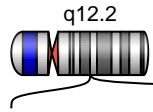
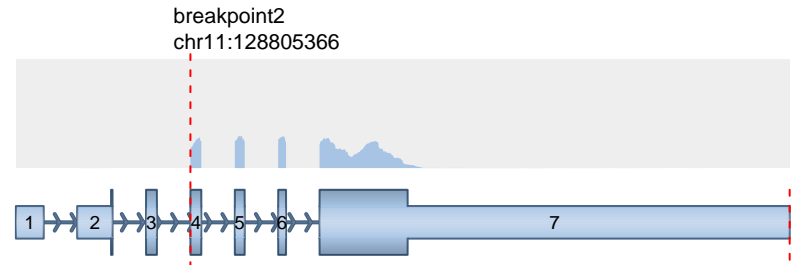
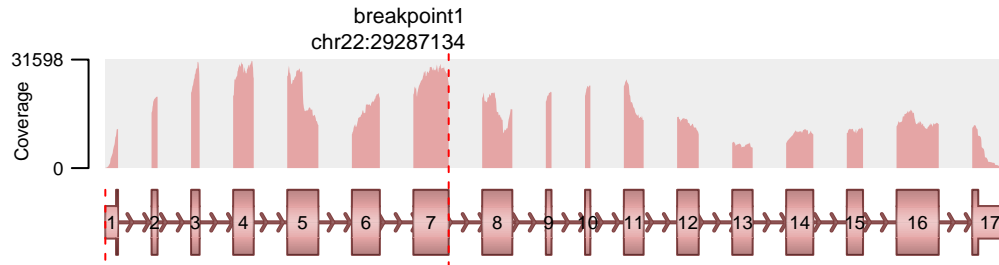
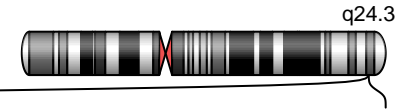


chromosome 22

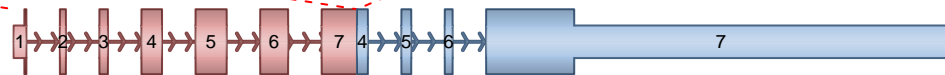


chromosome 11

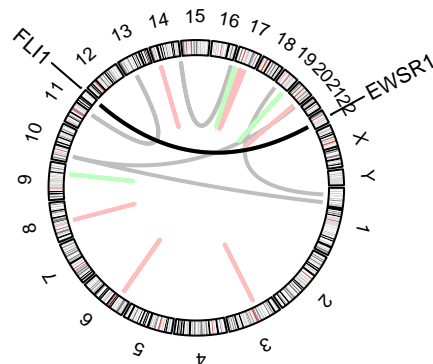


EWSR1
ENST00000406548.5

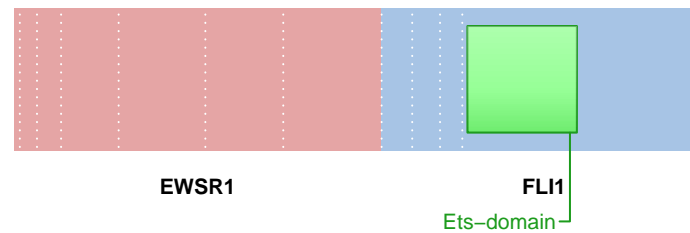
FLI1
ENST00000344954.10



2 kbp
introns not to scale



RETAINED PROTEIN DOMAINS
reading frame unclear

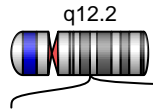


SUPPORTING READ COUNT

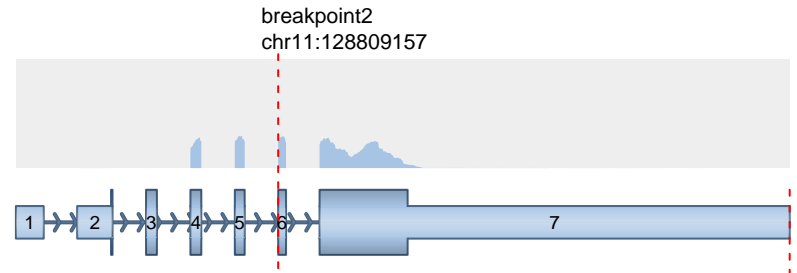
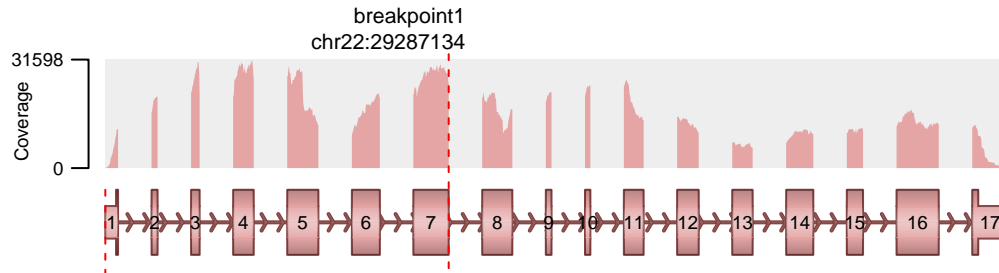
Split reads = 2316
Discordant mates = 6

— translocation — deletion
— duplication — inversion

chromosome 22

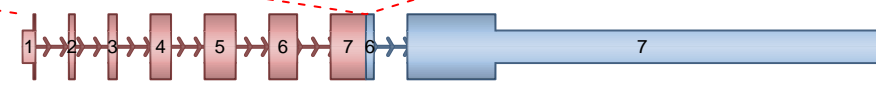


chromosome 11

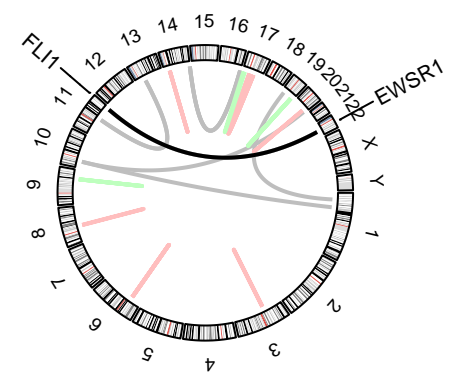


EWSR1
ENST00000406548.5

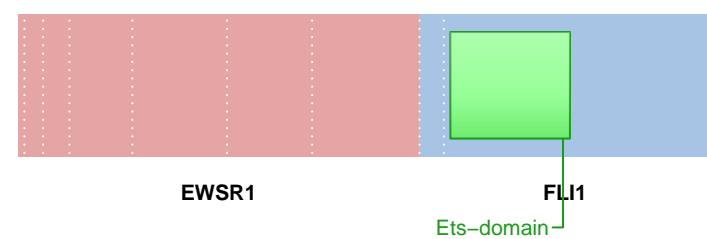
FLI1
ENST00000344954.10



2 kbp
introns not to scale



RETAINED PROTEIN DOMAINS
reading frame unclear

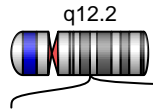


SUPPORTING READ COUNT

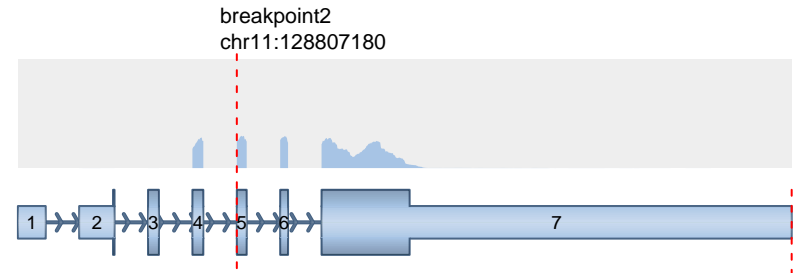
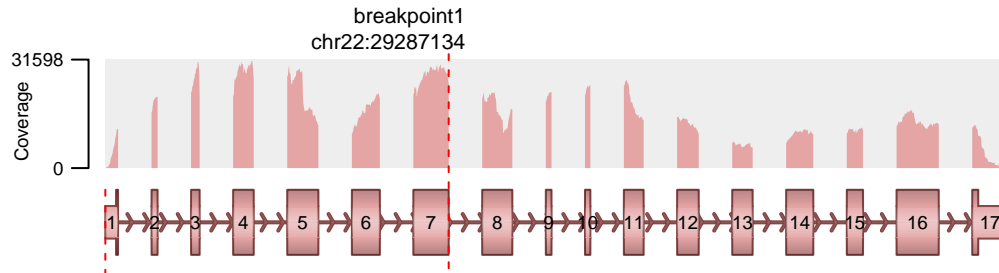
Split reads = 24
Discordant mates = 0

— translocation — deletion
— duplication — inversion

chromosome 22



chromosome 11

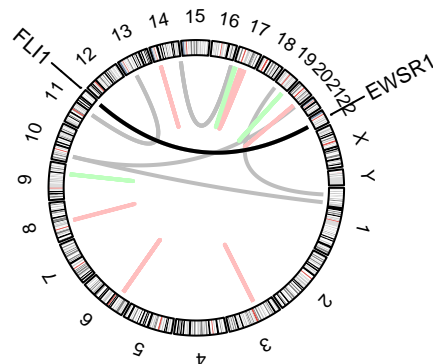


EWSR1
ENST00000406548.5

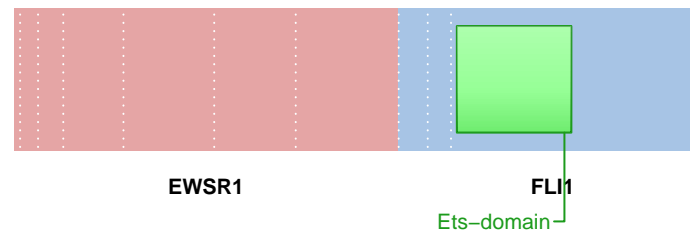
FLI1
ENST00000344954.10



2 kbp
introns not to scale



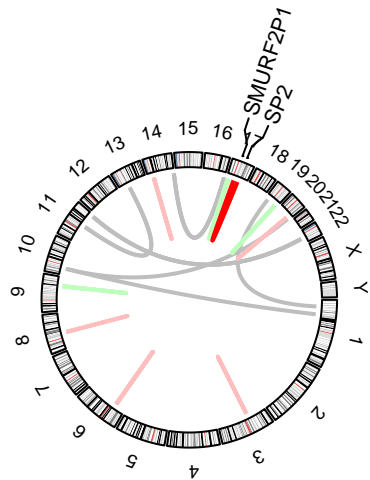
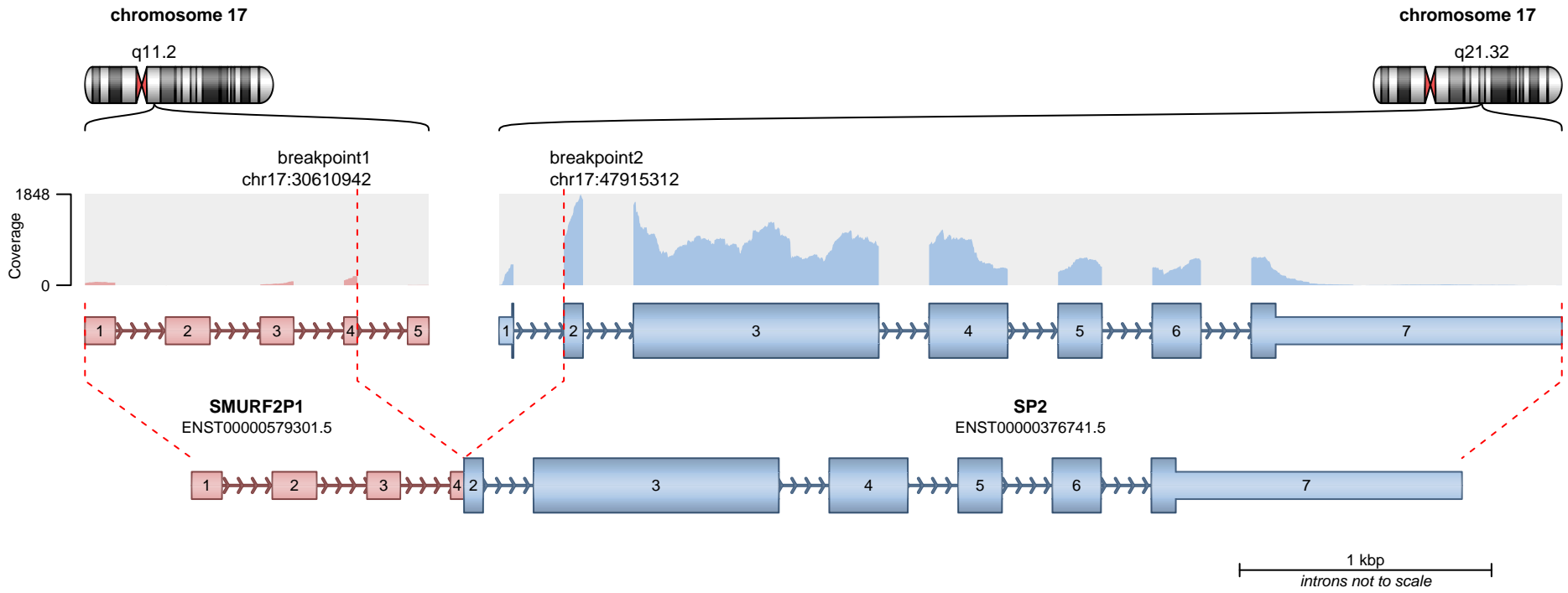
RETAINED PROTEIN DOMAINS
reading frame unclear



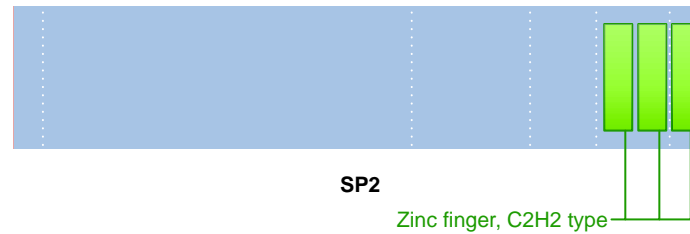
SUPPORTING READ COUNT

Split reads = 14
Discordant mates = 1

— translocation — deletion
— duplication — inversion



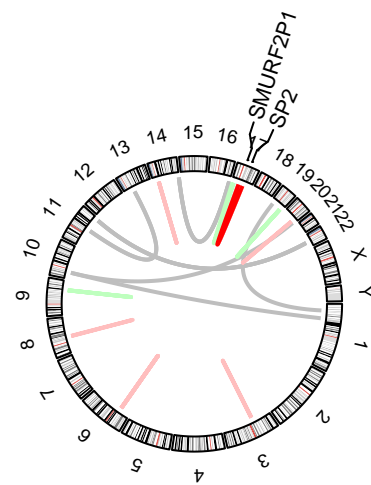
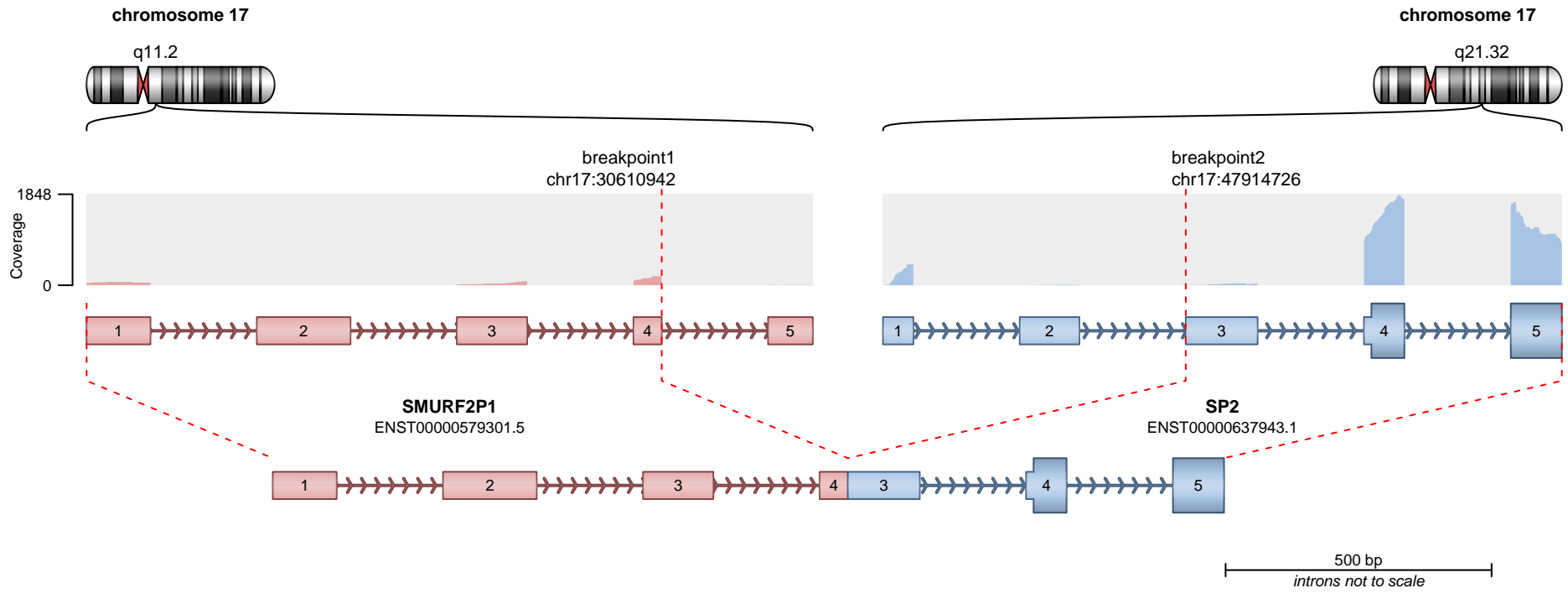
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 146
Discordant mates = 0

— translocation — deletion
— duplication — inversion

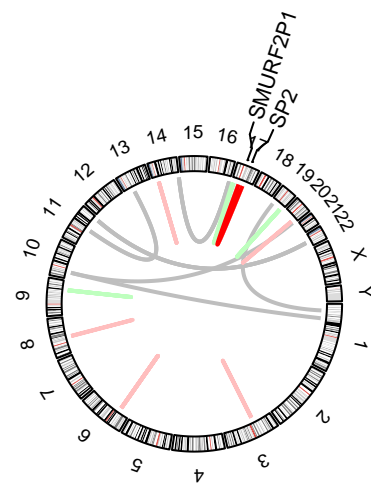
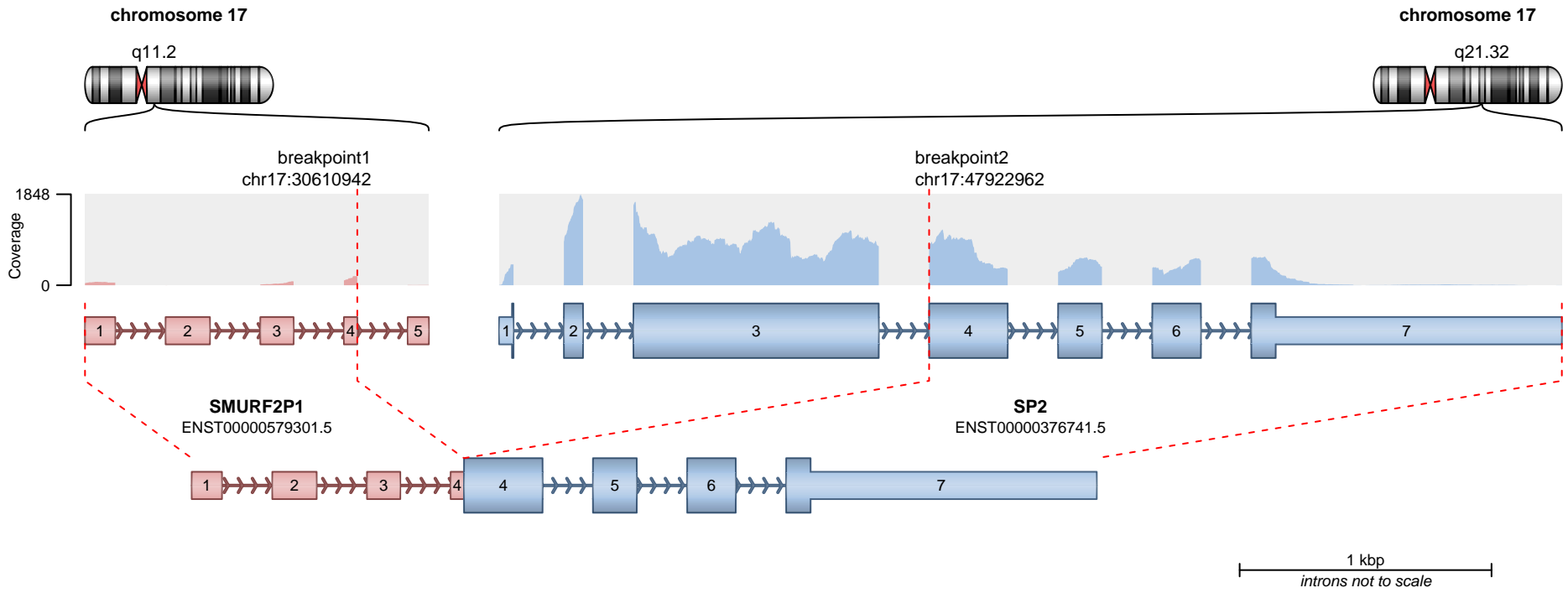


No protein domains retained in fusion.

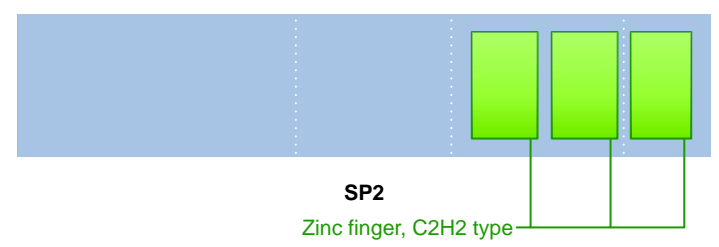
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 1

— translocation — deletion
— duplication — inversion



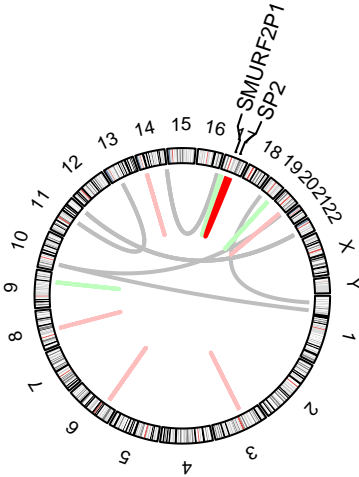
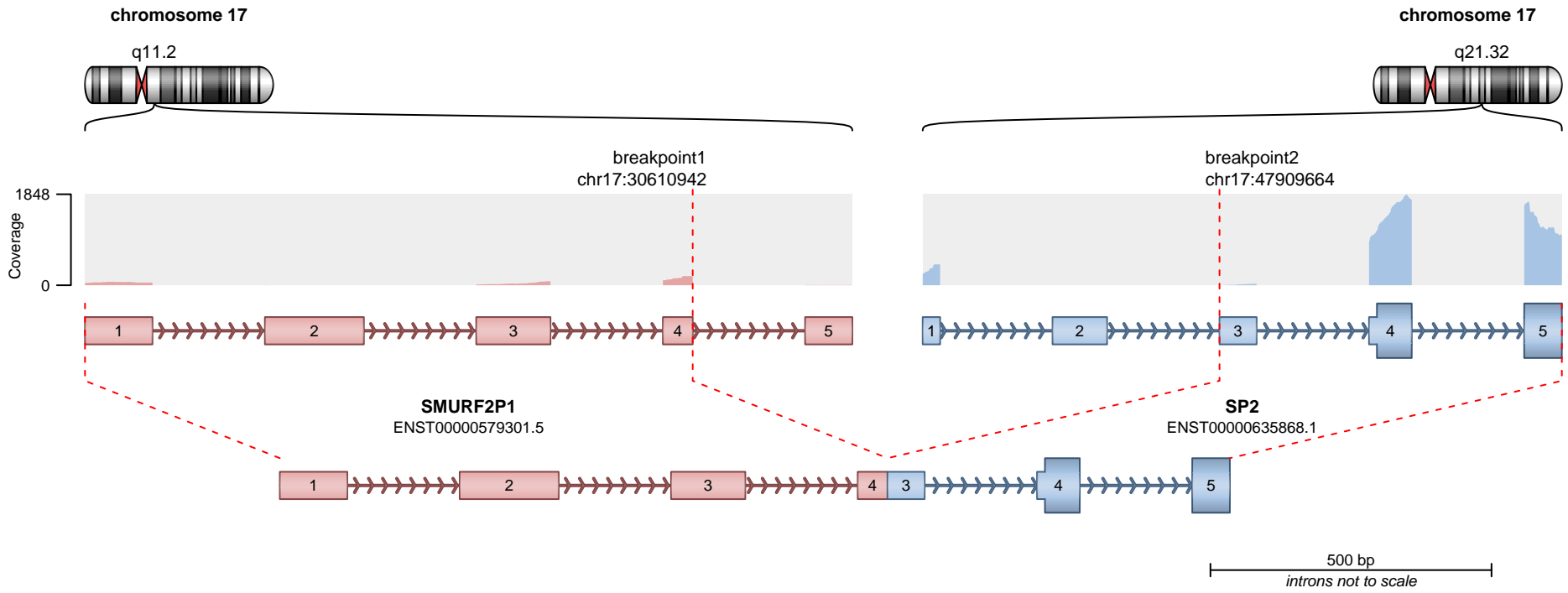
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

— translocation — deletion
— duplication — inversion

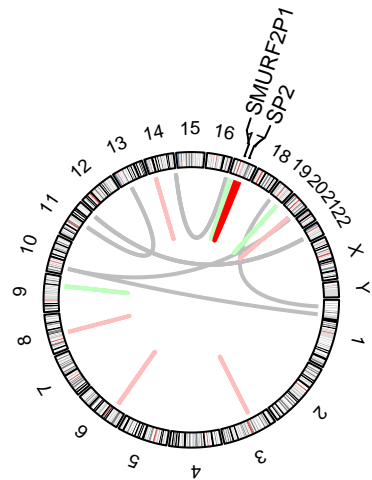
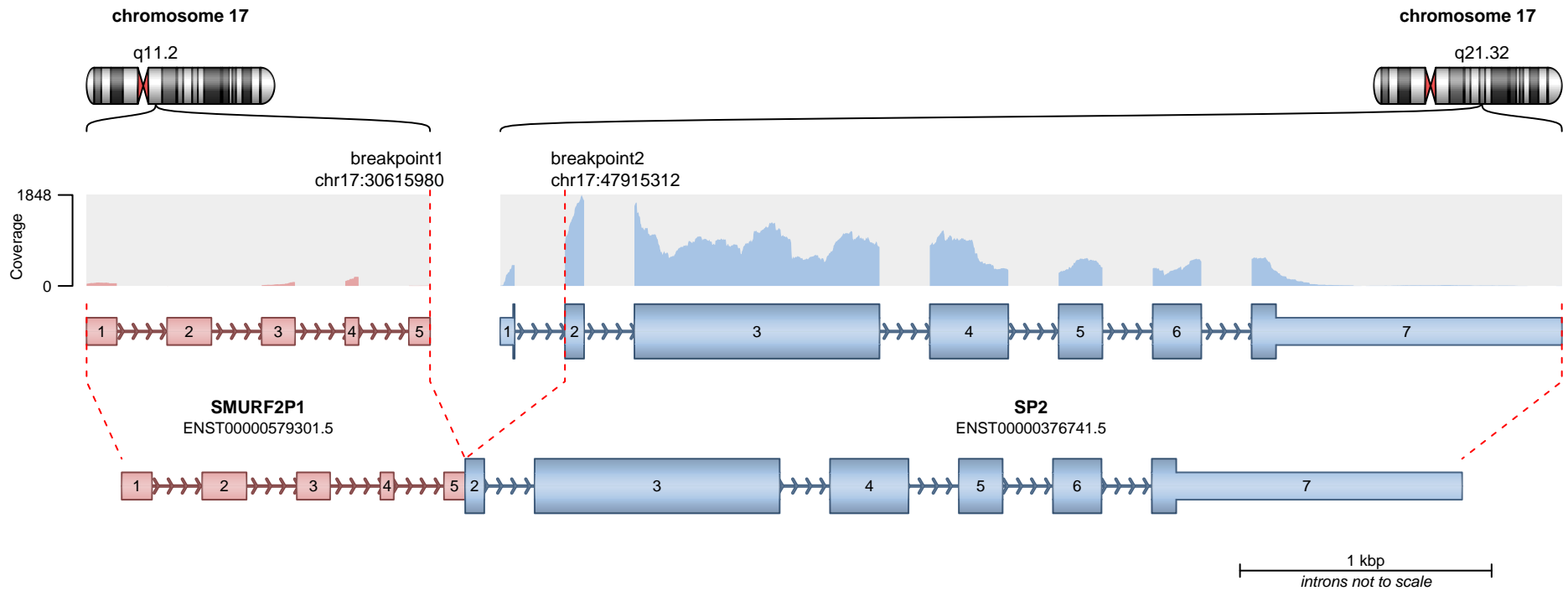


No protein domains retained in fusion.

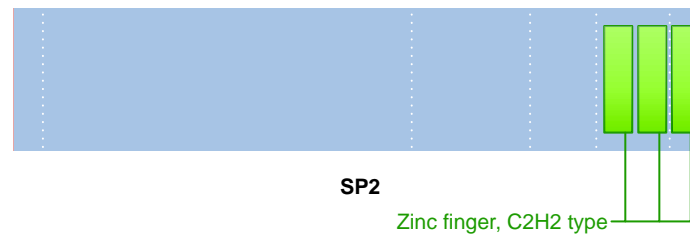
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



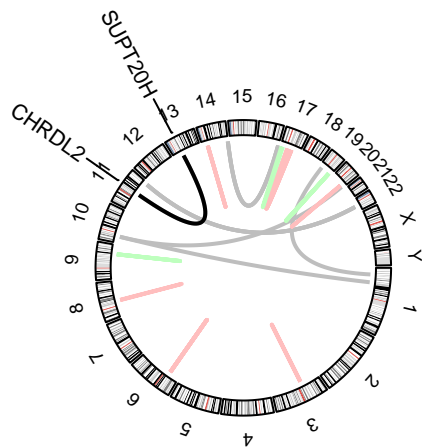
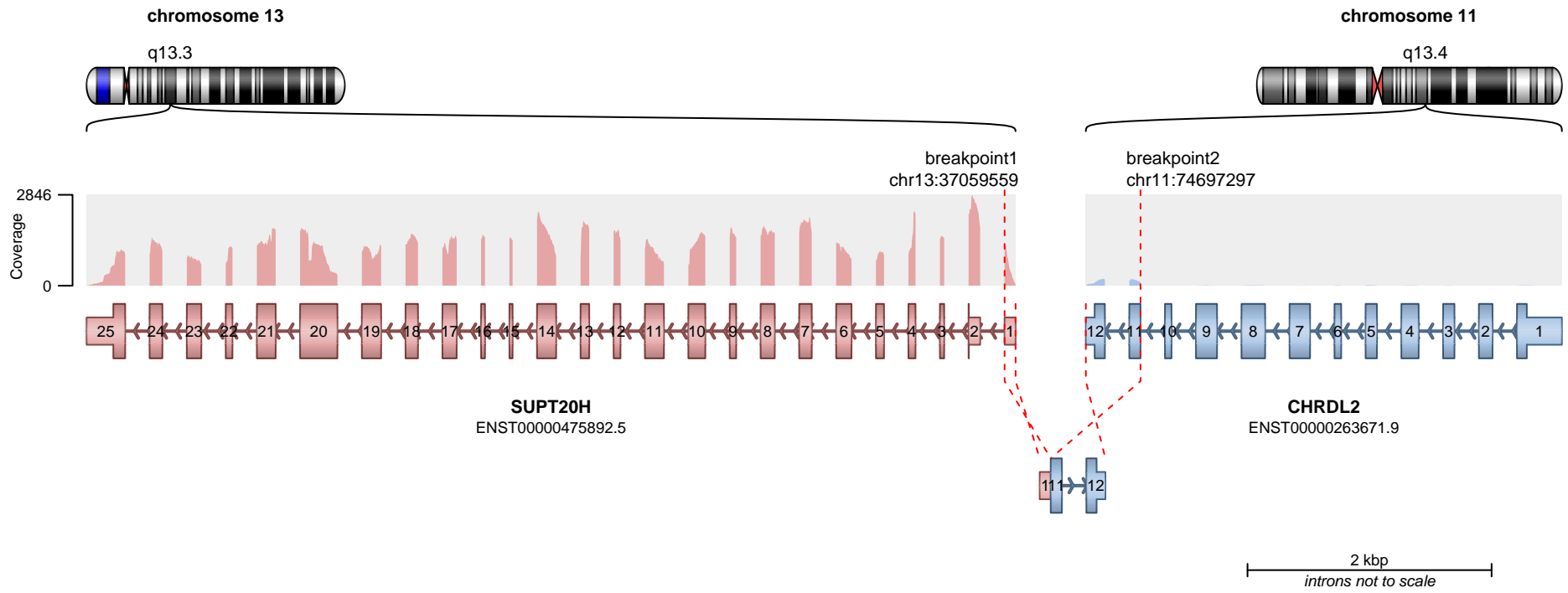
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion

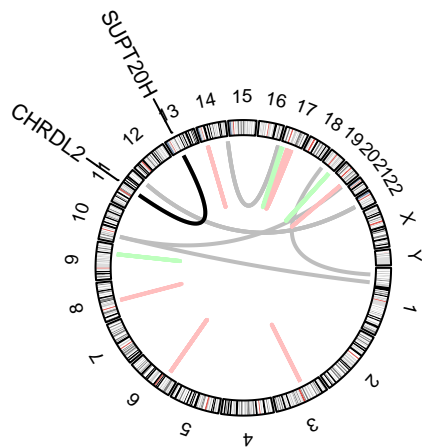
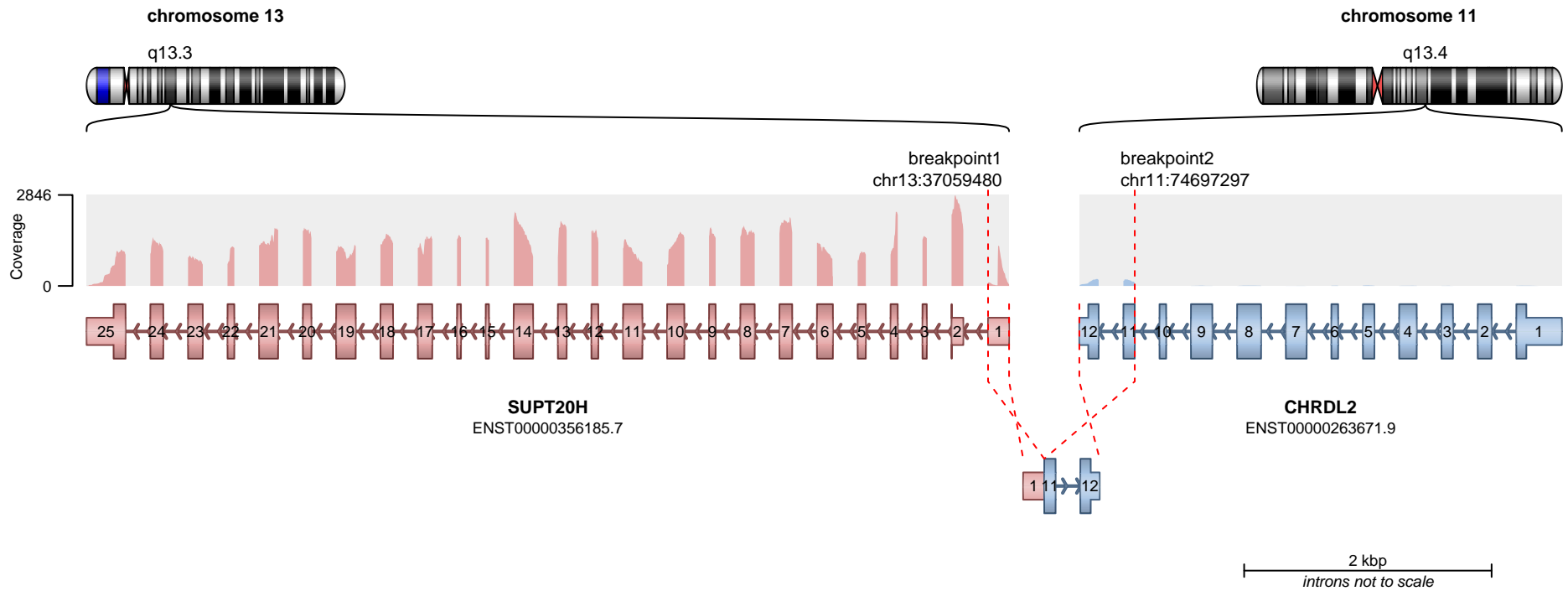


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 29
Discordant mates = 0

— translocation — deletion
— duplication — inversion

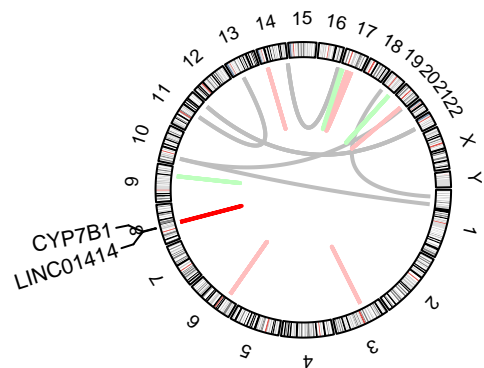
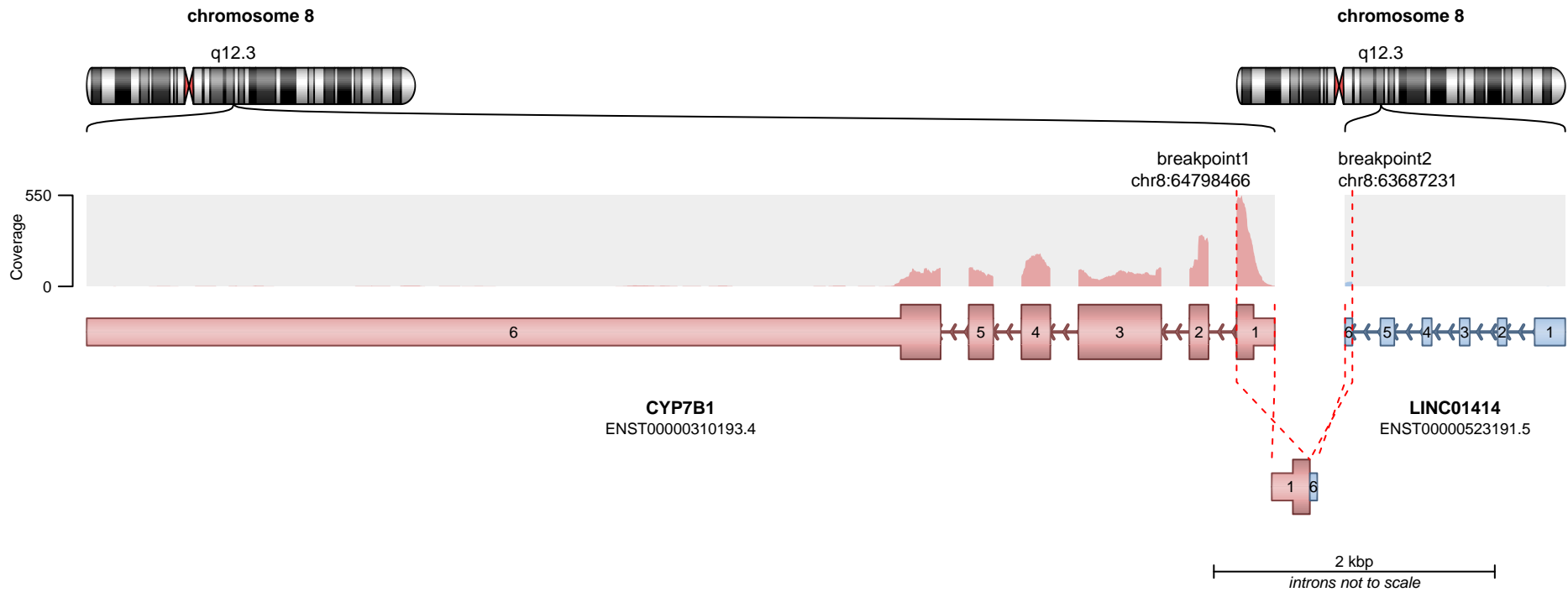


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 11
Discordant mates = 0

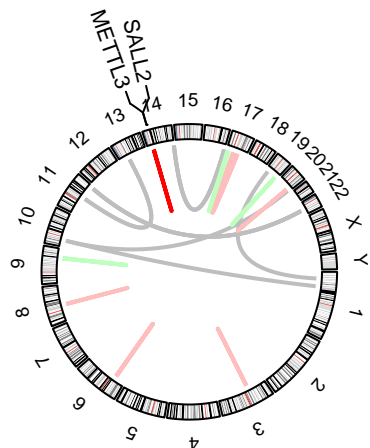
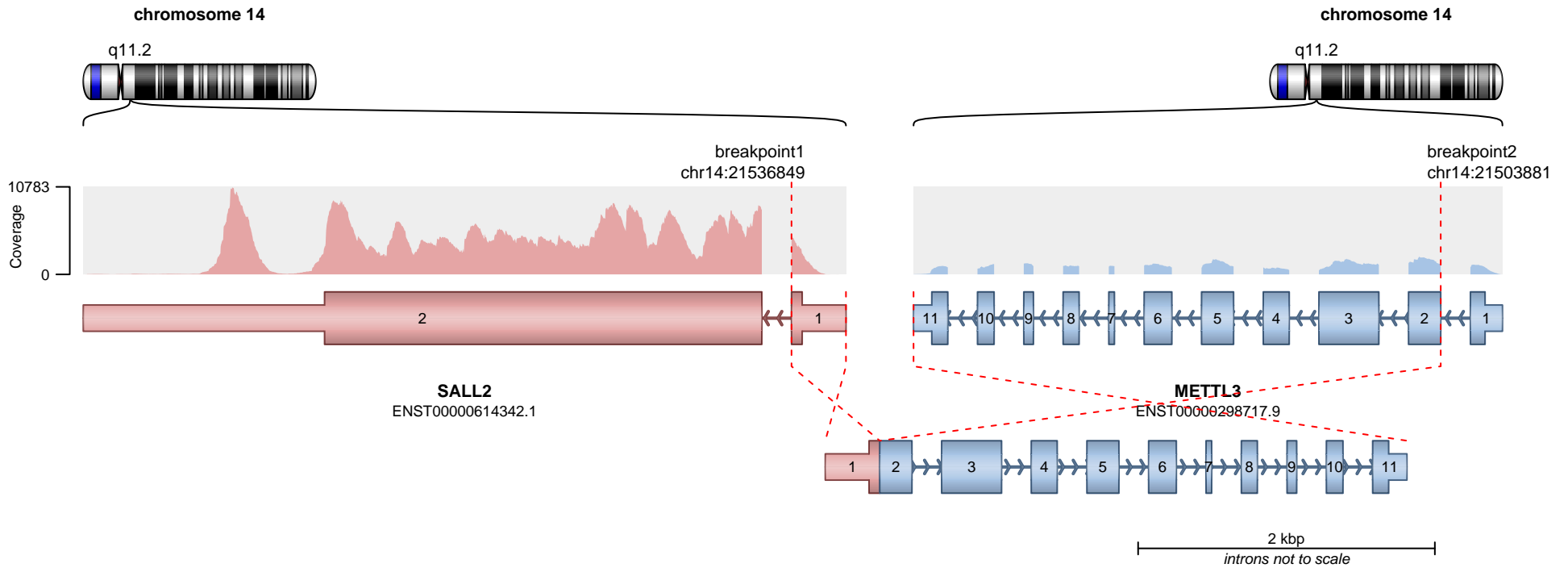


— translocation — deletion
— duplication — inversion

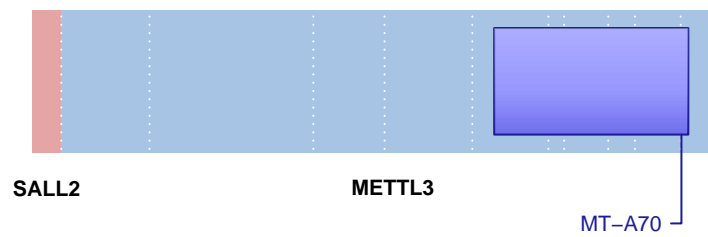
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 20
Discordant mates = 0



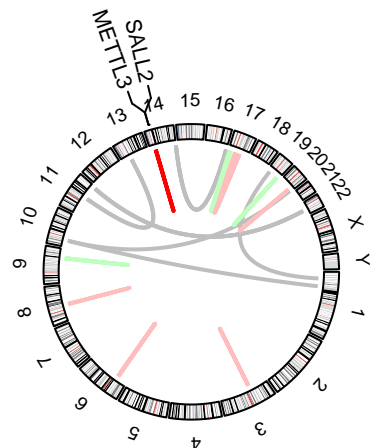
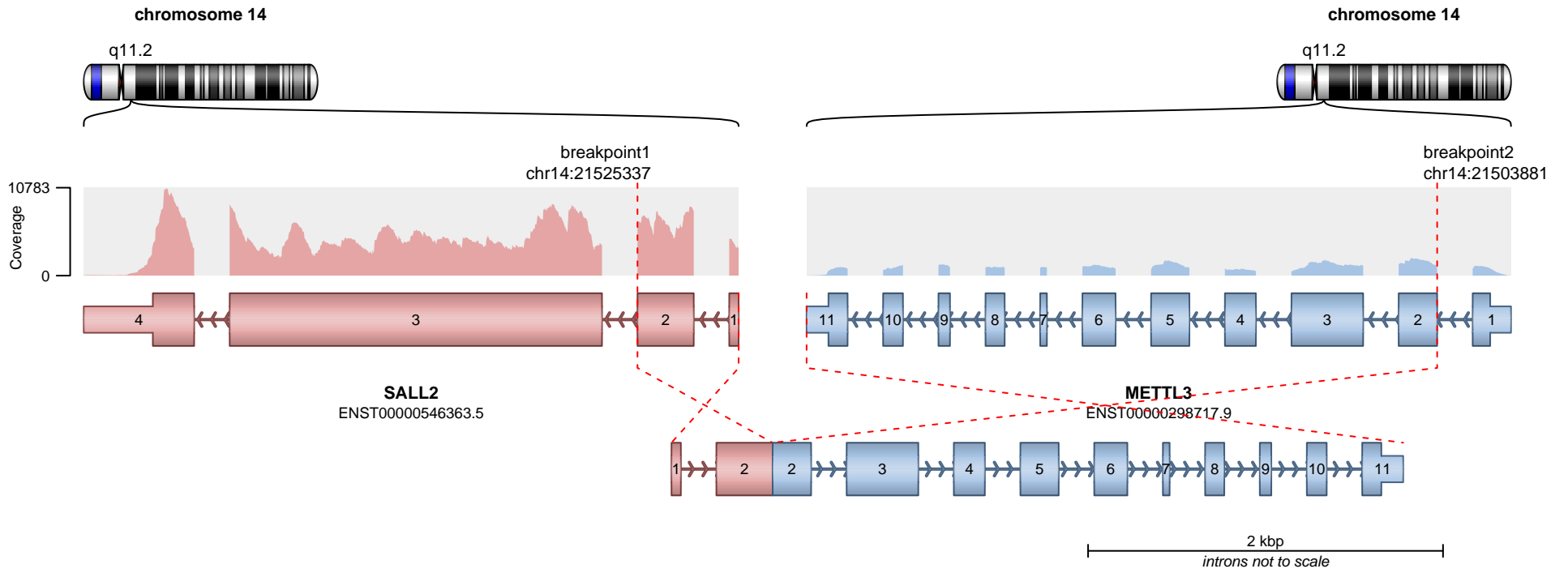
RETAINED PROTEIN DOMAINS
reading frame unclear



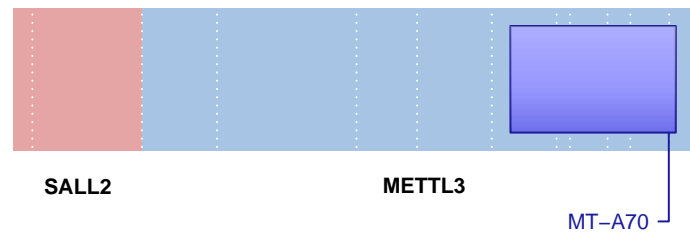
SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 0

— translocation — deletion
— duplication — inversion



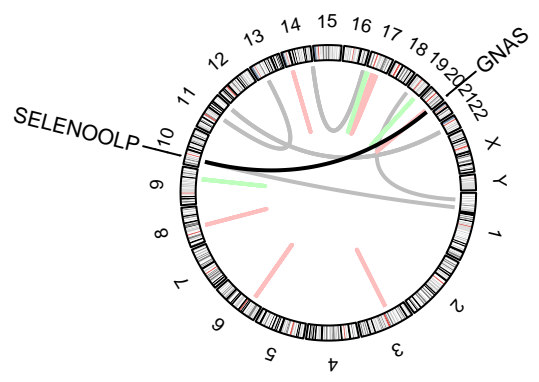
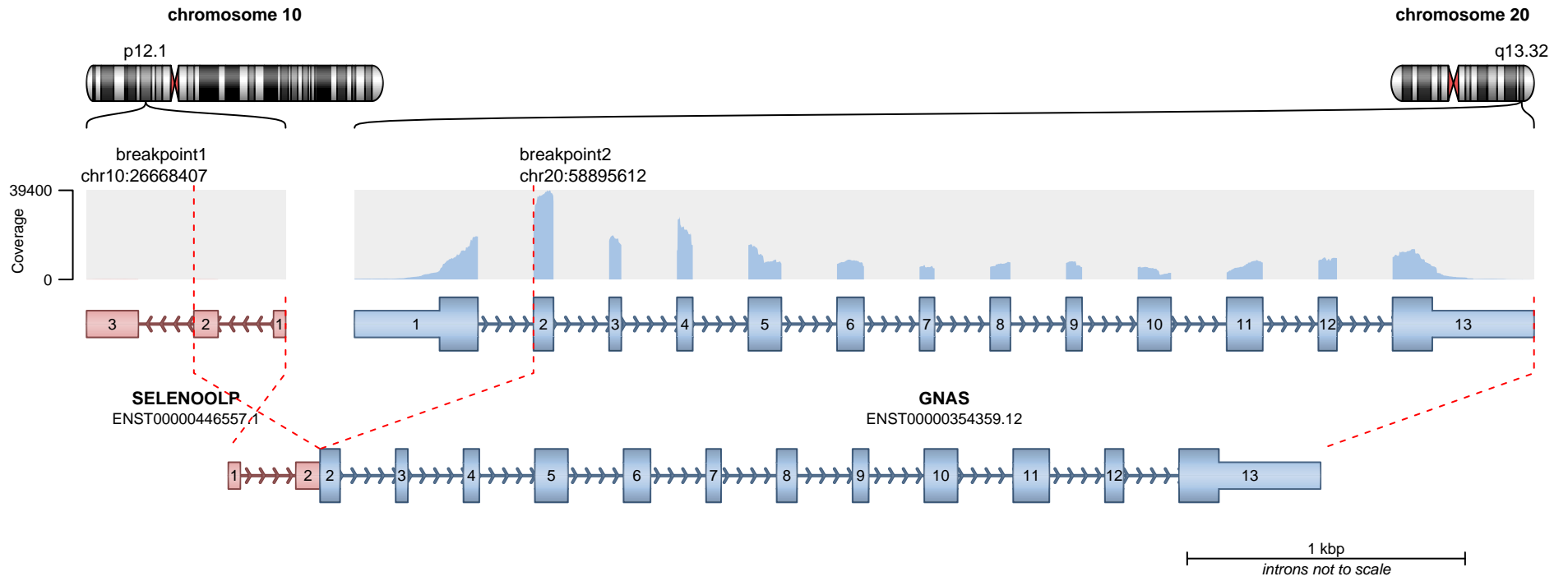
RETAINED PROTEIN DOMAINS
reading frame unclear



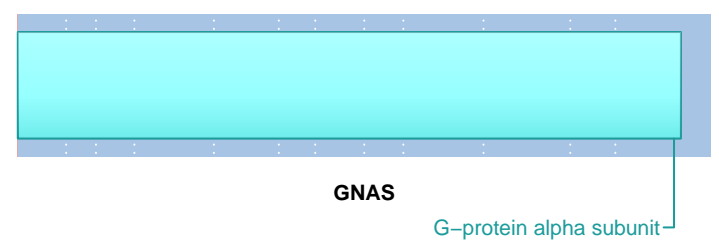
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

— translocation — deletion
— duplication — inversion



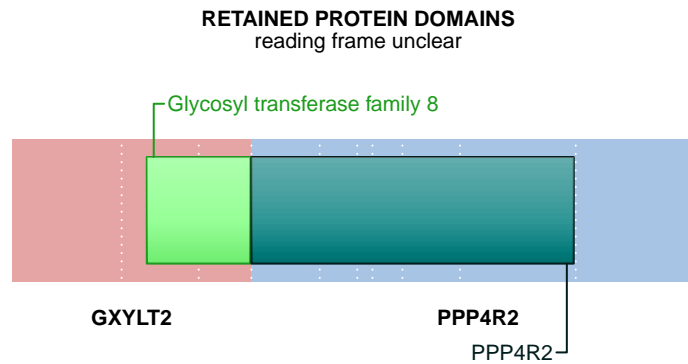
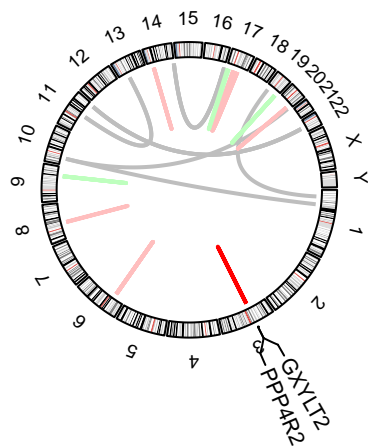
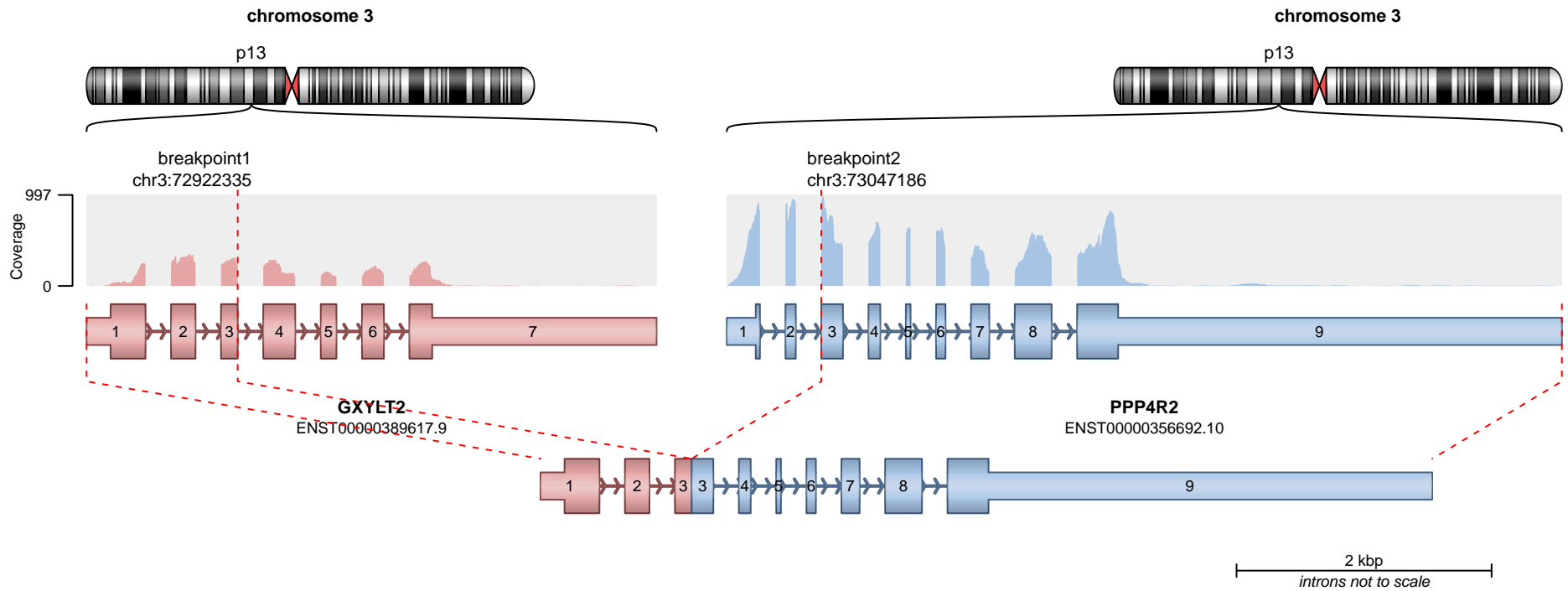
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 0

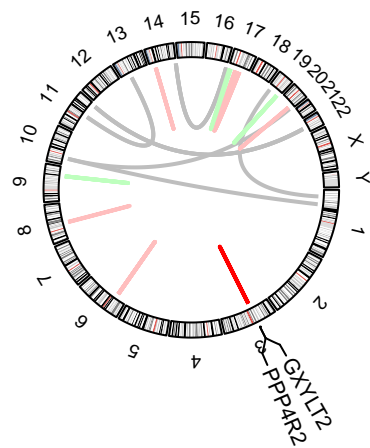
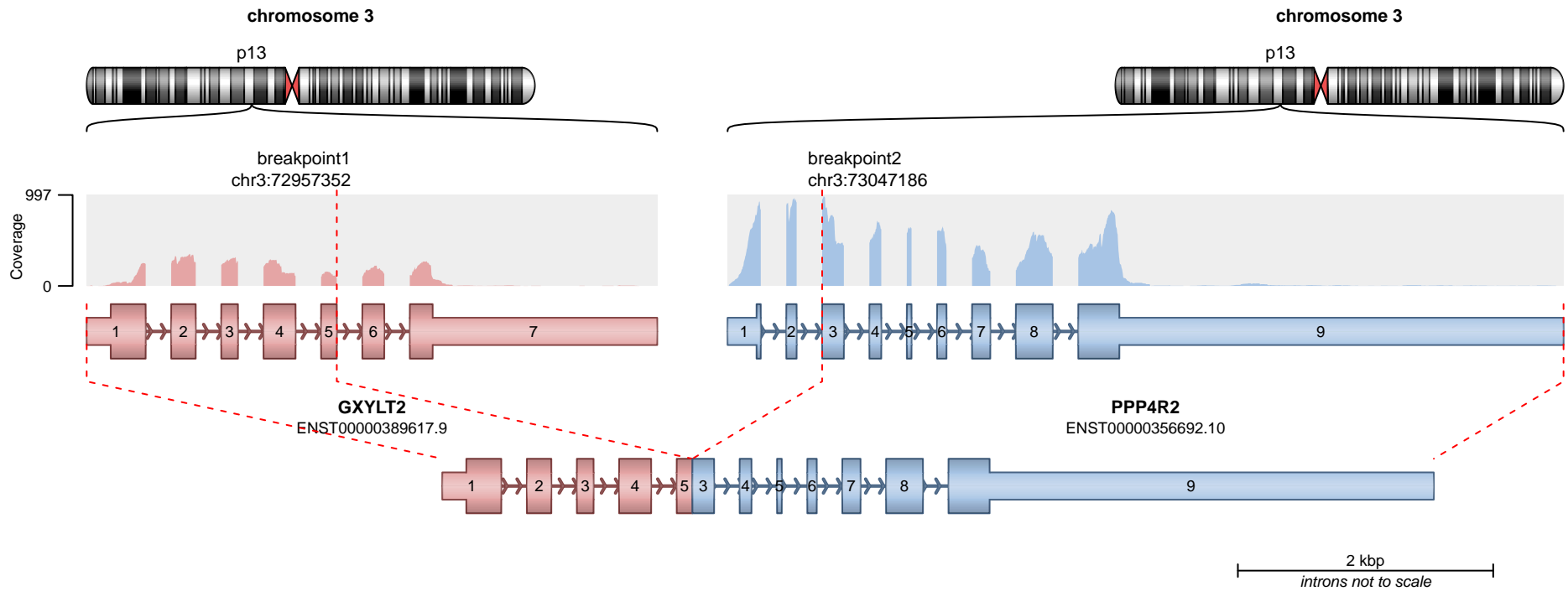
- translocation
- duplication
- deletion
- inversion



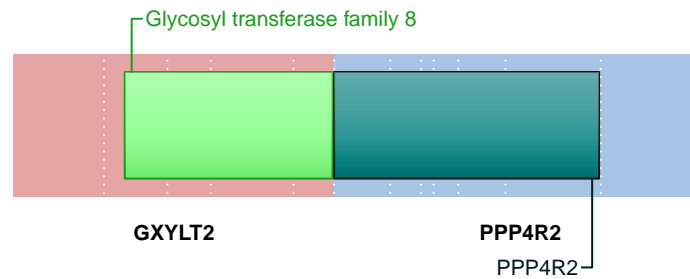
SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 0

— translocation — deletion
— duplication — inversion



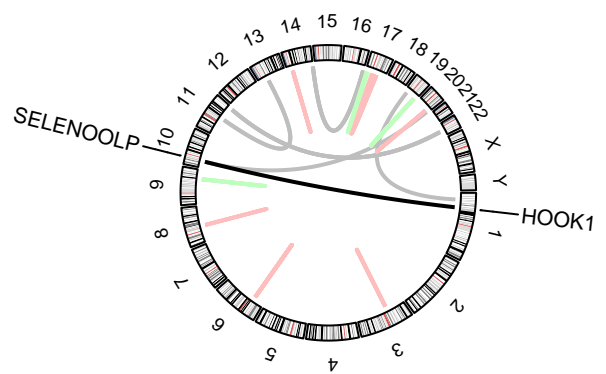
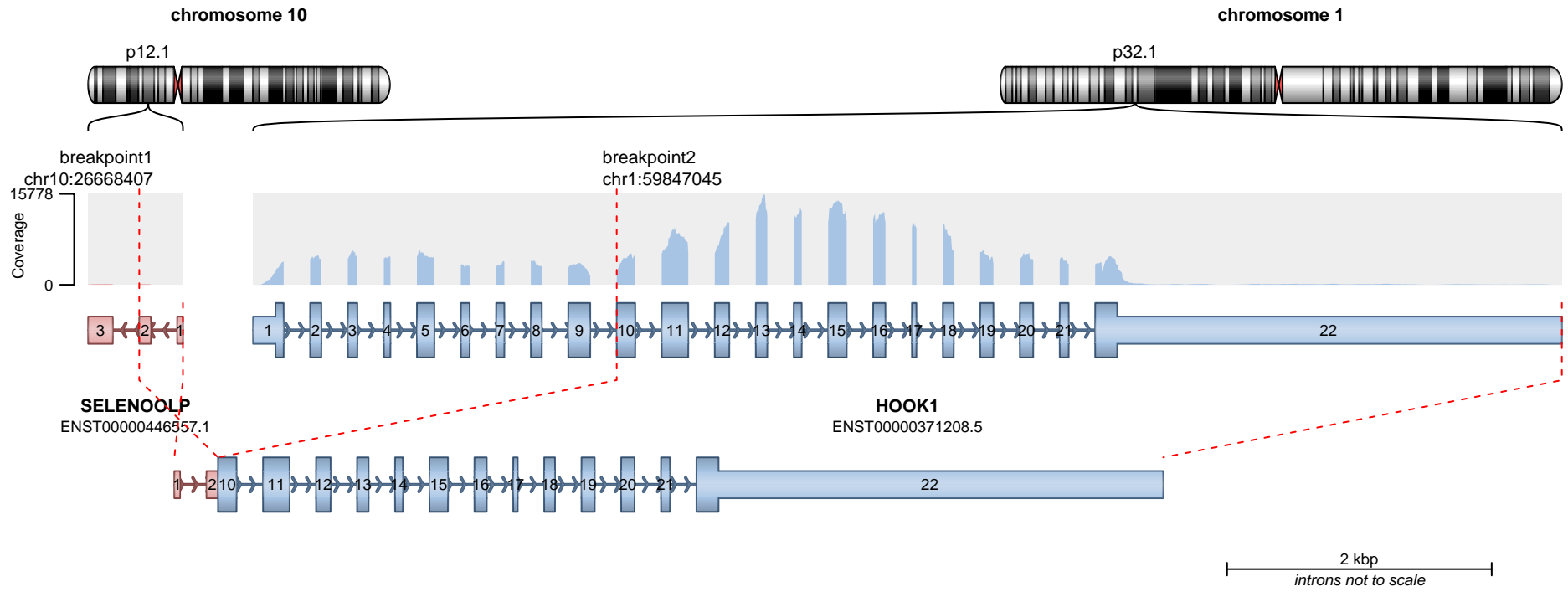
RETAINED PROTEIN DOMAINS
reading frame unclear



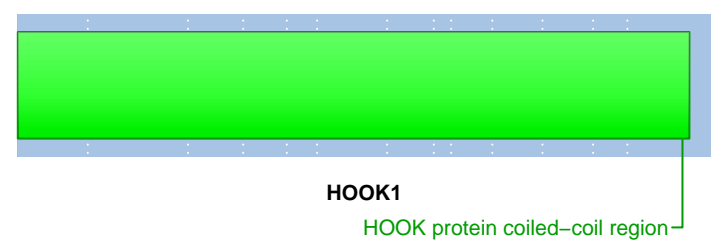
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



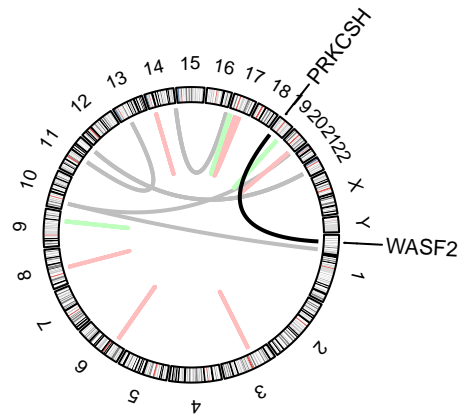
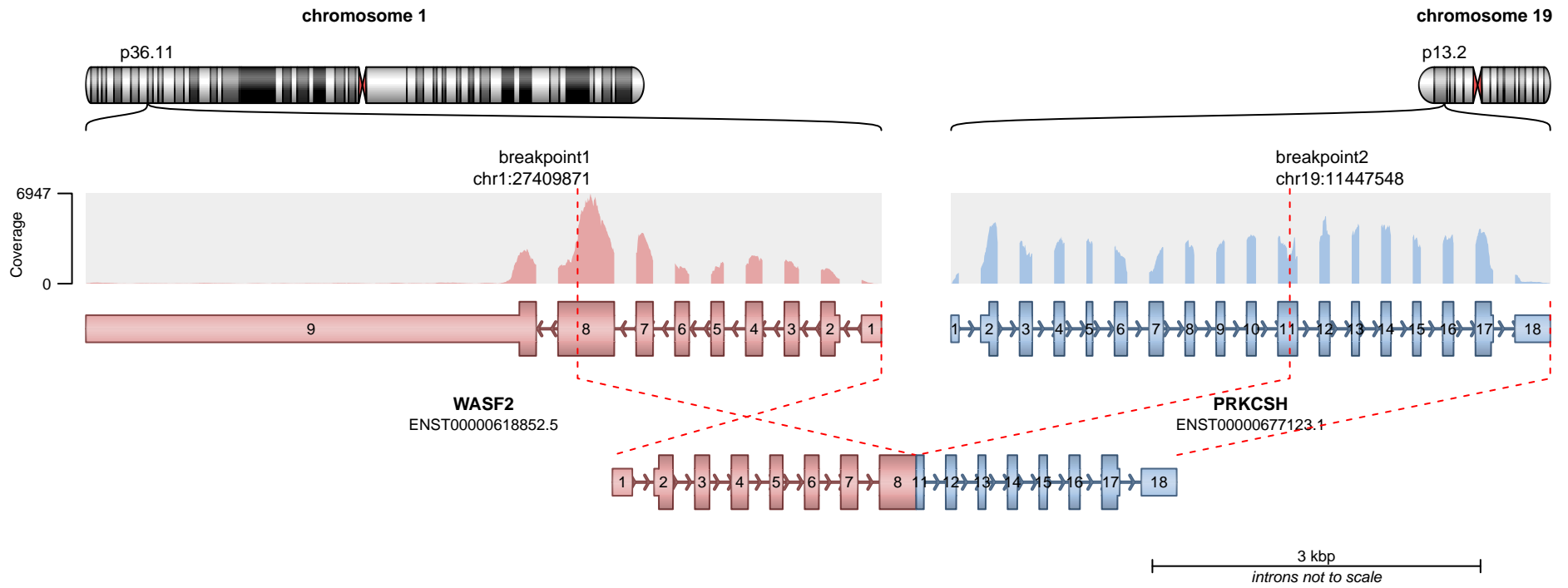
RETAINED PROTEIN DOMAINS
reading frame unclear



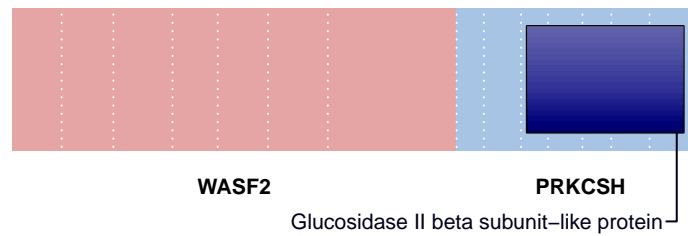
SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0

— translocation — deletion
— duplication — inversion



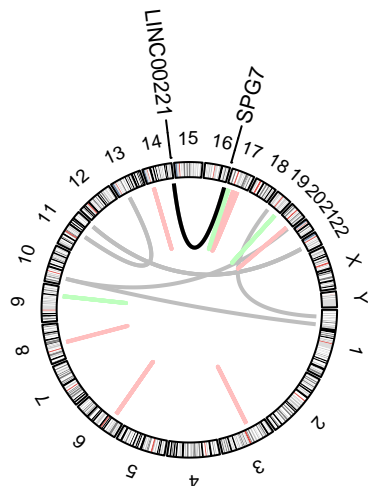
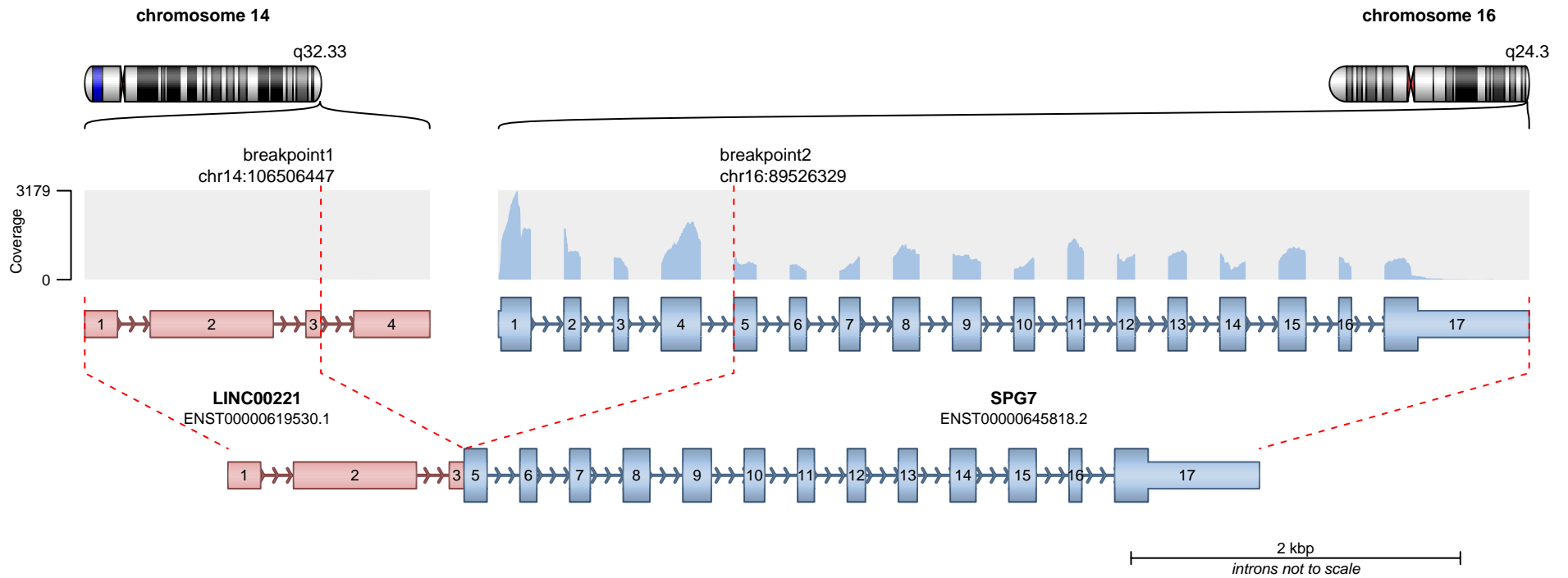
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

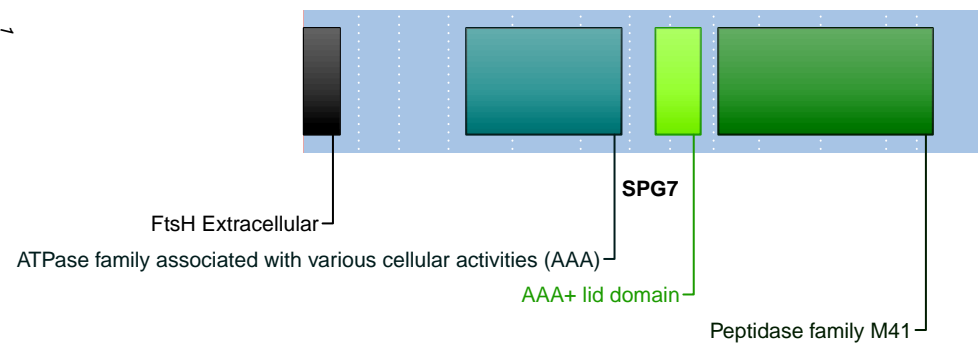
Split reads = 5
Discordant mates = 0

— translocation — deletion
— duplication — inversion



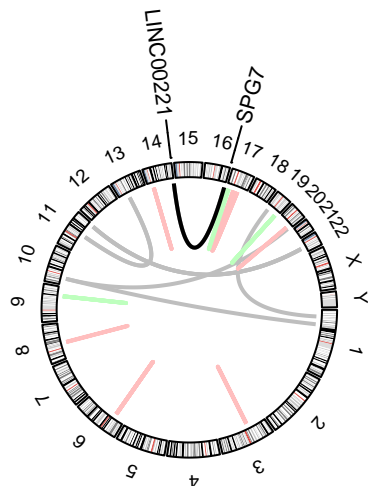
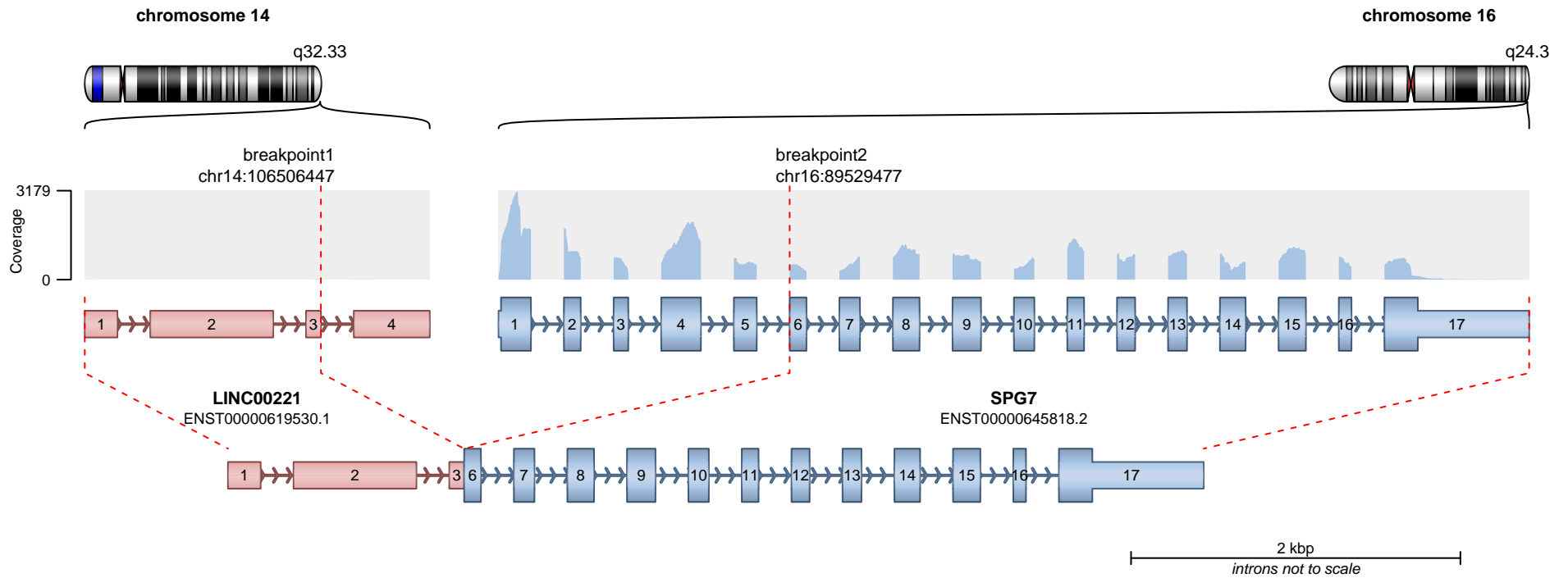
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0



RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

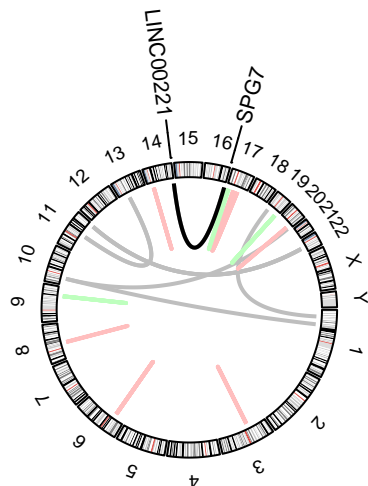
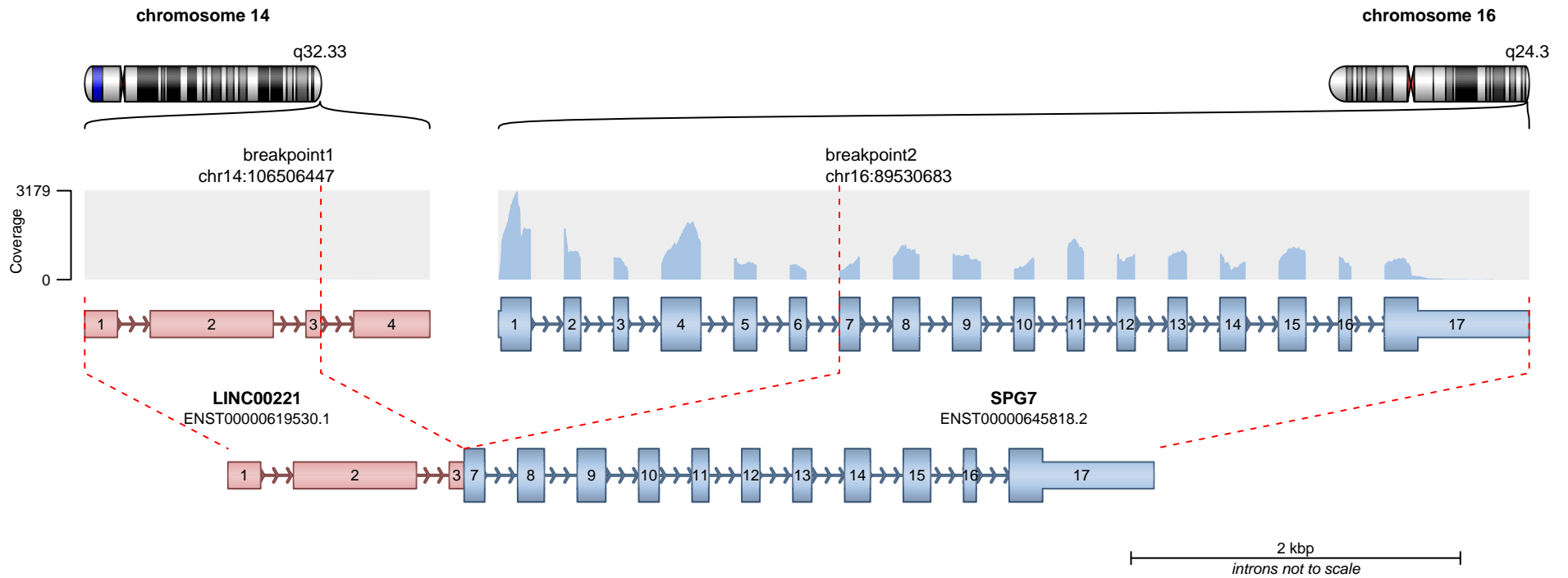
Split reads = 2
Discordant mates = 0

ATPase family associated with various cellular activities (AAA)

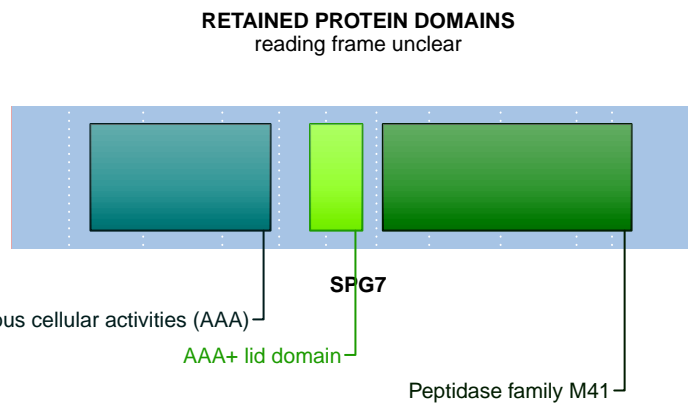
SPG7

Peptidase family M41

- translocation
- duplication
- deletion
- inversion



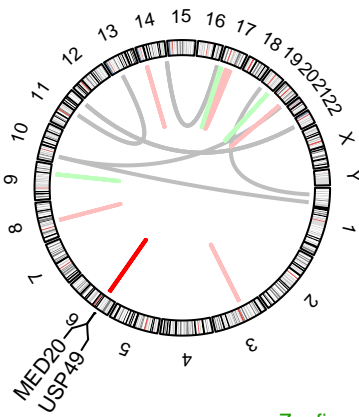
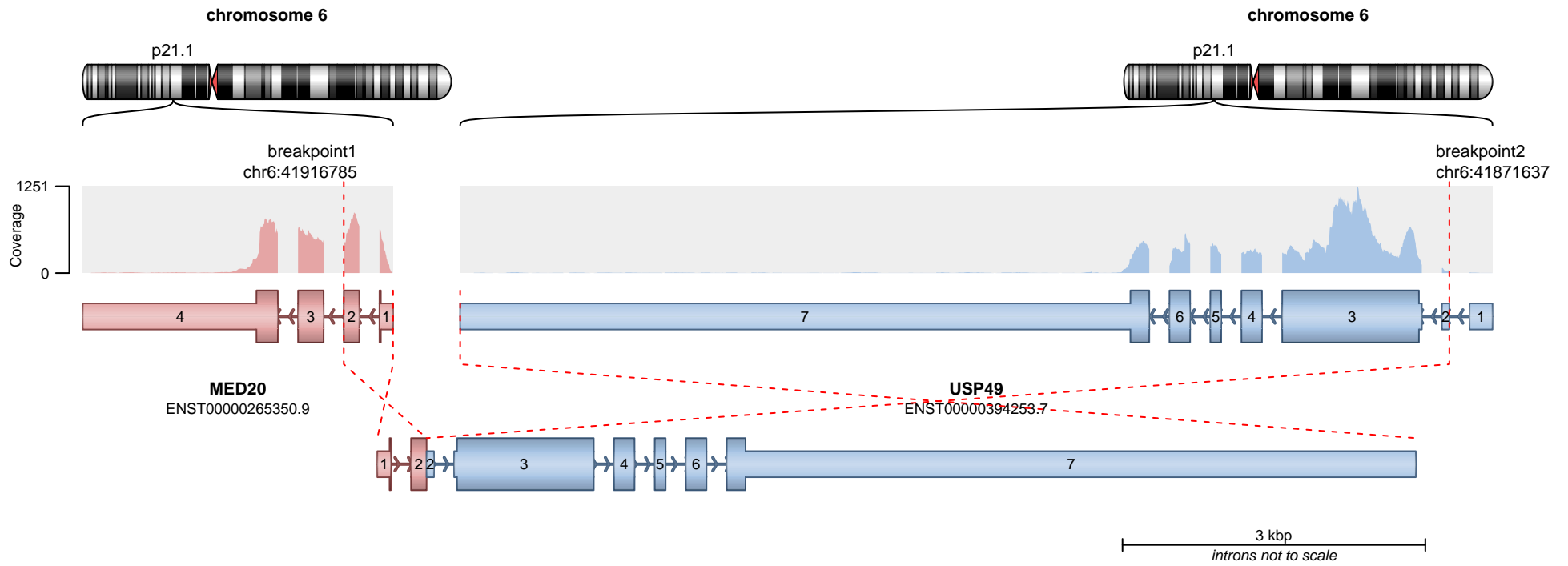
ATPase family associated with various cellular activities (AAA)



SUPPORTING READ COUNT

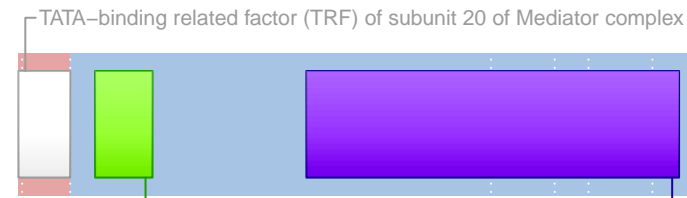
Split reads = 1
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



Zn-finger in ubiquitin-hydrolases and other protein

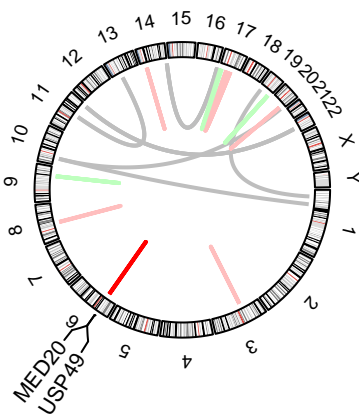
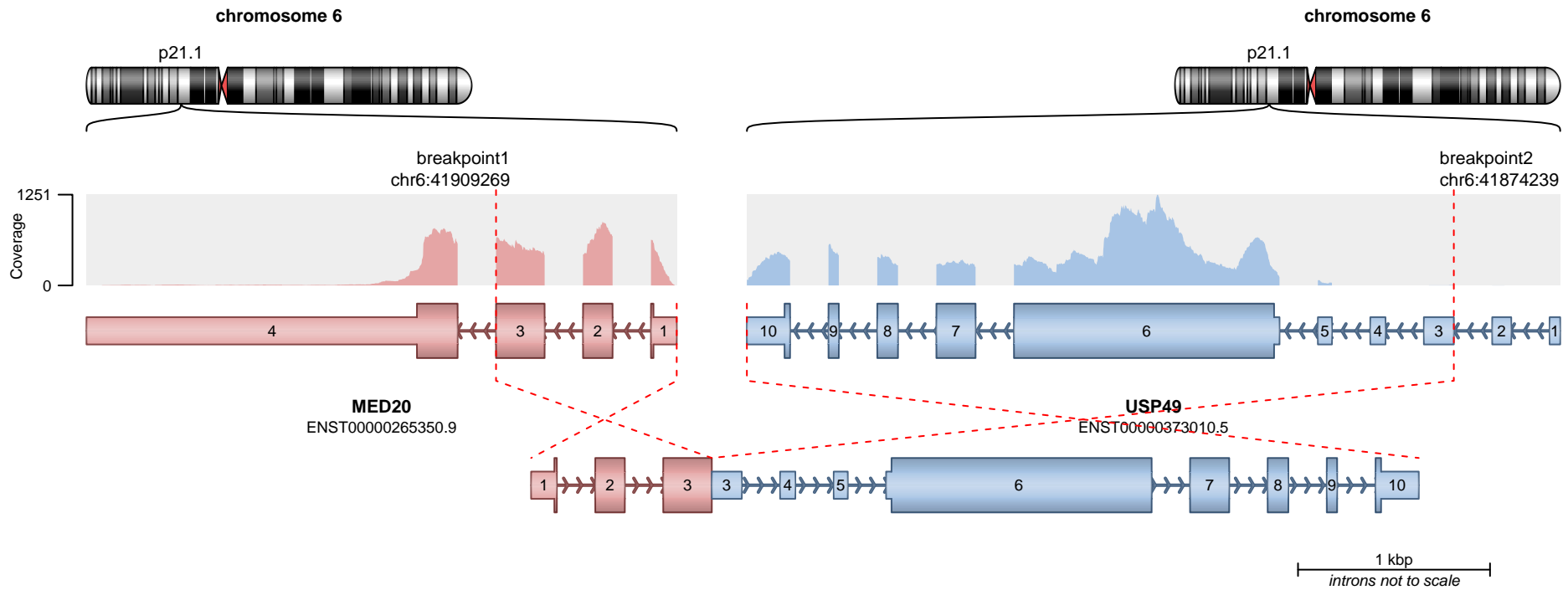
RETAINED PROTEIN DOMAINS
reading frame unclear



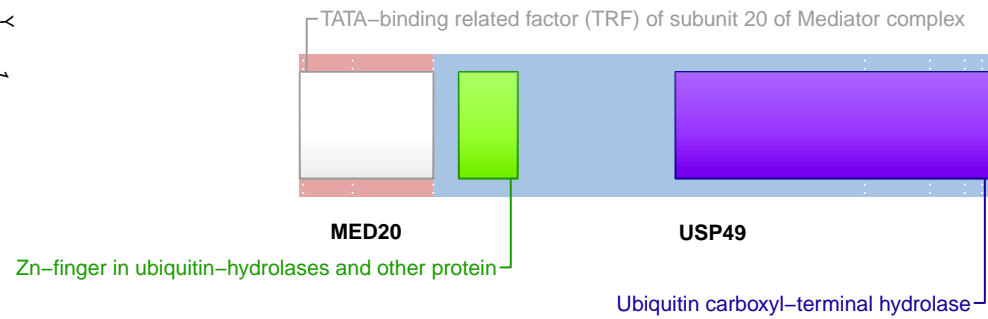
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



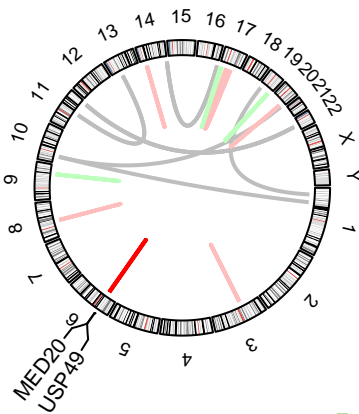
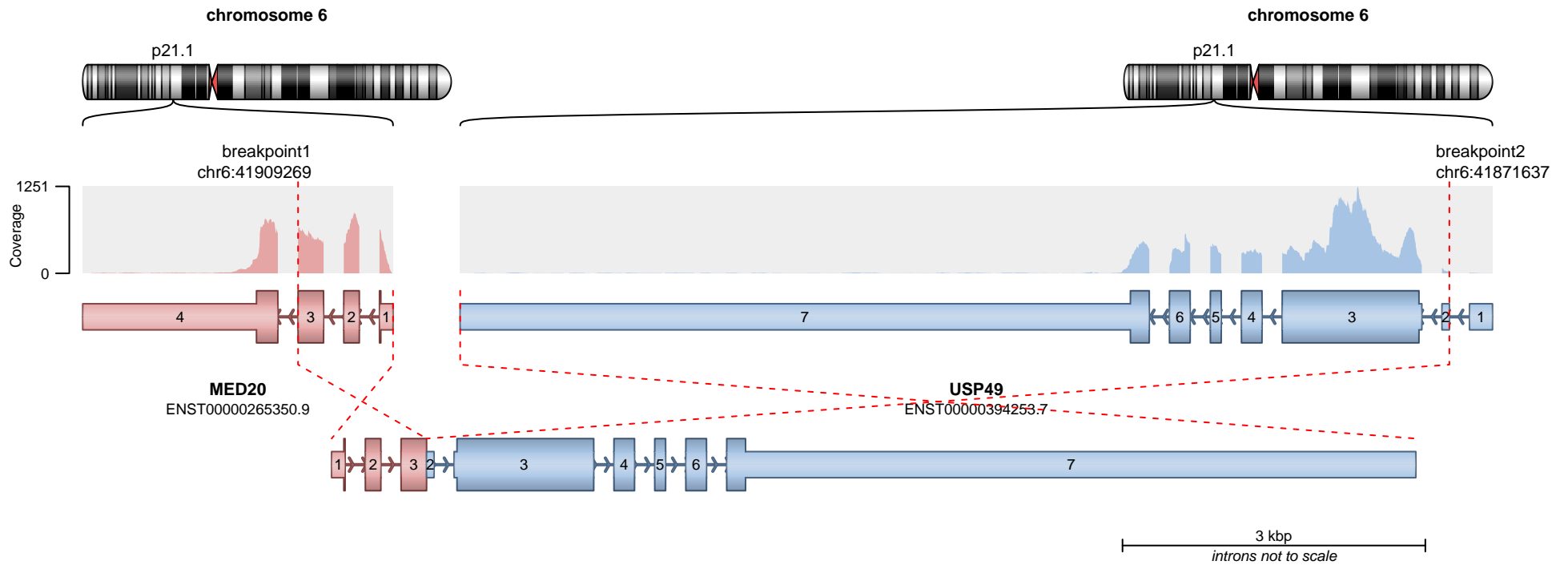
RETAINED PROTEIN DOMAINS
reading frame unclear



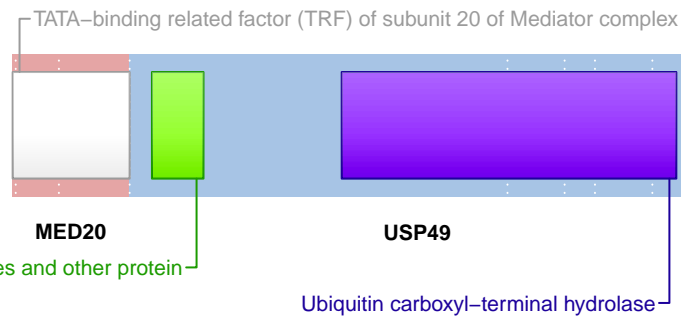
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



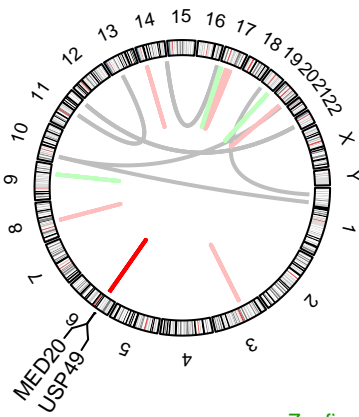
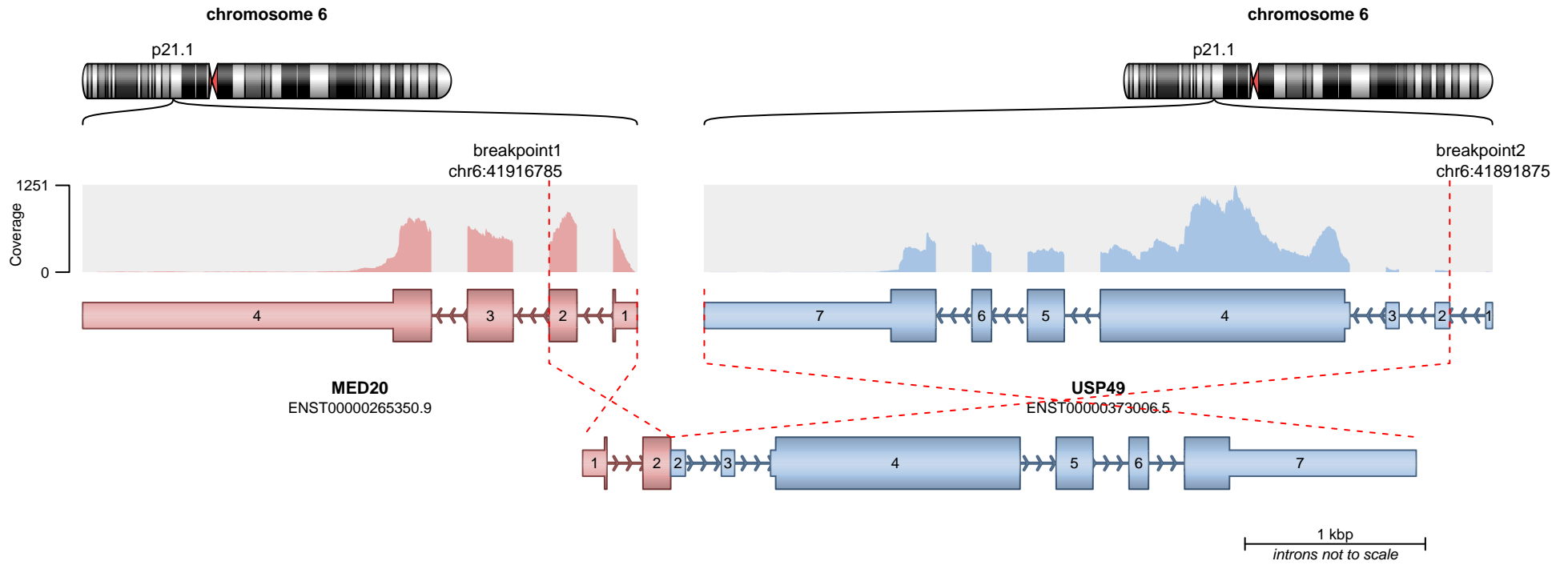
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

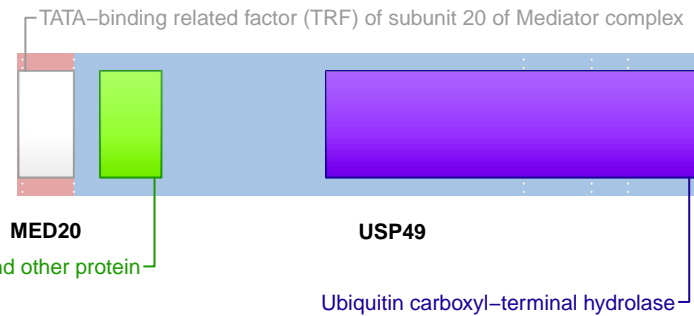
Split reads = 1
Discordant mates = 1

— translocation — deletion
— duplication — inversion



Zn-finger in ubiquitin-hydrolases and other protein

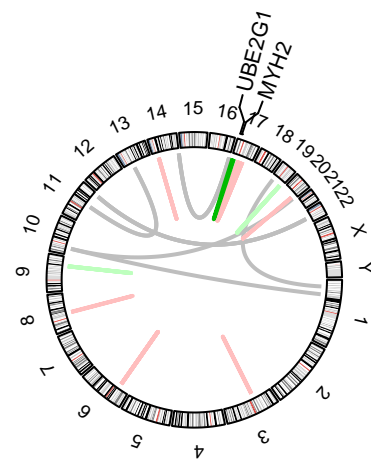
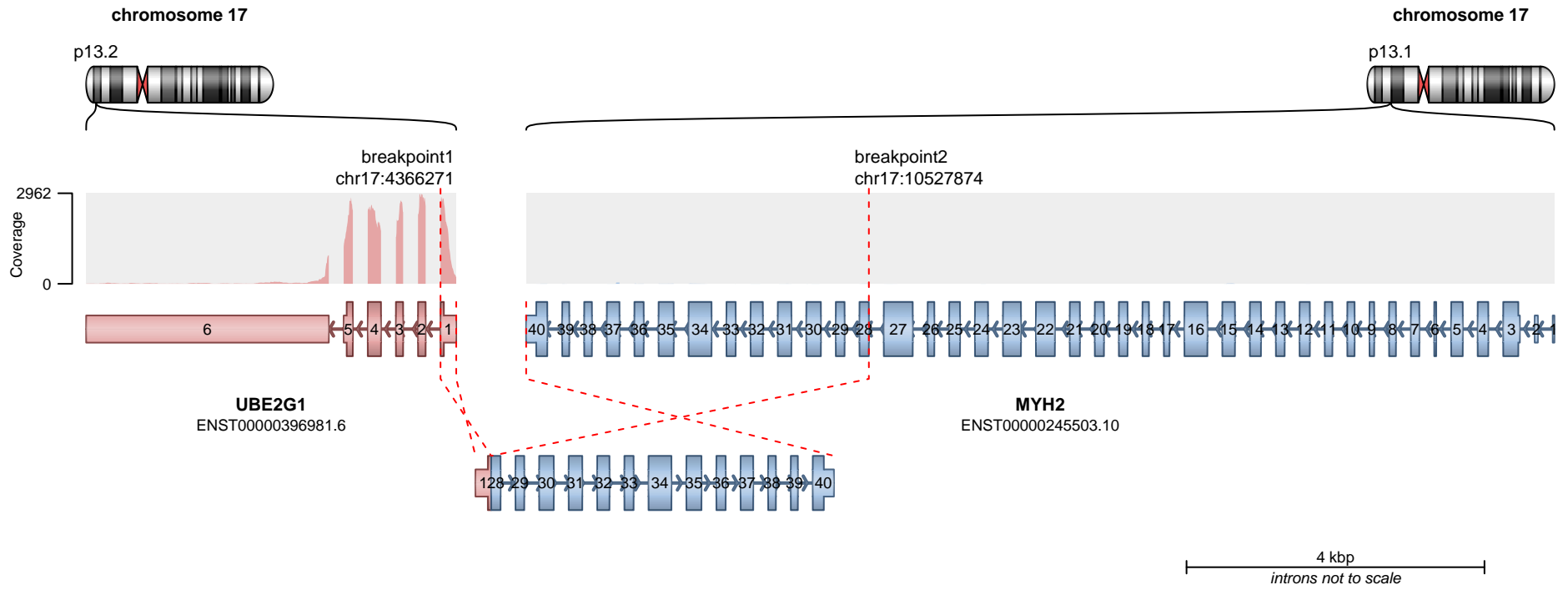
RETAINED PROTEIN DOMAINS
reading frame unclear



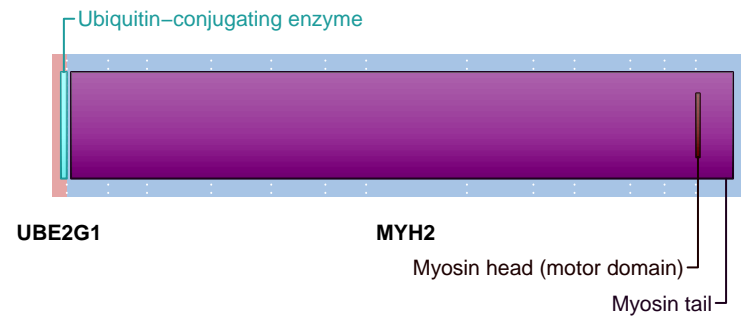
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

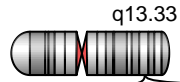


SUPPORTING READ COUNT

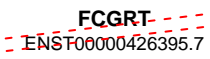
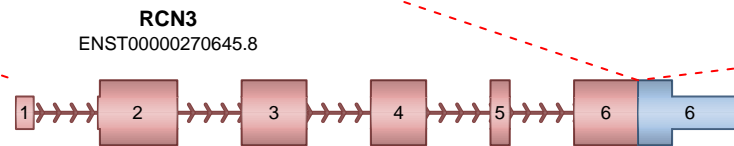
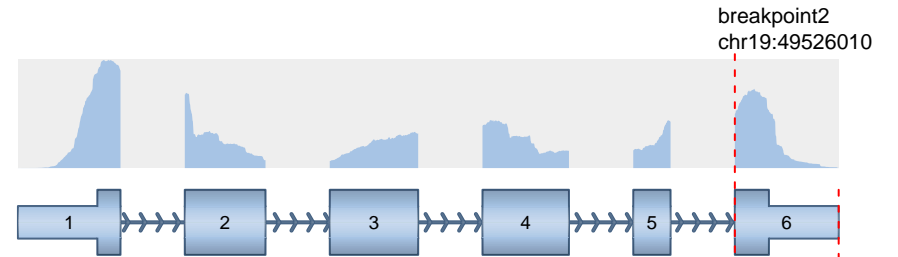
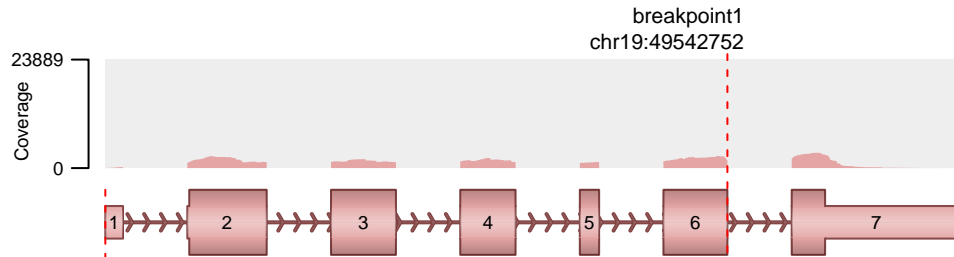
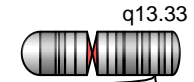
Split reads = 3
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

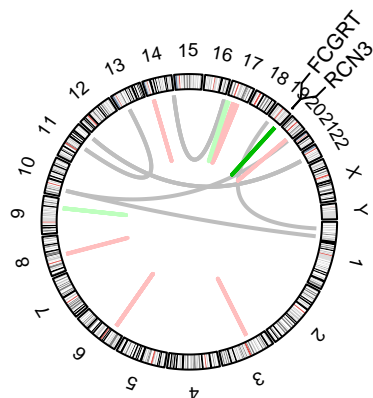
chromosome 19



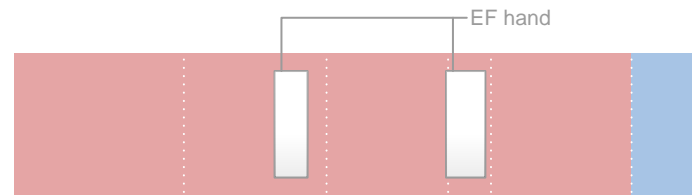
chromosome 19



1 kbp
introns not to scale



RETAINED PROTEIN DOMAINS
reading frame unclear



RCN3

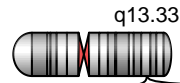
FCGRT

SUPPORTING READ COUNT

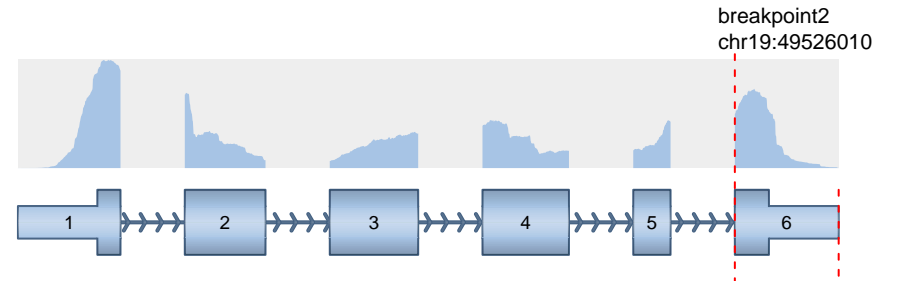
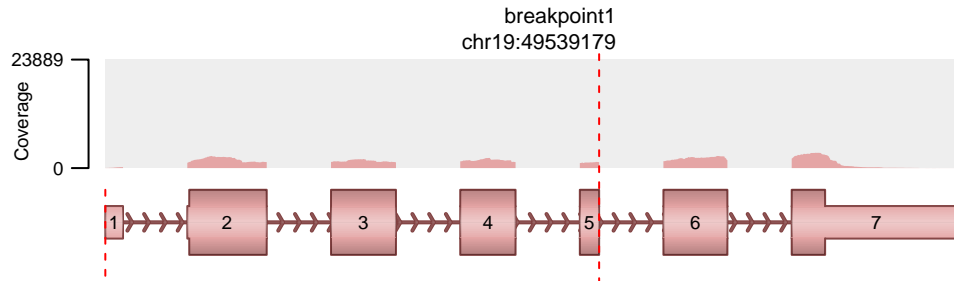
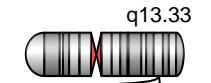
Split reads = 2
Discordant mates = 0

— translocation — deletion
— duplication — inversion

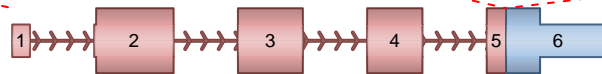
chromosome 19



chromosome 19

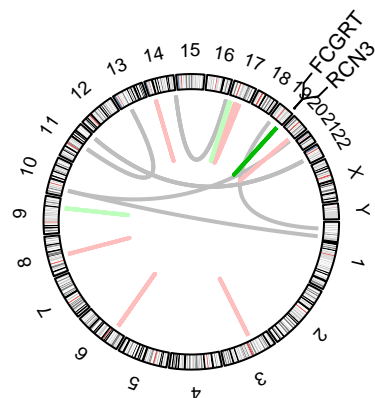


RCN3
ENST00000270645.8

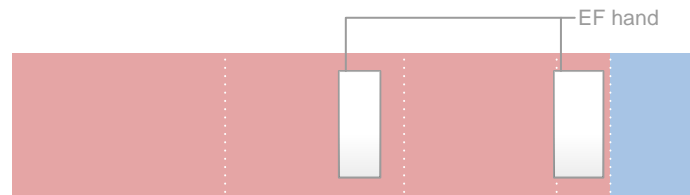


FCGRT
ENST00000426395.7

1 kbp
introns not to scale



RETAINED PROTEIN DOMAINS
reading frame unclear



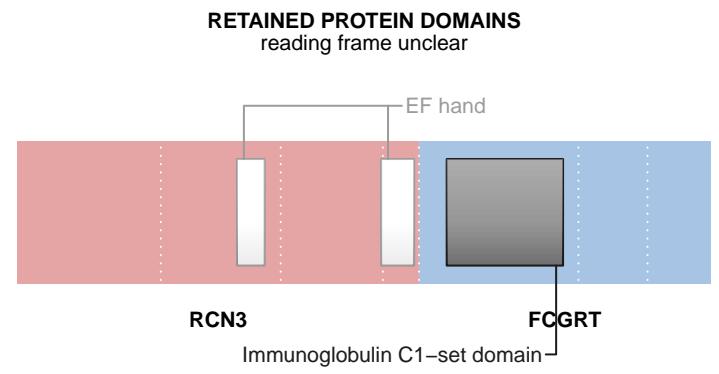
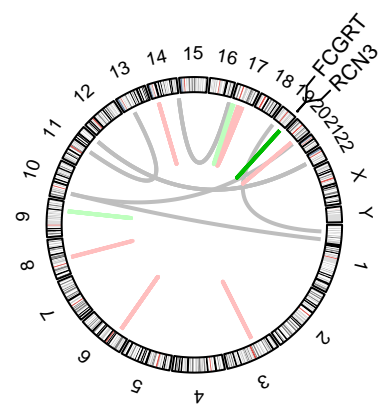
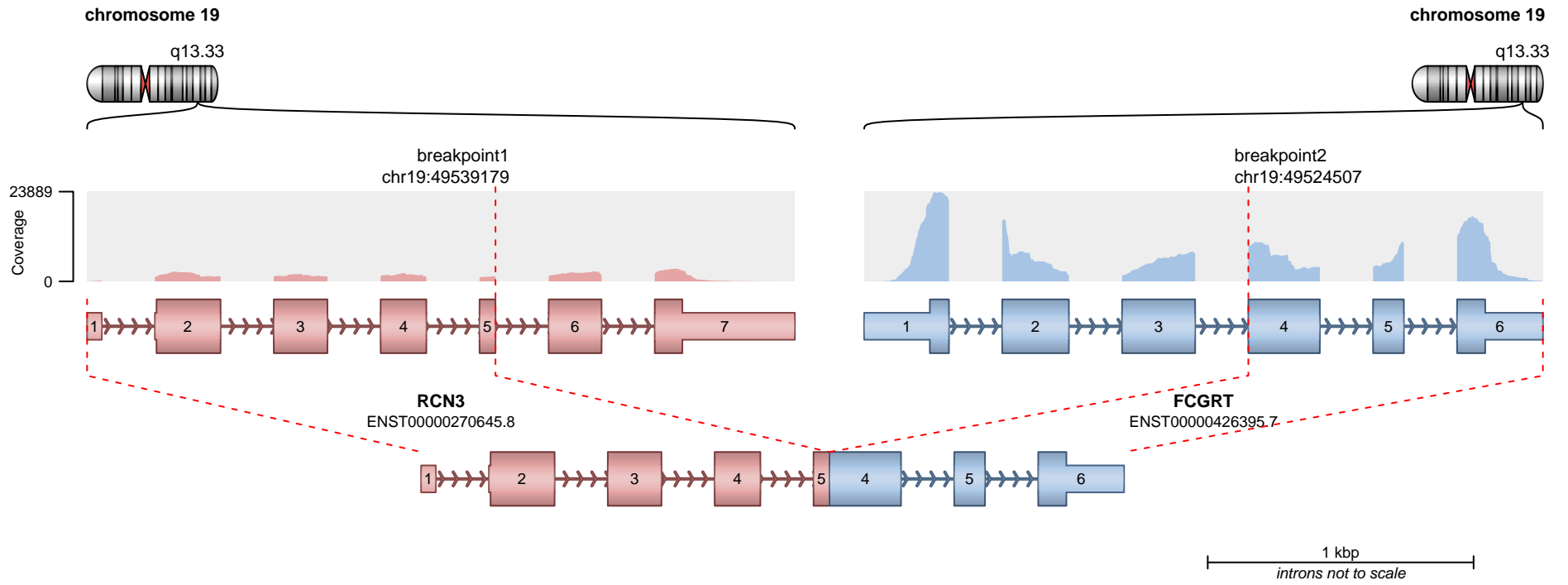
RCN3

FCGRT

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

— translocation — deletion
— duplication — inversion

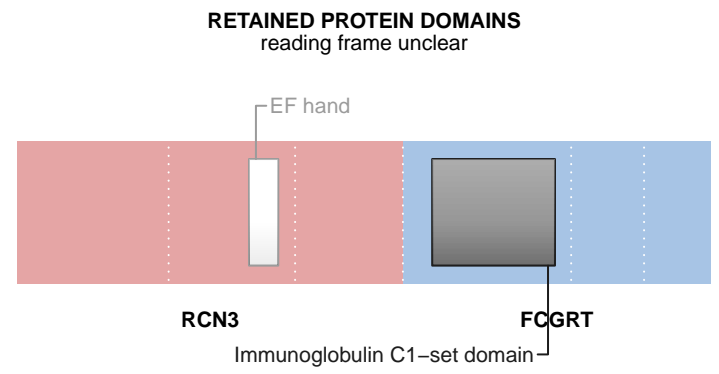
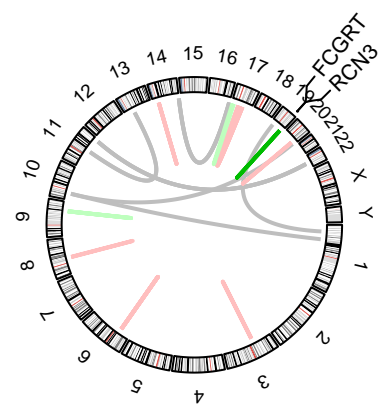
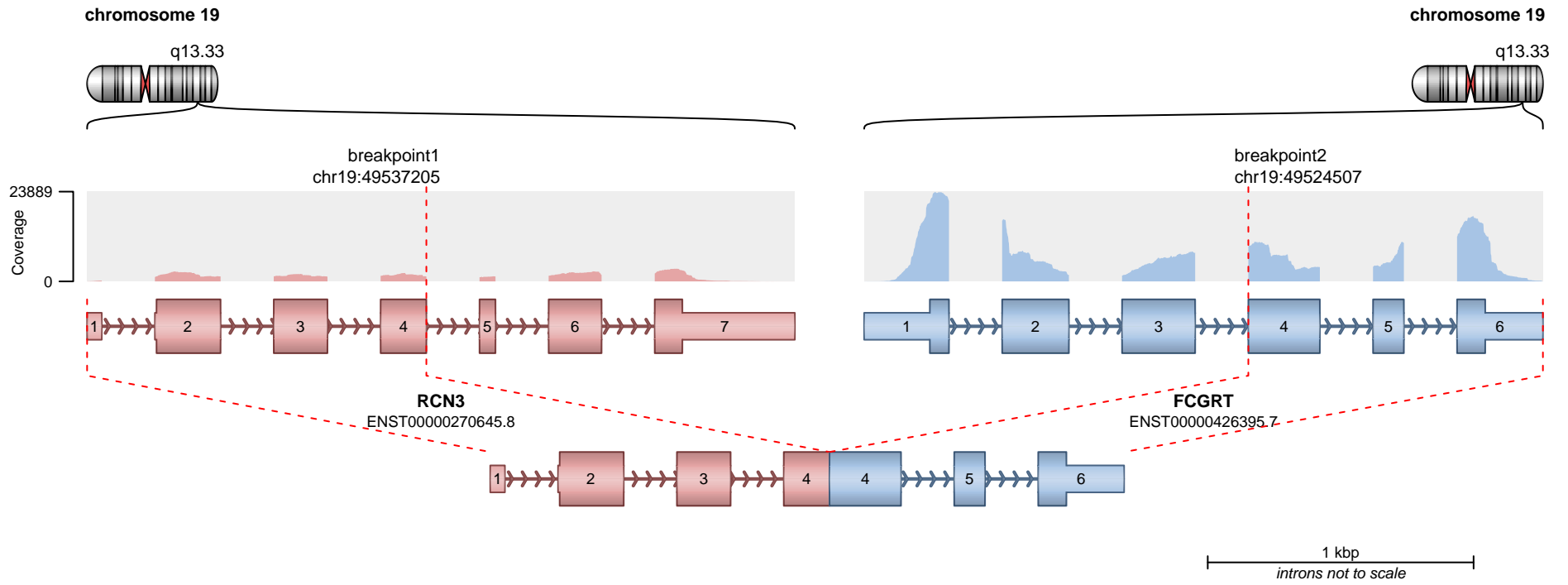


SUPPORTING READ COUNT

Split reads = 1

Discordant mates = 0

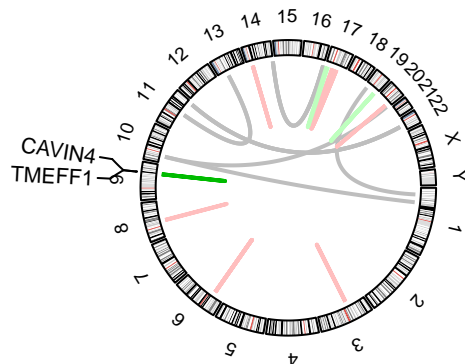
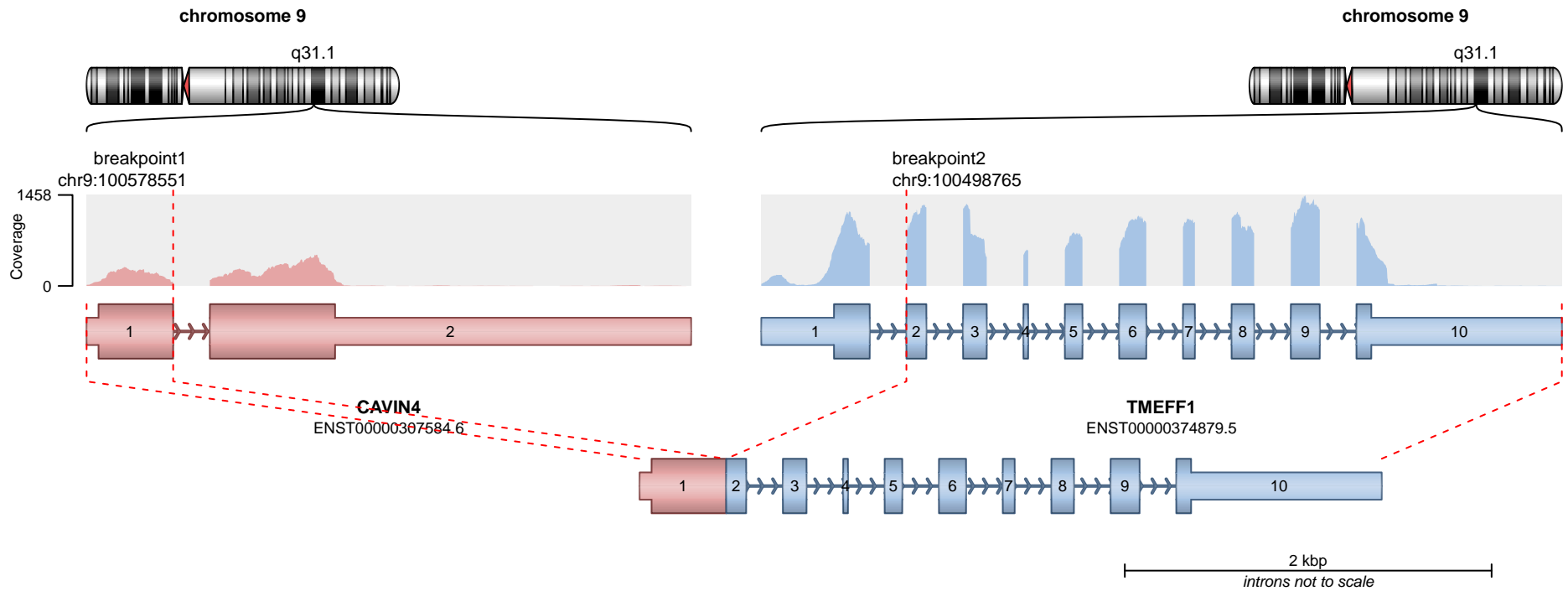
— translocation — deletion
— duplication — inversion



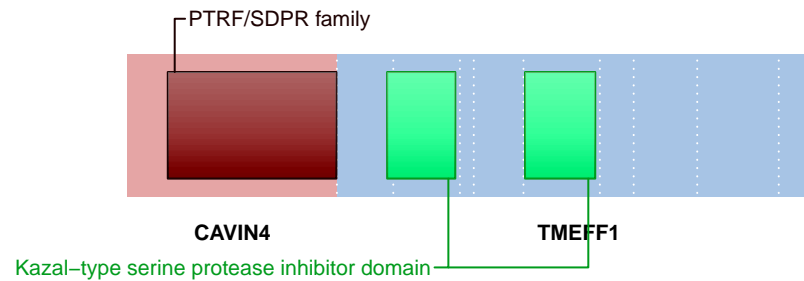
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



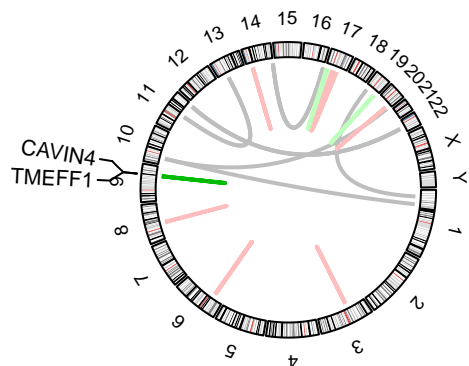
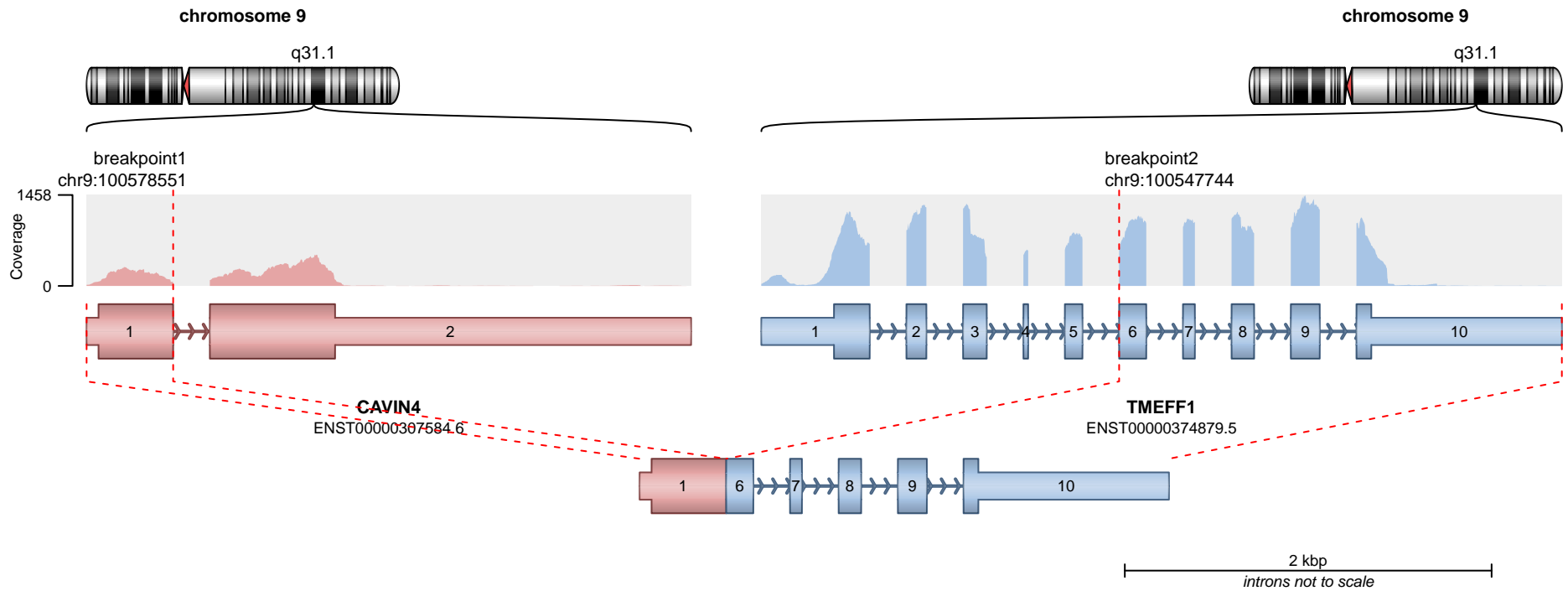
RETAINED PROTEIN DOMAINS
reading frame unclear



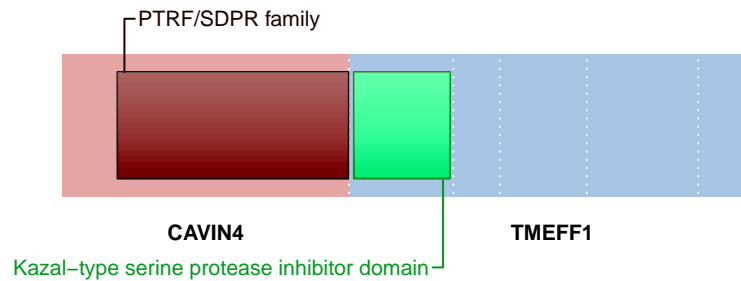
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



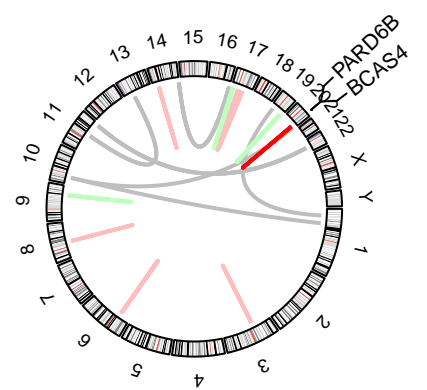
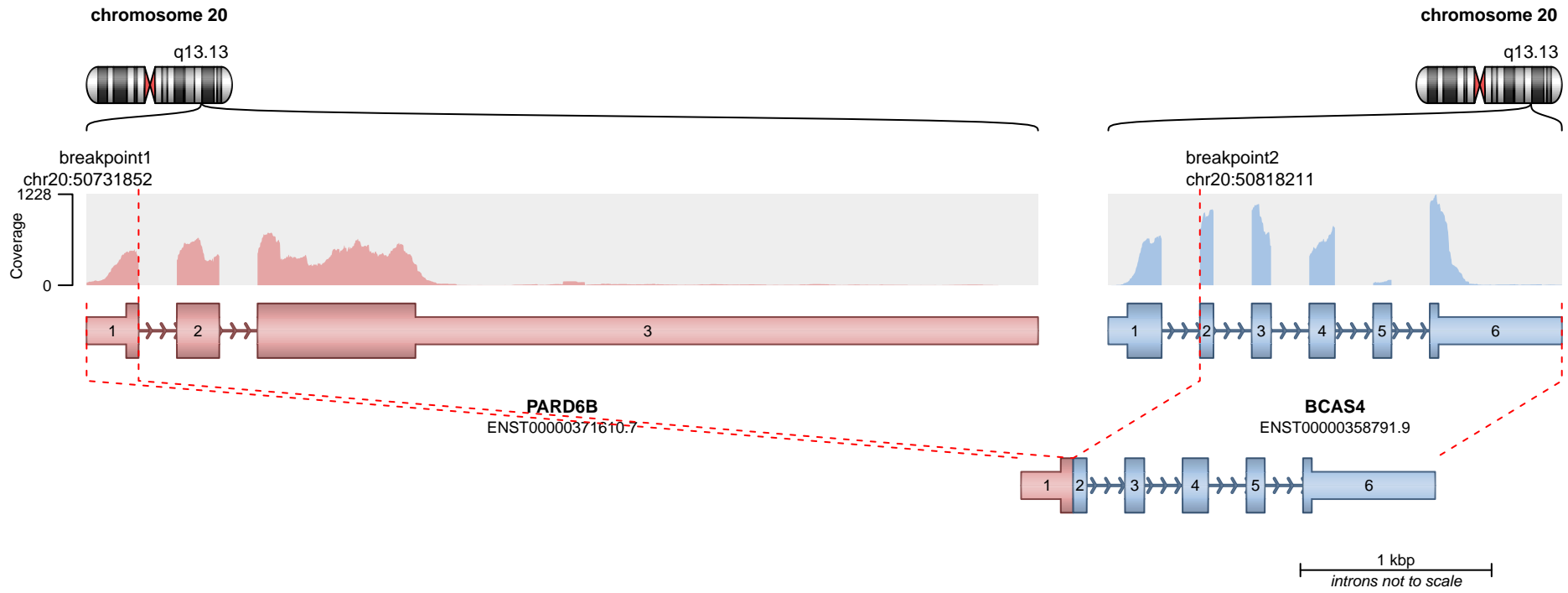
RETAINED PROTEIN DOMAINS
reading frame unclear



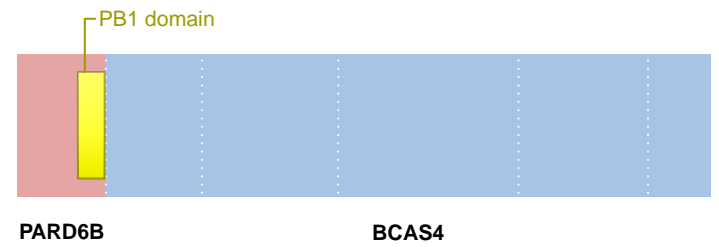
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion