

RETAINED PROTEIN DOMAINS
reading frame unclear

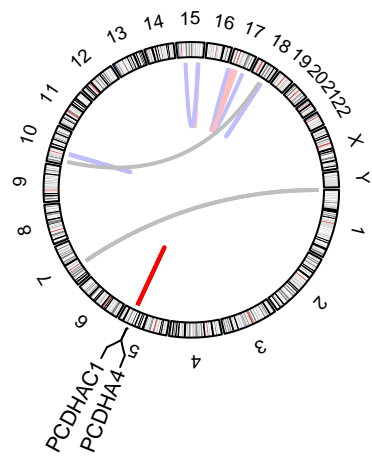
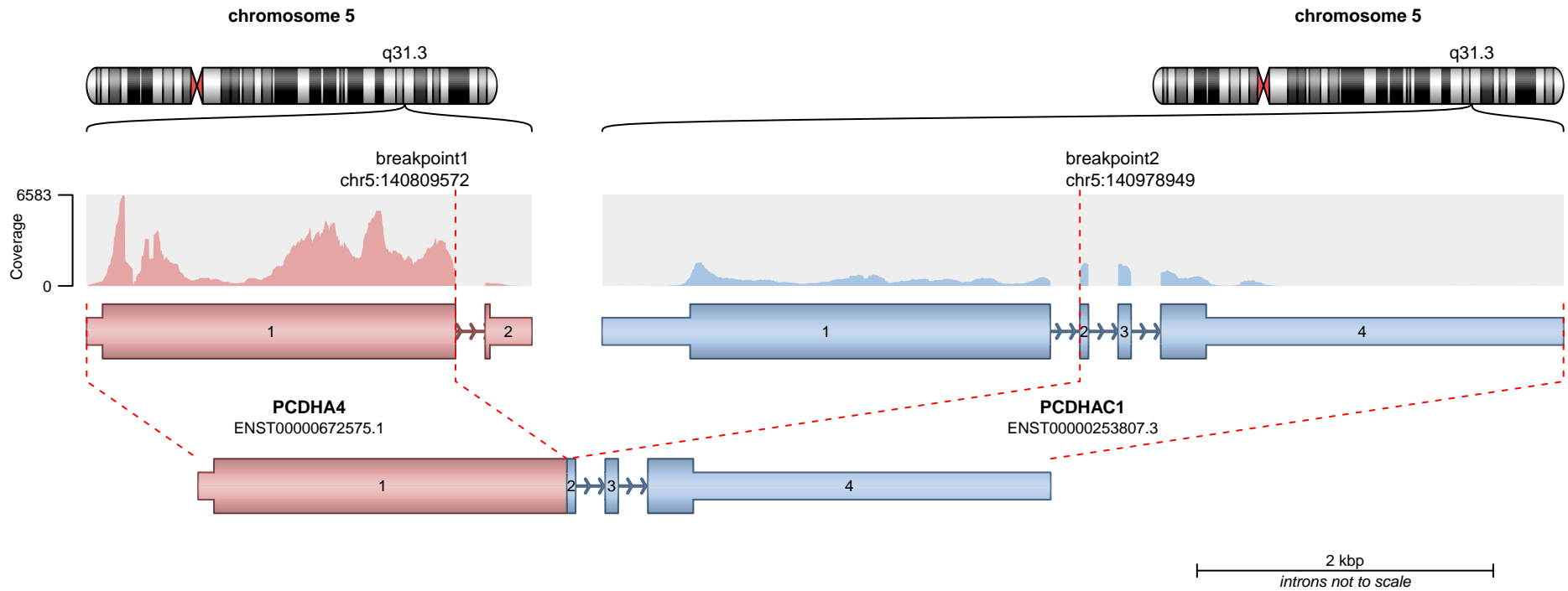


SUPPORTING READ COUNT

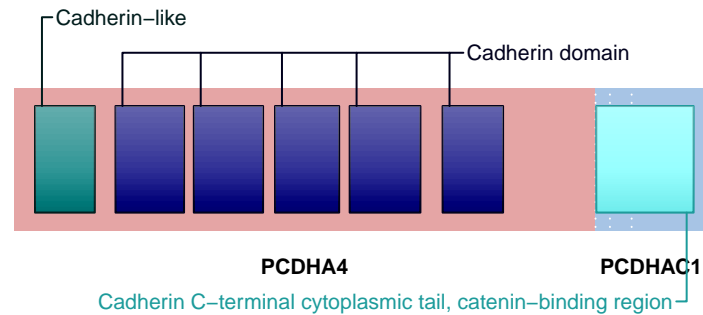
Split reads = 312
Discordant mates = 1

Putative golgin subfamily A member 2-like protein 5

- translocation
- duplication
- deletion
- inversion



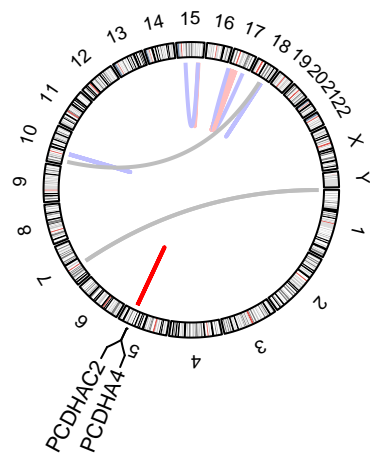
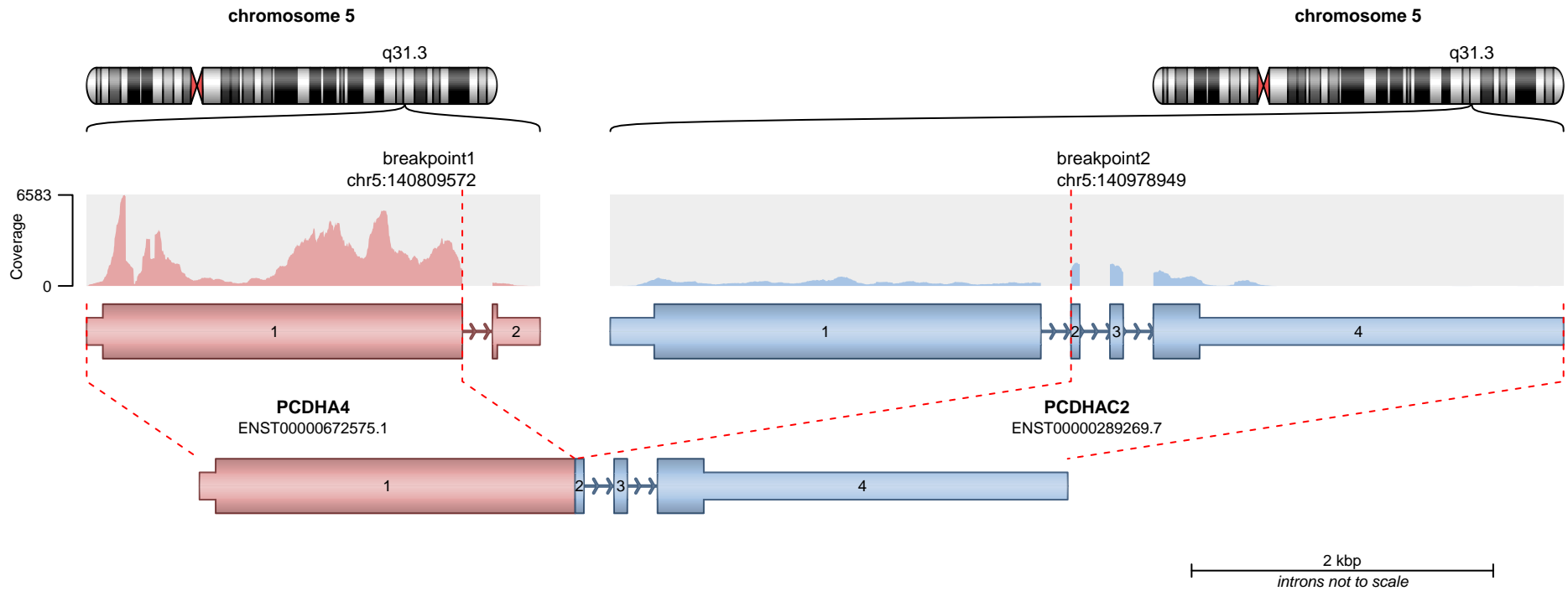
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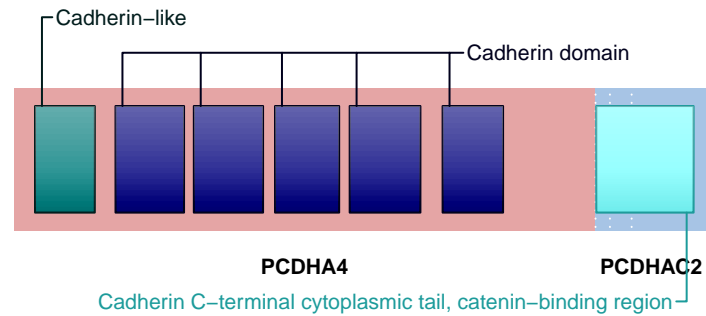
SUPPORTING READ COUNT

Split reads = 188
Discordant mates = 0

— translocation — deletion
— duplication — inversion



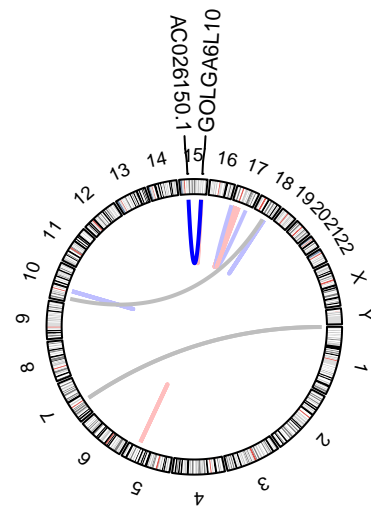
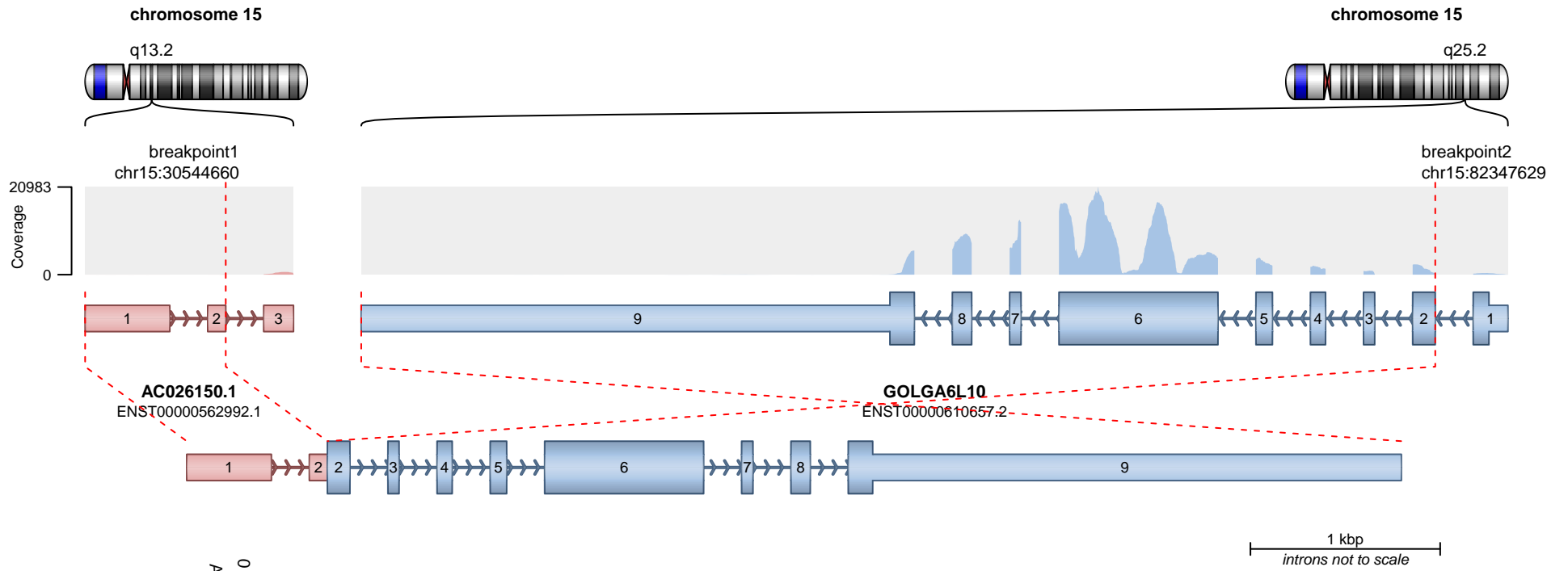
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reading frame unclear



SUPPORTING READ COUNT

Split reads = 188
Discordant mates = 0

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

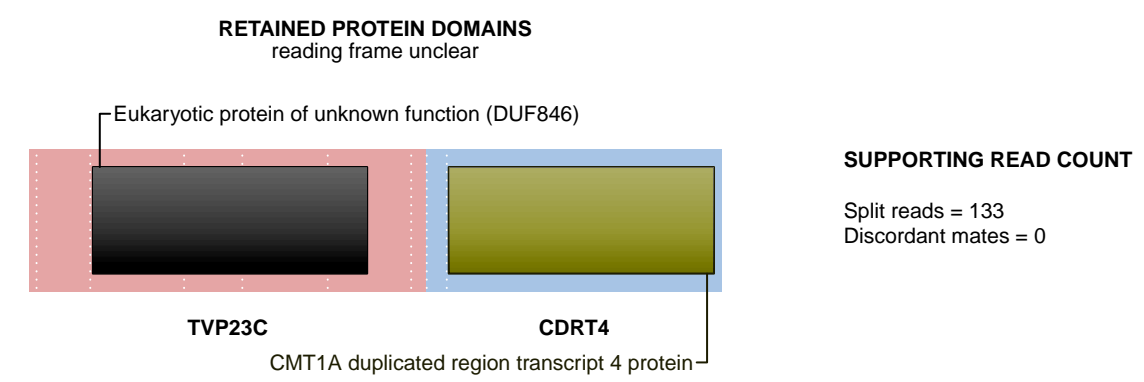
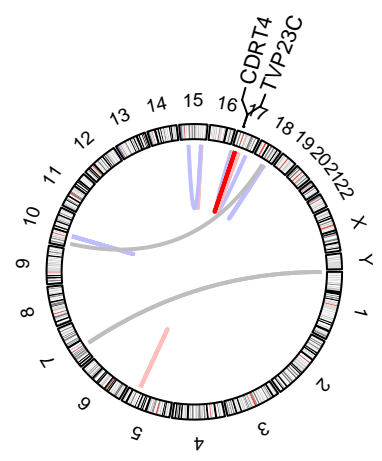
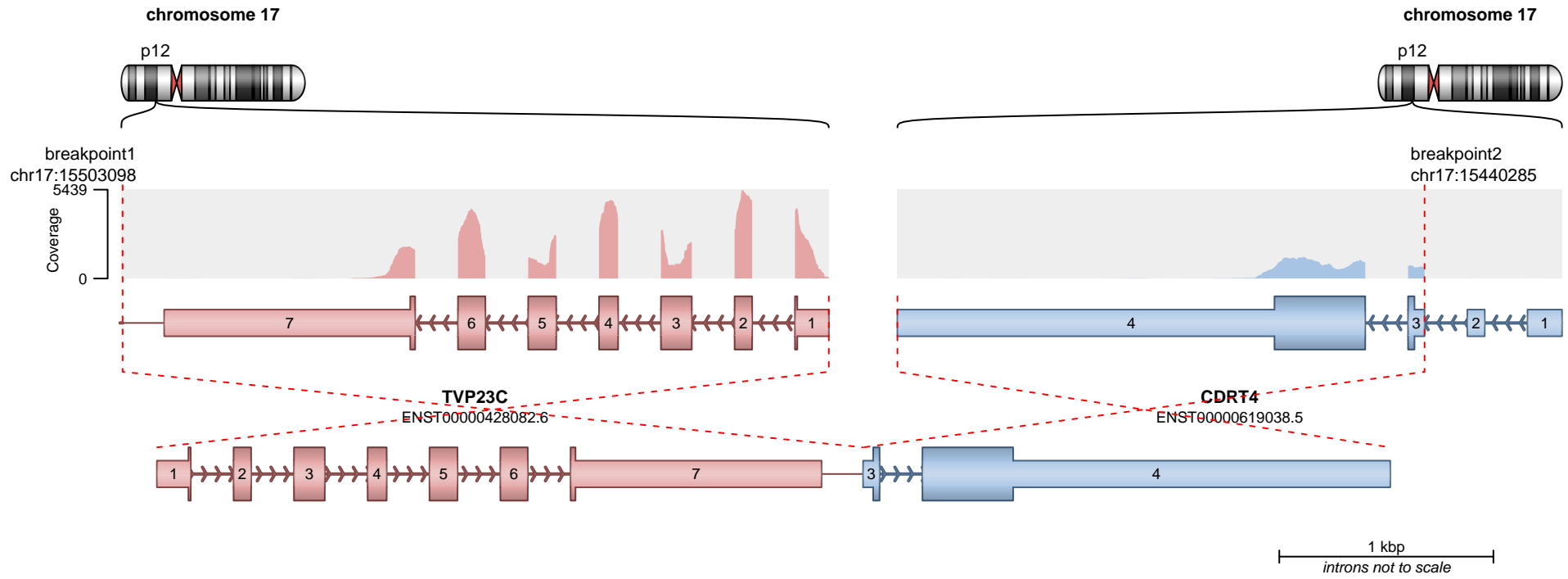


SUPPORTING READ COUNT

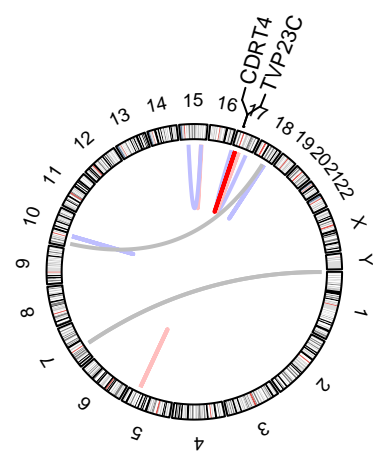
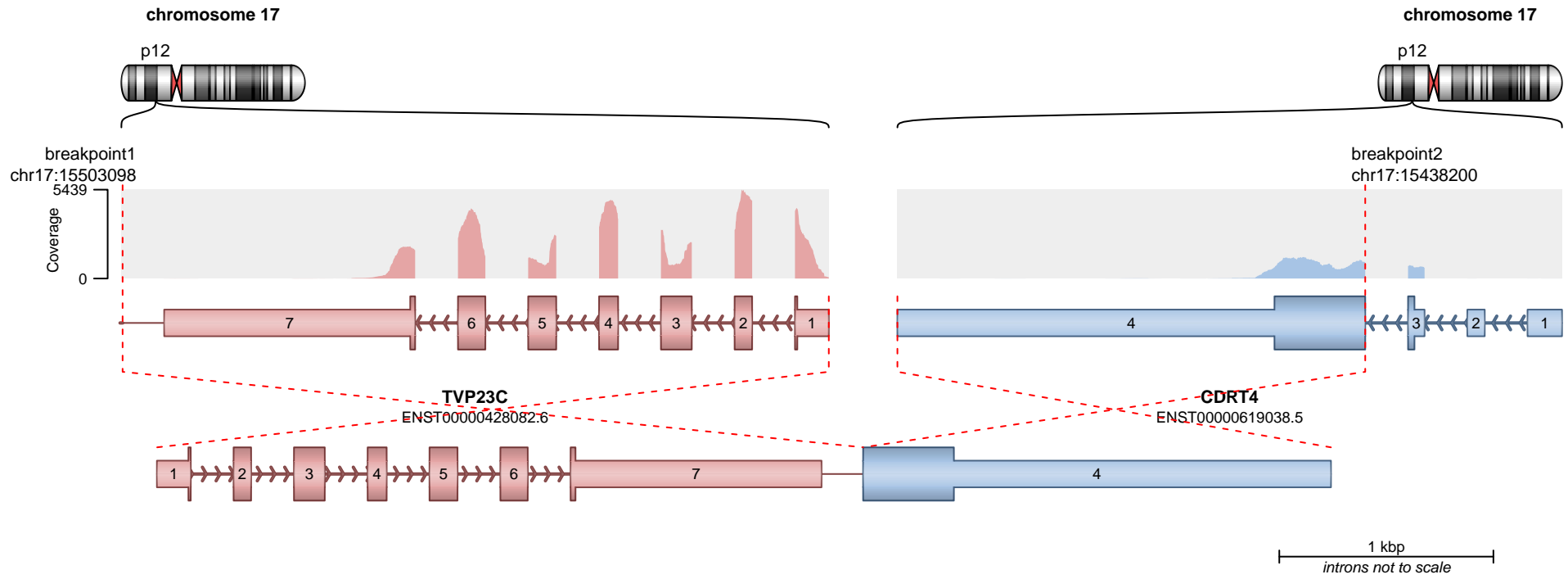
Split reads = 175
Discordant mates = 0

Putative golgin subfamily A member 2-like protein 5

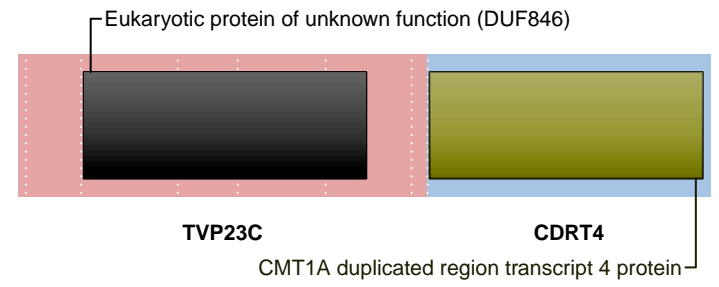
- translocation
- duplication
- deletion
- inversion



— translocation — deletion
— duplication — inversion



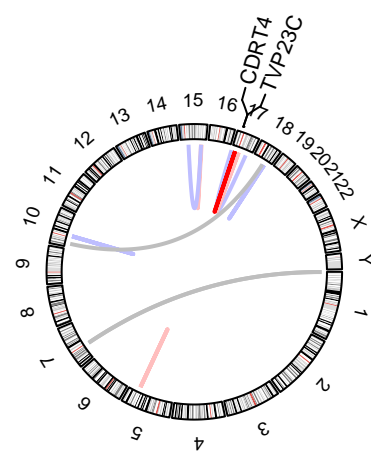
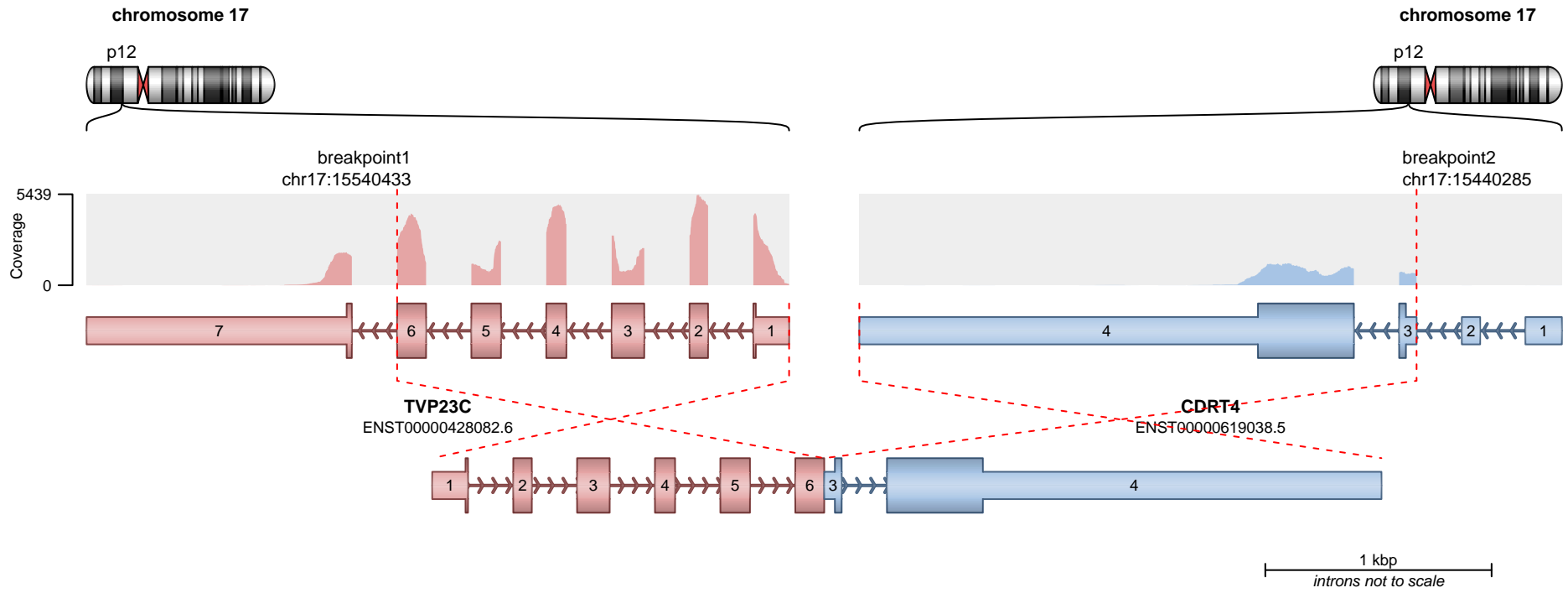
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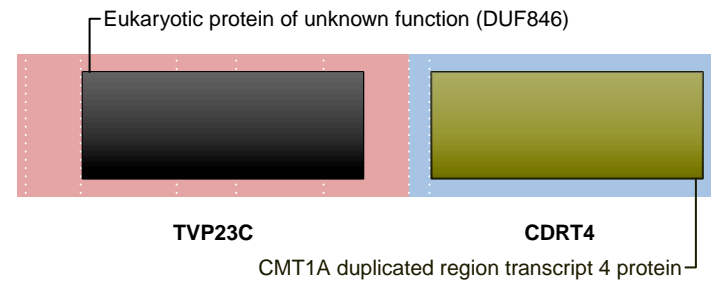
SUPPORTING READ COUNT

Split reads = 32
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



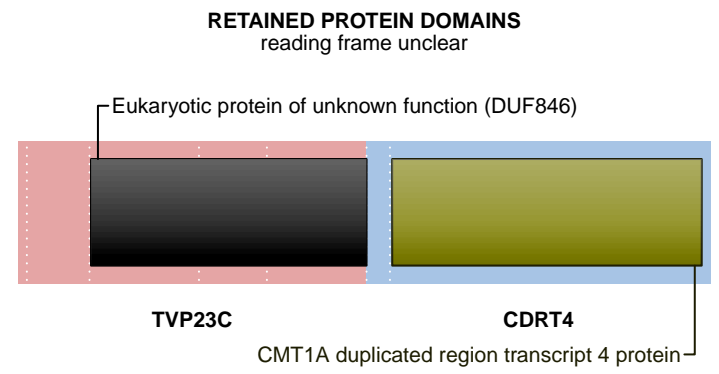
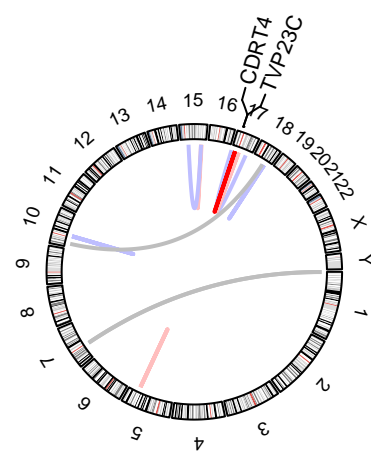
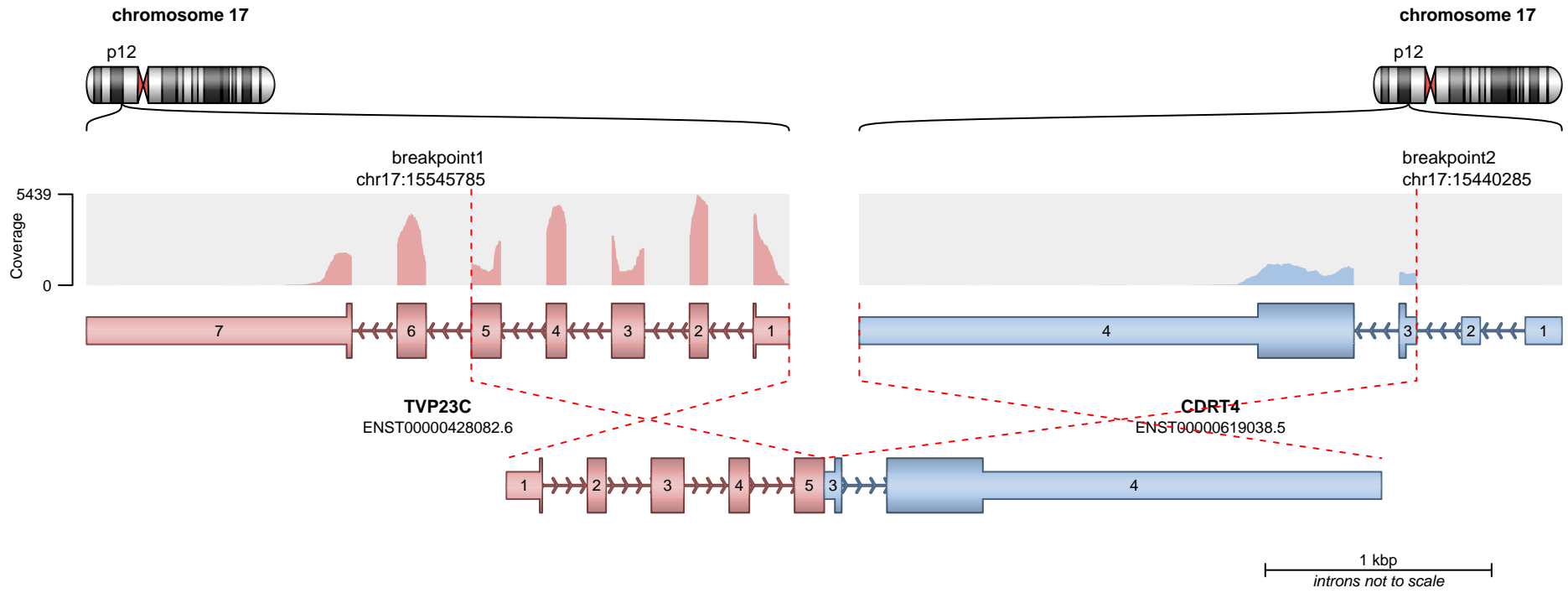
RETAINED PROTEIN DOMAINS
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SUPPORTING READ COUNT

Split reads = 20
Discordant mates = 0

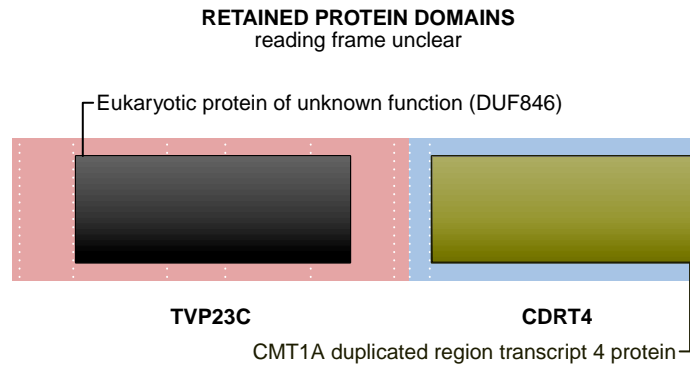
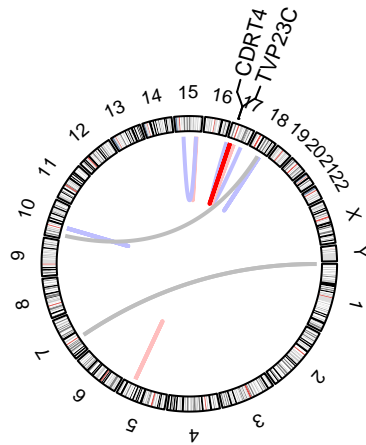
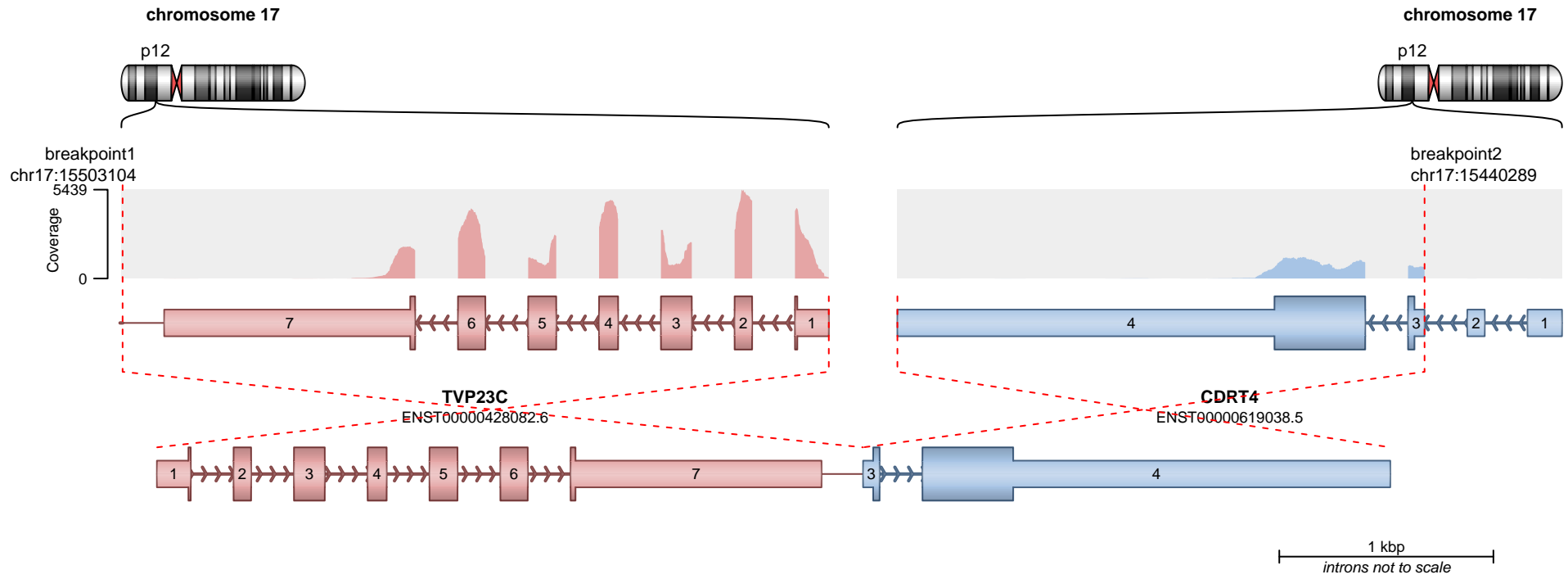
- translocation
- duplication
- deletion
- inversion



SUPPORTING READ COUNT

Split reads = 9
Discordant mates = 0

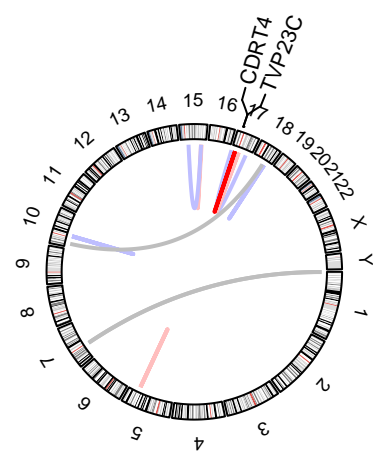
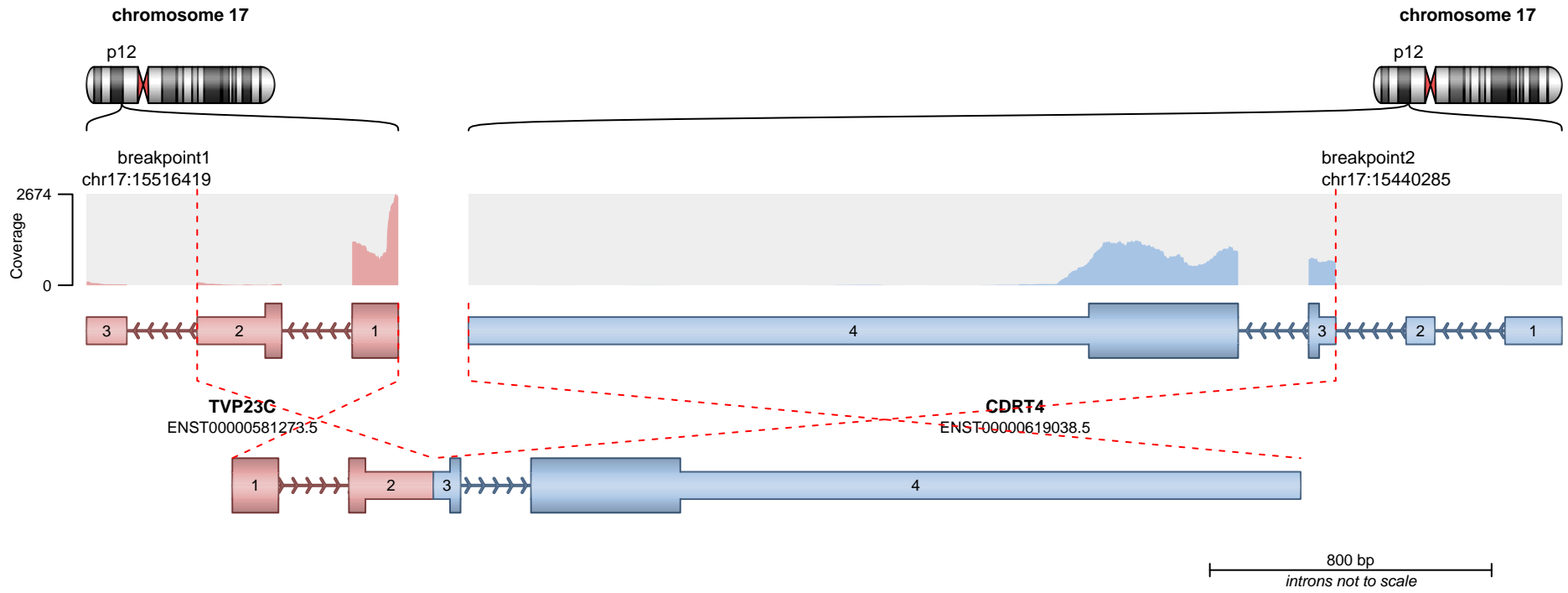
— translocation — deletion
— duplication — inversion



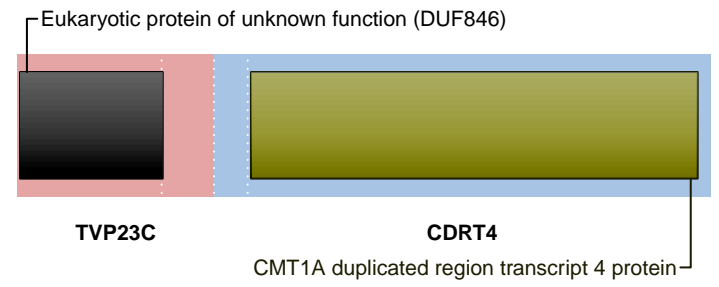
SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0

— translocation — deletion
— duplication — inversion



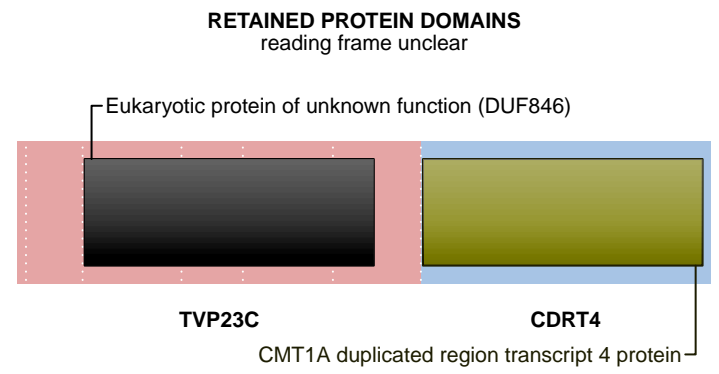
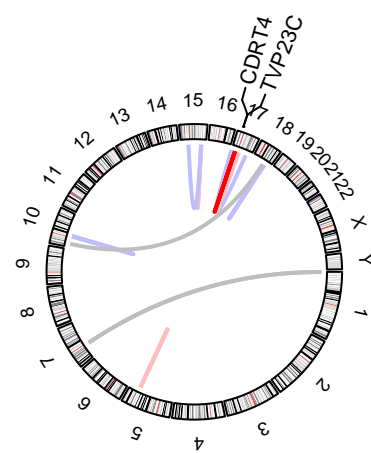
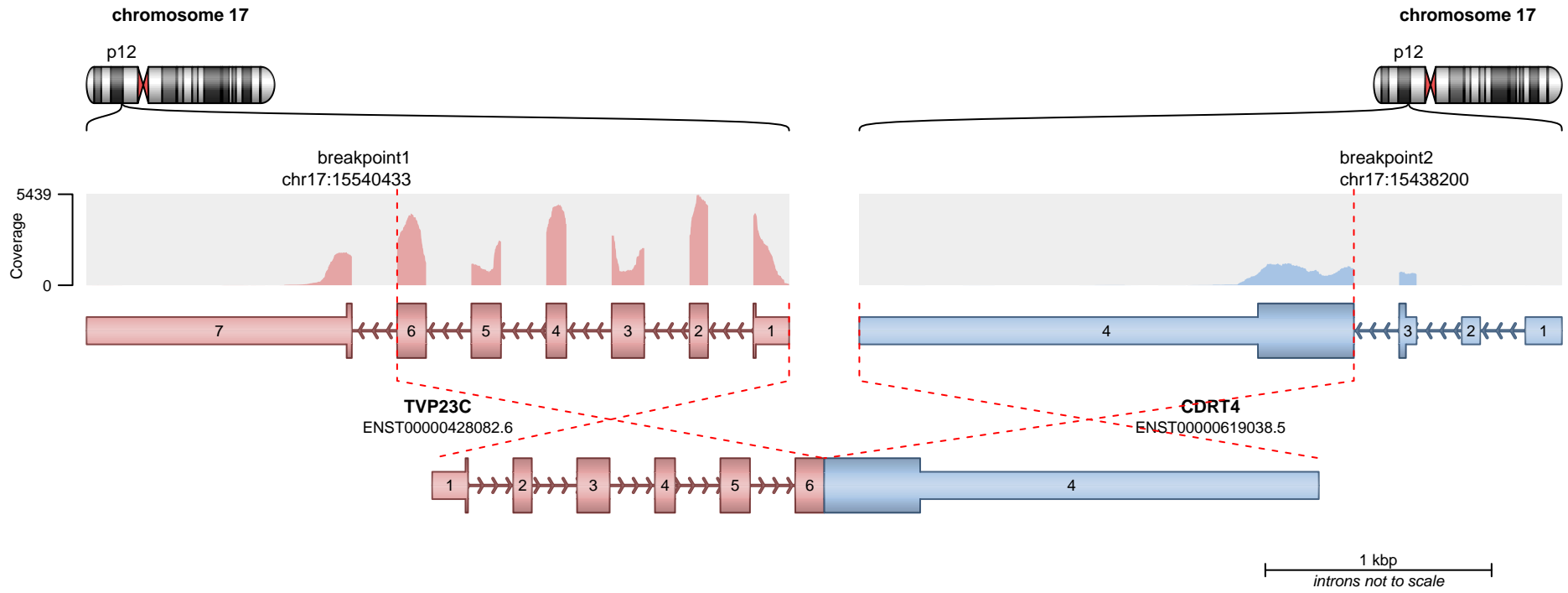
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SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

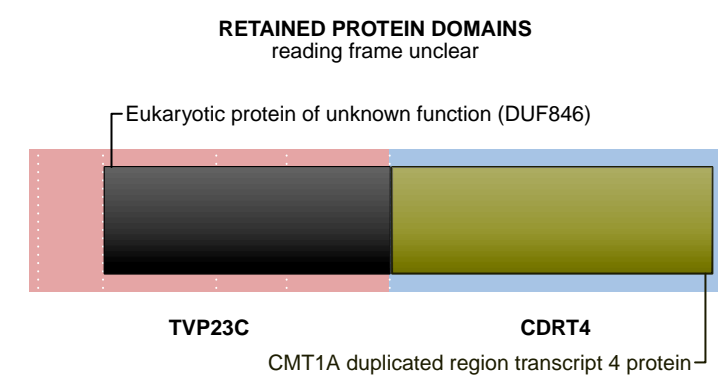
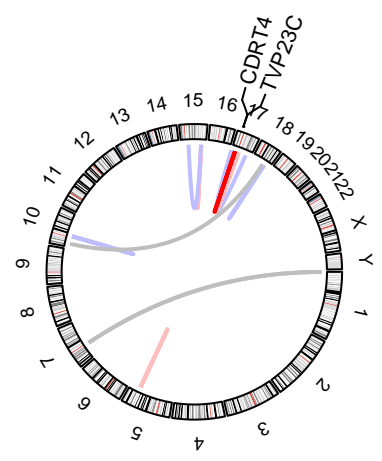
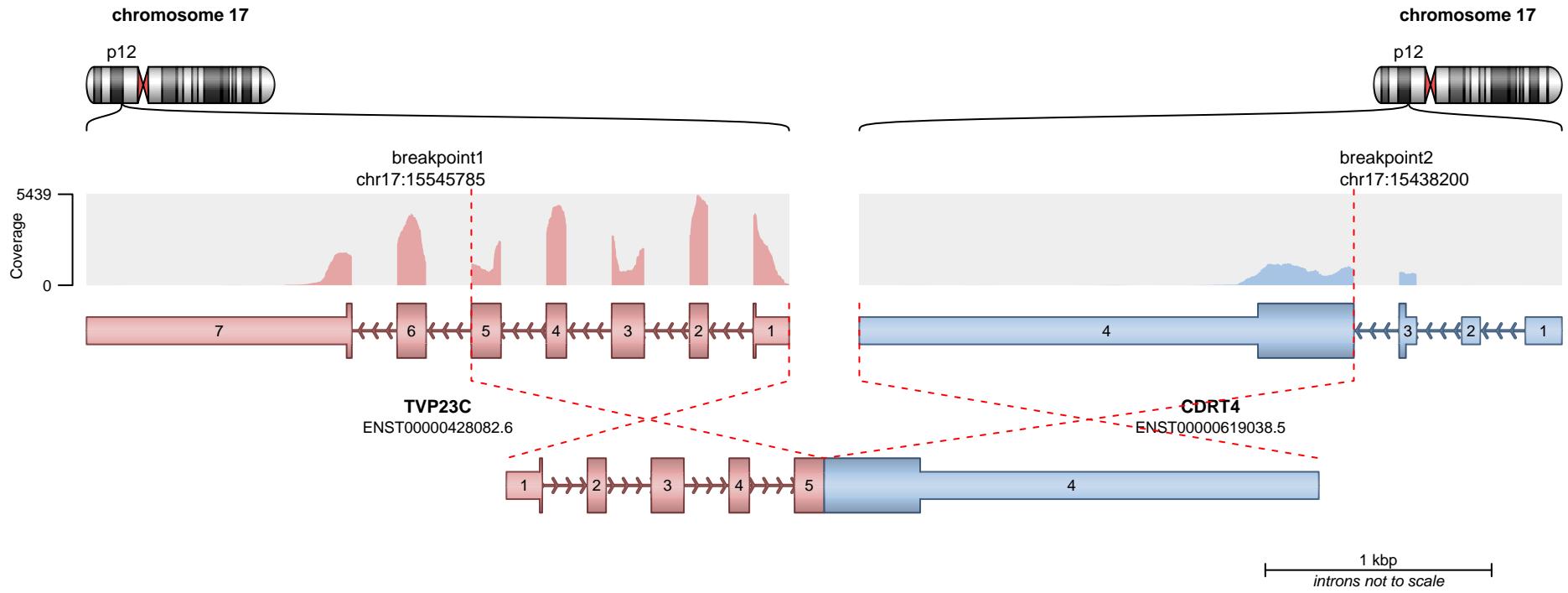
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

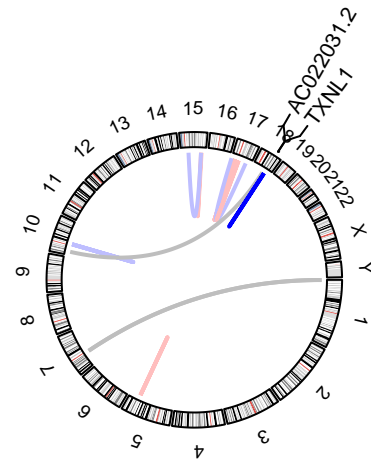
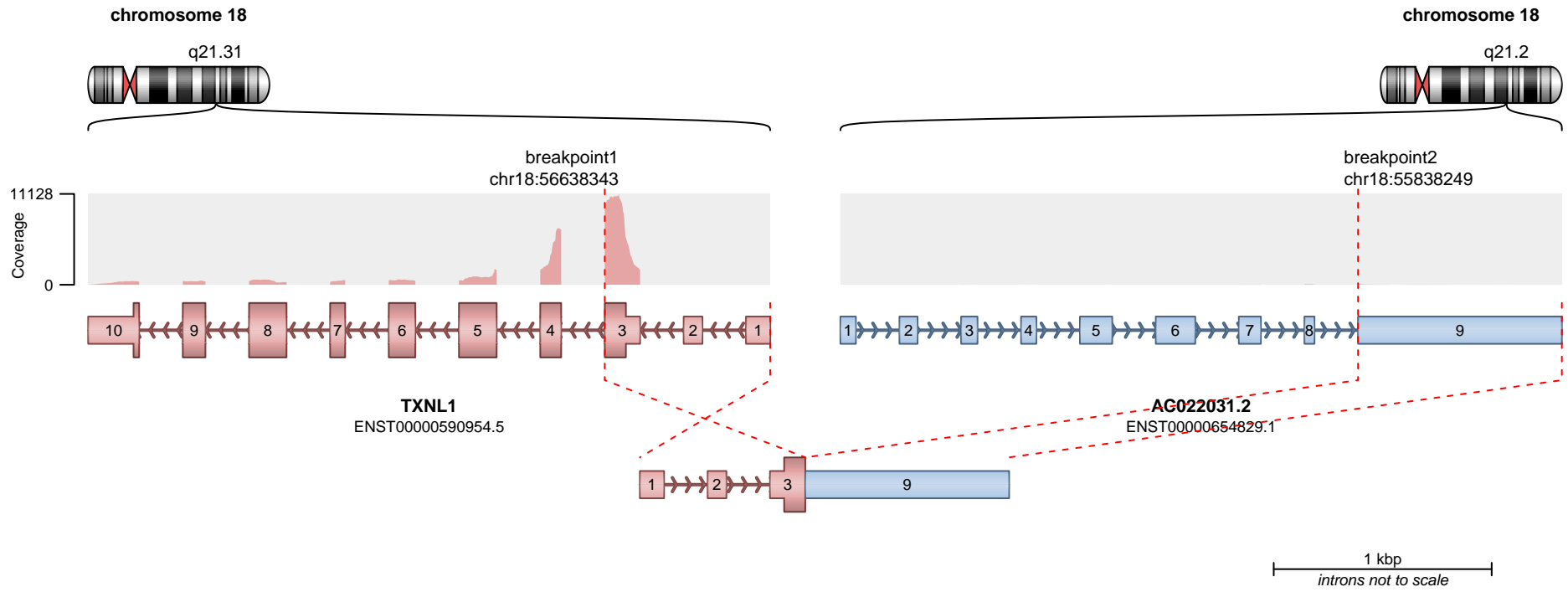
— translocation — deletion
— duplication — inversion



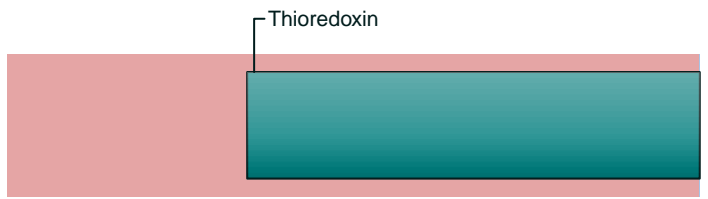
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

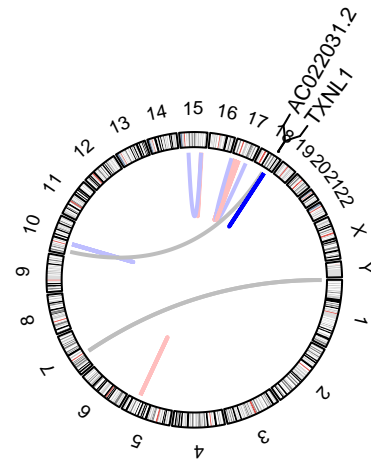
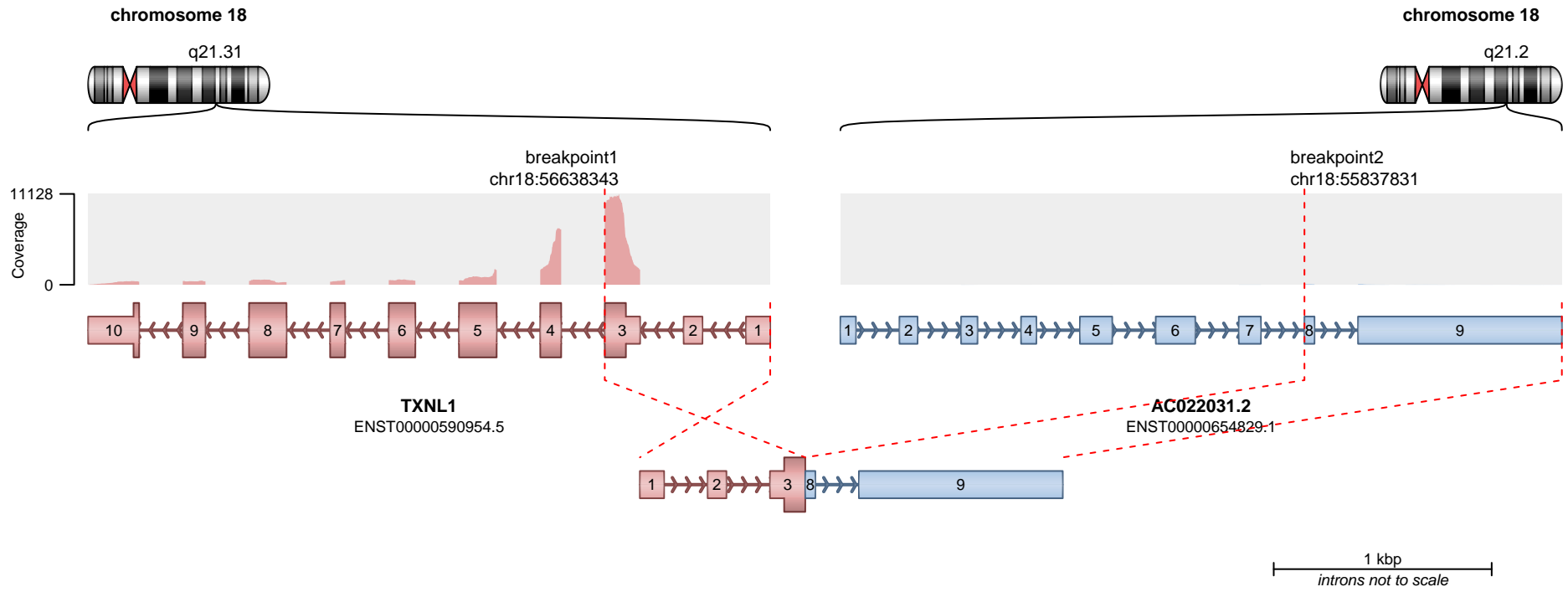


TXNL1

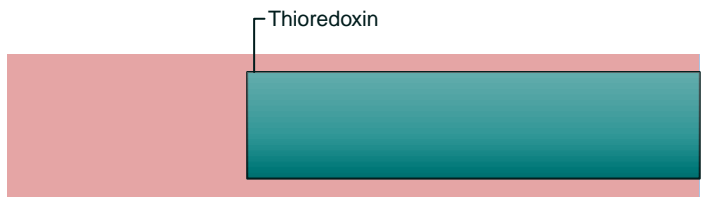
SUPPORTING READ COUNT

Split reads = 71
Discordant mates = 0

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

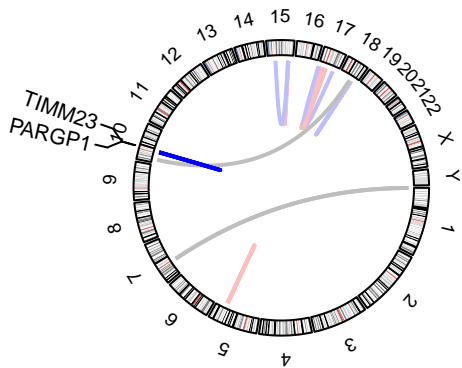
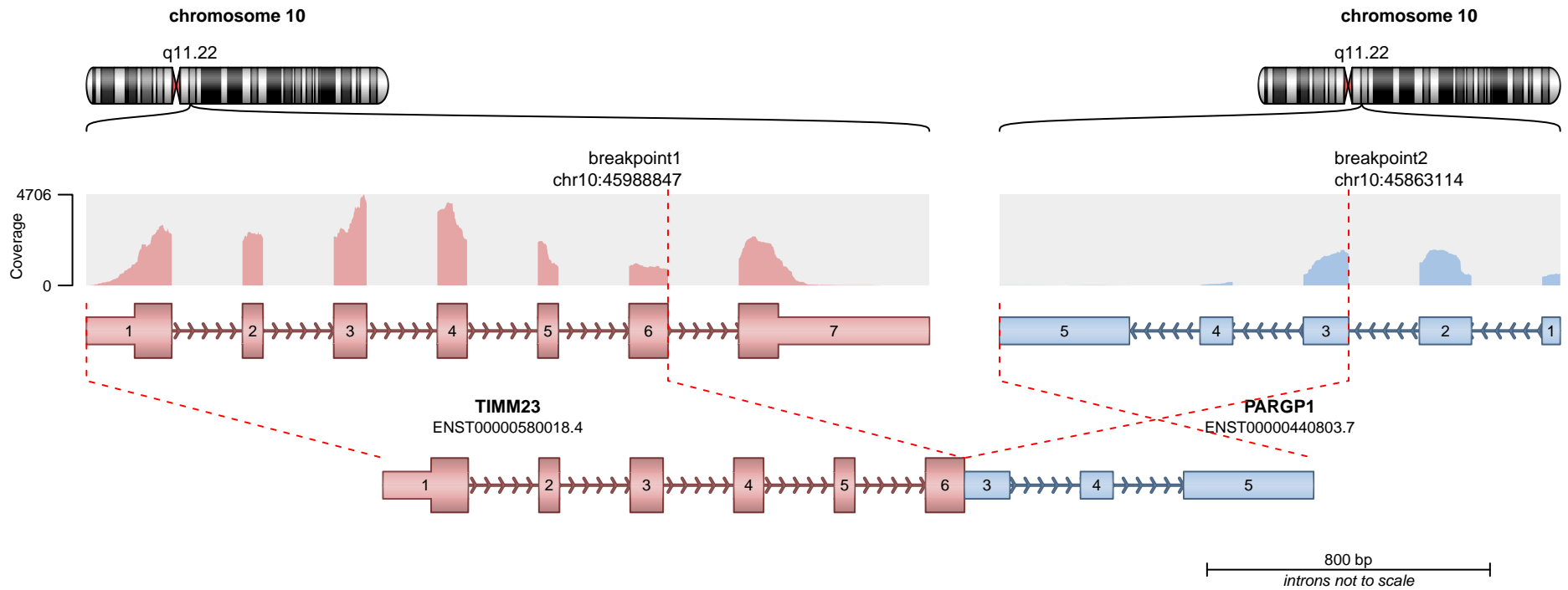


TXNL1

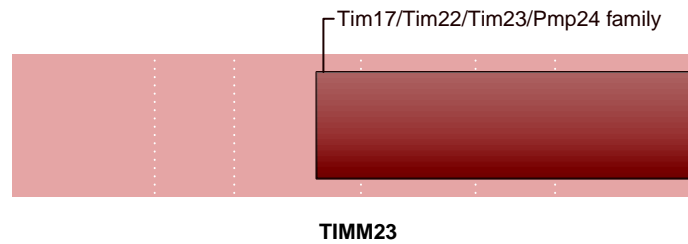
SUPPORTING READ COUNT

Split reads = 46
Discordant mates = 0

— translocation — deletion
— duplication — inversion



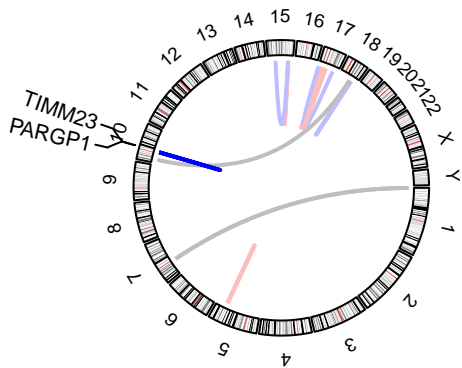
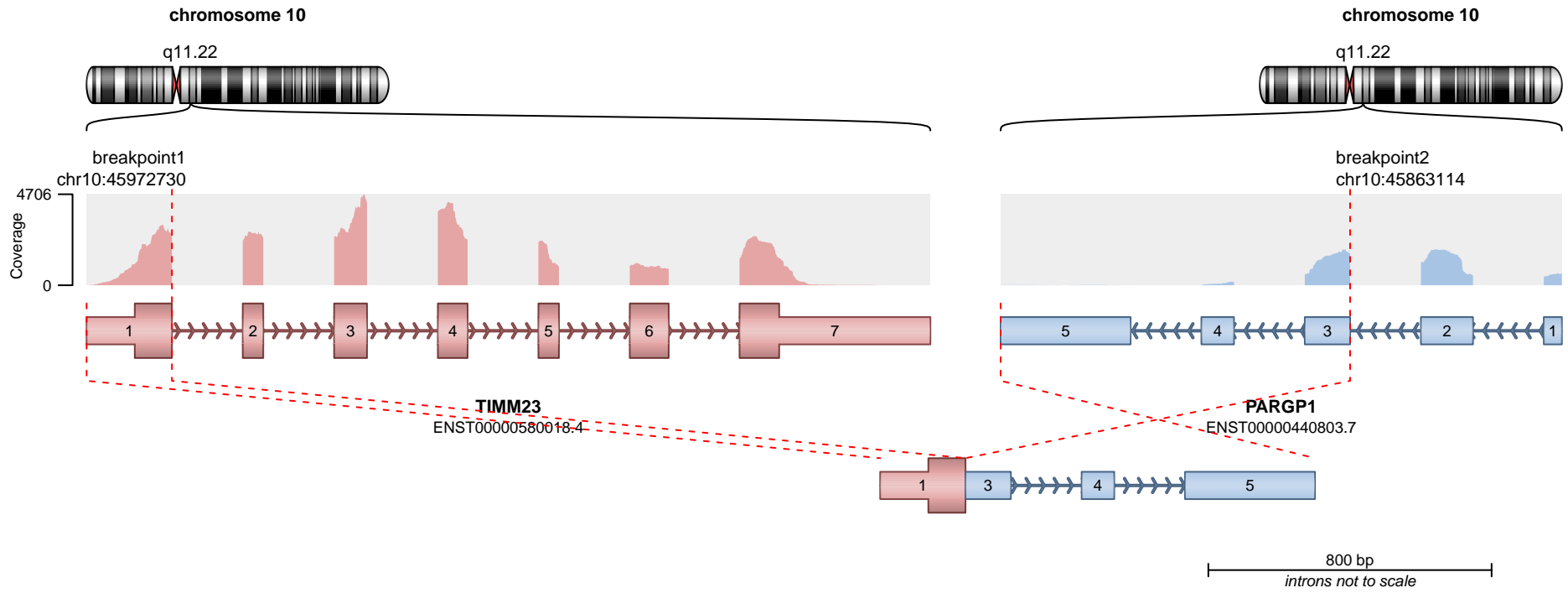
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 67
Discordant mates = 0

— translocation — deletion
— duplication — inversion

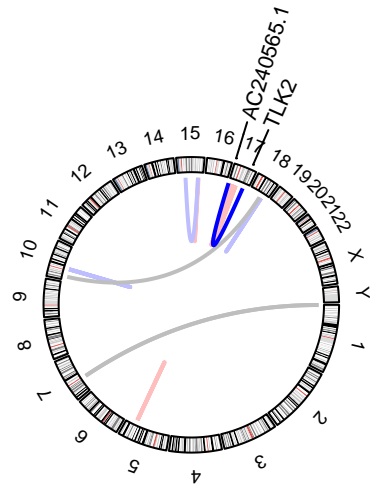
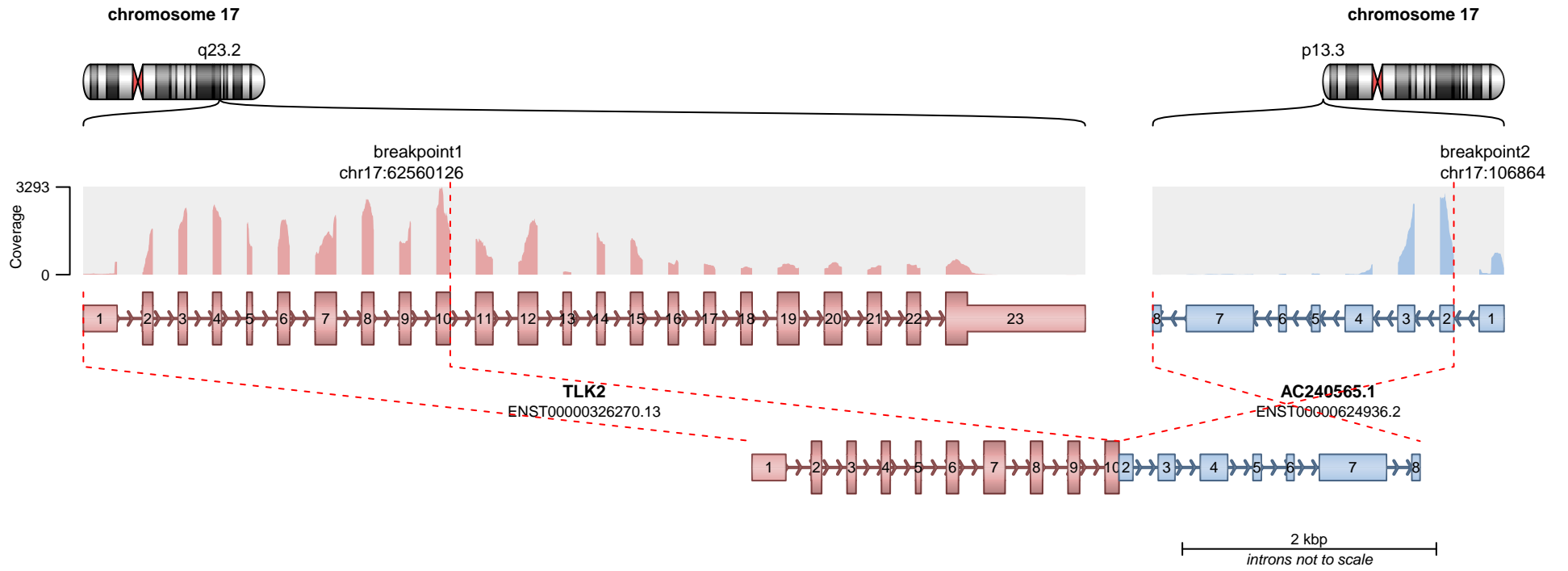


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion

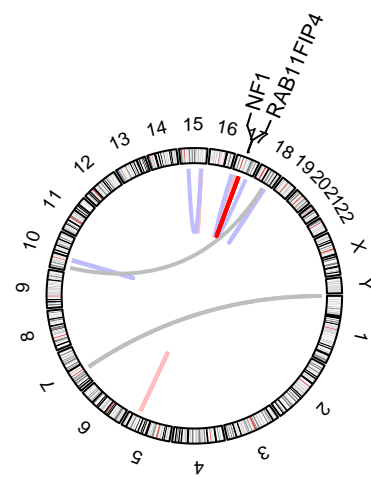
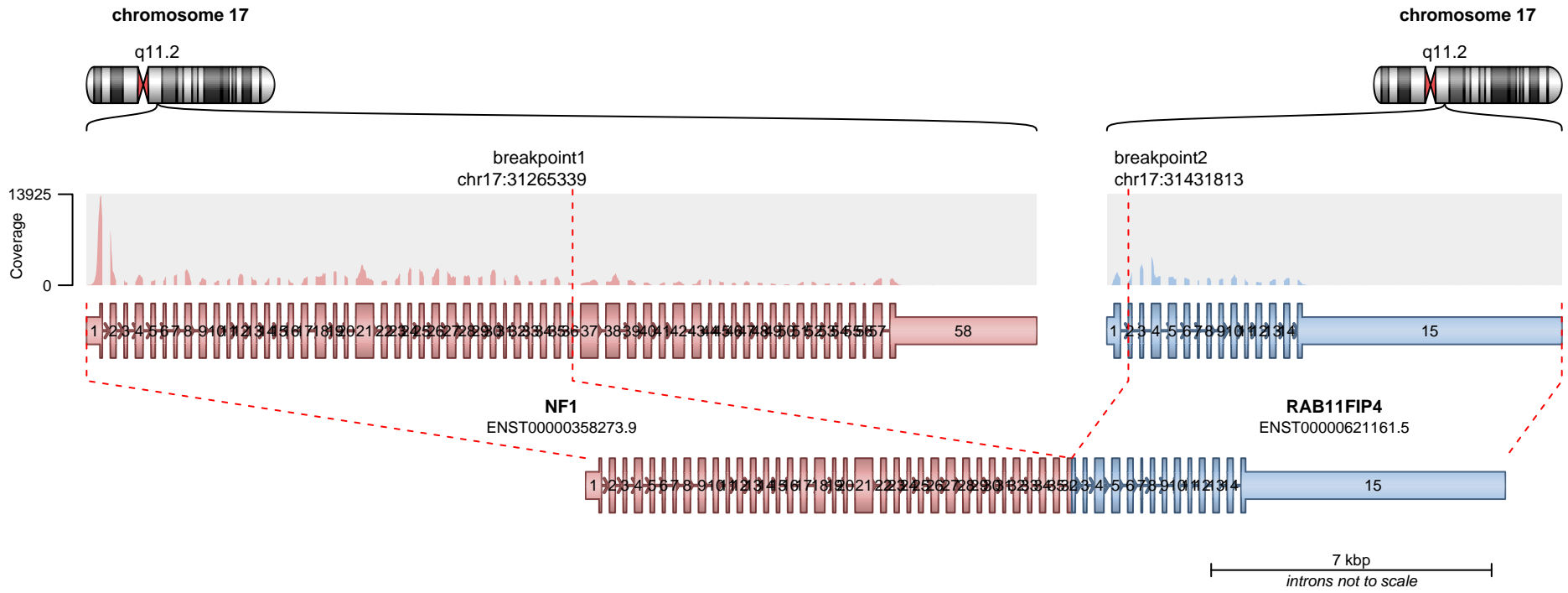


— translocation — deletion
— duplication — inversion

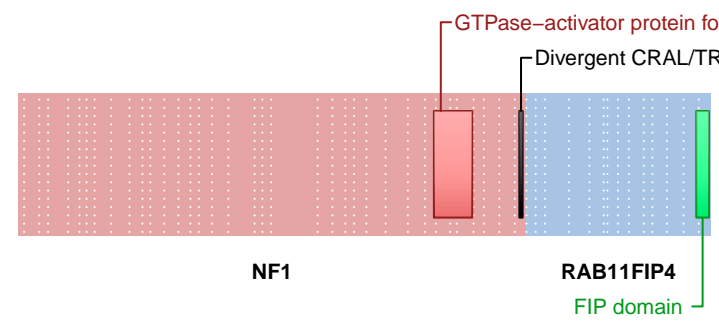
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 59
Discordant mates = 0



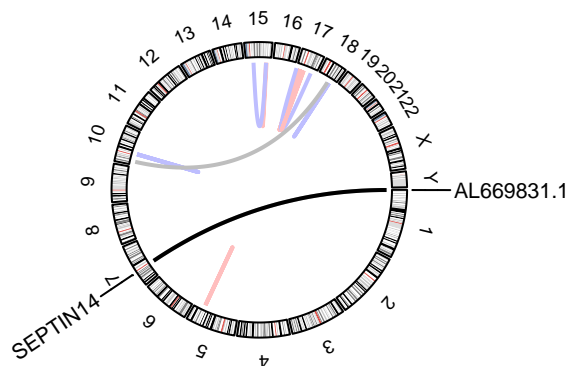
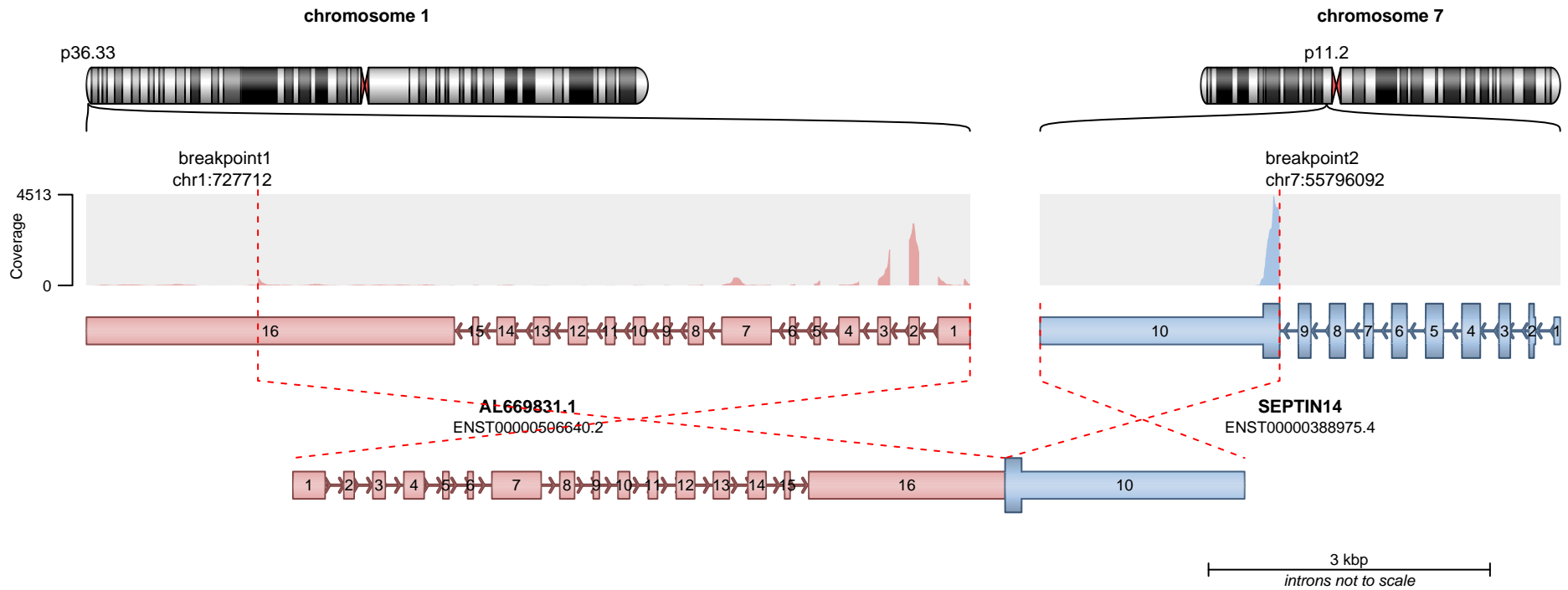
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 49
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

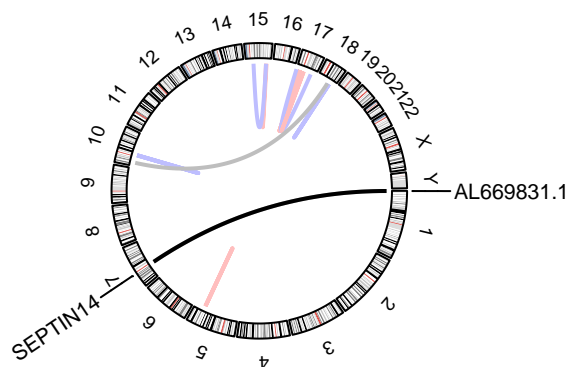
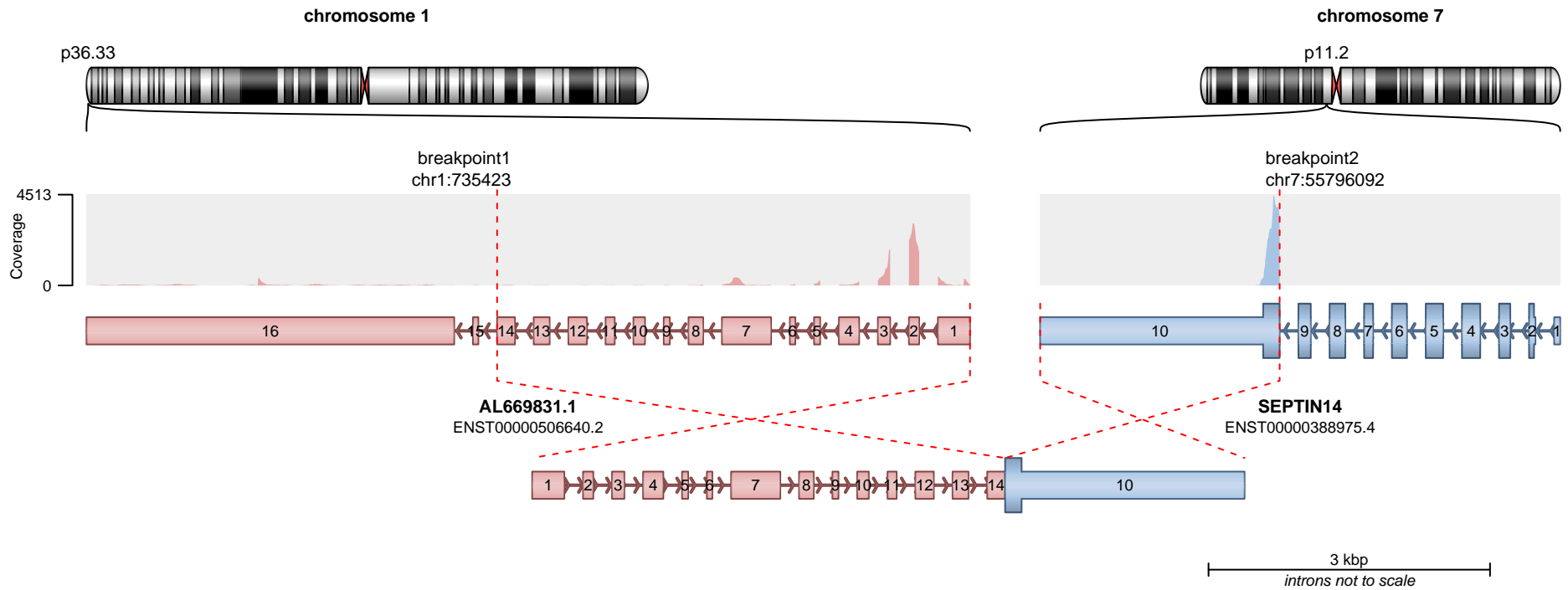


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 22
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

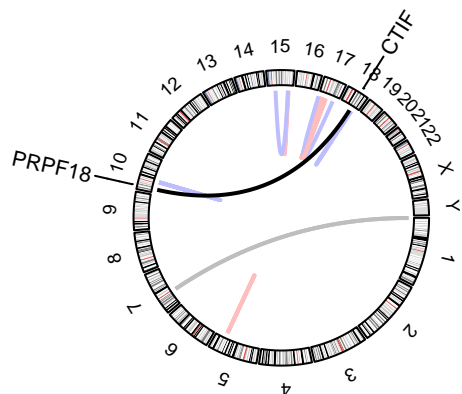
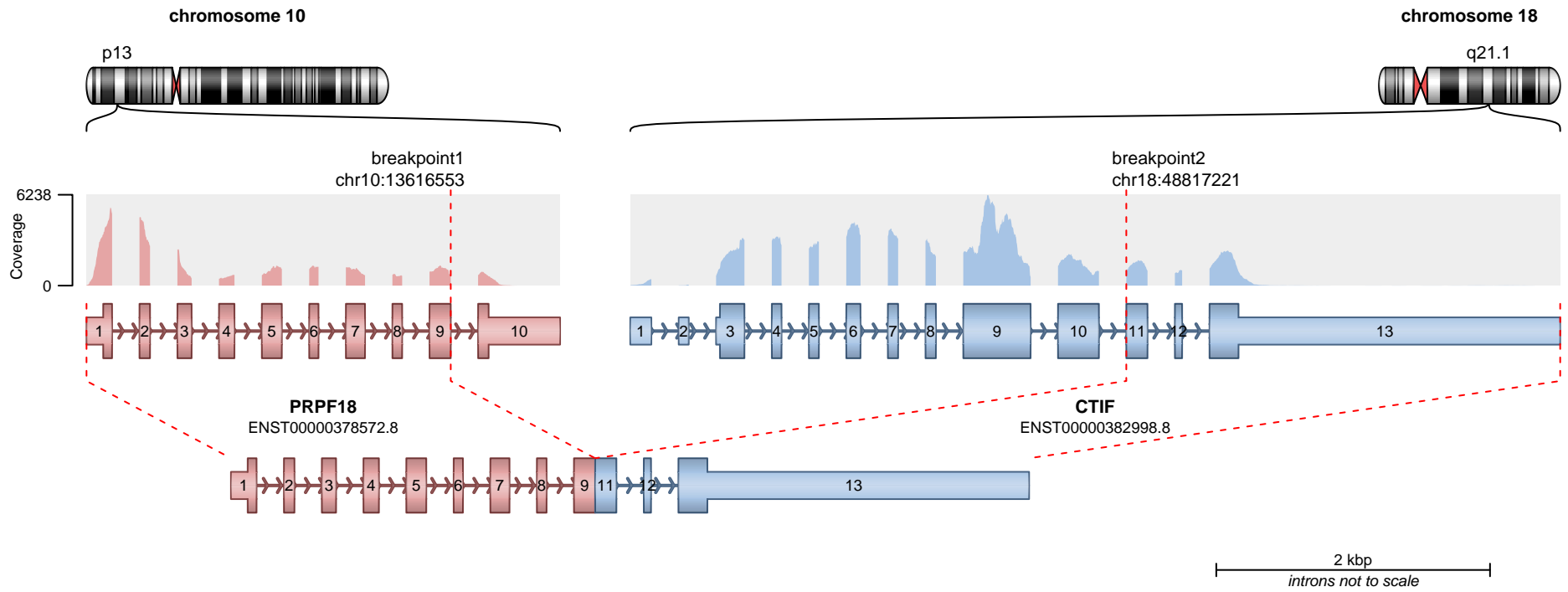


No protein domains retained in fusion.

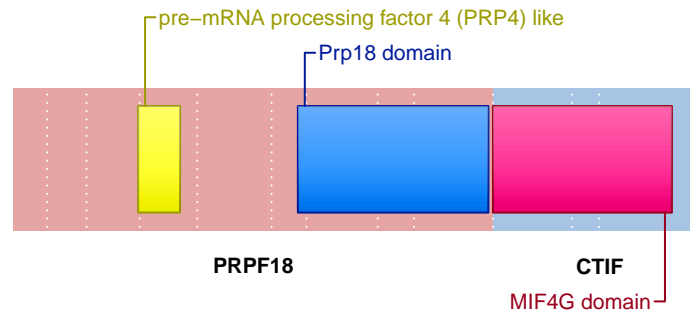
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 15
Discordant mates = 0

— translocation — deletion
— duplication — inversion