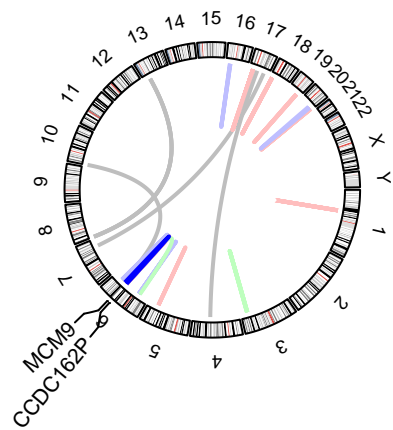
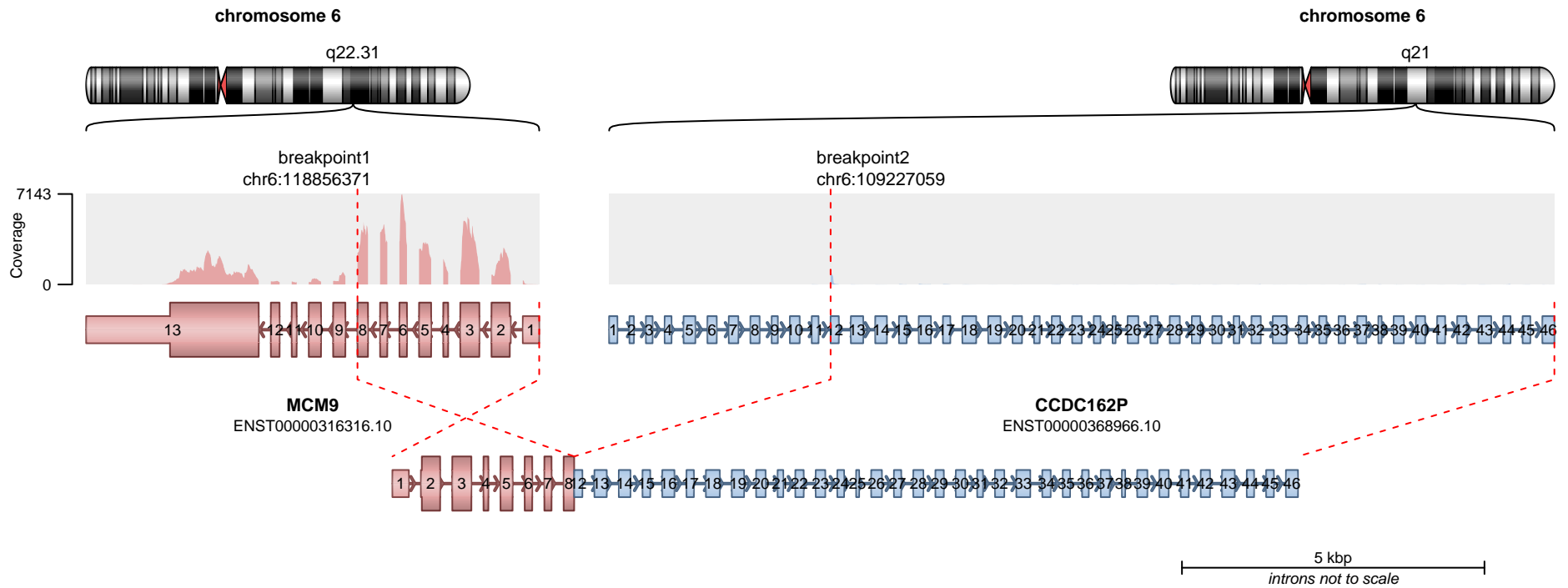


— translocation — deletion
— duplication — inversion

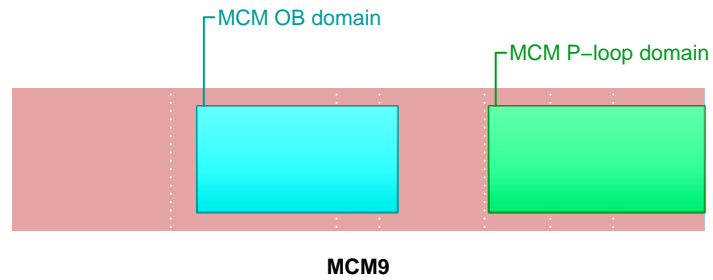
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 816
Discordant mates = 0



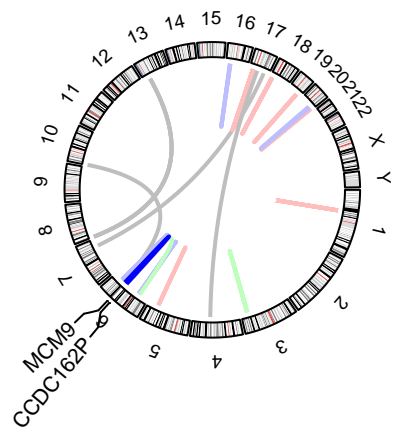
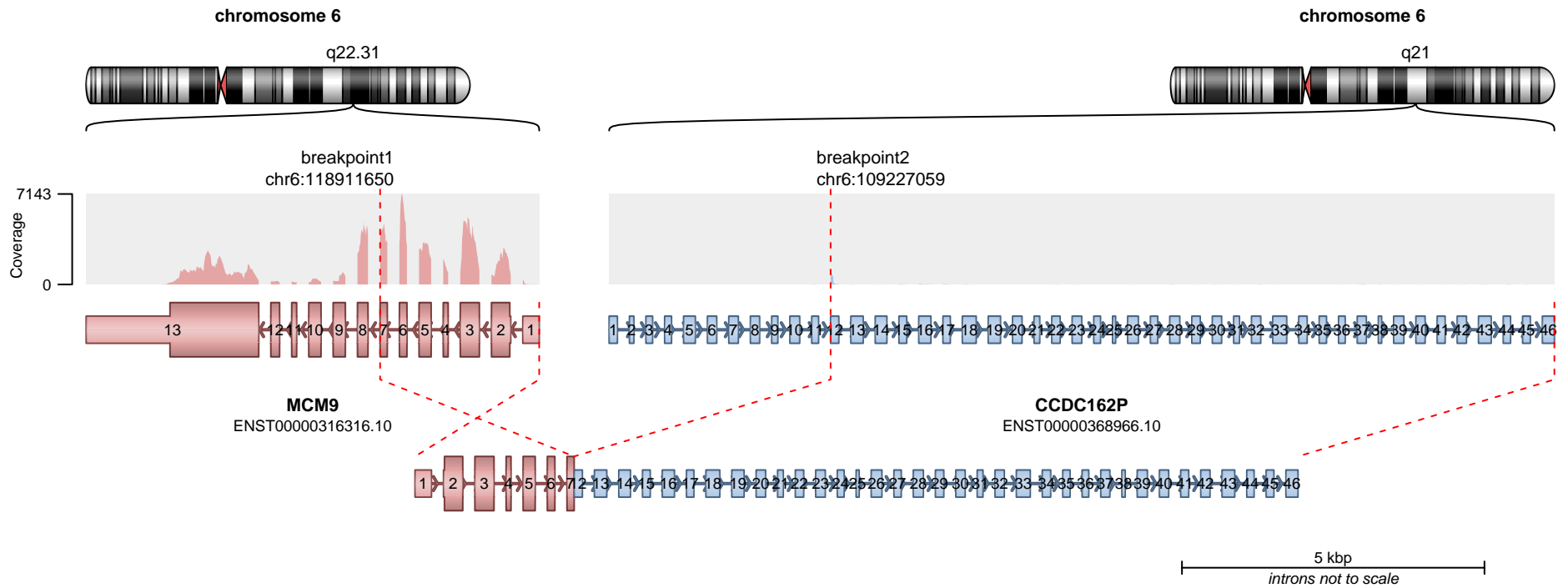
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

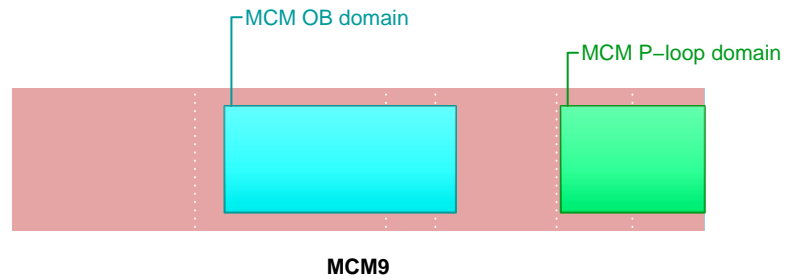
Split reads = 666
Discordant mates = 0

— translocation — deletion
— duplication — inversion



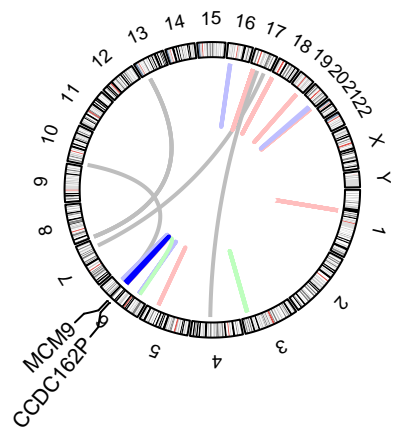
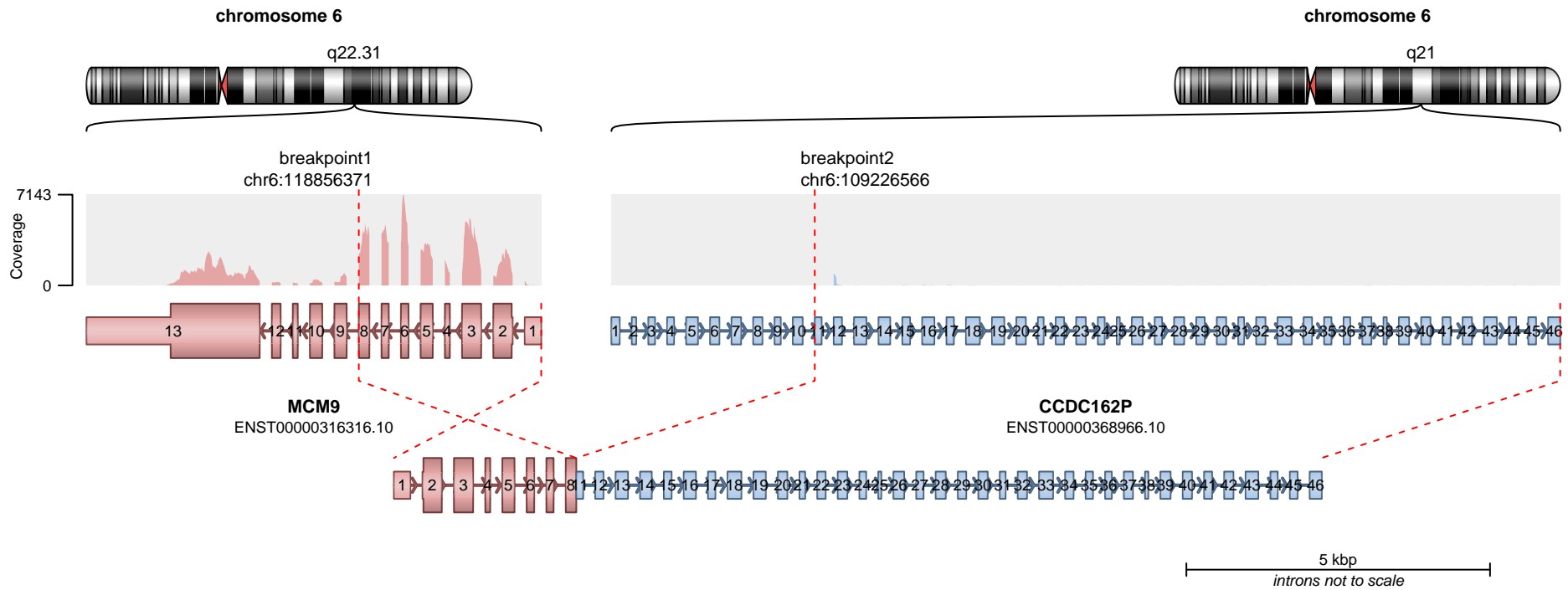
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear

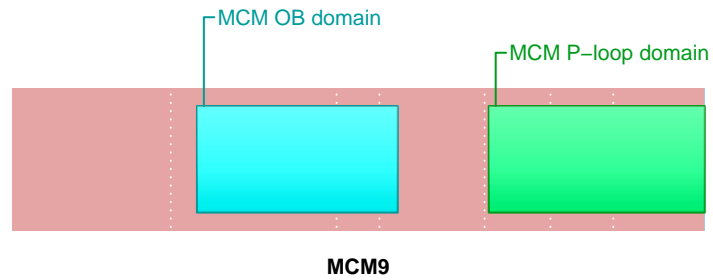


SUPPORTING READ COUNT

Split reads = 70
Discordant mates = 0



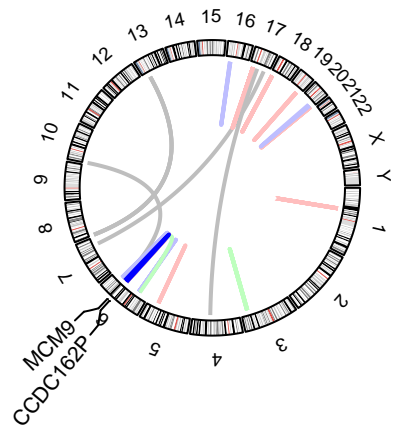
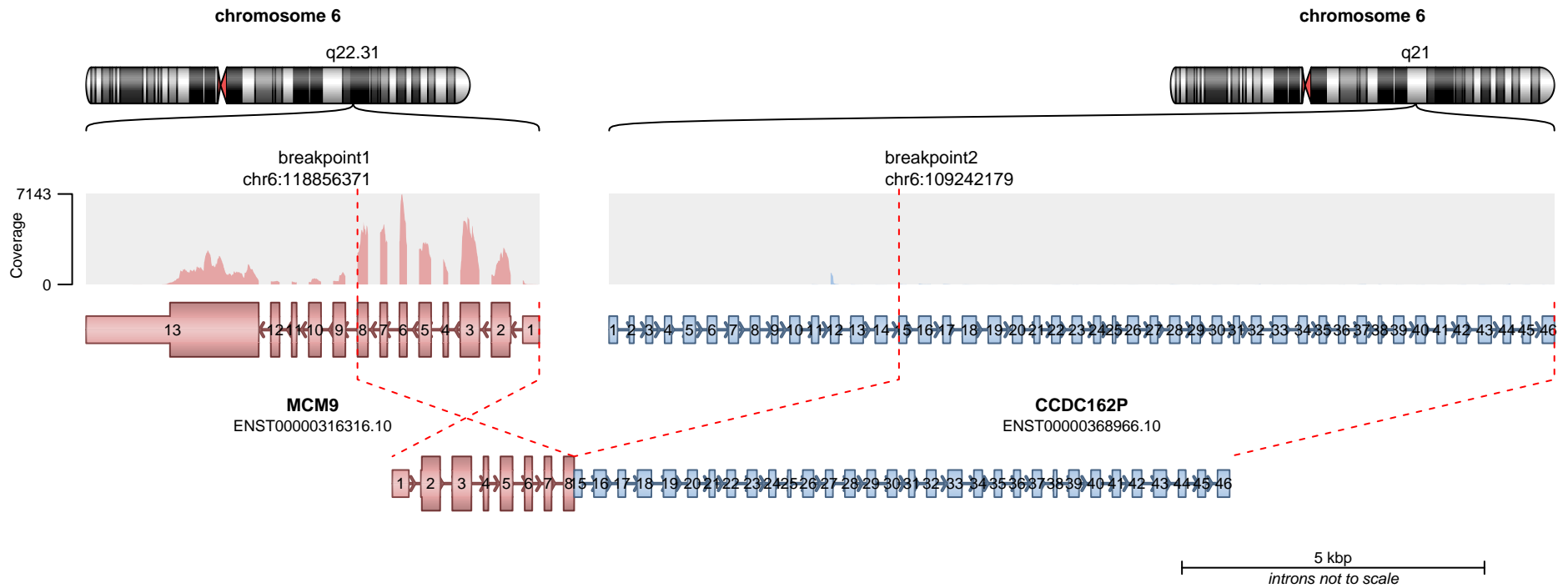
RETAINED PROTEIN DOMAINS
reading frame unclear



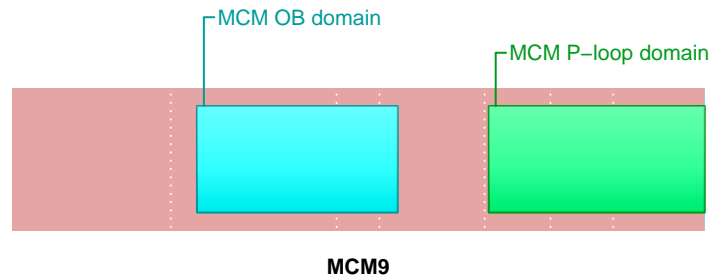
SUPPORTING READ COUNT

Split reads = 16
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



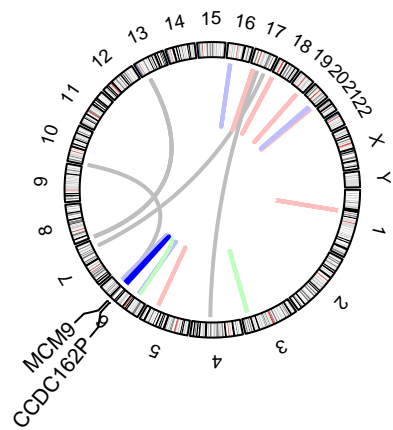
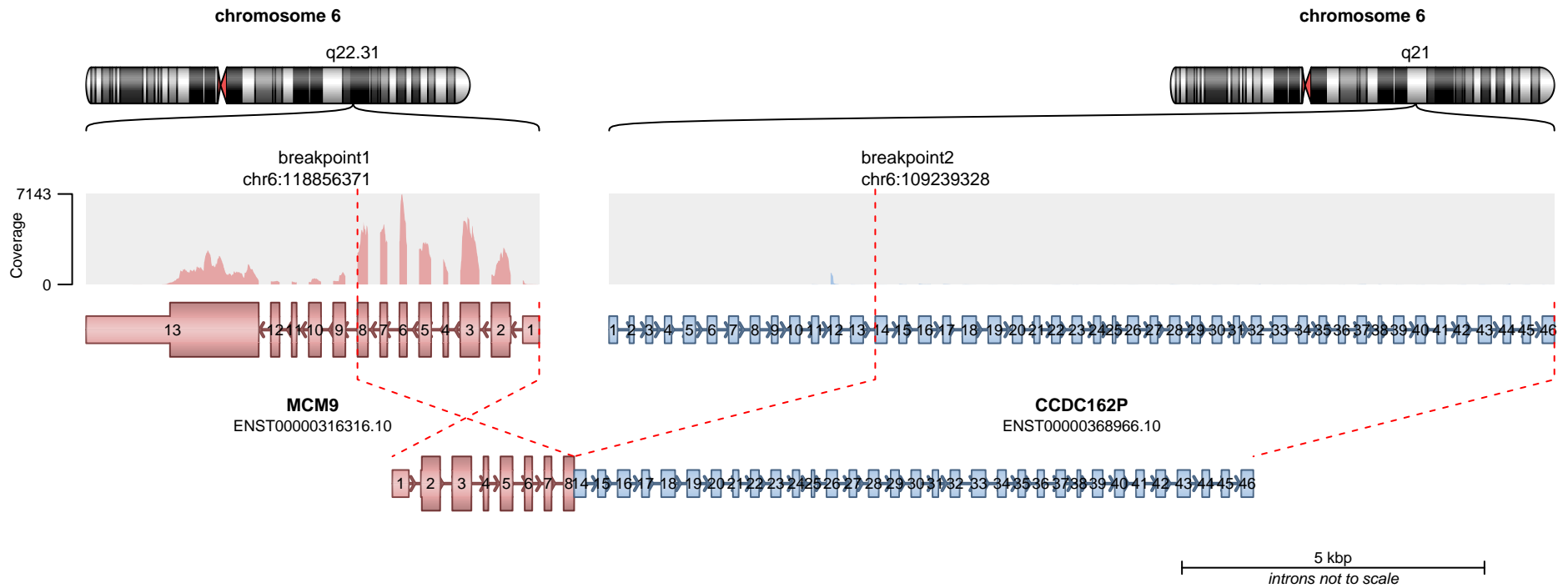
RETAINED PROTEIN DOMAINS
reading frame unclear



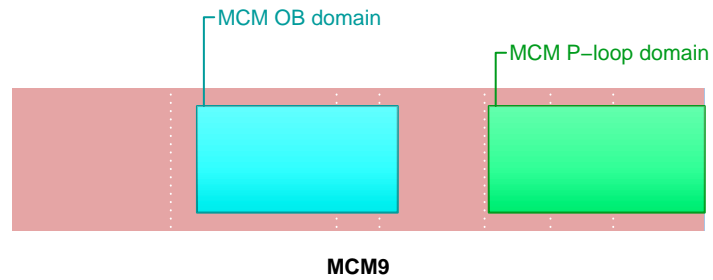
SUPPORTING READ COUNT

Split reads = 11
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



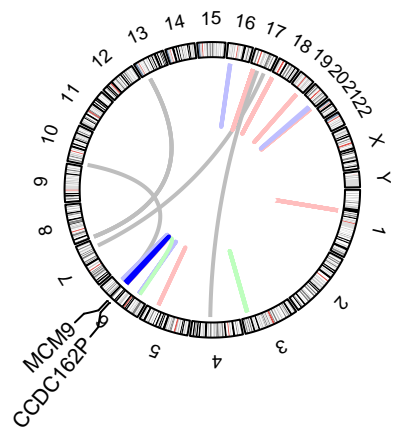
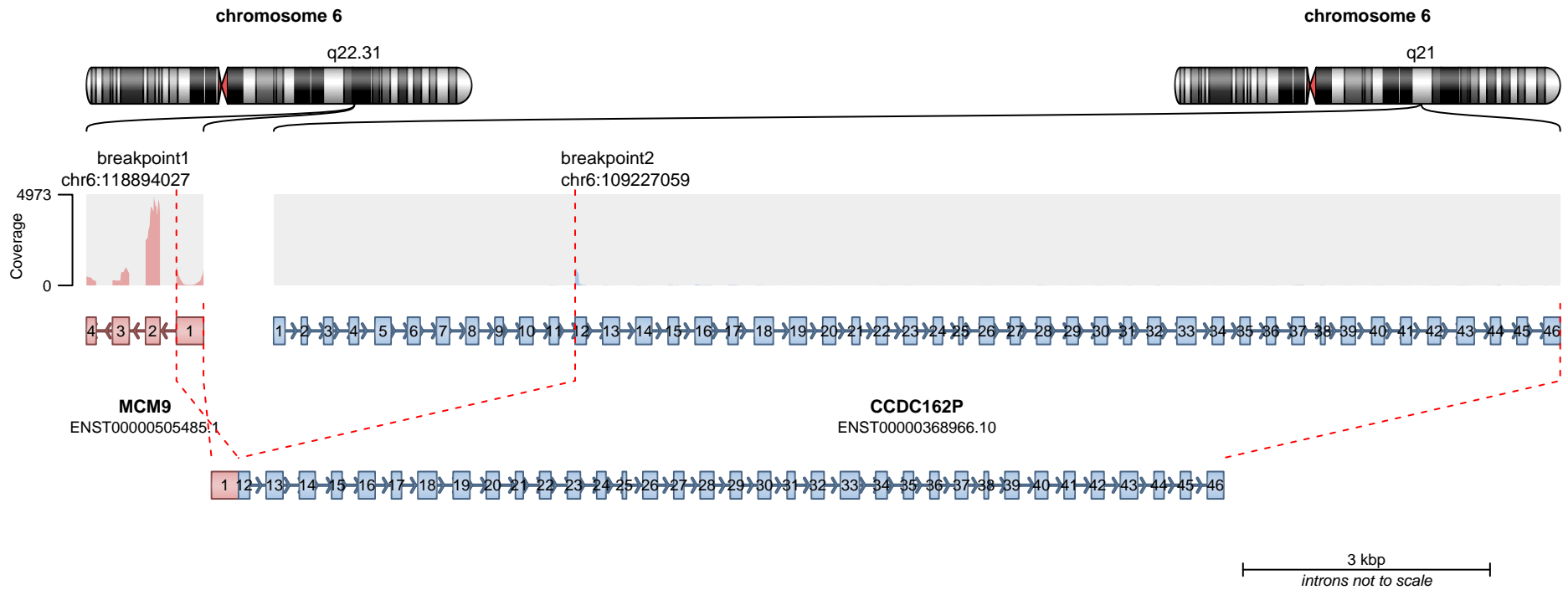
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

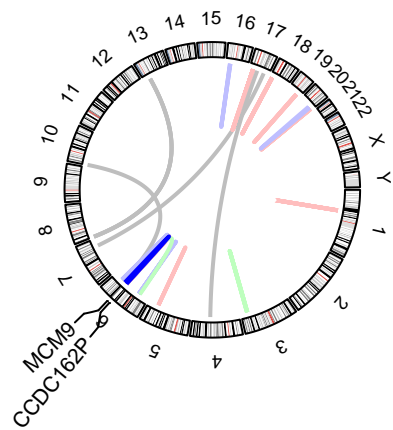
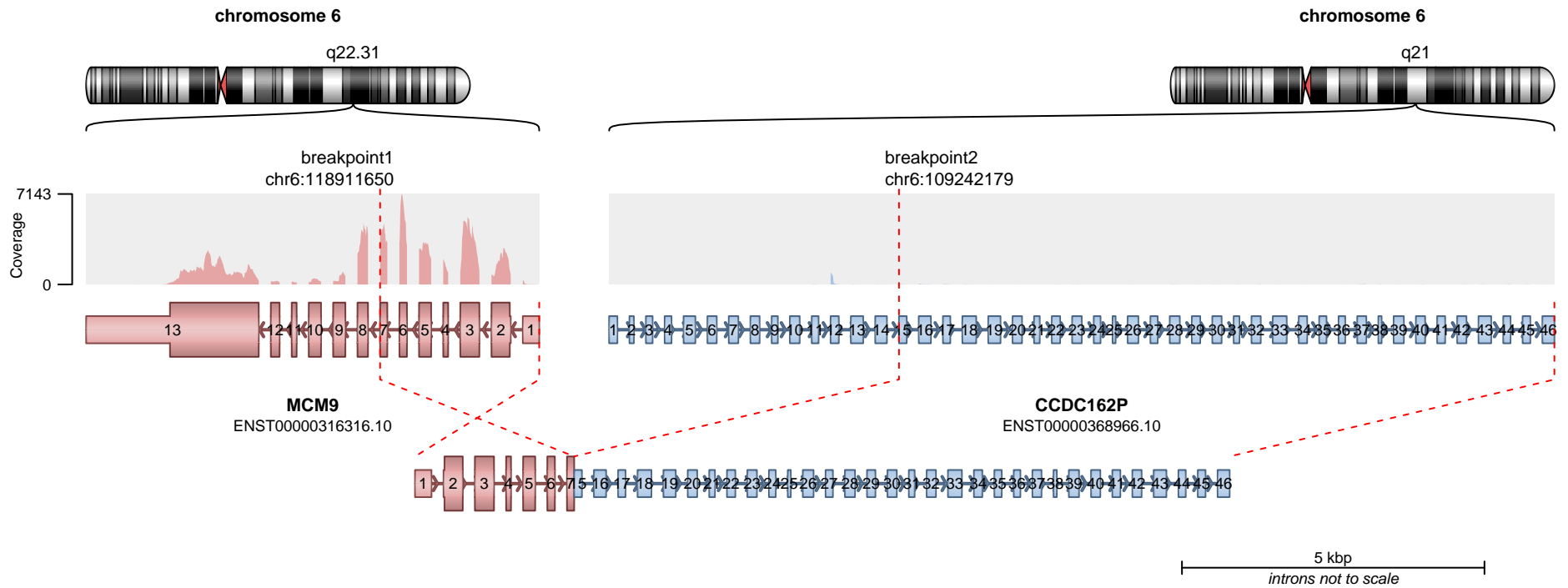


— translocation — deletion
— duplication — inversion

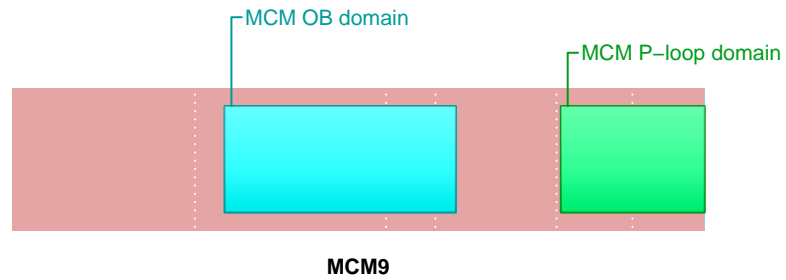
Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0



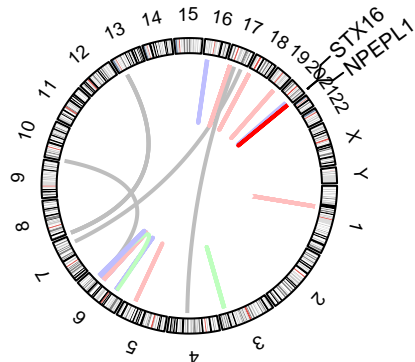
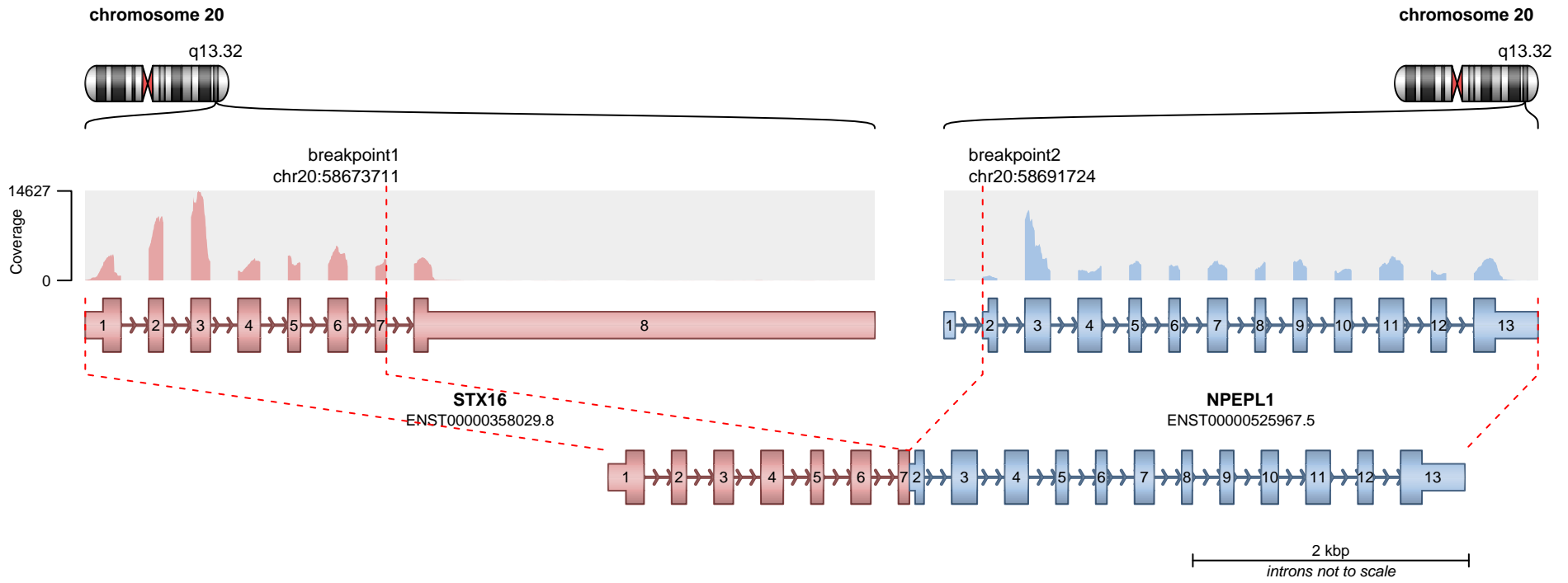
RETAINED PROTEIN DOMAINS
reading frame unclear



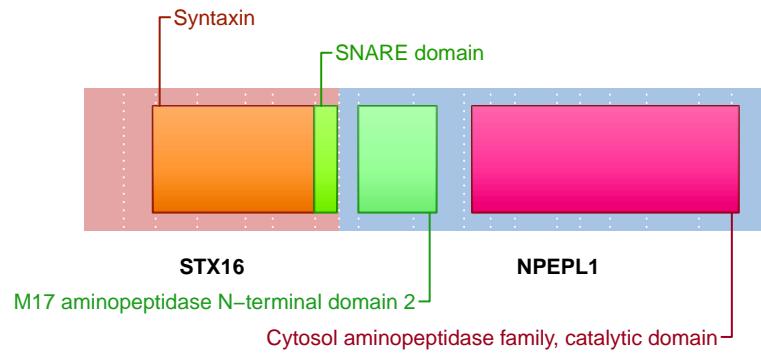
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



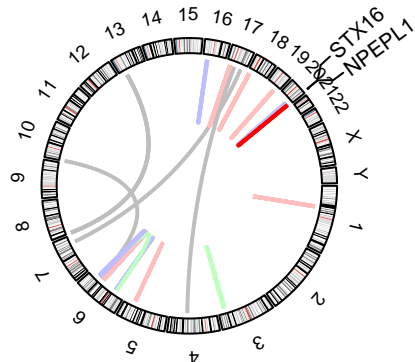
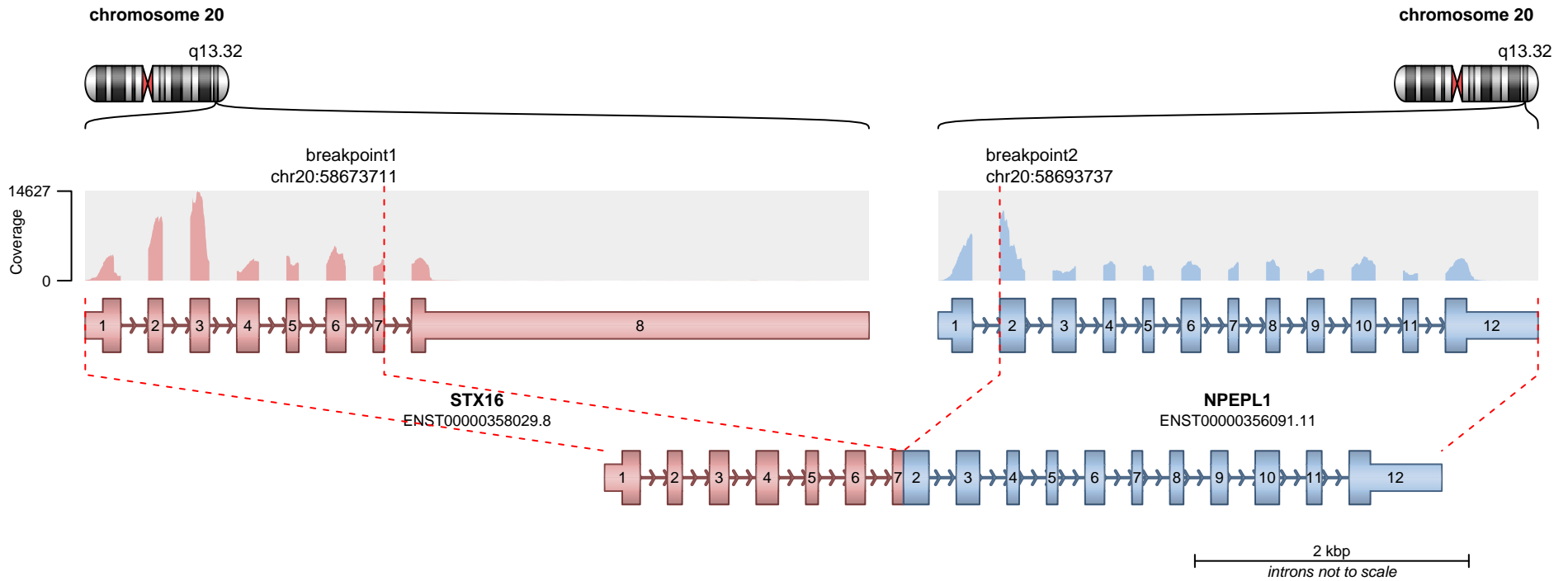
RETAINED PROTEIN DOMAINS
reading frame unclear



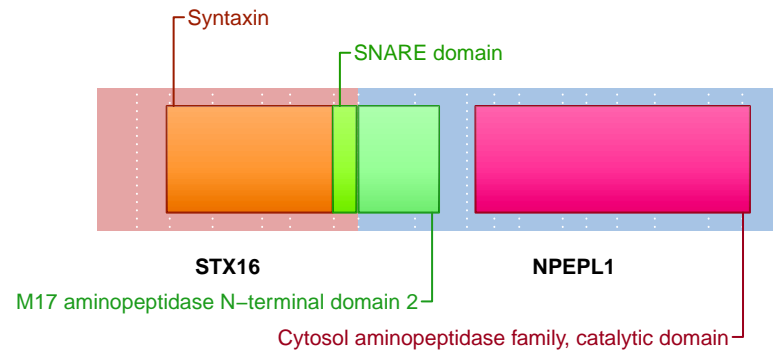
SUPPORTING READ COUNT

Split reads = 192
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



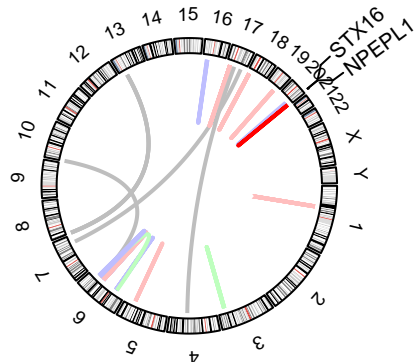
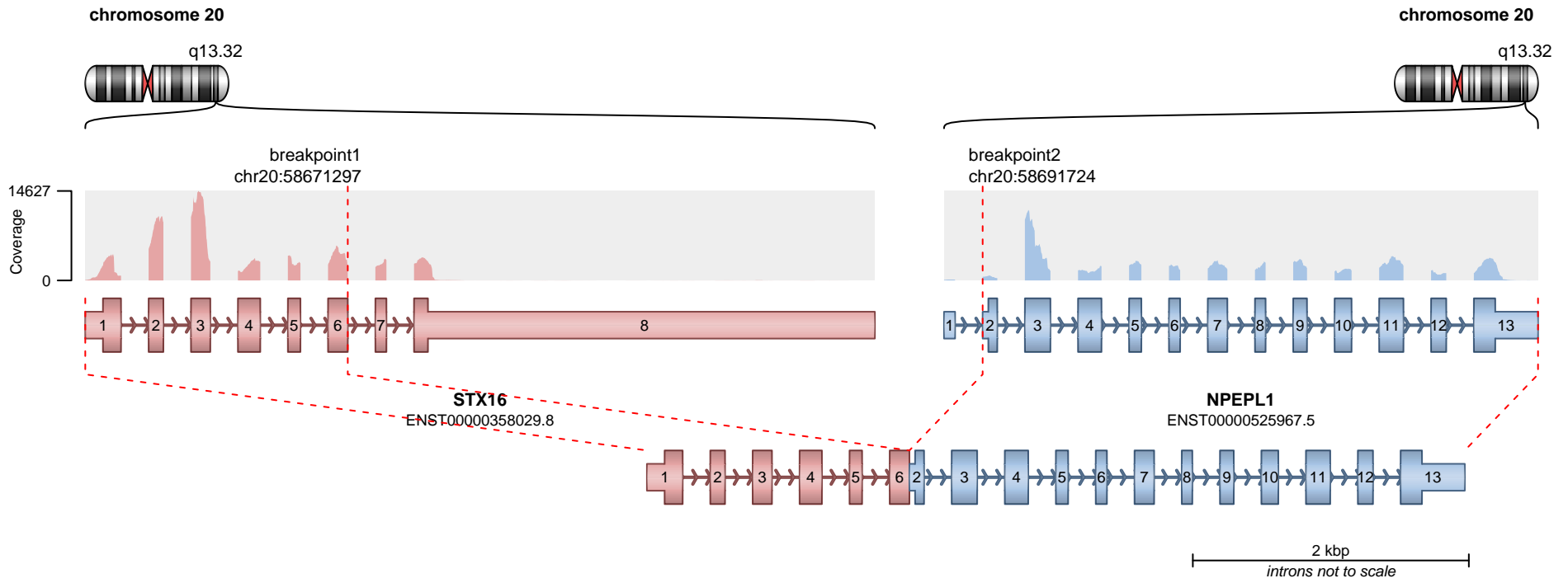
RETAINED PROTEIN DOMAINS
reading frame unclear



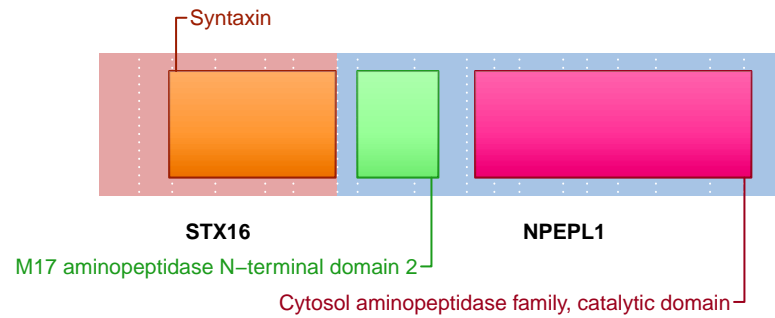
SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



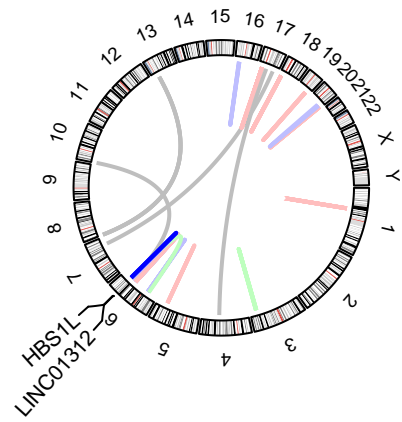
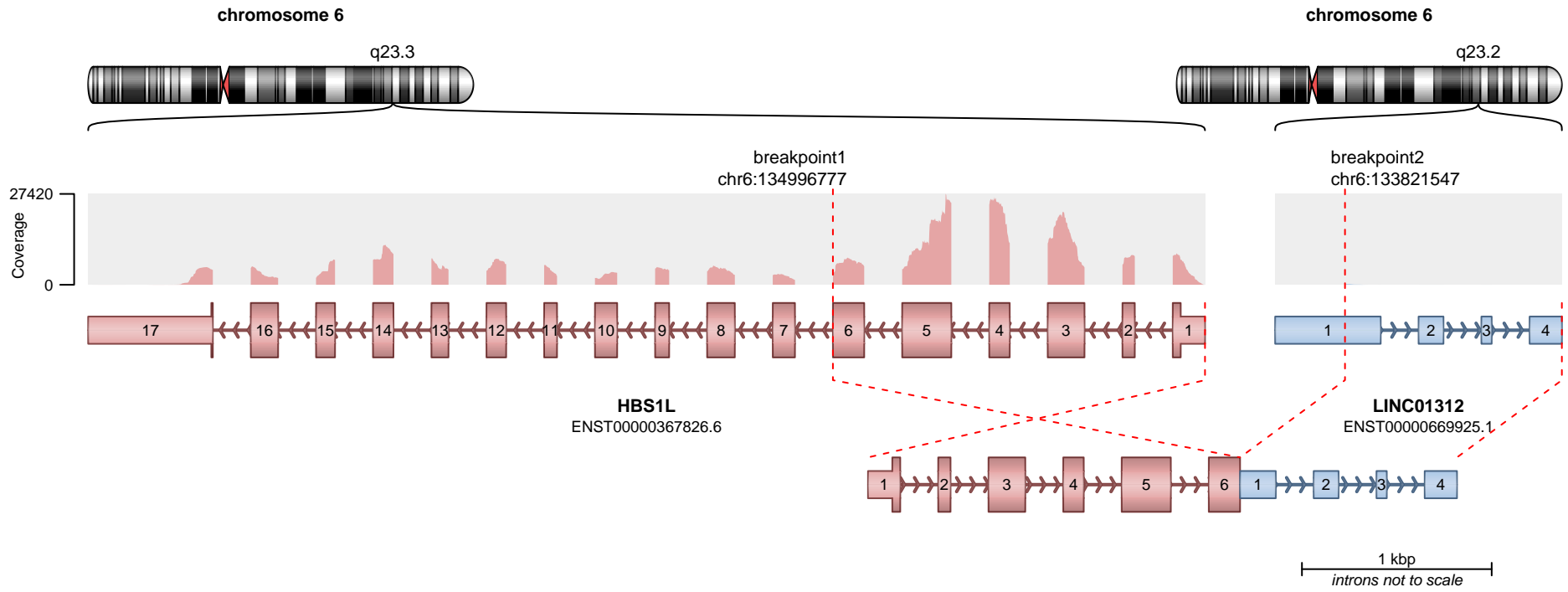
RETAINED PROTEIN DOMAINS
reading frame unclear



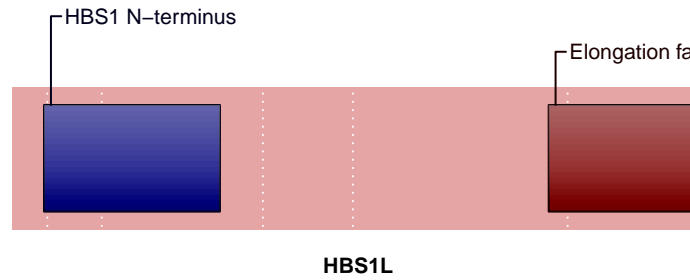
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



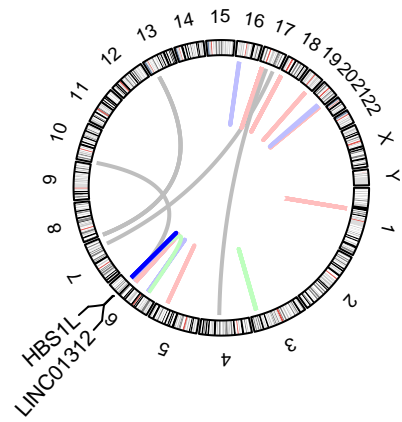
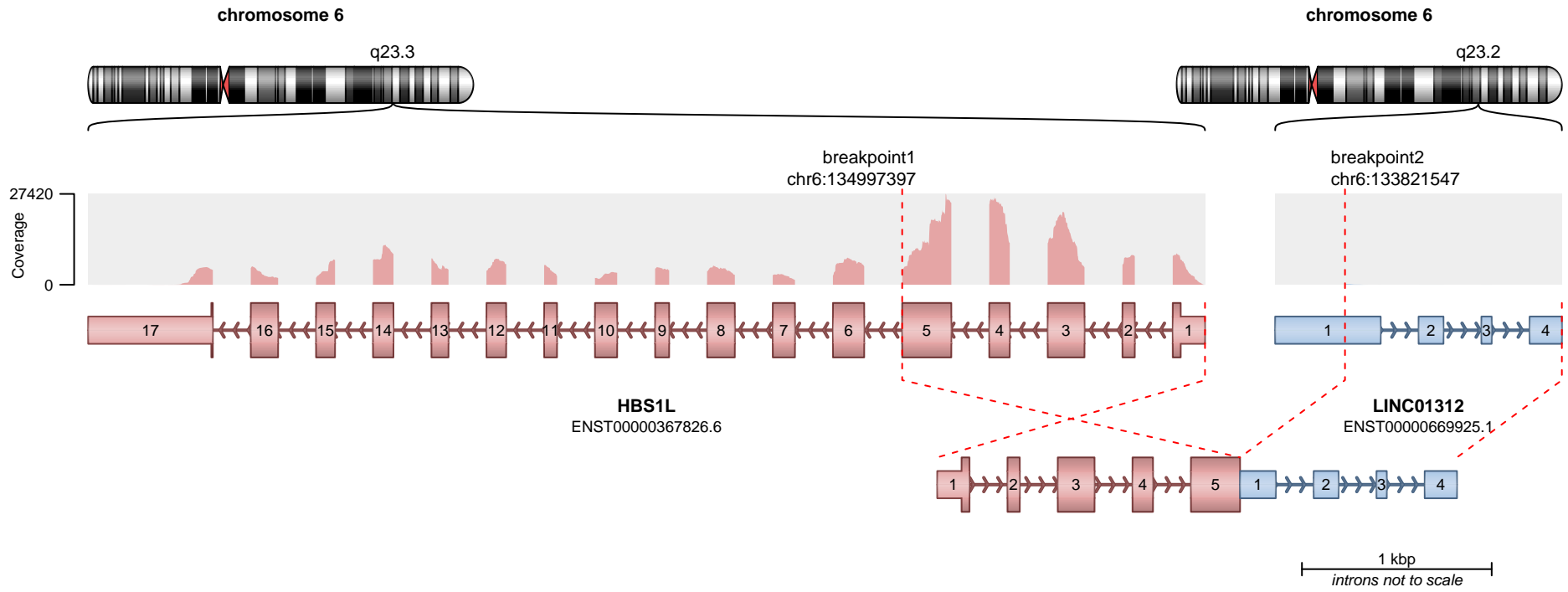
RETAINED PROTEIN DOMAINS
reading frame unclear



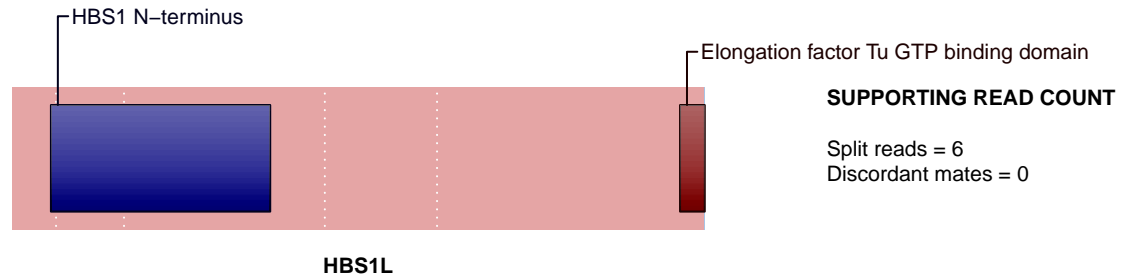
SUPPORTING READ COUNT

Split reads = 168
Discordant mates = 0

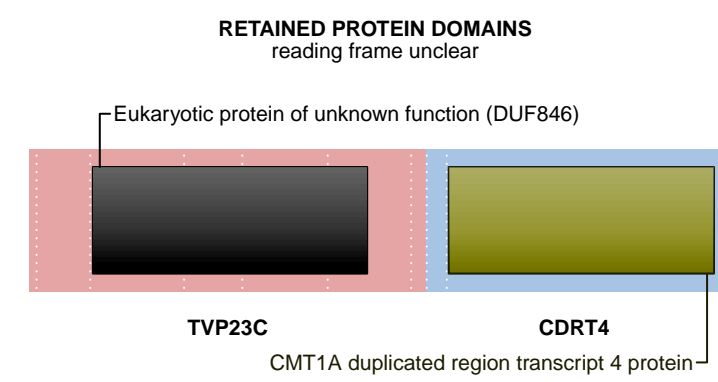
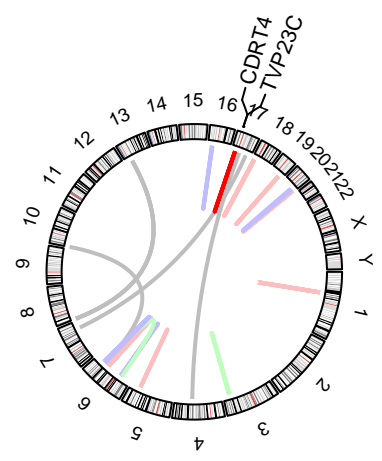
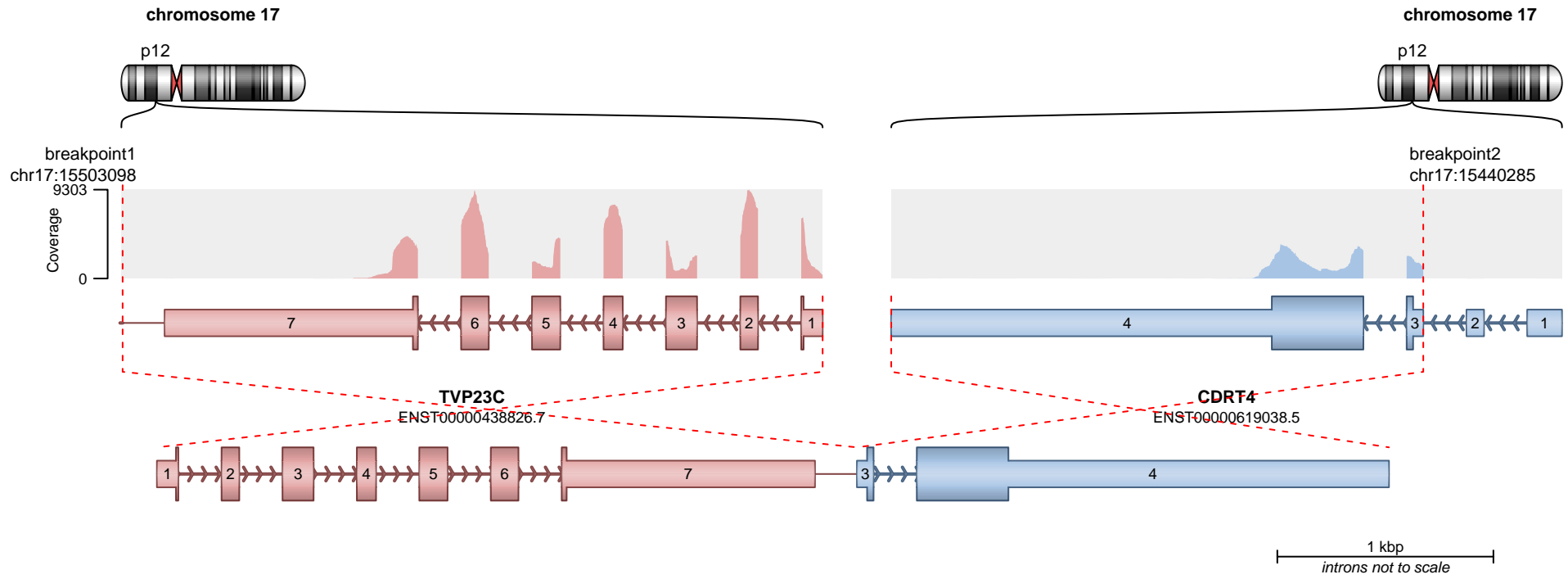
- translocation
- duplication
- deletion
- inversion



RETAINED PROTEIN DOMAINS
reading frame unclear



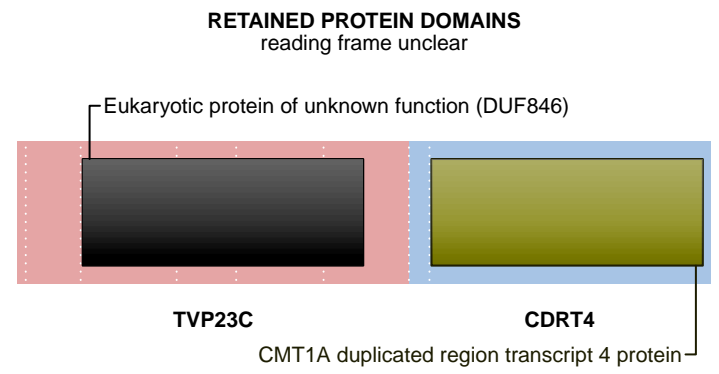
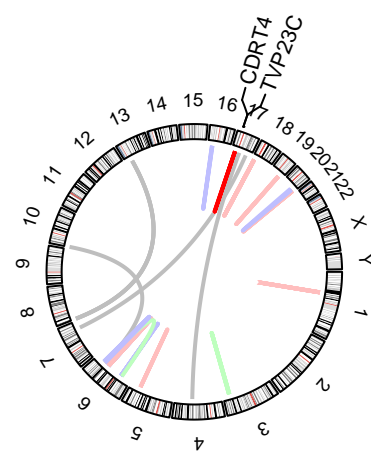
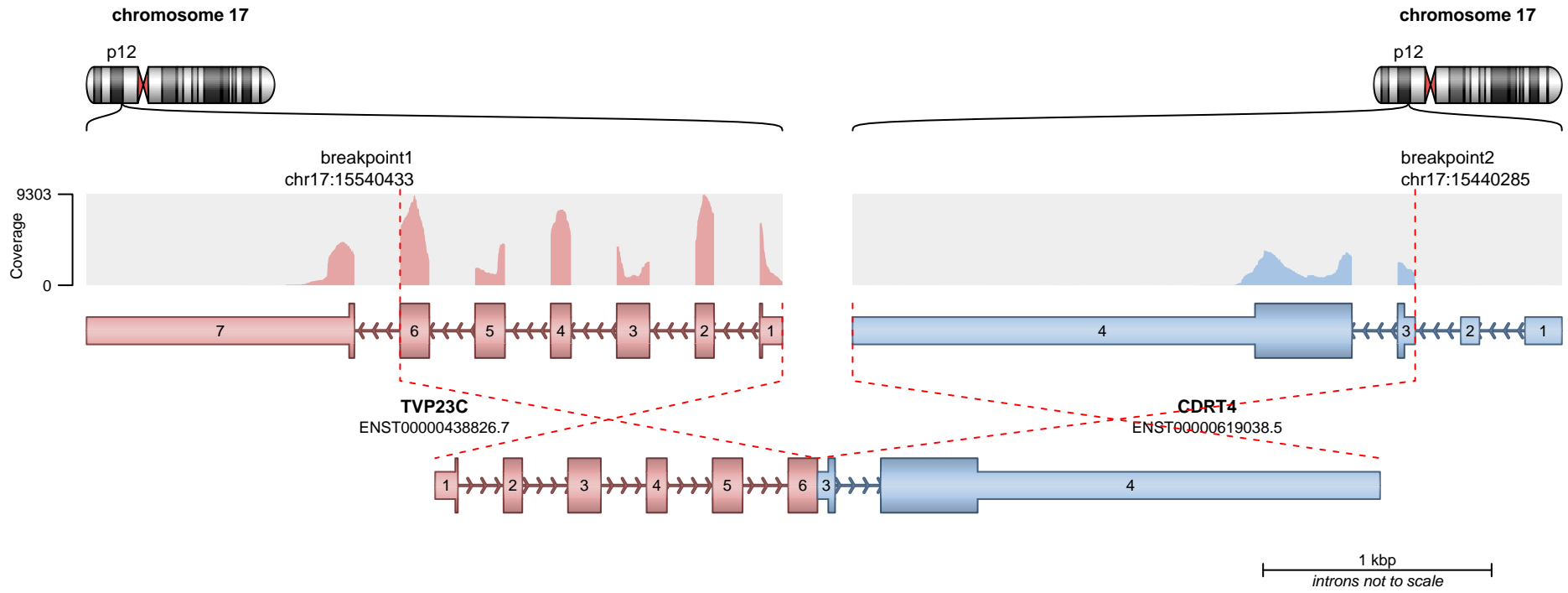
- translocation
- duplication
- deletion
- inversion



SUPPORTING READ COUNT

Split reads = 162
Discordant mates = 0

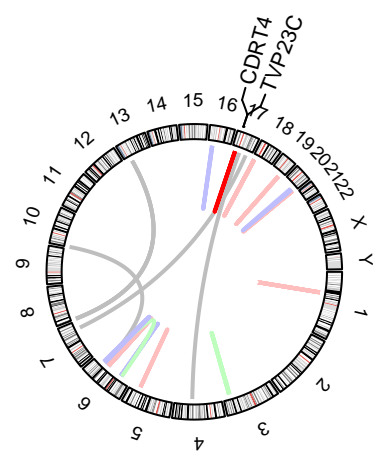
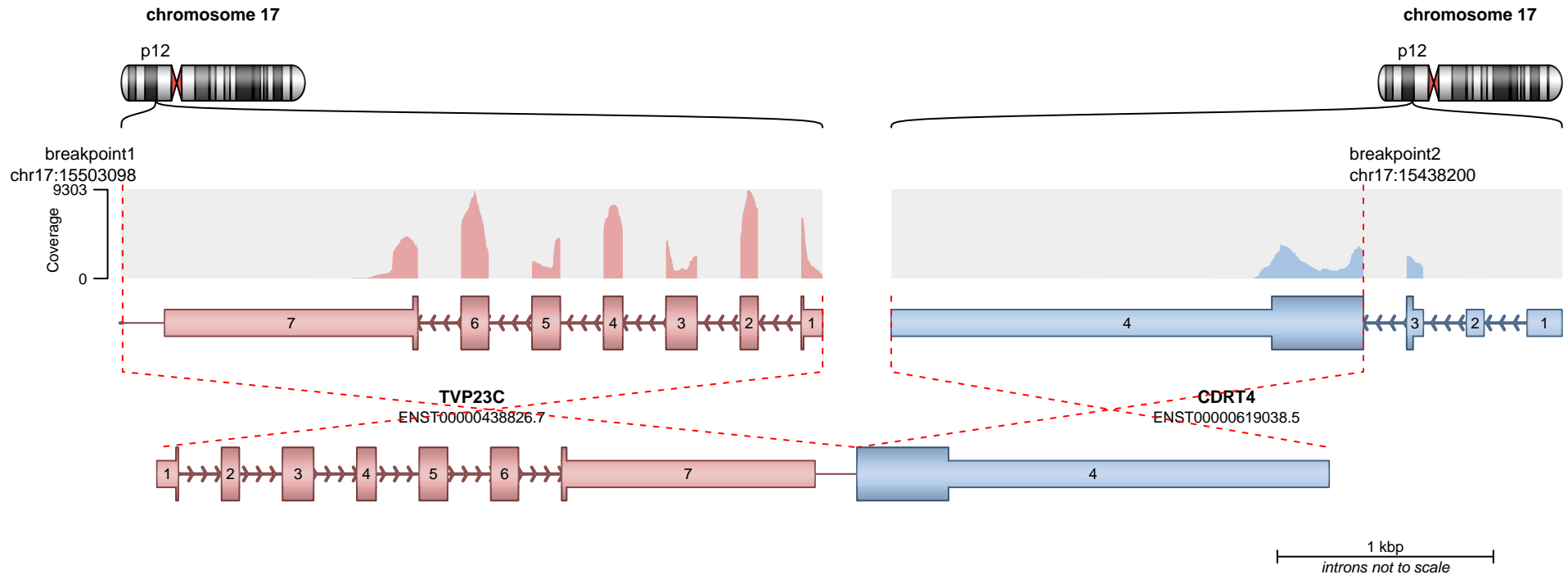
— translocation — deletion
— duplication — inversion



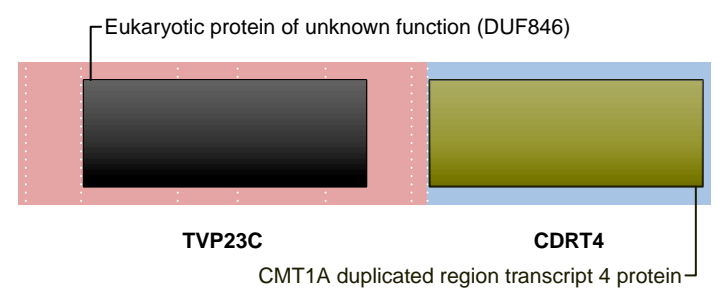
SUPPORTING READ COUNT

Split reads = 130
Discordant mates = 0

— translocation — deletion
— duplication — inversion



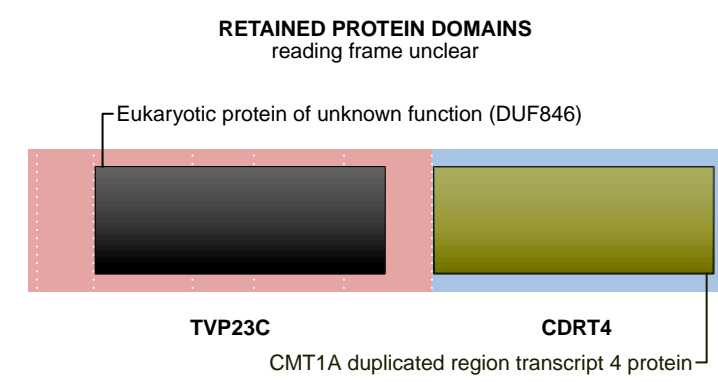
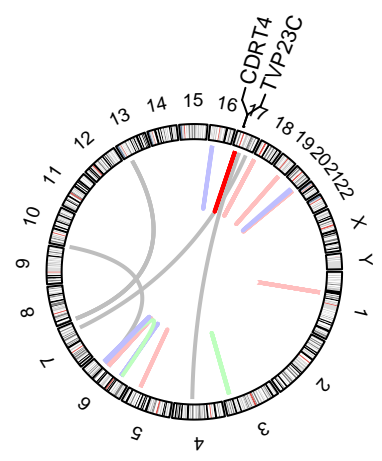
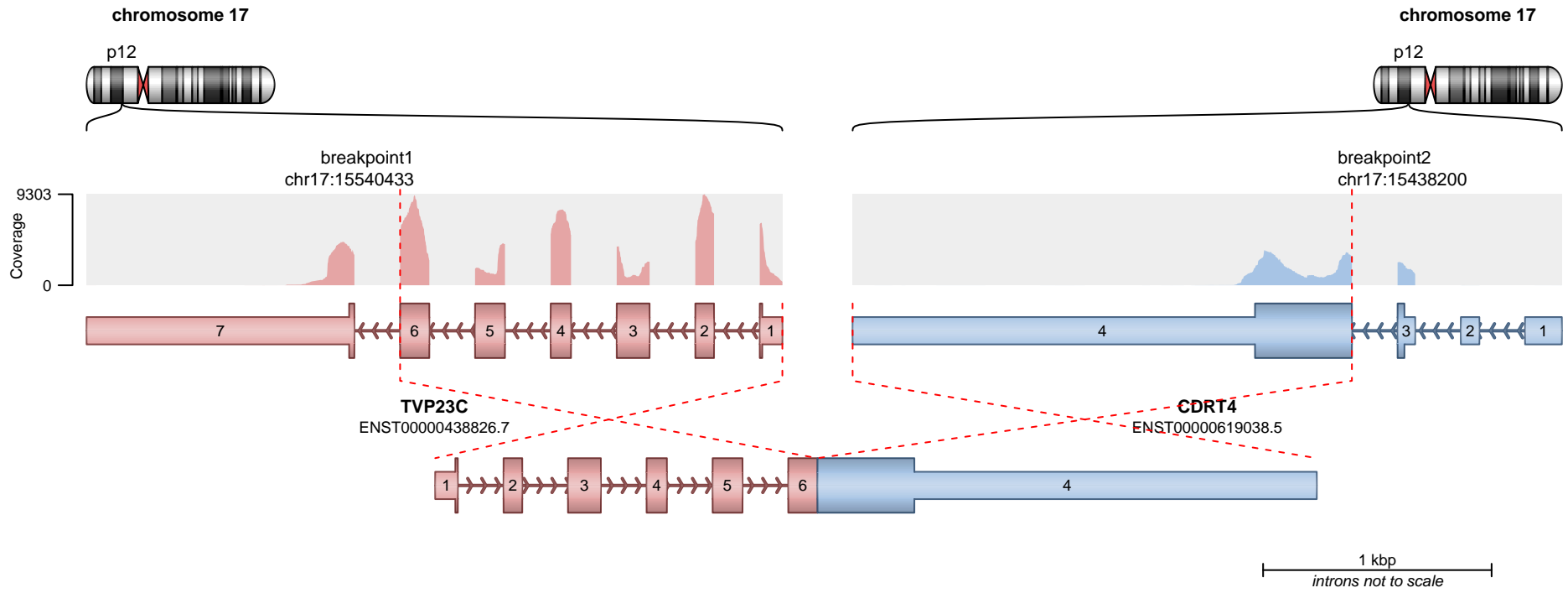
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 59
Discordant mates = 0

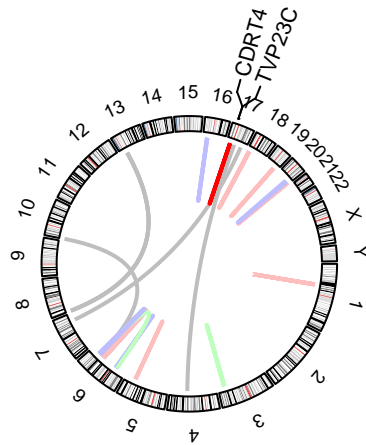
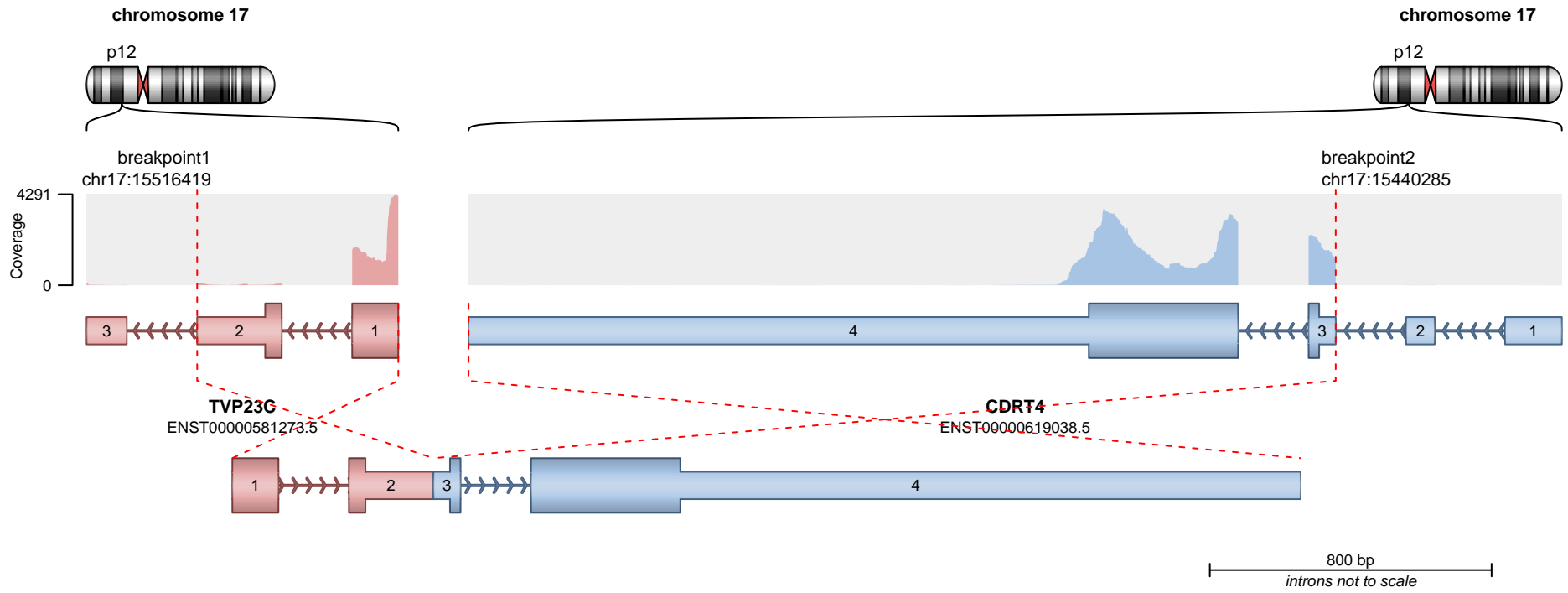
- translocation
- duplication
- deletion
- inversion



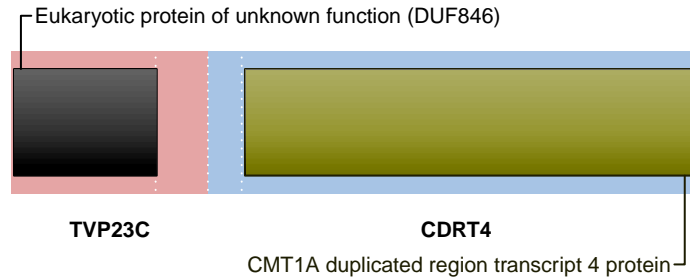
SUPPORTING READ COUNT

Split reads = 46
Discordant mates = 0

— translocation — deletion
— duplication — inversion



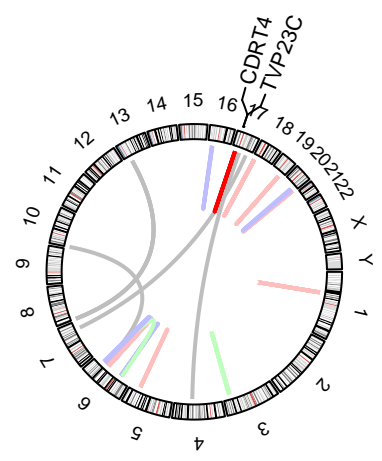
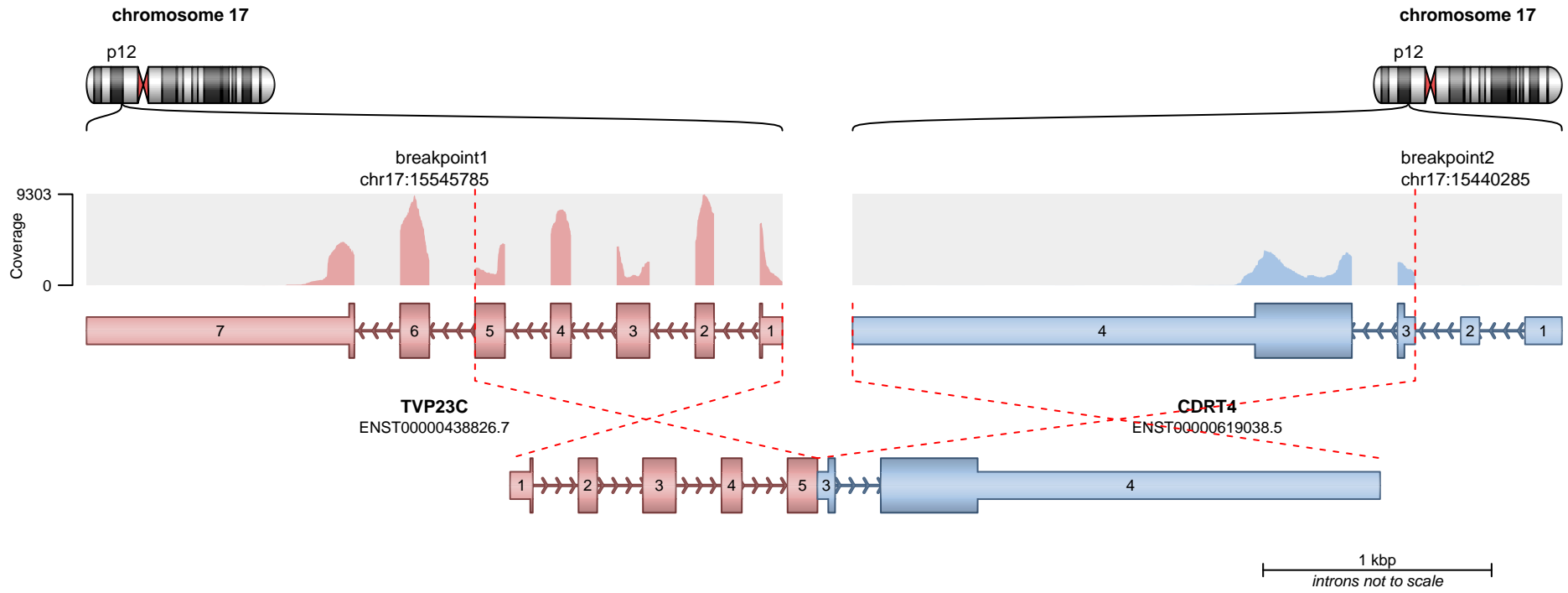
RETAINED PROTEIN DOMAINS
reading frame unclear



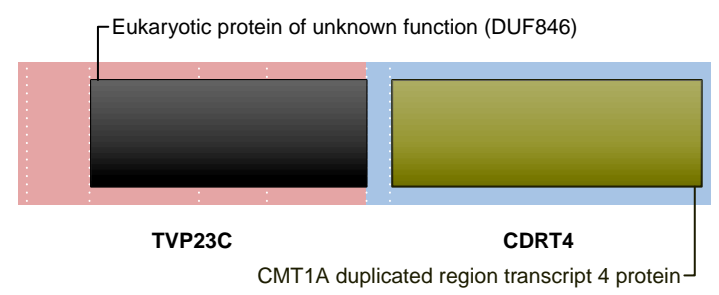
SUPPORTING READ COUNT

Split reads = 19
Discordant mates = 0

— translocation — deletion
— duplication — inversion



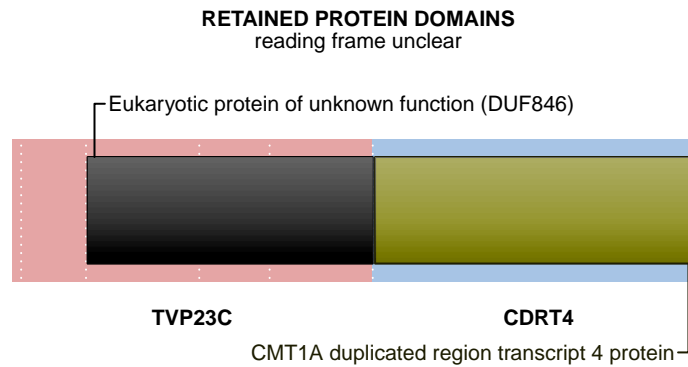
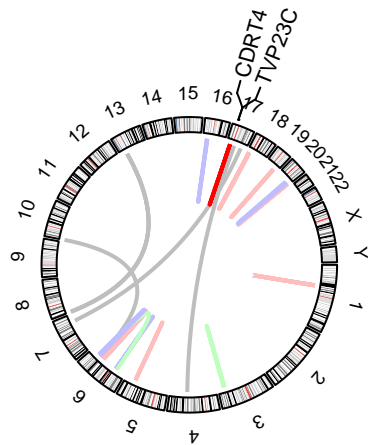
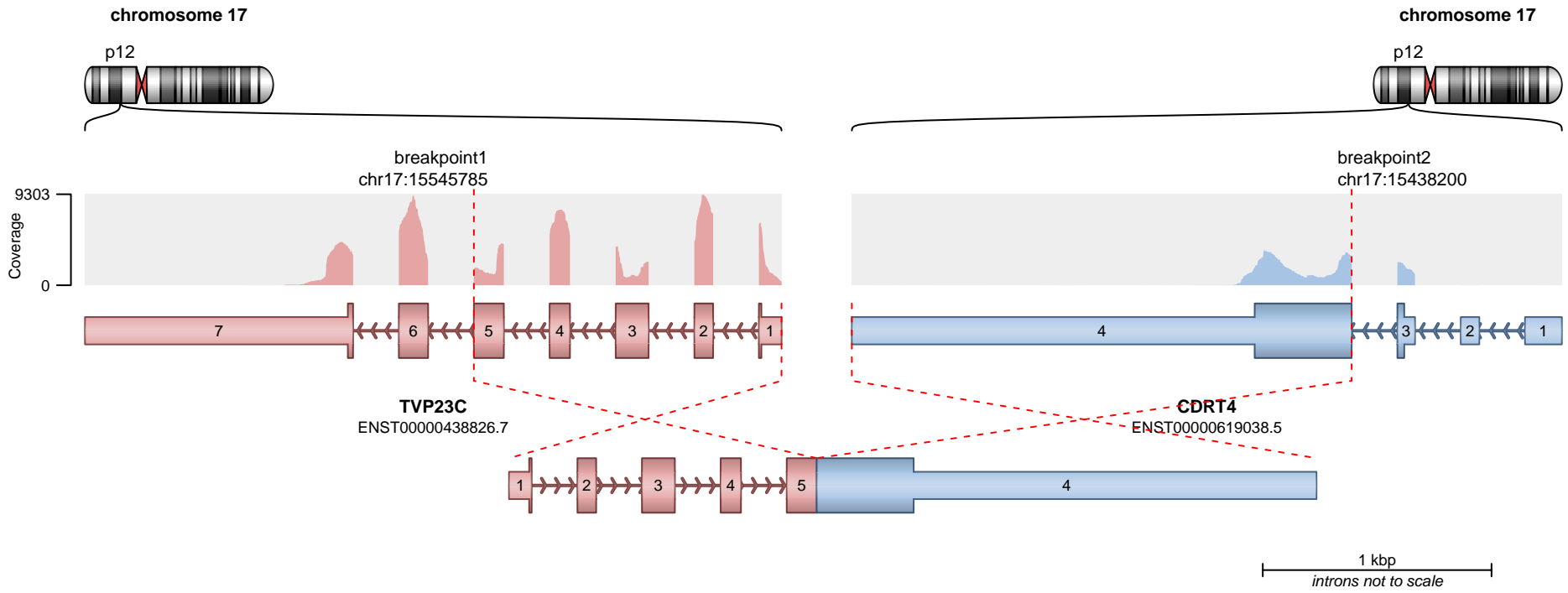
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 13
Discordant mates = 0

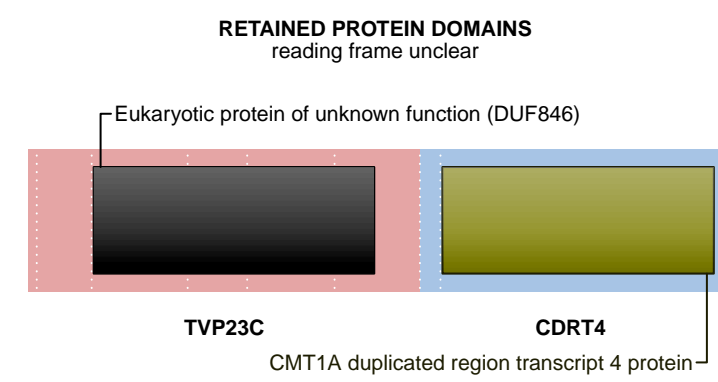
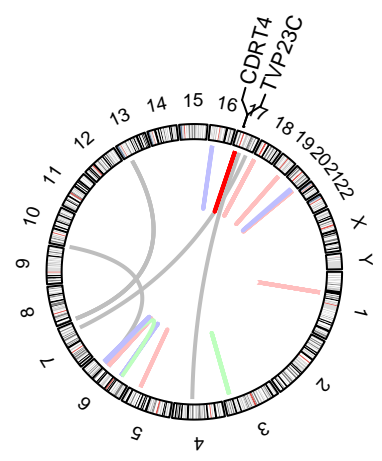
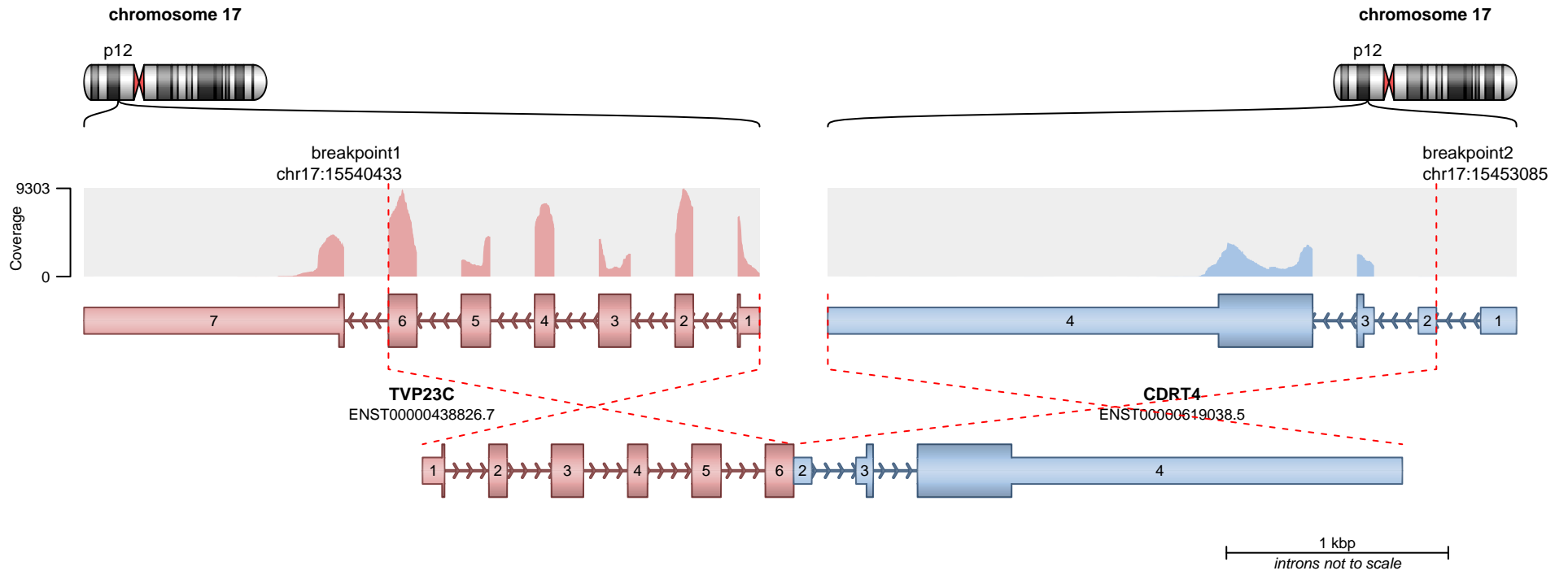
- translocation
- duplication
- deletion
- inversion



SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

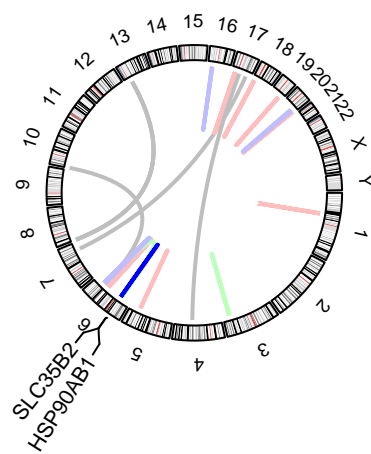
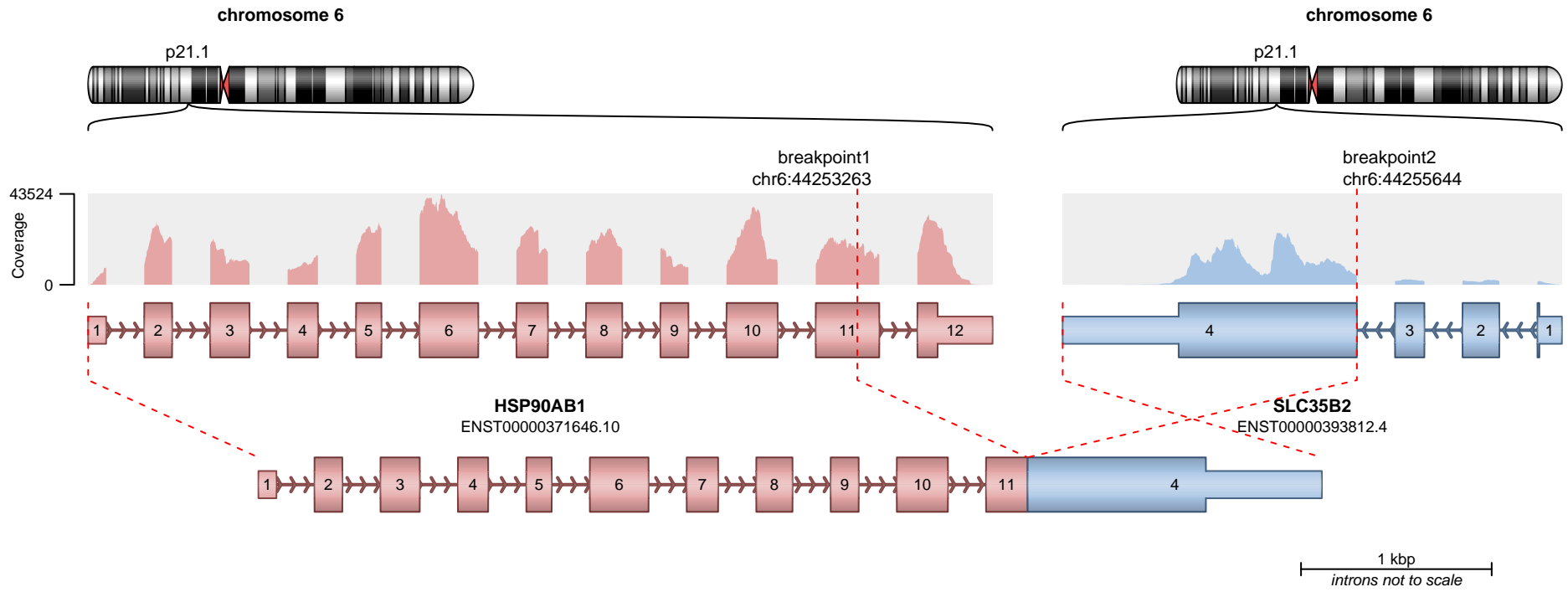
— translocation — deletion
— duplication — inversion



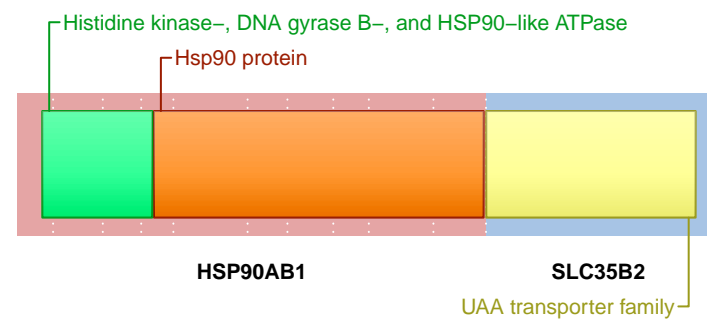
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



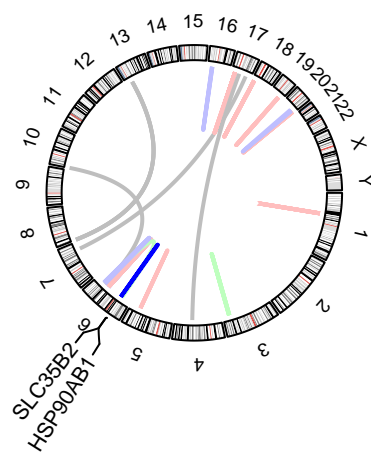
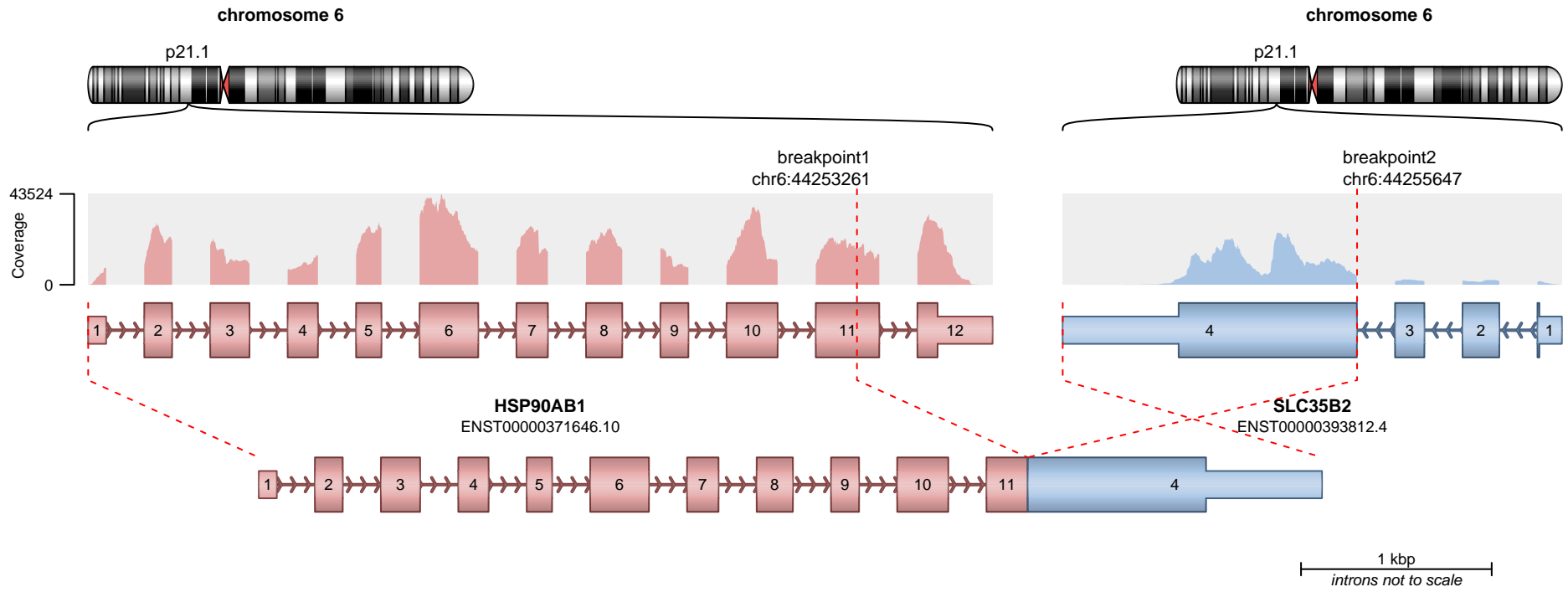
RETAINED PROTEIN DOMAINS
reading frame unclear



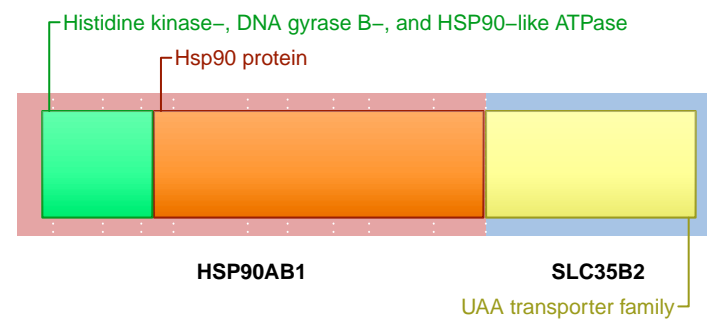
SUPPORTING READ COUNT

Split reads = 133
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



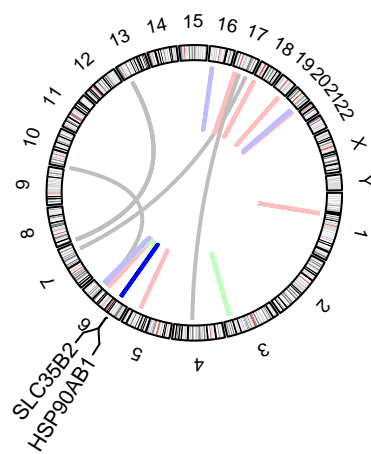
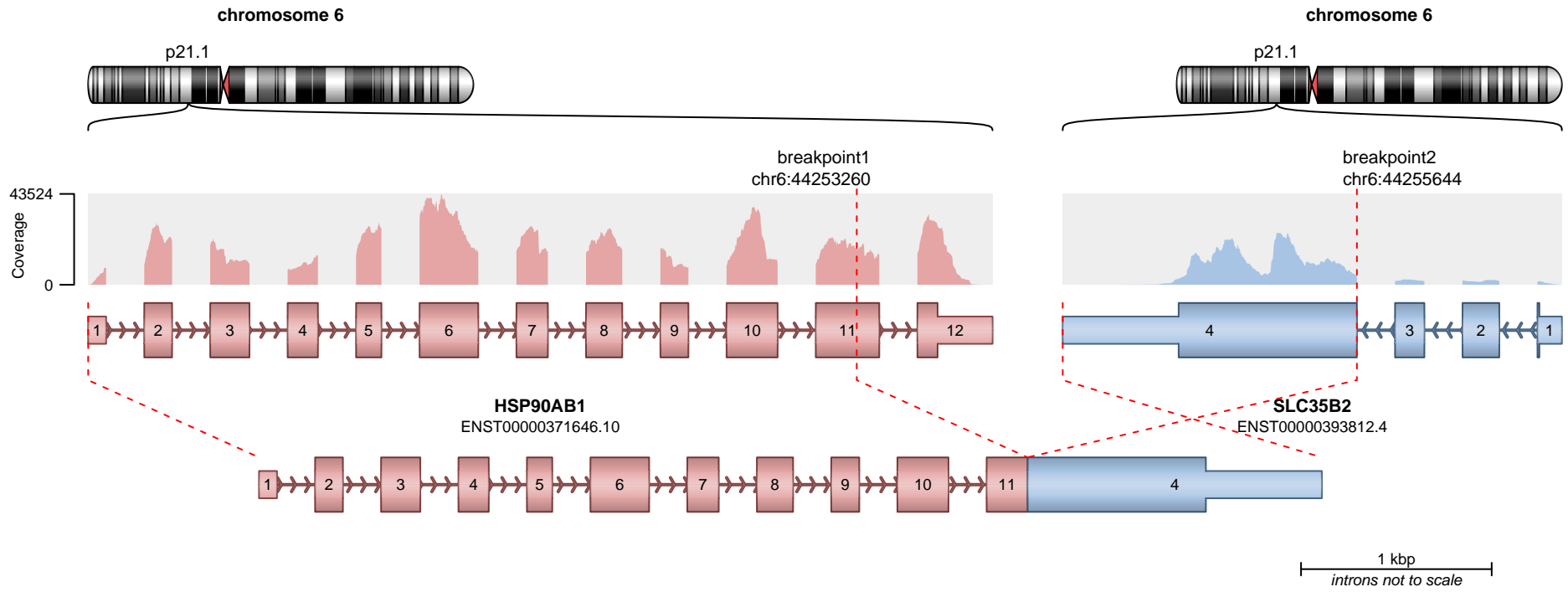
RETAINED PROTEIN DOMAINS
reading frame unclear



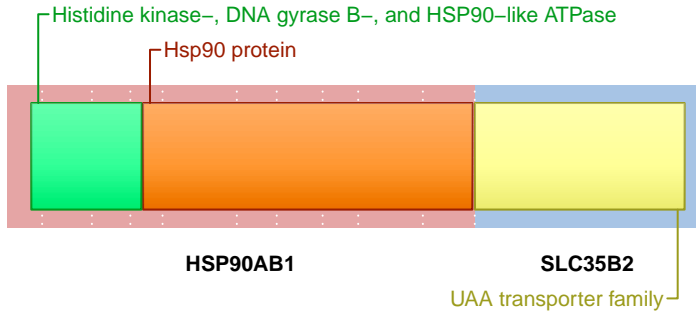
SUPPORTING READ COUNT

Split reads = 9
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



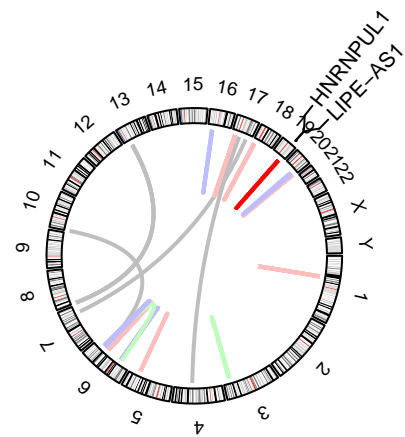
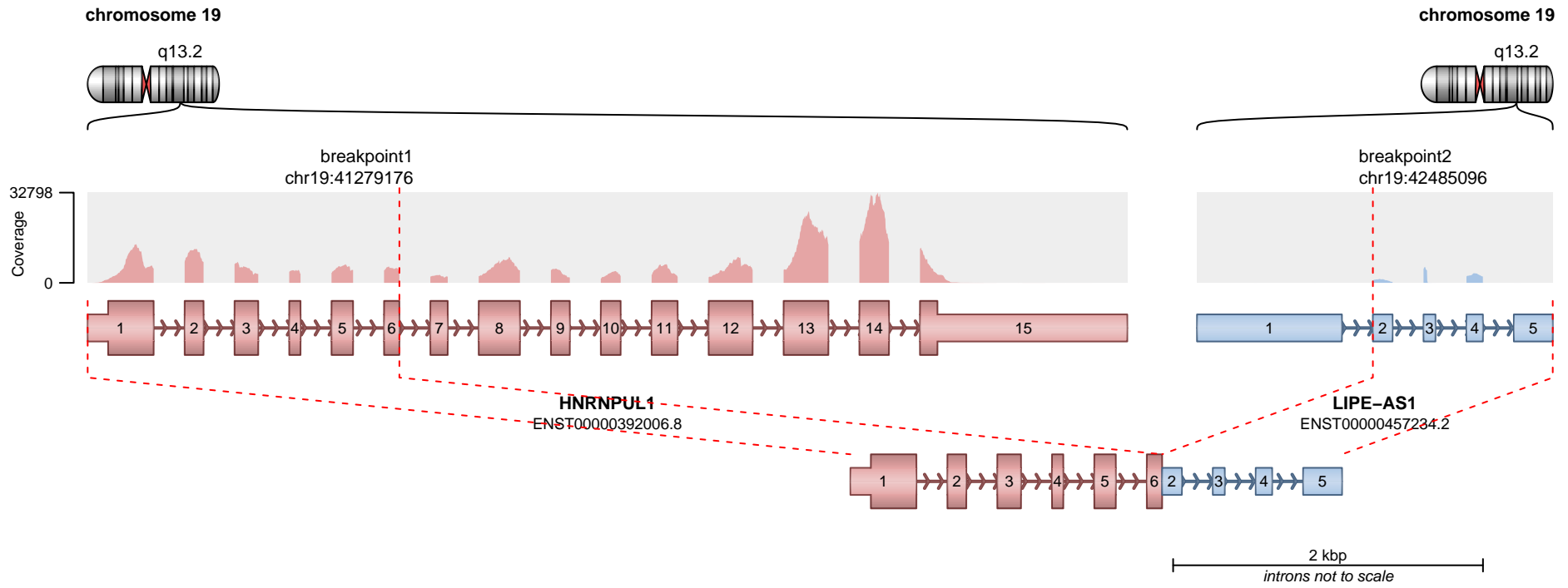
RETAINED PROTEIN DOMAINS
reading frame unclear



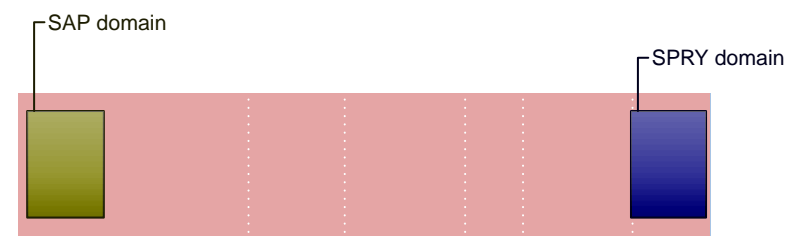
SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

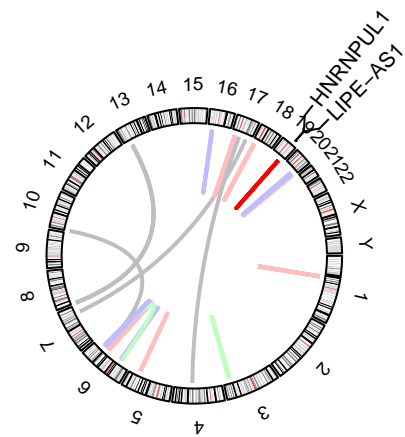
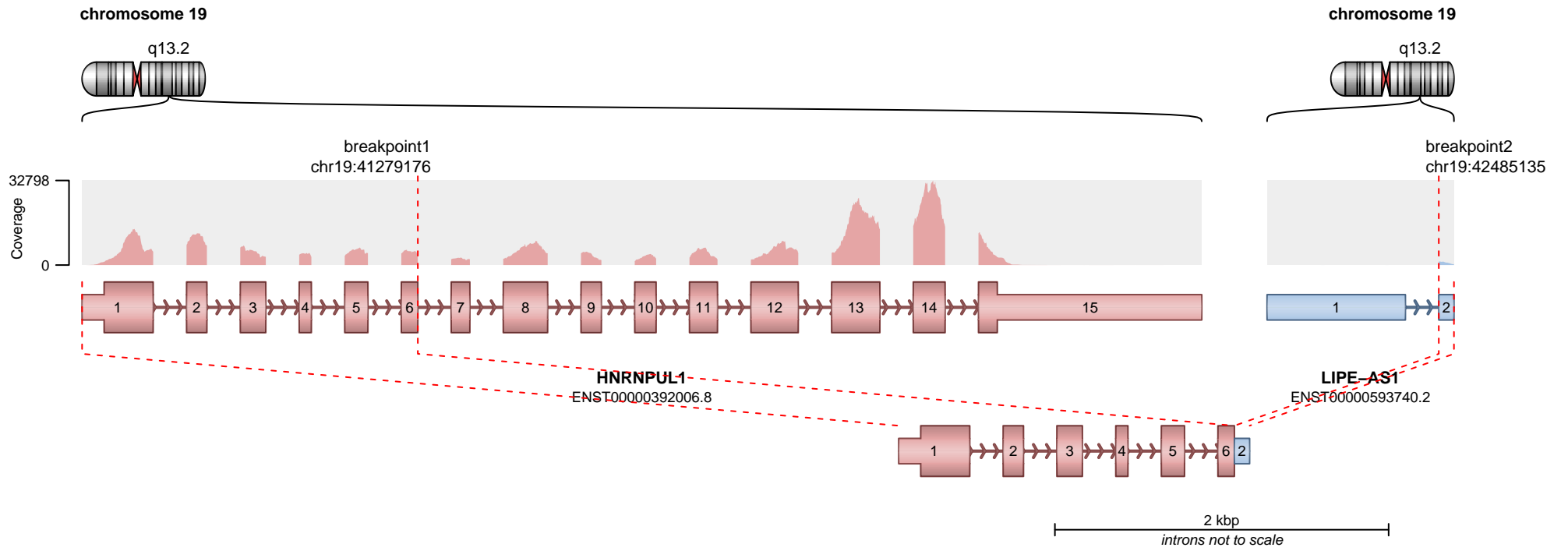


HNRNPUL1

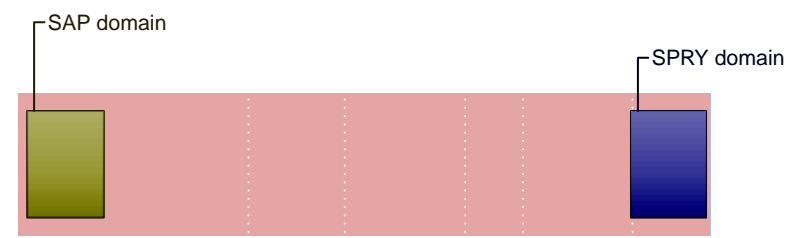
SUPPORTING READ COUNT

Split reads = 132
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

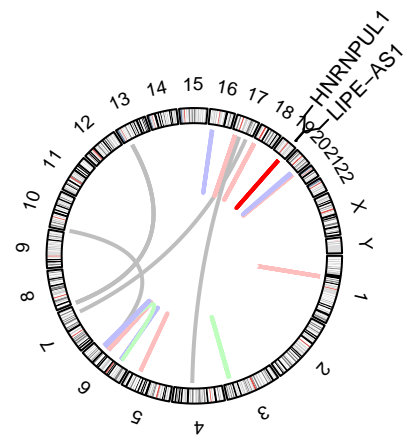
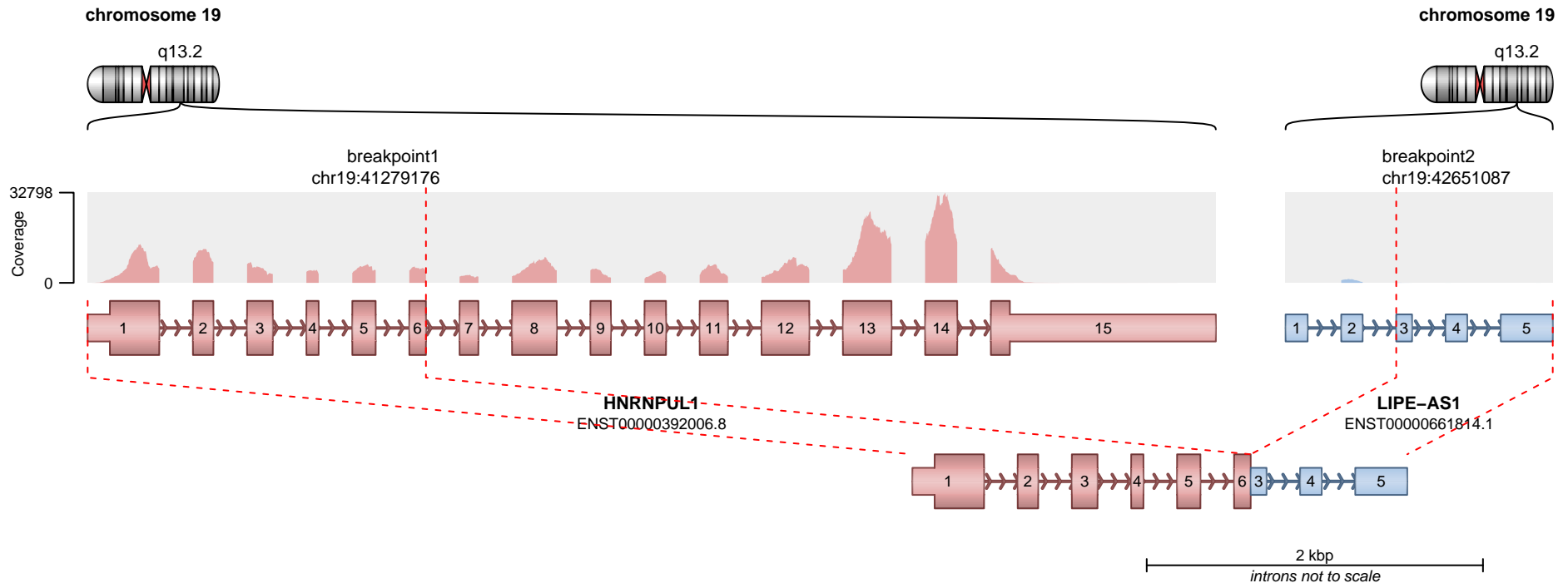


HNRNPUL1

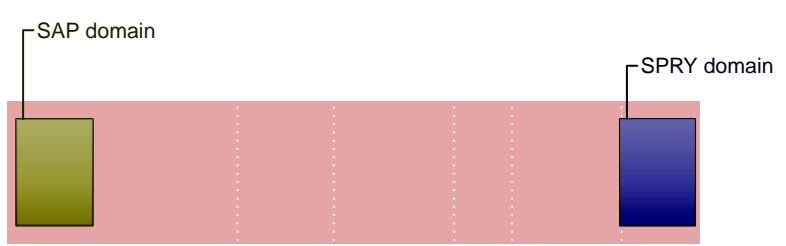
SUPPORTING READ COUNT

Split reads = 78
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



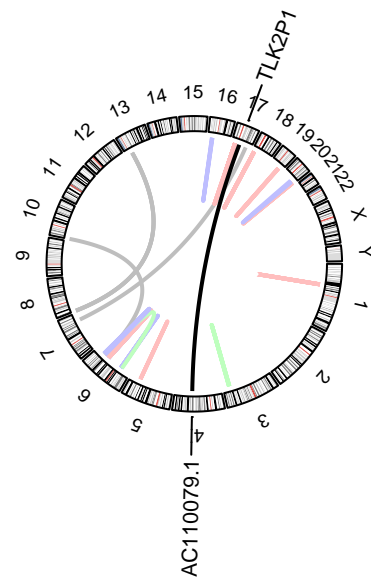
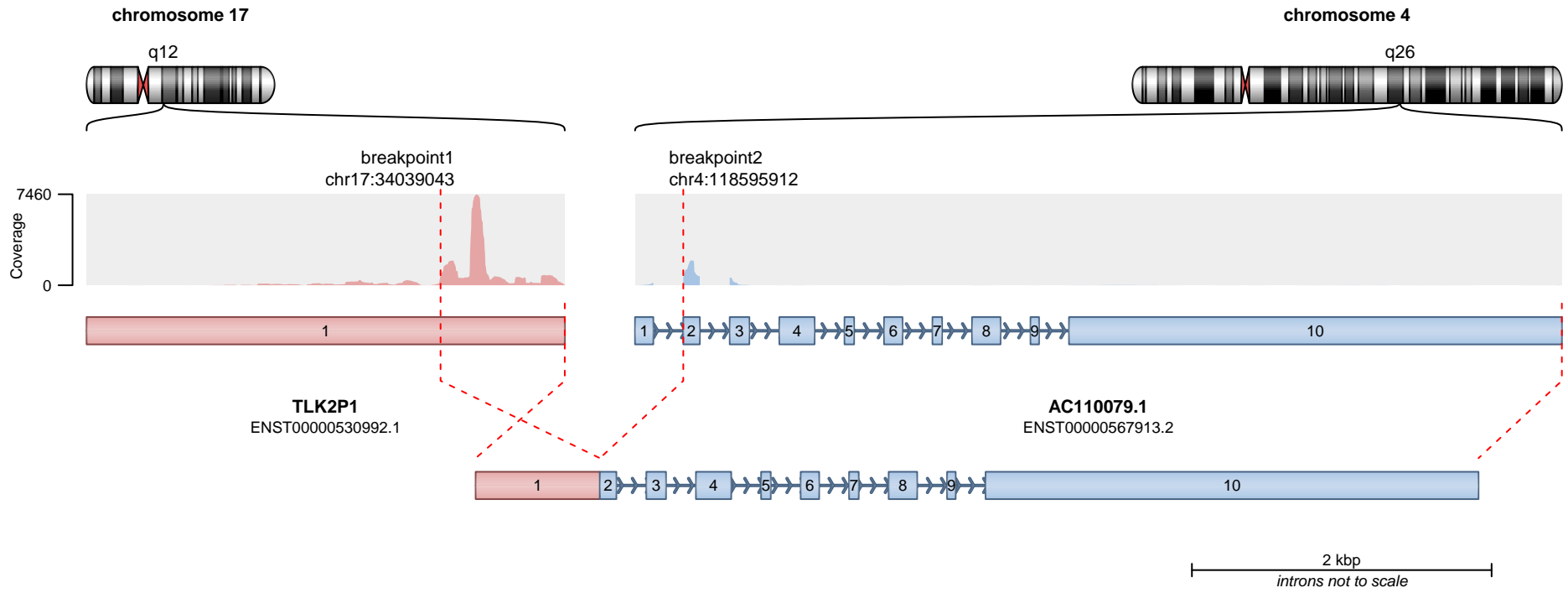
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 34
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

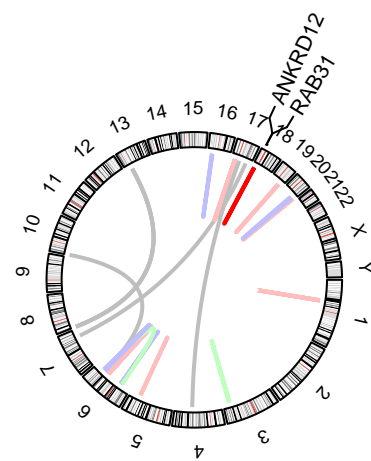
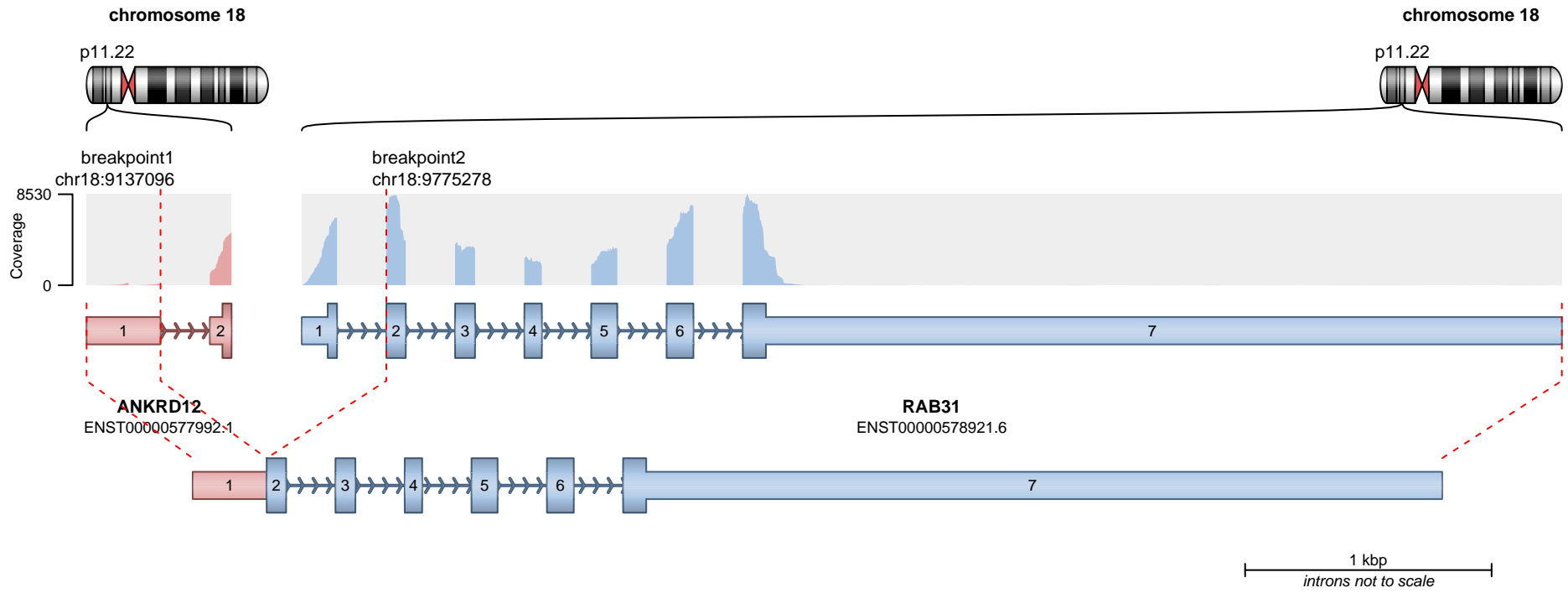


— translocation — deletion
 — duplication — inversion

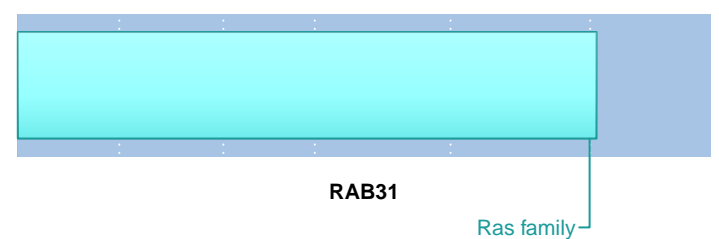
Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 95
Discordant mates = 0



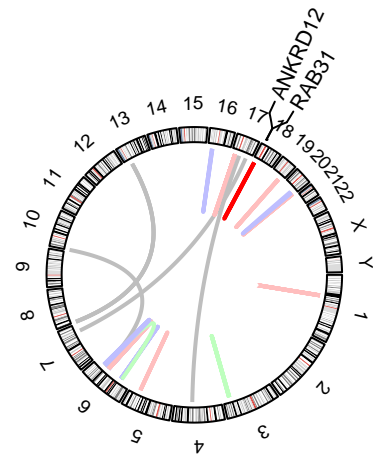
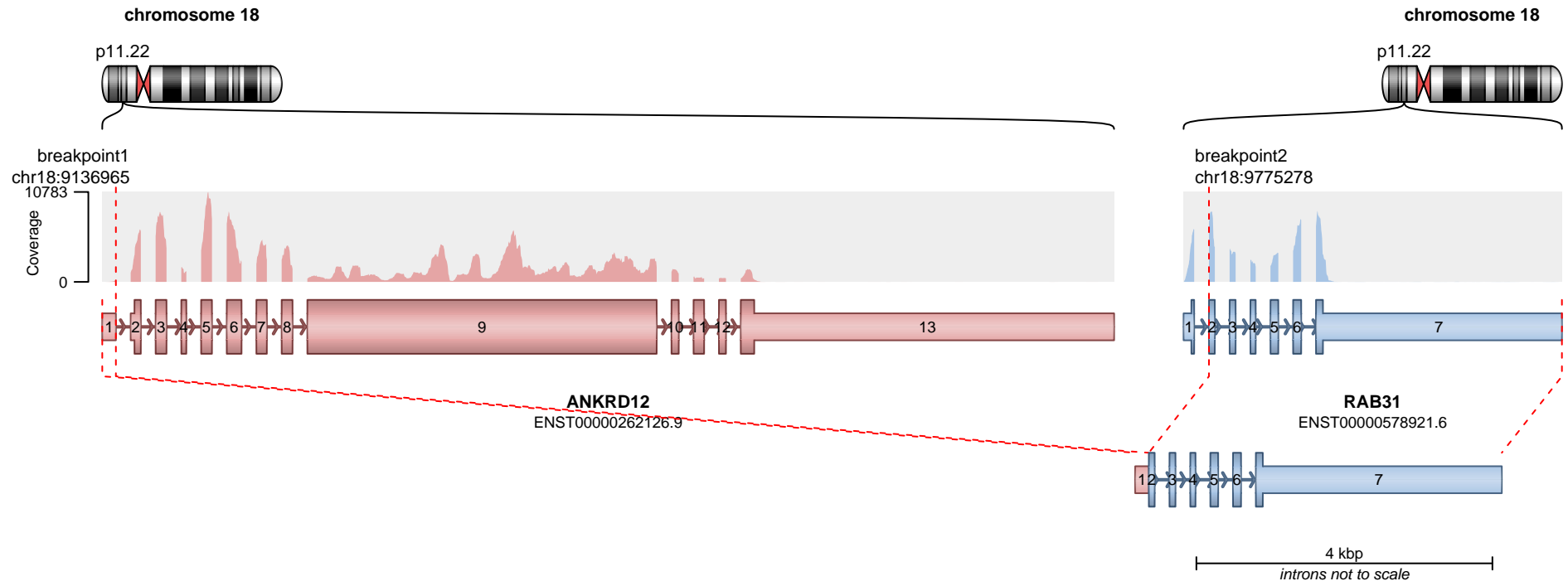
RETAINED PROTEIN DOMAINS
reading frame unclear



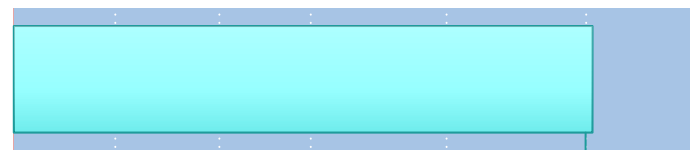
SUPPORTING READ COUNT

Split reads = 78
Discordant mates = 0

— translocation — deletion
— duplication — inversion



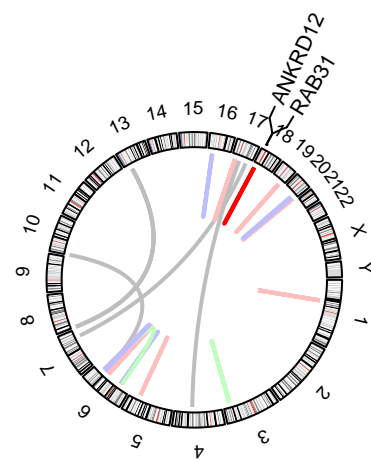
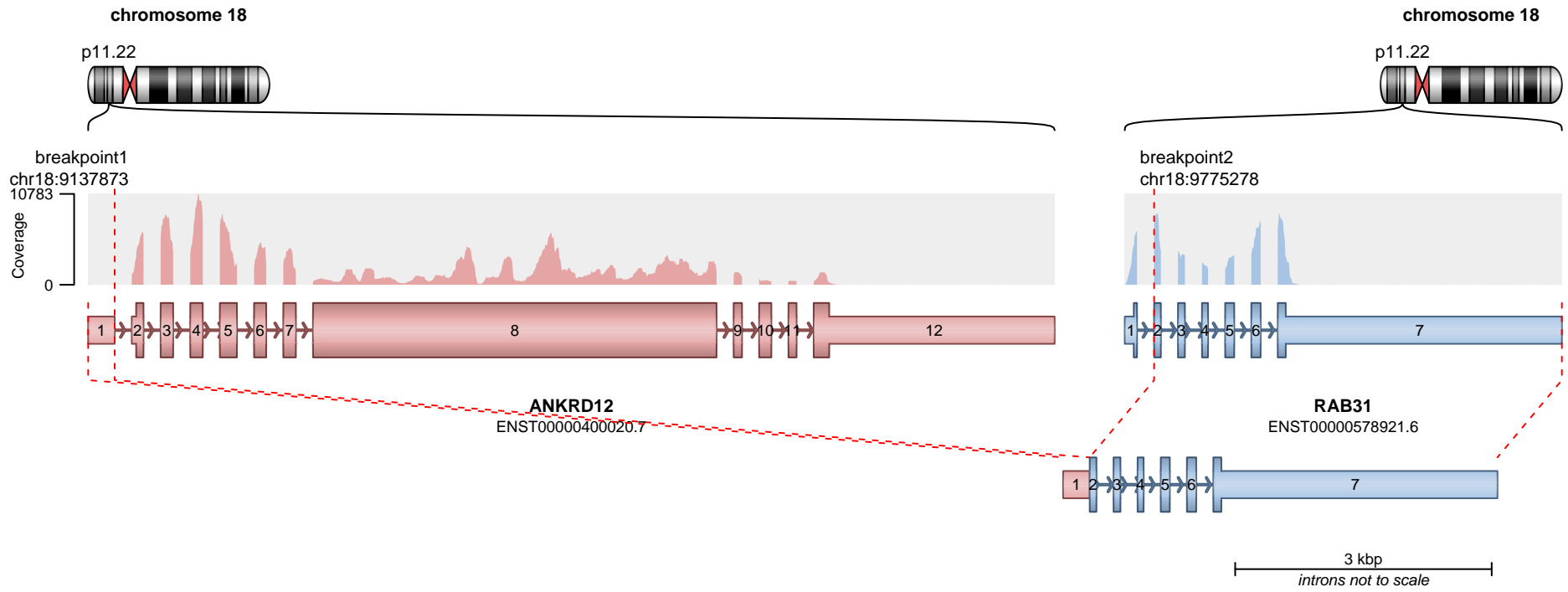
RETAINED PROTEIN DOMAINS
reading frame unclear



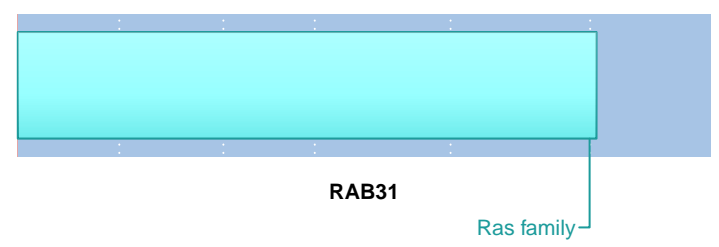
SUPPORTING READ COUNT

Split reads = 45
Discordant mates = 0

— translocation — deletion
— duplication — inversion



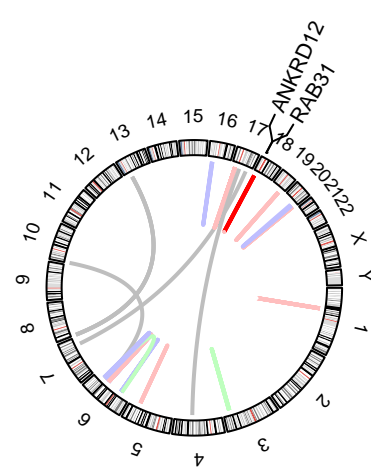
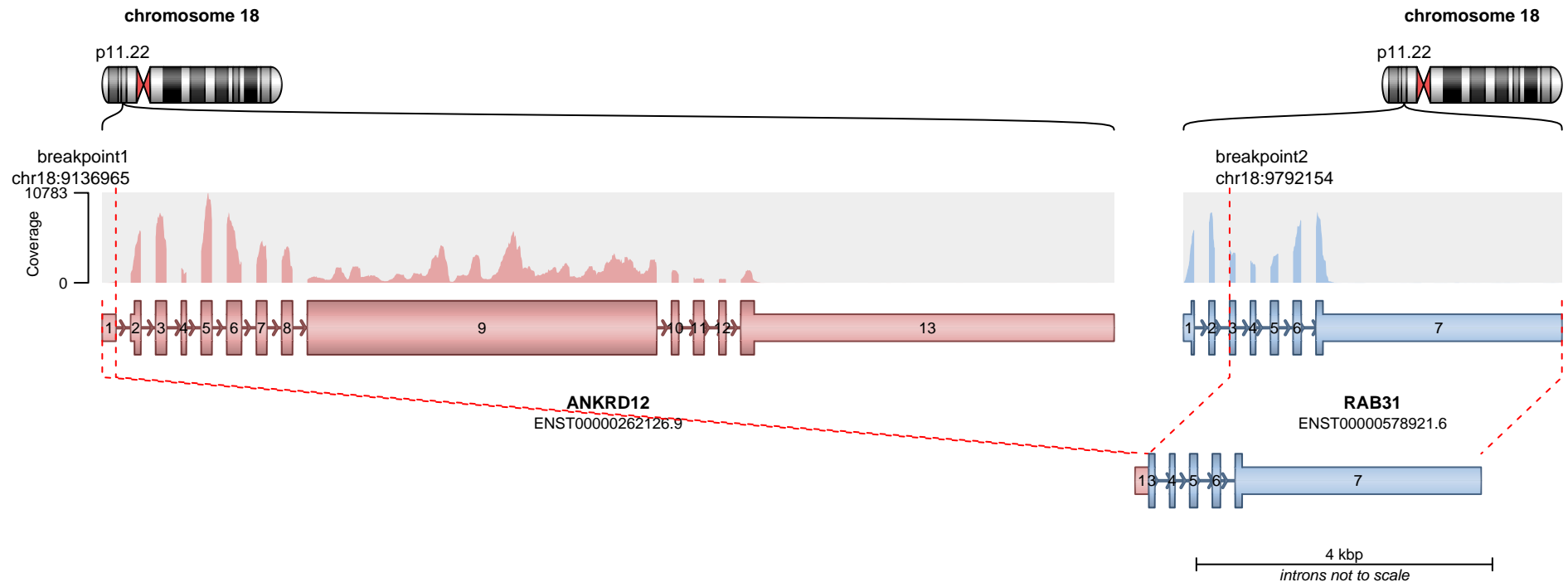
RETAINED PROTEIN DOMAINS
reading frame unclear



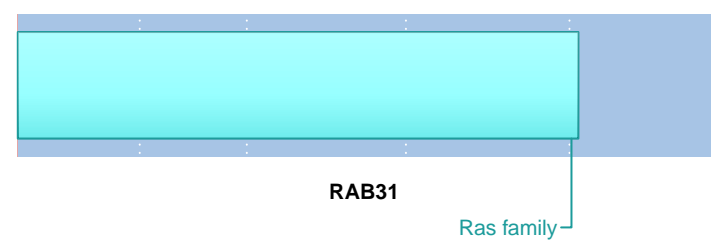
SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



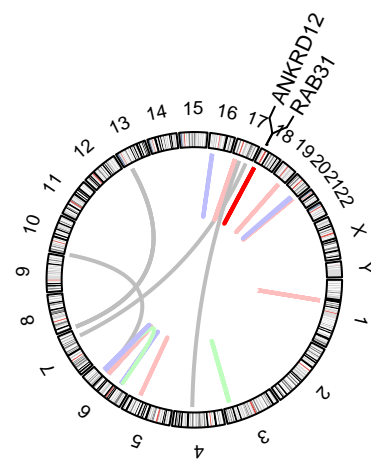
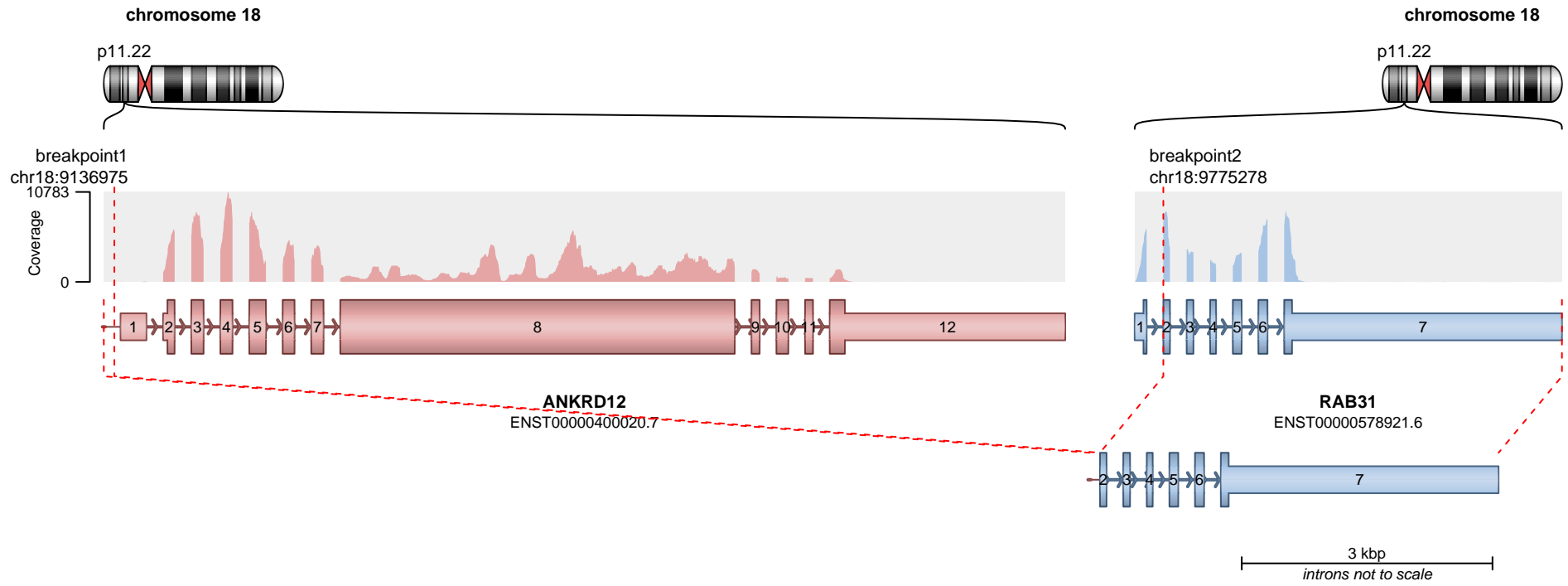
RETAINED PROTEIN DOMAINS
reading frame unclear



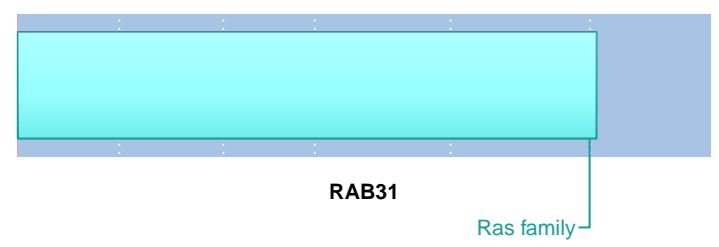
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



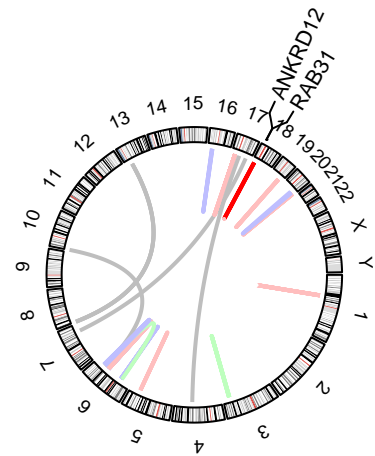
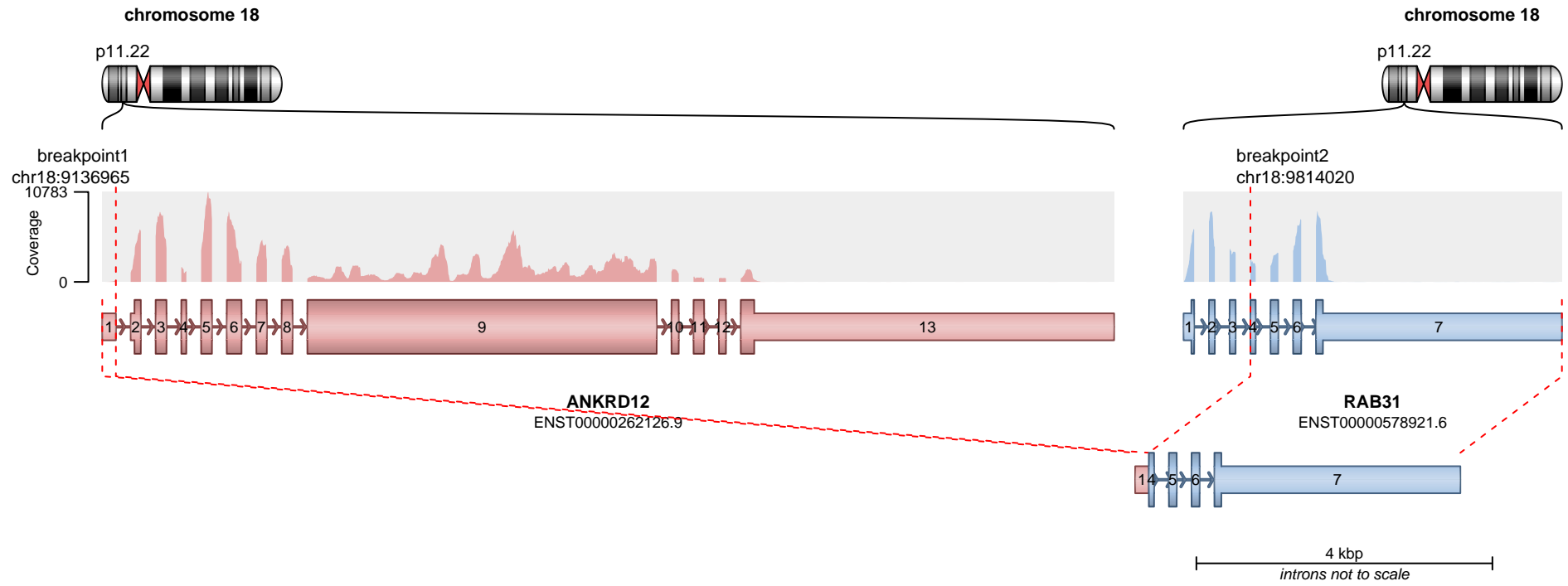
RETAINED PROTEIN DOMAINS
reading frame unclear



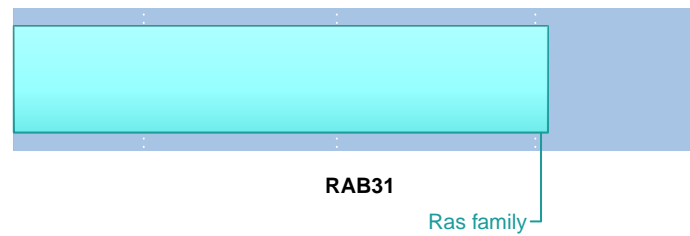
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



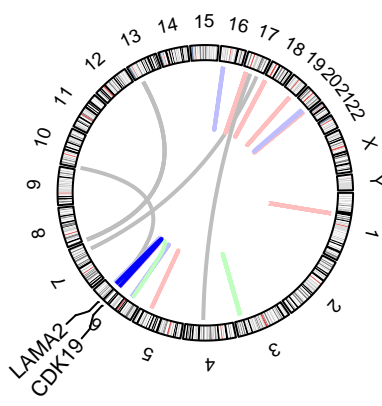
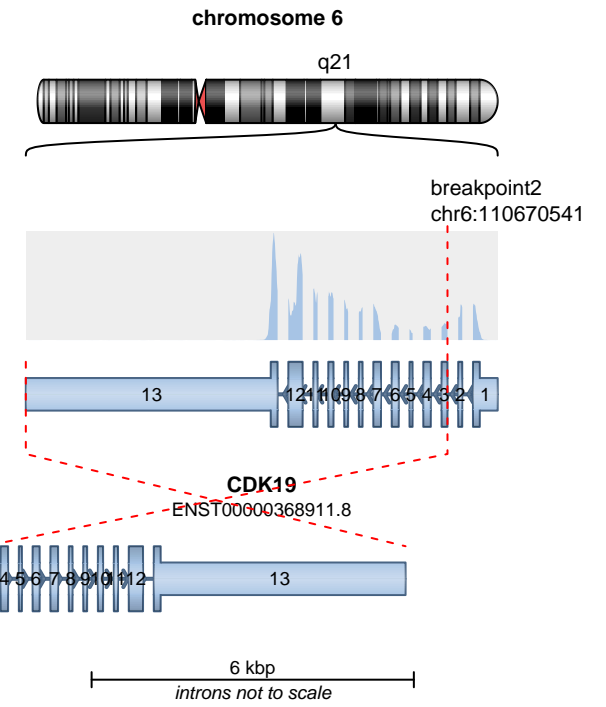
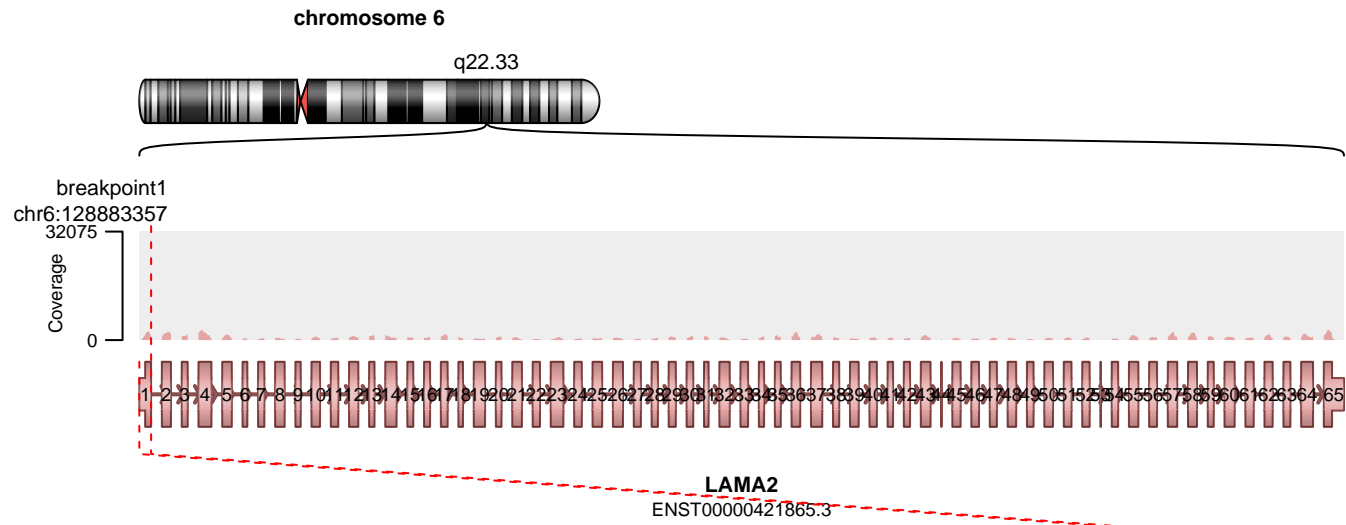
RETAINED PROTEIN DOMAINS
reading frame unclear



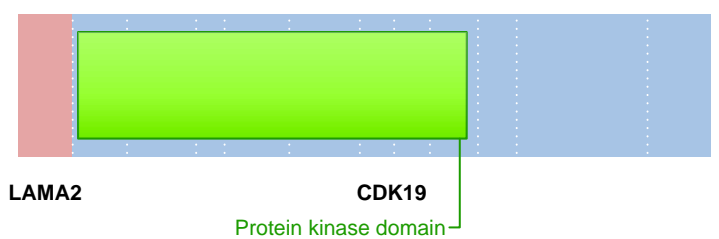
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



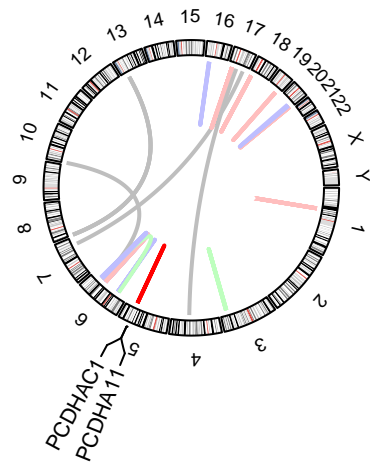
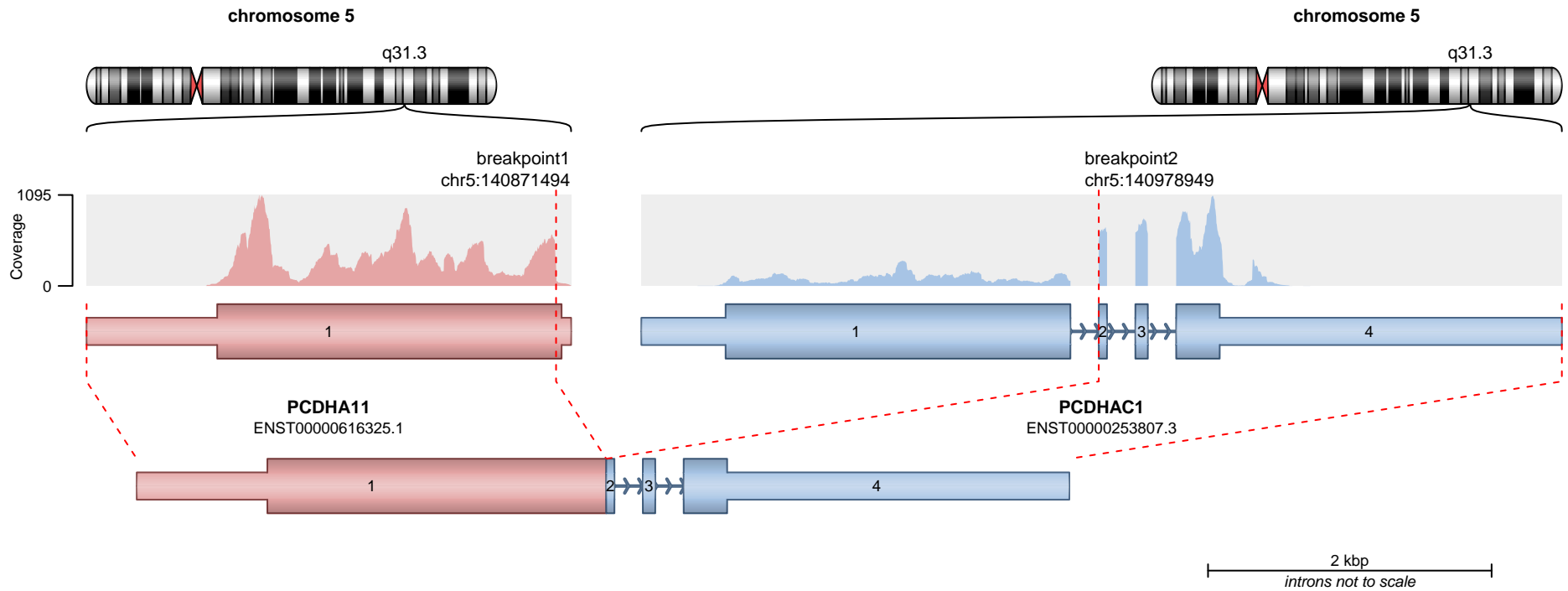
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

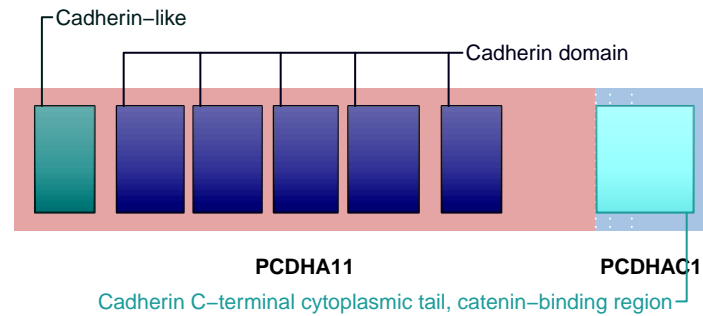
Split reads = 77
Discordant mates = 0

- translocation
- deletion
- duplication
- inversion



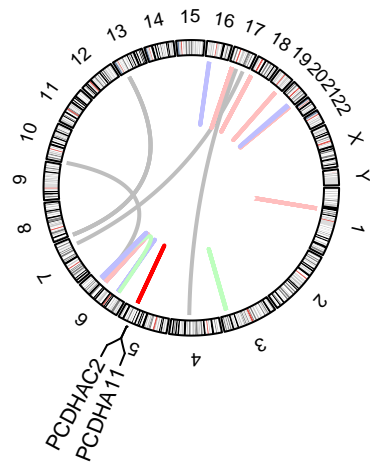
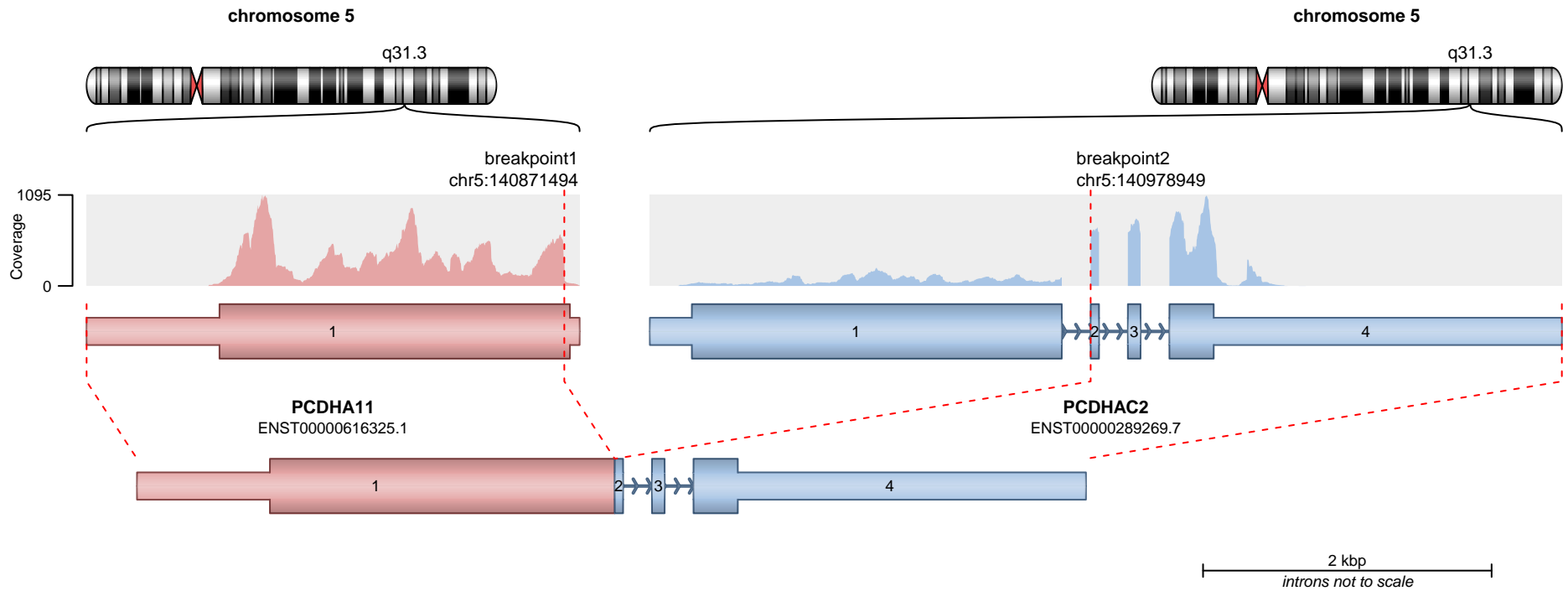
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



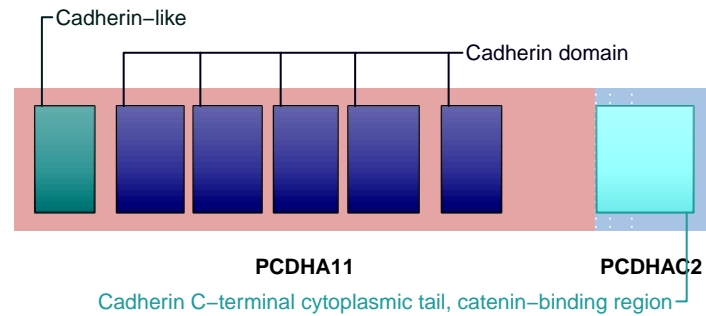
SUPPORTING READ COUNT

Split reads = 77
Discordant mates = 0



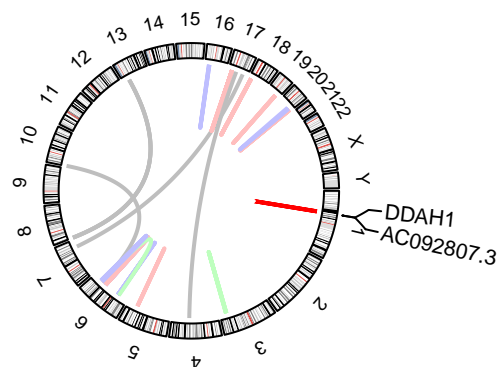
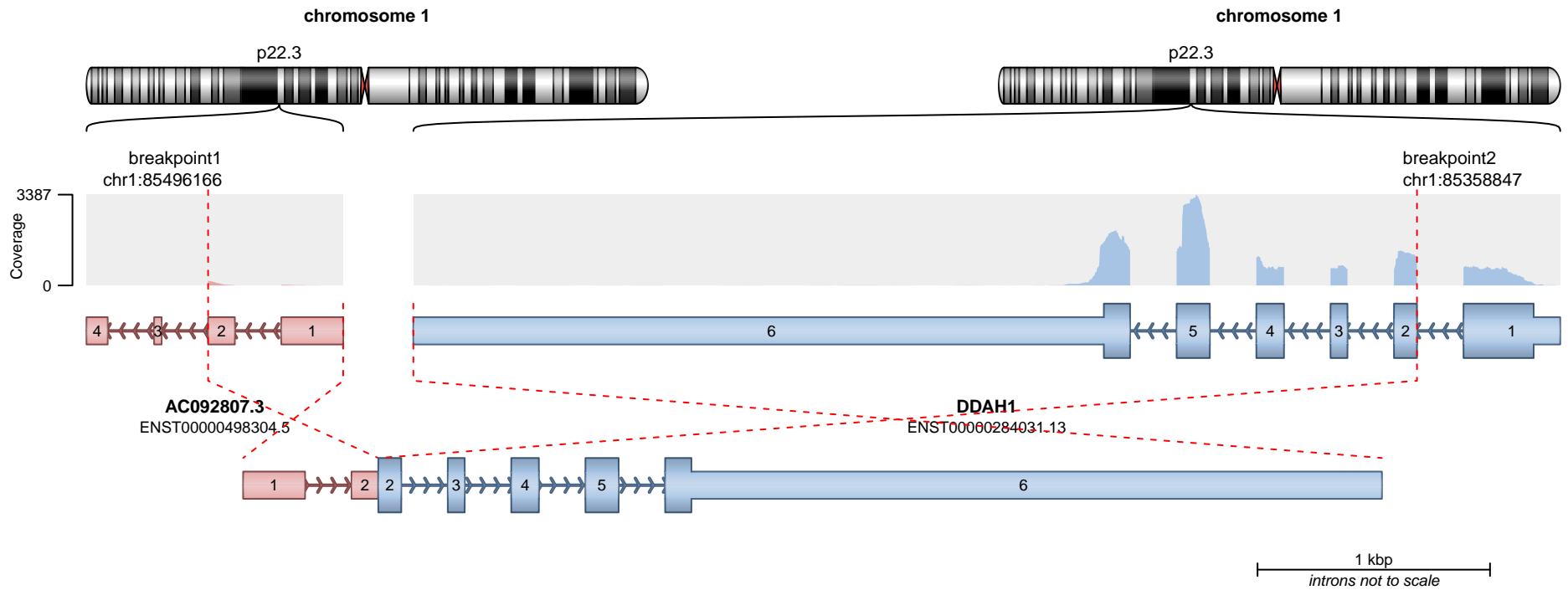
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear

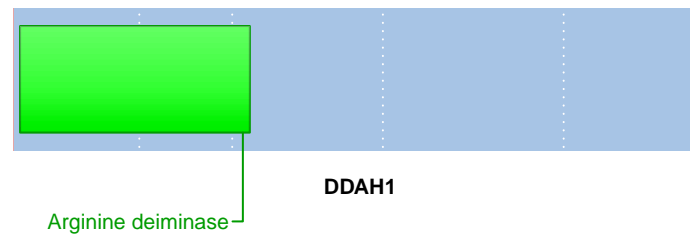


SUPPORTING READ COUNT

Split reads = 77
Discordant mates = 0



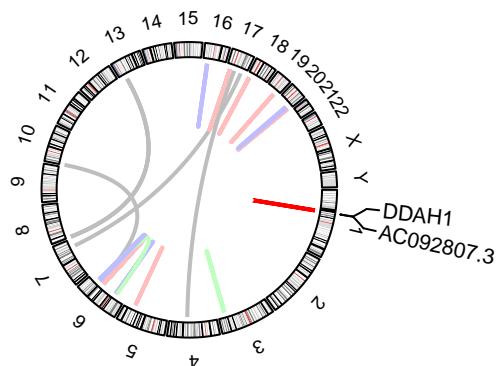
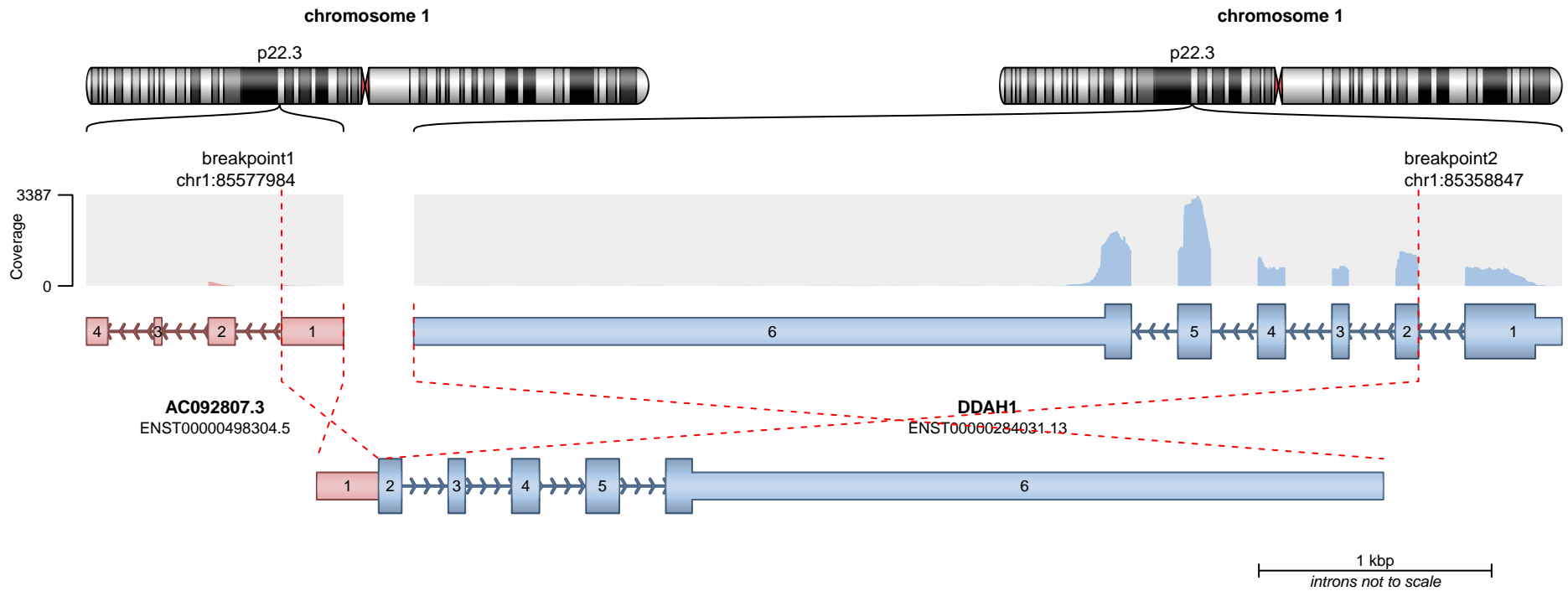
RETAINED PROTEIN DOMAINS
reading frame unclear



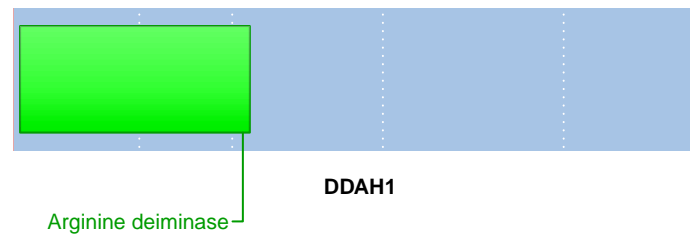
SUPPORTING READ COUNT

Split reads = 64
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



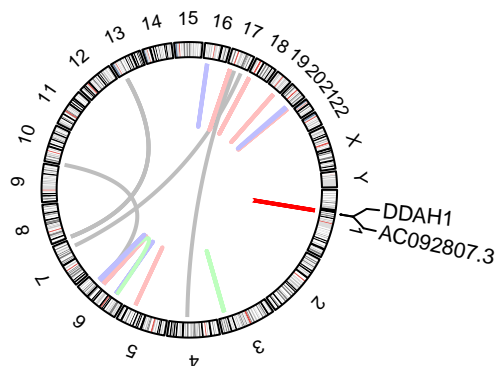
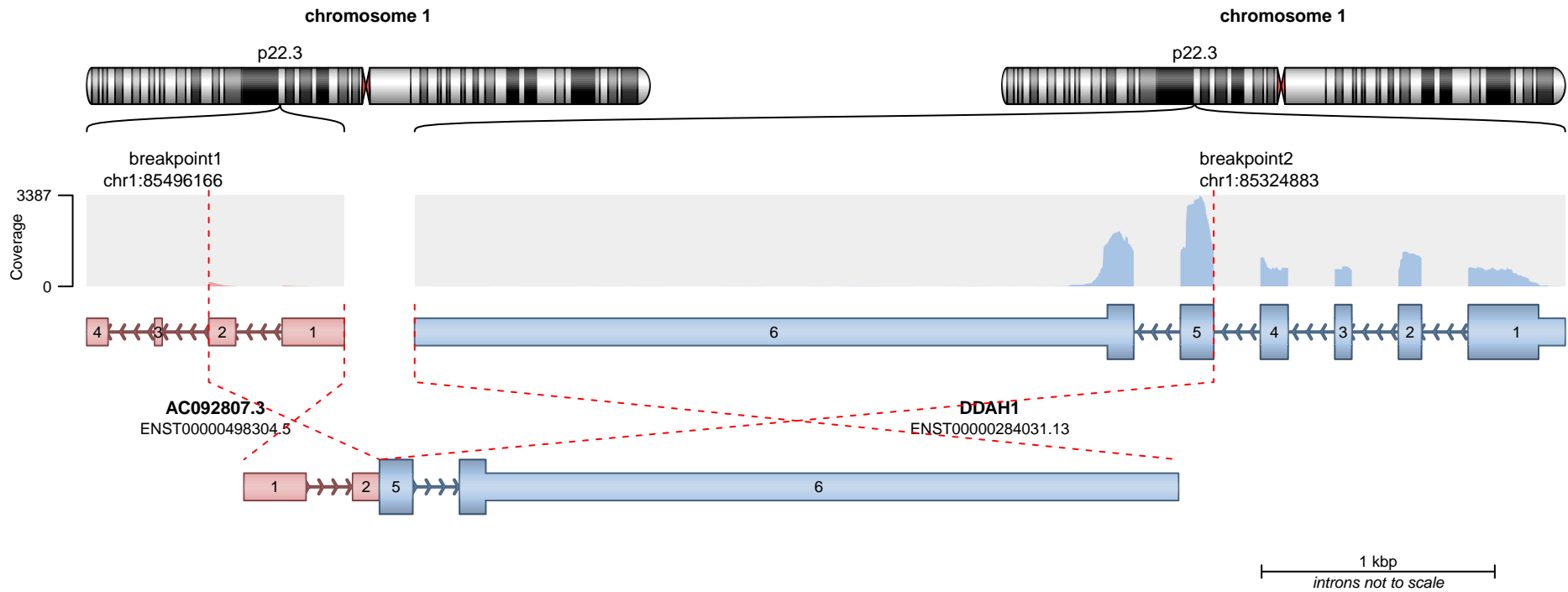
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 11
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

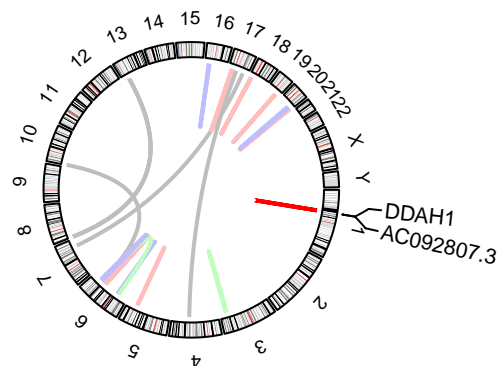
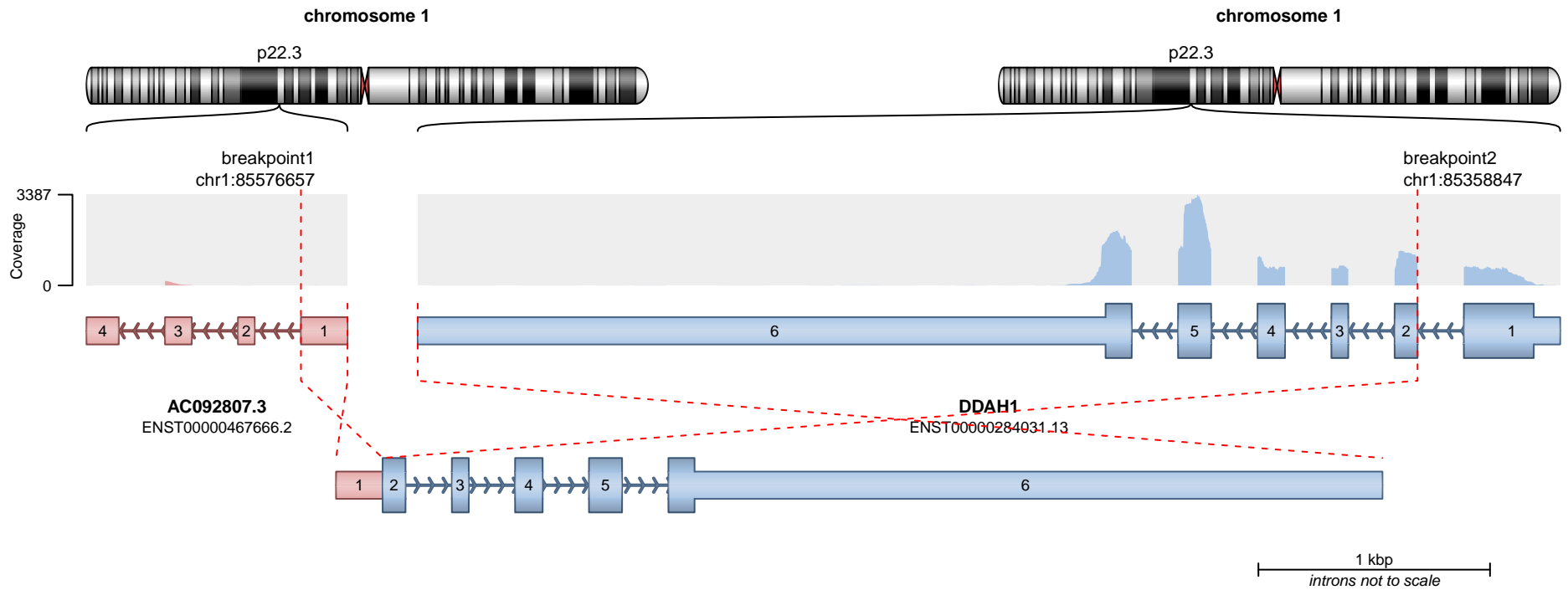


No protein domains retained in fusion.

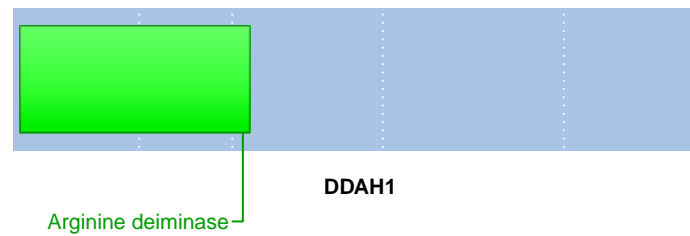
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



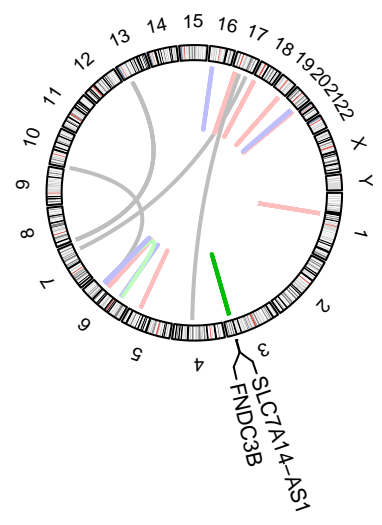
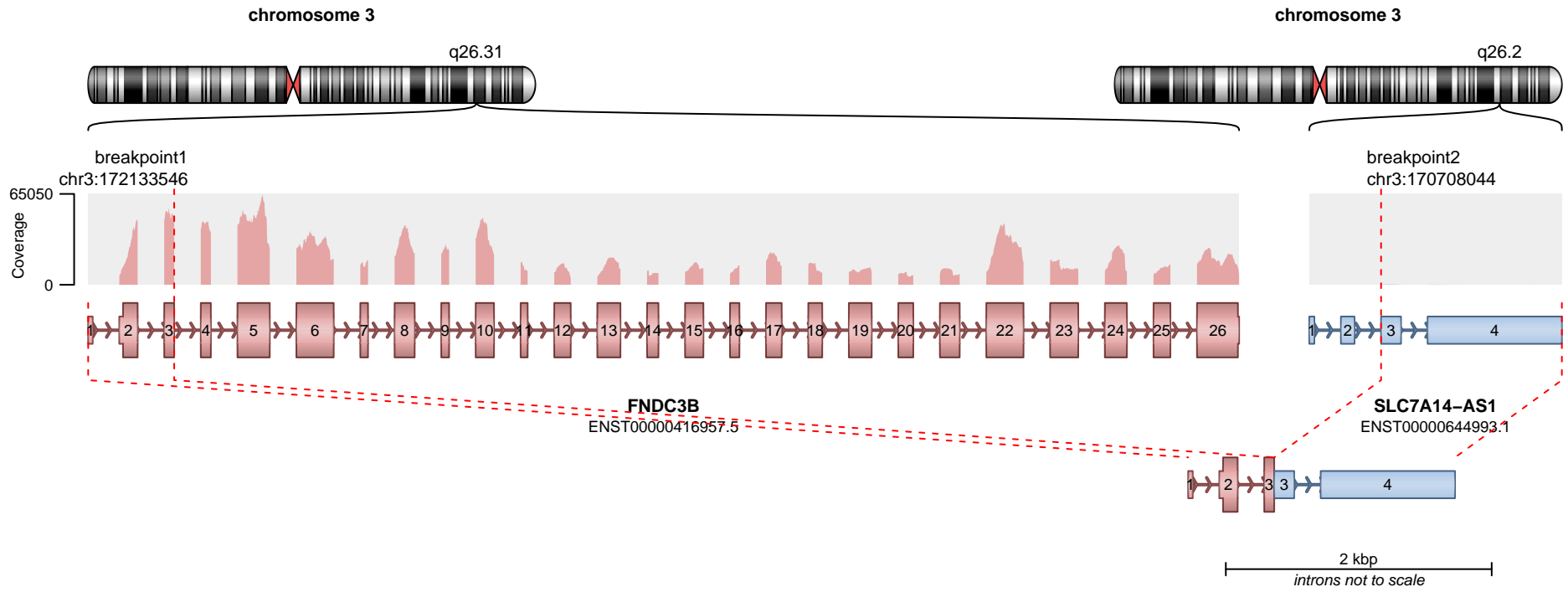
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

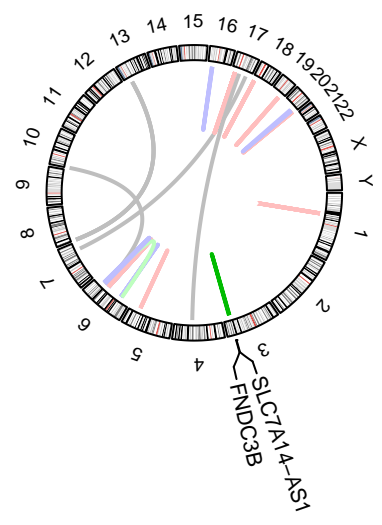
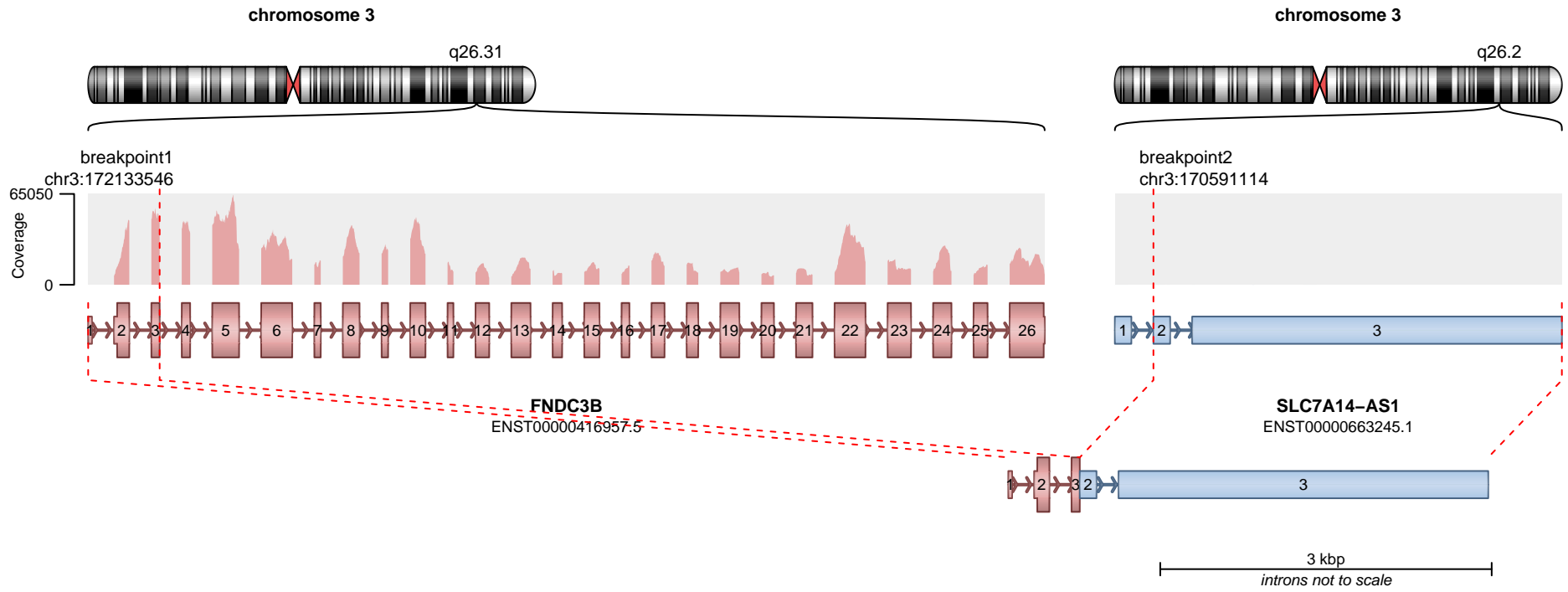


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 62
Discordant mates = 0

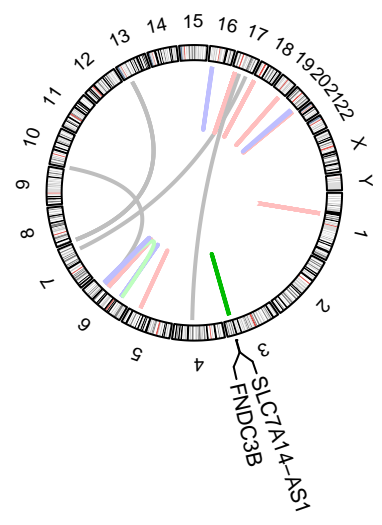
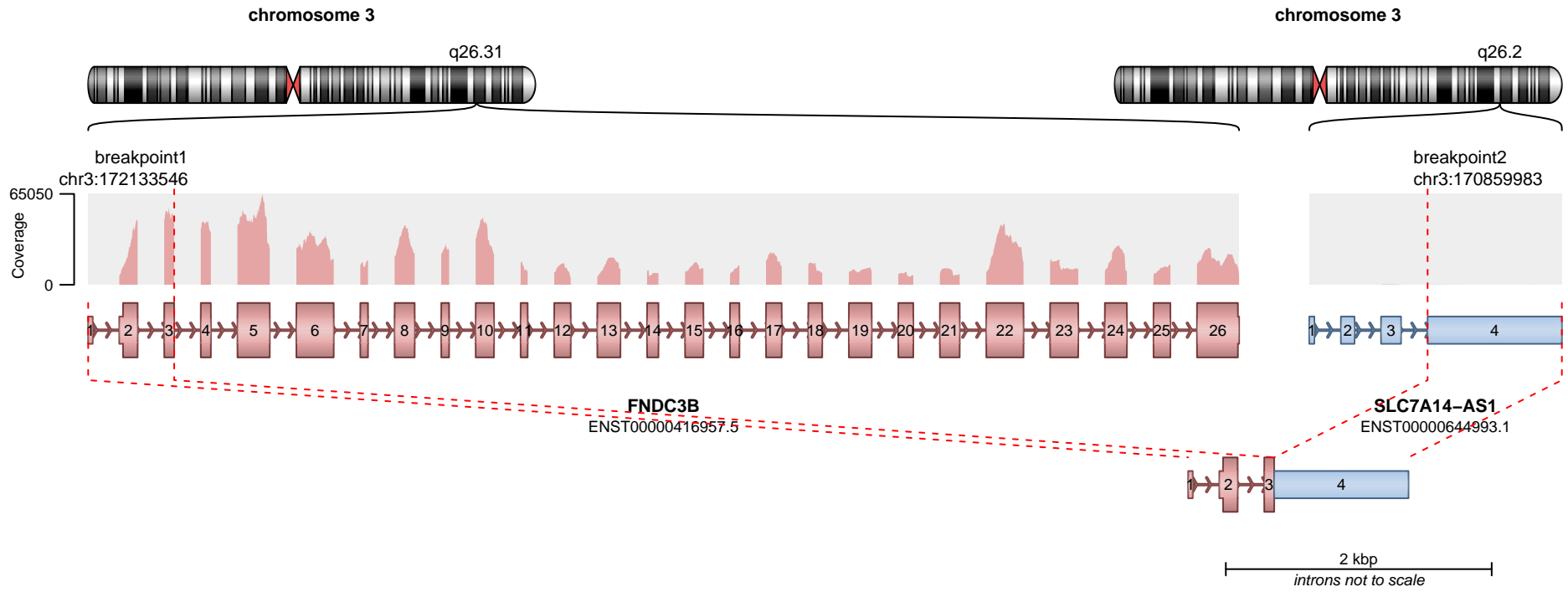


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 15
Discordant mates = 0

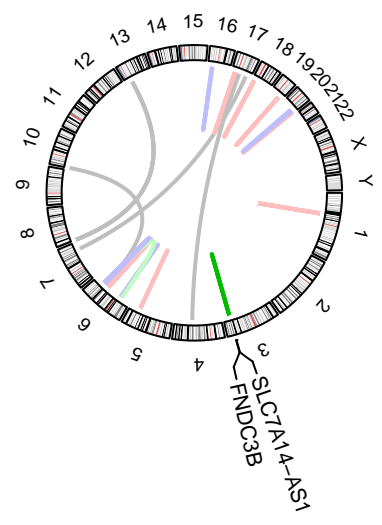
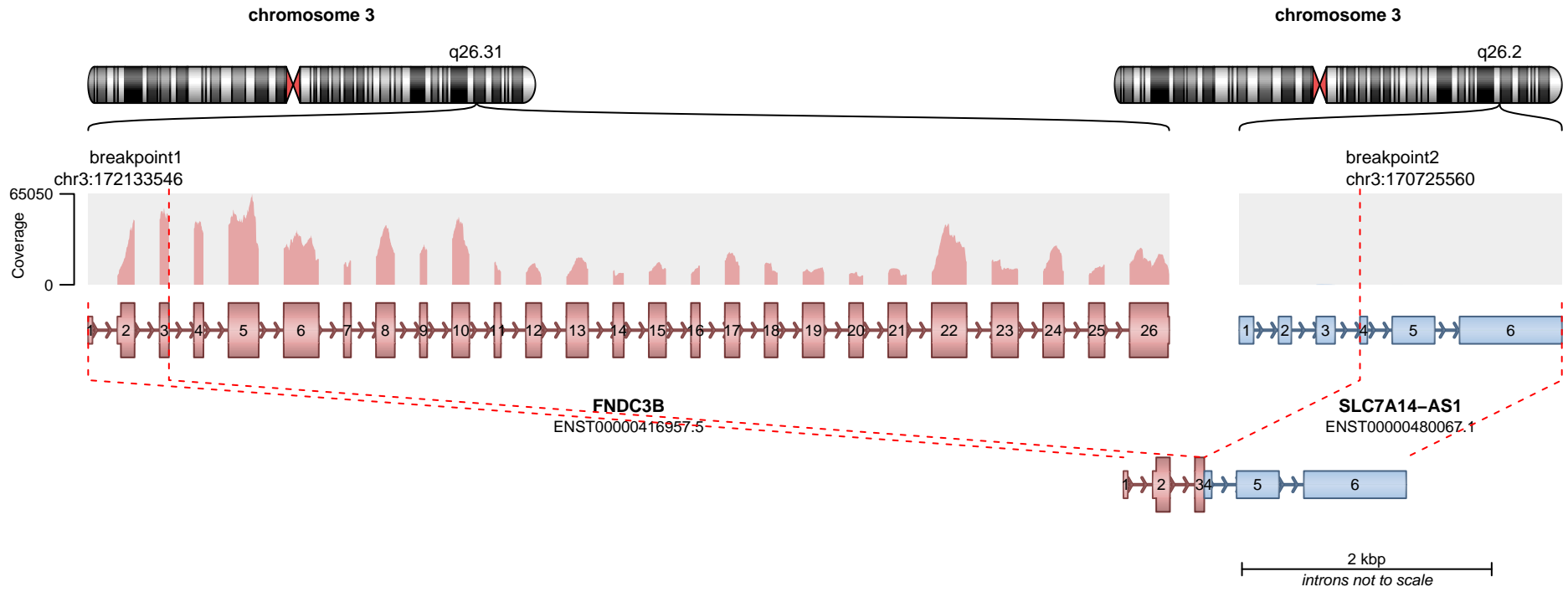


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 9
Discordant mates = 0

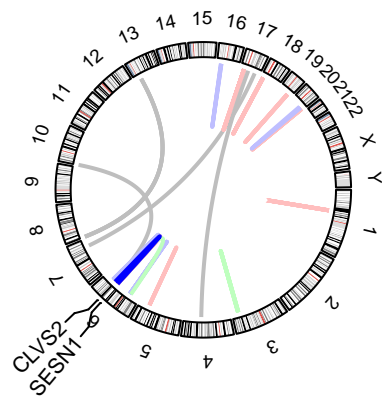
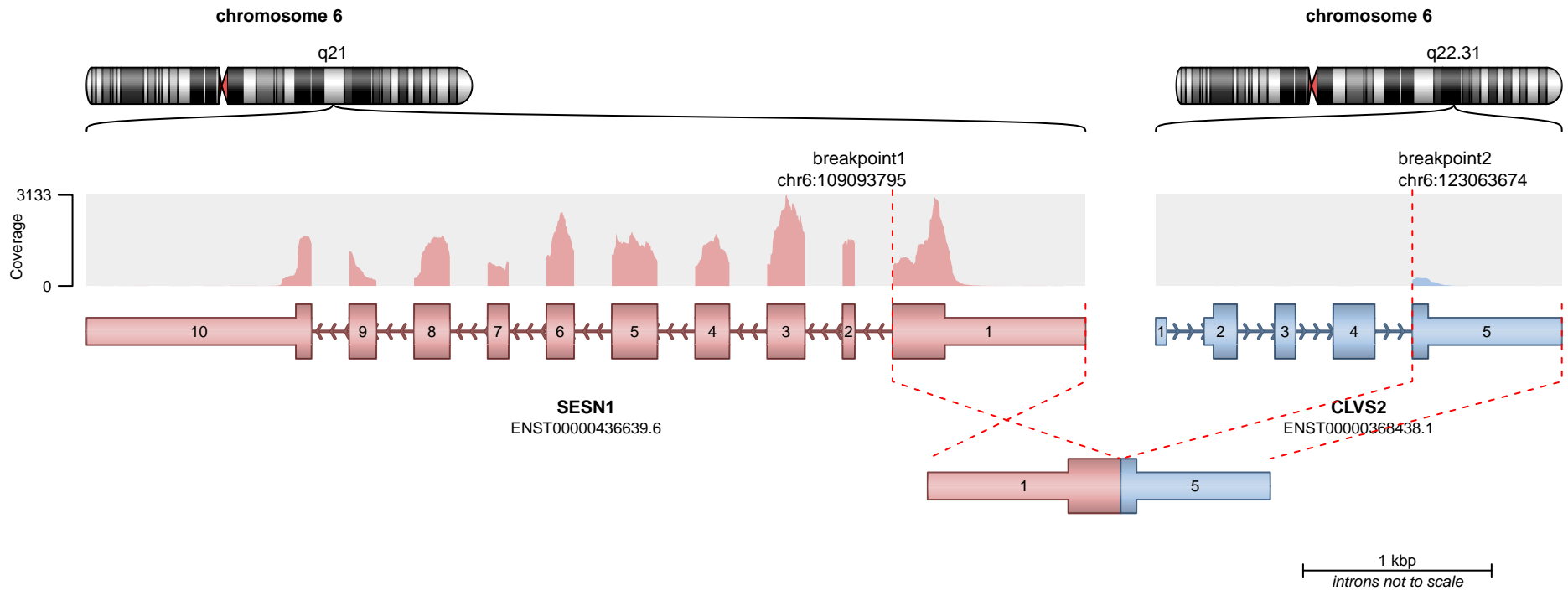


— translocation — deletion
 — duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 4
 Discordant mates = 0

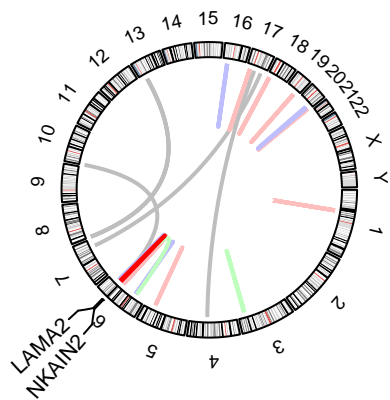
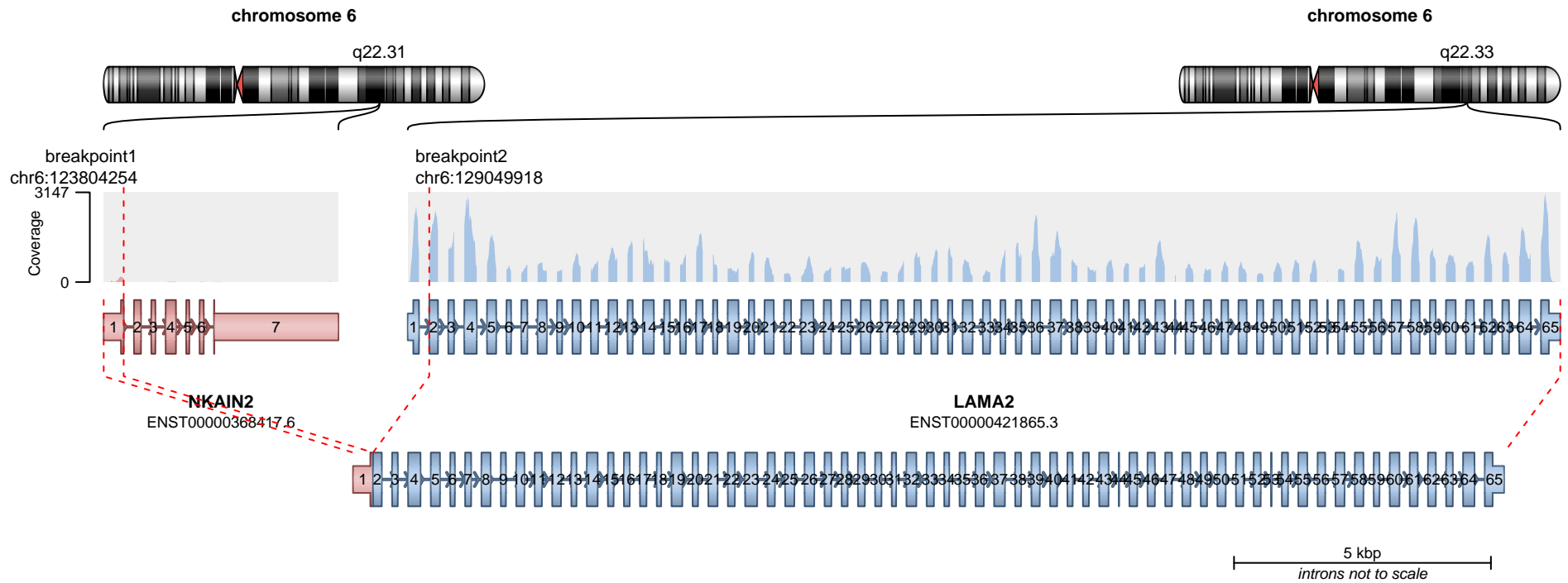


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

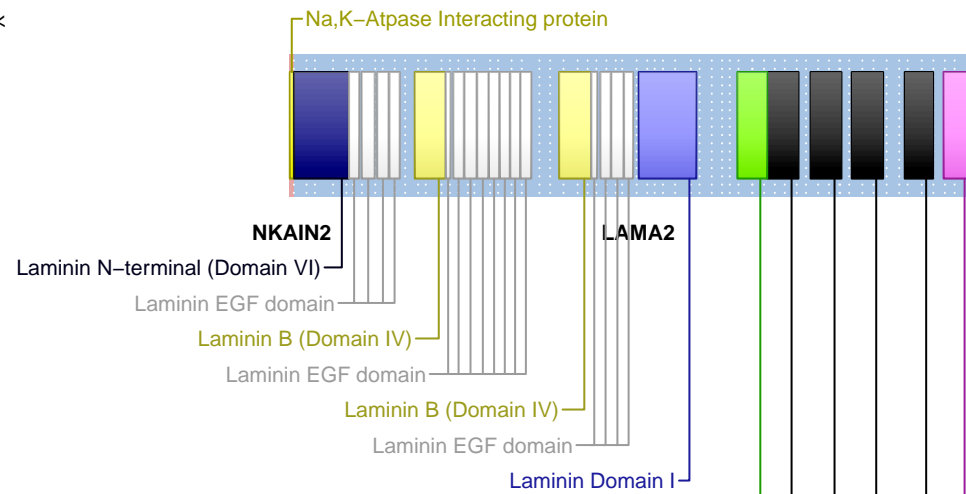
SUPPORTING READ COUNT

Split reads = 54
Discordant mates = 0



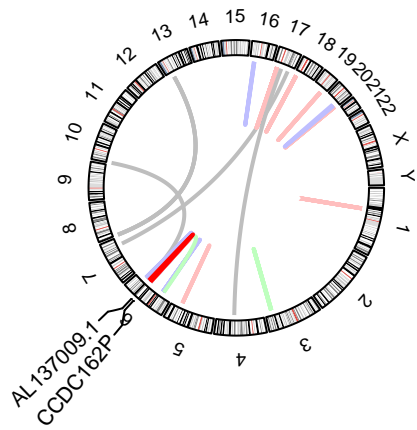
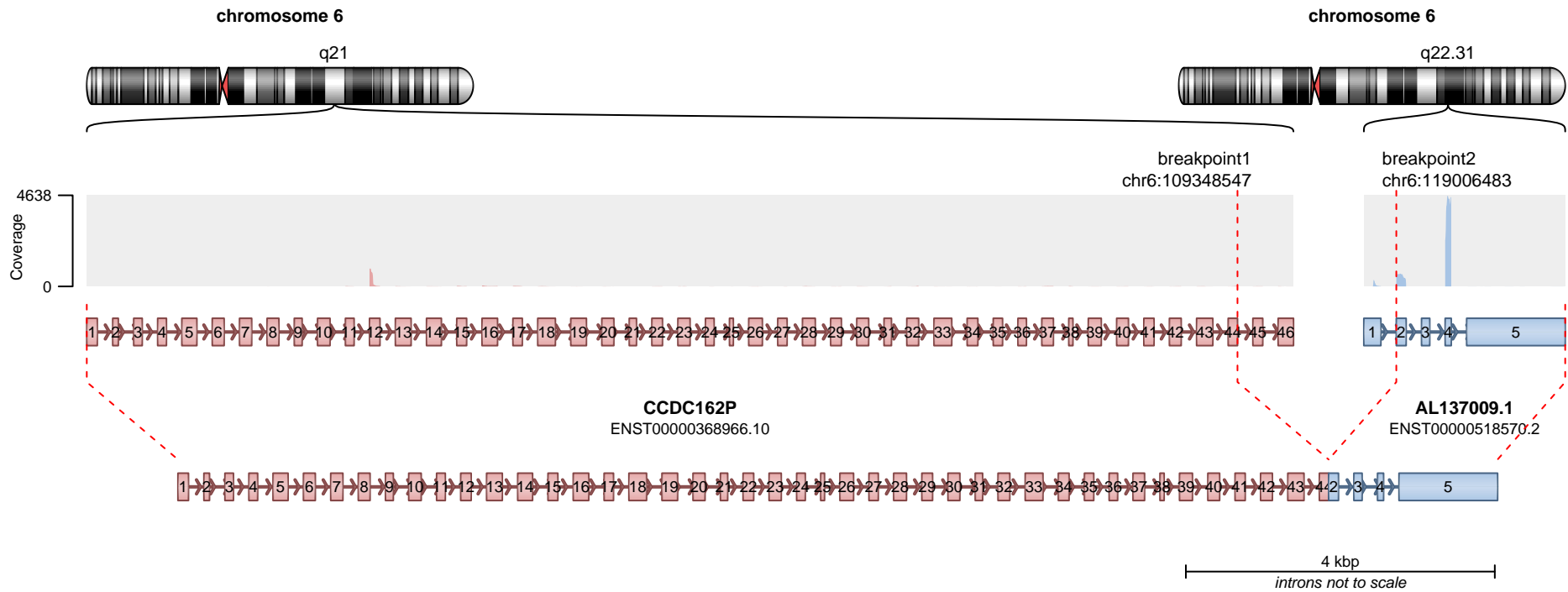
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 39
Discordant mates = 0

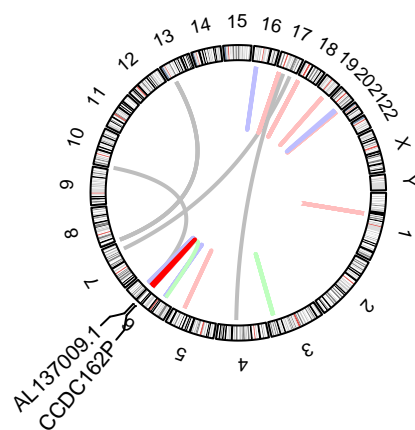
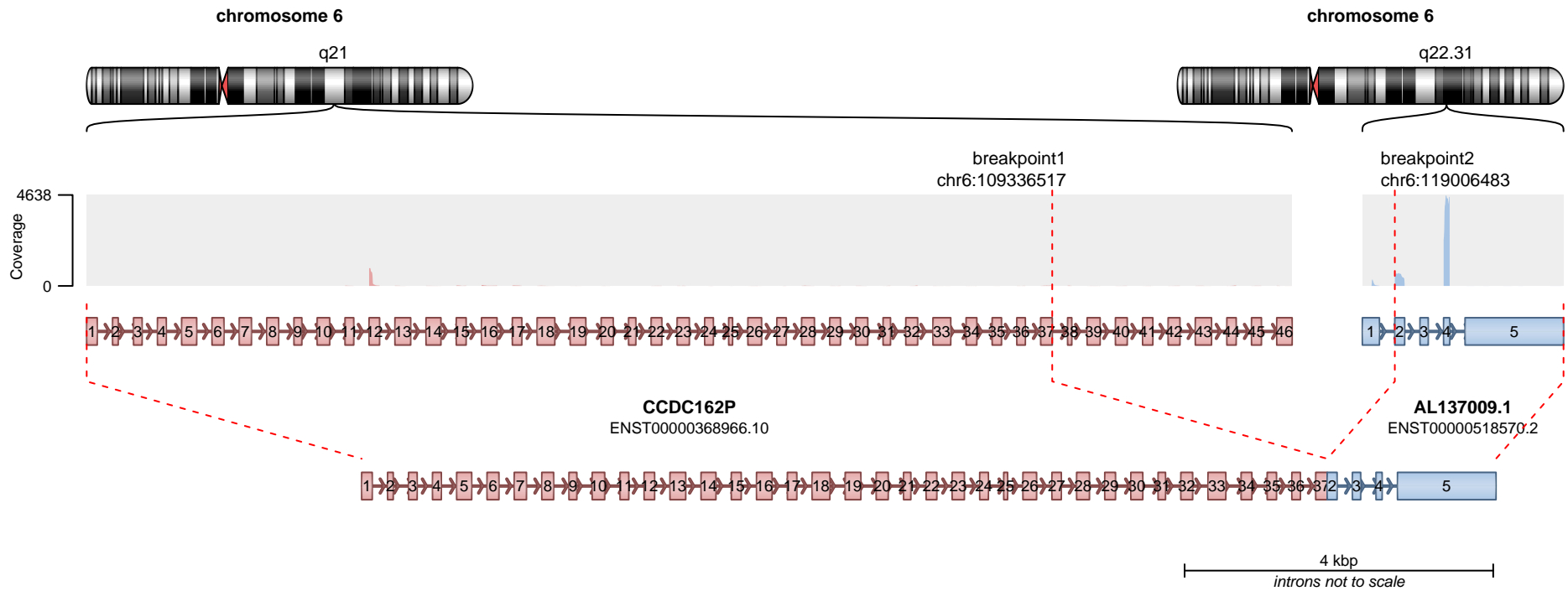


— translocation — deletion
— duplication — inversion

Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 27
Discordant mates = 0

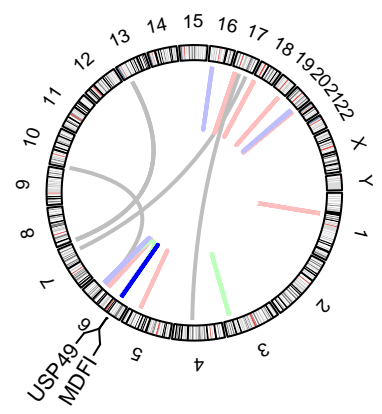
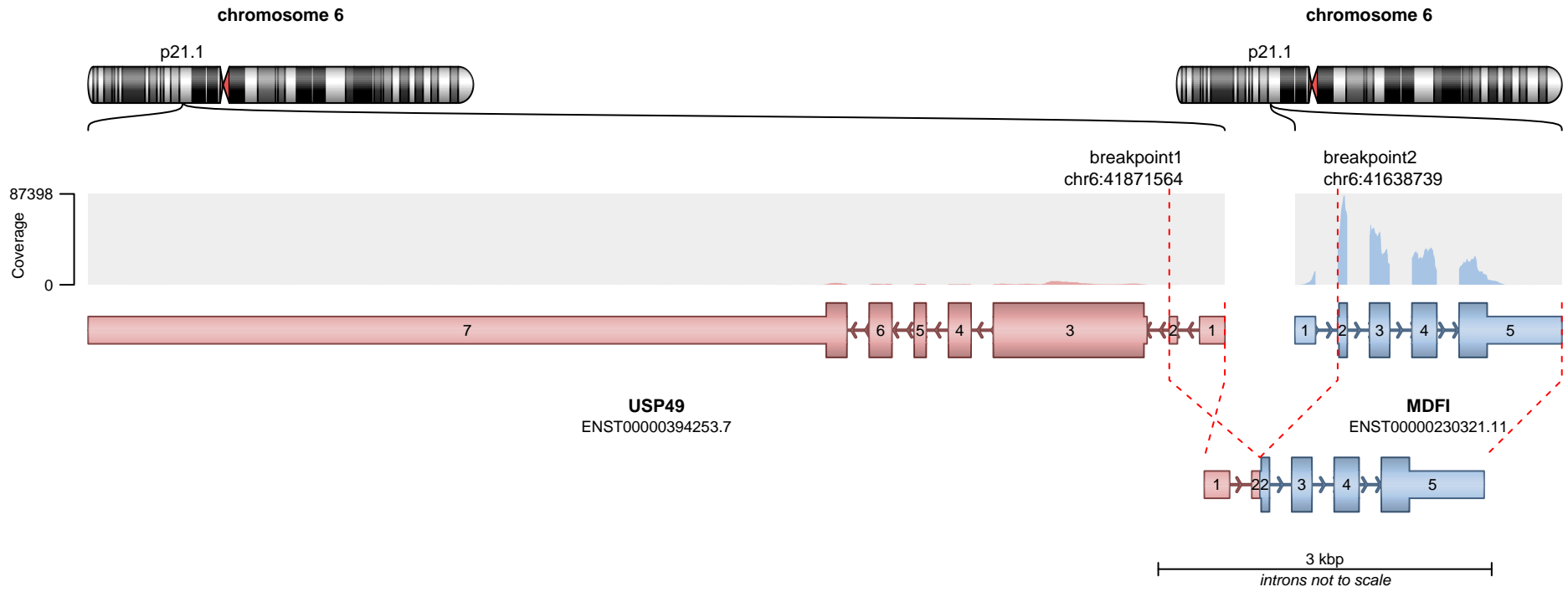


- translocation
- duplication
- deletion
- inversion

Genes are not protein-coding.

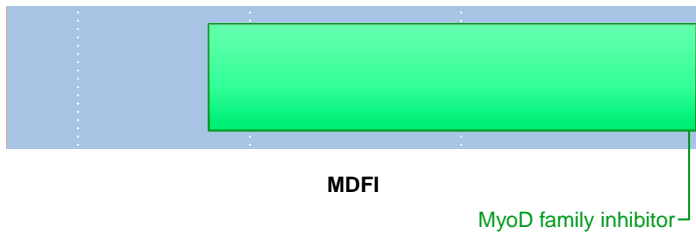
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0



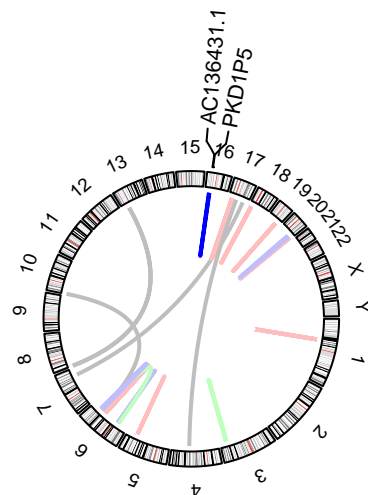
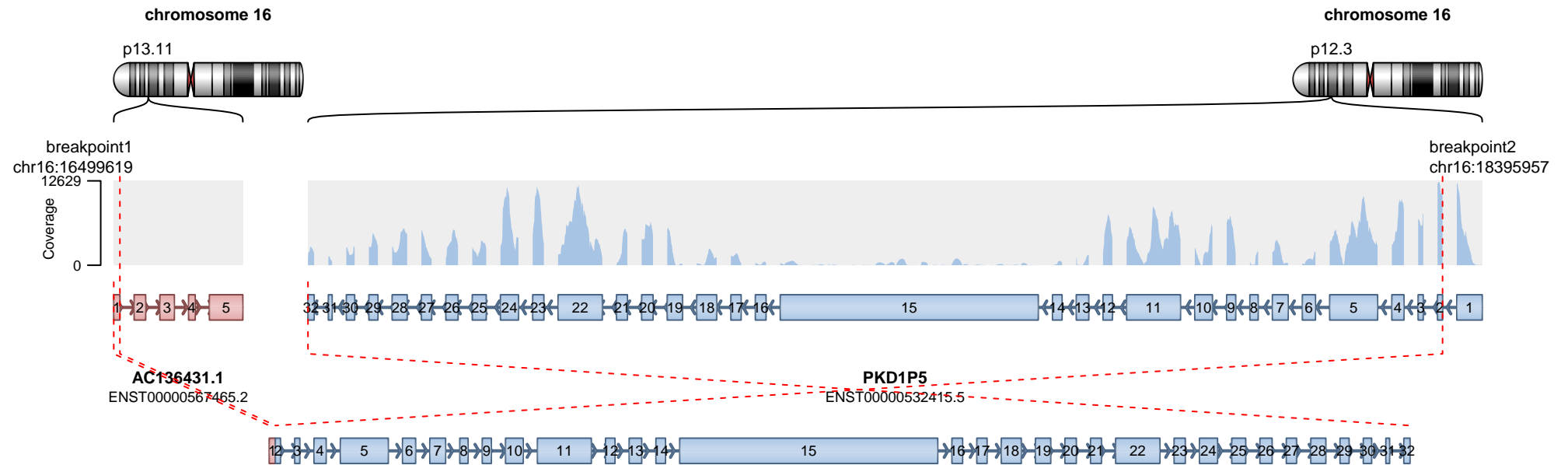
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 25
Discordant mates = 0

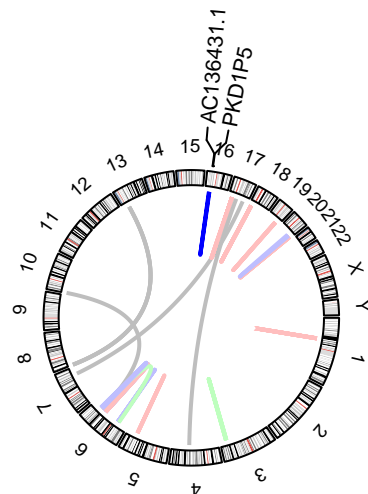
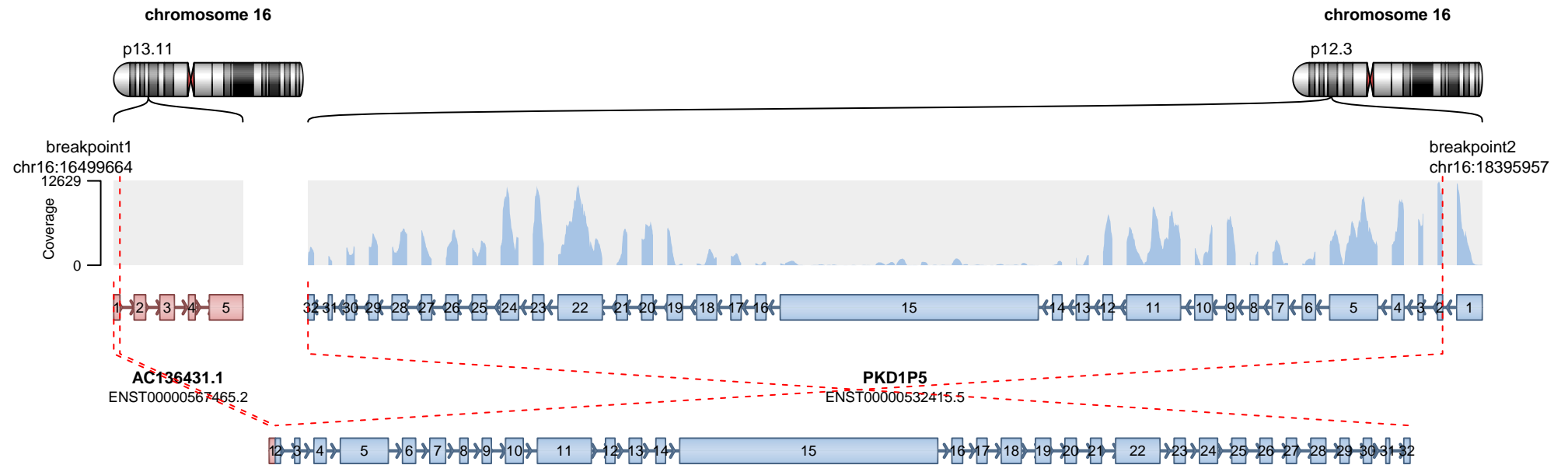


Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 24
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

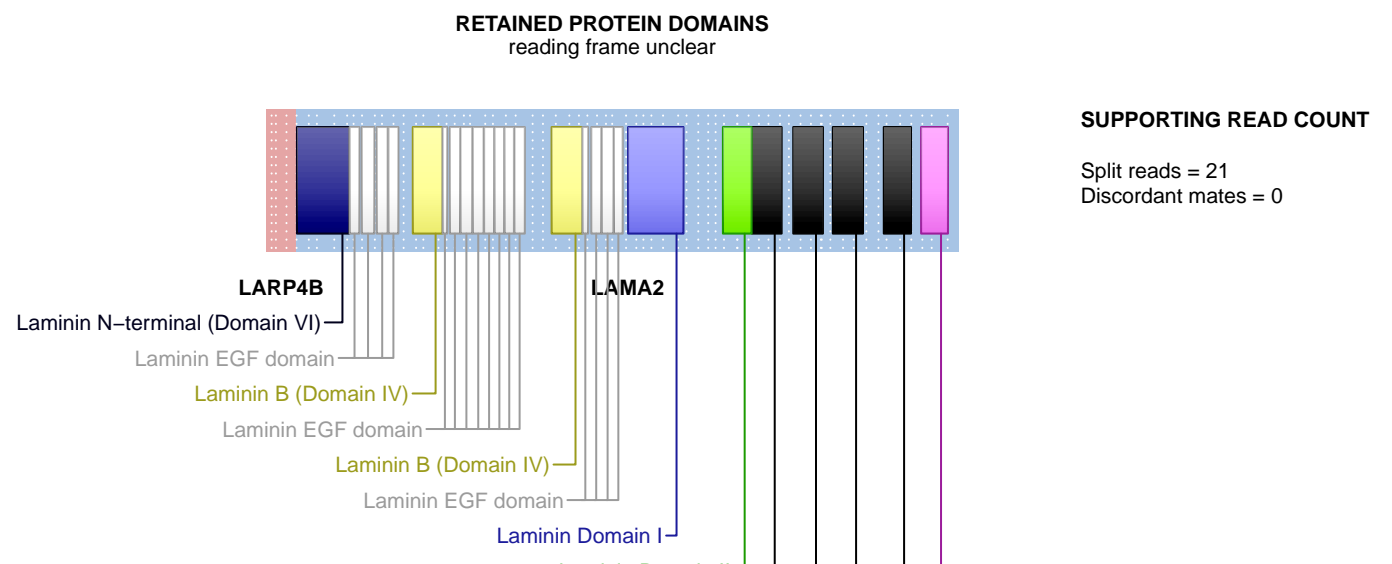
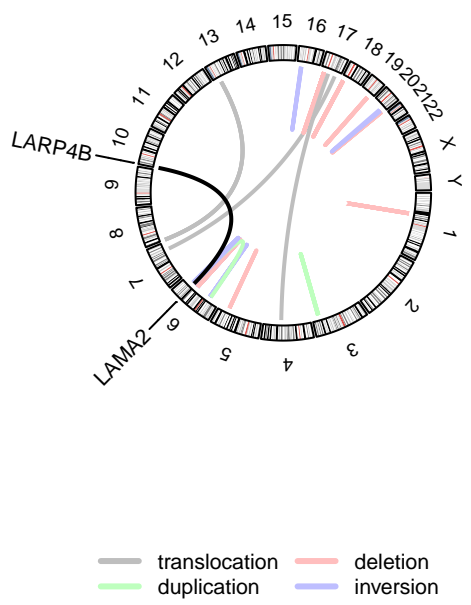
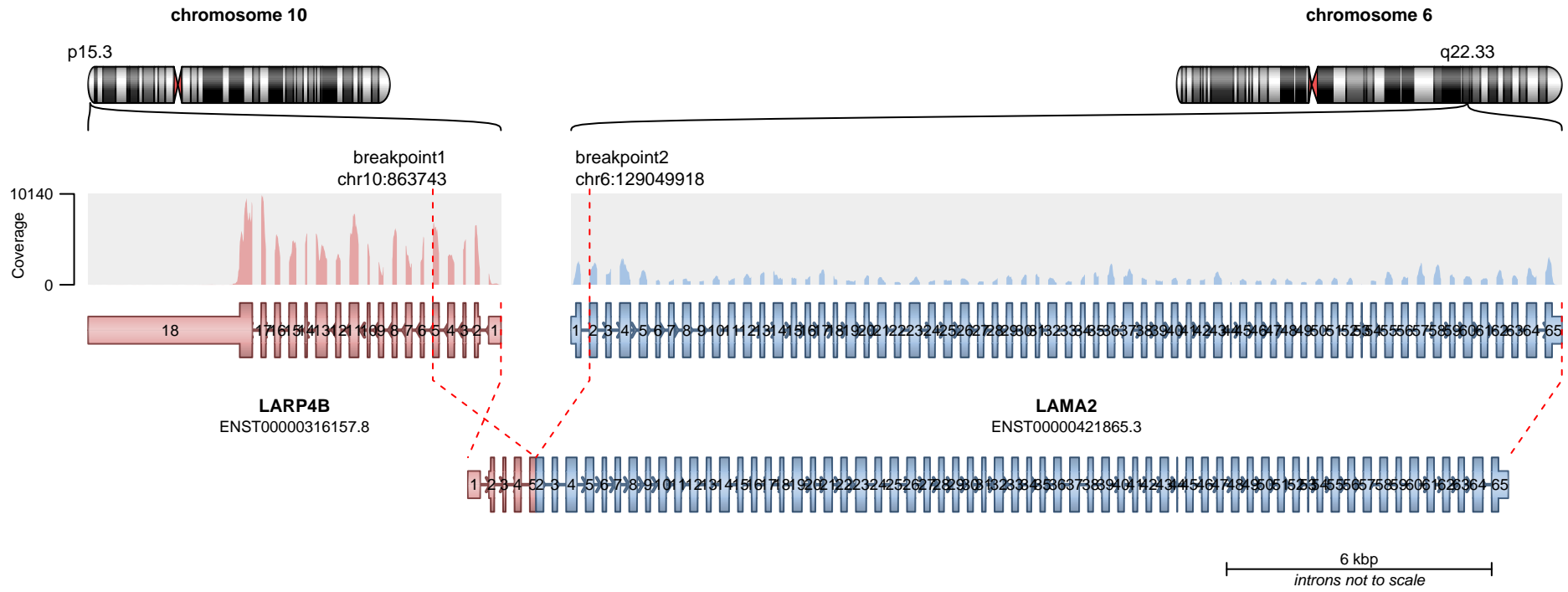


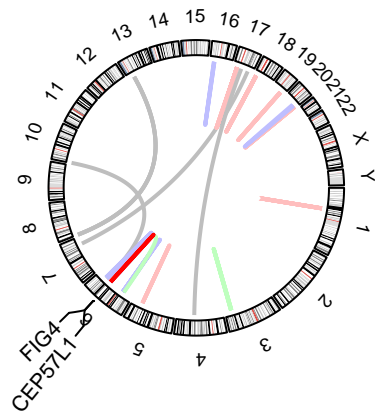
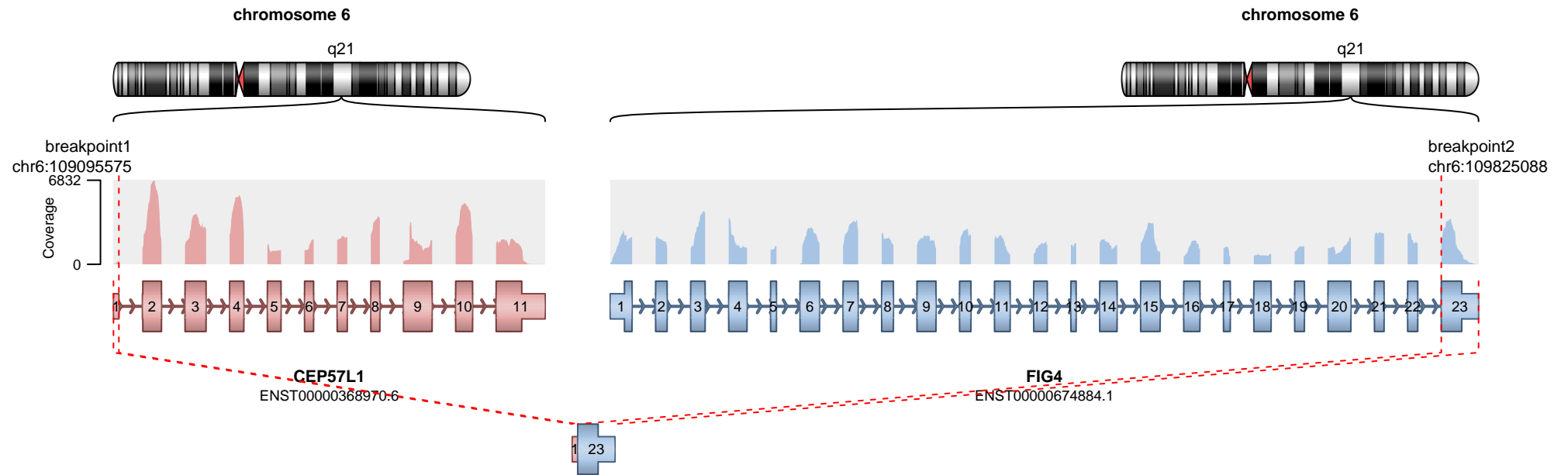
Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

— translocation — deletion
— duplication — inversion



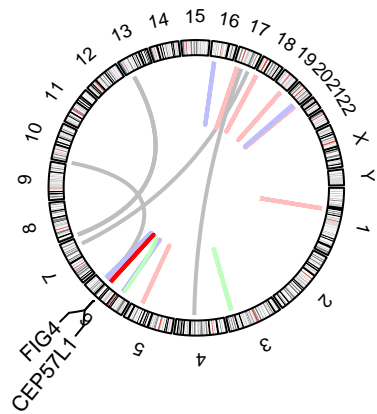
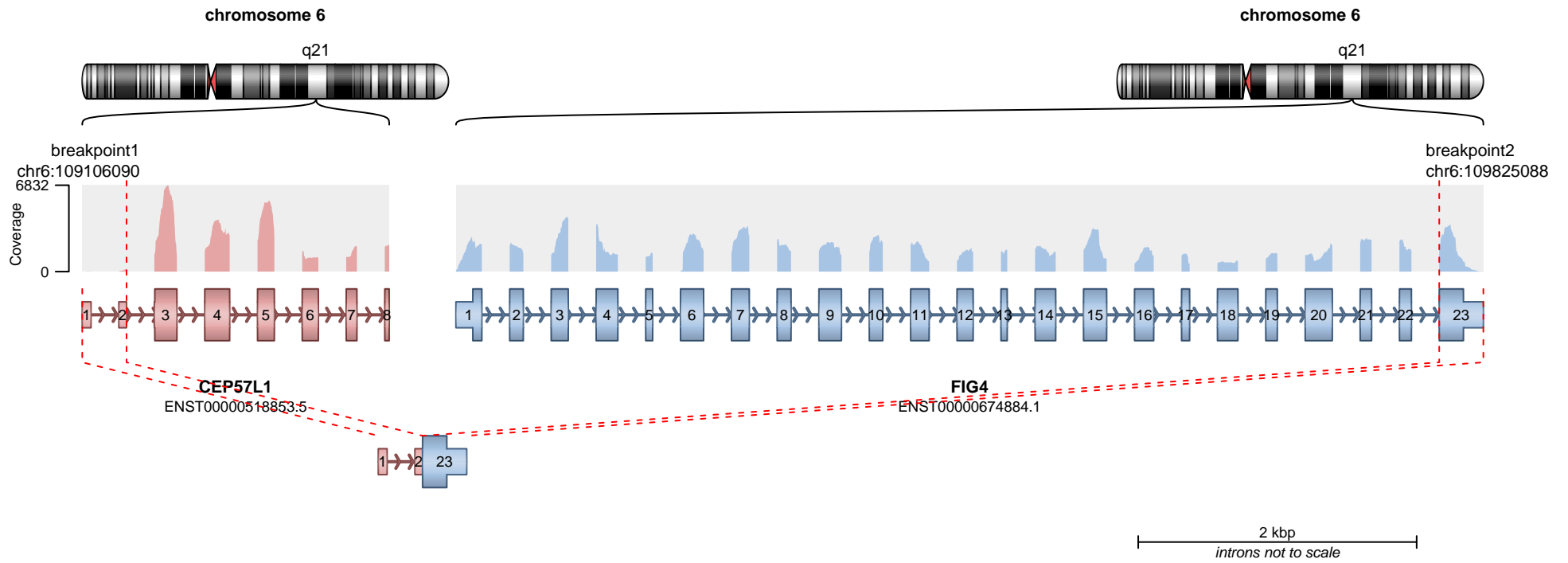


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 14
Discordant mates = 0

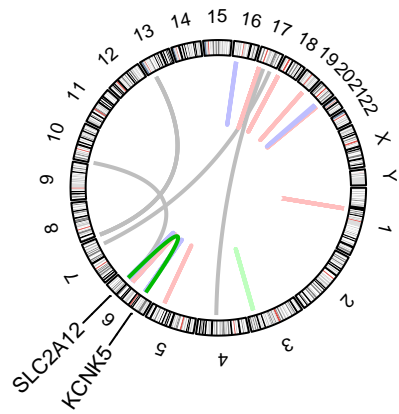
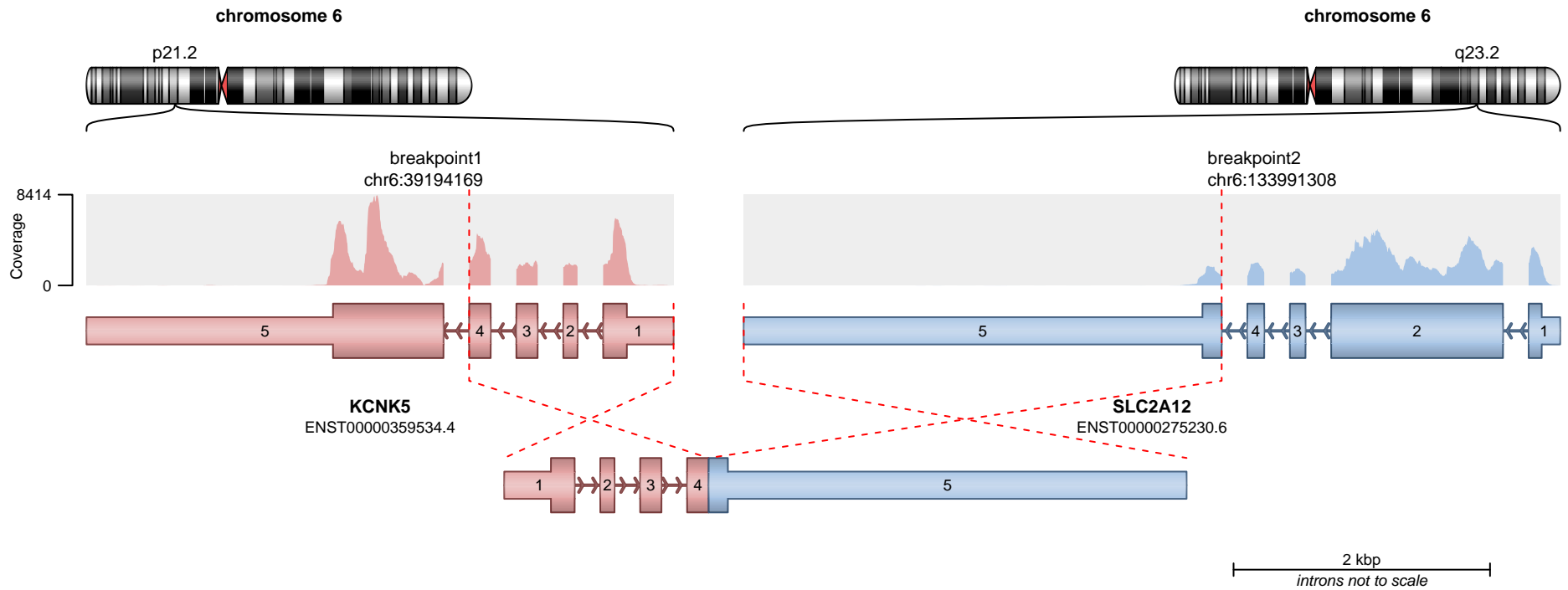


— translocation — deletion
— duplication — inversion

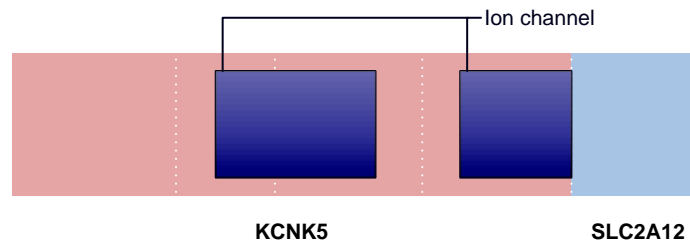
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0



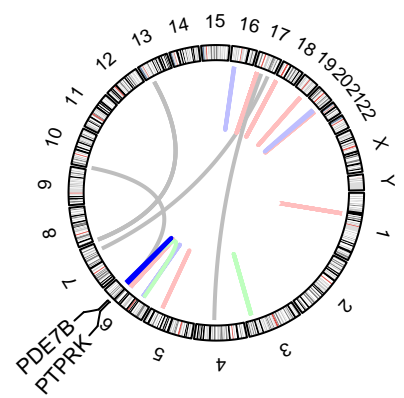
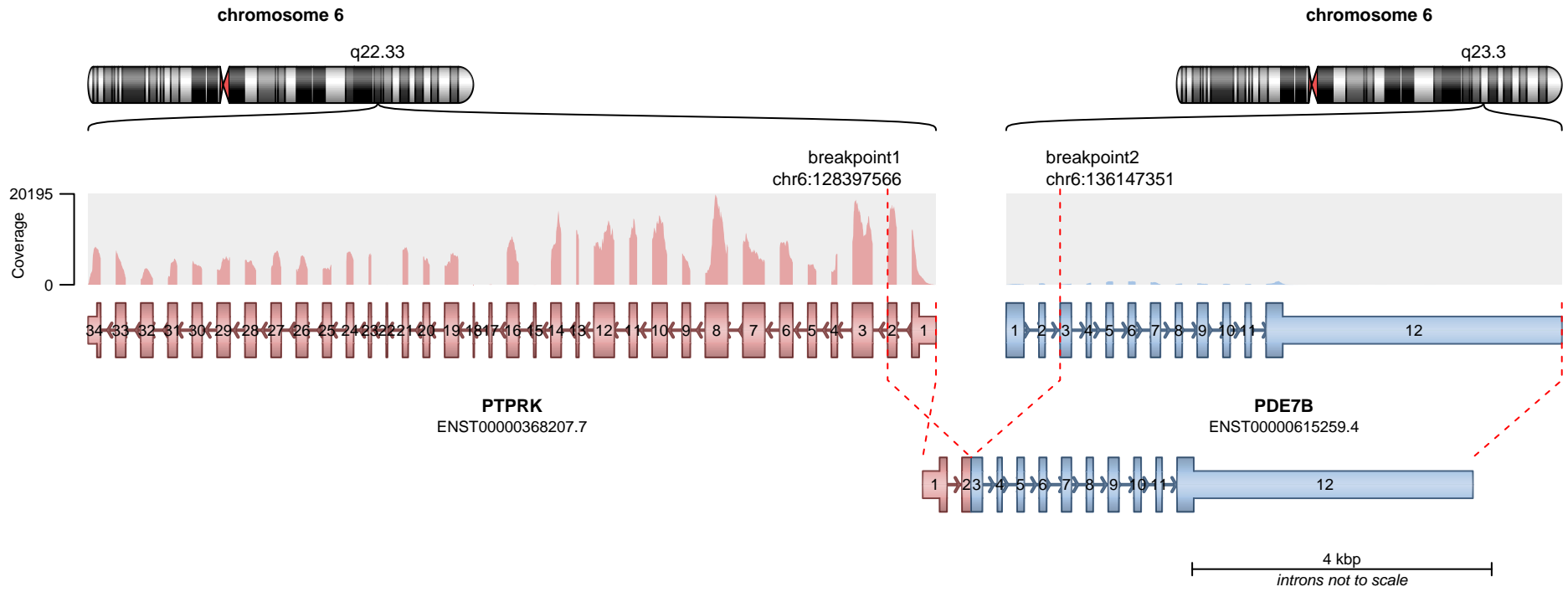
RETAINED PROTEIN DOMAINS
reading frame unclear



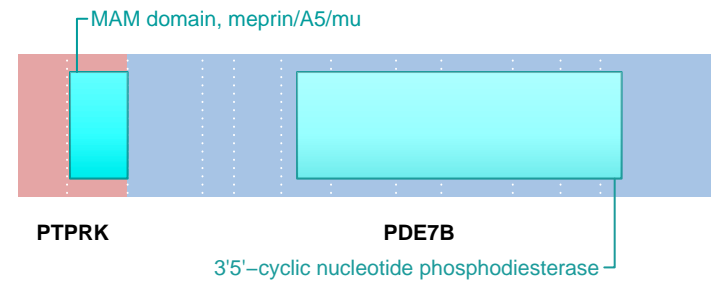
SUPPORTING READ COUNT

Split reads = 14
Discordant mates = 0

— translocation — deletion
— duplication — inversion



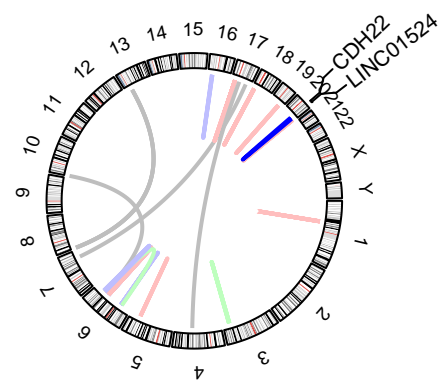
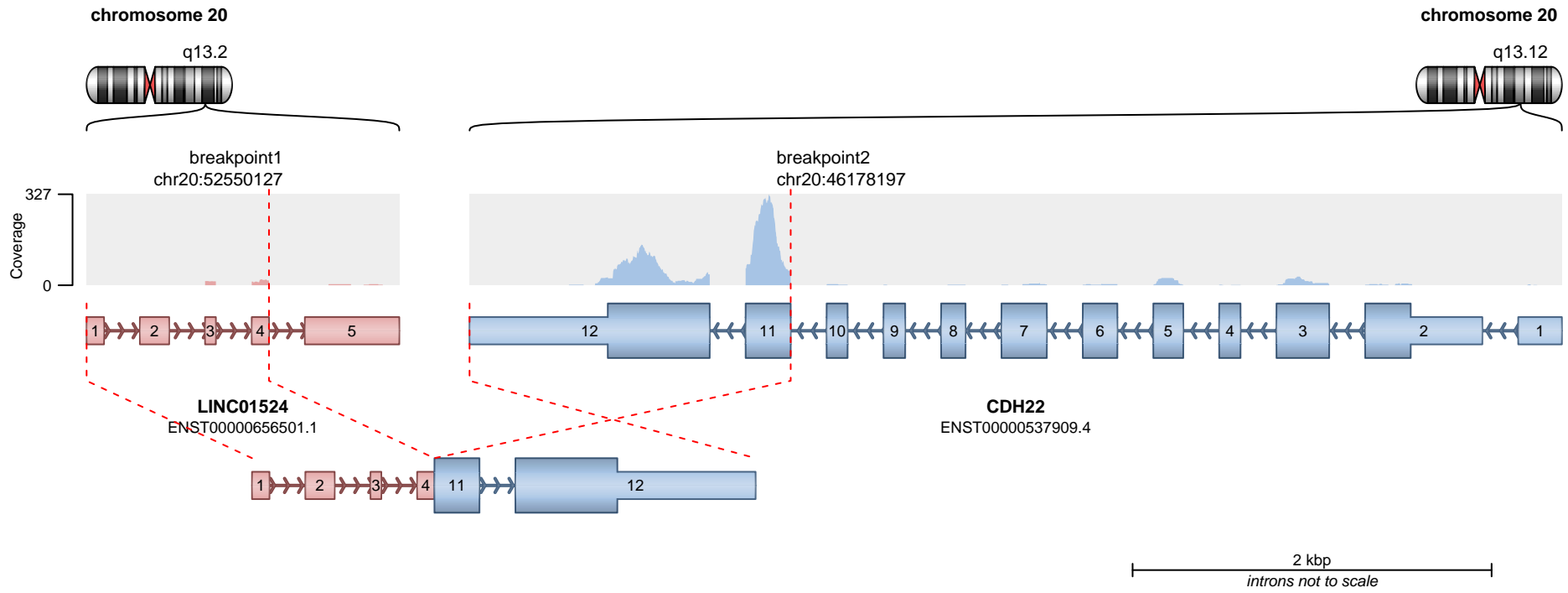
RETAINED PROTEIN DOMAINS
reading frame unclear



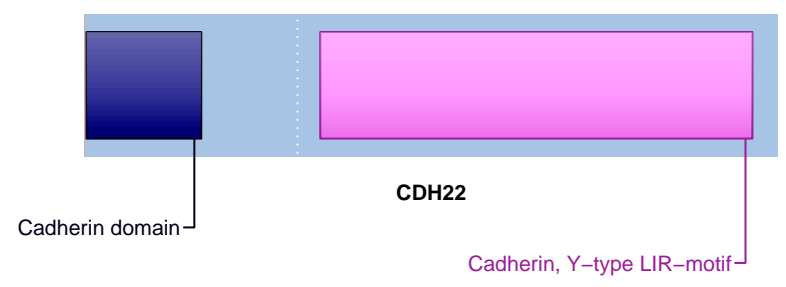
SUPPORTING READ COUNT

Split reads = 13
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



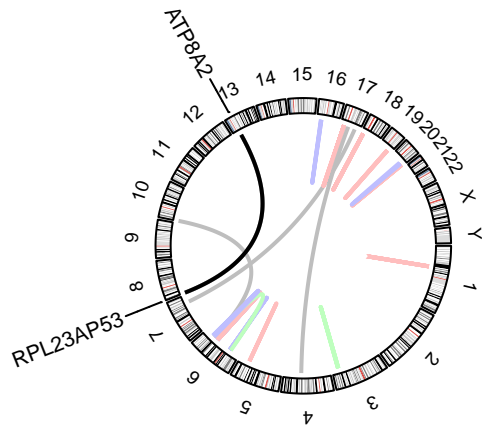
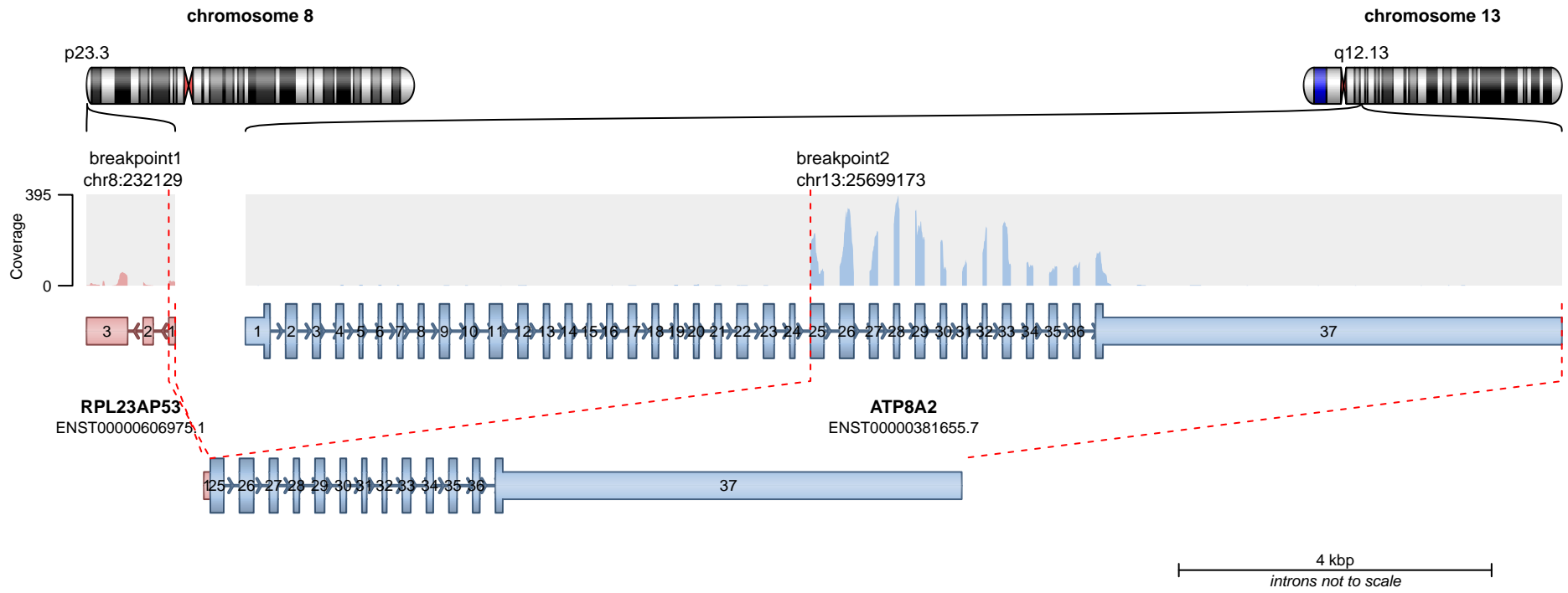
RETAINED PROTEIN DOMAINS
reading frame unclear



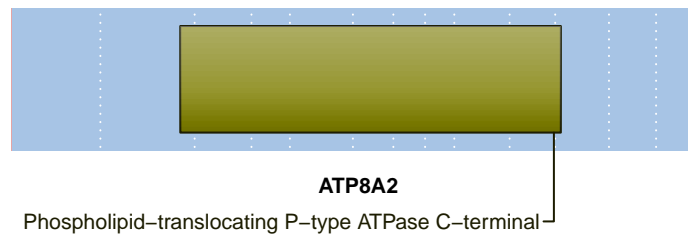
SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 0

— translocation — deletion
— duplication — inversion



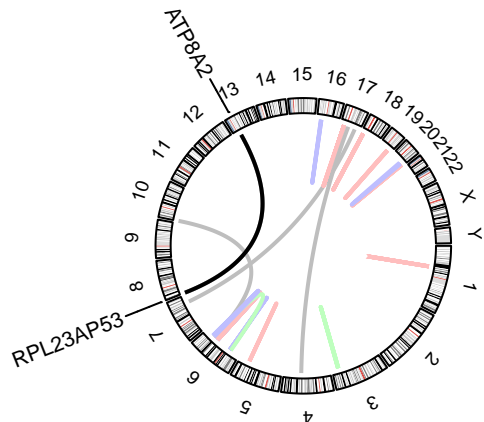
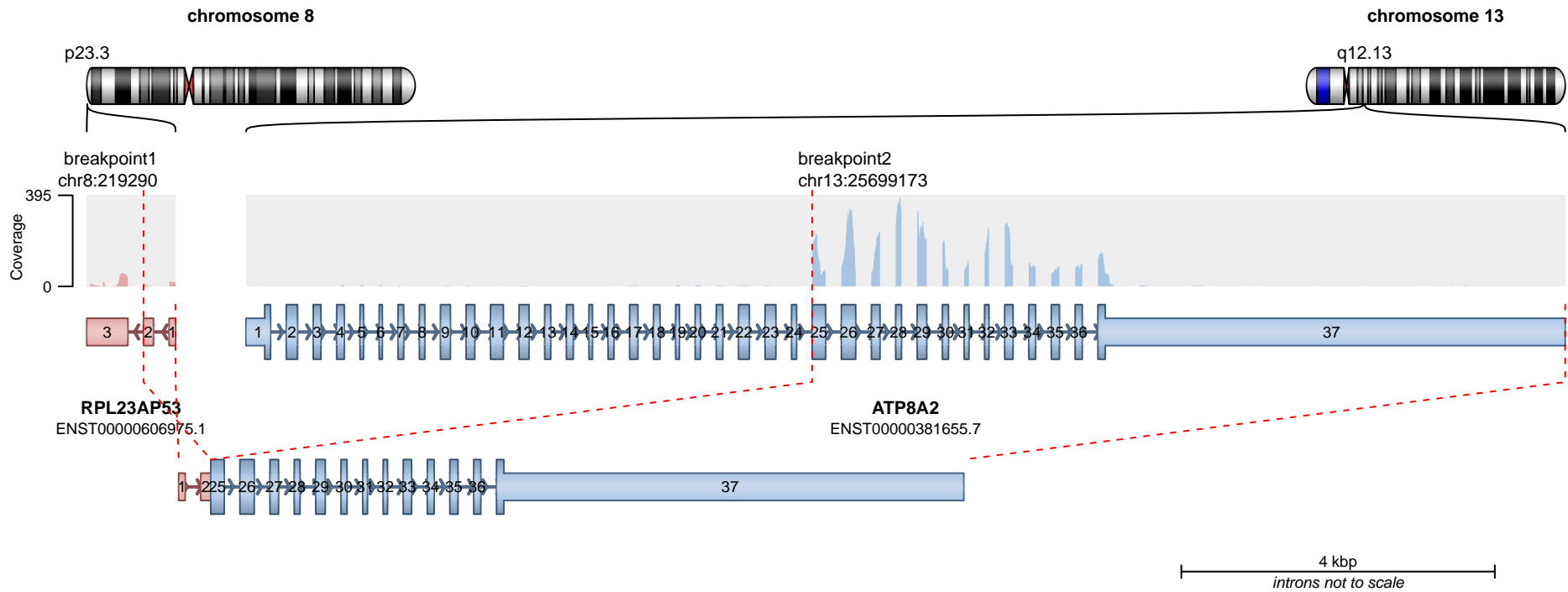
RETAINED PROTEIN DOMAINS
reading frame unclear



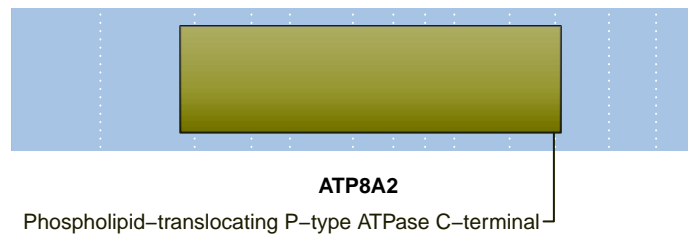
SUPPORTING READ COUNT

Split reads = 9
Discordant mates = 0

— translocation — deletion
— duplication — inversion



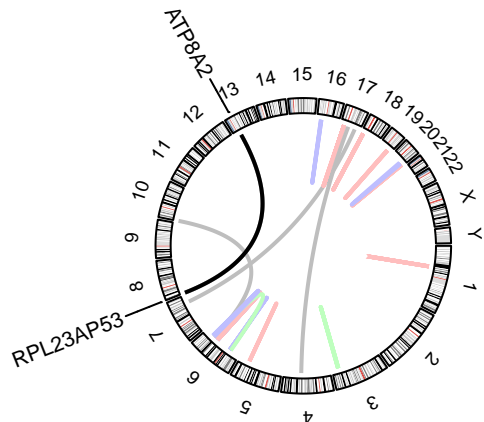
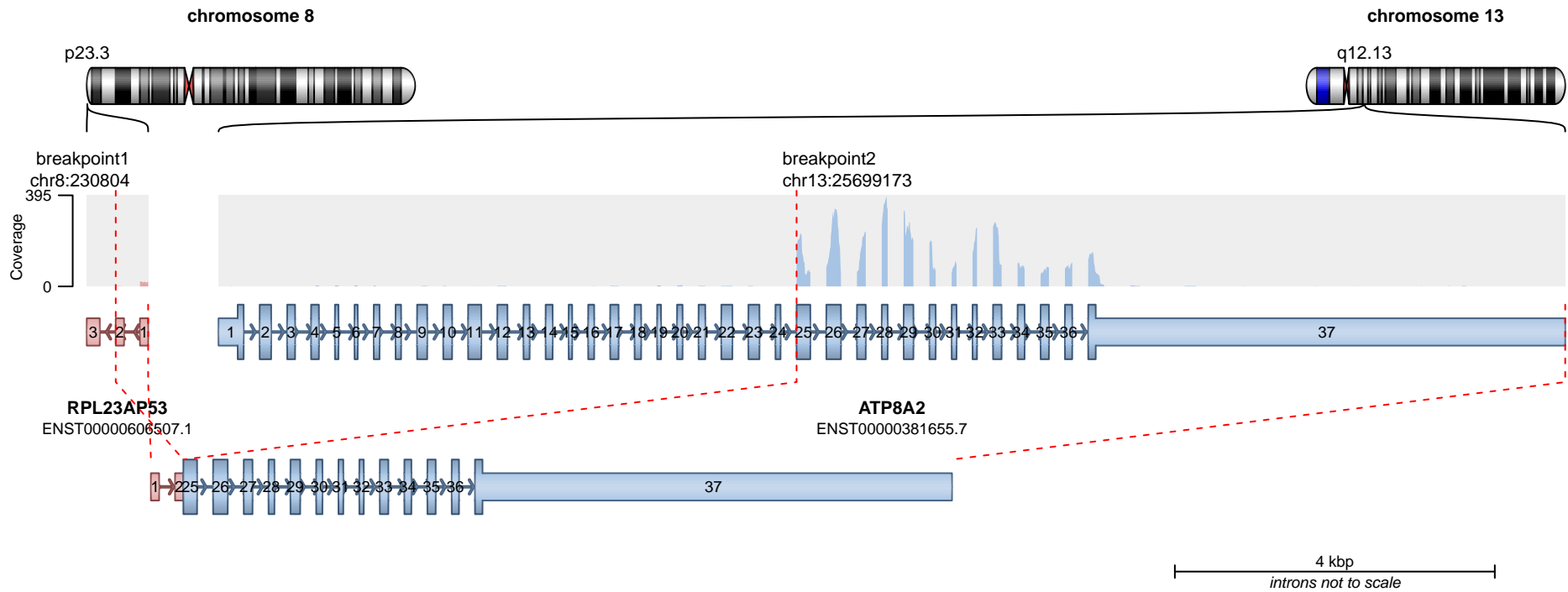
RETAINED PROTEIN DOMAINS
reading frame unclear



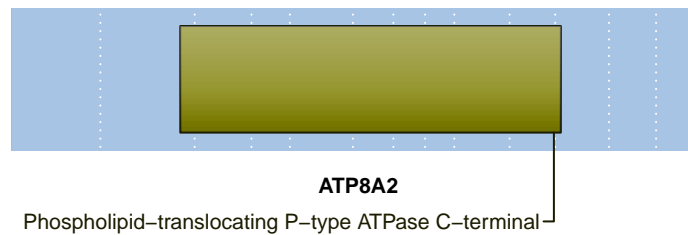
SUPPORTING READ COUNT

Split reads = 4
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