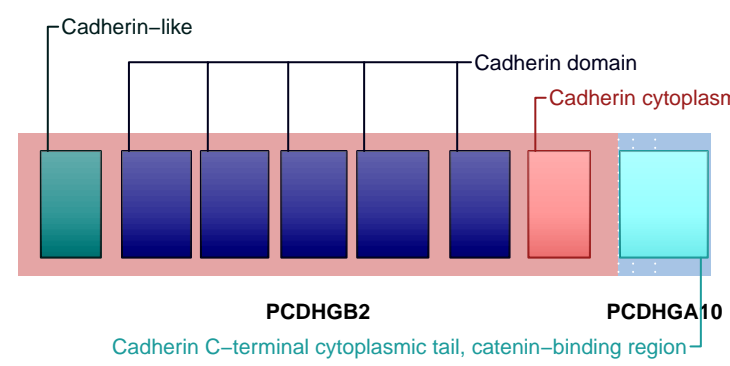


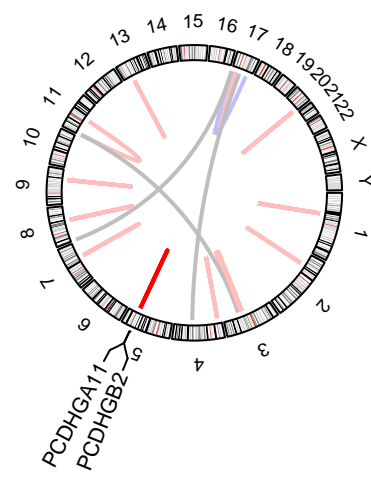
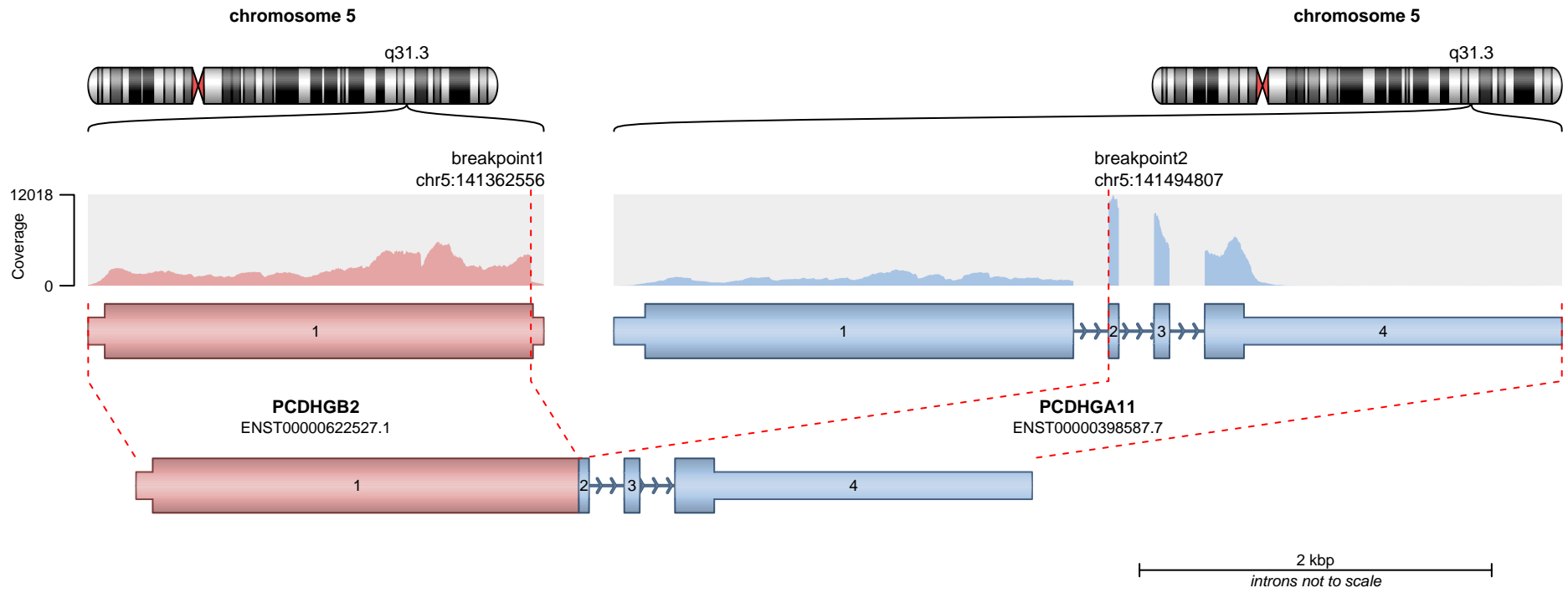
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

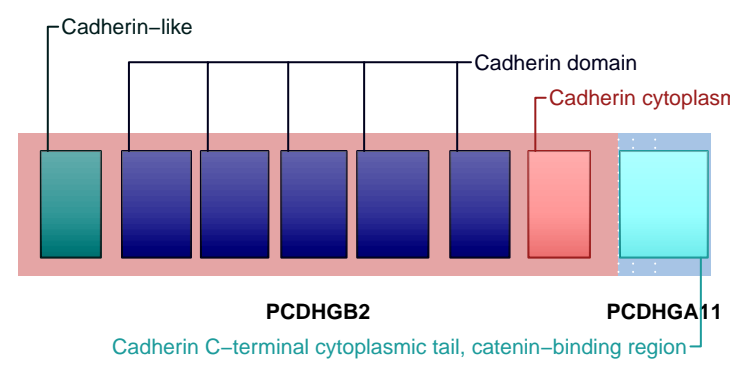
Split reads = 1181
Discordant mates = 5

- translocation
- duplication
- deletion
- inversion



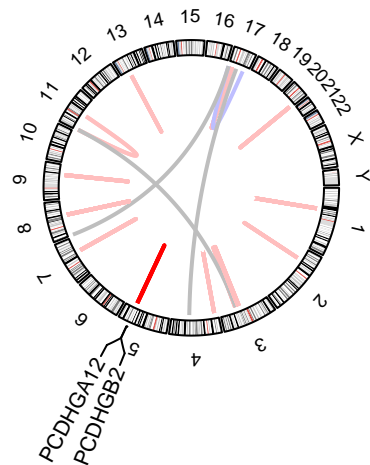
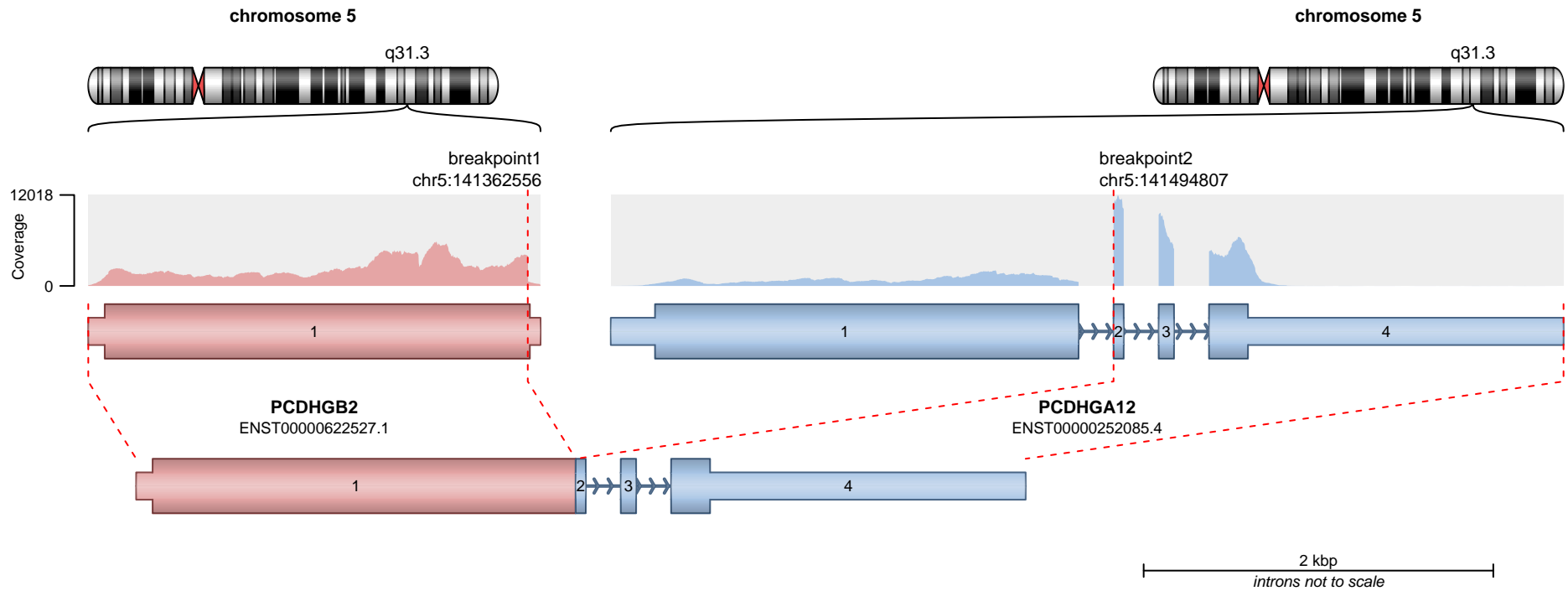
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear

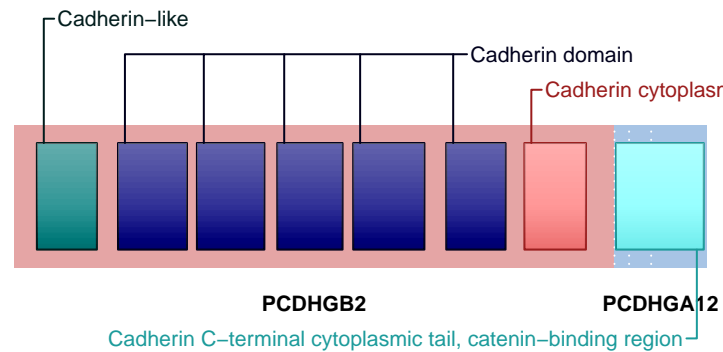


SUPPORTING READ COUNT

Split reads = 1181
Discordant mates = 5



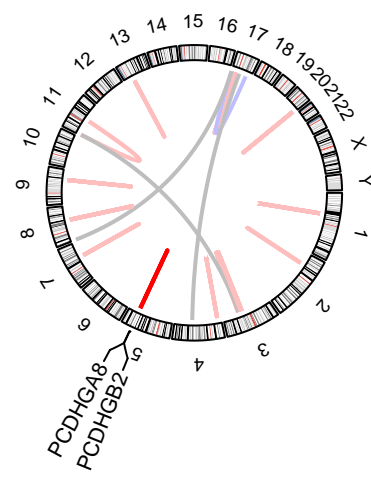
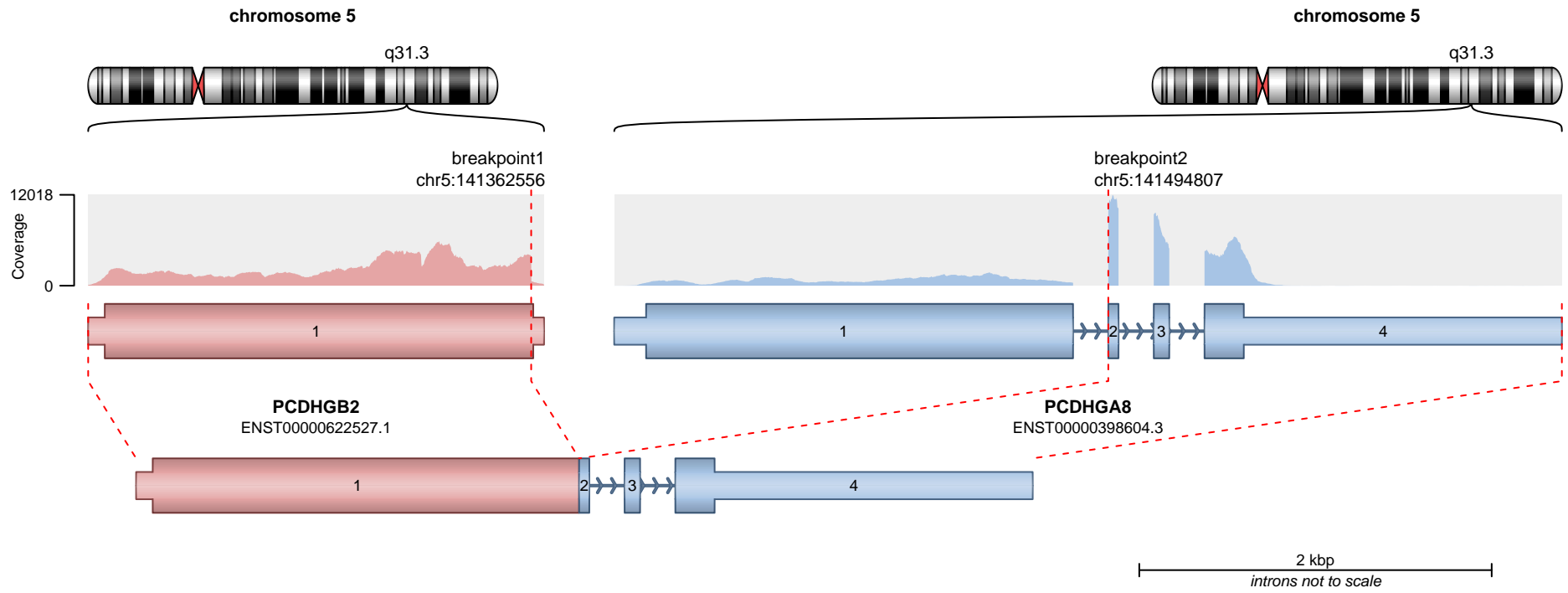
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

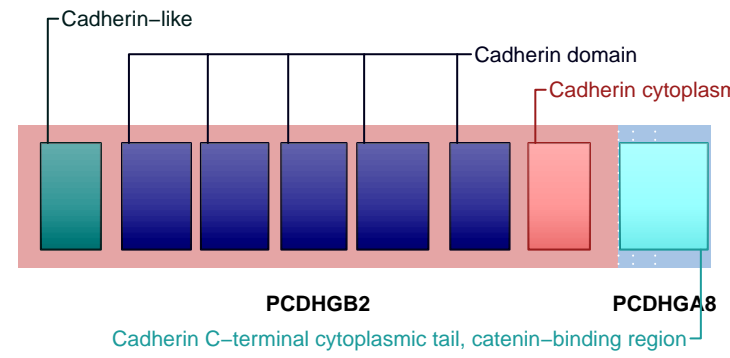
Split reads = 1181
Discordant mates = 5

— translocation — deletion
— duplication — inversion



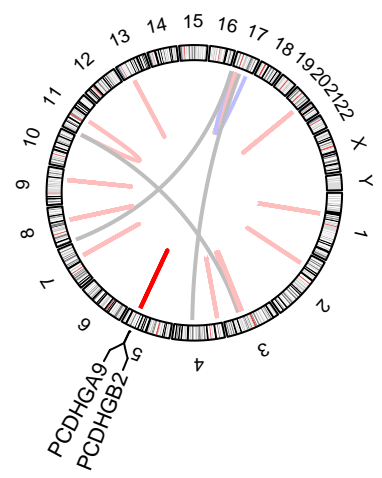
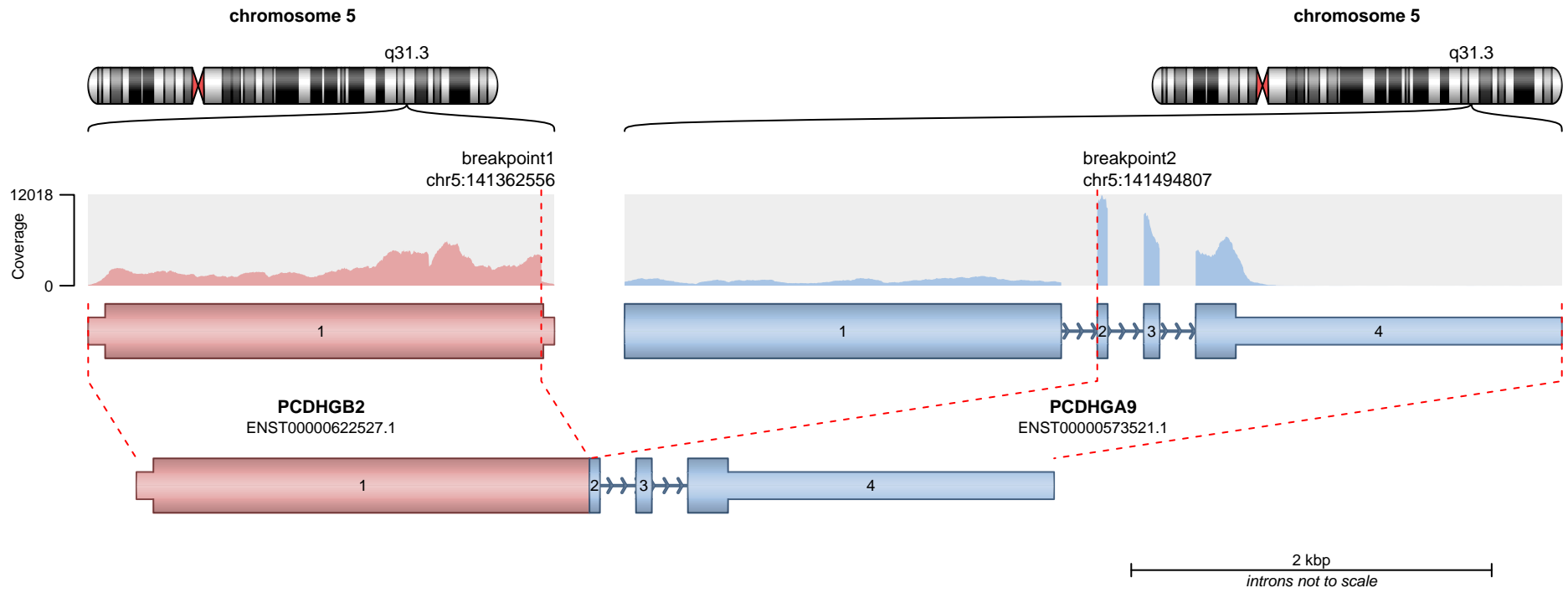
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear

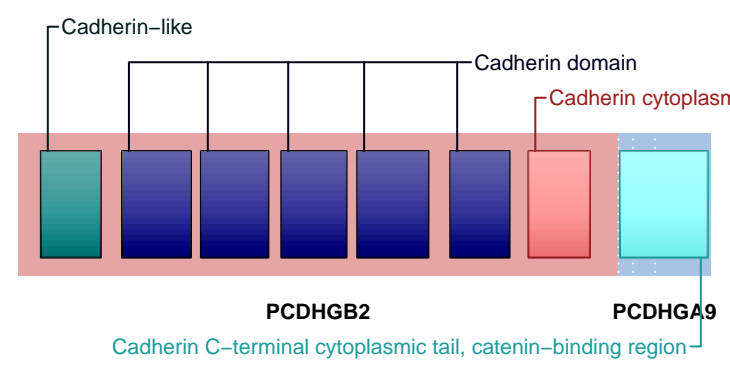


SUPPORTING READ COUNT

Split reads = 1181
Discordant mates = 5



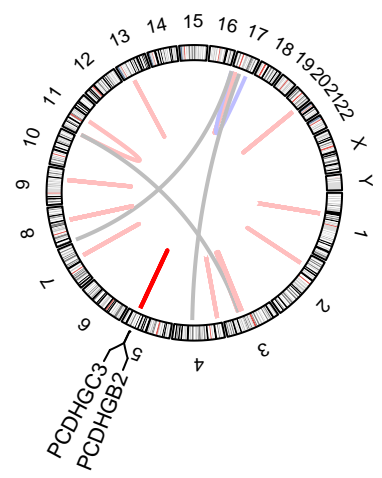
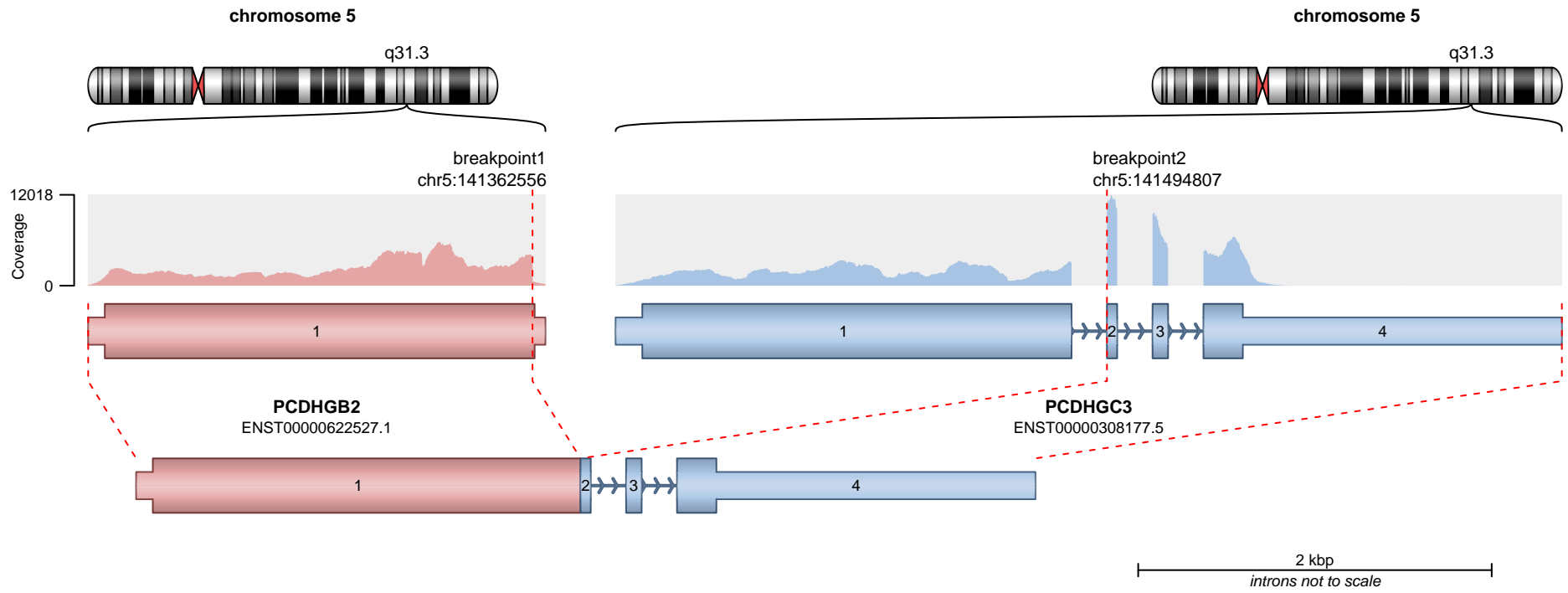
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

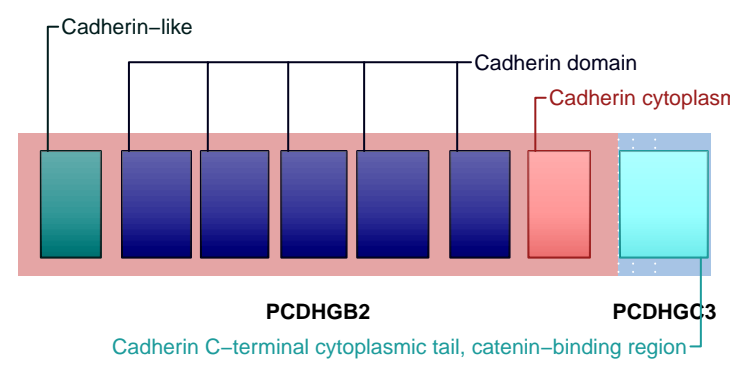
Split reads = 1181
Discordant mates = 5

- translocation
- duplication
- deletion
- inversion



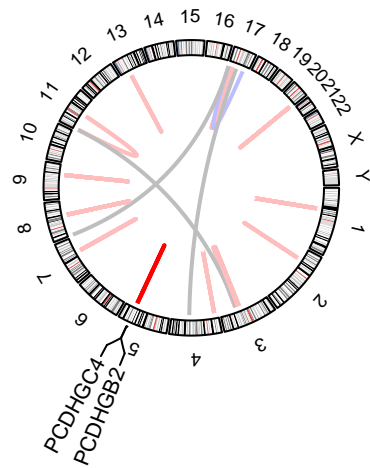
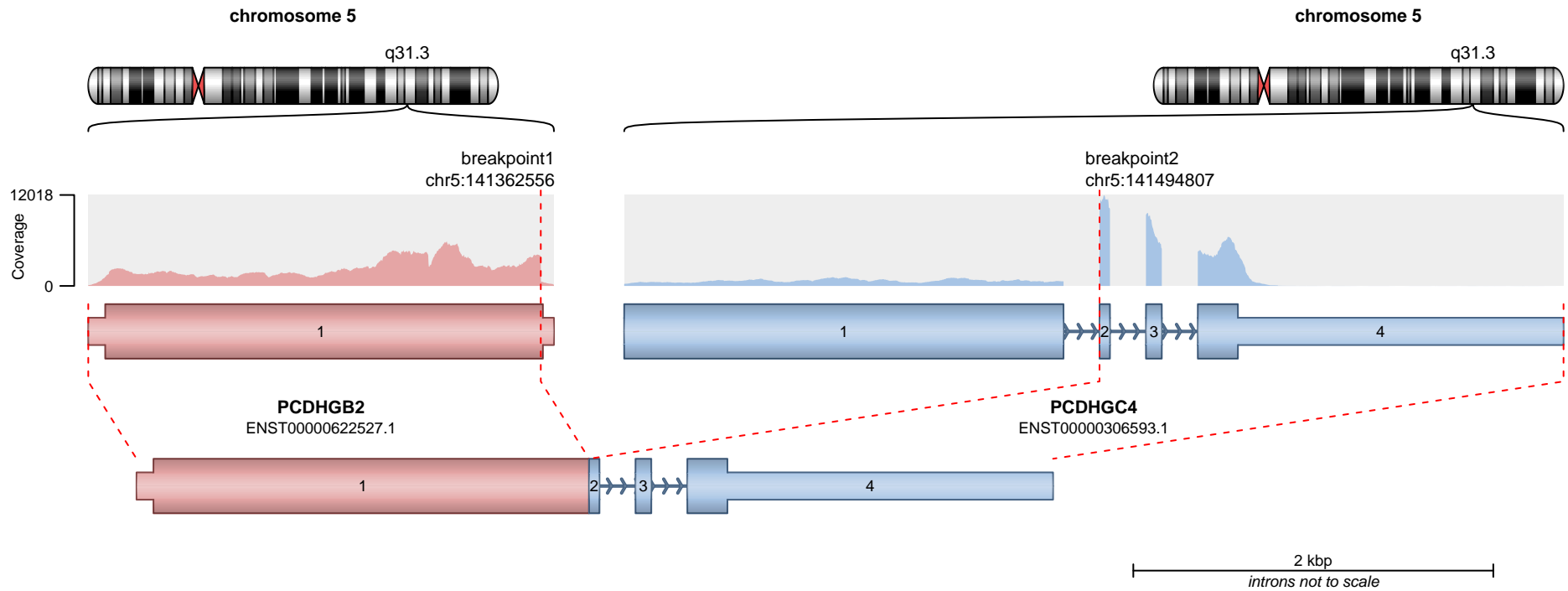
— translocation — deletion
 — duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear

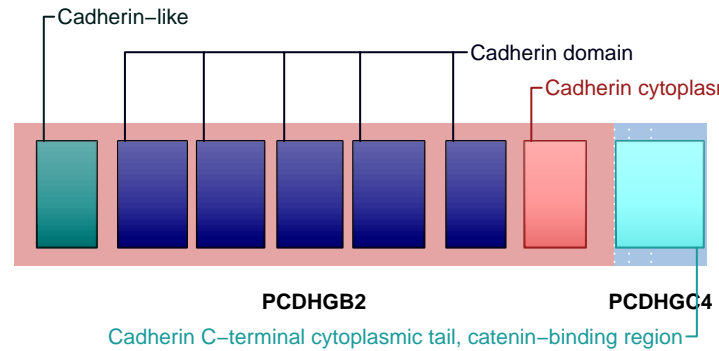


SUPPORTING READ COUNT

Split reads = 1181
 Discordant mates = 5



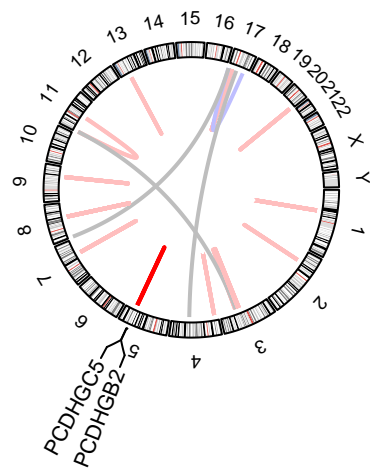
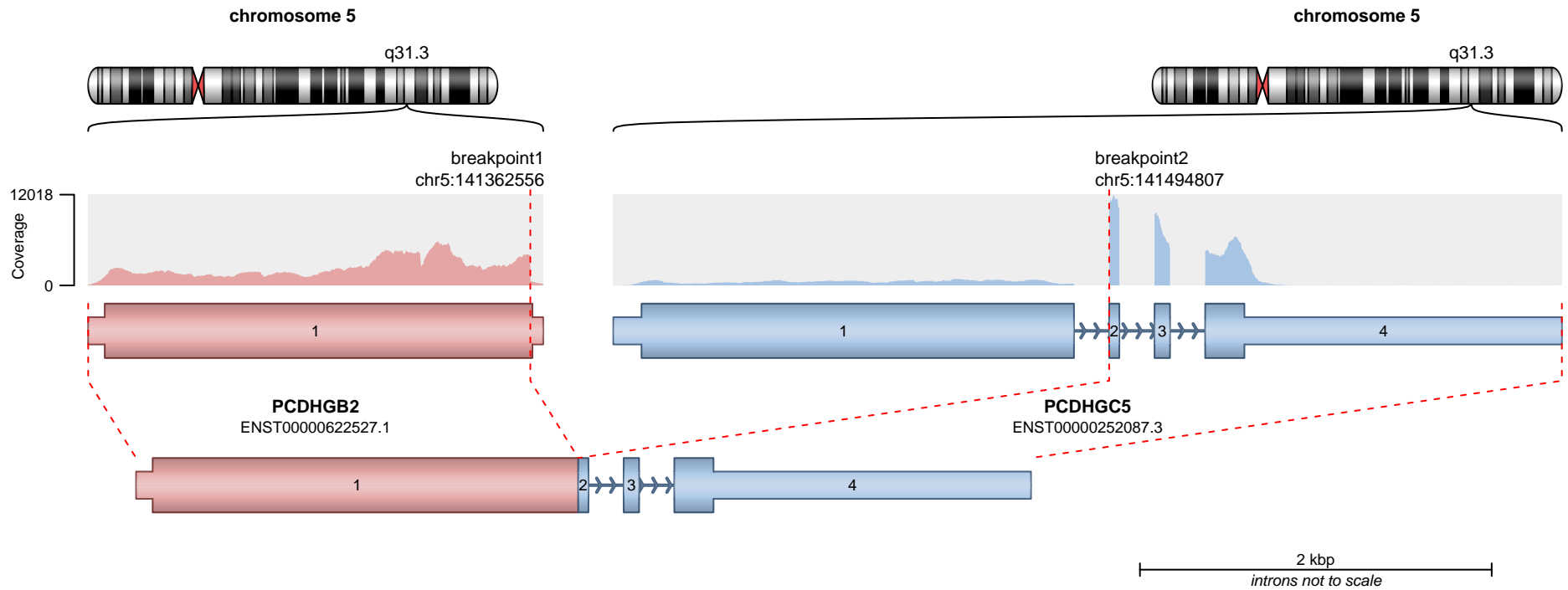
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1181
Discordant mates = 5

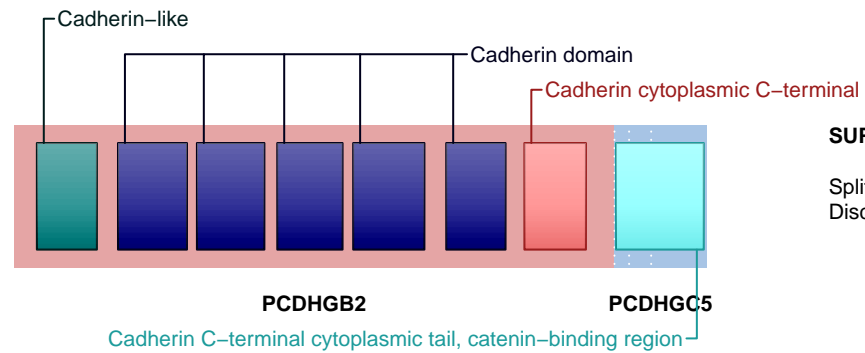
— translocation — deletion
— duplication — inversion



— translocation — deletion
— duplication — inversion

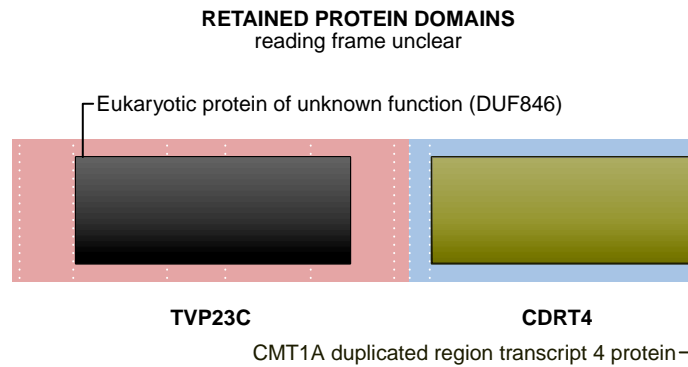
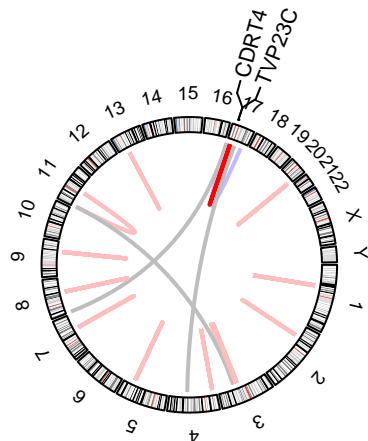
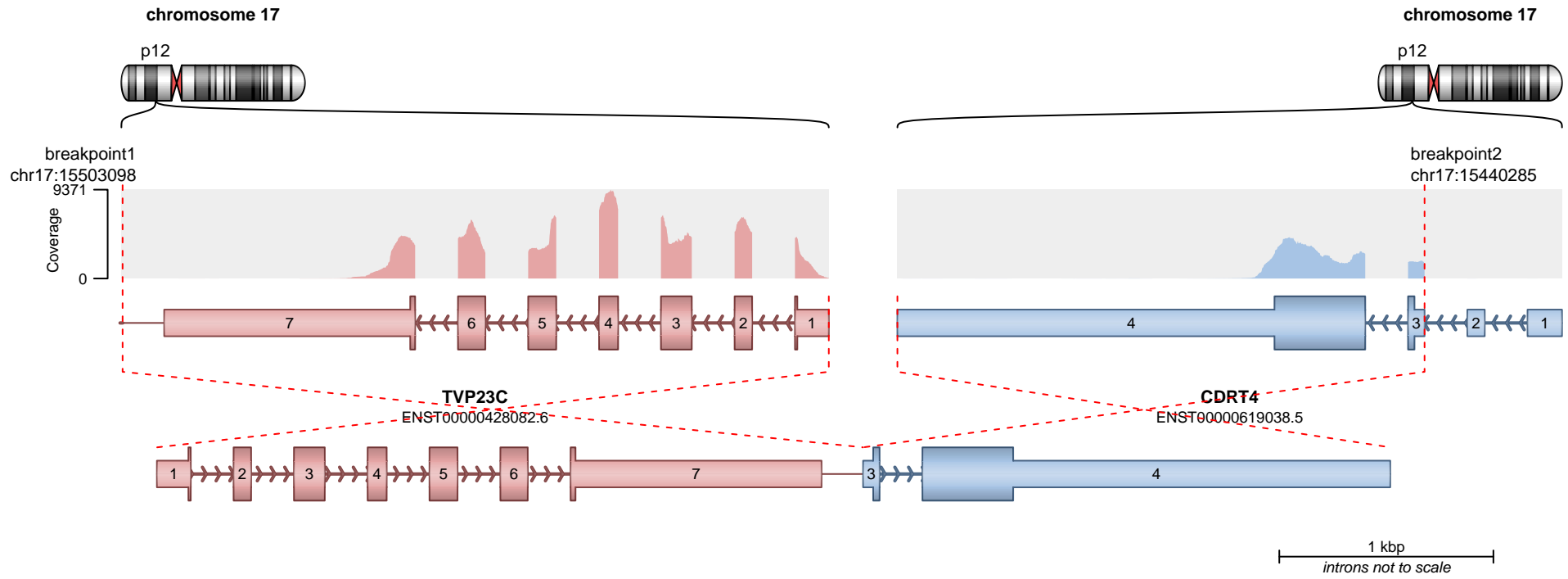
RETAINED PROTEIN DOMAINS

reading frame unclear



SUPPORTING READ COUNT

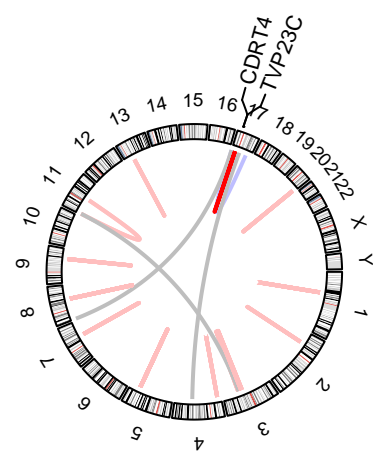
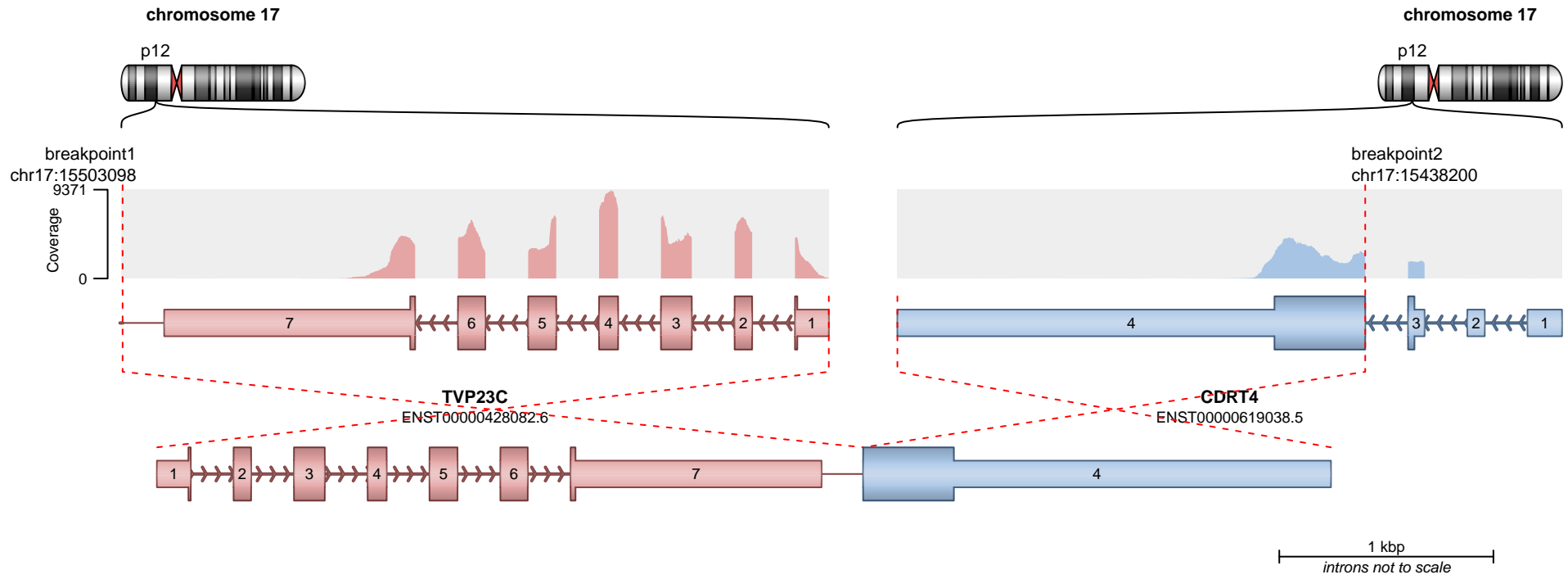
Split reads = 1181
Discordant mates = 5



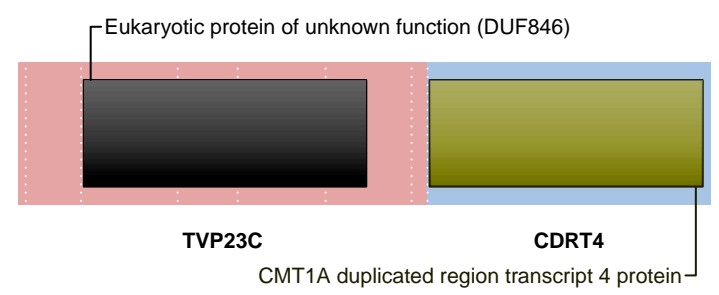
SUPPORTING READ COUNT

Split reads = 326
Discordant mates = 6

- translocation
- duplication
- deletion
- inversion



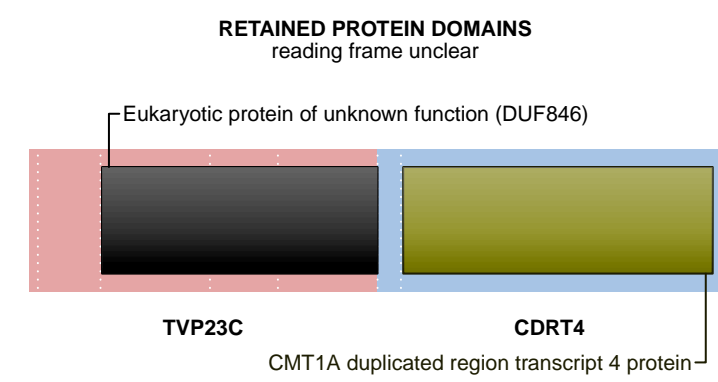
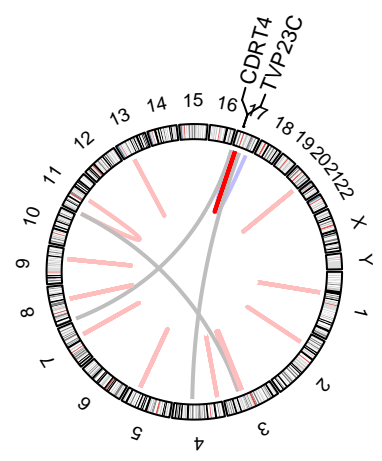
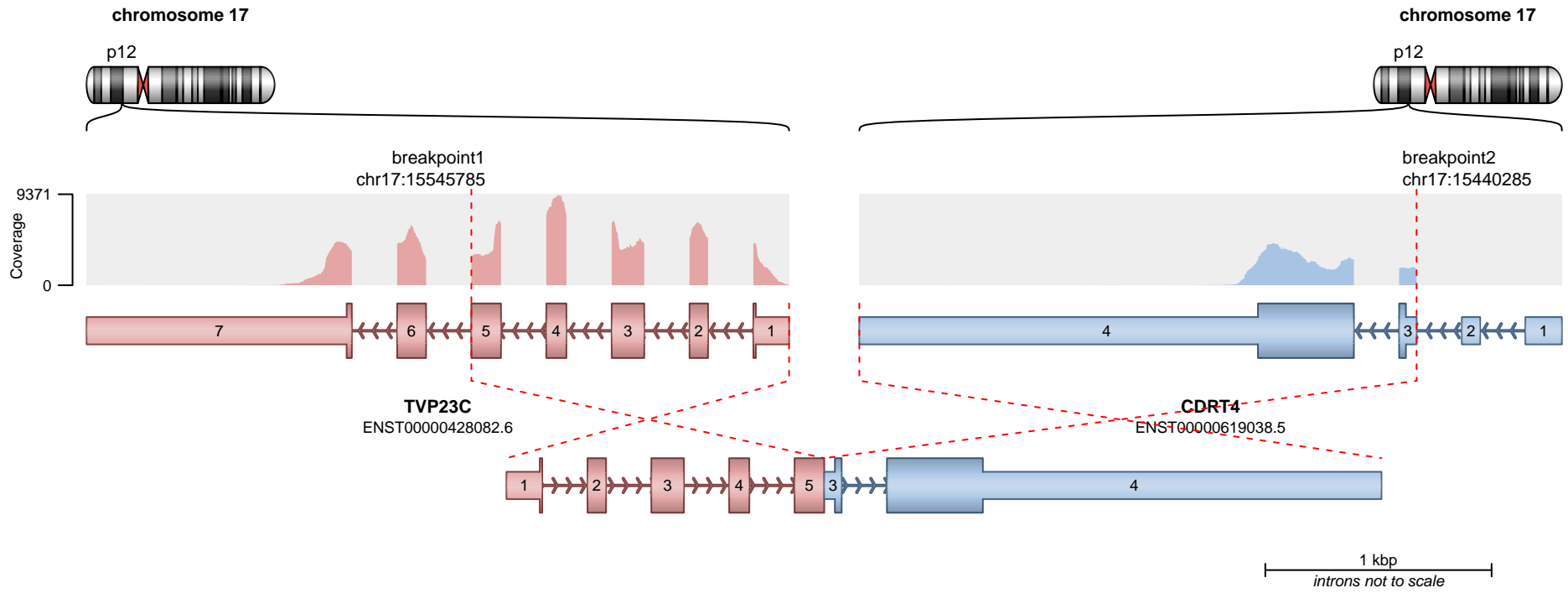
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 174
Discordant mates = 1

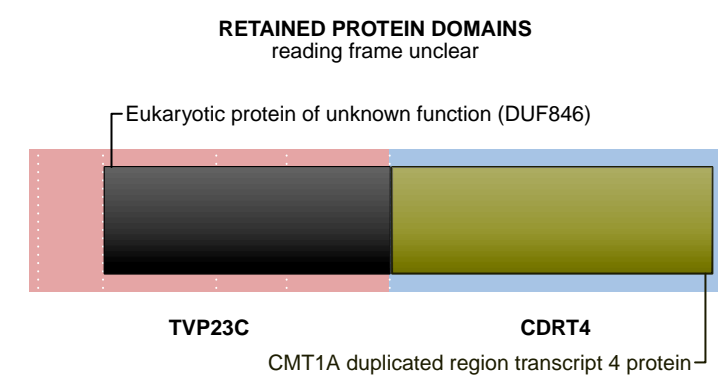
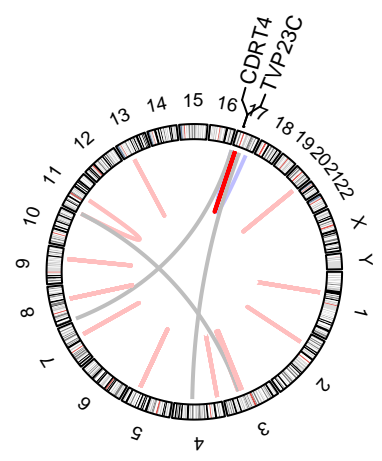
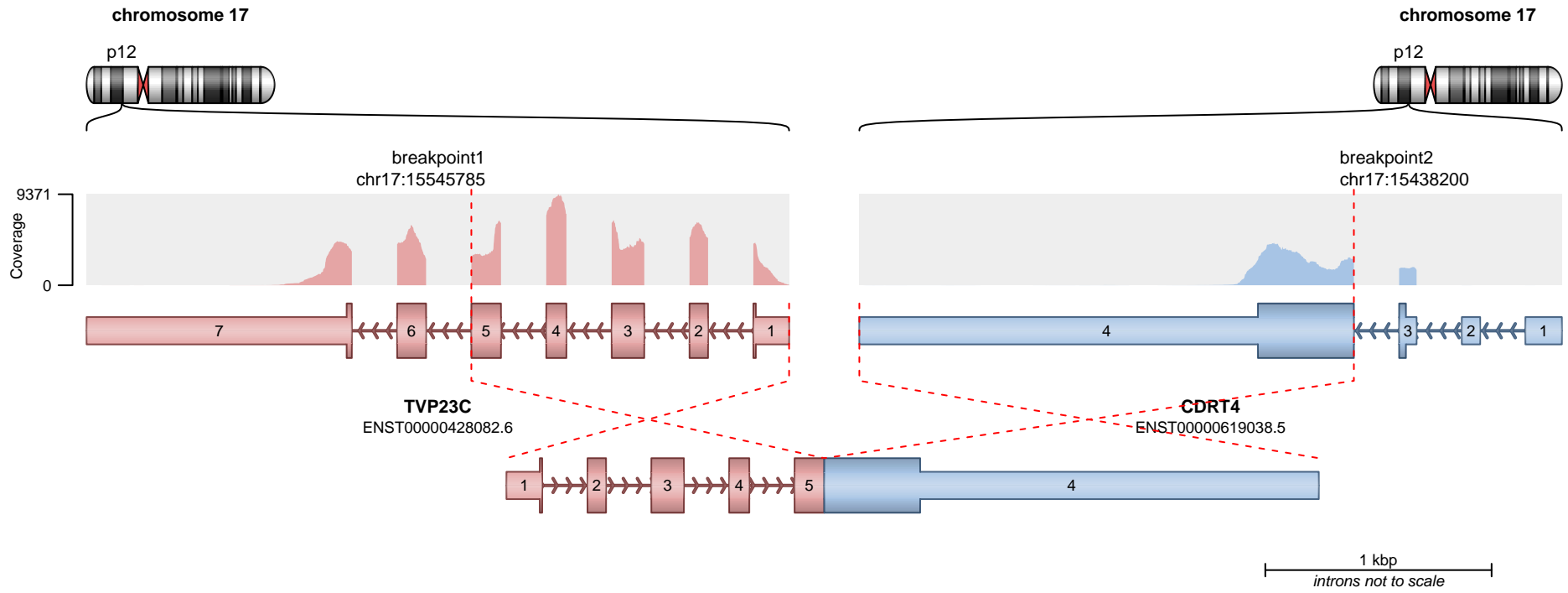
- translocation
- duplication
- deletion
- inversion



SUPPORTING READ COUNT

Split reads = 168
Discordant mates = 3

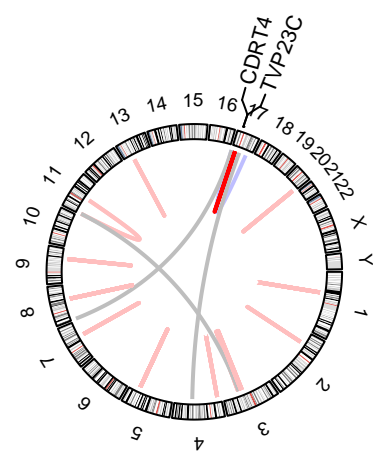
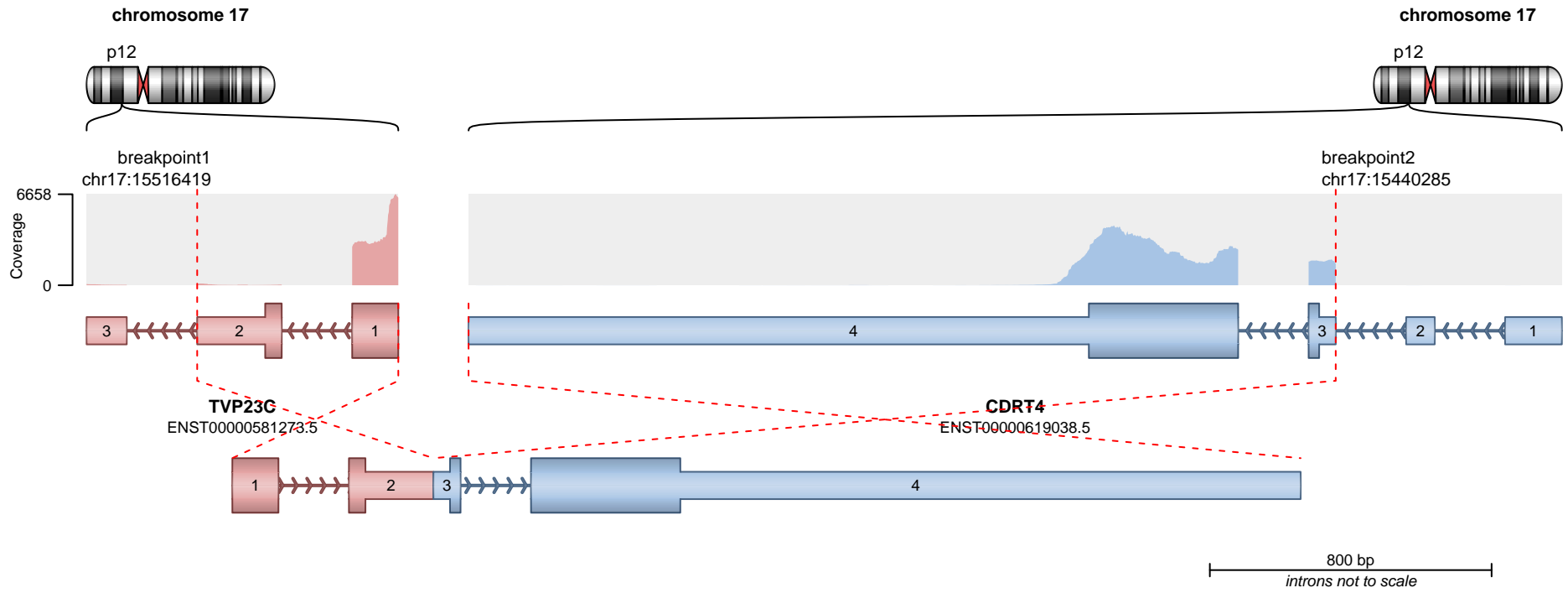
— translocation — deletion
— duplication — inversion



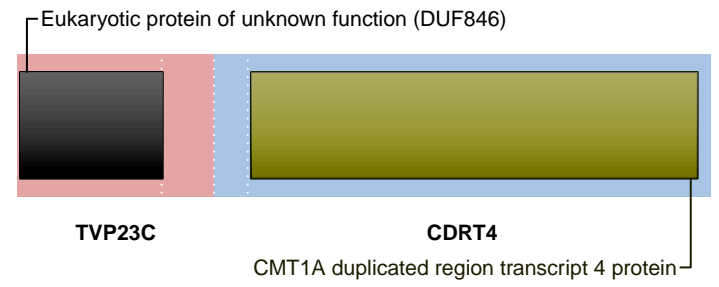
SUPPORTING READ COUNT

Split reads = 93
Discordant mates = 0

— translocation — deletion
— duplication — inversion



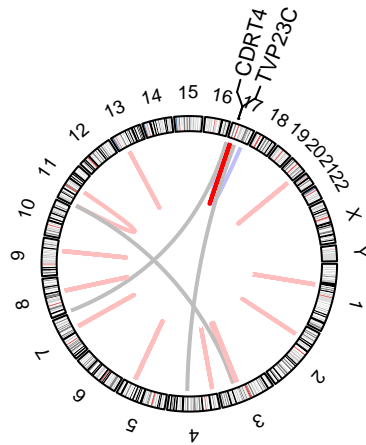
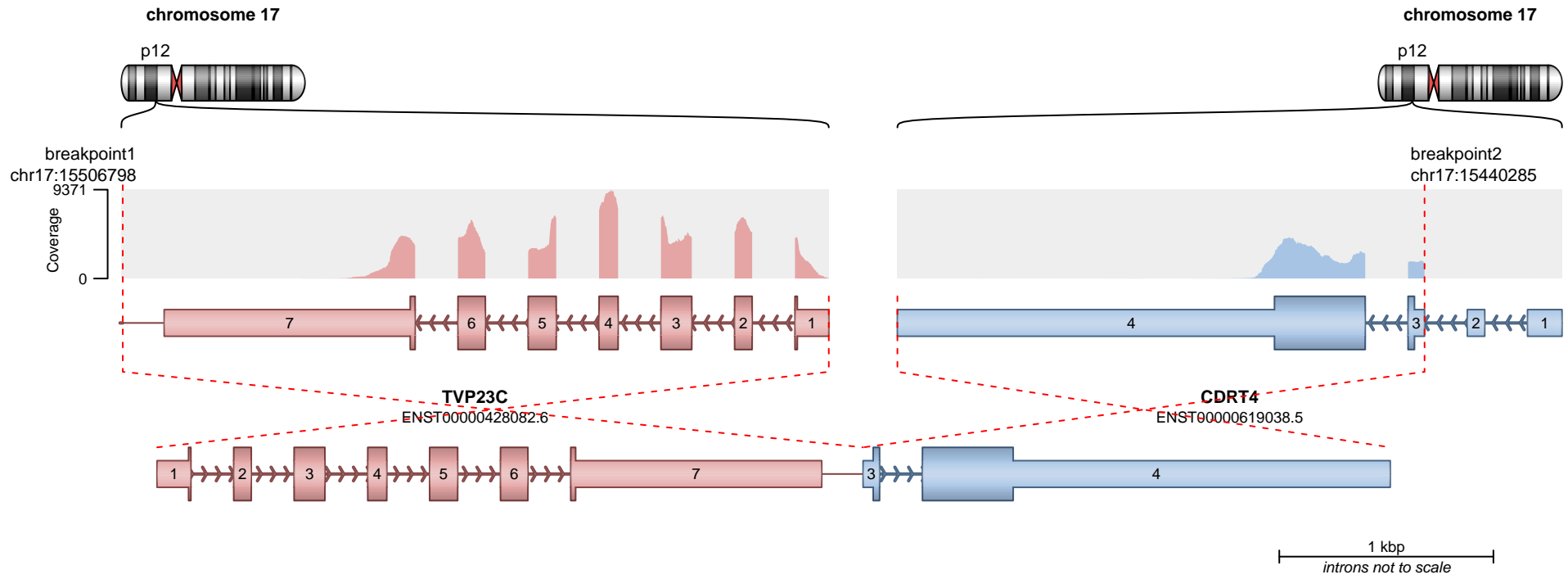
RETAINED PROTEIN DOMAINS
reading frame unclear



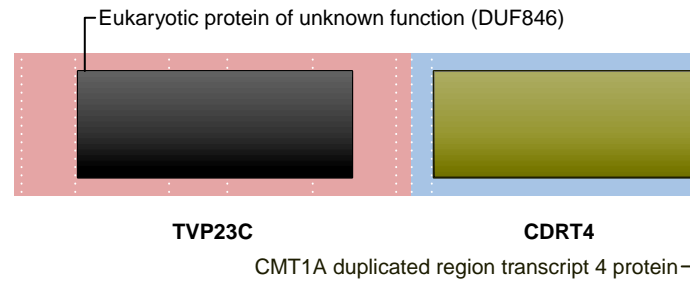
SUPPORTING READ COUNT

Split reads = 17
Discordant mates = 3

- translocation
- deletion
- duplication
- inversion



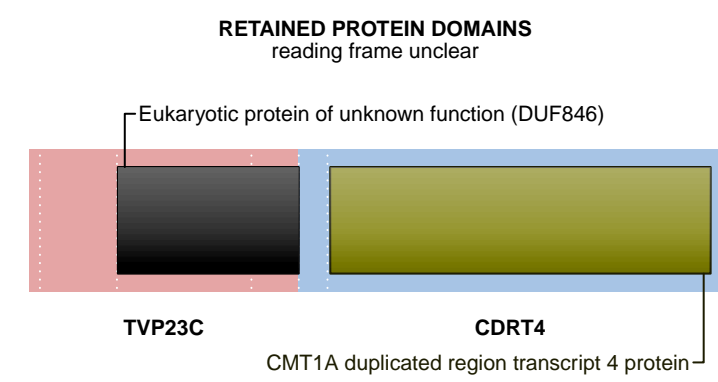
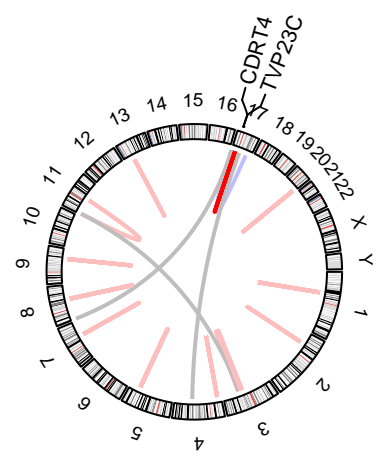
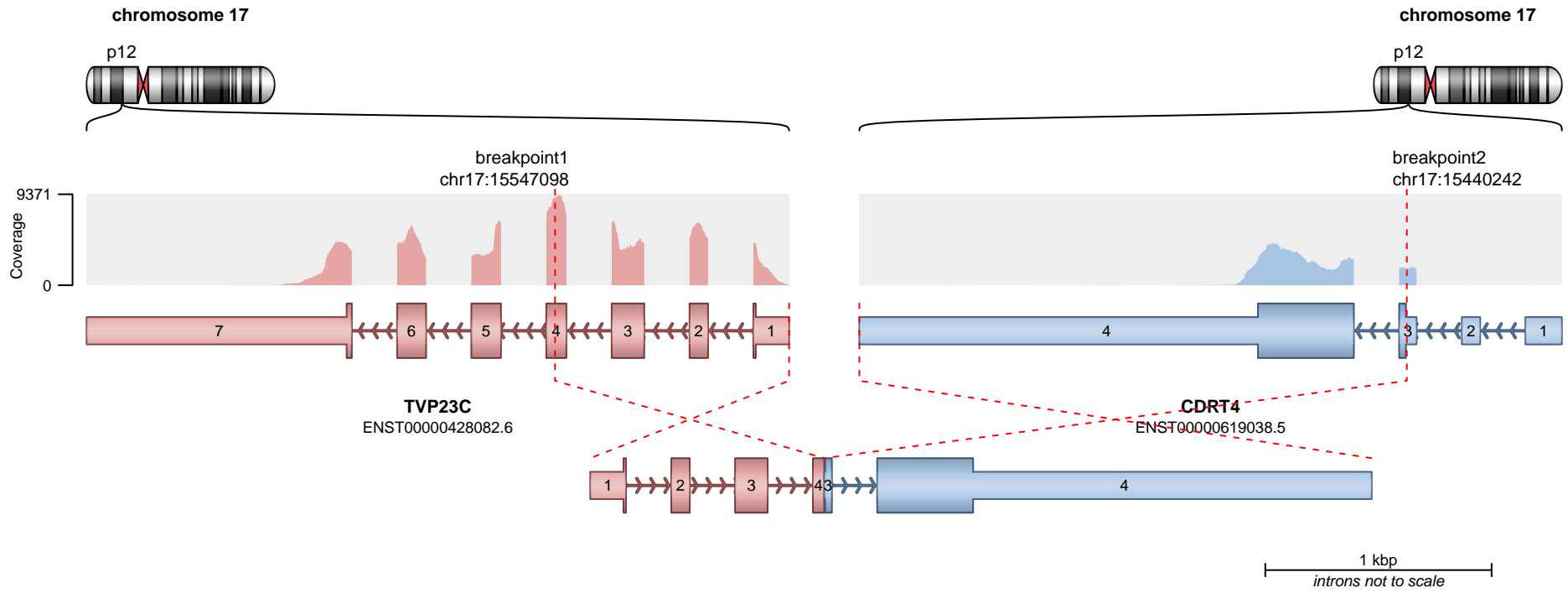
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 4

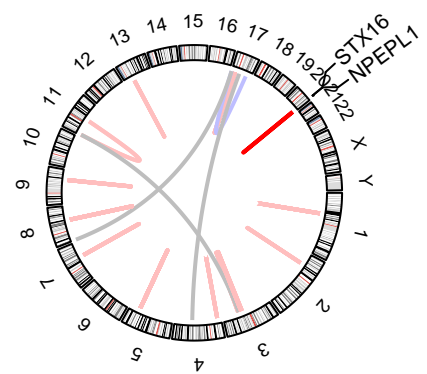
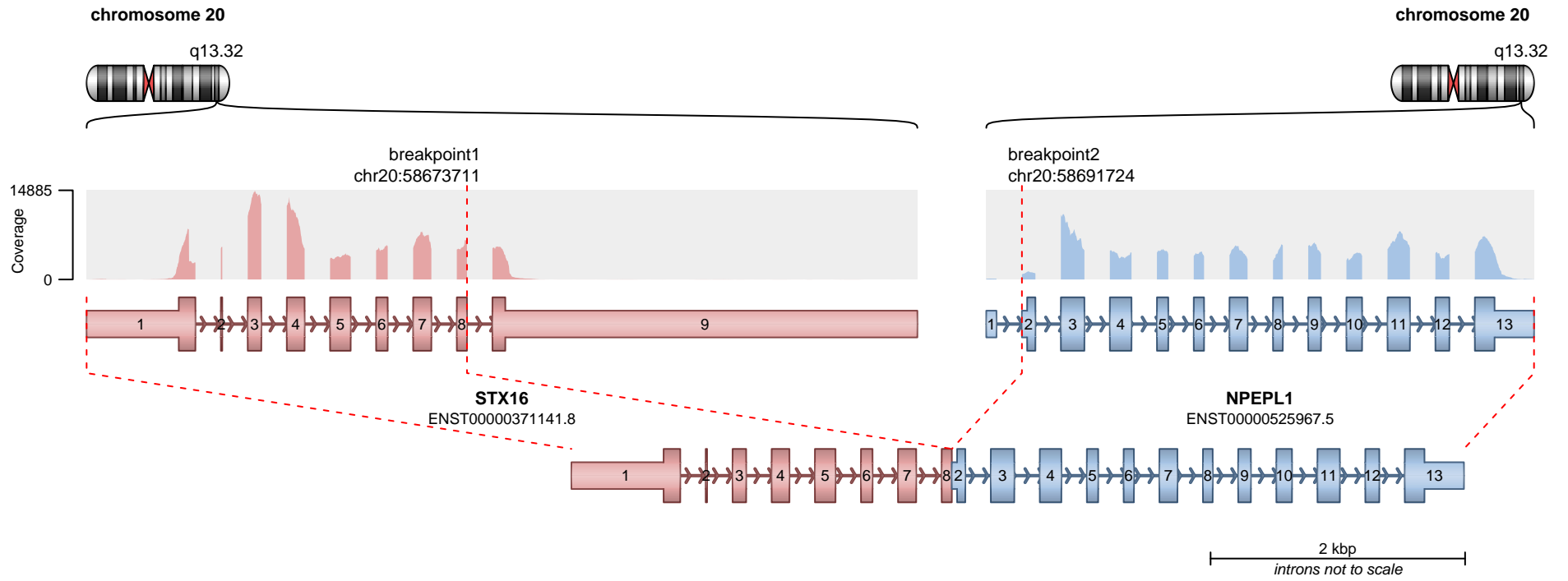
- translocation
- duplication
- deletion
- inversion



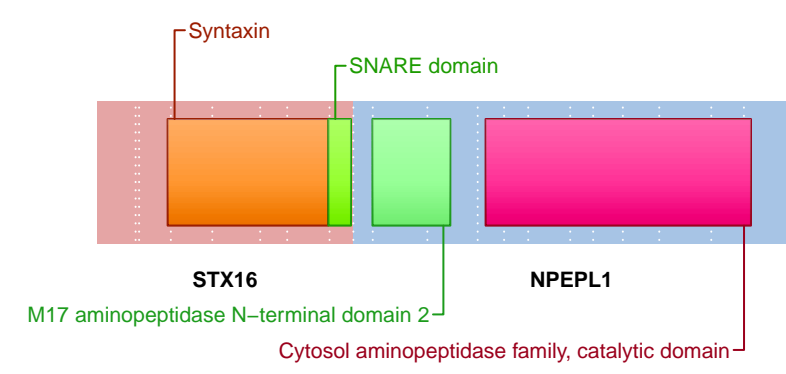
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

— translocation — deletion
— duplication — inversion



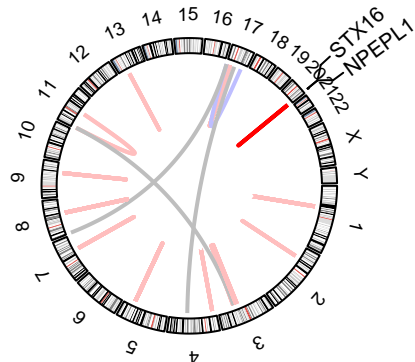
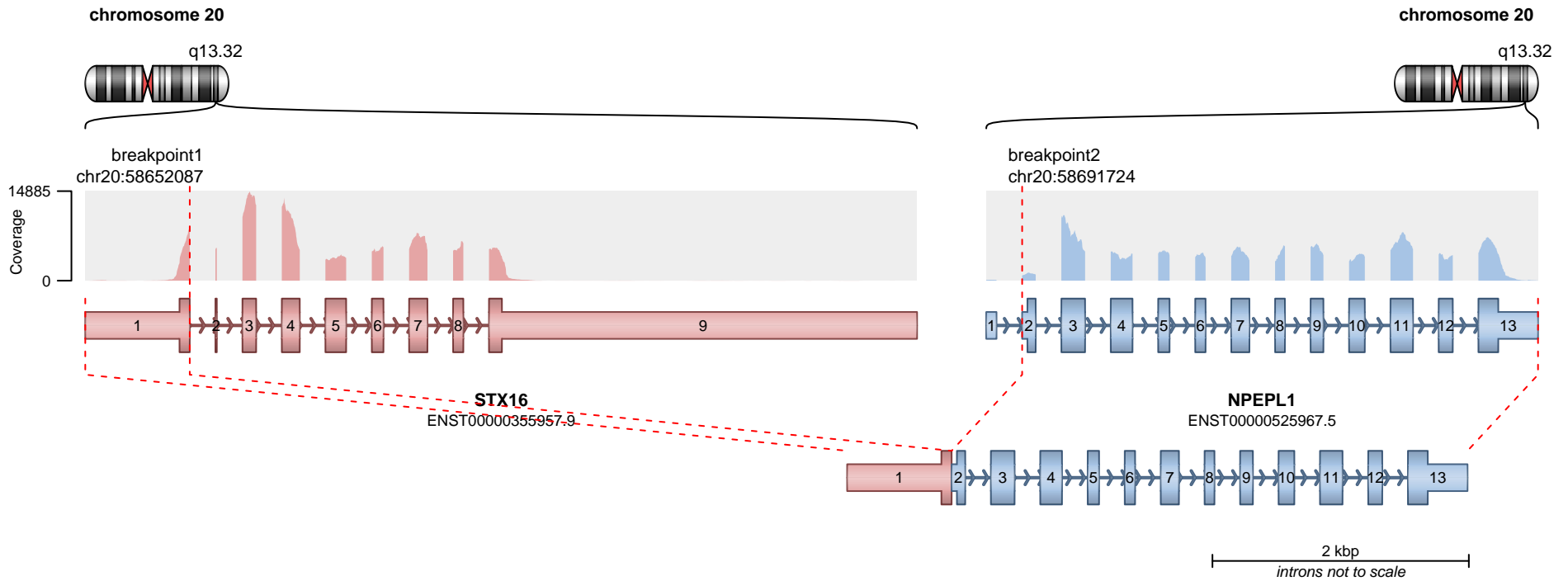
RETAINED PROTEIN DOMAINS
reading frame unclear



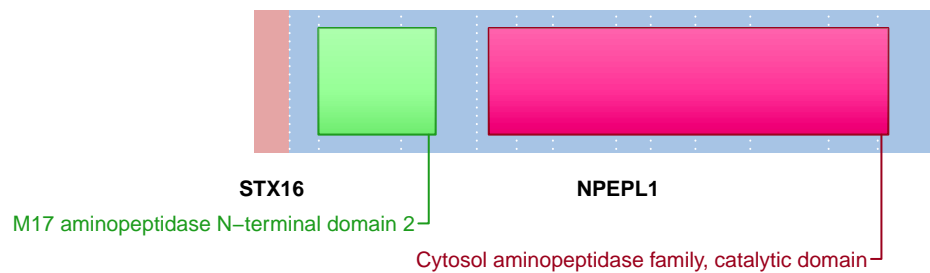
SUPPORTING READ COUNT

Split reads = 180
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



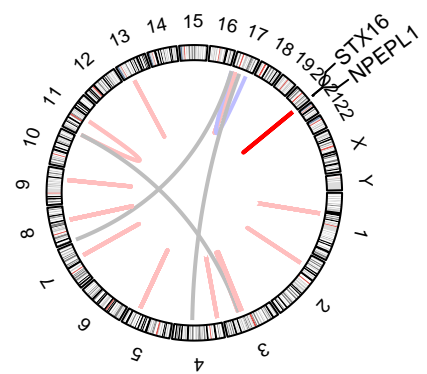
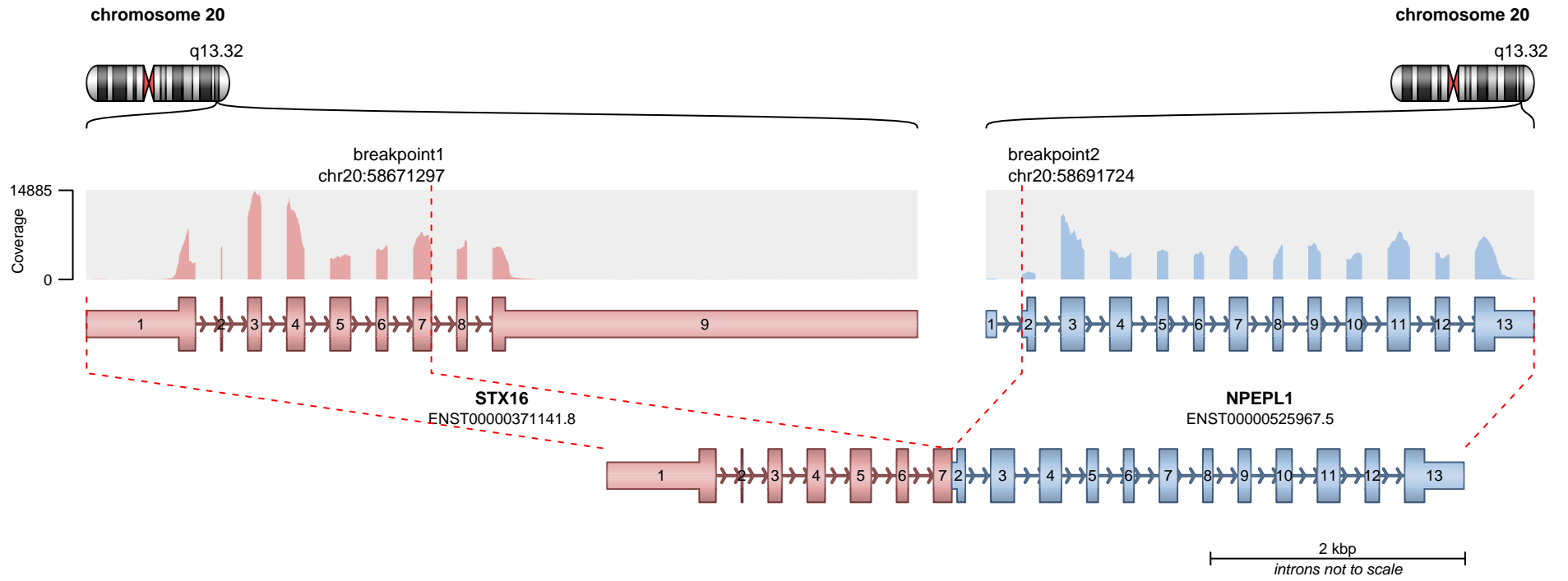
RETAINED PROTEIN DOMAINS
reading frame unclear



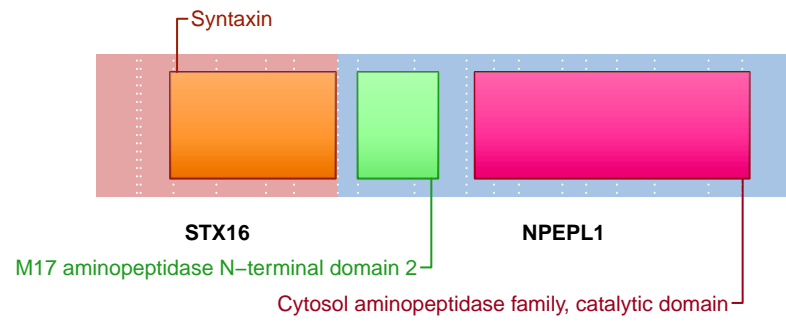
SUPPORTING READ COUNT

Split reads = 11
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



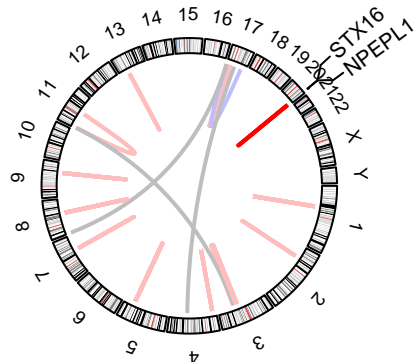
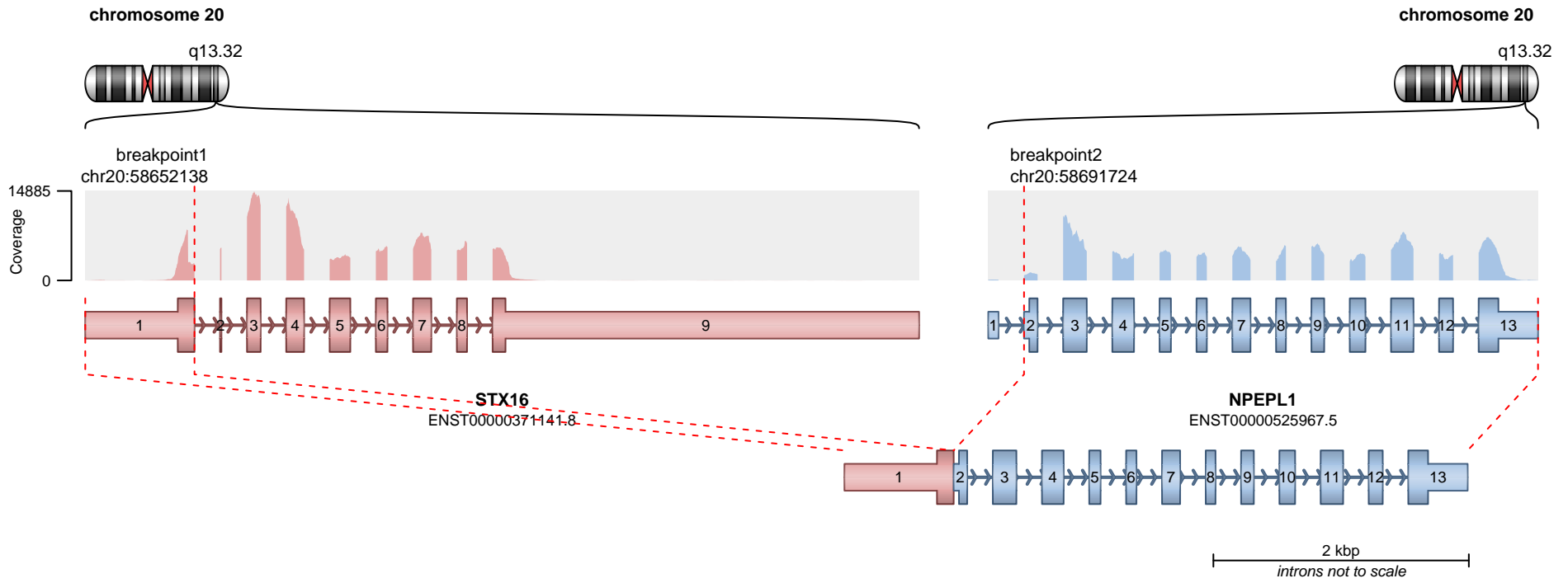
RETAINED PROTEIN DOMAINS
reading frame unclear



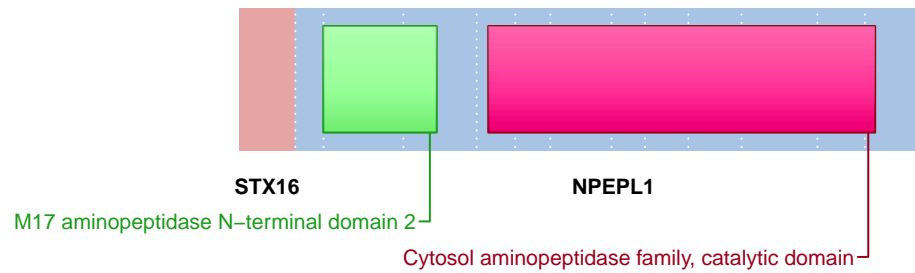
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



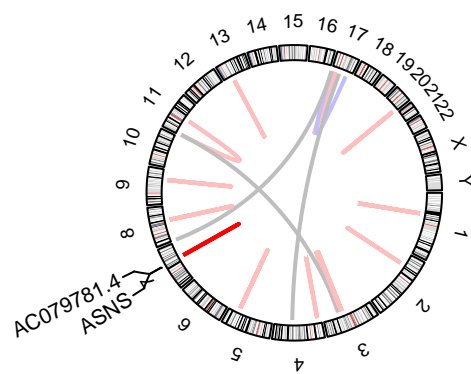
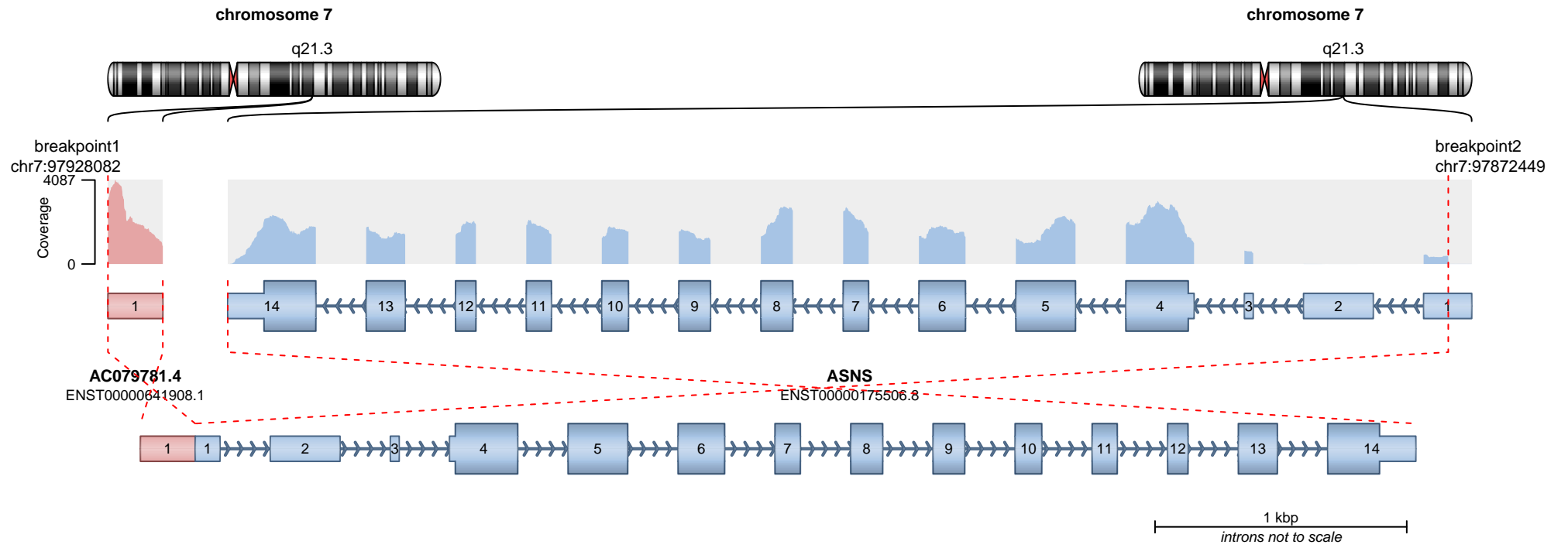
RETAINED PROTEIN DOMAINS
reading frame unclear



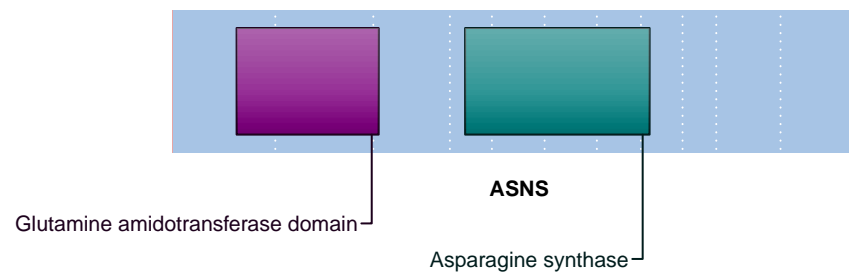
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



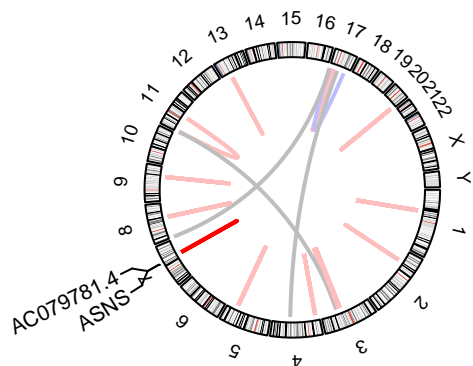
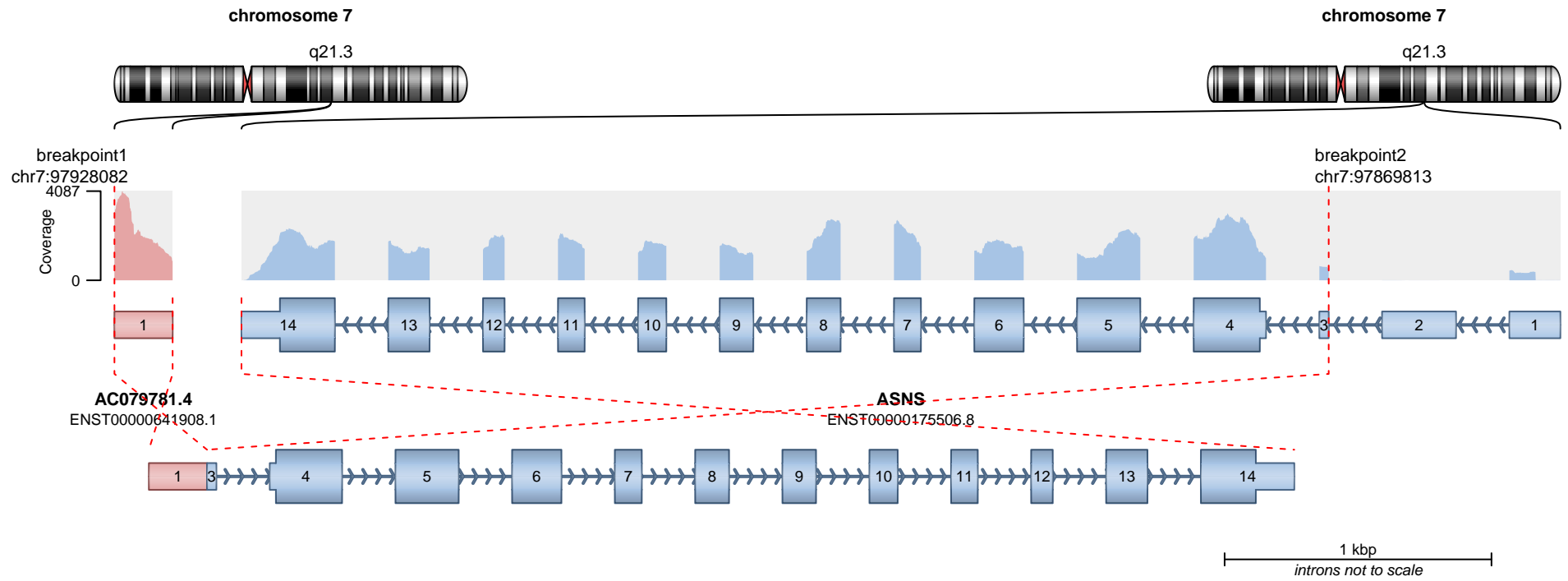
RETAINED PROTEIN DOMAINS
reading frame unclear



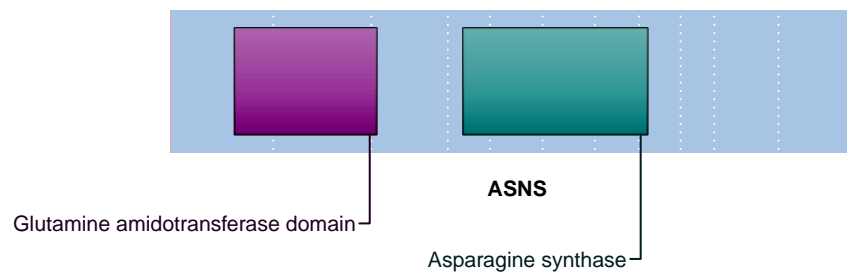
SUPPORTING READ COUNT

Split reads = 171
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



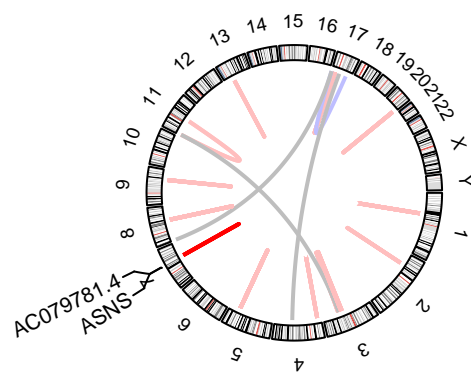
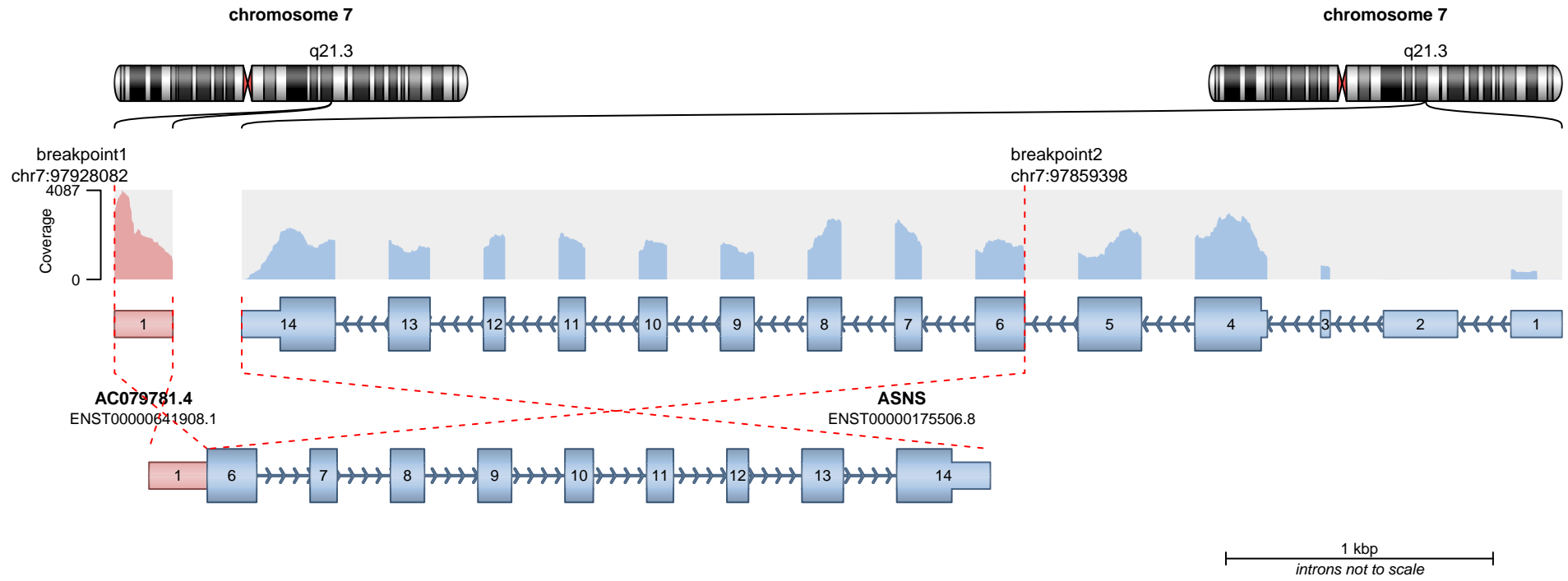
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

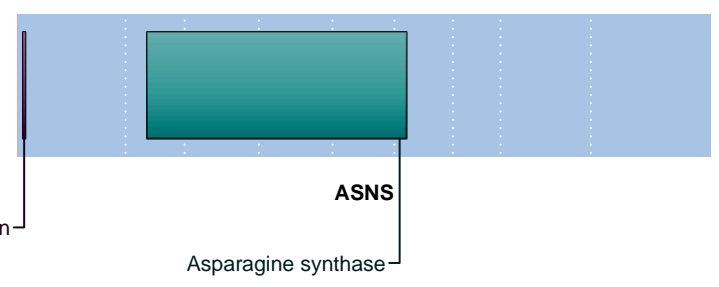
Split reads = 18
Discordant mates = 0

— translocation — deletion
— duplication — inversion



Glutamine amidotransferase domain

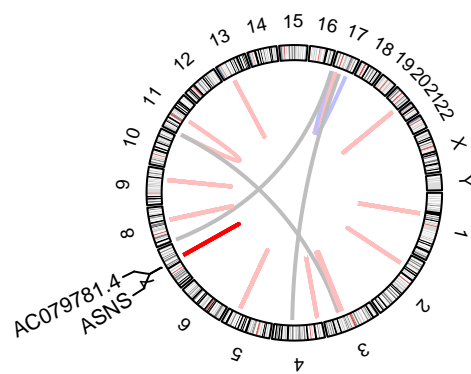
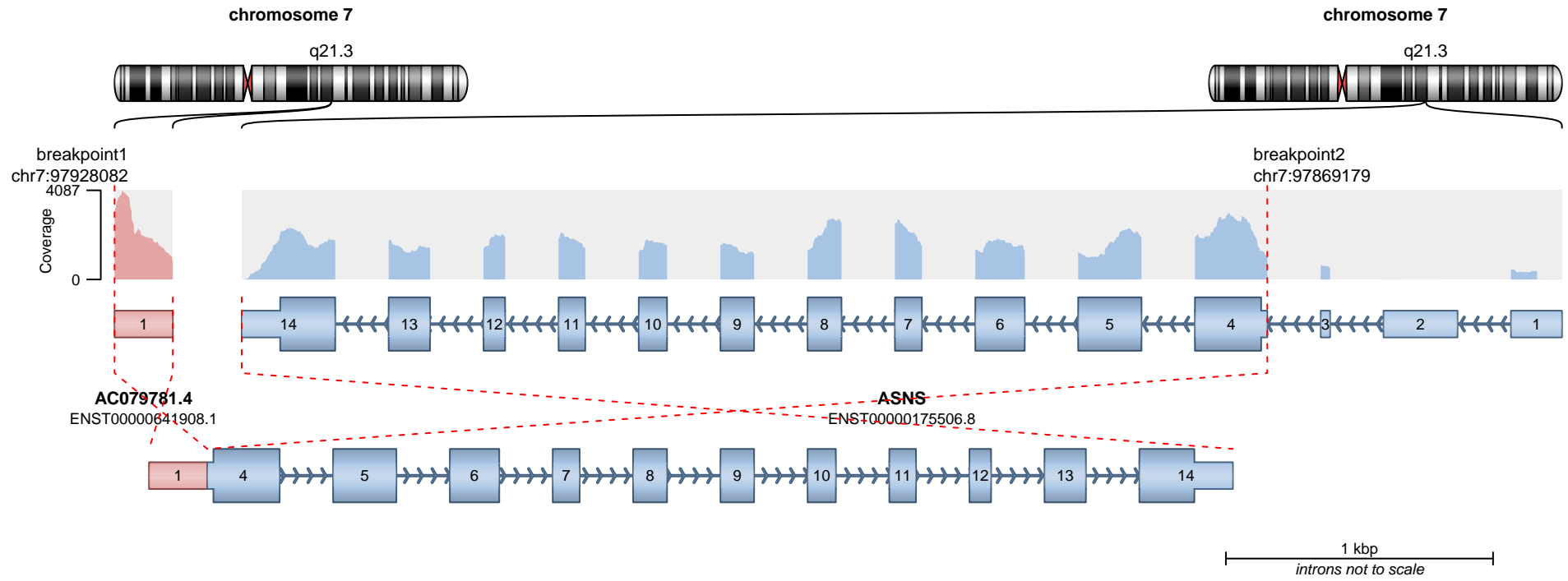
RETAINED PROTEIN DOMAINS
reading frame unclear



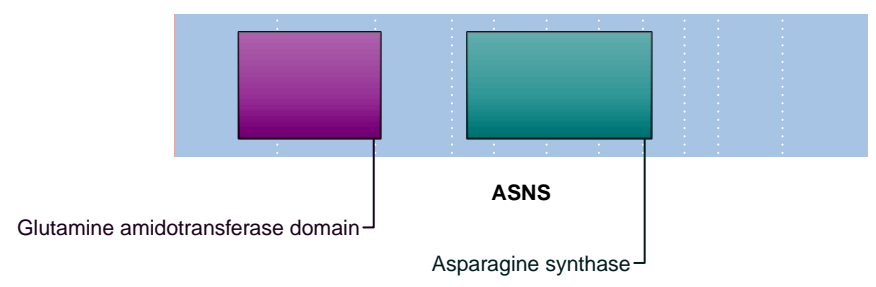
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



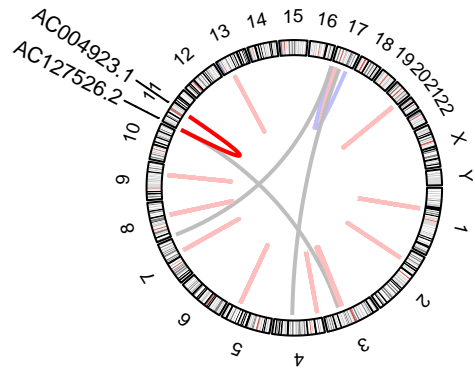
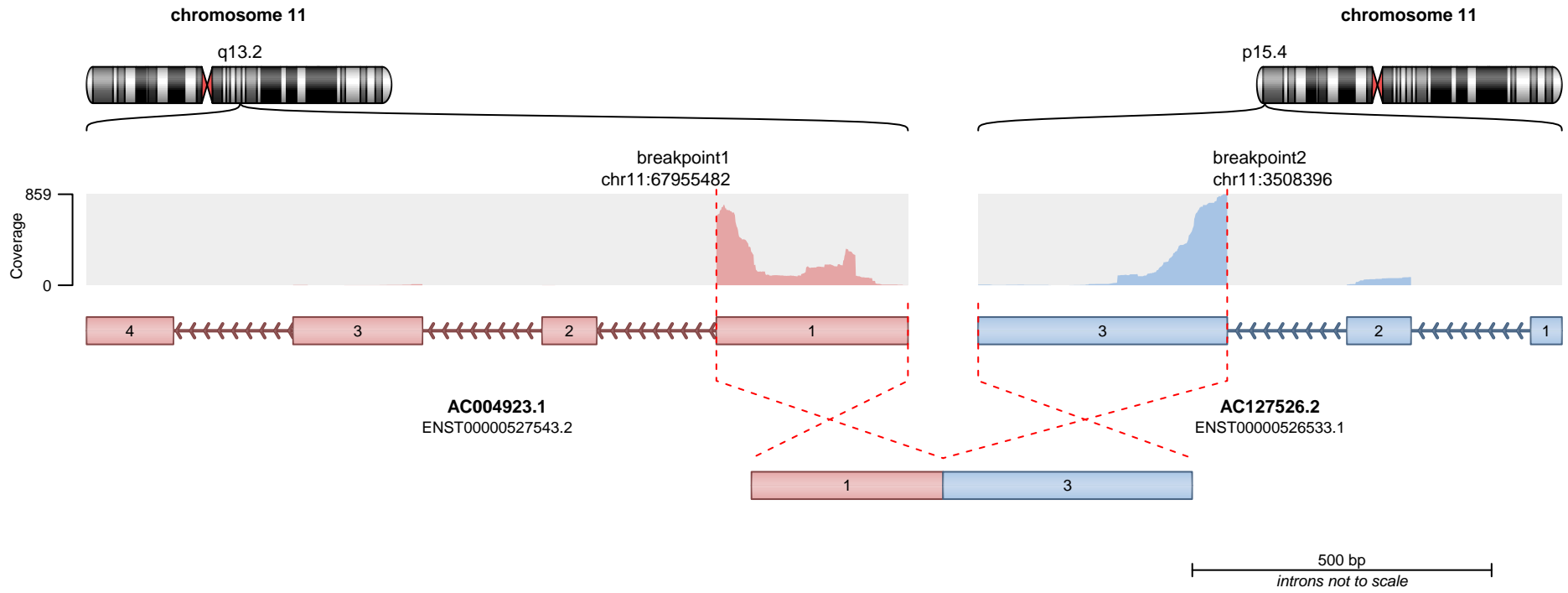
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

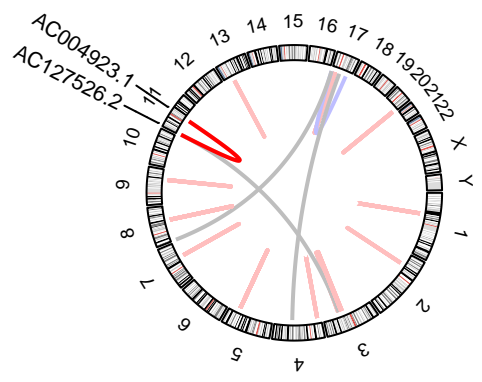
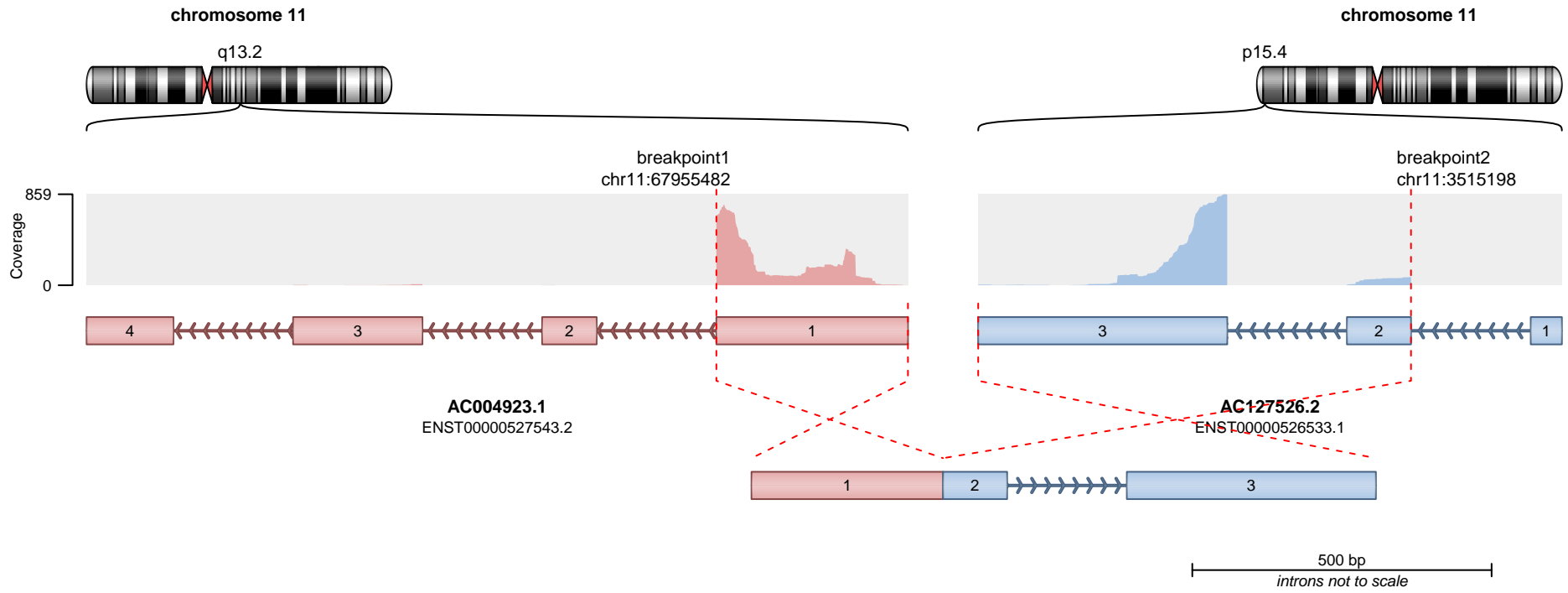


— translocation — deletion
— duplication — inversion

Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 162
Discordant mates = 0

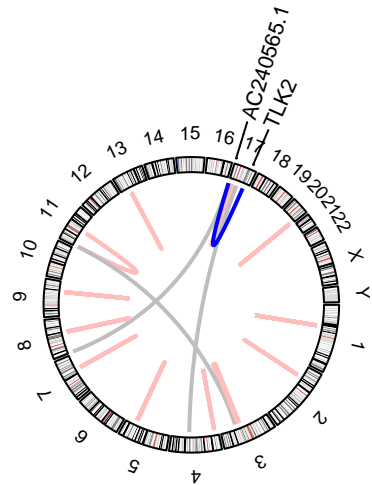
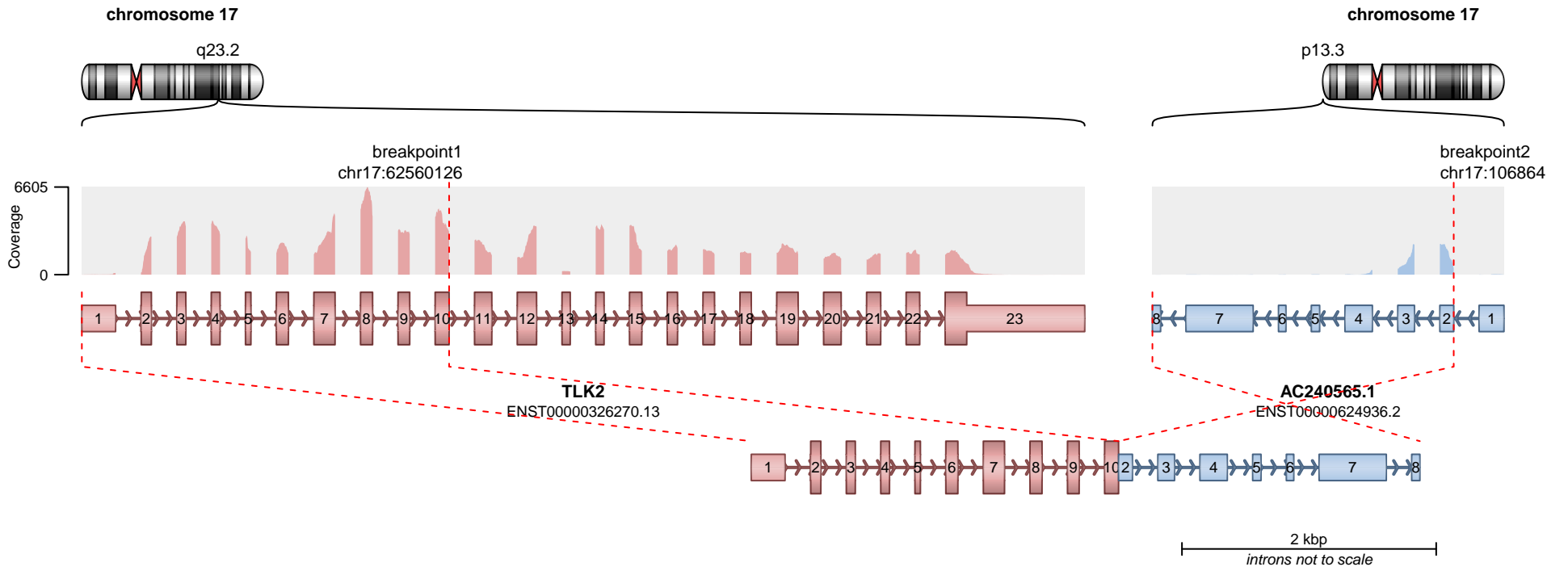


— translocation — deletion
— duplication — inversion

Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 15
Discordant mates = 0

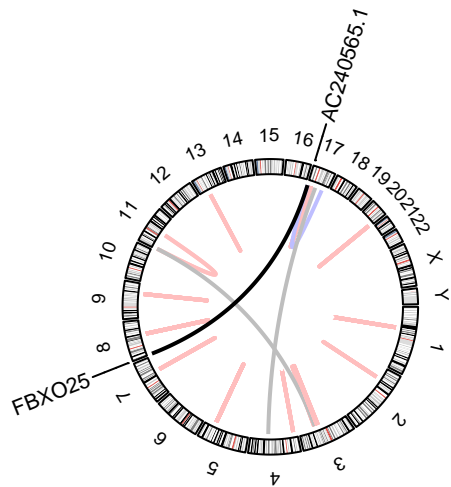
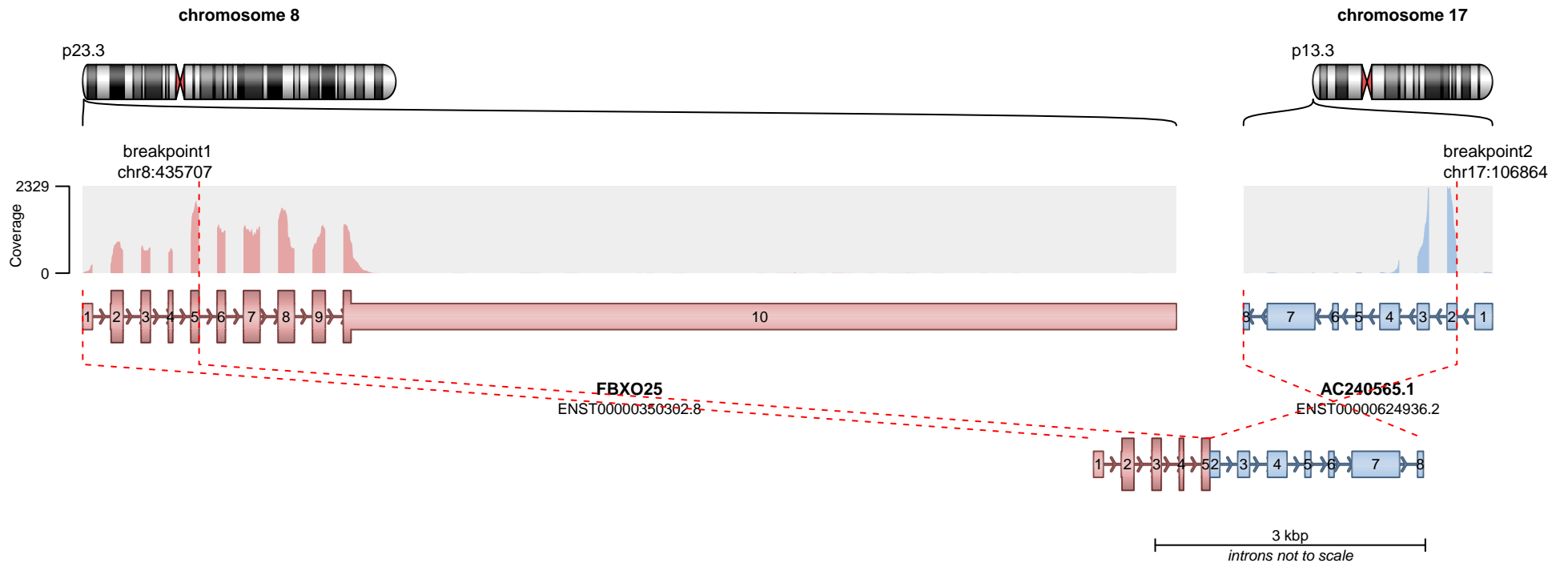


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 157
Discordant mates = 1

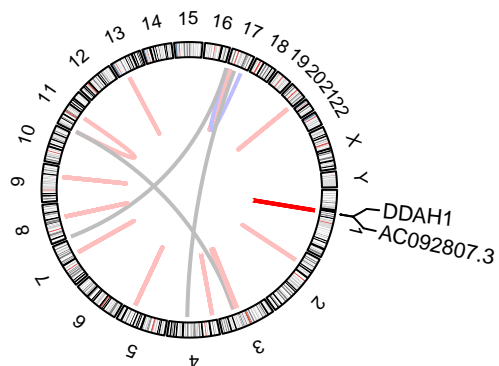
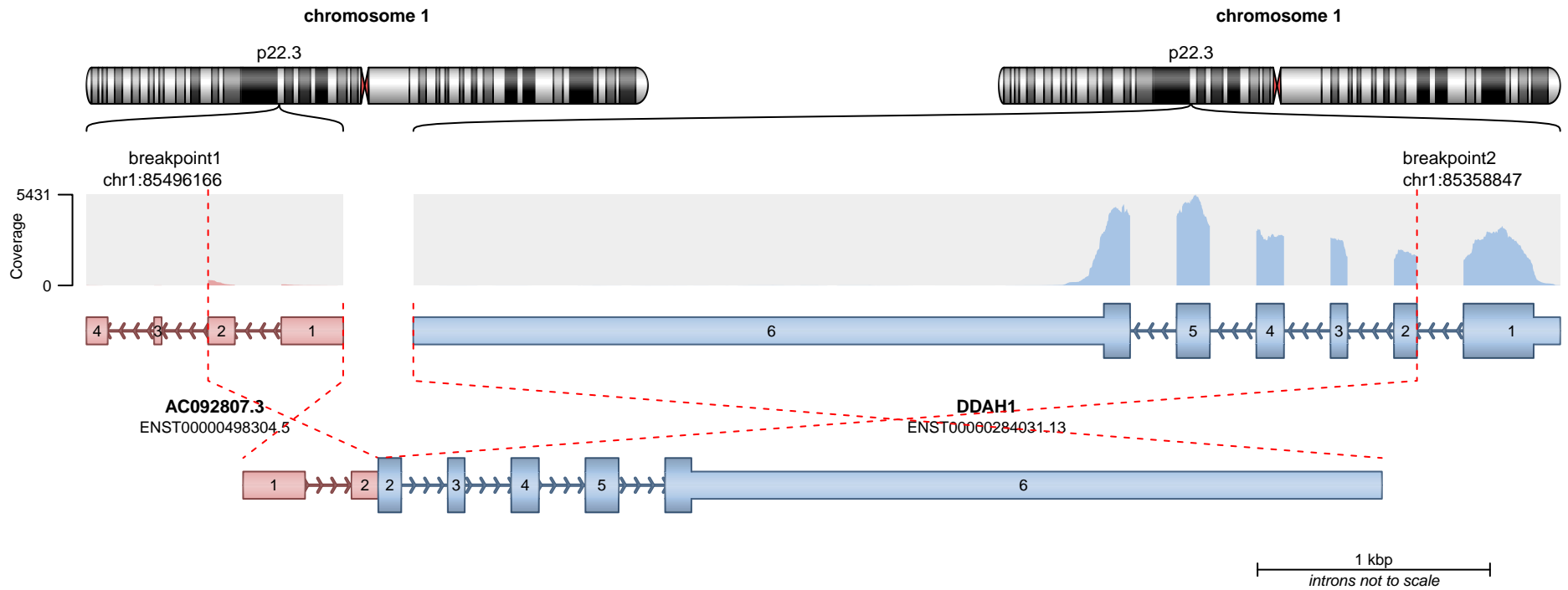


No protein domains retained in fusion.

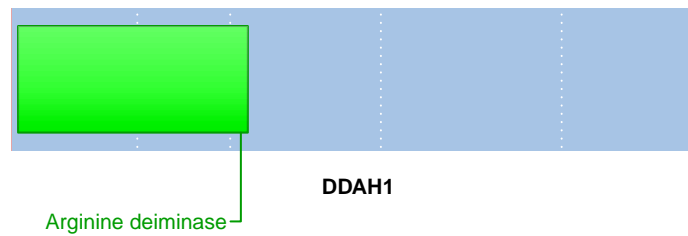
SUPPORTING READ COUNT

Split reads = 155
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



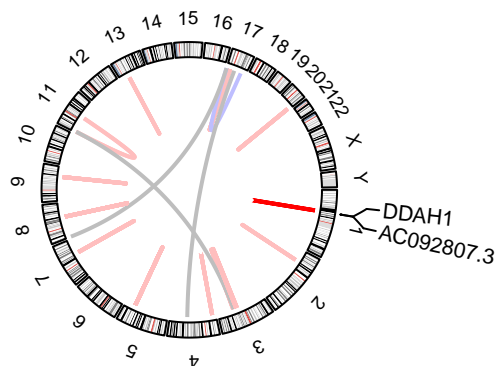
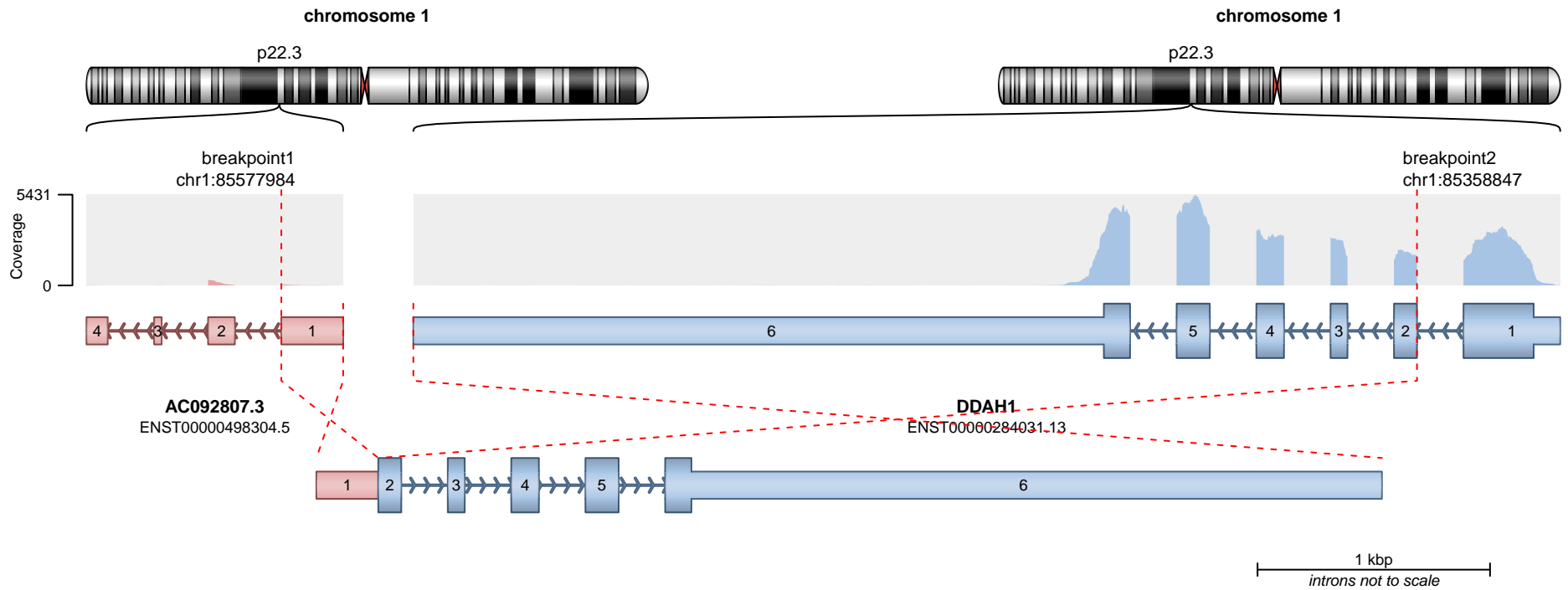
RETAINED PROTEIN DOMAINS
reading frame unclear



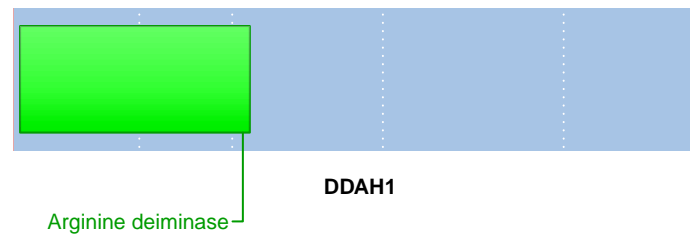
SUPPORTING READ COUNT

Split reads = 127
Discordant mates = 3

- translocation
- duplication
- deletion
- inversion



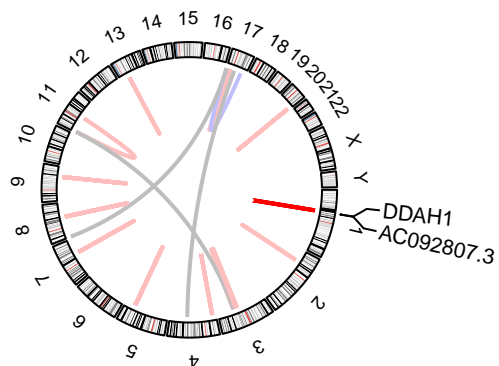
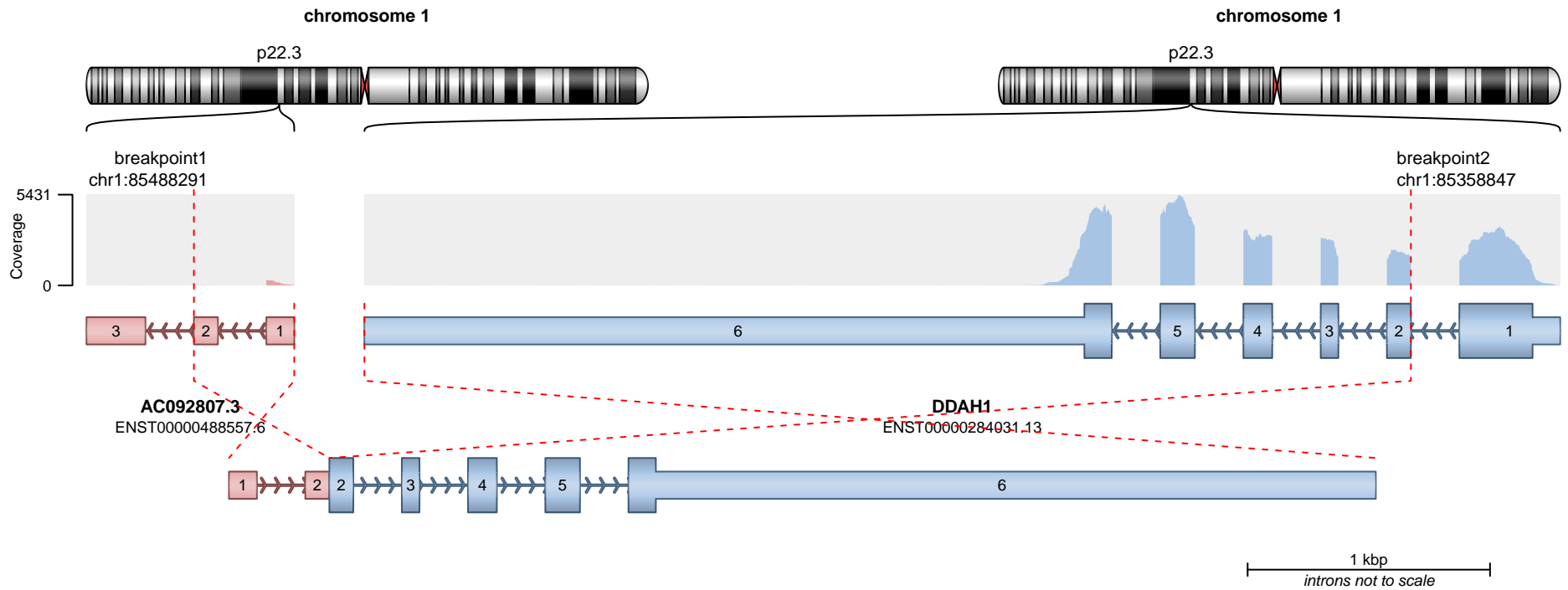
RETAINED PROTEIN DOMAINS
reading frame unclear



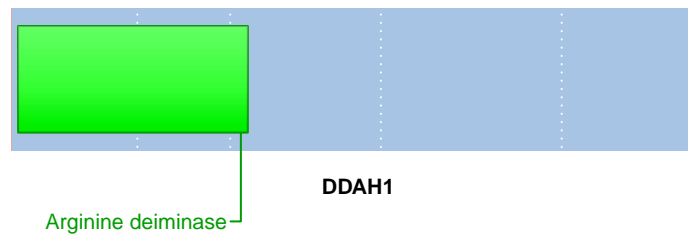
SUPPORTING READ COUNT

Split reads = 25
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



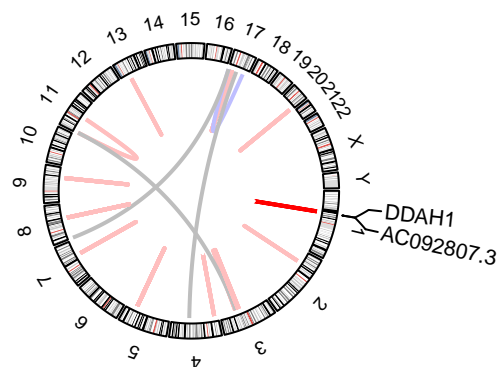
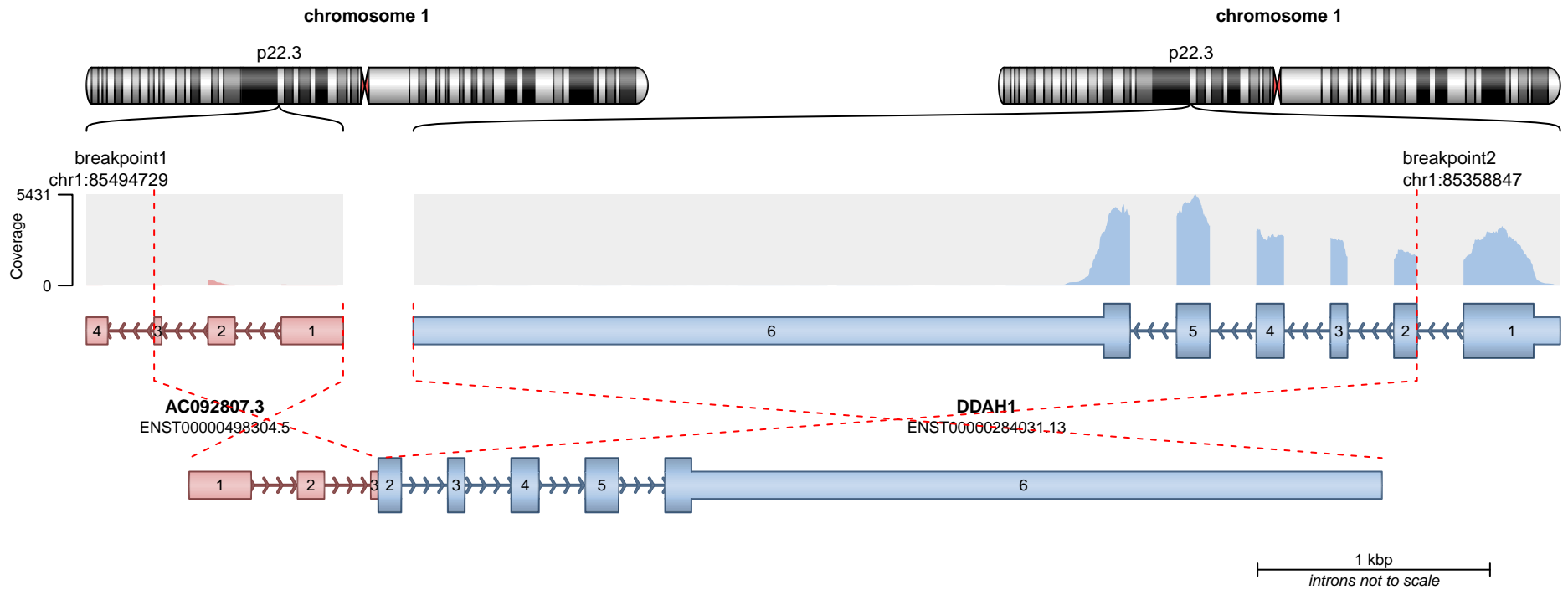
RETAINED PROTEIN DOMAINS
reading frame unclear



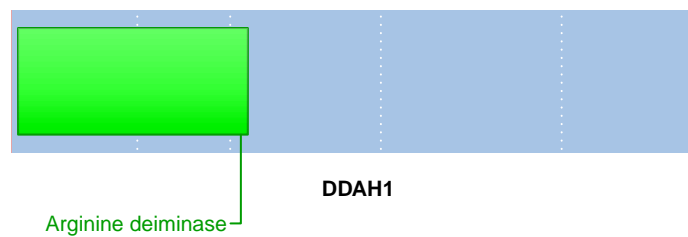
SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 3

- translocation
- duplication
- deletion
- inversion



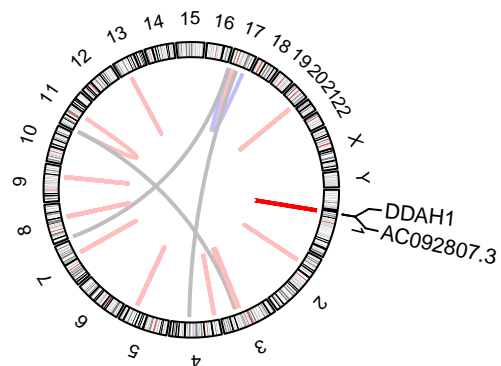
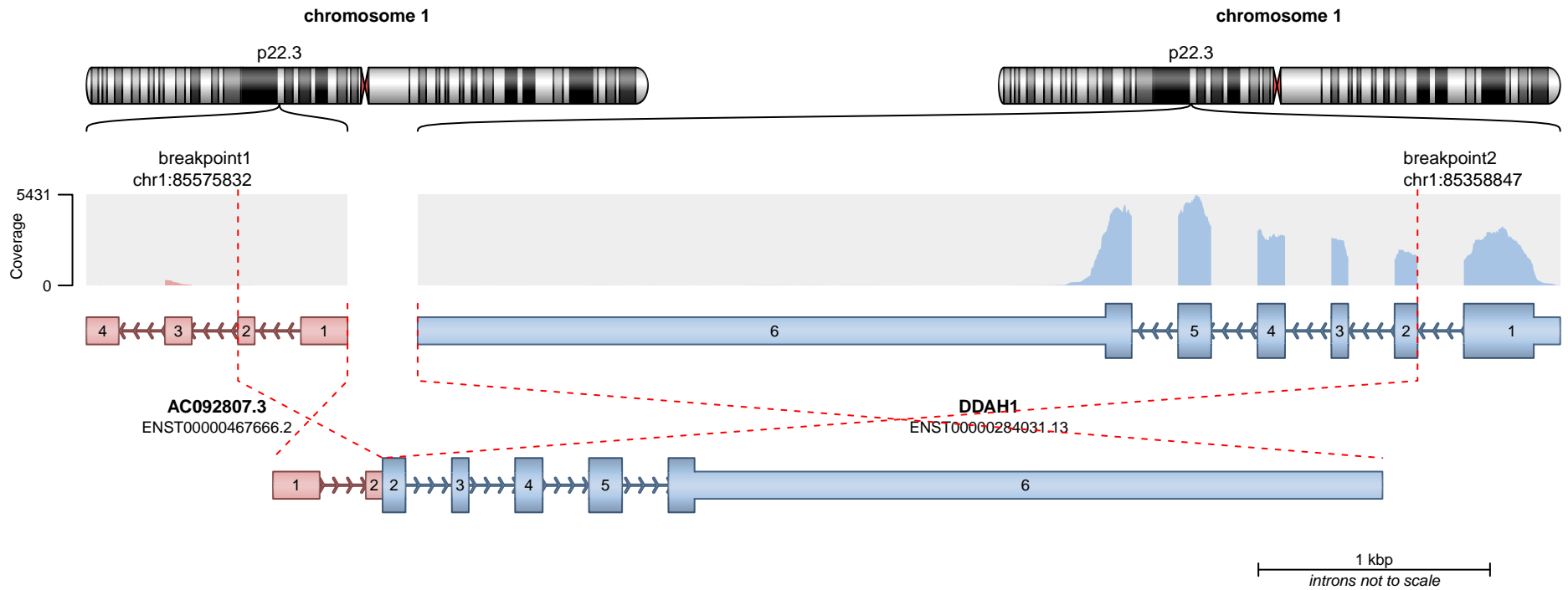
RETAINED PROTEIN DOMAINS
reading frame unclear



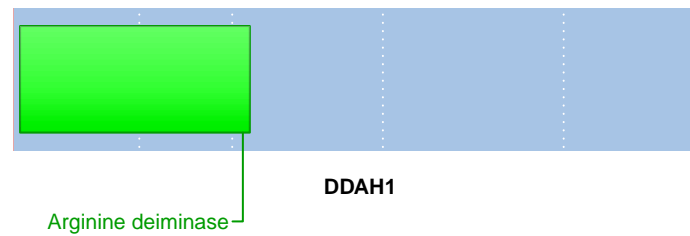
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 3

— translocation — deletion
— duplication — inversion



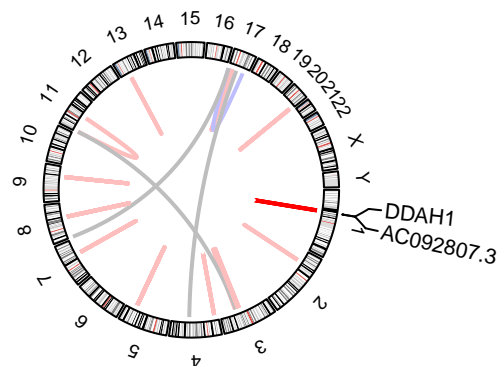
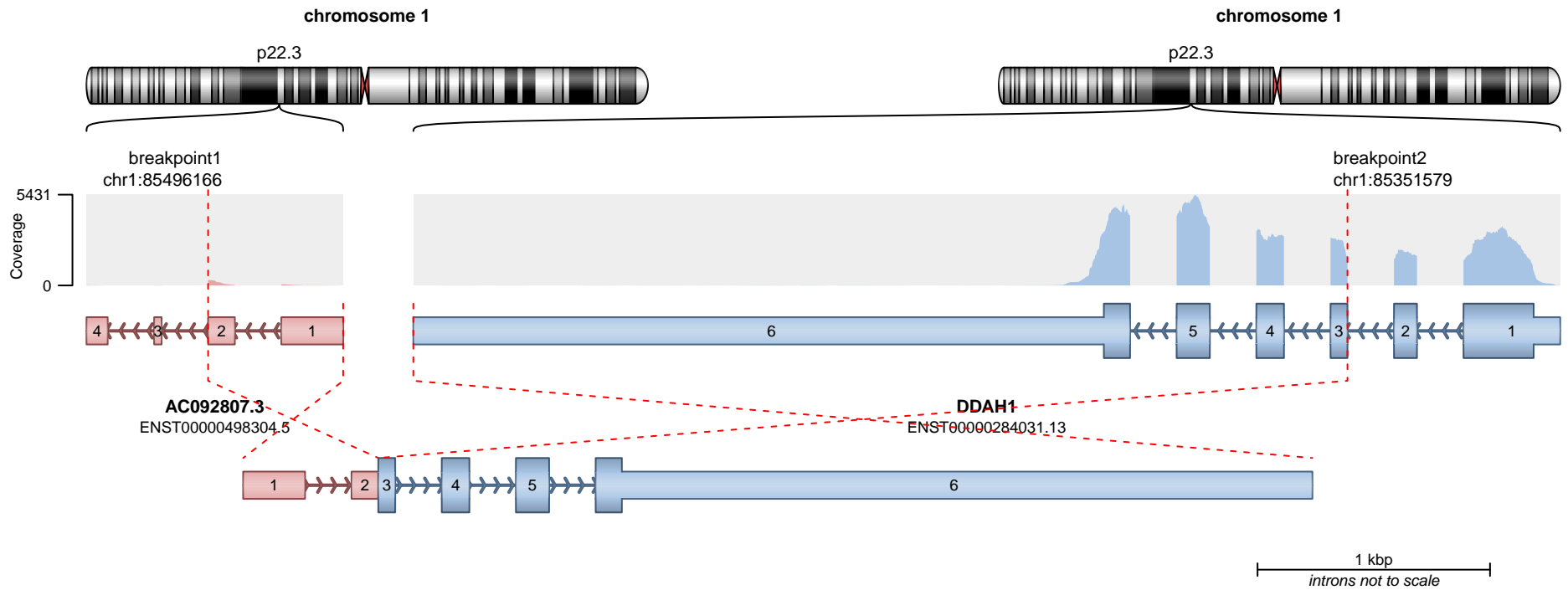
RETAINED PROTEIN DOMAINS
reading frame unclear



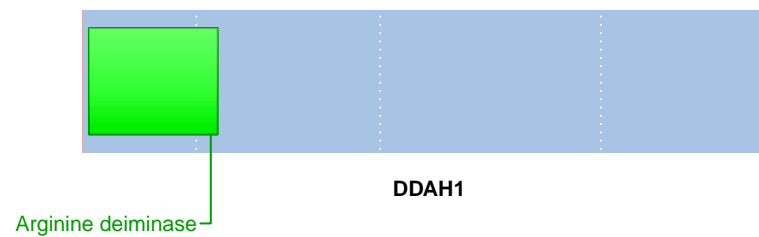
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



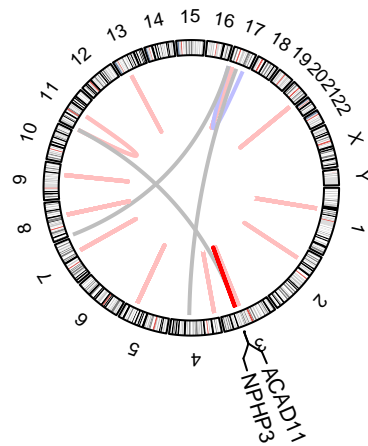
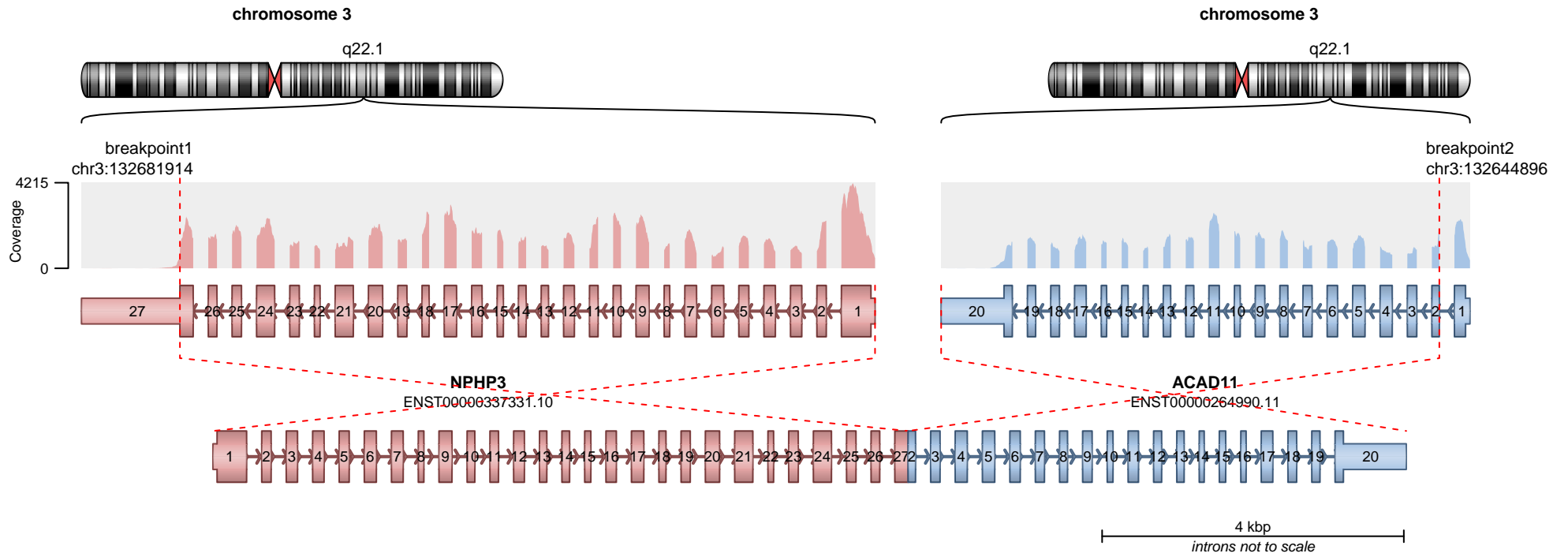
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

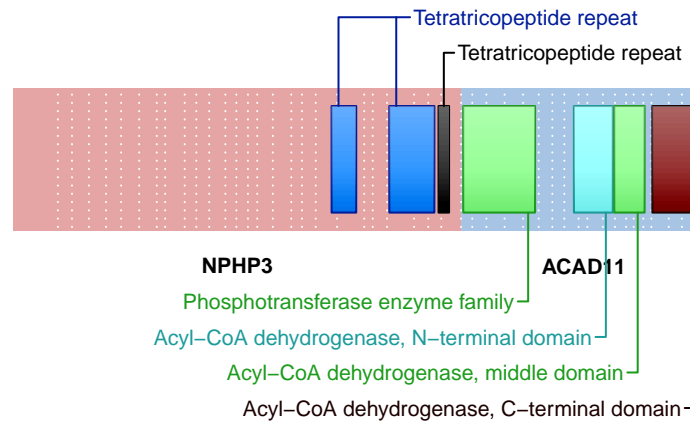
Split reads = 1
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



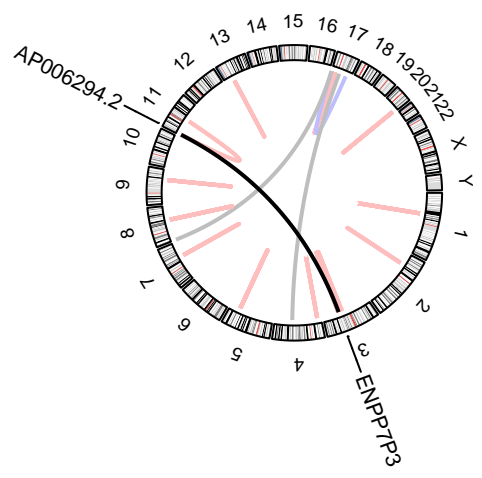
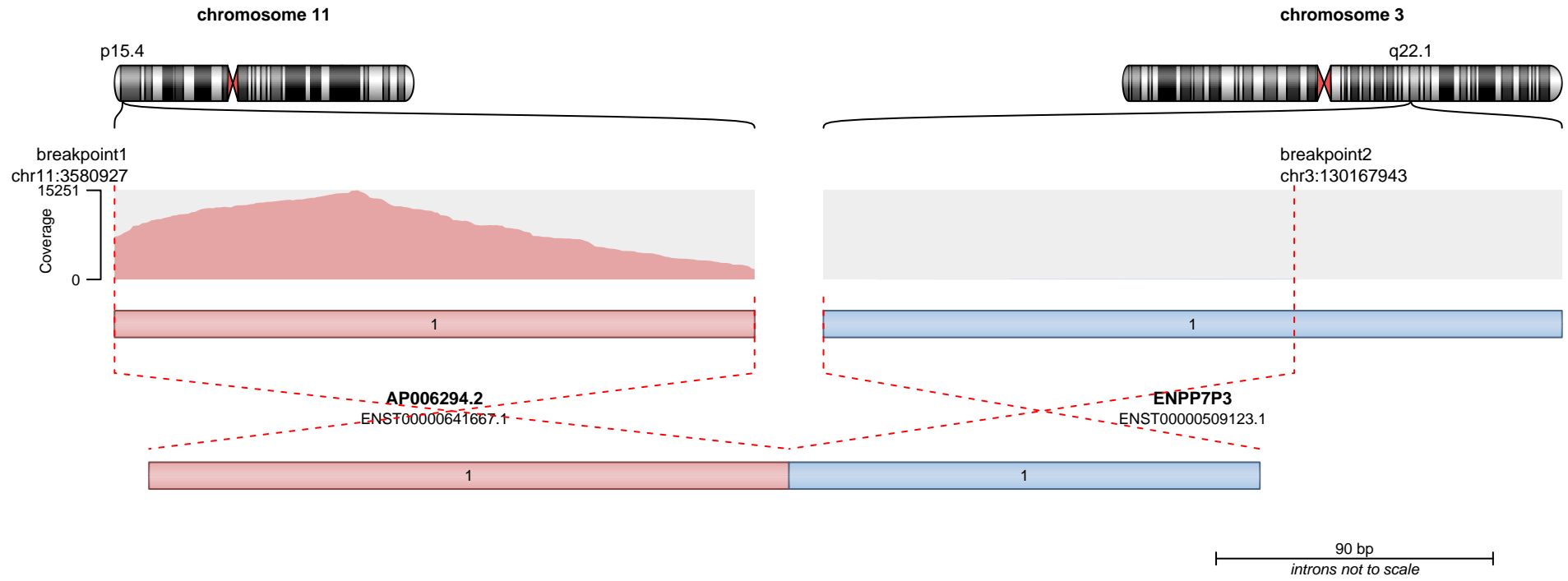
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 85
Discordant mates = 2

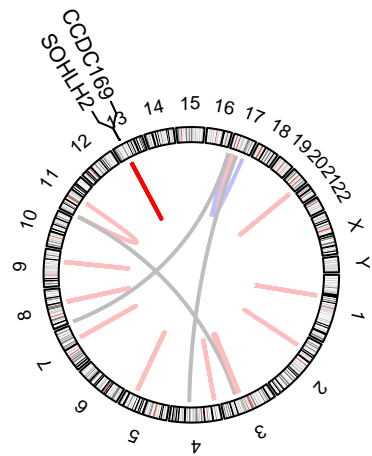
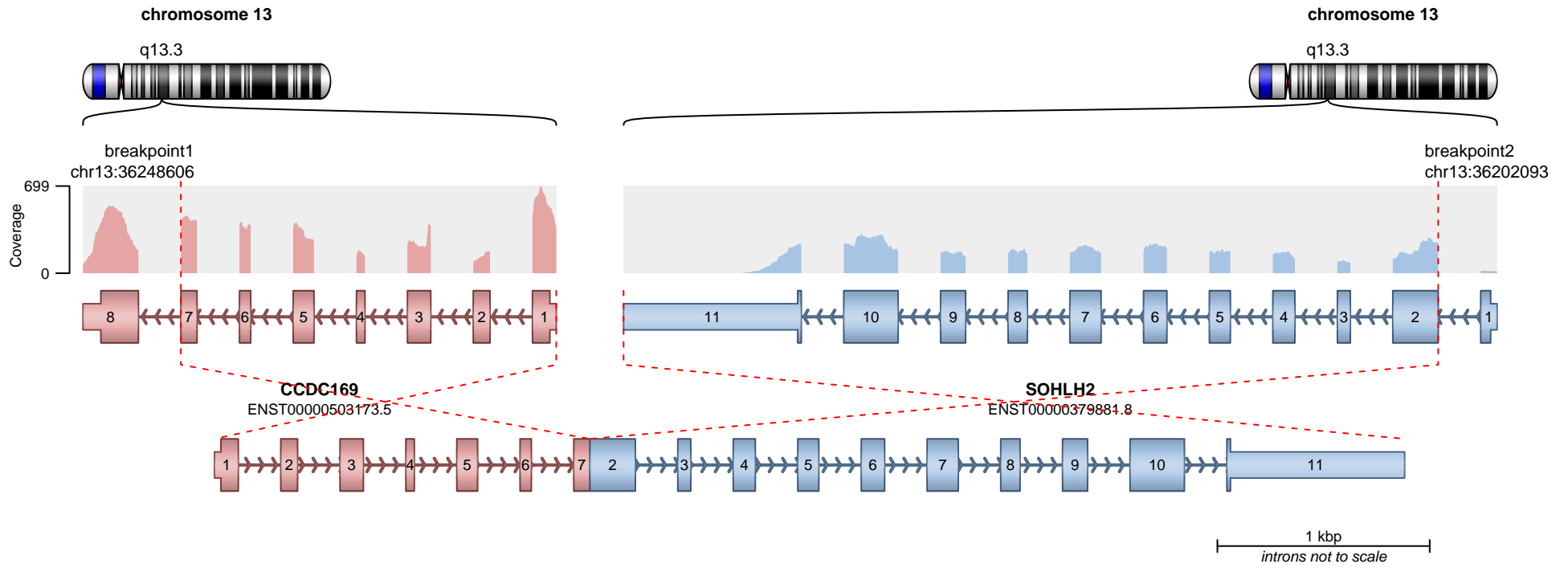


— translocation — deletion
— duplication — inversion

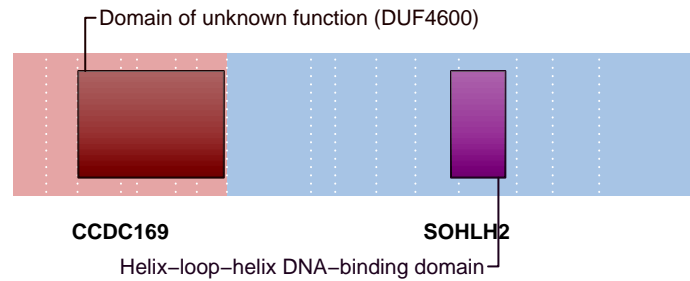
Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 65
Discordant mates = 1



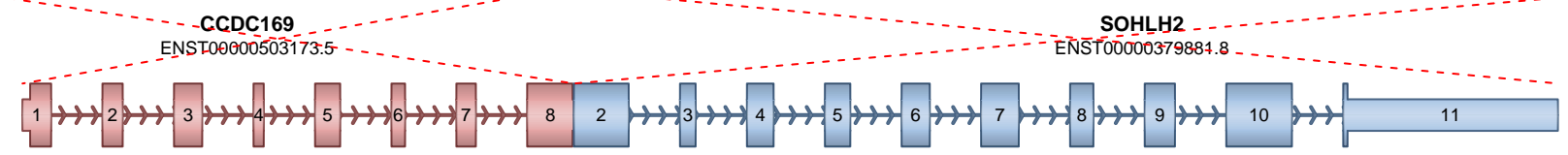
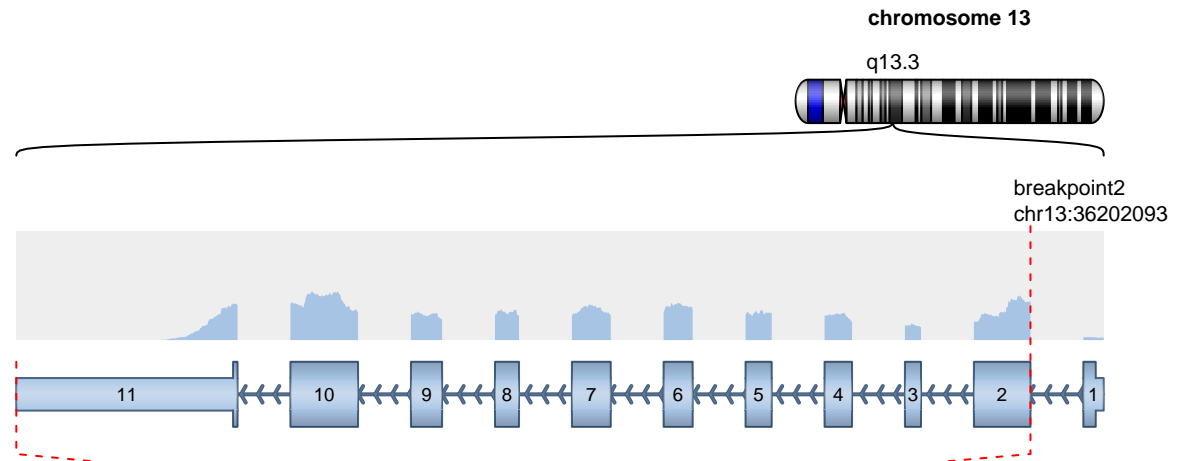
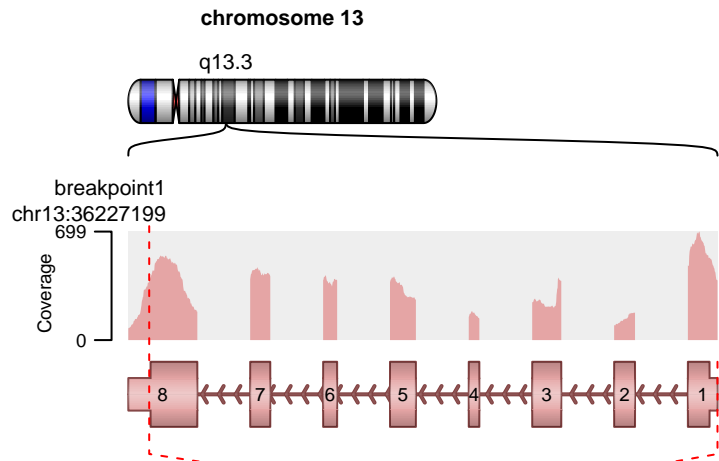
RETAINED PROTEIN DOMAINS
reading frame unclear



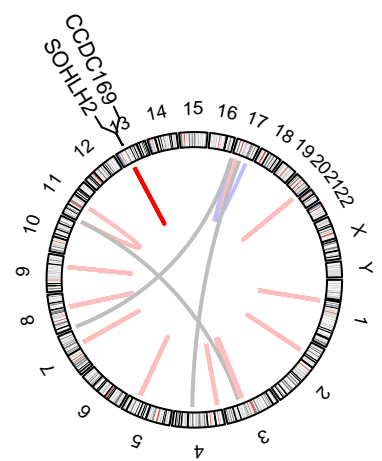
SUPPORTING READ COUNT

Split reads = 62
Discordant mates = 0

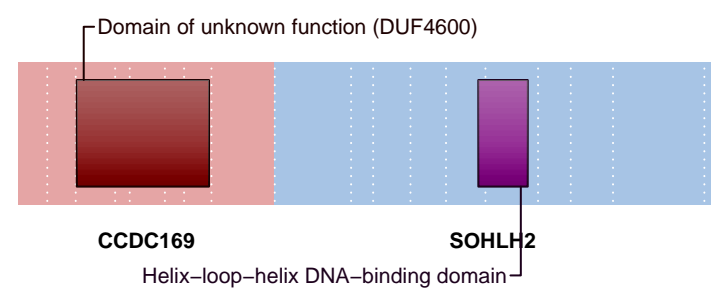
- translocation
- duplication
- deletion
- inversion



1 kbp
introns not to scale



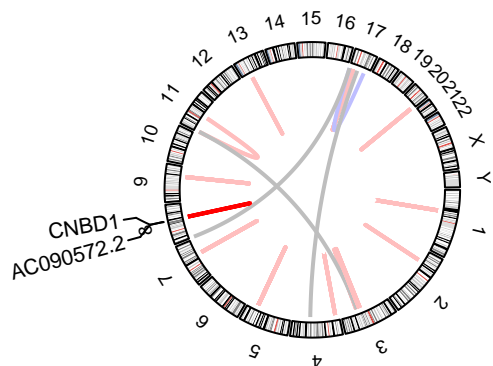
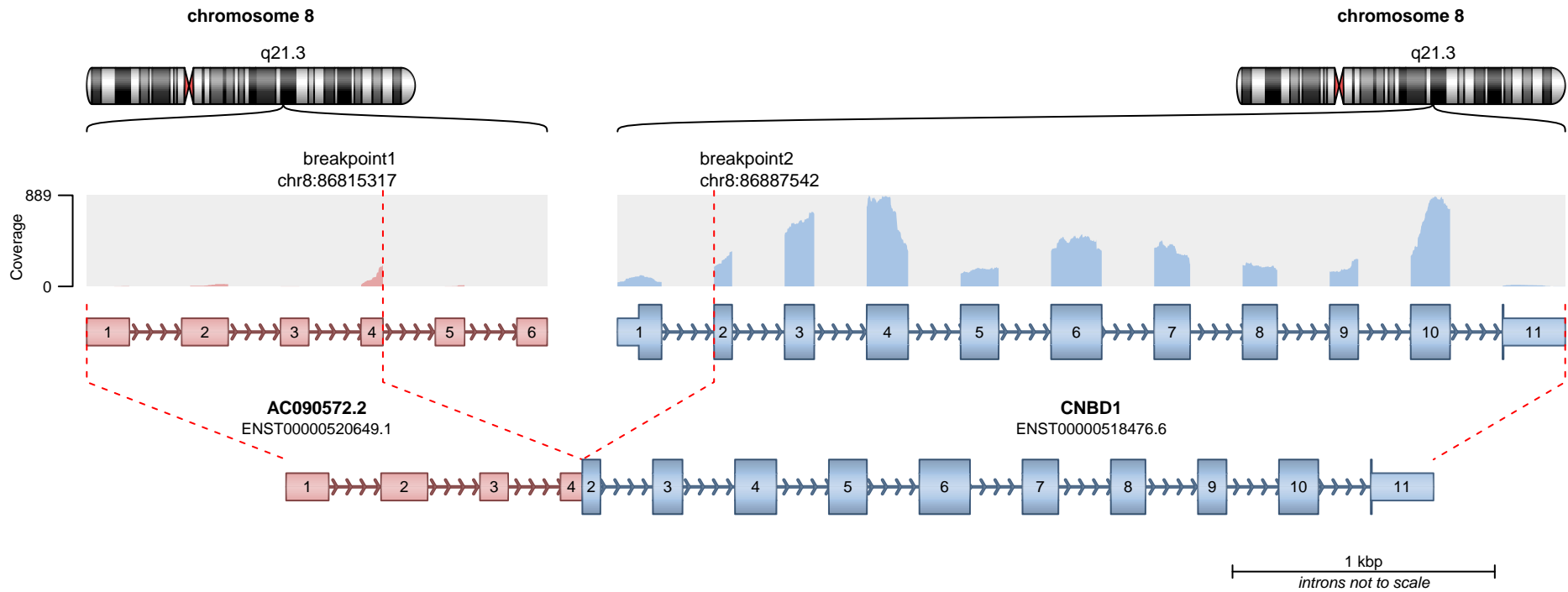
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

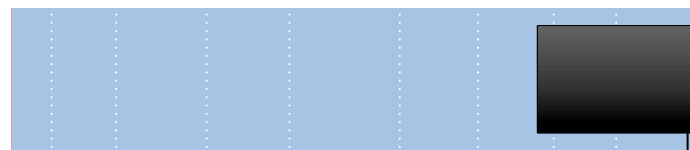
Split reads = 9
Discordant mates = 0

— translocation — deletion
— duplication — inversion



— translocation — deletion
— duplication — inversion

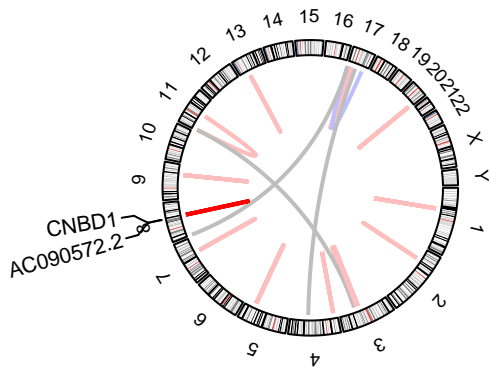
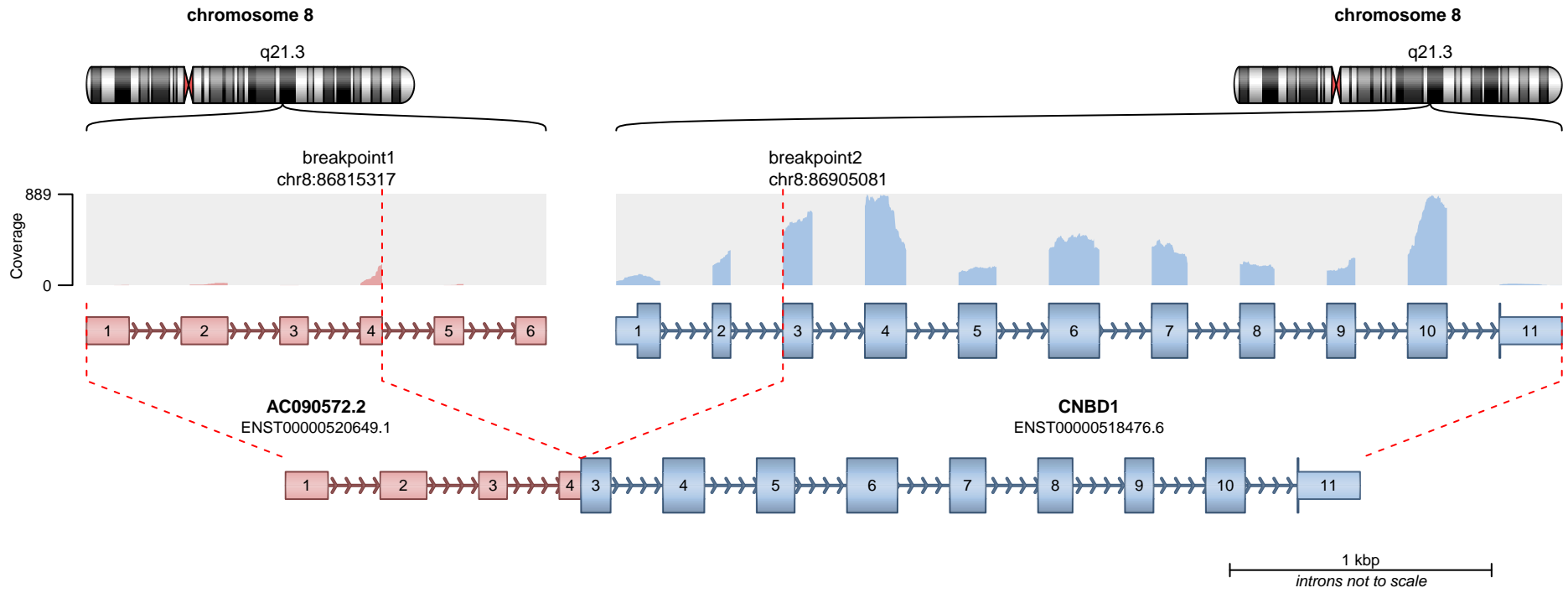
RETAINED PROTEIN DOMAINS
reading frame unclear



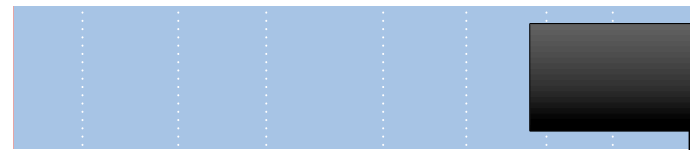
CNBD1
Cyclic nucleotide-binding domain

SUPPORTING READ COUNT

Split reads = 57
Discordant mates = 2



RETAINED PROTEIN DOMAINS
reading frame unclear

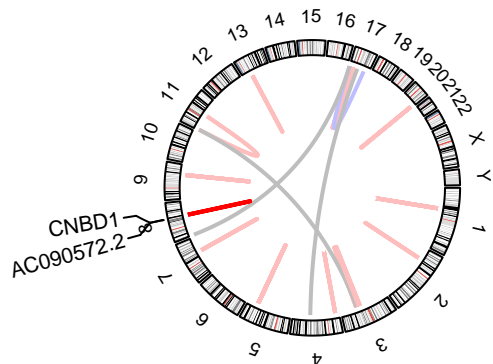
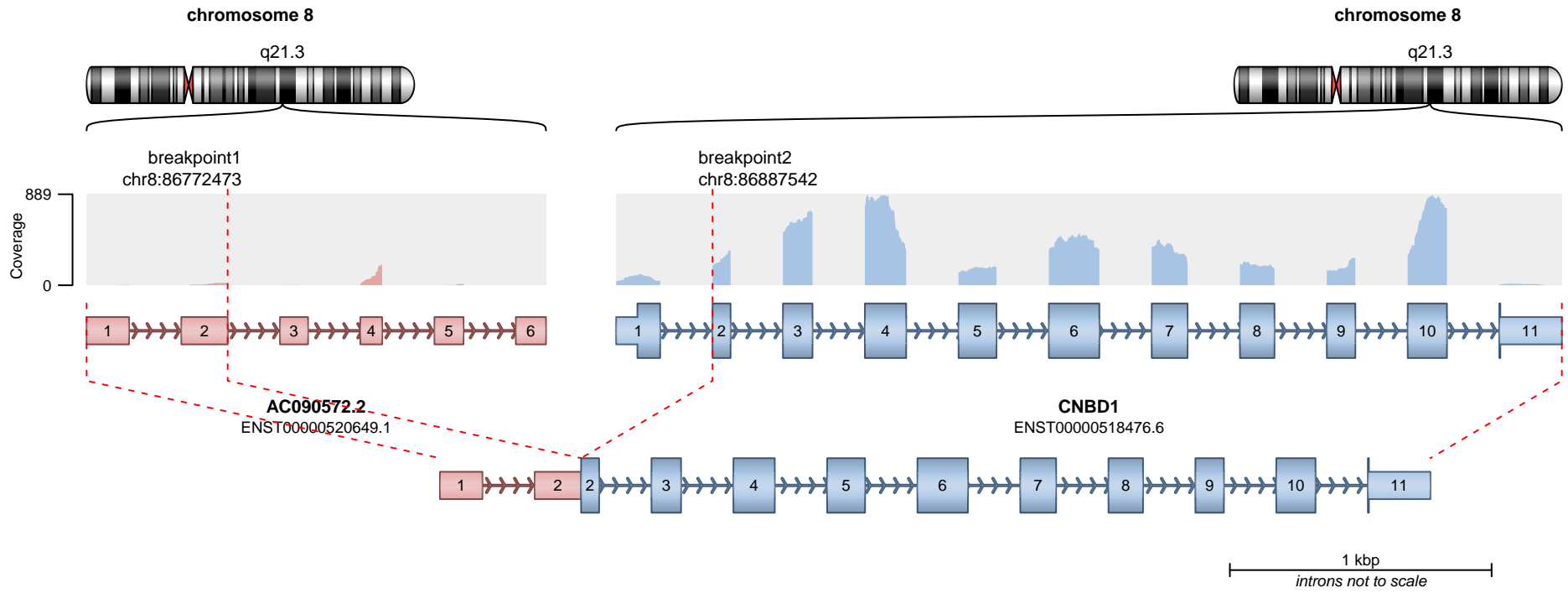


CNBD1
Cyclic nucleotide-binding domain

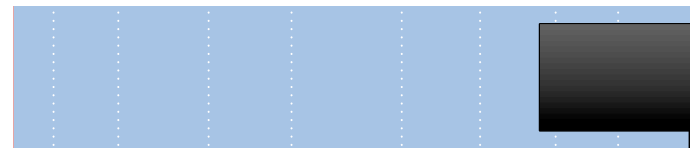
SUPPORTING READ COUNT

Split reads = 28
Discordant mates = 0

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

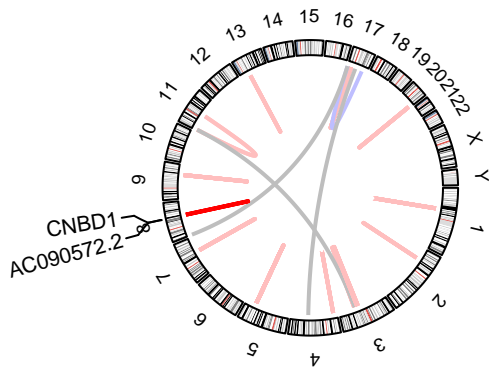
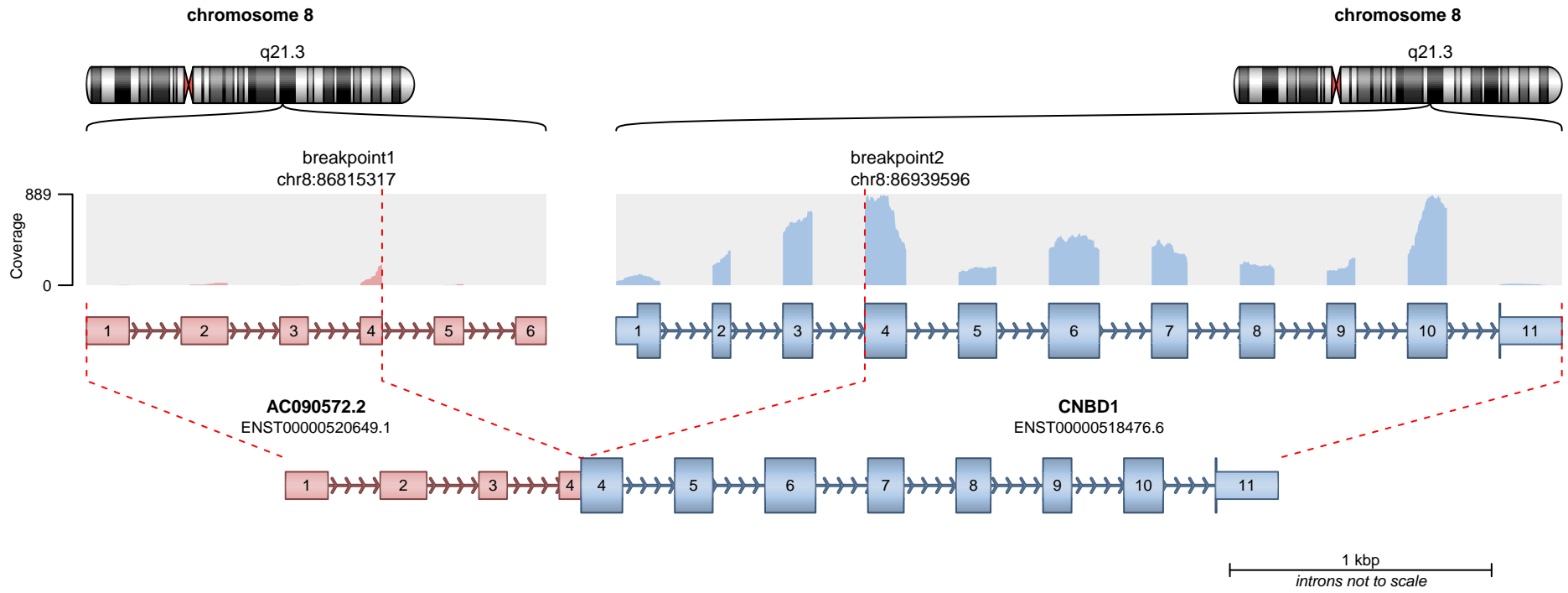


CNBD1
Cyclic nucleotide-binding domain

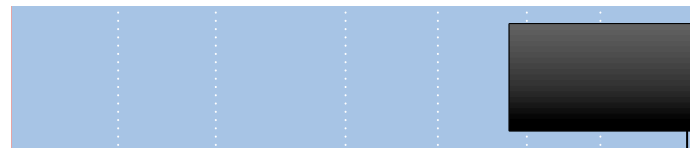
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

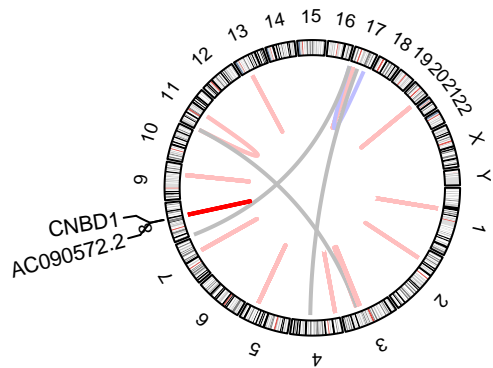
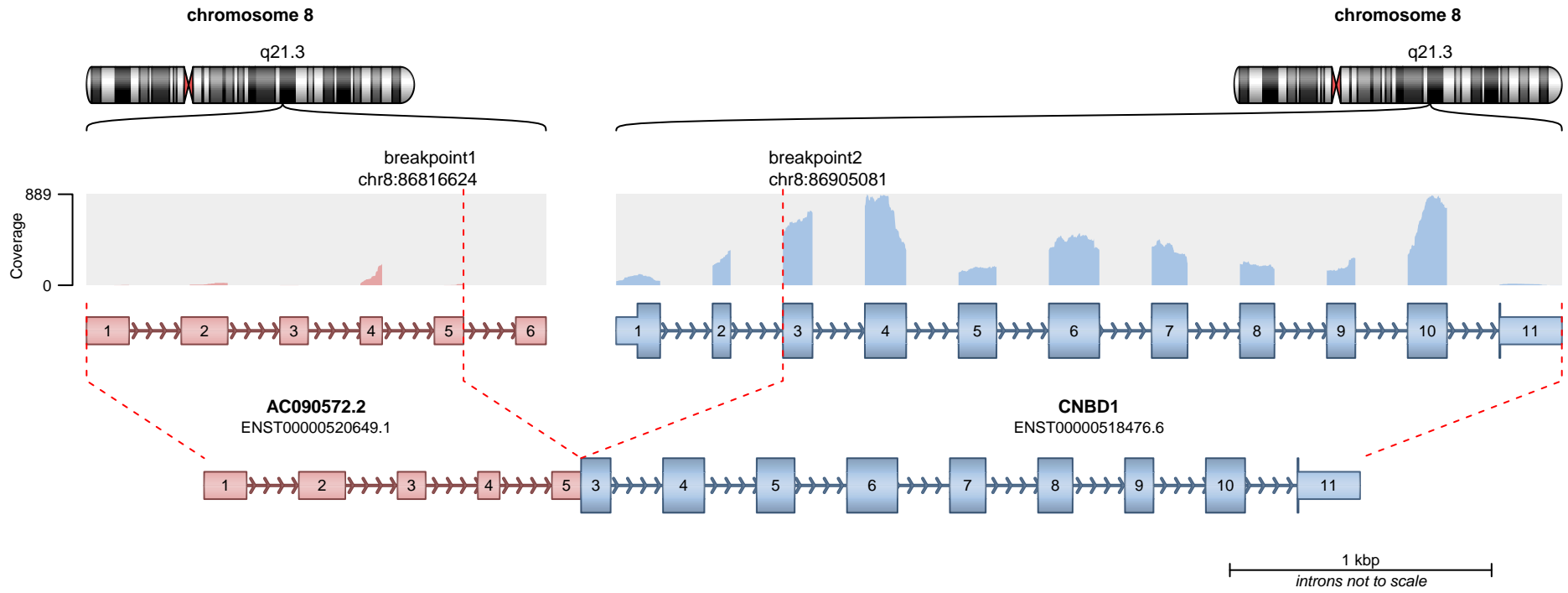


CNBD1
Cyclic nucleotide-binding domain

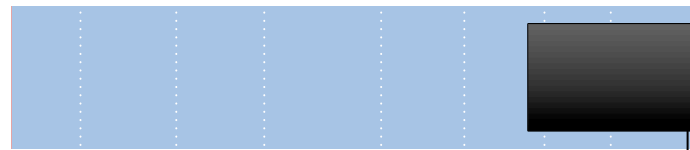
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

— translocation — deletion
— duplication — inversion



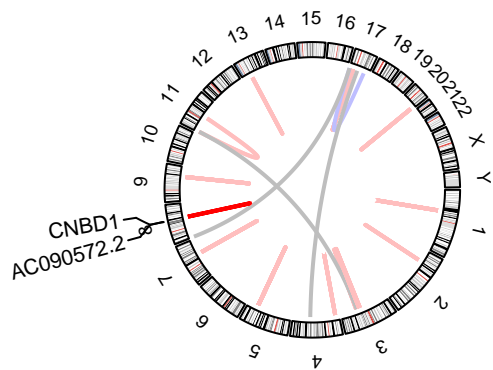
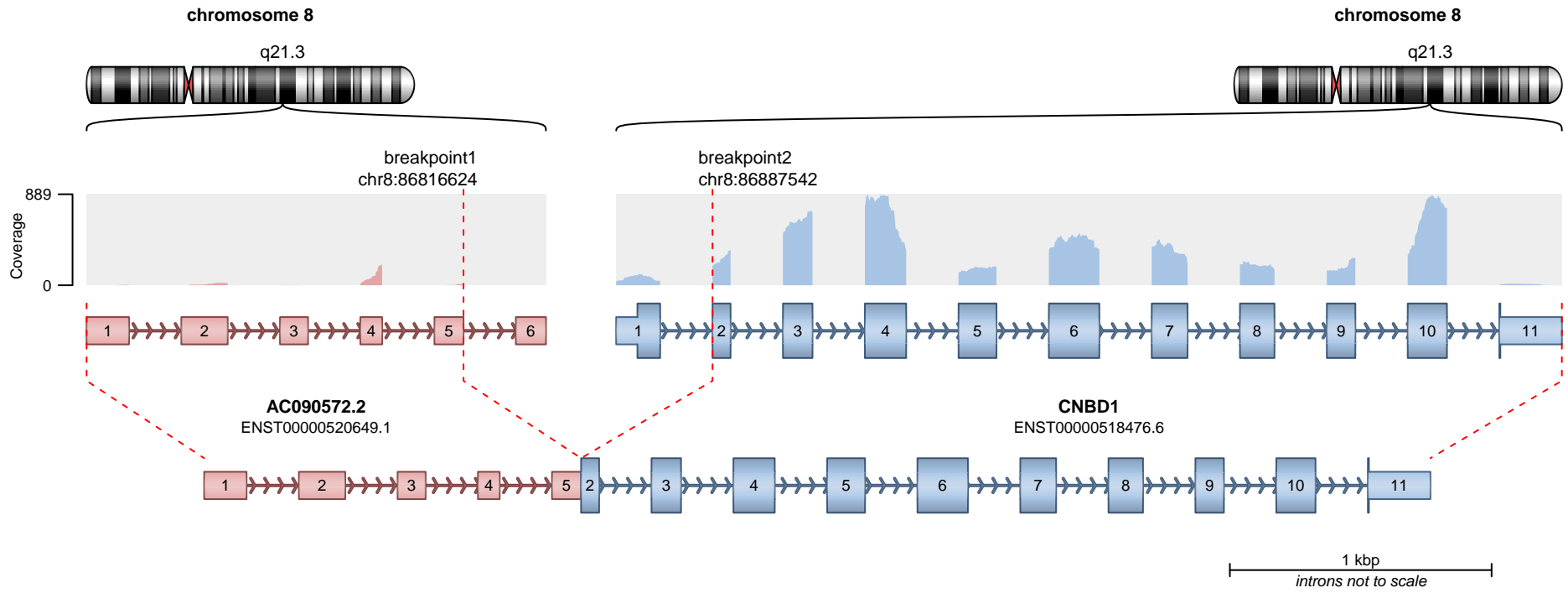
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

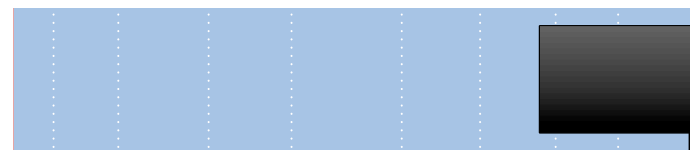
Split reads = 3
Discordant mates = 0

— translocation — deletion
— duplication — inversion



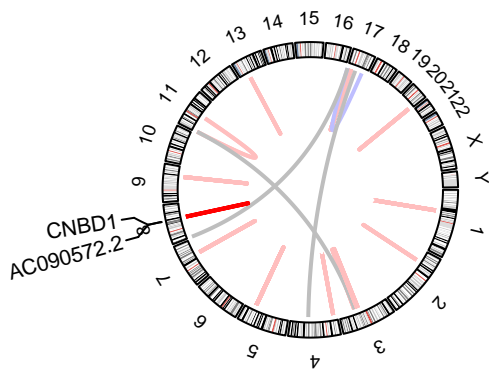
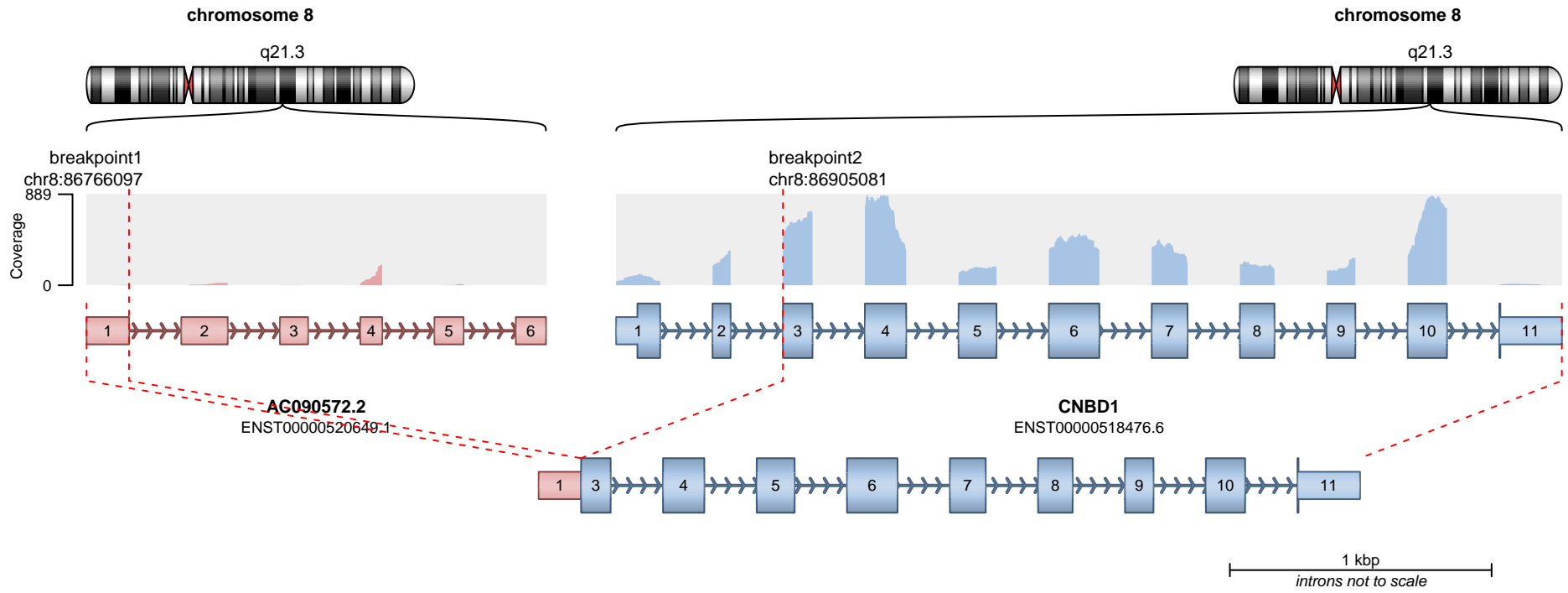
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 2



RETAINED PROTEIN DOMAINS
reading frame unclear

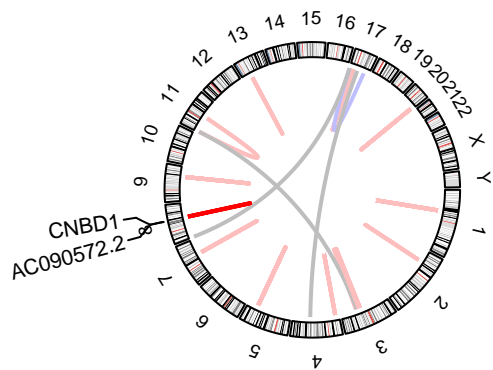
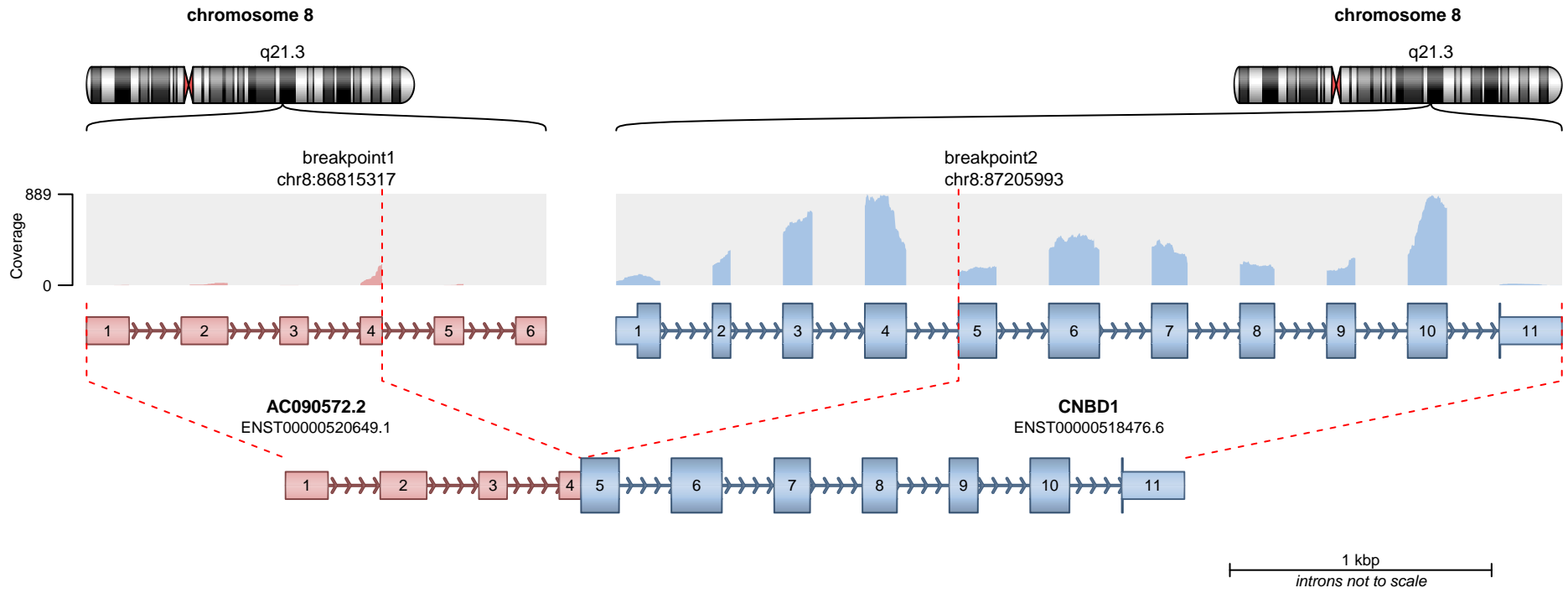


CNBD1
Cyclic nucleotide-binding domain

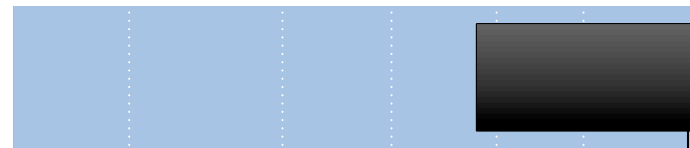
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

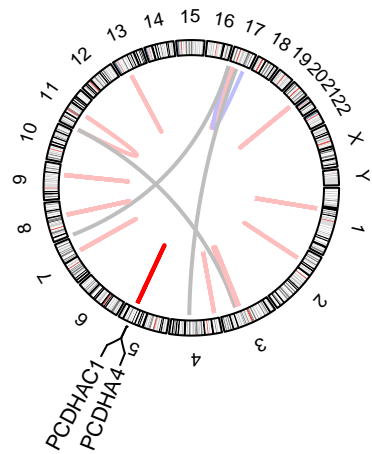
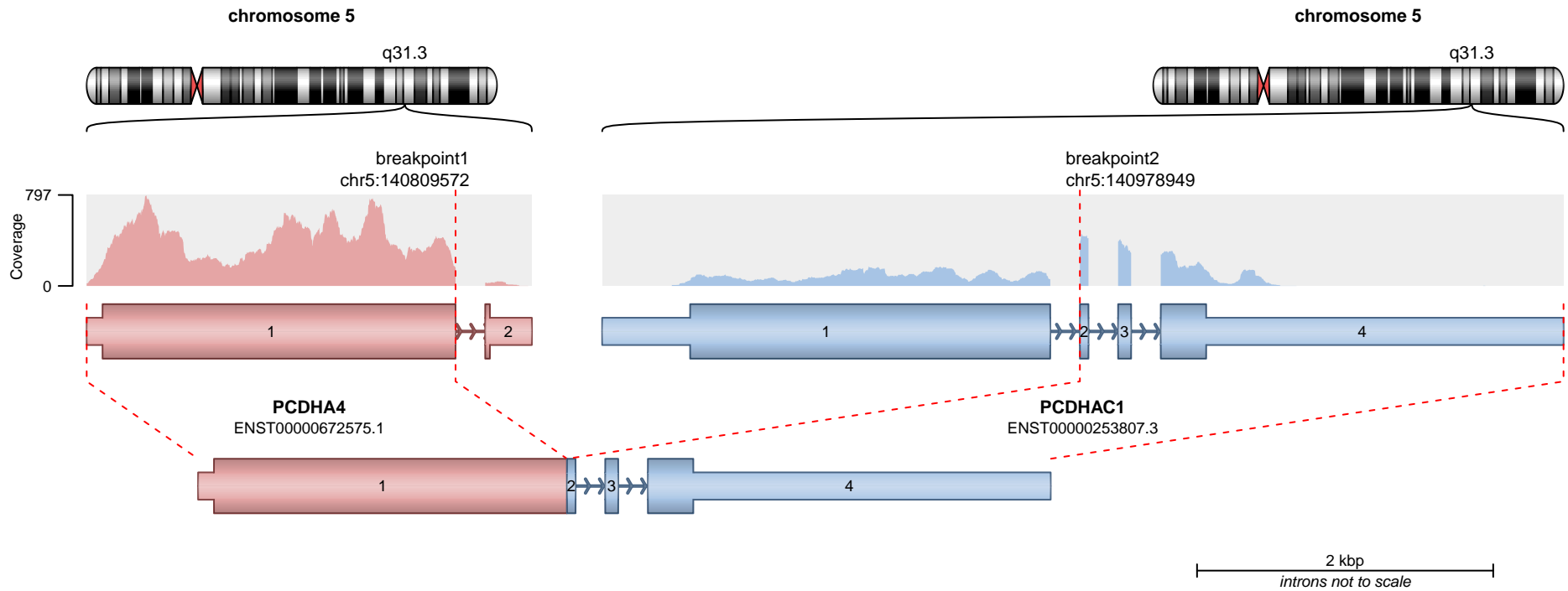


CNBD1
Cyclic nucleotide-binding domain

SUPPORTING READ COUNT

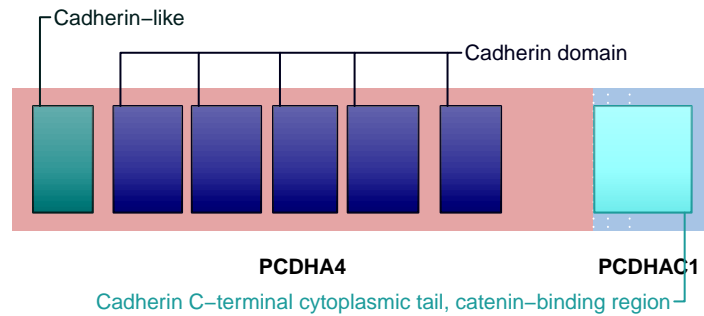
Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



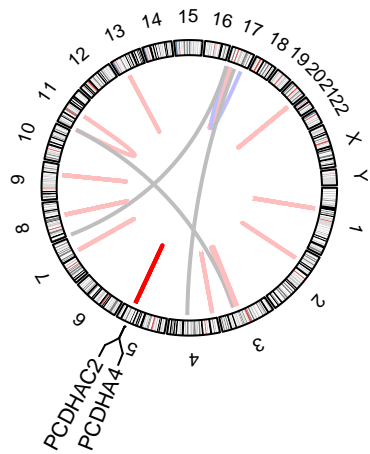
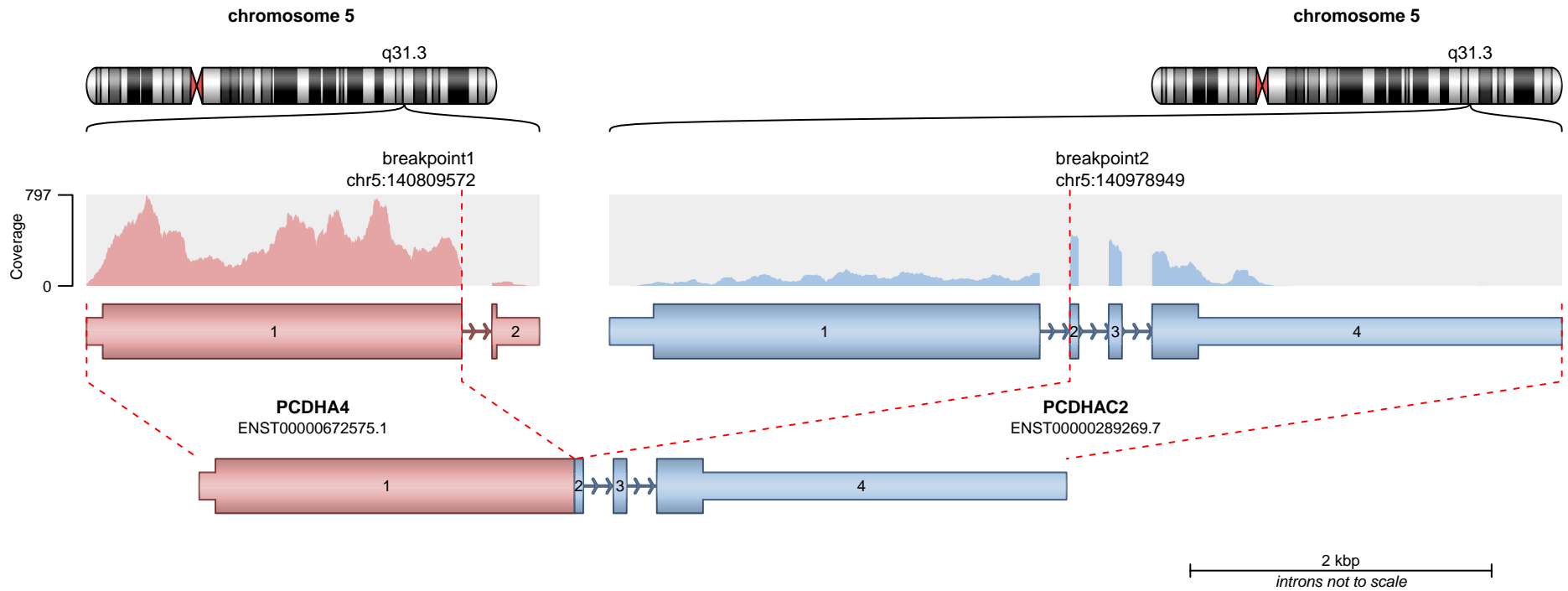
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



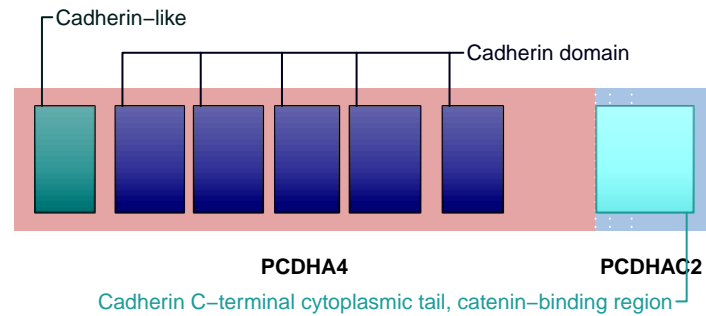
SUPPORTING READ COUNT

Split reads = 57
Discordant mates = 1



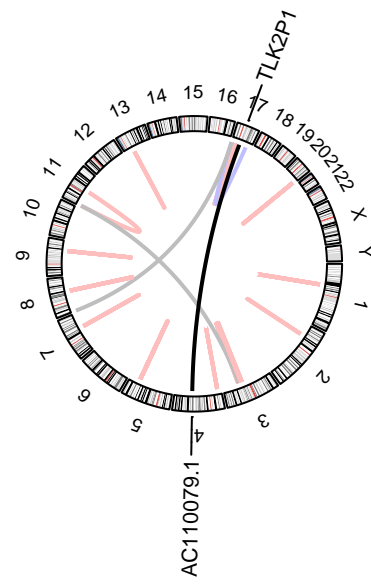
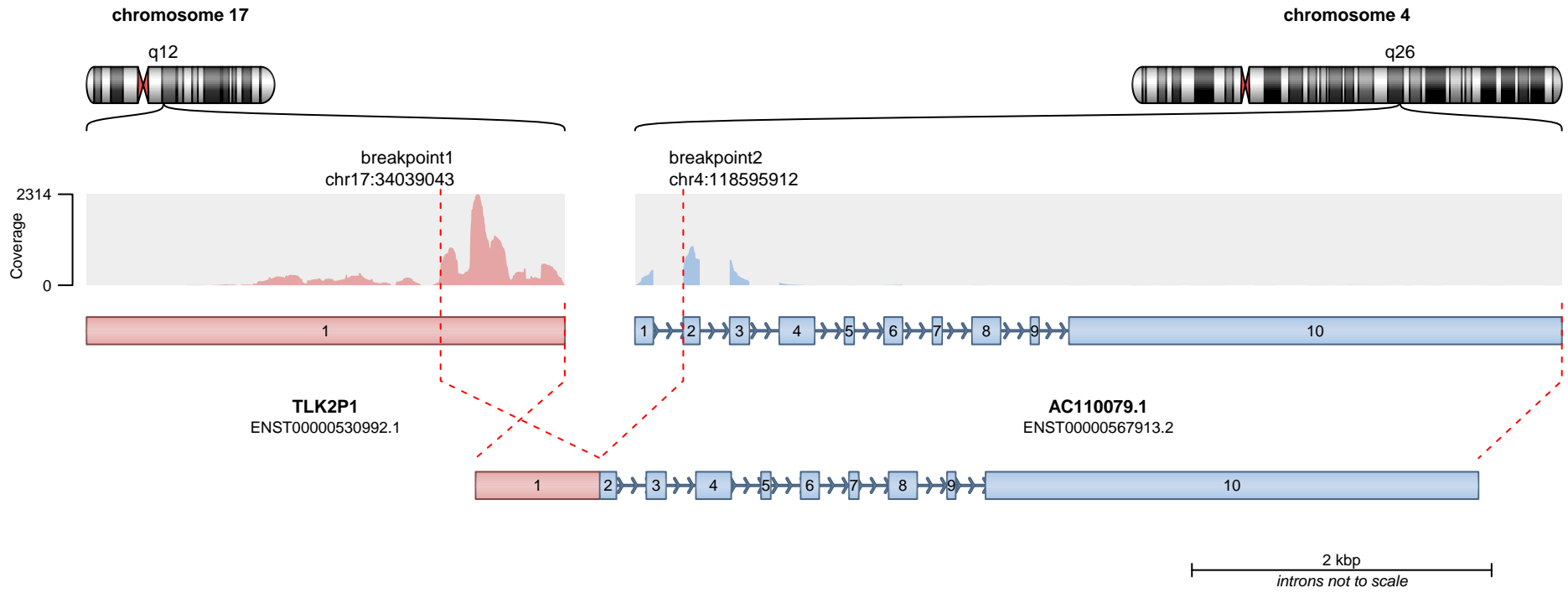
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 57
Discordant mates = 1

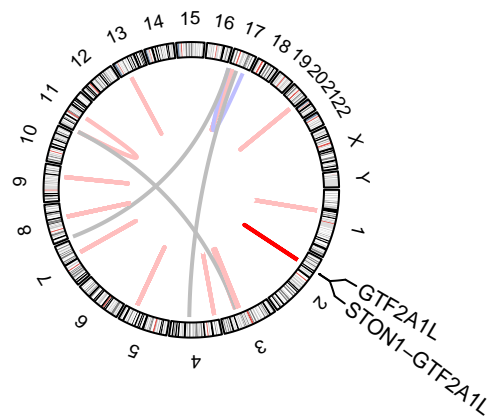
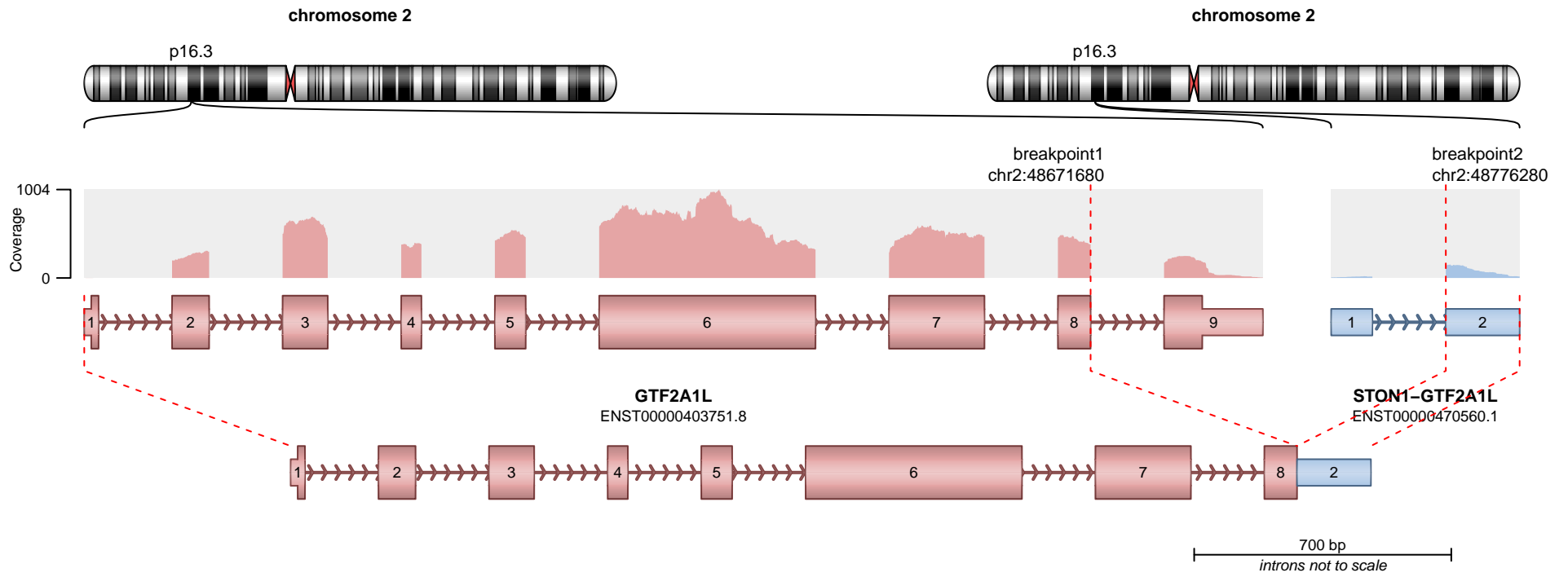


— translocation — deletion
 — duplication — inversion

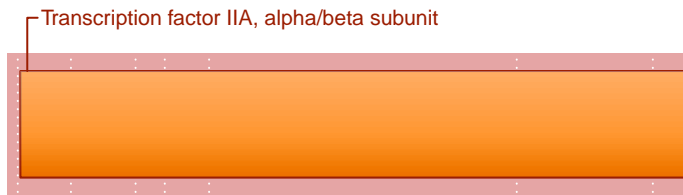
Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 52
 Discordant mates = 0



RETAINED PROTEIN DOMAINS
reading frame unclear

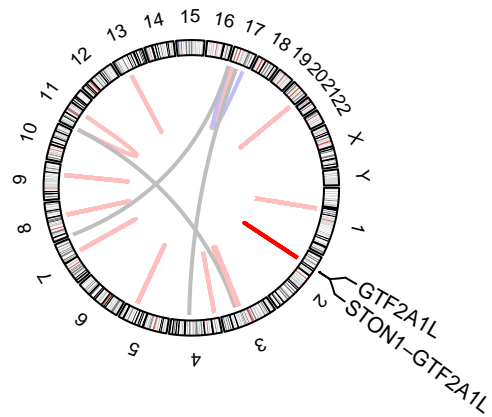
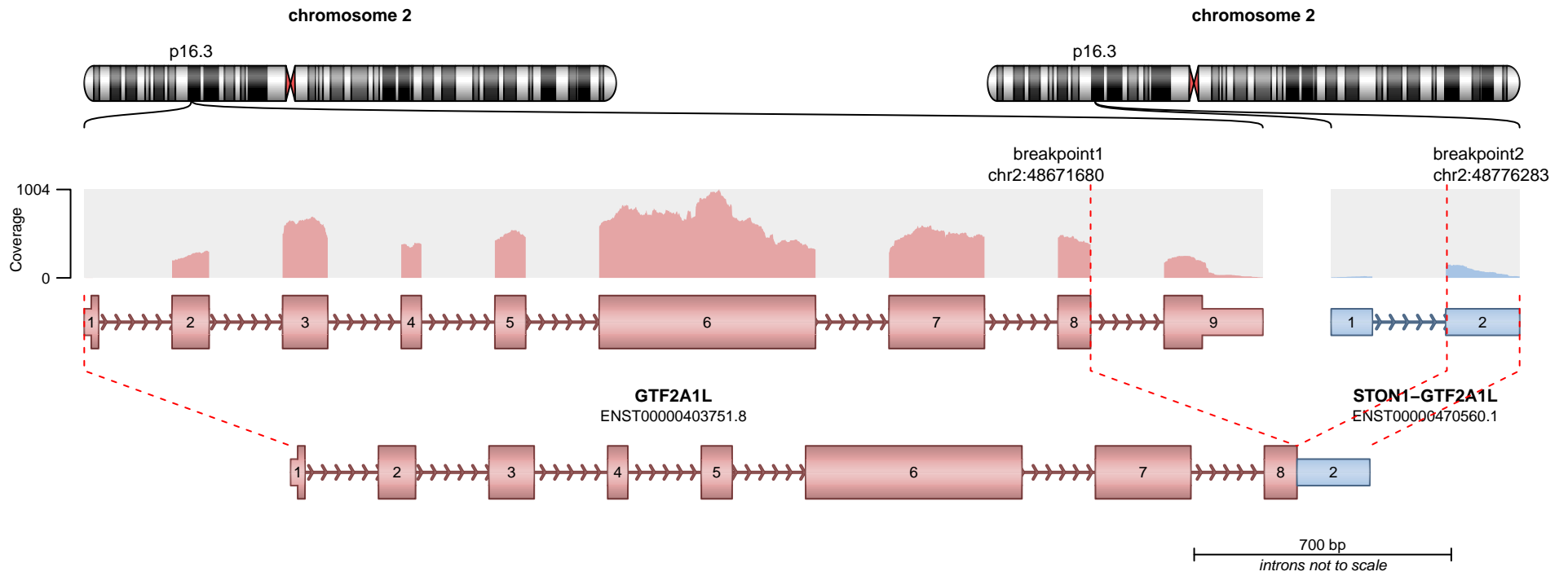


GTF2A1L

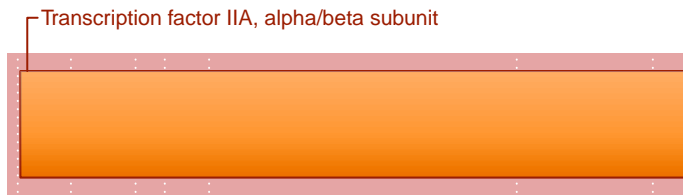
SUPPORTING READ COUNT

Split reads = 36
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

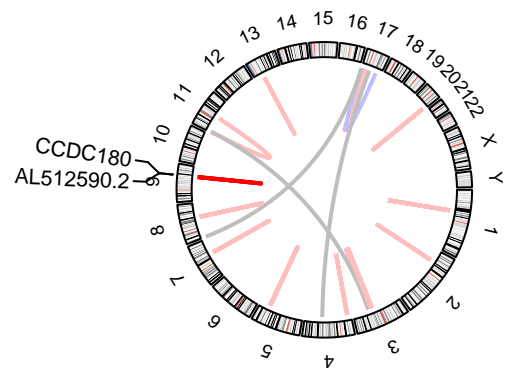
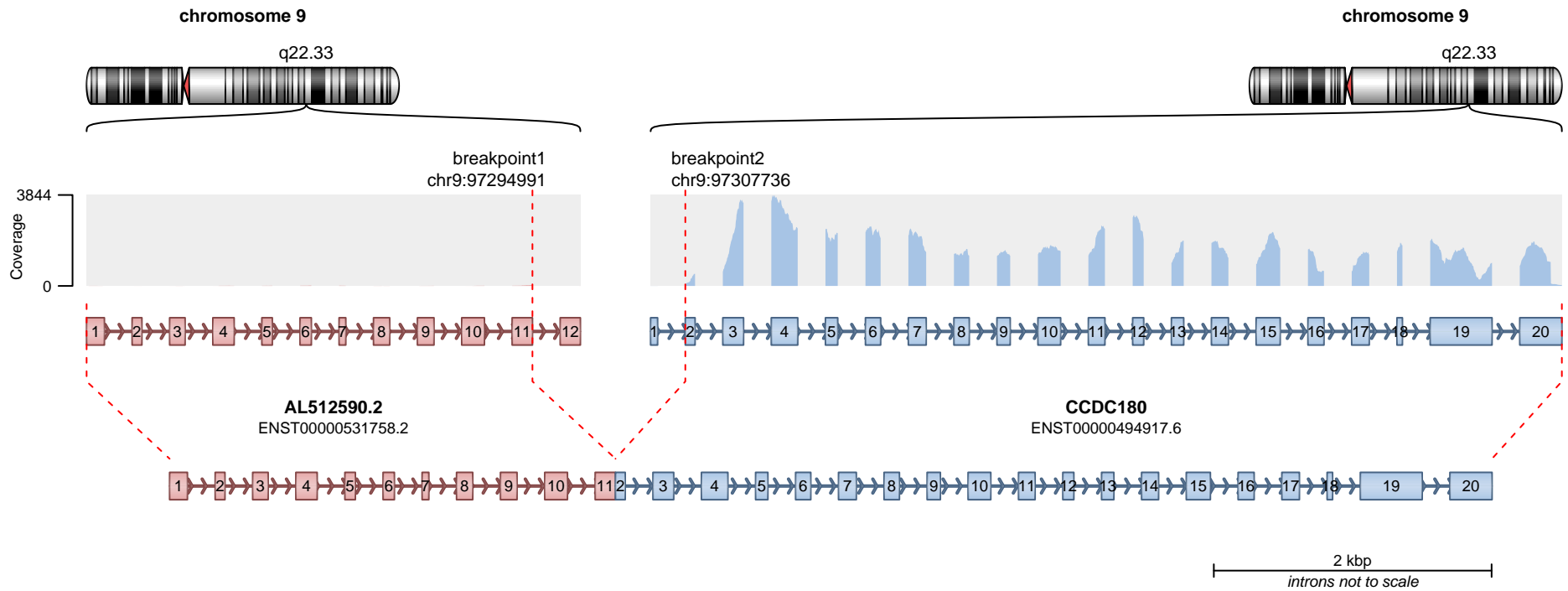


GTF2A1L

SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion

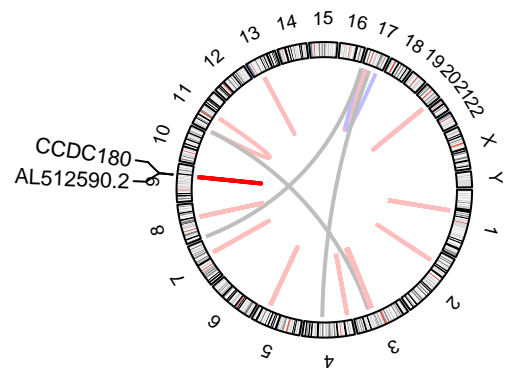
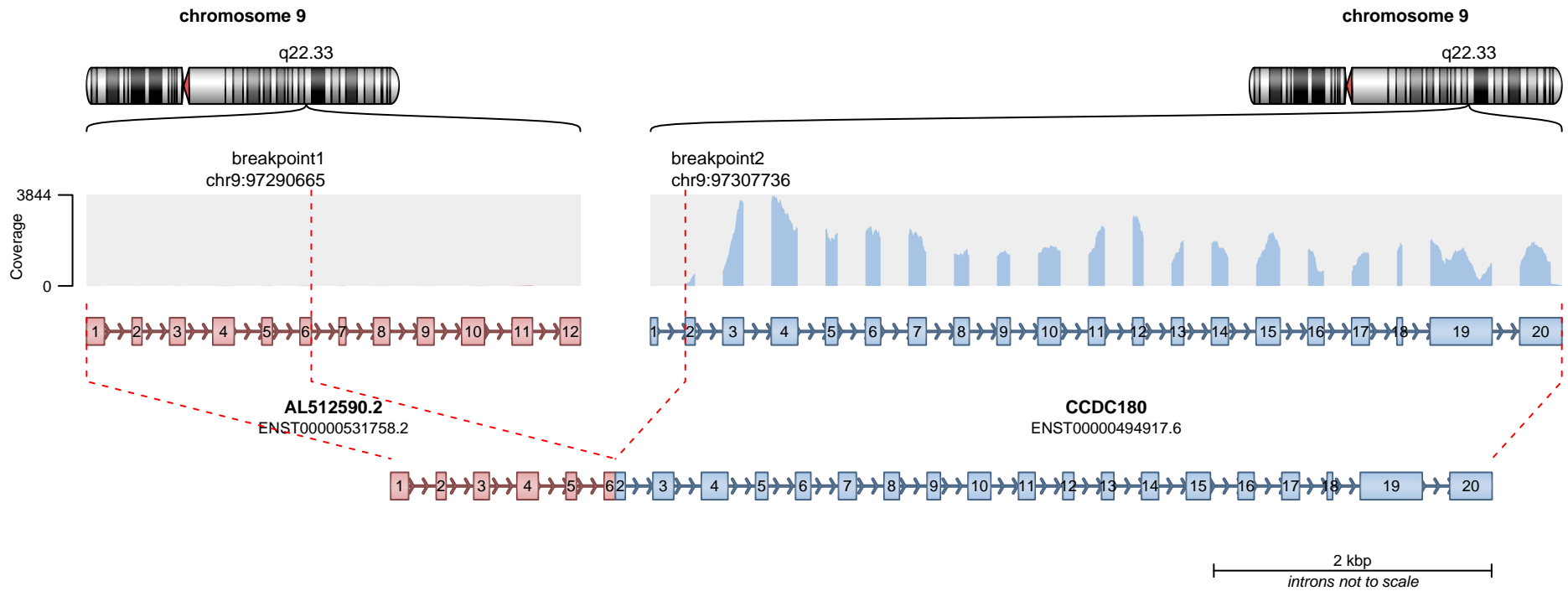


— translocation — deletion
— duplication — inversion

Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 26
Discordant mates = 5

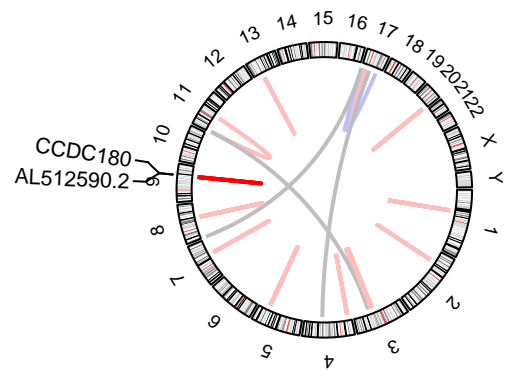
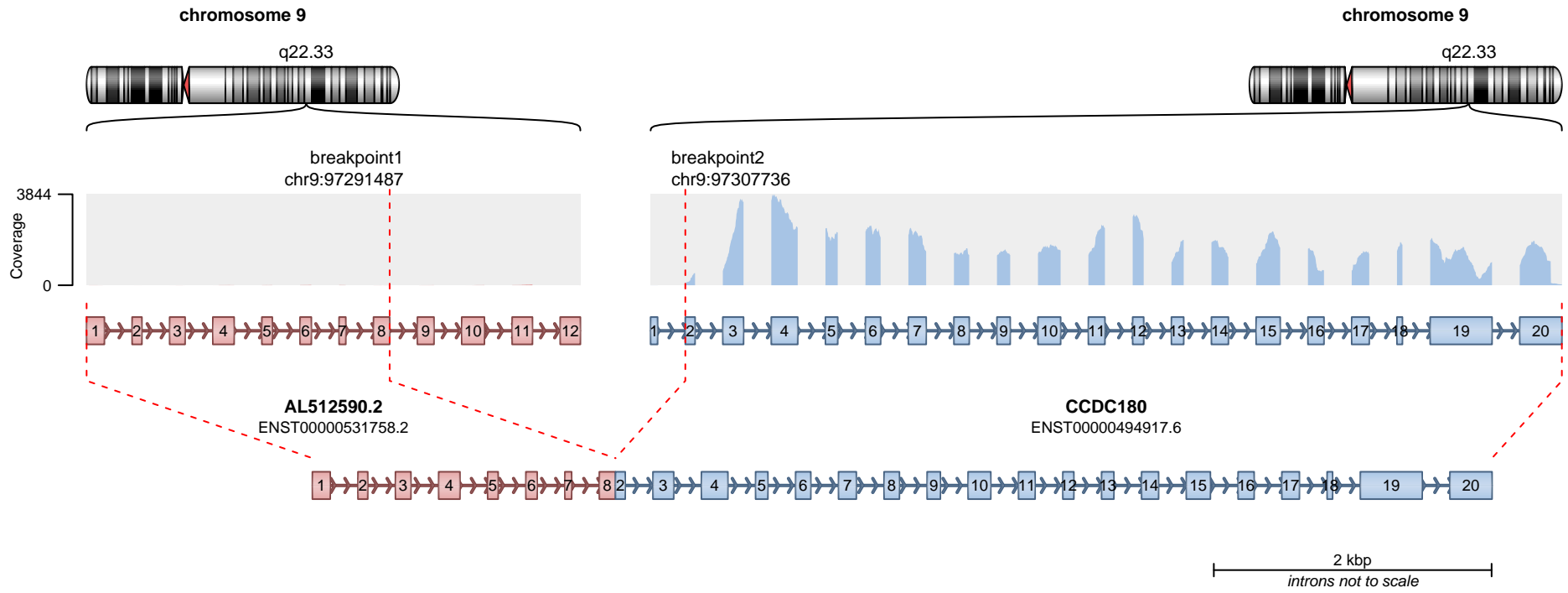


— translocation — deletion
— duplication — inversion

Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 1

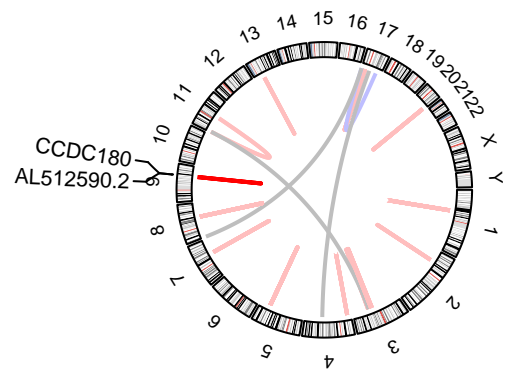
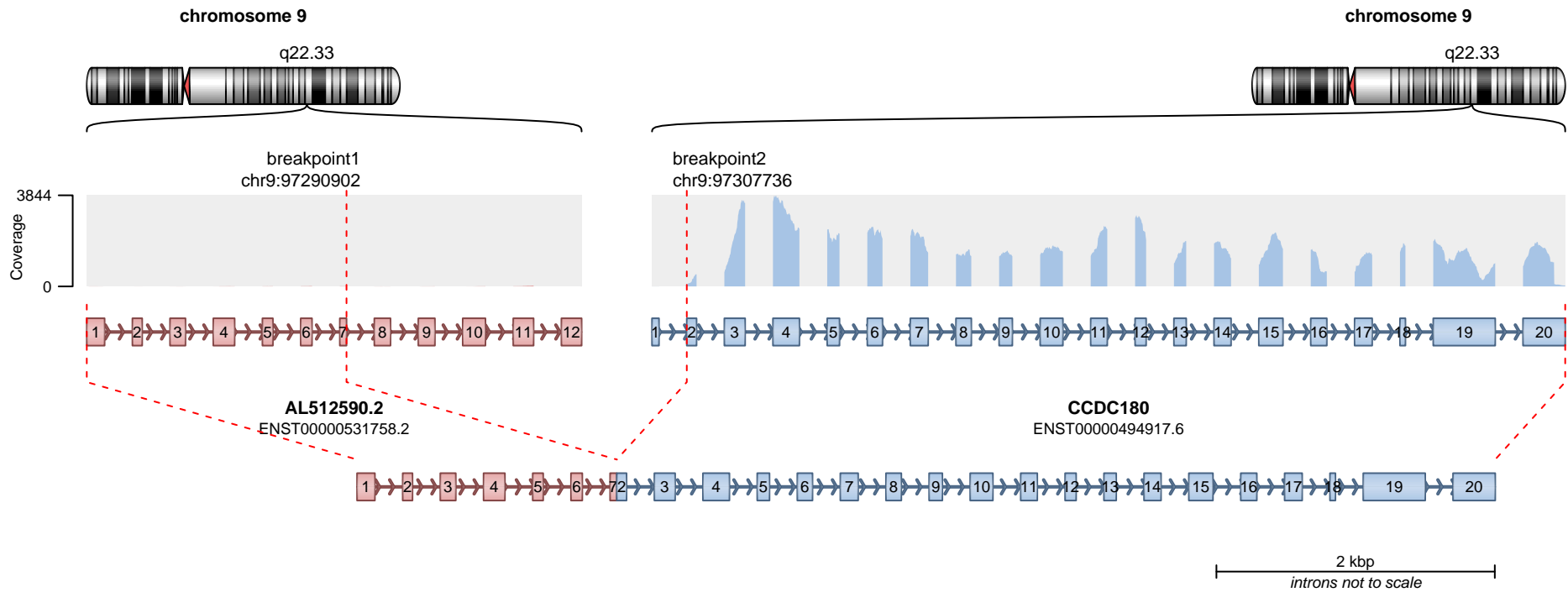


— translocation — deletion
— duplication — inversion

Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 2

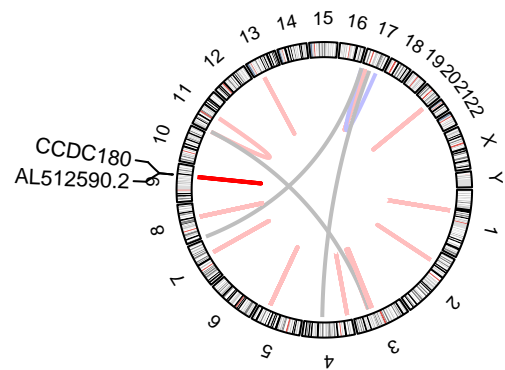
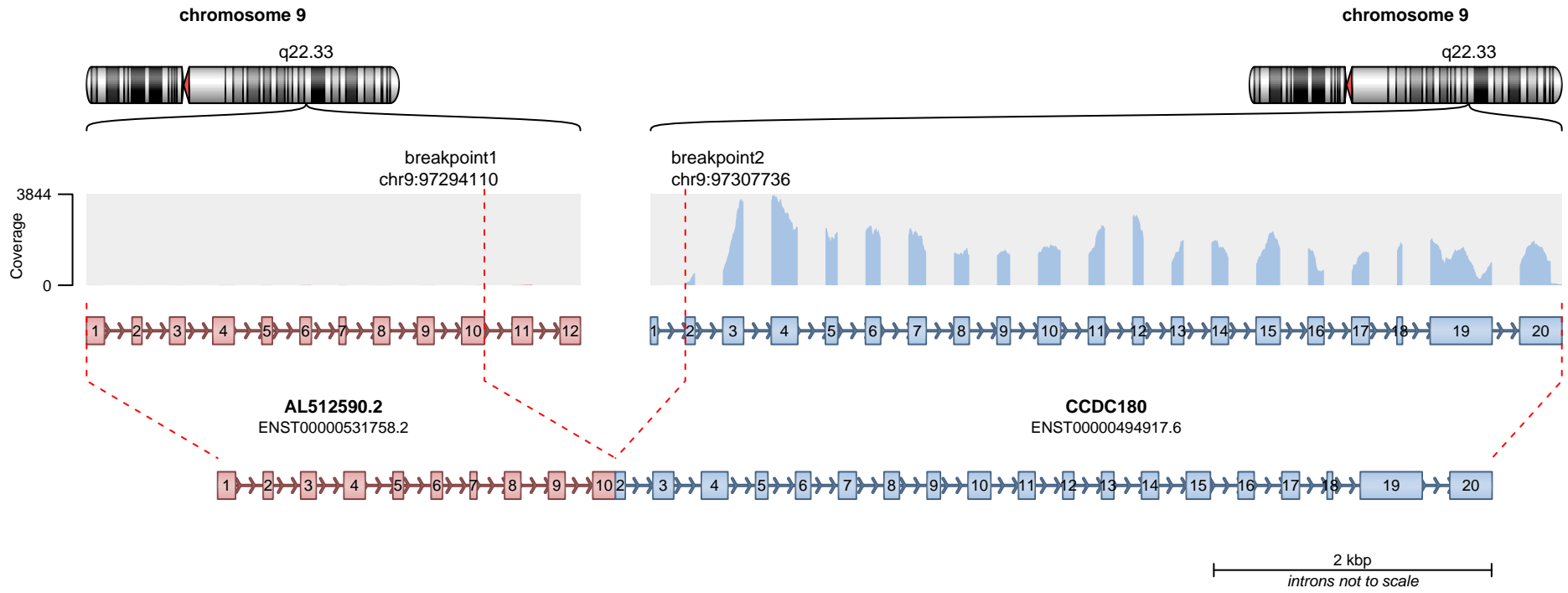


— translocation — deletion
— duplication — inversion

Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 2

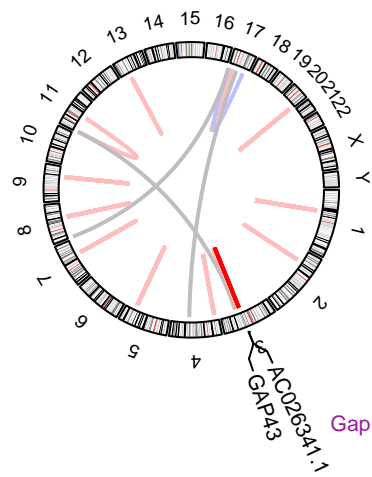
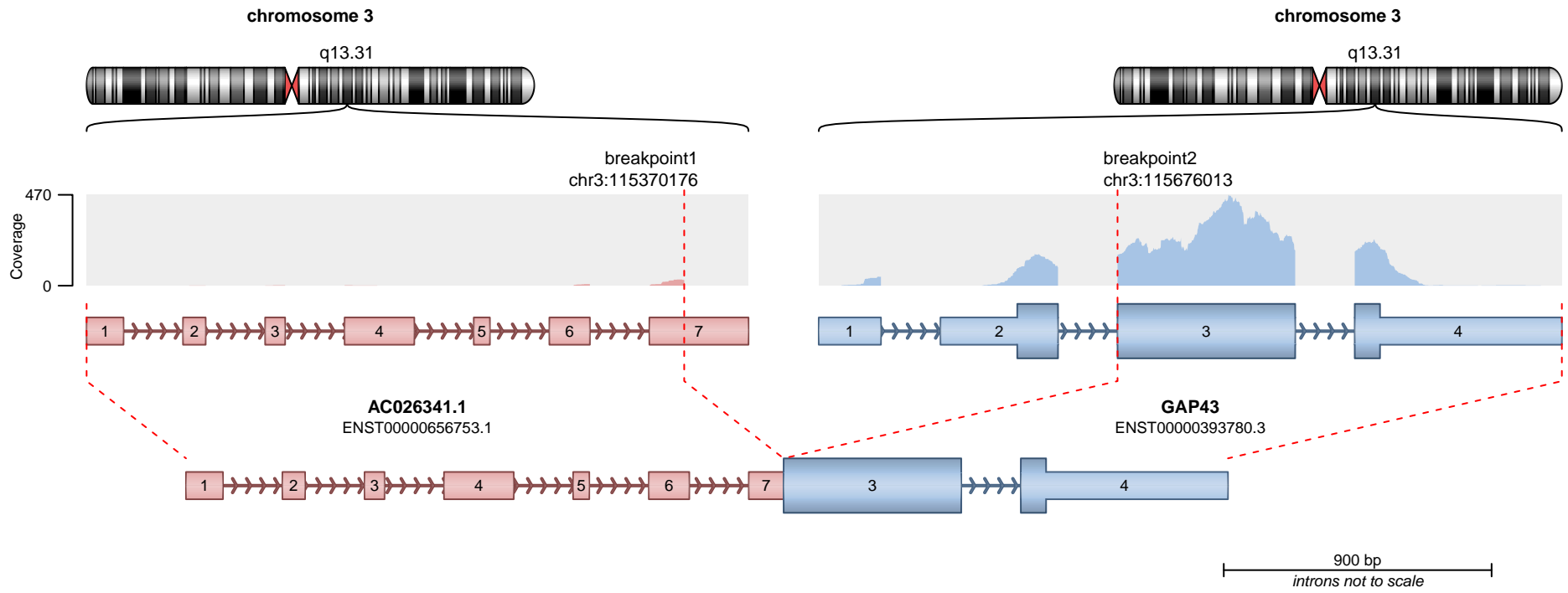


— translocation — deletion
— duplication — inversion

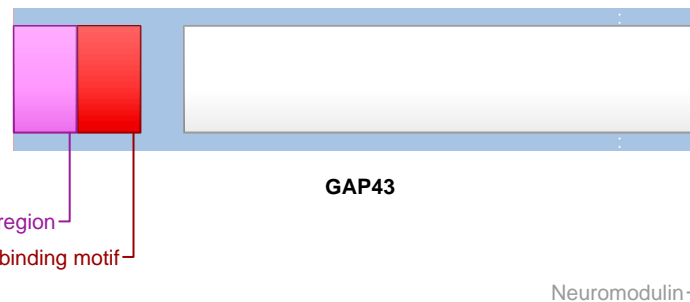
Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 2



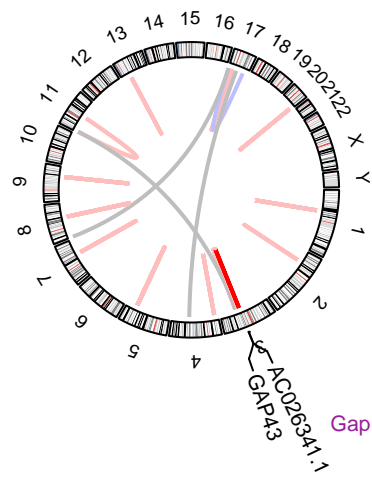
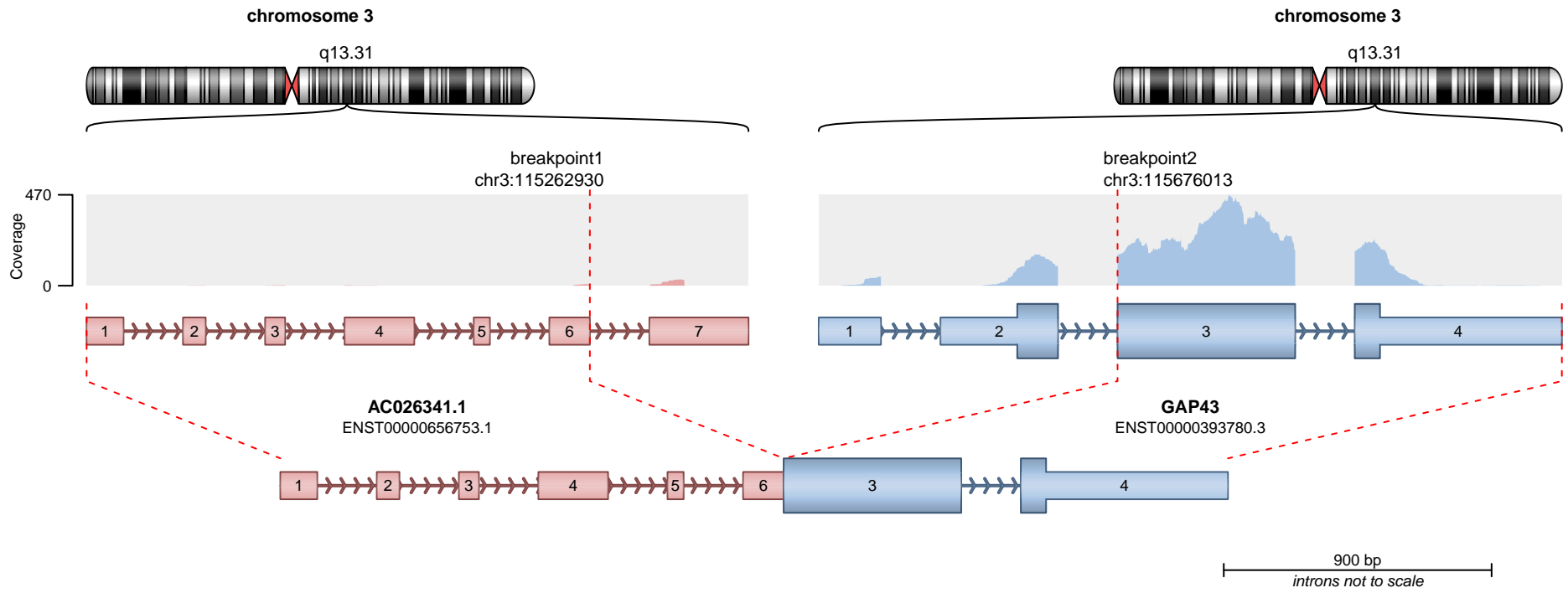
RETAINED PROTEIN DOMAINS
reading frame unclear



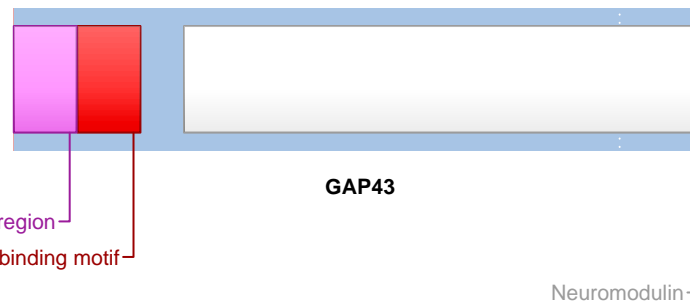
SUPPORTING READ COUNT

Split reads = 19
Discordant mates = 0

— translocation — deletion
— duplication — inversion



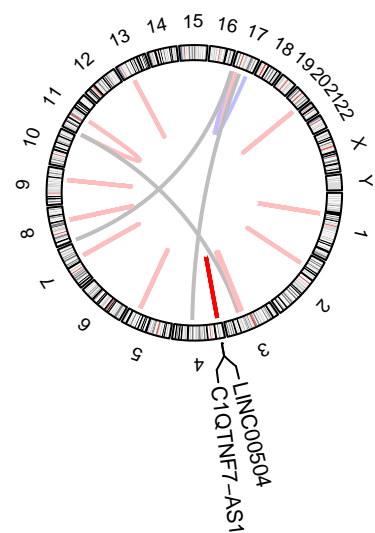
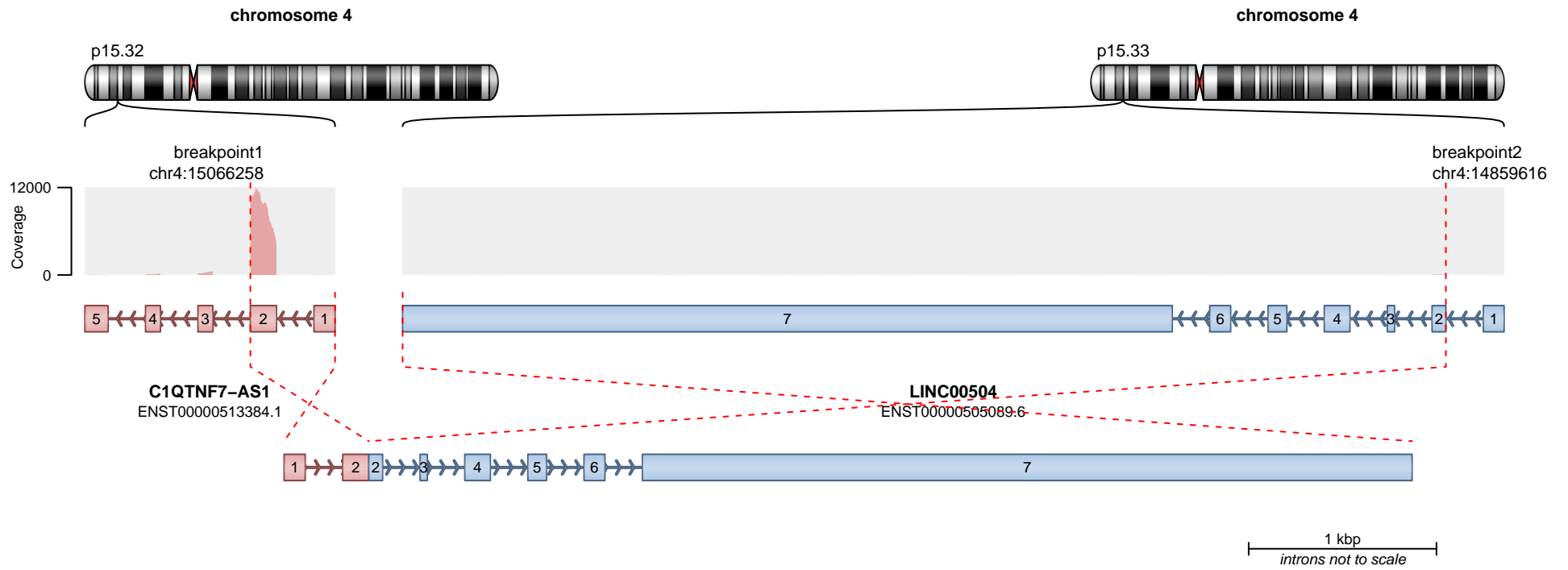
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 0

— translocation — deletion
— duplication — inversion

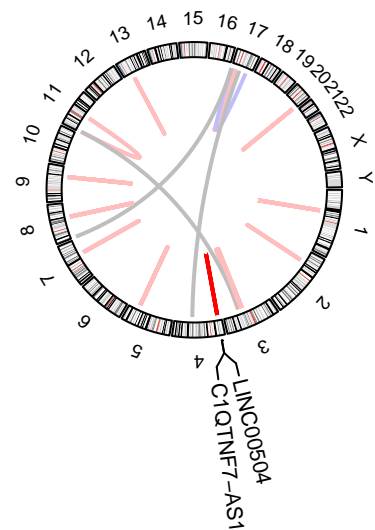
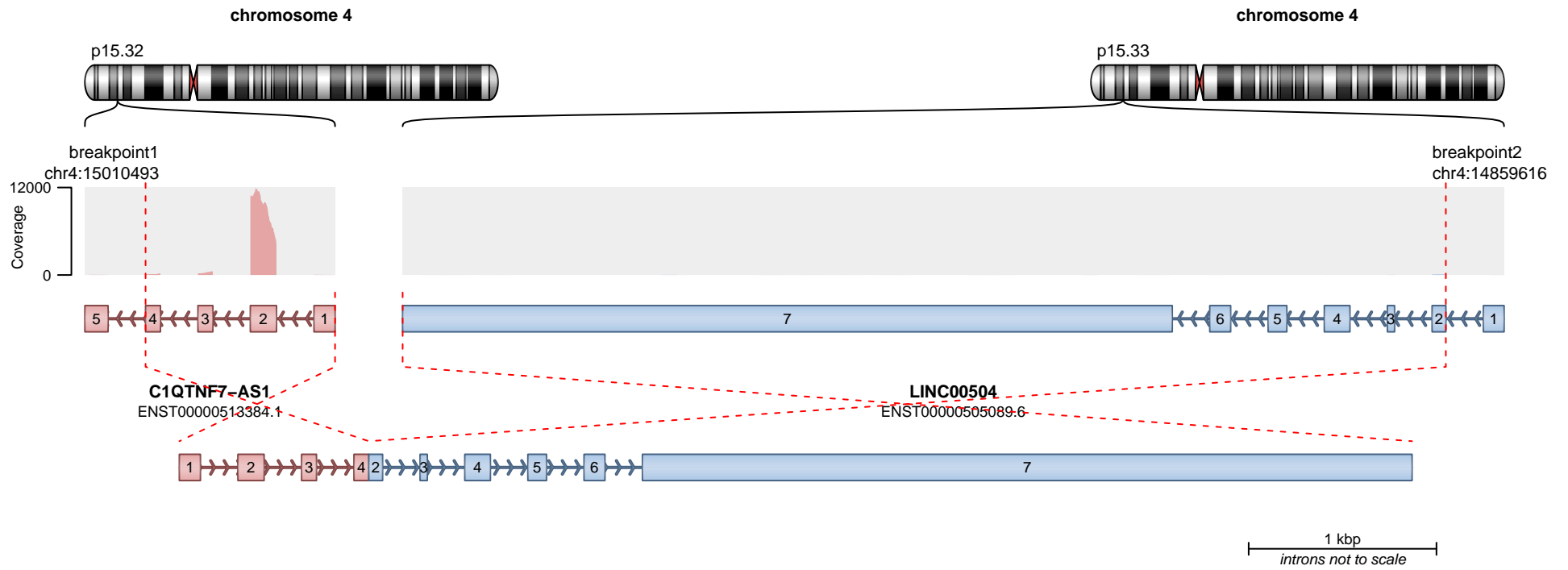


— translocation — deletion
— duplication — inversion

Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 1

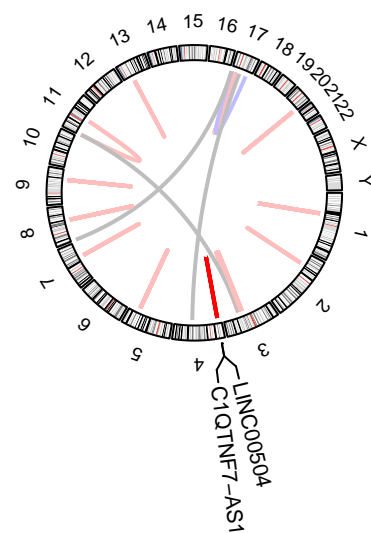
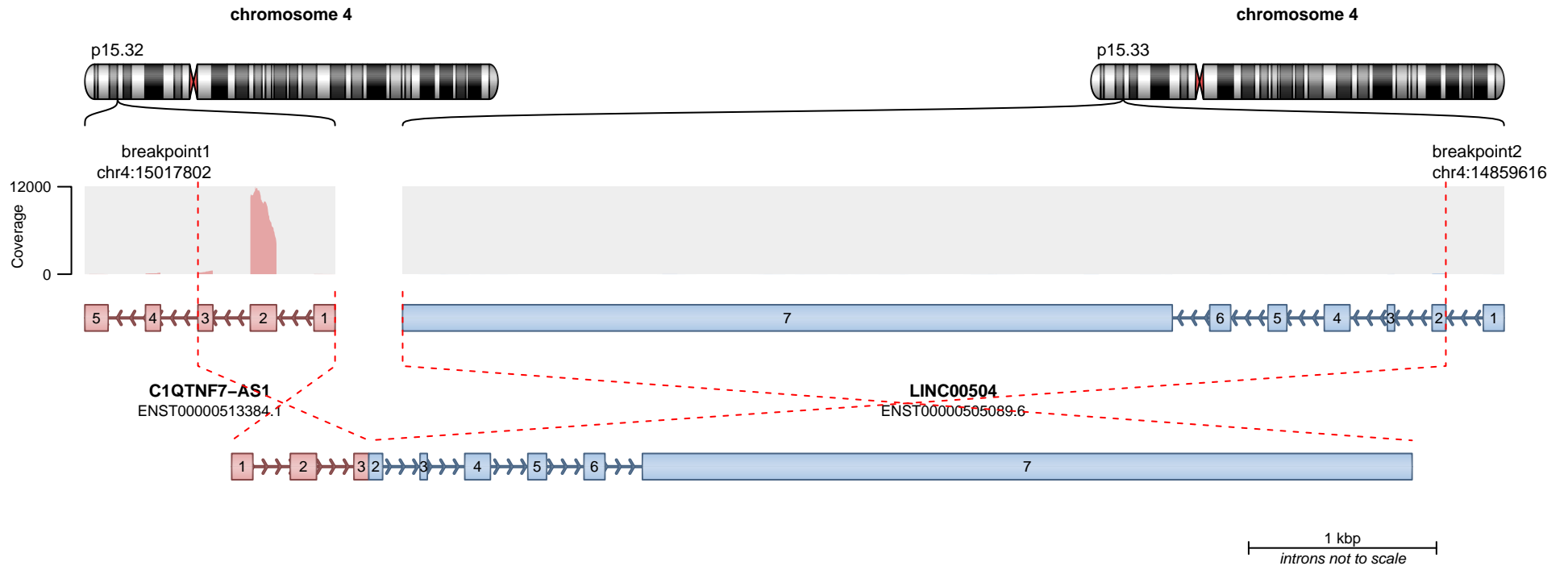


— translocation — deletion
— duplication — inversion

Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 1

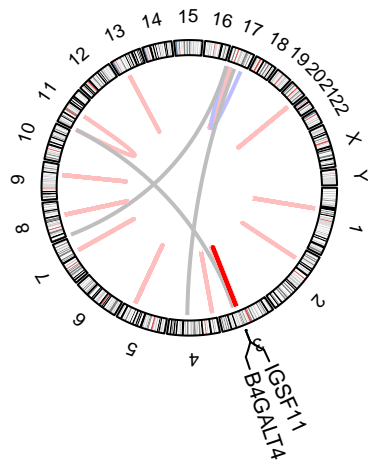
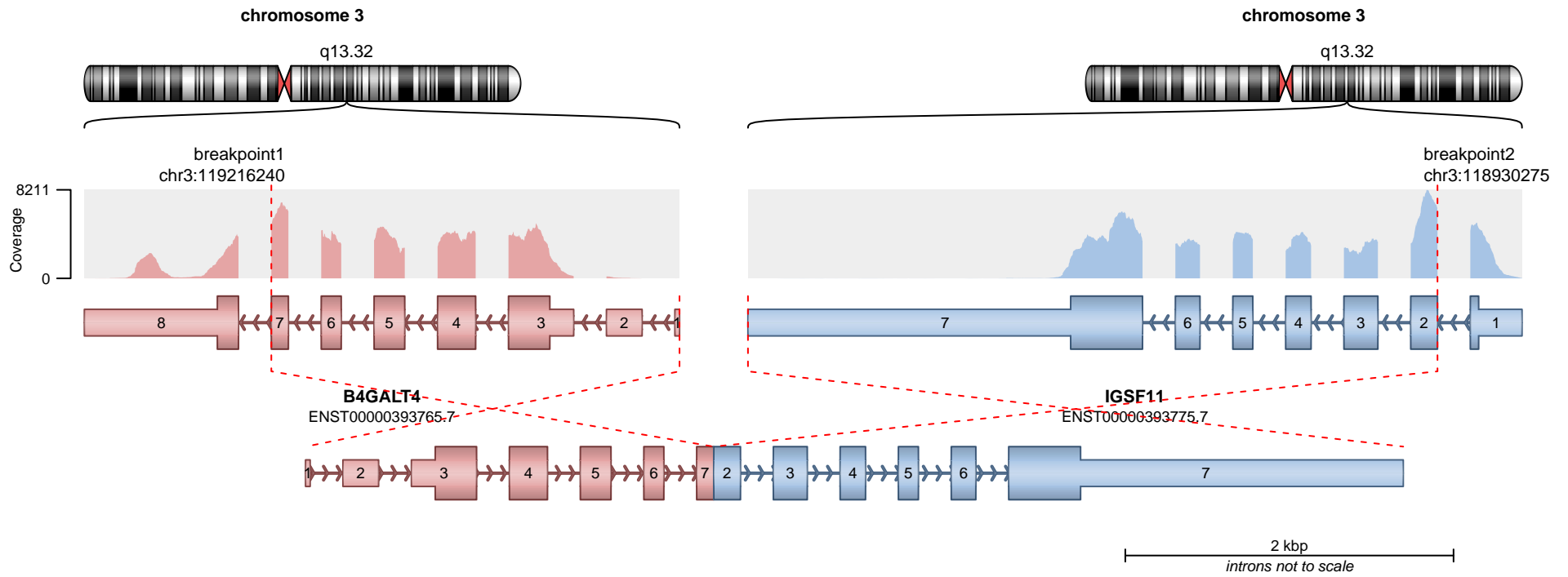


— translocation — deletion
— duplication — inversion

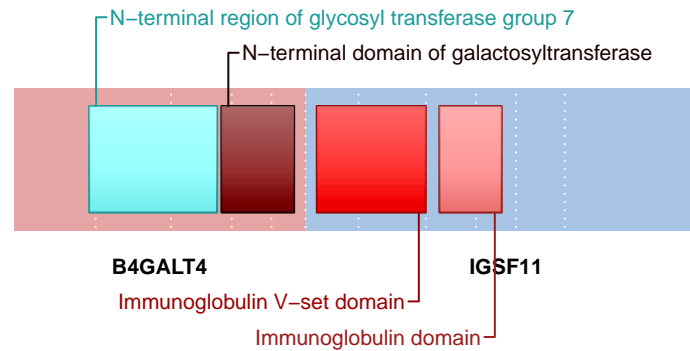
Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1



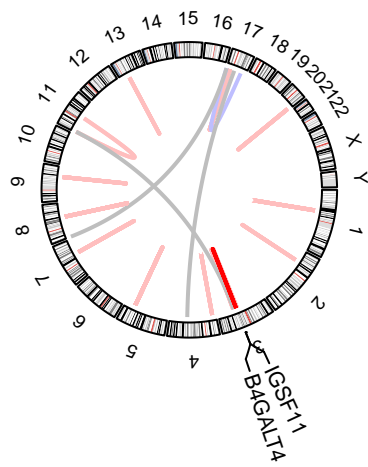
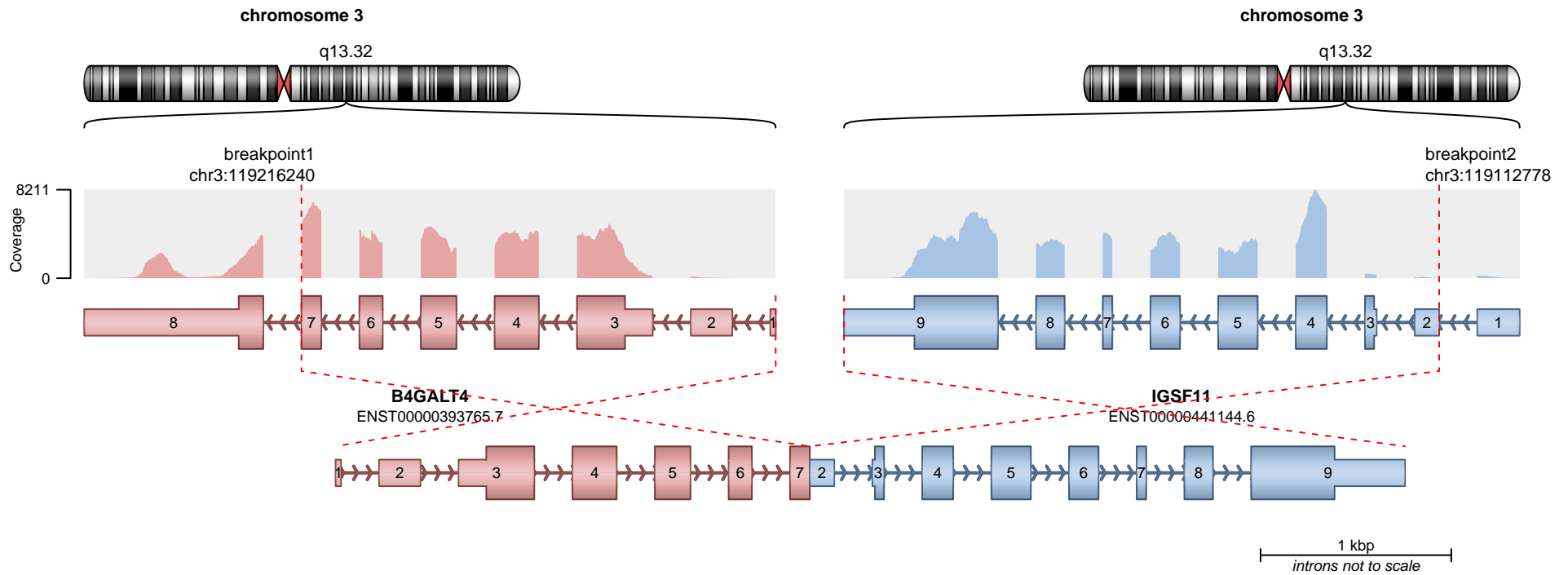
RETAINED PROTEIN DOMAINS
reading frame unclear



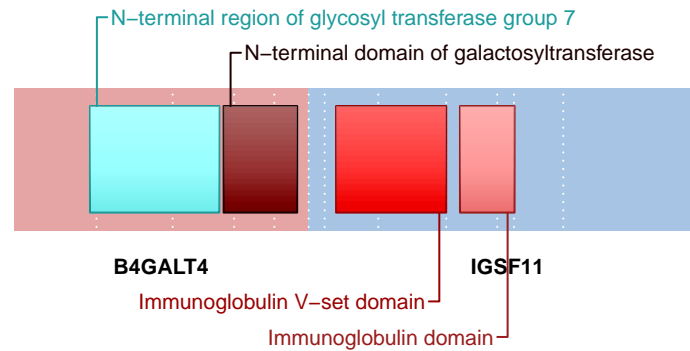
SUPPORTING READ COUNT

Split reads = 11
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion