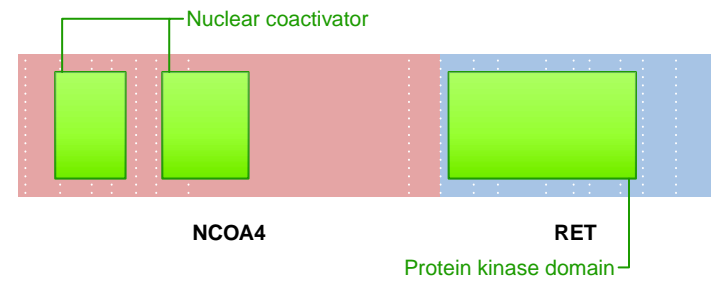


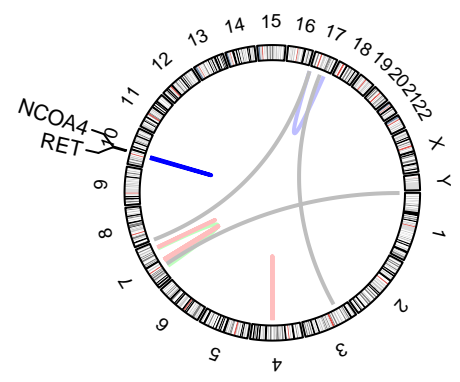
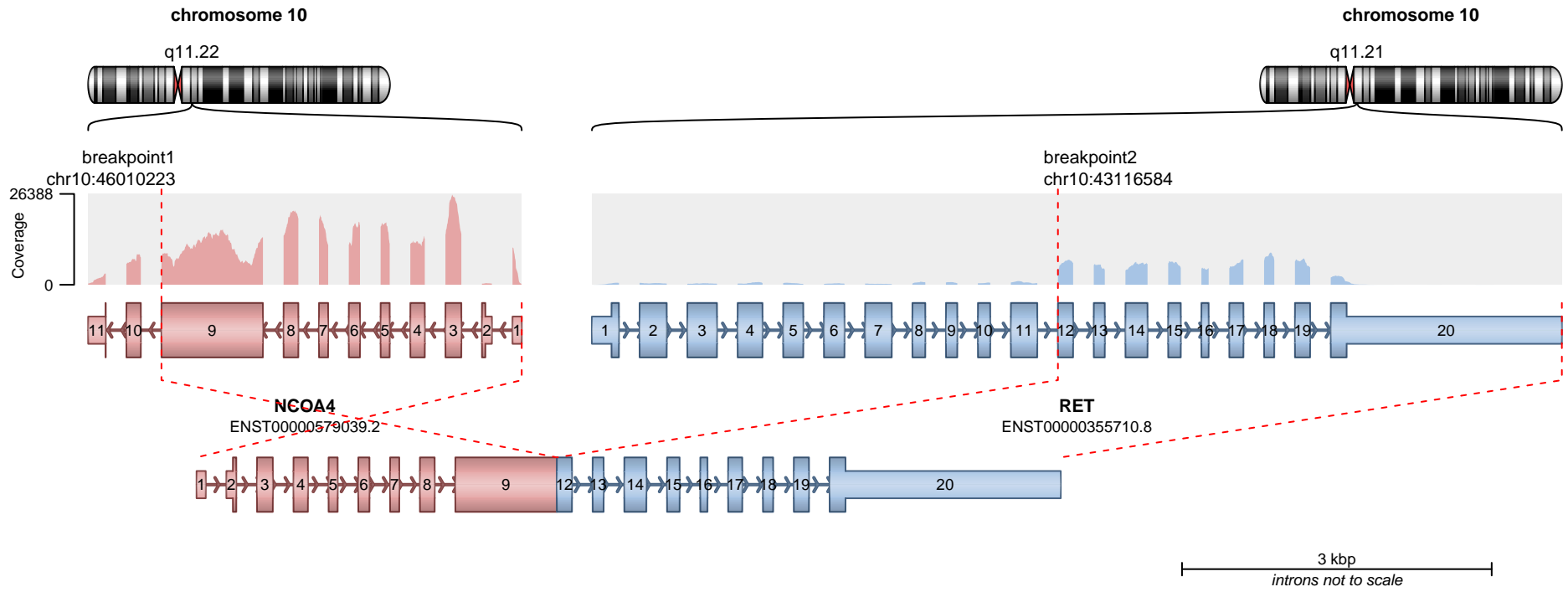
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



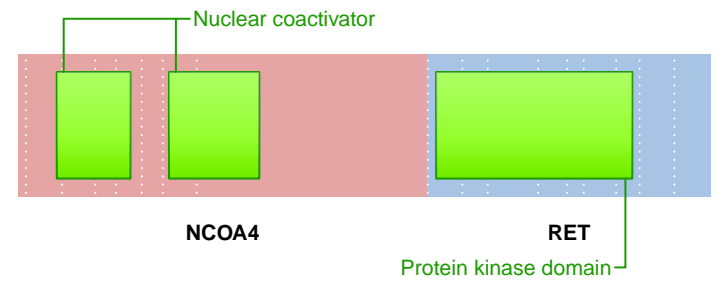
**SUPPORTING READ COUNT**

Split reads = 1043  
Discordant mates = 5

- translocation
- duplication
- deletion
- inversion



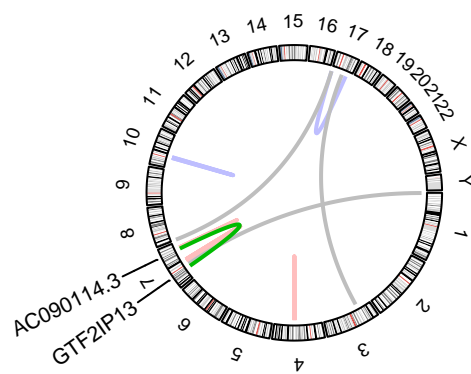
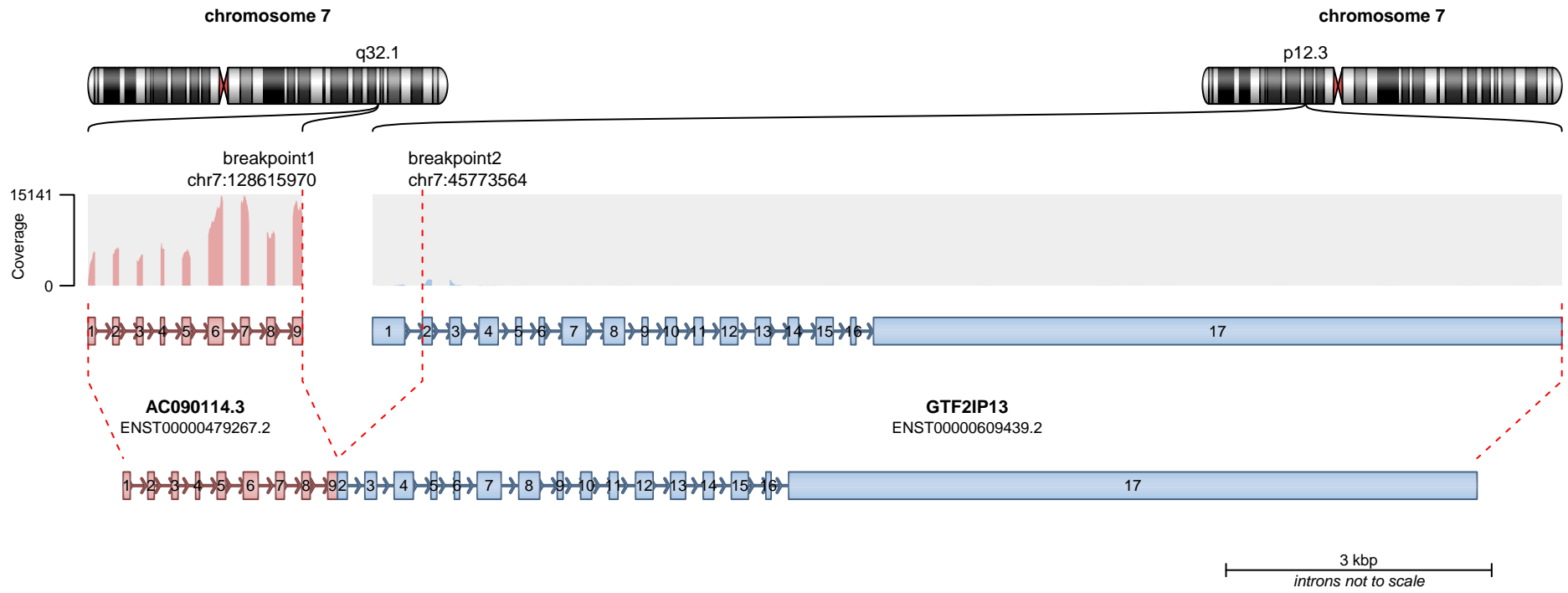
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 7  
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion

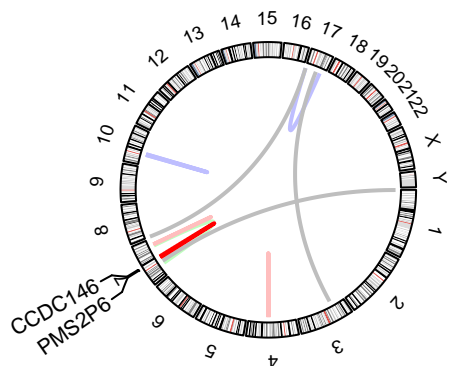
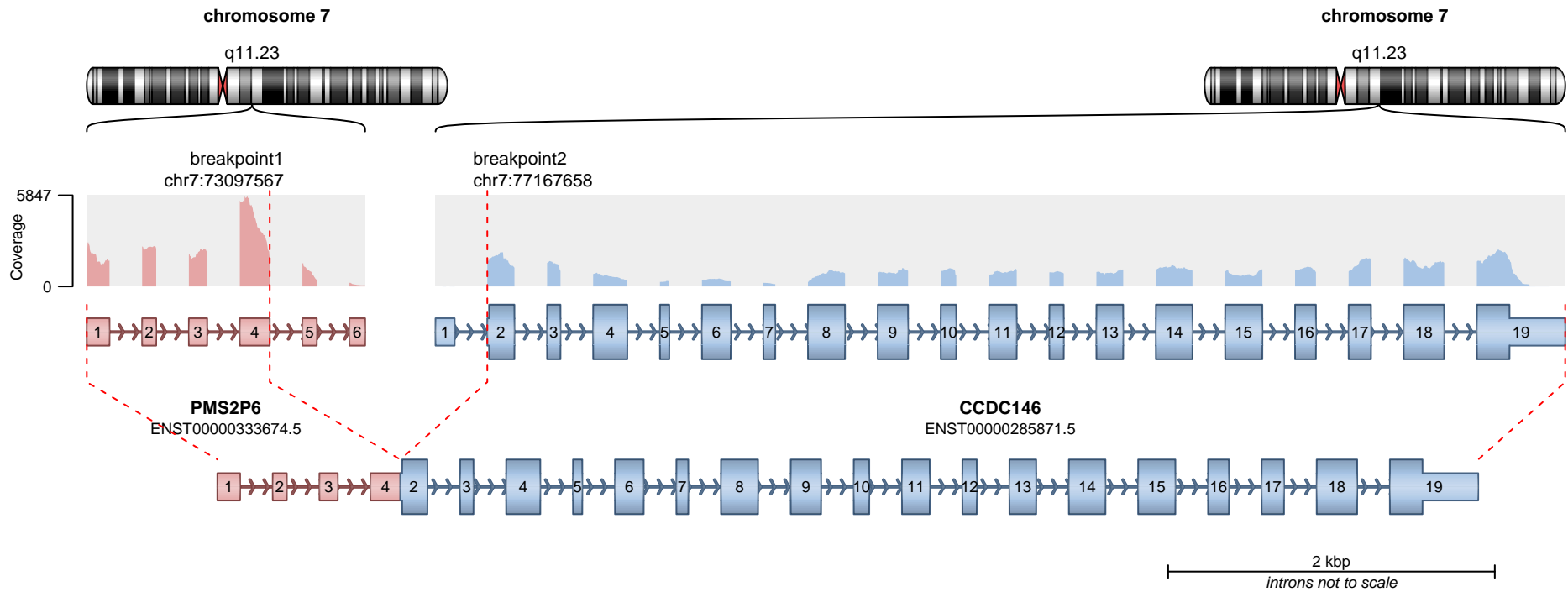


— translocation — deletion  
— duplication — inversion

Genes are not protein-coding.

**SUPPORTING READ COUNT**

Split reads = 458  
Discordant mates = 3

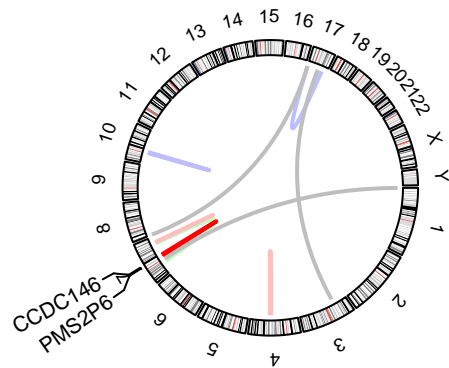
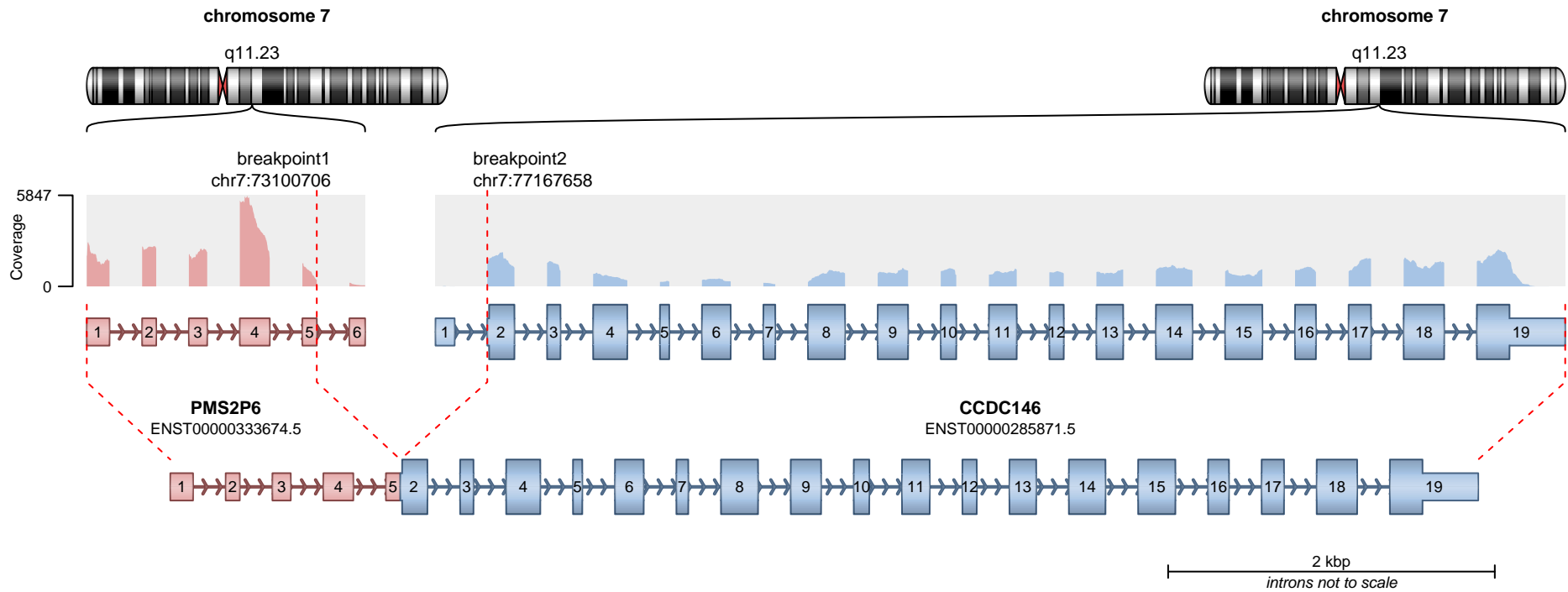


— translocation — deletion  
— duplication — inversion

No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 273  
Discordant mates = 3

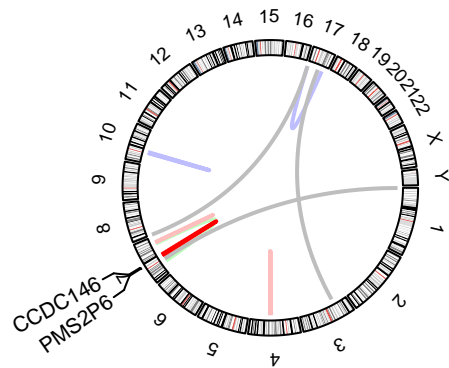
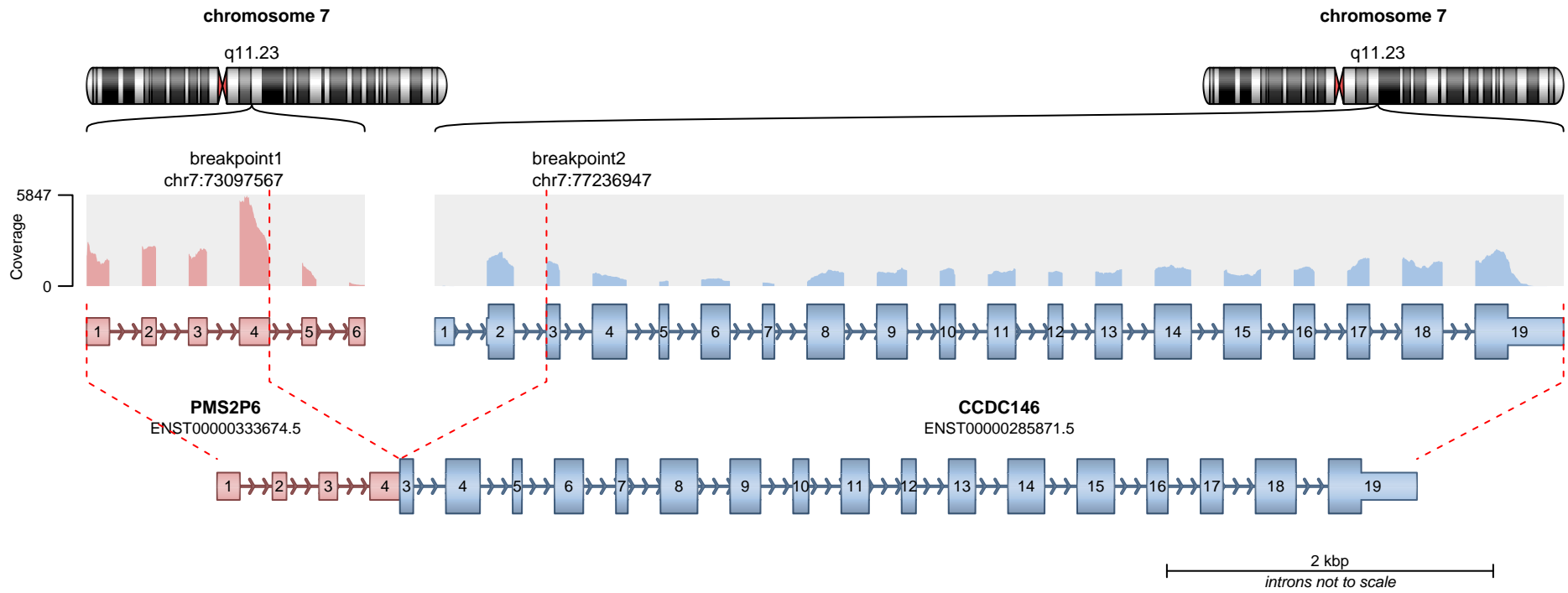


— translocation    — deletion  
 — duplication    — inversion

No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 51  
 Discordant mates = 3

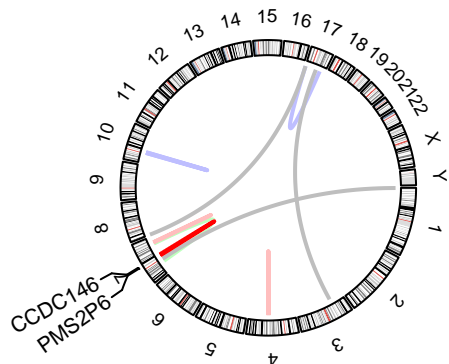
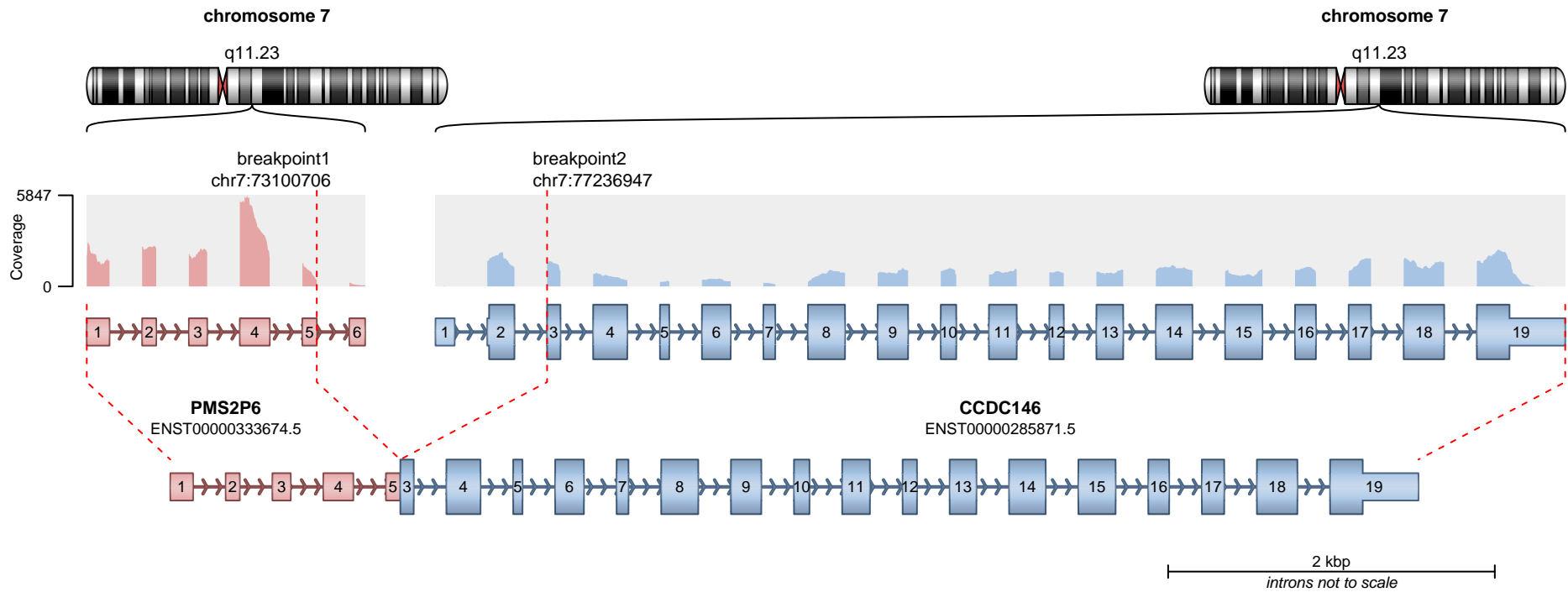


— translocation — deletion  
— duplication — inversion

No protein domains retained in fusion.

#### SUPPORTING READ COUNT

Split reads = 25  
Discordant mates = 2

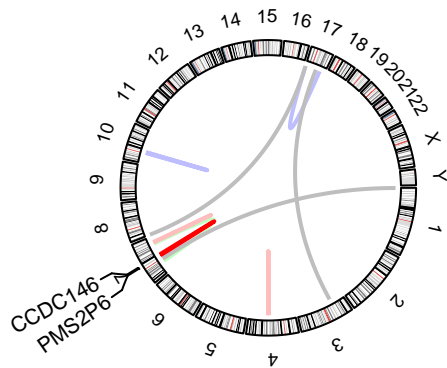
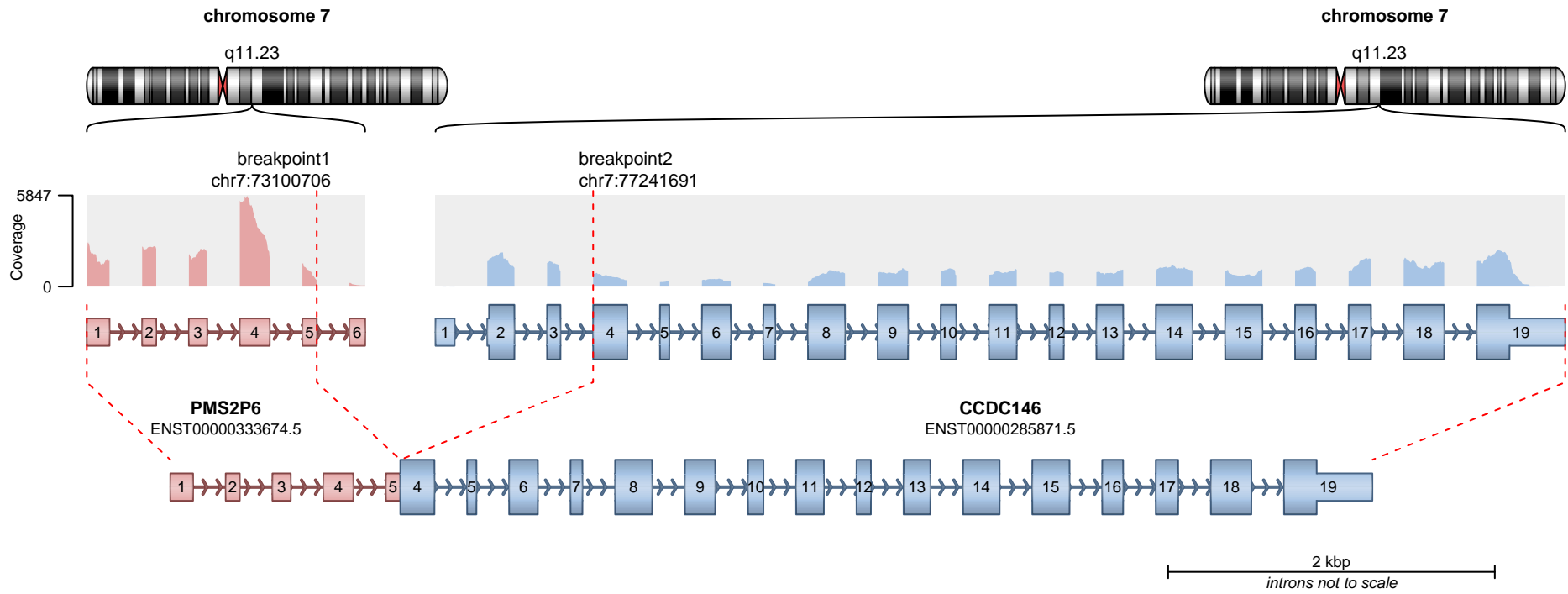


— translocation — deletion  
— duplication — inversion

No protein domains retained in fusion.

#### SUPPORTING READ COUNT

Split reads = 8  
Discordant mates = 2

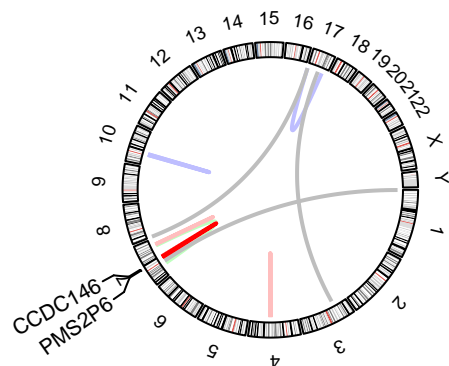
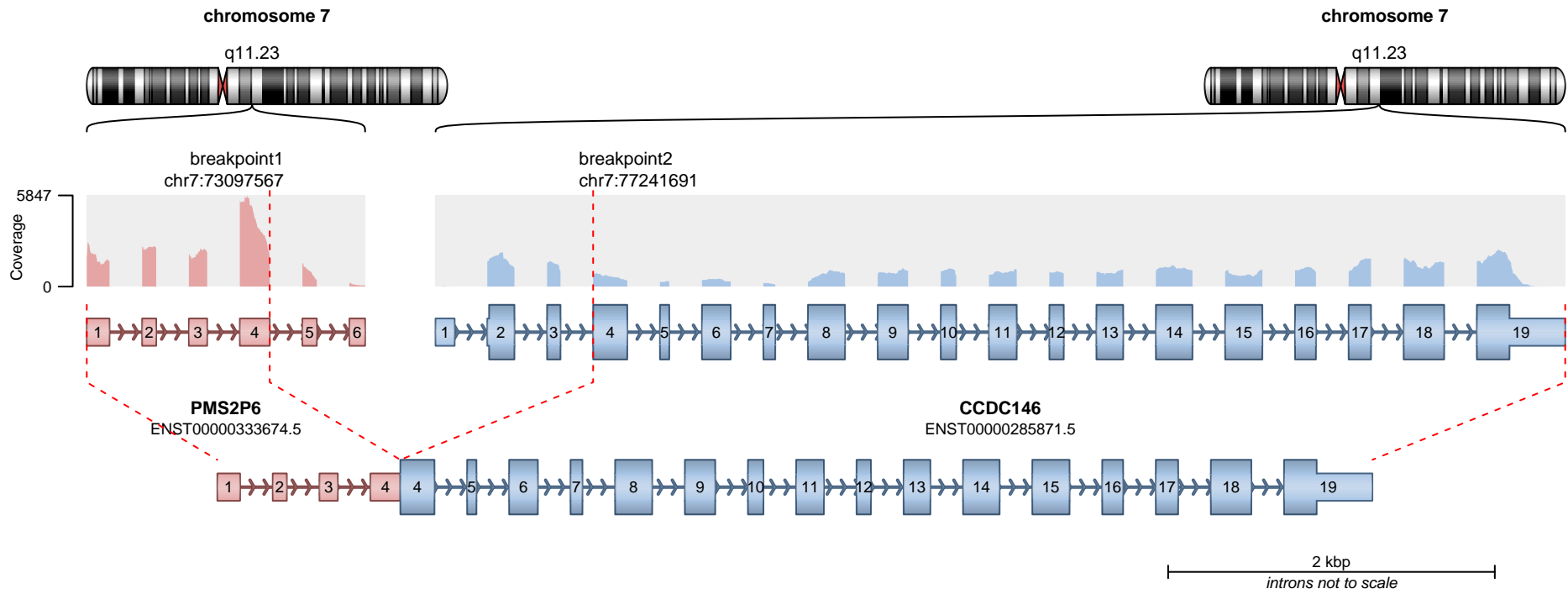


— translocation    — deletion  
— duplication    — inversion

No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0

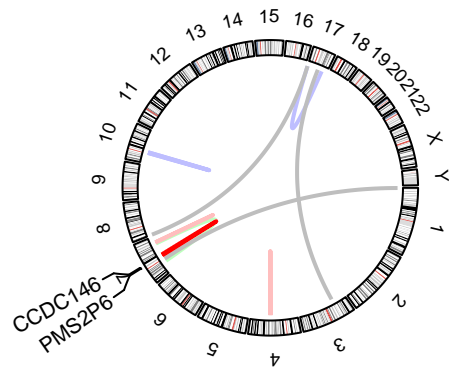
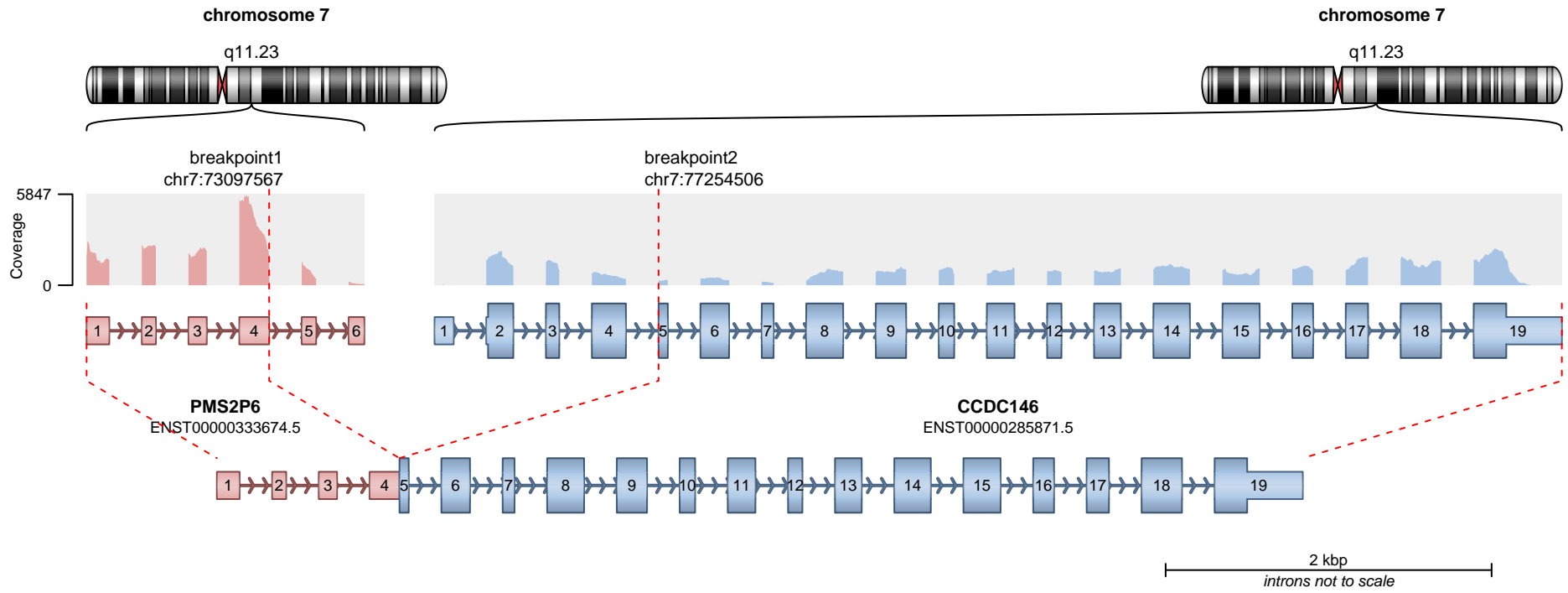


— translocation — deletion  
— duplication — inversion

No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 2  
Discordant mates = 0

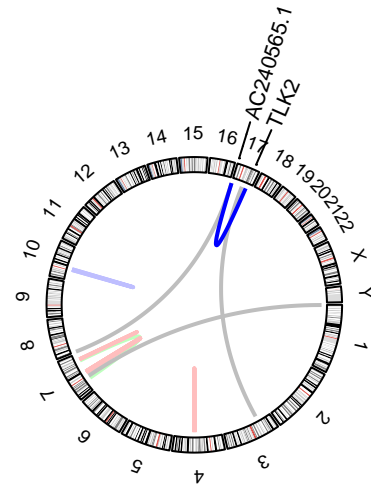
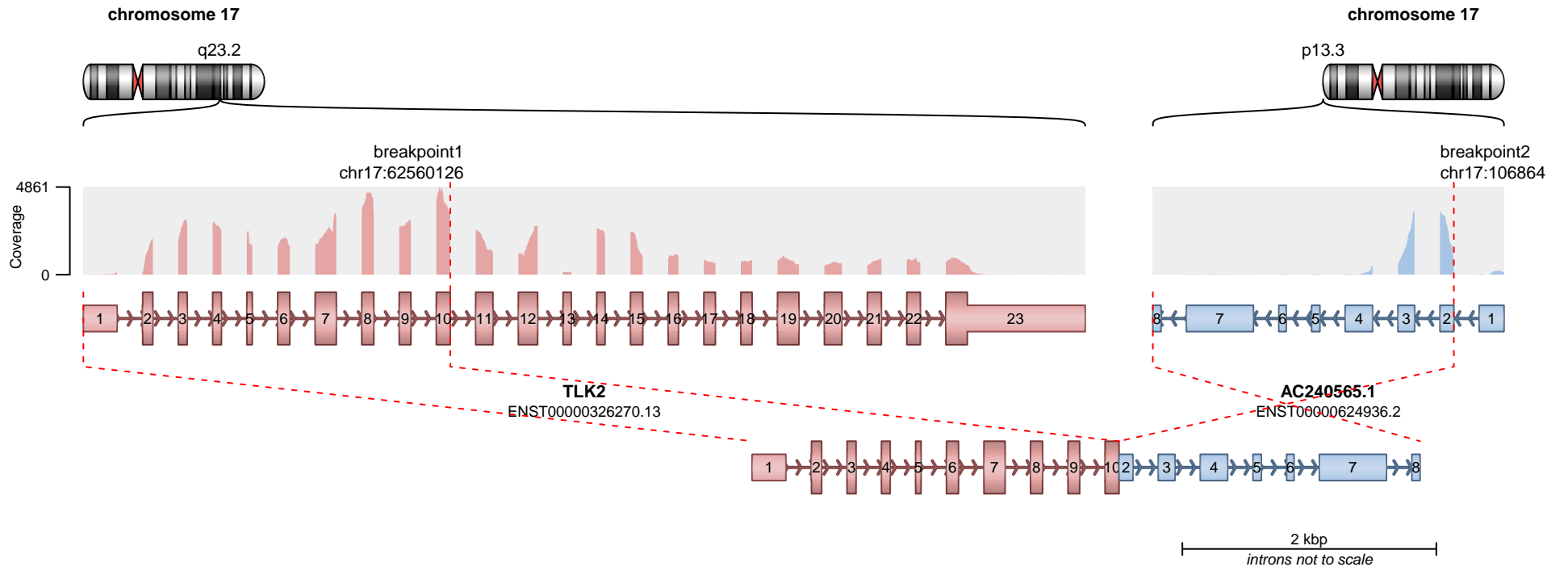


— translocation    — deletion  
 — duplication    — inversion

No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 1  
 Discordant mates = 0

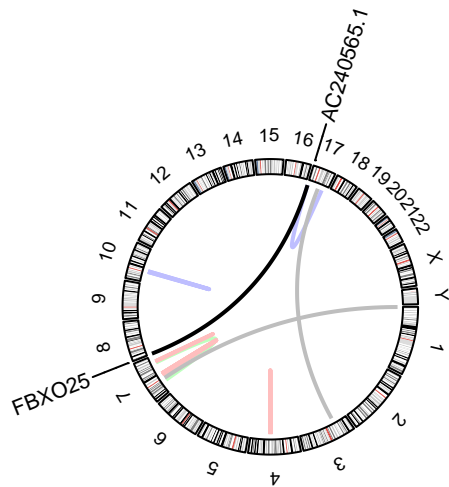
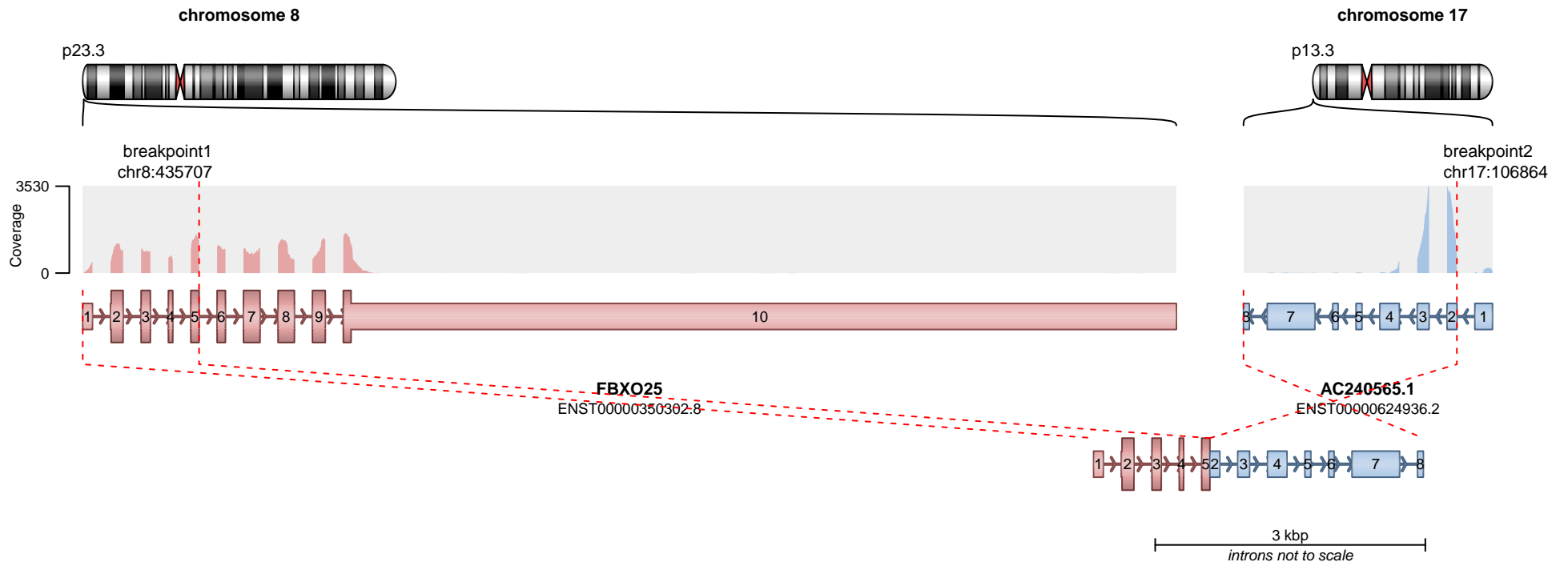


No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 200  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion

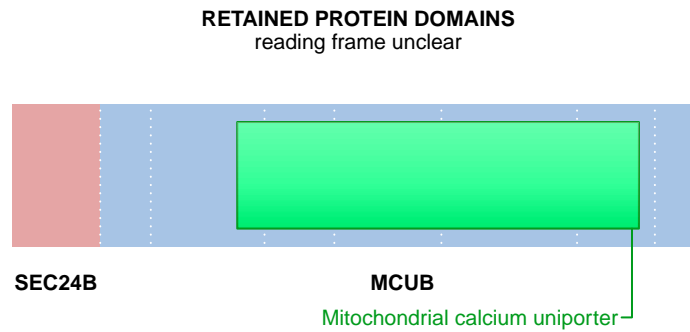
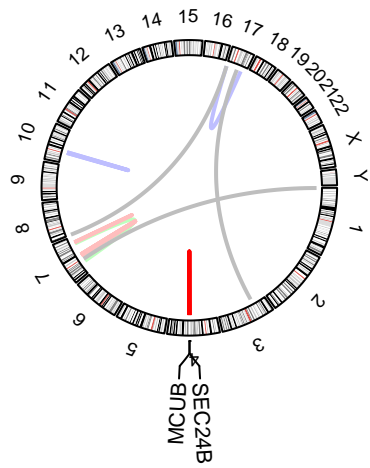
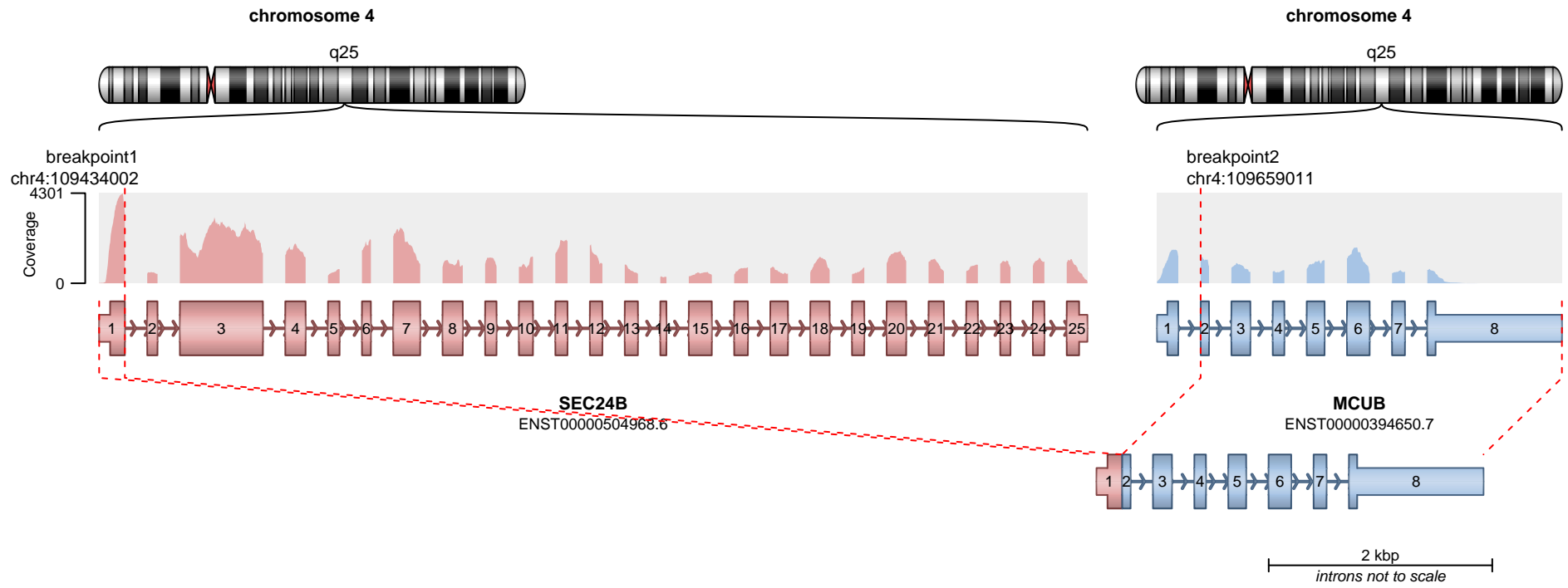


No protein domains retained in fusion.

**SUPPORTING READ COUNT**

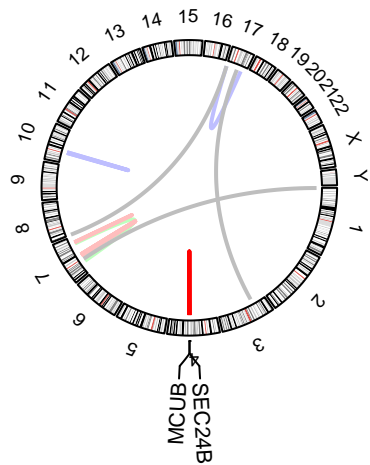
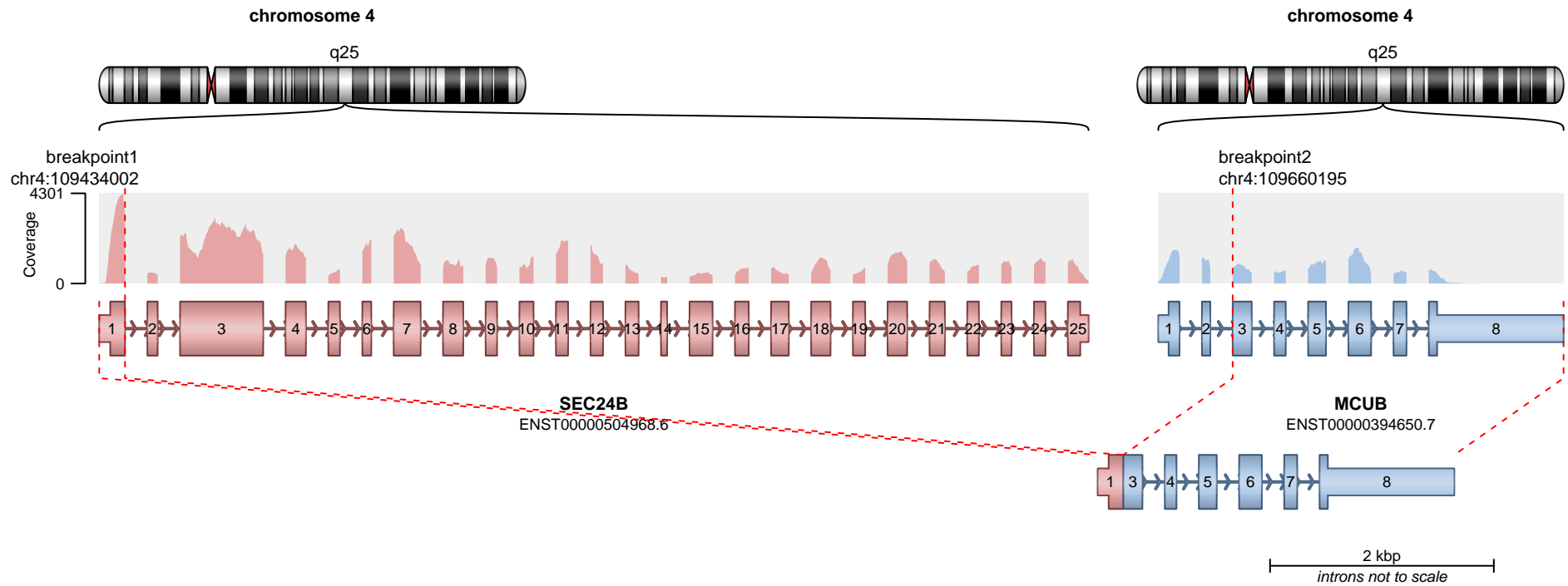
Split reads = 170  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

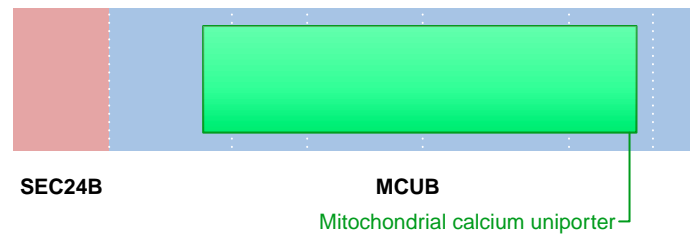


**SUPPORTING READ COUNT**

Split reads = 108  
Discordant mates = 5



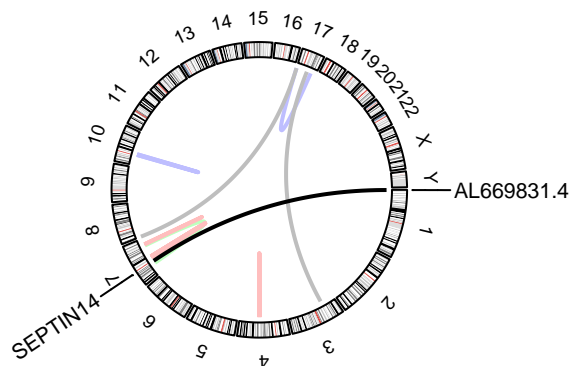
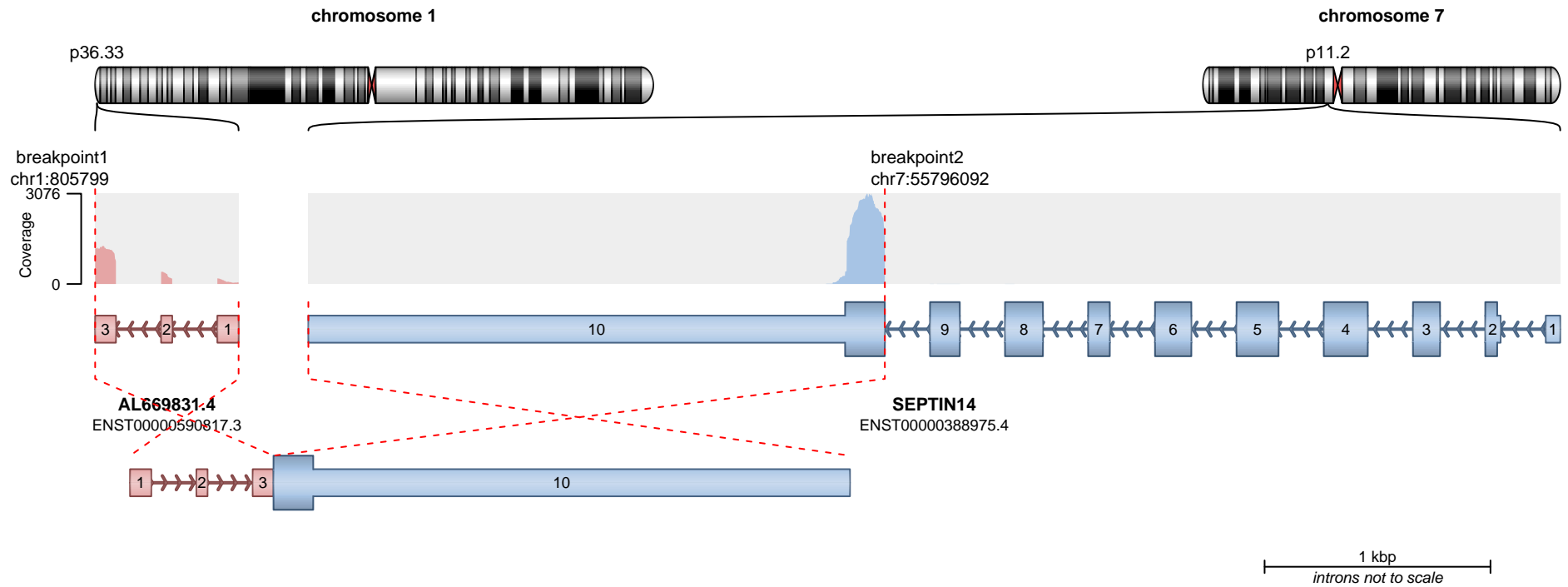
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 9  
Discordant mates = 0

— translocation — deletion  
— duplication — inversion

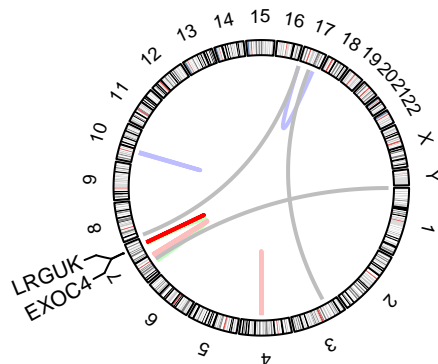
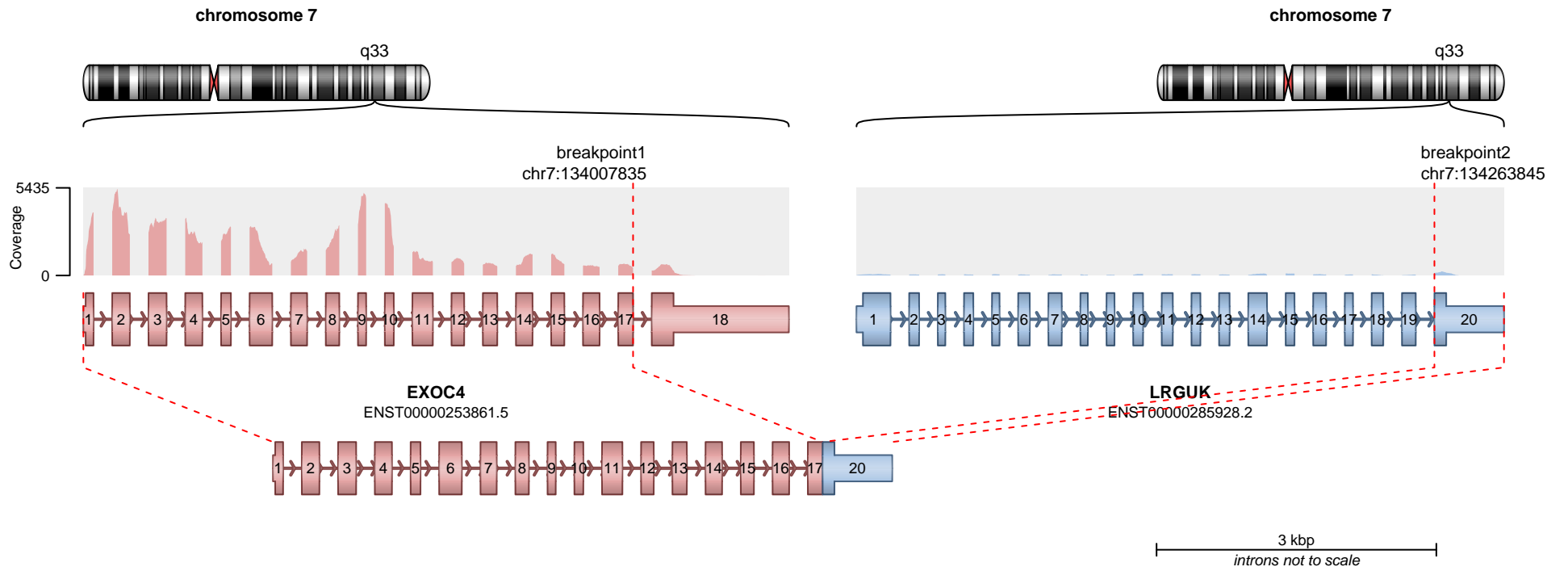


No protein domains retained in fusion.

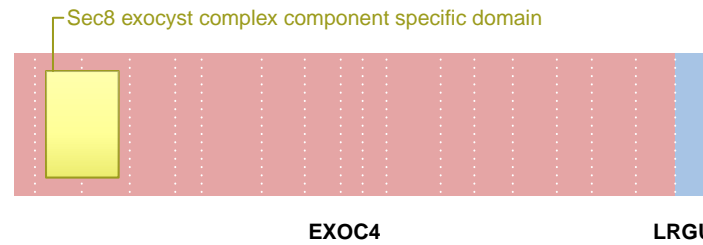
**SUPPORTING READ COUNT**

Split reads = 64  
Discordant mates = 1

— translocation    — deletion  
— duplication    — inversion



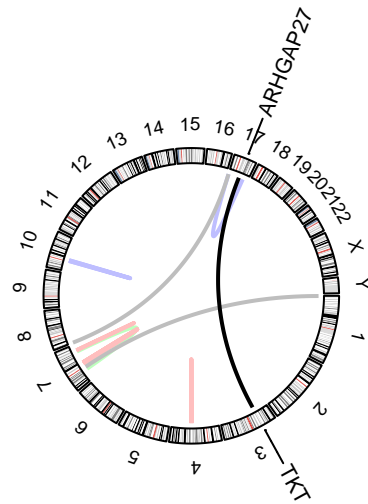
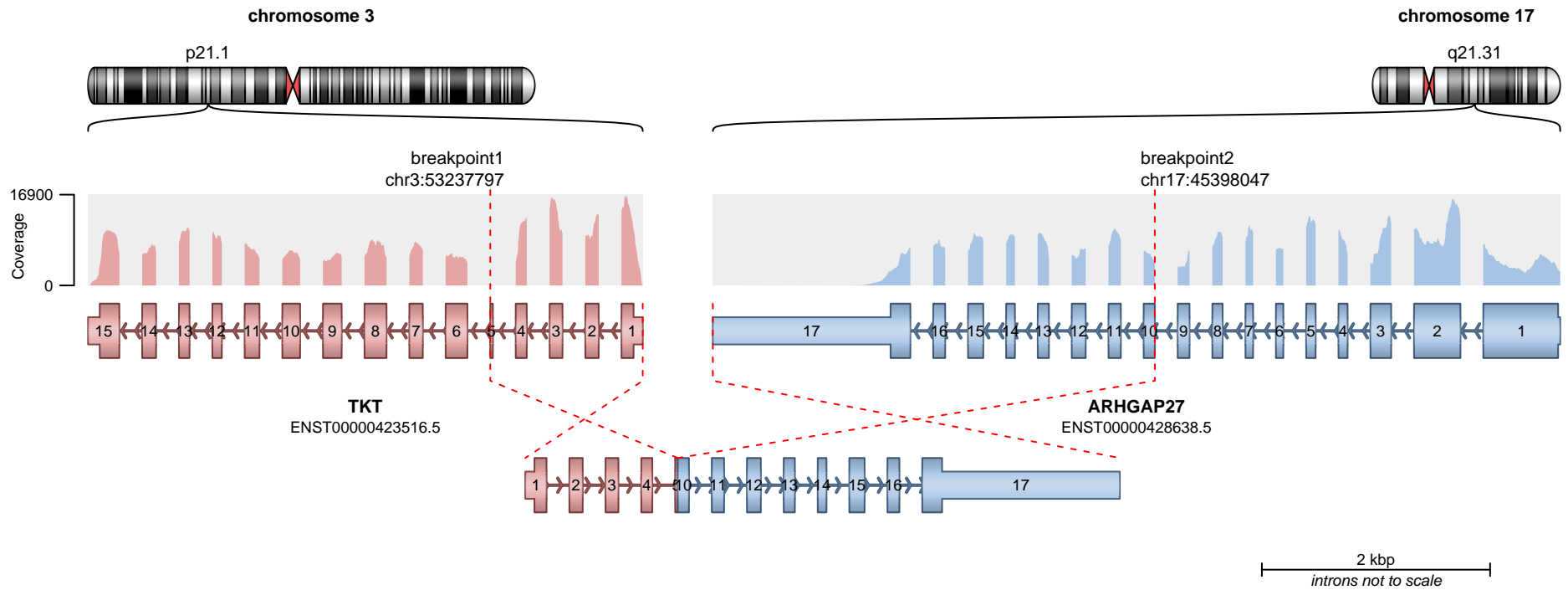
**RETAINED PROTEIN DOMAINS**  
reading frame unclear



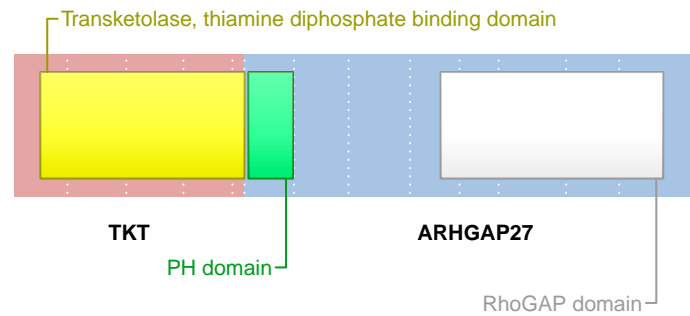
**SUPPORTING READ COUNT**

Split reads = 39  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



**RETAINED PROTEIN DOMAINS**  
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 12  
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion