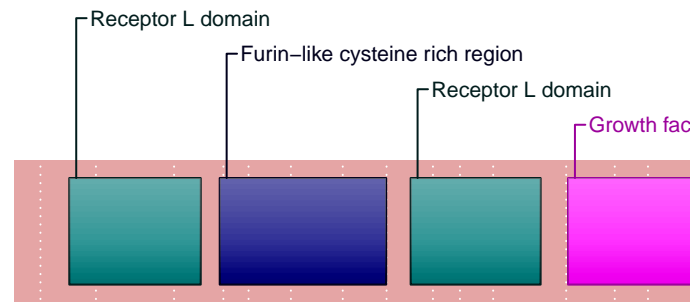


**RETAINED PROTEIN DOMAINS**  
reading frame unclear

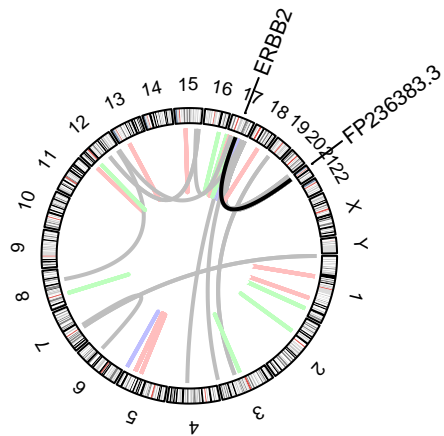
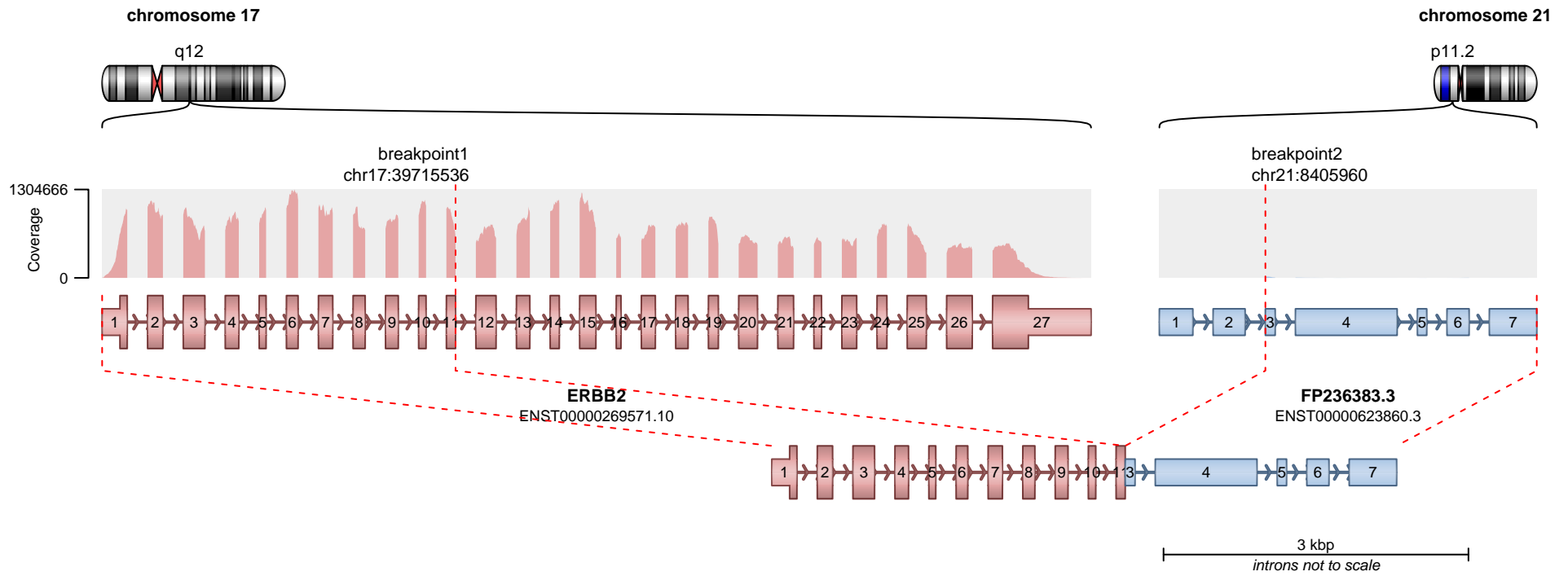


**ERBB2**

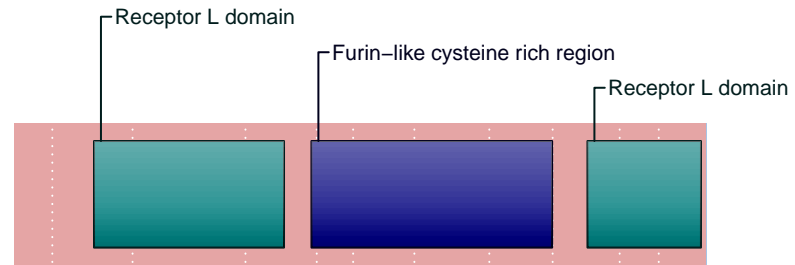
**SUPPORTING READ COUNT**

Split reads = 4057  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



**RETAINED PROTEIN DOMAINS**  
reading frame unclear

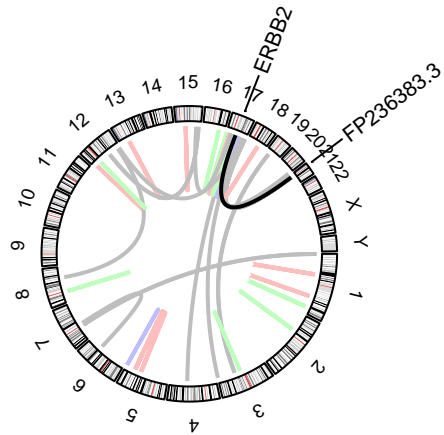
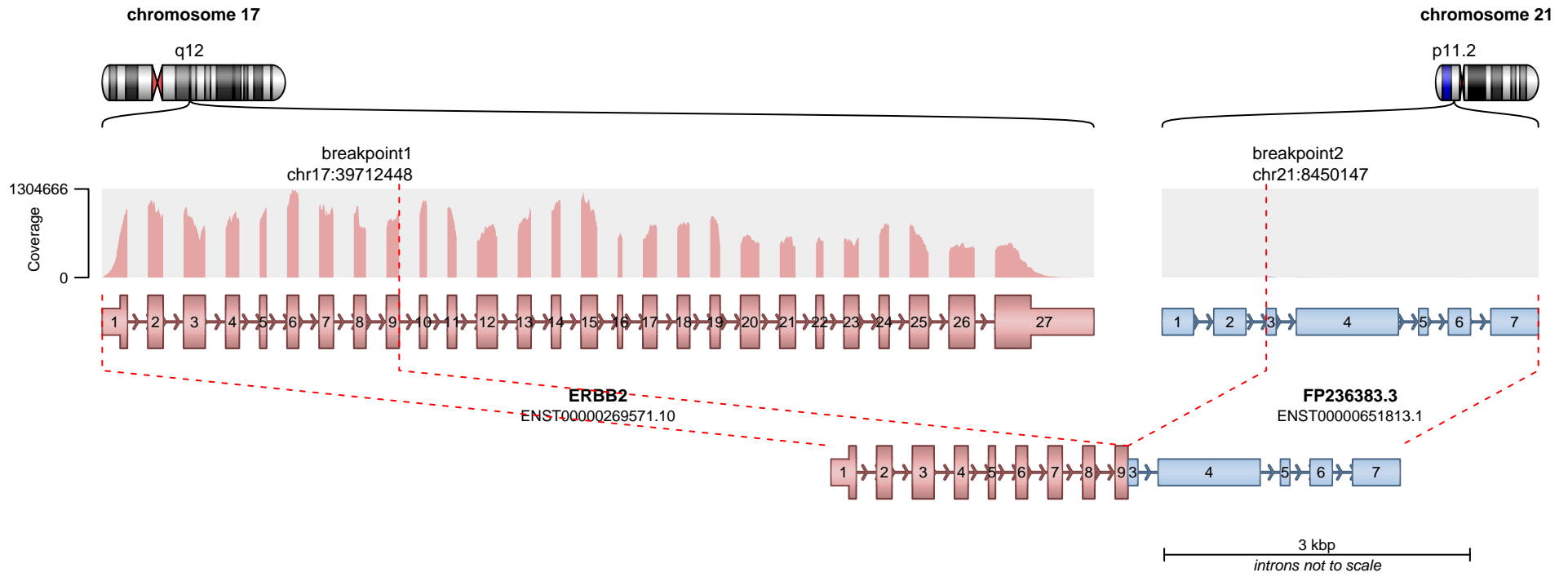


**ERBB2**

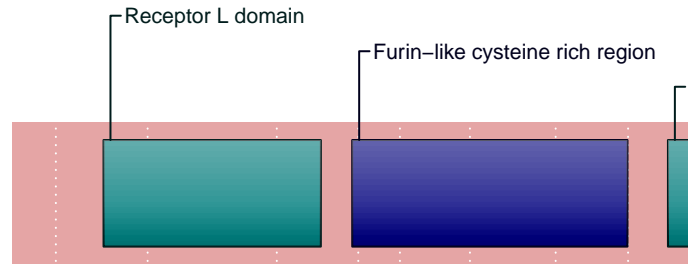
**SUPPORTING READ COUNT**

Split reads = 448  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



**RETAINED PROTEIN DOMAINS**  
reading frame unclear

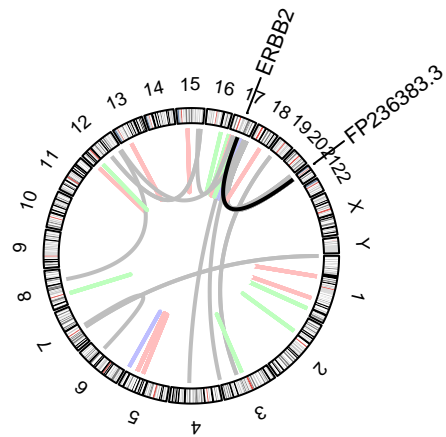
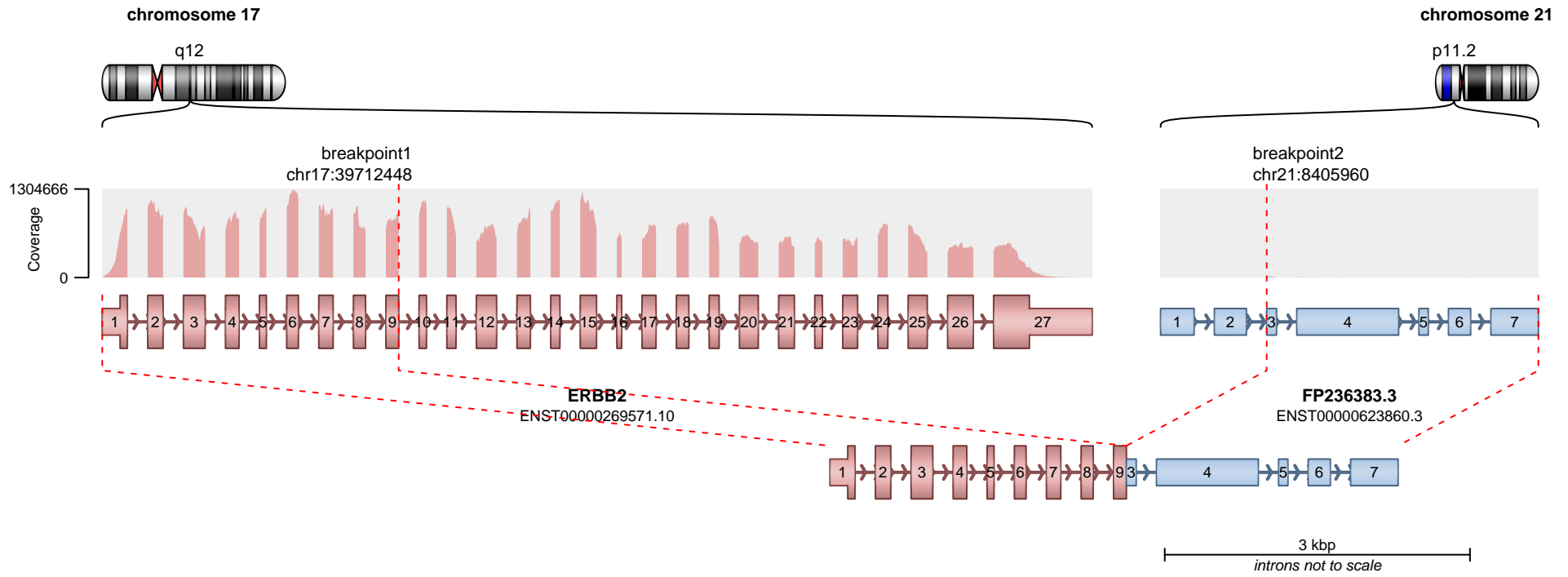


**ERBB2**

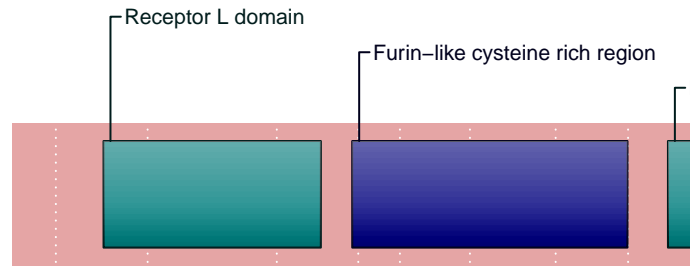
**SUPPORTING READ COUNT**

Split reads = 91  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



**RETAINED PROTEIN DOMAINS**  
reading frame unclear

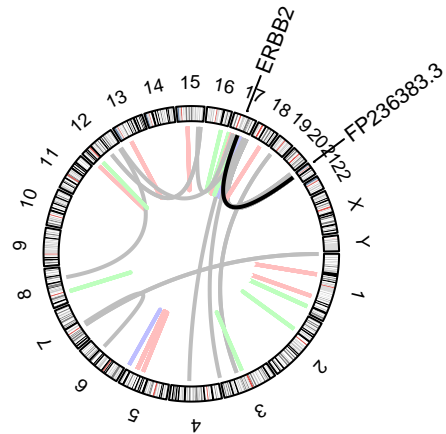
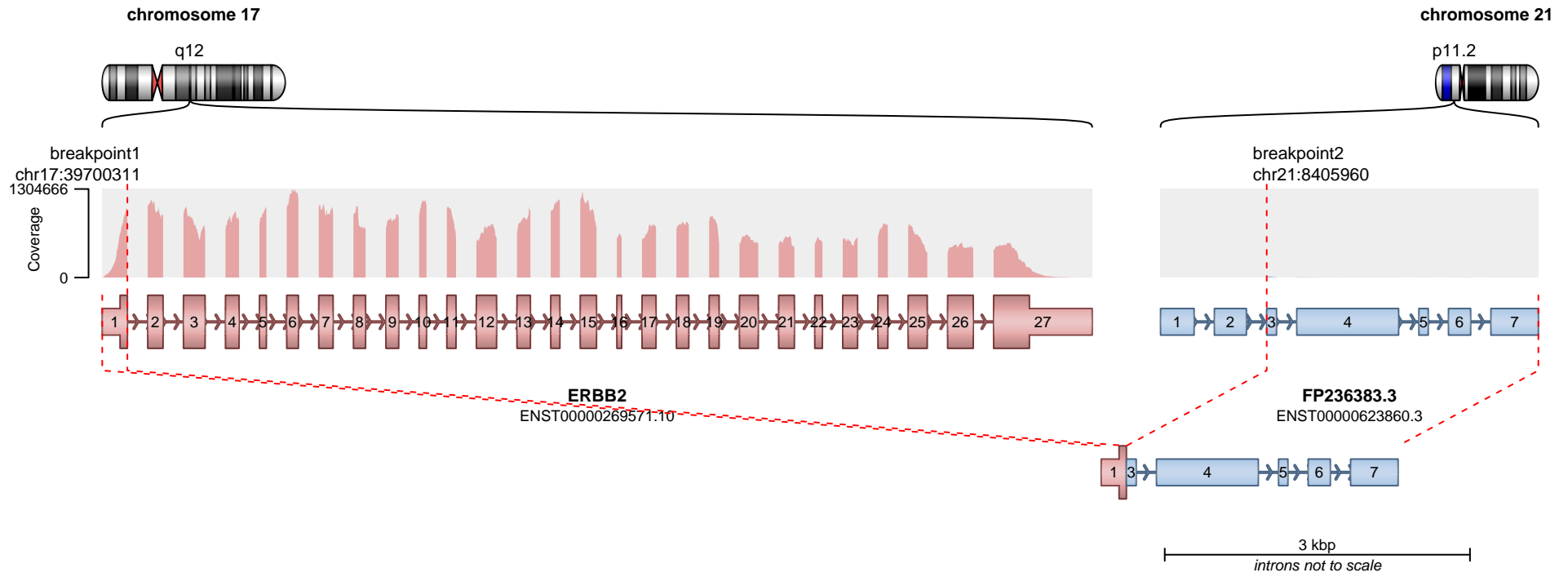


**ERBB2**

**SUPPORTING READ COUNT**

Split reads = 91  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



— translocation — deletion  
— duplication — inversion

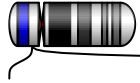
No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 15  
Discordant mates = 0

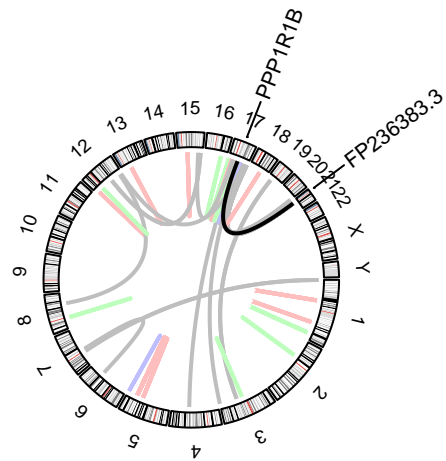
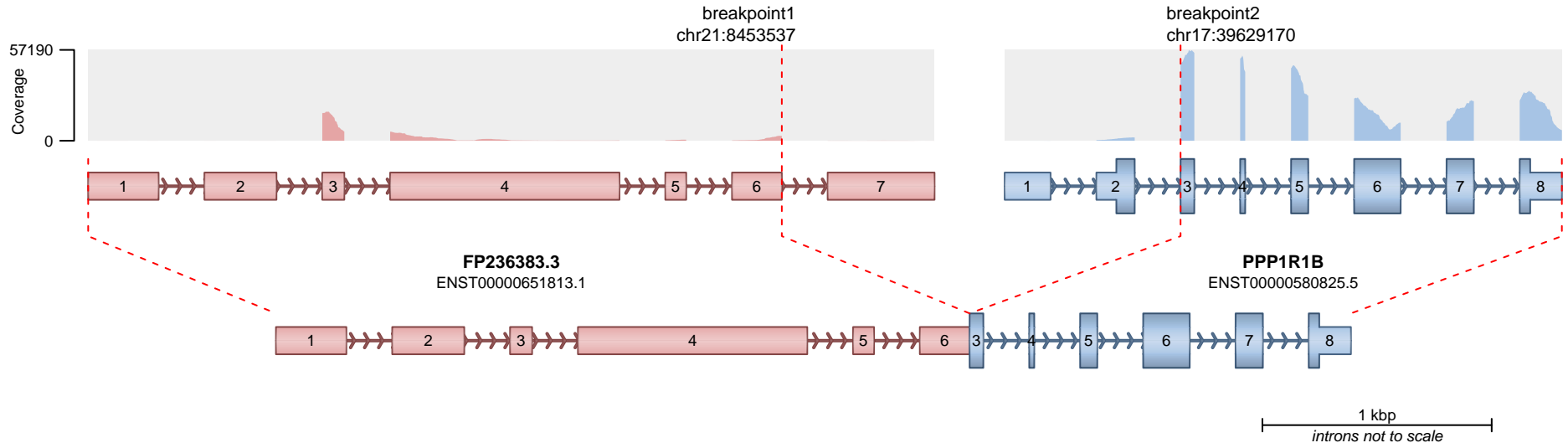
chromosome 21

p11.2



chromosome 17

q12



RETAINED PROTEIN DOMAINS  
reading frame unclear



**PPP1R1B**

Protein phosphatase inhibitor 1/DARPP-32

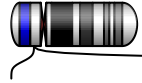
**SUPPORTING READ COUNT**

Split reads = 1835  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion

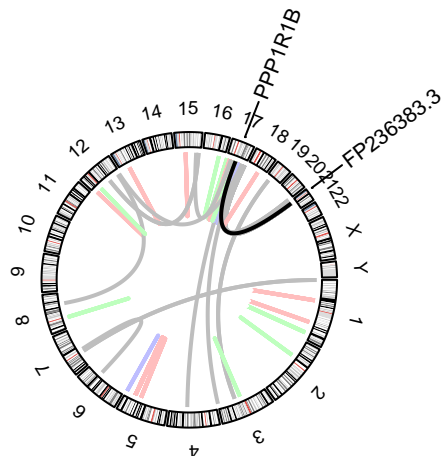
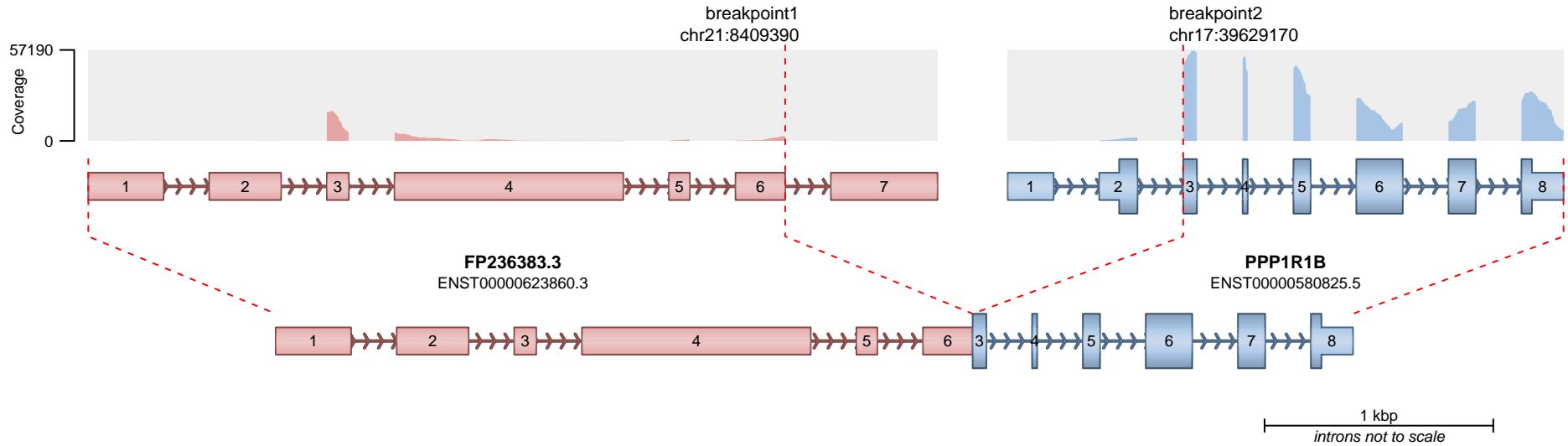
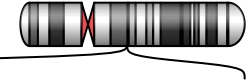
chromosome 21

p11.2

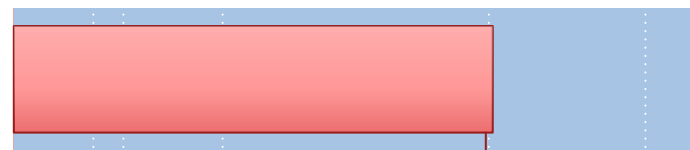


chromosome 17

q12



RETAINED PROTEIN DOMAINS  
reading frame unclear



**PPP1R1B**

Protein phosphatase inhibitor 1/DARPP-32

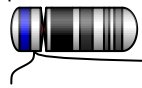
**SUPPORTING READ COUNT**

Split reads = 1827  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion

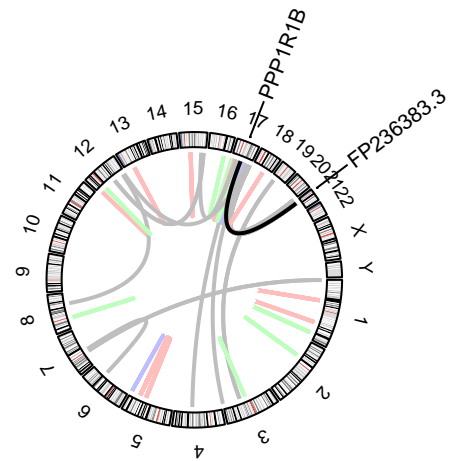
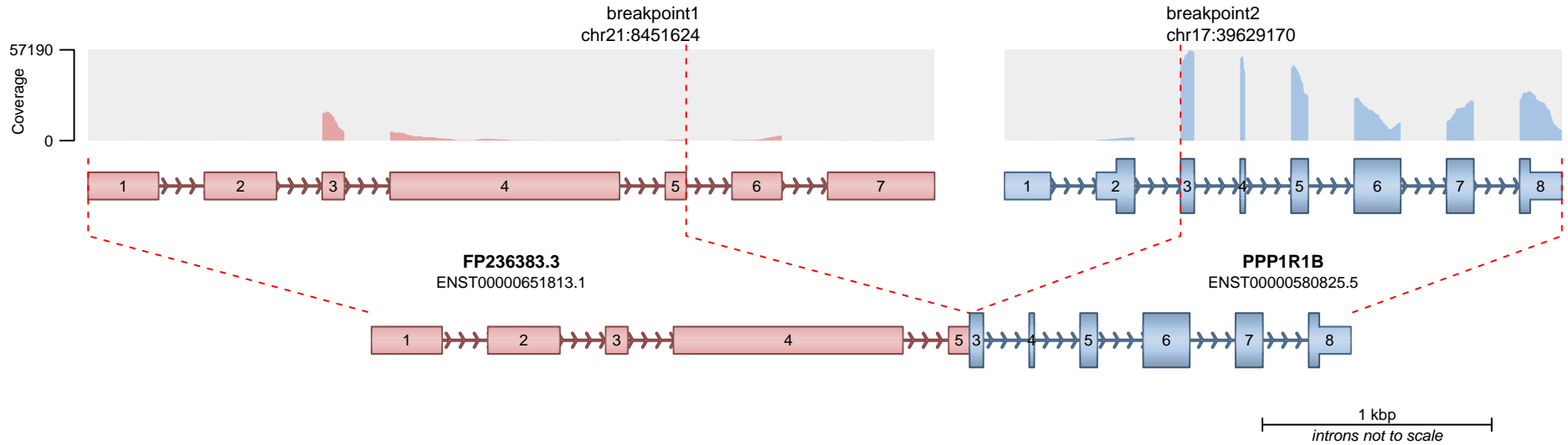
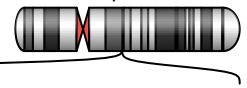
chromosome 21

p11.2



chromosome 17

q12



RETAINED PROTEIN DOMAINS  
reading frame unclear



PPP1R1B

Protein phosphatase inhibitor 1/DARPP-32

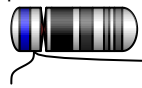
SUPPORTING READ COUNT

Split reads = 355  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion

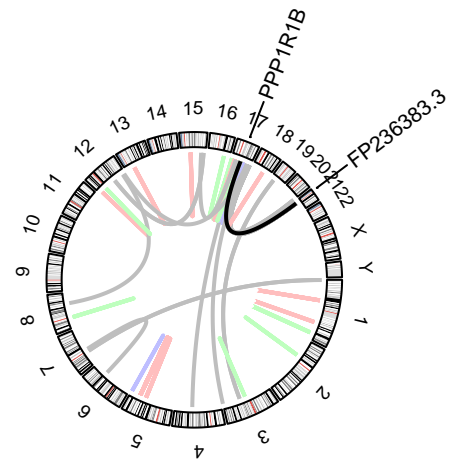
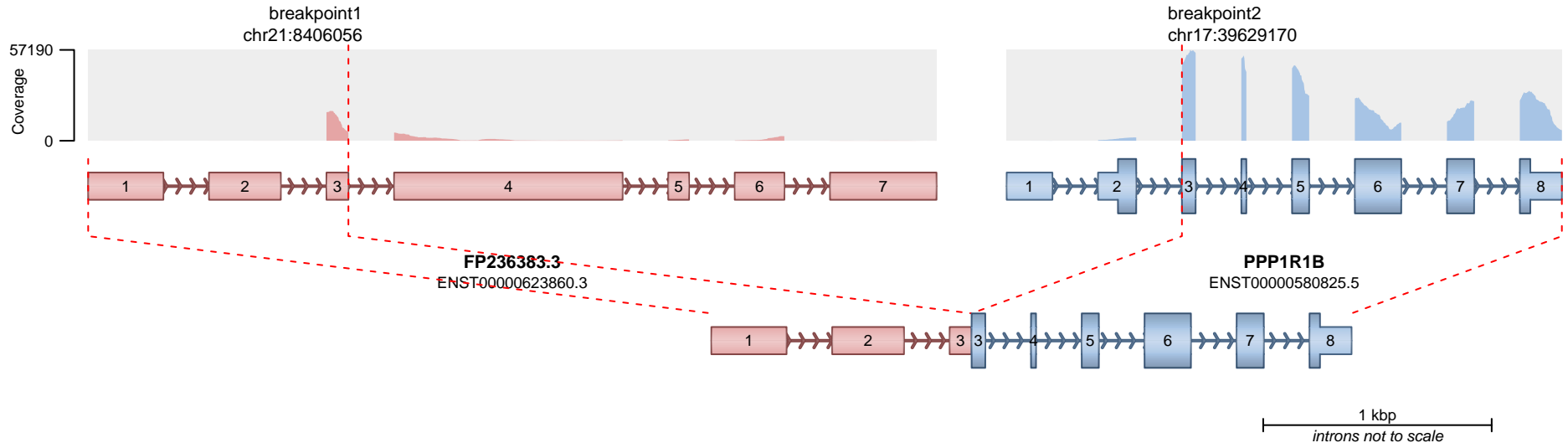
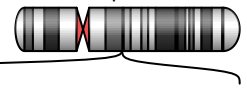
chromosome 21

p11.2

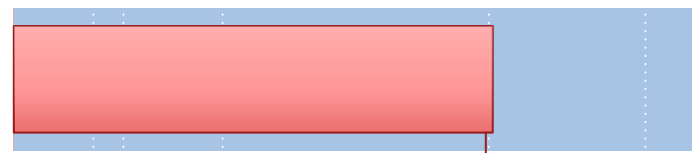


chromosome 17

q12



RETAINED PROTEIN DOMAINS  
reading frame unclear



**PPP1R1B**

Protein phosphatase inhibitor 1/DARPP-32

**SUPPORTING READ COUNT**

Split reads = 27  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion

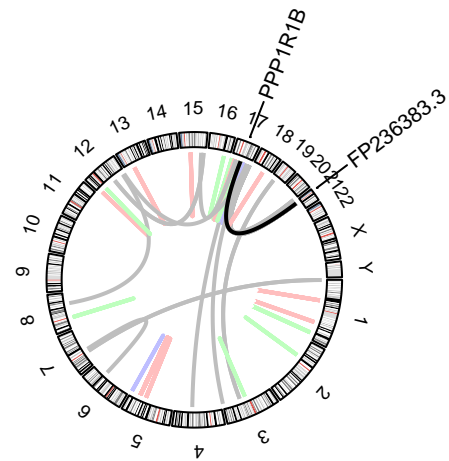
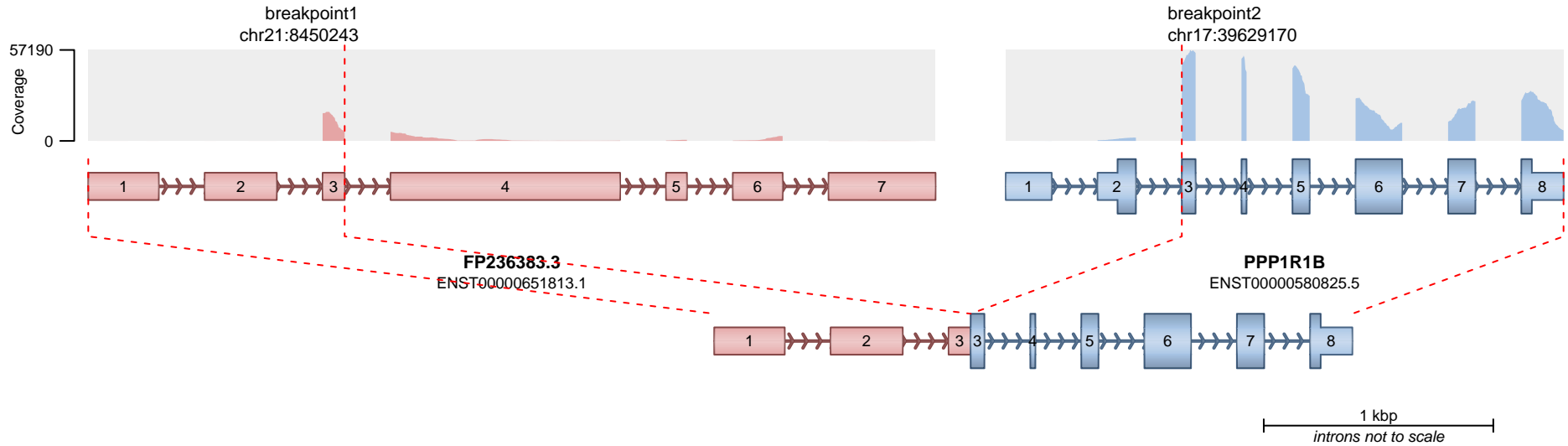
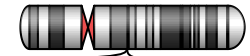
chromosome 21

p11.2

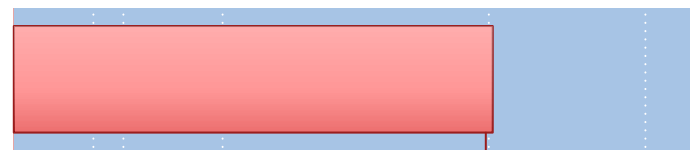


chromosome 17

q12



RETAINED PROTEIN DOMAINS  
reading frame unclear



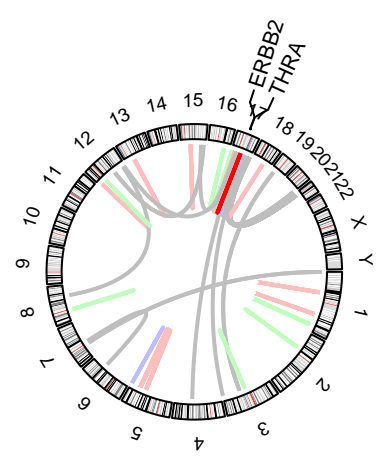
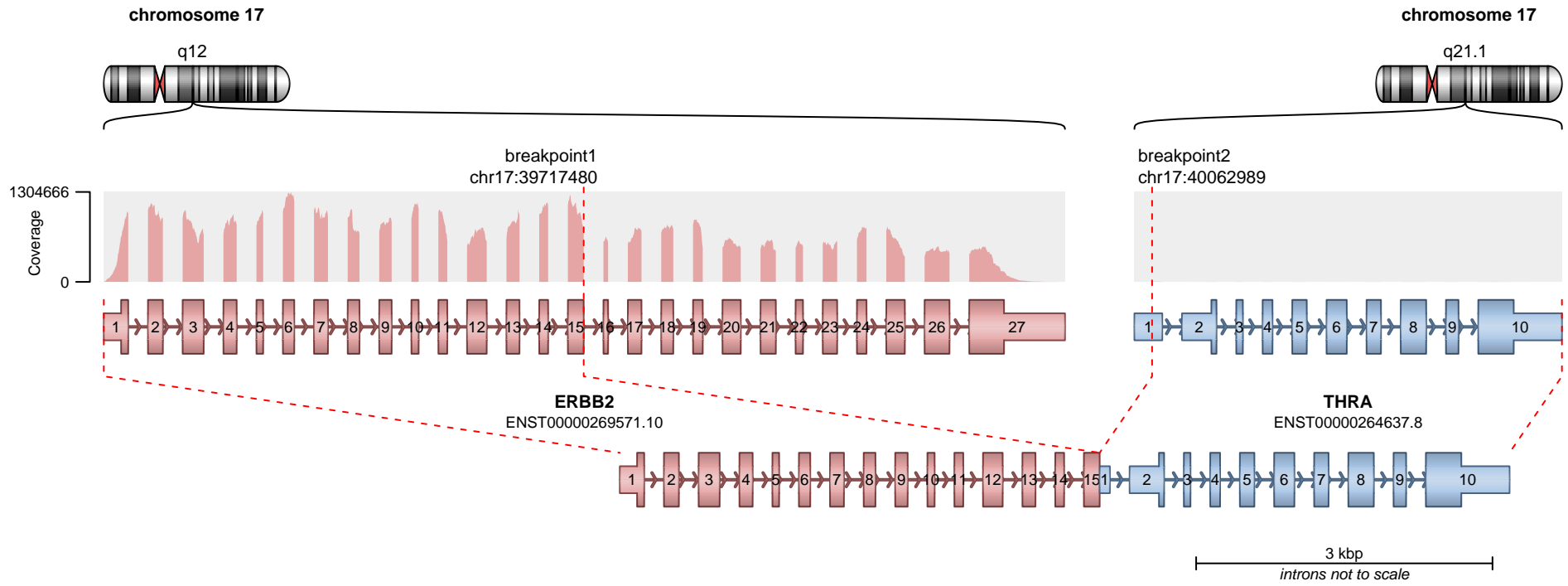
PPP1R1B

Protein phosphatase inhibitor 1/DARPP-32

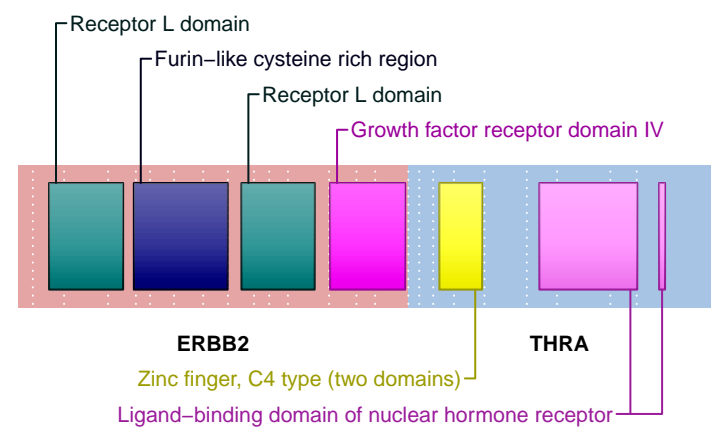
SUPPORTING READ COUNT

Split reads = 27  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



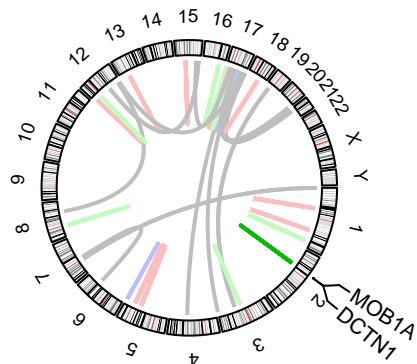
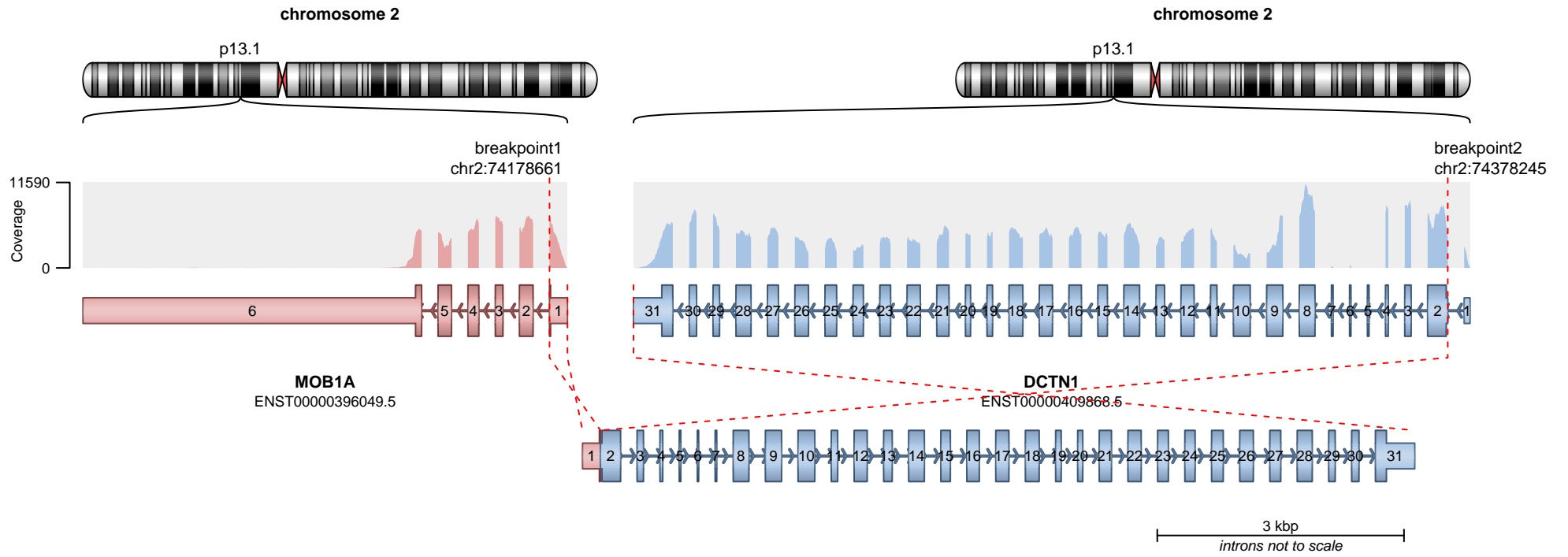
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



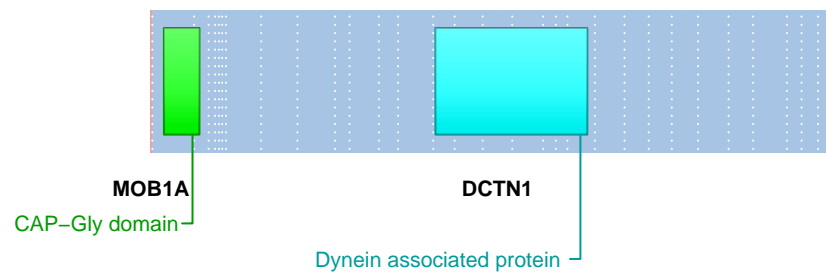
**SUPPORTING READ COUNT**

Split reads = 1066  
Discordant mates = 2

- translocation
- duplication
- deletion
- inversion



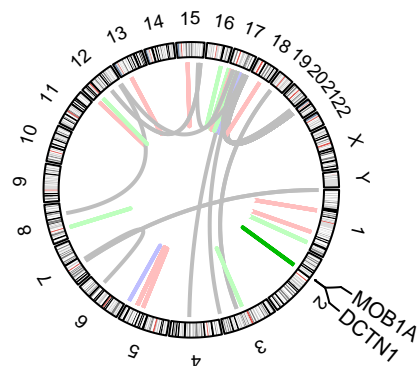
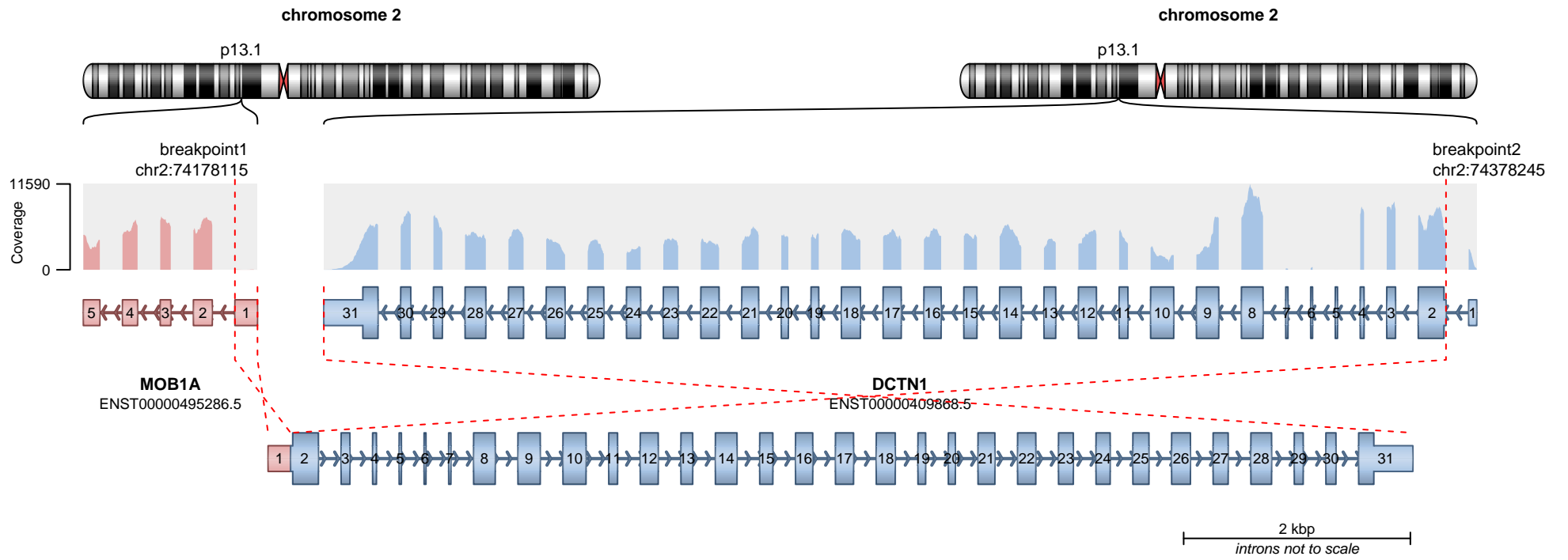
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



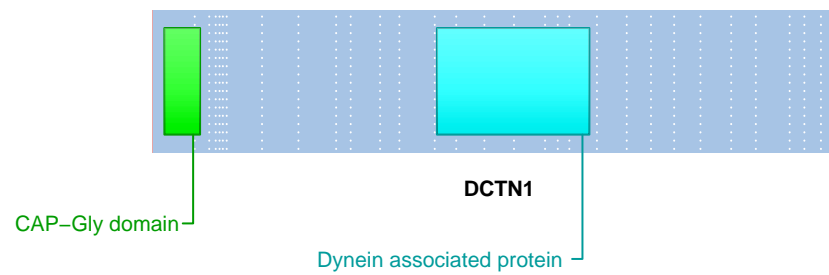
**SUPPORTING READ COUNT**

Split reads = 499  
Discordant mates = 15

- translocation
- duplication
- deletion
- inversion



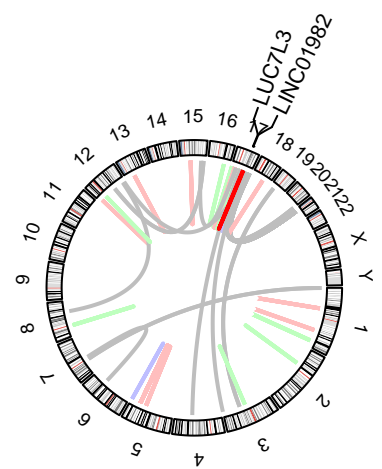
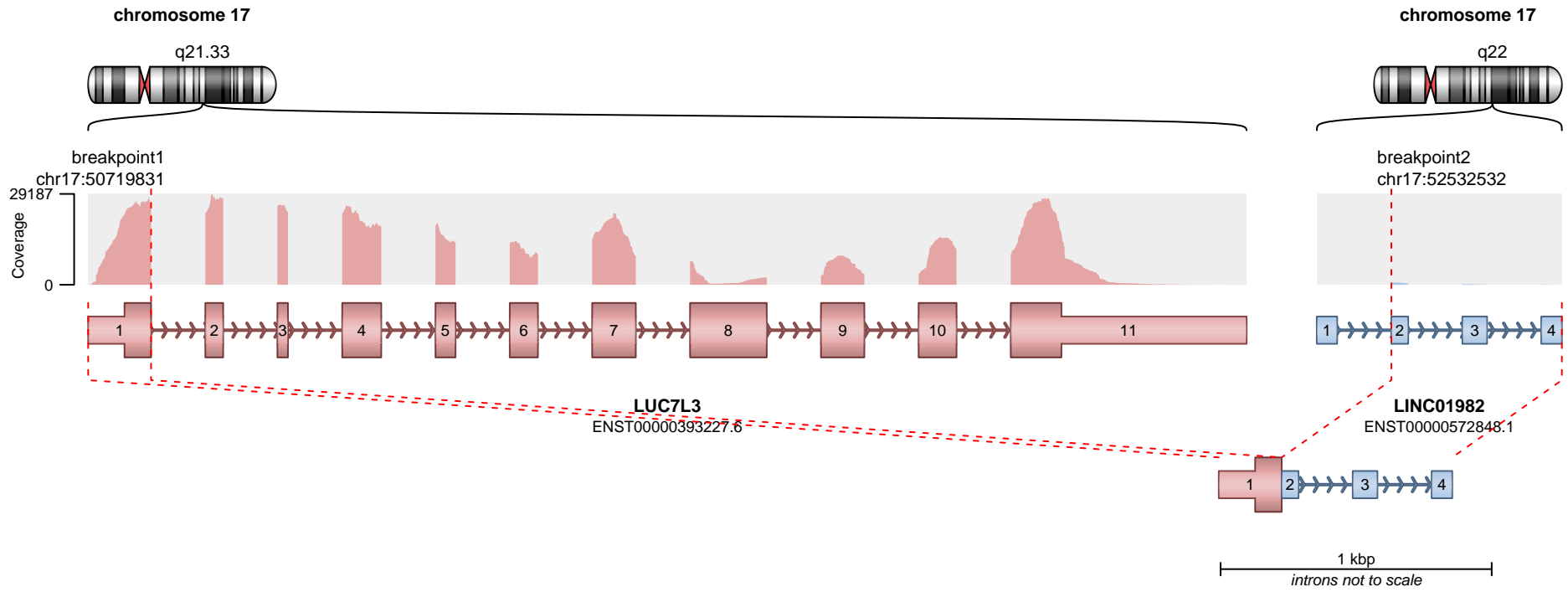
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



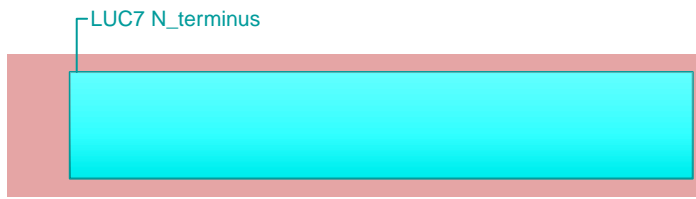
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 15

- translocation
- duplication
- deletion
- inversion



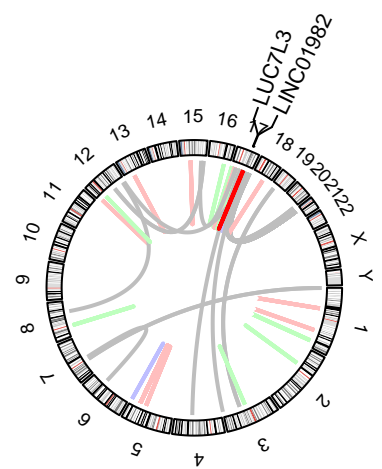
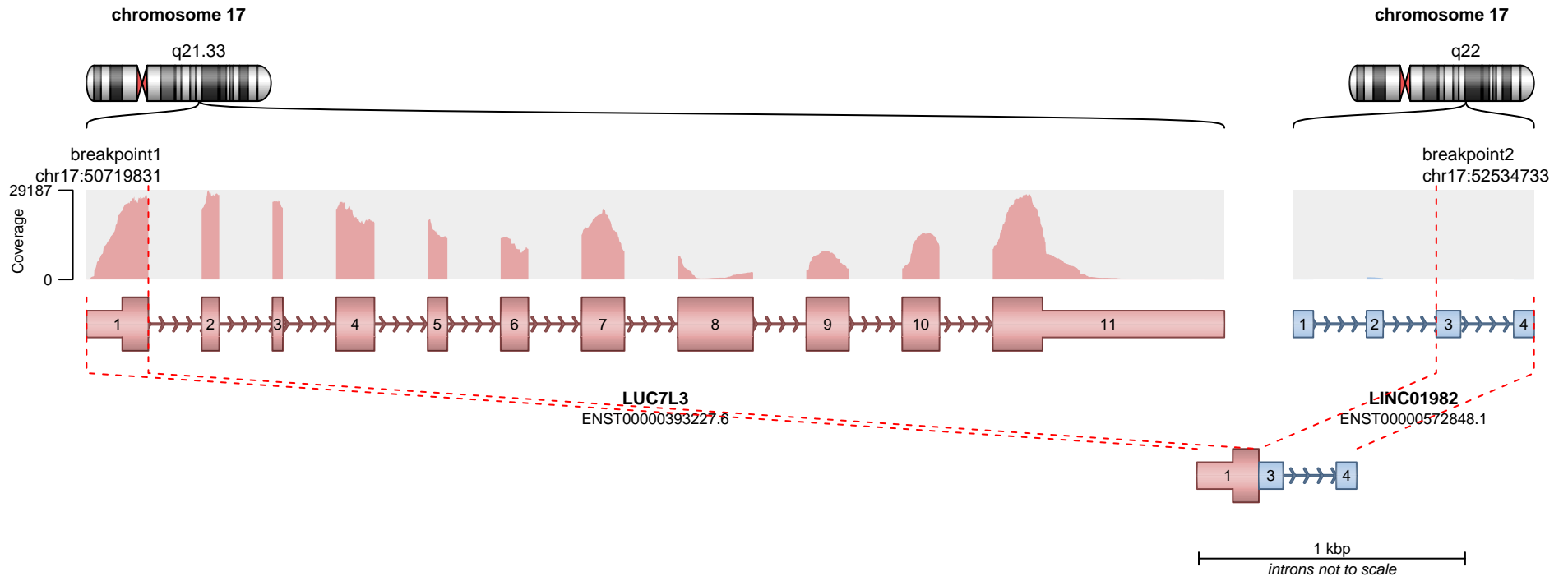
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



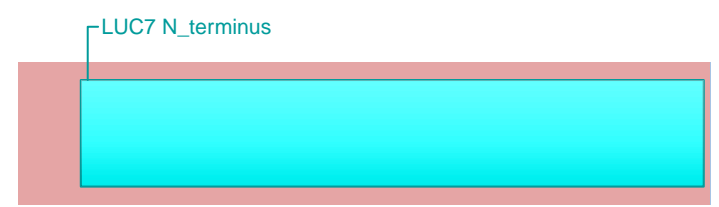
**SUPPORTING READ COUNT**

Split reads = 446  
Discordant mates = 14

- translocation
- duplication
- deletion
- inversion



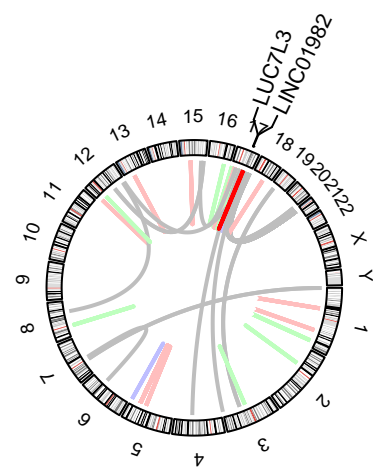
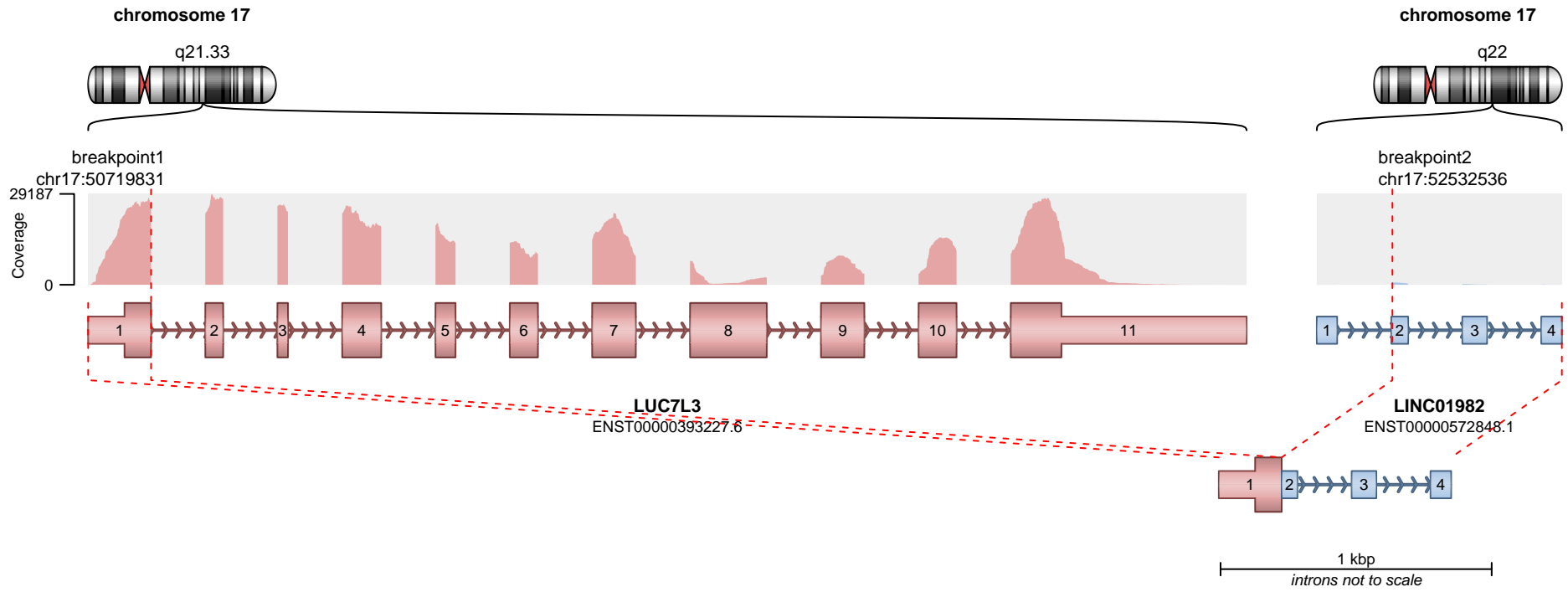
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



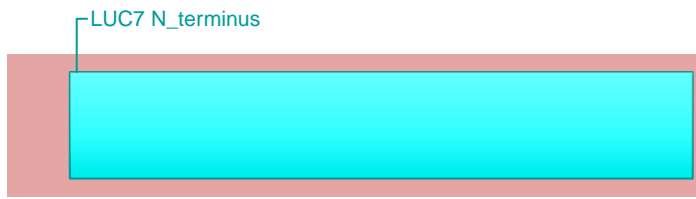
**SUPPORTING READ COUNT**

Split reads = 12  
Discordant mates = 4

- translocation
- duplication
- deletion
- inversion



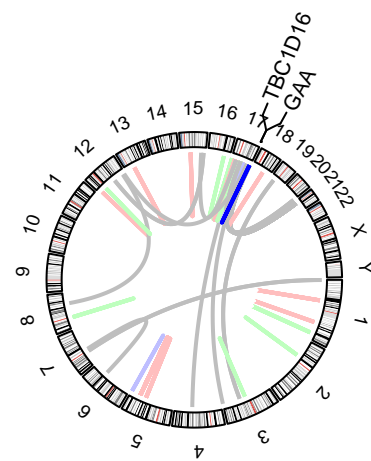
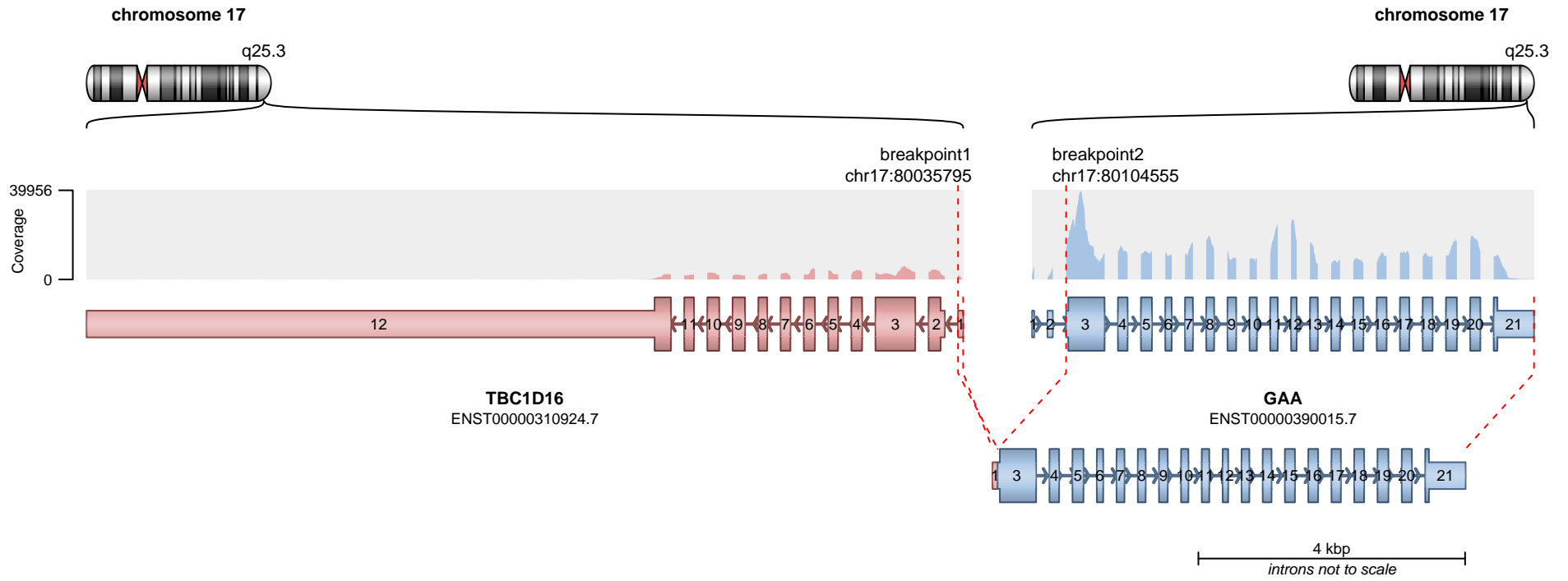
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



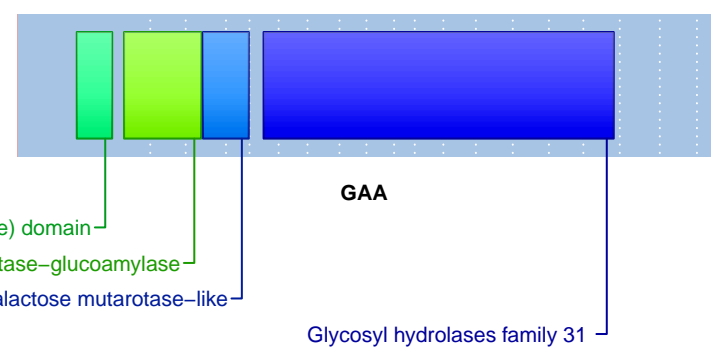
**SUPPORTING READ COUNT**

Split reads = 7  
Discordant mates = 14

- translocation
- duplication
- deletion
- inversion



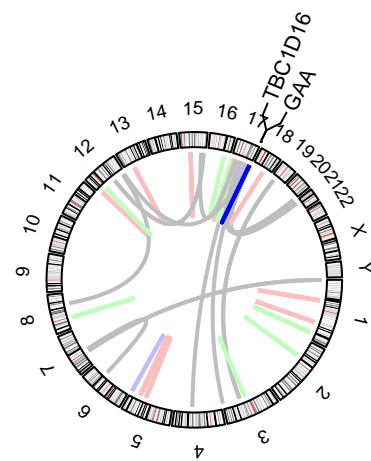
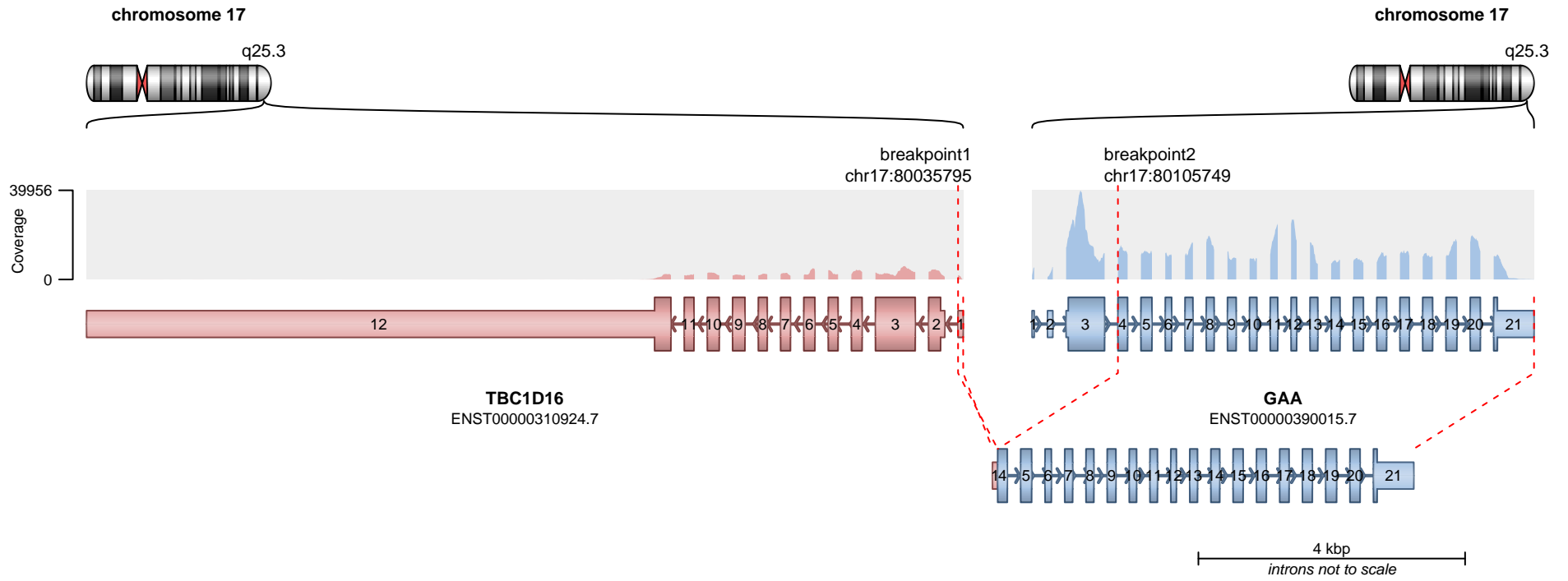
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

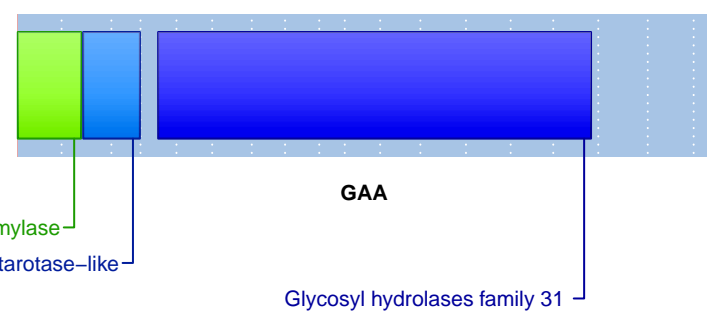
Split reads = 448  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



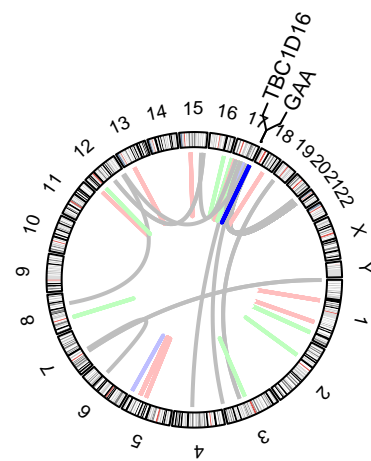
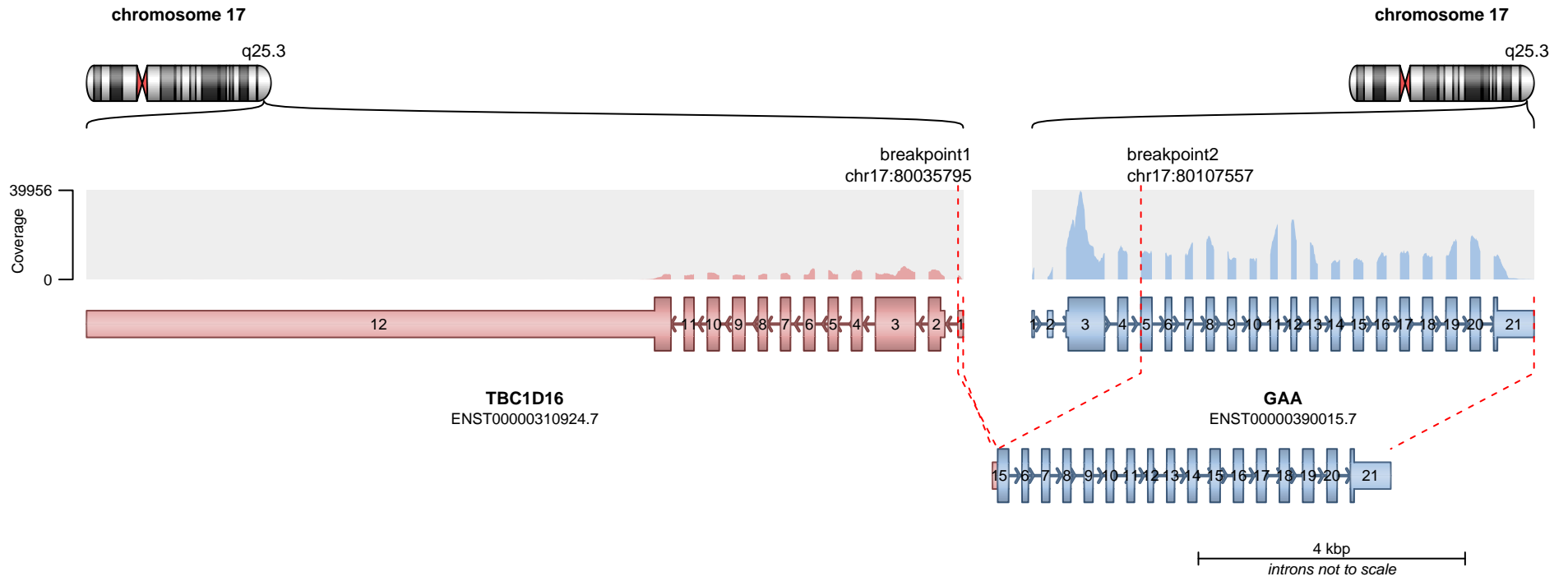
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

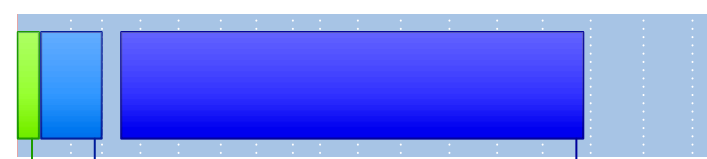
Split reads = 18  
Discordant mates = 0



N-terminal barrel of NtMGAM and CtMGAM, maltase-glucoamylase

Galactose mutarotase-like

RETAINED PROTEIN DOMAINS  
reading frame unclear

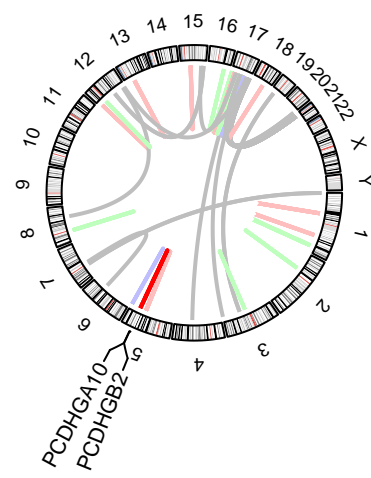
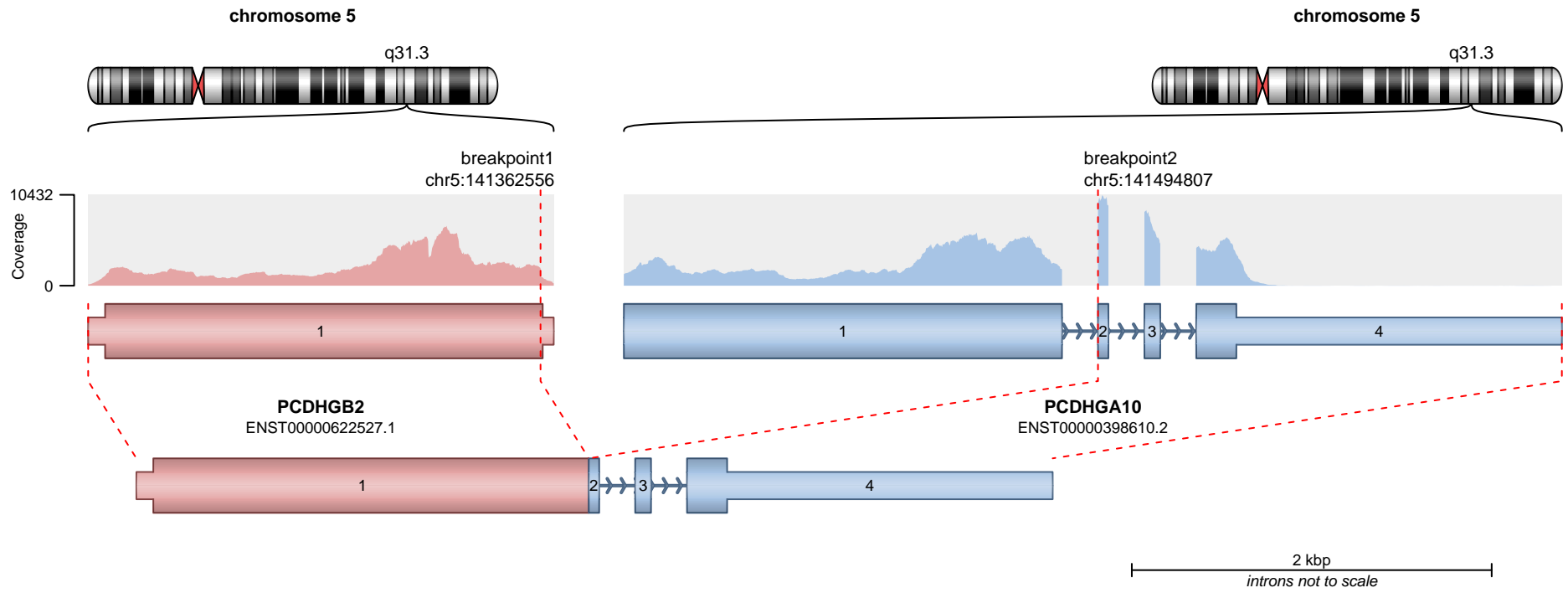


Glycosyl hydrolases family 31

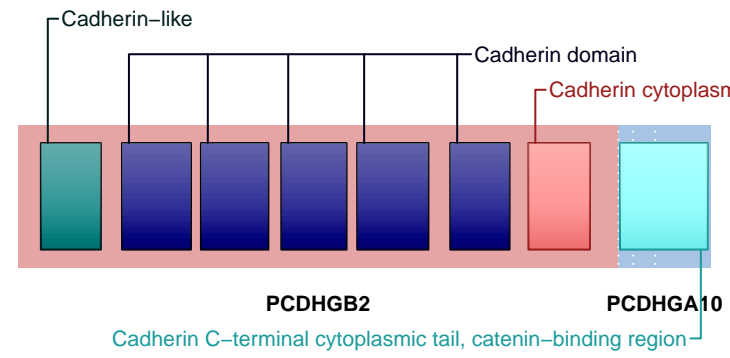
SUPPORTING READ COUNT

Split reads = 3  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



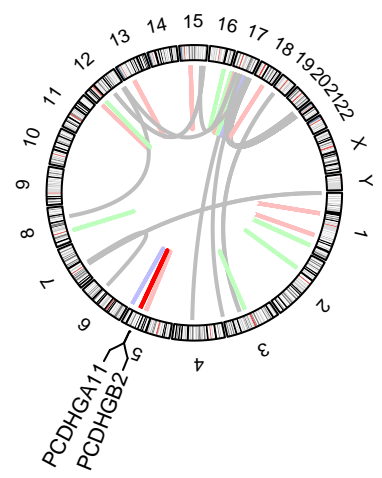
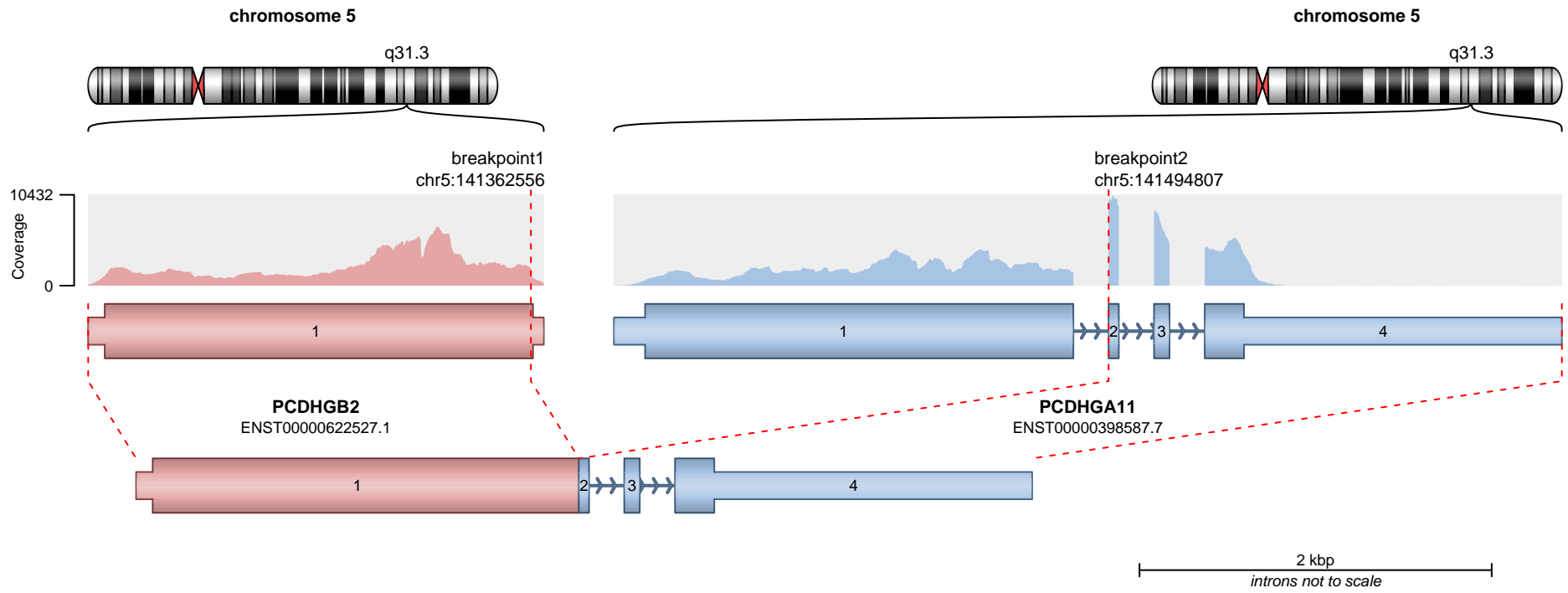
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



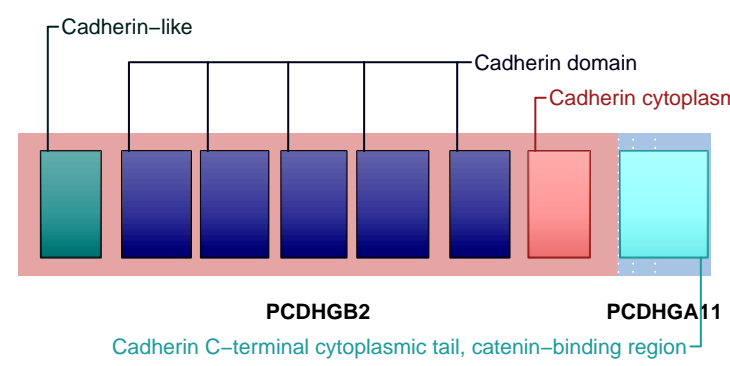
**SUPPORTING READ COUNT**

Split reads = 250  
Discordant mates = 2

- translocation
- duplication
- deletion
- inversion



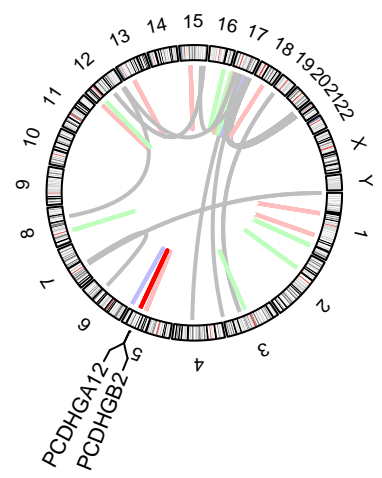
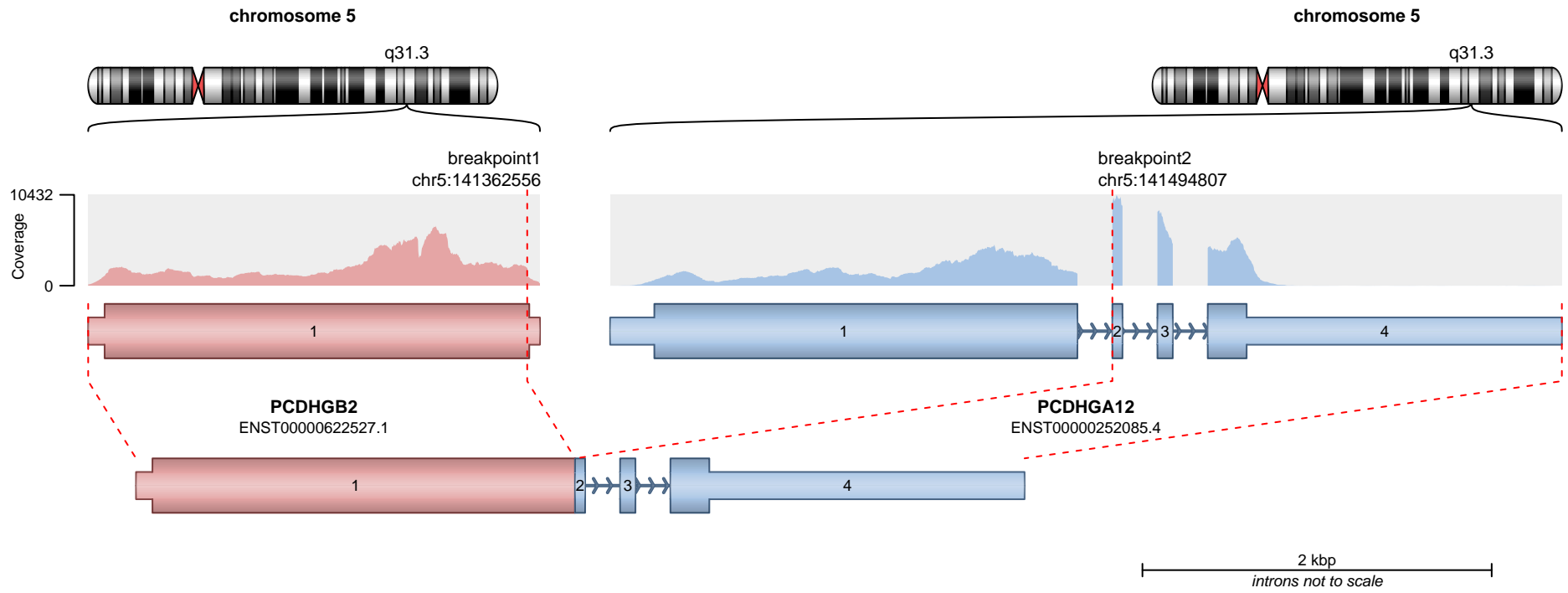
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

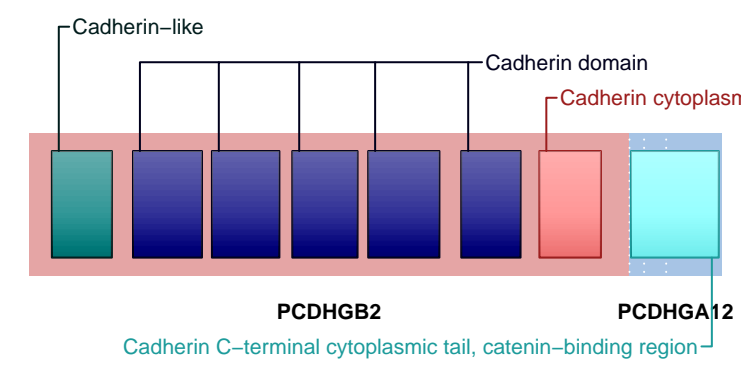
Split reads = 250  
Discordant mates = 2

- translocation
- duplication
- deletion
- inversion



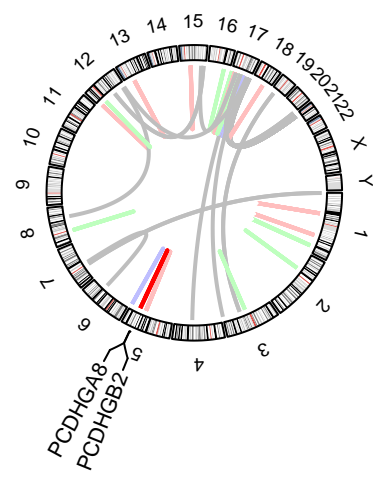
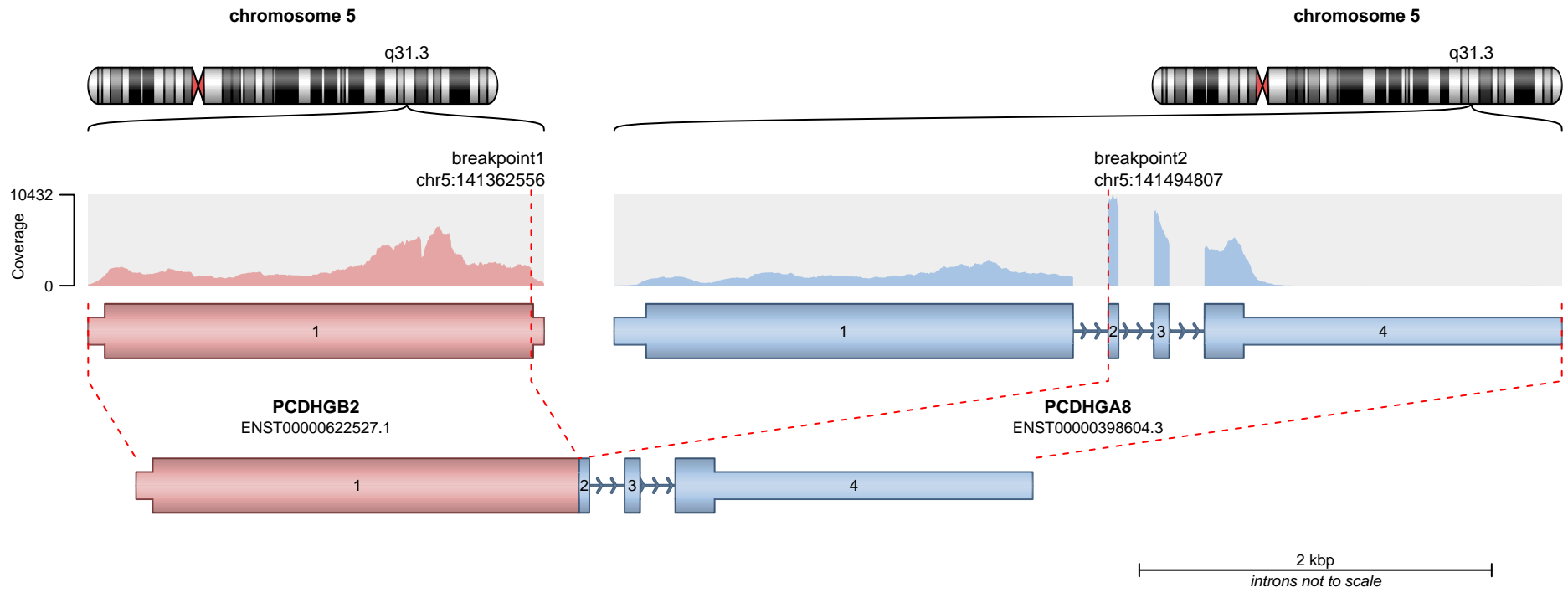
— translocation    — deletion  
 — duplication    — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



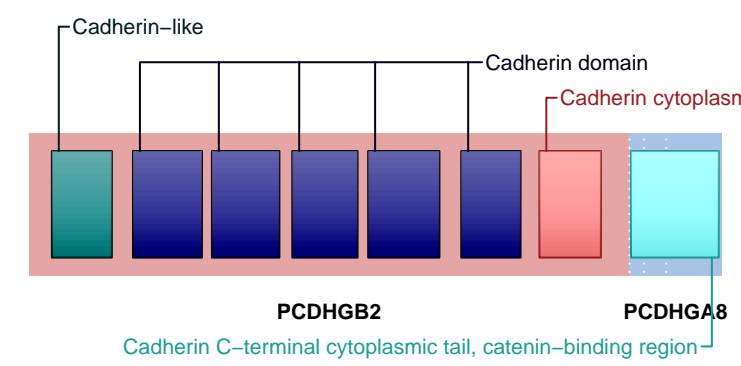
**SUPPORTING READ COUNT**

Split reads = 250  
 Discordant mates = 2



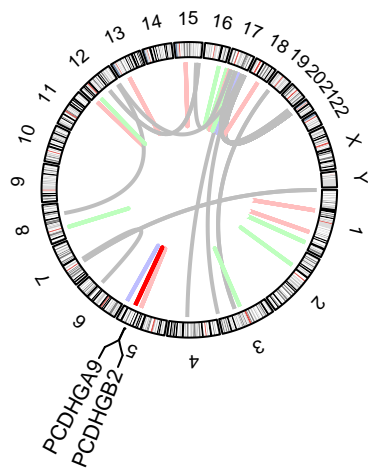
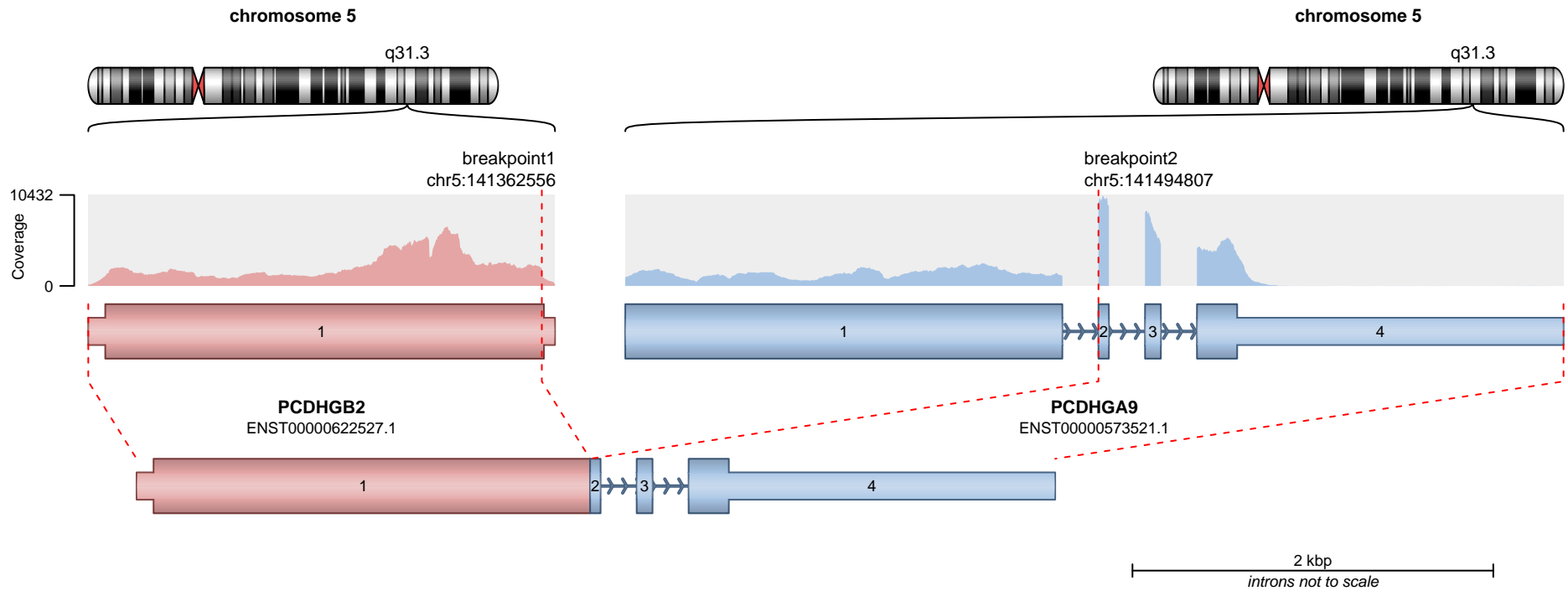
— translocation    — deletion  
 — duplication    — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



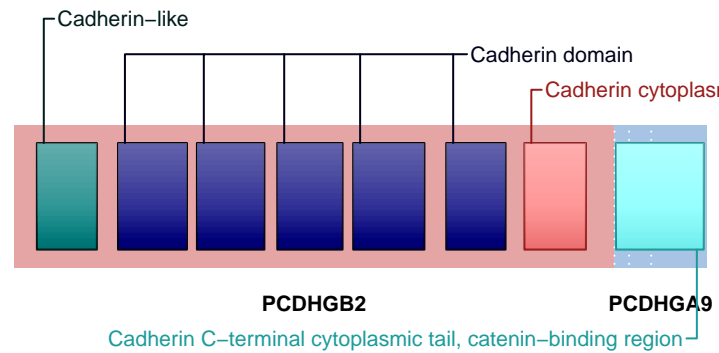
**SUPPORTING READ COUNT**

Split reads = 250  
 Discordant mates = 2



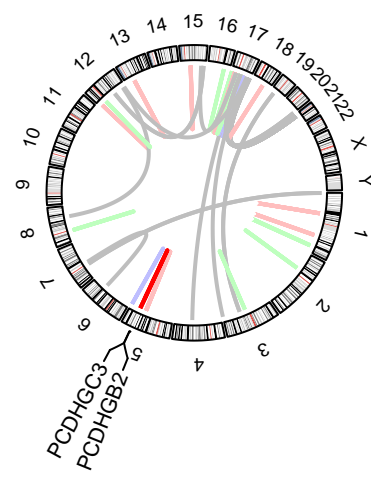
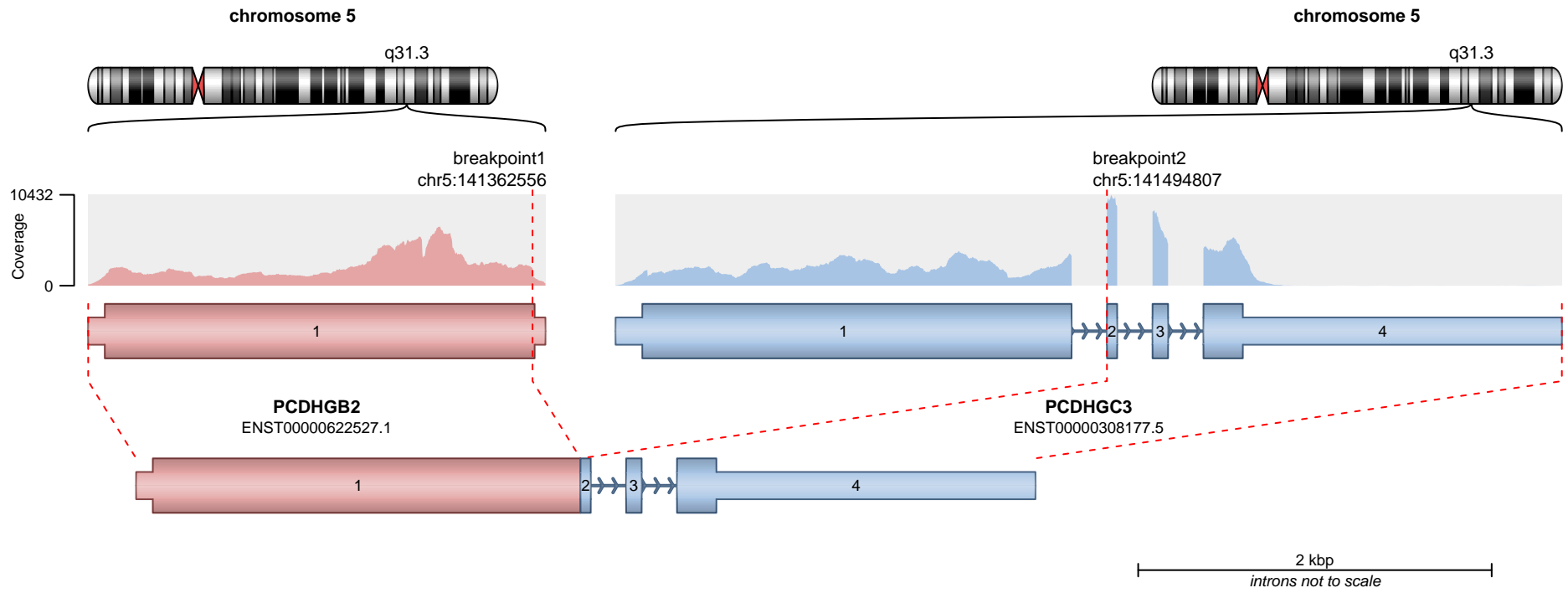
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



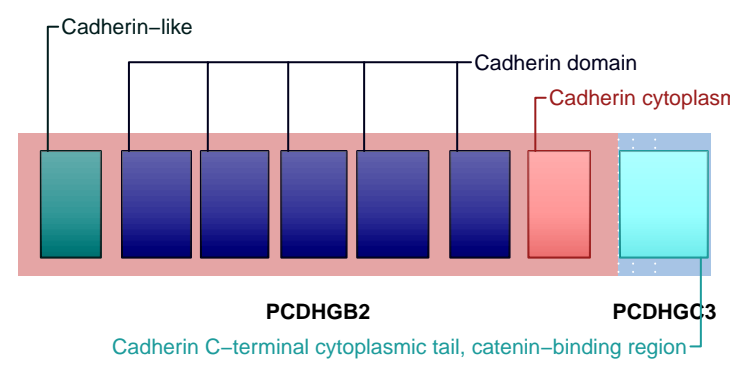
**SUPPORTING READ COUNT**

Split reads = 250  
Discordant mates = 2



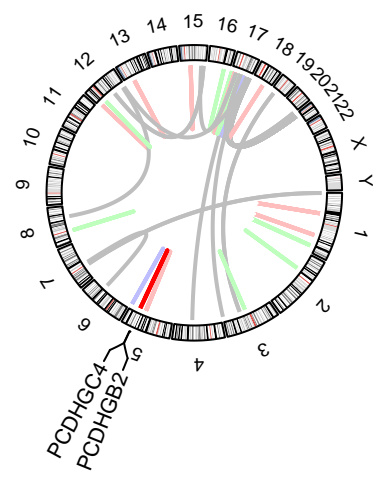
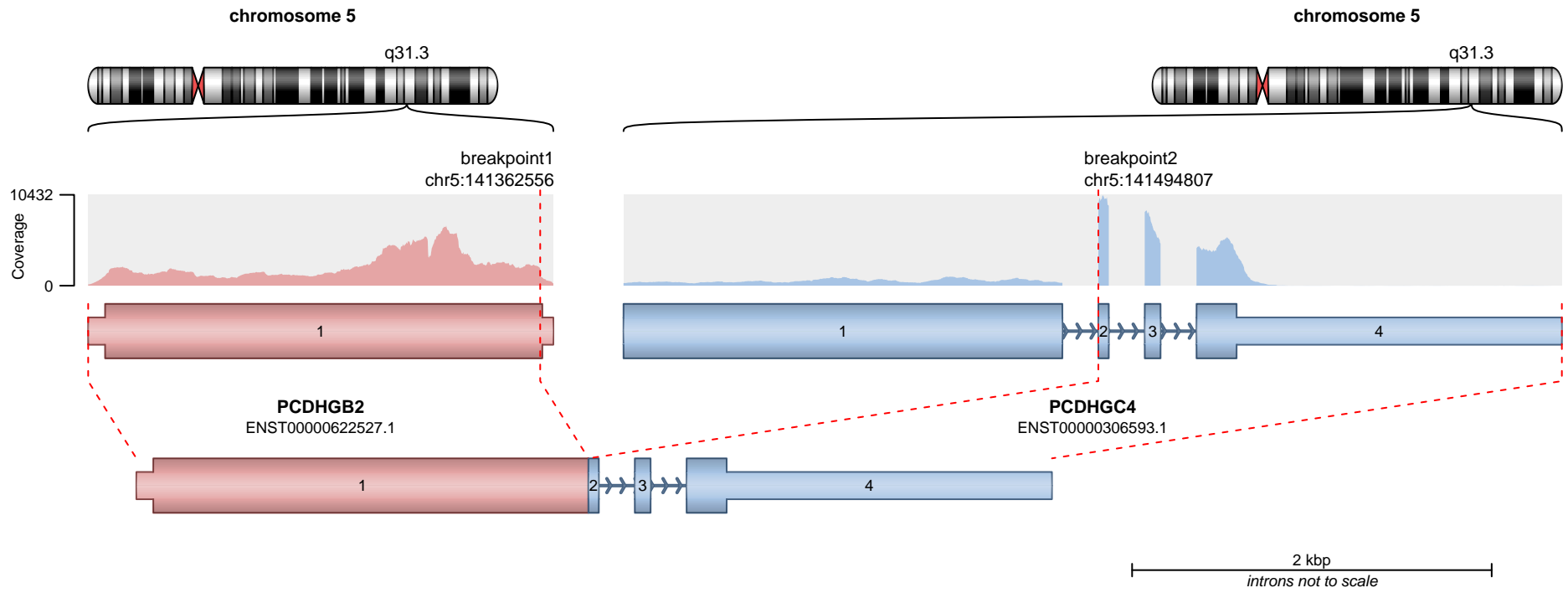
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



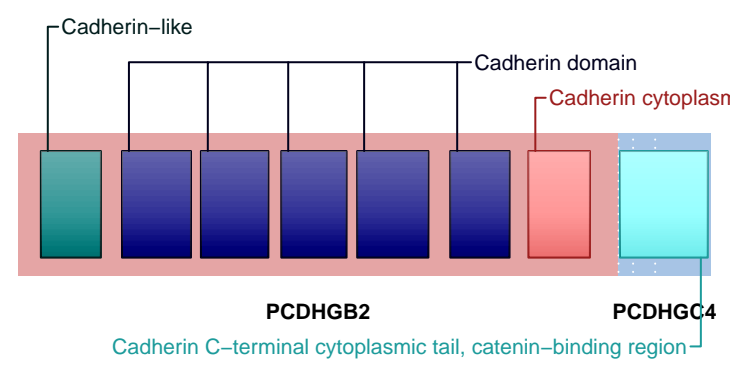
**SUPPORTING READ COUNT**

Split reads = 250  
Discordant mates = 2



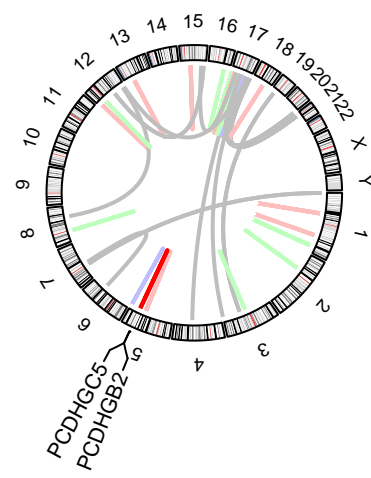
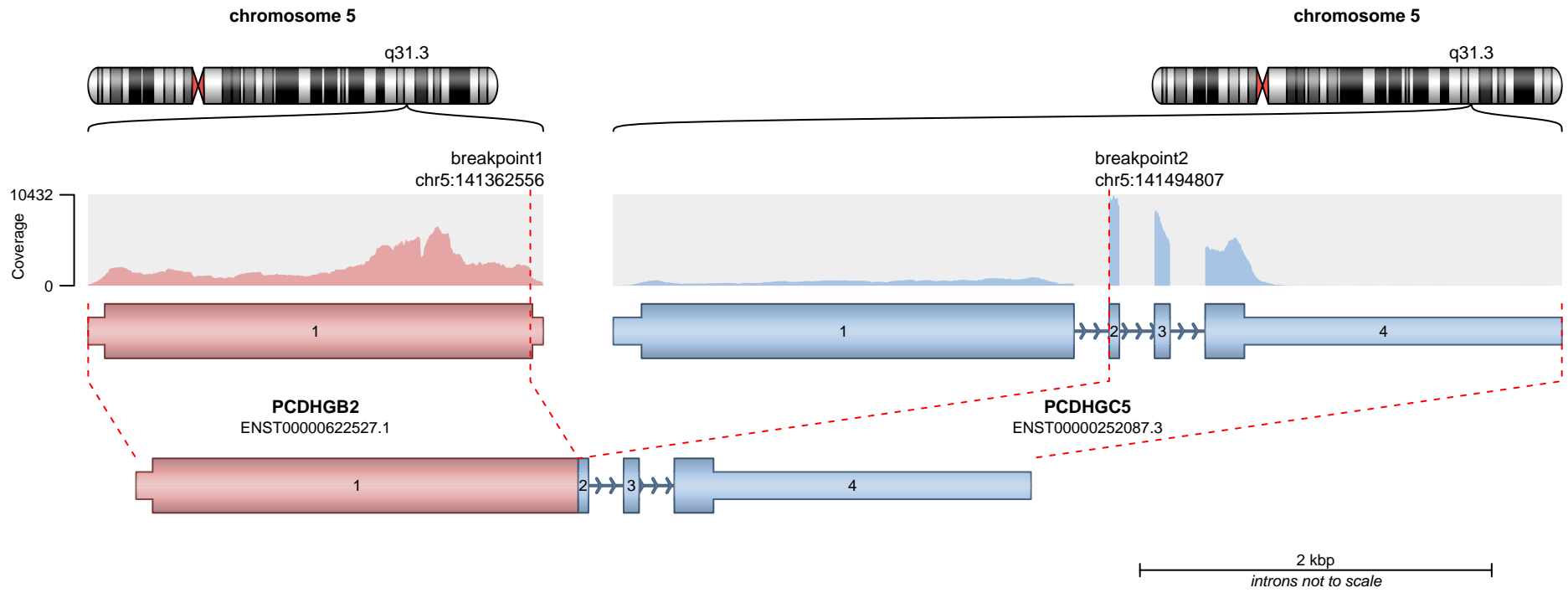
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



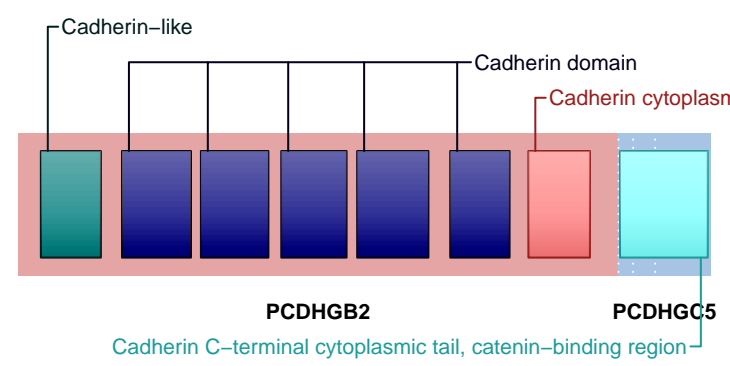
**SUPPORTING READ COUNT**

Split reads = 250  
Discordant mates = 2



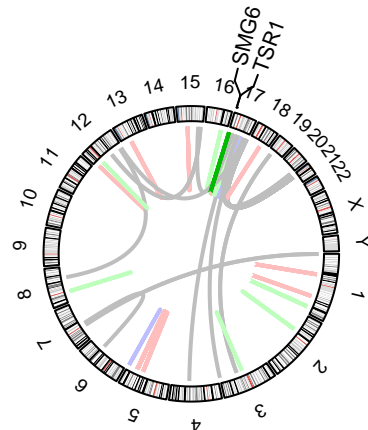
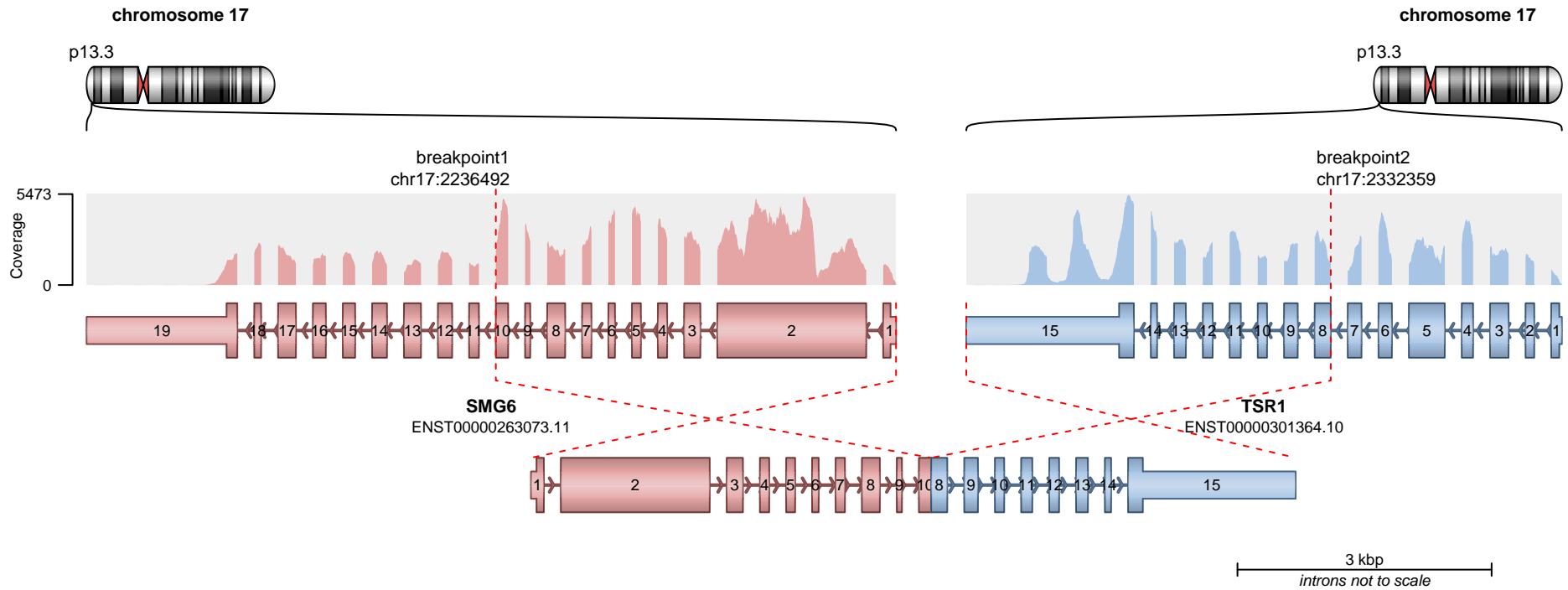
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear

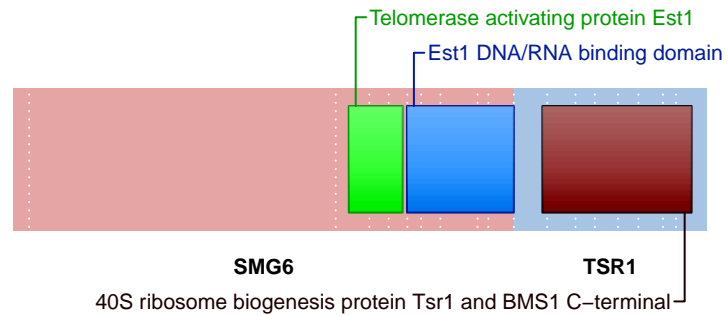


**SUPPORTING READ COUNT**

Split reads = 250  
Discordant mates = 2



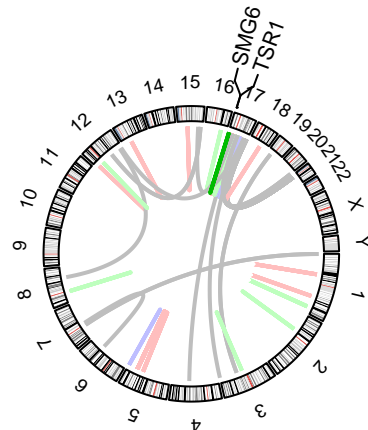
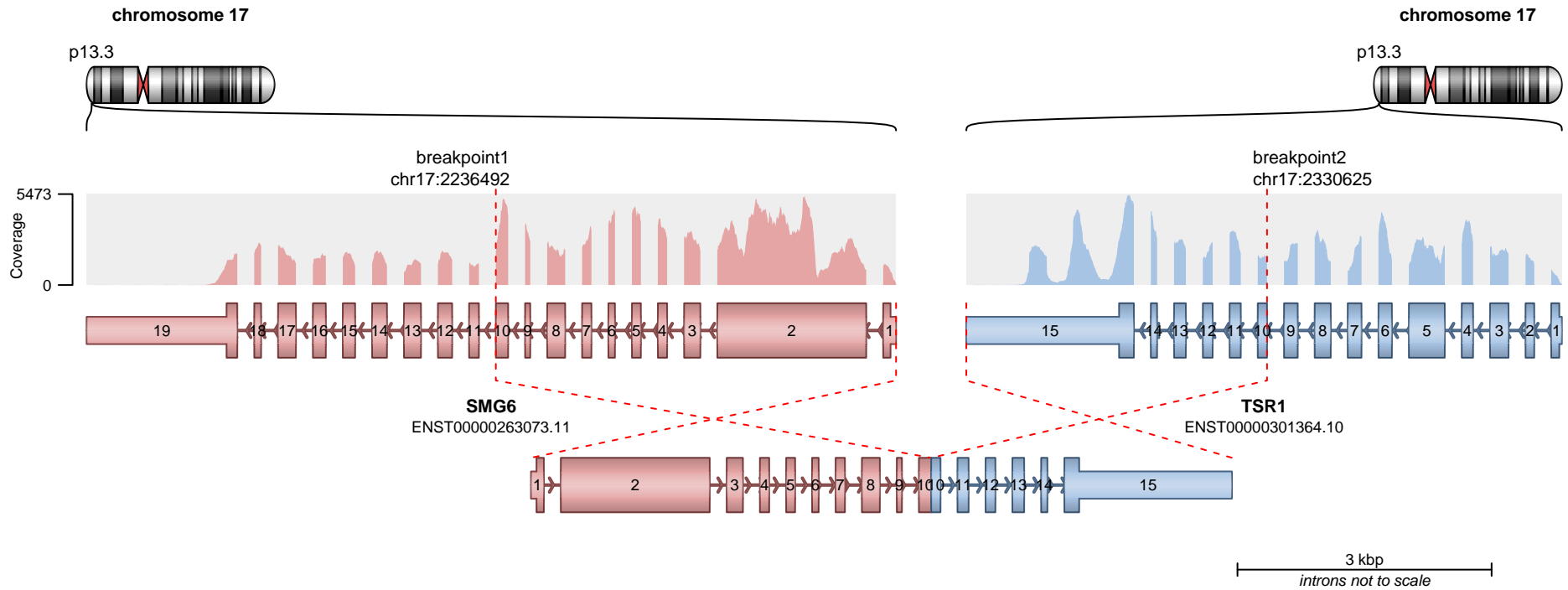
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



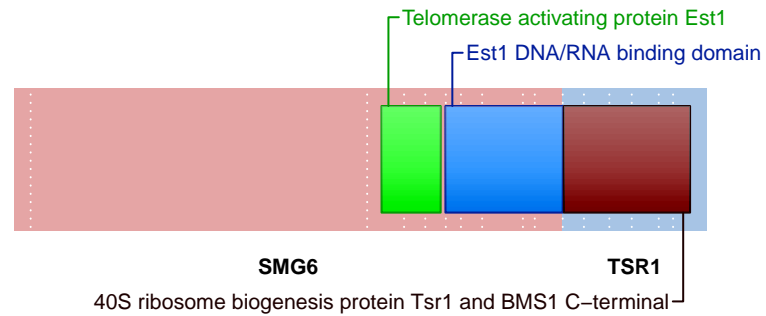
**SUPPORTING READ COUNT**

Split reads = 179  
Discordant mates = 5

— translocation — deletion  
— duplication — inversion



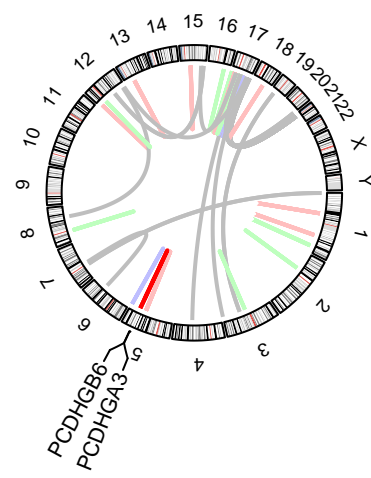
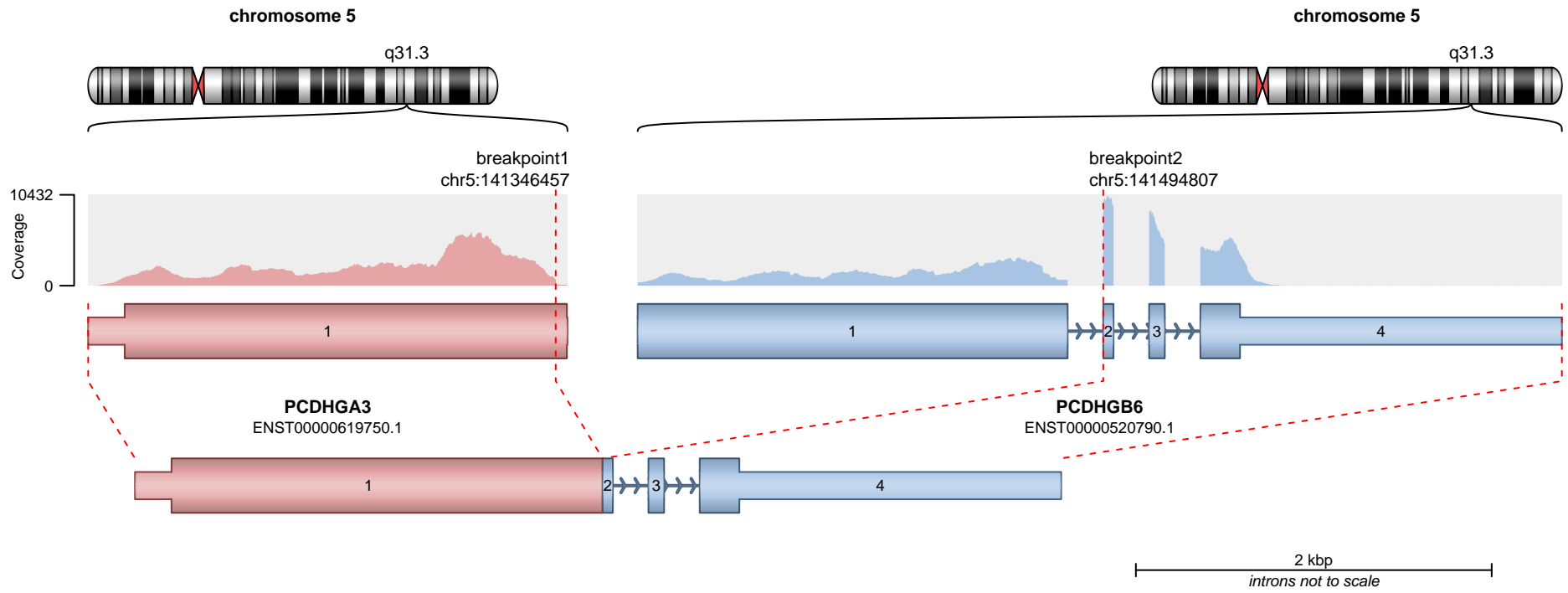
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

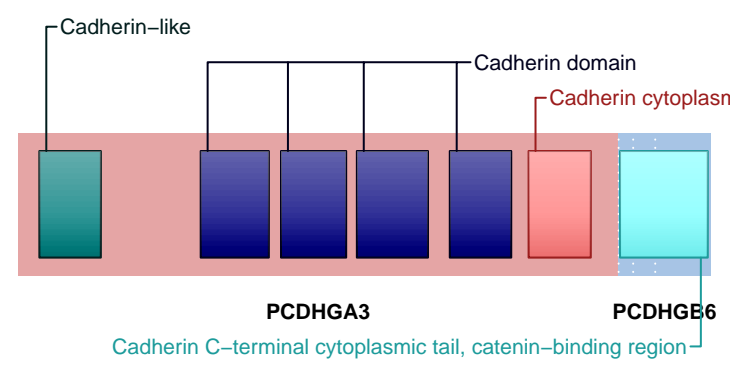
Split reads = 1  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



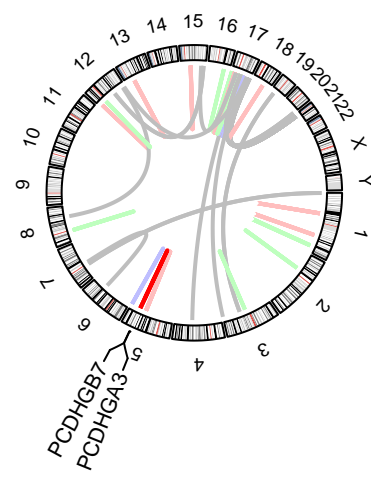
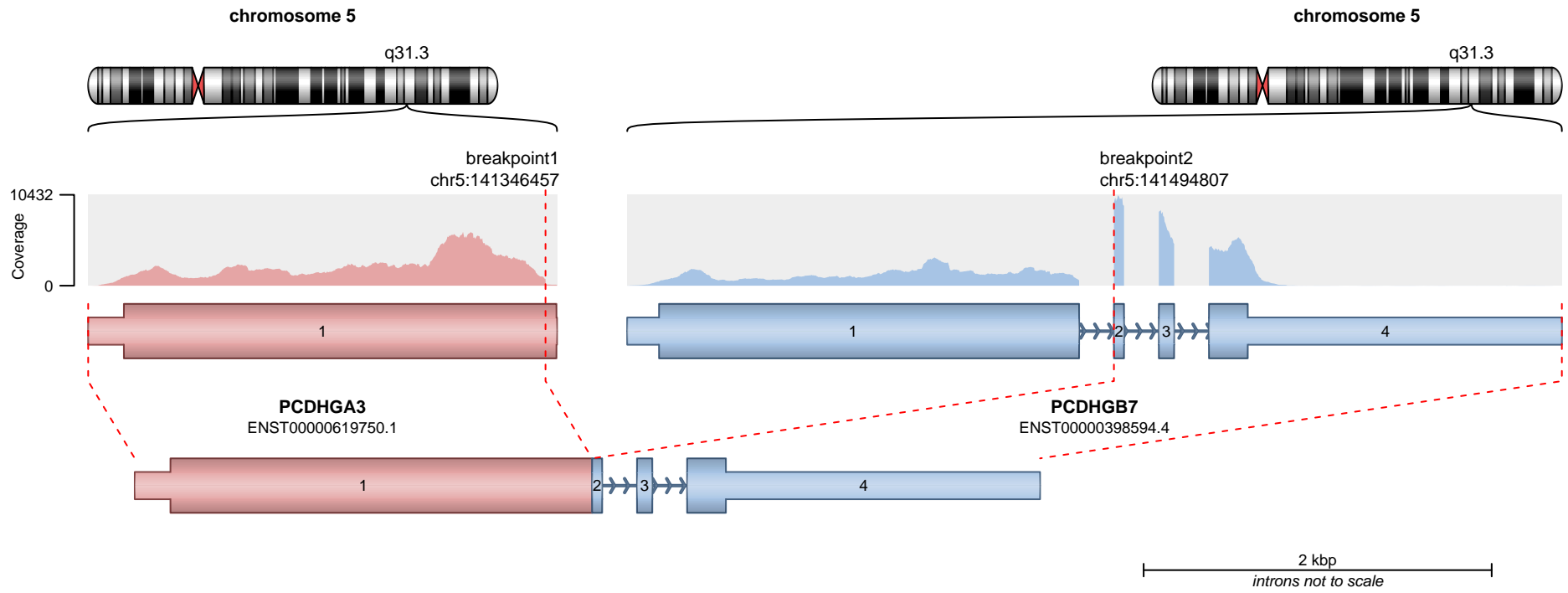
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



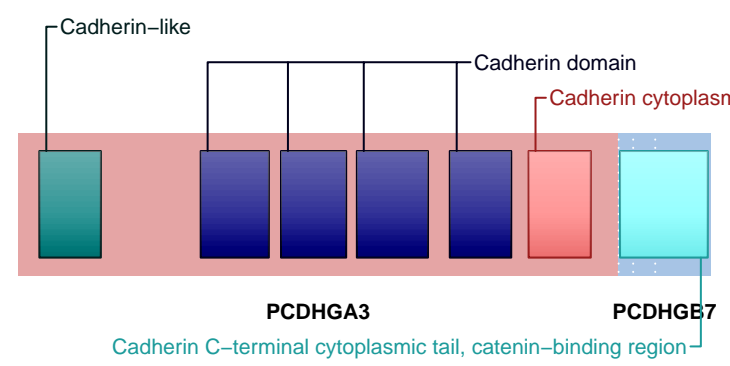
**SUPPORTING READ COUNT**

Split reads = 173  
Discordant mates = 4



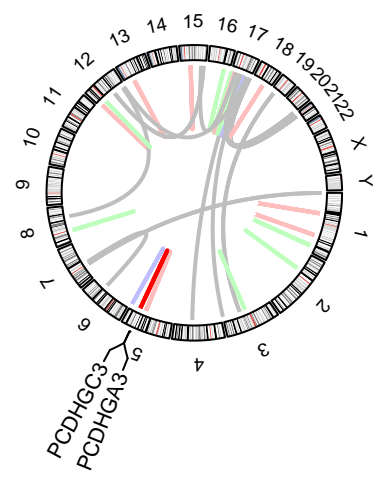
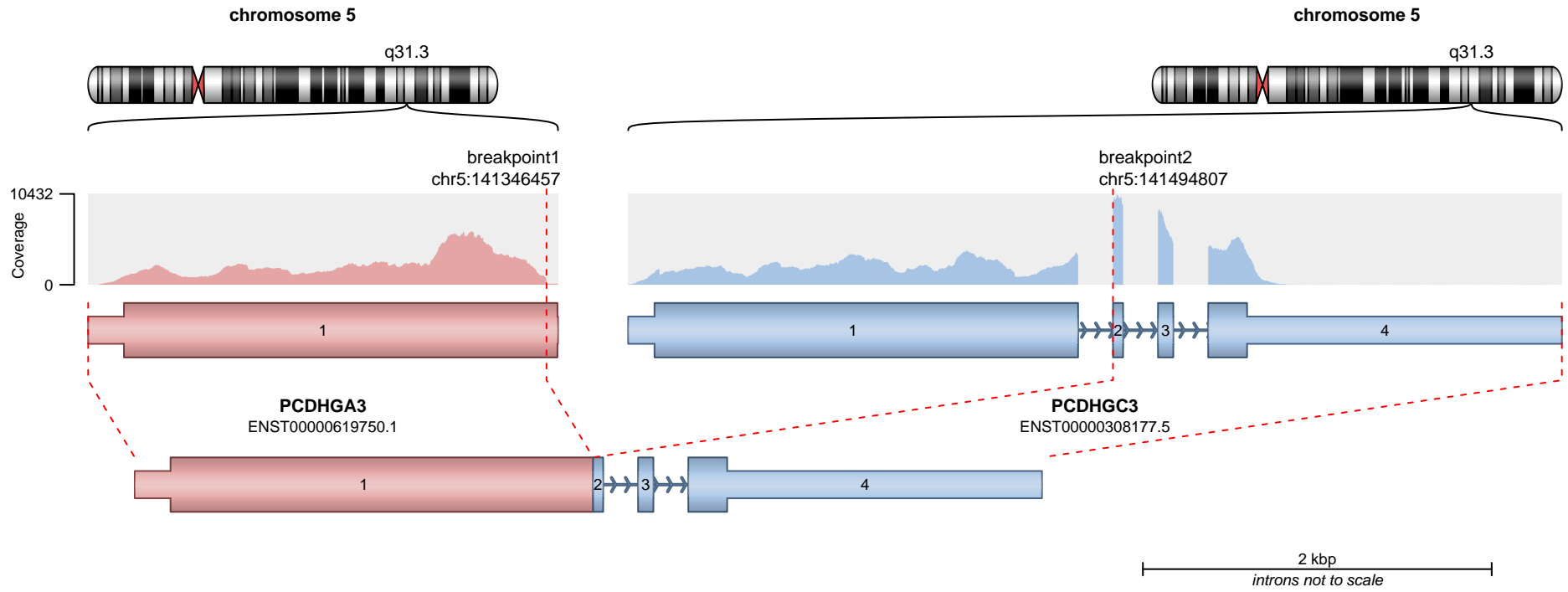
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



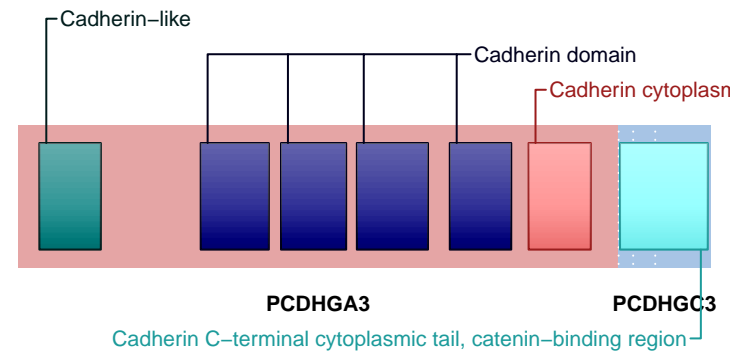
**SUPPORTING READ COUNT**

Split reads = 173  
Discordant mates = 4



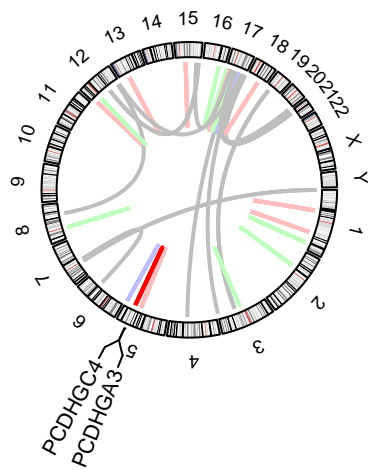
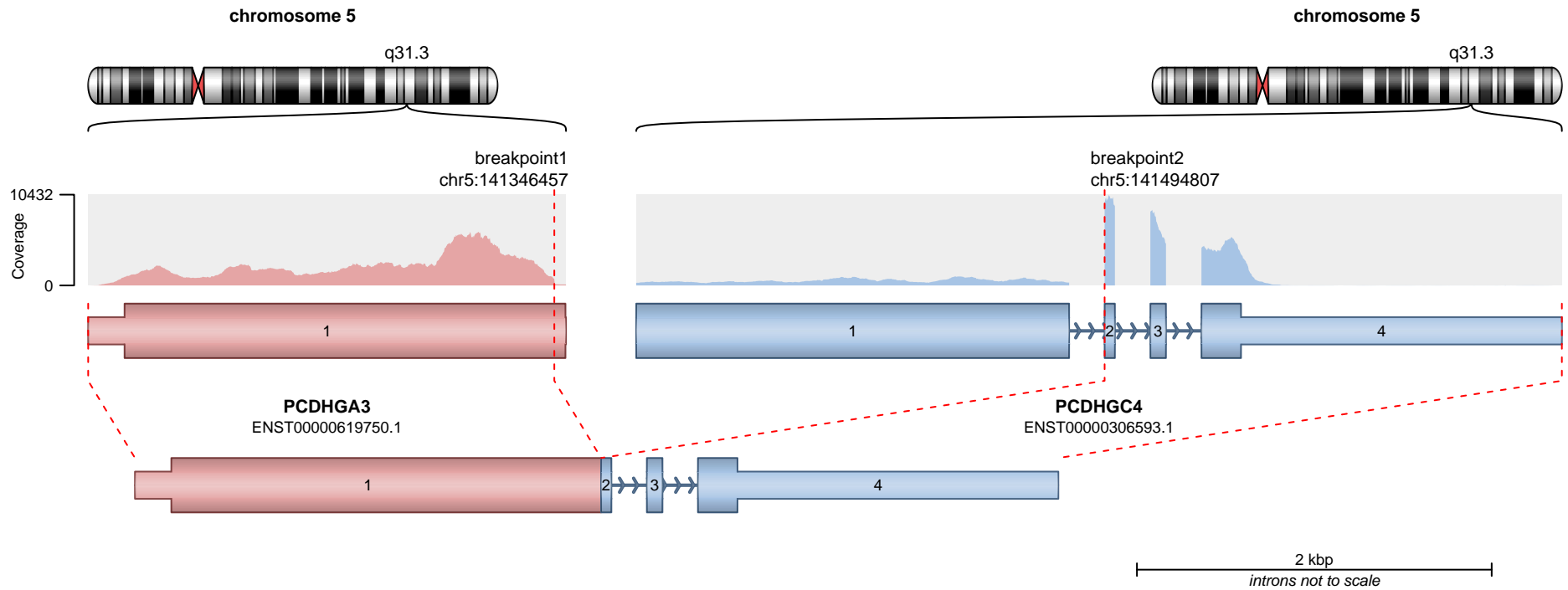
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear

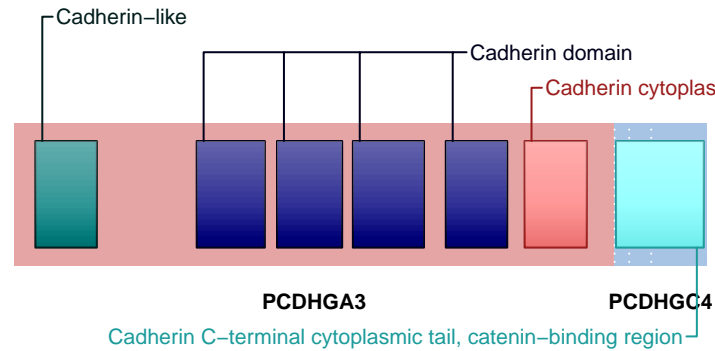


**SUPPORTING READ COUNT**

Split reads = 173  
Discordant mates = 4



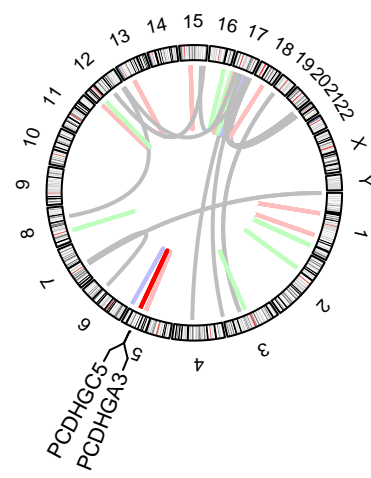
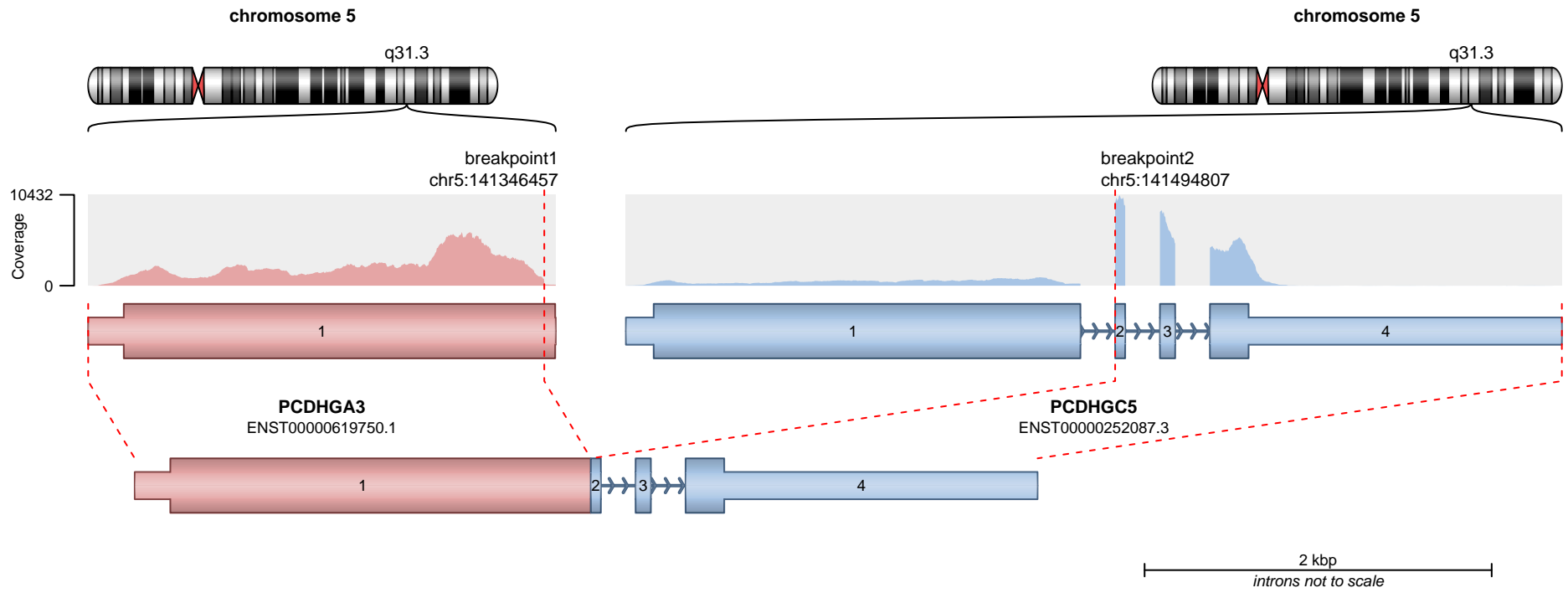
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

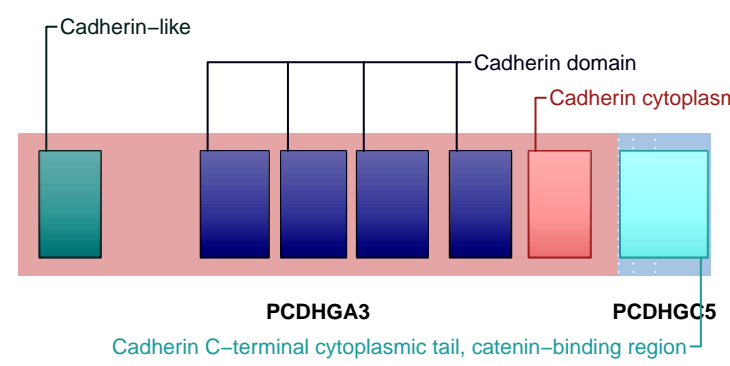
Split reads = 173  
Discordant mates = 4

— translocation — deletion  
— duplication — inversion



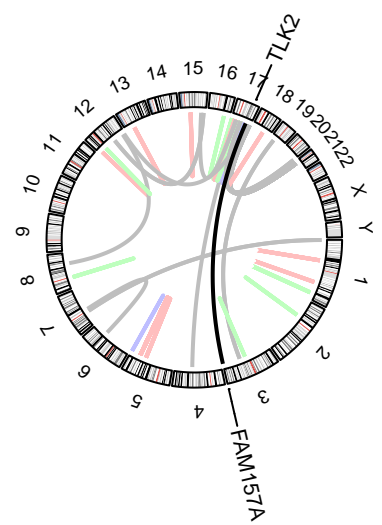
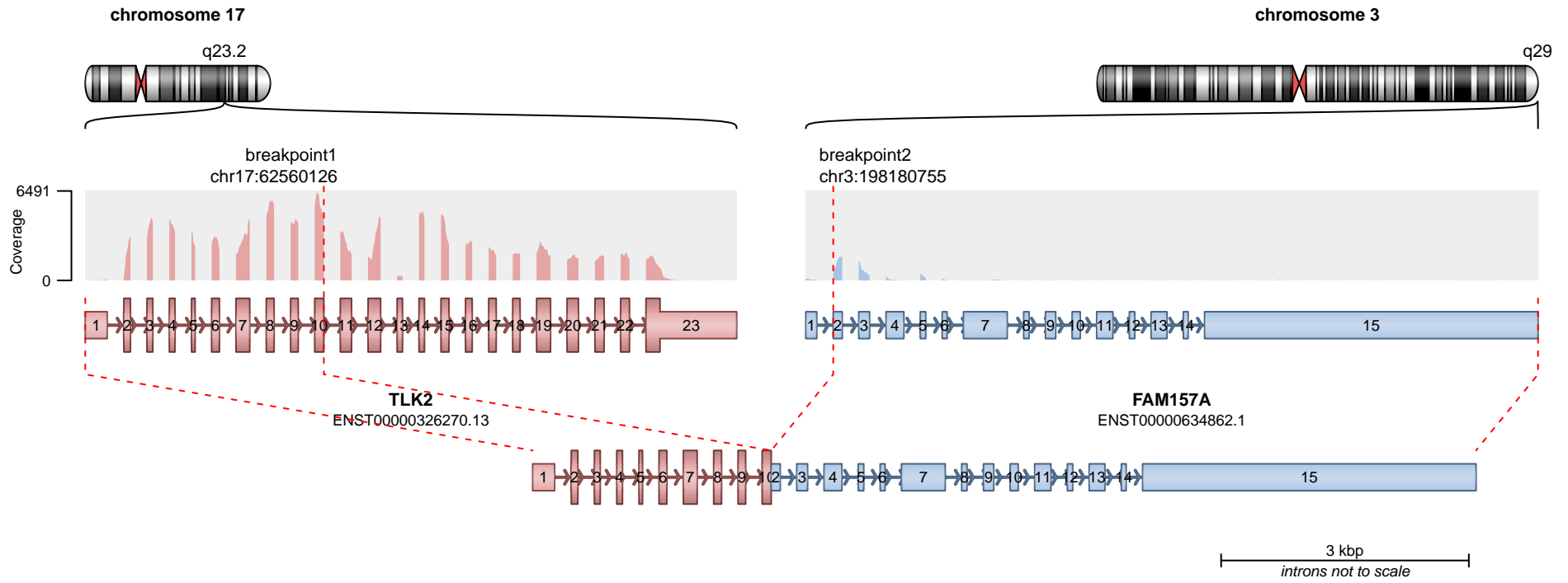
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 173  
Discordant mates = 4

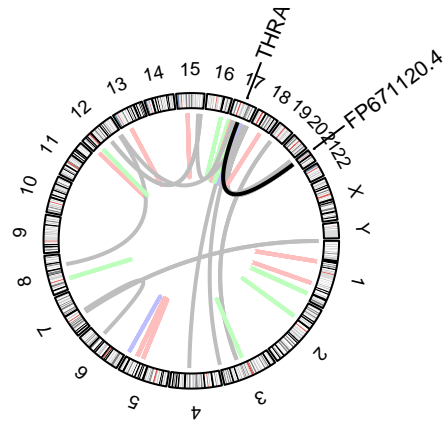
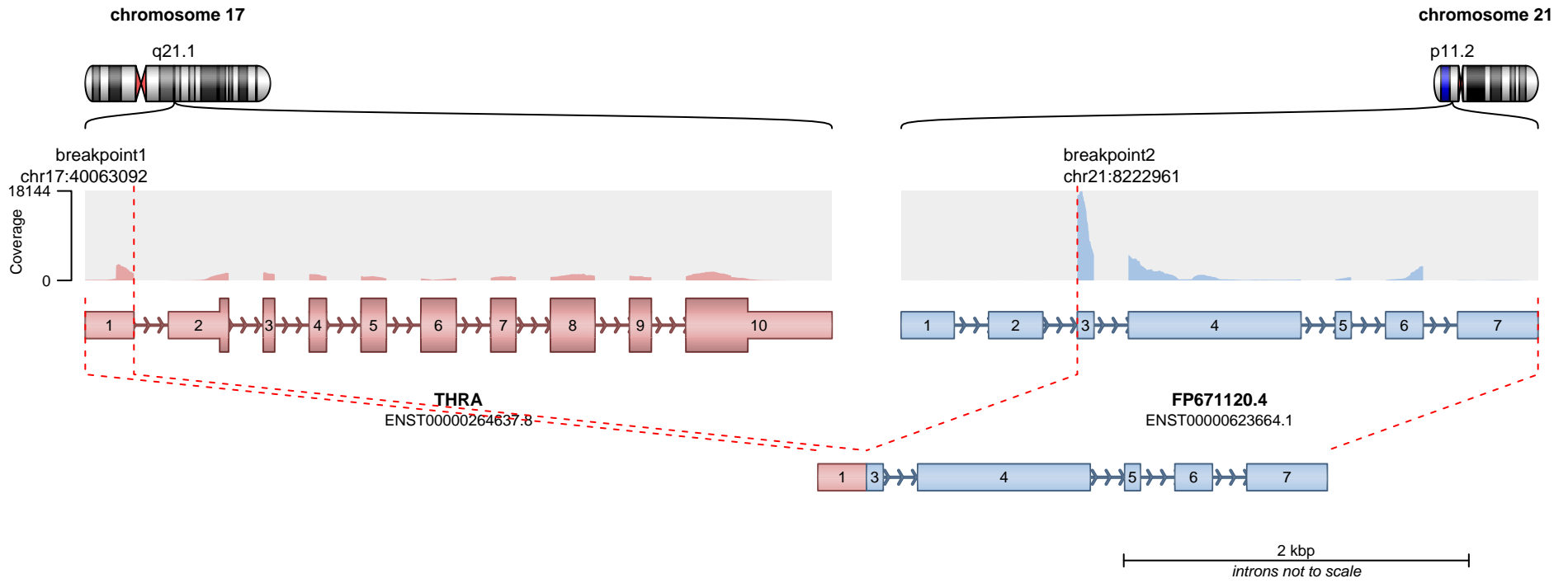


— translocation    — deletion  
— duplication    — inversion

No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 147  
Discordant mates = 3

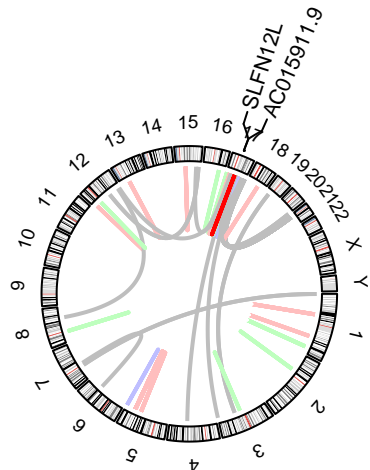
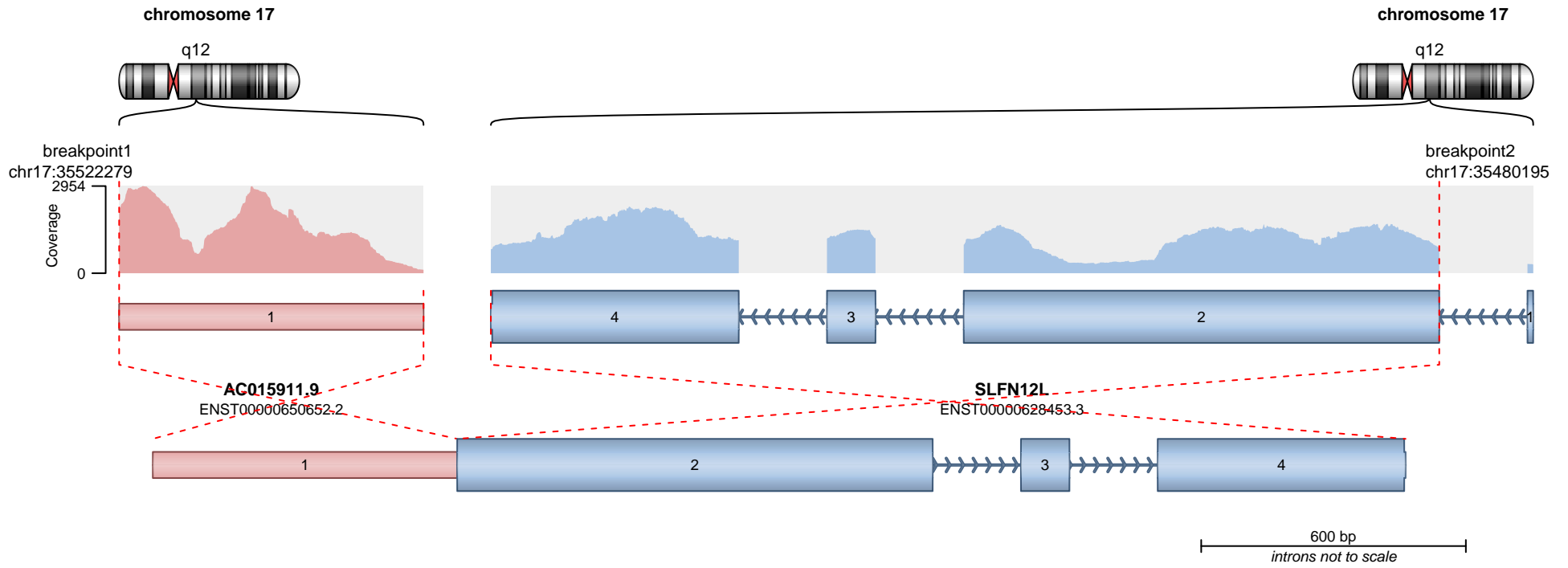


No coding regions retained in fusion transcript.

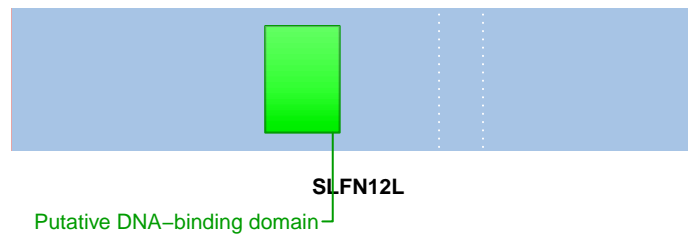
**SUPPORTING READ COUNT**

Split reads = 143  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



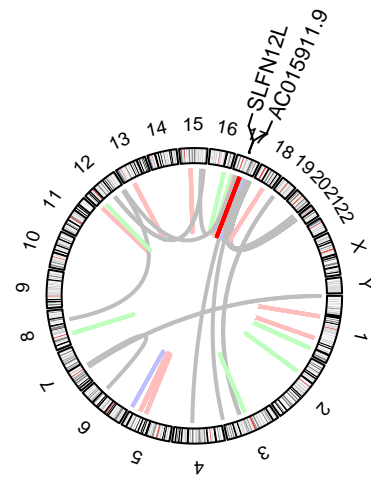
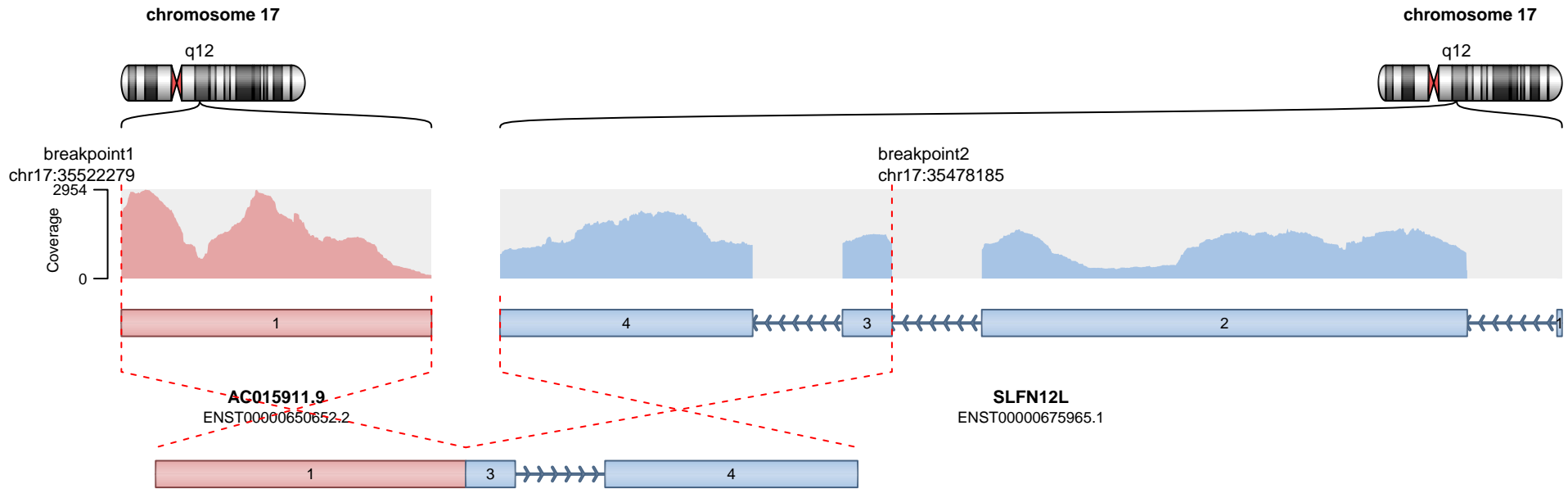
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 128  
Discordant mates = 9

— translocation — deletion  
— duplication — inversion

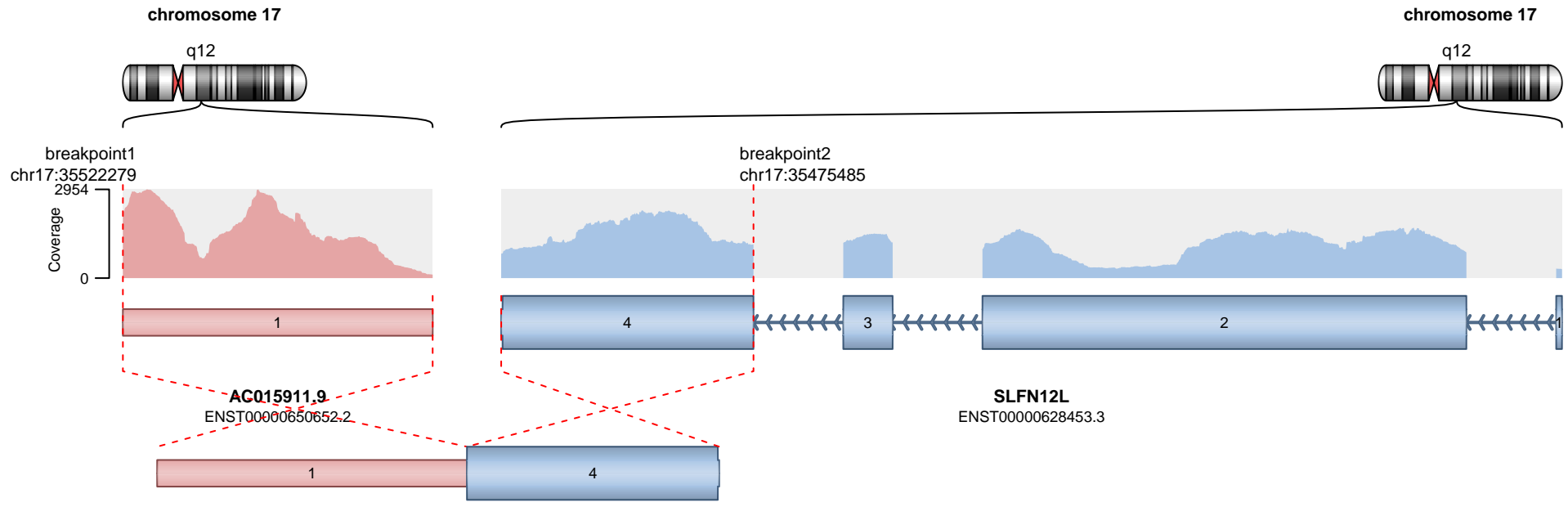


— translocation    — deletion  
— duplication    — inversion

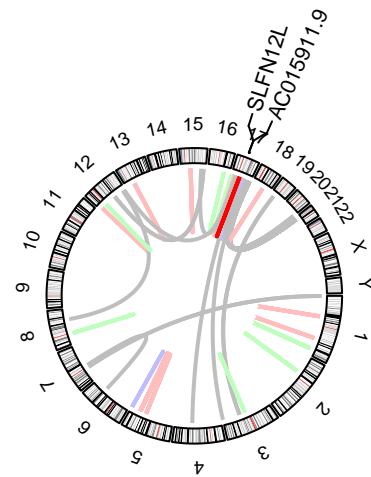
Genes are not protein-coding.

**SUPPORTING READ COUNT**

Split reads = 45  
Discordant mates = 1



600 bp  
introns not to scale

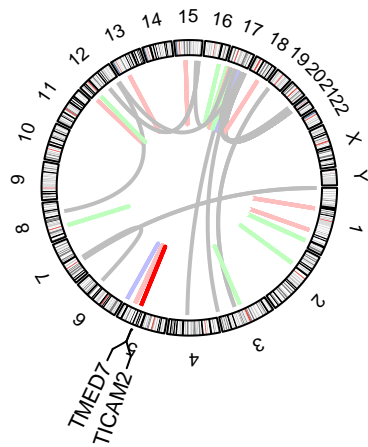
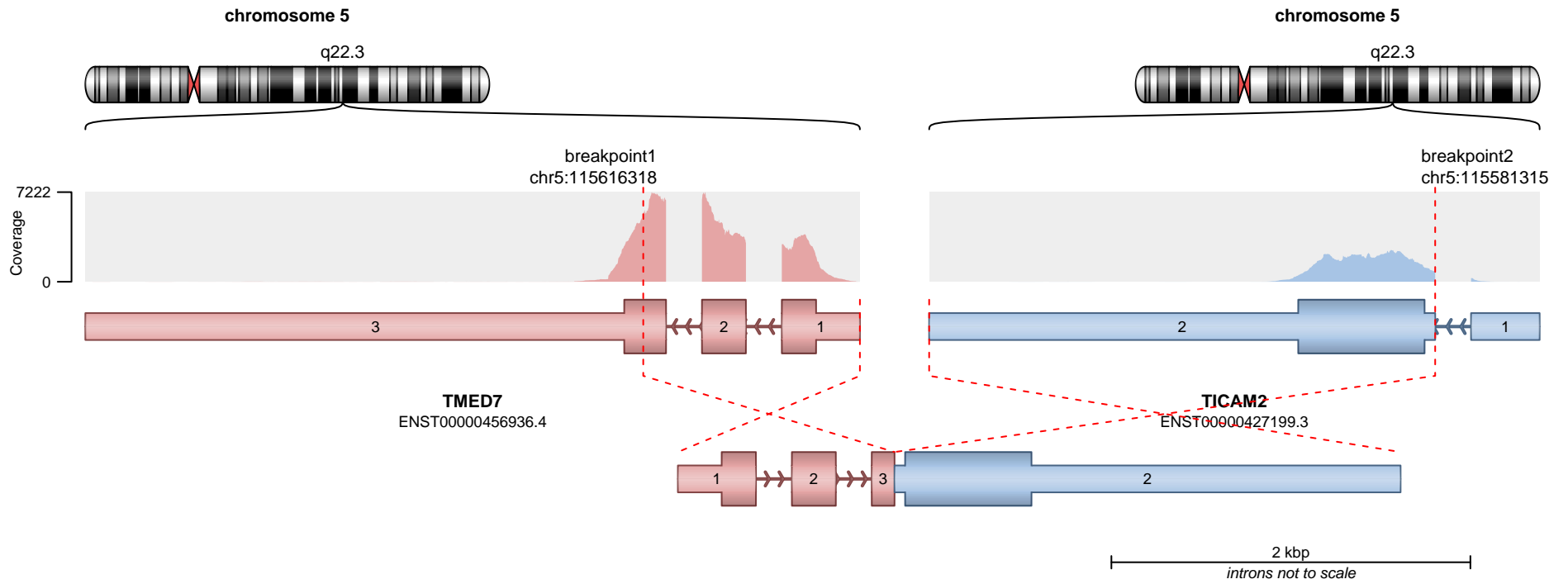


— translocation    — deletion  
— duplication    — inversion

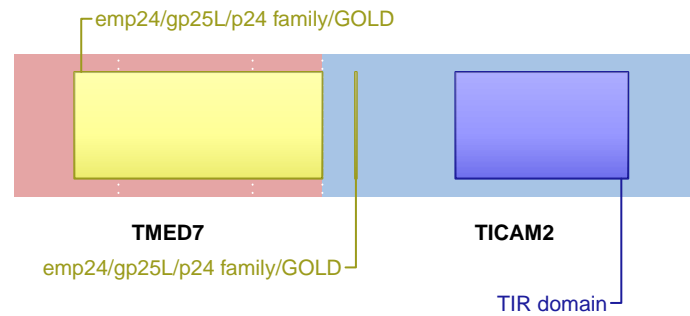
No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0



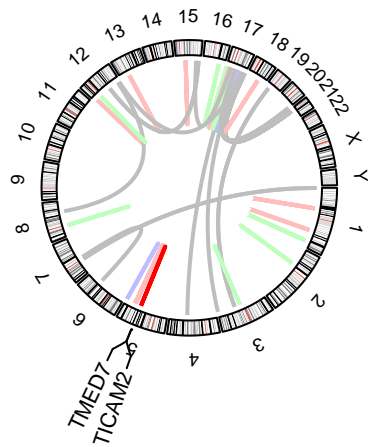
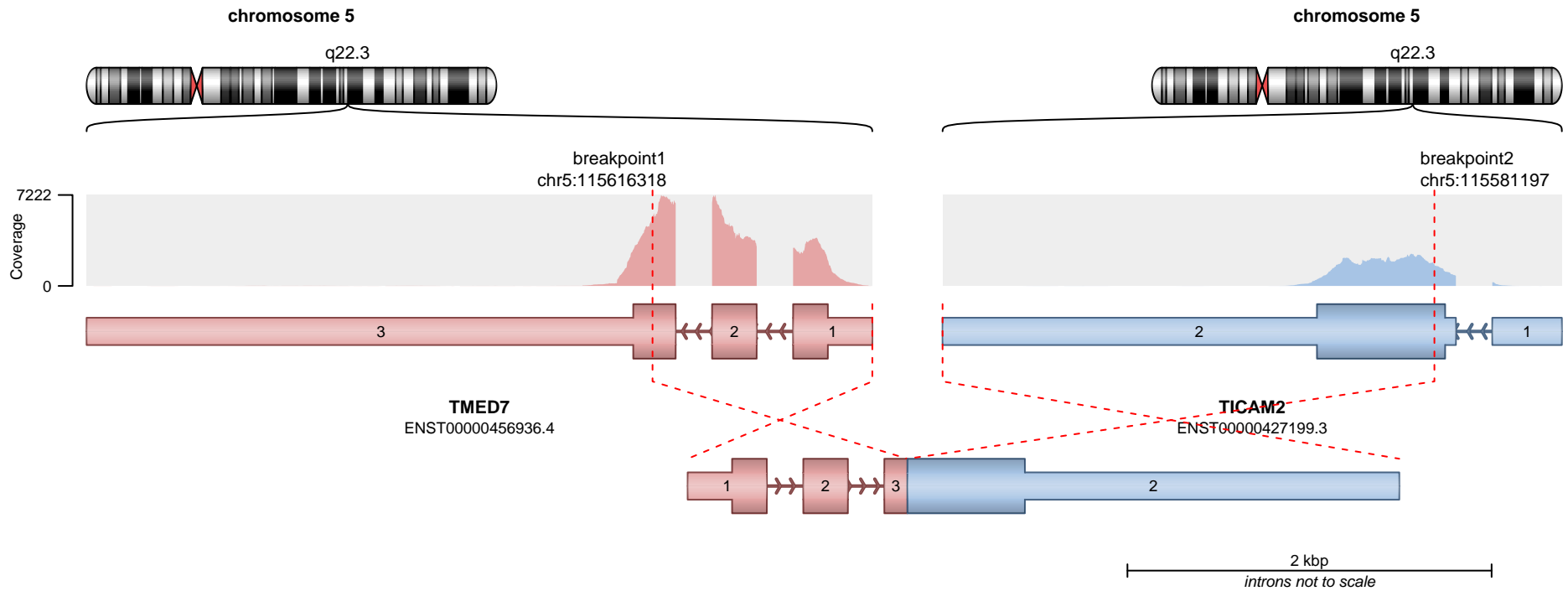
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



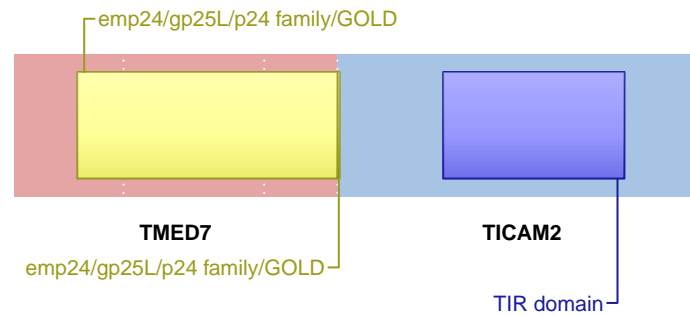
**SUPPORTING READ COUNT**

Split reads = 110  
Discordant mates = 3

- translocation
- duplication
- deletion
- inversion



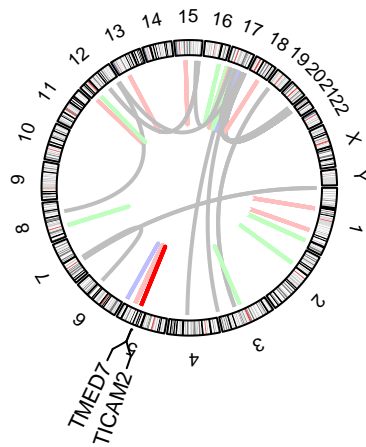
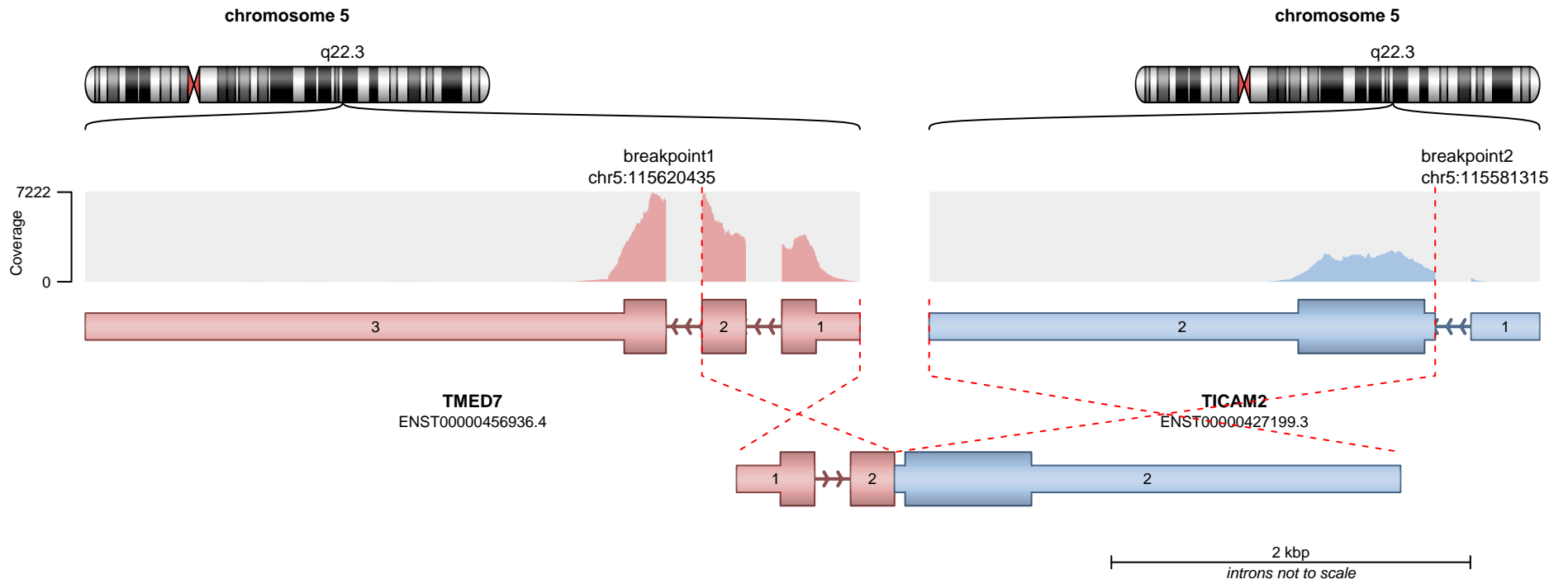
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



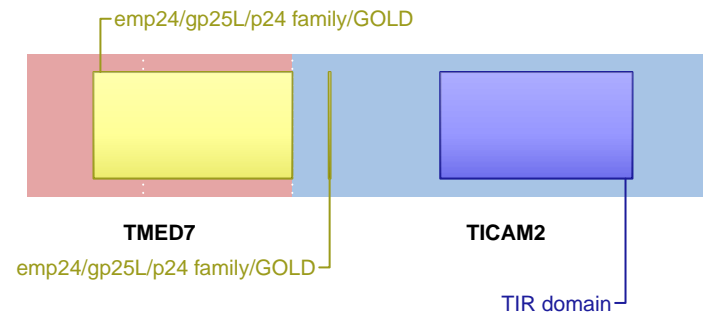
**SUPPORTING READ COUNT**

Split reads = 17  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



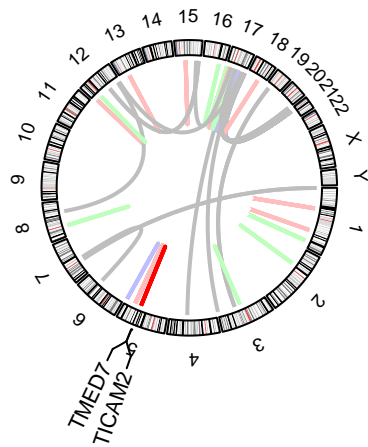
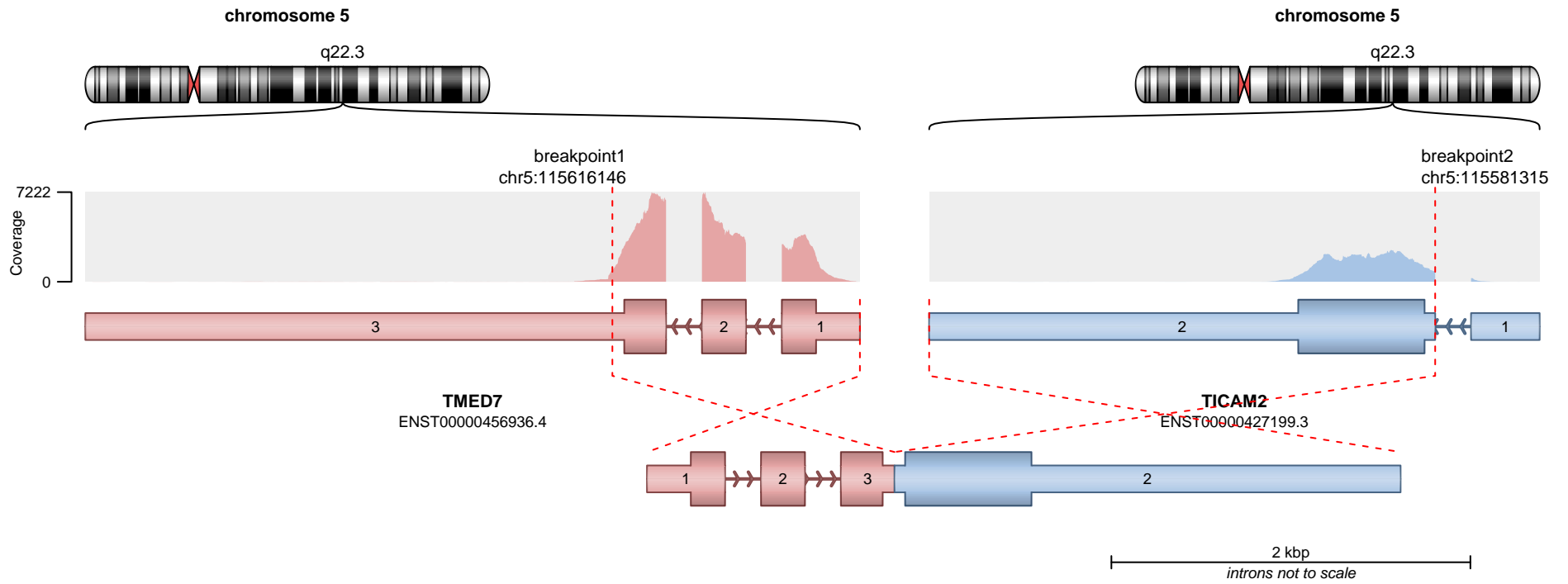
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



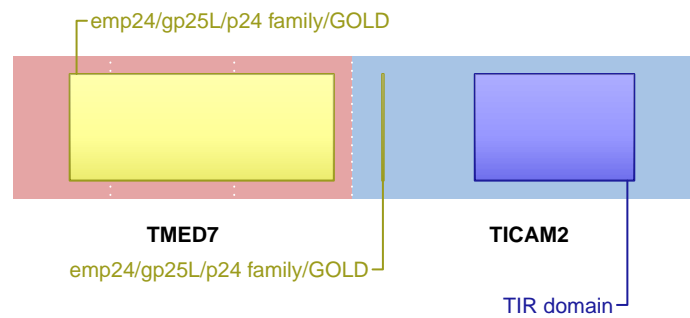
**SUPPORTING READ COUNT**

Split reads = 9  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



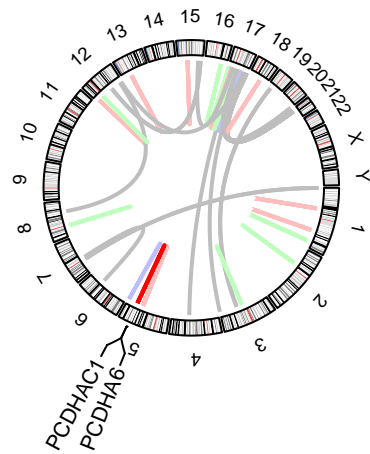
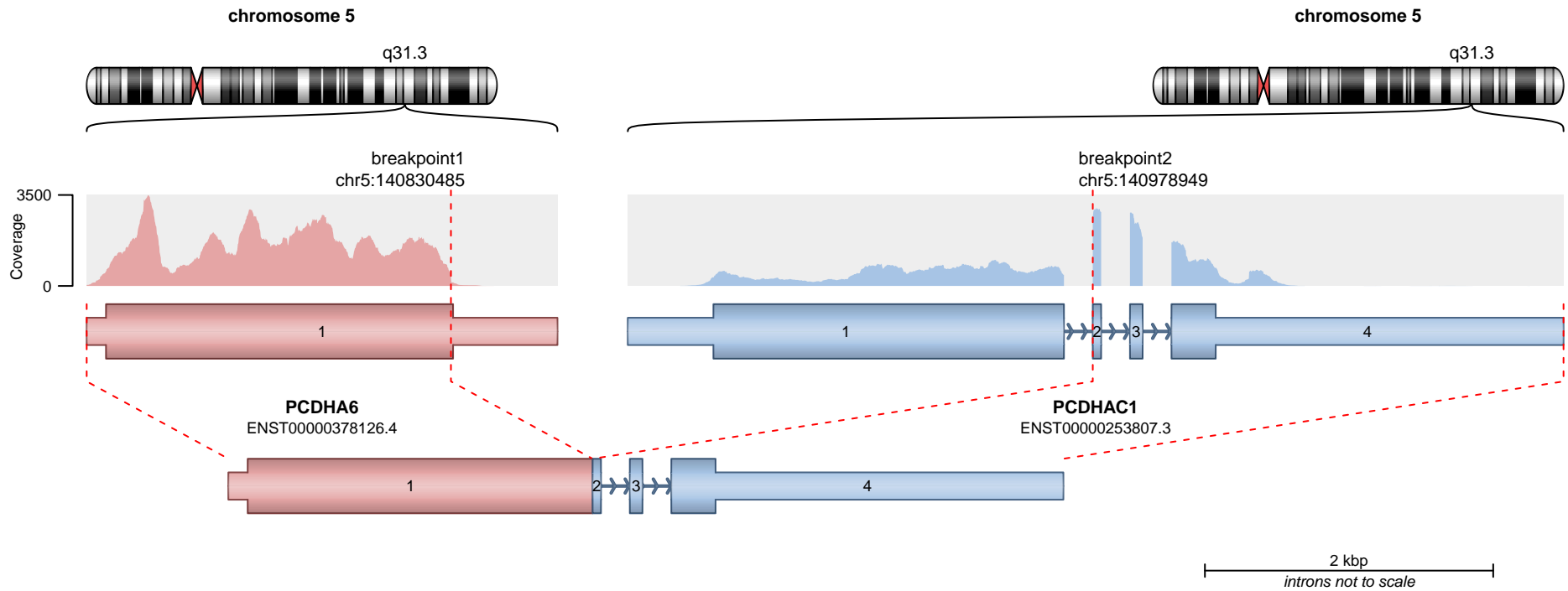
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

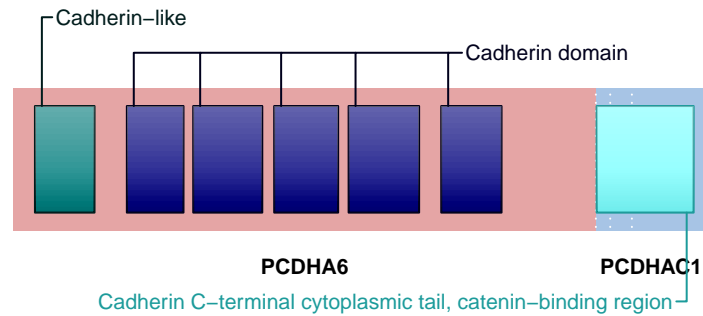
Split reads = 3  
Discordant mates = 3

— translocation — deletion  
— duplication — inversion



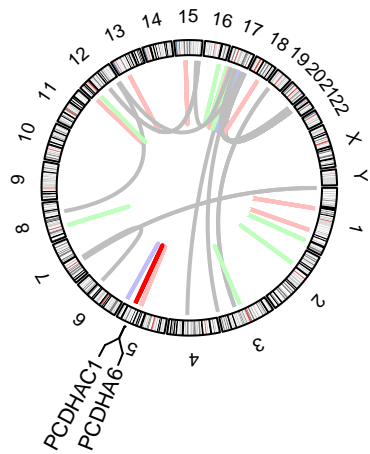
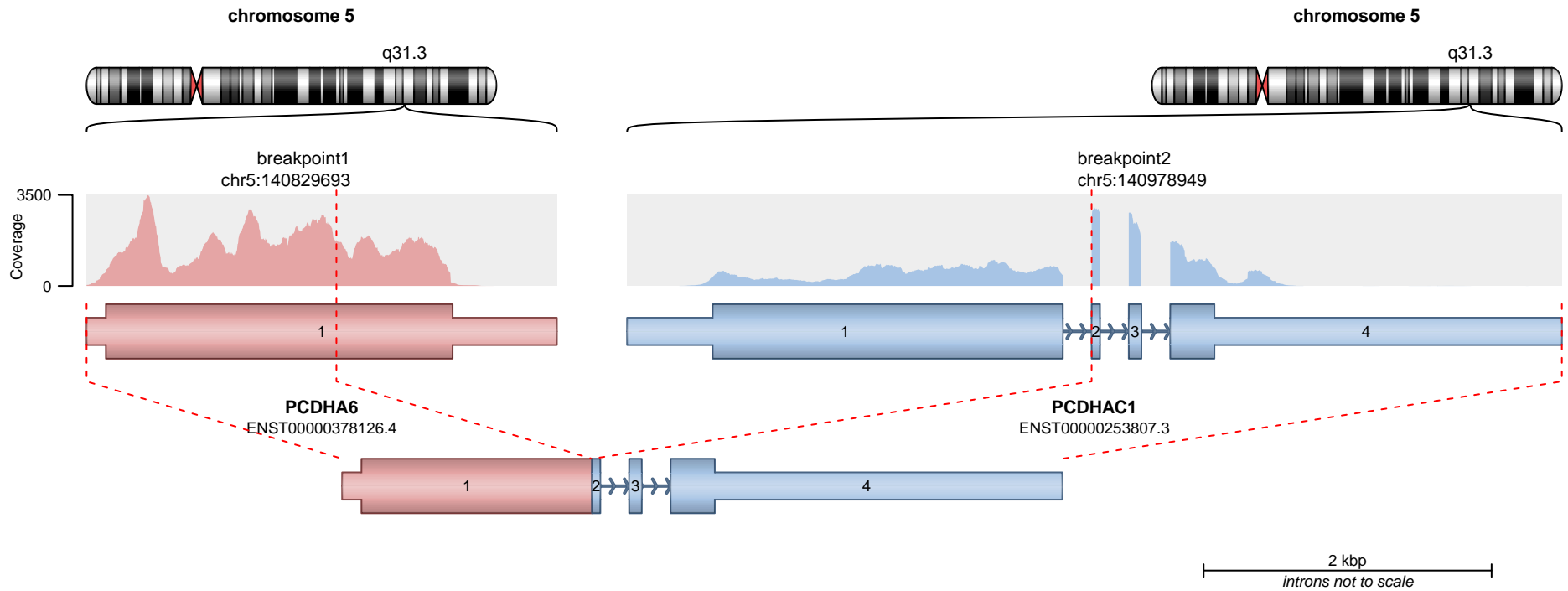
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear

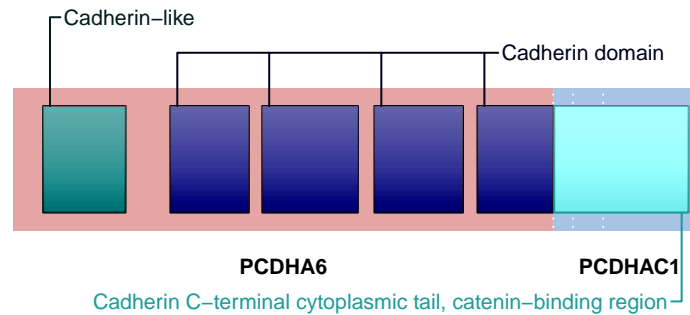


**SUPPORTING READ COUNT**

Split reads = 105  
Discordant mates = 5



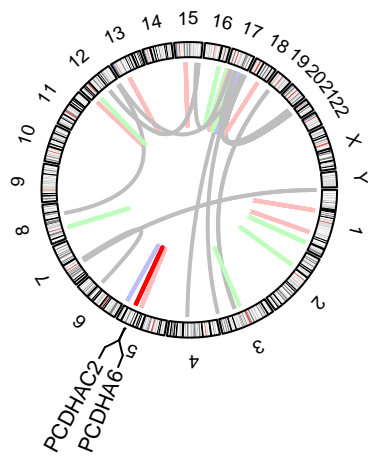
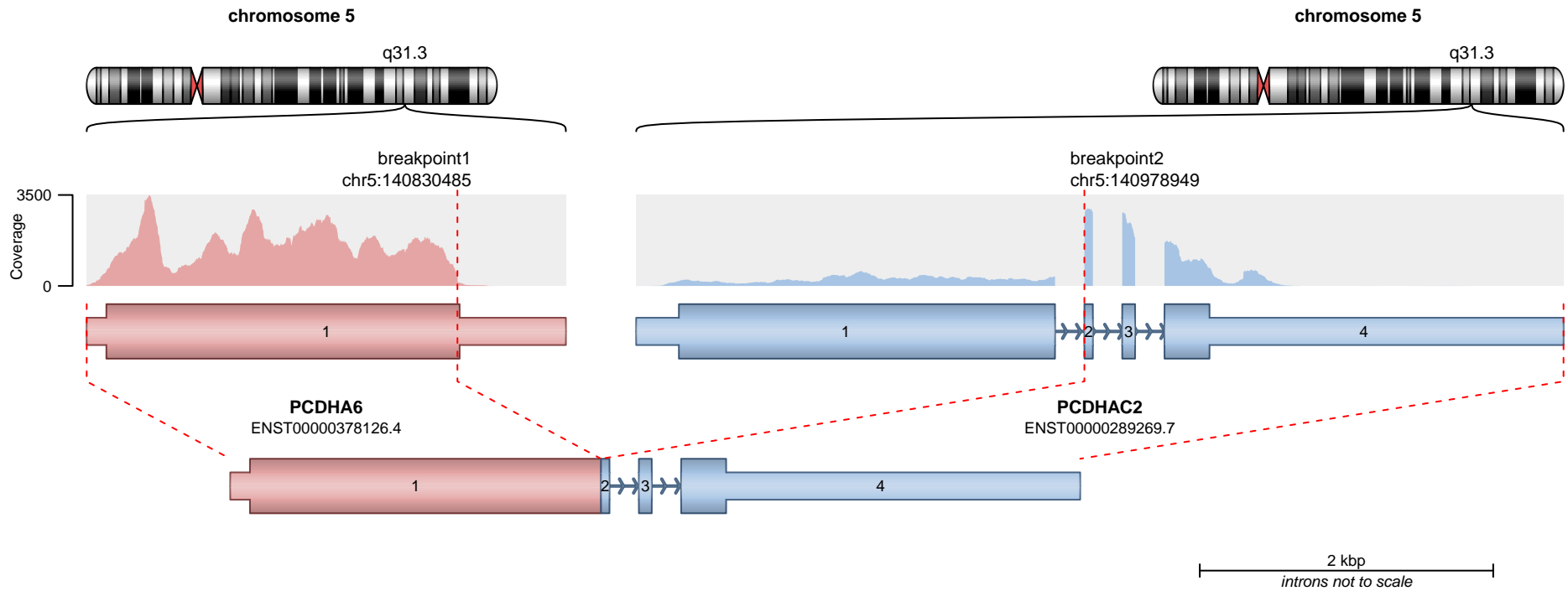
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



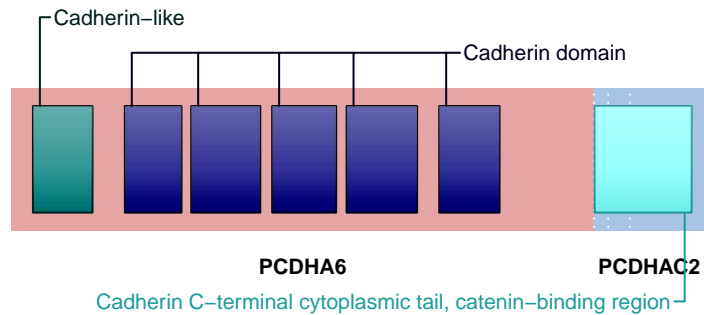
**SUPPORTING READ COUNT**

Split reads = 29  
Discordant mates = 1

— translocation — deletion  
— duplication — inversion



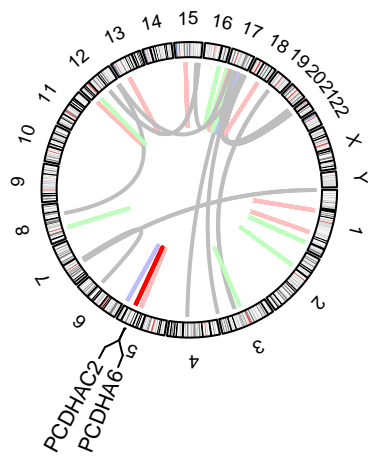
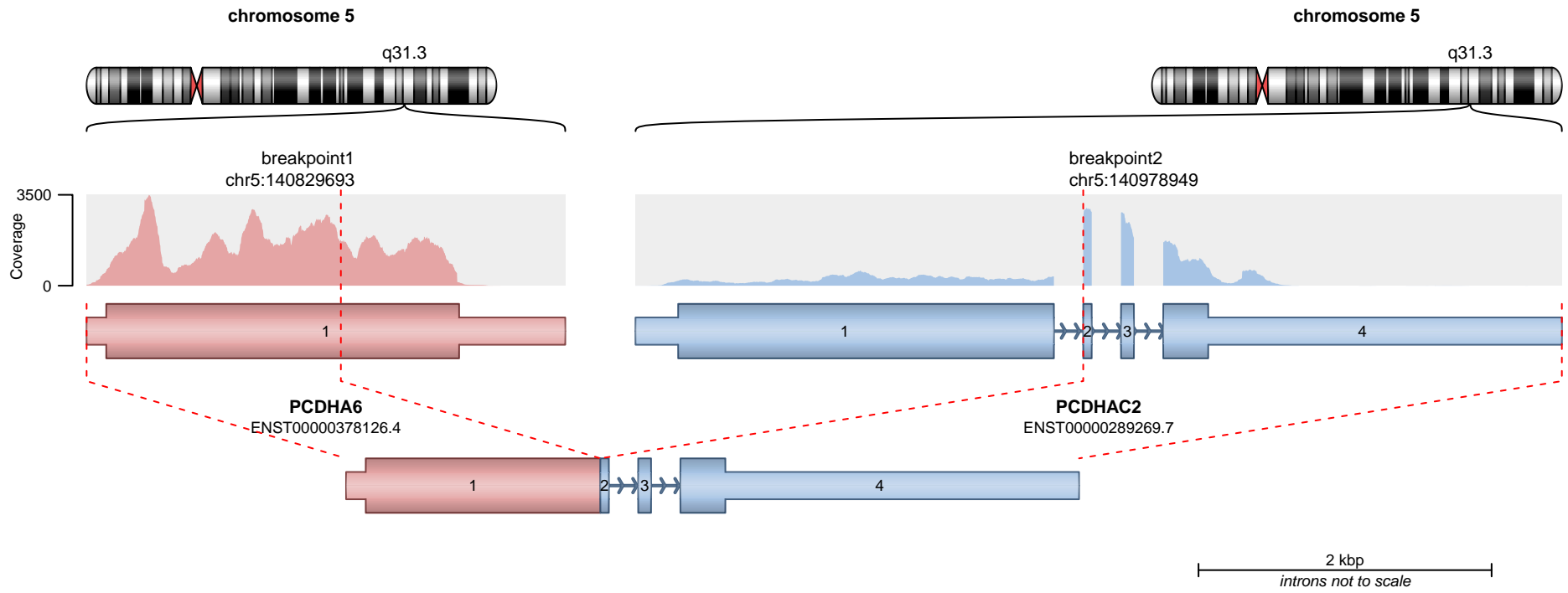
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



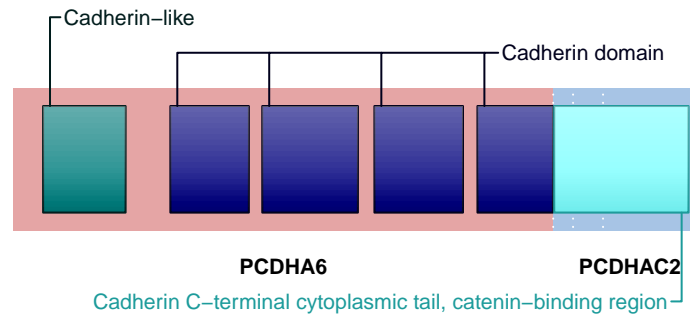
**SUPPORTING READ COUNT**

Split reads = 105  
Discordant mates = 5

— translocation — deletion  
— duplication — inversion



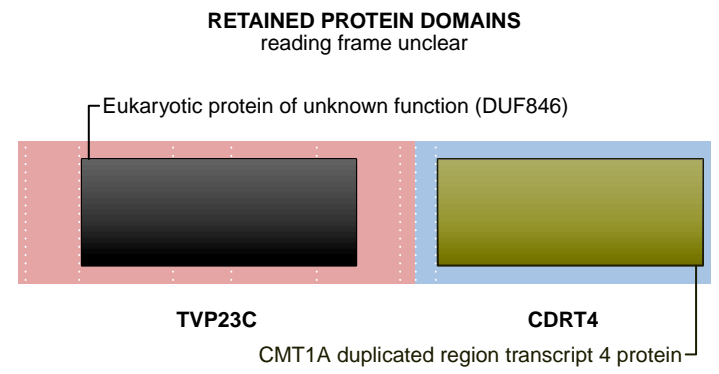
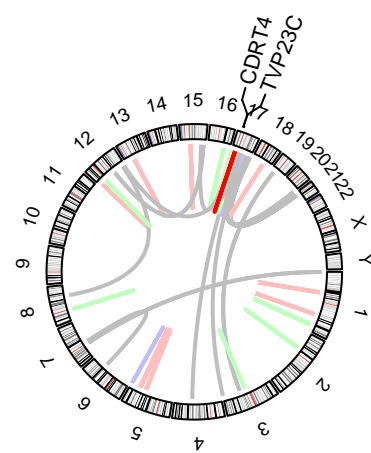
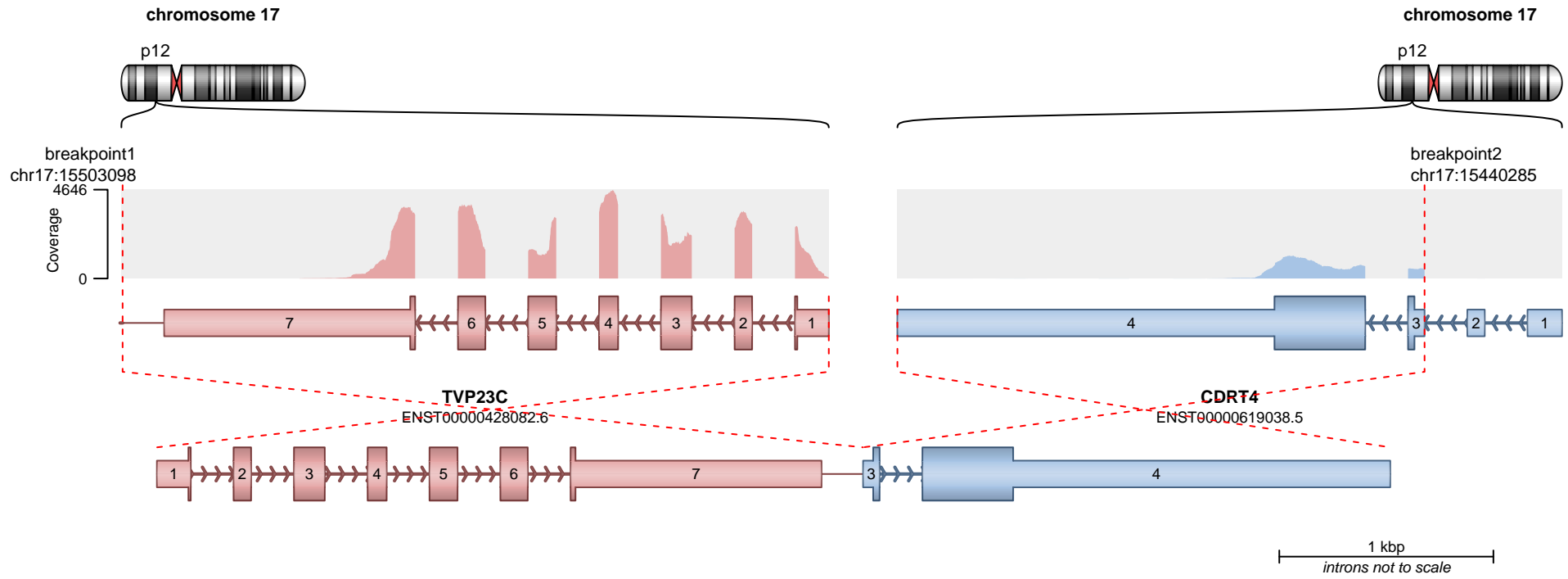
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 29  
Discordant mates = 1

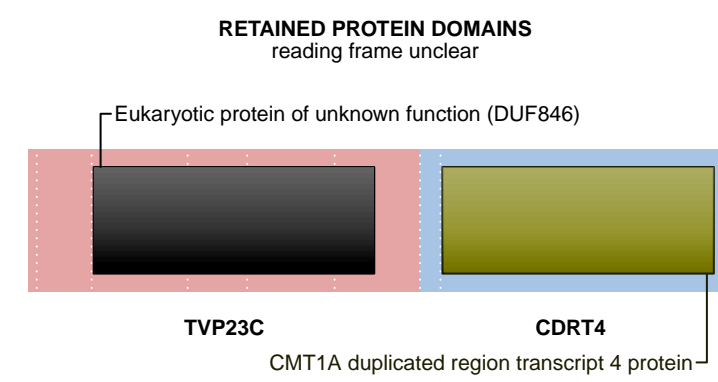
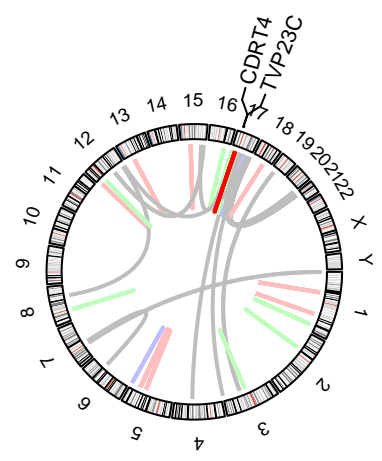
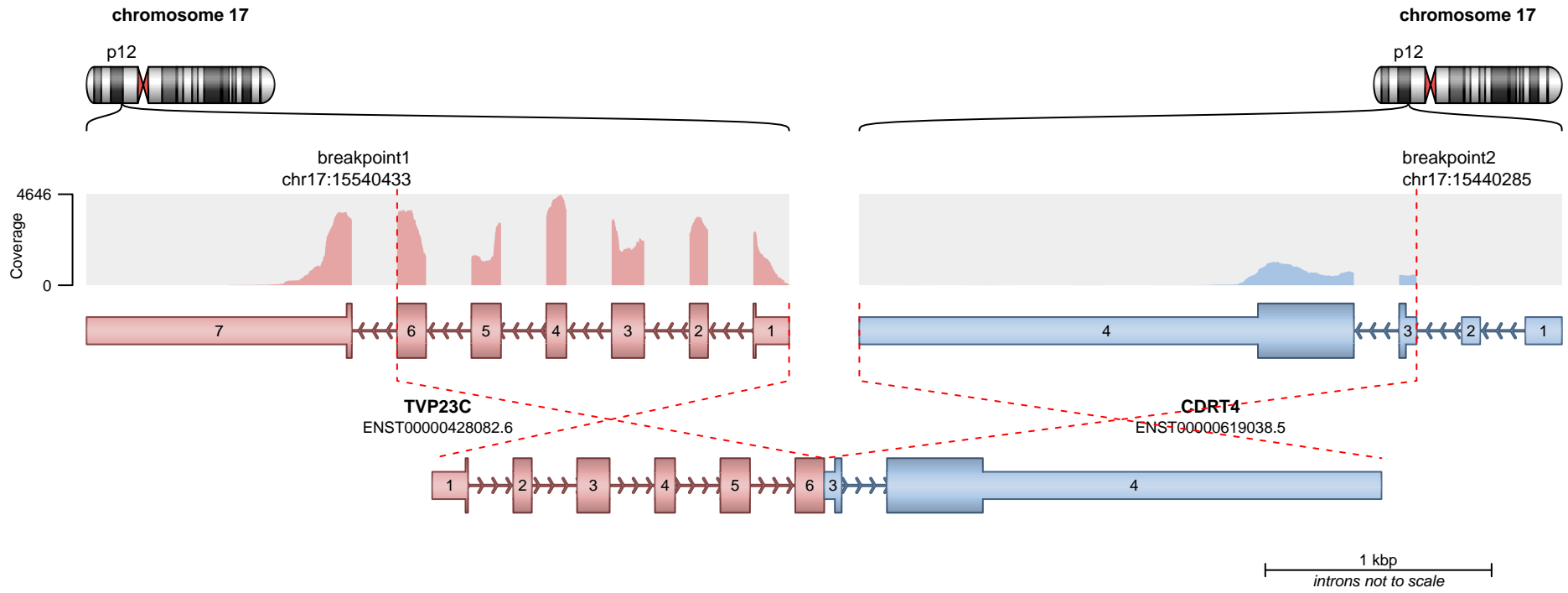
— translocation    — deletion  
— duplication    — inversion



**SUPPORTING READ COUNT**

Split reads = 92  
Discordant mates = 1

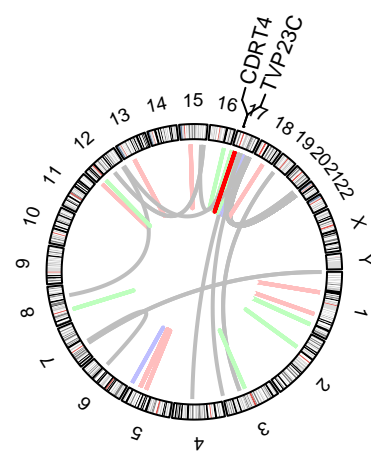
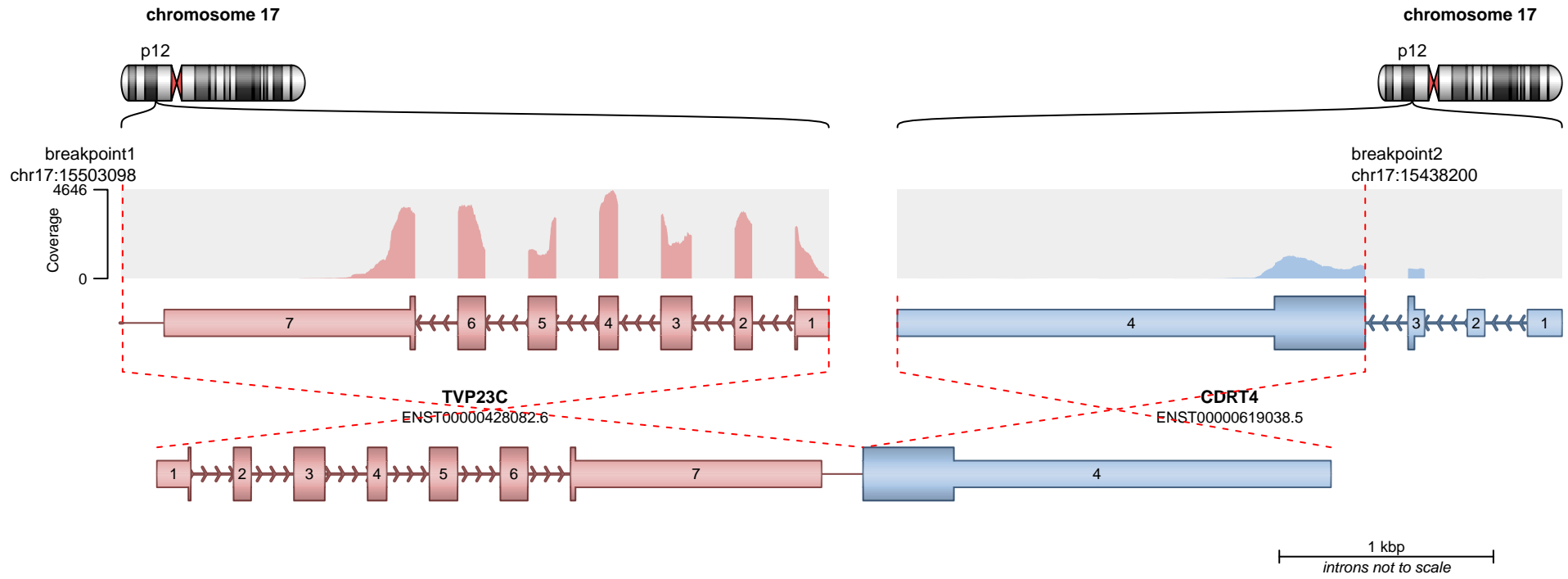
— translocation — deletion  
— duplication — inversion



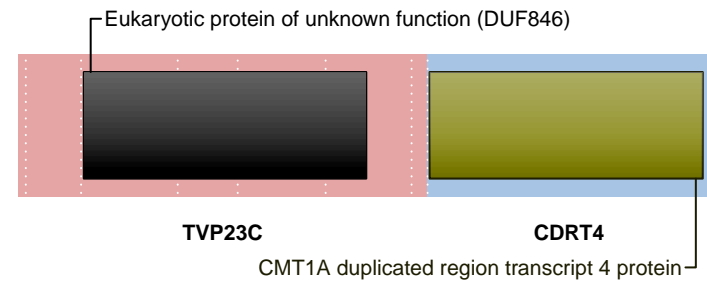
**SUPPORTING READ COUNT**

Split reads = 42  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



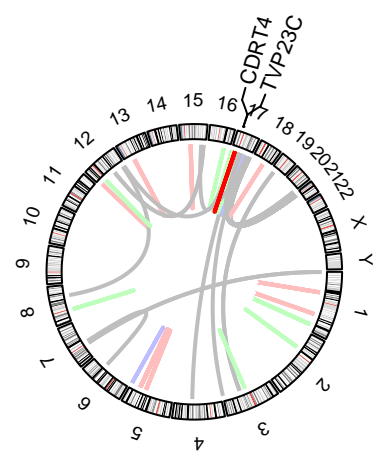
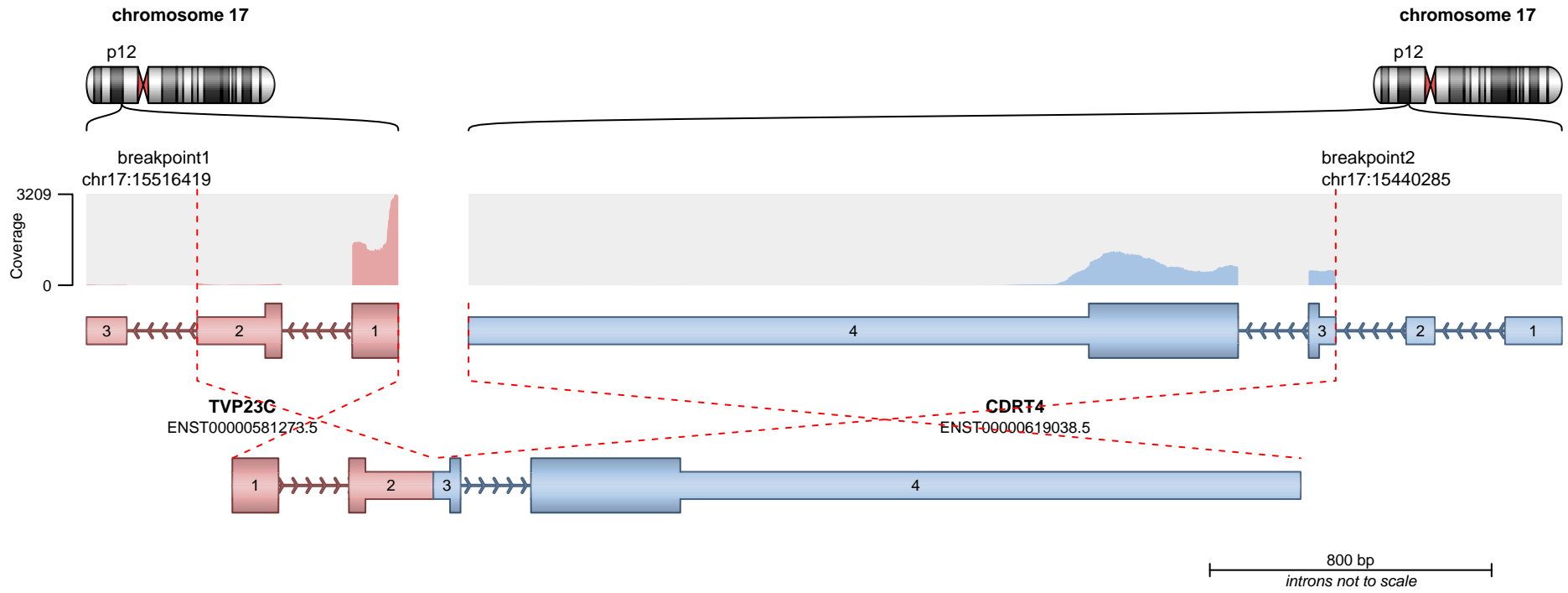
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



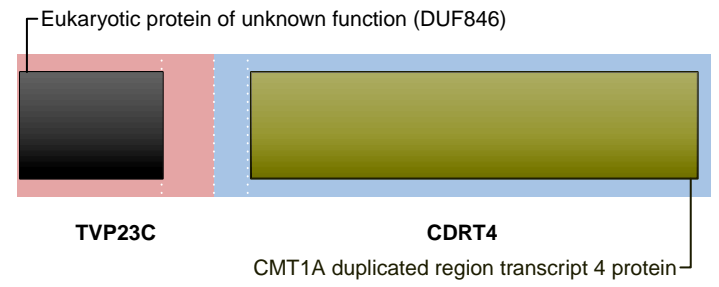
**SUPPORTING READ COUNT**

Split reads = 25  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



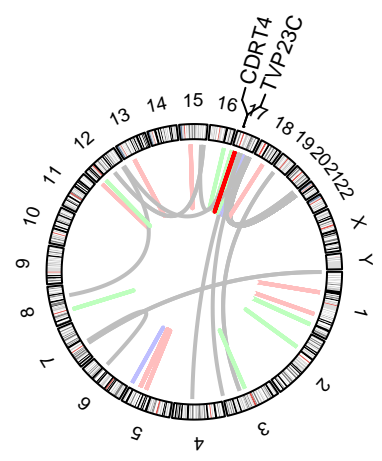
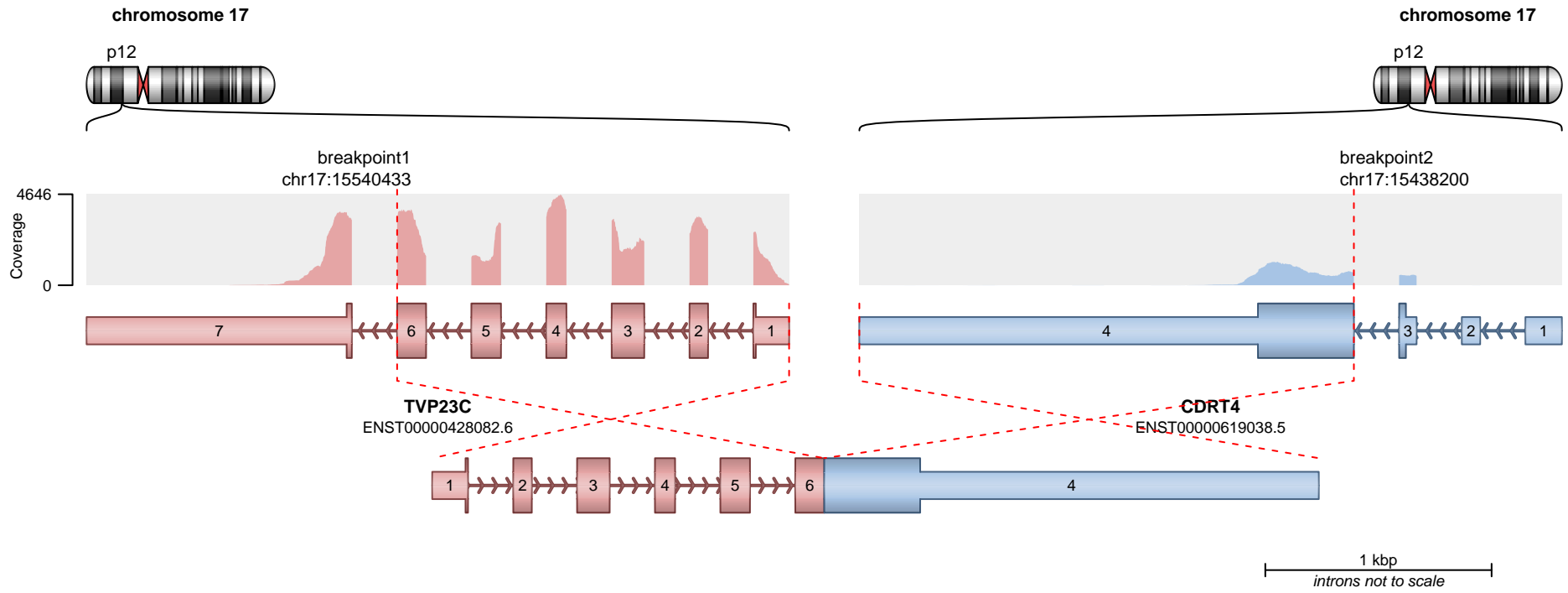
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



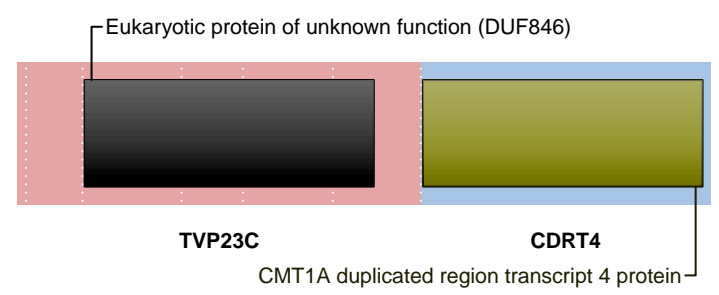
**SUPPORTING READ COUNT**

Split reads = 13  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



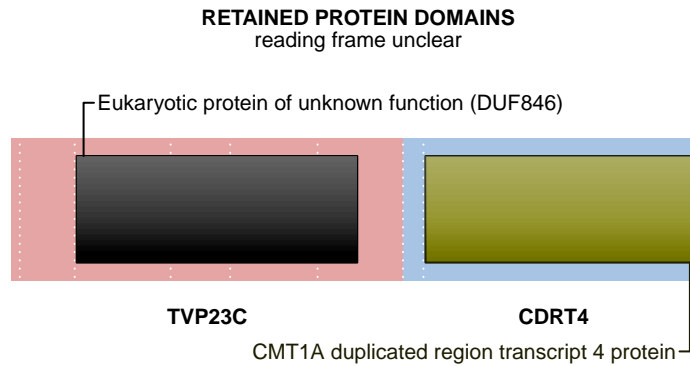
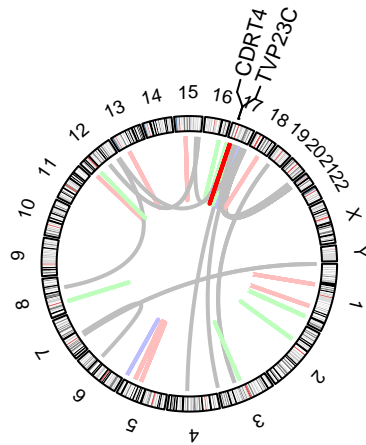
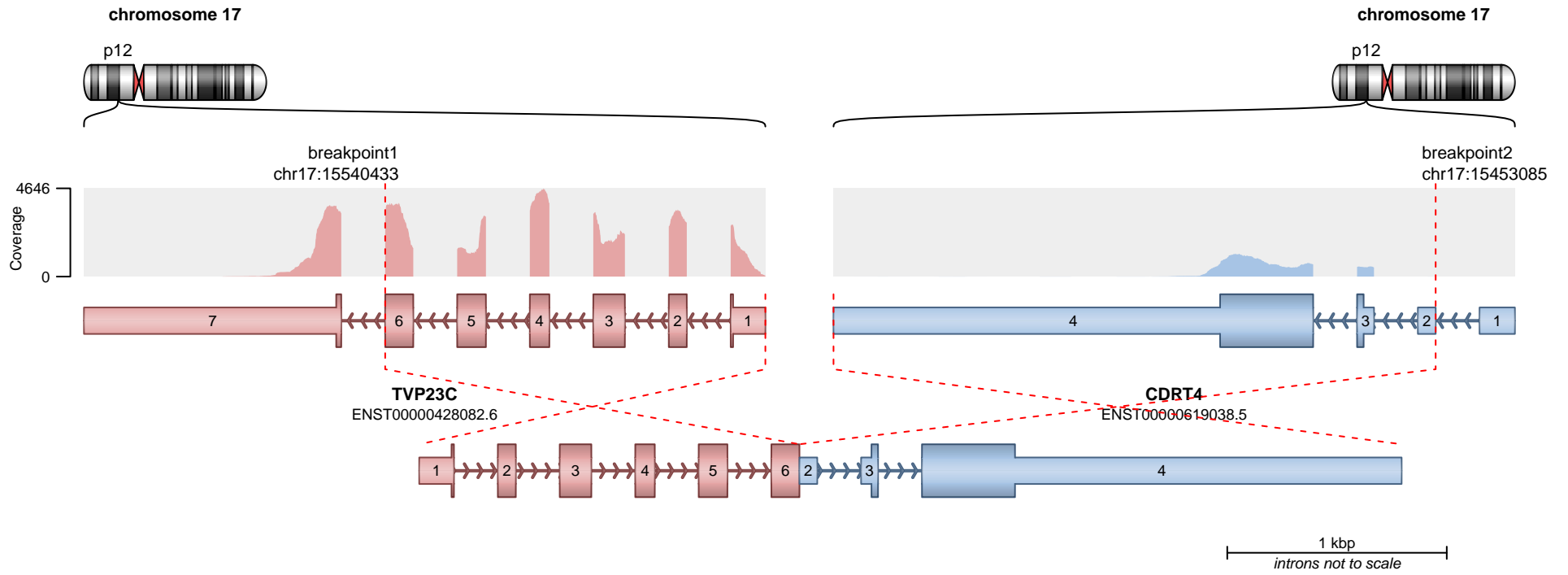
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 0

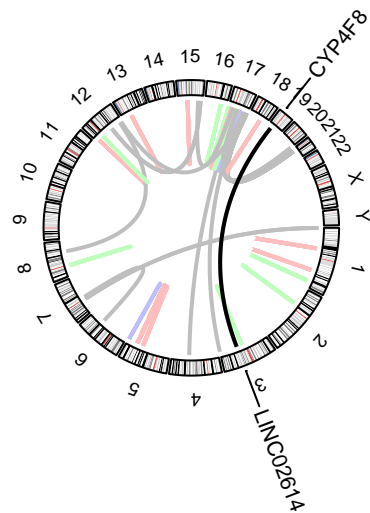
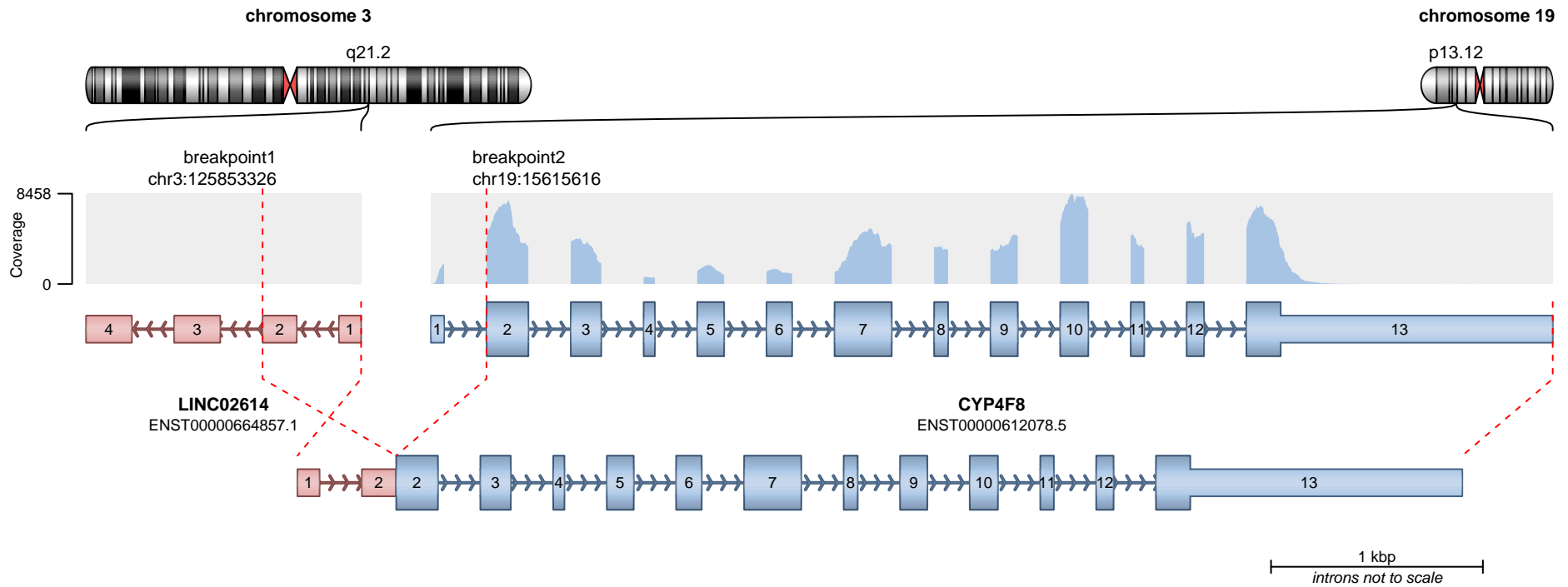
- translocation
- duplication
- deletion
- inversion



**SUPPORTING READ COUNT**

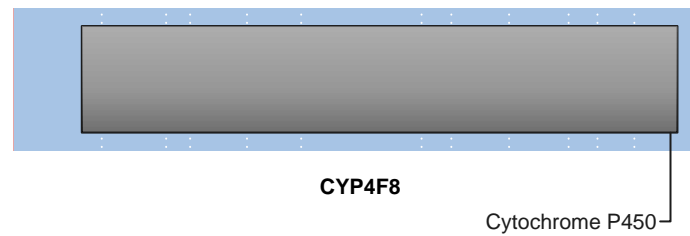
Split reads = 1  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



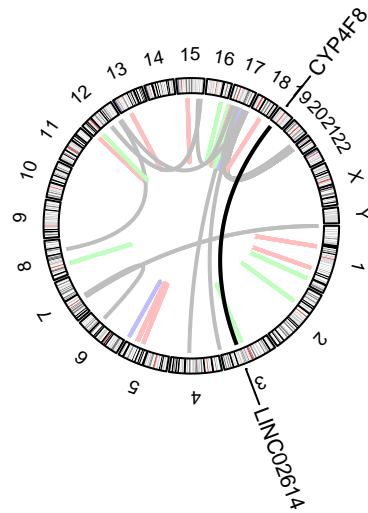
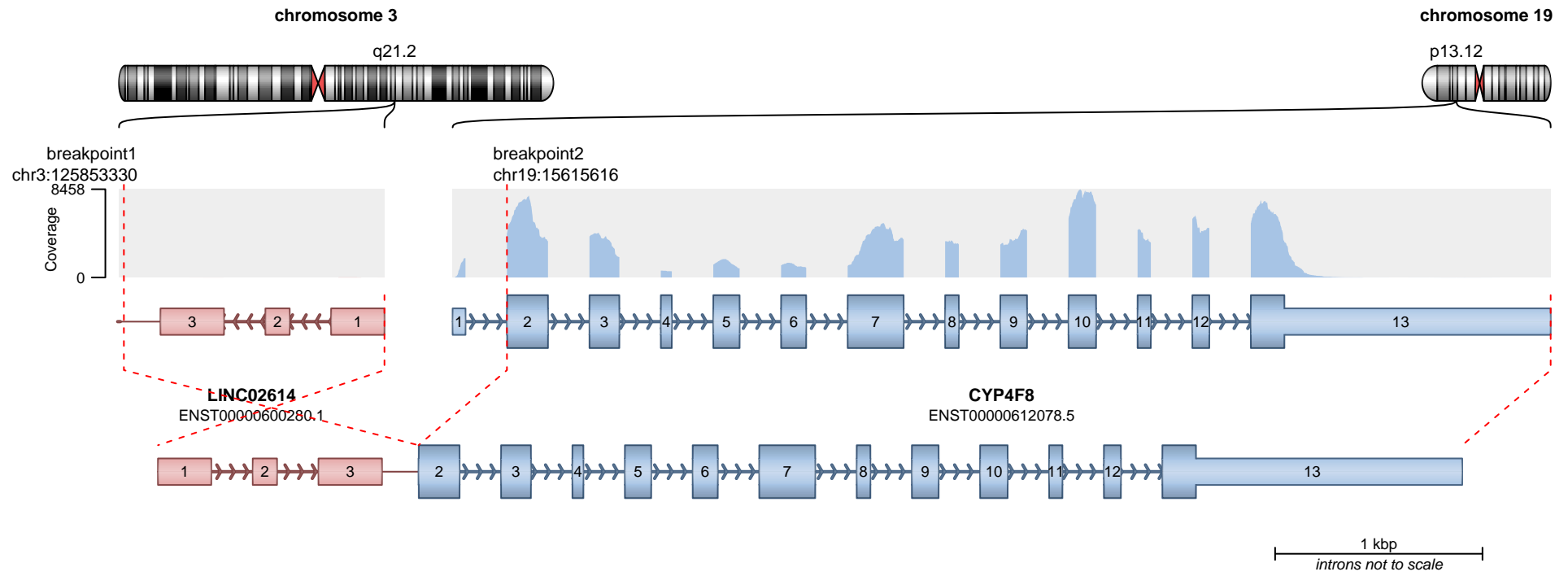
— translocation — deletion  
— duplication — inversion

RETAINED PROTEIN DOMAINS  
reading frame unclear



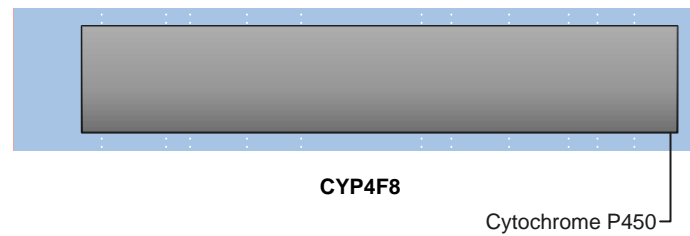
SUPPORTING READ COUNT

Split reads = 76  
Discordant mates = 0



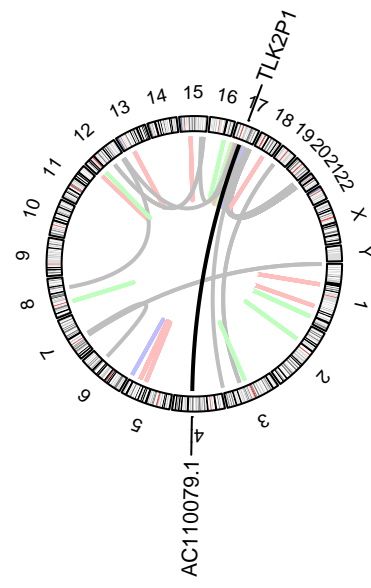
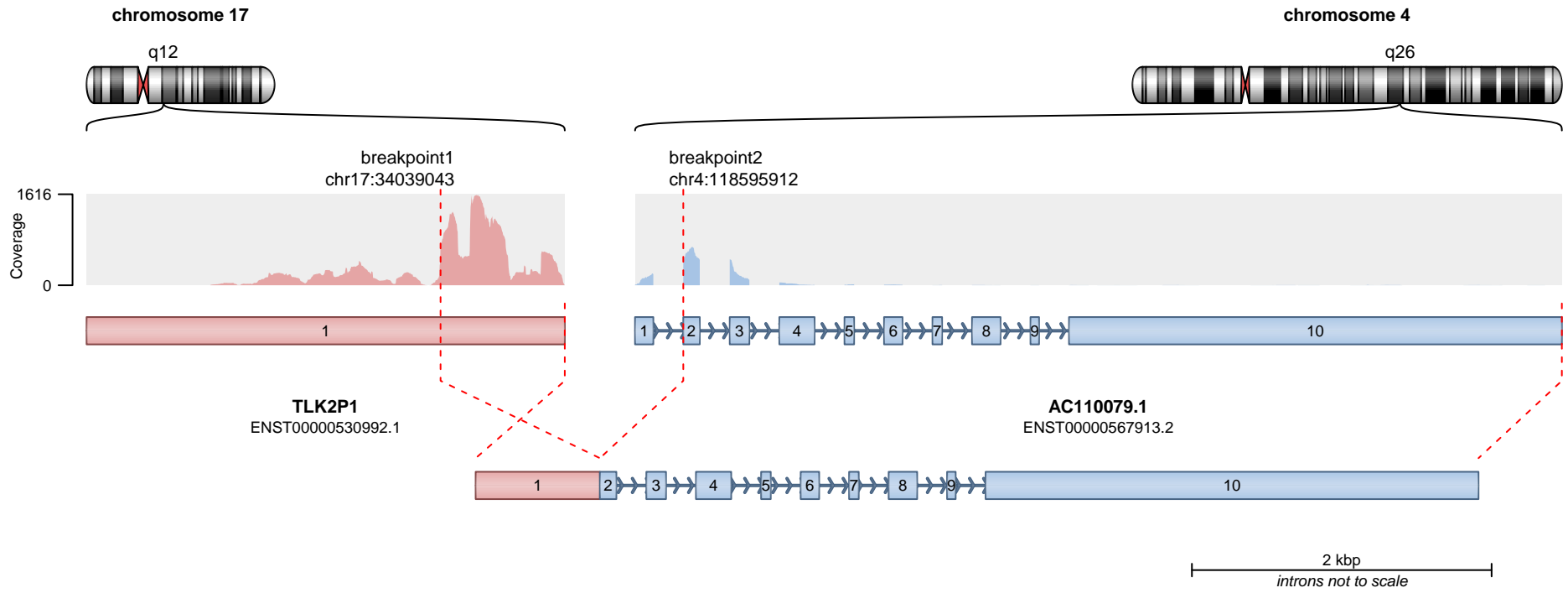
— translocation — deletion  
— duplication — inversion

RETAINED PROTEIN DOMAINS  
reading frame unclear



SUPPORTING READ COUNT

Split reads = 10  
Discordant mates = 0

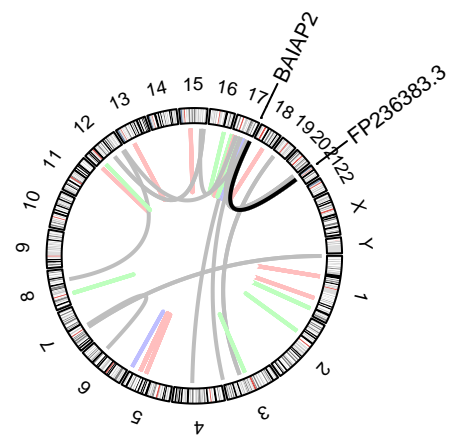
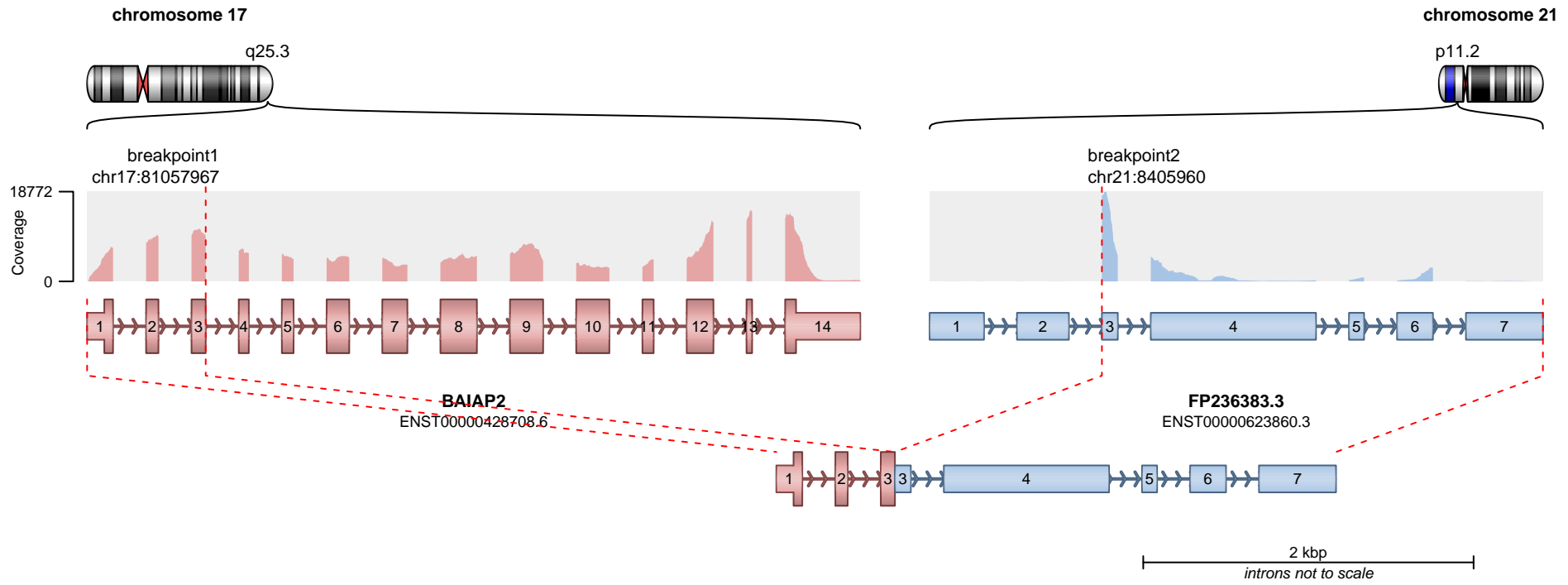


— translocation    — deletion  
 — duplication    — inversion

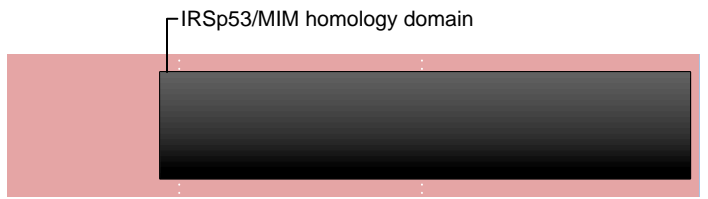
Genes are not protein-coding.

**SUPPORTING READ COUNT**

Split reads = 72  
Discordant mates = 1



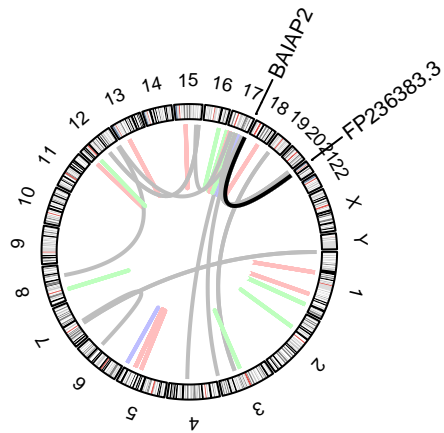
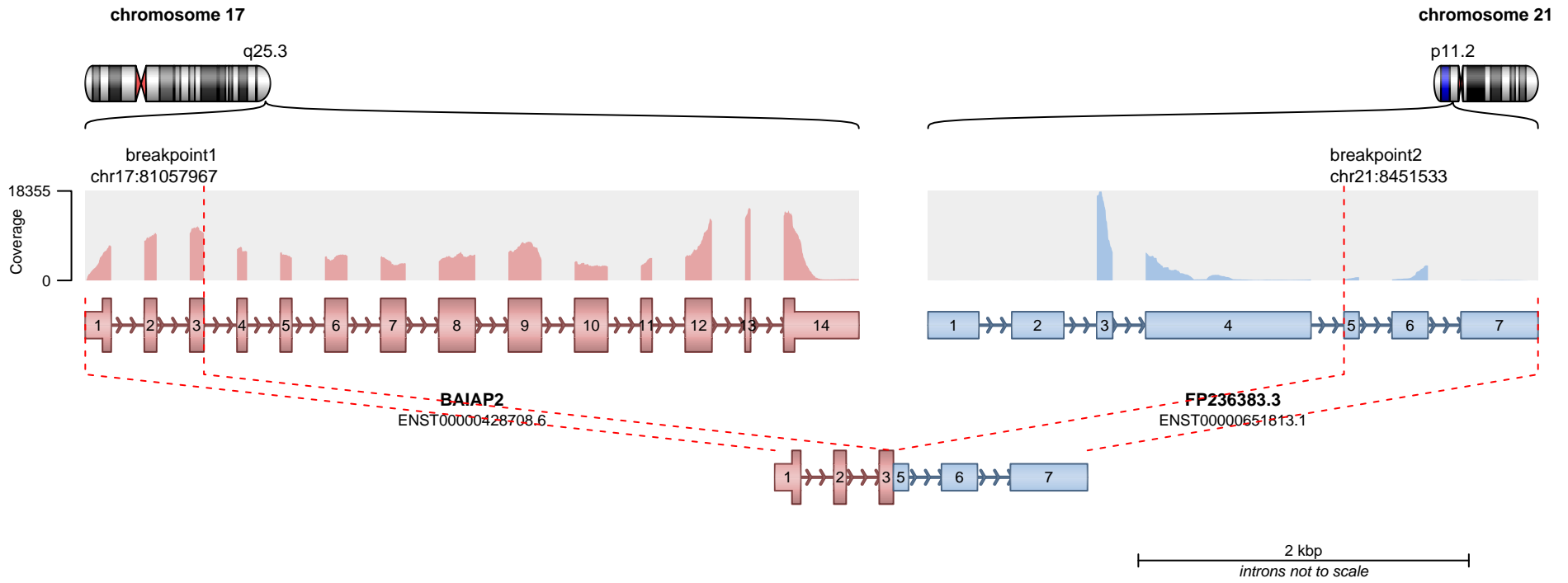
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 58  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



**RETAINED PROTEIN DOMAINS**  
reading frame unclear

IRSp53/MIM homology domain

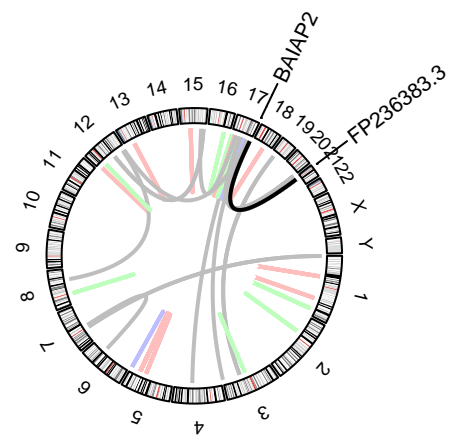
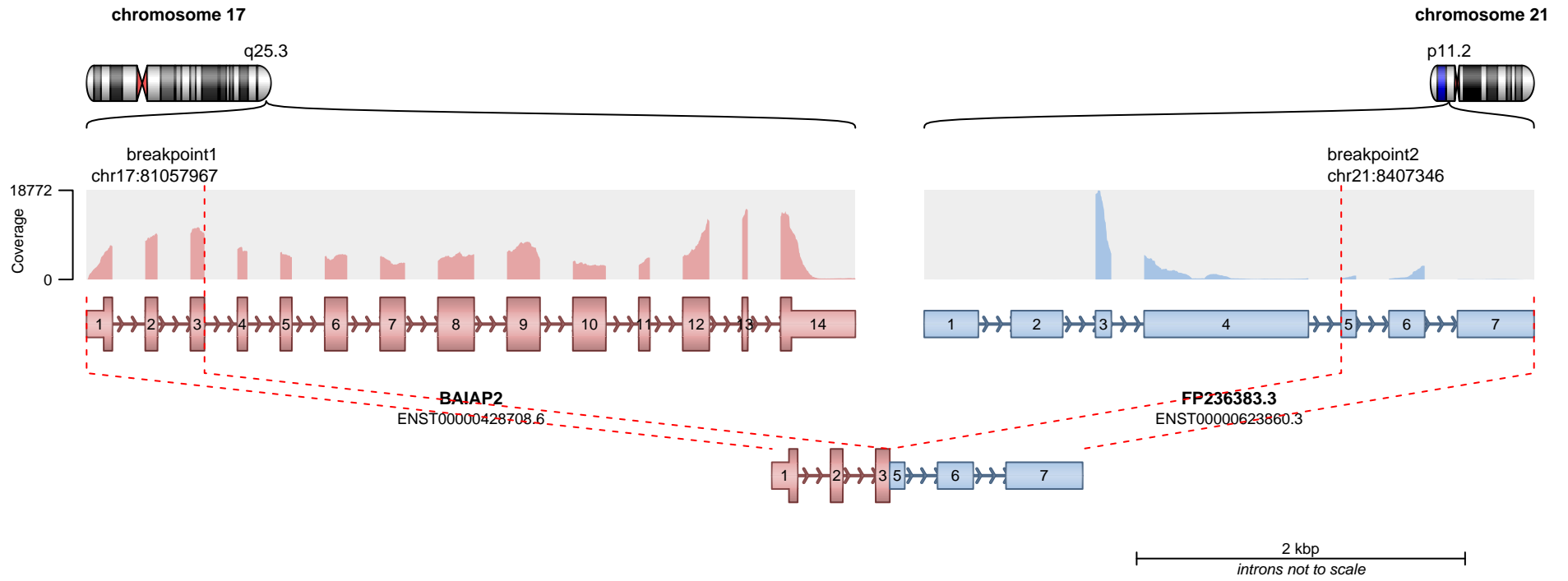


**BAIAP2**

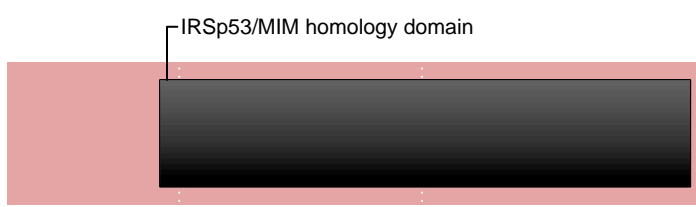
**SUPPORTING READ COUNT**

Split reads = 15  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



**RETAINED PROTEIN DOMAINS**  
reading frame unclear

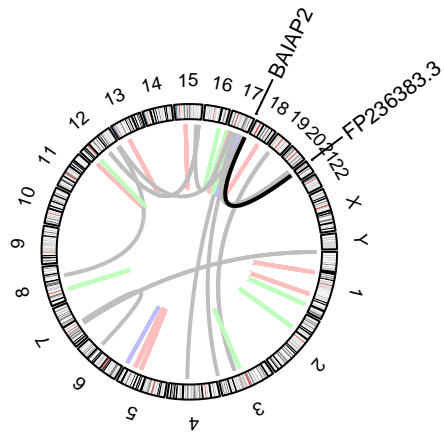
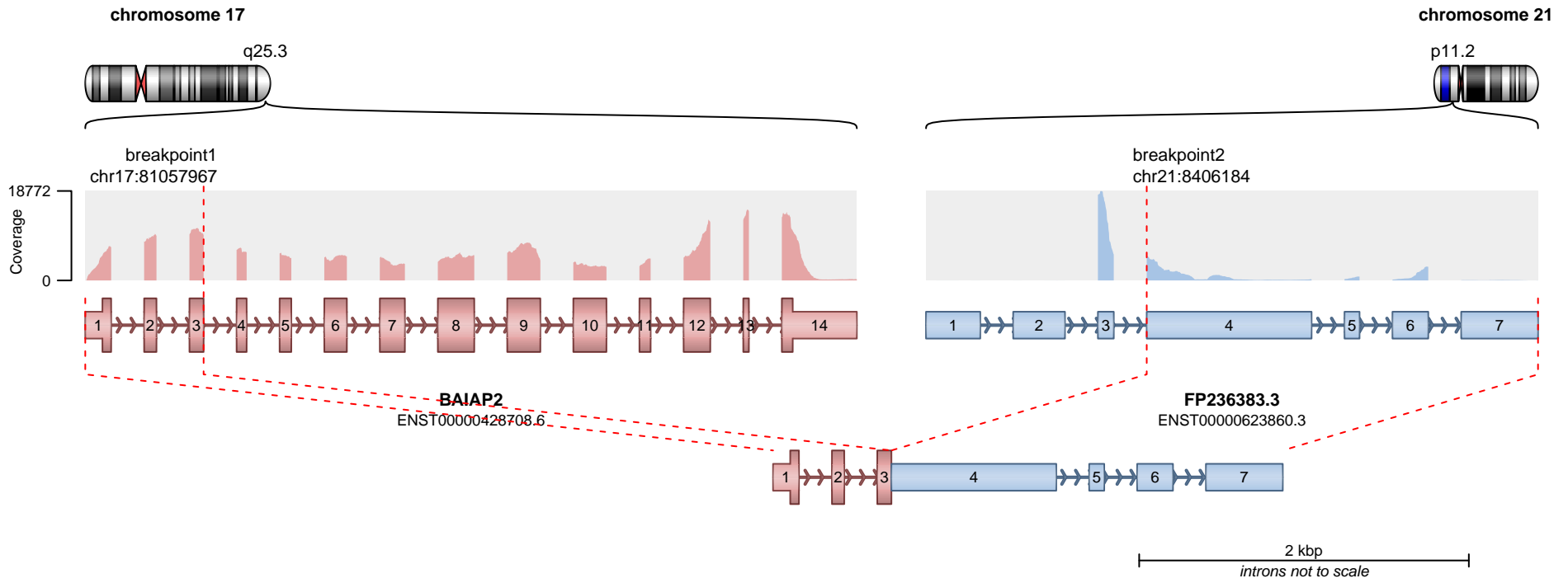


**BAIAP2**

**SUPPORTING READ COUNT**

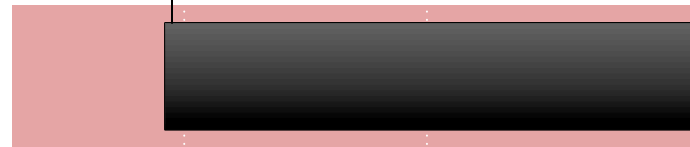
Split reads = 15  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



**RETAINED PROTEIN DOMAINS**  
reading frame unclear

IRSp53/MIM homology domain

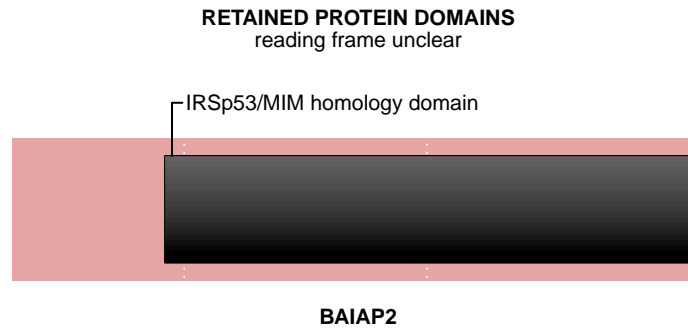
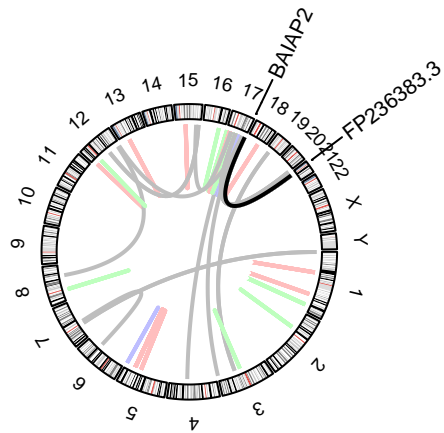
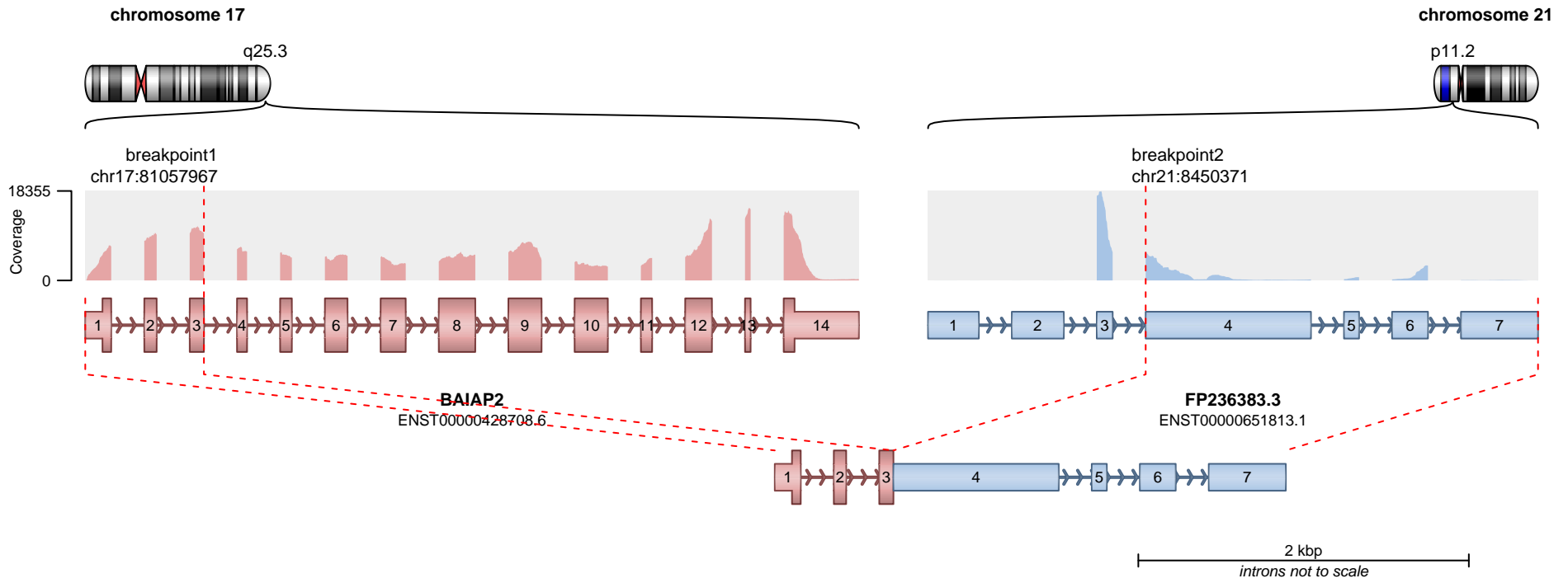


**BAIAP2**

**SUPPORTING READ COUNT**

Split reads = 7  
Discordant mates = 0

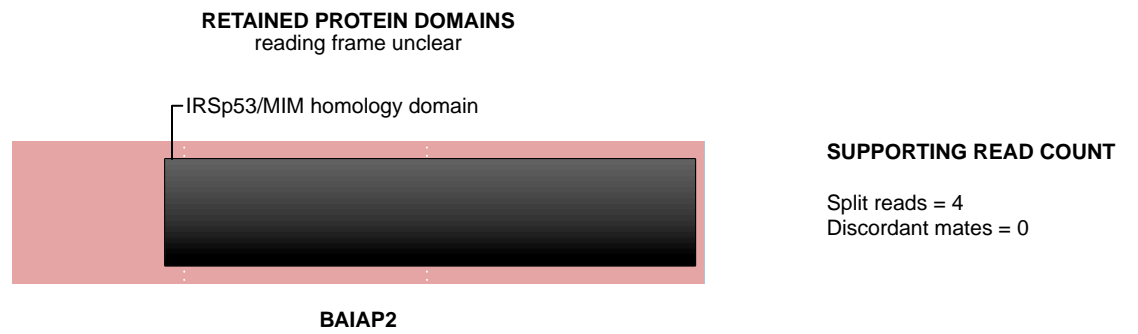
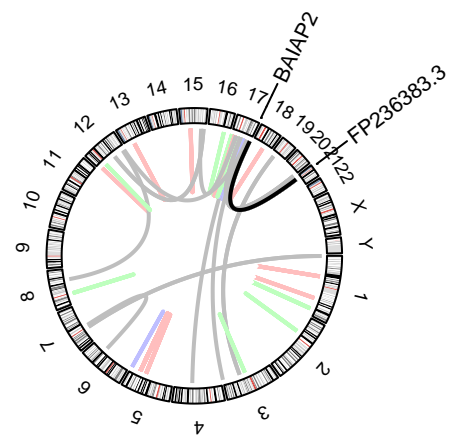
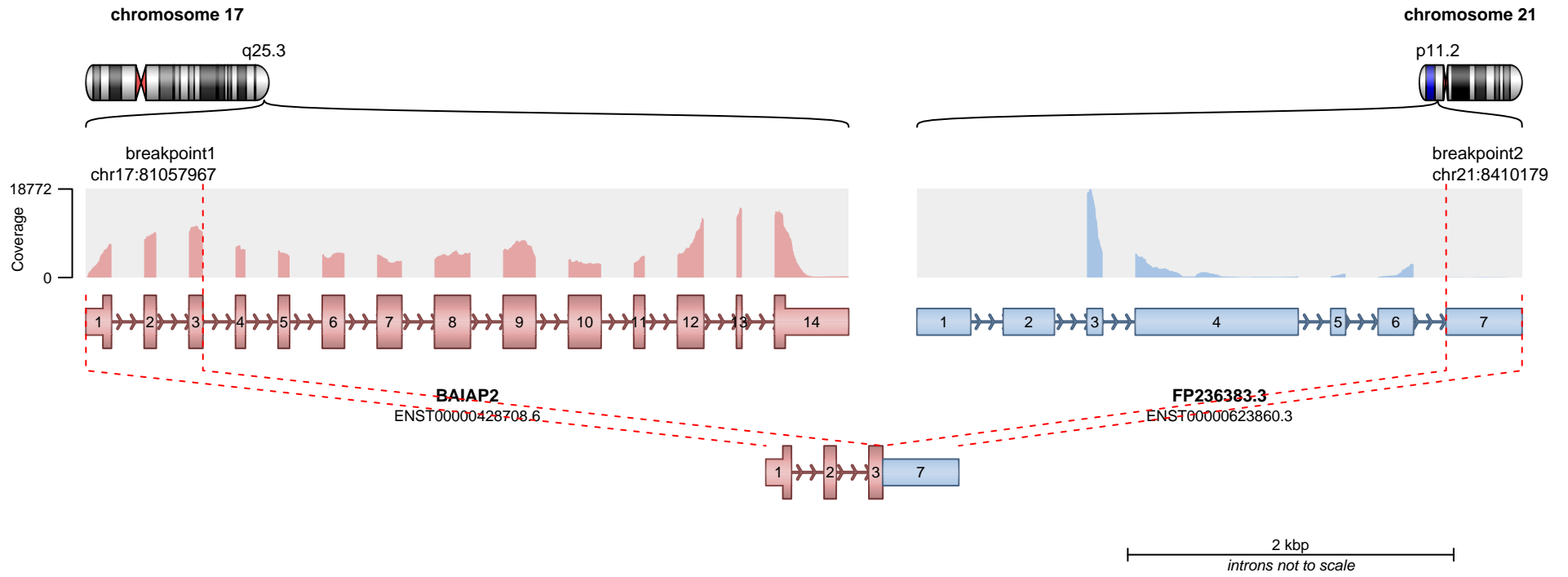
- translocation
- duplication
- deletion
- inversion



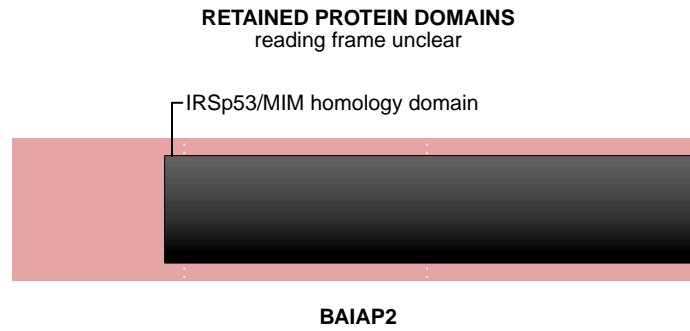
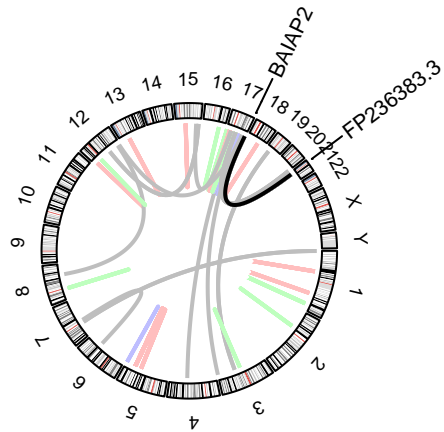
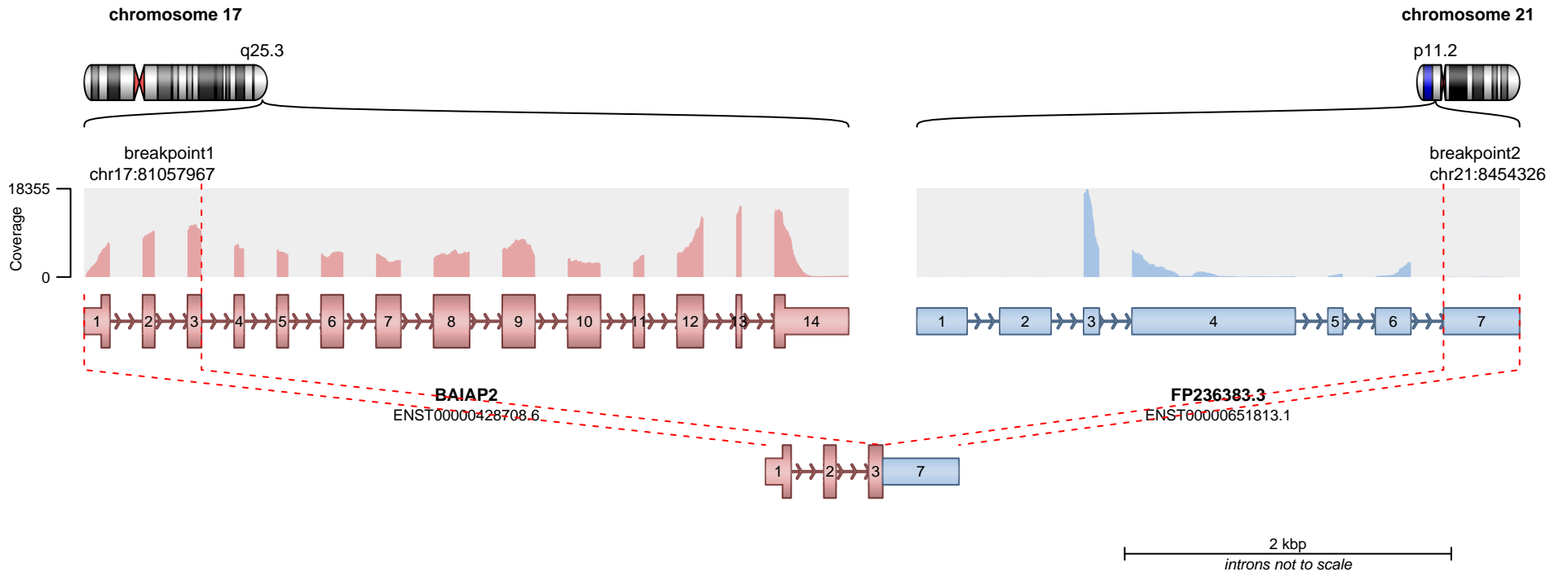
**SUPPORTING READ COUNT**

Split reads = 7  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



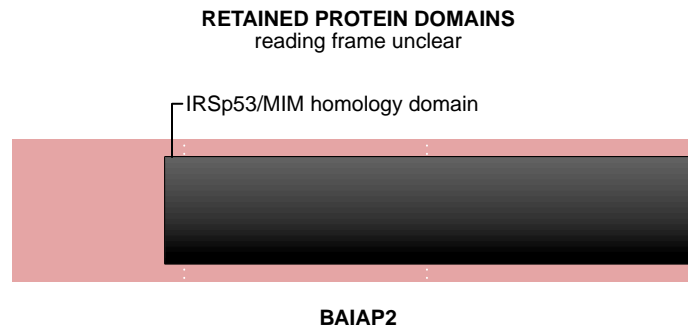
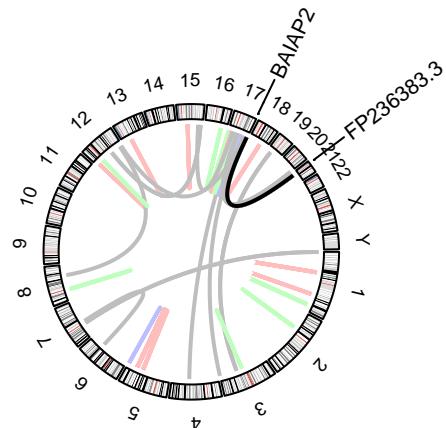
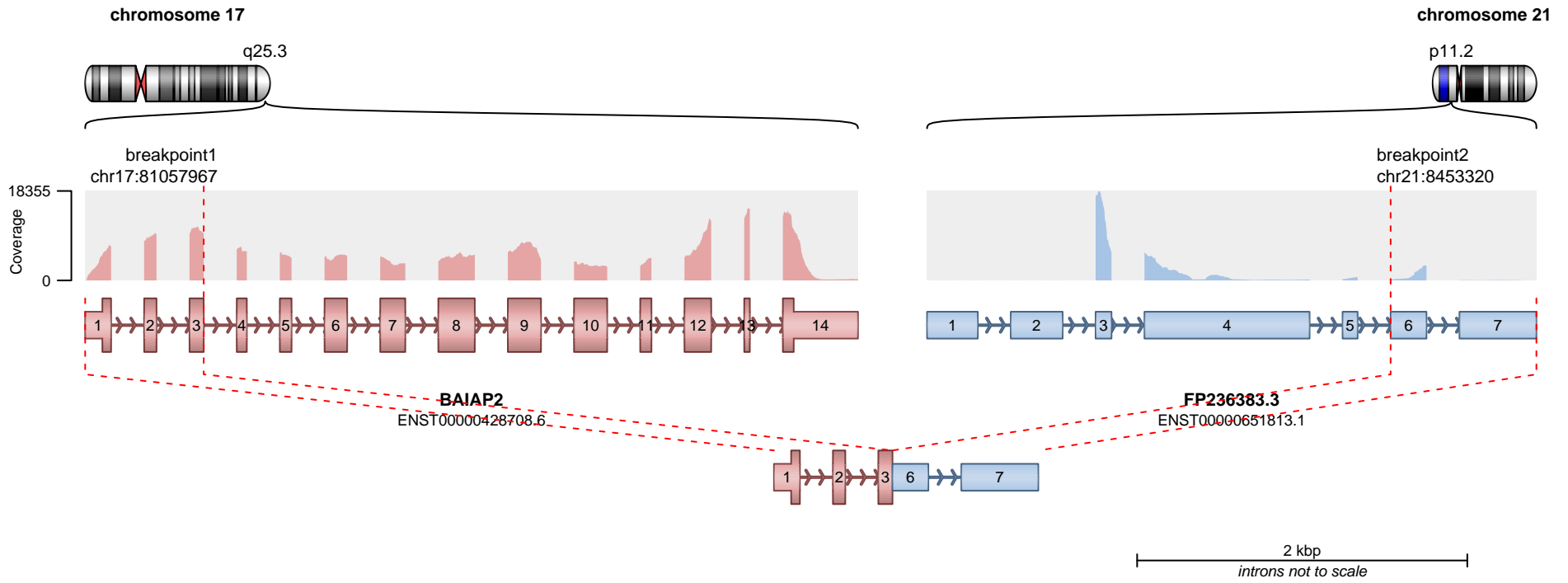
— translocation    — deletion  
 — duplication    — inversion



**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 0

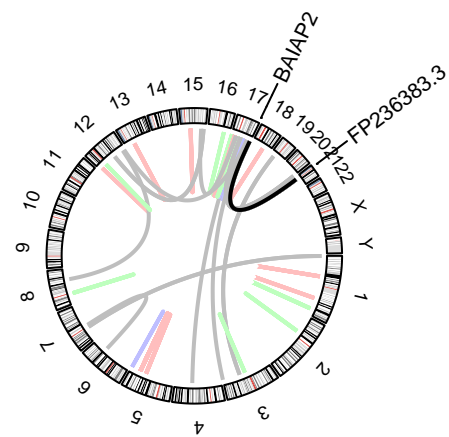
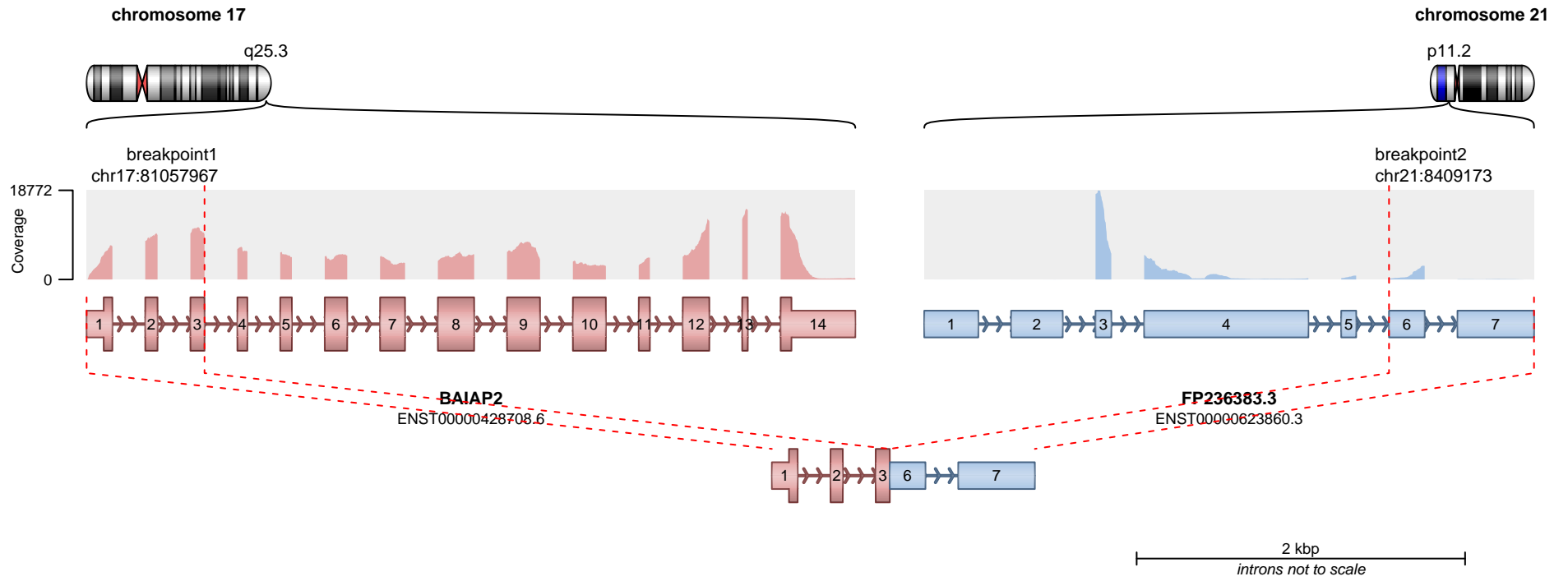
— translocation    — deletion  
— duplication    — inversion



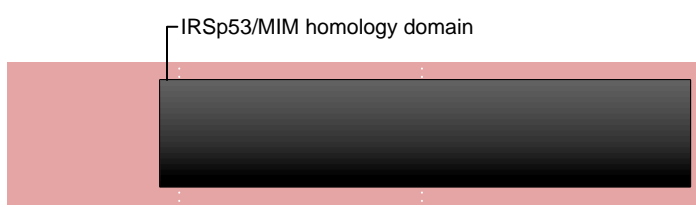
**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



**RETAINED PROTEIN DOMAINS**  
reading frame unclear

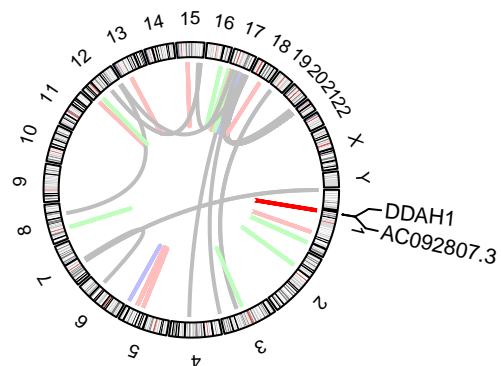
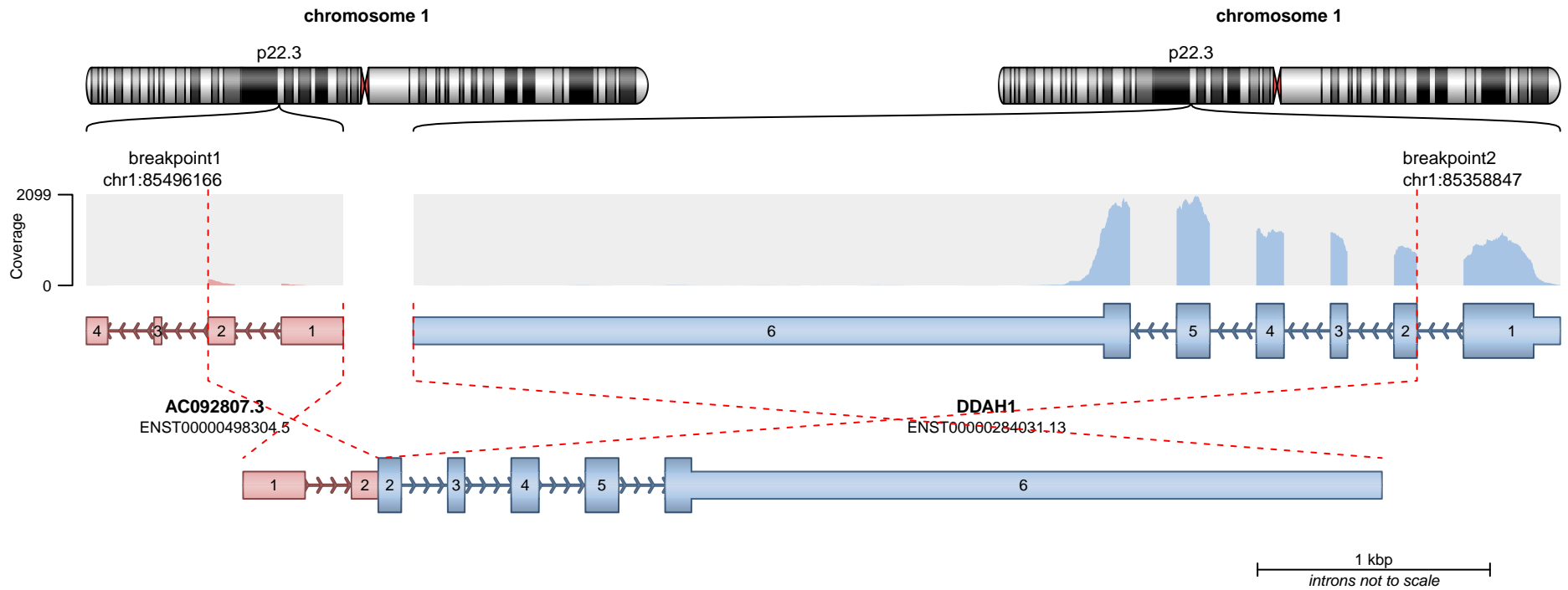


**BAIAP2**

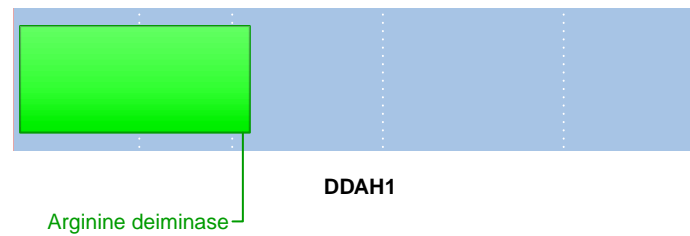
**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



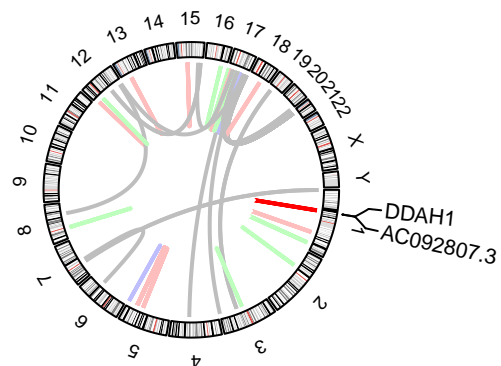
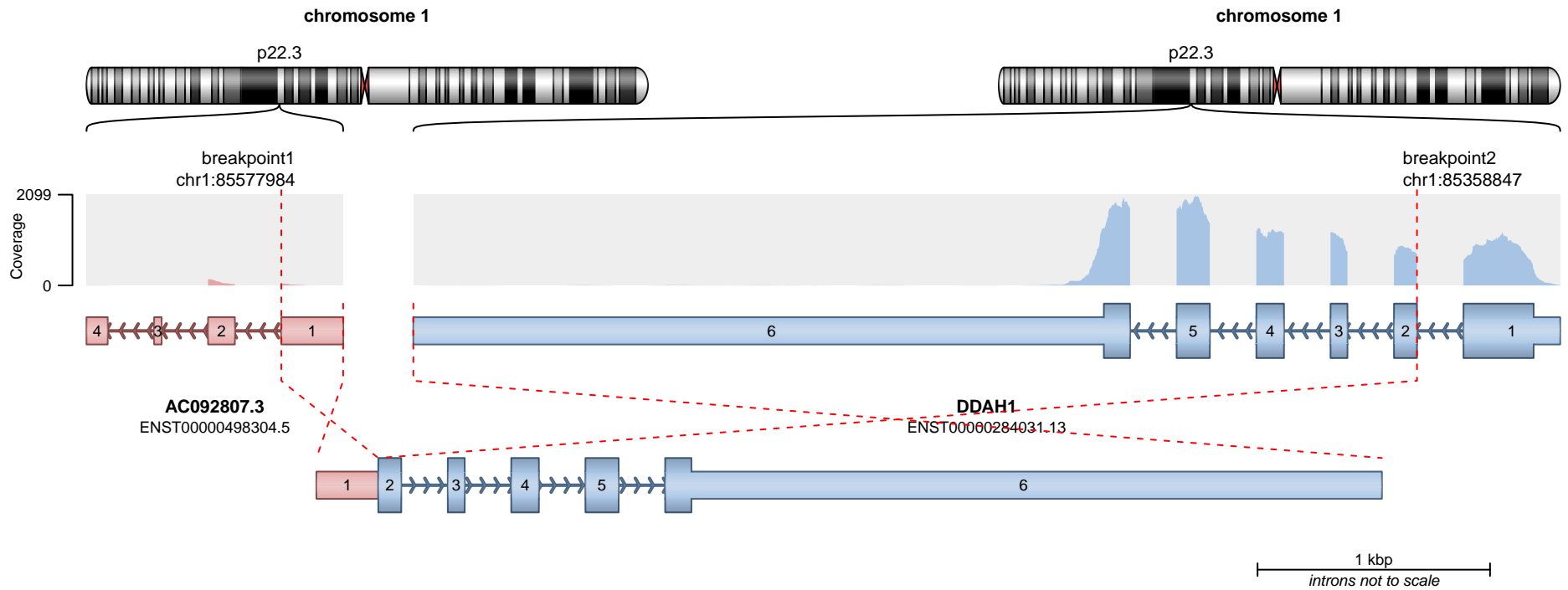
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



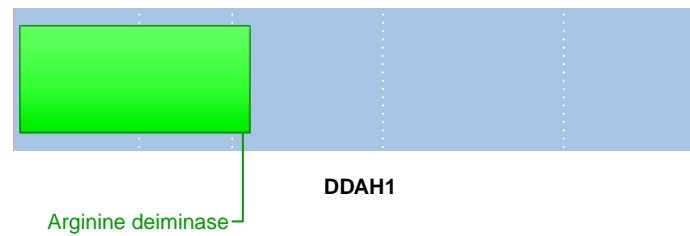
**SUPPORTING READ COUNT**

Split reads = 54  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



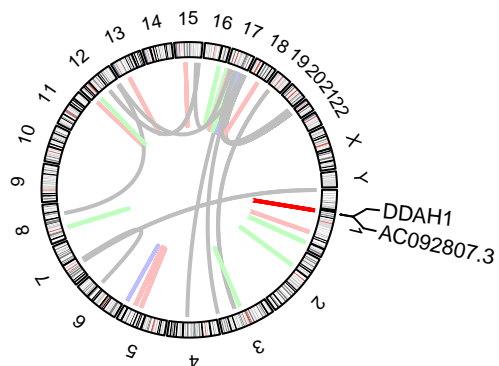
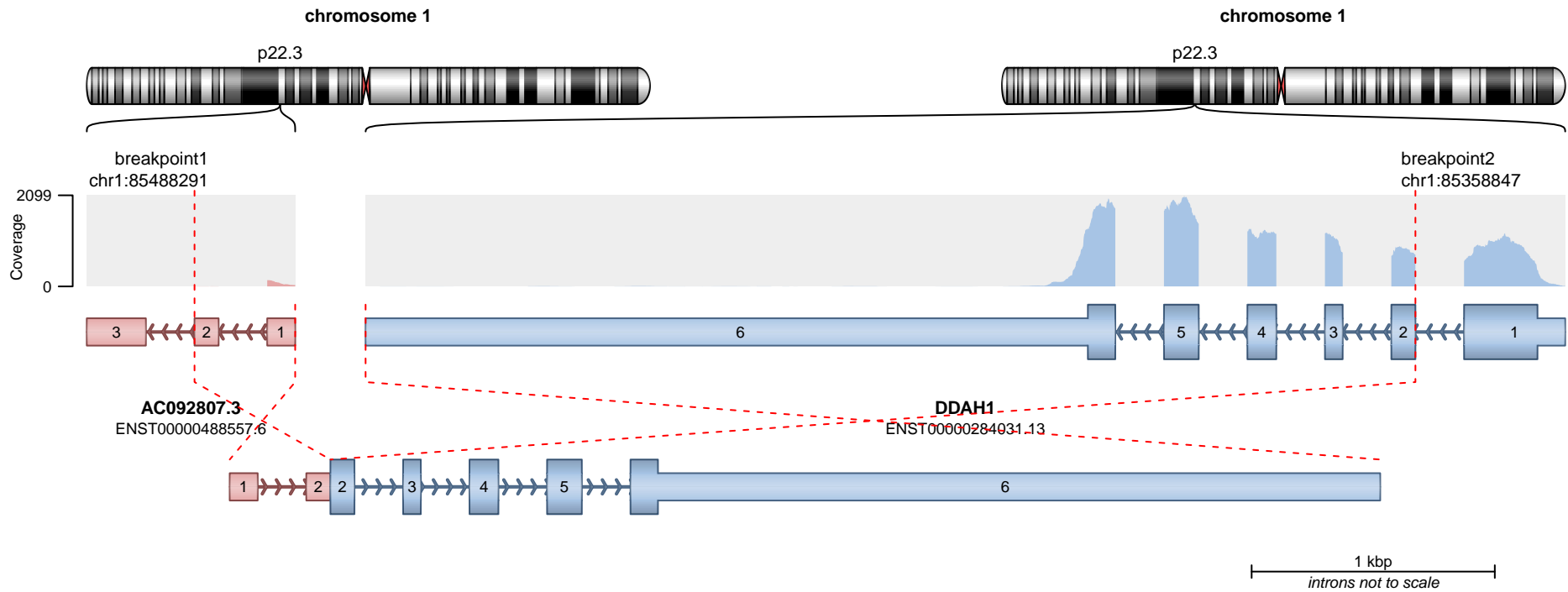
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



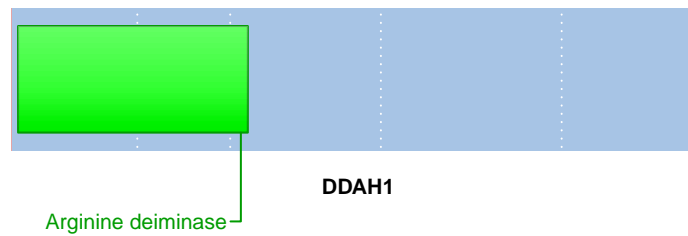
**SUPPORTING READ COUNT**

Split reads = 8  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



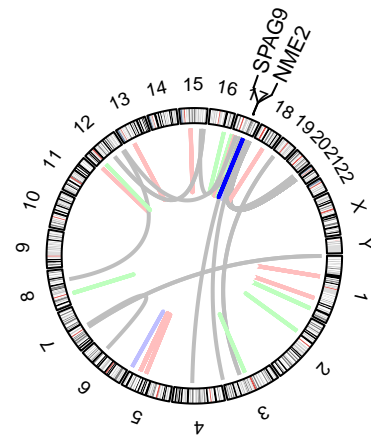
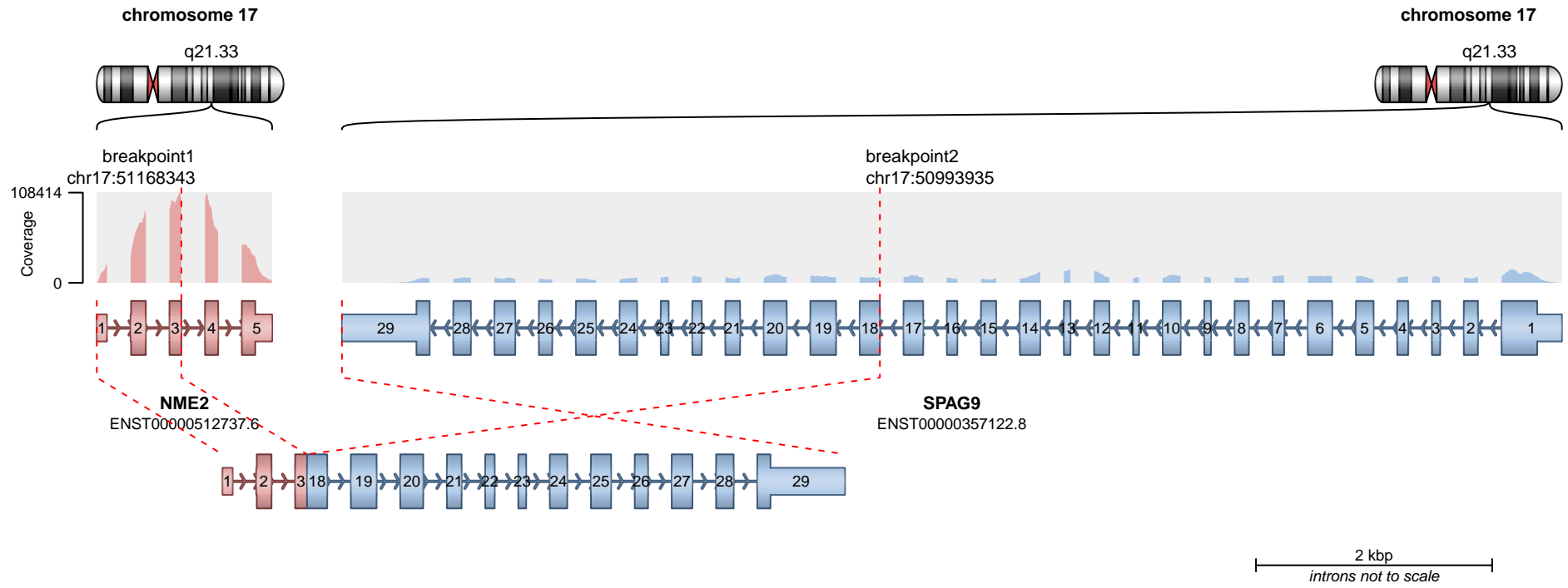
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

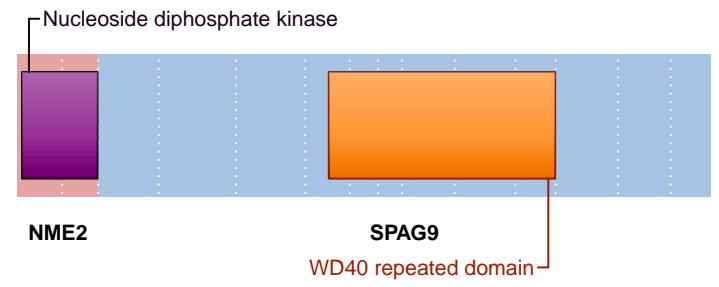
Split reads = 1  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



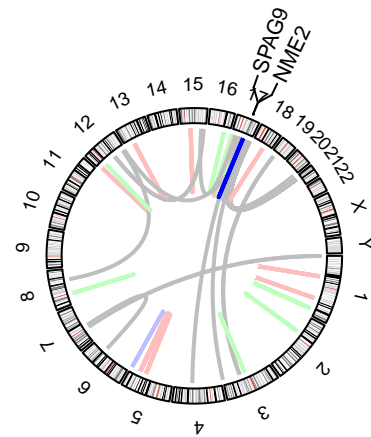
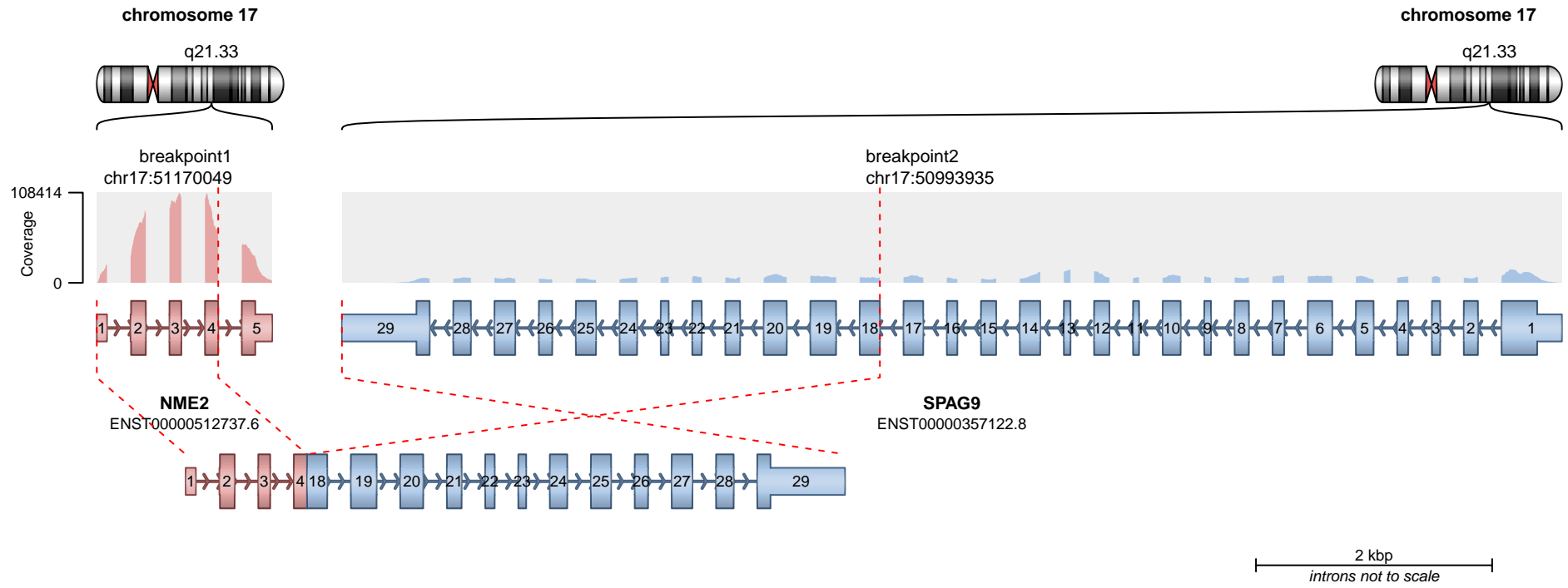
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear

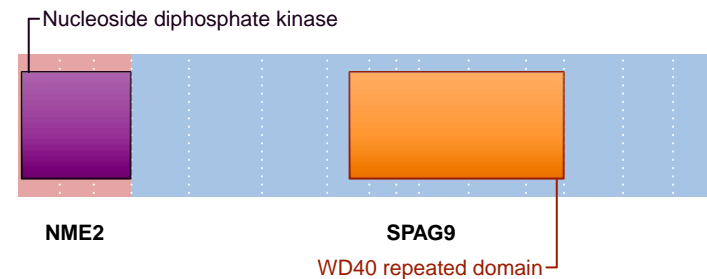


**SUPPORTING READ COUNT**

Split reads = 52  
Discordant mates = 1



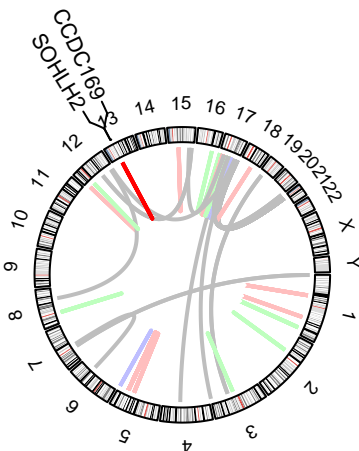
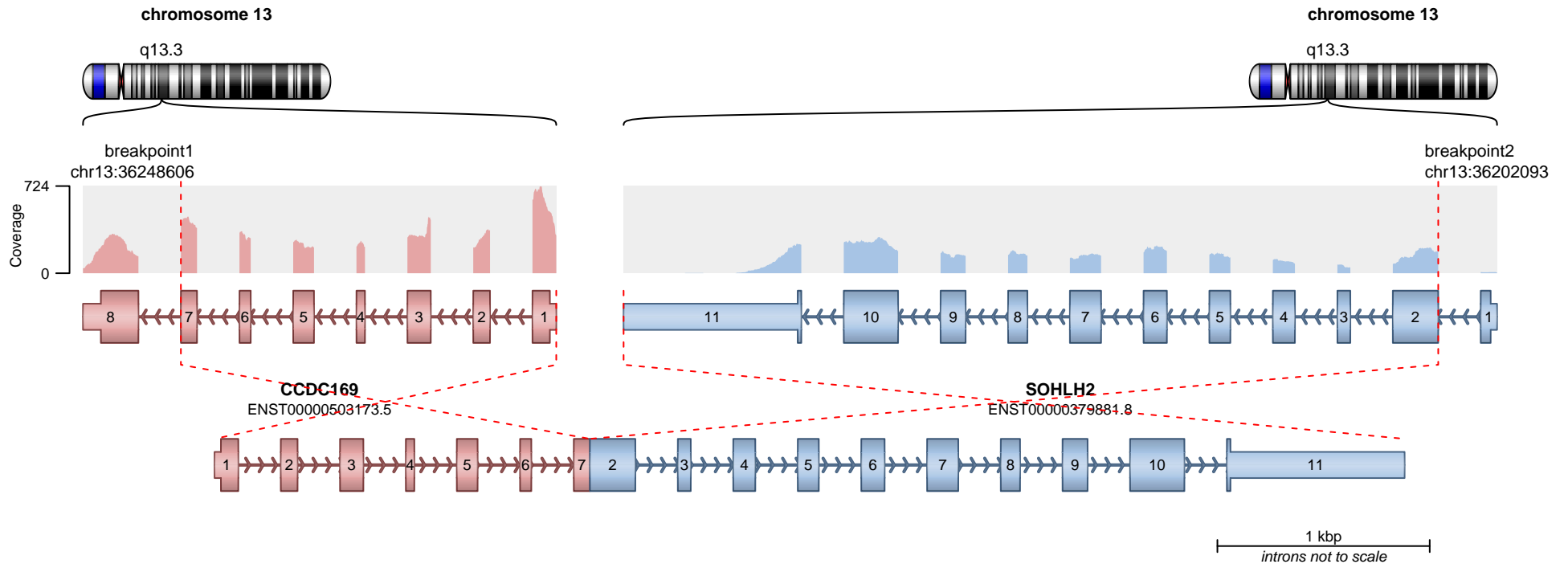
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



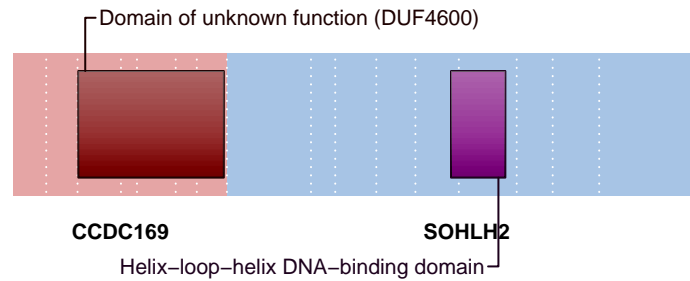
**SUPPORTING READ COUNT**

Split reads = 6  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



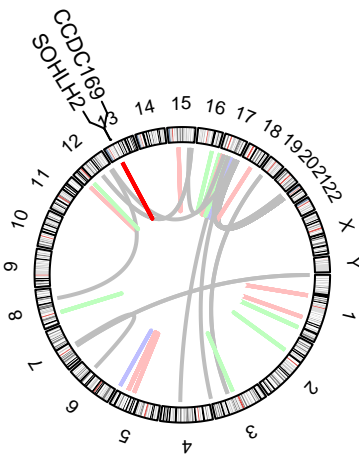
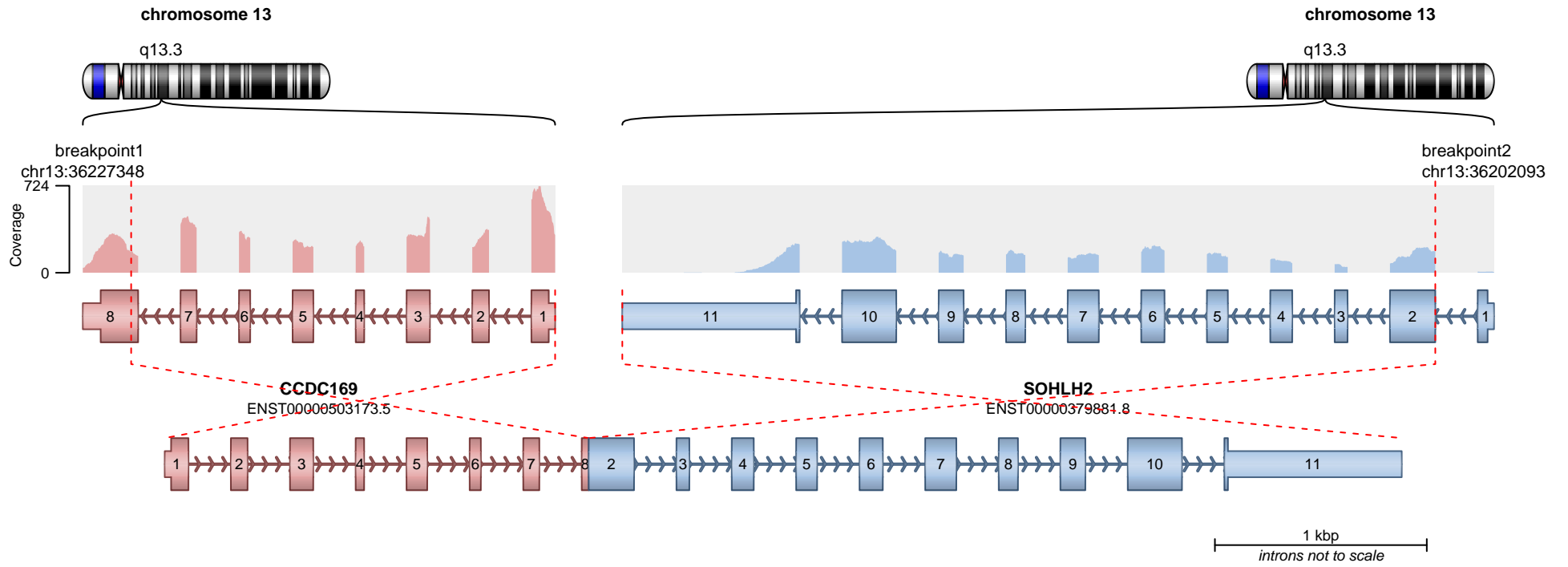
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



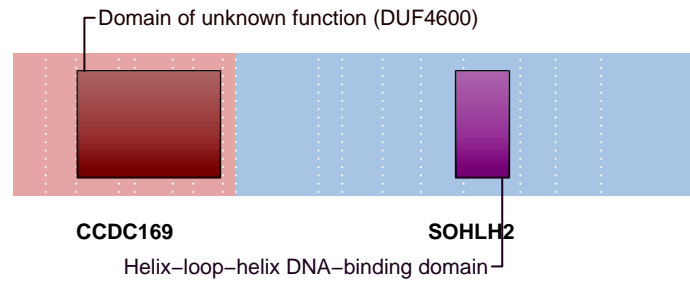
**SUPPORTING READ COUNT**

Split reads = 48  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



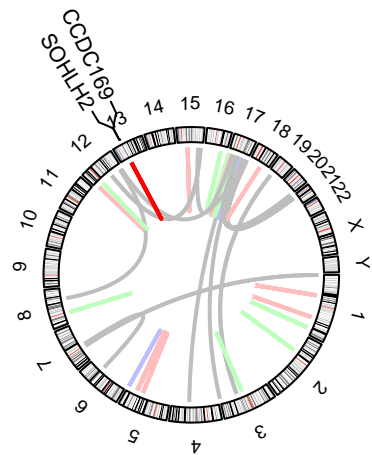
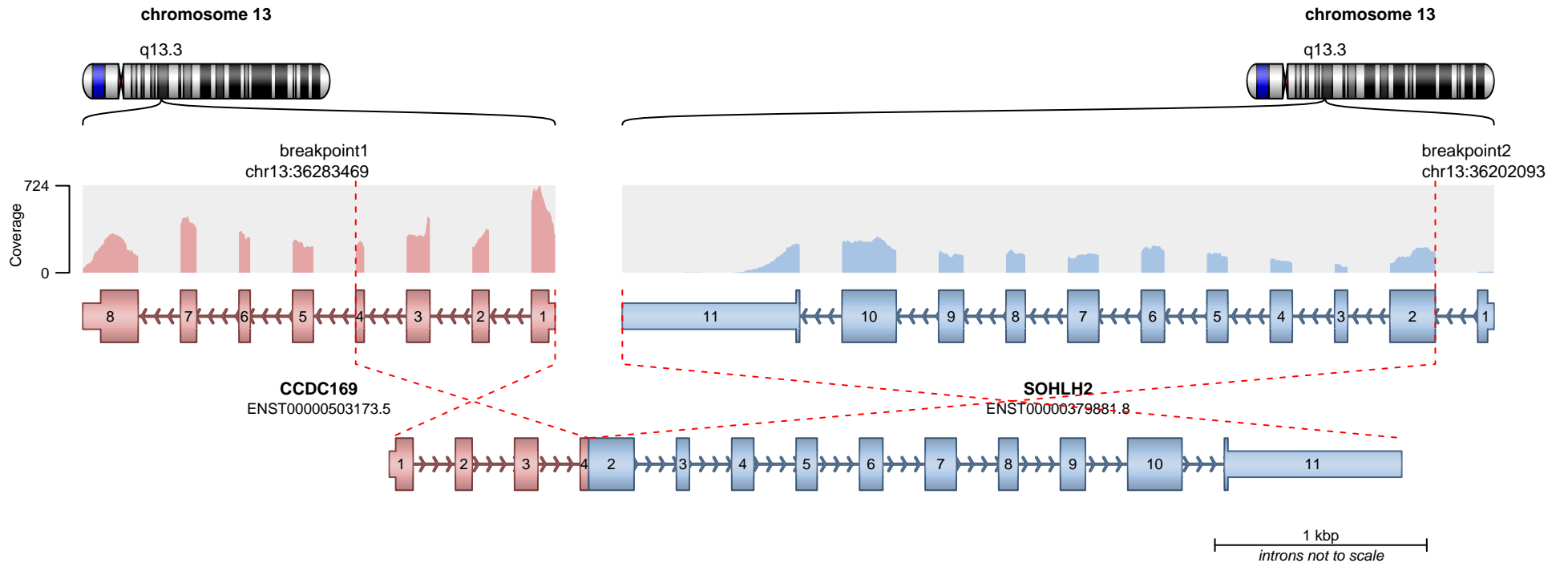
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



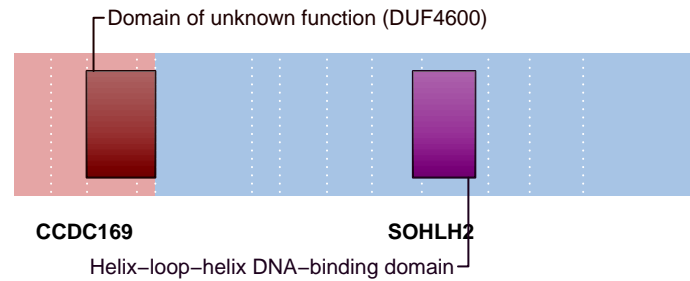
**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



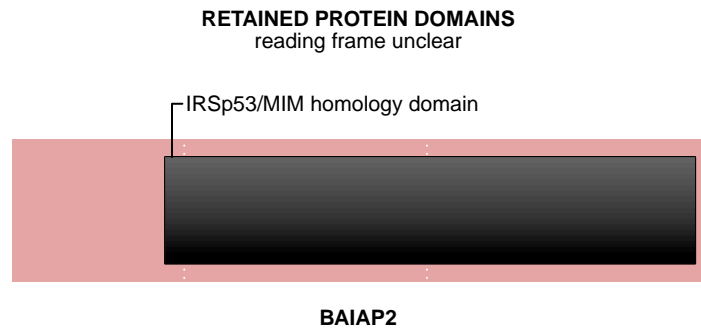
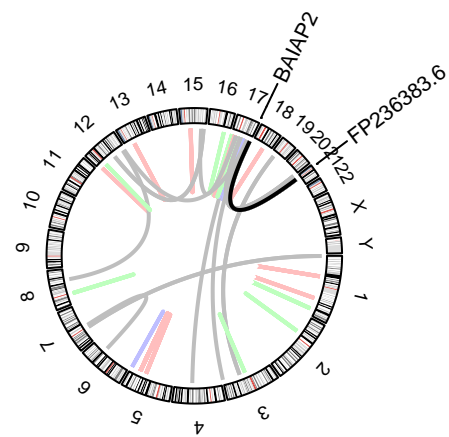
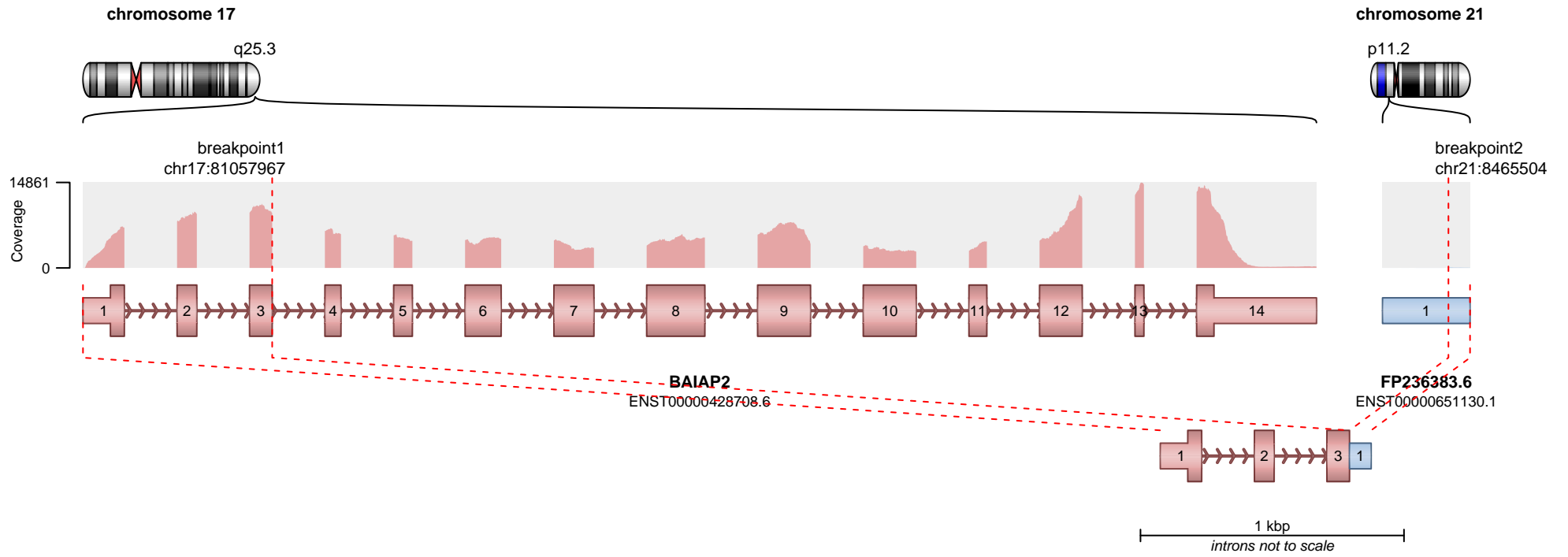
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

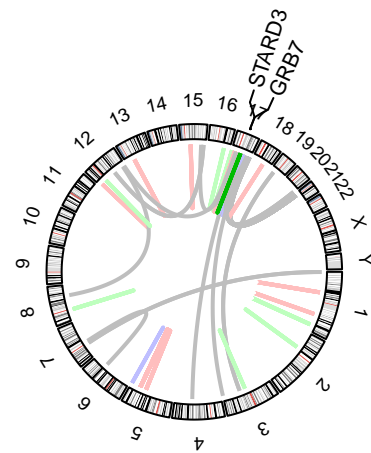
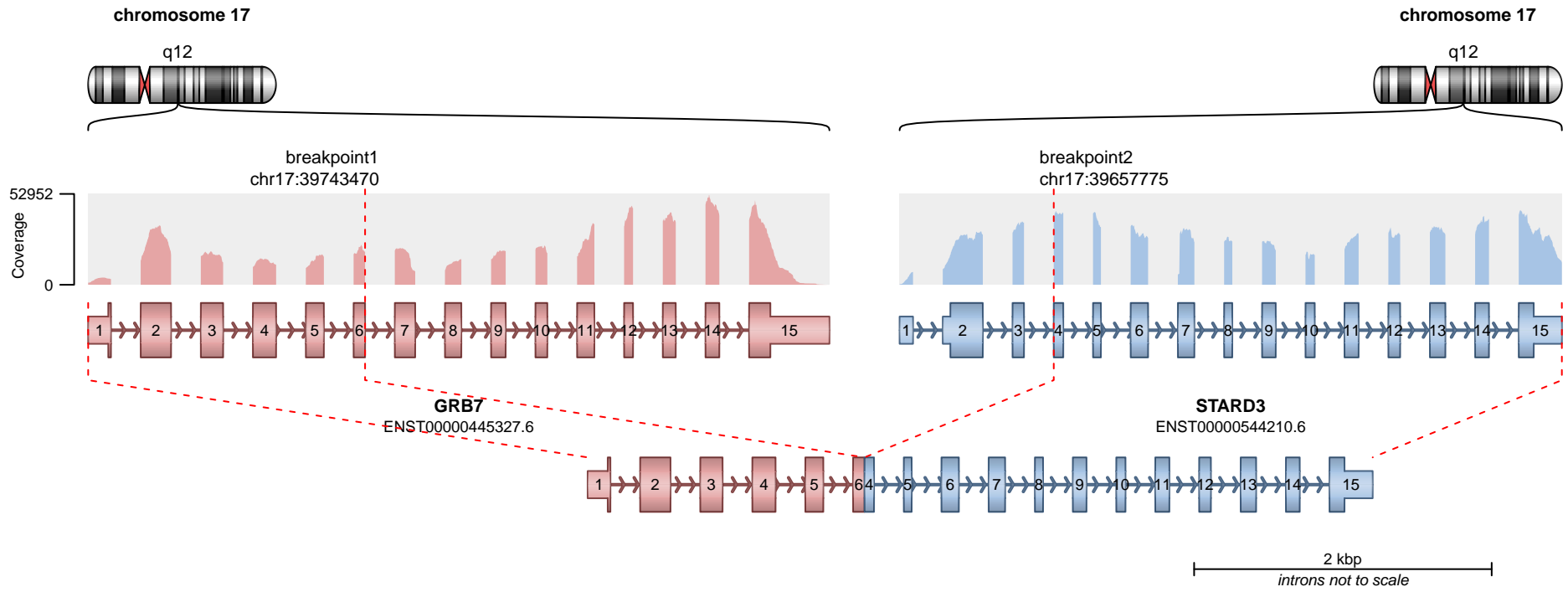
— translocation    — deletion  
— duplication    — inversion



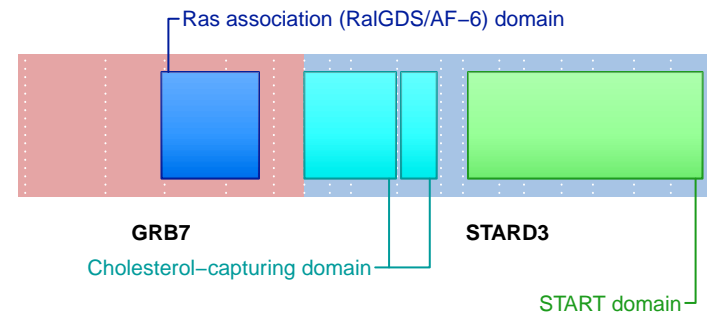
**SUPPORTING READ COUNT**

Split reads = 43  
Discordant mates = 1

— translocation    — deletion  
— duplication    — inversion



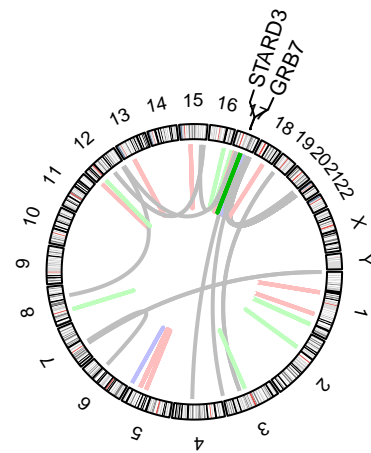
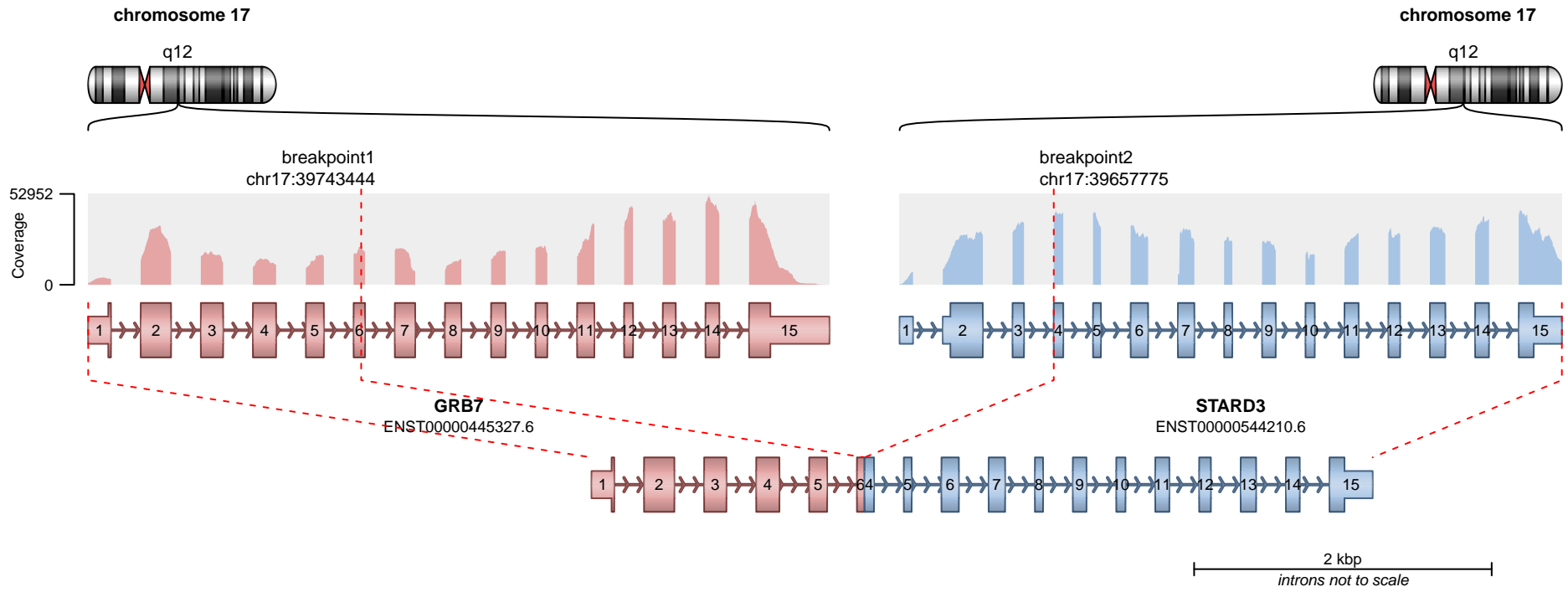
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



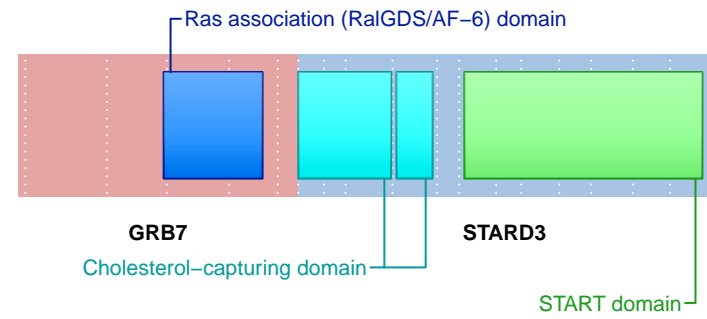
**SUPPORTING READ COUNT**

Split reads = 34  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



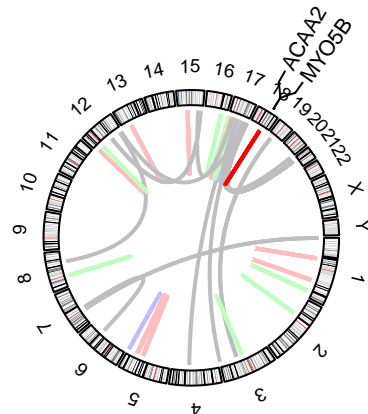
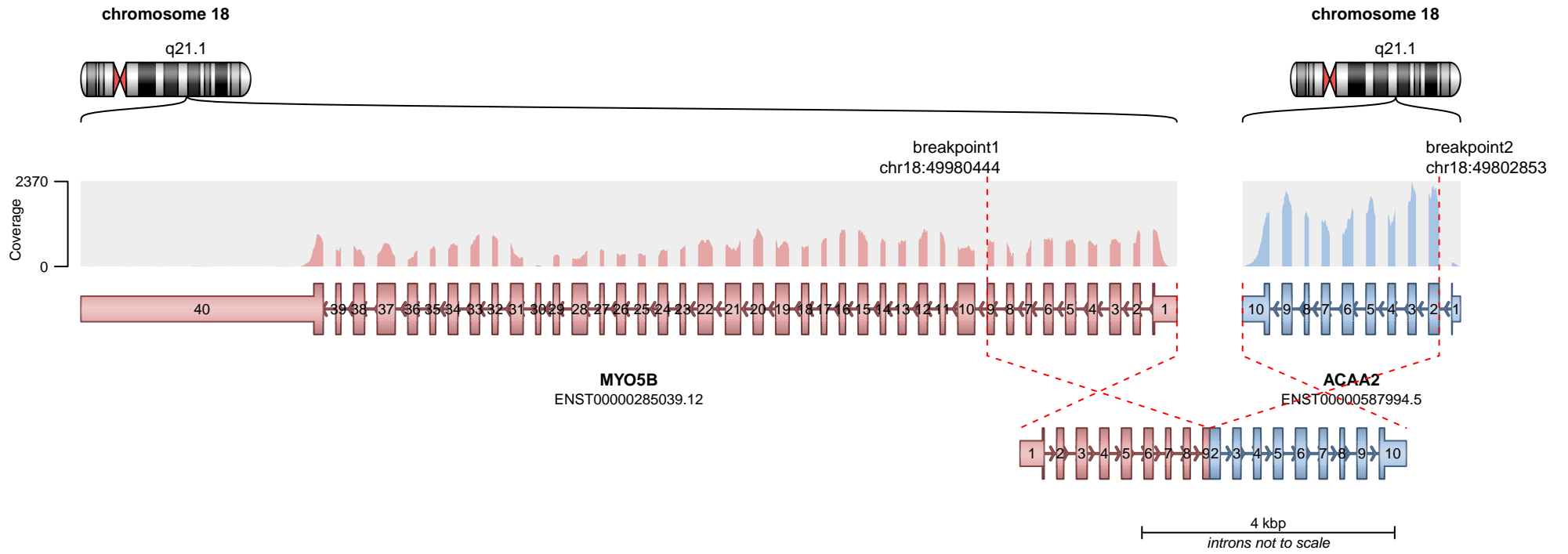
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



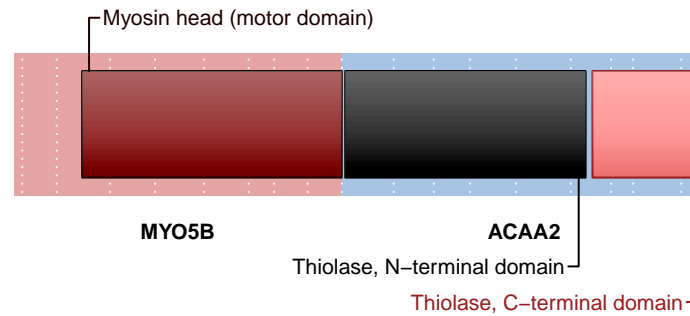
**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



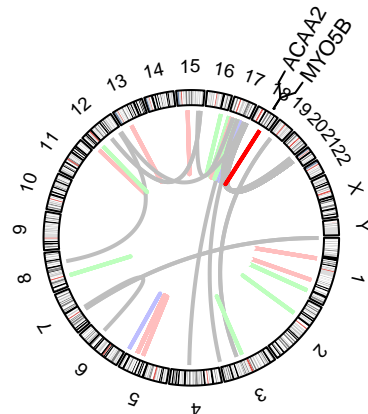
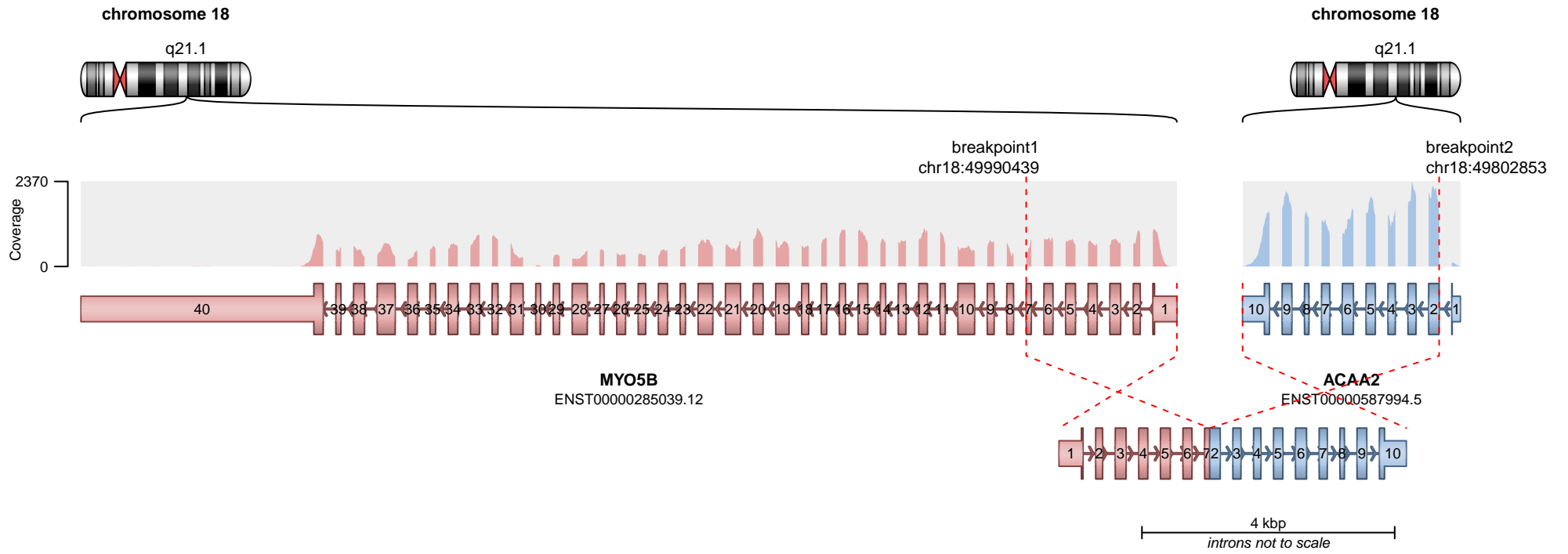
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



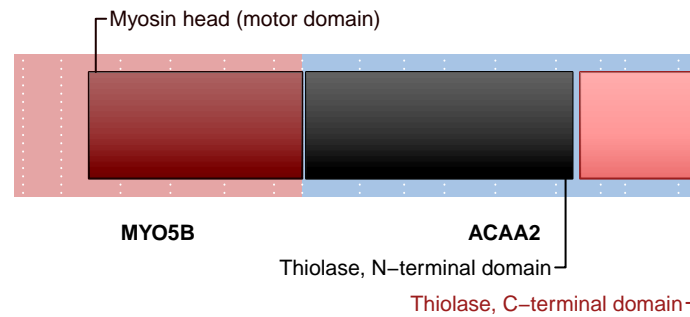
**SUPPORTING READ COUNT**

Split reads = 33  
Discordant mates = 2

- translocation
- duplication
- deletion
- inversion



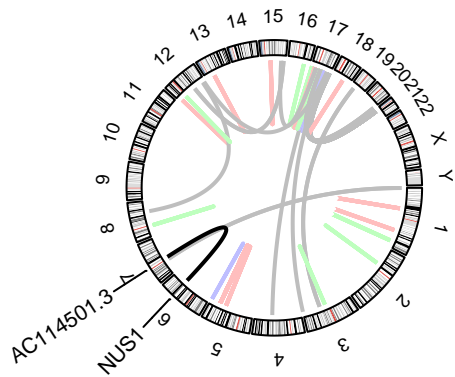
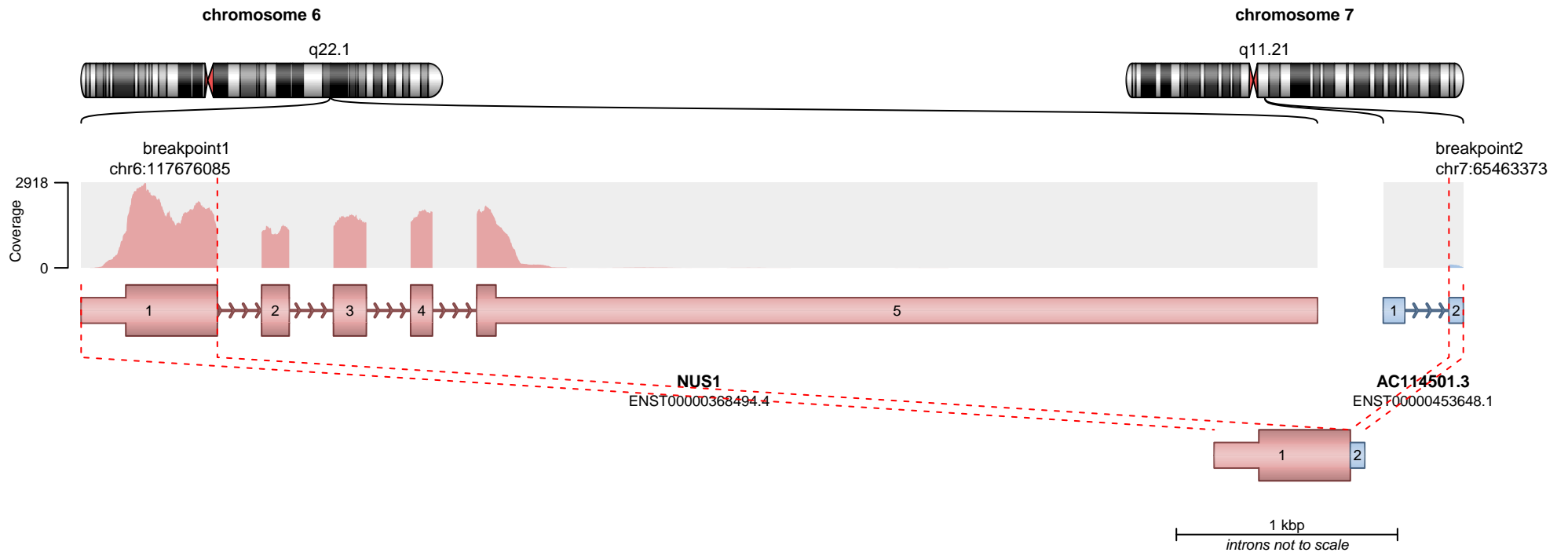
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

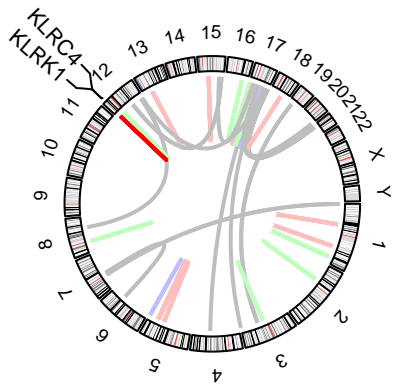
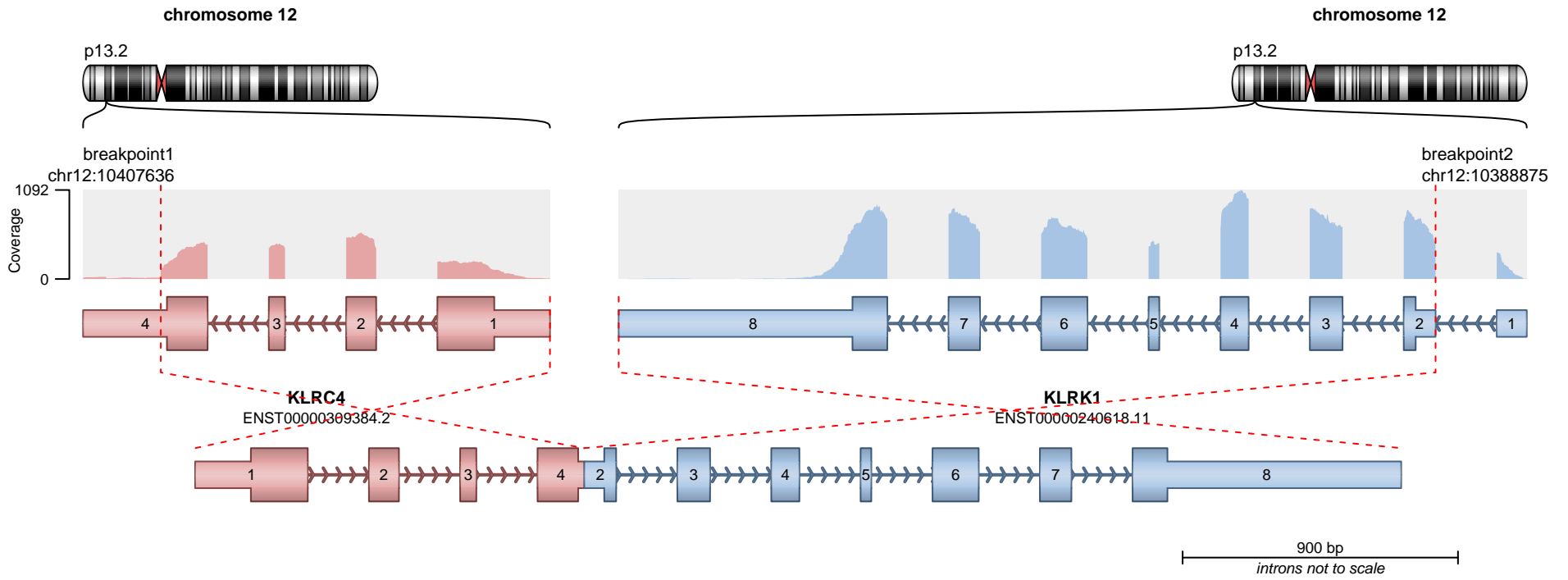


— translocation    — deletion  
— duplication      — inversion

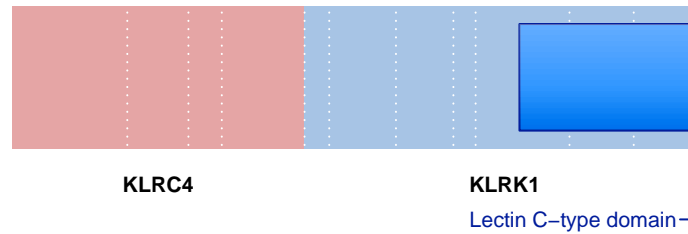
No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 32  
Discordant mates = 0



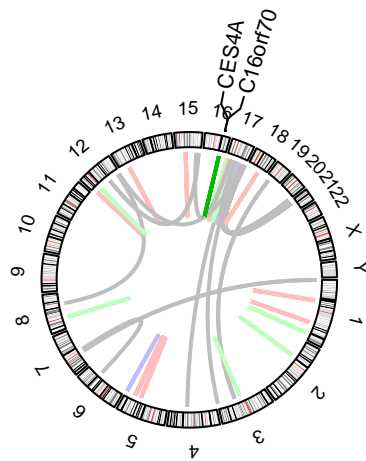
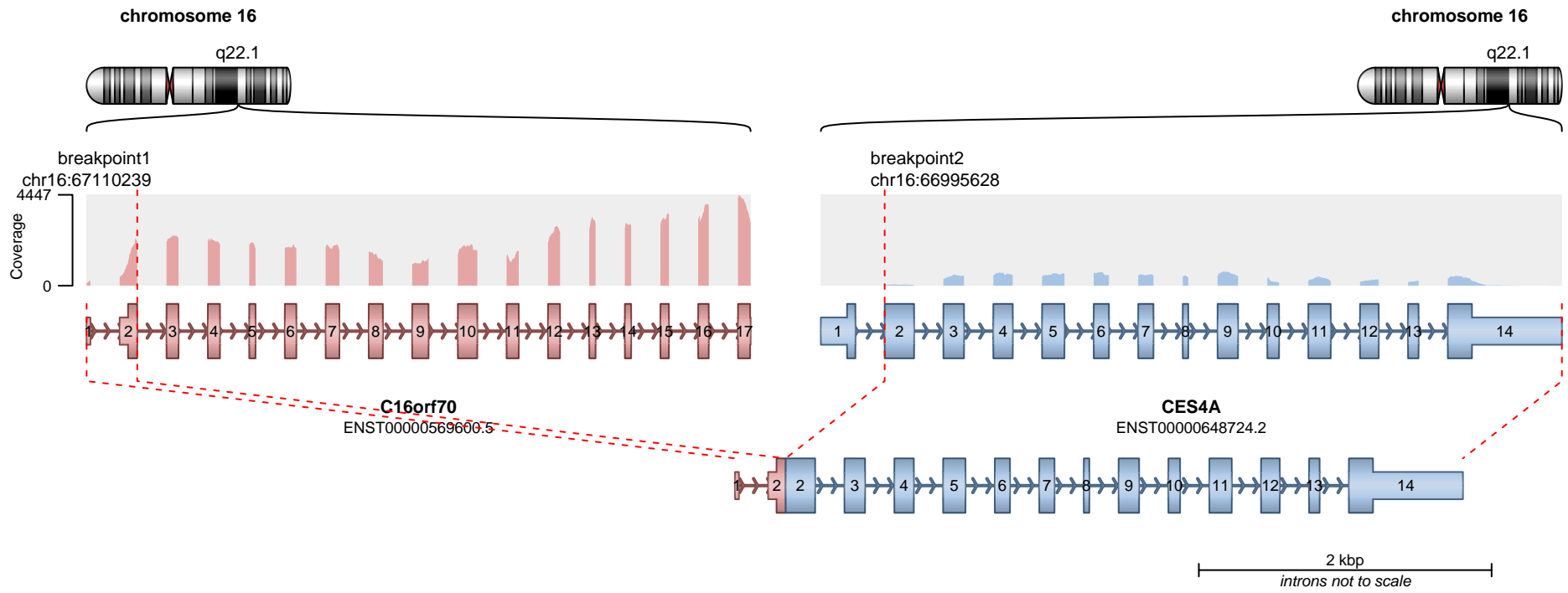
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



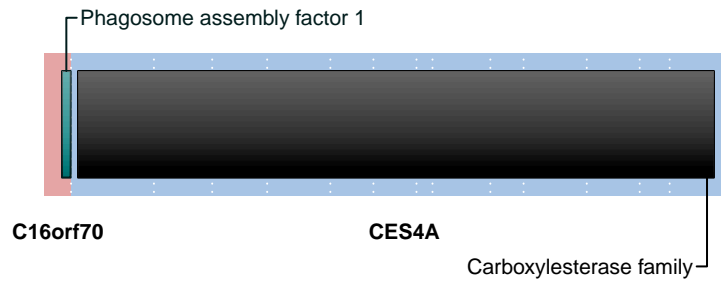
**SUPPORTING READ COUNT**

Split reads = 31  
Discordant mates = 2

— translocation — deletion  
— duplication — inversion



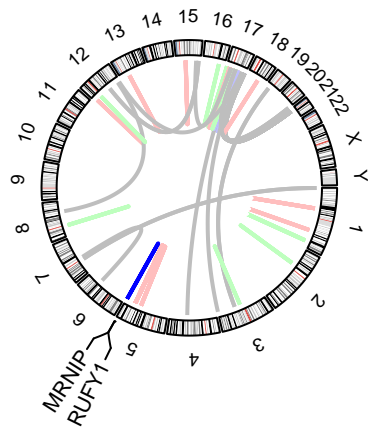
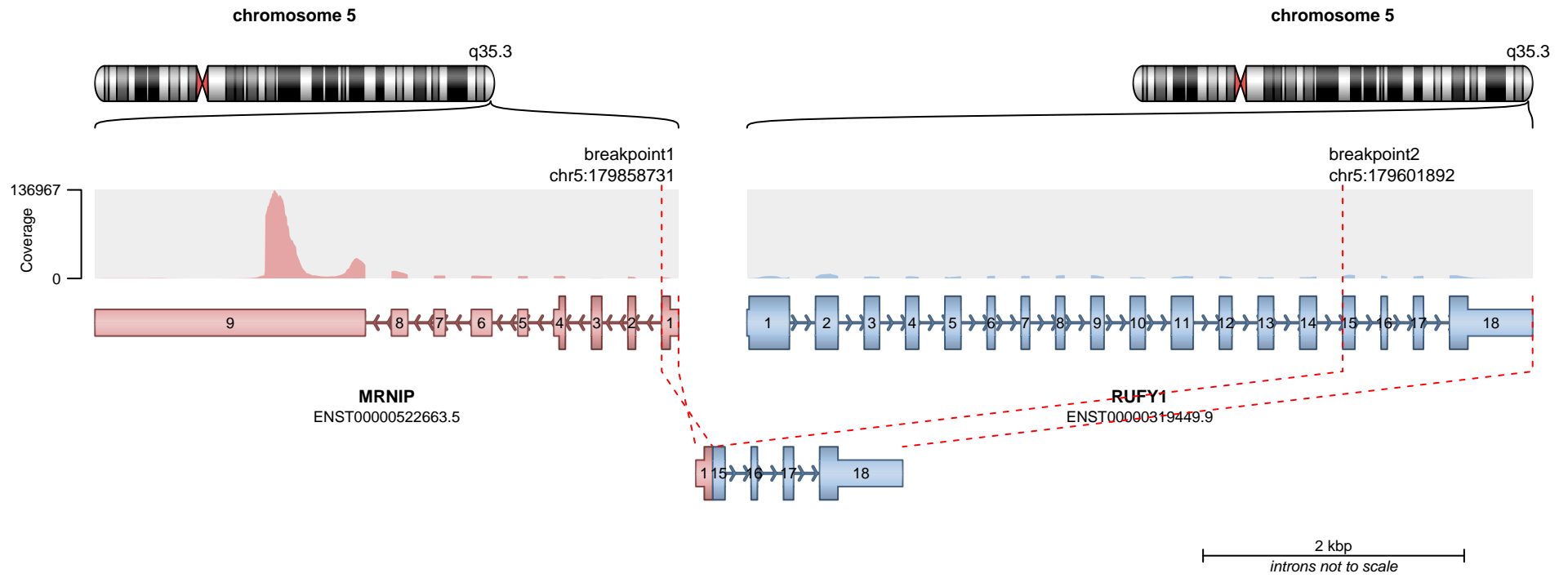
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

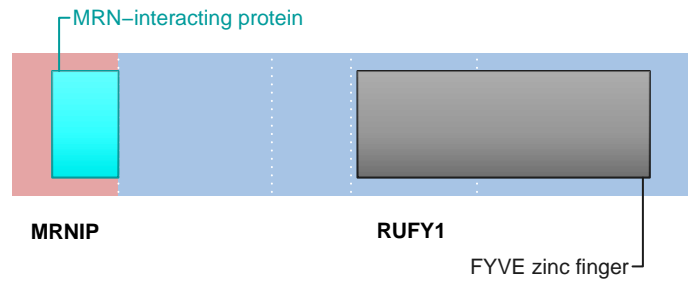
Split reads = 27  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



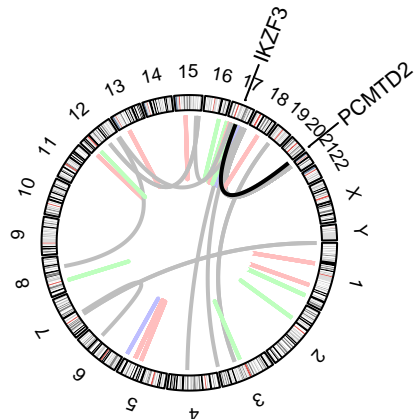
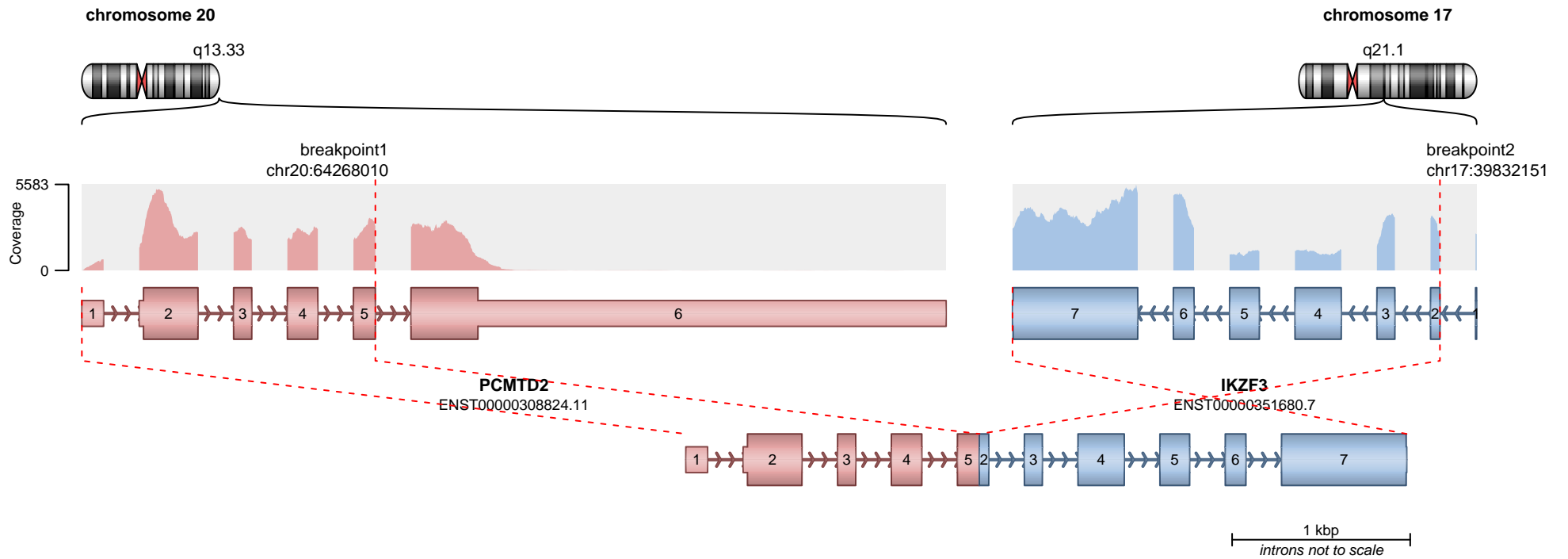
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear

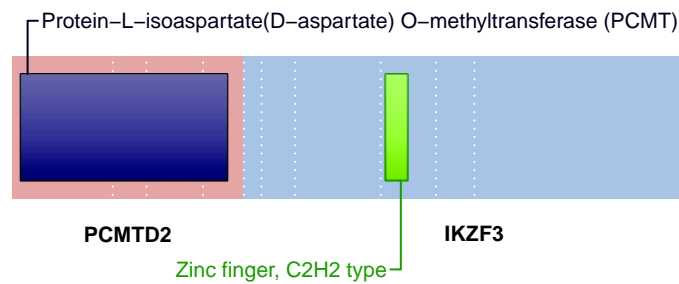


**SUPPORTING READ COUNT**

Split reads = 27  
Discordant mates = 0



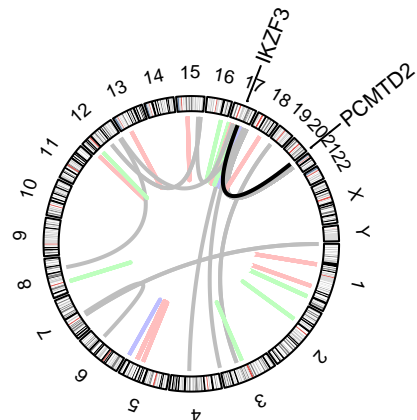
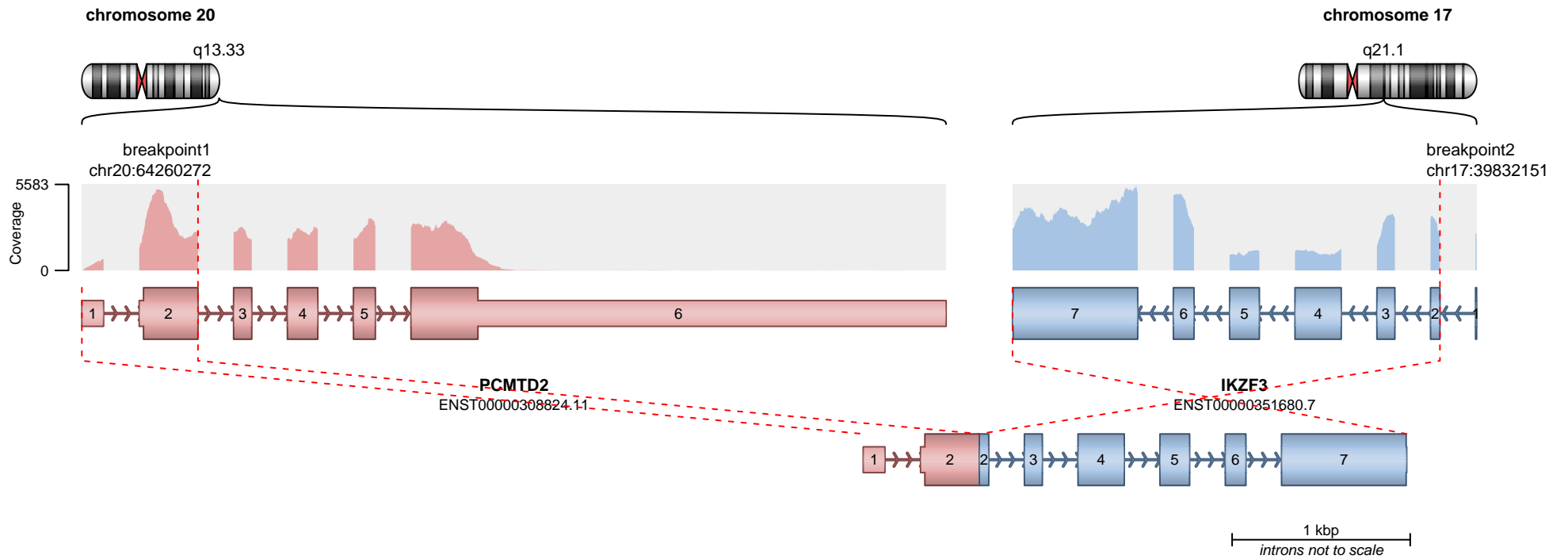
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



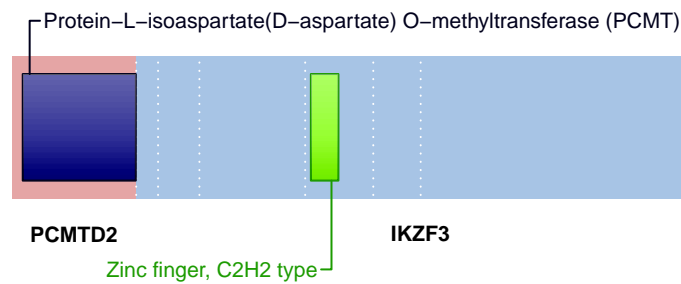
**SUPPORTING READ COUNT**

Split reads = 25  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



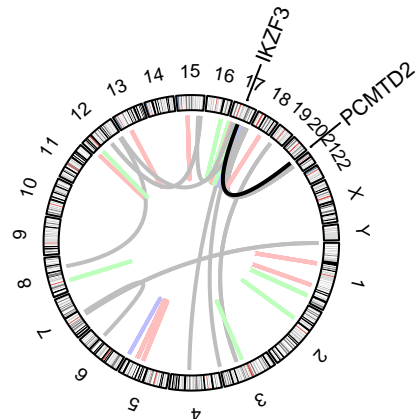
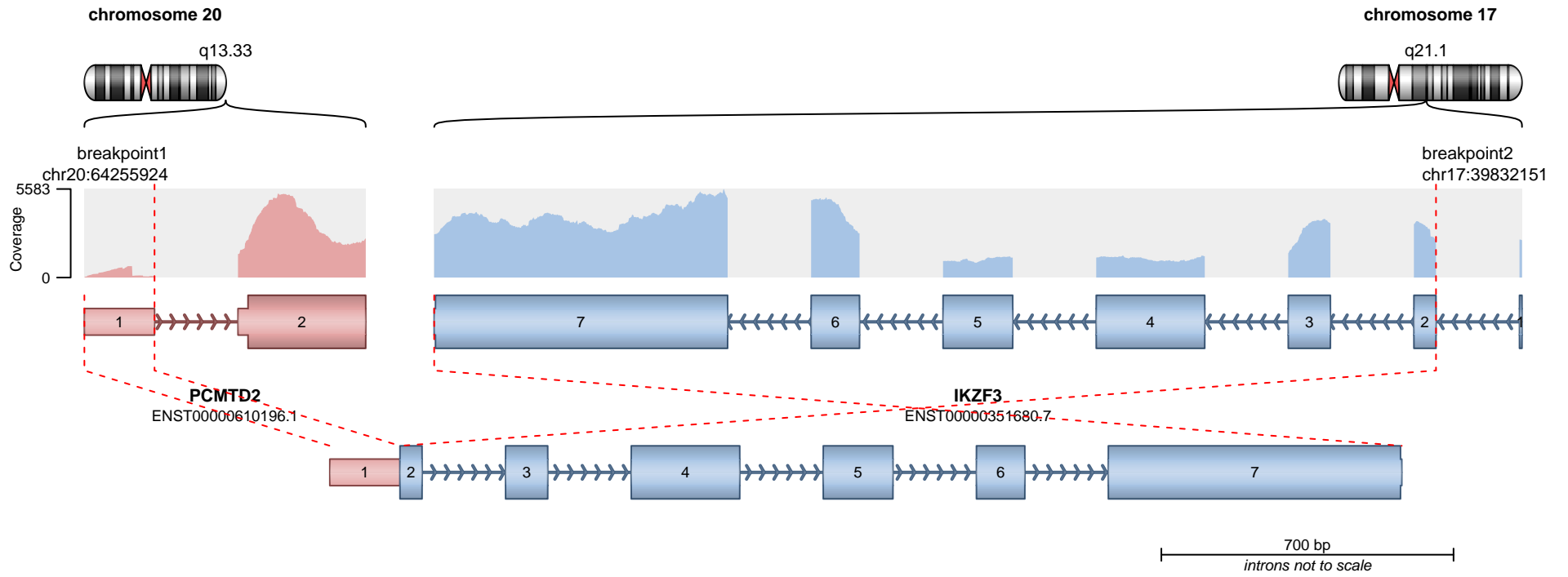
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



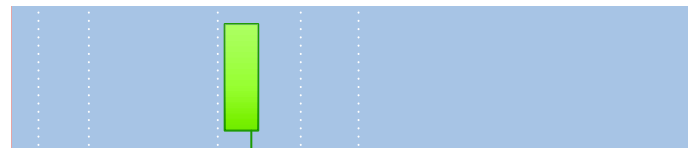
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



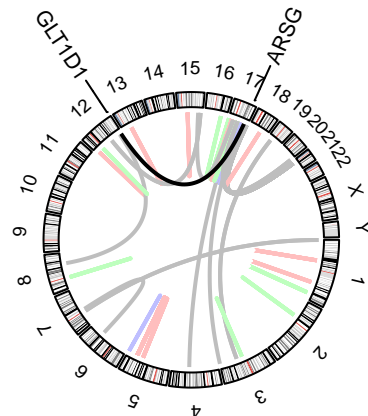
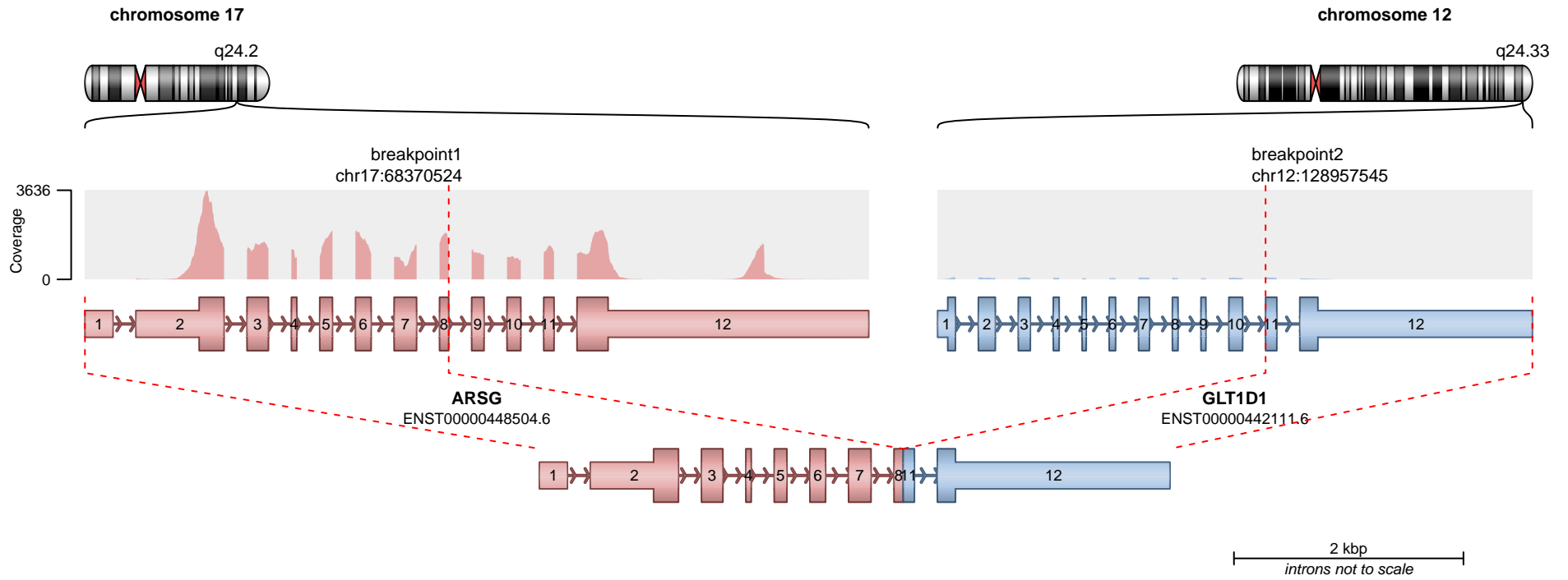
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



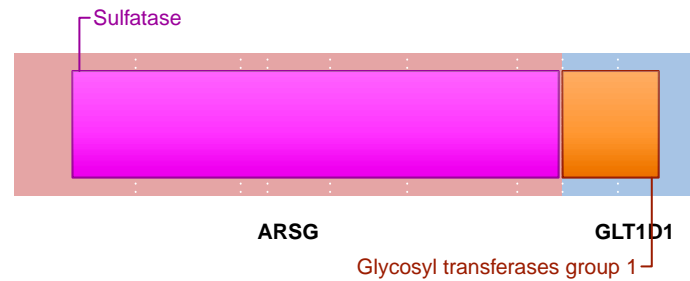
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

— translocation    — deletion  
— duplication    — inversion



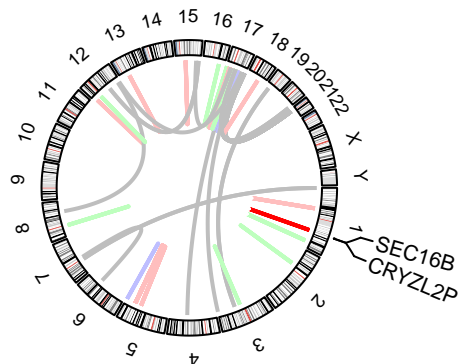
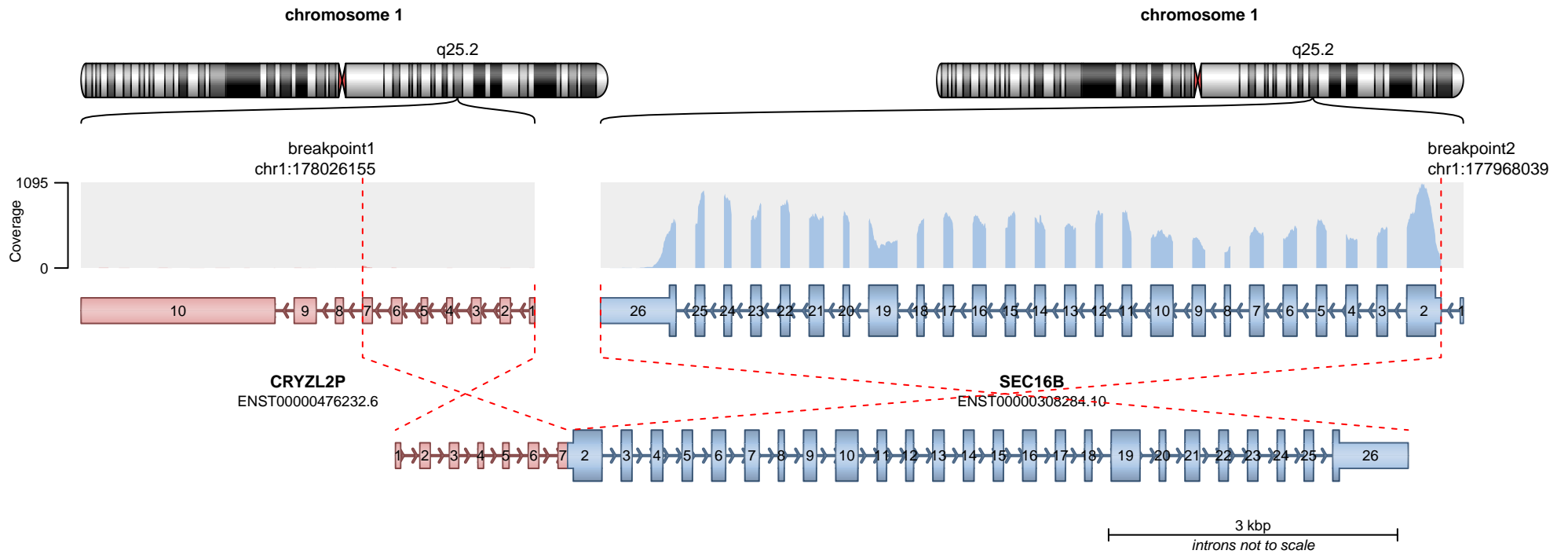
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



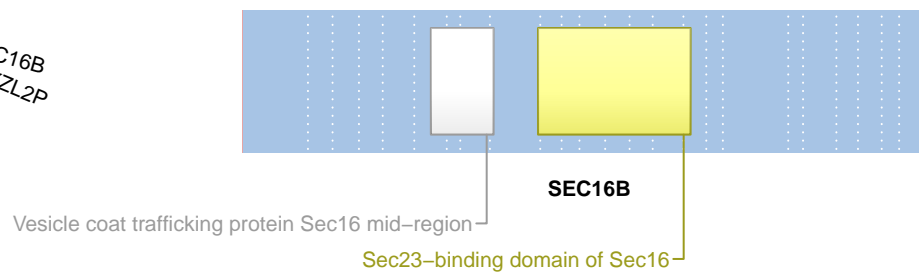
**SUPPORTING READ COUNT**

Split reads = 16  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion



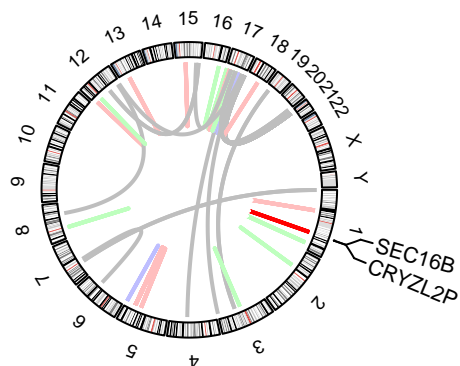
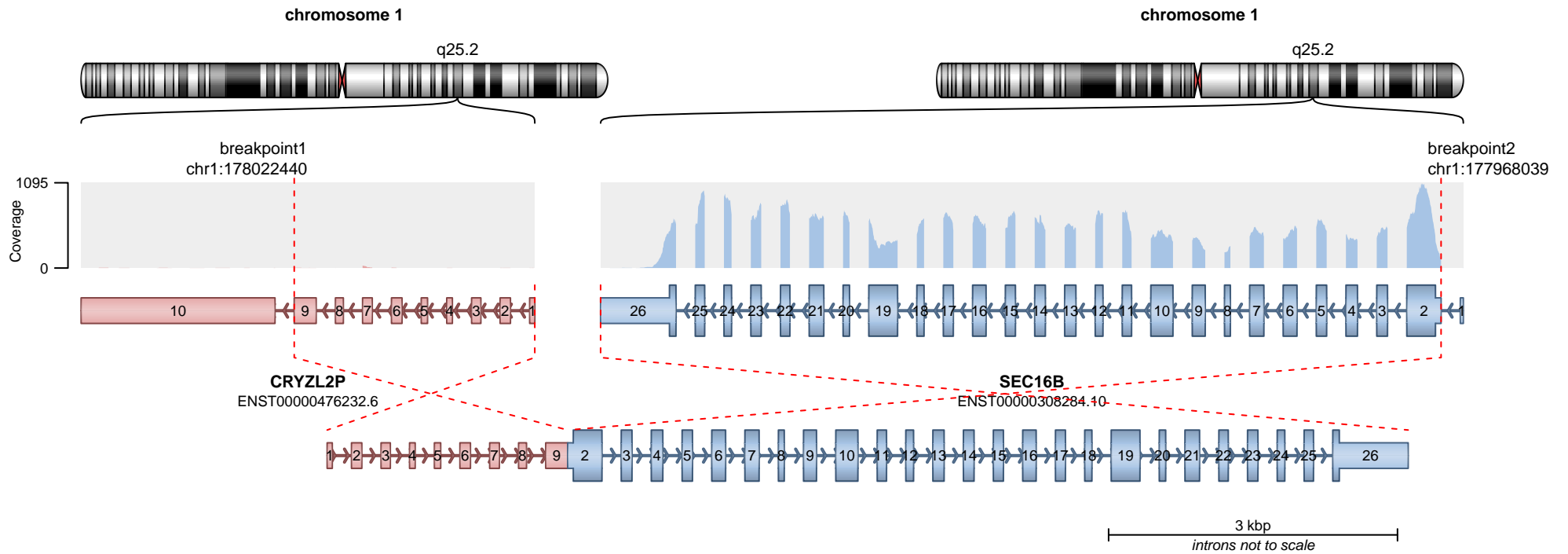
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



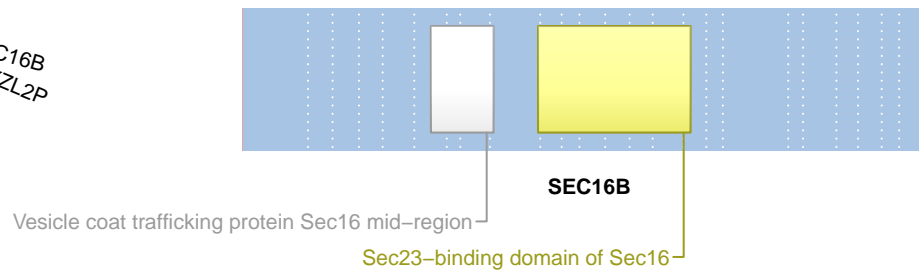
**SUPPORTING READ COUNT**

Split reads = 16  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



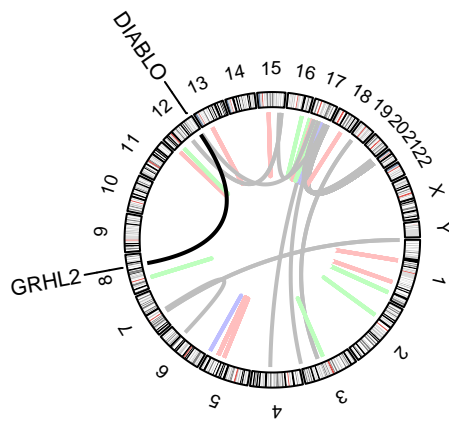
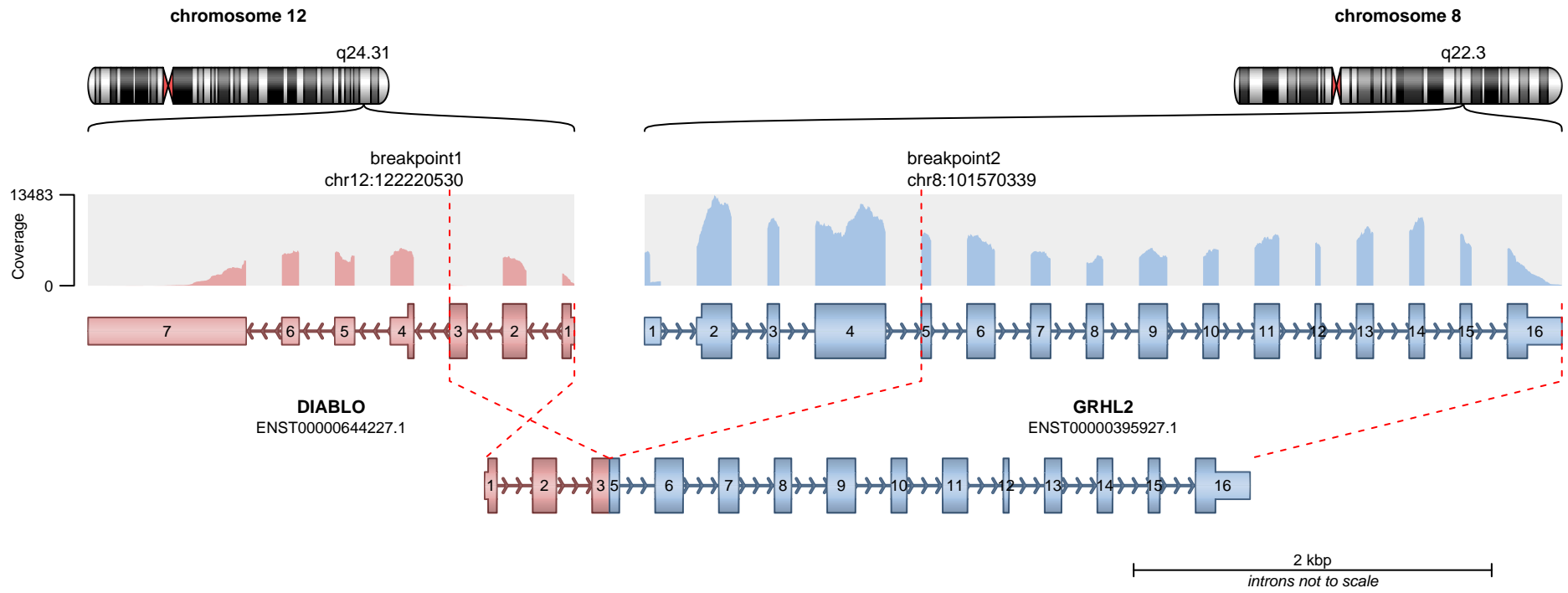
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



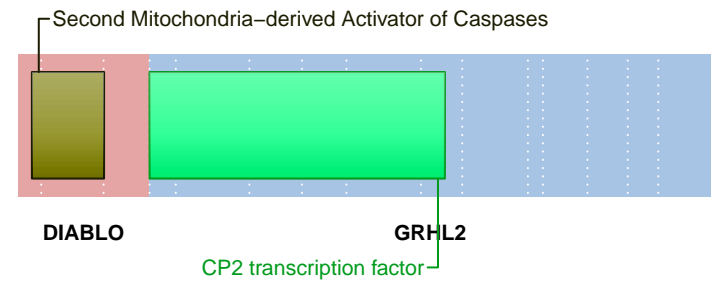
**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



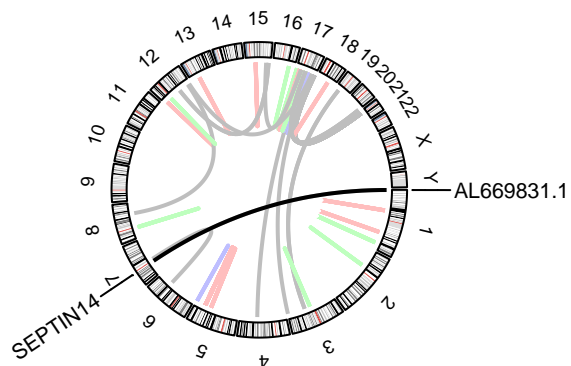
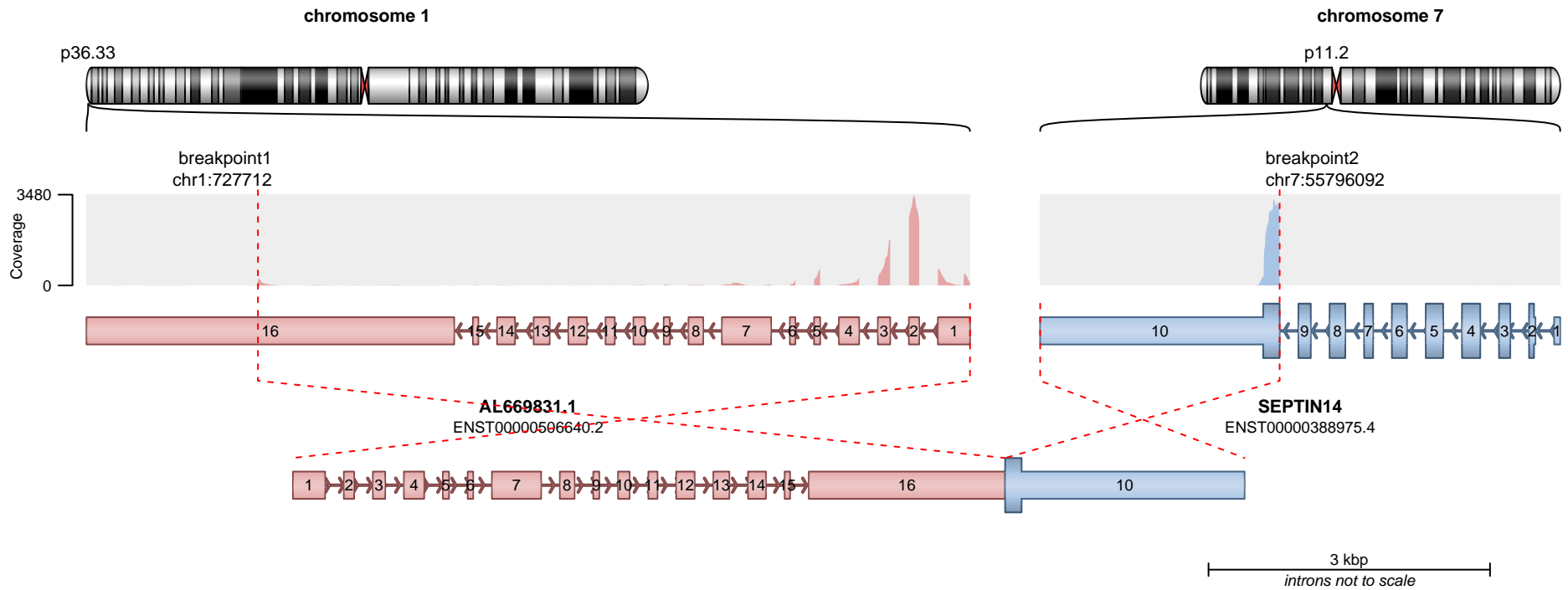
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 16  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

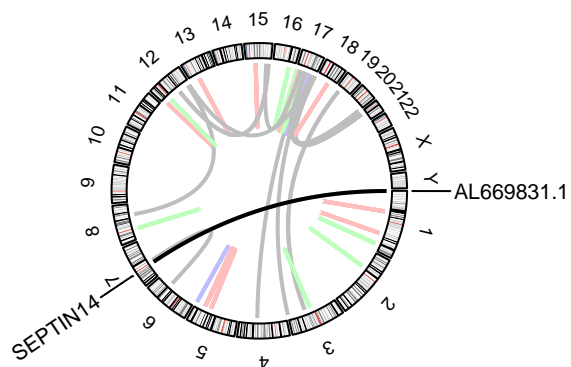
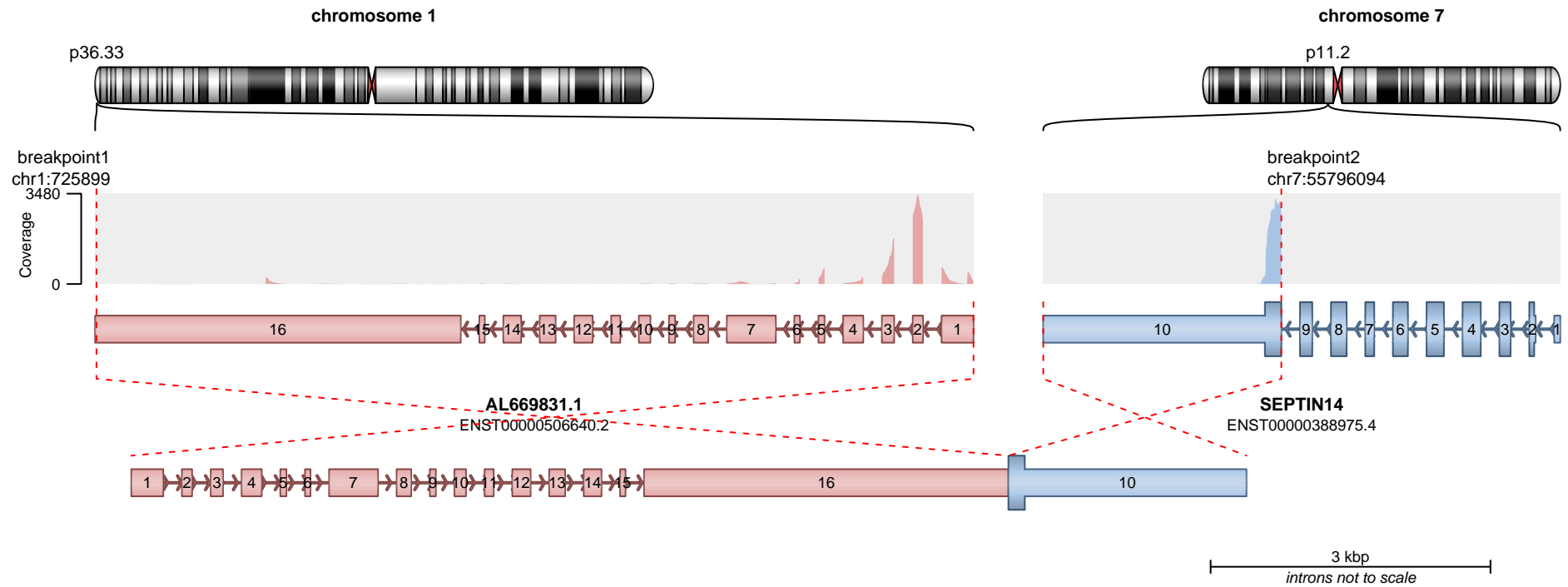


No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 15  
Discordant mates = 2

- translocation
- duplication
- deletion
- inversion

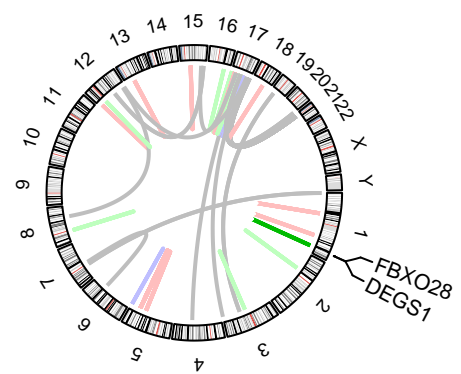
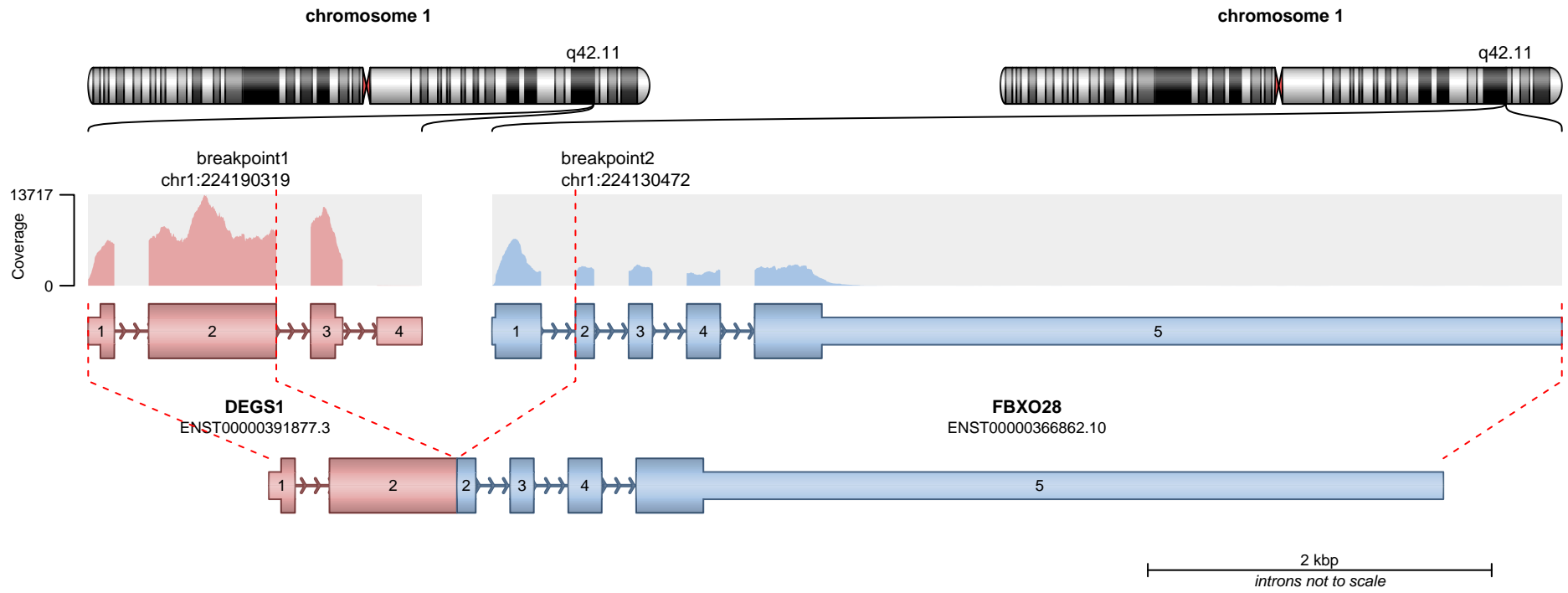


No protein domains retained in fusion.

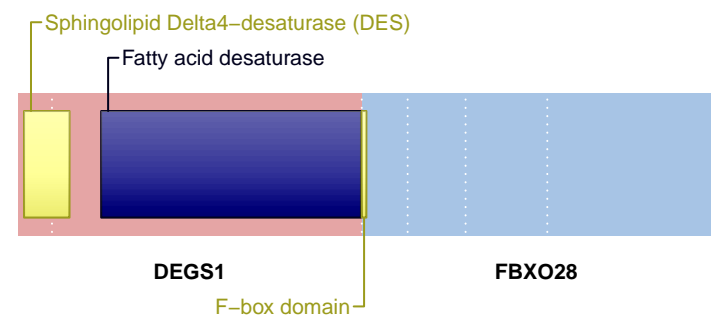
**SUPPORTING READ COUNT**

Split reads = 4  
Discordant mates = 2

- translocation
- duplication
- deletion
- inversion



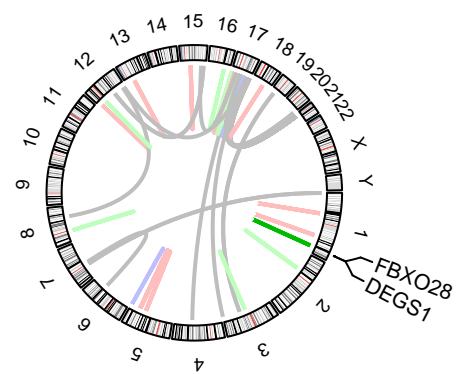
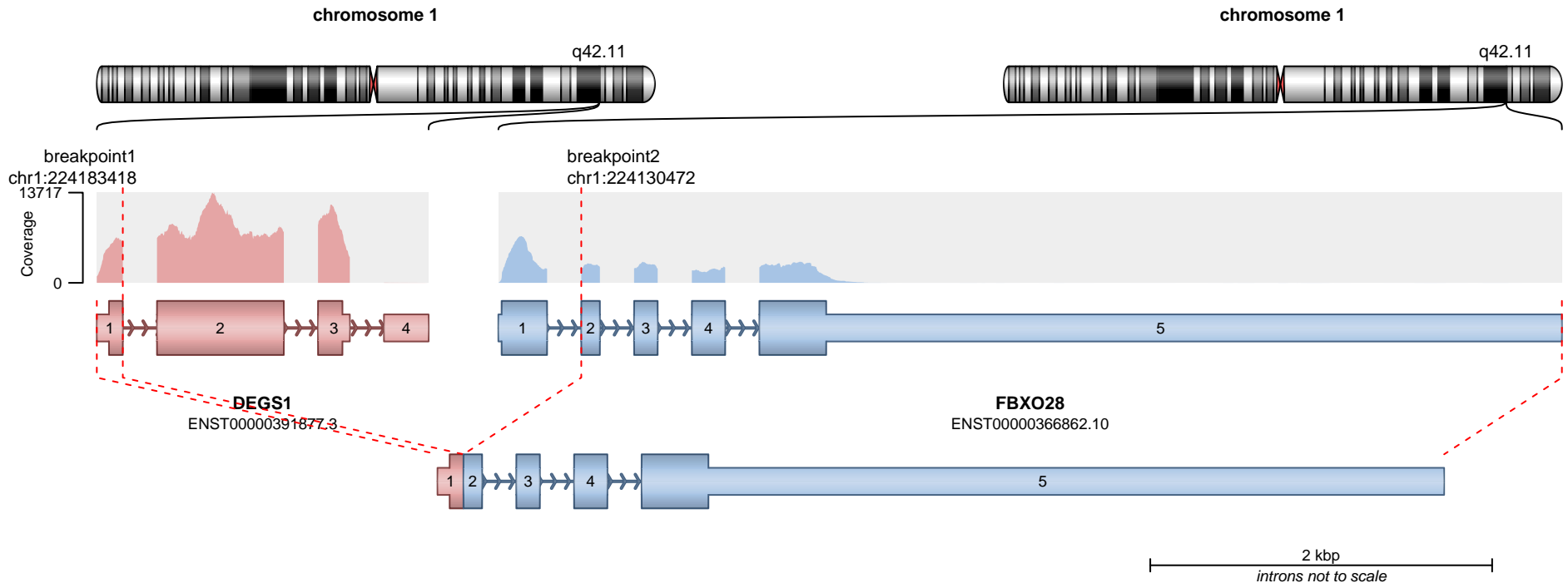
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



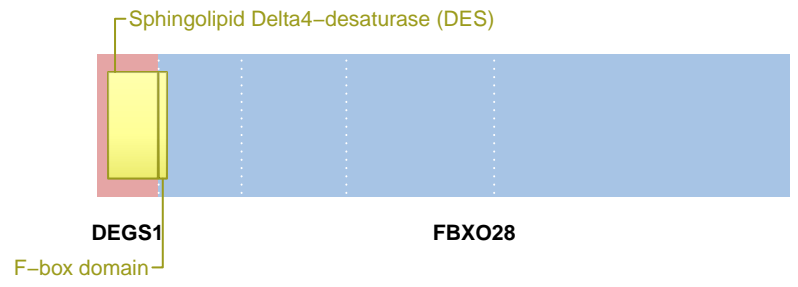
**SUPPORTING READ COUNT**

Split reads = 13  
Discordant mates = 2

- translocation
- duplication
- deletion
- inversion



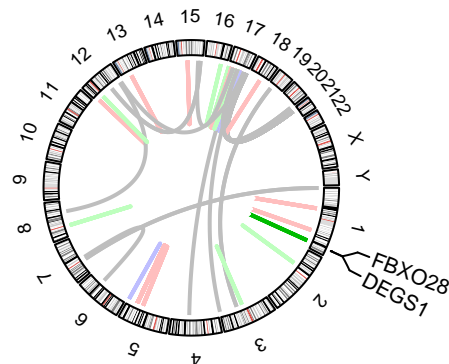
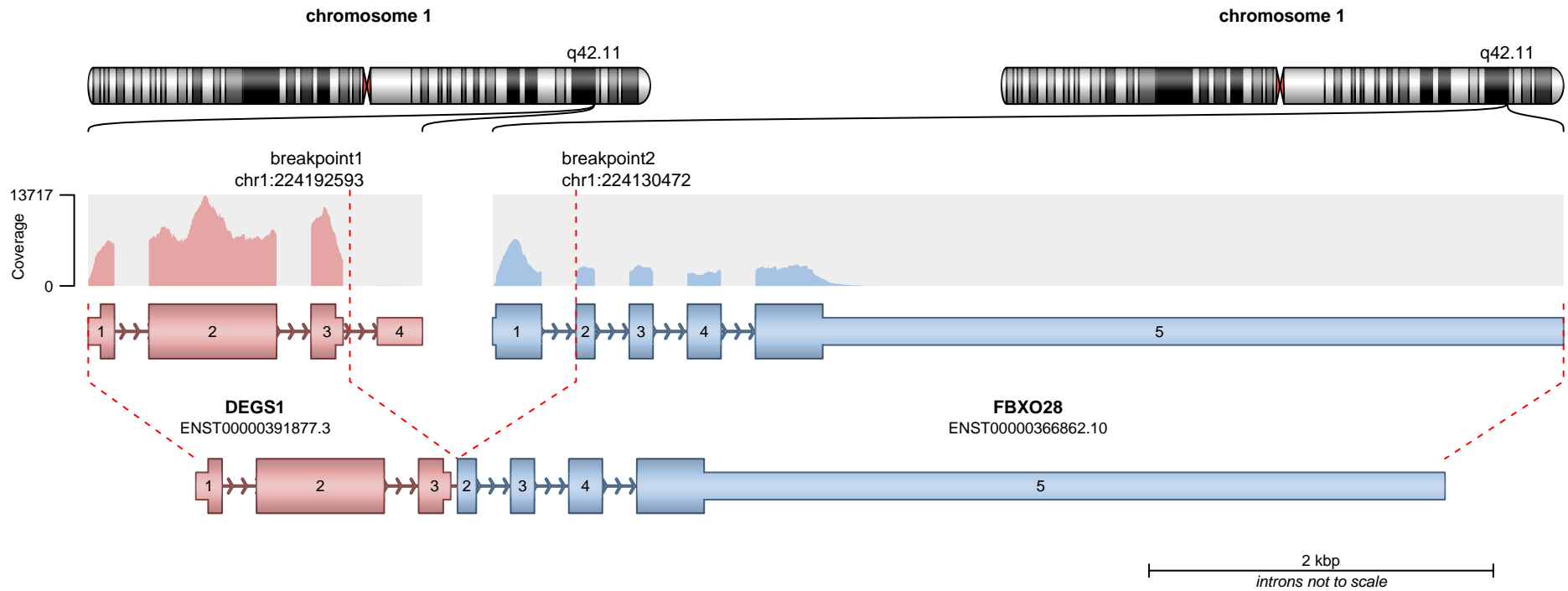
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



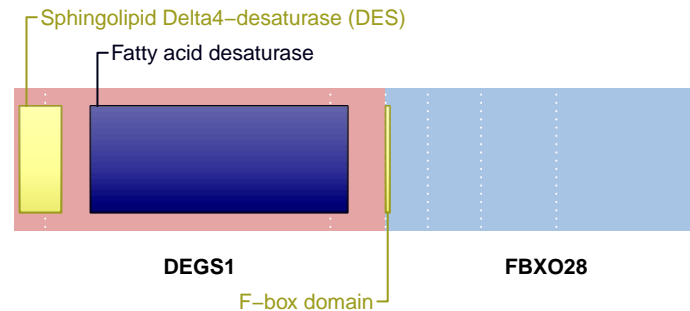
**SUPPORTING READ COUNT**

Split reads = 7  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



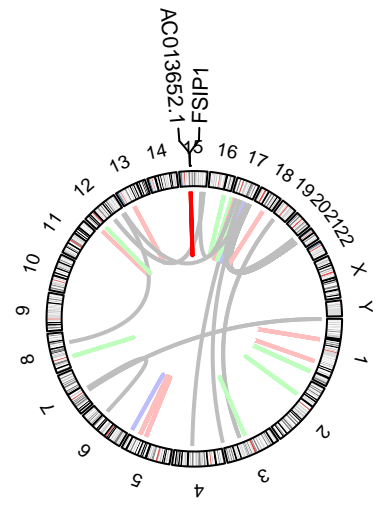
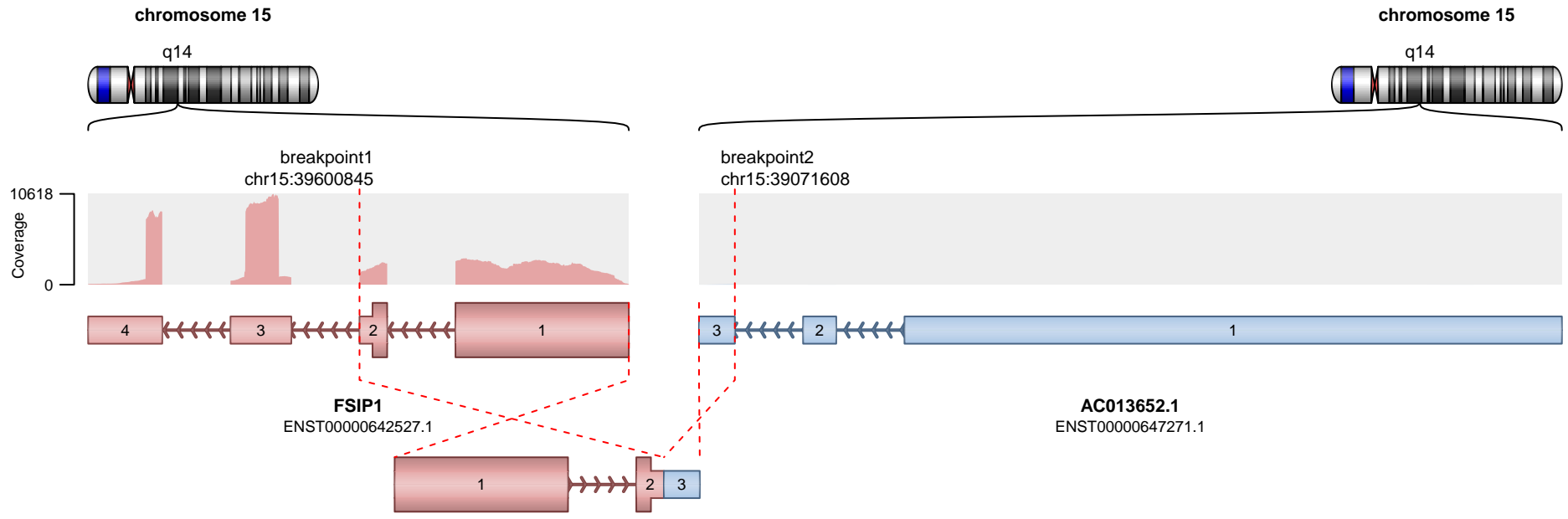
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 3  
Discordant mates = 2

- translocation
- duplication
- deletion
- inversion

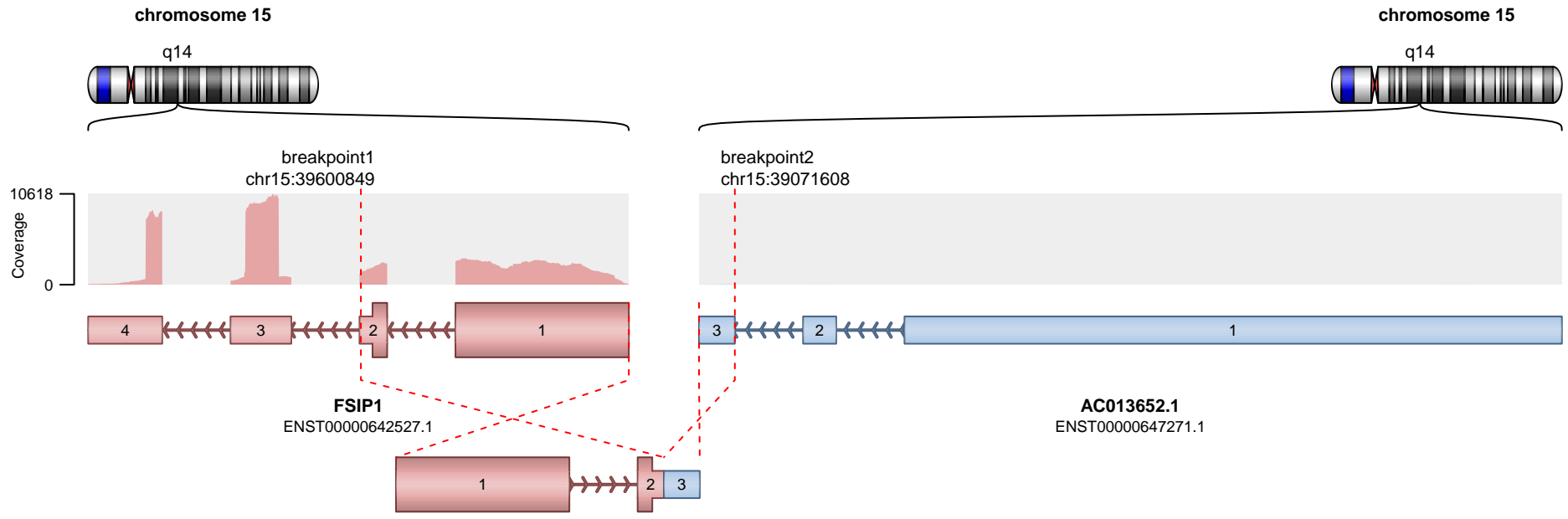


— translocation    — deletion  
 — duplication    — inversion

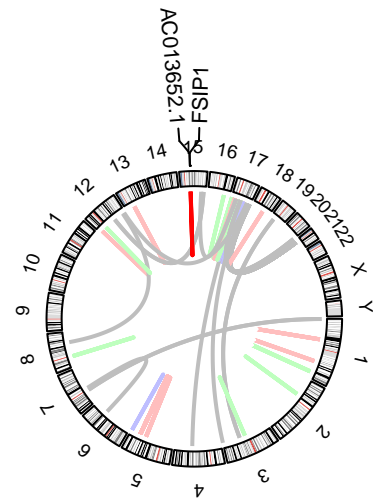
No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 13  
Discordant mates = 0



800 bp  
introns not to scale

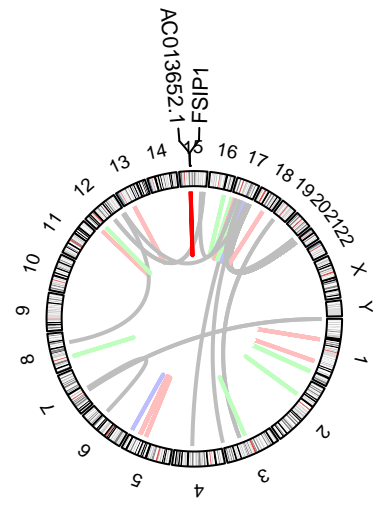
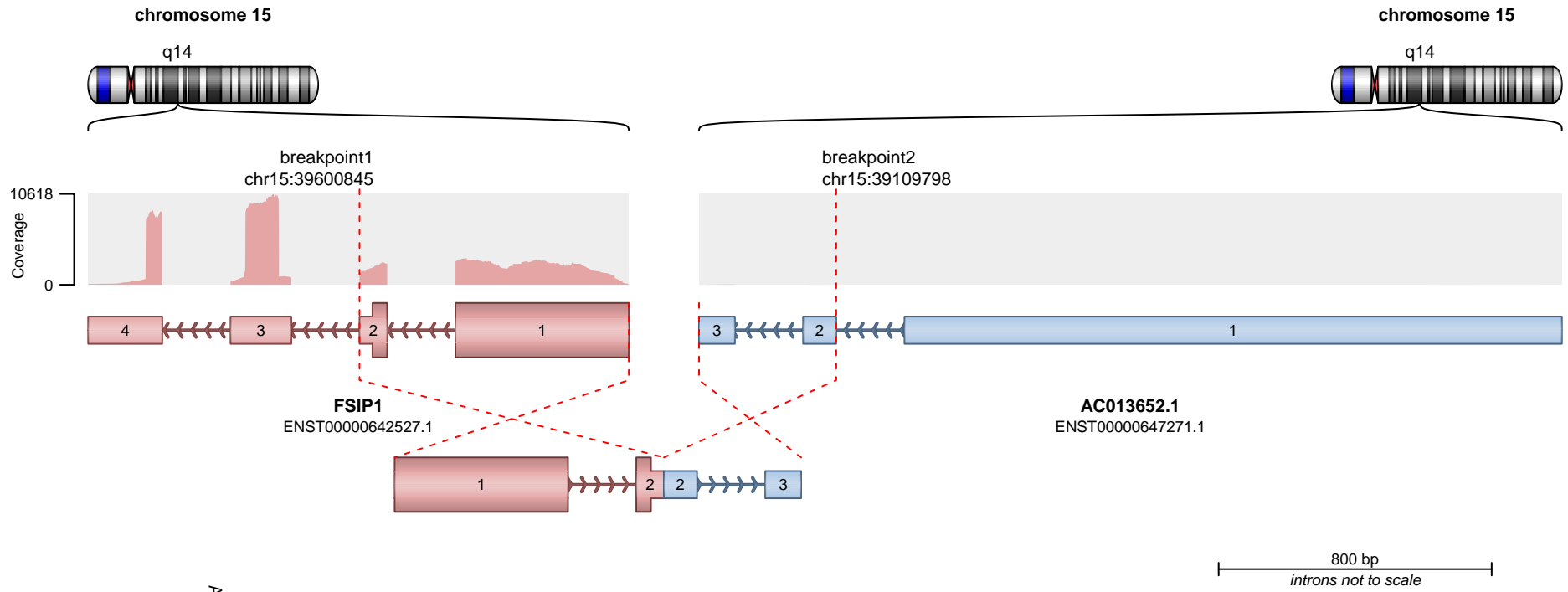


— translocation    — deletion  
— duplication    — inversion

No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 7  
Discordant mates = 0

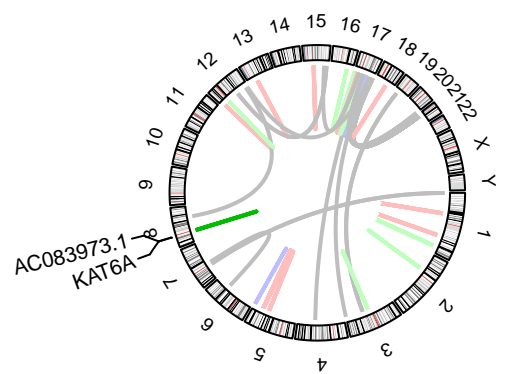
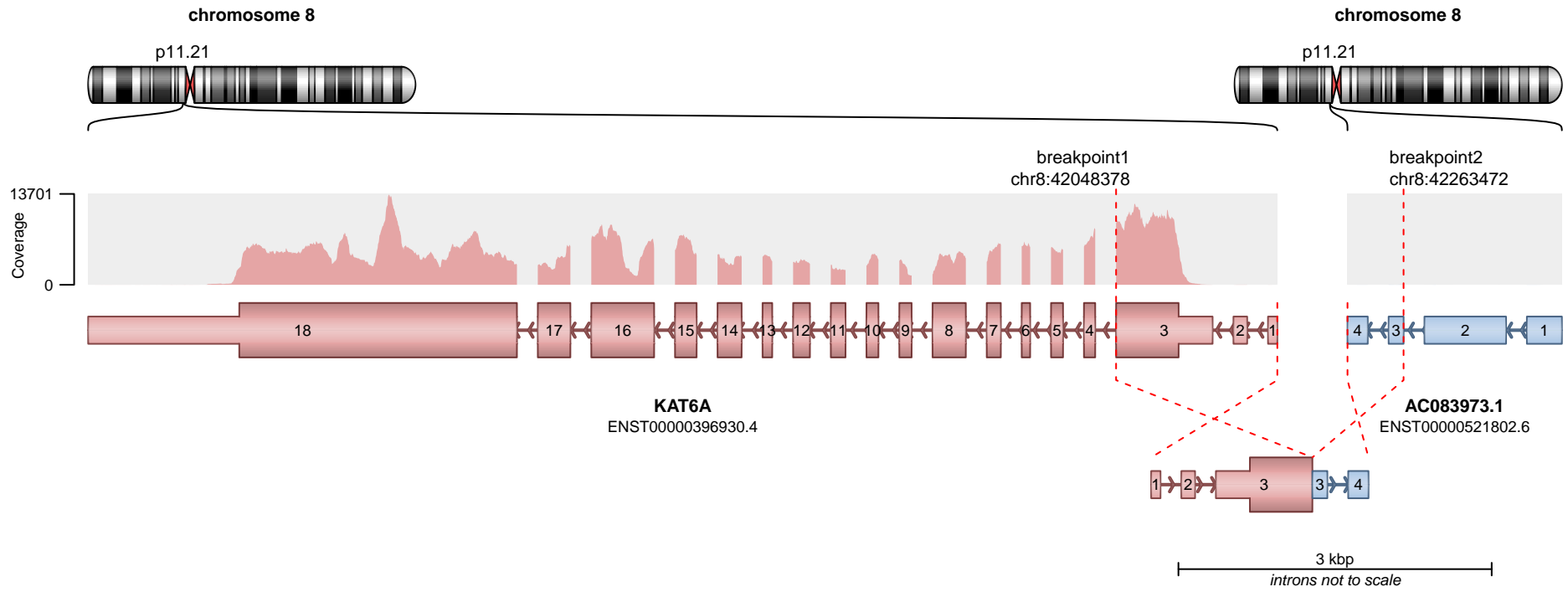


— translocation — deletion  
— duplication — inversion

No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

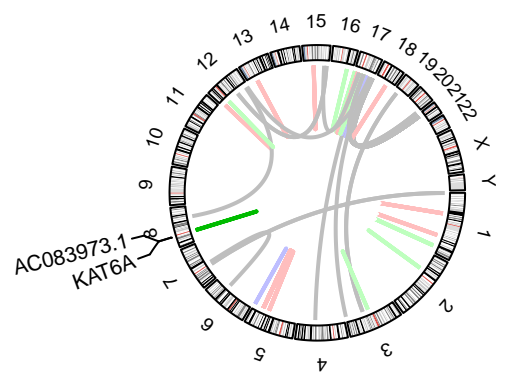
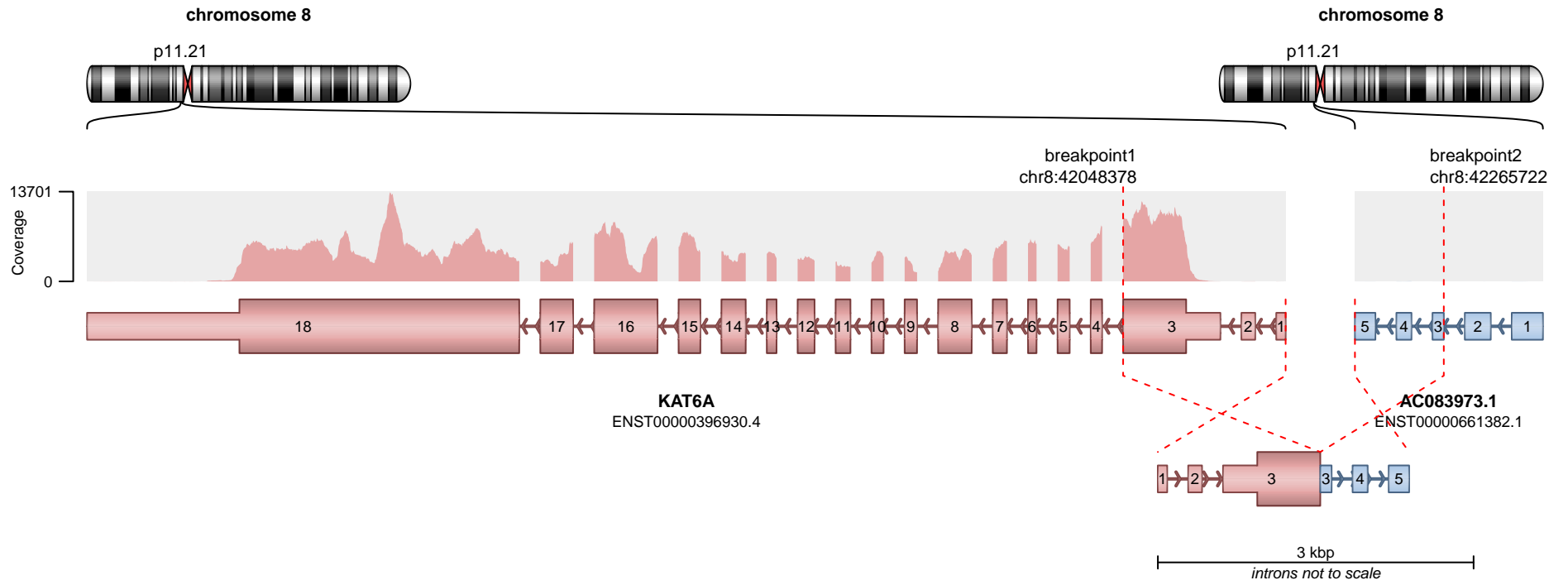


— translocation    — deletion  
 — duplication    — inversion

No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 12  
 Discordant mates = 0

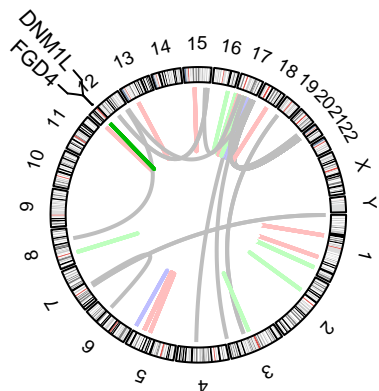
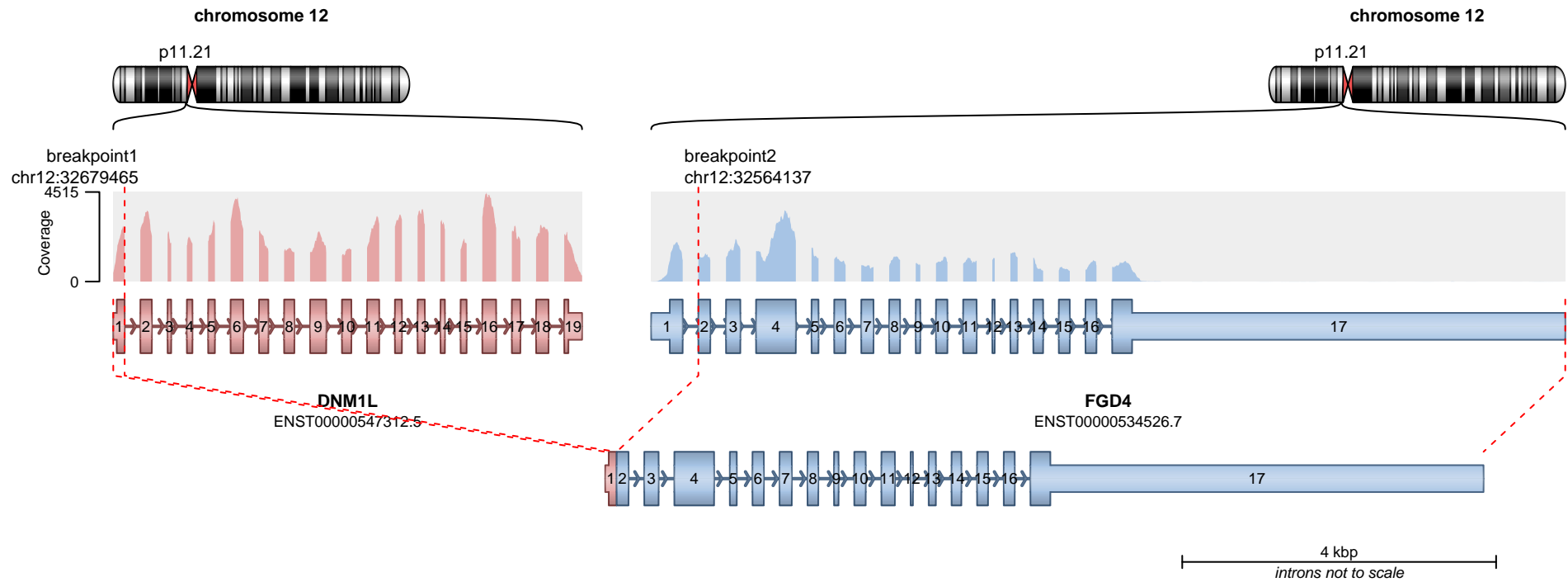


— translocation    — deletion  
— duplication    — inversion

No protein domains retained in fusion.

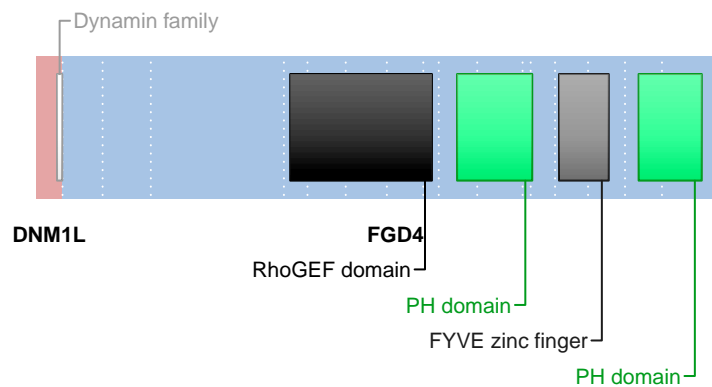
**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0



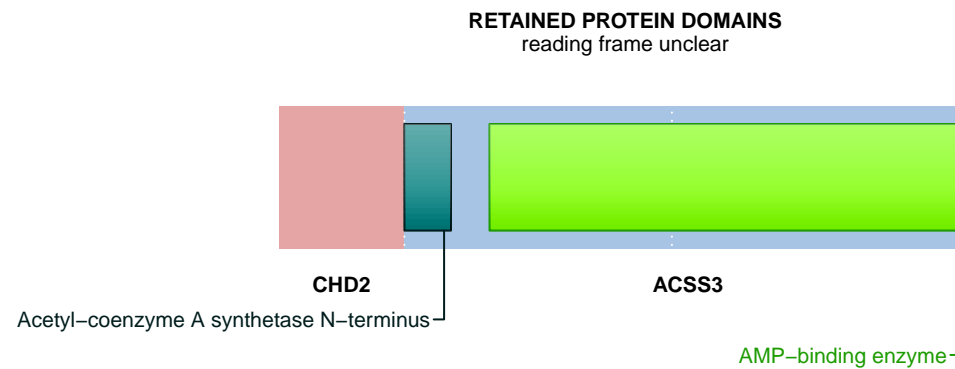
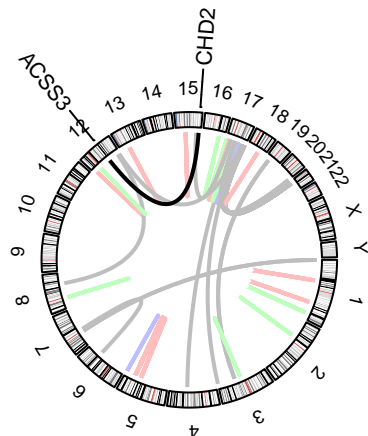
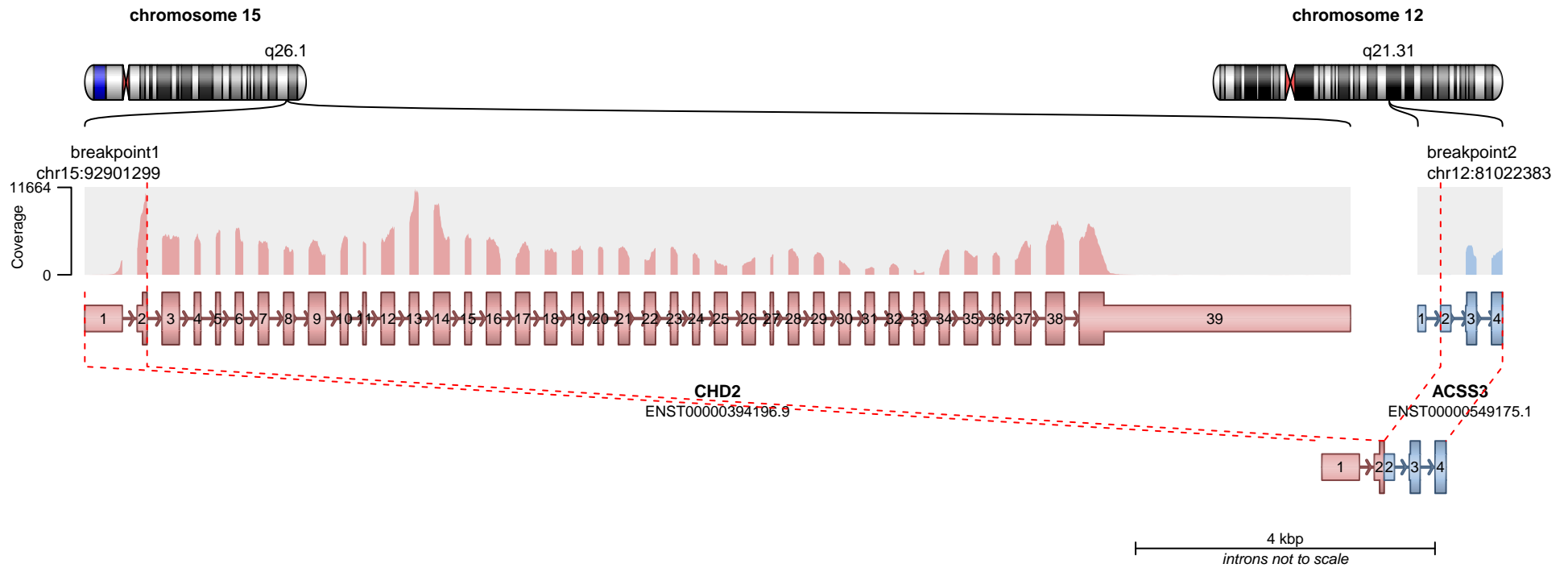
— translocation — deletion  
— duplication — inversion

**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

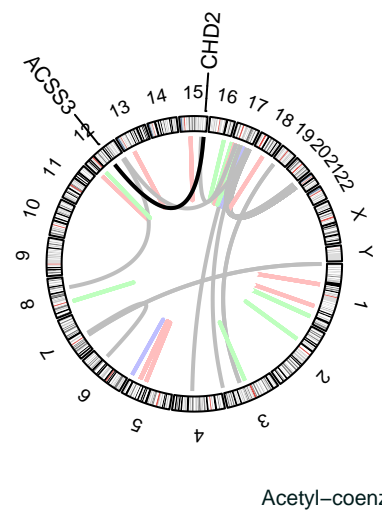
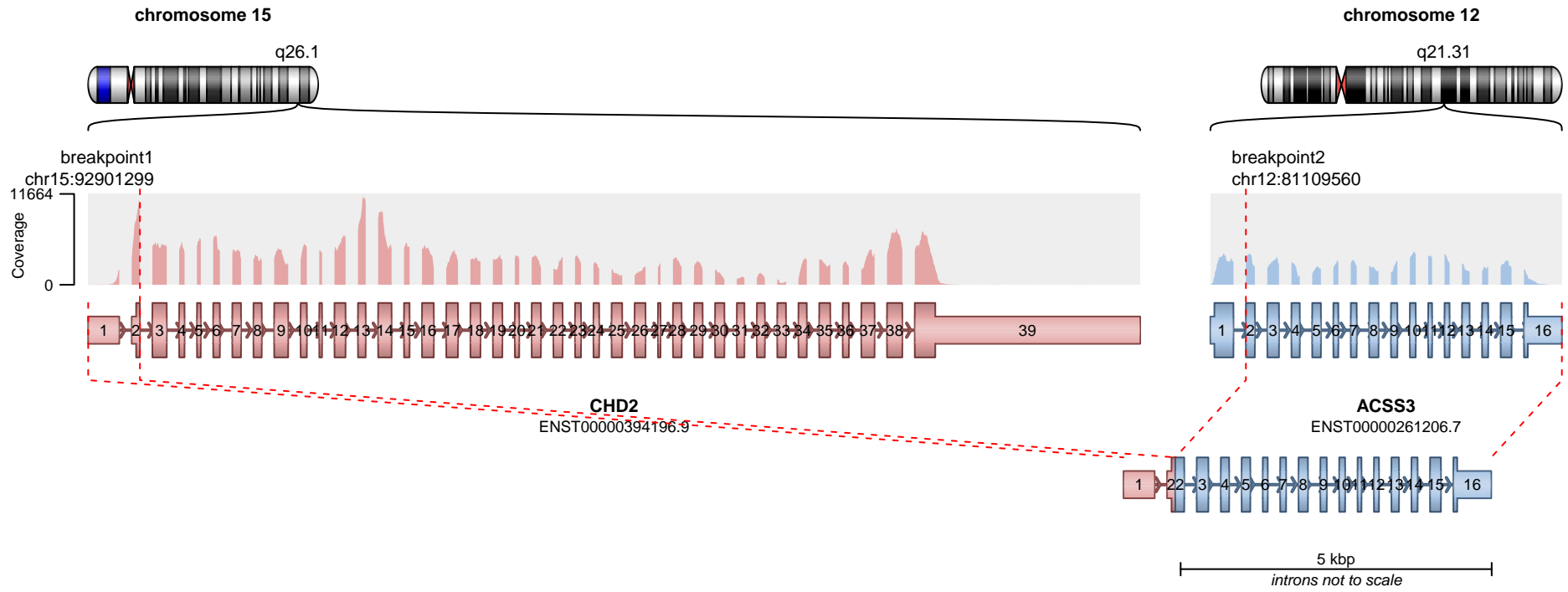
Split reads = 10  
Discordant mates = 0



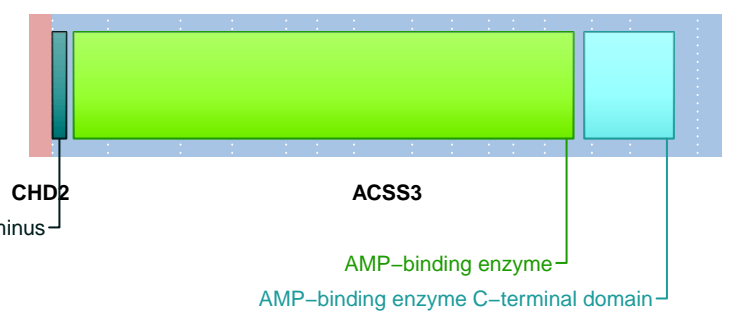
**SUPPORTING READ COUNT**

Split reads = 9  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



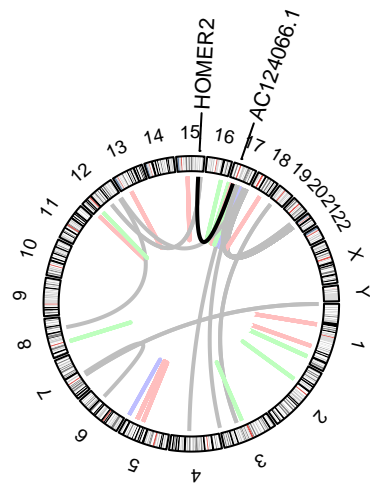
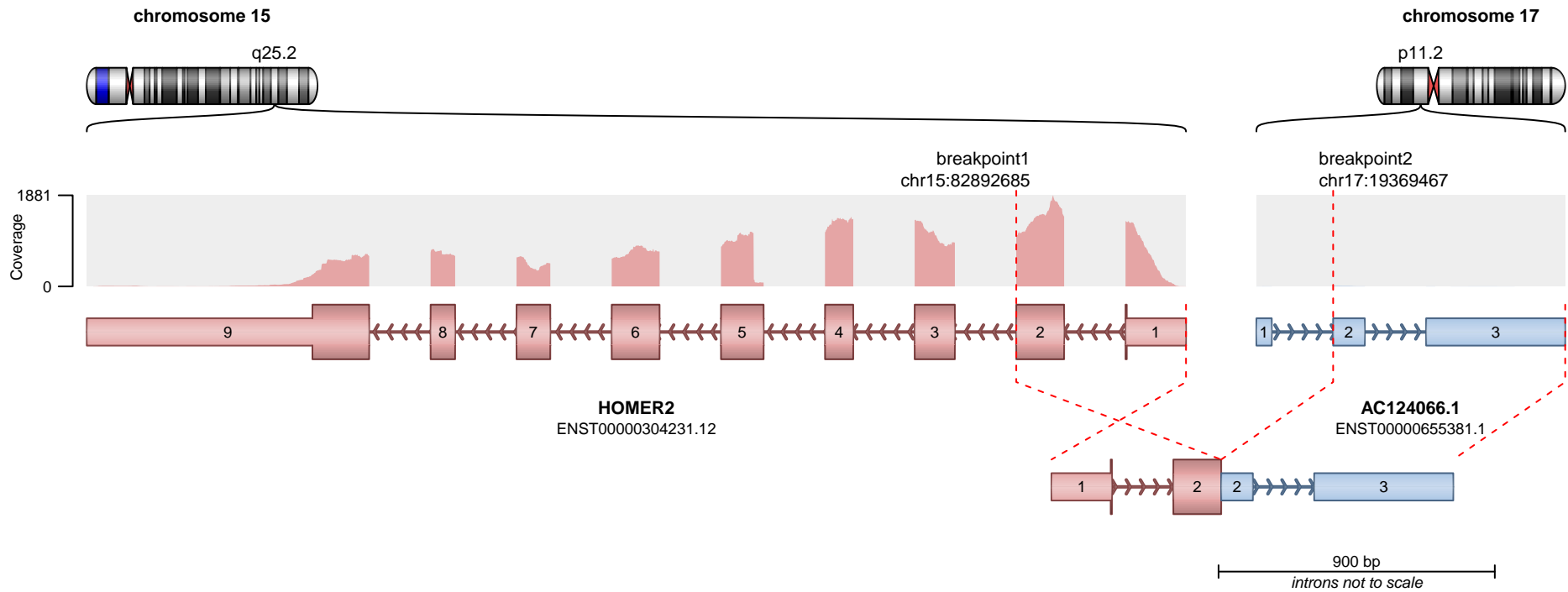
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



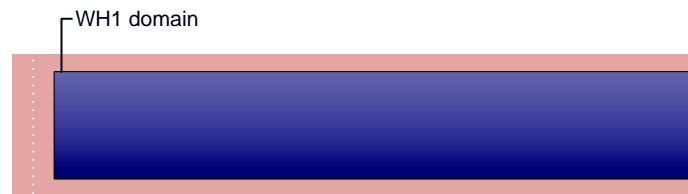
**SUPPORTING READ COUNT**

Split reads = 5  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



**RETAINED PROTEIN DOMAINS**  
reading frame unclear

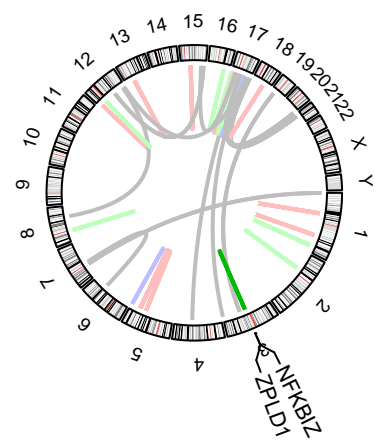
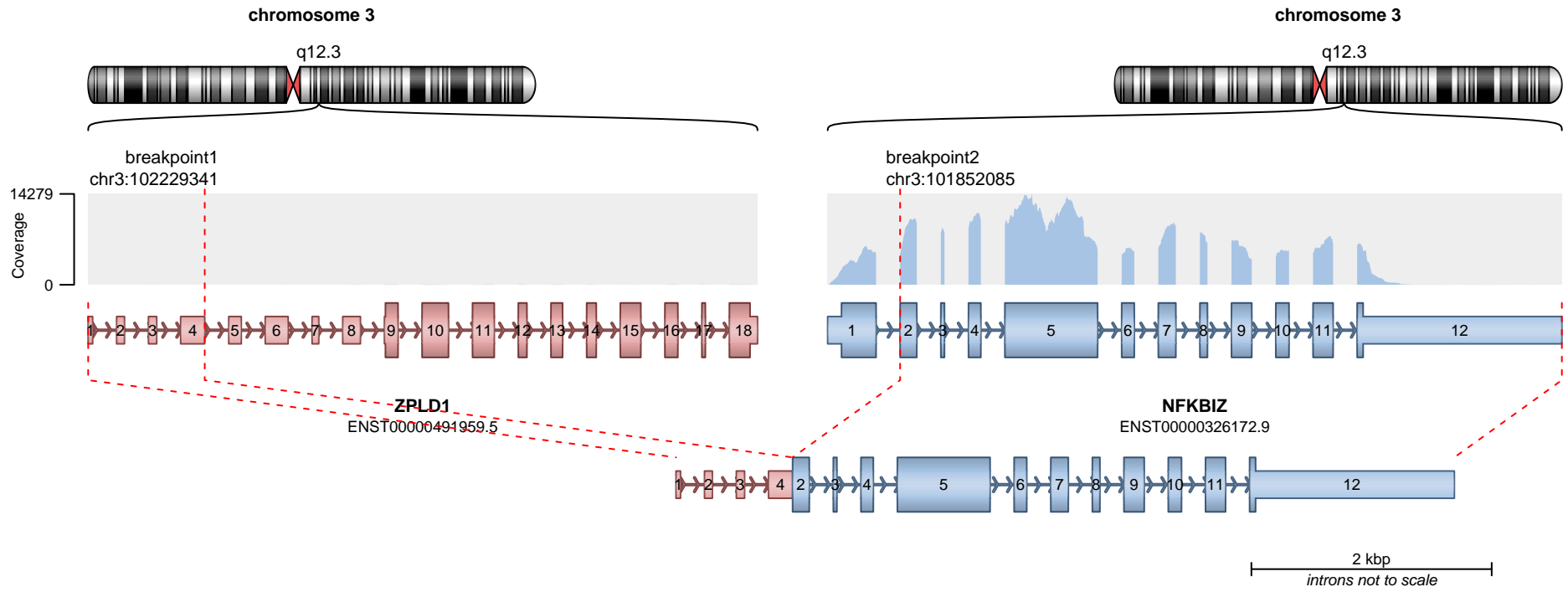


**SUPPORTING READ COUNT**

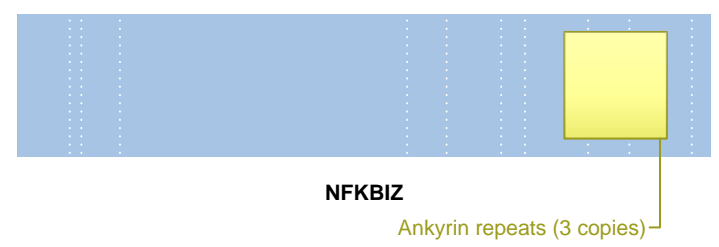
Split reads = 9  
Discordant mates = 0

**HOMER2**

- translocation
- duplication
- deletion
- inversion



**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 1  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion