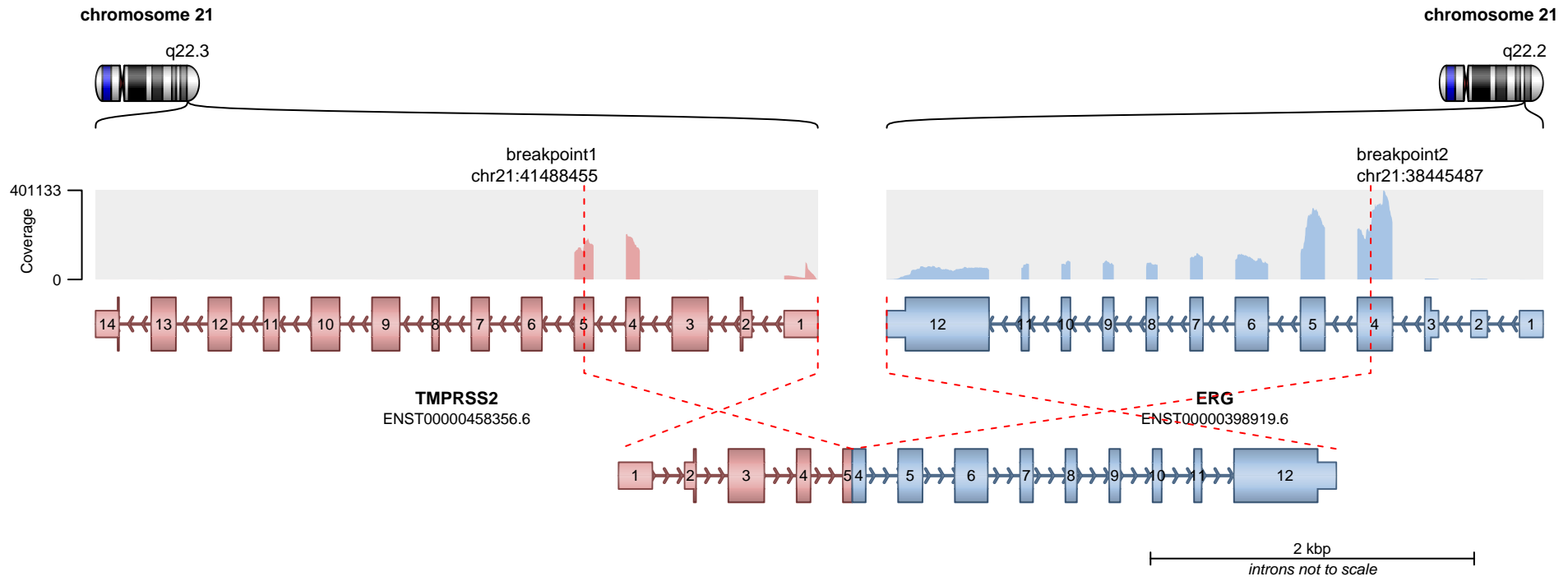
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



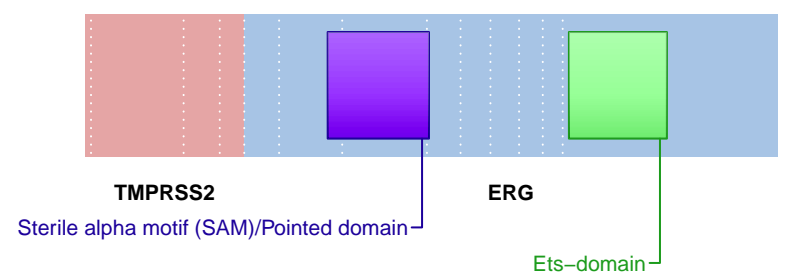
**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 11

- translocation
- duplication
- deletion
- inversion



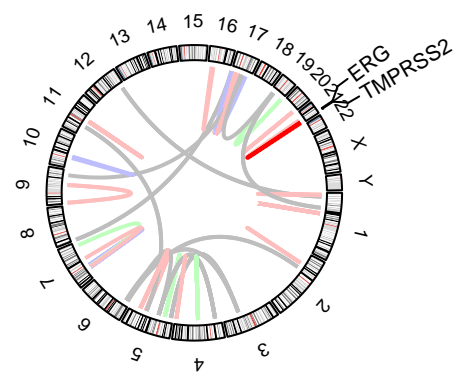
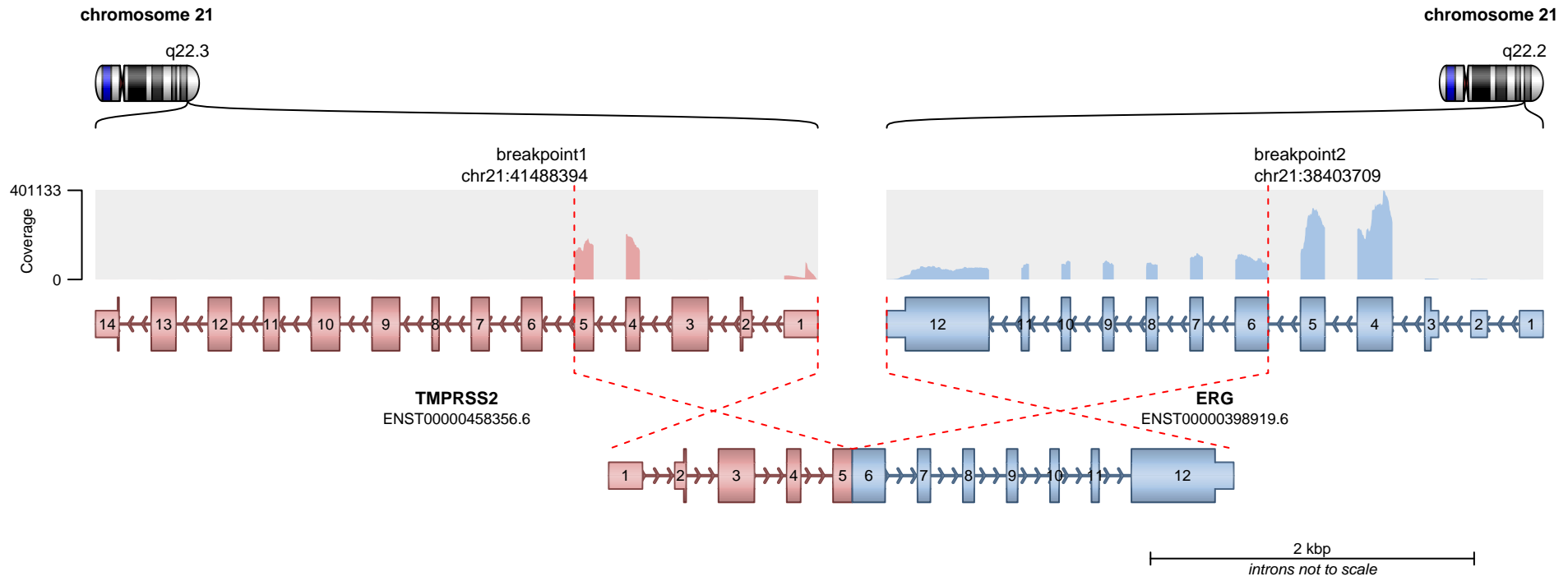
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



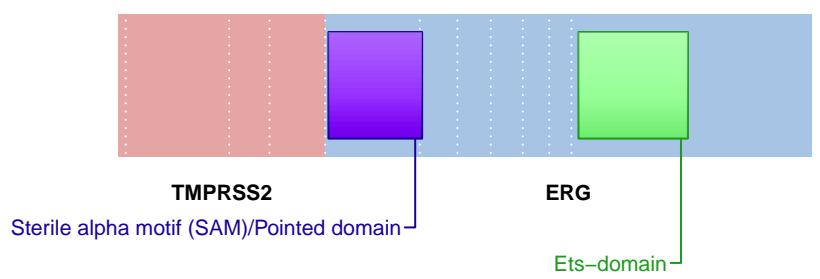
**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 15

- translocation
- duplication
- deletion
- inversion



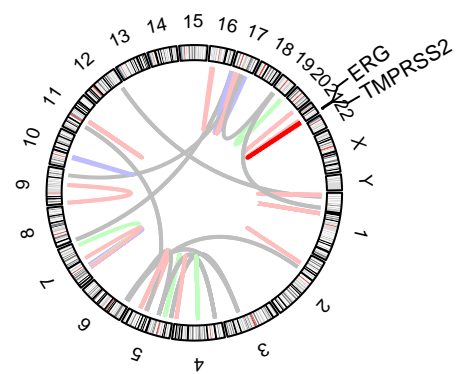
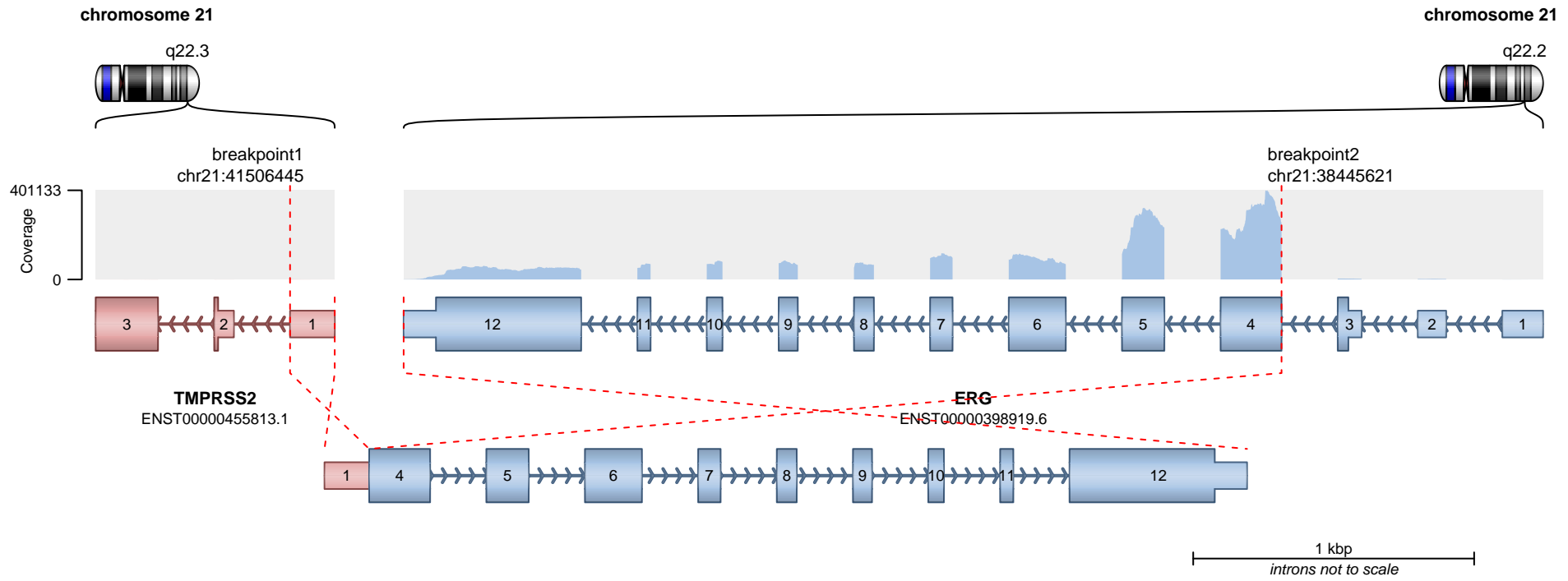
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

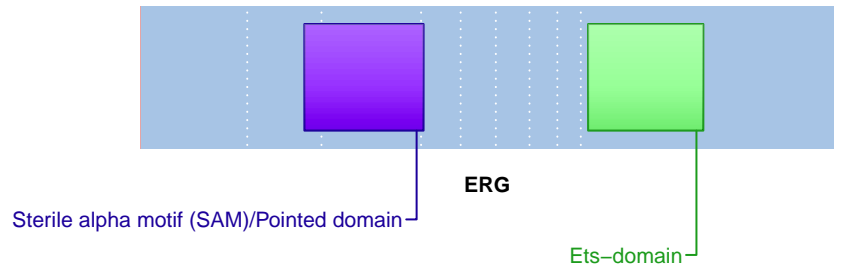
Split reads = 6  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



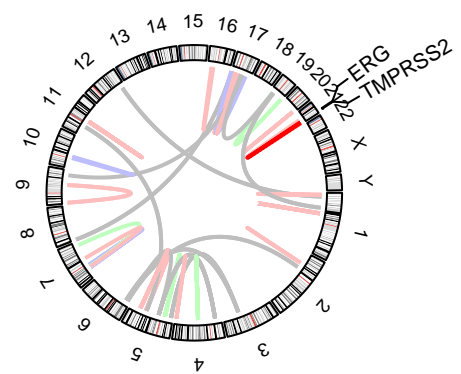
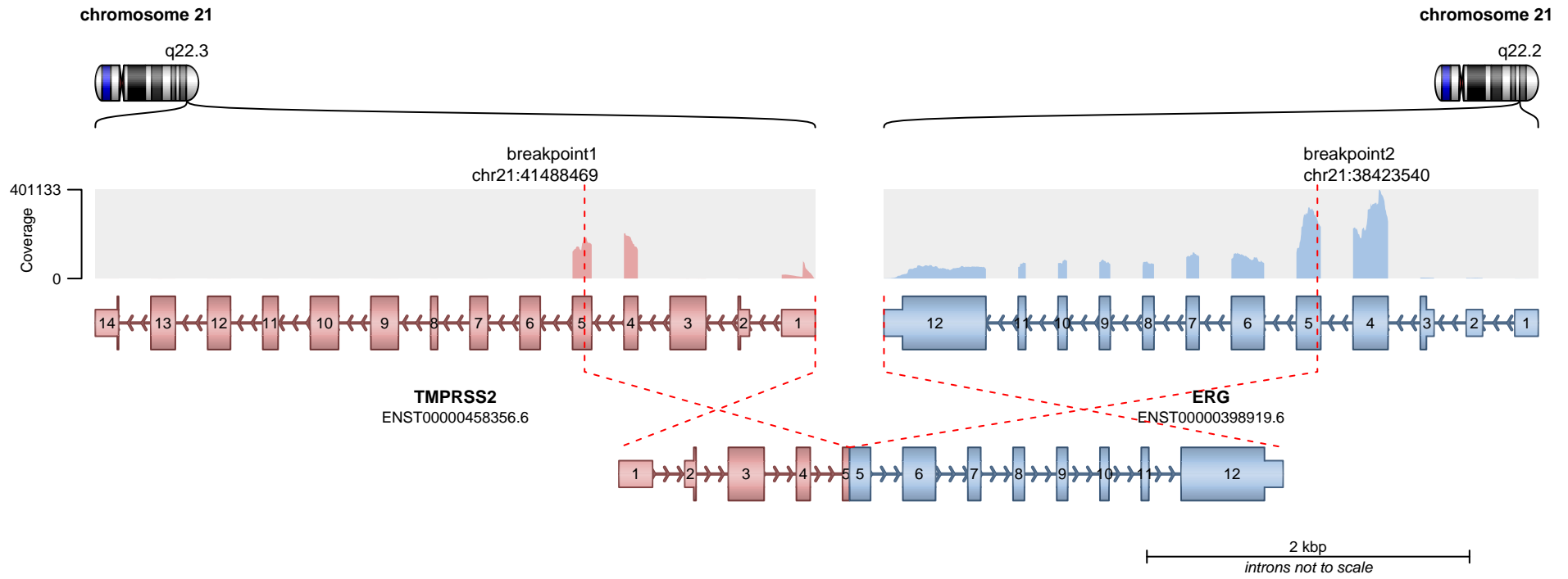
— translocation    — deletion  
— duplication    — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear

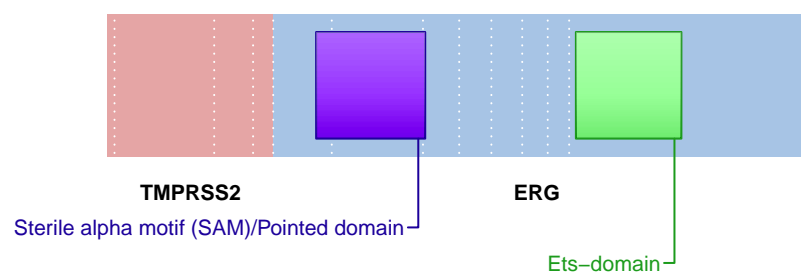


**SUPPORTING READ COUNT**

Split reads = 5  
Discordant mates = 2



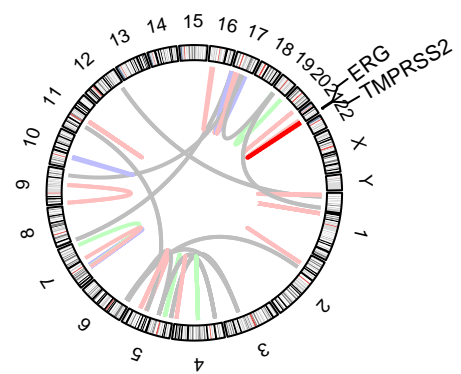
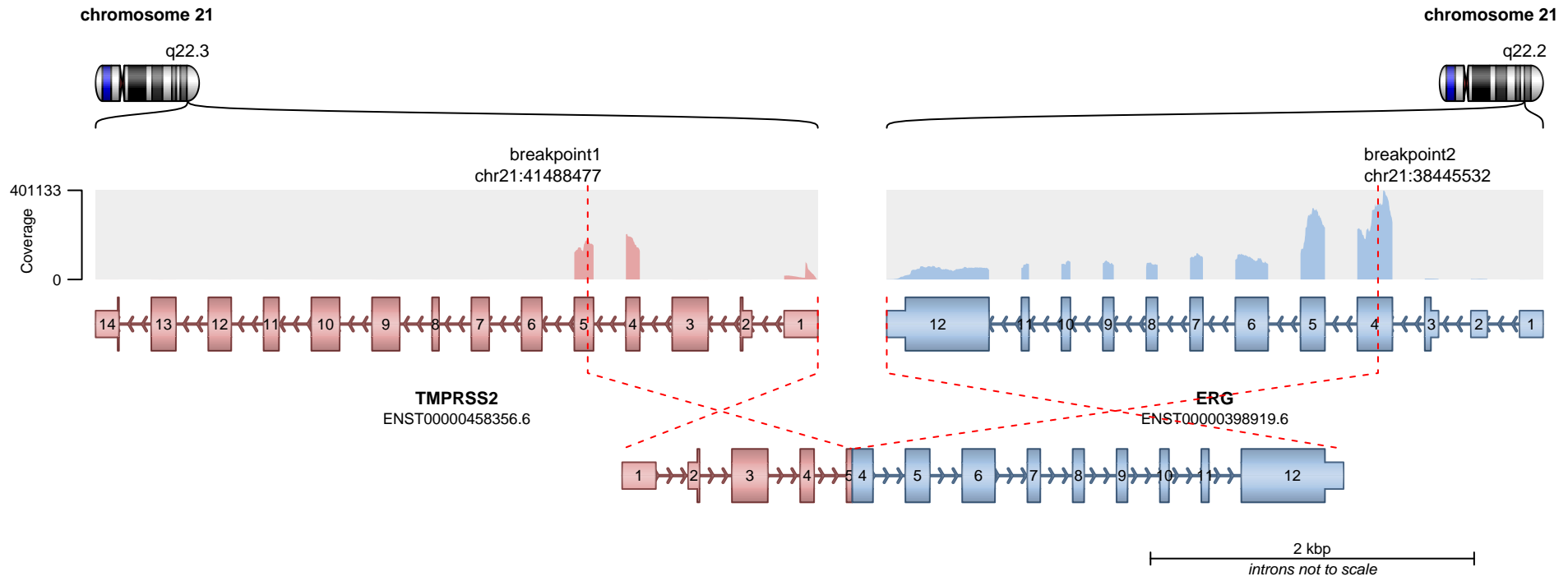
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



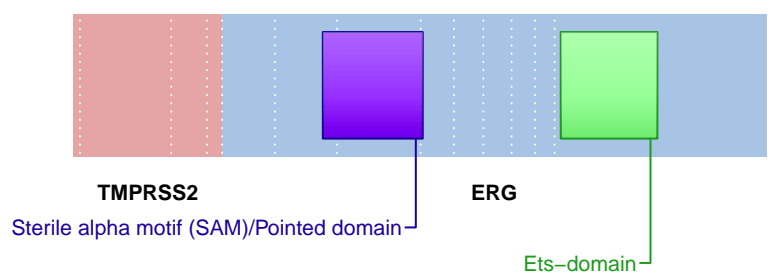
**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 2

- translocation
- duplication
- deletion
- inversion



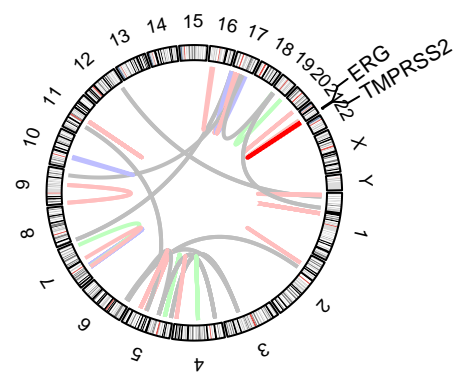
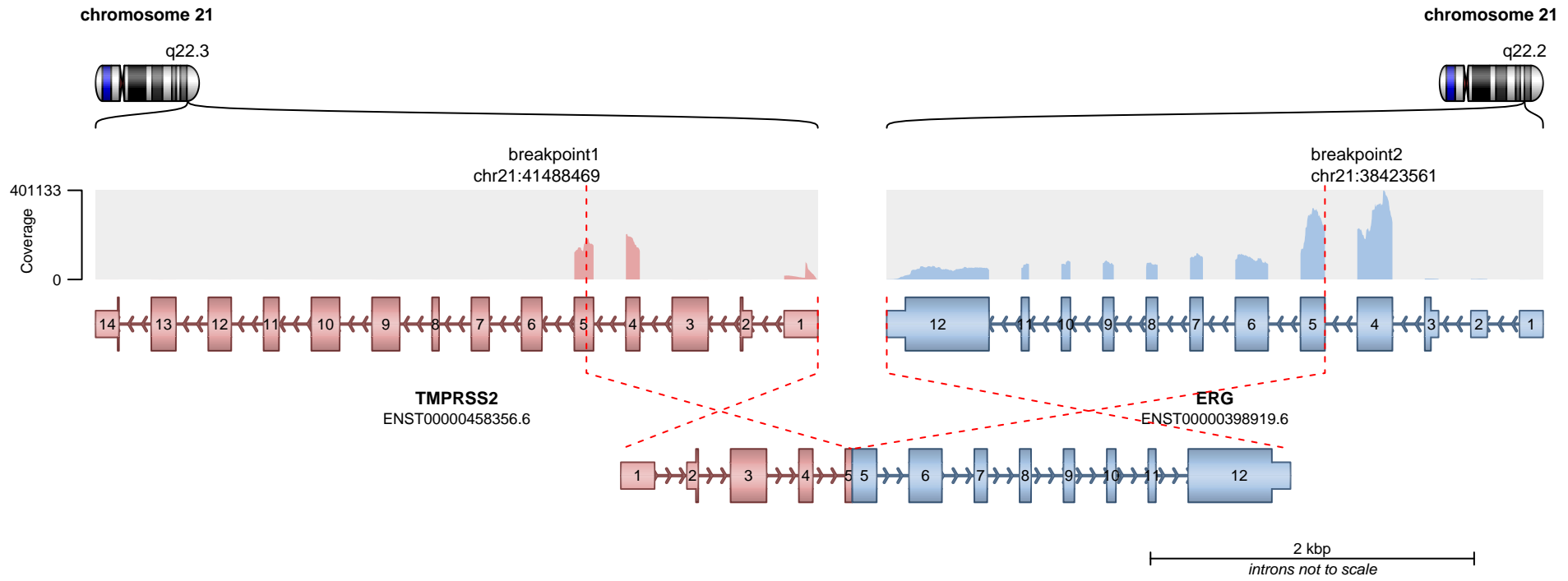
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



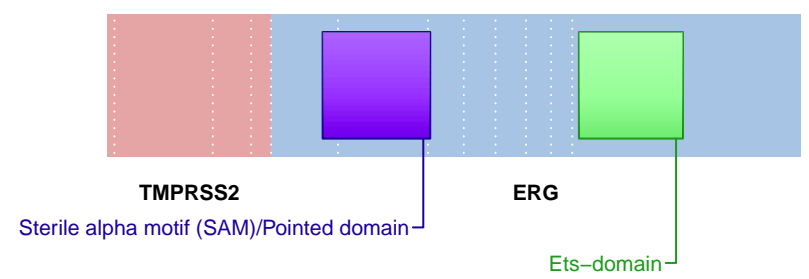
**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 4

- translocation
- duplication
- deletion
- inversion



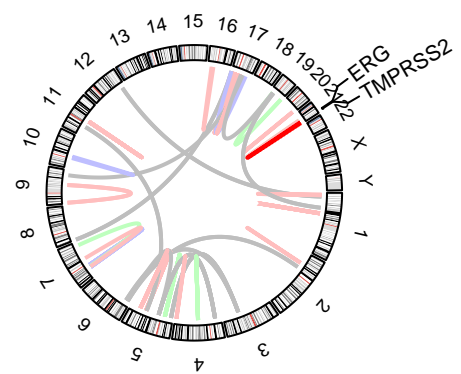
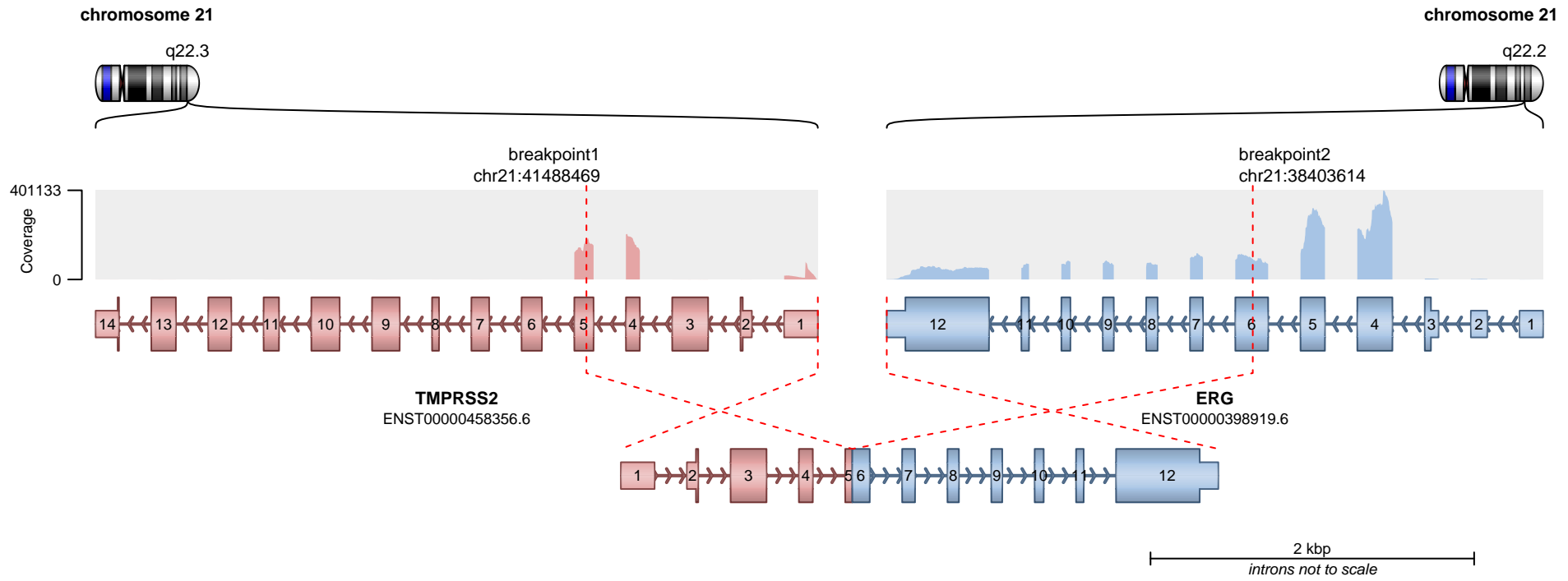
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



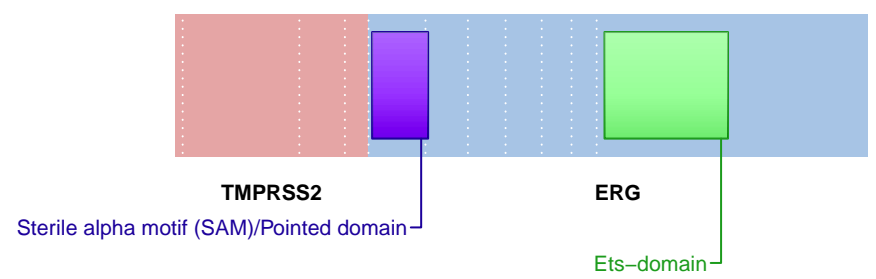
**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 3

- translocation
- duplication
- deletion
- inversion



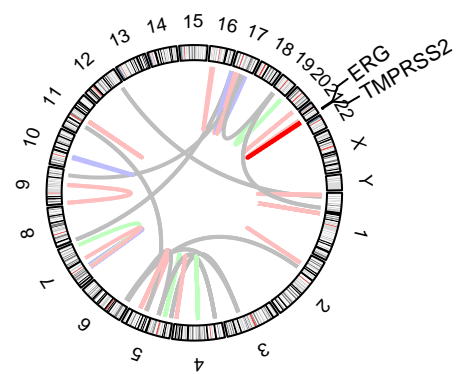
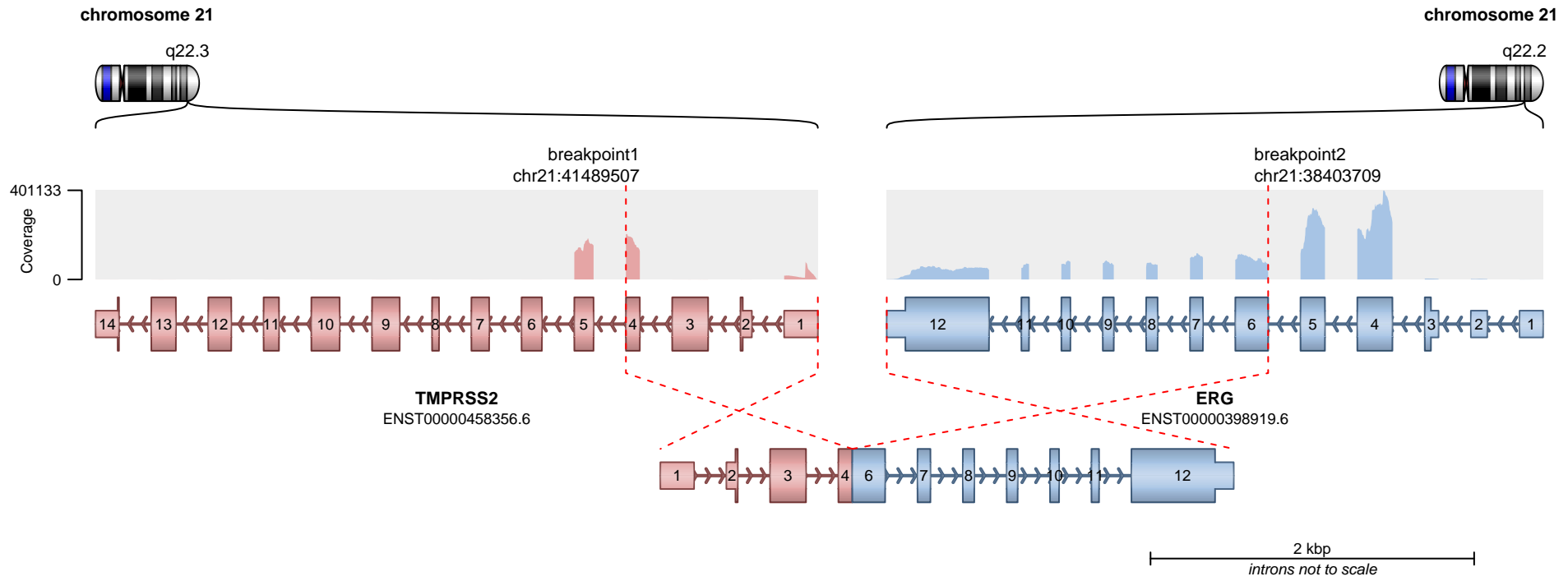
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



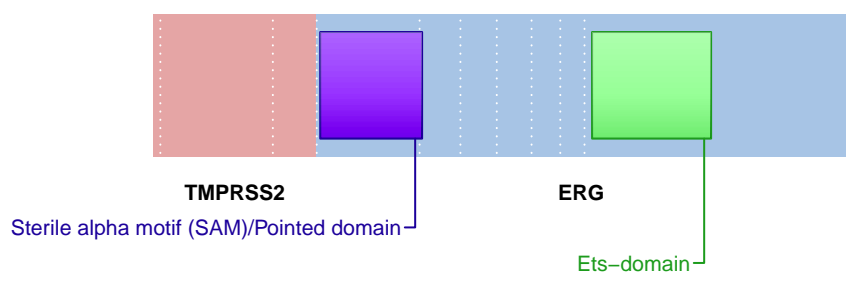
**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



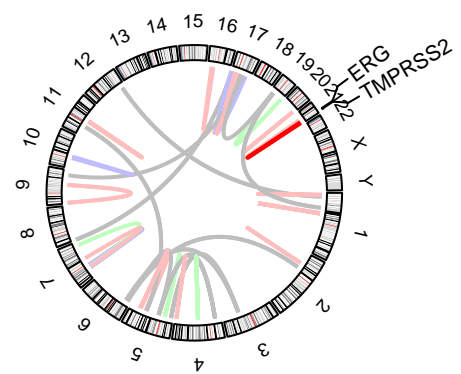
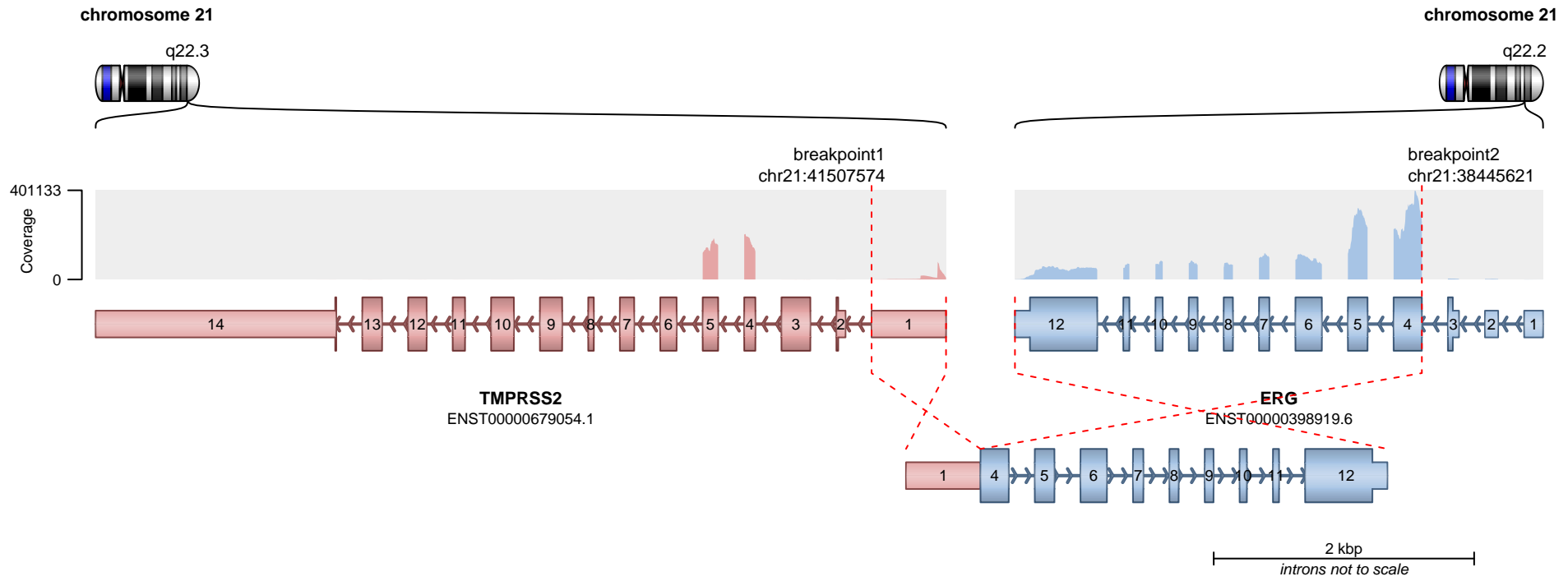
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

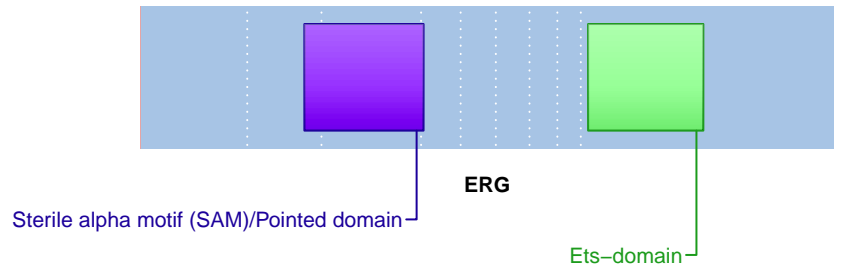
Split reads = 3  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



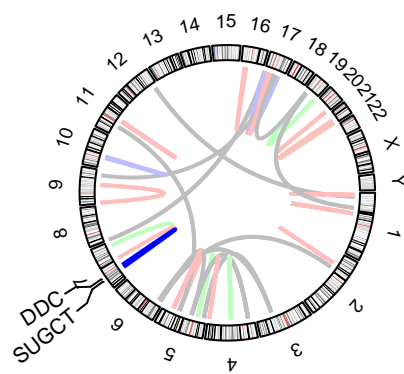
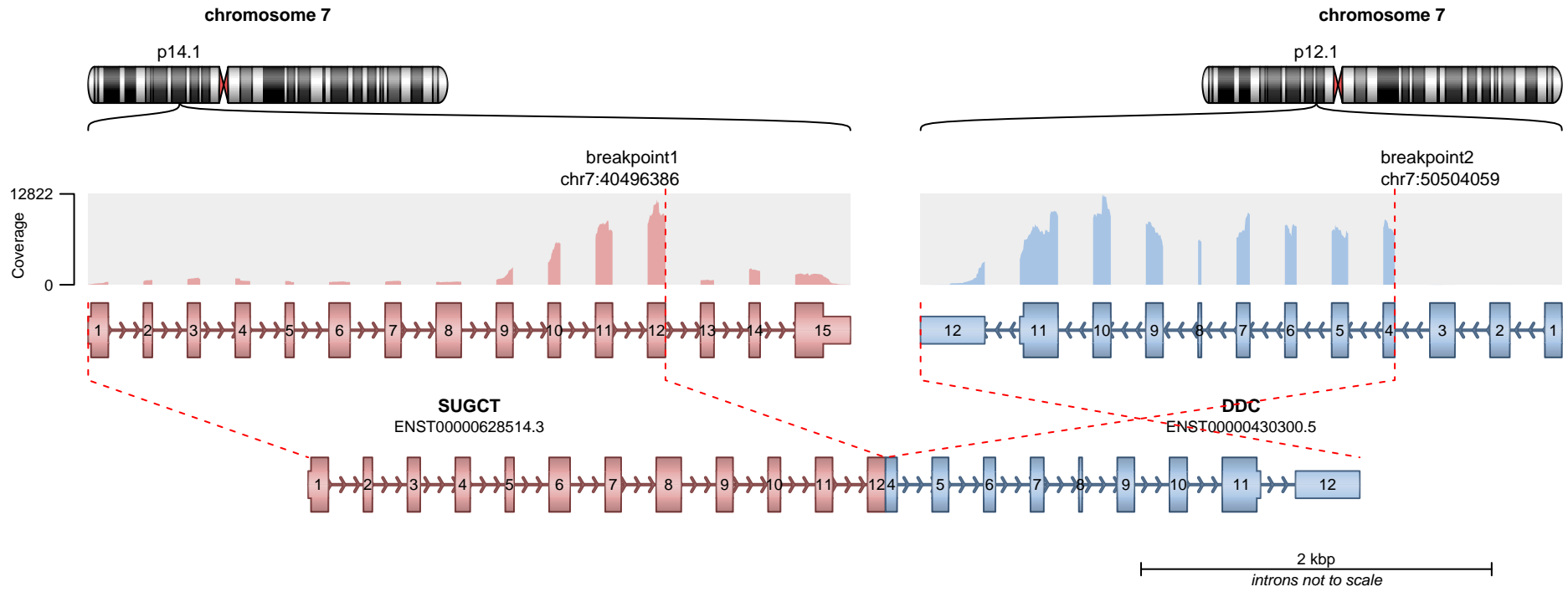
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear

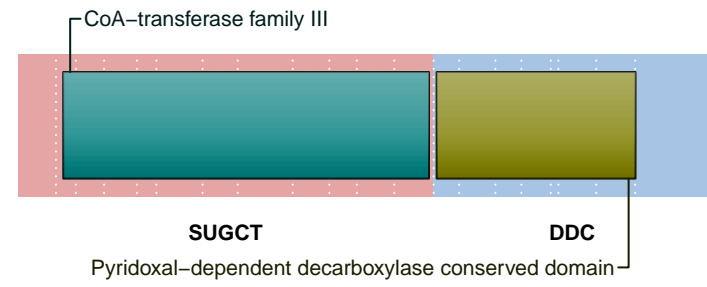


**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 2



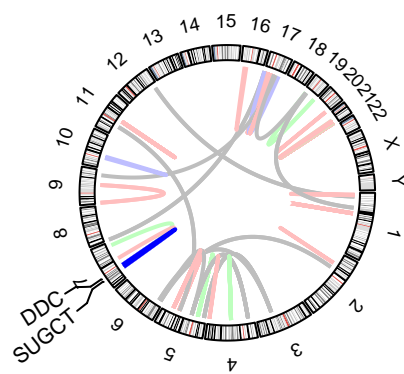
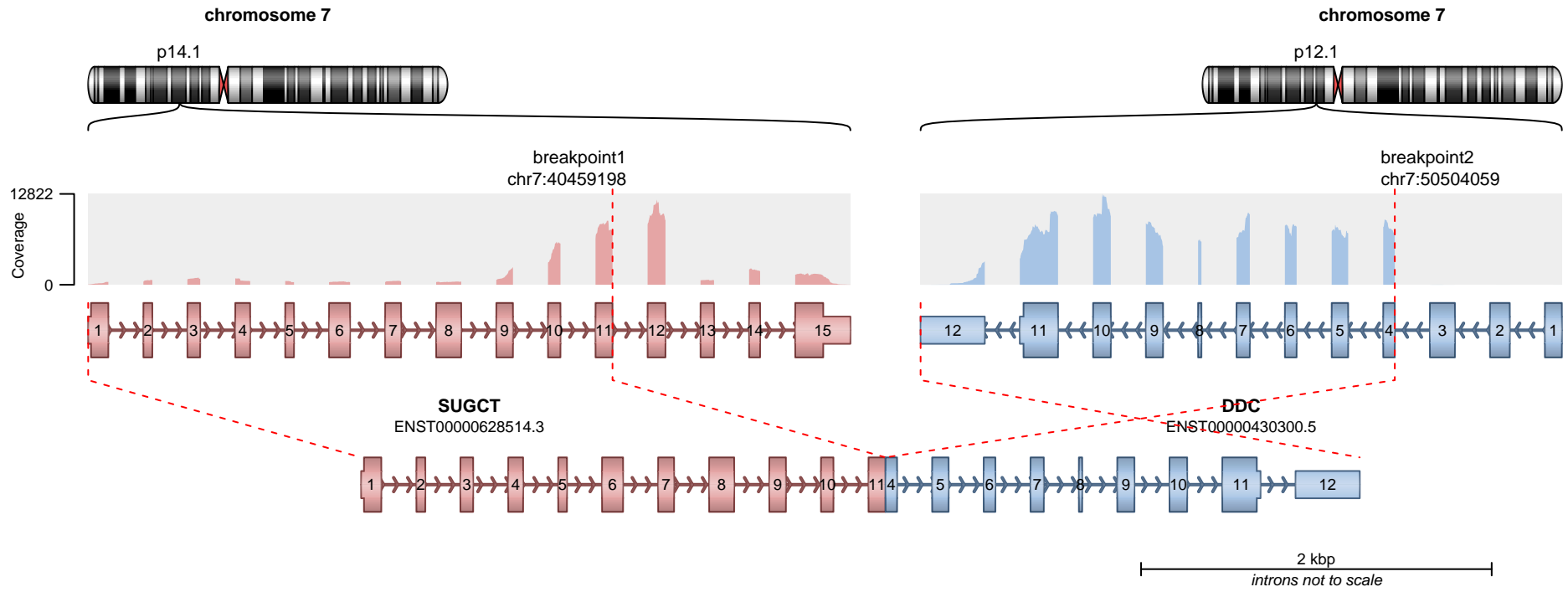
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



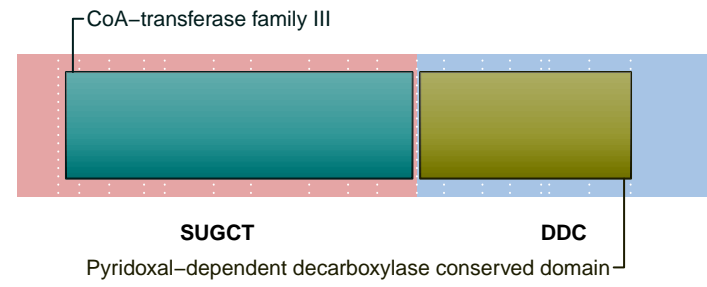
**SUPPORTING READ COUNT**

Split reads = 3302  
Discordant mates = 97

- translocation
- duplication
- deletion
- inversion



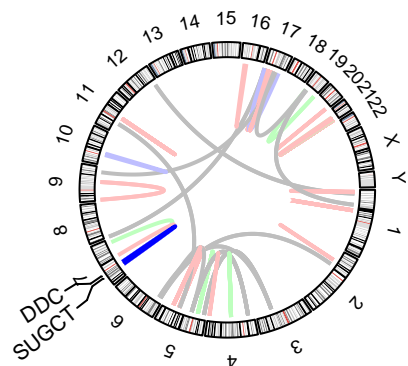
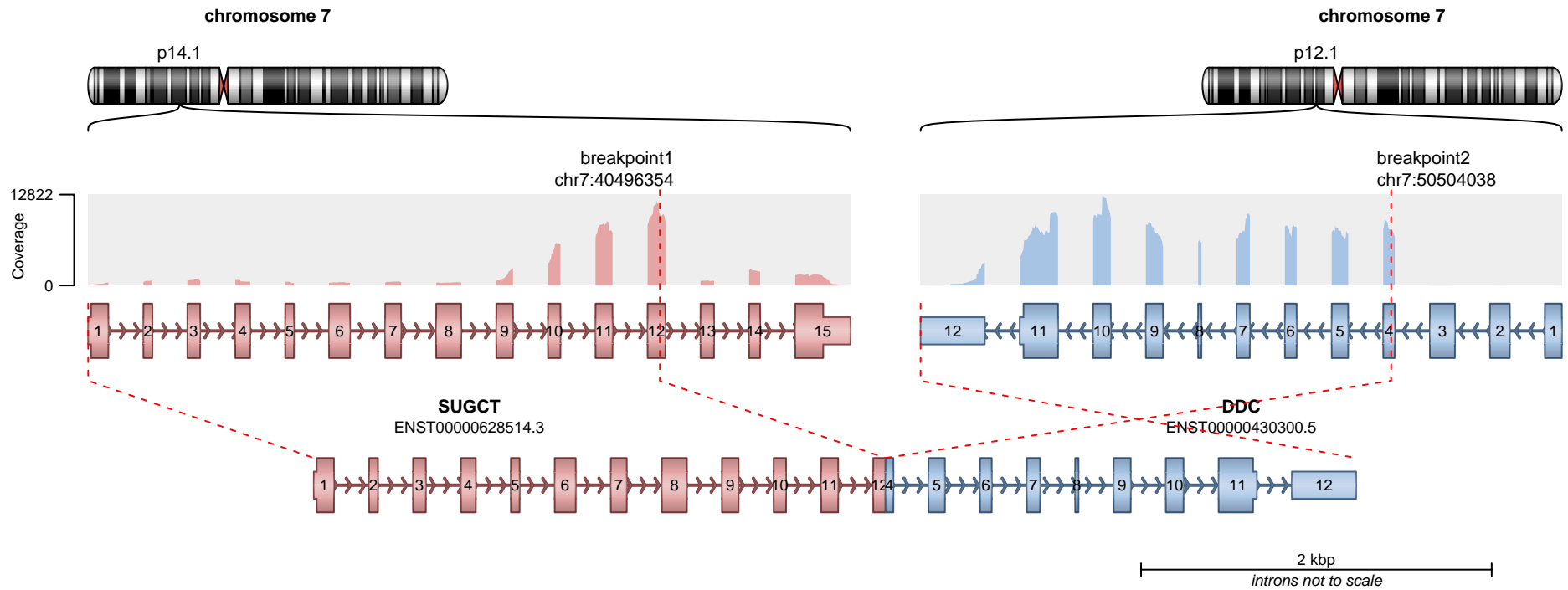
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



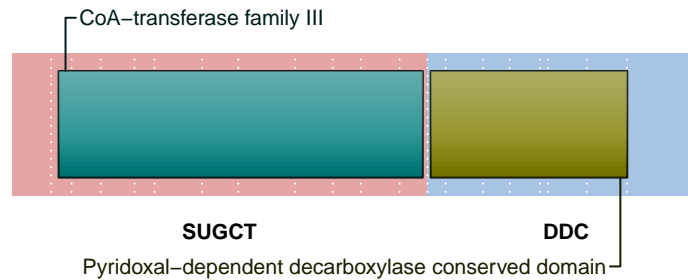
**SUPPORTING READ COUNT**

Split reads = 12  
Discordant mates = 7

- translocation
- duplication
- deletion
- inversion



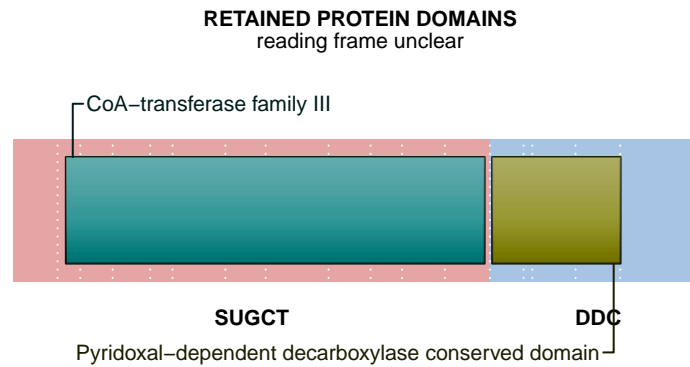
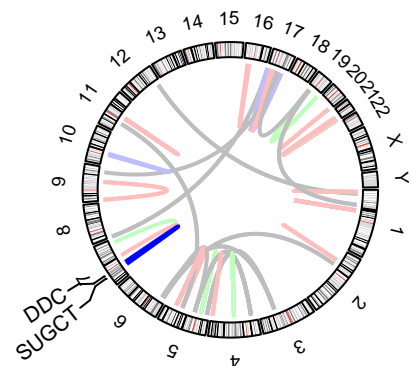
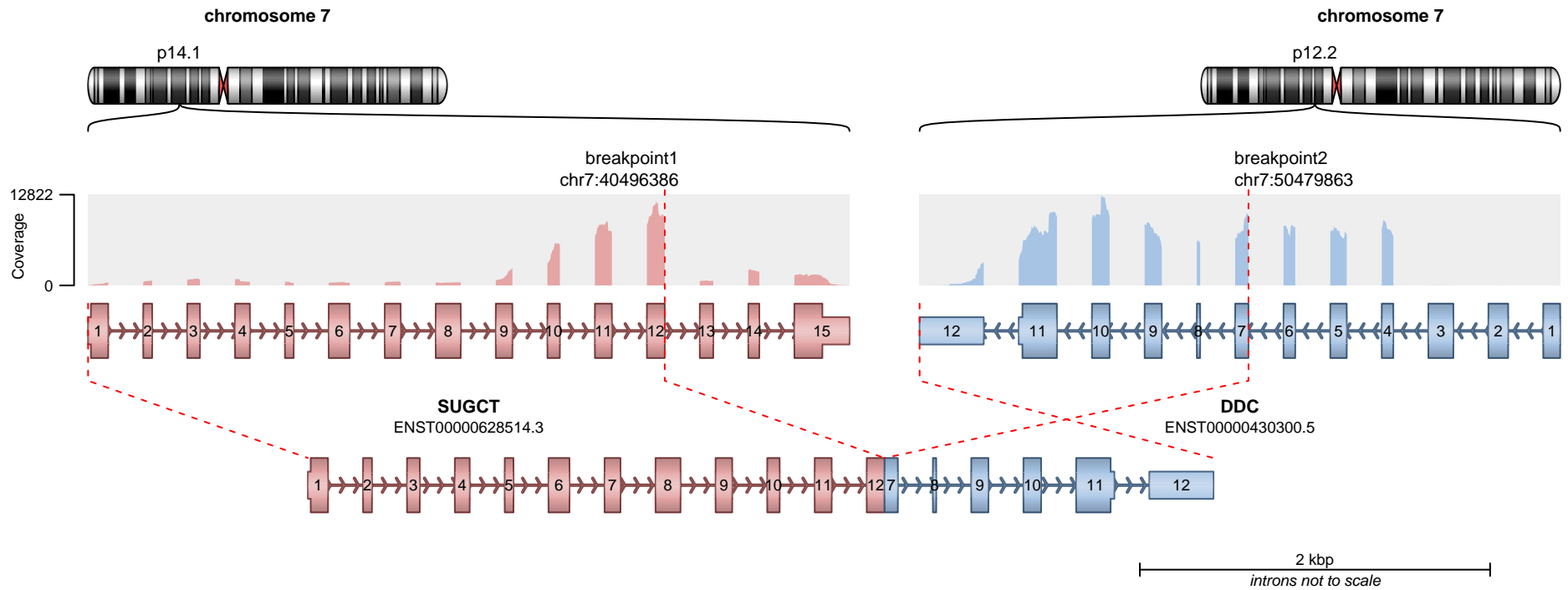
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 29

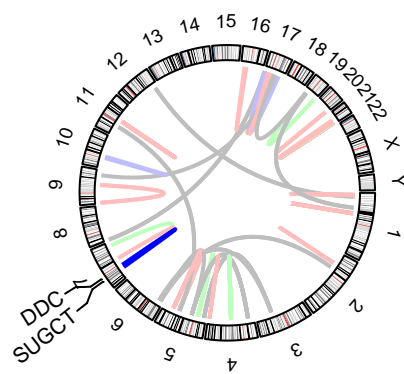
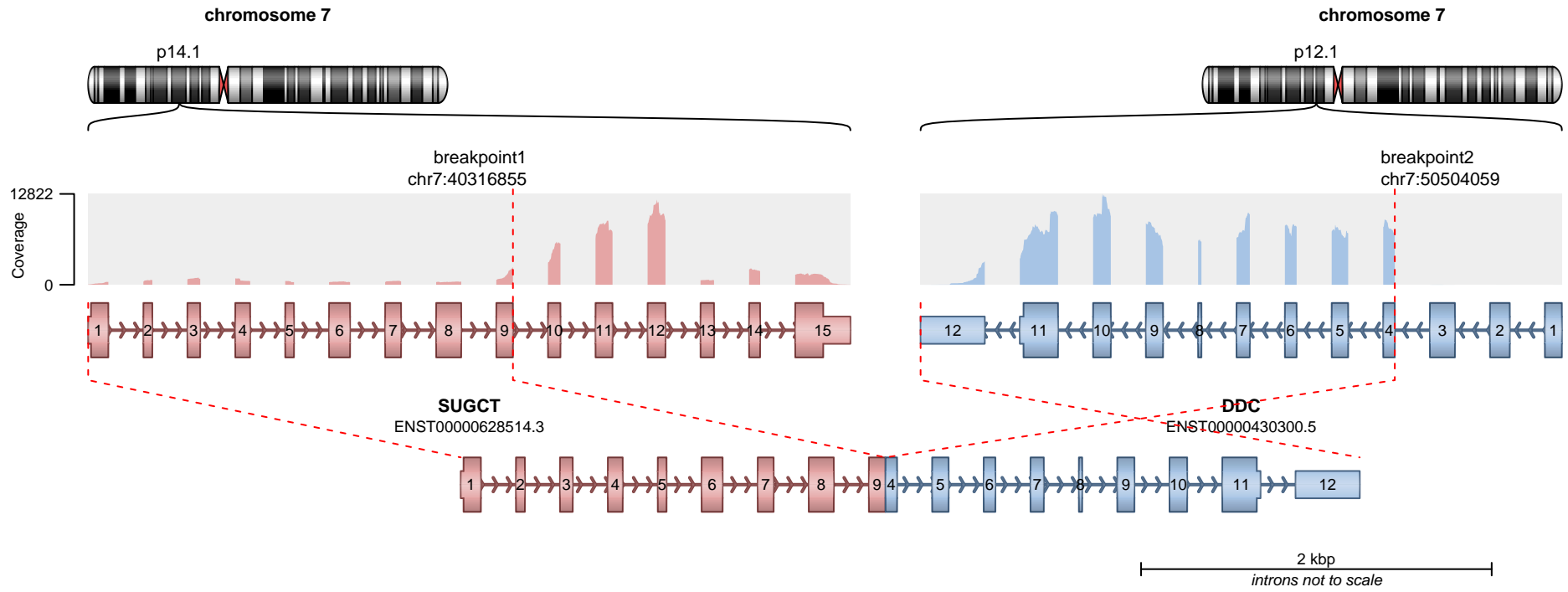
- translocation
- duplication
- deletion
- inversion



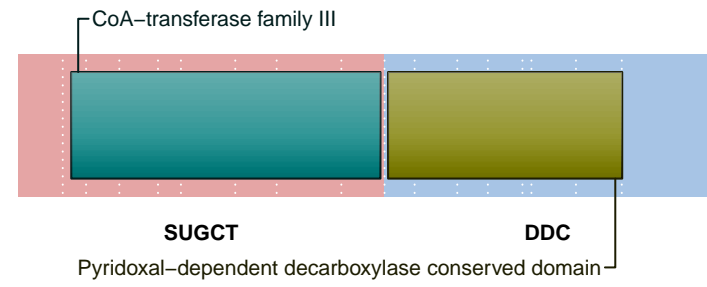
**SUPPORTING READ COUNT**

Split reads = 5  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



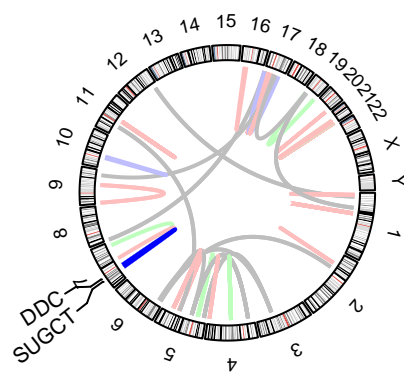
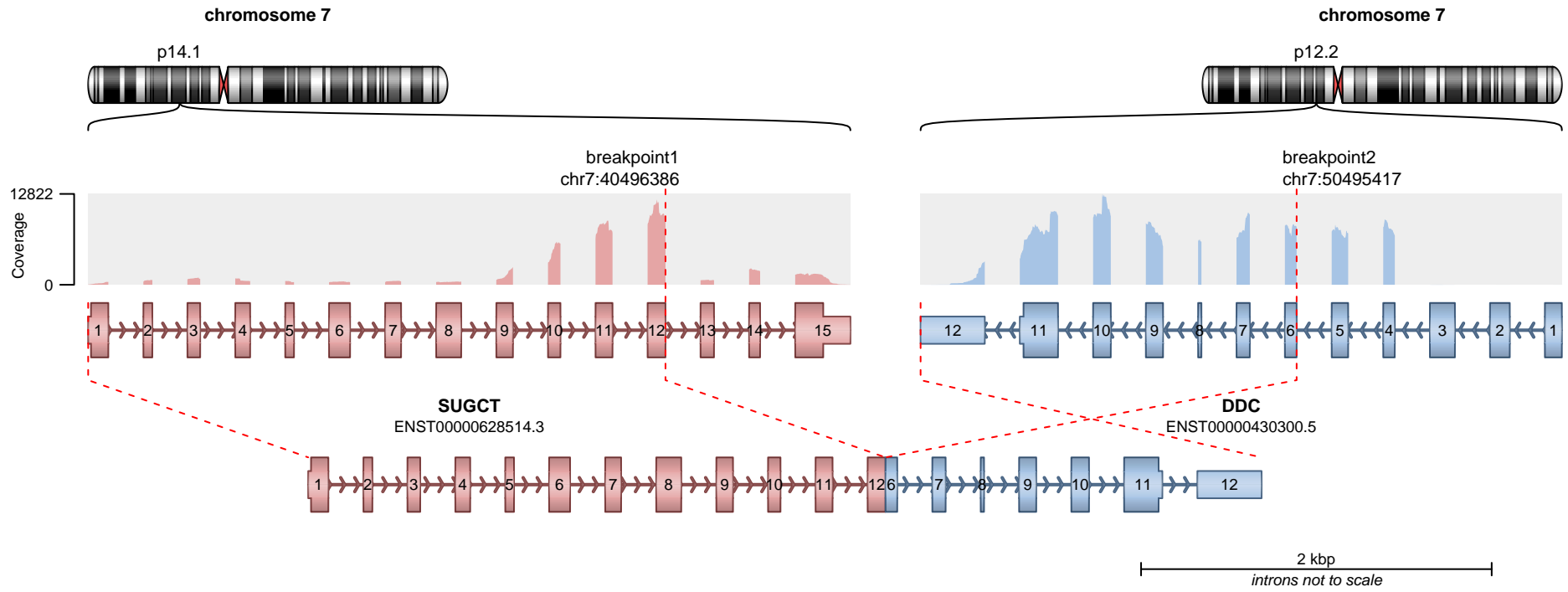
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



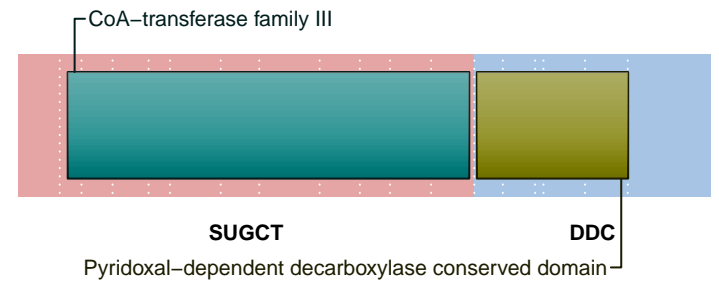
**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



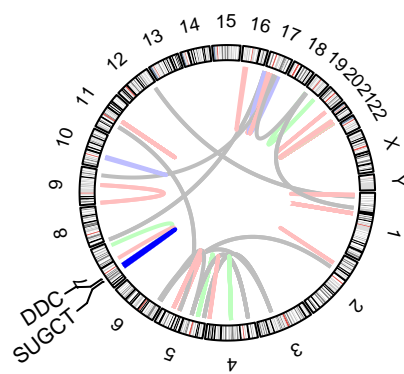
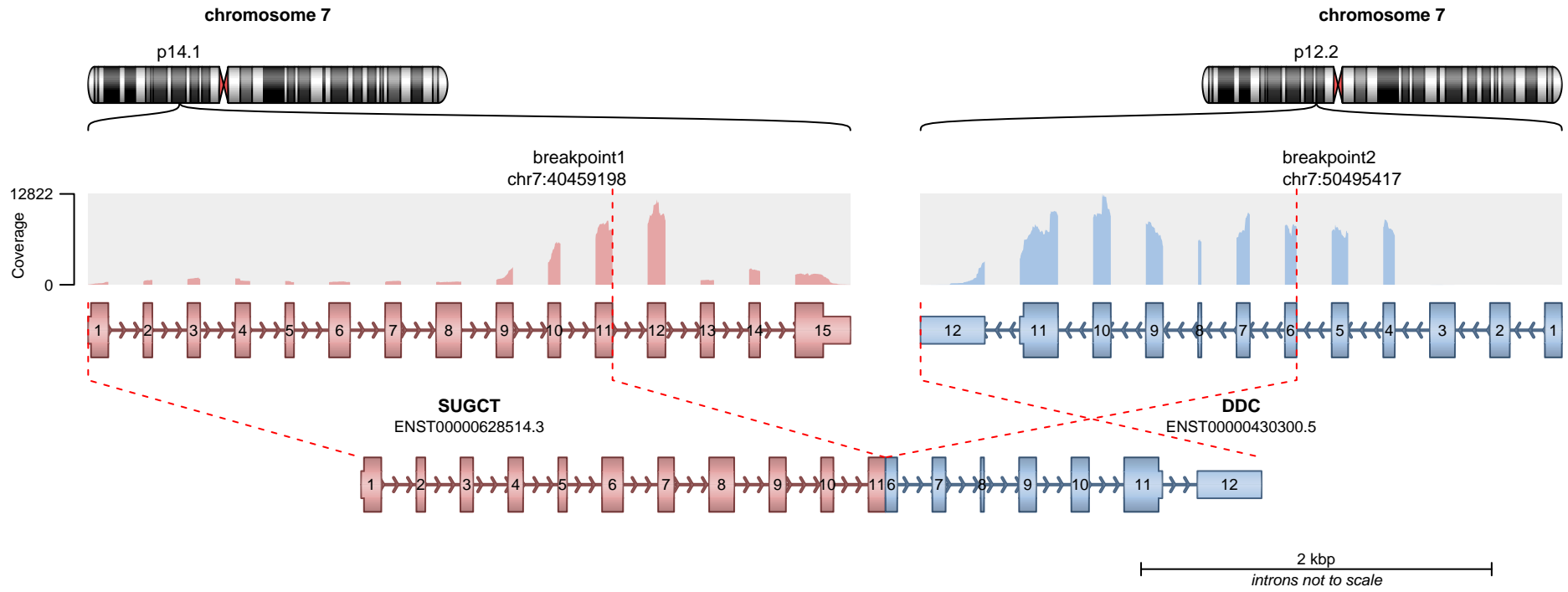
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



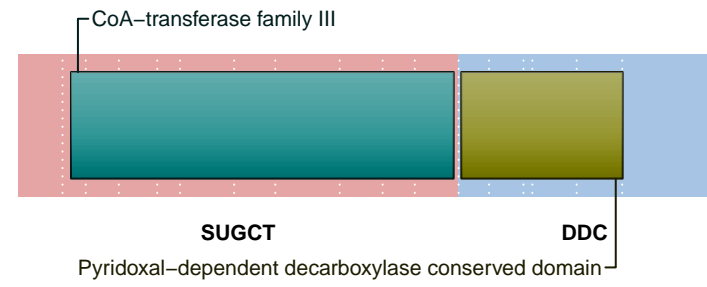
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 5

- translocation
- duplication
- deletion
- inversion



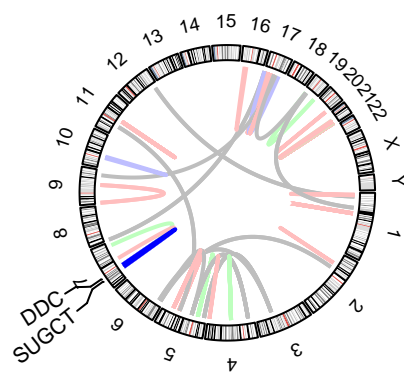
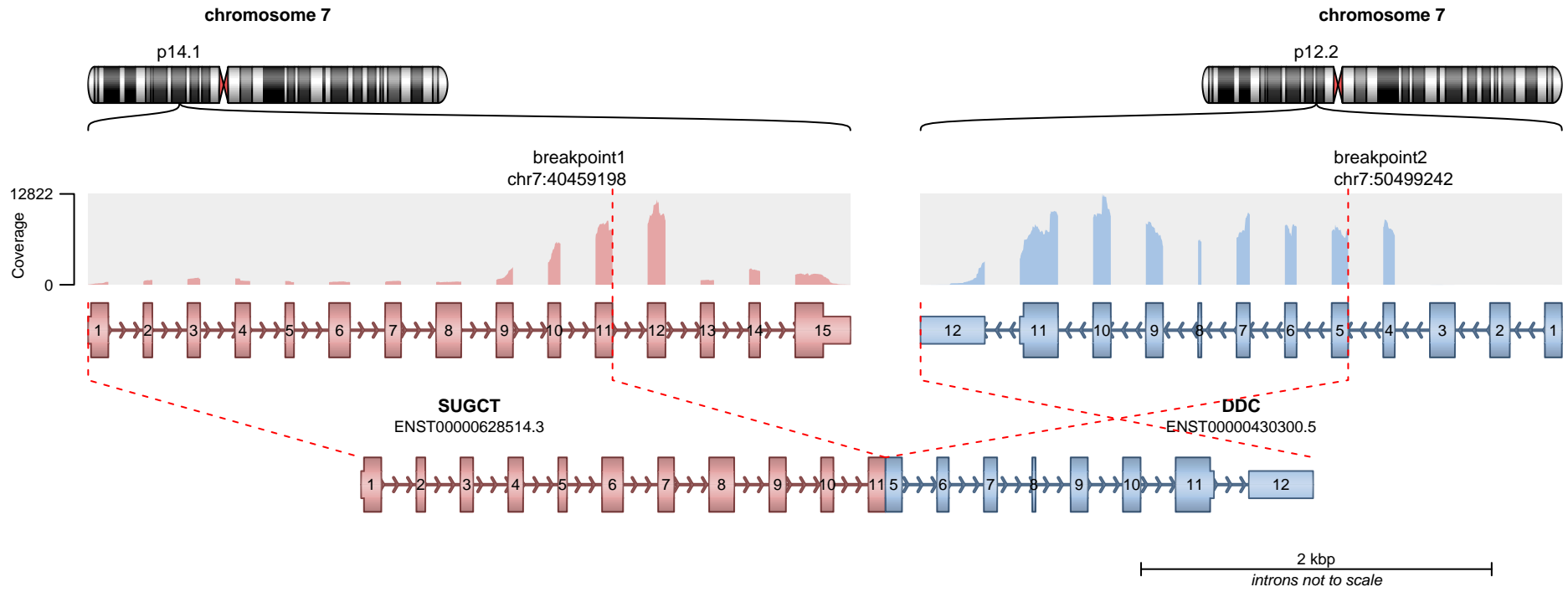
**RETAINED PROTEIN DOMAINS**  
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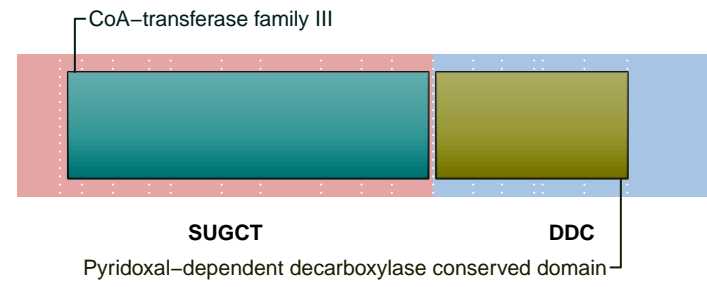
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



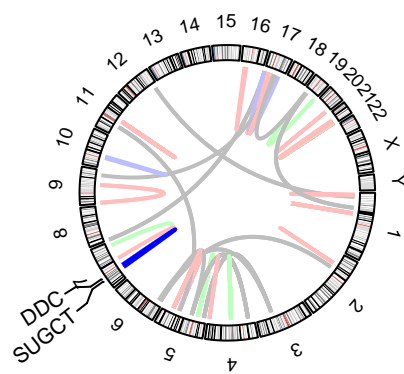
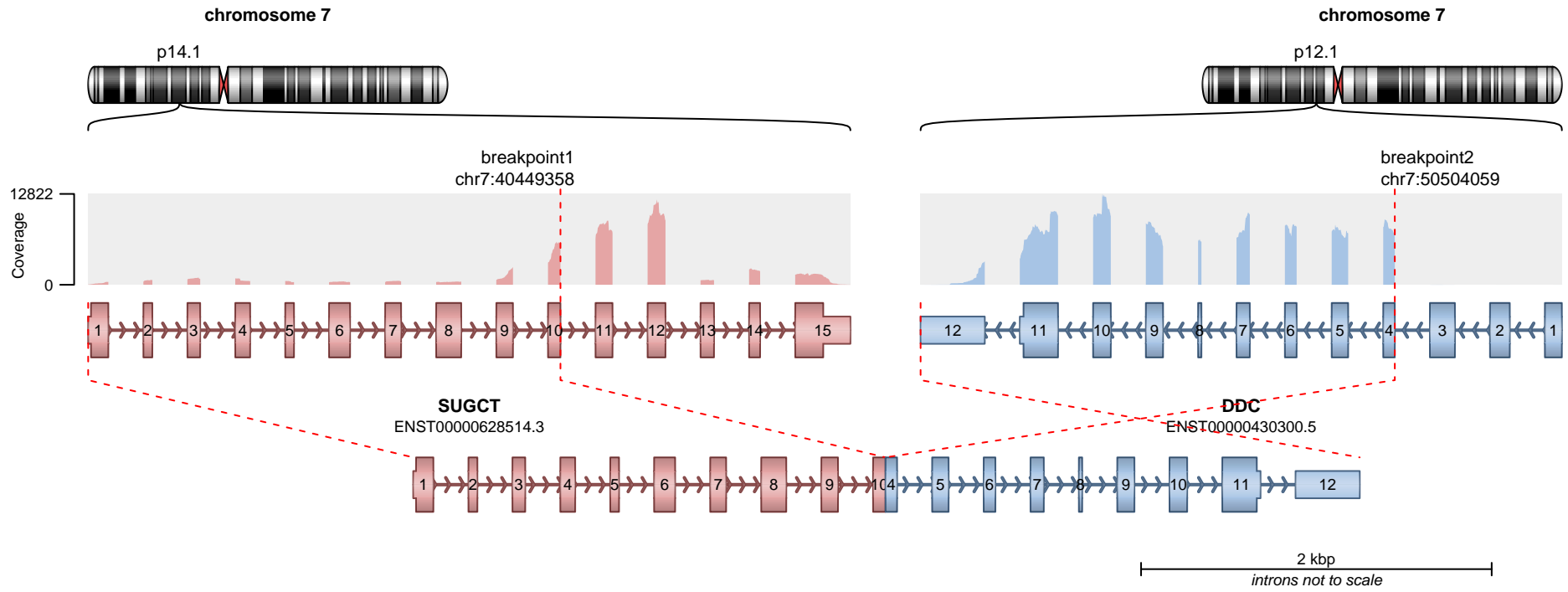
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



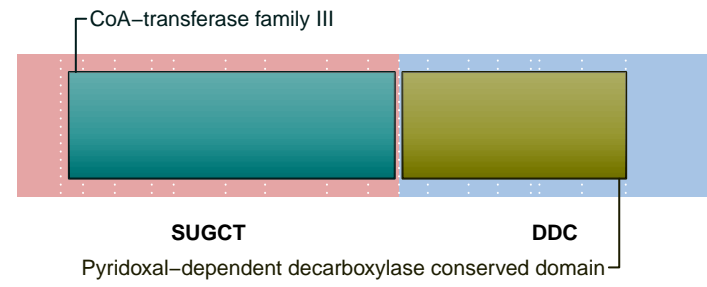
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



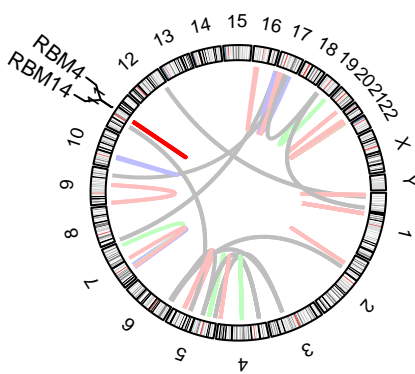
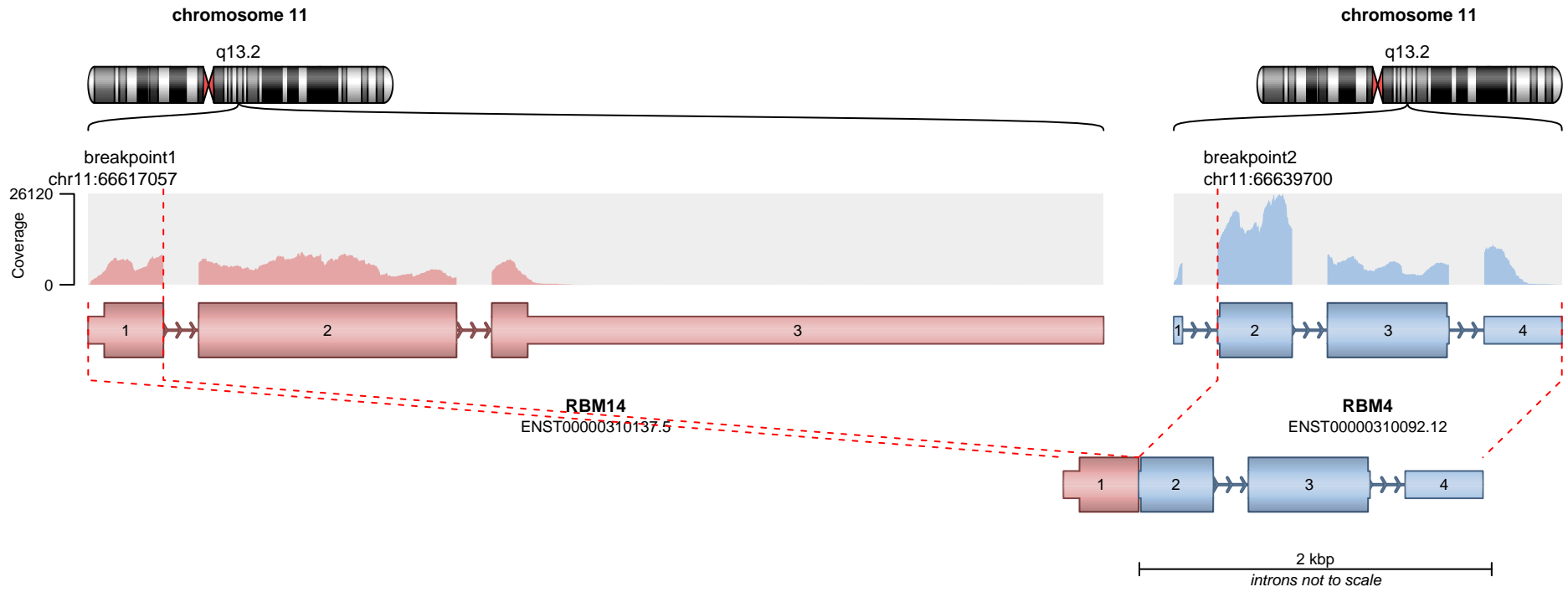
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



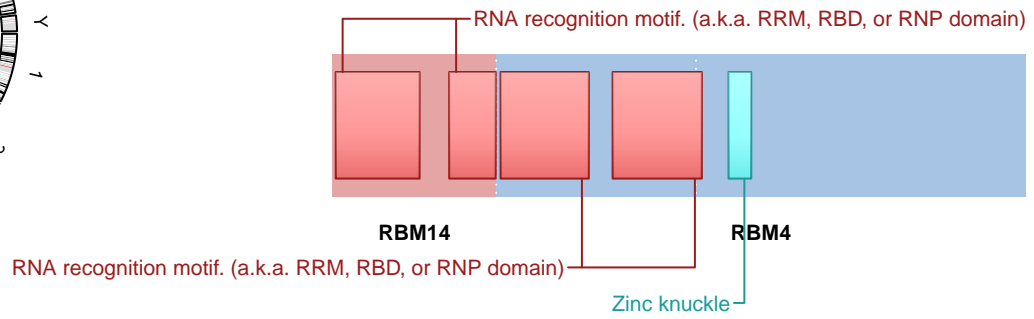
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



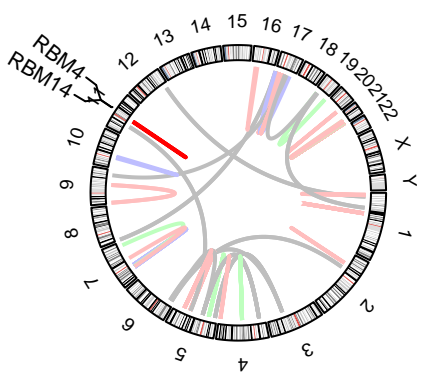
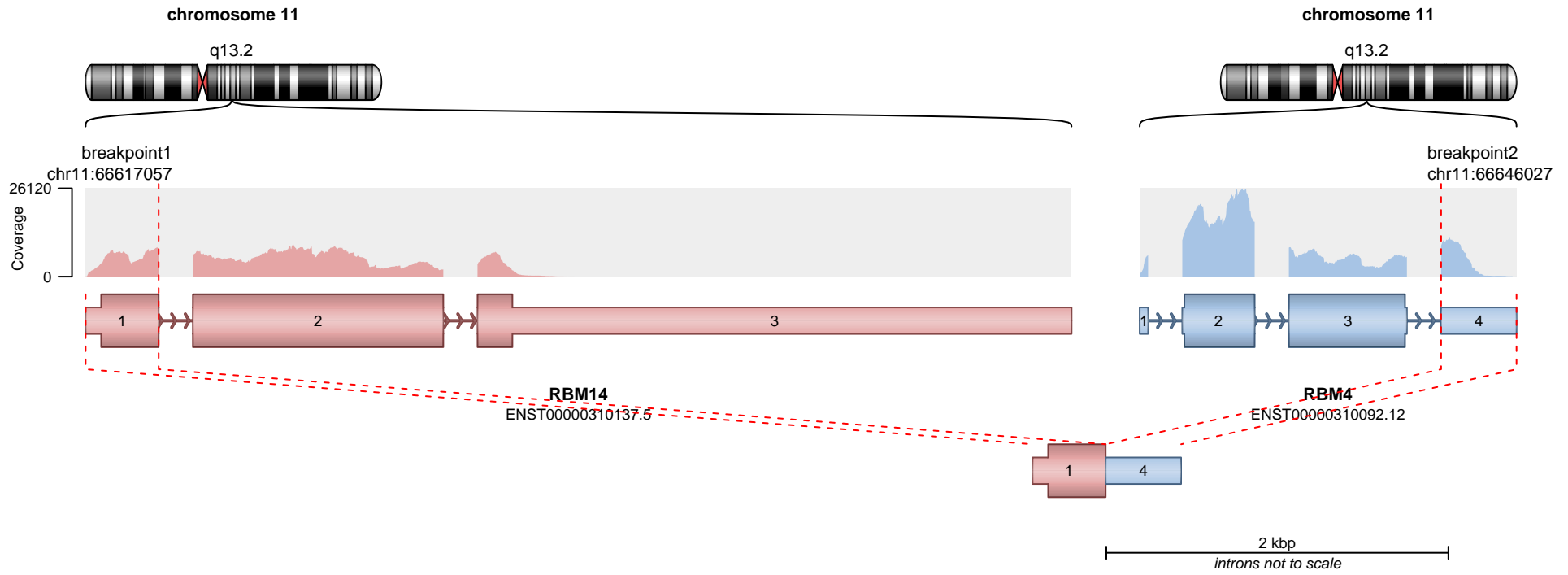
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



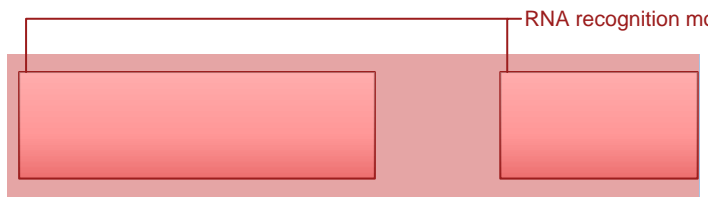
**SUPPORTING READ COUNT**

Split reads = 768  
Discordant mates = 28

- translocation
- duplication
- deletion
- inversion



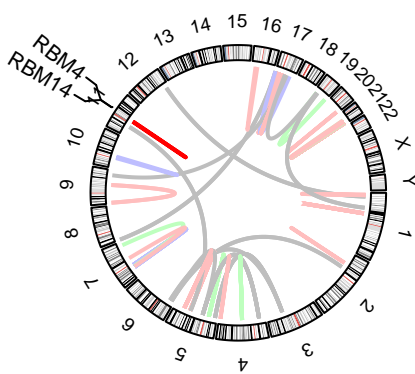
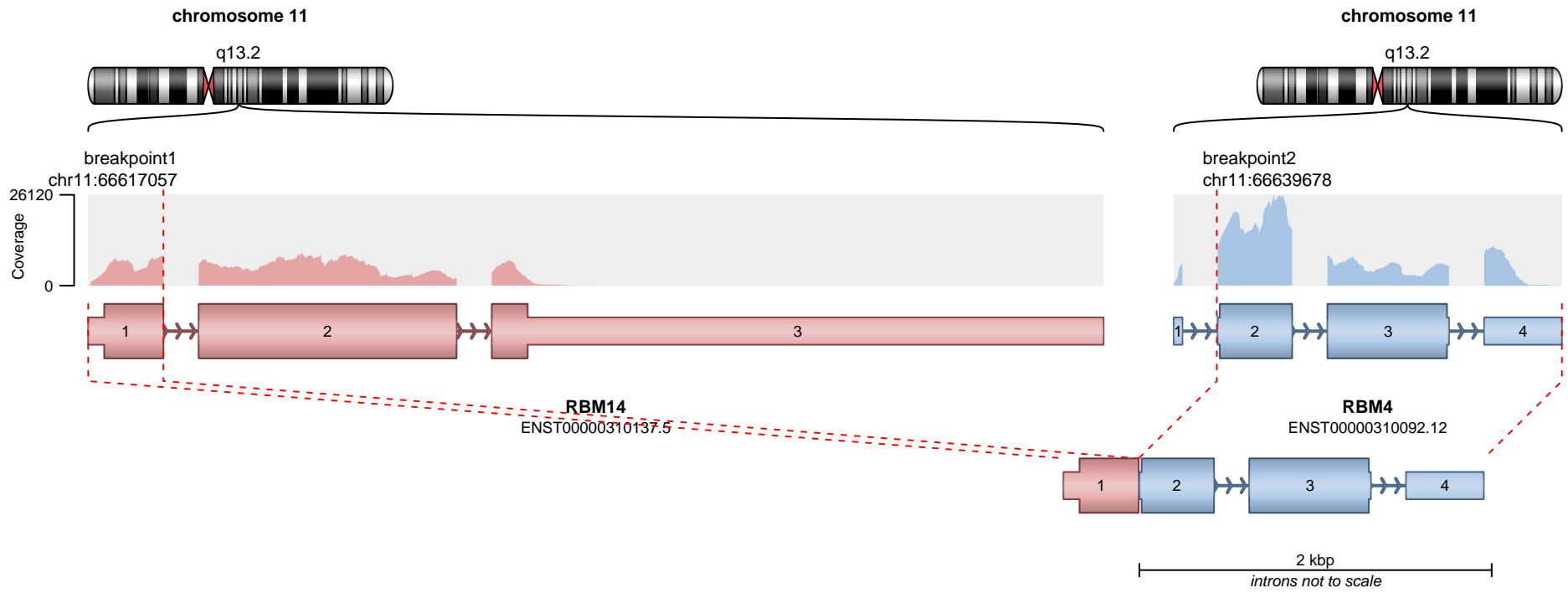
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



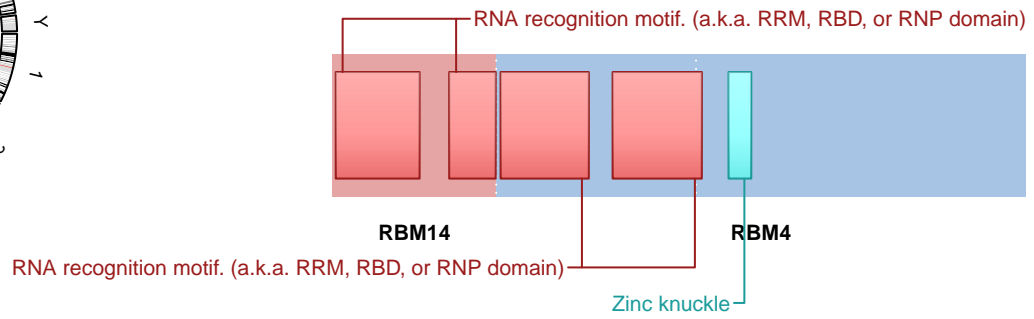
**SUPPORTING READ COUNT**

Split reads = 94  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



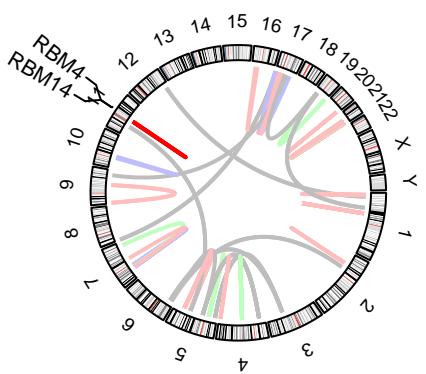
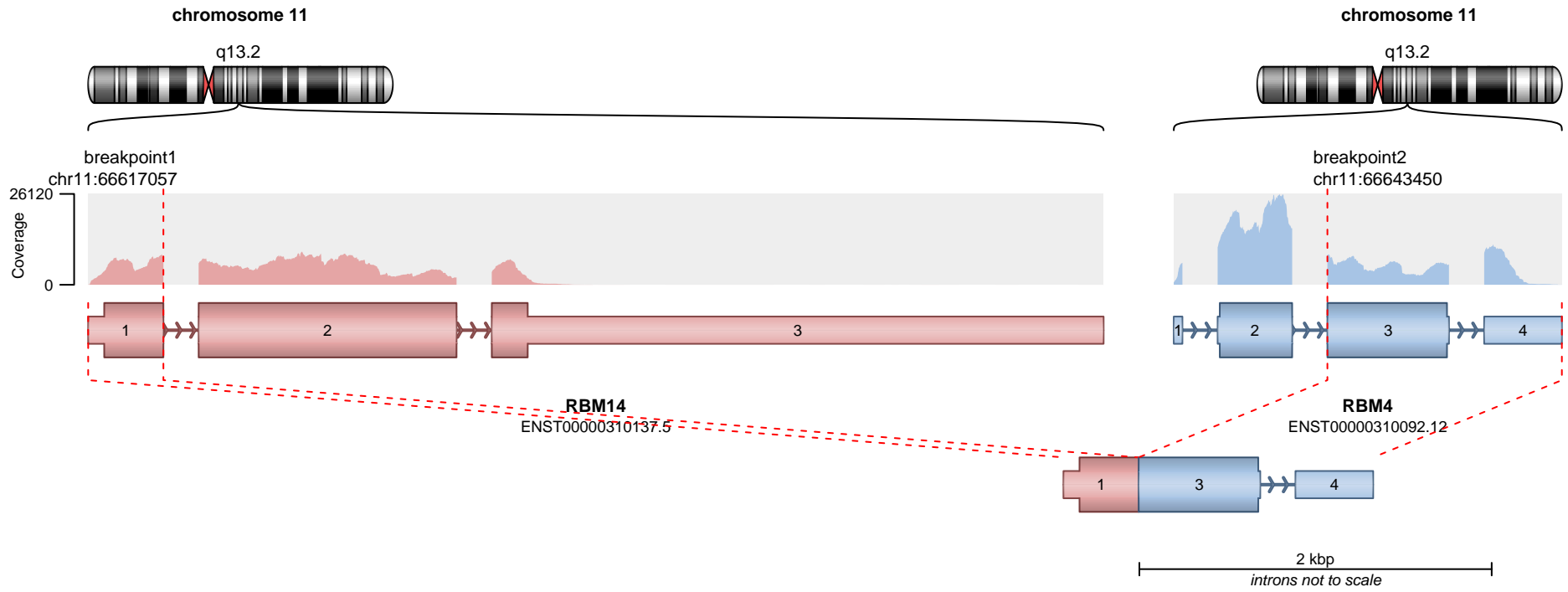
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



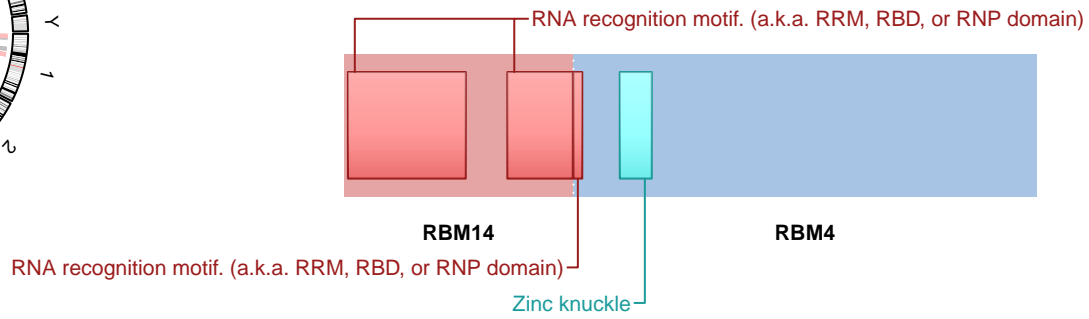
**SUPPORTING READ COUNT**

Split reads = 12  
Discordant mates = 29

- translocation
- duplication
- deletion
- inversion



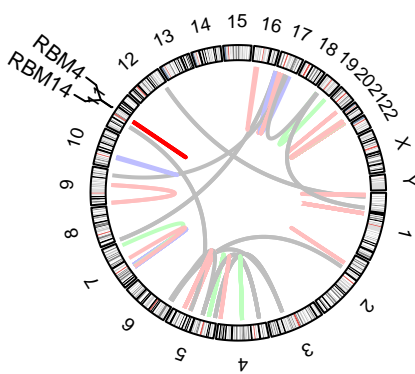
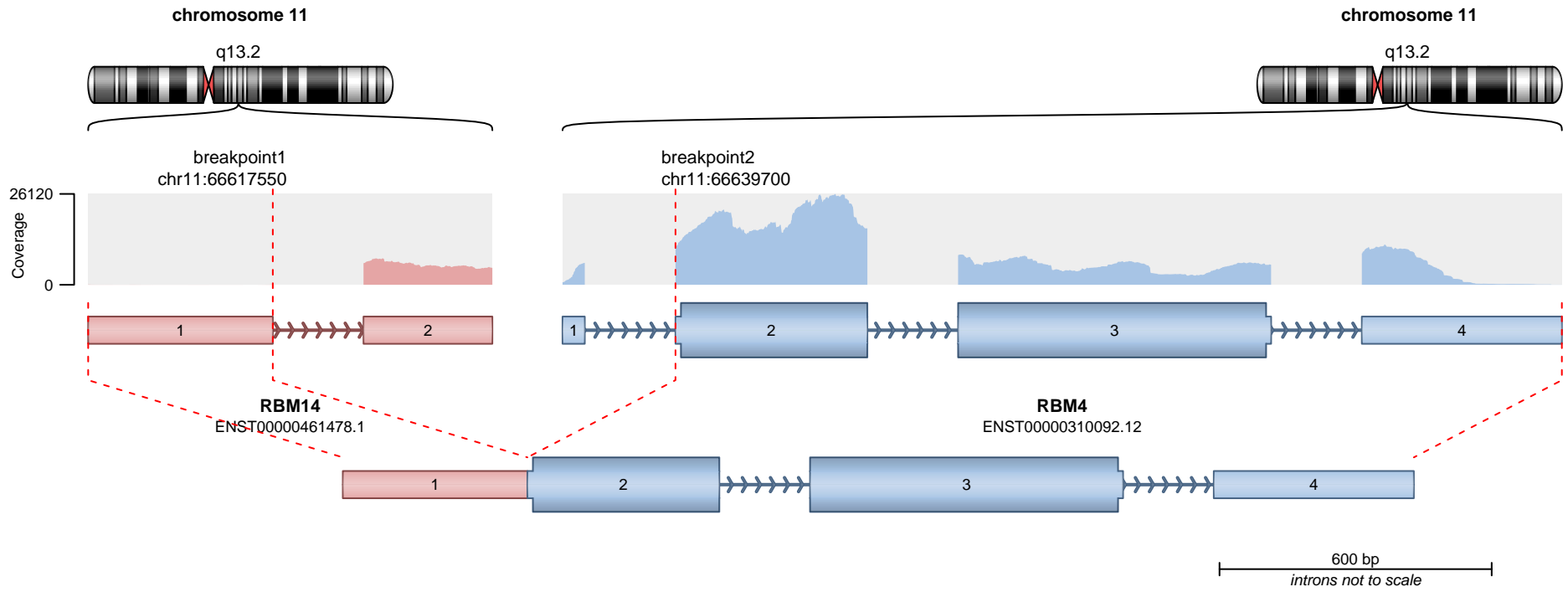
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

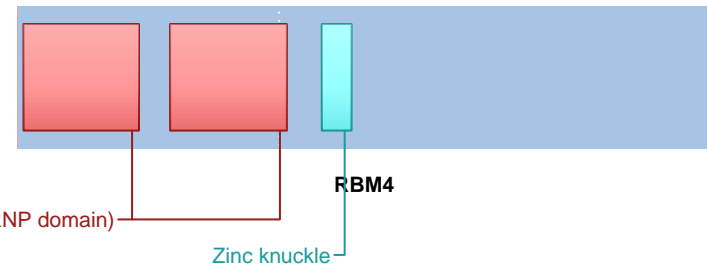
Split reads = 18  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)

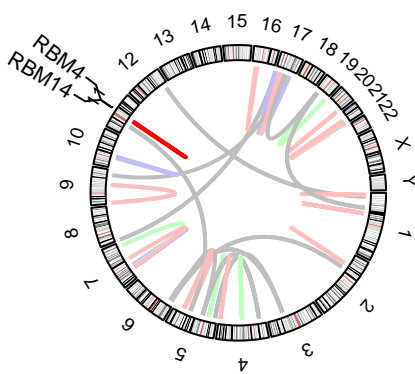
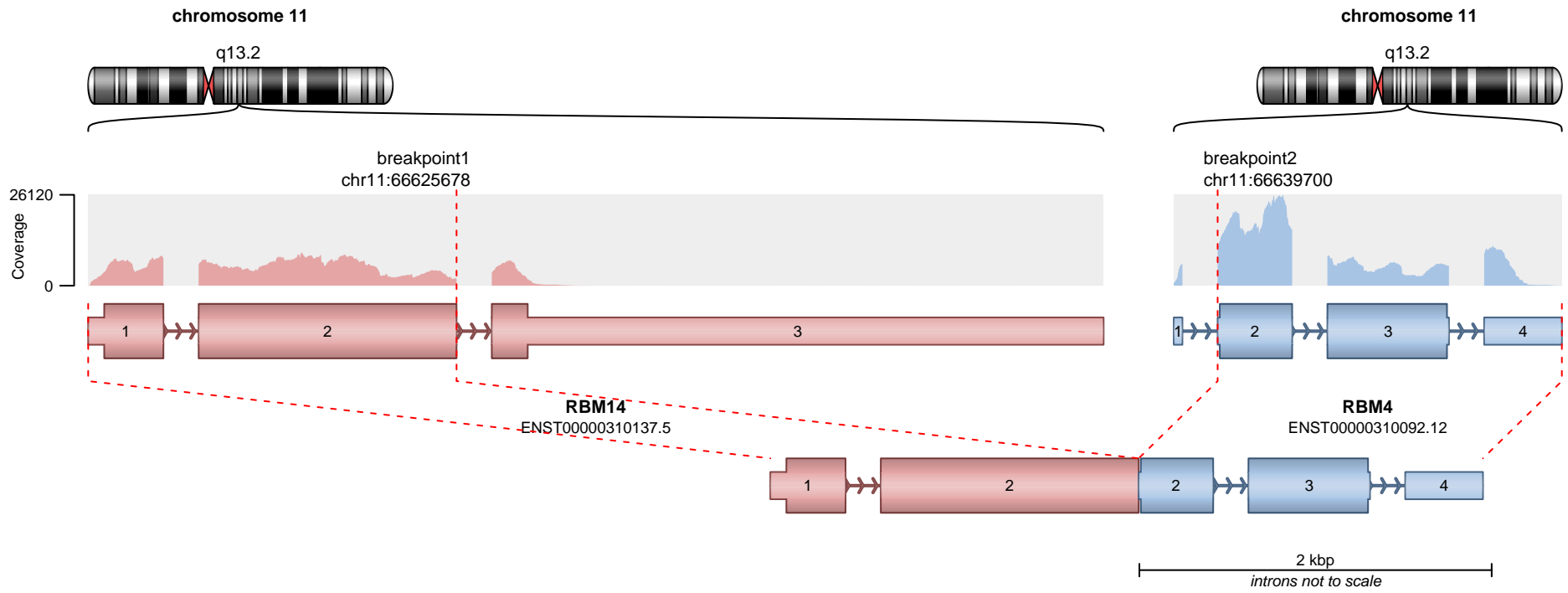
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



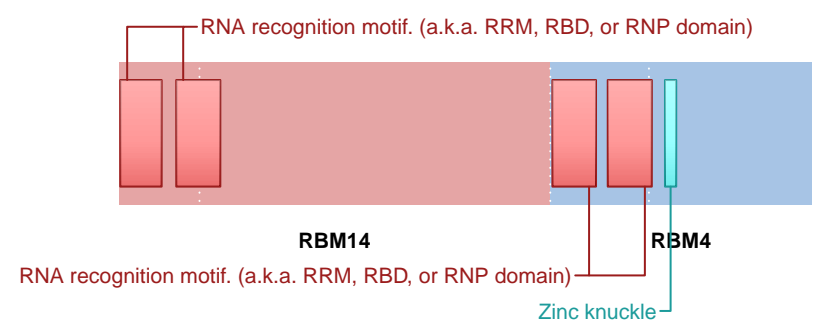
**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 28

- translocation
- duplication
- deletion
- inversion



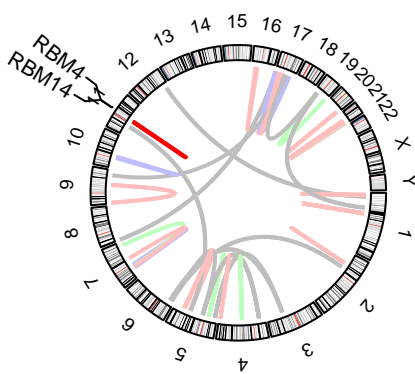
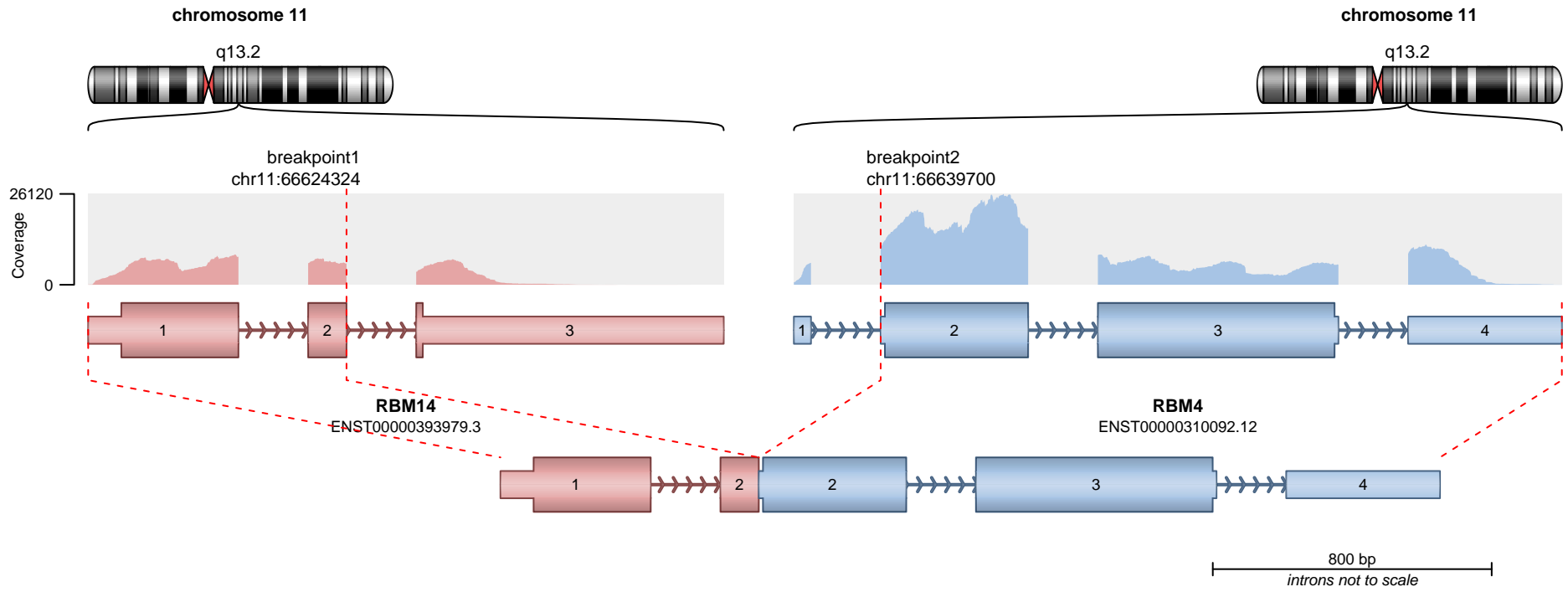
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



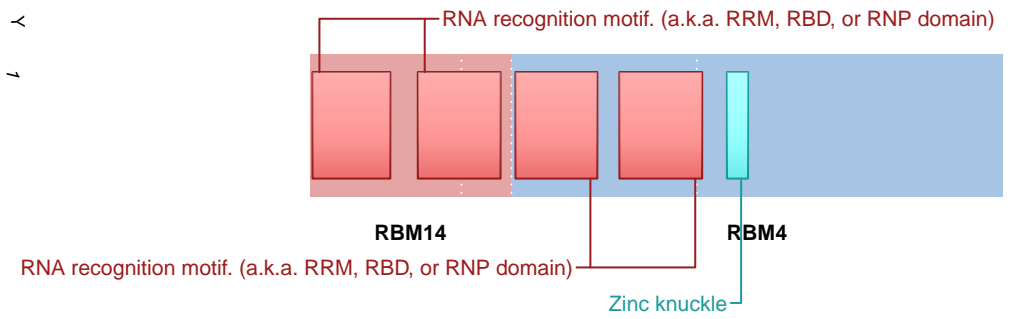
**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 28

- translocation
- duplication
- deletion
- inversion



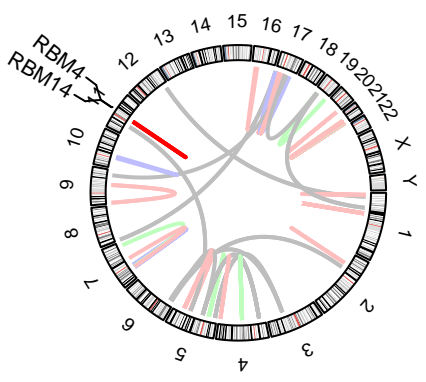
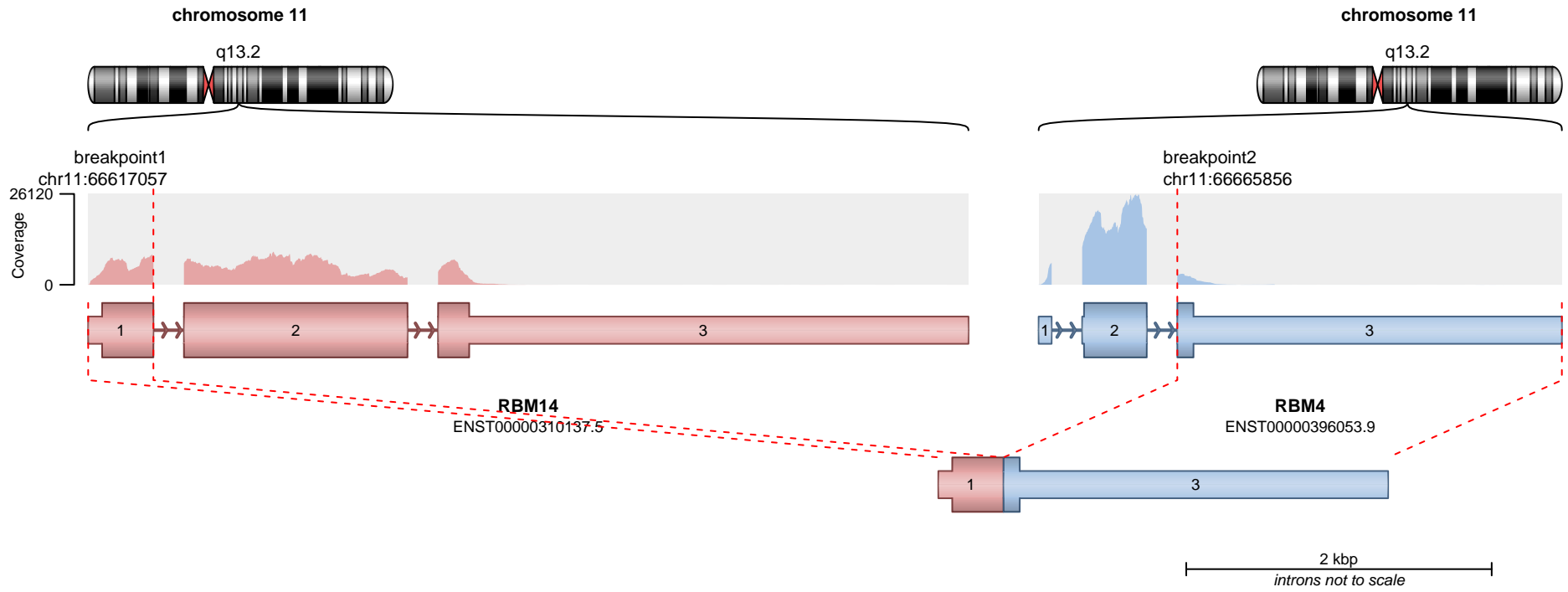
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



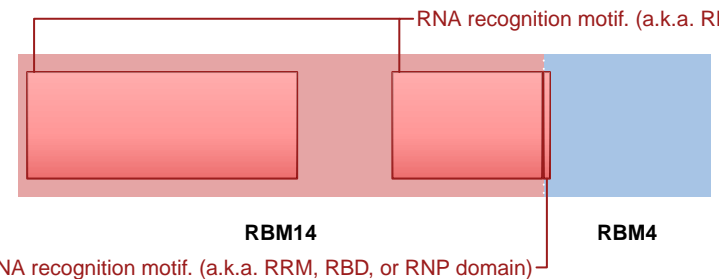
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 28

- translocation
- duplication
- deletion
- inversion



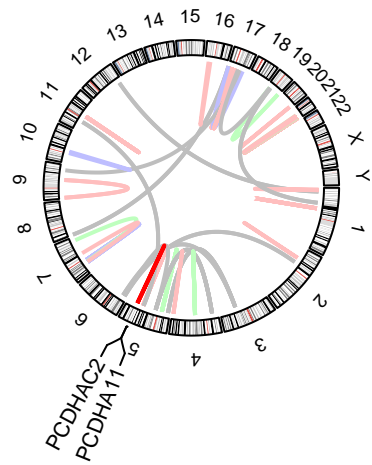
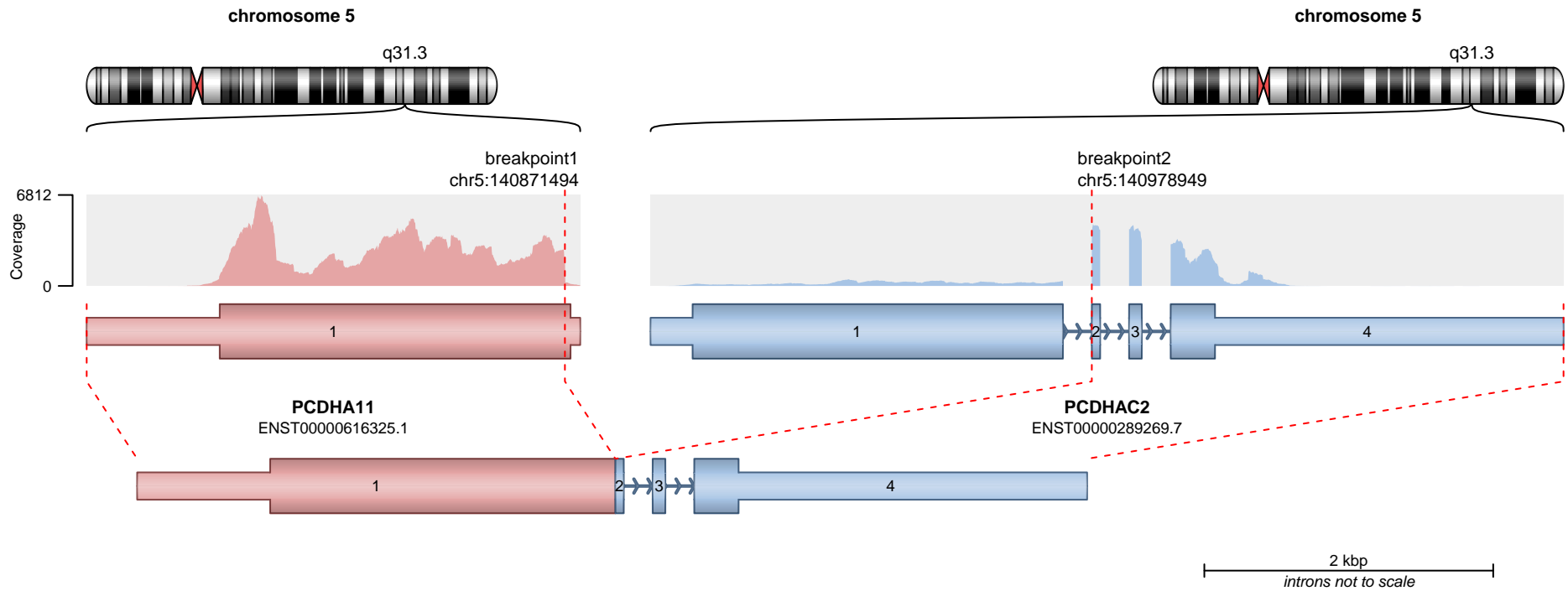
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



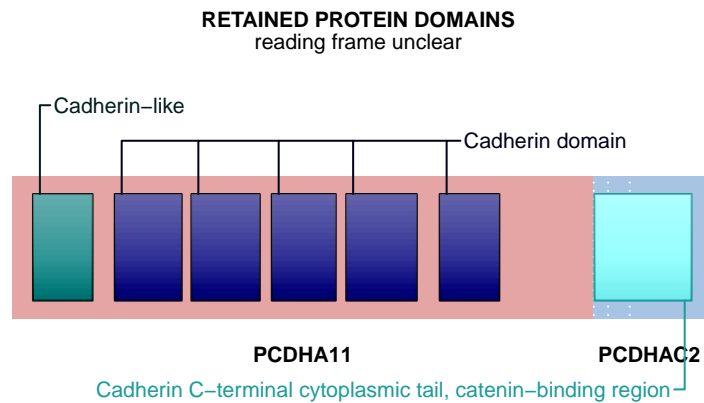
**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

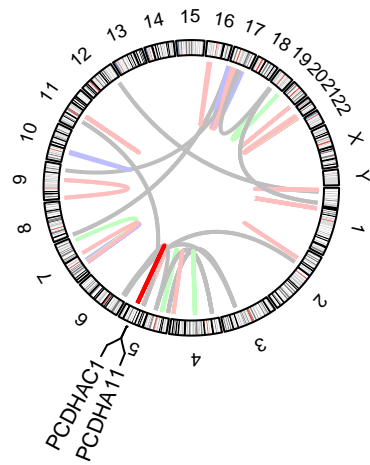
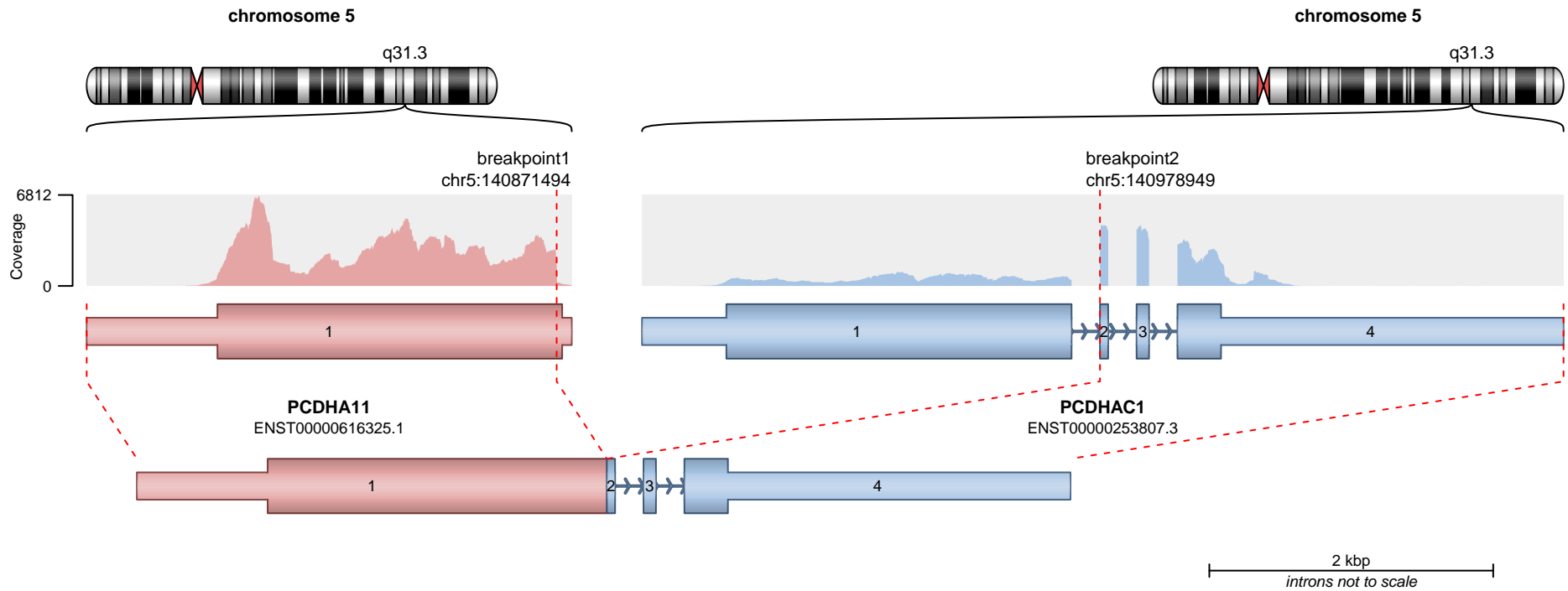


— translocation — deletion  
— duplication — inversion

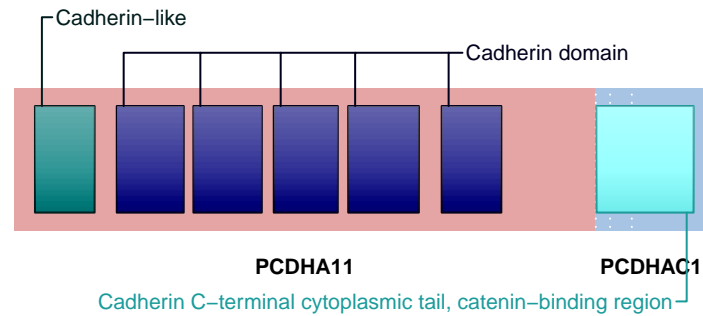


**SUPPORTING READ COUNT**

Split reads = 670  
Discordant mates = 37



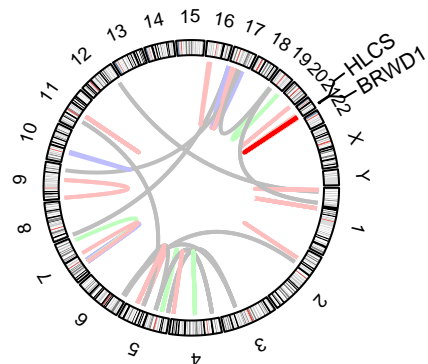
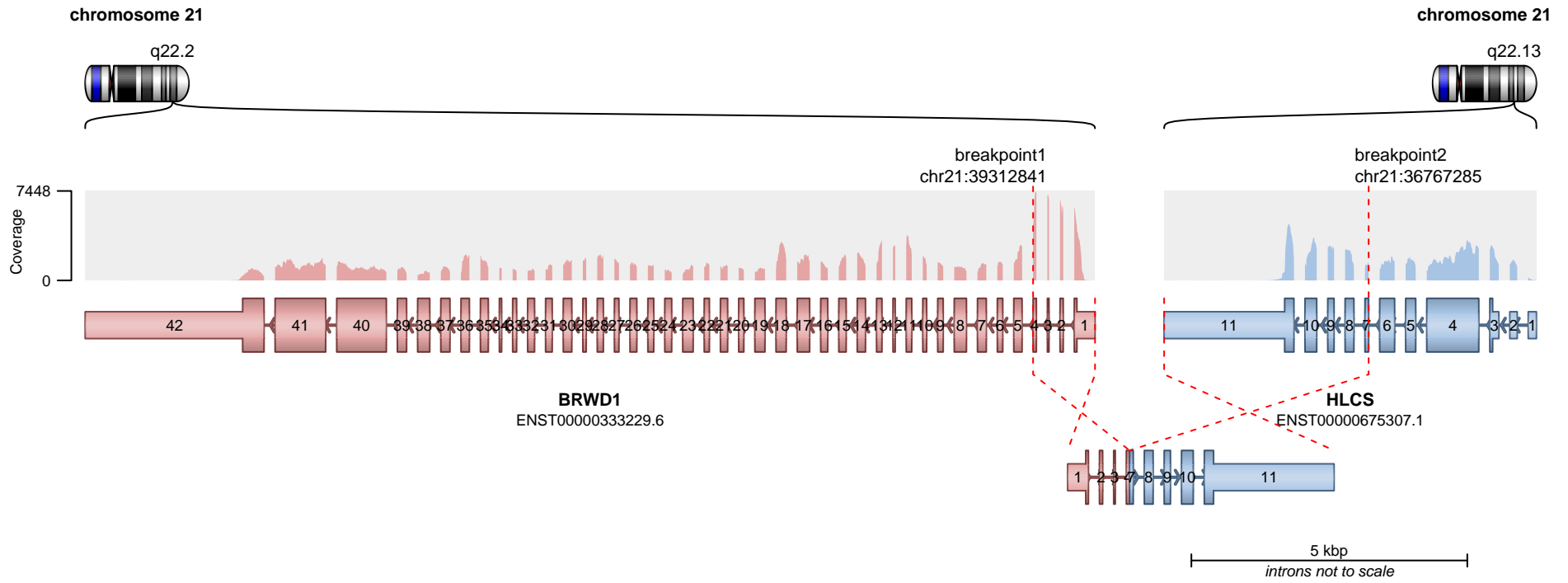
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



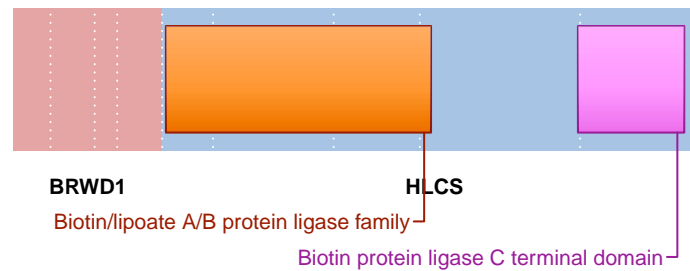
**SUPPORTING READ COUNT**

Split reads = 668  
Discordant mates = 36

— translocation — deletion  
— duplication — inversion



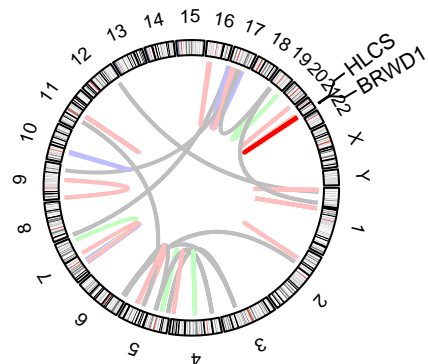
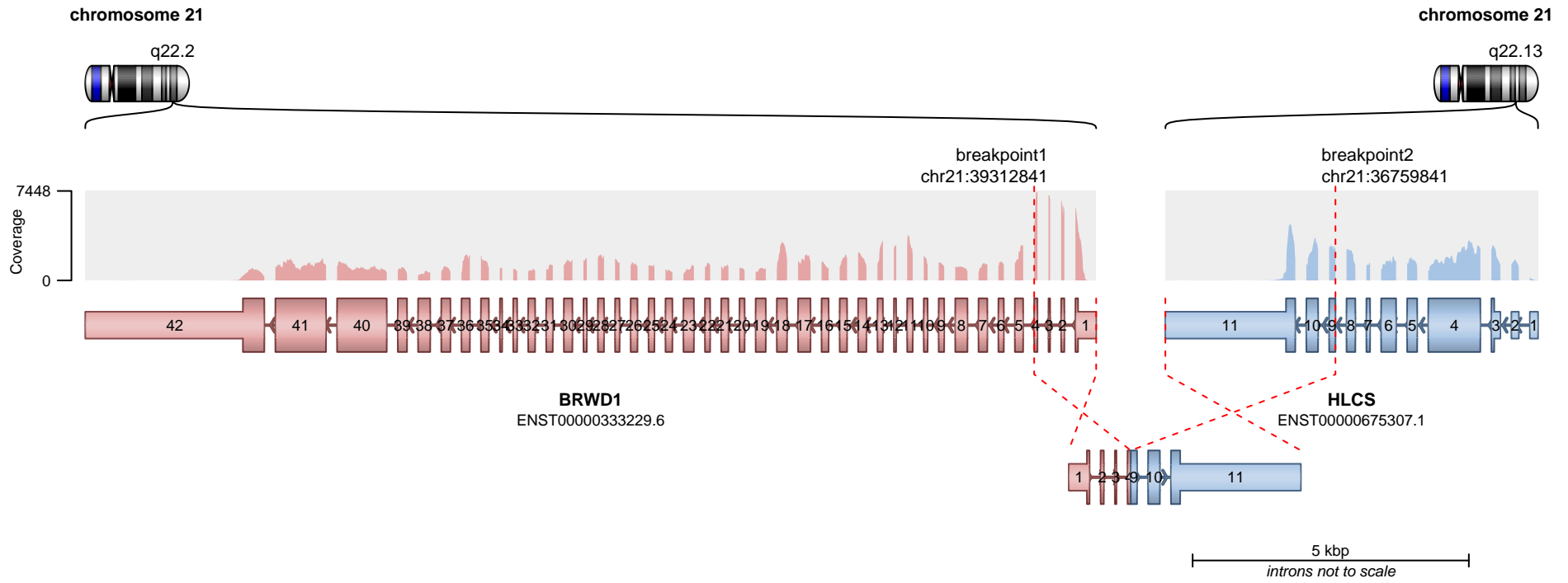
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



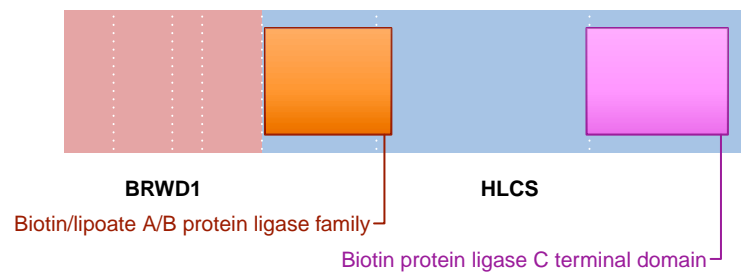
**SUPPORTING READ COUNT**

Split reads = 494  
Discordant mates = 10

- translocation
- duplication
- deletion
- inversion



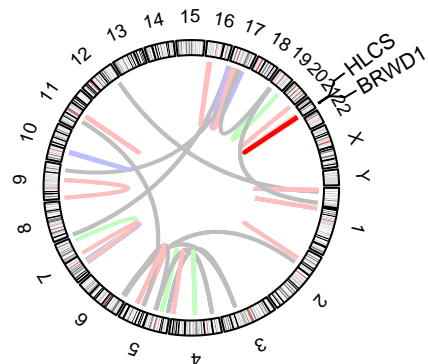
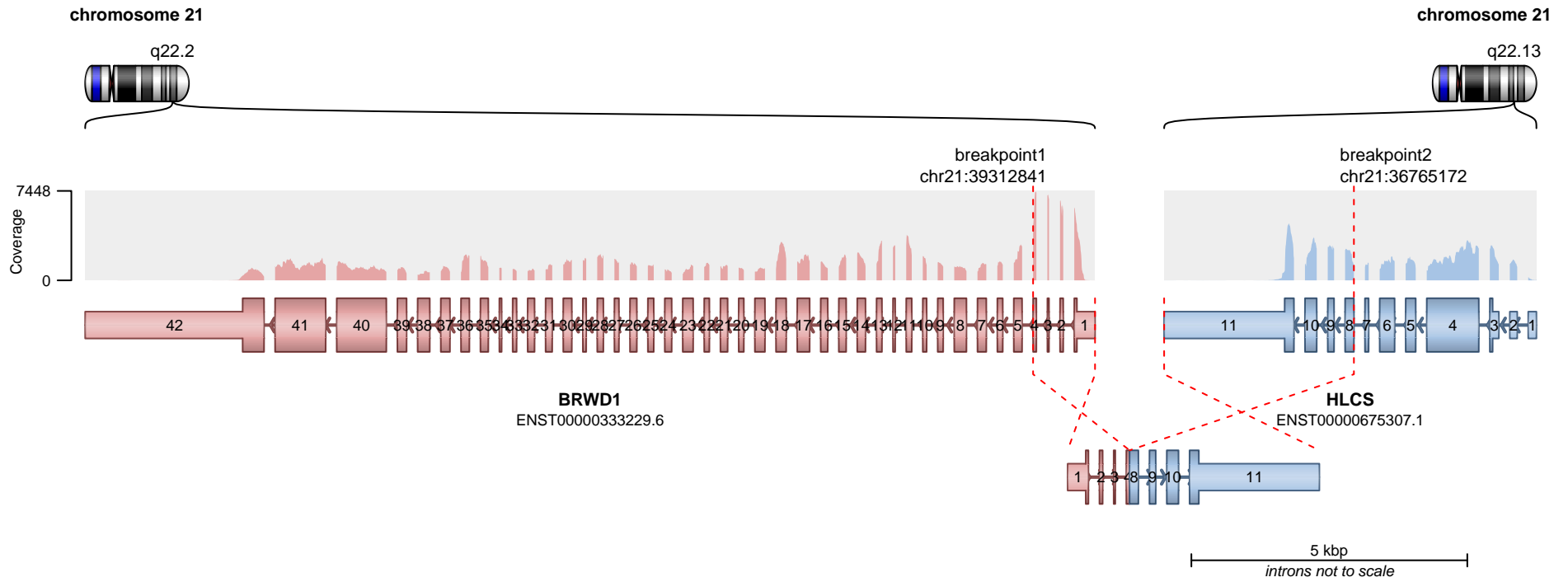
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



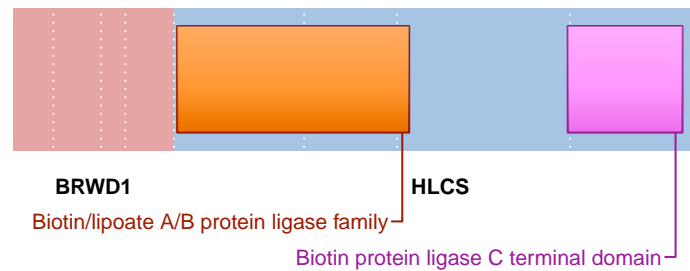
**SUPPORTING READ COUNT**

Split reads = 16  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



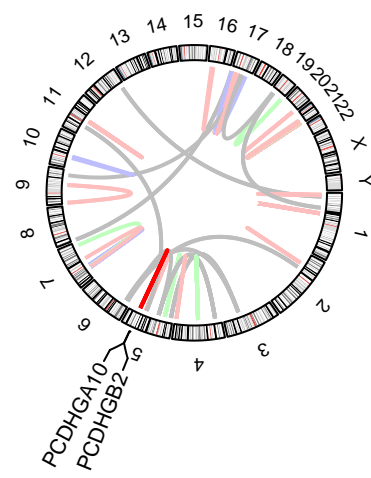
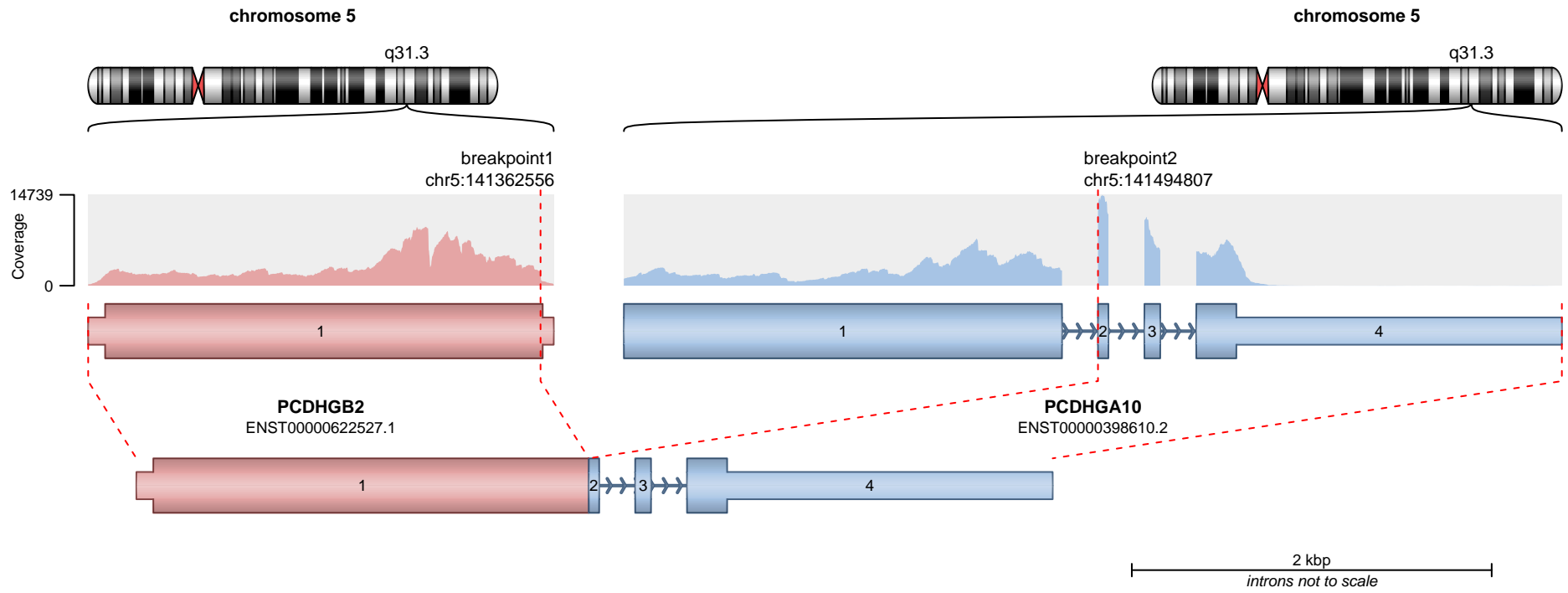
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



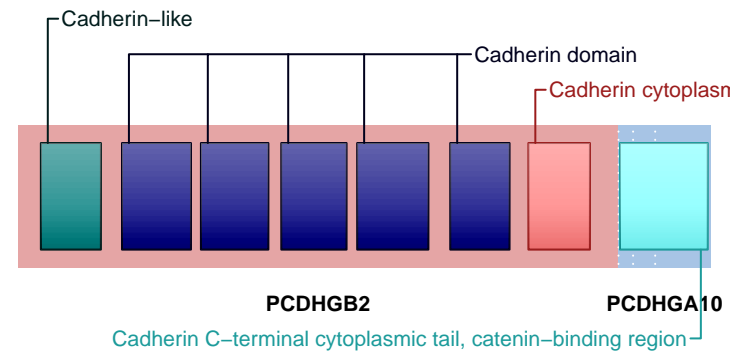
**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 8

- translocation
- duplication
- deletion
- inversion



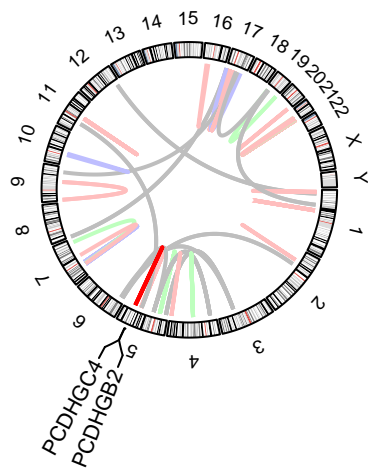
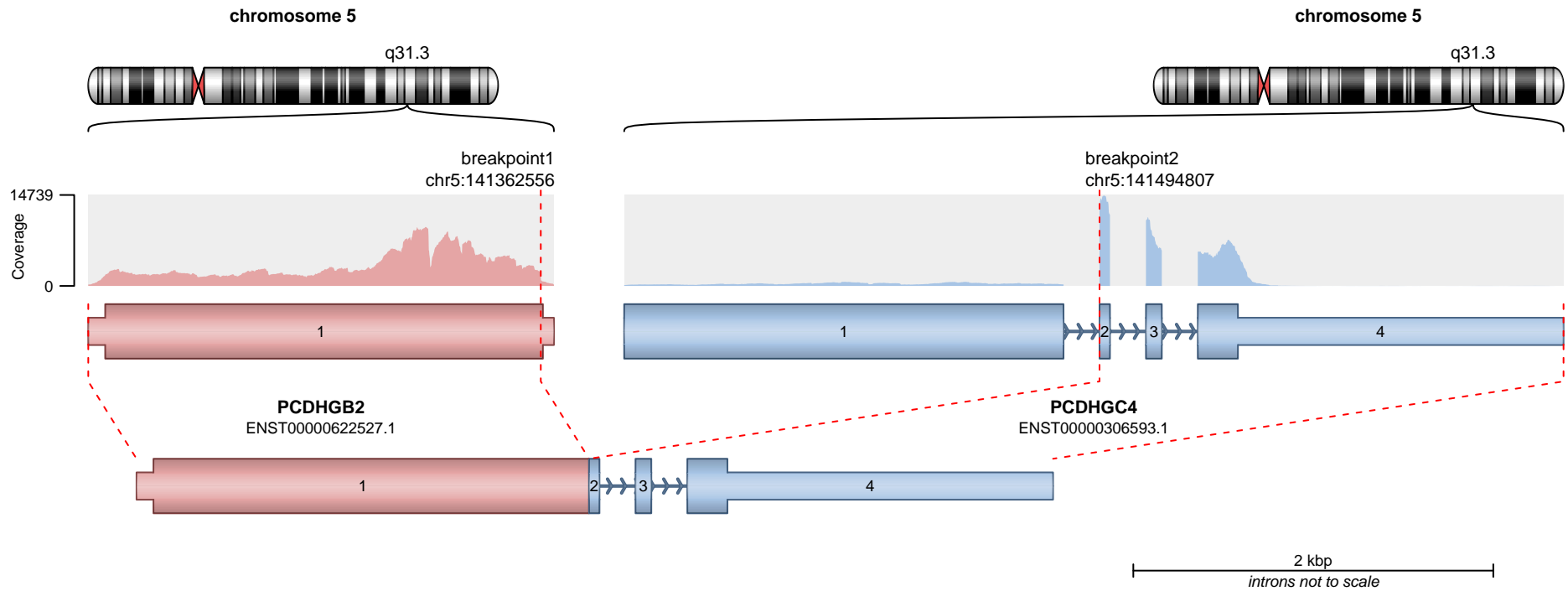
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



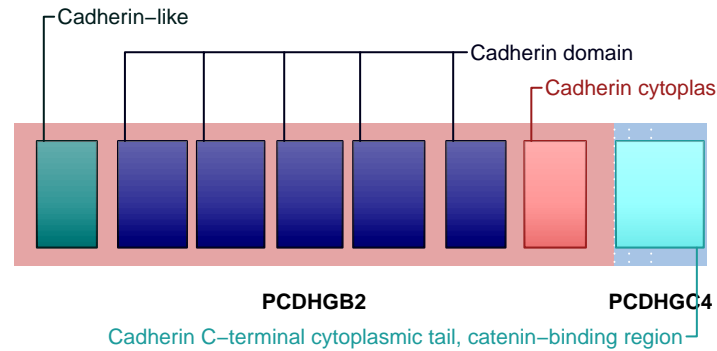
**SUPPORTING READ COUNT**

Split reads = 416  
Discordant mates = 3

- translocation
- duplication
- deletion
- inversion



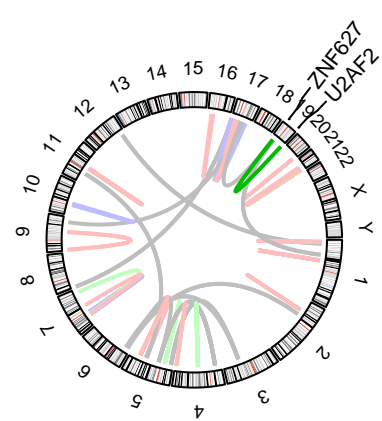
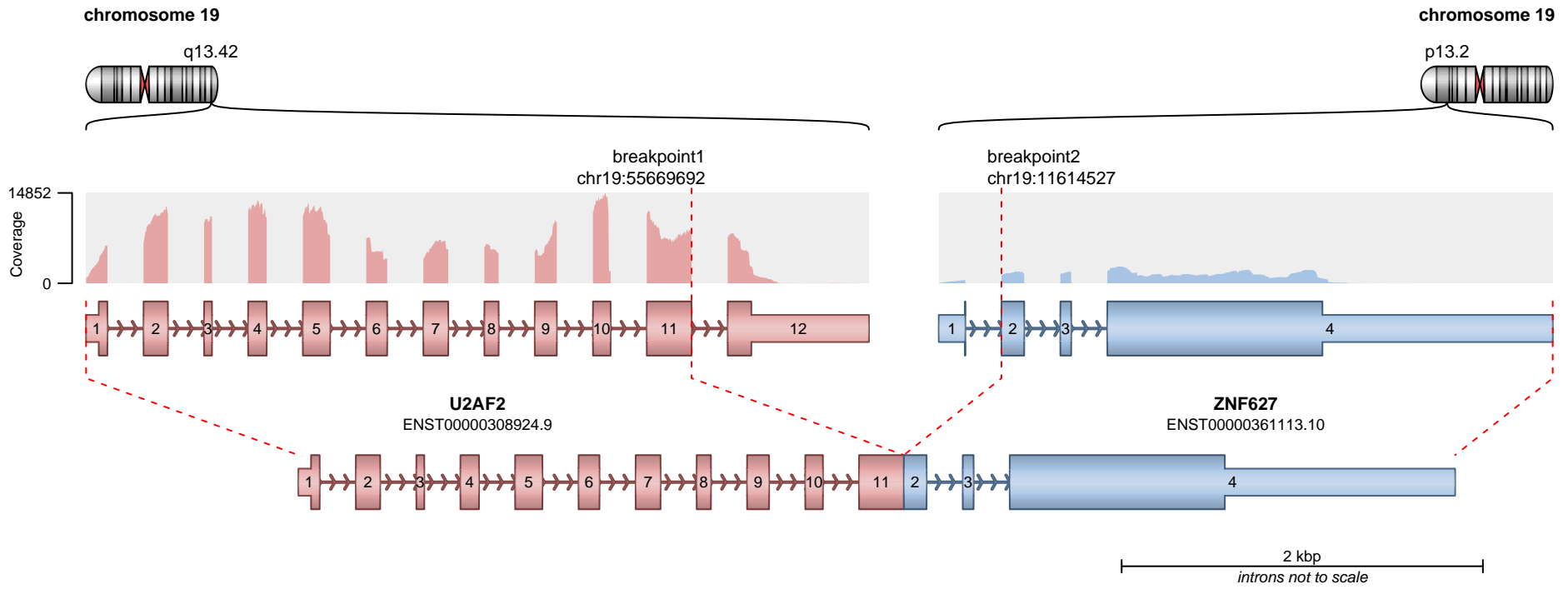
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



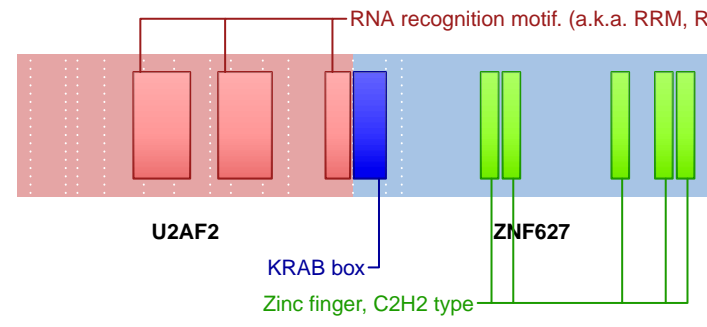
**SUPPORTING READ COUNT**

Split reads = 416  
Discordant mates = 3

— translocation — deletion  
— duplication — inversion



**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

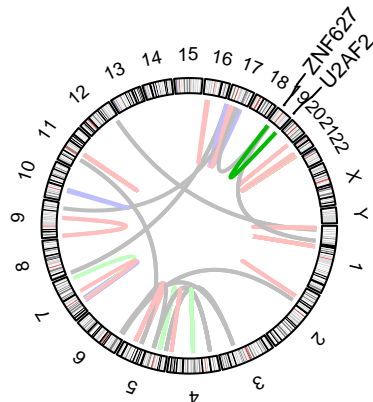
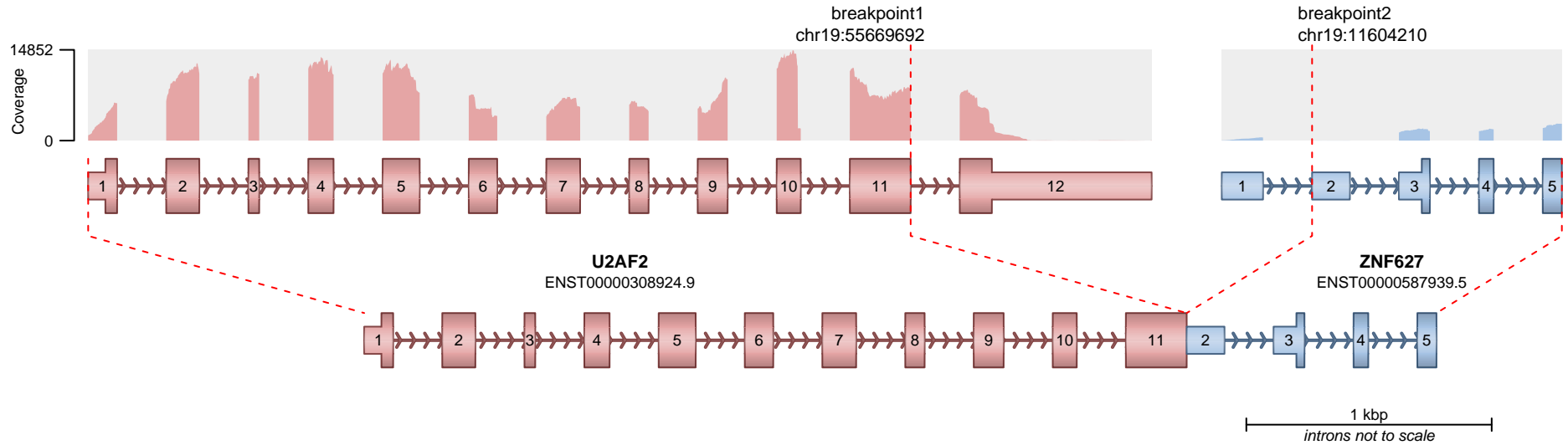
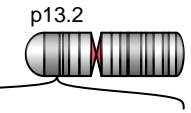
Split reads = 341  
Discordant mates = 10

- translocation
- duplication
- deletion
- inversion

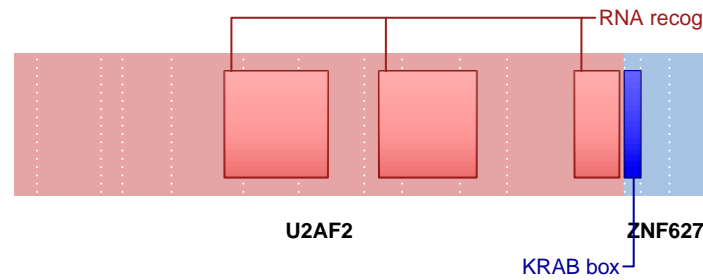
chromosome 19



chromosome 19



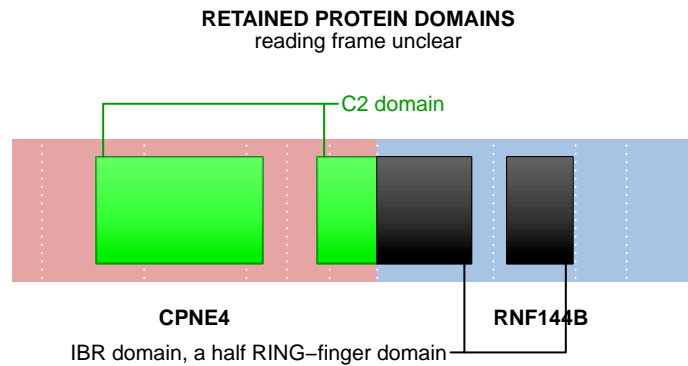
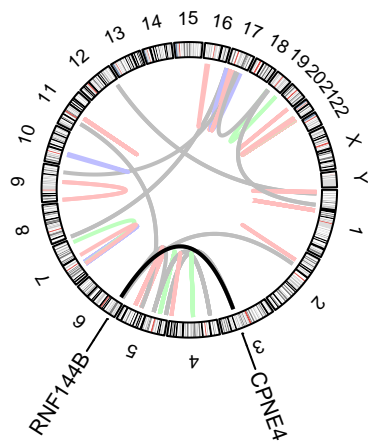
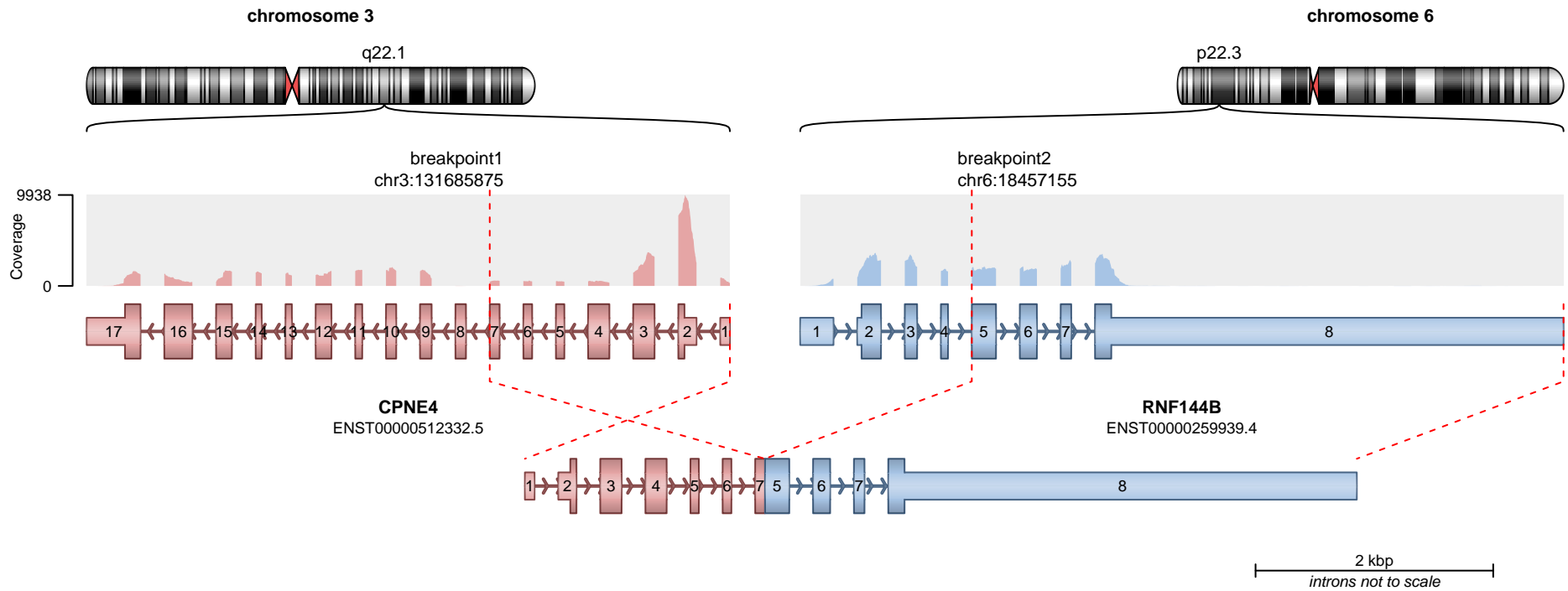
RETAINED PROTEIN DOMAINS  
reading frame unclear



SUPPORTING READ COUNT

Split reads = 10  
Discordant mates = 10

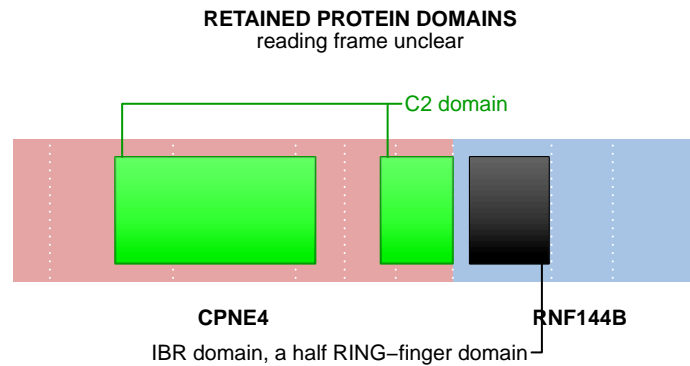
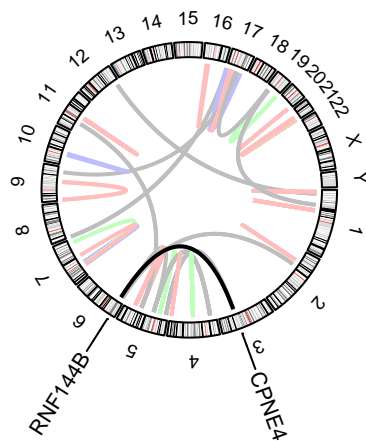
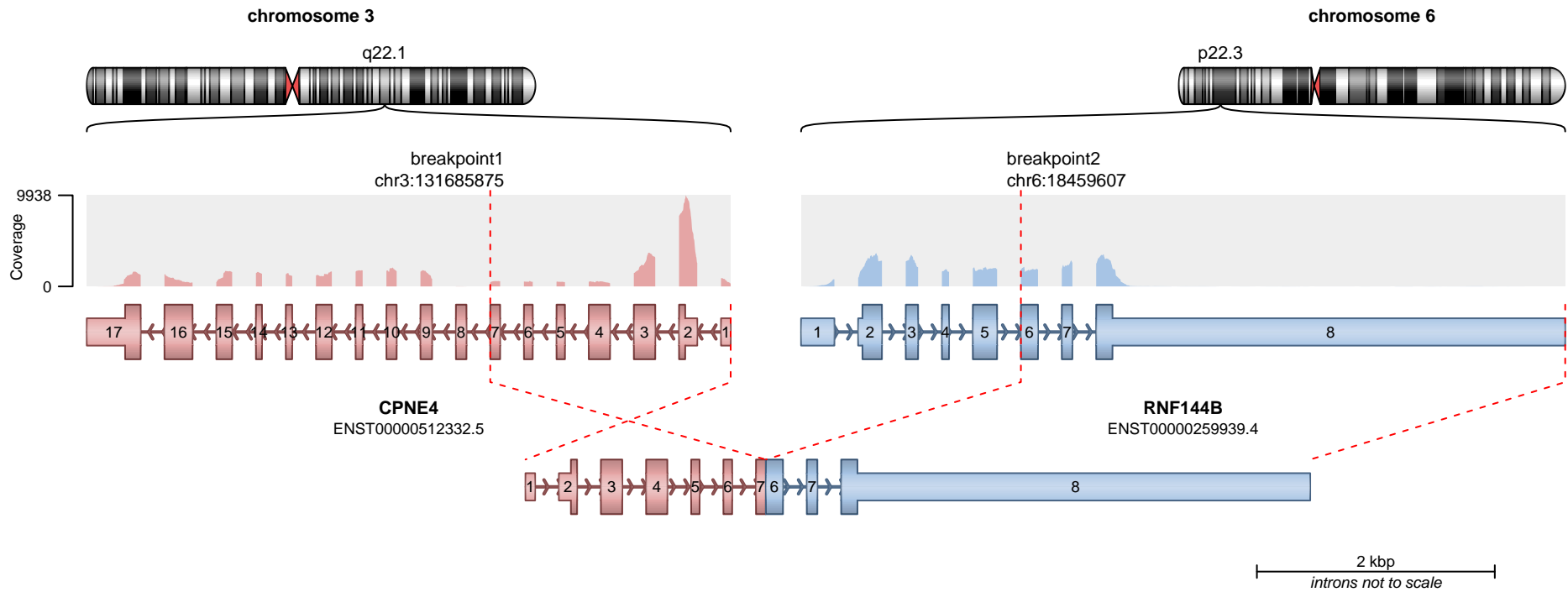
— translocation    — deletion  
— duplication    — inversion



**SUPPORTING READ COUNT**

Split reads = 245  
Discordant mates = 24

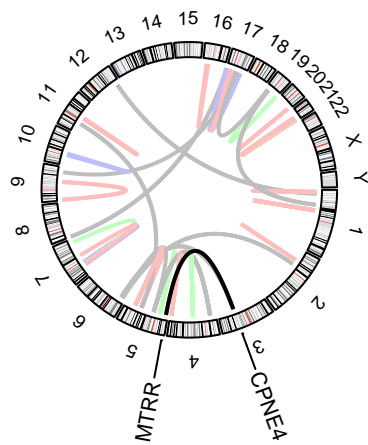
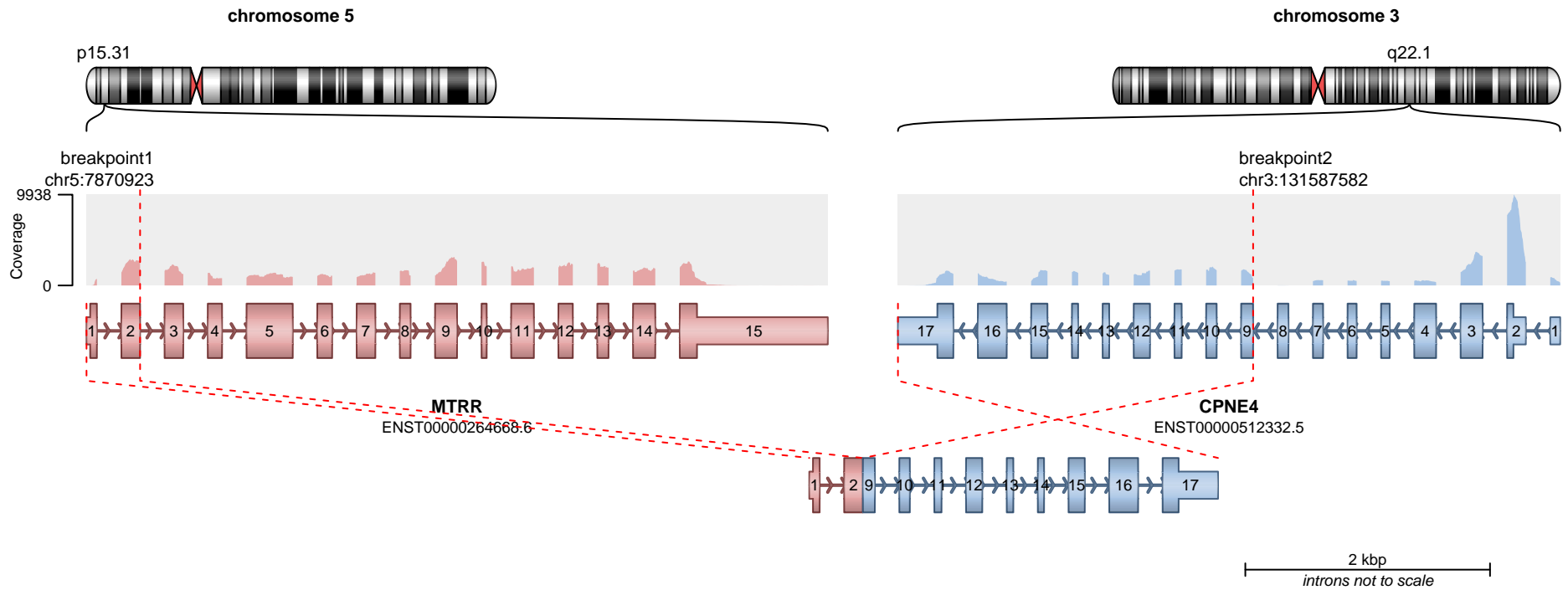
— translocation — deletion  
— duplication — inversion



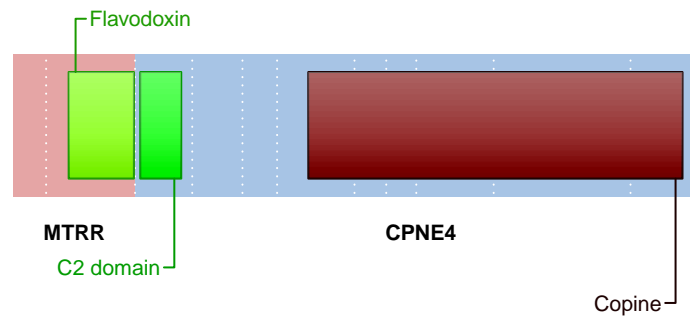
**SUPPORTING READ COUNT**

Split reads = 17  
Discordant mates = 1

— translocation — deletion  
— duplication — inversion



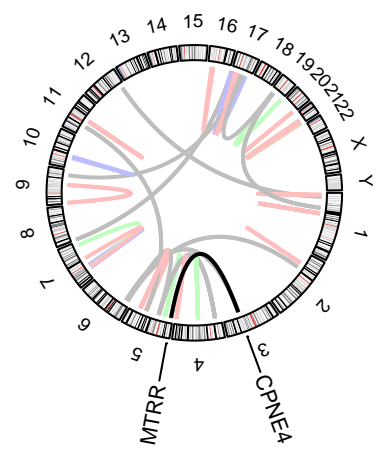
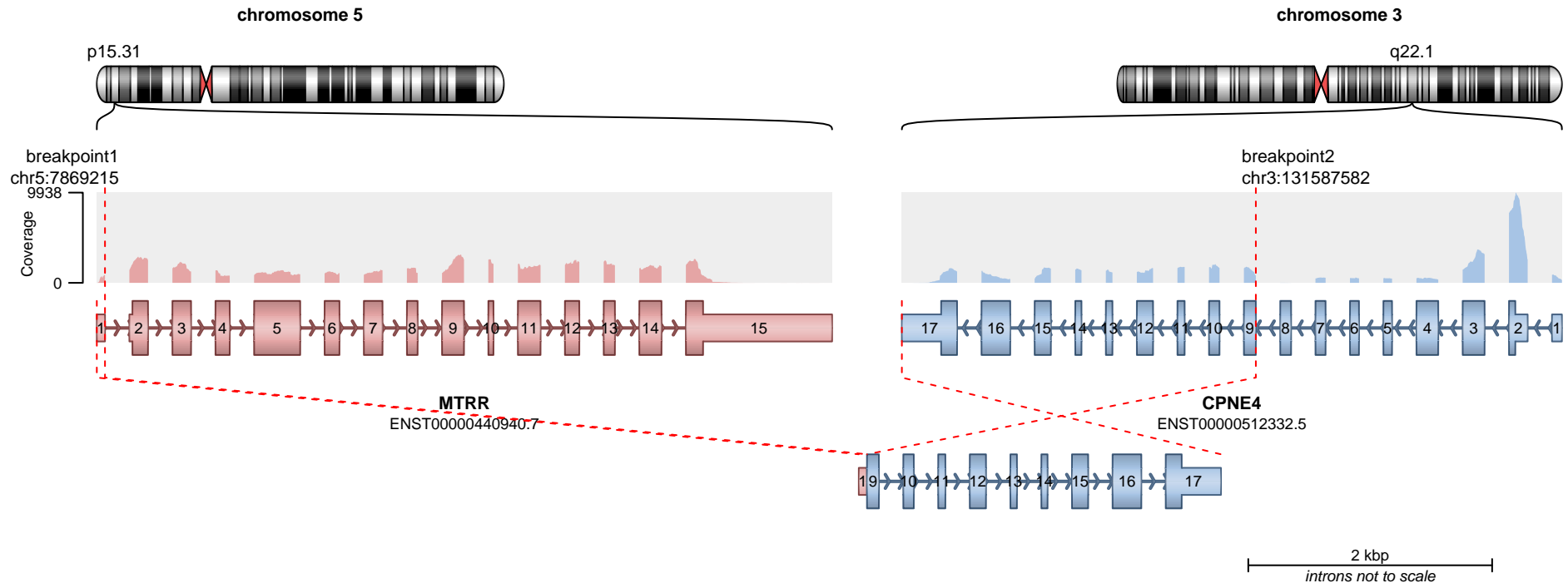
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



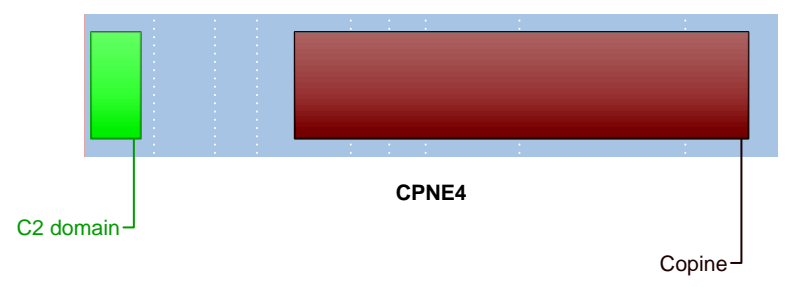
**SUPPORTING READ COUNT**

Split reads = 233  
Discordant mates = 10

— translocation — deletion  
— duplication — inversion



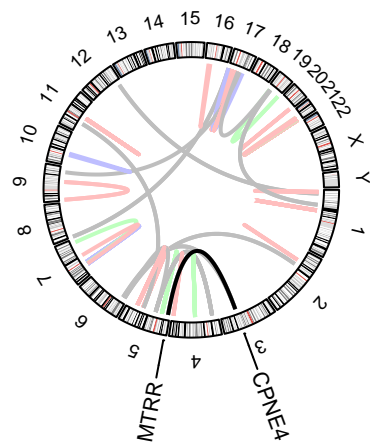
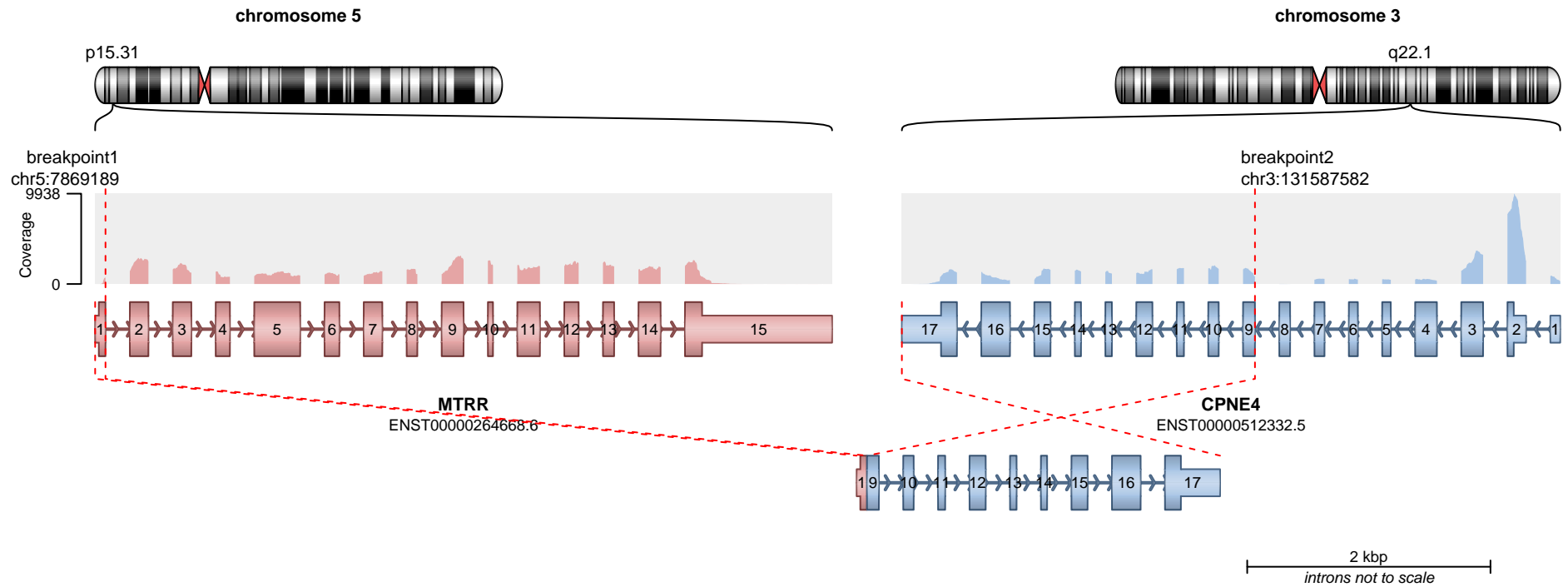
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



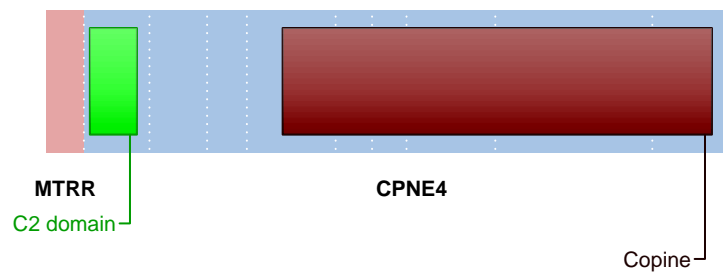
**SUPPORTING READ COUNT**

Split reads = 120  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



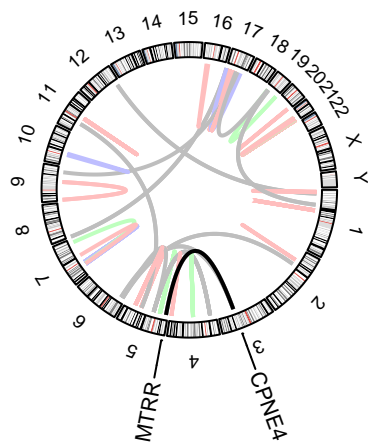
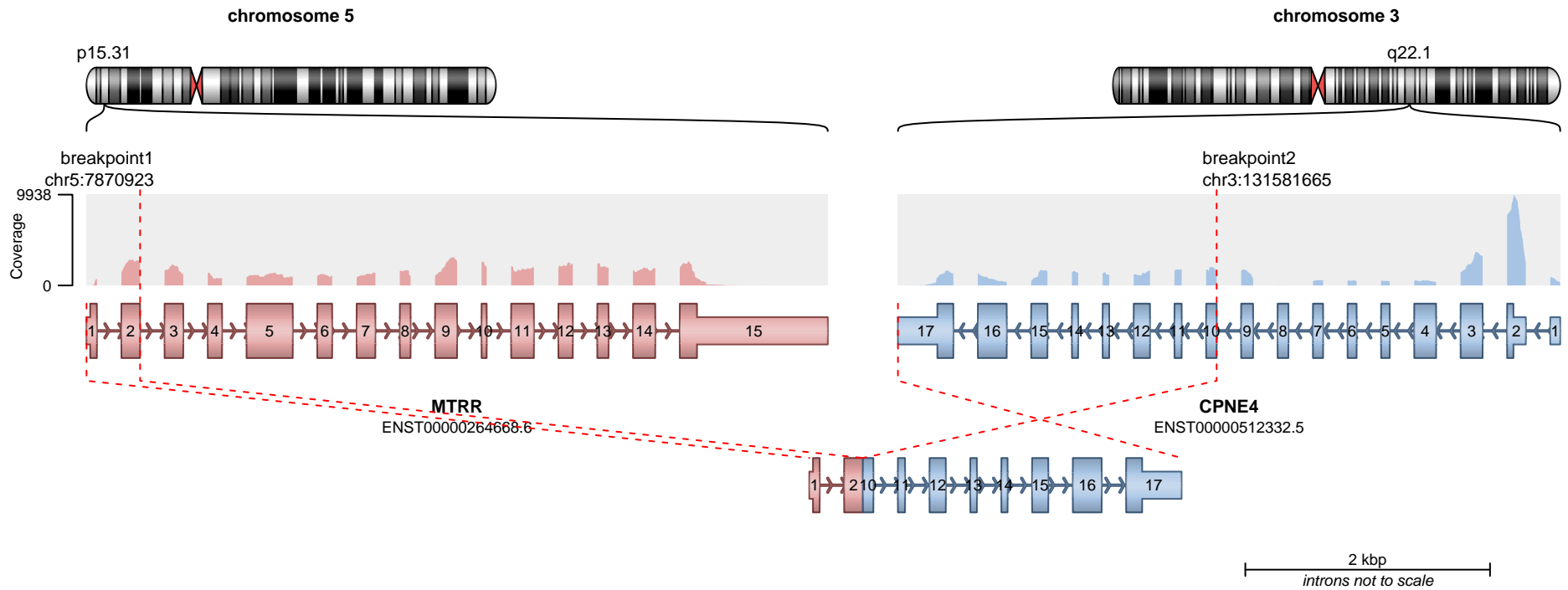
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



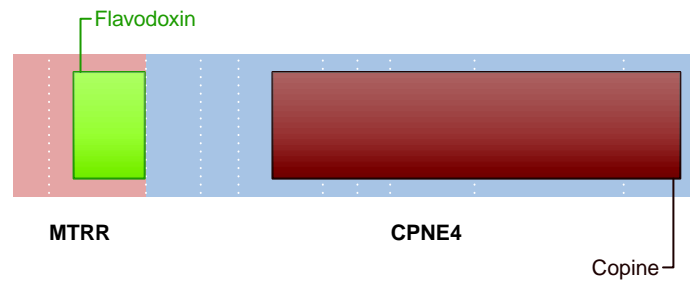
**SUPPORTING READ COUNT**

Split reads = 24  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



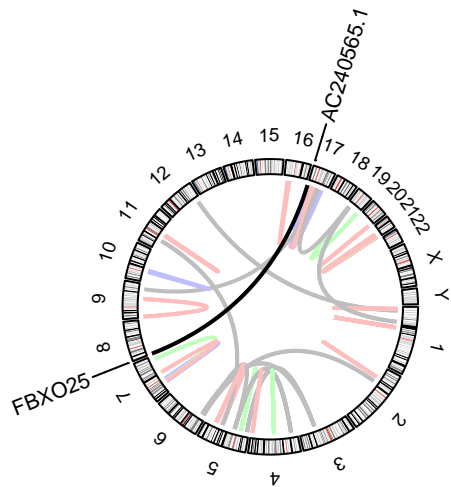
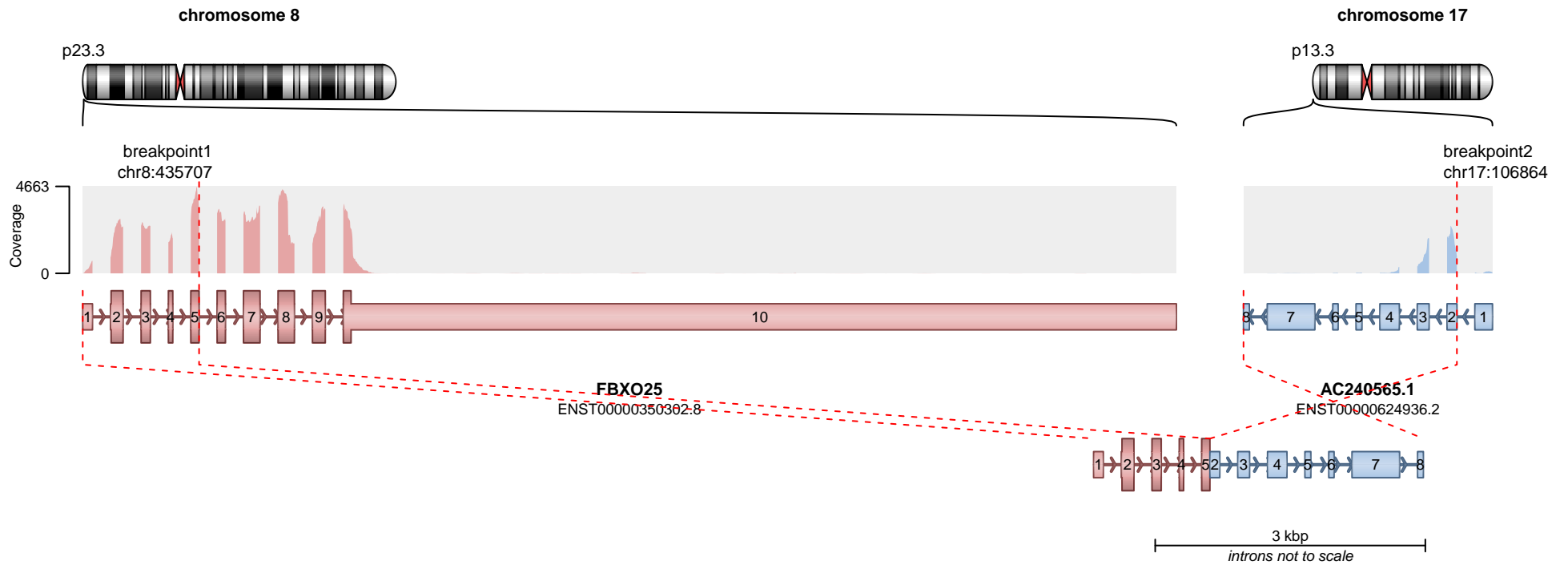
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 2

- translocation
- duplication
- deletion
- inversion

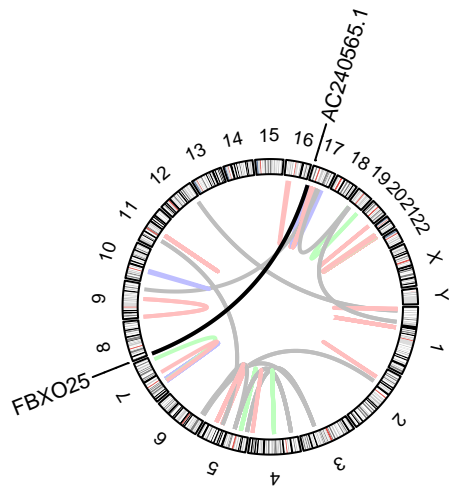
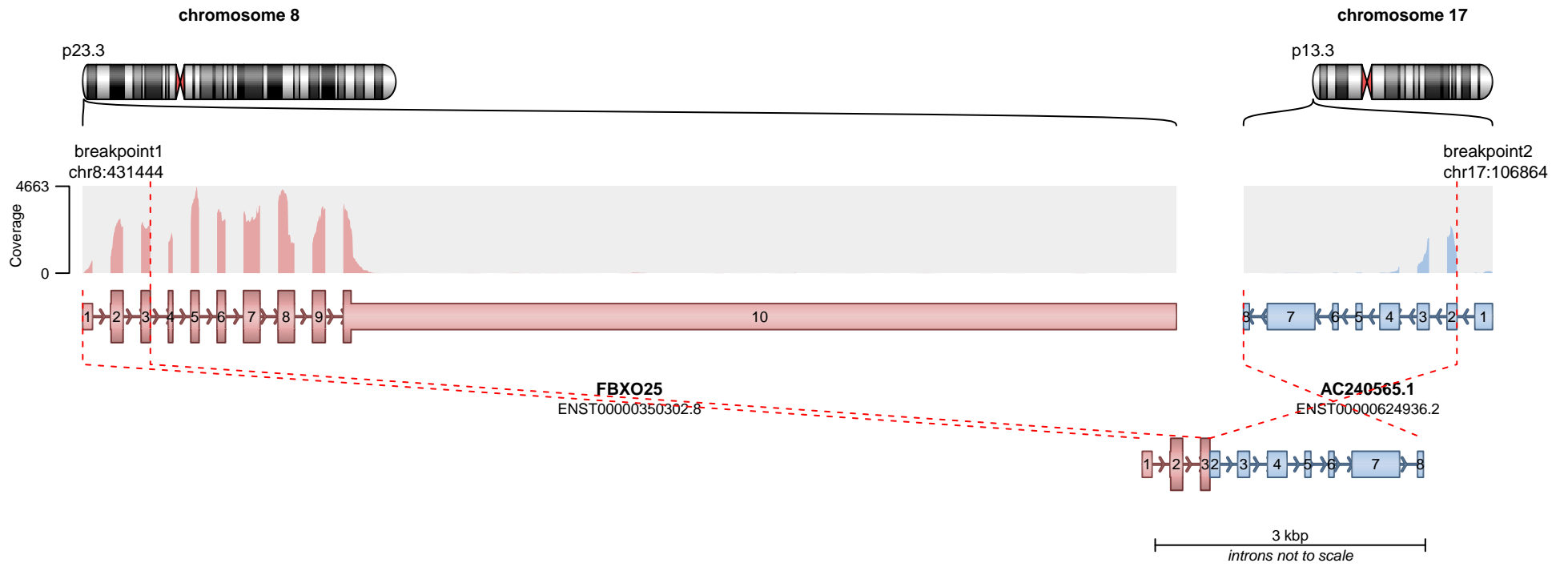


No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 231  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion

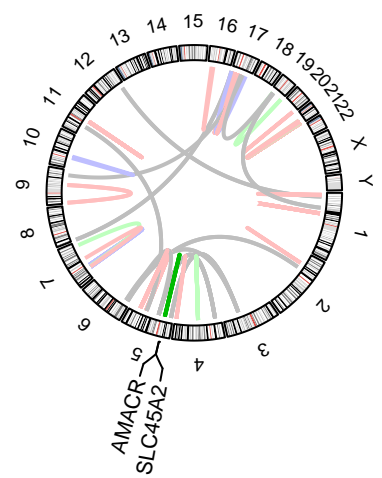
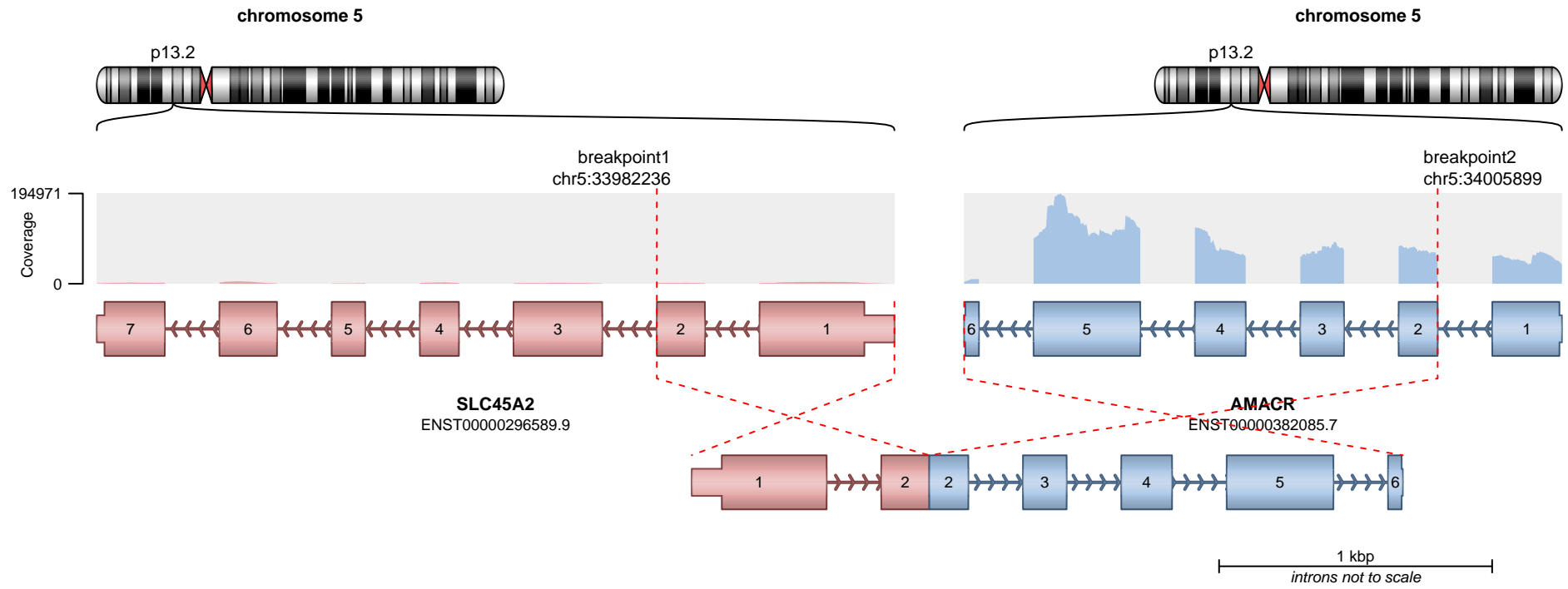


No protein domains retained in fusion.

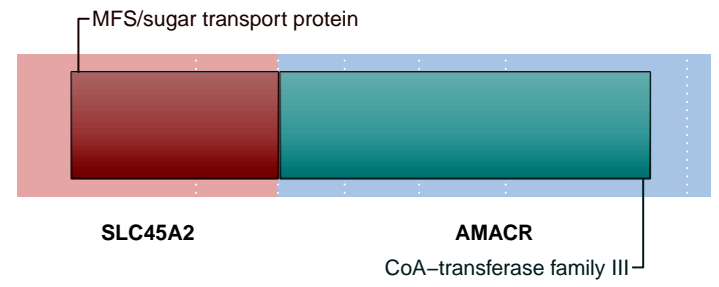
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



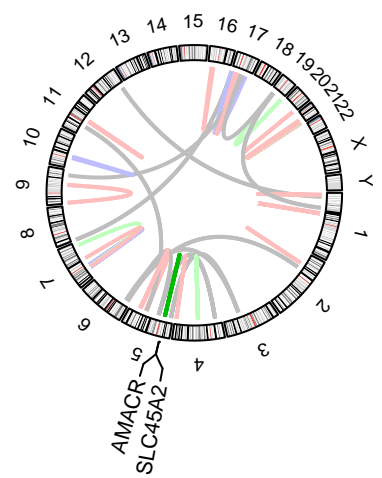
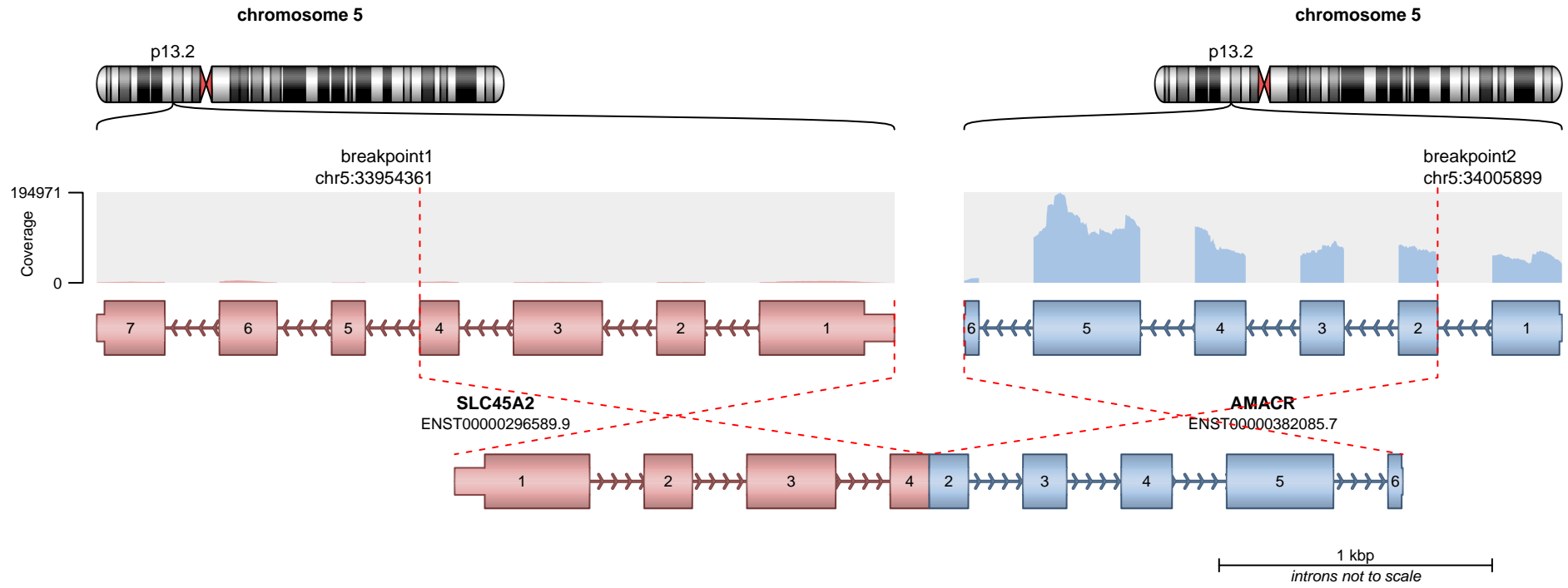
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



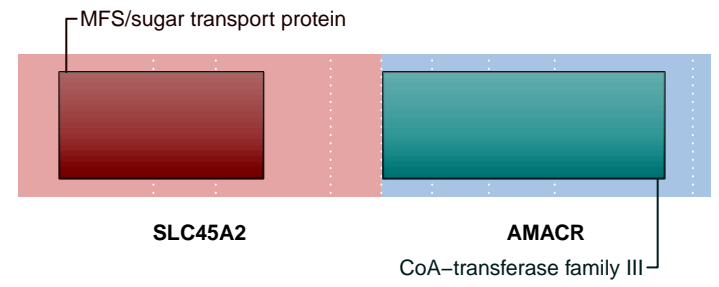
**SUPPORTING READ COUNT**

Split reads = 186  
Discordant mates = 12

— translocation — deletion  
— duplication — inversion



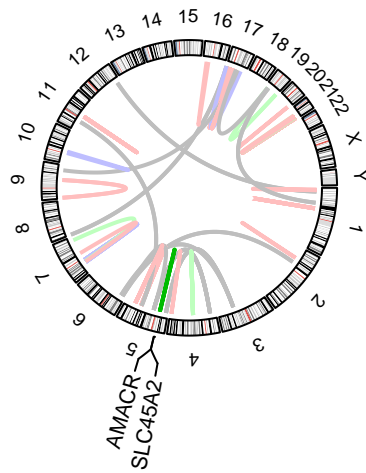
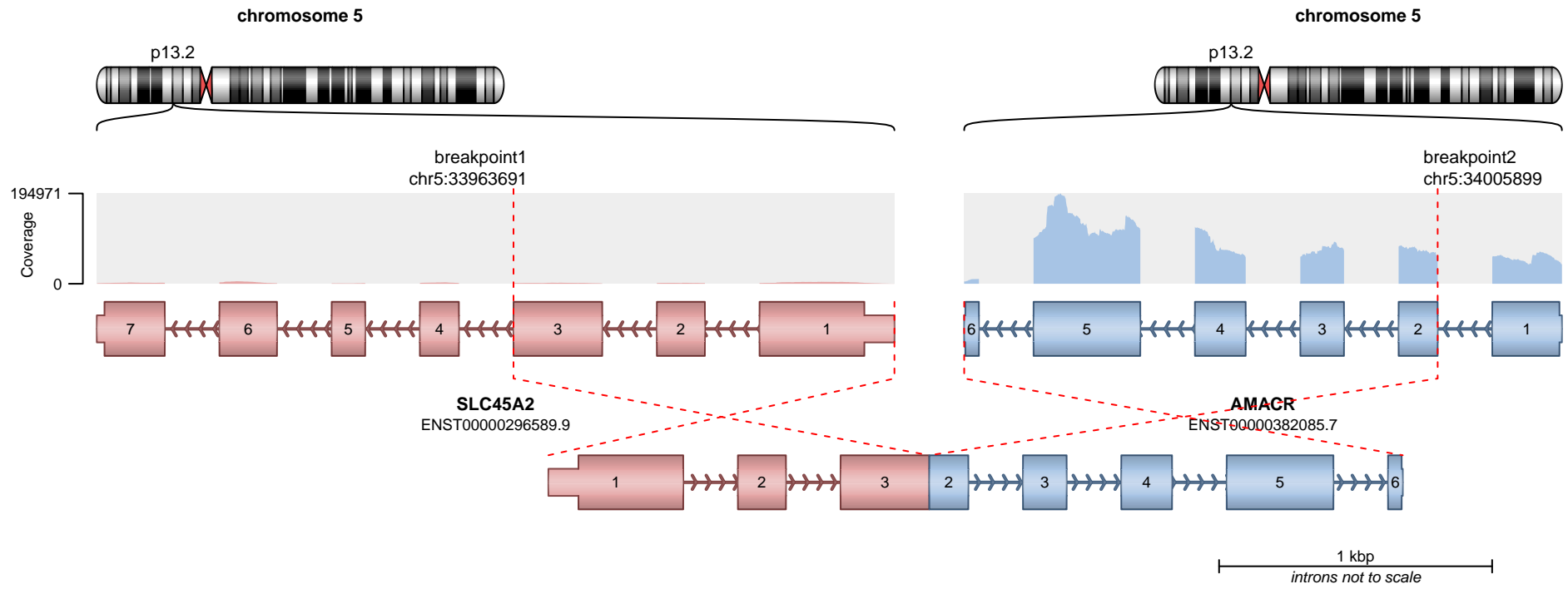
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



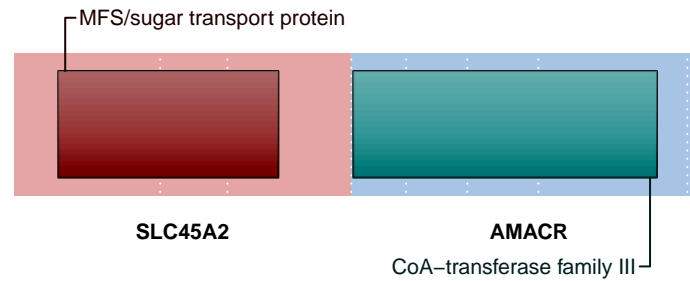
**SUPPORTING READ COUNT**

Split reads = 22  
Discordant mates = 16

- translocation
- duplication
- deletion
- inversion



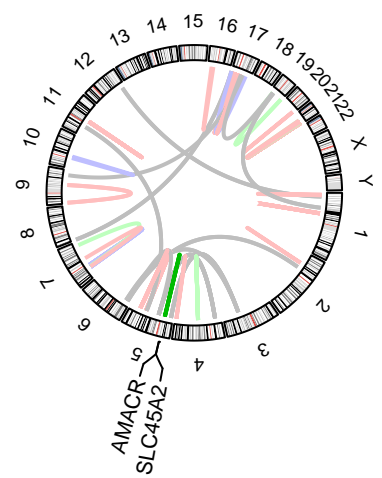
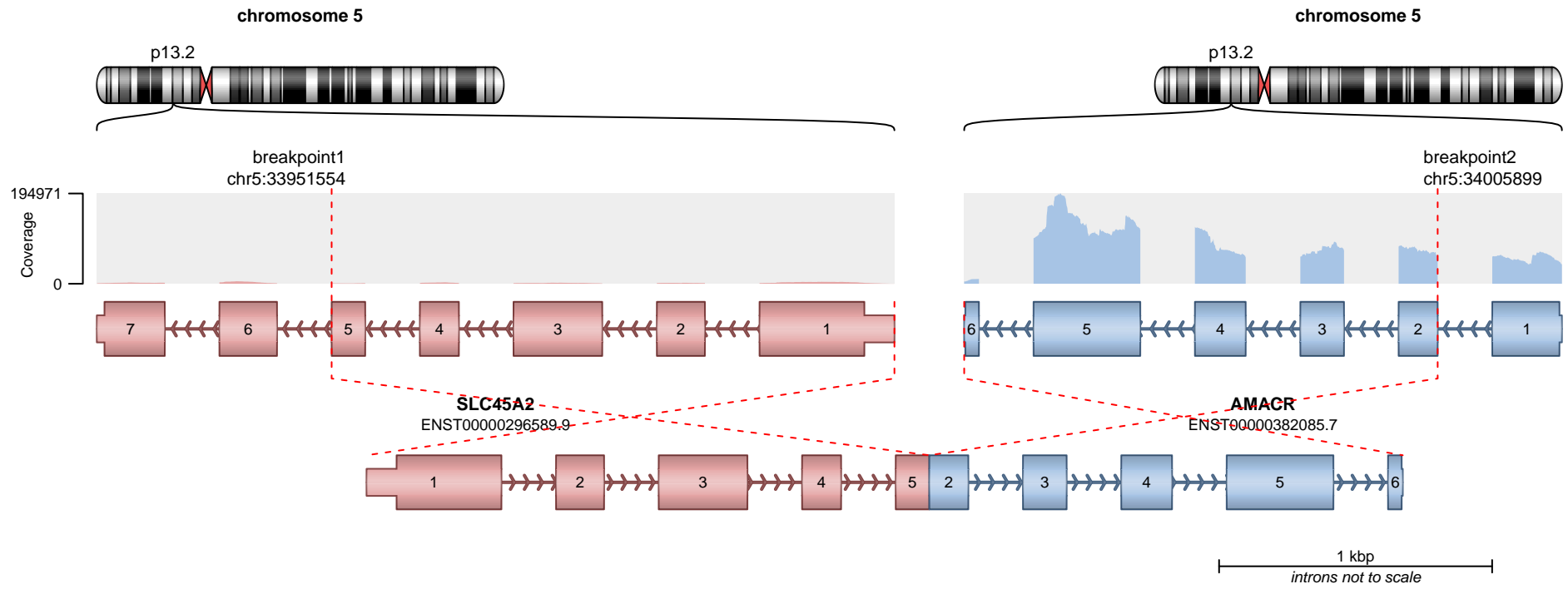
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



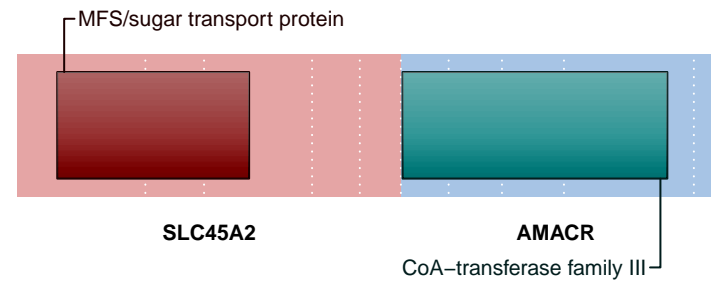
**SUPPORTING READ COUNT**

Split reads = 17  
Discordant mates = 16

— translocation    — deletion  
— duplication    — inversion



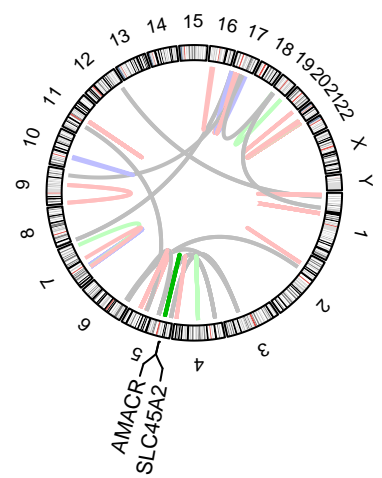
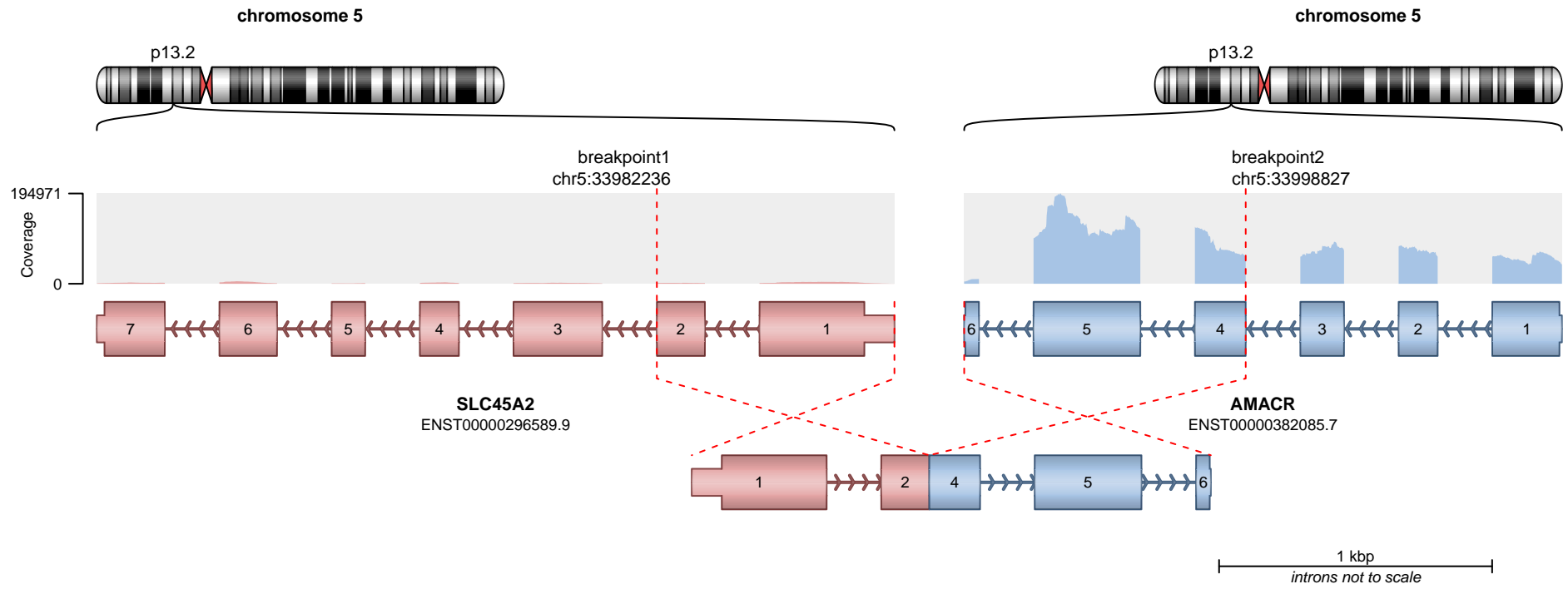
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



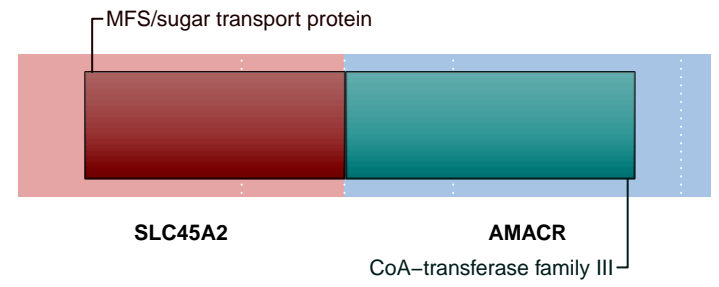
**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 18

- translocation
- duplication
- deletion
- inversion



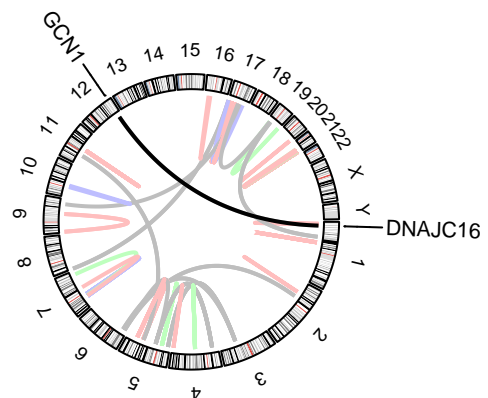
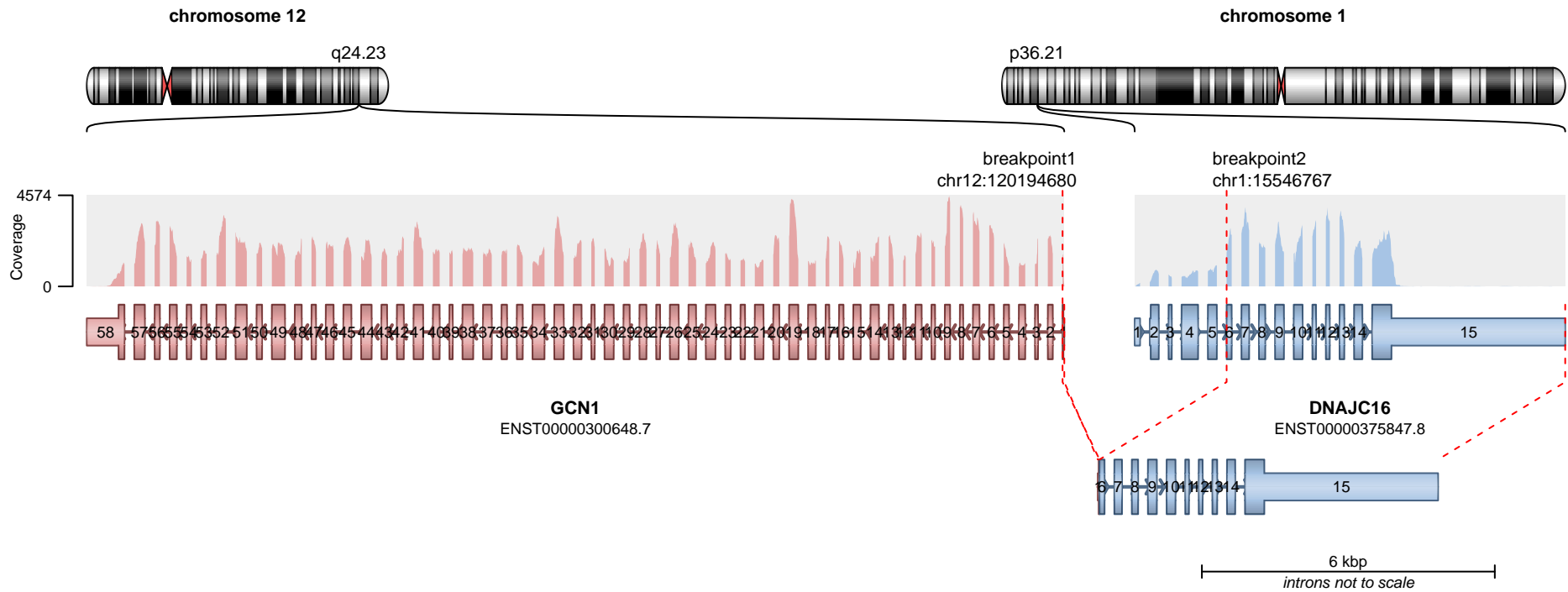
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion

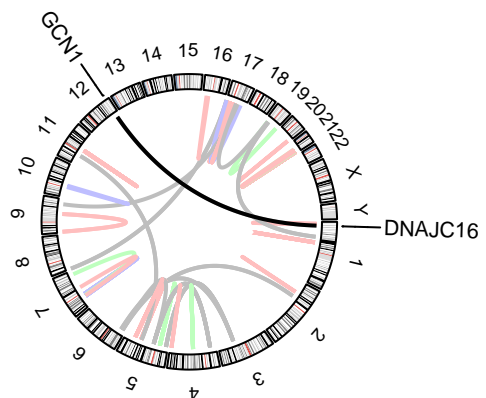
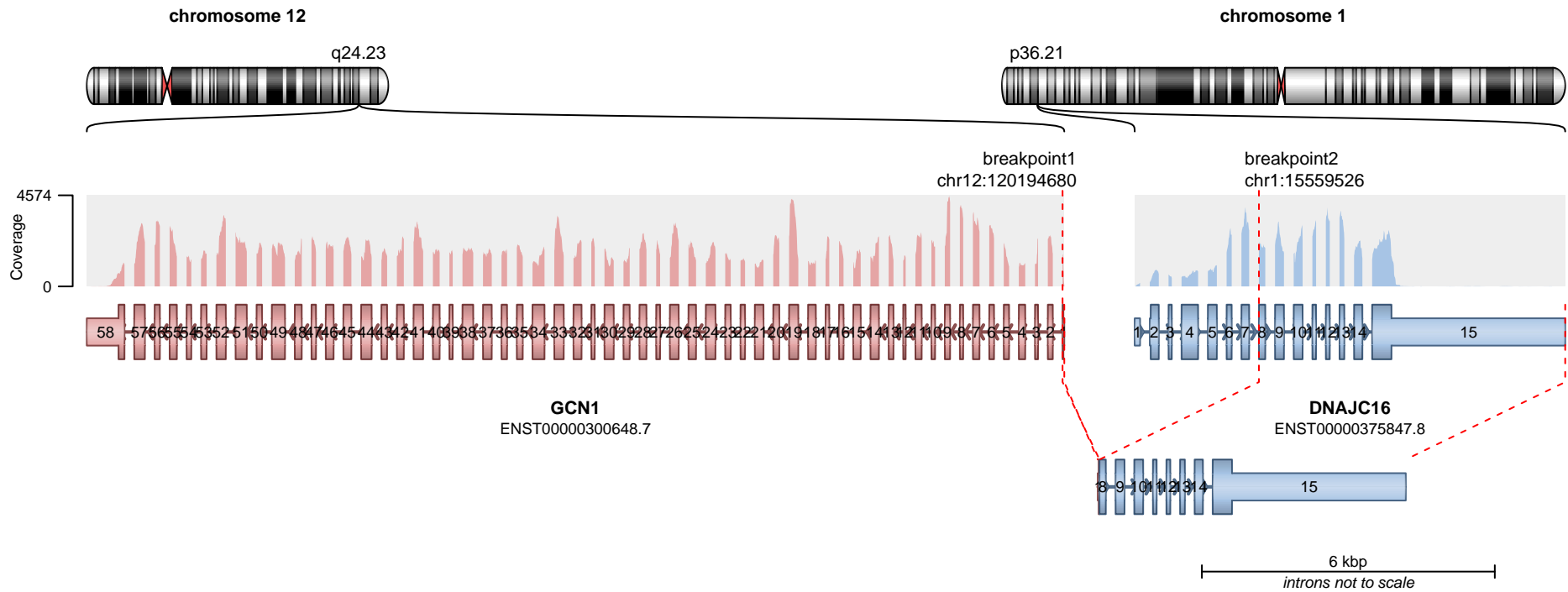


No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 162  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

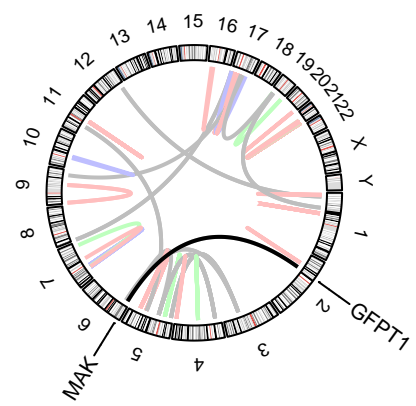
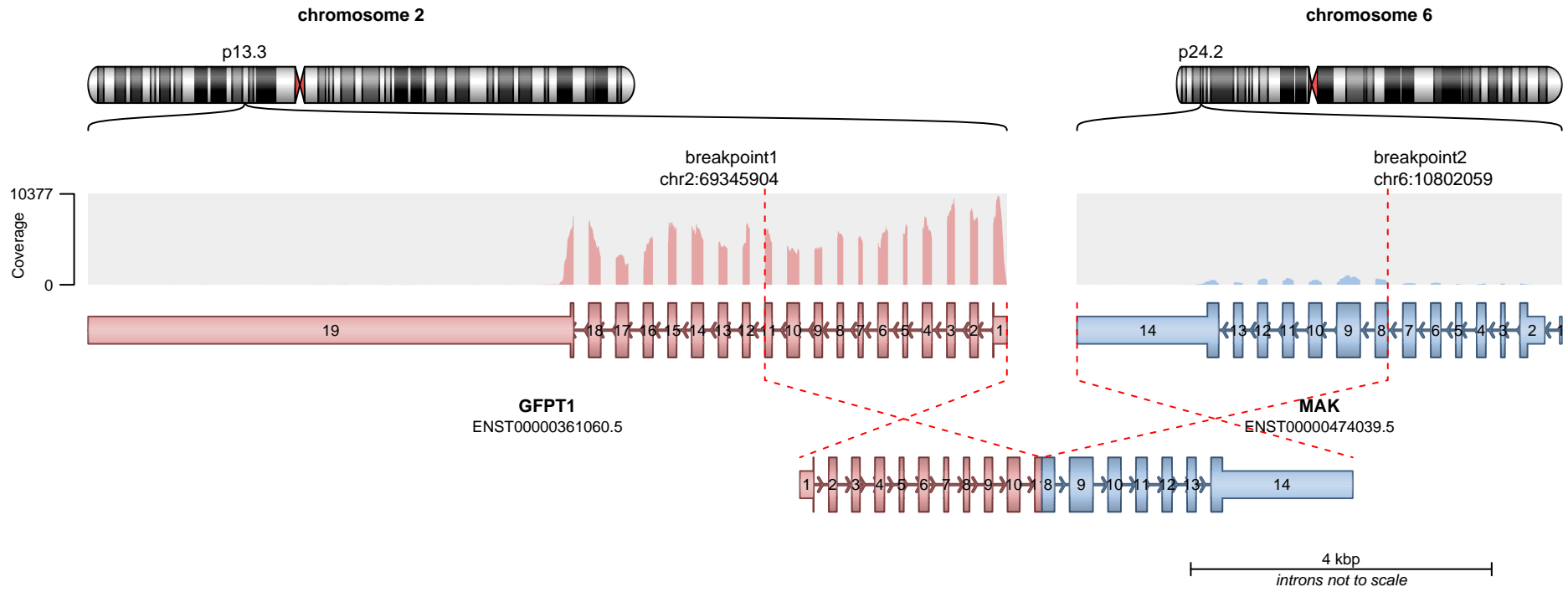


No protein domains retained in fusion.

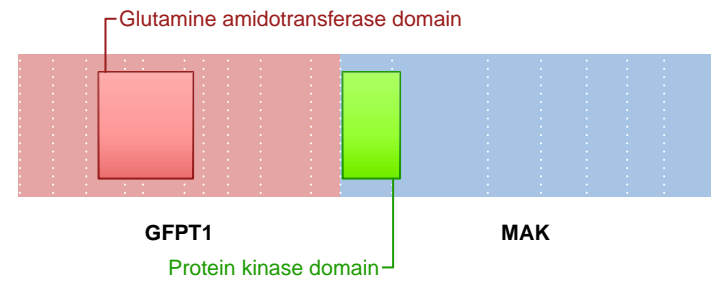
**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



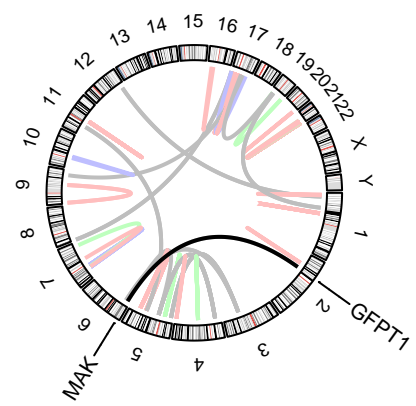
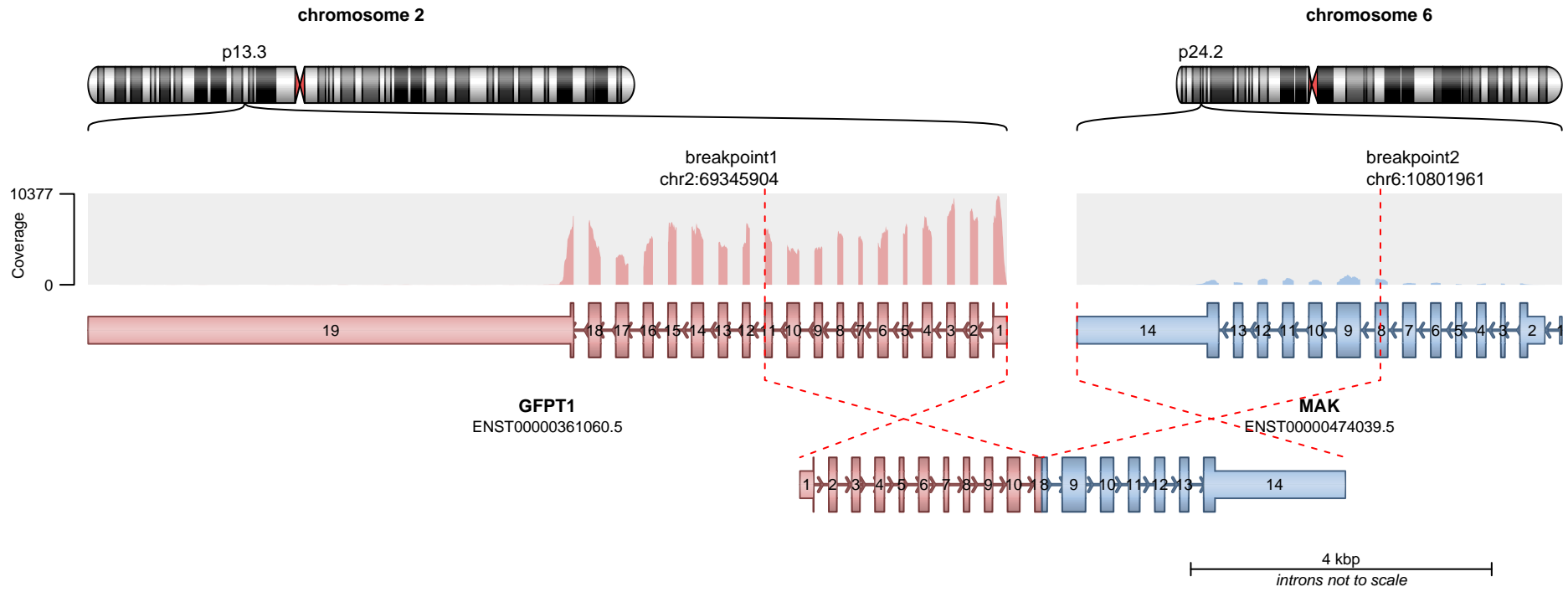
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



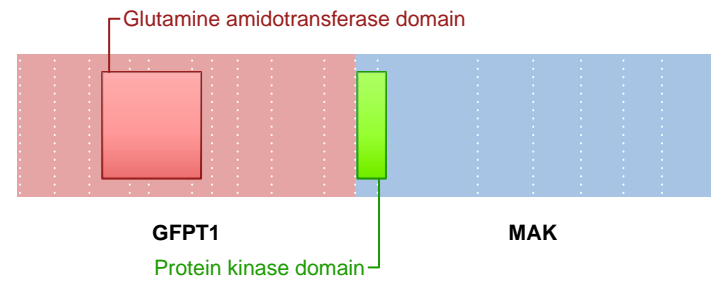
**SUPPORTING READ COUNT**

Split reads = 136  
Discordant mates = 16

- translocation
- duplication
- deletion
- inversion



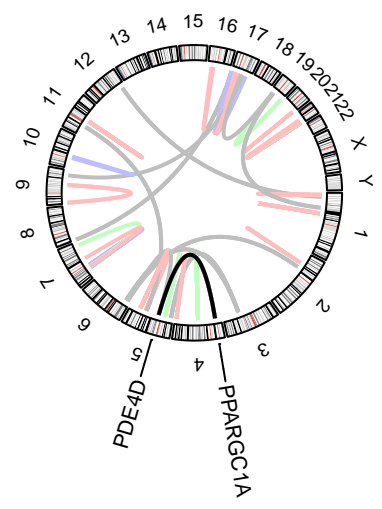
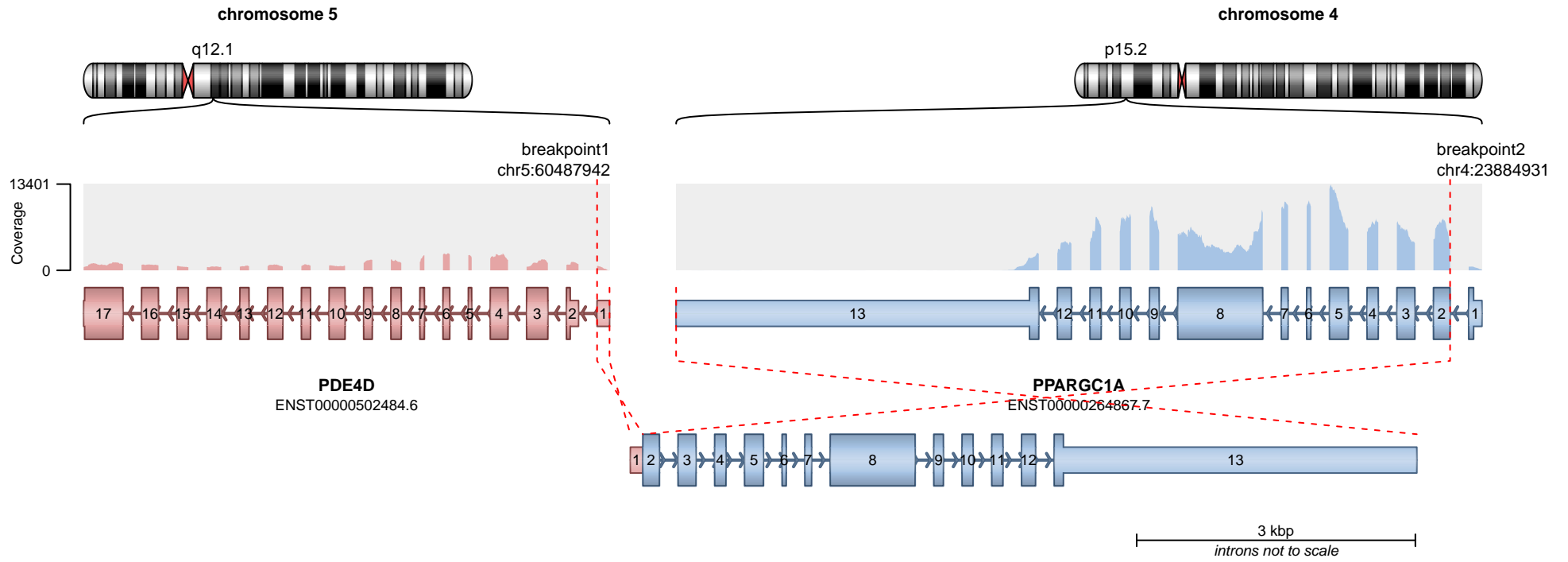
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

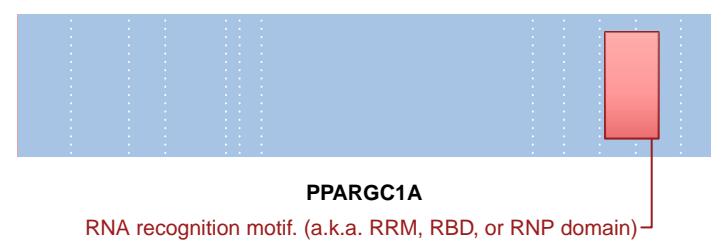
Split reads = 27  
Discordant mates = 4

- translocation
- duplication
- deletion
- inversion



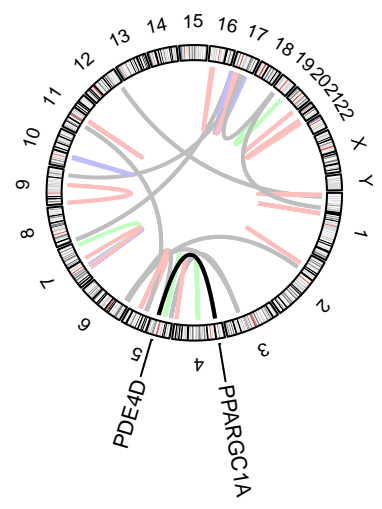
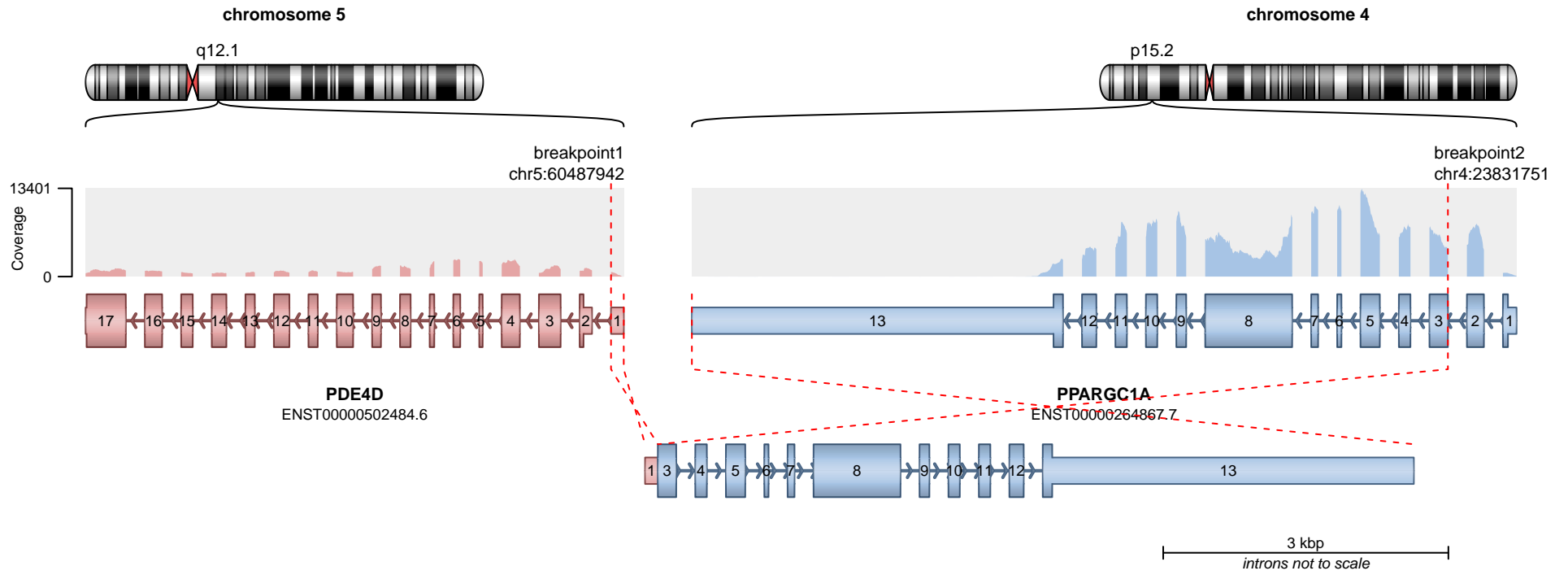
— translocation    — deletion  
 — duplication    — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 132  
Discordant mates = 3



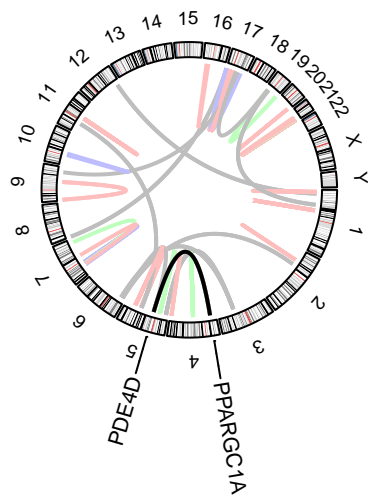
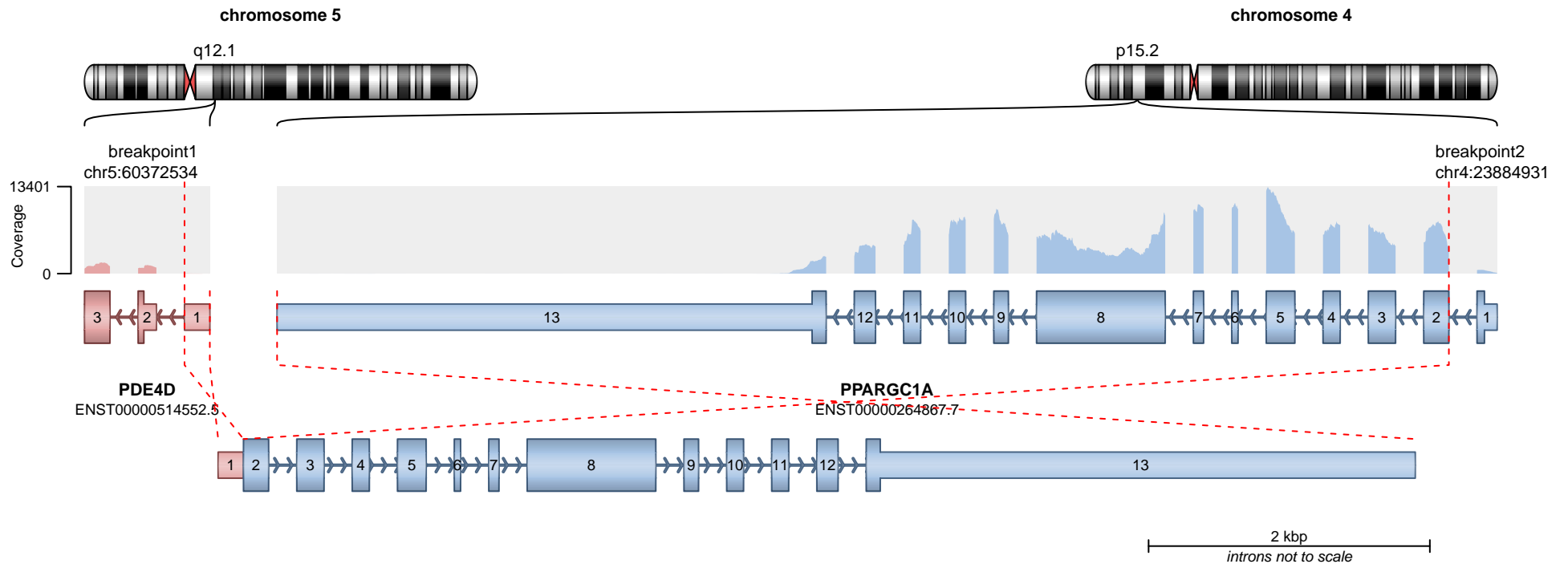
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



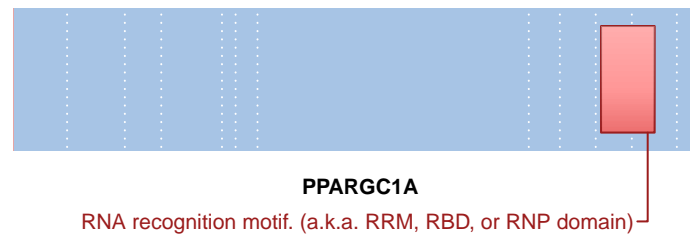
**SUPPORTING READ COUNT**

Split reads = 13  
Discordant mates = 0



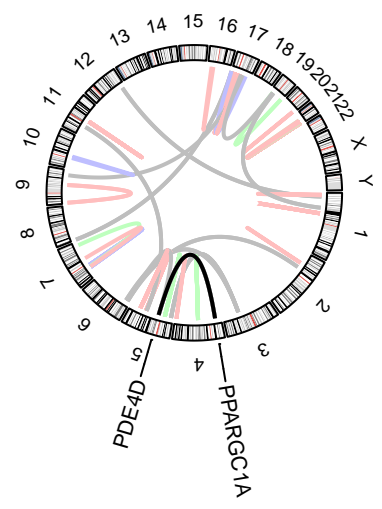
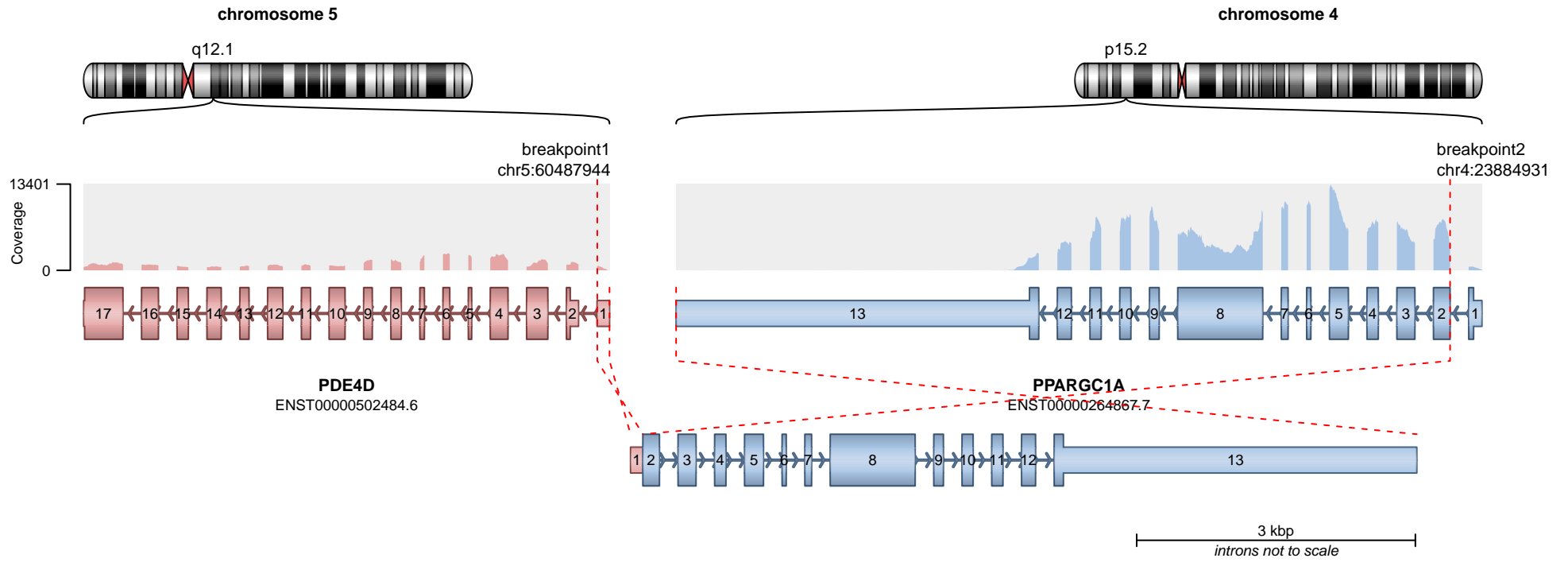
— translocation    — deletion  
 — duplication    — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



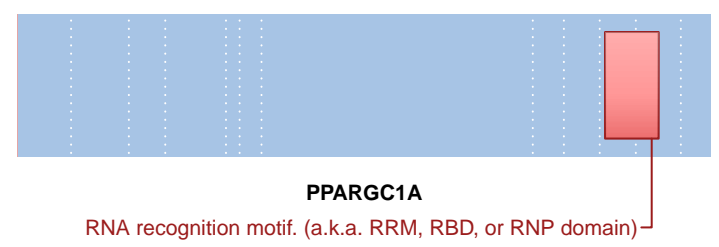
**SUPPORTING READ COUNT**

Split reads = 6  
Discordant mates = 3



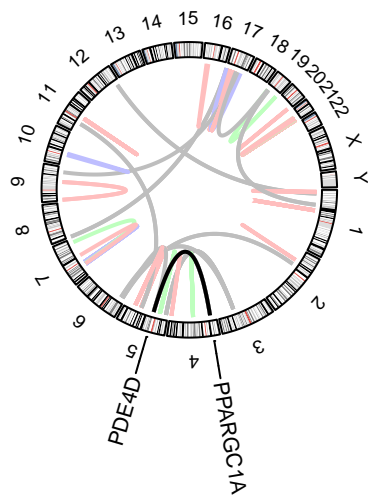
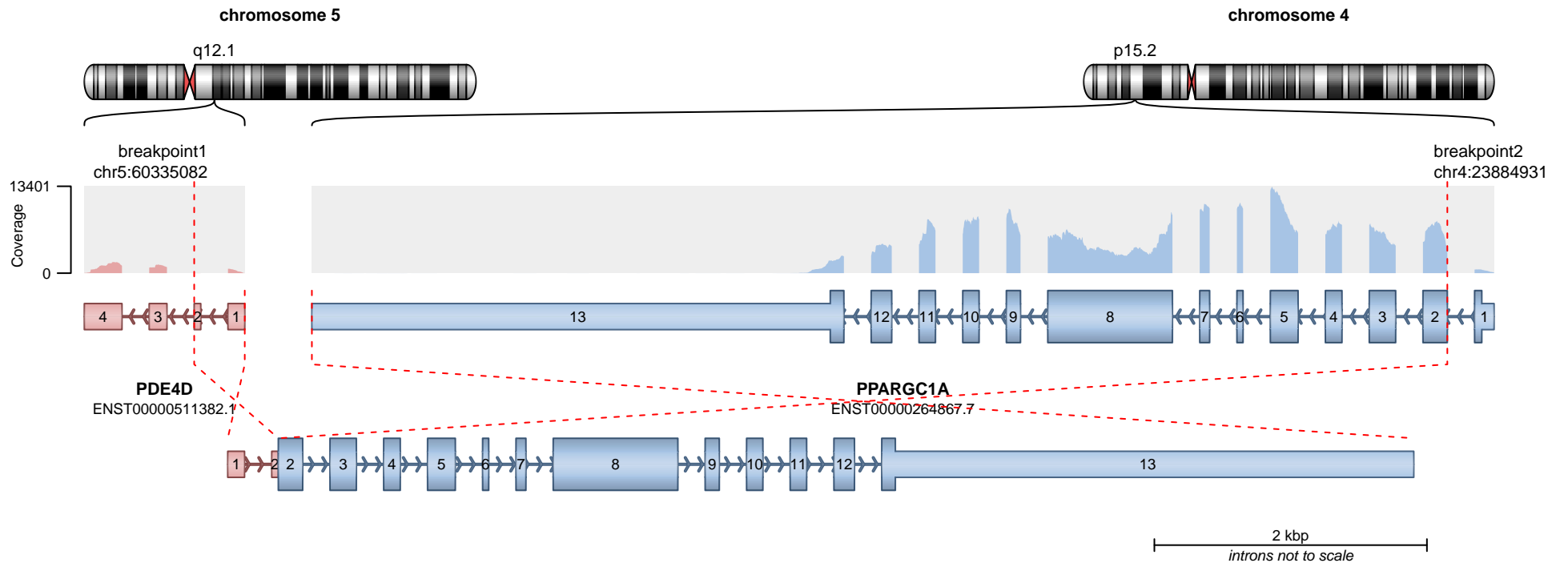
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 5  
Discordant mates = 3



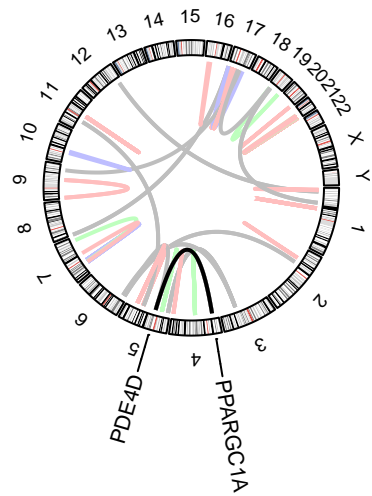
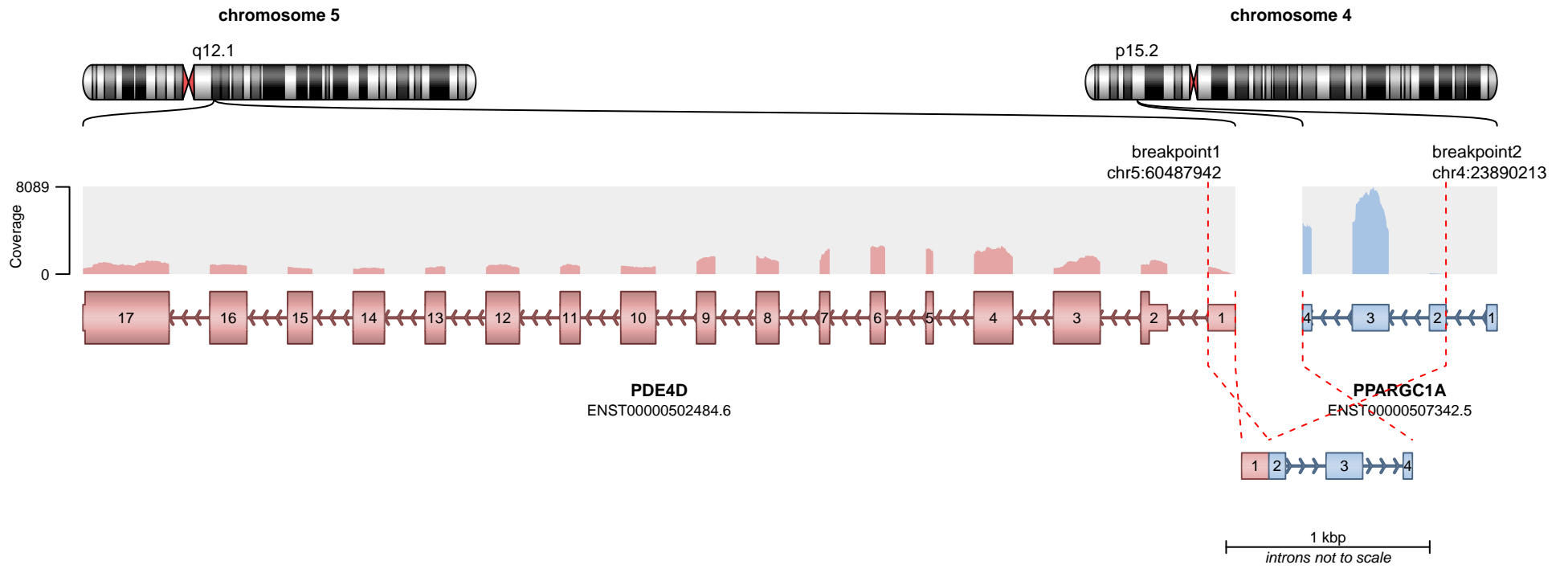
— translocation  
— duplication  
— deletion  
— inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 3

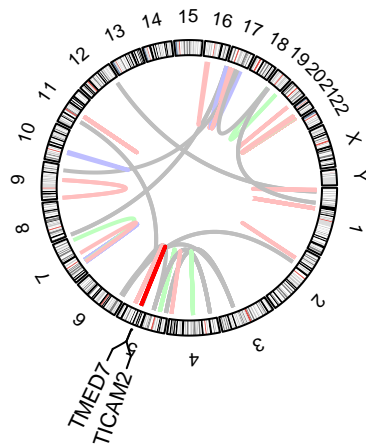
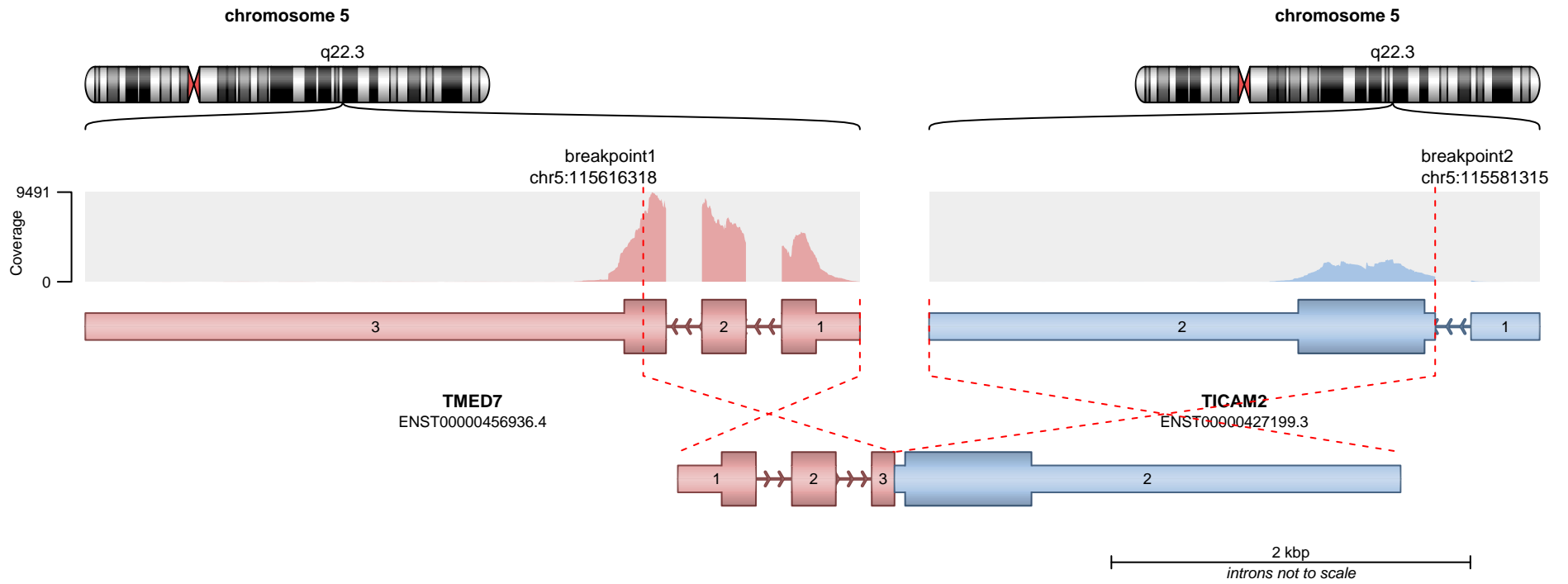


— translocation — deletion  
— duplication — inversion

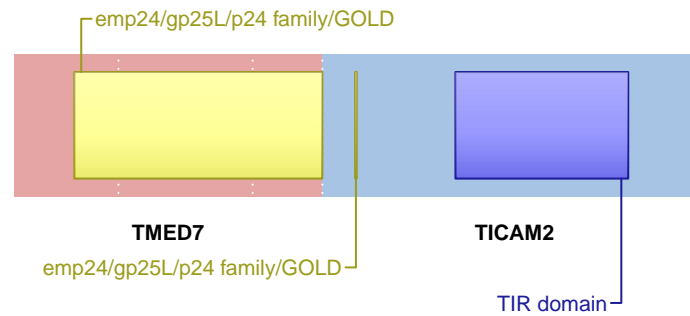
No coding regions retained in fusion transcript.

**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 3



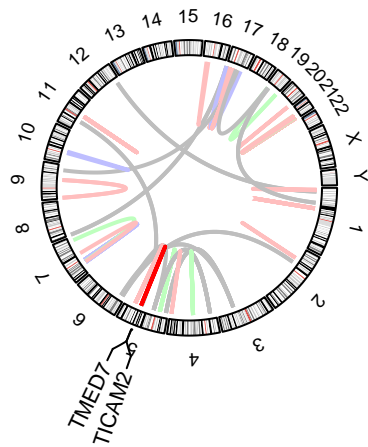
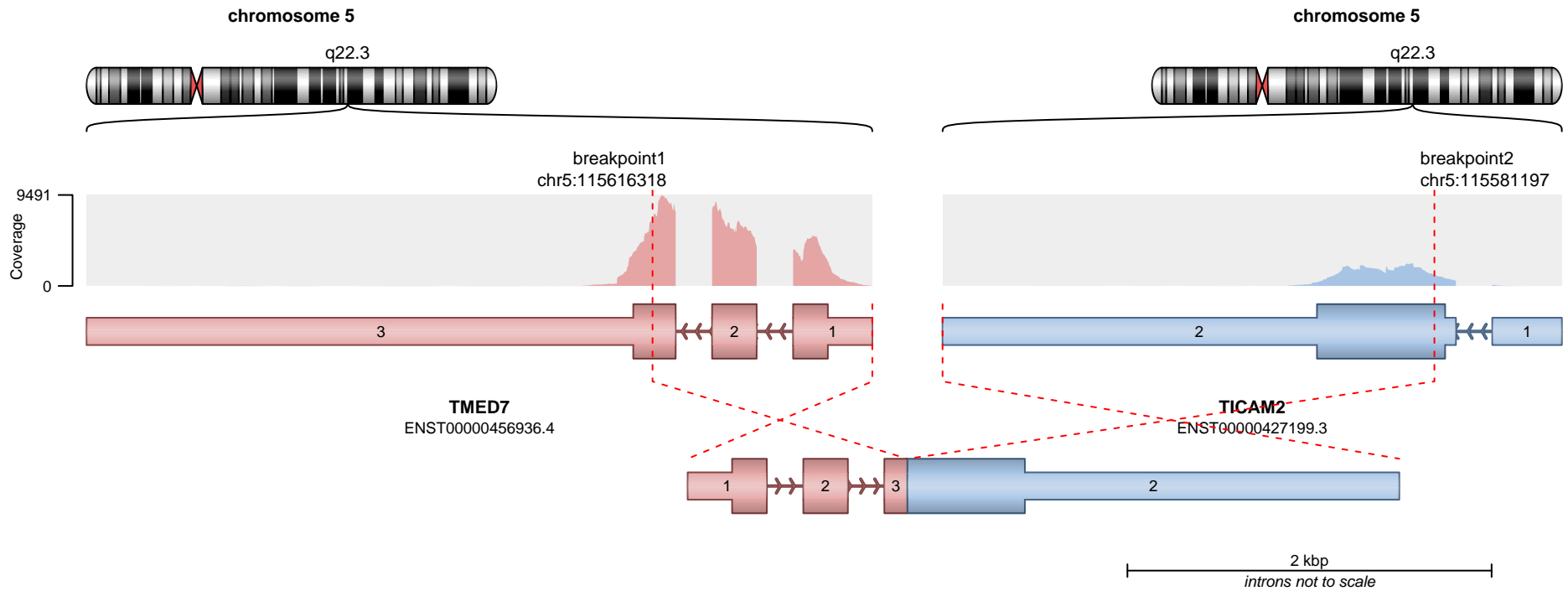
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



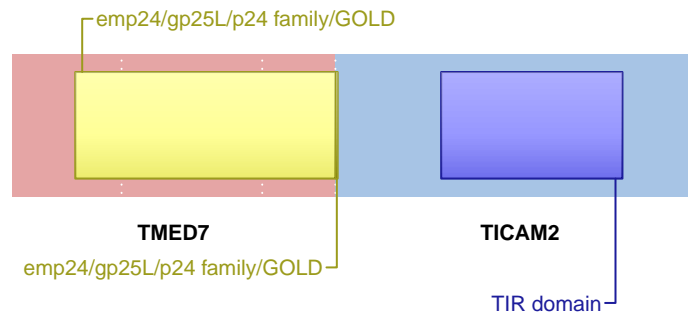
**SUPPORTING READ COUNT**

Split reads = 129  
Discordant mates = 8

— translocation — deletion  
— duplication — inversion



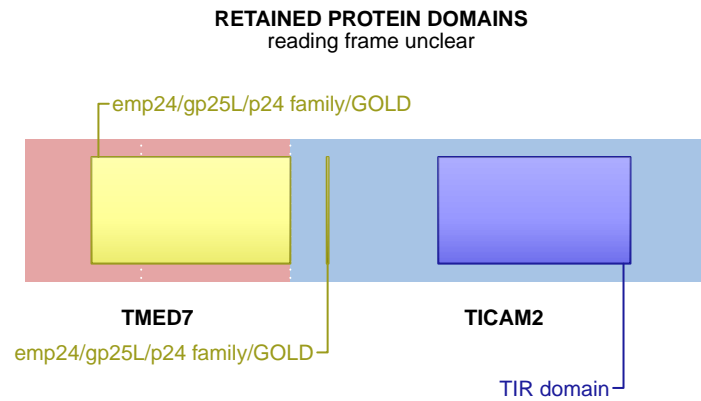
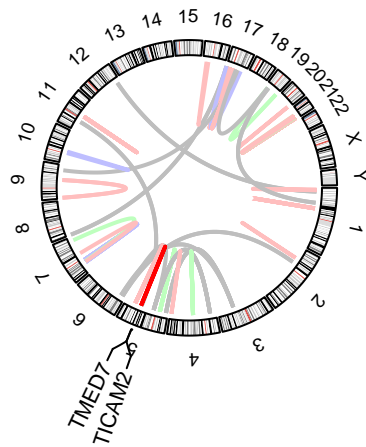
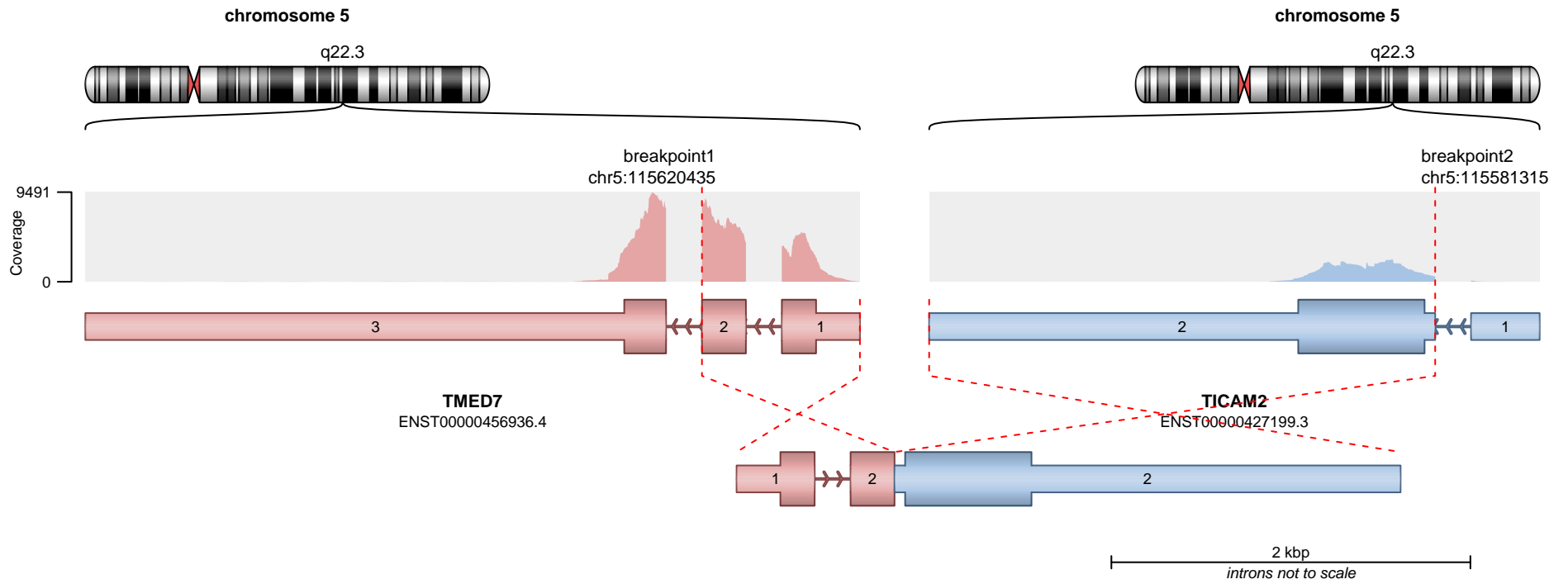
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 30  
Discordant mates = 5

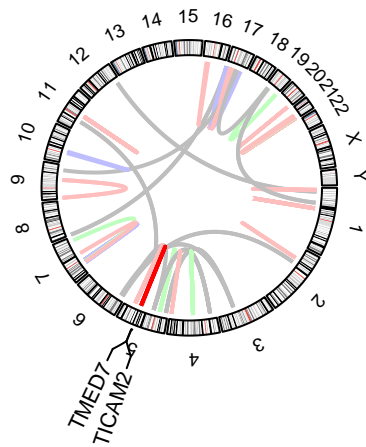
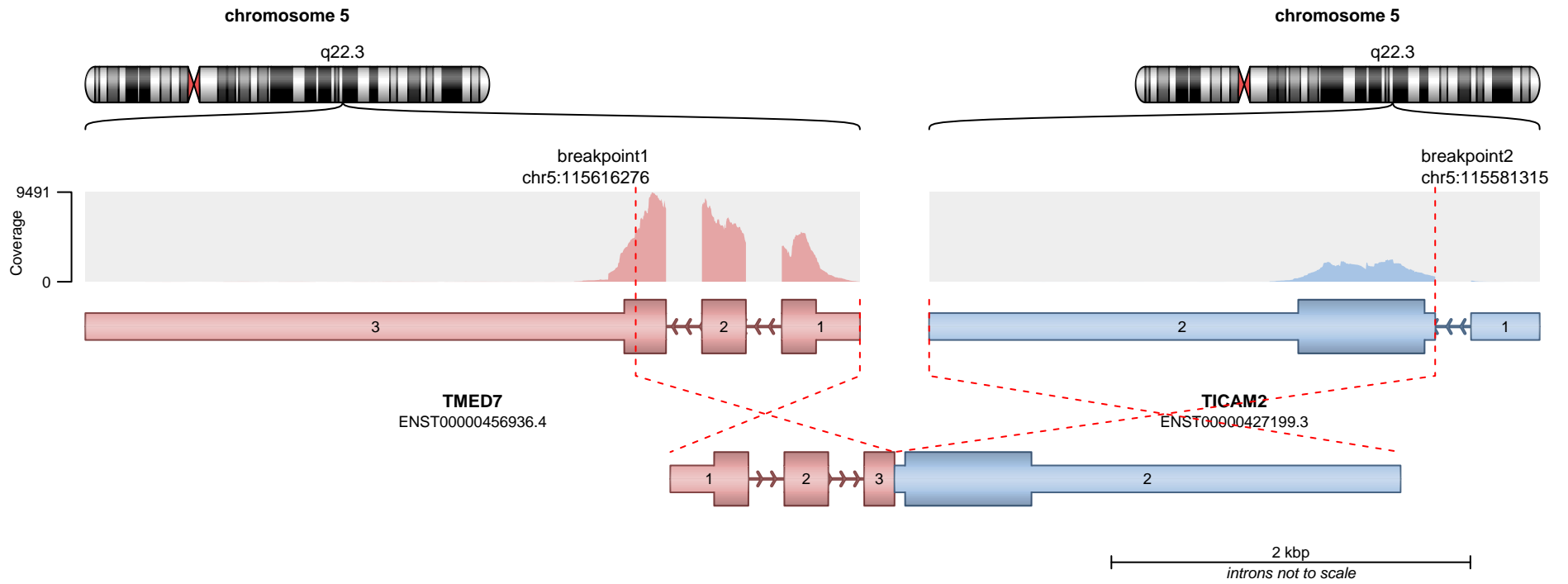
- translocation
- duplication
- deletion
- inversion



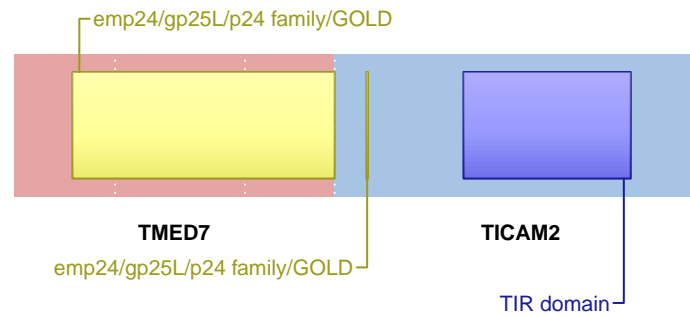
**SUPPORTING READ COUNT**

Split reads = 10  
Discordant mates = 1

— translocation — deletion  
— duplication — inversion



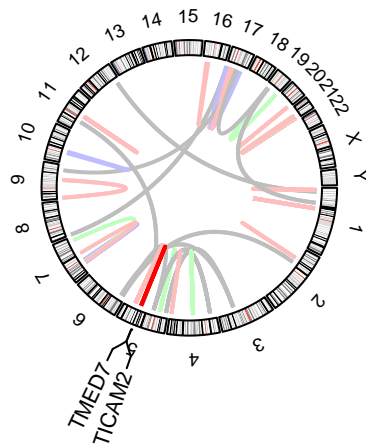
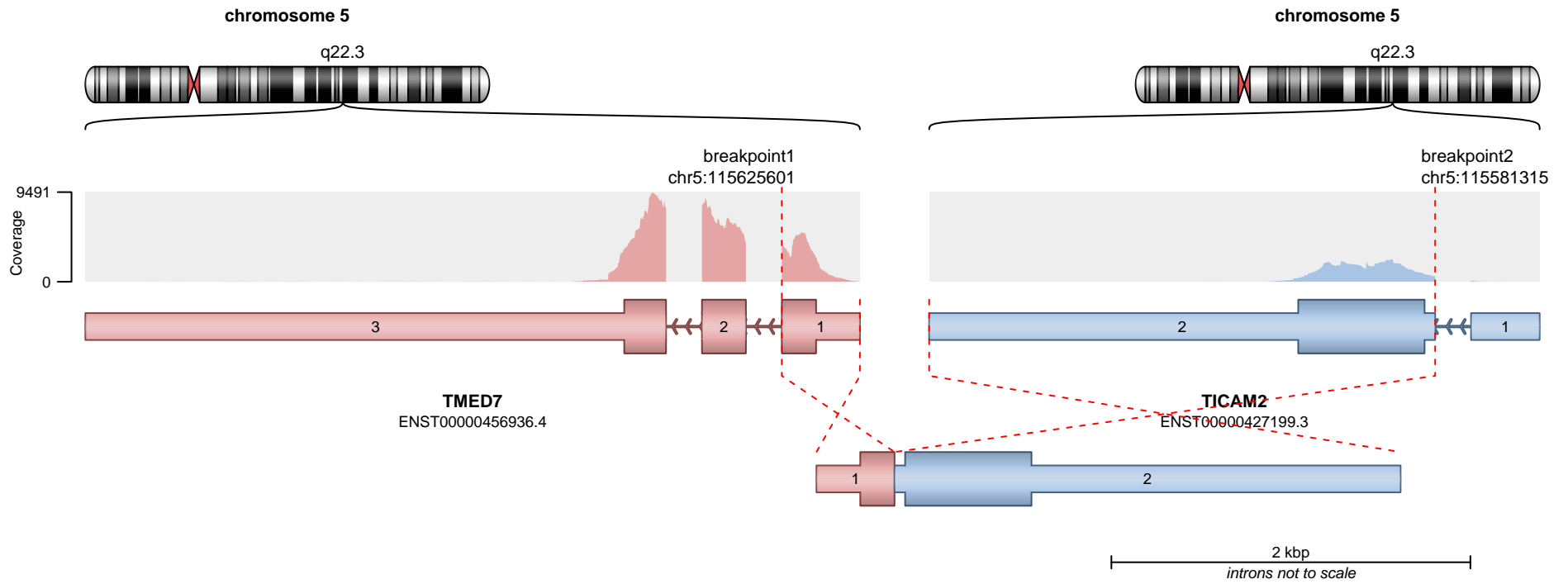
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



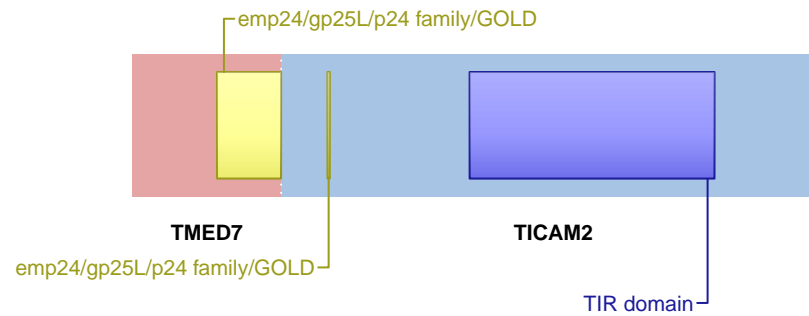
**SUPPORTING READ COUNT**

Split reads = 5  
Discordant mates = 9

— translocation — deletion  
— duplication — inversion



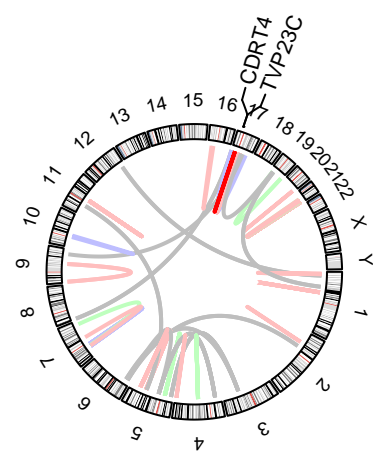
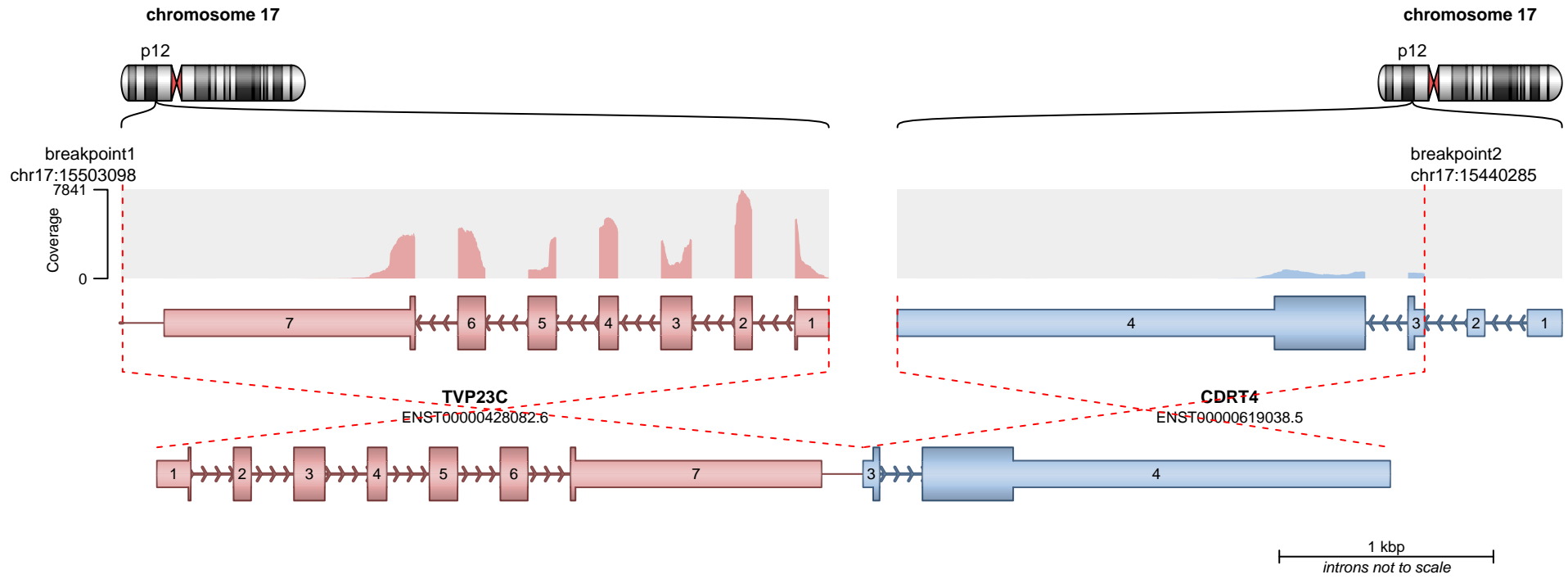
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



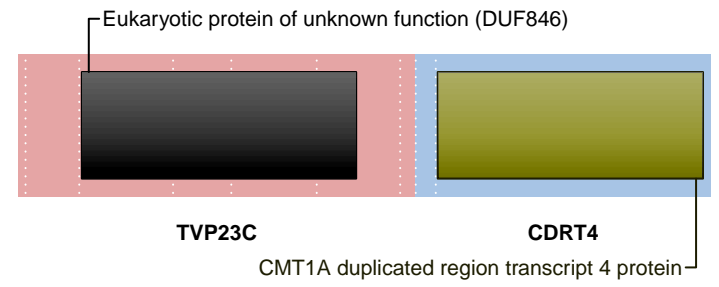
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 1

— translocation — deletion  
— duplication — inversion



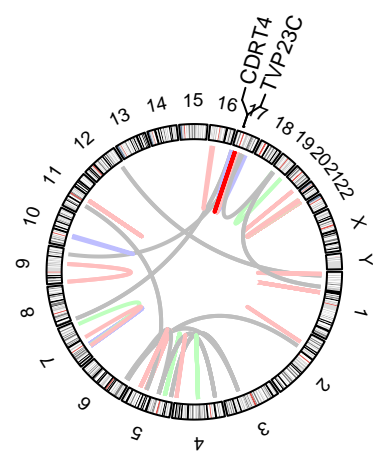
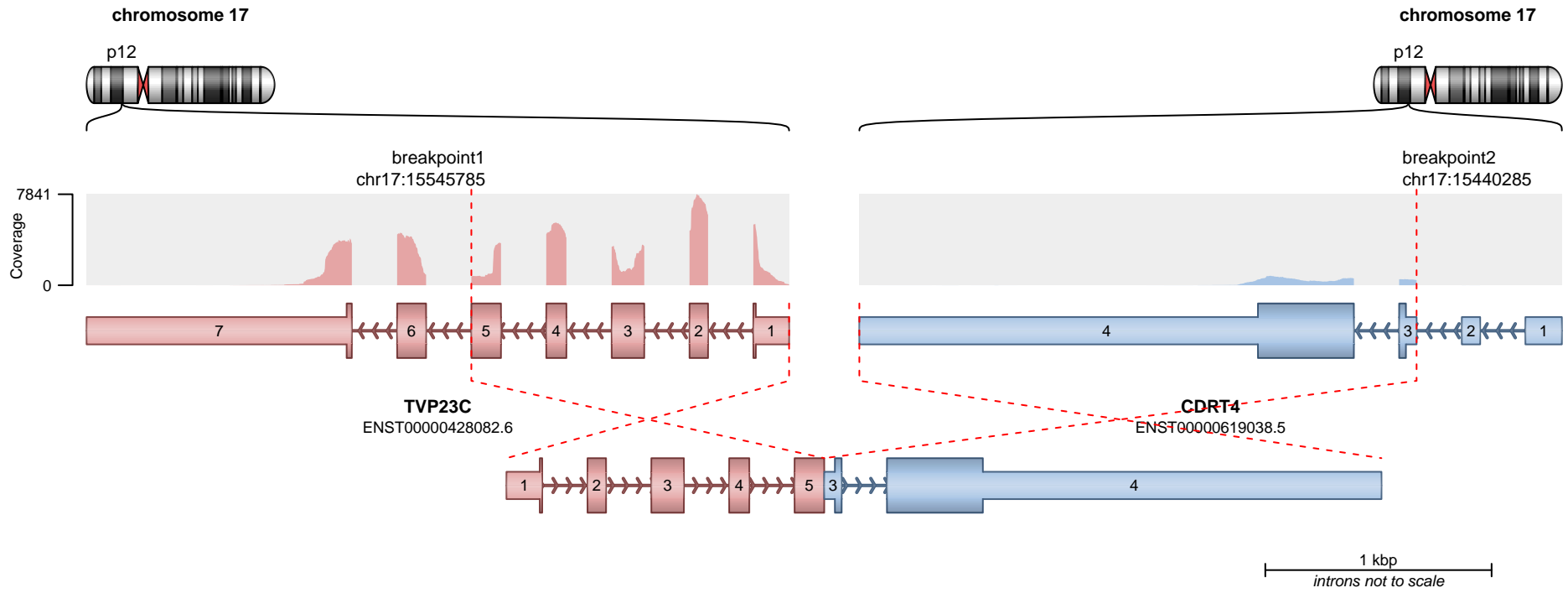
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



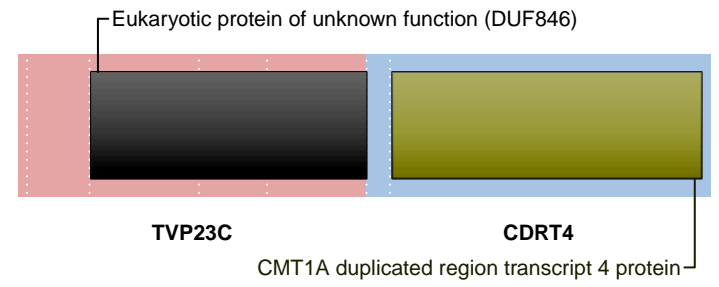
**SUPPORTING READ COUNT**

Split reads = 104  
Discordant mates = 2

- translocation
- duplication
- deletion
- inversion



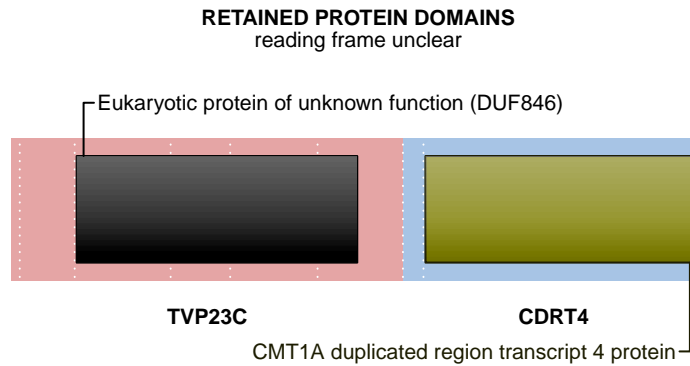
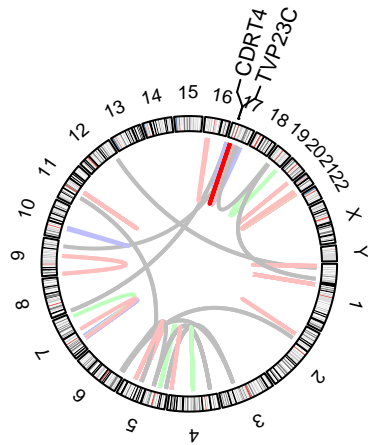
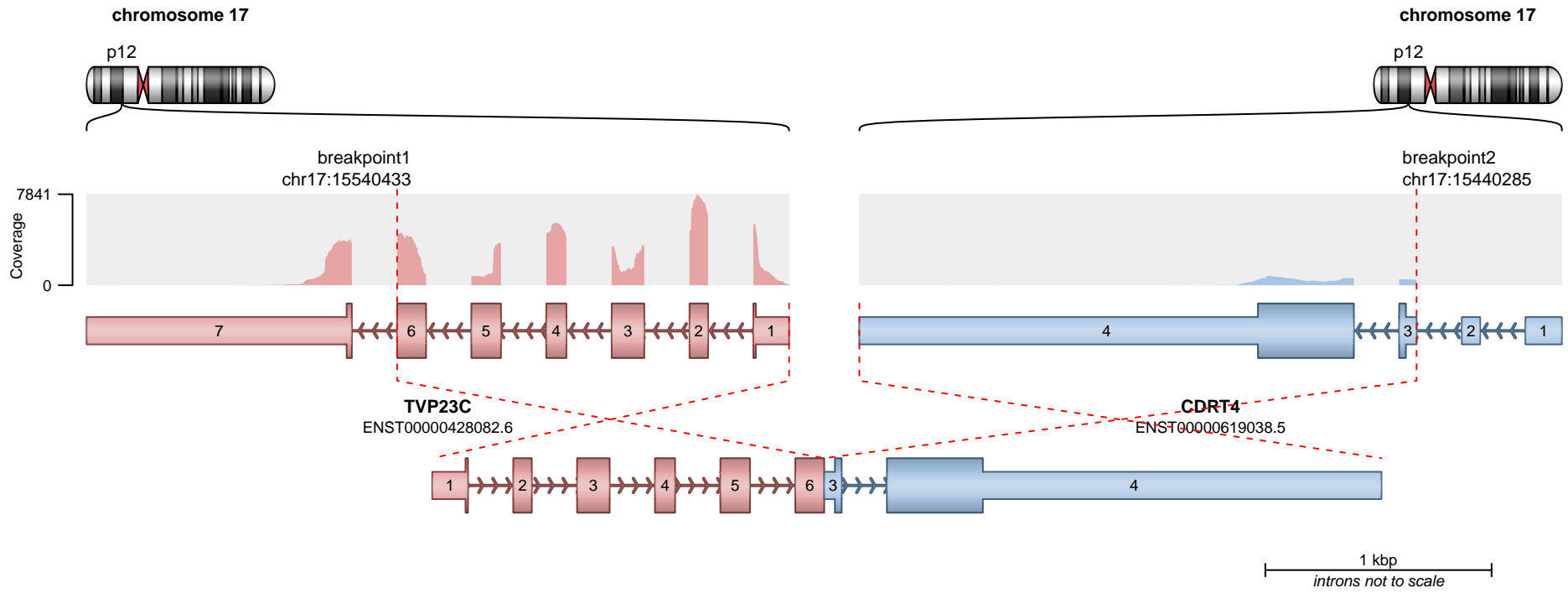
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 37  
Discordant mates = 0

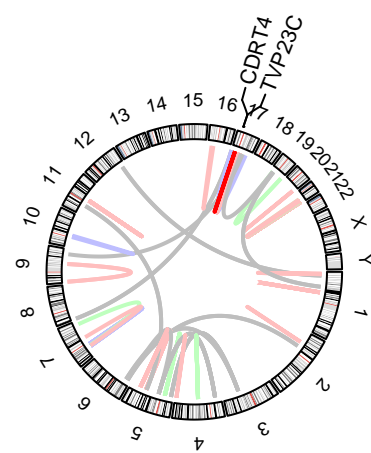
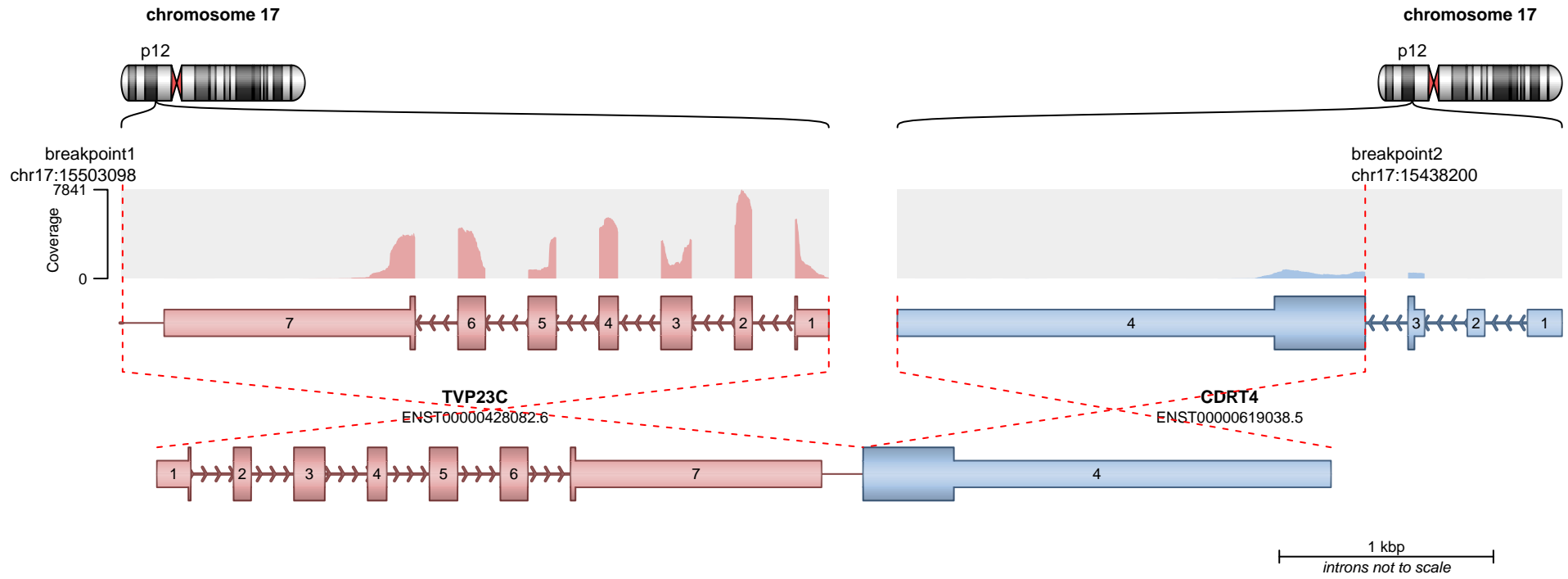
- translocation
- duplication
- deletion
- inversion



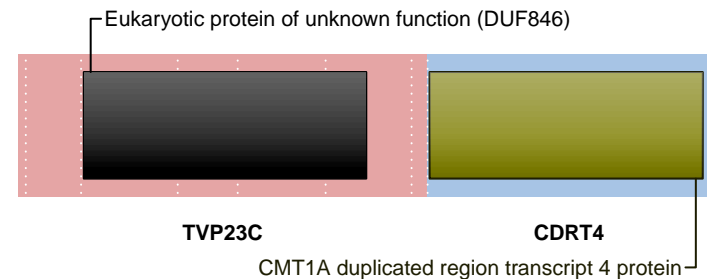
**SUPPORTING READ COUNT**

Split reads = 20  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



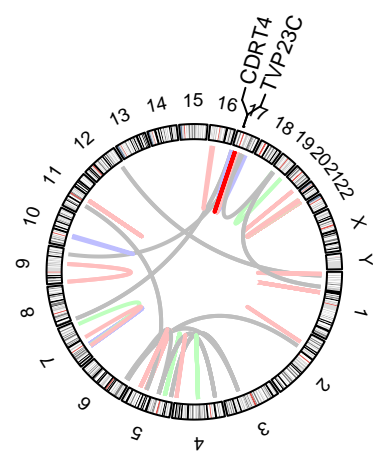
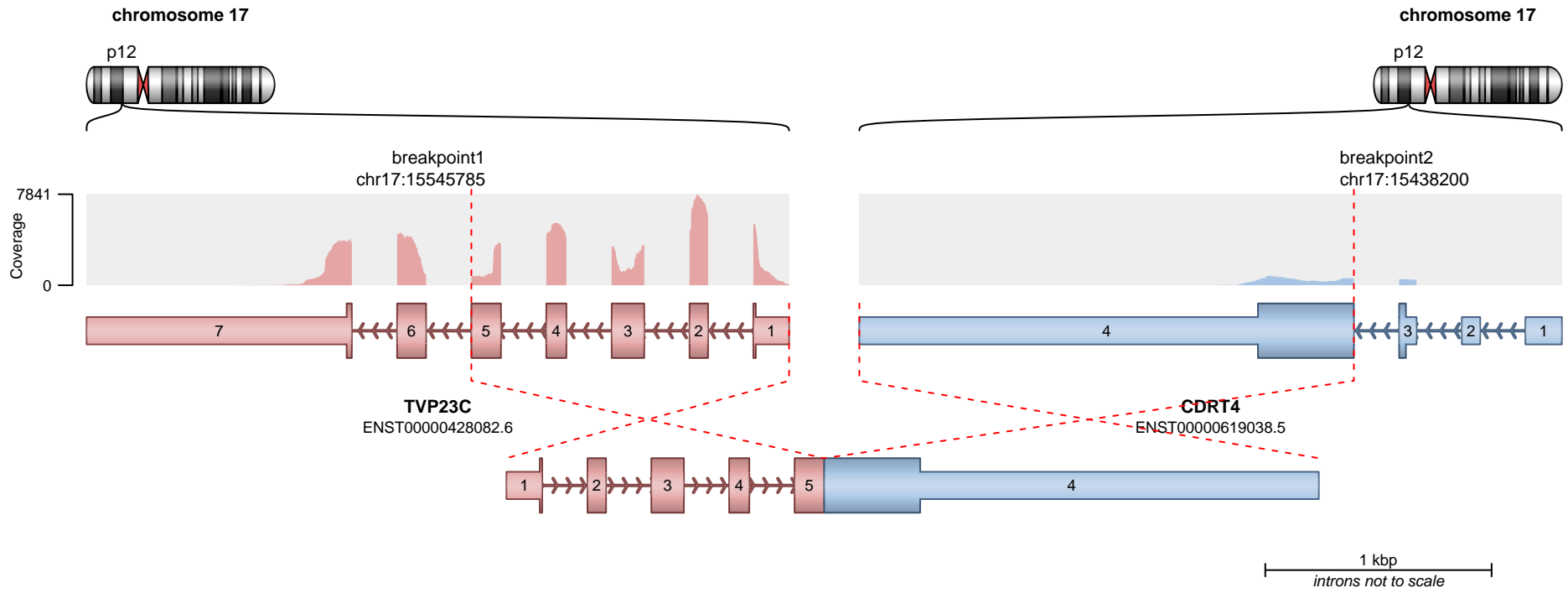
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



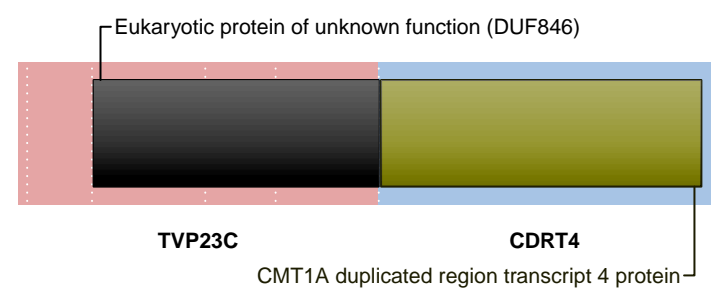
**SUPPORTING READ COUNT**

Split reads = 12  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



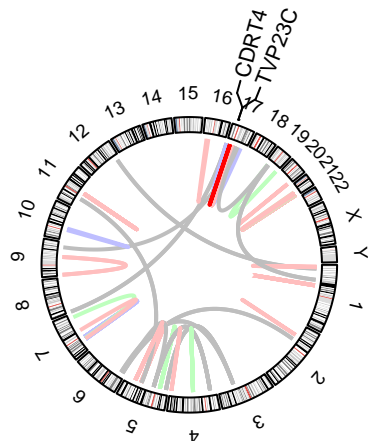
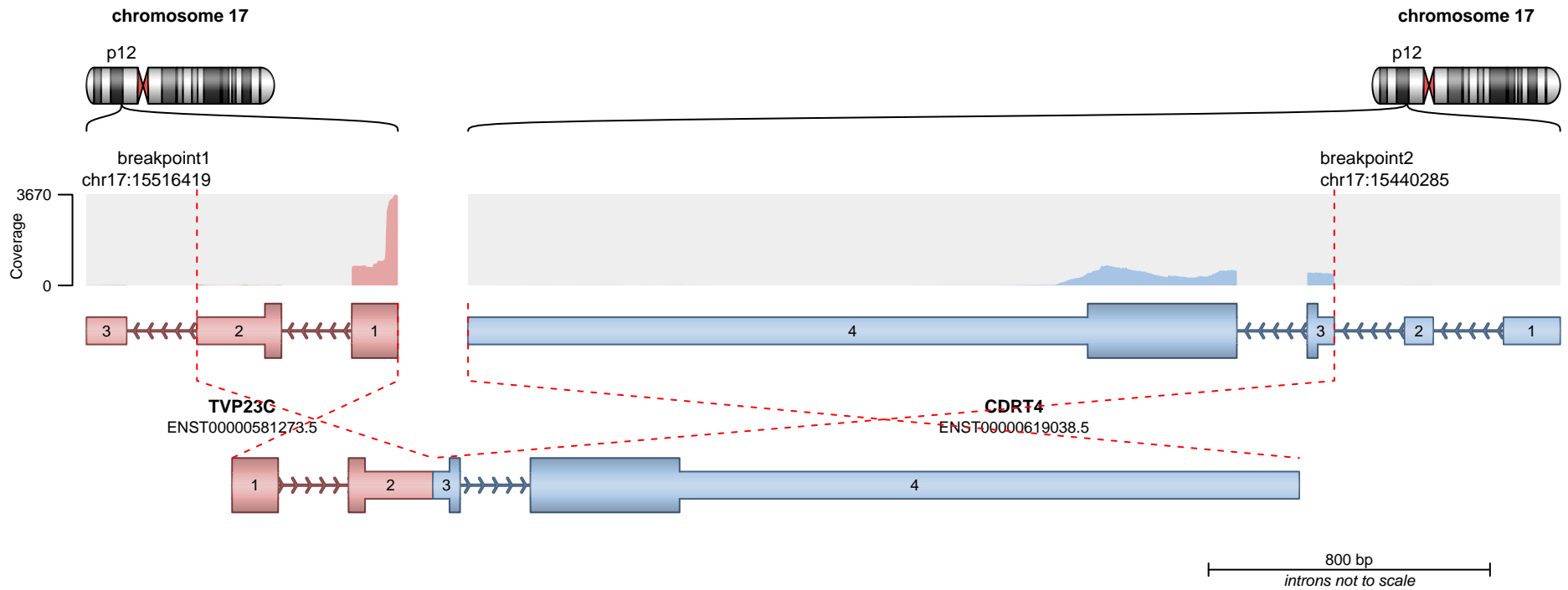
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



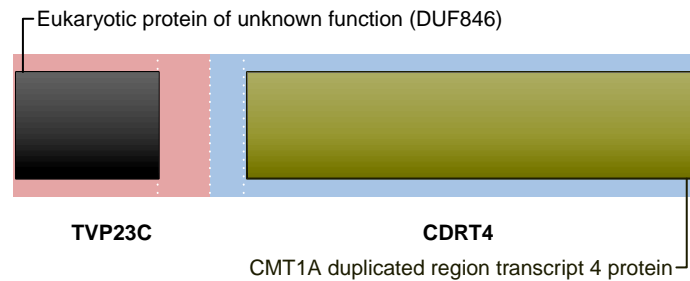
**SUPPORTING READ COUNT**

Split reads = 7  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



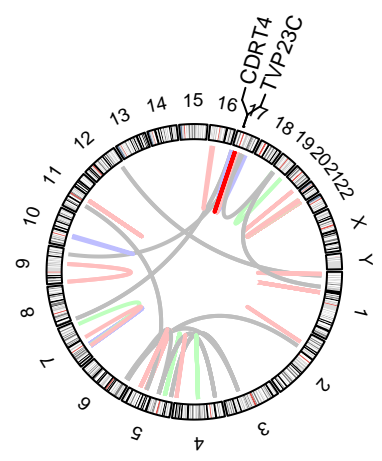
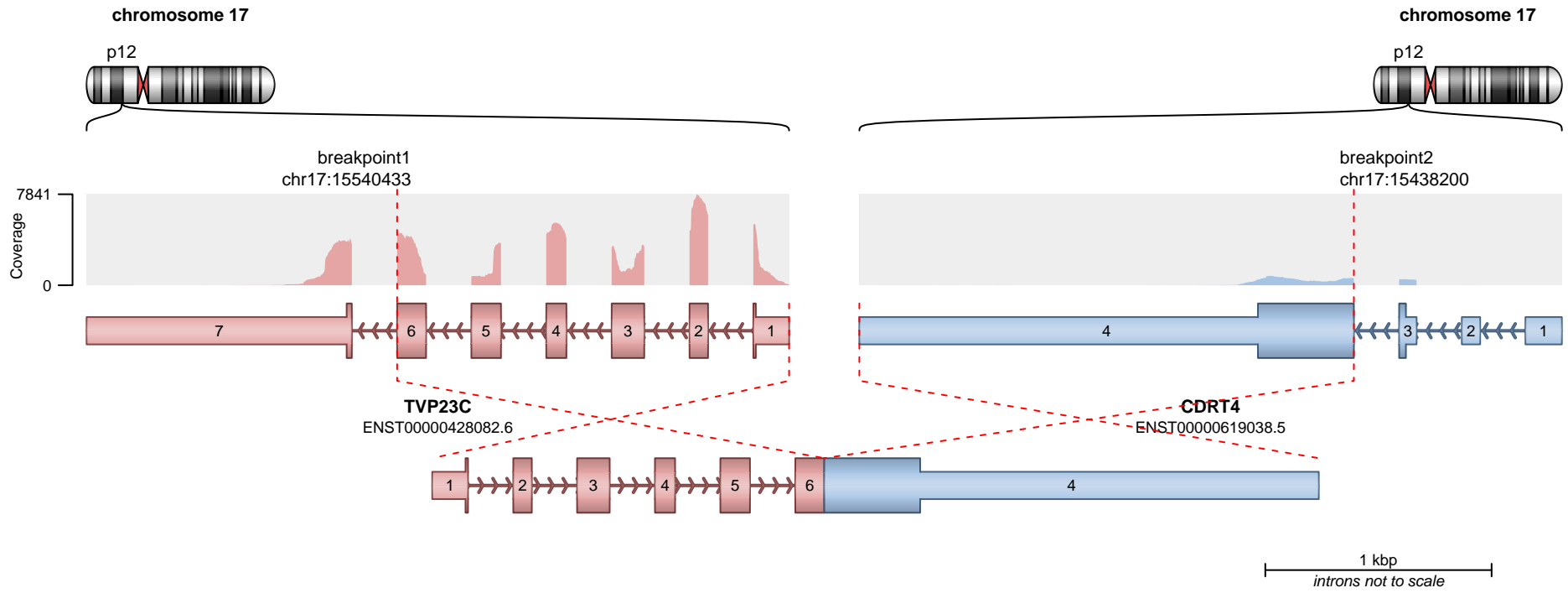
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



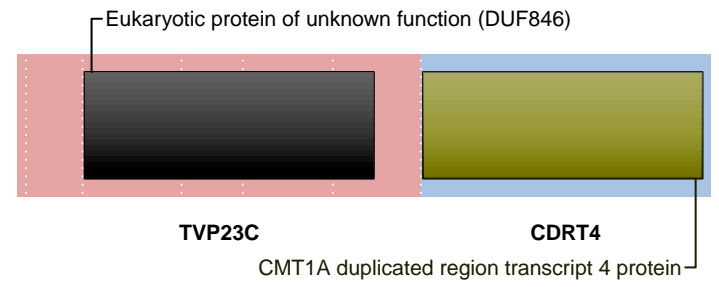
**SUPPORTING READ COUNT**

Split reads = 6  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



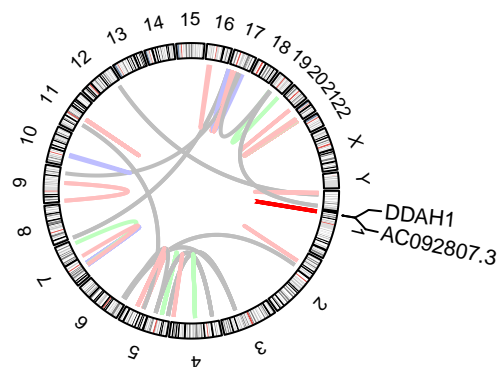
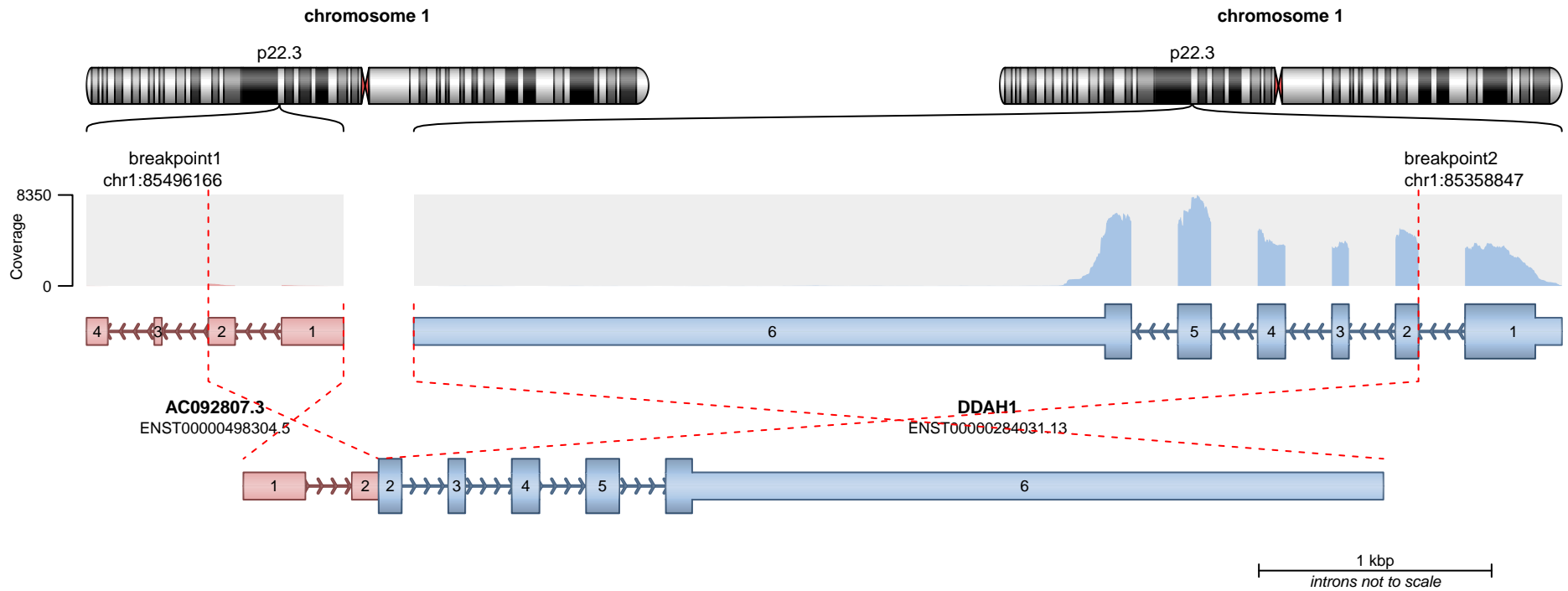
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



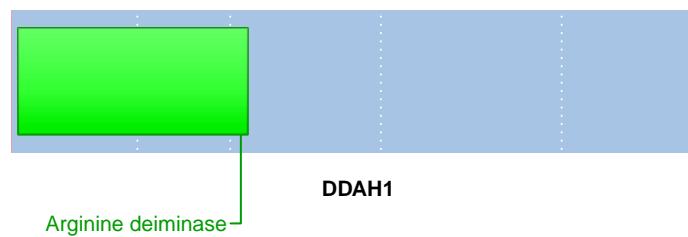
**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



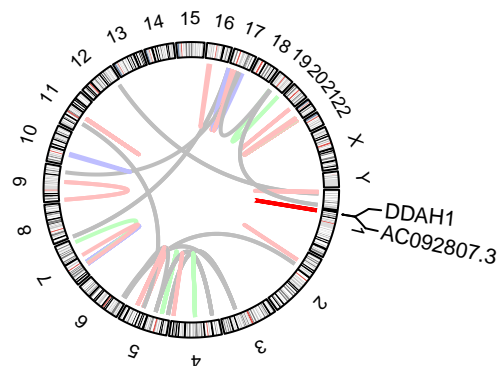
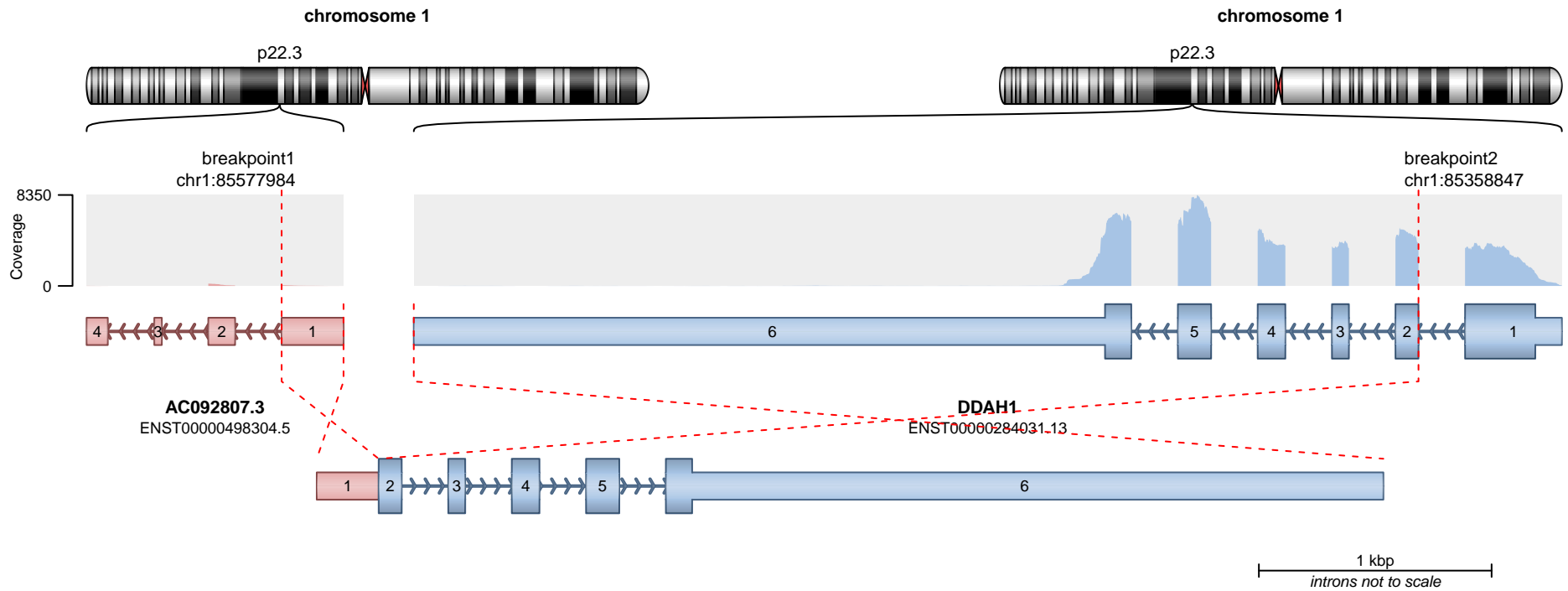
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



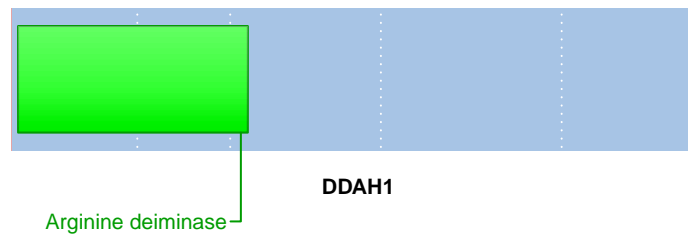
**SUPPORTING READ COUNT**

Split reads = 101  
Discordant mates = 4

- translocation
- duplication
- deletion
- inversion



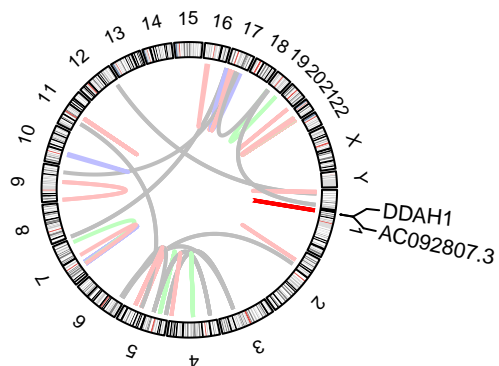
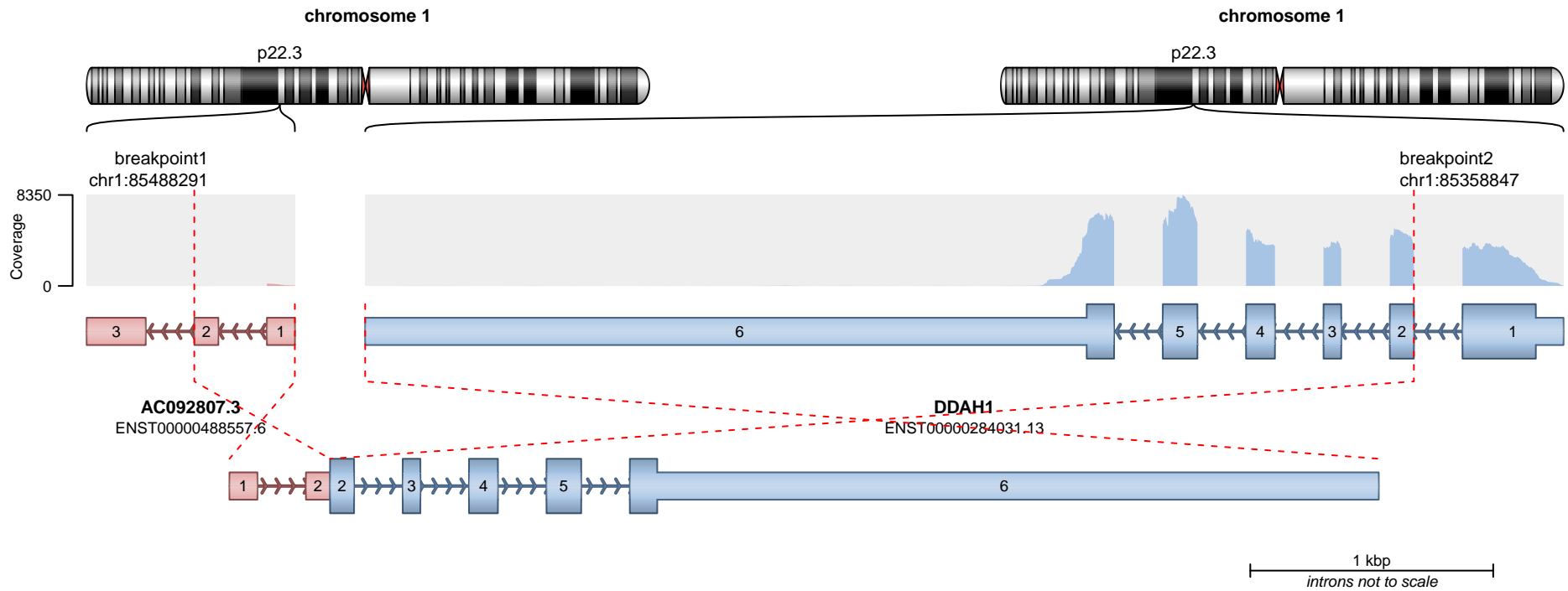
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



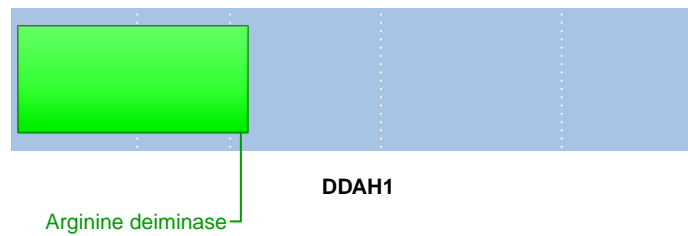
**SUPPORTING READ COUNT**

Split reads = 21  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



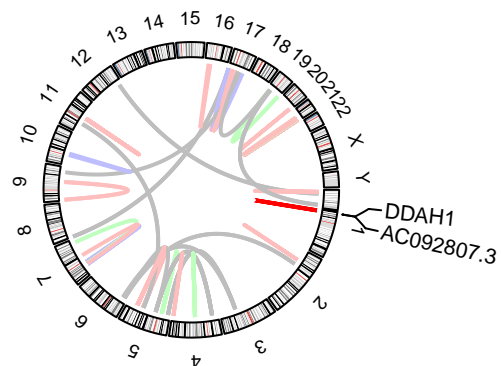
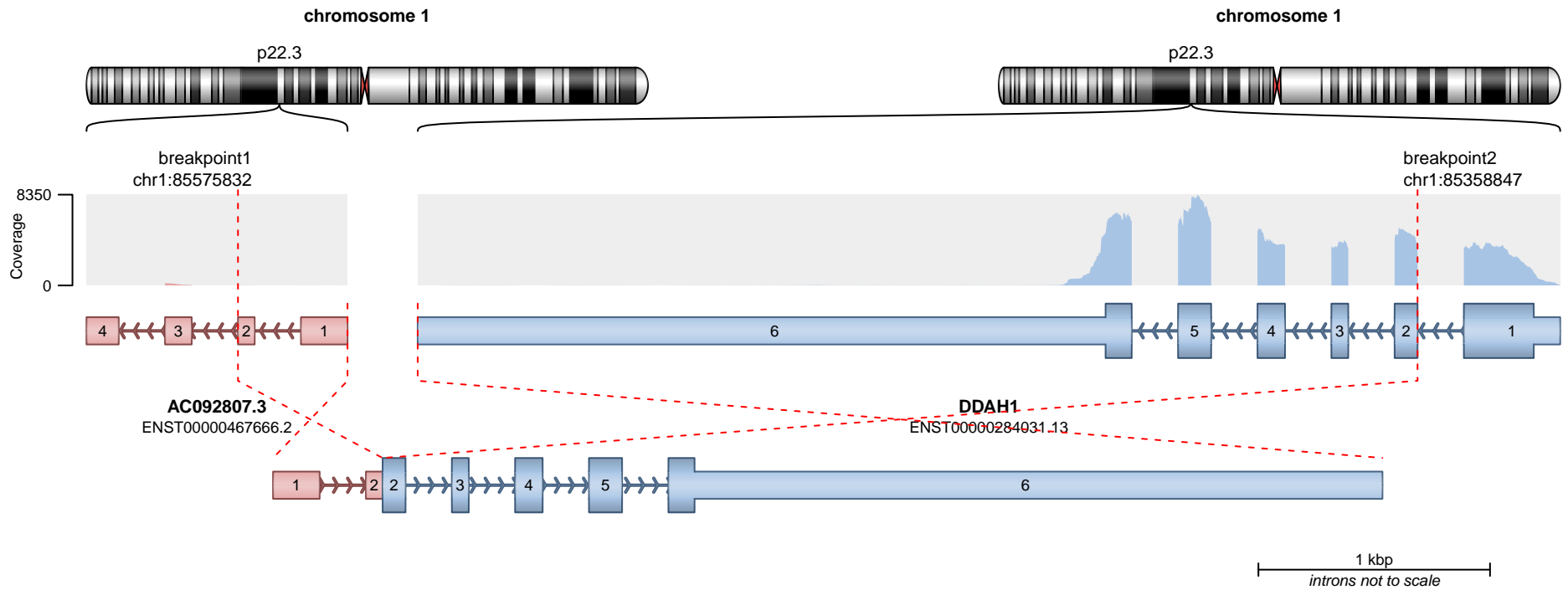
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



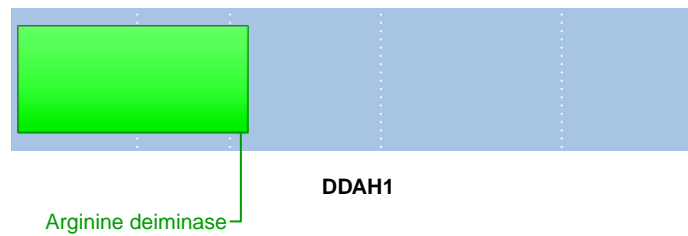
**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 4

- translocation
- duplication
- deletion
- inversion



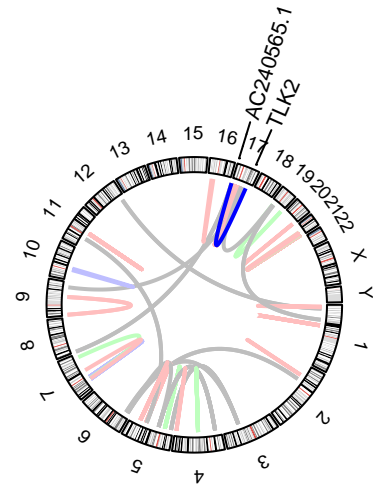
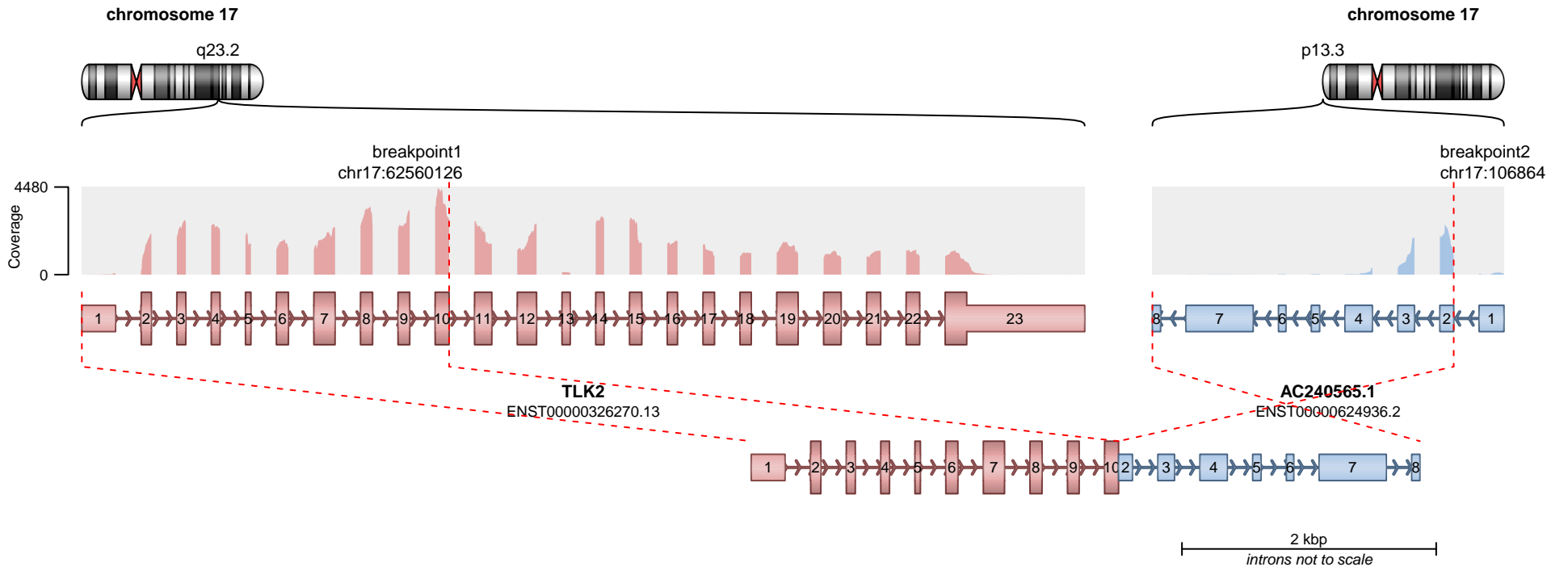
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion

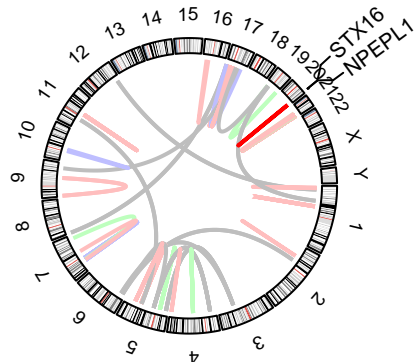
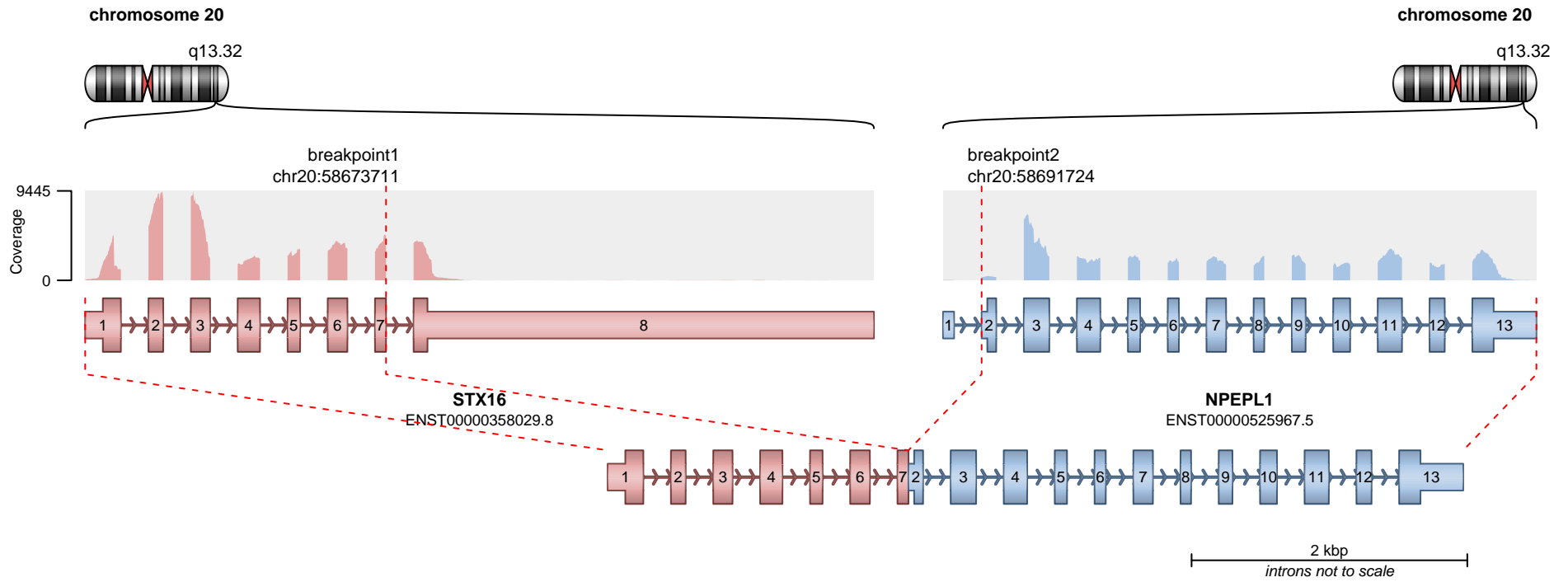


— translocation — deletion  
— duplication — inversion

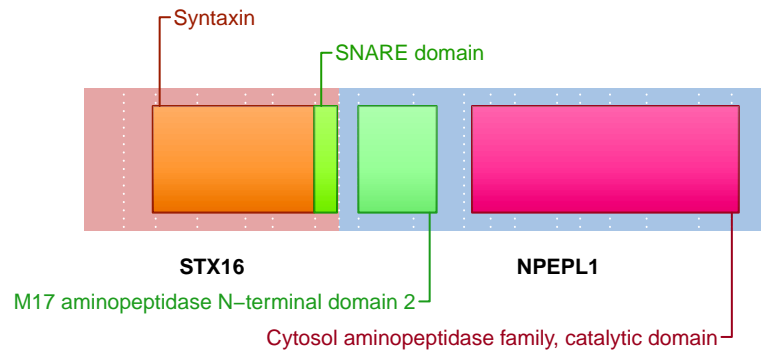
No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 80  
Discordant mates = 0



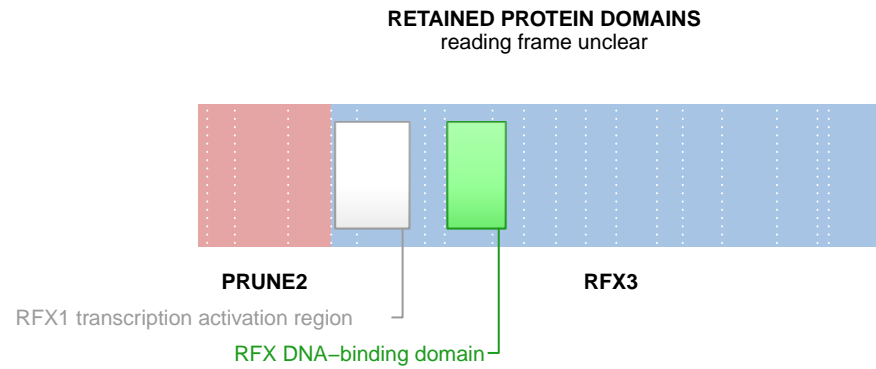
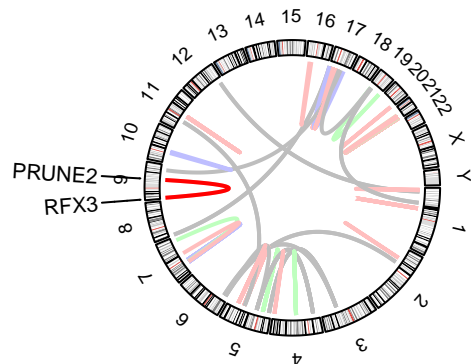
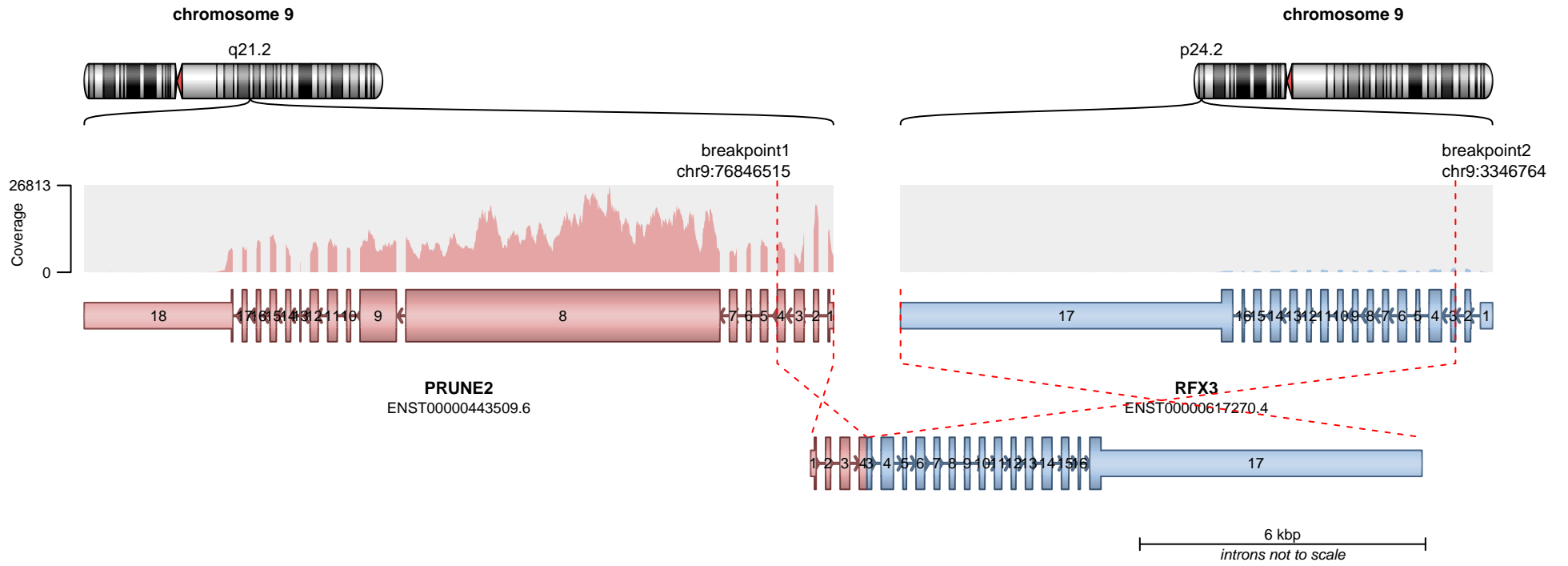
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 76  
Discordant mates = 1

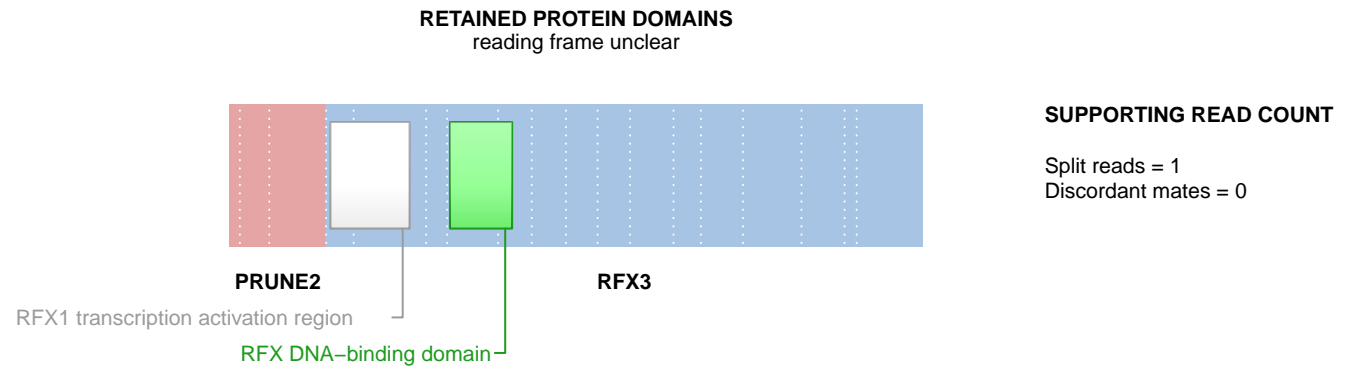
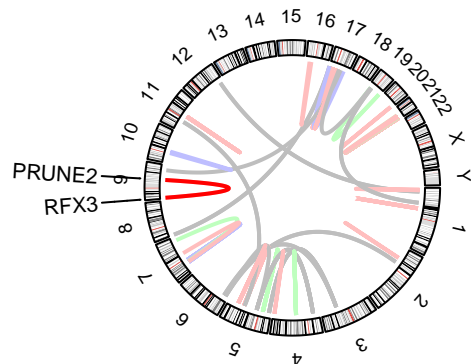
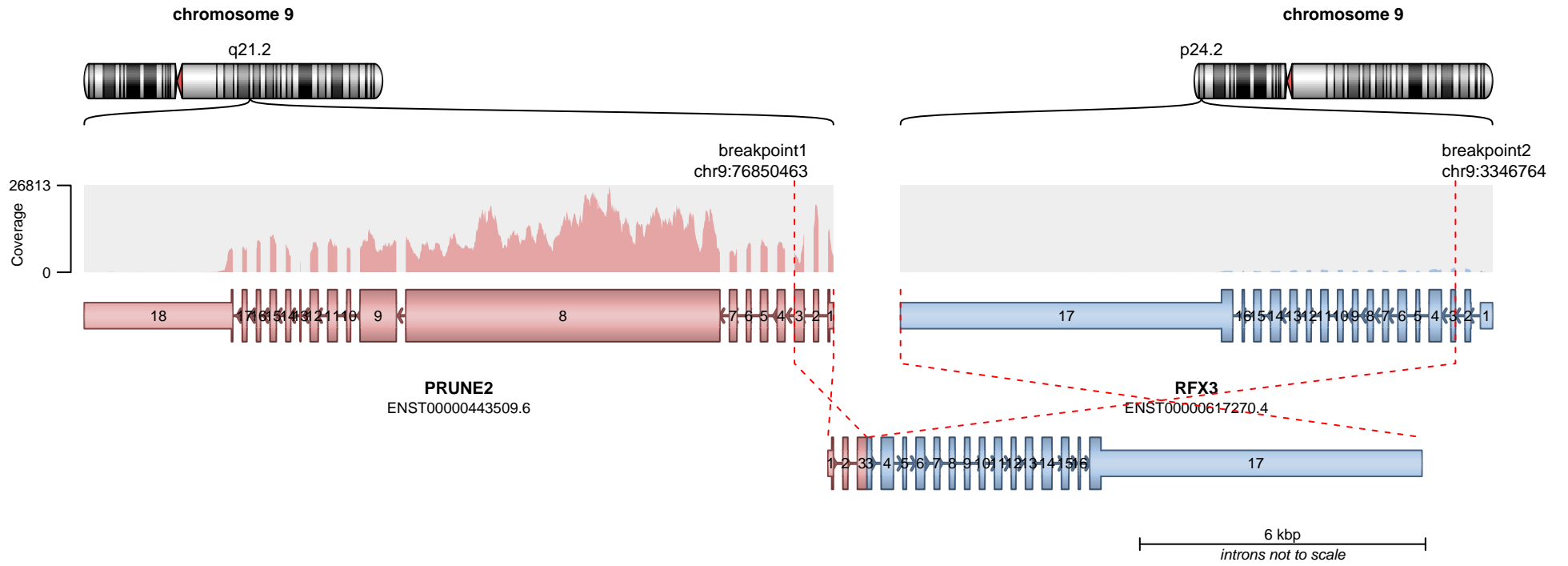
- translocation
- duplication
- deletion
- inversion



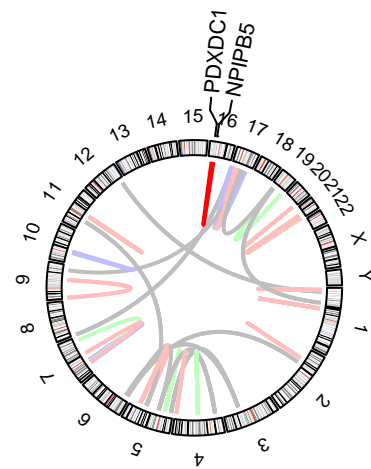
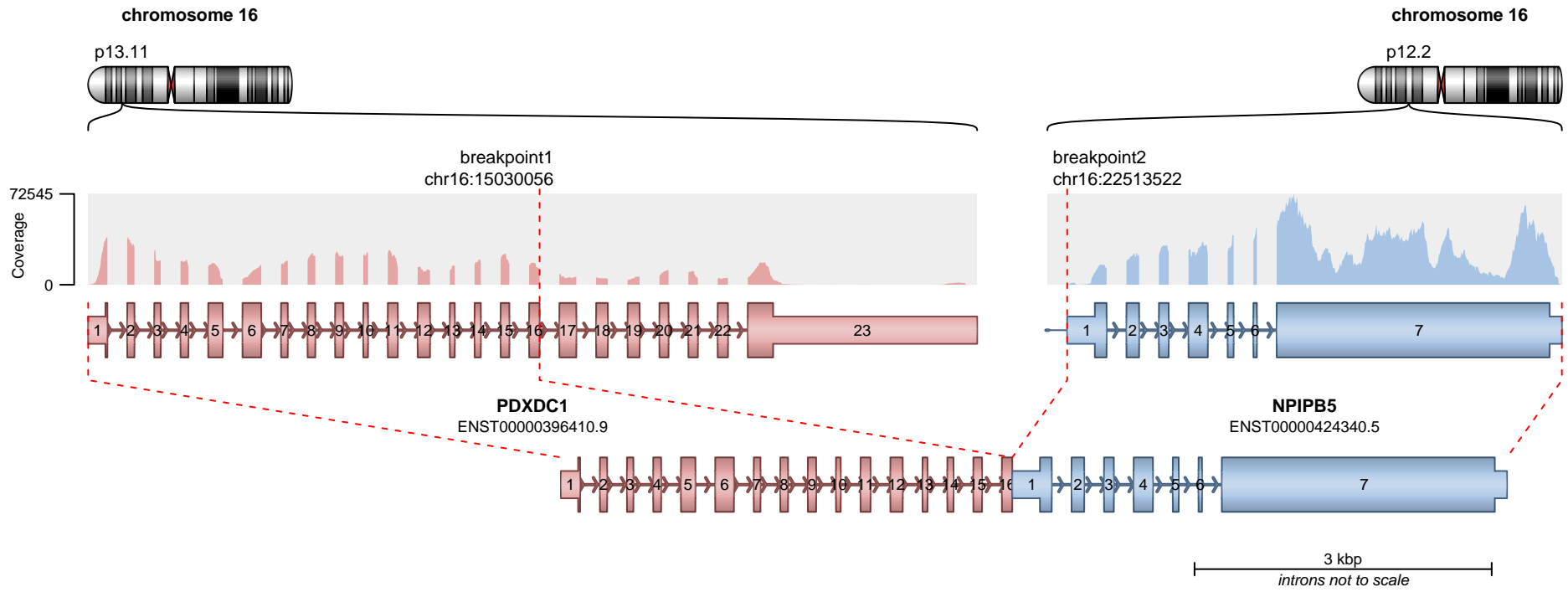
**SUPPORTING READ COUNT**

Split reads = 36  
Discordant mates = 0

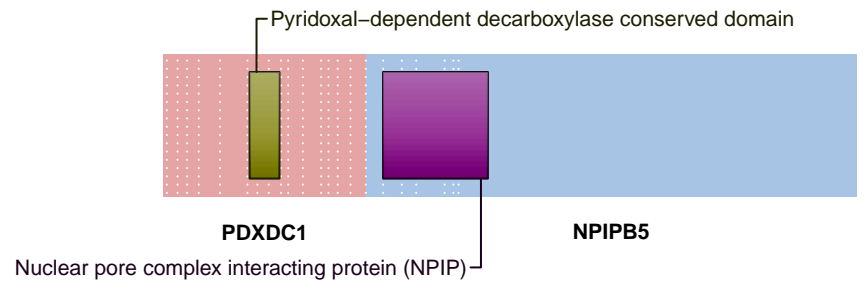
- translocation
- duplication
- deletion
- inversion



— translocation    — deletion  
— duplication    — inversion



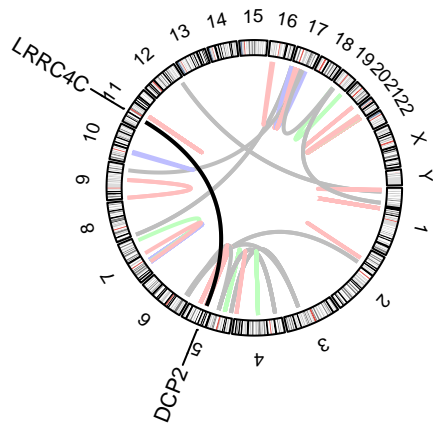
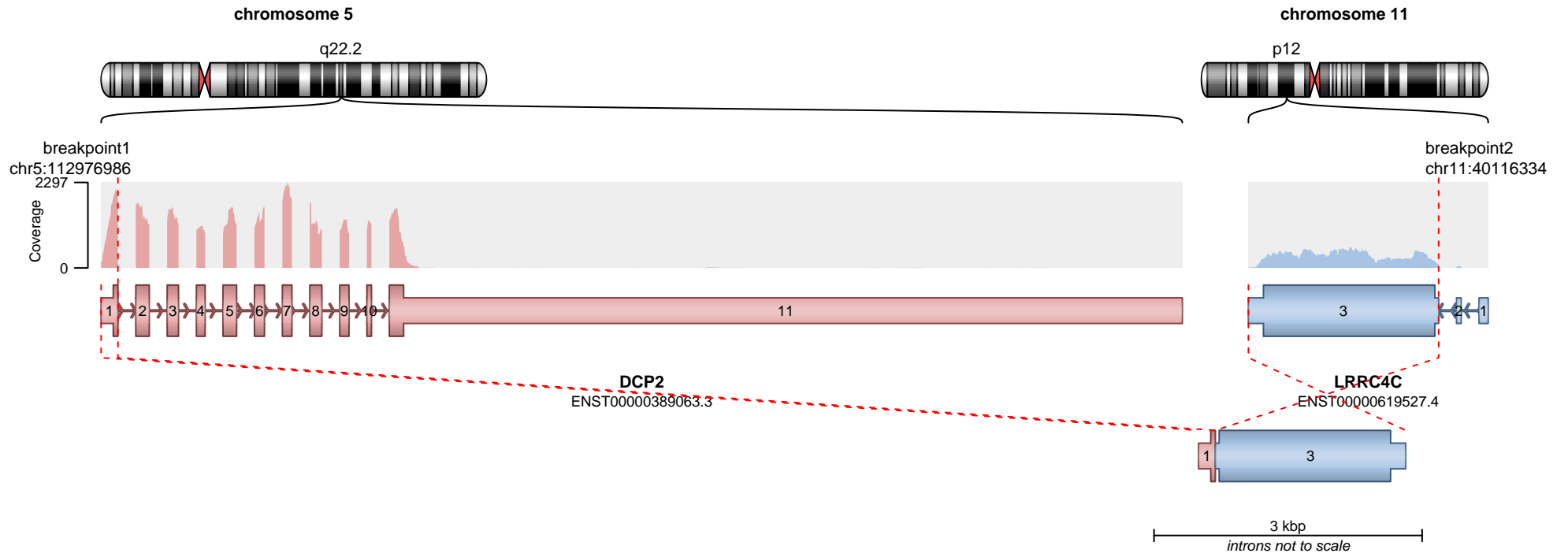
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



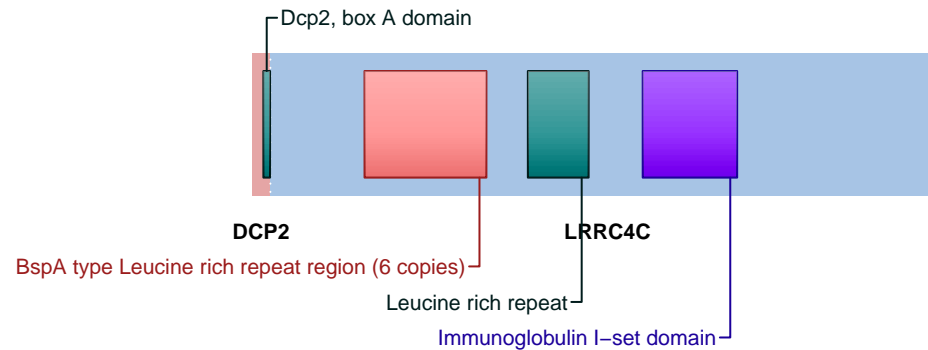
**SUPPORTING READ COUNT**

Split reads = 34  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



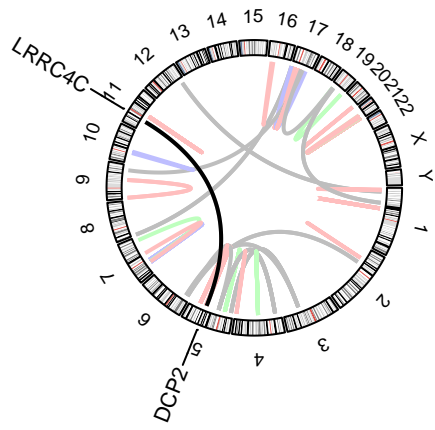
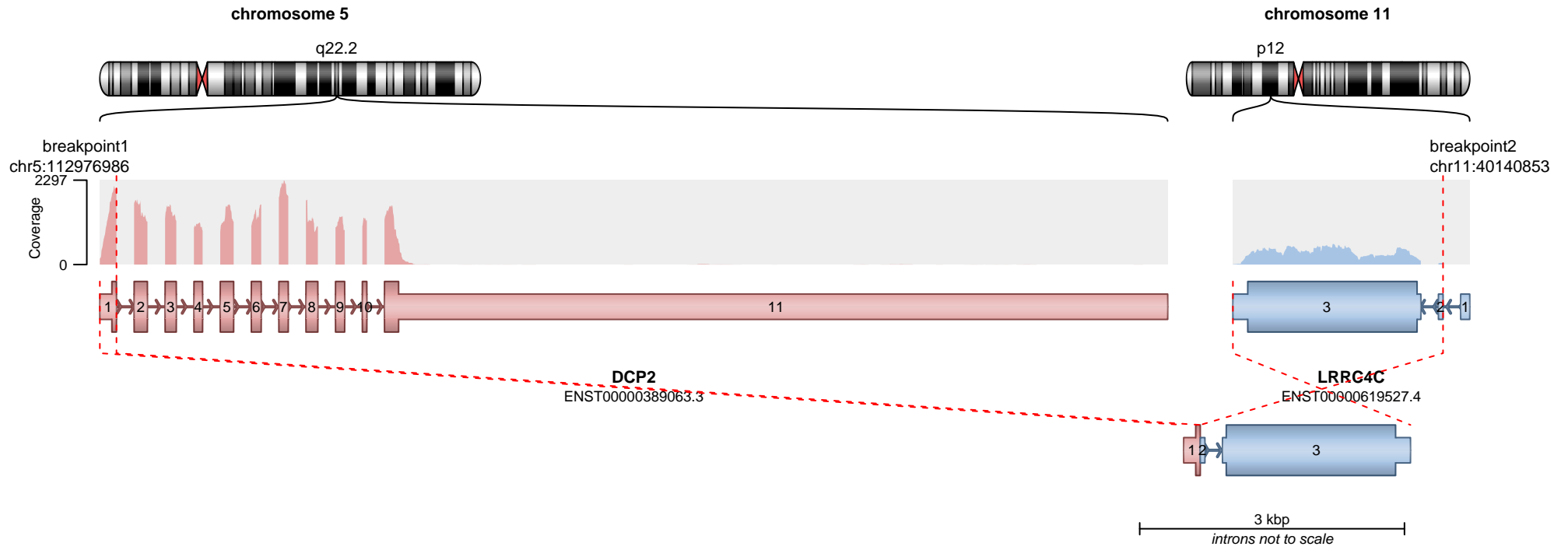
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



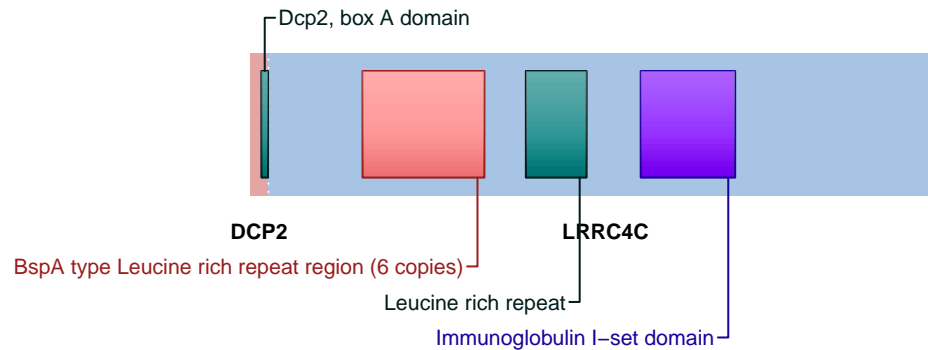
**SUPPORTING READ COUNT**

Split reads = 29  
Discordant mates = 6

- translocation
- duplication
- deletion
- inversion



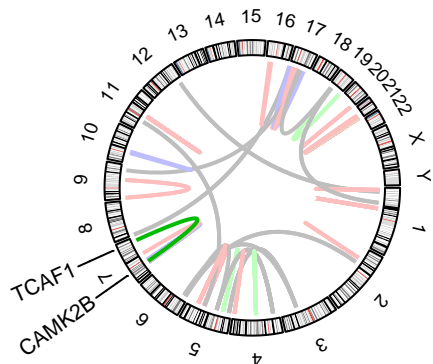
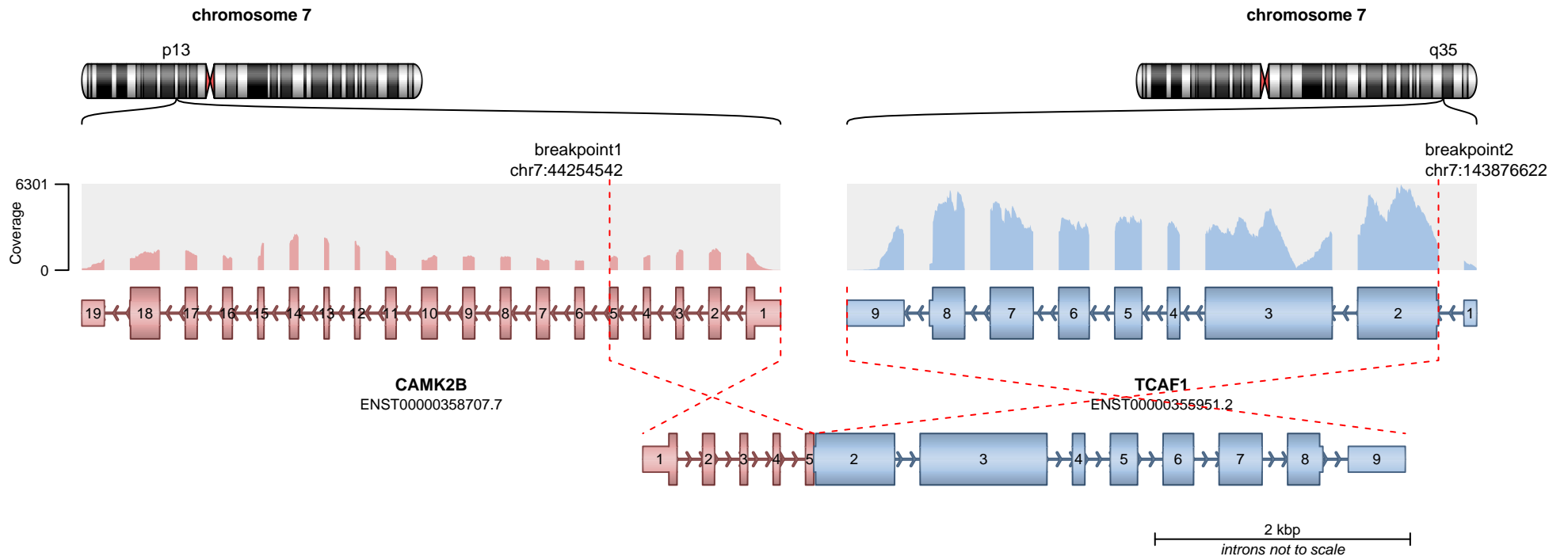
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



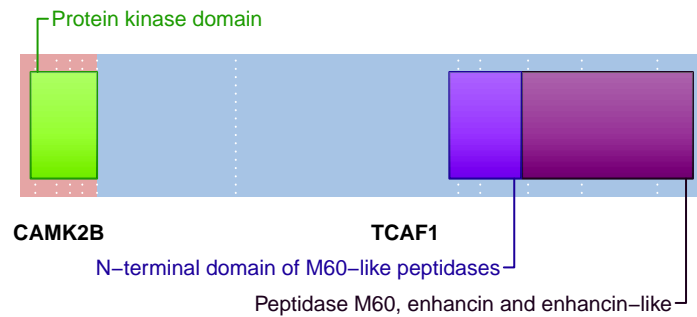
**SUPPORTING READ COUNT**

Split reads = 28  
Discordant mates = 7

— translocation — deletion  
— duplication — inversion



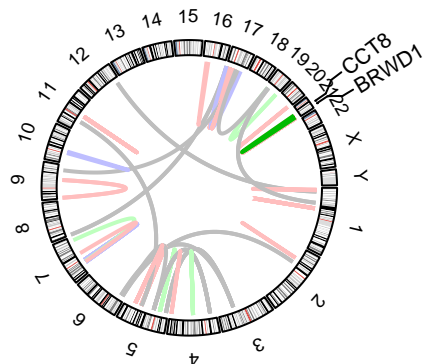
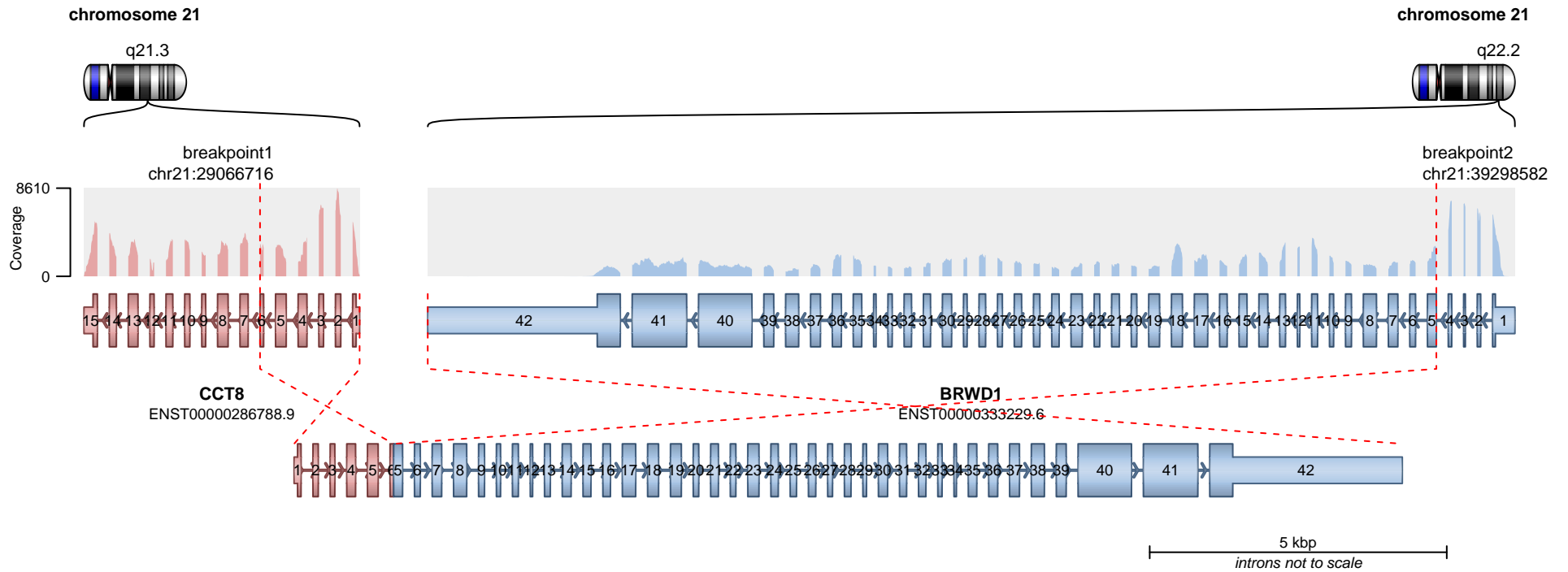
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



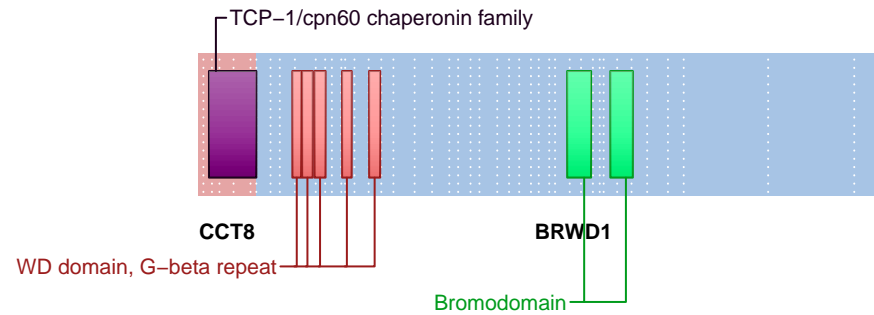
**SUPPORTING READ COUNT**

Split reads = 27  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



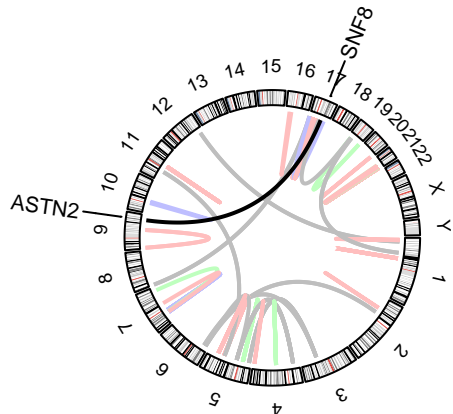
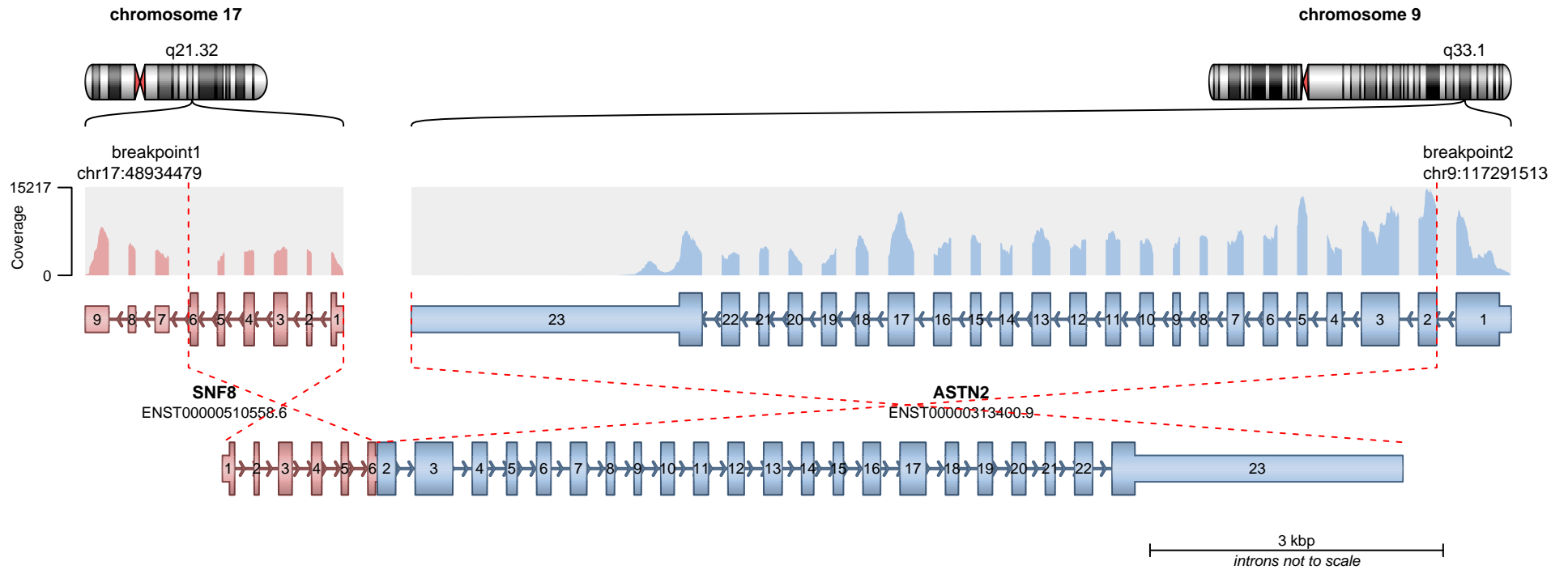
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

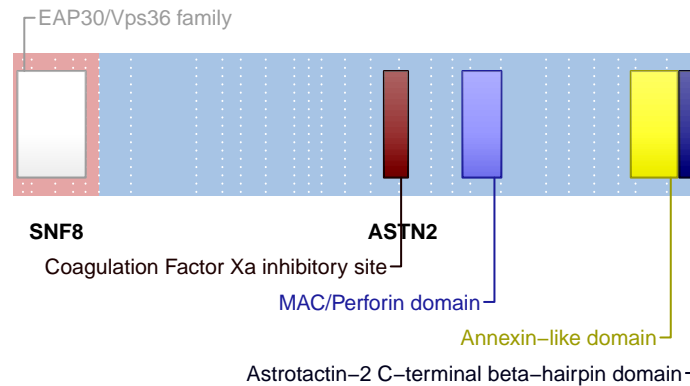
Split reads = 25  
Discordant mates = 2

- translocation
- duplication
- deletion
- inversion



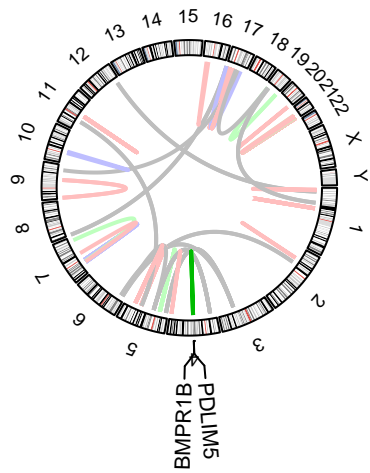
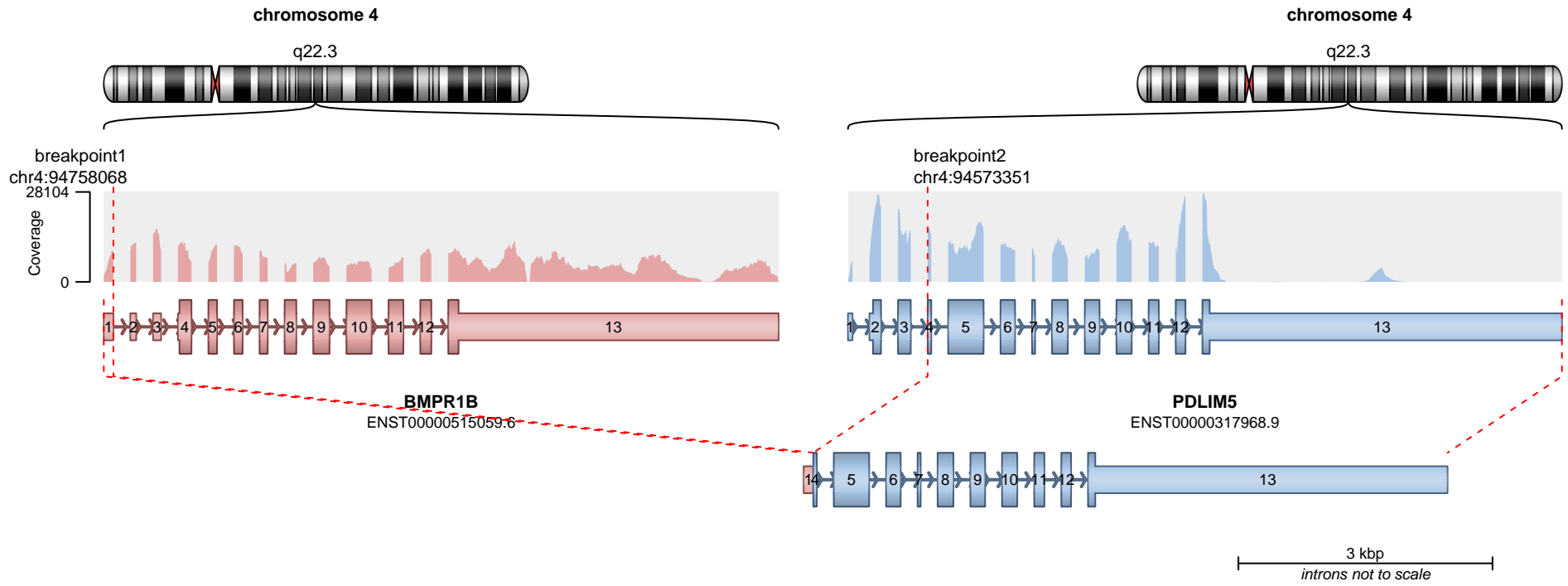
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



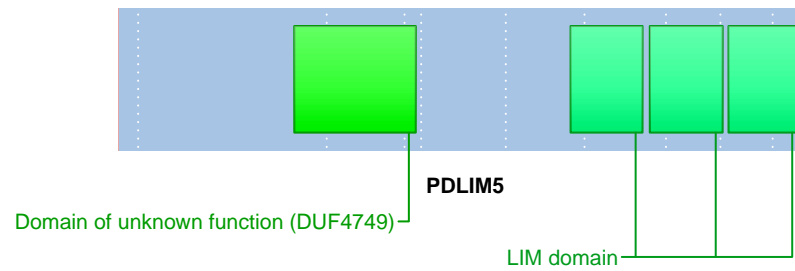
**SUPPORTING READ COUNT**

Split reads = 25  
Discordant mates = 0



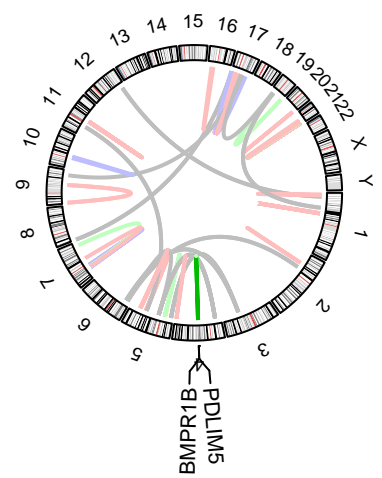
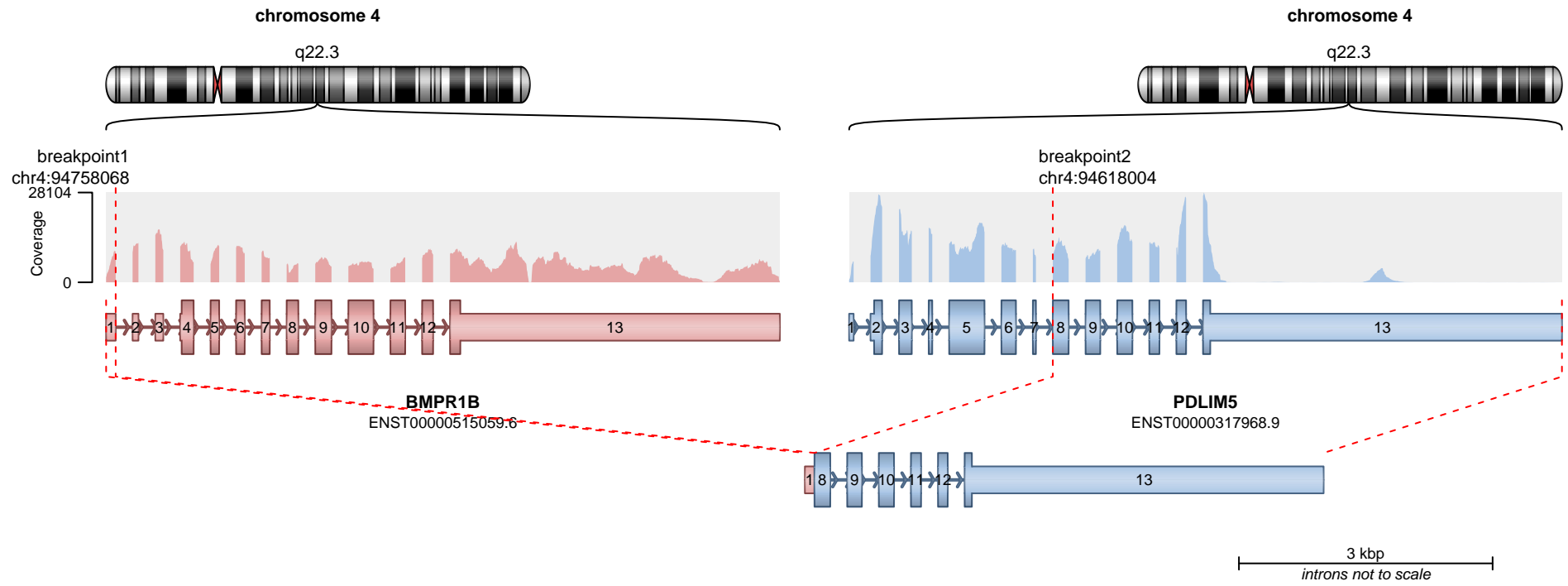
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear

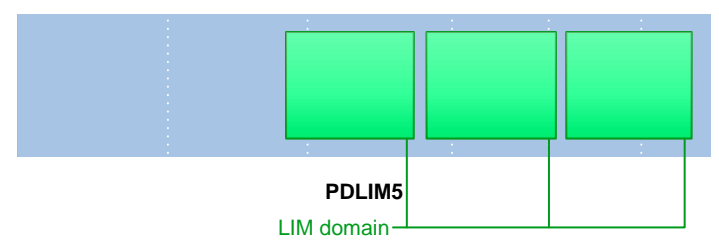


**SUPPORTING READ COUNT**

Split reads = 23  
Discordant mates = 0



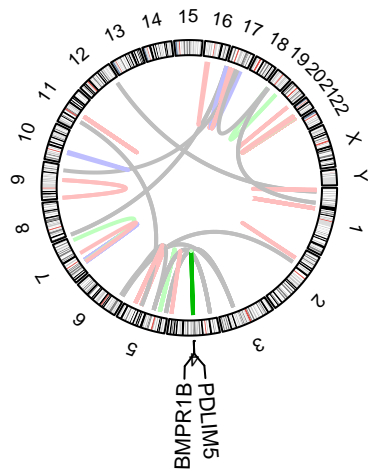
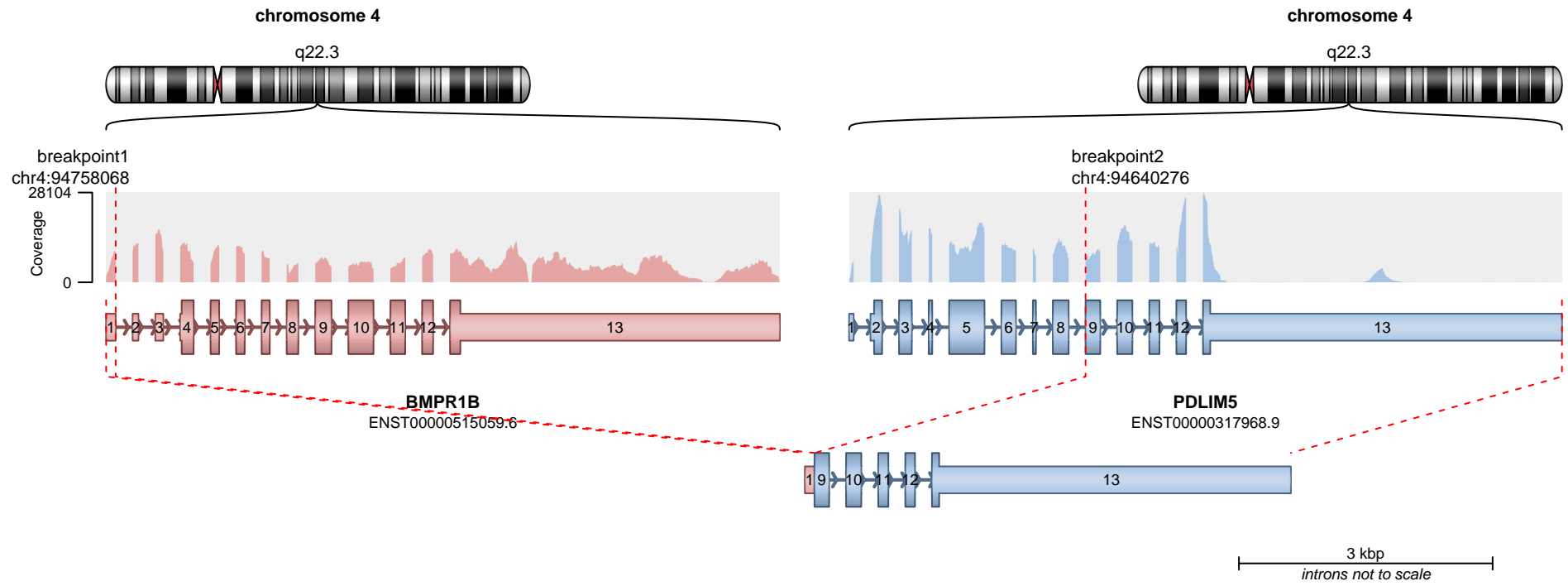
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

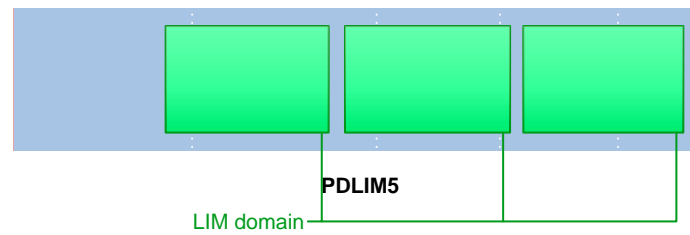
Split reads = 5  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



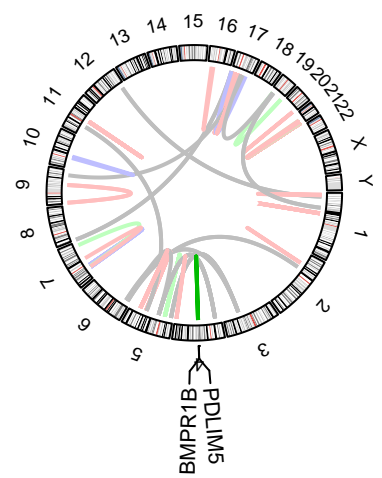
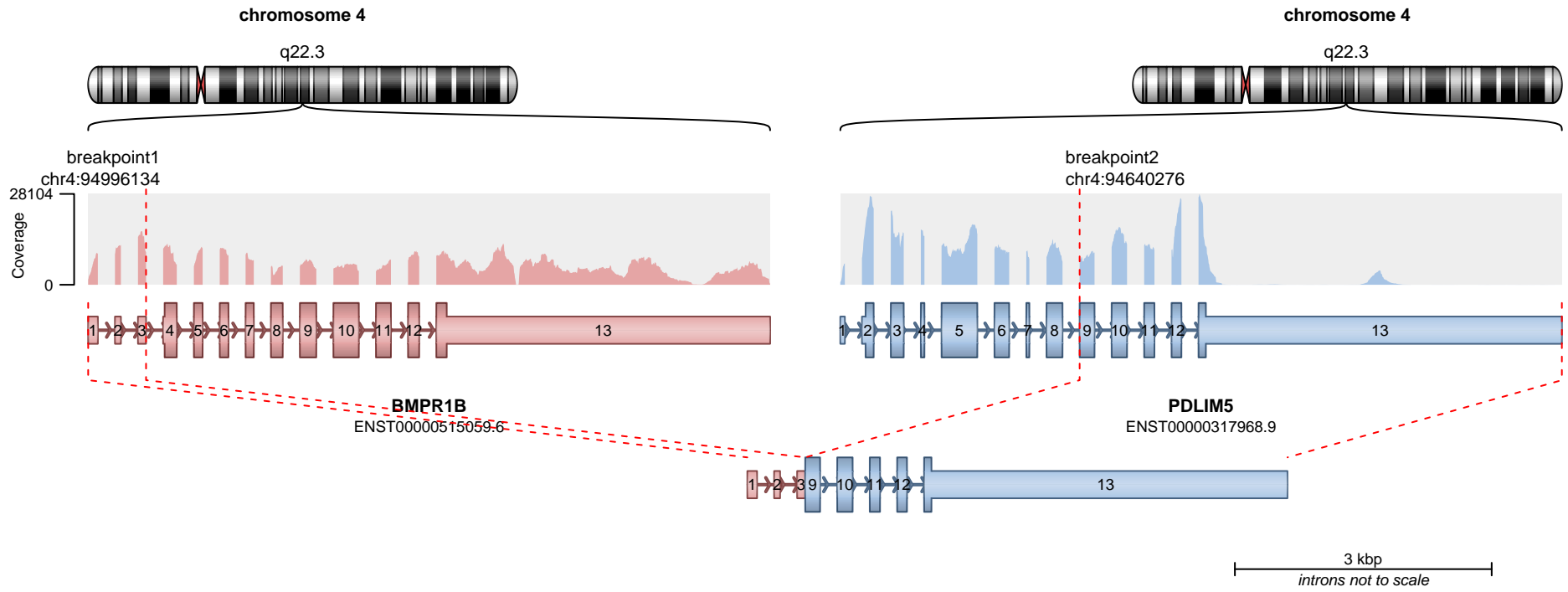
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



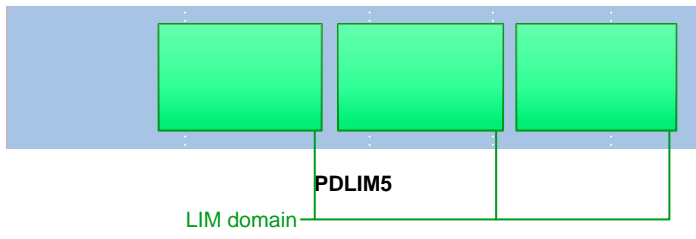
**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0



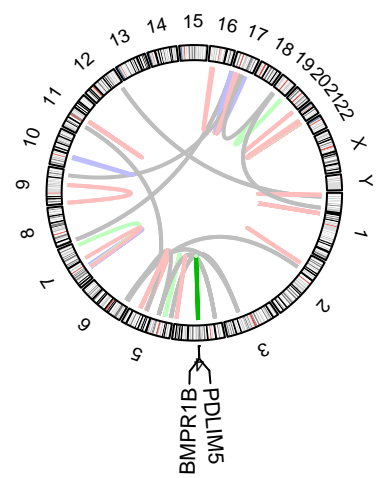
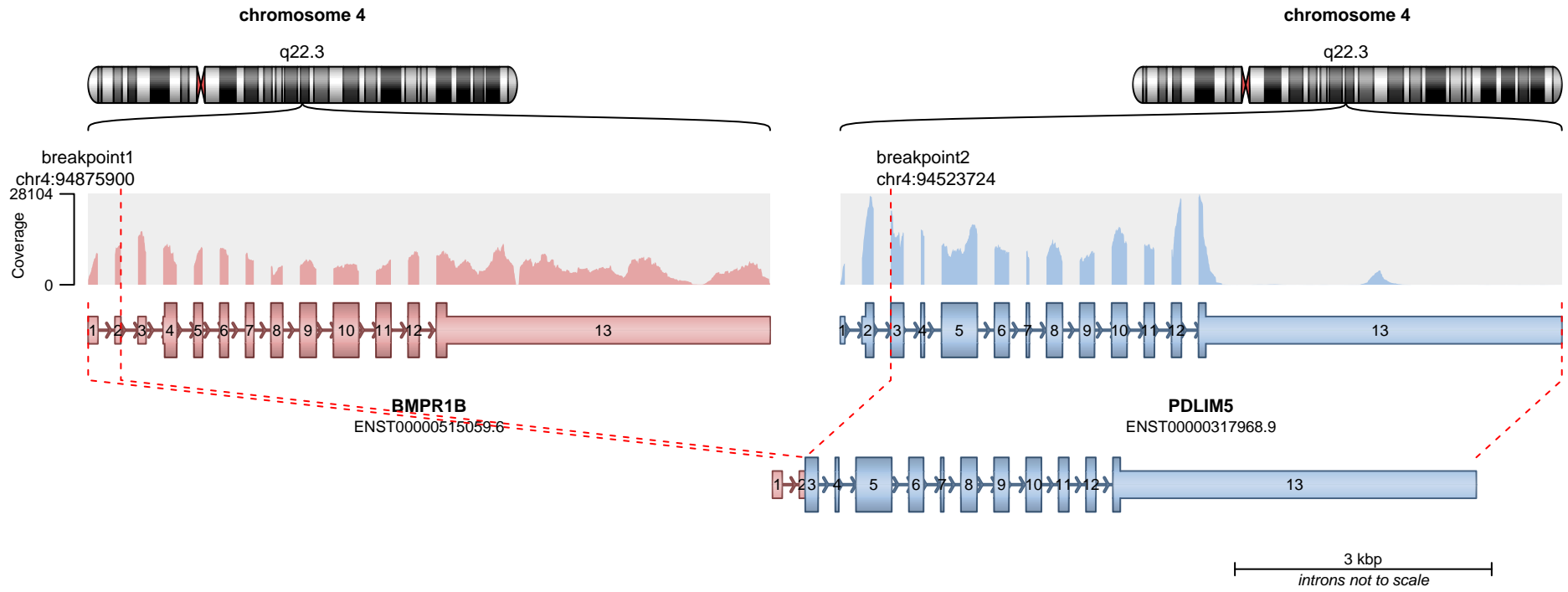
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear

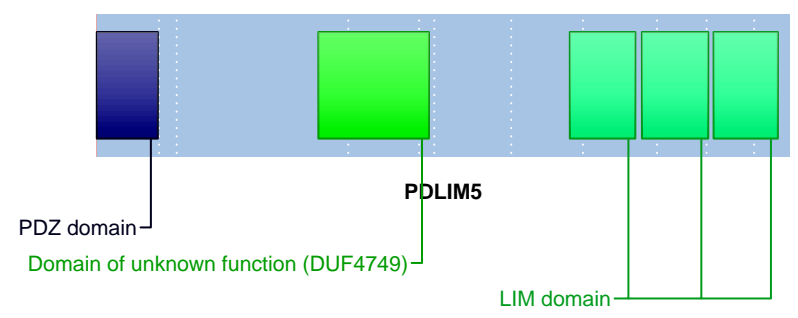


**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0



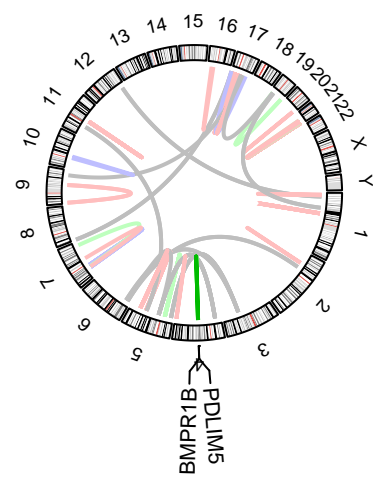
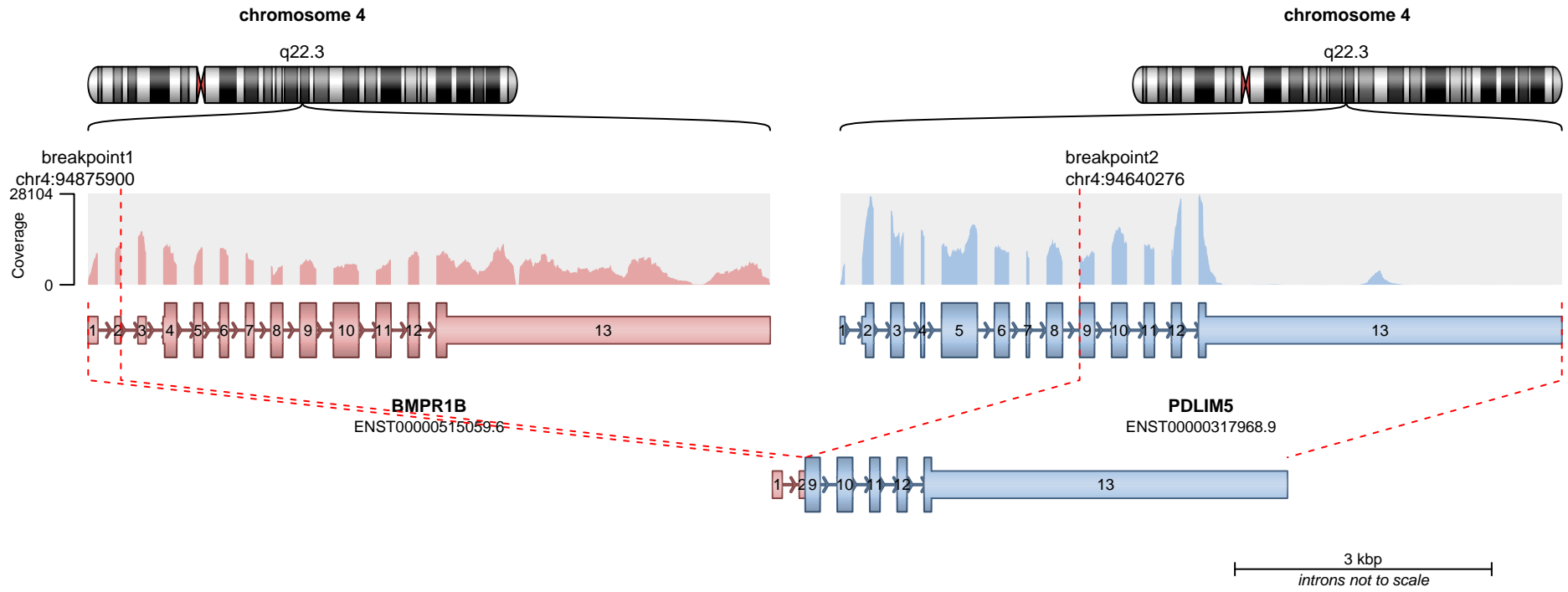
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

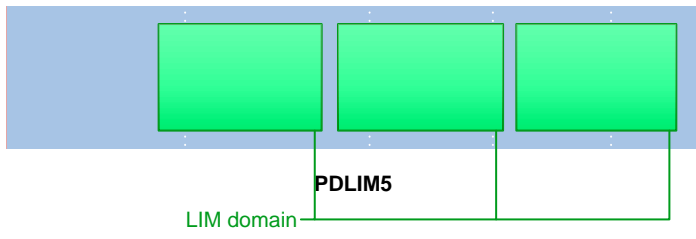
Split reads = 2  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



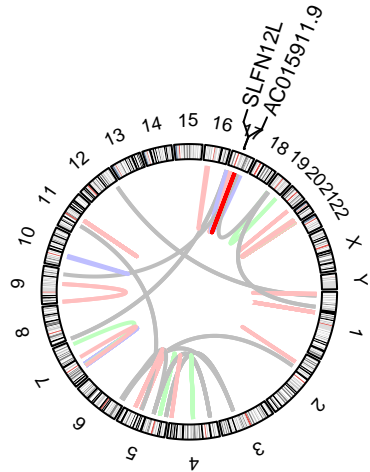
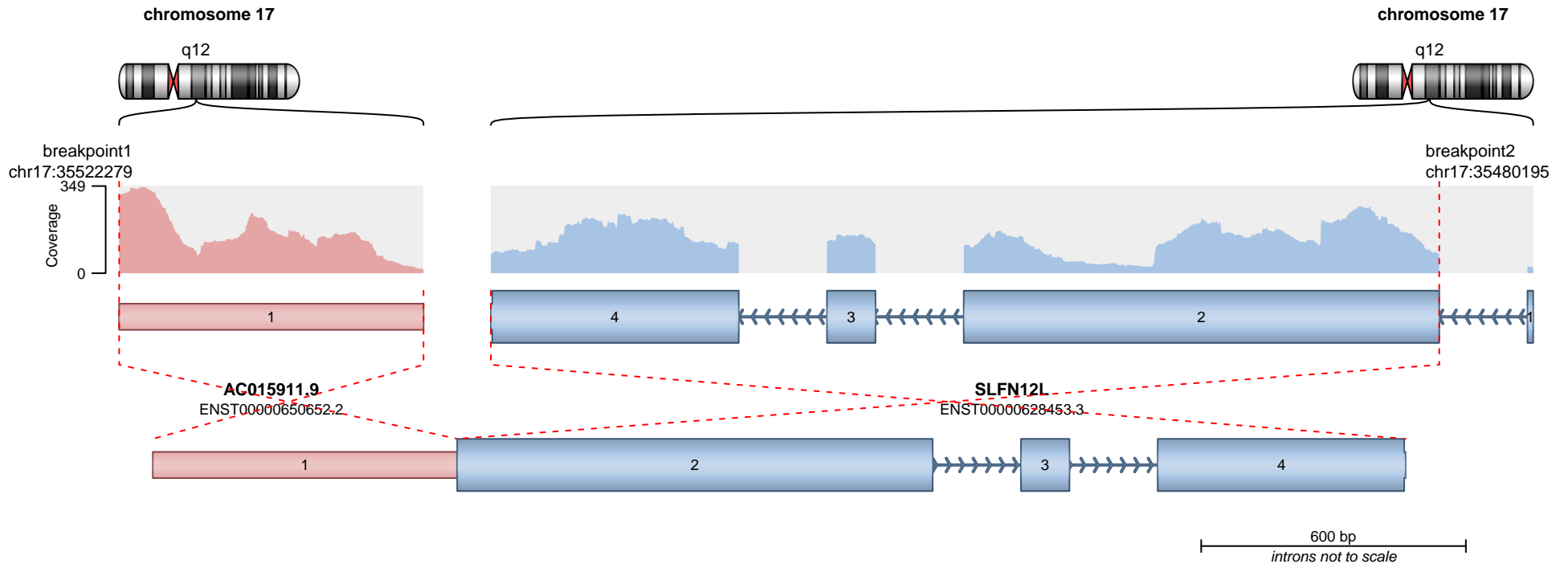
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear

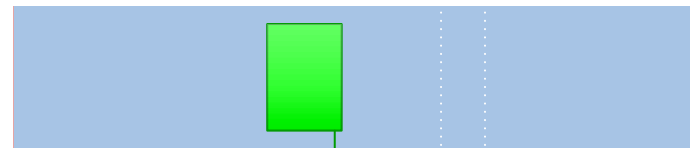


**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0



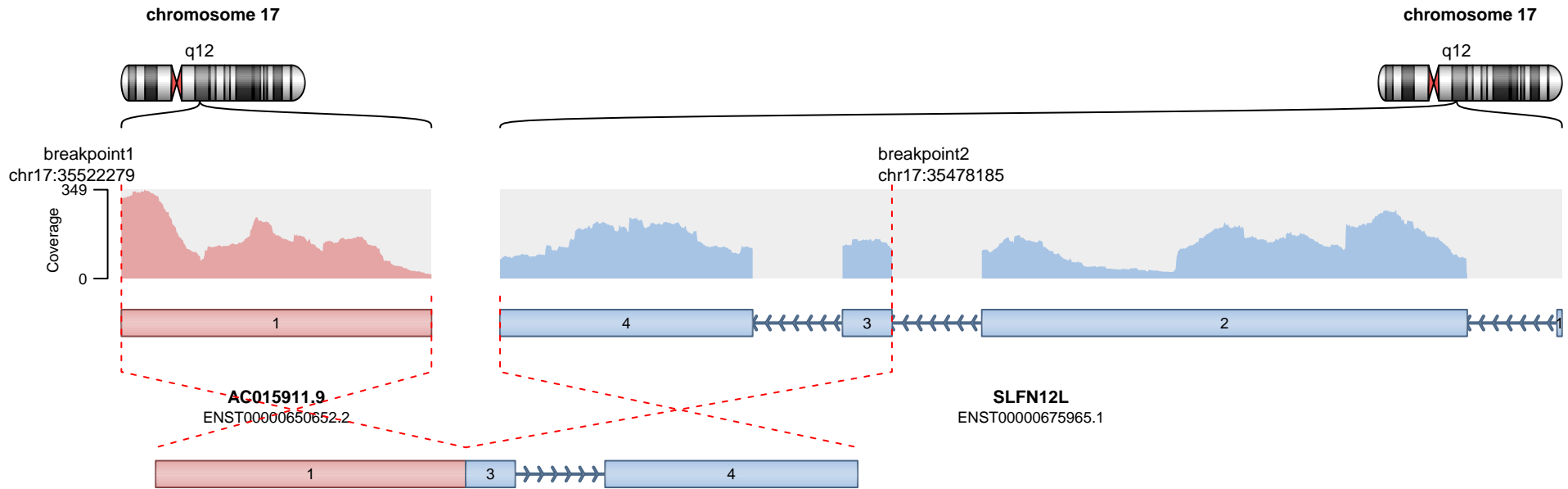
RETAINED PROTEIN DOMAINS  
reading frame unclear



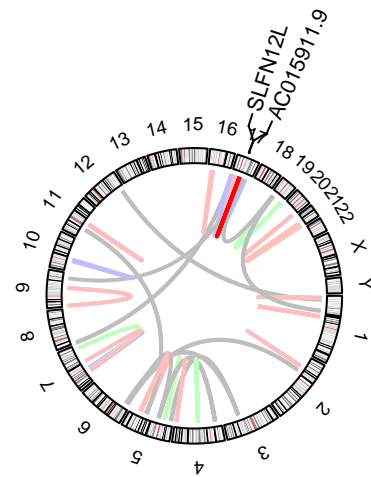
SUPPORTING READ COUNT

Split reads = 20  
Discordant mates = 4

— translocation — deletion  
— duplication — inversion



600 bp  
introns not to scale

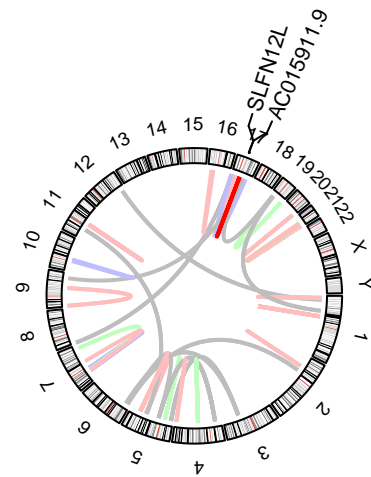
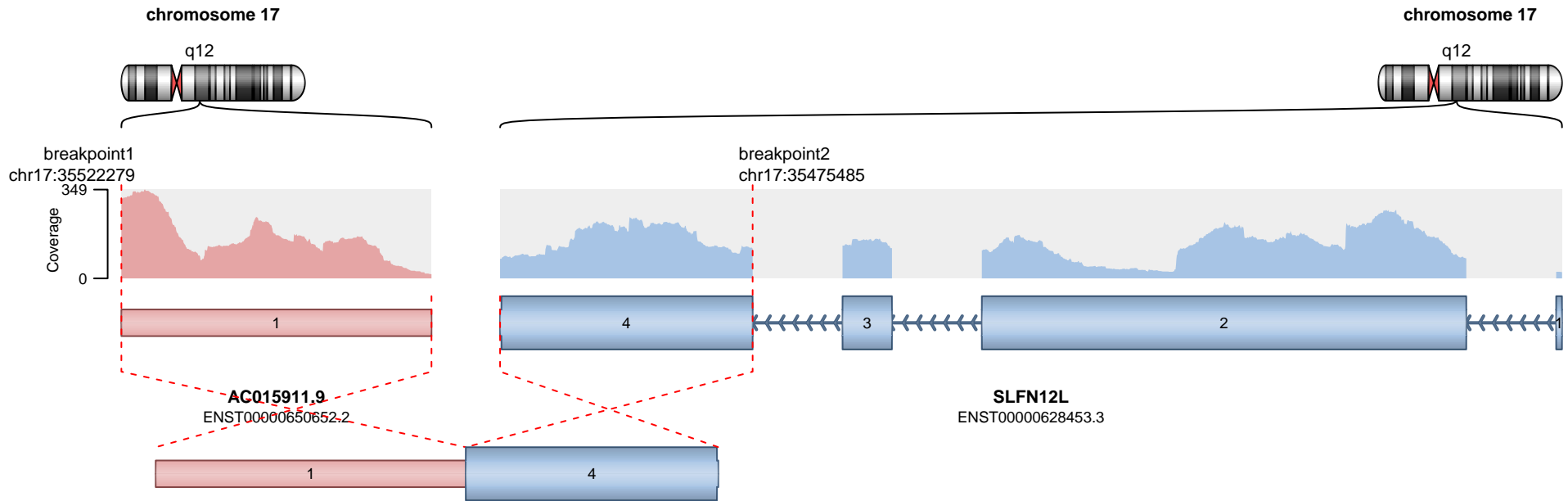


— translocation — deletion  
— duplication — inversion

Genes are not protein-coding.

**SUPPORTING READ COUNT**

Split reads = 8  
Discordant mates = 1

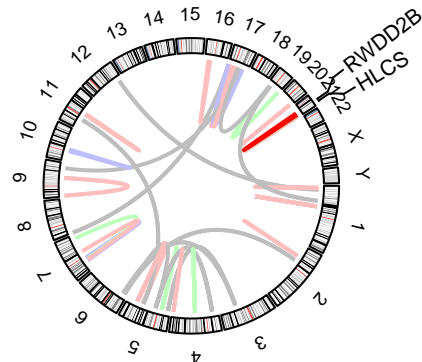
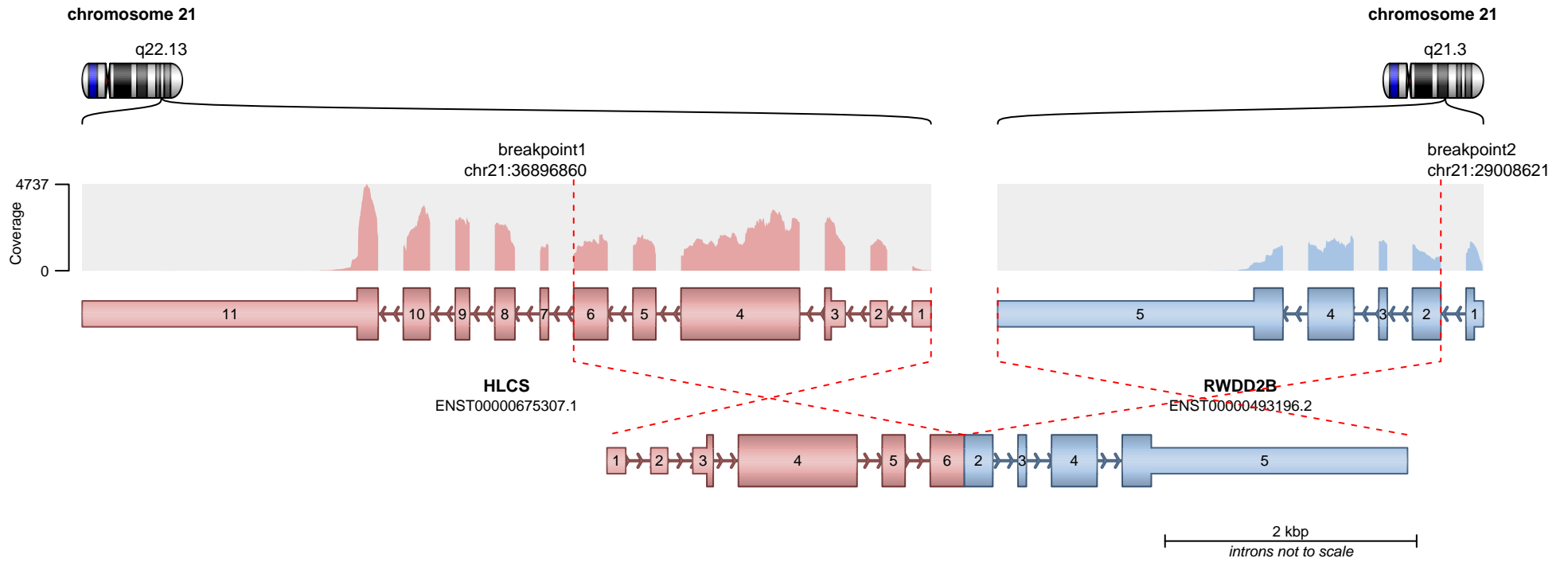


— translocation    — deletion  
— duplication    — inversion

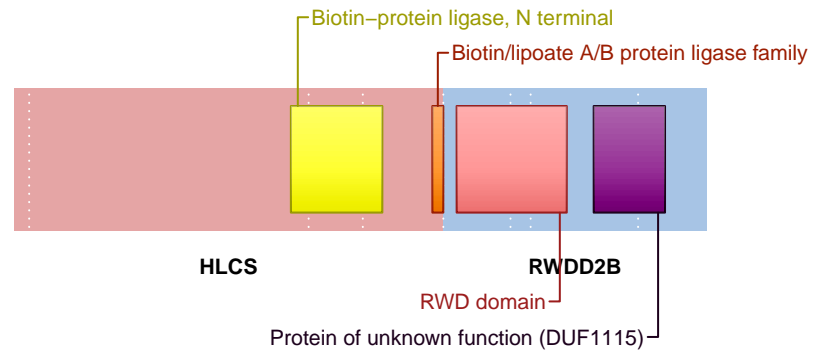
No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0



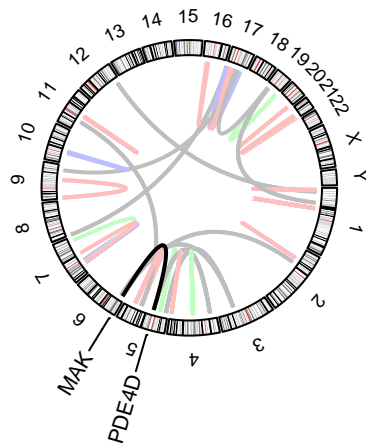
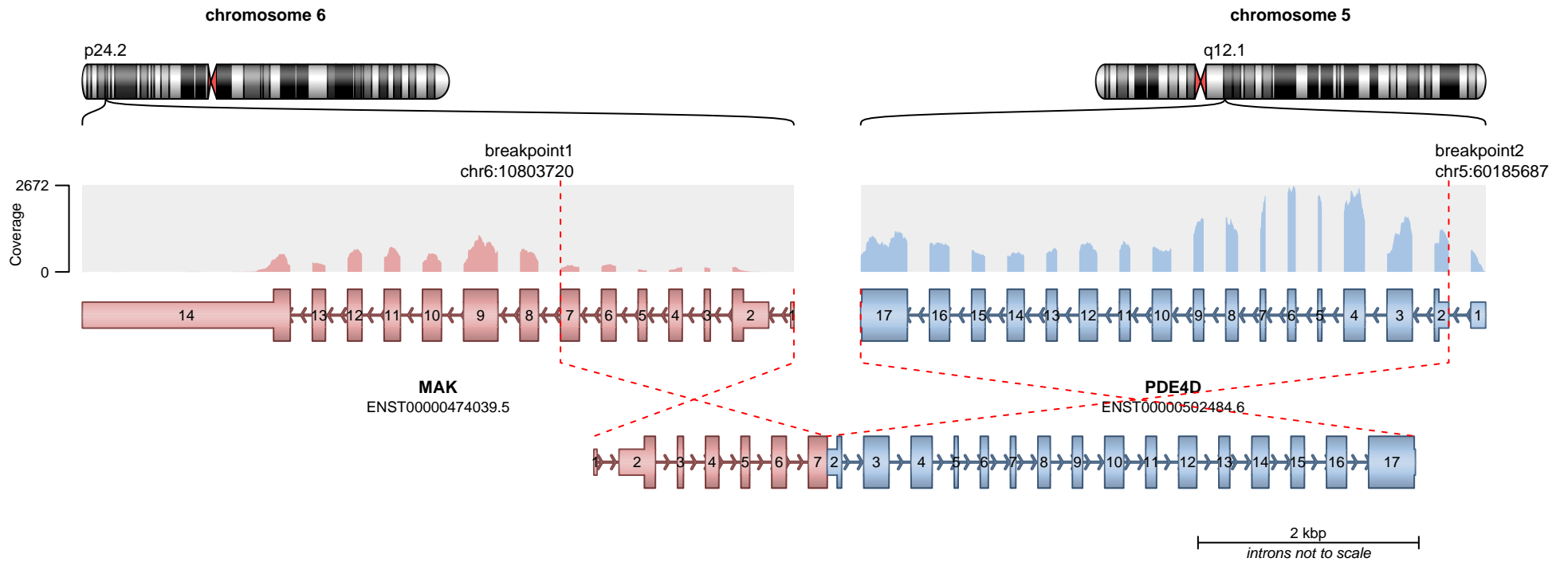
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



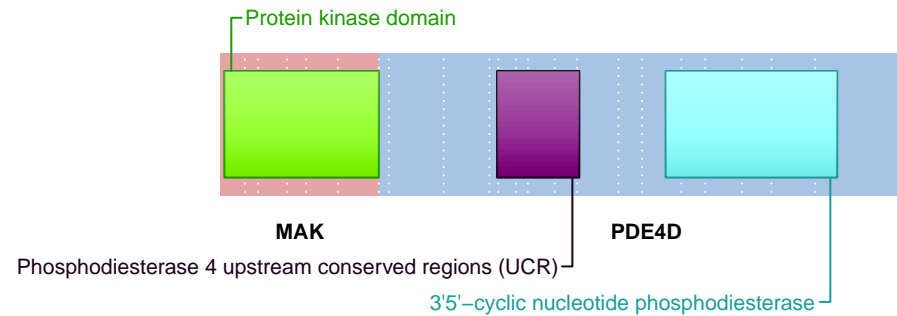
**SUPPORTING READ COUNT**

Split reads = 21  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



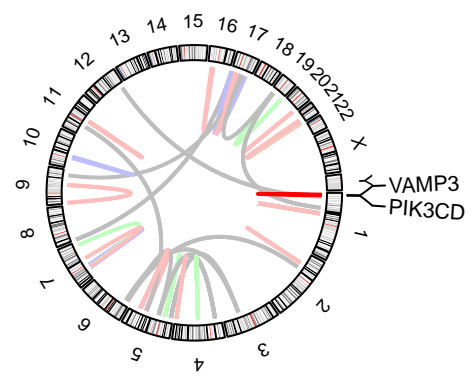
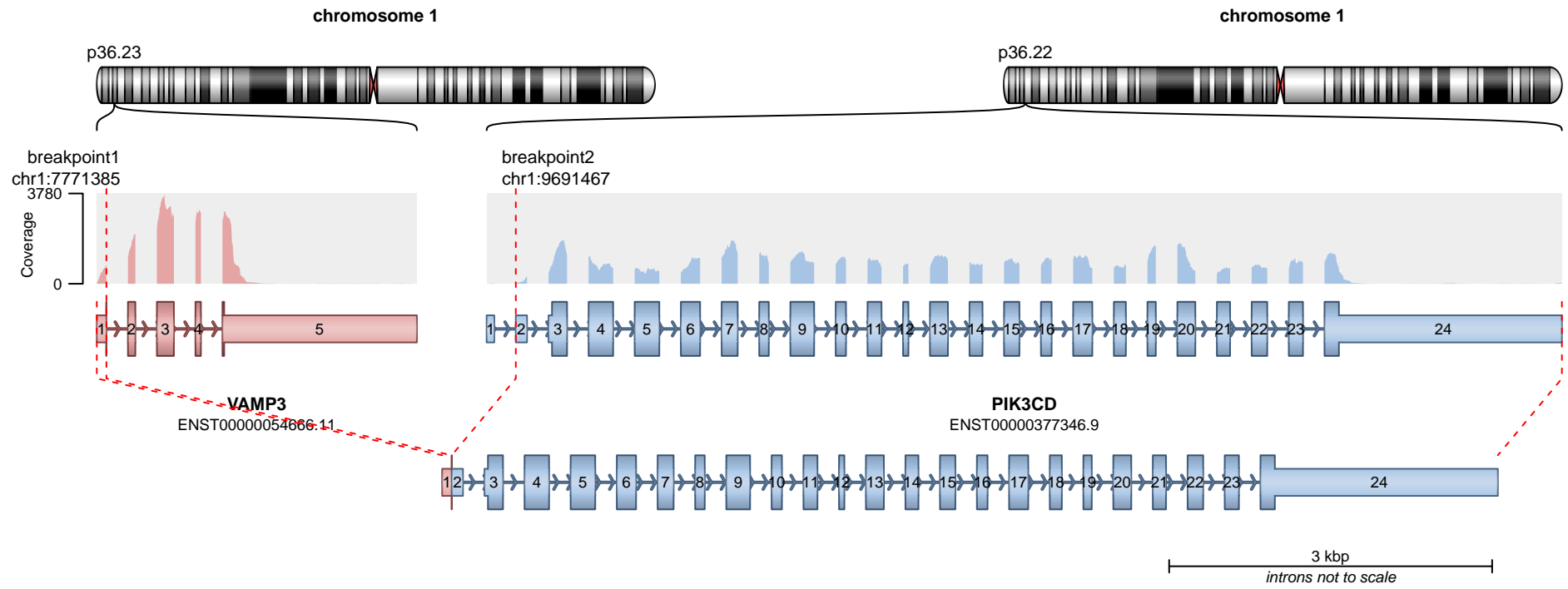
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

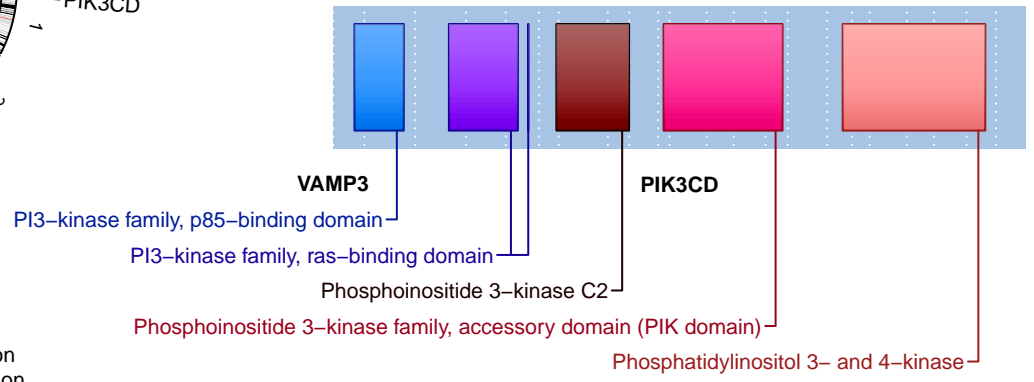
Split reads = 18  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



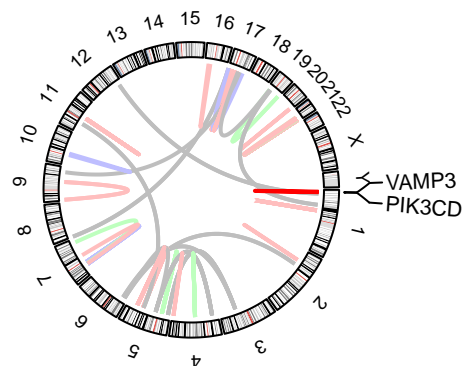
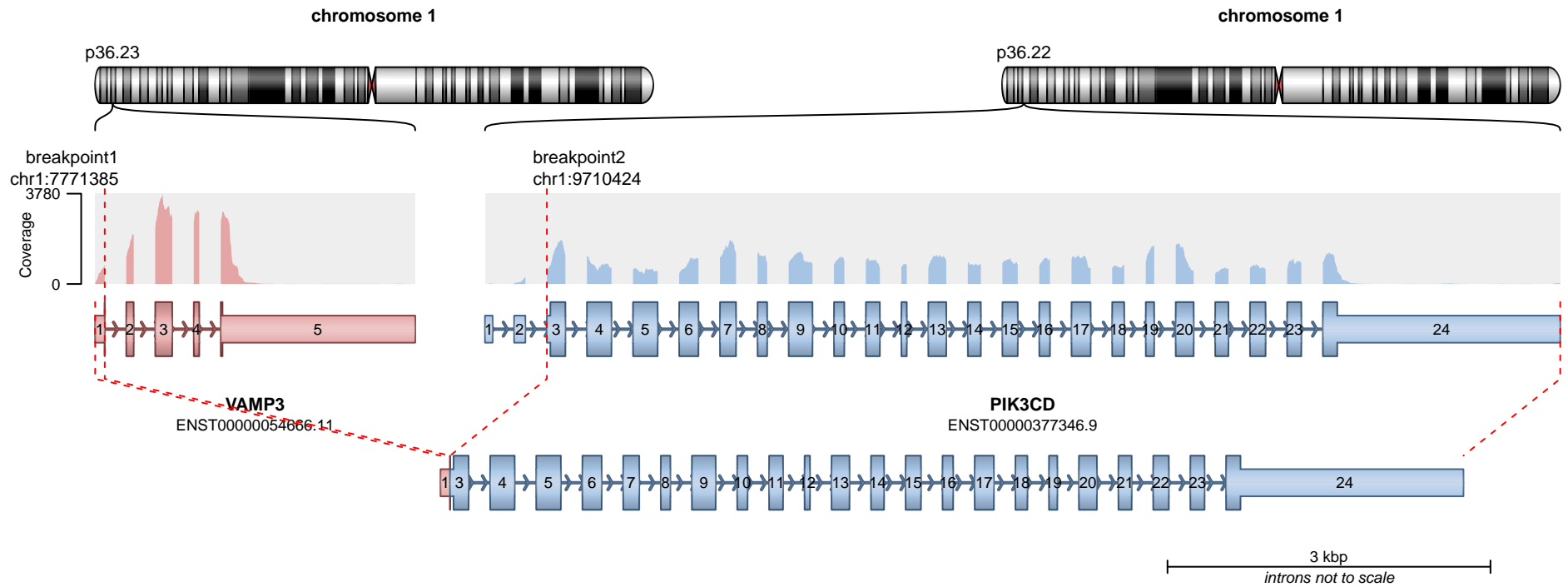
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



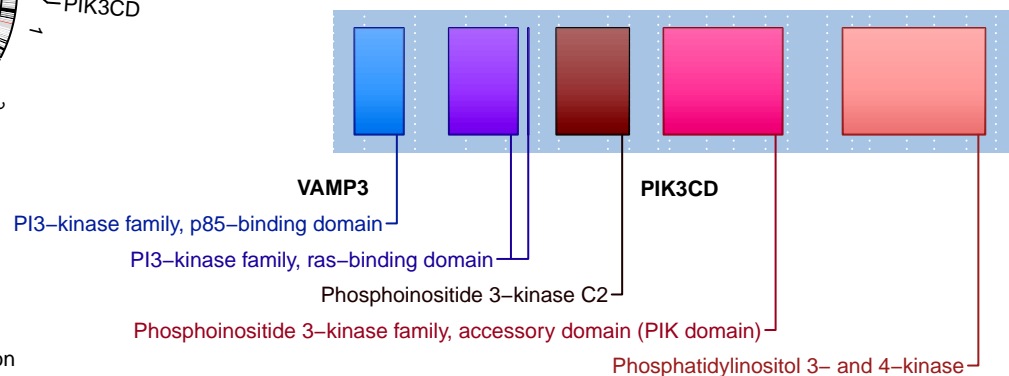
**SUPPORTING READ COUNT**

Split reads = 18  
Discordant mates = 0



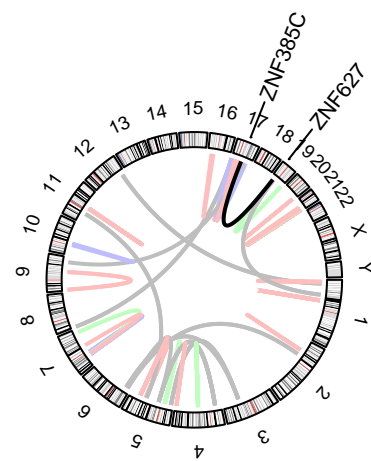
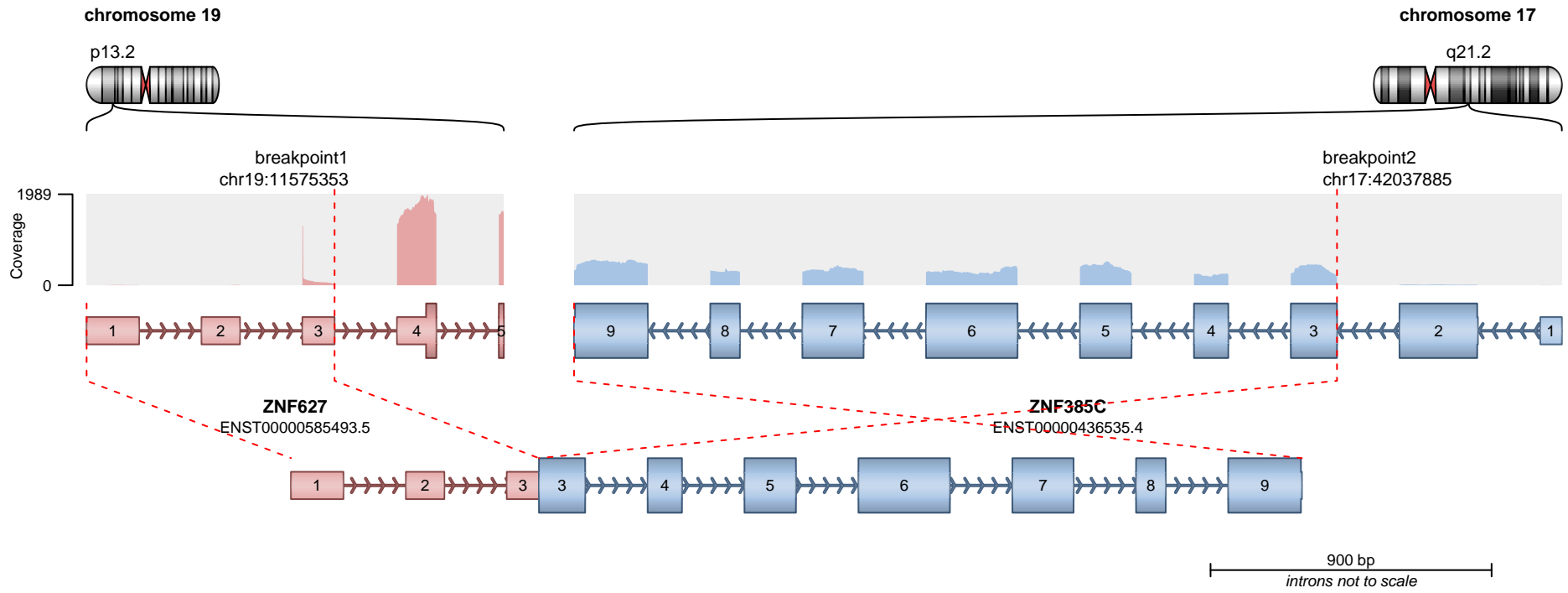
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear

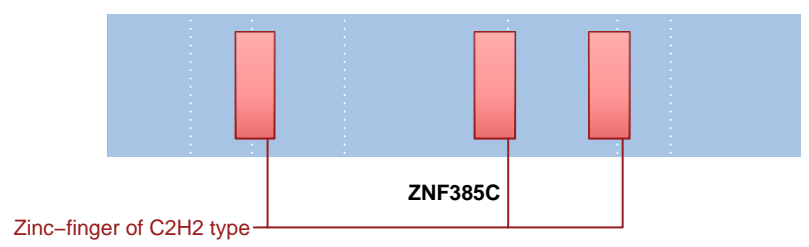


**SUPPORTING READ COUNT**

Split reads = 7  
Discordant mates = 0



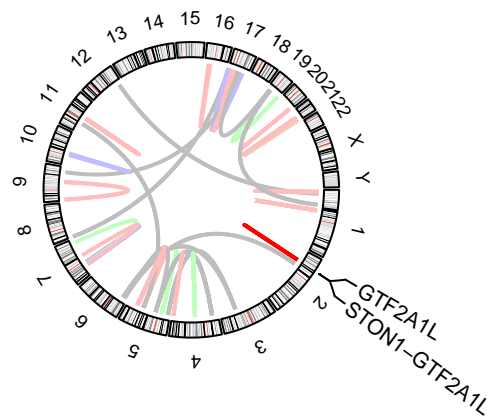
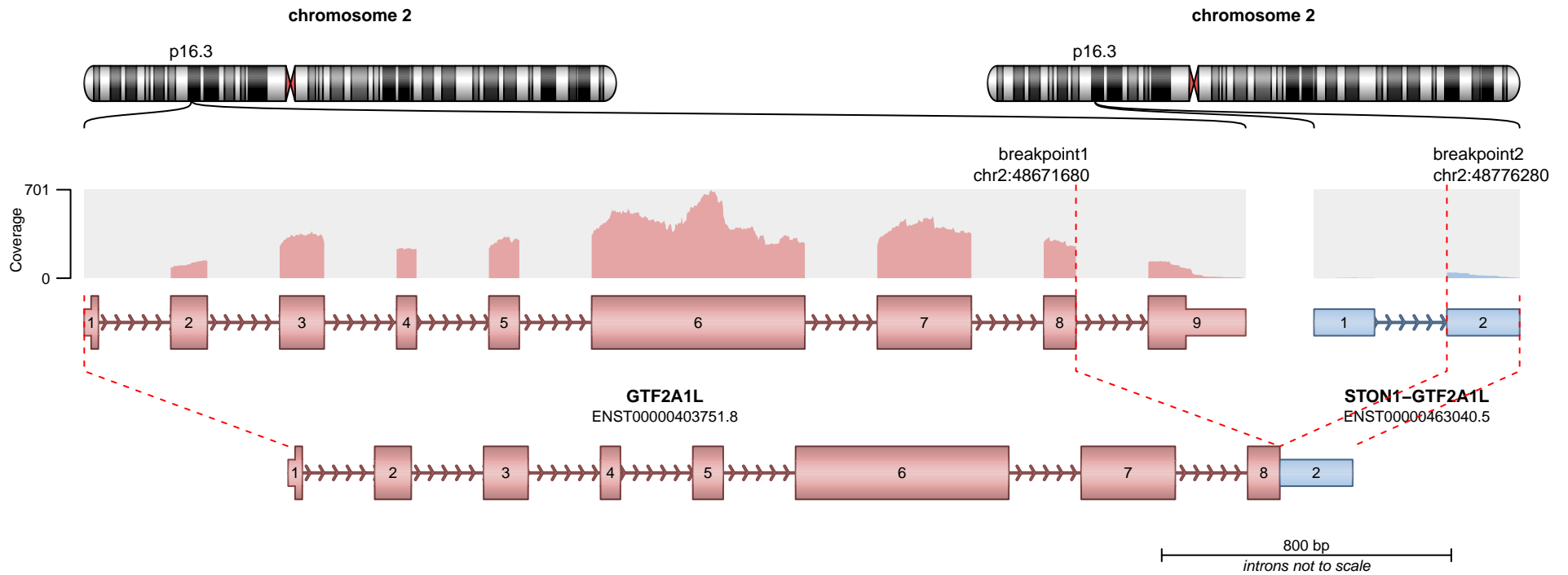
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



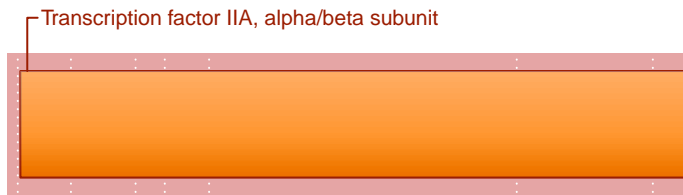
**SUPPORTING READ COUNT**

Split reads = 15  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



**RETAINED PROTEIN DOMAINS**  
reading frame unclear

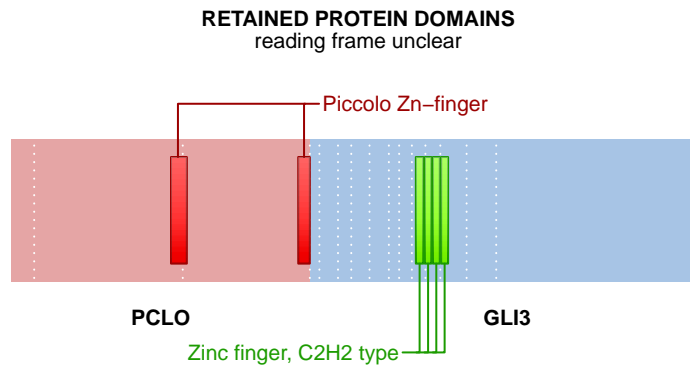
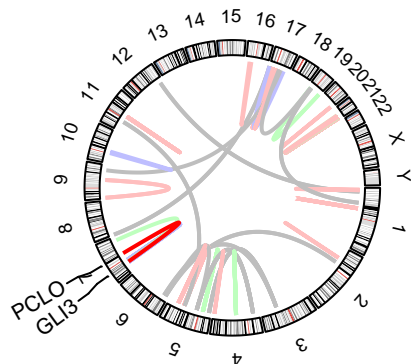
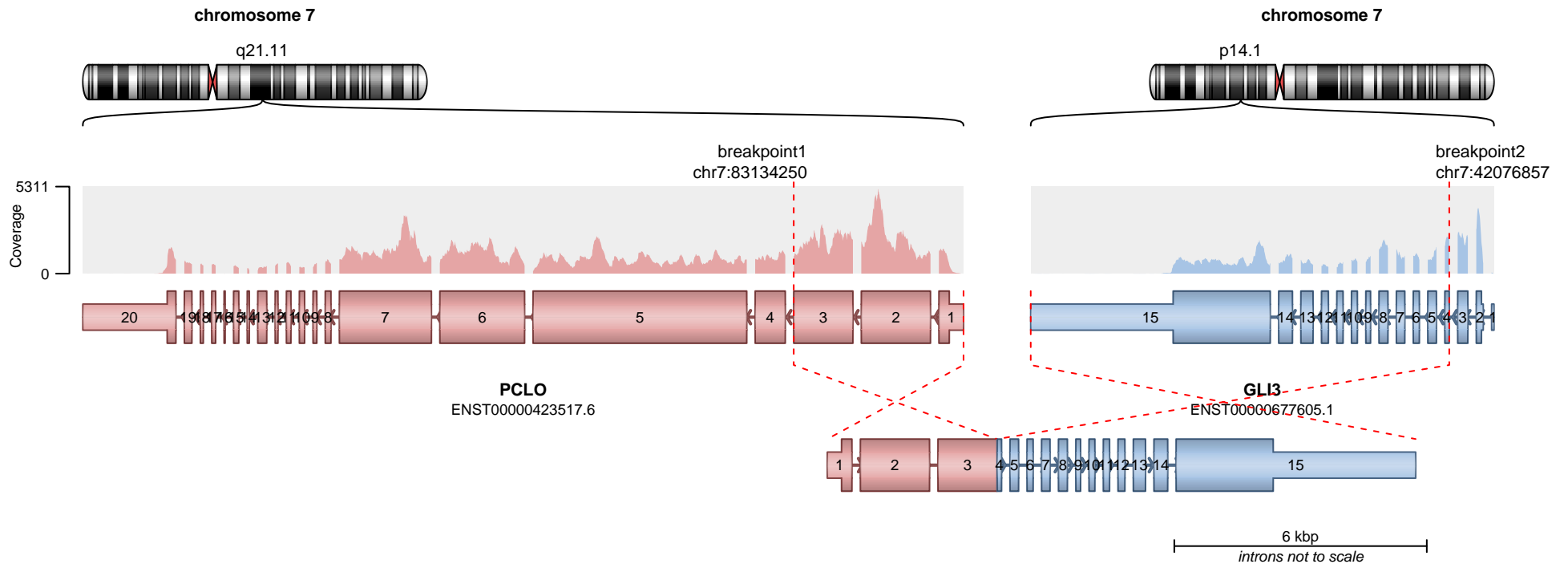


GTF2A1L

**SUPPORTING READ COUNT**

Split reads = 13  
Discordant mates = 0

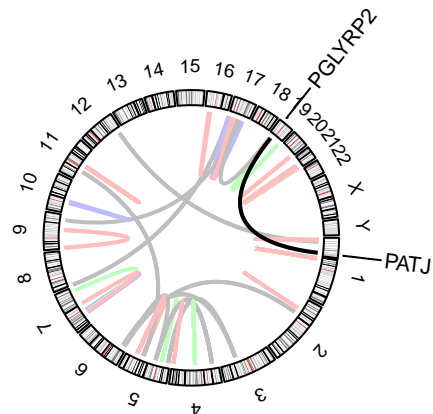
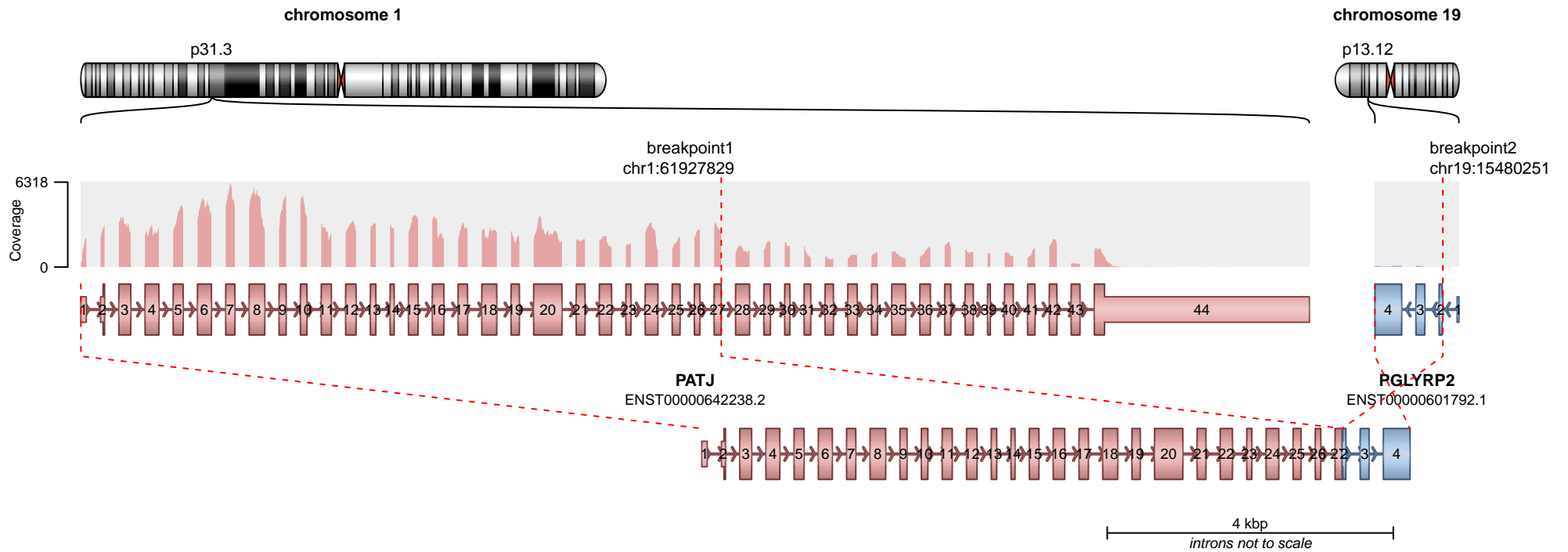
- translocation
- duplication
- deletion
- inversion



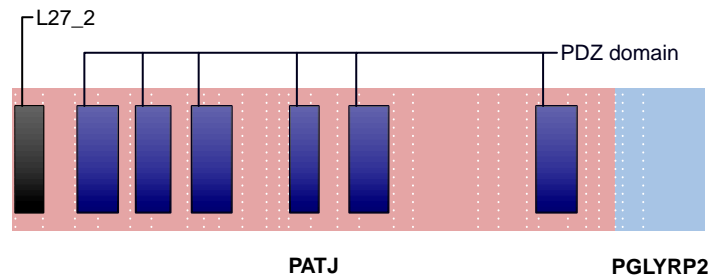
**SUPPORTING READ COUNT**

Split reads = 12  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



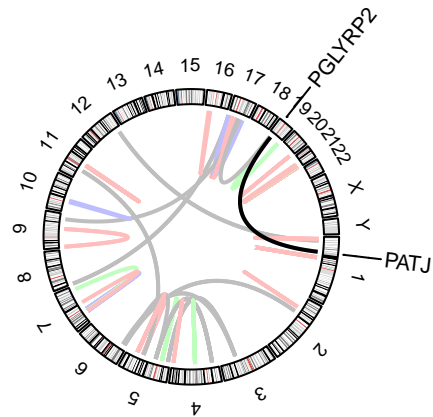
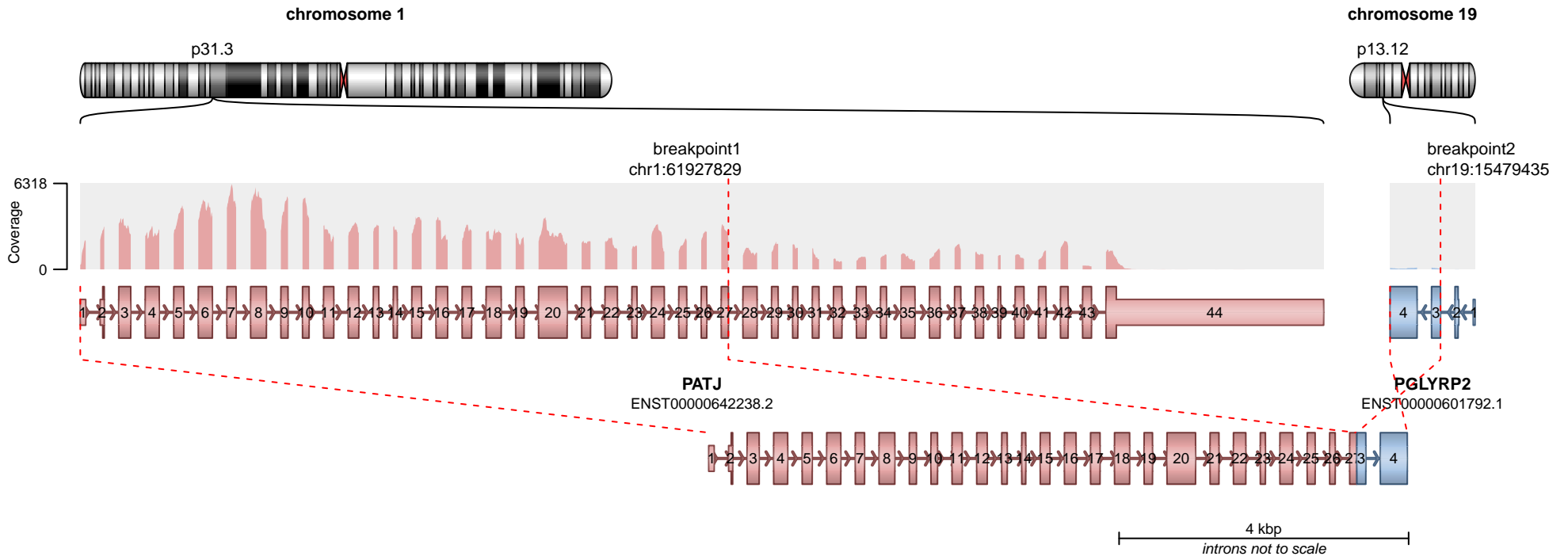
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



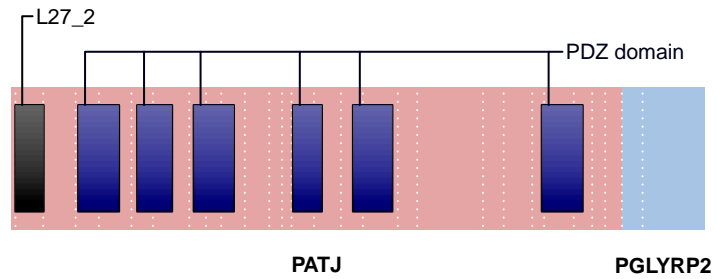
**SUPPORTING READ COUNT**

Split reads = 10  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



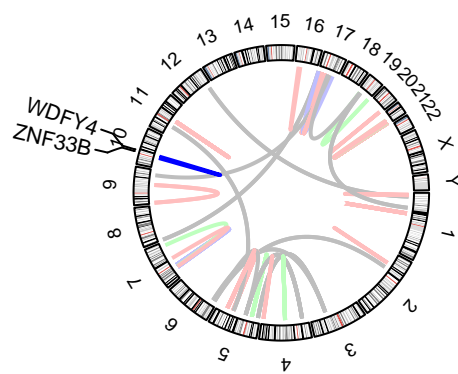
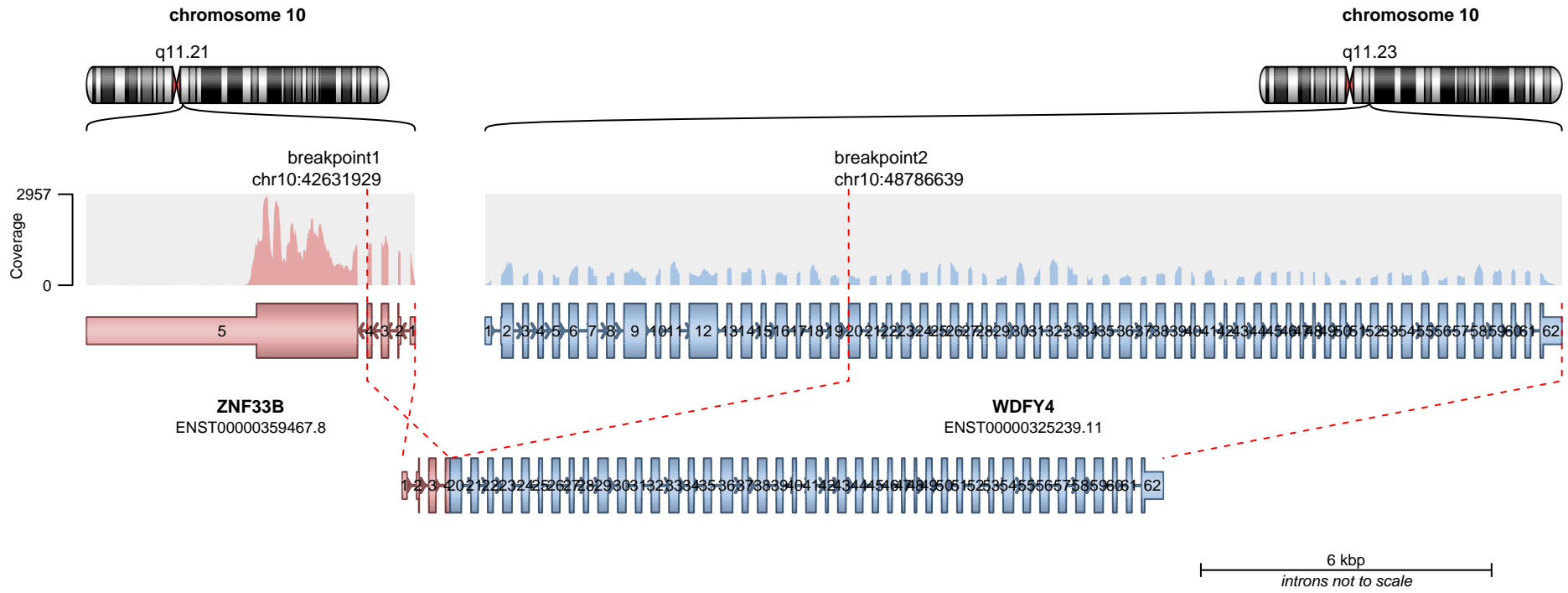
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

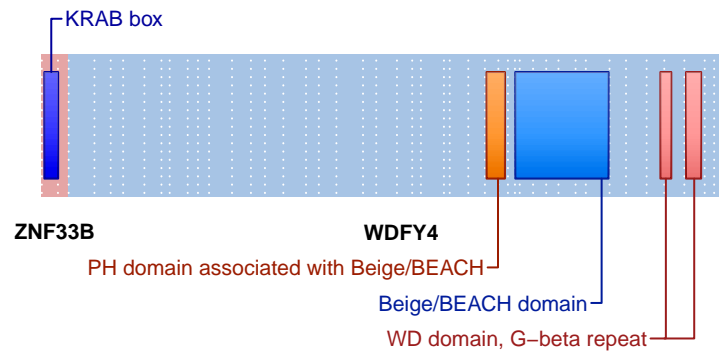
Split reads = 8  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



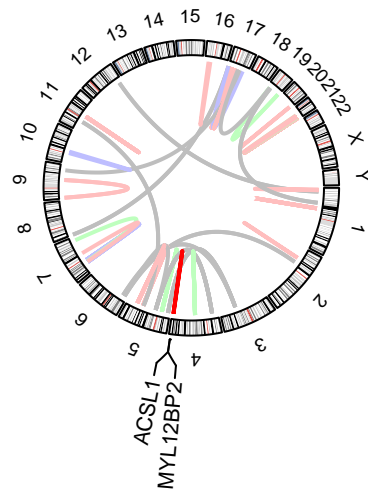
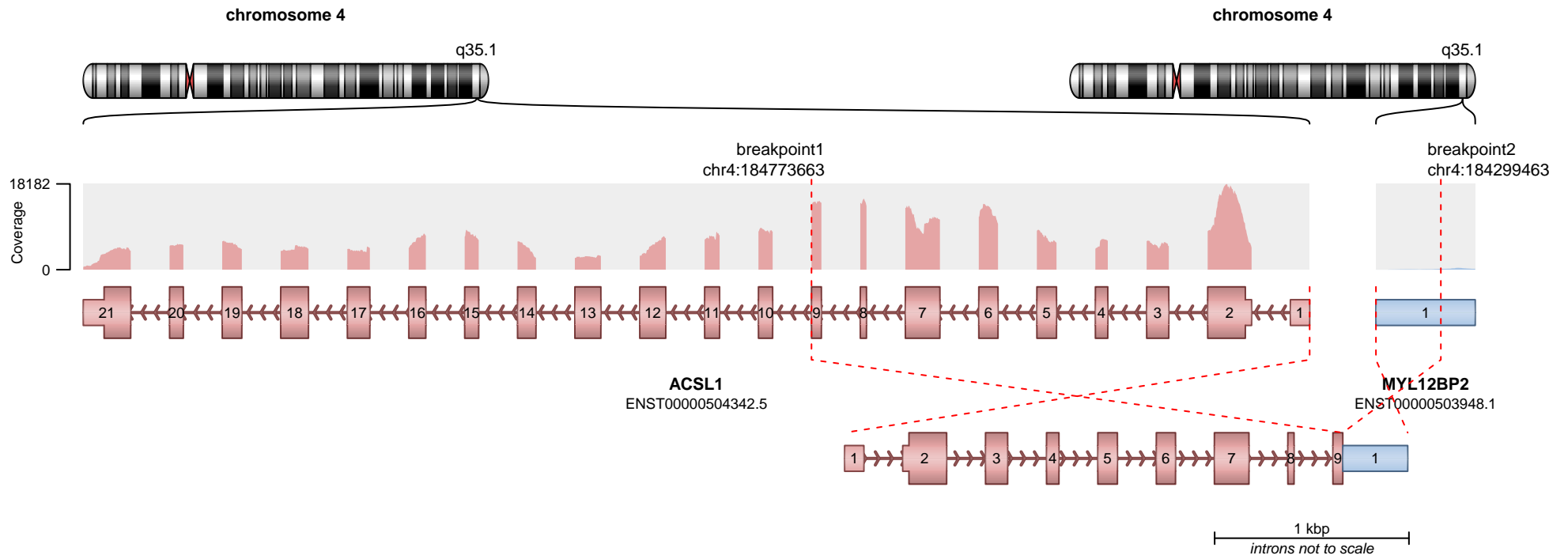
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear

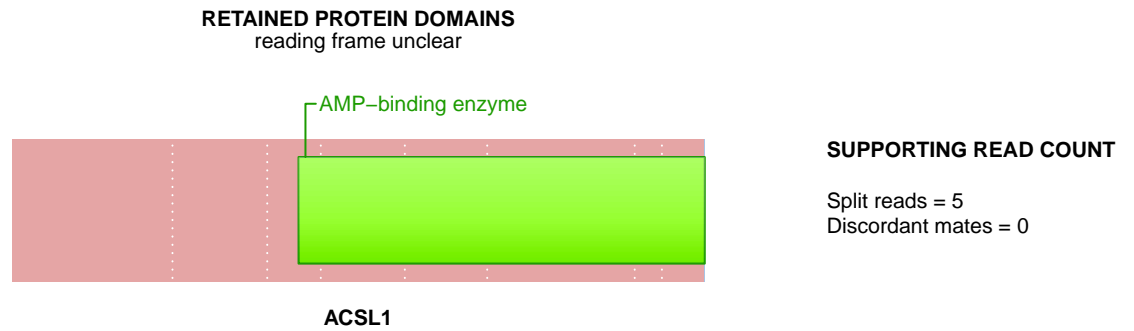


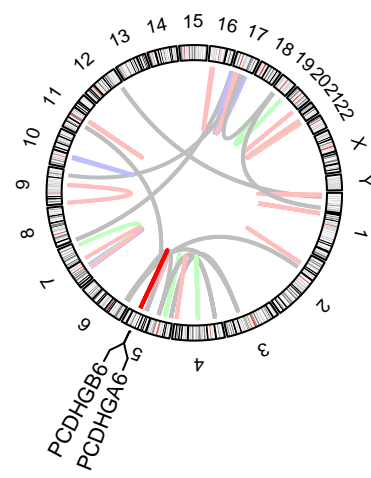
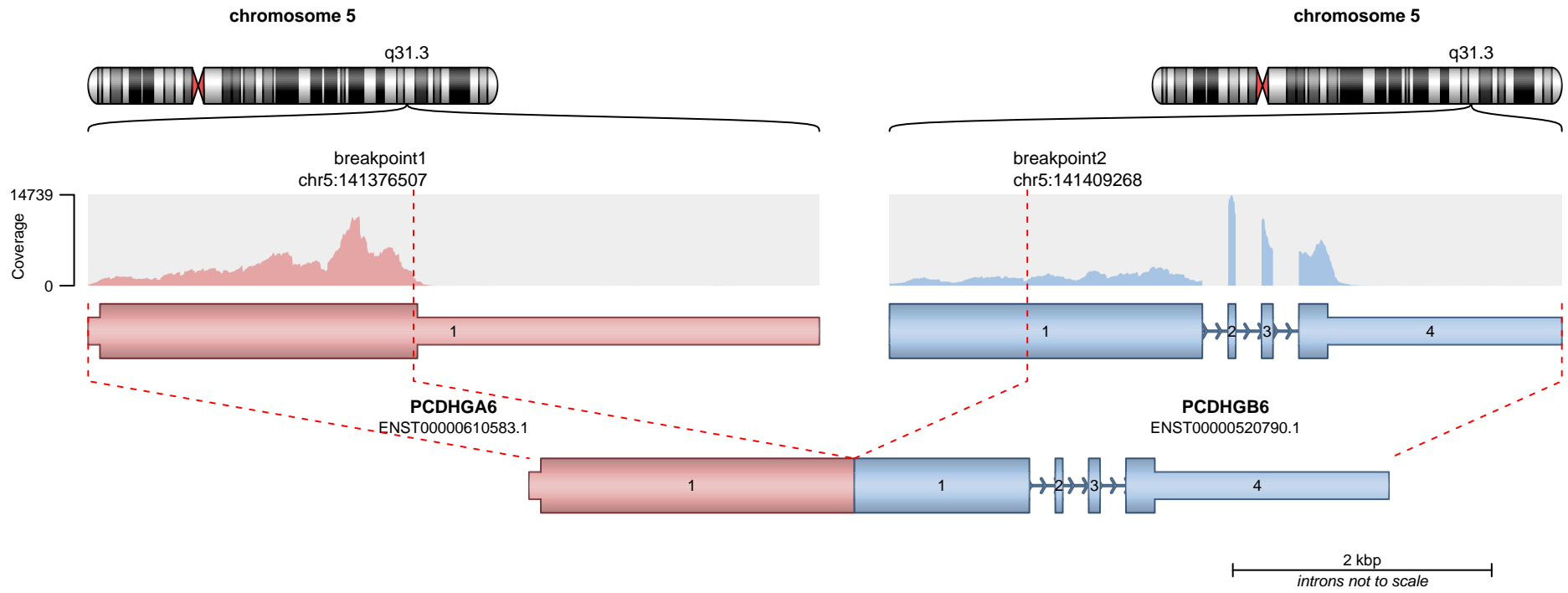
**SUPPORTING READ COUNT**

Split reads = 9  
Discordant mates = 1



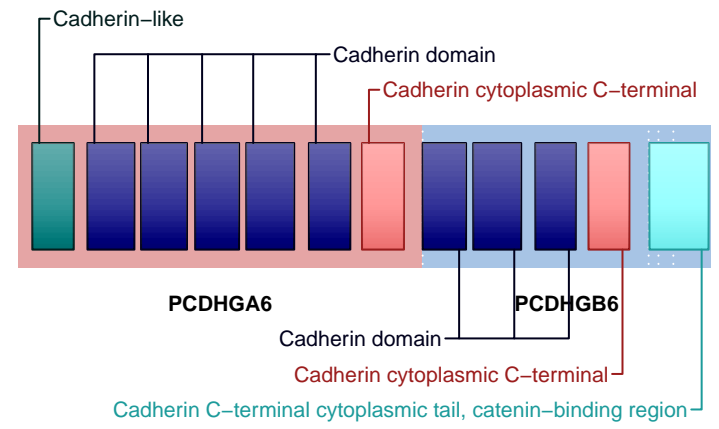
— translocation — deletion  
— duplication — inversion





— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 5  
Discordant mates = 0