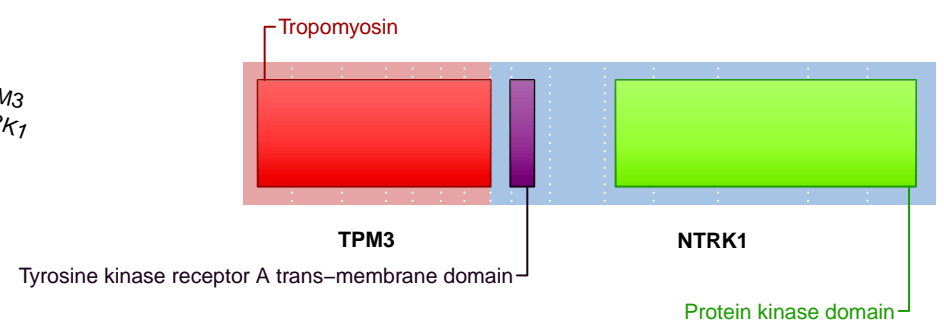


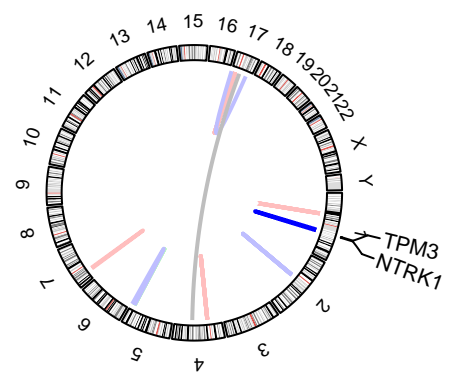
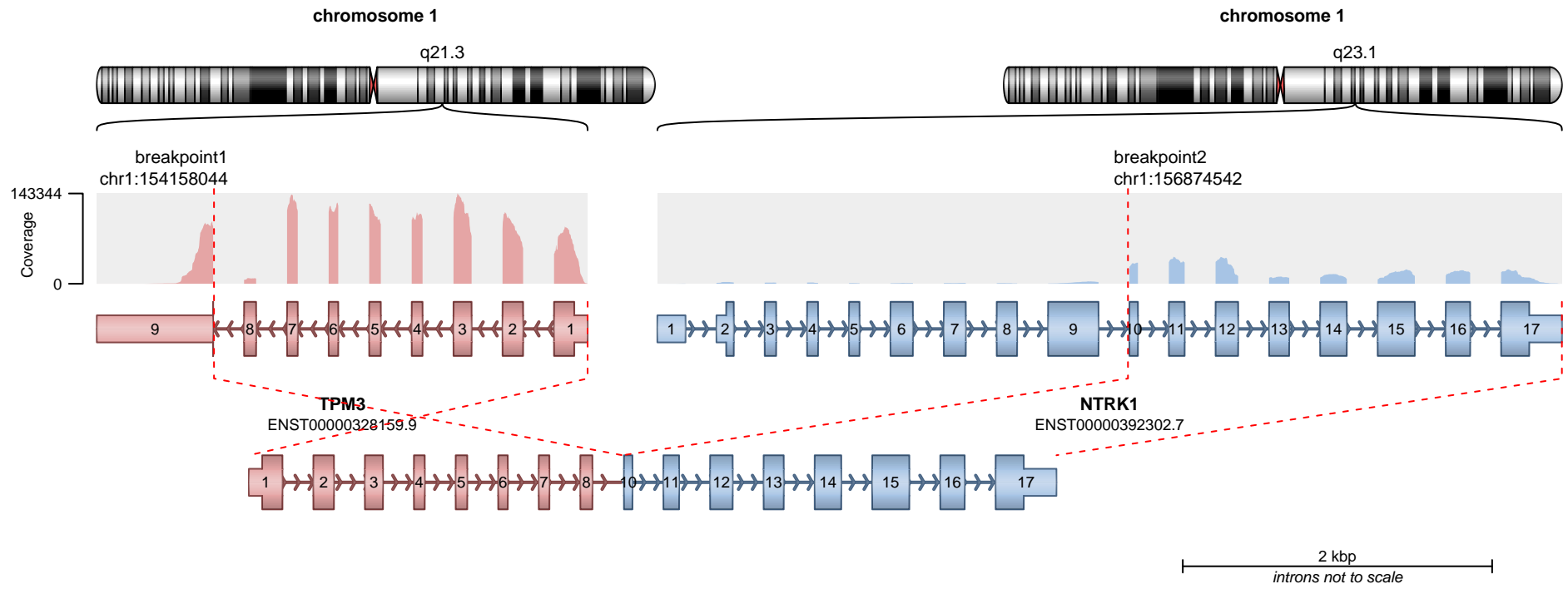
RETAINED PROTEIN DOMAINS
reading frame unclear



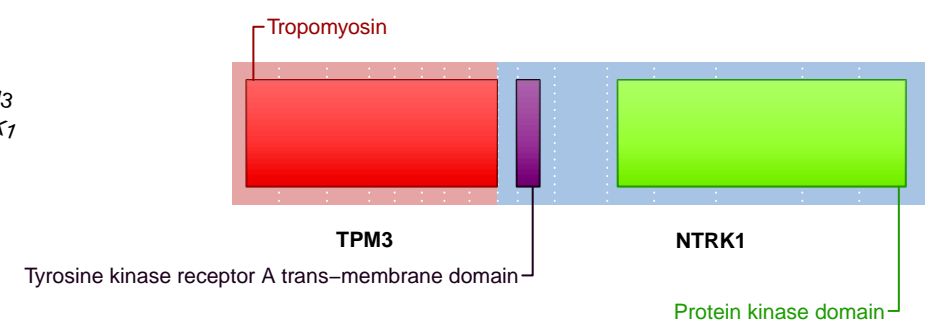
SUPPORTING READ COUNT

Split reads = 8669
Discordant mates = 36

- translocation
- duplication
- deletion
- inversion



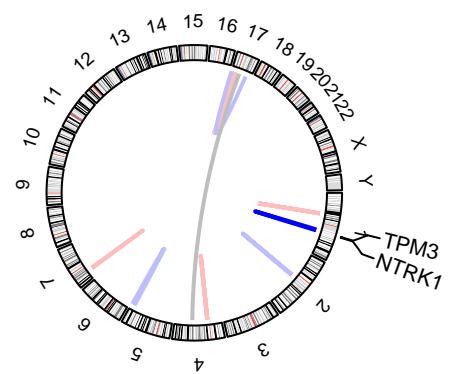
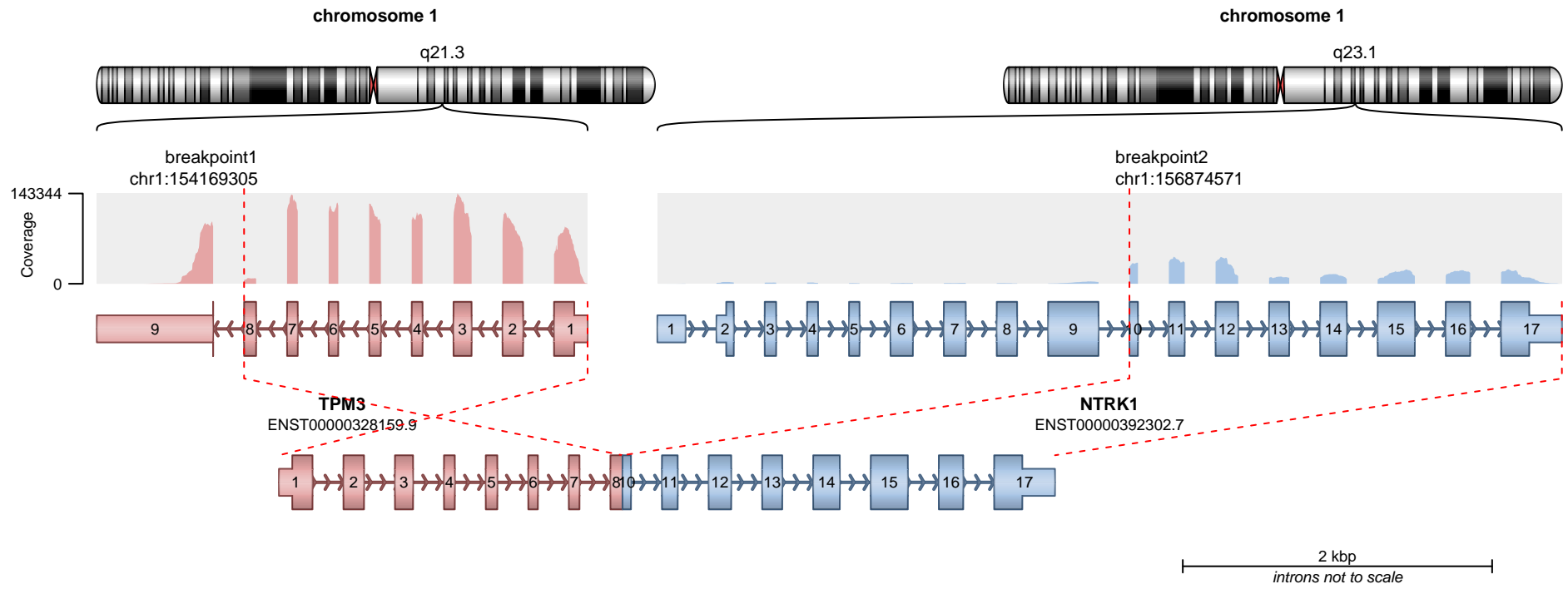
RETAINED PROTEIN DOMAINS
reading frame unclear



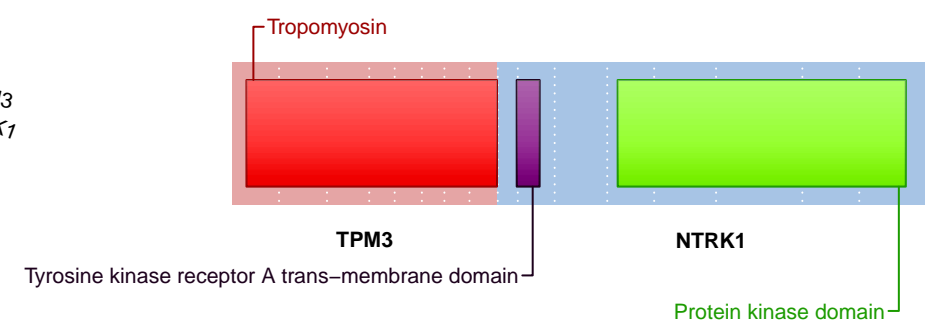
SUPPORTING READ COUNT

Split reads = 201
Discordant mates = 39

- translocation
- duplication
- deletion
- inversion



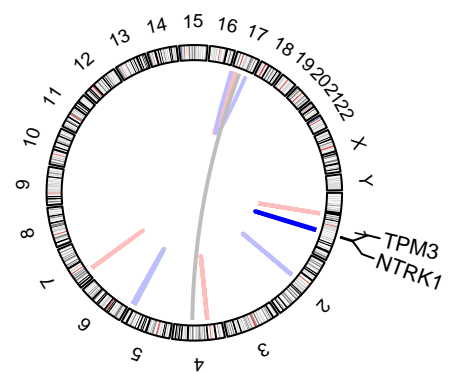
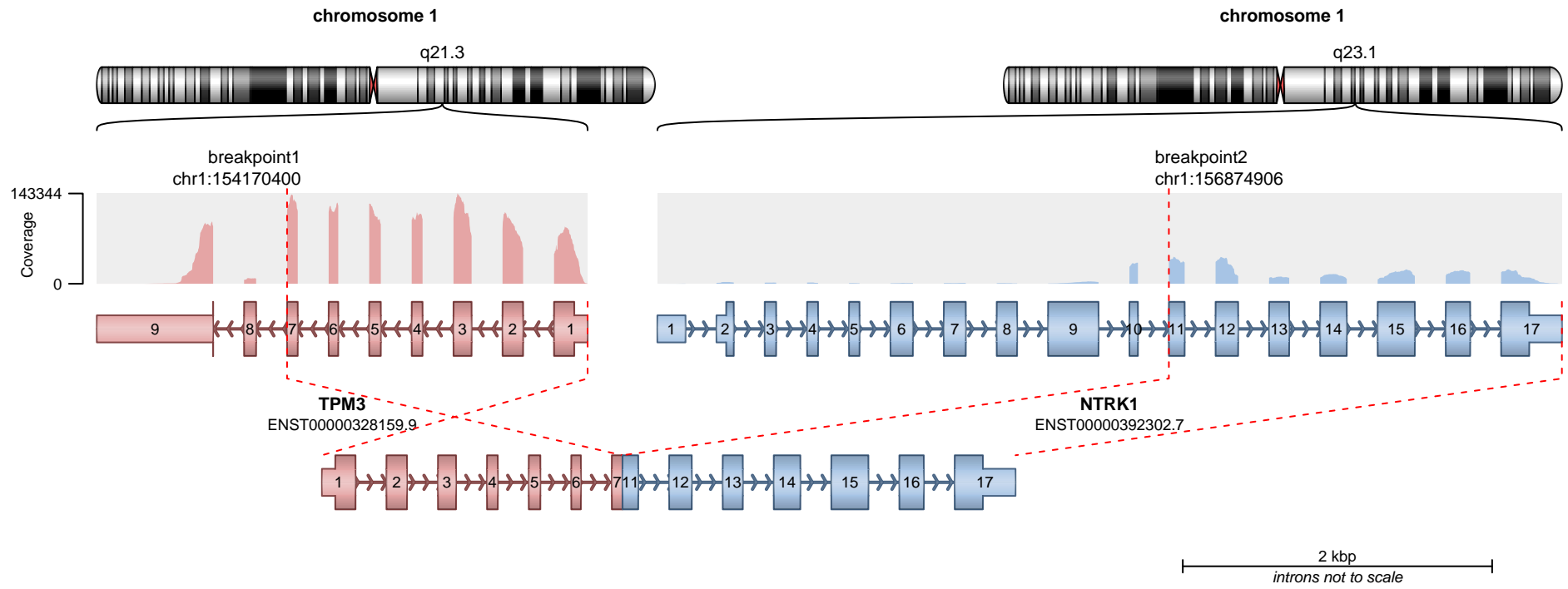
RETAINED PROTEIN DOMAINS
reading frame unclear



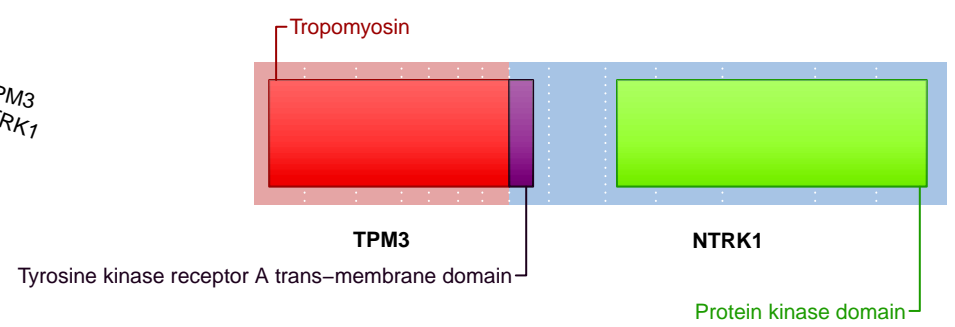
SUPPORTING READ COUNT

Split reads = 173
Discordant mates = 36

- translocation
- duplication
- deletion
- inversion



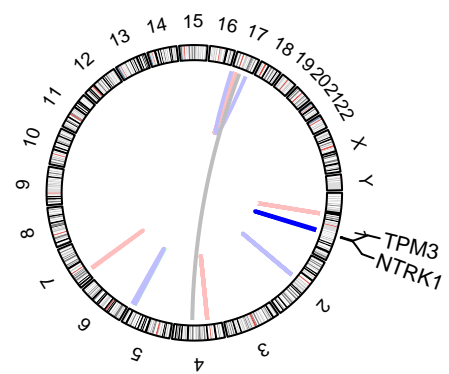
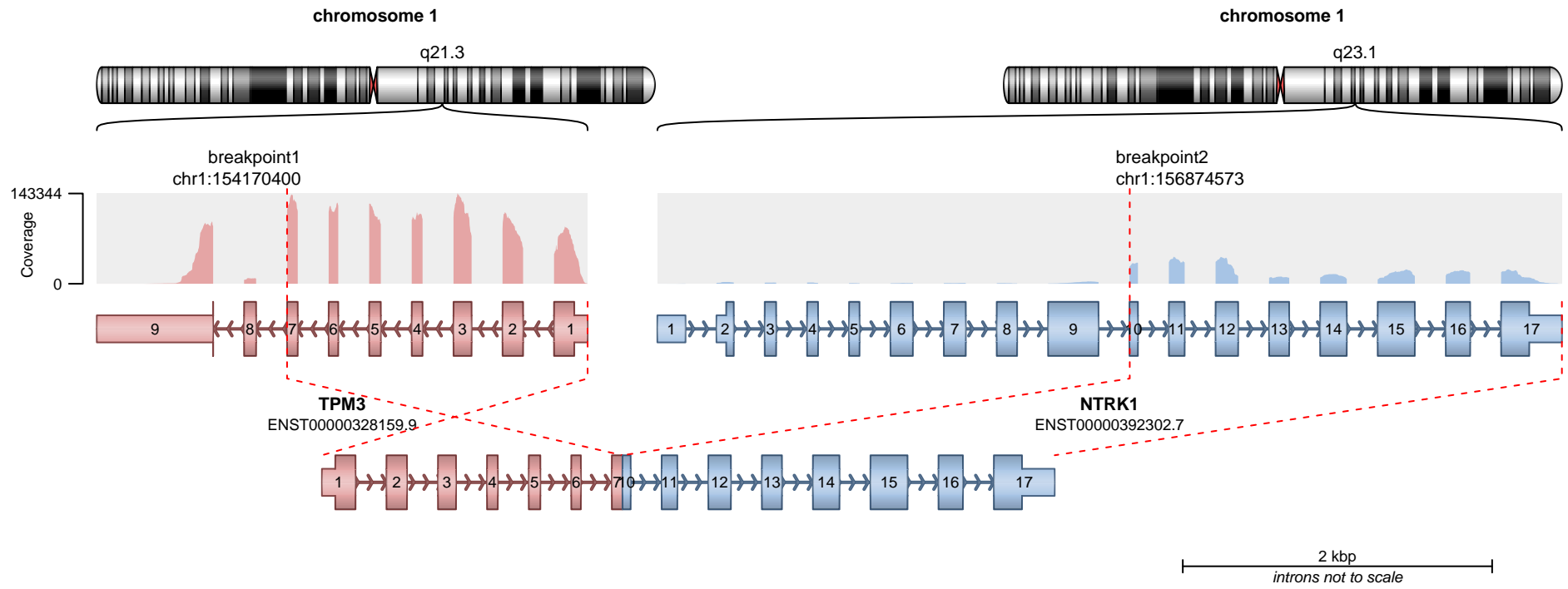
RETAINED PROTEIN DOMAINS
reading frame unclear



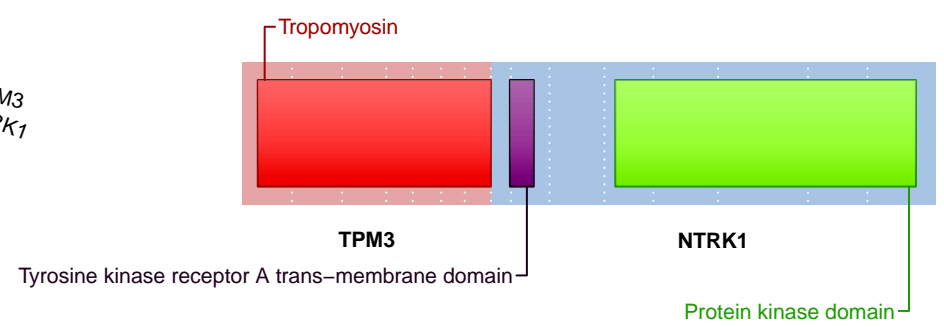
SUPPORTING READ COUNT

Split reads = 26
Discordant mates = 9

- translocation
- duplication
- deletion
- inversion



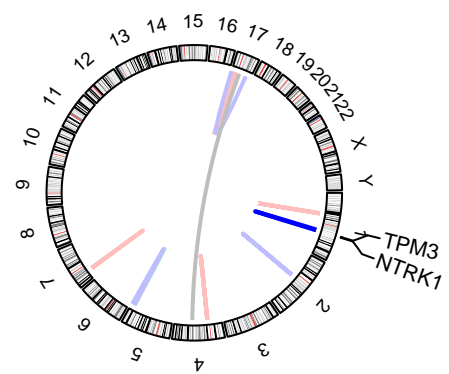
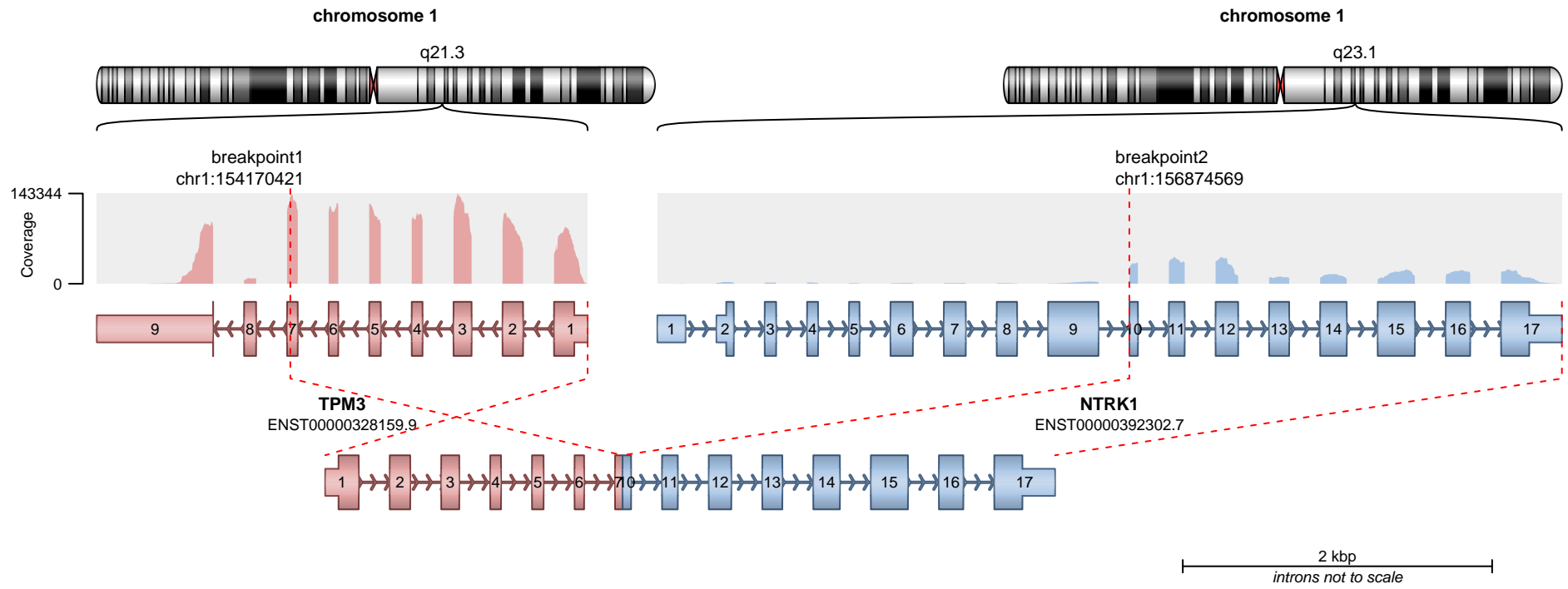
RETAINED PROTEIN DOMAINS
reading frame unclear



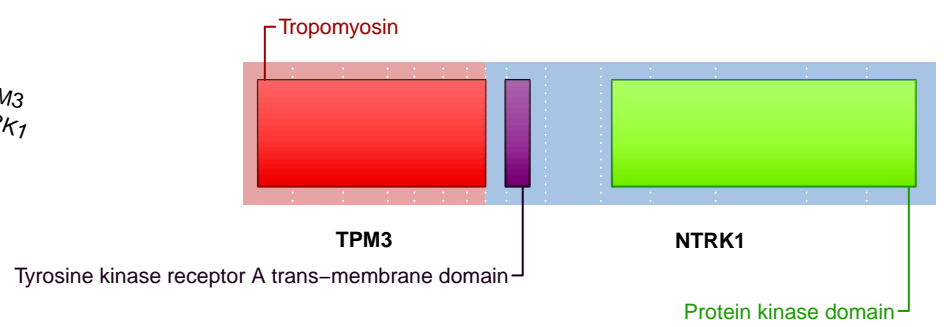
SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 36

- translocation
- duplication
- deletion
- inversion



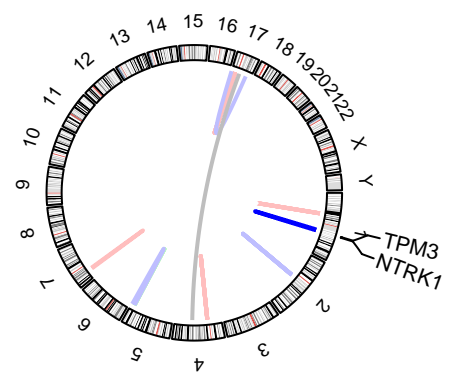
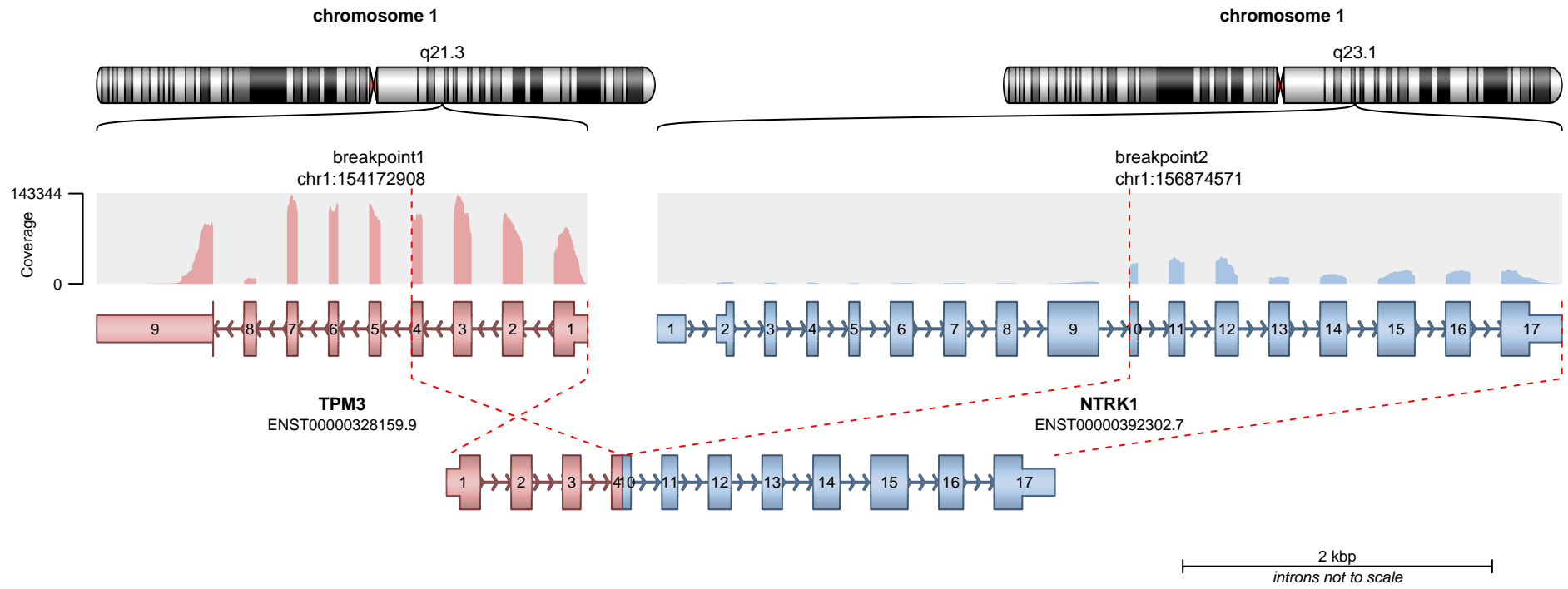
RETAINED PROTEIN DOMAINS
reading frame unclear



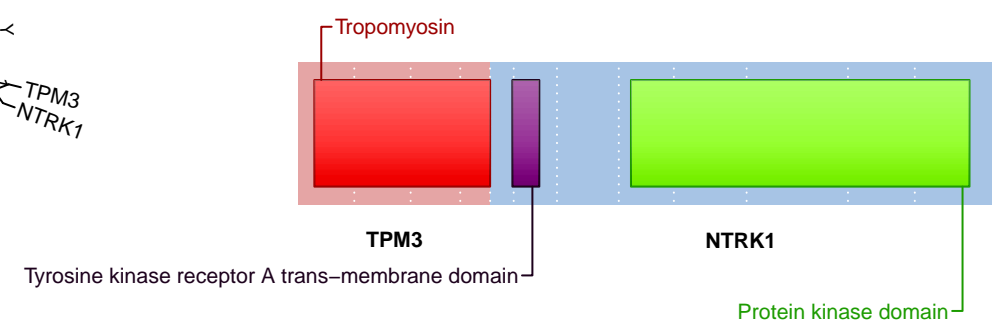
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 20

- translocation
- duplication
- deletion
- inversion



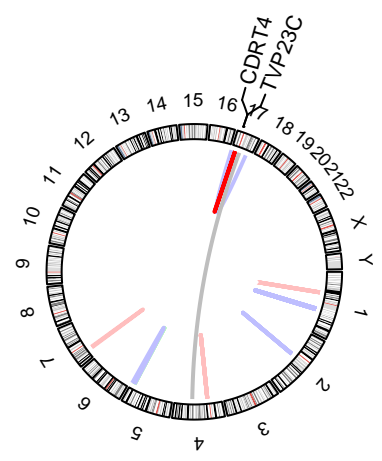
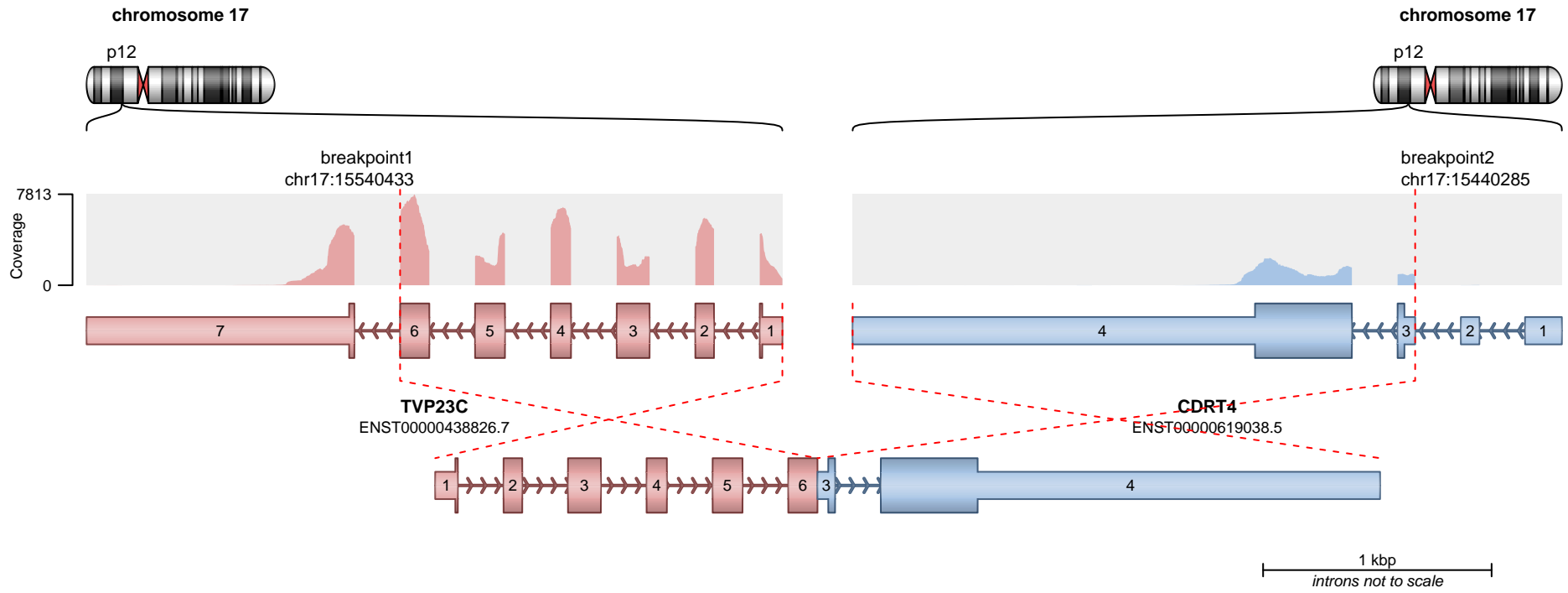
RETAINED PROTEIN DOMAINS
reading frame unclear



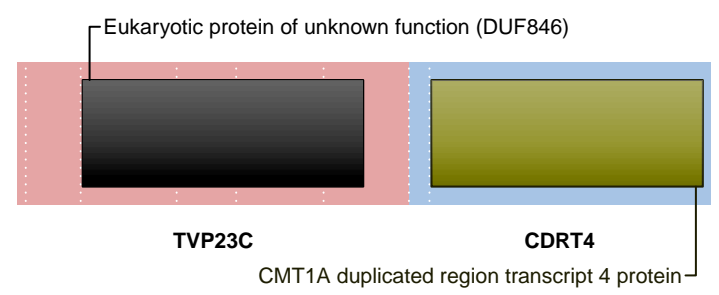
SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



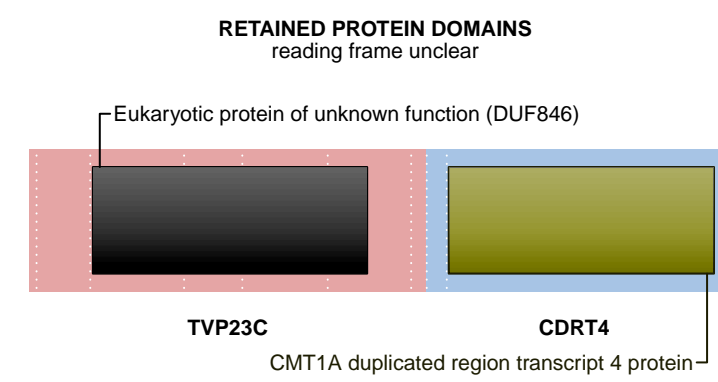
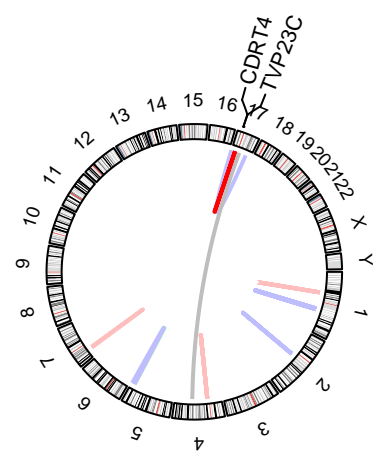
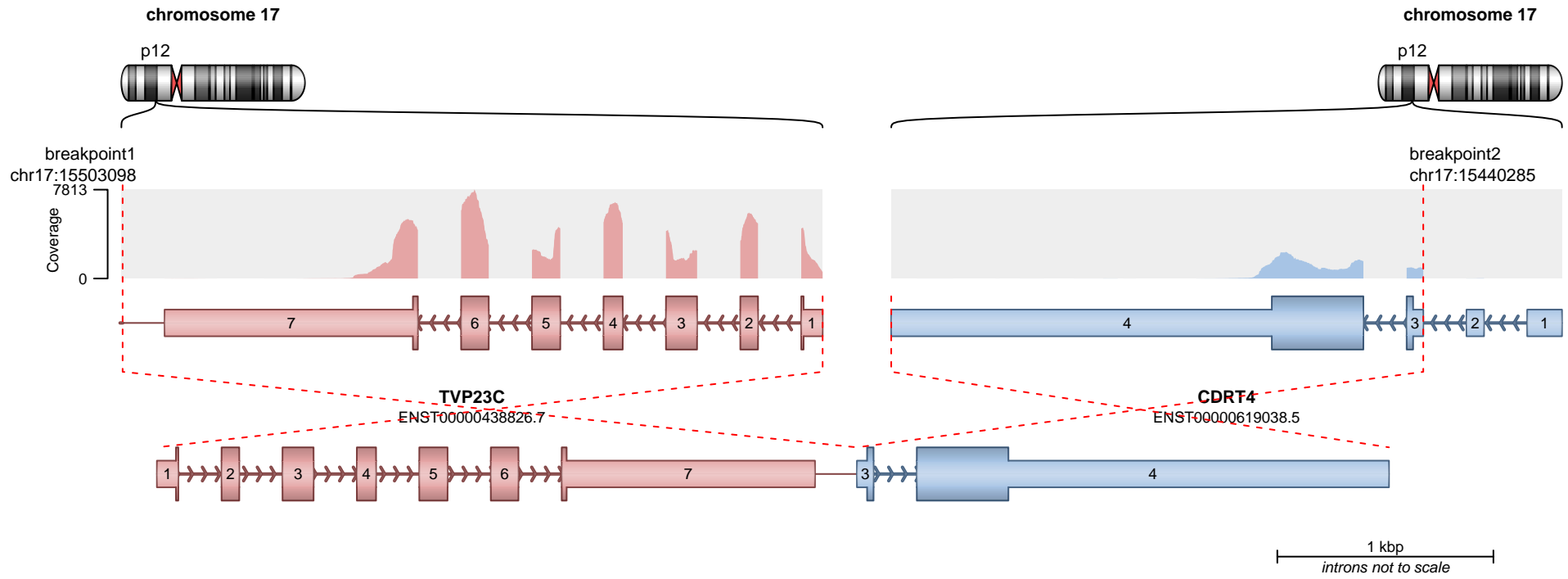
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 160
Discordant mates = 2

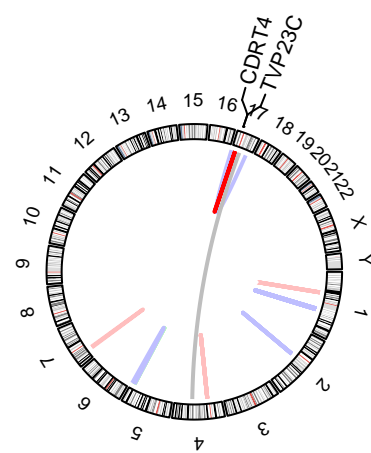
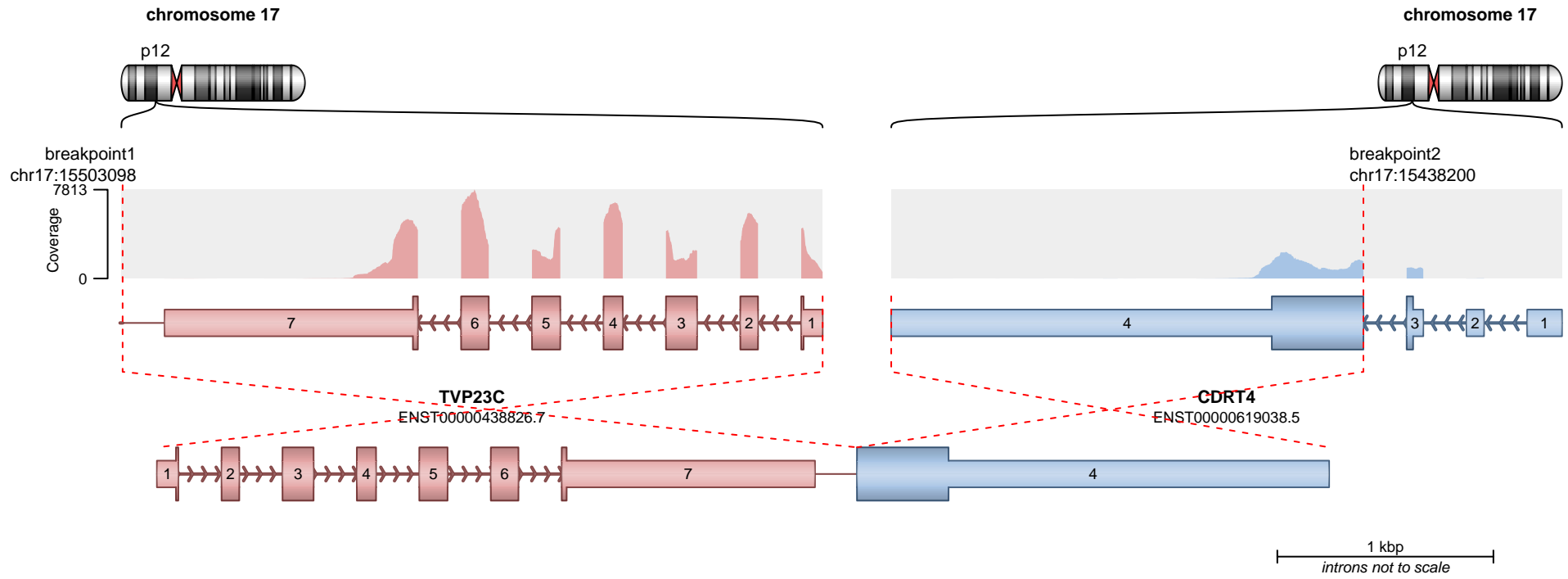
- translocation
- duplication
- deletion
- inversion



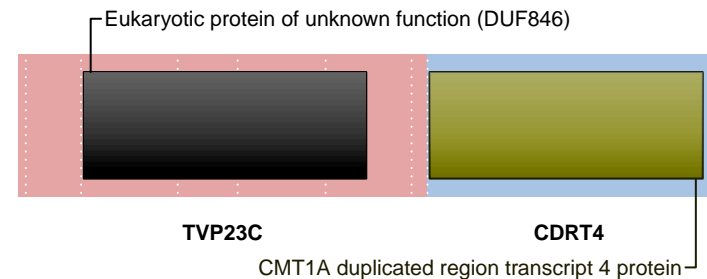
SUPPORTING READ COUNT

Split reads = 116
Discordant mates = 2

— translocation — deletion
— duplication — inversion



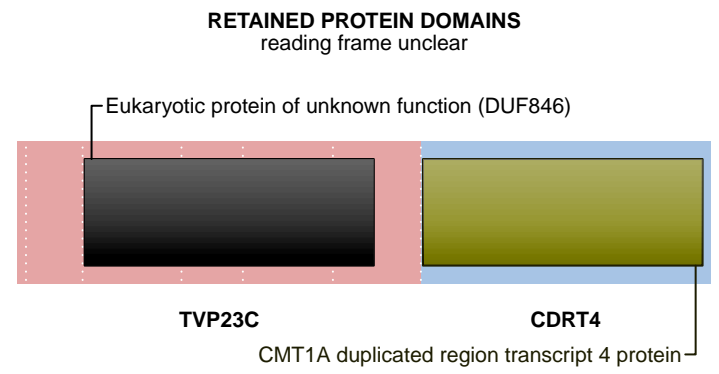
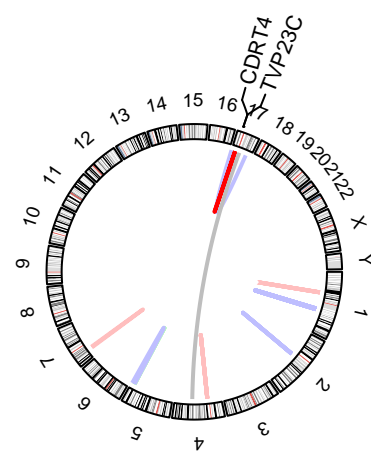
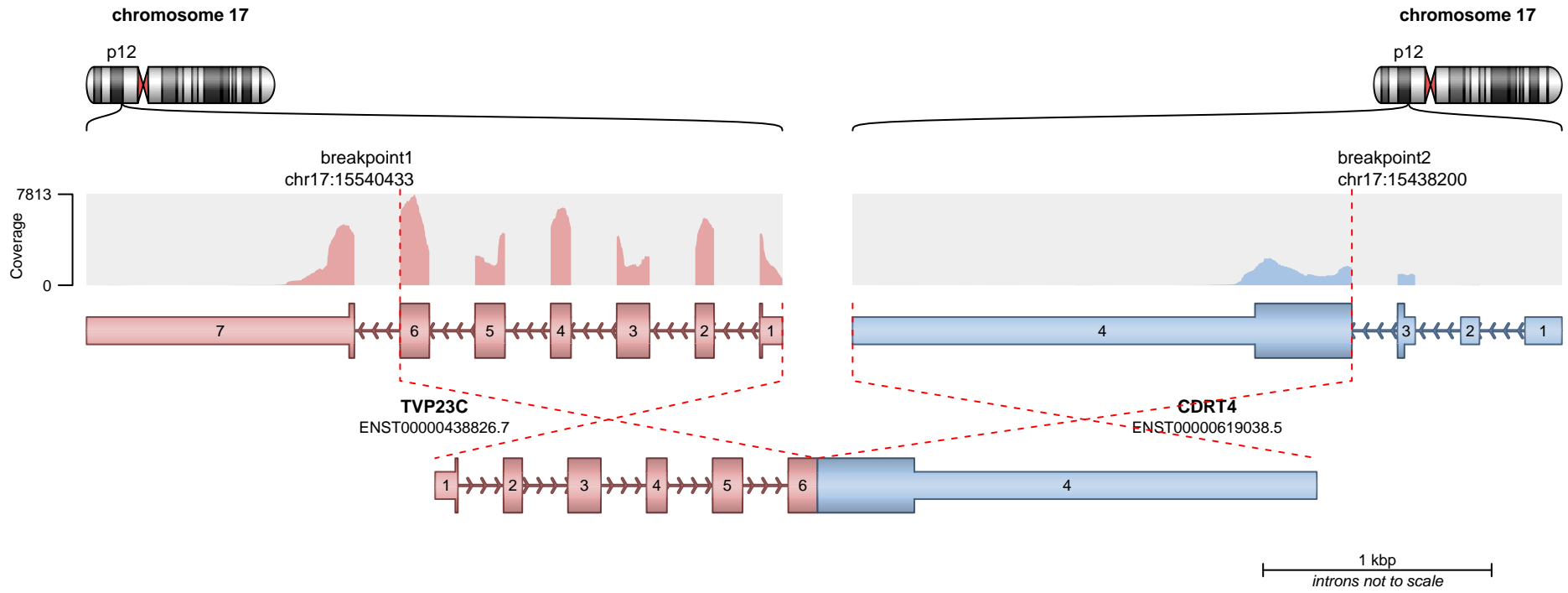
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 112
Discordant mates = 1

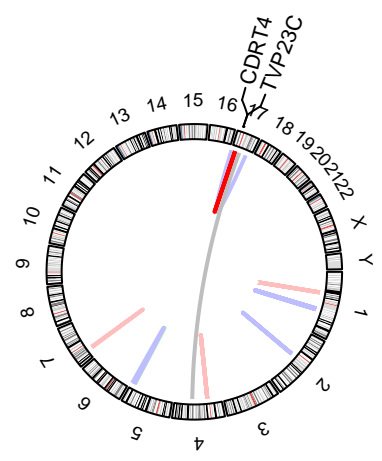
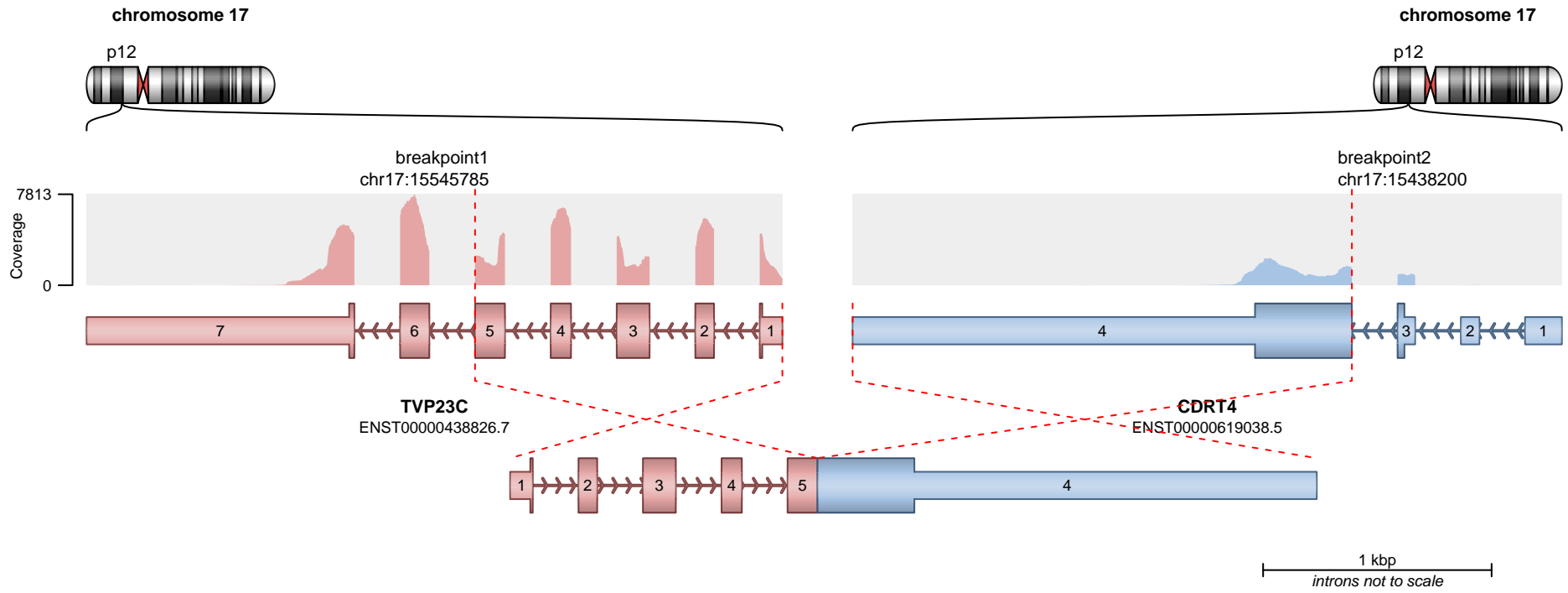
- translocation
- deletion
- duplication
- inversion



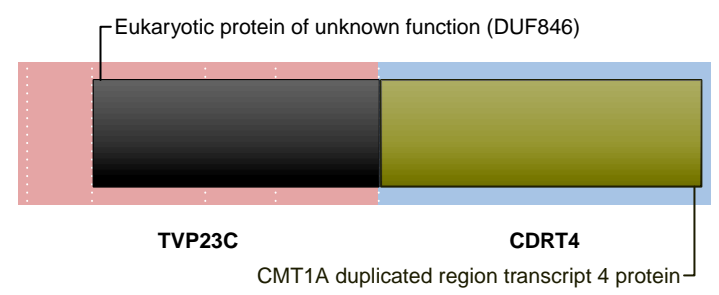
SUPPORTING READ COUNT

Split reads = 87
Discordant mates = 1

— translocation — deletion
— duplication — inversion



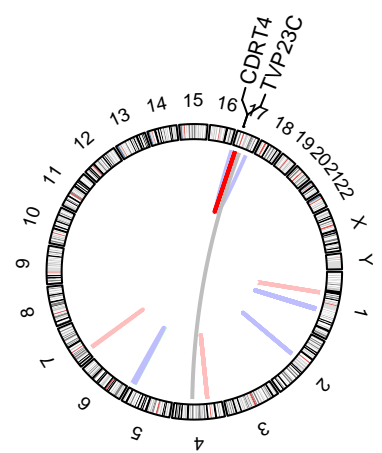
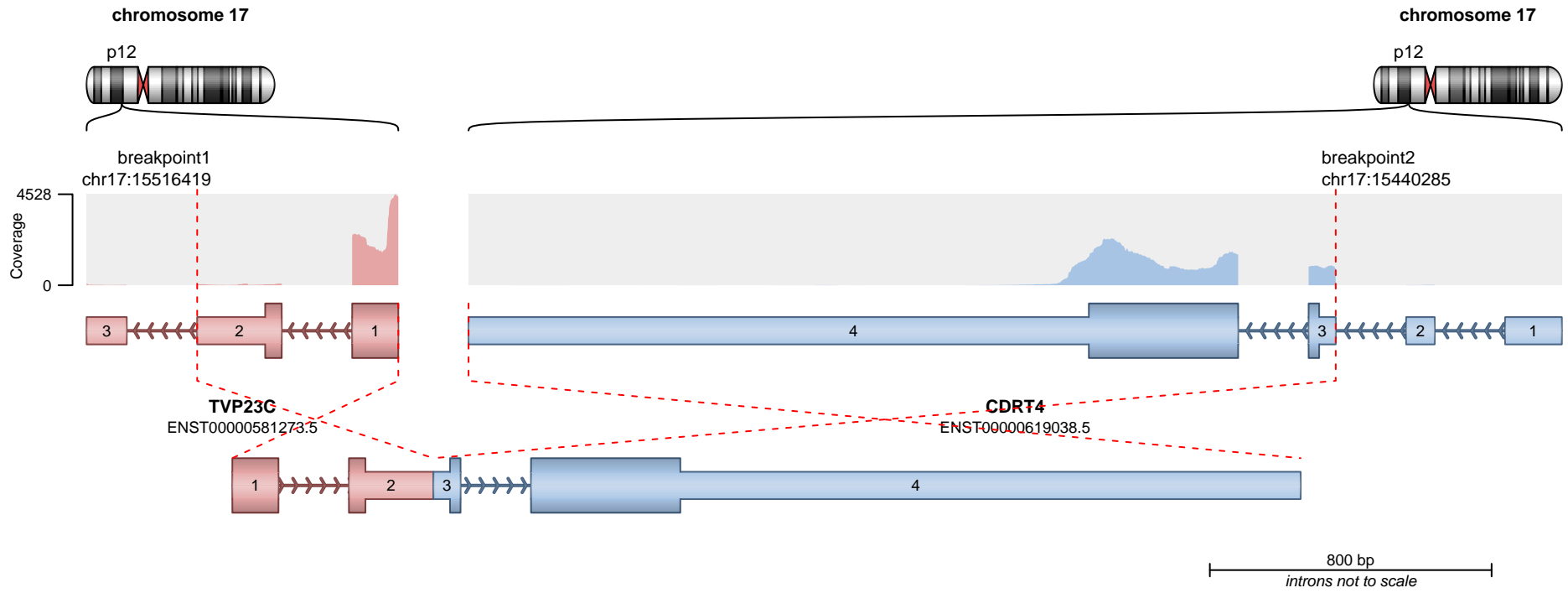
RETAINED PROTEIN DOMAINS
reading frame unclear



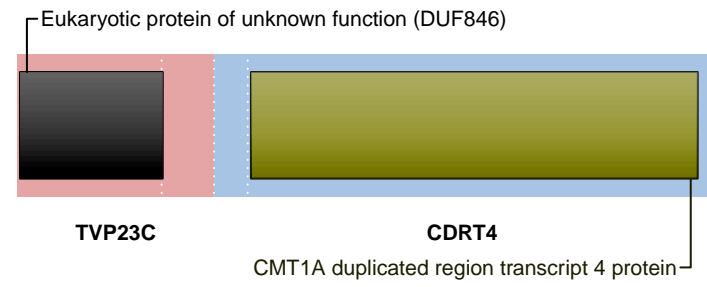
SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



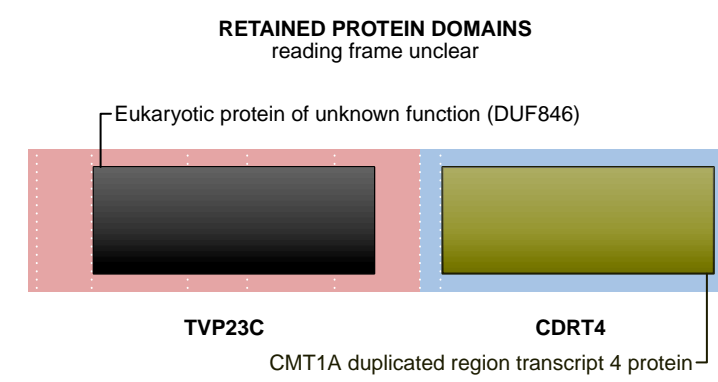
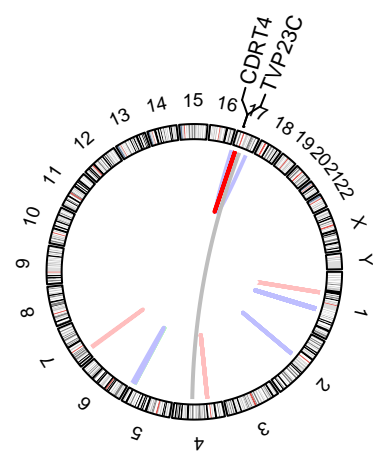
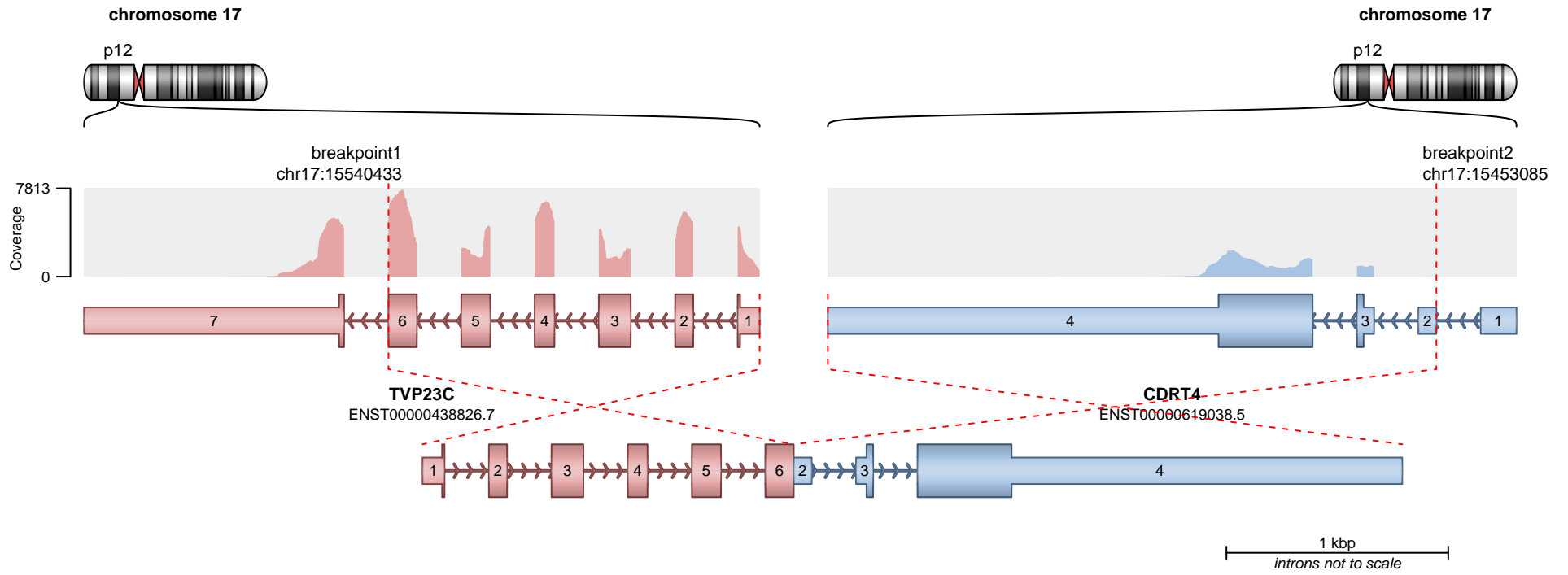
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 2

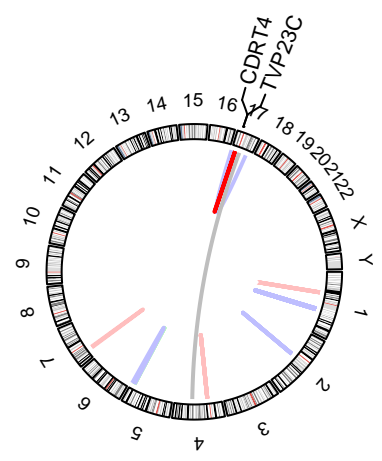
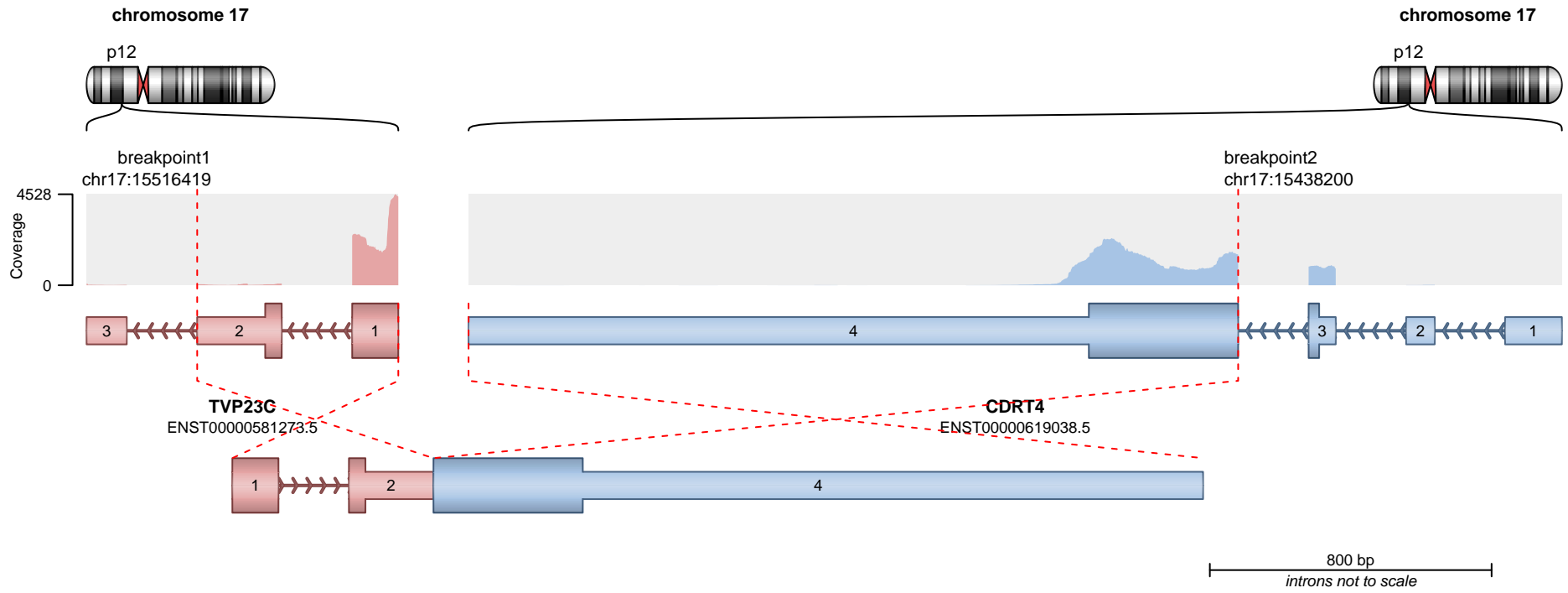
- translocation
- duplication
- deletion
- inversion



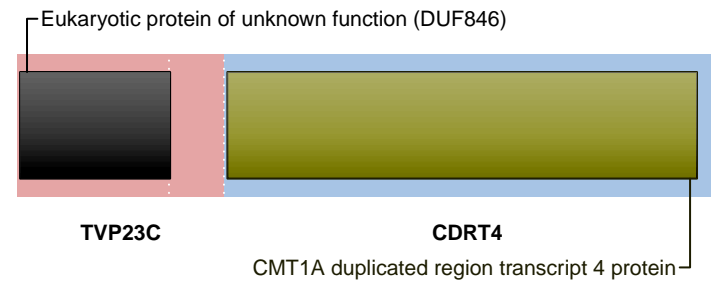
SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 2

— translocation — deletion
— duplication — inversion



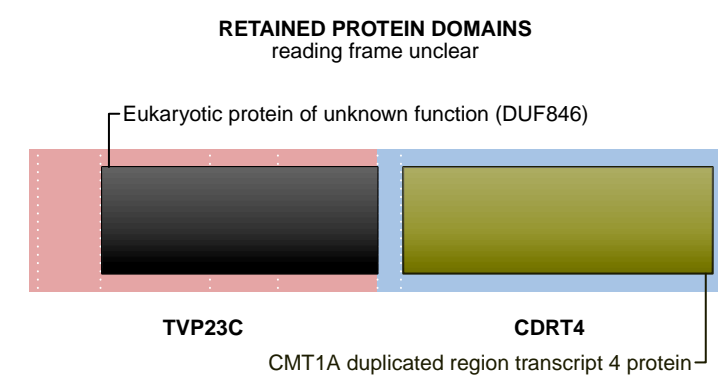
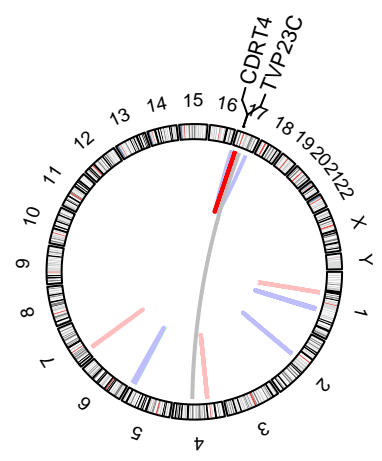
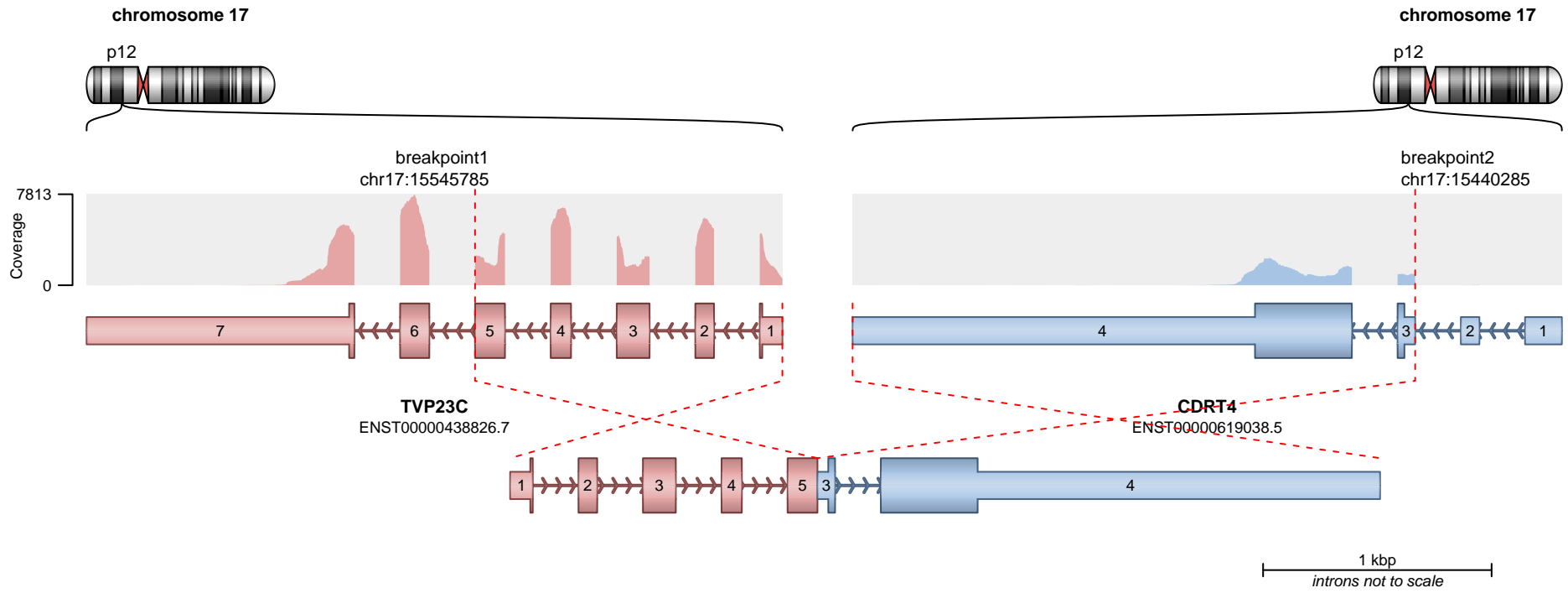
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 1

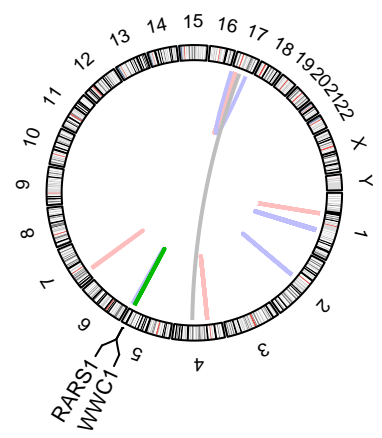
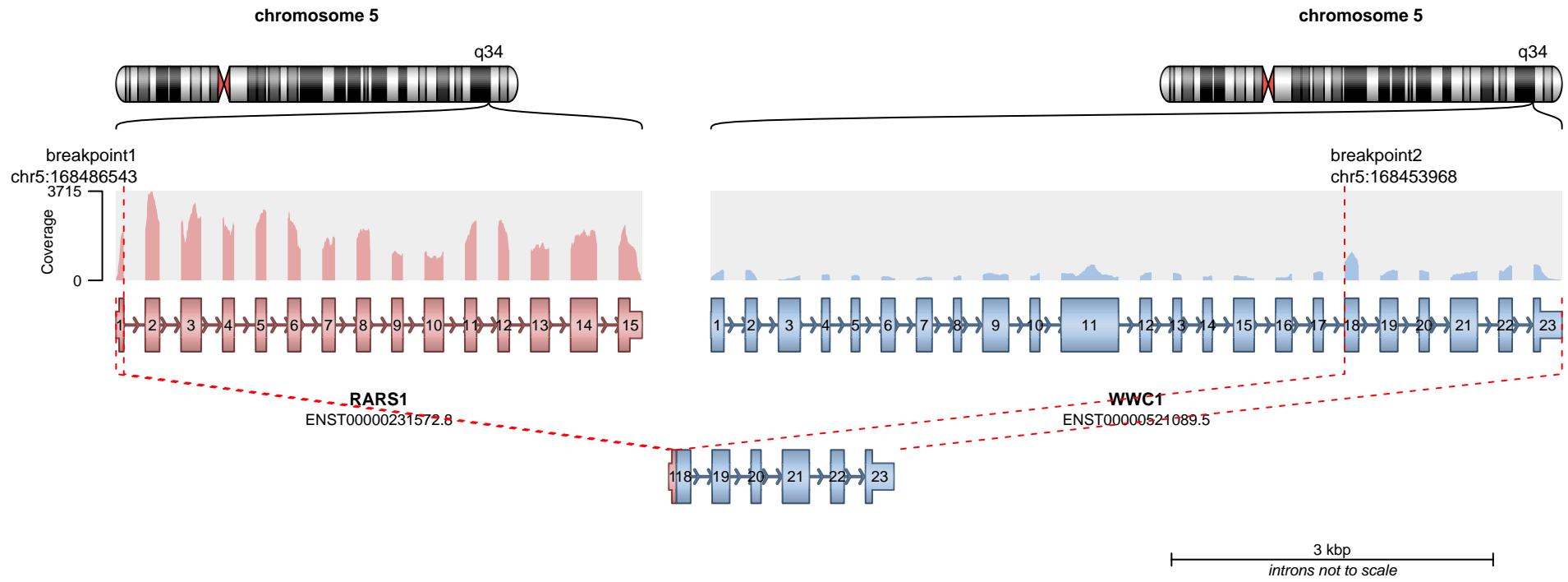
- translocation
- duplication
- deletion
- inversion



SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

— translocation — deletion
— duplication — inversion

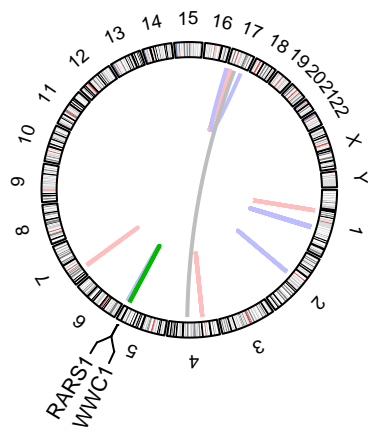
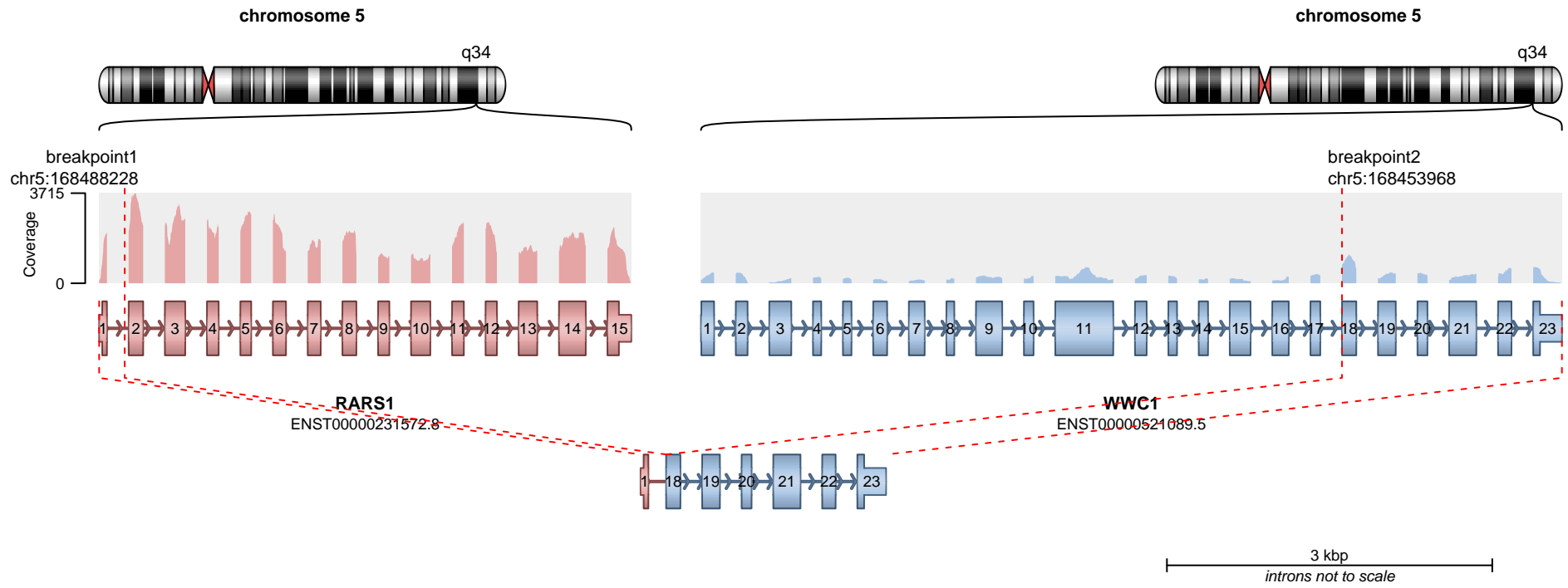


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 124
Discordant mates = 0

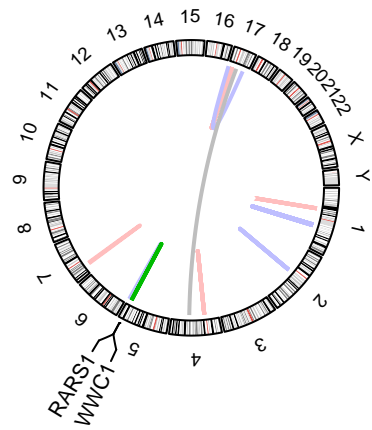
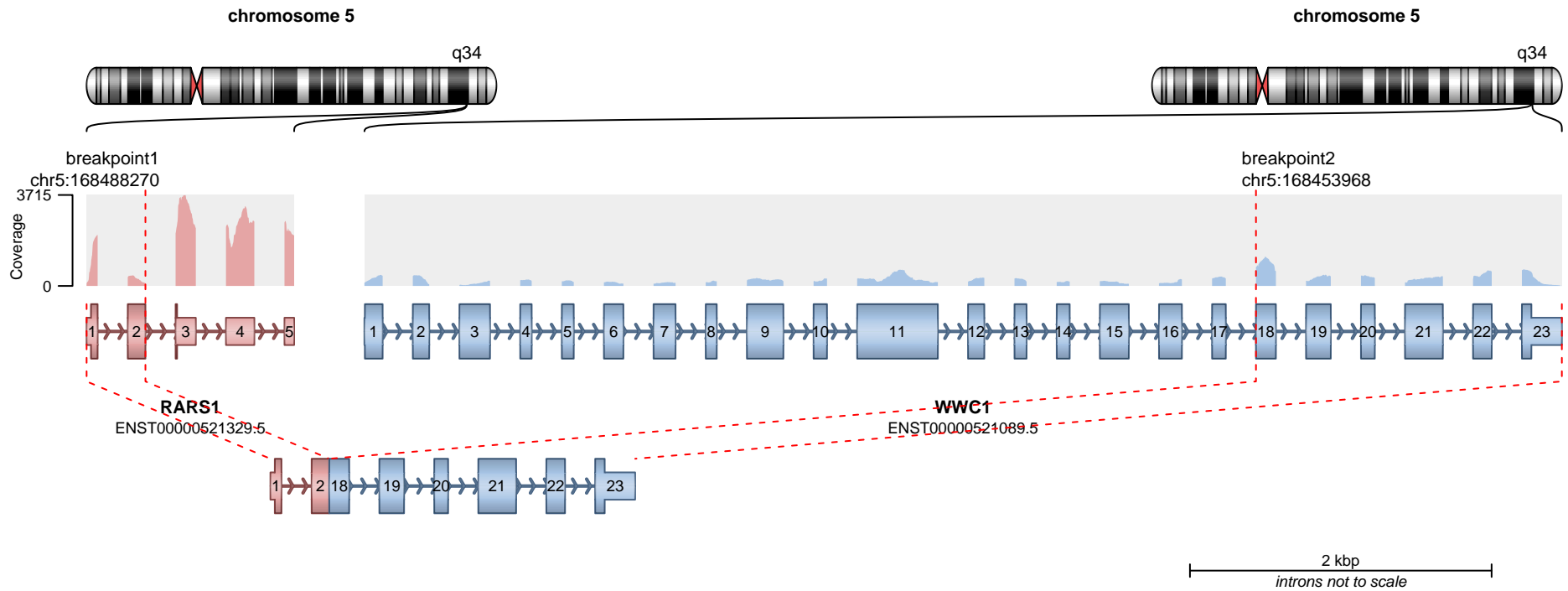


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

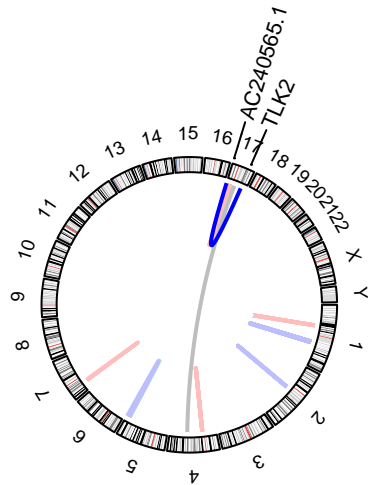
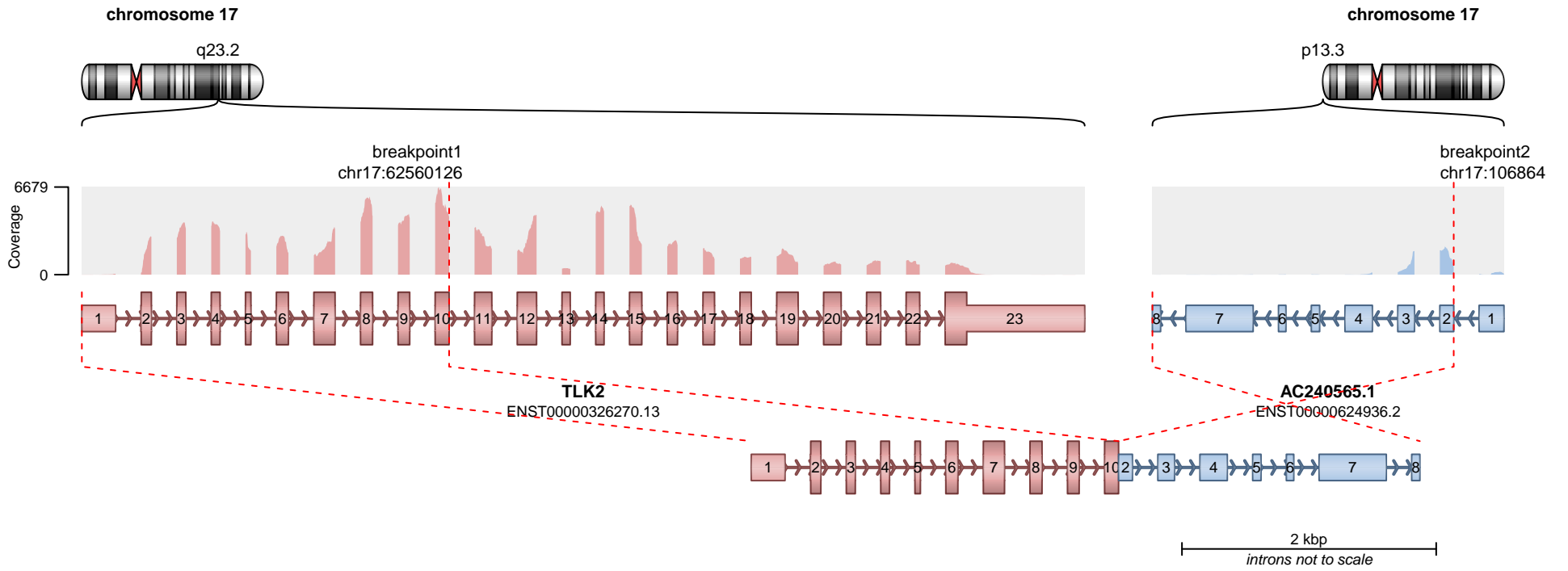


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

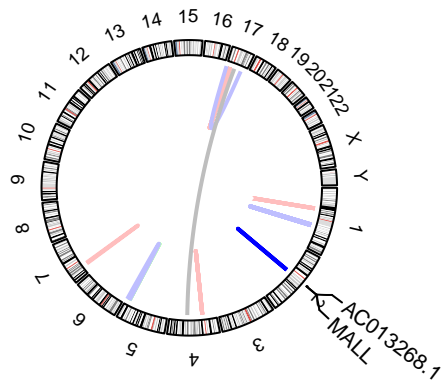
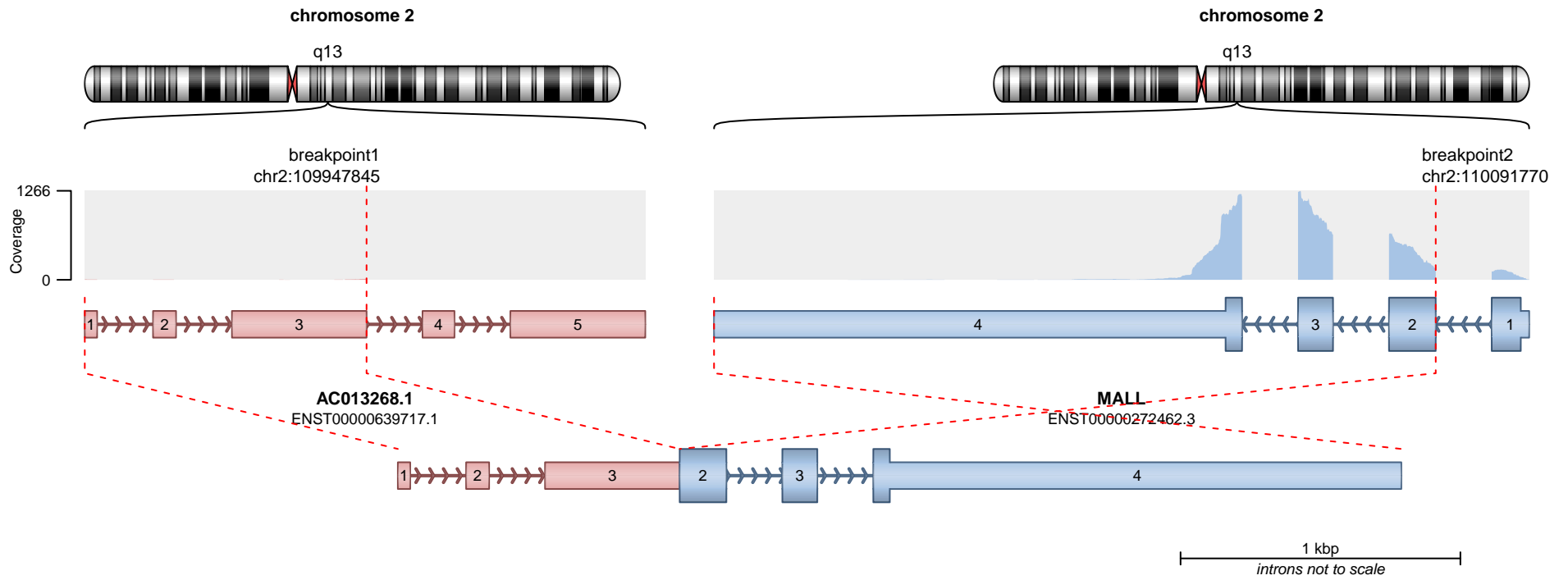


No protein domains retained in fusion.

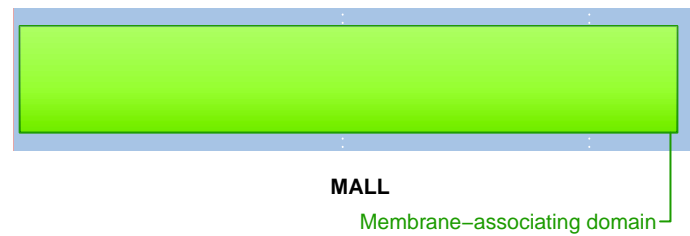
SUPPORTING READ COUNT

Split reads = 92
Discordant mates = 0

— translocation — deletion
— duplication — inversion



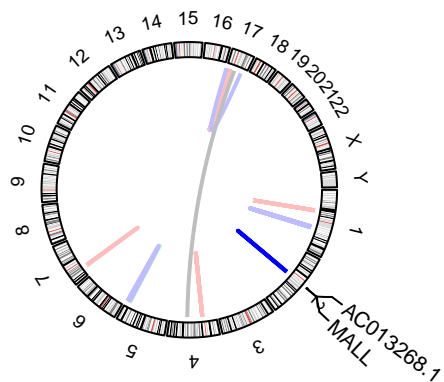
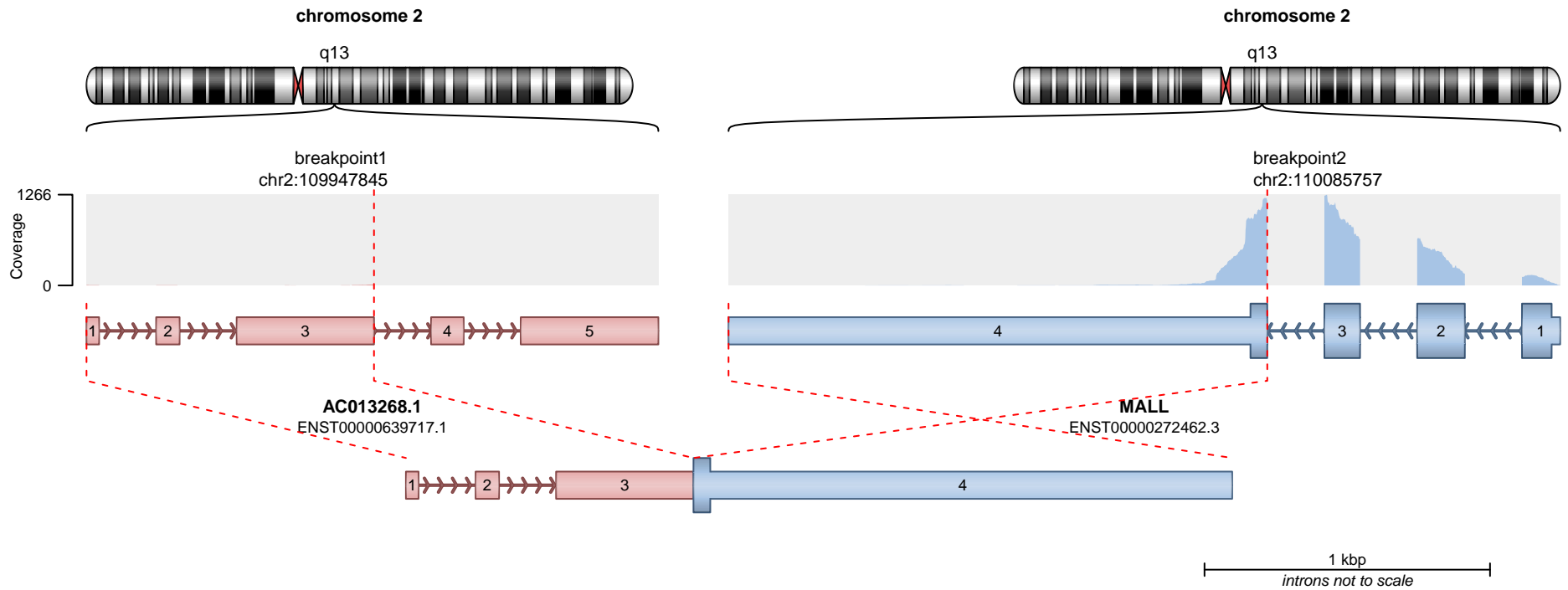
RETAINED PROTEIN DOMAINS
reading frame unclear



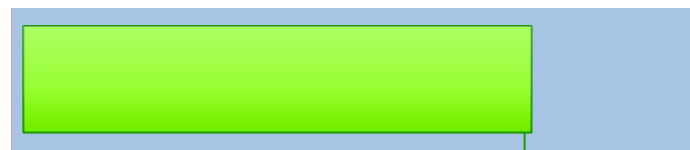
SUPPORTING READ COUNT

Split reads = 80
Discordant mates = 0

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

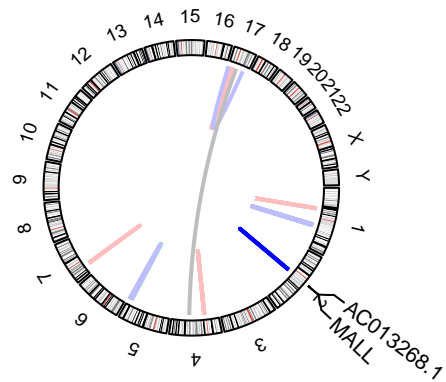
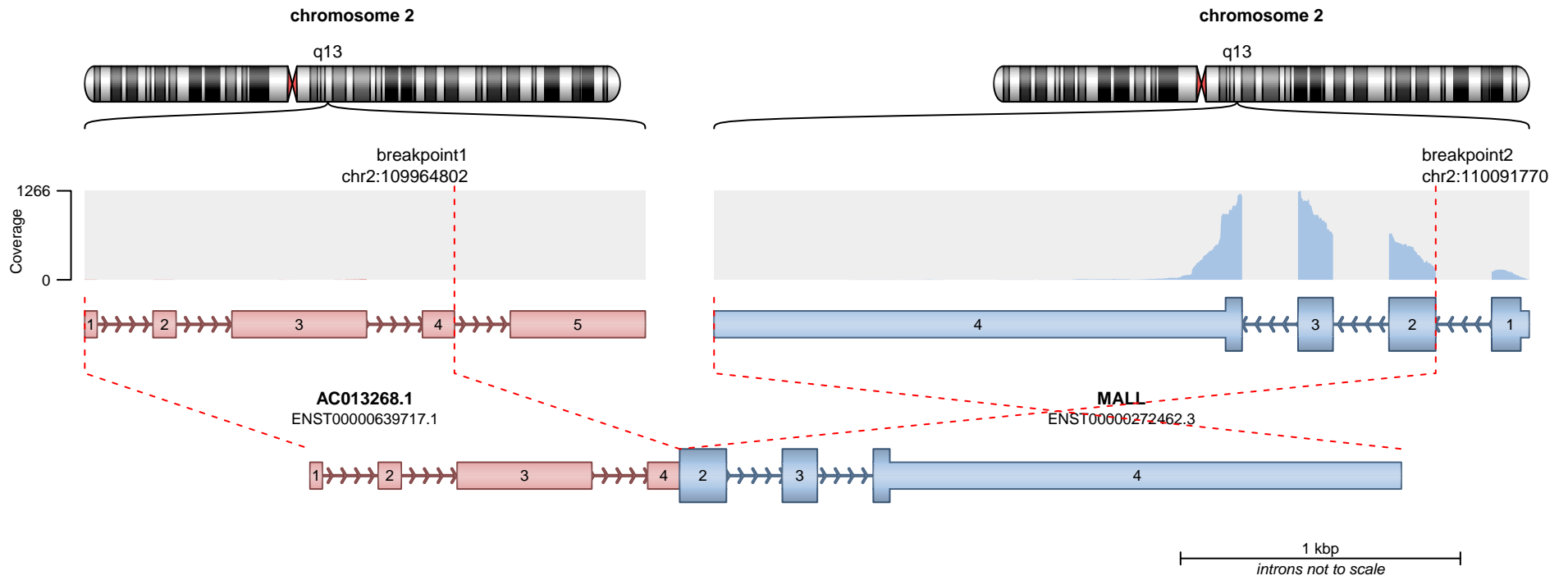


MALL
Membrane-associating domain

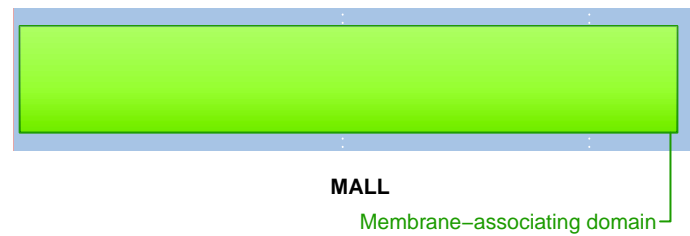
SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 0

— translocation — deletion
— duplication — inversion



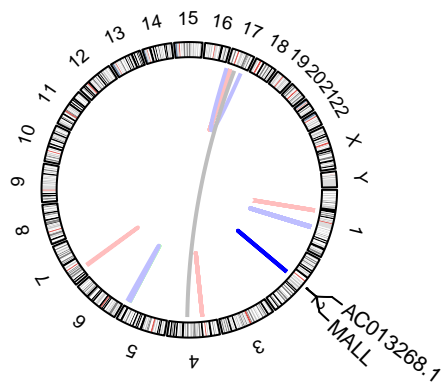
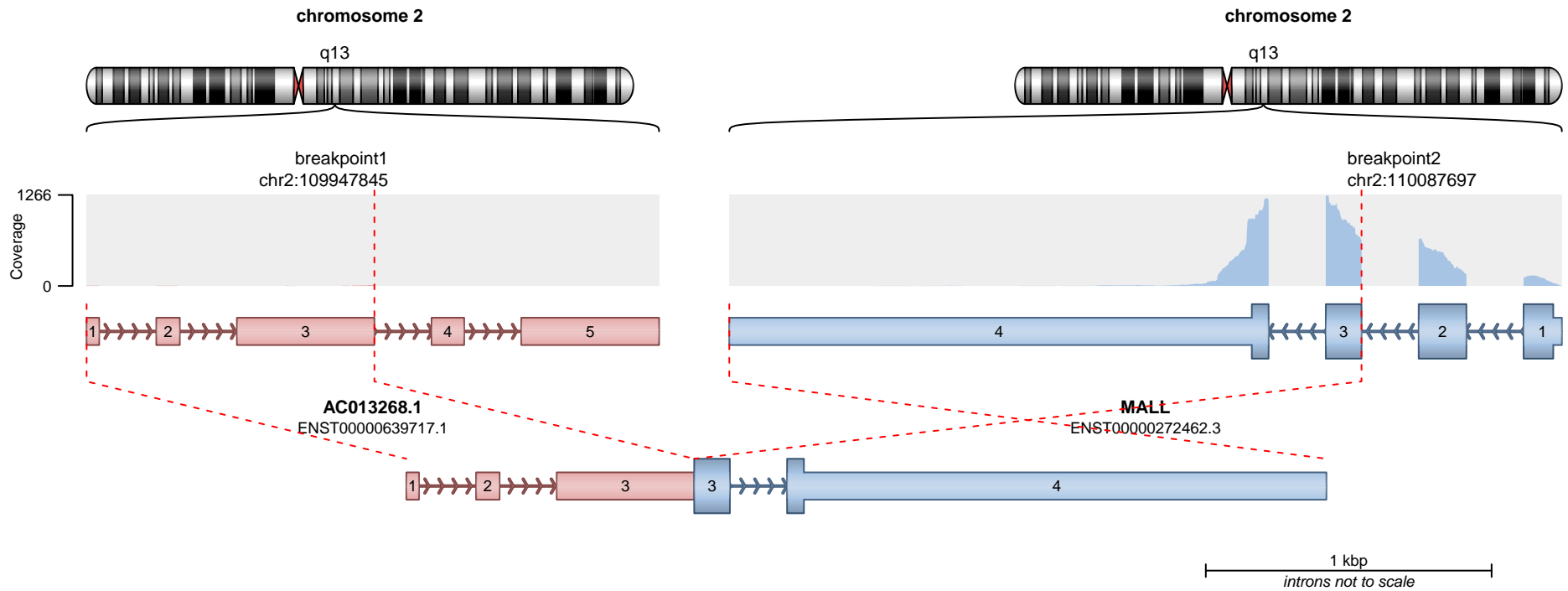
RETAINED PROTEIN DOMAINS
reading frame unclear



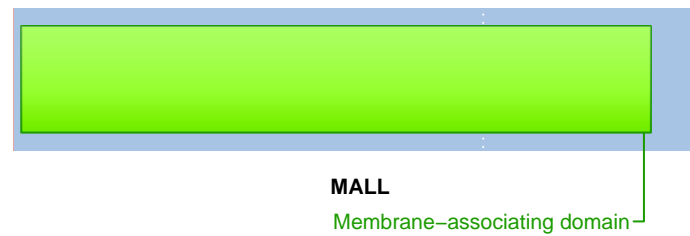
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

— translocation — deletion
— duplication — inversion



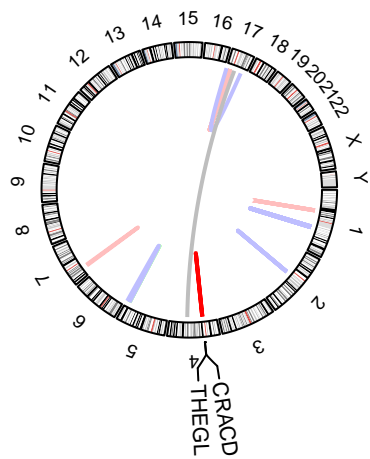
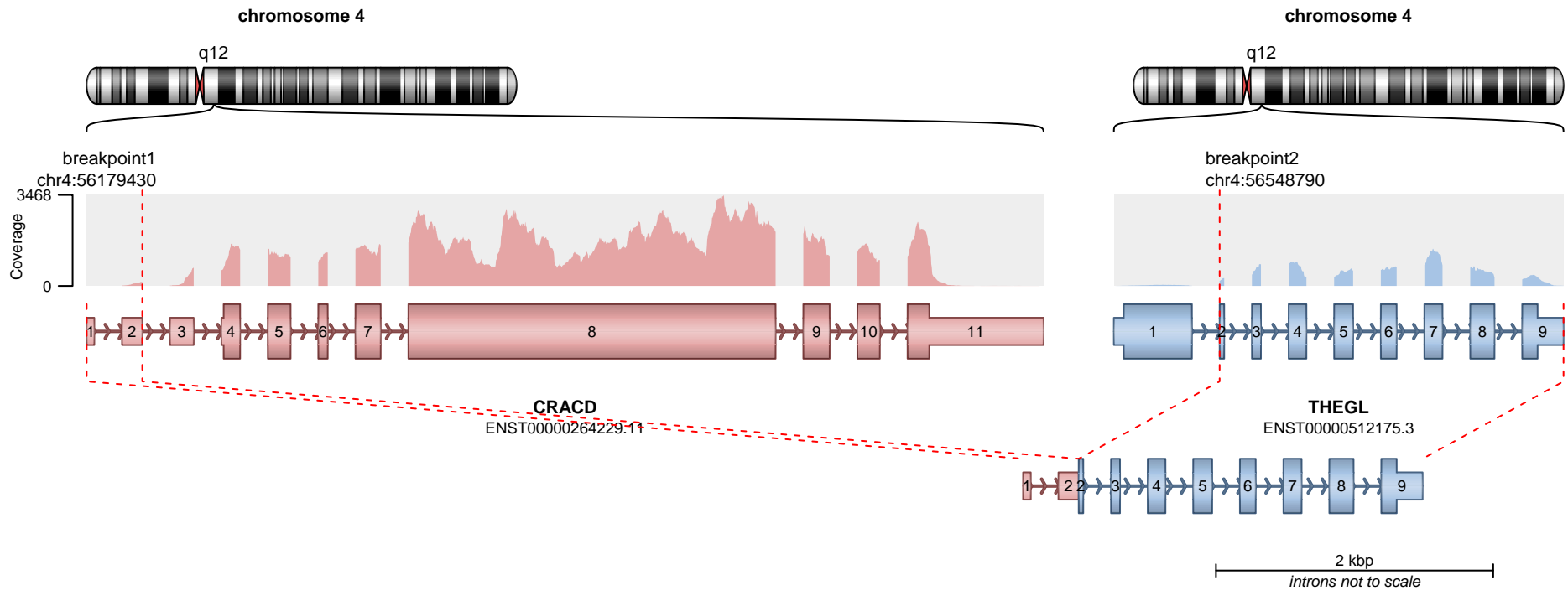
RETAINED PROTEIN DOMAINS
reading frame unclear



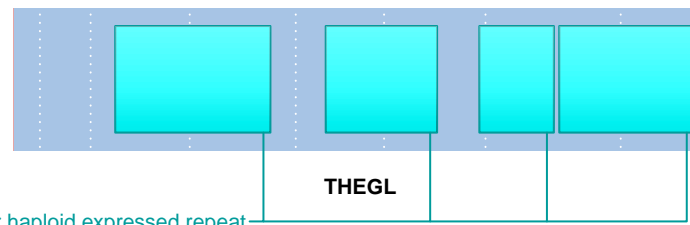
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



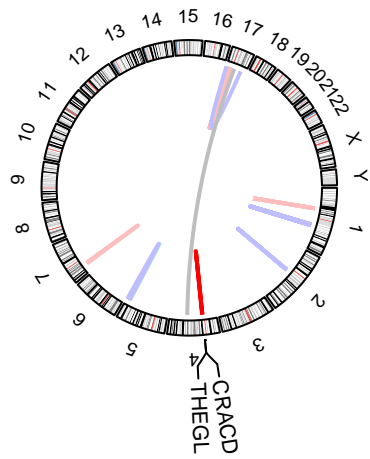
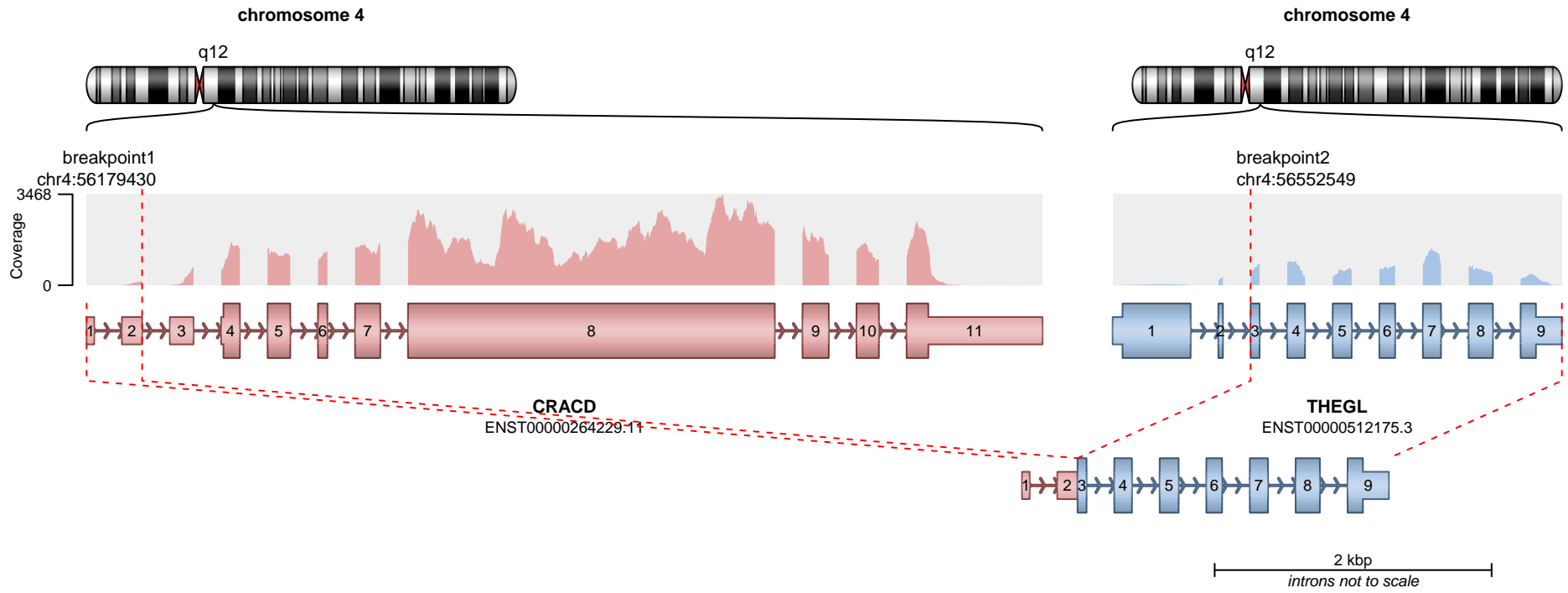
RETAINED PROTEIN DOMAINS
reading frame unclear



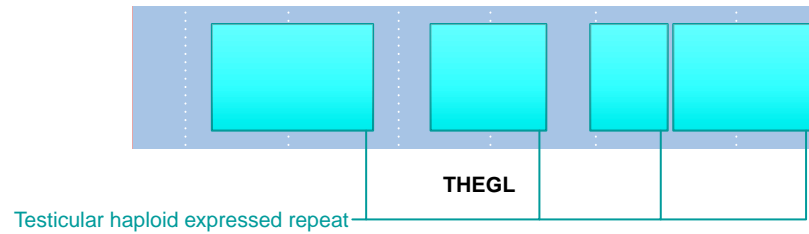
SUPPORTING READ COUNT

Split reads = 78
Discordant mates = 2

- translocation
- duplication
- deletion
- inversion



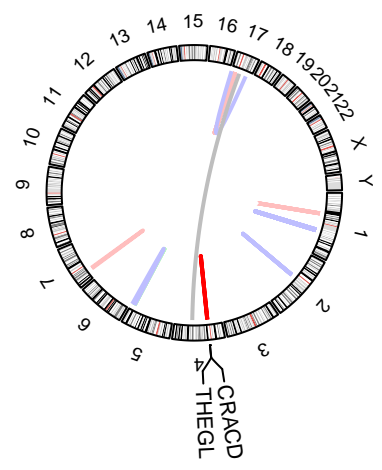
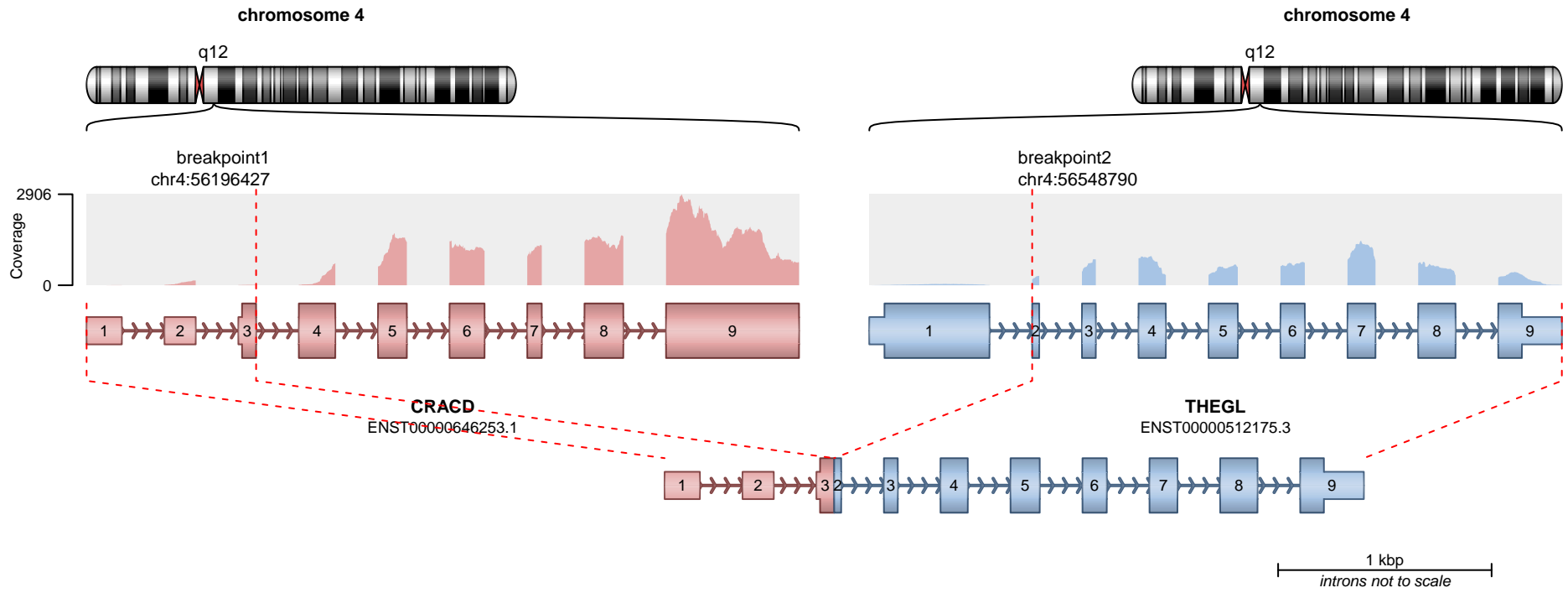
RETAINED PROTEIN DOMAINS
reading frame unclear



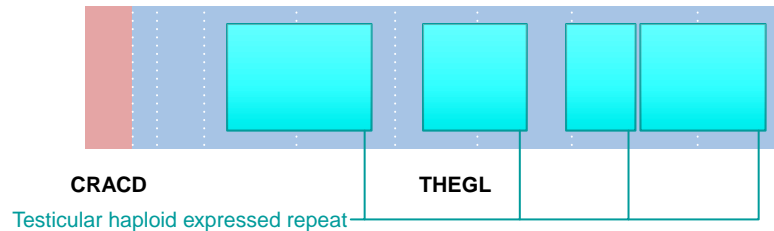
SUPPORTING READ COUNT

Split reads = 28
Discordant mates = 2

- translocation
- duplication
- deletion
- inversion



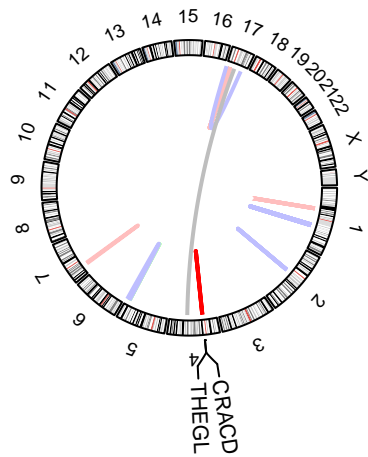
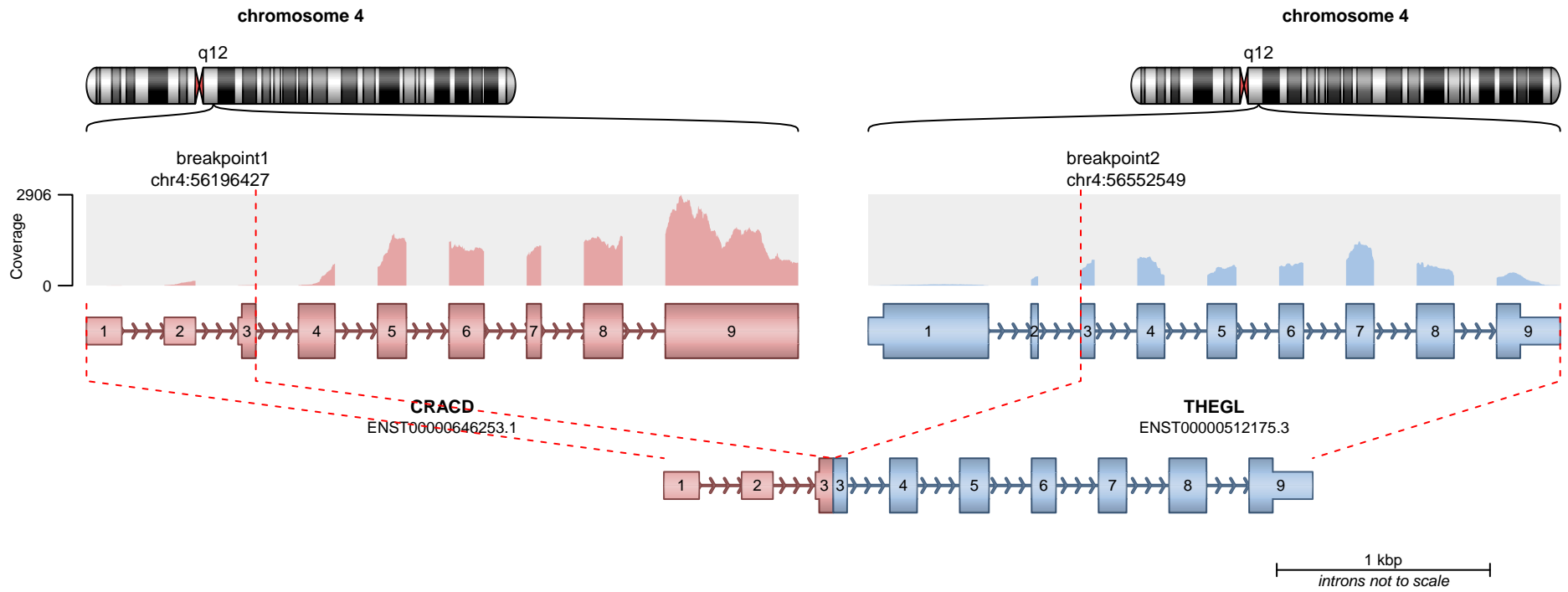
RETAINED PROTEIN DOMAINS
reading frame unclear



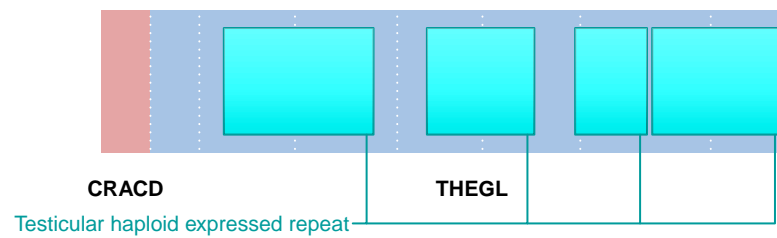
SUPPORTING READ COUNT

Split reads = 9
Discordant mates = 4

- translocation
- duplication
- deletion
- inversion



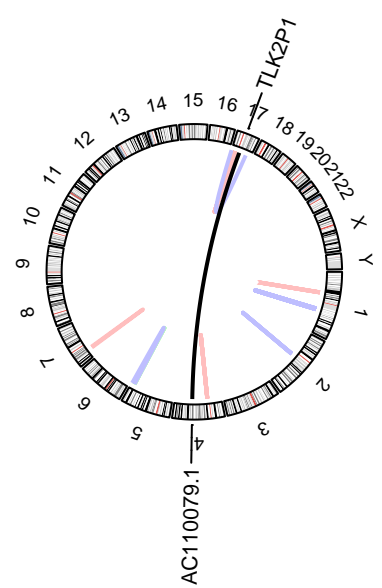
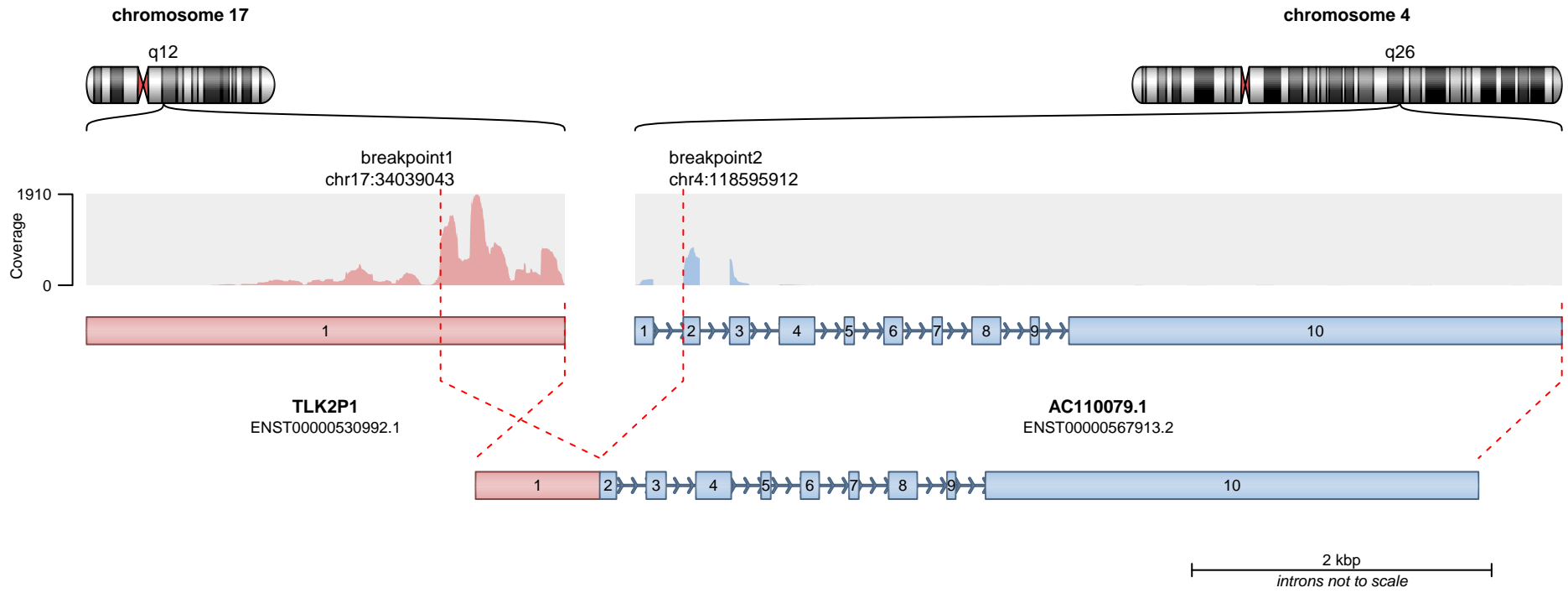
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 4

- translocation
- duplication
- deletion
- inversion

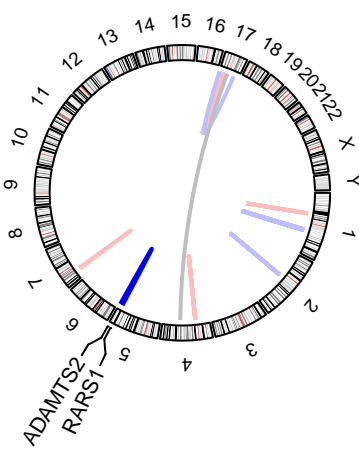
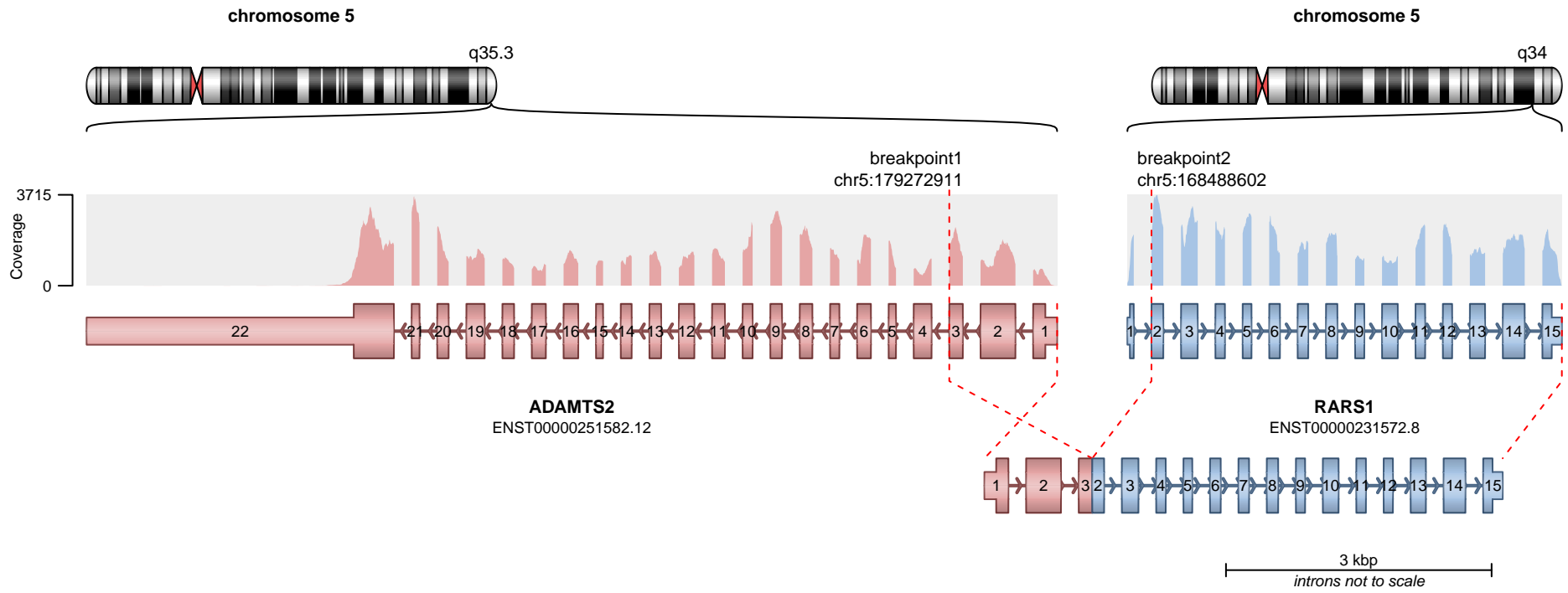


— translocation — deletion
 — duplication — inversion

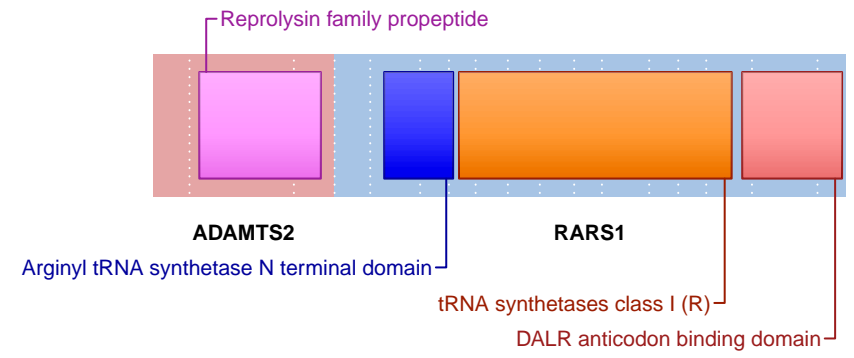
Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 64
Discordant mates = 0



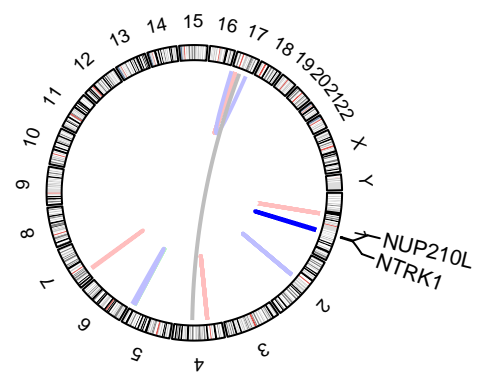
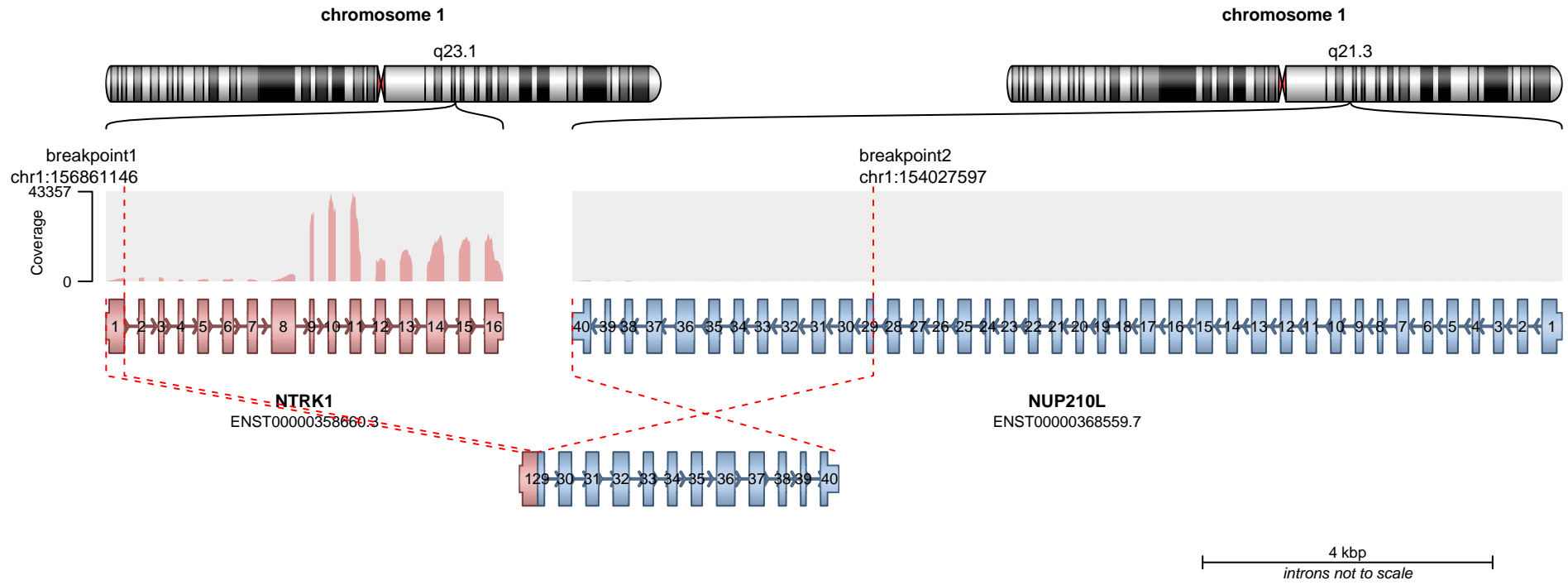
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 45
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

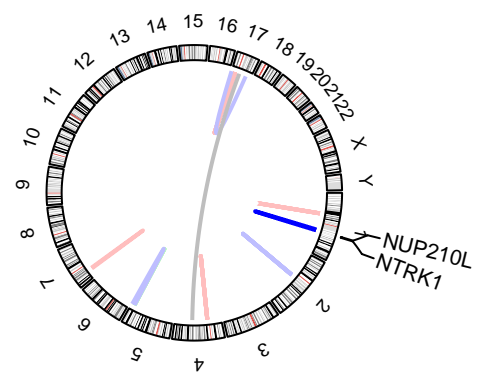
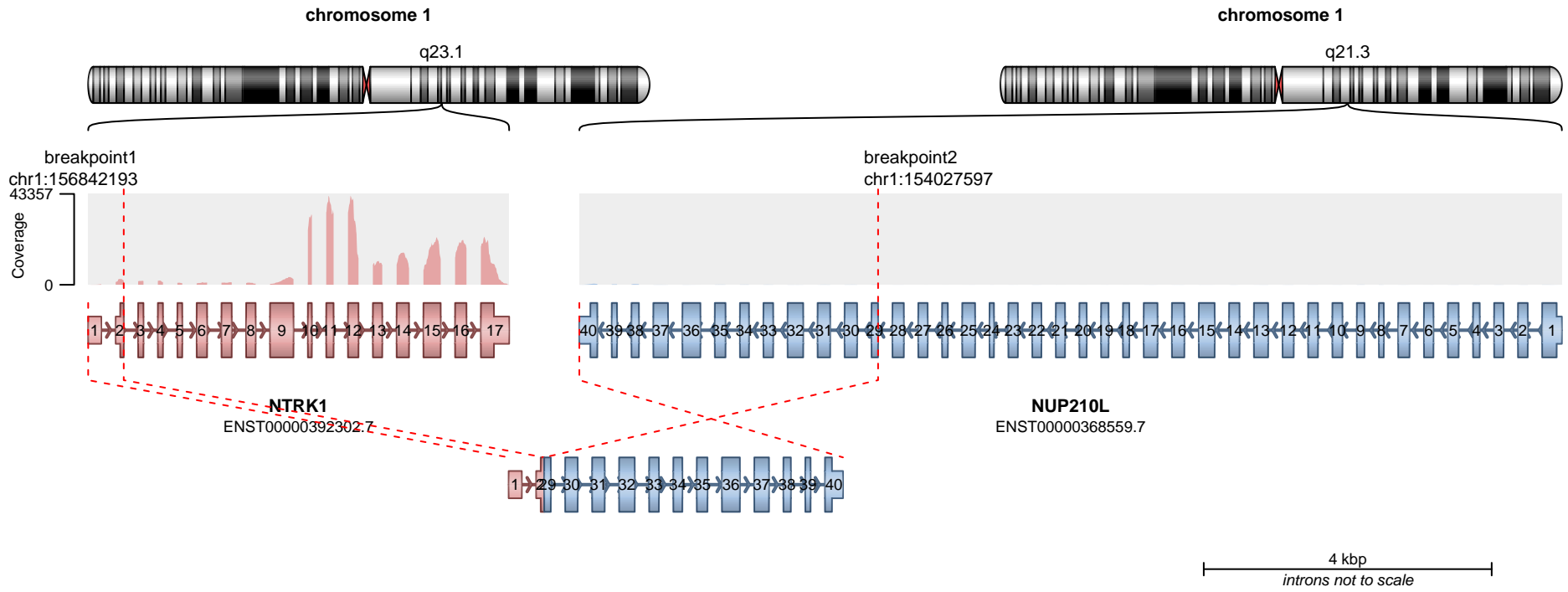


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 28
Discordant mates = 1

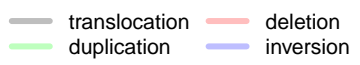
- translocation
- duplication
- deletion
- inversion

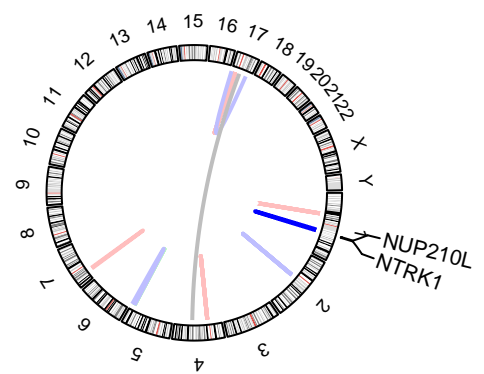
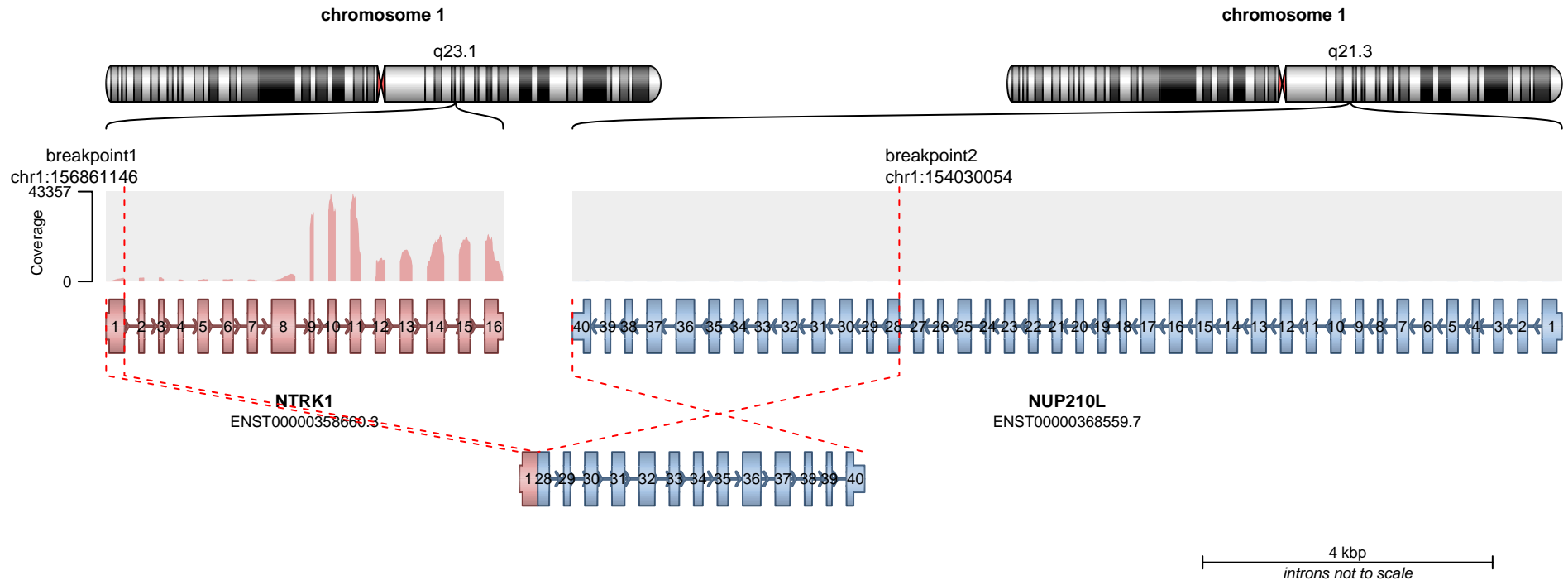


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 0



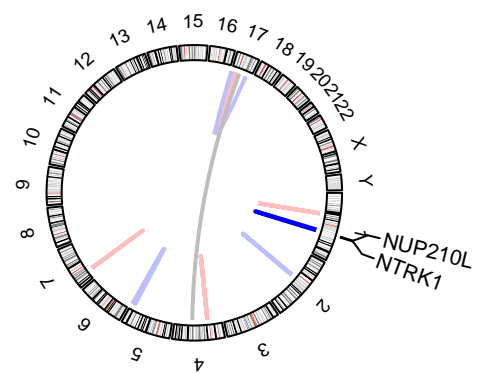
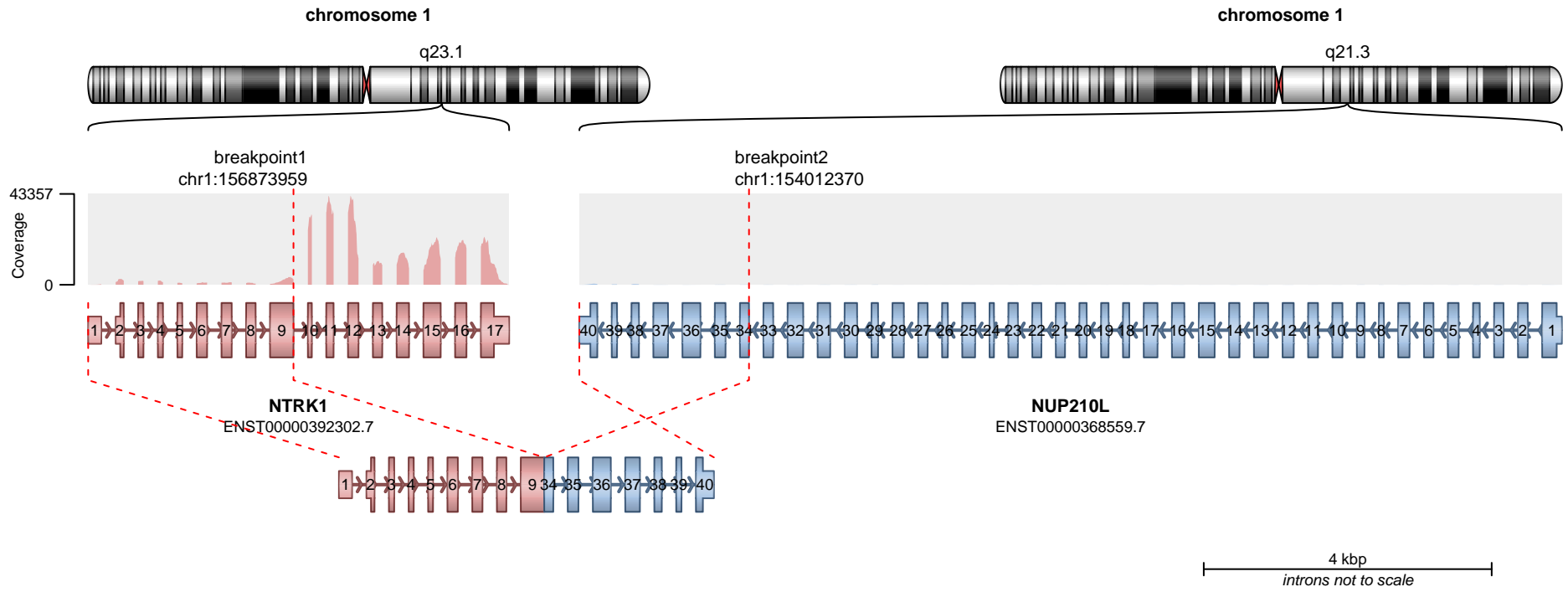


No protein domains retained in fusion.

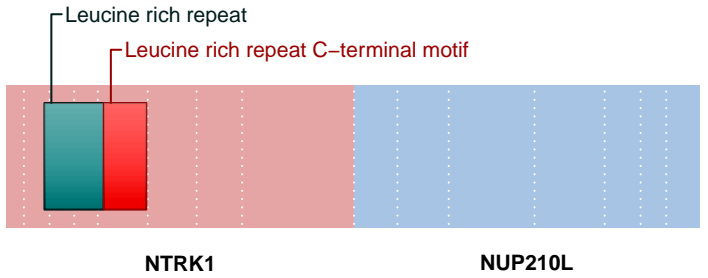
SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



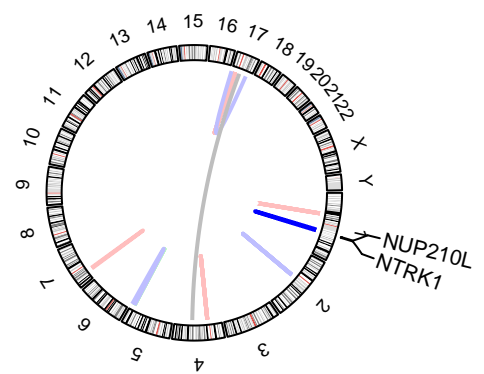
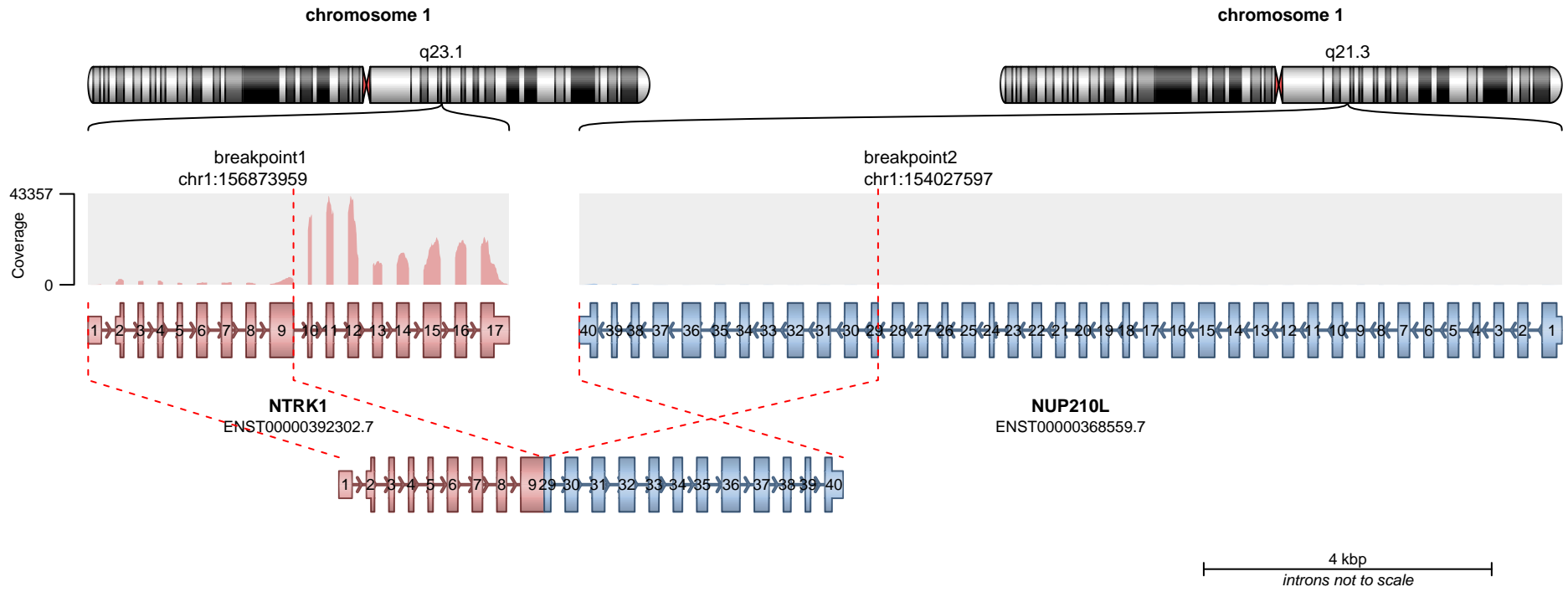
RETAINED PROTEIN DOMAINS
reading frame unclear



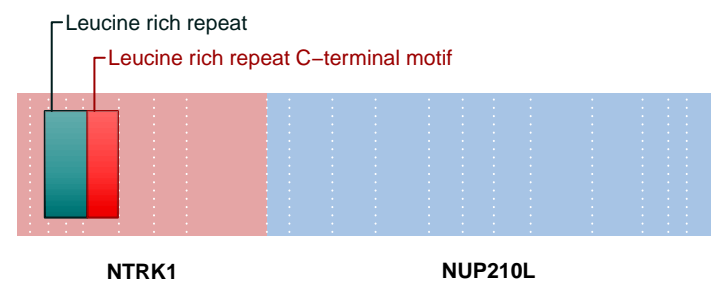
SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



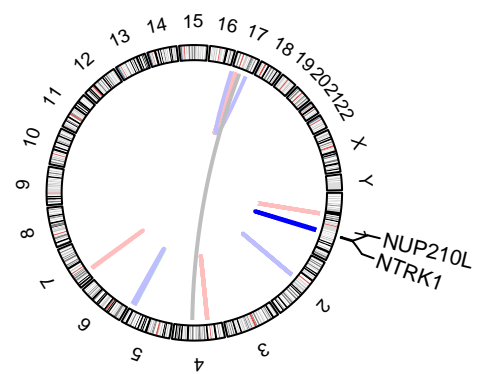
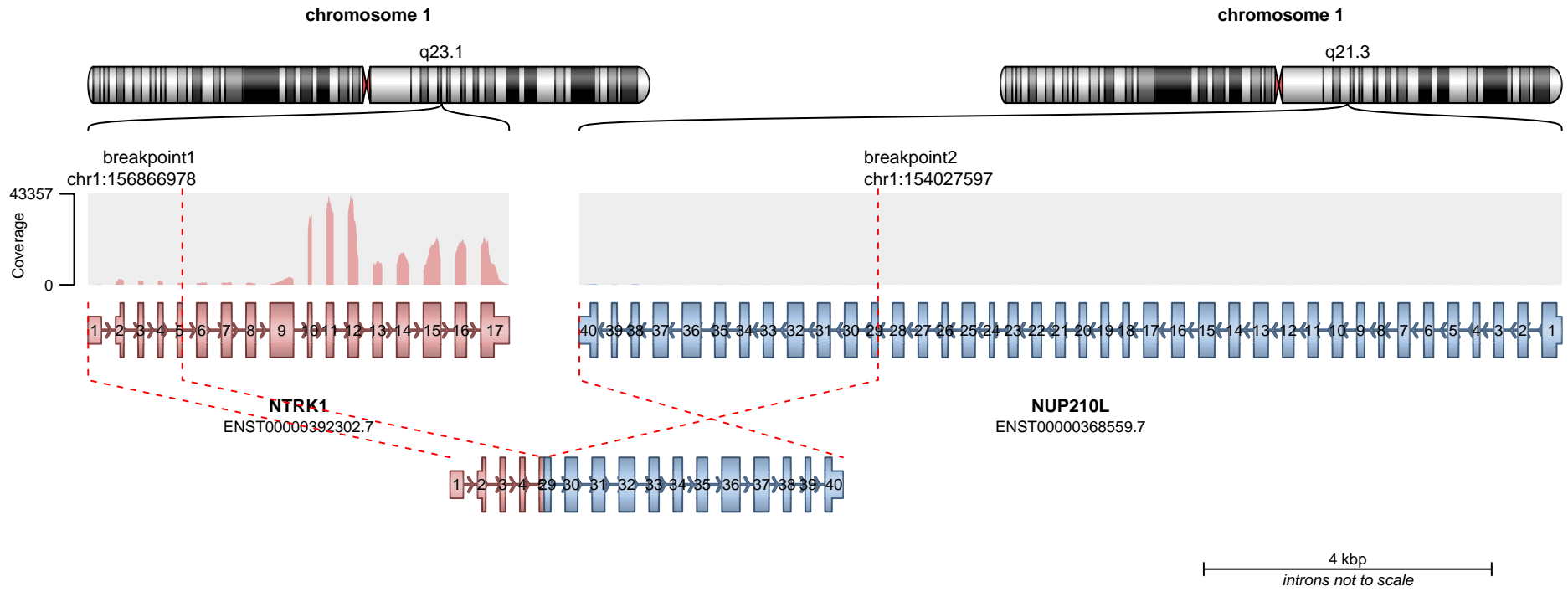
RETAINED PROTEIN DOMAINS
reading frame unclear



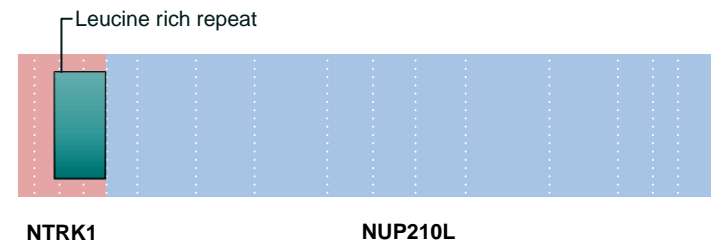
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



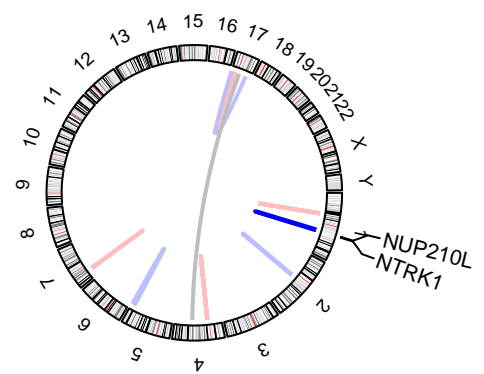
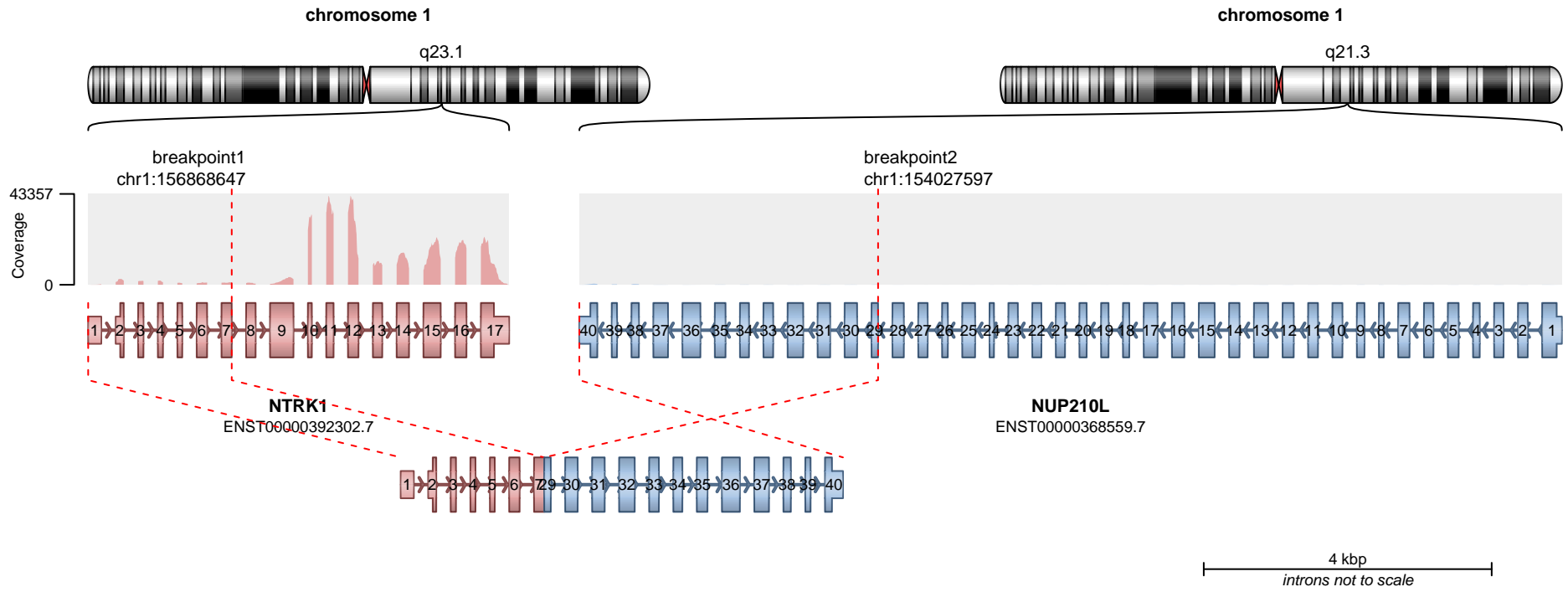
RETAINED PROTEIN DOMAINS
reading frame unclear



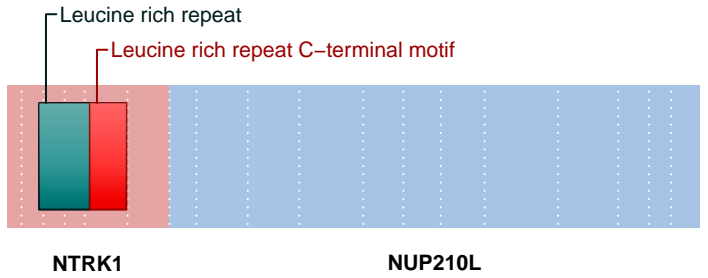
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



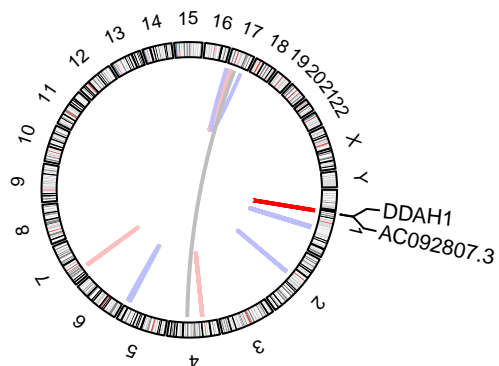
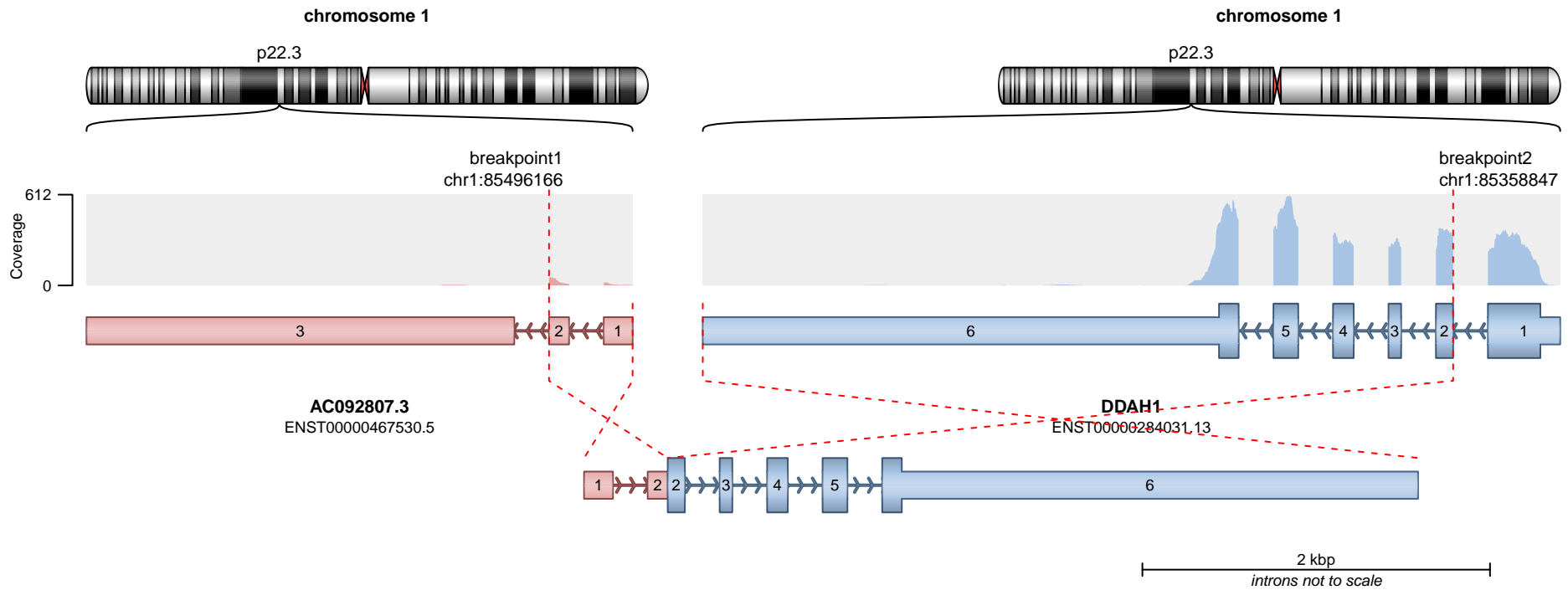
RETAINED PROTEIN DOMAINS
reading frame unclear



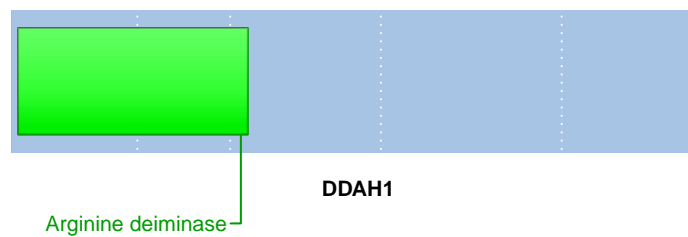
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



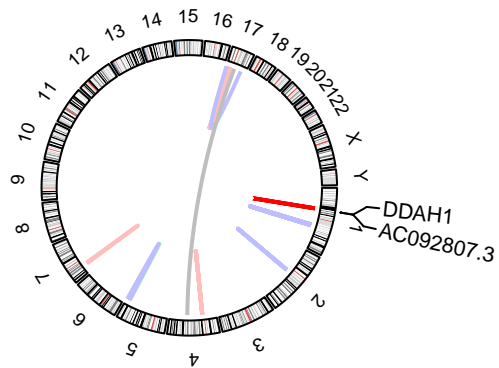
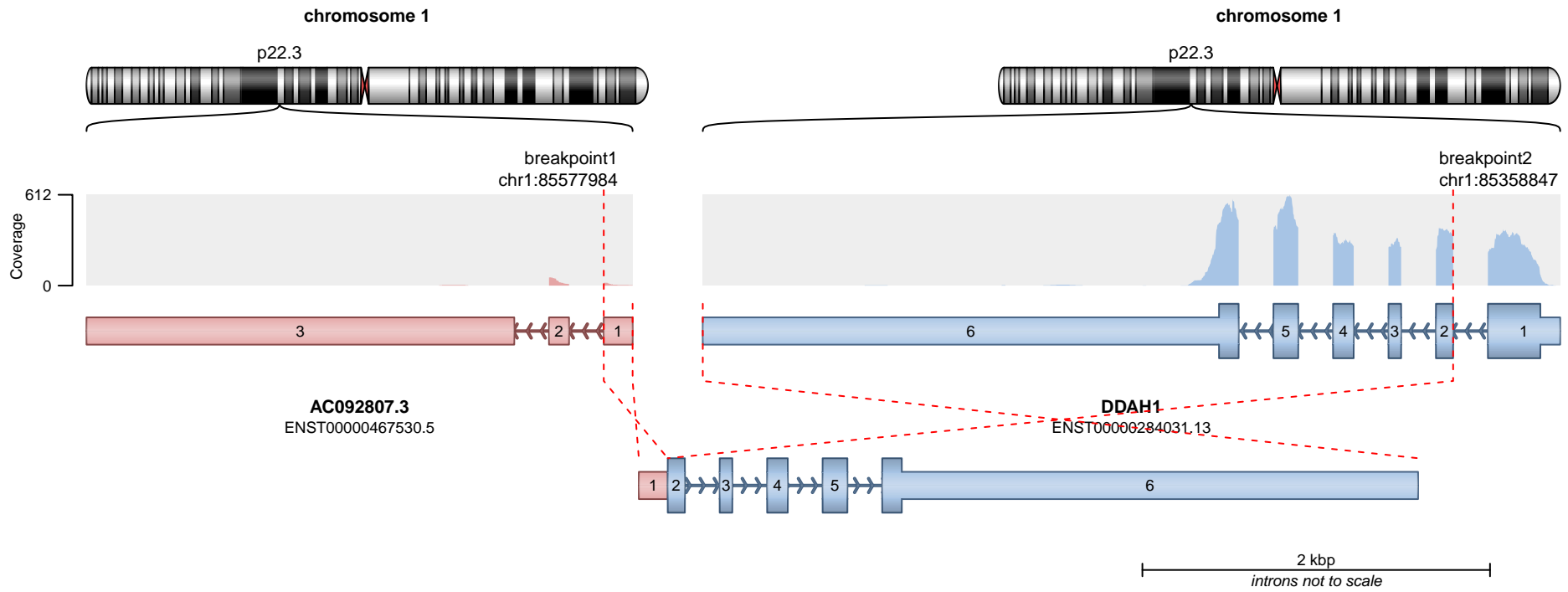
RETAINED PROTEIN DOMAINS
reading frame unclear



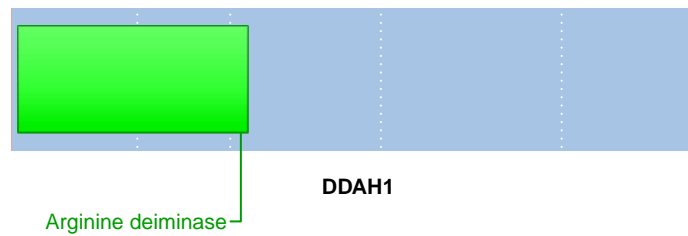
SUPPORTING READ COUNT

Split reads = 23
Discordant mates = 2

- translocation
- duplication
- deletion
- inversion



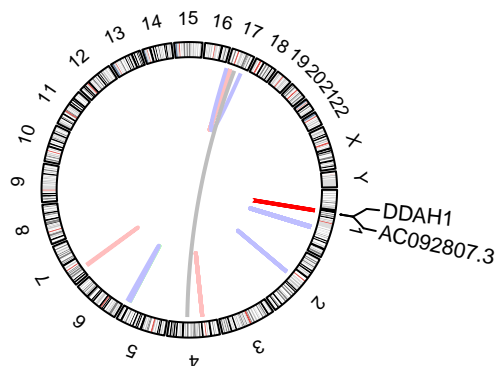
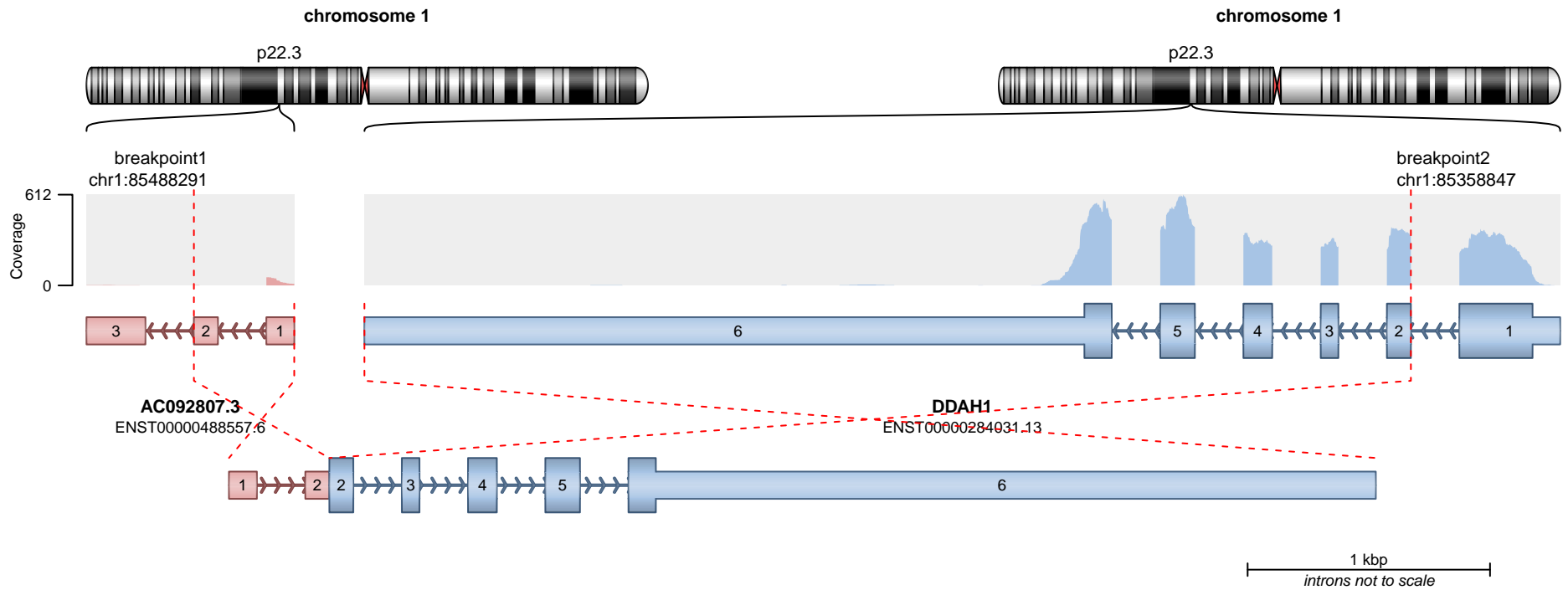
RETAINED PROTEIN DOMAINS
reading frame unclear



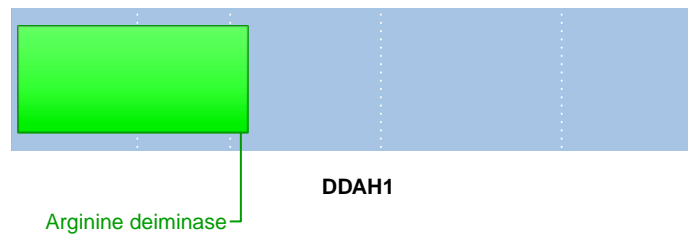
SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



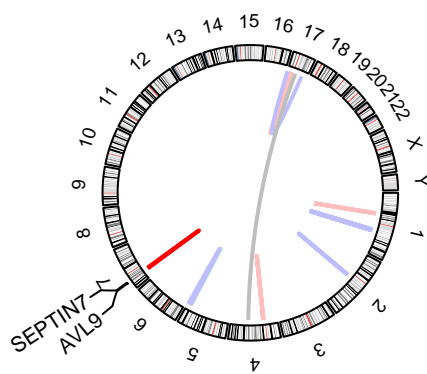
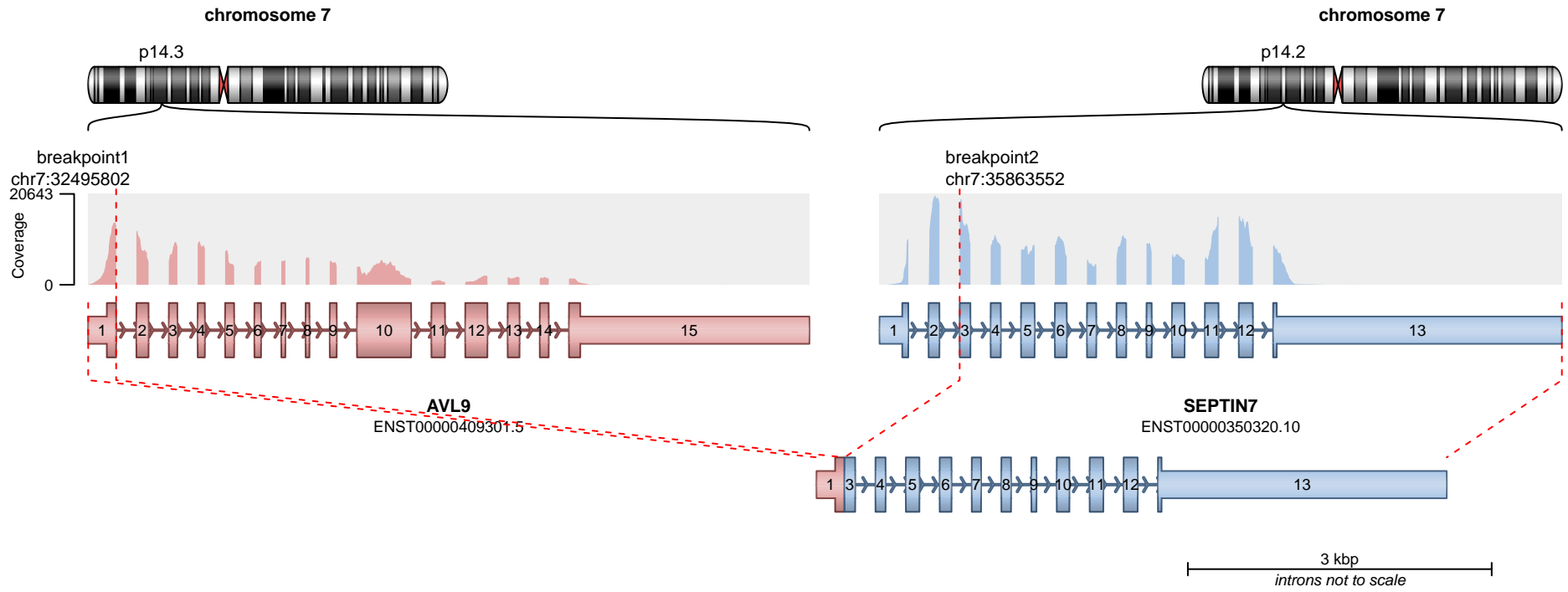
RETAINED PROTEIN DOMAINS
reading frame unclear



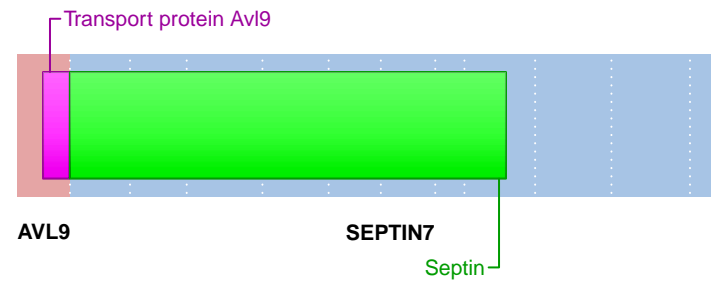
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 2

- translocation
- duplication
- deletion
- inversion



RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion