

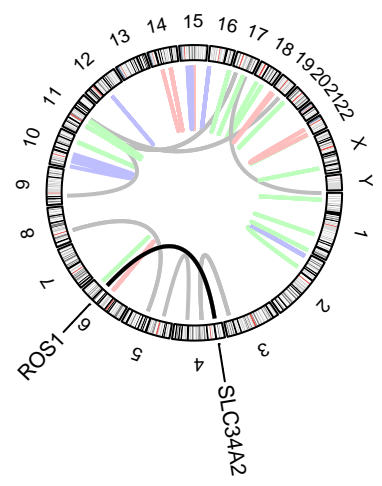
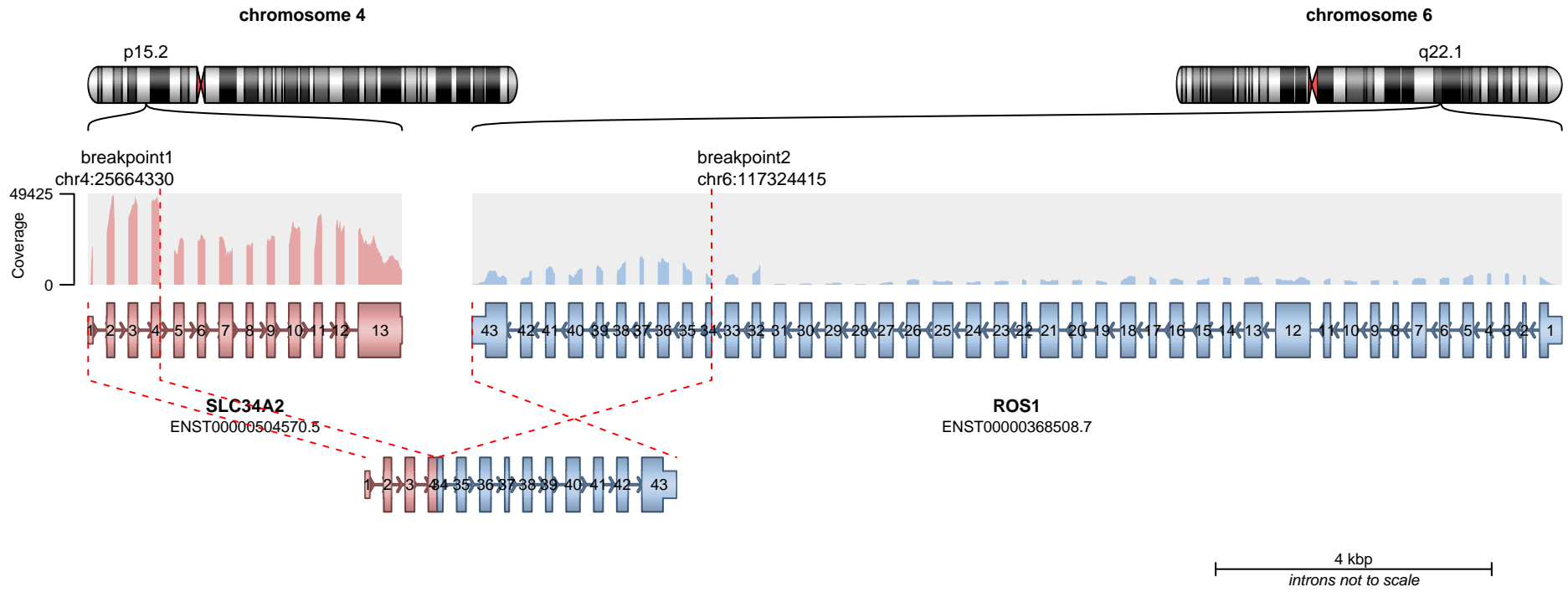
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 3993
Discordant mates = 86

- translocation
- duplication
- deletion
- inversion



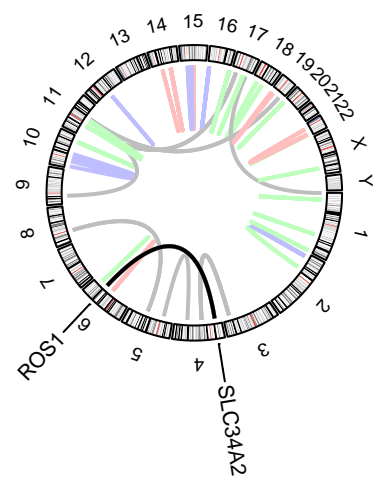
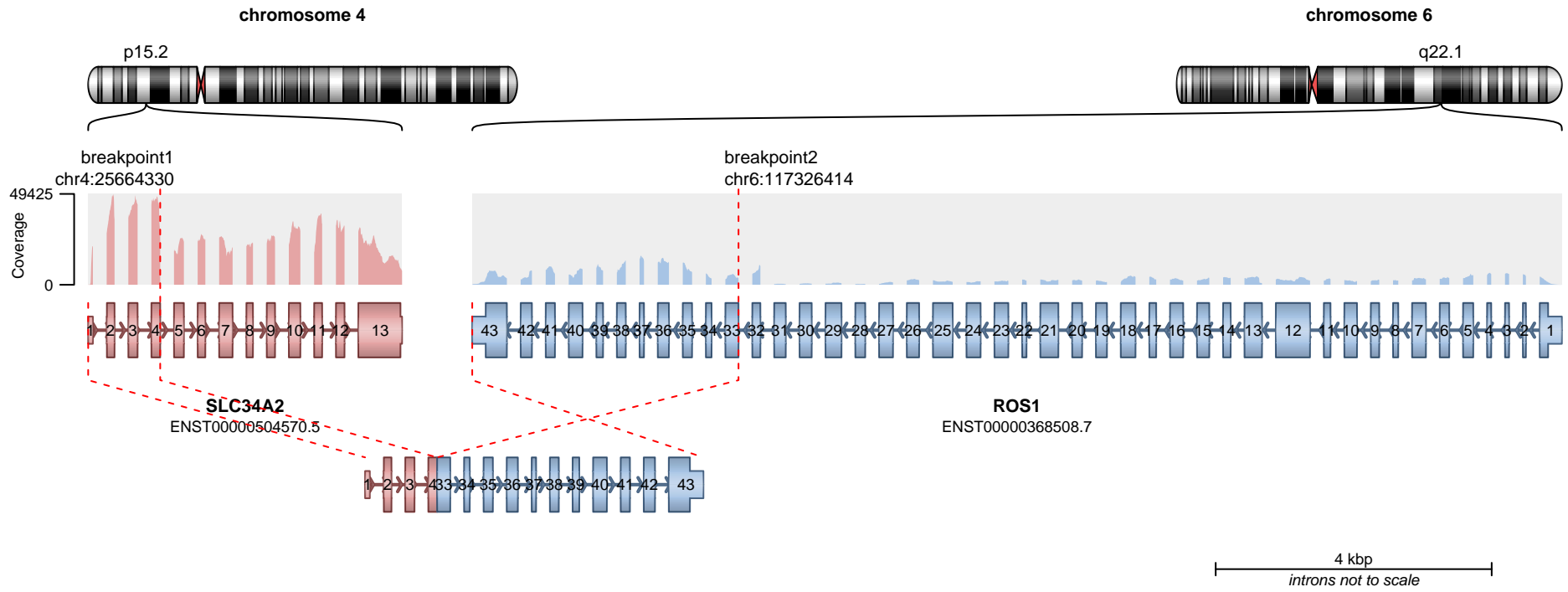
RETAINED PROTEIN DOMAINS
reading frame unclear



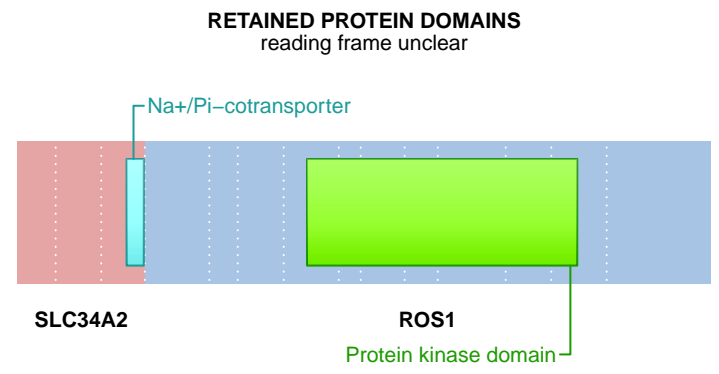
SUPPORTING READ COUNT

Split reads = 277
Discordant mates = 17

- translocation
- duplication
- deletion
- inversion

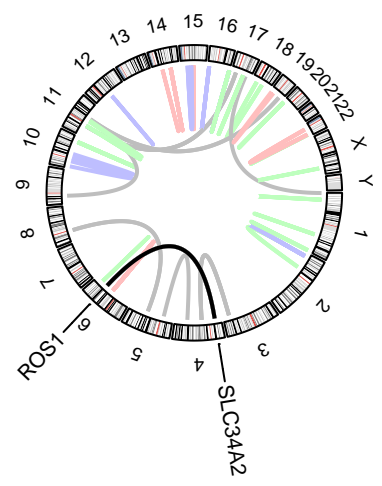
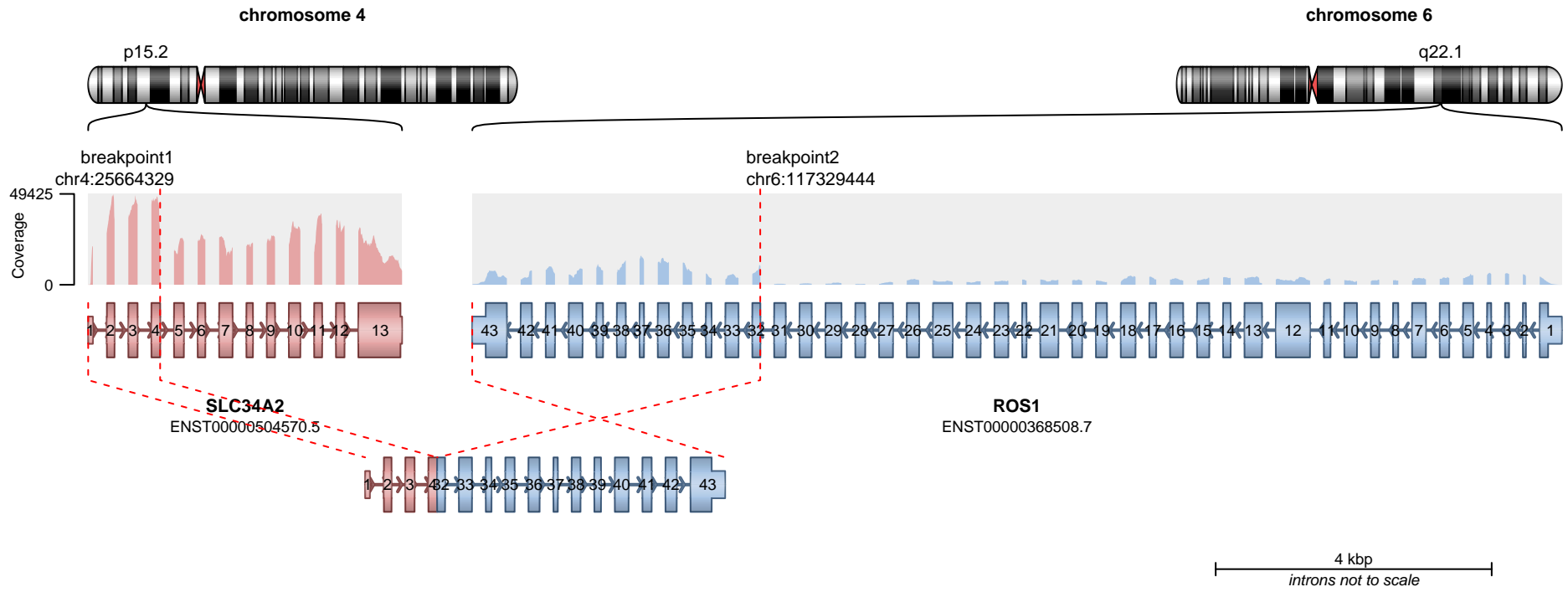


— translocation — deletion
— duplication — inversion

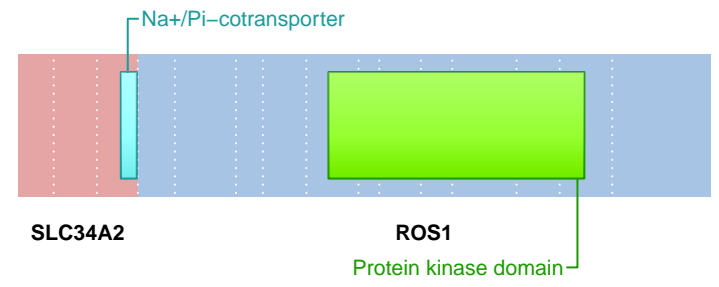


SUPPORTING READ COUNT

Split reads = 53
Discordant mates = 17



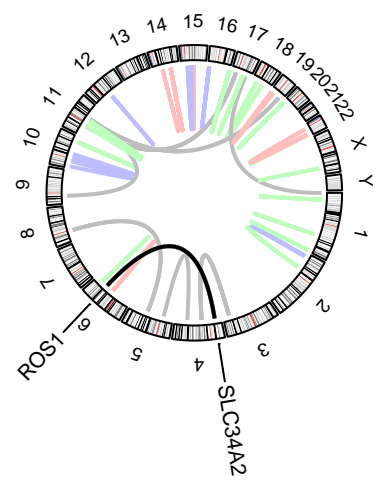
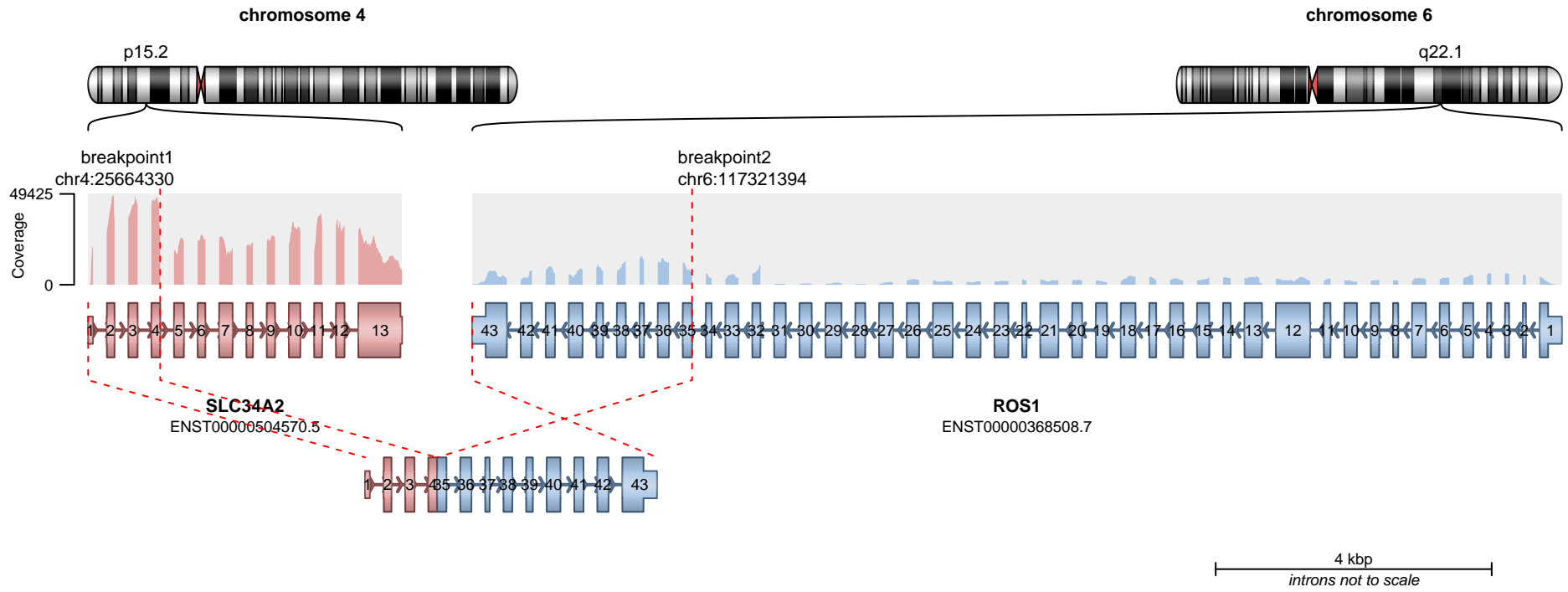
RETAINED PROTEIN DOMAINS
reading frame unclear



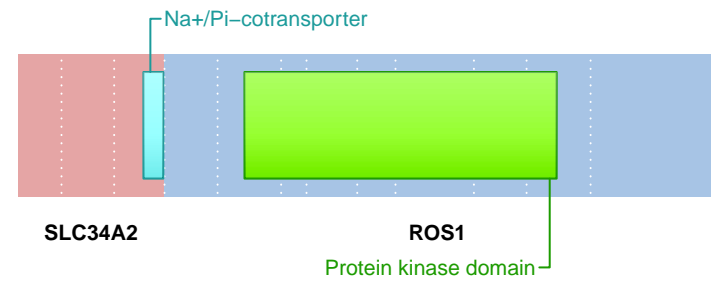
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 86

- translocation
- duplication
- deletion
- inversion



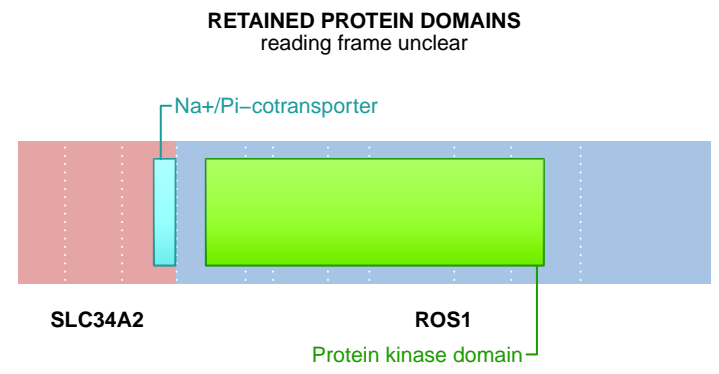
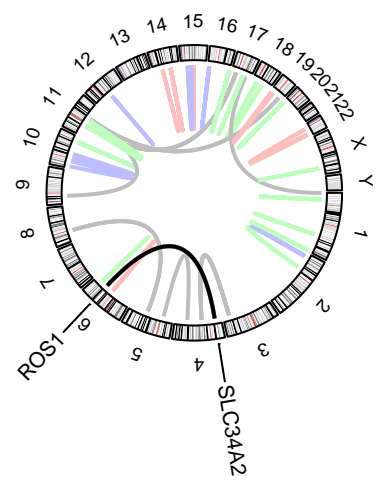
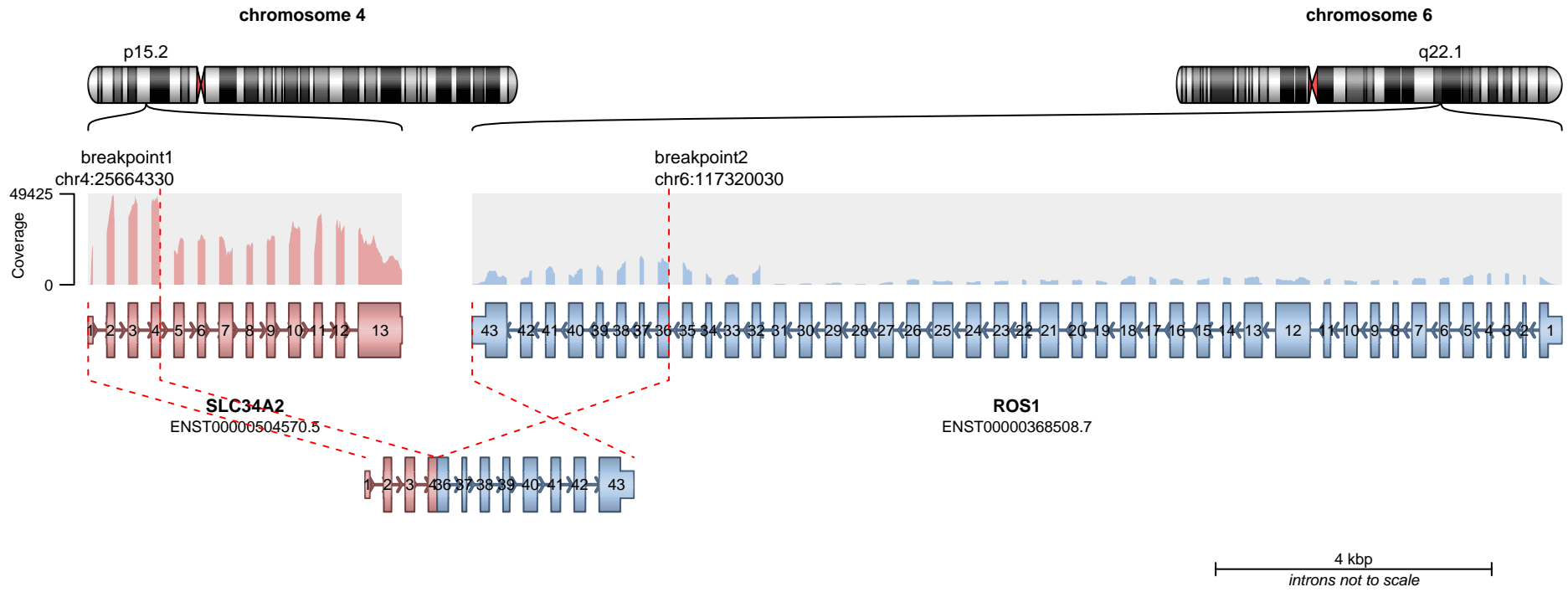
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 20
Discordant mates = 3

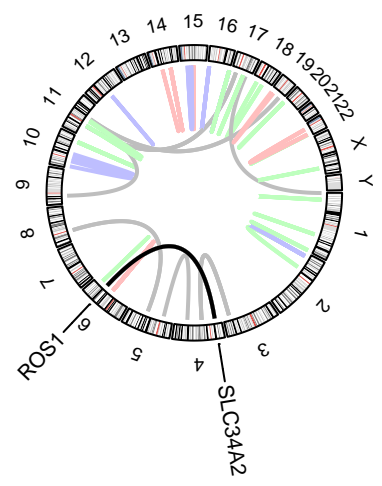
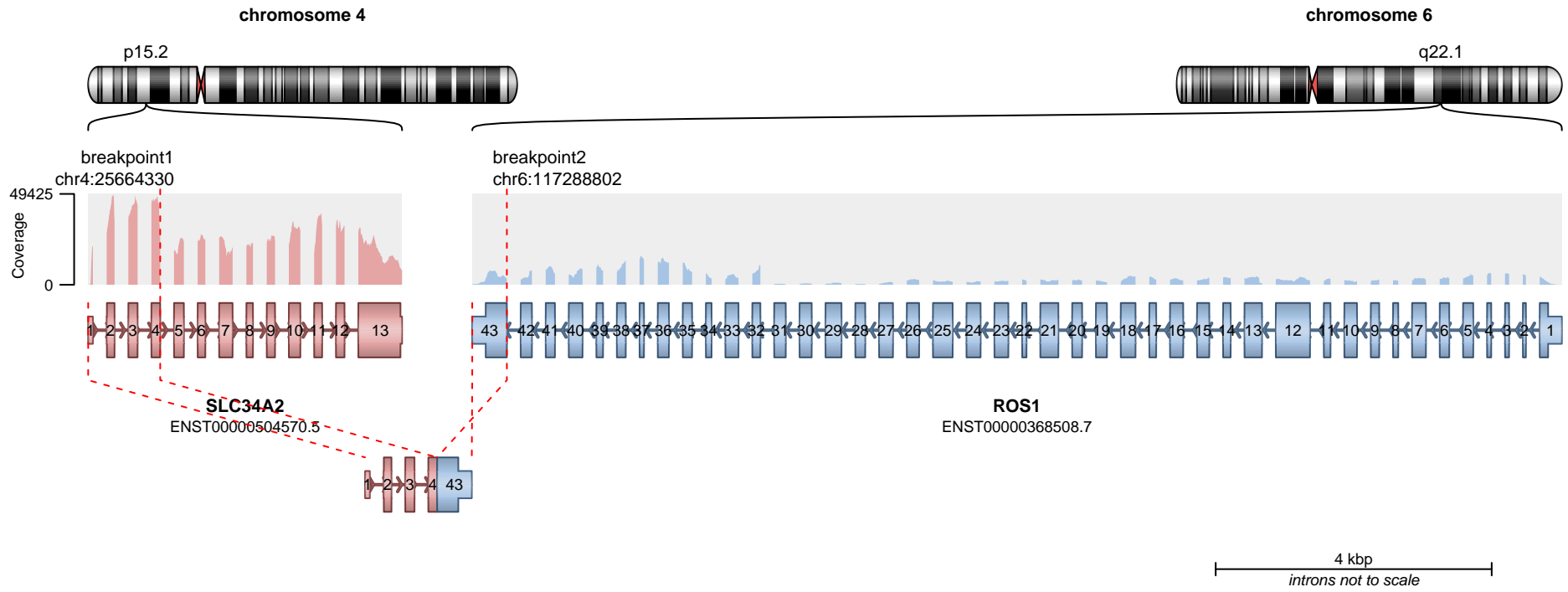
- translocation
- duplication
- deletion
- inversion



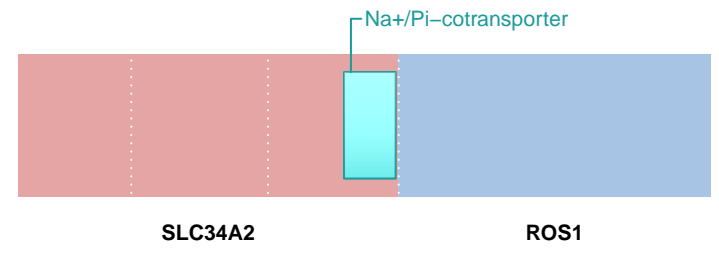
SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 1

— translocation — deletion
— duplication — inversion



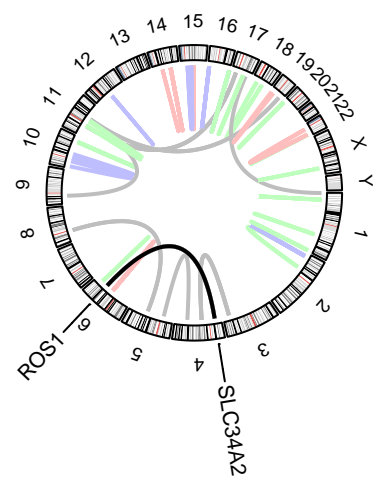
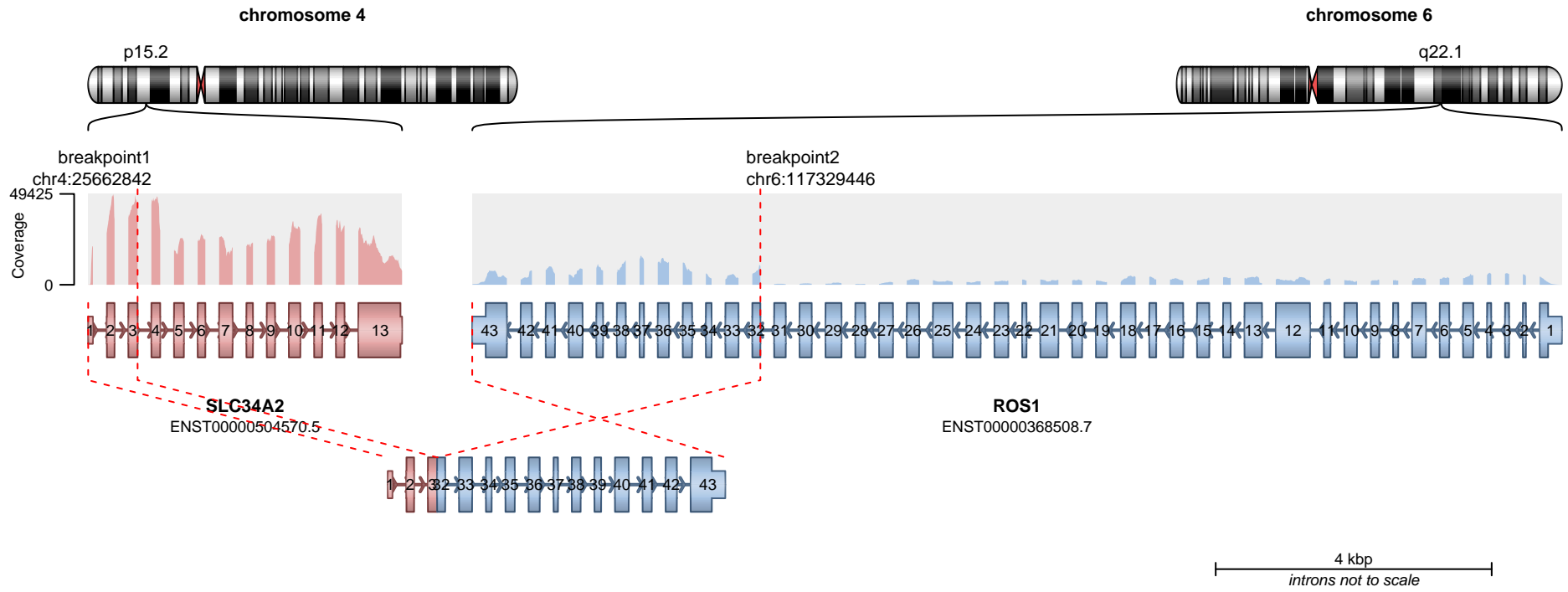
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

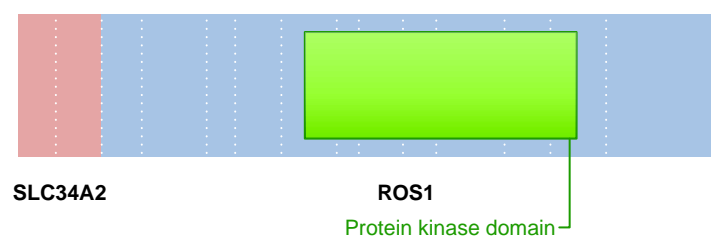
Split reads = 3
Discordant mates = 0

— translocation — deletion
— duplication — inversion



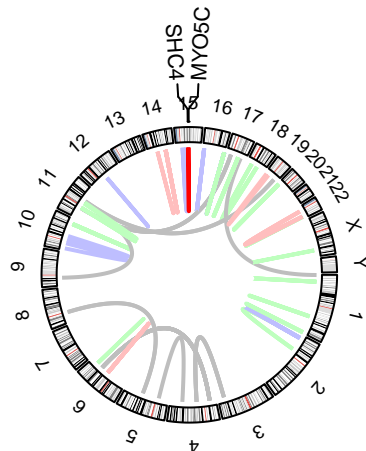
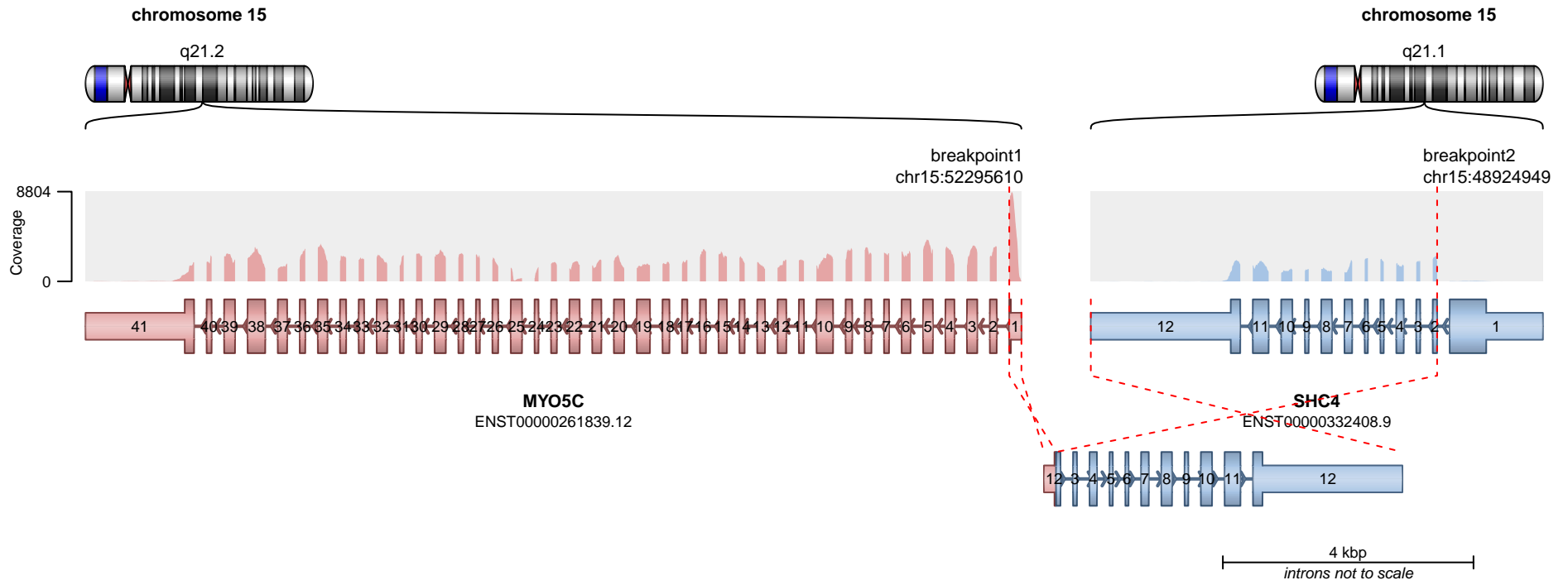
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear

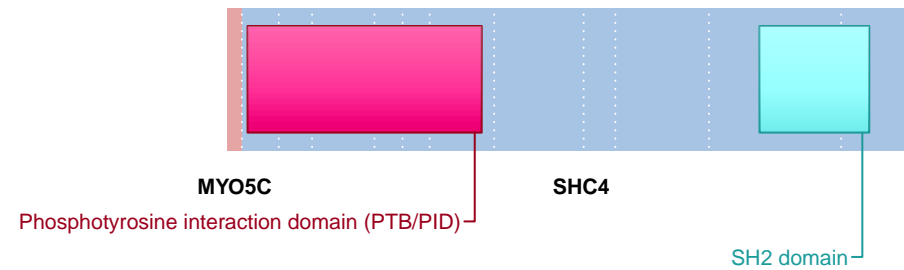


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 7



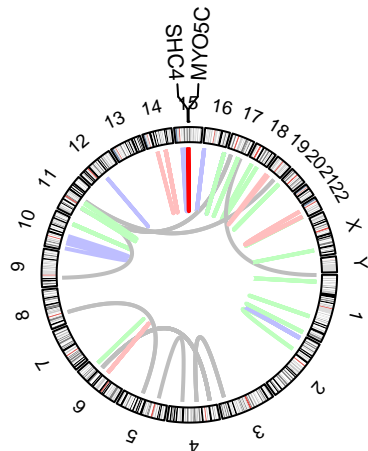
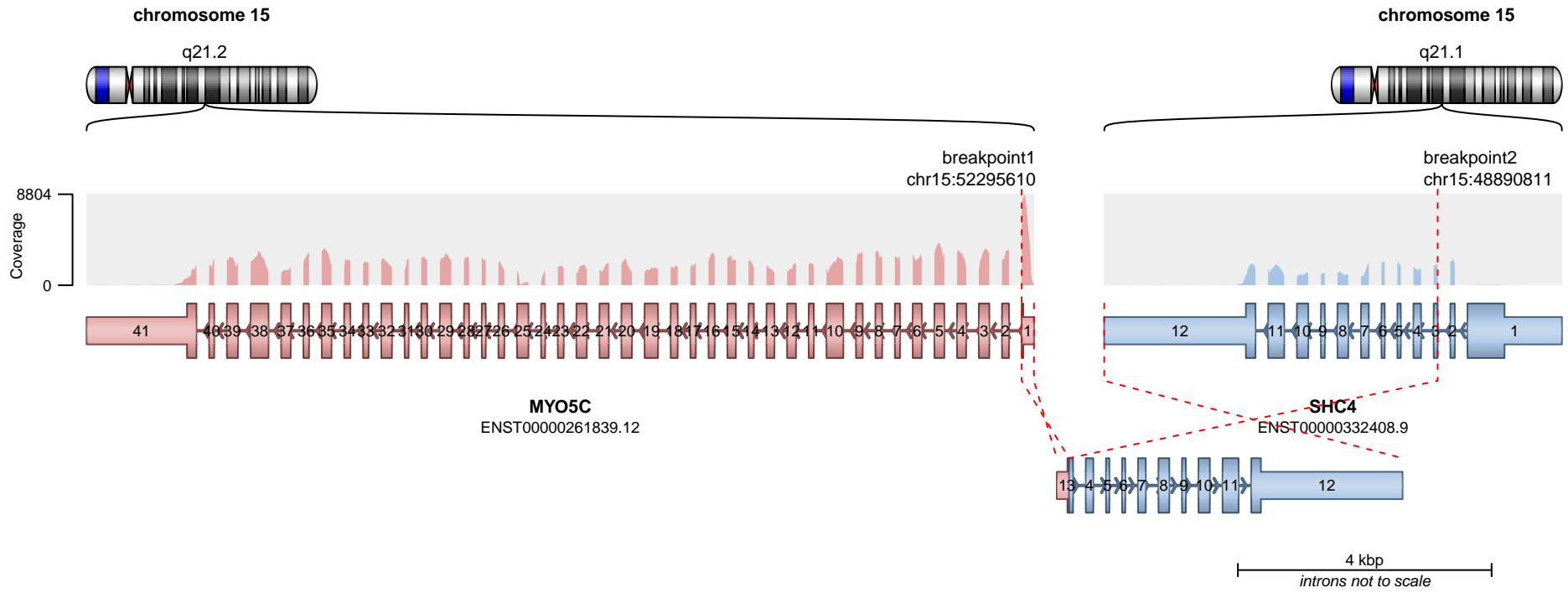
RETAINED PROTEIN DOMAINS
reading frame unclear



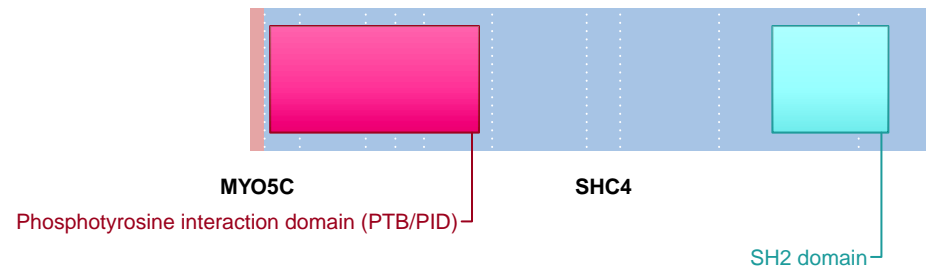
SUPPORTING READ COUNT

Split reads = 1118
Discordant mates = 28

- translocation
- duplication
- deletion
- inversion



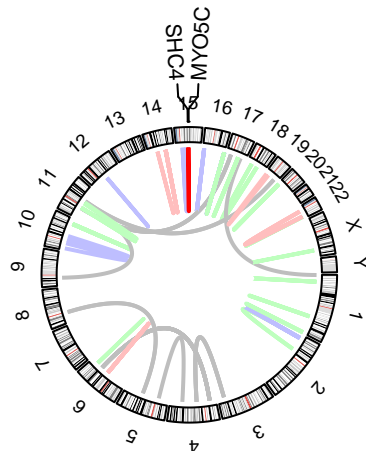
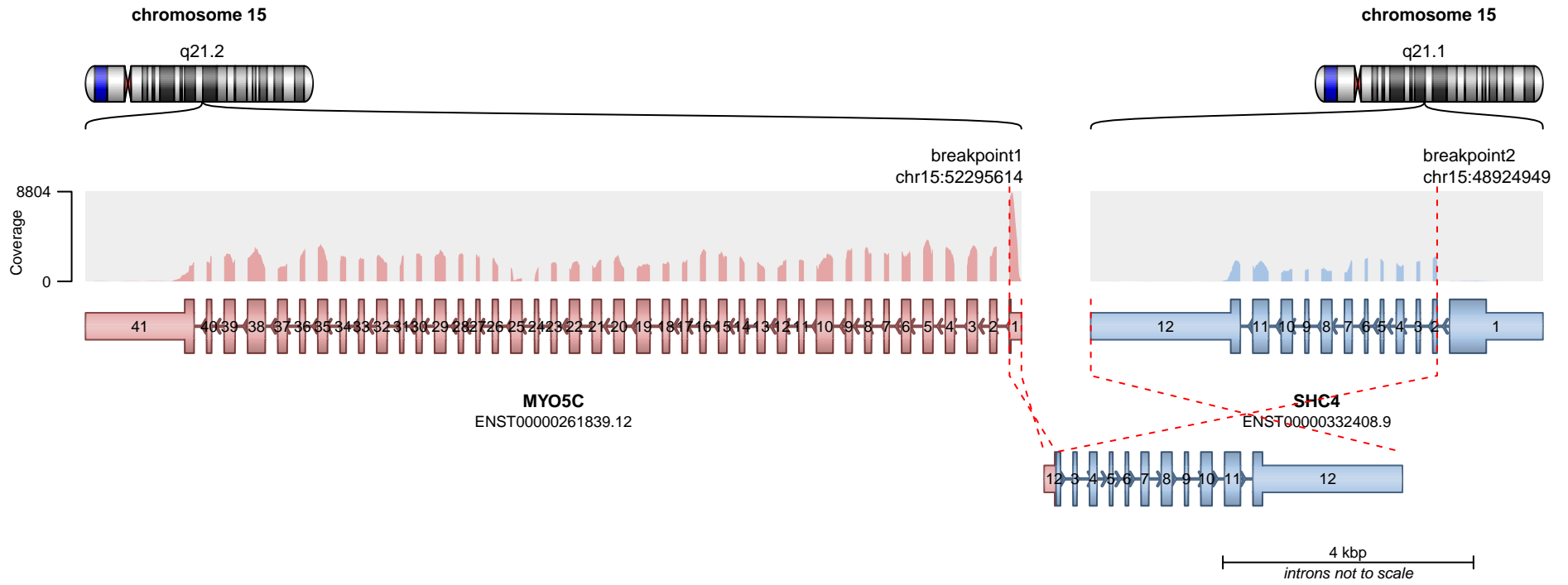
RETAINED PROTEIN DOMAINS
reading frame unclear



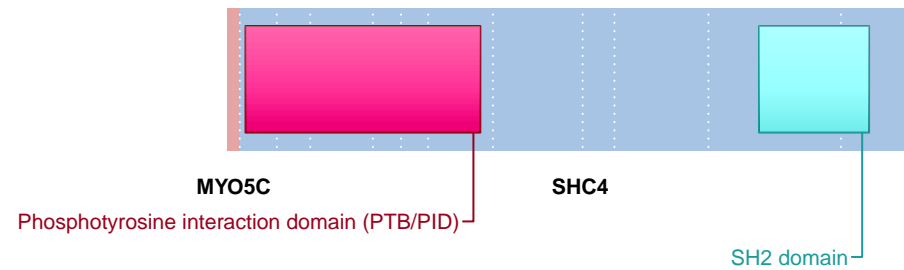
SUPPORTING READ COUNT

Split reads = 26
Discordant mates = 12

- translocation
- duplication
- deletion
- inversion



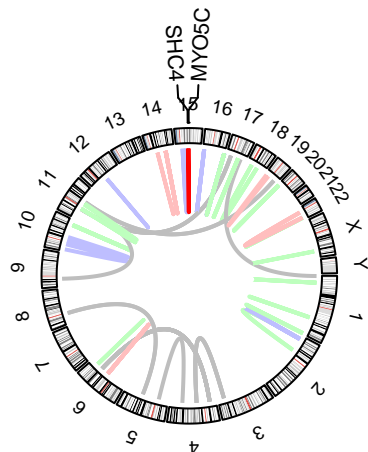
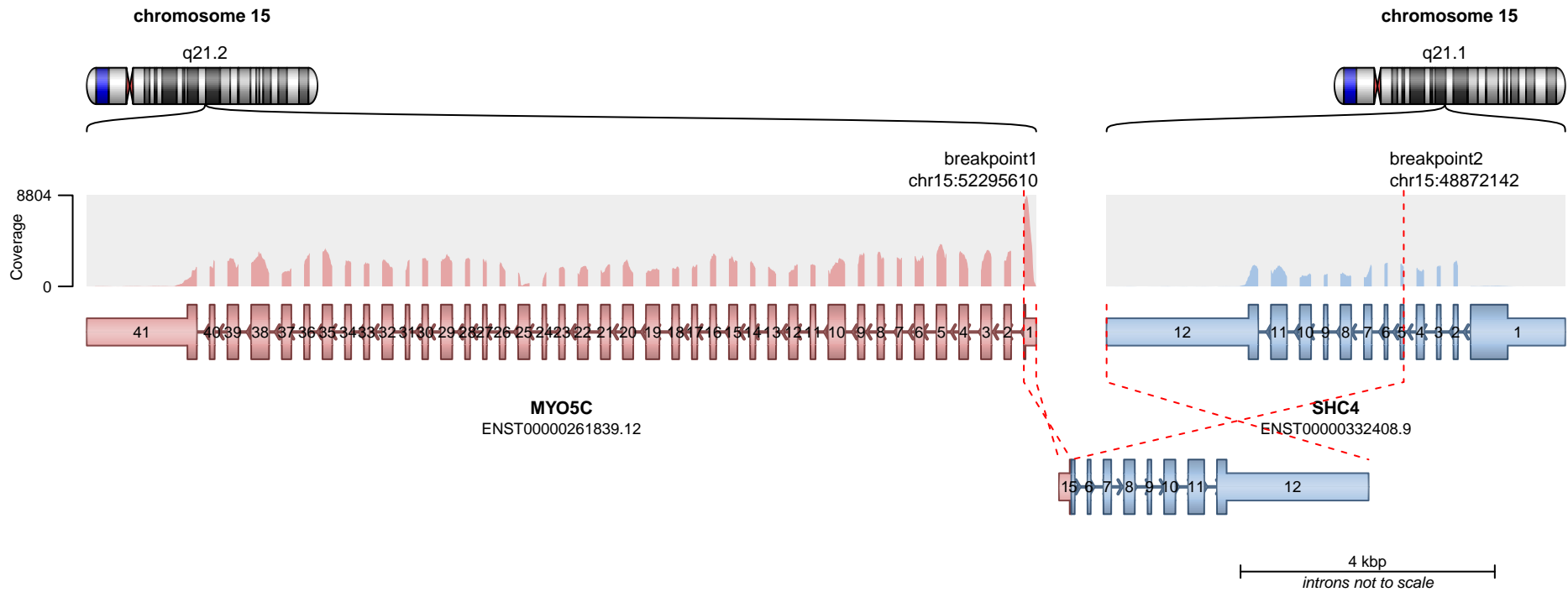
RETAINED PROTEIN DOMAINS
reading frame unclear



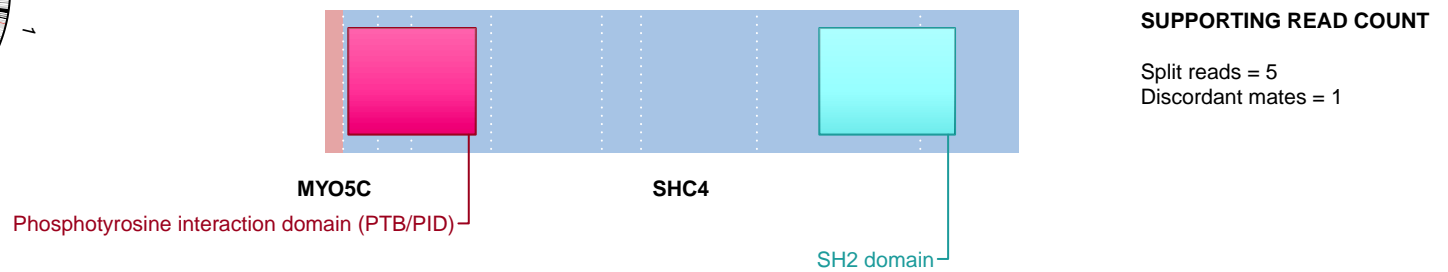
SUPPORTING READ COUNT

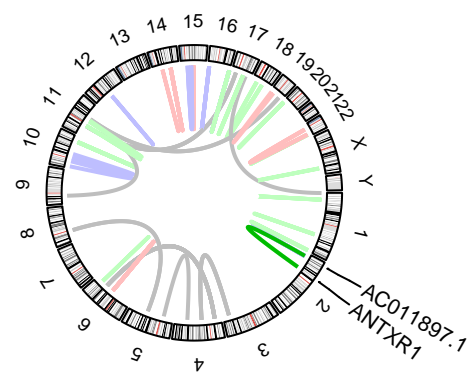
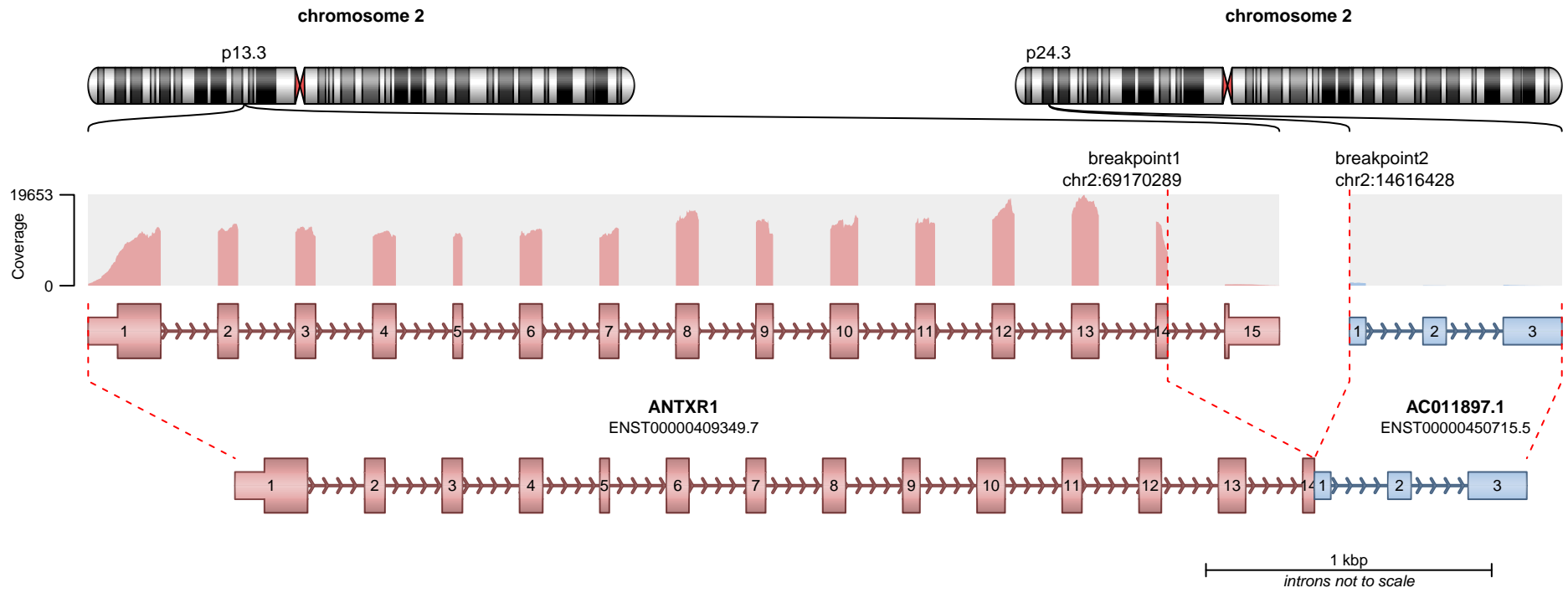
Split reads = 7
Discordant mates = 28

- translocation
- duplication
- deletion
- inversion

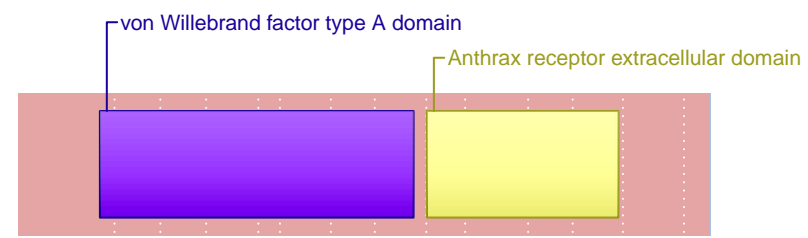


RETAINED PROTEIN DOMAINS
reading frame unclear





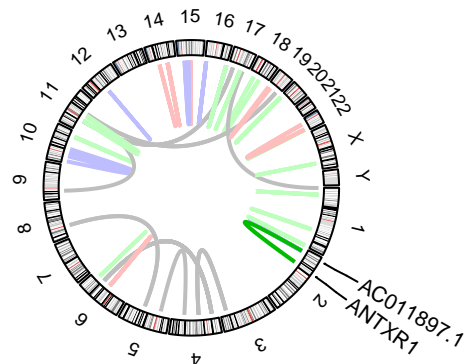
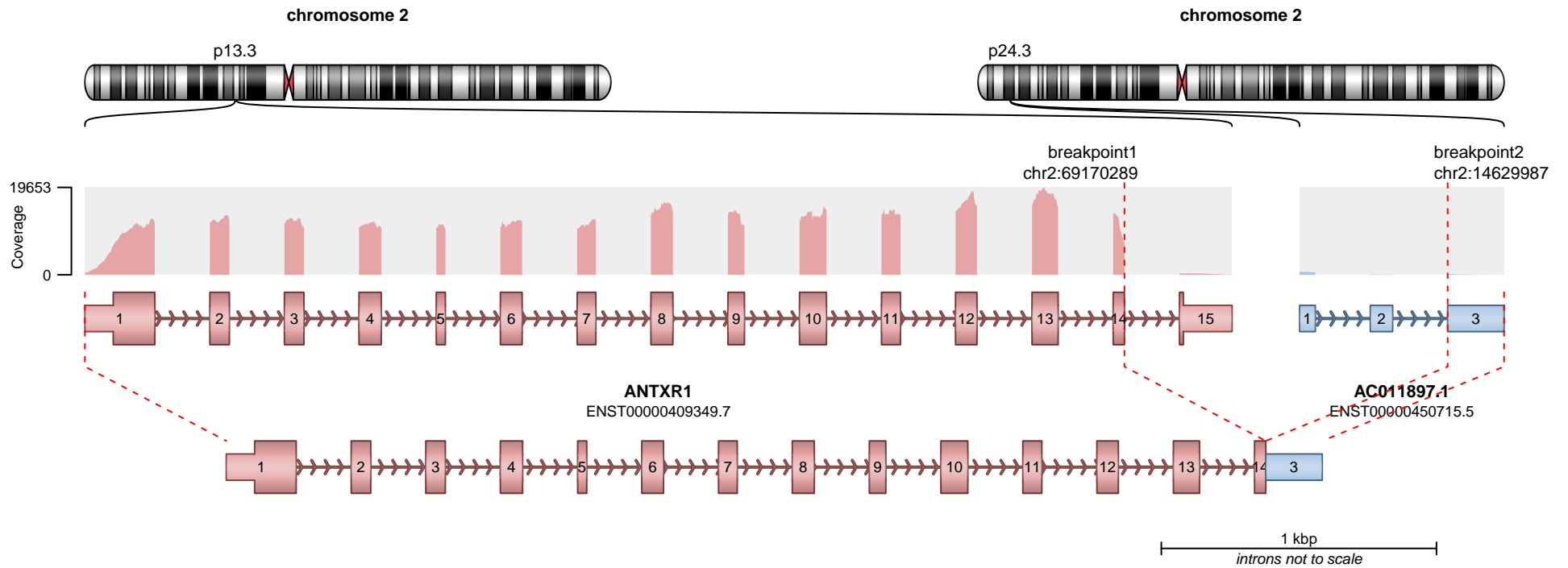
RETAINED PROTEIN DOMAINS
reading frame unclear



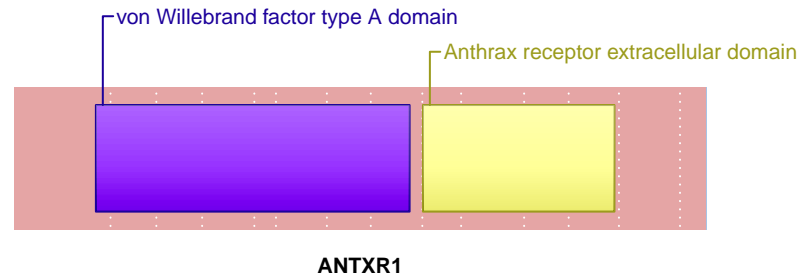
SUPPORTING READ COUNT

Split reads = 652
Discordant mates = 20

- translocation
- duplication
- deletion
- inversion



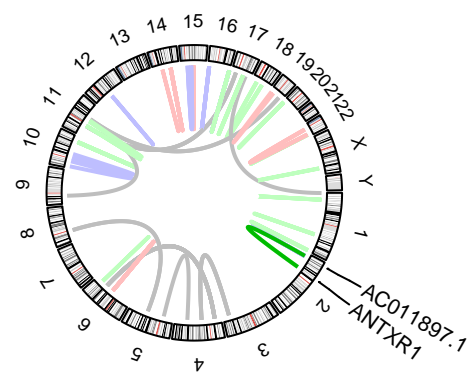
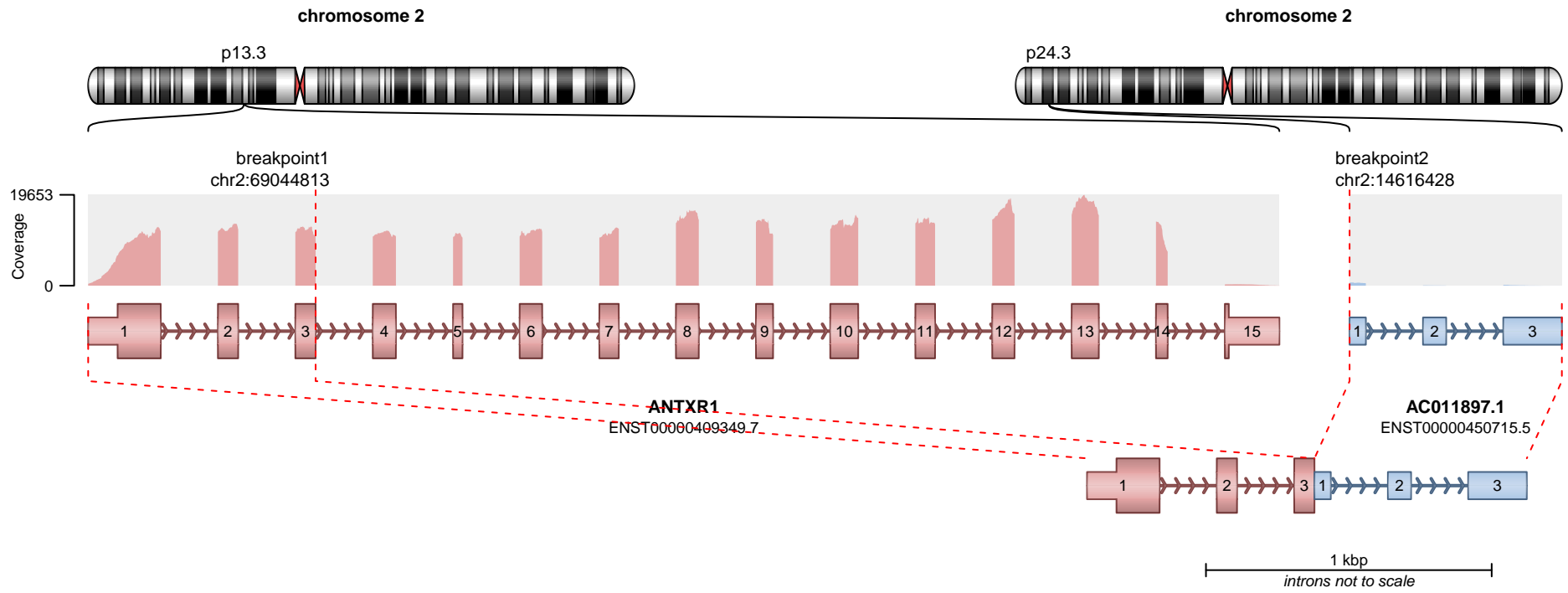
RETAINED PROTEIN DOMAINS
reading frame unclear



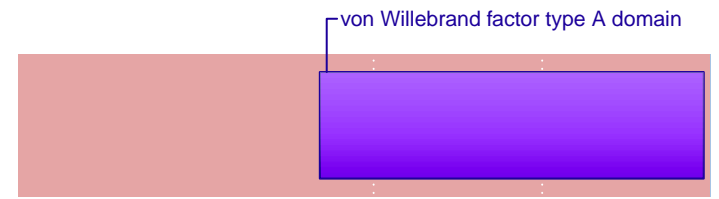
SUPPORTING READ COUNT

Split reads = 9
Discordant mates = 3

— translocation — deletion
— duplication — inversion



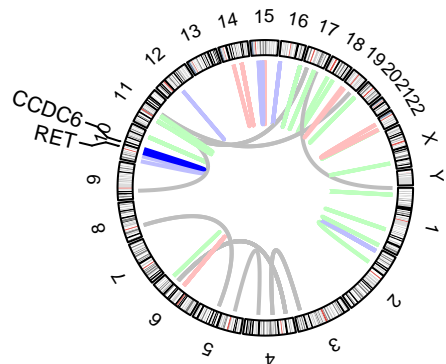
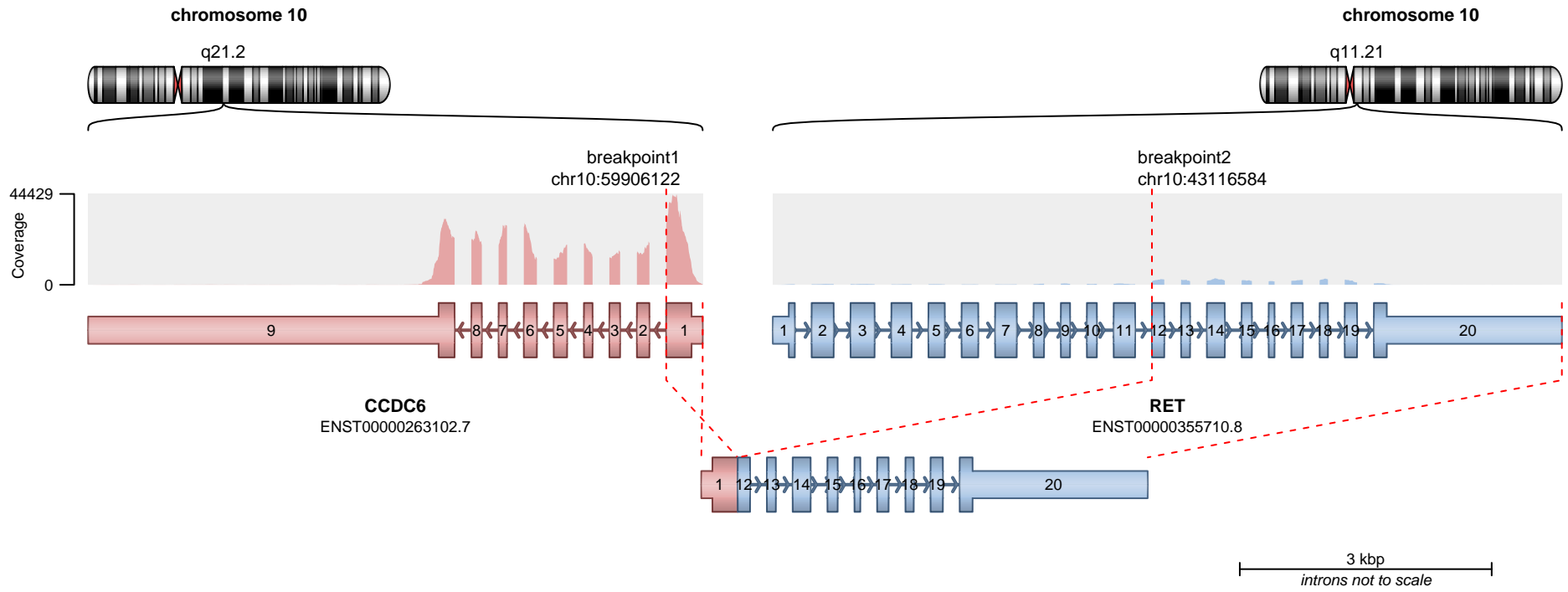
RETAINED PROTEIN DOMAINS
reading frame unclear



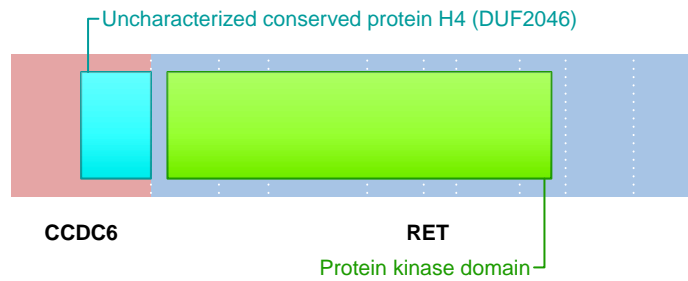
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



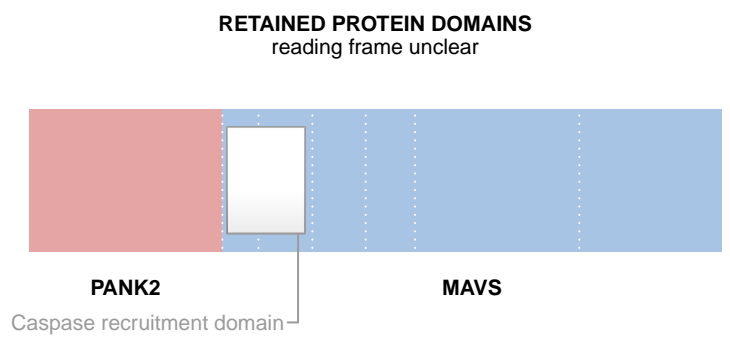
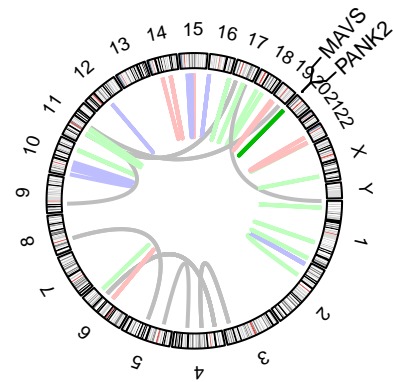
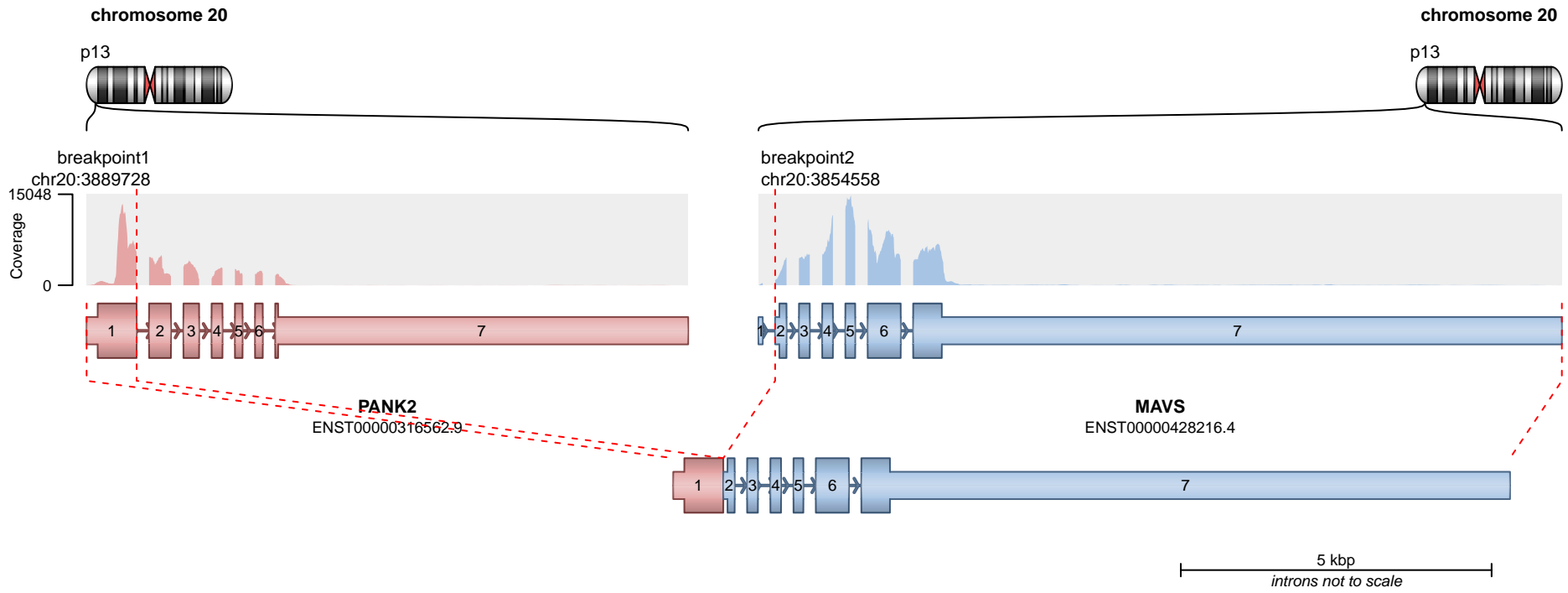
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 570
Discordant mates = 22

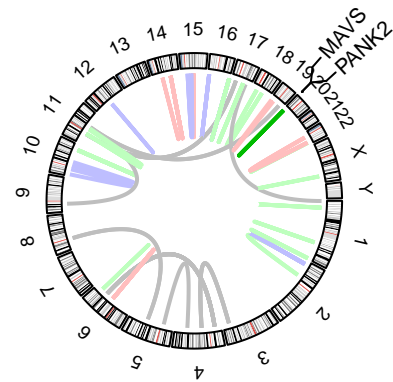
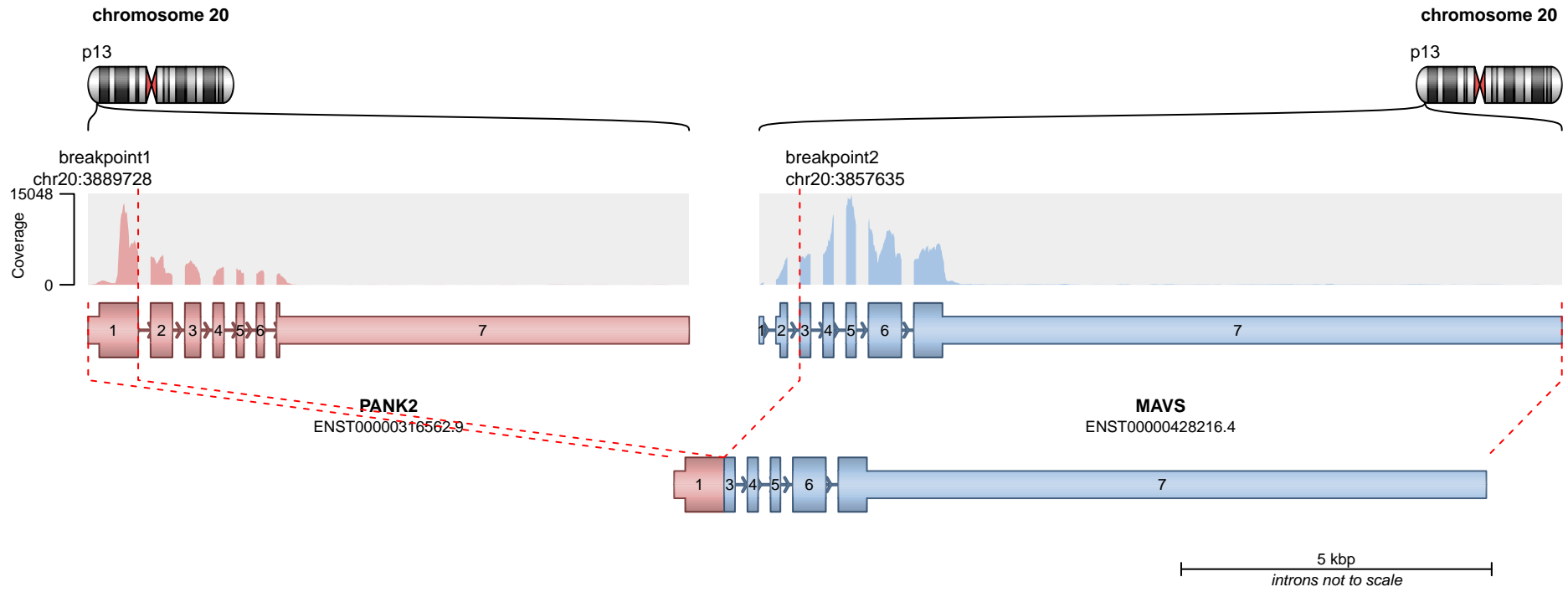
- translocation
- duplication
- deletion
- inversion



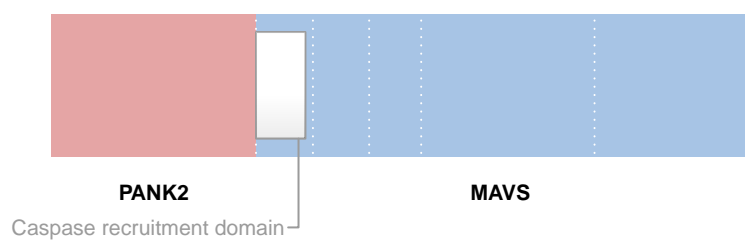
SUPPORTING READ COUNT

Split reads = 217
Discordant mates = 5

— translocation — deletion
— duplication — inversion



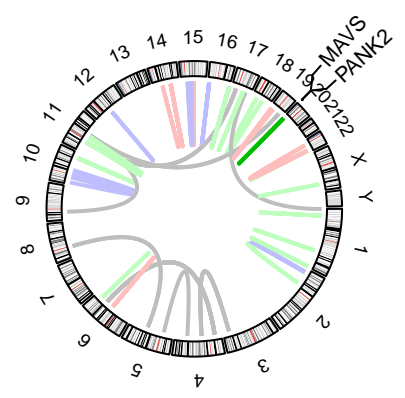
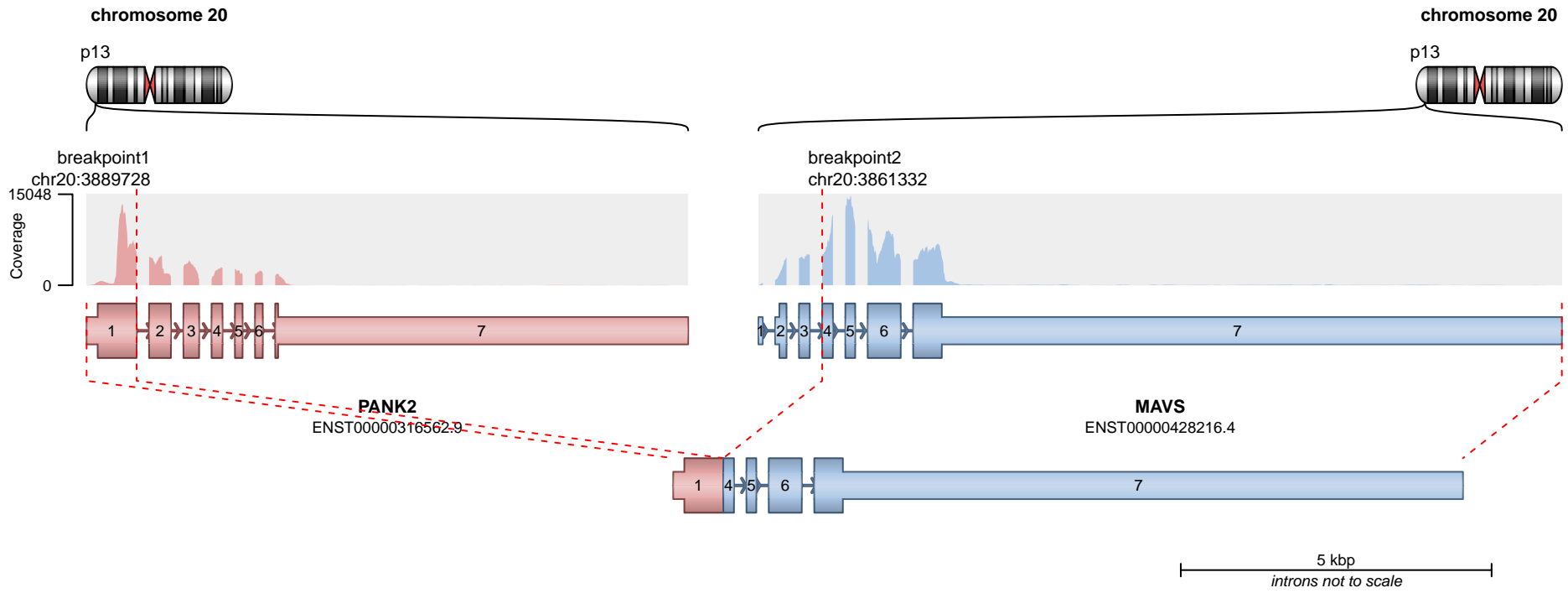
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

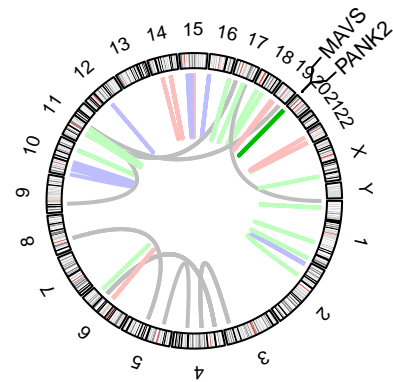
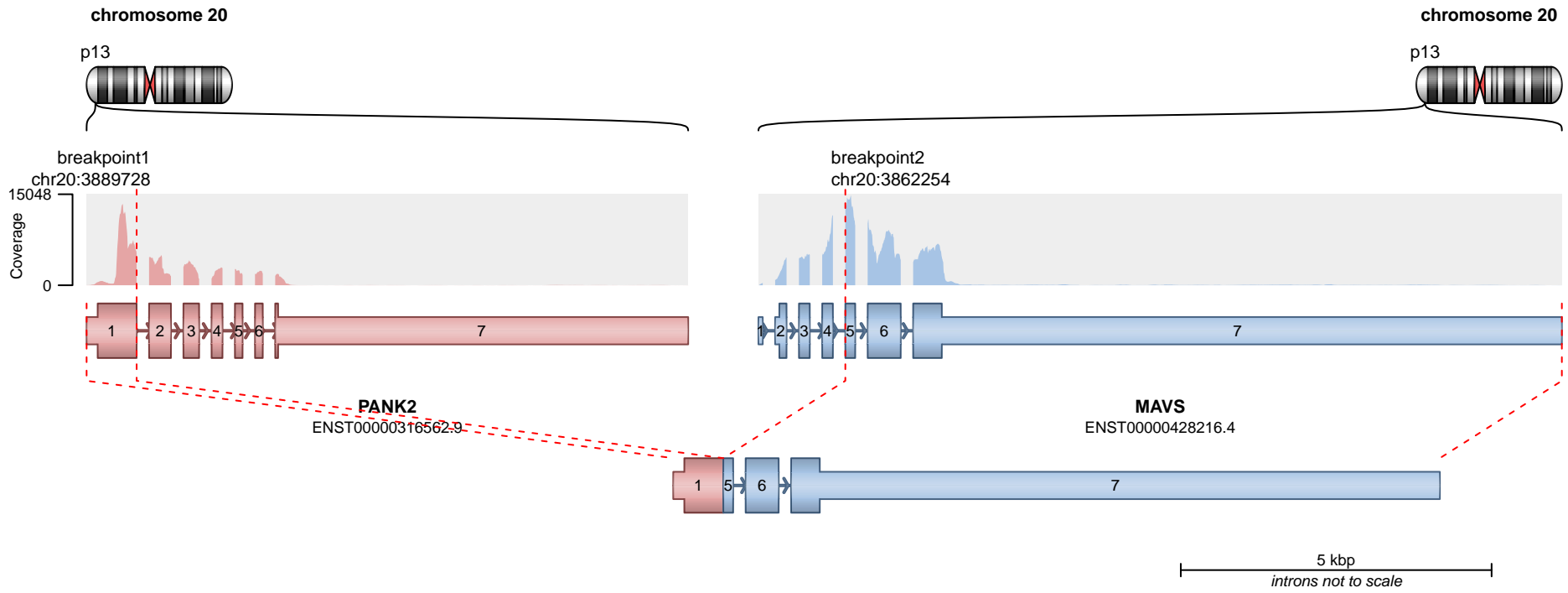


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 0

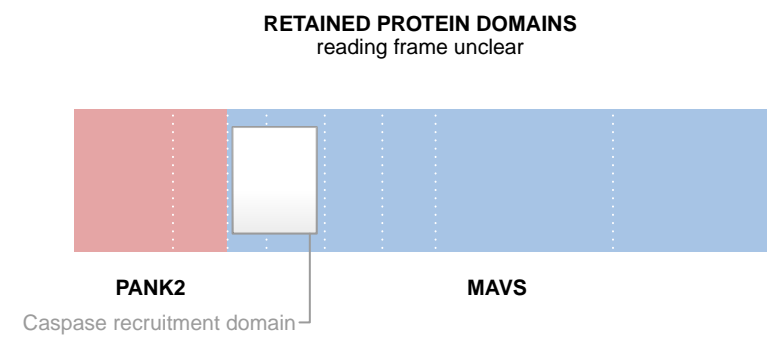
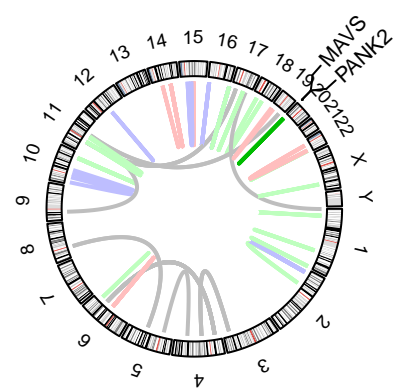
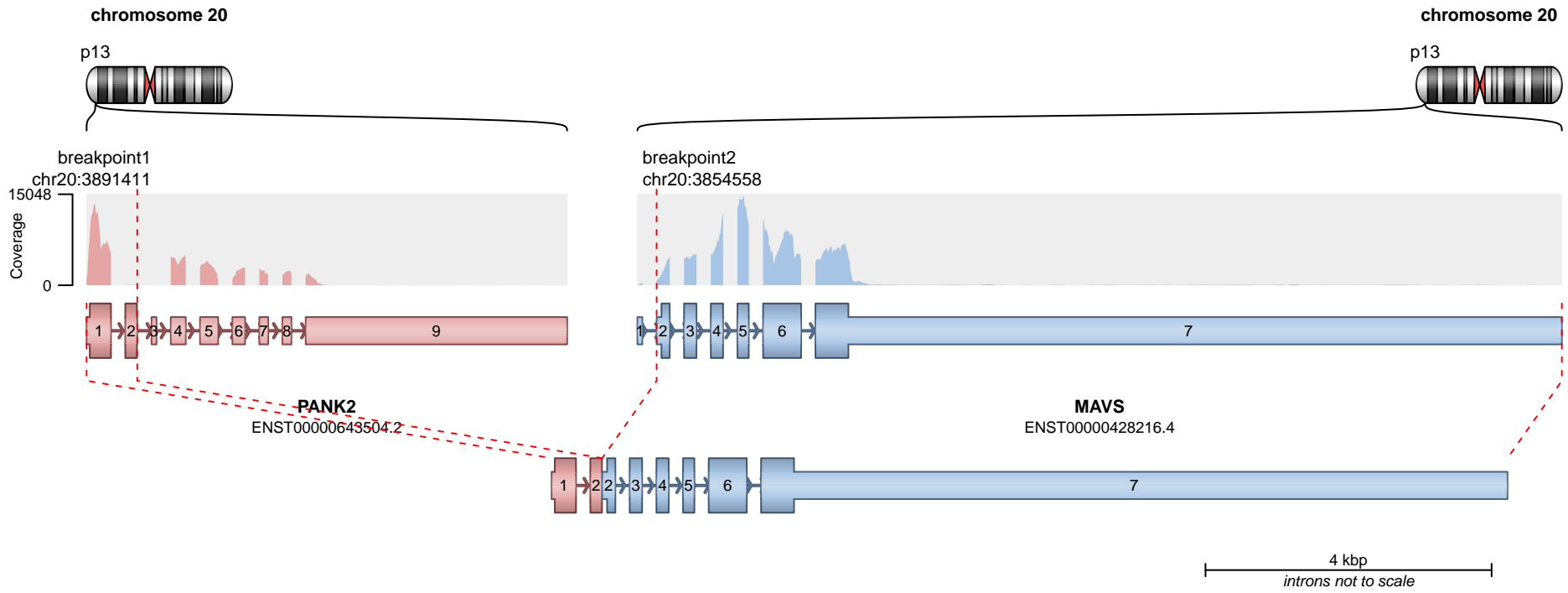


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

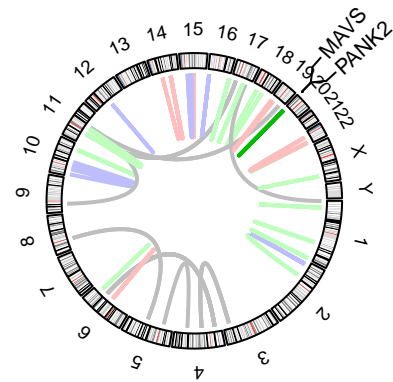
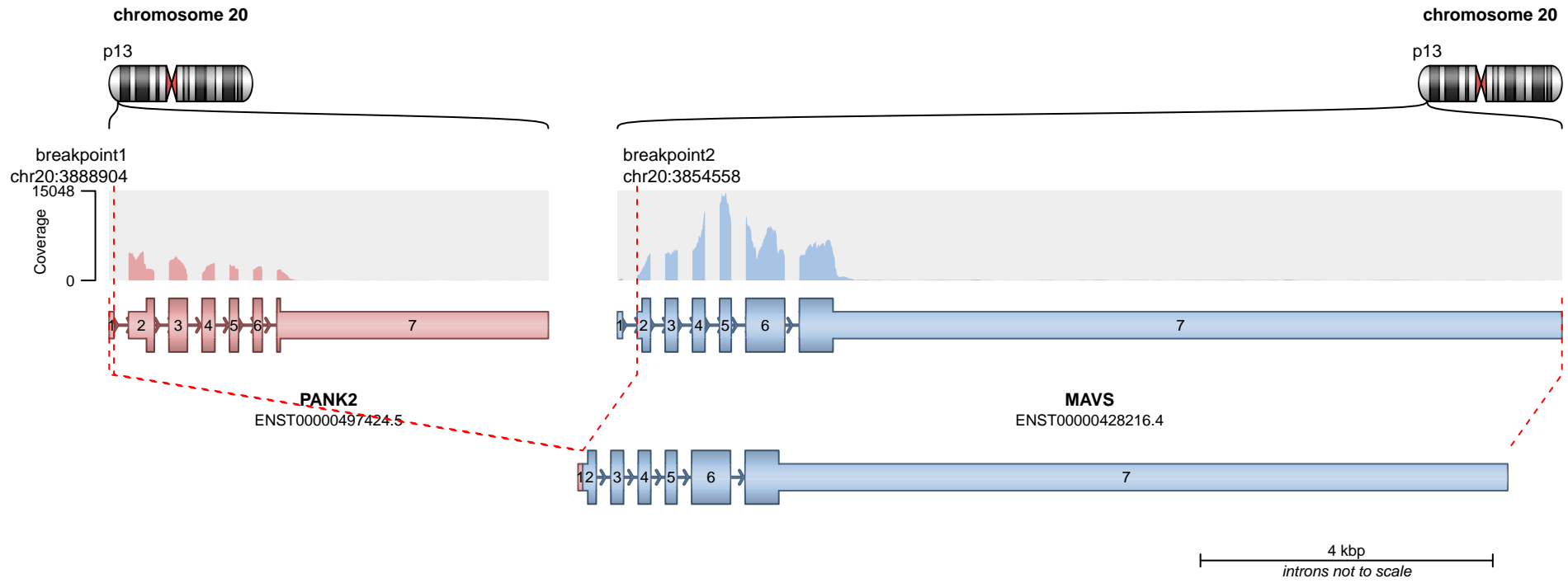
Split reads = 3
Discordant mates = 0



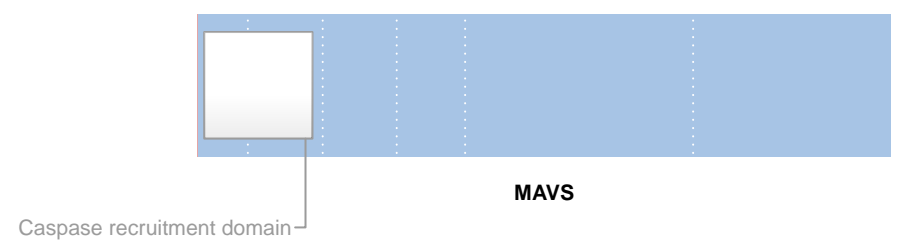
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 5

— translocation — deletion
— duplication — inversion



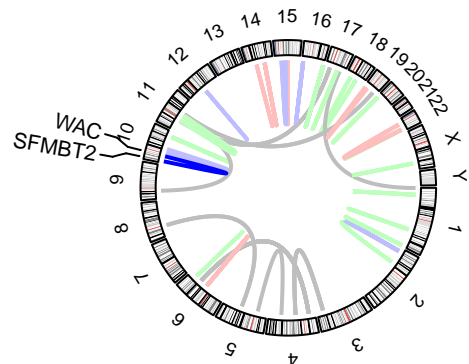
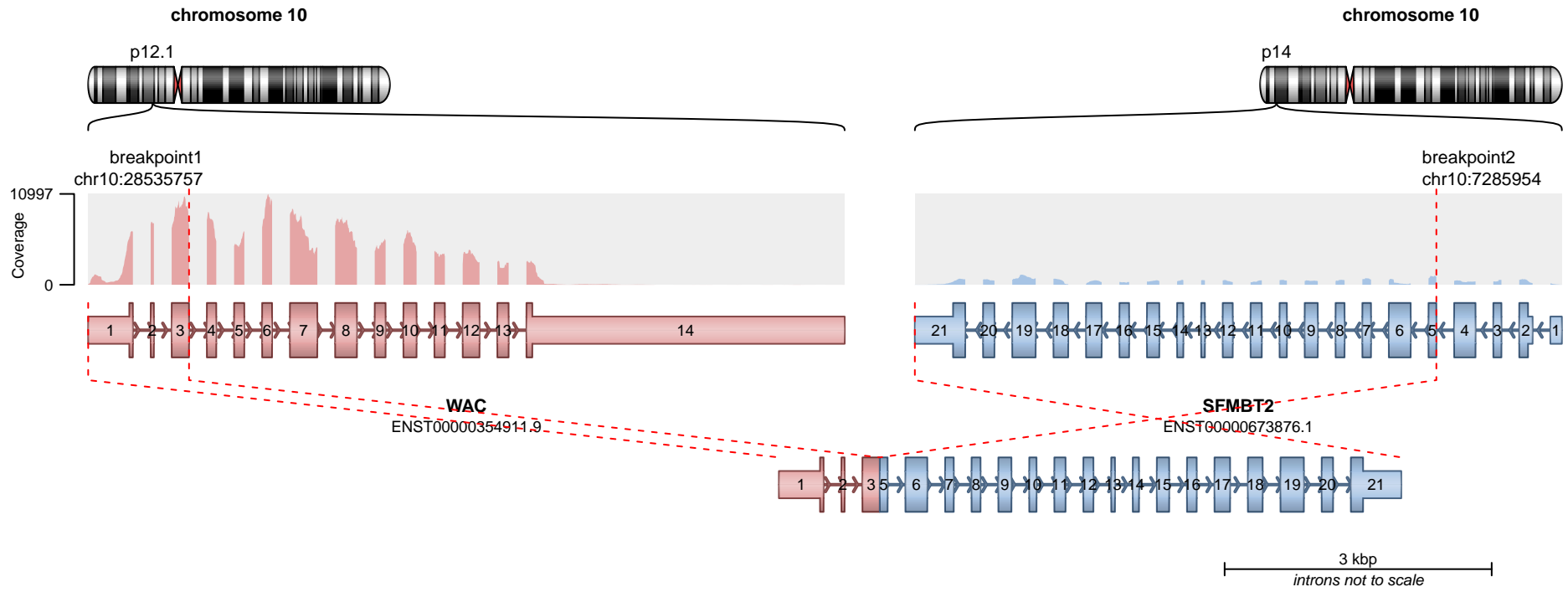
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

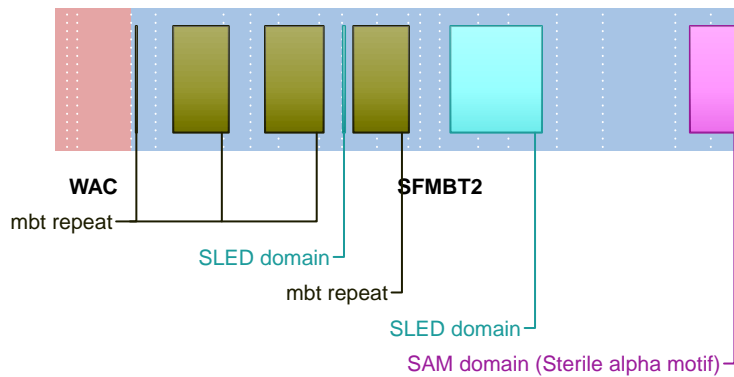
Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



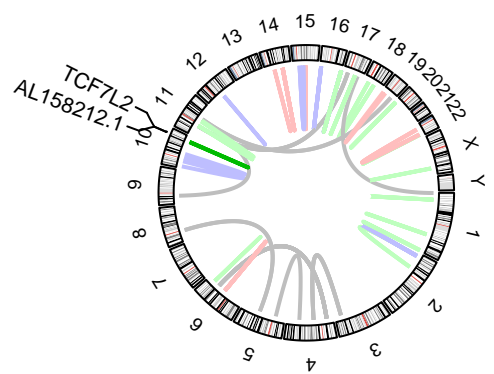
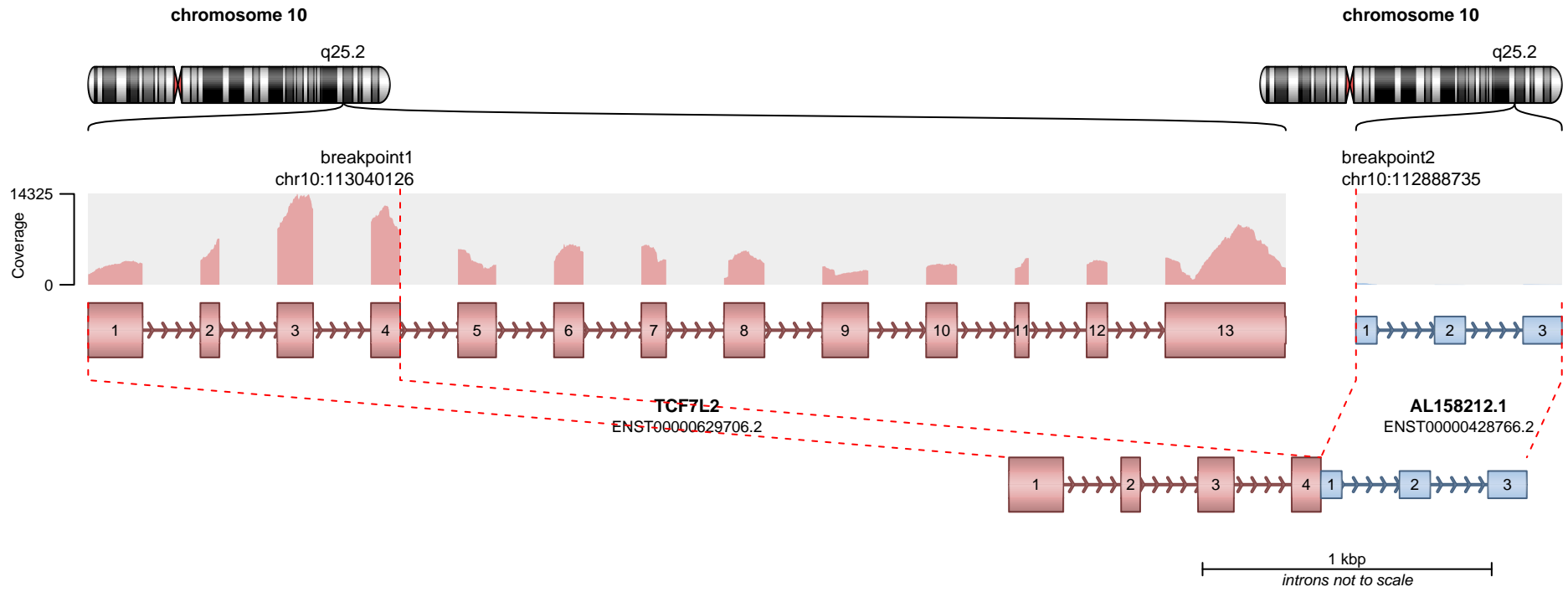
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear

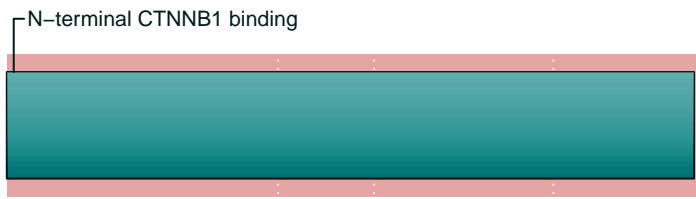


SUPPORTING READ COUNT

Split reads = 154
Discordant mates = 4



RETAINED PROTEIN DOMAINS
reading frame unclear

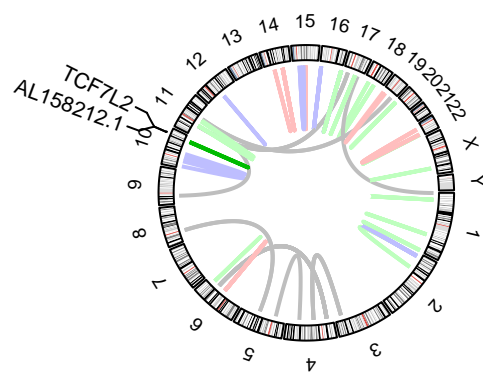
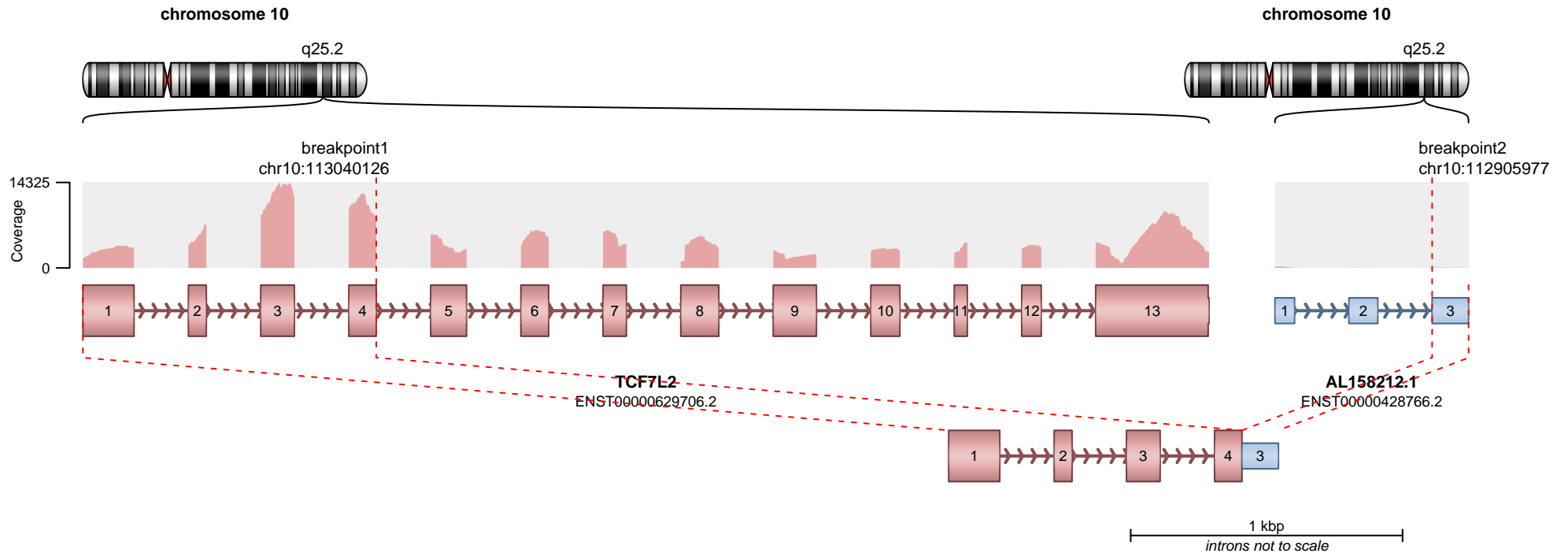


TCF7L2

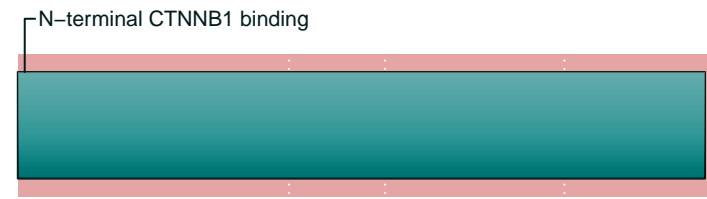
SUPPORTING READ COUNT

Split reads = 130
Discordant mates = 5

- translocation
- duplication
- deletion
- inversion



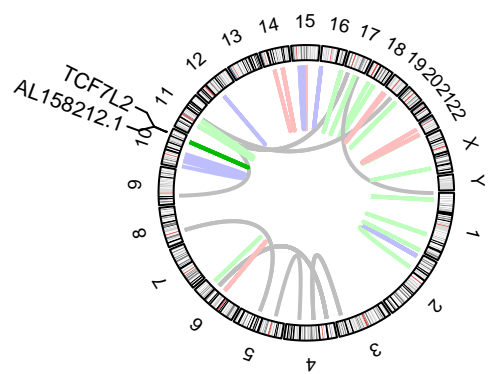
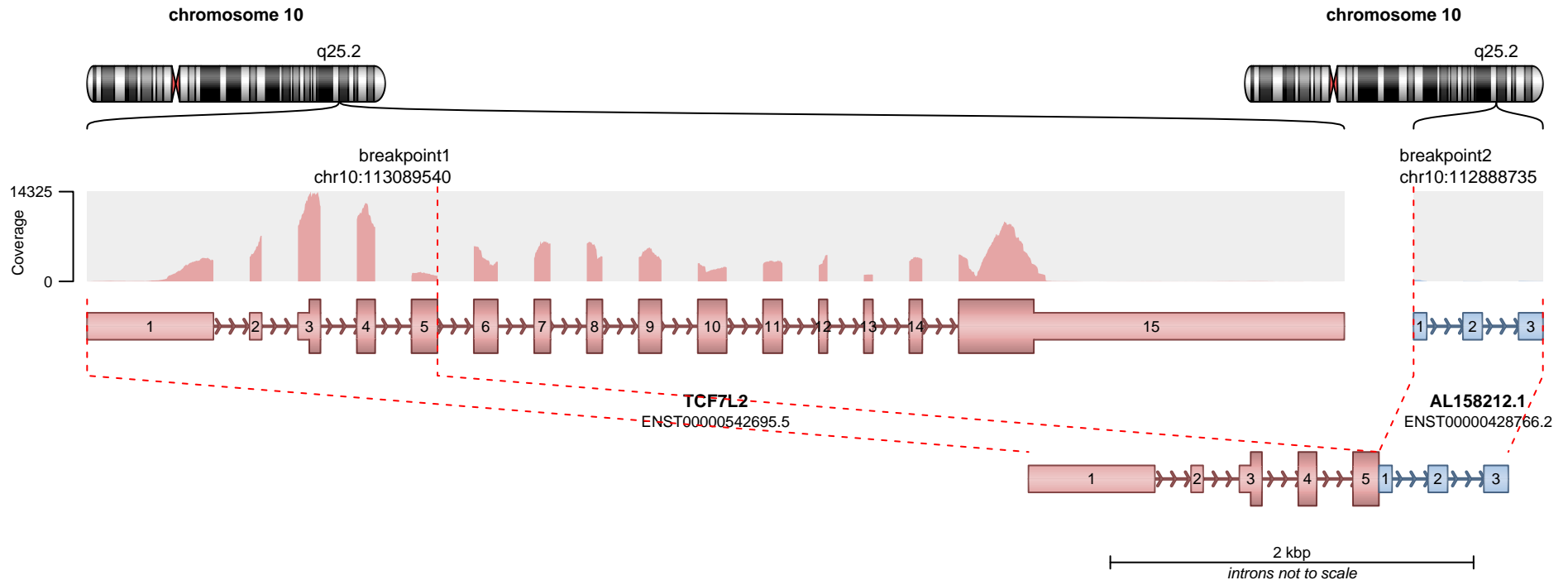
RETAINED PROTEIN DOMAINS
reading frame unclear



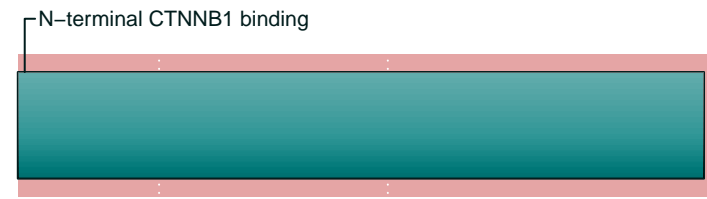
SUPPORTING READ COUNT

Split reads = 35
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

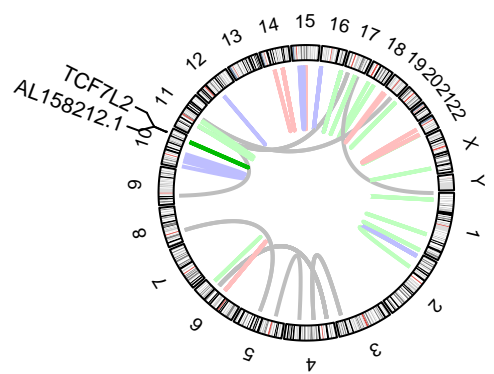
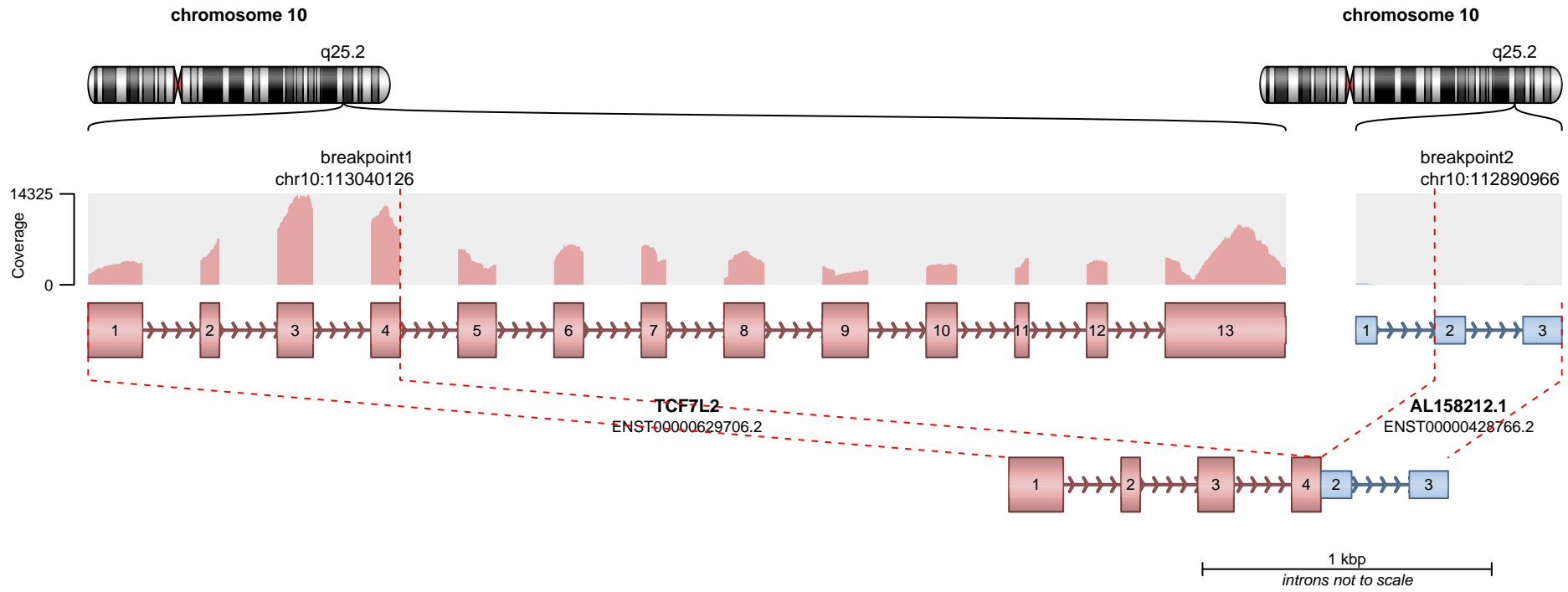


TCF7L2

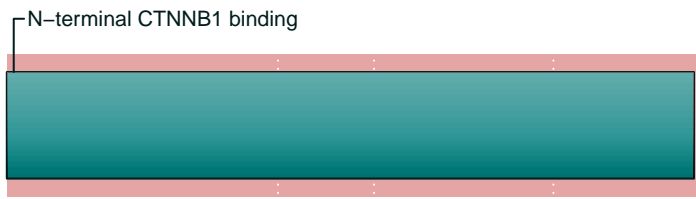
SUPPORTING READ COUNT

Split reads = 15
Discordant mates = 5

- translocation
- duplication
- deletion
- inversion



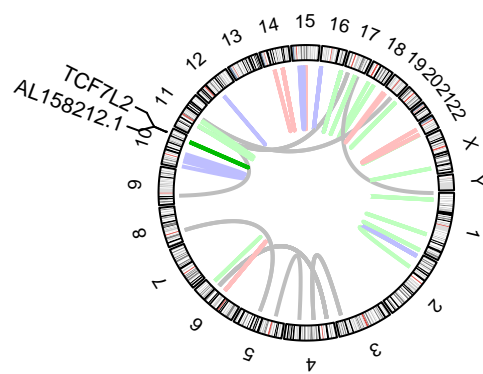
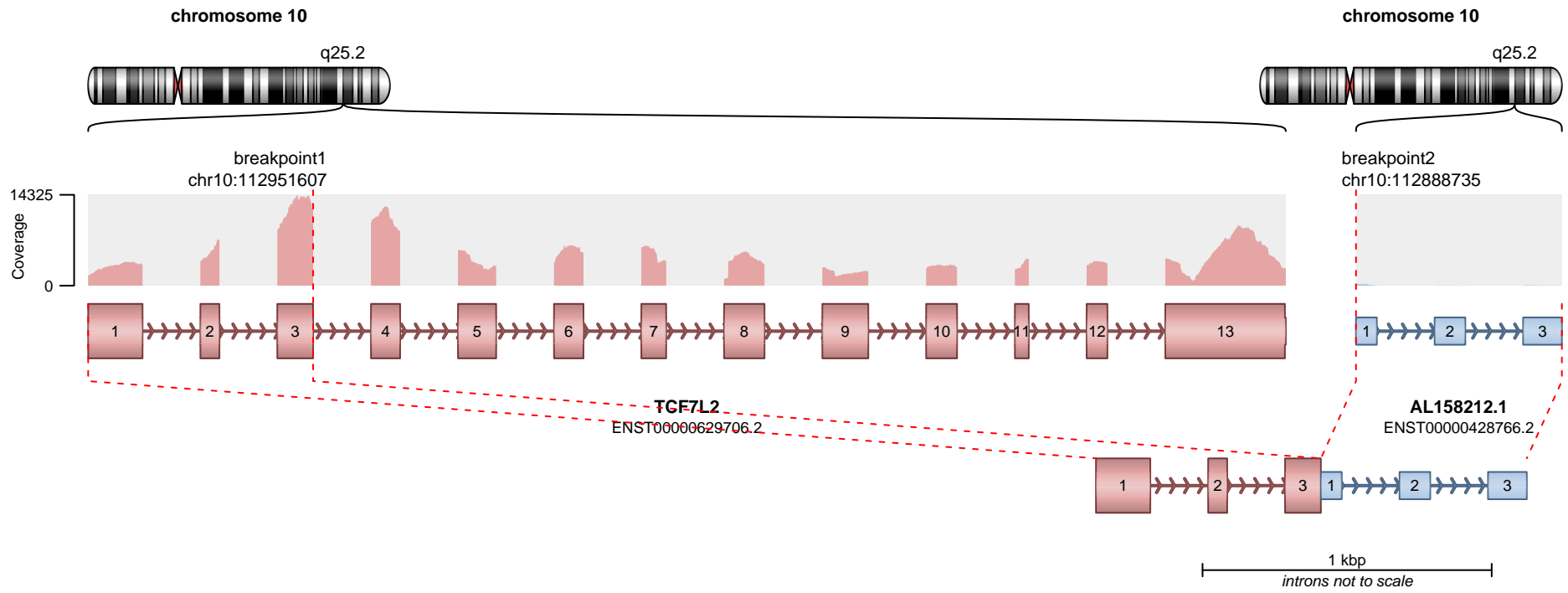
RETAINED PROTEIN DOMAINS
reading frame unclear



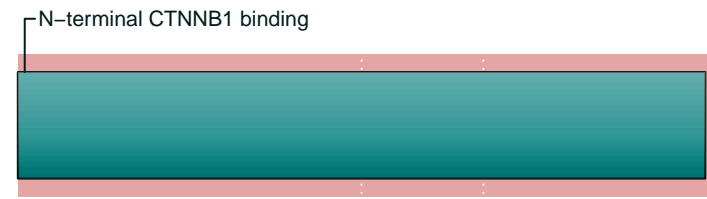
SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

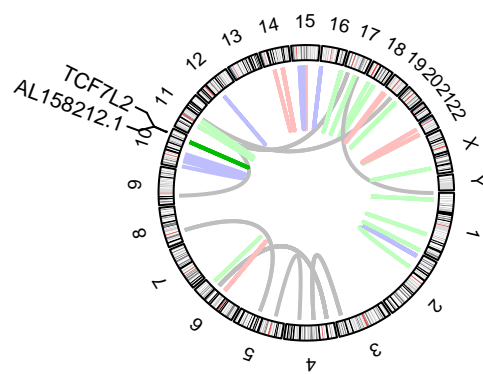
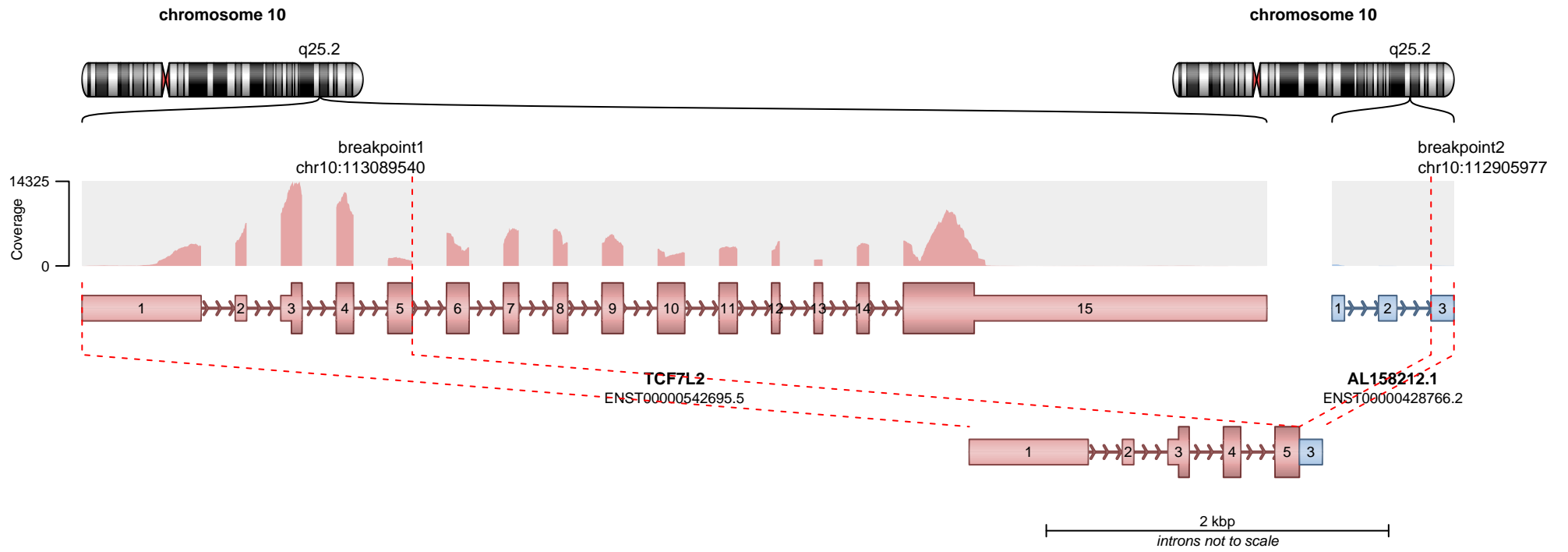


TCF7L2

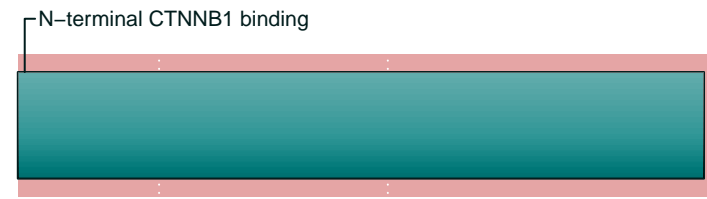
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



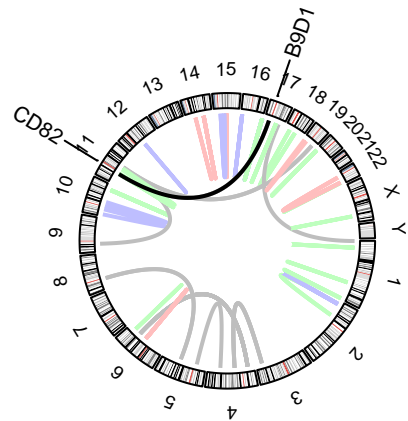
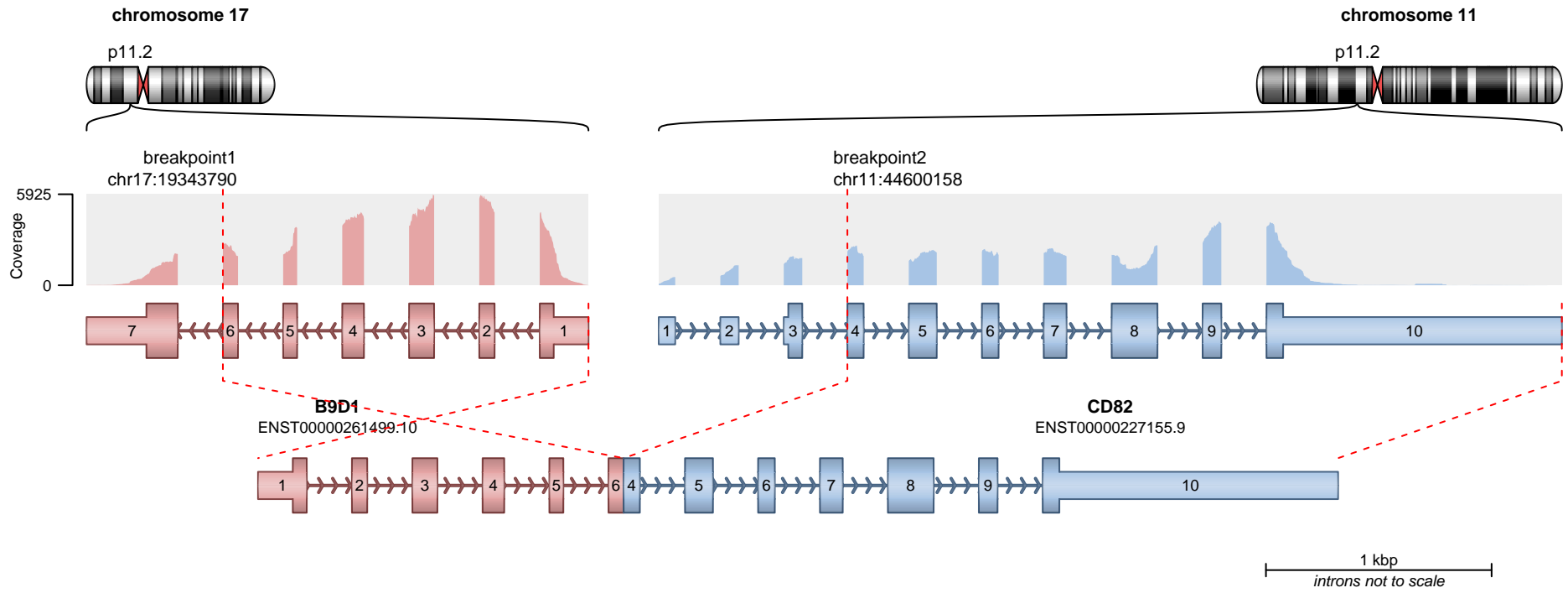
RETAINED PROTEIN DOMAINS
reading frame unclear



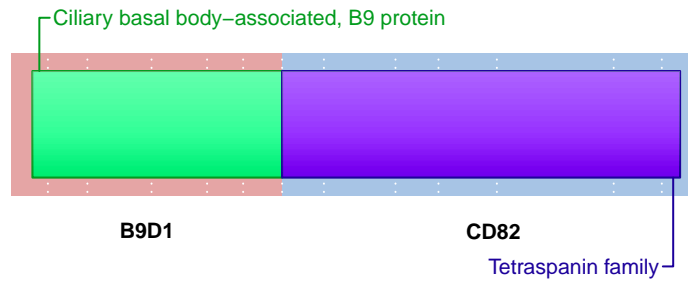
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



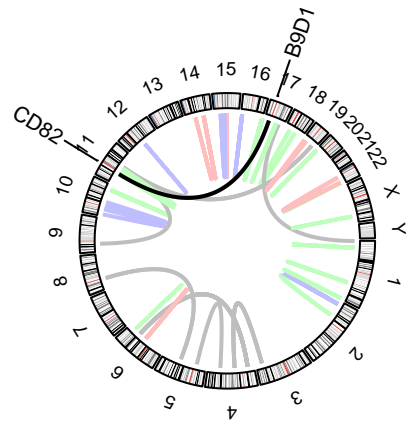
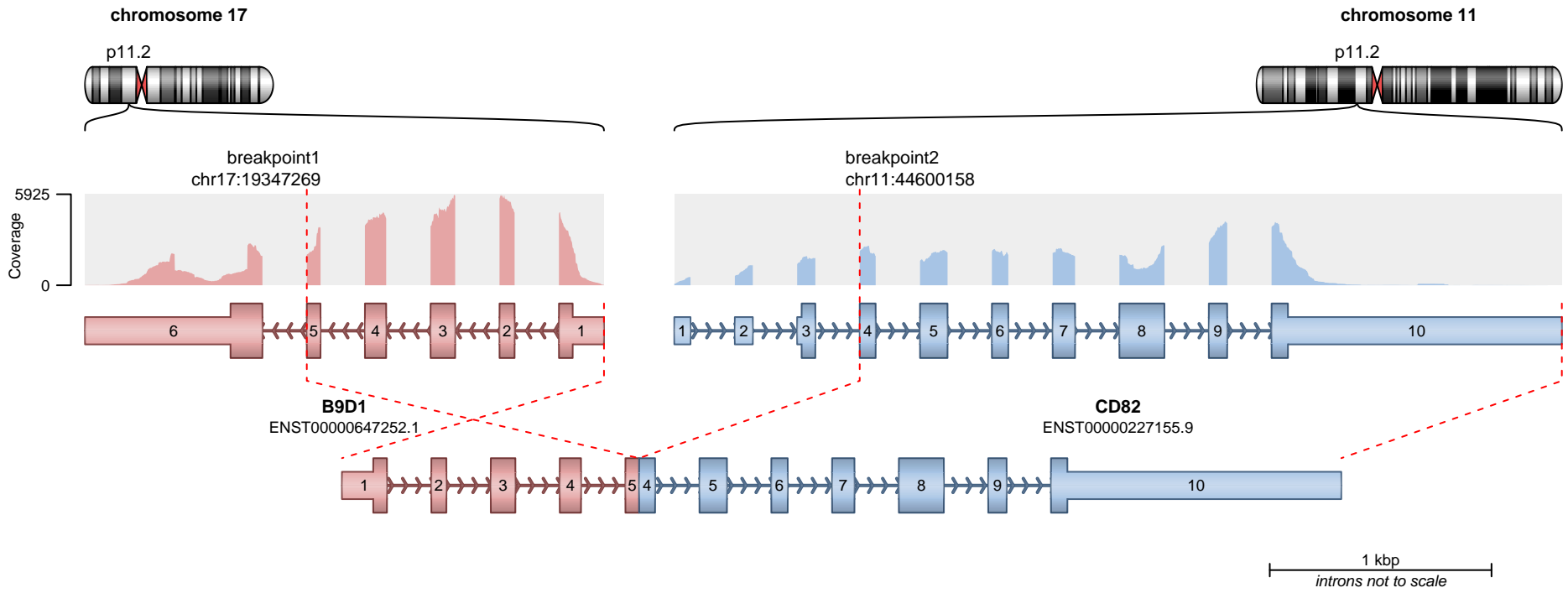
RETAINED PROTEIN DOMAINS
reading frame unclear



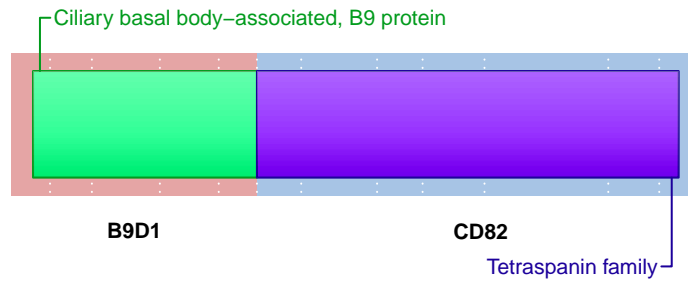
SUPPORTING READ COUNT

Split reads = 115
Discordant mates = 7

— translocation — deletion
— duplication — inversion



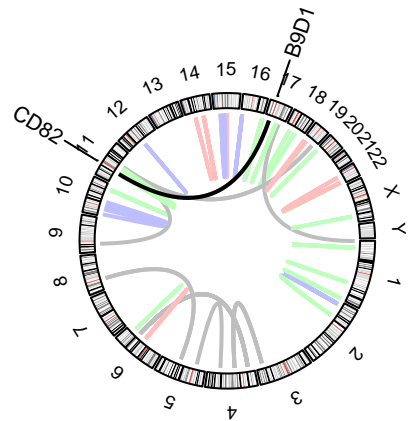
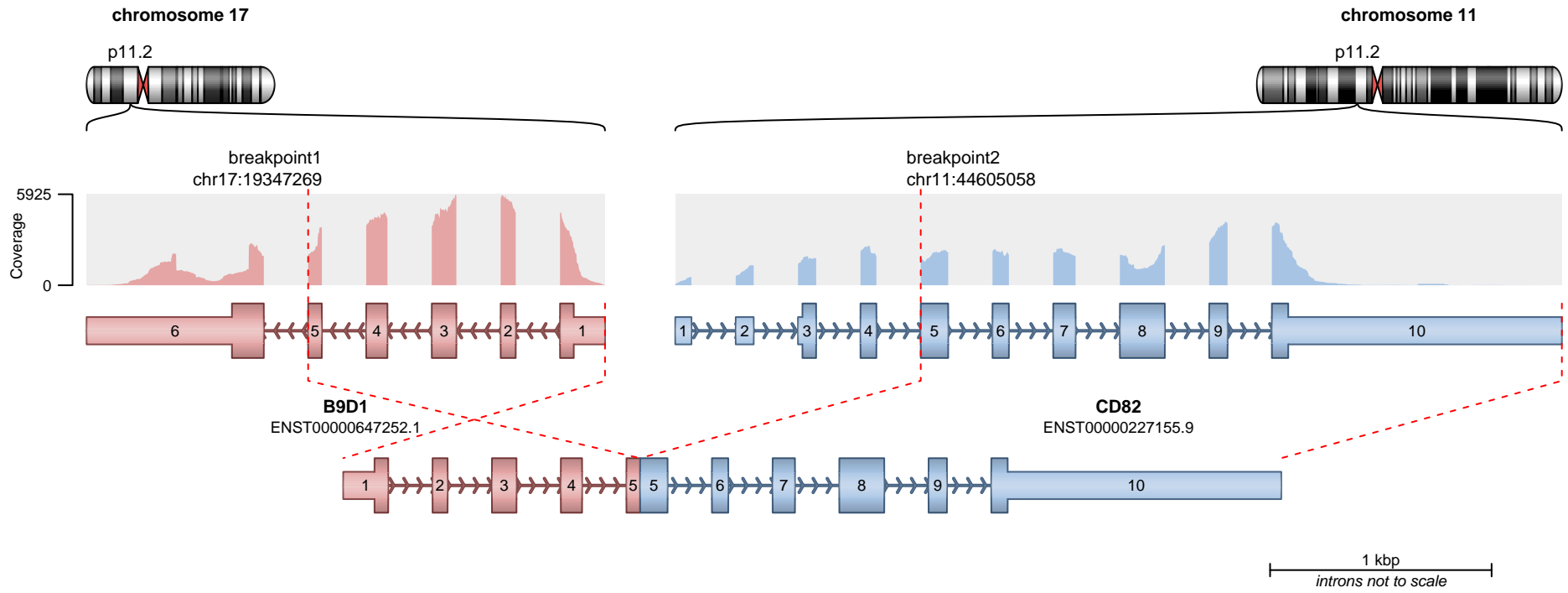
RETAINED PROTEIN DOMAINS
reading frame unclear



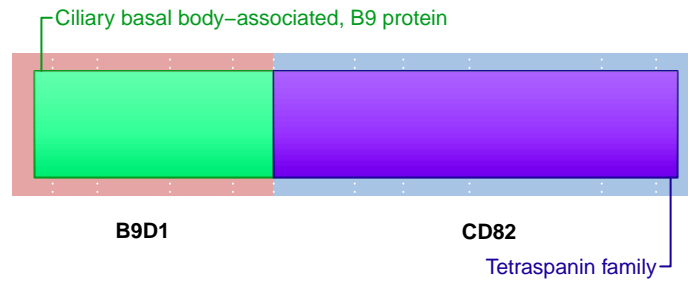
SUPPORTING READ COUNT

Split reads = 13
Discordant mates = 3

— translocation — deletion
— duplication — inversion



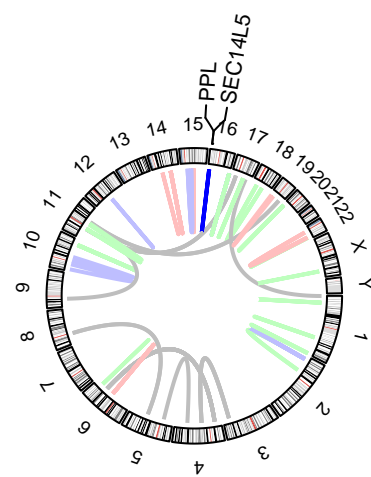
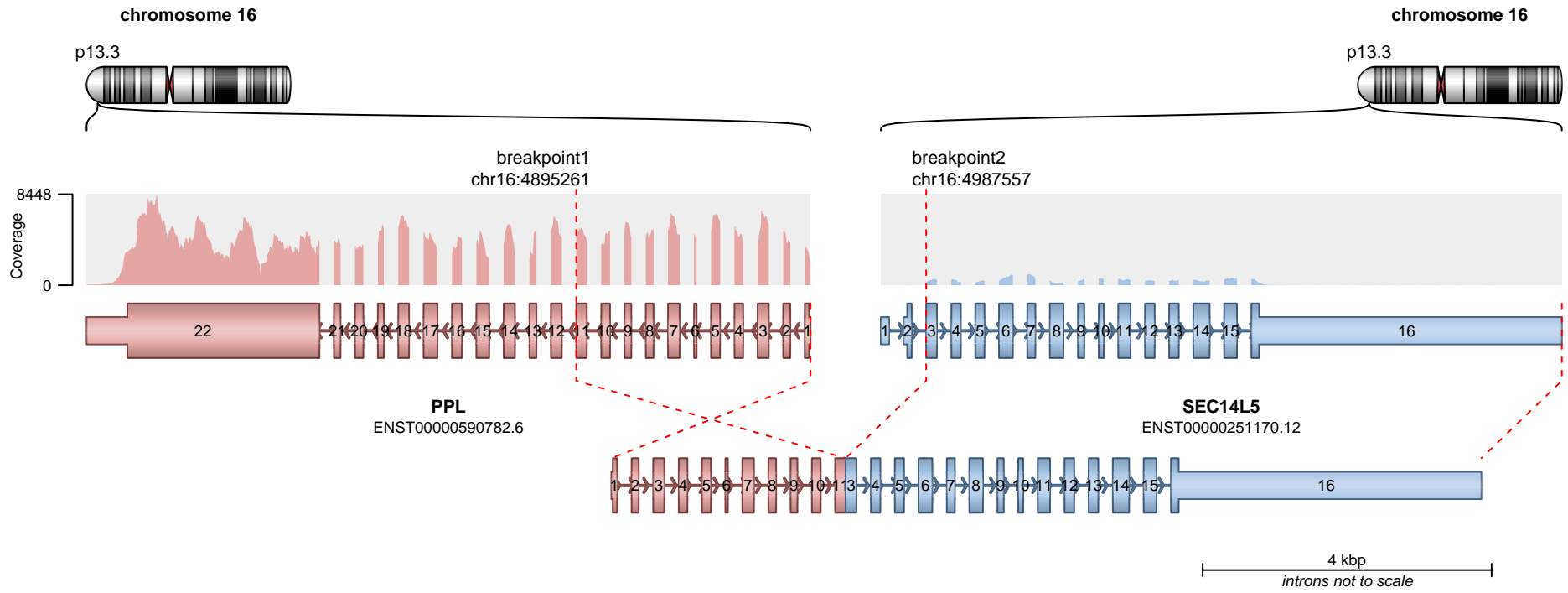
RETAINED PROTEIN DOMAINS
reading frame unclear



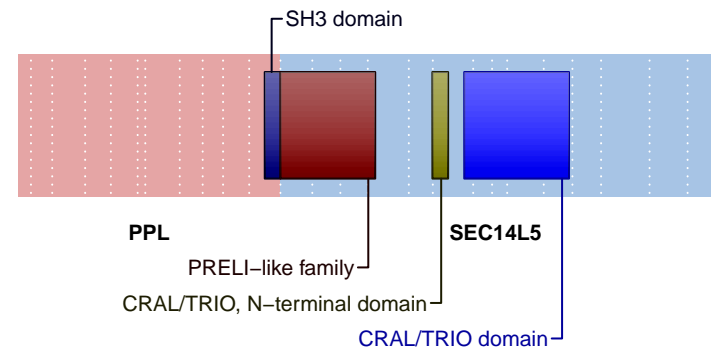
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



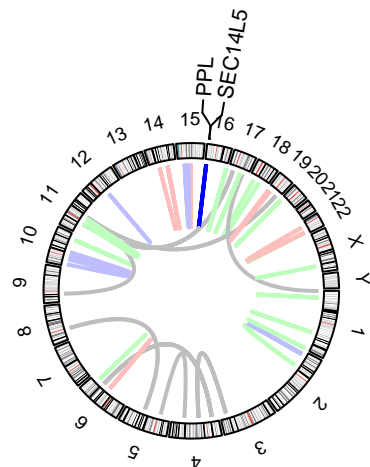
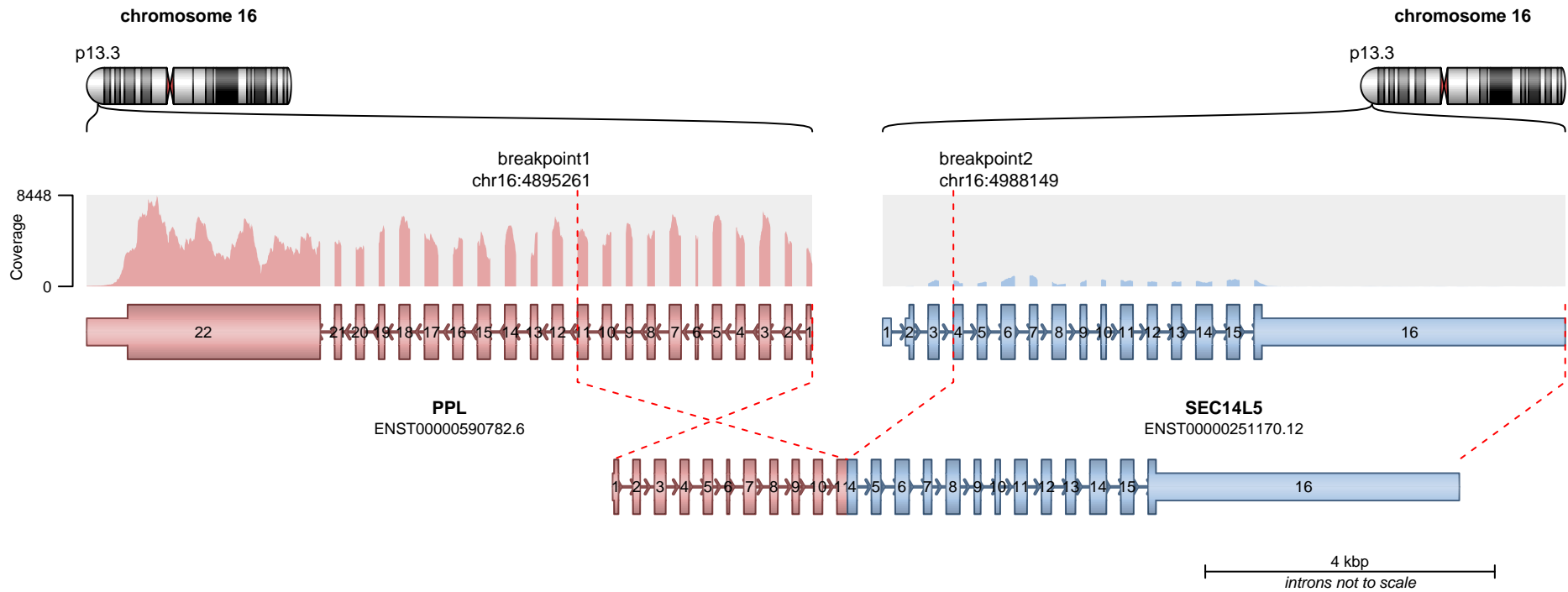
RETAINED PROTEIN DOMAINS
reading frame unclear



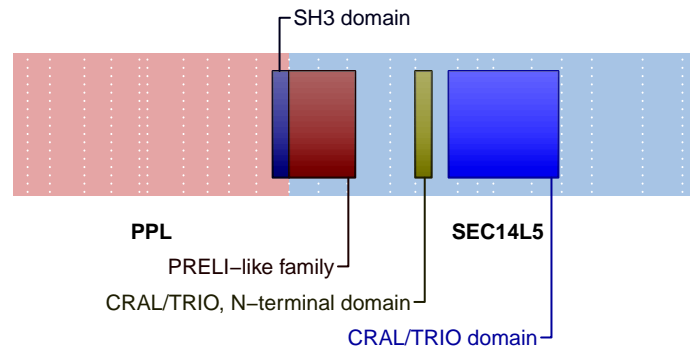
SUPPORTING READ COUNT

Split reads = 92
Discordant mates = 6

- translocation
- duplication
- deletion
- inversion



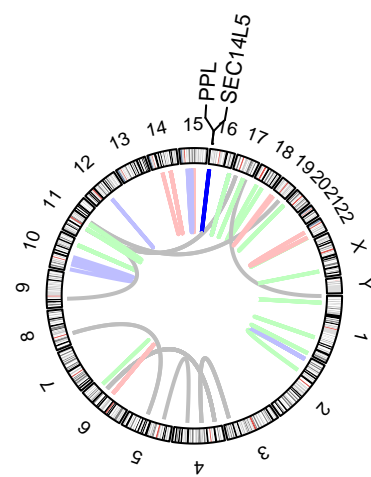
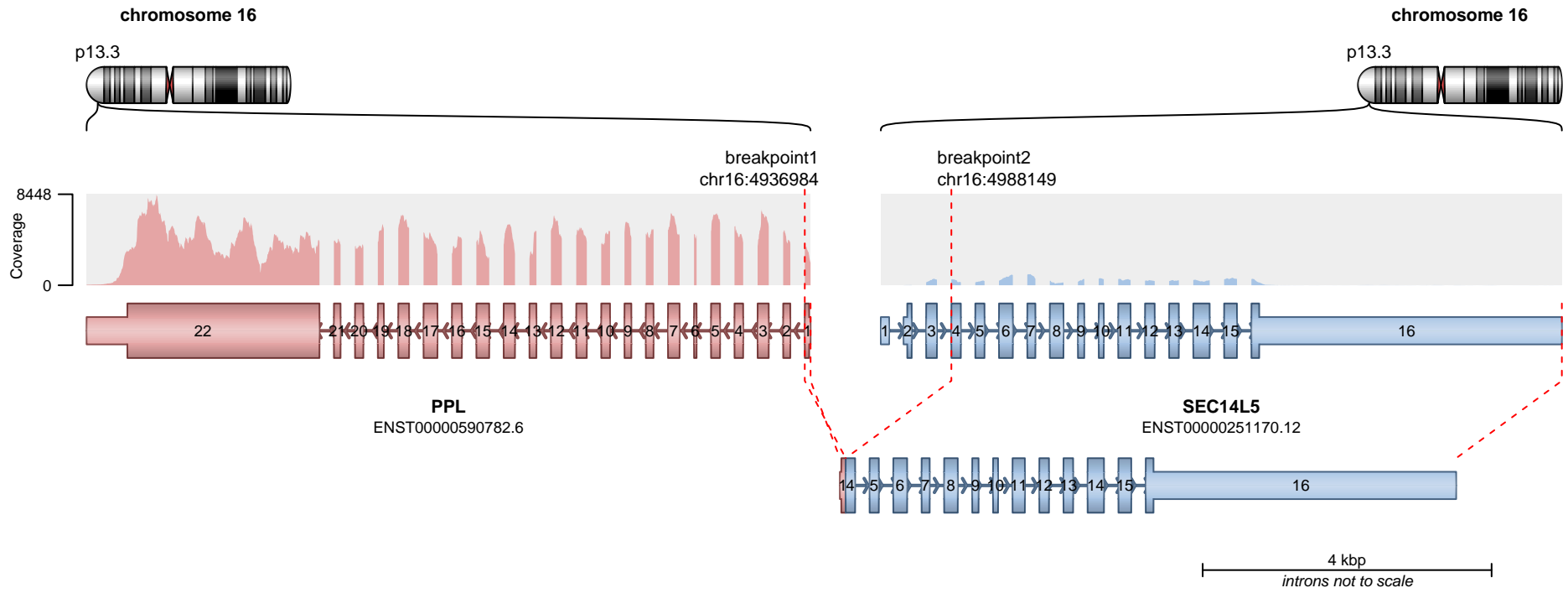
RETAINED PROTEIN DOMAINS
reading frame unclear



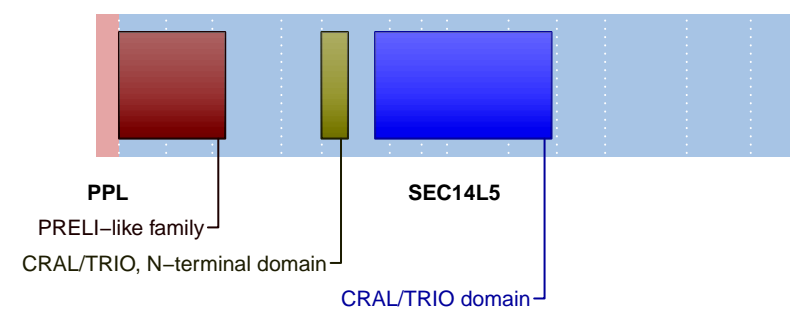
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

— translocation — deletion
— duplication — inversion



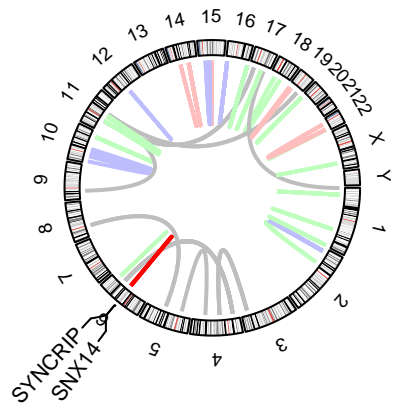
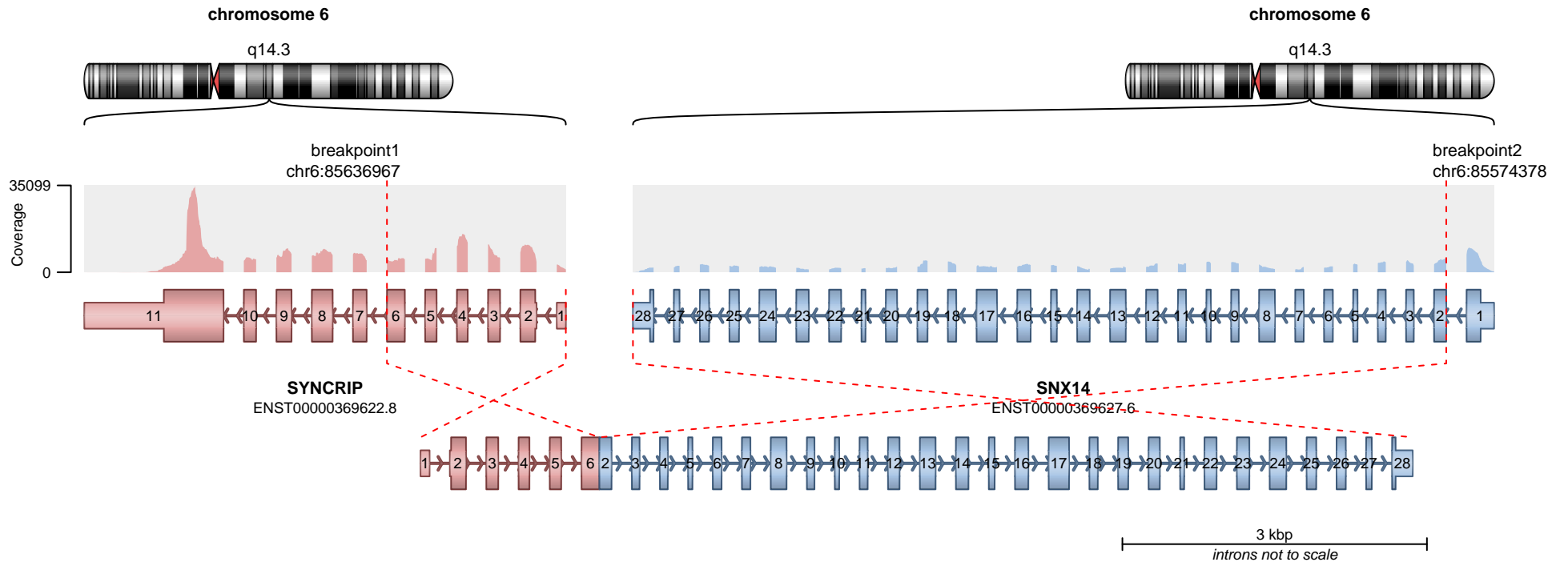
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

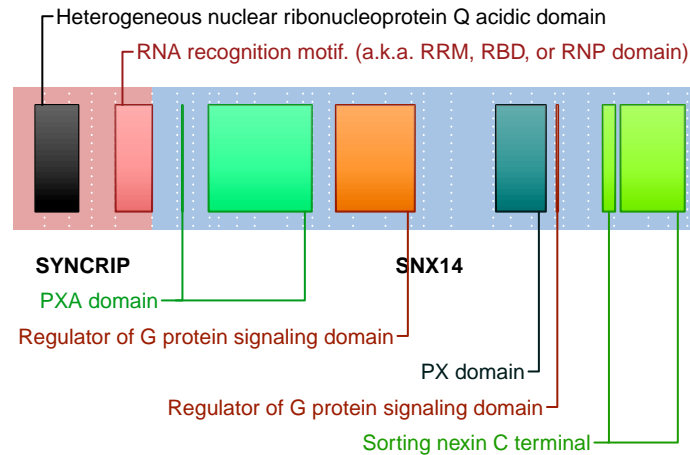
Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



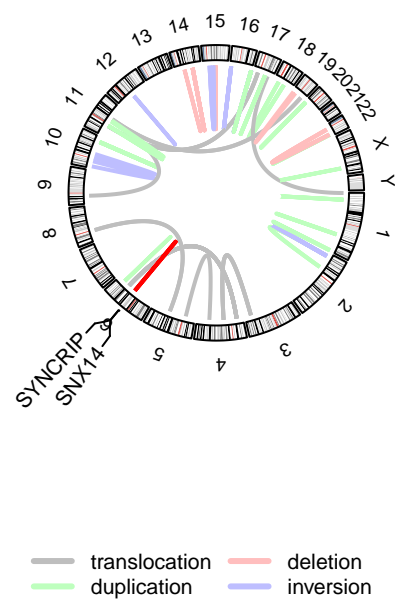
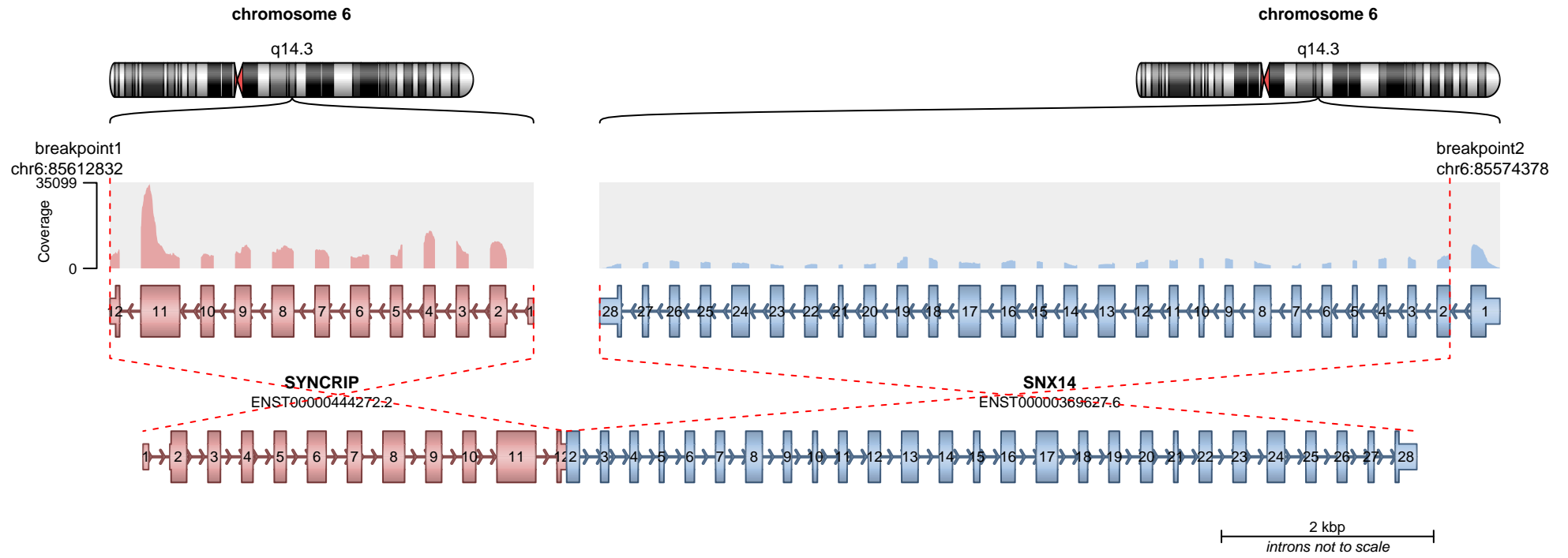
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear

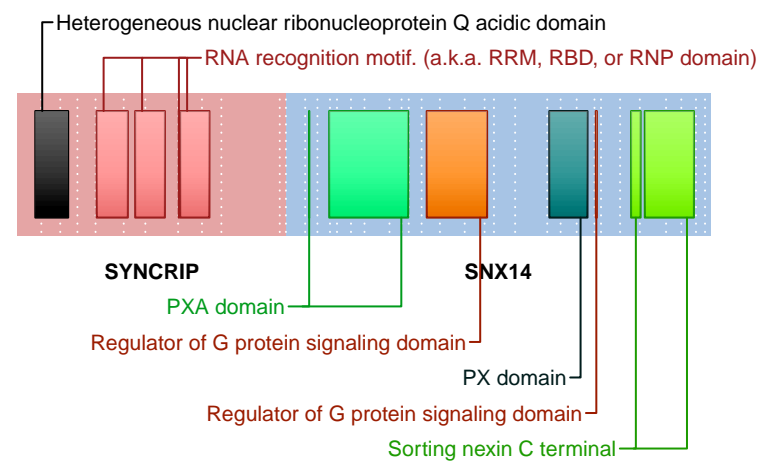


SUPPORTING READ COUNT

Split reads = 89
Discordant mates = 4

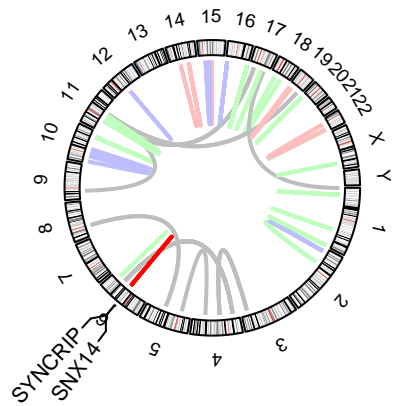
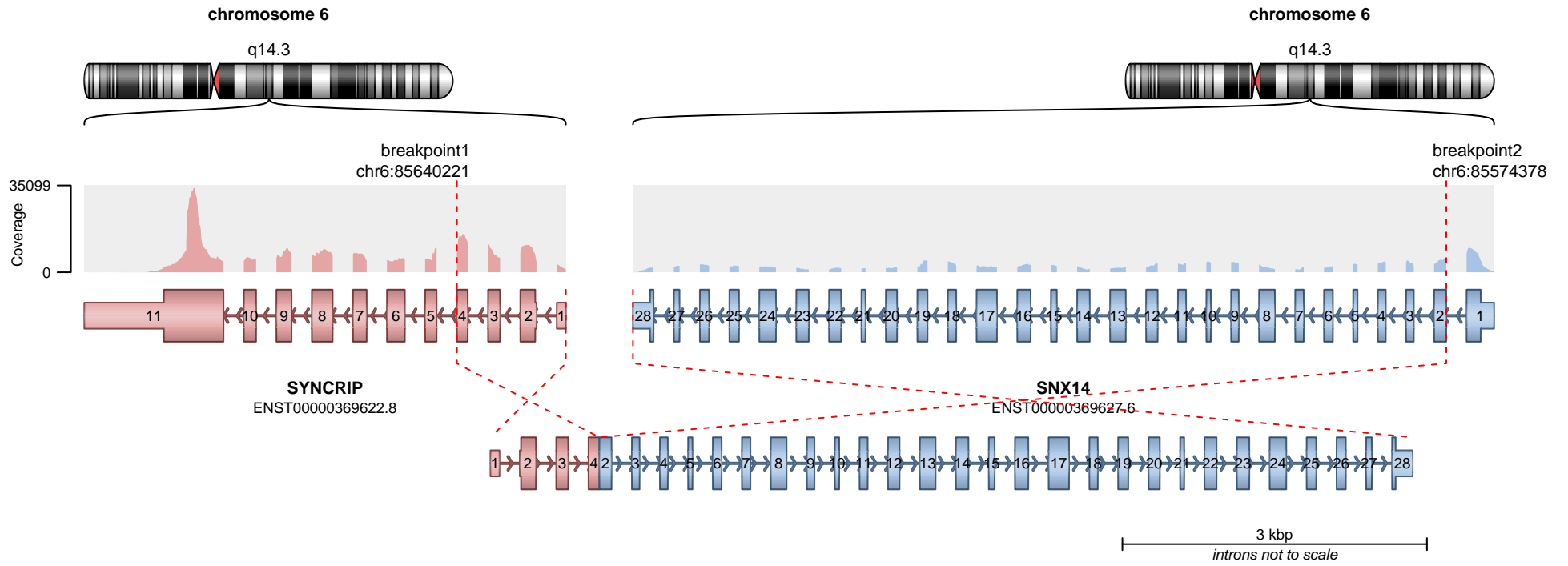


RETAINED PROTEIN DOMAINS
reading frame unclear



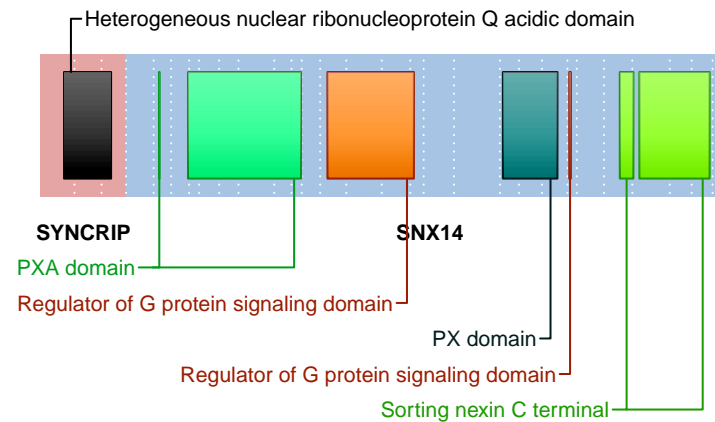
SUPPORTING READ COUNT

Split reads = 72
Discordant mates = 5



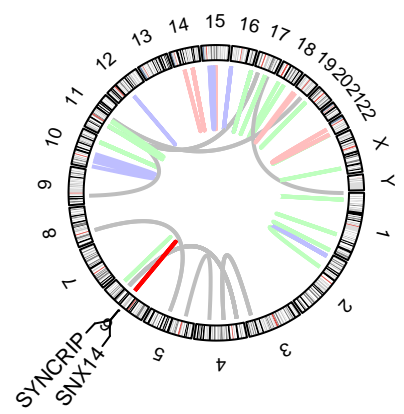
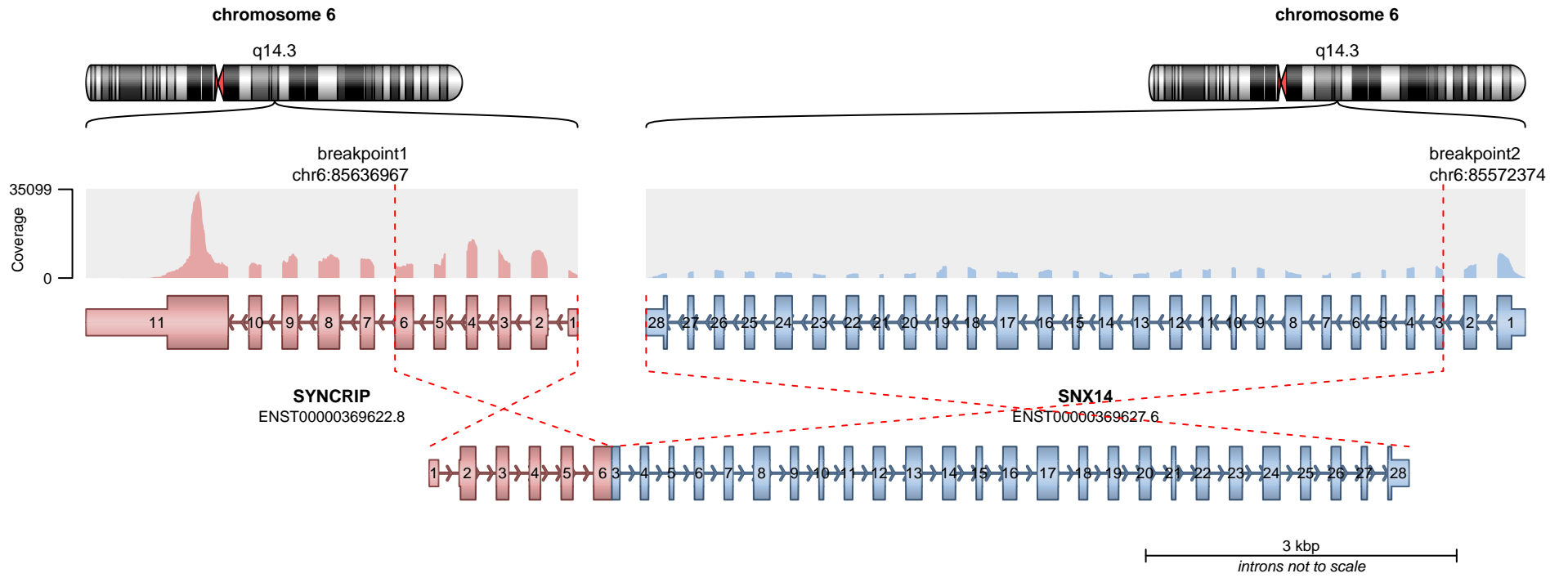
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



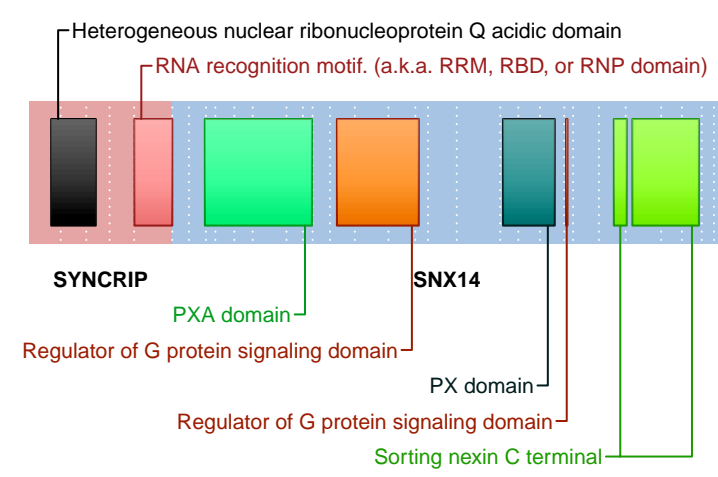
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0



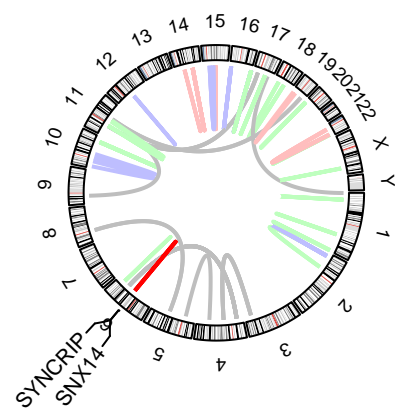
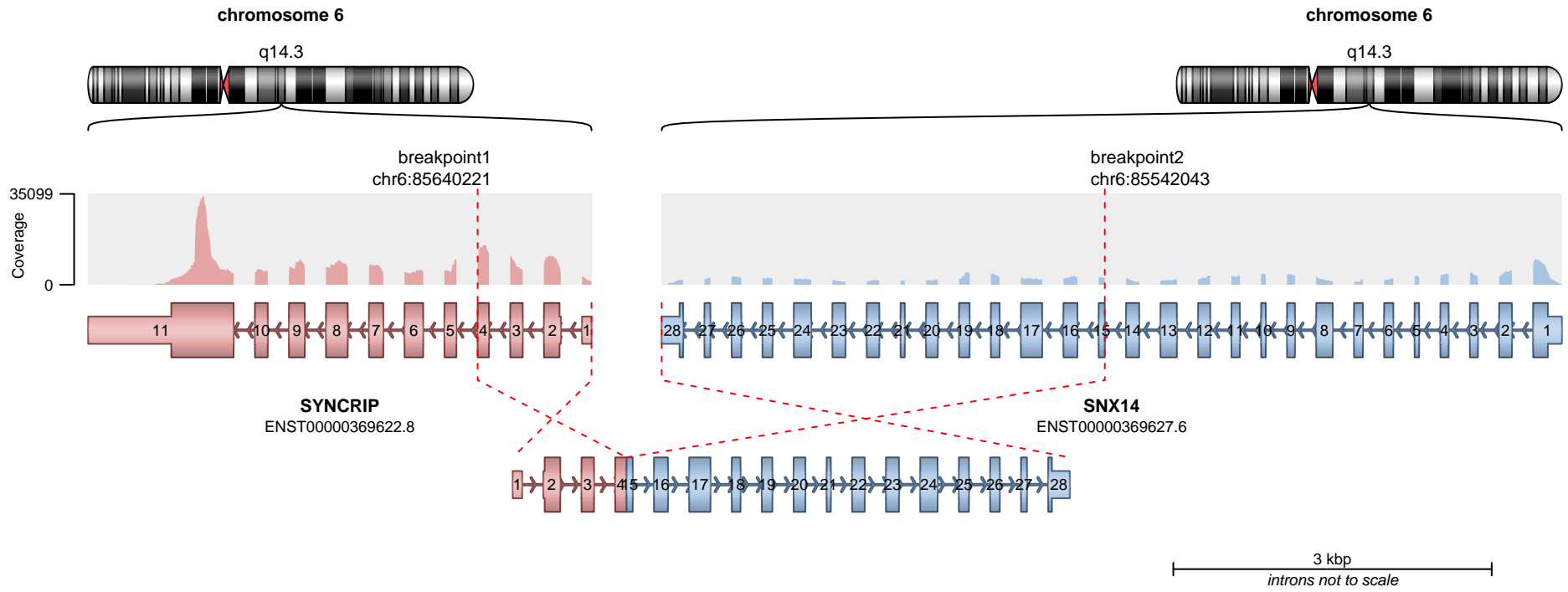
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



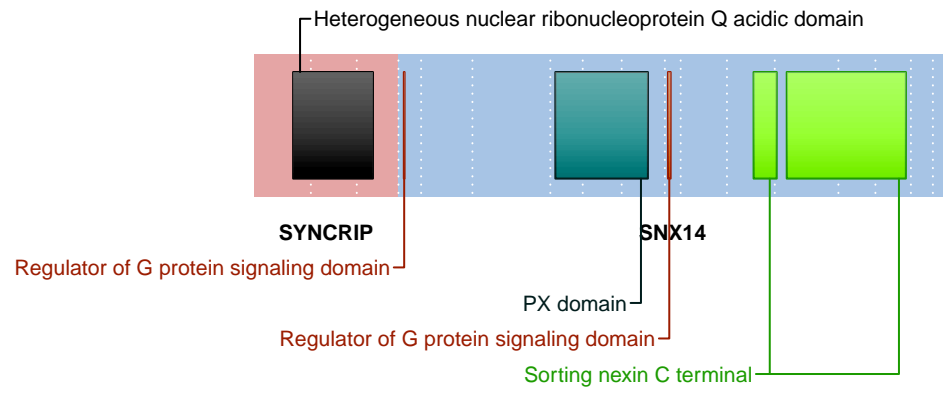
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



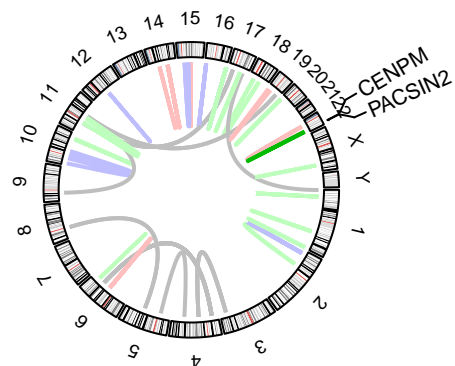
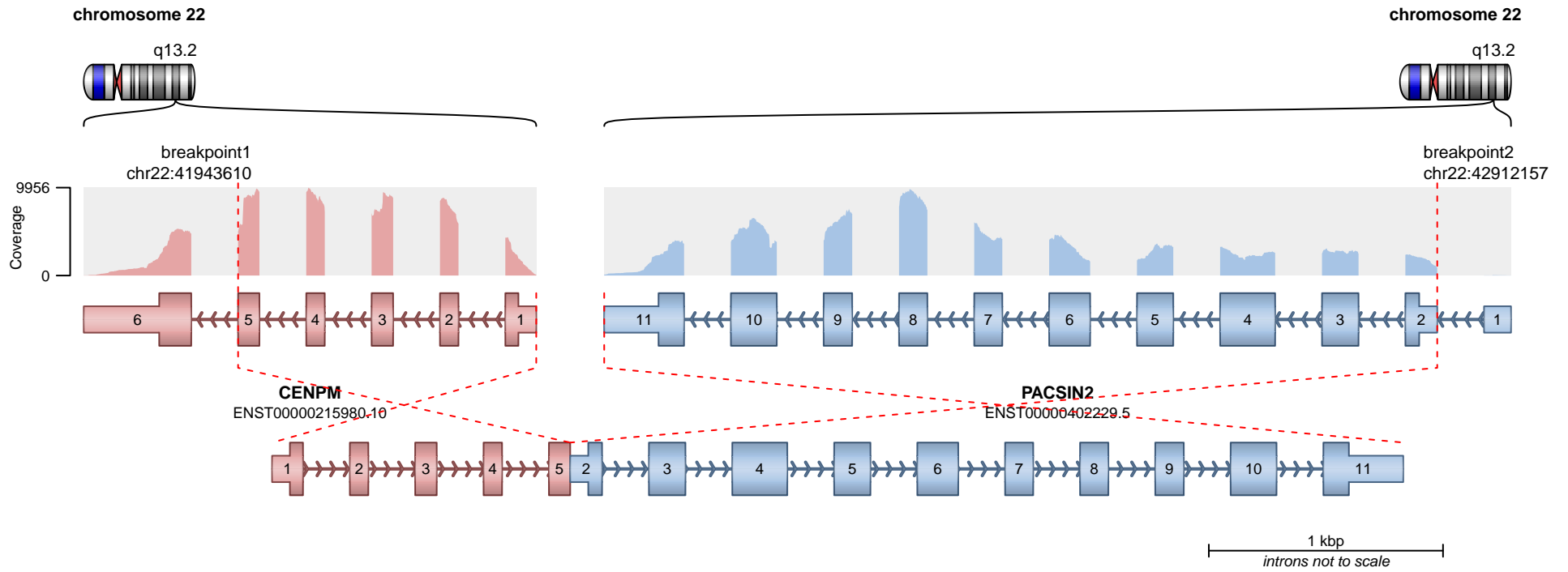
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear

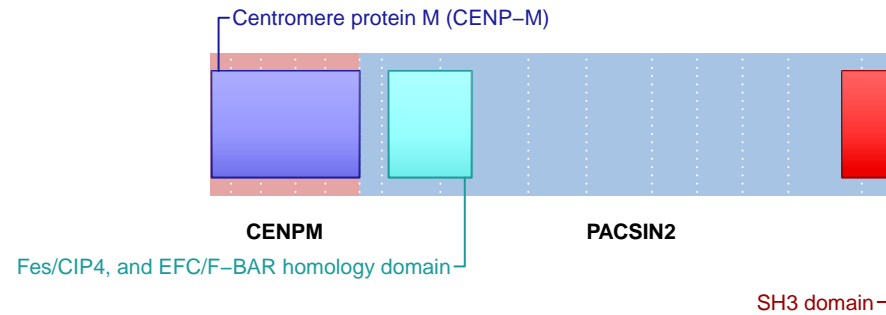


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



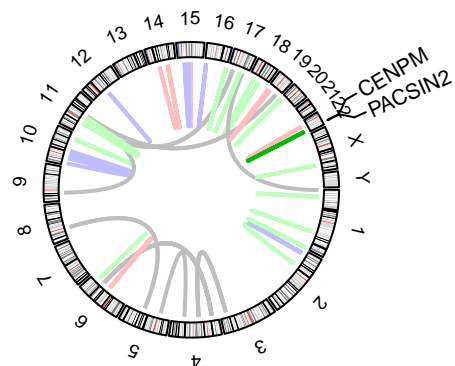
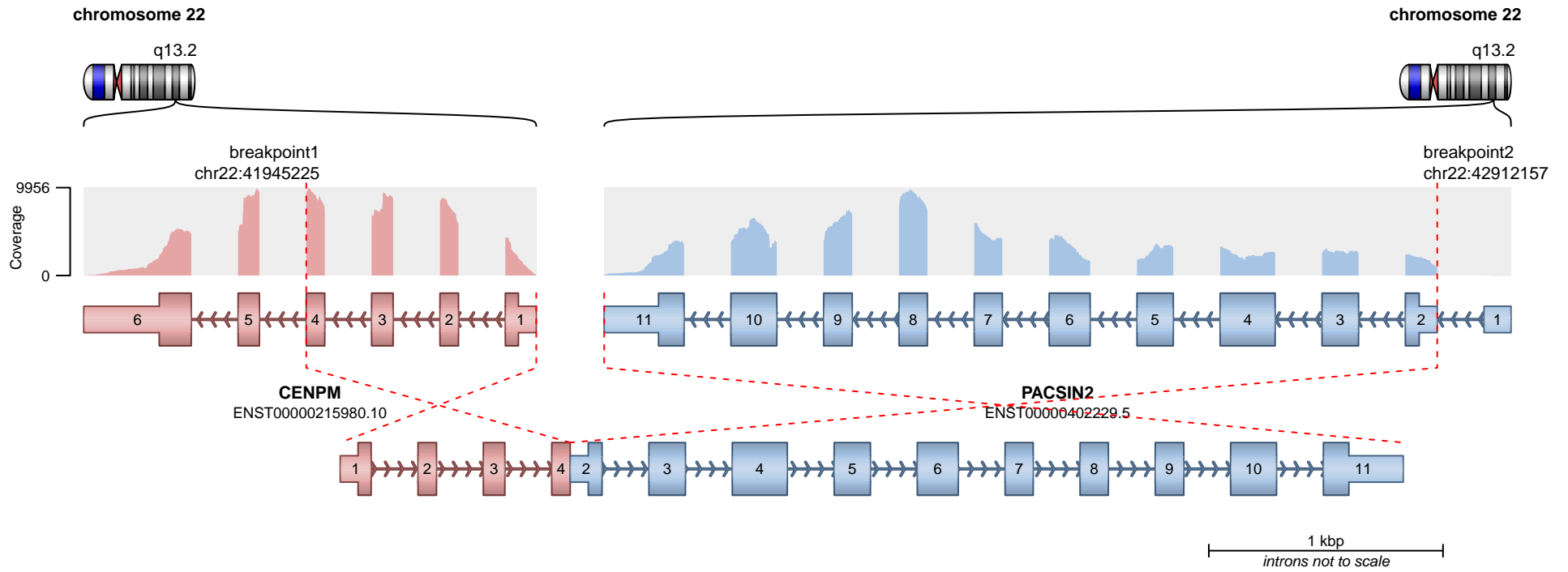
RETAINED PROTEIN DOMAINS
reading frame unclear



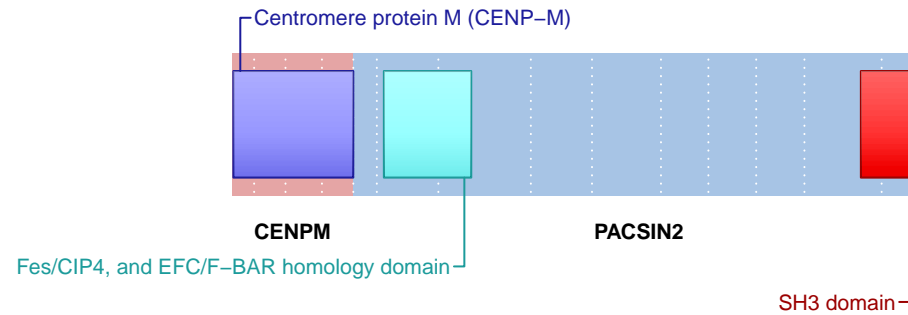
SUPPORTING READ COUNT

Split reads = 86
Discordant mates = 6

— translocation — deletion
— duplication — inversion



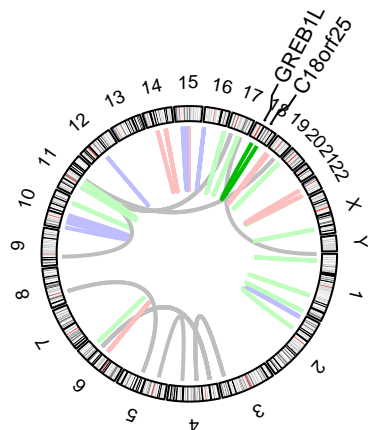
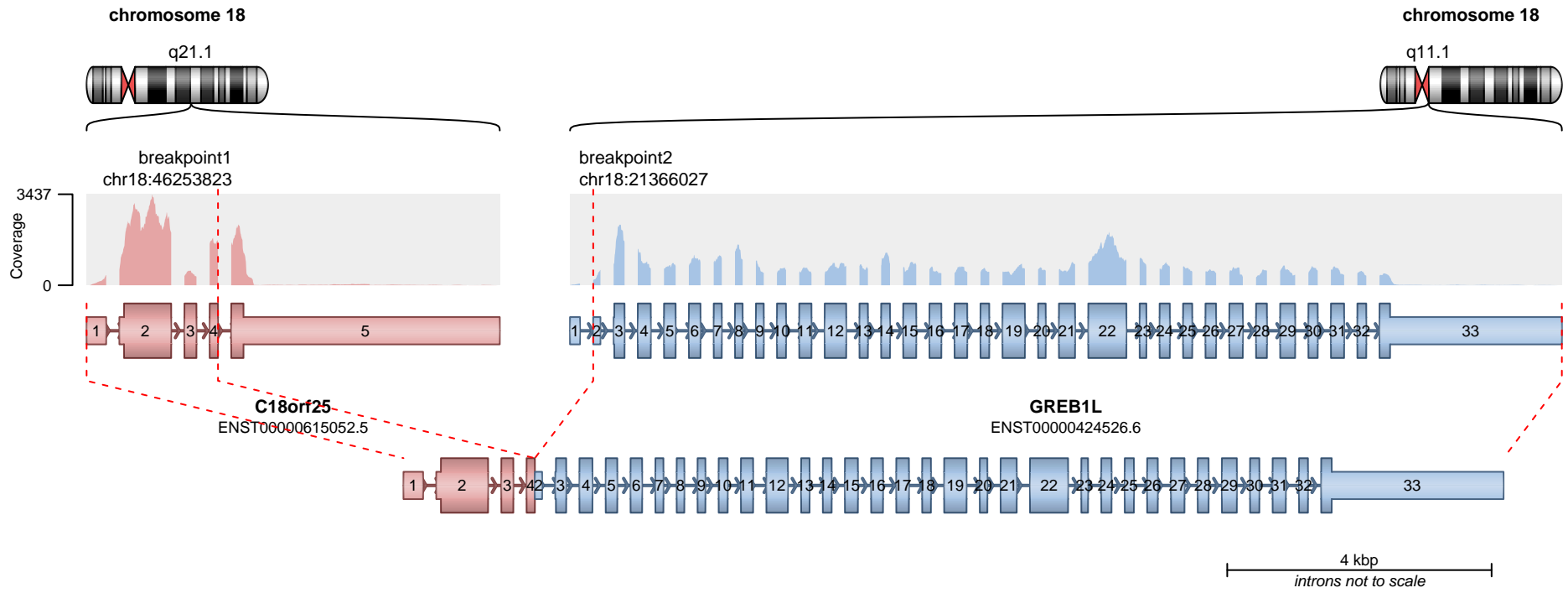
RETAINED PROTEIN DOMAINS
reading frame unclear



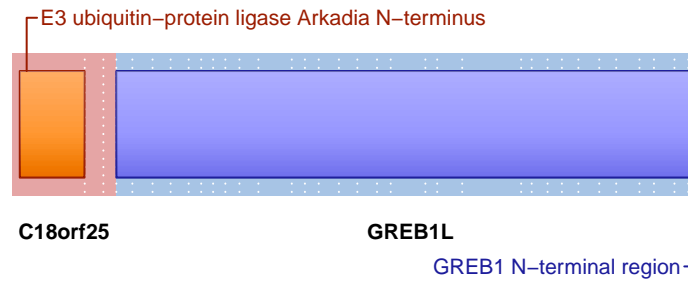
SUPPORTING READ COUNT

Split reads = 27
Discordant mates = 1

— translocation — deletion
— duplication — inversion



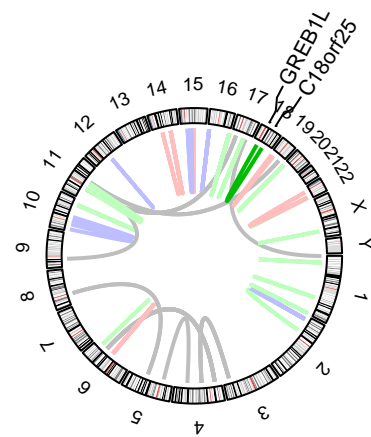
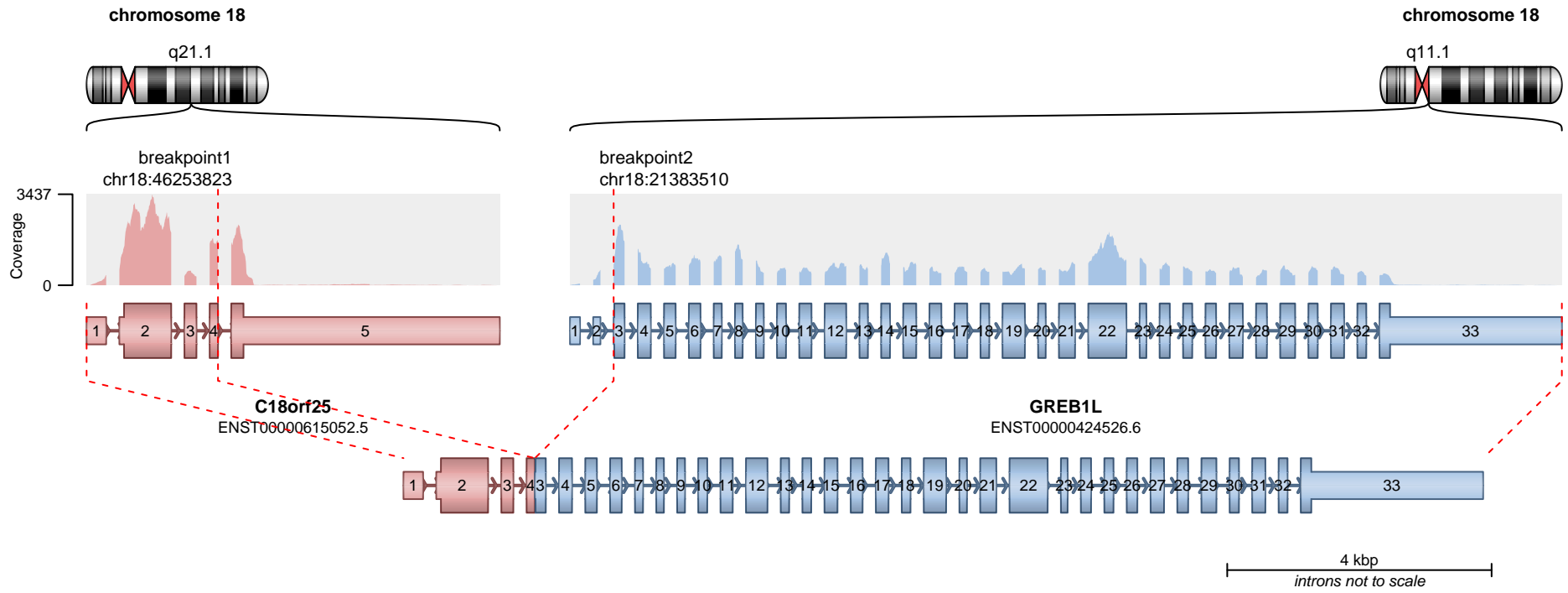
RETAINED PROTEIN DOMAINS
reading frame unclear



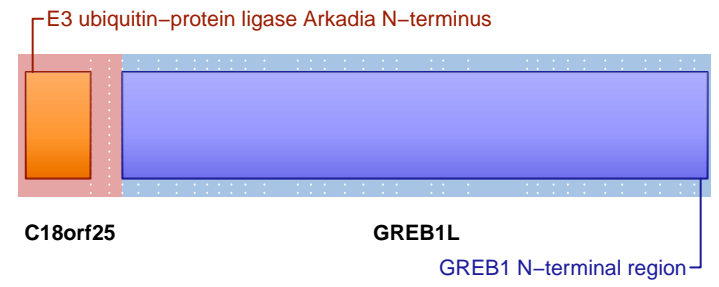
SUPPORTING READ COUNT

Split reads = 81
Discordant mates = 3

— translocation — deletion
— duplication — inversion



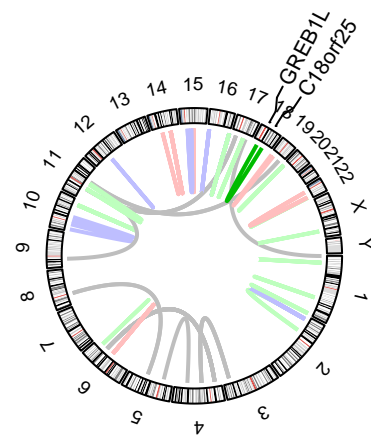
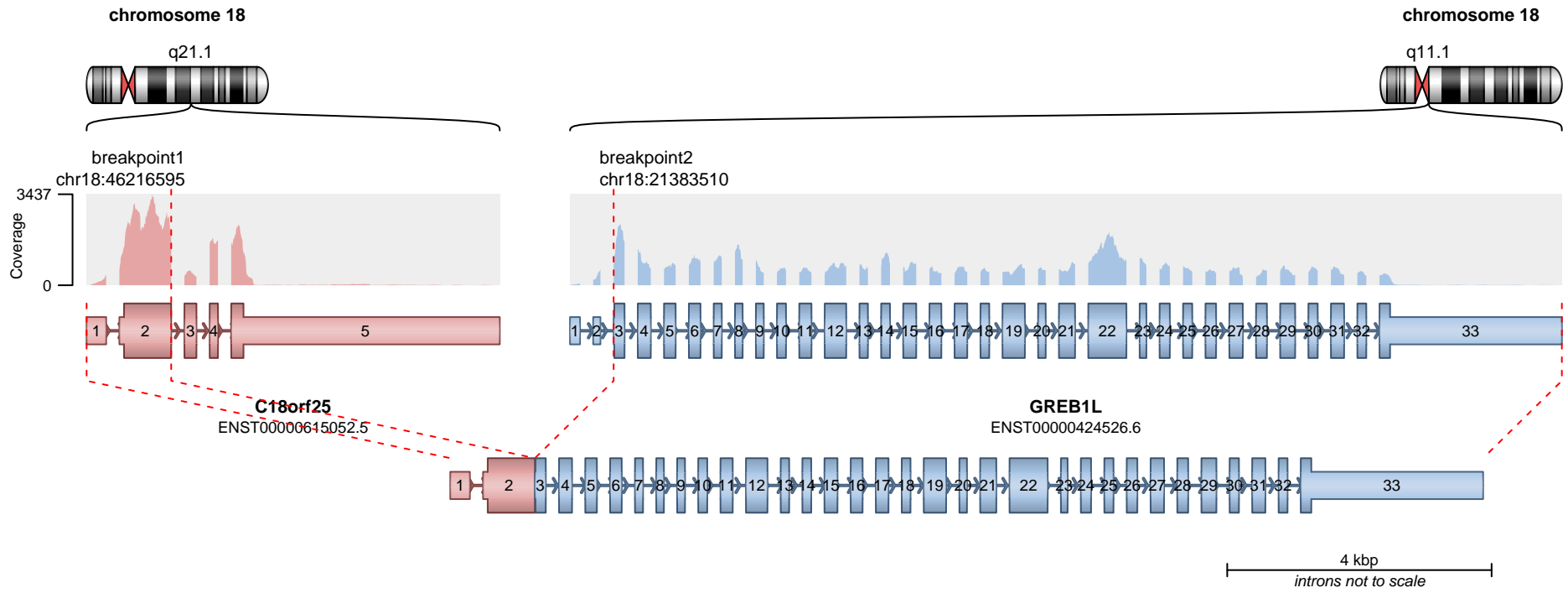
RETAINED PROTEIN DOMAINS
reading frame unclear



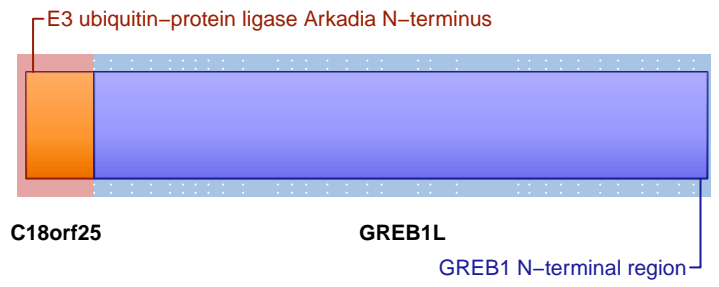
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 3

— translocation — deletion
— duplication — inversion



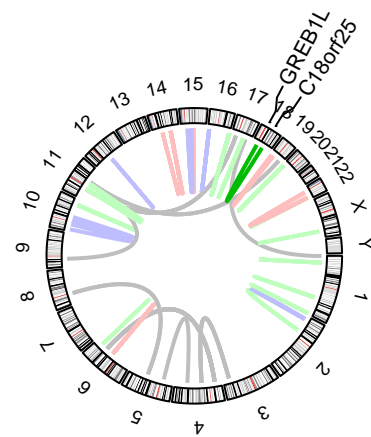
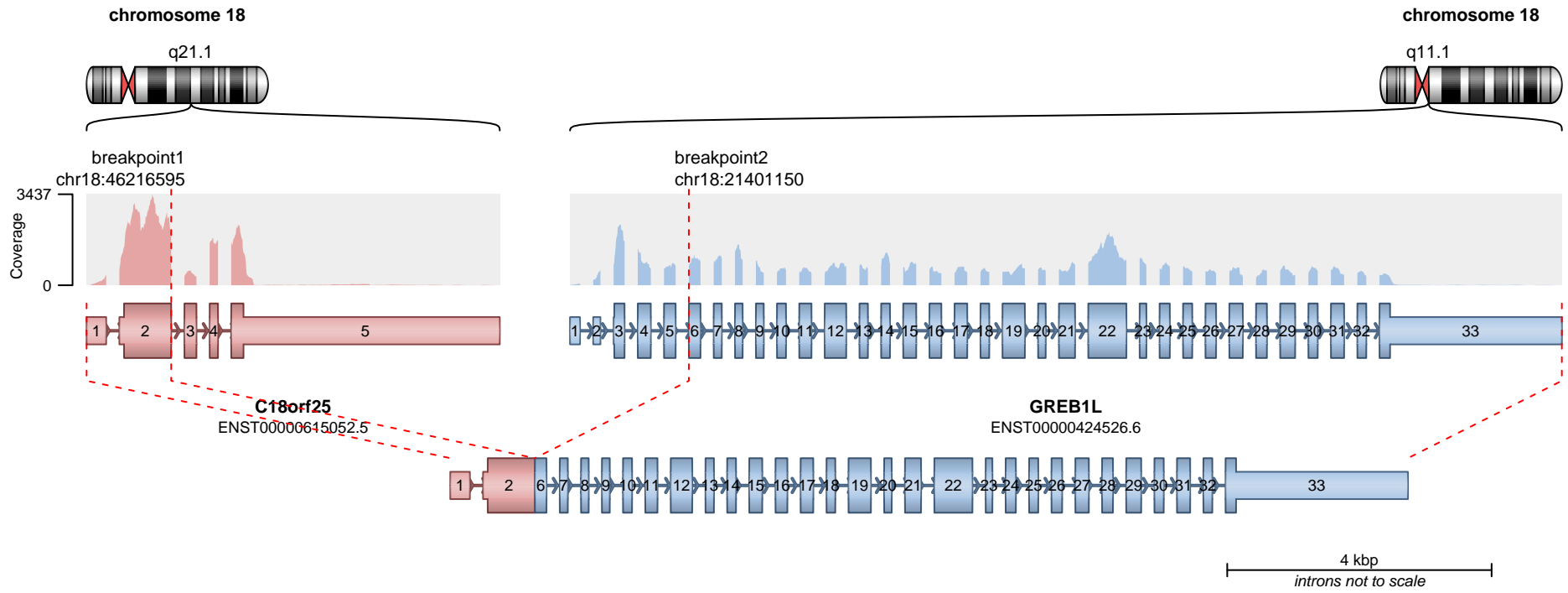
RETAINED PROTEIN DOMAINS
reading frame unclear



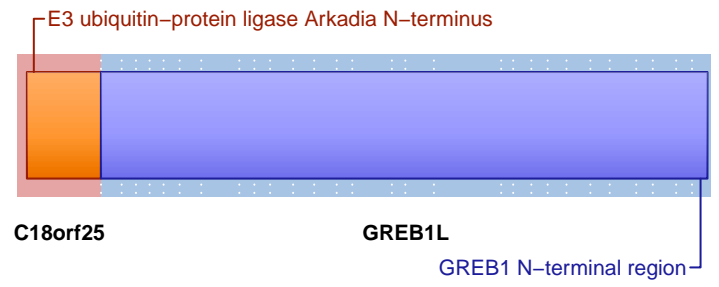
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



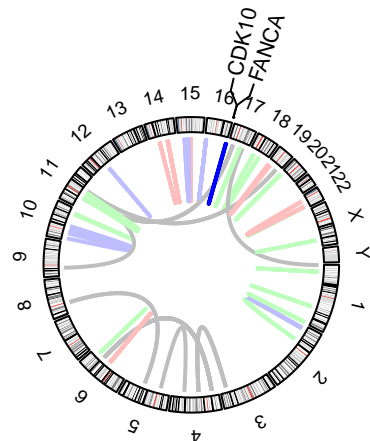
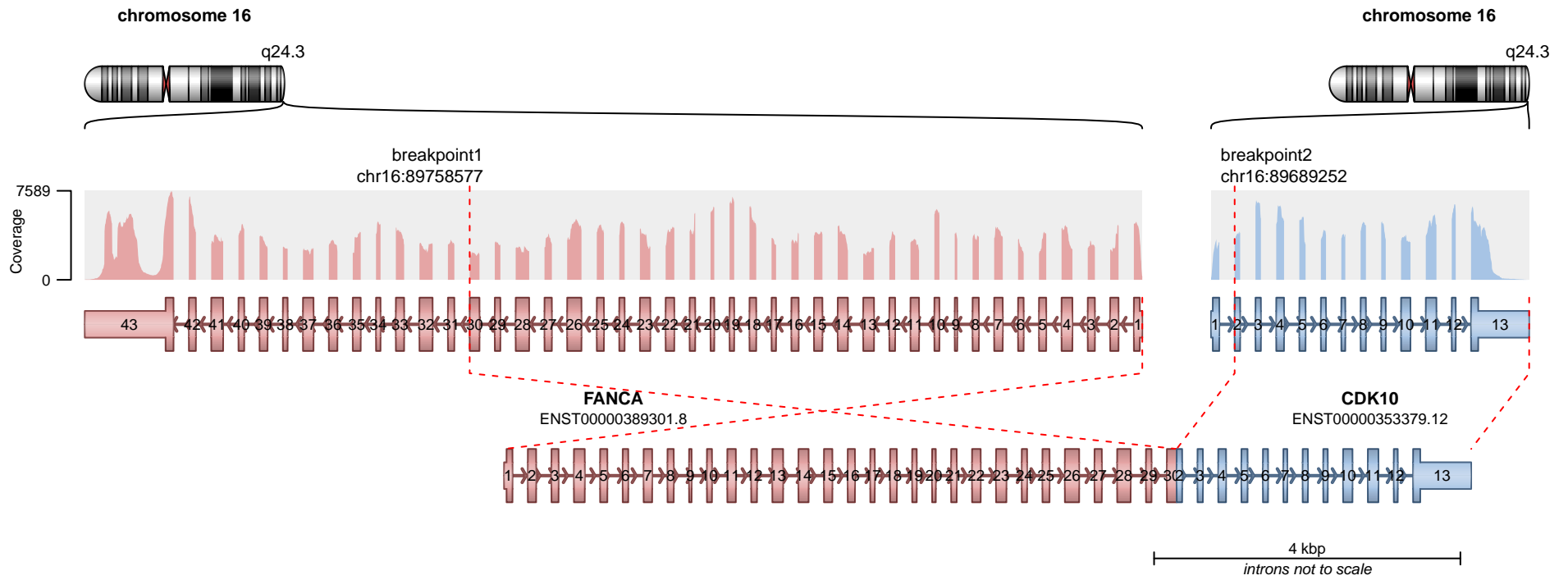
RETAINED PROTEIN DOMAINS
reading frame unclear



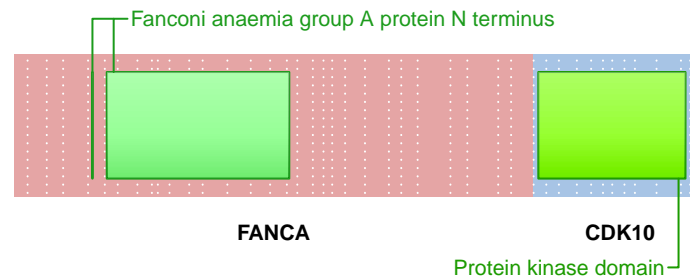
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



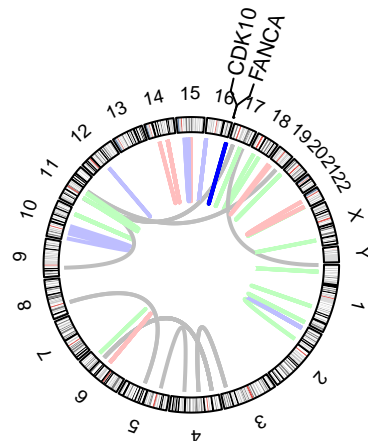
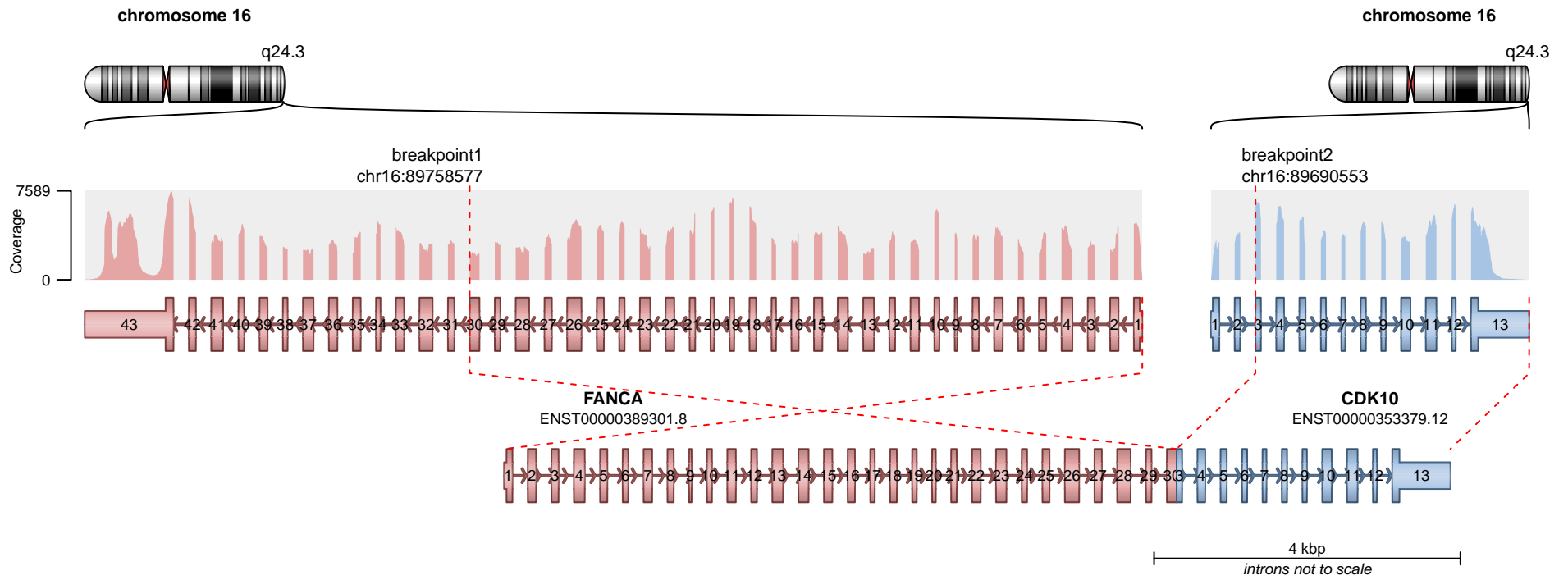
RETAINED PROTEIN DOMAINS
reading frame unclear



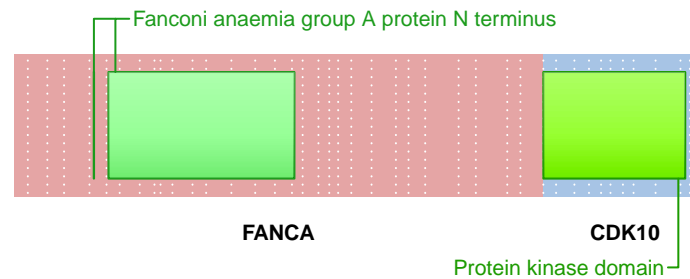
SUPPORTING READ COUNT

Split reads = 73
Discordant mates = 4

- translocation
- duplication
- deletion
- inversion



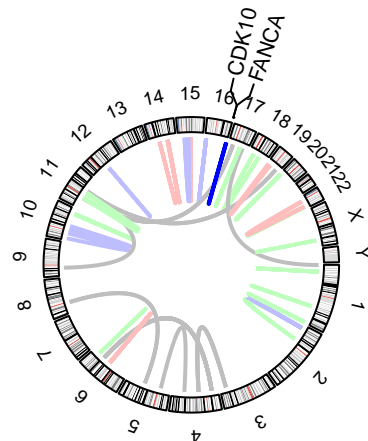
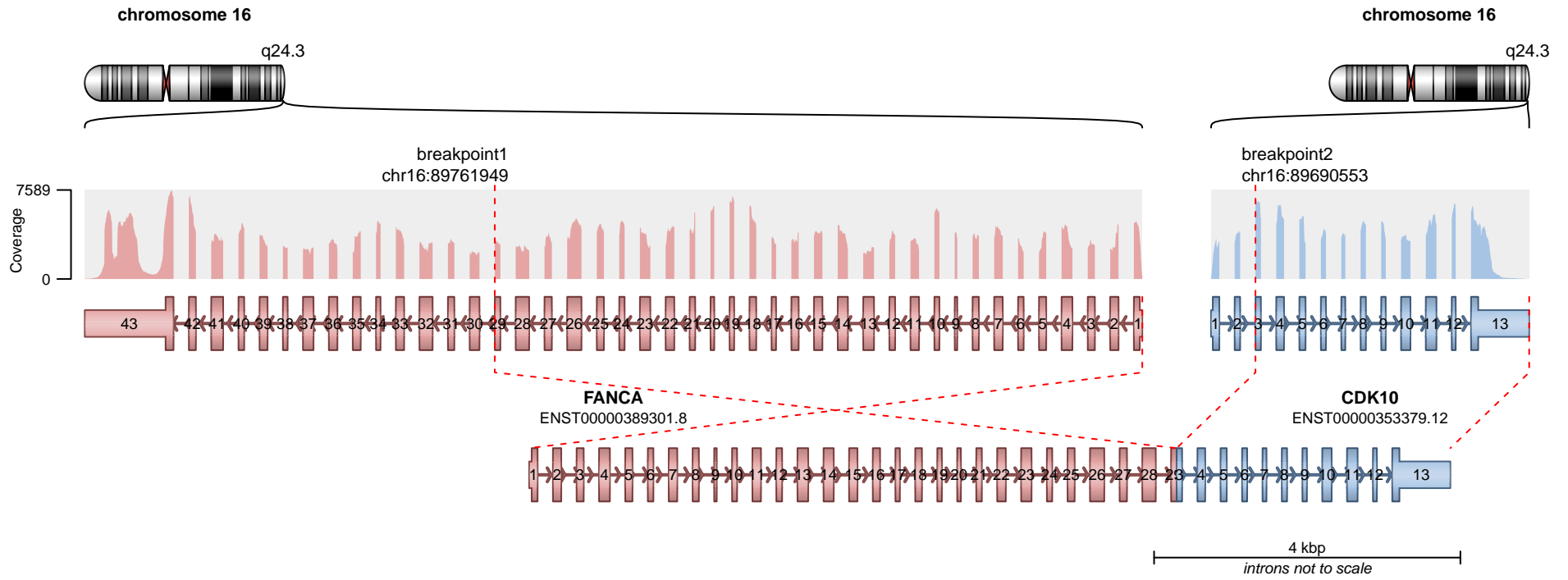
RETAINED PROTEIN DOMAINS
reading frame unclear



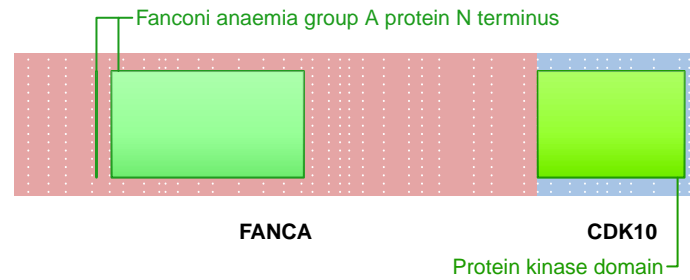
SUPPORTING READ COUNT

Split reads = 35
Discordant mates = 4

— translocation — deletion
— duplication — inversion



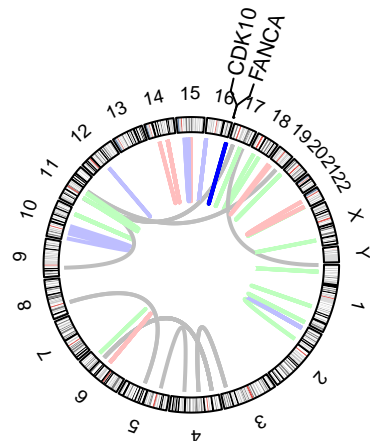
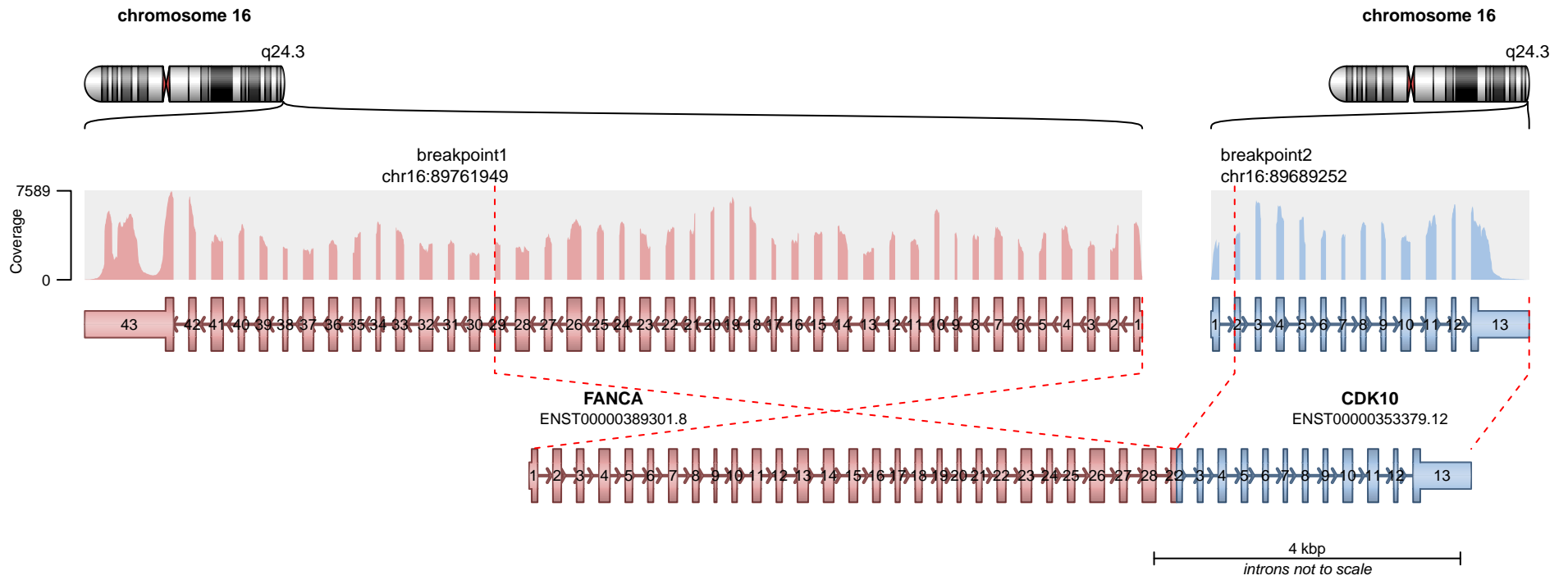
RETAINED PROTEIN DOMAINS
reading frame unclear



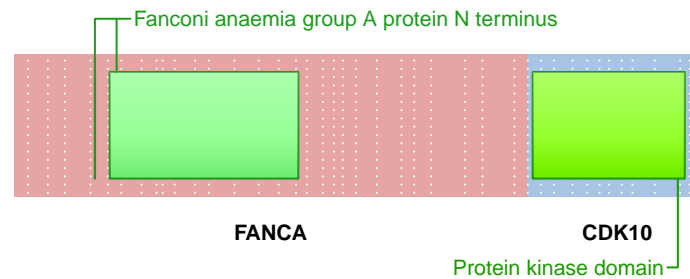
SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



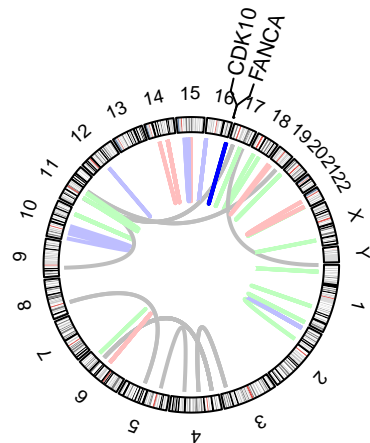
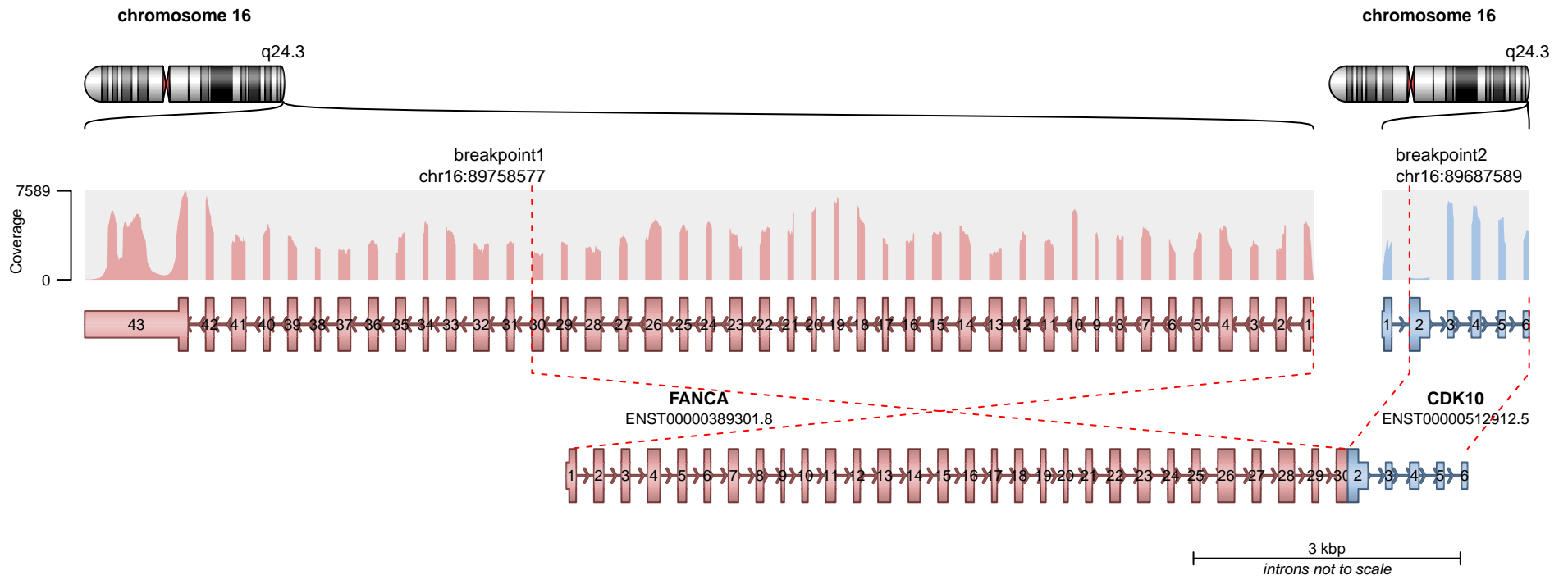
RETAINED PROTEIN DOMAINS
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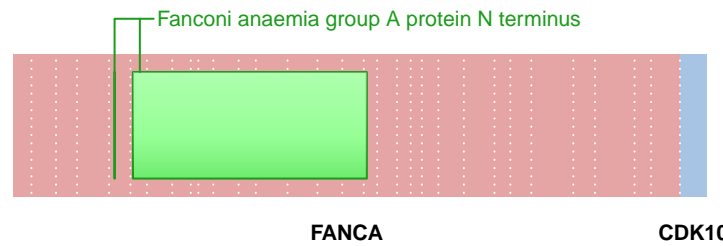
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



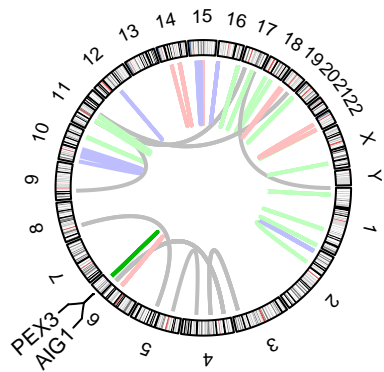
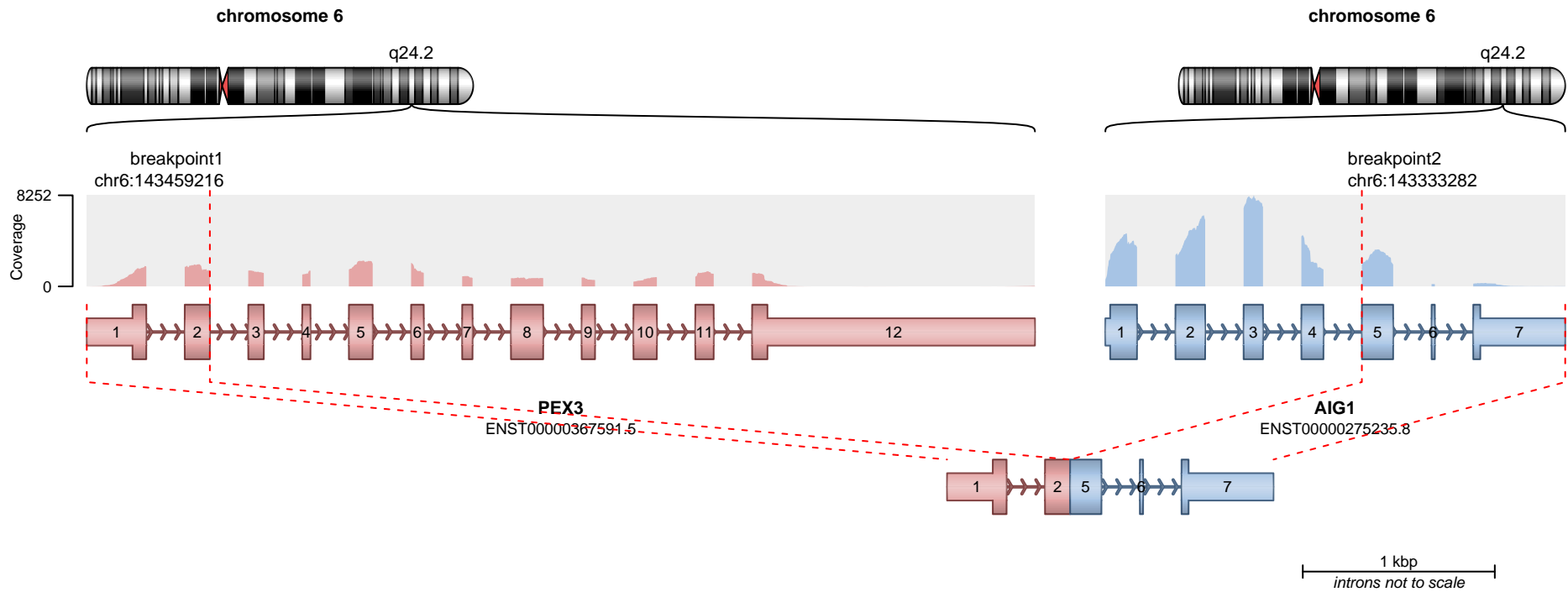
RETAINED PROTEIN DOMAINS
reading frame unclear



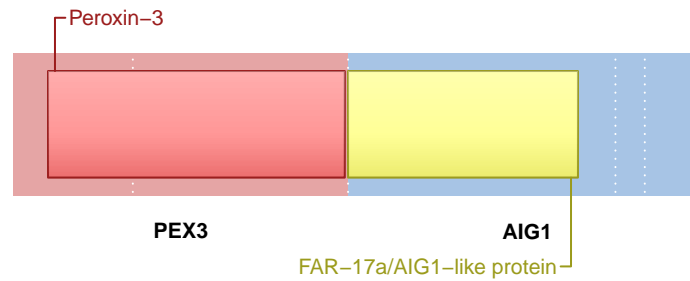
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 4

— translocation — deletion
— duplication — inversion



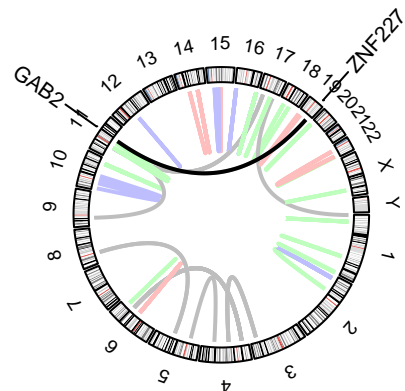
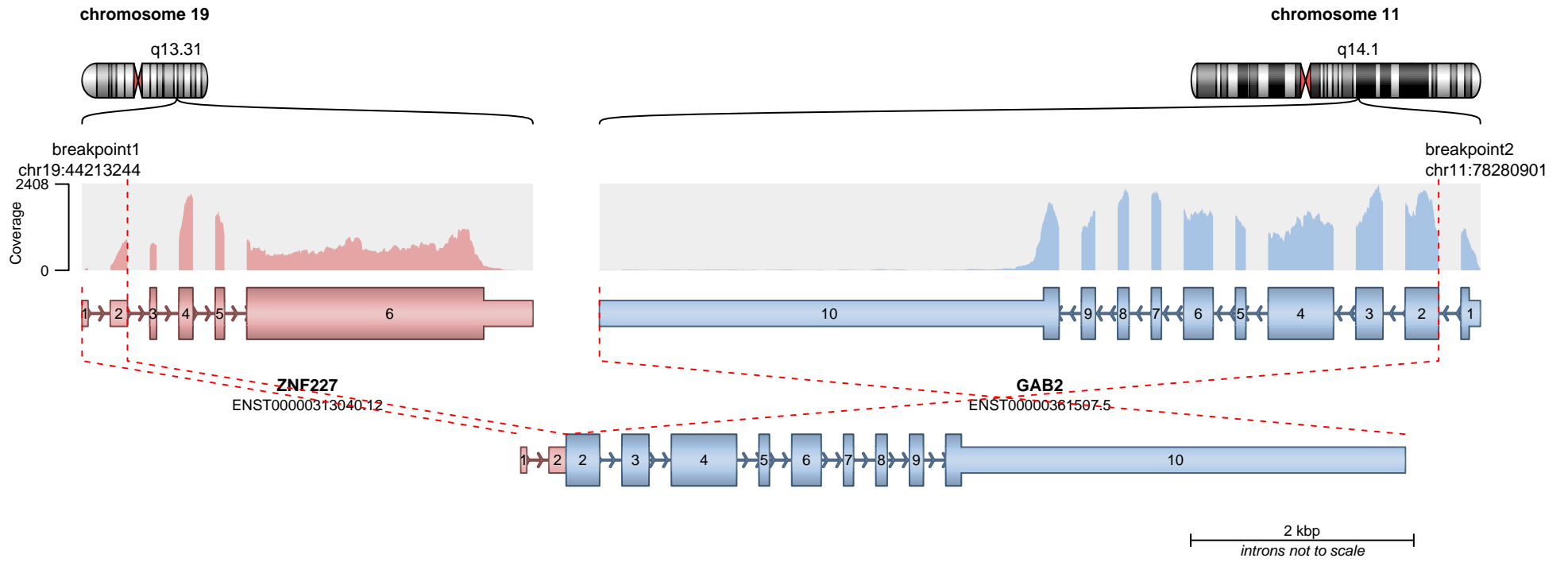
RETAINED PROTEIN DOMAINS
reading frame unclear



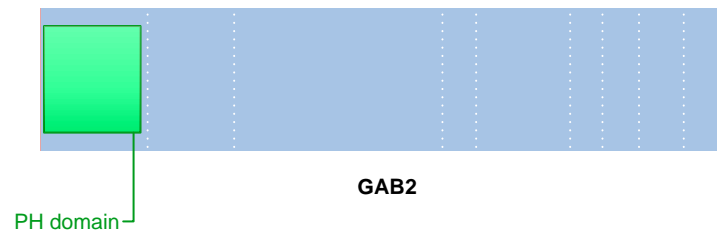
SUPPORTING READ COUNT

Split reads = 67
Discordant mates = 1

— translocation — deletion
— duplication — inversion



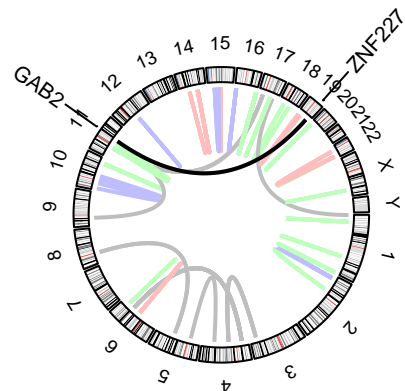
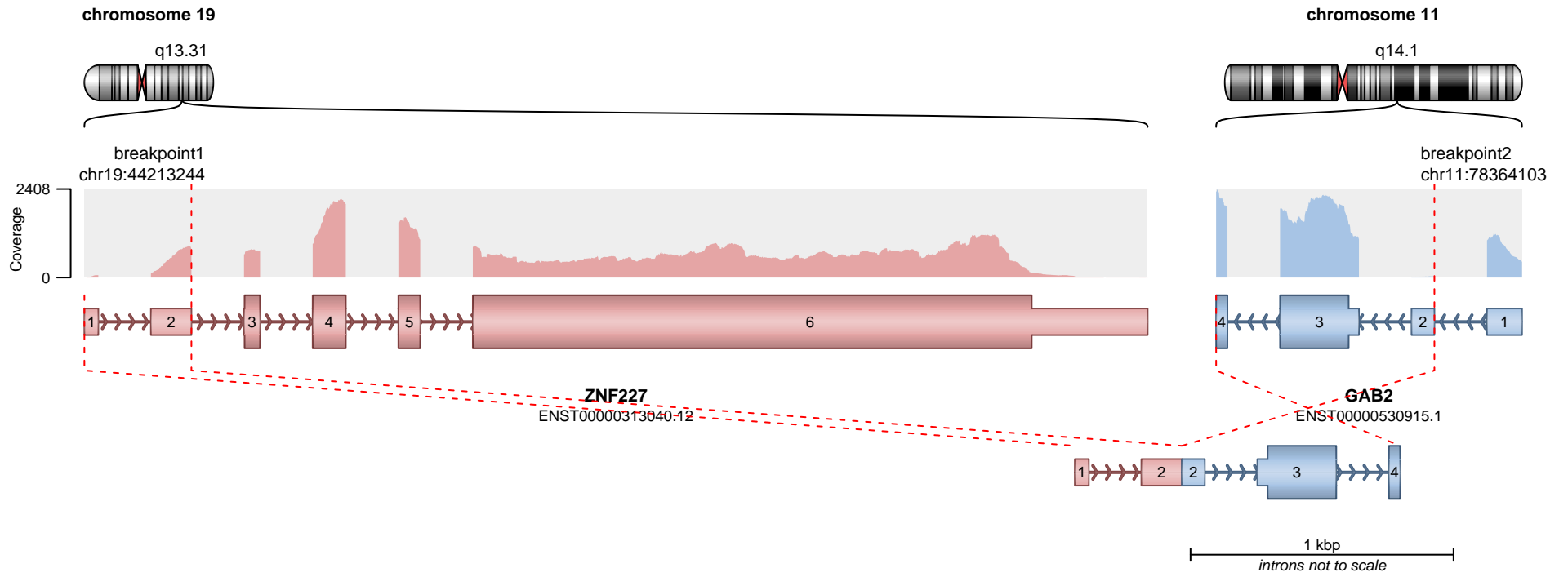
RETAINED PROTEIN DOMAINS
reading frame unclear



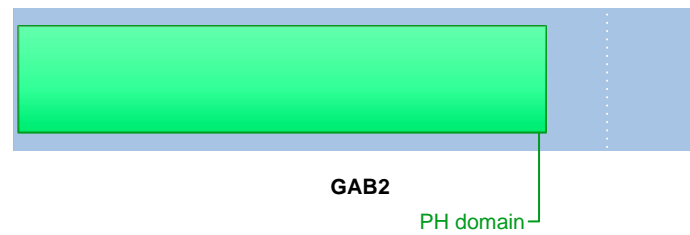
SUPPORTING READ COUNT

Split reads = 66
Discordant mates = 3

— translocation — deletion
— duplication — inversion



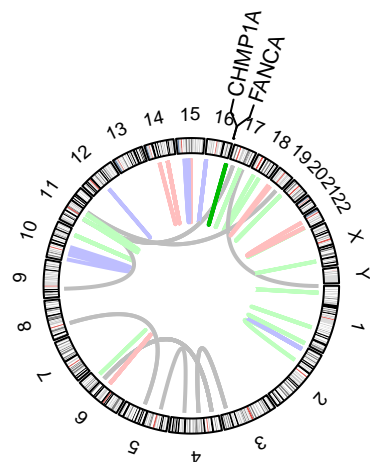
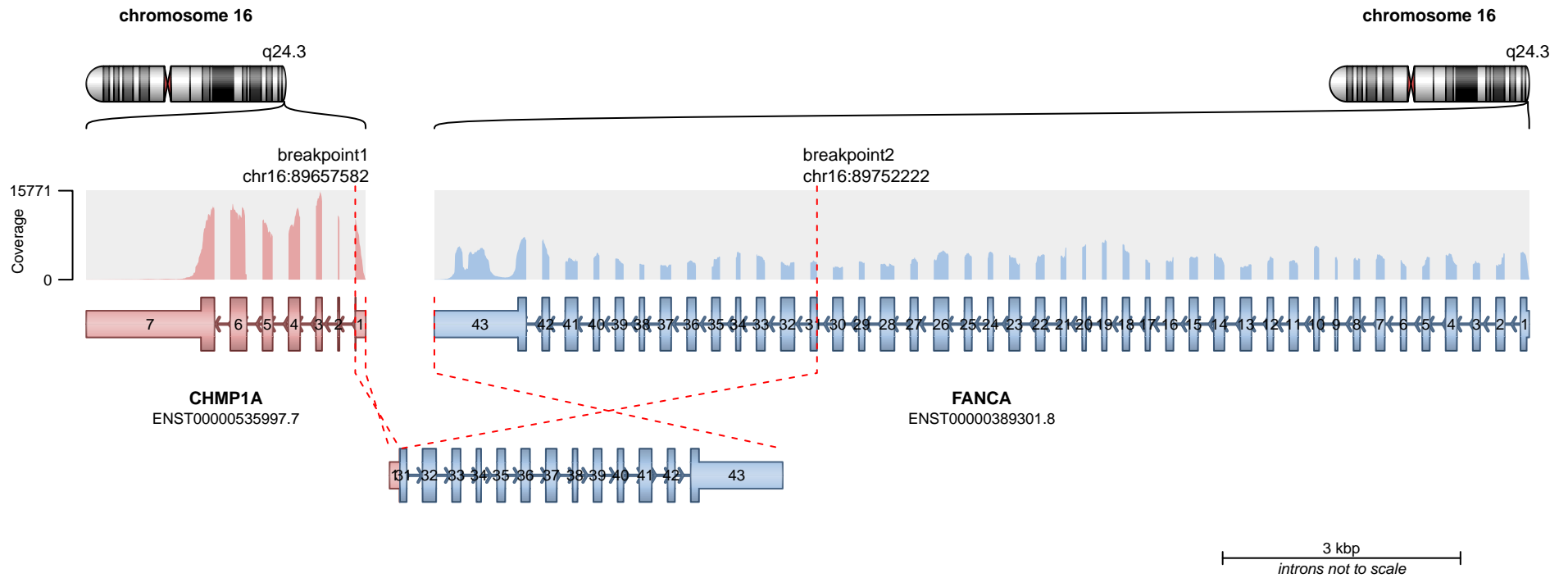
RETAINED PROTEIN DOMAINS
reading frame unclear



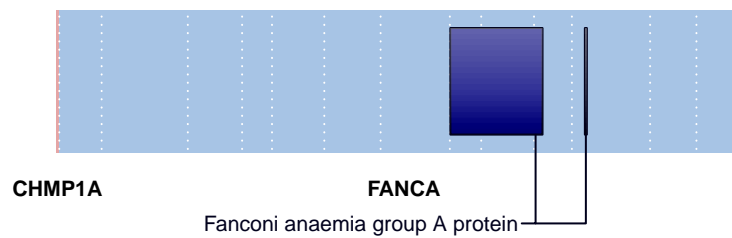
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 3

— translocation — deletion
— duplication — inversion



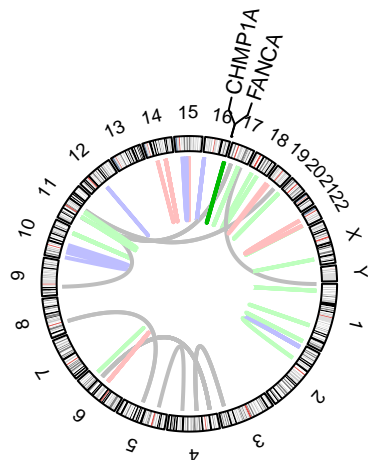
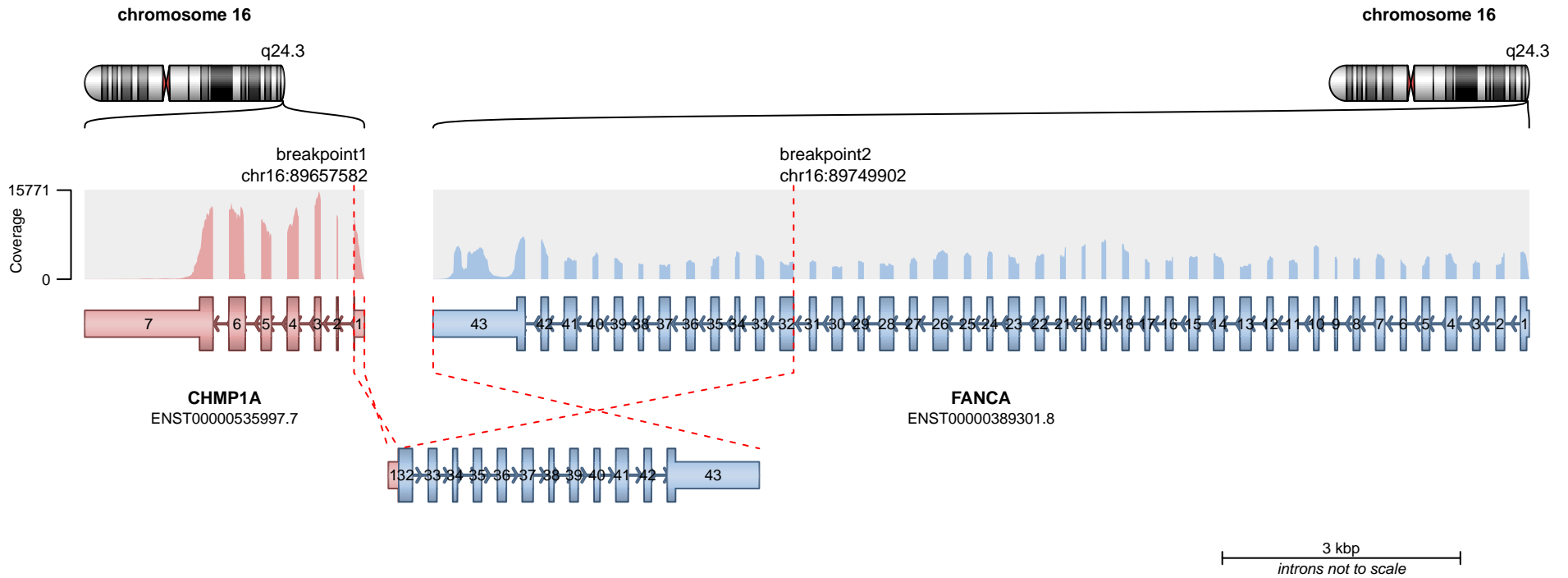
RETAINED PROTEIN DOMAINS
reading frame unclear



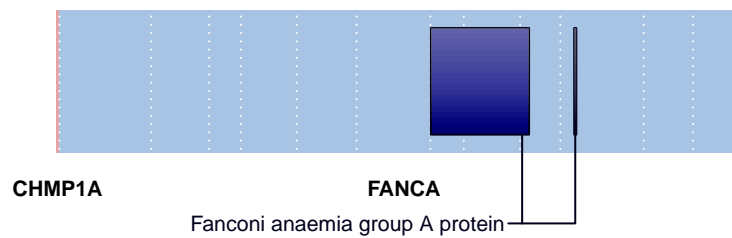
SUPPORTING READ COUNT

Split reads = 65
Discordant mates = 0

— translocation — deletion
— duplication — inversion



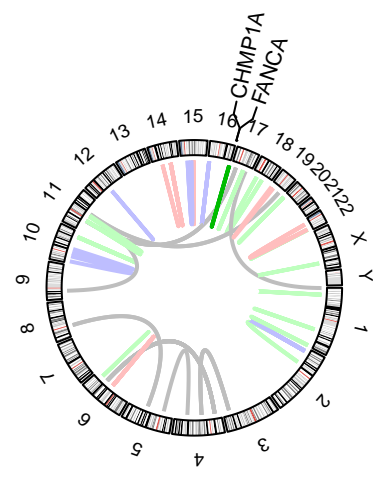
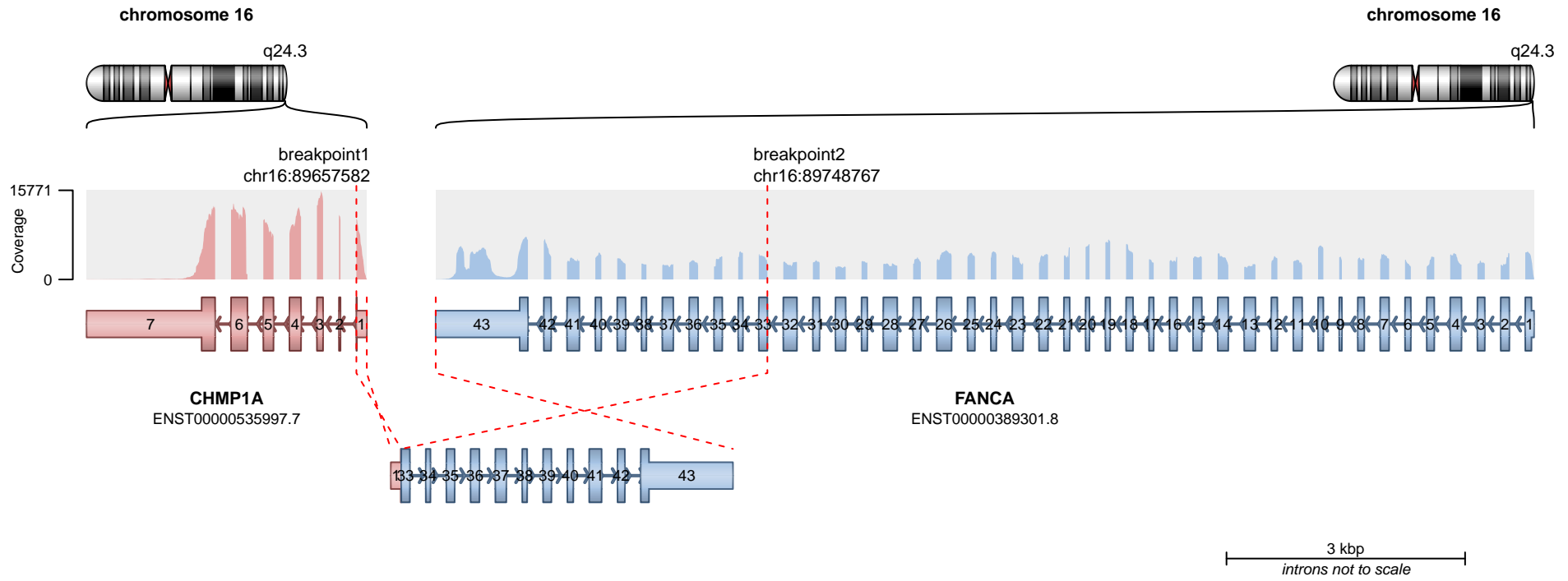
RETAINED PROTEIN DOMAINS
reading frame unclear



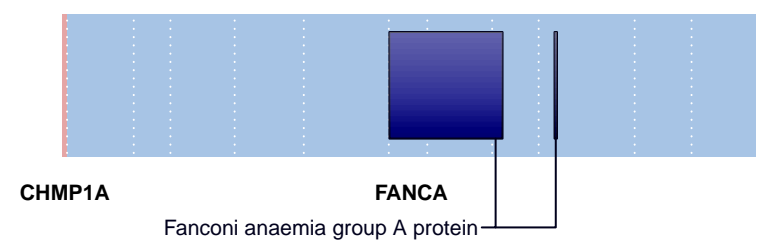
SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 0

— translocation — deletion
— duplication — inversion



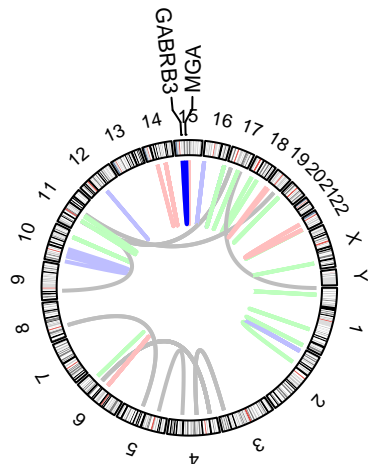
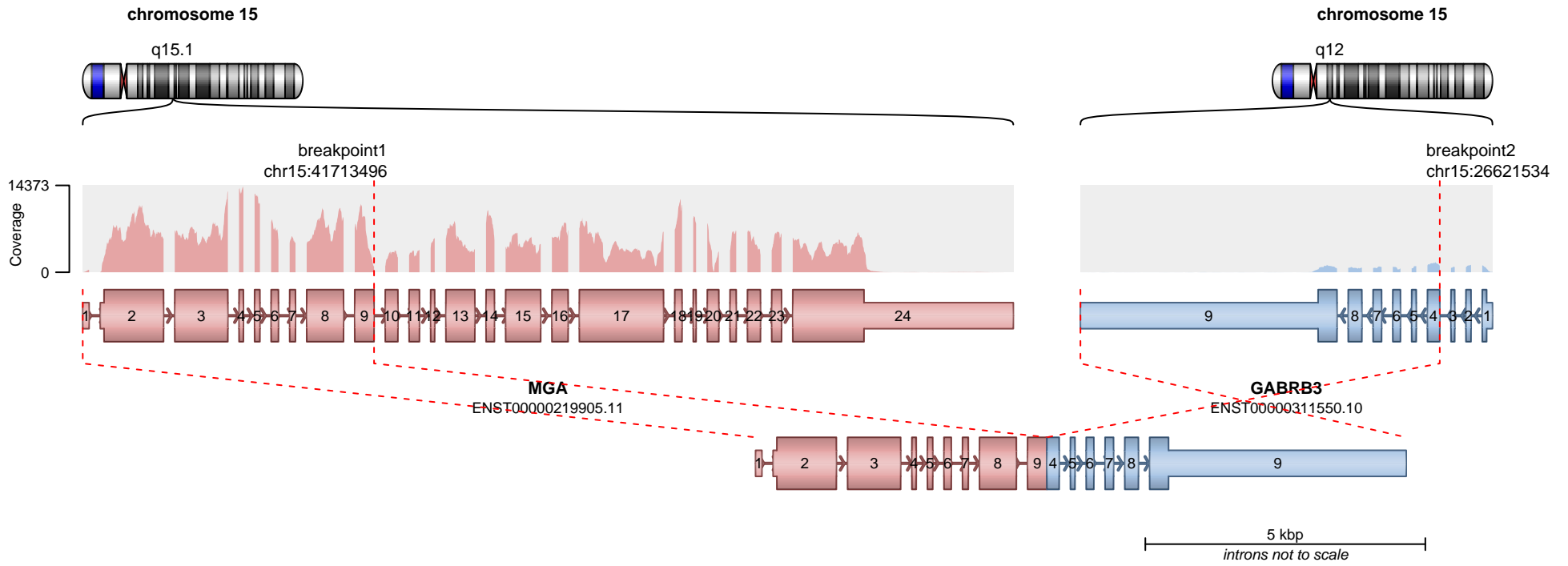
RETAINED PROTEIN DOMAINS
reading frame unclear



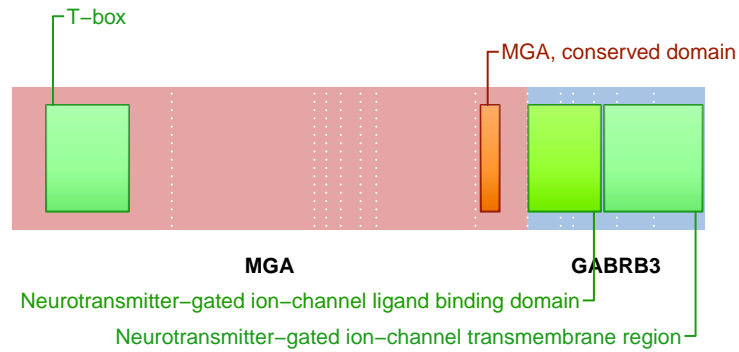
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



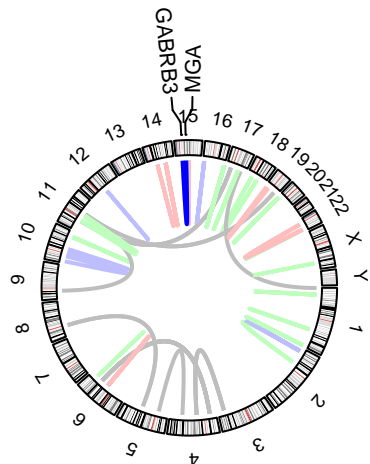
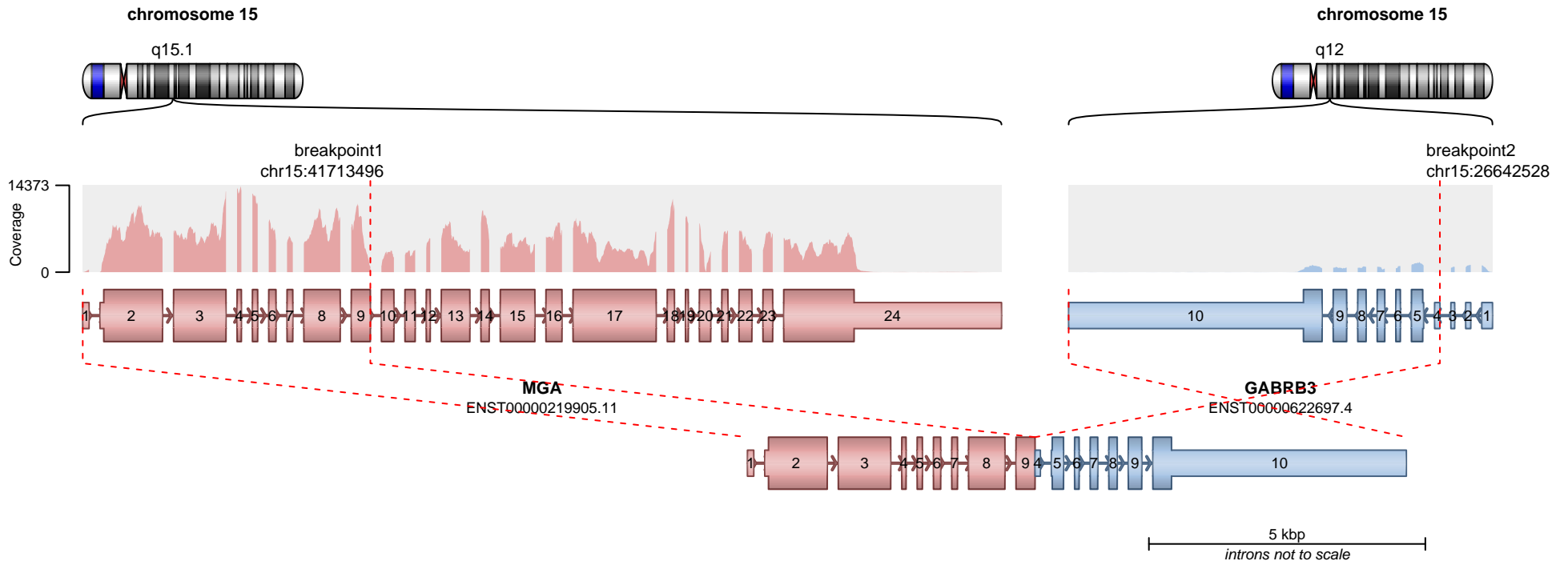
RETAINED PROTEIN DOMAINS
reading frame unclear



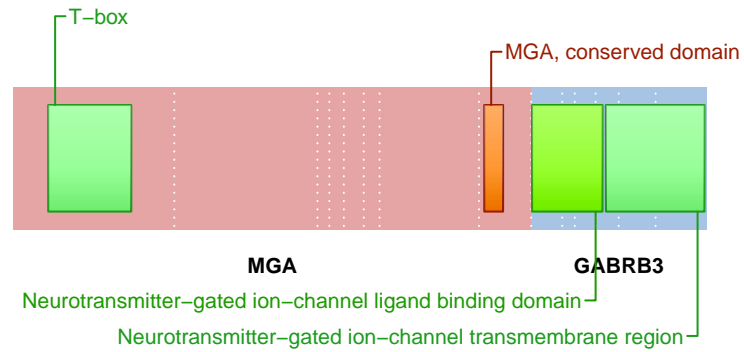
SUPPORTING READ COUNT

Split reads = 60
Discordant mates = 1

— translocation — deletion
— duplication — inversion



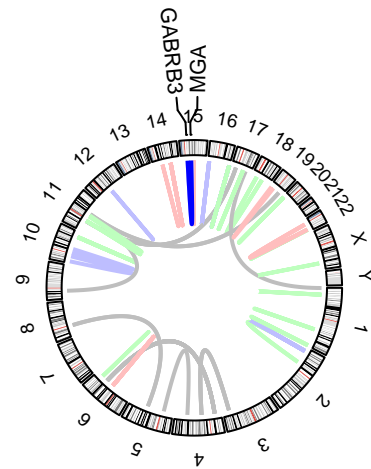
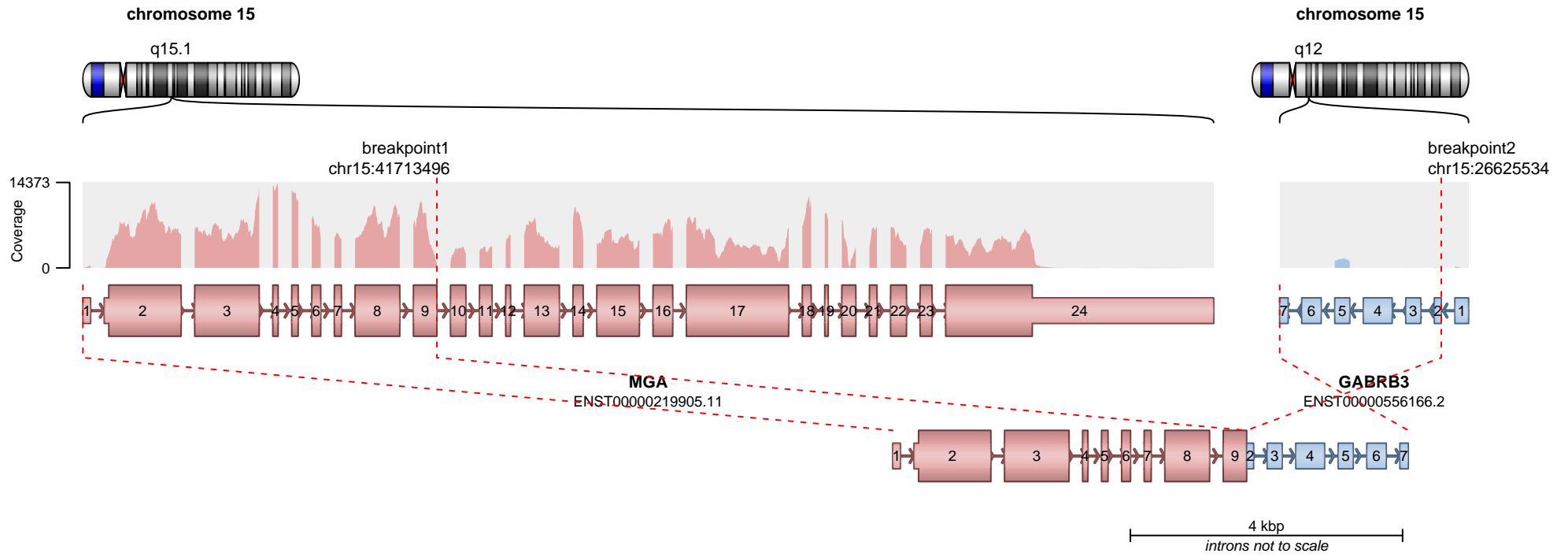
RETAINED PROTEIN DOMAINS
reading frame unclear



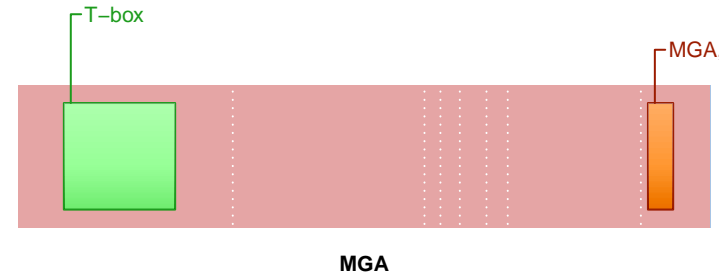
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 2

— translocation — deletion
— duplication — inversion



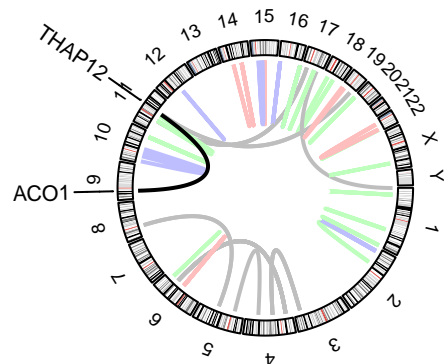
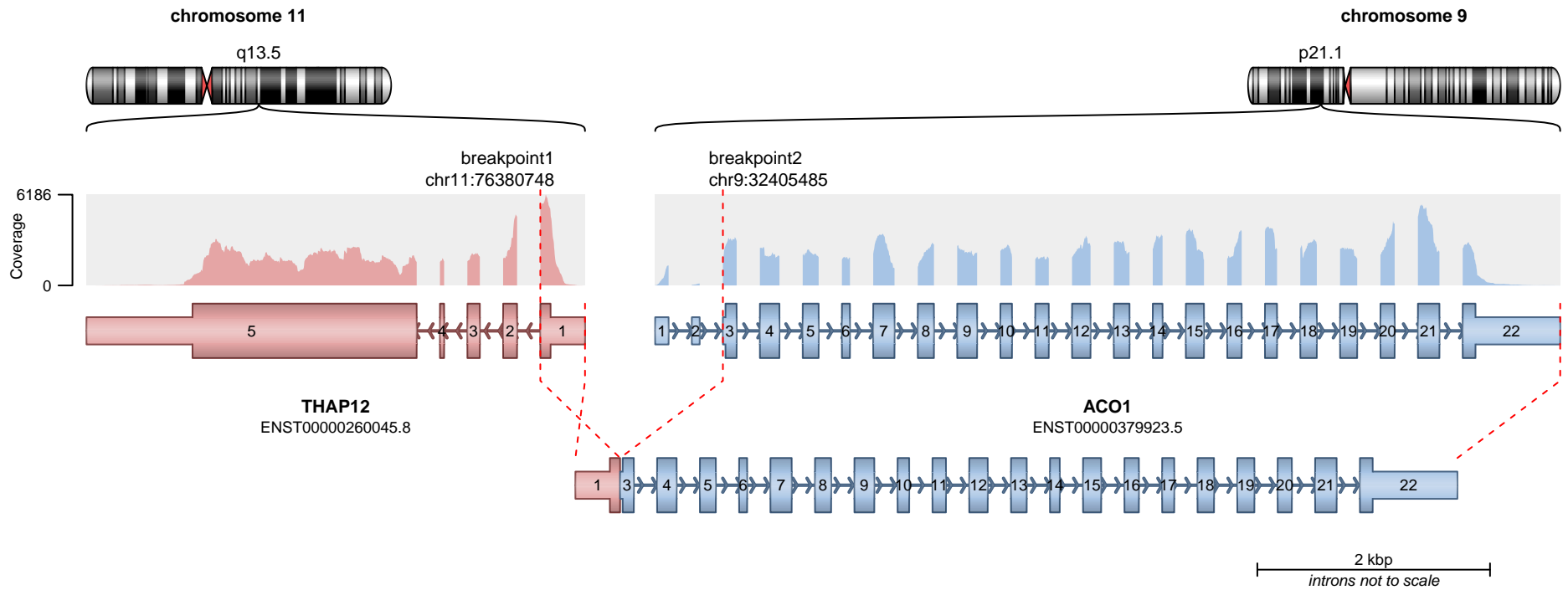
RETAINED PROTEIN DOMAINS
reading frame unclear



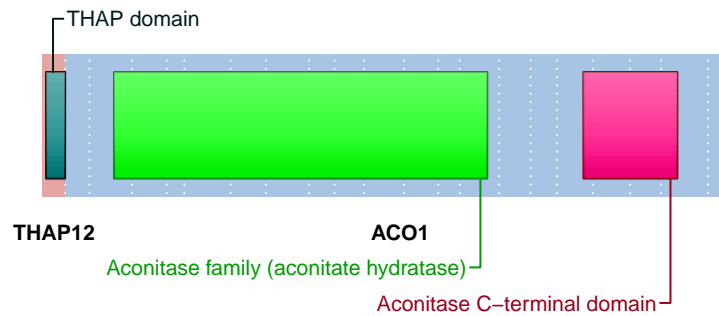
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



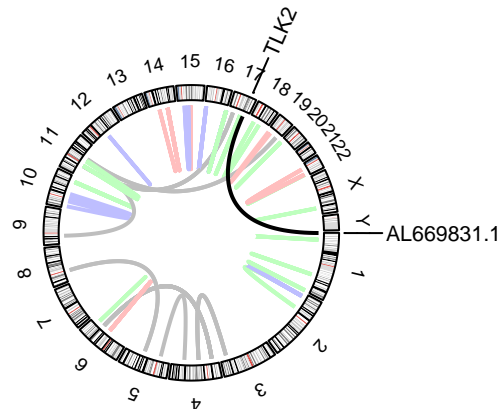
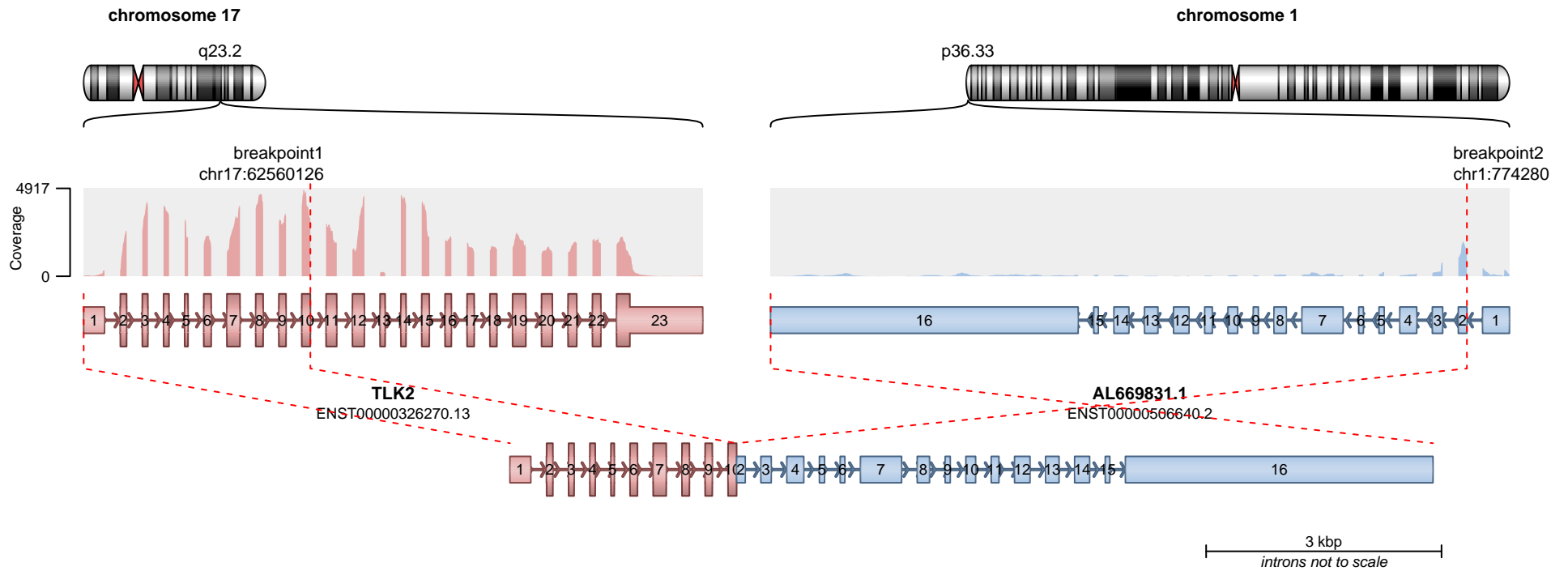
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 60
Discordant mates = 0

— translocation — deletion
— duplication — inversion

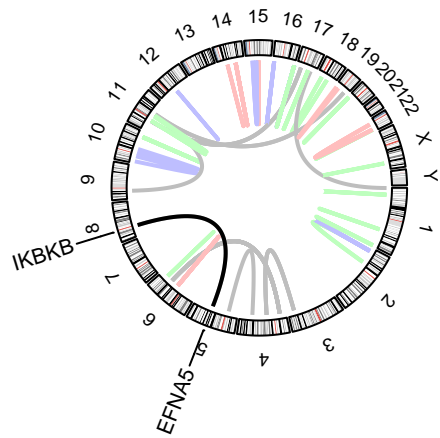
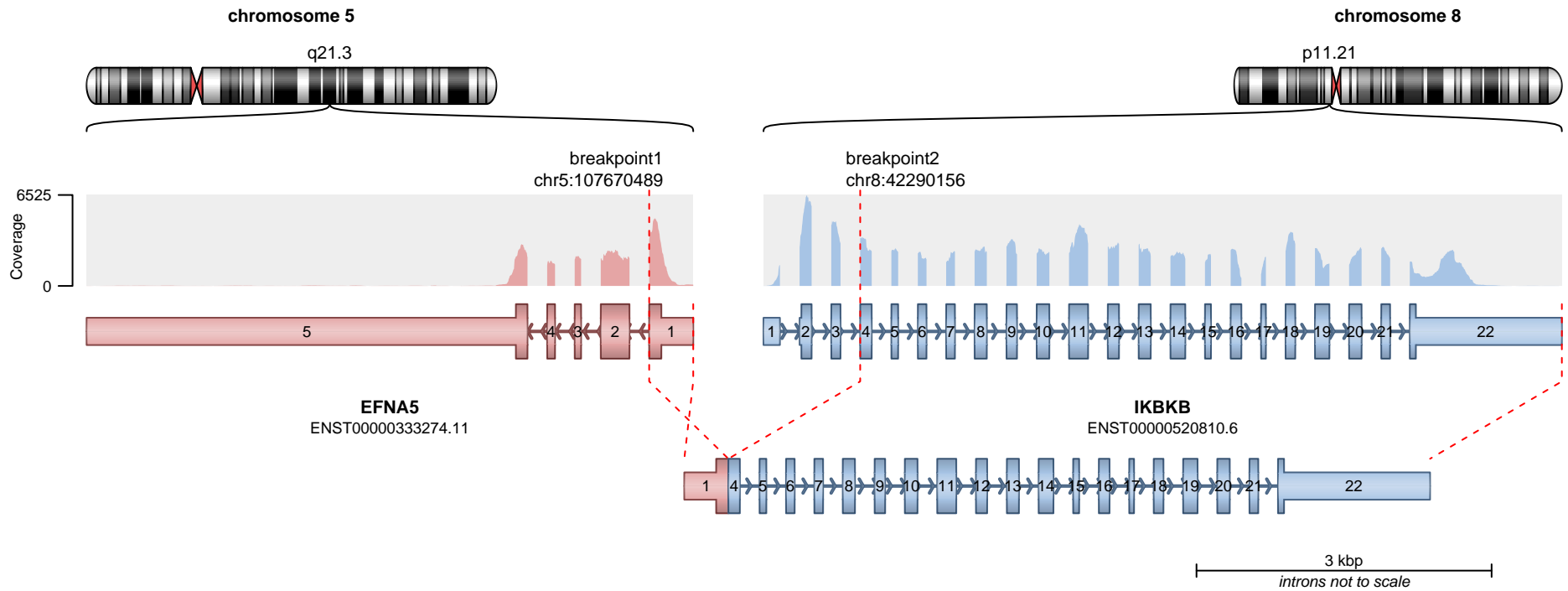


No protein domains retained in fusion.

SUPPORTING READ COUNT

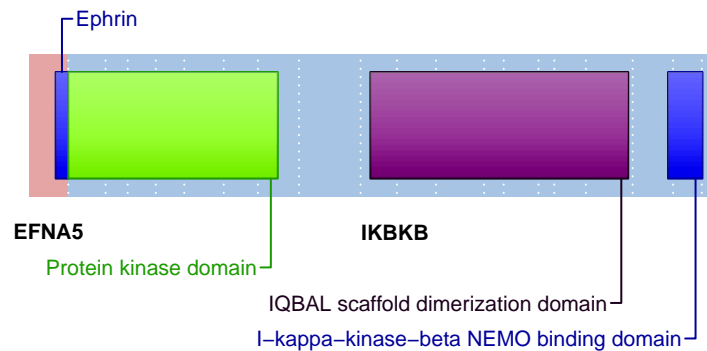
Split reads = 58
Discordant mates = 0

— translocation — deletion
— duplication — inversion



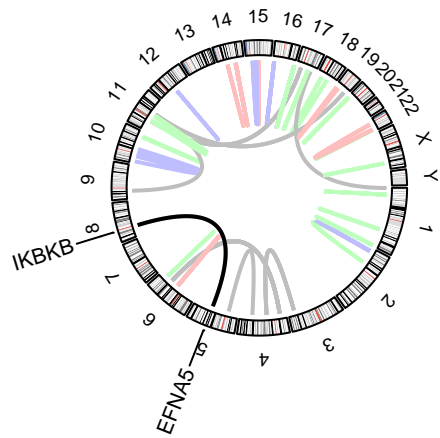
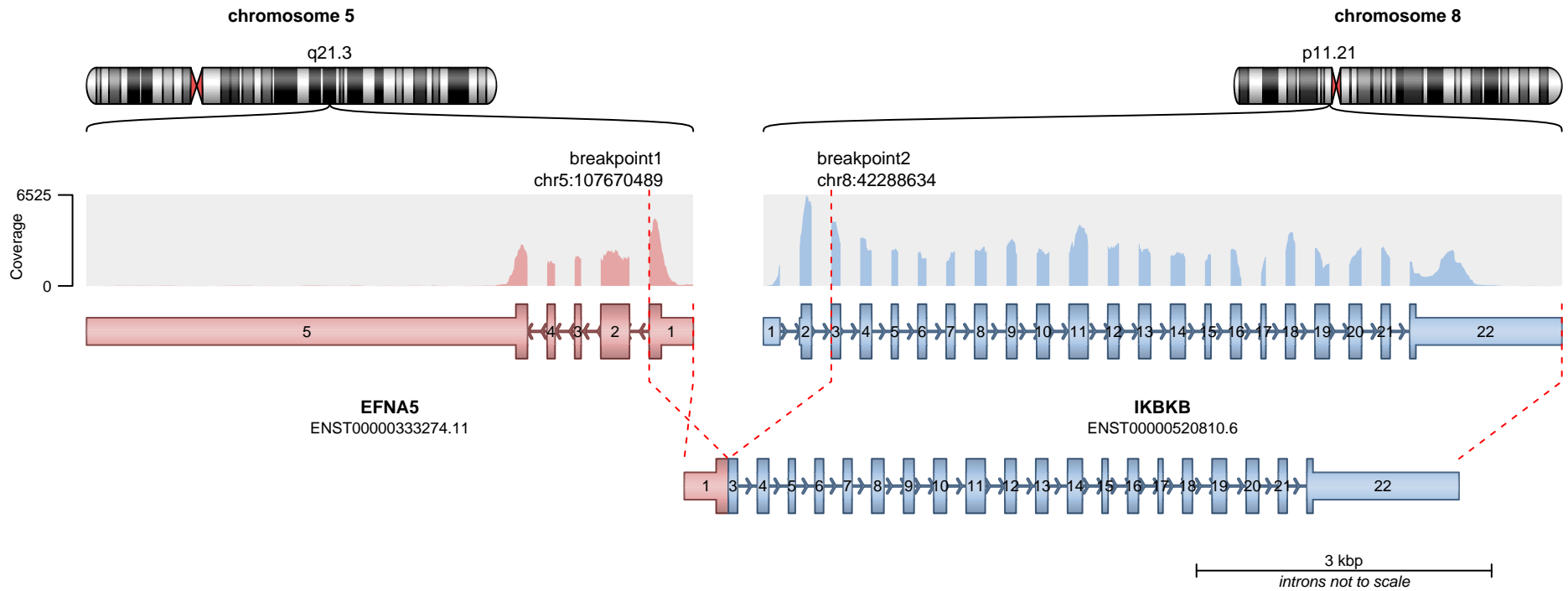
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



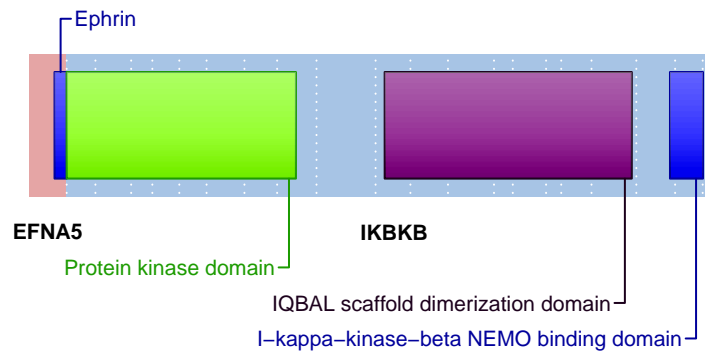
SUPPORTING READ COUNT

Split reads = 41
Discordant mates = 0



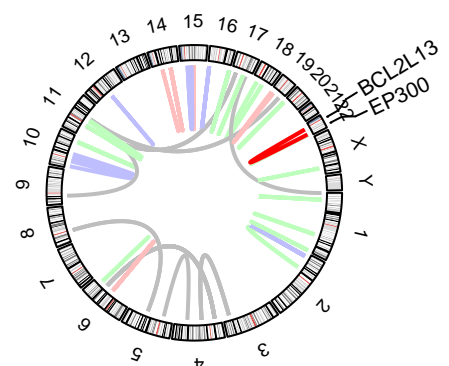
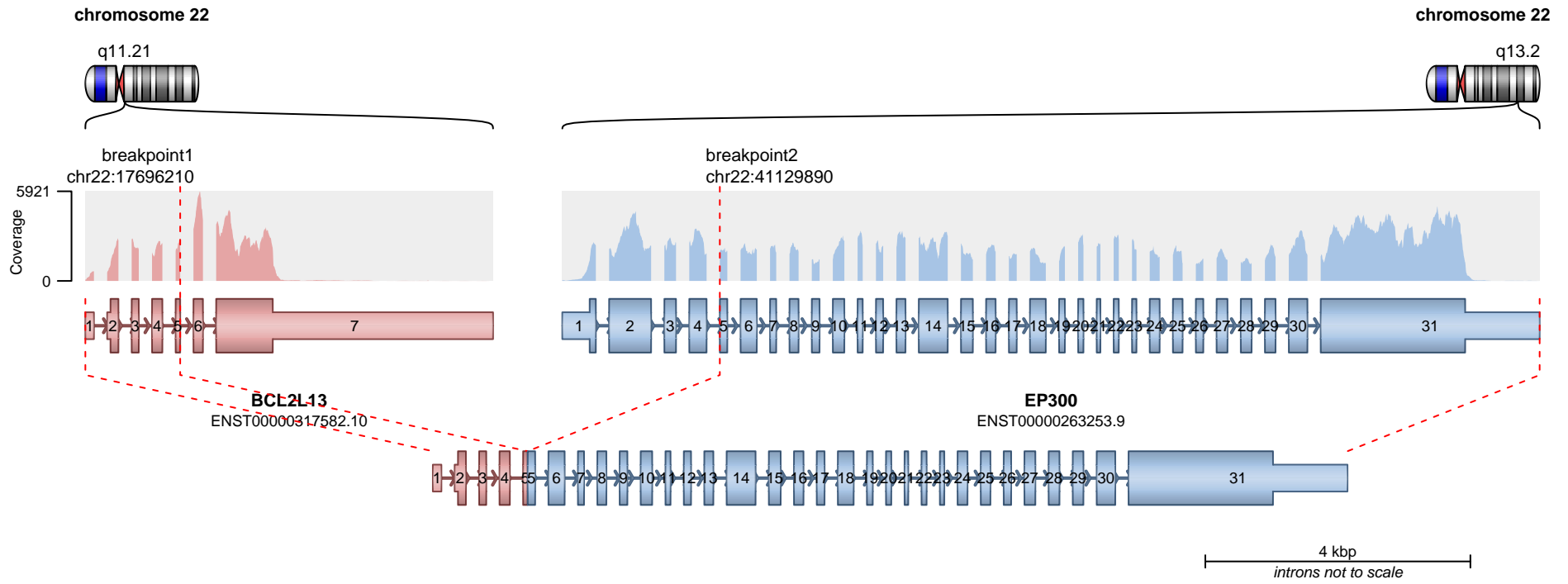
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



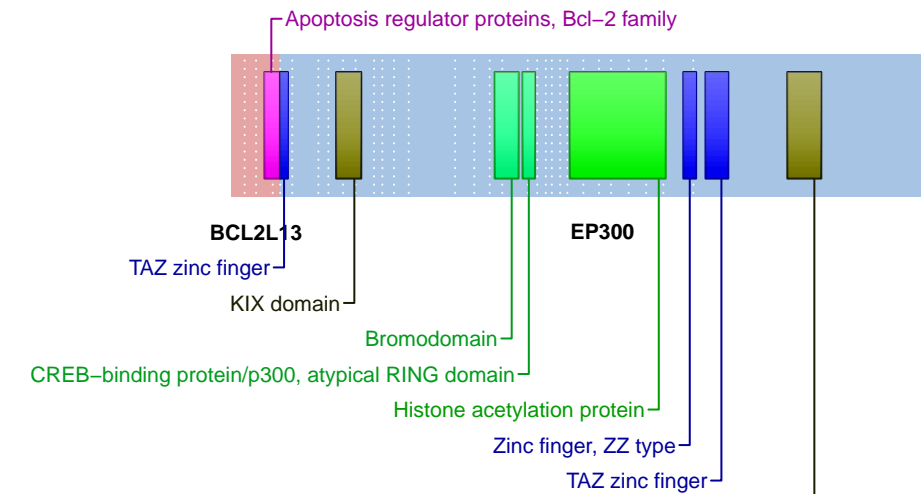
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 2



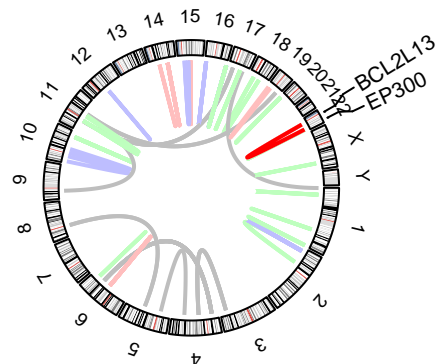
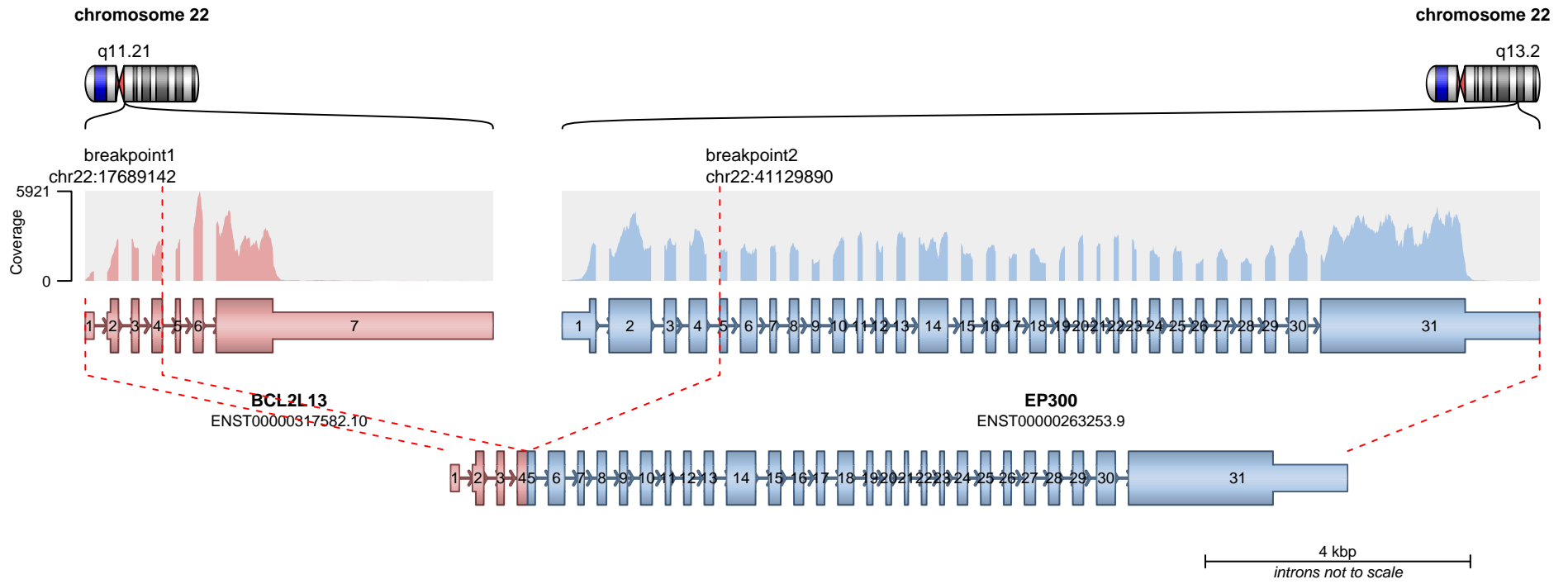
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



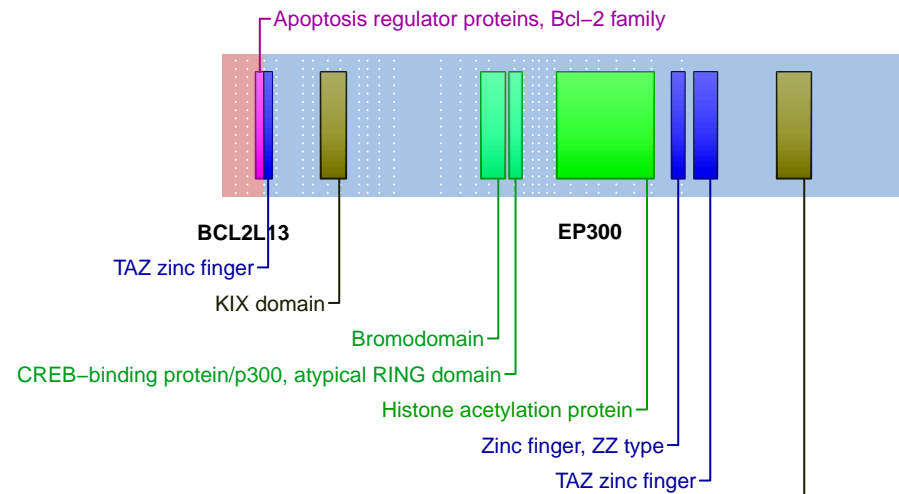
SUPPORTING READ COUNT

Split reads = 34
Discordant mates = 7



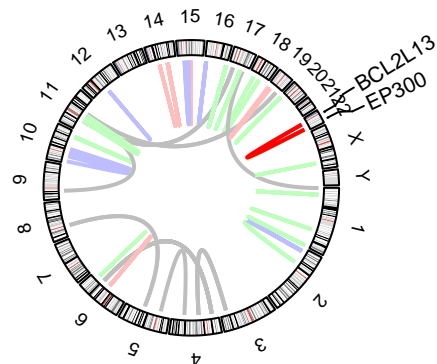
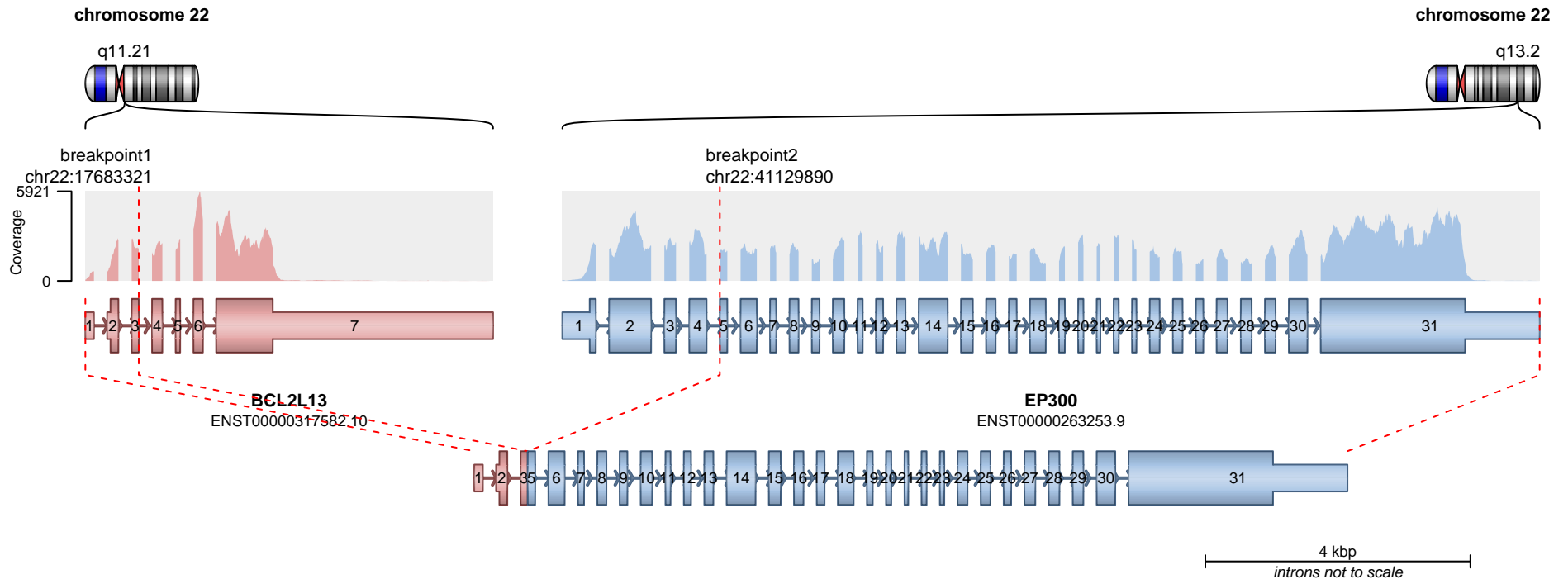
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



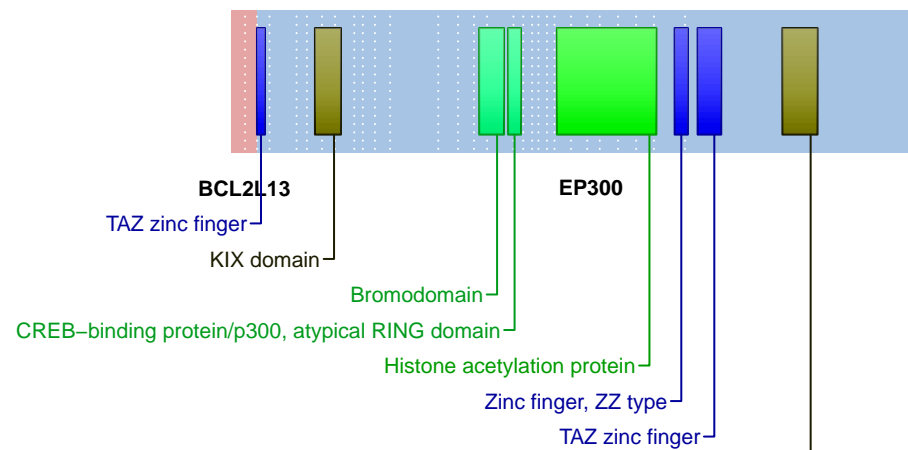
SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 1



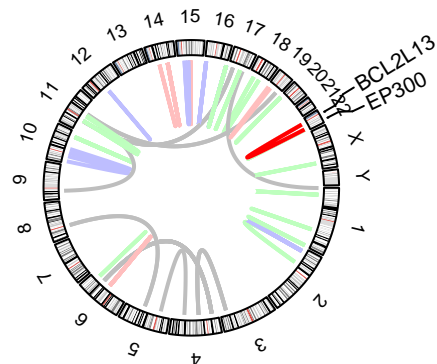
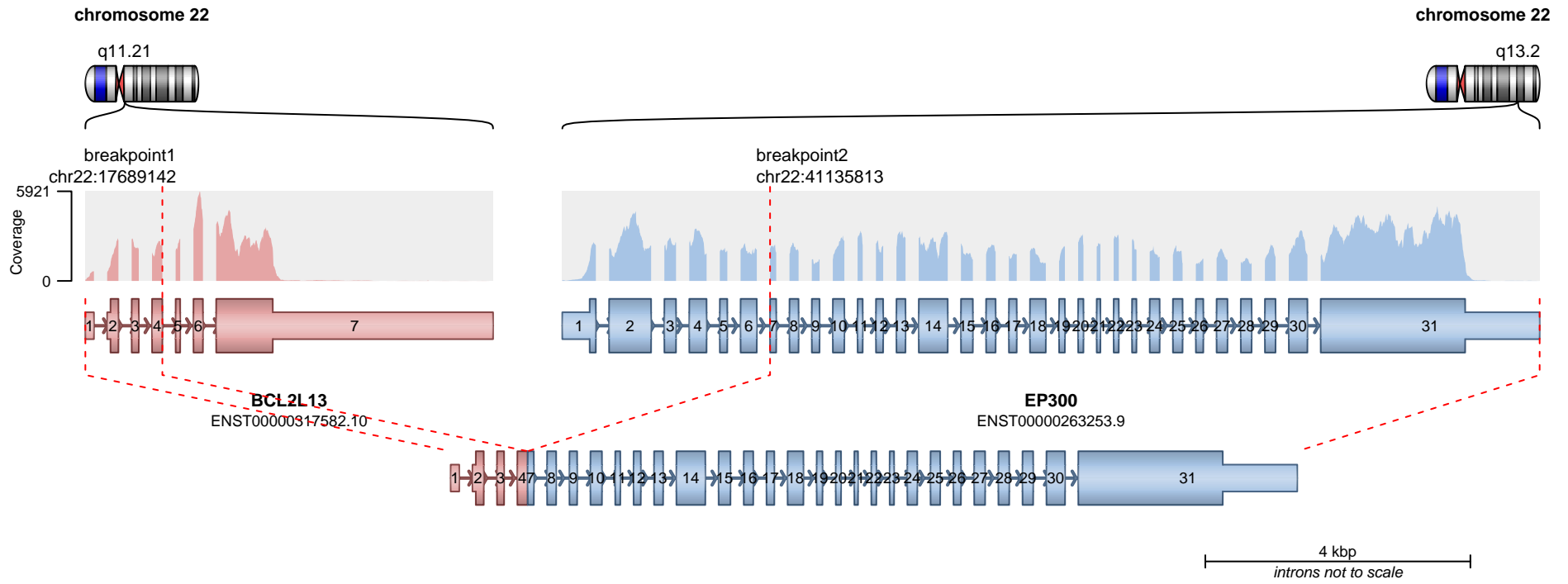
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



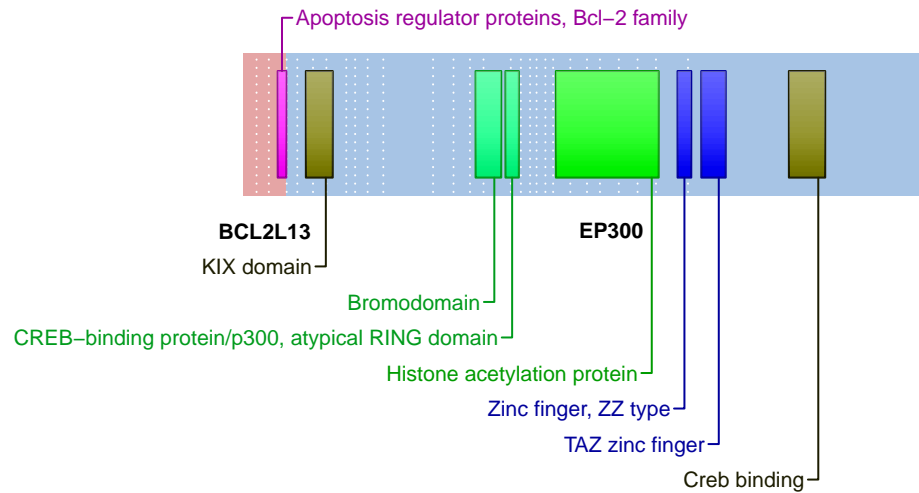
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



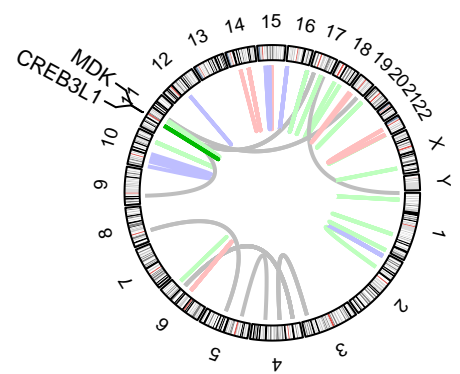
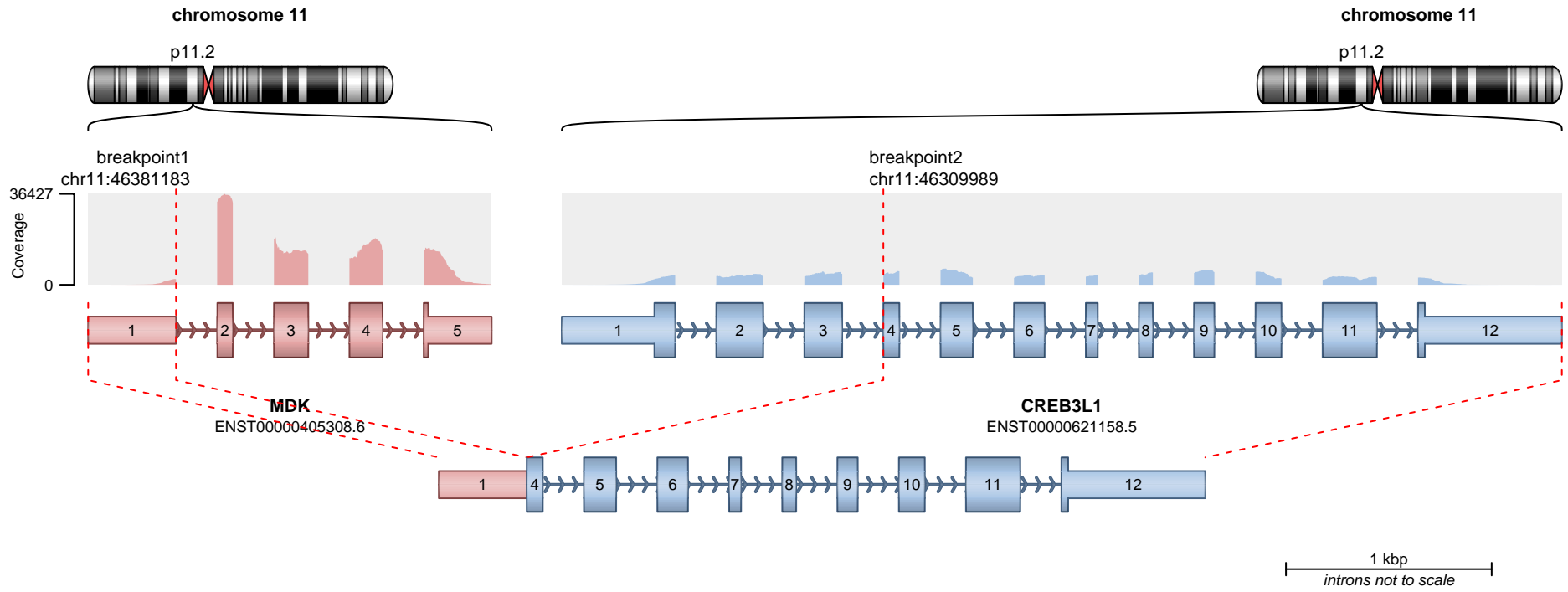
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



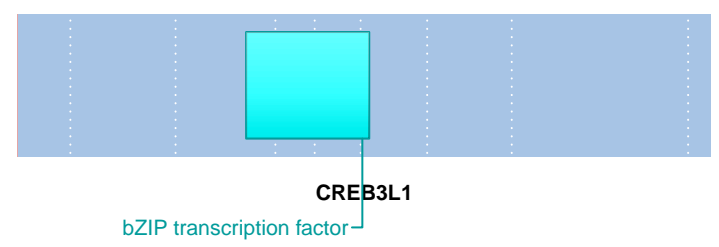
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



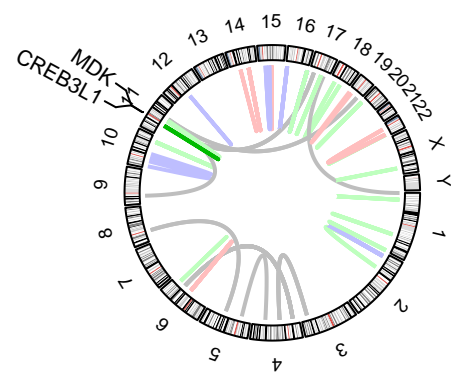
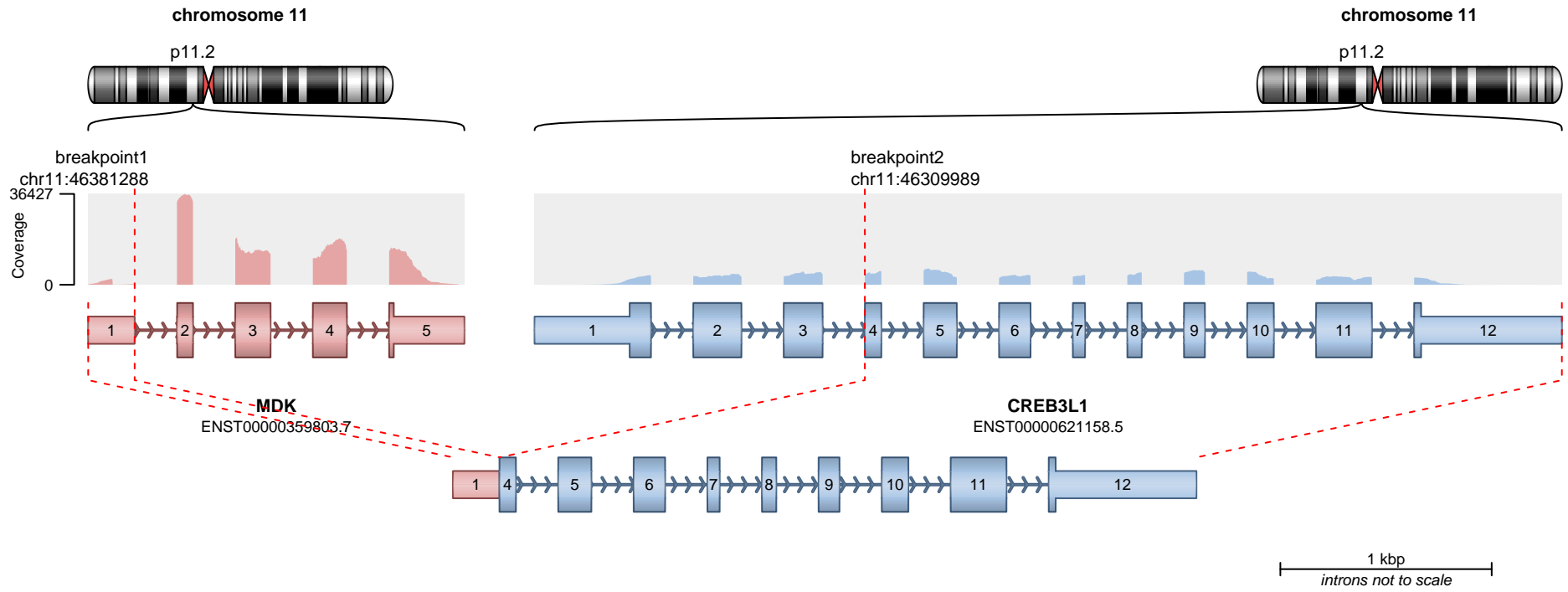
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



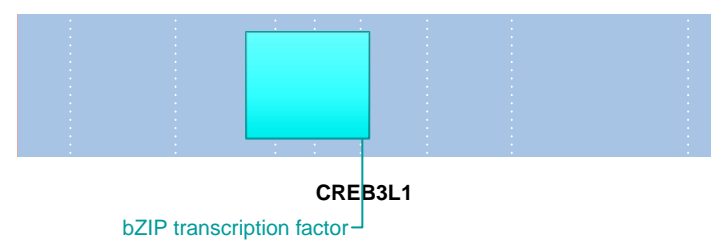
SUPPORTING READ COUNT

Split reads = 29
Discordant mates = 0



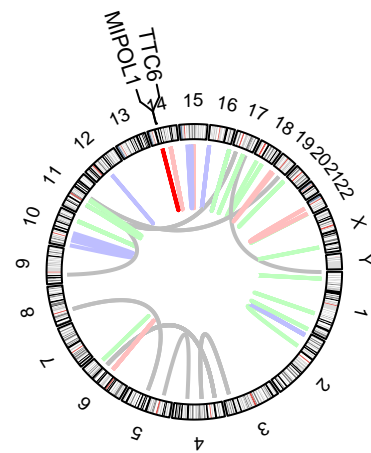
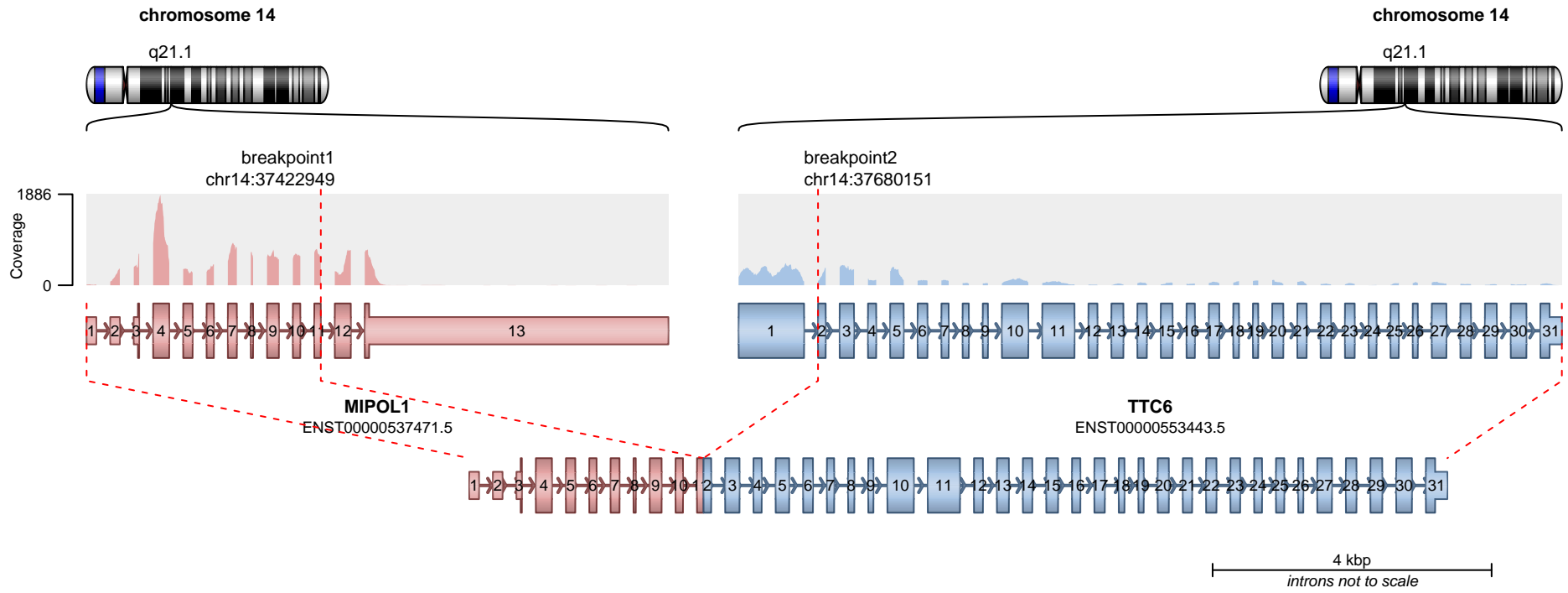
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



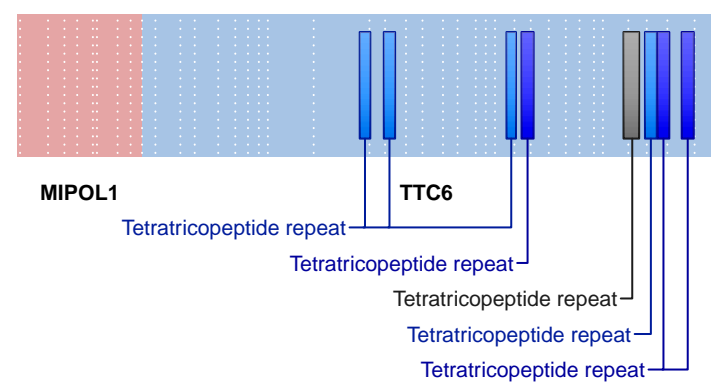
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0



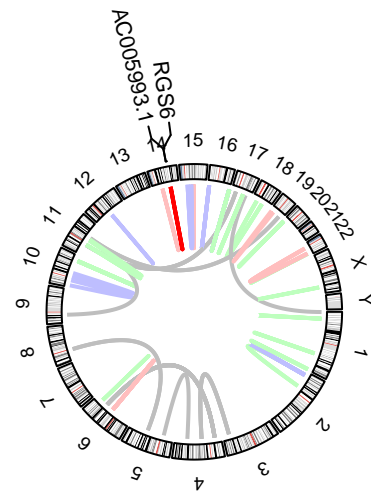
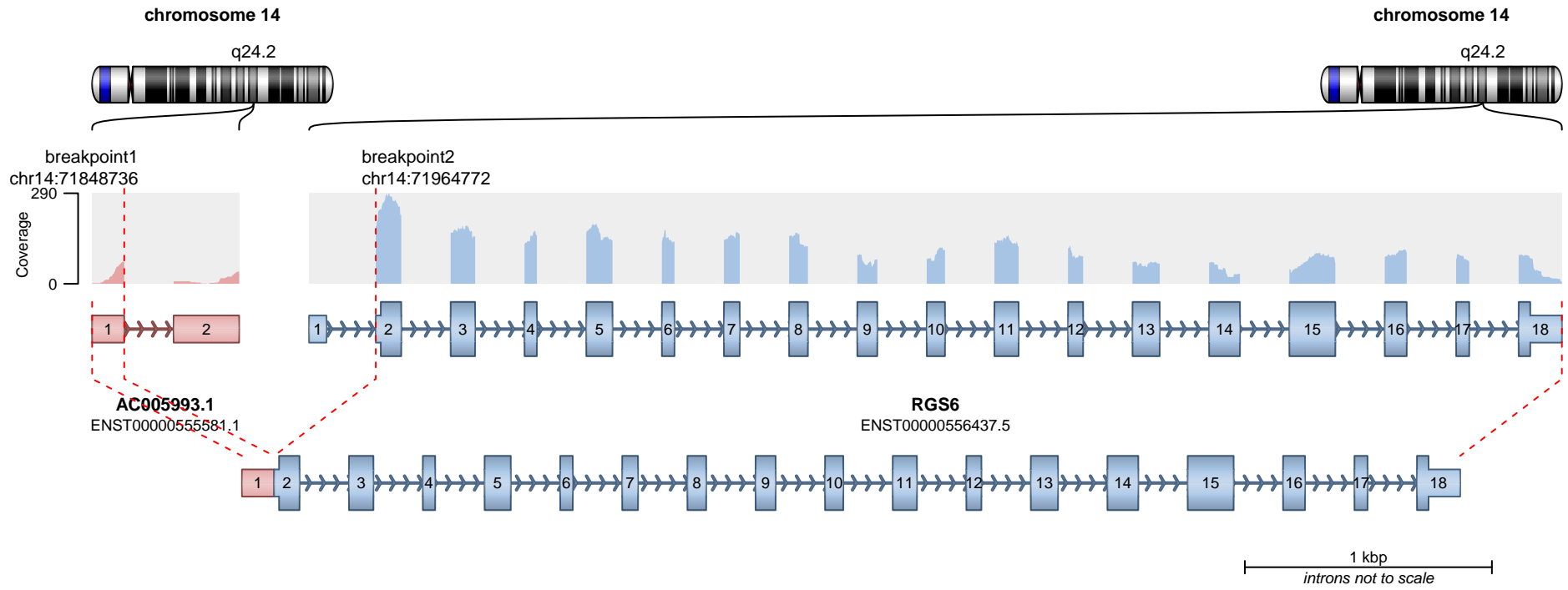
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear

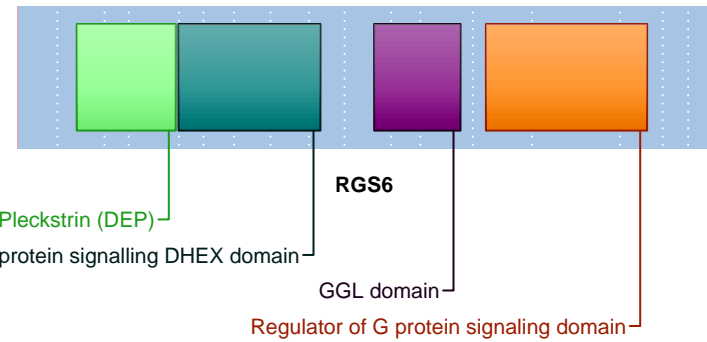


SUPPORTING READ COUNT

Split reads = 27
Discordant mates = 2



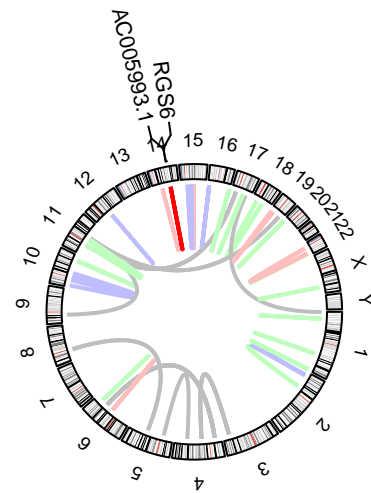
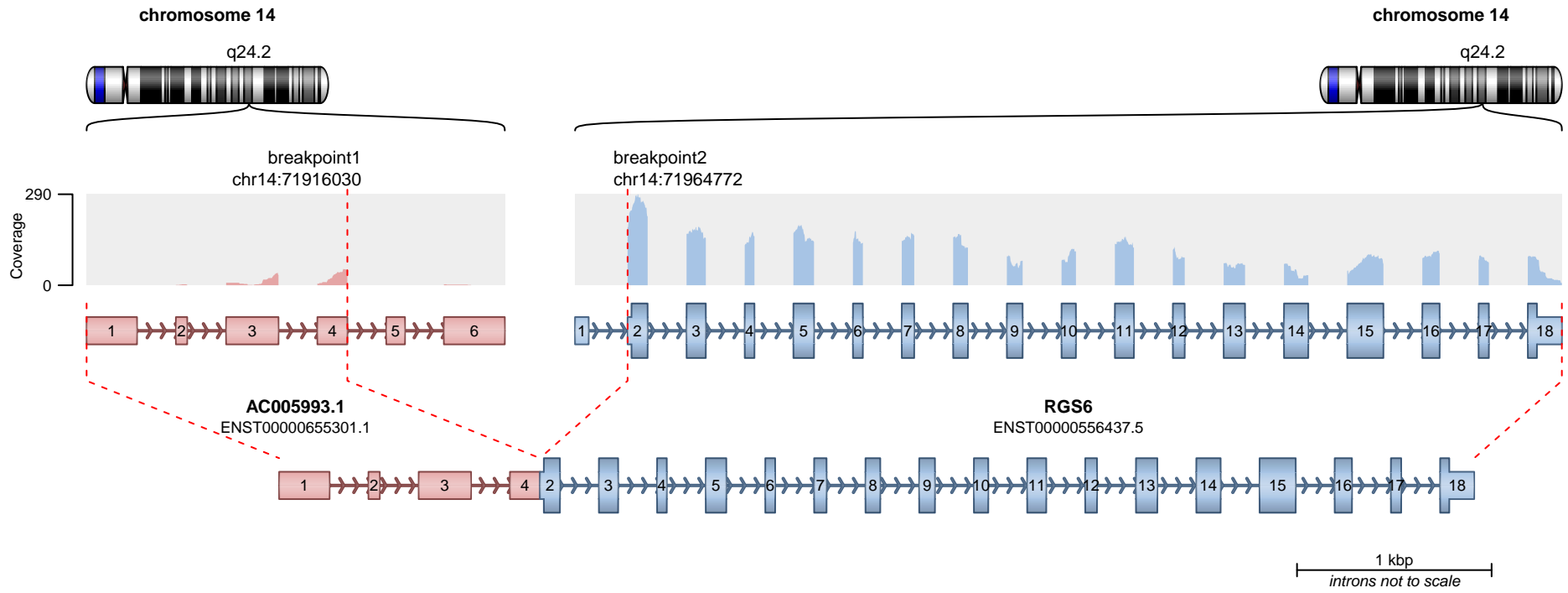
RETAINED PROTEIN DOMAINS
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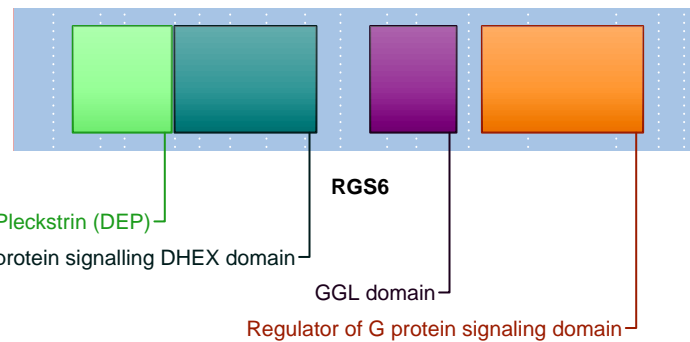
SUPPORTING READ COUNT

Split reads = 26
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



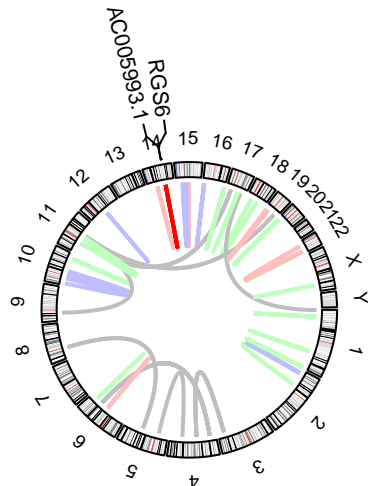
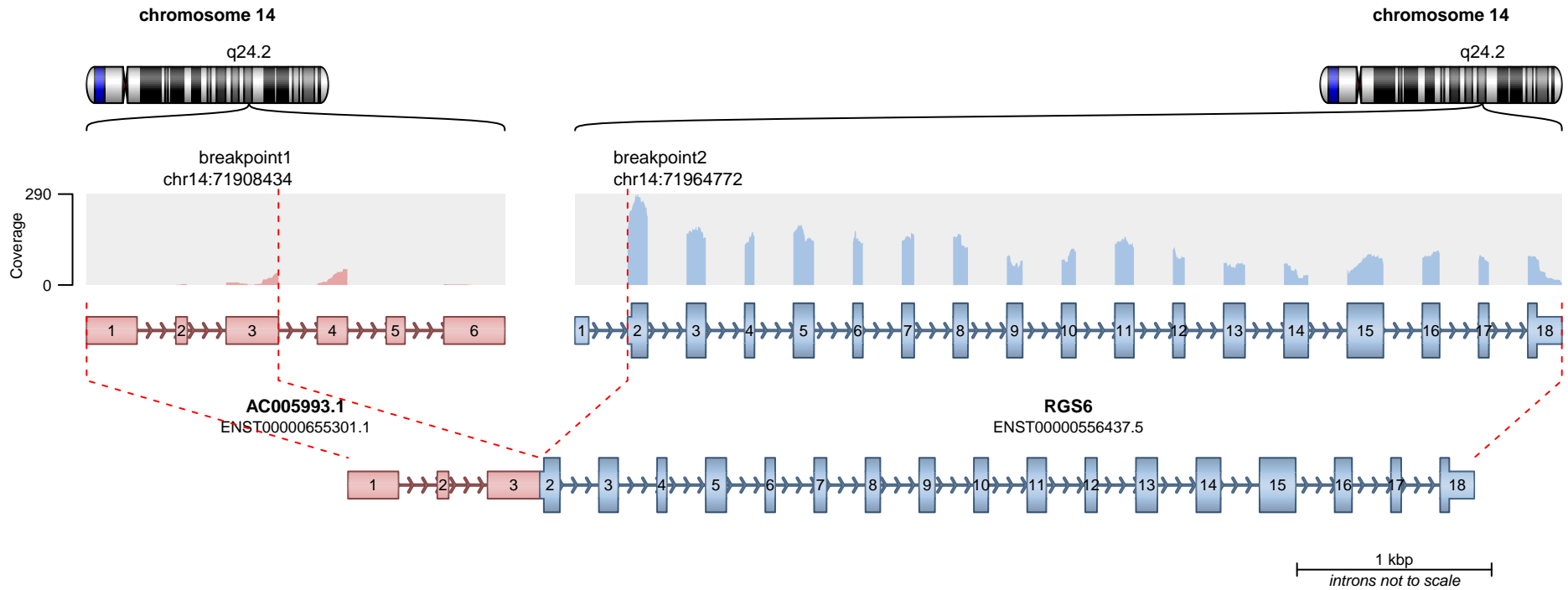
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 22
Discordant mates = 2

- translocation
- duplication
- deletion
- inversion



Domain found in Dishevelled, Egl-10, and Pleckstrin (DEP)

Regulator of G-protein signalling DHEX domain

RGS6

GGL domain

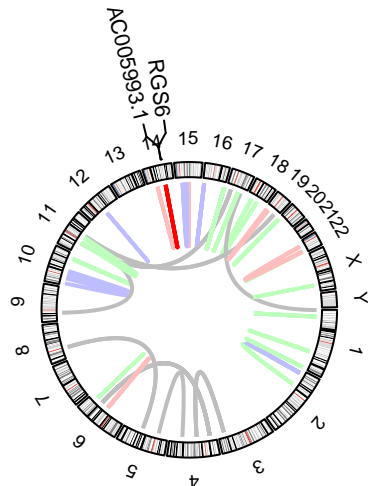
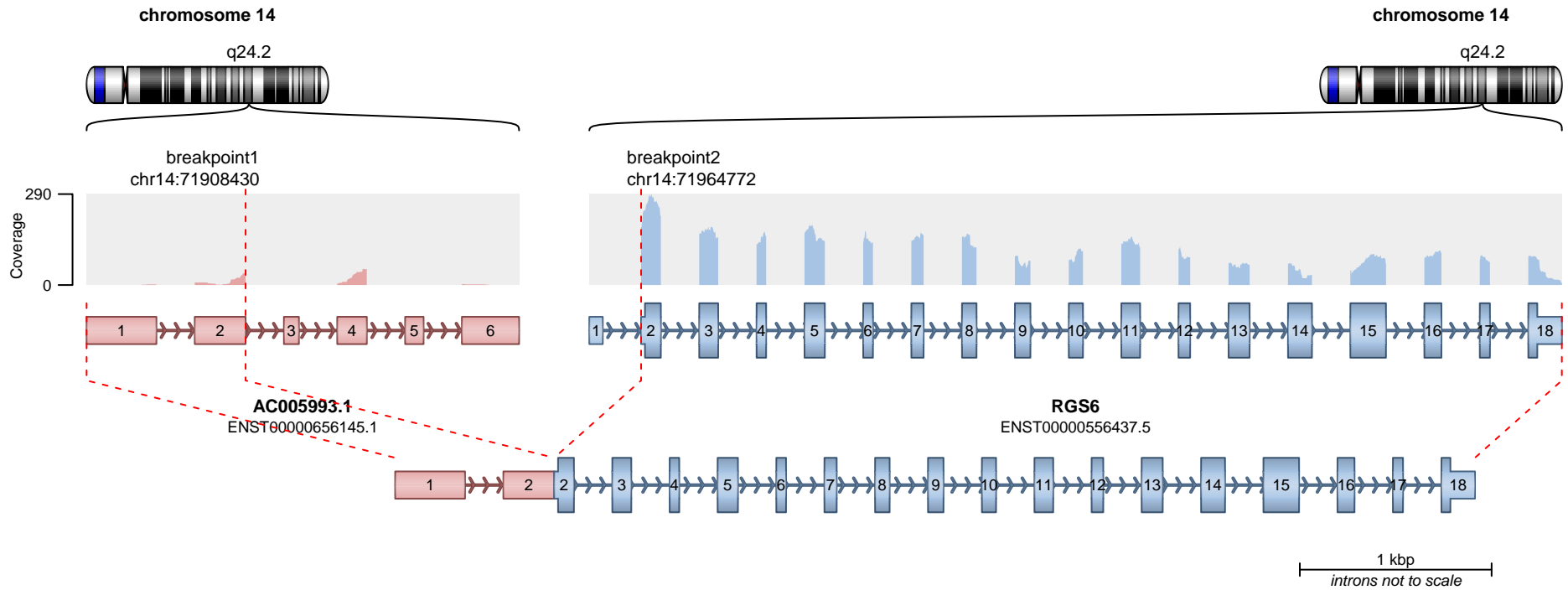
Regulator of G protein signaling domain

RETAINED PROTEIN DOMAINS
reading frame unclear

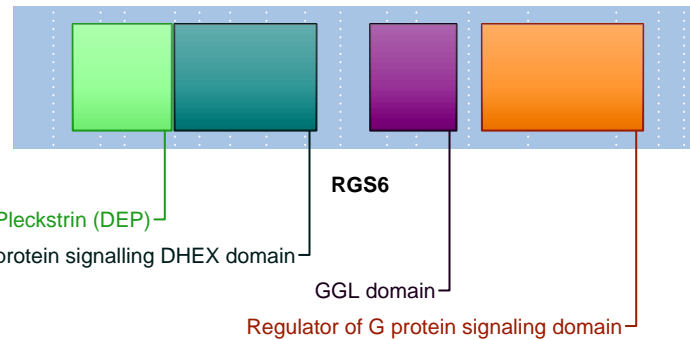
SUPPORTING READ COUNT

Split reads = 14
Discordant mates = 2

— translocation — deletion
— duplication — inversion



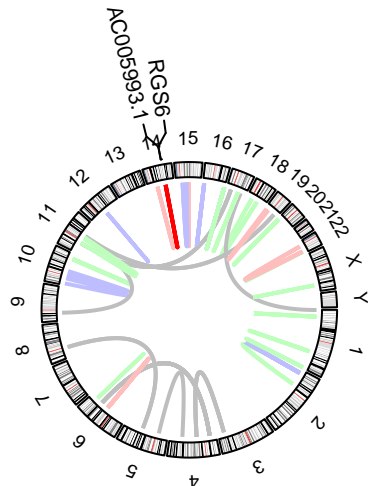
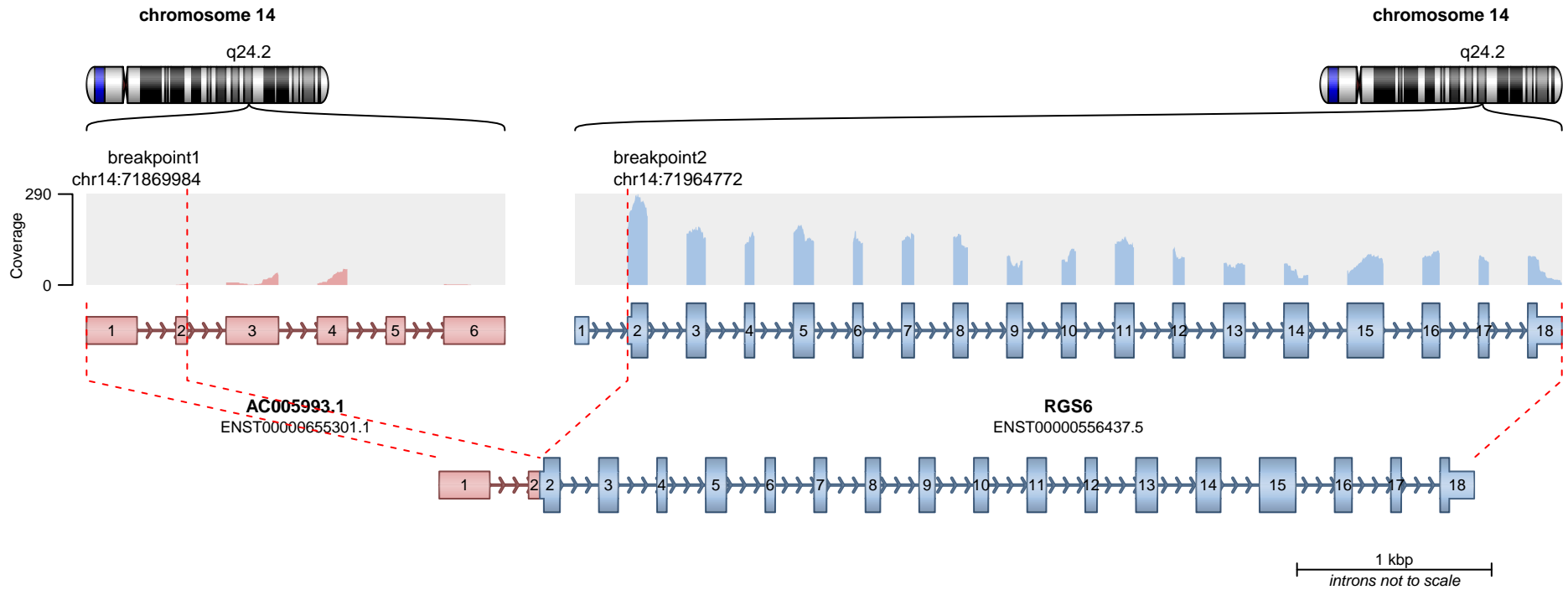
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 2

- translocation
- duplication
- deletion
- inversion



Domain found in Dishevelled, Egl-10, and Pleckstrin (DEP)

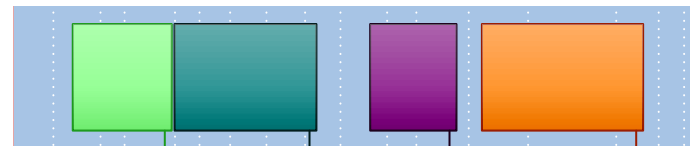
Regulator of G-protein signalling DHEX domain

RGS6

GGL domain

Regulator of G protein signaling domain

RETAINED PROTEIN DOMAINS
reading frame unclear

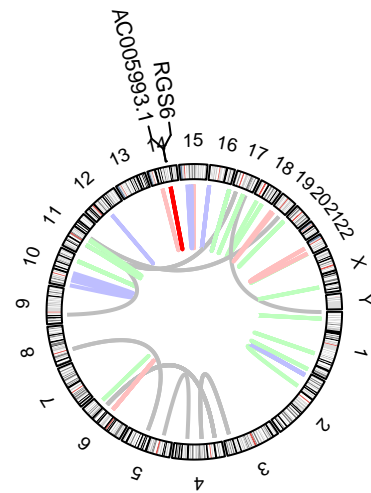
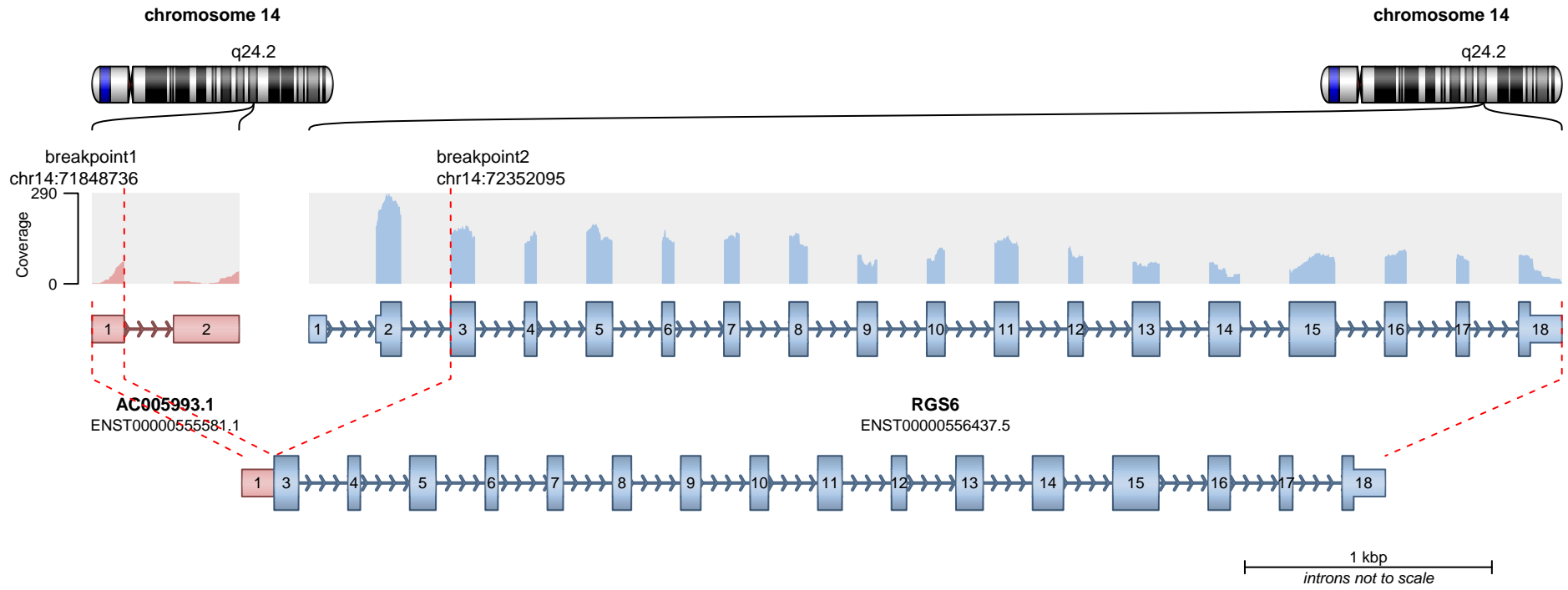


SUPPORTING READ COUNT

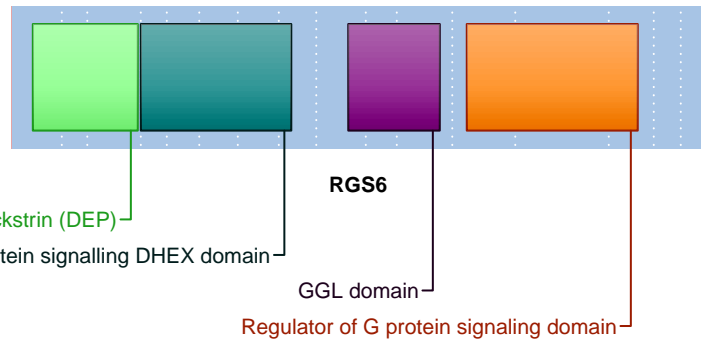
Split reads = 1

Discordant mates = 1

— translocation — deletion
— duplication — inversion



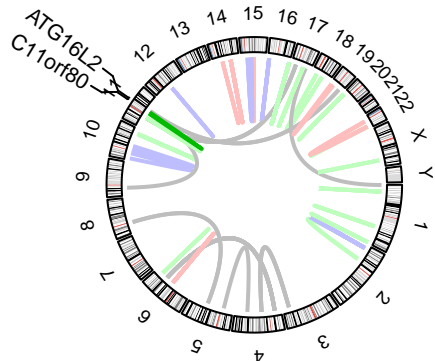
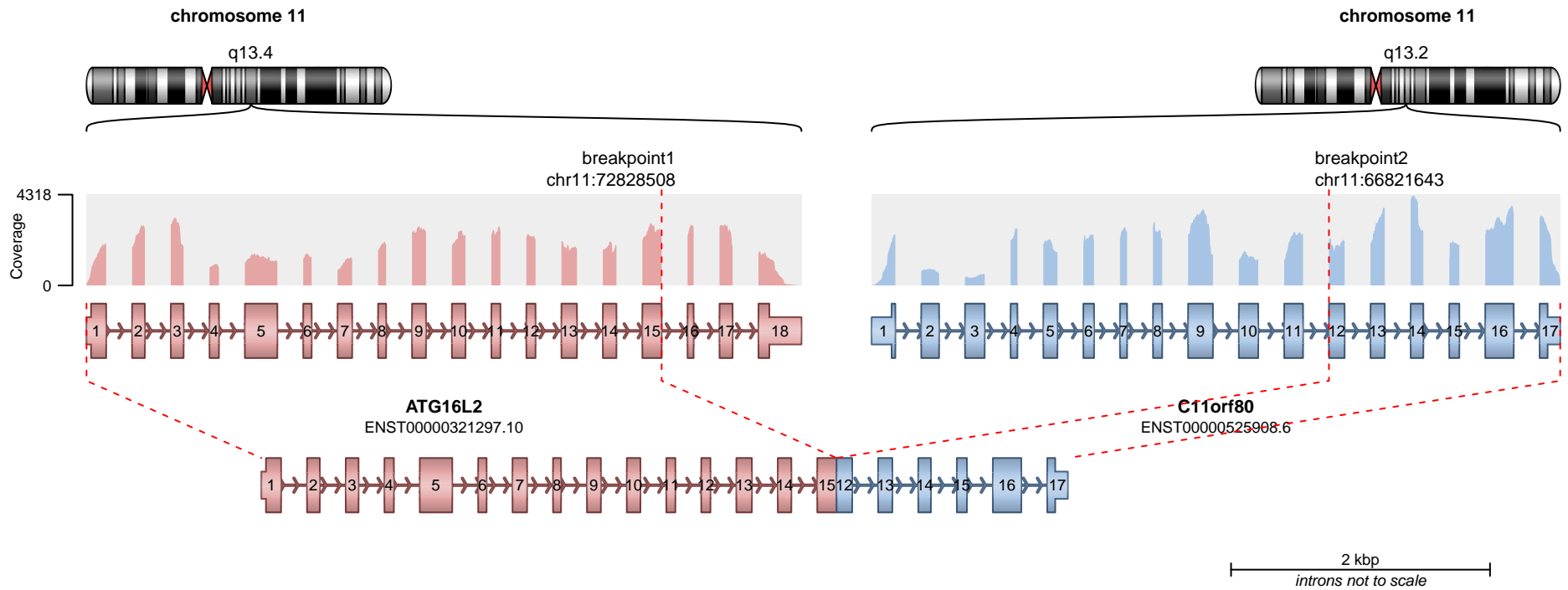
RETAINED PROTEIN DOMAINS
reading frame unclear



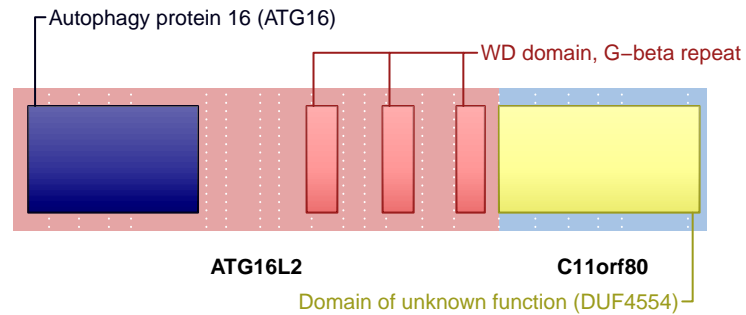
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



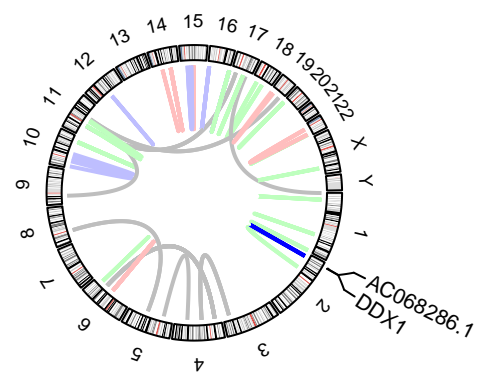
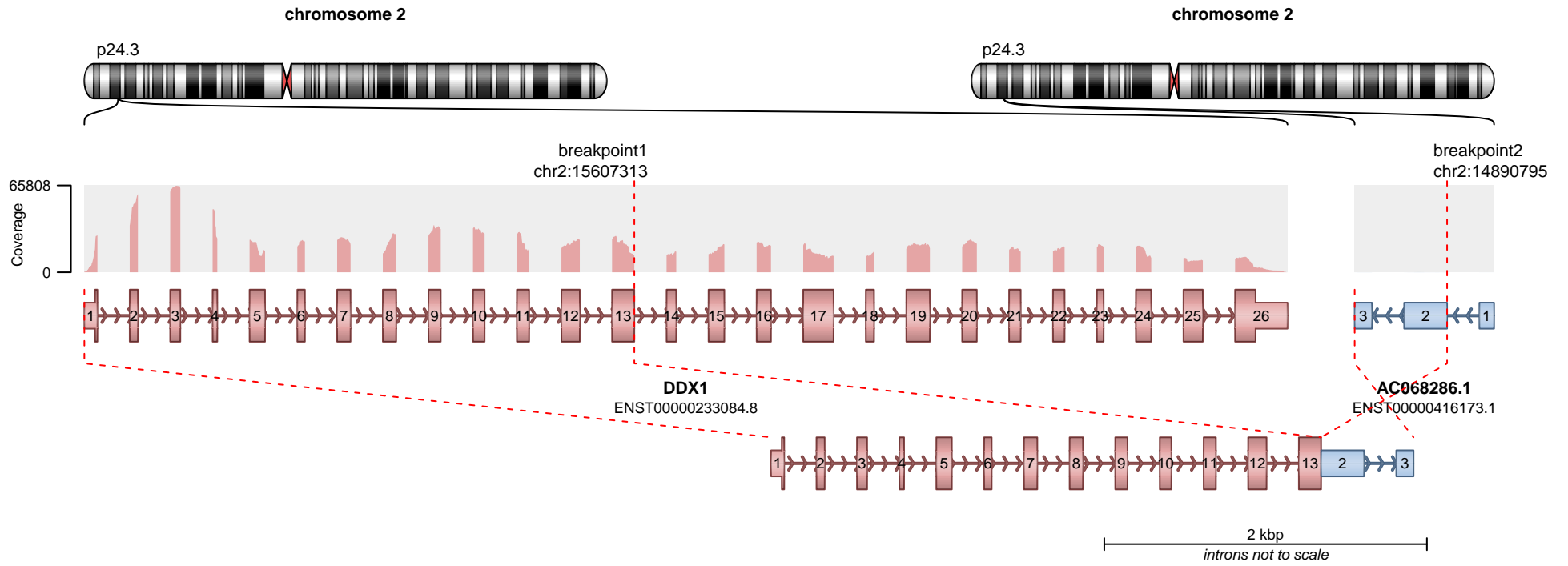
RETAINED PROTEIN DOMAINS
reading frame unclear



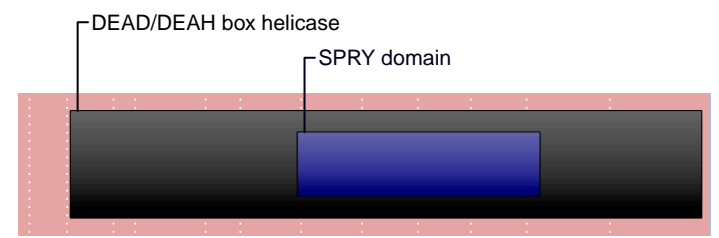
SUPPORTING READ COUNT

Split reads = 26
Discordant mates = 1

— translocation — deletion
— duplication — inversion



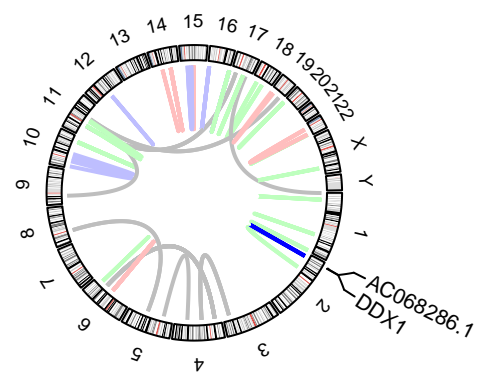
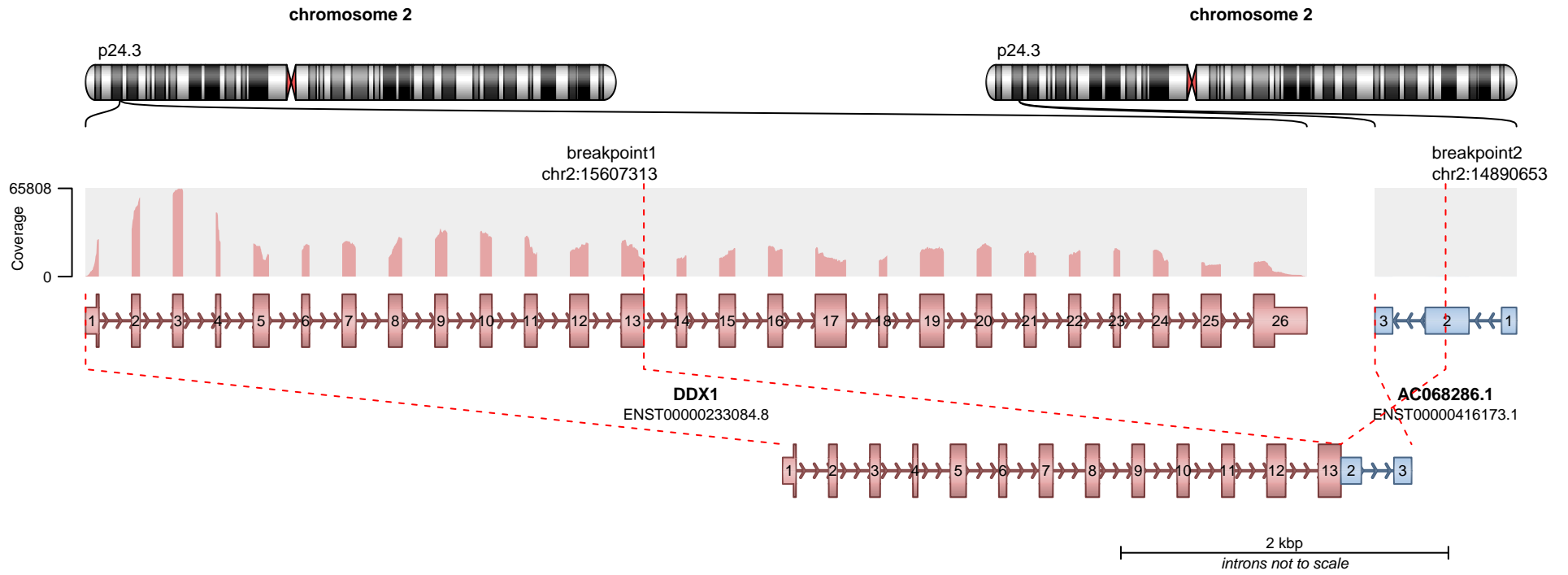
RETAINED PROTEIN DOMAINS
reading frame unclear



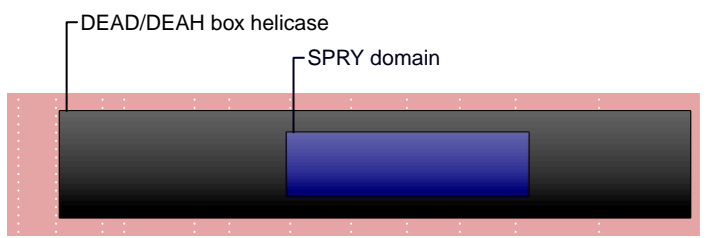
SUPPORTING READ COUNT

Split reads = 22
Discordant mates = 3

- translocation
- duplication
- deletion
- inversion



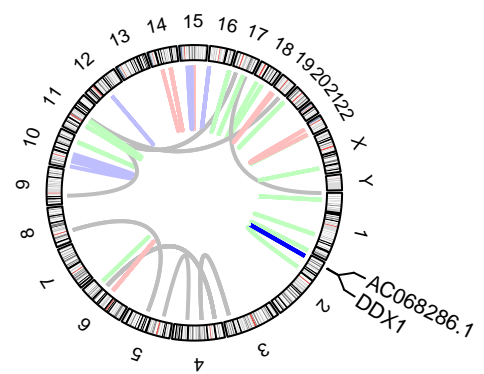
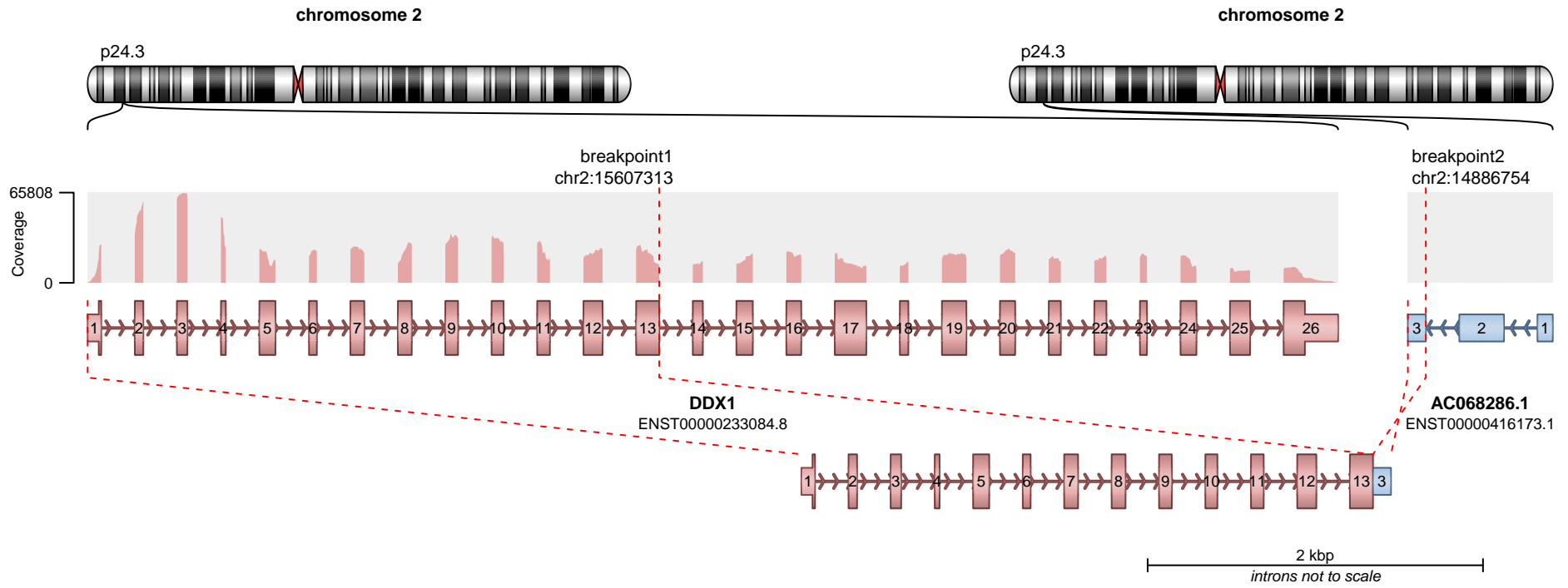
RETAINED PROTEIN DOMAINS
reading frame unclear



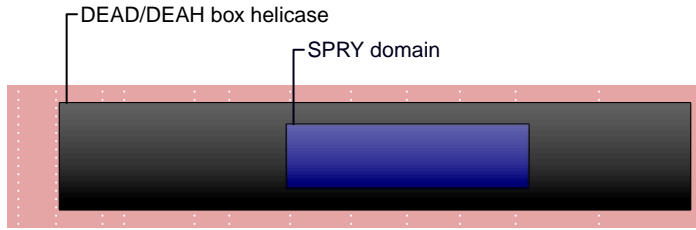
SUPPORTING READ COUNT

Split reads = 18
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



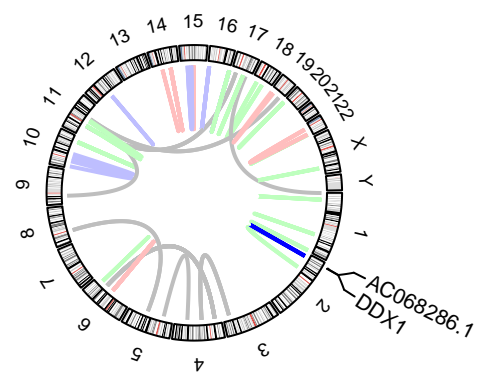
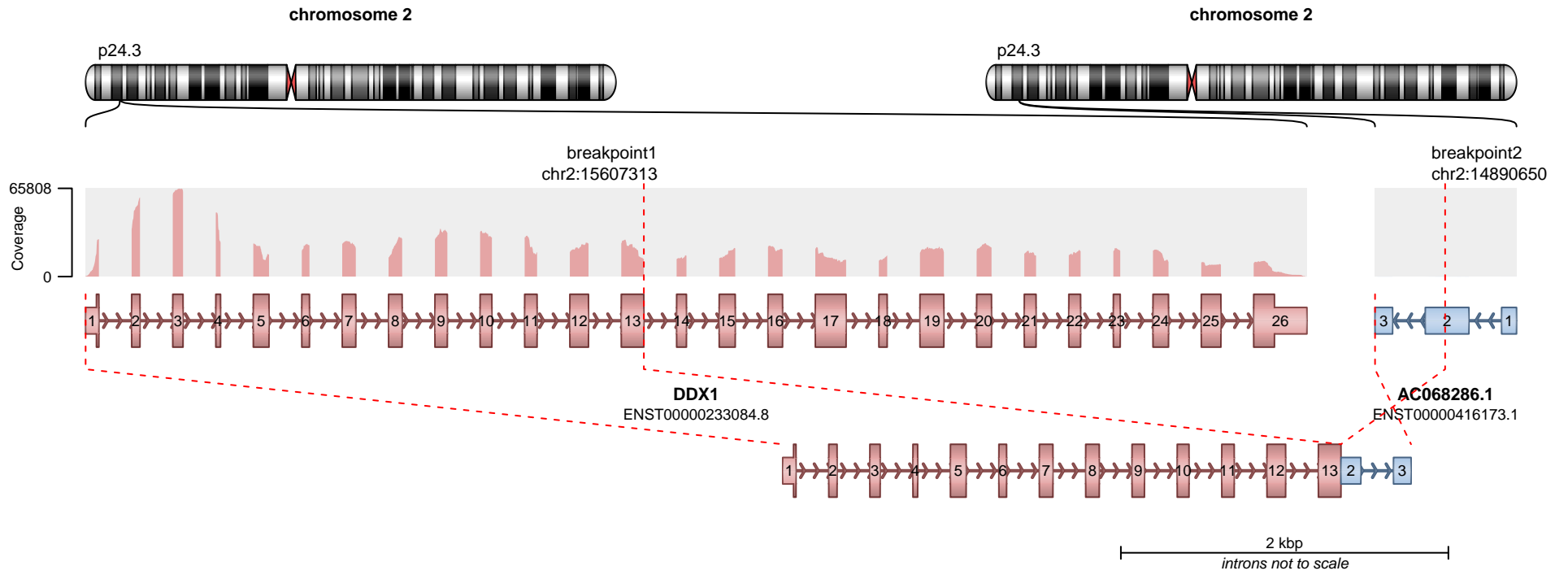
RETAINED PROTEIN DOMAINS
reading frame unclear



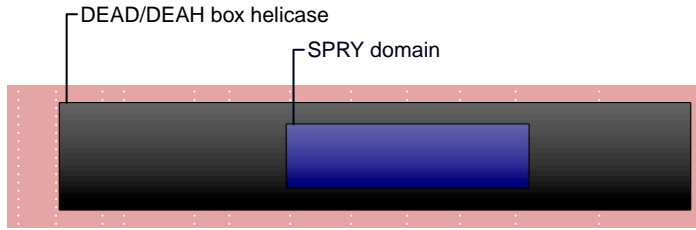
SUPPORTING READ COUNT

Split reads = 17
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



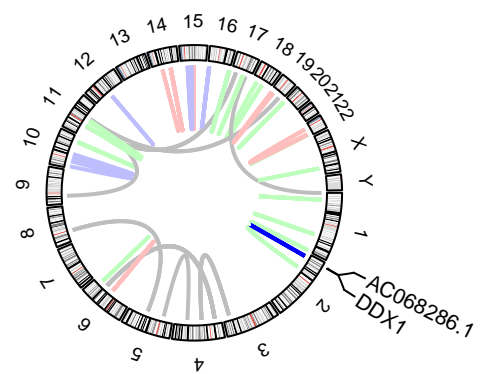
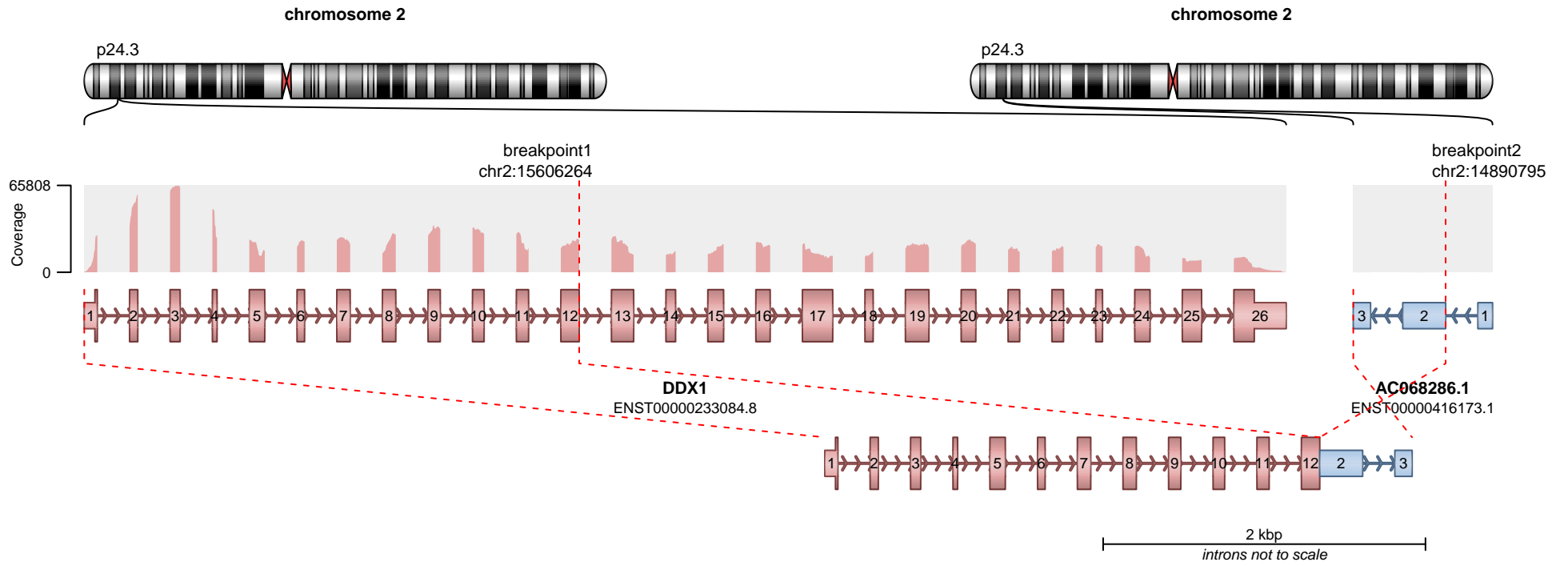
RETAINED PROTEIN DOMAINS
reading frame unclear



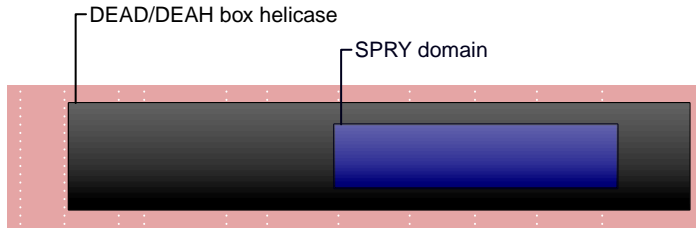
SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

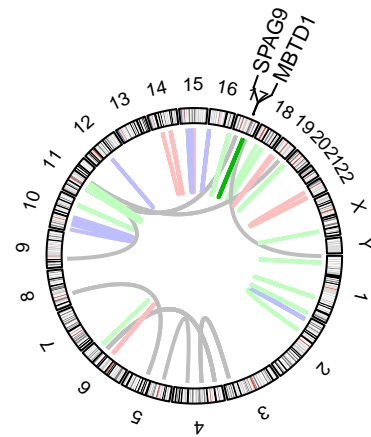
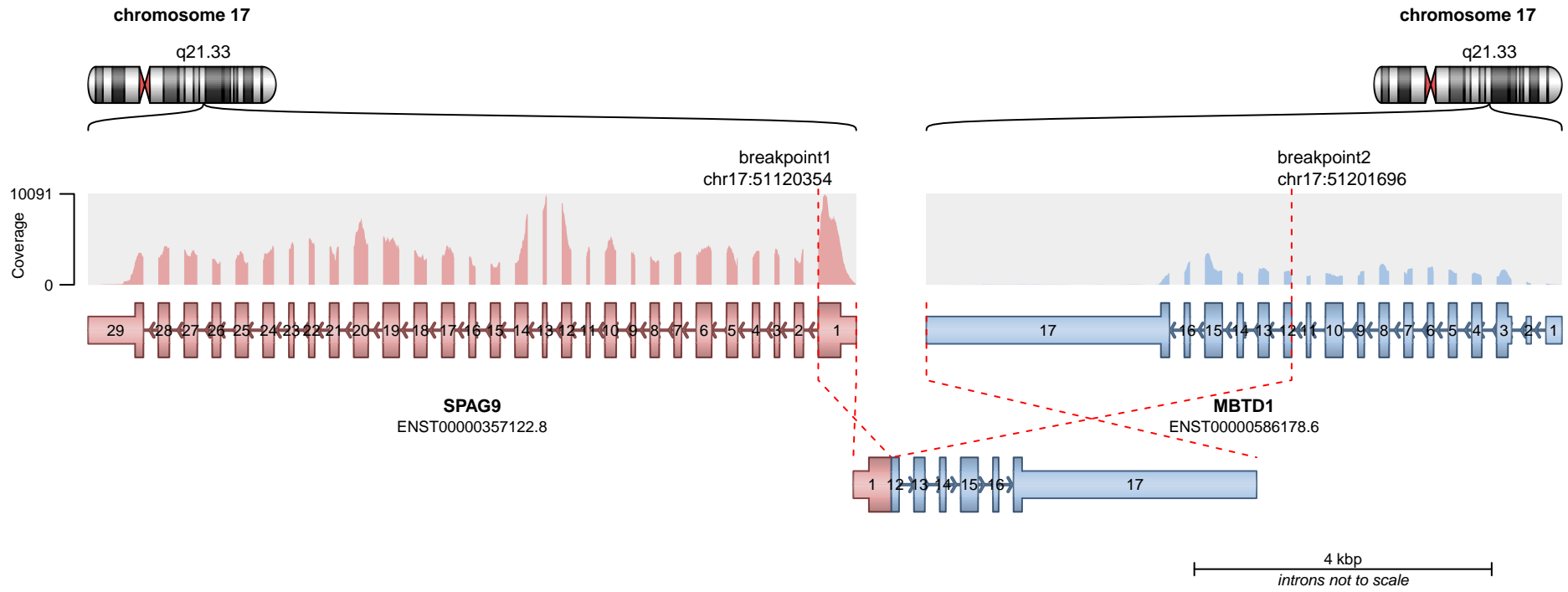


DDX1

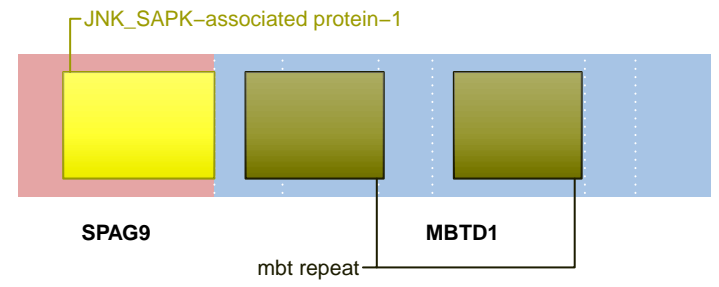
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



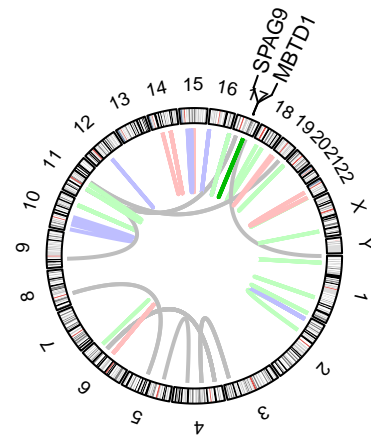
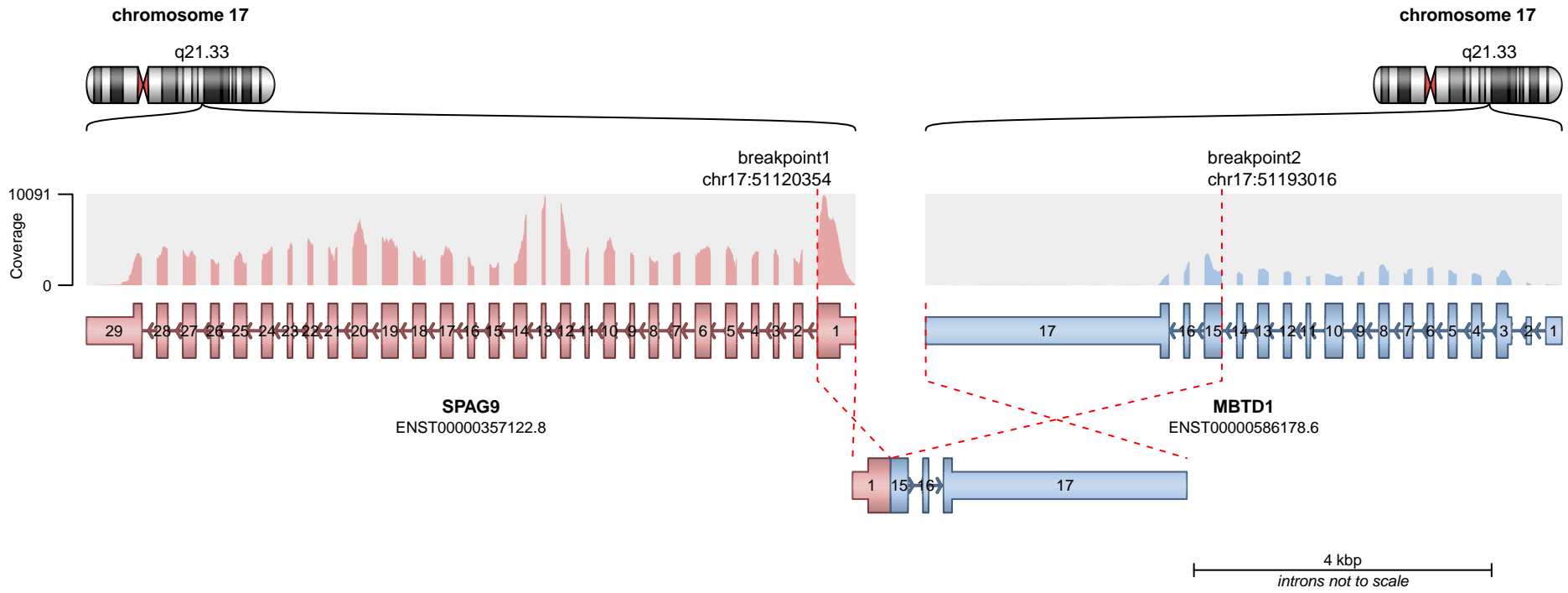
RETAINED PROTEIN DOMAINS
reading frame unclear



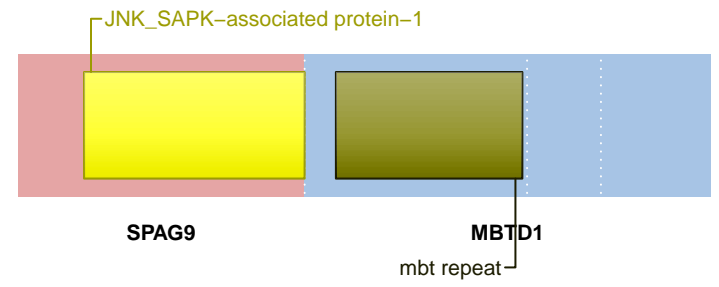
SUPPORTING READ COUNT

Split reads = 18
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



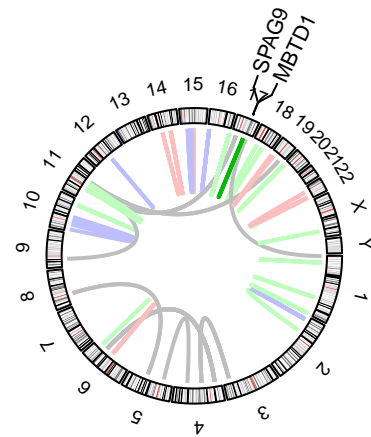
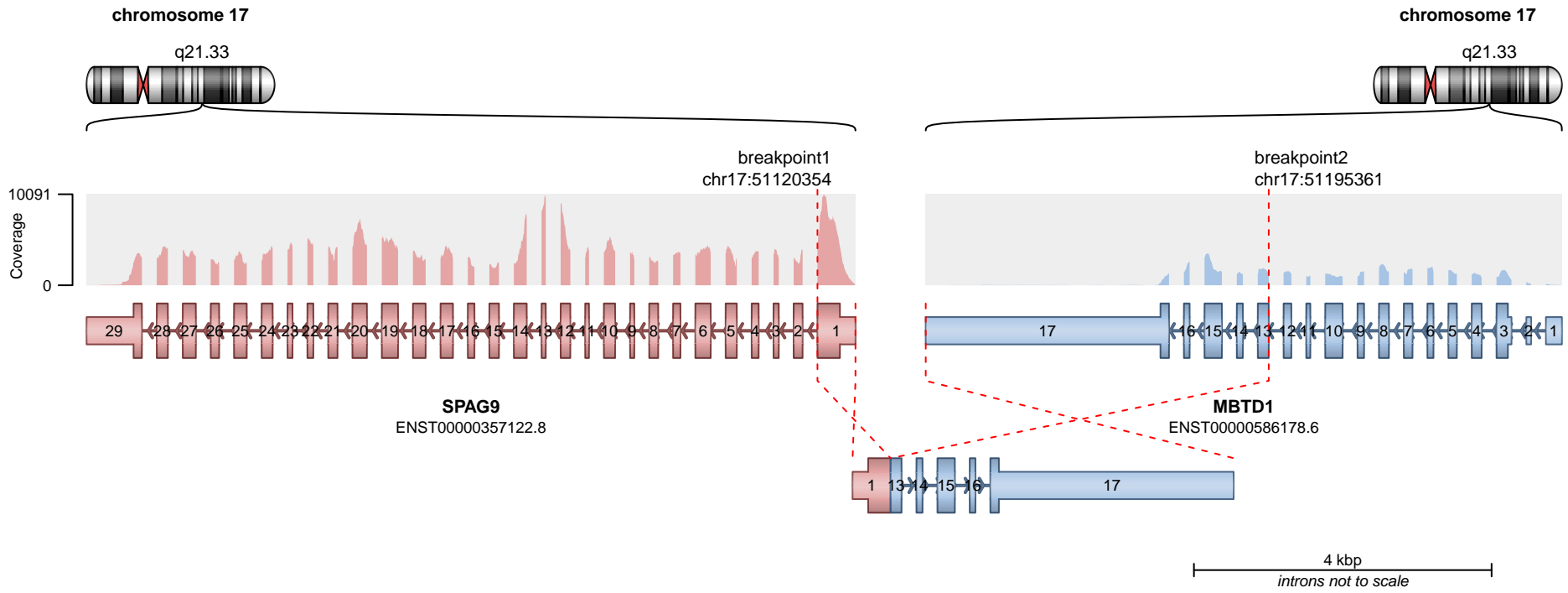
RETAINED PROTEIN DOMAINS
reading frame unclear



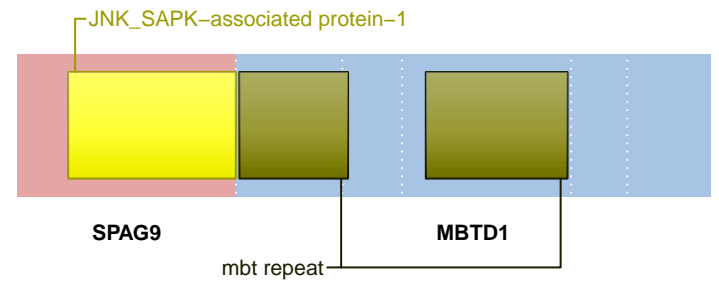
SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



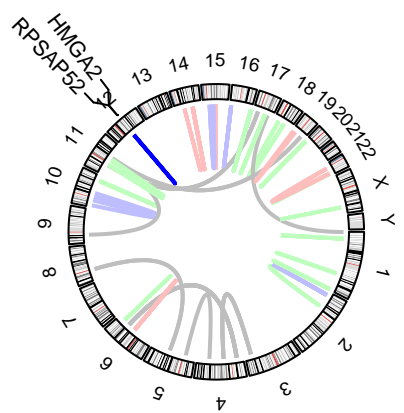
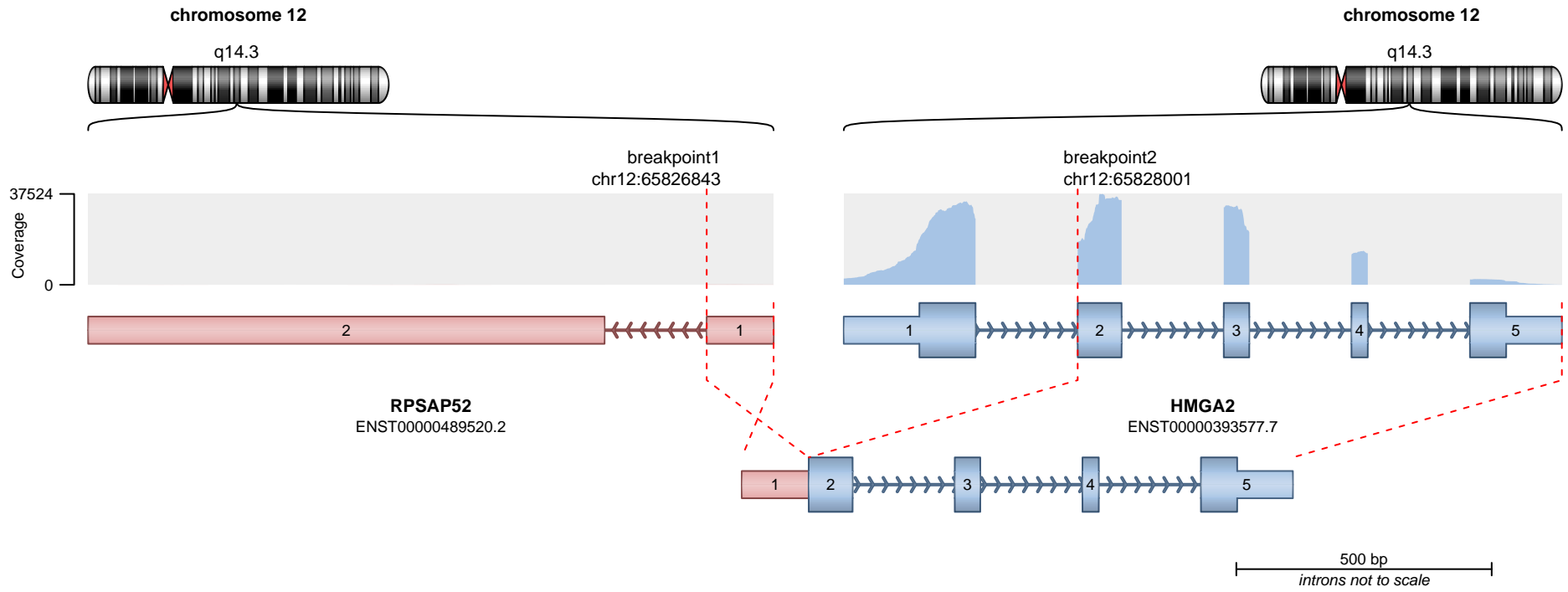
RETAINED PROTEIN DOMAINS
reading frame unclear



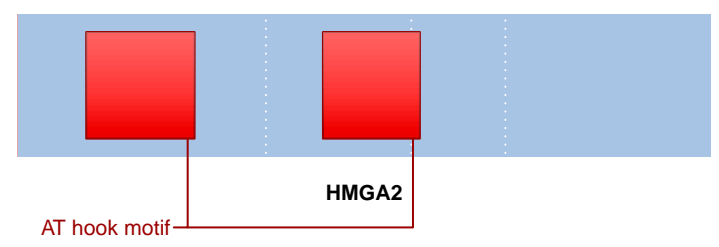
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



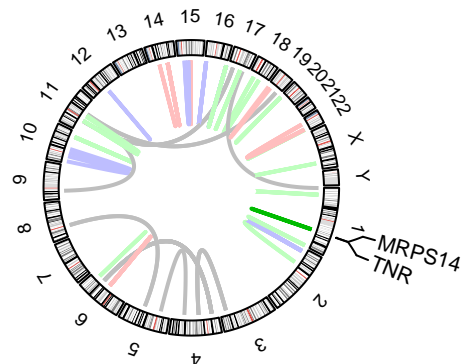
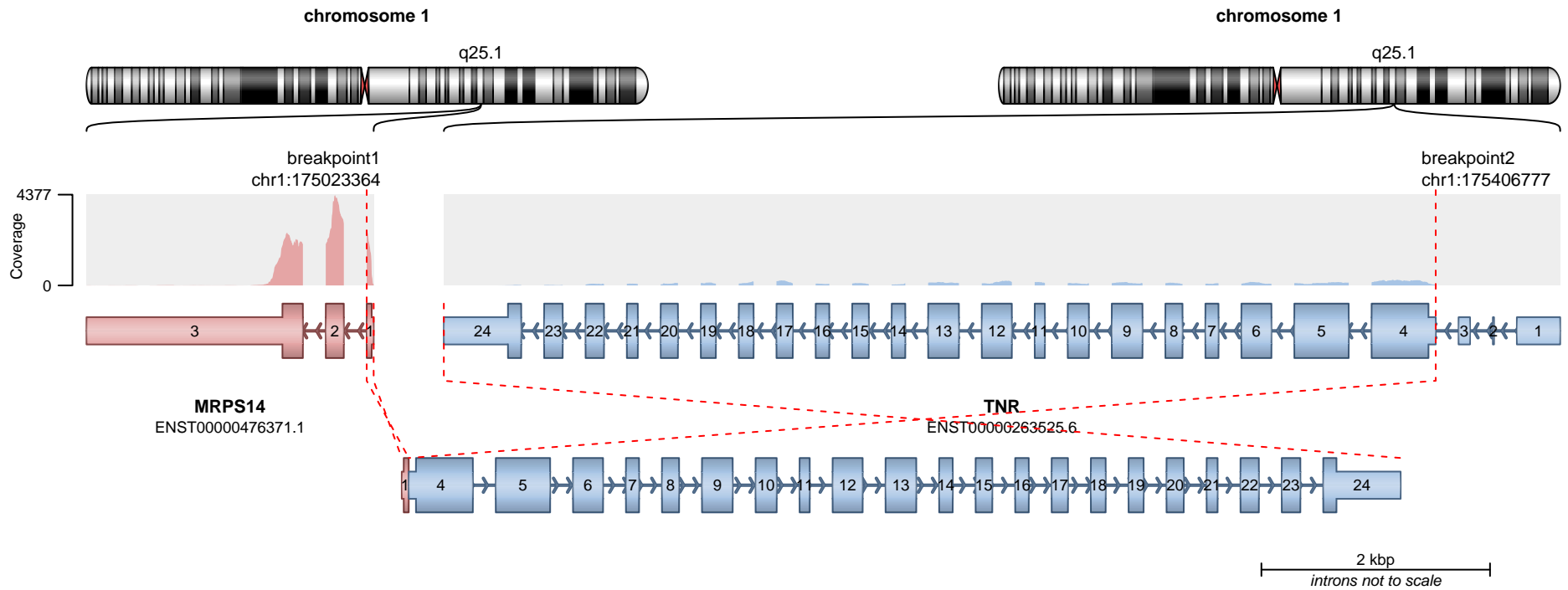
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

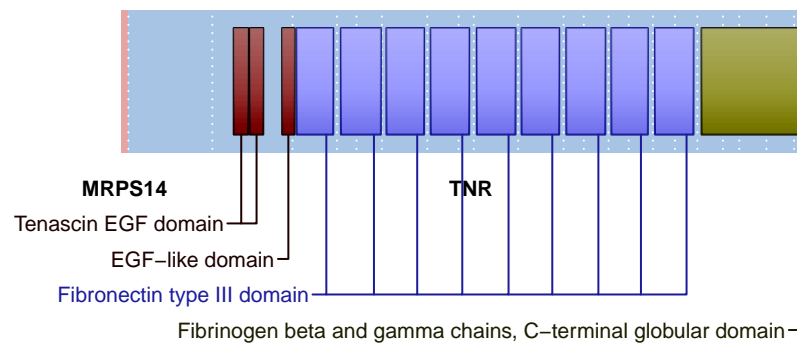
Split reads = 18
Discordant mates = 0

— translocation — deletion
— duplication — inversion



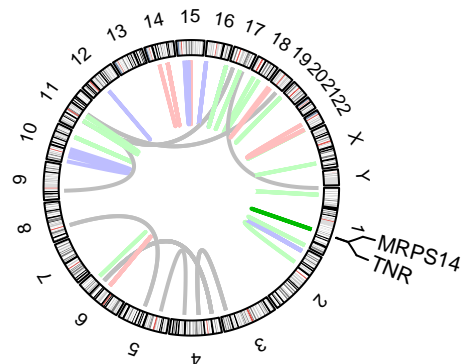
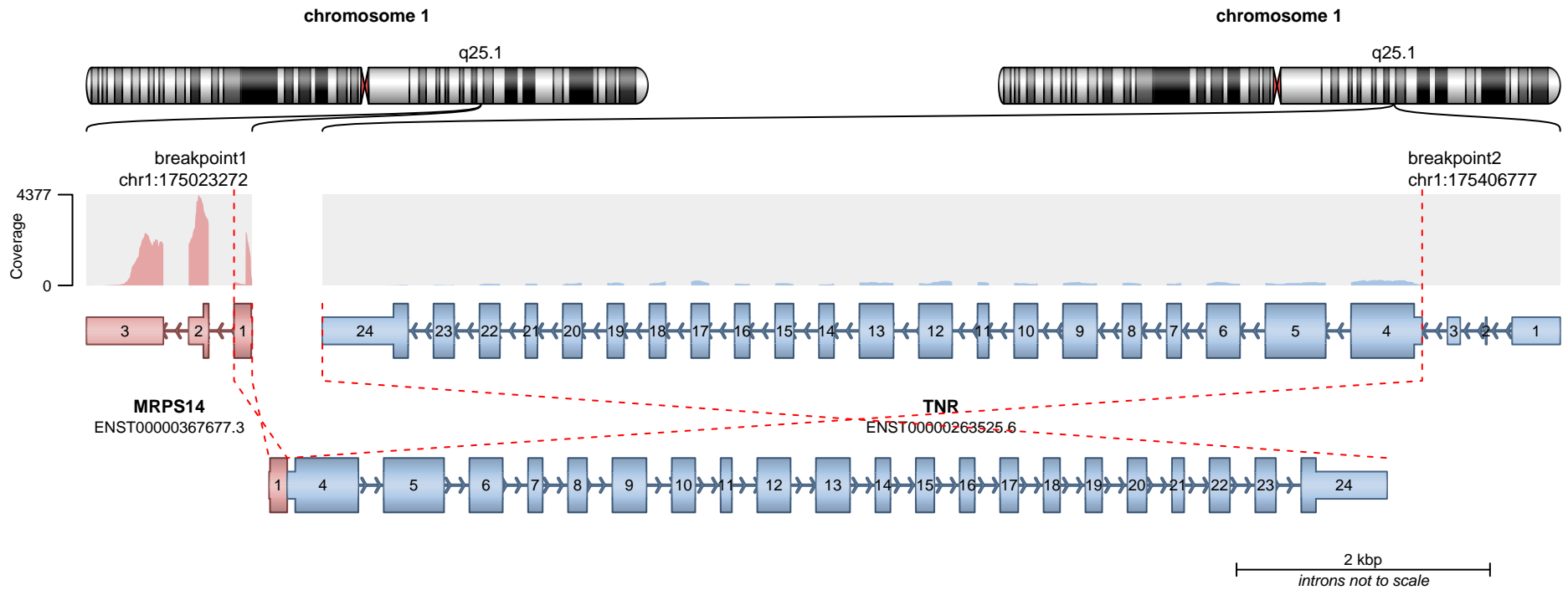
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



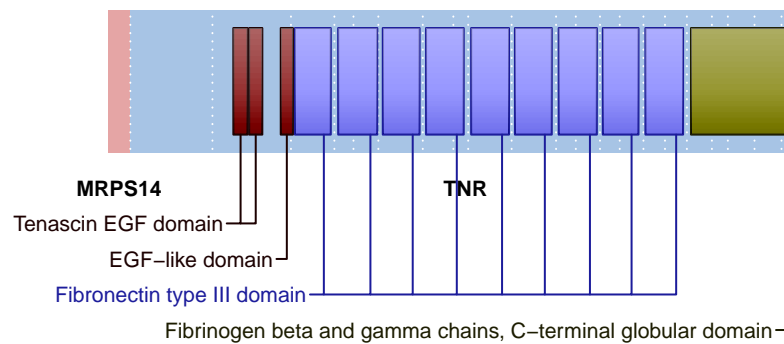
SUPPORTING READ COUNT

Split reads = 17
Discordant mates = 0



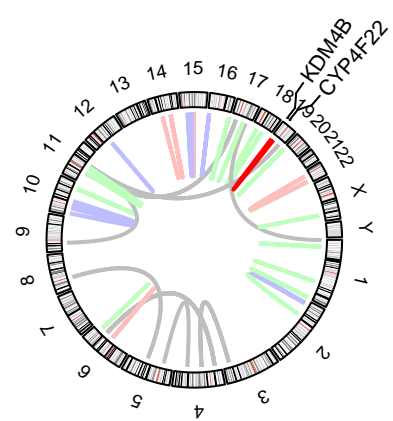
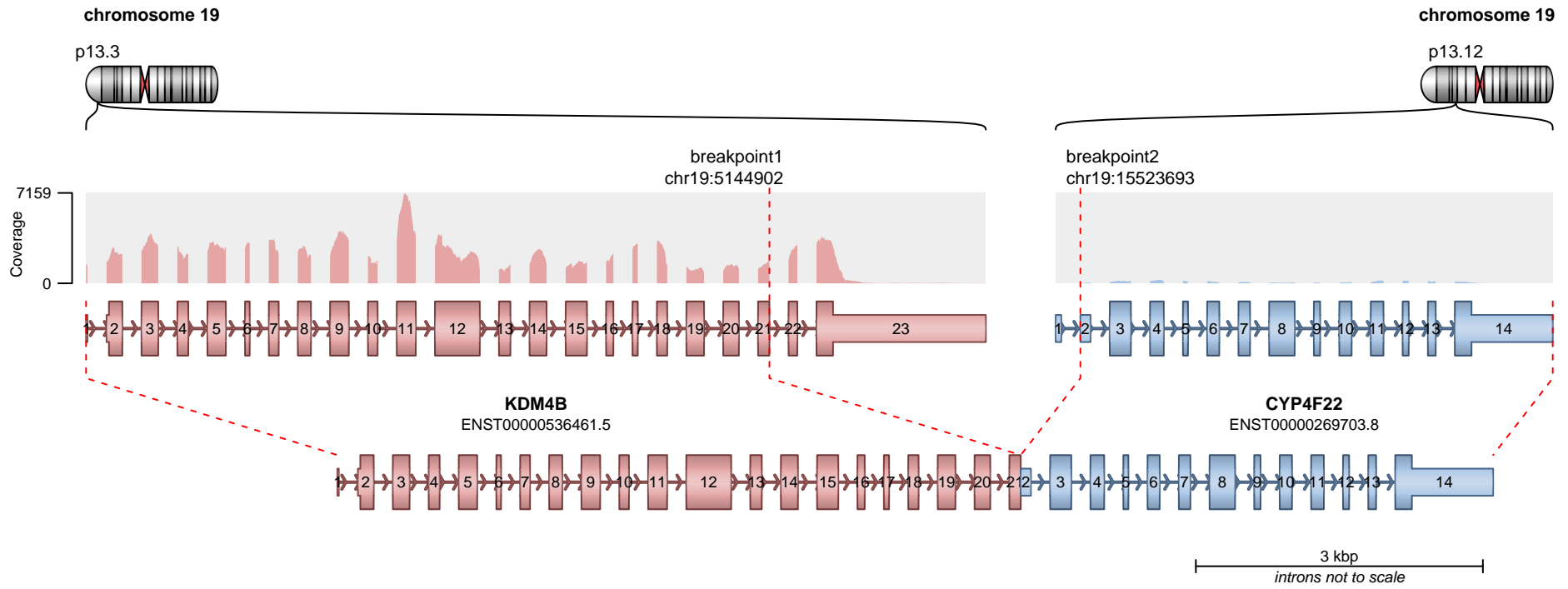
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear

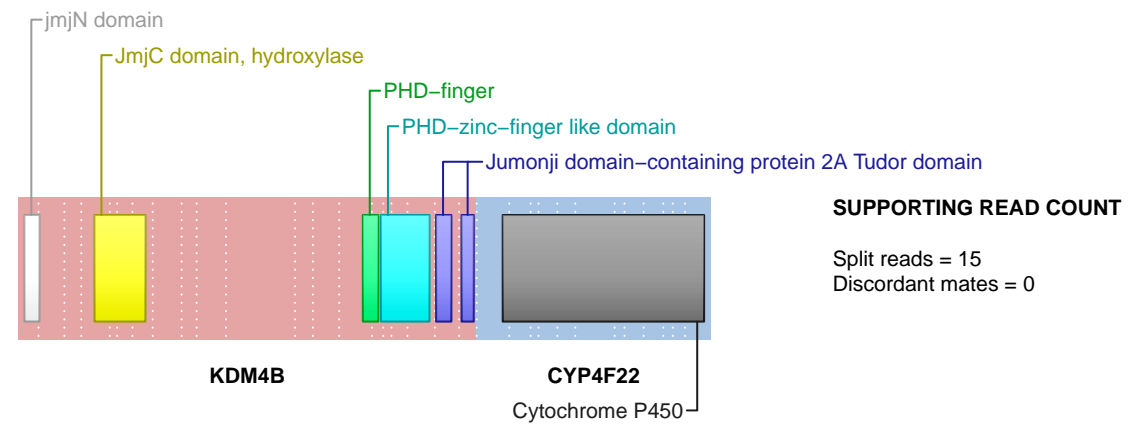


SUPPORTING READ COUNT

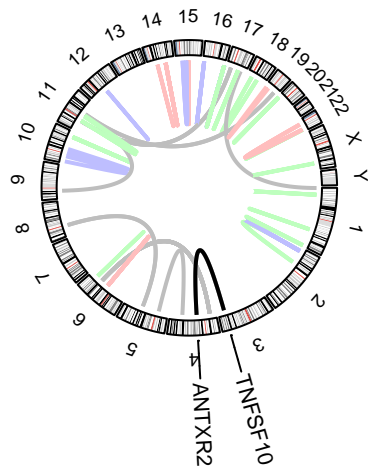
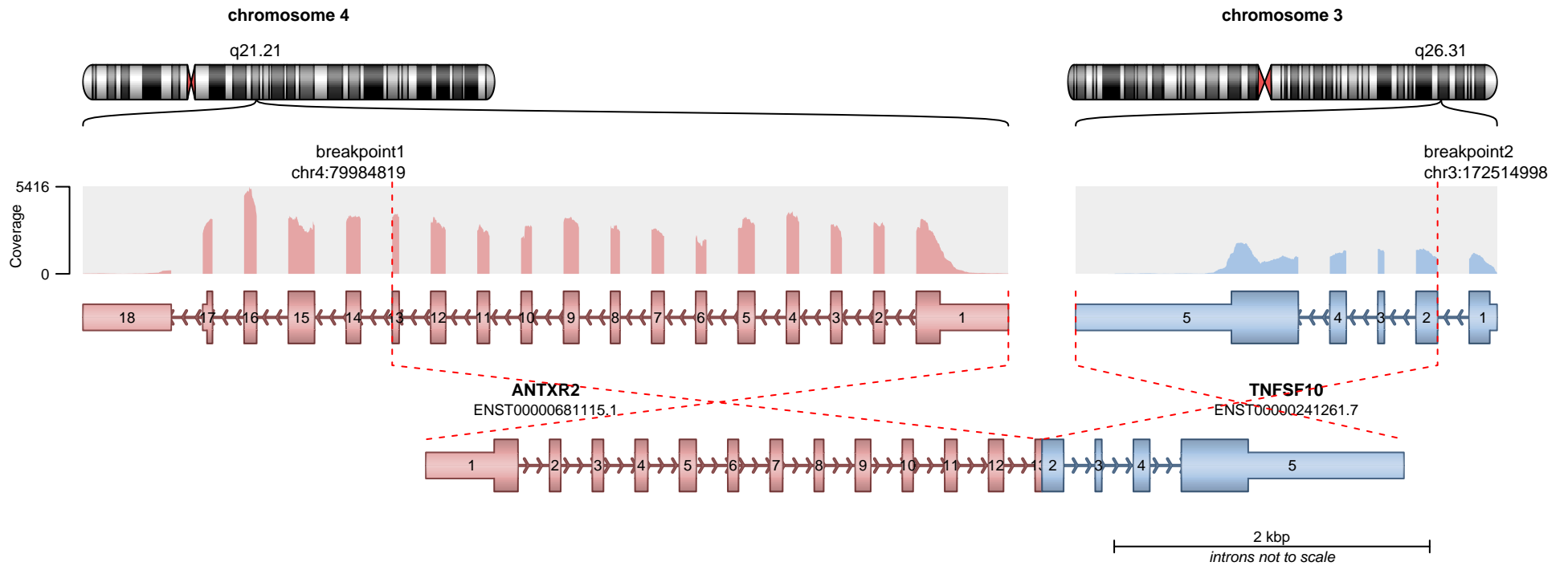
Split reads = 2
Discordant mates = 0



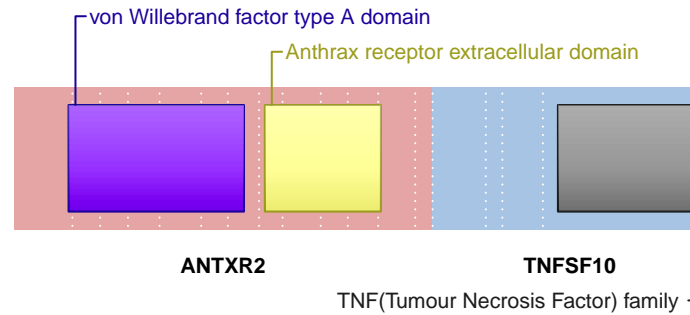
RETAINED PROTEIN DOMAINS
reading frame unclear



- translocation
- duplication
- deletion
- inversion



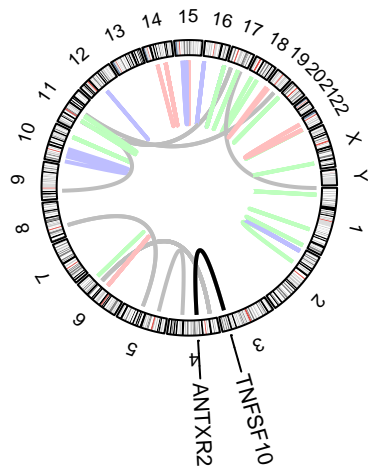
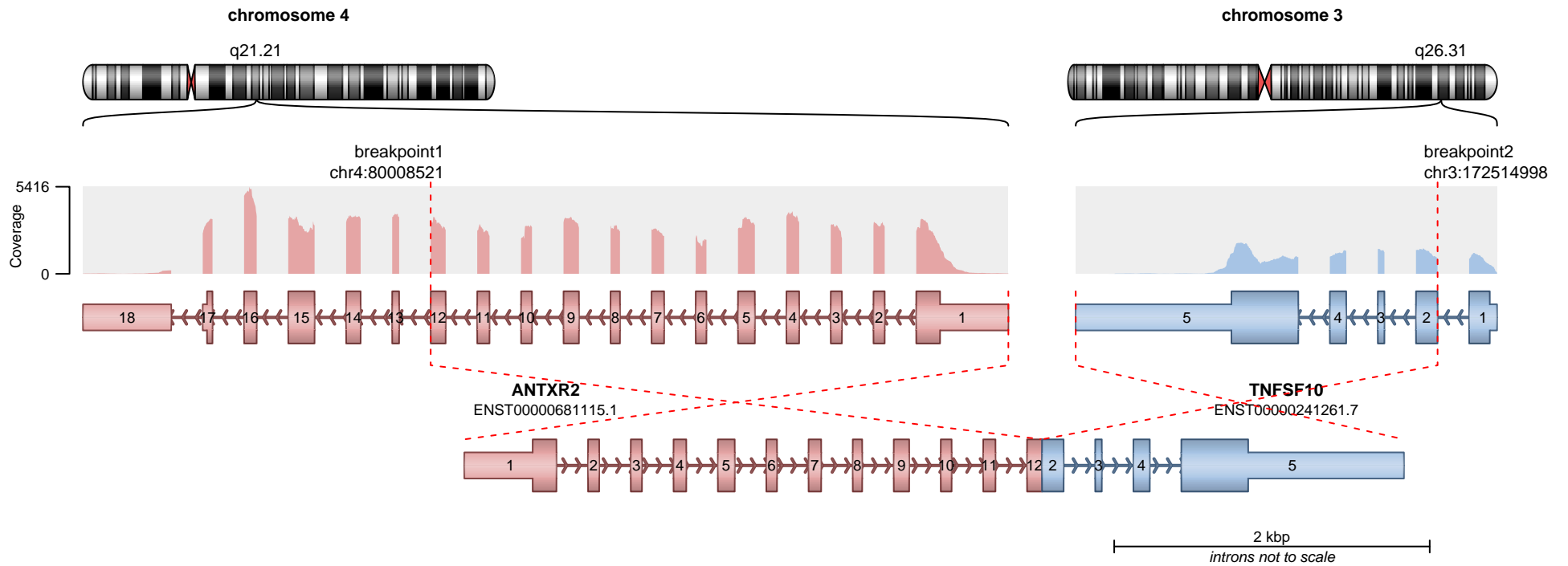
RETAINED PROTEIN DOMAINS
reading frame unclear



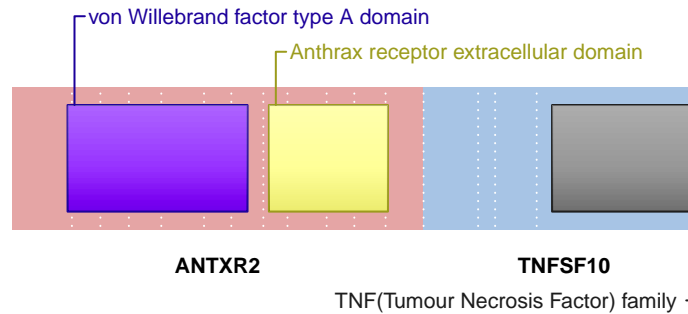
SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 0

— translocation — deletion
— duplication — inversion



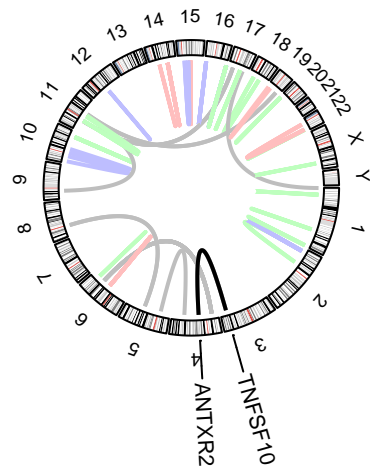
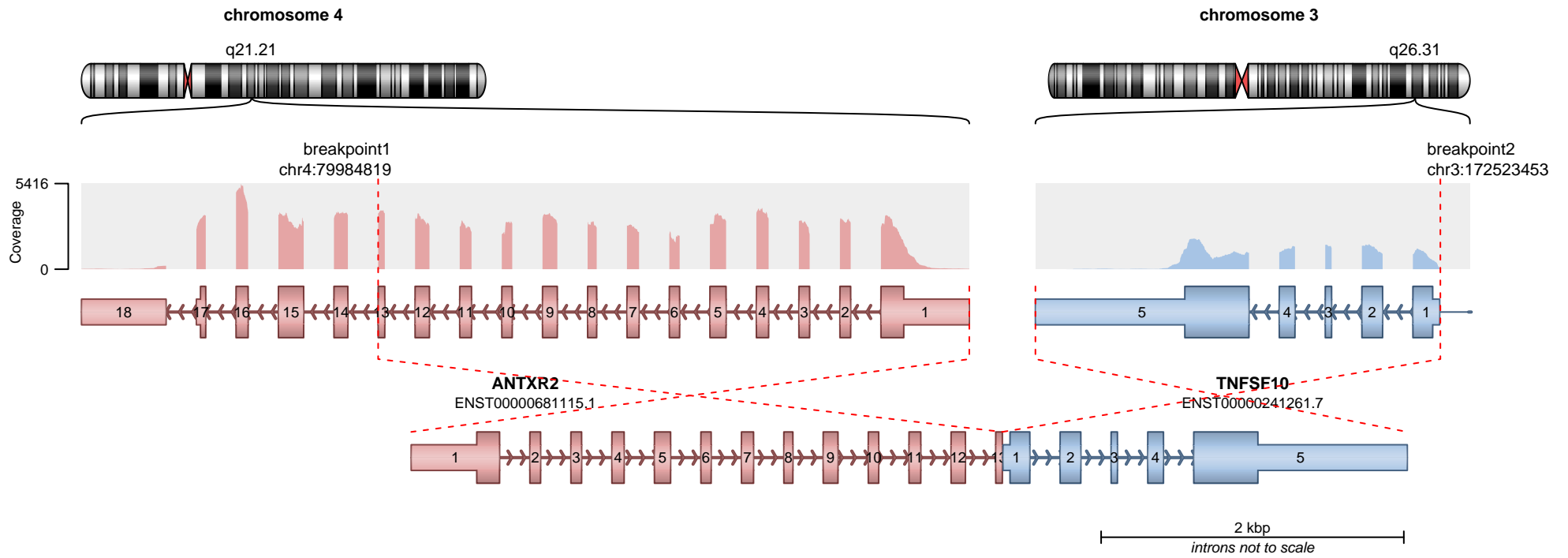
RETAINED PROTEIN DOMAINS
reading frame unclear



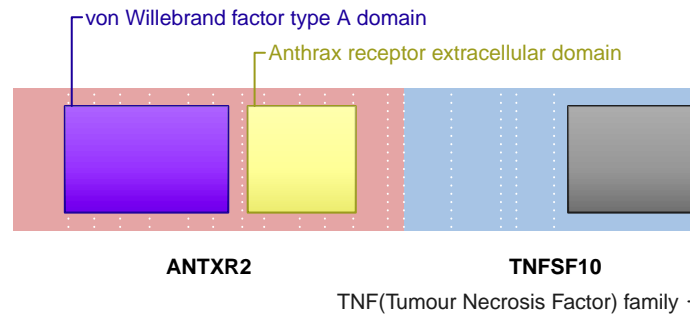
SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 0

— translocation — deletion
— duplication — inversion



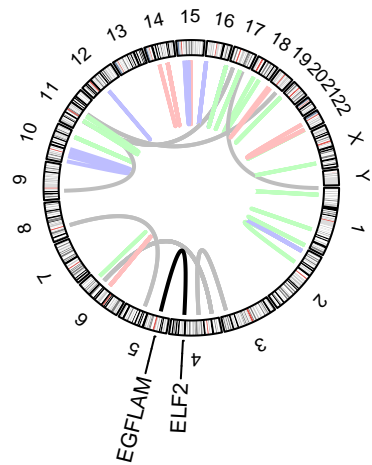
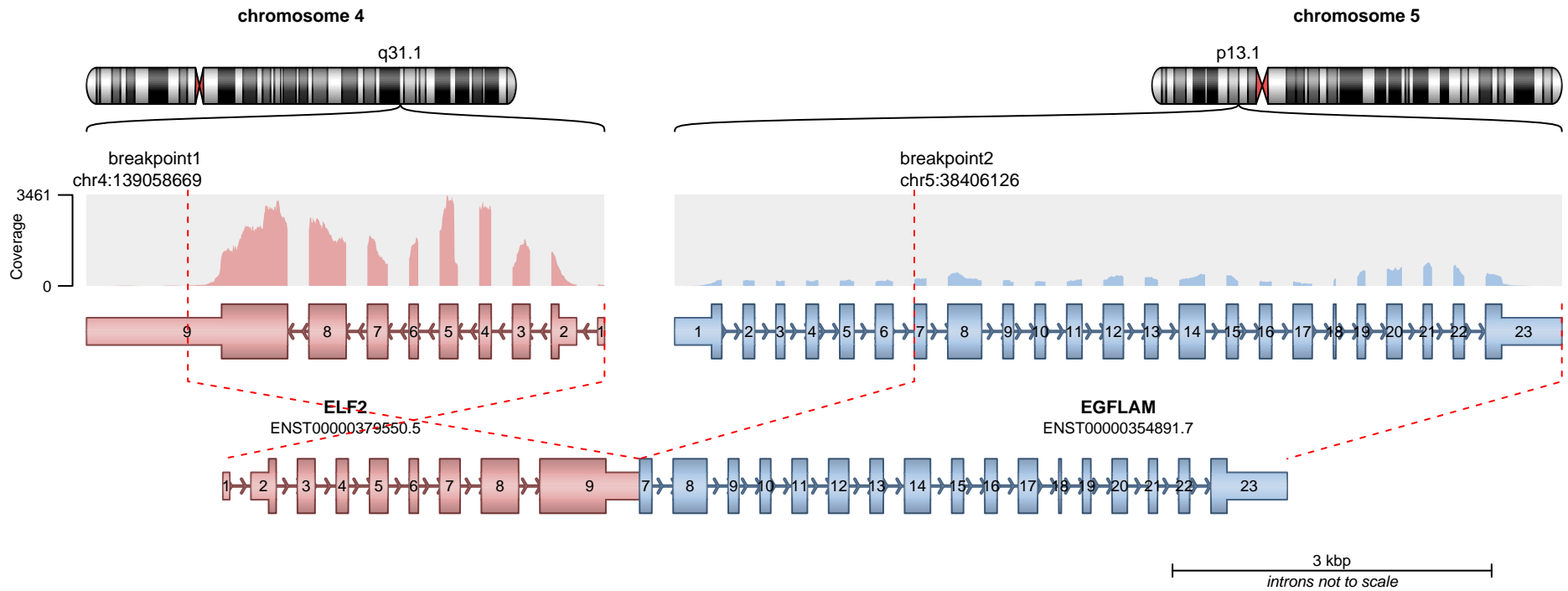
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

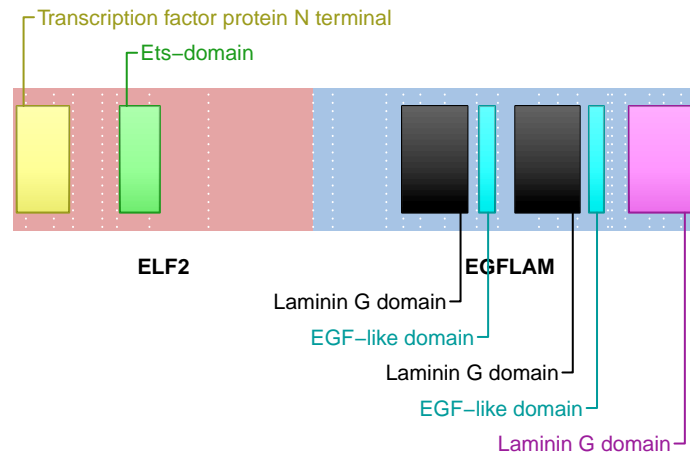
Split reads = 5
Discordant mates = 0

— translocation — deletion
— duplication — inversion



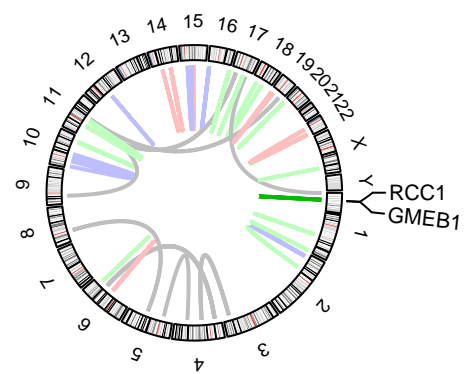
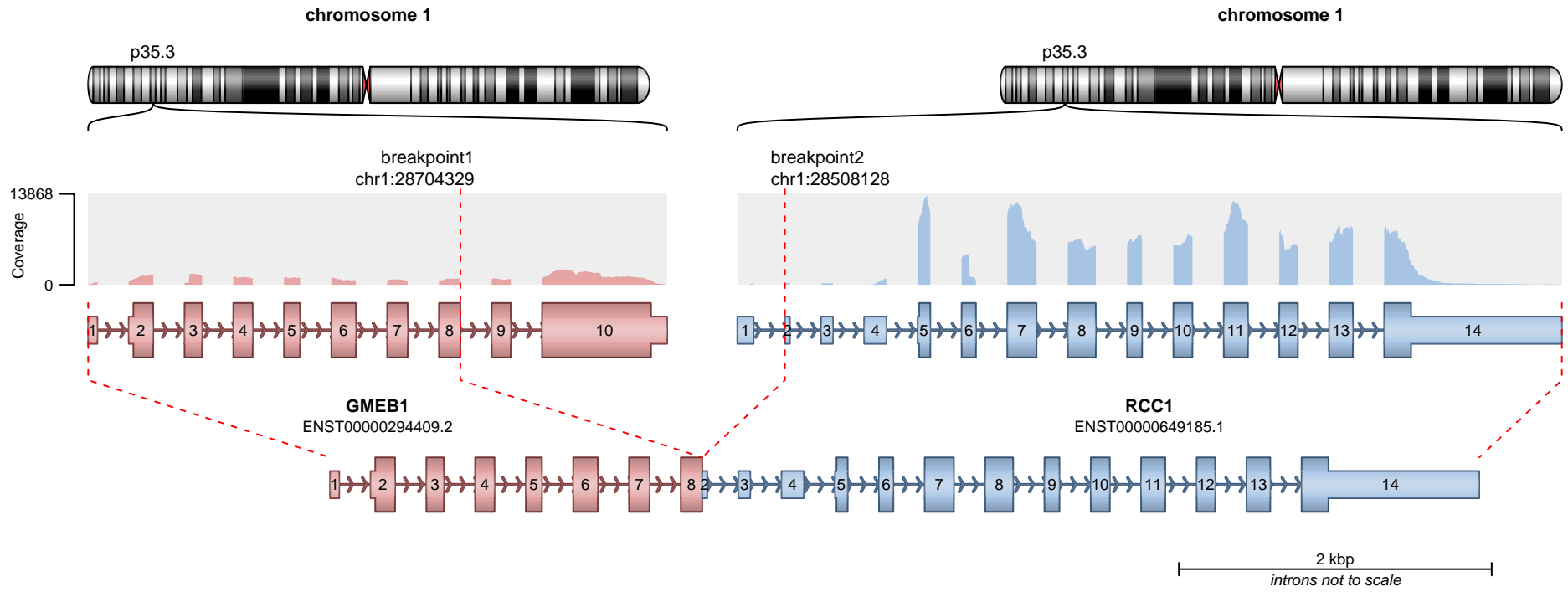
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear

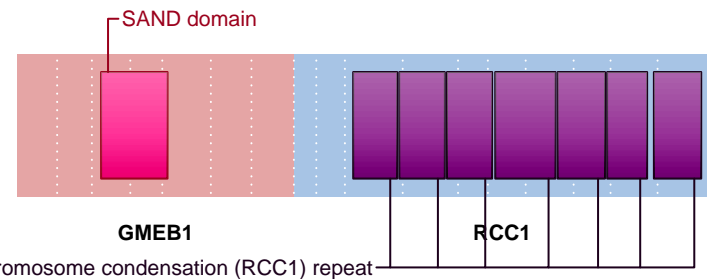


SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 0



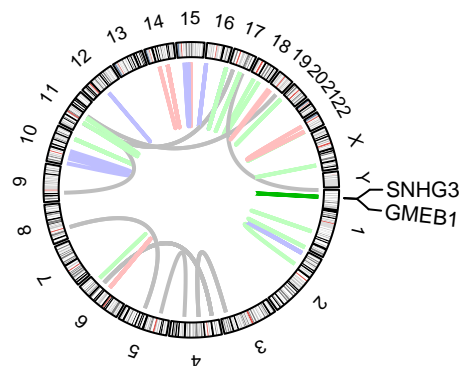
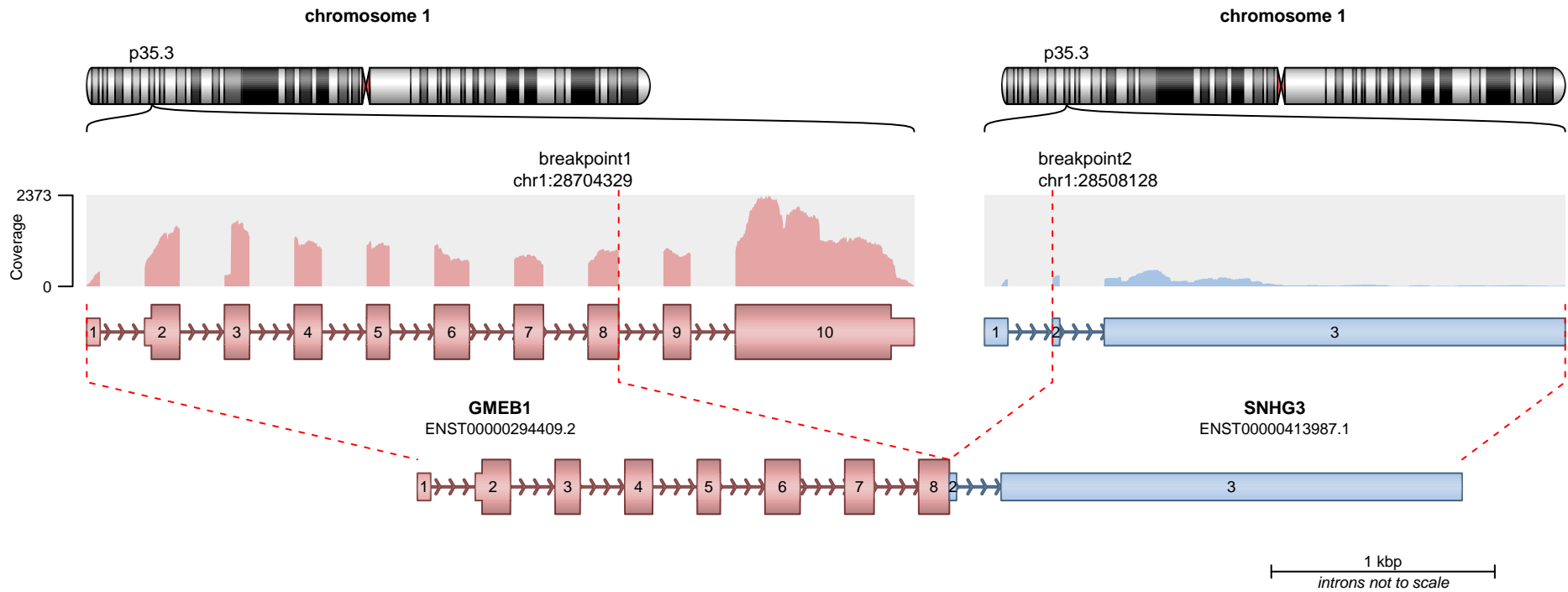
RETAINED PROTEIN DOMAINS
reading frame unclear



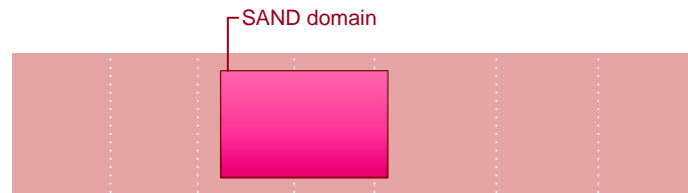
SUPPORTING READ COUNT

Split reads = 11
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



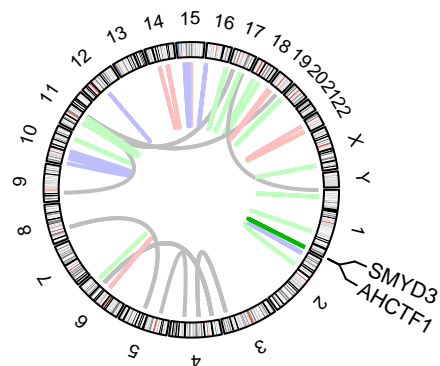
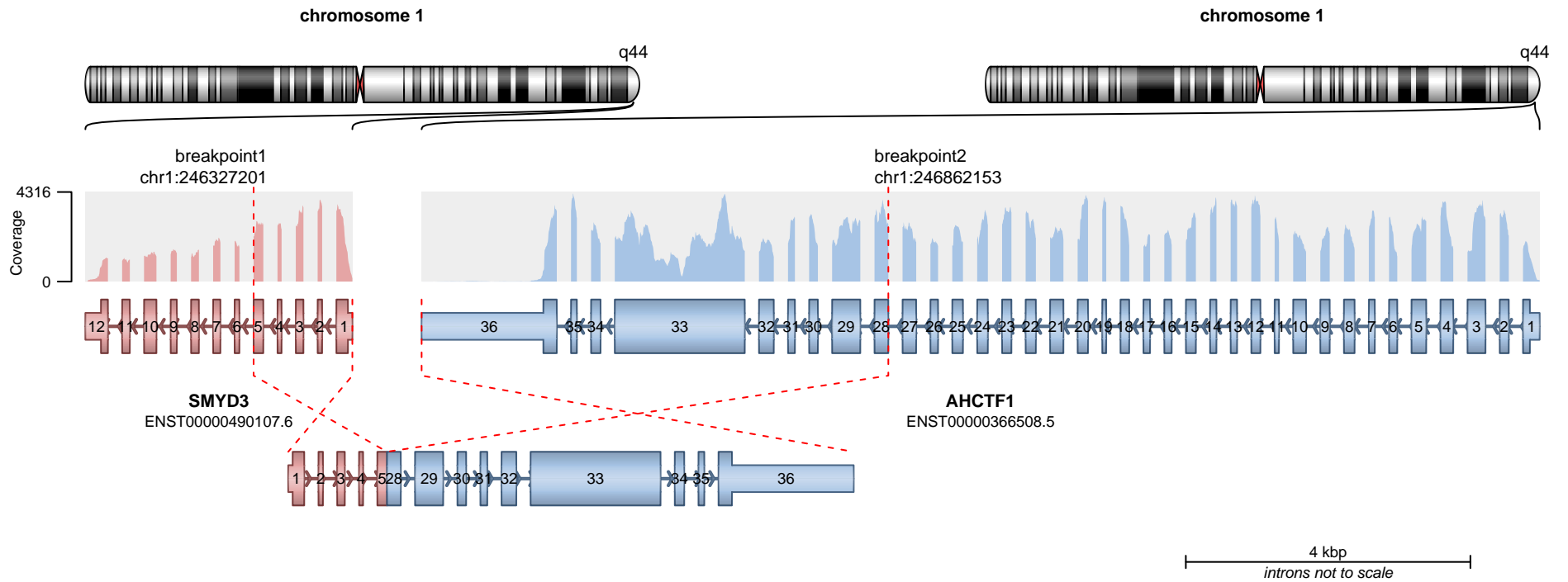
RETAINED PROTEIN DOMAINS
reading frame unclear



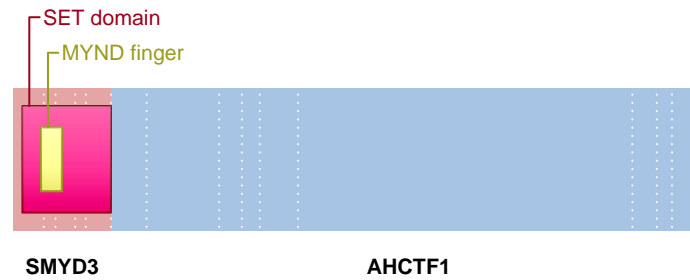
SUPPORTING READ COUNT

Split reads = 11
Discordant mates = 0

— translocation — deletion
— duplication — inversion



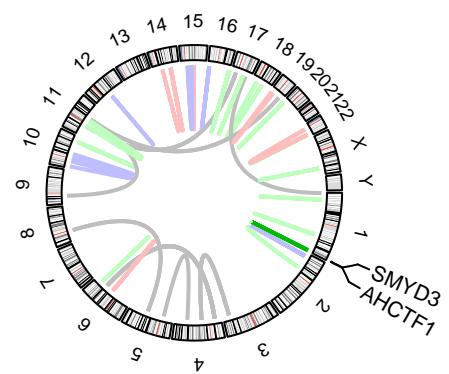
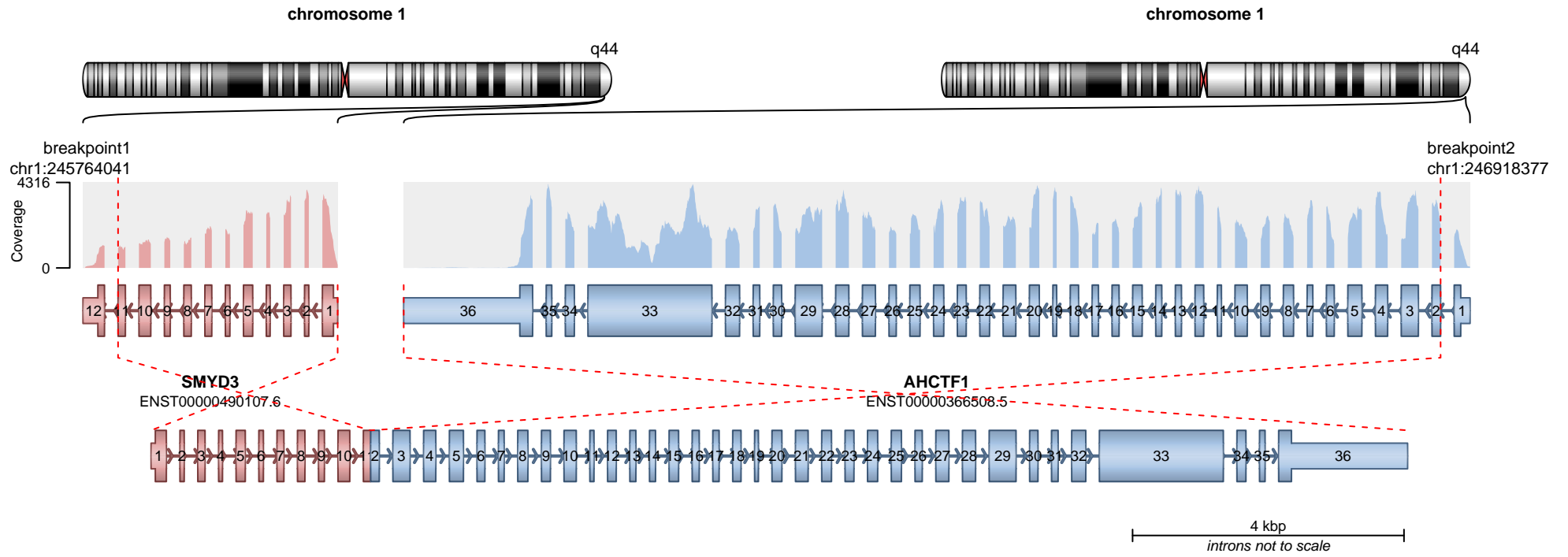
RETAINED PROTEIN DOMAINS
reading frame unclear



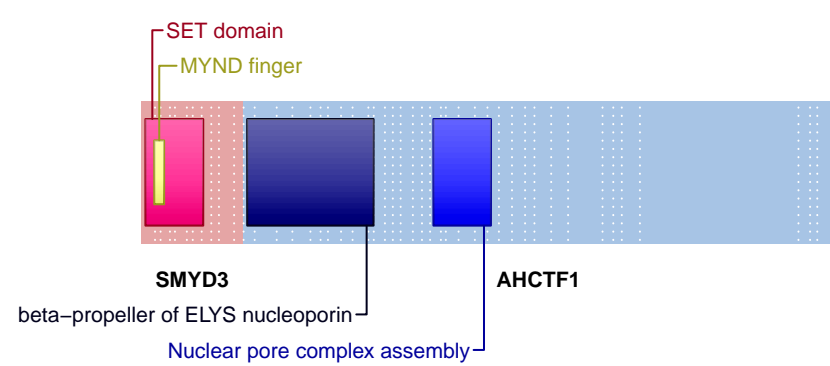
SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 0

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion