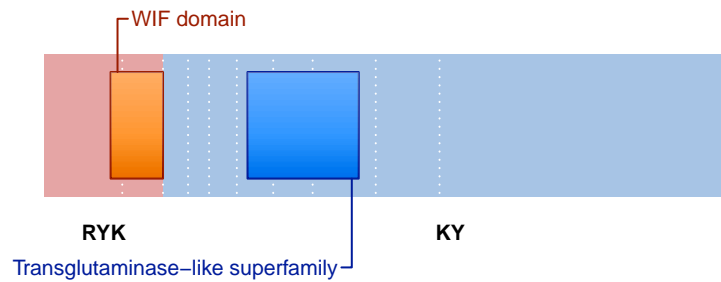


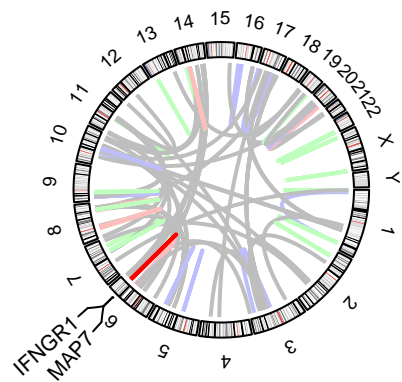
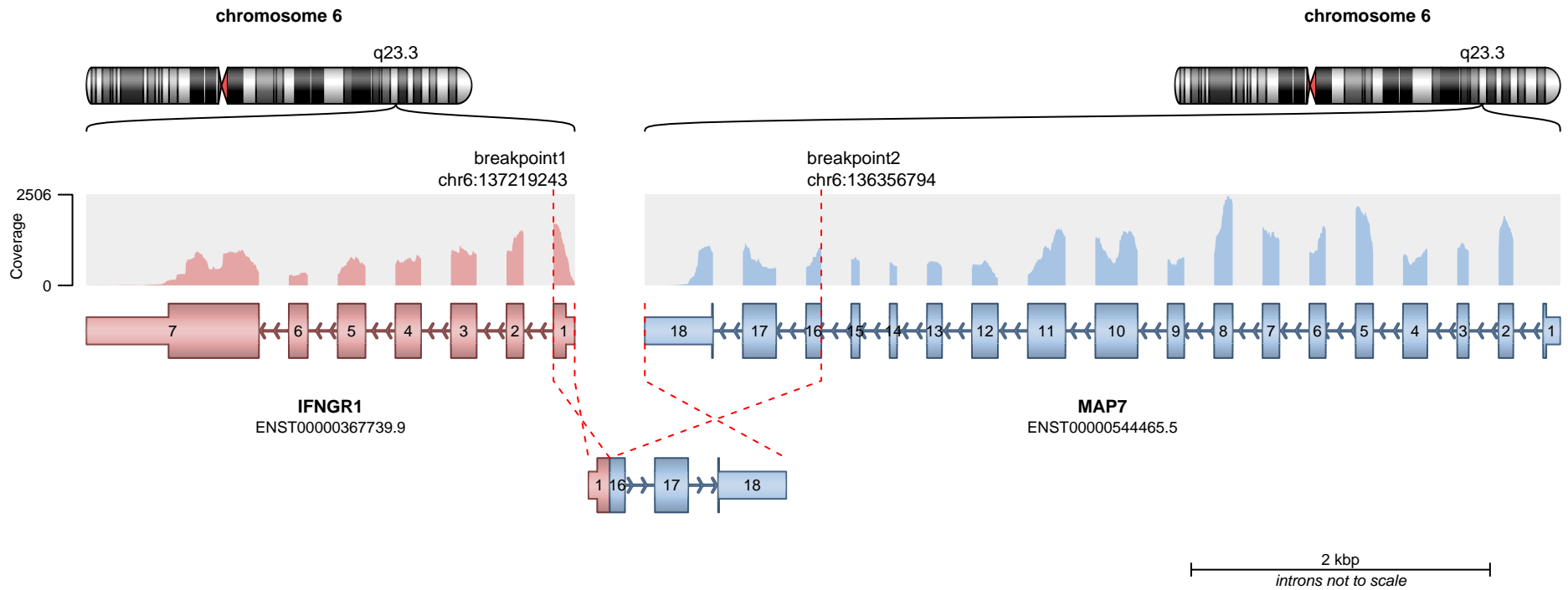
RETAINED PROTEIN DOMAINS
reading frame unclear



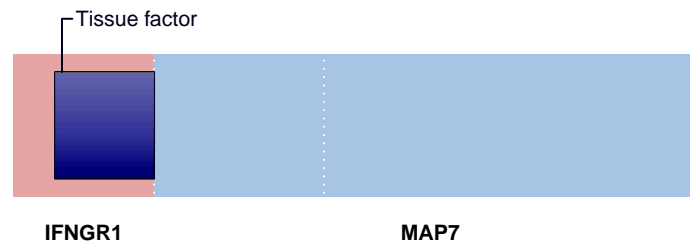
SUPPORTING READ COUNT

Split reads = 264
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



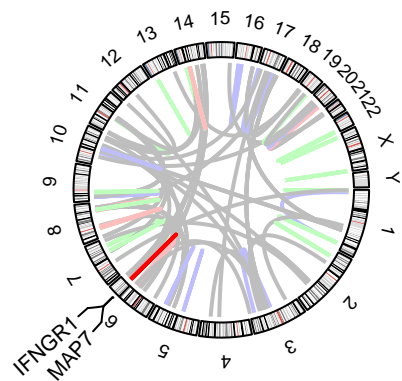
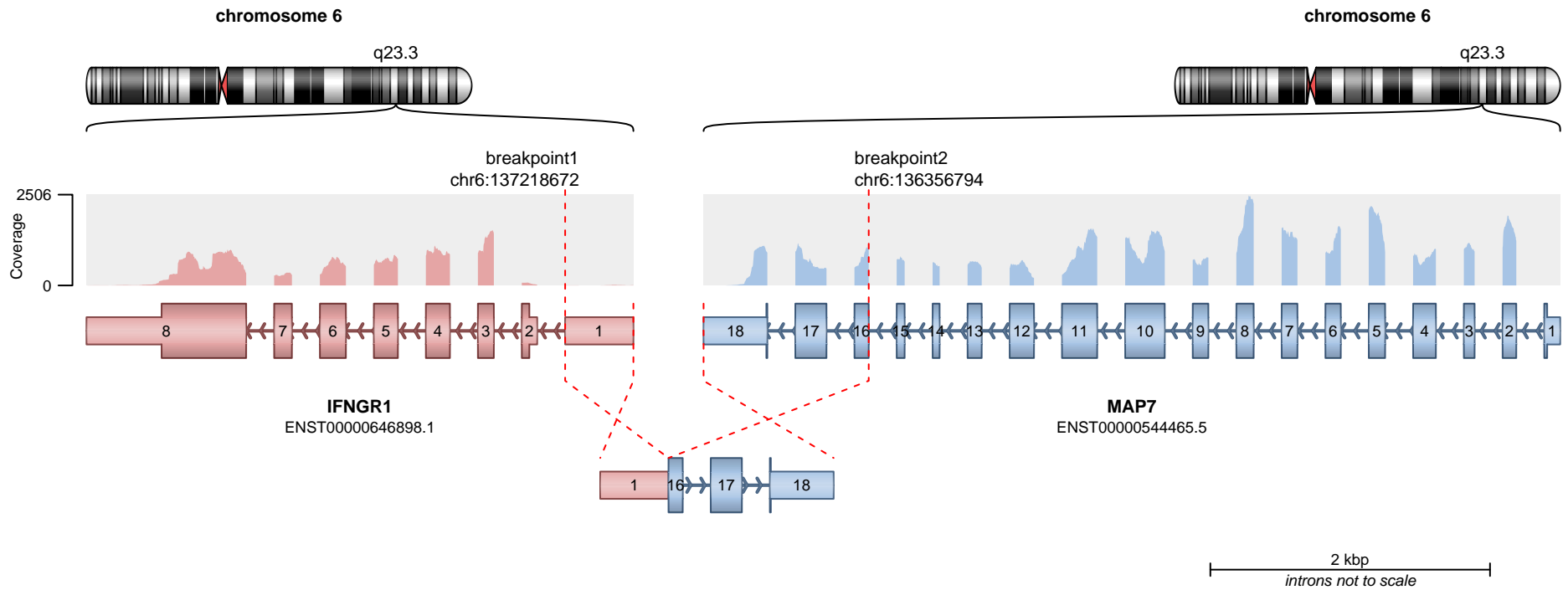
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 184
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

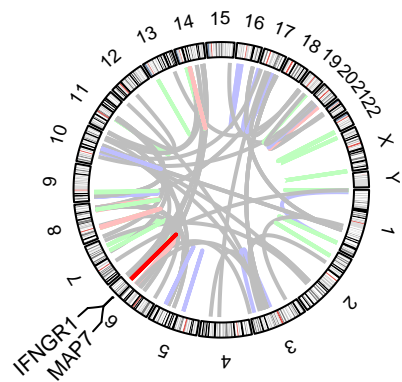
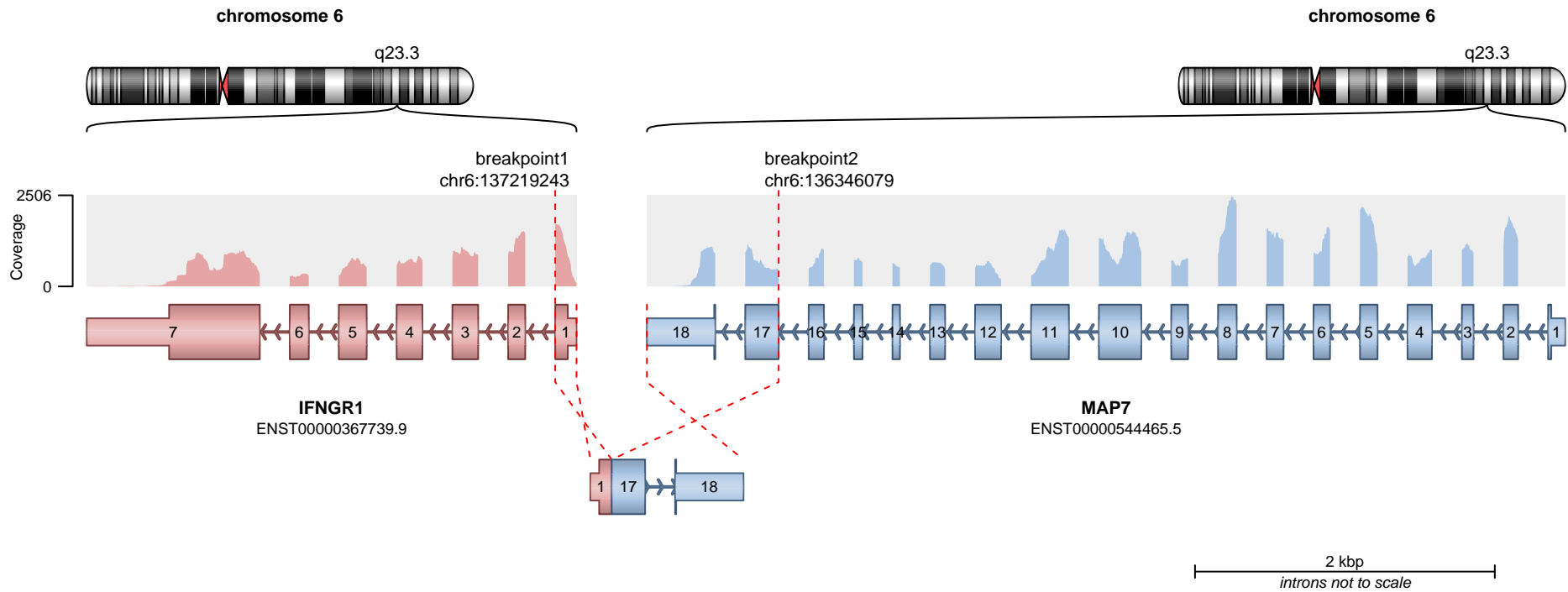


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



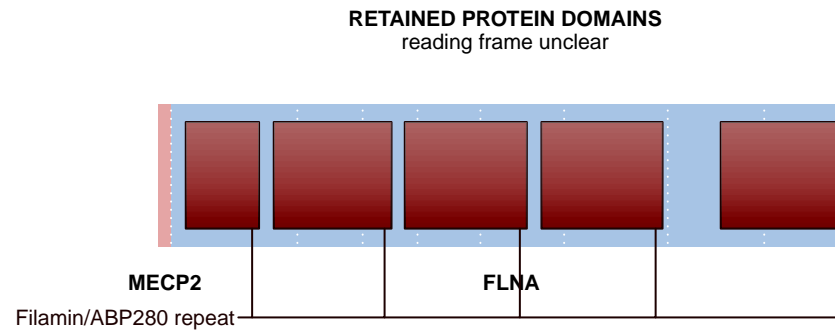
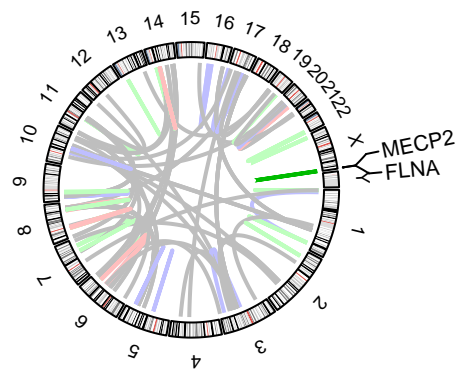
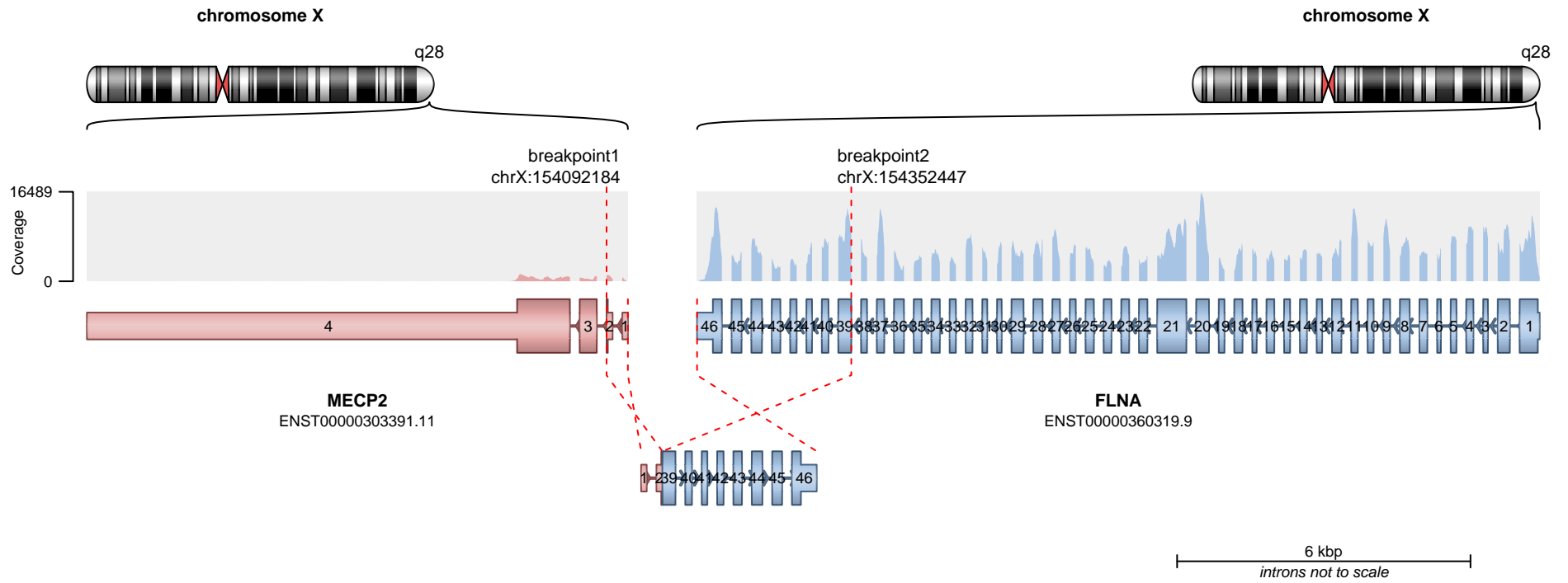
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

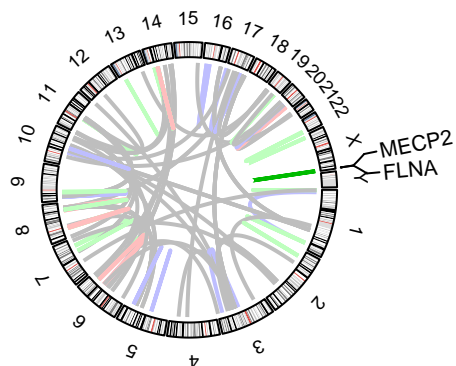
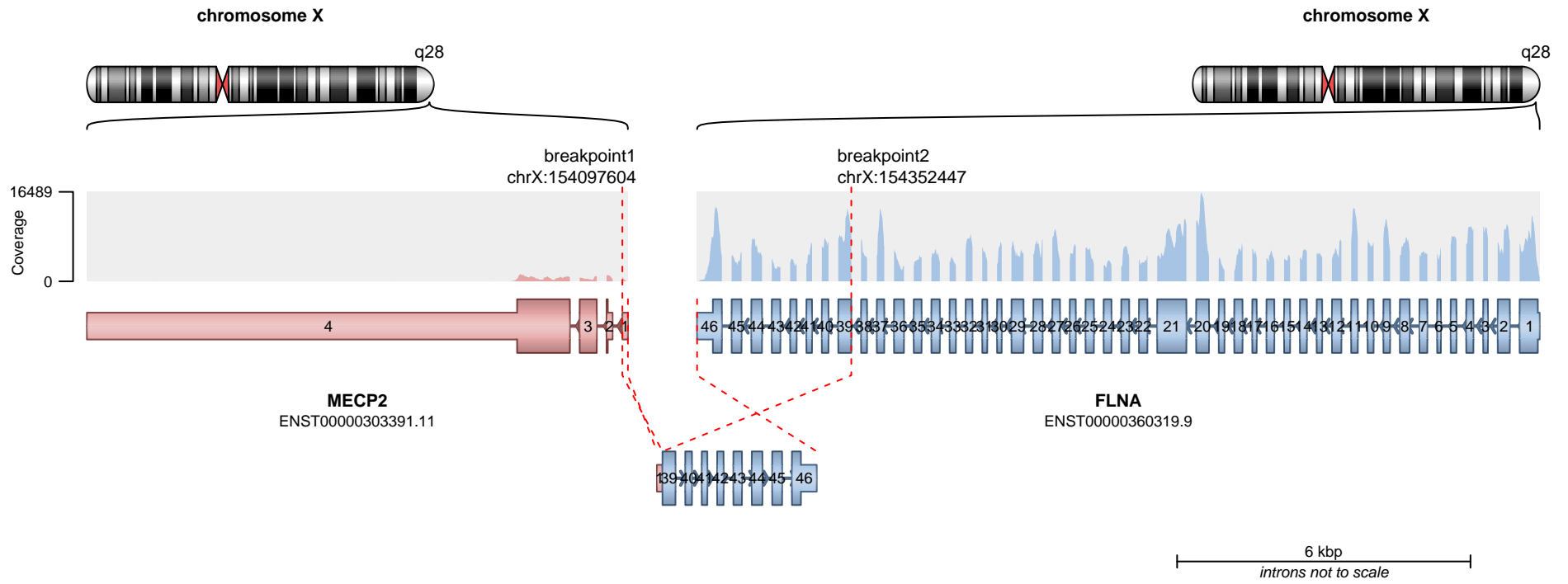
- translocation
- duplication
- deletion
- inversion



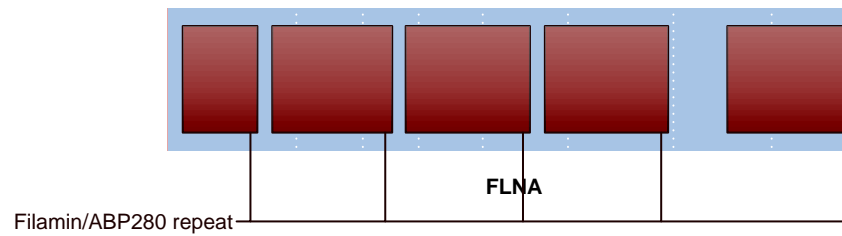
SUPPORTING READ COUNT

Split reads = 183
Discordant mates = 0

— translocation — deletion
— duplication — inversion



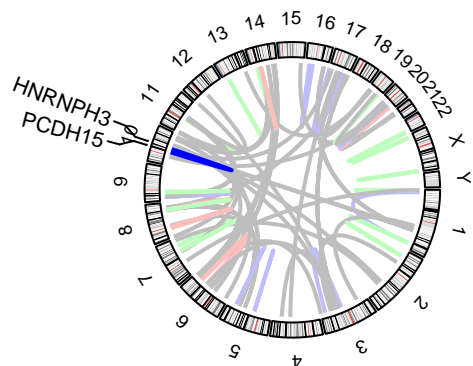
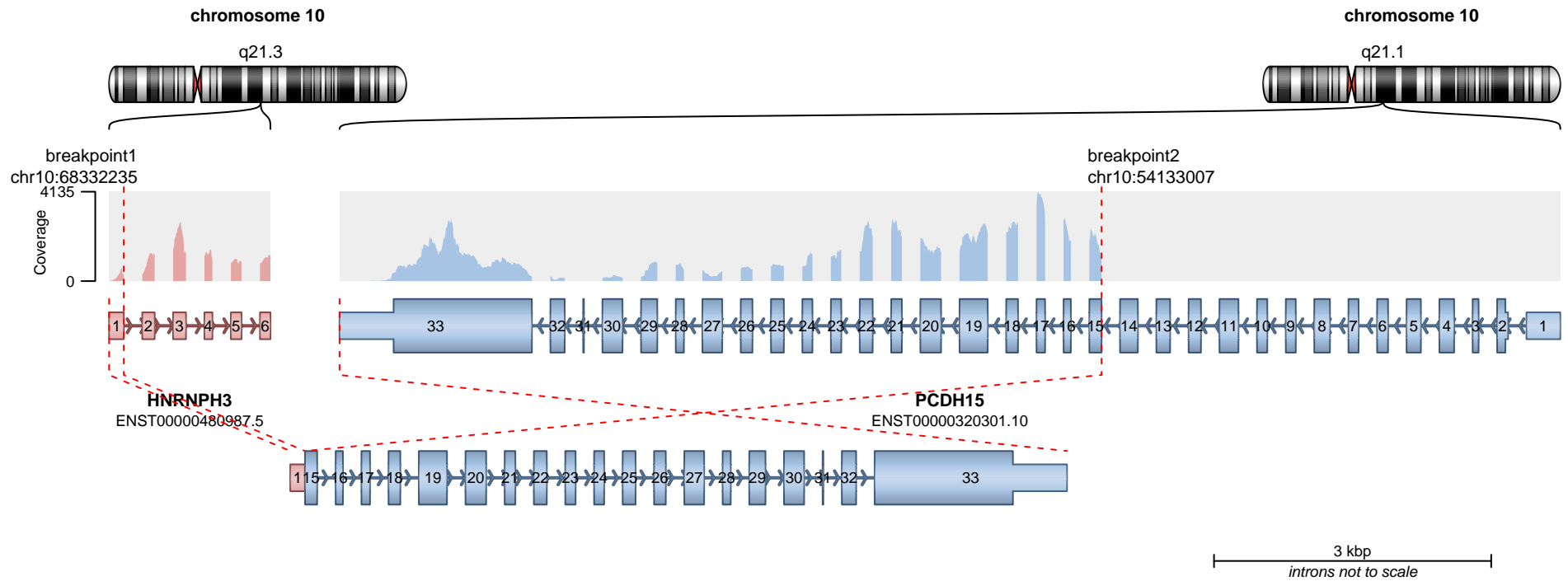
RETAINED PROTEIN DOMAINS
reading frame unclear



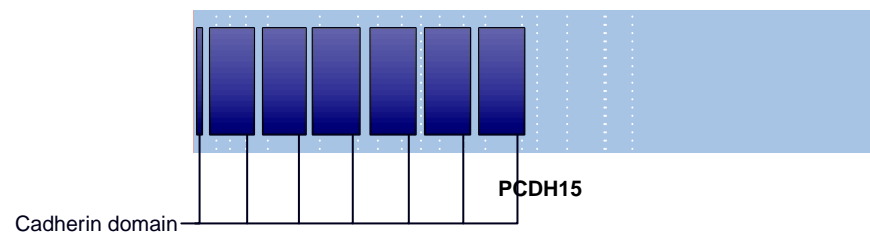
SUPPORTING READ COUNT

Split reads = 52
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



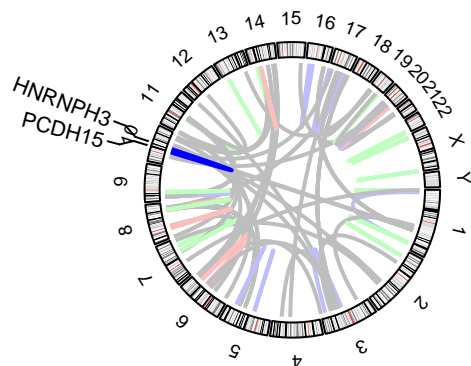
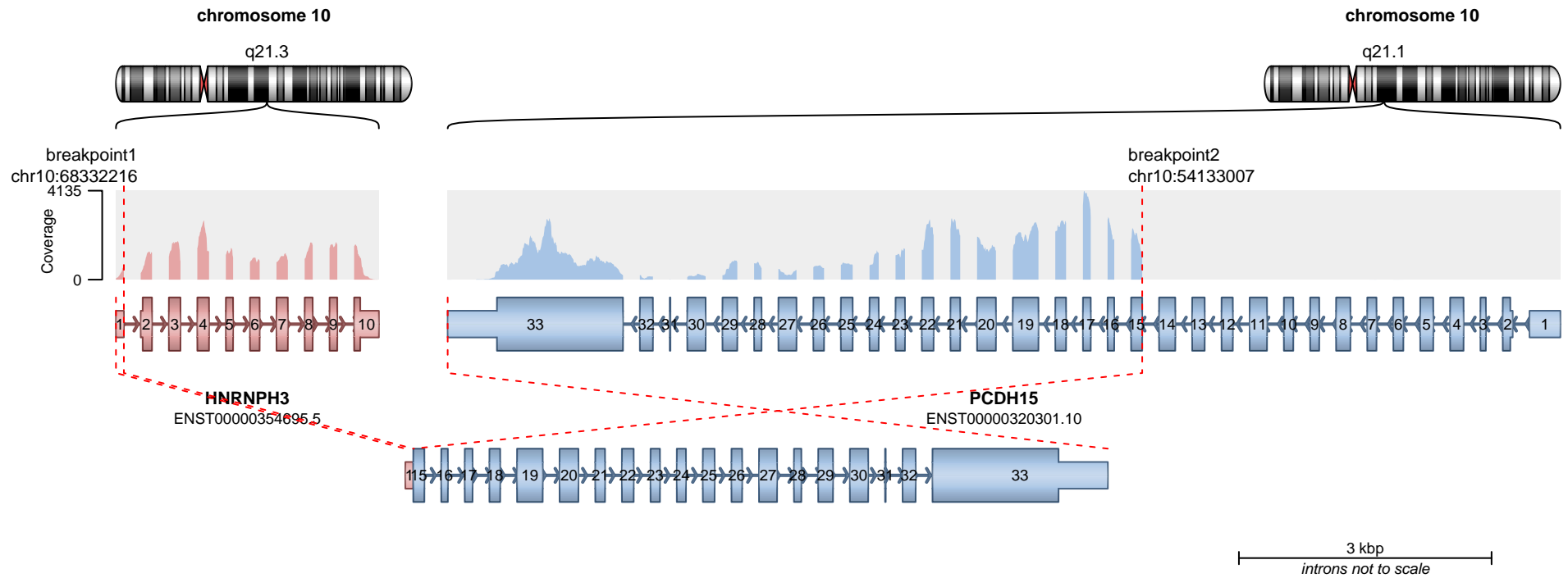
RETAINED PROTEIN DOMAINS
reading frame unclear



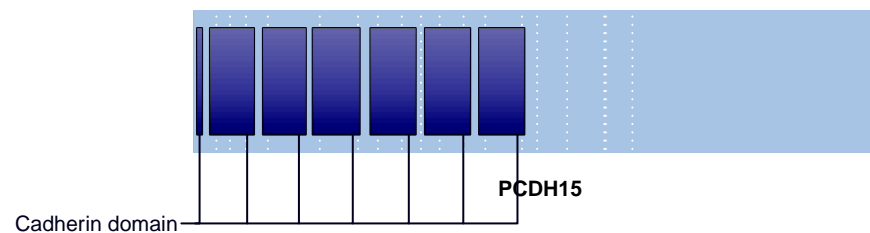
SUPPORTING READ COUNT

Split reads = 162
Discordant mates = 0

— translocation — deletion
— duplication — inversion



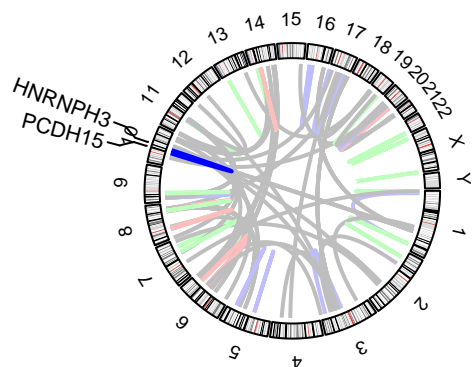
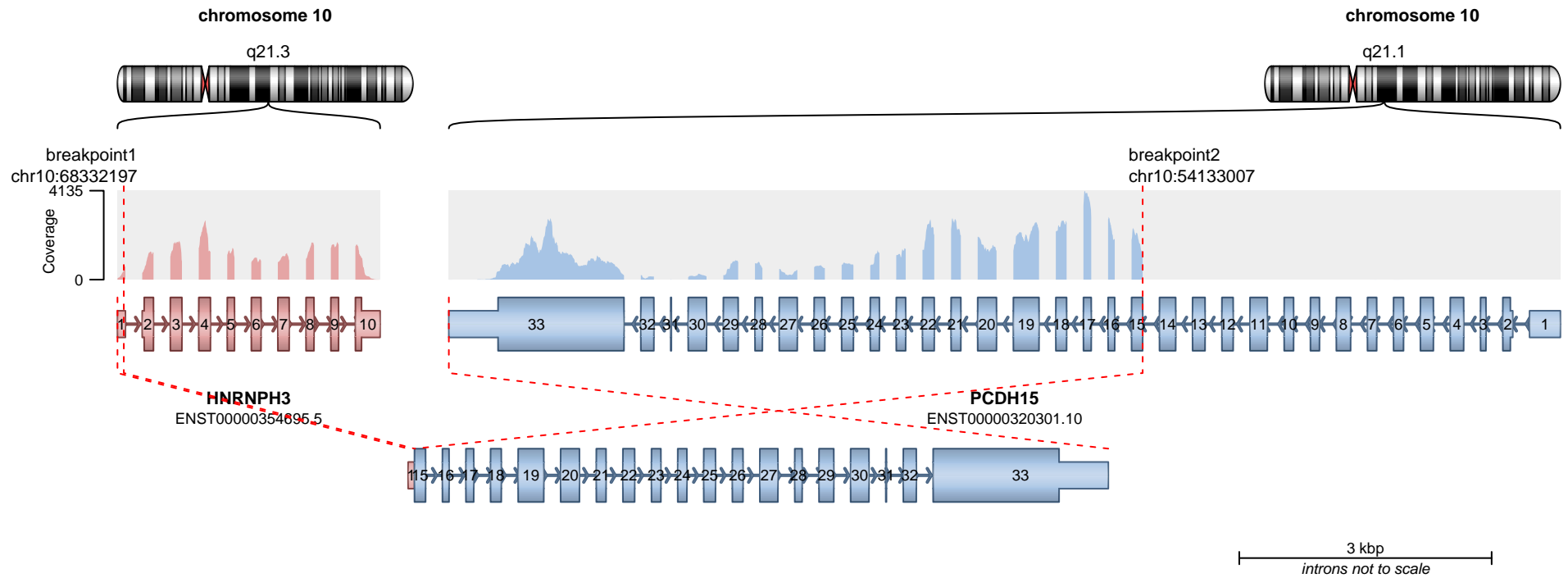
RETAINED PROTEIN DOMAINS
reading frame unclear



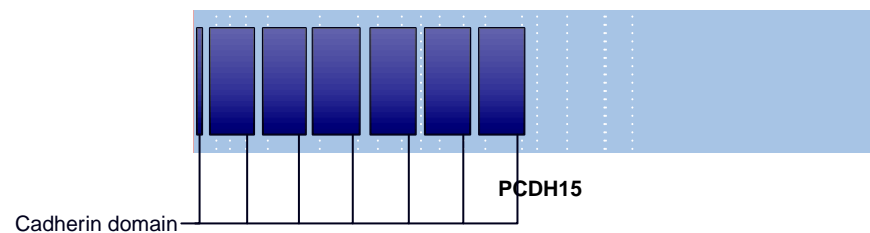
SUPPORTING READ COUNT

Split reads = 144
Discordant mates = 0

— translocation — deletion
— duplication — inversion



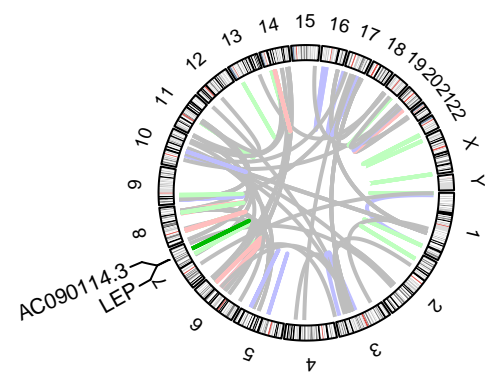
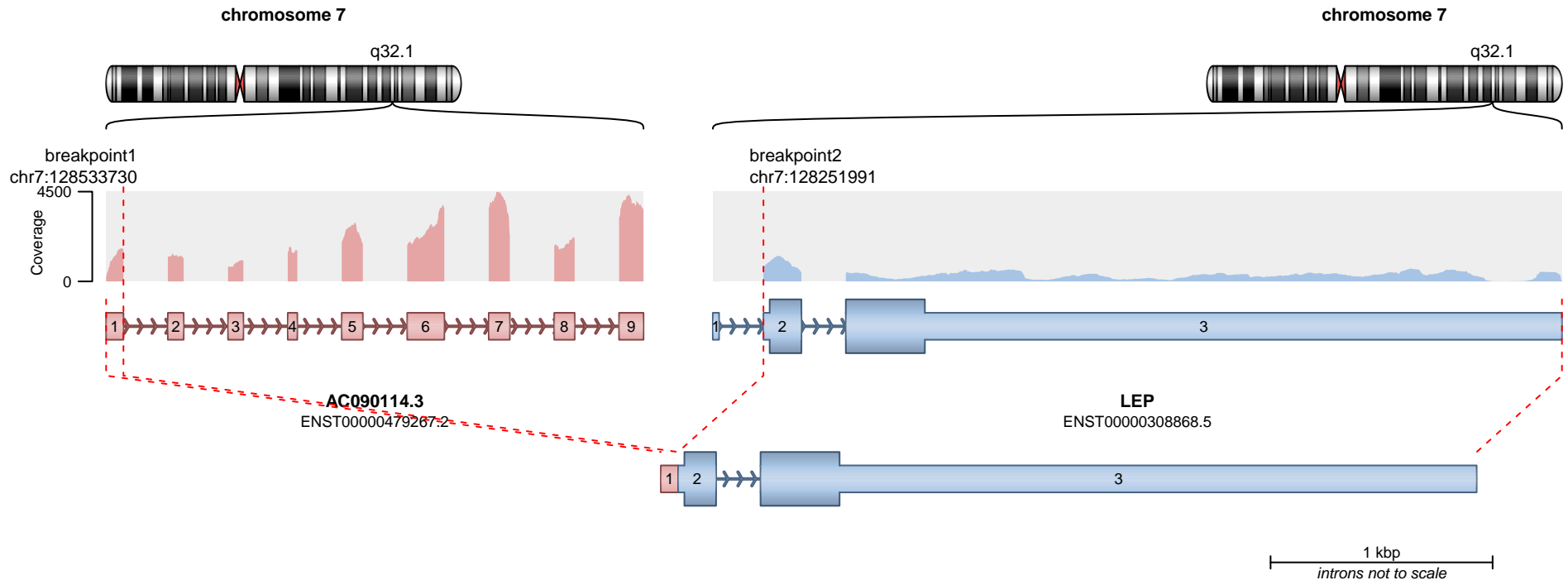
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

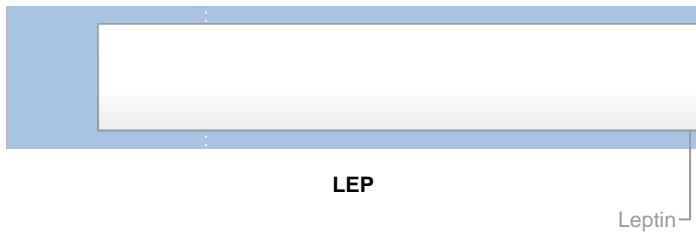
Split reads = 3
Discordant mates = 0

— translocation — deletion
— duplication — inversion



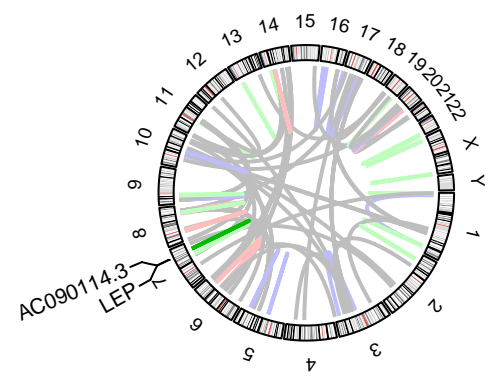
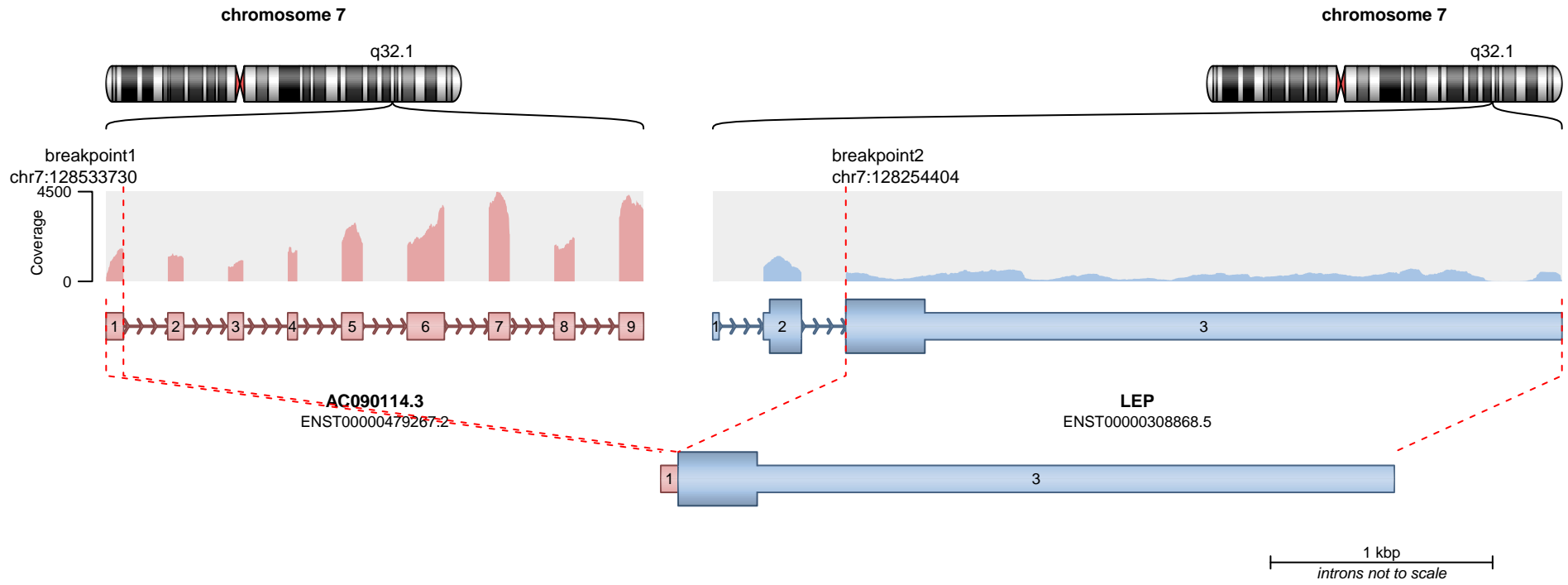
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear

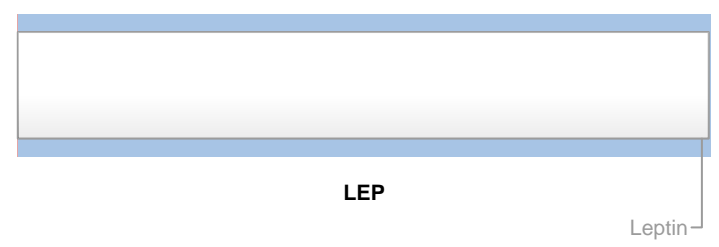


SUPPORTING READ COUNT

Split reads = 118
Discordant mates = 0



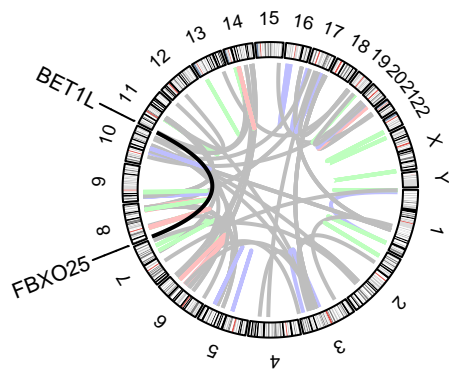
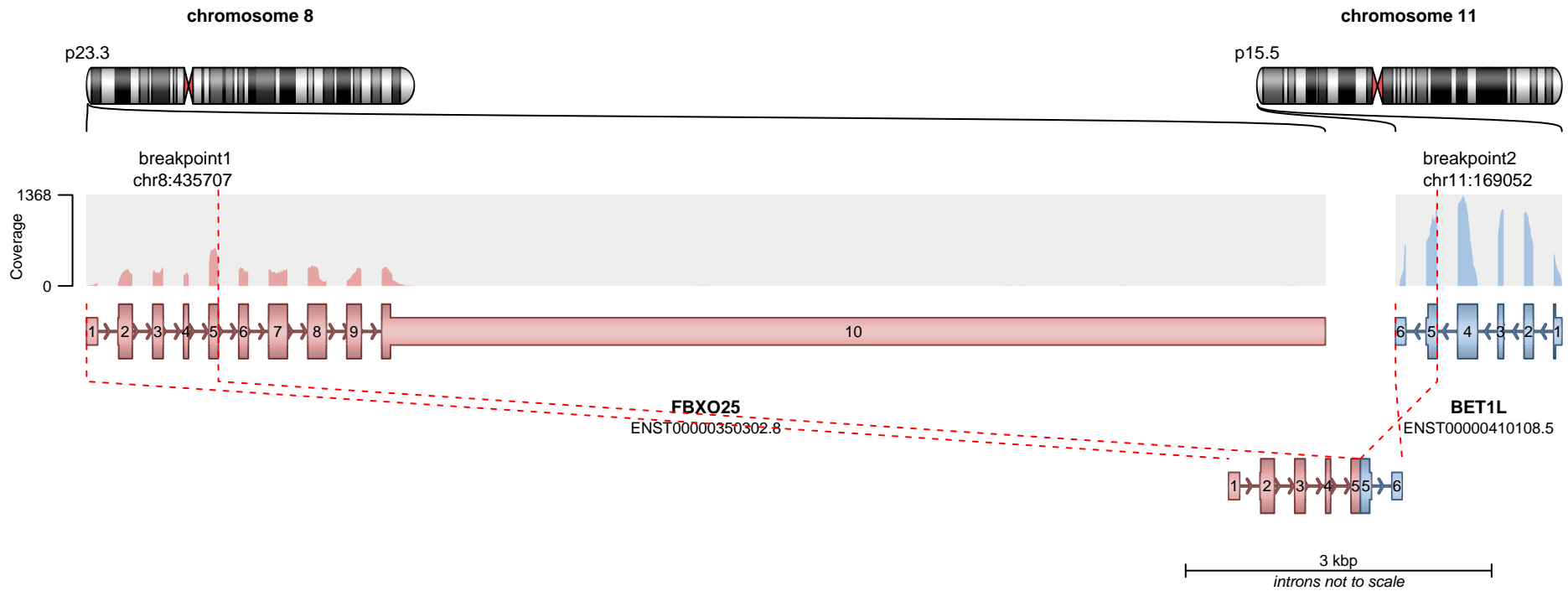
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

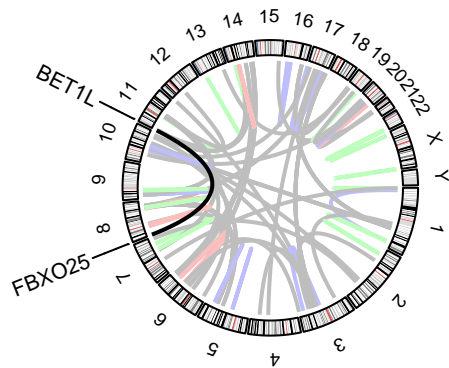
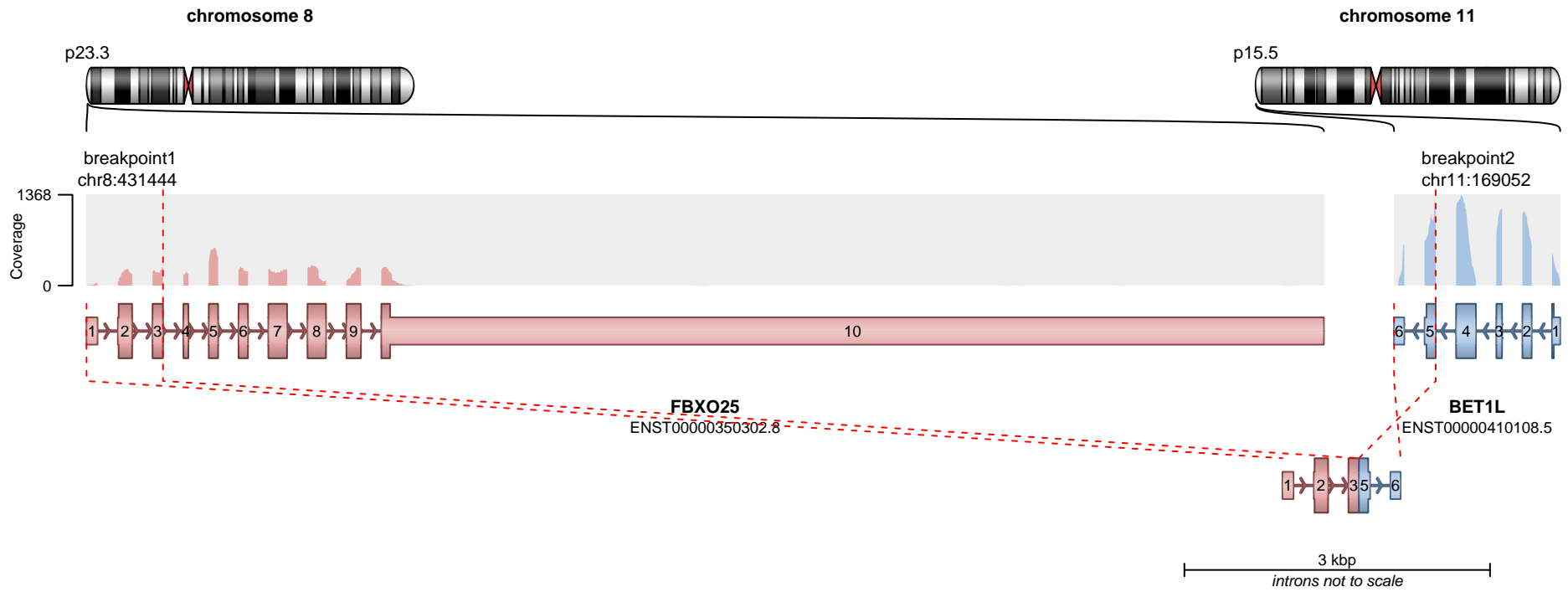


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 96
Discordant mates = 0

— translocation — deletion
— duplication — inversion

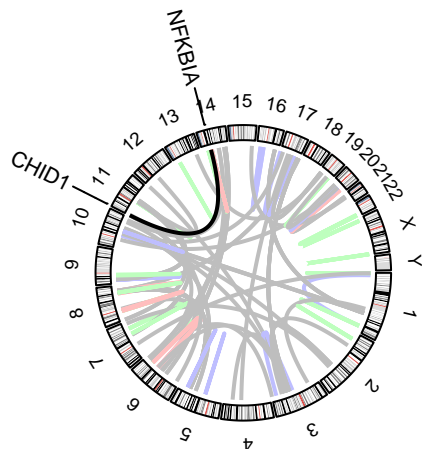
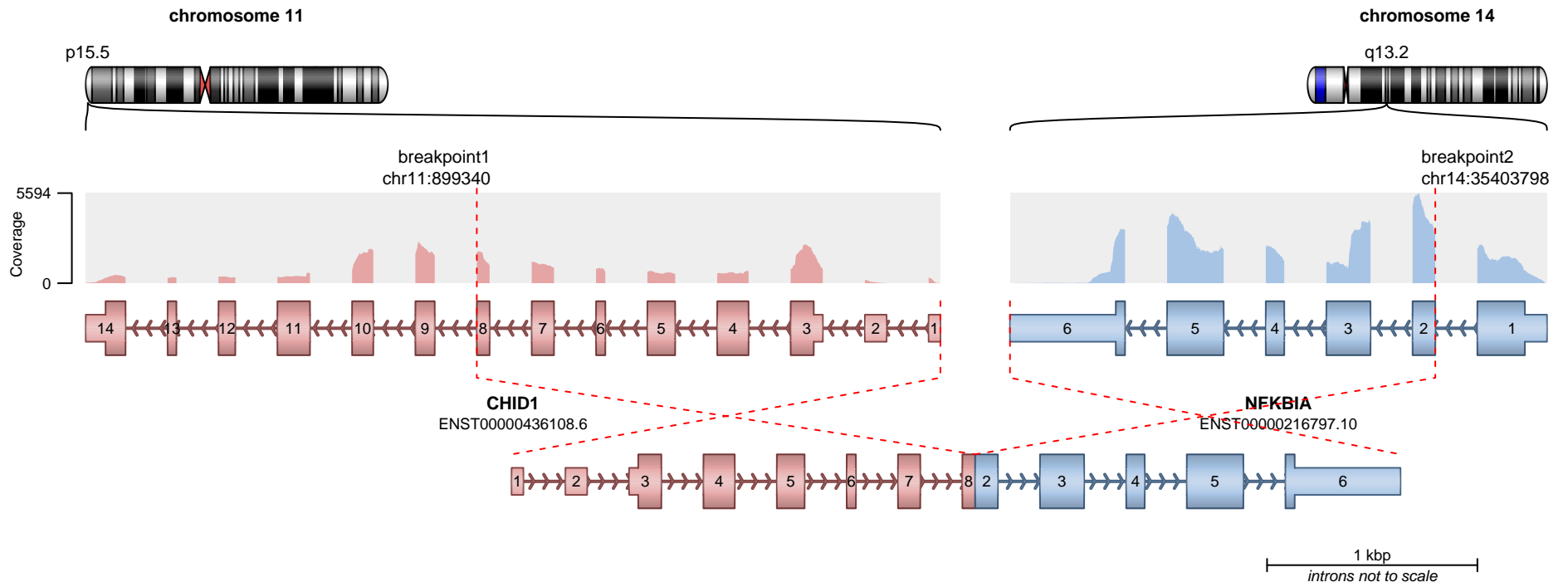


No protein domains retained in fusion.

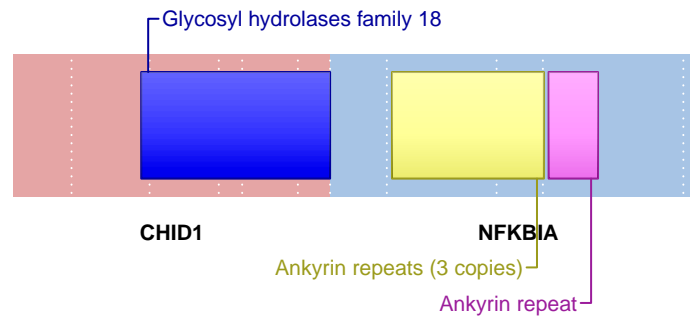
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



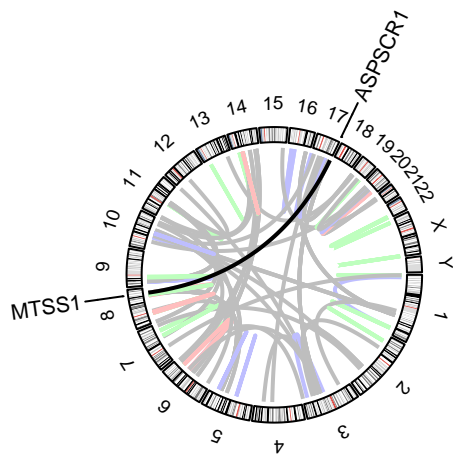
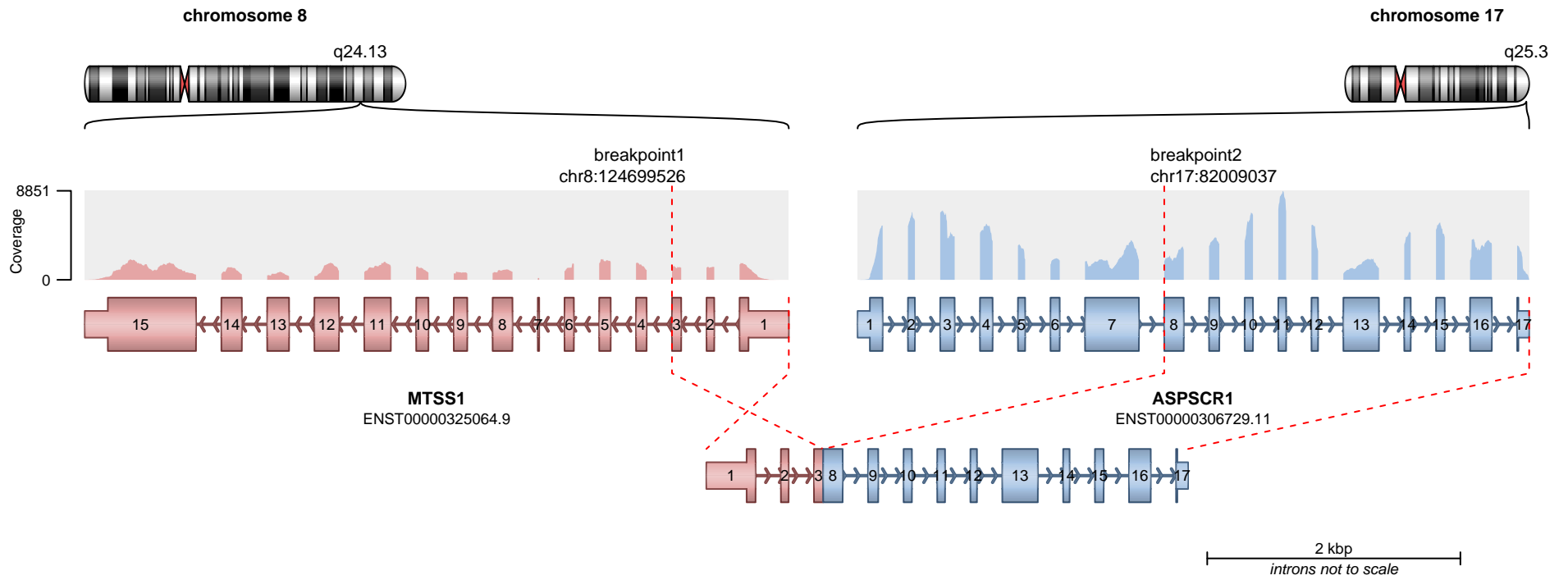
RETAINED PROTEIN DOMAINS
reading frame unclear



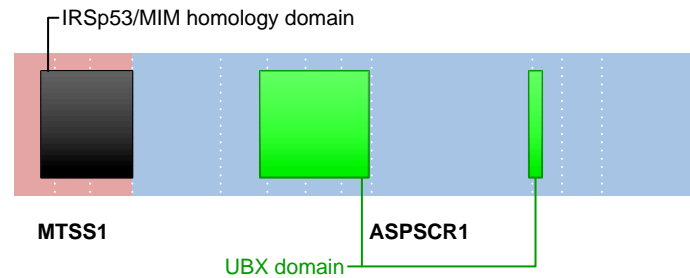
SUPPORTING READ COUNT

Split reads = 80
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



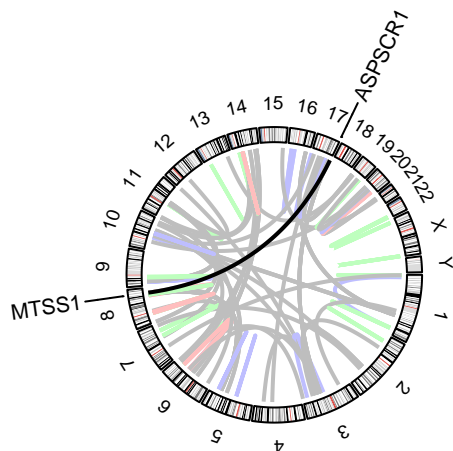
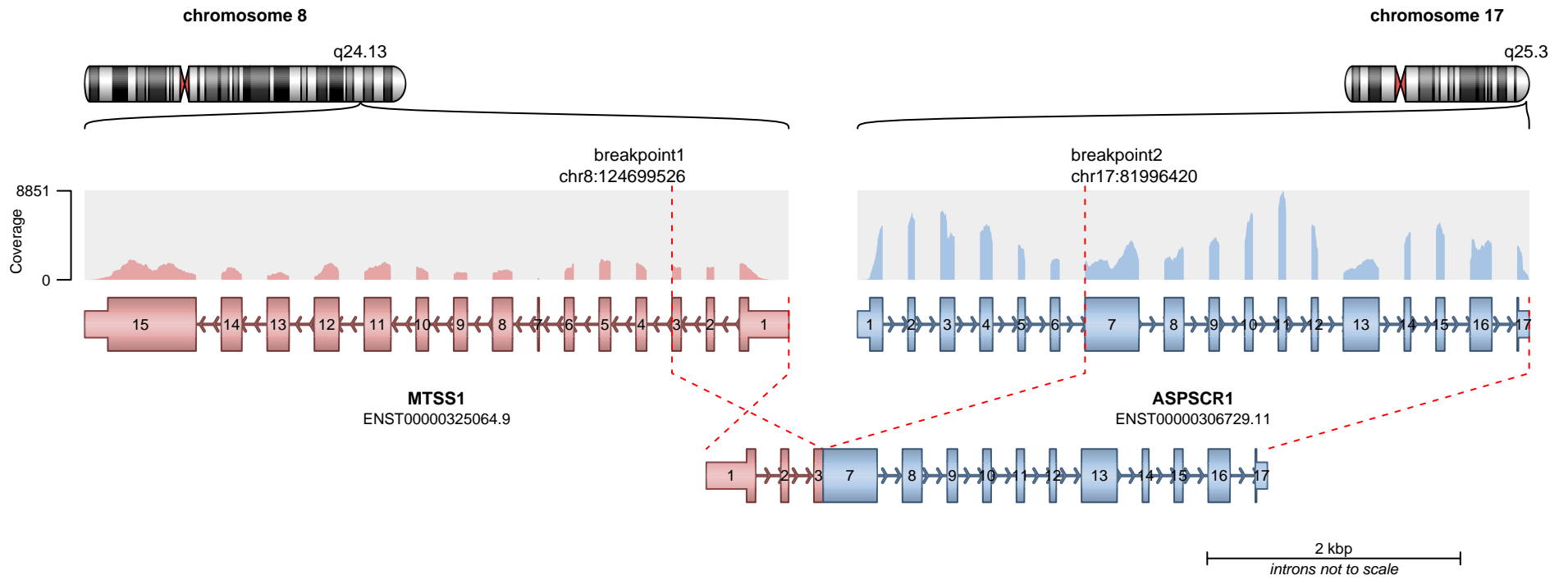
RETAINED PROTEIN DOMAINS
reading frame unclear



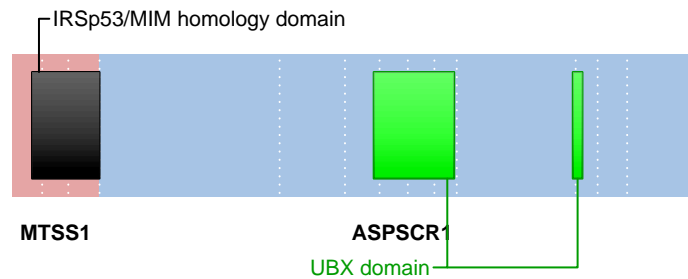
SUPPORTING READ COUNT

Split reads = 65
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



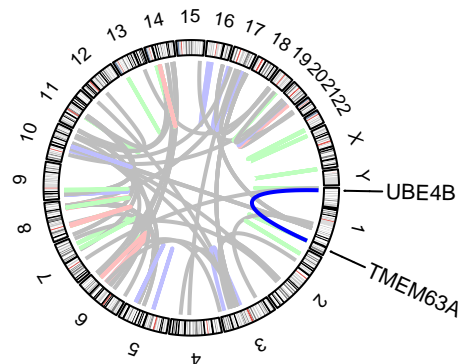
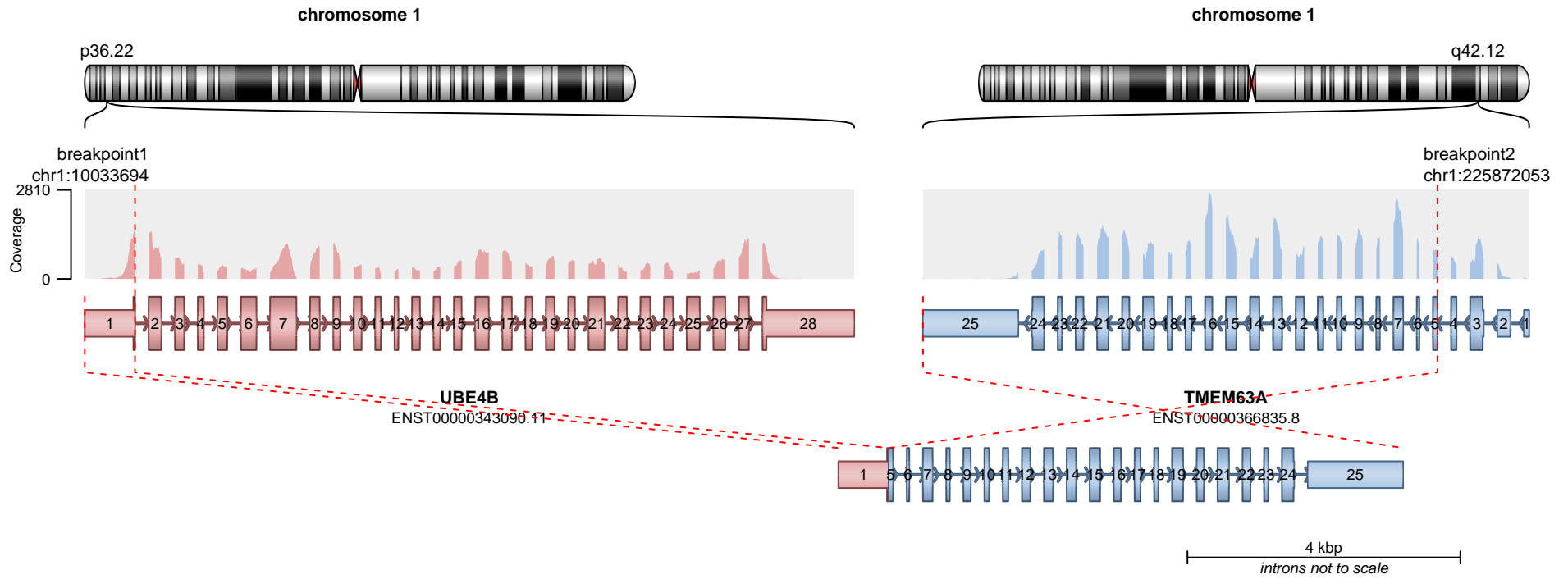
RETAINED PROTEIN DOMAINS
reading frame unclear



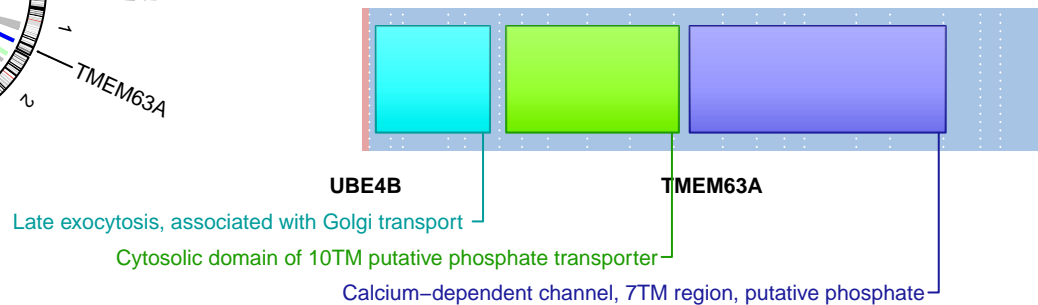
SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



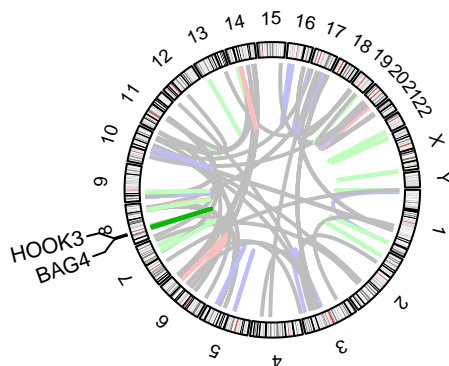
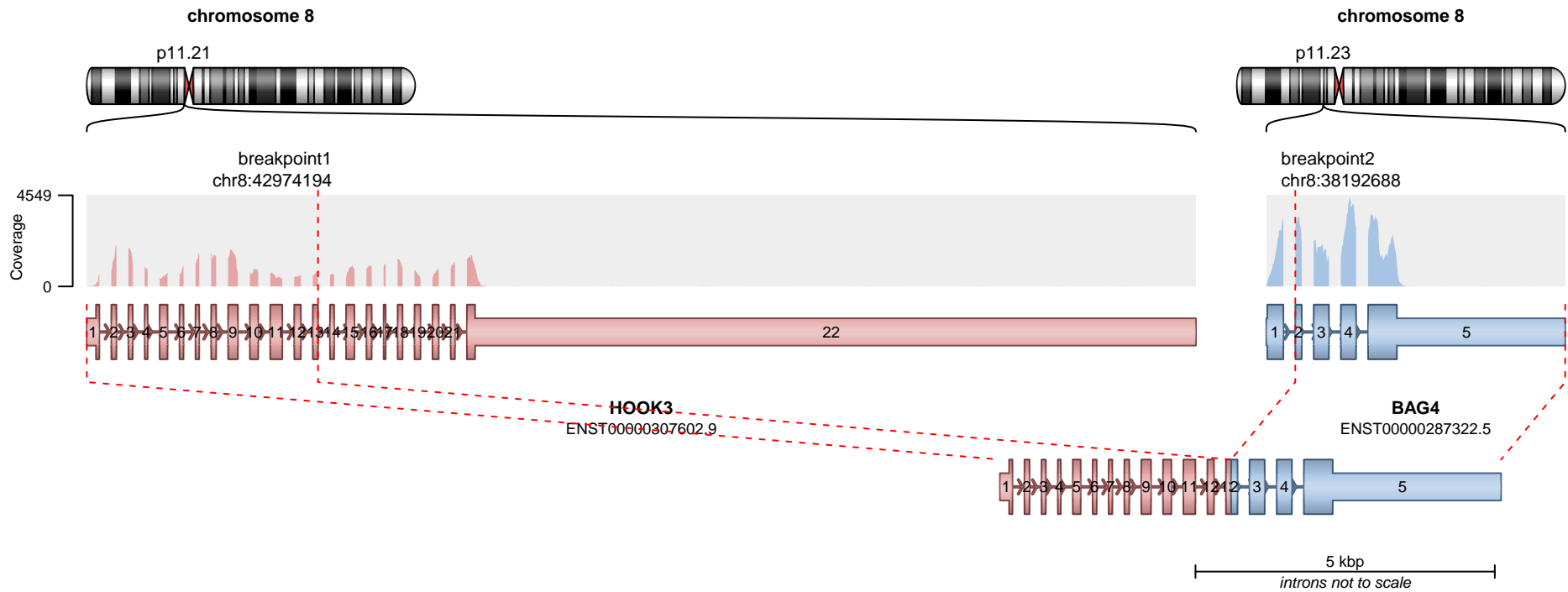
RETAINED PROTEIN DOMAINS
reading frame unclear



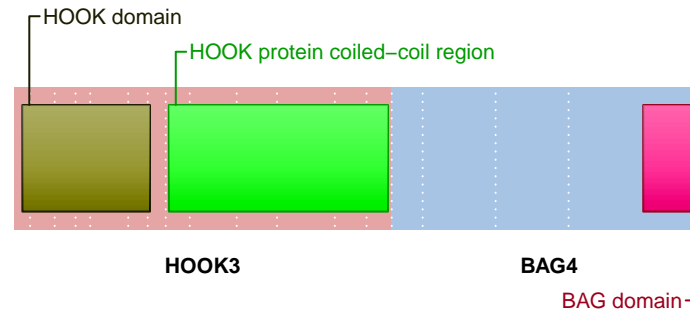
SUPPORTING READ COUNT

Split reads = 52
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



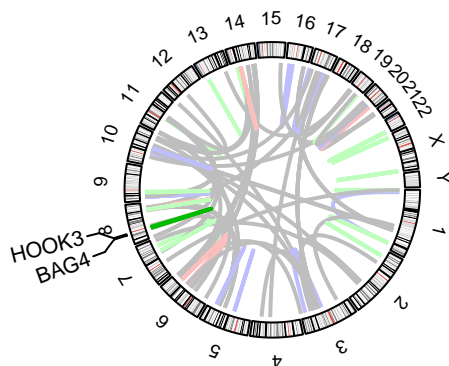
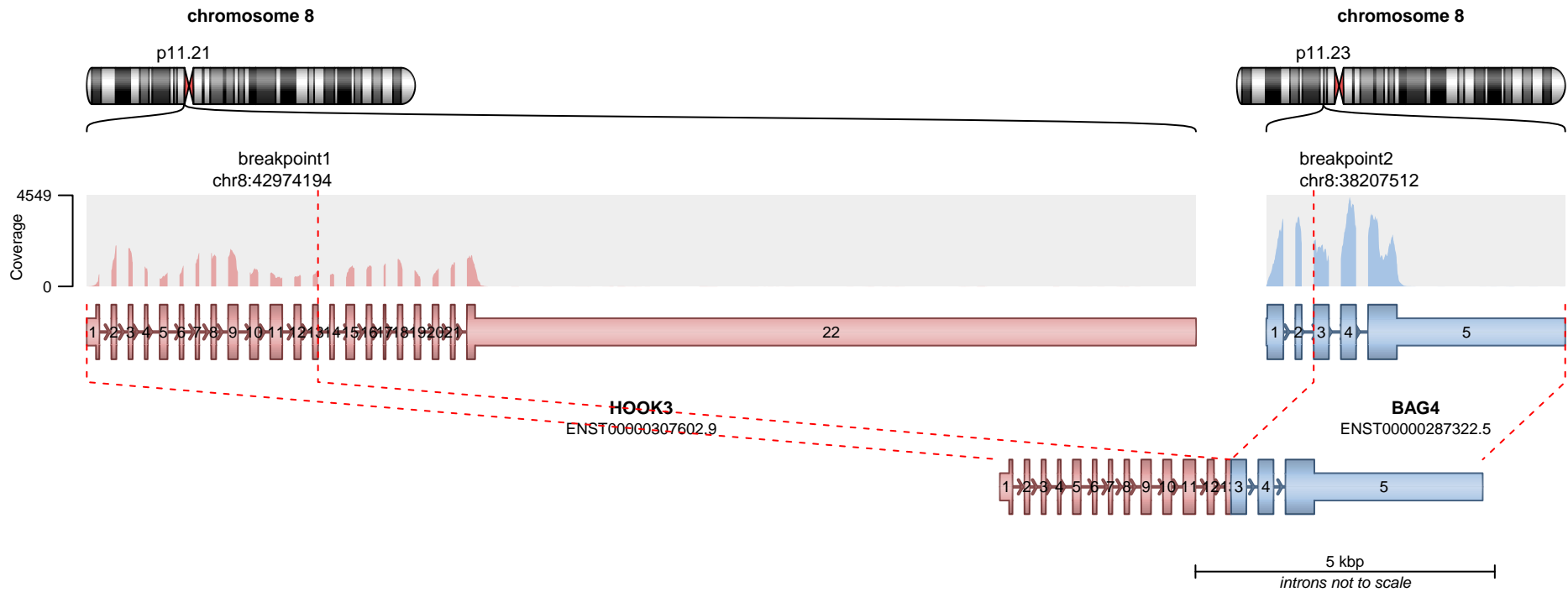
RETAINED PROTEIN DOMAINS
reading frame unclear



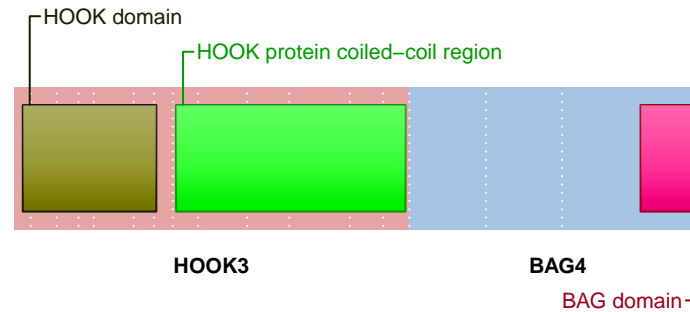
SUPPORTING READ COUNT

Split reads = 49
Discordant mates = 2

— translocation — deletion
— duplication — inversion



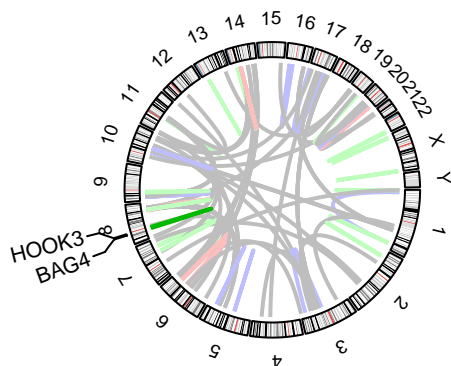
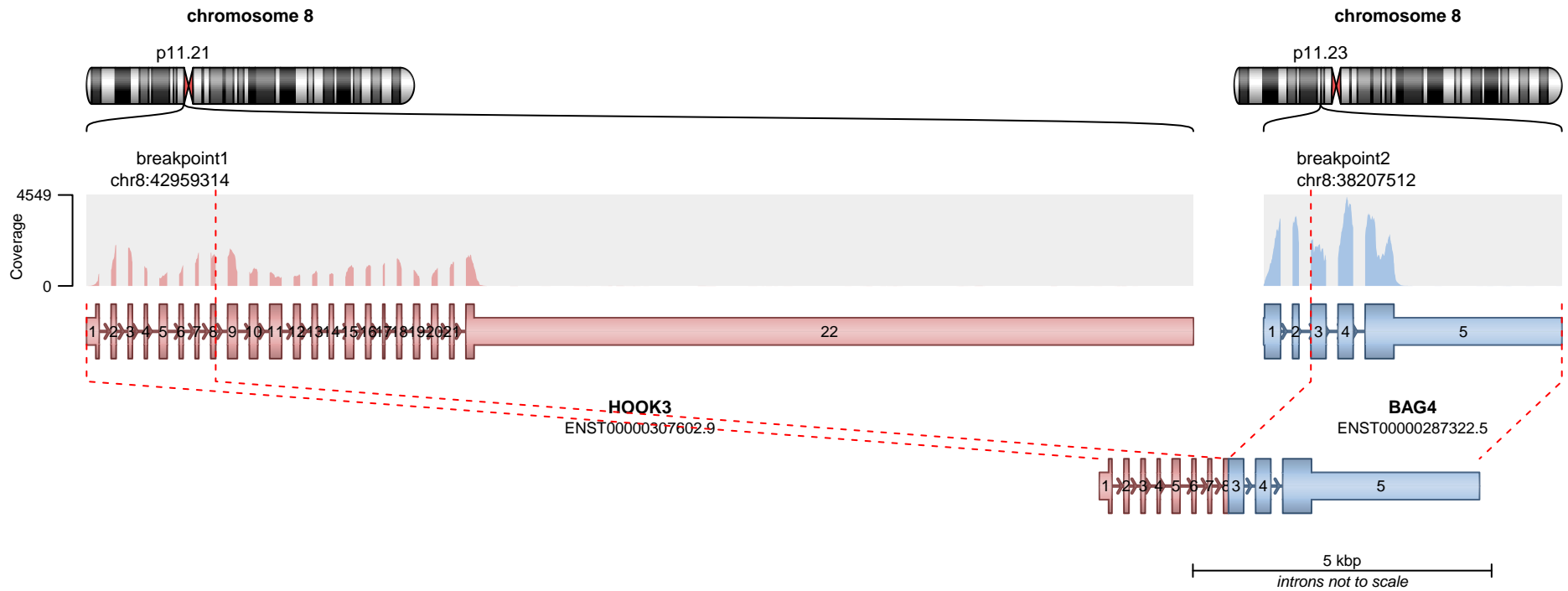
RETAINED PROTEIN DOMAINS
reading frame unclear



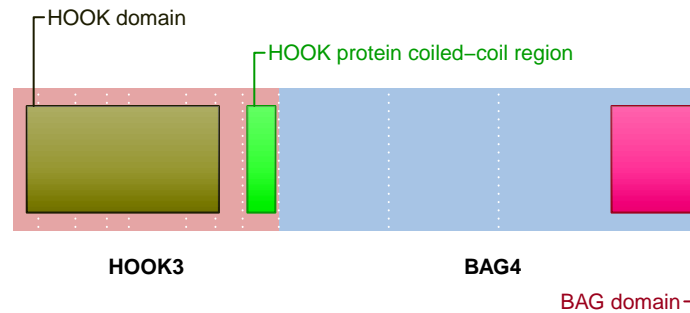
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

— translocation — deletion
— duplication — inversion



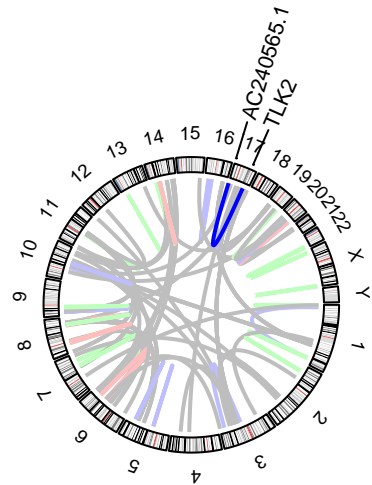
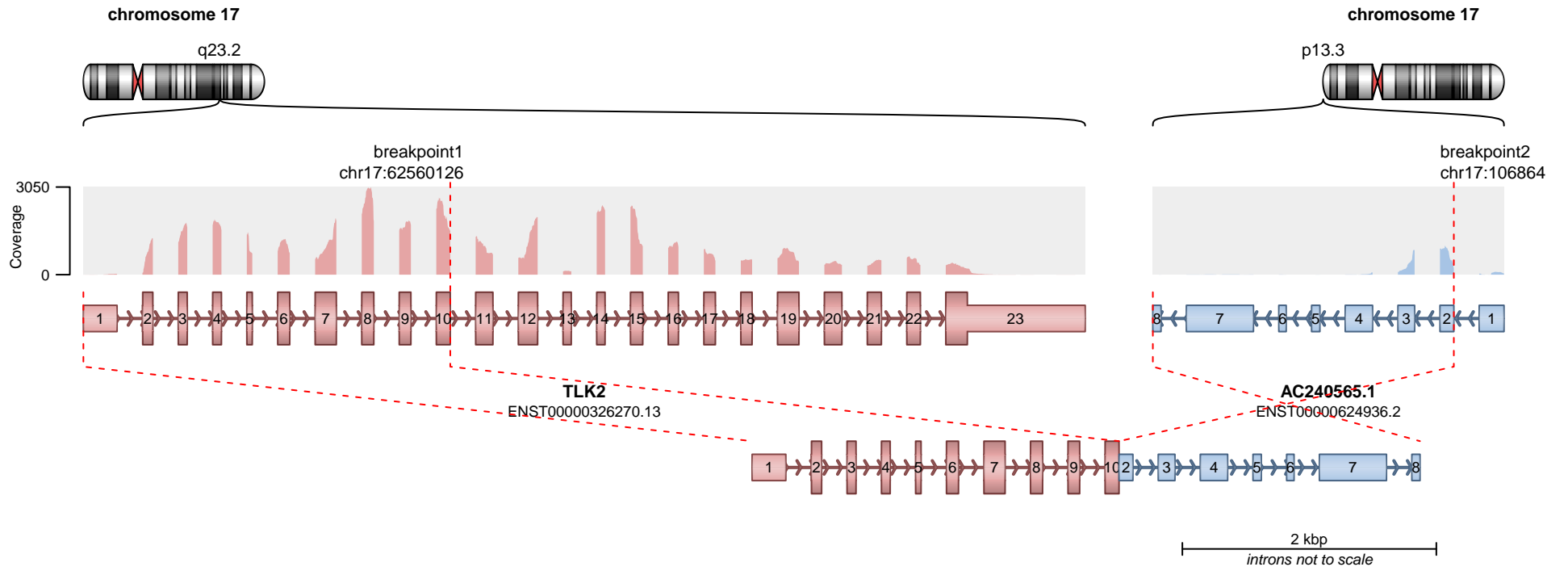
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion

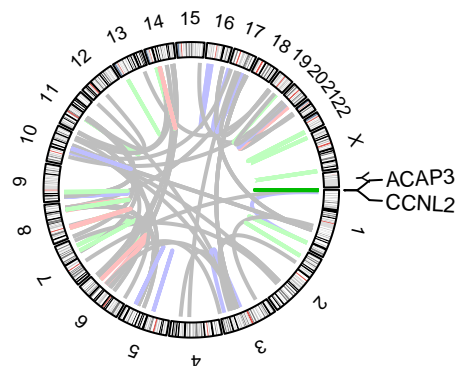
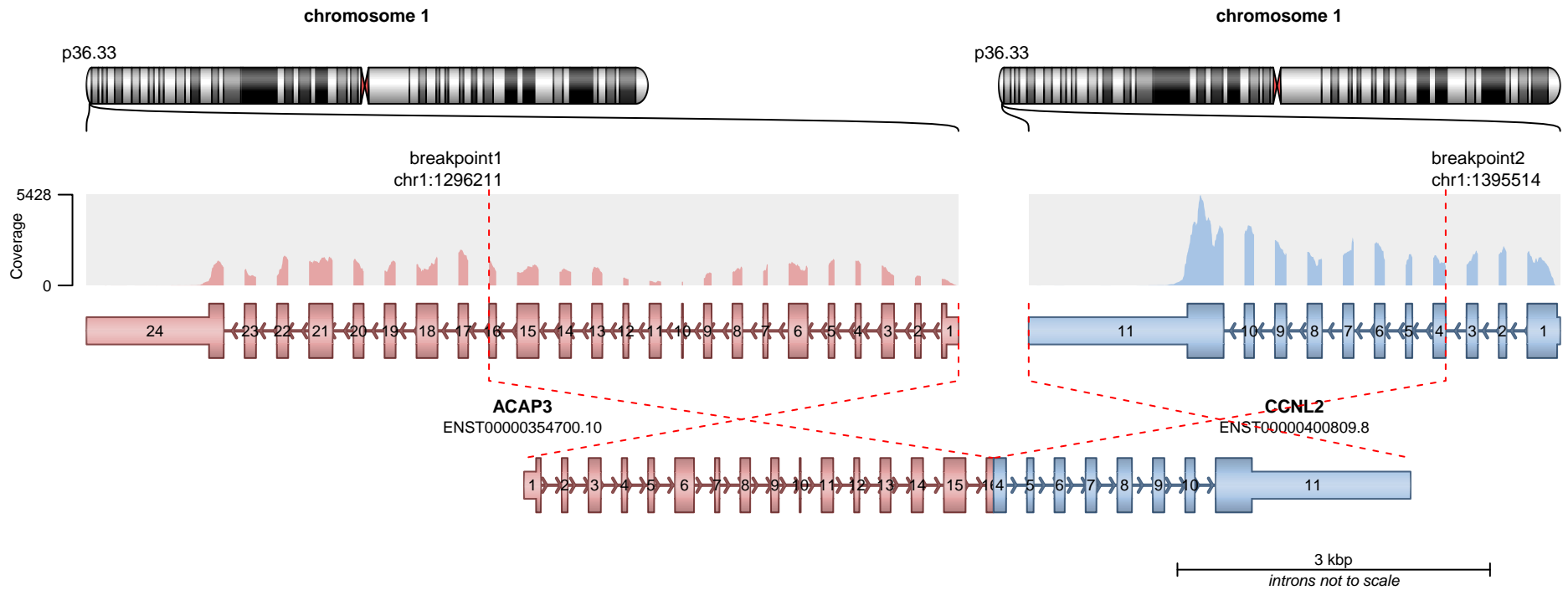


No protein domains retained in fusion.

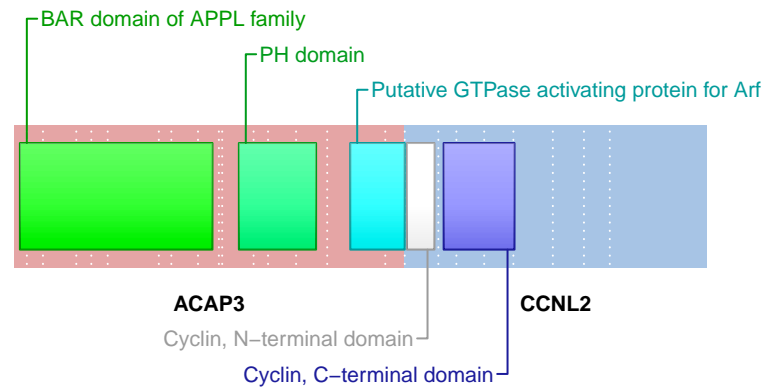
SUPPORTING READ COUNT

Split reads = 47
Discordant mates = 0

— translocation — deletion
— duplication — inversion



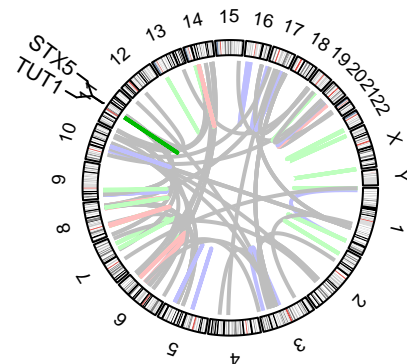
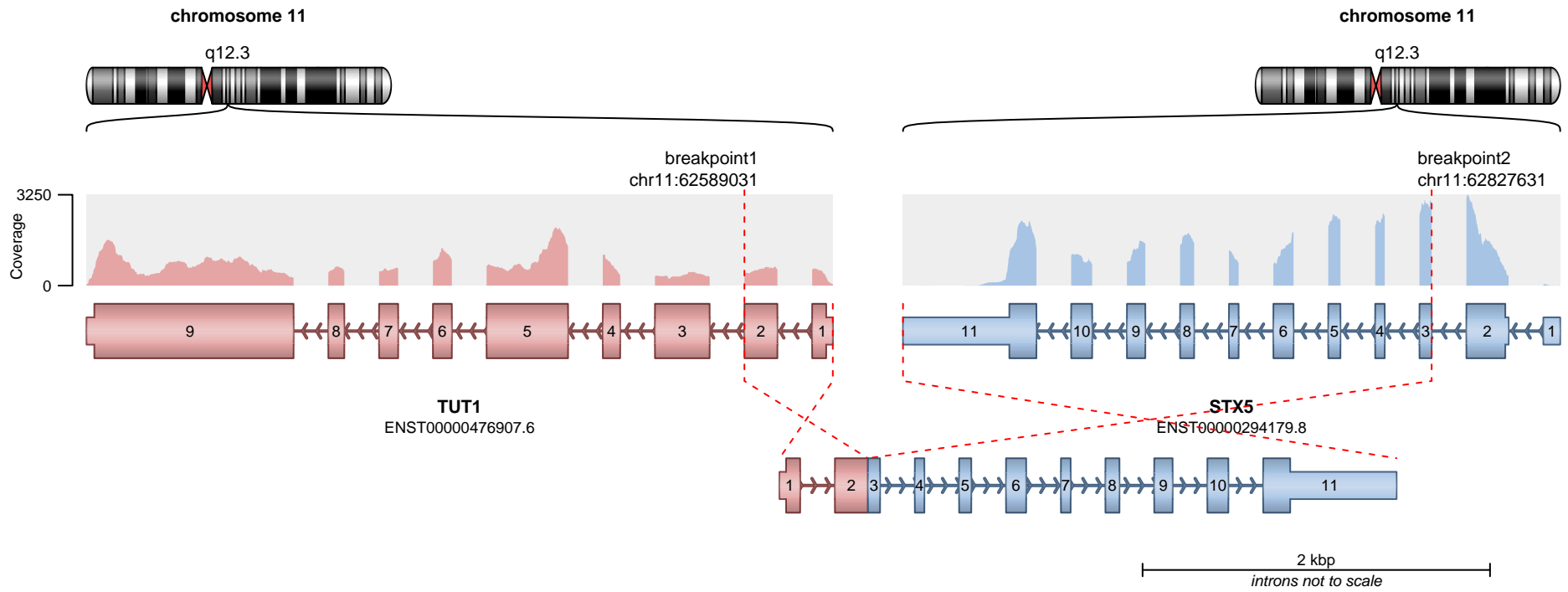
RETAINED PROTEIN DOMAINS
reading frame unclear



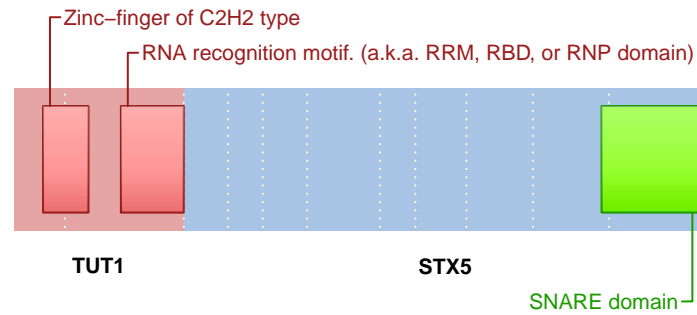
SUPPORTING READ COUNT

Split reads = 46
Discordant mates = 1

— translocation — deletion
— duplication — inversion



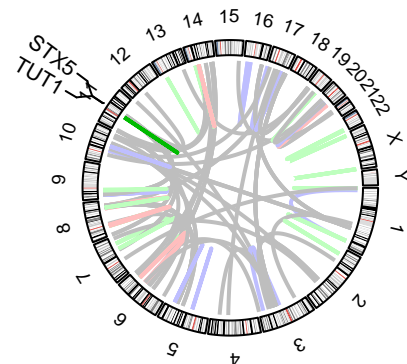
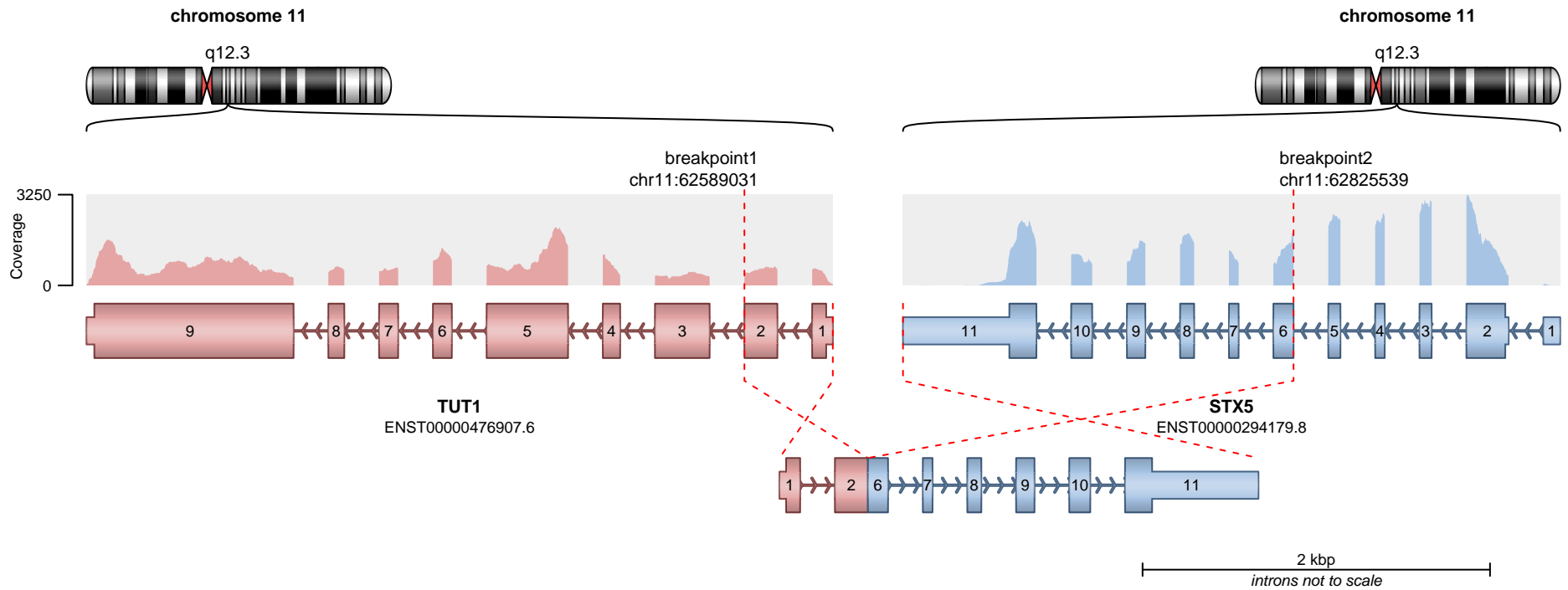
RETAINED PROTEIN DOMAINS
reading frame unclear



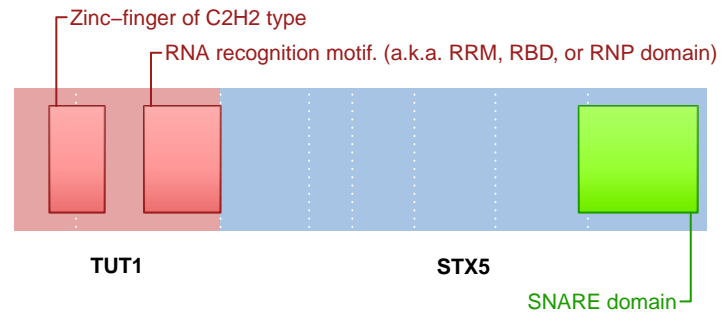
SUPPORTING READ COUNT

Split reads = 45
Discordant mates = 0

— translocation — deletion
— duplication — inversion



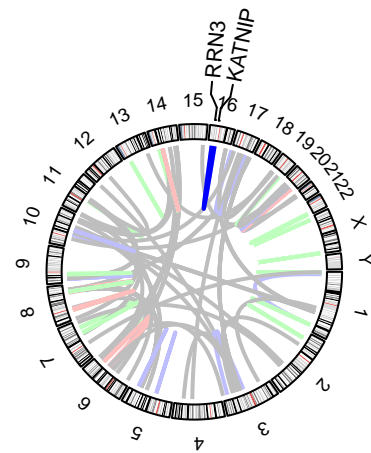
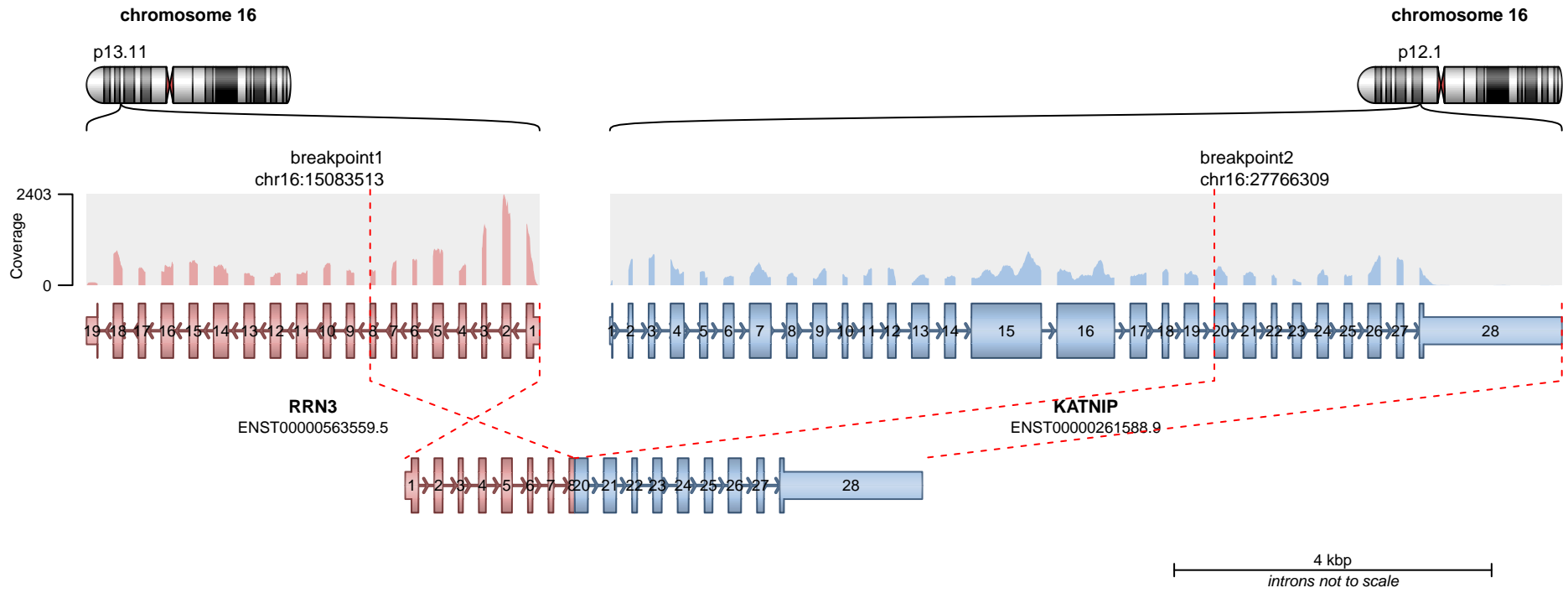
RETAINED PROTEIN DOMAINS
reading frame unclear



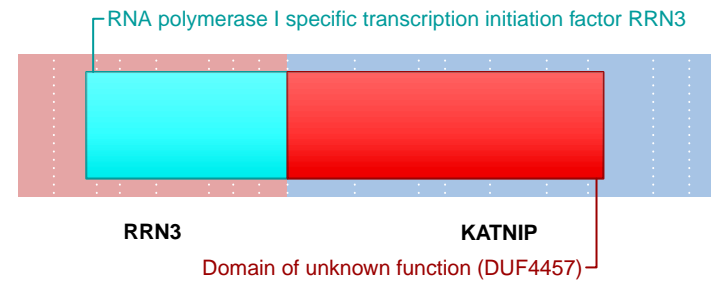
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



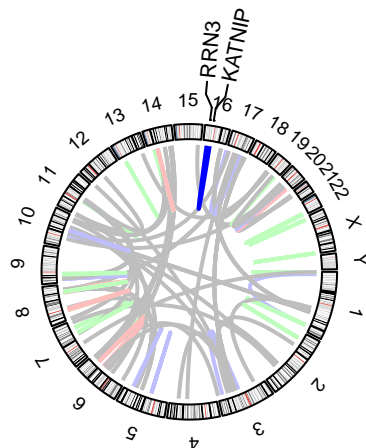
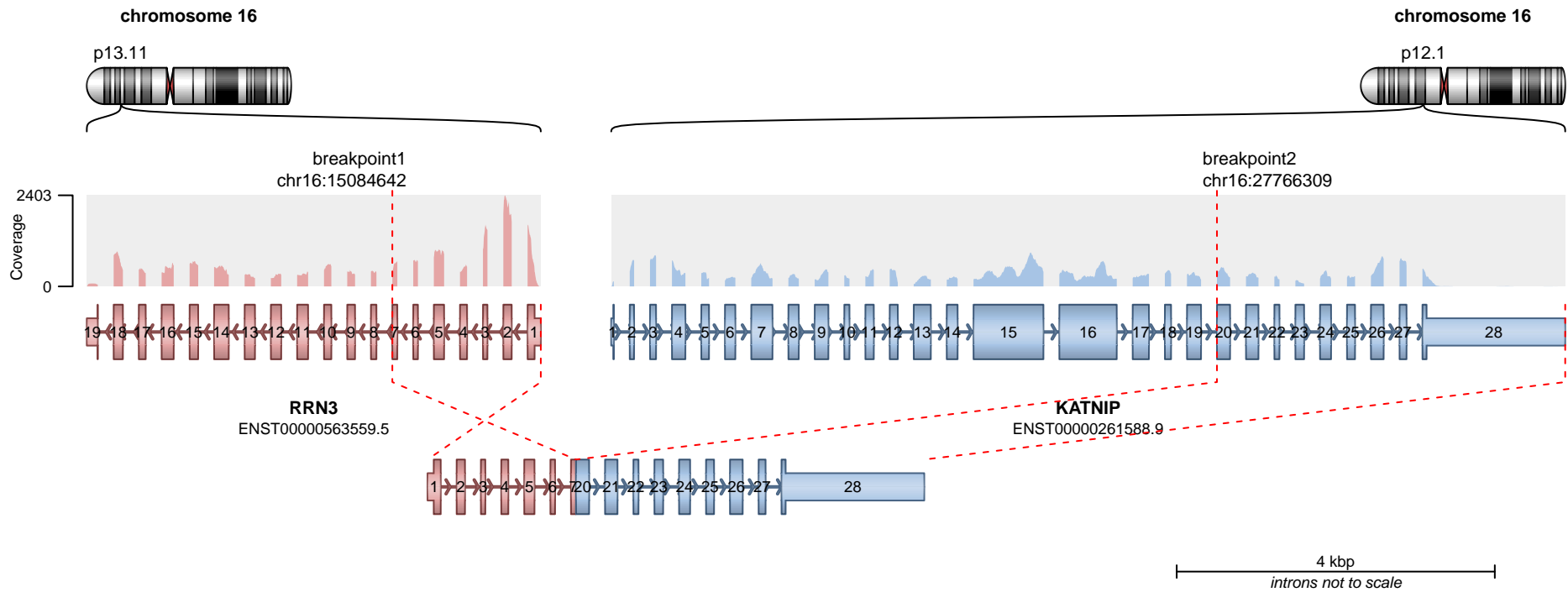
RETAINED PROTEIN DOMAINS
reading frame unclear



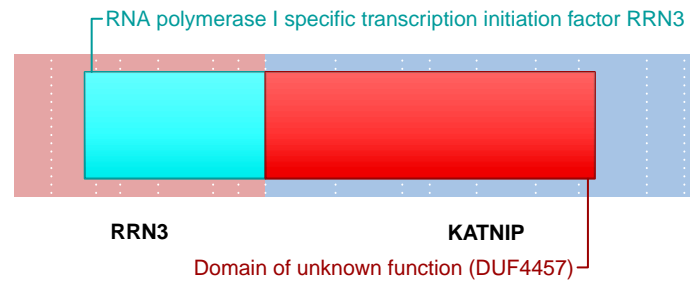
SUPPORTING READ COUNT

Split reads = 44
Discordant mates = 2

- translocation
- duplication
- deletion
- inversion



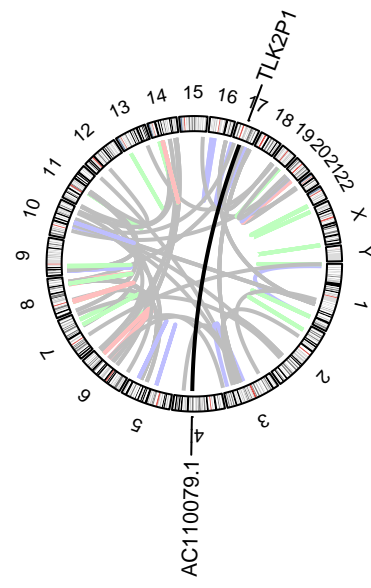
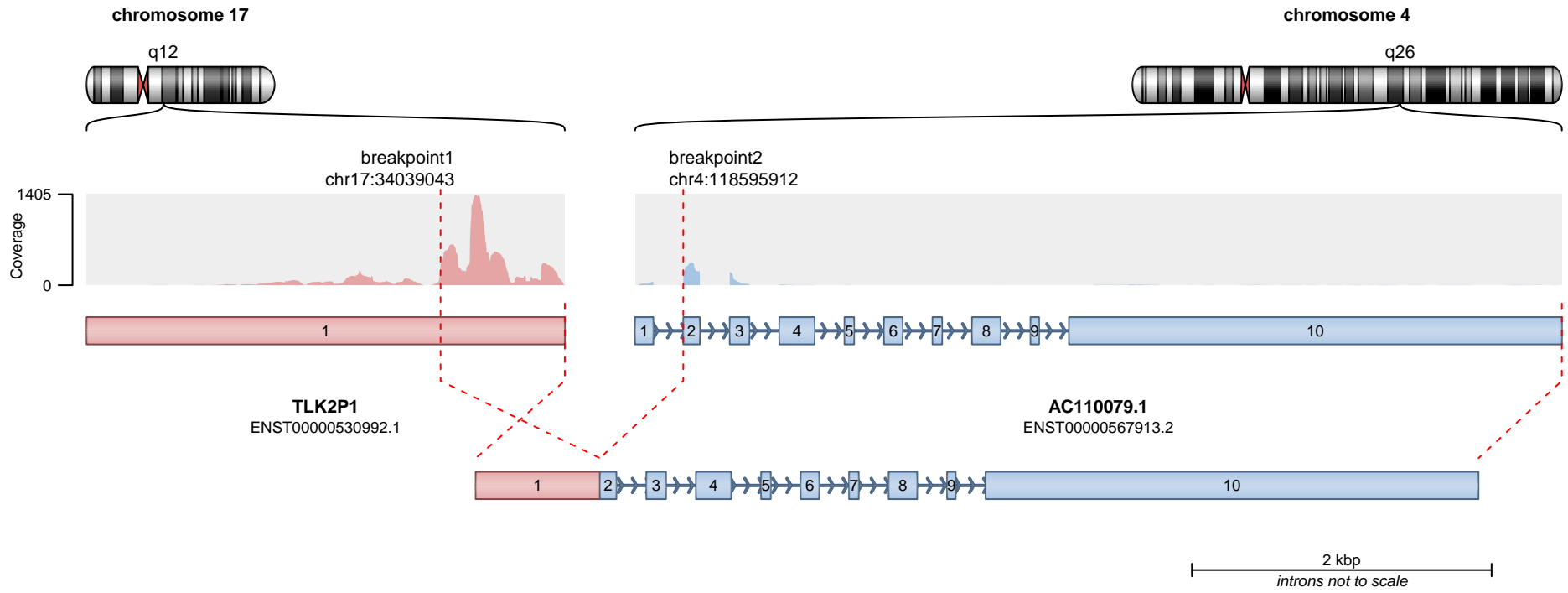
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 11
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion

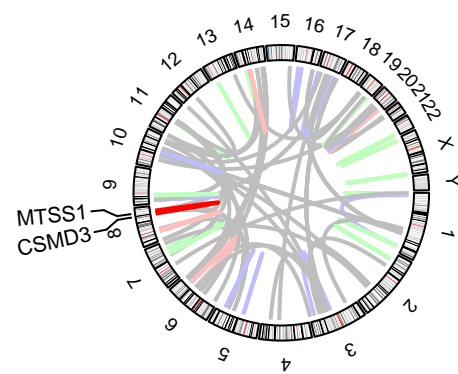
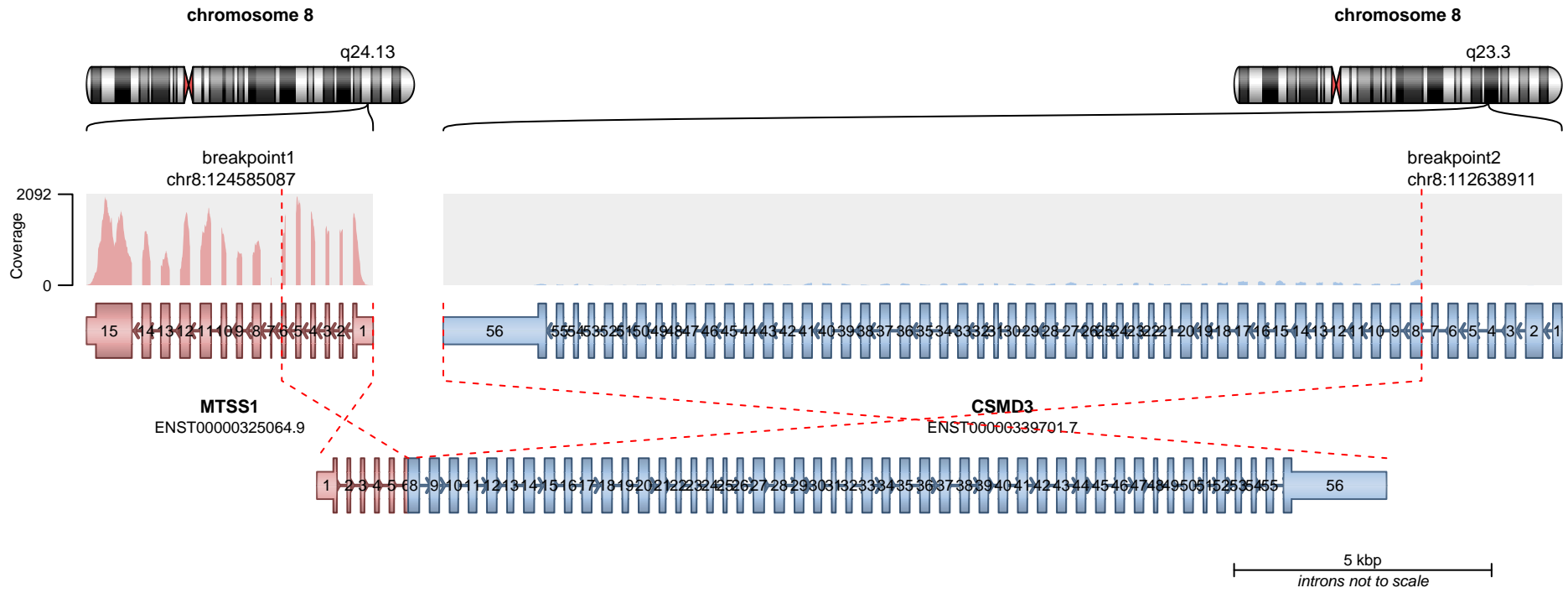


— translocation — deletion
 — duplication — inversion

Genes are not protein-coding.

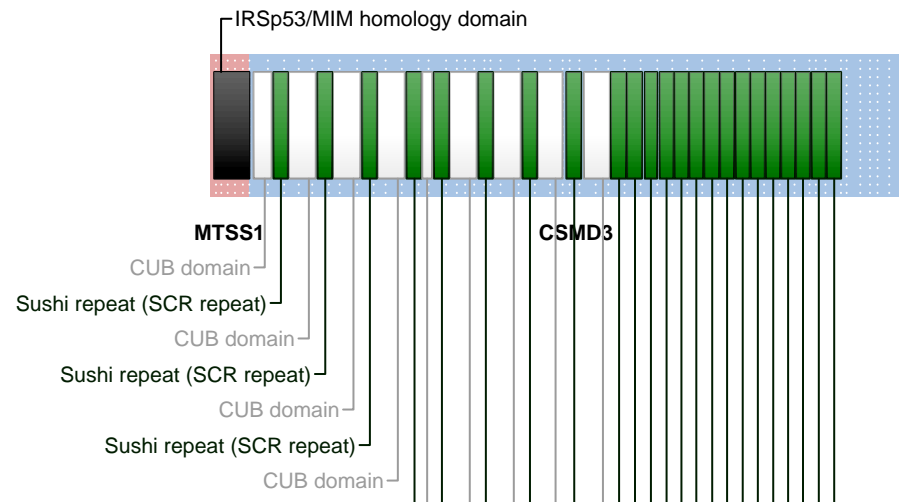
SUPPORTING READ COUNT

Split reads = 44
 Discordant mates = 0



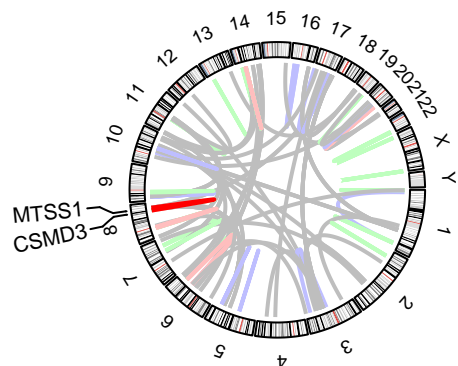
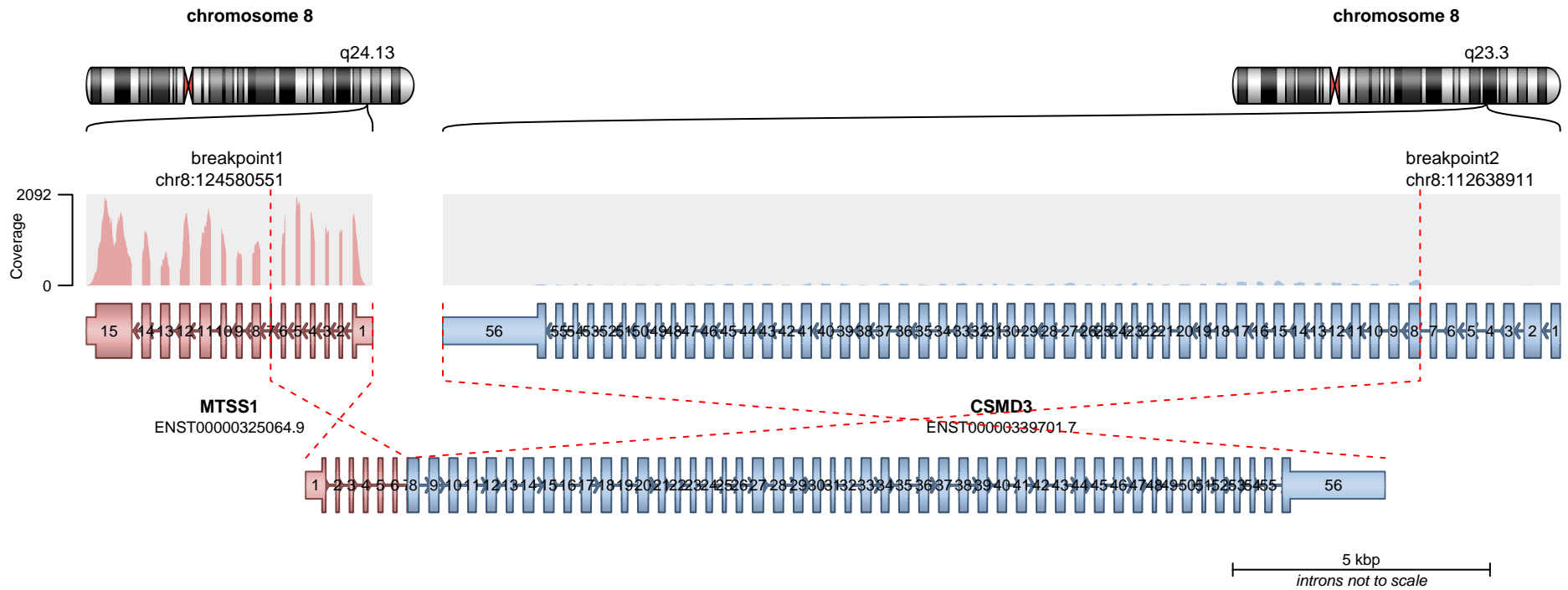
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



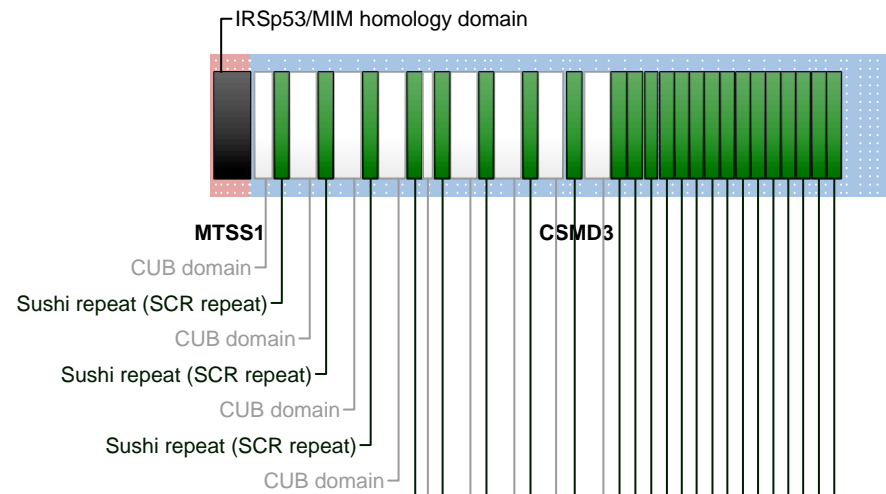
SUPPORTING READ COUNT

Split reads = 35
Discordant mates = 0



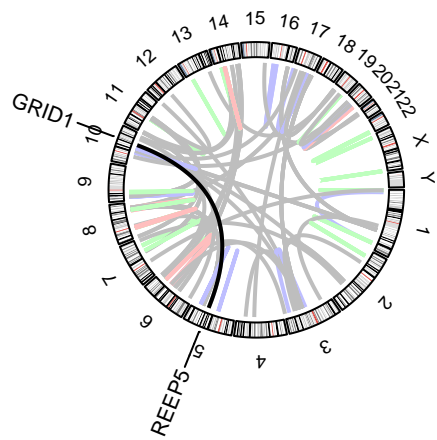
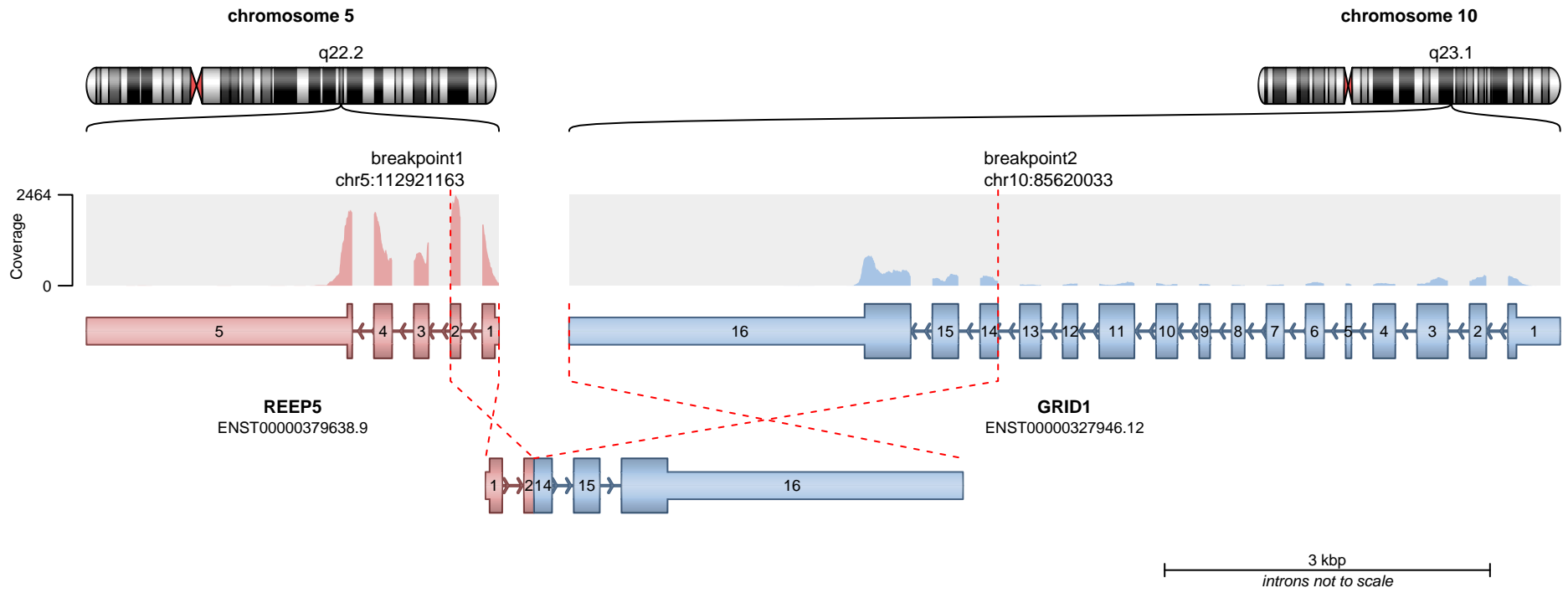
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear

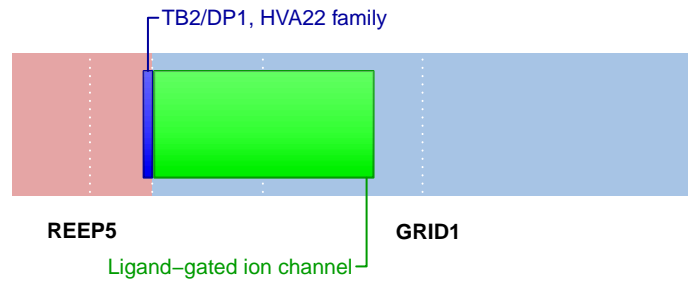


SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 0



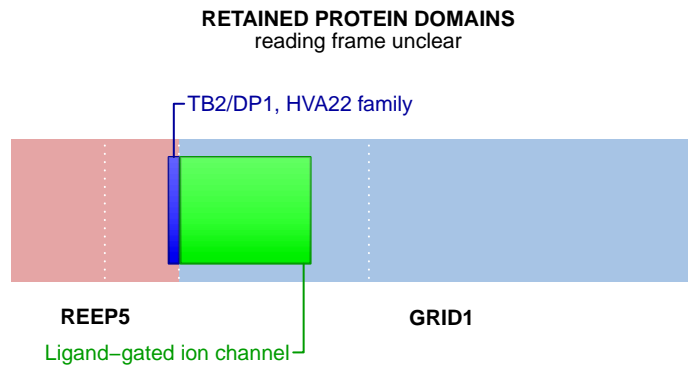
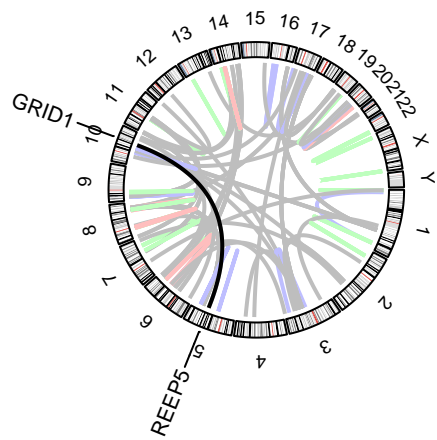
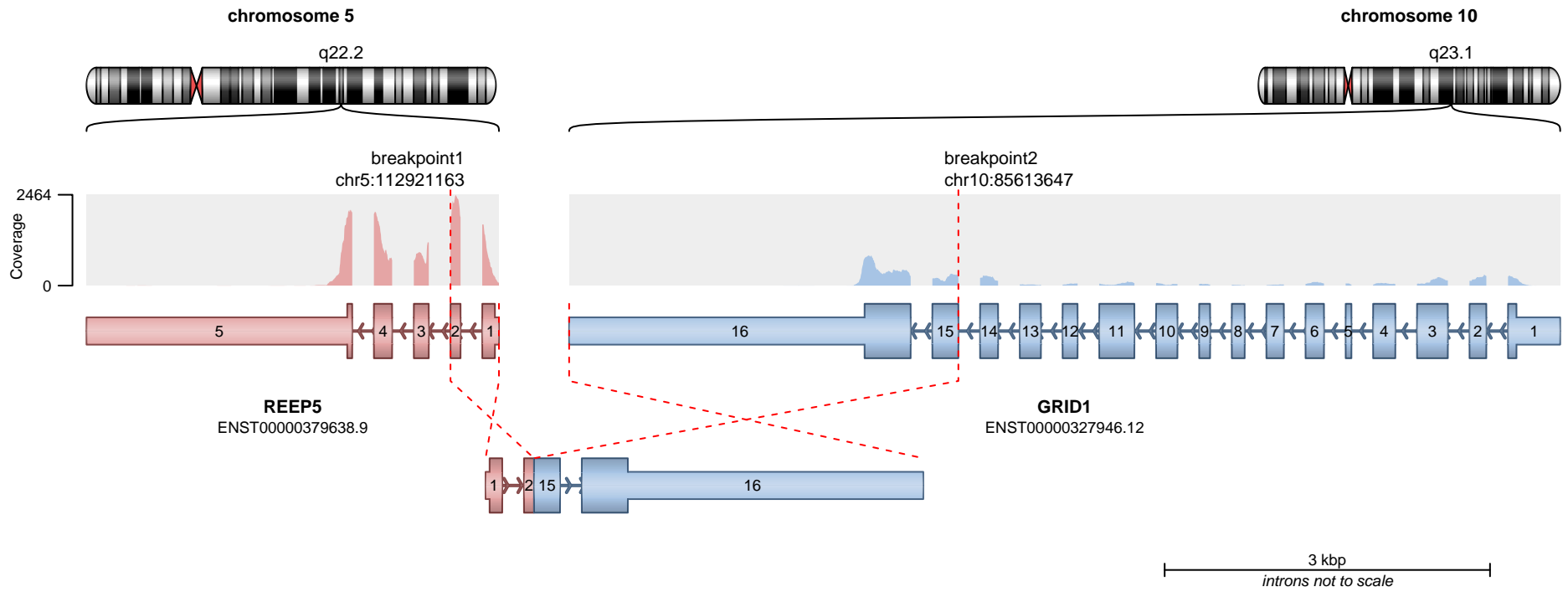
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 31
Discordant mates = 1

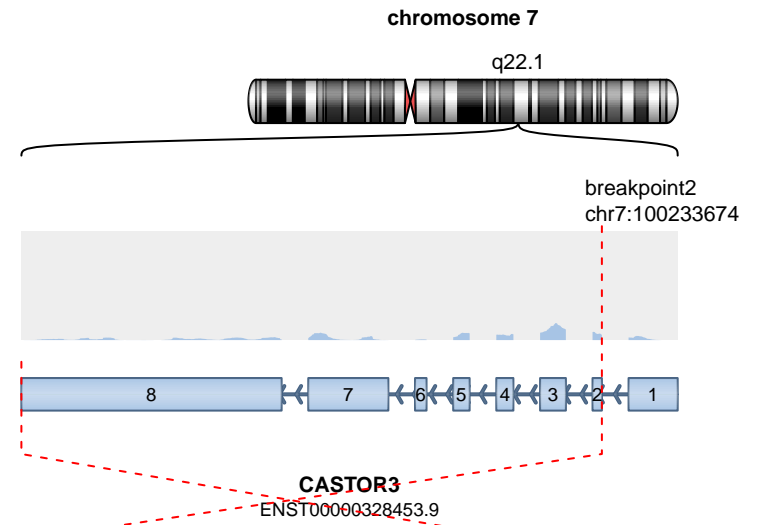
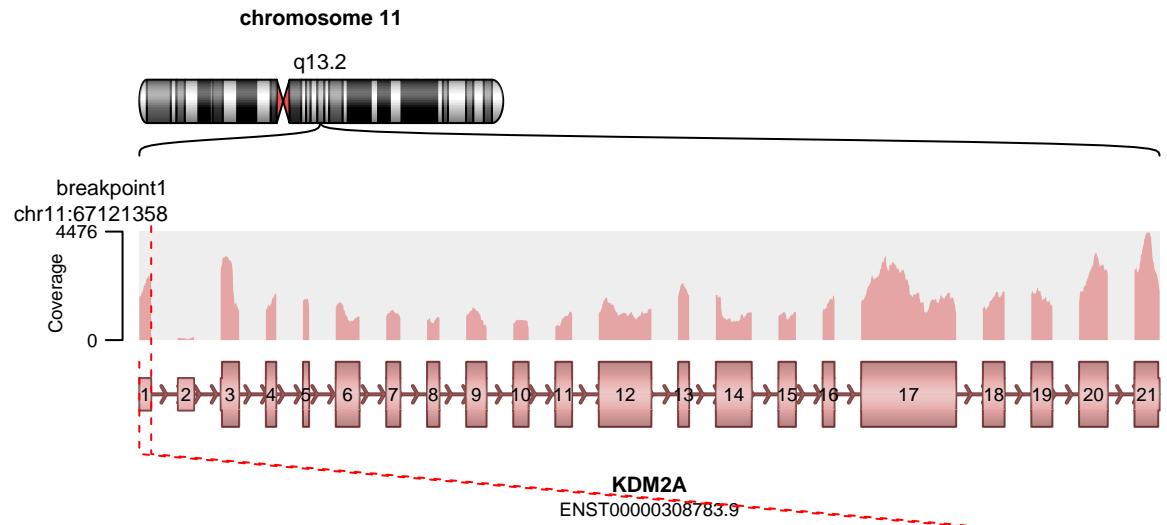
- translocation
- duplication
- deletion
- inversion



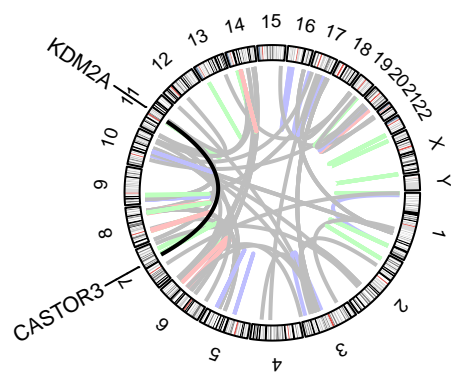
SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



3 kbp
introns not to scale

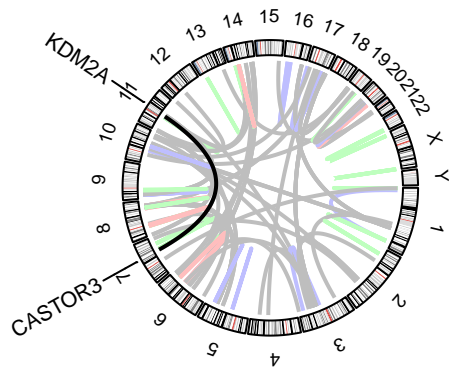
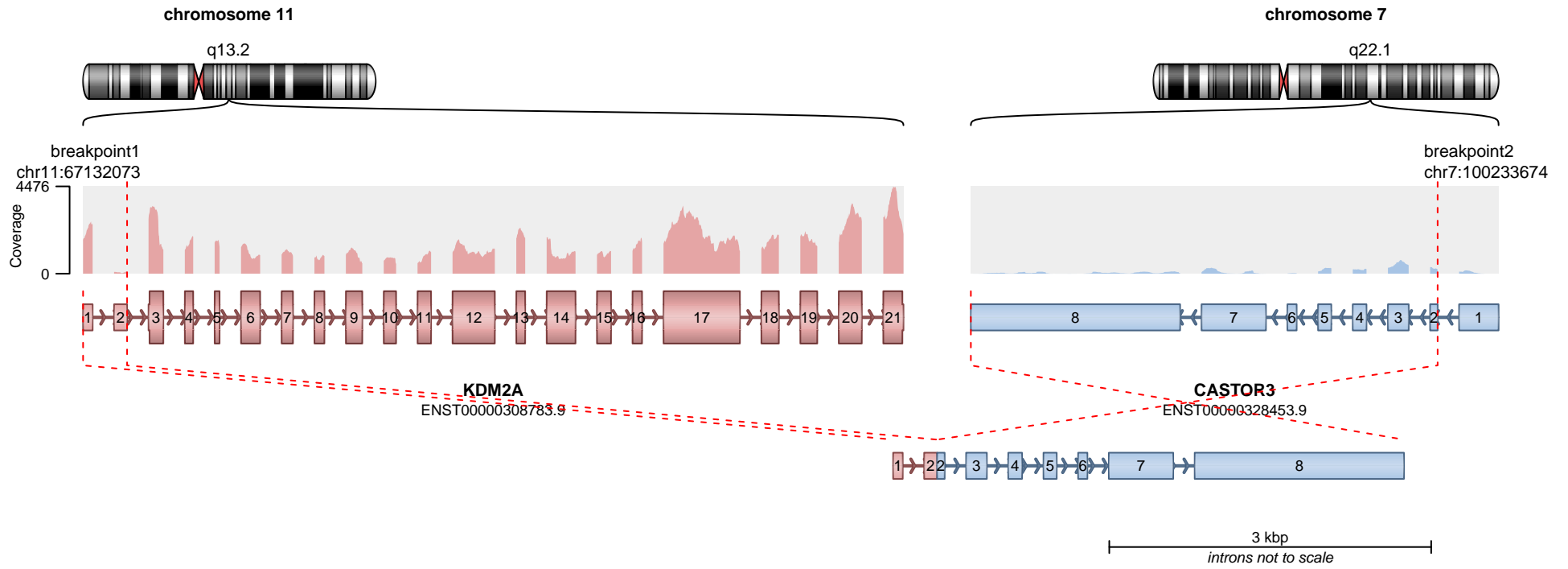


No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 29
Discordant mates = 3

- translocation
- duplication
- deletion
- inversion

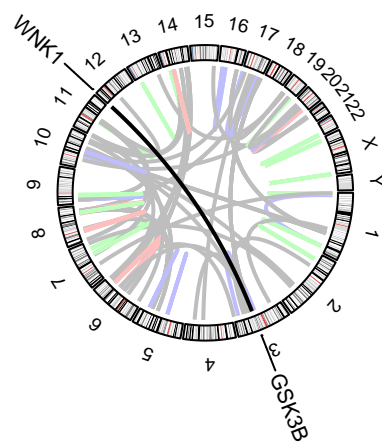
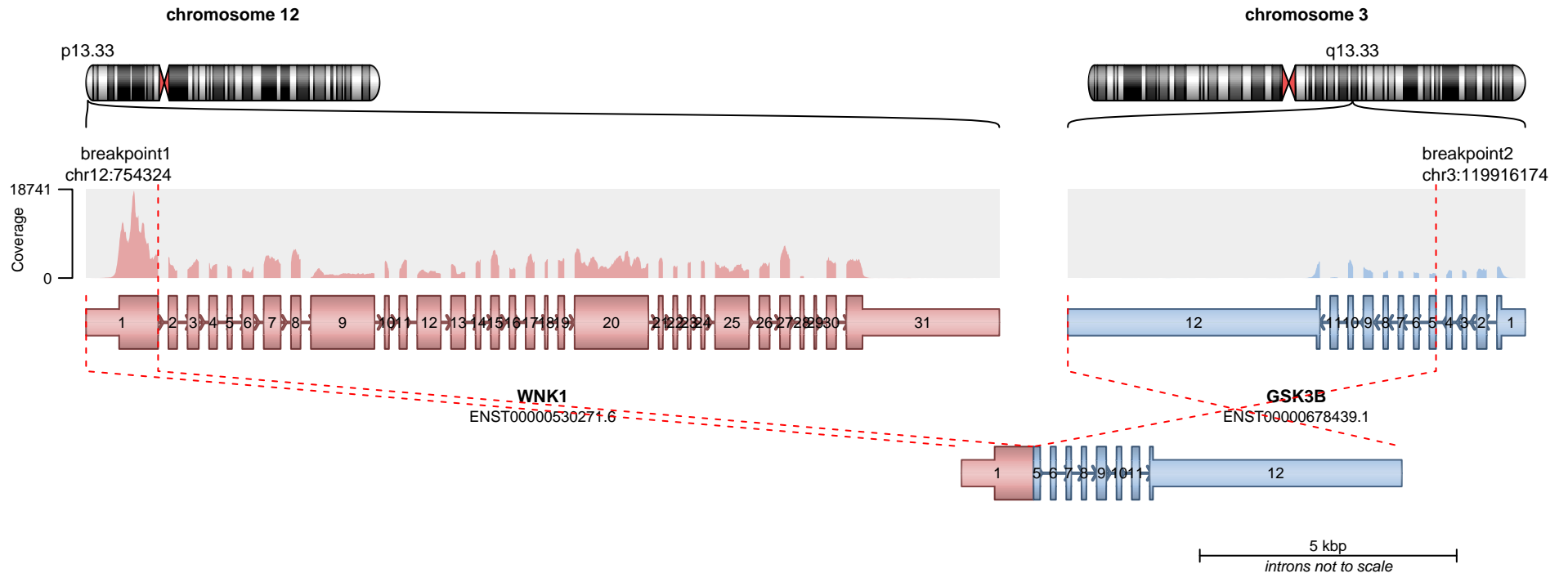


No coding regions retained in fusion transcript.

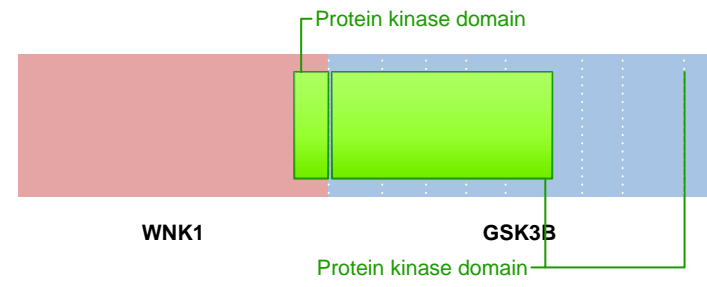
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 3

- translocation
- duplication
- deletion
- inversion



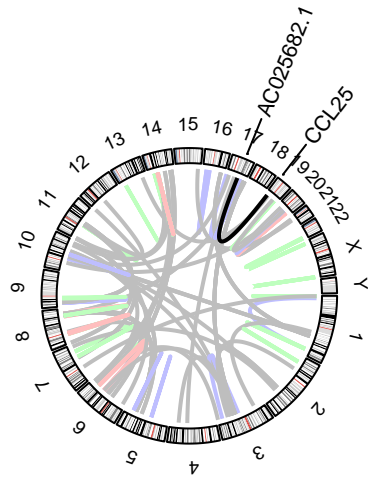
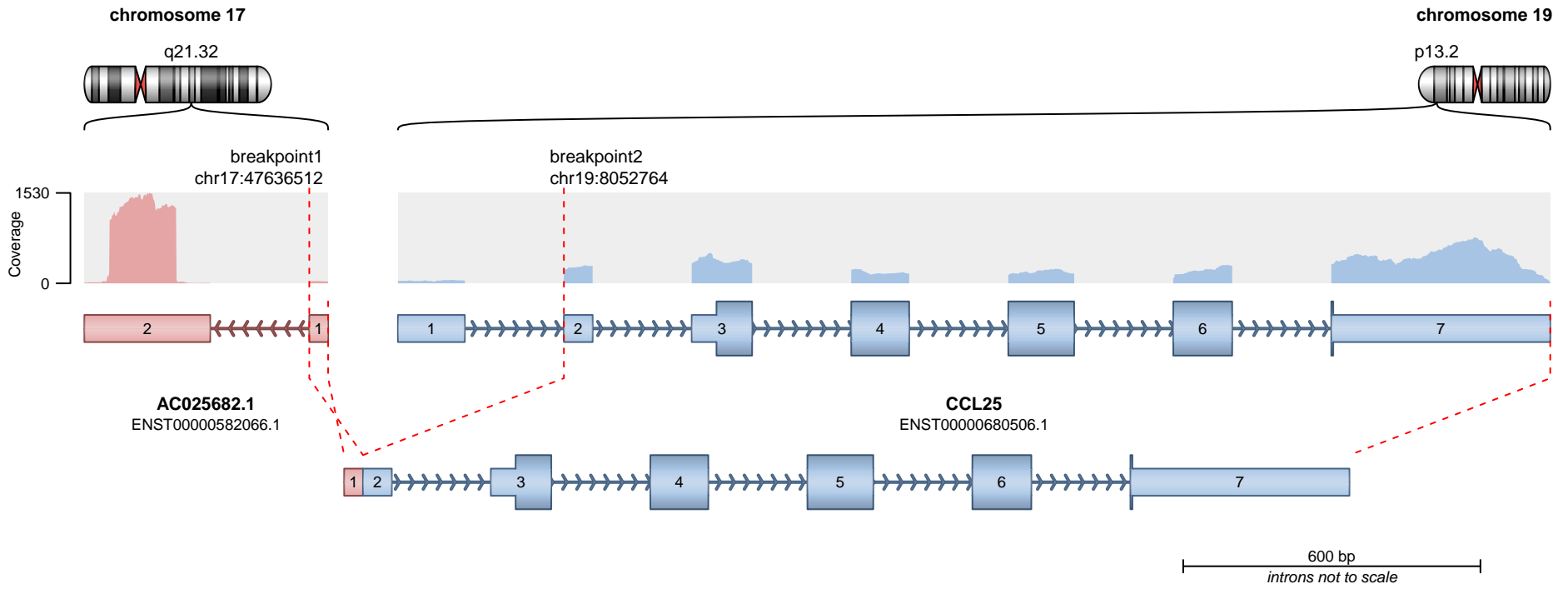
RETAINED PROTEIN DOMAINS
reading frame unclear



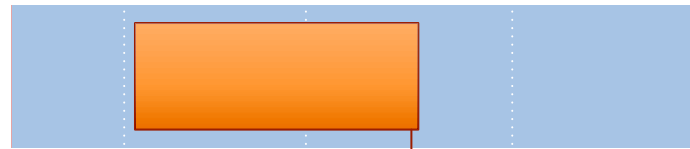
SUPPORTING READ COUNT

Split reads = 27
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



RETAINED PROTEIN DOMAINS
reading frame unclear



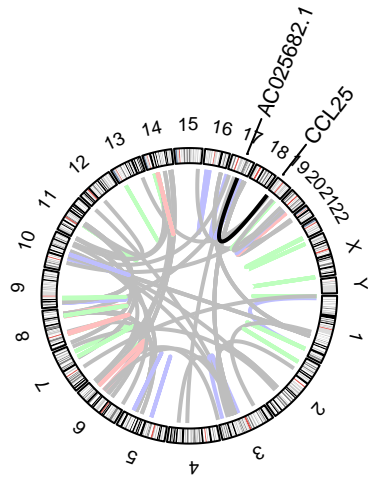
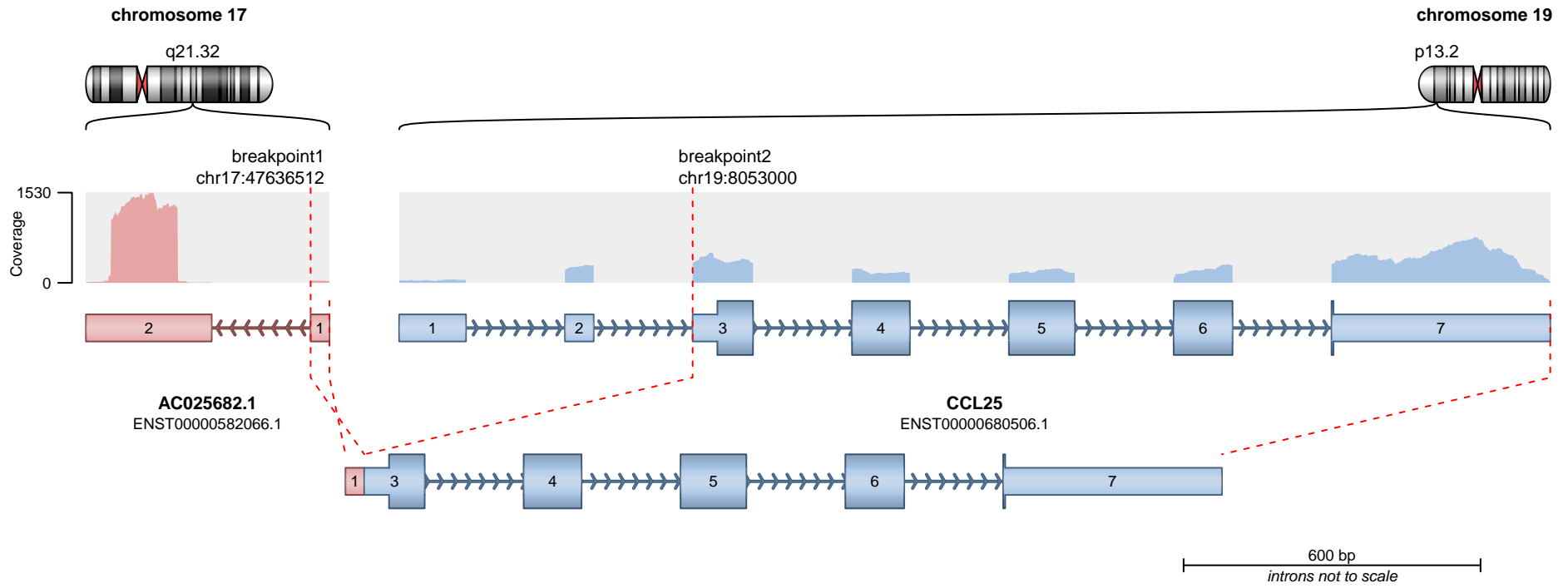
CCL25

Small cytokines (intecrine/chemokine), interleukin-8 like

SUPPORTING READ COUNT

Split reads = 25
Discordant mates = 0

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS
reading frame unclear



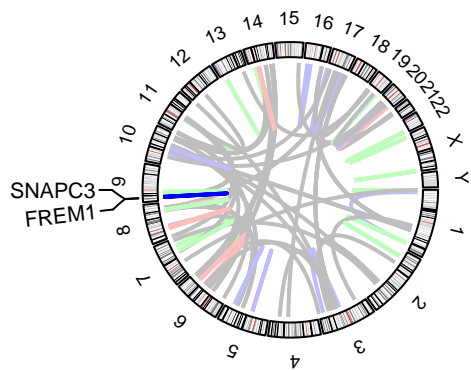
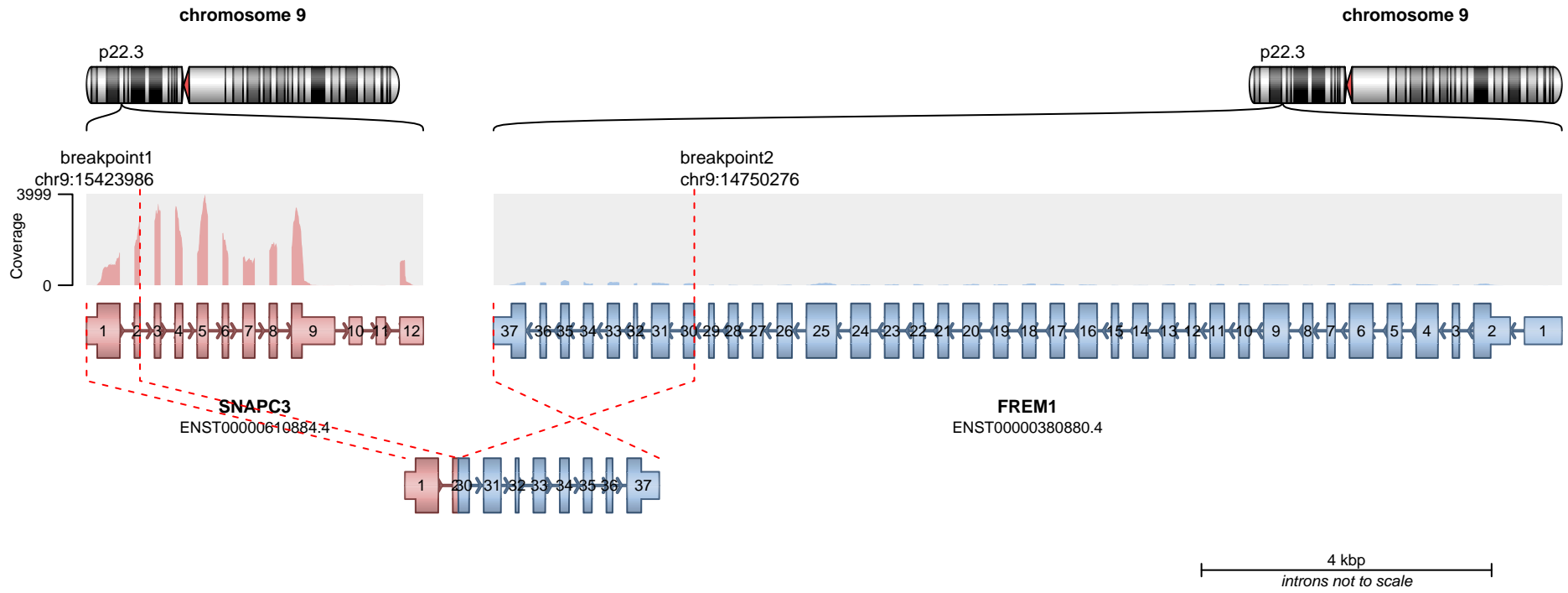
CCL25

Small cytokines (intecrine/chemokine), interleukin-8 like

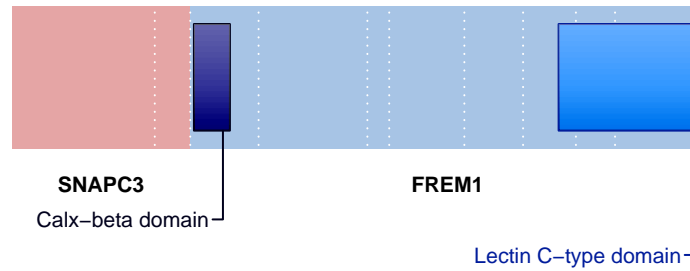
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



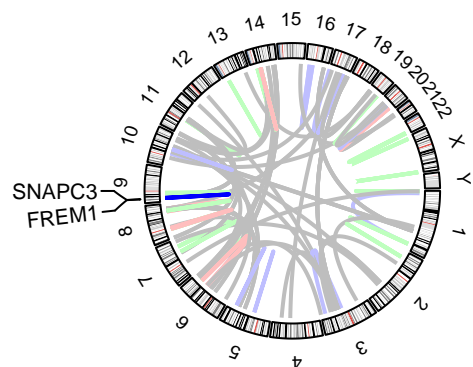
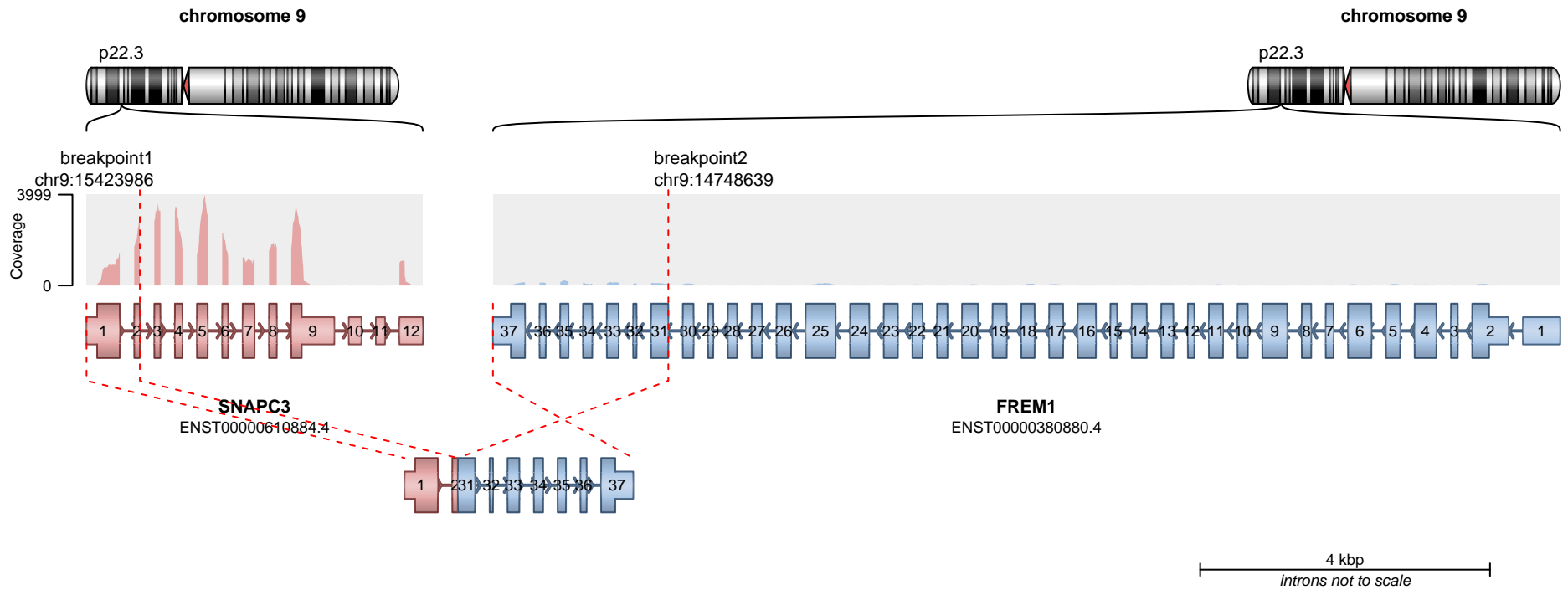
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 23
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



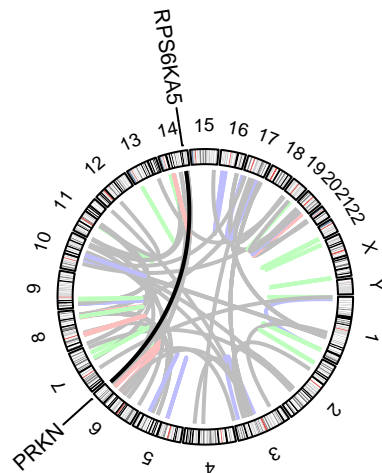
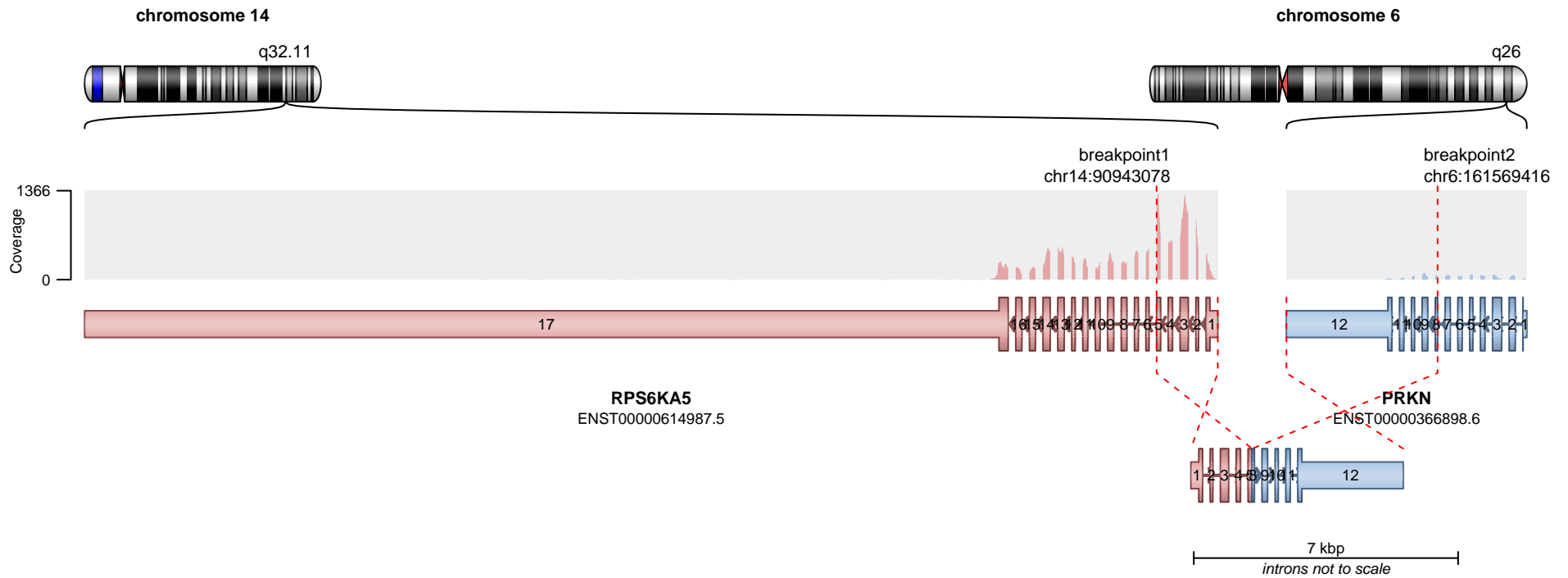
RETAINED PROTEIN DOMAINS
reading frame unclear



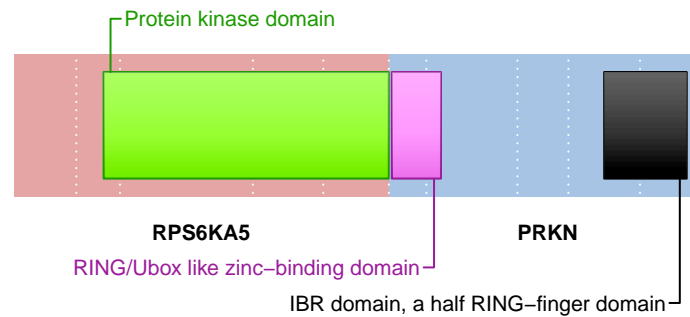
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



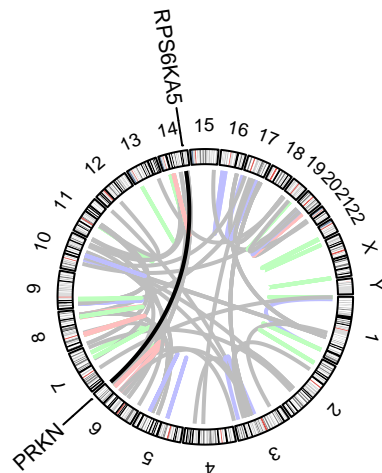
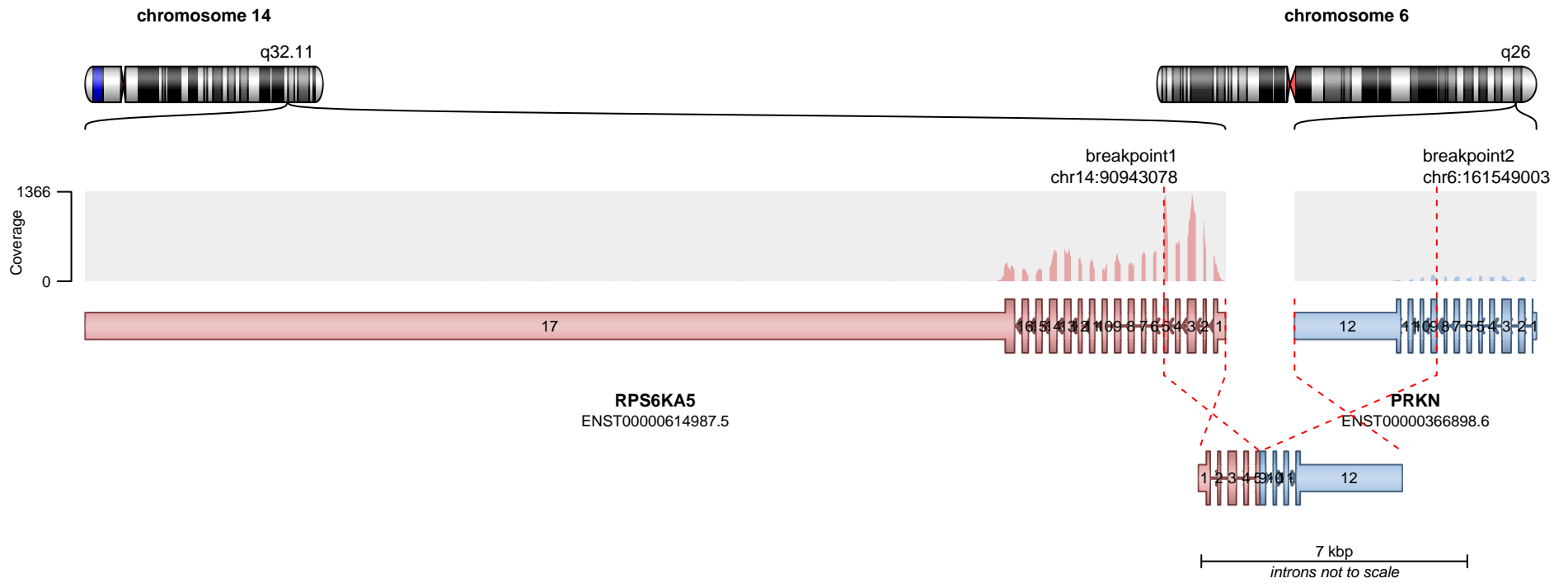
RETAINED PROTEIN DOMAINS
reading frame unclear



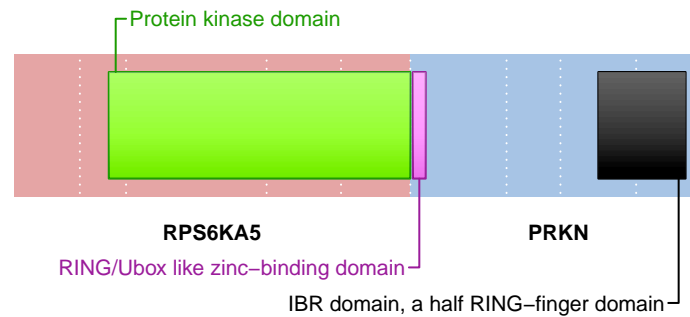
SUPPORTING READ COUNT

Split reads = 21
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



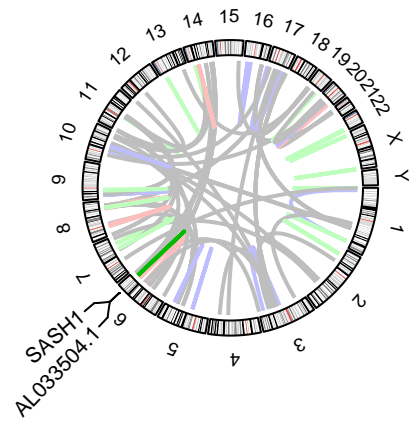
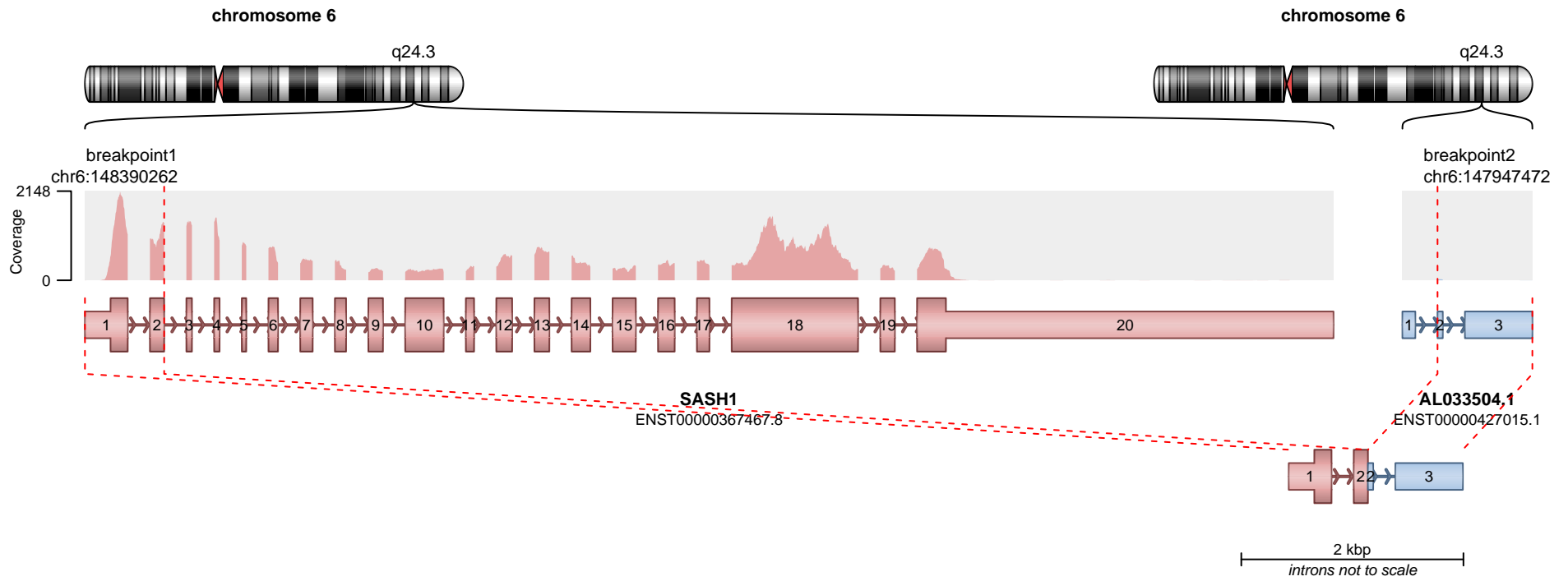
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

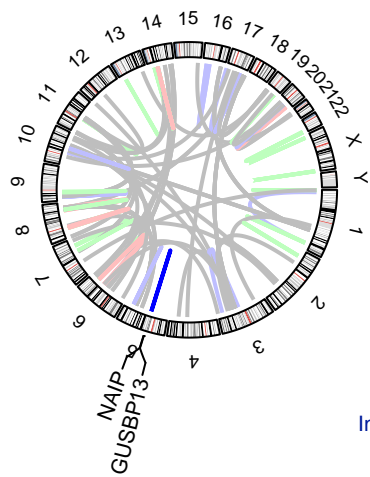
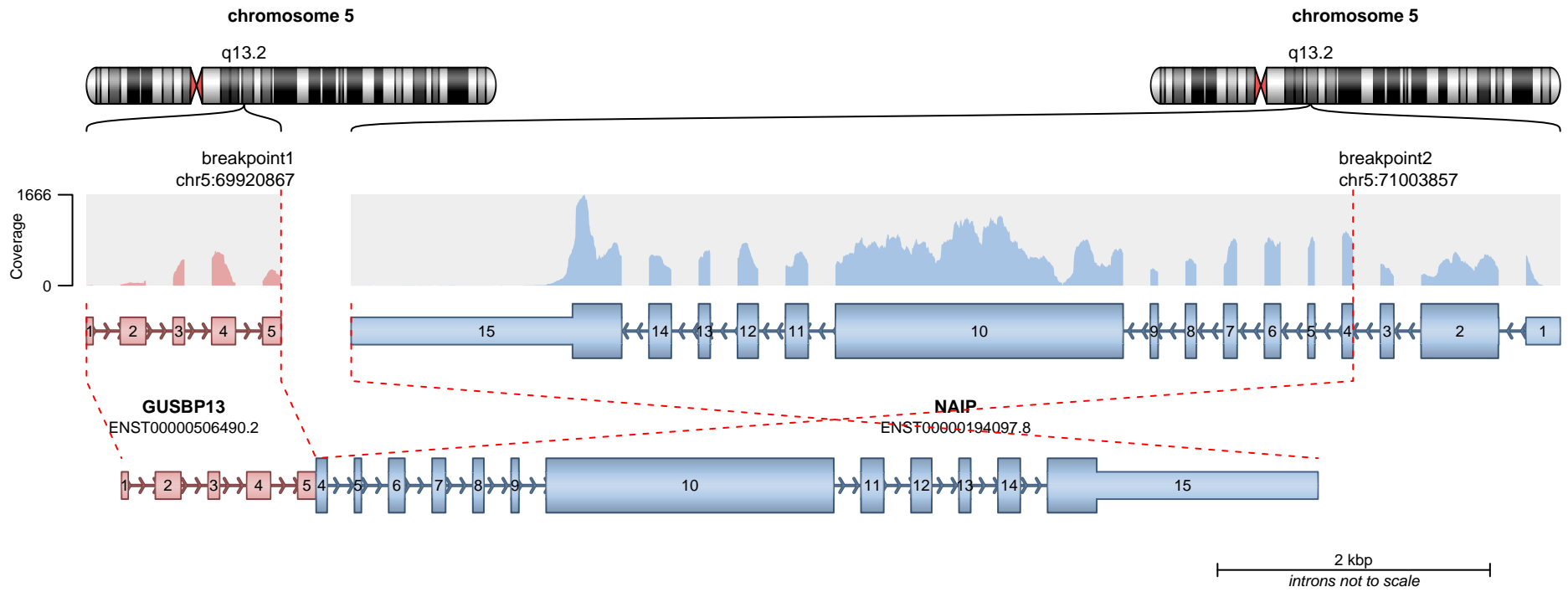


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

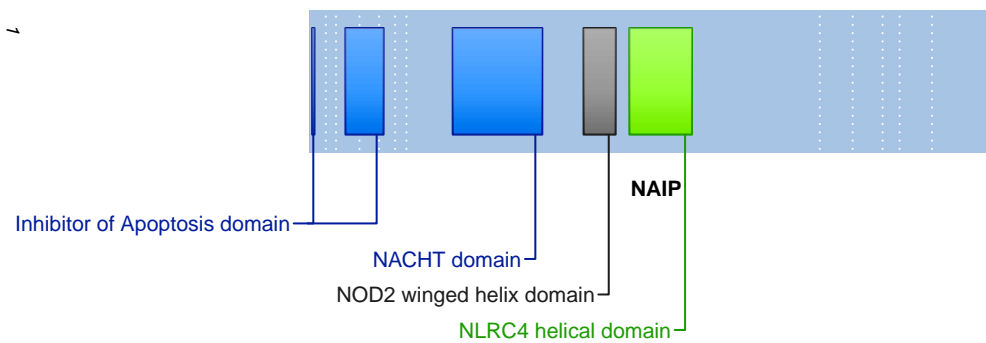
SUPPORTING READ COUNT

Split reads = 21
Discordant mates = 0



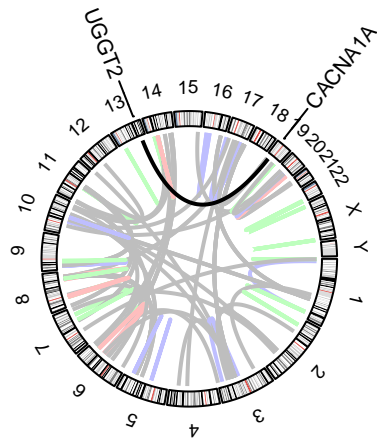
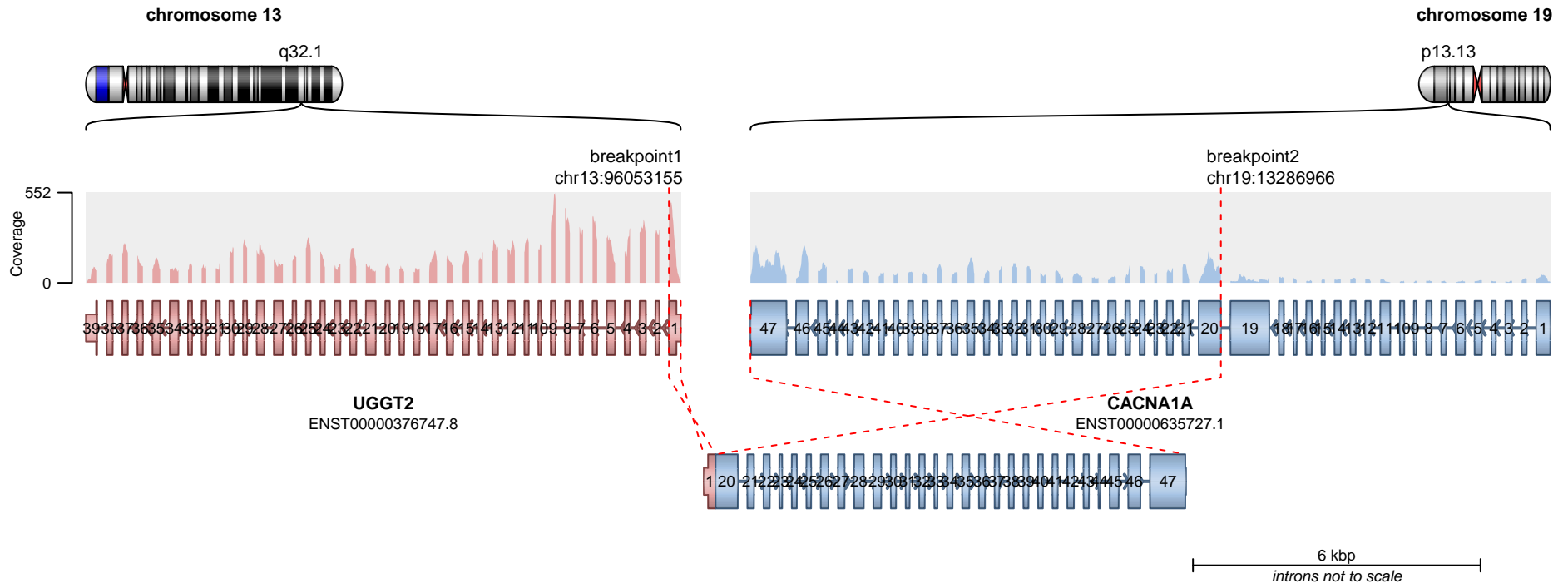
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear

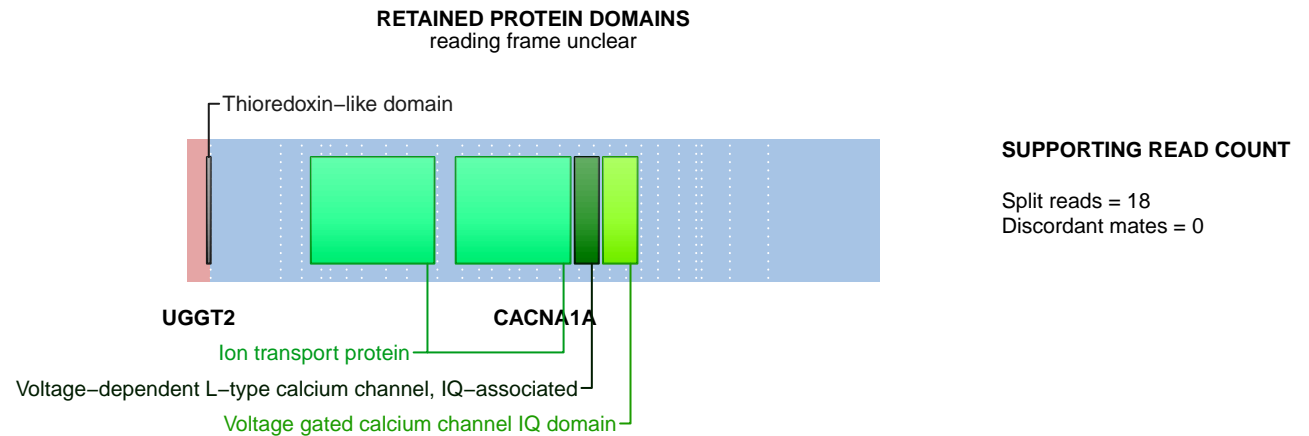


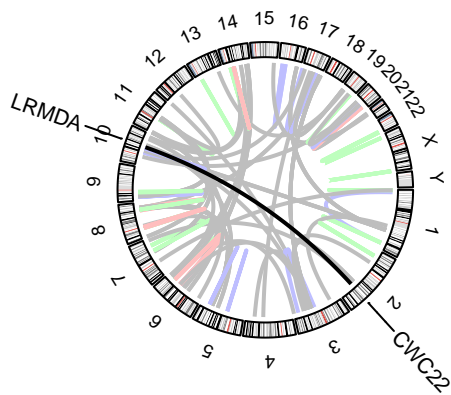
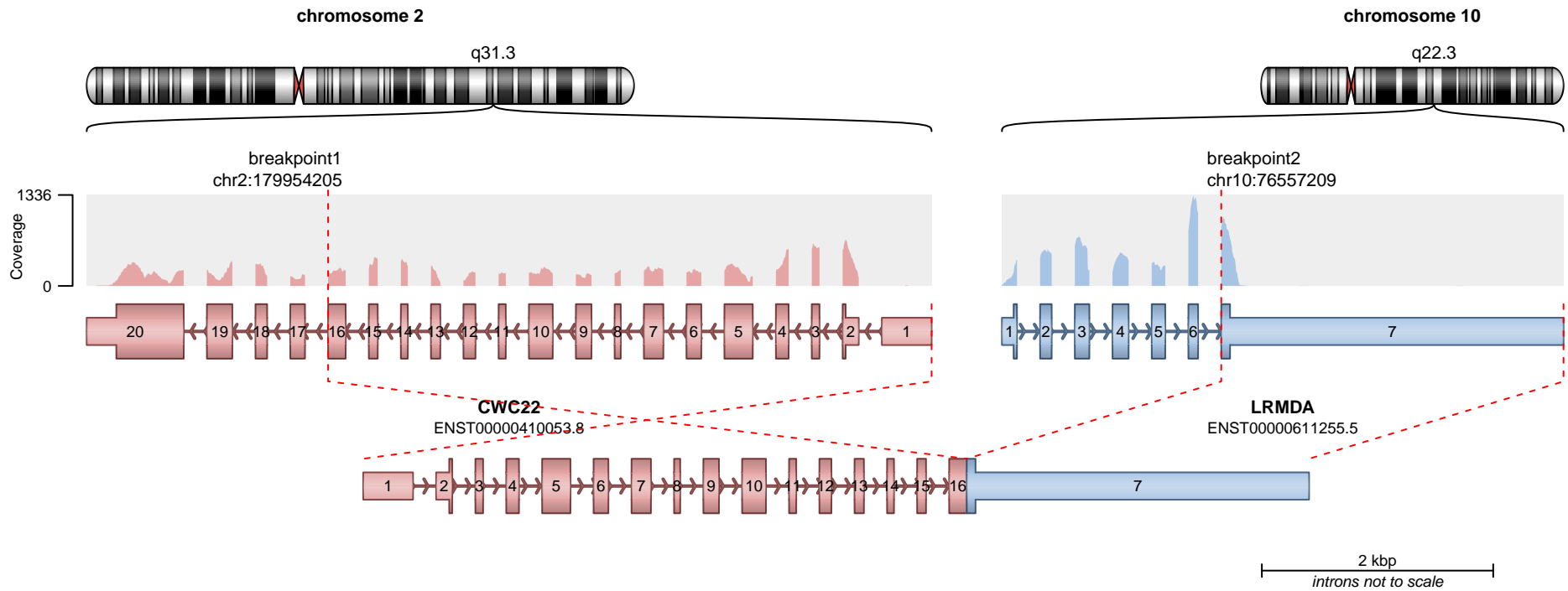
SUPPORTING READ COUNT

Split reads = 18
Discordant mates = 0

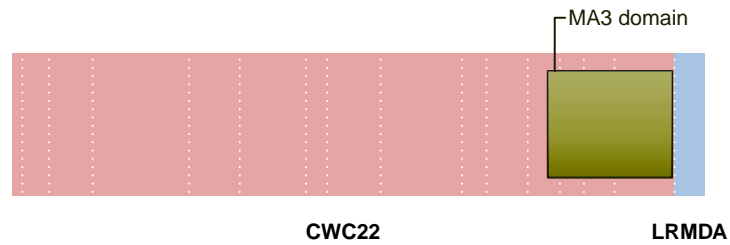


— translocation — deletion
— duplication — inversion





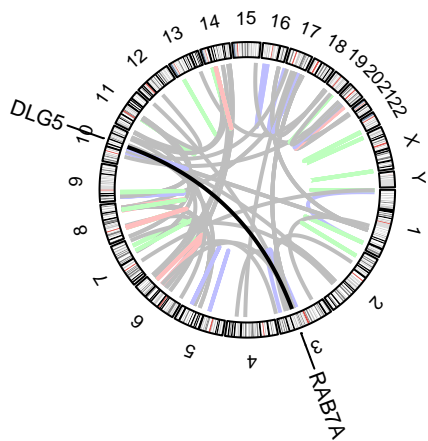
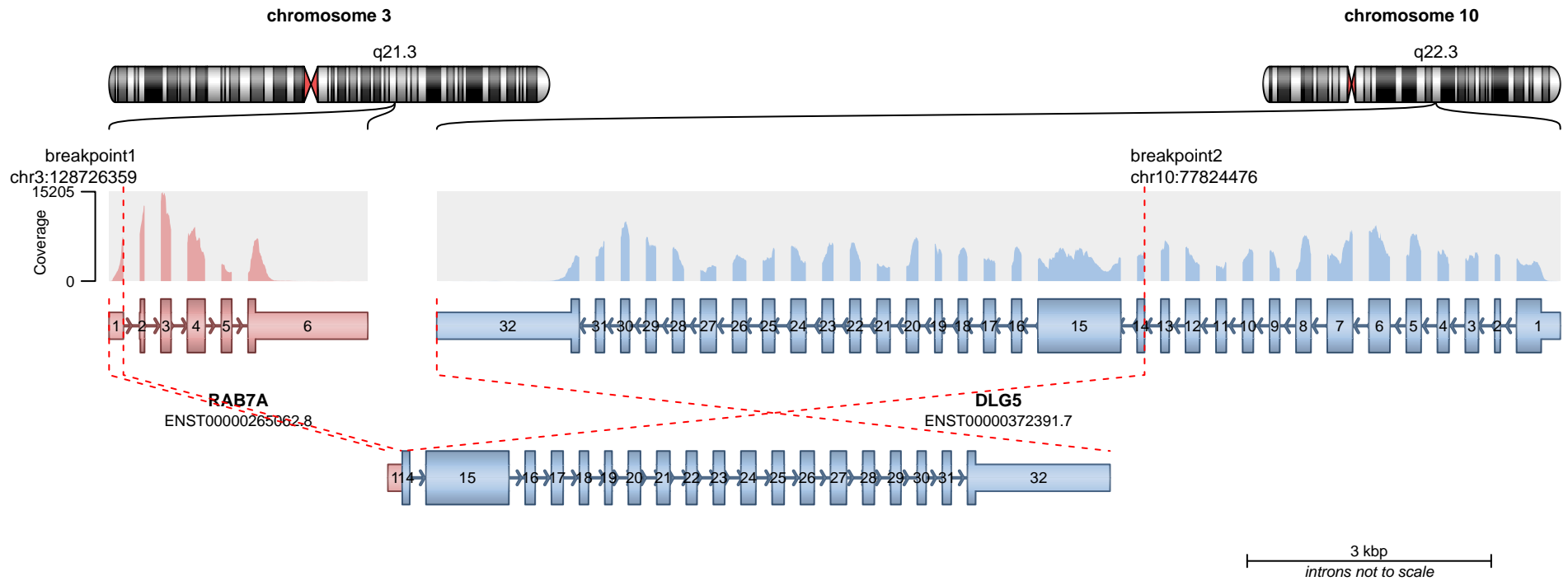
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

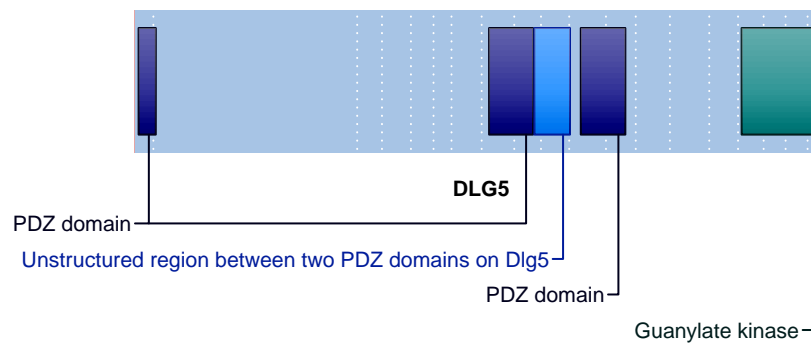
Split reads = 16
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



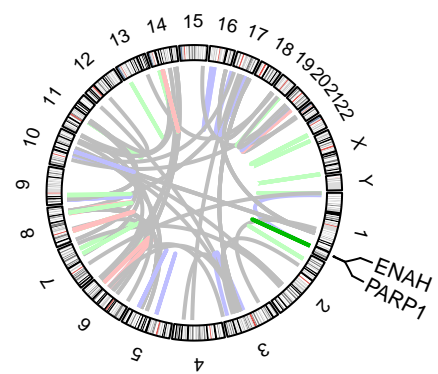
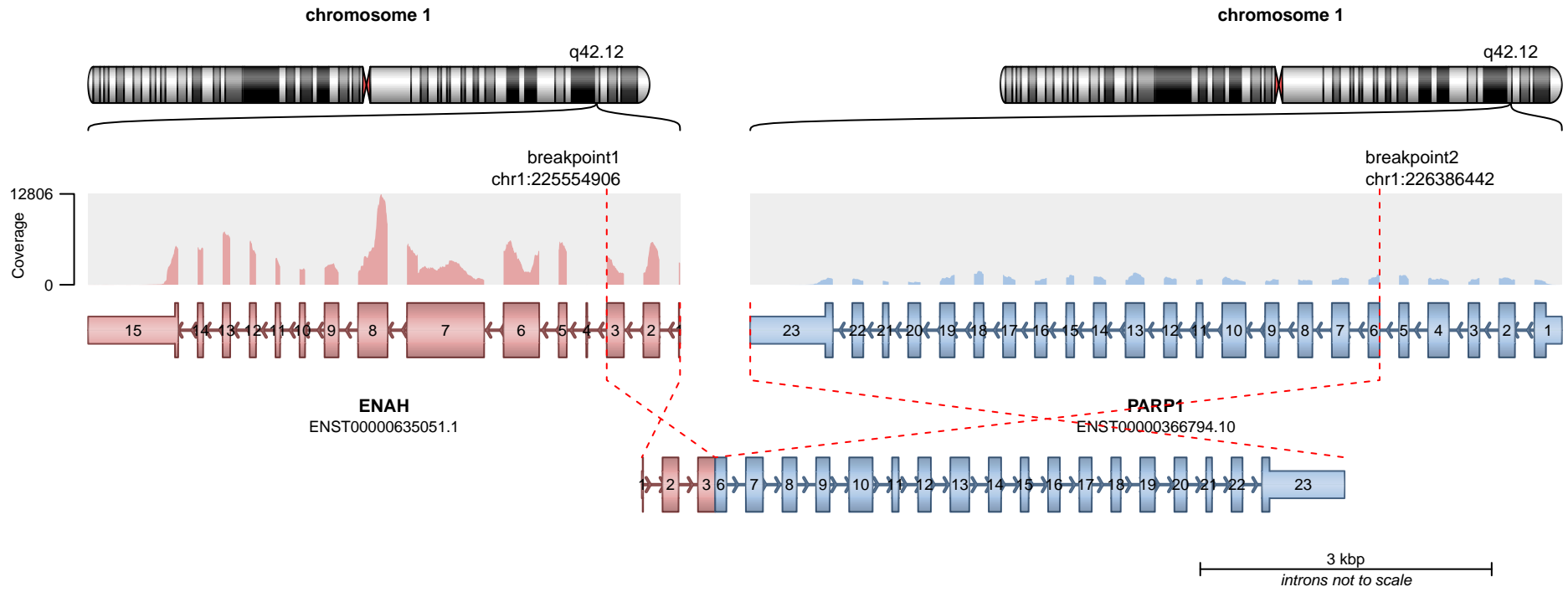
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



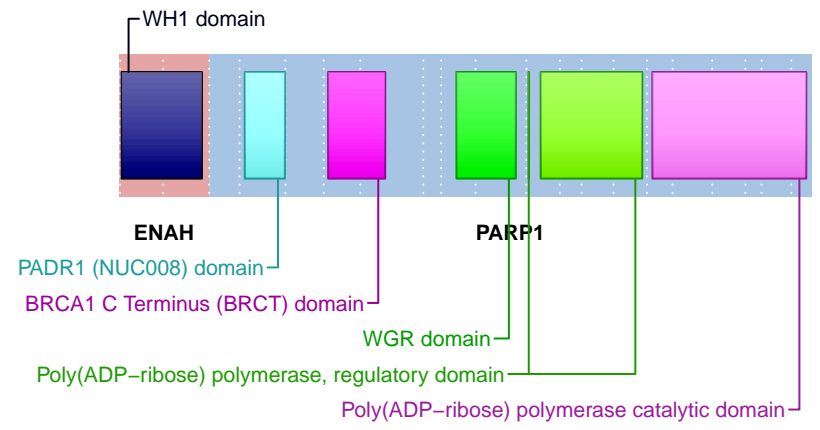
SUPPORTING READ COUNT

Split reads = 16
Discordant mates = 0



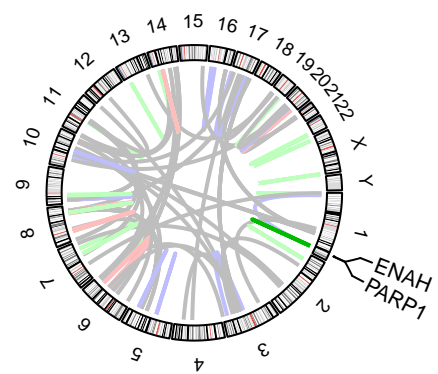
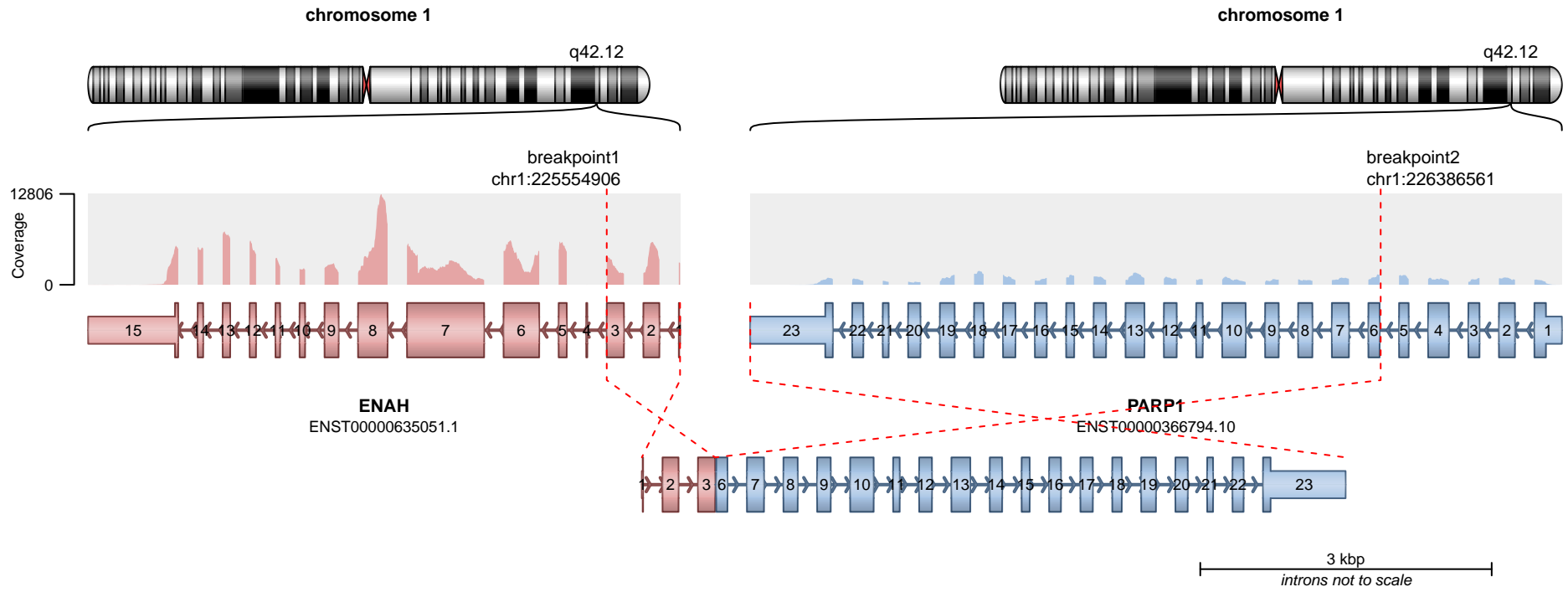
- translocation
- duplication
- deletion
- inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



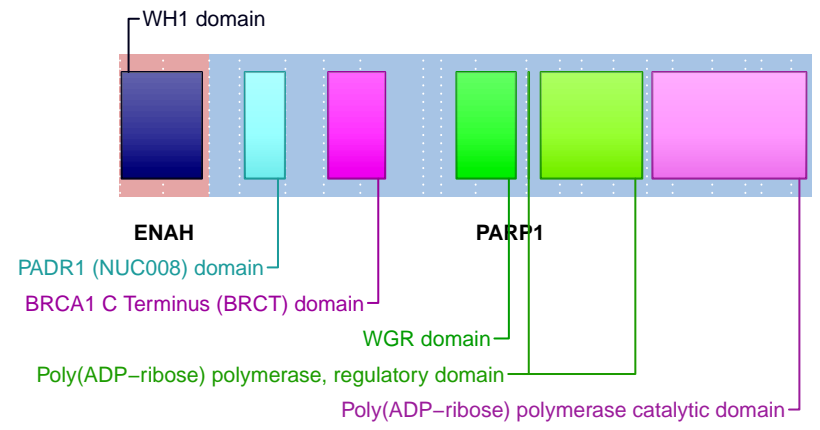
SUPPORTING READ COUNT

Split reads = 14
Discordant mates = 0



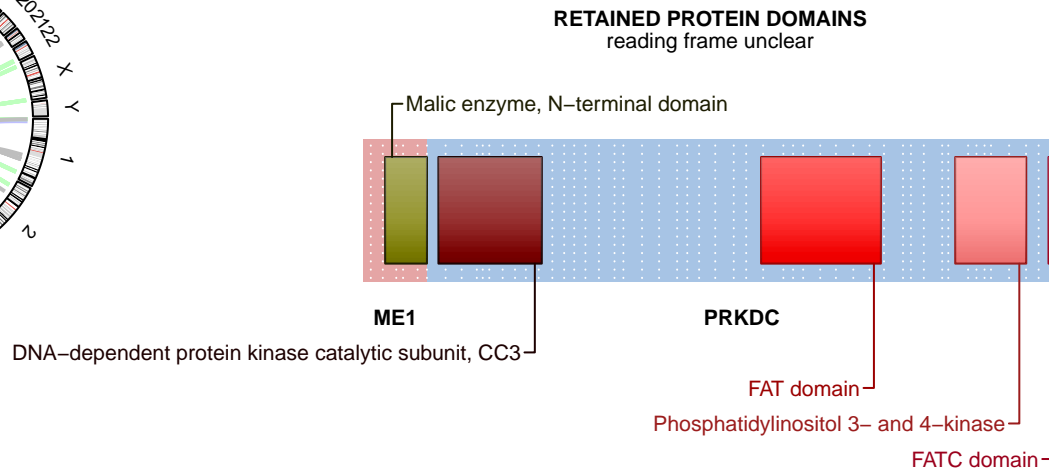
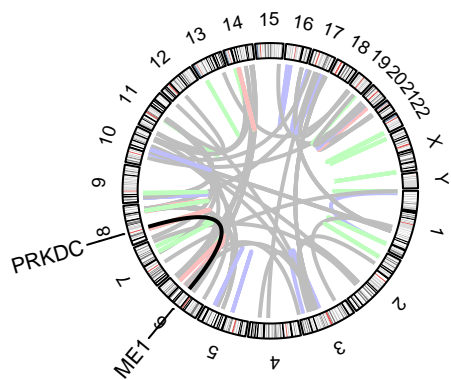
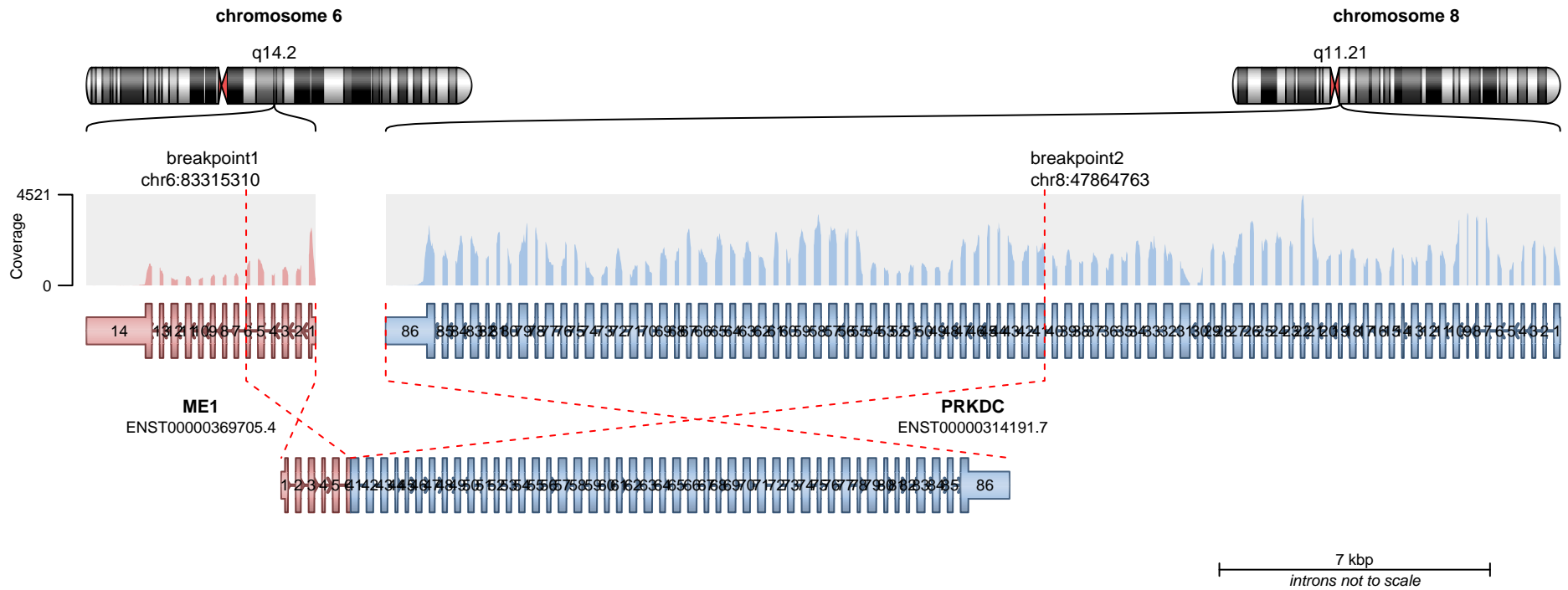
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

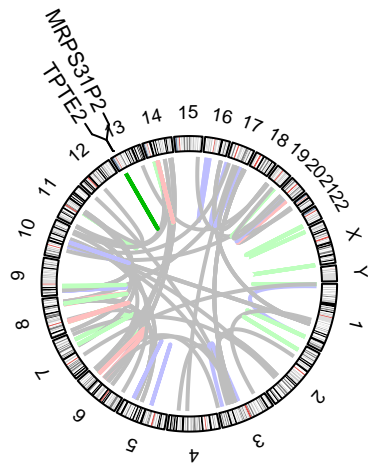
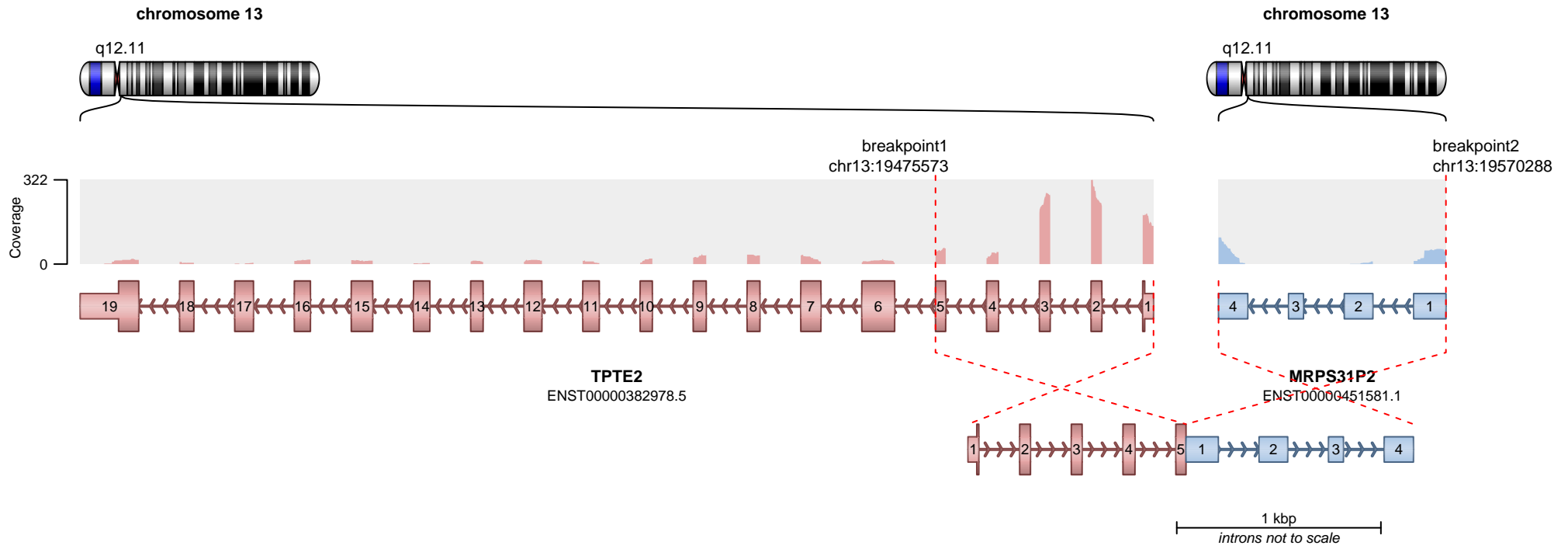
Split reads = 4
Discordant mates = 0



SUPPORTING READ COUNT

Split reads = 13
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

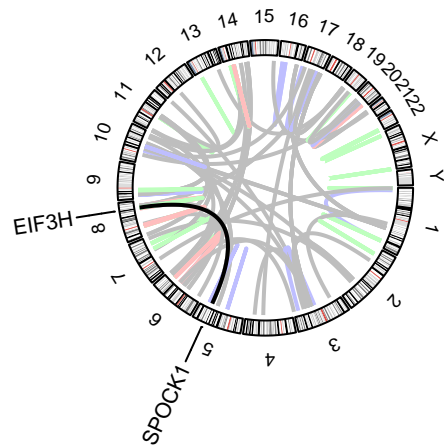
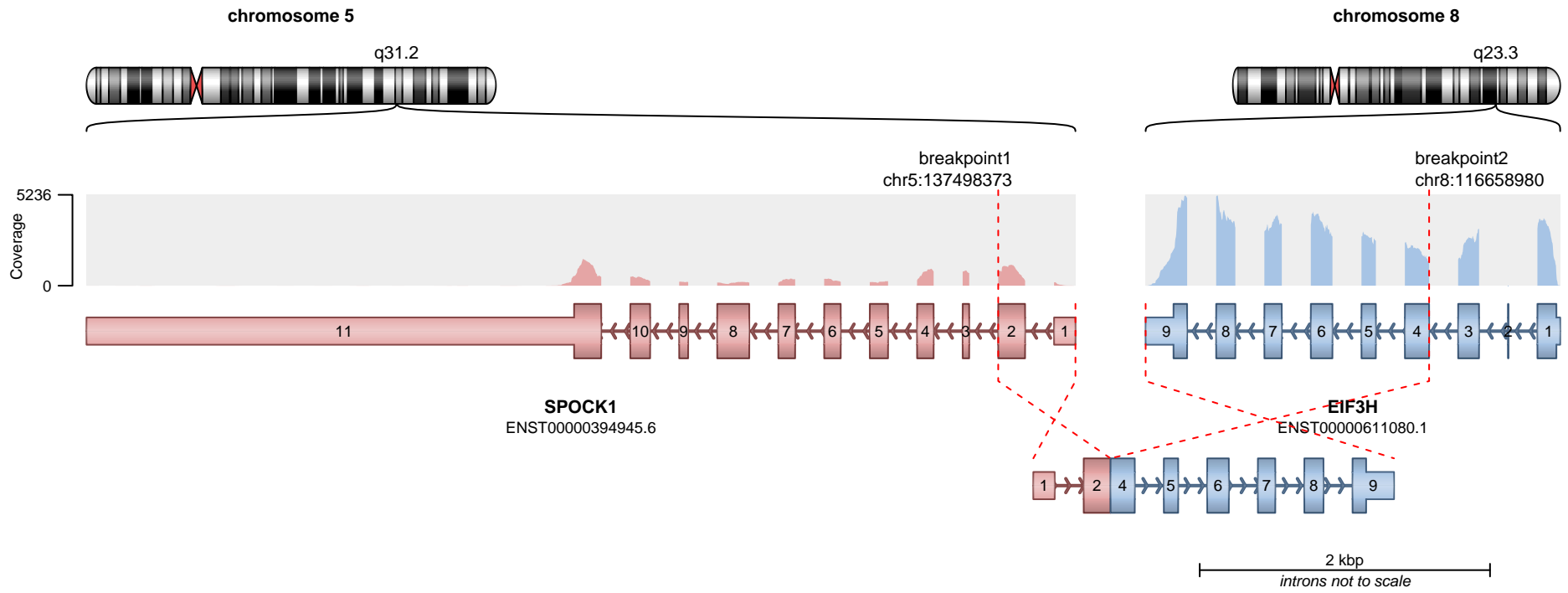


— translocation — deletion
— duplication — inversion

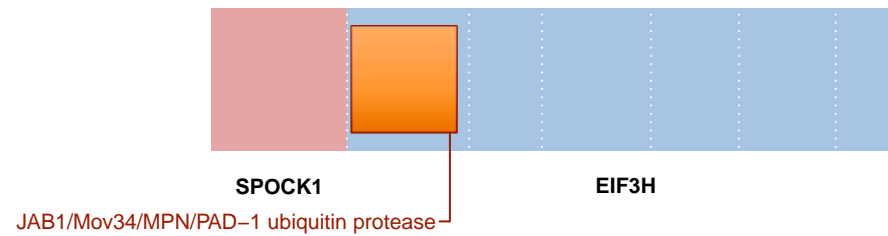
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 11
Discordant mates = 0



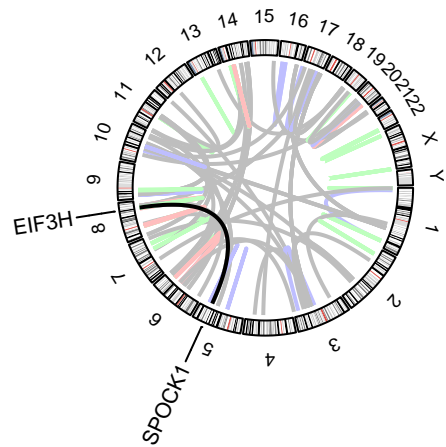
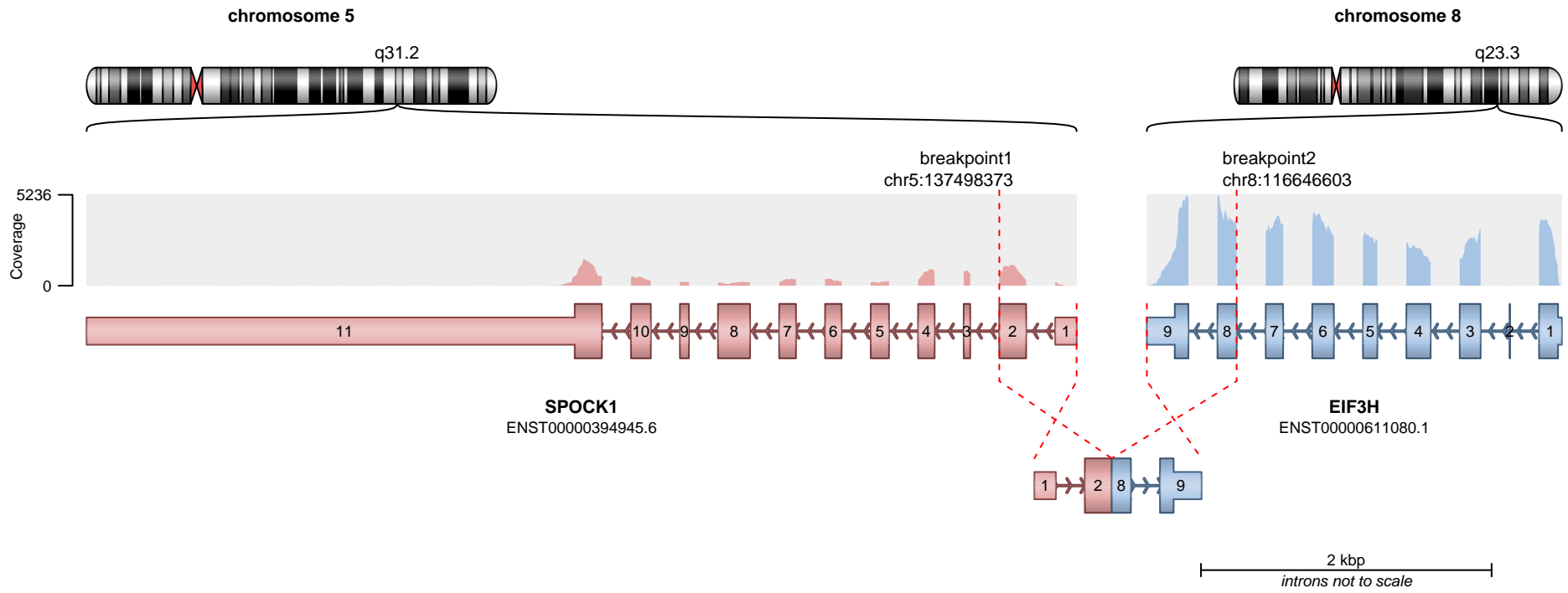
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

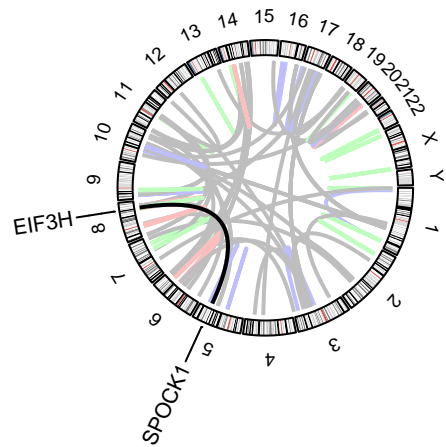
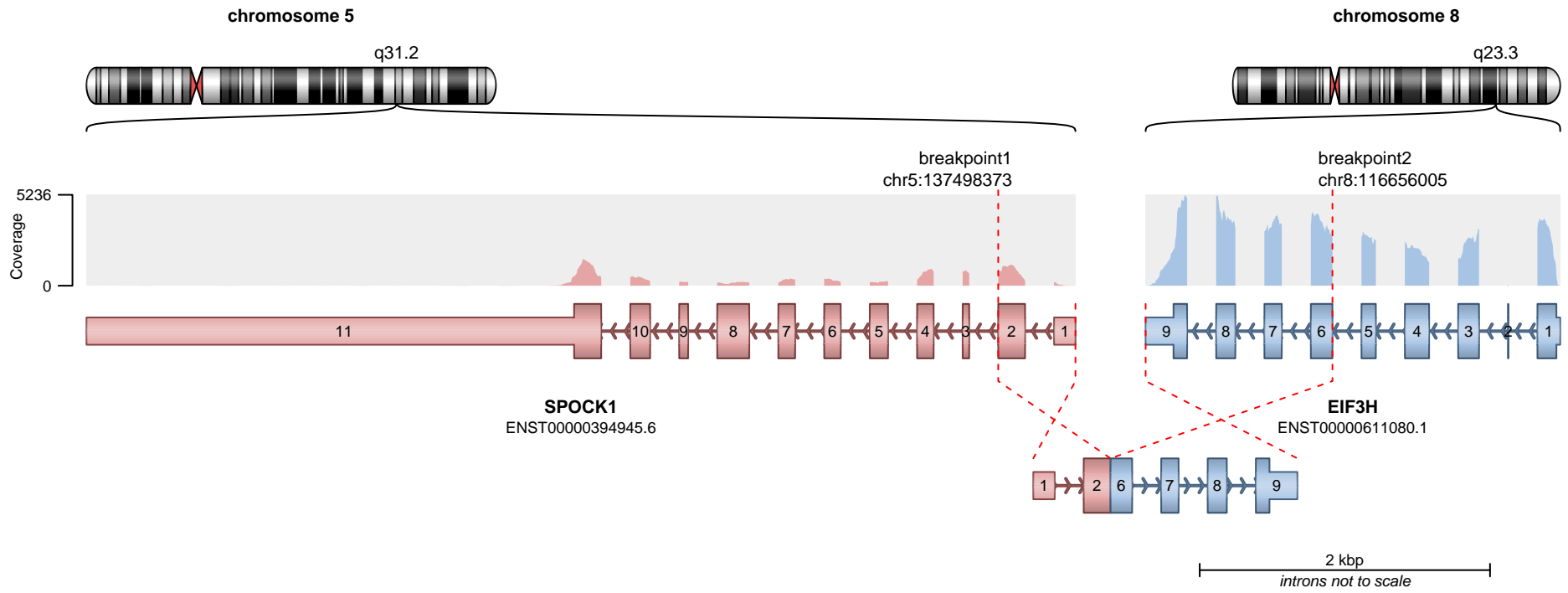


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 0

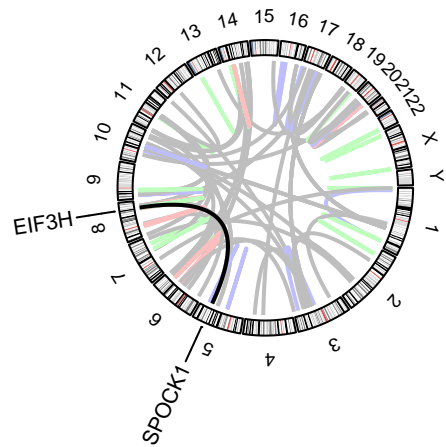
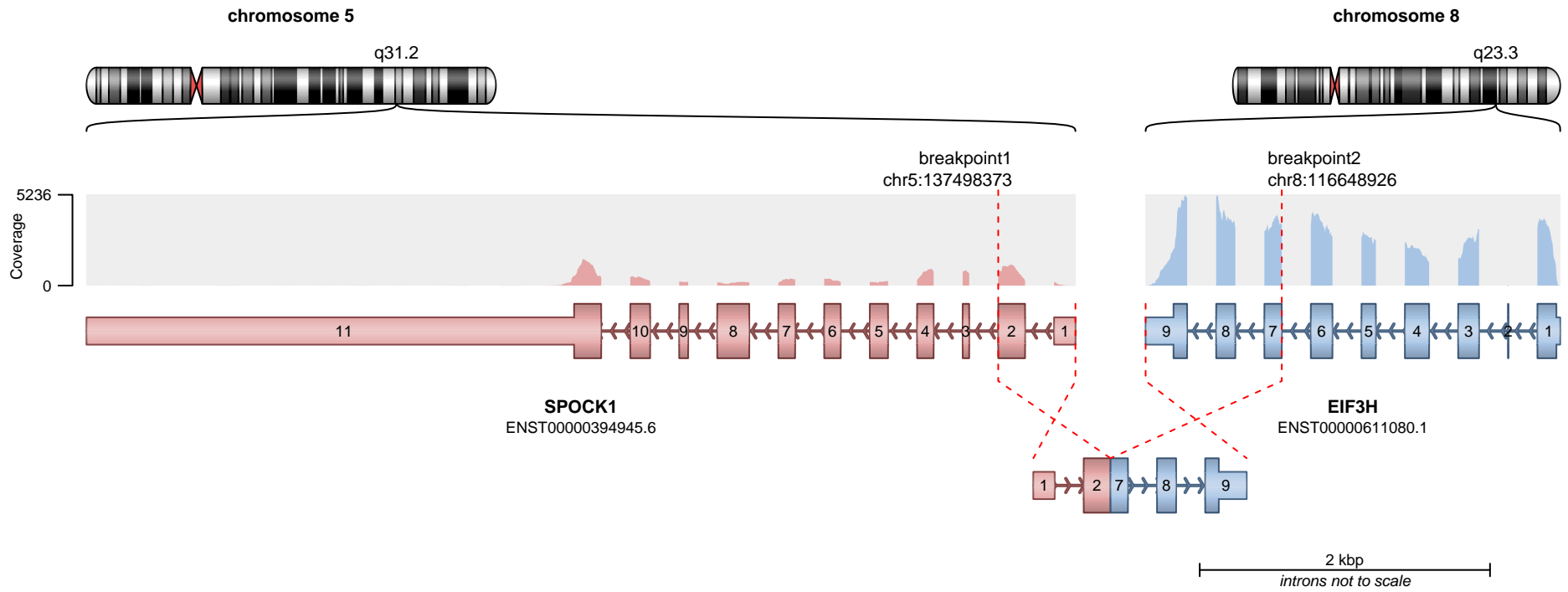


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

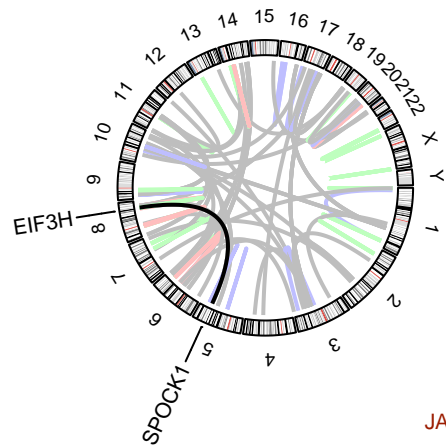
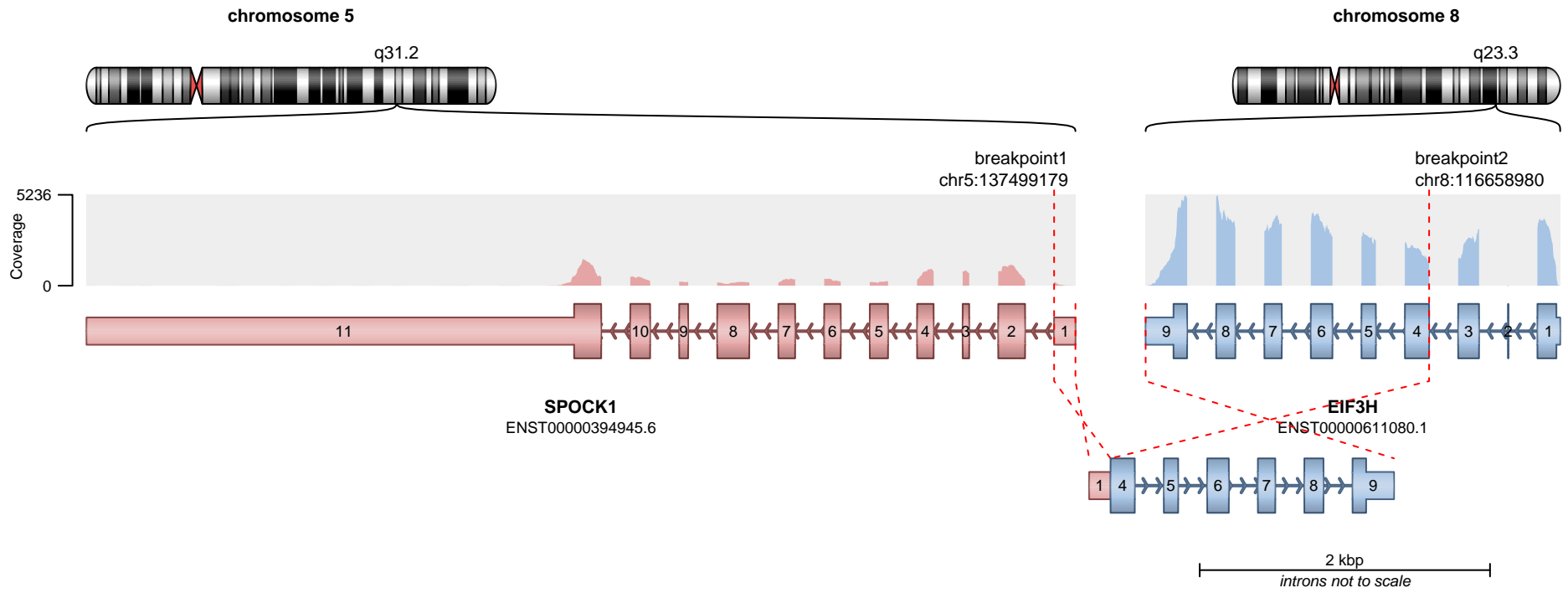


— translocation — deletion
— duplication — inversion

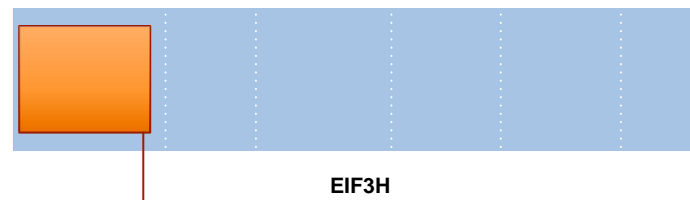
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



RETAINED PROTEIN DOMAINS
reading frame unclear

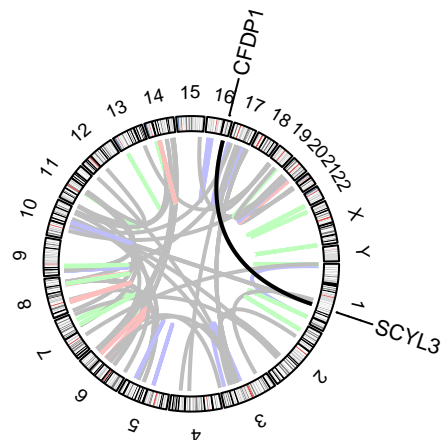
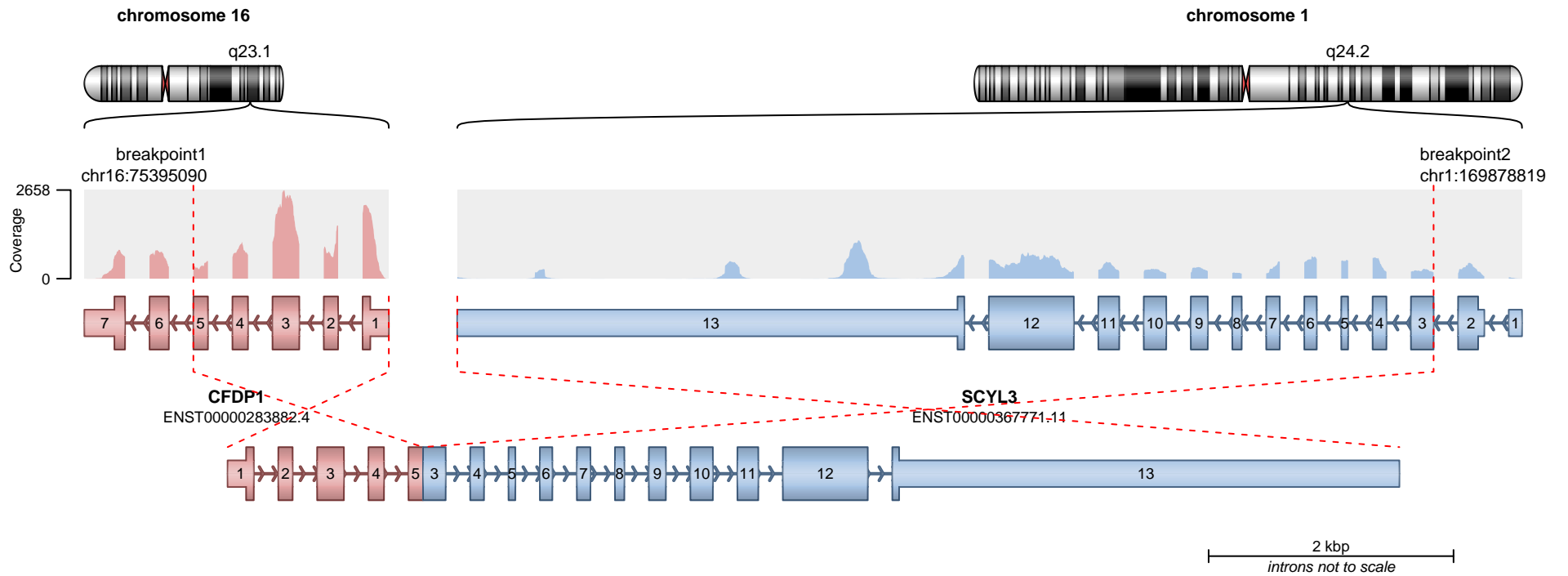


JAB1/Mov34/MPN/PAD-1 ubiquitin protease

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion

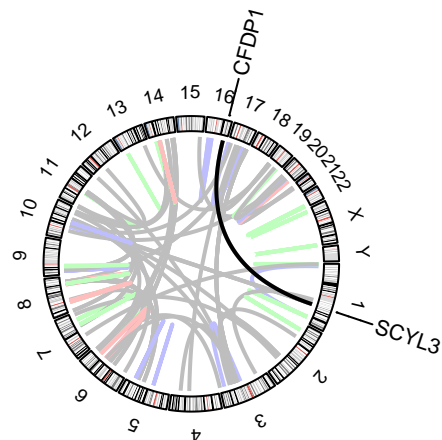
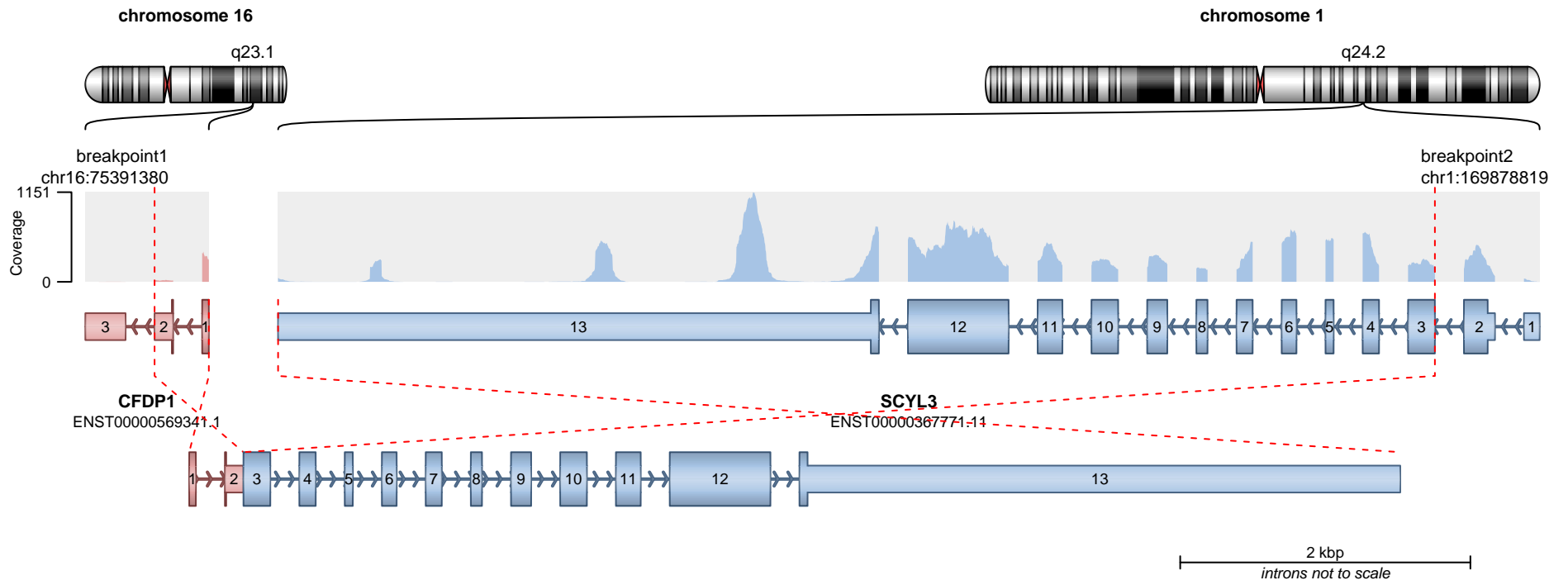


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 9
Discordant mates = 0

— translocation — deletion
— duplication — inversion

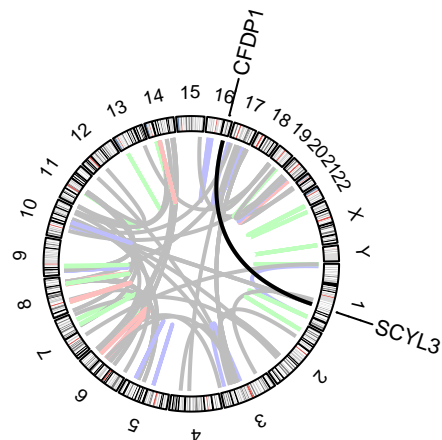
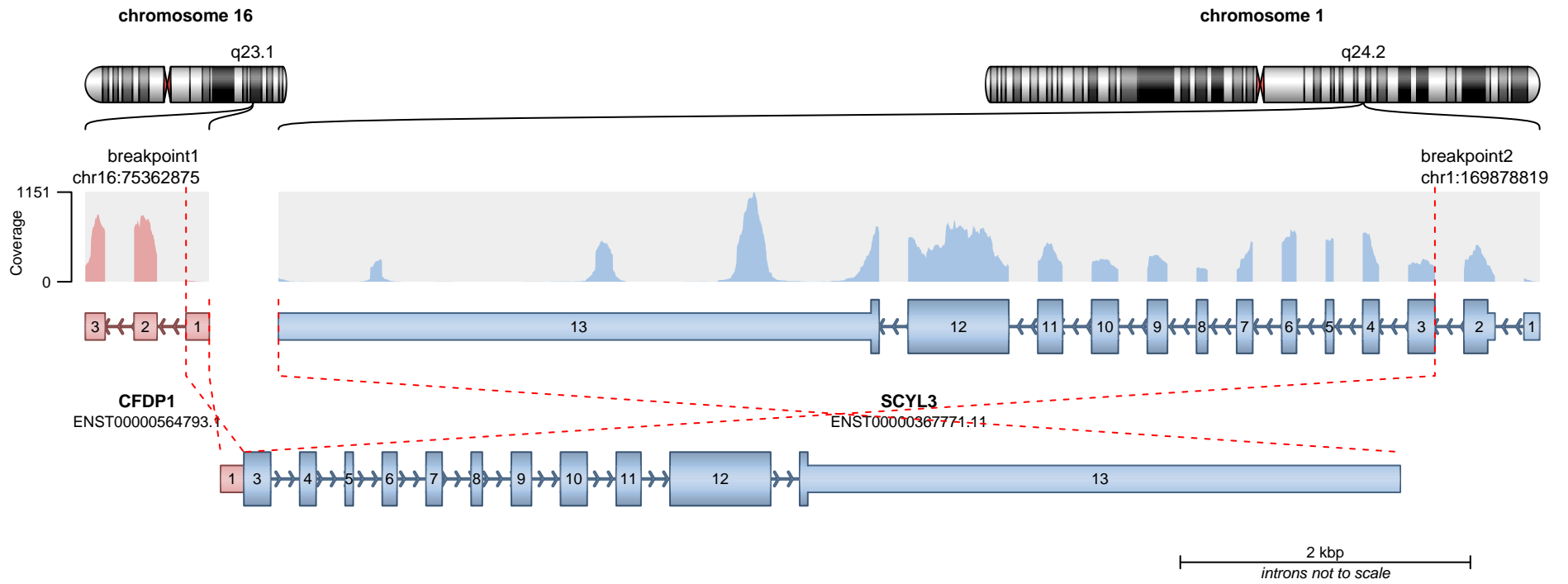


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 0

— translocation — deletion
— duplication — inversion

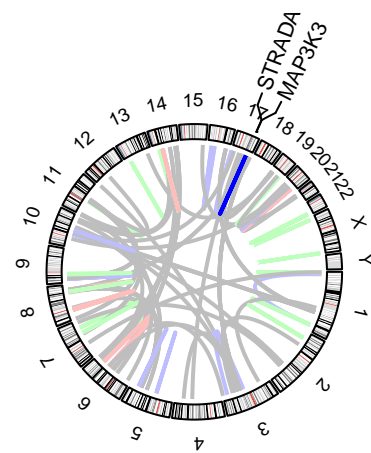
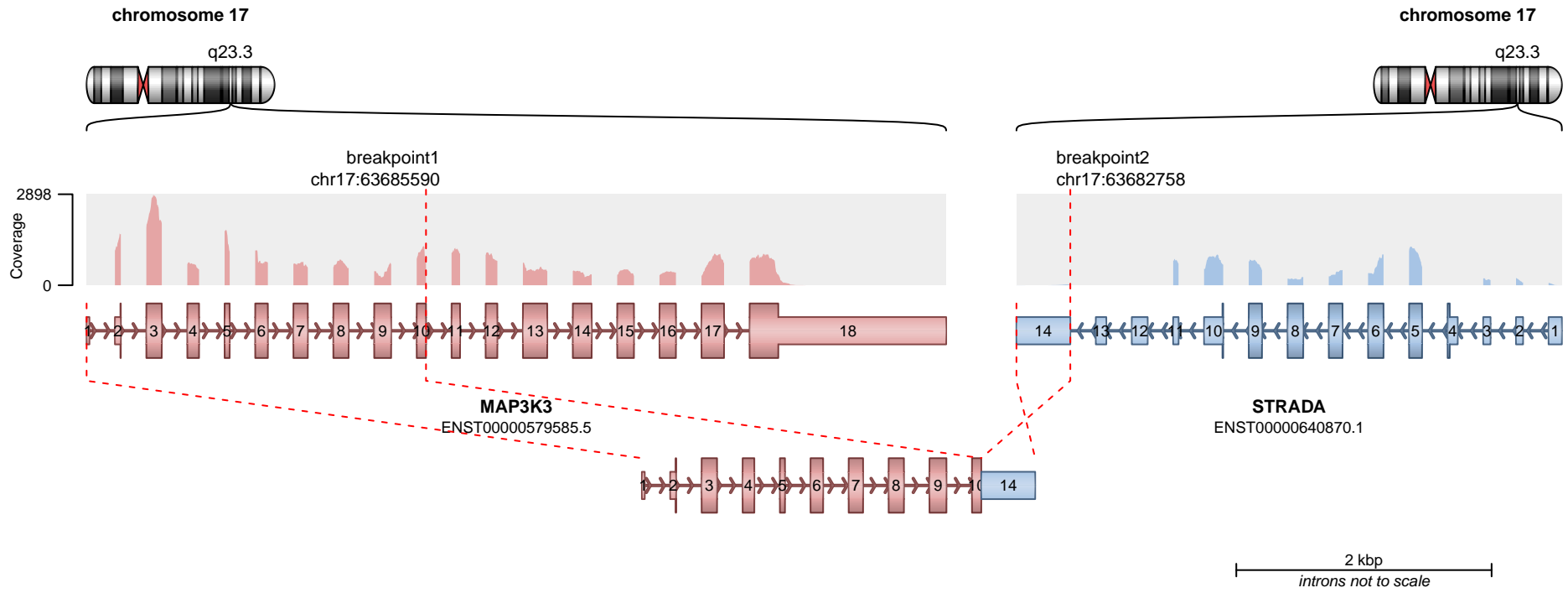


No protein domains retained in fusion.

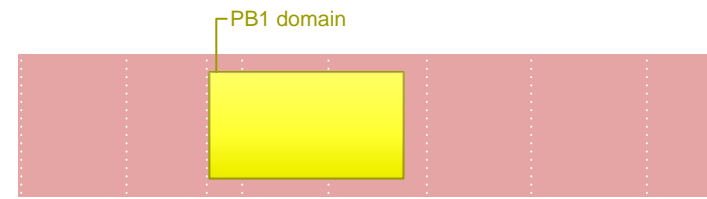
SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 0

— translocation — deletion
— duplication — inversion



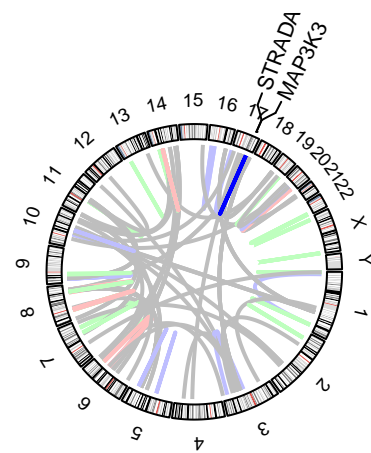
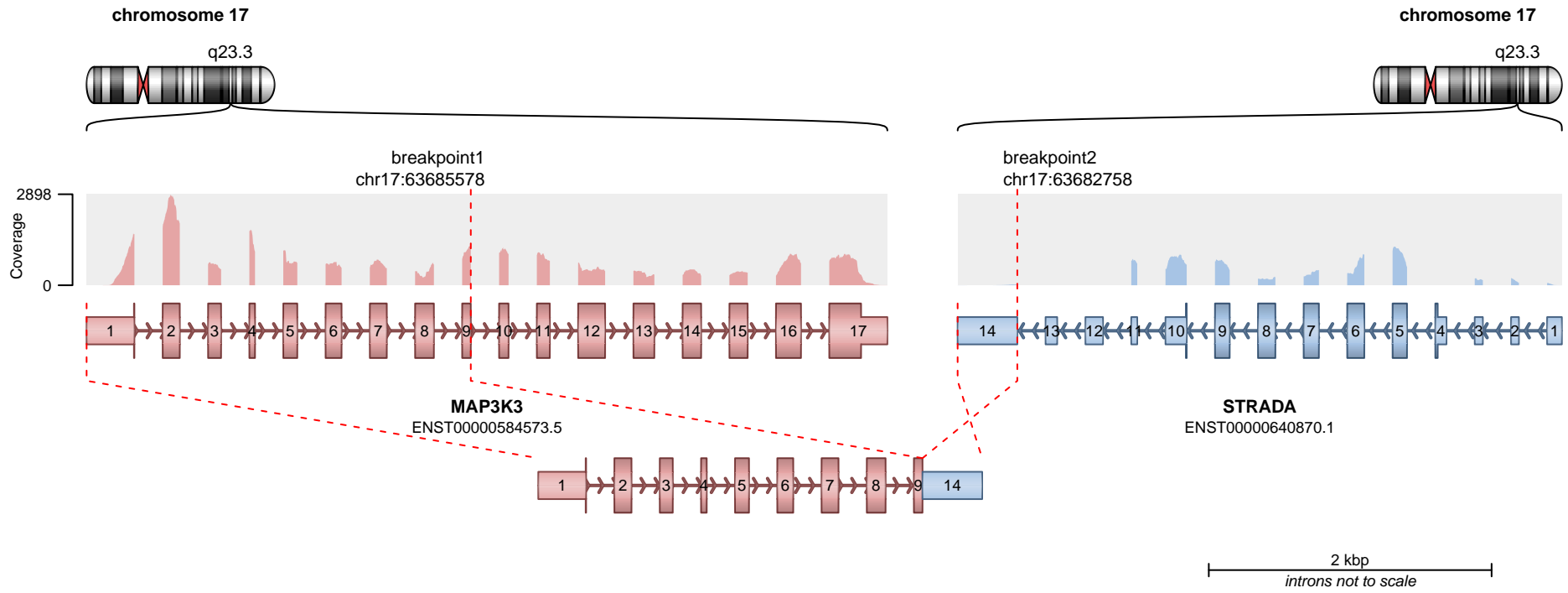
RETAINED PROTEIN DOMAINS
reading frame unclear



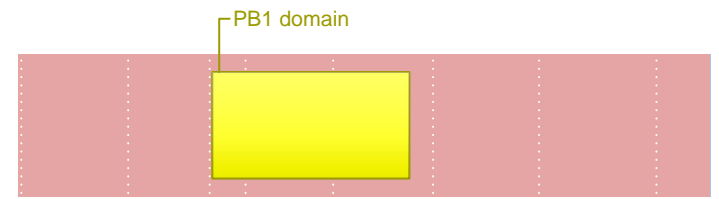
SUPPORTING READ COUNT

Split reads = 9
Discordant mates = 0

— translocation — deletion
— duplication — inversion



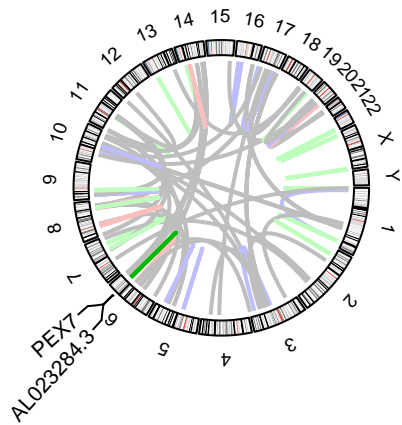
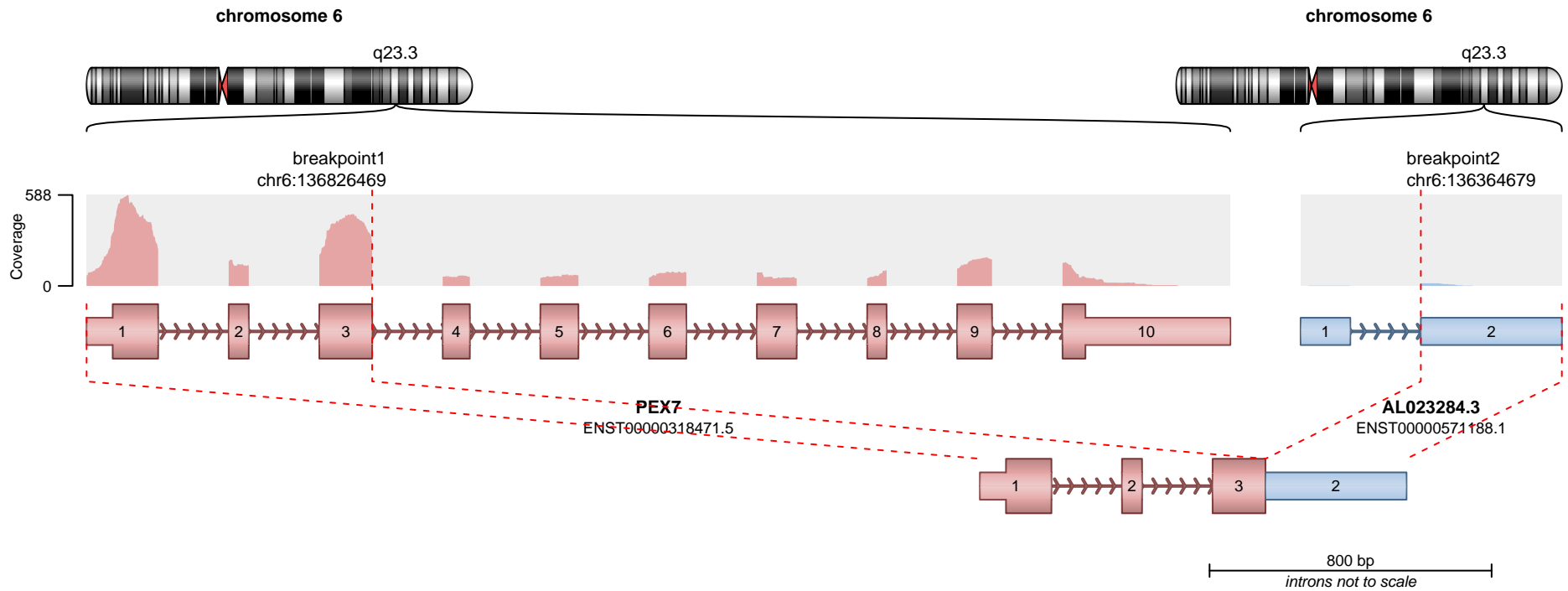
RETAINED PROTEIN DOMAINS
reading frame unclear



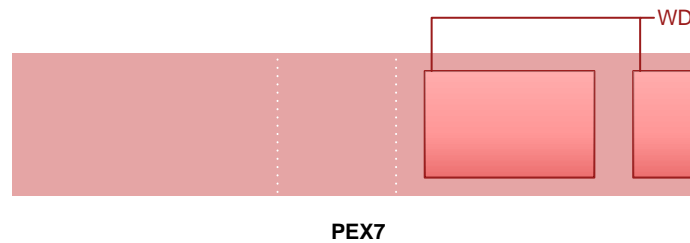
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



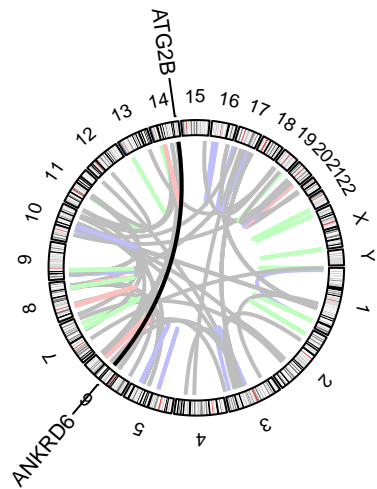
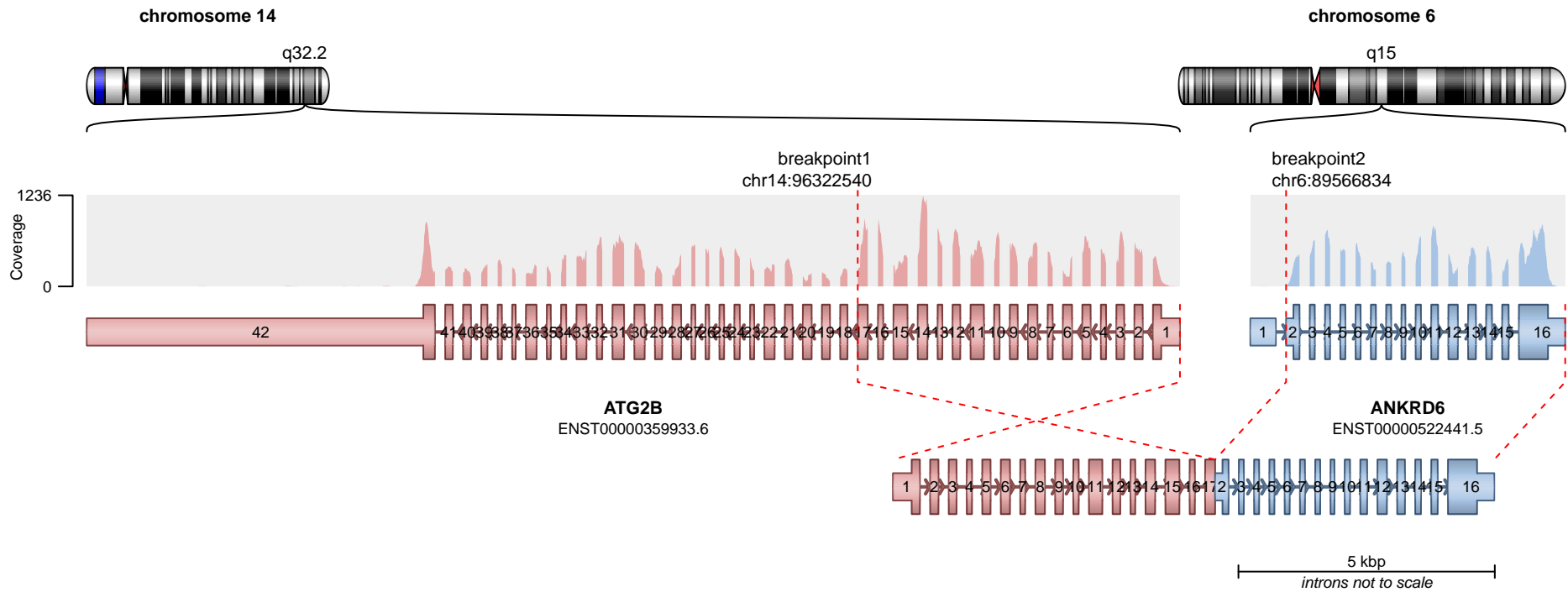
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

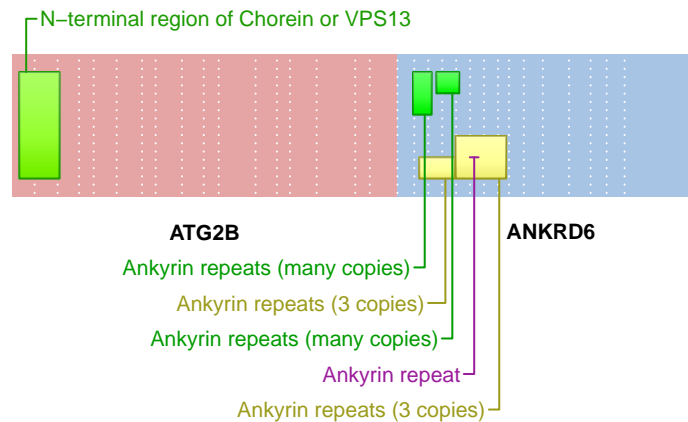
Split reads = 9
Discordant mates = 0

— translocation — deletion
— duplication — inversion



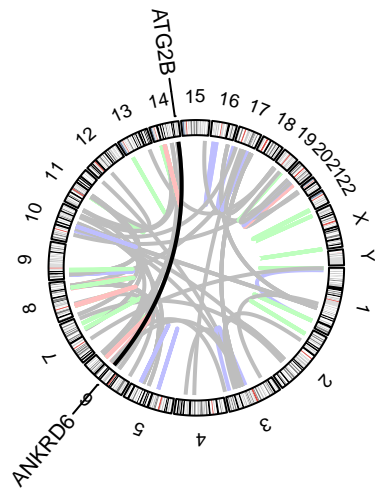
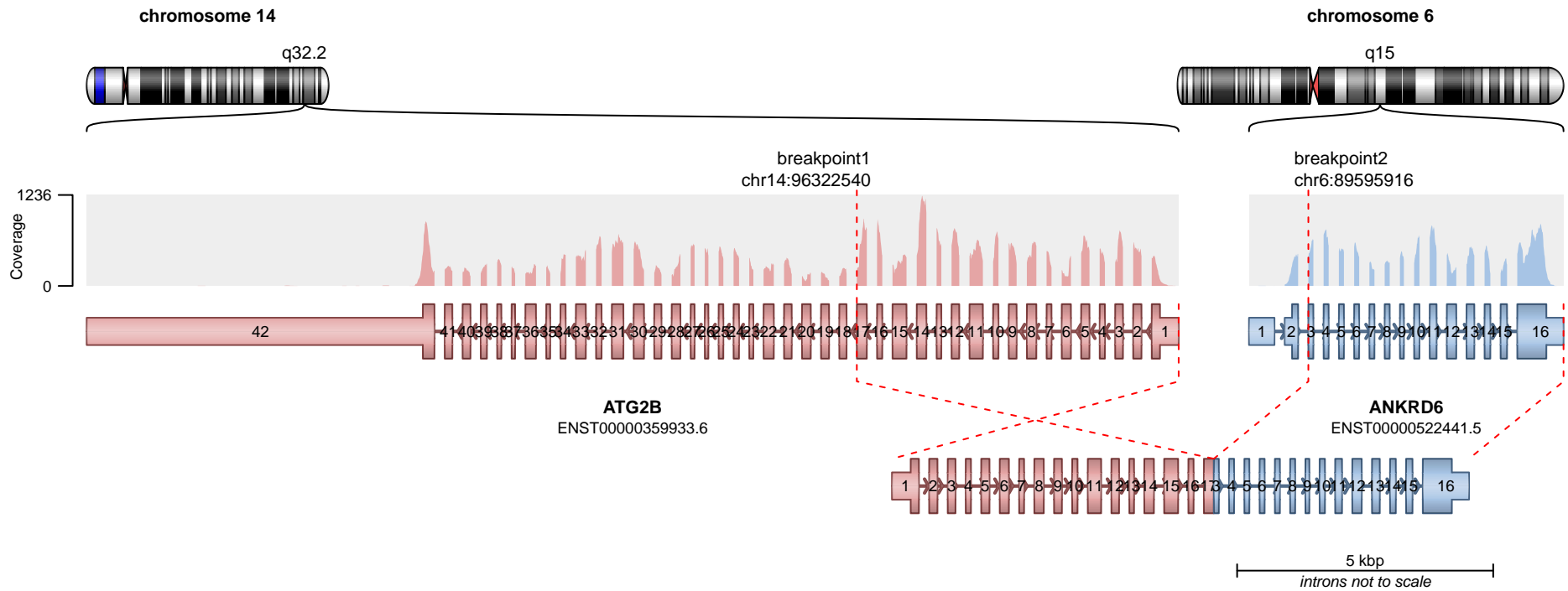
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear

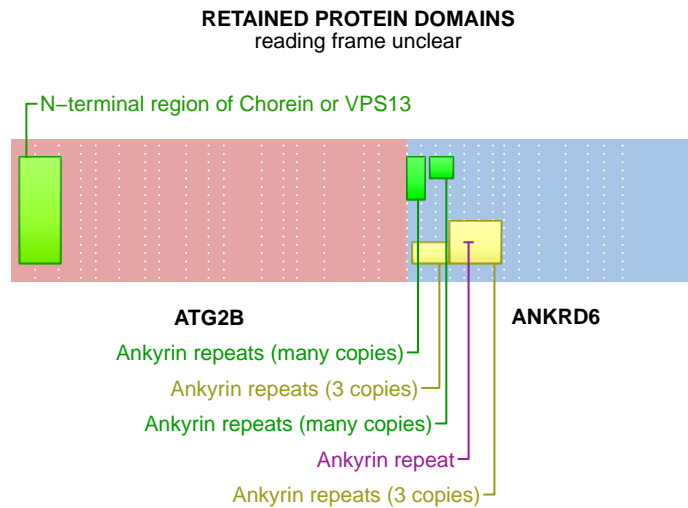


SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 1

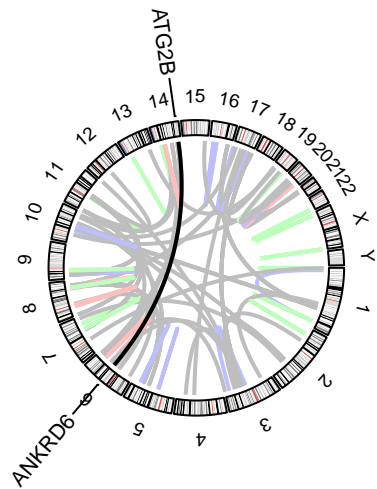
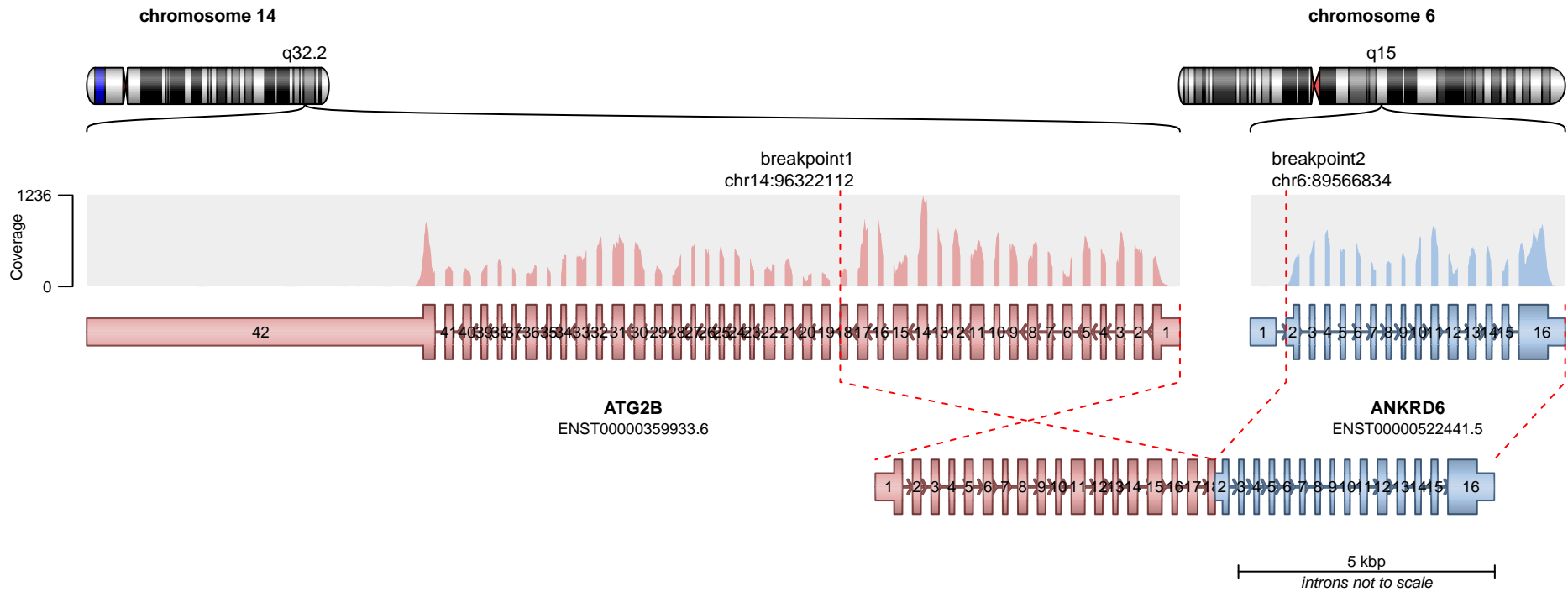


— translocation — deletion
— duplication — inversion



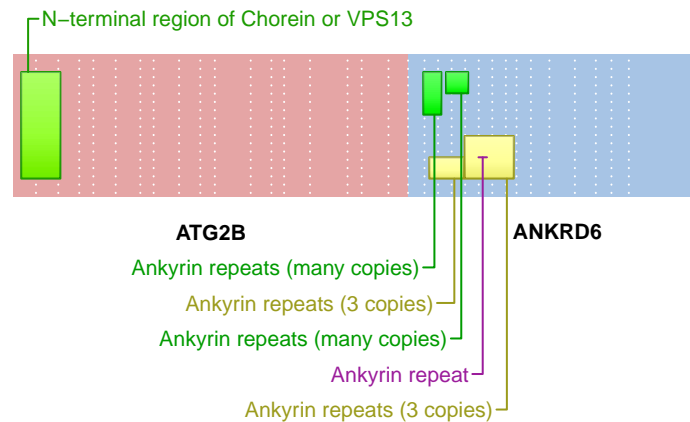
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0



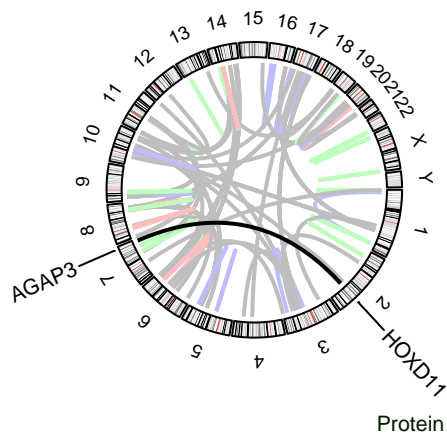
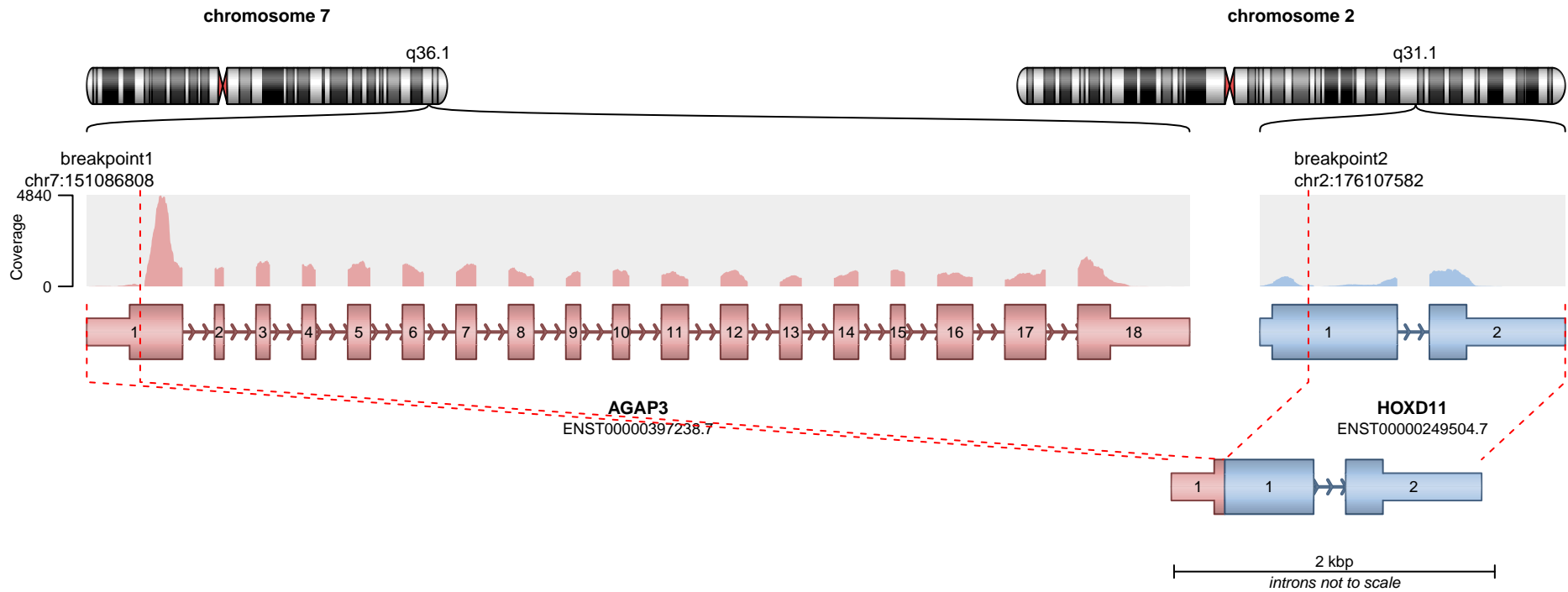
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear

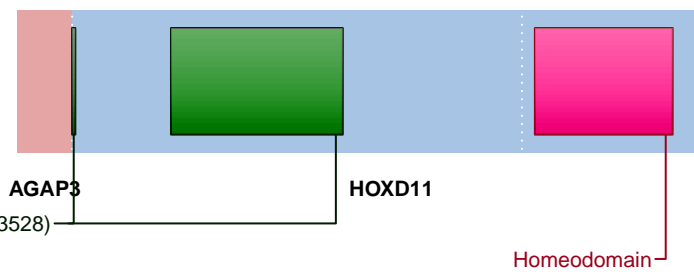


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 1



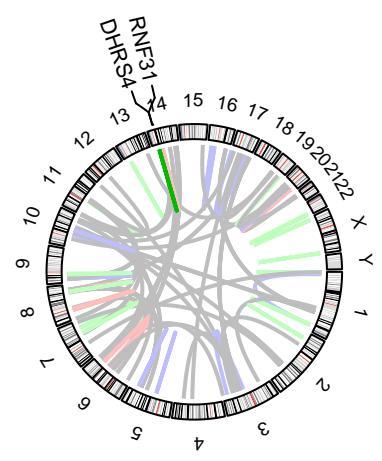
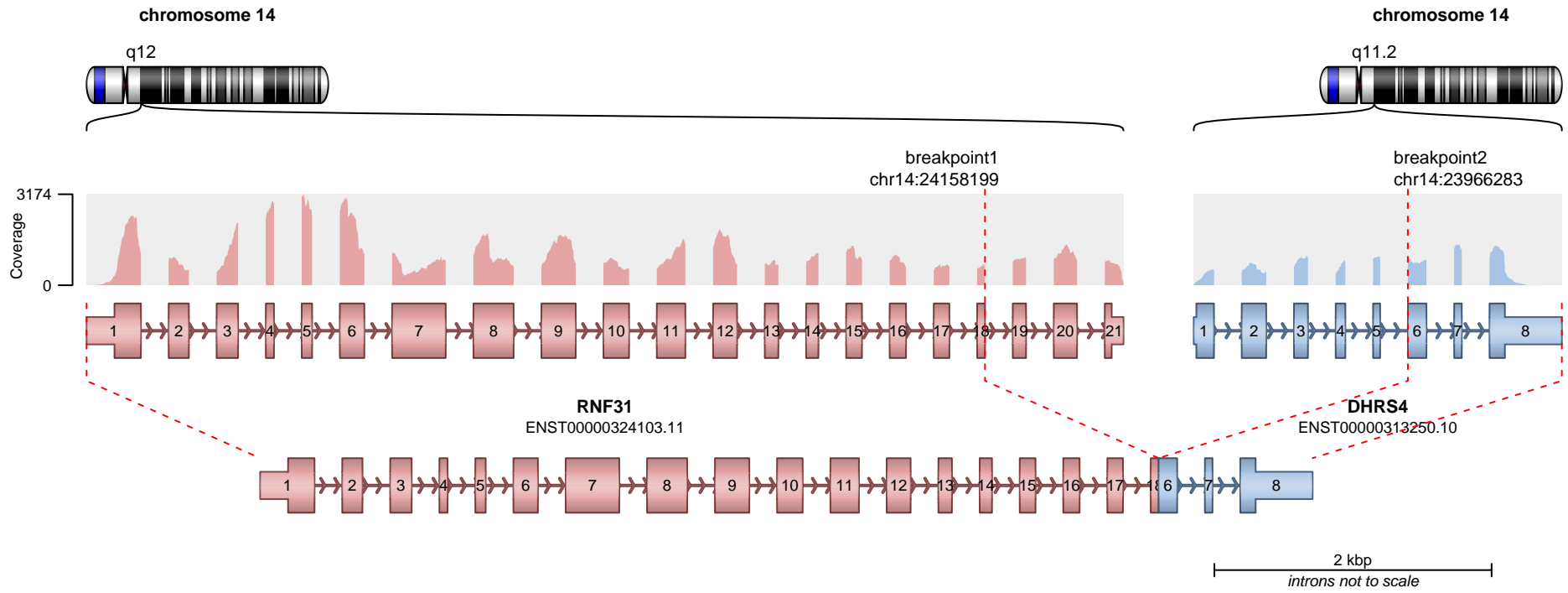
RETAINED PROTEIN DOMAINS
reading frame unclear



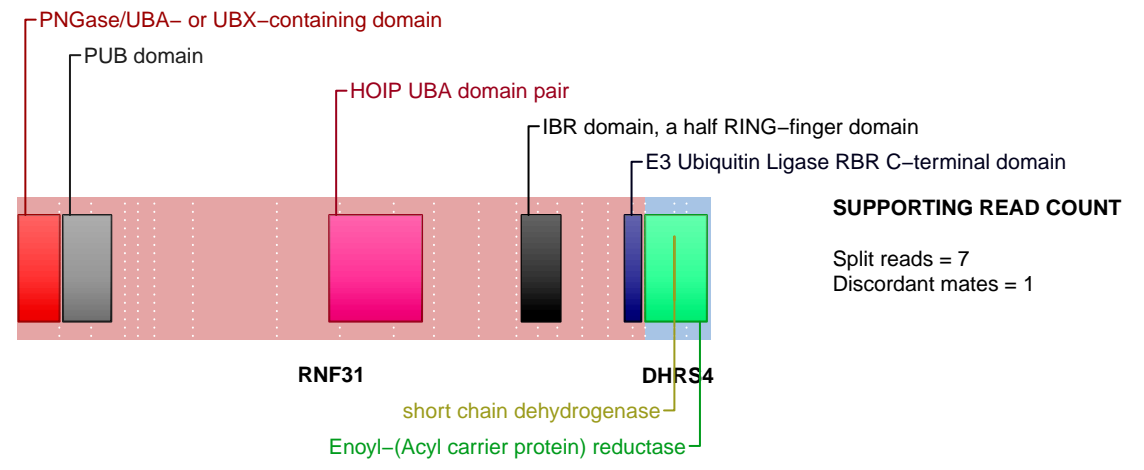
SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 0

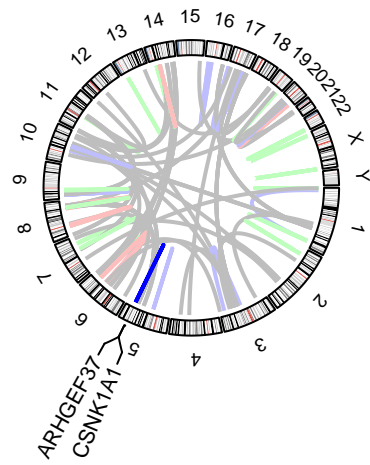
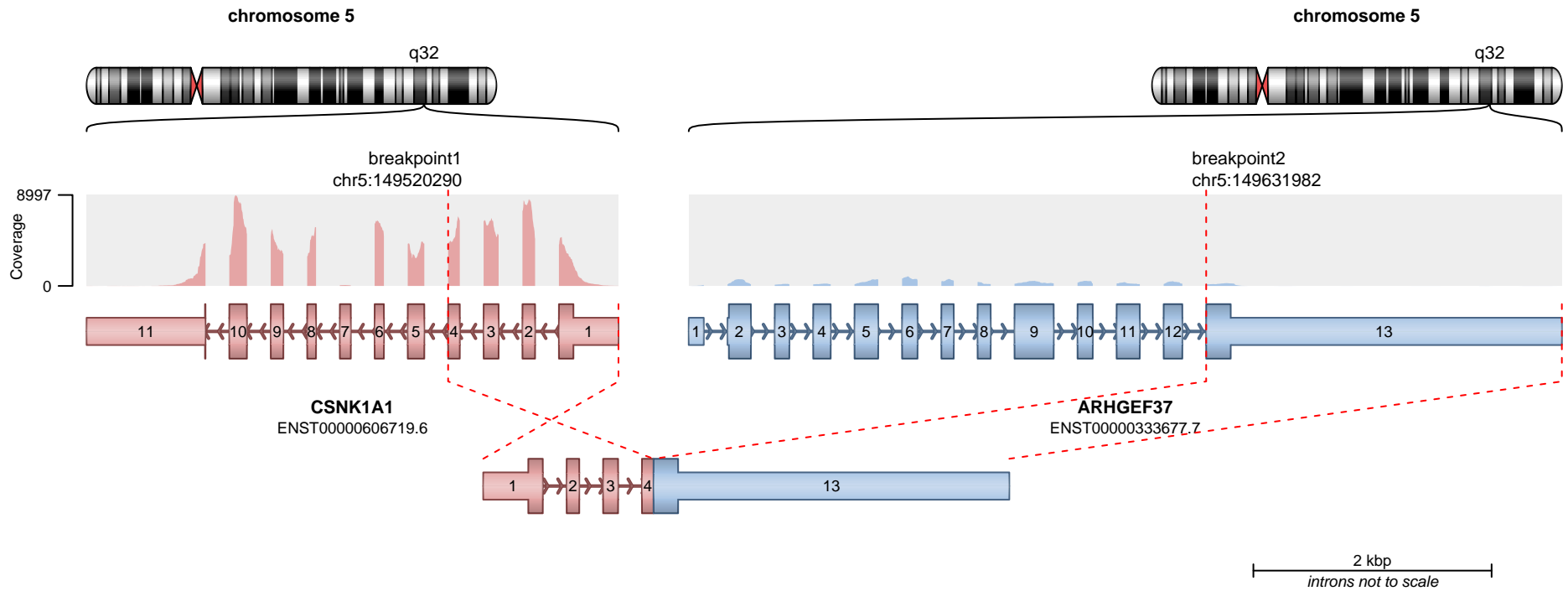
- translocation
- duplication
- deletion
- inversion



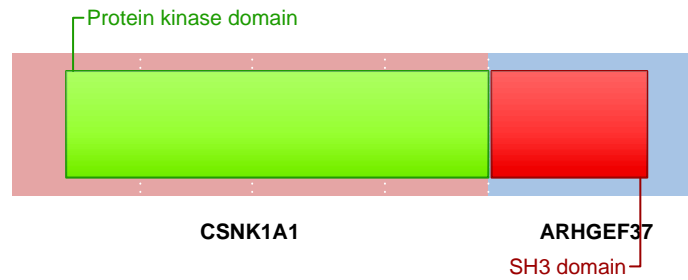
RETAINED PROTEIN DOMAINS
reading frame unclear



- translocation
- duplication
- deletion
- inversion



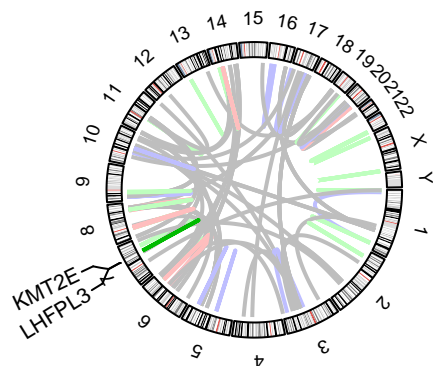
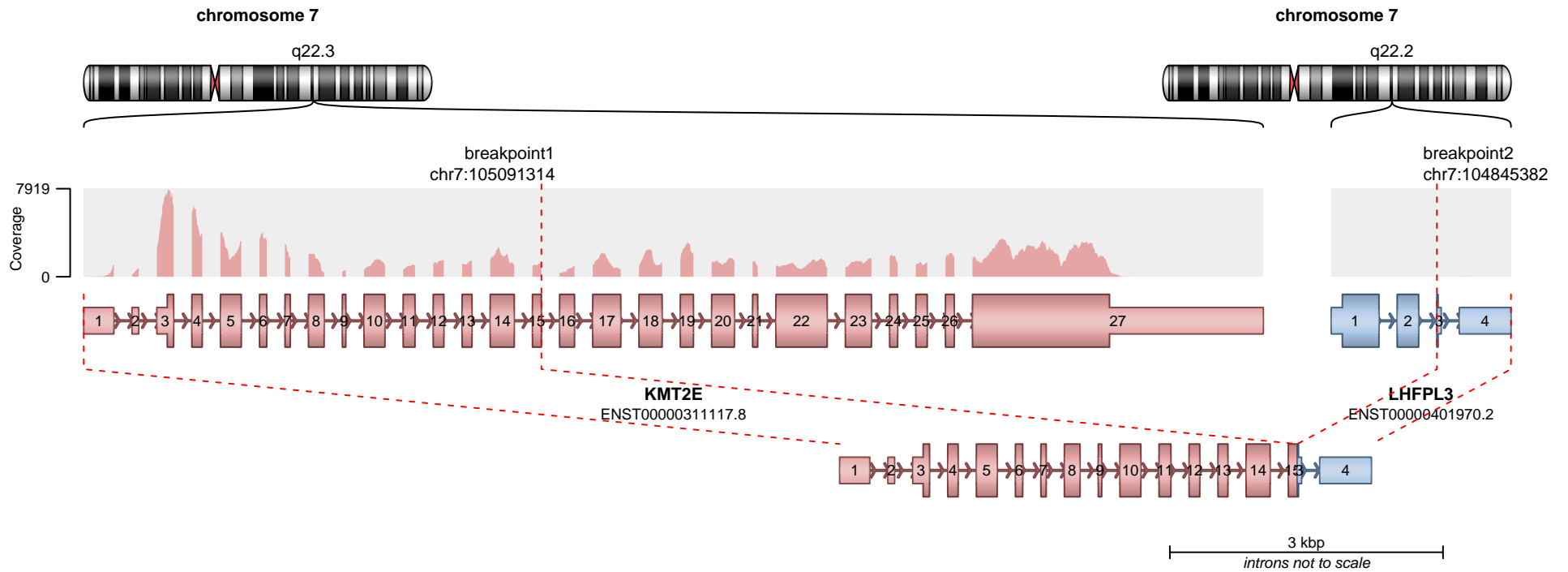
RETAINED PROTEIN DOMAINS
reading frame unclear



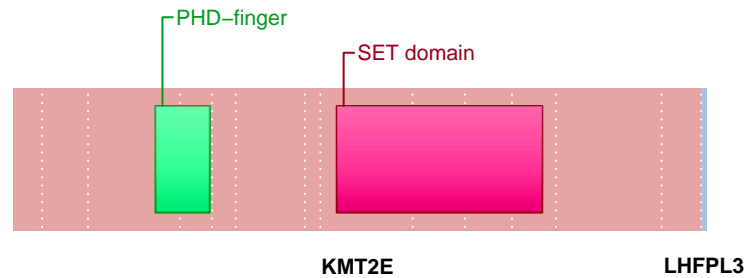
SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 0

— translocation — deletion
— duplication — inversion



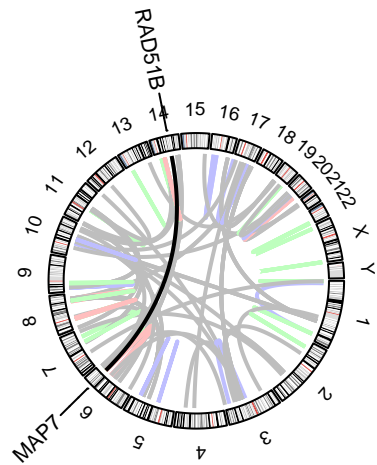
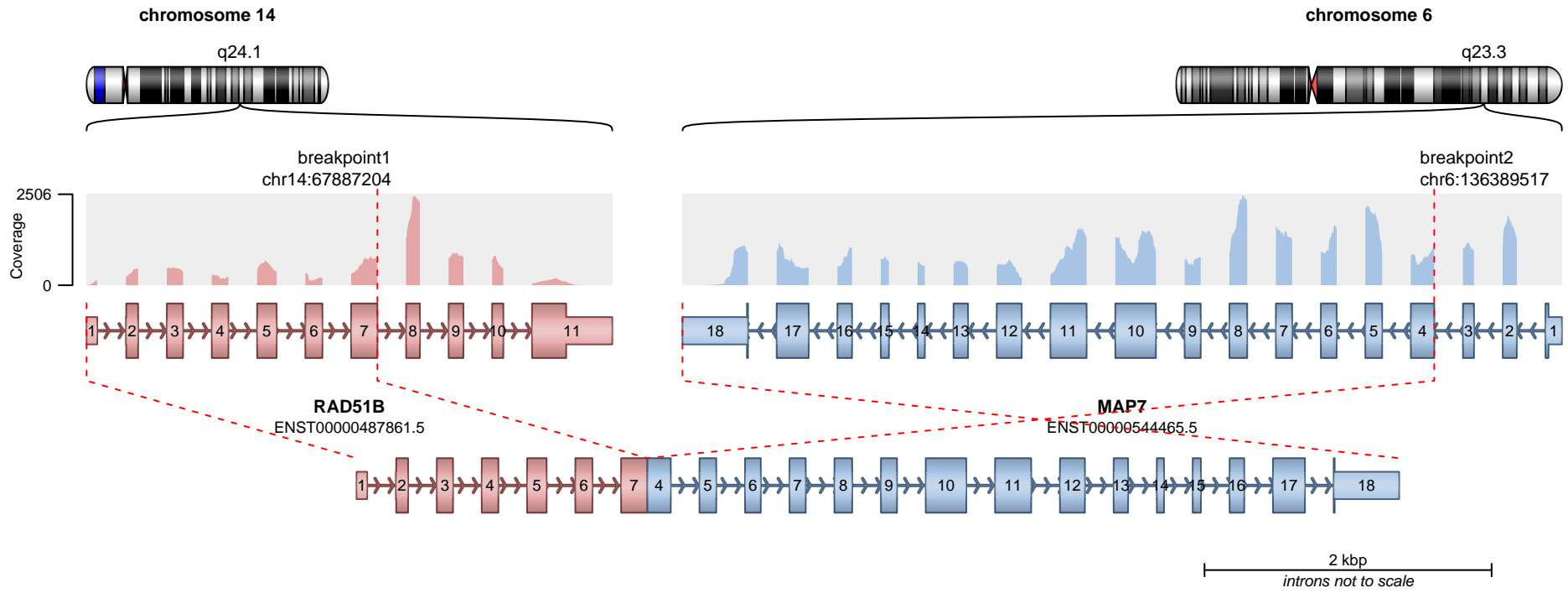
RETAINED PROTEIN DOMAINS
reading frame unclear



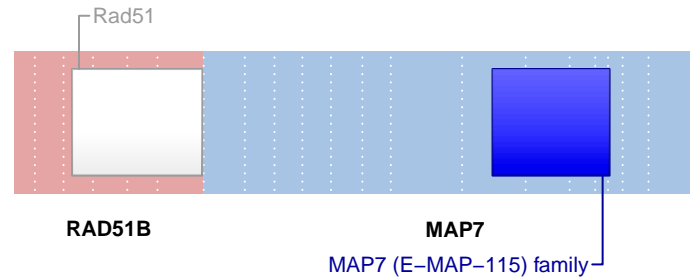
SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 0

— translocation — deletion
— duplication — inversion



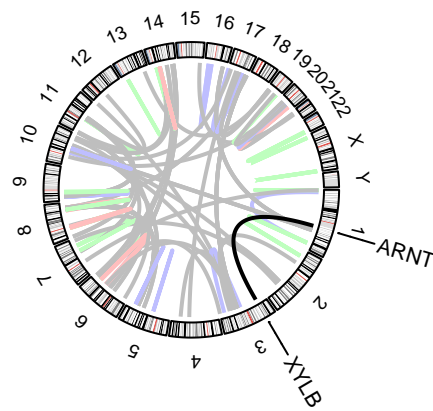
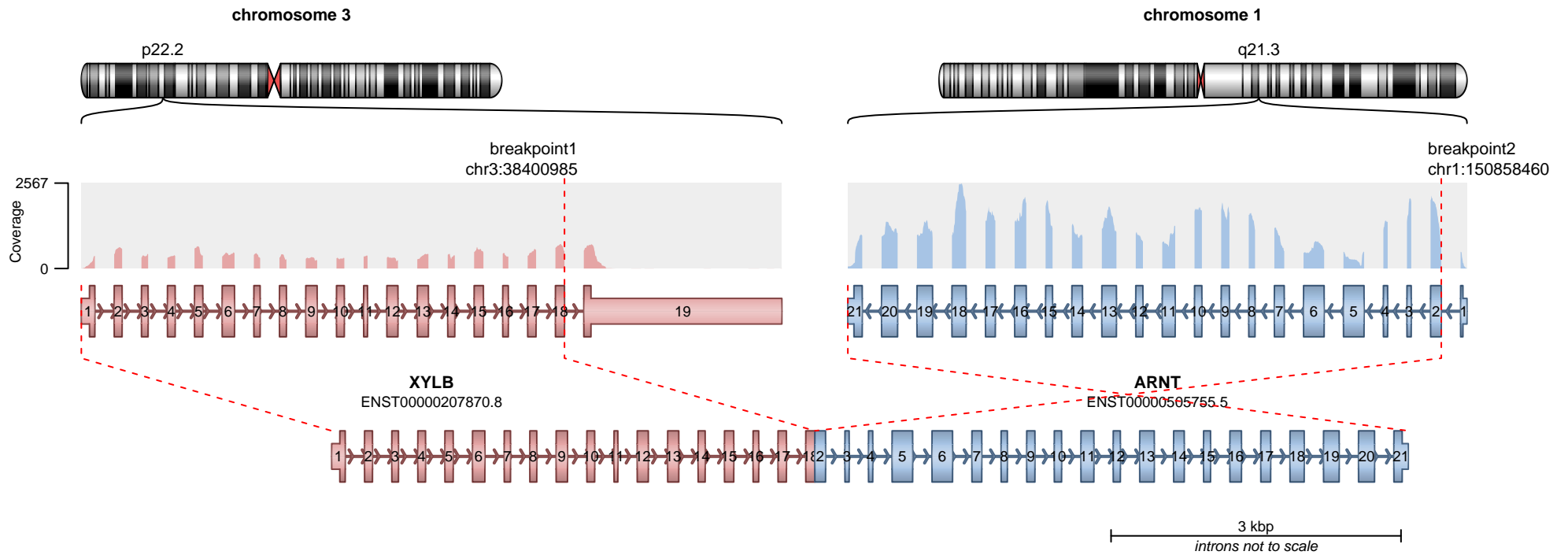
RETAINED PROTEIN DOMAINS
reading frame unclear



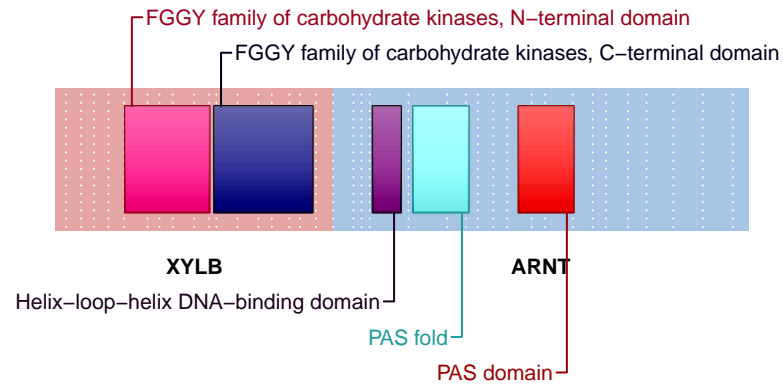
SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



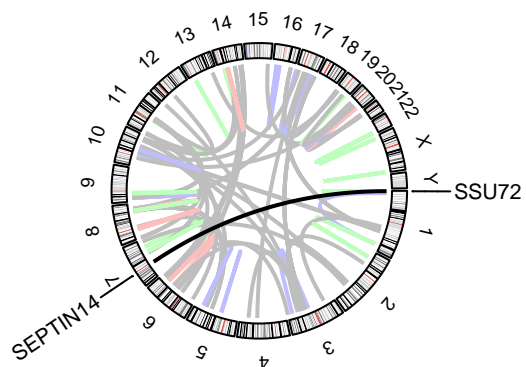
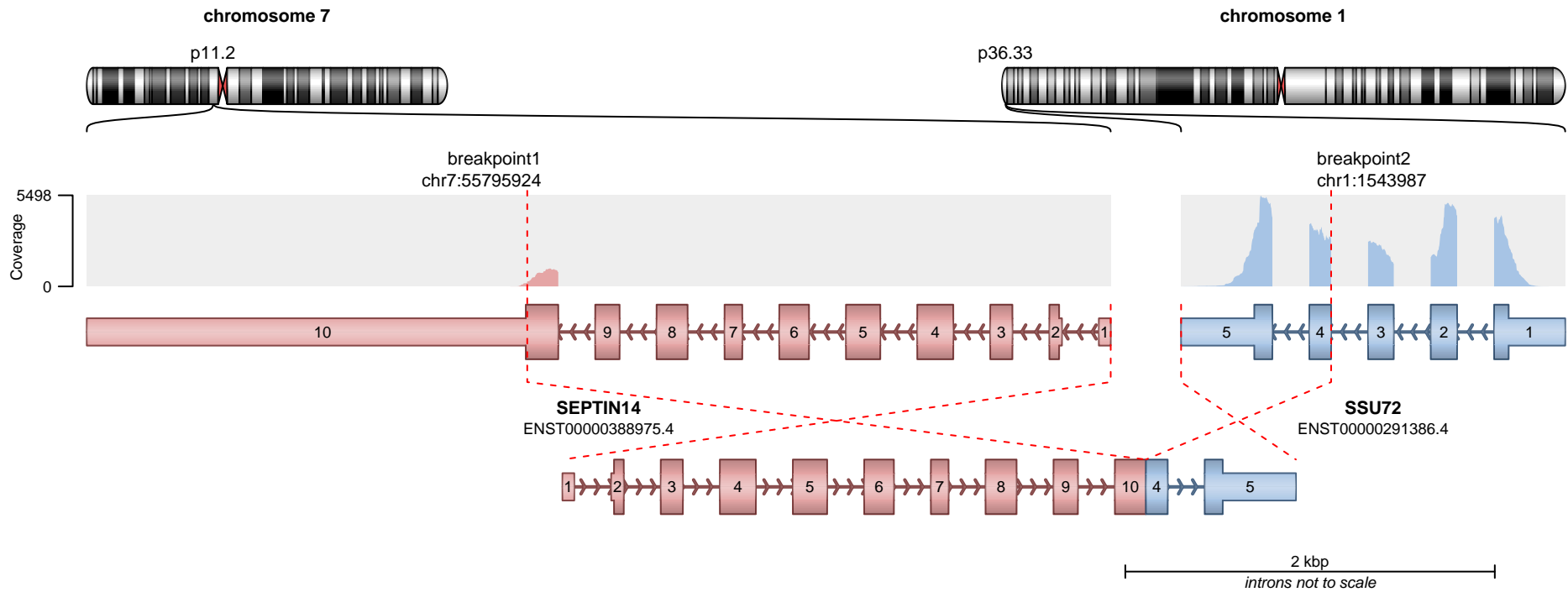
RETAINED PROTEIN DOMAINS
reading frame unclear



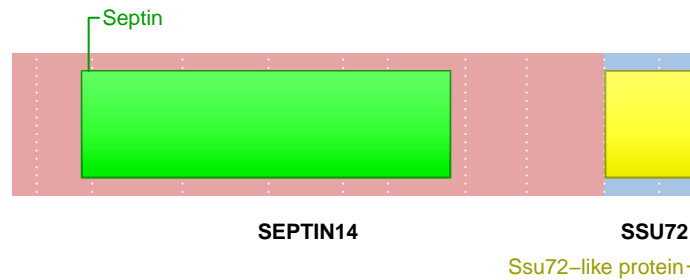
SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



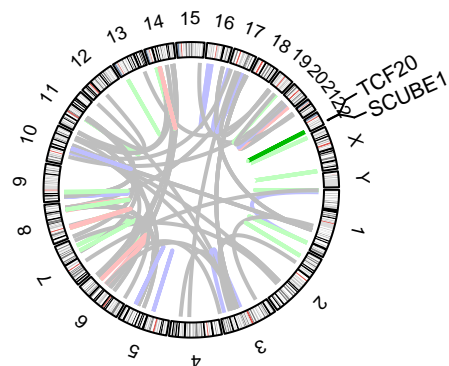
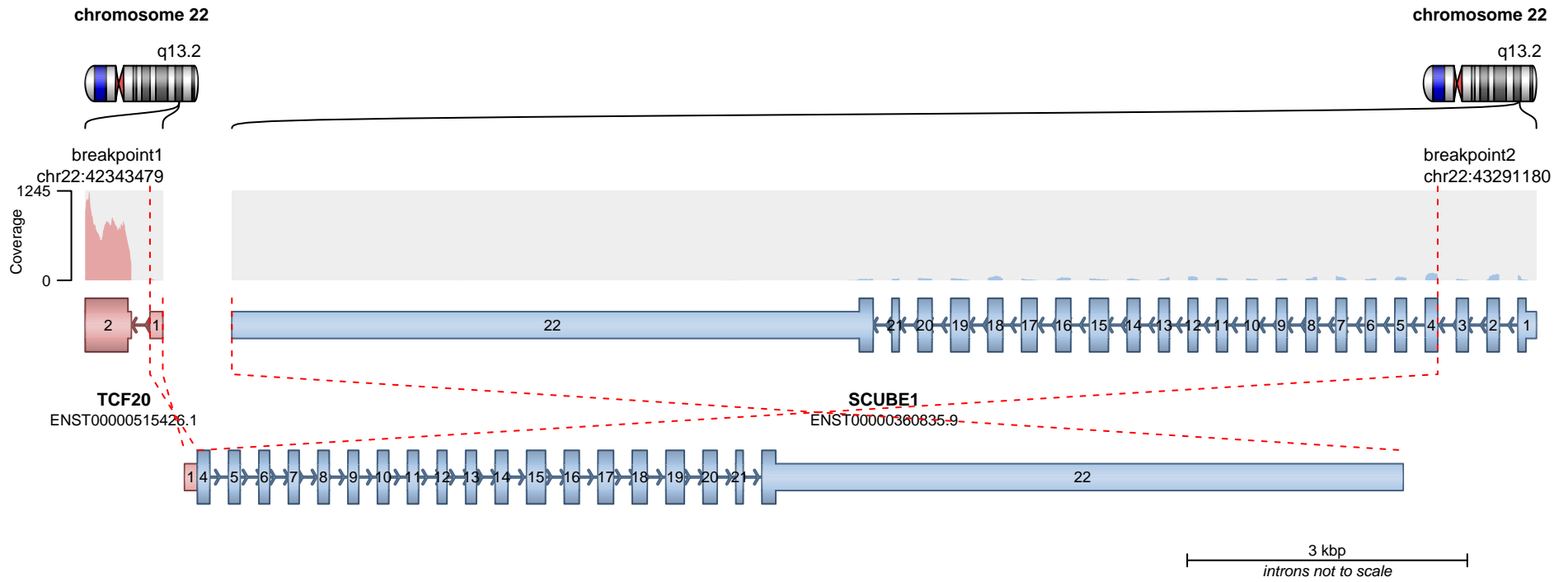
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

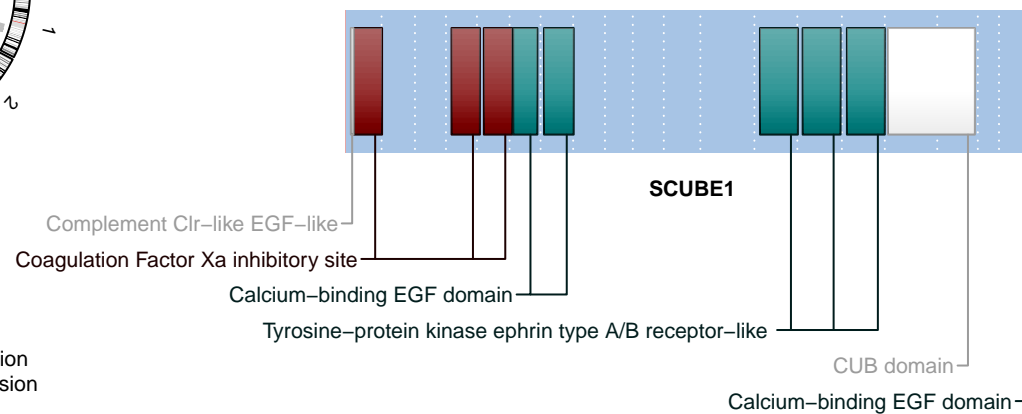
Split reads = 6
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



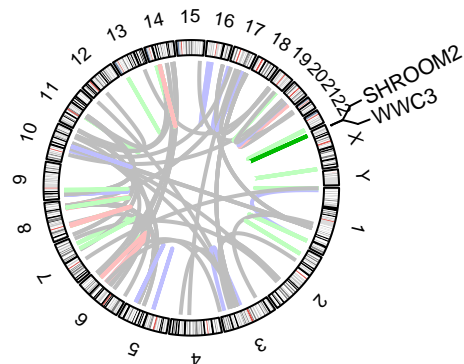
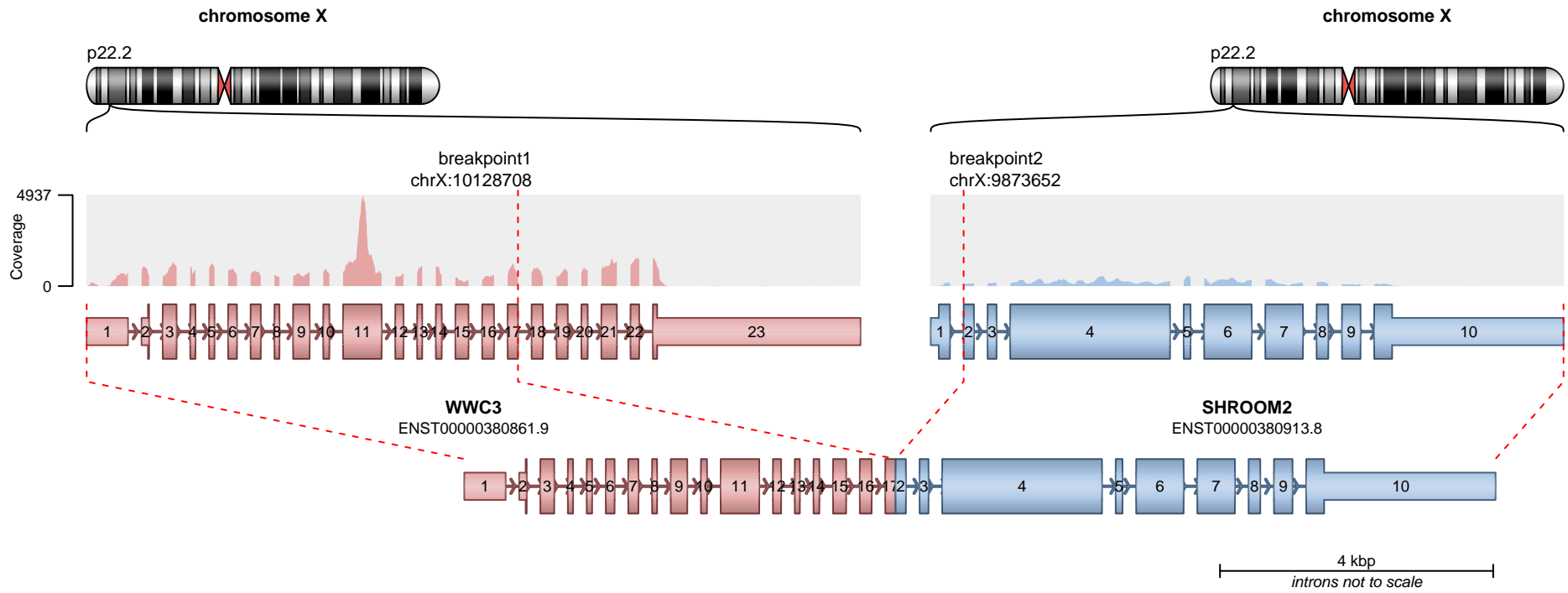
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear

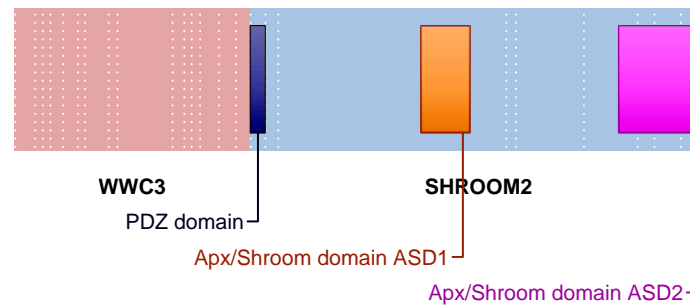


SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 0



RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion

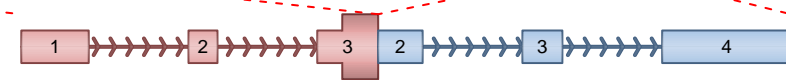
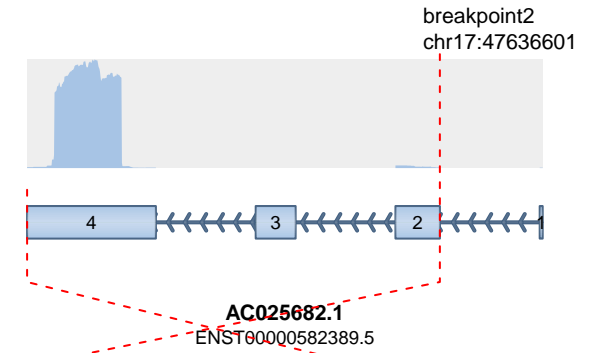
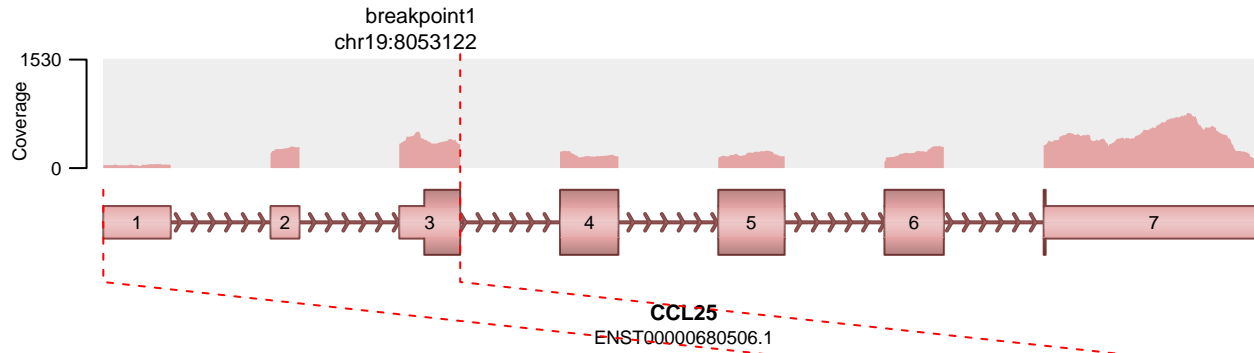
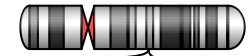
chromosome 19

p13.2

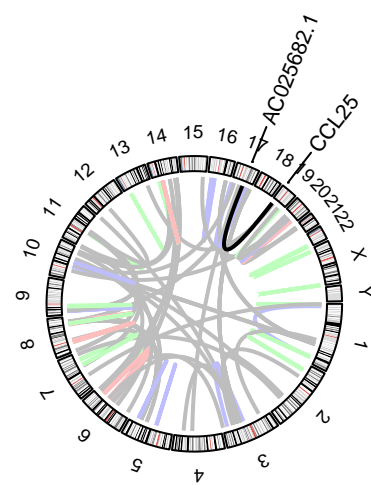


chromosome 17

q21.32



700 bp
introns not to scale

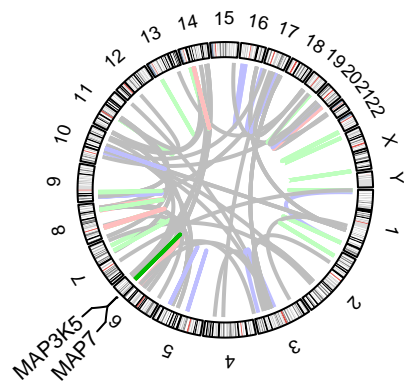
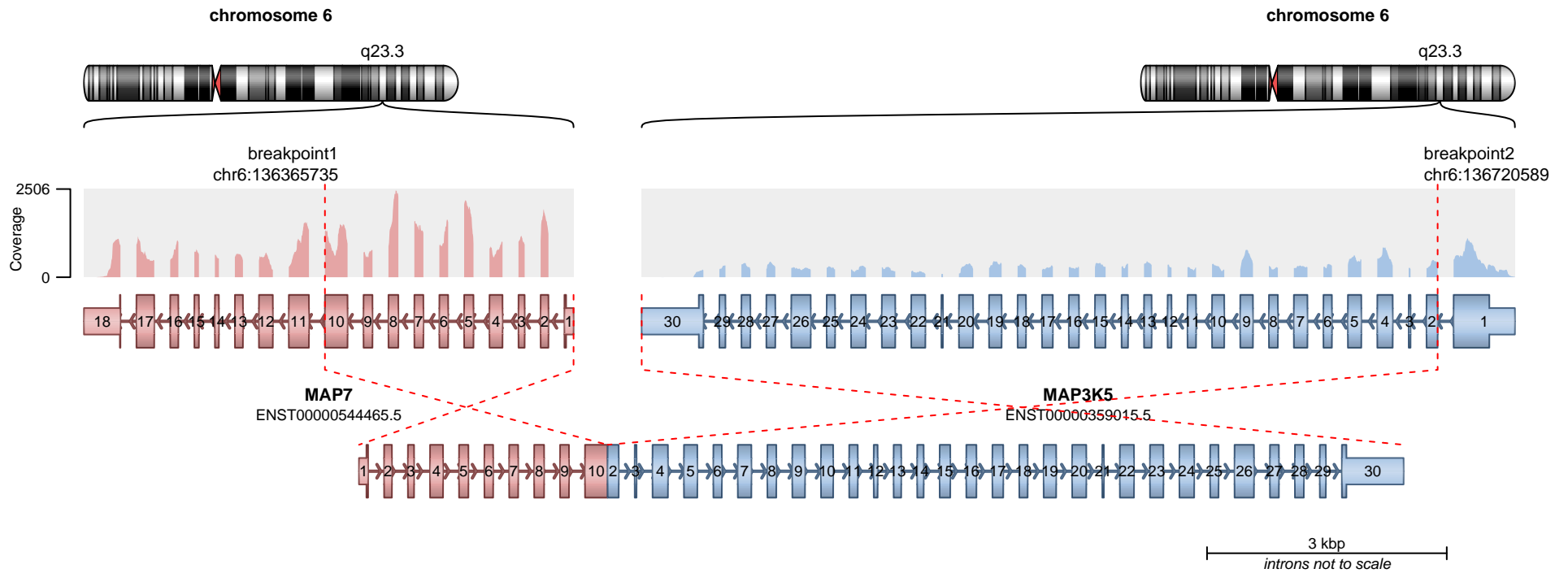


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

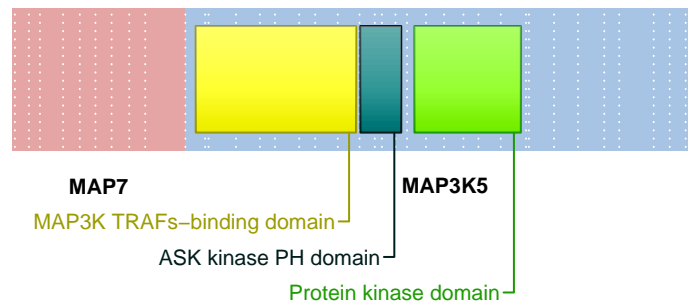
SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0



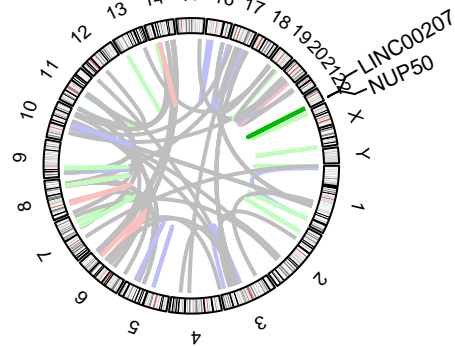
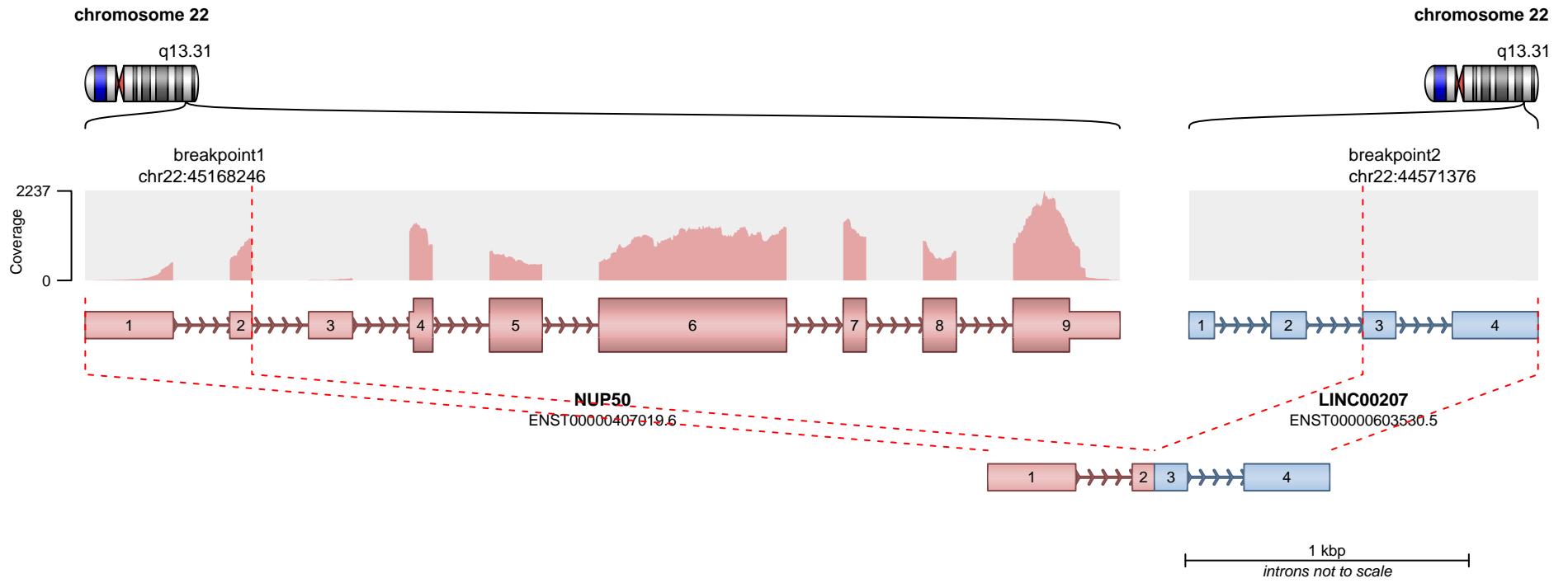
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0



No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

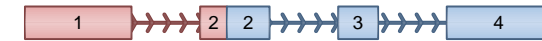
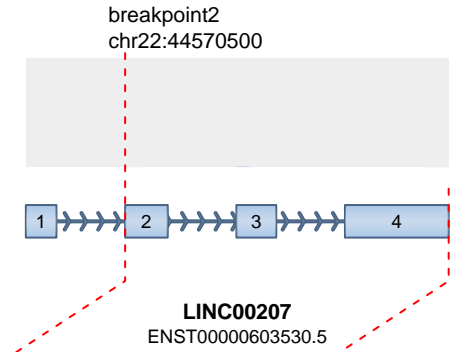
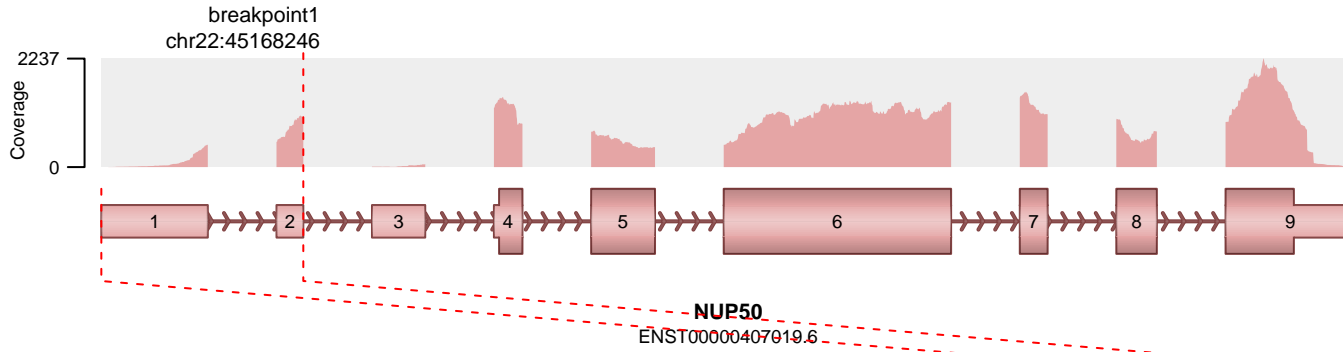
Split reads = 5
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

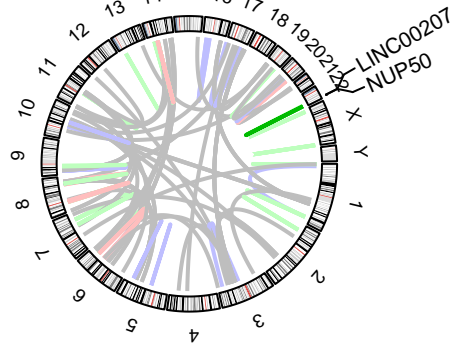
chromosome 22



chromosome 22



1 kbp
introns not to scale

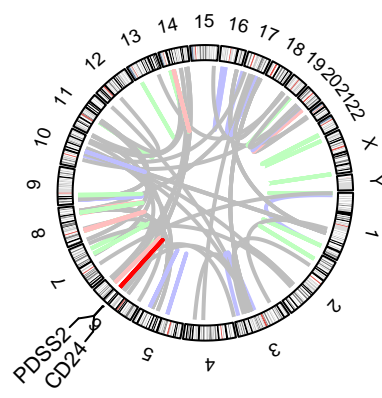
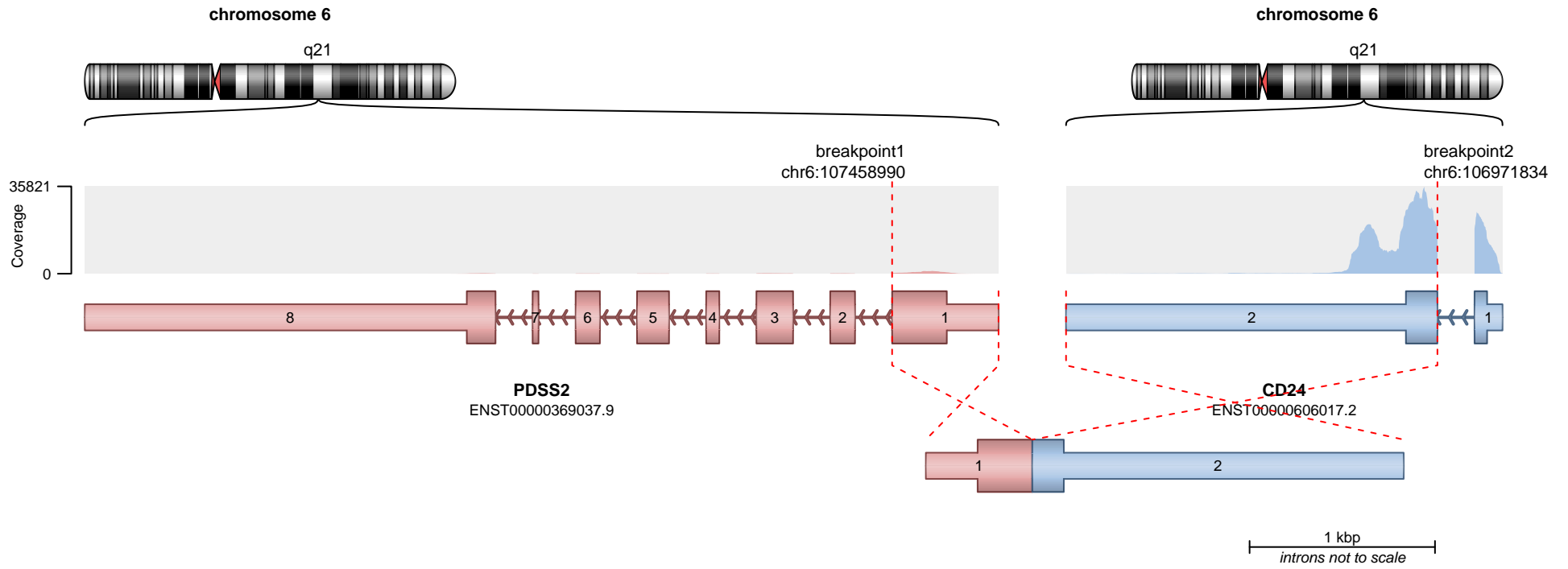


No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



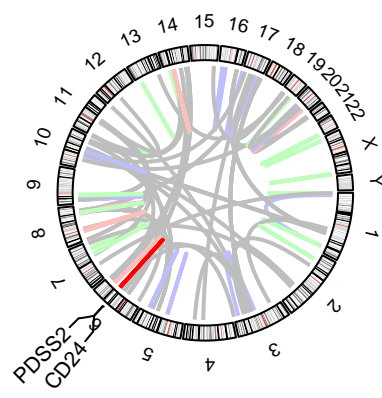
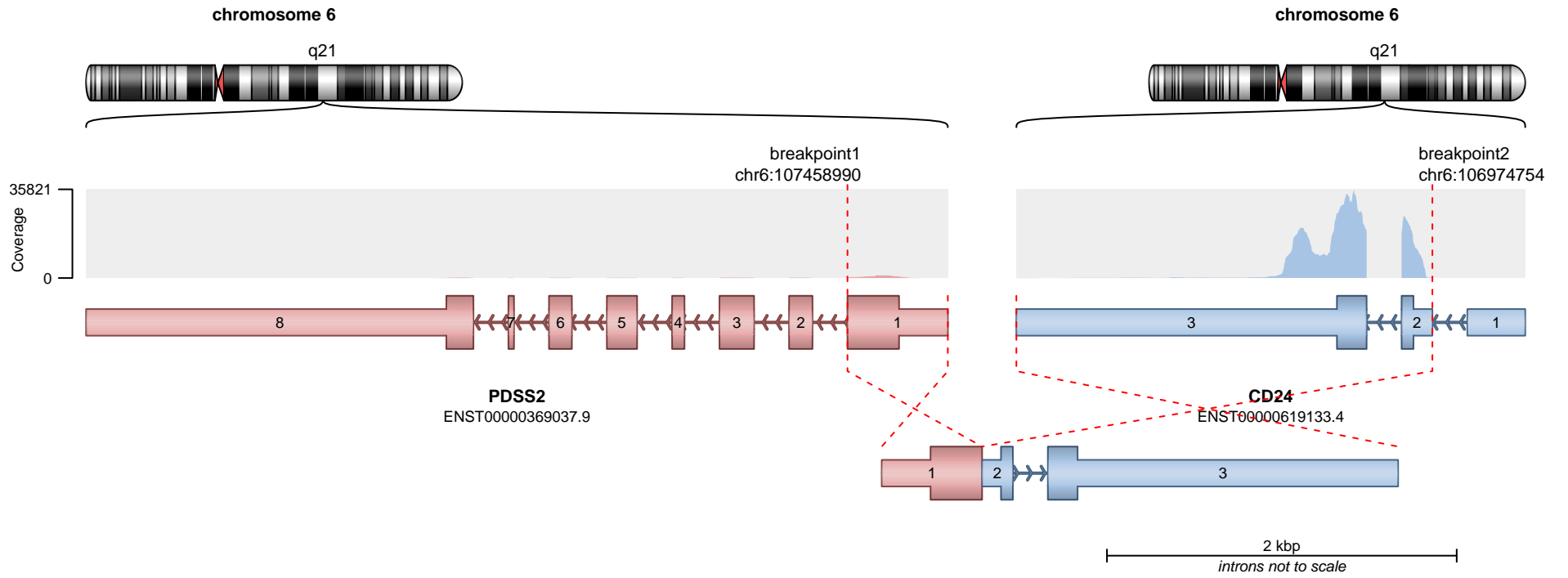
RETAINED PROTEIN DOMAINS
reading frame unclear



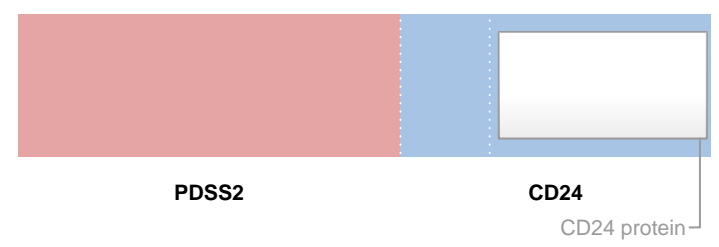
SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0

— translocation — deletion
— duplication — inversion



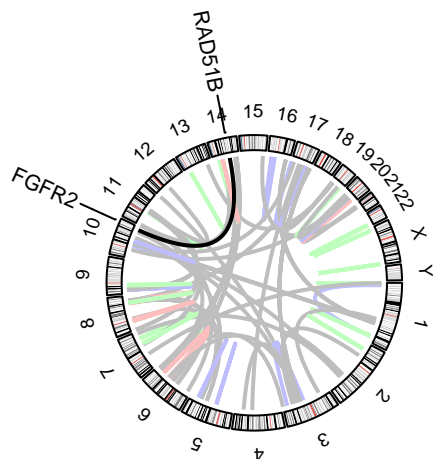
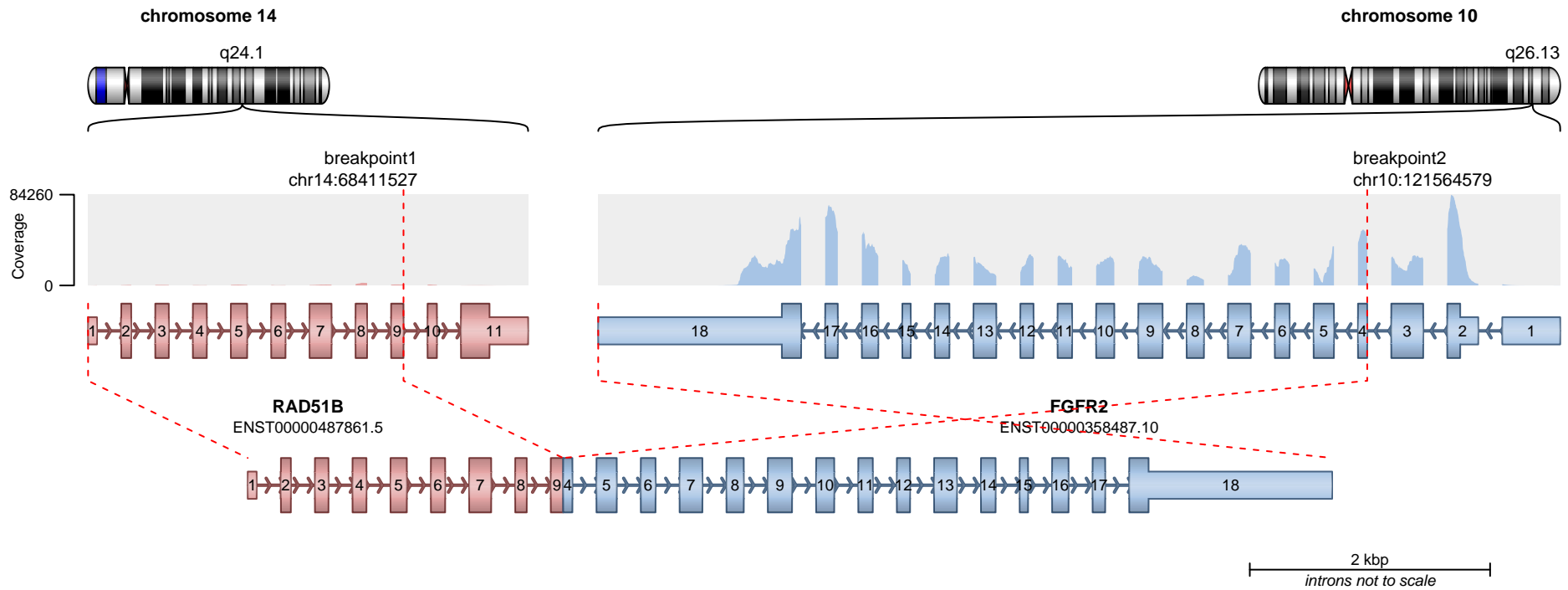
RETAINED PROTEIN DOMAINS
reading frame unclear



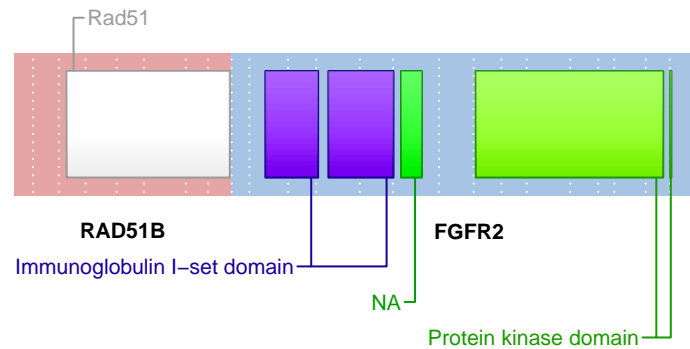
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

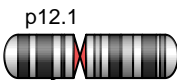


SUPPORTING READ COUNT

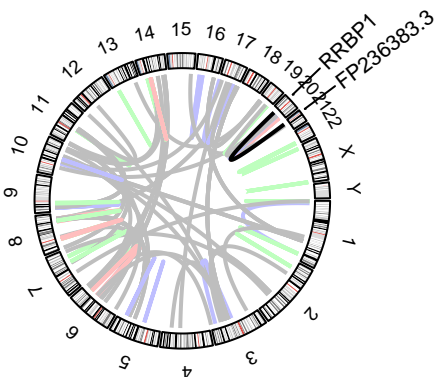
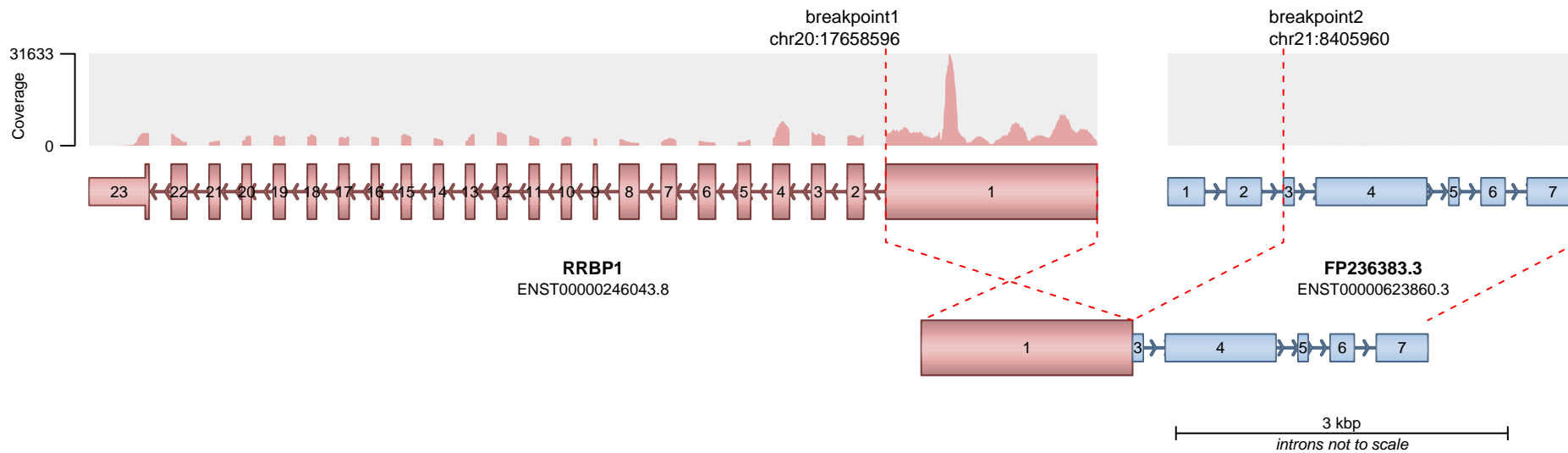
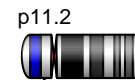
Split reads = 5
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

chromosome 20



chromosome 21



RETAINED PROTEIN DOMAINS
reading frame unclear

Ribosome receptor lysine/proline rich region



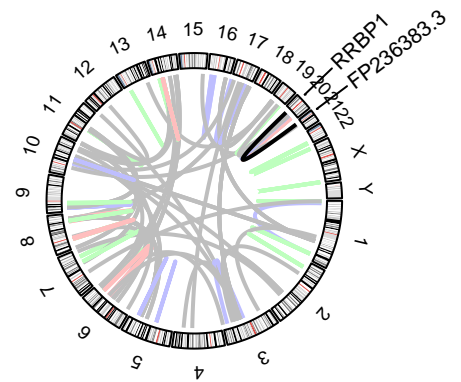
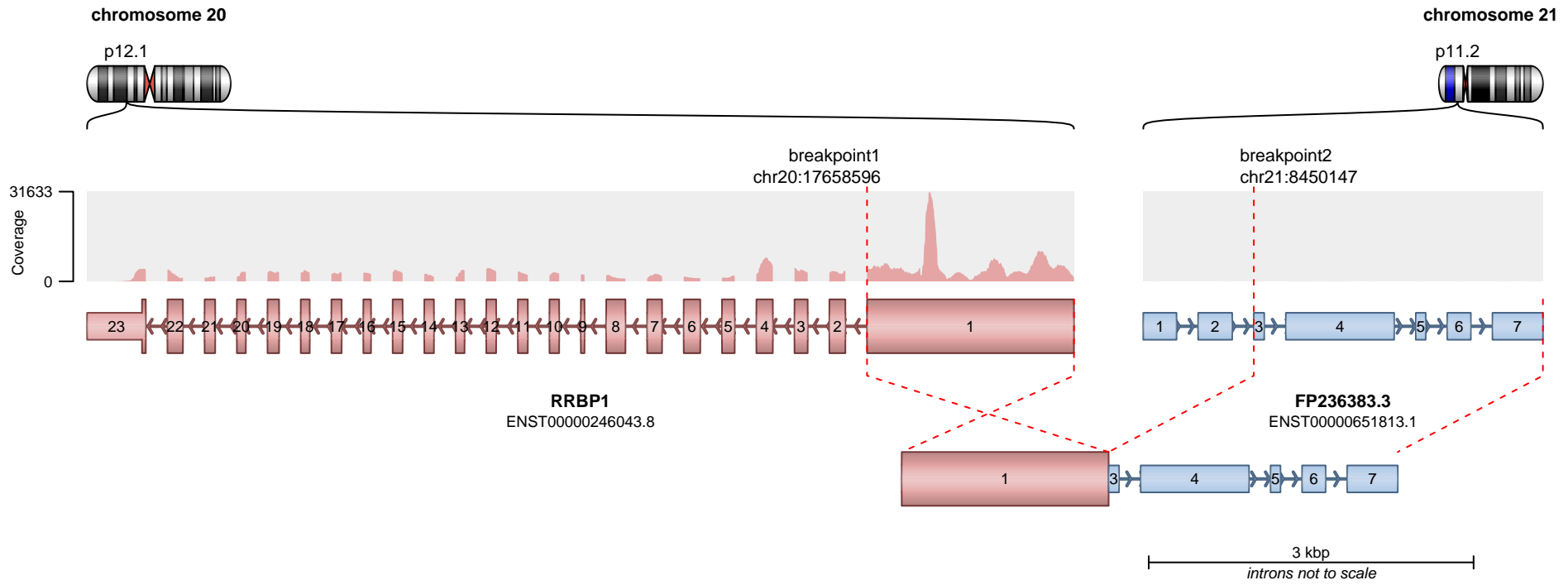
RRBP1

SUPPORTING READ COUNT

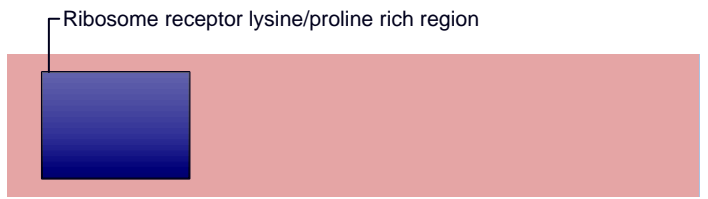
Split reads = 5

Discordant mates = 0

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

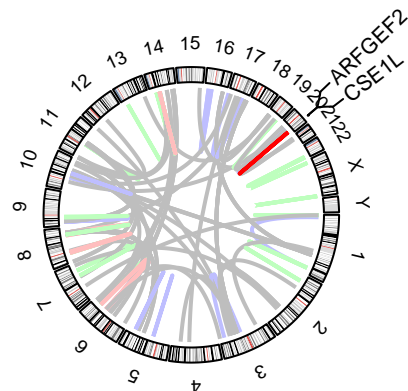
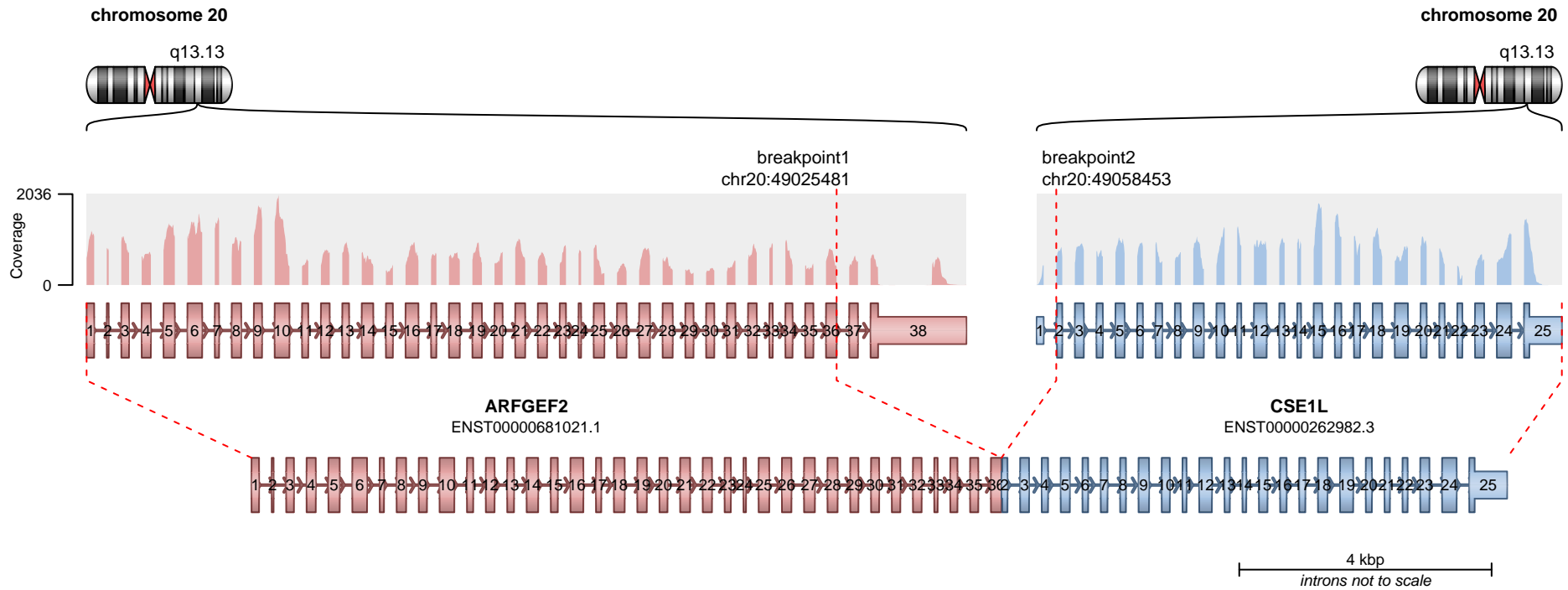


RRBP1

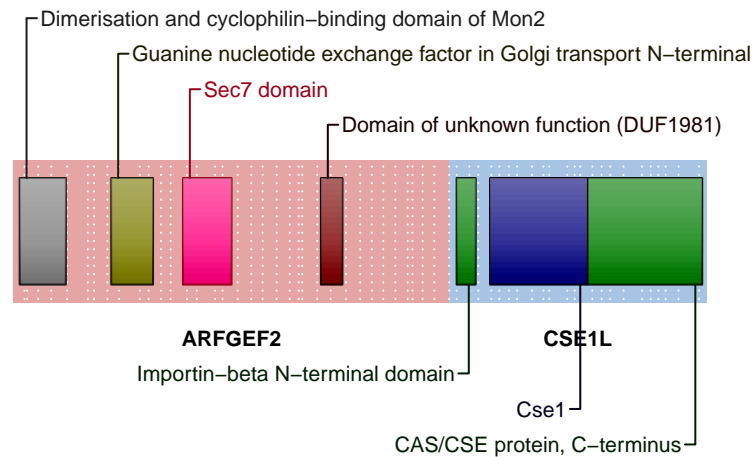
SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



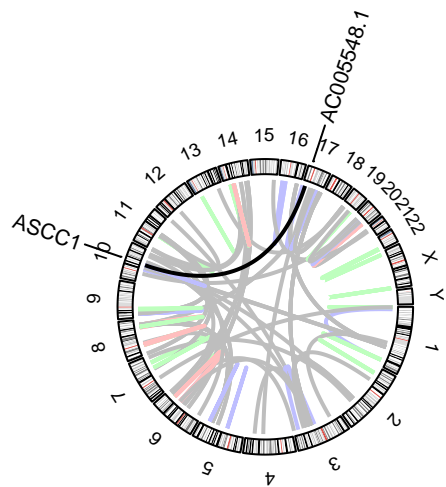
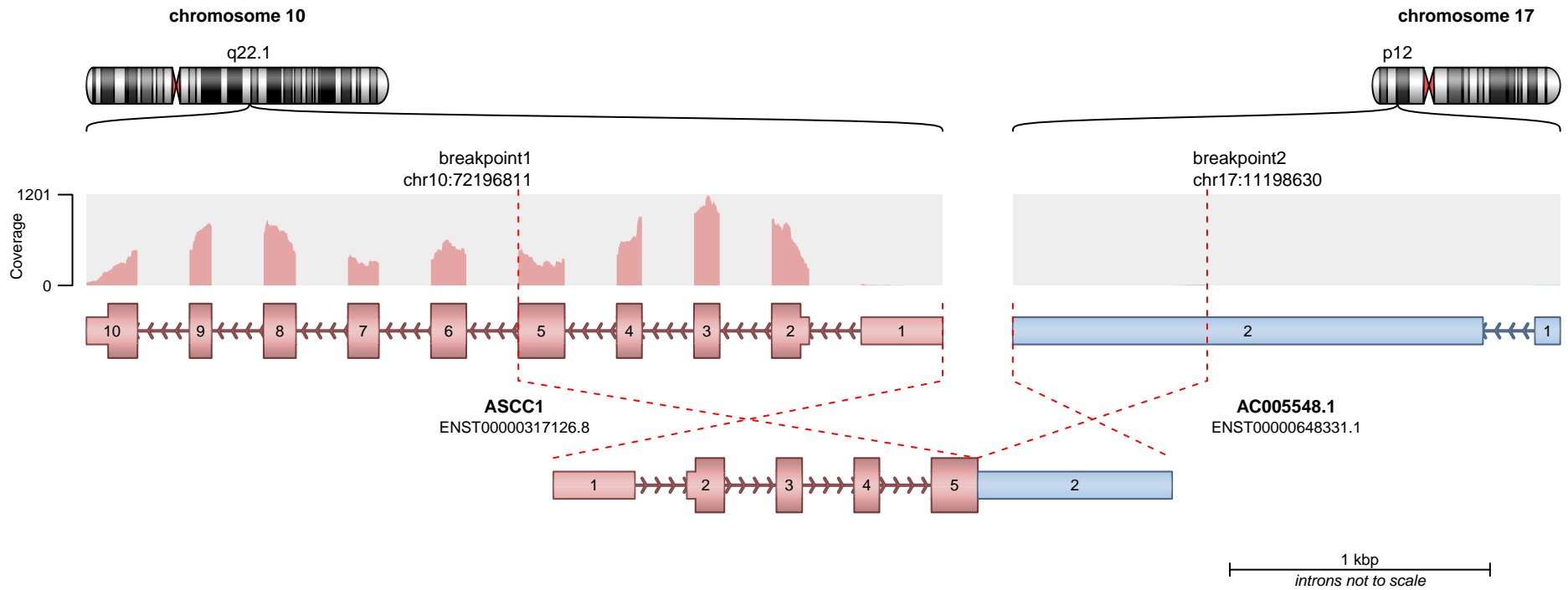
RETAINED PROTEIN DOMAINS
reading frame unclear



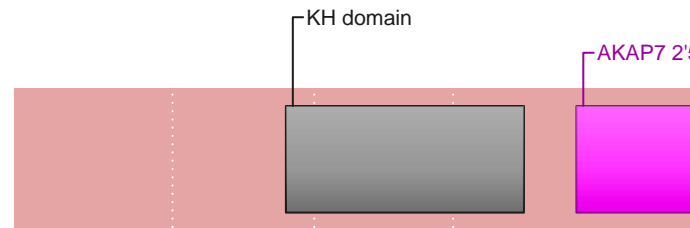
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

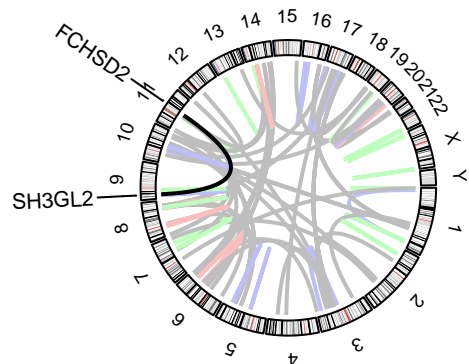
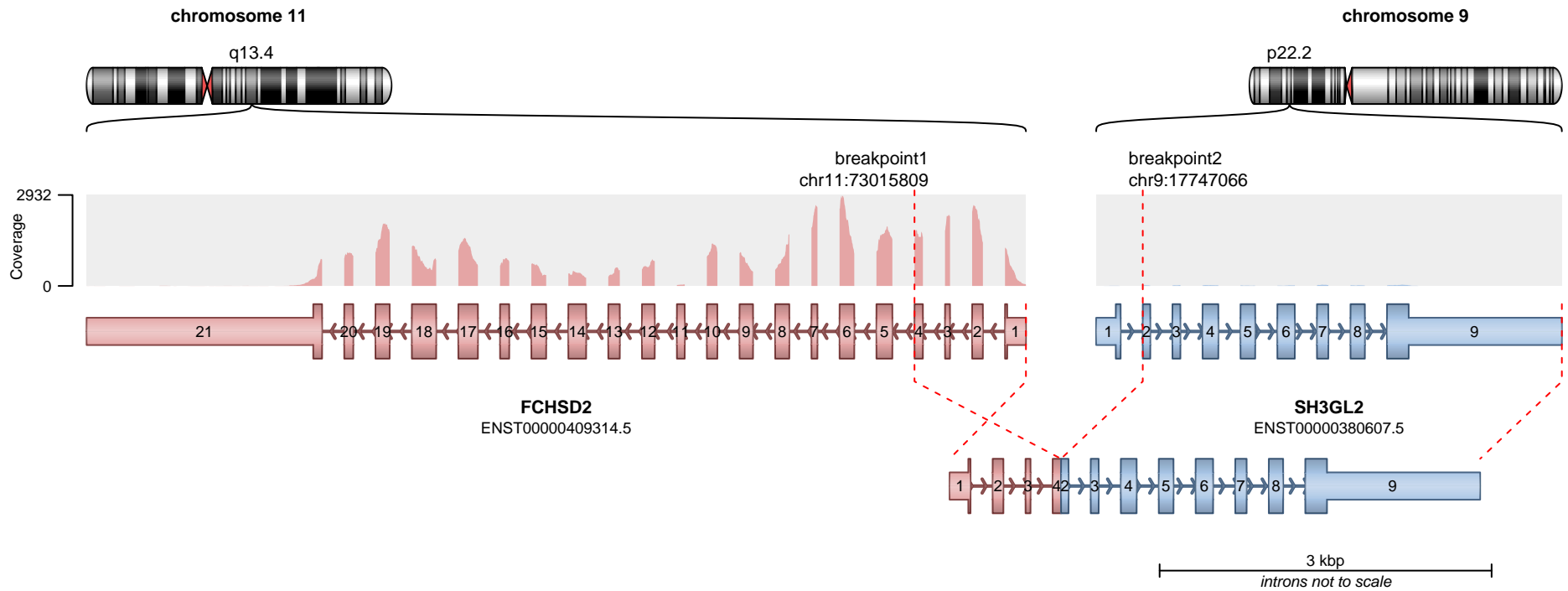


SUPPORTING READ COUNT

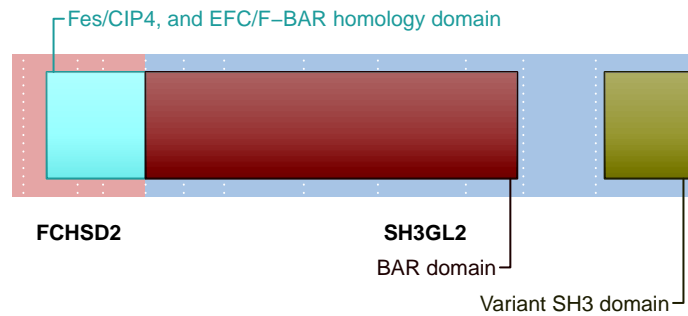
Split reads = 4
Discordant mates = 0

— translocation — deletion
— duplication — inversion

ASCC1



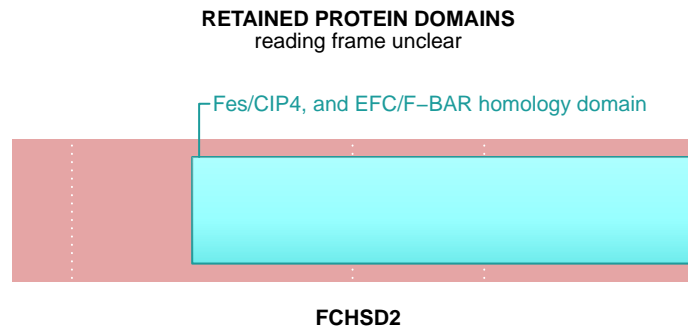
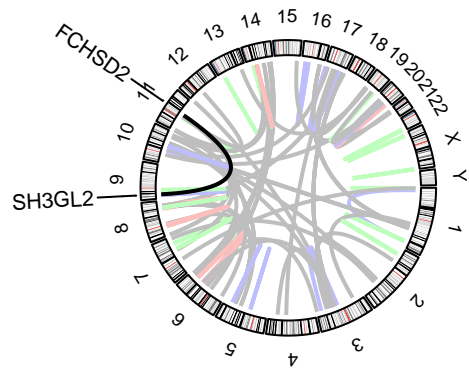
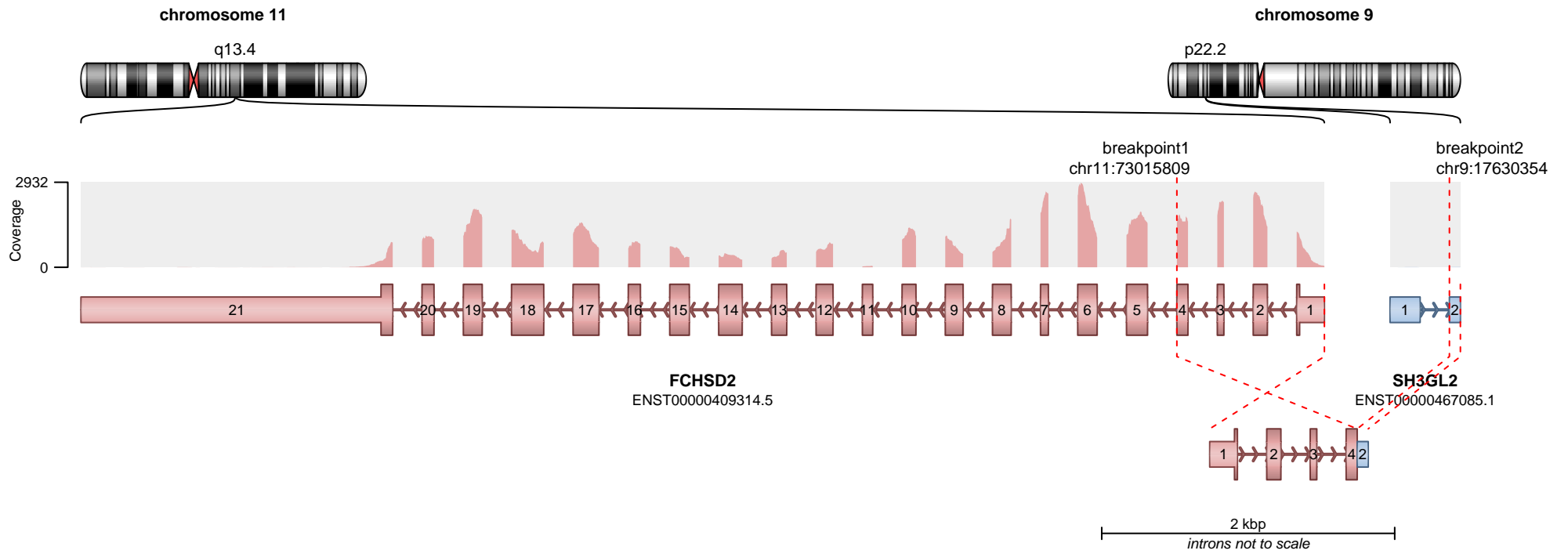
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

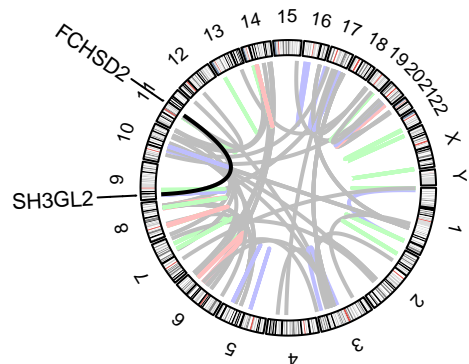
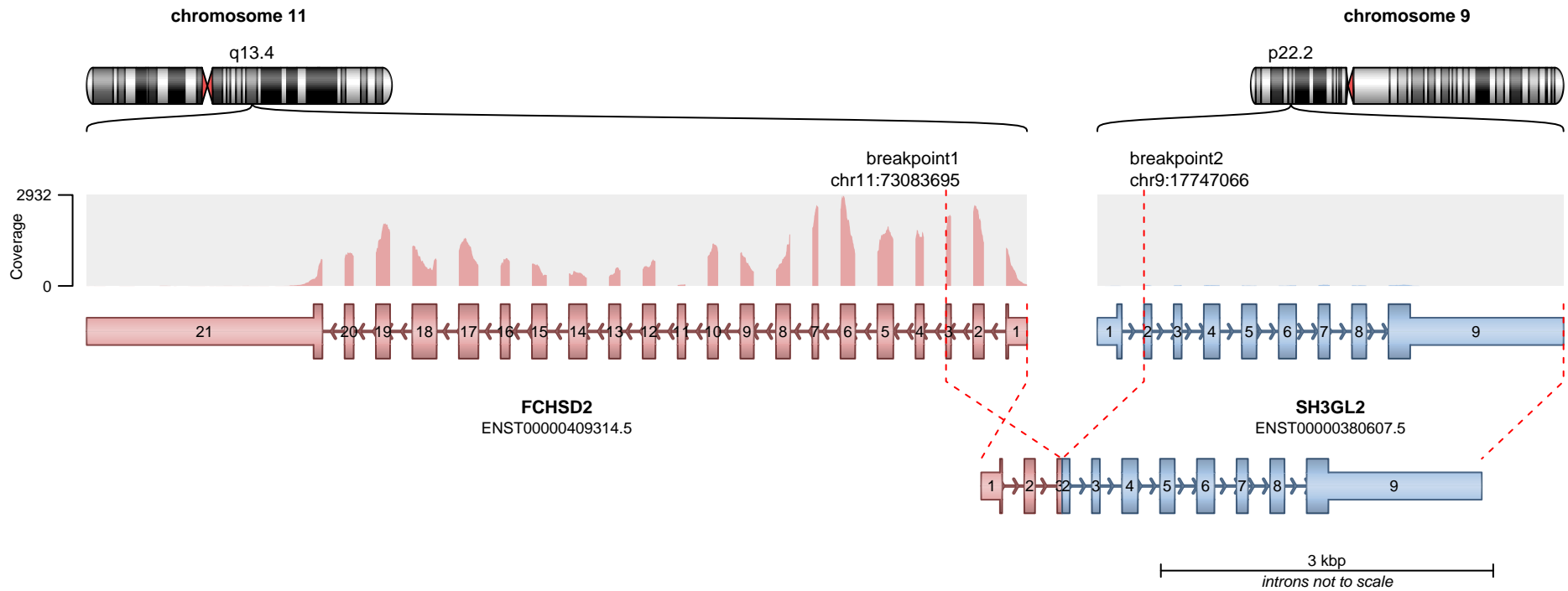
- translocation
- duplication
- deletion
- inversion



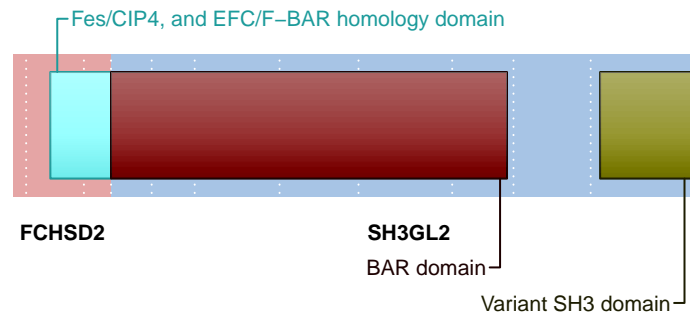
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



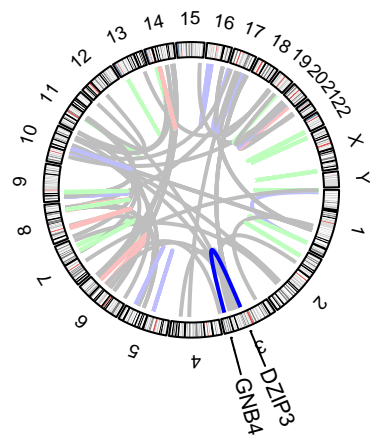
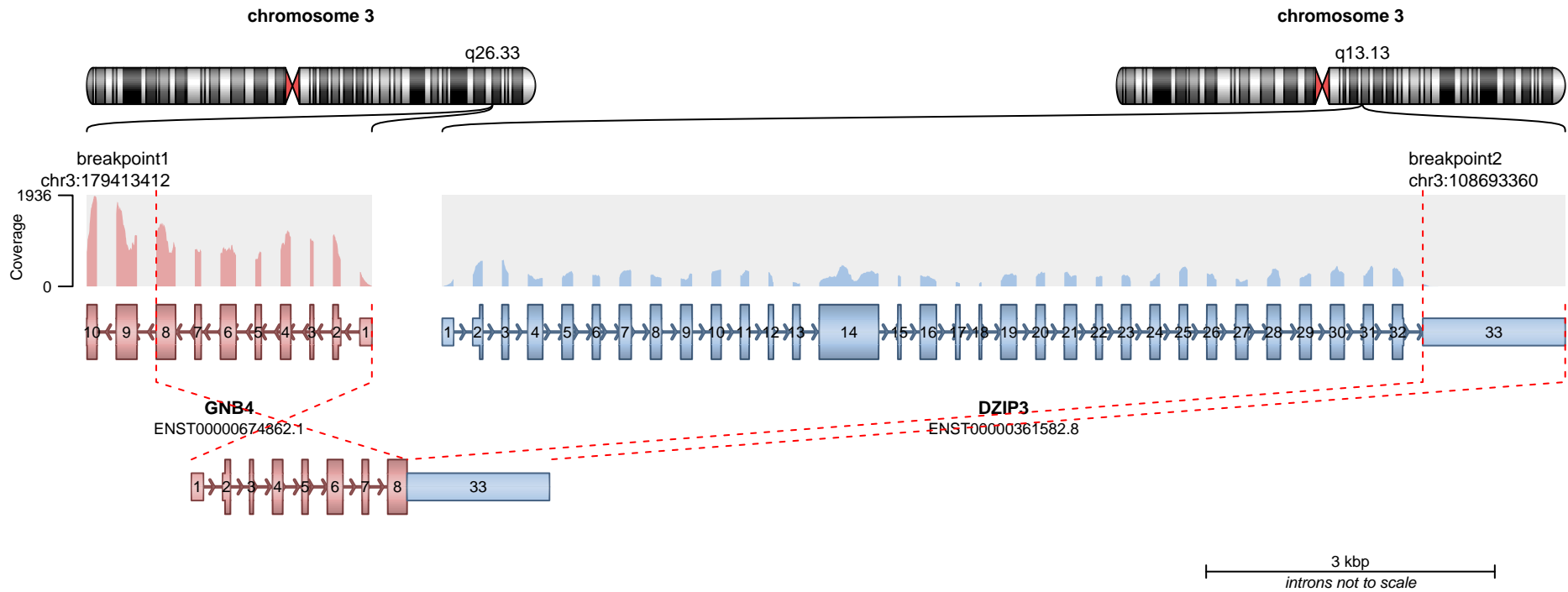
RETAINED PROTEIN DOMAINS
reading frame unclear



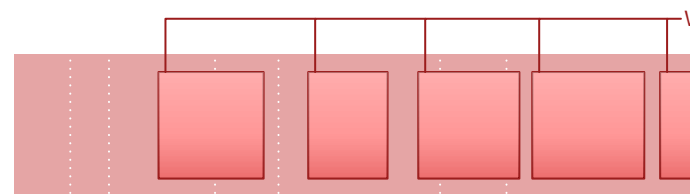
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

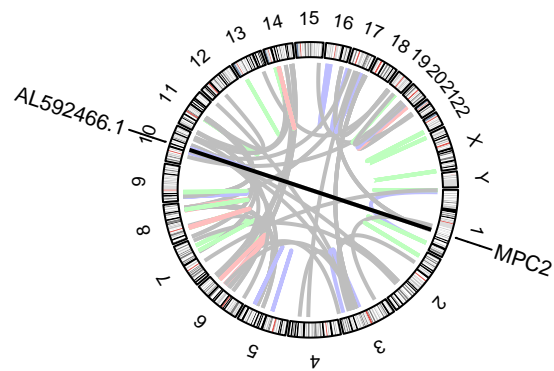
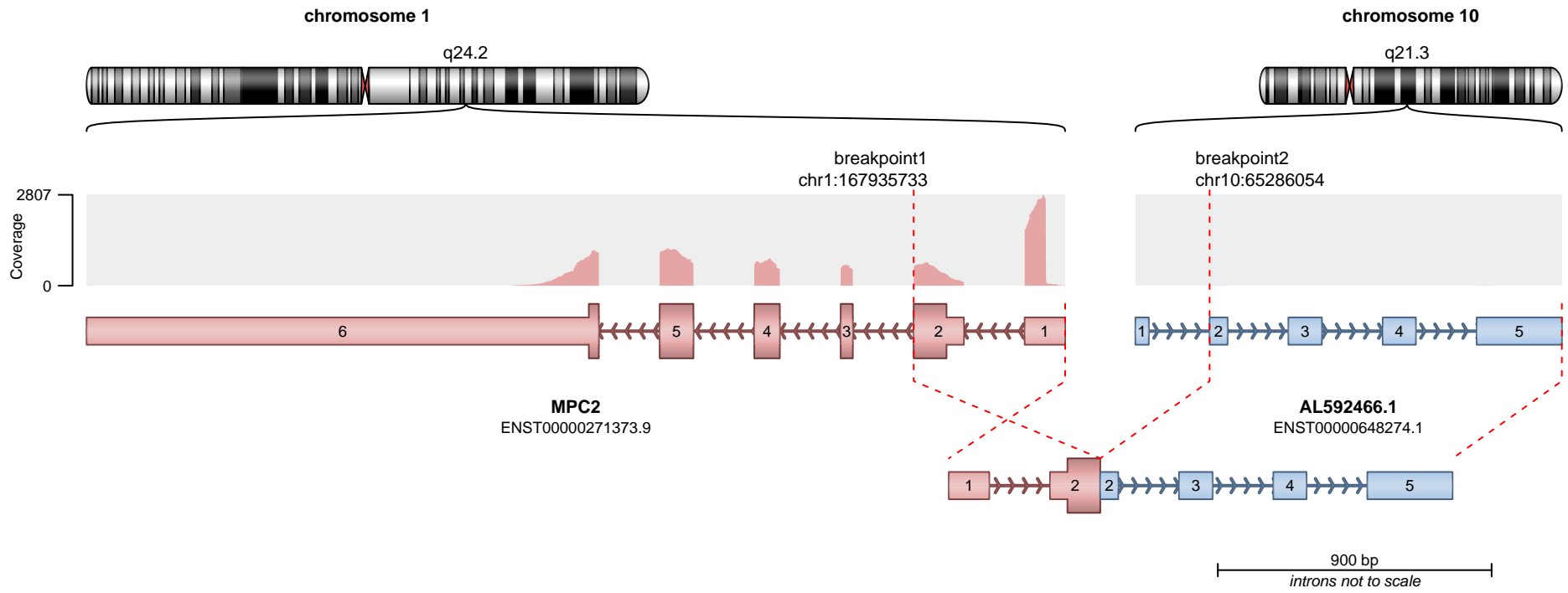


GNB4

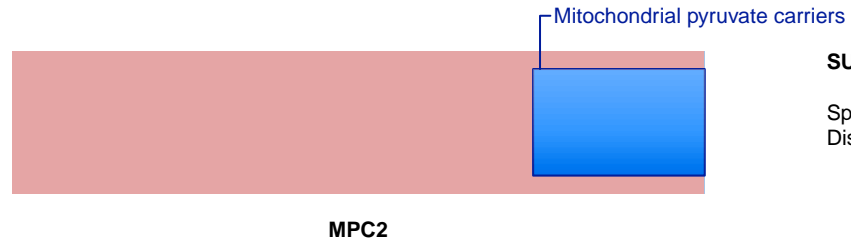
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

— translocation — deletion
— duplication — inversion



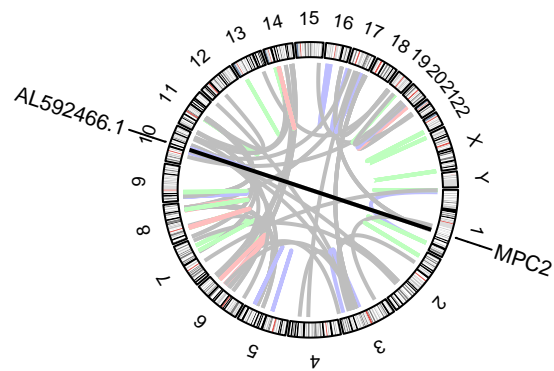
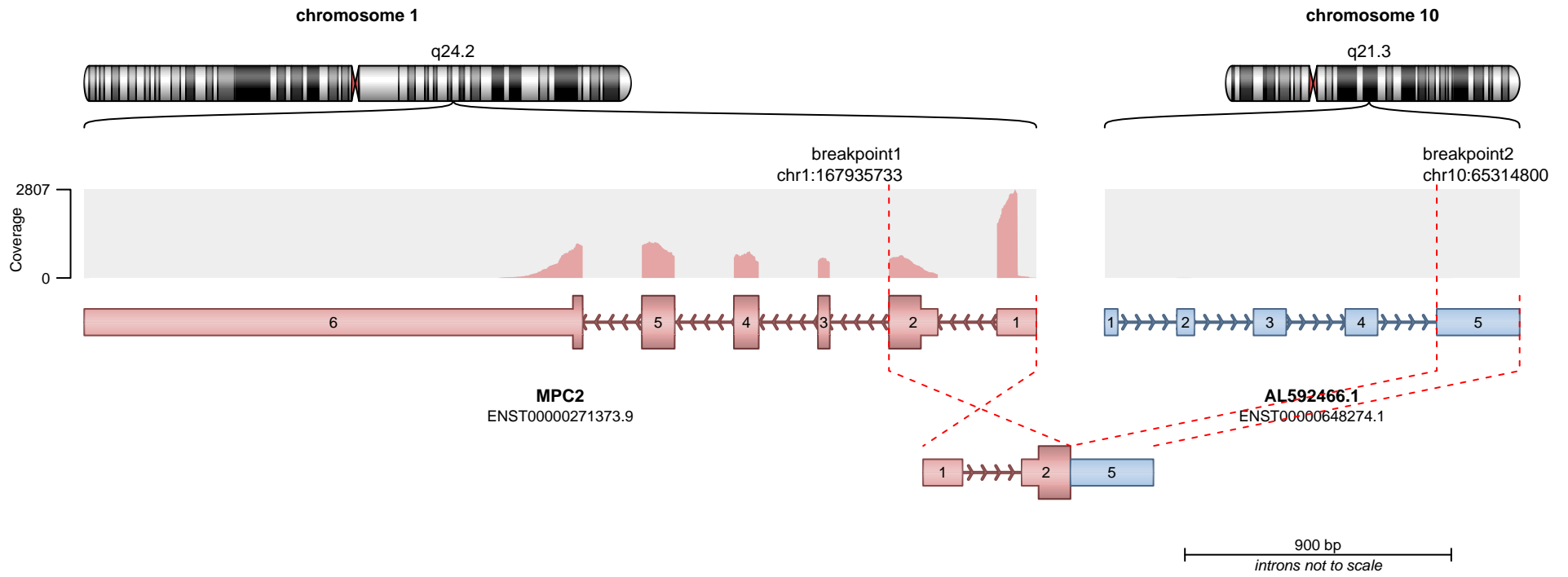
RETAINED PROTEIN DOMAINS
reading frame unclear



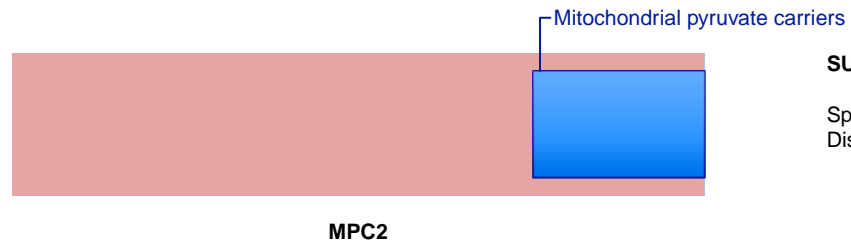
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

— translocation — deletion
— duplication — inversion



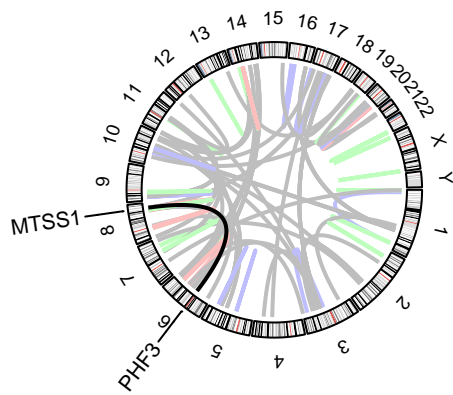
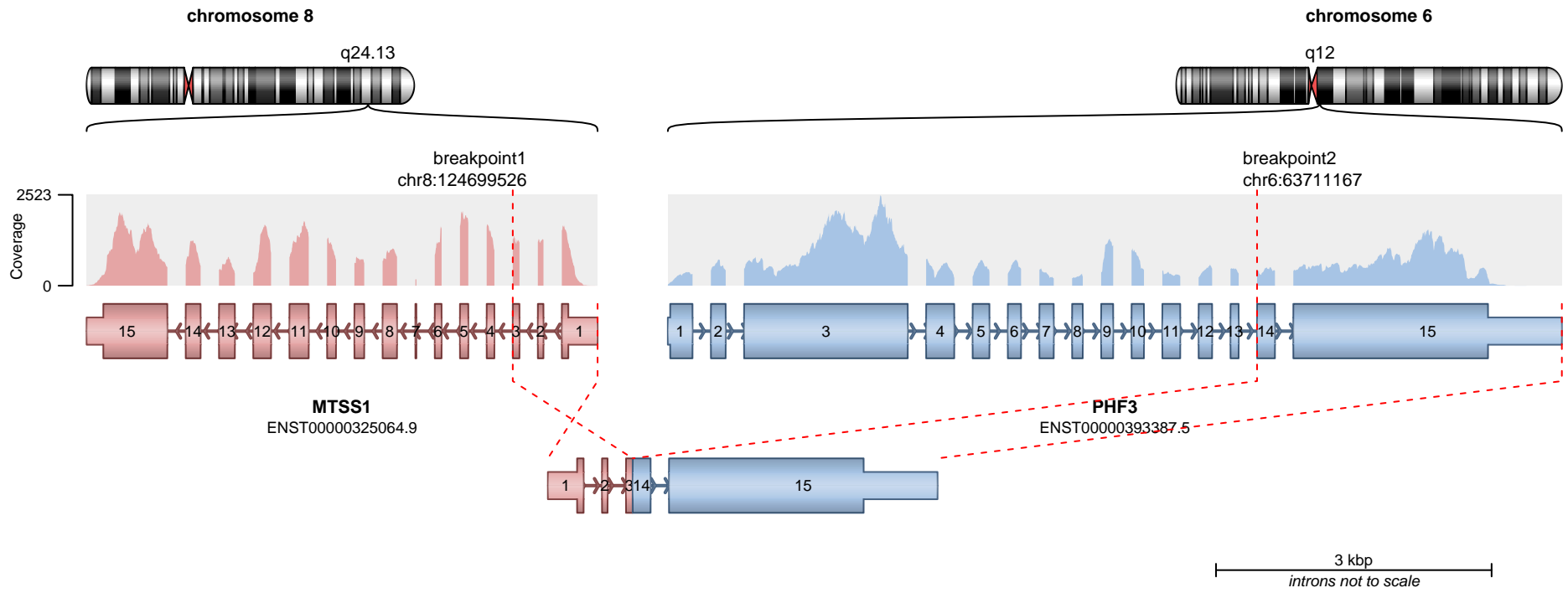
RETAINED PROTEIN DOMAINS
reading frame unclear



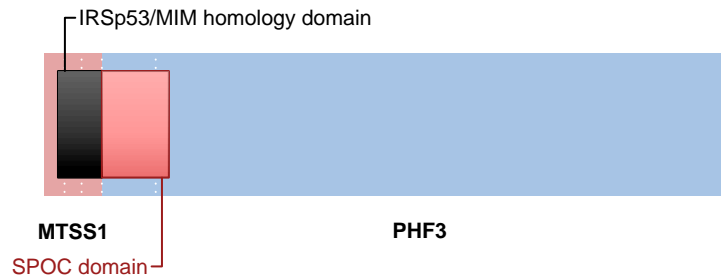
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



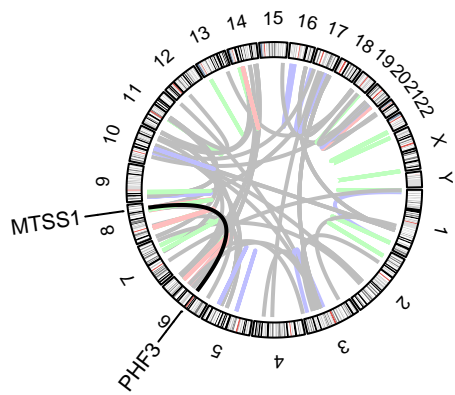
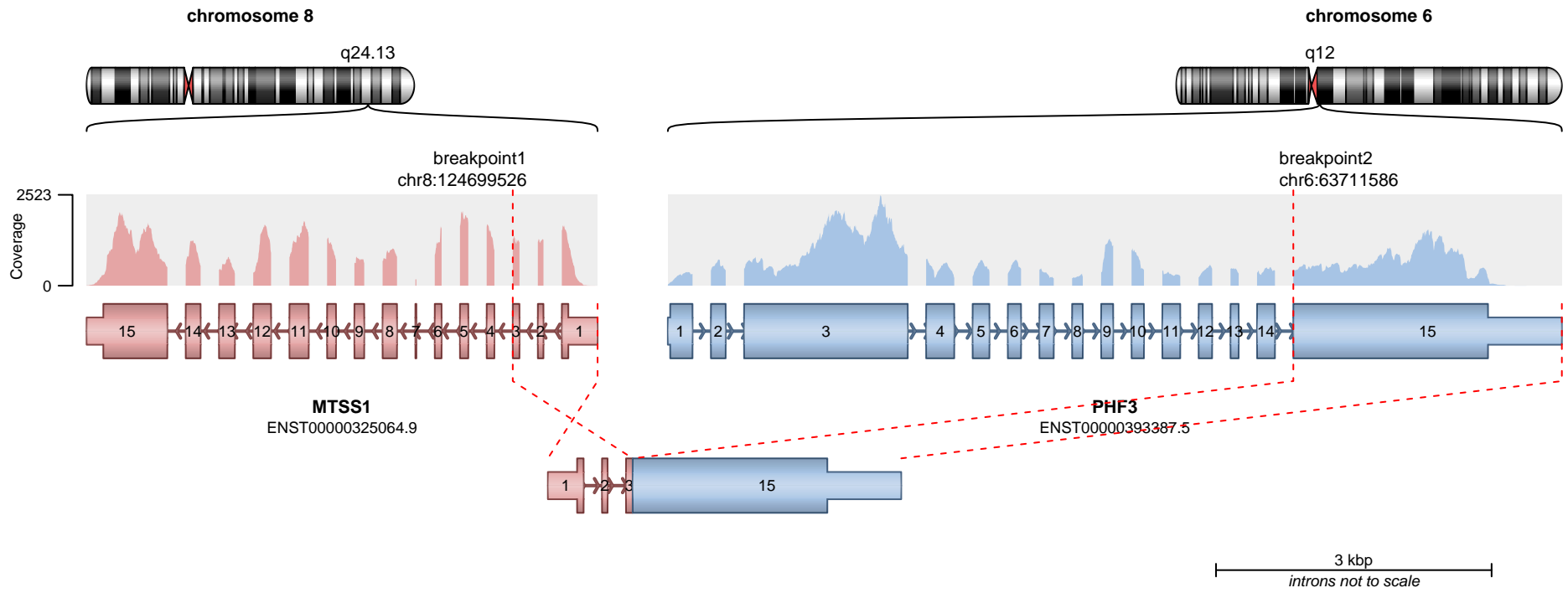
RETAINED PROTEIN DOMAINS
reading frame unclear



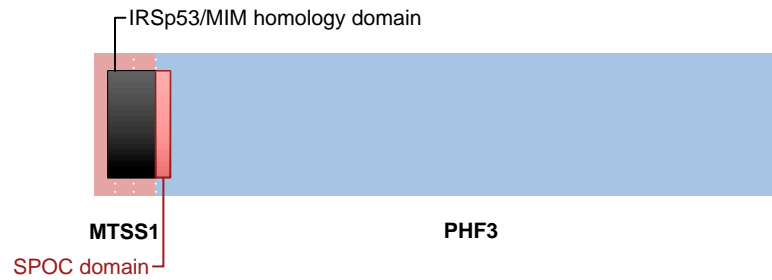
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



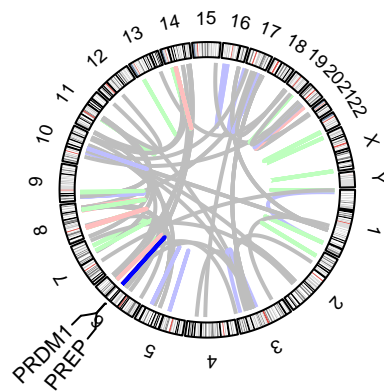
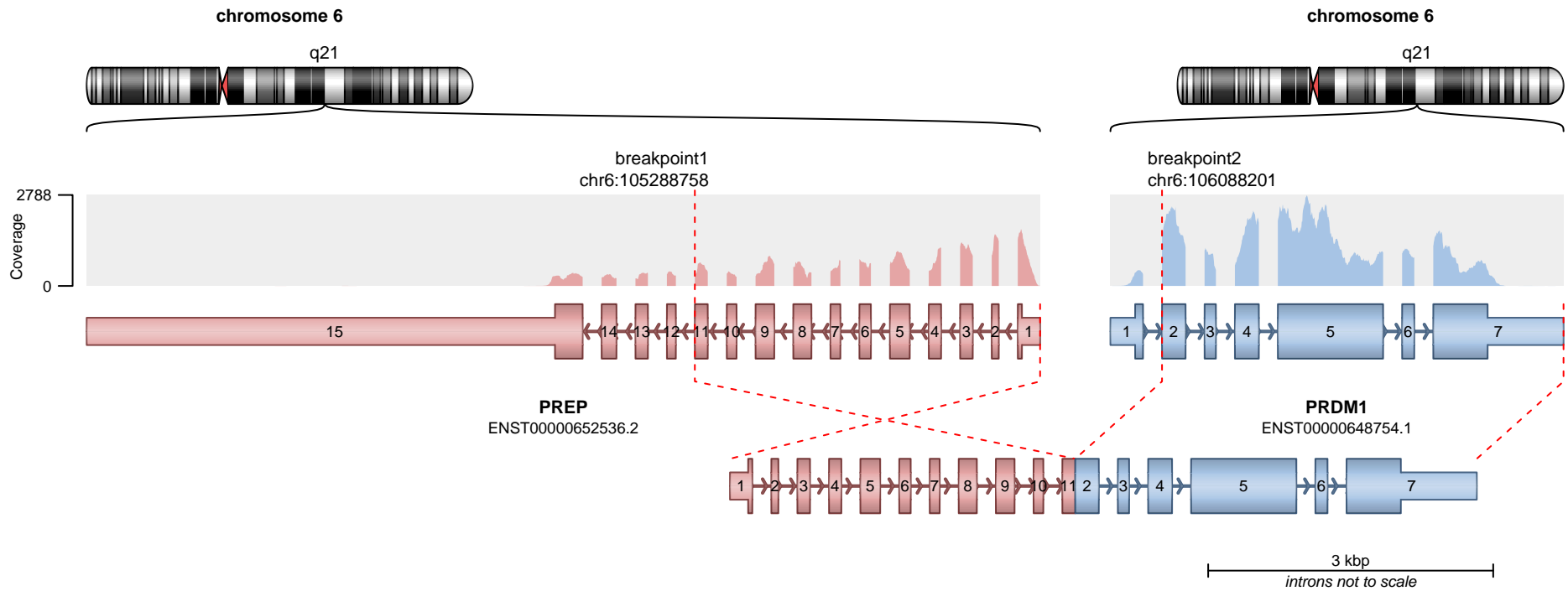
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

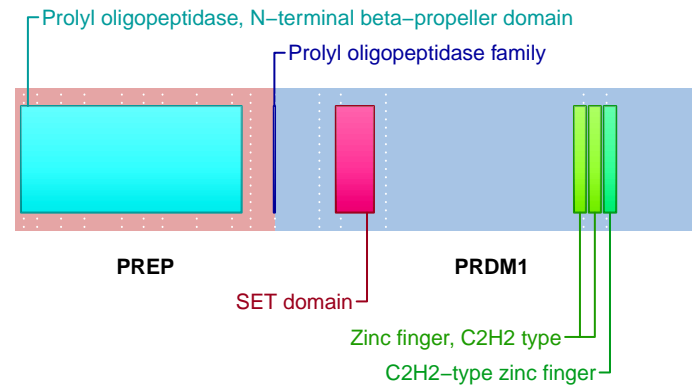
Split reads = 3
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



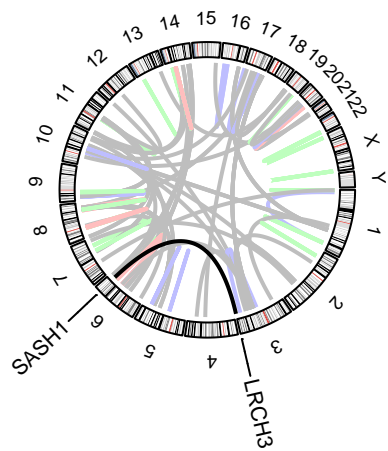
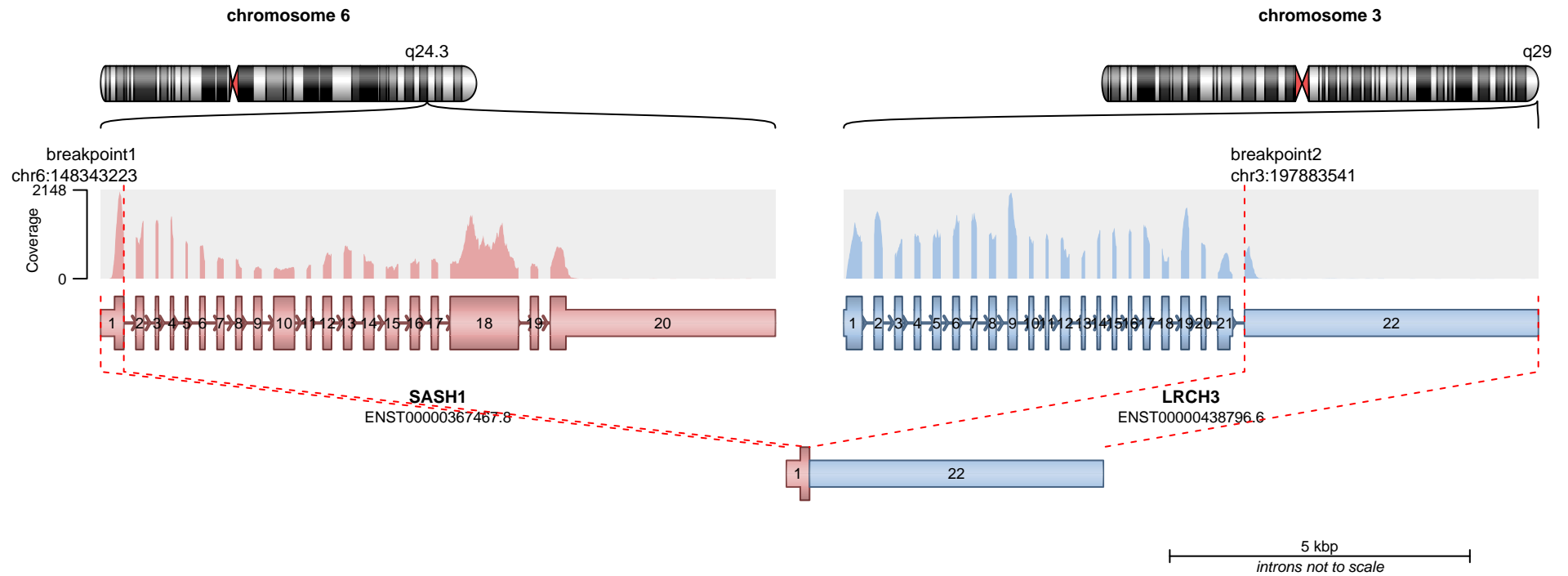
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

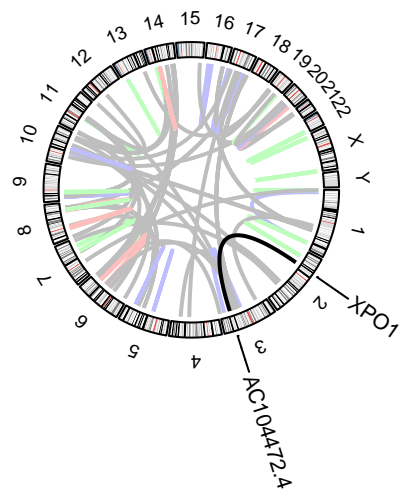
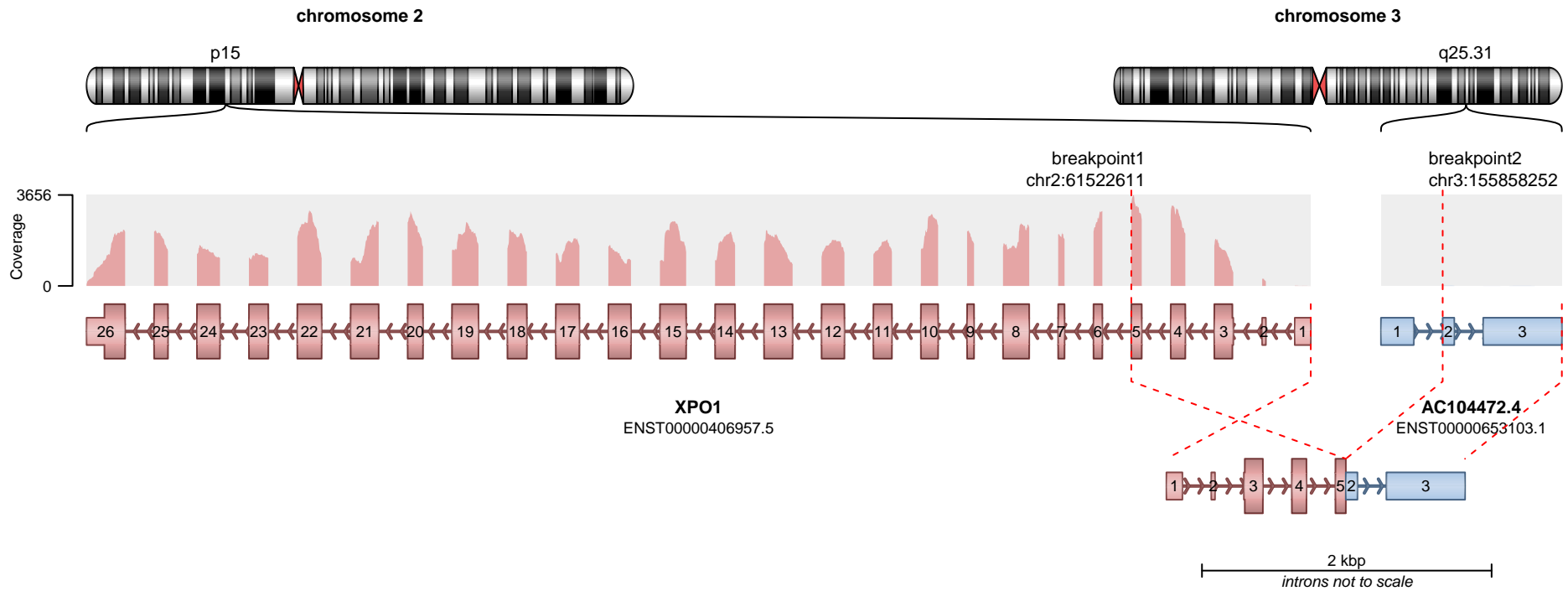


— translocation — deletion
— duplication — inversion

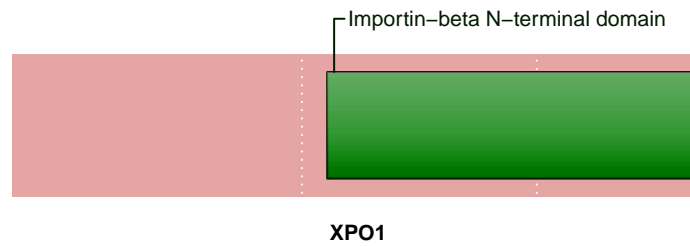
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0



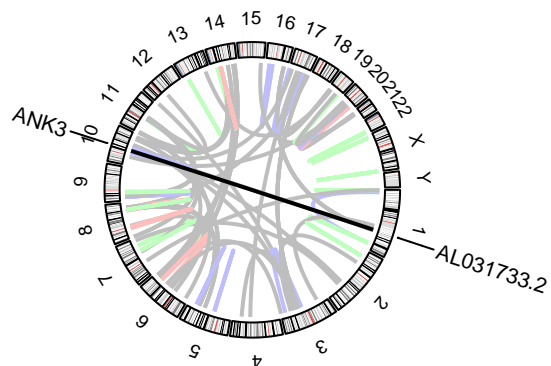
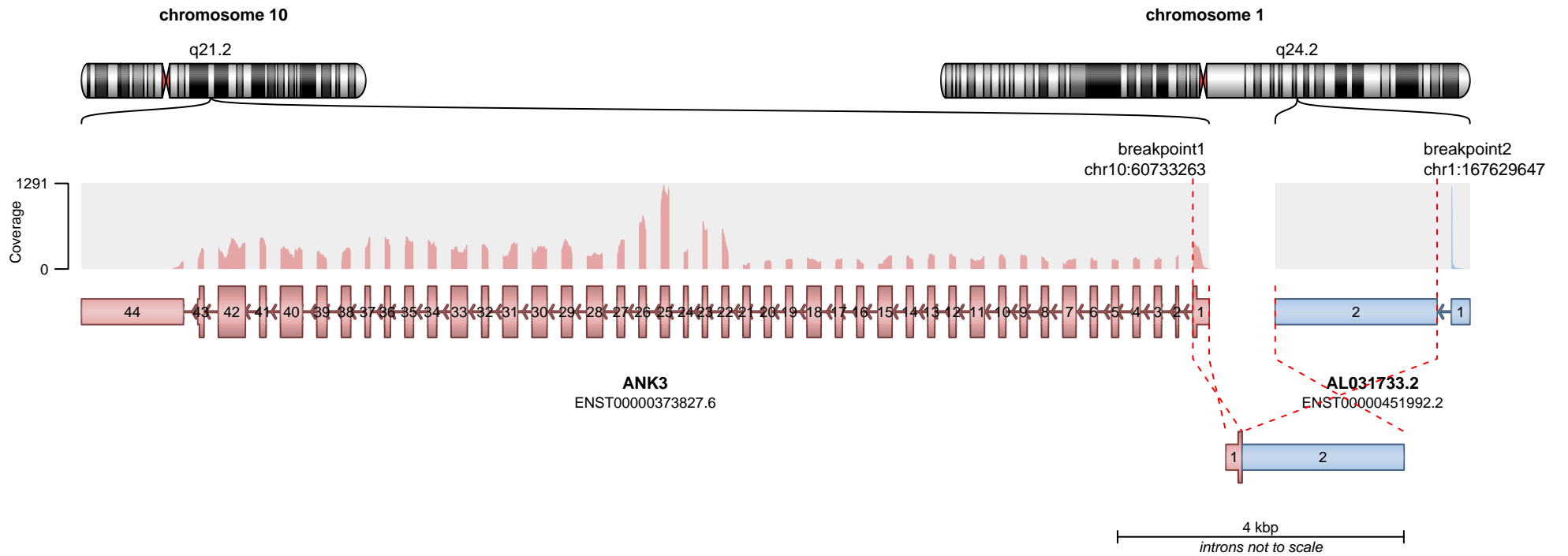
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

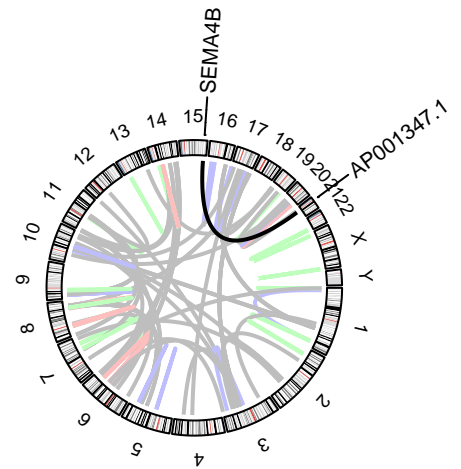
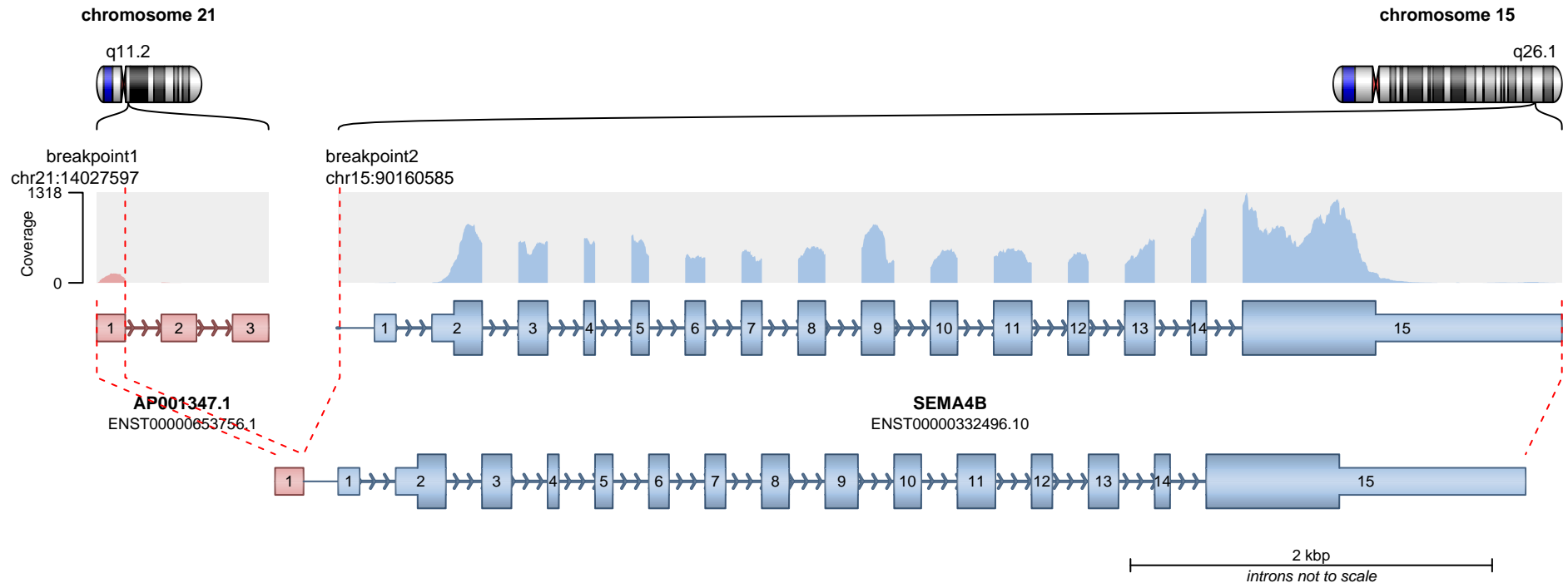


— translocation — deletion
— duplication — inversion

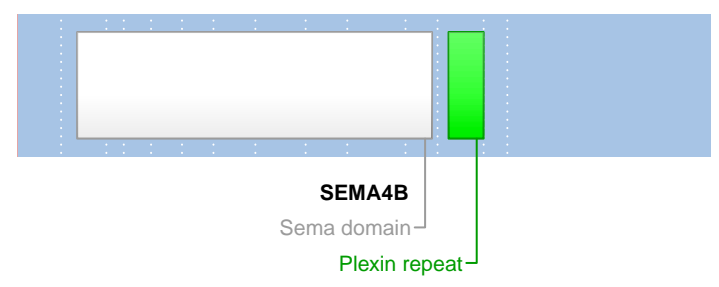
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0



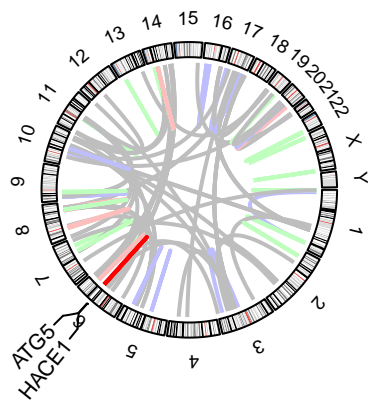
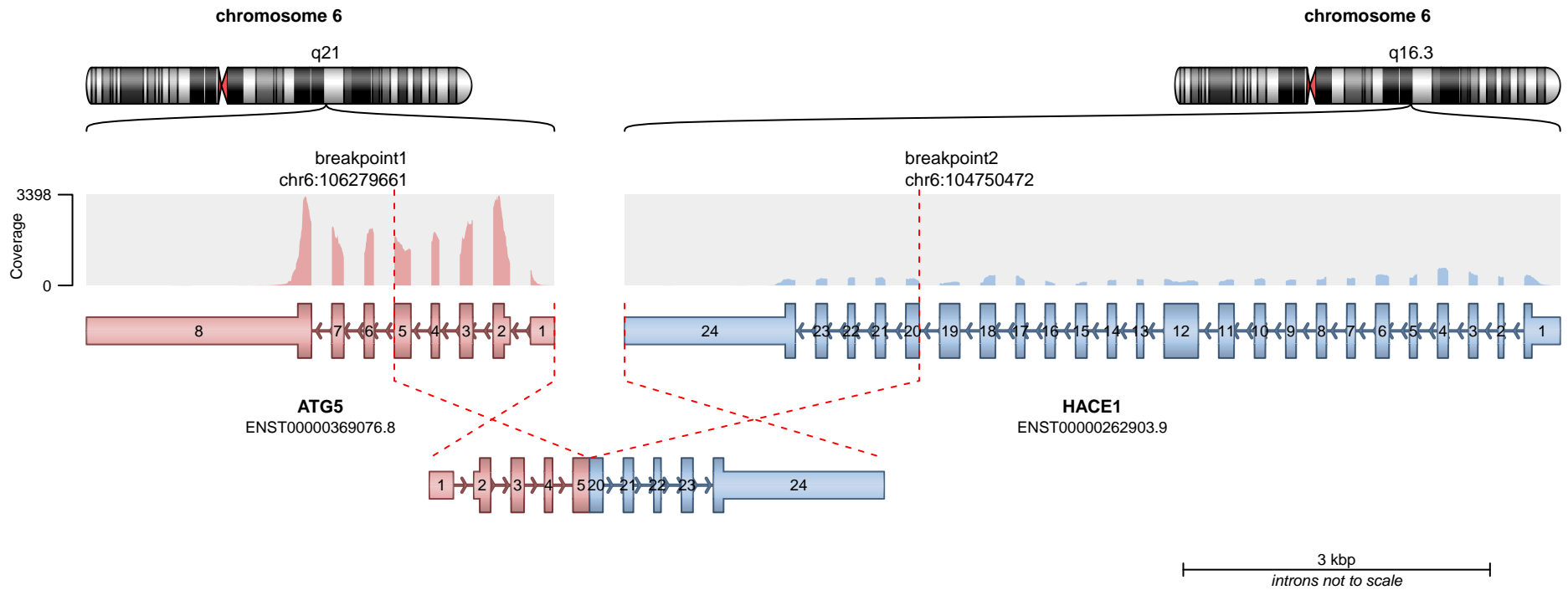
RETAINED PROTEIN DOMAINS
reading frame unclear



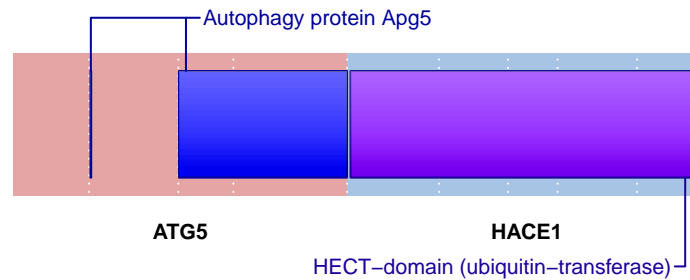
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



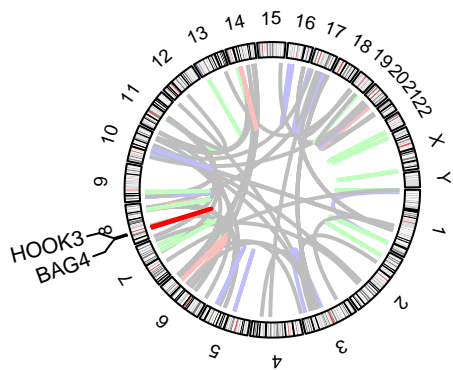
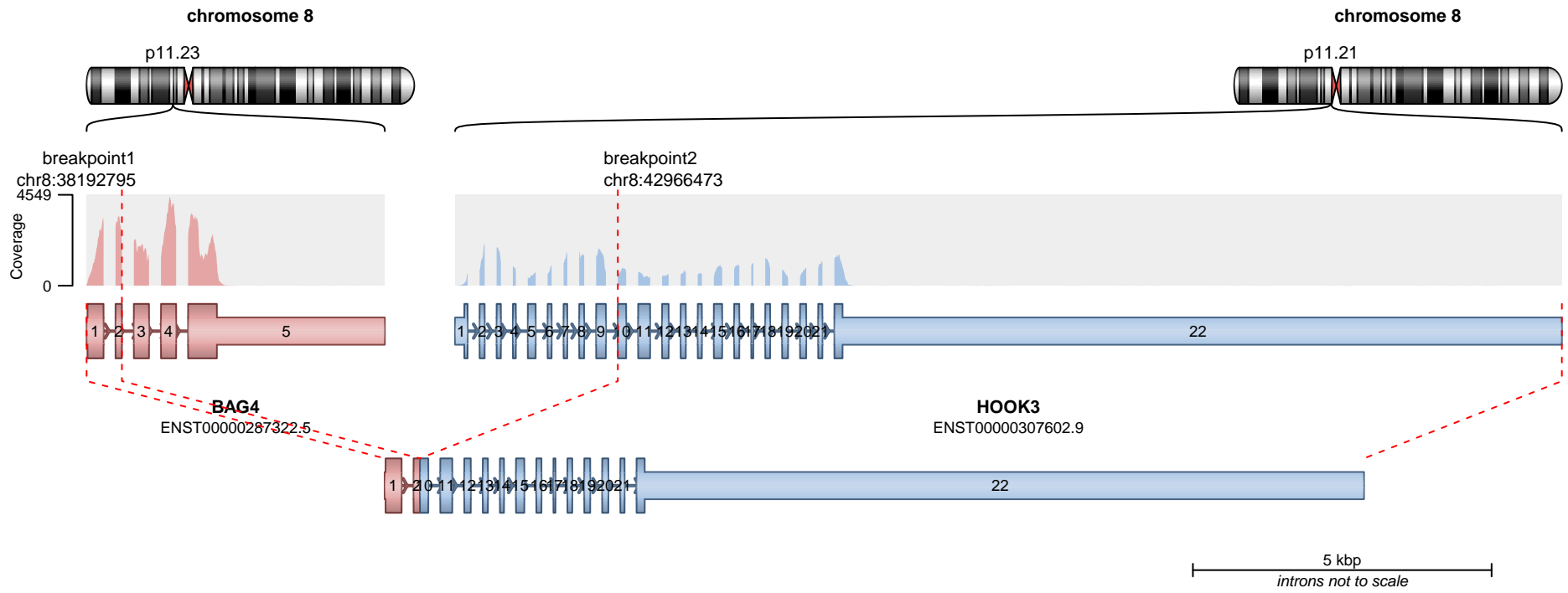
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



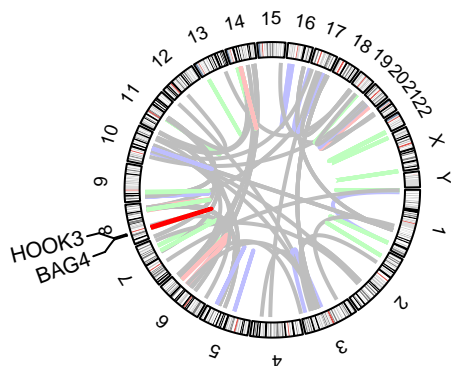
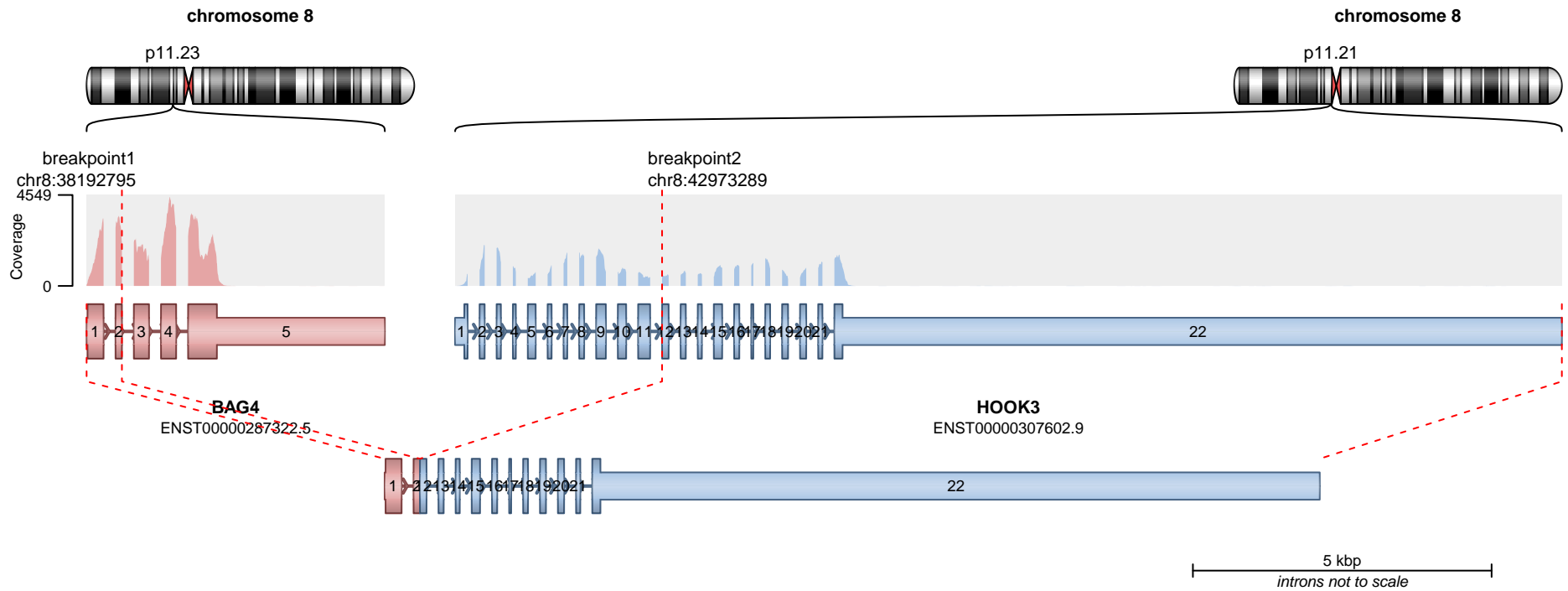
RETAINED PROTEIN DOMAINS
reading frame unclear



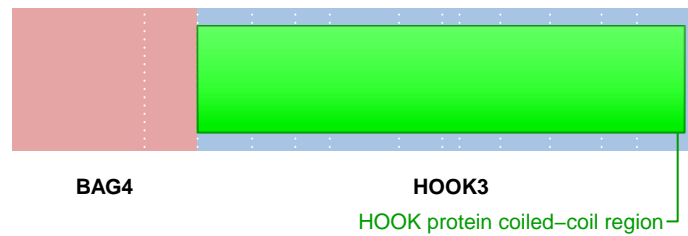
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



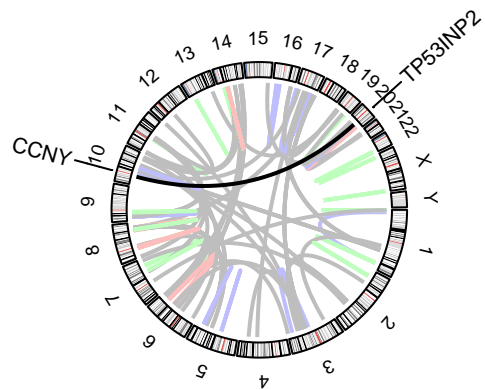
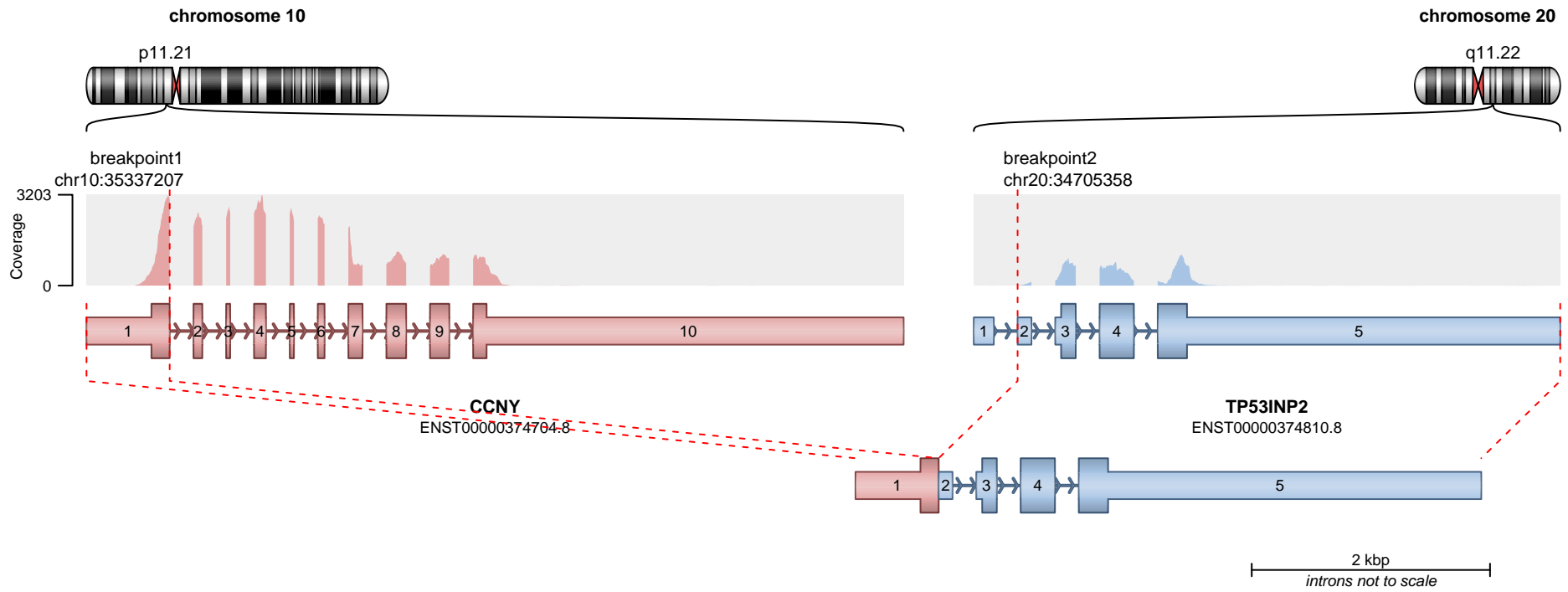
RETAINED PROTEIN DOMAINS
reading frame unclear



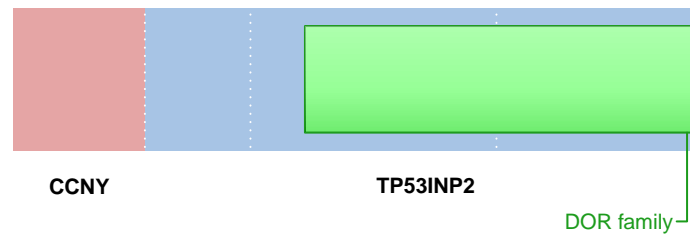
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



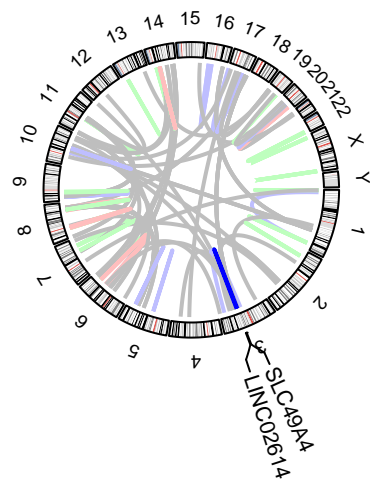
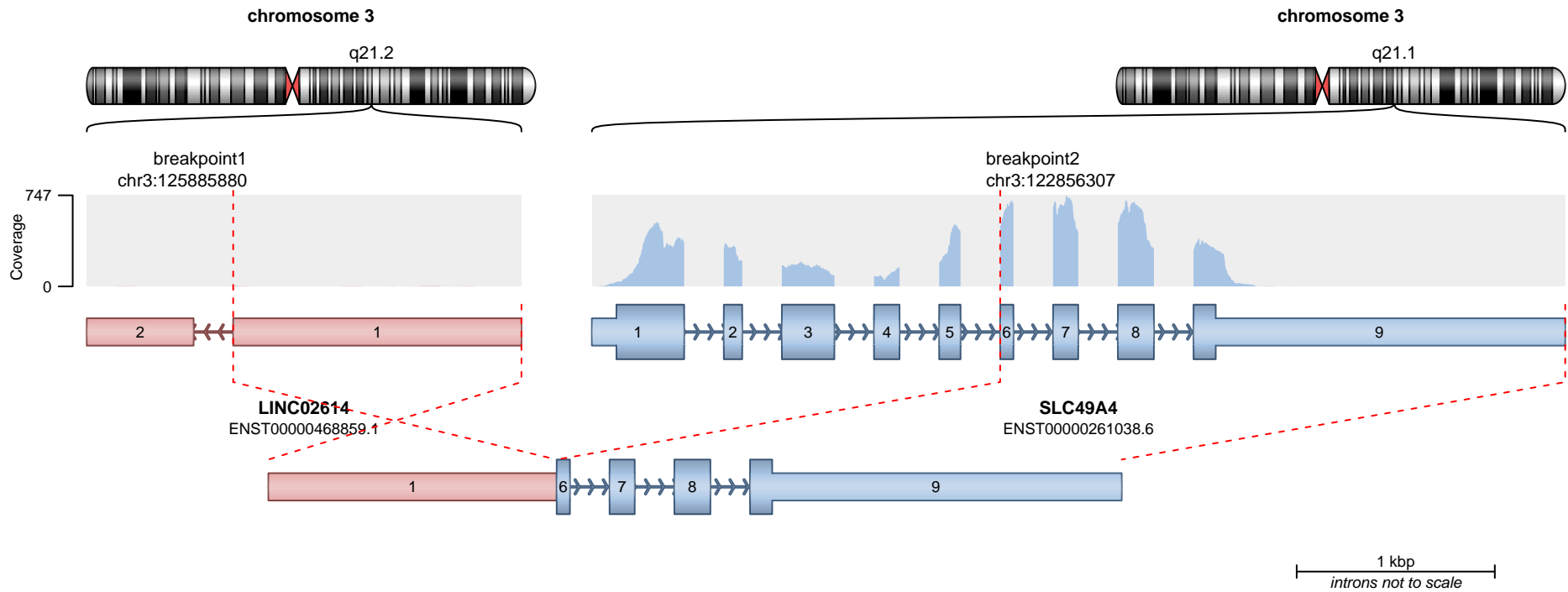
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

— translocation — deletion
— duplication — inversion

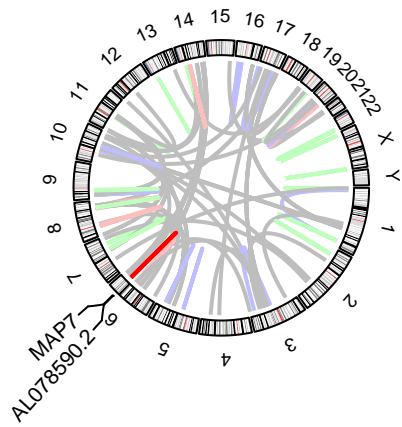
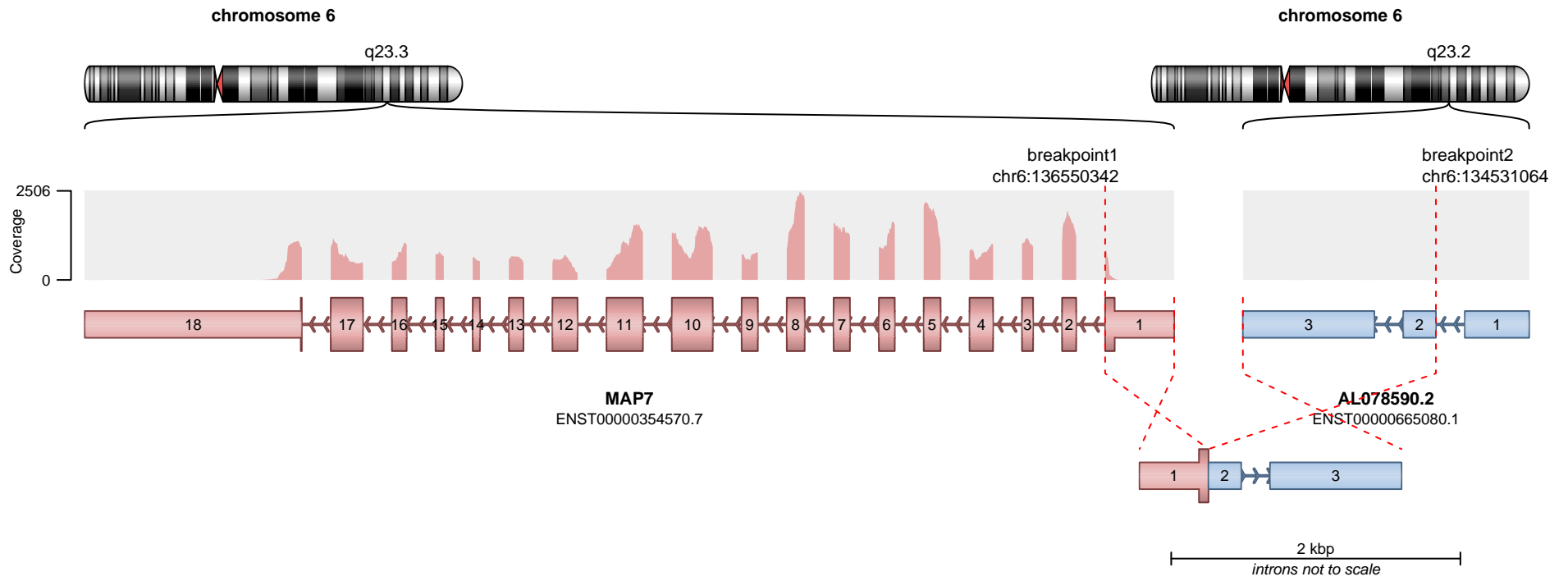


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

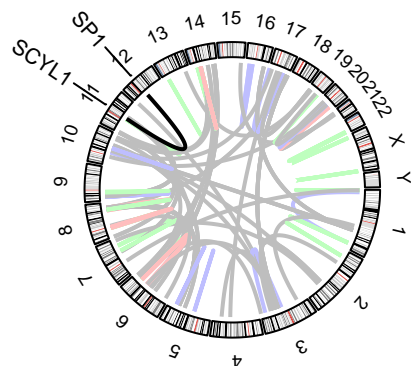
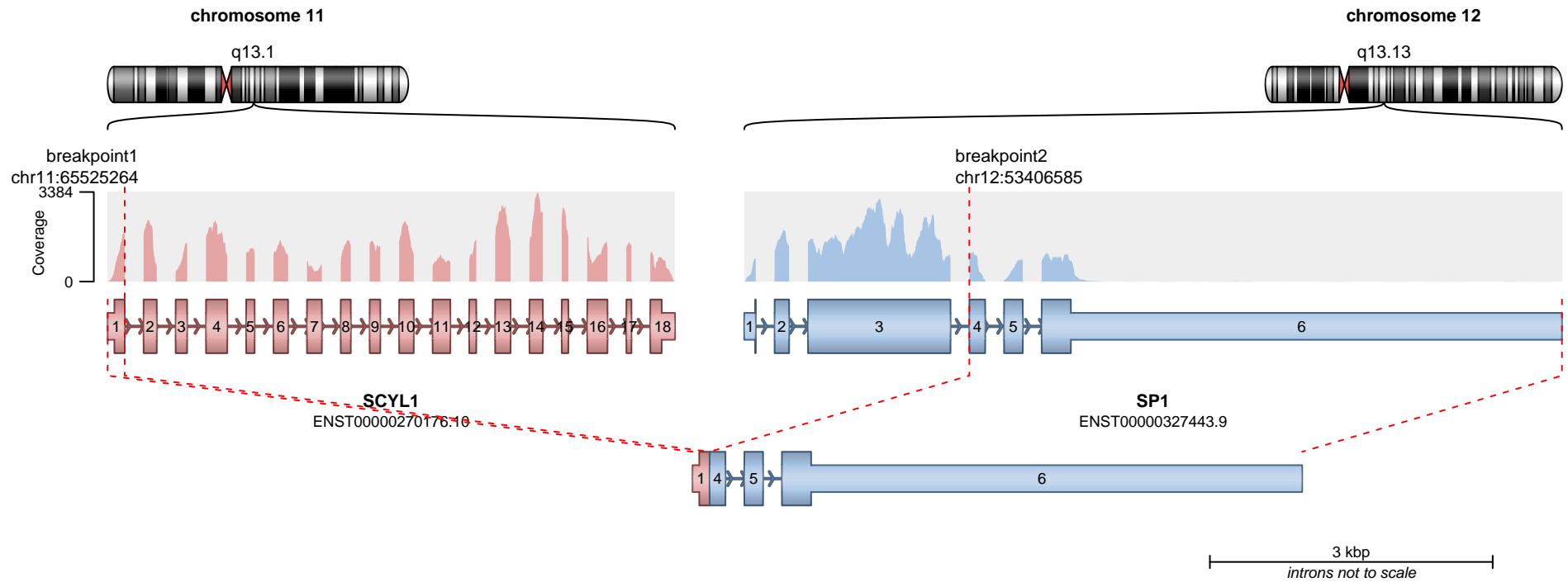


— translocation — deletion
— duplication — inversion

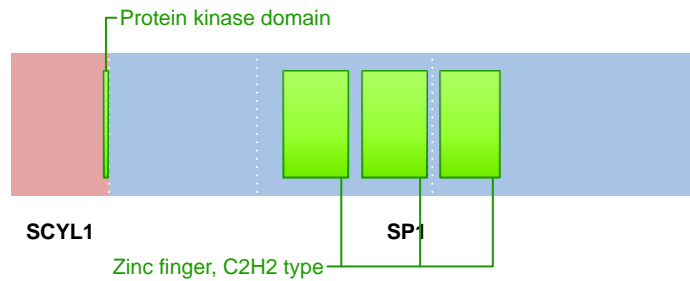
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0



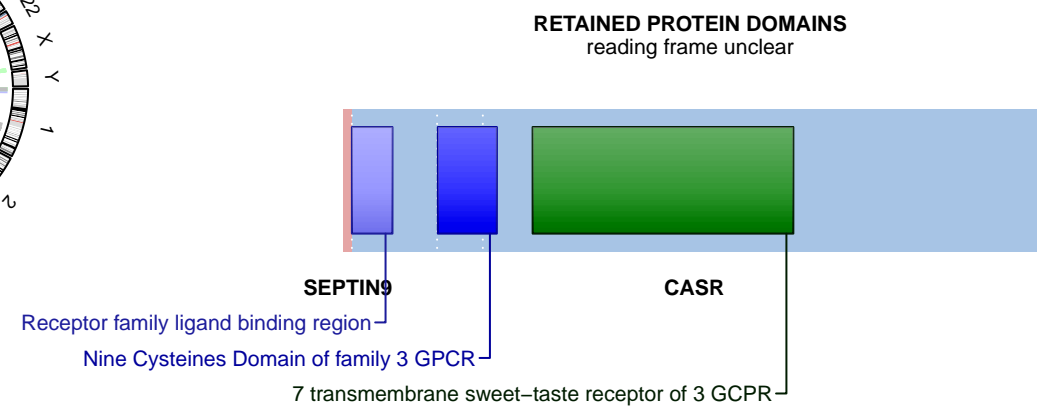
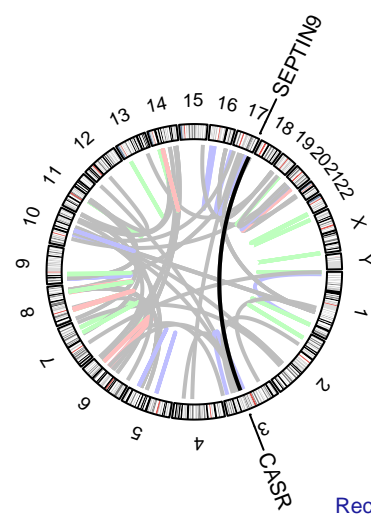
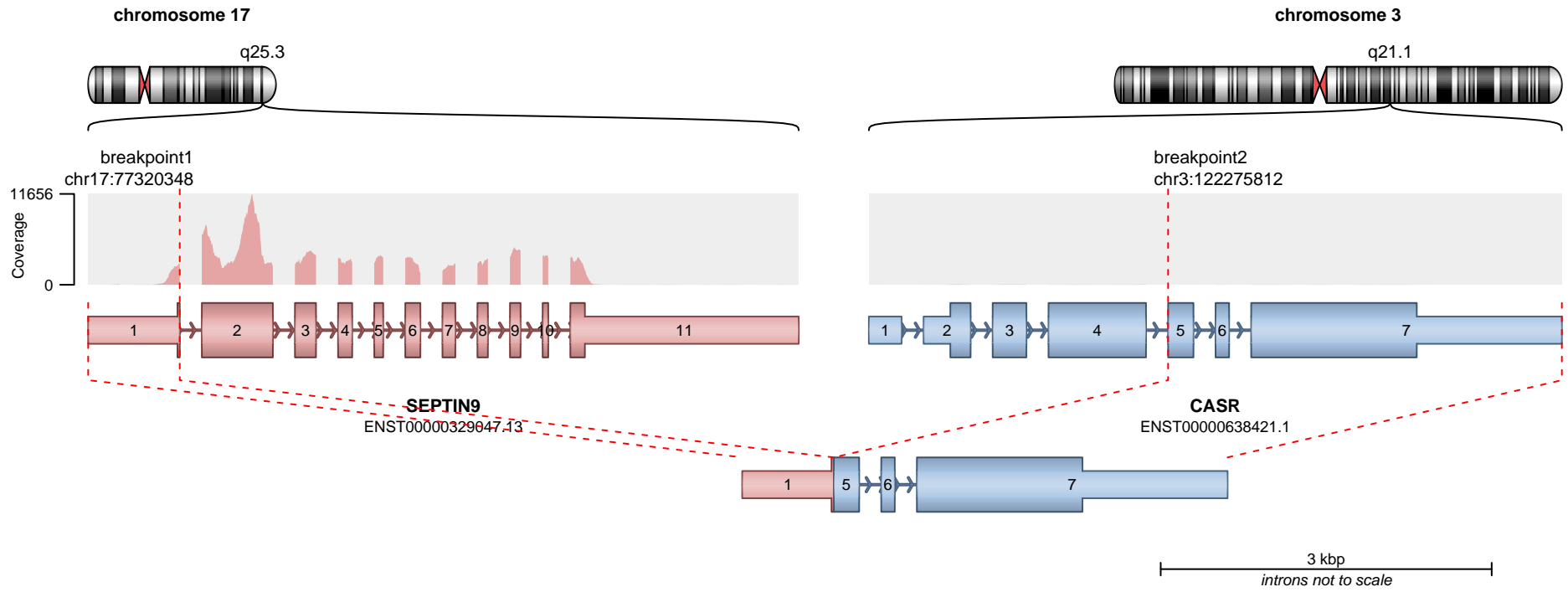
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

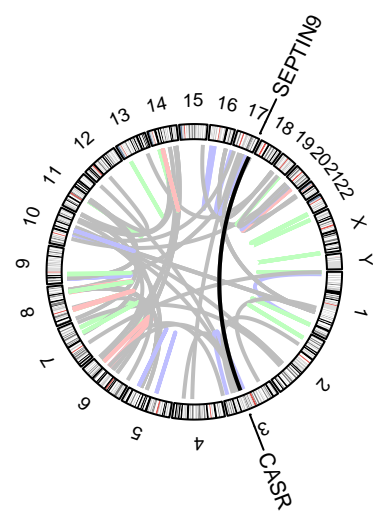
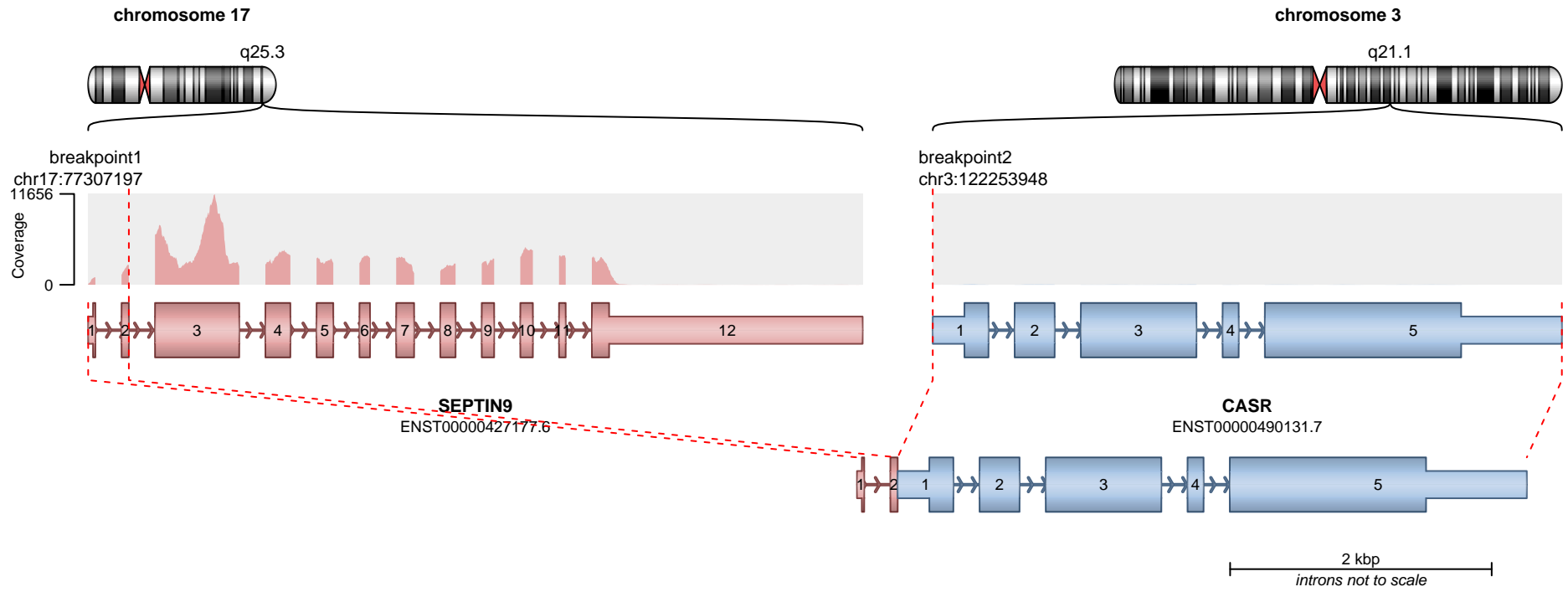
— translocation — deletion
— duplication — inversion



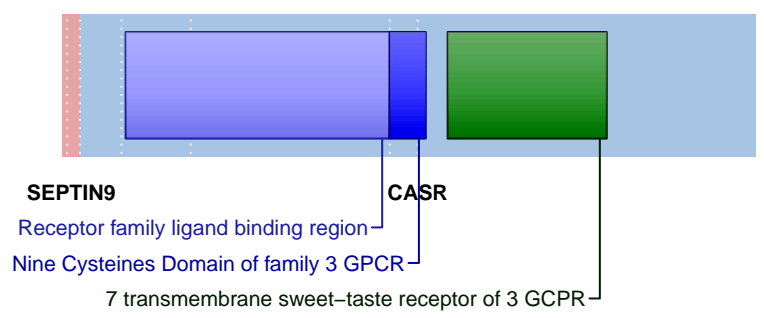
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

— translocation — deletion
— duplication — inversion



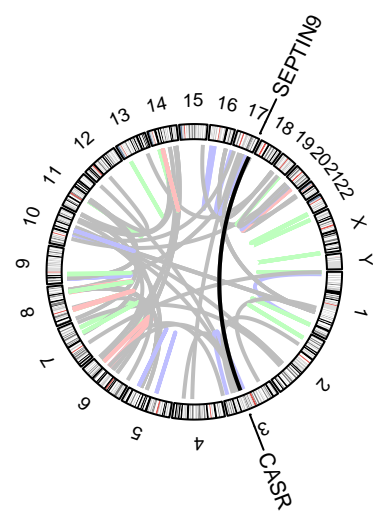
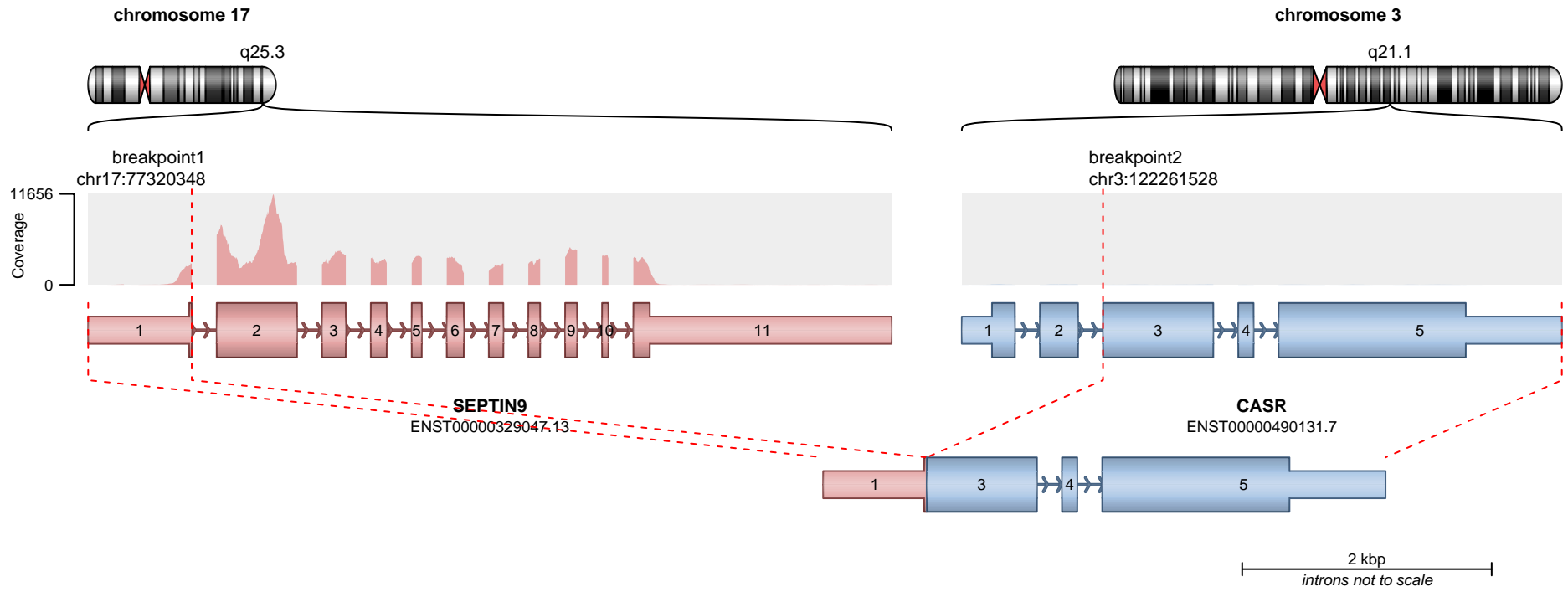
RETAINED PROTEIN DOMAINS
reading frame unclear



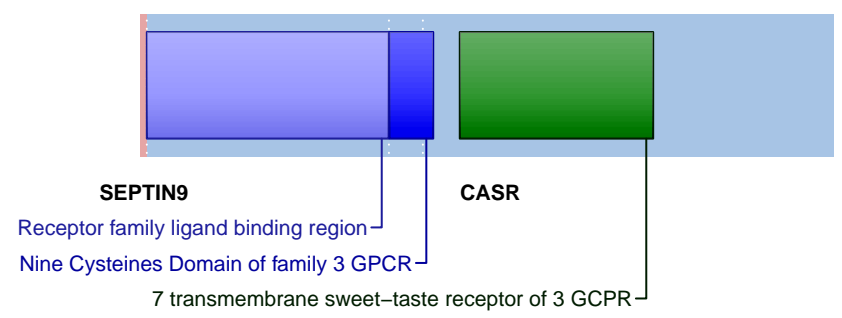
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



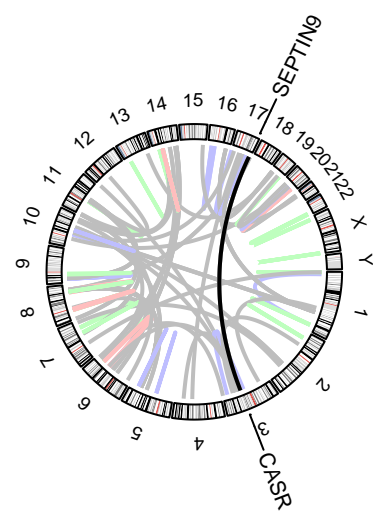
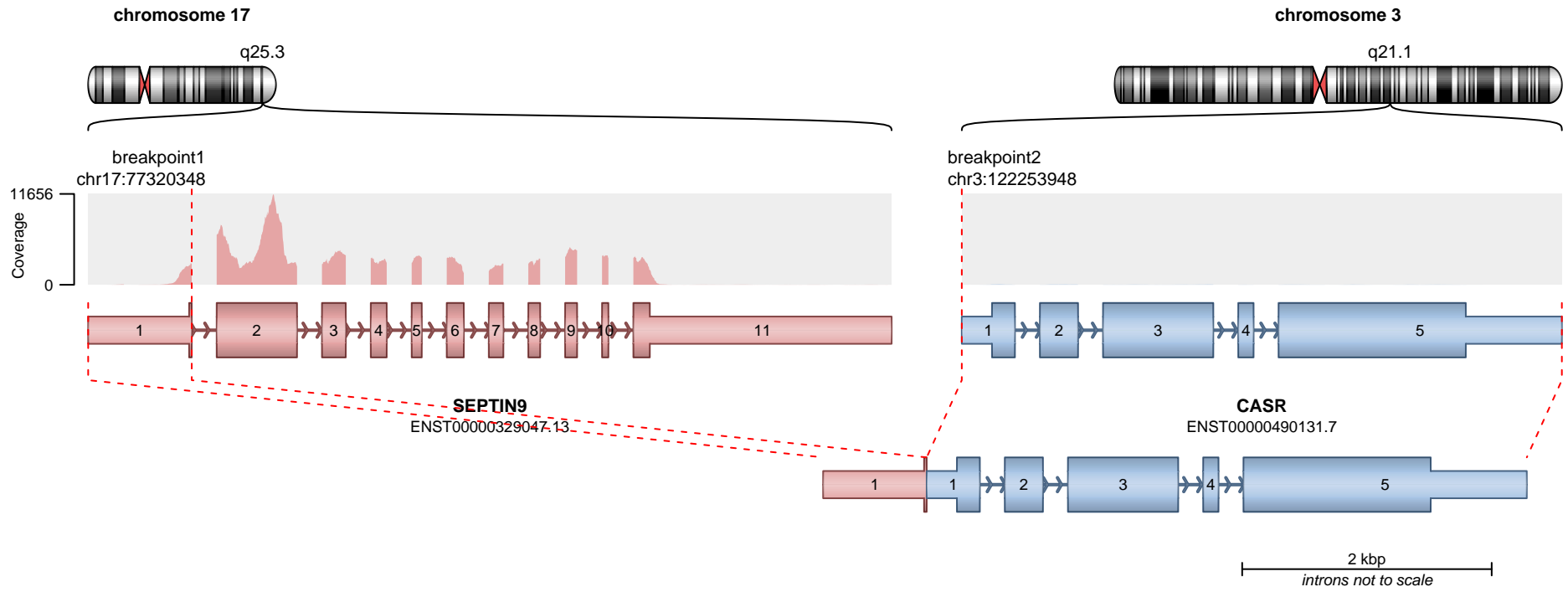
RETAINED PROTEIN DOMAINS
reading frame unclear



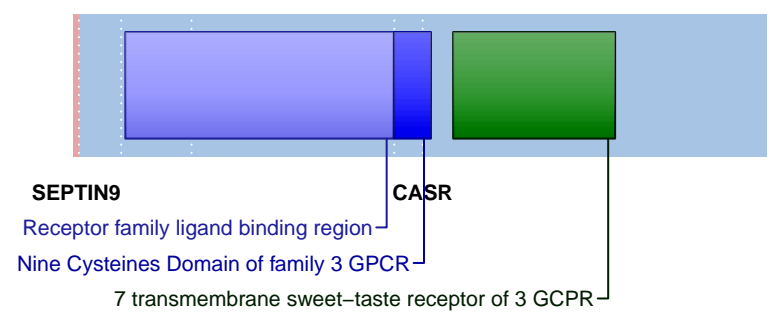
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



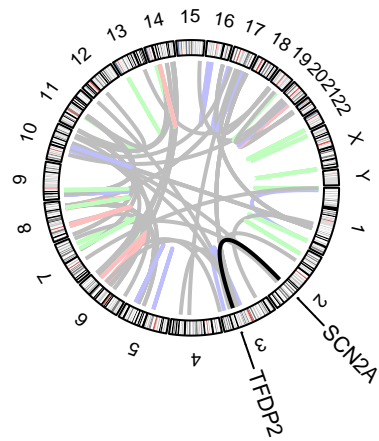
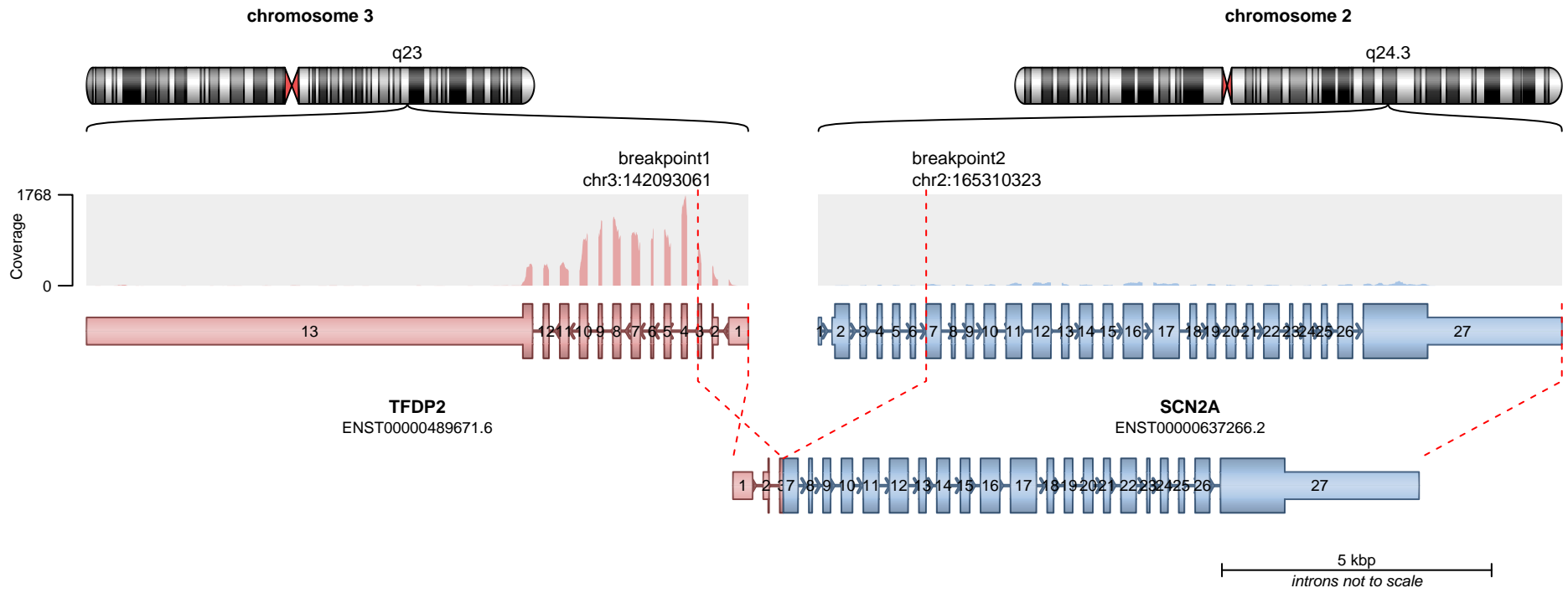
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

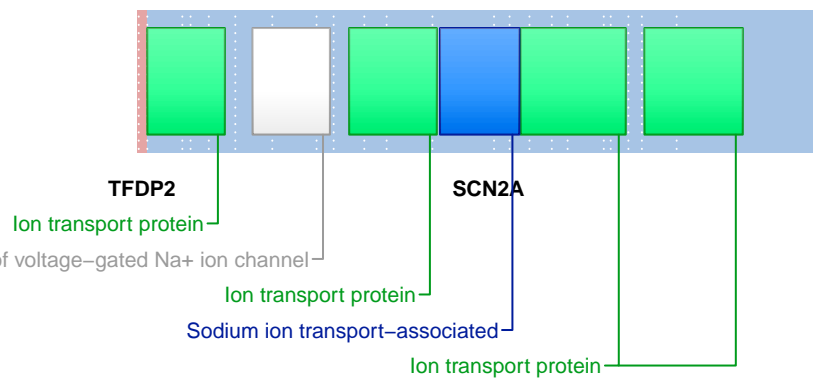
Split reads = 1
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



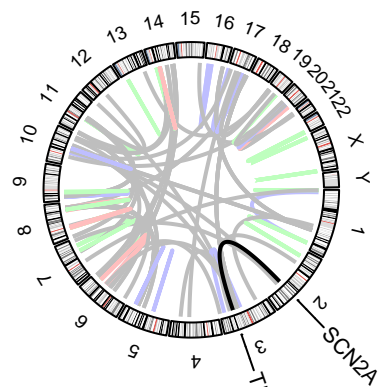
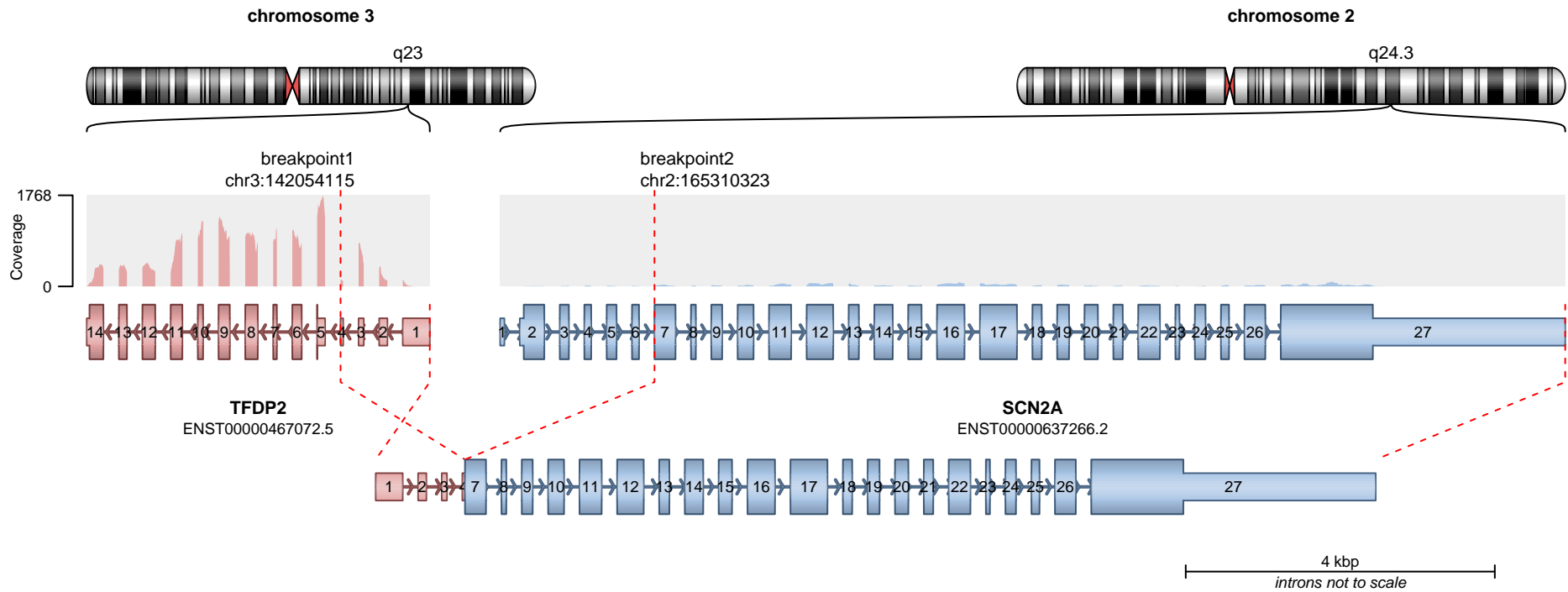
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



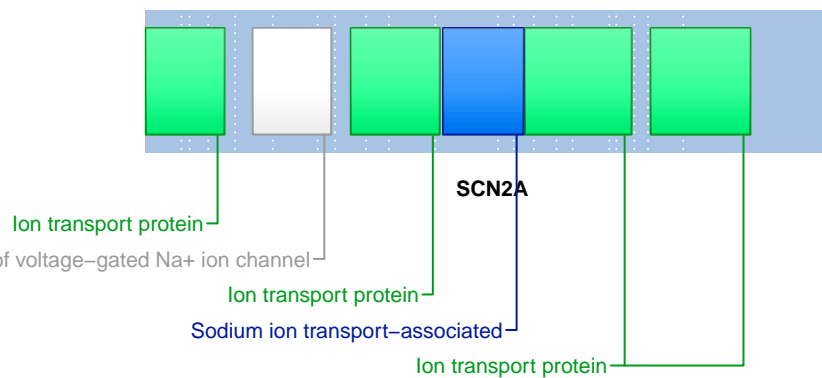
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0



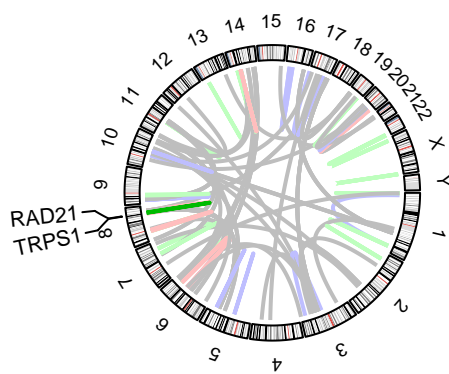
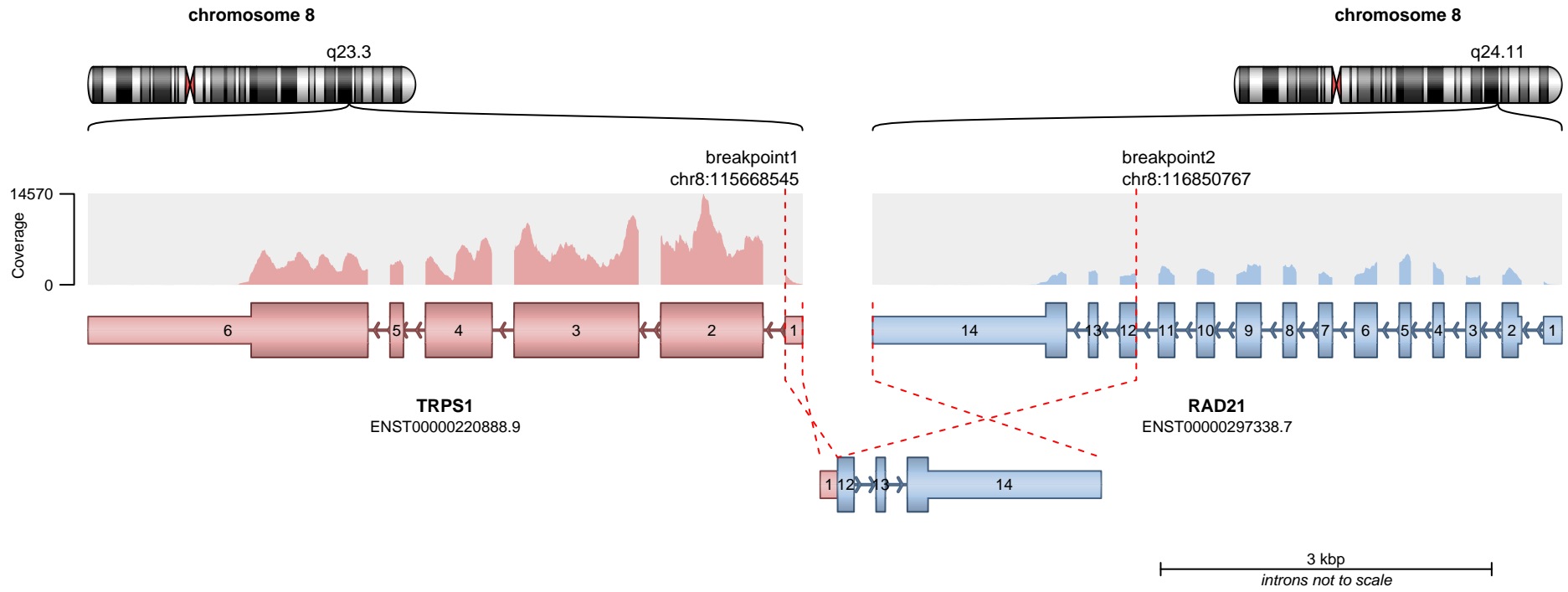
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear

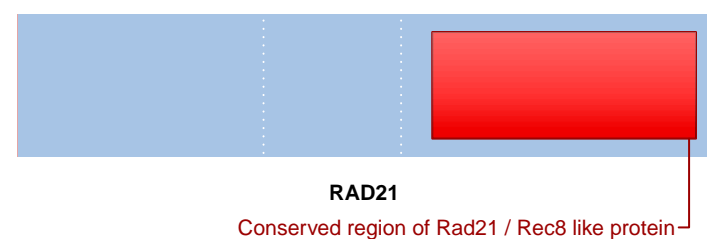


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



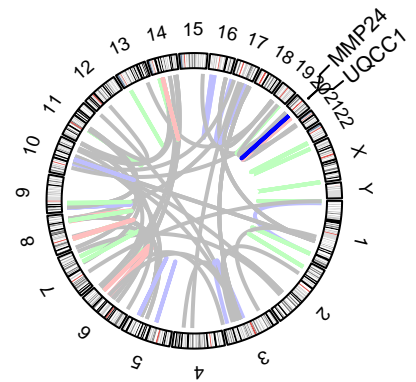
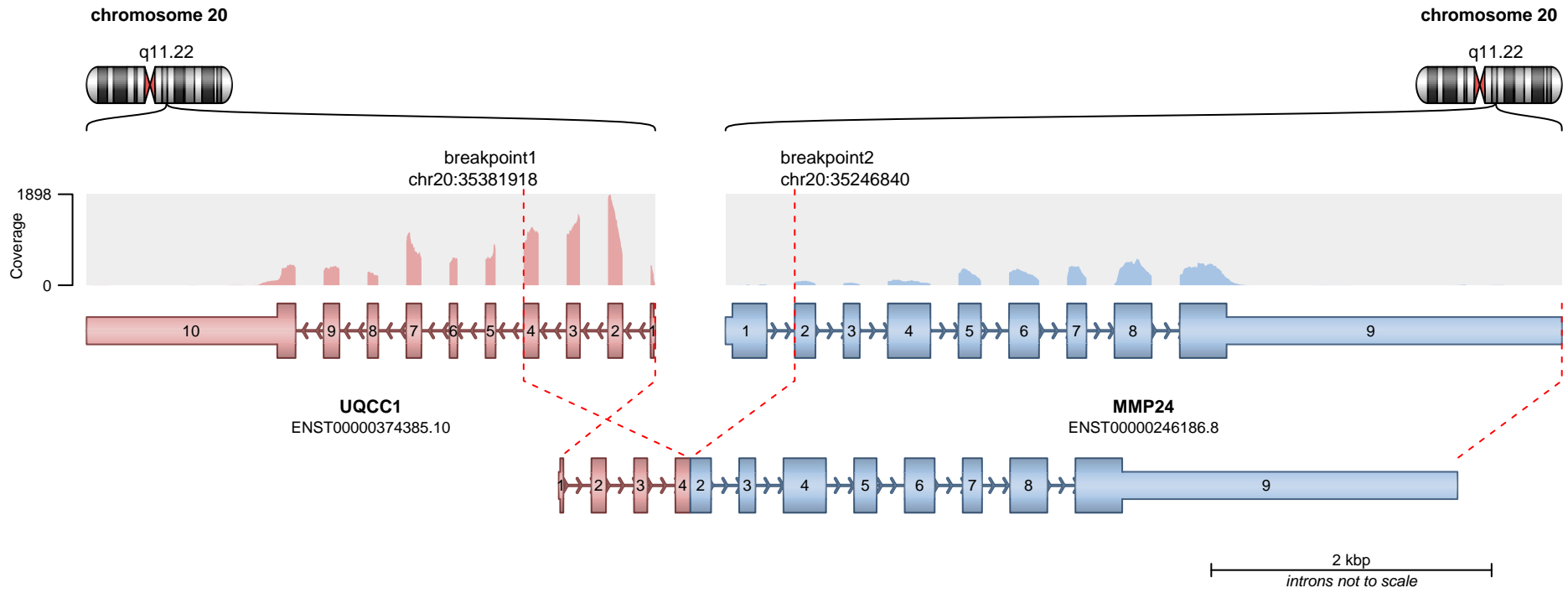
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

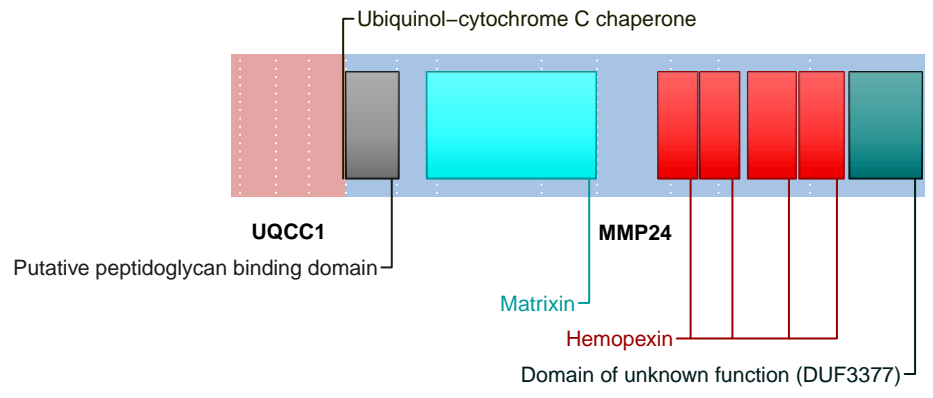
Split reads = 3
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



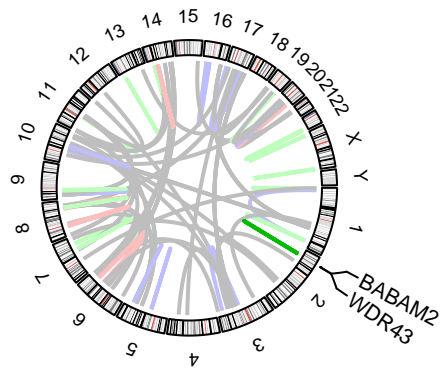
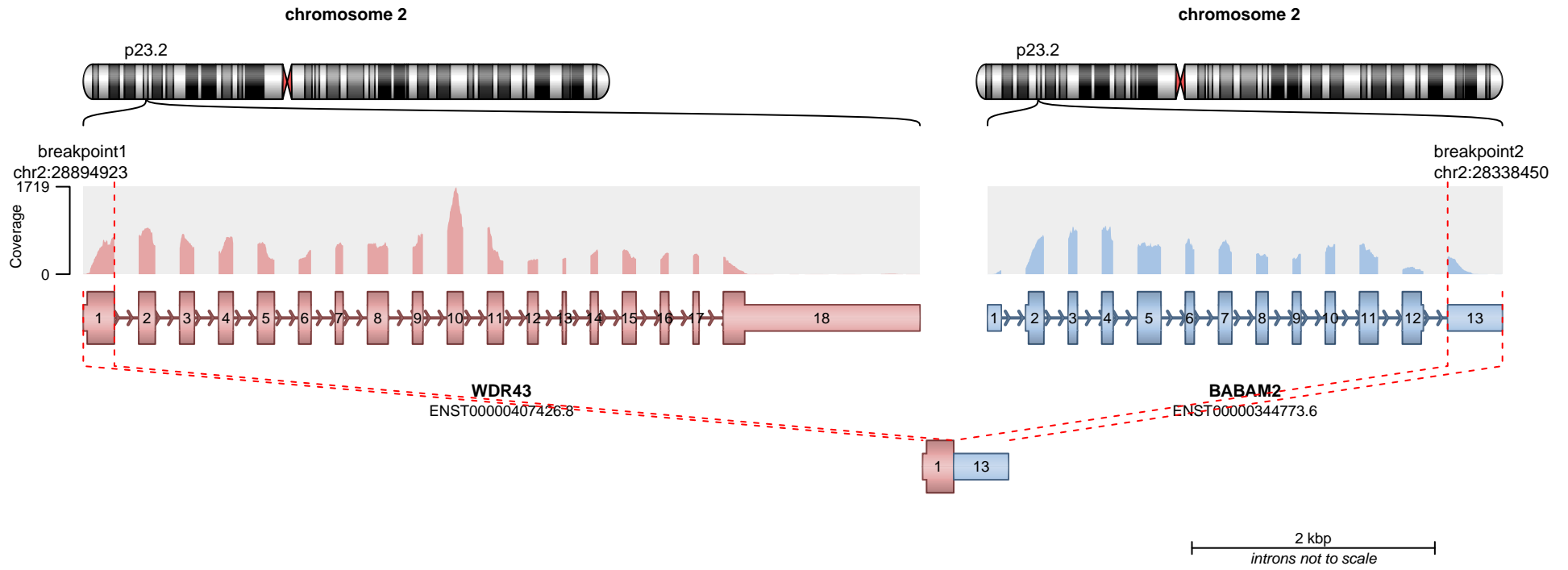
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

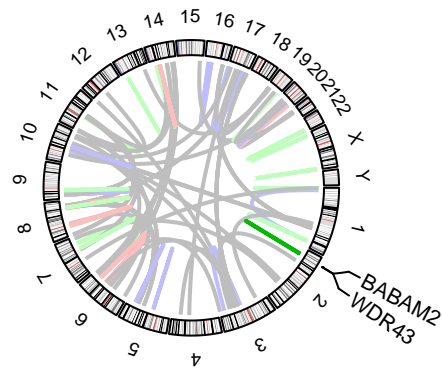
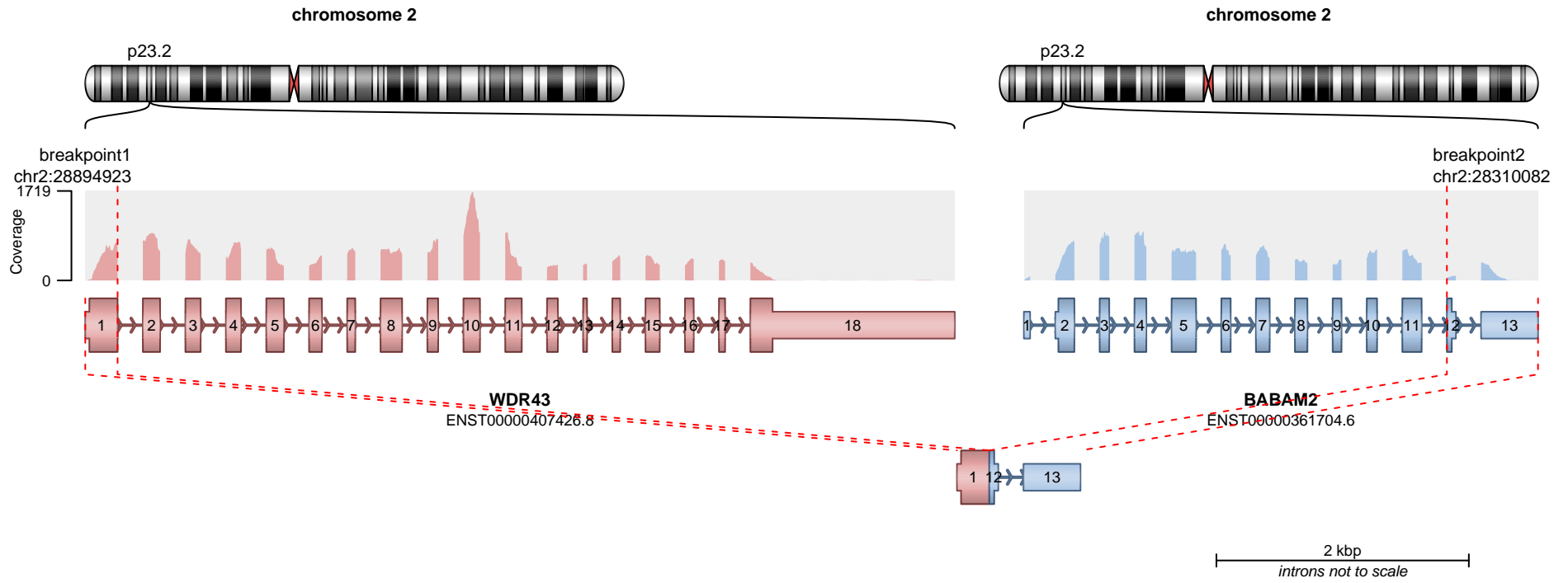


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

— translocation — deletion
— duplication — inversion

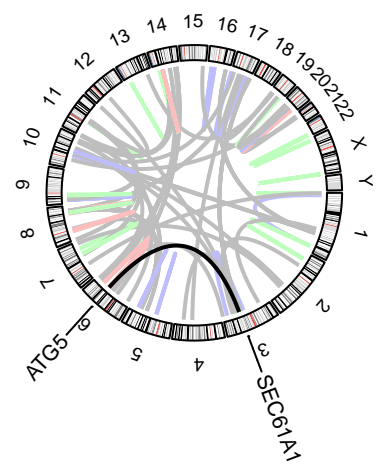
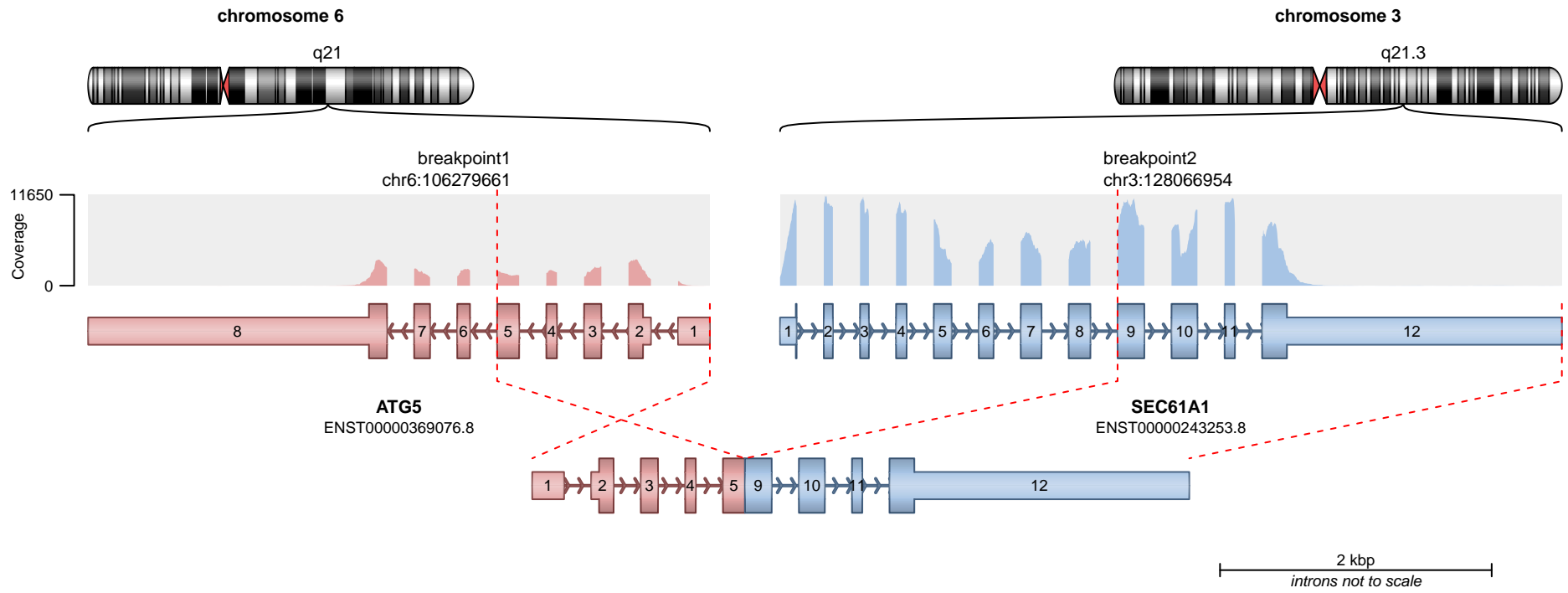


No protein domains retained in fusion.

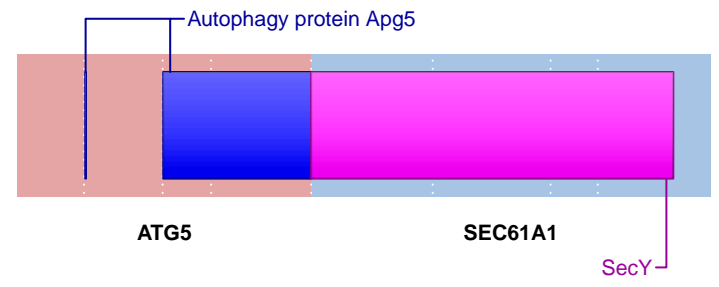
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



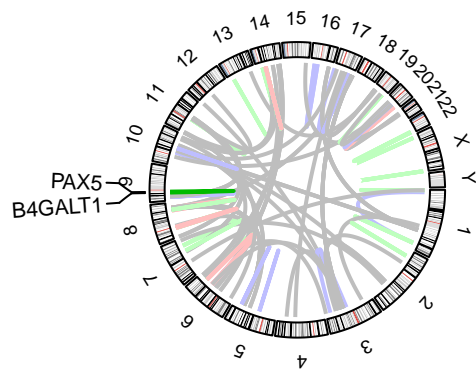
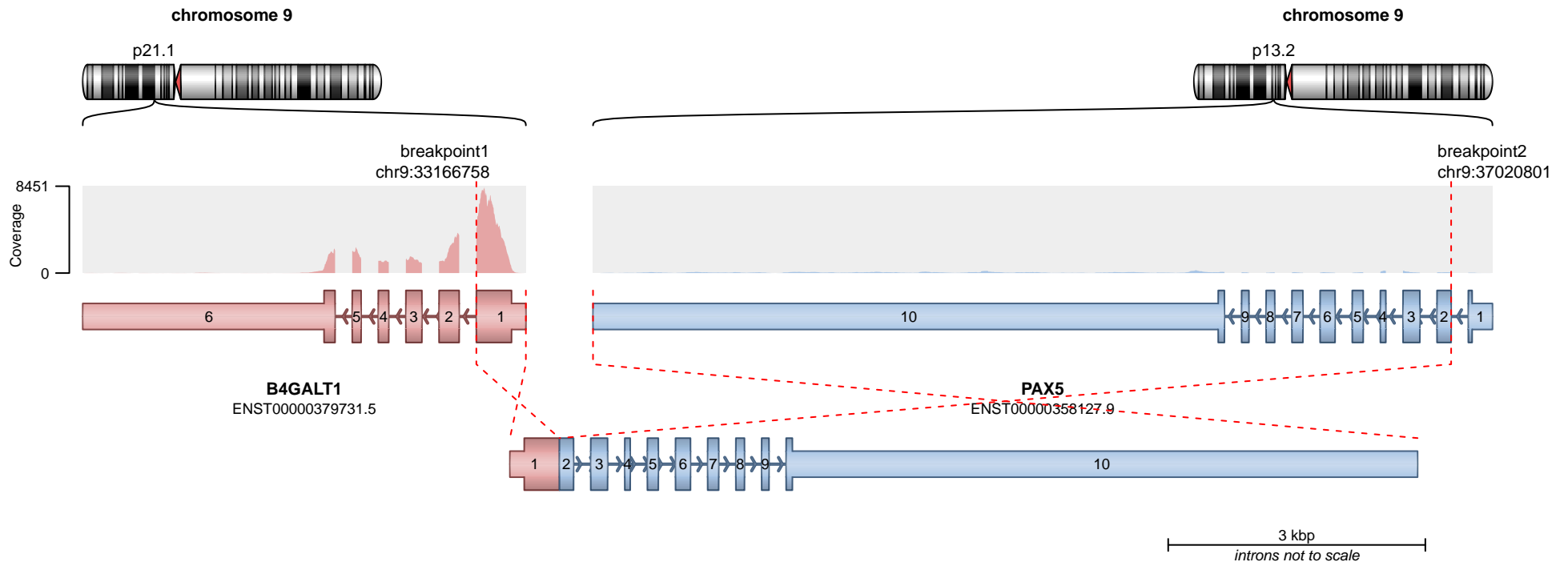
RETAINED PROTEIN DOMAINS
reading frame unclear



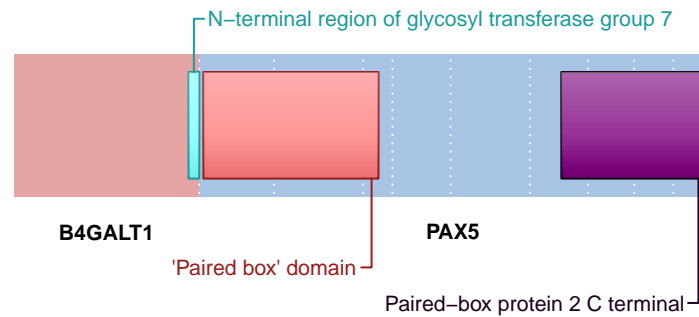
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



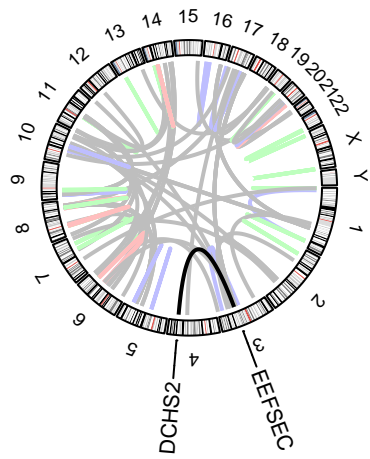
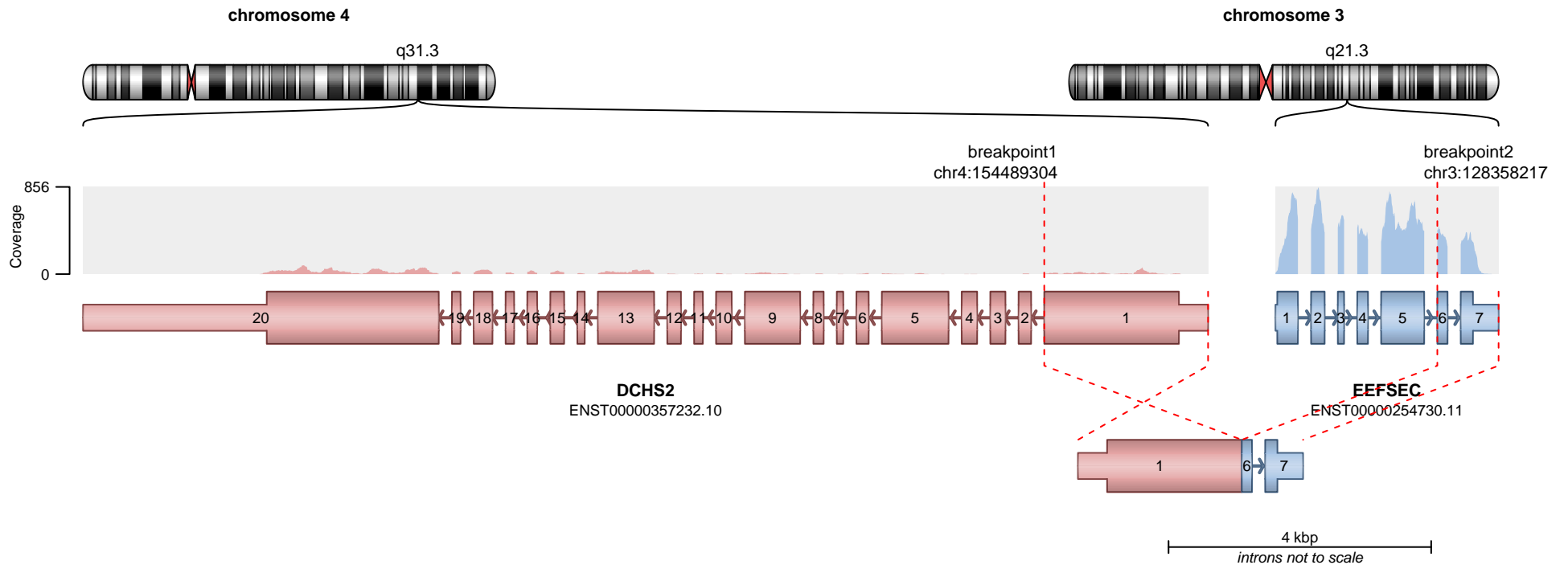
RETAINED PROTEIN DOMAINS
reading frame unclear



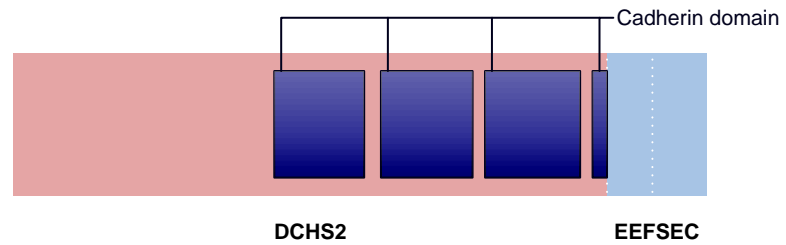
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



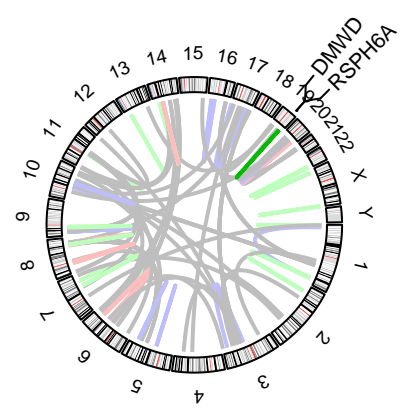
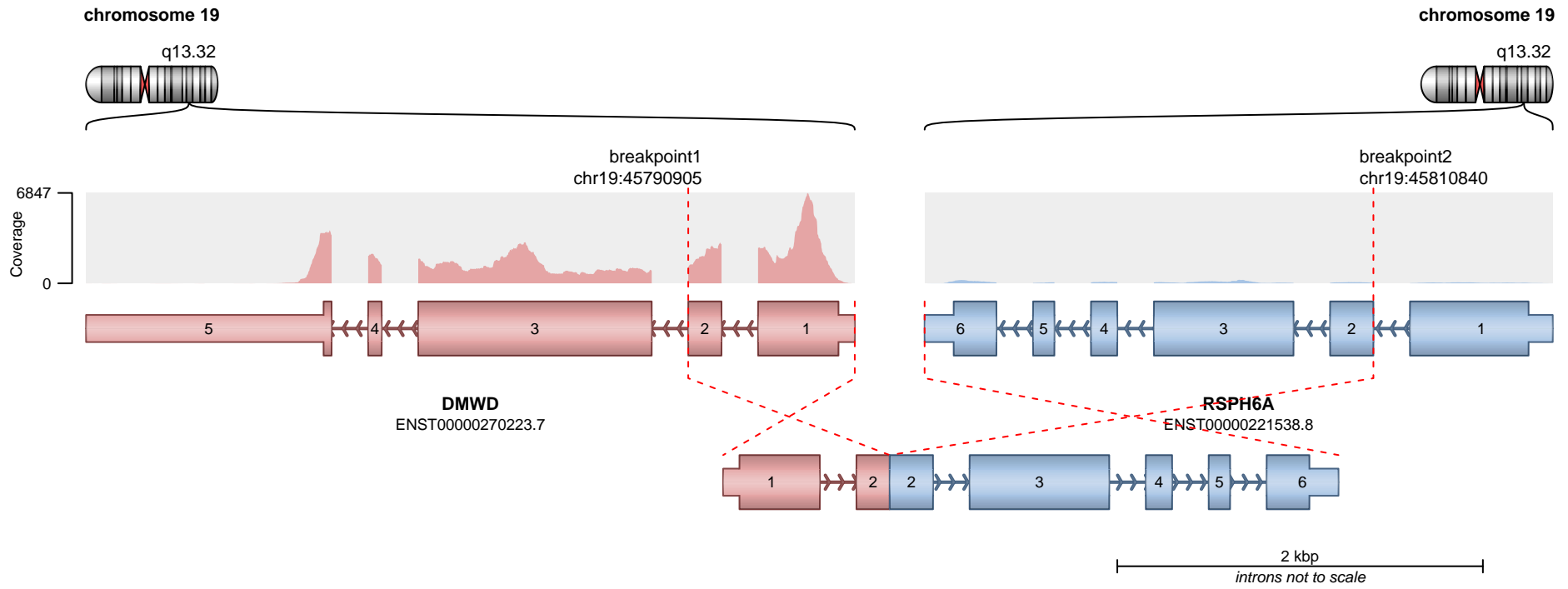
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



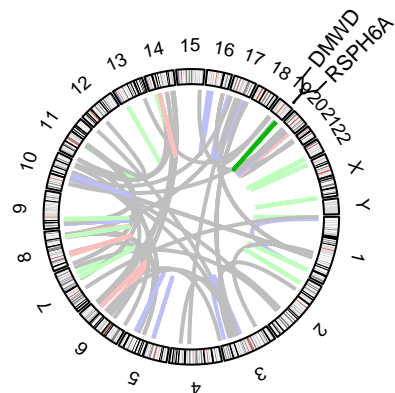
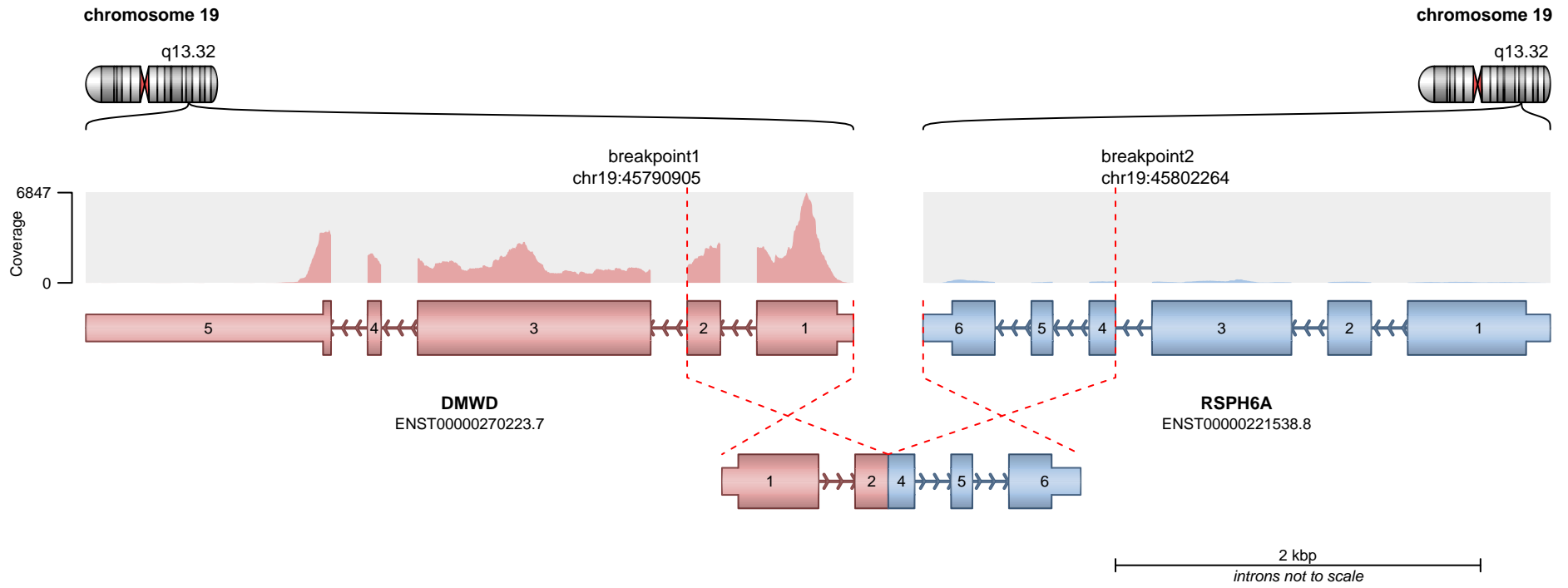
RETAINED PROTEIN DOMAINS
reading frame unclear



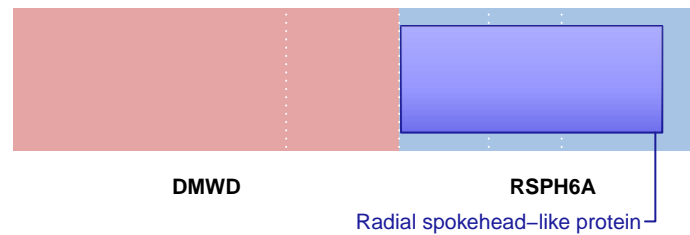
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

— translocation — deletion
— duplication — inversion



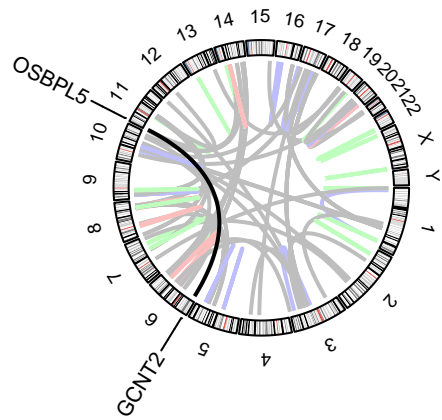
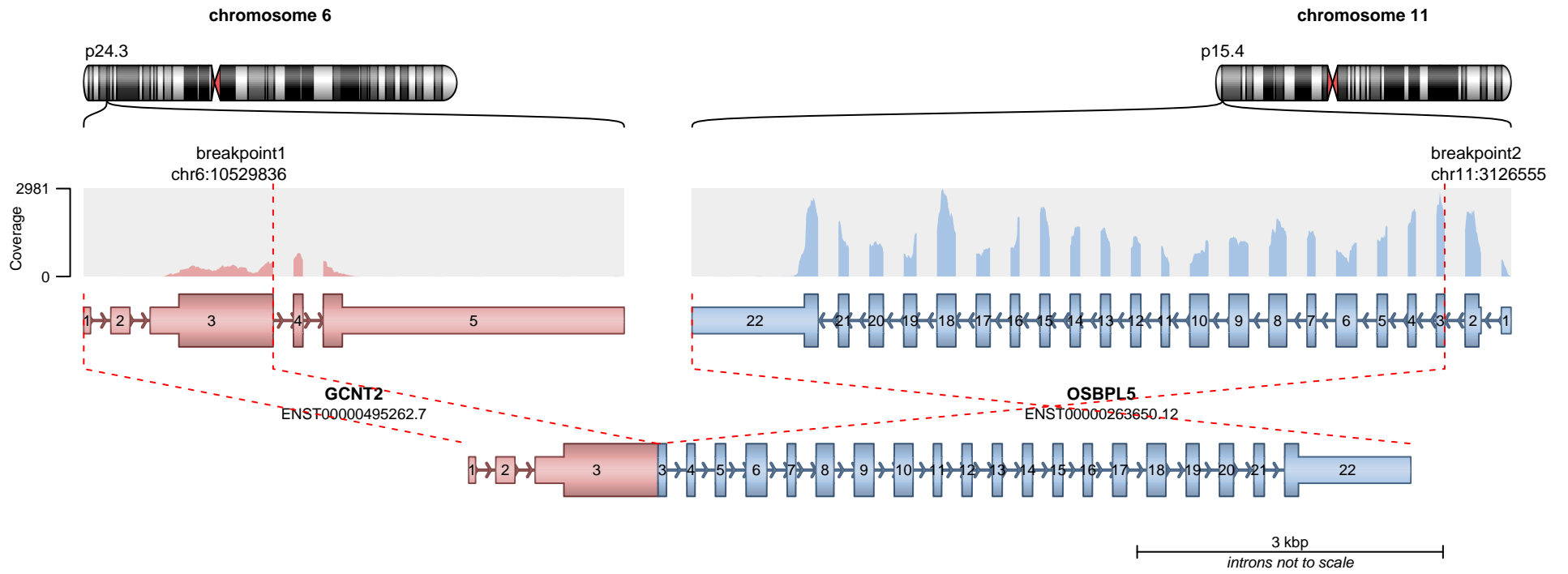
RETAINED PROTEIN DOMAINS
reading frame unclear



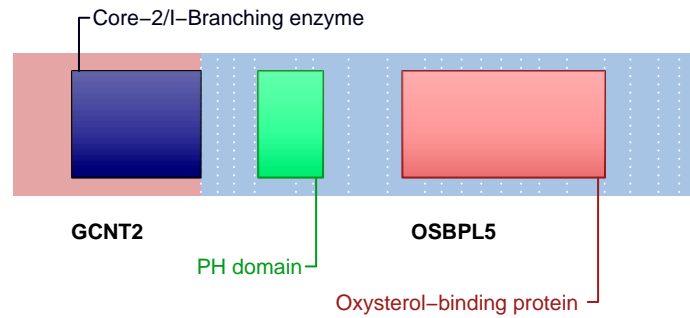
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



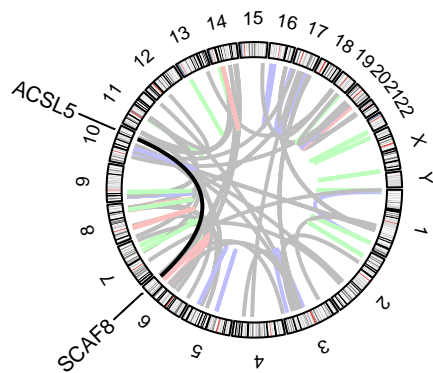
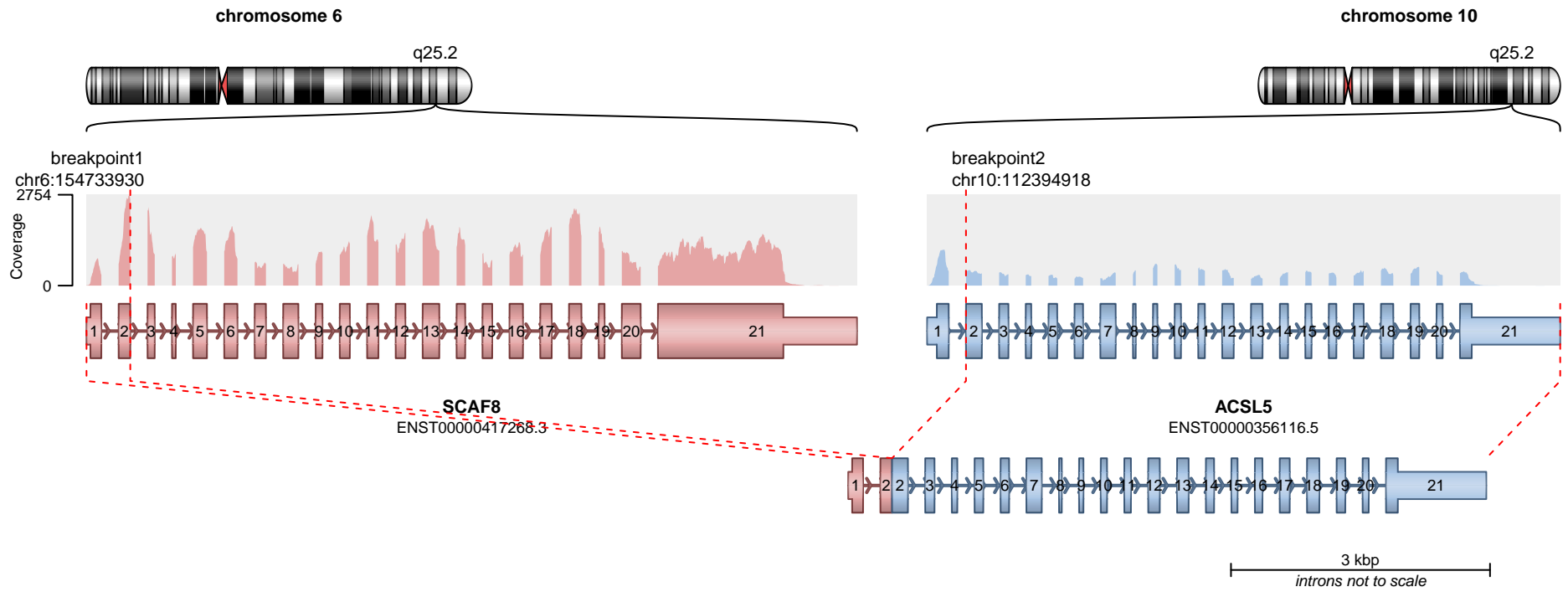
RETAINED PROTEIN DOMAINS
reading frame unclear



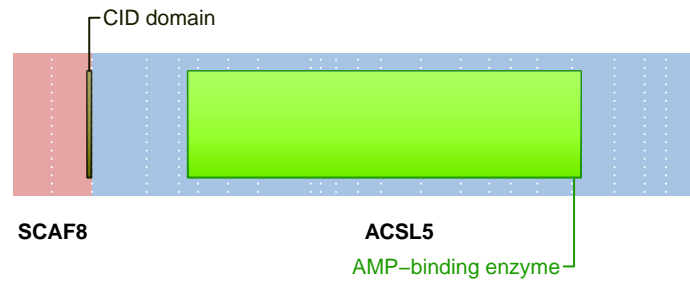
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



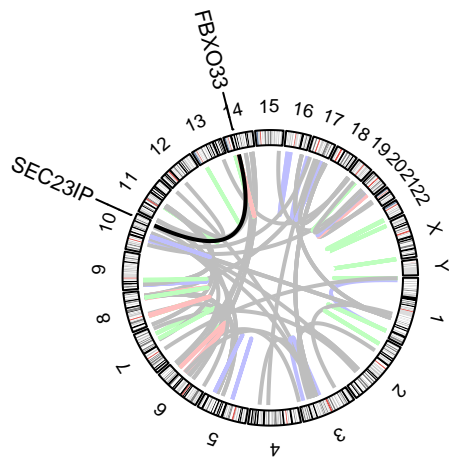
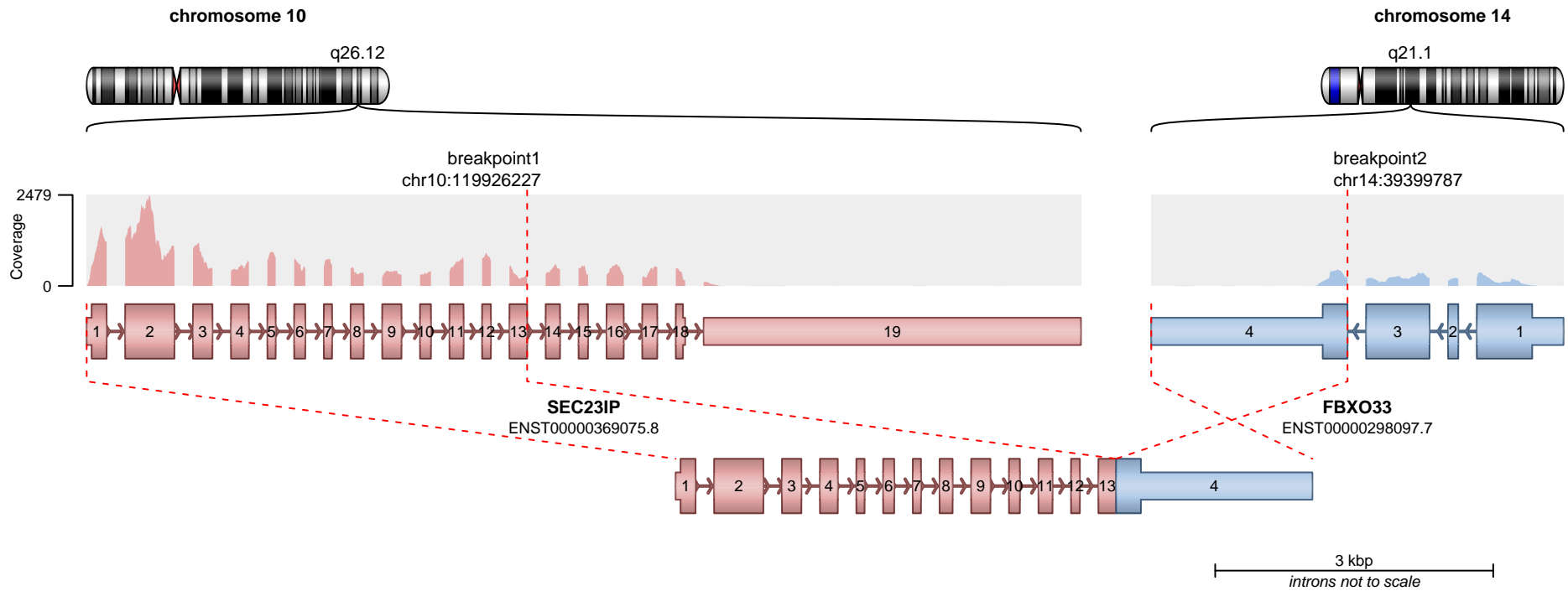
RETAINED PROTEIN DOMAINS
 reading frame unclear



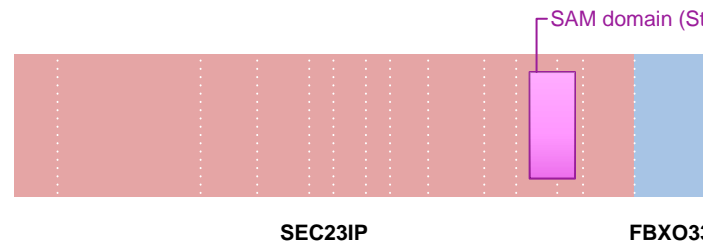
SUPPORTING READ COUNT

Split reads = 2
 Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



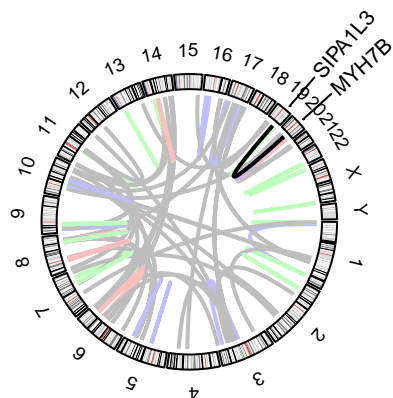
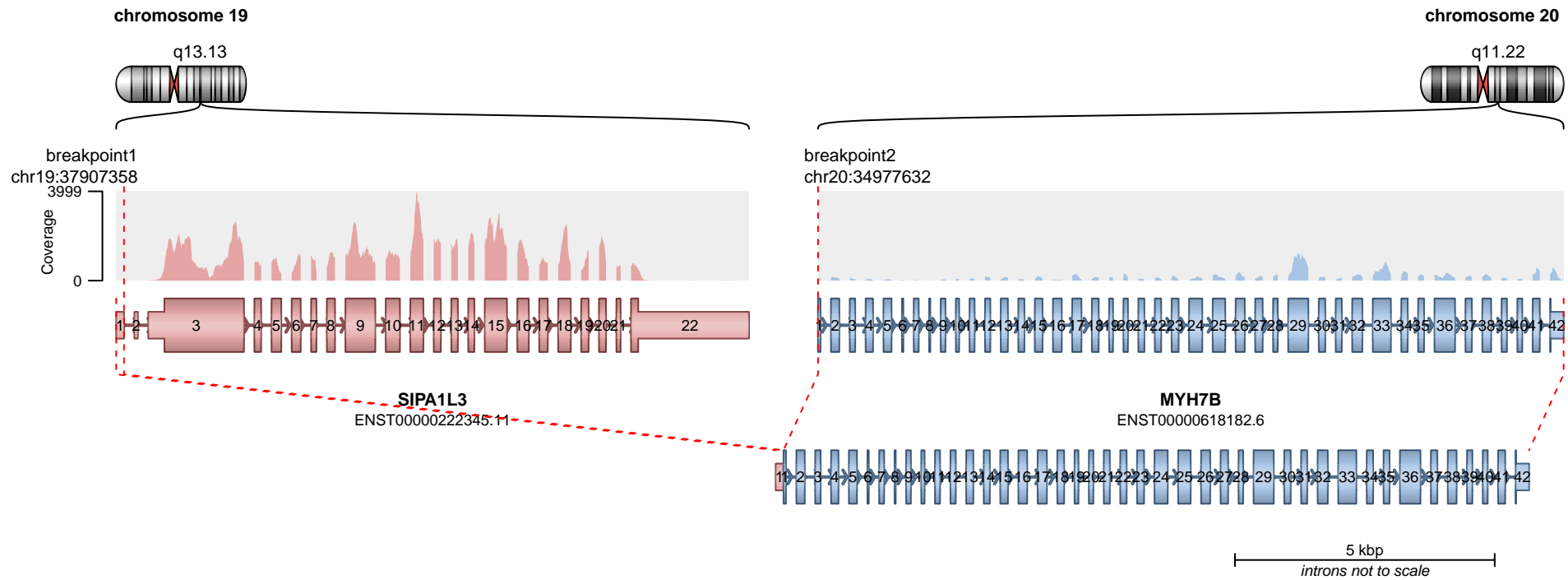
RETAINED PROTEIN DOMAINS
reading frame unclear



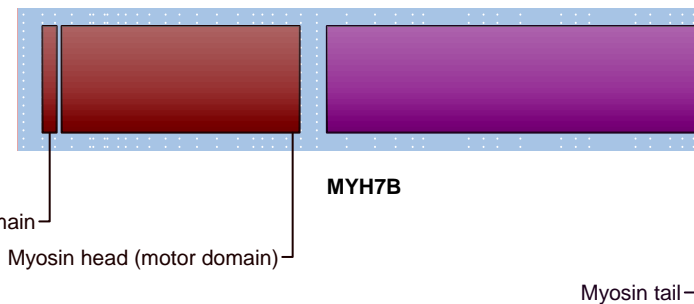
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

— translocation — deletion
— duplication — inversion



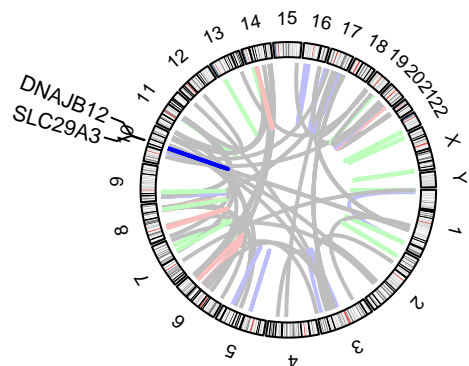
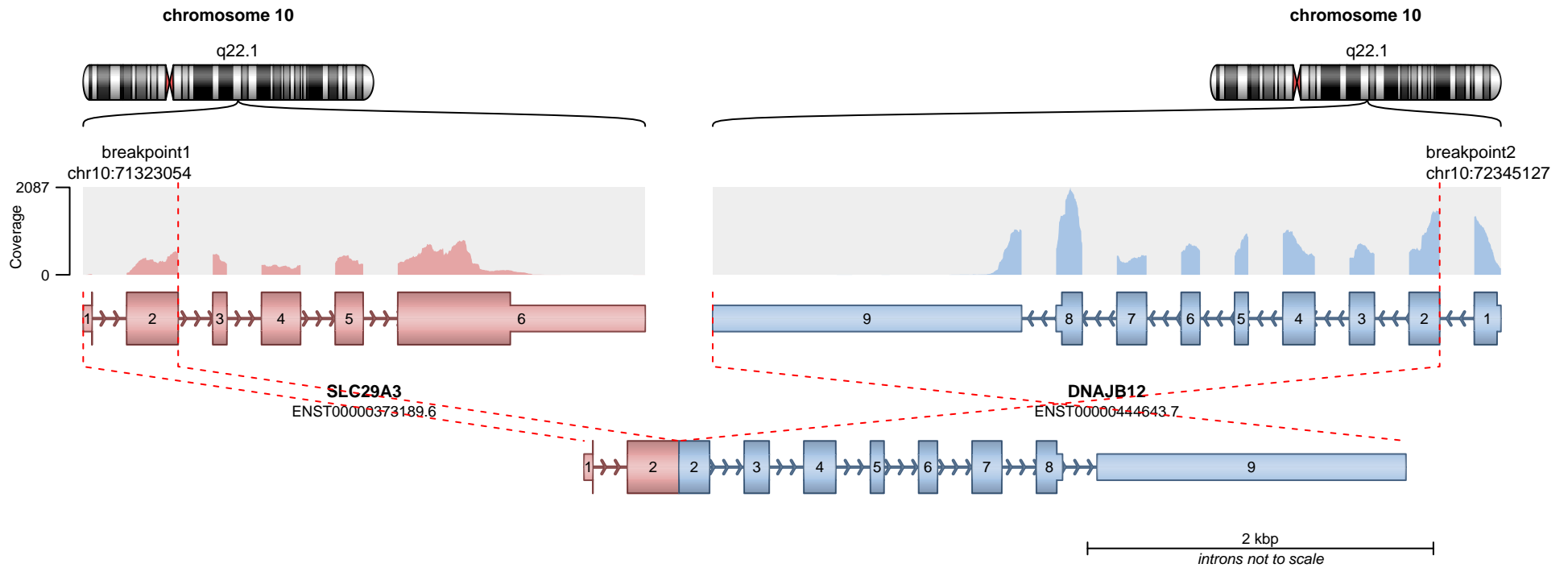
RETAINED PROTEIN DOMAINS
reading frame unclear



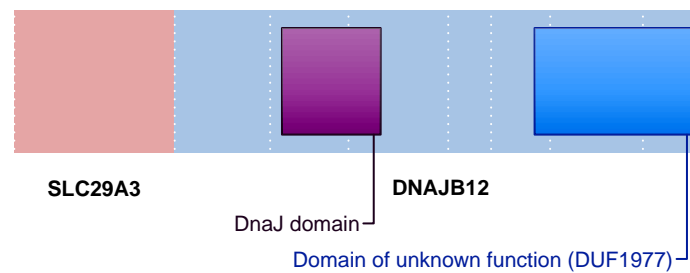
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

— translocation — deletion
— duplication — inversion



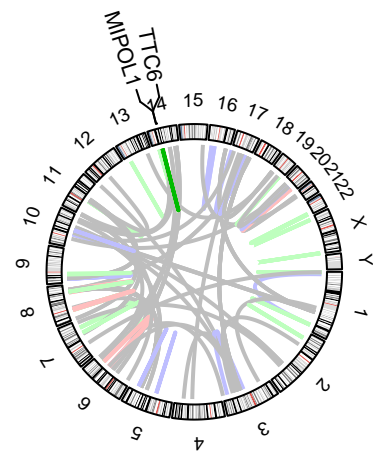
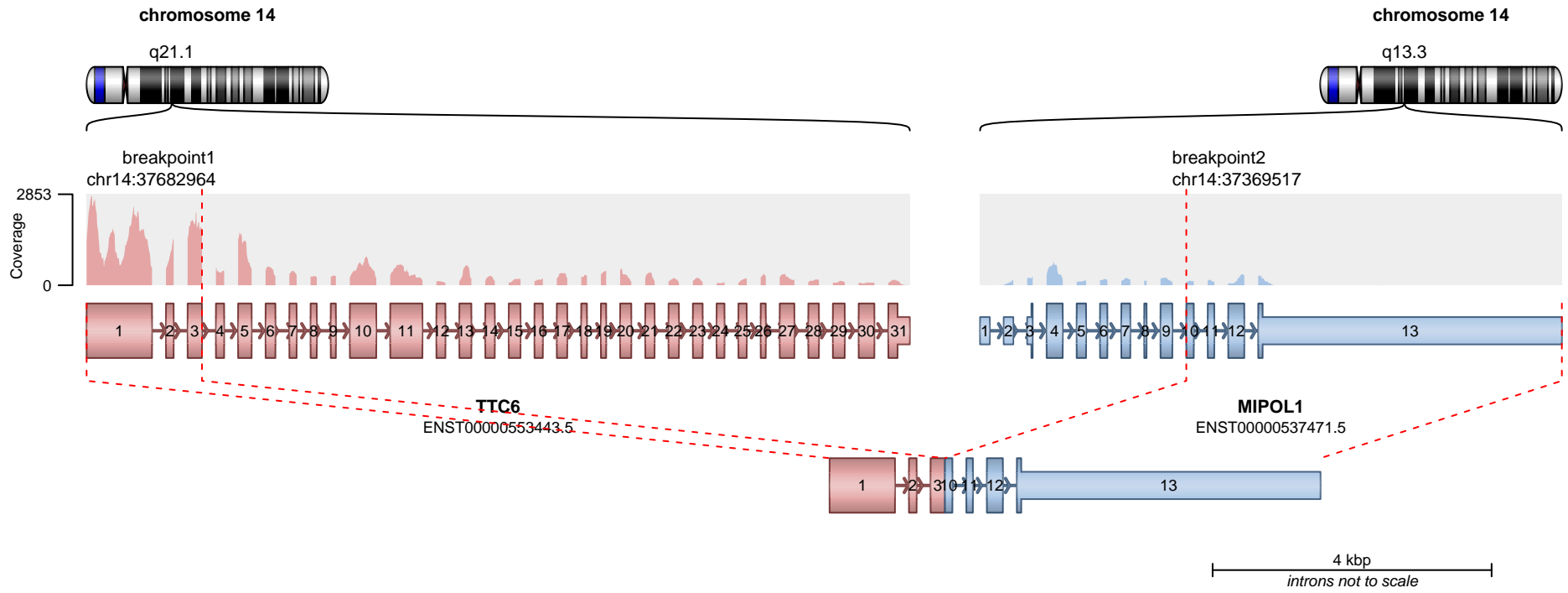
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

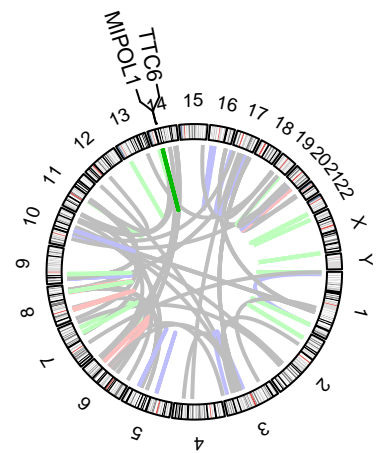
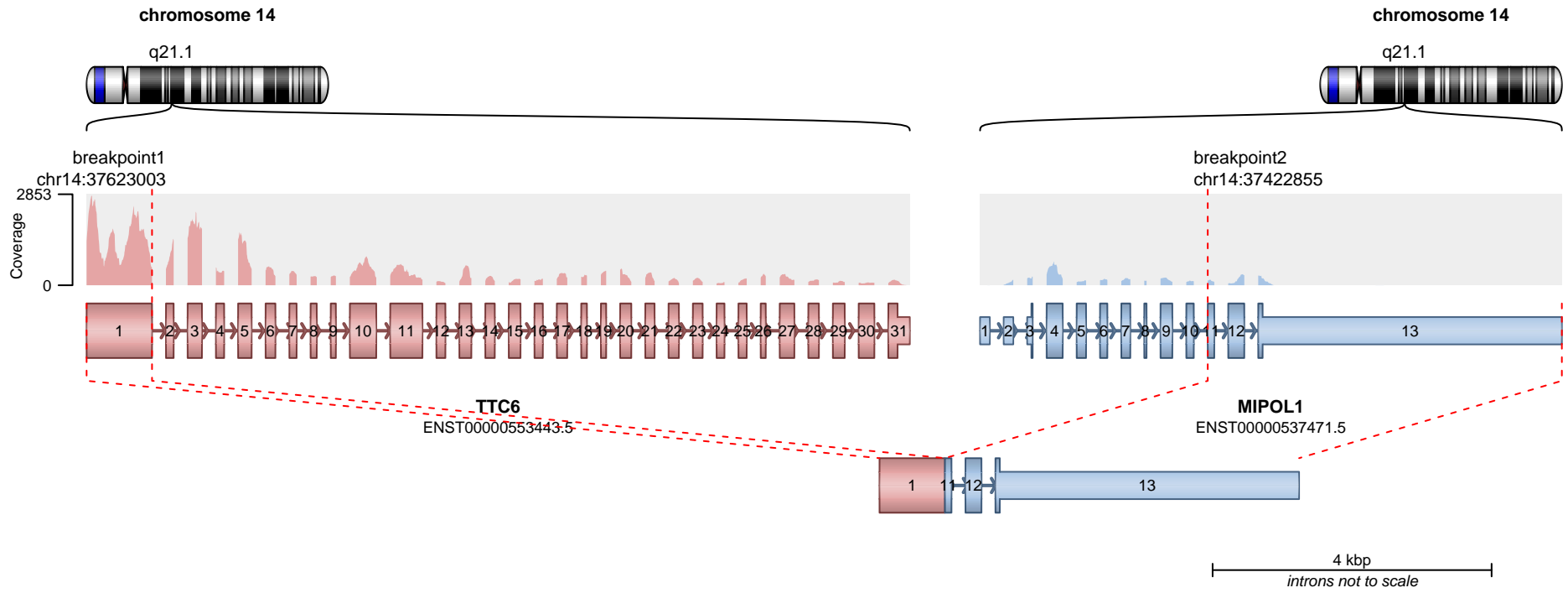


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

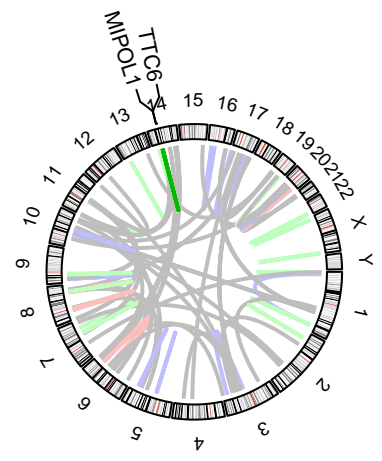
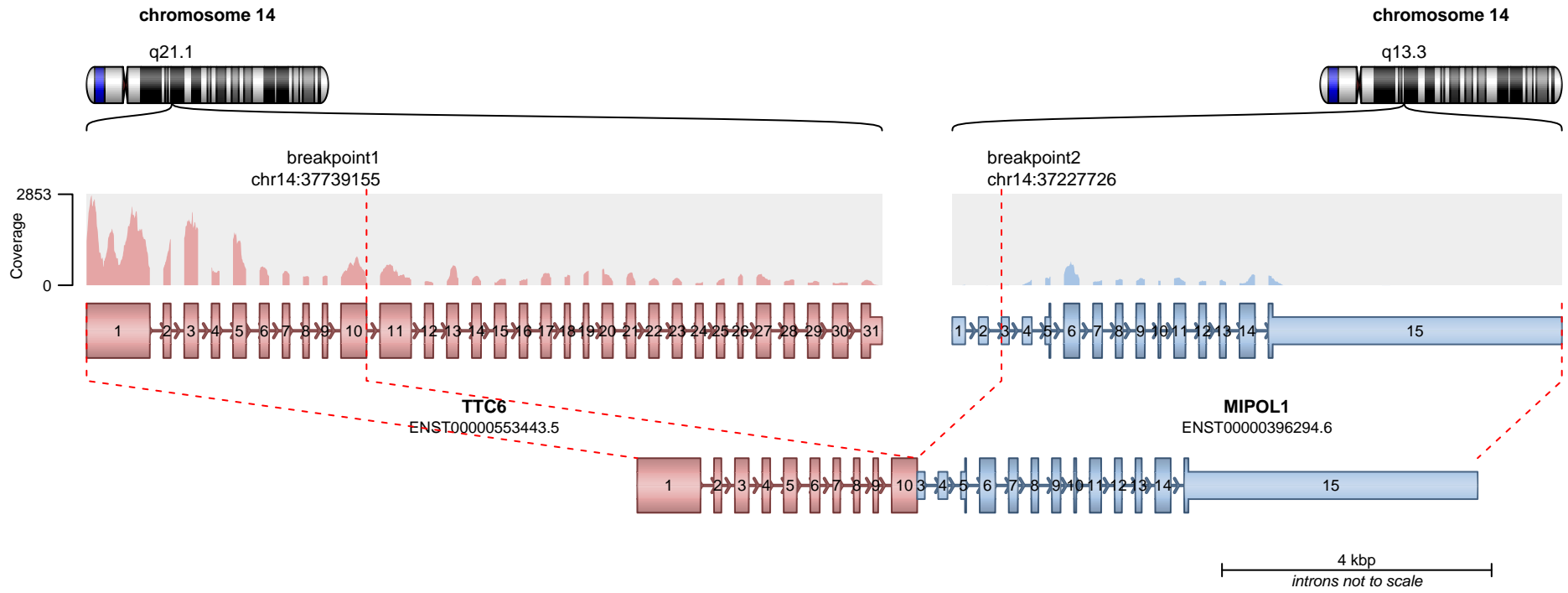


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

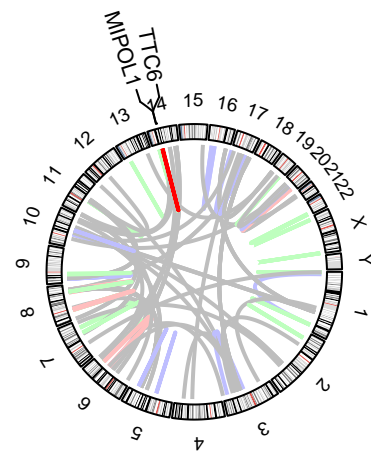
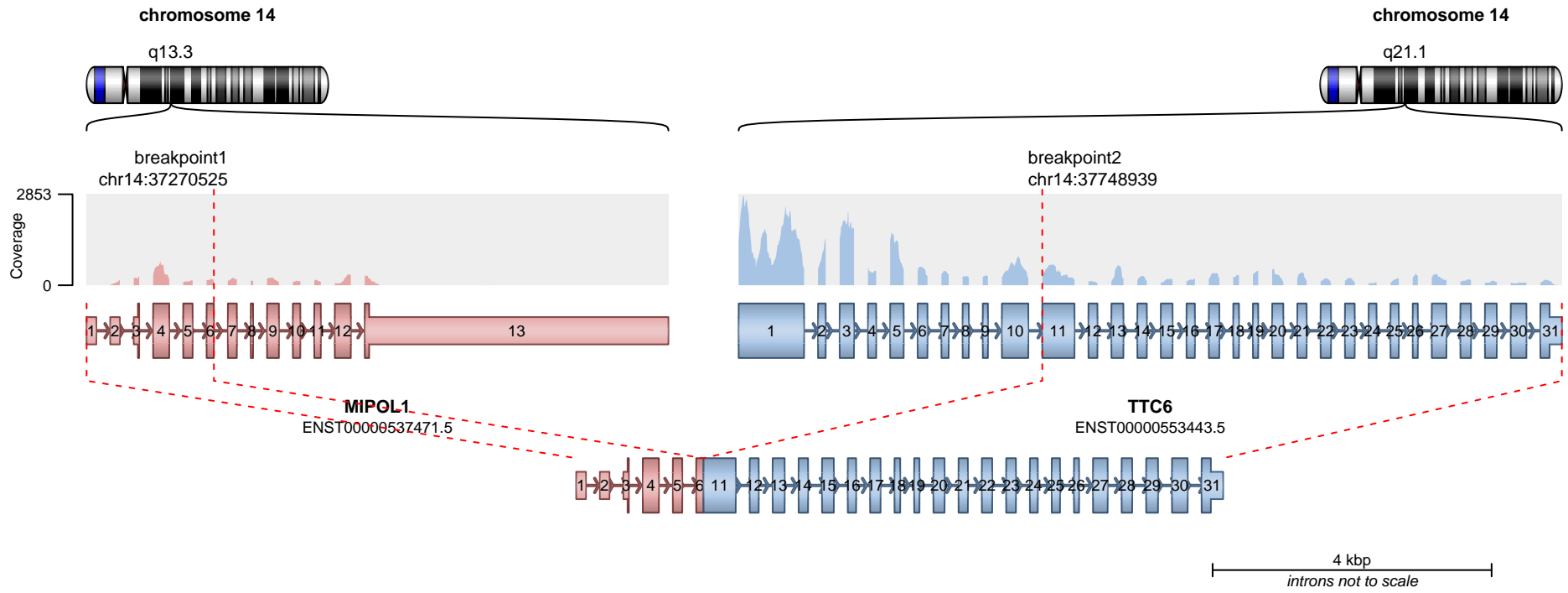


No protein domains retained in fusion.

SUPPORTING READ COUNT

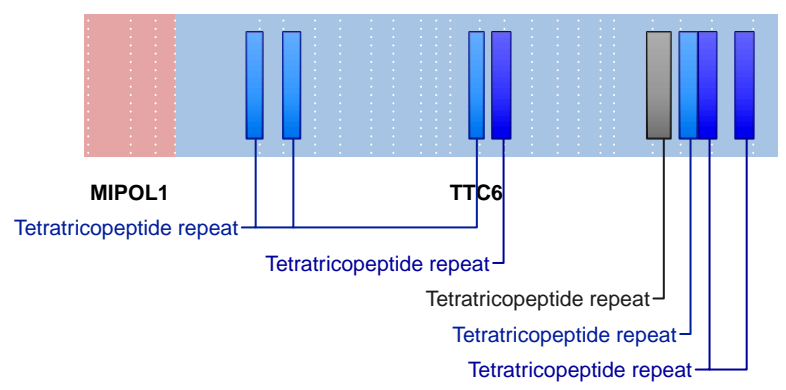
Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



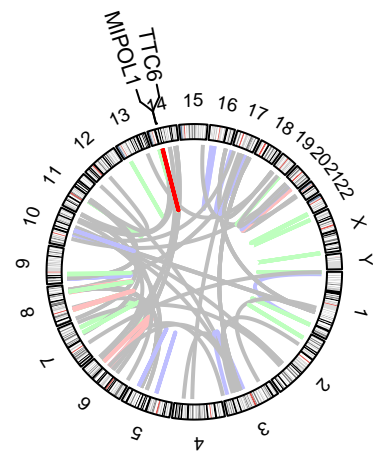
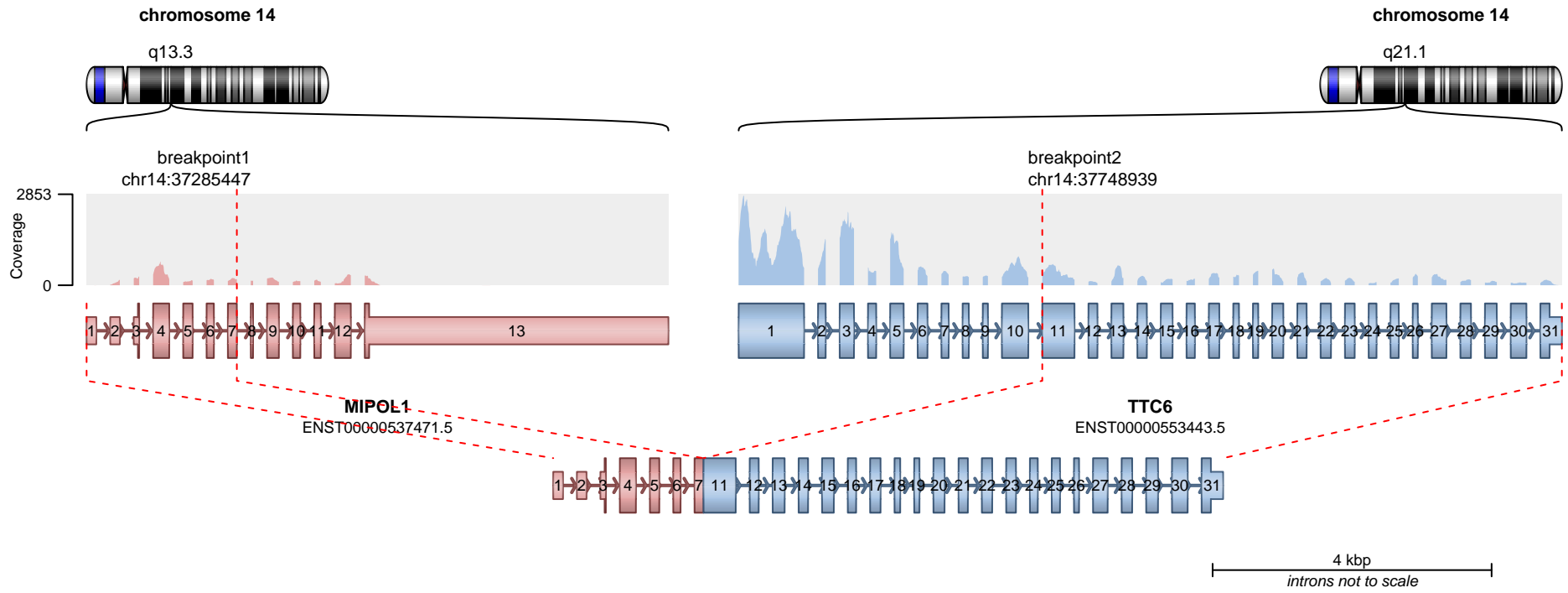
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



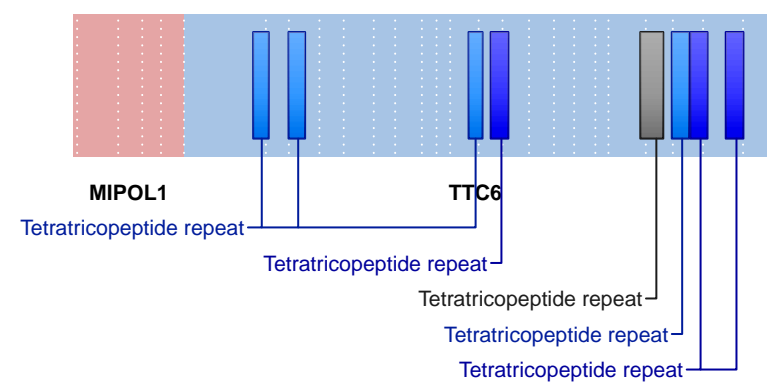
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



— translocation
— duplication
— deletion
— inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0