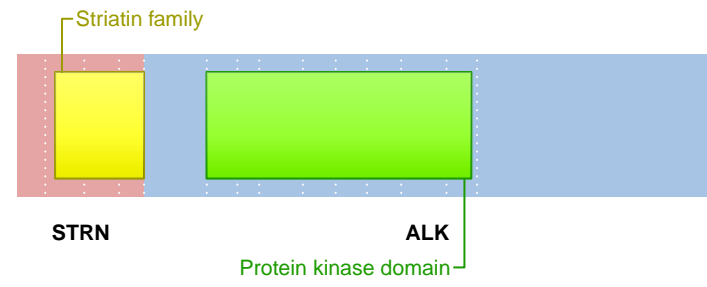


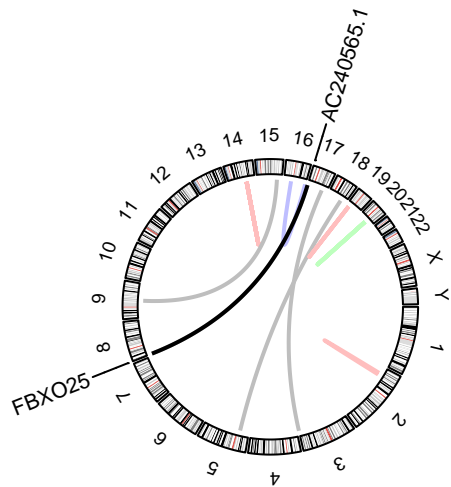
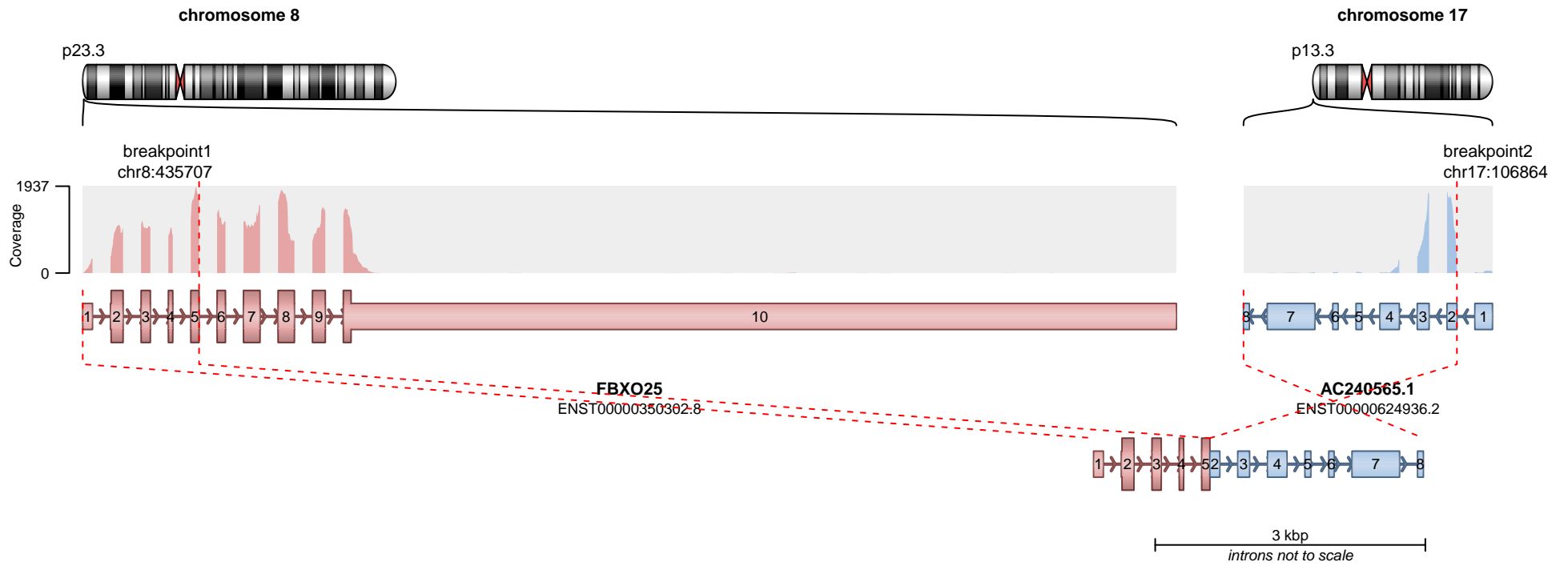
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 872
Discordant mates = 4

- translocation
- duplication
- deletion
- inversion

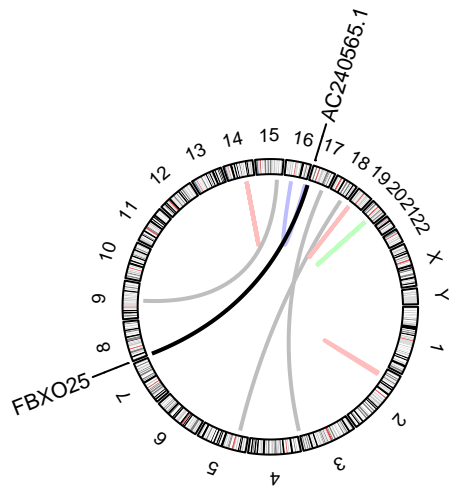
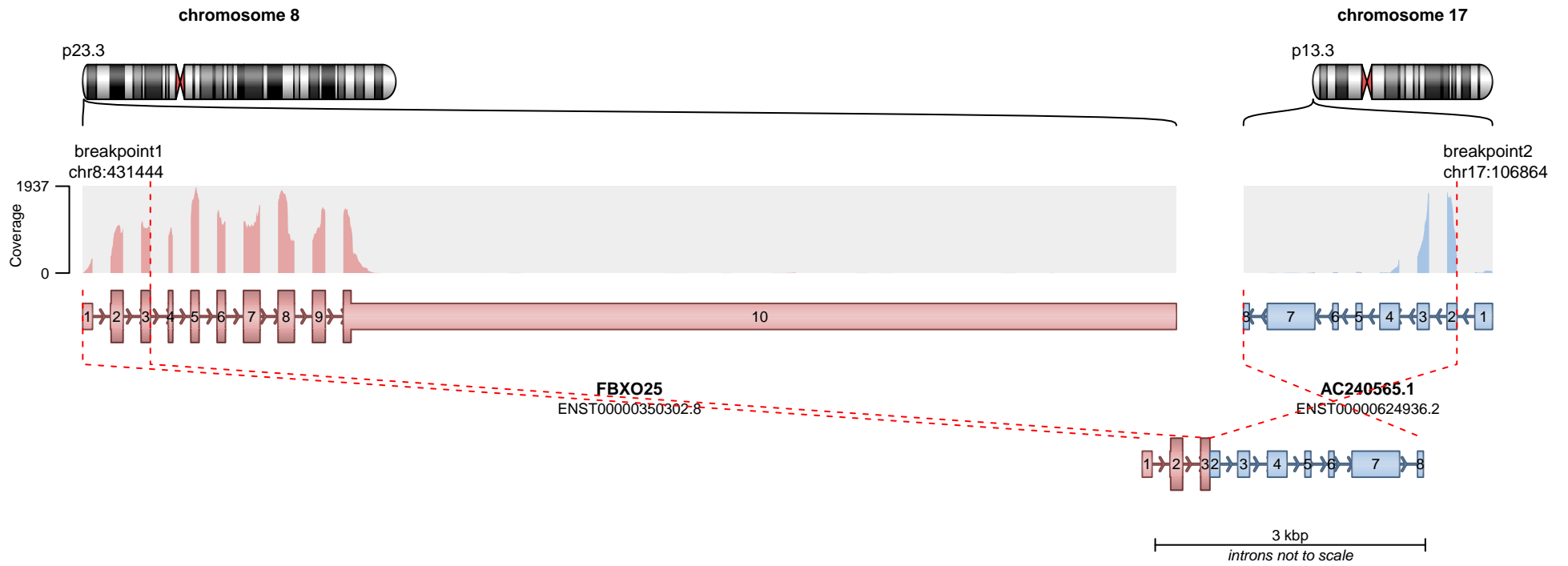


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 223
Discordant mates = 0

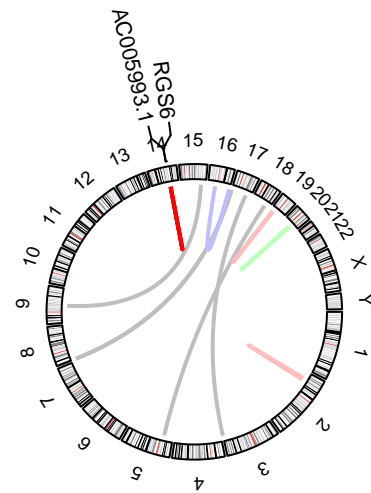
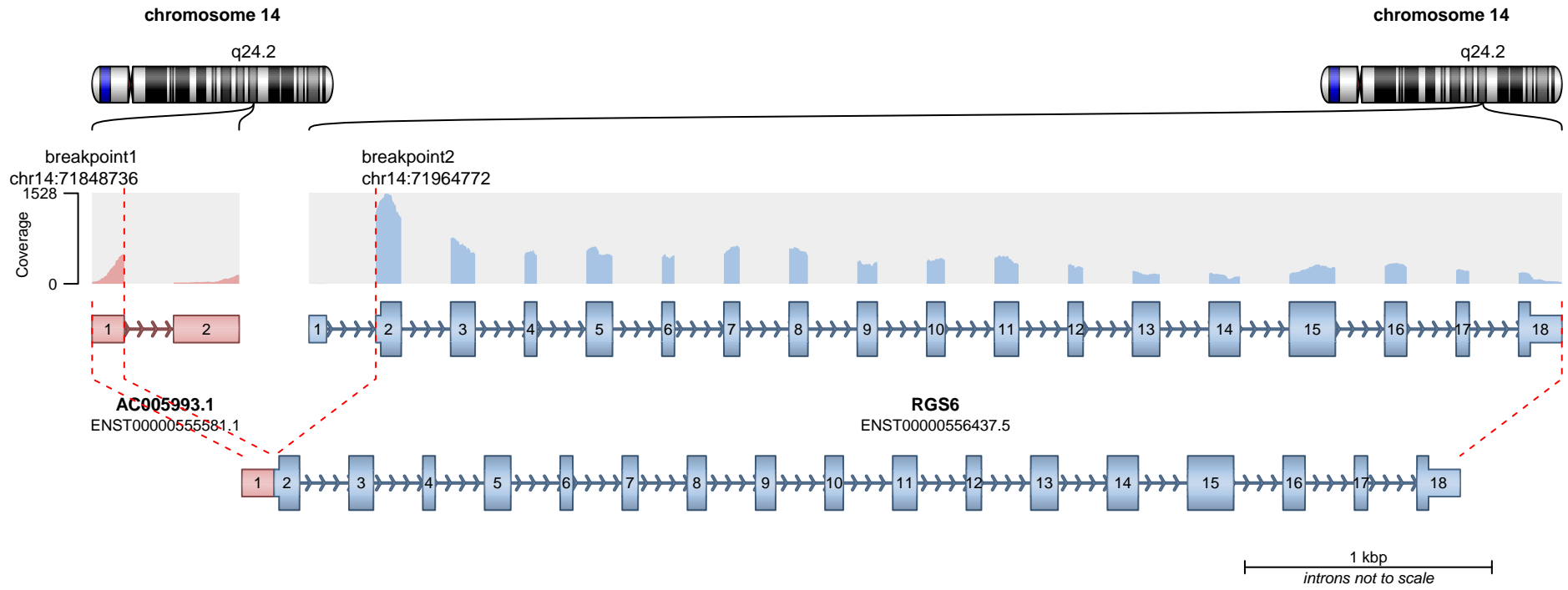


— translocation — deletion
— duplication — inversion

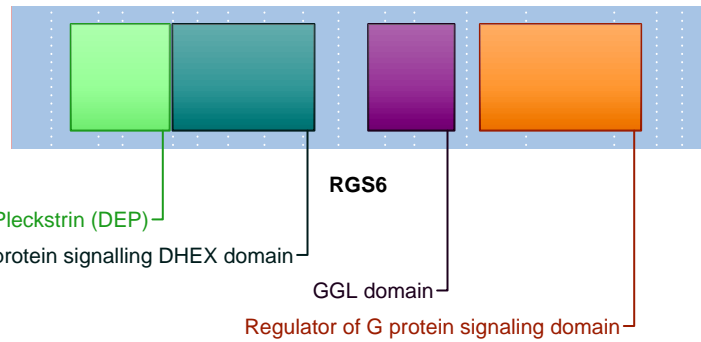
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



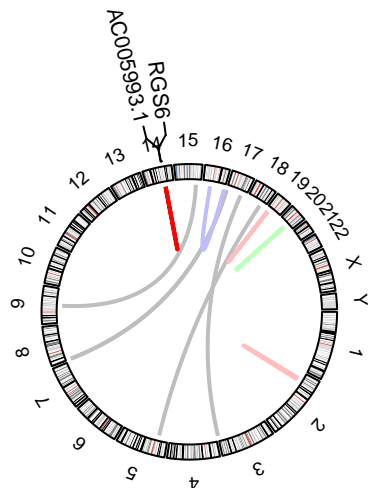
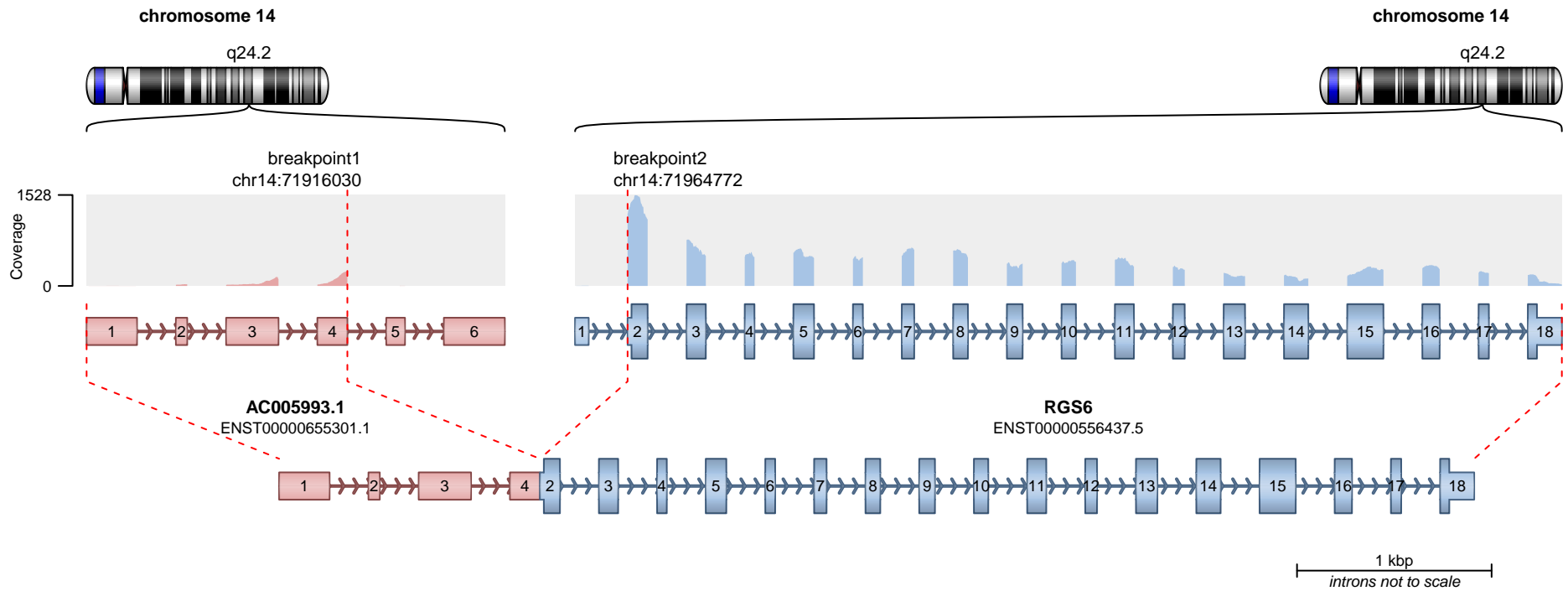
RETAINED PROTEIN DOMAINS
reading frame unclear



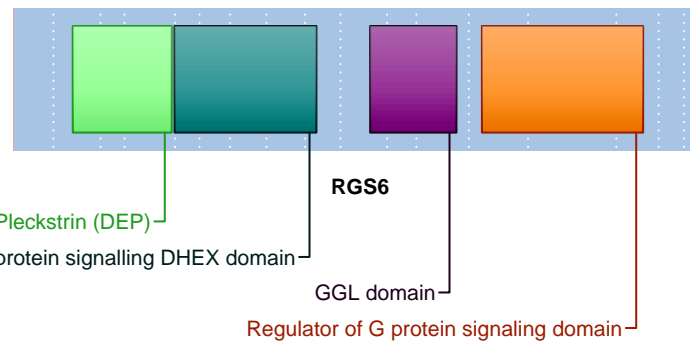
SUPPORTING READ COUNT

Split reads = 215
Discordant mates = 6

- translocation
- duplication
- deletion
- inversion



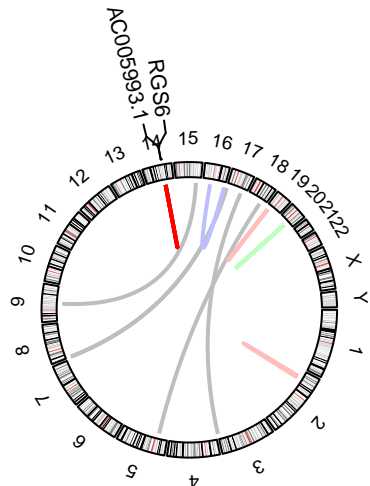
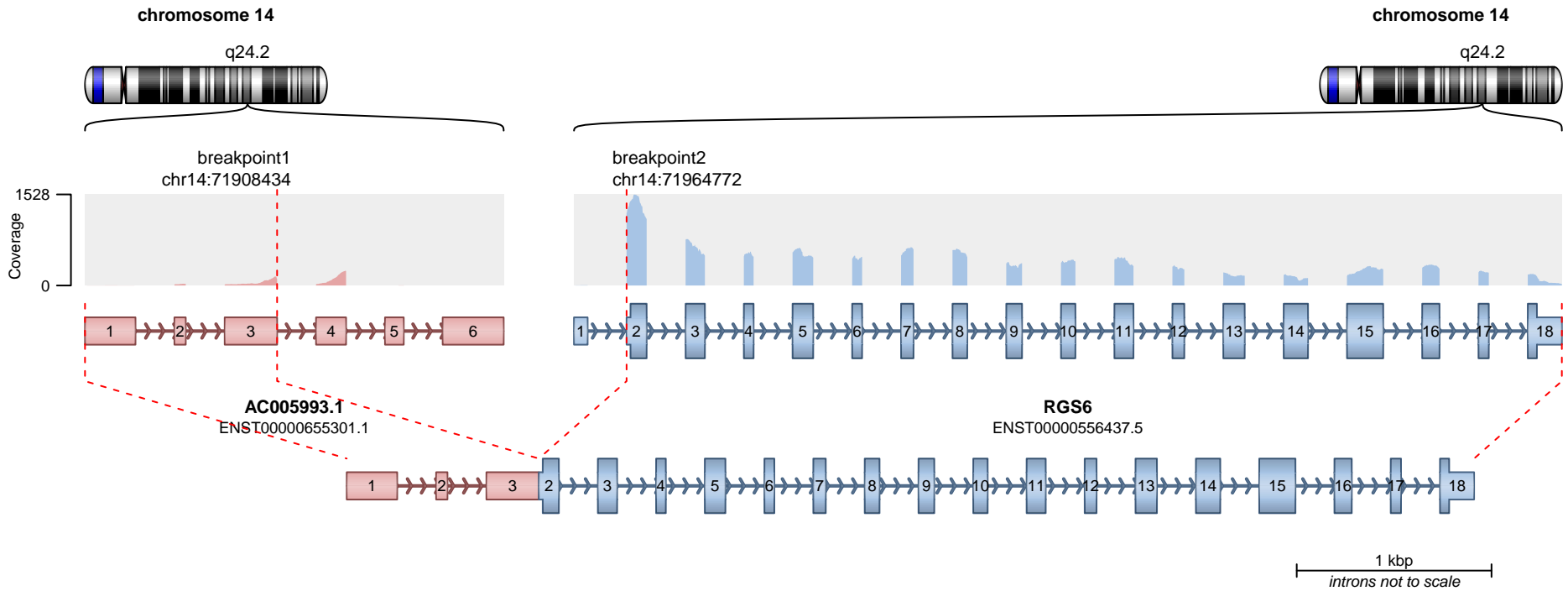
RETAINED PROTEIN DOMAINS
reading frame unclear



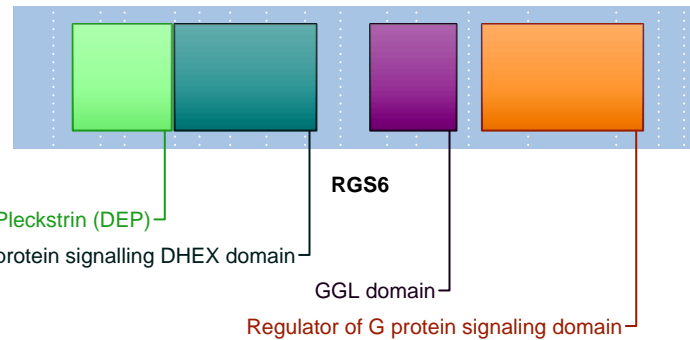
SUPPORTING READ COUNT

Split reads = 111
Discordant mates = 14

- translocation
- duplication
- deletion
- inversion



RETAINED PROTEIN DOMAINS
reading frame unclear



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

Regulator of G-protein signalling DHEX domain

RGS6

GGL domain

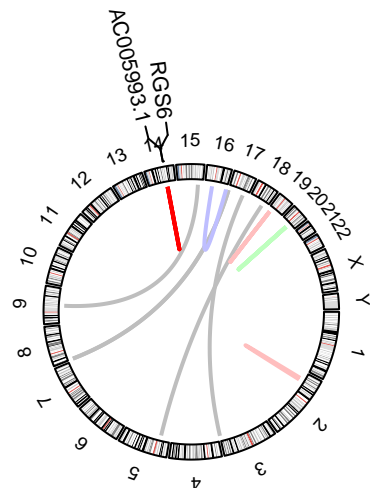
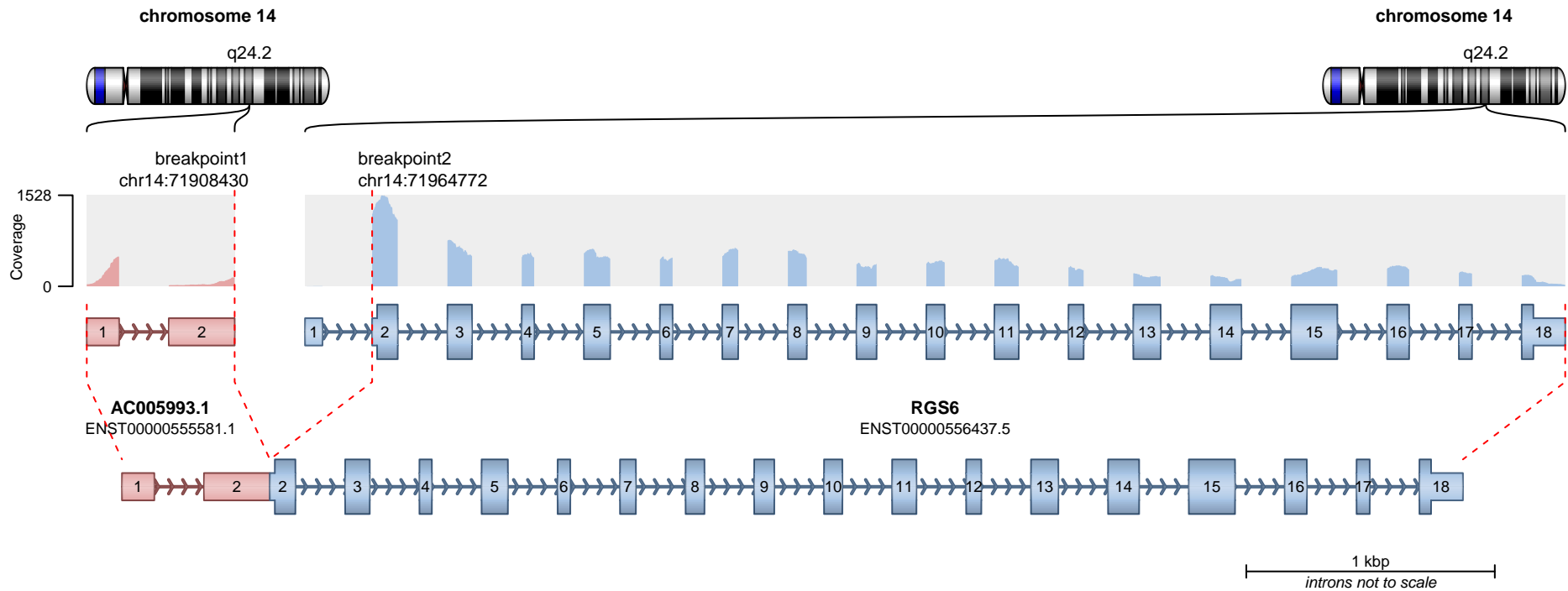
Regulator of G protein signaling domain

SUPPORTING READ COUNT

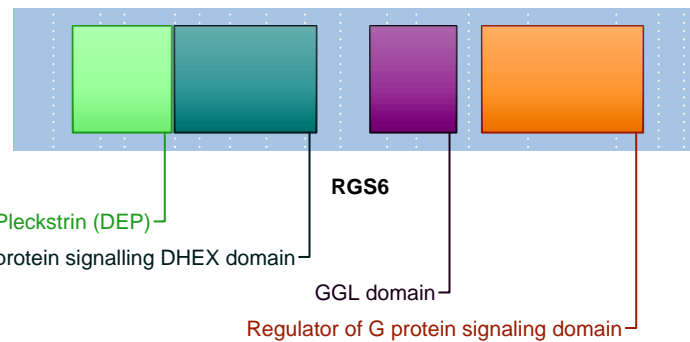
Split reads = 48

Discordant mates = 10

- translocation
- duplication
- deletion
- inversion



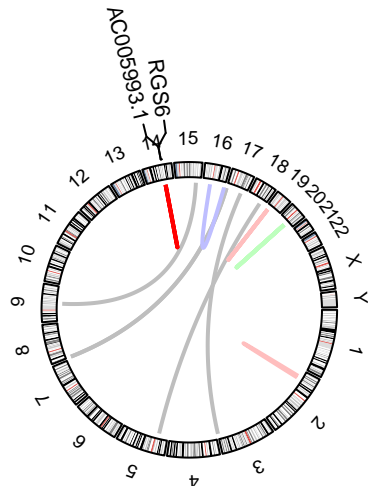
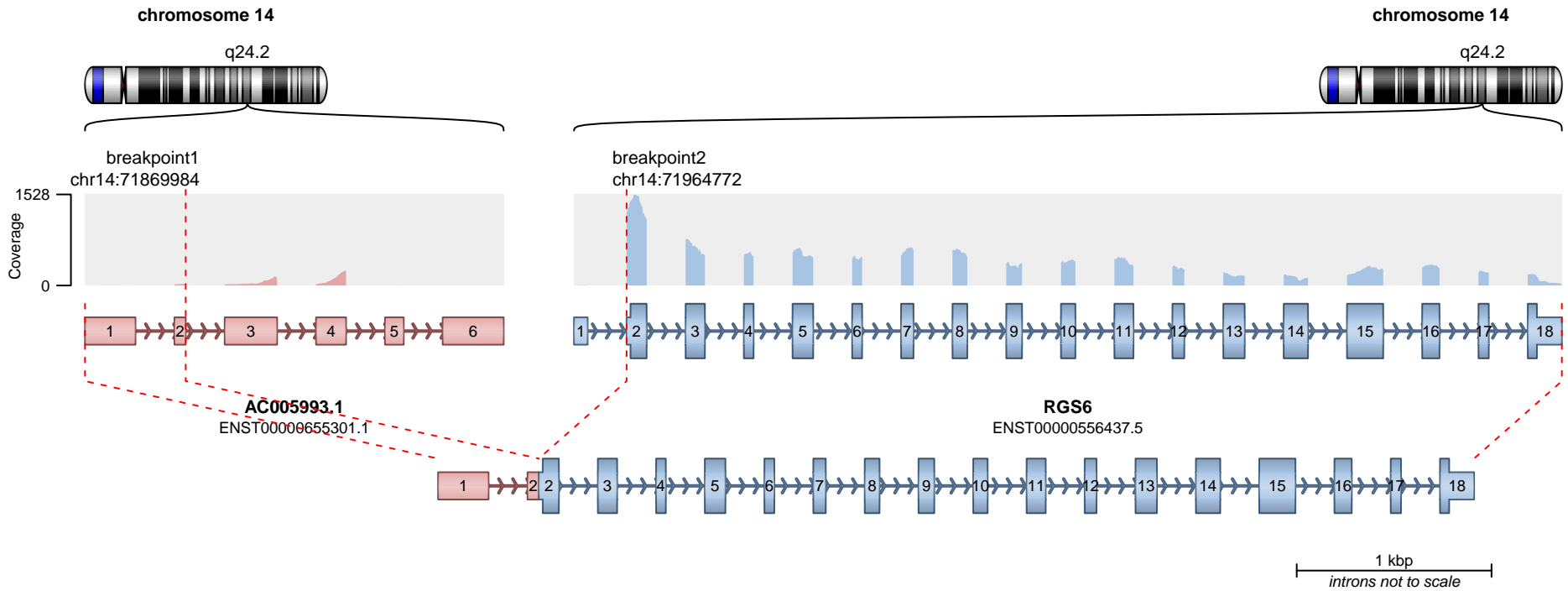
RETAINED PROTEIN DOMAINS
reading frame unclear



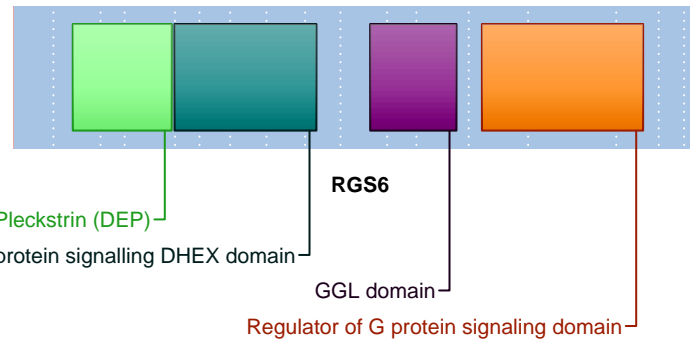
SUPPORTING READ COUNT

Split reads = 15
Discordant mates = 10

— translocation — deletion
— duplication — inversion



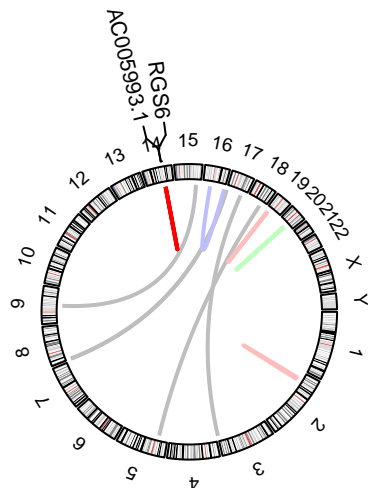
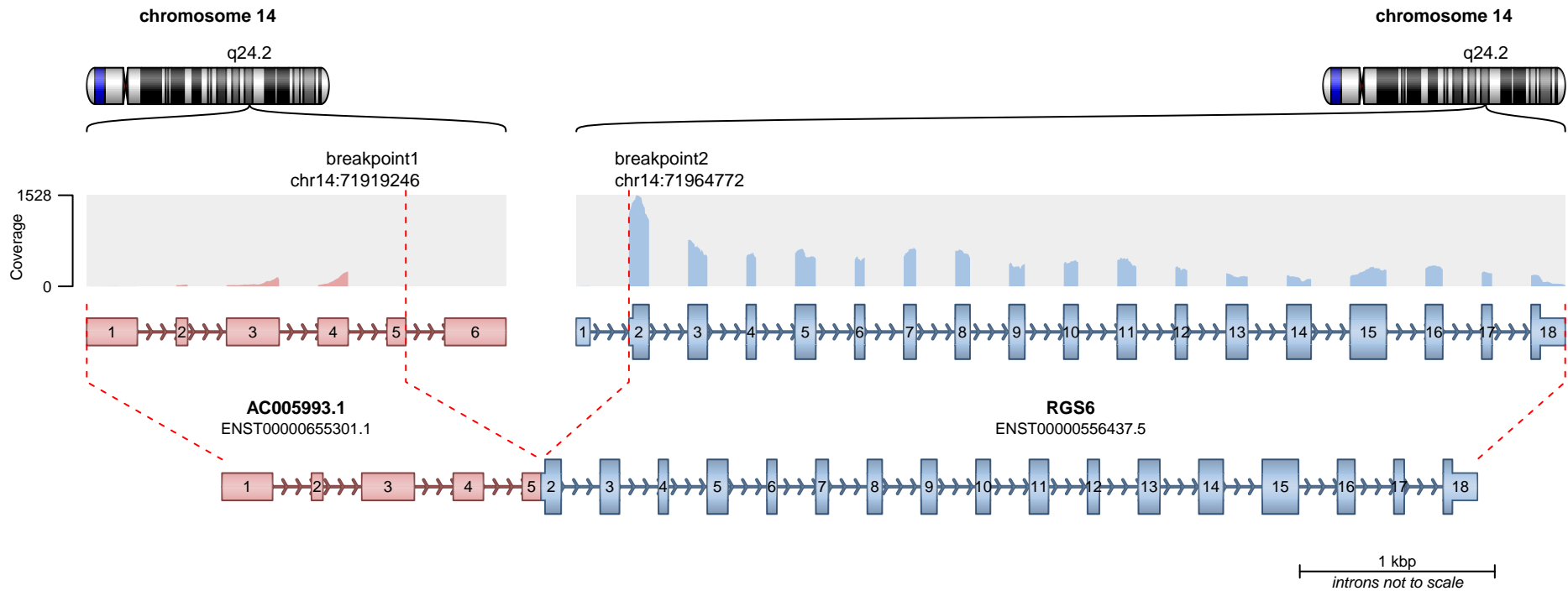
RETAINED PROTEIN DOMAINS
reading frame unclear



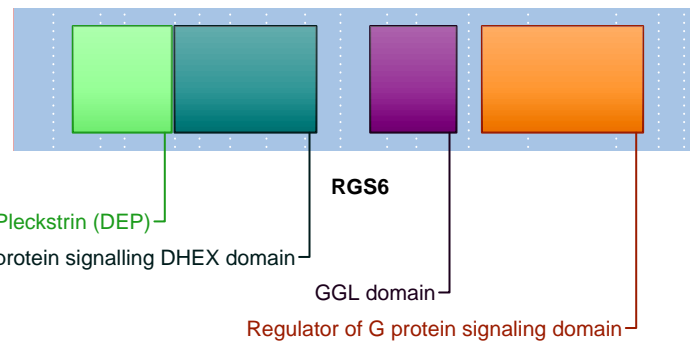
SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 6

- translocation
- duplication
- deletion
- inversion



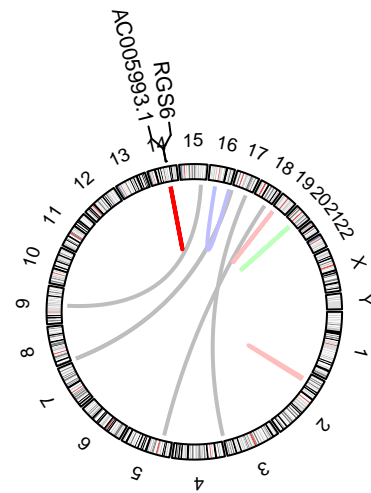
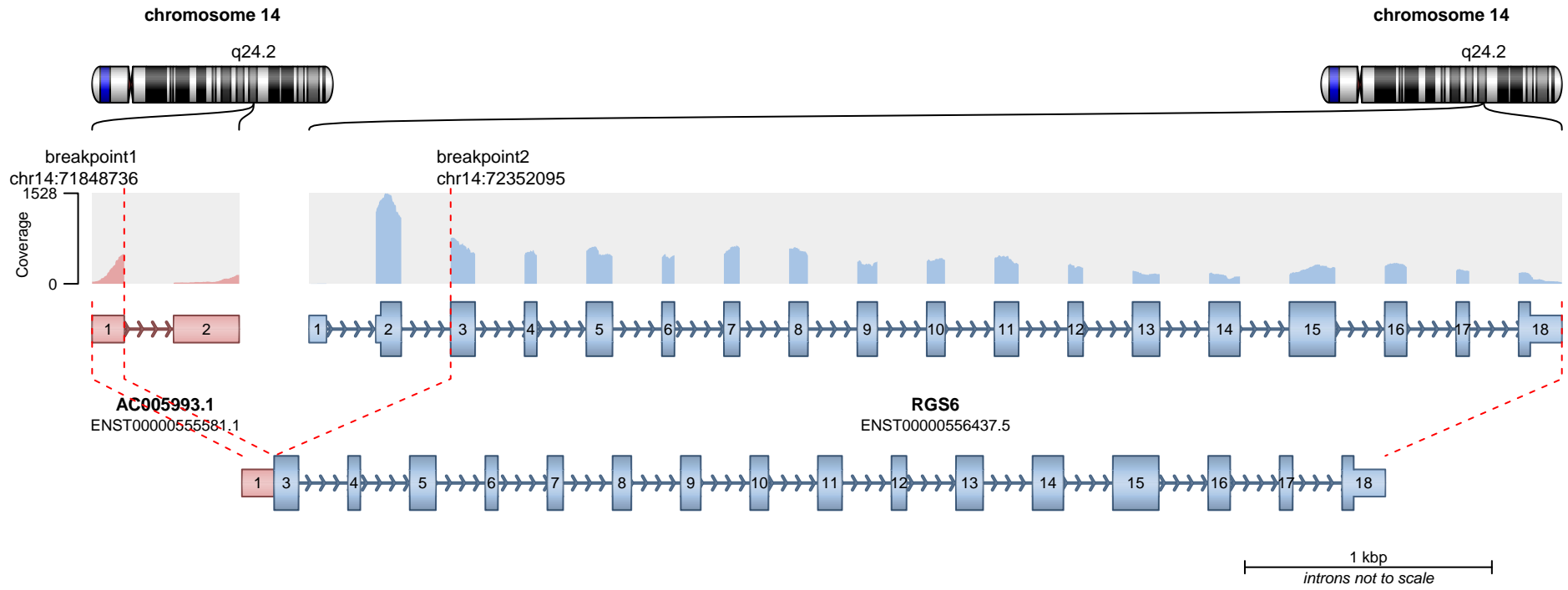
RETAINED PROTEIN DOMAINS
reading frame unclear



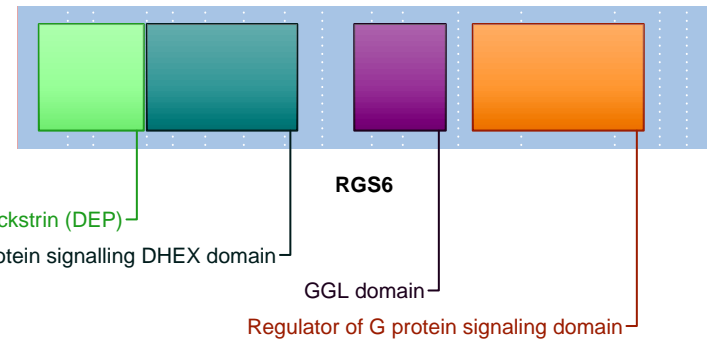
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 14

- translocation
- duplication
- deletion
- inversion



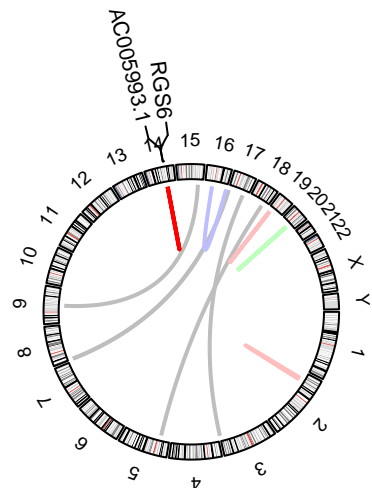
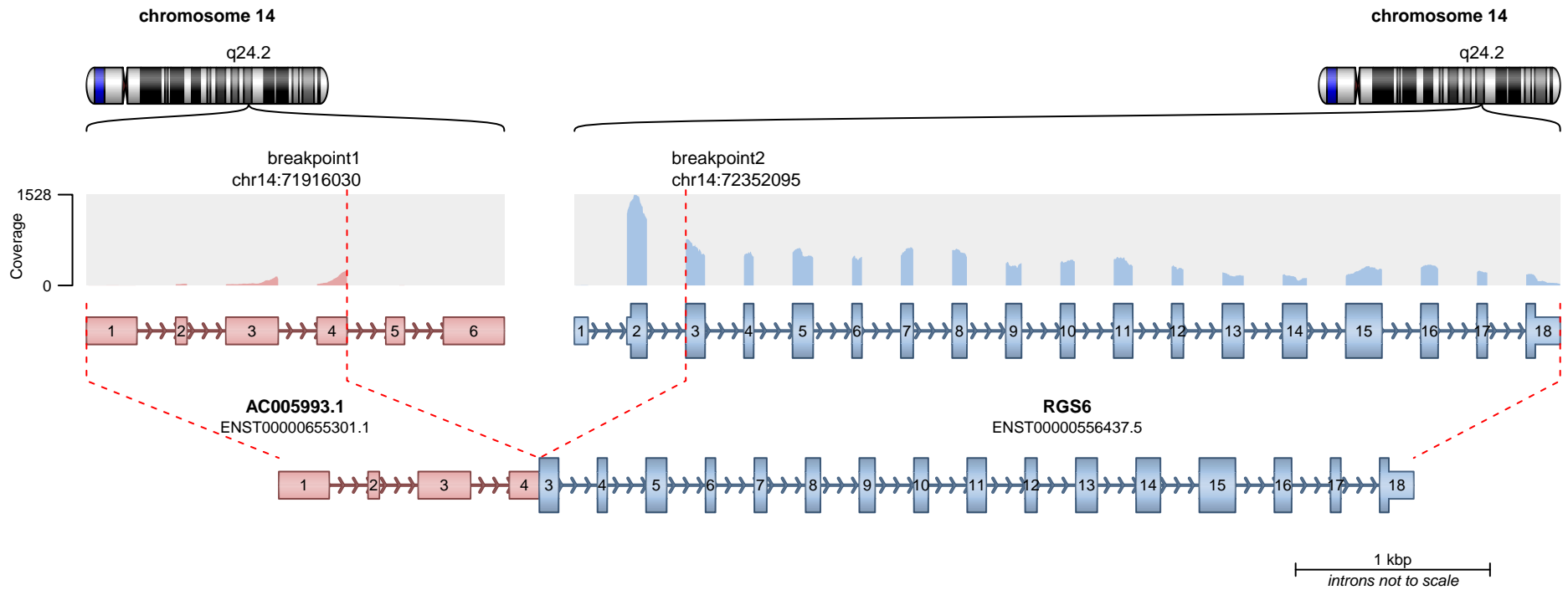
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 1

- 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

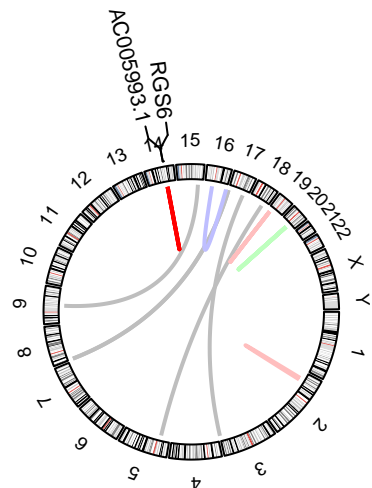
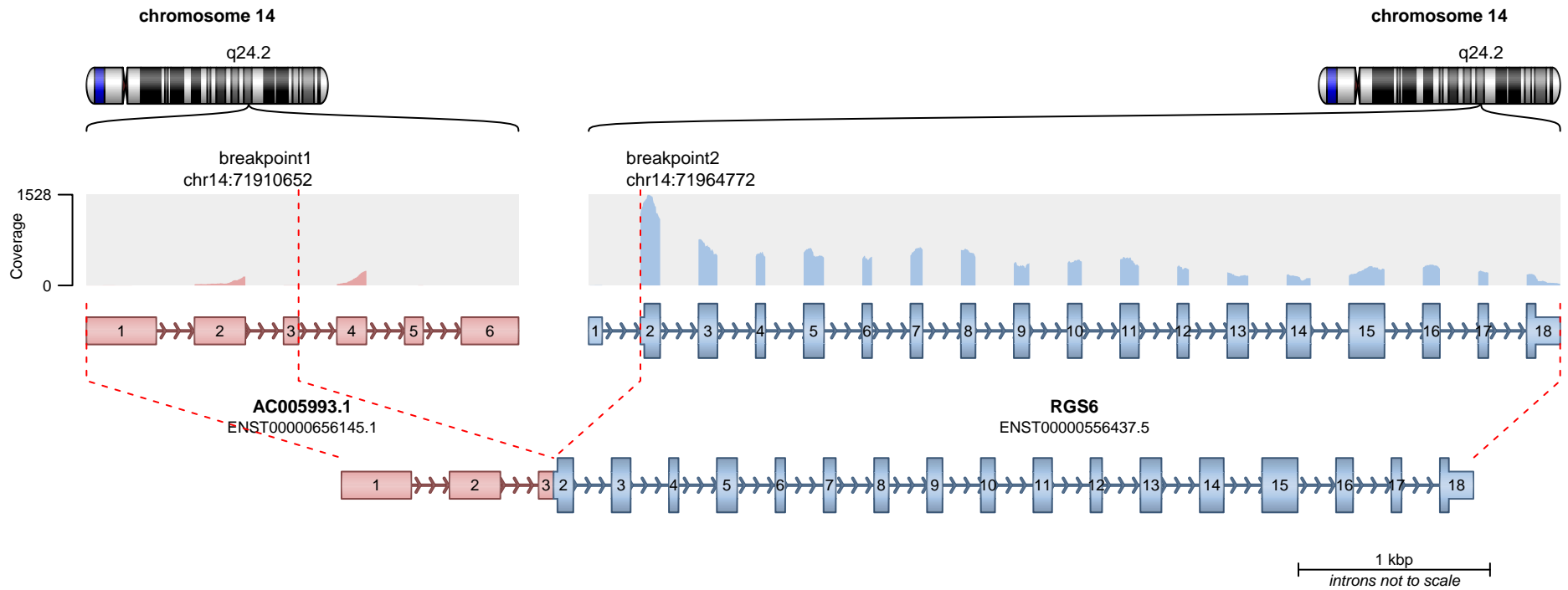
RETAINED PROTEIN DOMAINS
reading frame unclear

SUPPORTING READ COUNT

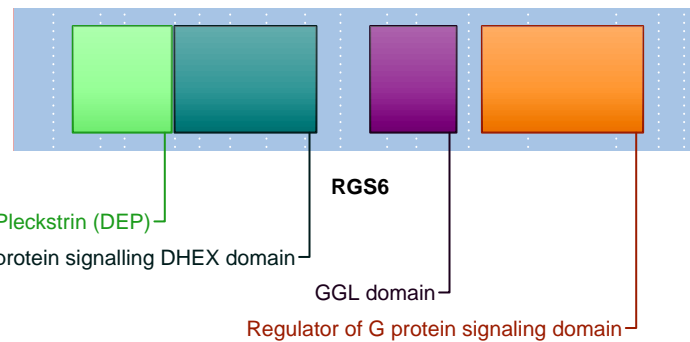
Split reads = 3

Discordant mates = 3

— translocation — deletion
— duplication — inversion



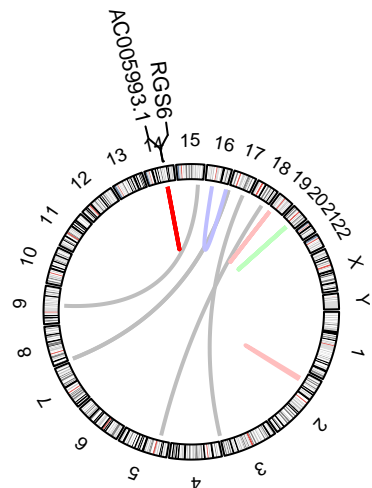
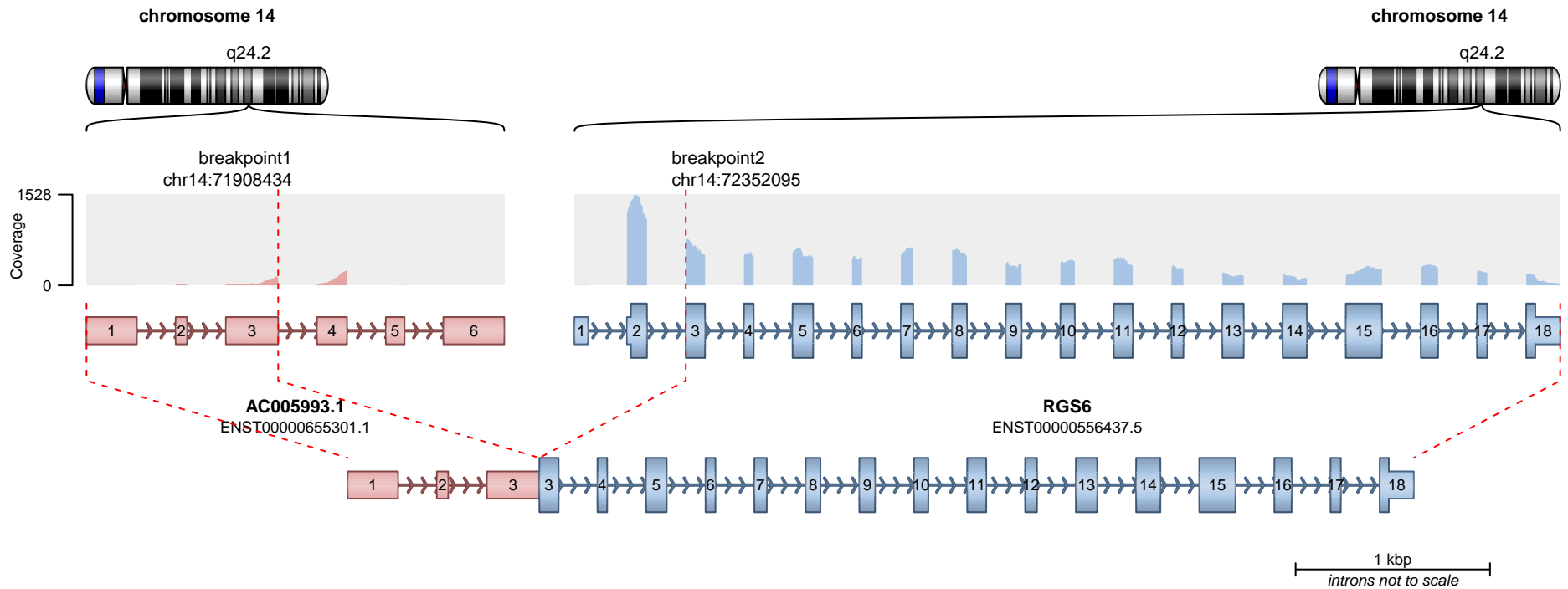
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 10

- 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

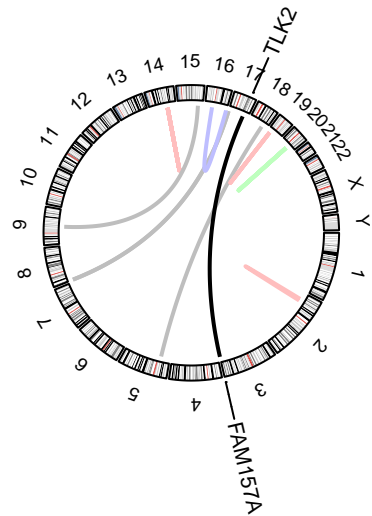
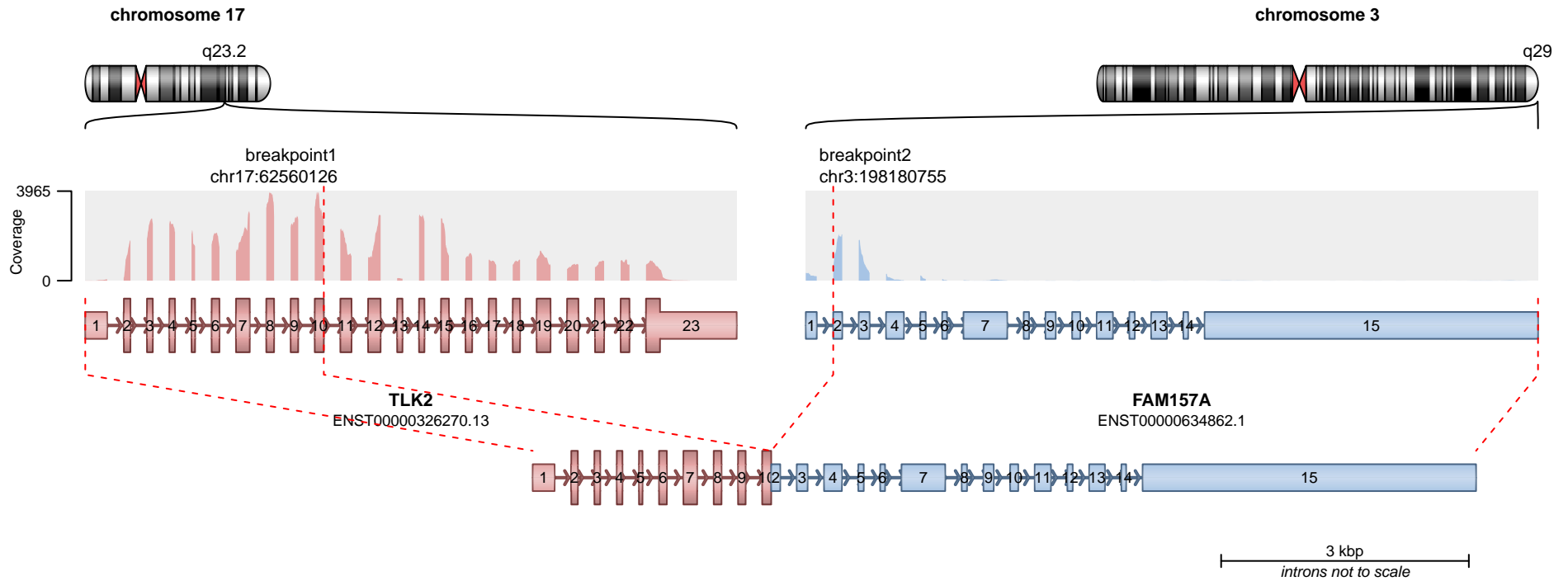
RETAINED PROTEIN DOMAINS
reading frame unclear

SUPPORTING READ COUNT

Split reads = 1

Discordant mates = 3

— translocation — deletion
— duplication — inversion

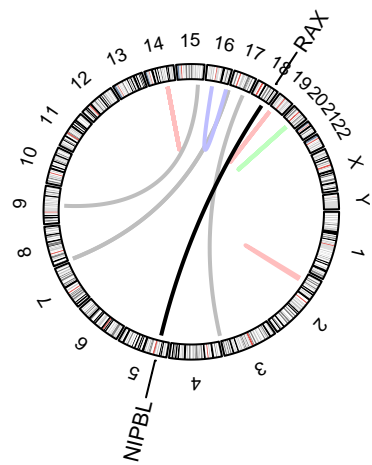
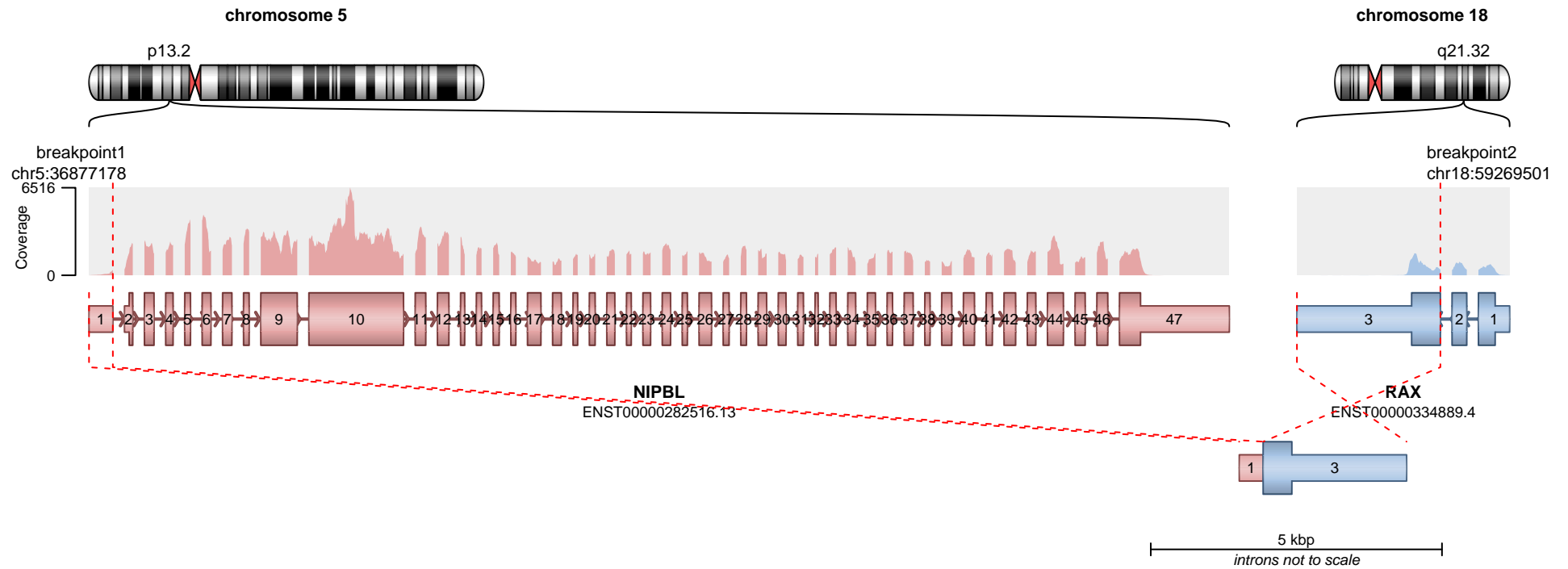


— translocation — deletion
— duplication — inversion

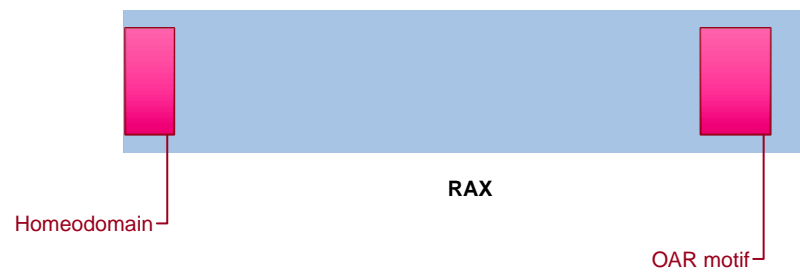
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 111
Discordant mates = 0



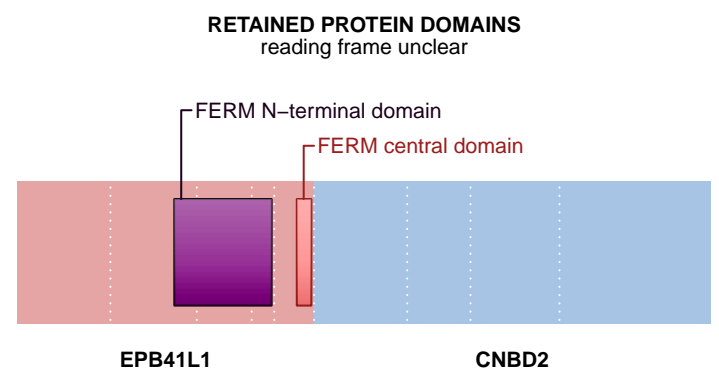
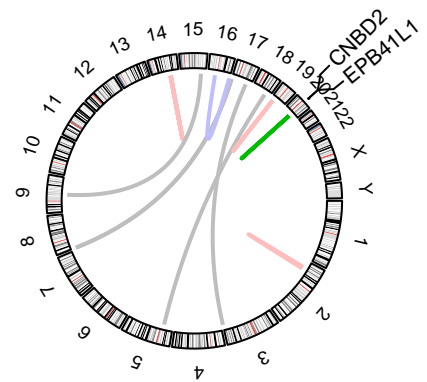
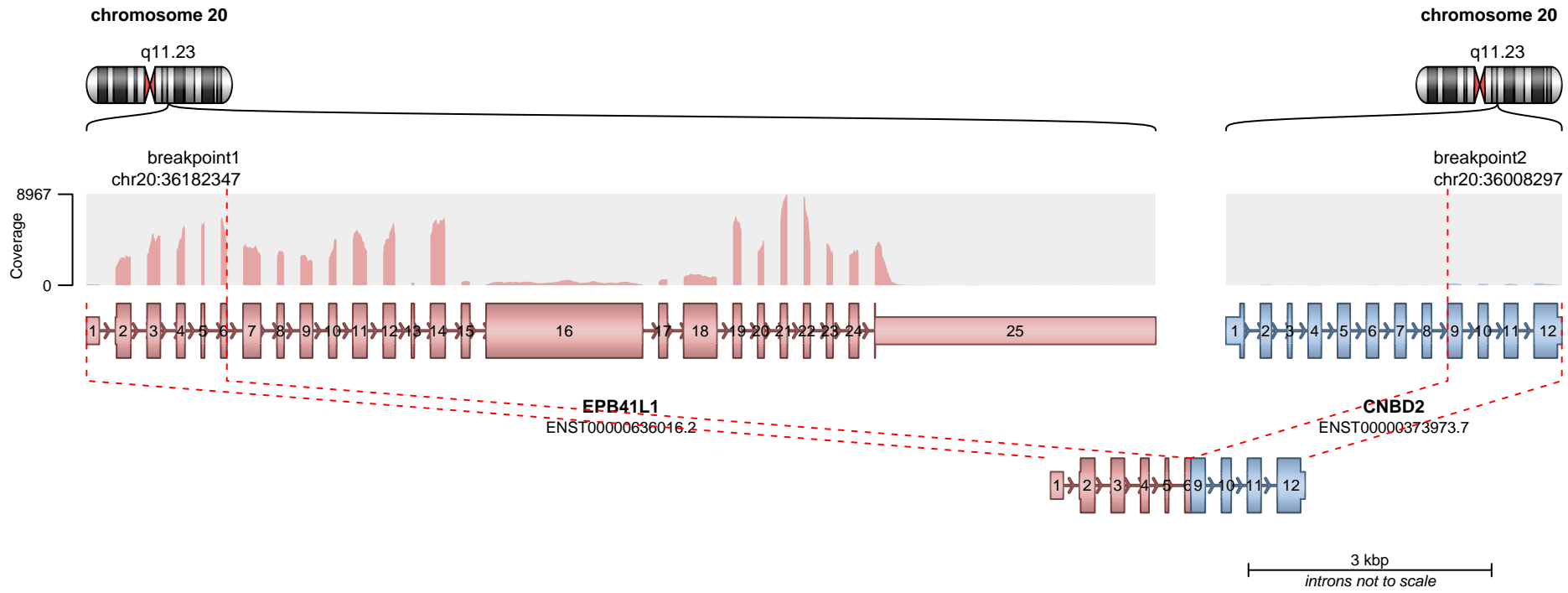
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 56
Discordant mates = 2

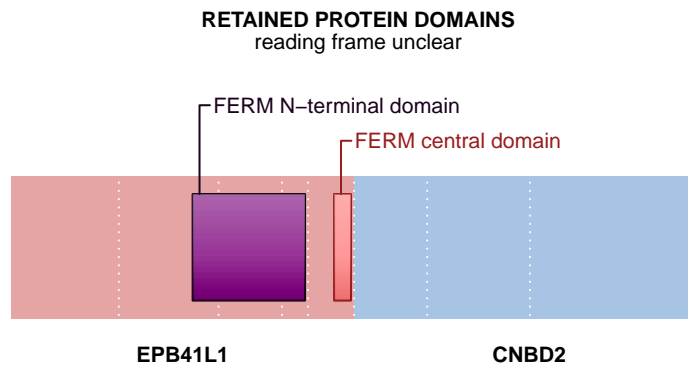
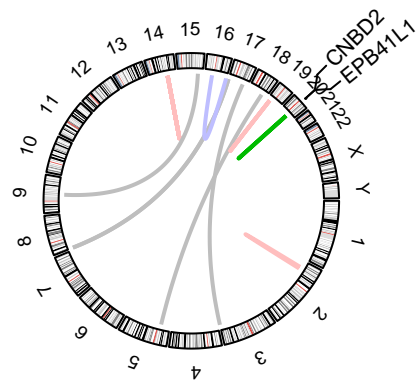
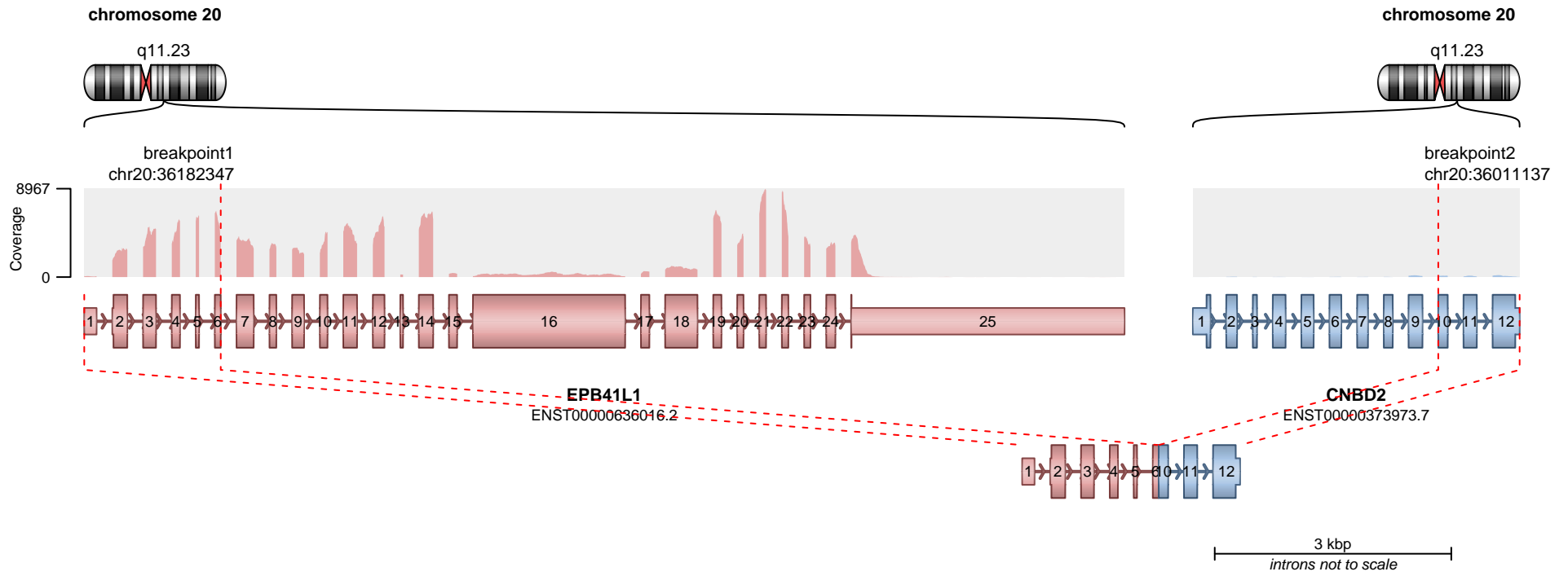
- translocation
- duplication
- deletion
- inversion



SUPPORTING READ COUNT

Split reads = 46
Discordant mates = 2

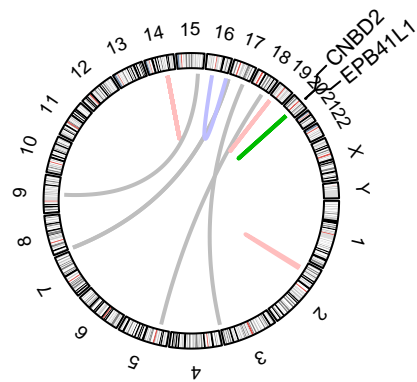
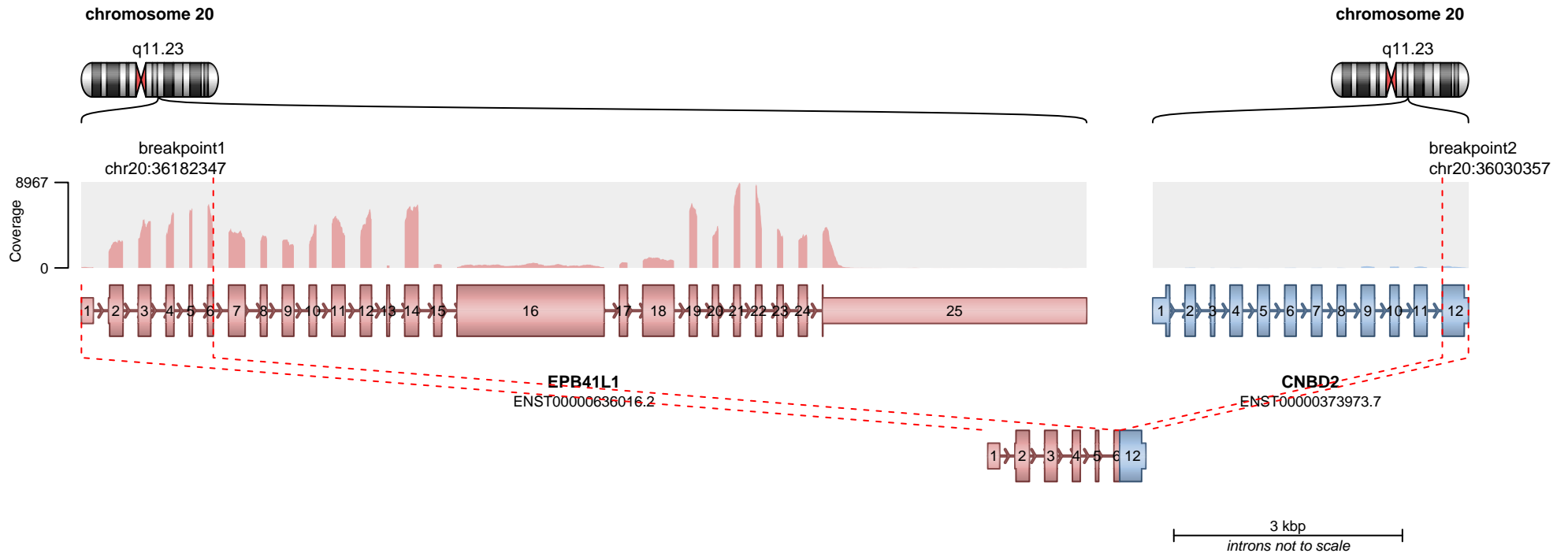
— translocation — deletion
— duplication — inversion



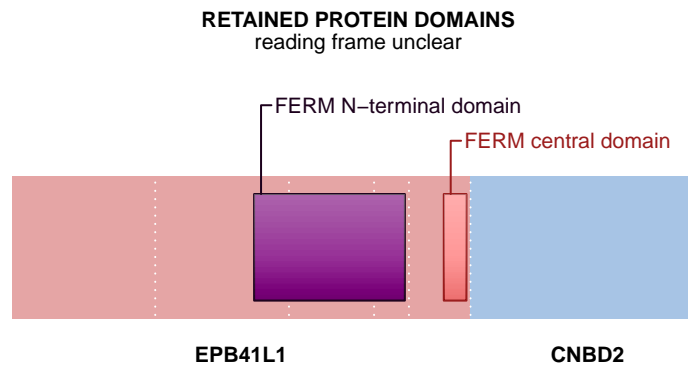
SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 1

— translocation — deletion
— duplication — inversion

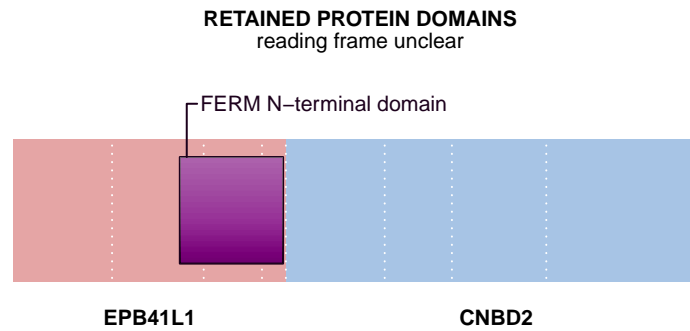
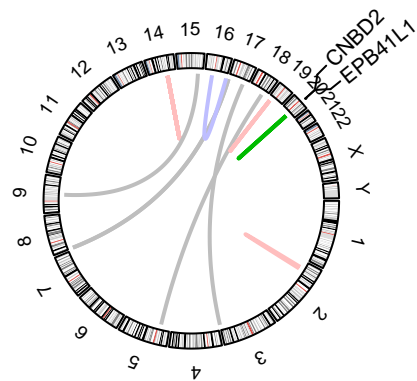
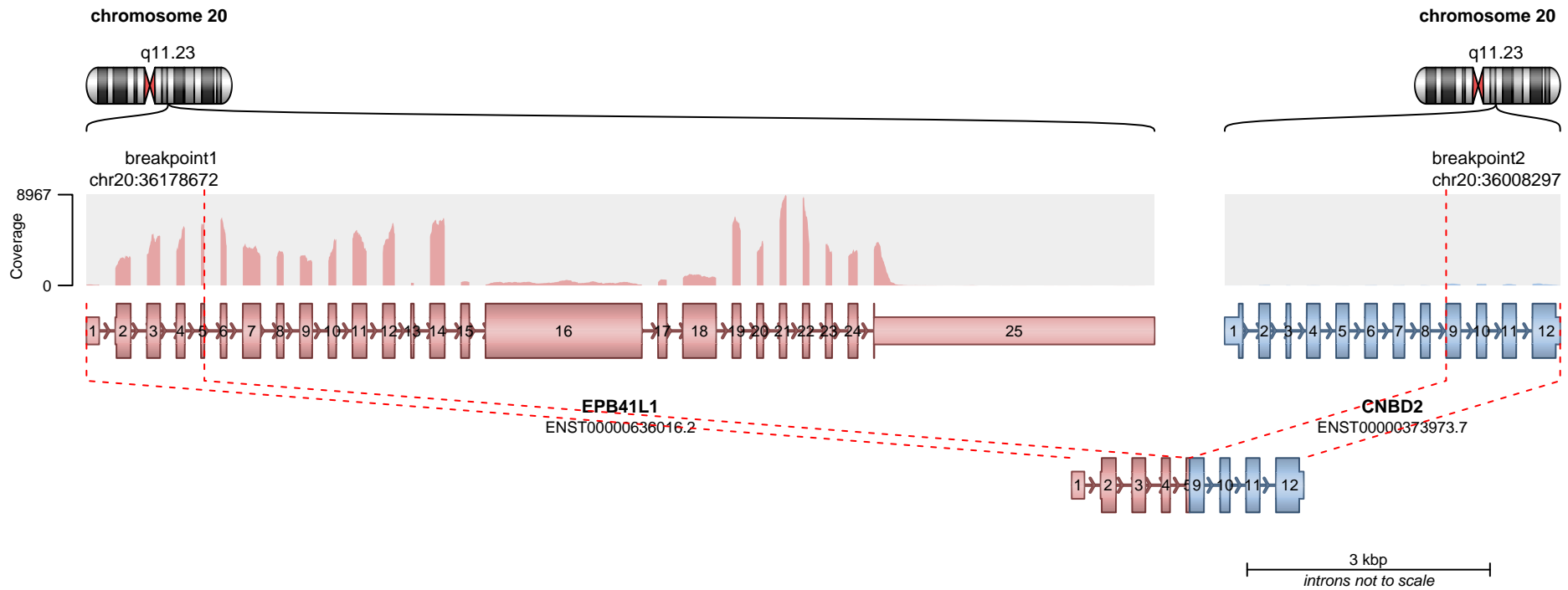


— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

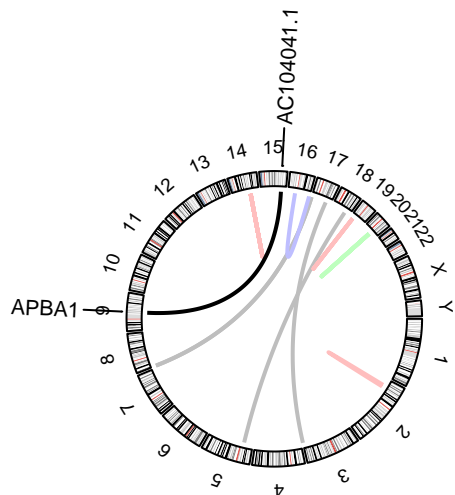
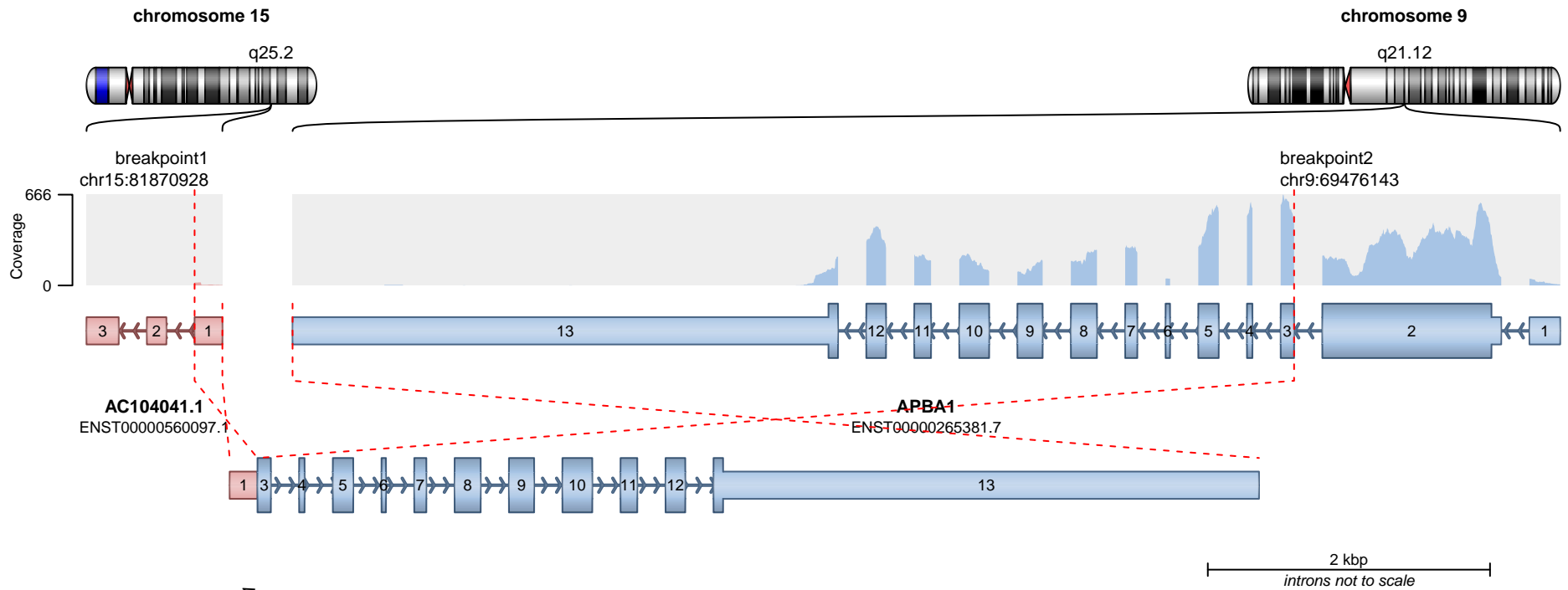
Split reads = 10
Discordant mates = 0



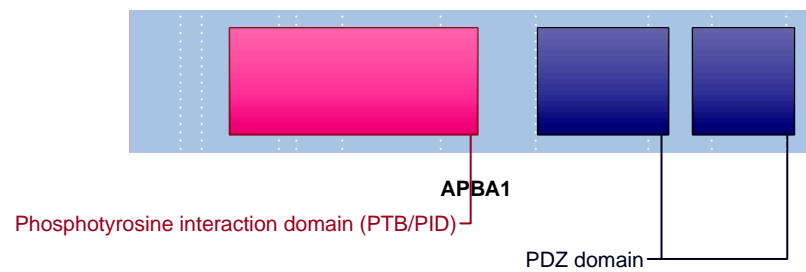
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

— translocation — deletion
— duplication — inversion



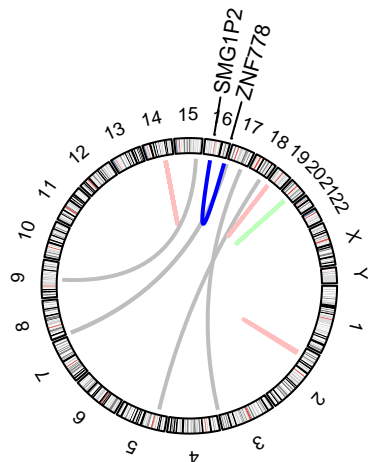
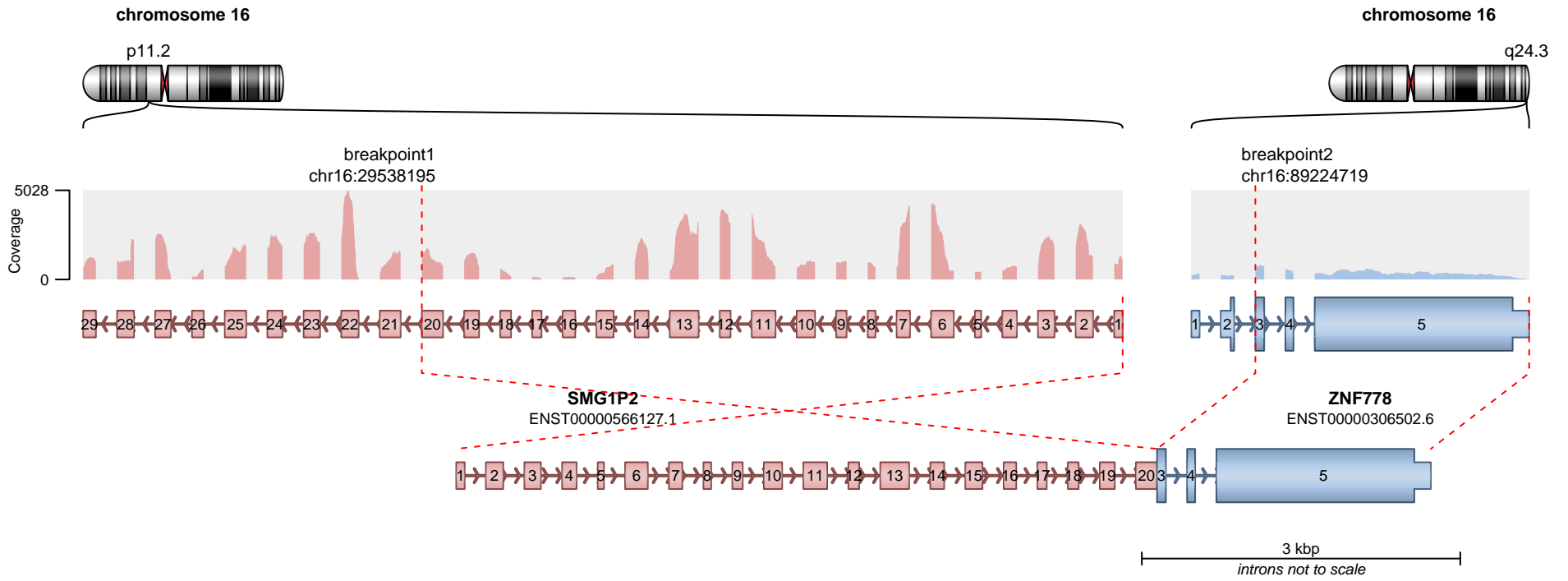
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

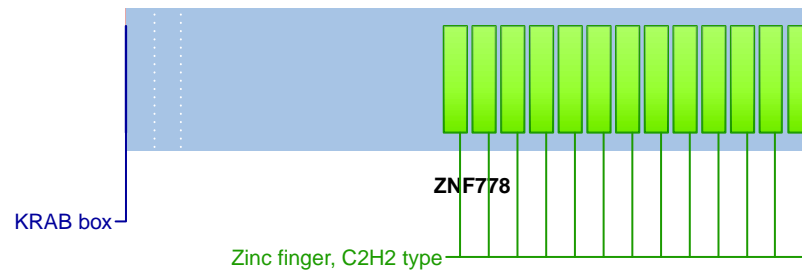
Split reads = 46
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



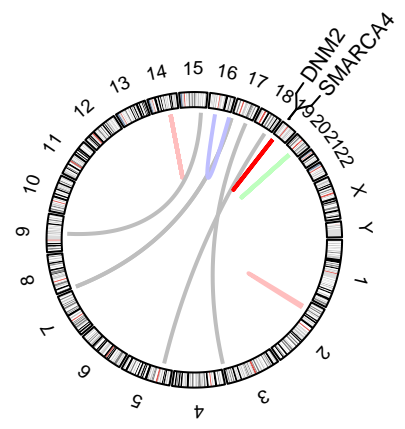
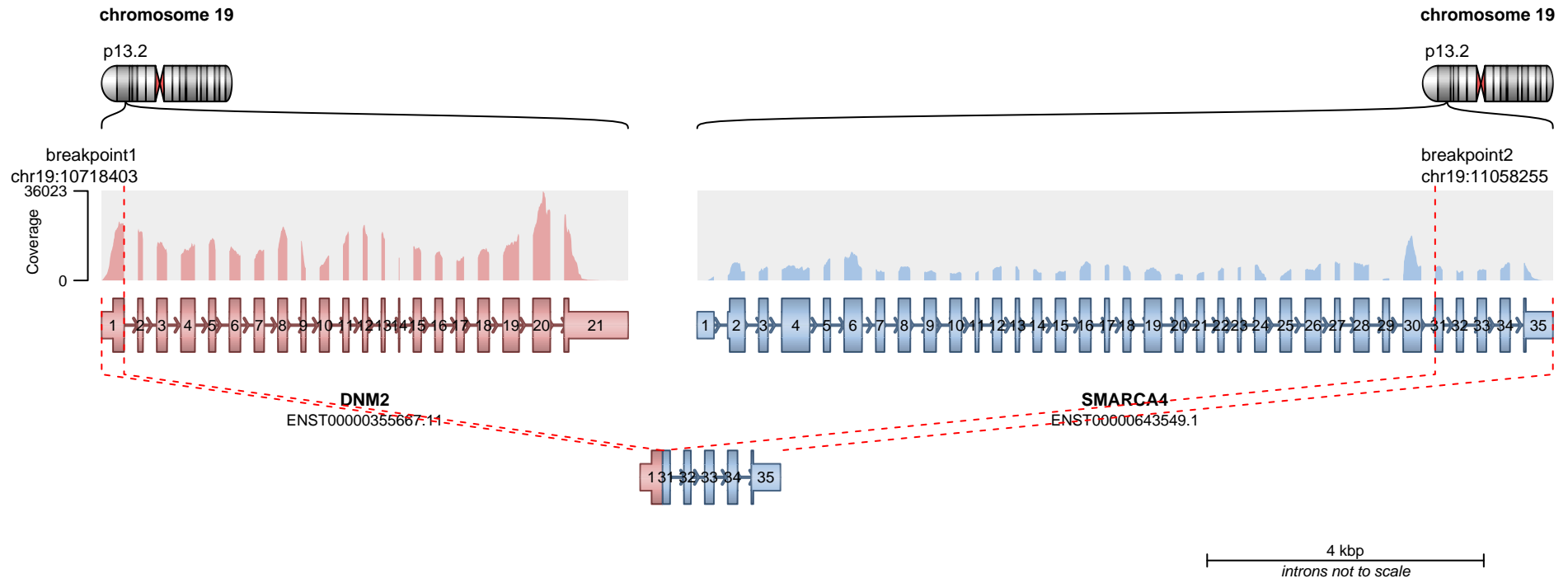
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear

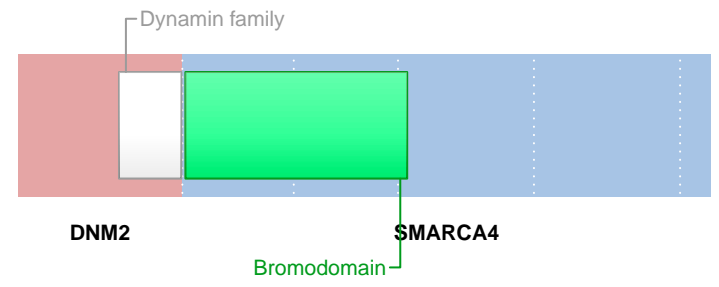


SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 1



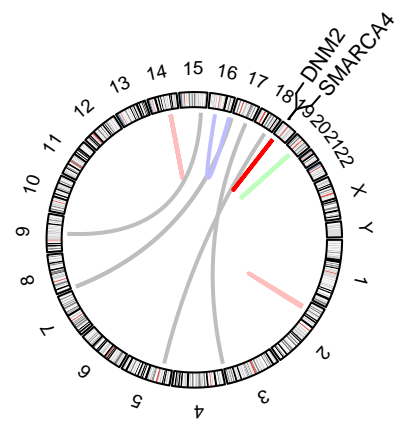
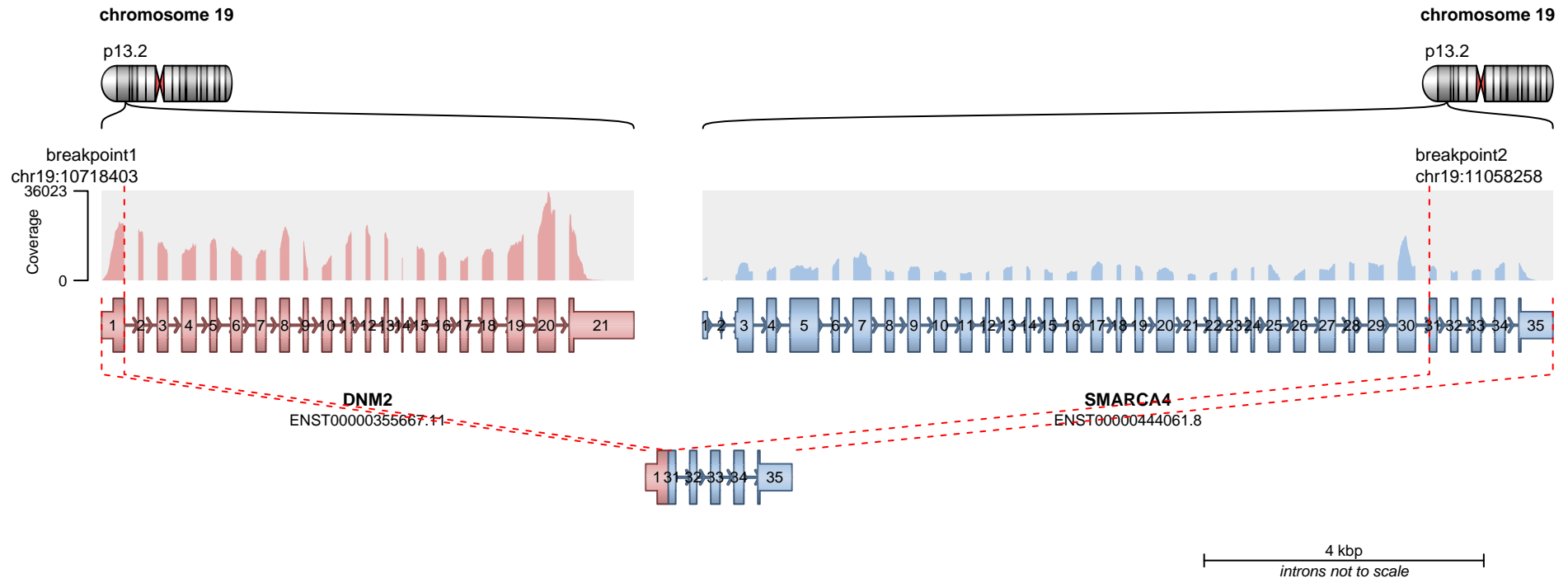
RETAINED PROTEIN DOMAINS
reading frame unclear



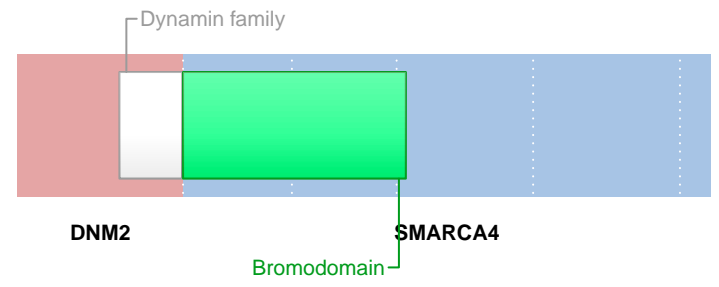
SUPPORTING READ COUNT

Split reads = 9
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion