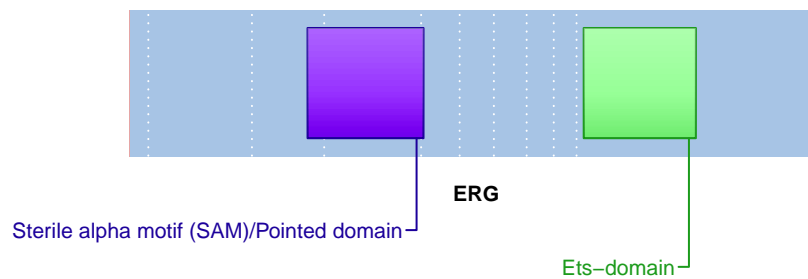


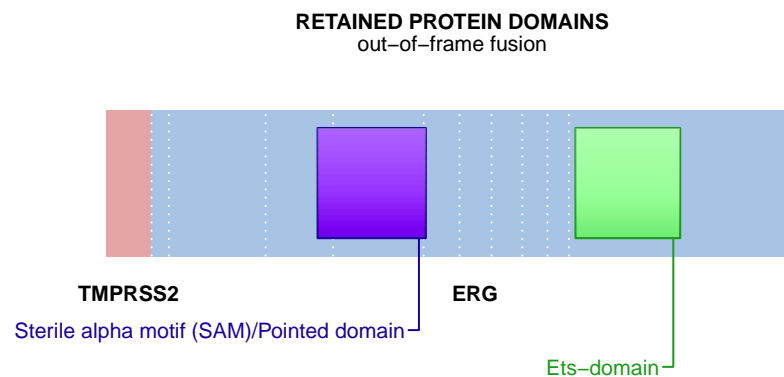
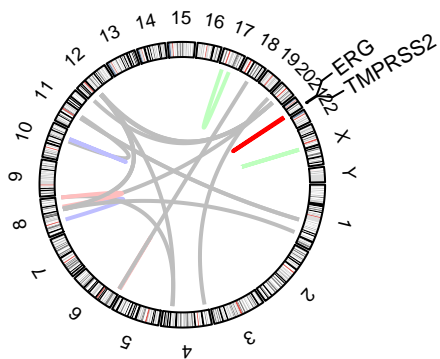
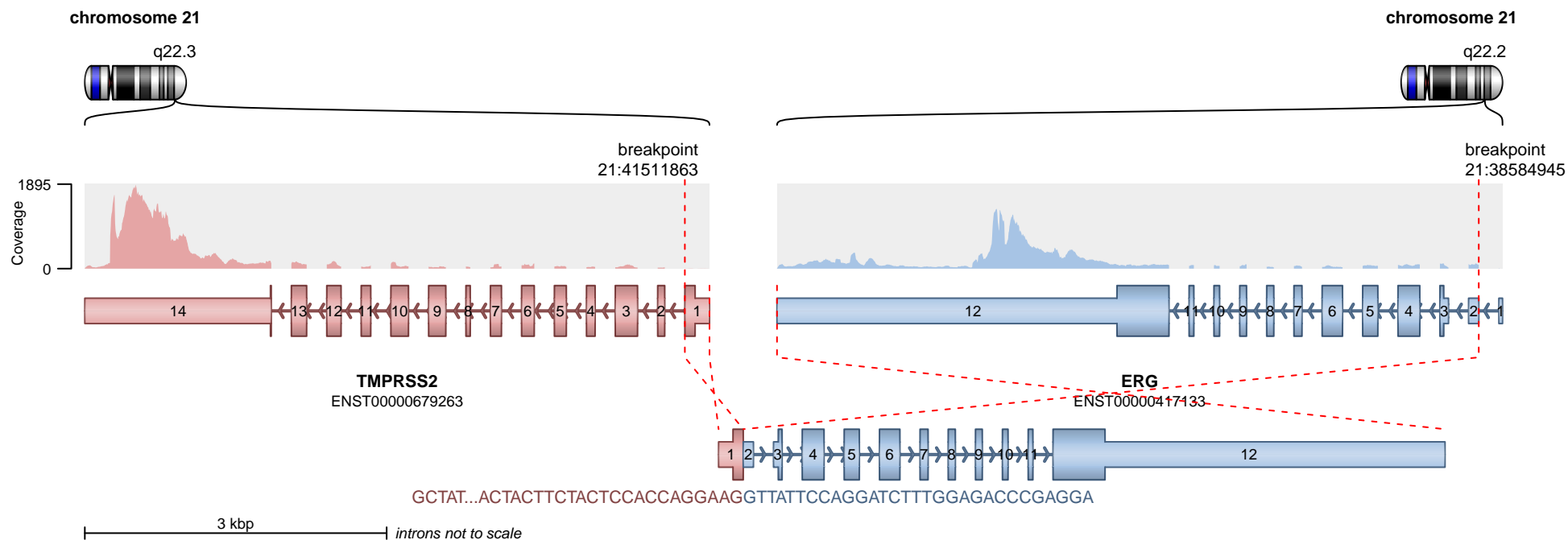
RETAINED PROTEIN DOMAINS reading frame unclear



SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 70

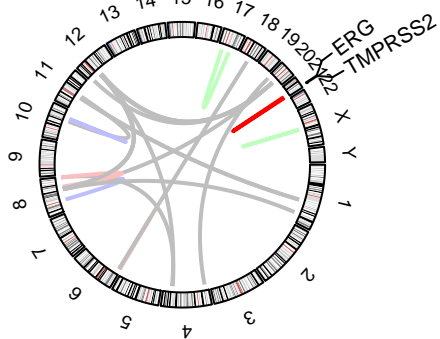
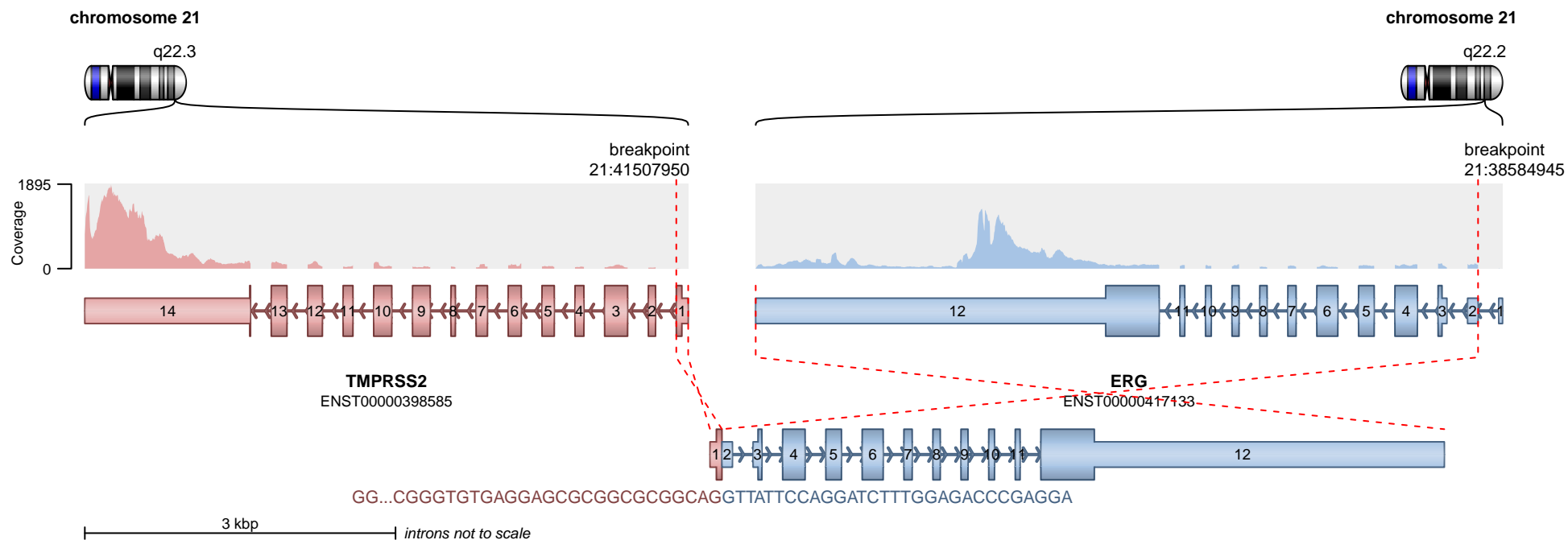
— translocation — deletion
— duplication — inversion



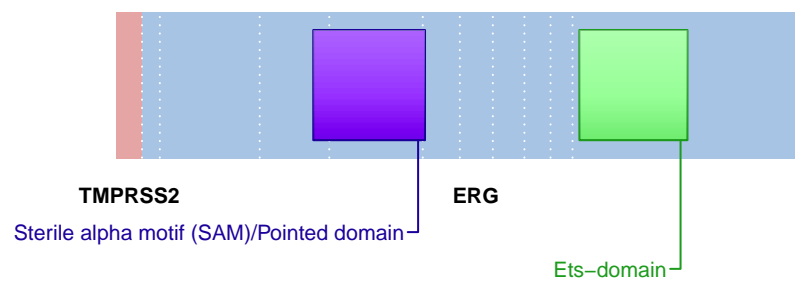
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 3

— translocation — deletion
— duplication — inversion



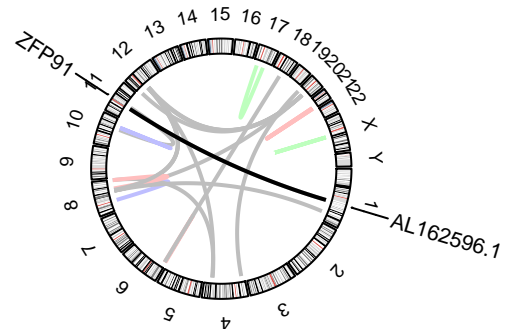
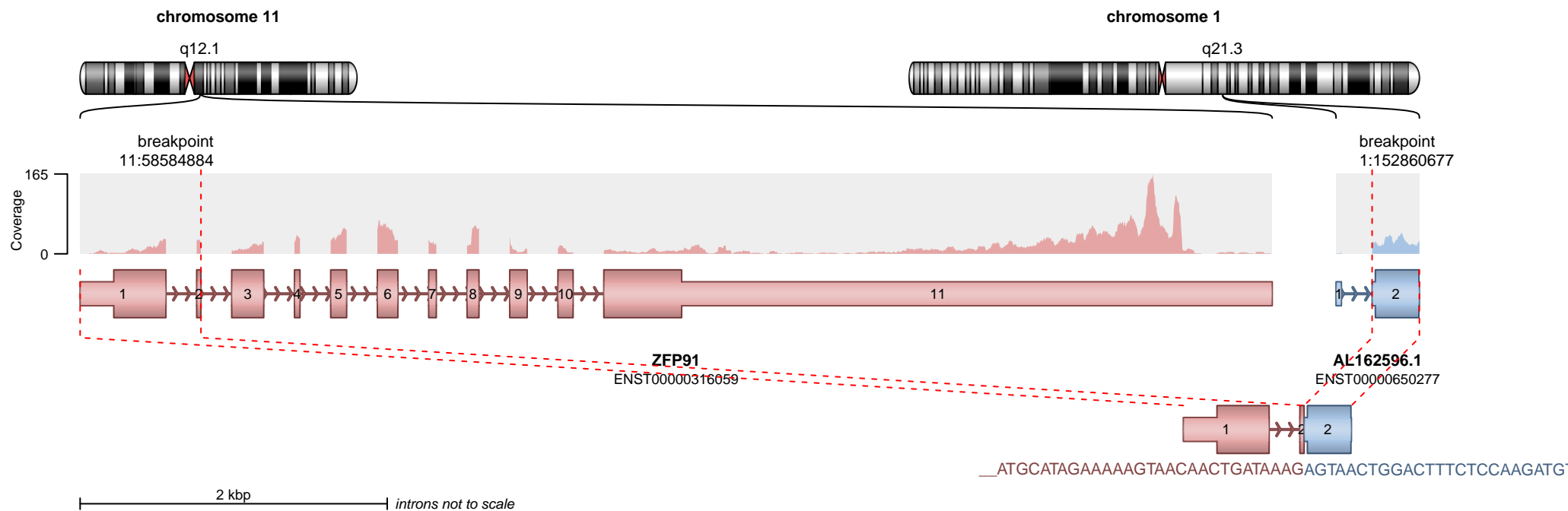
RETAINED PROTEIN DOMAINS reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 71

— translocation — deletion
— duplication — inversion

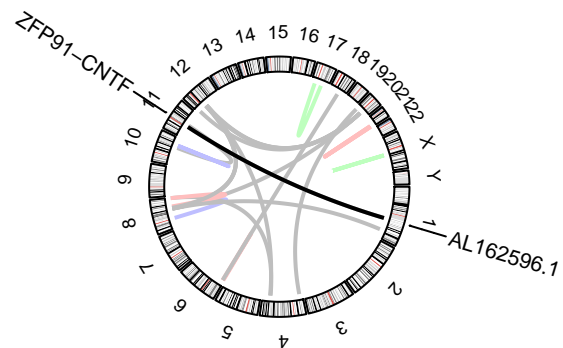
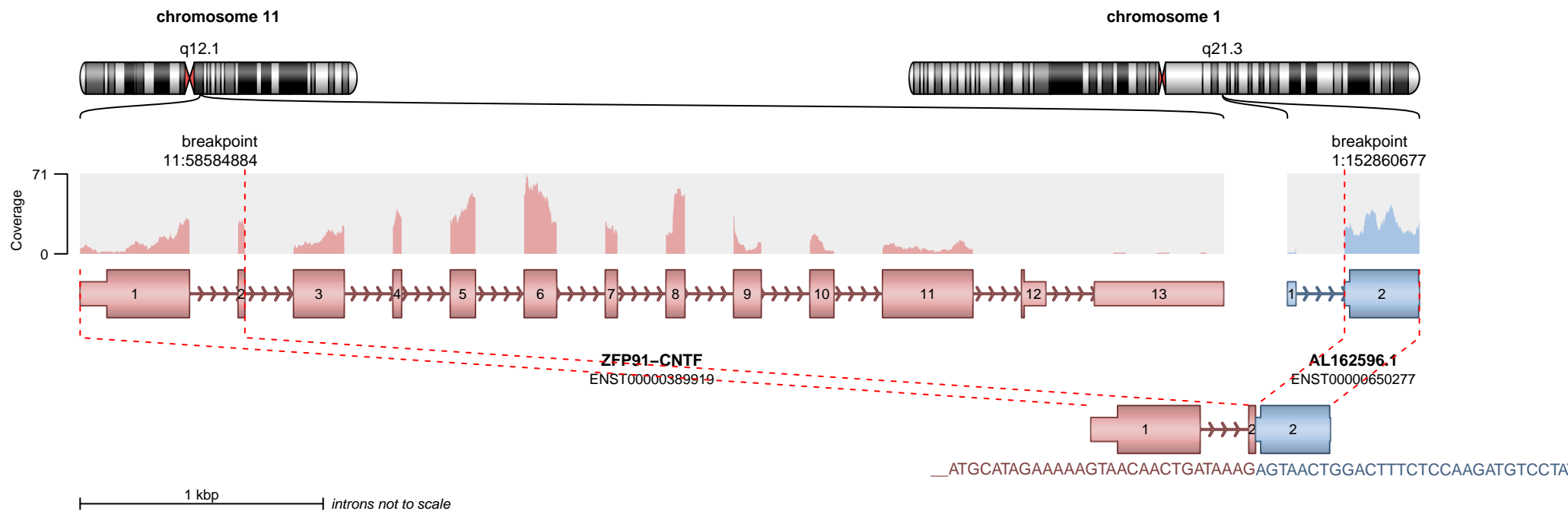


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 11
Discordant mates = 37

— translocation — deletion
— duplication — inversion

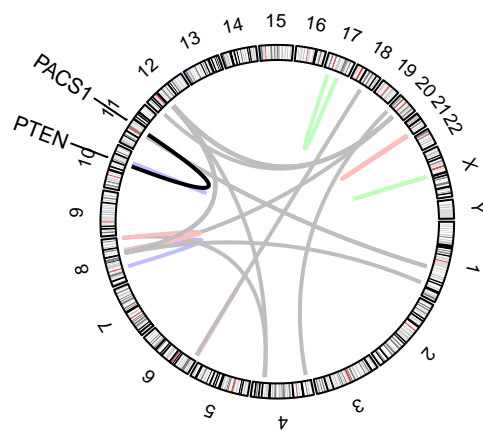
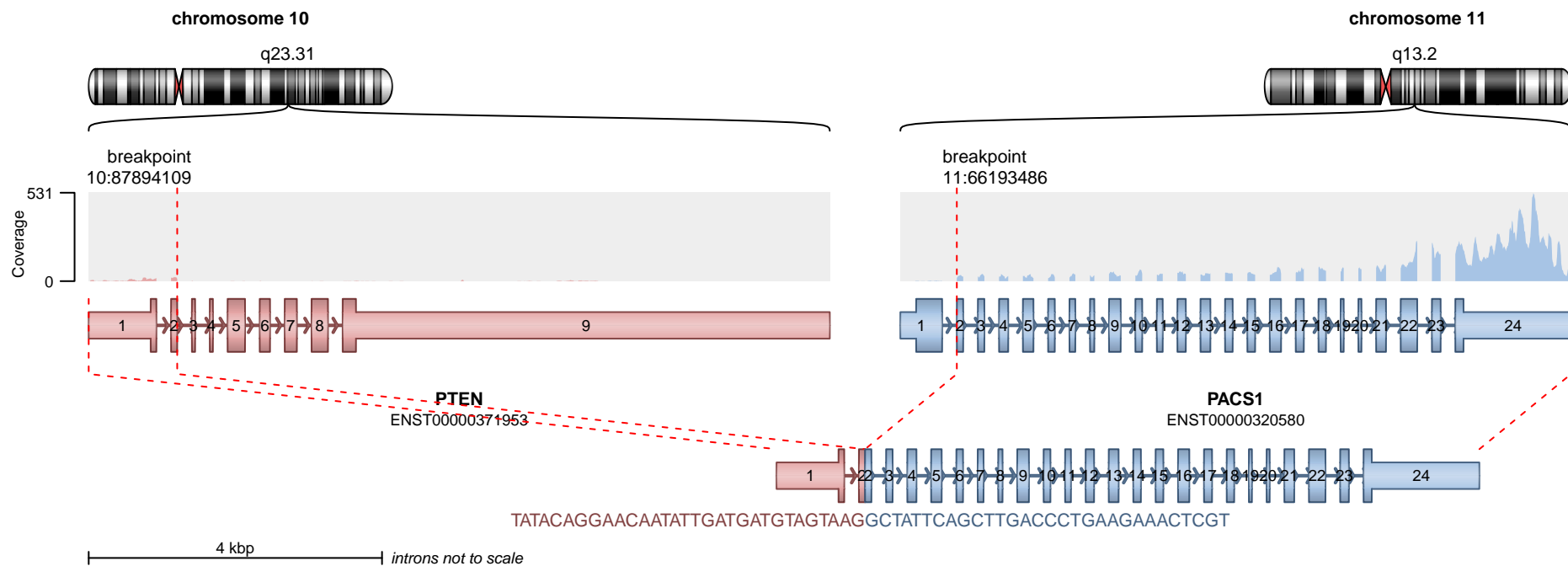


No protein domains retained in fusion.

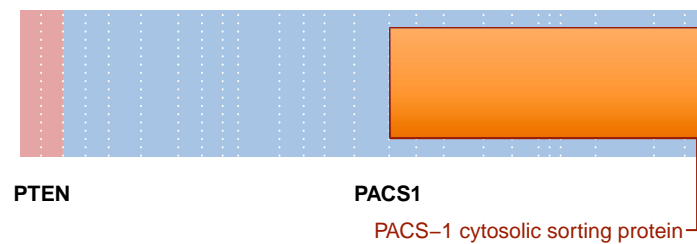
SUPPORTING READ COUNT

Split reads = 11
Discordant mates = 37

translocation deletion
duplication inversion



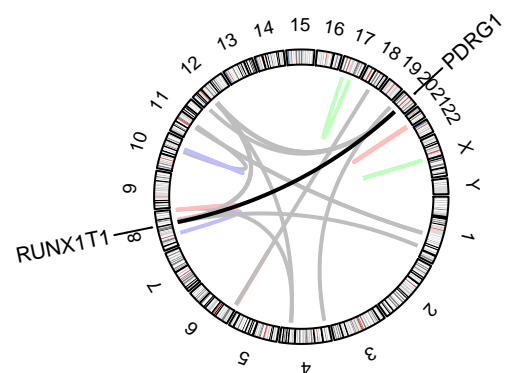
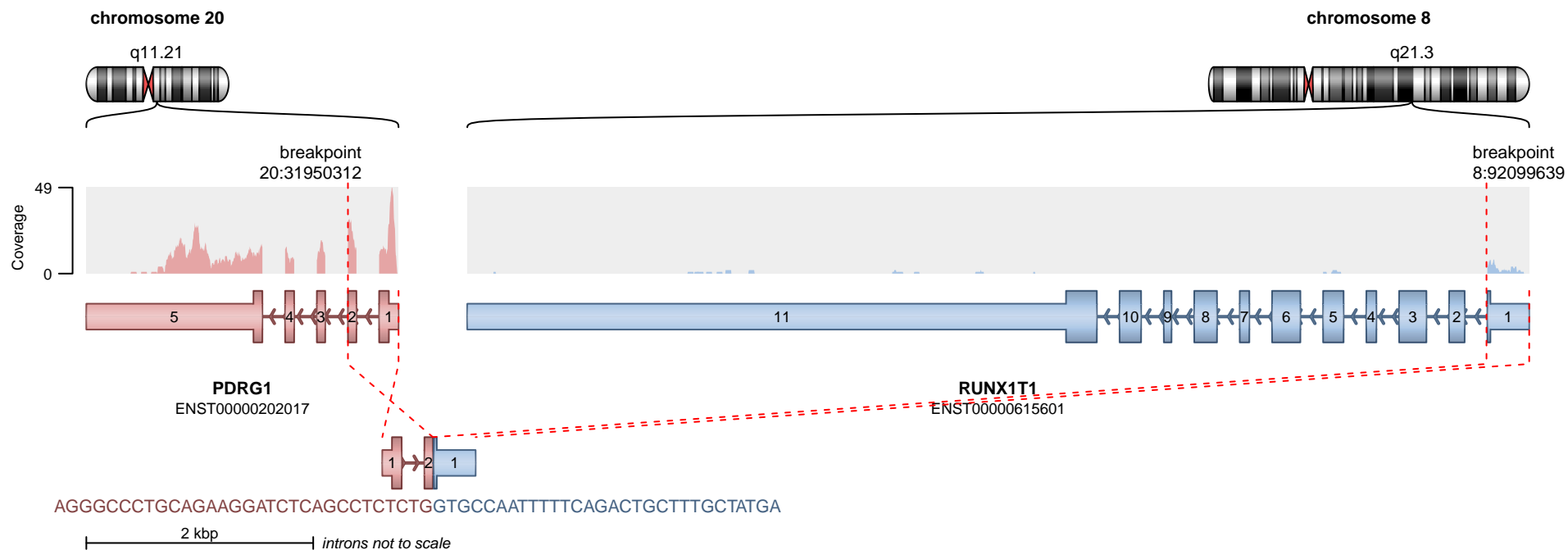
RETAINED PROTEIN DOMAINS in-frame fusion



SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 27

— translocation — deletion
— duplication — inversion

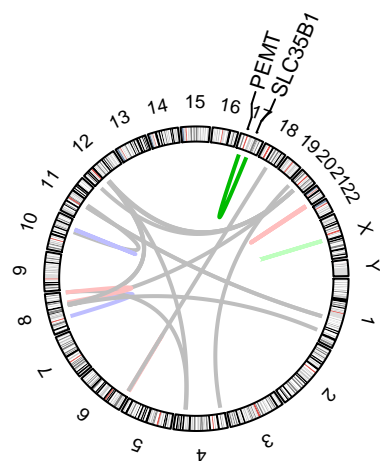
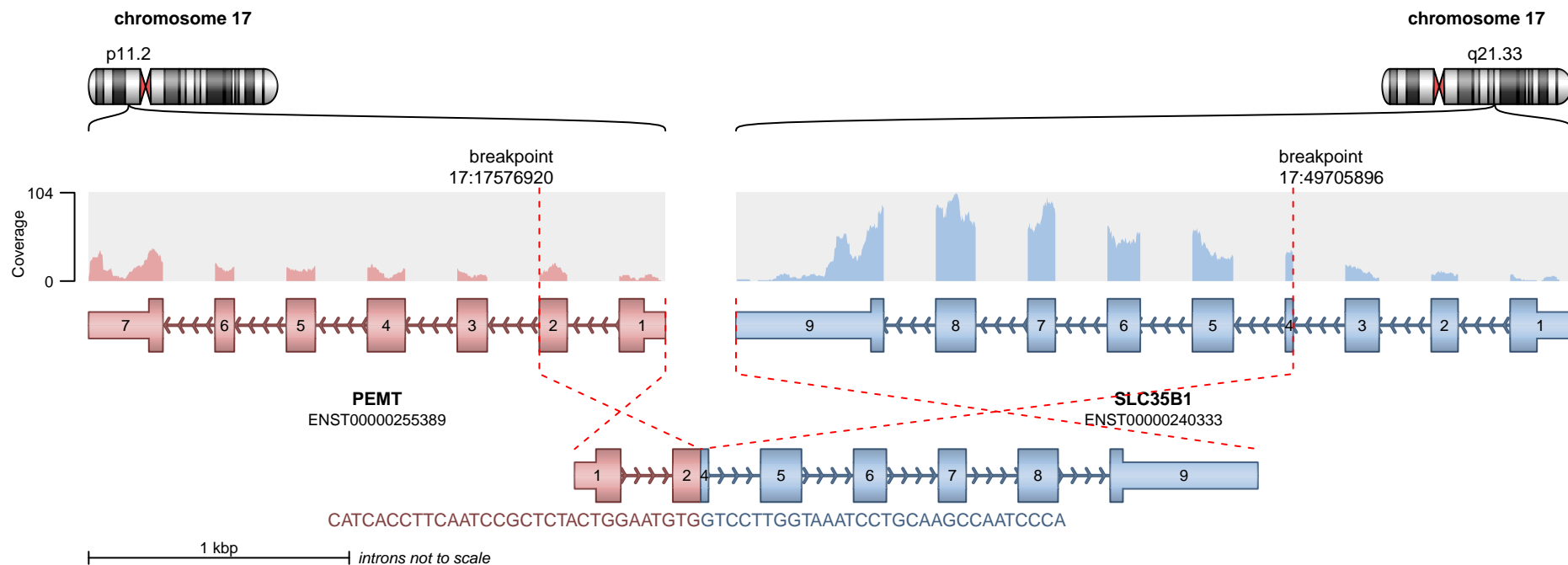


— translocation — deletion
— duplication — inversion

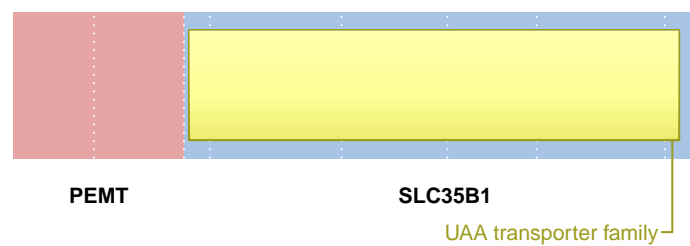
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 25



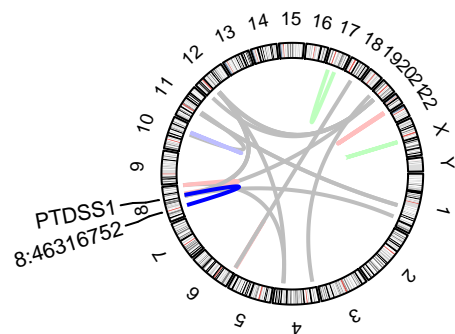
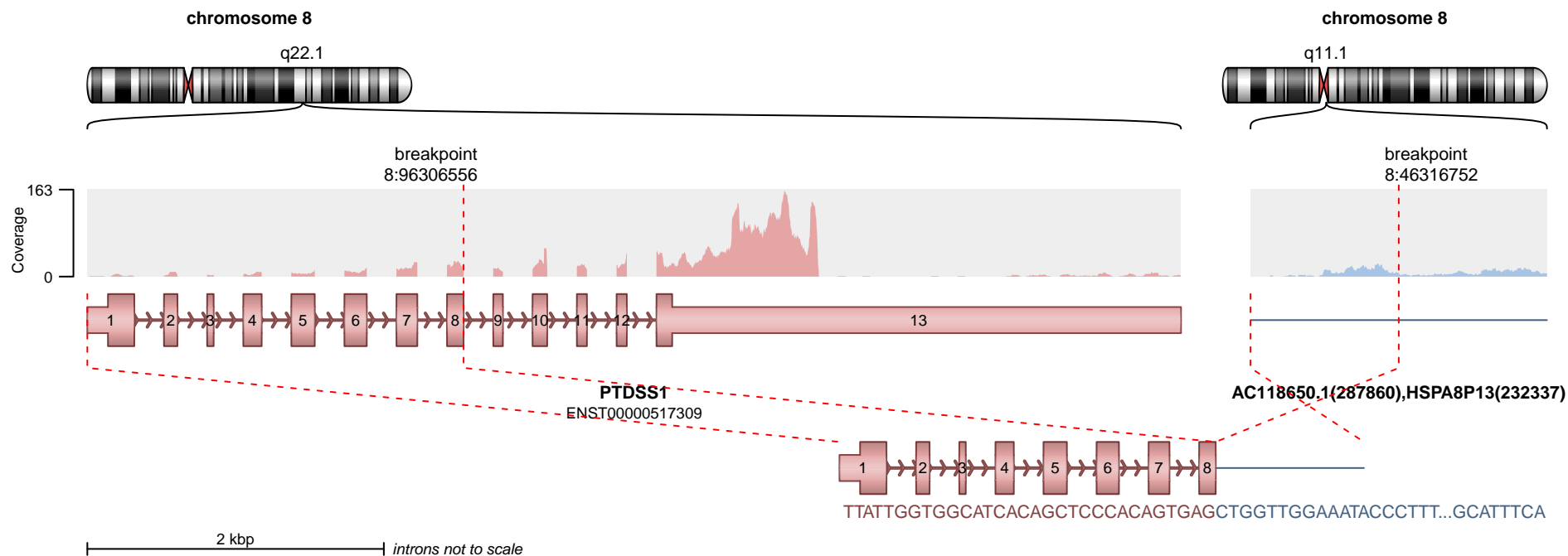
RETAINED PROTEIN DOMAINS in-frame fusion



SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 10

translocation deletion
duplication inversion

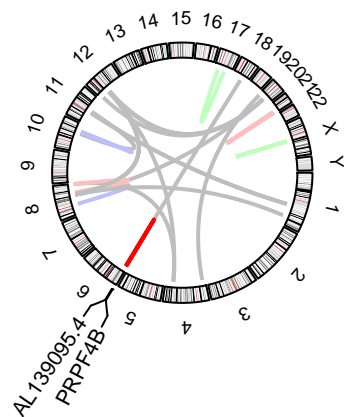
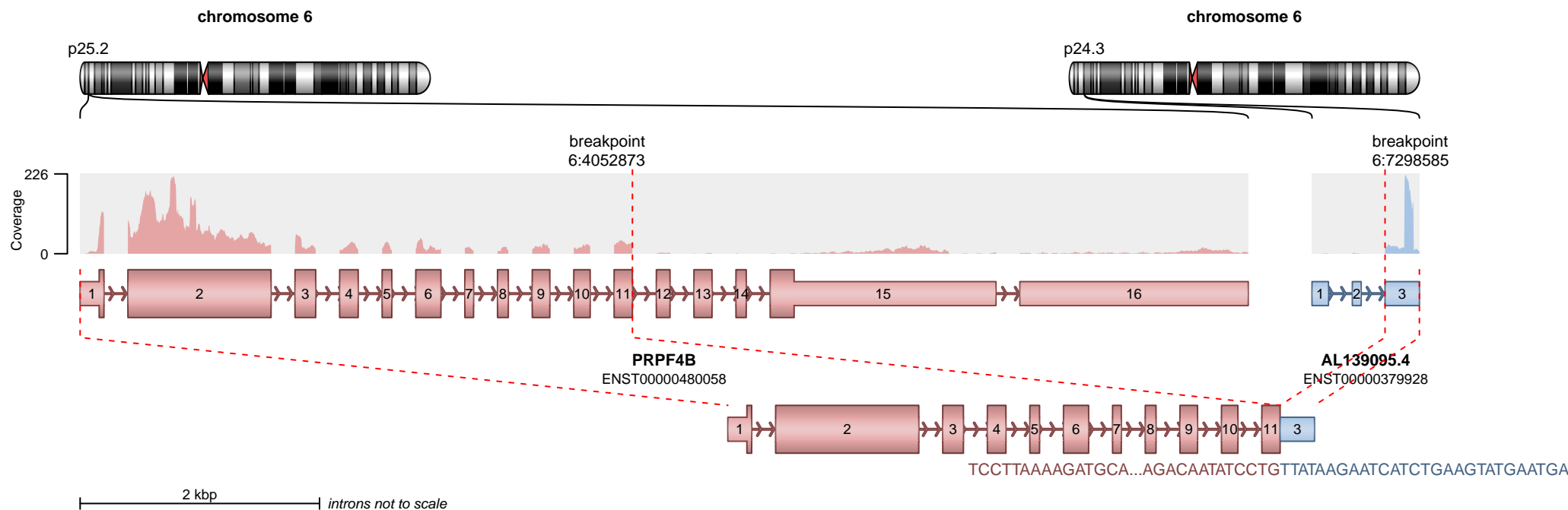


No protein domains retained in fusion.

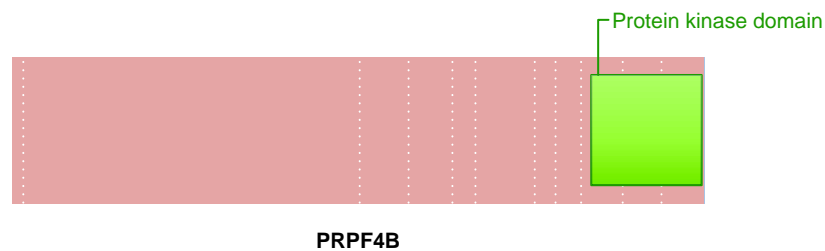
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 5

— translocation — deletion
— duplication — inversion



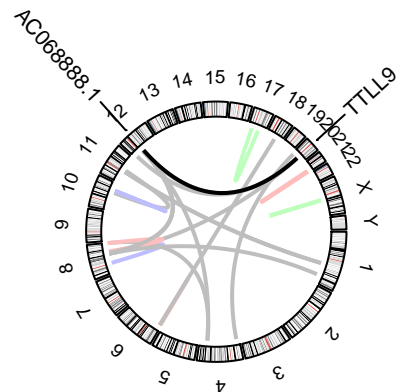
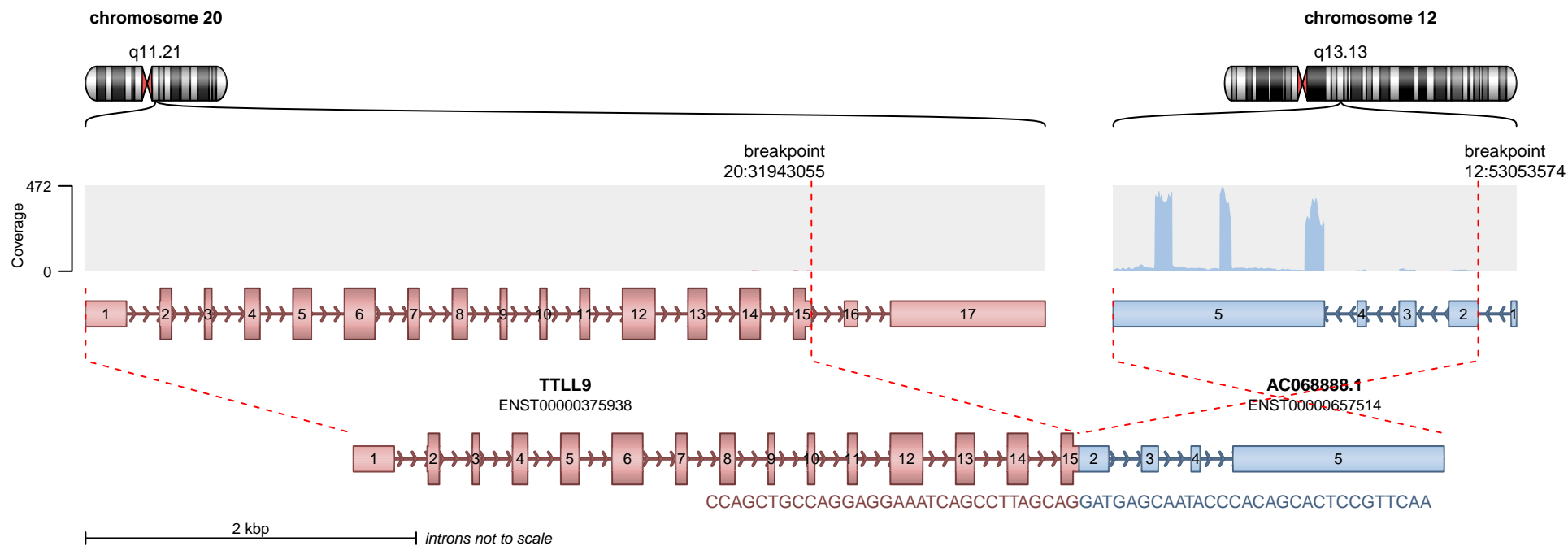
RETAINED PROTEIN DOMAINS out-of-frame fusion



SUPPORTING READ COUNT

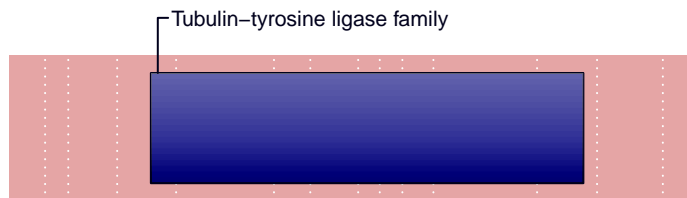
Split reads = 1
Discordant mates = 4

translocation deletion
duplication inversion



RETAINED PROTEIN DOMAINS

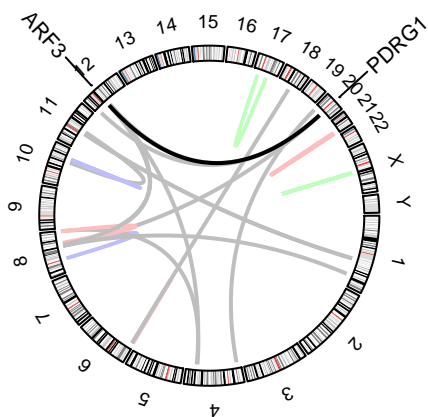
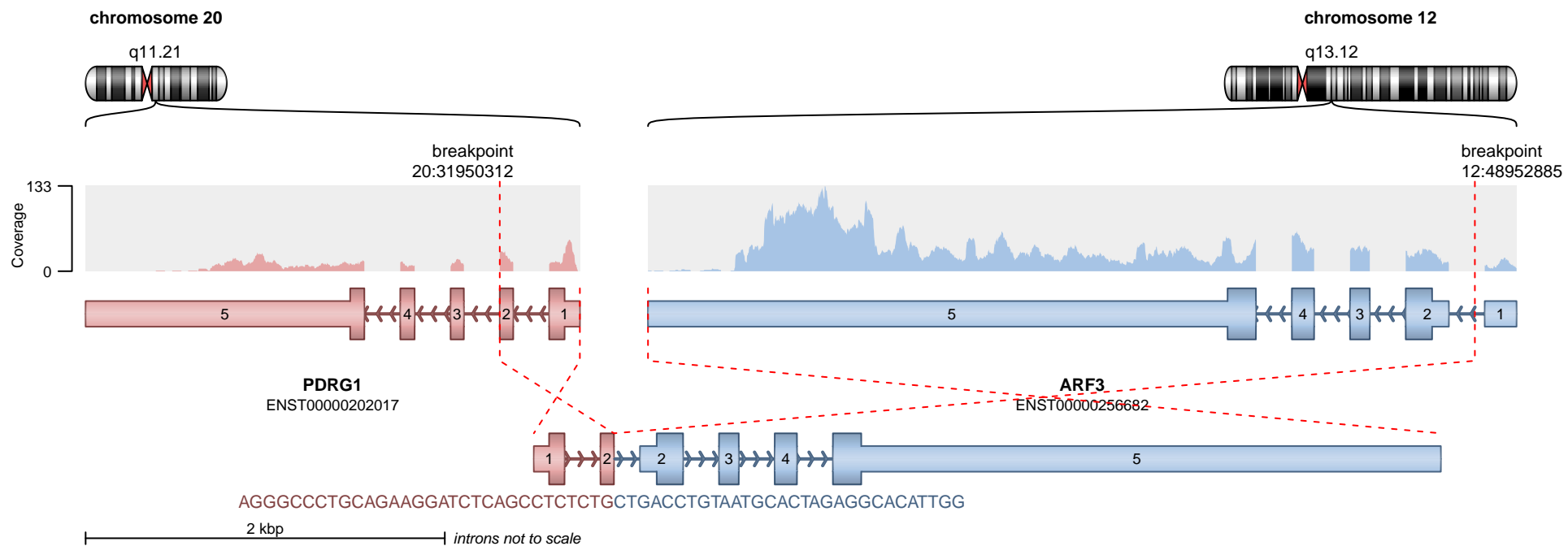
reading frame unclear



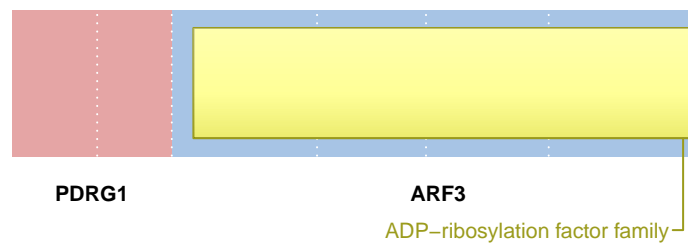
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 3

— translocation — deletion
— duplication — inversion



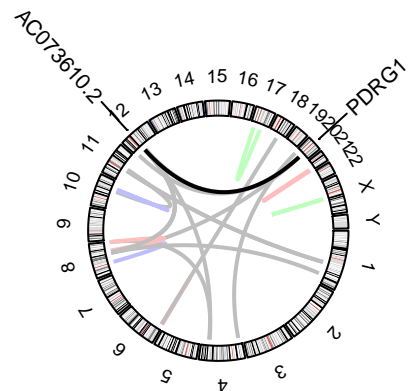
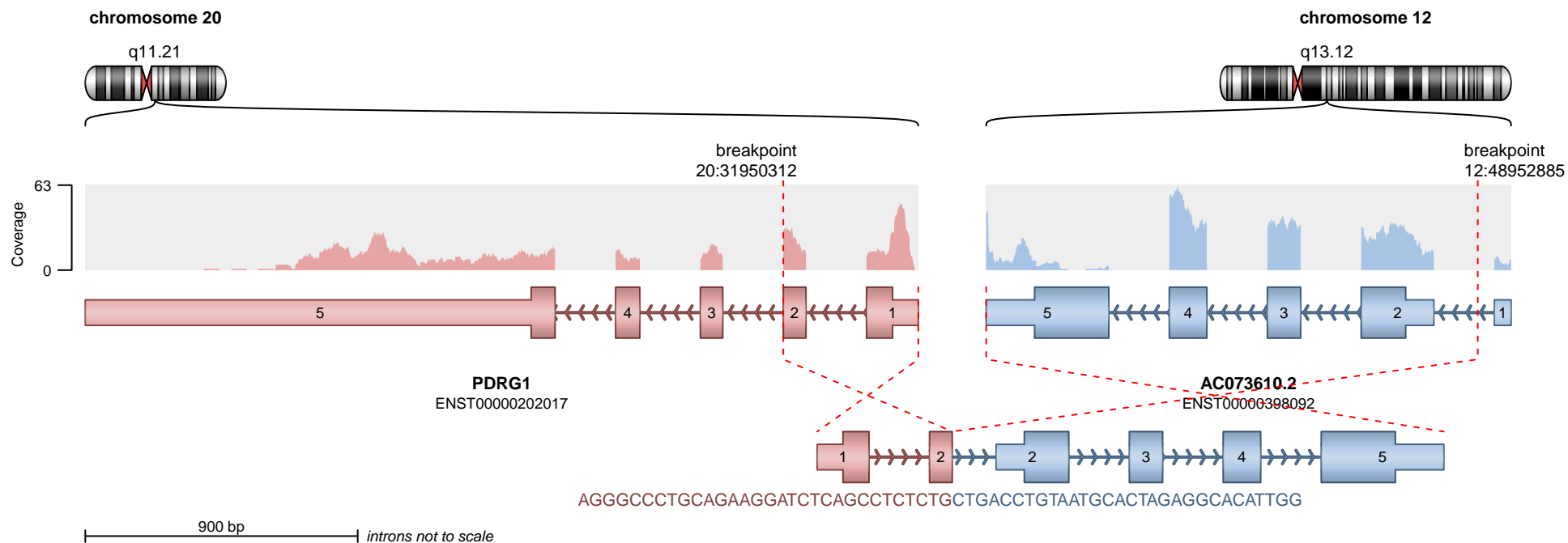
RETAINED PROTEIN DOMAINS out-of-frame fusion



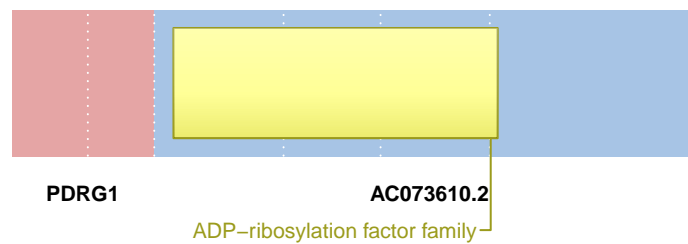
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 1

— translocation — deletion
— duplication — inversion



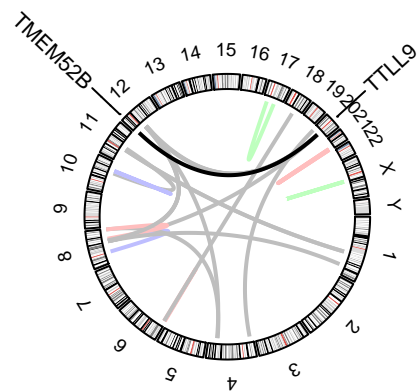
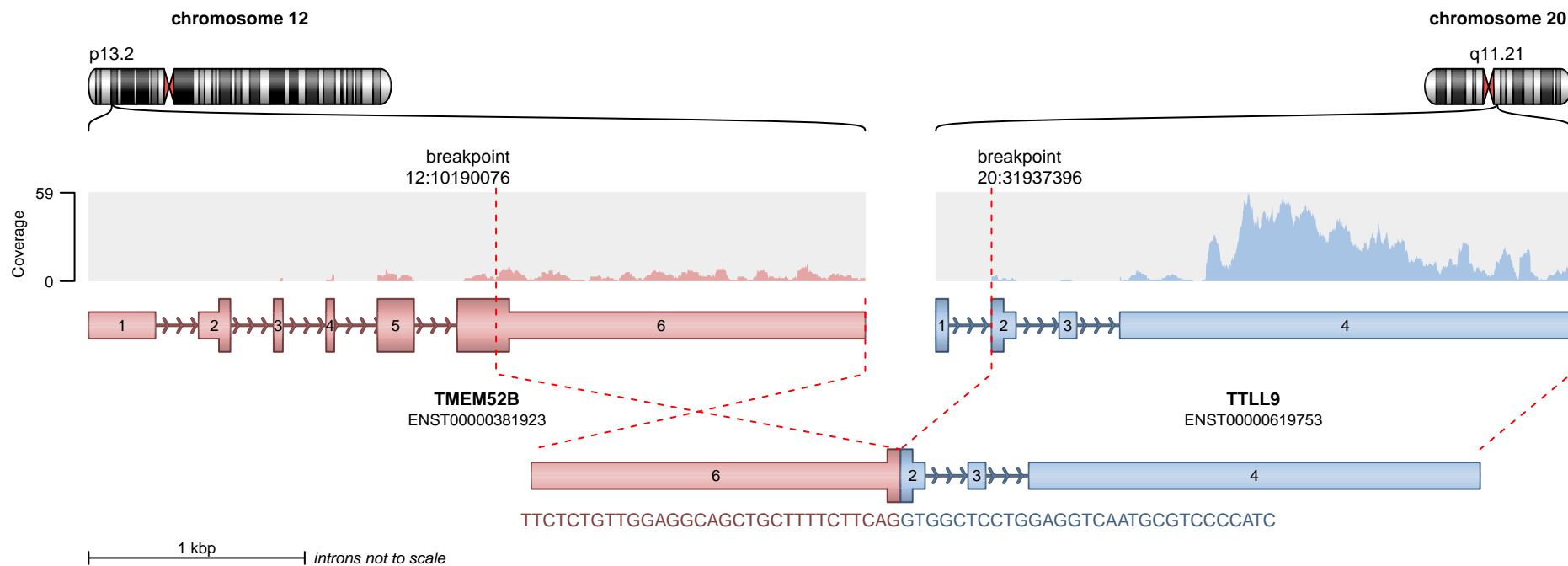
RETAINED PROTEIN DOMAINS out-of-frame fusion



SUPPORTING READ COUNT

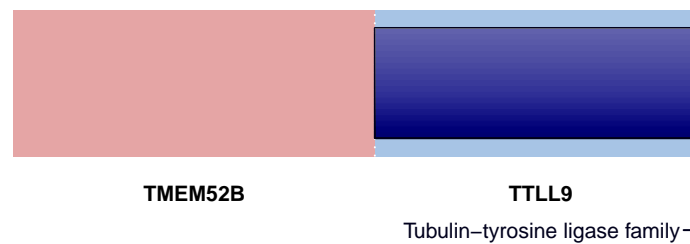
Split reads = 2
Discordant mates = 1

translocation deletion
duplication inversion



RETAINED PROTEIN DOMAINS

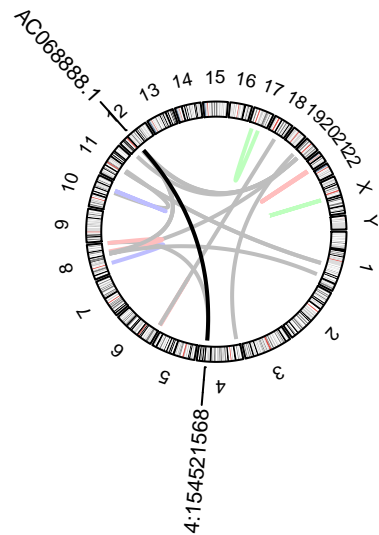
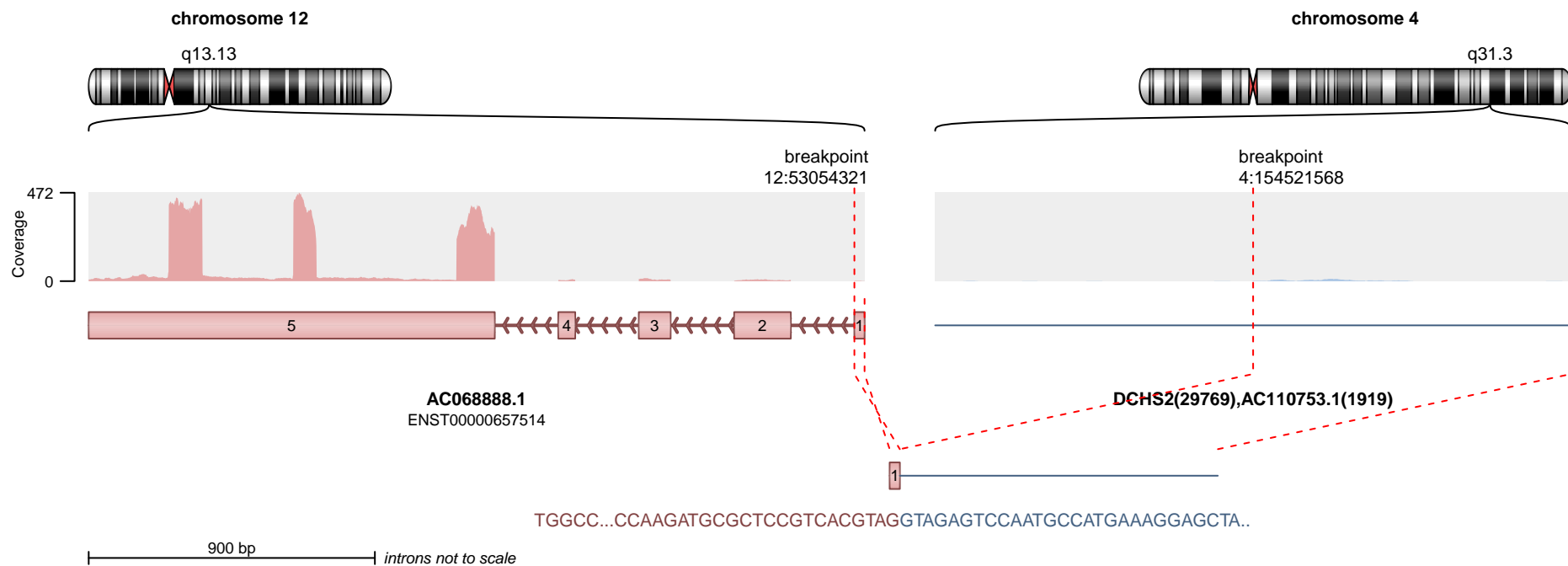
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

— translocation — deletion
— duplication — inversion

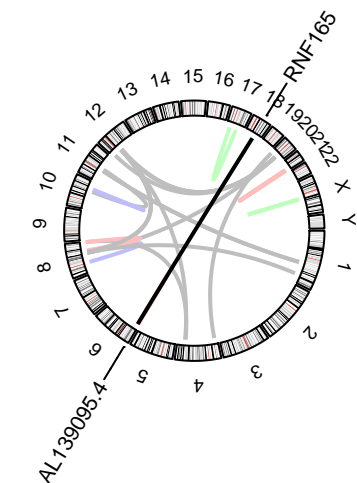
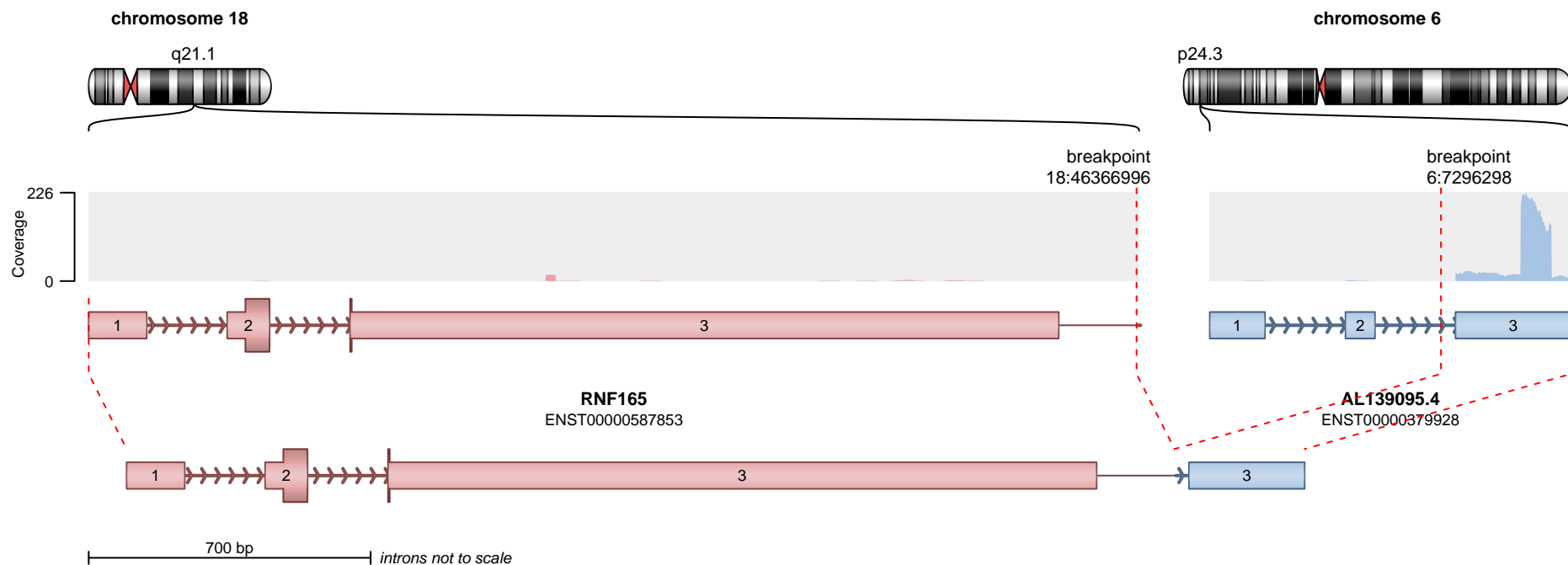


— translocation — deletion
— duplication — inversion

Genes are not protein-coding.

SUPPORTING READ COUNT

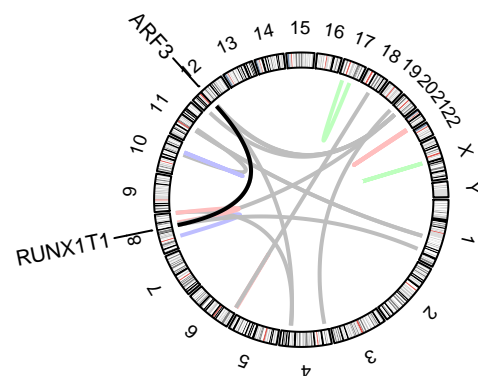
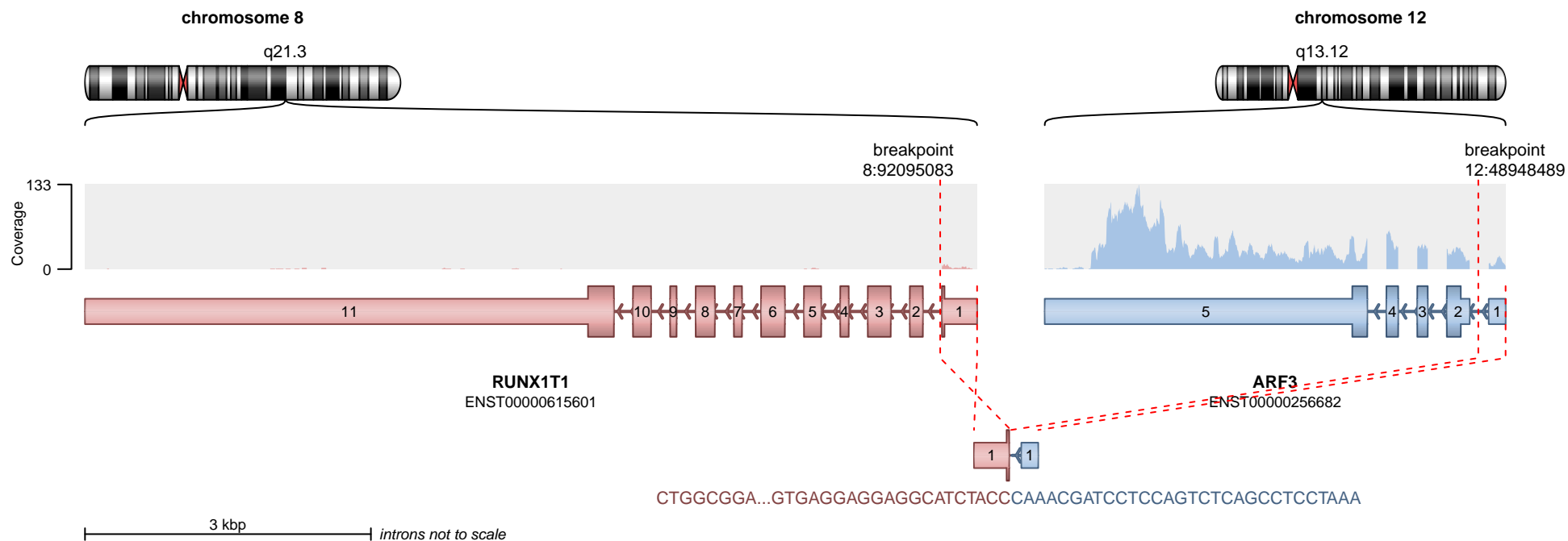
Split reads = 1
Discordant mates = 1



No coding regions due to antisense transcription.

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 33

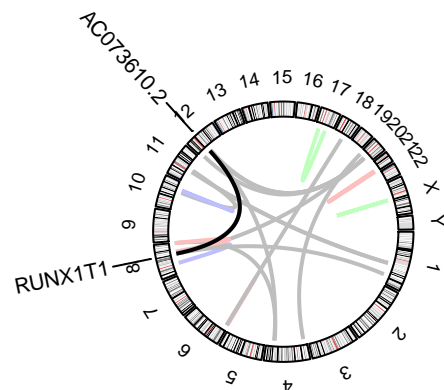
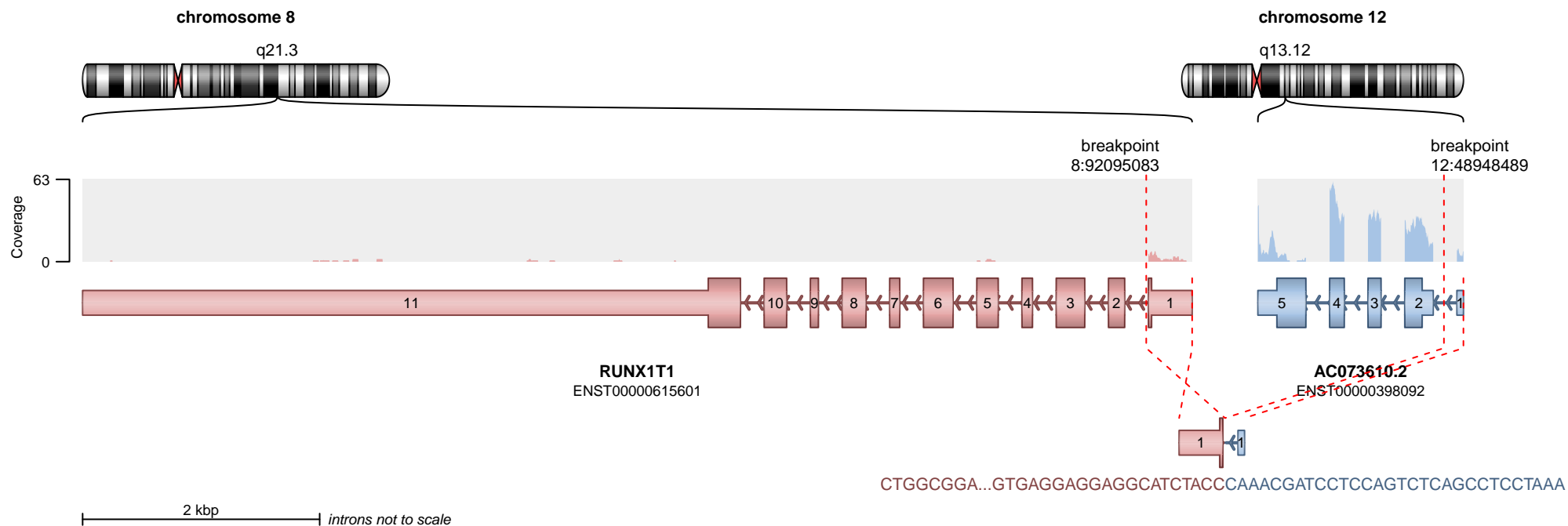


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 9

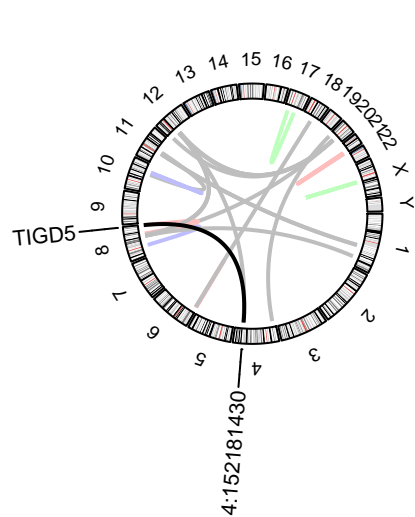
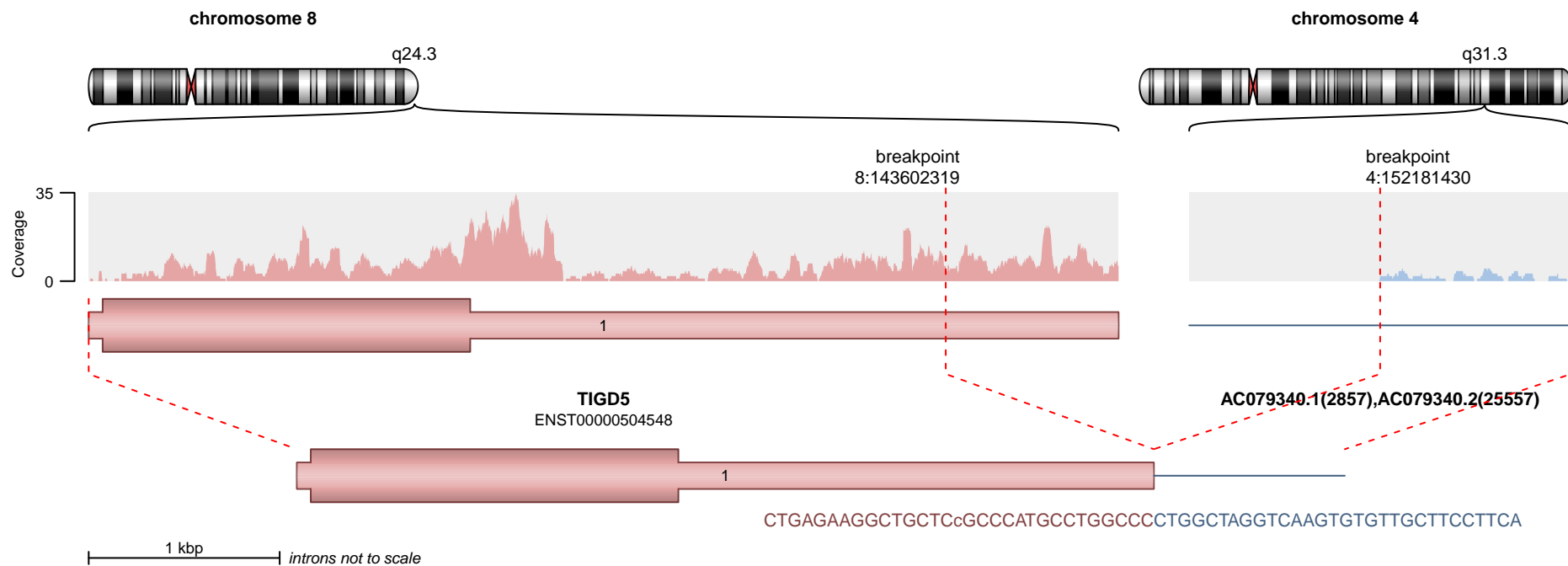


No protein domains retained in fusion.

SUPPORTING READ COUNT

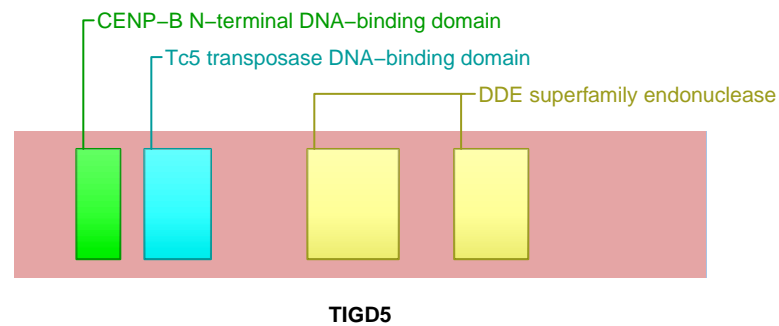
Split reads = 1
Discordant mates = 9

— translocation — deletion
— duplication — inversion



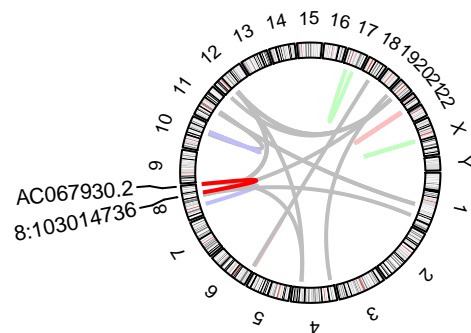
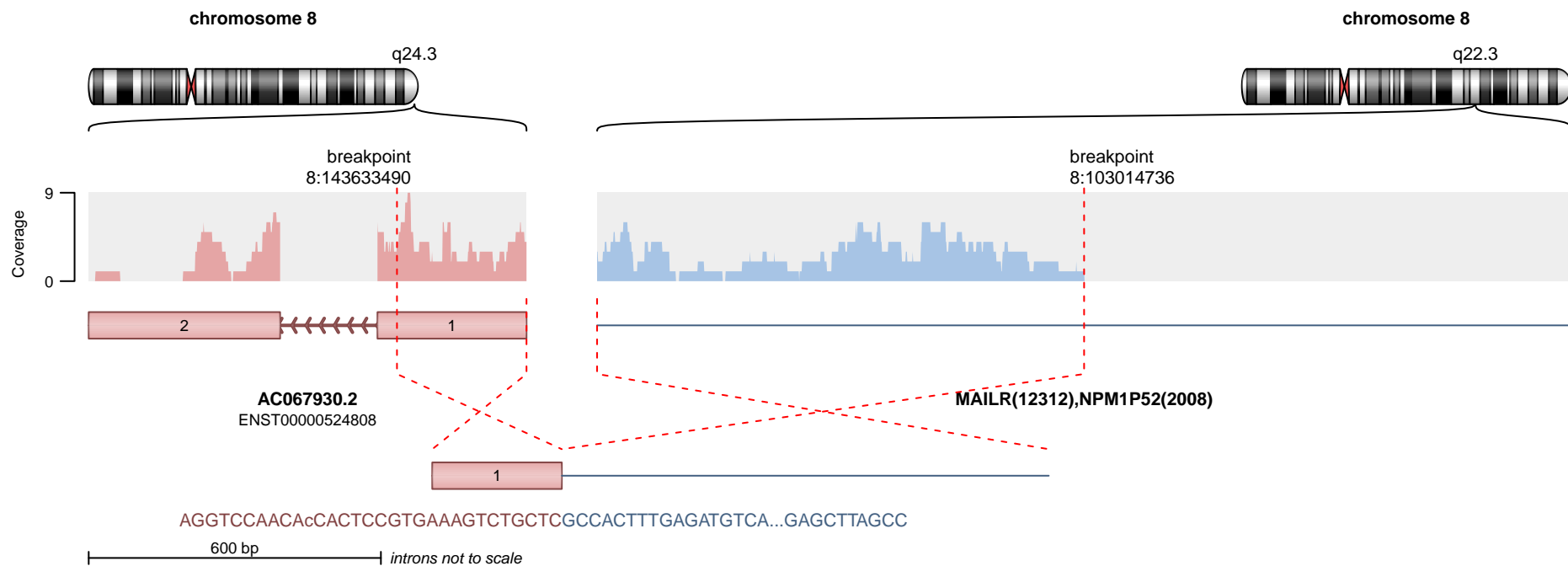
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 4

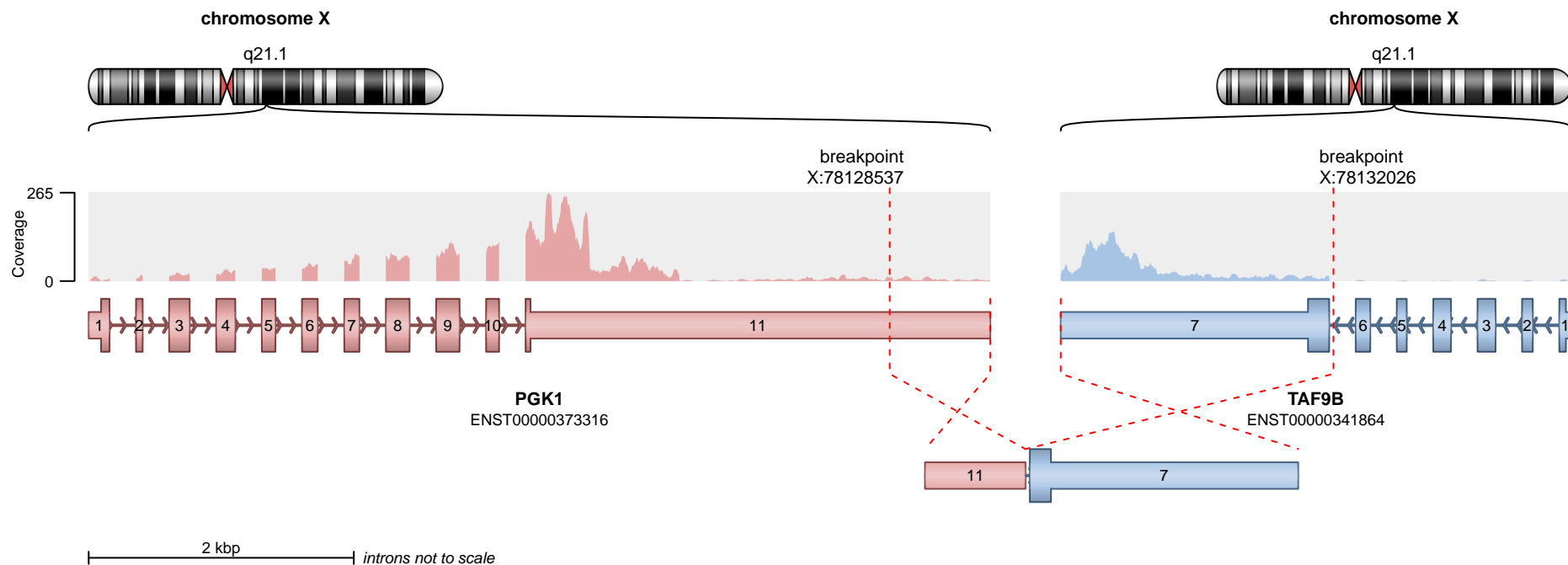


— translocation — deletion
— duplication — inversion

Genes are not protein-coding.

SUPPORTING READ COUNT

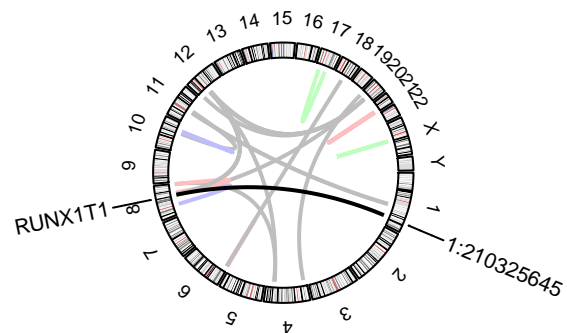
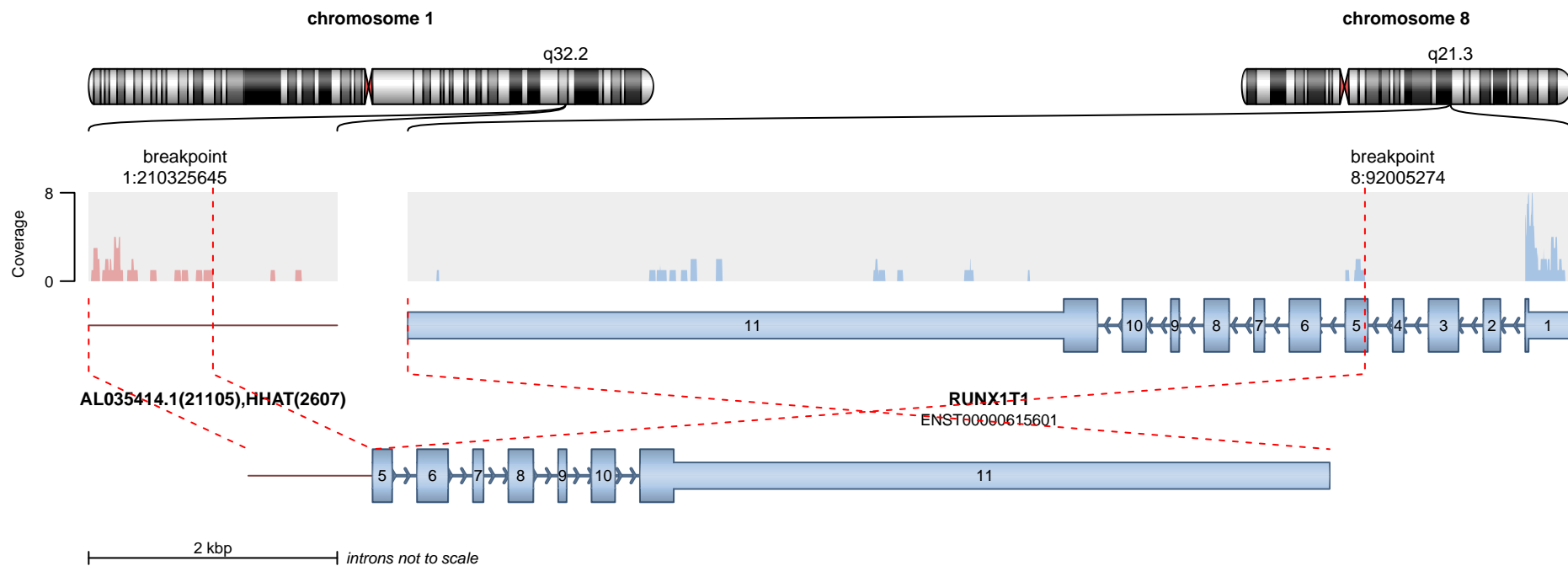
Split reads = 1
Discordant mates = 2



No coding regions due to antisense transcription.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 2

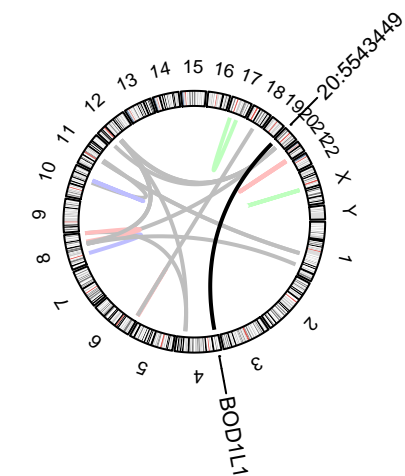
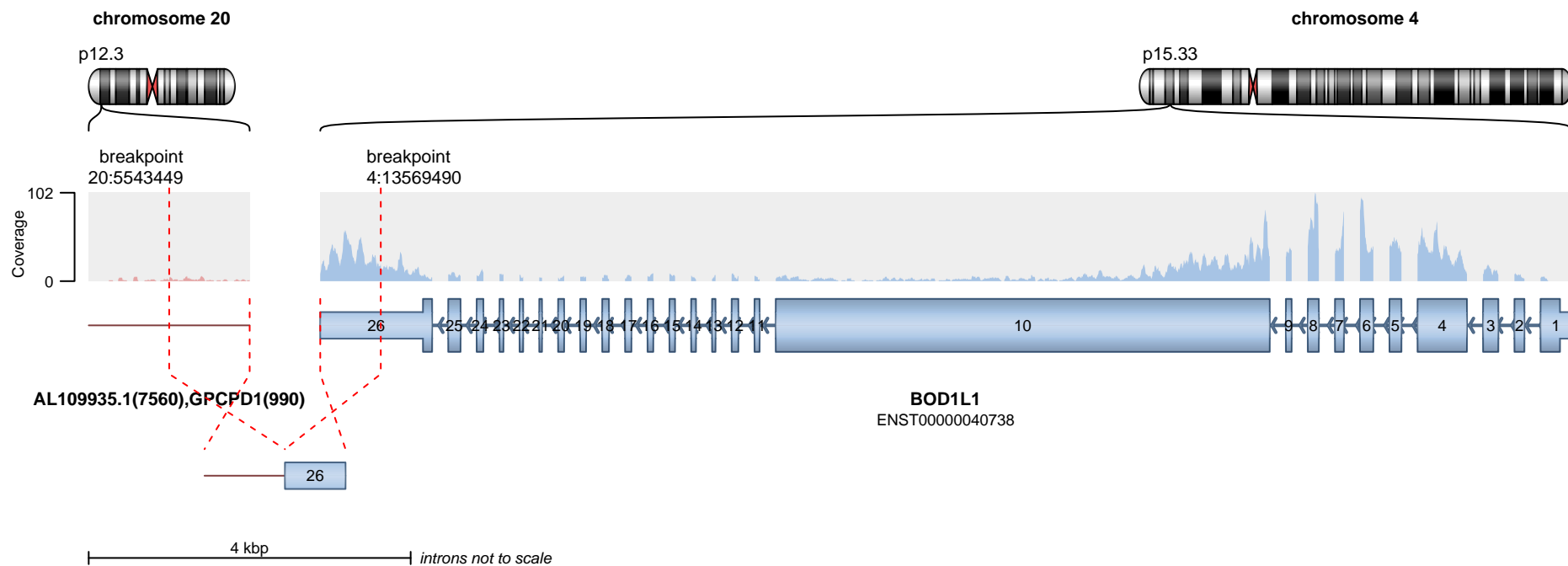


No coding regions due to antisense transcription.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

translocation deletion
duplication inversion

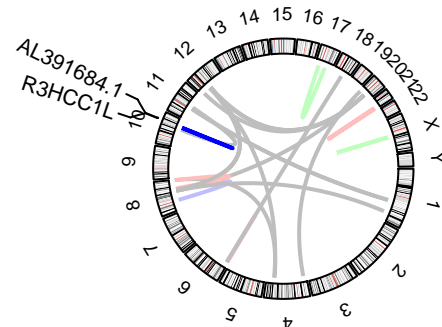
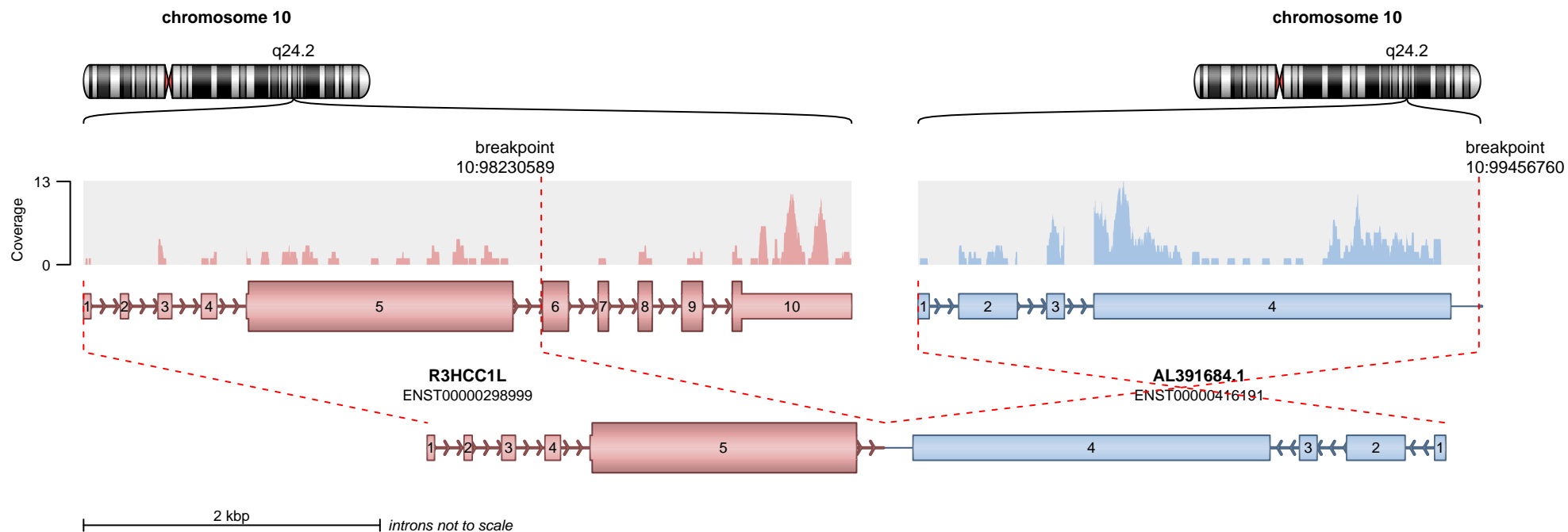


translocation deletion
duplication inversion

No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

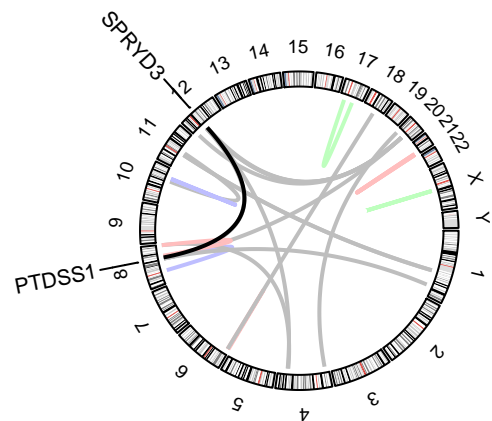
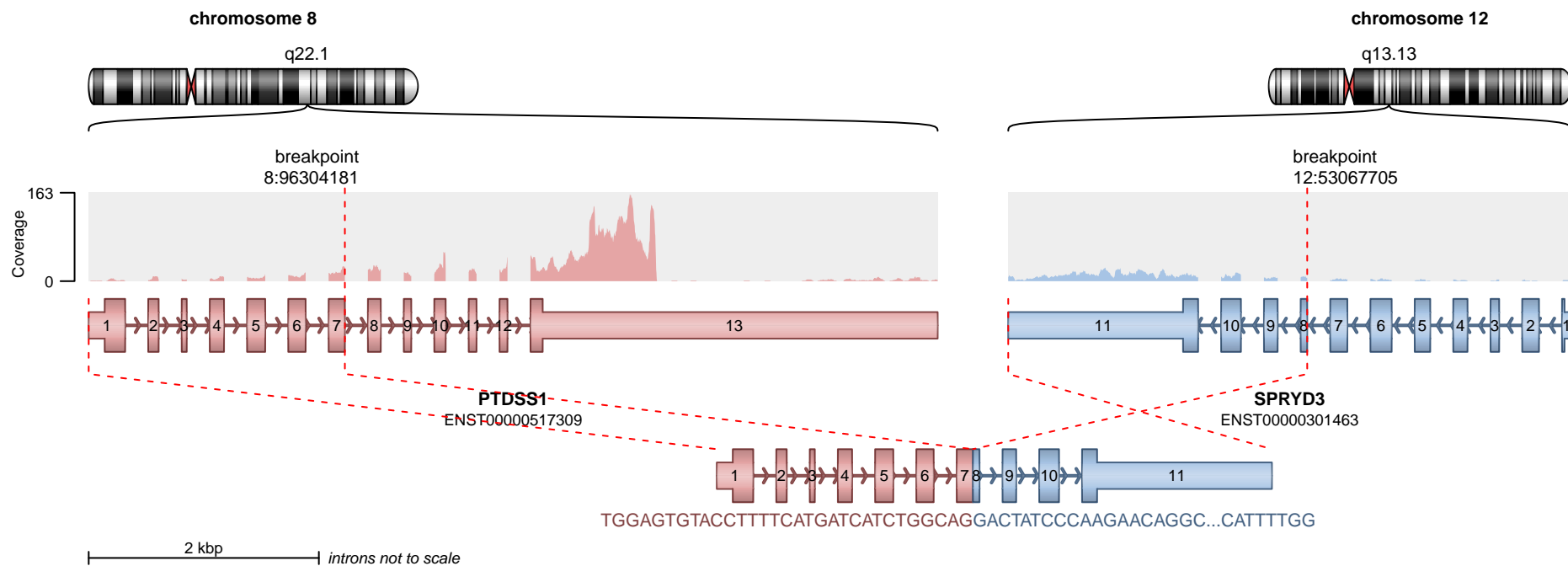


No coding regions due to antisense transcription.

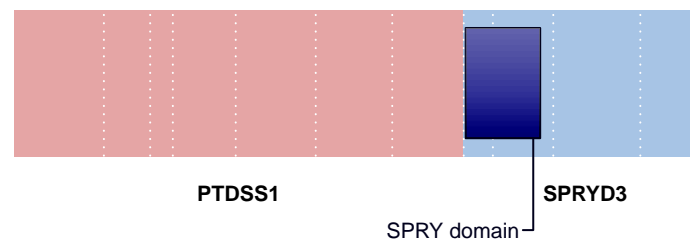
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

— translocation — deletion
— duplication — inversion



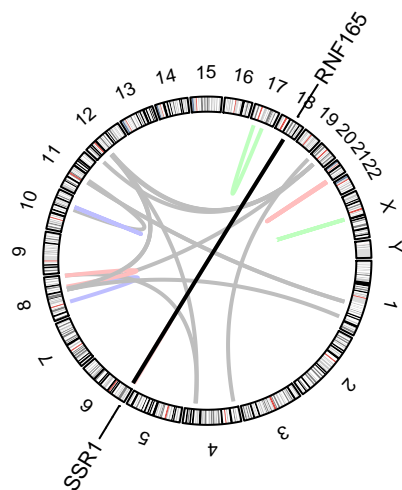
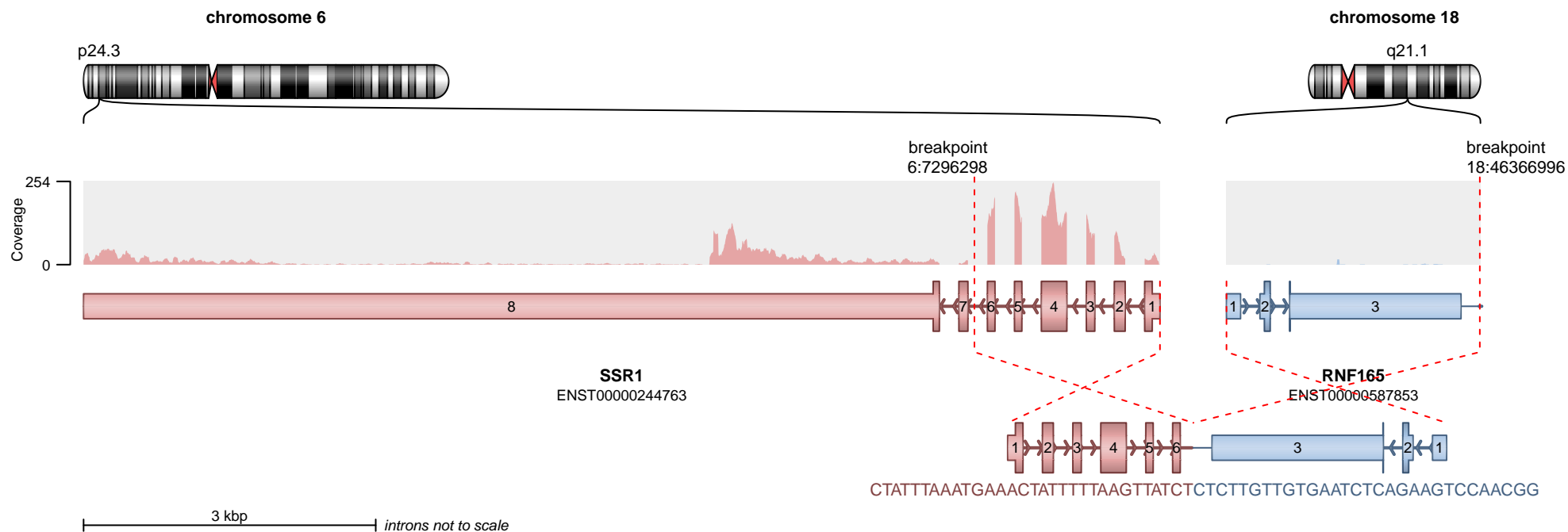
RETAINED PROTEIN DOMAINS in-frame fusion



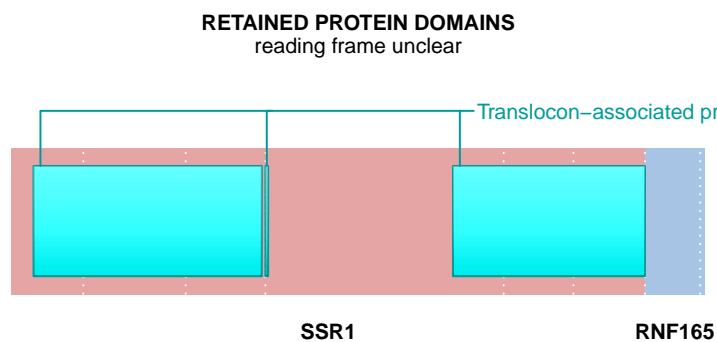
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

— translocation — deletion
— duplication — inversion

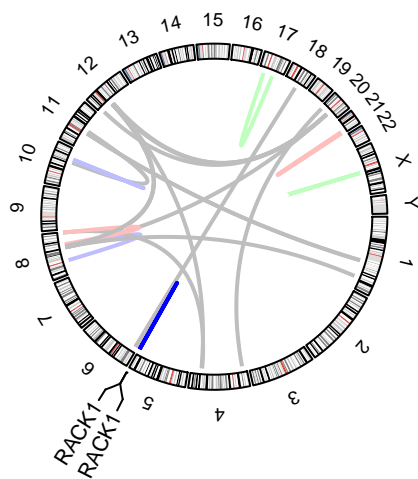
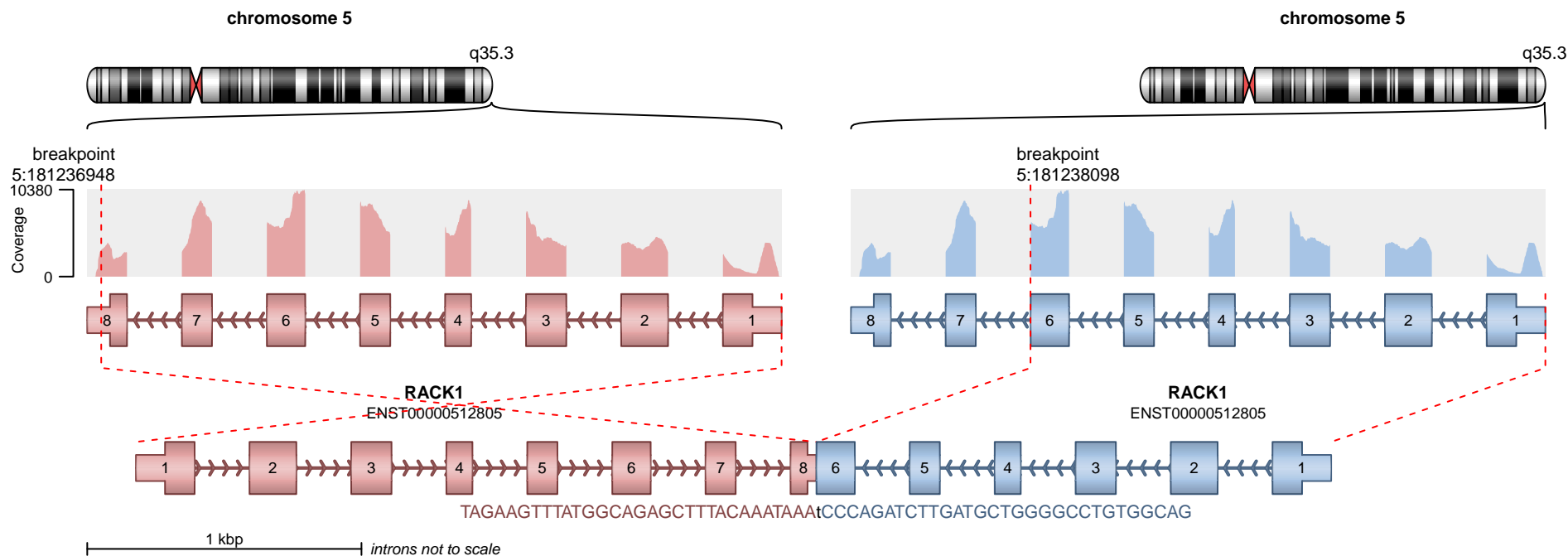


— translocation — deletion
— duplication — inversion

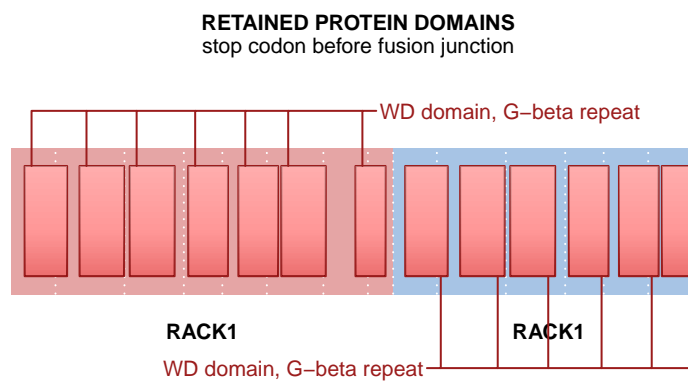


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 128

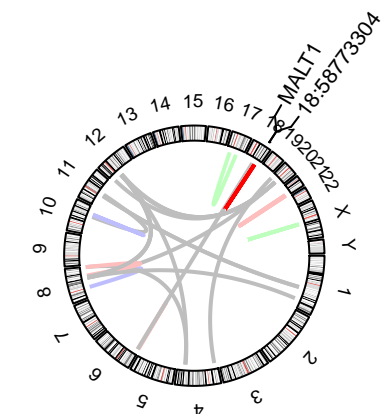
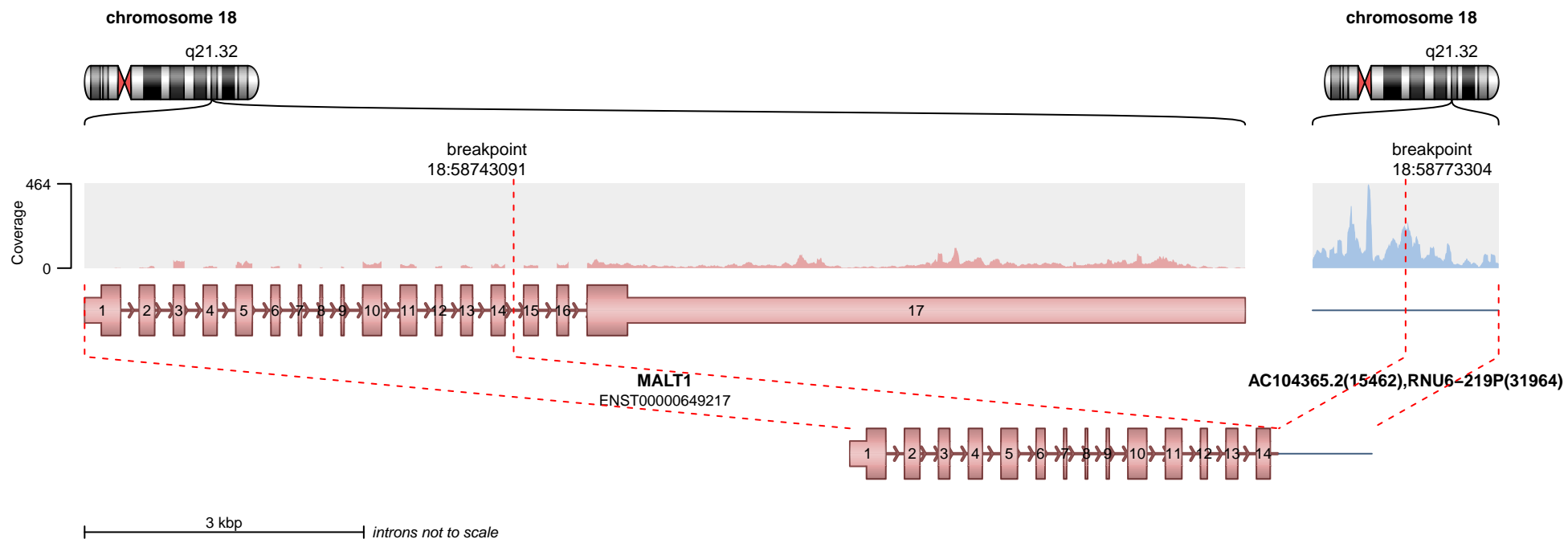


— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 59

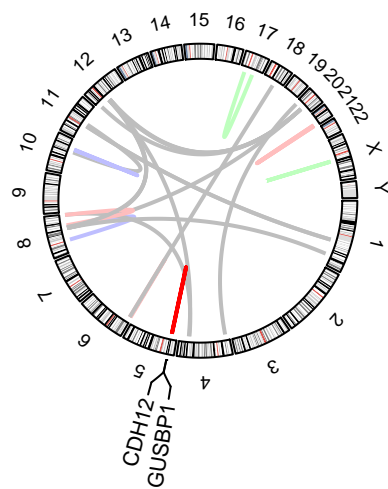
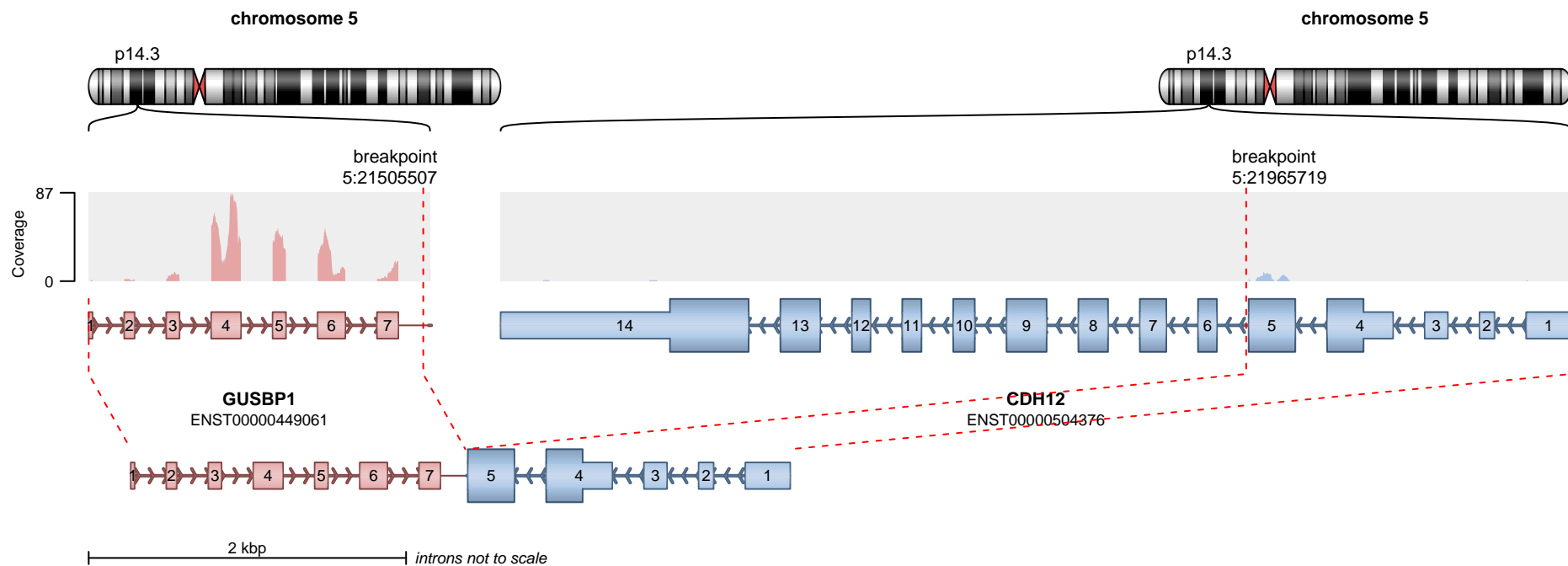


No coding regions due to antisense transcription.

SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 12

translocation deletion
duplication inversion

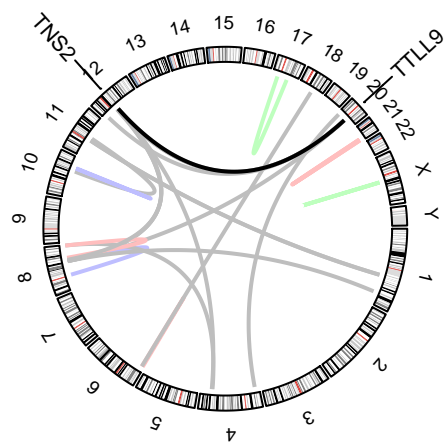
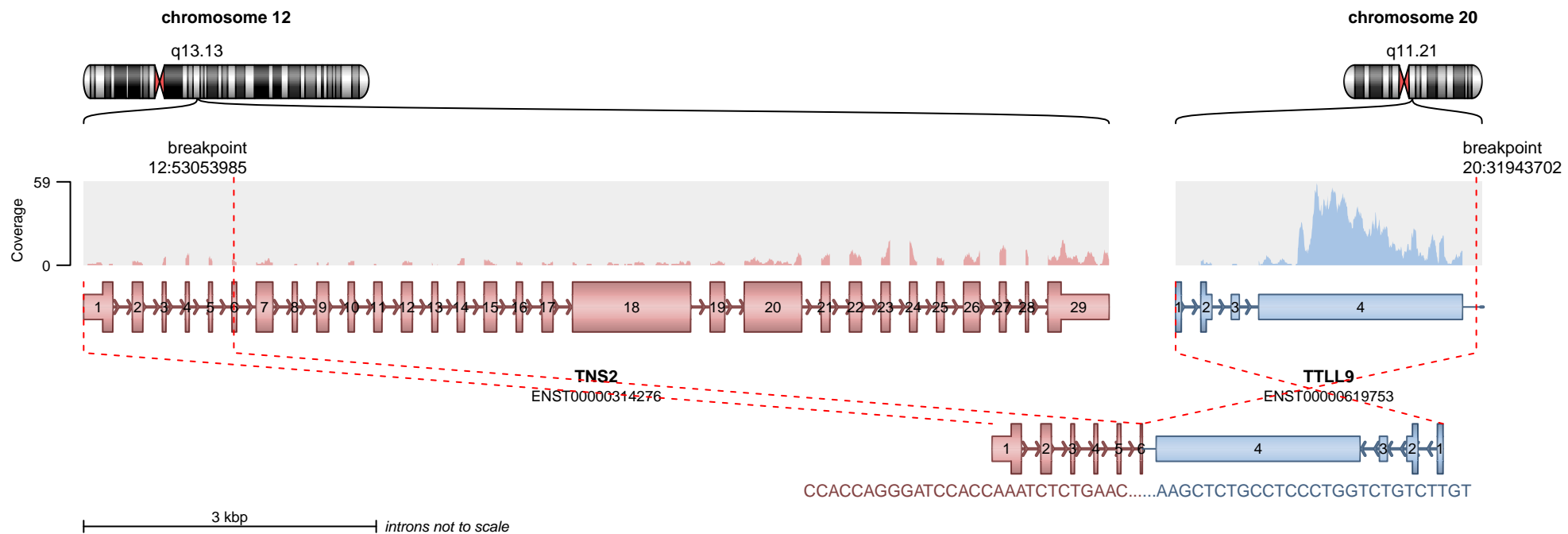


translocation duplication deletion inversion

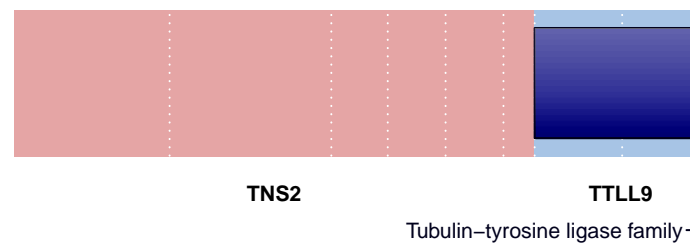
No coding regions due to antisense transcription.

SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 11



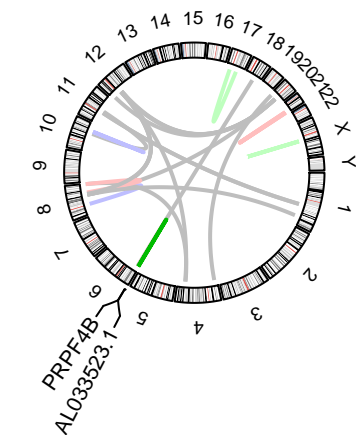
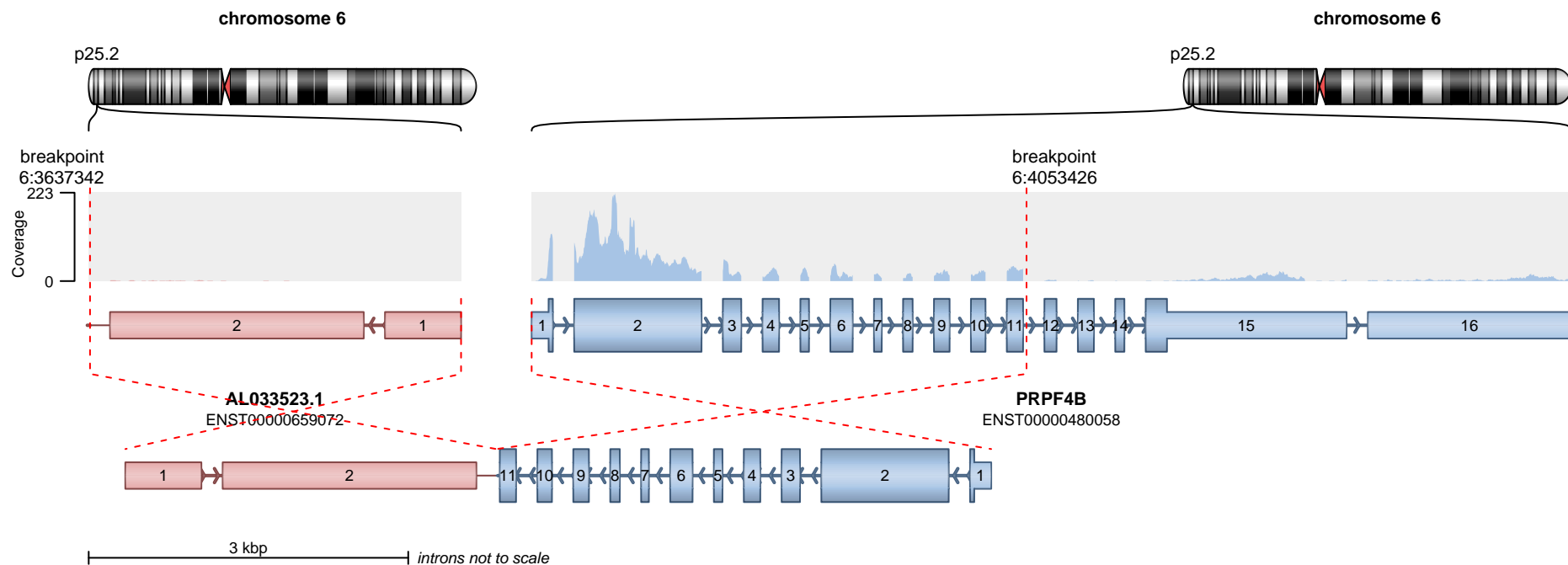
RETAINED PROTEIN DOMAINS reading frame unclear



SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 8

— translocation — deletion
— duplication — inversion

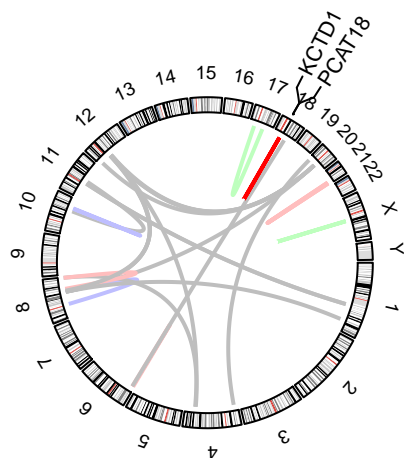
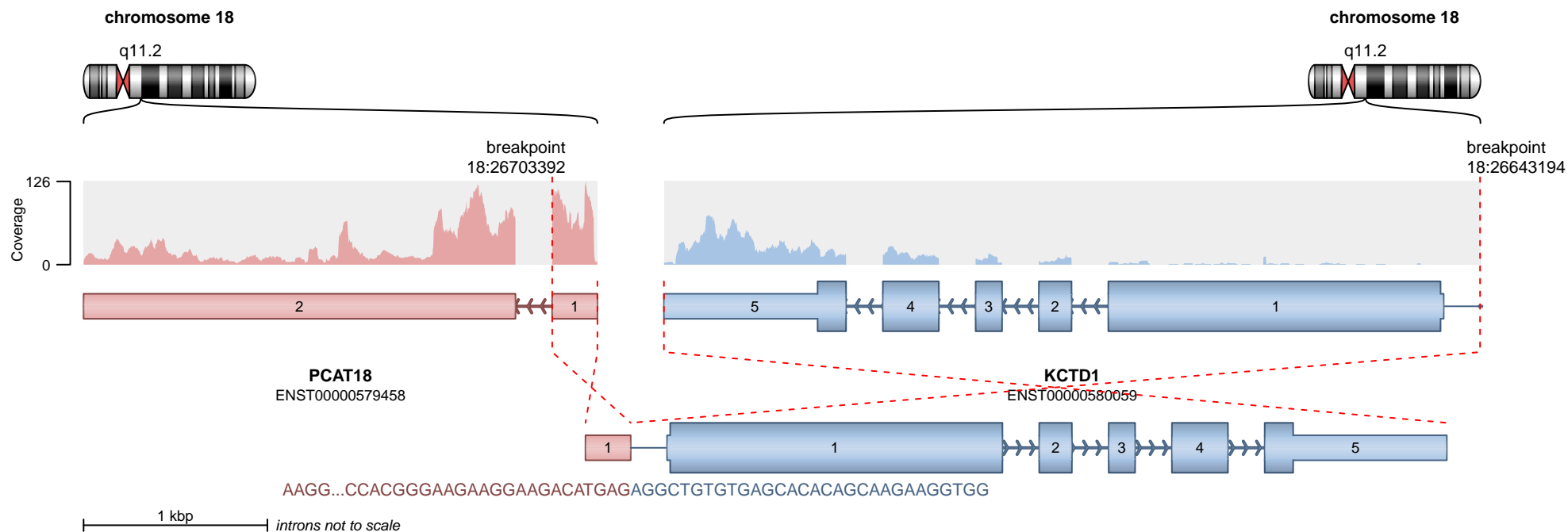


— translocation — deletion
— duplication — inversion

No coding regions due to antisense transcription.

SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 5

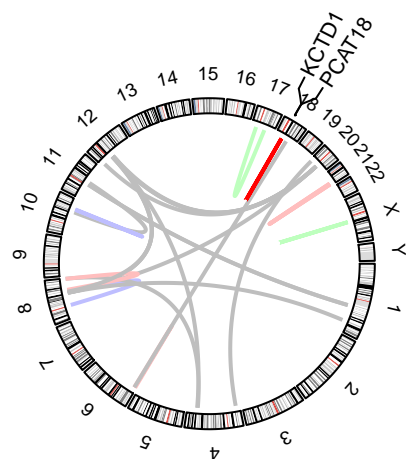
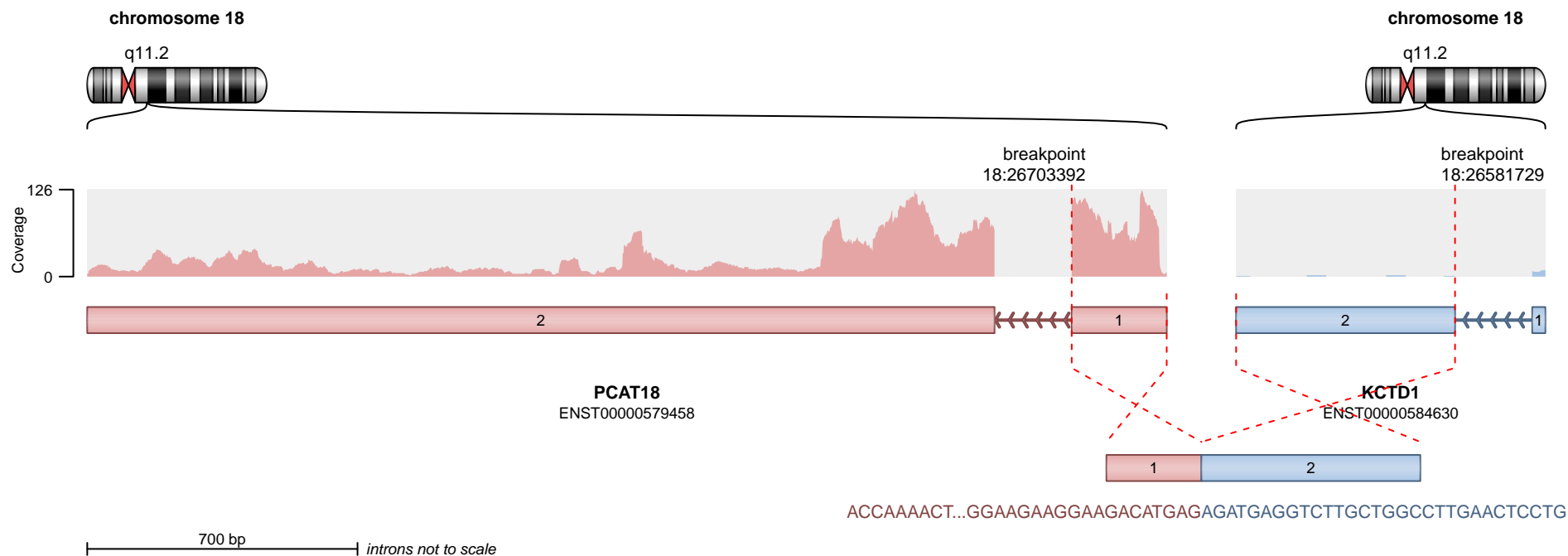


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 4

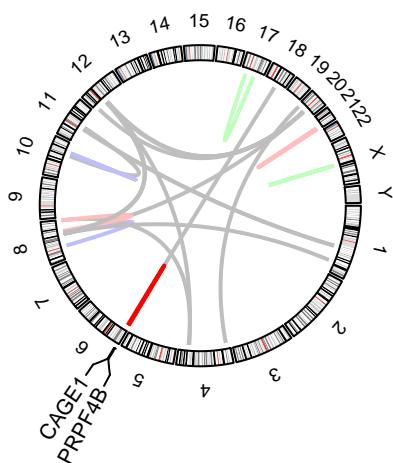
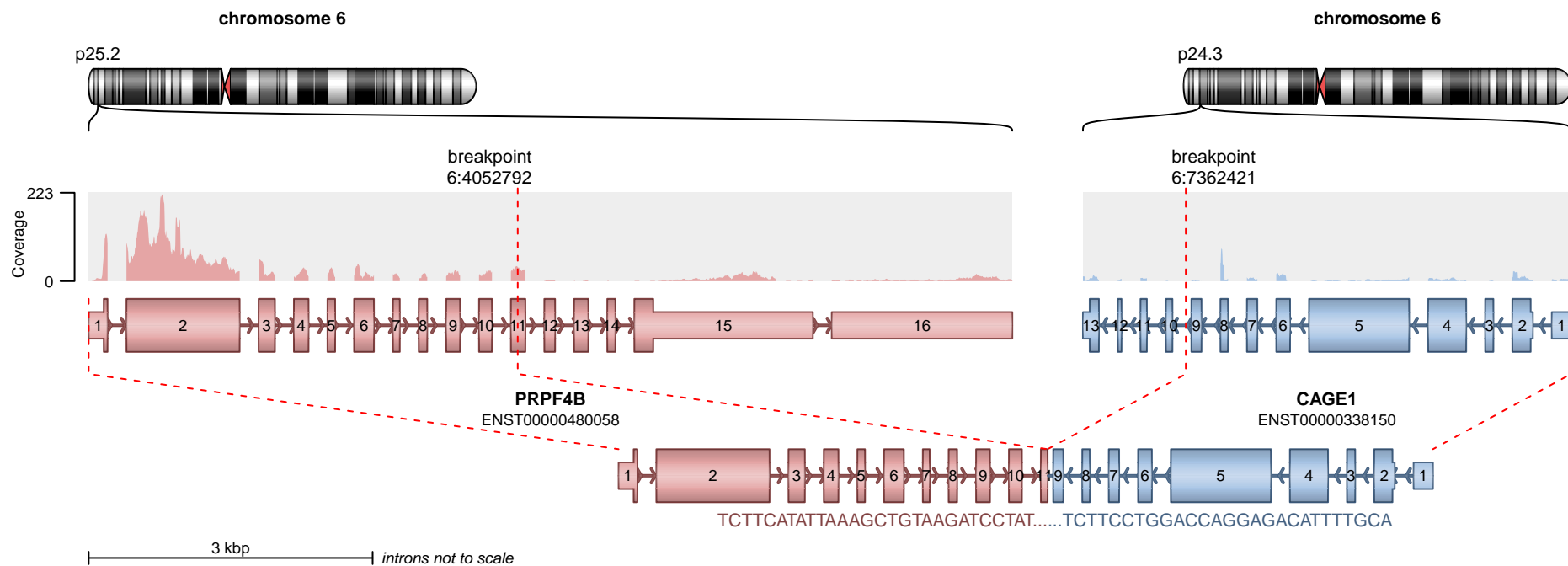


— translocation — deletion
— duplication — inversion

Genes are not protein-coding.

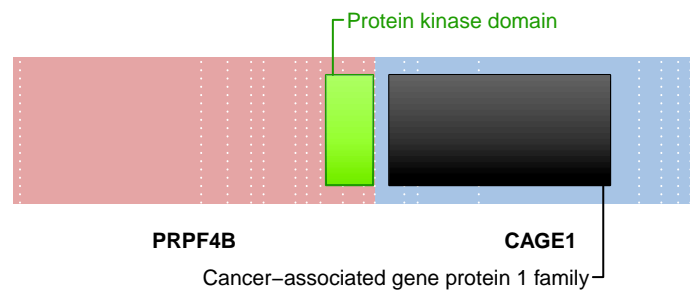
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



RETAINED PROTEIN DOMAINS

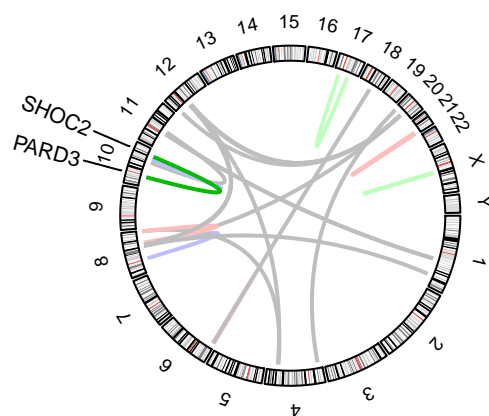
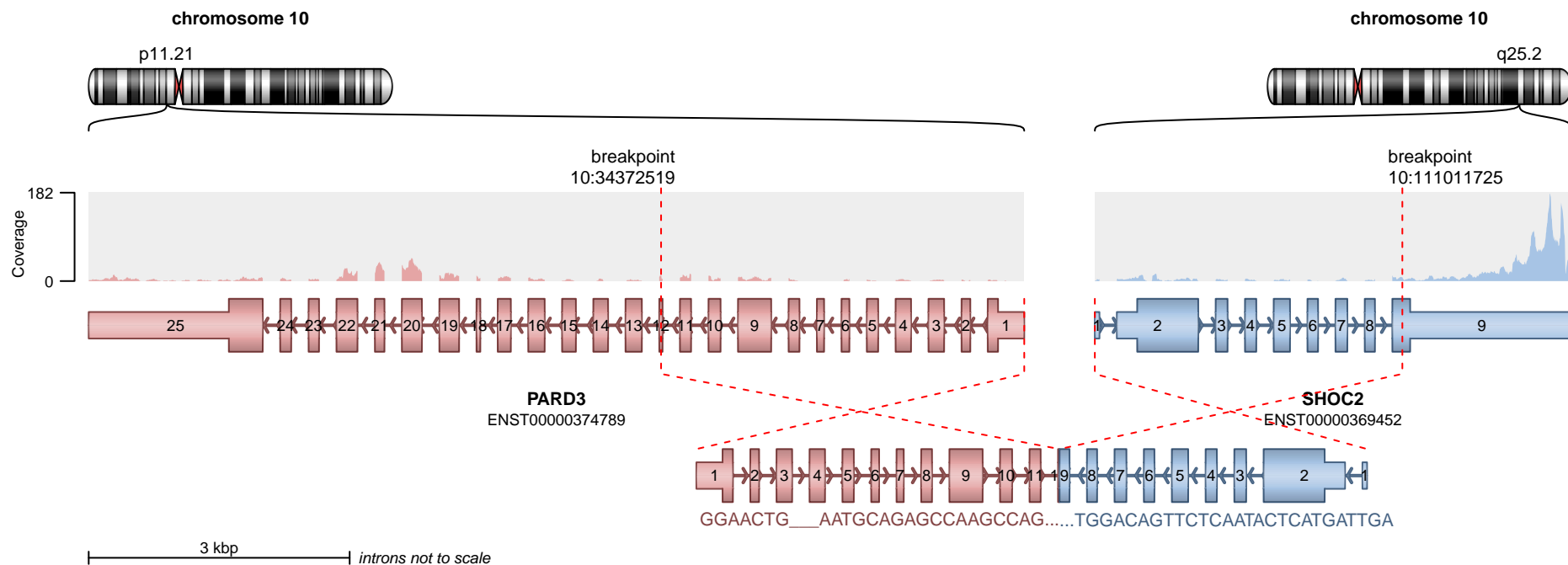
reading frame unclear



SUPPORTING READ COUNT

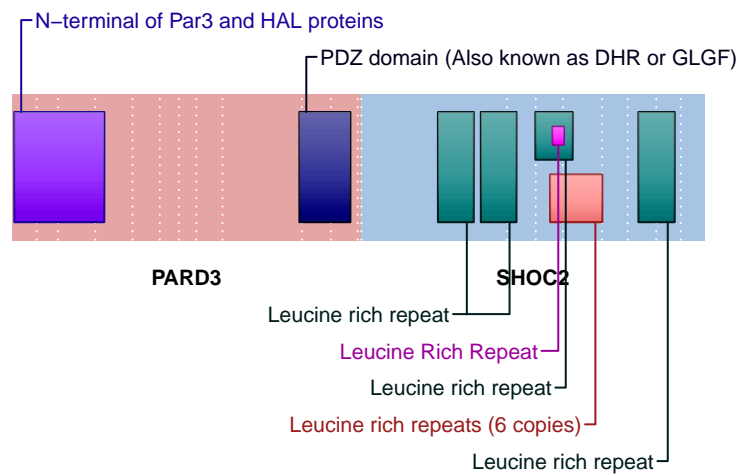
Split reads = 0
Discordant mates = 5

translocation deletion
duplication inversion



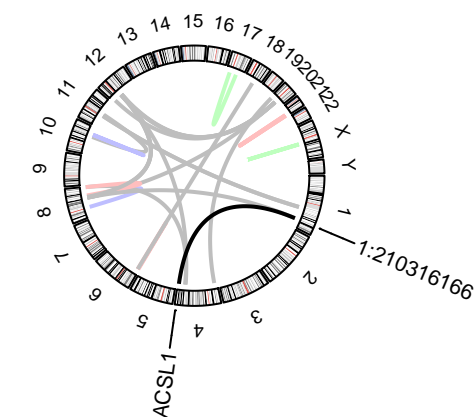
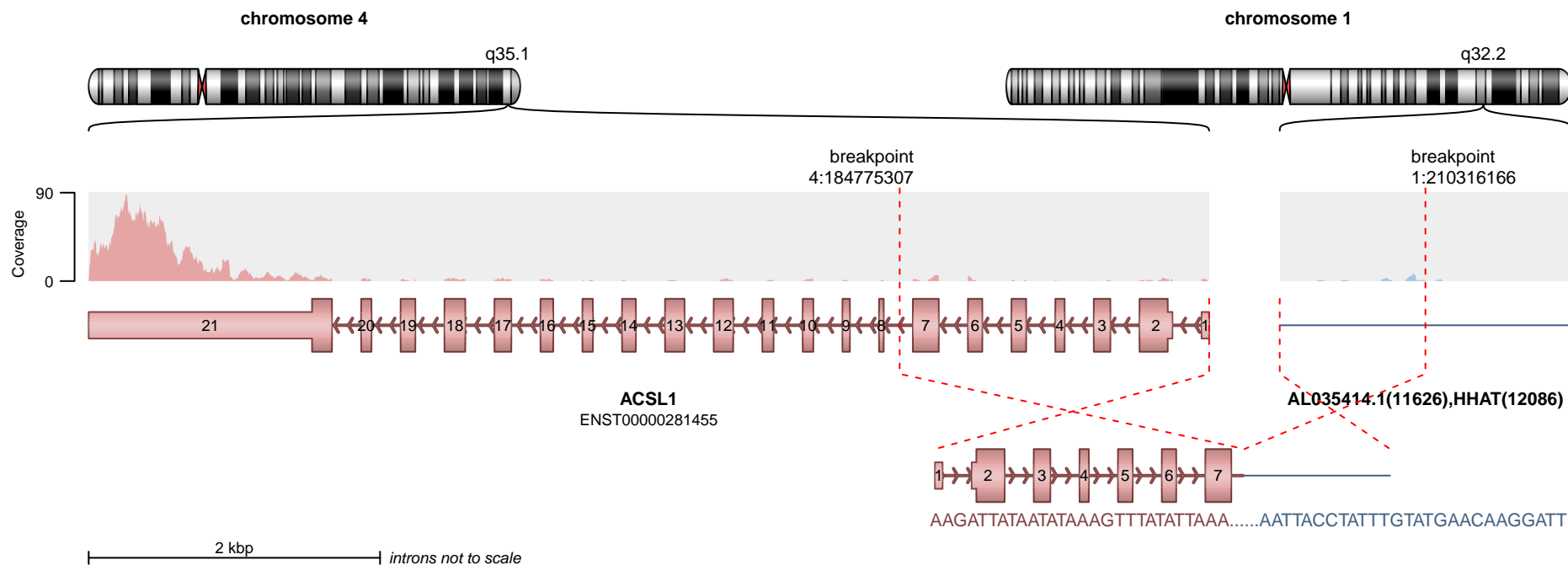
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS reading frame unclear



SUPPORTING READ COUNT

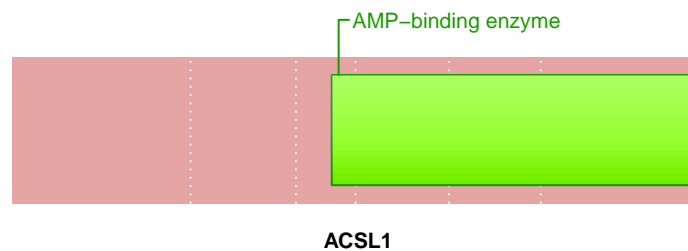
Split reads = 0
Discordant mates = 5



translocation deletion
duplication inversion

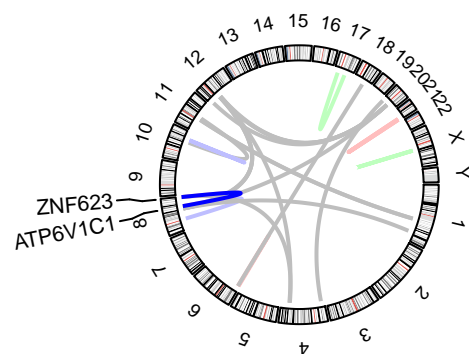
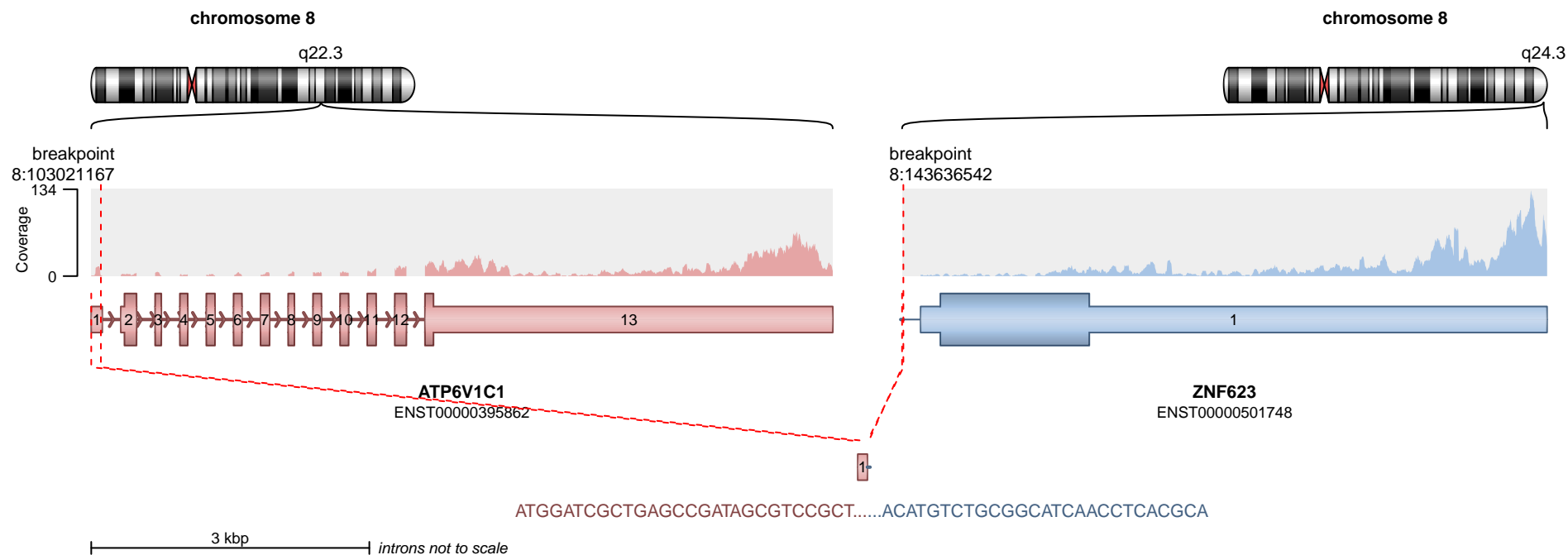
RETAINED PROTEIN DOMAINS

reading frame unclear



SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 4

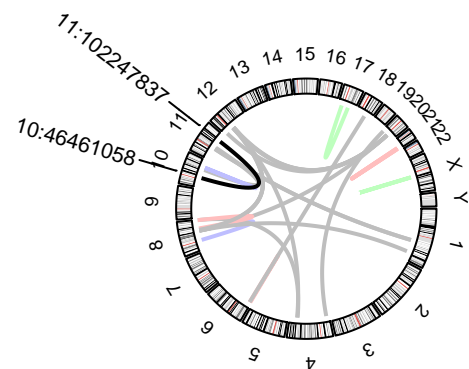
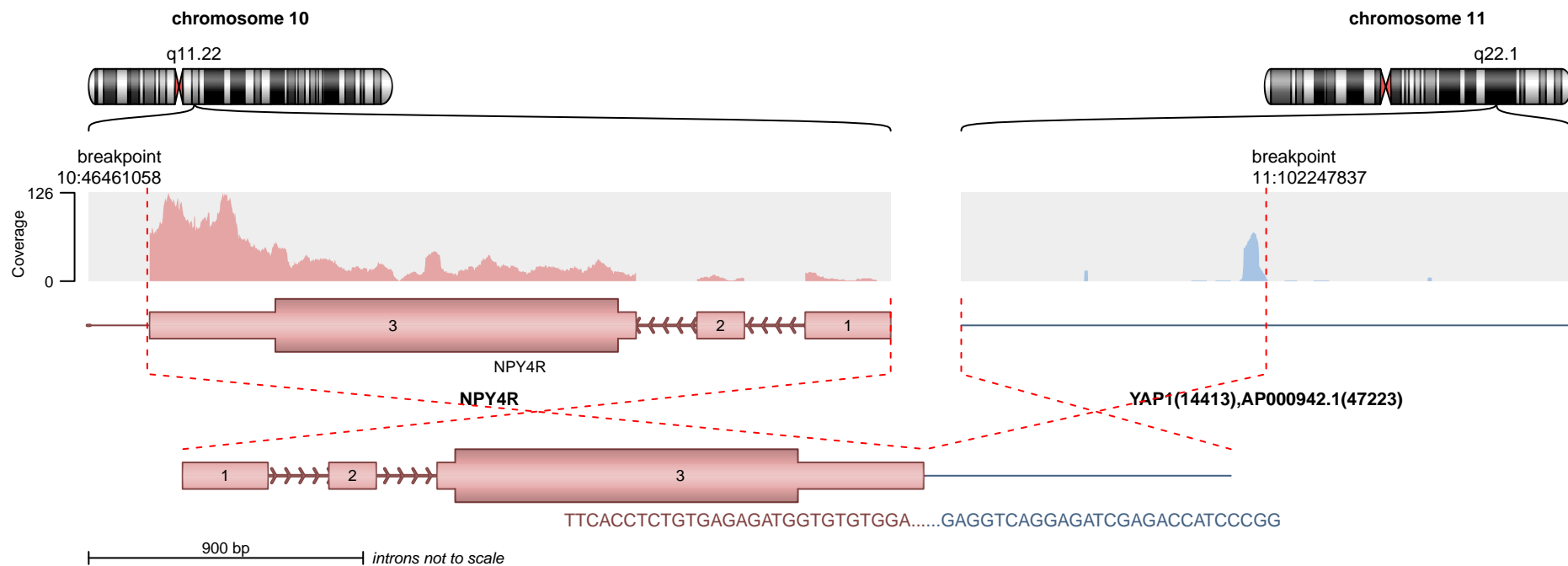


No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 4

translocation deletion
duplication inversion

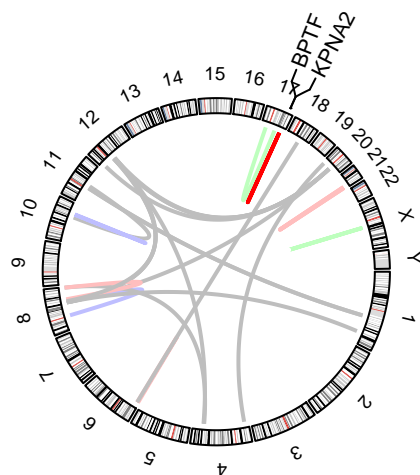
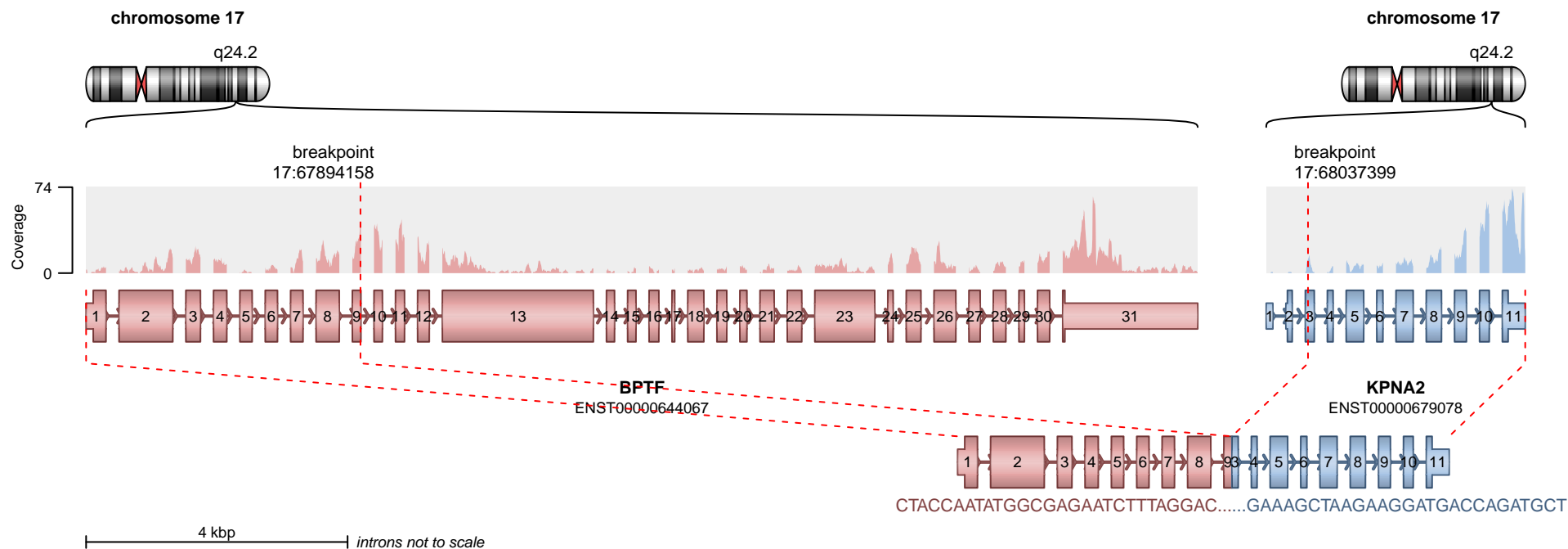


No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

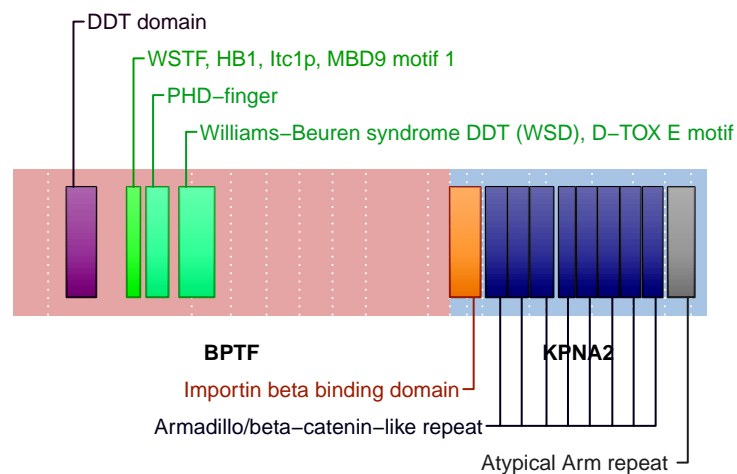
Split reads = 0
Discordant mates = 4

— translocation — deletion
— duplication — inversion



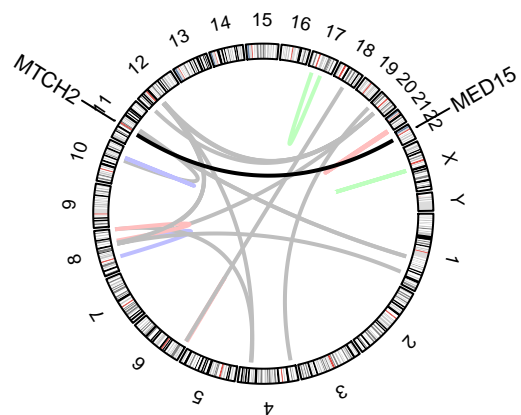
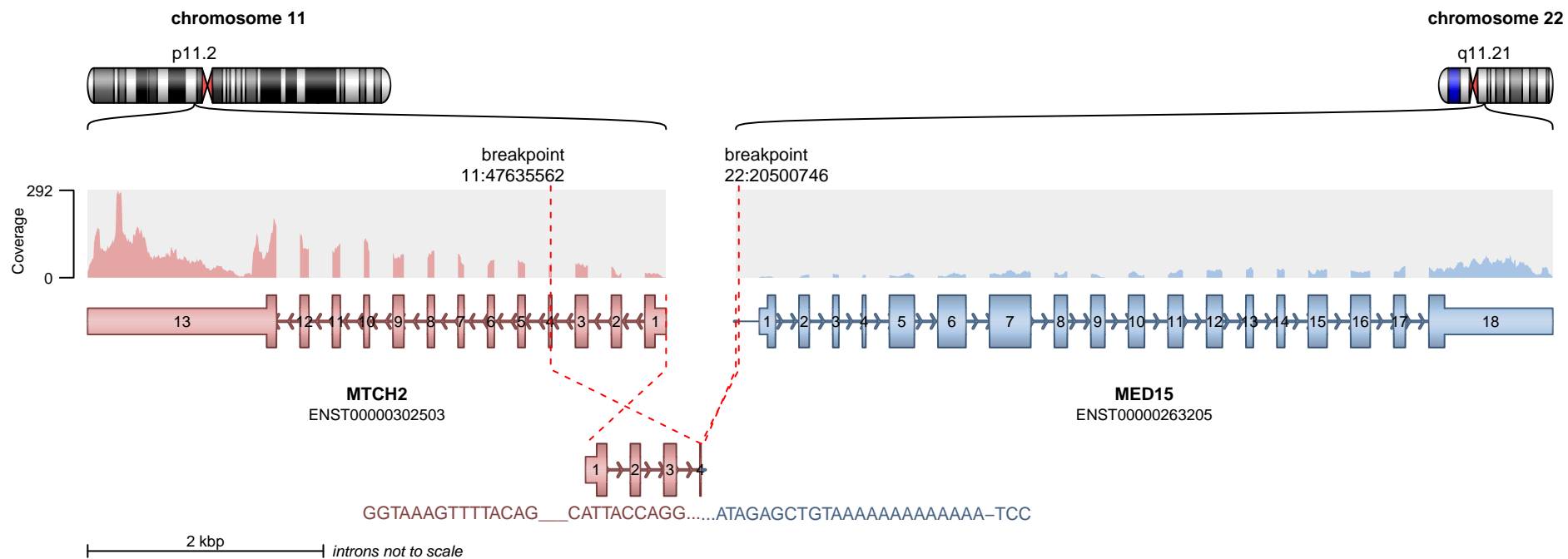
RETAINED PROTEIN DOMAINS

reading frame unclear



SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 4

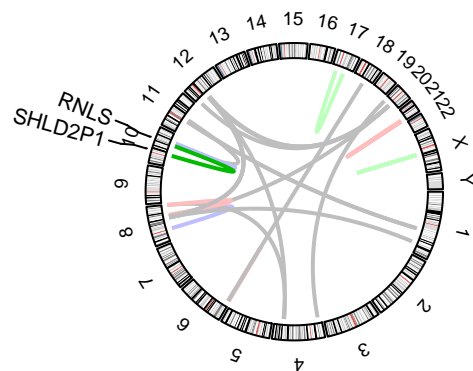
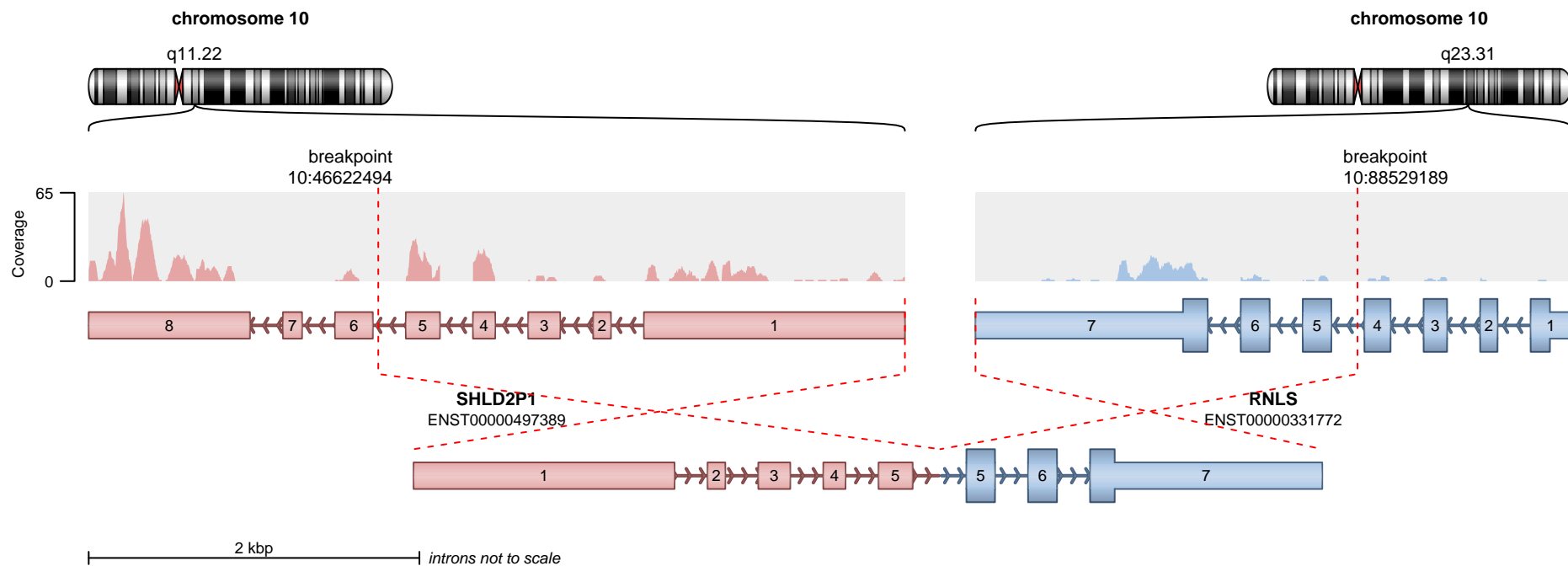


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 4

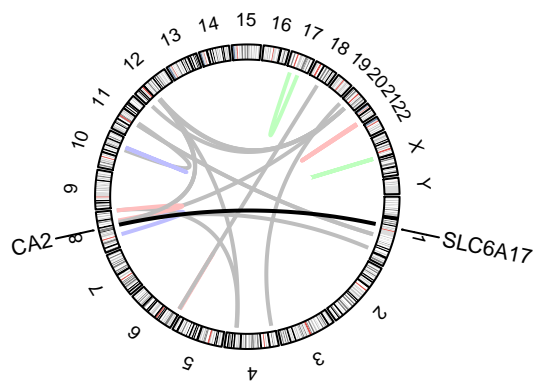
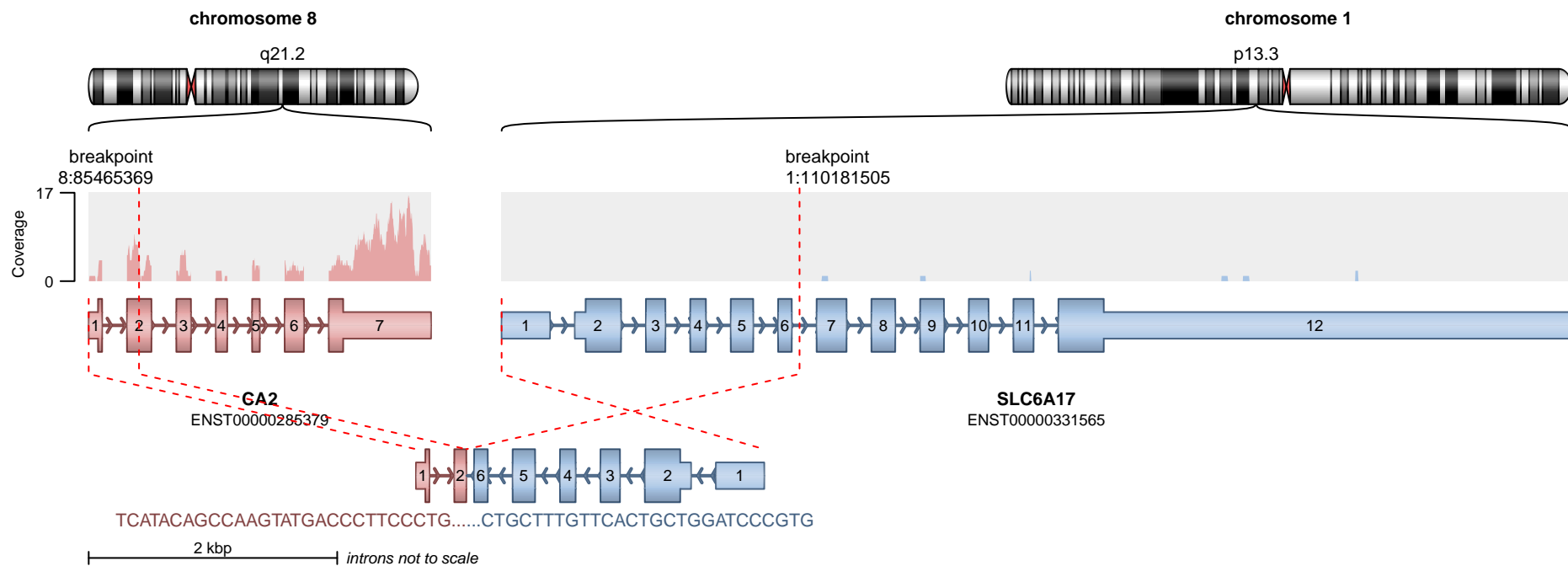


No coding regions due to antisense transcription.

SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 3

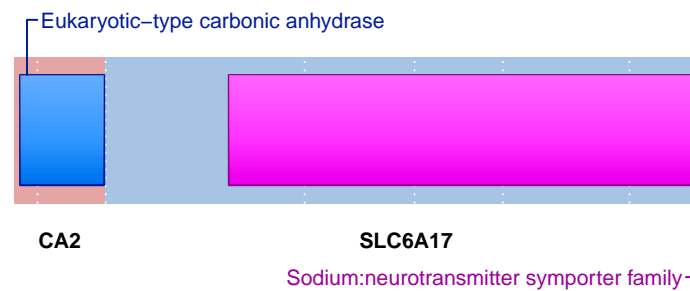
translocation deletion
duplication inversion



— translocation — deletion
— duplication — inversion

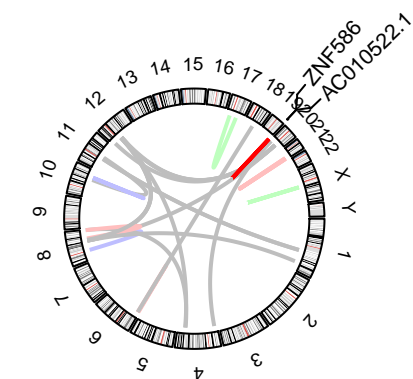
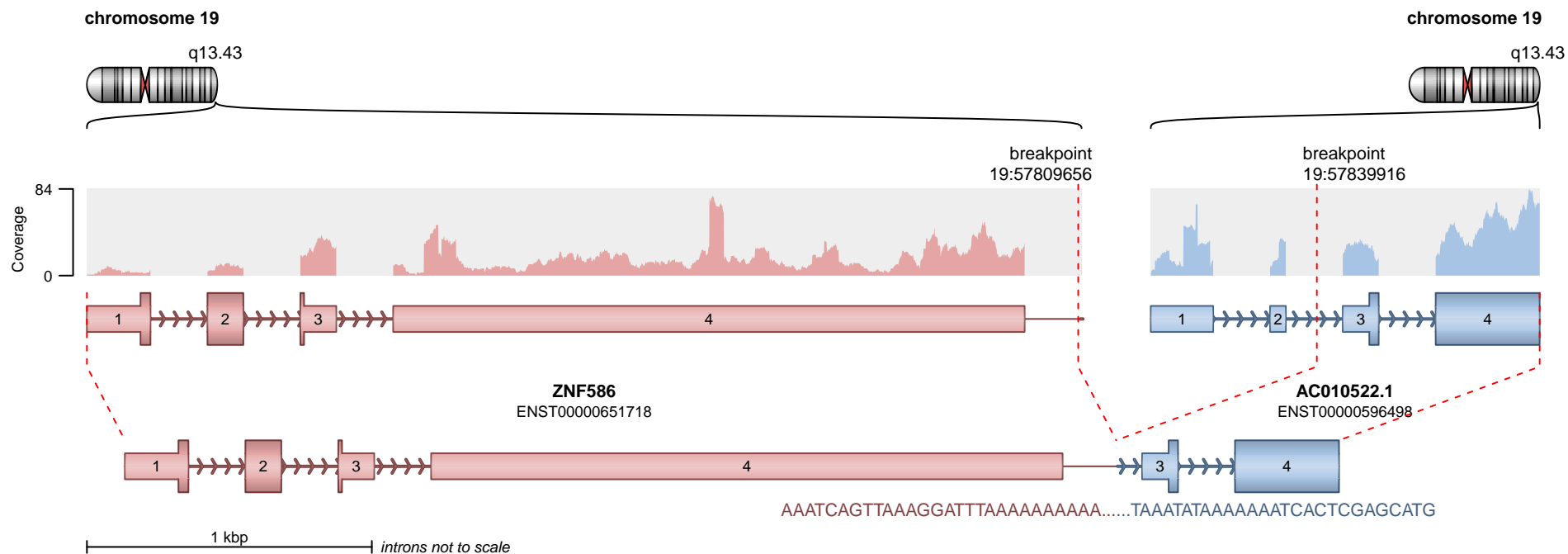
RETAINED PROTEIN DOMAINS

reading frame unclear



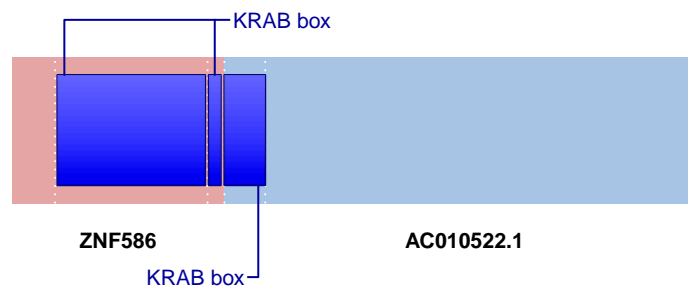
SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 3



RETAINED PROTEIN DOMAINS

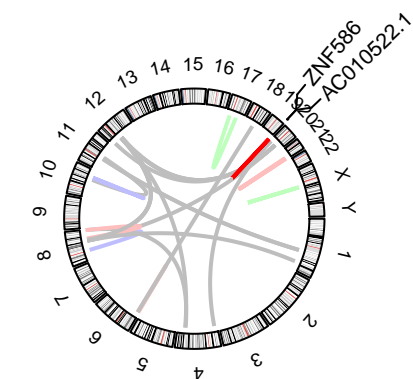
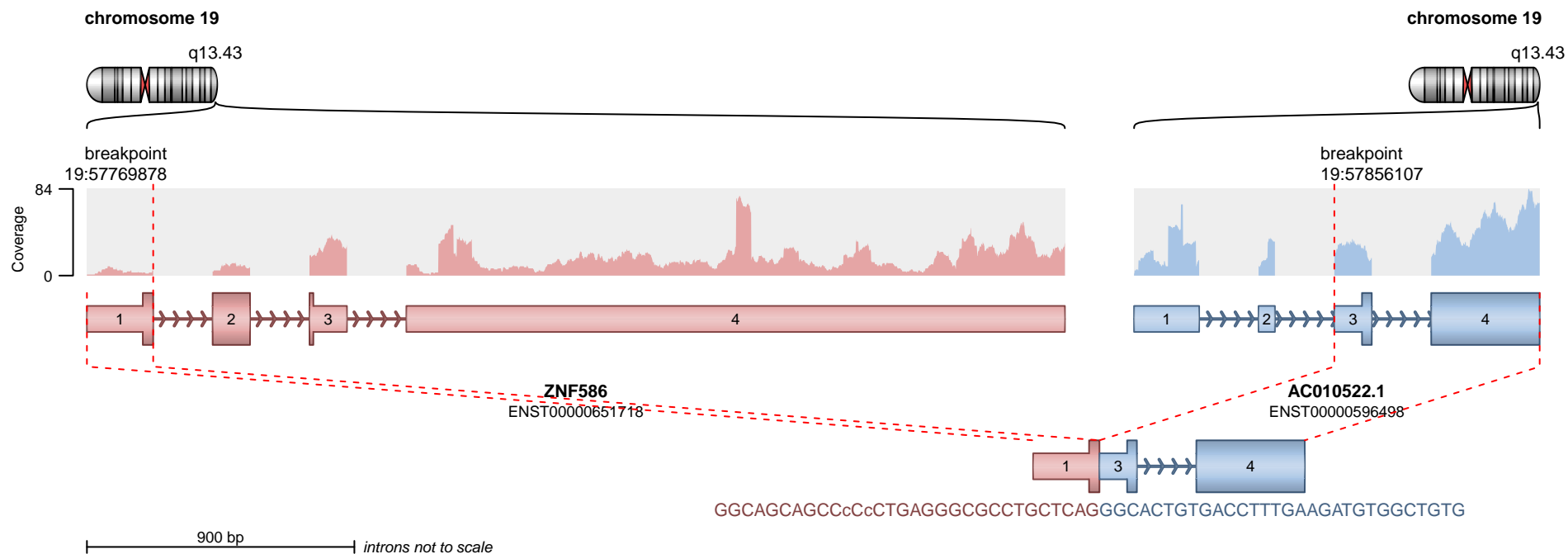
reading frame unclear



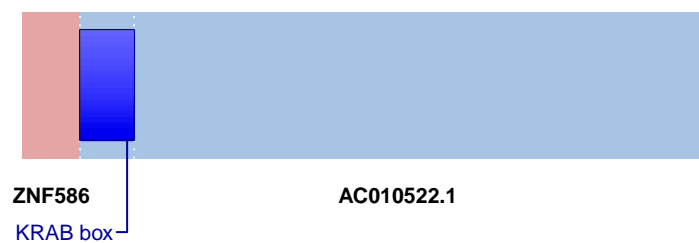
SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 3

— translocation — deletion
— duplication — inversion



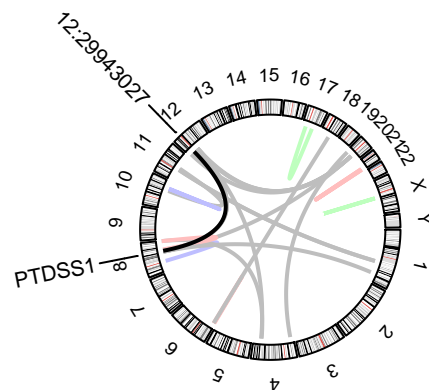
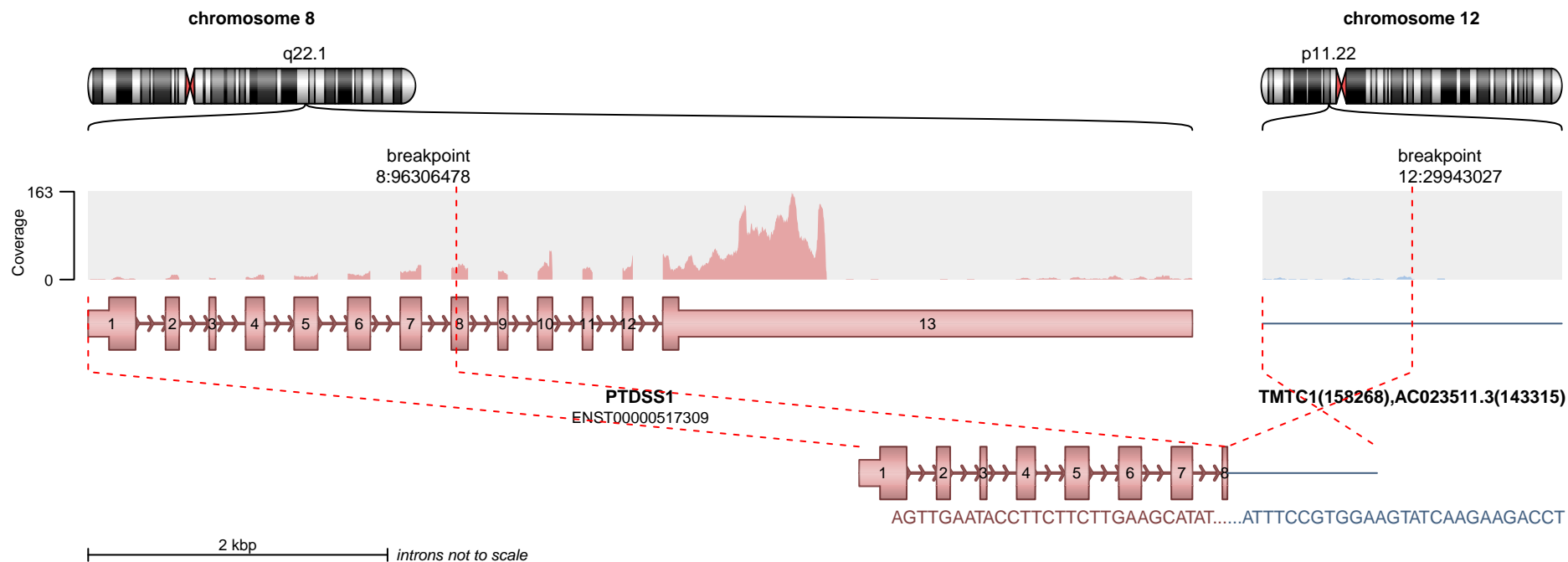
RETAINED PROTEIN DOMAINS in-frame fusion



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

translocation deletion
duplication inversion

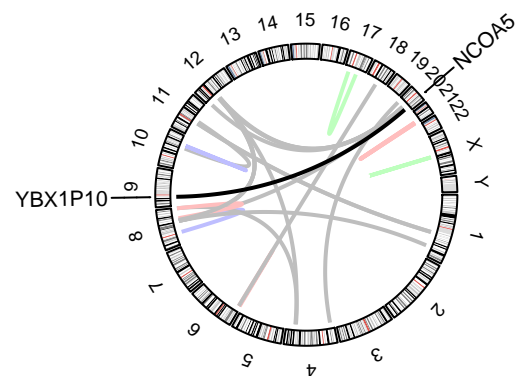
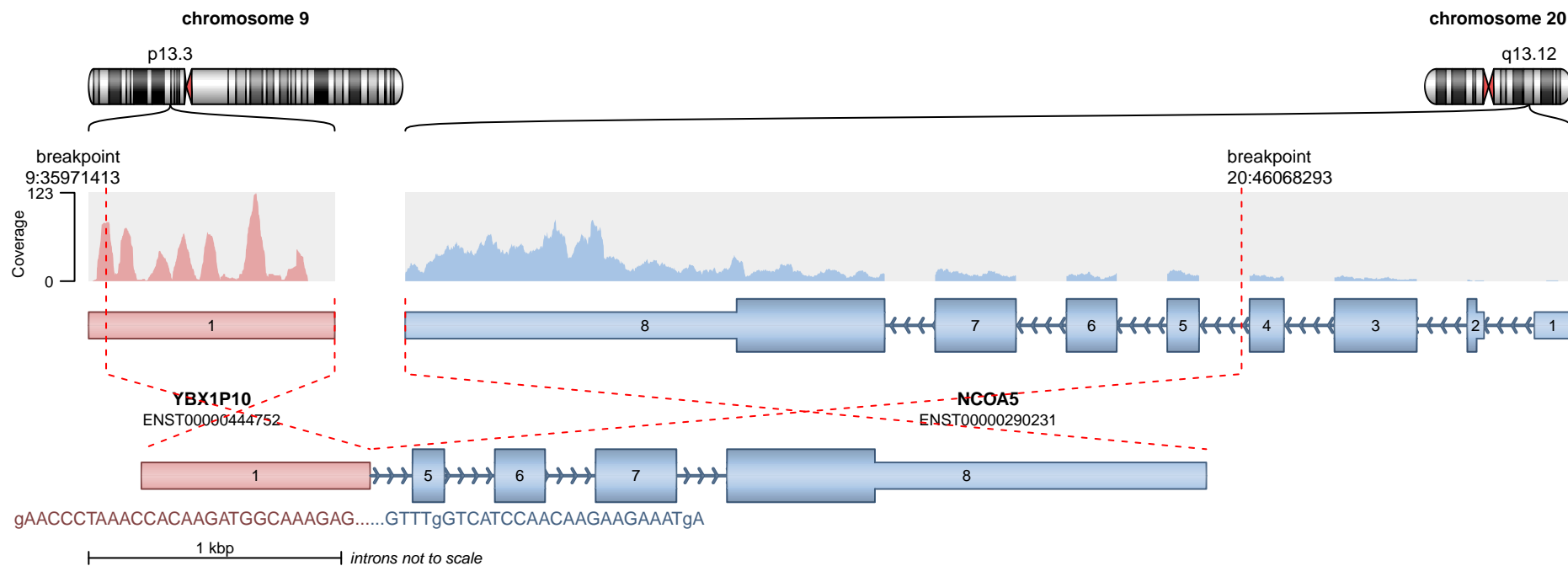


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 3

— translocation — deletion
— duplication — inversion

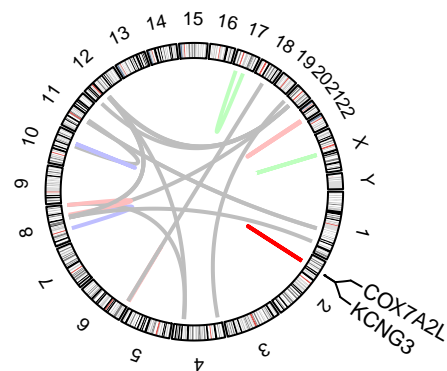
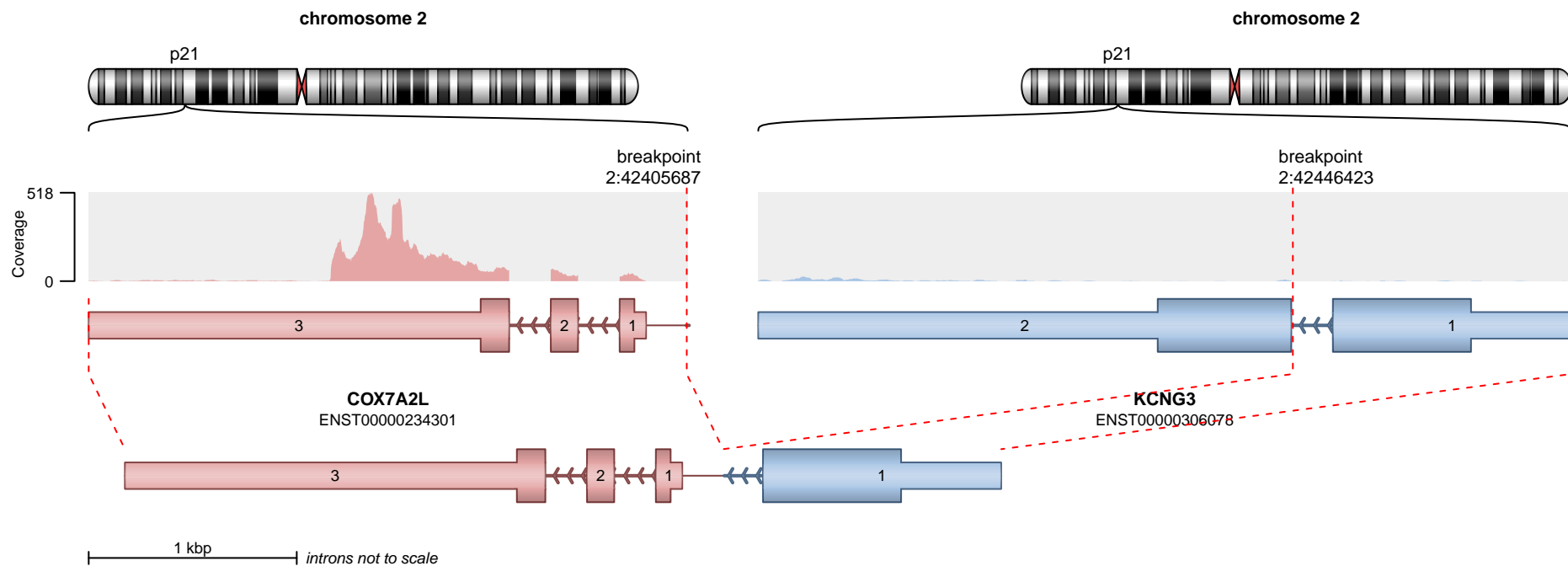


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 2



No coding regions due to antisense transcription.

SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 2

translocation deletion
duplication inversion