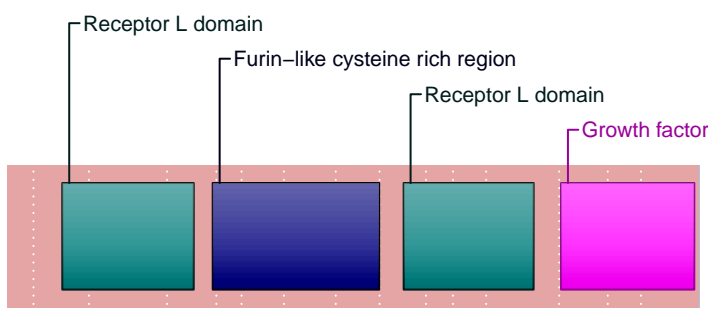


RETAINED PROTEIN DOMAINS
reading frame unclear

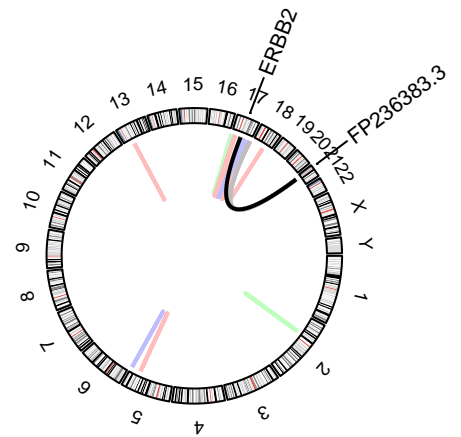
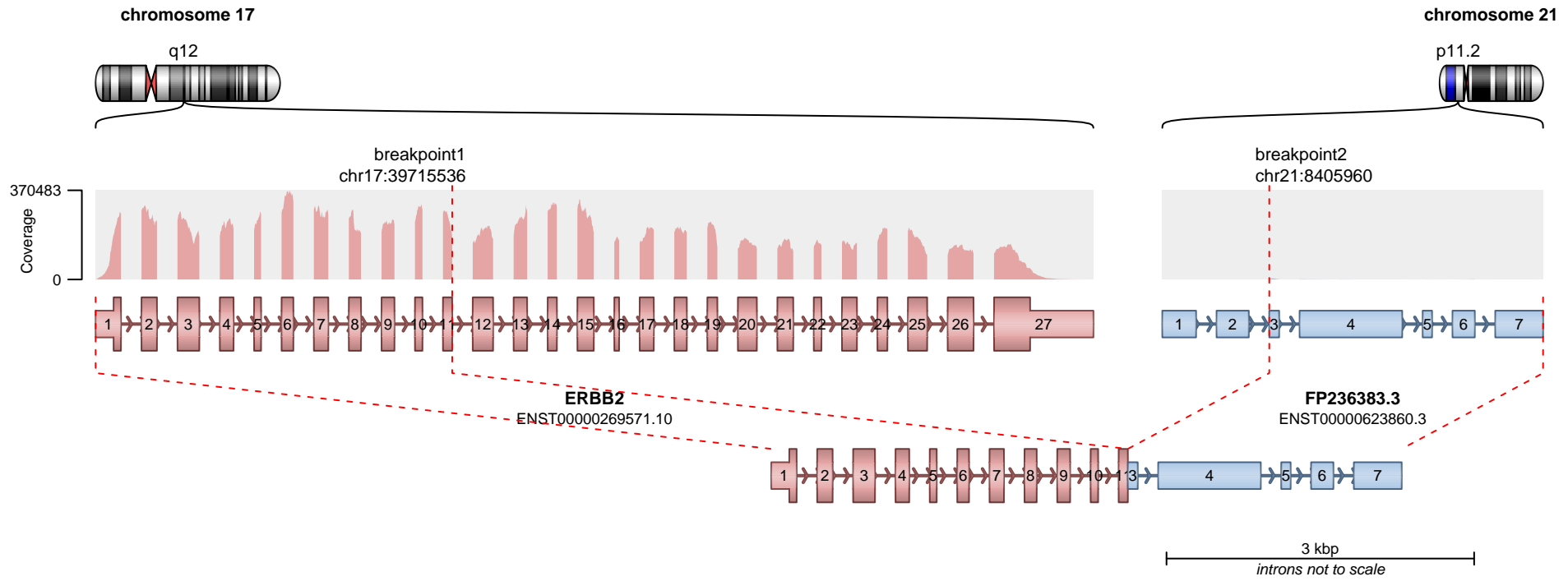


ERBB2

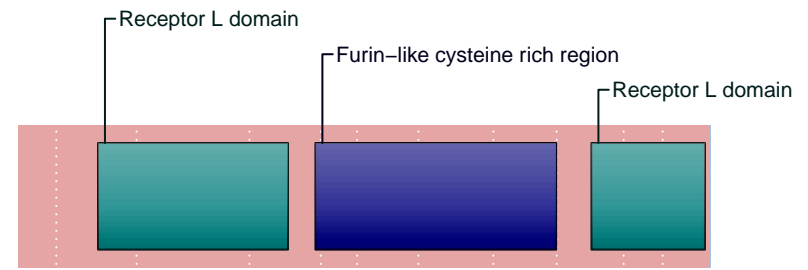
SUPPORTING READ COUNT

Split reads = 1161
Discordant mates = 0

- translocation
- deletion
- duplication
- inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

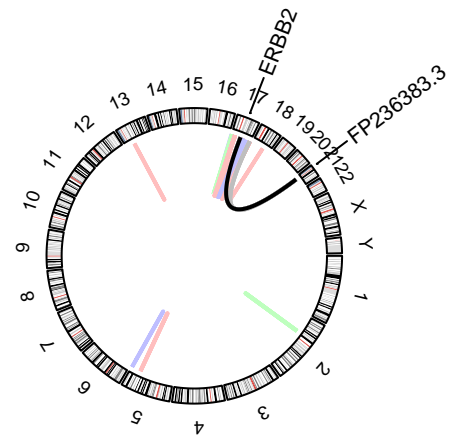
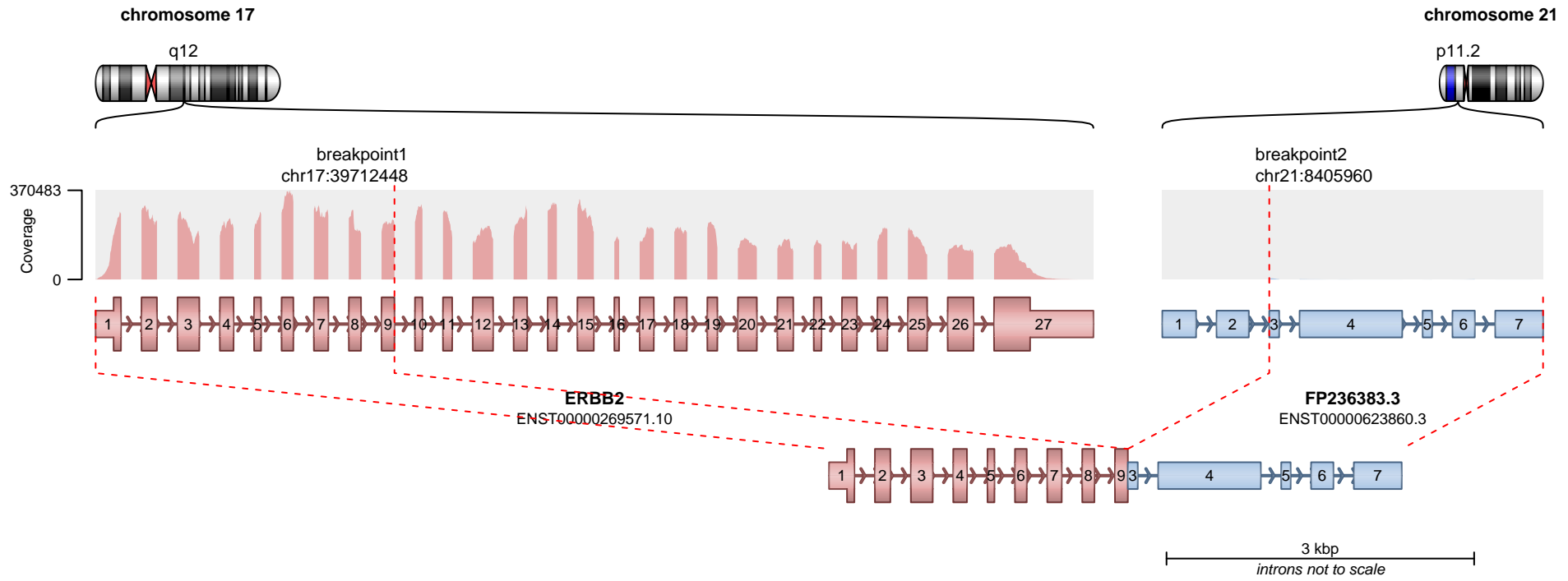


ERBB2

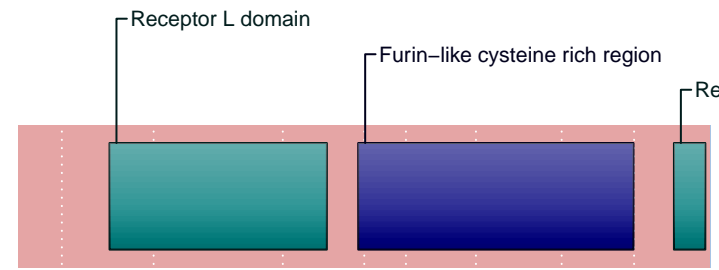
SUPPORTING READ COUNT

Split reads = 116
Discordant mates = 0

- translocation
- deletion
- duplication
- inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

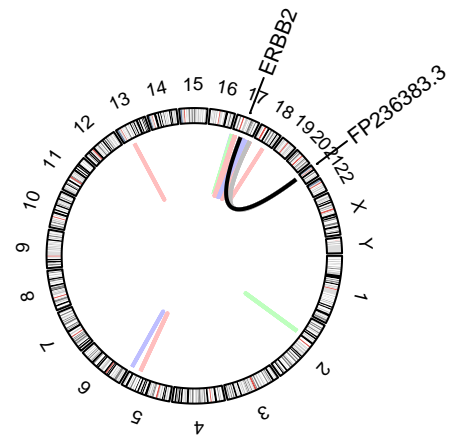
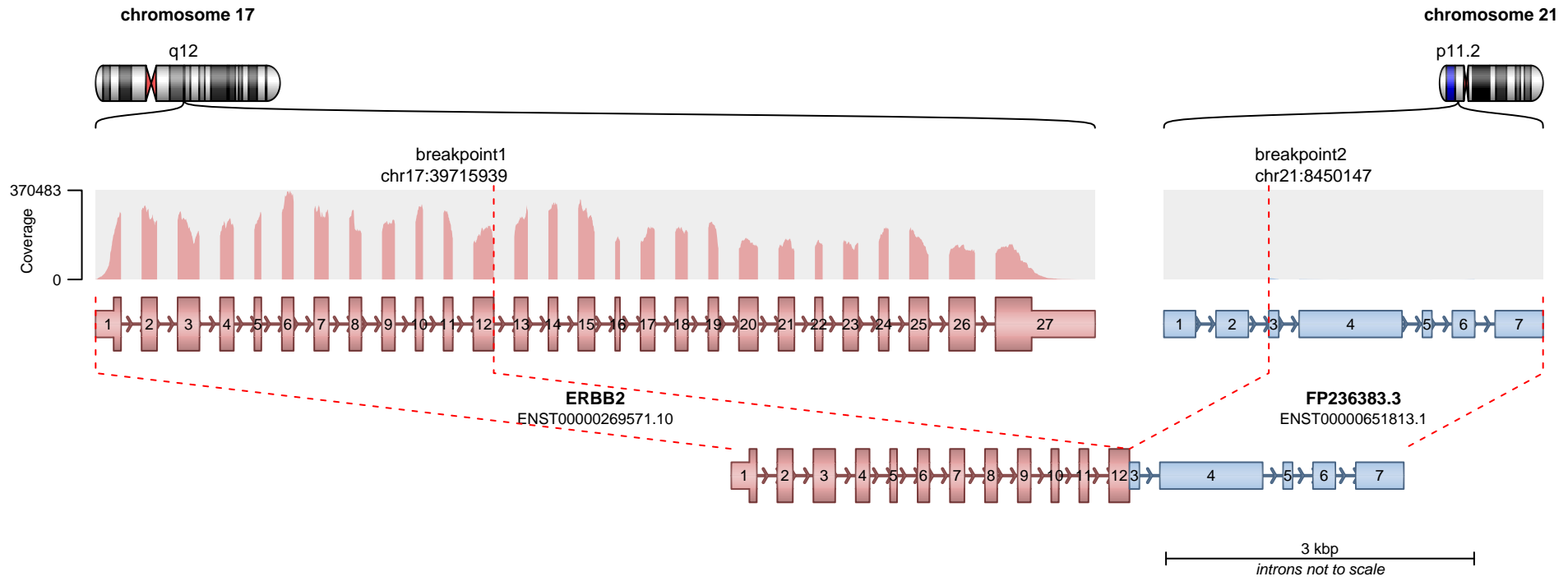


ERBB2

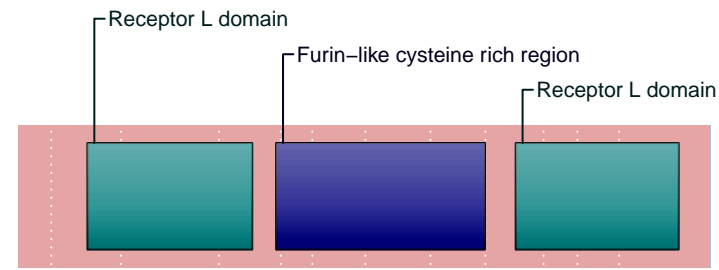
SUPPORTING READ COUNT

Split reads = 19
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

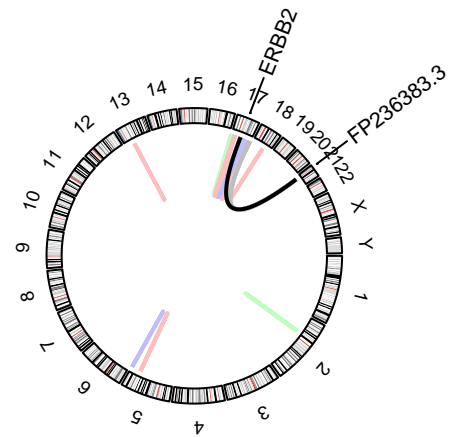
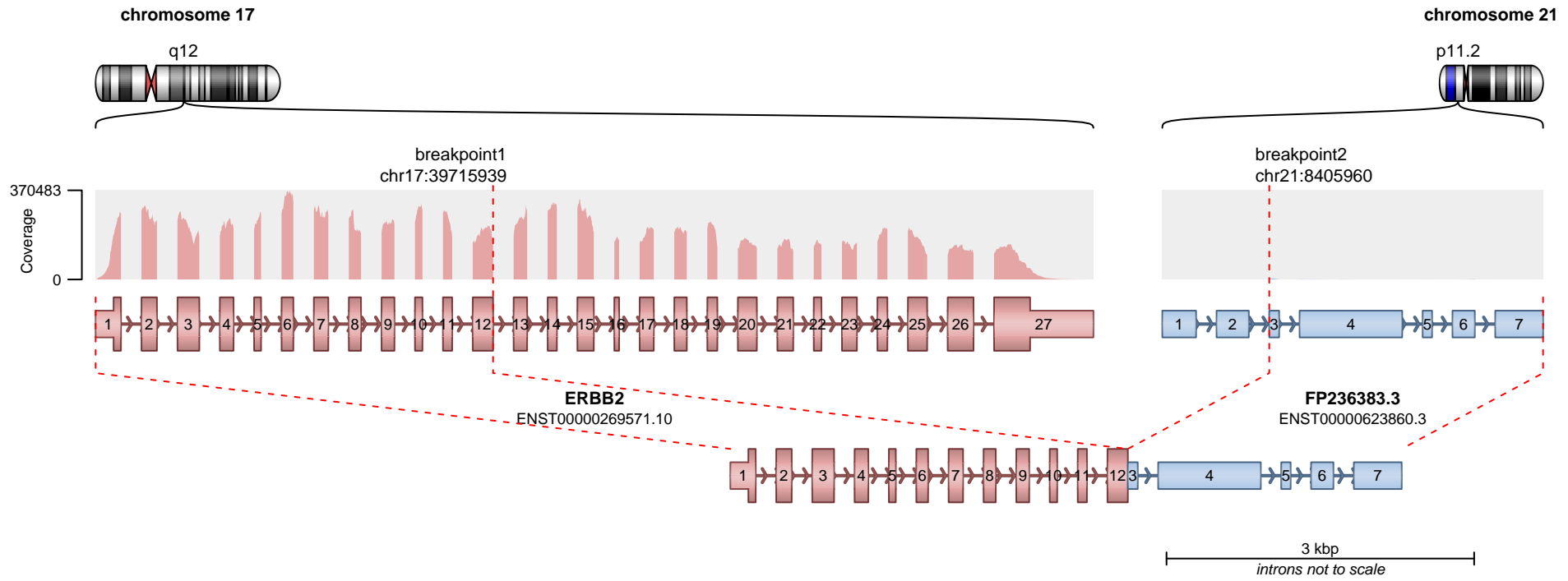


ERBB2

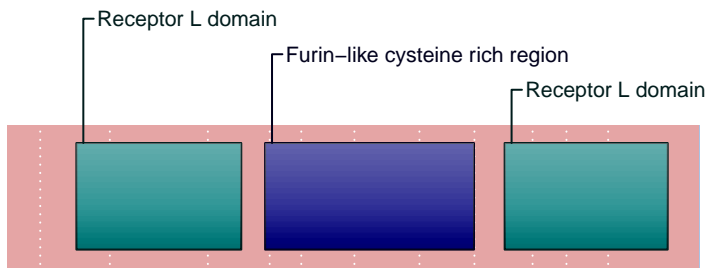
SUPPORTING READ COUNT

Split reads = 14
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

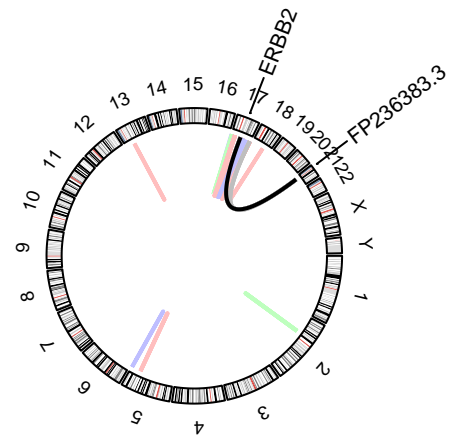
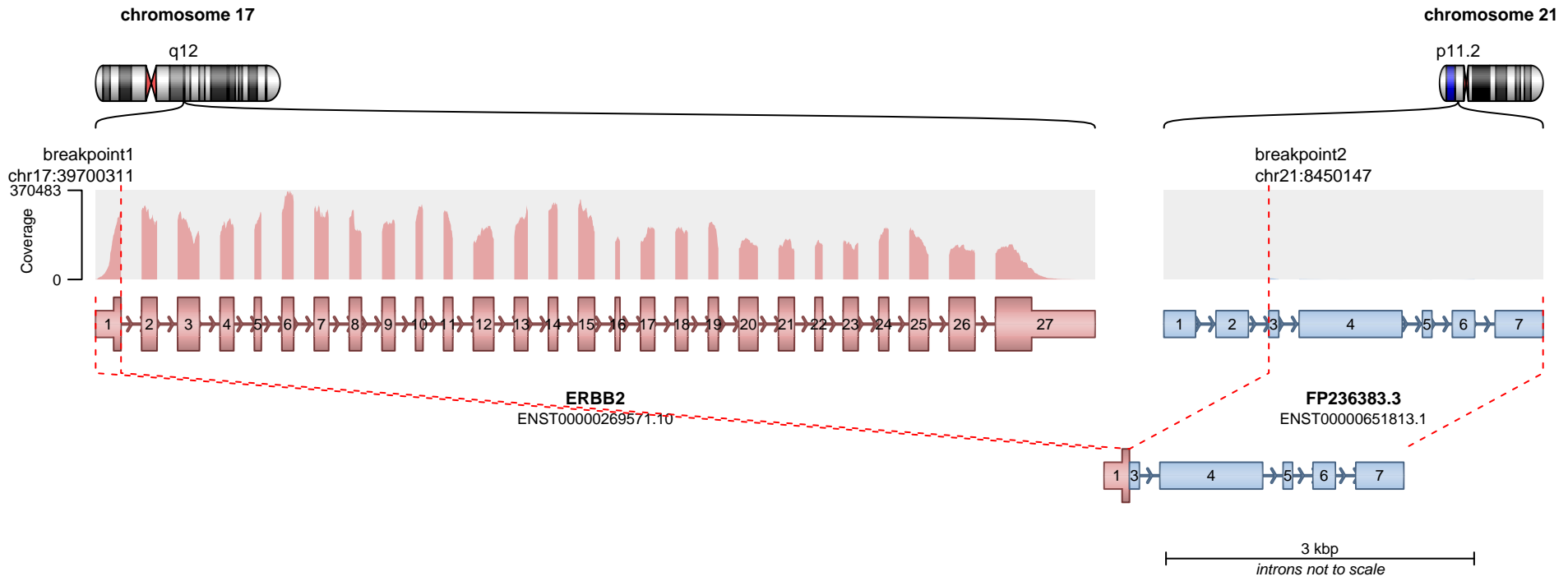


ERBB2

SUPPORTING READ COUNT

Split reads = 14
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

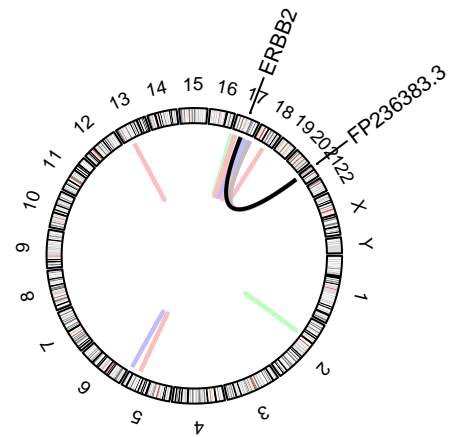
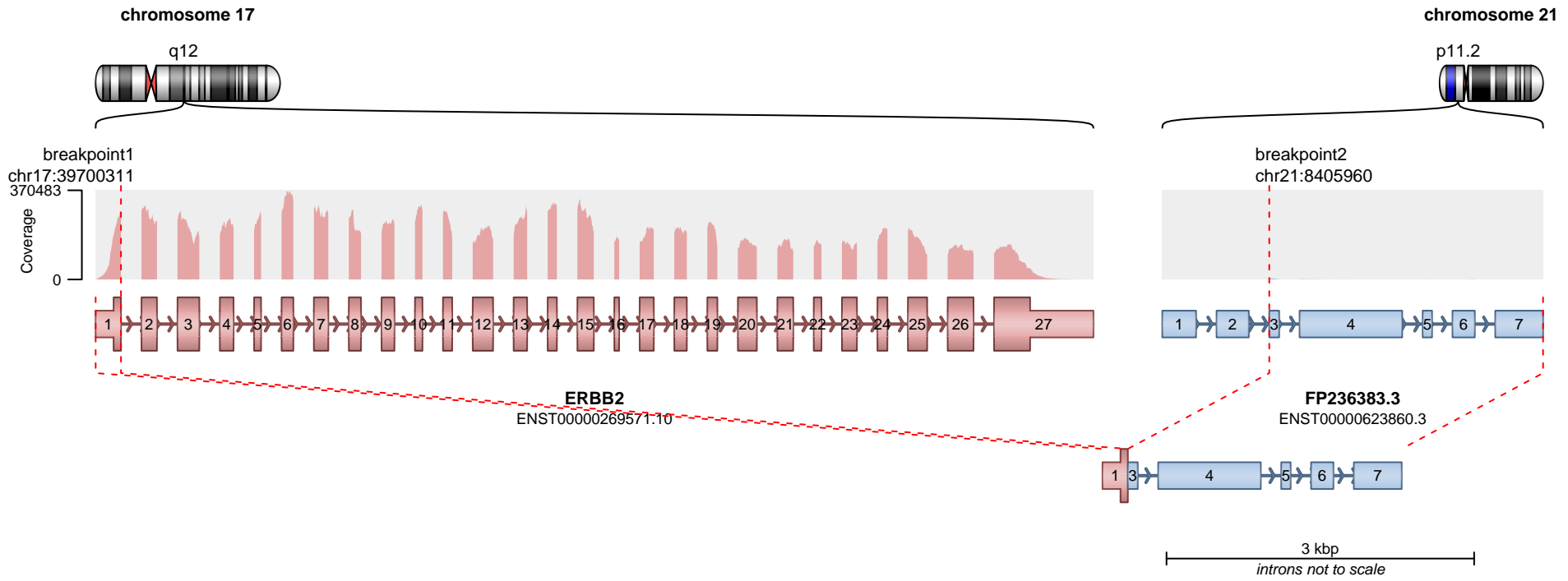


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 11
Discordant mates = 0

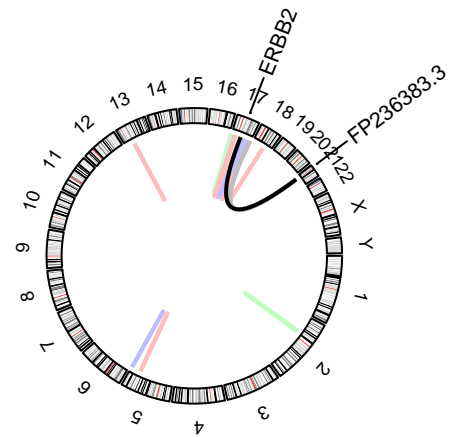
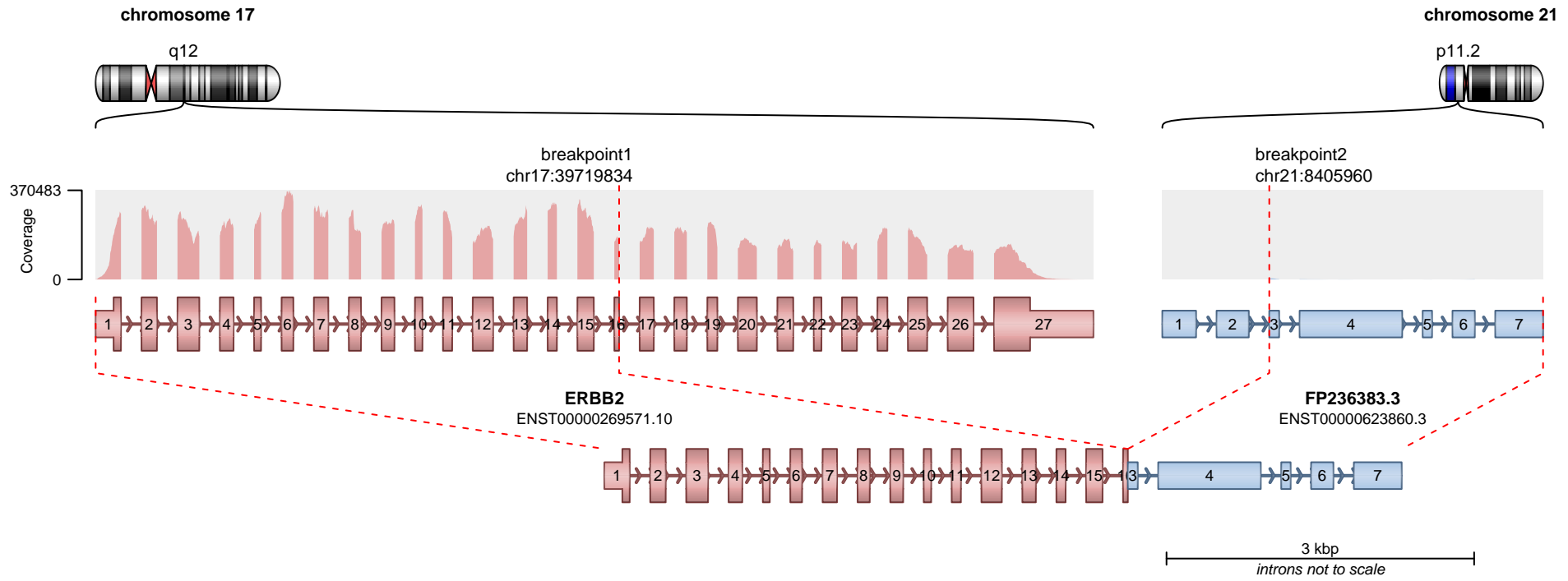


No protein domains retained in fusion.

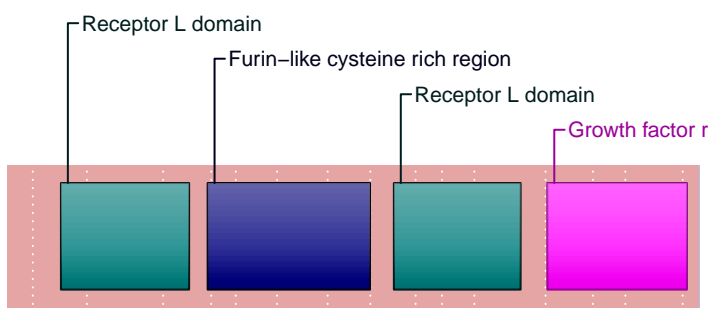
SUPPORTING READ COUNT

Split reads = 11
Discordant mates = 0

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

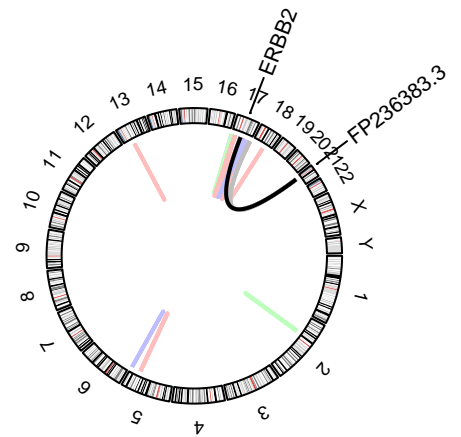
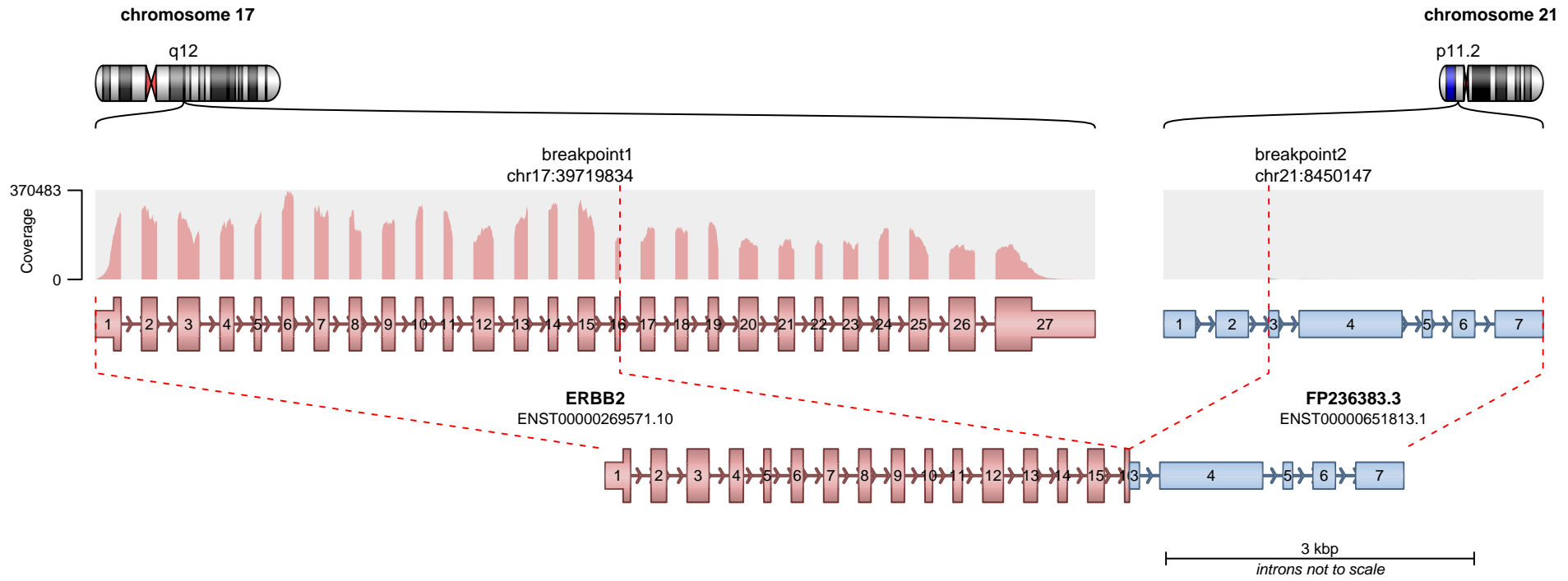


ERBB2

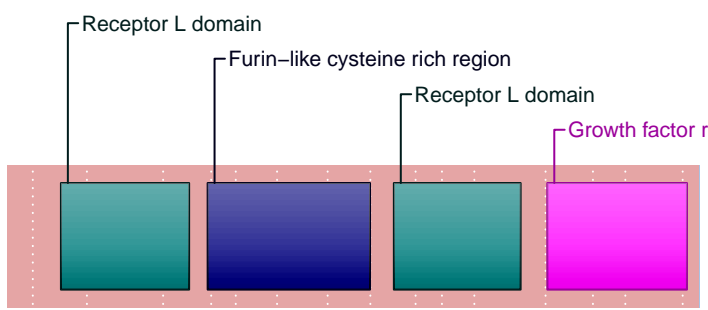
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

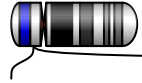
Split reads = 2
Discordant mates = 0

ERBB2

- translocation
- duplication
- deletion
- inversion

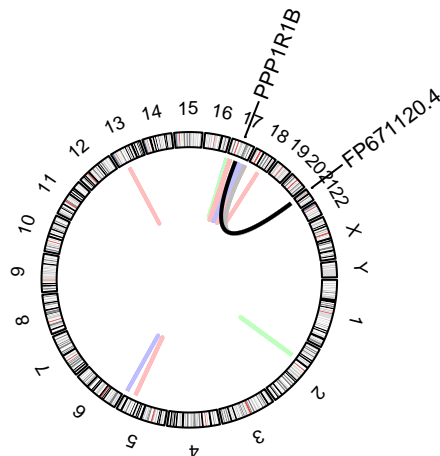
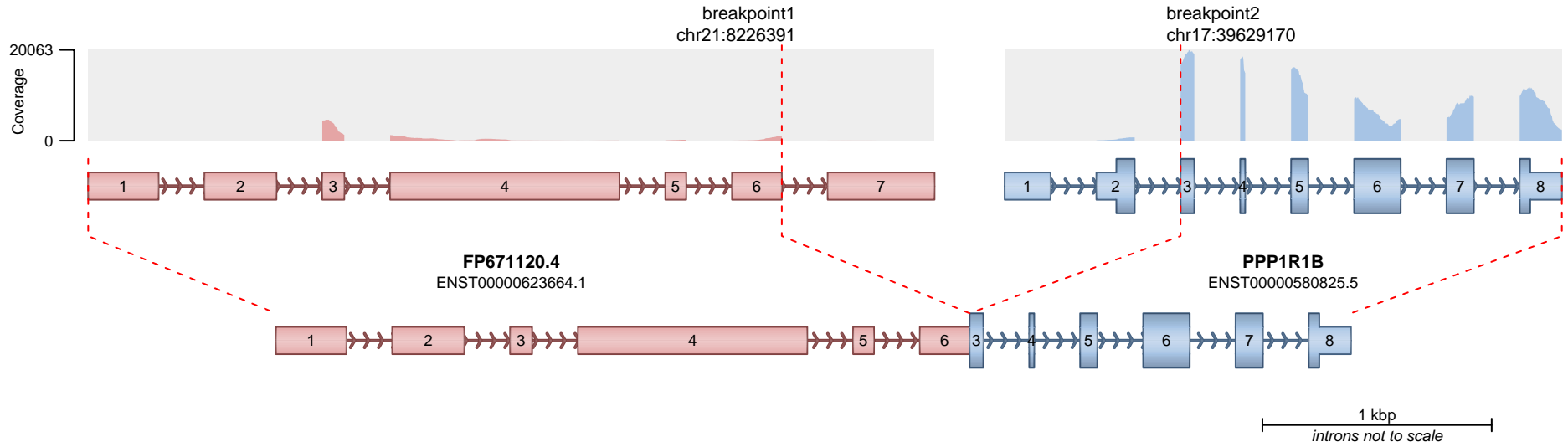
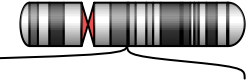
chromosome 21

p11.2

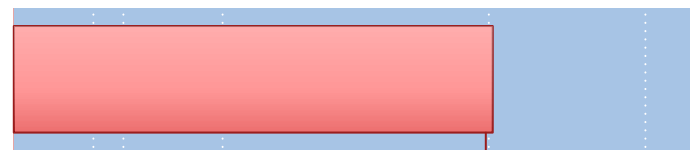


chromosome 17

q12



RETAINED PROTEIN DOMAINS
reading frame unclear



PPP1R1B

Protein phosphatase inhibitor 1/DARPP-32

SUPPORTING READ COUNT

Split reads = 673

Discordant mates = 12

— translocation — deletion
— duplication — inversion

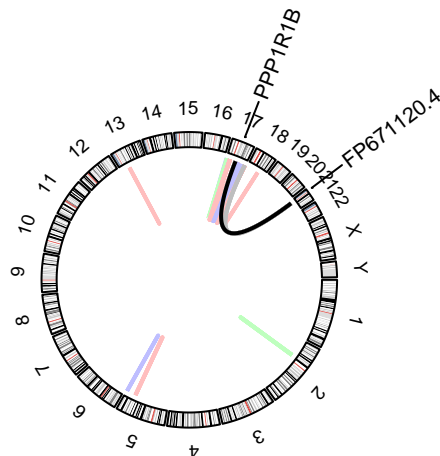
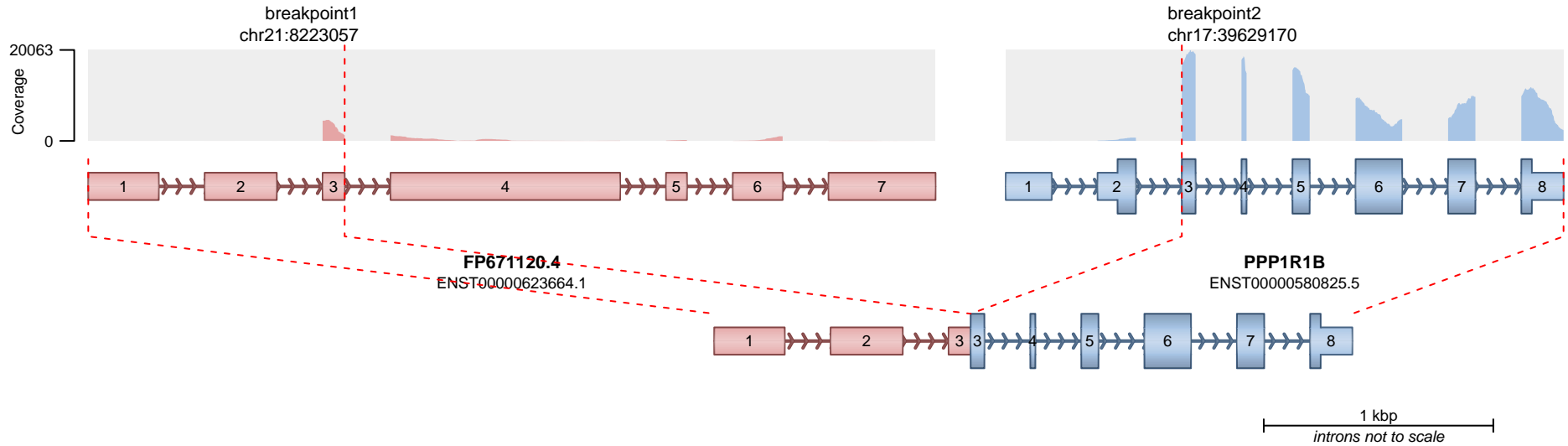
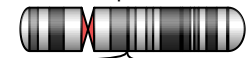
chromosome 21

p11.2

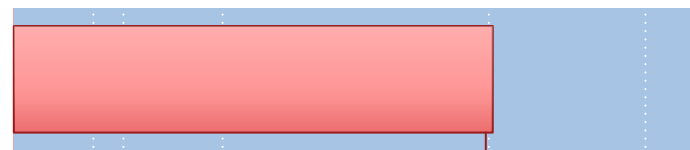


chromosome 17

q12



RETAINED PROTEIN DOMAINS
reading frame unclear



PPP1R1B

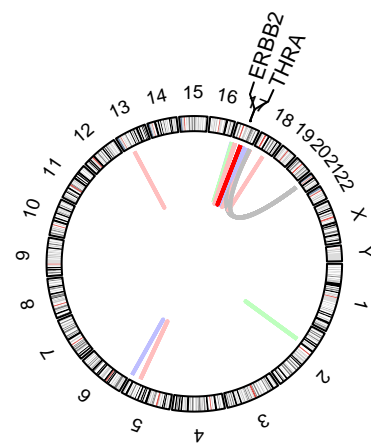
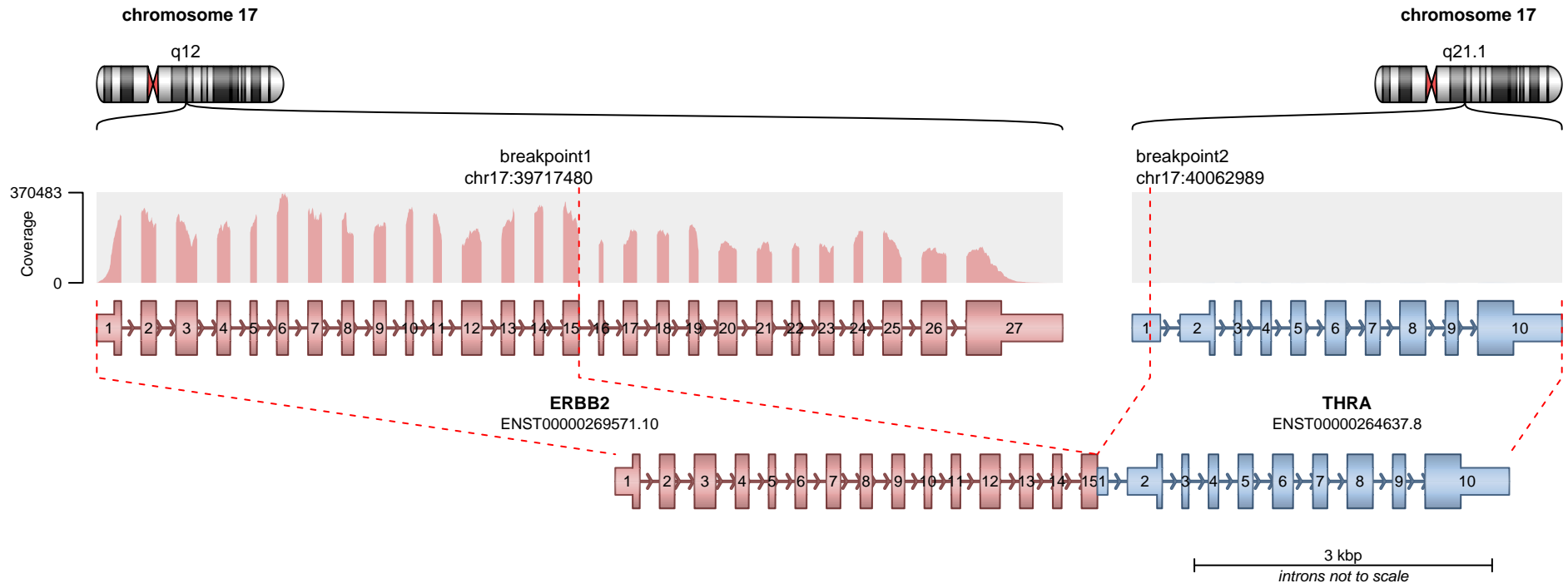
Protein phosphatase inhibitor 1/DARPP-32

SUPPORTING READ COUNT

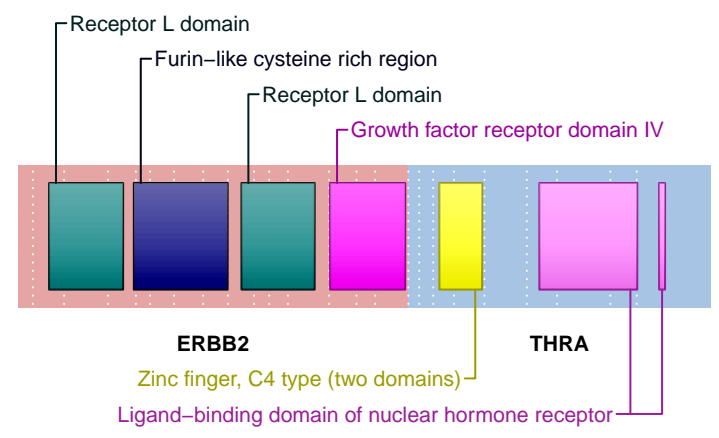
Split reads = 9

Discordant mates = 0

— translocation — deletion
— duplication — inversion



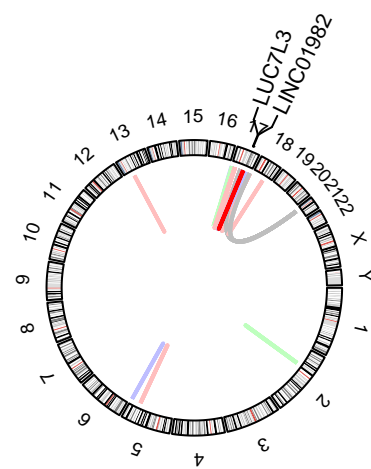
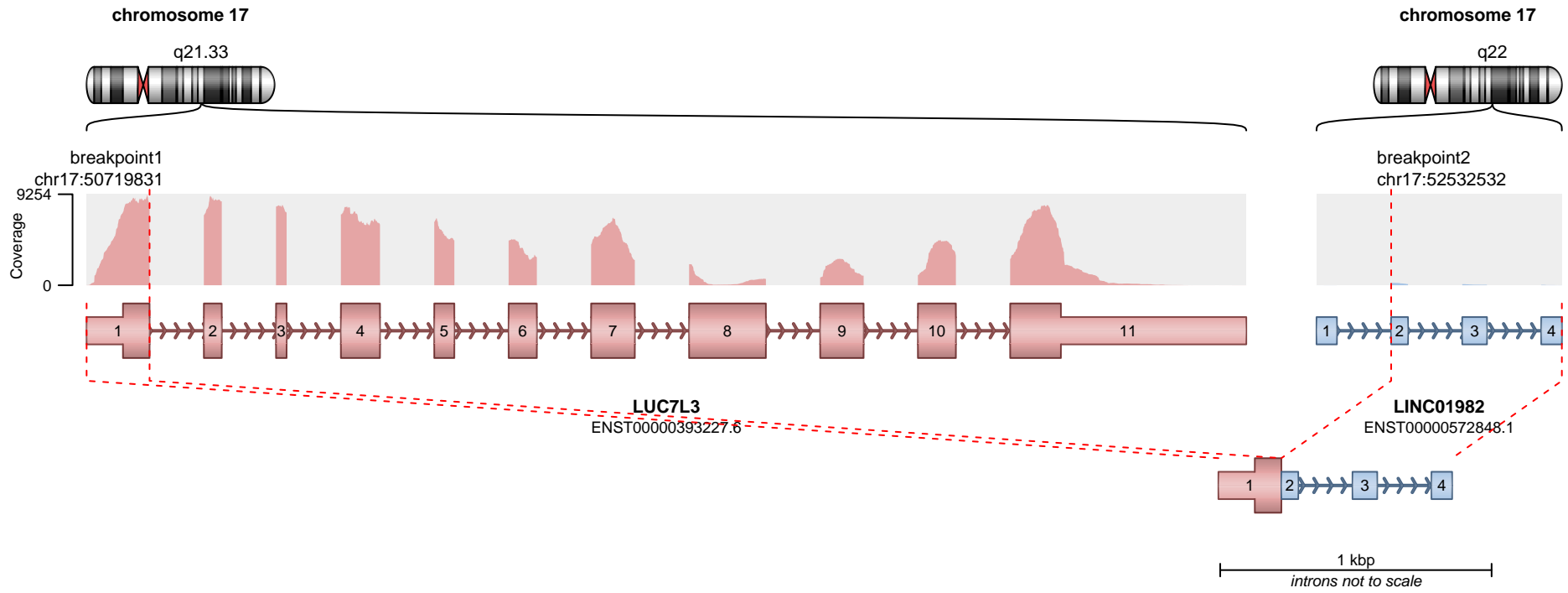
RETAINED PROTEIN DOMAINS
reading frame unclear



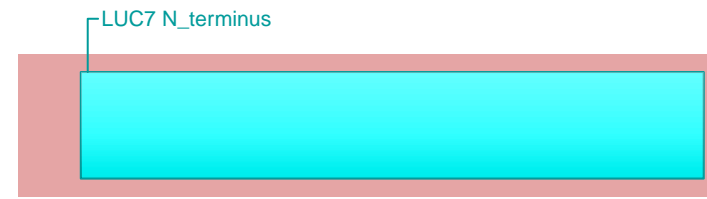
SUPPORTING READ COUNT

Split reads = 316
Discordant mates = 0

- translocation
- deletion
- duplication
- inversion



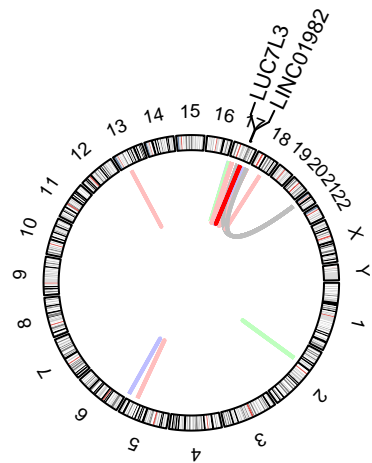
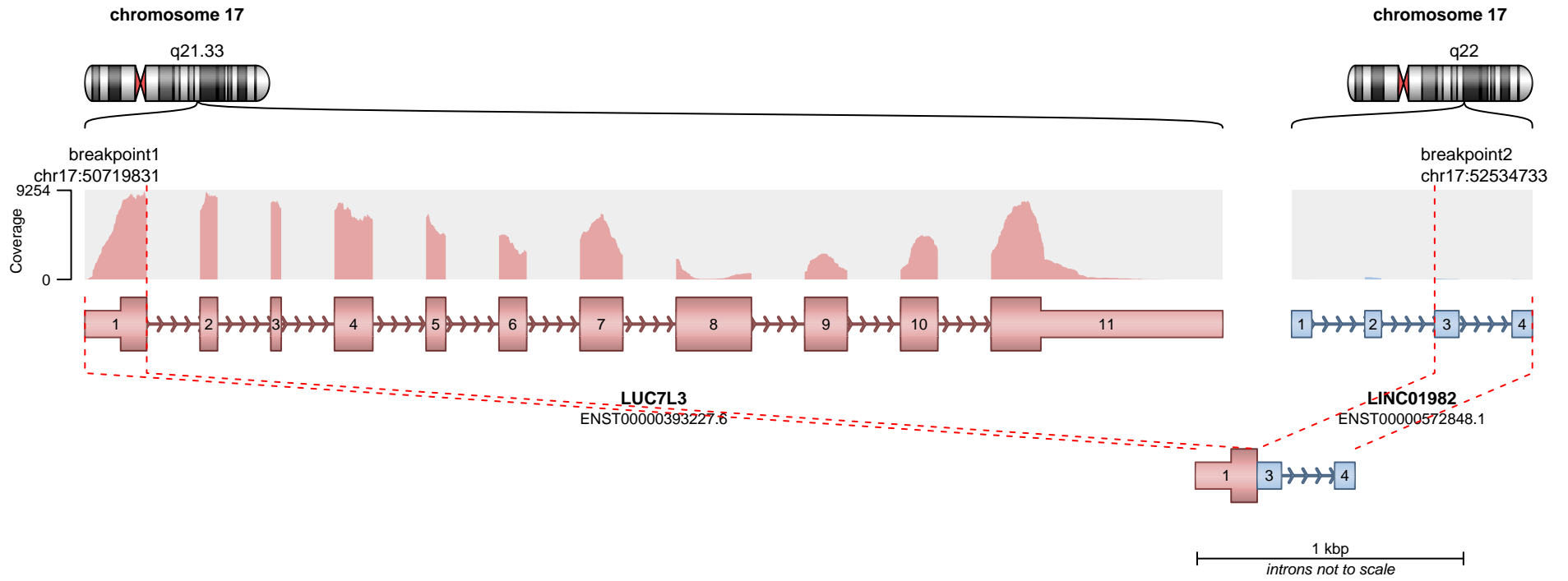
RETAINED PROTEIN DOMAINS
reading frame unclear



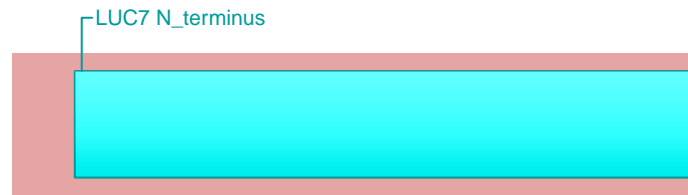
SUPPORTING READ COUNT

Split reads = 174
Discordant mates = 8

— translocation — deletion
— duplication — inversion



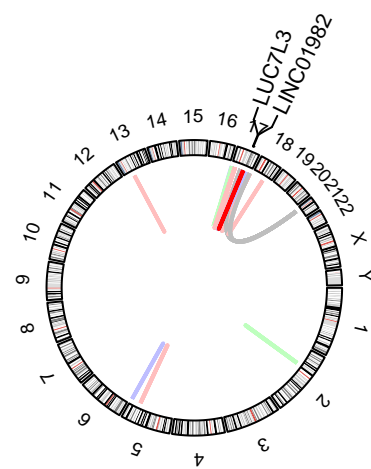
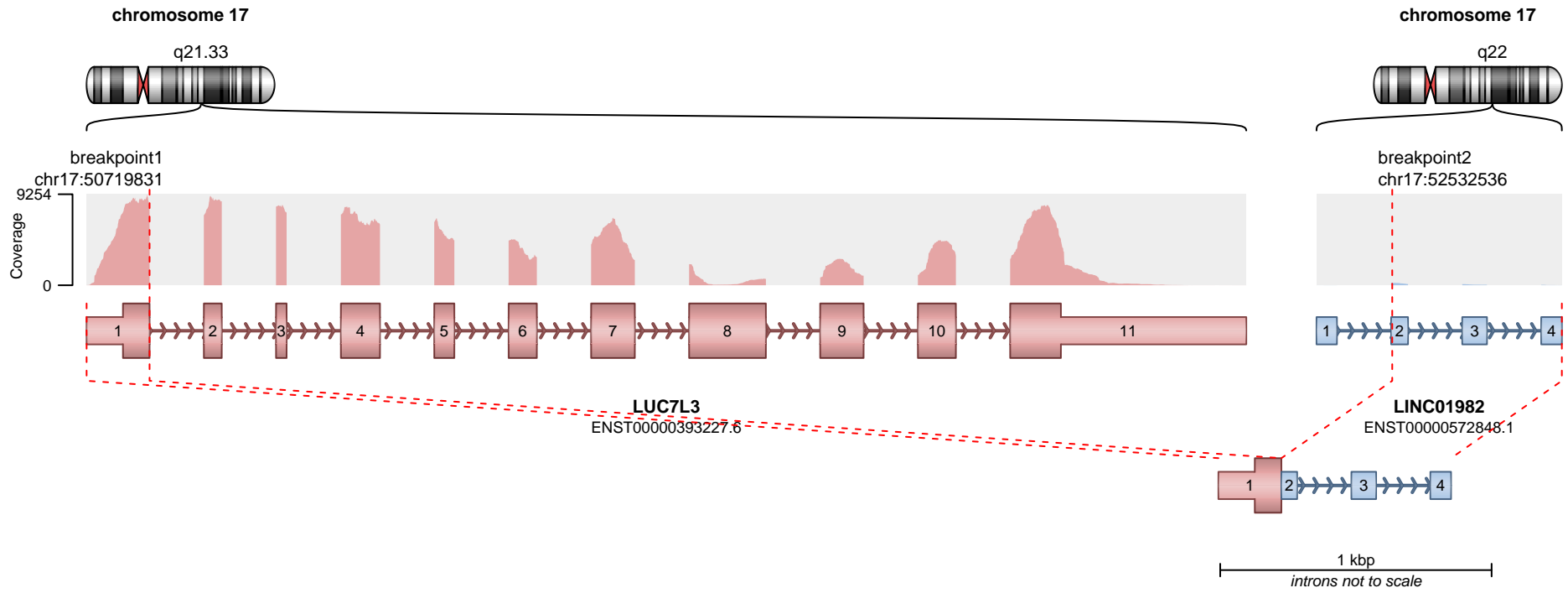
RETAINED PROTEIN DOMAINS
reading frame unclear



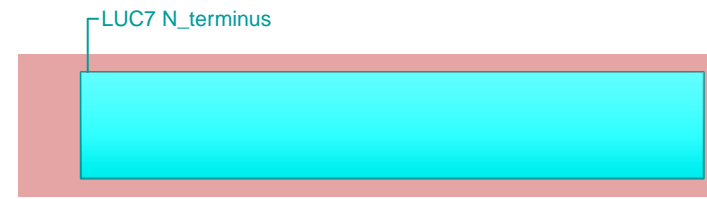
SUPPORTING READ COUNT

Split reads = 11
Discordant mates = 3

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

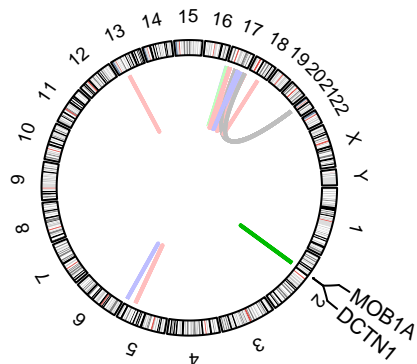
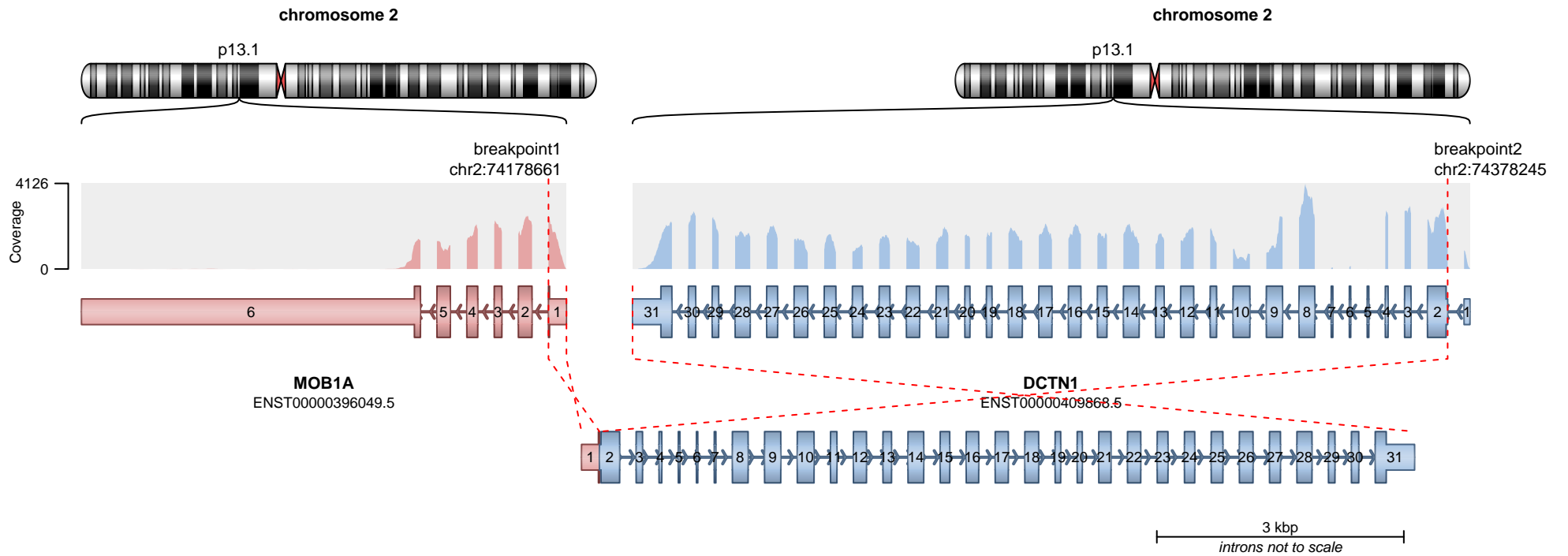


SUPPORTING READ COUNT

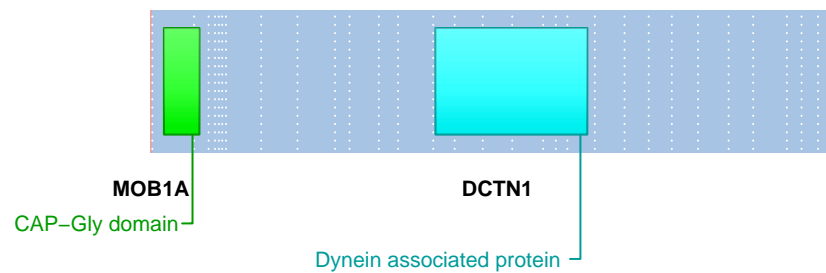
Split reads = 4
Discordant mates = 8

— translocation — deletion
— duplication — inversion

LUC7L3



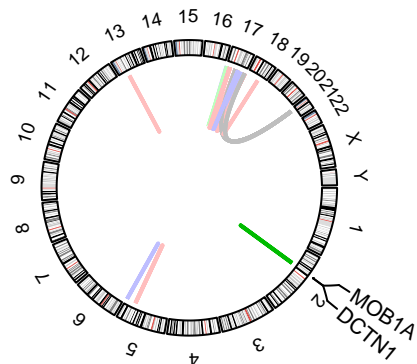
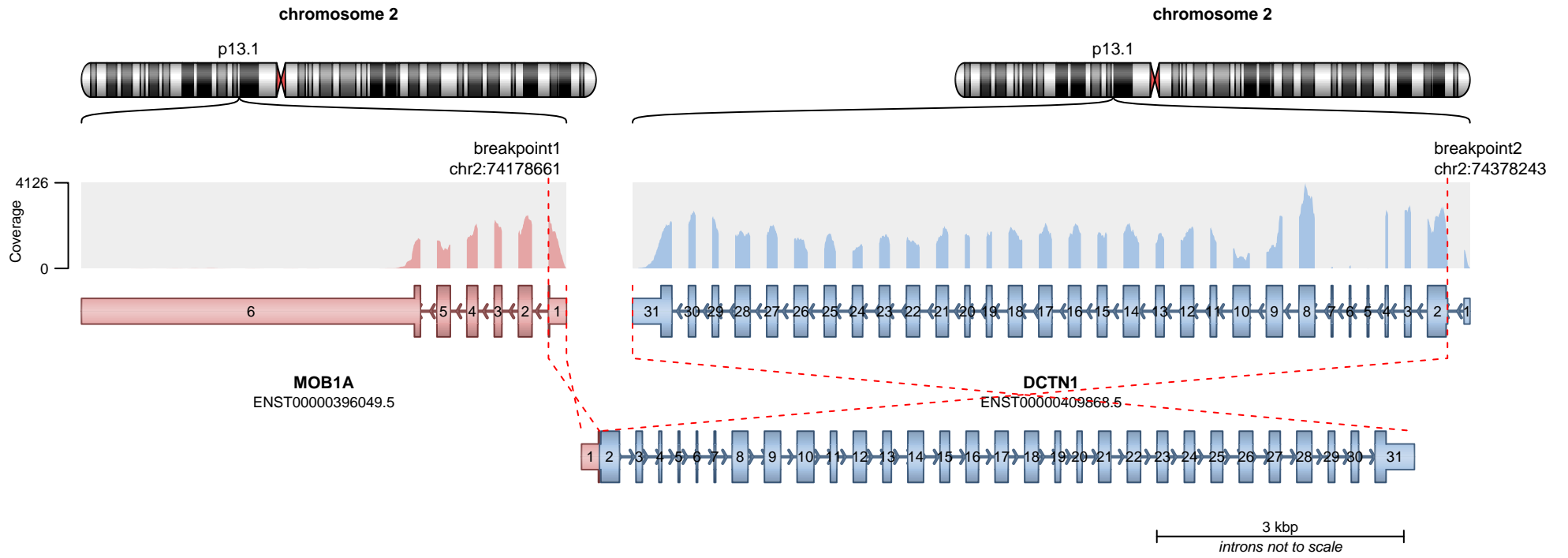
RETAINED PROTEIN DOMAINS
reading frame unclear



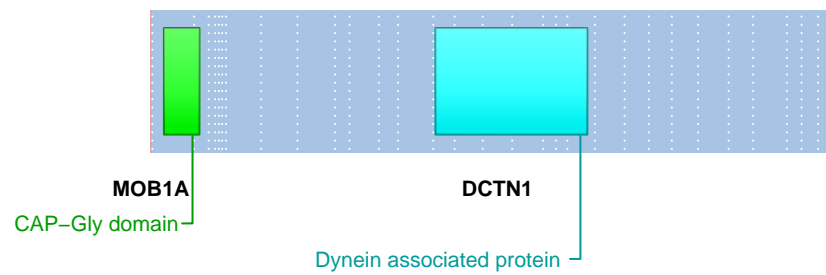
SUPPORTING READ COUNT

Split reads = 157
Discordant mates = 11

- translocation
- duplication
- deletion
- inversion



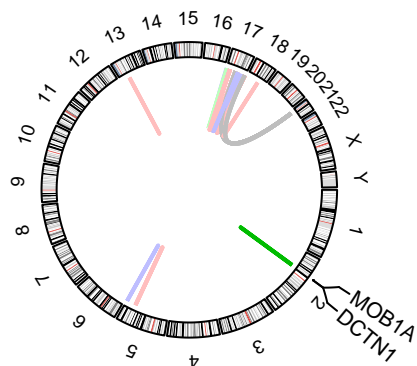
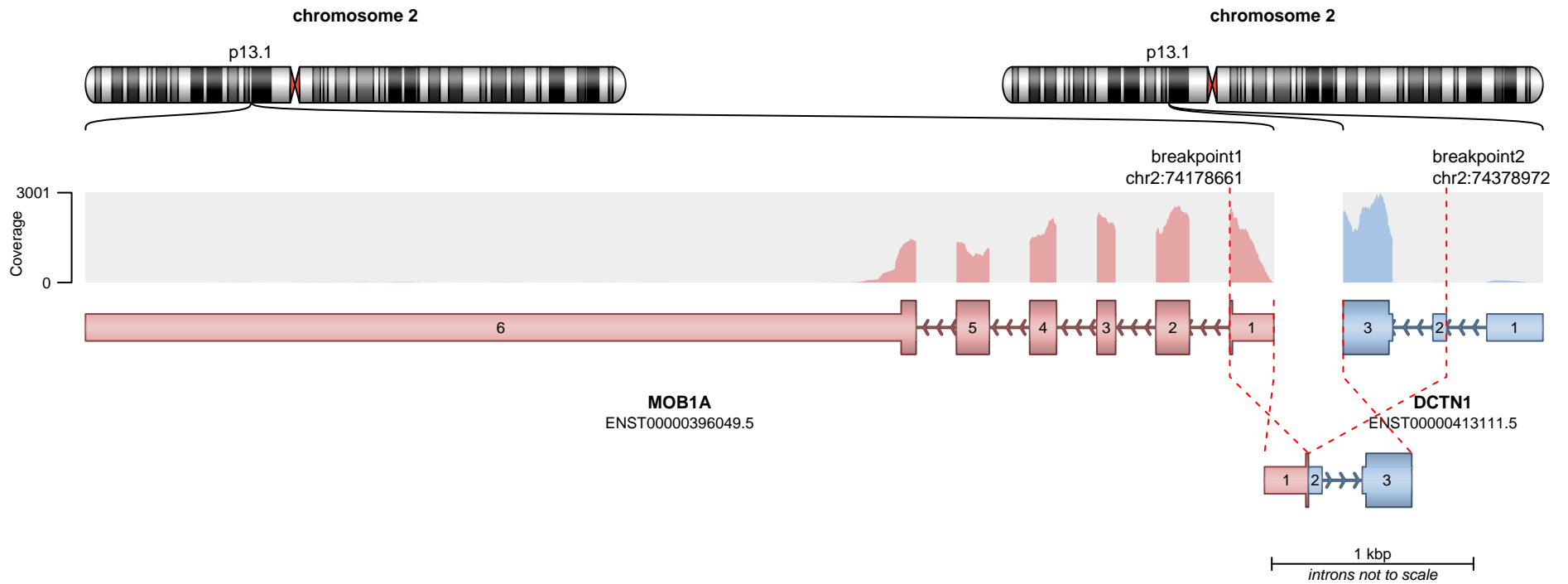
RETAINED PROTEIN DOMAINS
reading frame unclear



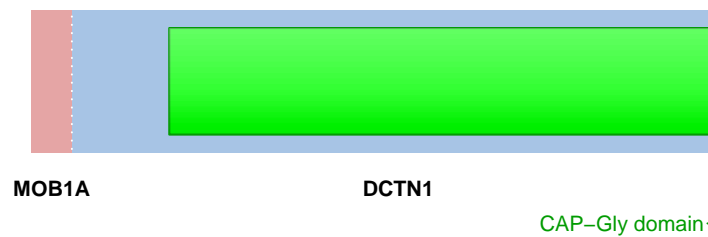
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 11

- translocation
- duplication
- deletion
- inversion



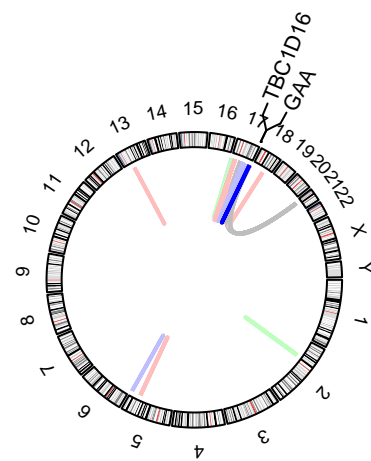
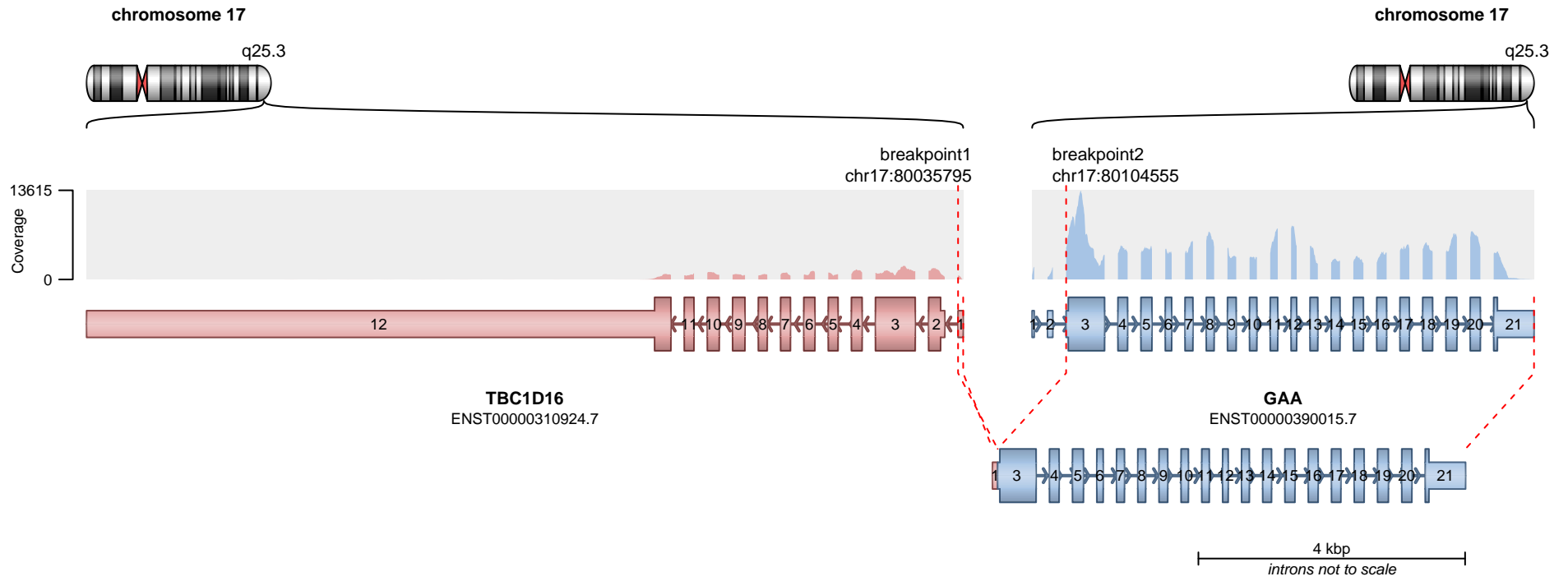
RETAINED PROTEIN DOMAINS
reading frame unclear



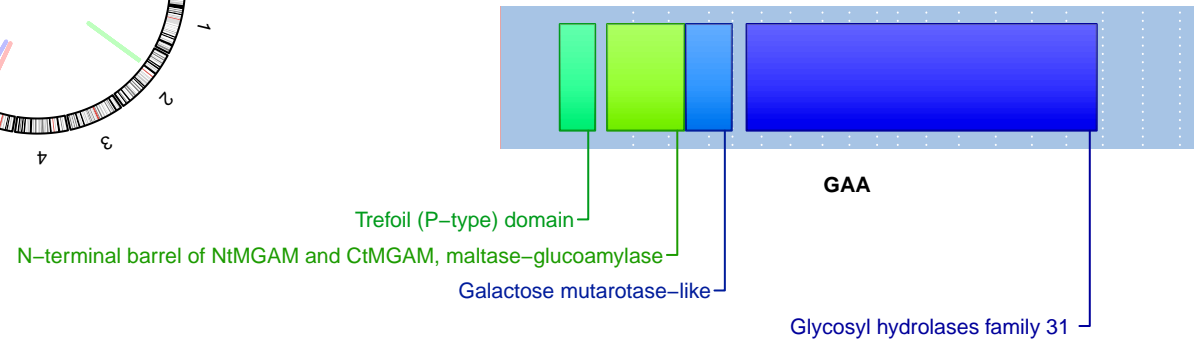
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 11

- translocation
- deletion
- duplication
- inversion



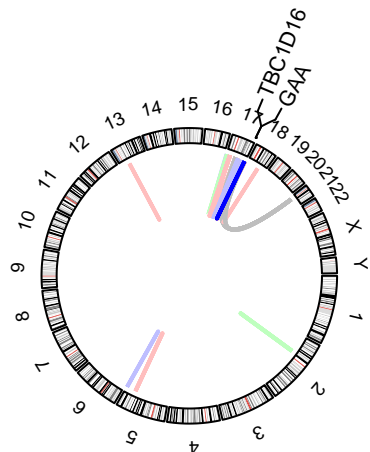
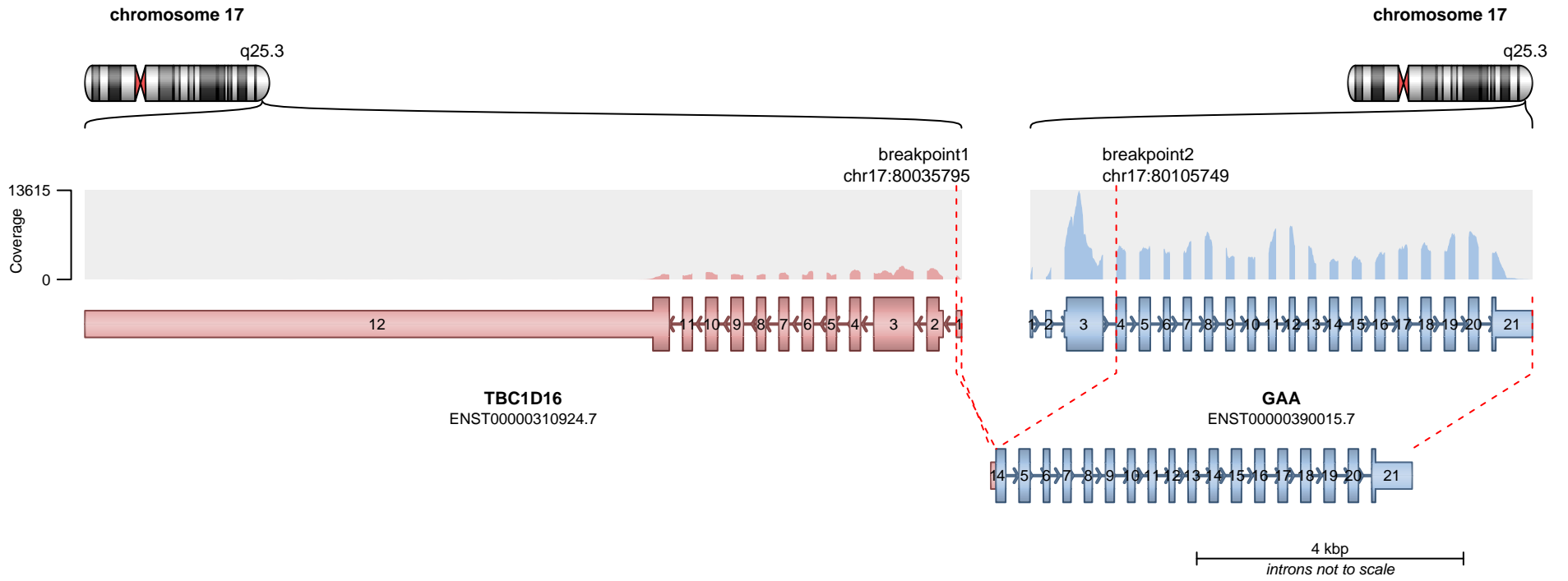
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 128
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



N-terminal barrel of NtMGAM and CtMGAM, maltase-glucoamylase

Galactose mutarotase-like

RETAINED PROTEIN DOMAINS
reading frame unclear



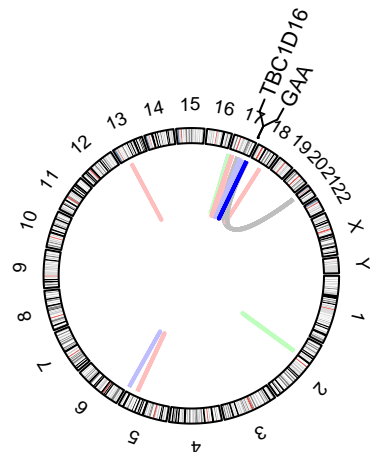
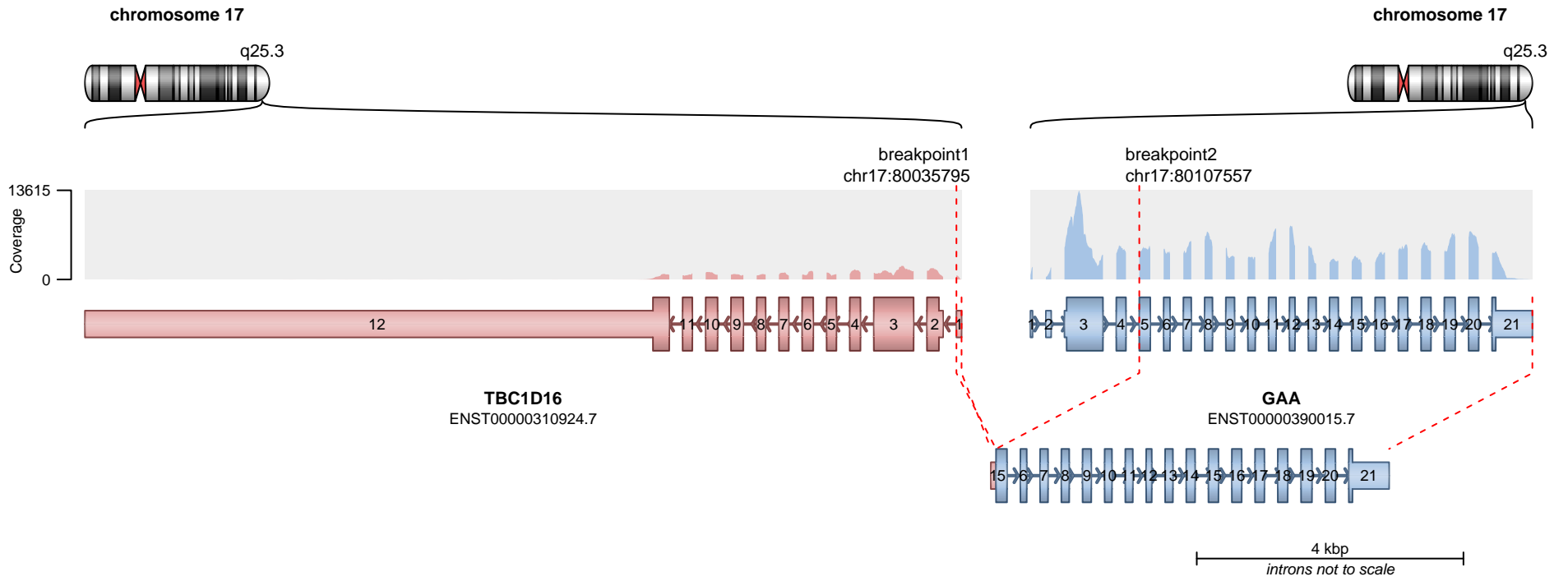
Glycosyl hydrolases family 31

SUPPORTING READ COUNT

Split reads = 5

Discordant mates = 0

— translocation — deletion
— duplication — inversion



N-terminal barrel of NtMGAM and CtMGAM, maltase-glucoamylase

Galactose mutarotase-like

RETAINED PROTEIN DOMAINS
reading frame unclear



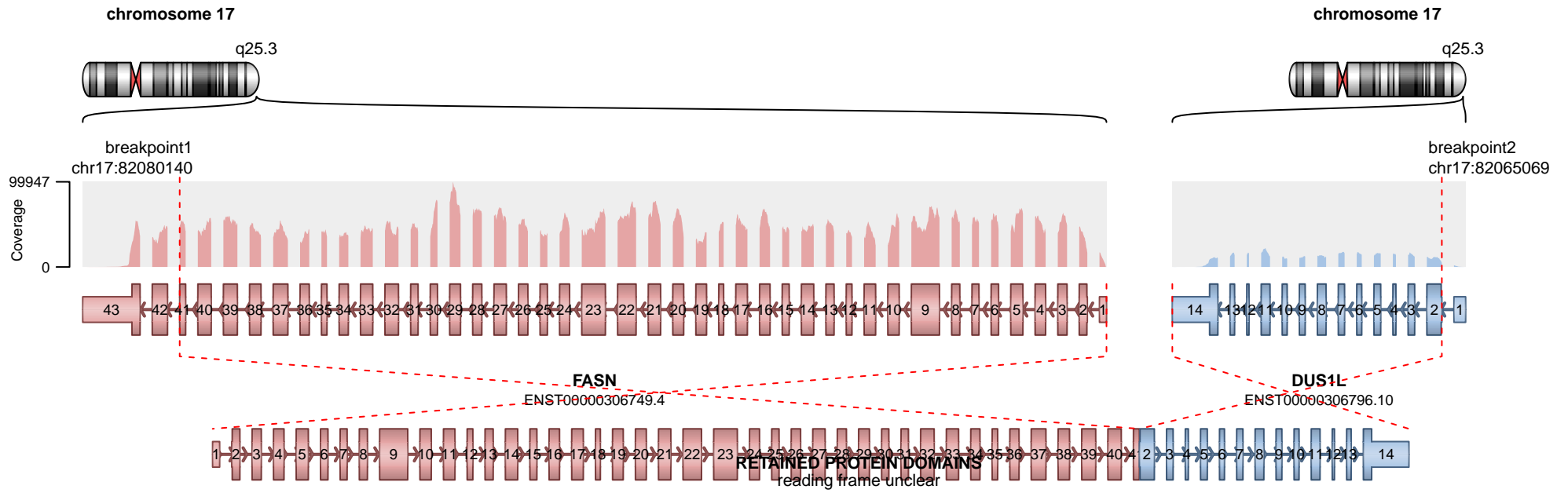
Glycosyl hydrolases family 31

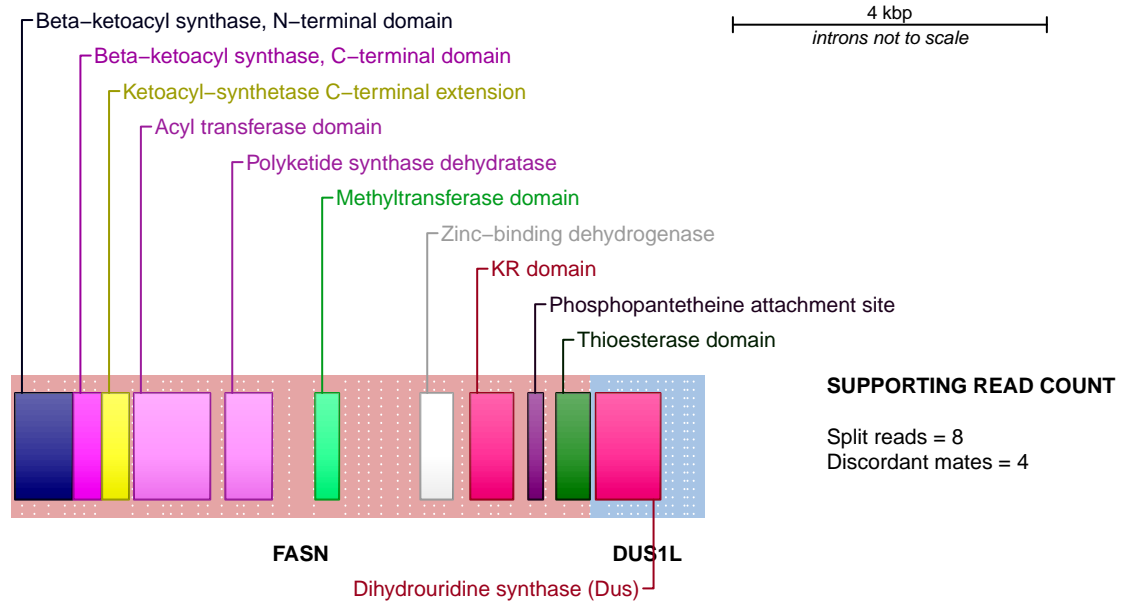
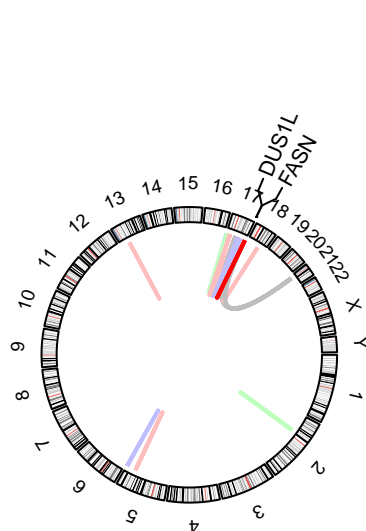
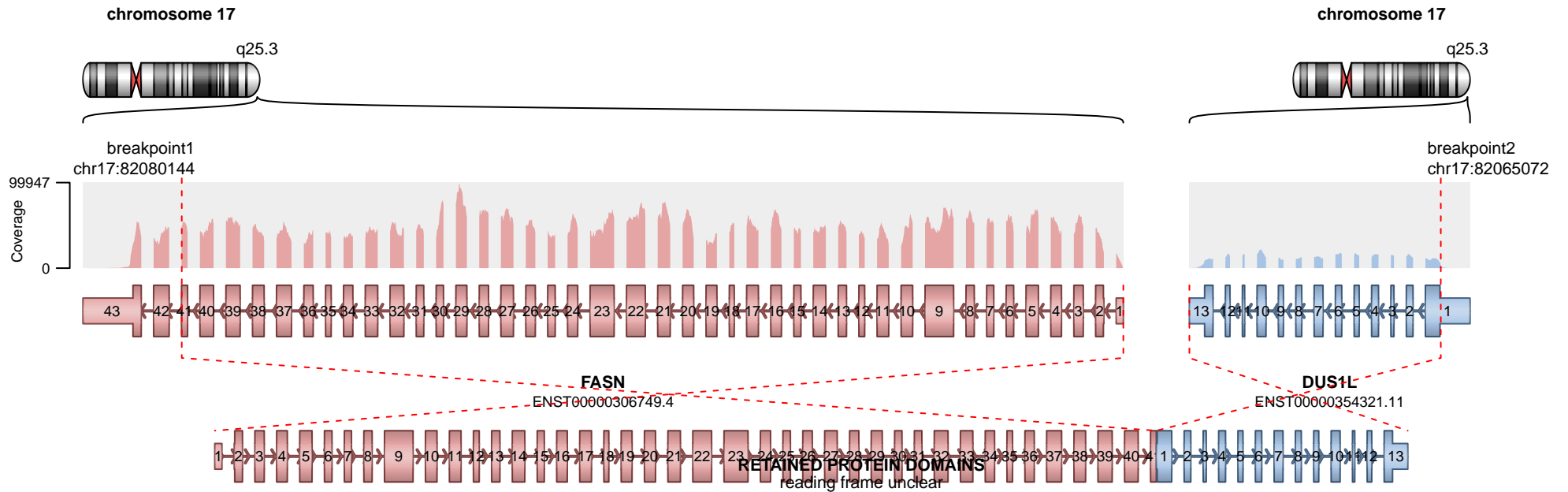
SUPPORTING READ COUNT

Split reads = 3

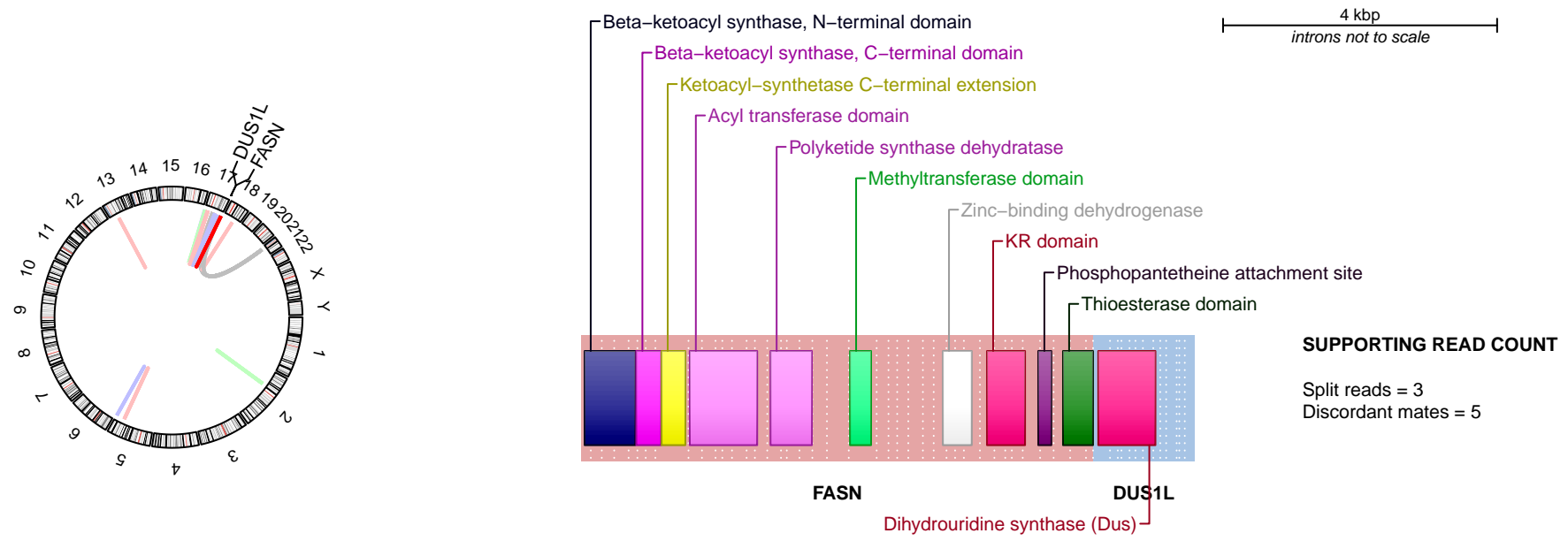
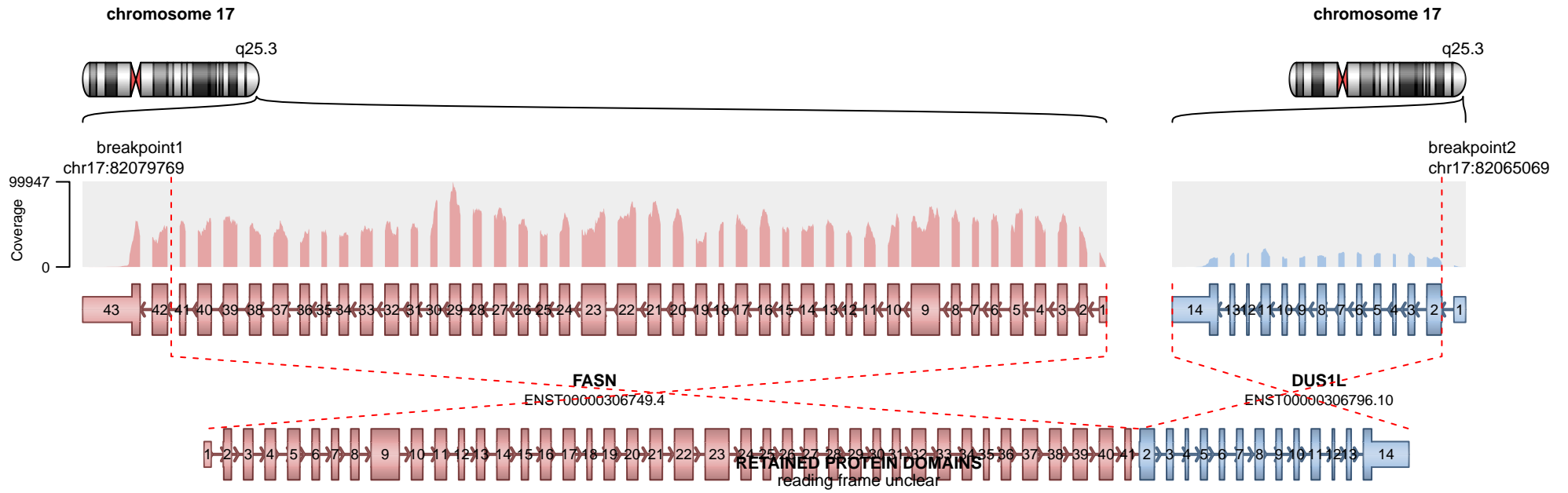
Discordant mates = 0

— translocation — deletion
— duplication — inversion

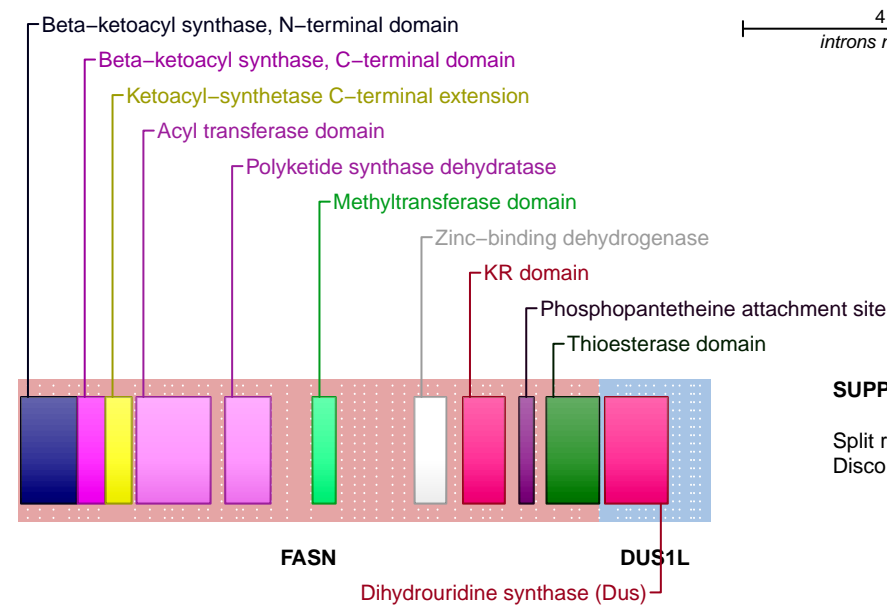
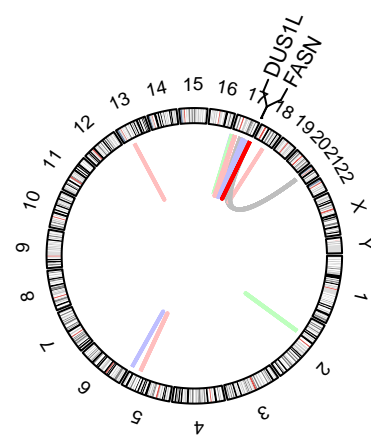
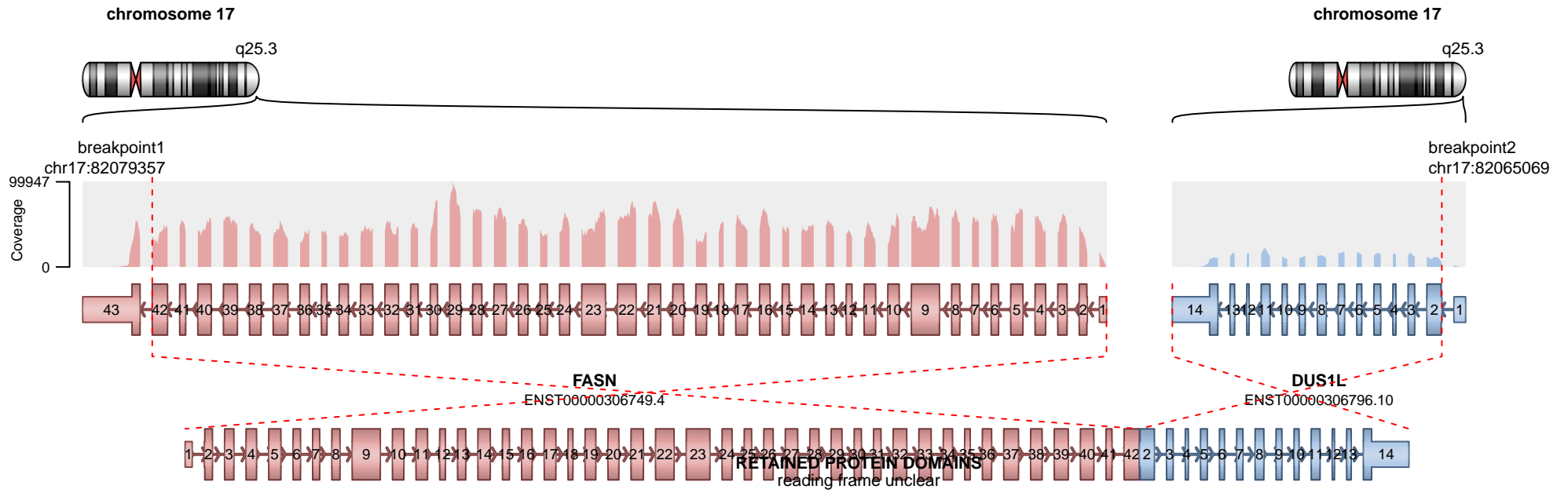




— translocation — deletion
— duplication — inversion



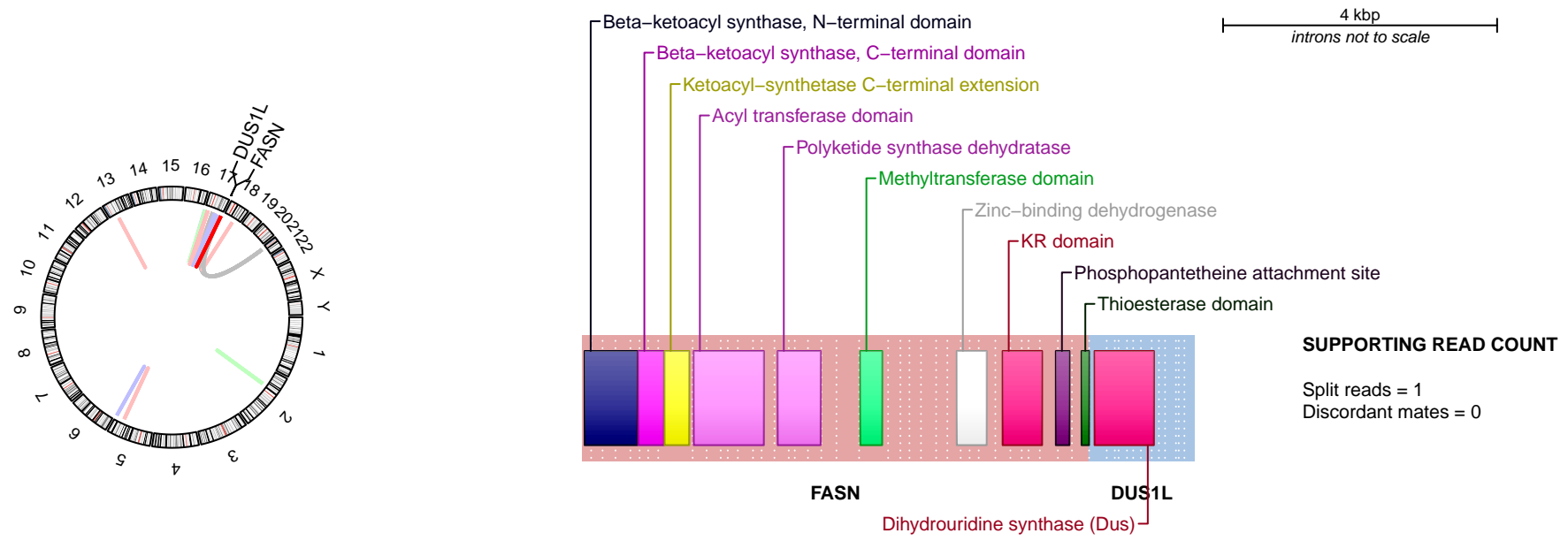
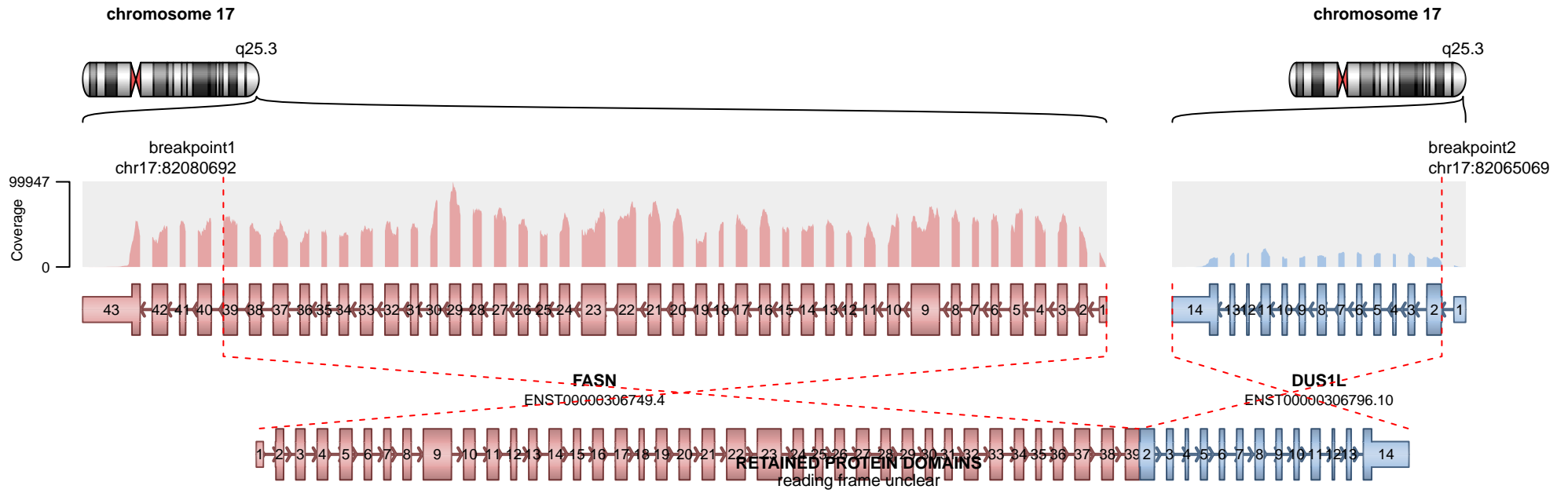
— translocation — deletion
— duplication — inversion



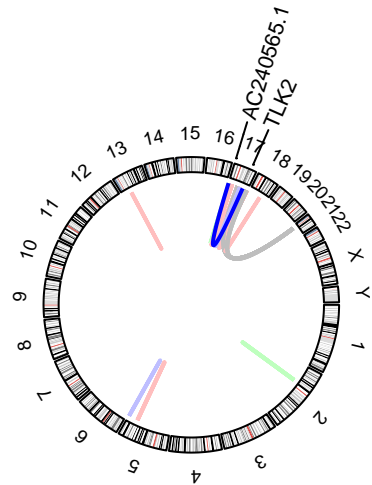
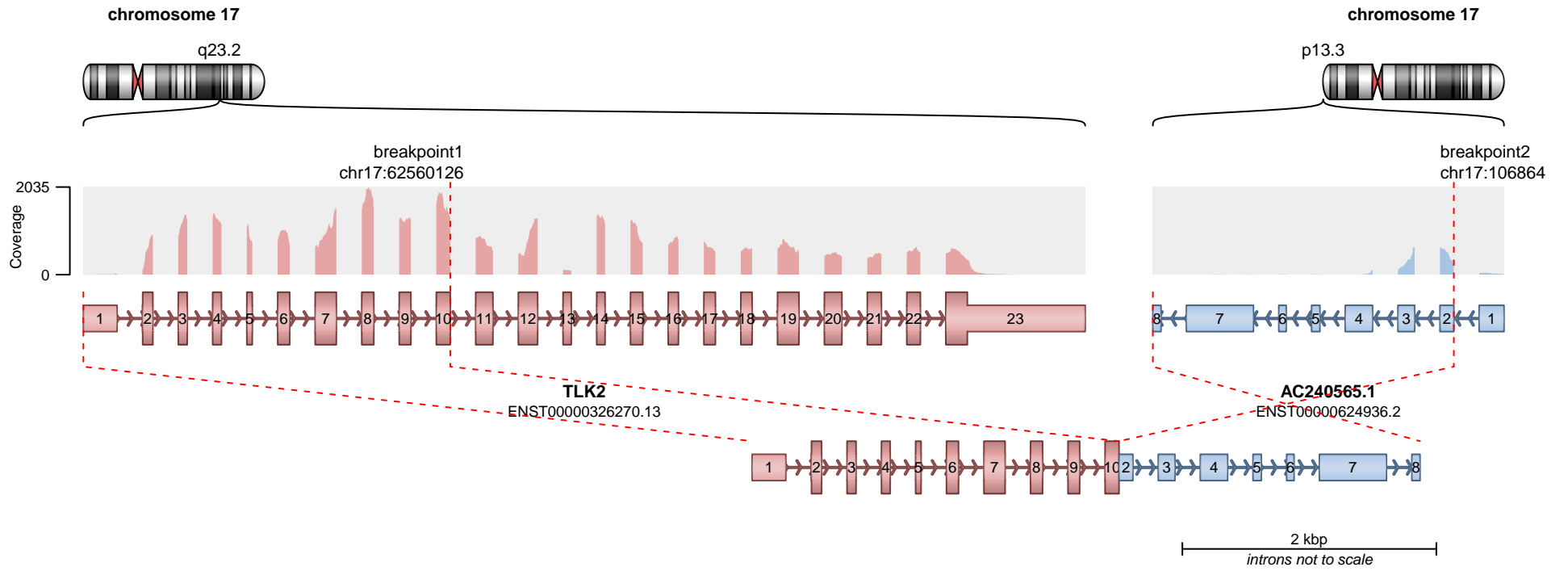
4 kbp
introns not to scale

SUPPORTING READ COUNT
Split reads = 1
Discordant mates = 5

— translocation — deletion
— duplication — inversion



— translocation — deletion
— duplication — inversion

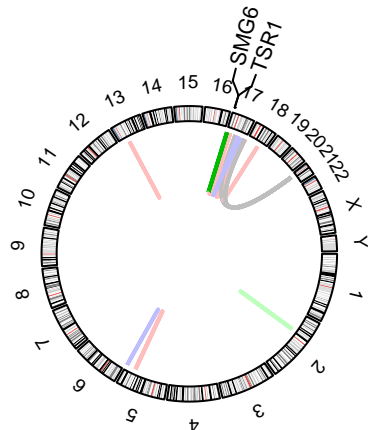
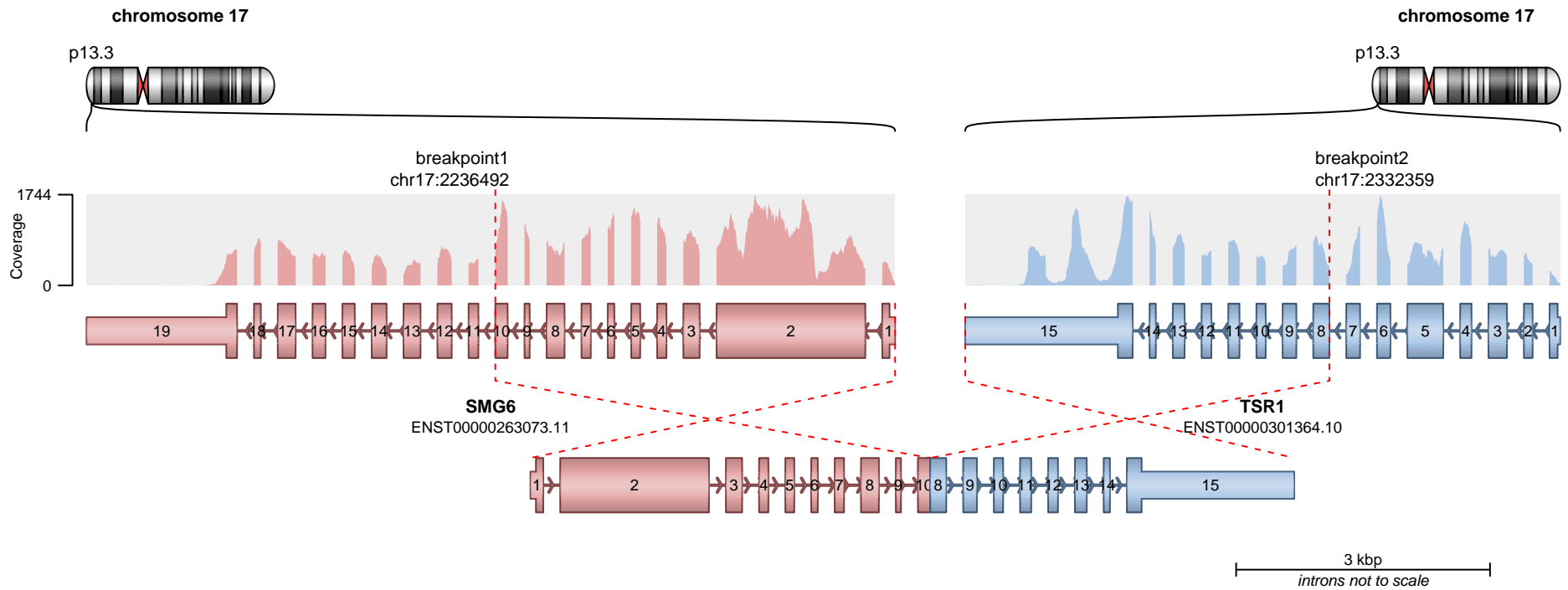


No protein domains retained in fusion.

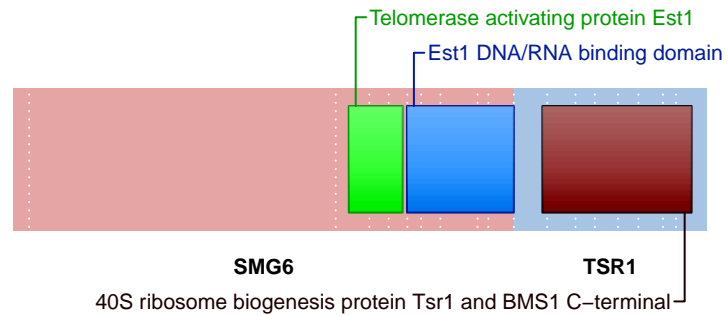
SUPPORTING READ COUNT

Split reads = 68
Discordant mates = 1

— translocation — deletion
— duplication — inversion



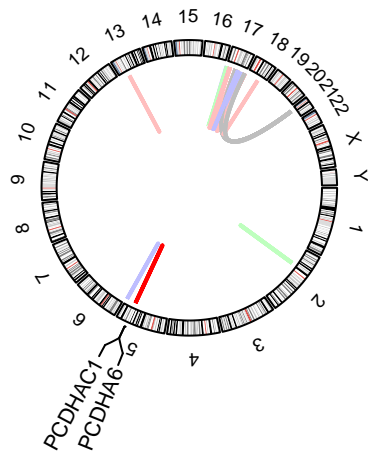
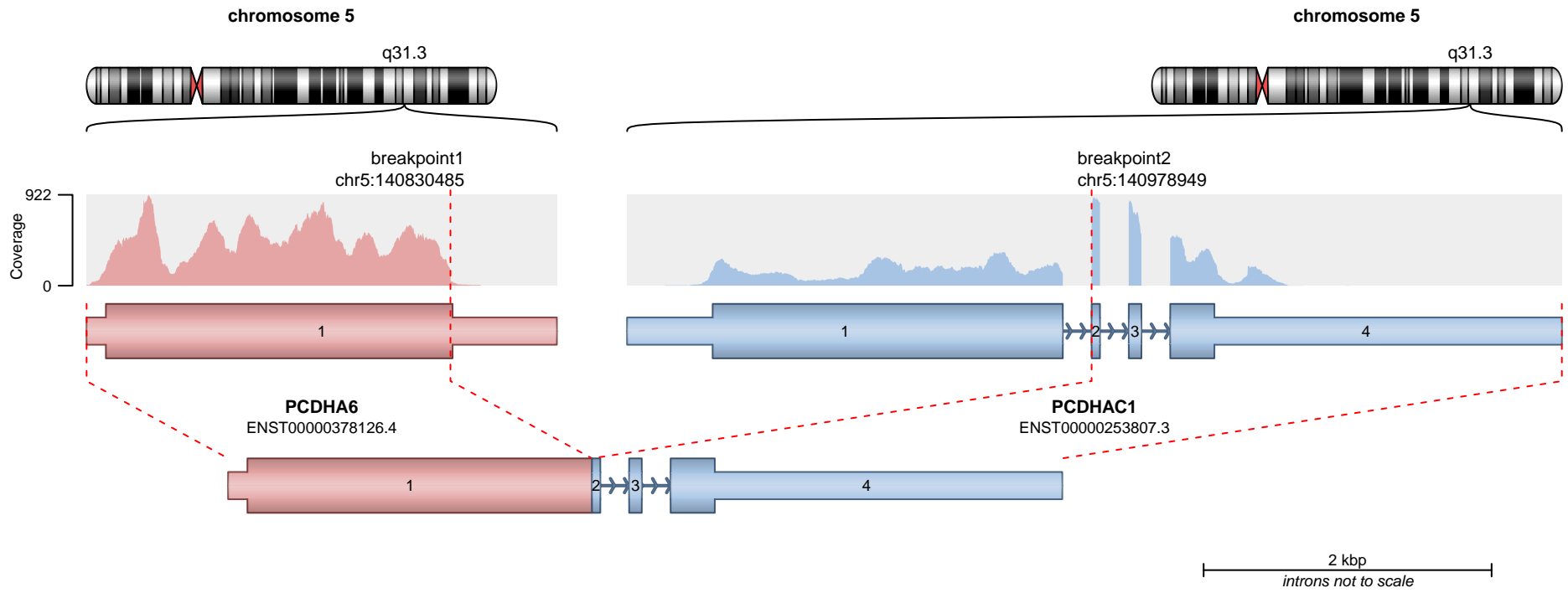
RETAINED PROTEIN DOMAINS
reading frame unclear



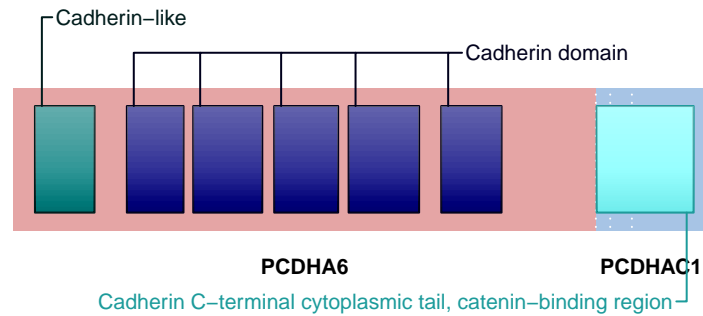
SUPPORTING READ COUNT

Split reads = 43
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



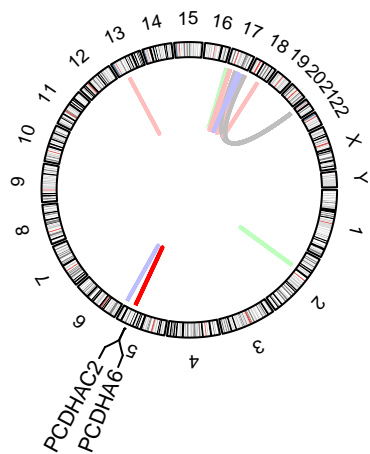
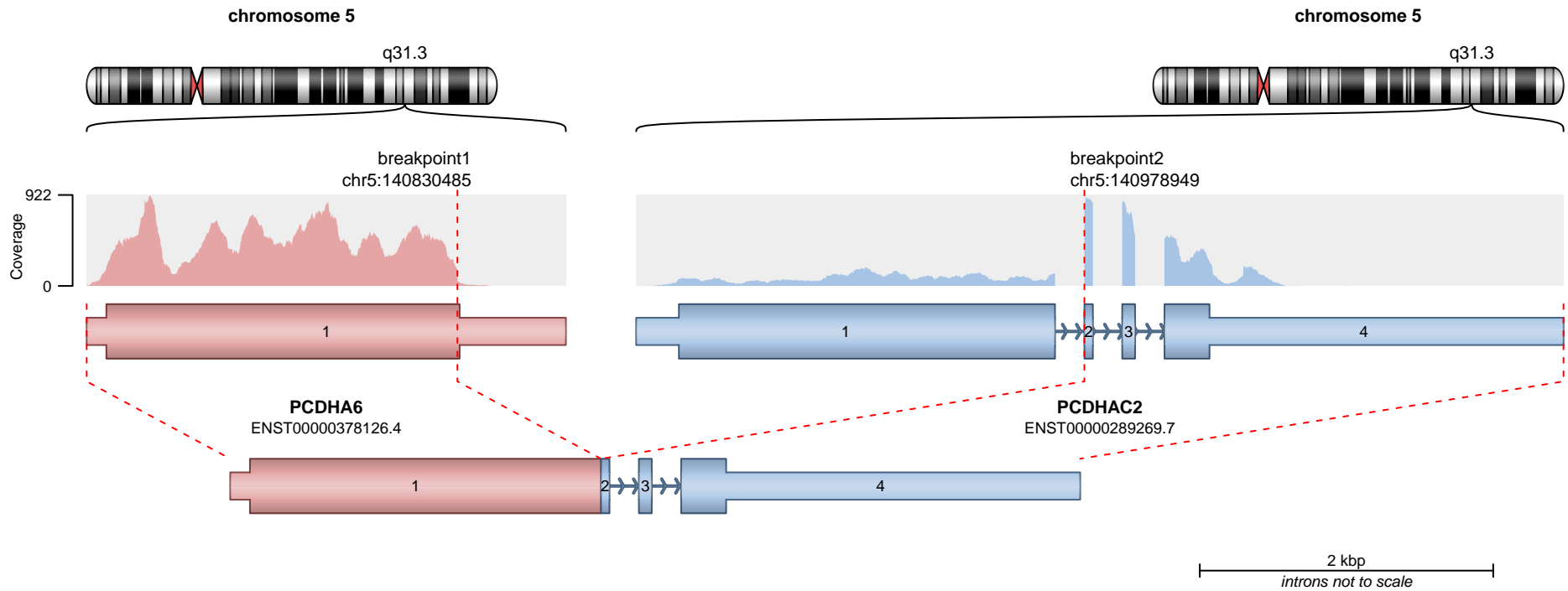
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

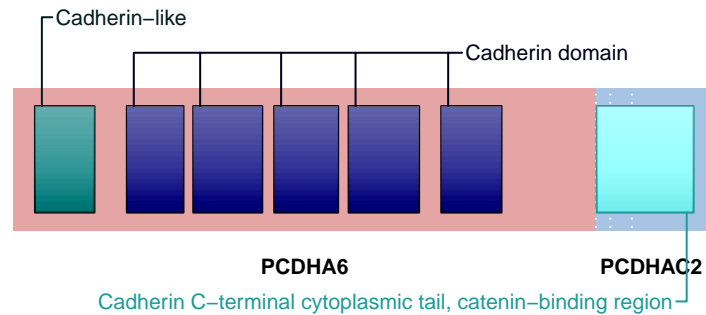
Split reads = 34
Discordant mates = 0

— translocation — deletion
— duplication — inversion



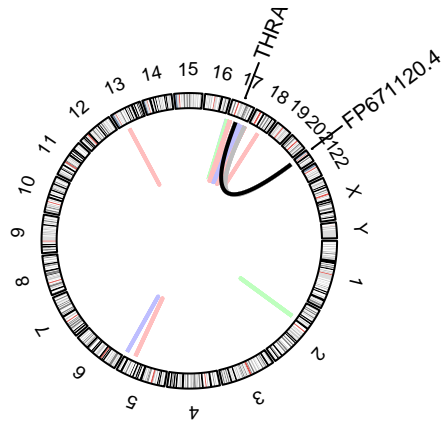
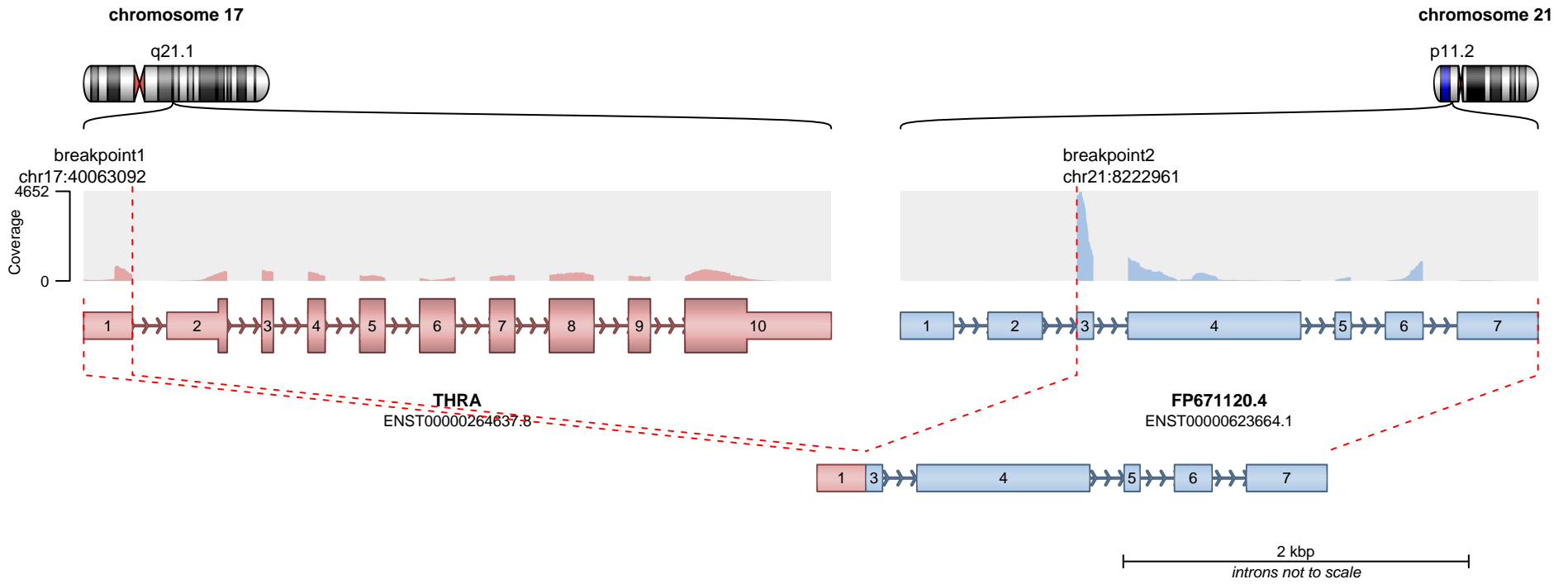
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 34
Discordant mates = 0

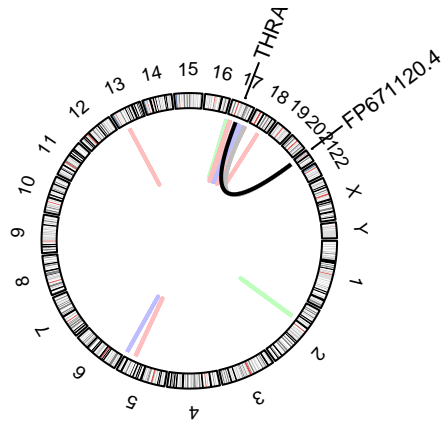
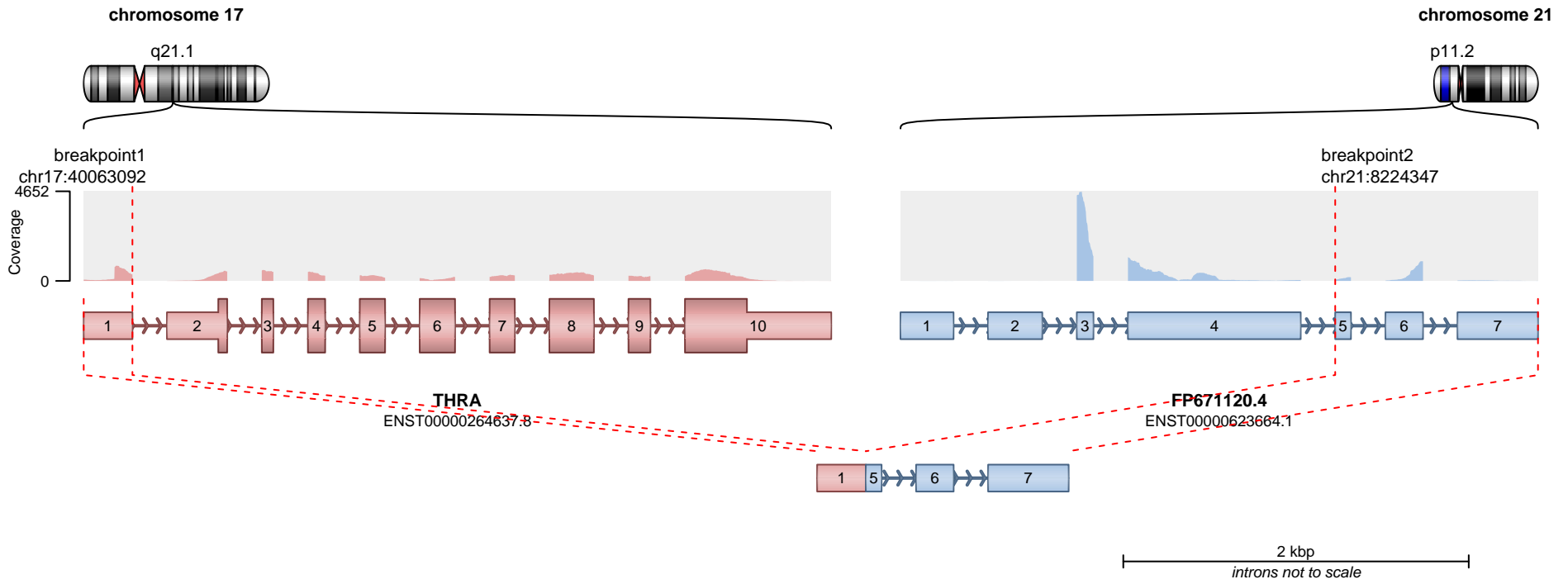


No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 30
Discordant mates = 0

— translocation — deletion
— duplication — inversion

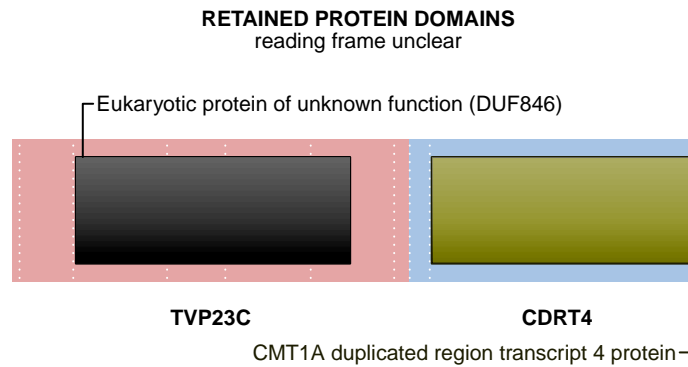
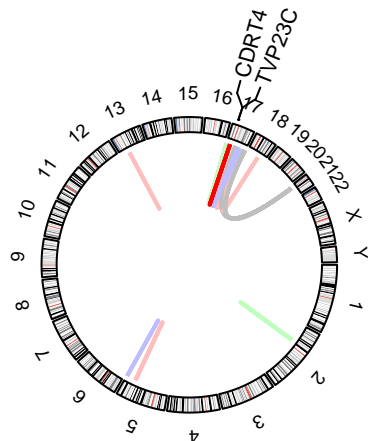
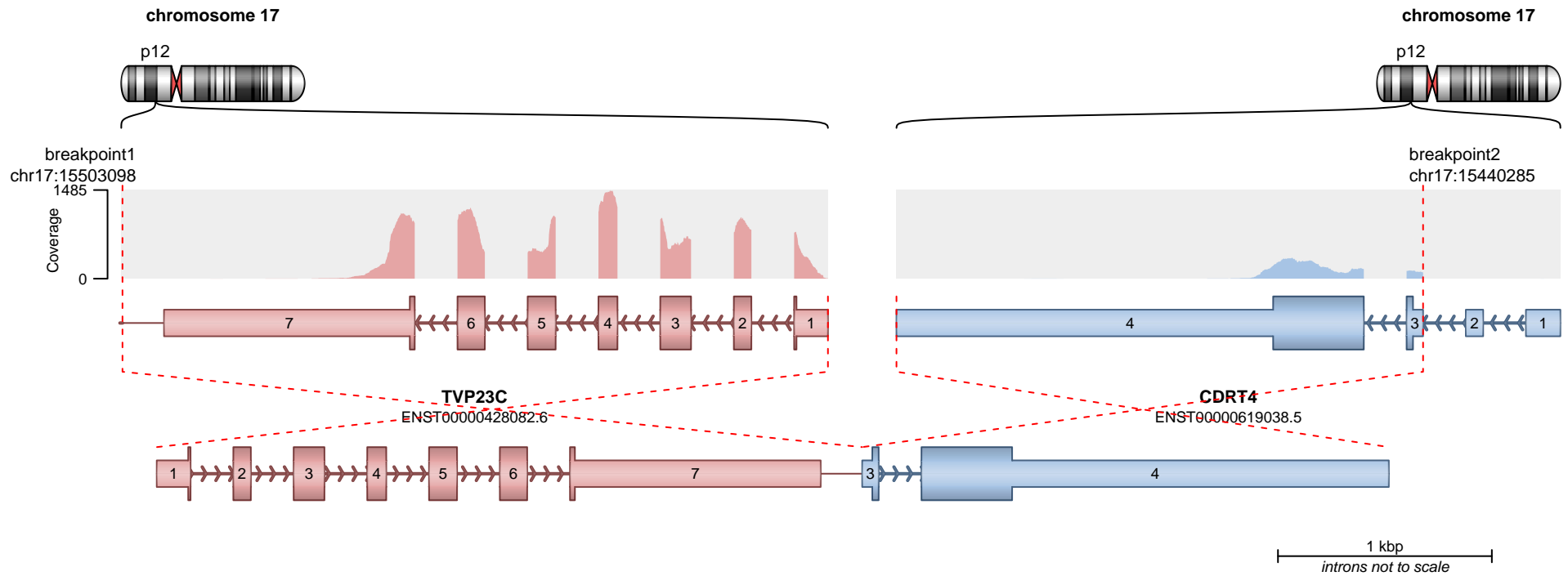


No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

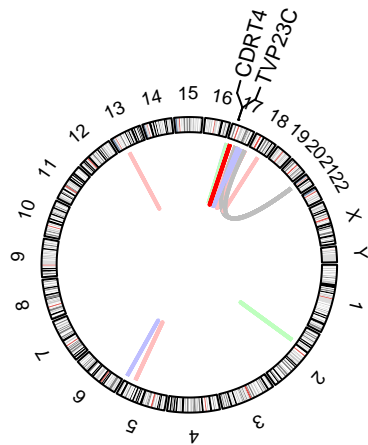
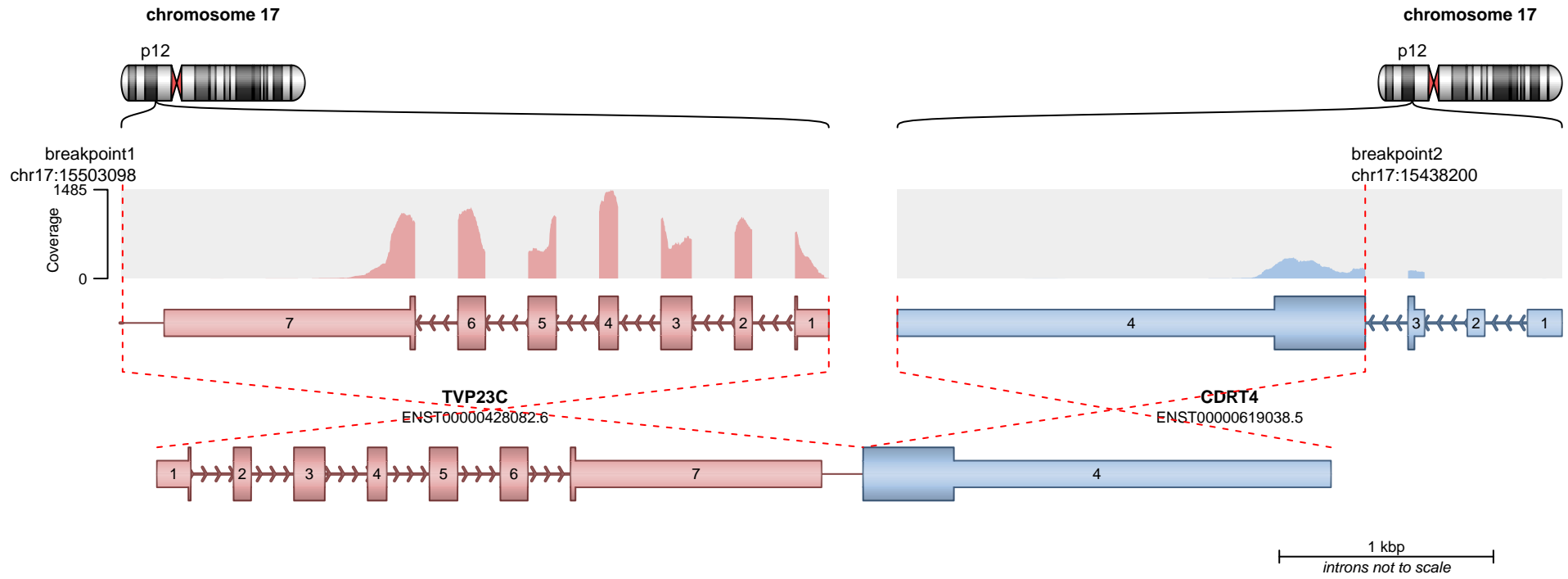
— translocation — deletion
— duplication — inversion



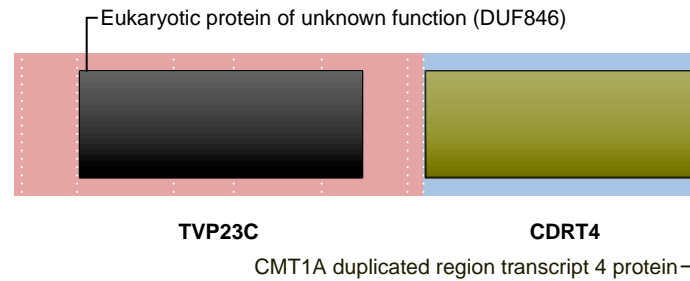
SUPPORTING READ COUNT

Split reads = 20
Discordant mates = 0

— translocation — deletion
— duplication — inversion



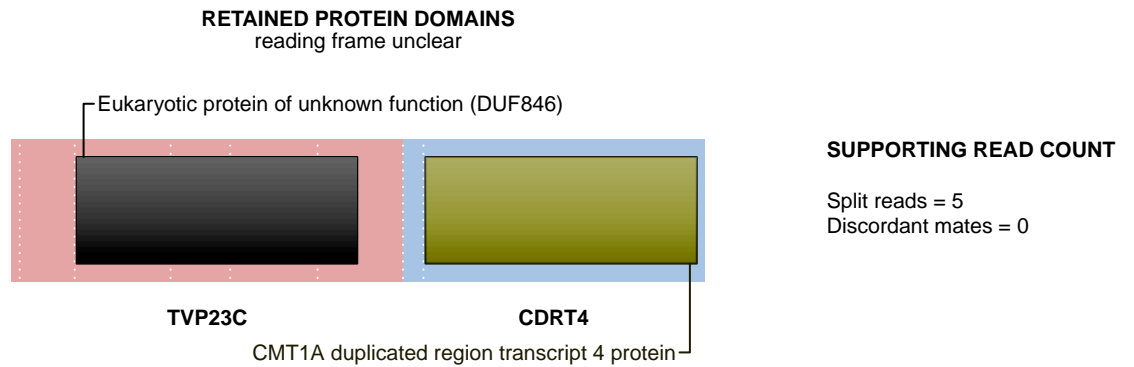
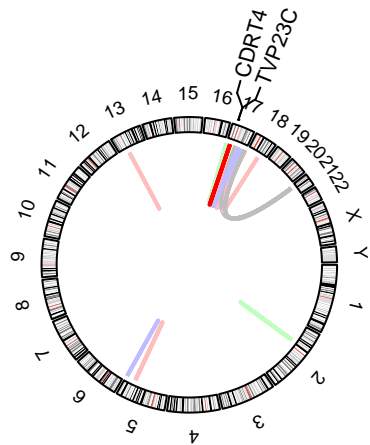
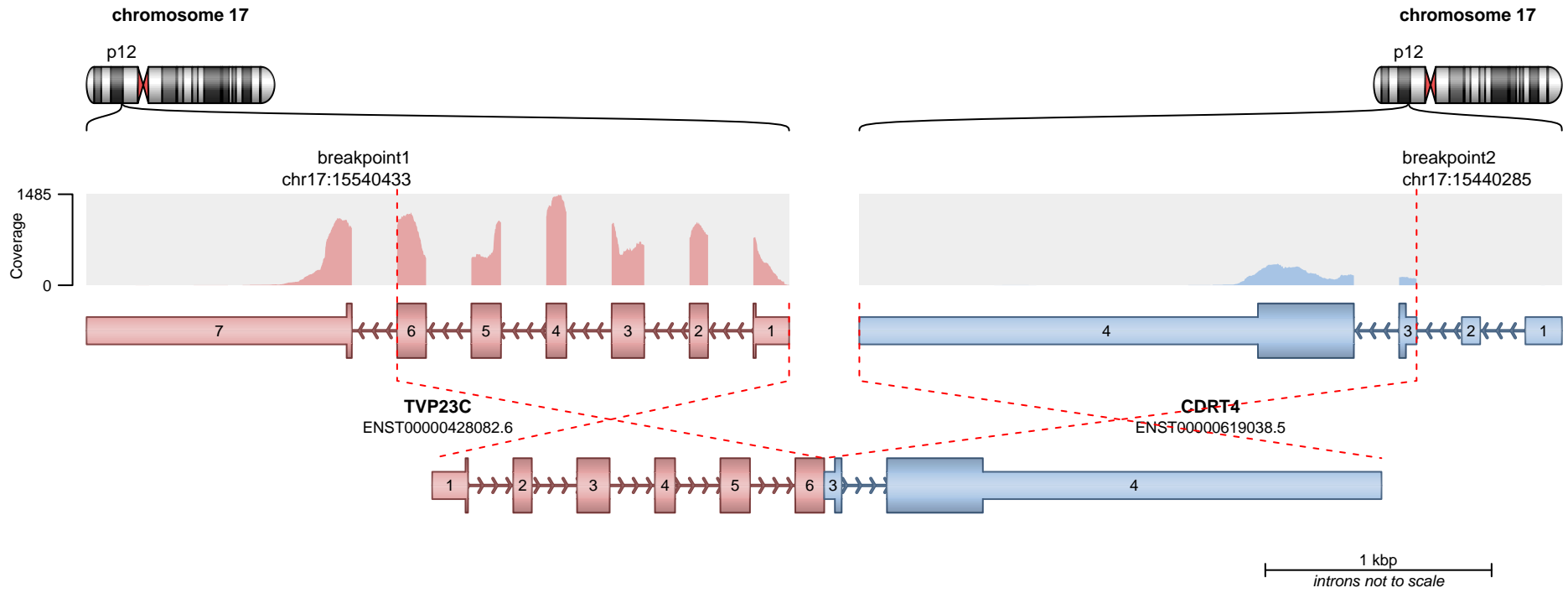
RETAINED PROTEIN DOMAINS
reading frame unclear



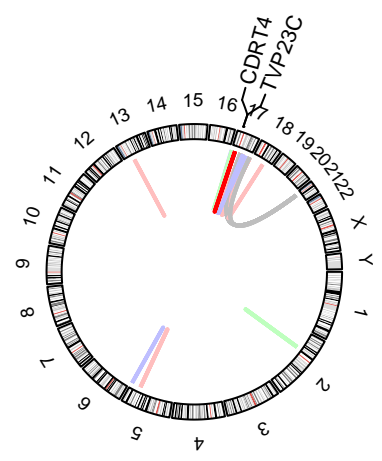
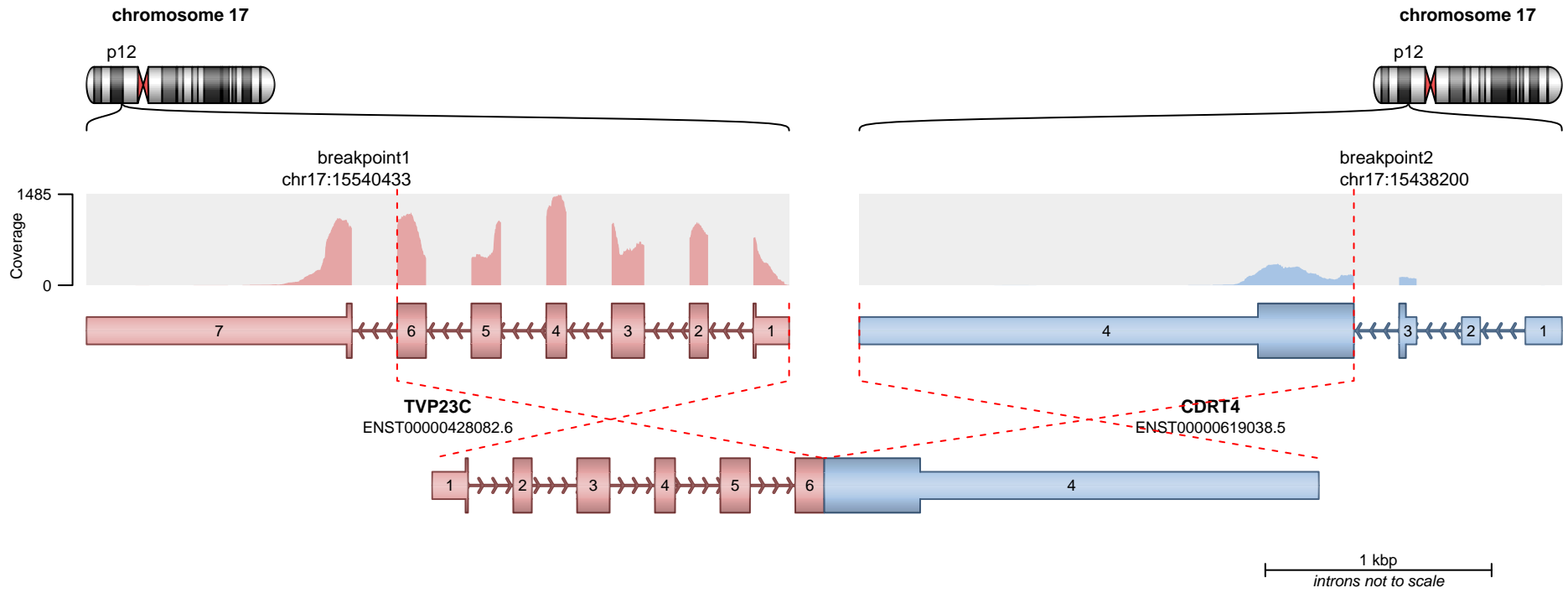
SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 0

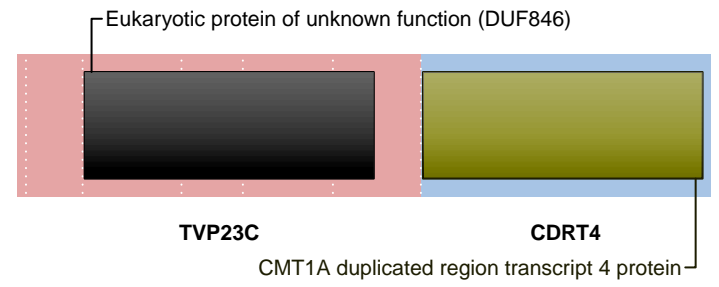
— translocation — deletion
— duplication — inversion



— translocation — deletion
— duplication — inversion



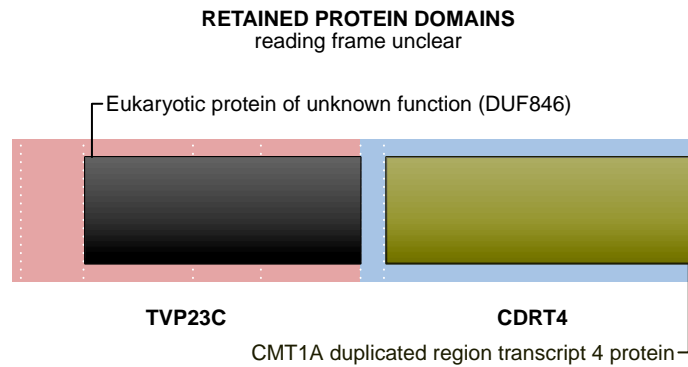
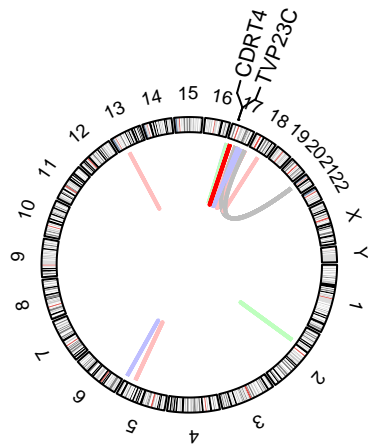
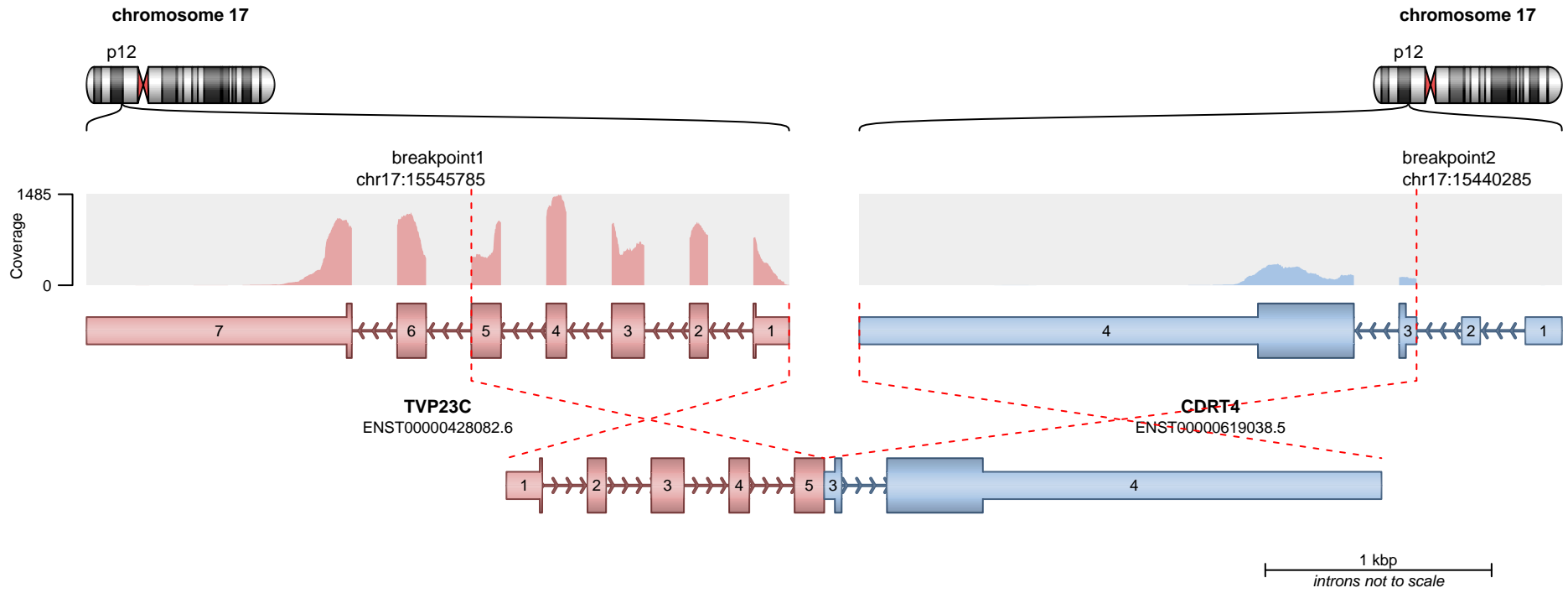
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

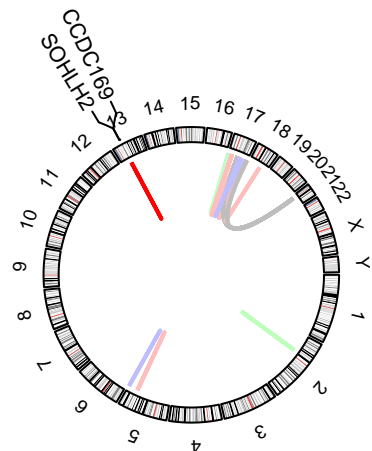
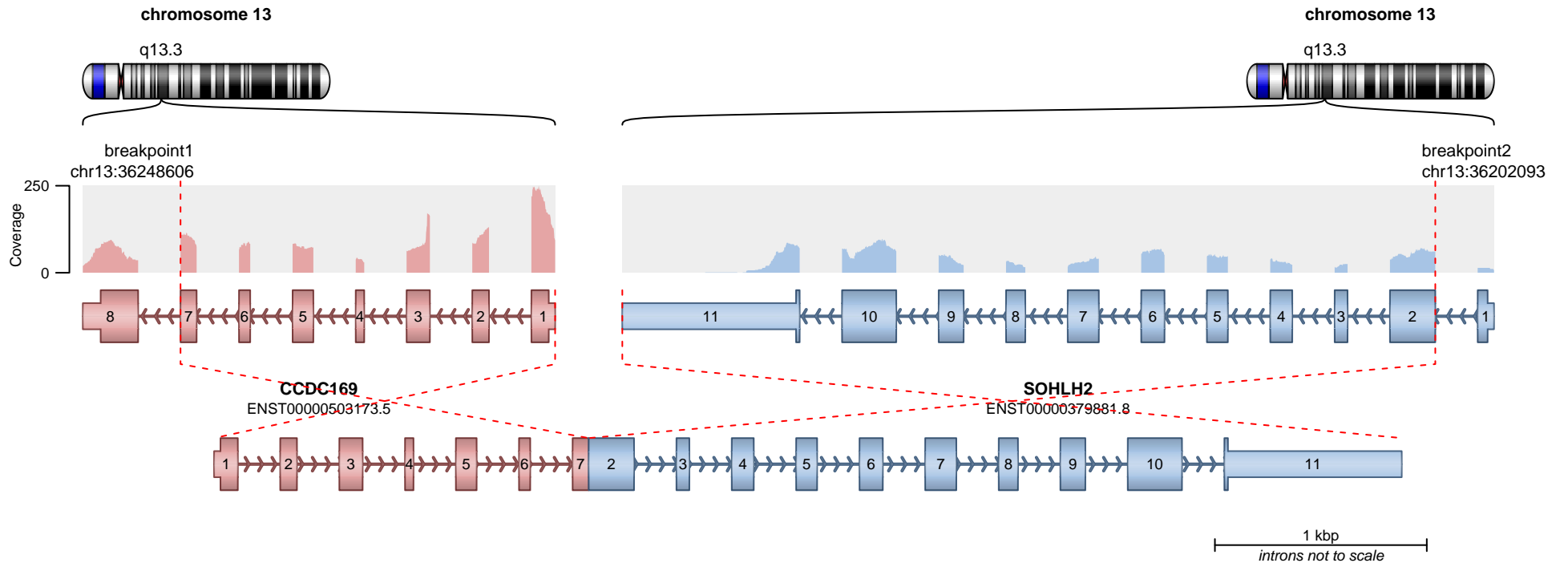
- translocation
- duplication
- deletion
- inversion



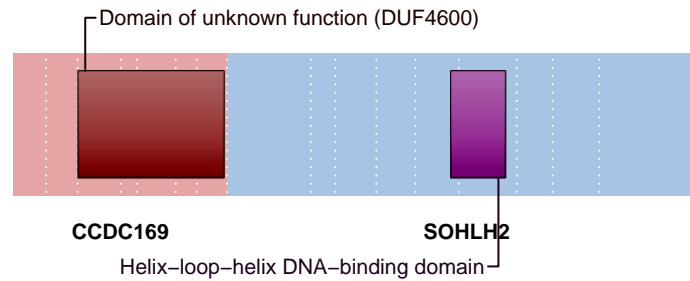
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



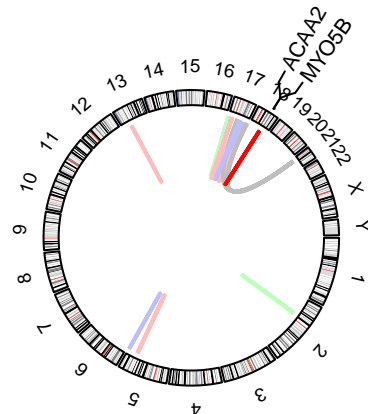
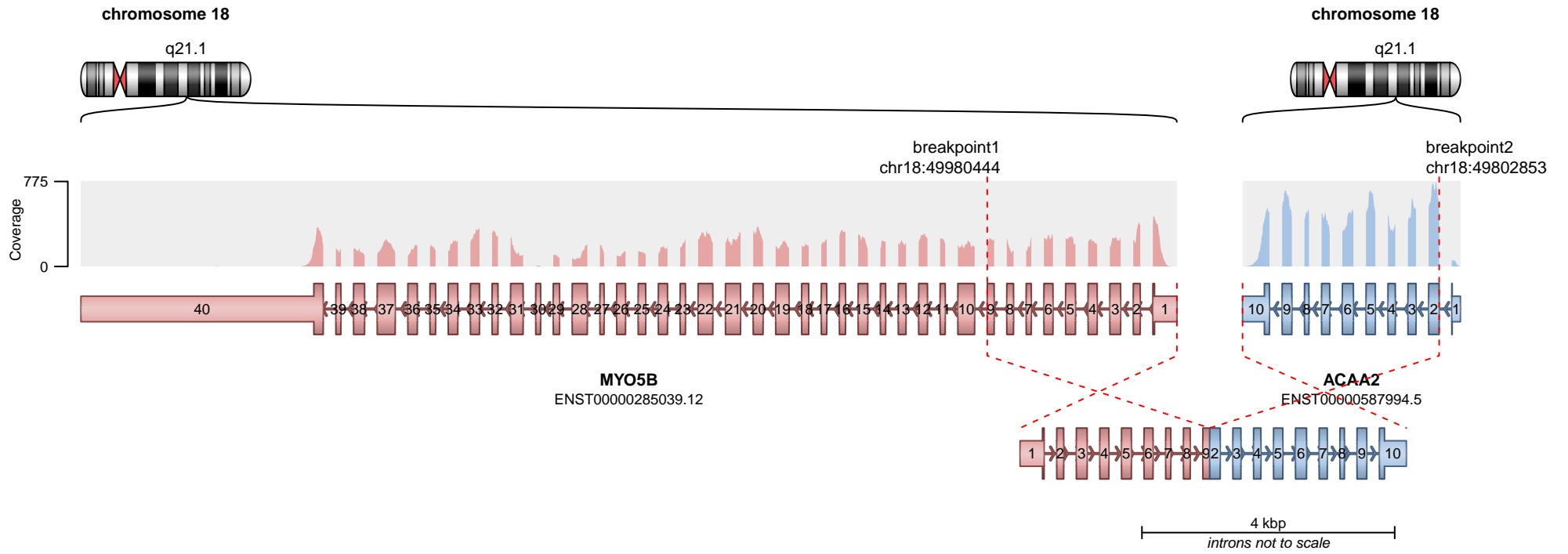
RETAINED PROTEIN DOMAINS
reading frame unclear



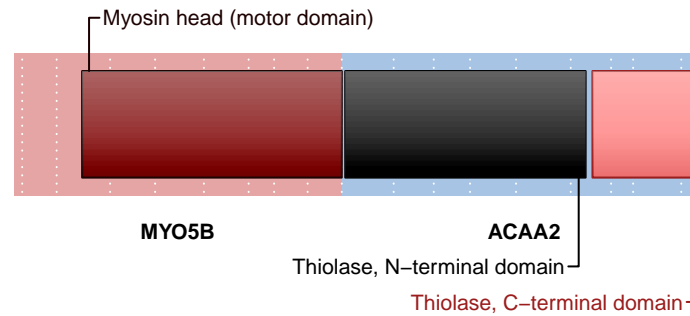
SUPPORTING READ COUNT

Split reads = 18
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



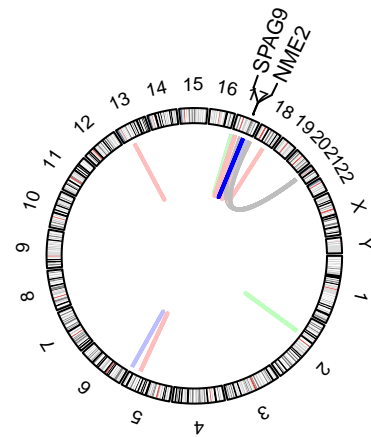
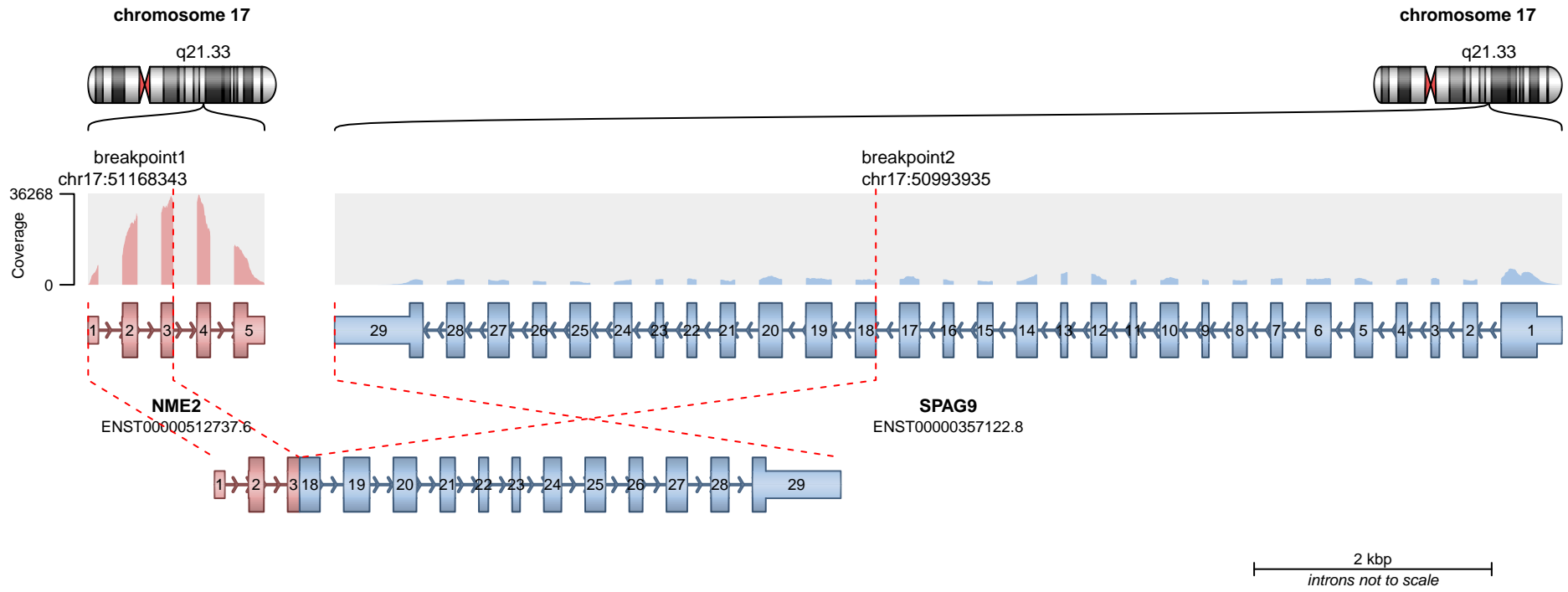
RETAINED PROTEIN DOMAINS
reading frame unclear



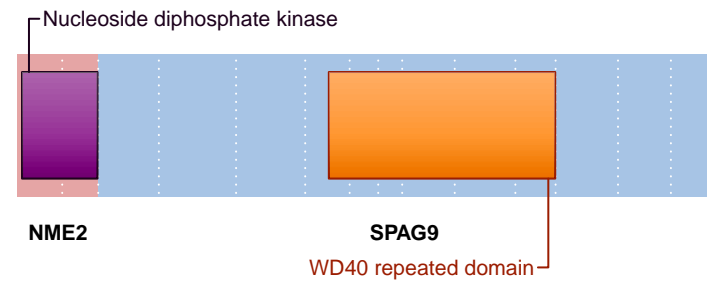
SUPPORTING READ COUNT

Split reads = 16
Discordant mates = 2

- translocation
- duplication
- deletion
- inversion



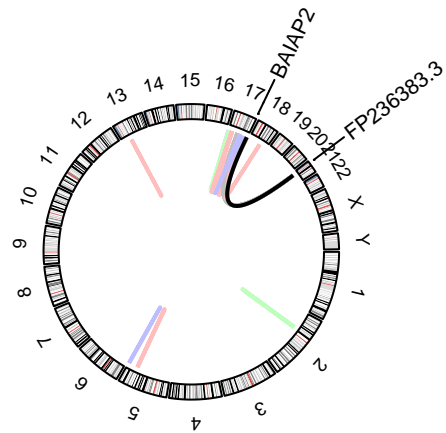
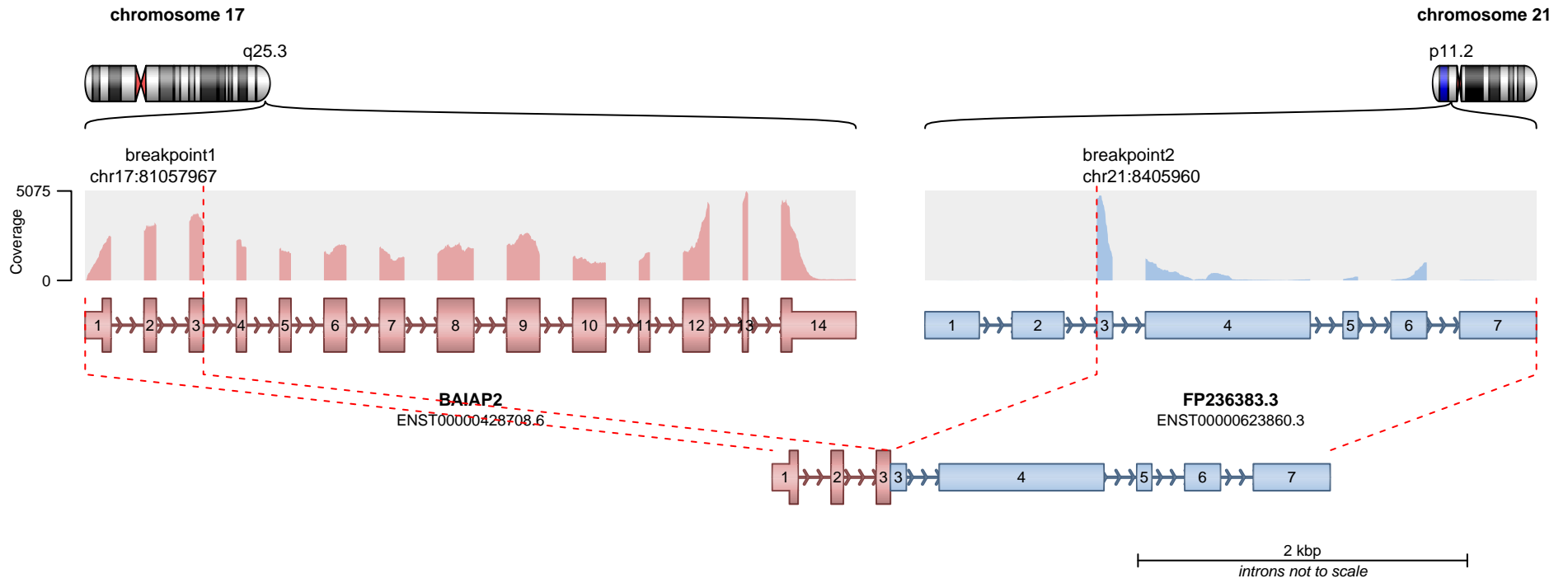
RETAINED PROTEIN DOMAINS
reading frame unclear



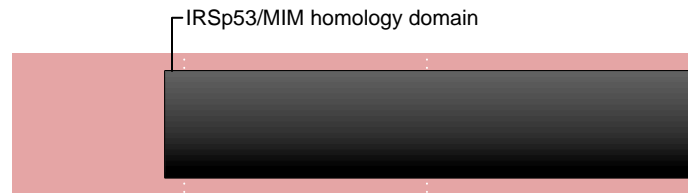
SUPPORTING READ COUNT

Split reads = 16
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



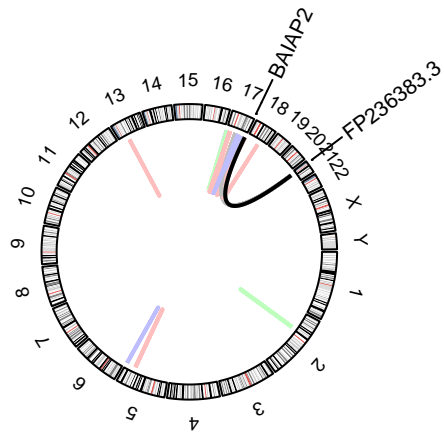
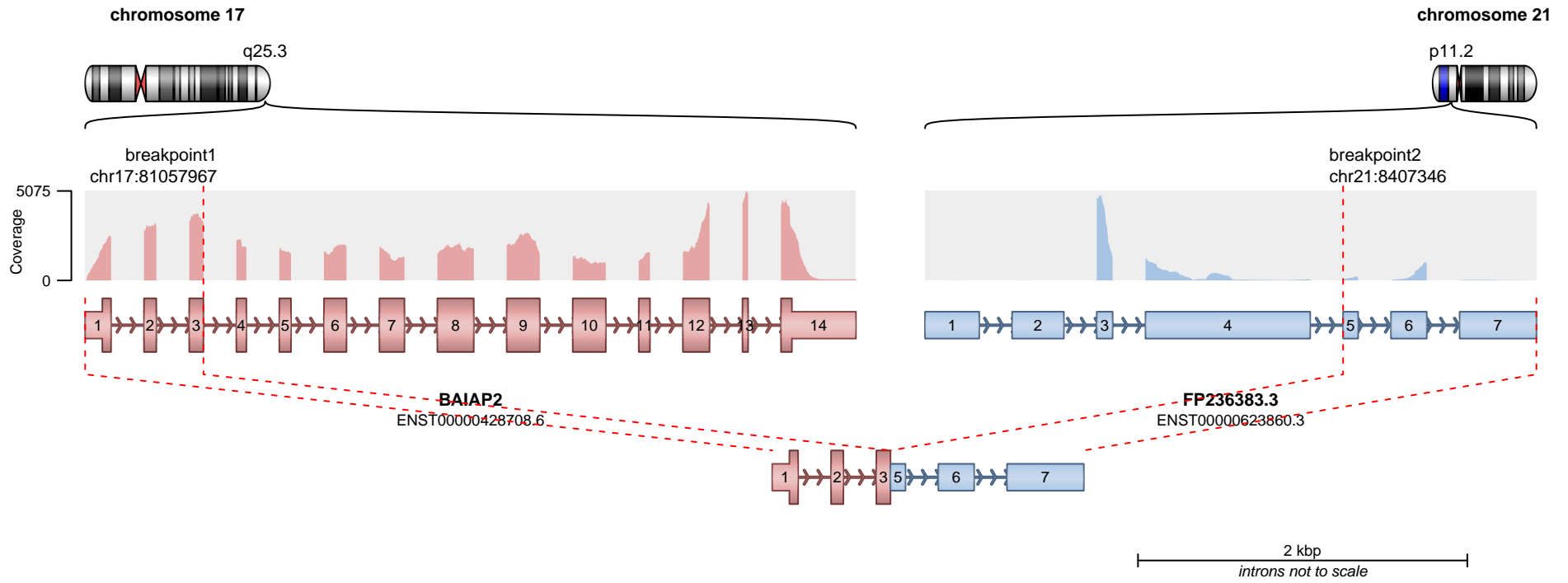
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

IRSp53/MIM homology domain

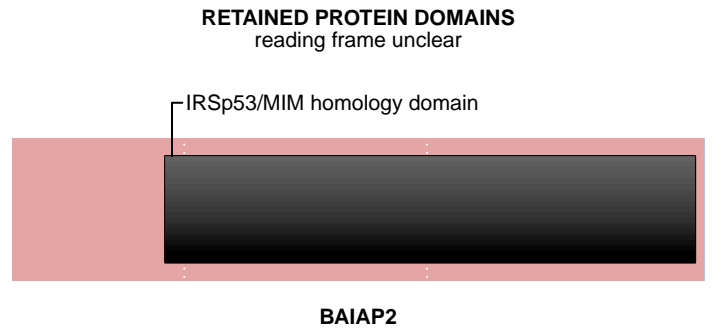
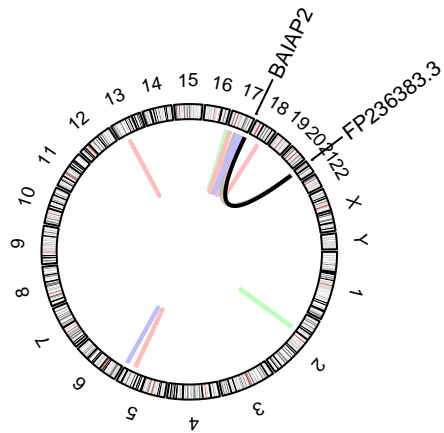
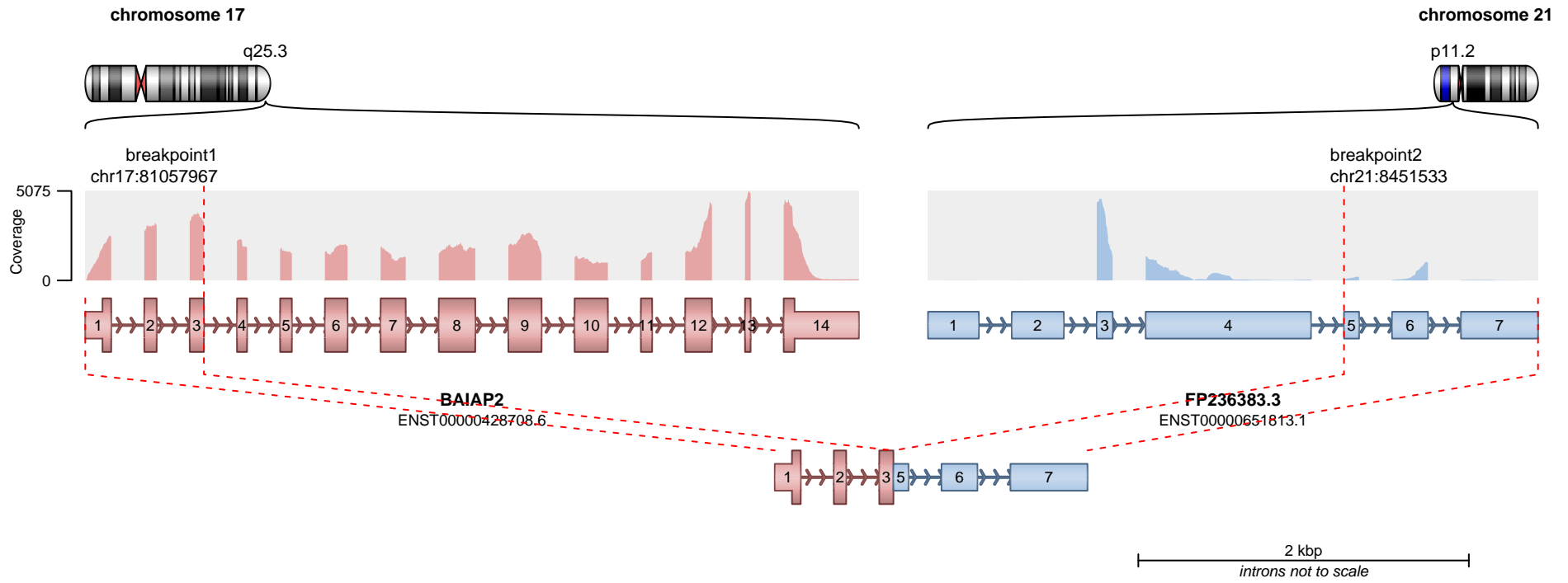


BAIAP2

SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

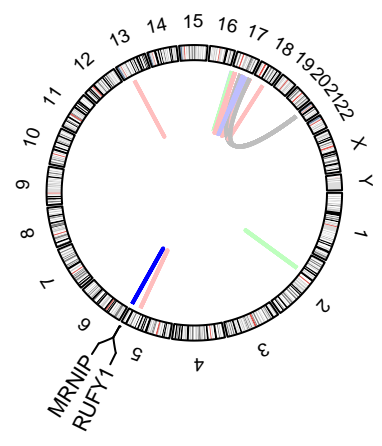
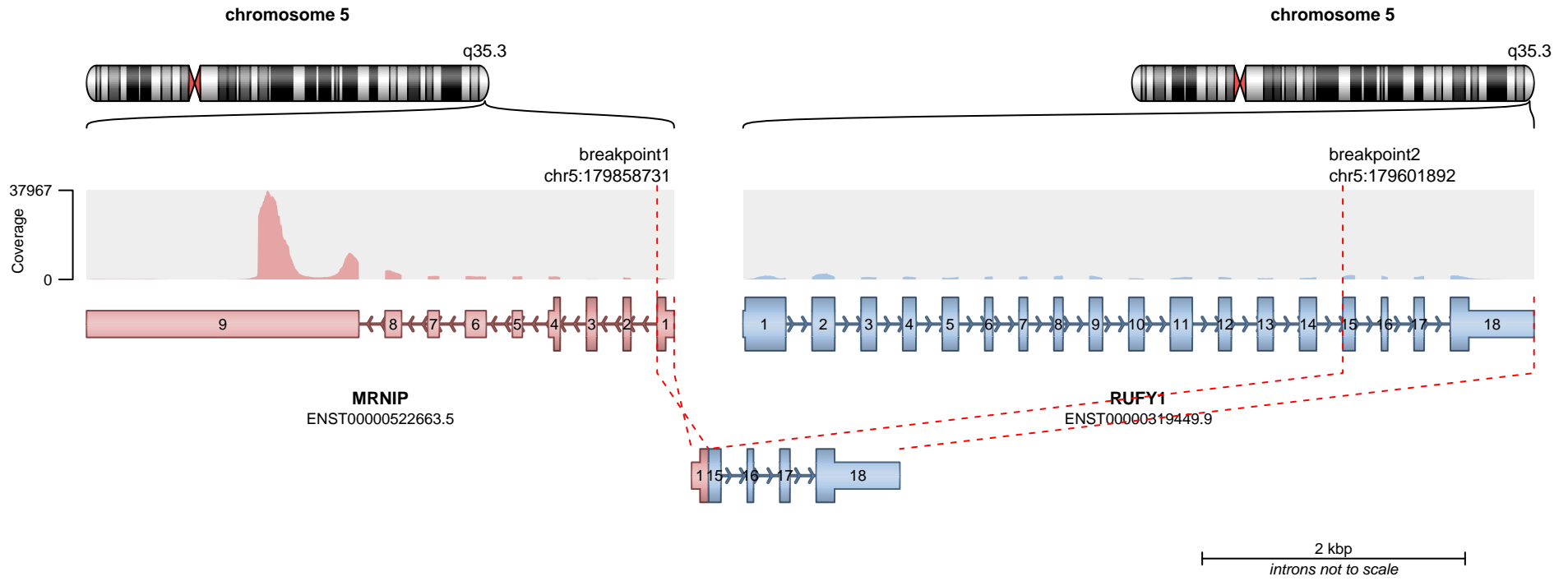
- translocation
- duplication
- deletion
- inversion



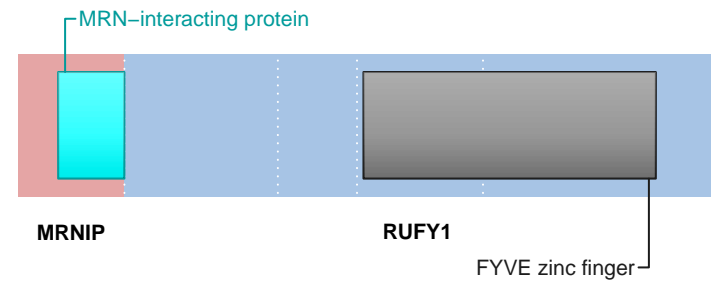
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 11
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion