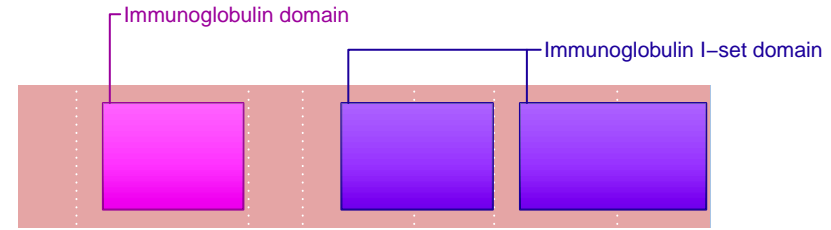


RETAINED PROTEIN DOMAINS
reading frame unclear

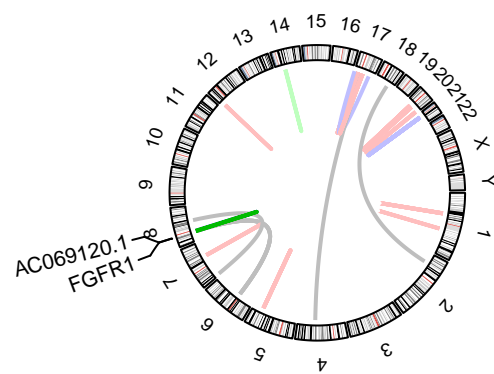
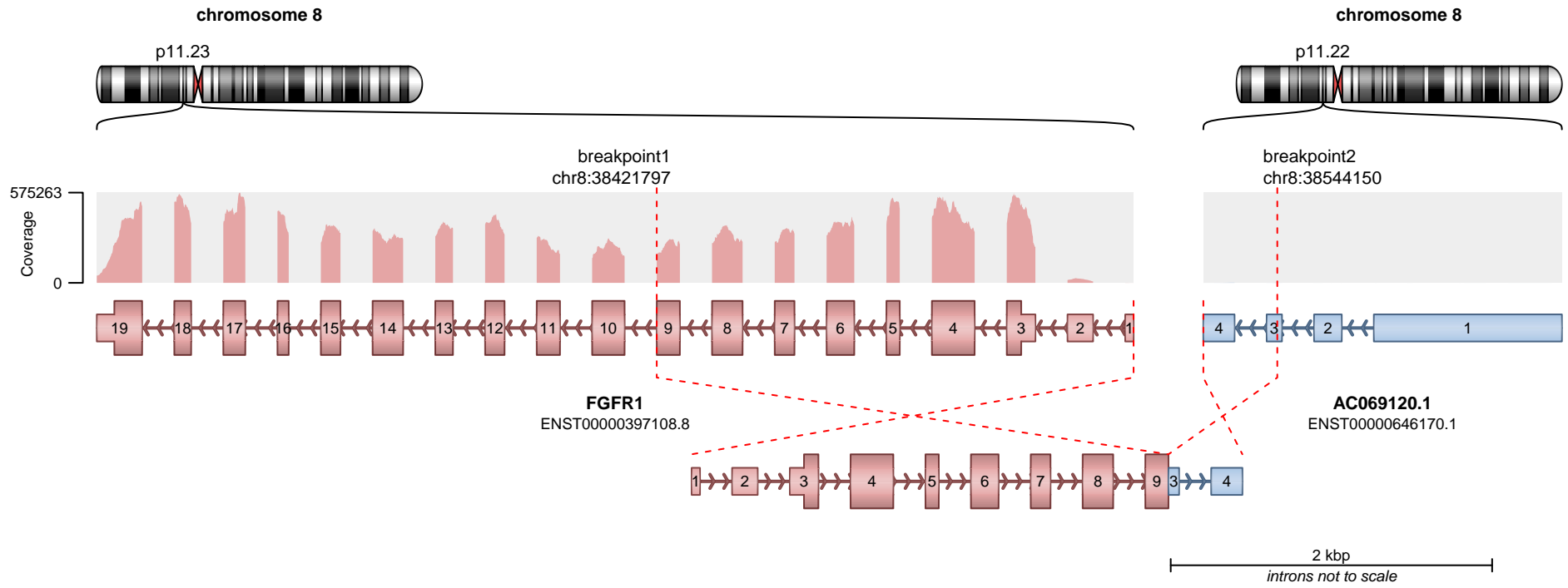


FGFR1

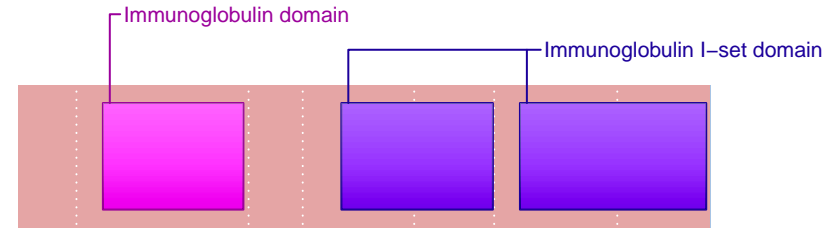
SUPPORTING READ COUNT

Split reads = 655
Discordant mates = 2

- translocation
- duplication
- deletion
- inversion



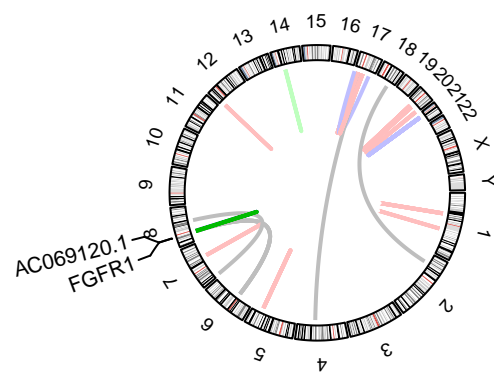
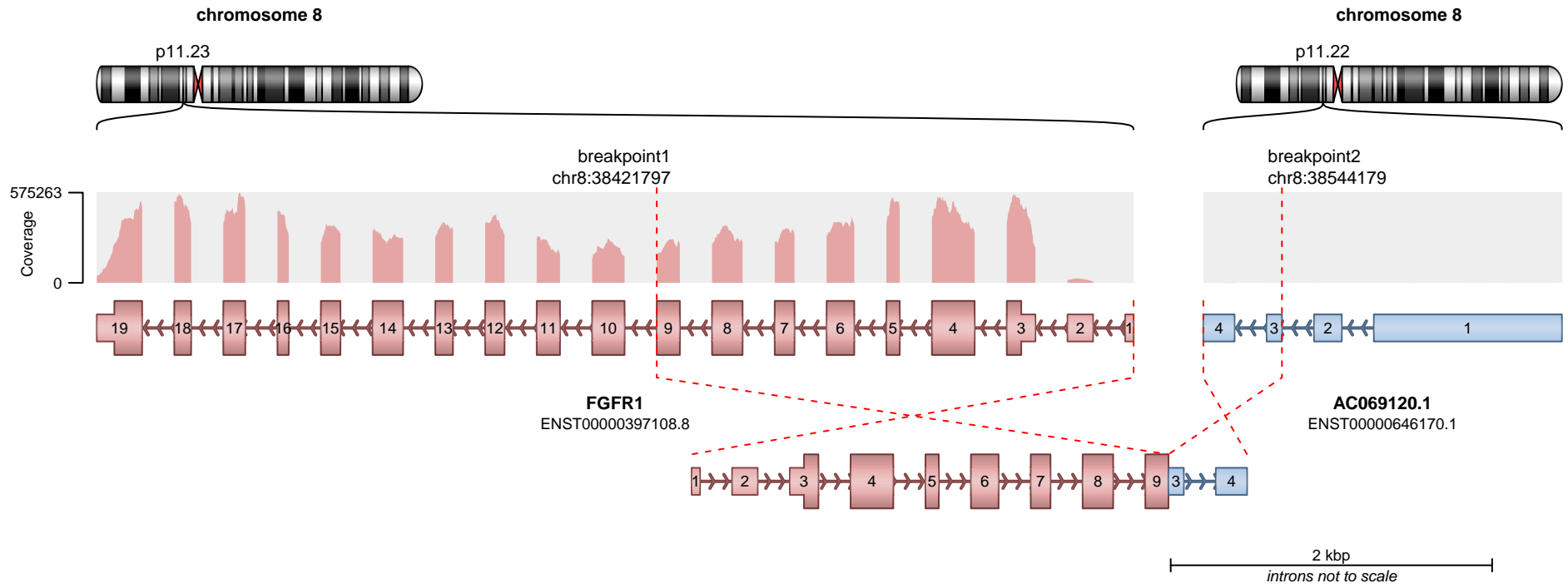
RETAINED PROTEIN DOMAINS
reading frame unclear



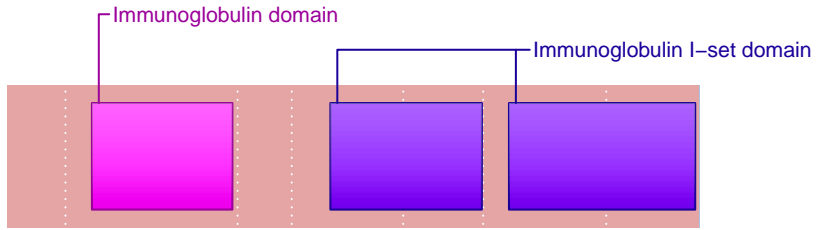
SUPPORTING READ COUNT

Split reads = 147
Discordant mates = 3

- translocation
- duplication
- deletion
- inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

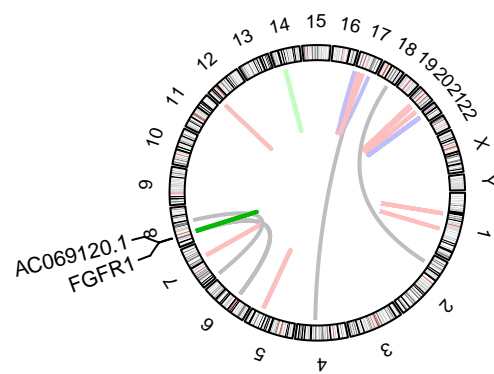
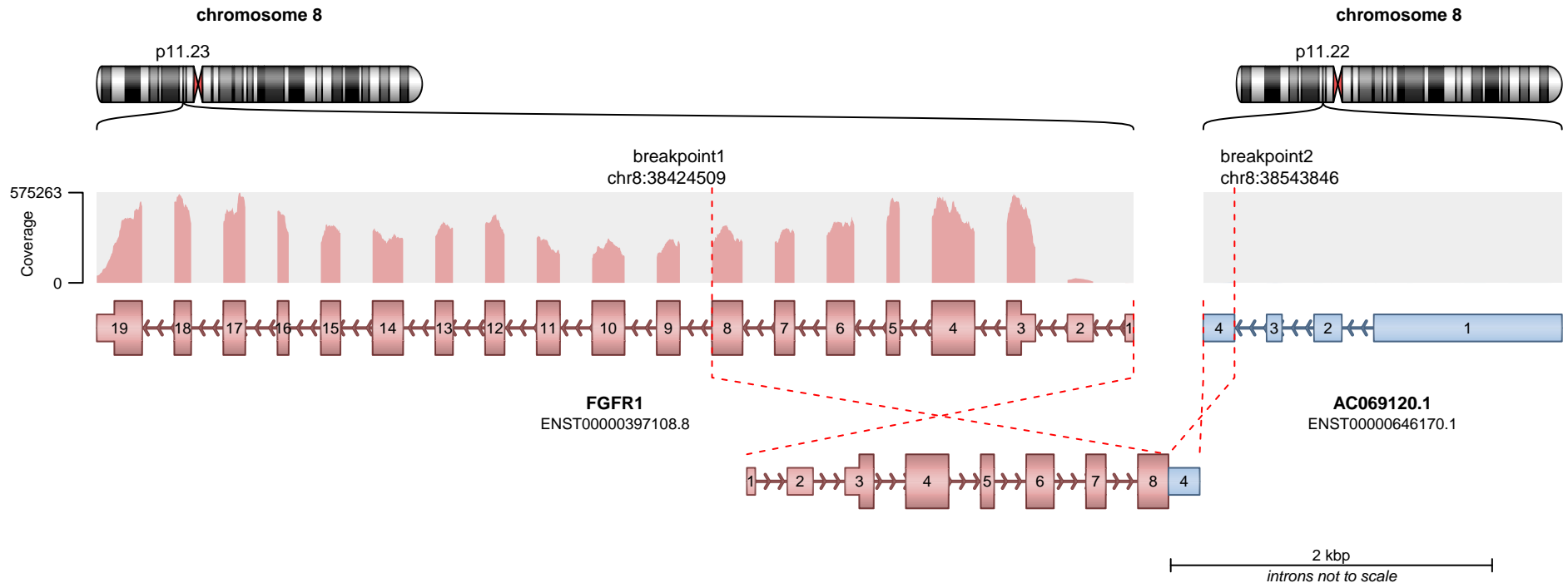


FGFR1

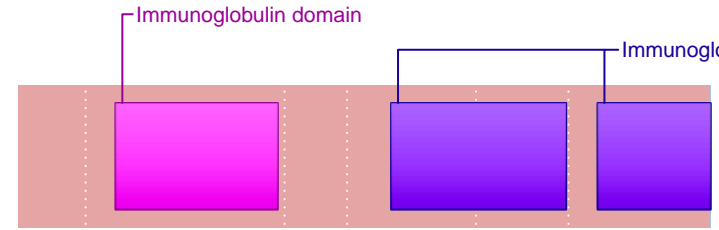
SUPPORTING READ COUNT

Split reads = 73
Discordant mates = 3

- translocation
- duplication
- deletion
- inversion



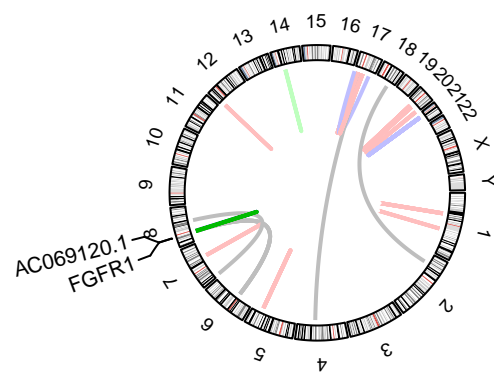
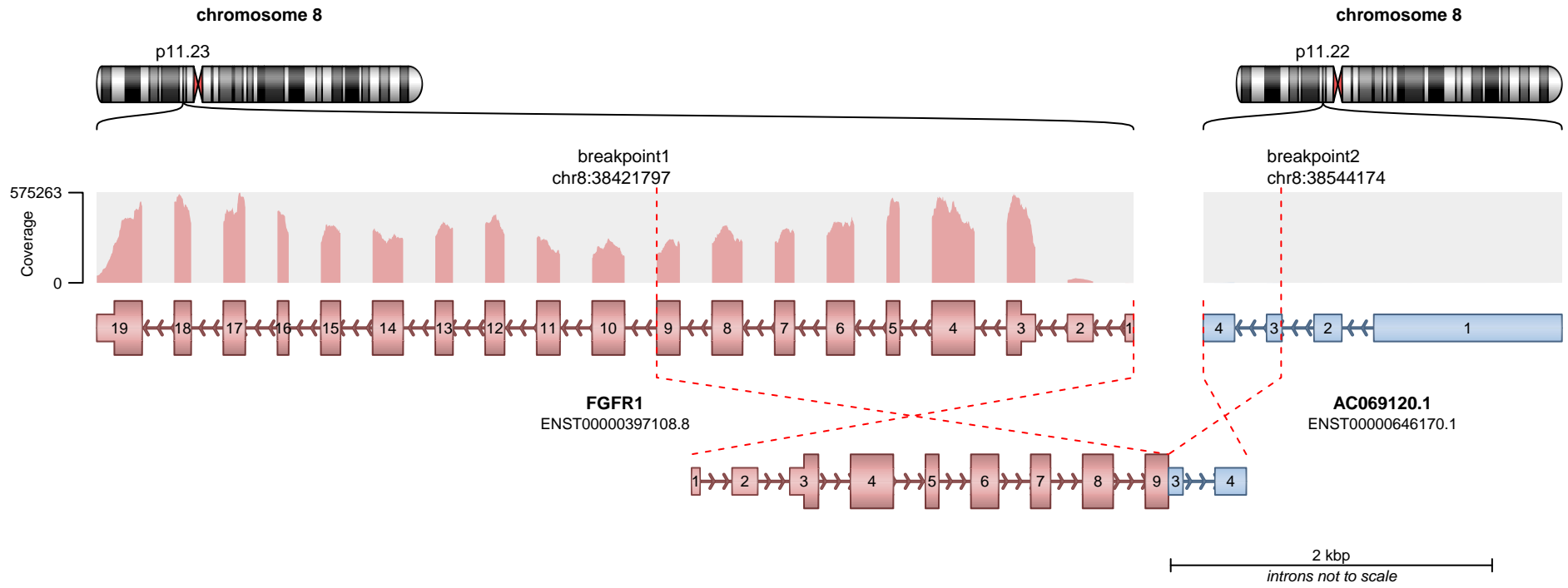
RETAINED PROTEIN DOMAINS
reading frame unclear



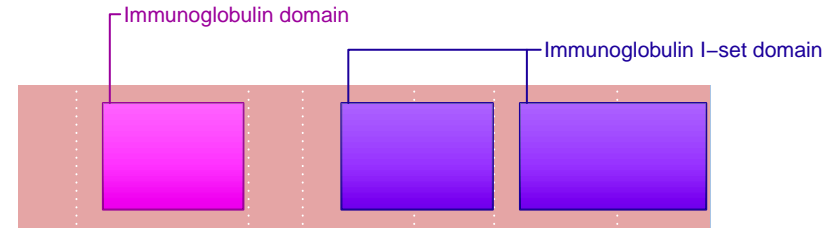
SUPPORTING READ COUNT

Split reads = 43
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

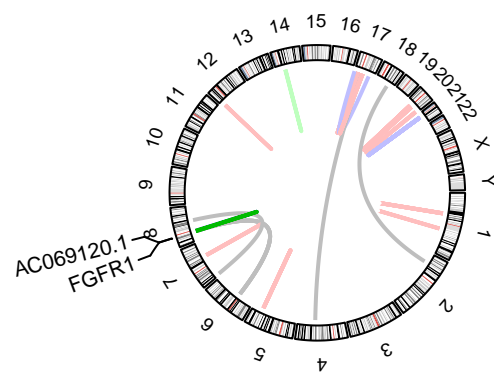
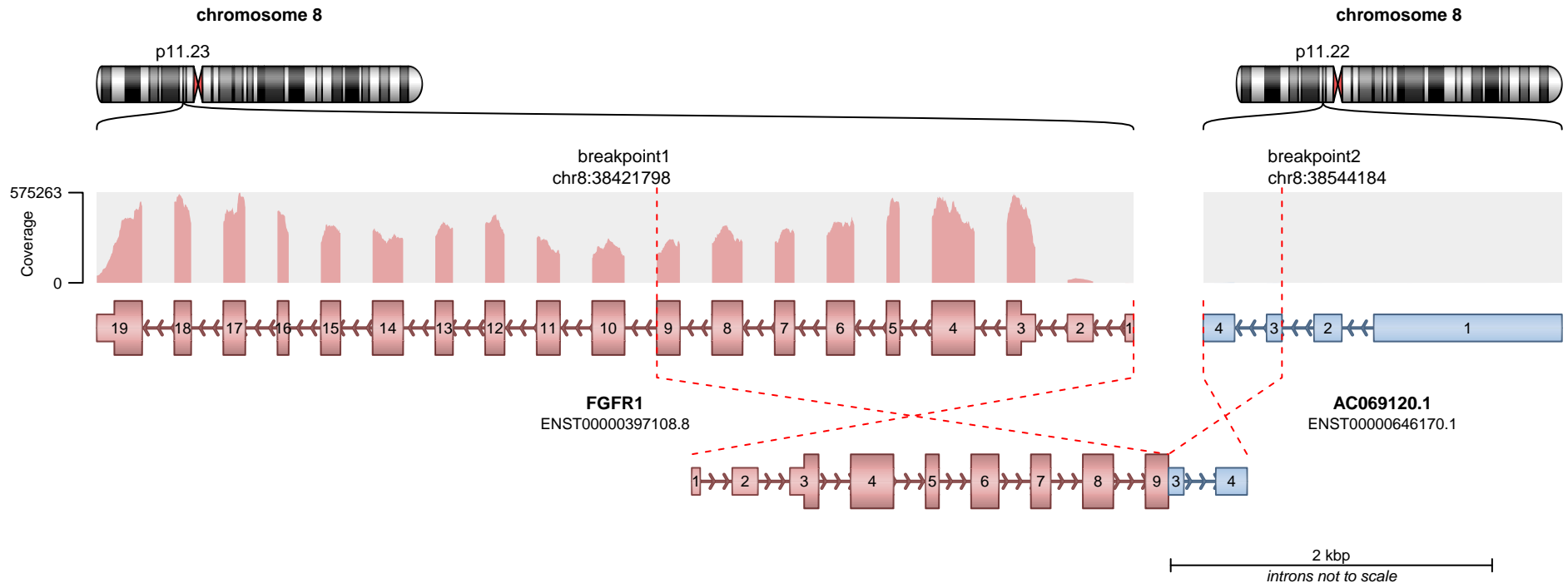


FGFR1

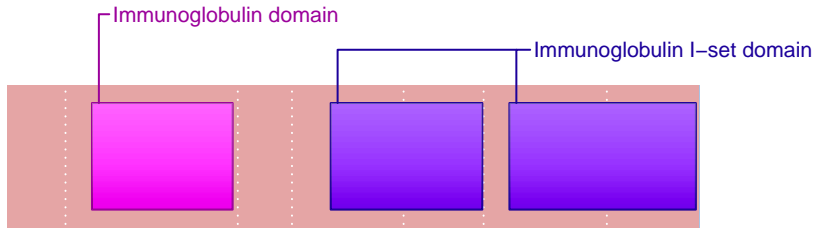
SUPPORTING READ COUNT

Split reads = 21
Discordant mates = 3

- translocation
- duplication
- deletion
- inversion



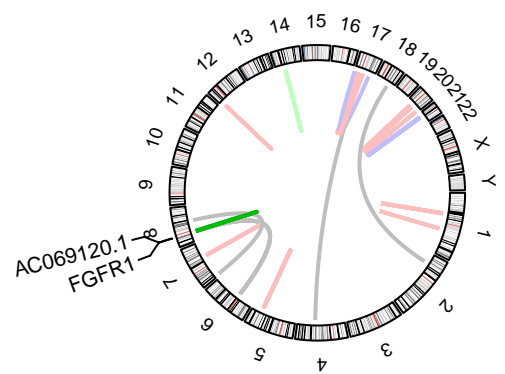
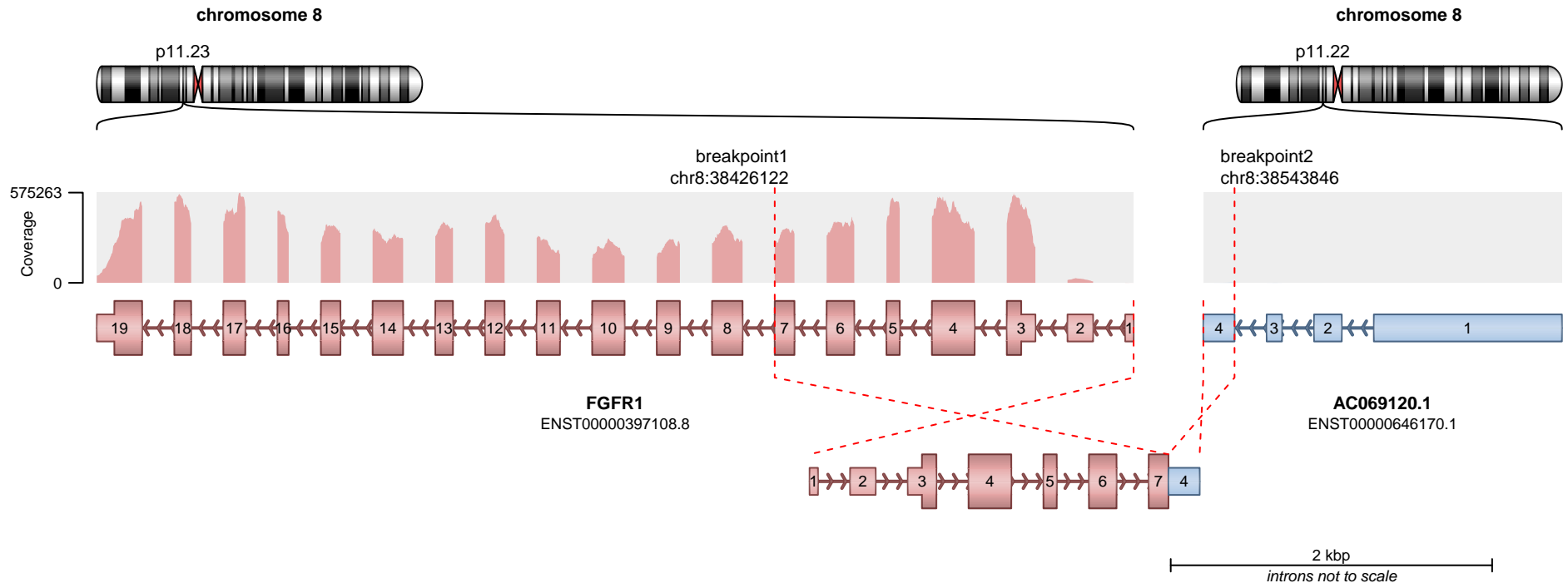
RETAINED PROTEIN DOMAINS
reading frame unclear



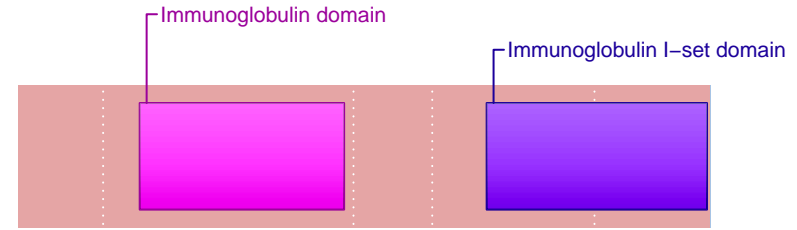
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 3

- translocation
- duplication
- deletion
- inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

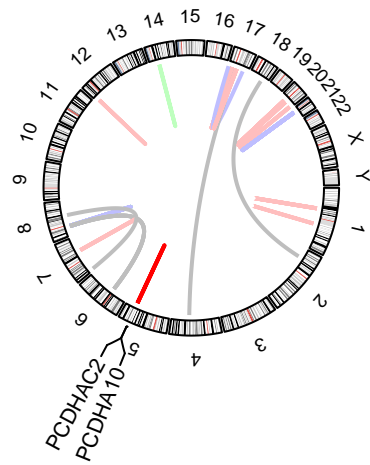
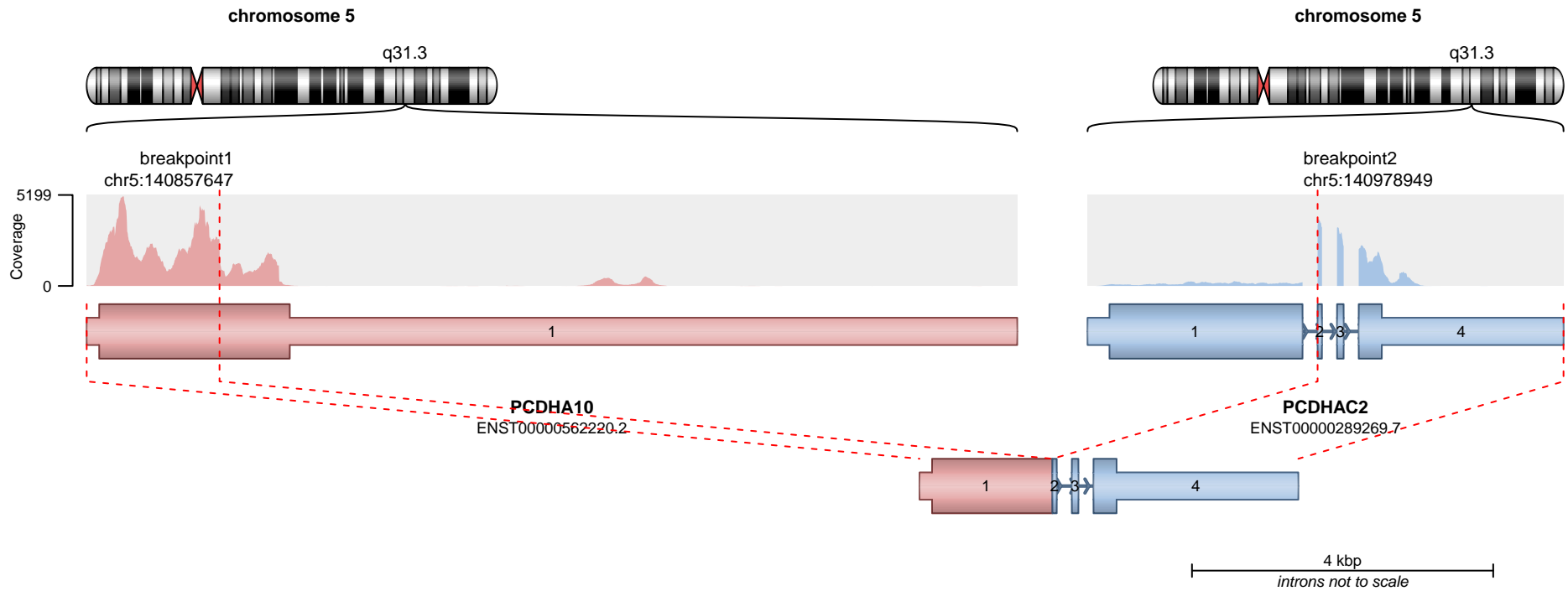


FGFR1

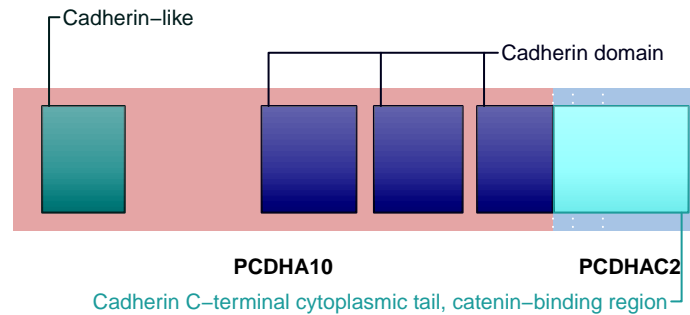
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



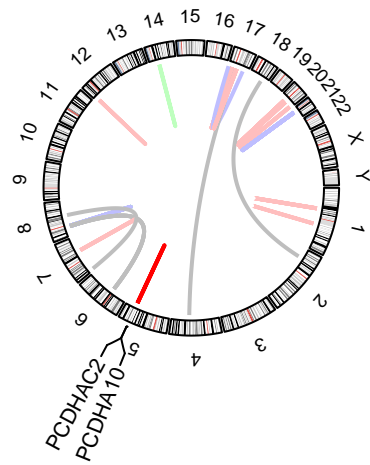
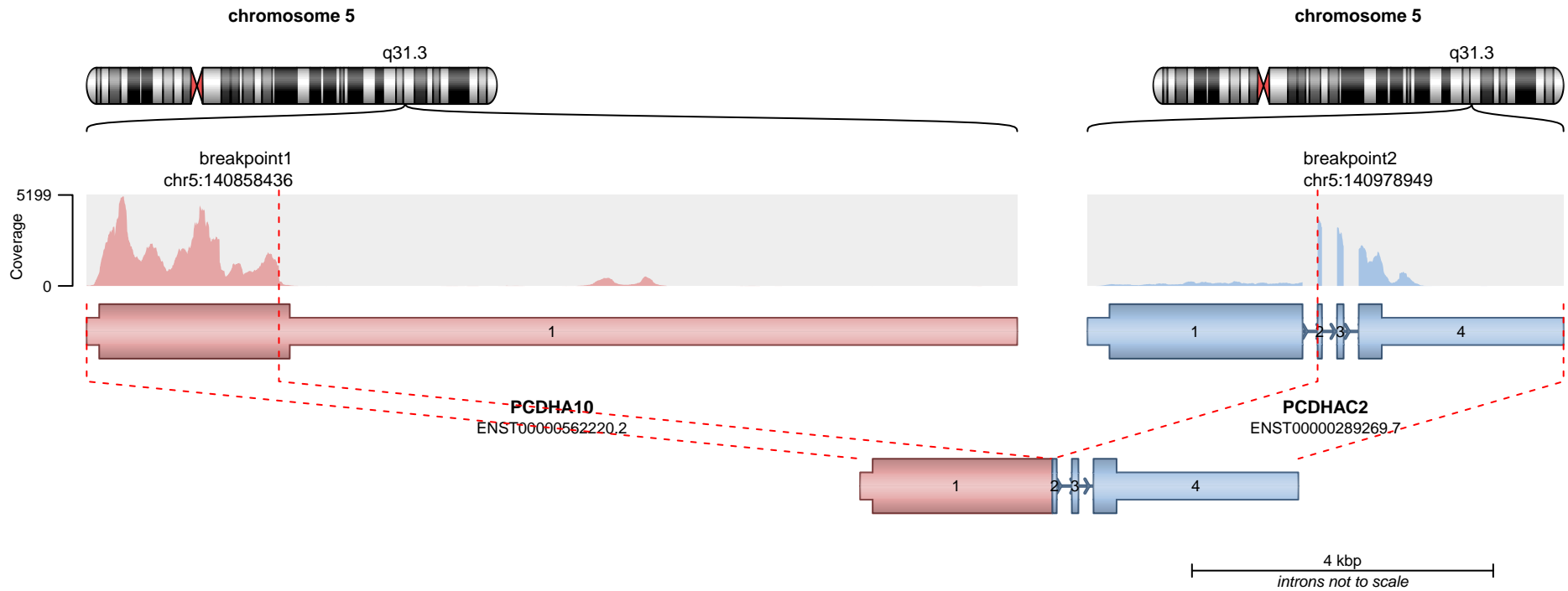
RETAINED PROTEIN DOMAINS
reading frame unclear



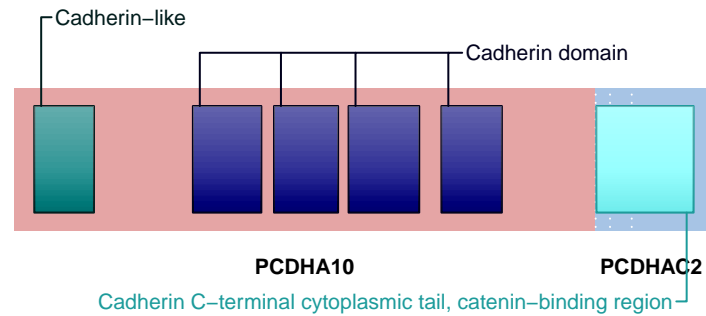
SUPPORTING READ COUNT

Split reads = 406
Discordant mates = 6

— translocation — deletion
— duplication — inversion



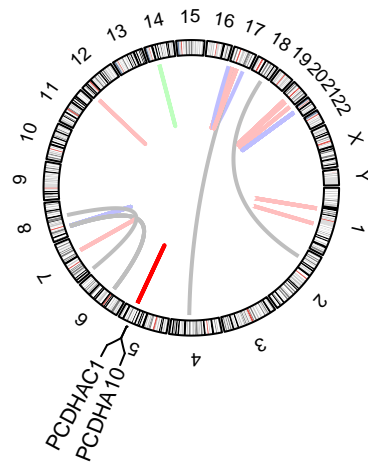
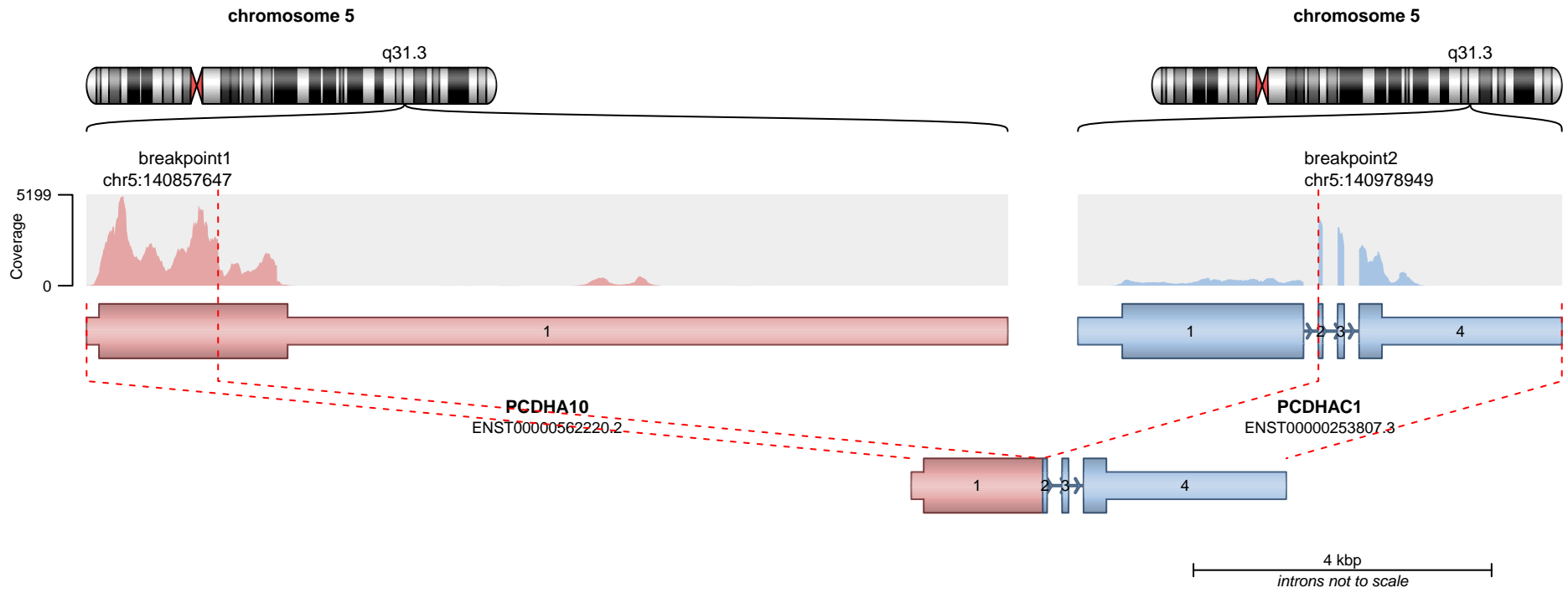
RETAINED PROTEIN DOMAINS
reading frame unclear



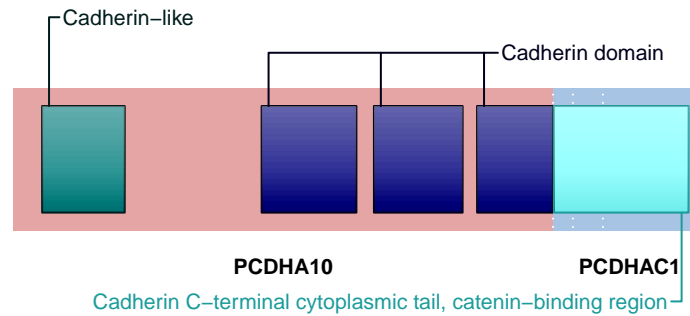
SUPPORTING READ COUNT

Split reads = 275
Discordant mates = 10

— translocation — deletion
— duplication — inversion



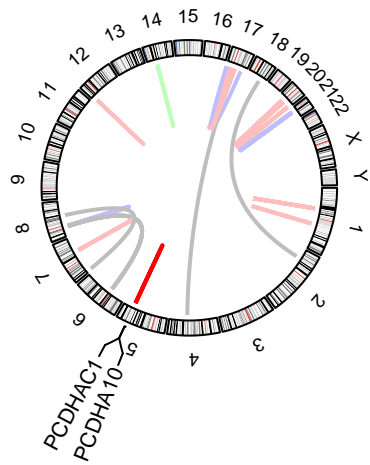
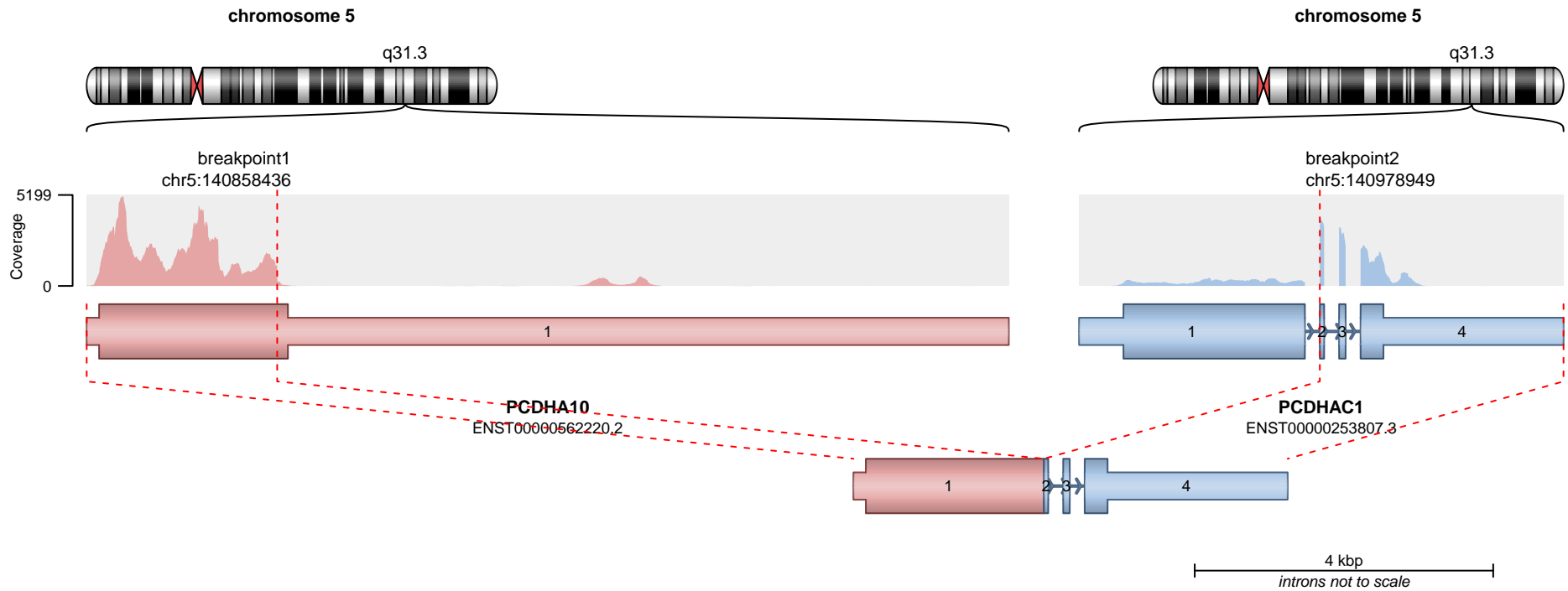
RETAINED PROTEIN DOMAINS
reading frame unclear



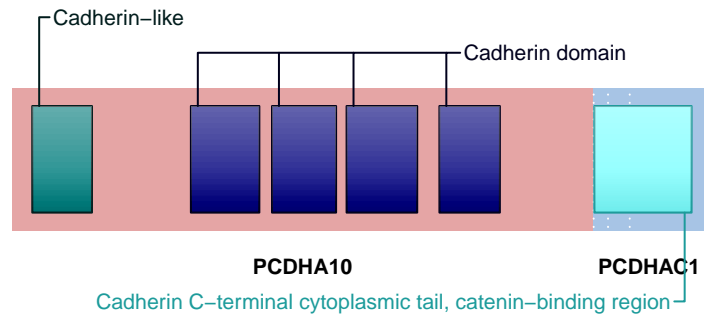
SUPPORTING READ COUNT

Split reads = 406
Discordant mates = 4

- translocation
- duplication
- deletion
- inversion



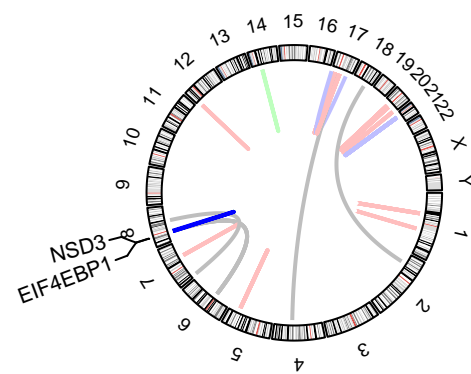
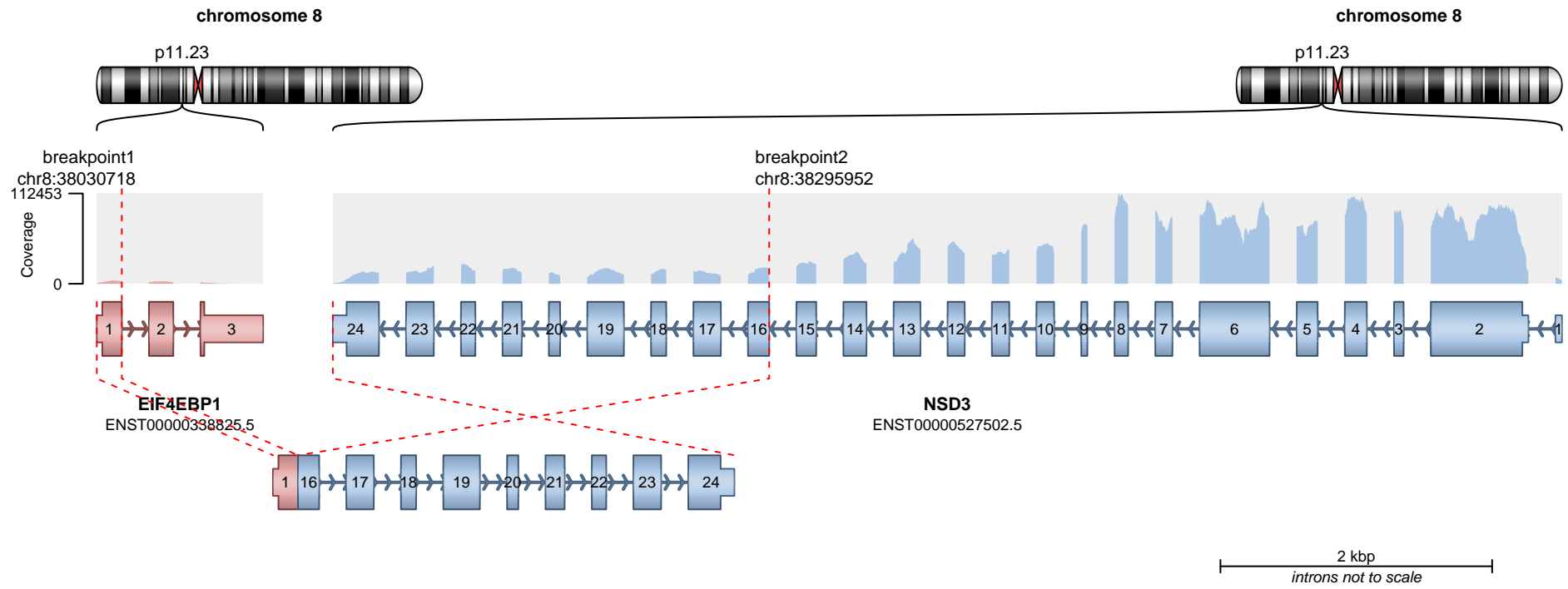
RETAINED PROTEIN DOMAINS
reading frame unclear



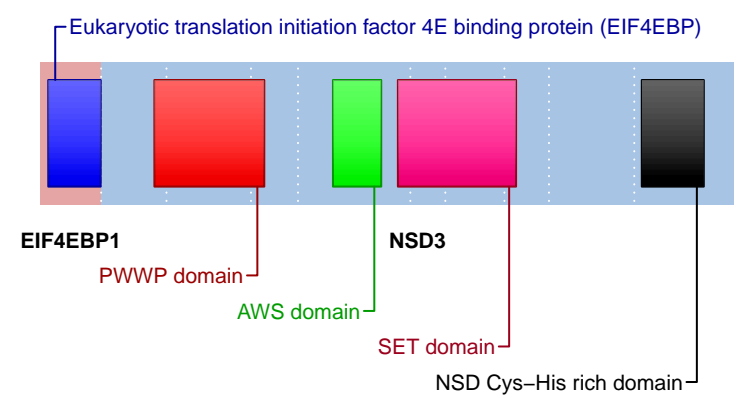
SUPPORTING READ COUNT

Split reads = 275
Discordant mates = 8

— translocation — deletion
— duplication — inversion

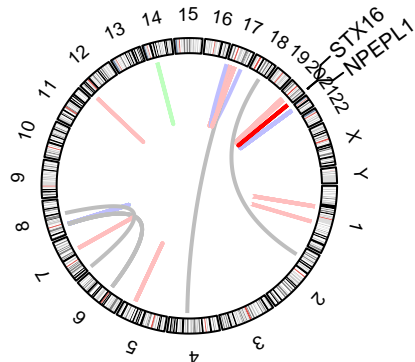
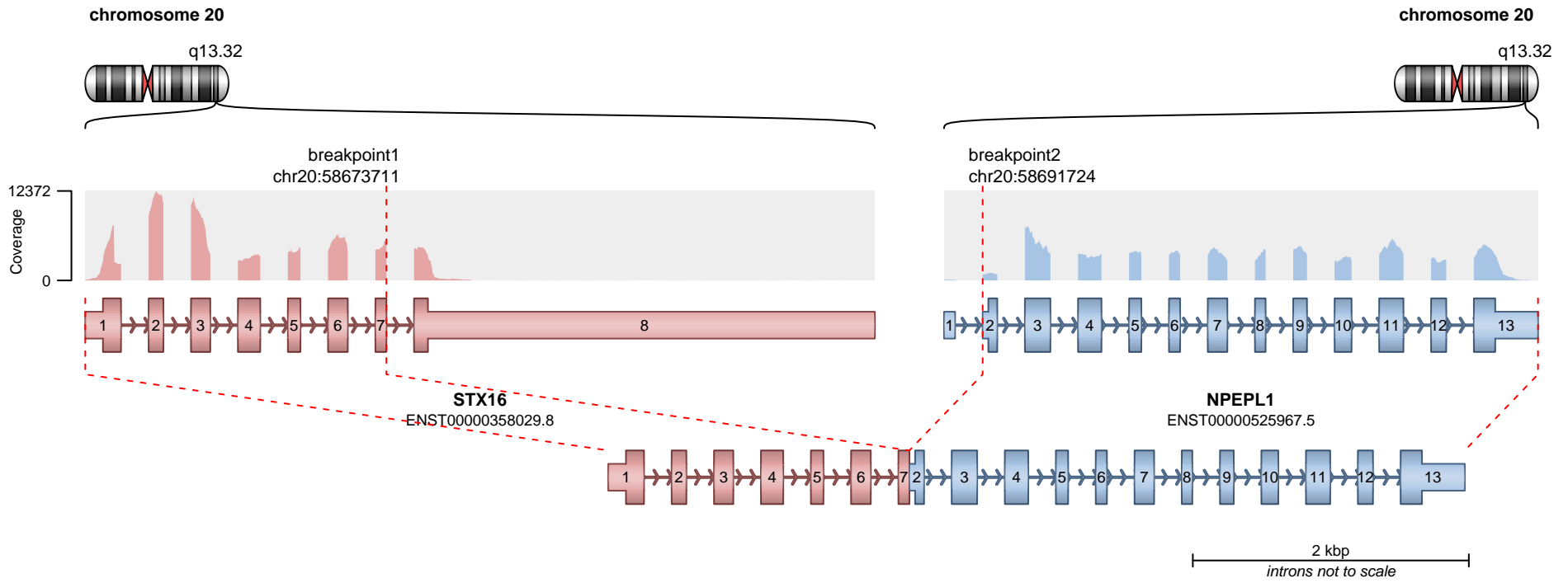


RETAINED PROTEIN DOMAINS
reading frame unclear

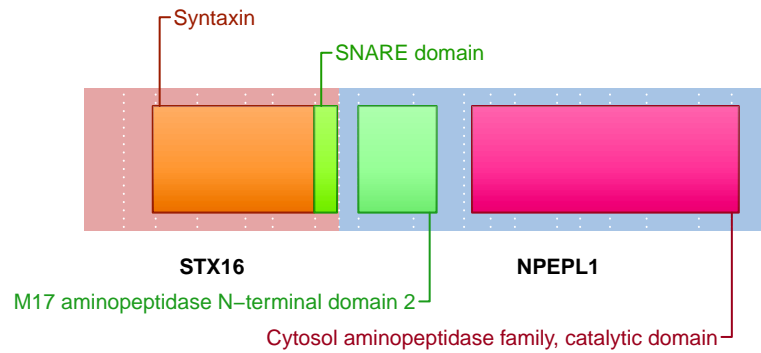


SUPPORTING READ COUNT

Split reads = 315
Discordant mates = 4



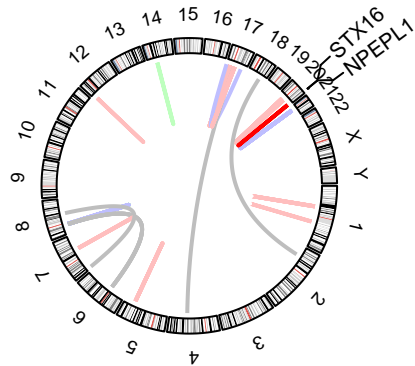
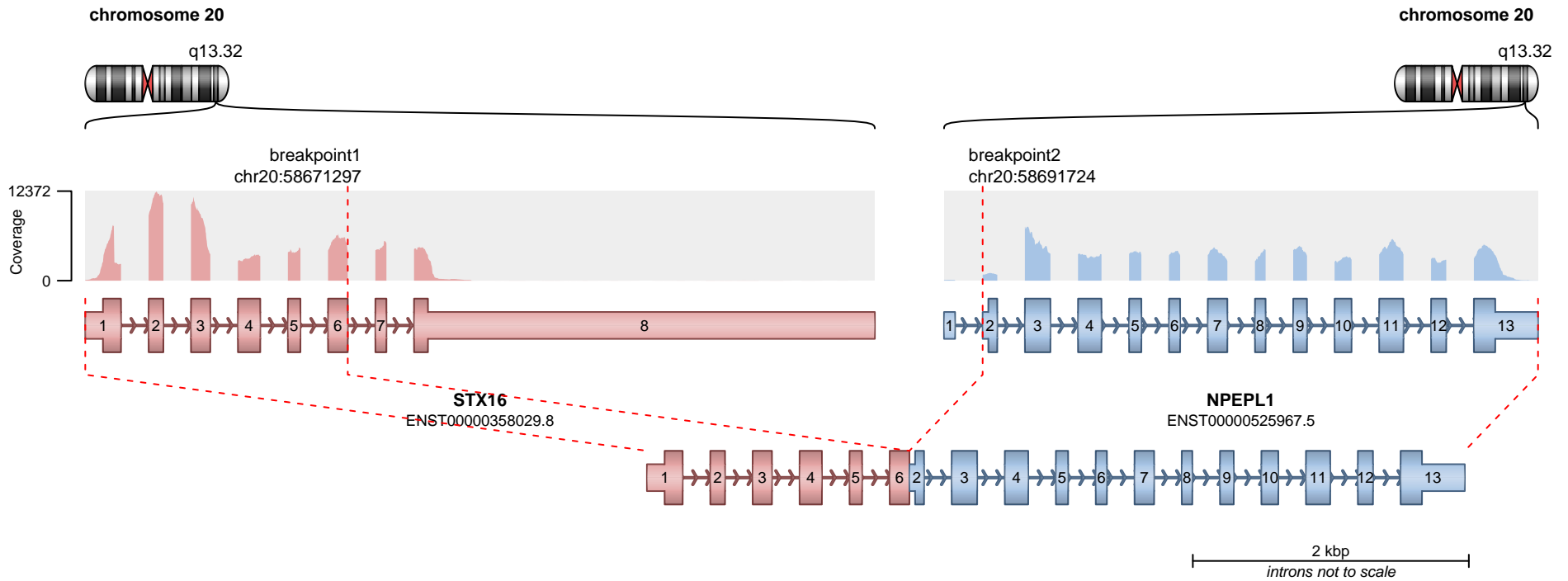
RETAINED PROTEIN DOMAINS
reading frame unclear



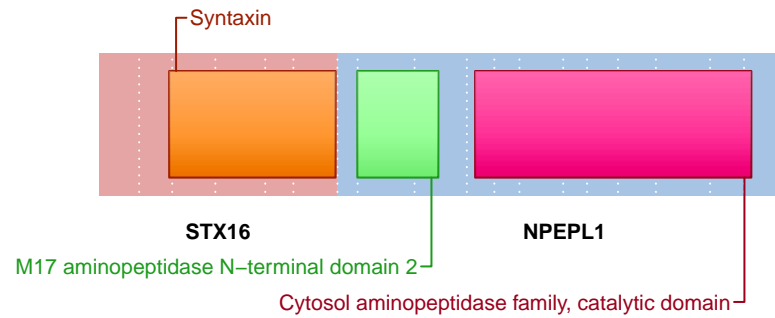
SUPPORTING READ COUNT

Split reads = 249
Discordant mates = 11

- translocation
- duplication
- deletion
- inversion



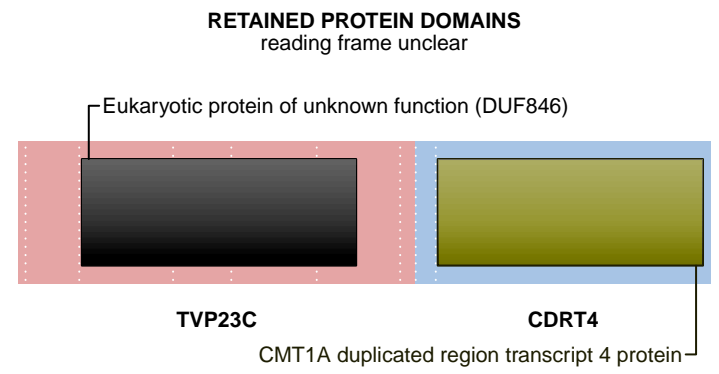
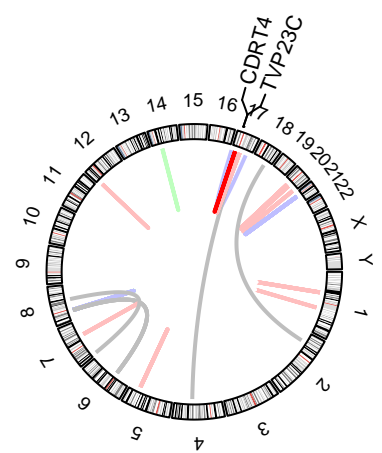
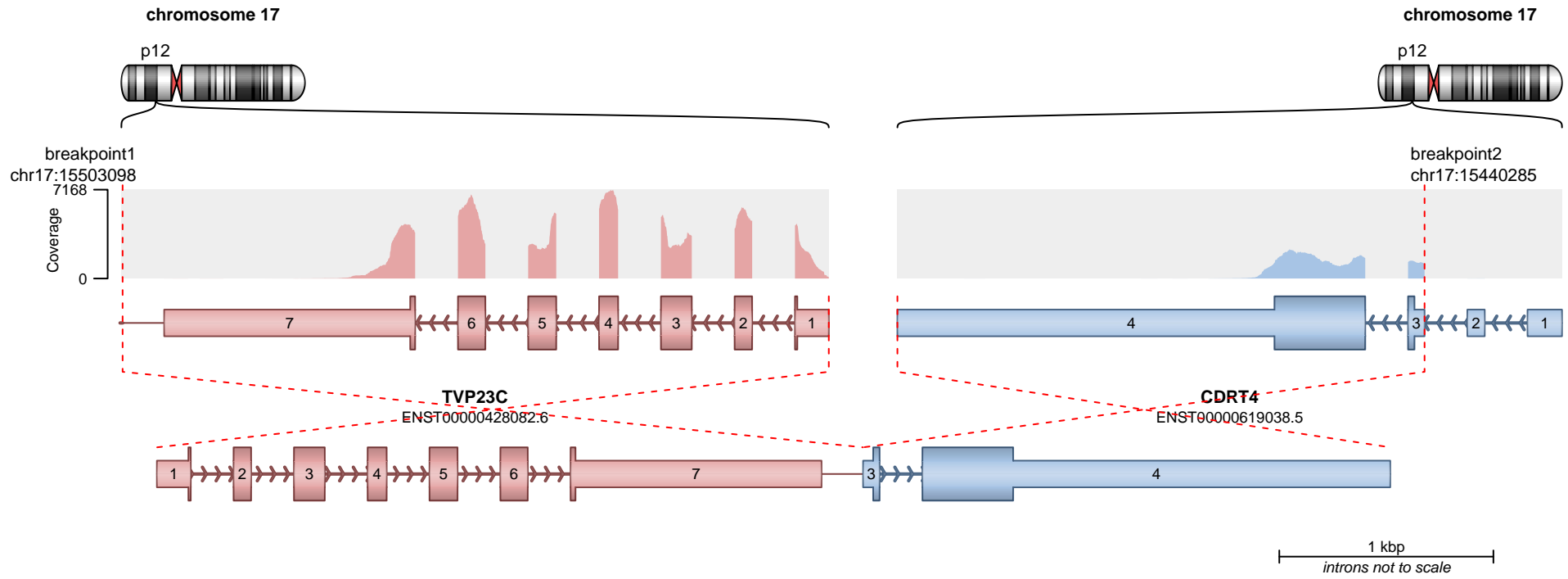
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 5

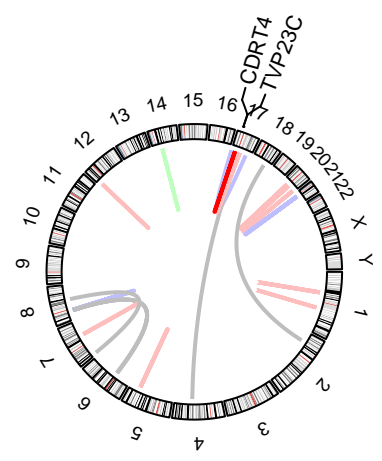
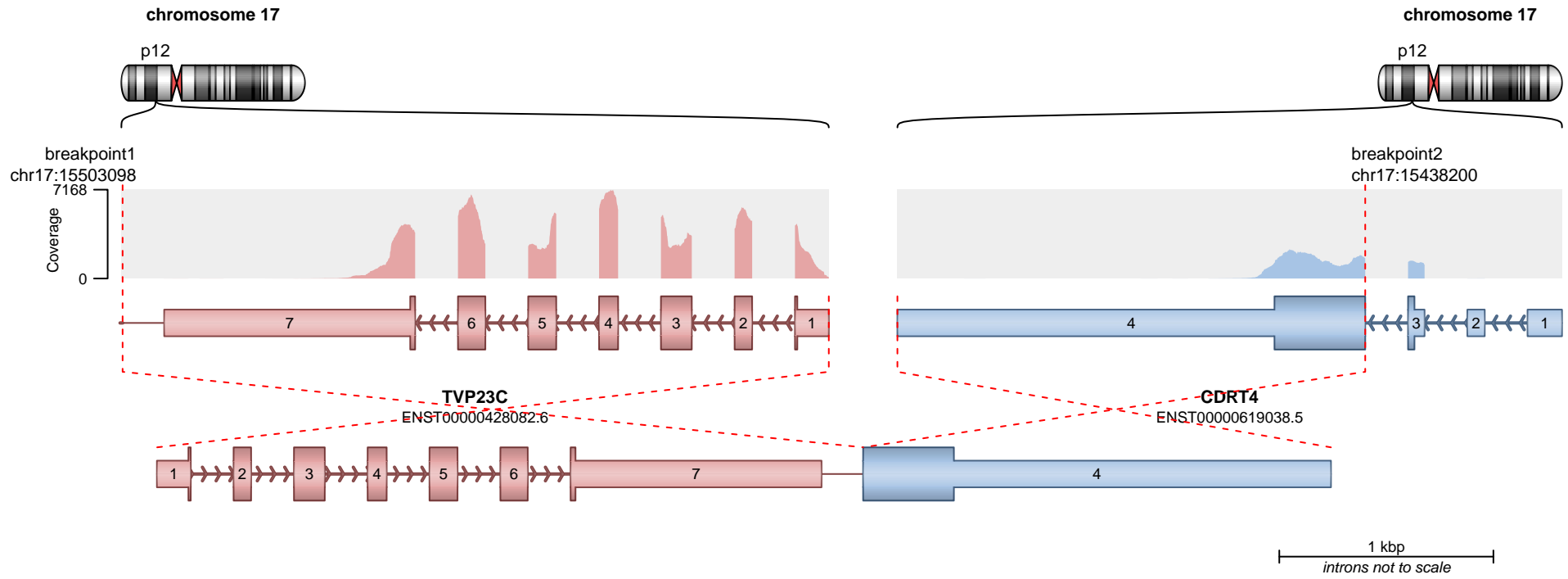
- translocation
- duplication
- deletion
- inversion



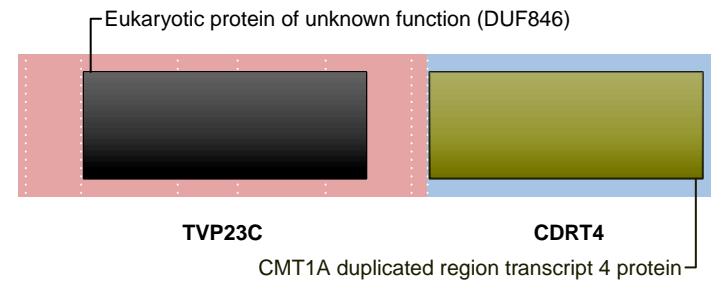
SUPPORTING READ COUNT

Split reads = 236
Discordant mates = 6

— translocation — deletion
— duplication — inversion



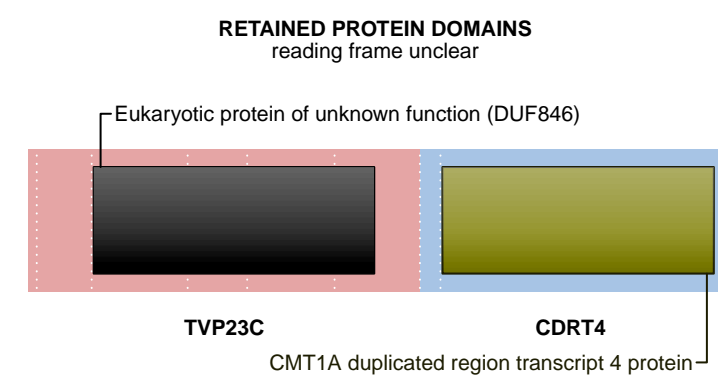
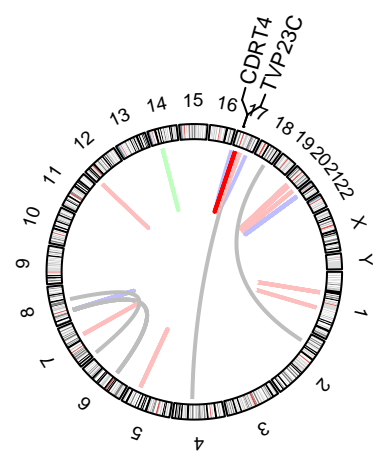
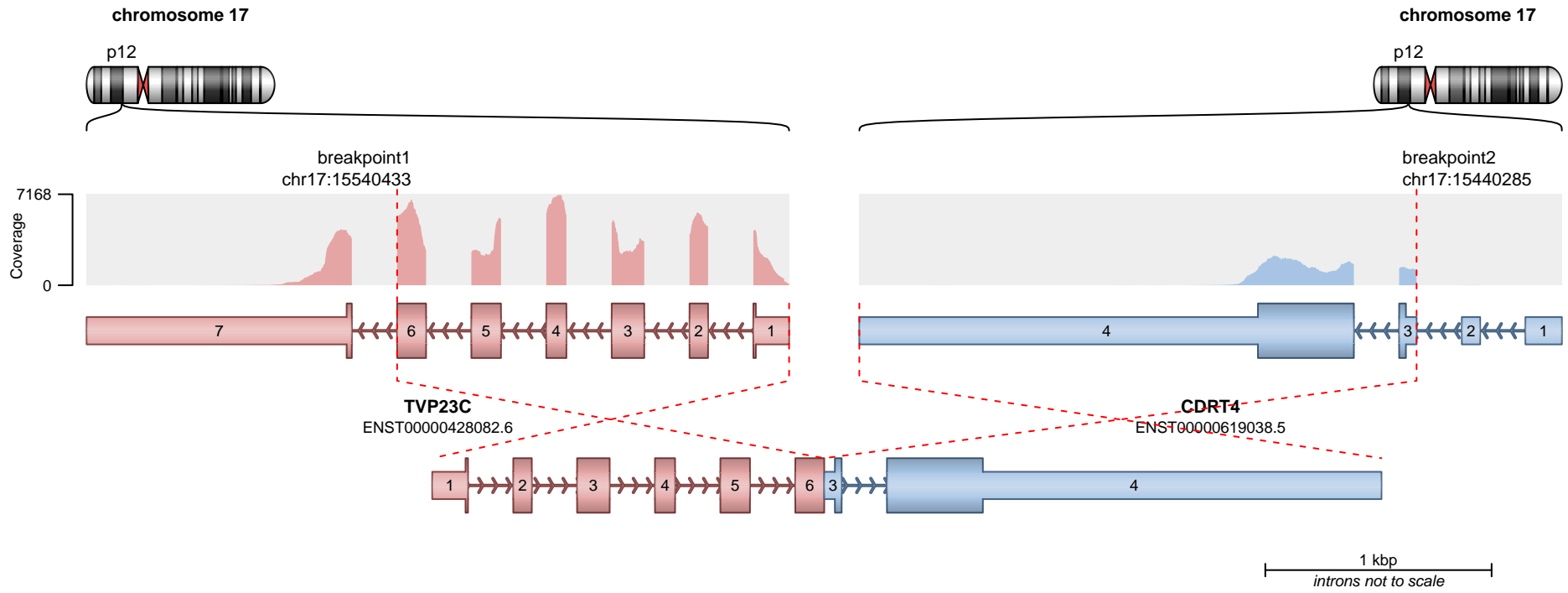
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 60
Discordant mates = 2

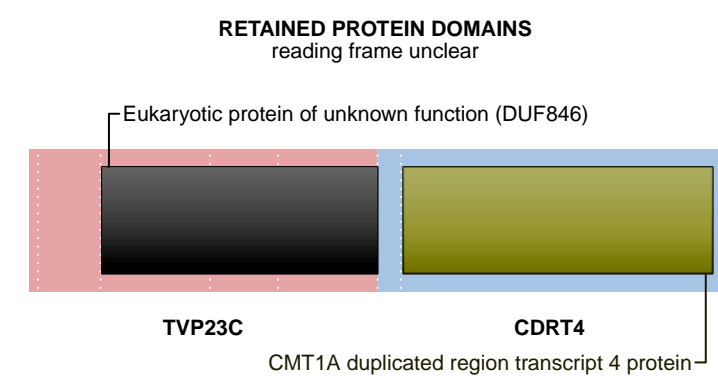
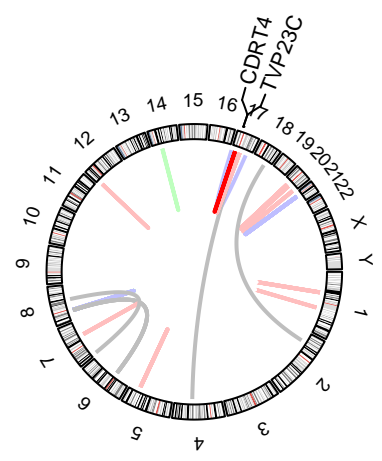
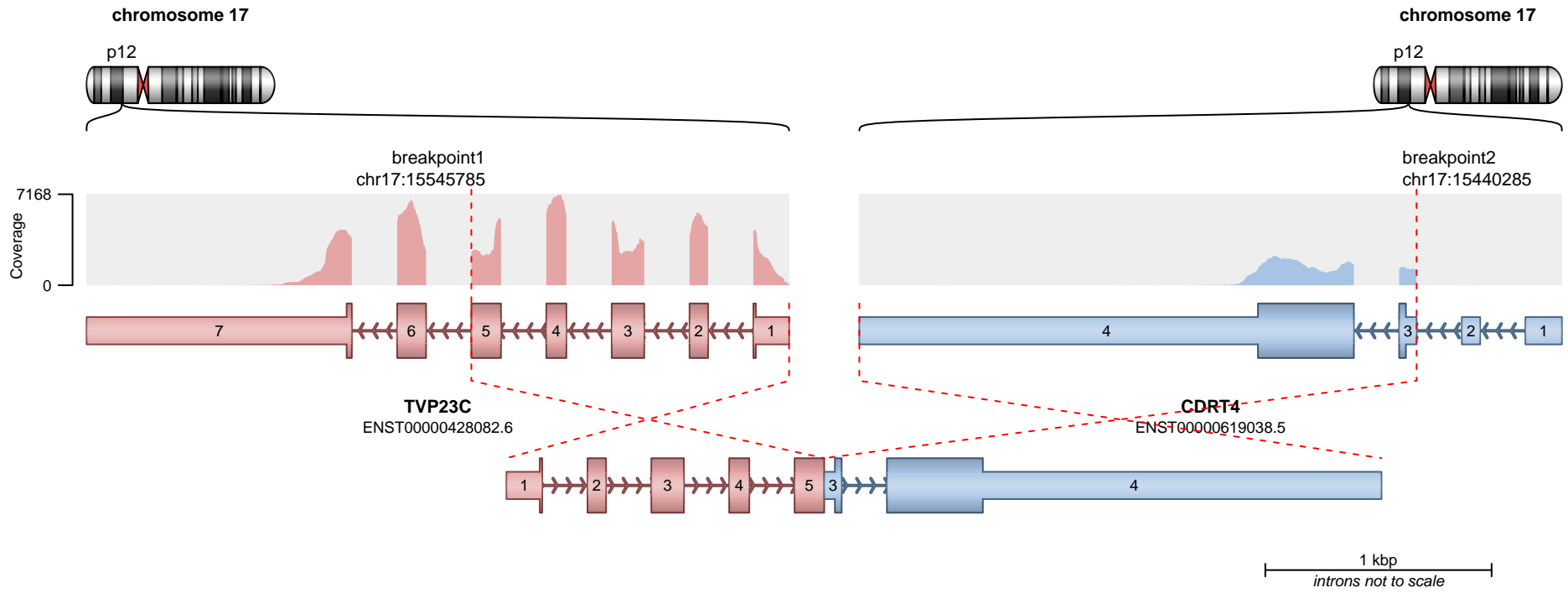
- translocation
- duplication
- deletion
- inversion



SUPPORTING READ COUNT

Split reads = 48
Discordant mates = 3

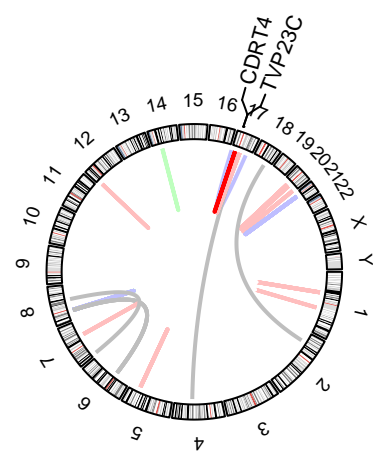
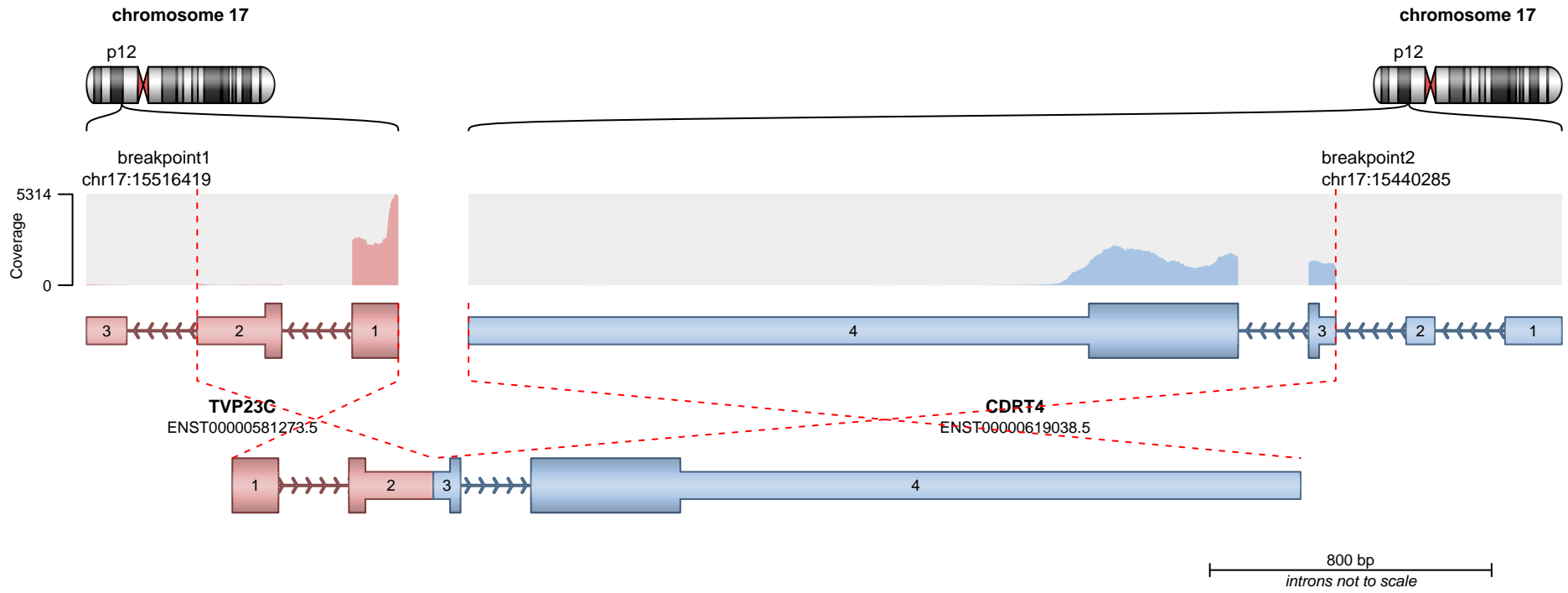
— translocation — deletion
— duplication — inversion



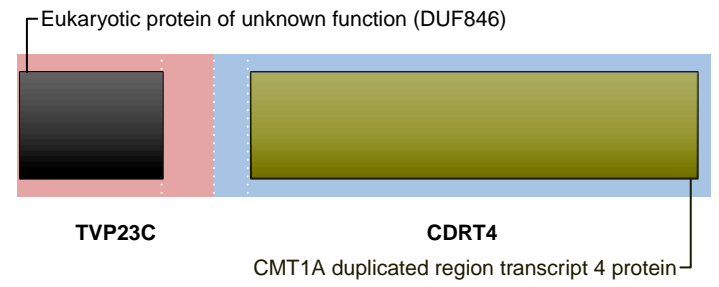
SUPPORTING READ COUNT

Split reads = 43
Discordant mates = 2

— translocation — deletion
— duplication — inversion



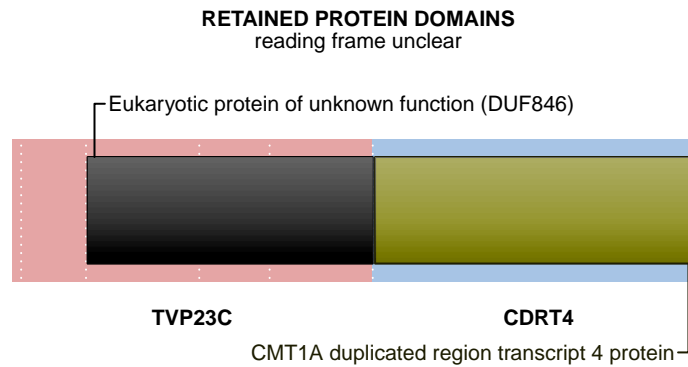
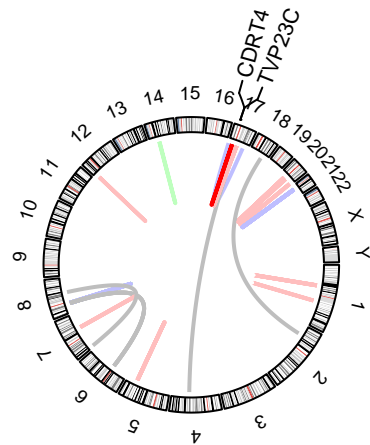
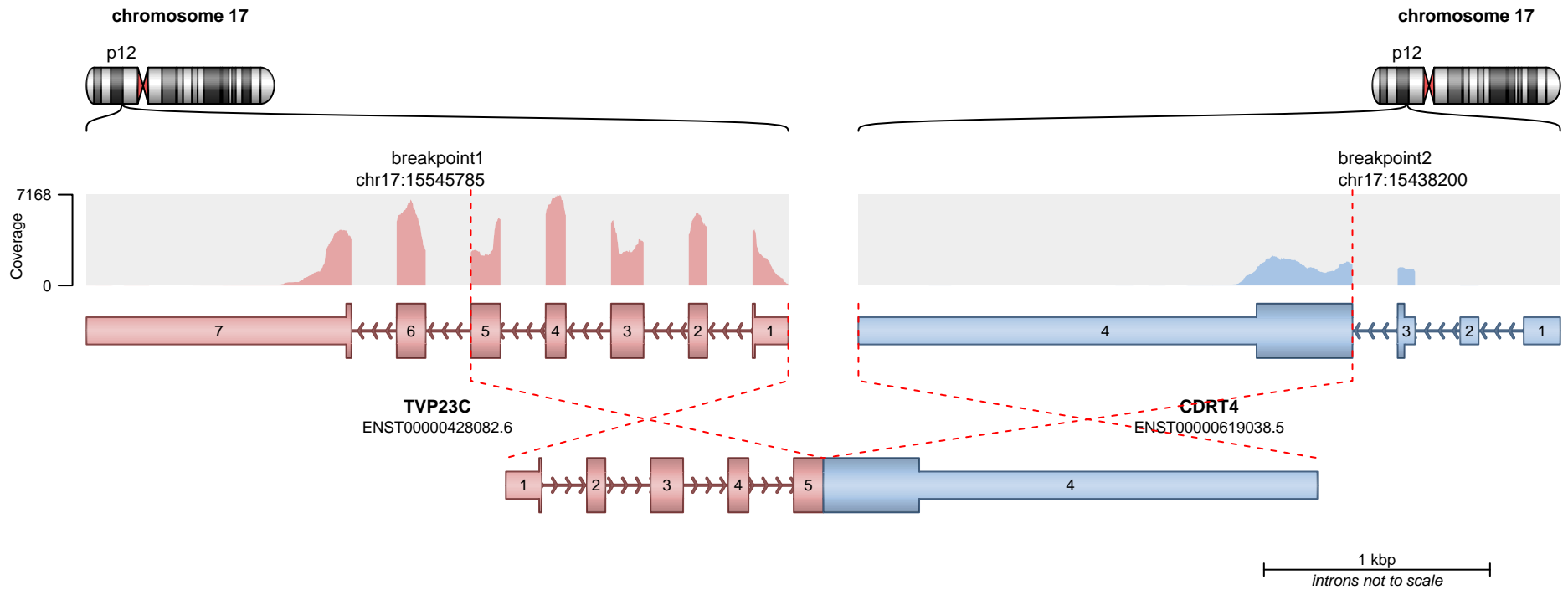
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 20
Discordant mates = 3

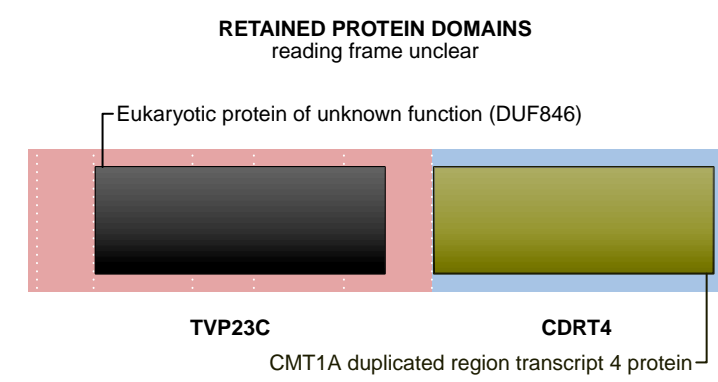
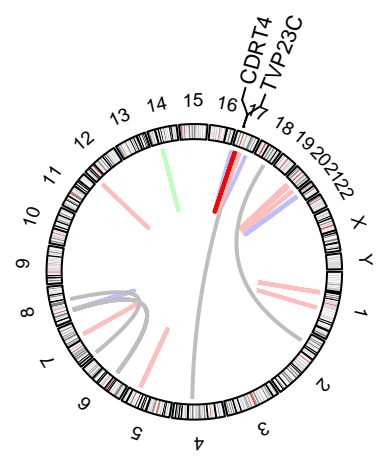
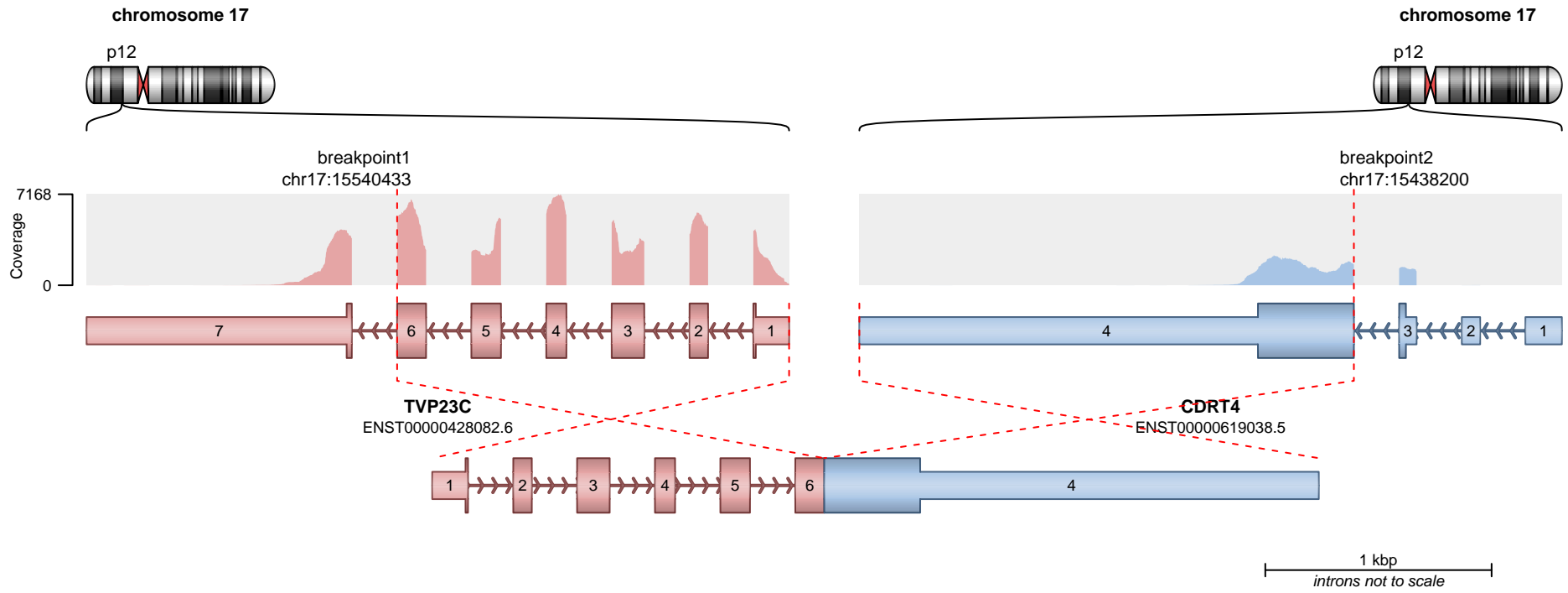
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 1

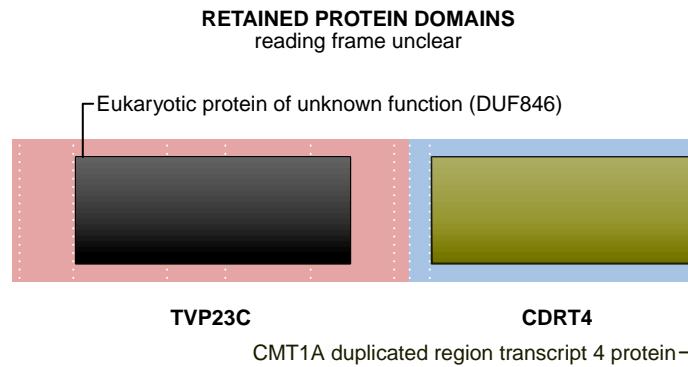
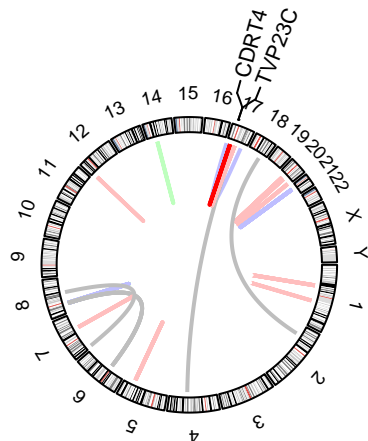
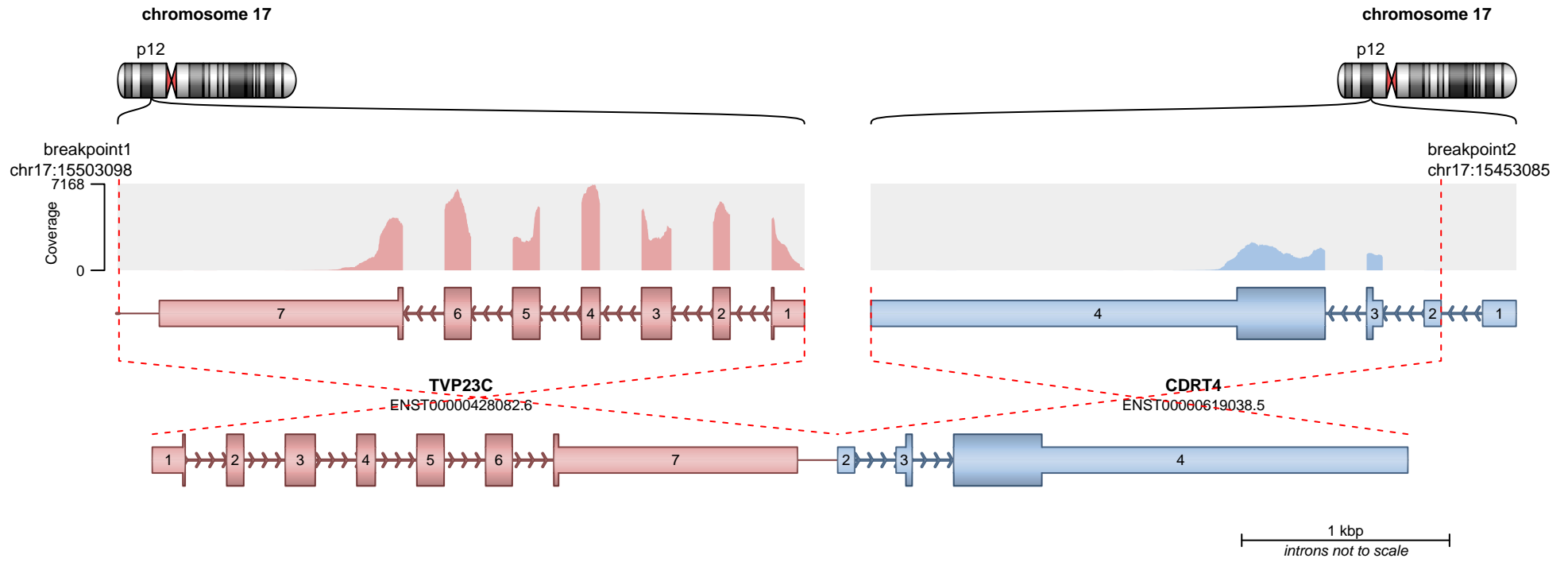
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 2

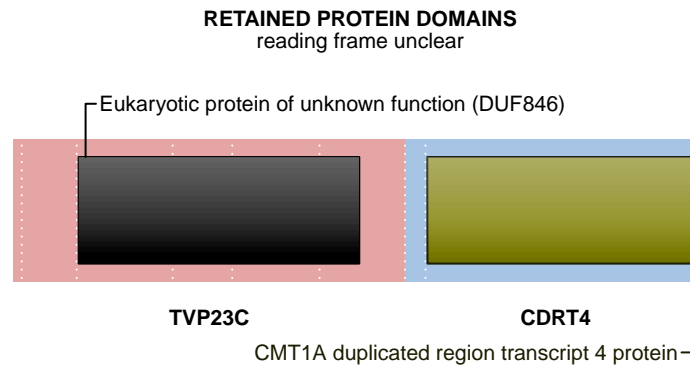
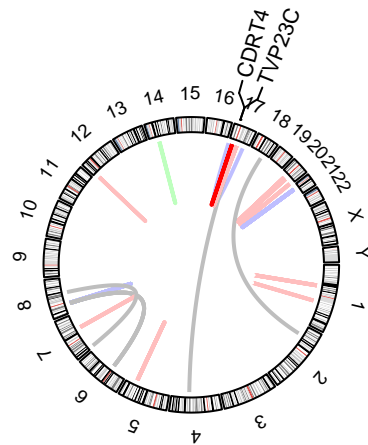
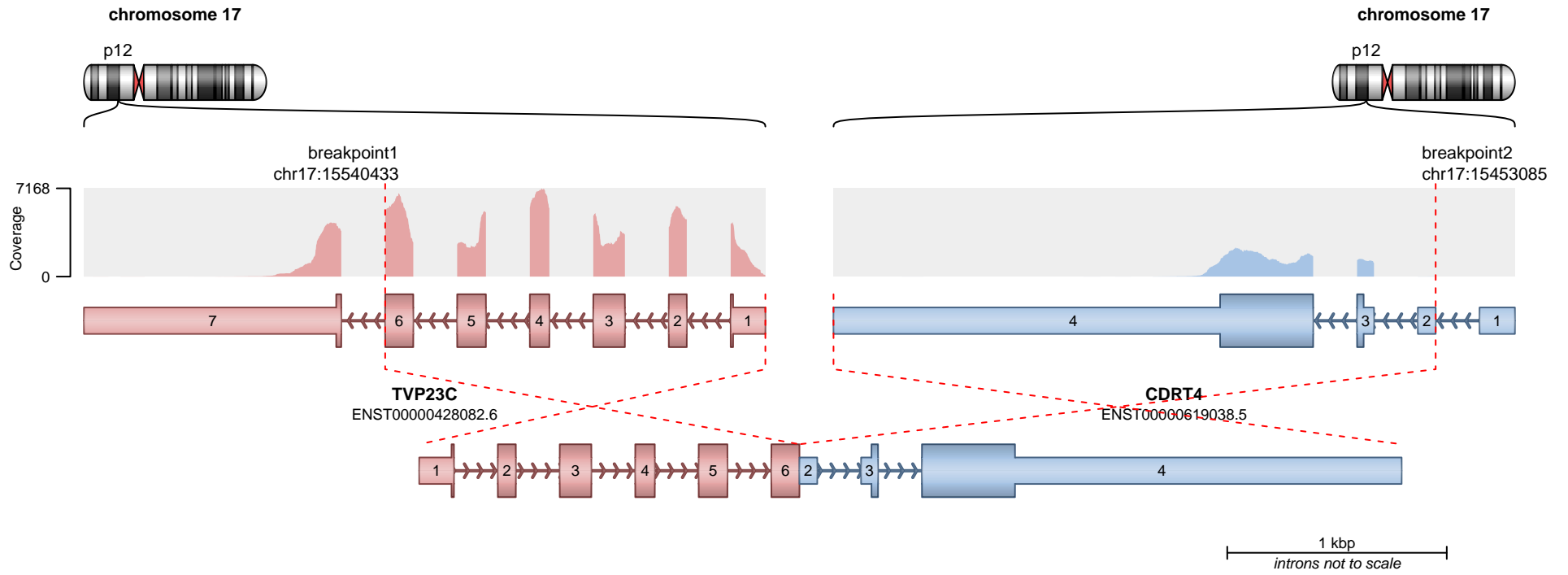
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 6

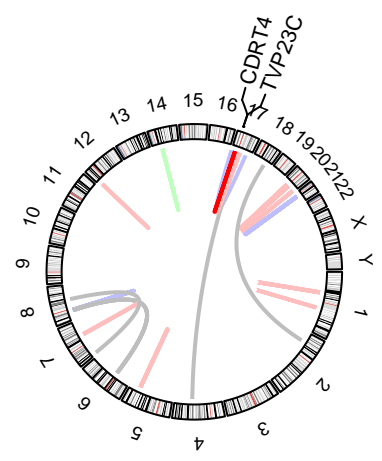
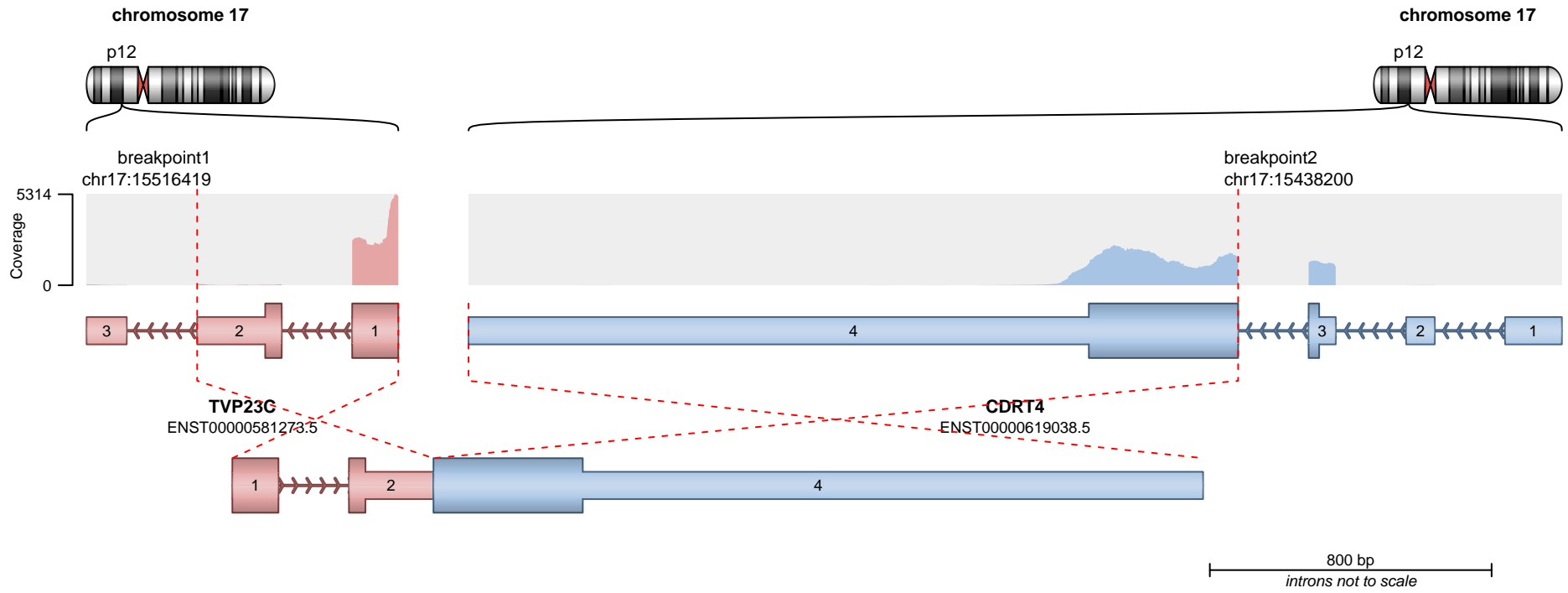
— translocation — deletion
— duplication — inversion



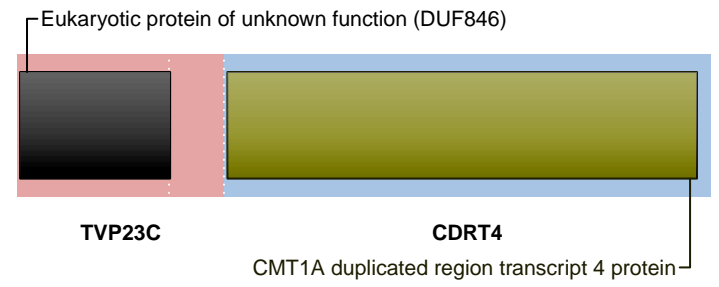
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 3

— translocation — deletion
— duplication — inversion



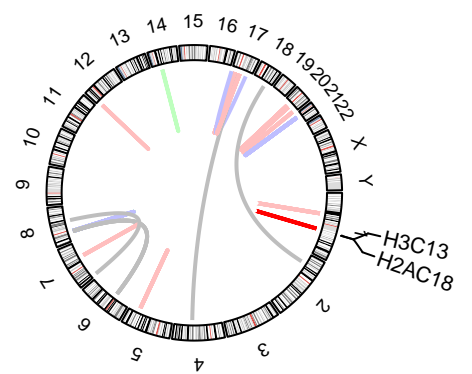
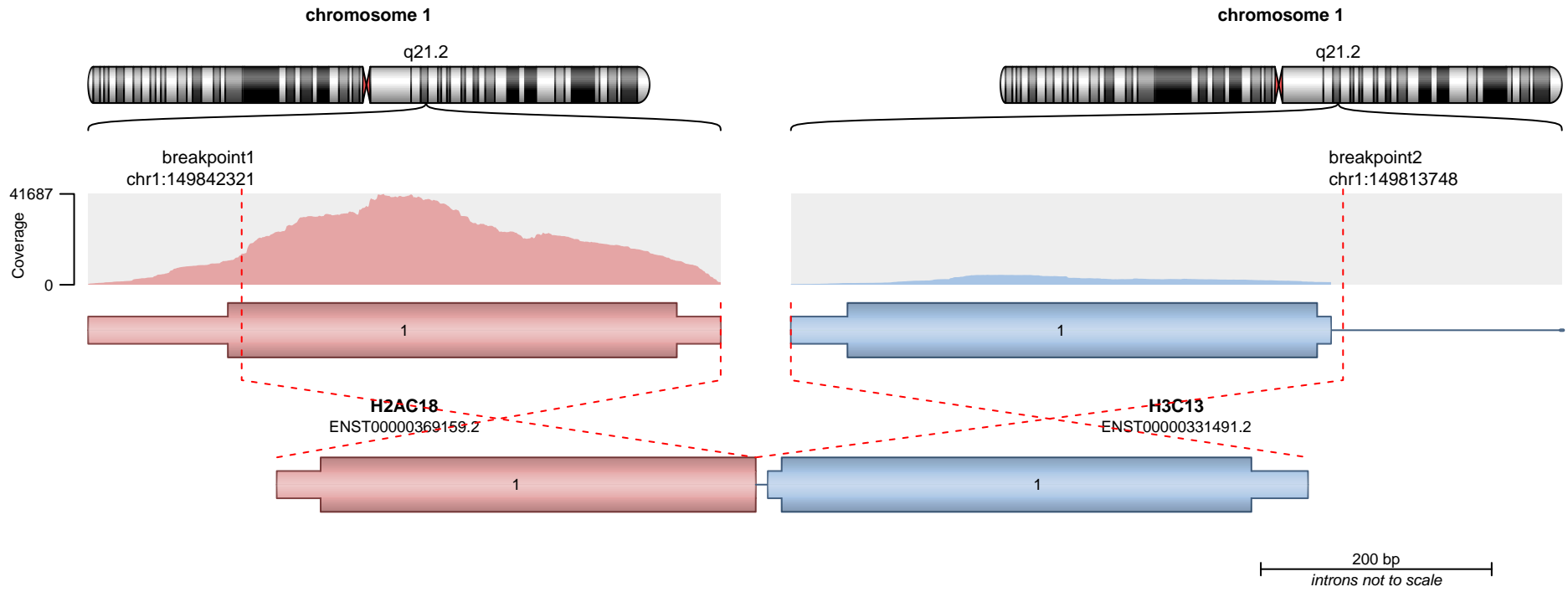
RETAINED PROTEIN DOMAINS
reading frame unclear



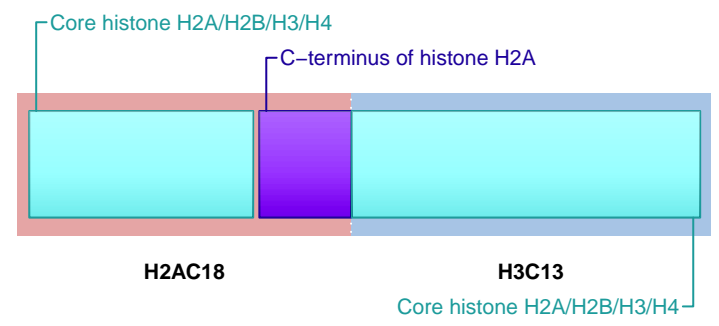
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 2

- translocation
- duplication
- deletion
- inversion



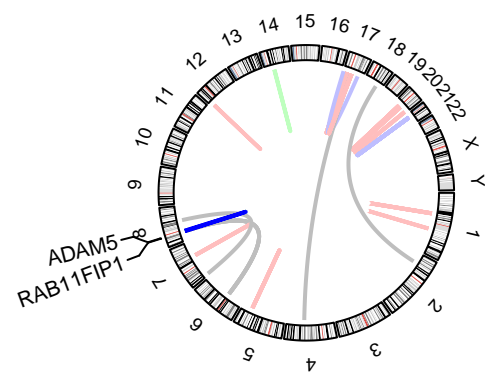
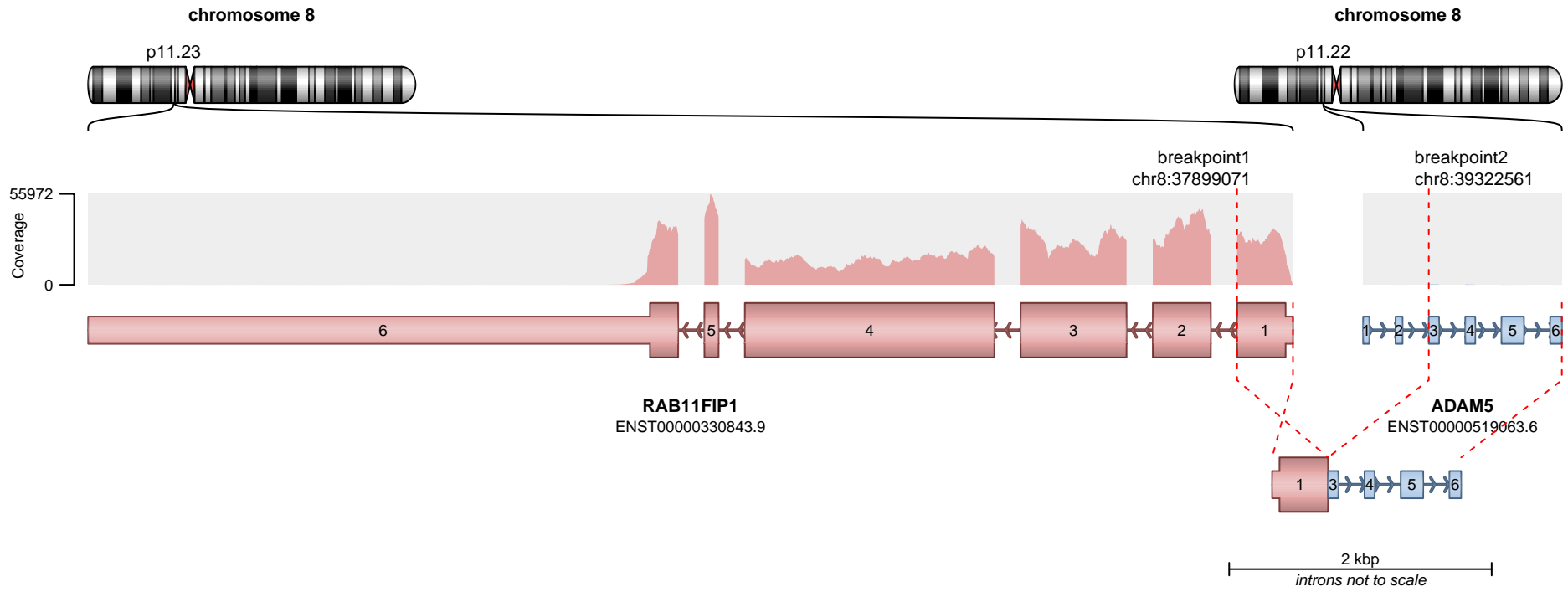
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 203
Discordant mates = 2

- translocation
- duplication
- deletion
- inversion



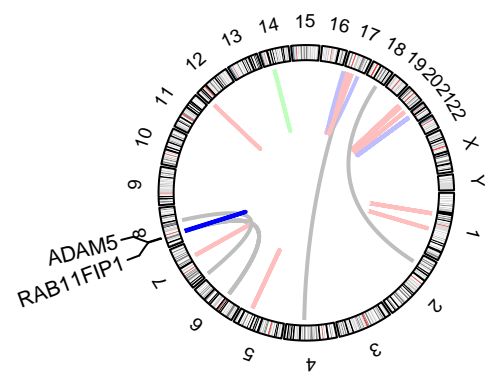
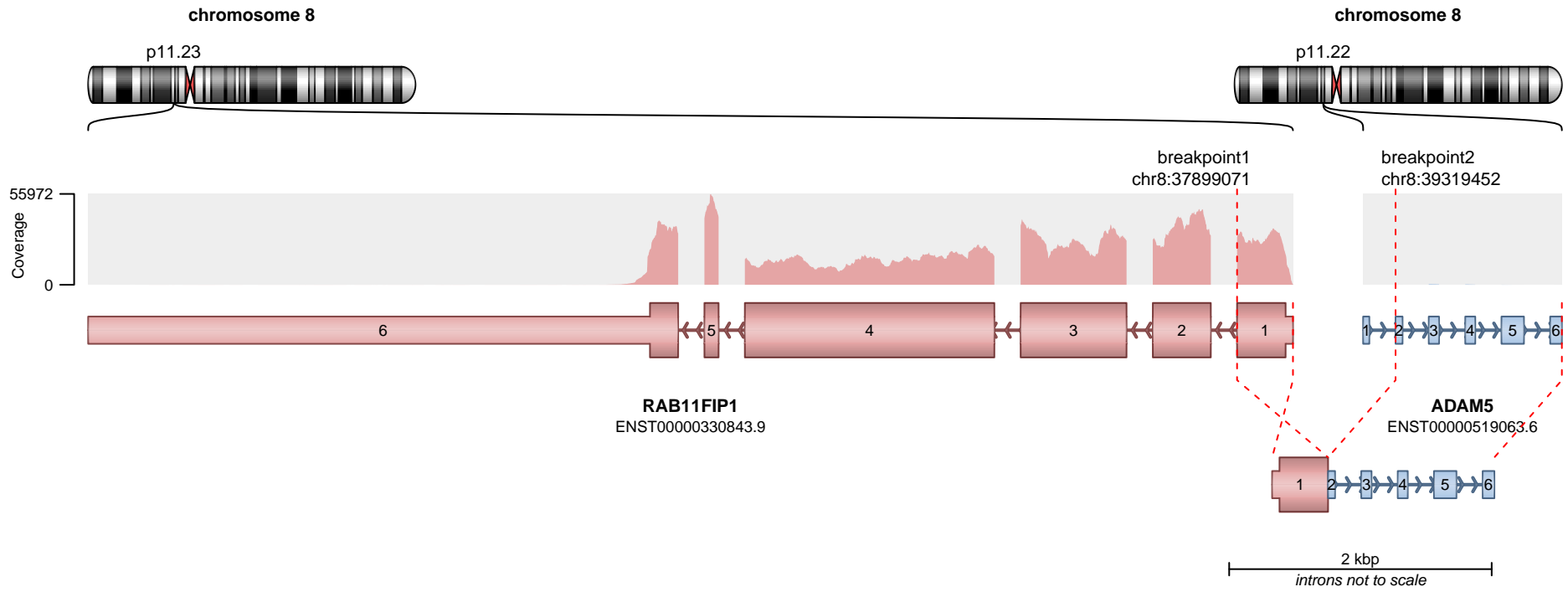
RETAINED PROTEIN DOMAINS
reading frame unclear



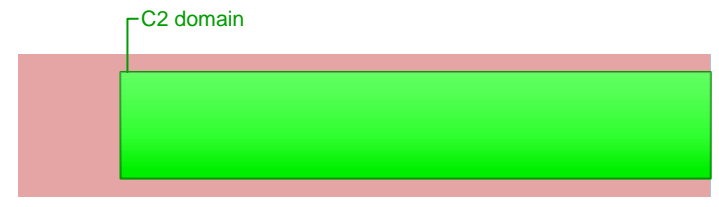
SUPPORTING READ COUNT

Split reads = 198
Discordant mates = 21

- translocation
- duplication
- deletion
- inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

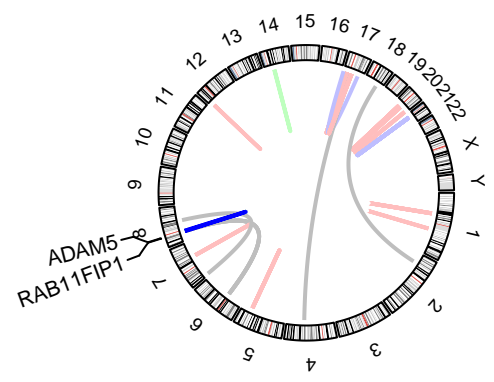
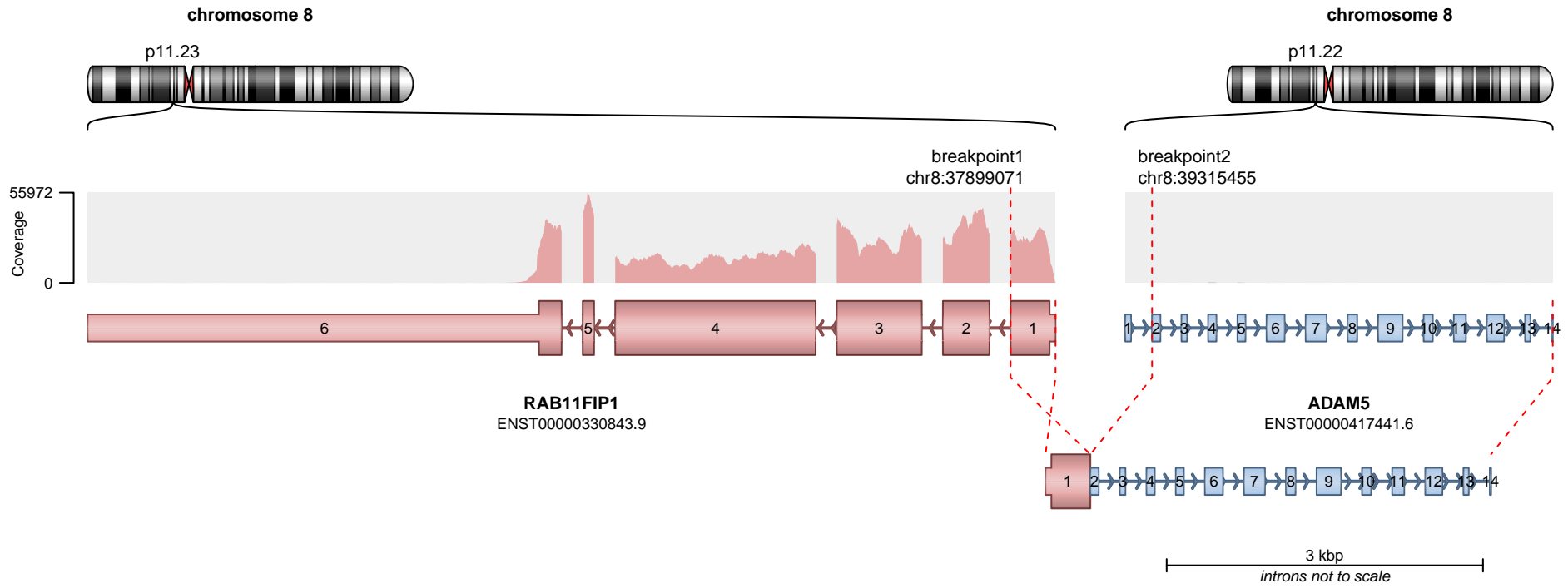


RAB11FIP1

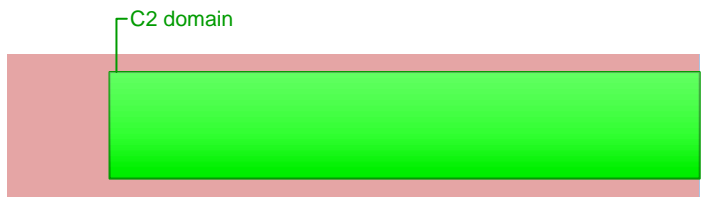
SUPPORTING READ COUNT

Split reads = 9
Discordant mates = 21

- translocation
- duplication
- deletion
- inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

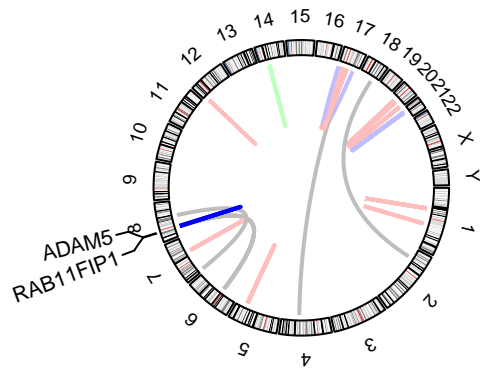
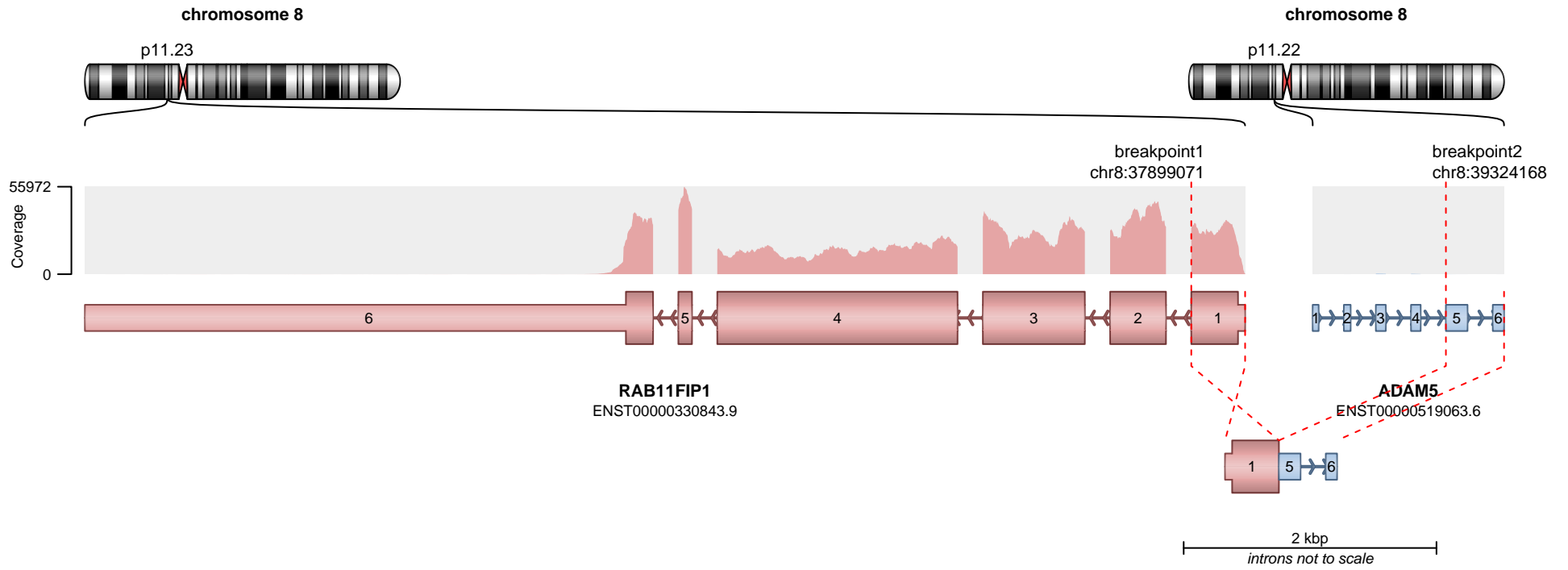


RAB11FIP1

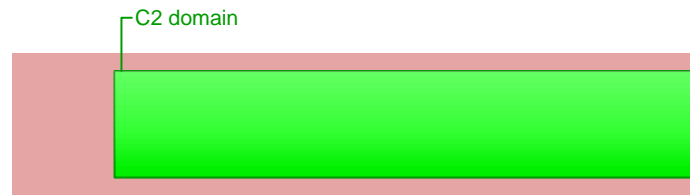
SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 21

- translocation
- duplication
- deletion
- inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

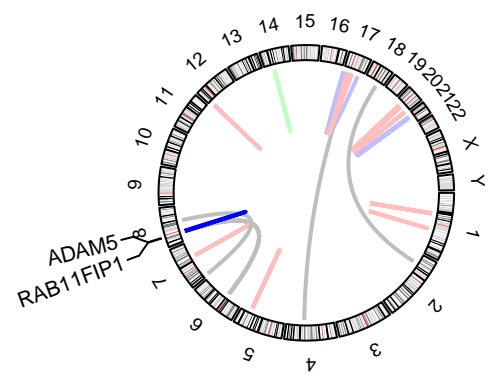
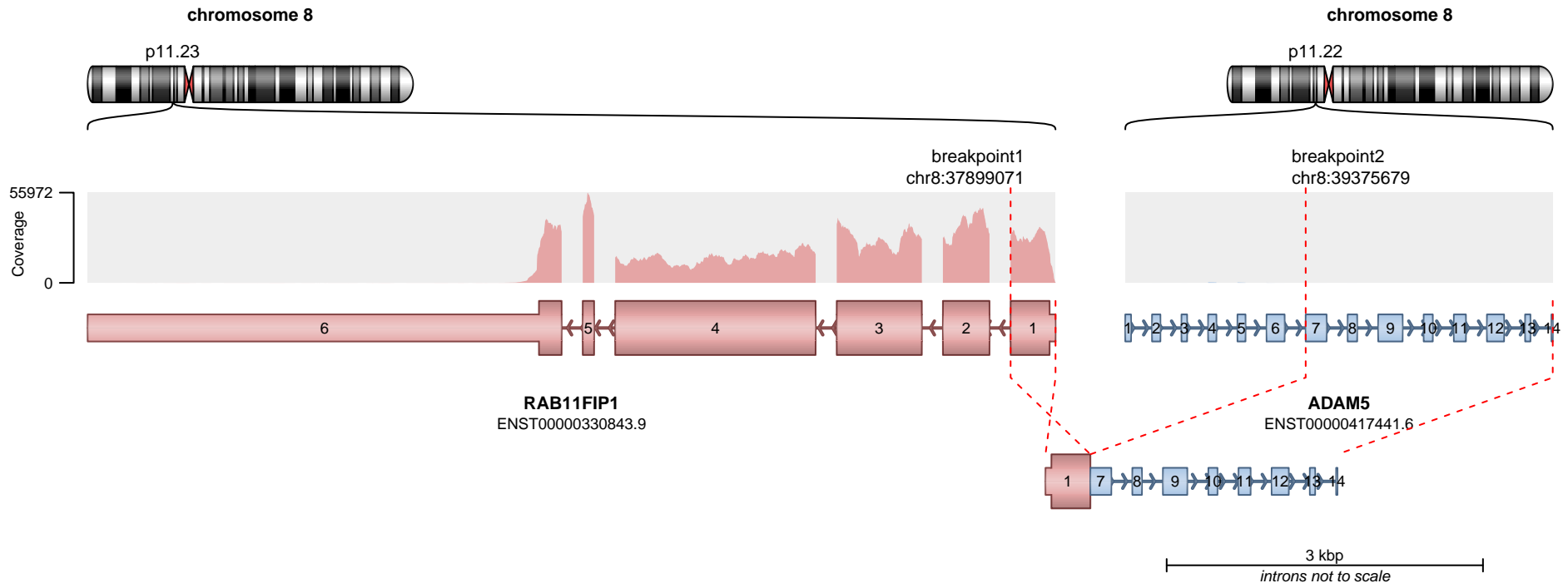


RAB11FIP1

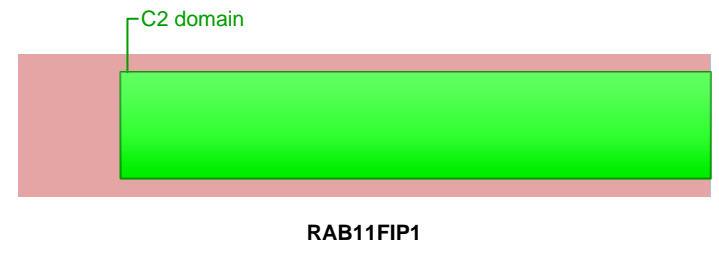
SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 0

— translocation — deletion
— duplication — inversion



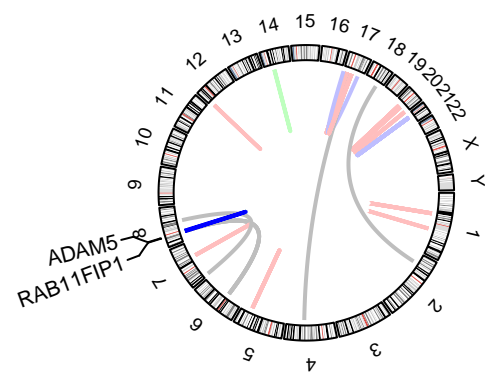
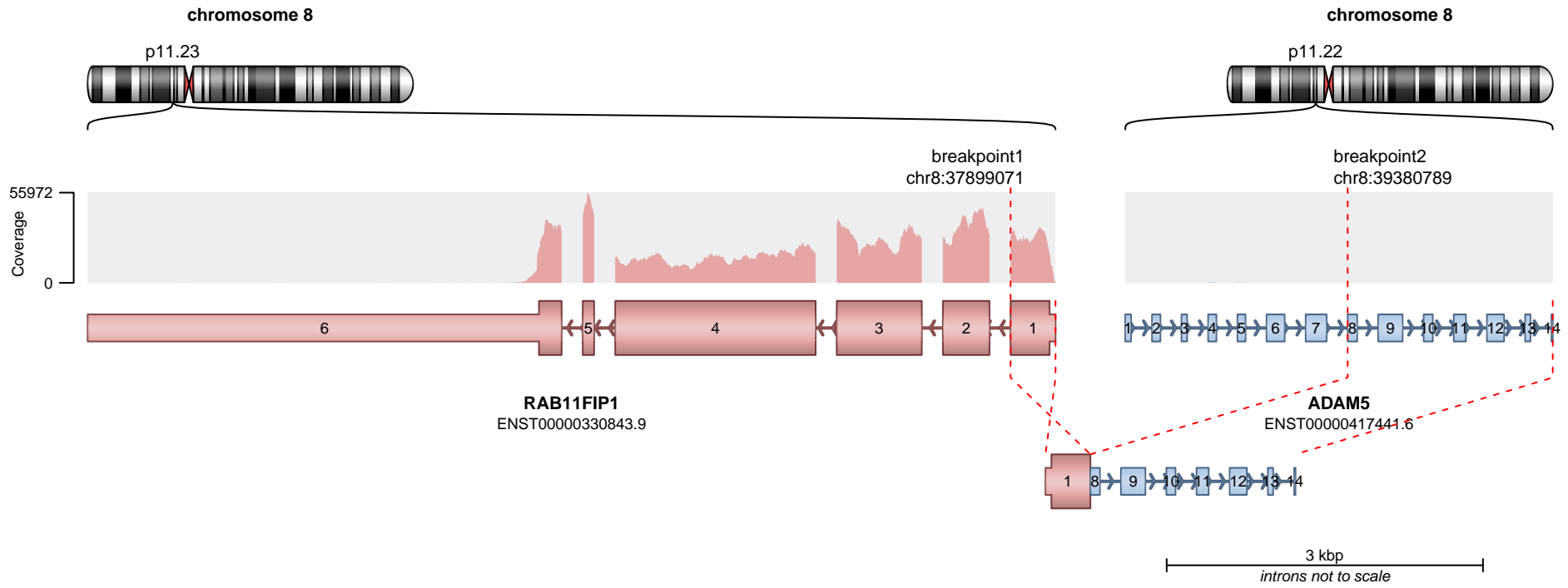
RETAINED PROTEIN DOMAINS
reading frame unclear



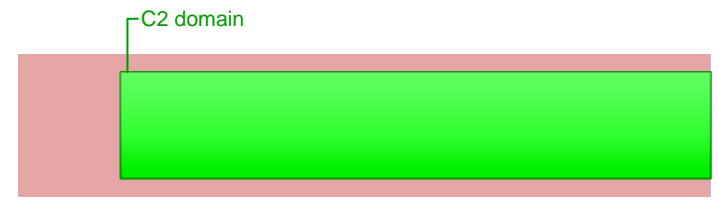
SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



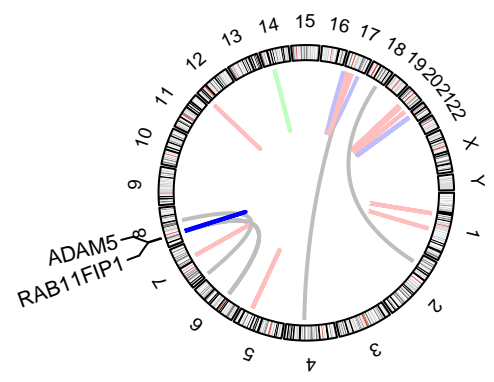
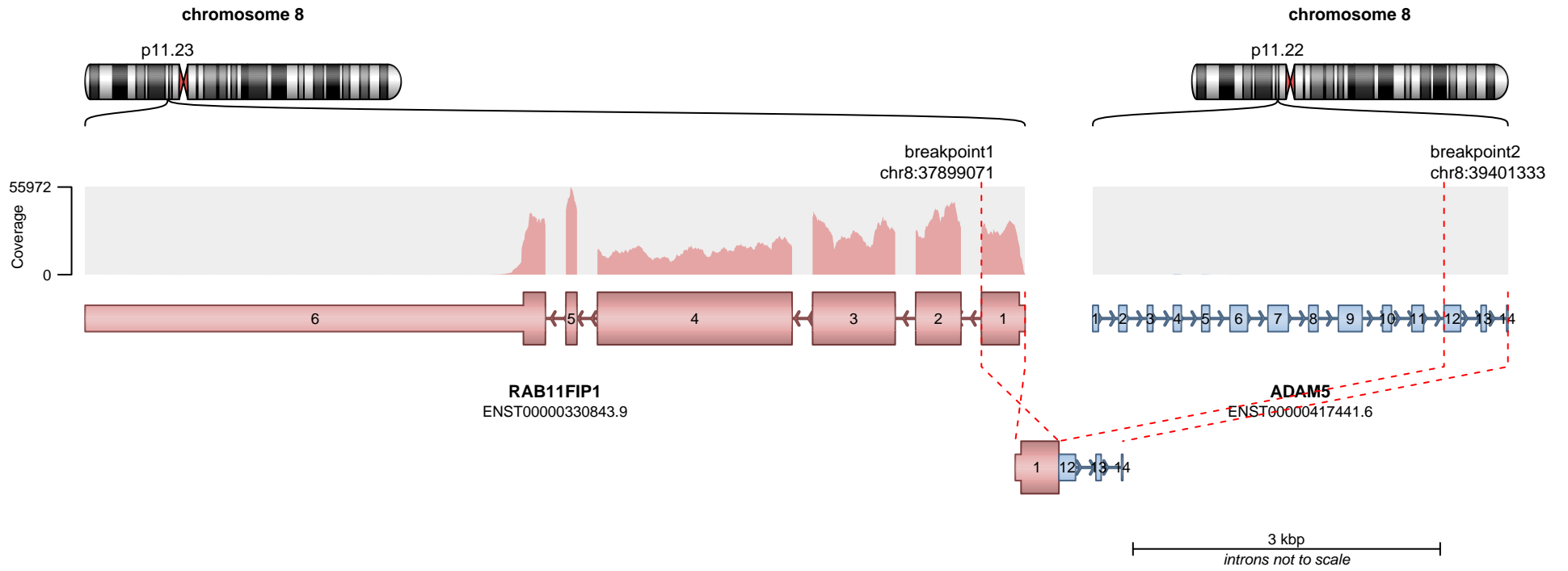
RETAINED PROTEIN DOMAINS
reading frame unclear



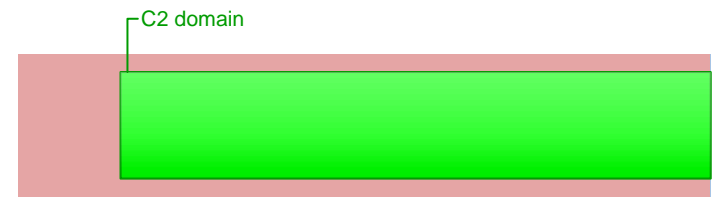
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

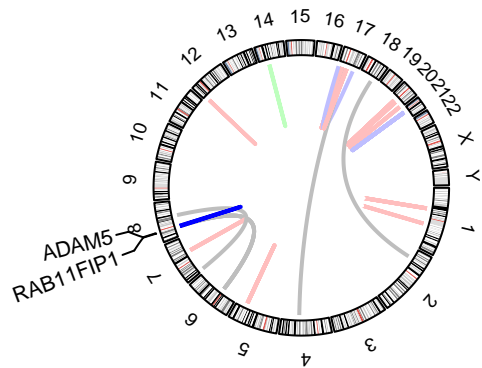
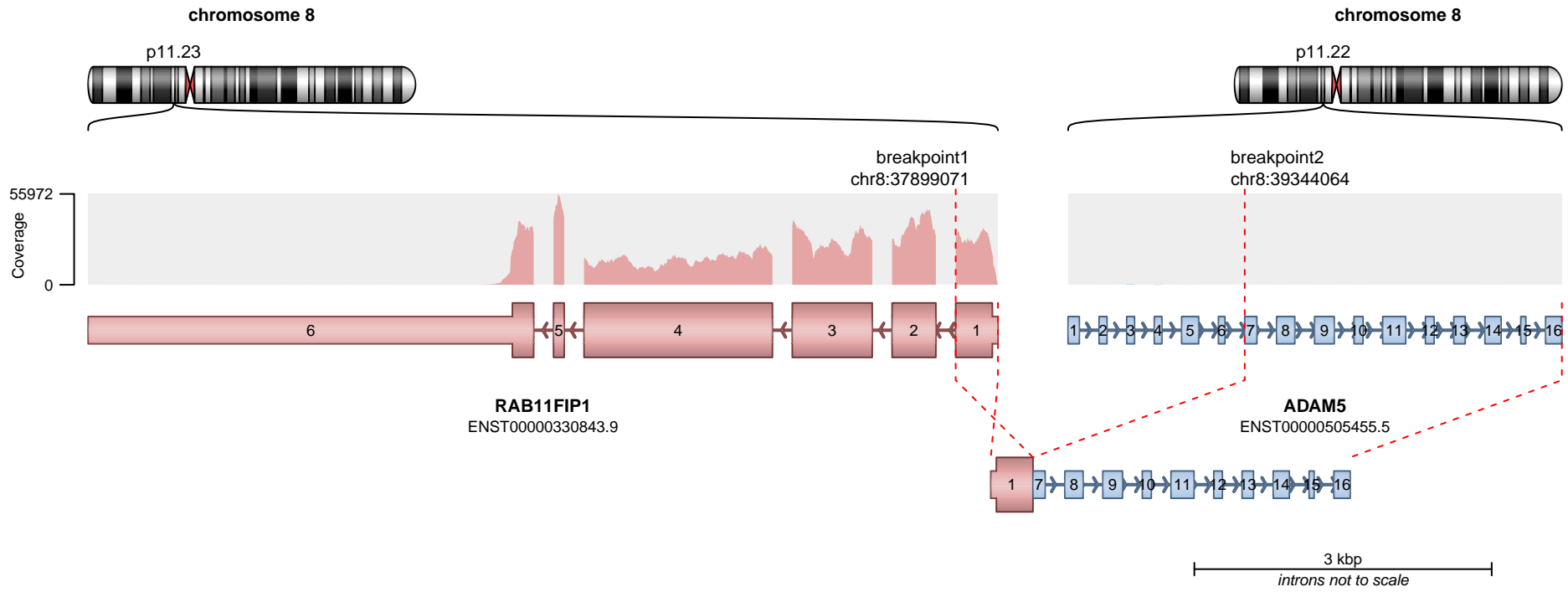


RAB11FIP1

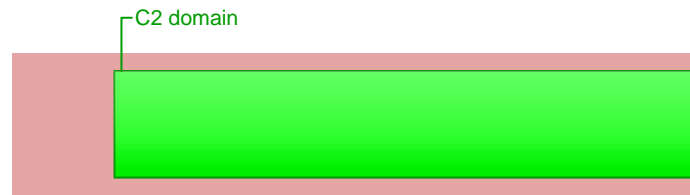
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



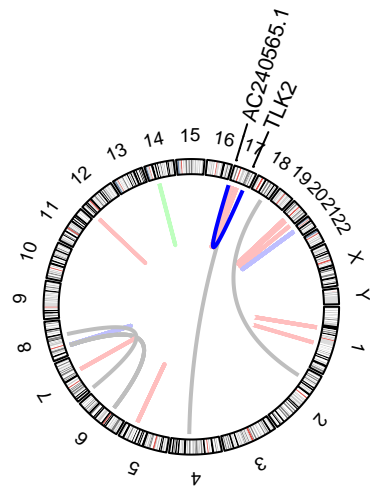
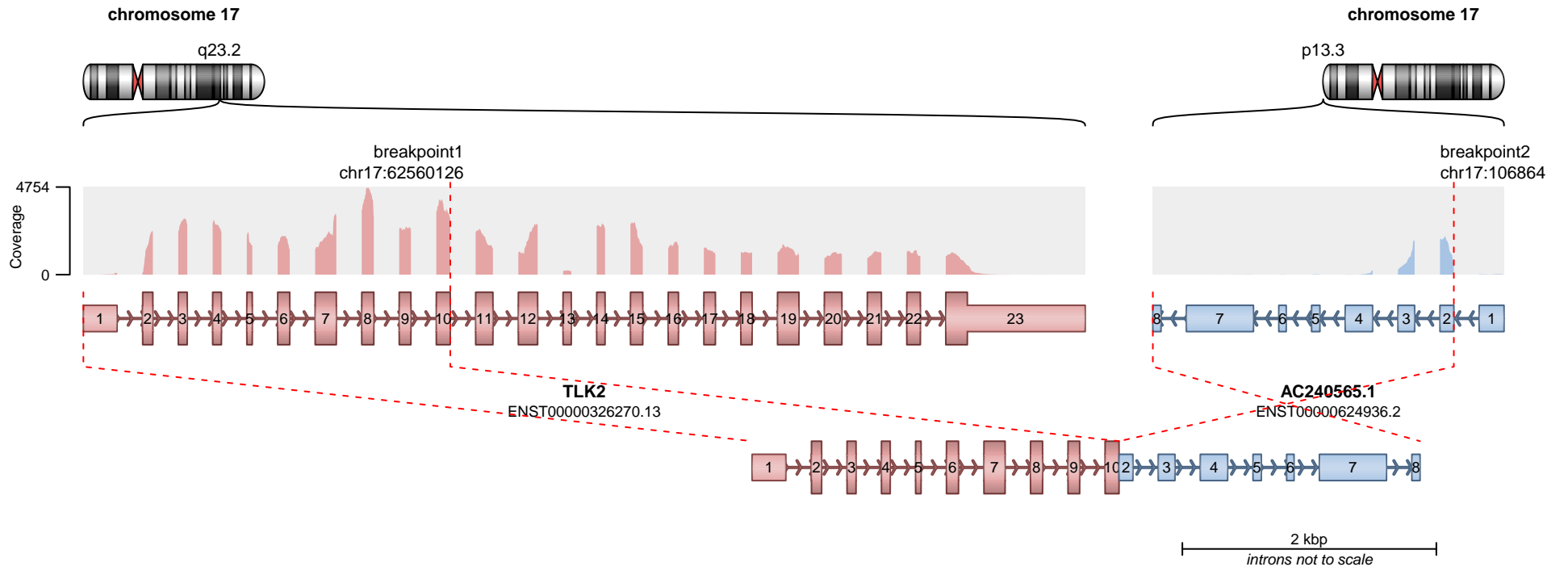
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

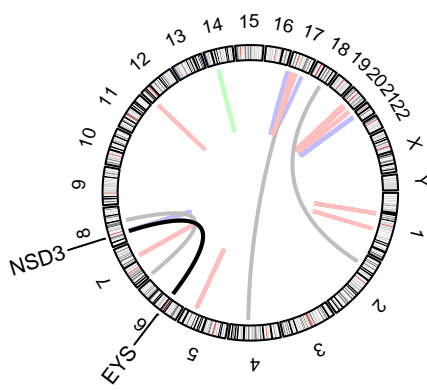
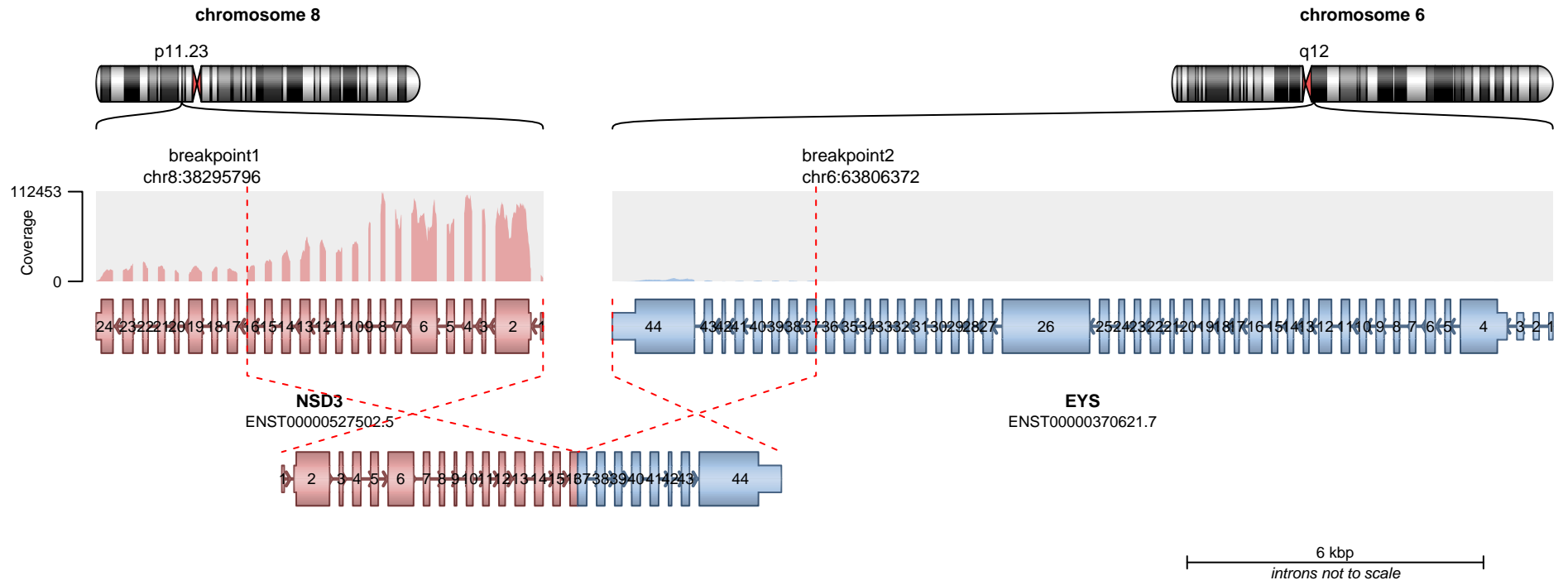


No protein domains retained in fusion.

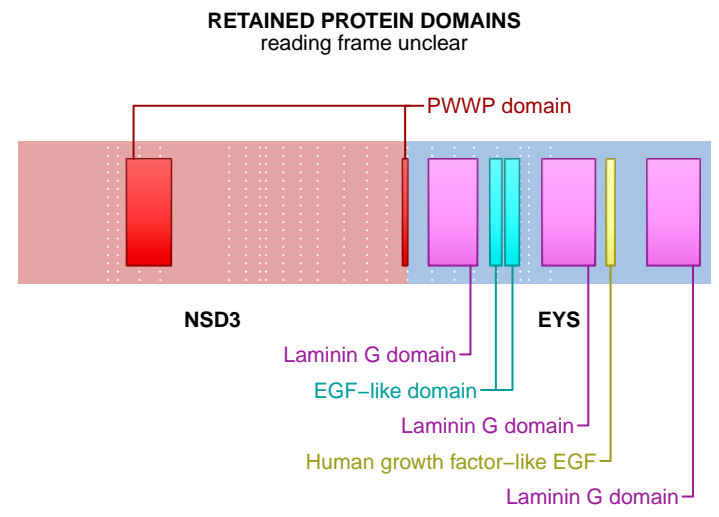
SUPPORTING READ COUNT

Split reads = 134
Discordant mates = 2

— translocation — deletion
— duplication — inversion

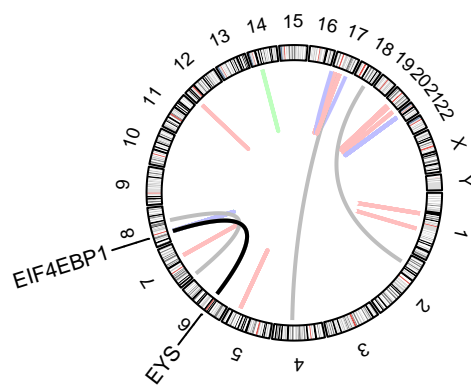
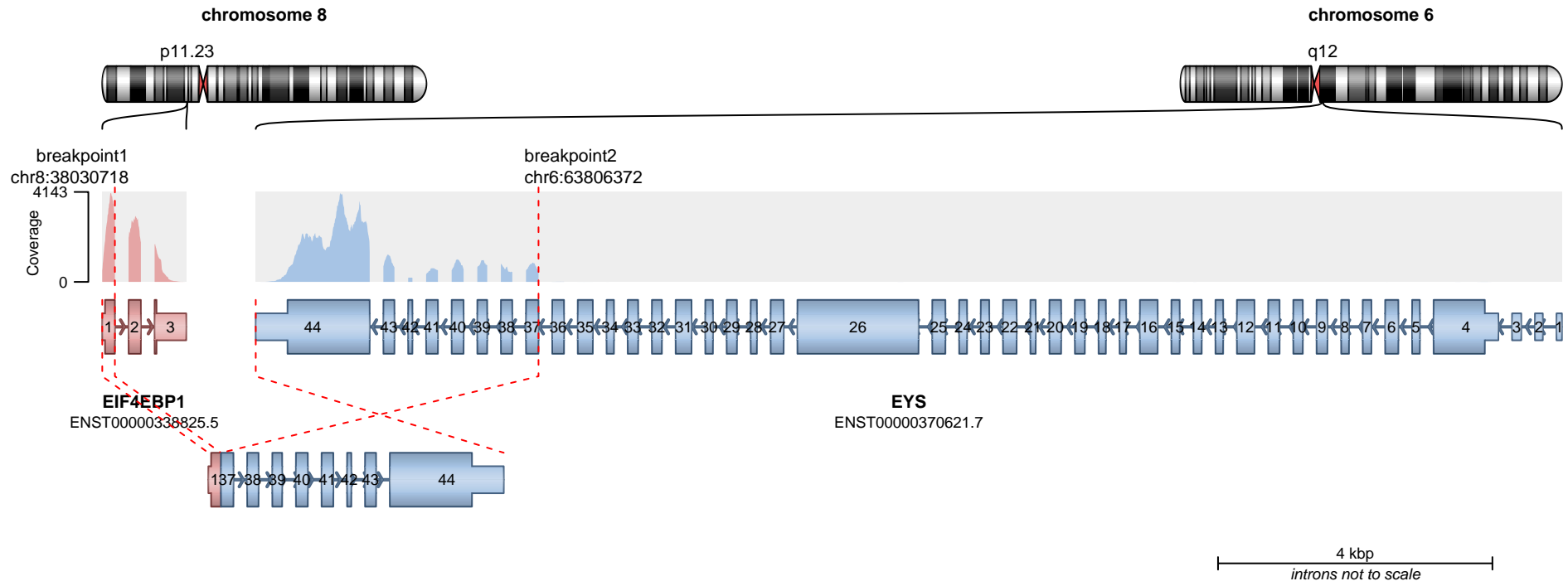


— translocation — deletion
— duplication — inversion



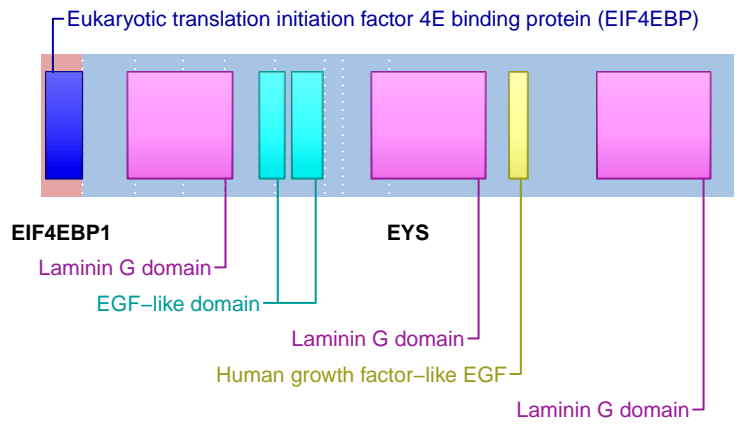
SUPPORTING READ COUNT

Split reads = 112
Discordant mates = 0



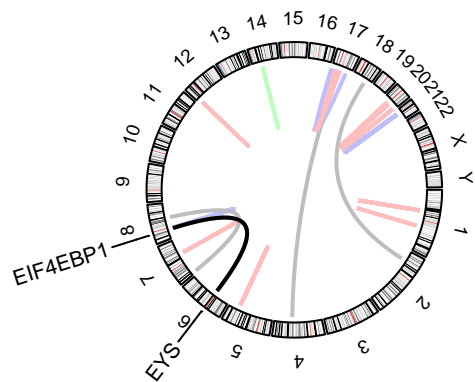
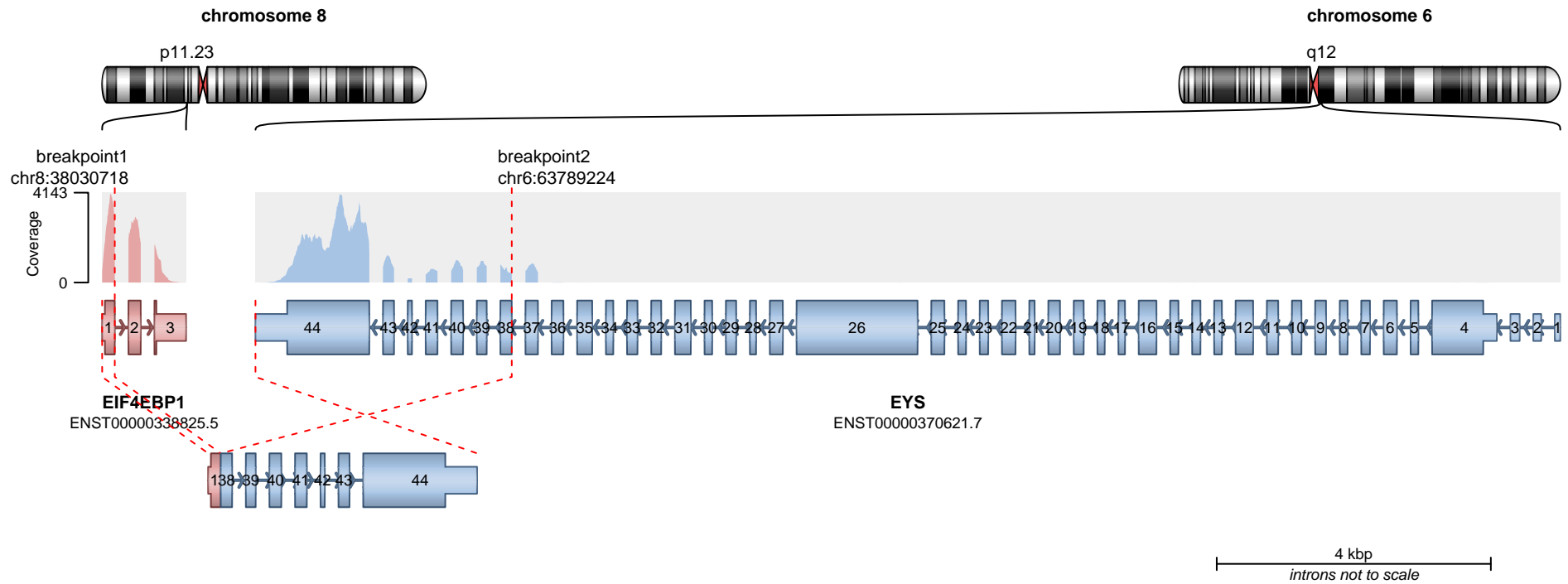
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



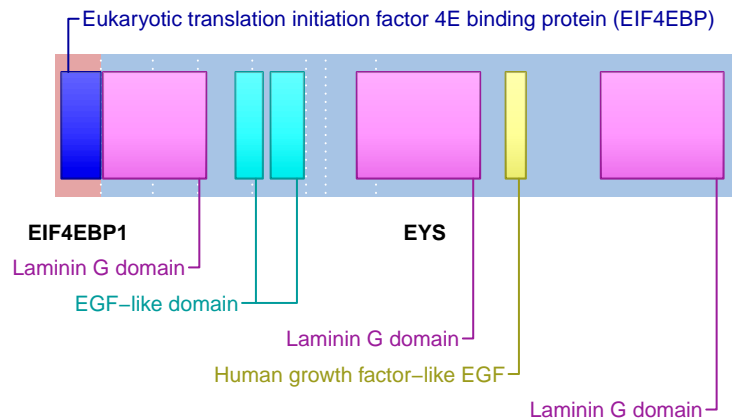
SUPPORTING READ COUNT

Split reads = 108
Discordant mates = 2



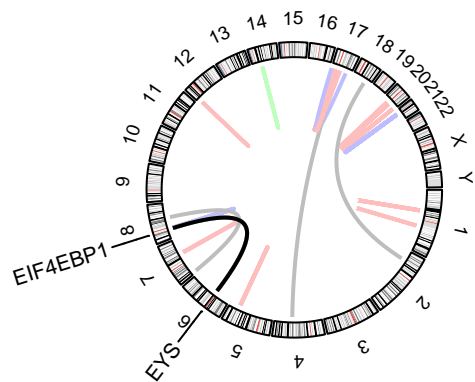
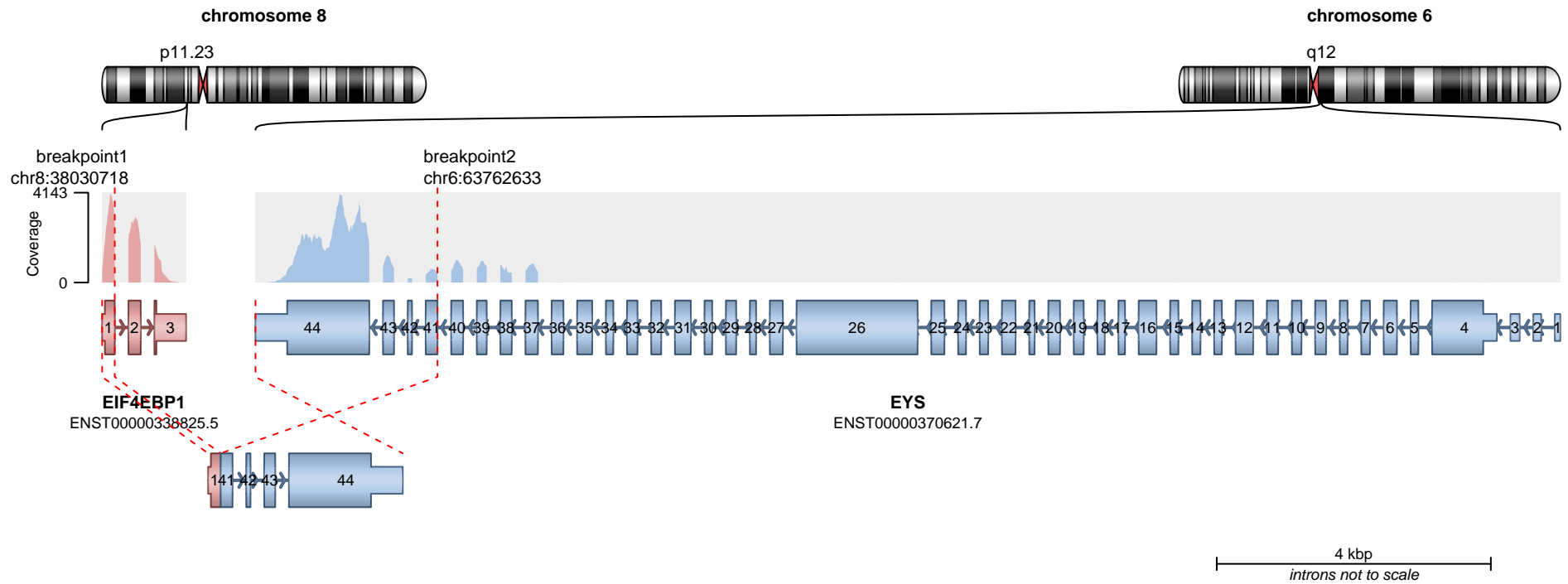
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



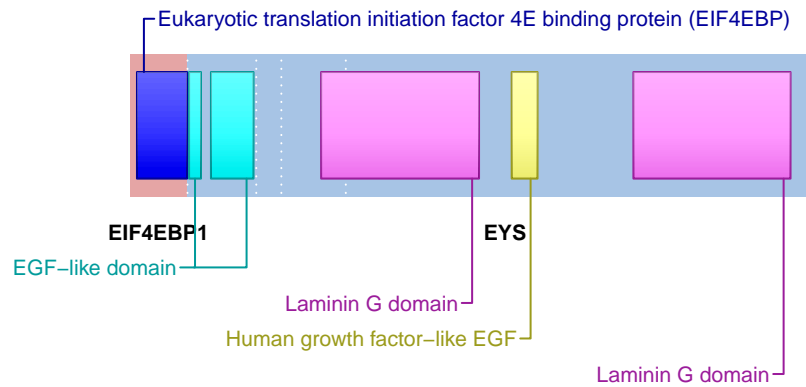
SUPPORTING READ COUNT

Split reads = 9
Discordant mates = 0



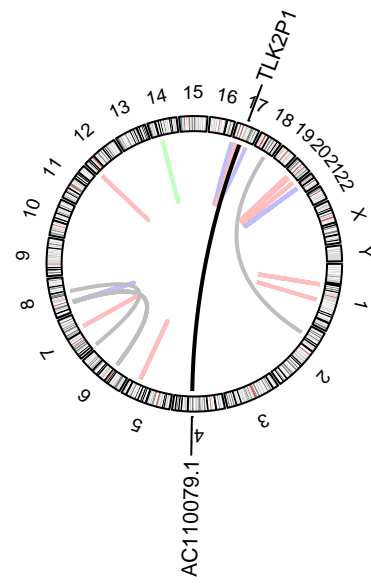
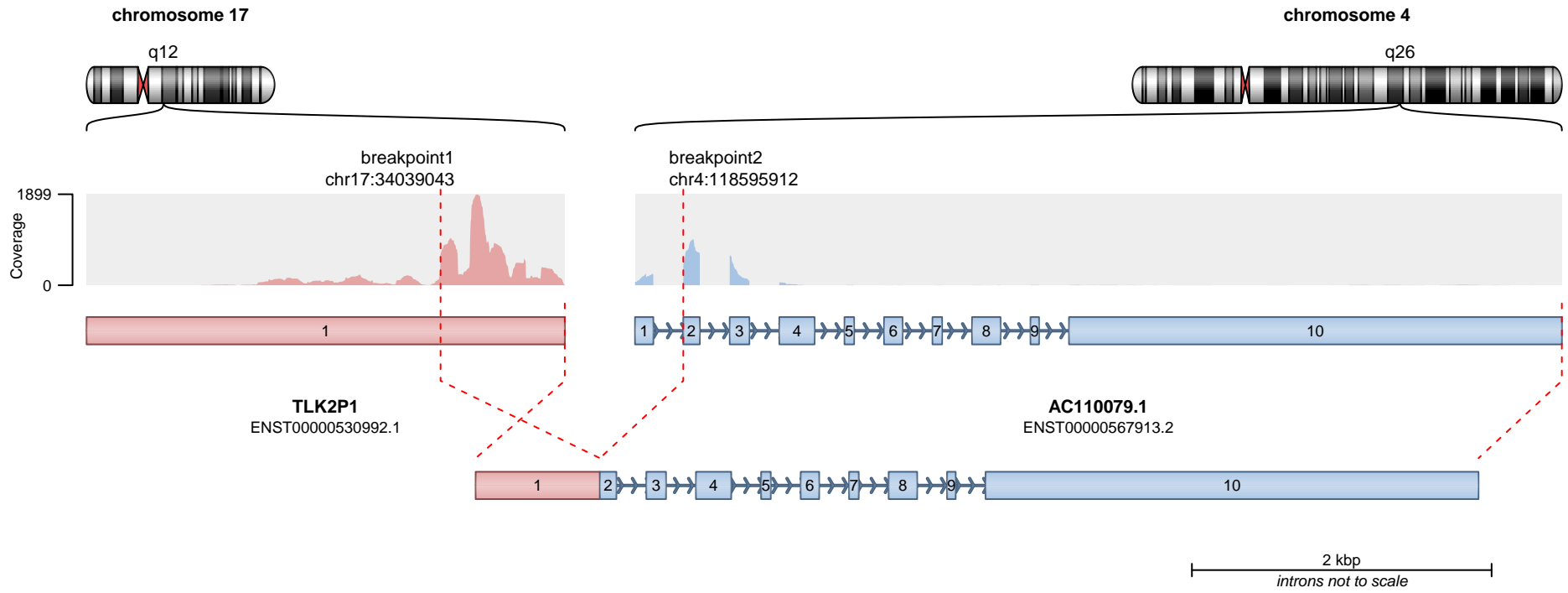
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

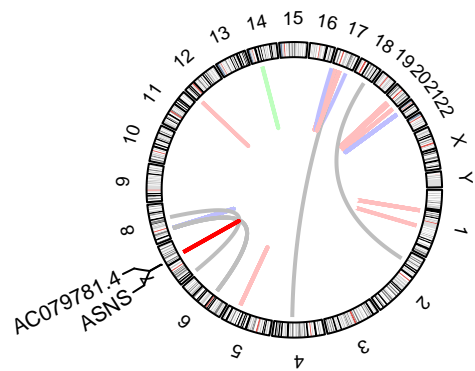
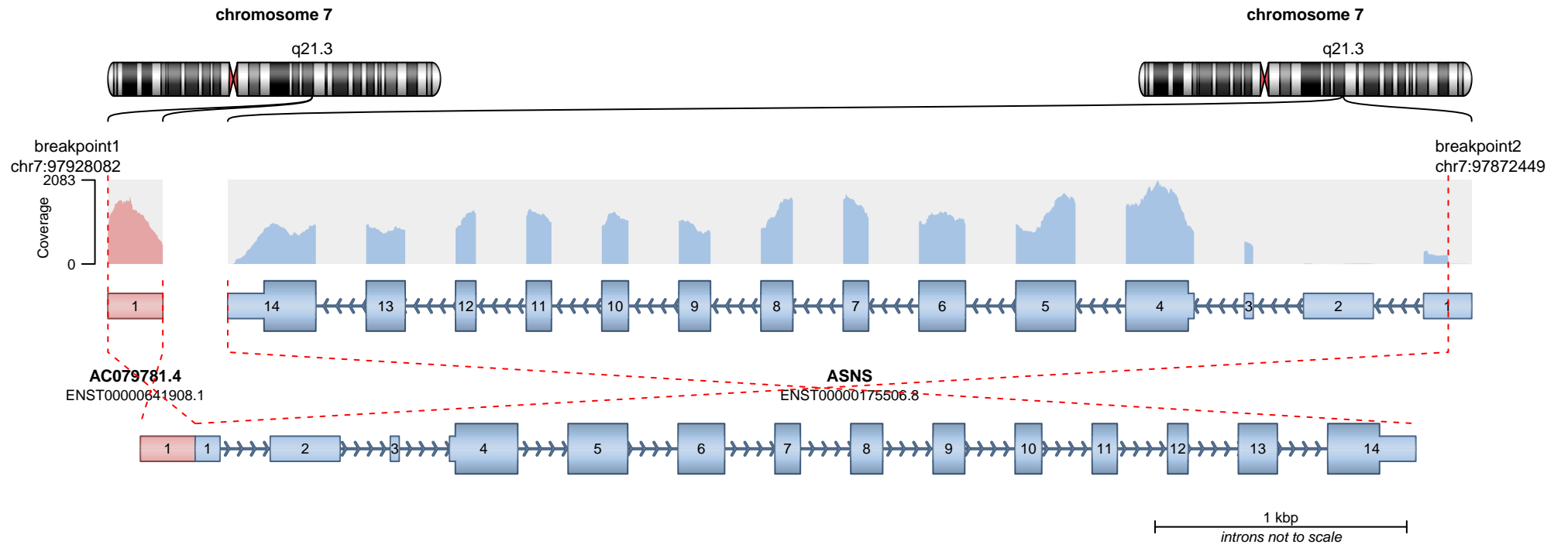


— translocation — deletion
 — duplication — inversion

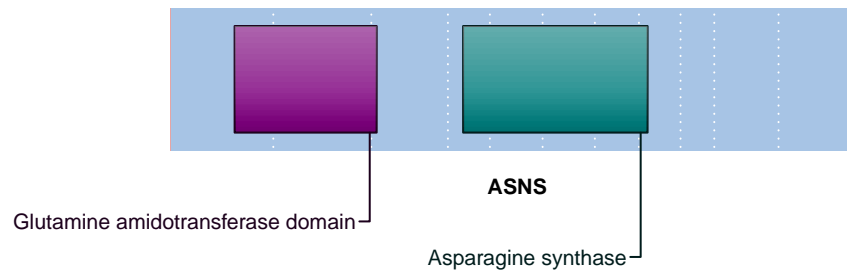
Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 101
 Discordant mates = 2



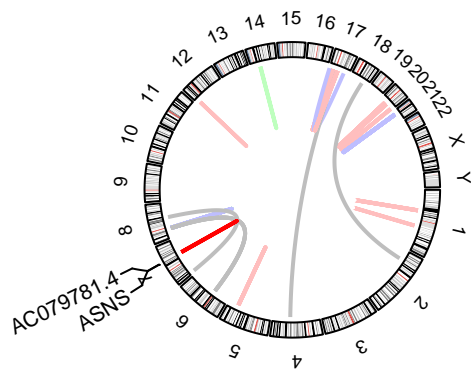
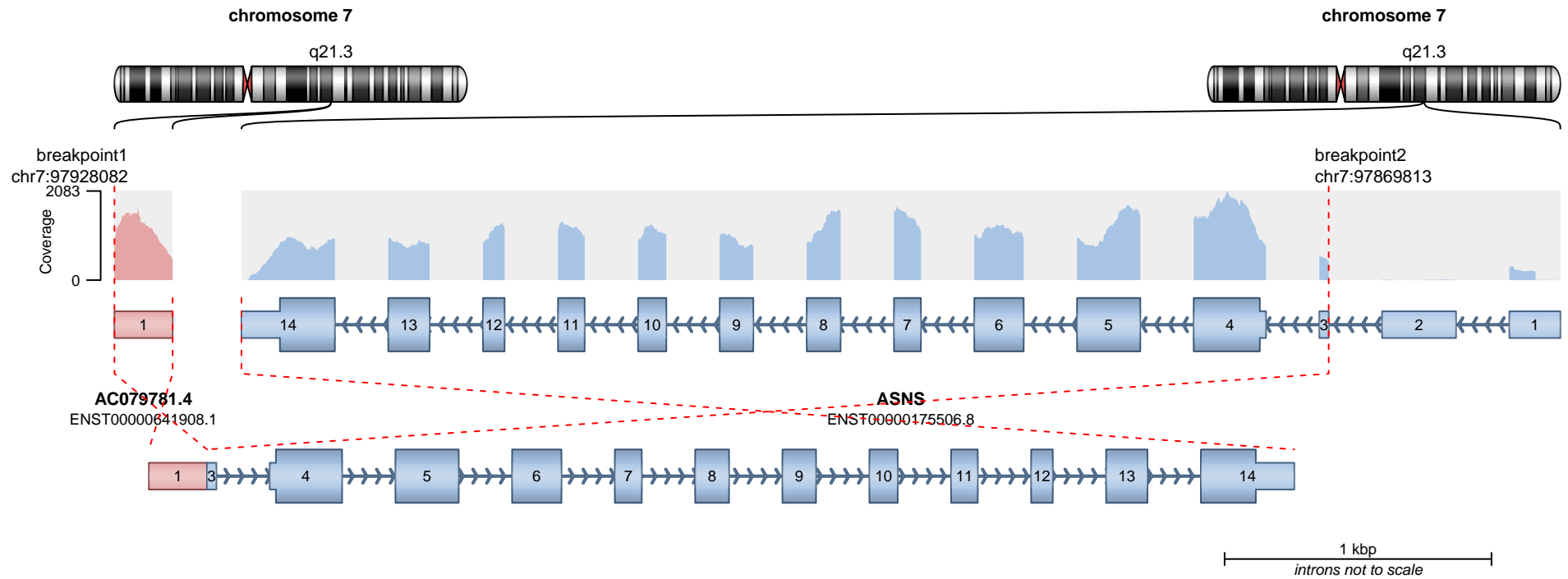
RETAINED PROTEIN DOMAINS
reading frame unclear



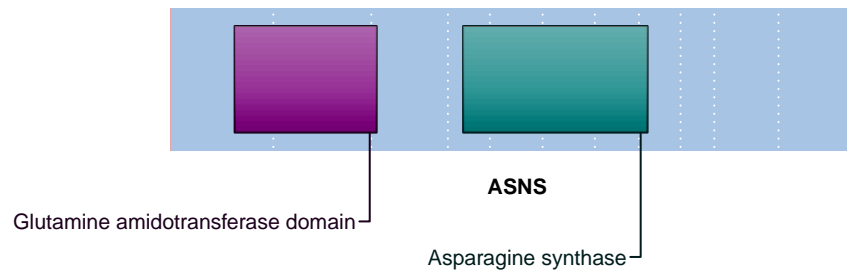
SUPPORTING READ COUNT

Split reads = 87
Discordant mates = 0

— translocation — deletion
— duplication — inversion



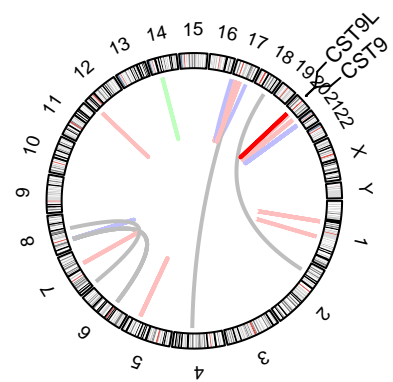
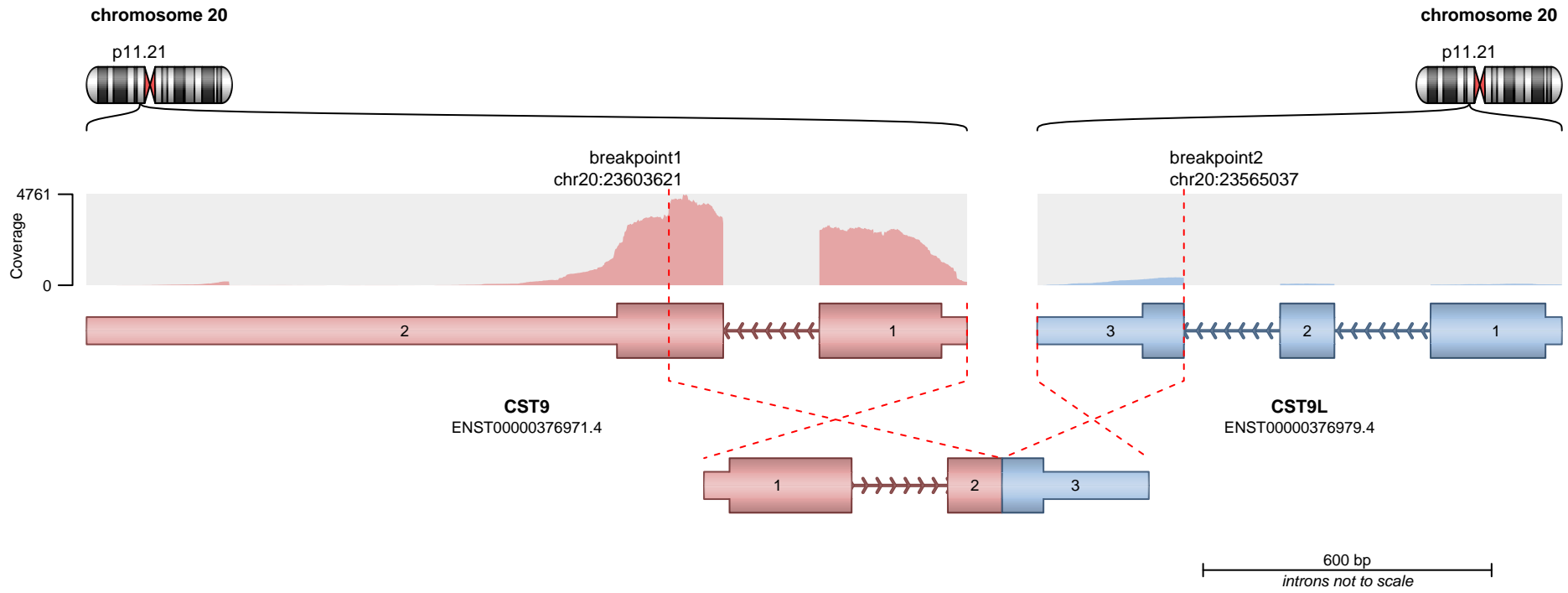
RETAINED PROTEIN DOMAINS
reading frame unclear



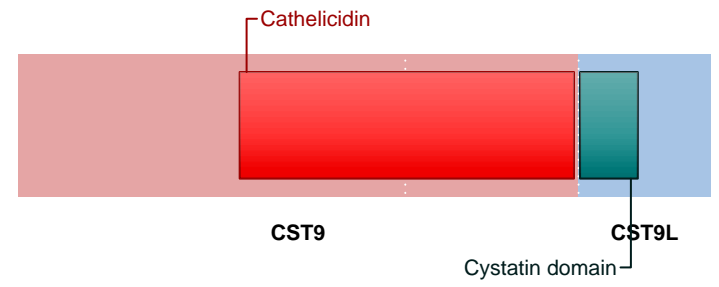
SUPPORTING READ COUNT

Split reads = 28
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



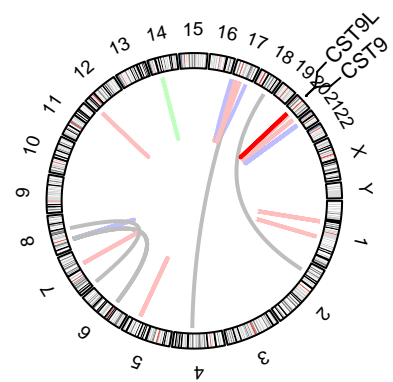
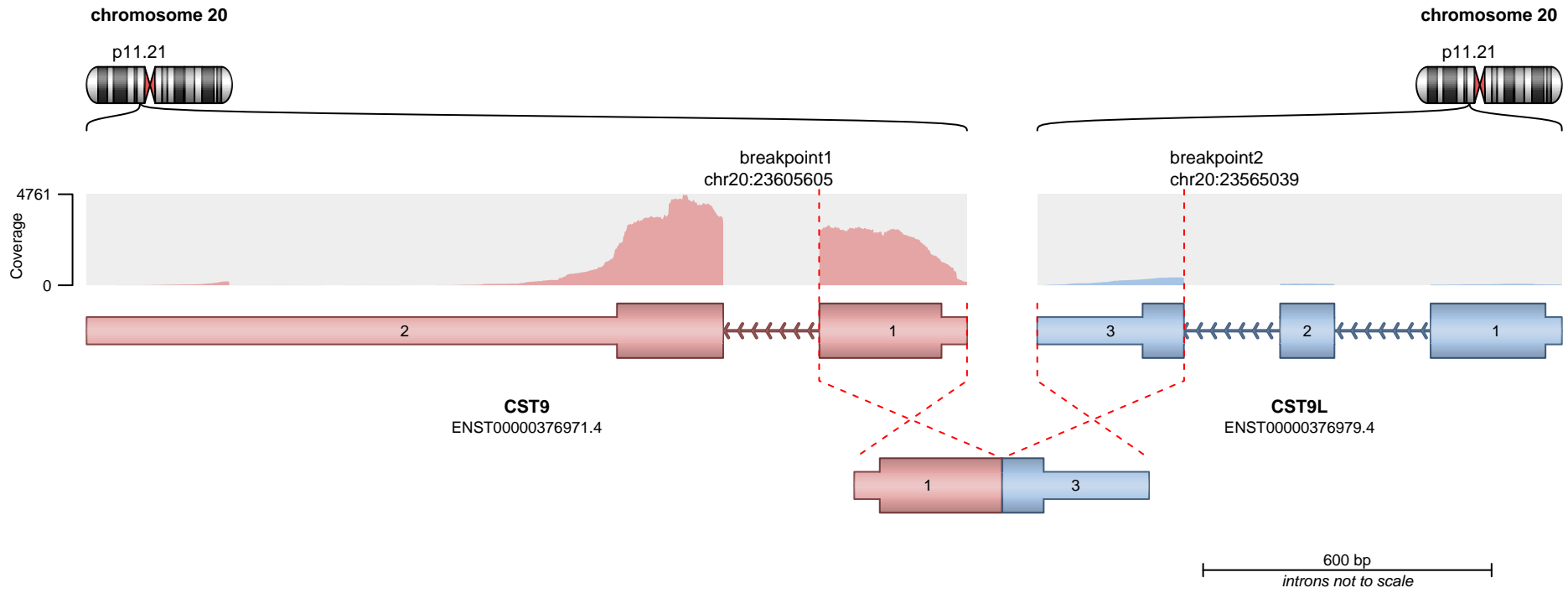
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

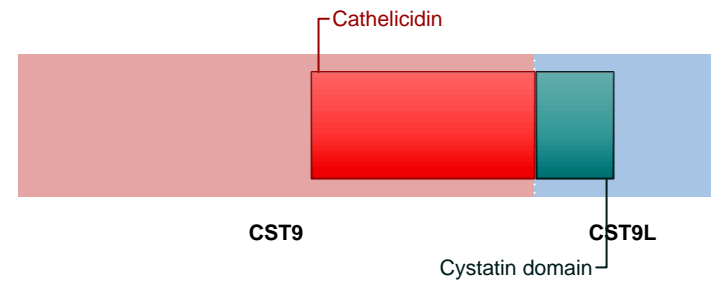
Split reads = 80
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



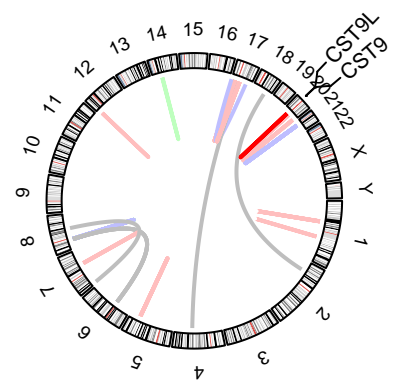
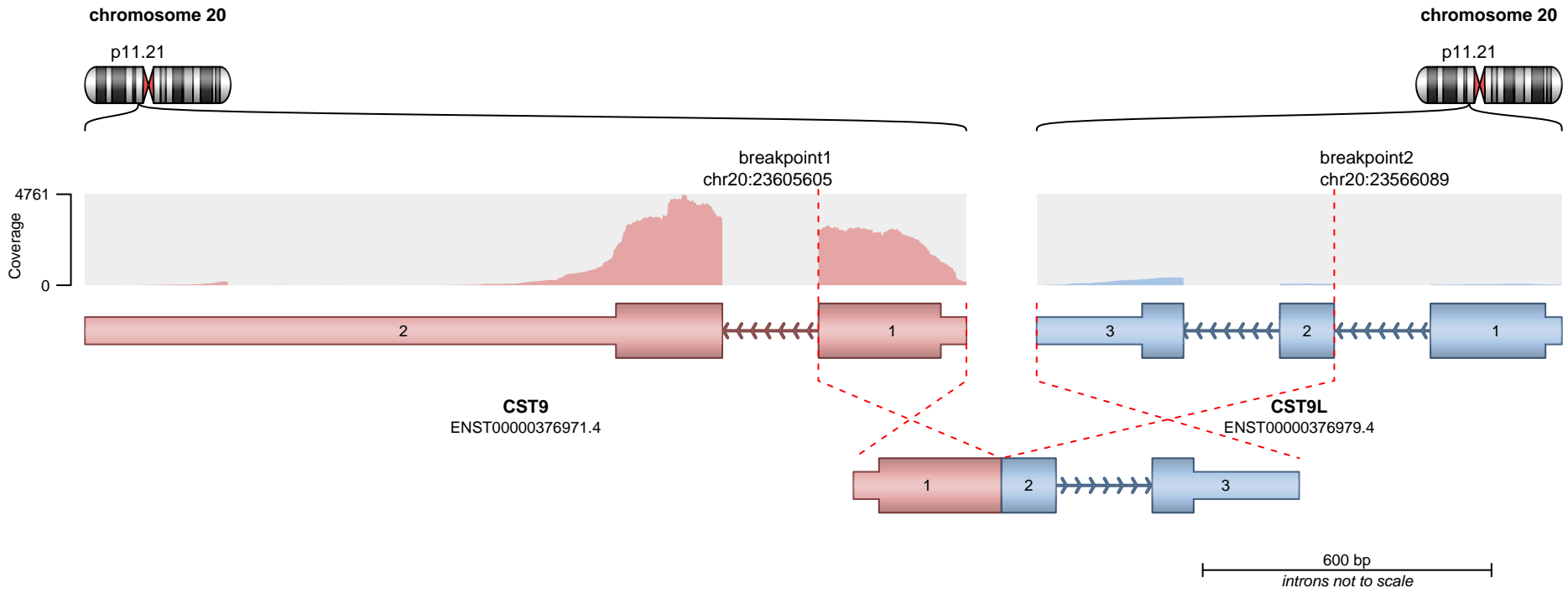
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear

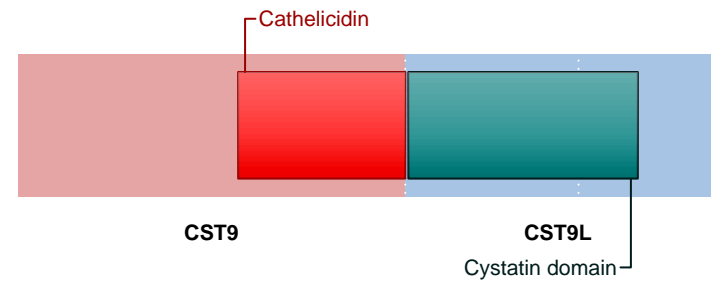


SUPPORTING READ COUNT

Split reads = 27
Discordant mates = 0



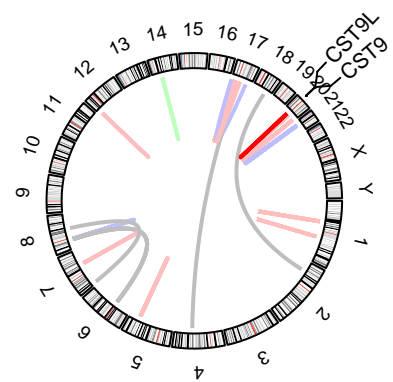
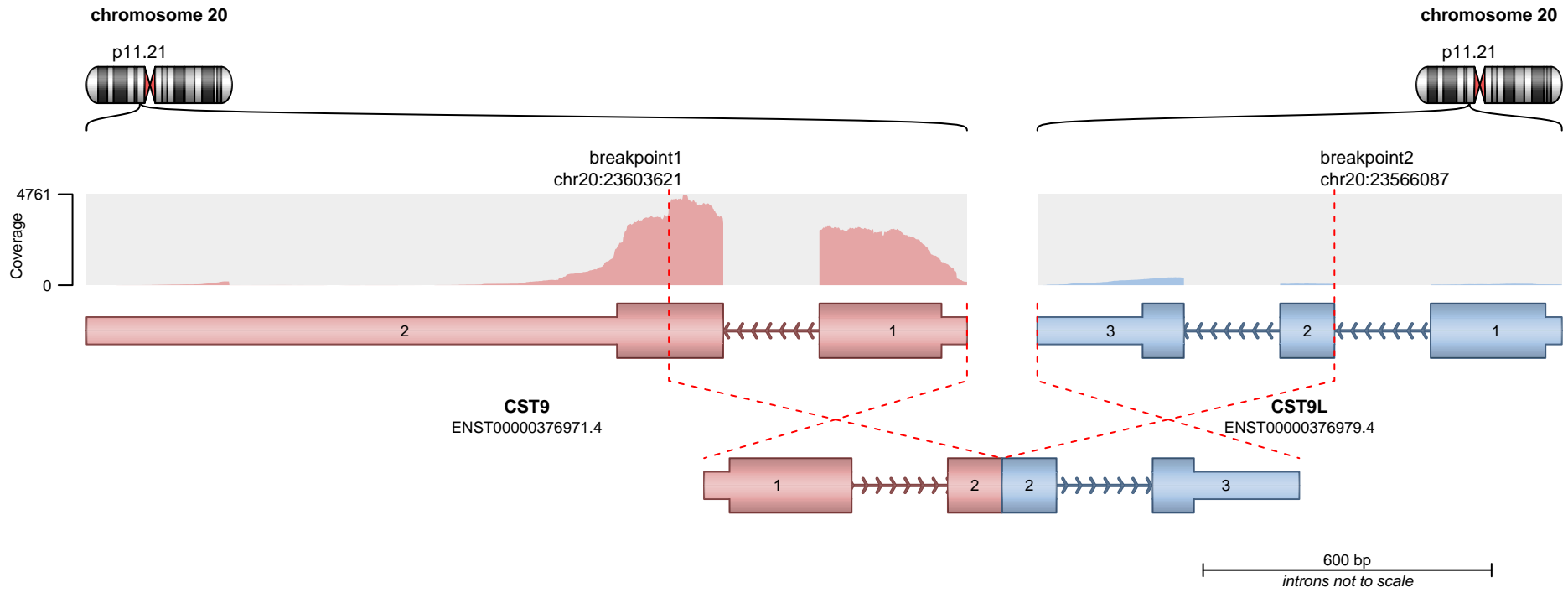
RETAINED PROTEIN DOMAINS
reading frame unclear



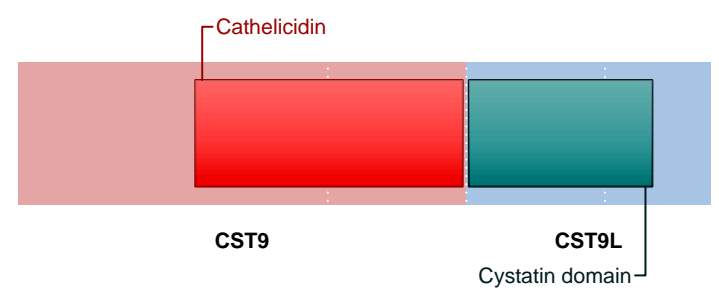
SUPPORTING READ COUNT

Split reads = 15
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



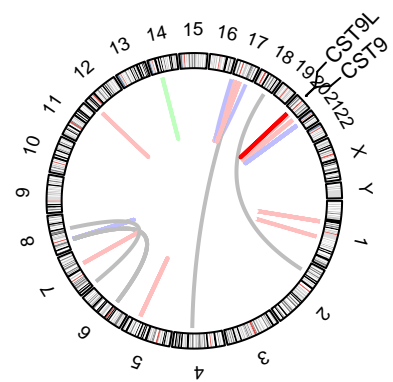
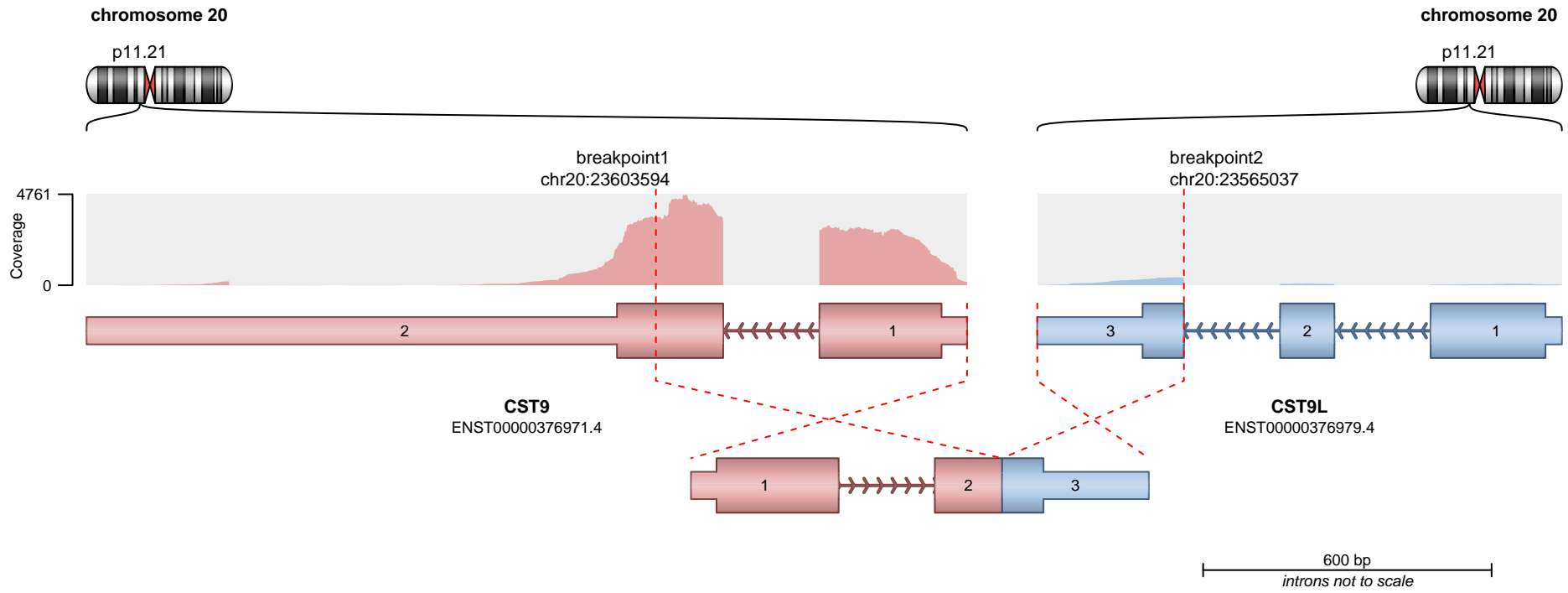
RETAINED PROTEIN DOMAINS
reading frame unclear



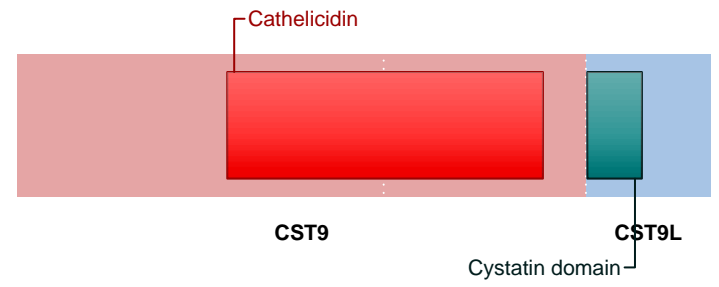
SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



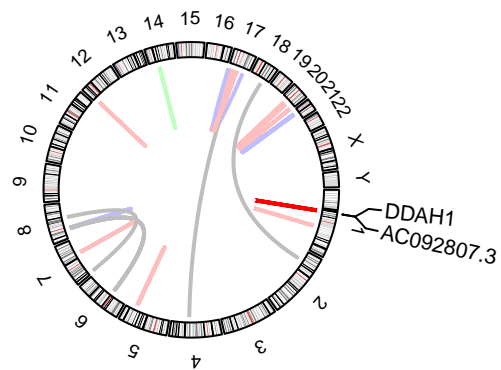
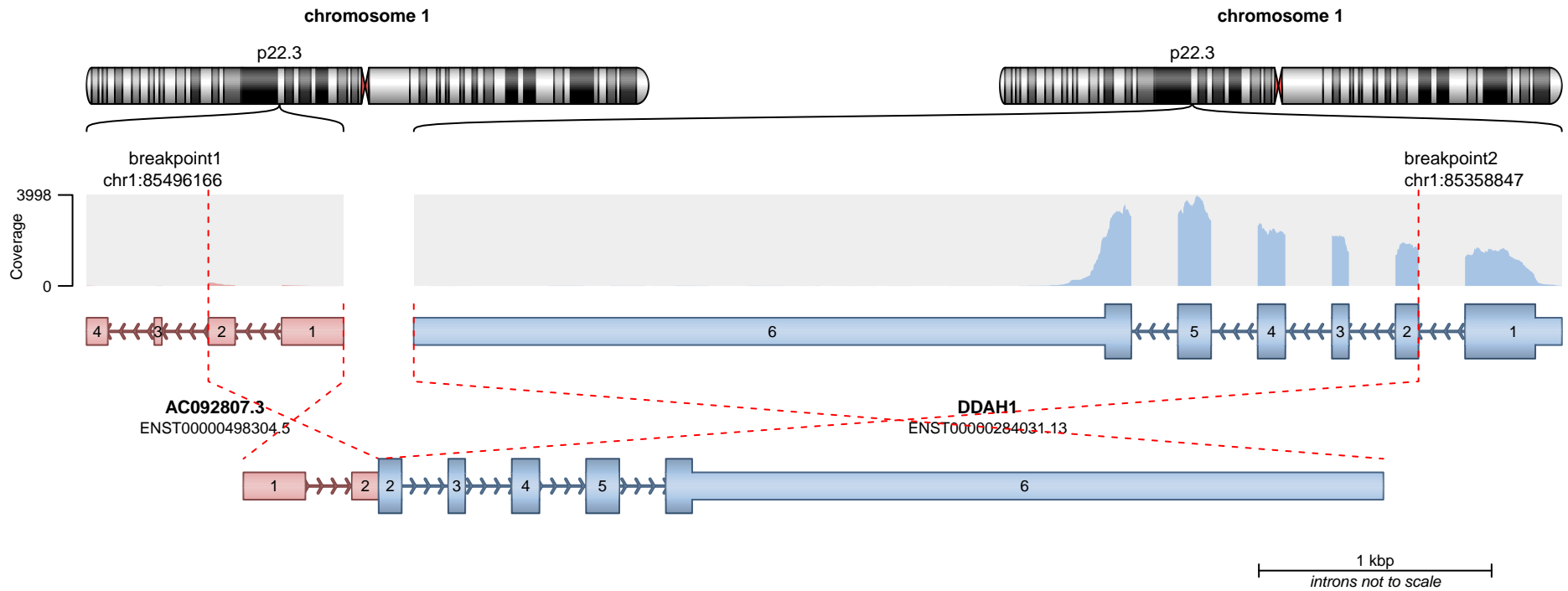
RETAINED PROTEIN DOMAINS
reading frame unclear



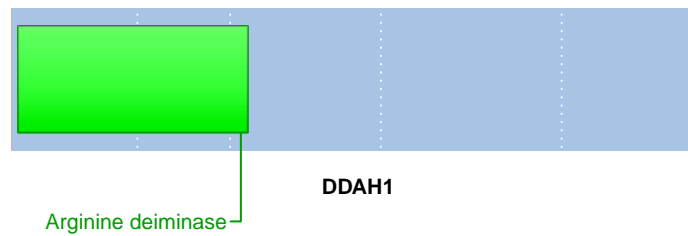
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



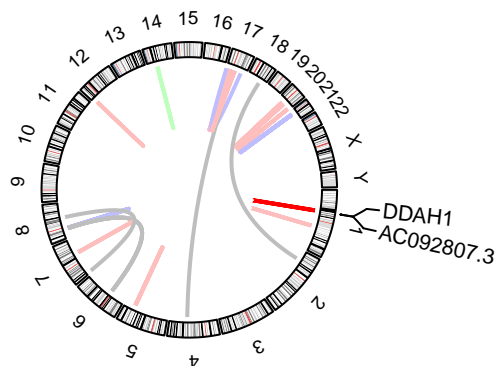
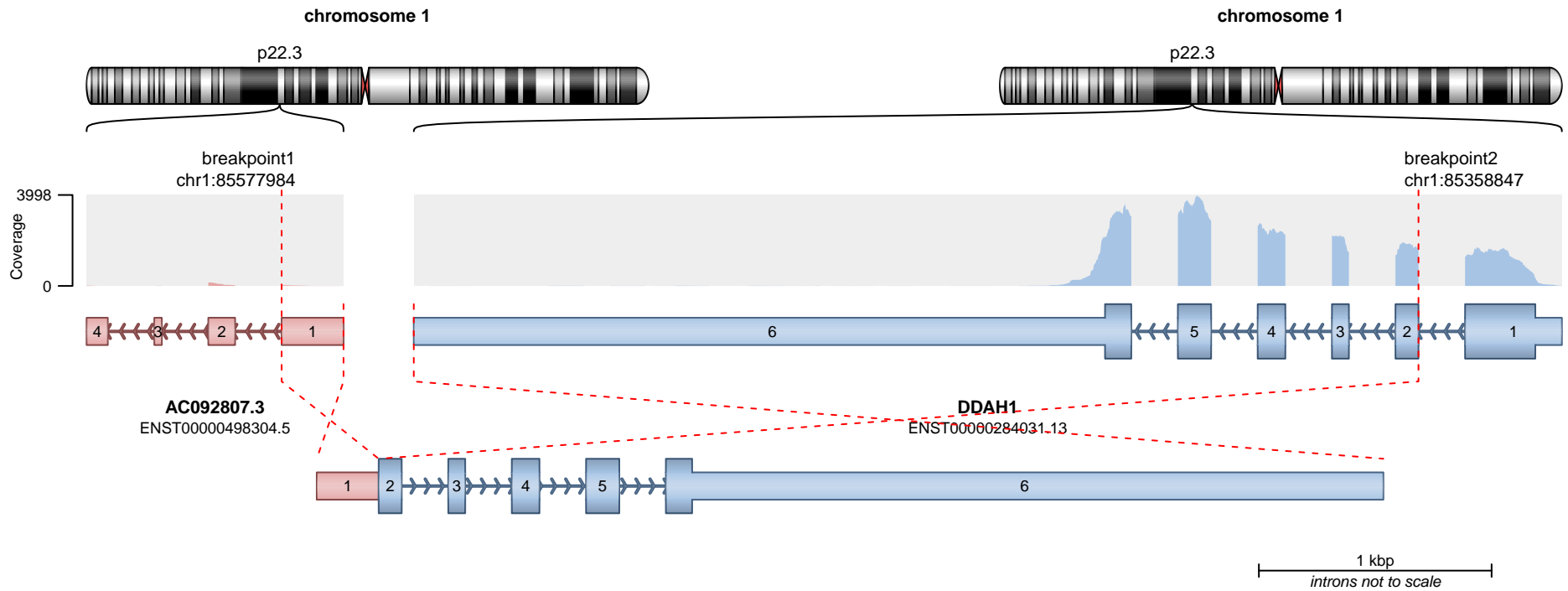
RETAINED PROTEIN DOMAINS
reading frame unclear



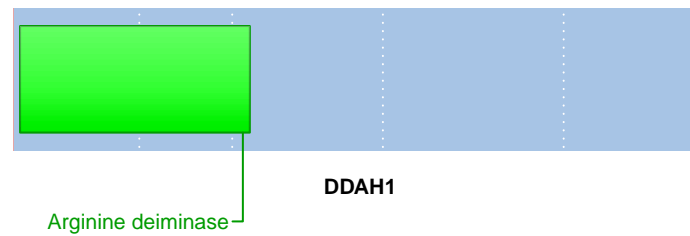
SUPPORTING READ COUNT

Split reads = 57
Discordant mates = 2

— translocation — deletion
— duplication — inversion



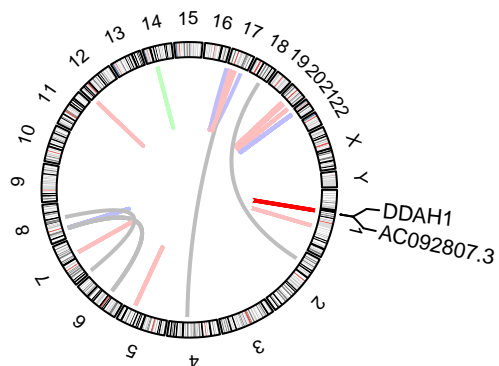
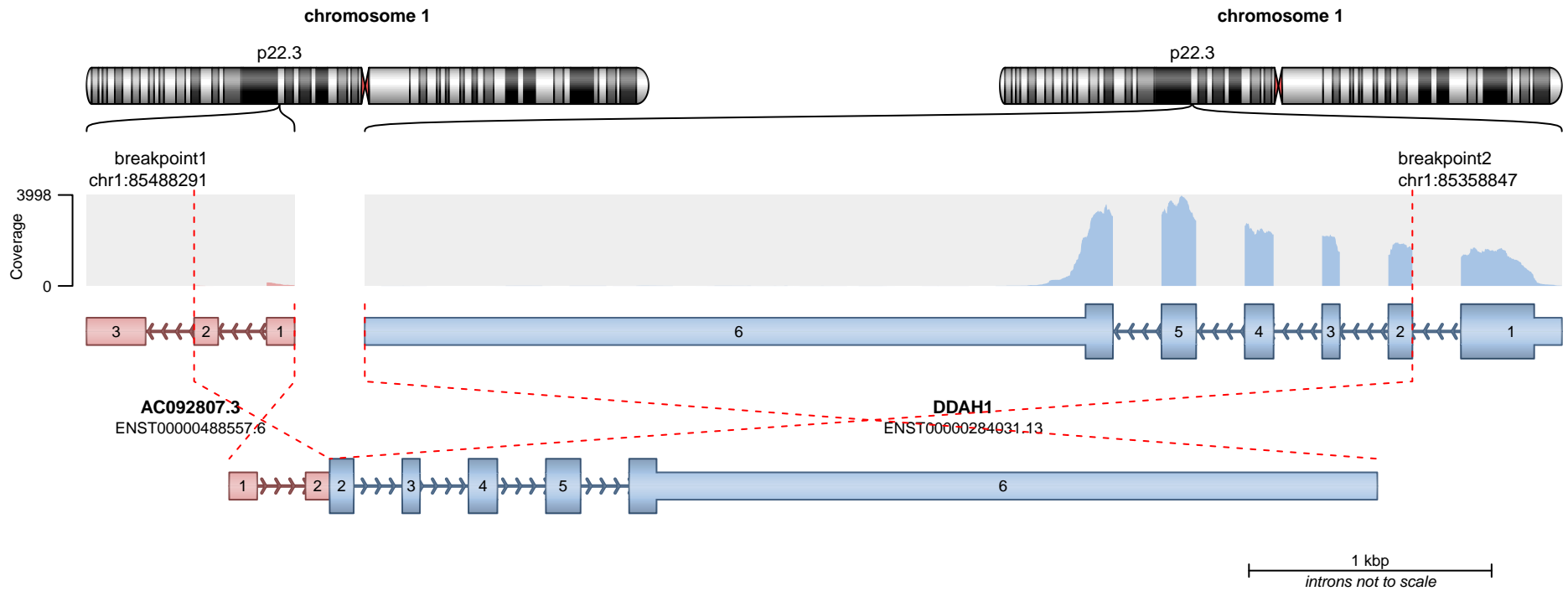
RETAINED PROTEIN DOMAINS
reading frame unclear



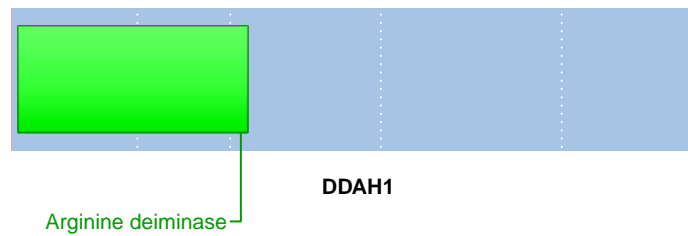
SUPPORTING READ COUNT

Split reads = 15
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



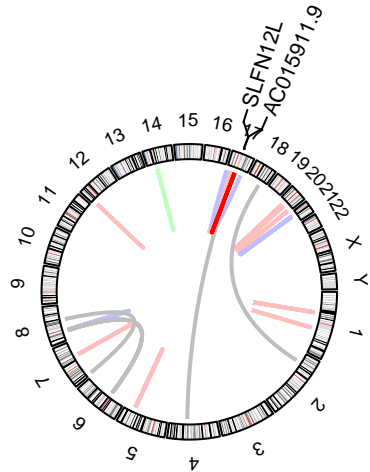
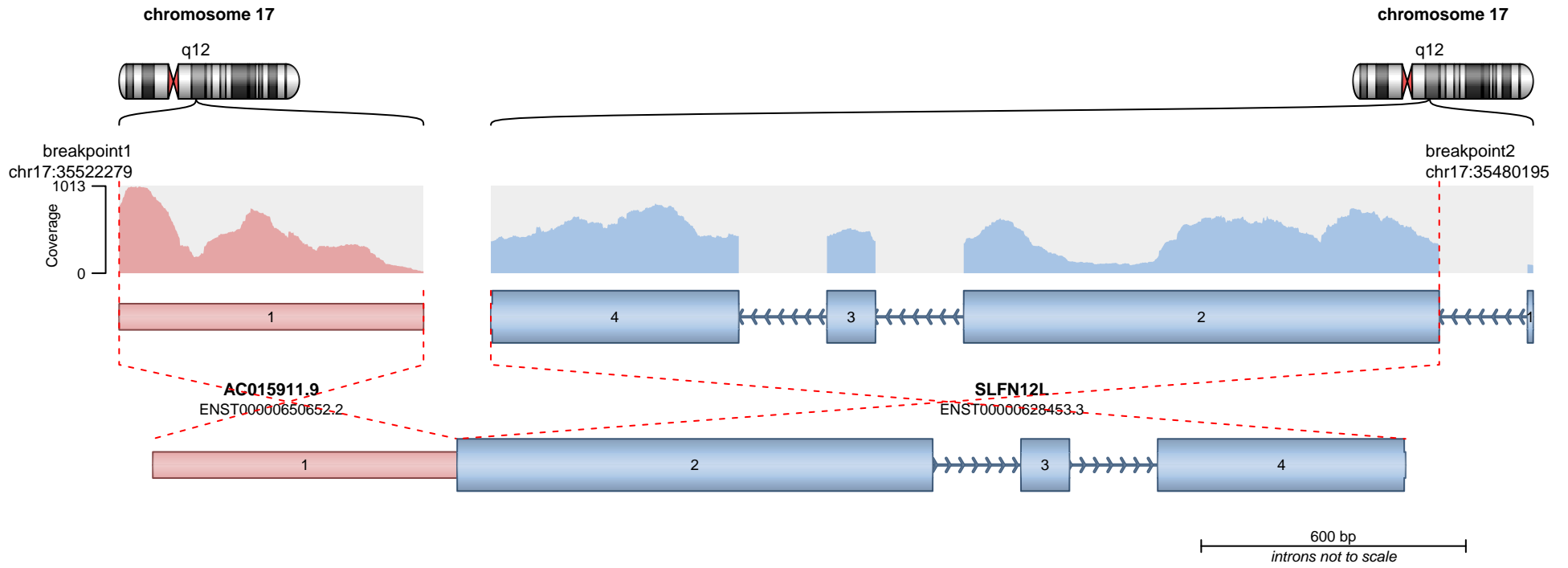
RETAINED PROTEIN DOMAINS
reading frame unclear



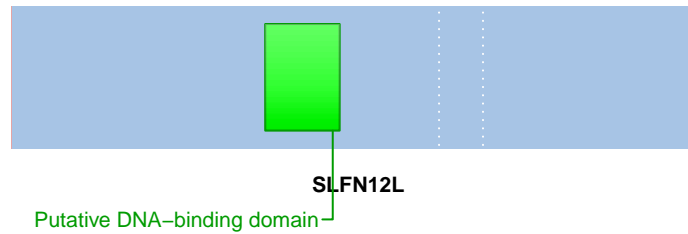
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 2

- translocation
- duplication
- deletion
- inversion



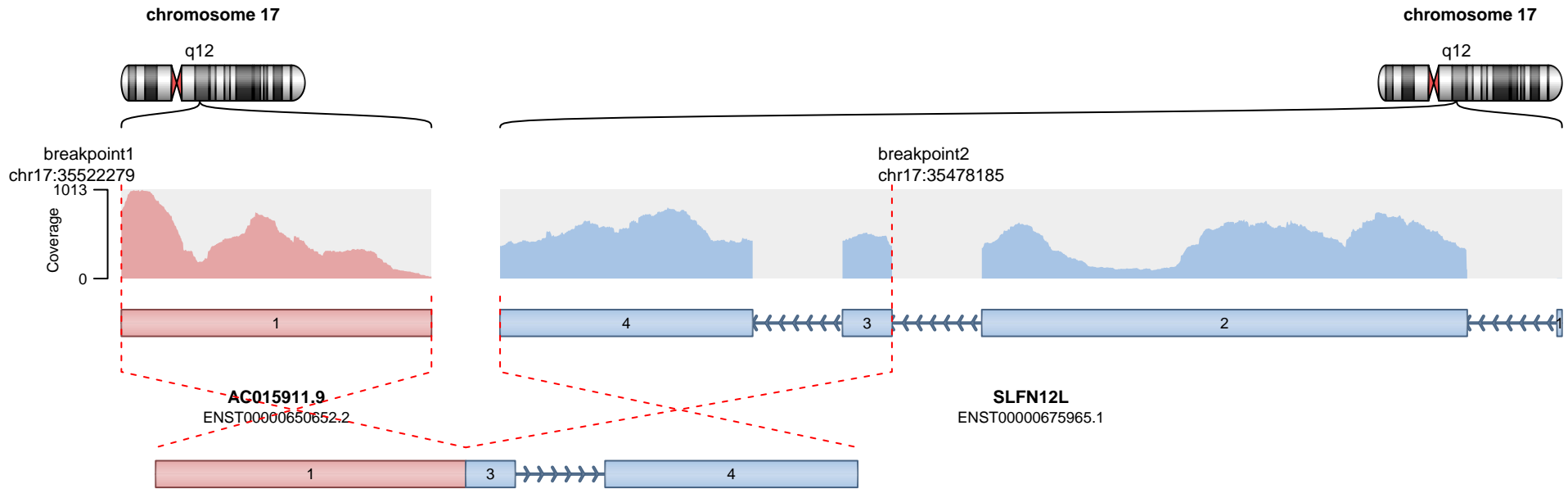
RETAINED PROTEIN DOMAINS
reading frame unclear



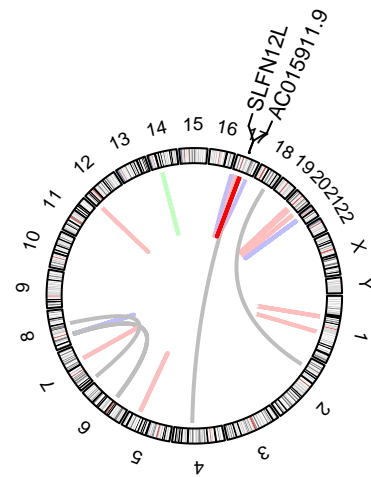
SUPPORTING READ COUNT

Split reads = 56
Discordant mates = 2

— translocation — deletion
— duplication — inversion



600 bp
introns not to scale

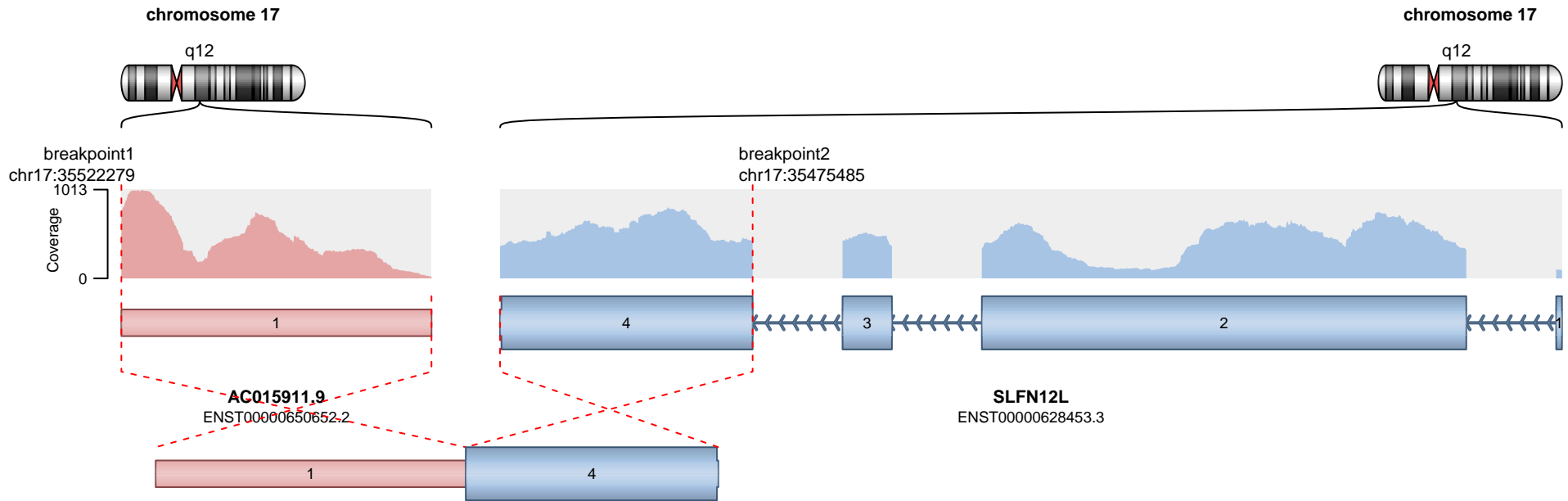


— translocation — deletion
— duplication — inversion

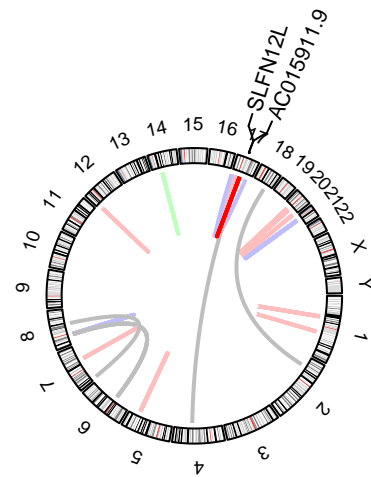
Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 19
Discordant mates = 0



600 bp
introns not to scale

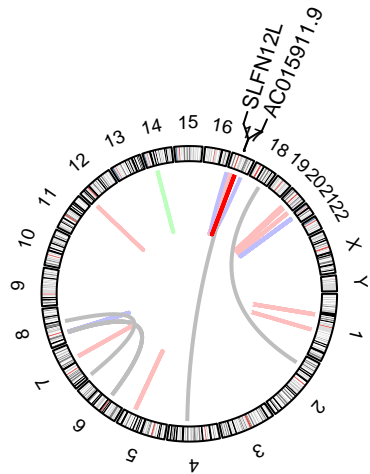
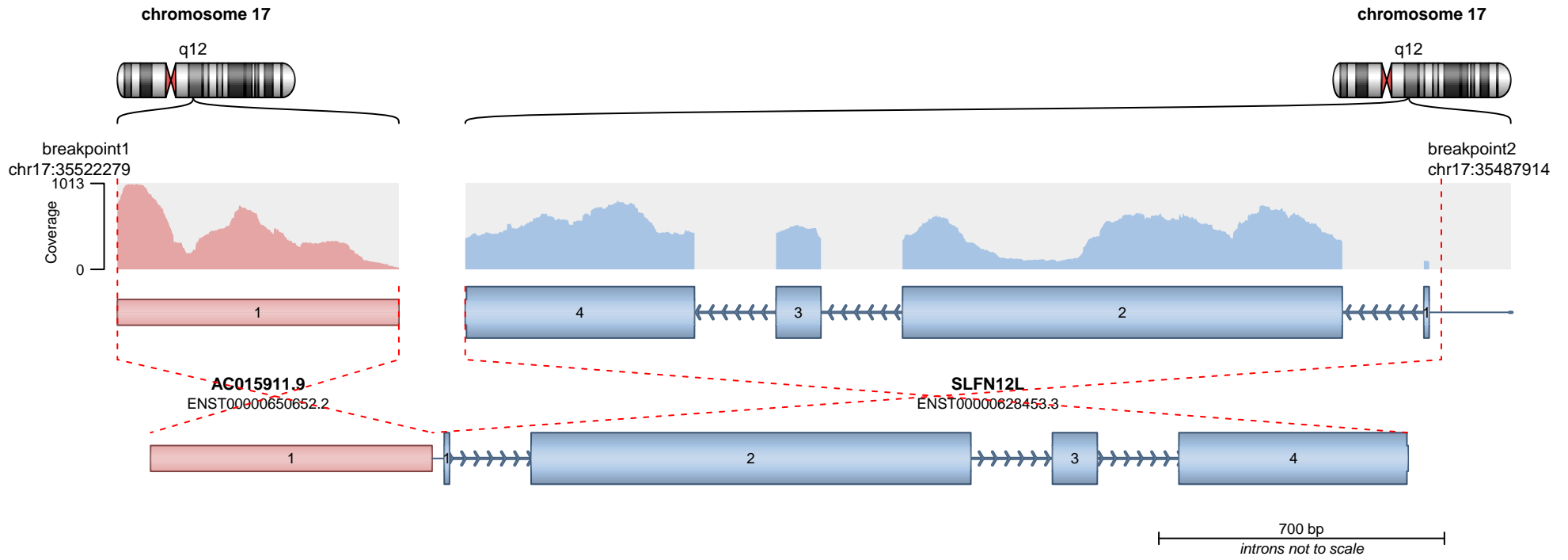


— translocation — deletion
— duplication — inversion

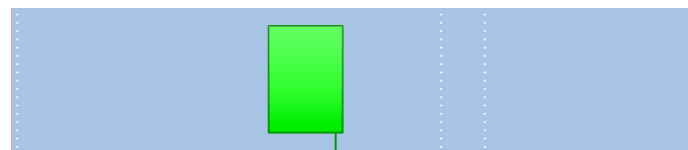
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0



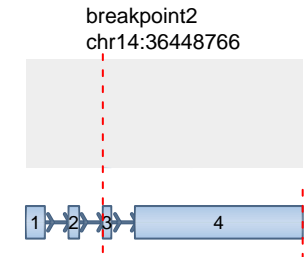
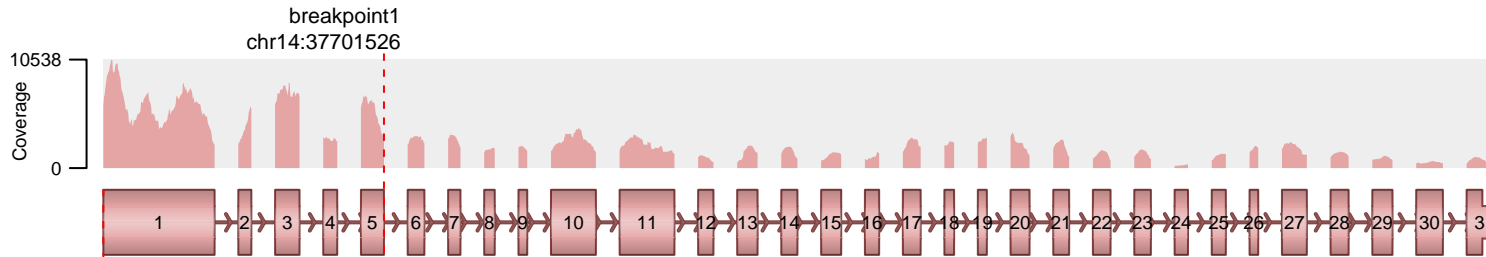
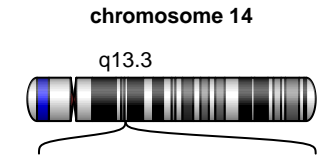
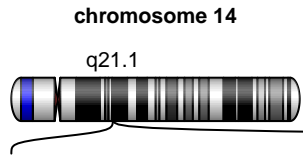
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 2

— translocation — deletion
— duplication — inversion

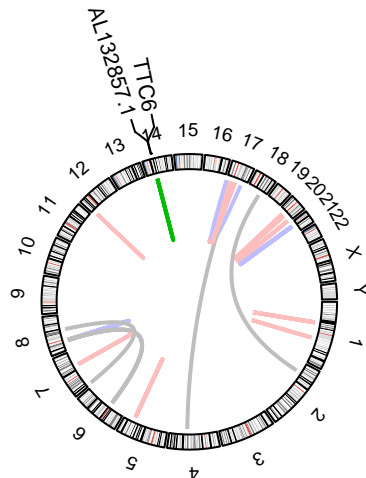


TTC6
ENST00000563443.5

AL132857.1
ENST00000634305.1



3 kbp
introns not to scale

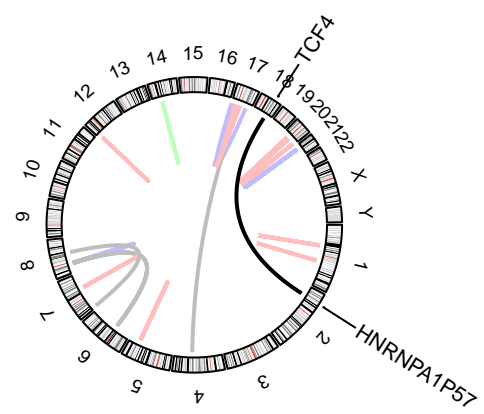
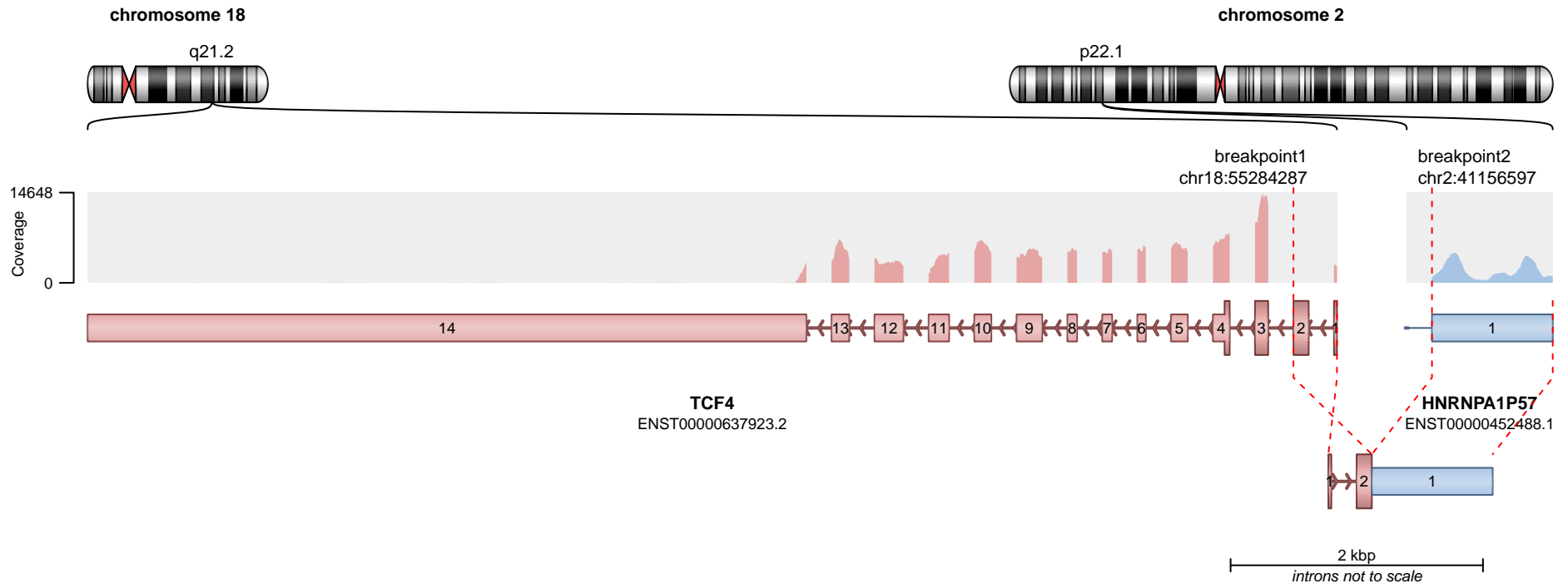


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 44
Discordant mates = 0

— translocation — deletion
— duplication — inversion

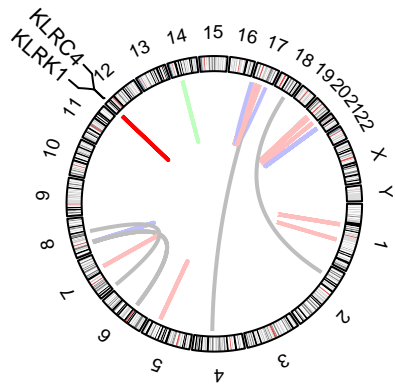
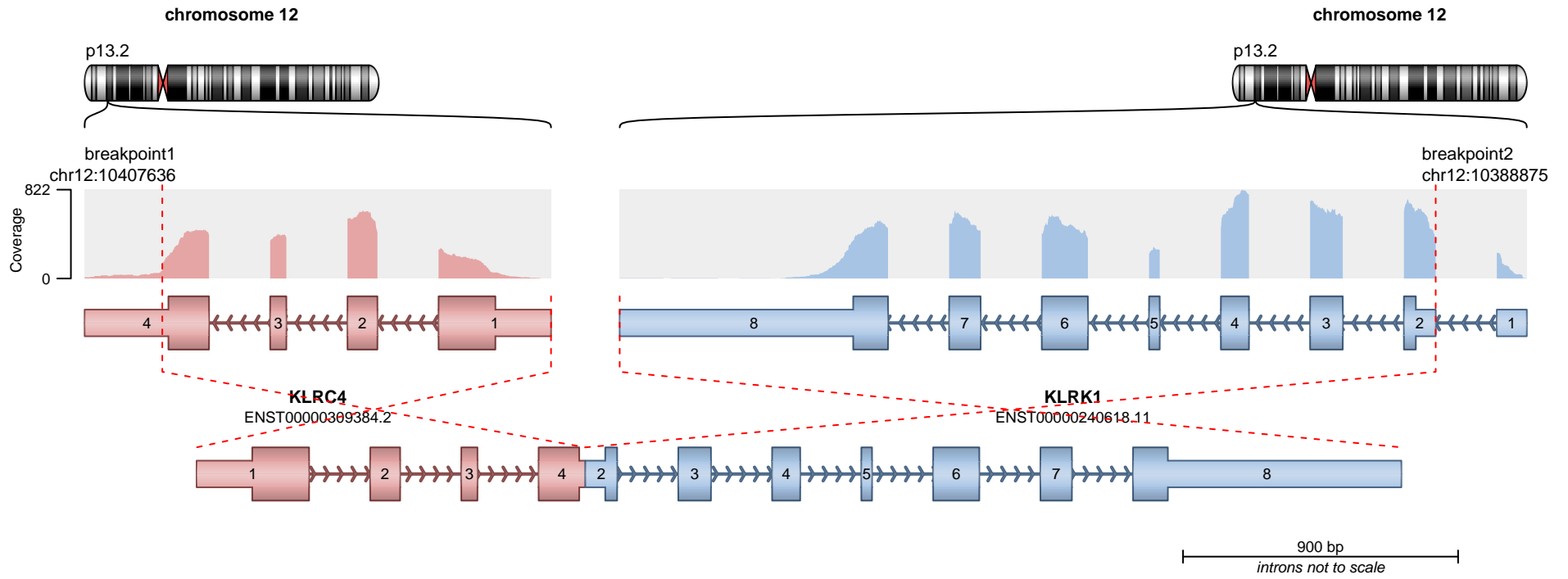


No protein domains retained in fusion.

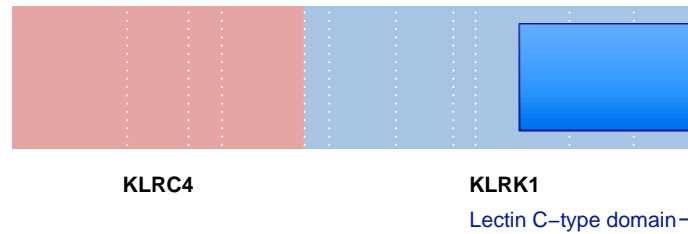
SUPPORTING READ COUNT

Split reads = 20
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



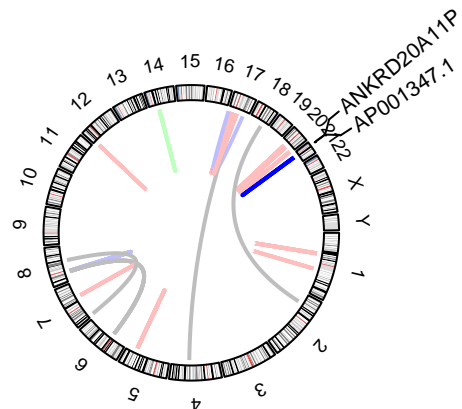
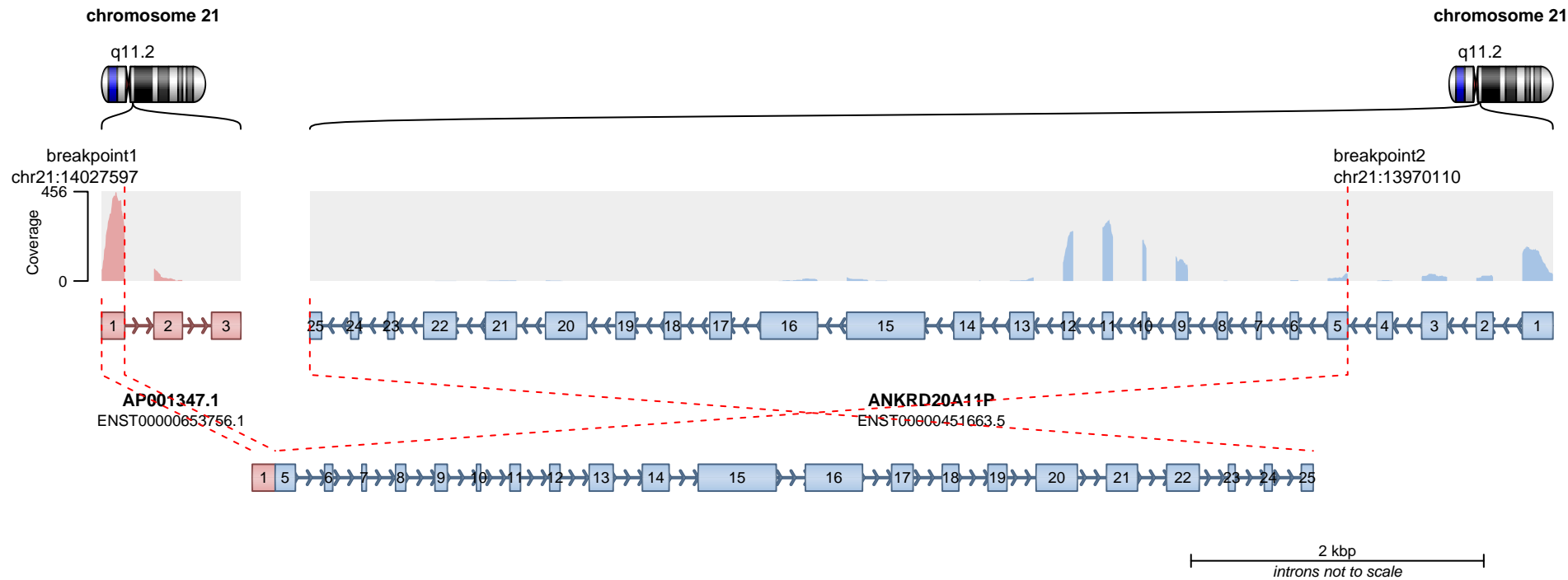
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 17
Discordant mates = 1

— translocation — deletion
— duplication — inversion

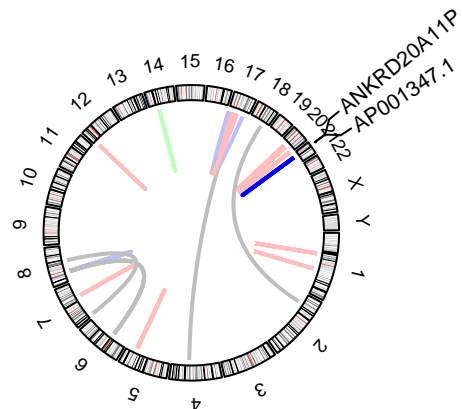
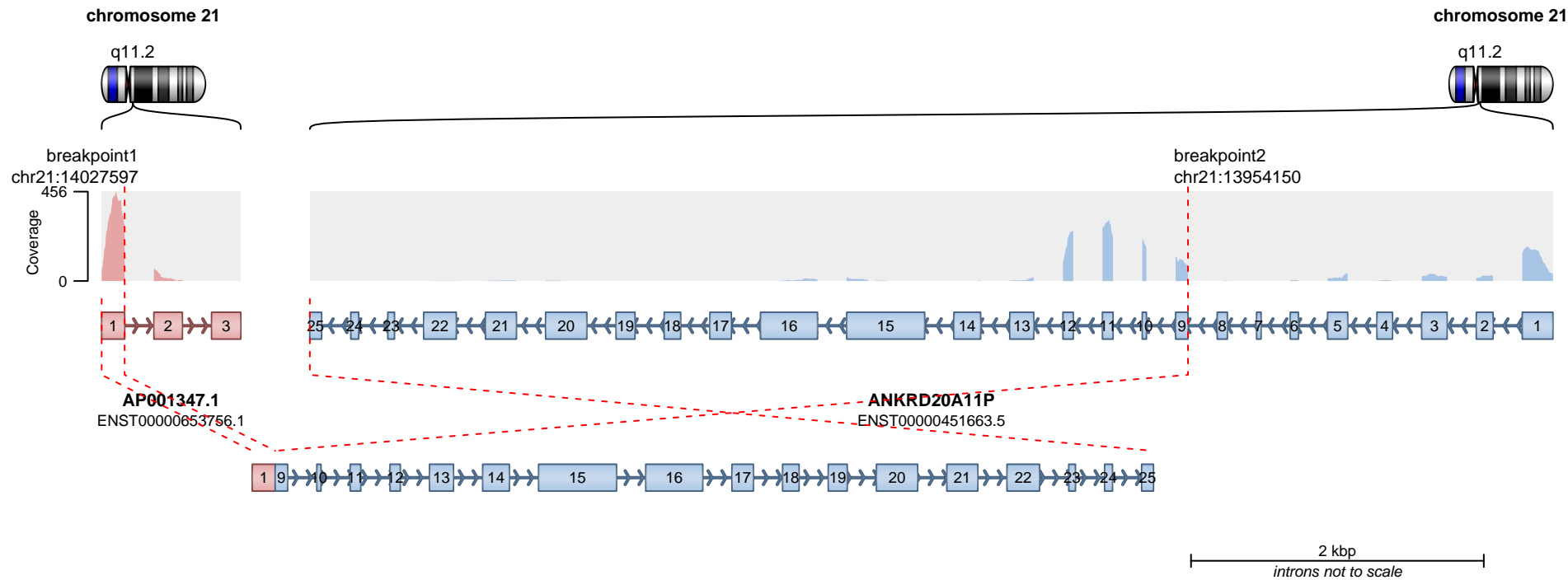


— translocation — deletion
— duplication — inversion

Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 1

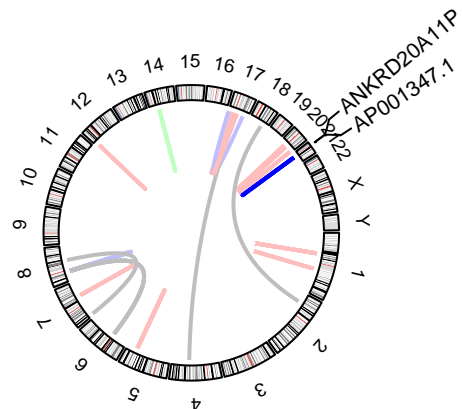
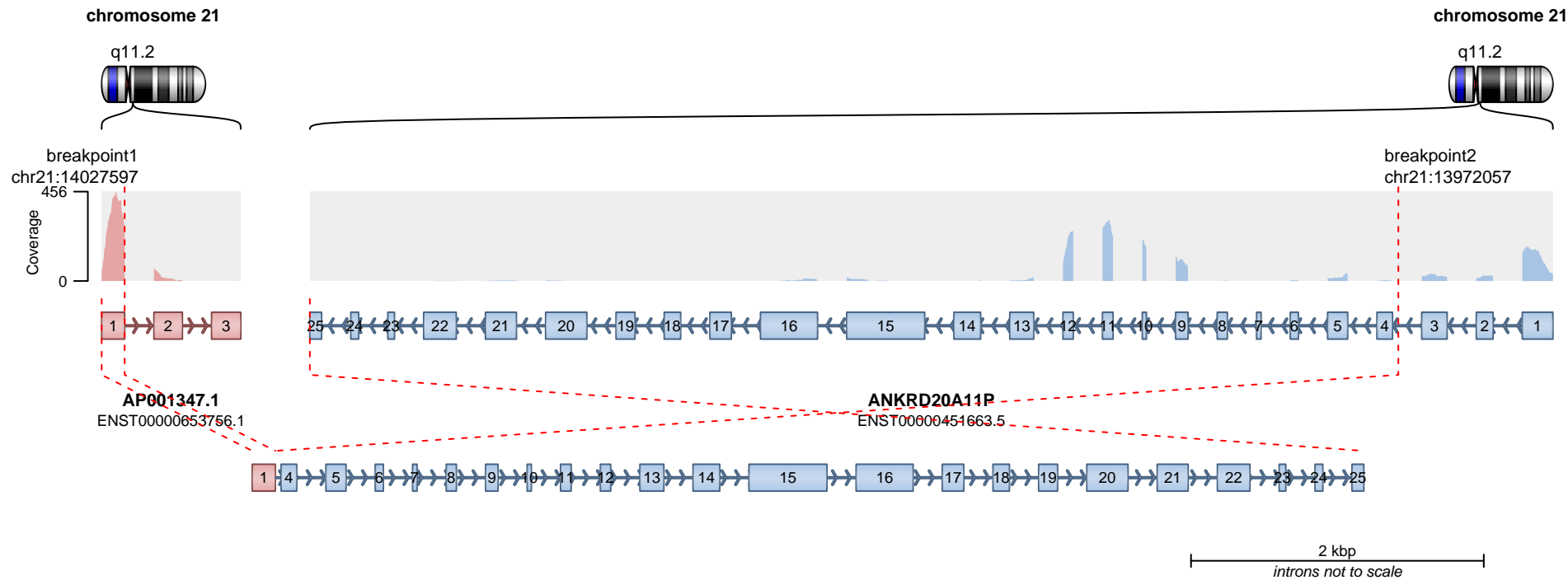


— translocation — deletion
— duplication — inversion

Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 0



— translocation — deletion
— duplication — inversion

Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 1

chromosome 21

chromosome 21

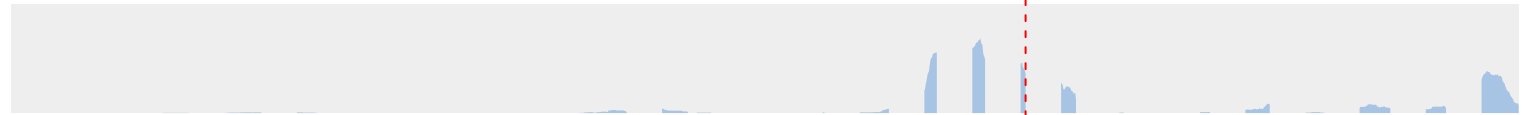
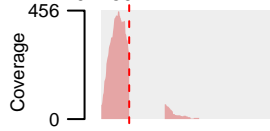
q11.2

q11.2



breakpoint1
chr21:14027597

breakpoint2
chr21:13951260

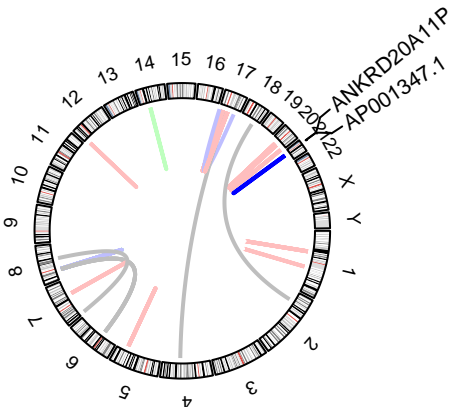


AP001347.1
ENST00000653756.1

ANKRD20A11P
ENST00000451663.5



2 kbp
introns not to scale



Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

— translocation — deletion
— duplication — inversion

chromosome 21

chromosome 21

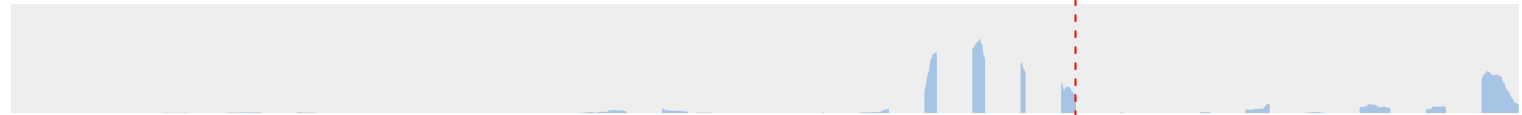
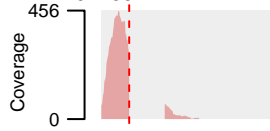
q11.2

q11.2



breakpoint1
chr21:14027597

breakpoint2
chr21:13954147

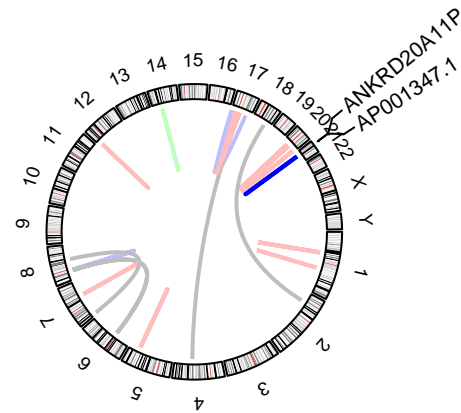


AP001347.1
ENST00000653756.1

ANKRD20A11P
ENST00000451663.5



2 kbp
introns not to scale

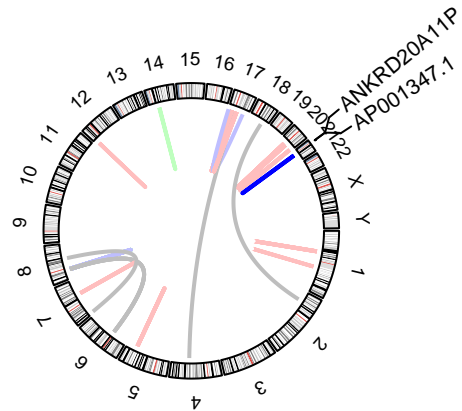
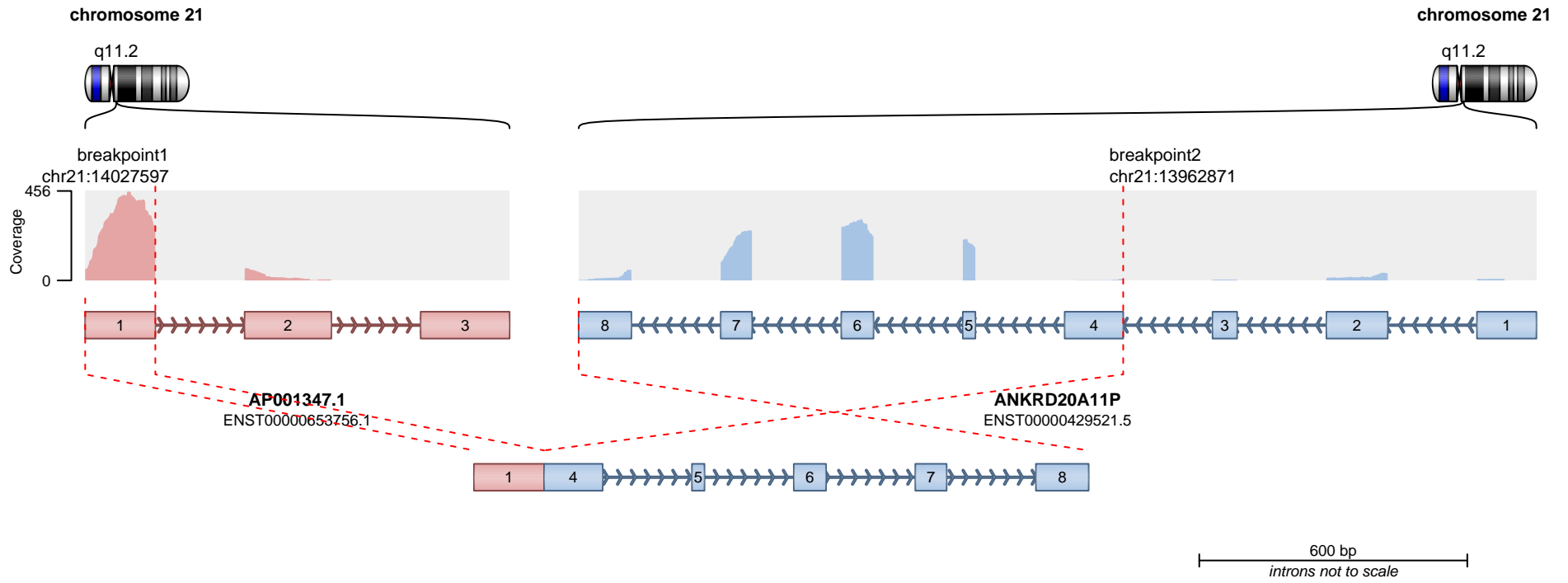


Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

— translocation — deletion
— duplication — inversion

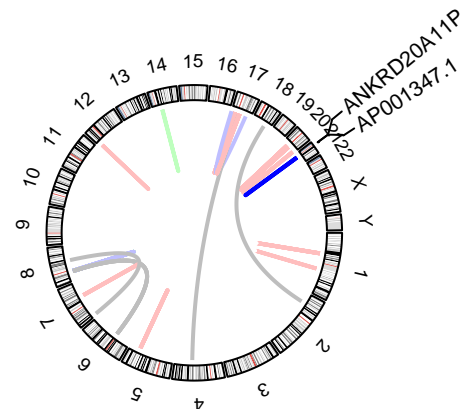
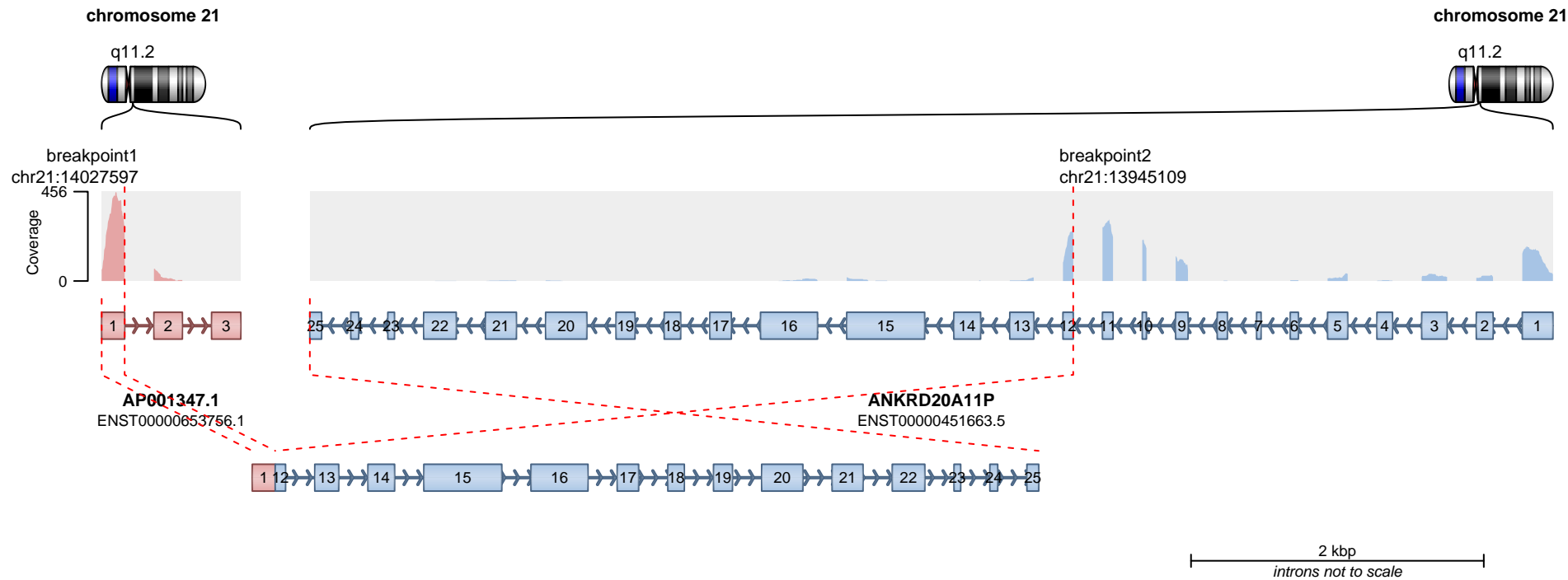


Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion

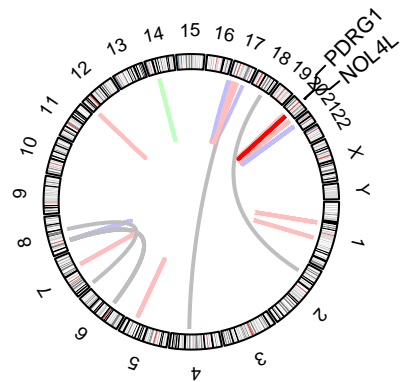
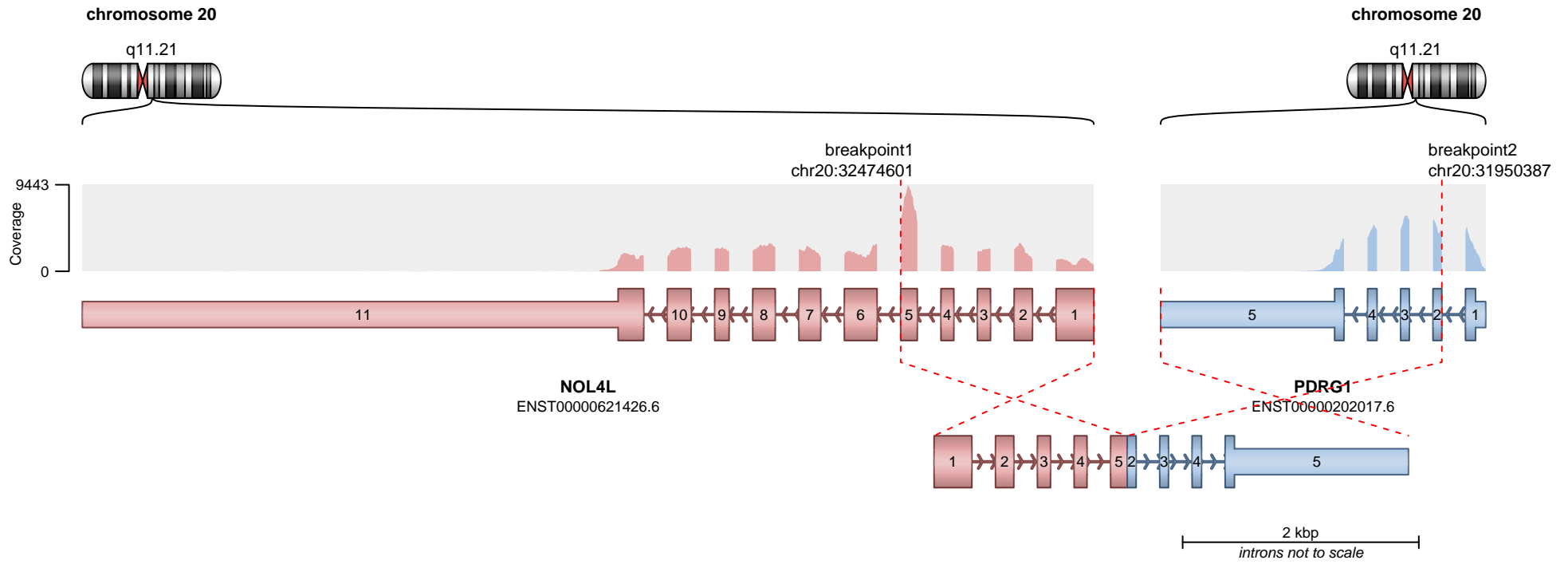


Genes are not protein-coding.

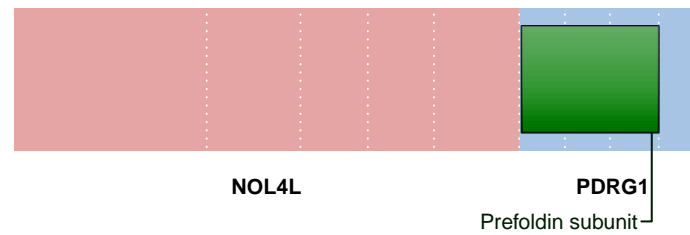
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



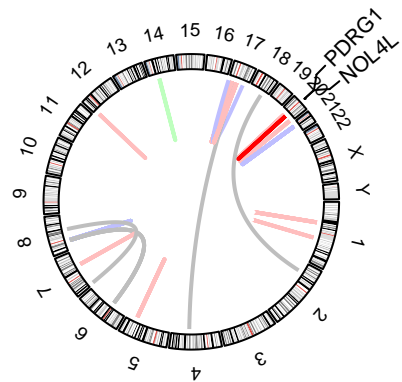
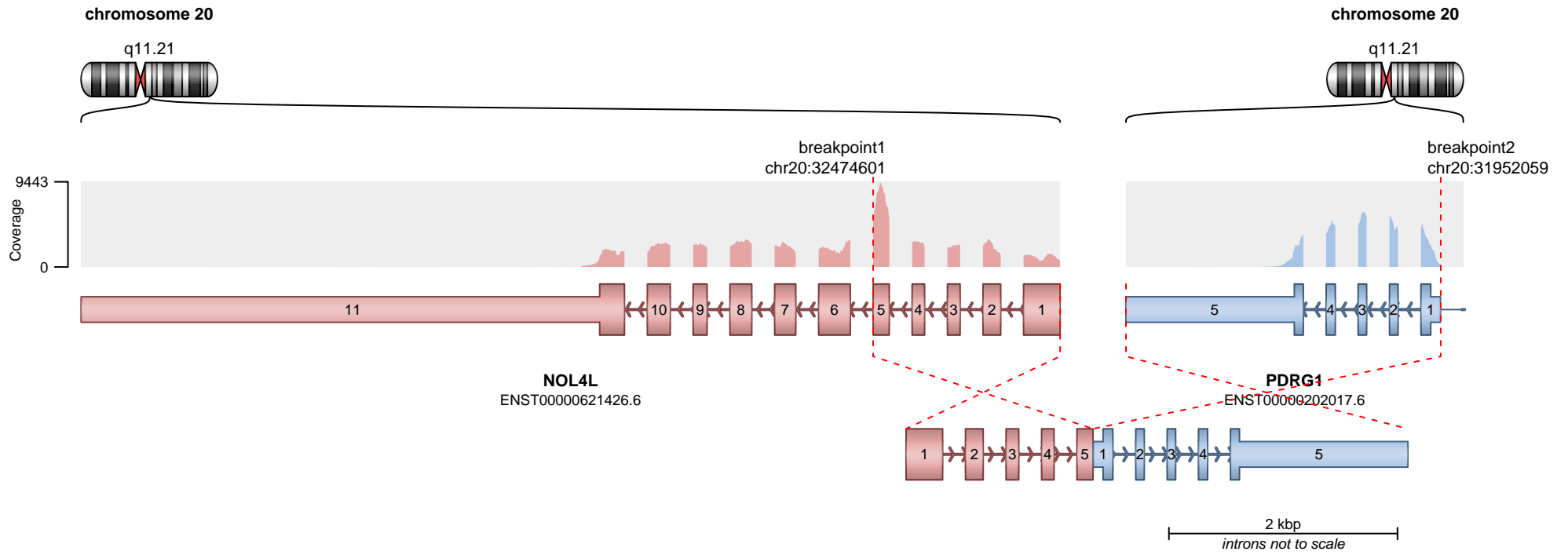
RETAINED PROTEIN DOMAINS
reading frame unclear



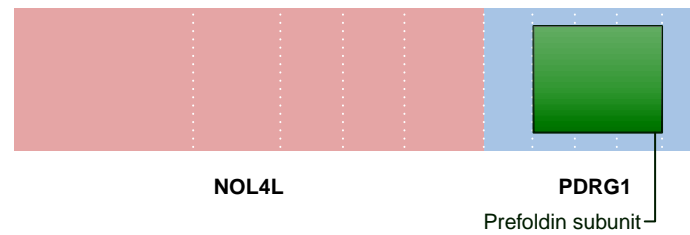
SUPPORTING READ COUNT

Split reads = 9
Discordant mates = 0

— translocation — deletion
— duplication — inversion



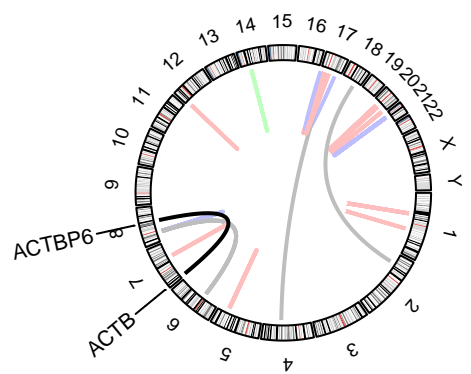
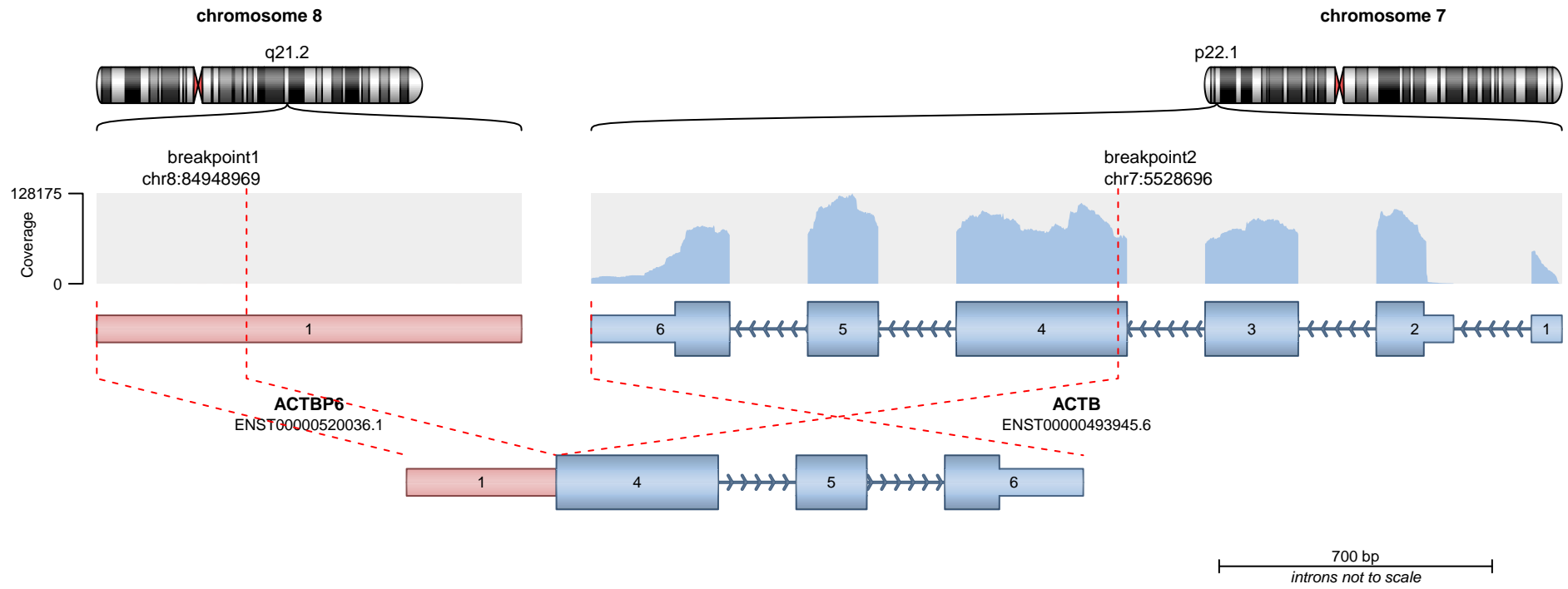
RETAINED PROTEIN DOMAINS
reading frame unclear



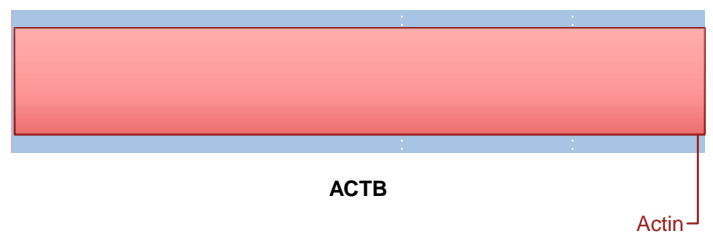
SUPPORTING READ COUNT

Split reads = 9
Discordant mates = 0

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

— translocation — deletion
— duplication — inversion