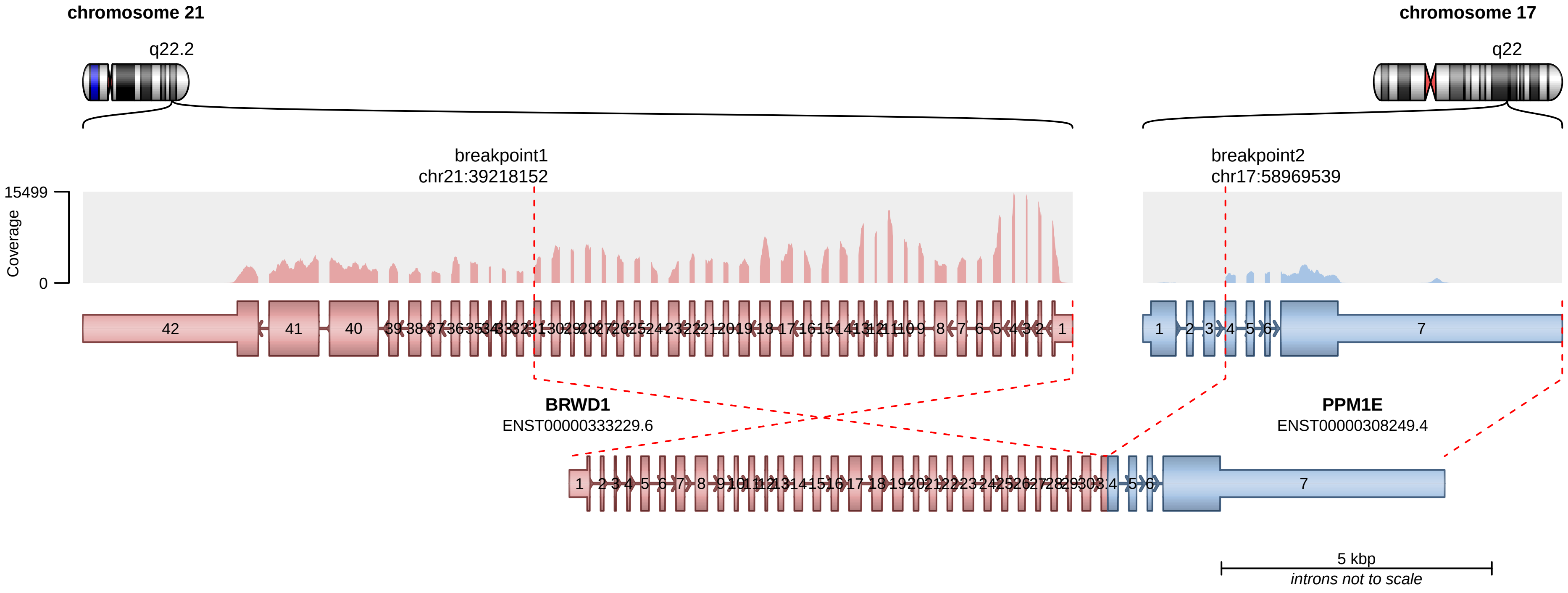
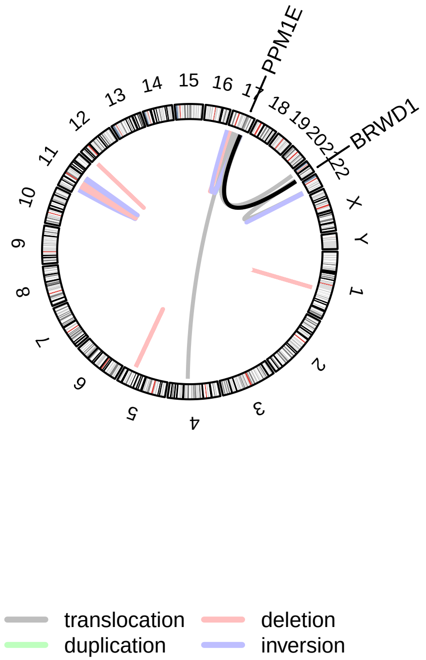
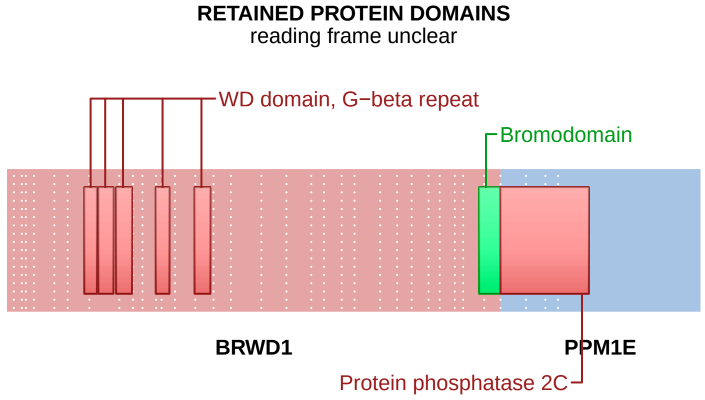
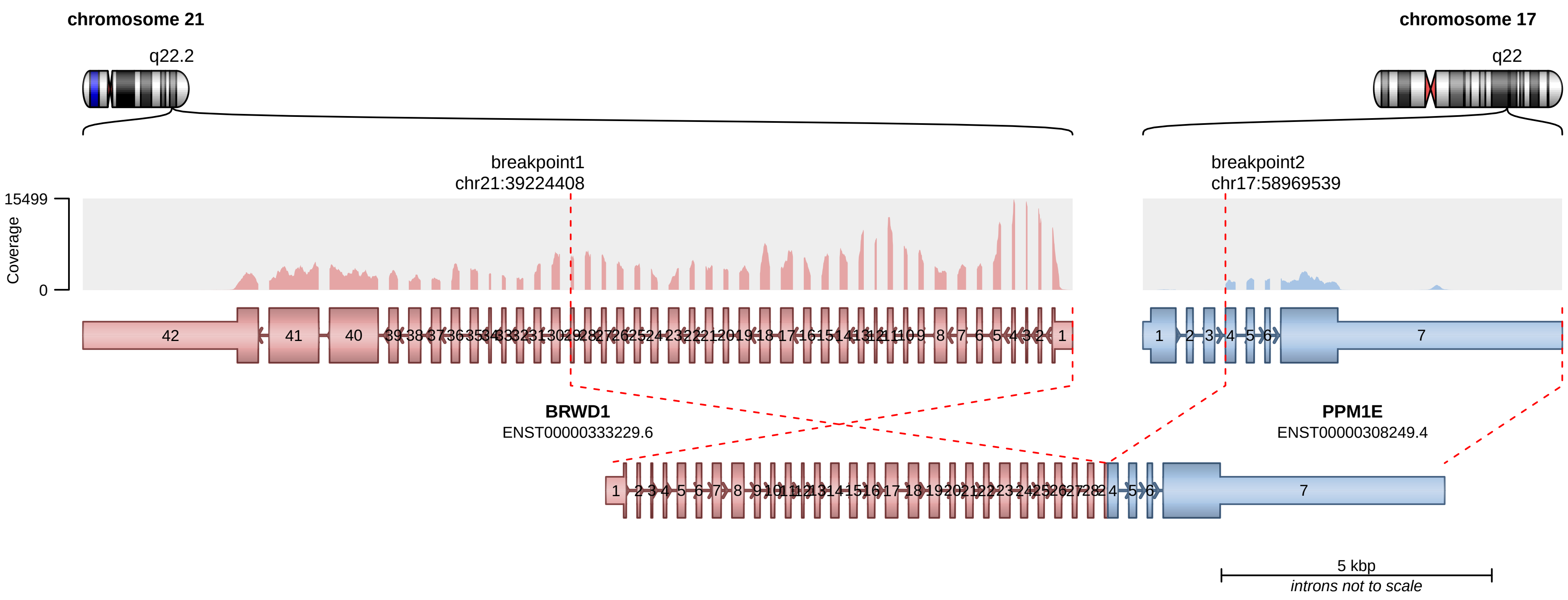


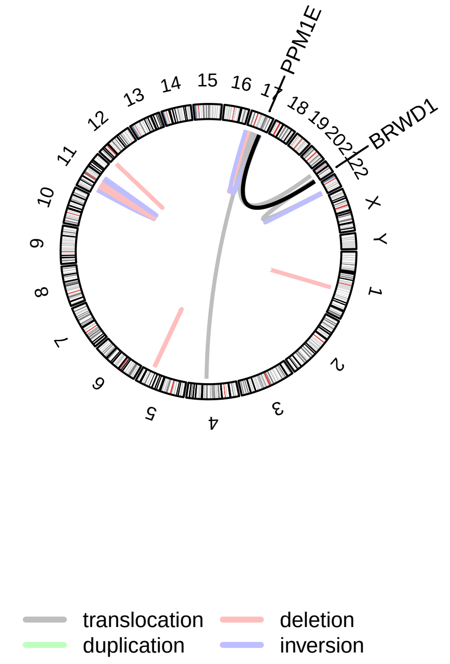


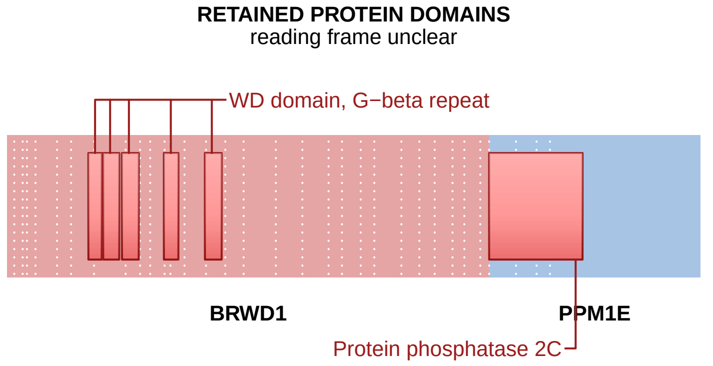


SUPPORTING READ COUNT

Split reads = 304
Discordant mates = 2

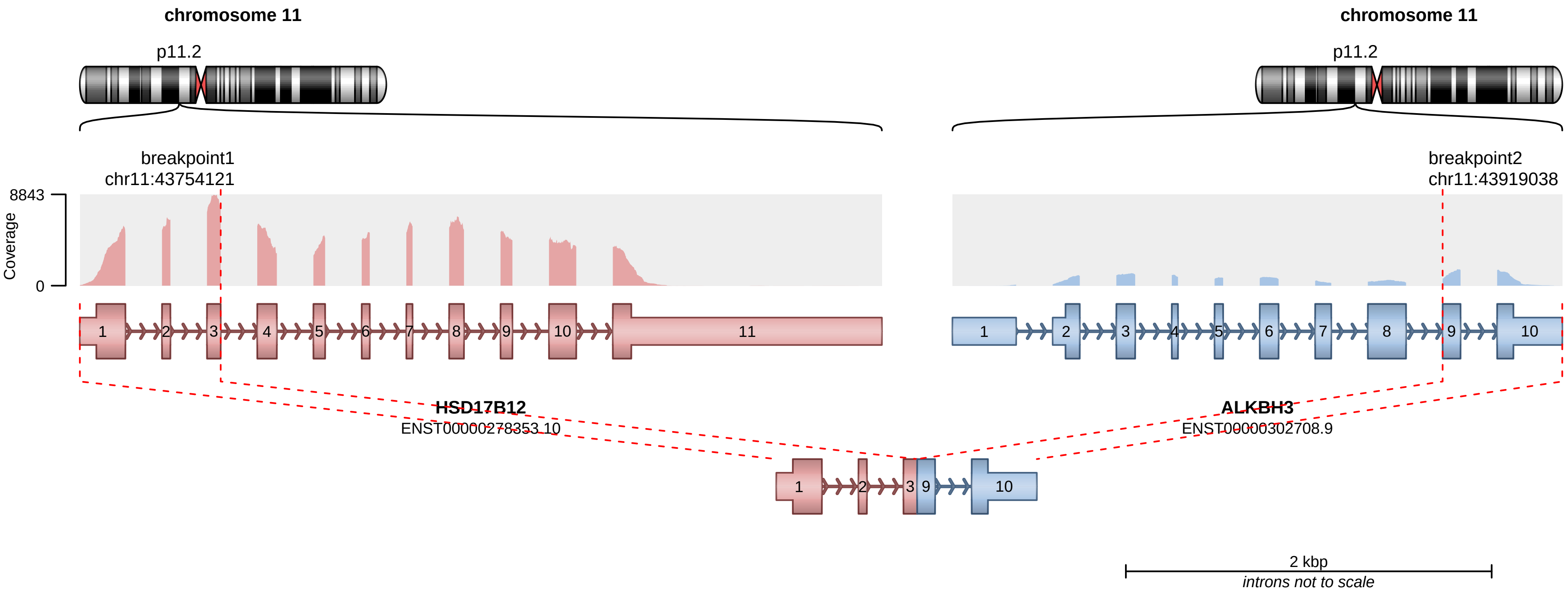


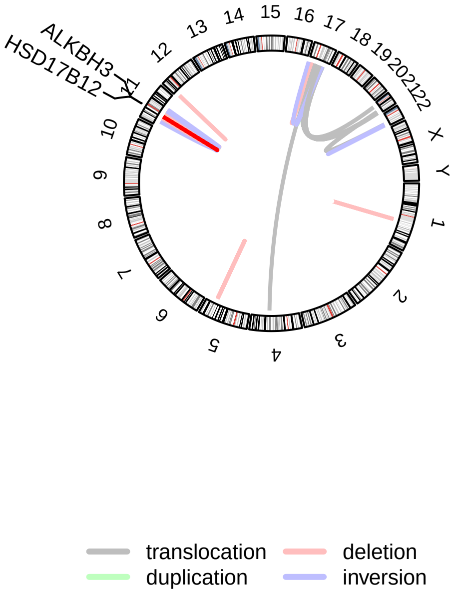


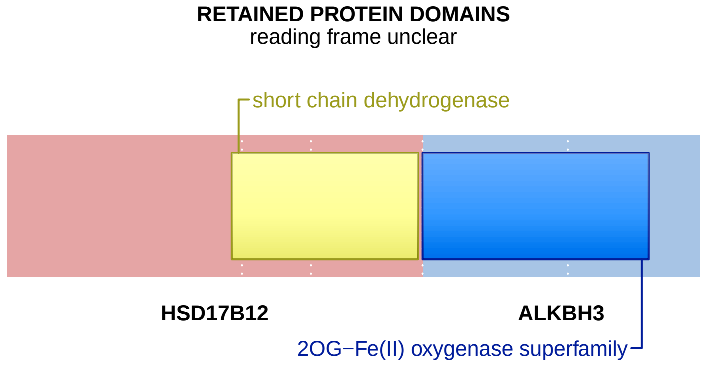


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

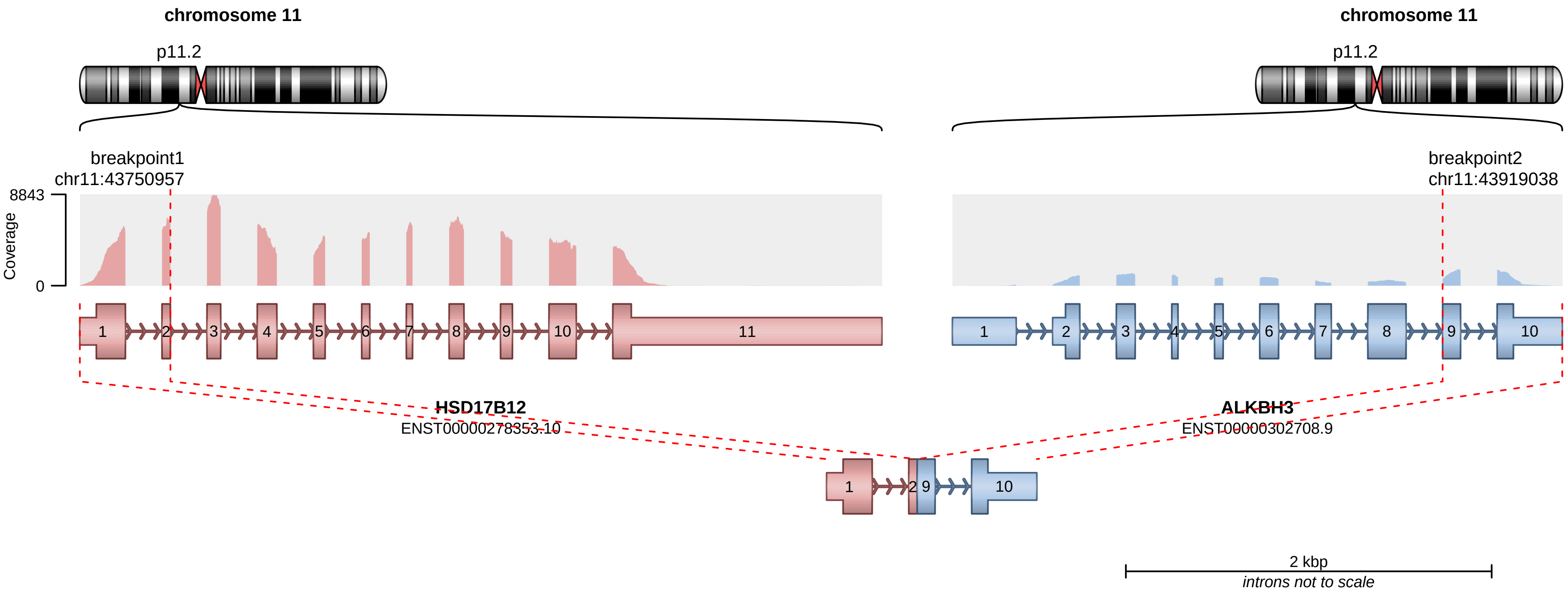


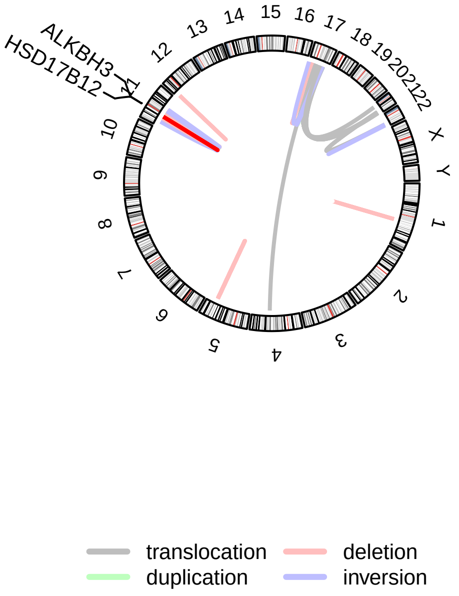


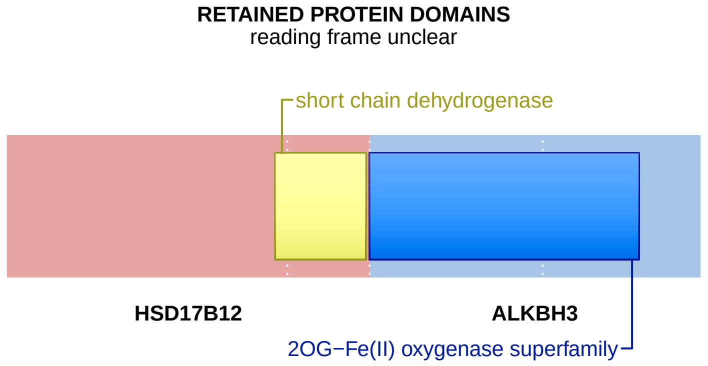


SUPPORTING READ COUNT

Split reads = 200
Discordant mates = 1

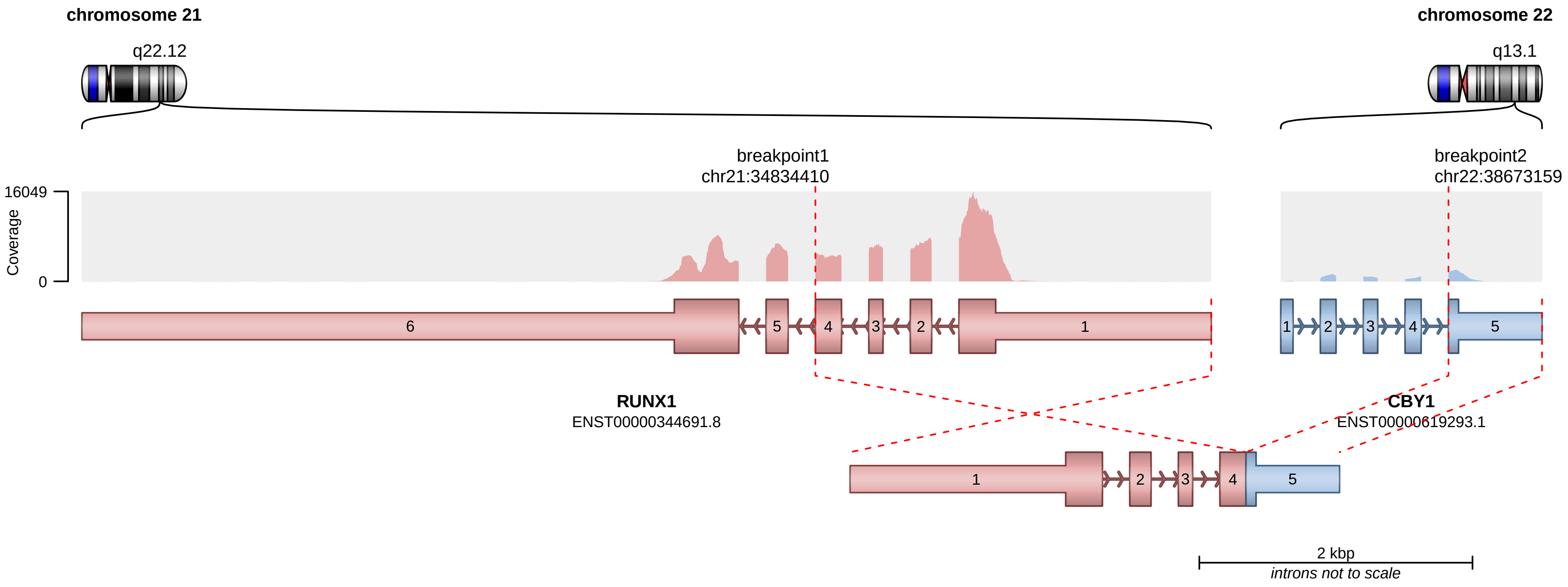


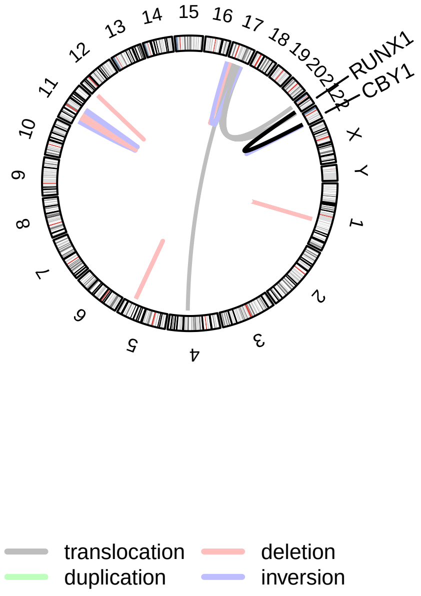




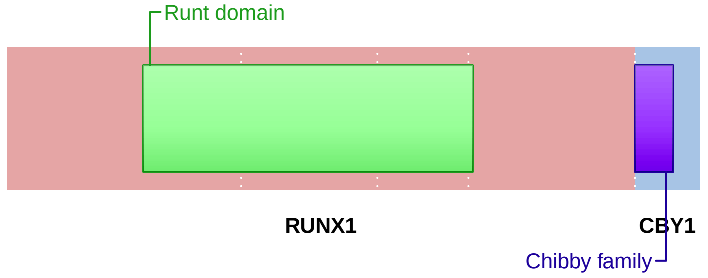
SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 1



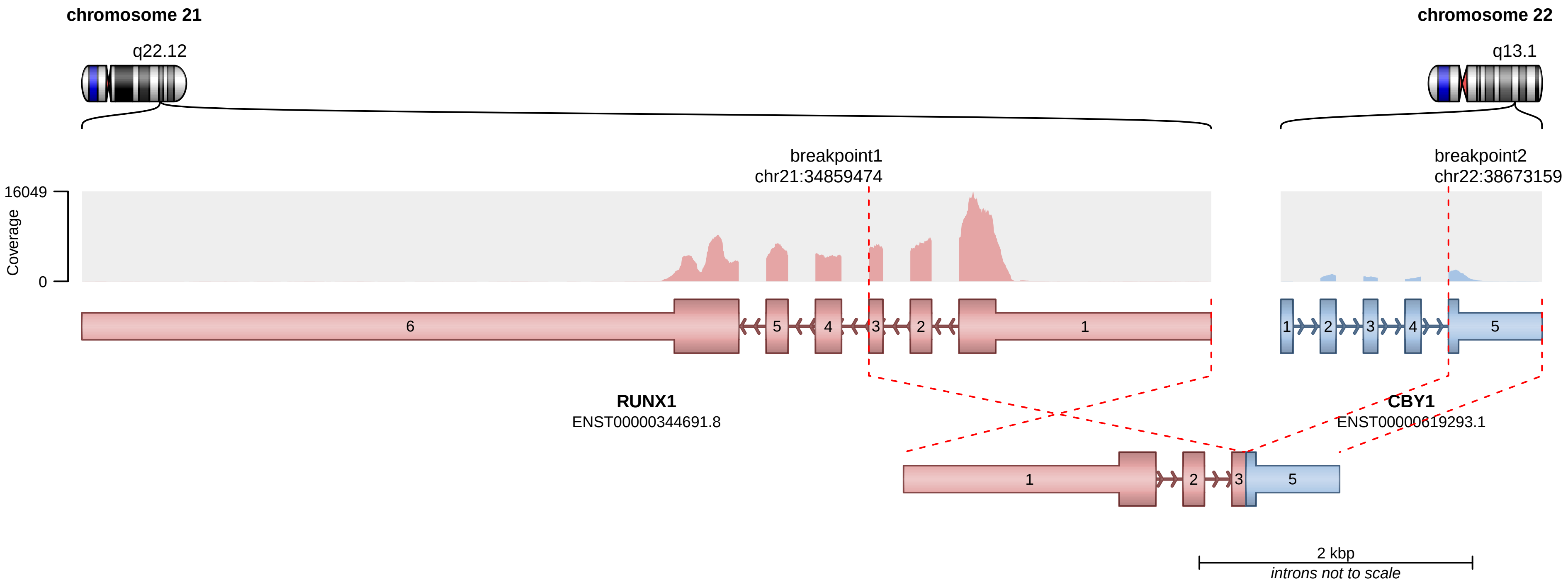


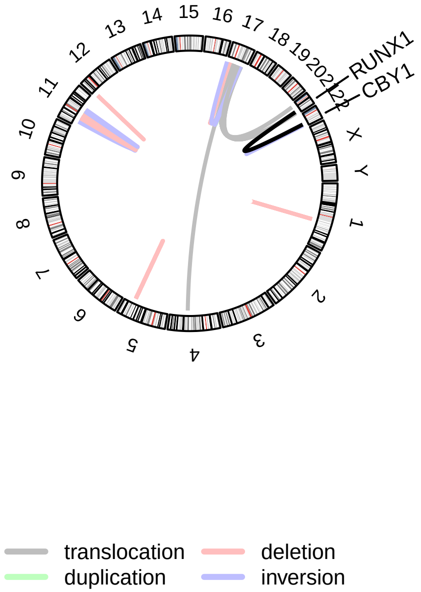
RETAINED PROTEIN DOMAINS
reading frame unclear



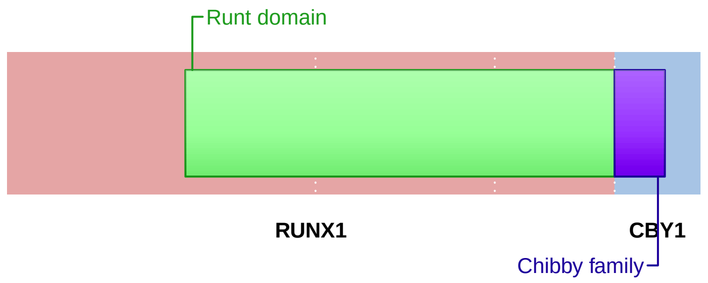
SUPPORTING READ COUNT

Split reads = 192
Discordant mates = 0



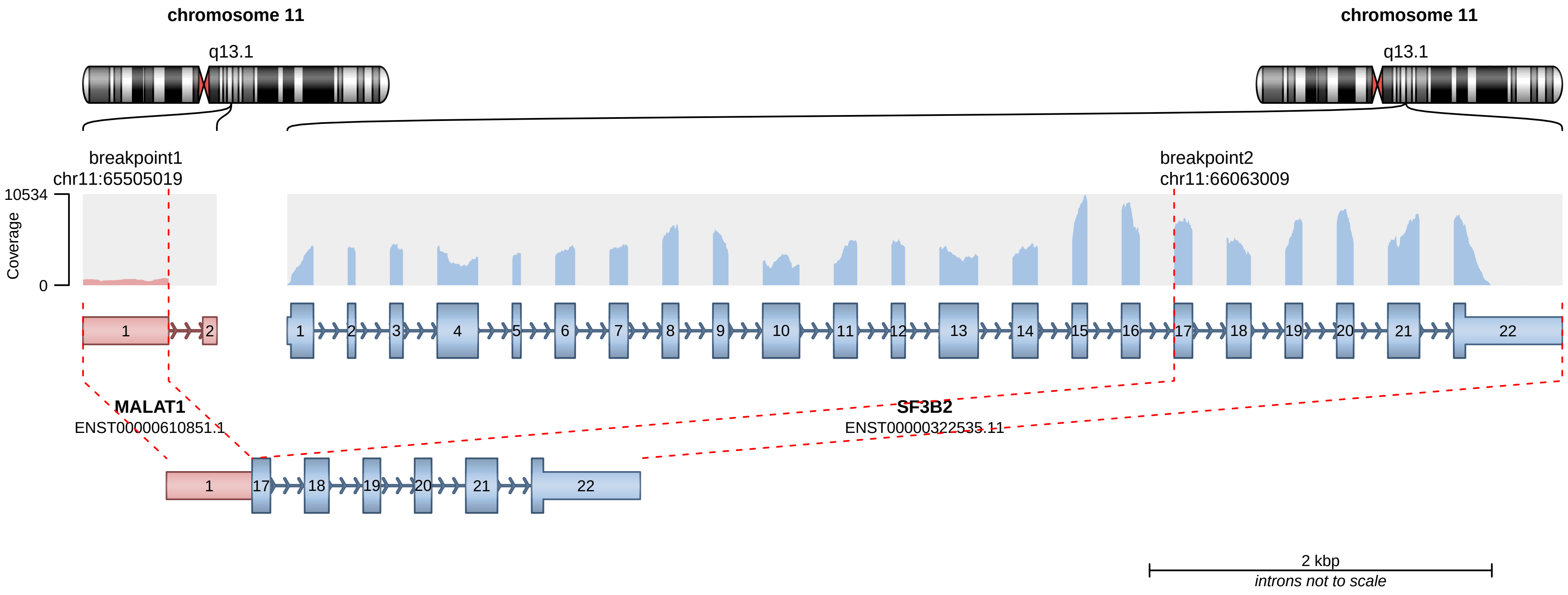


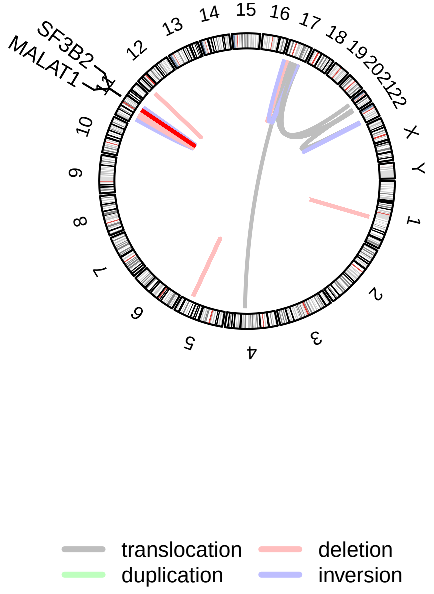
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 28
Discordant mates = 0

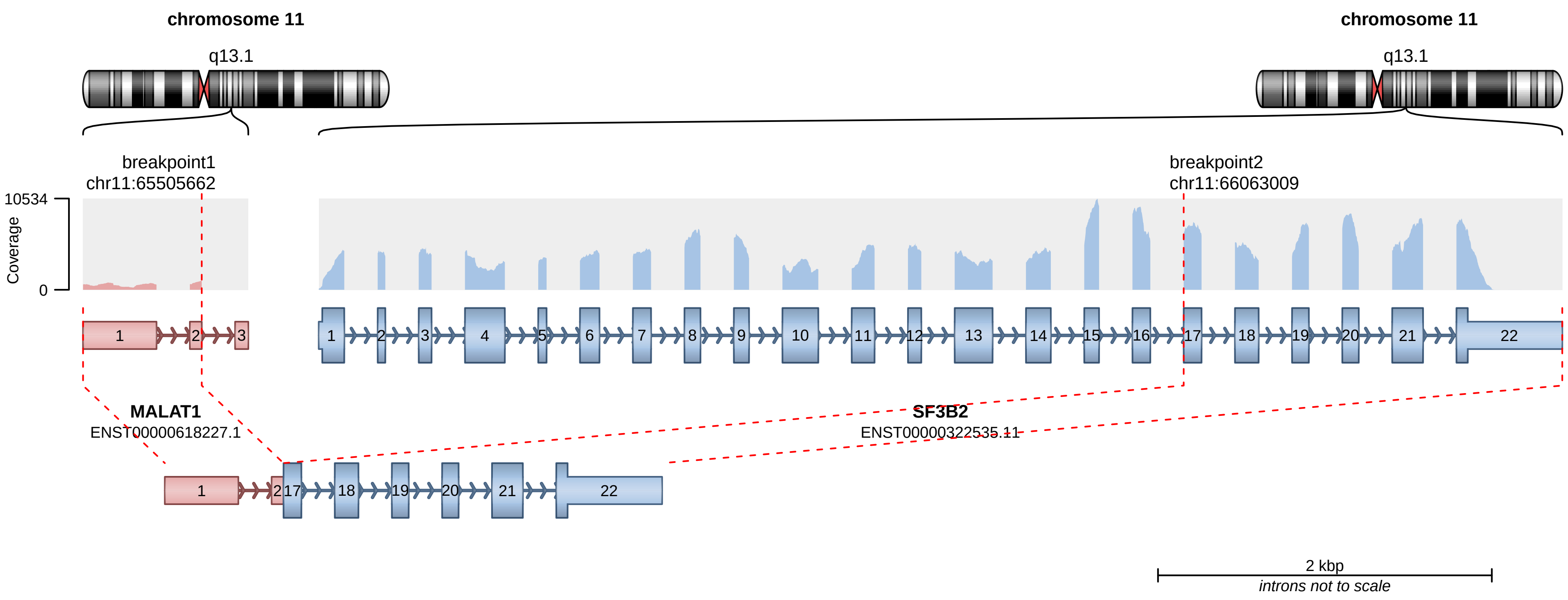


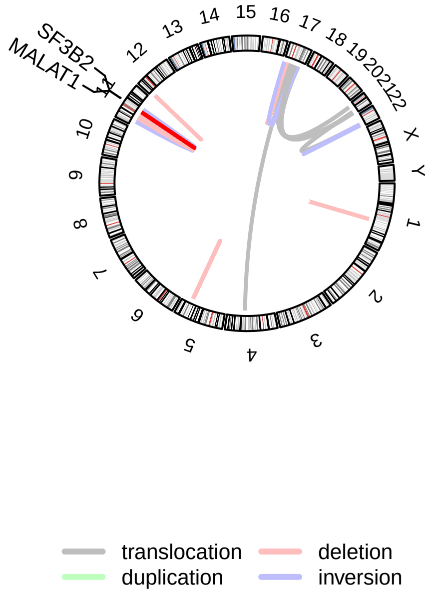


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 164
Discordant mates = 0

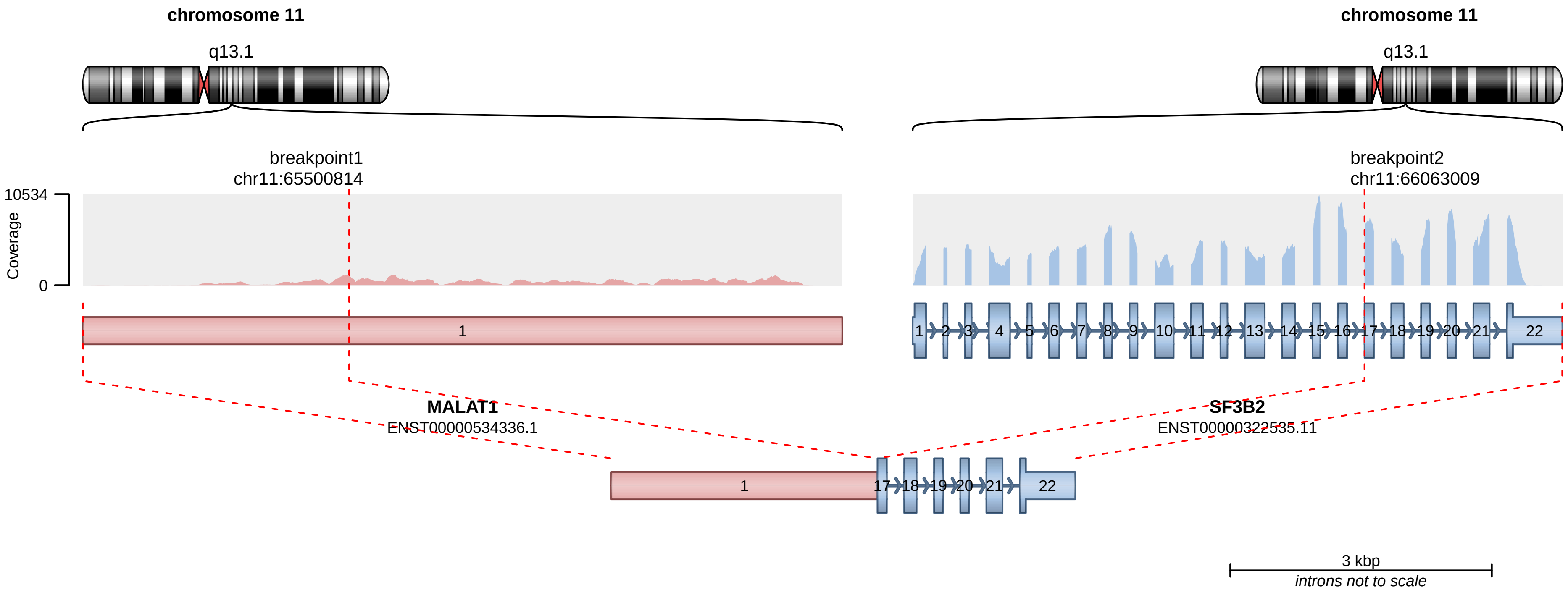


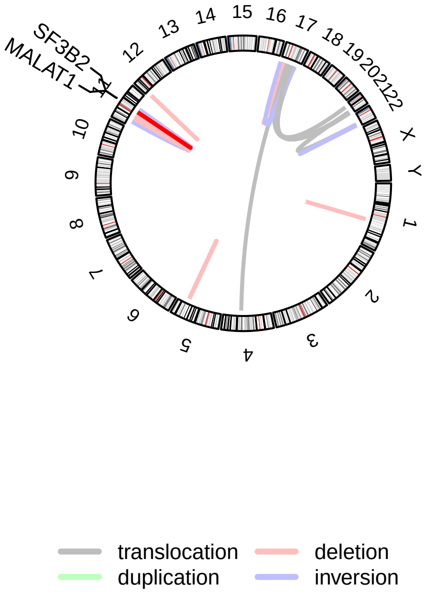


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 77
Discordant mates = 0

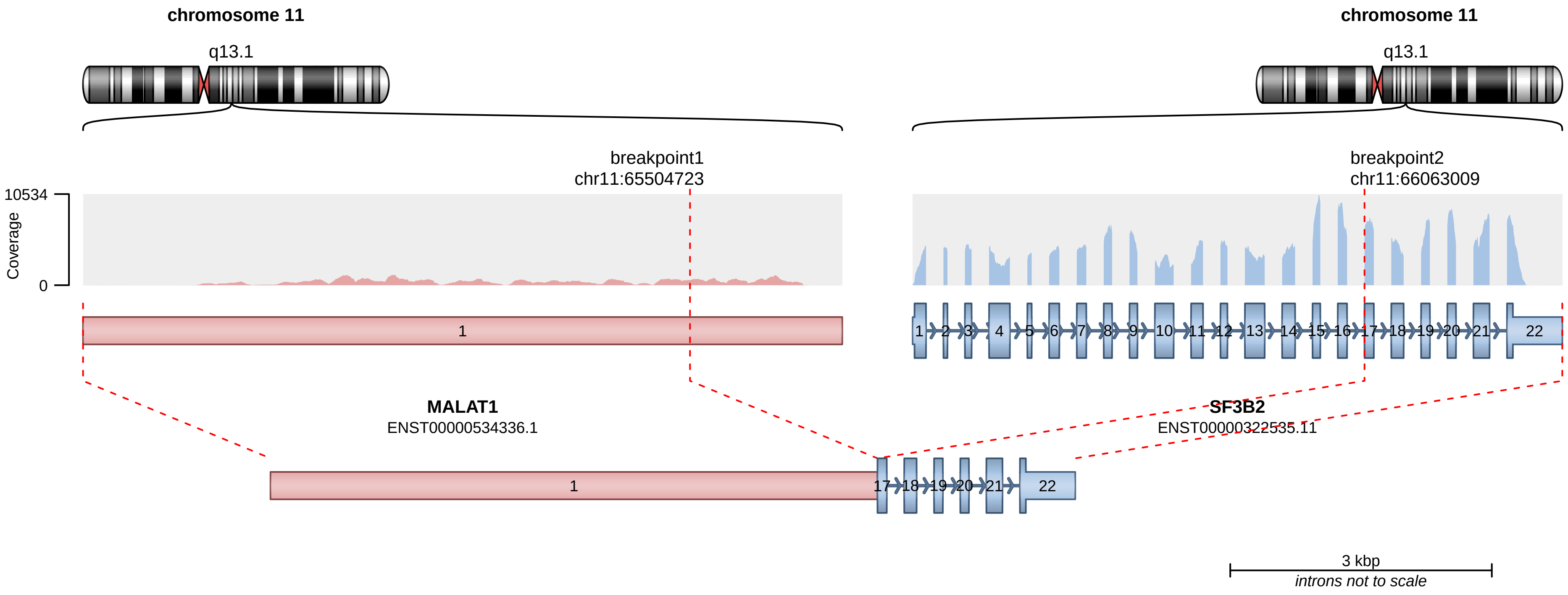


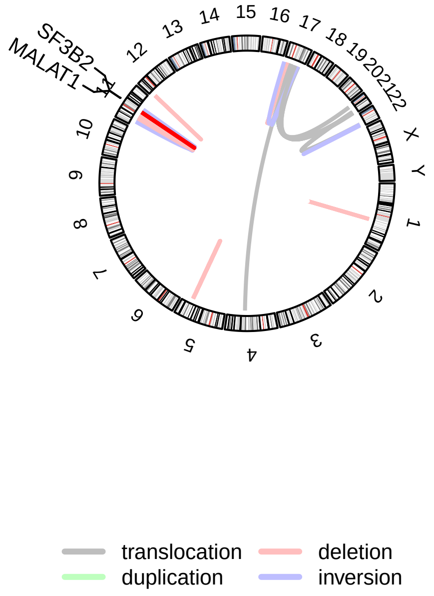


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 0

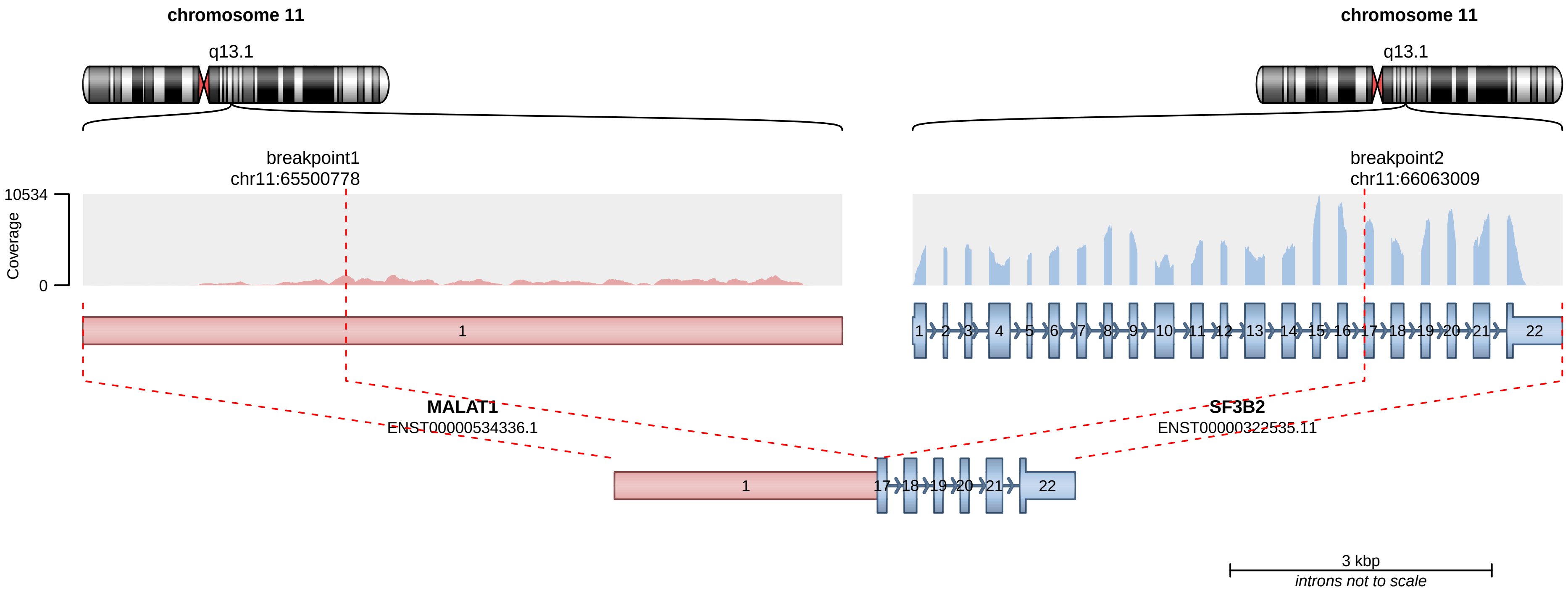


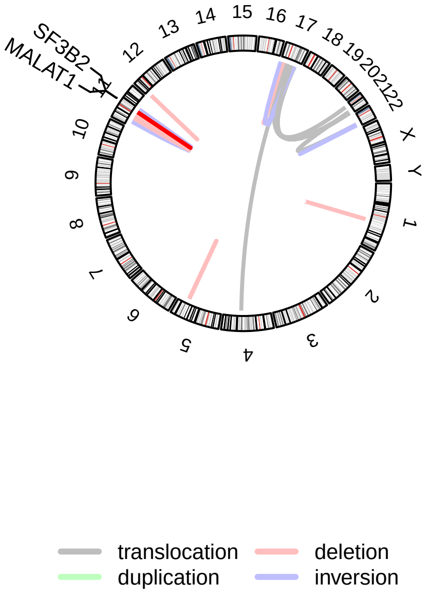


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0

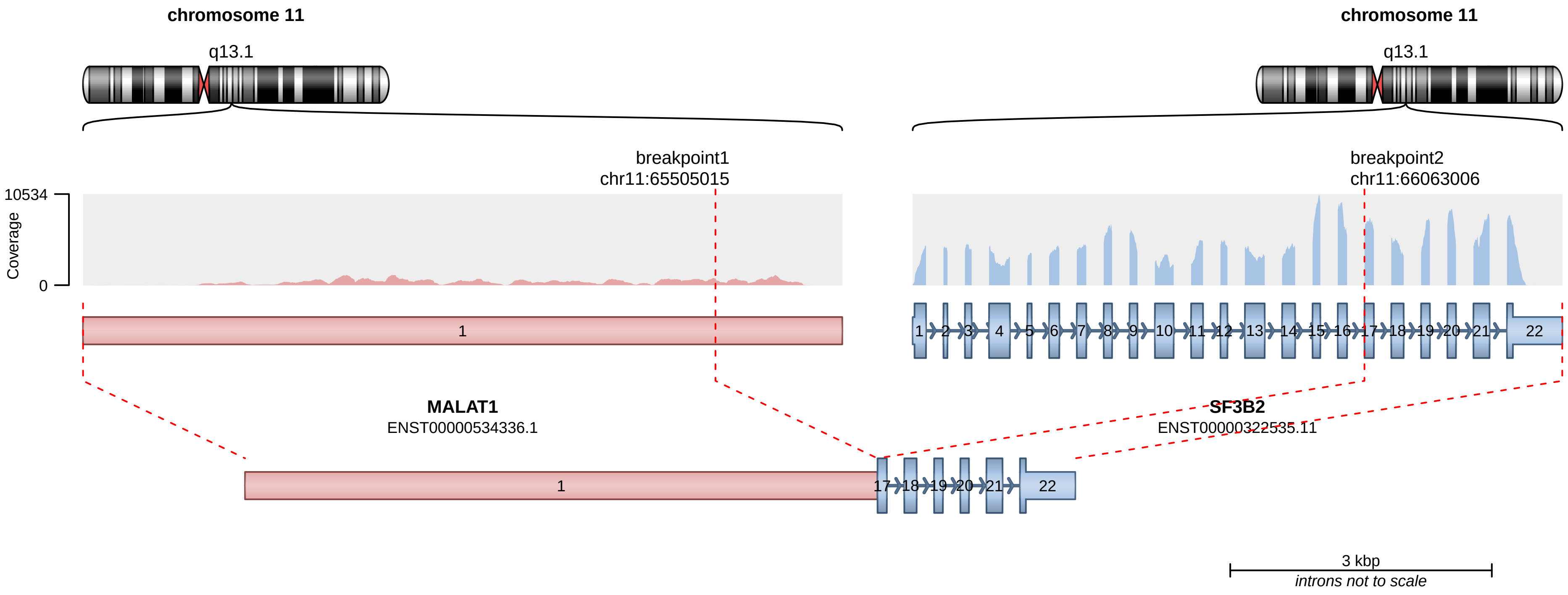


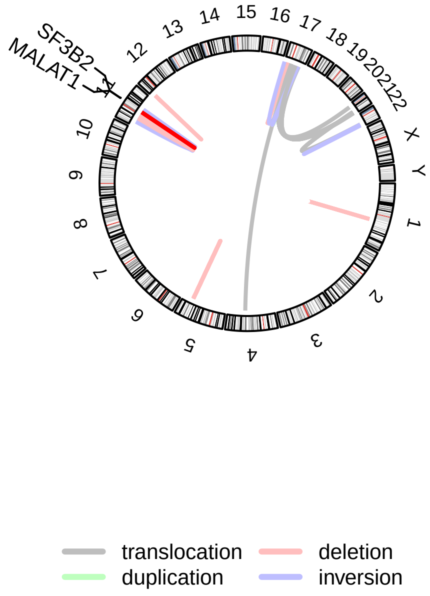


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

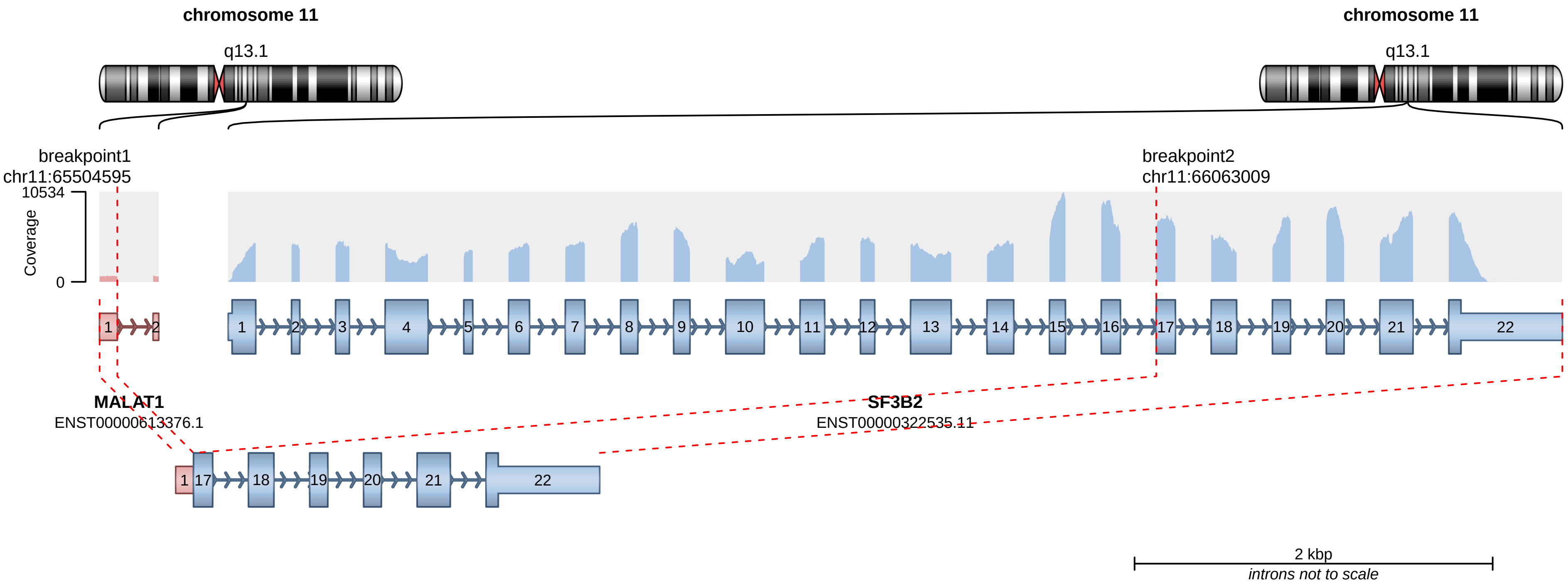


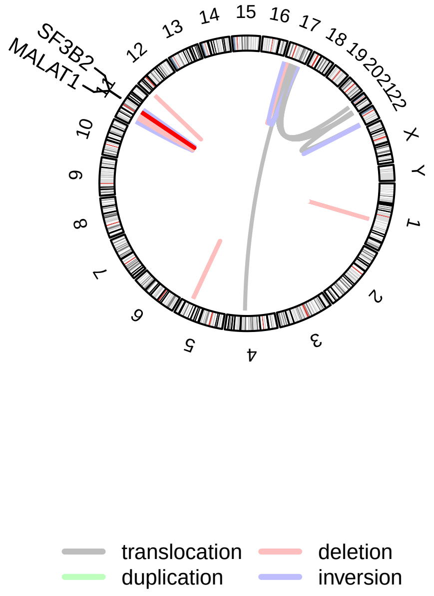


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

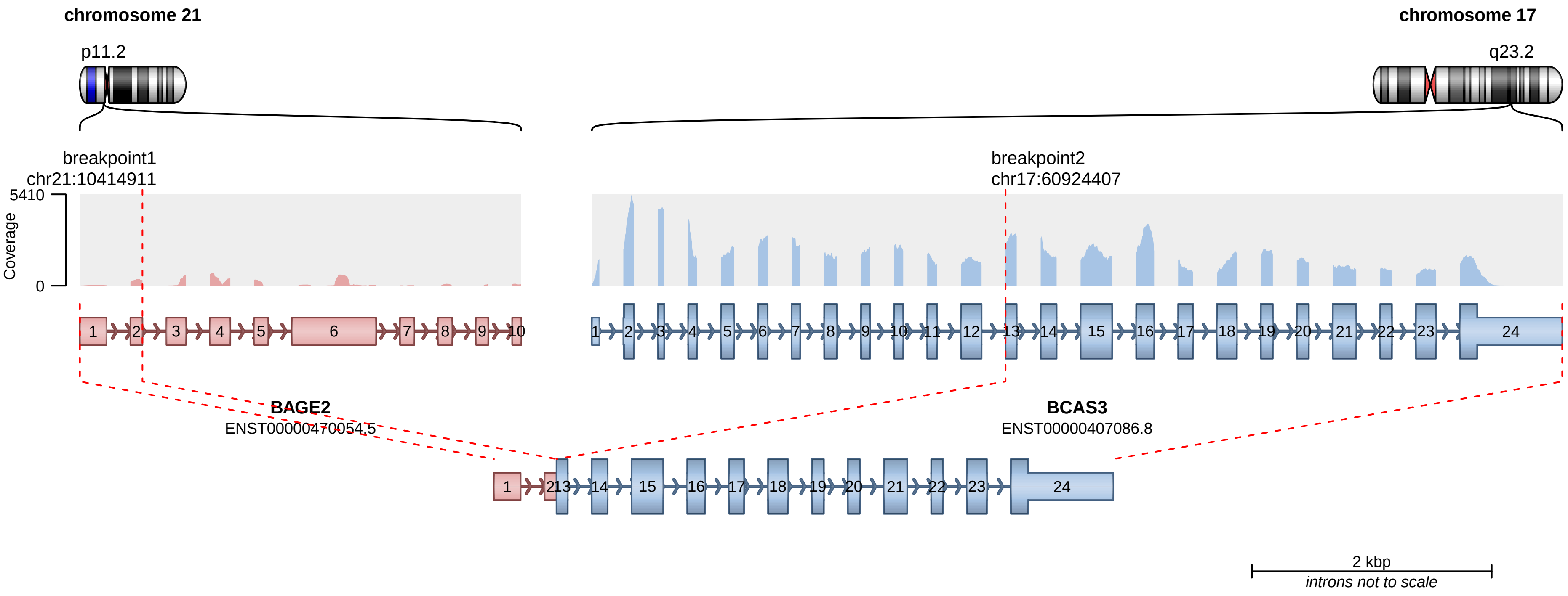


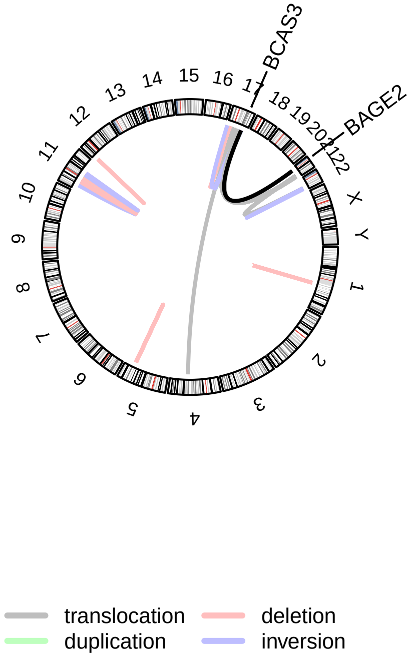


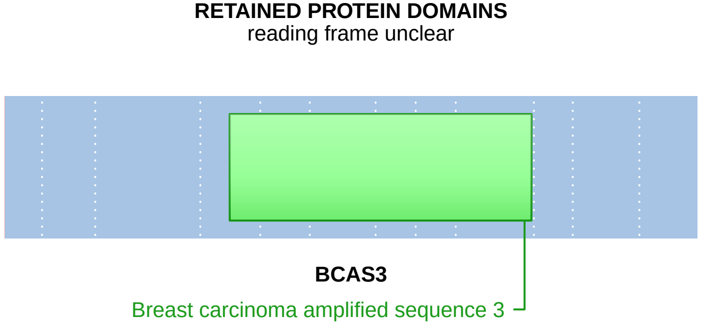
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

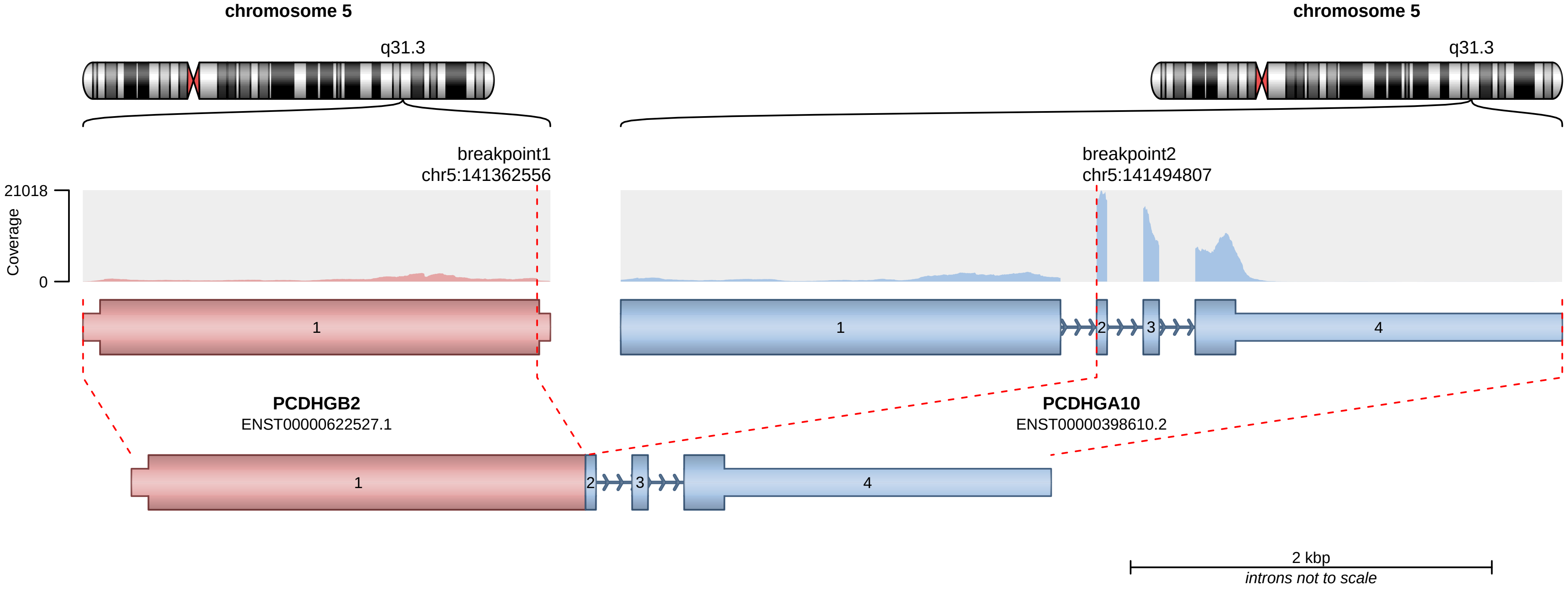


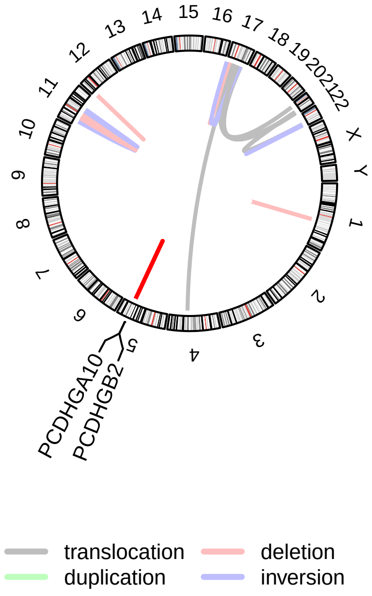




SUPPORTING READ COUNT

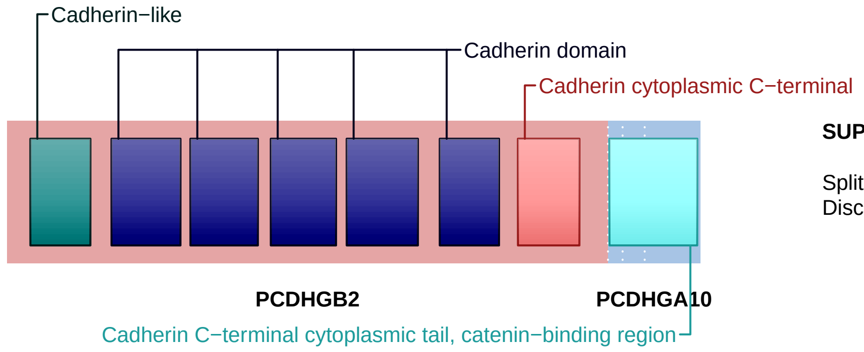
Split reads = 163
Discordant mates = 0





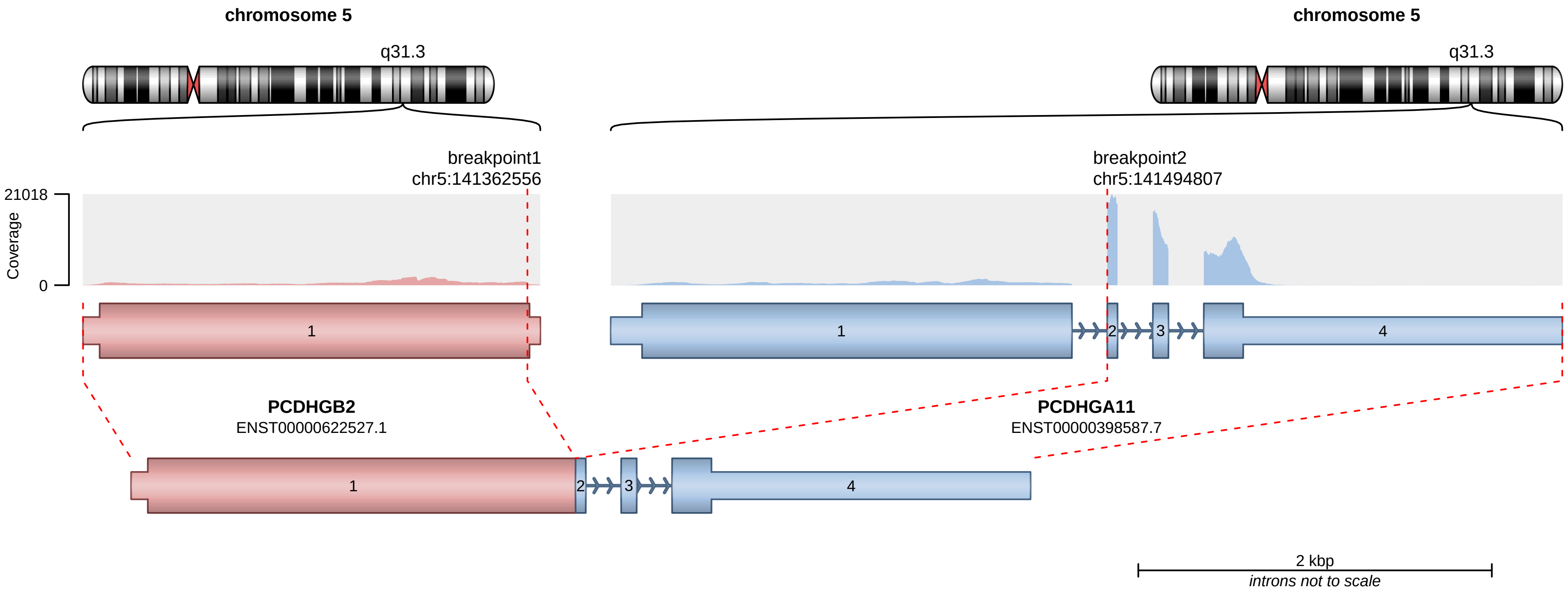
RETAINED PROTEIN DOMAINS

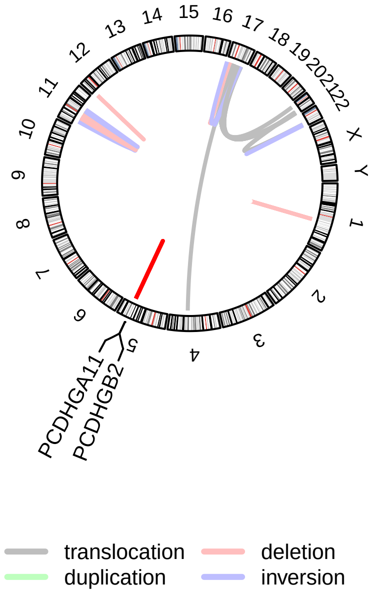
reading frame unclear

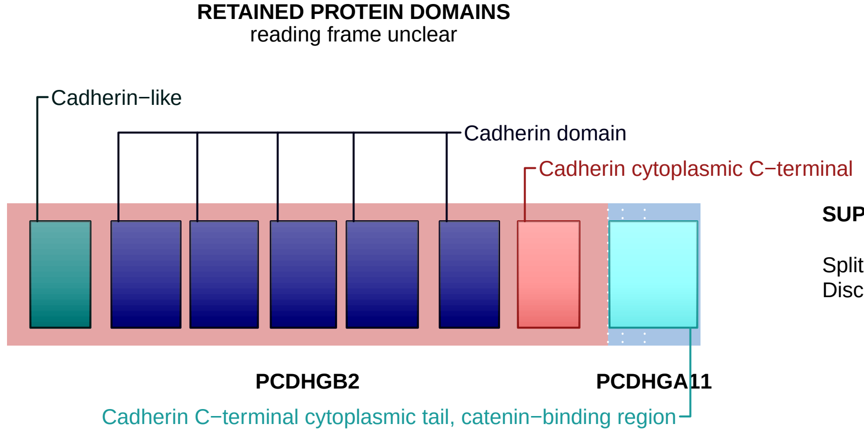


SUPPORTING READ COUNT

Split reads = 140
Discordant mates = 1

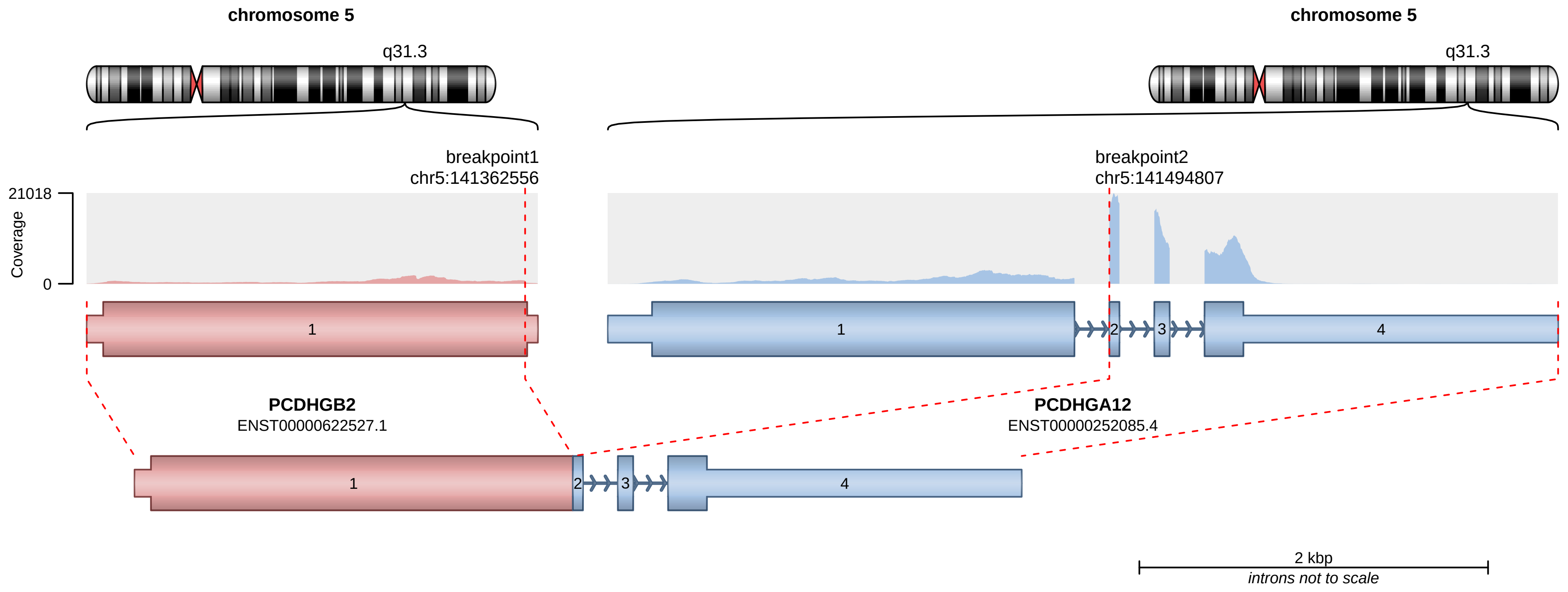


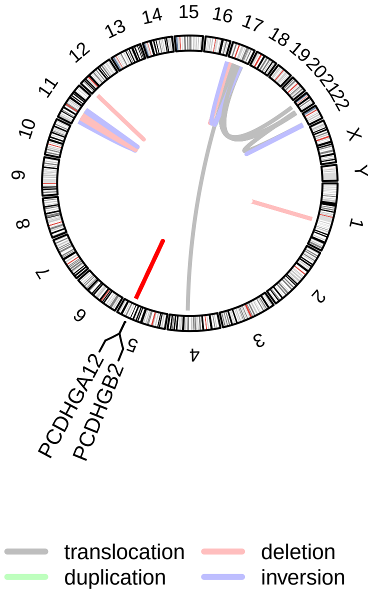


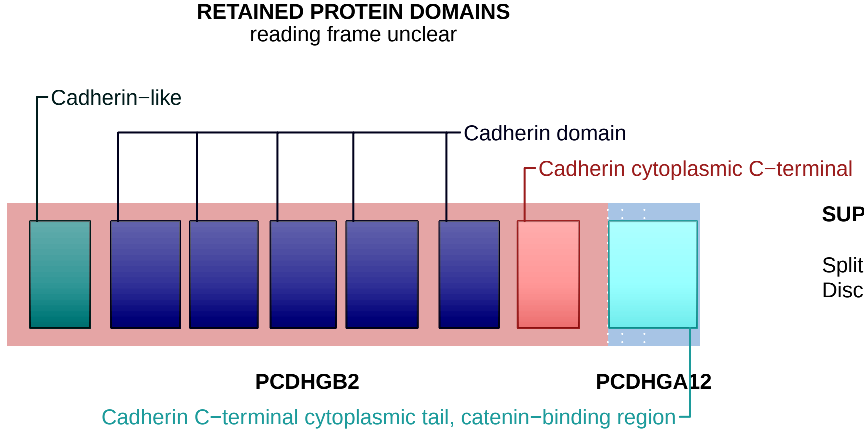


SUPPORTING READ COUNT

Split reads = 140
Discordant mates = 1

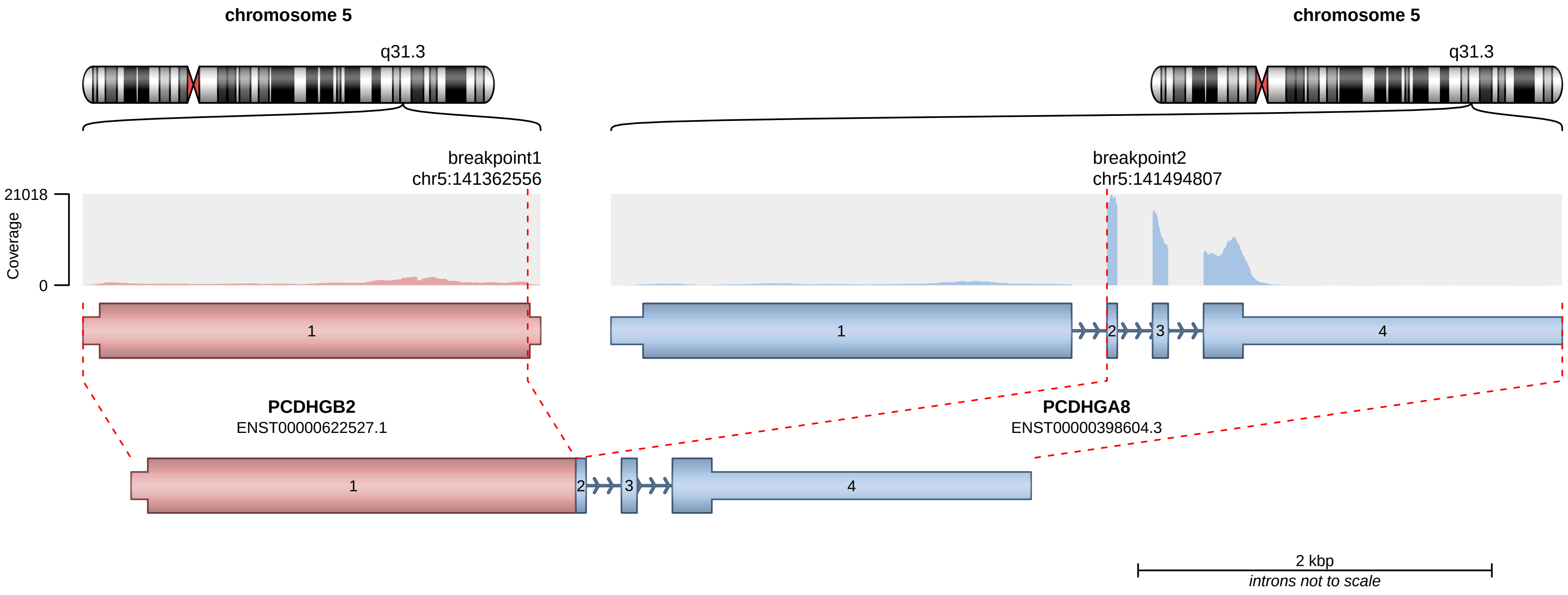


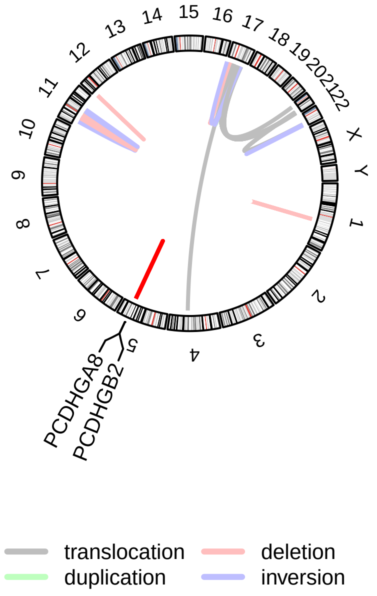


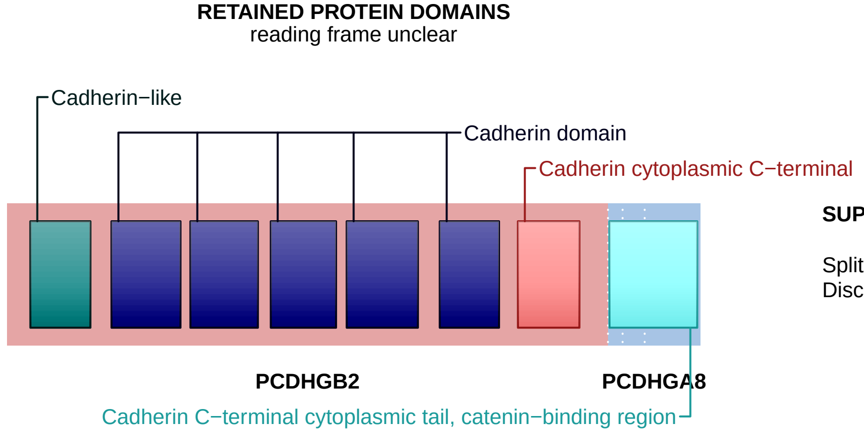


SUPPORTING READ COUNT

Split reads = 140
Discordant mates = 1

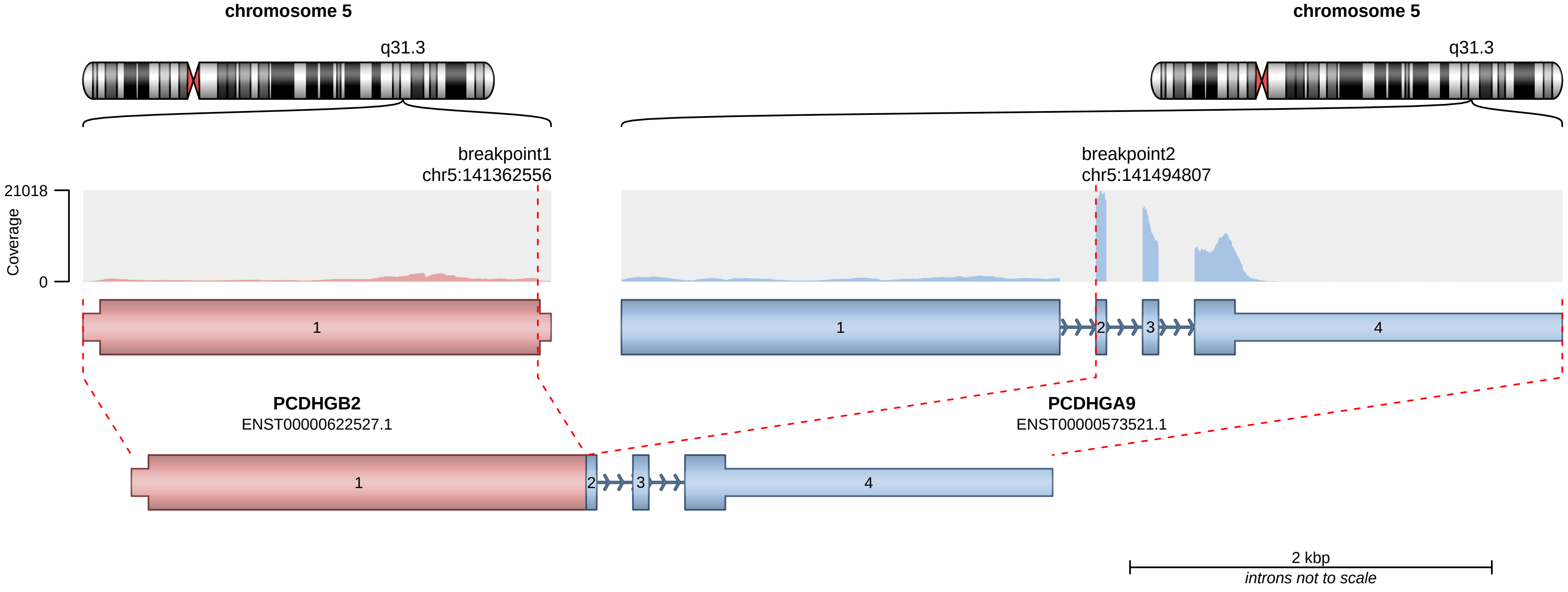


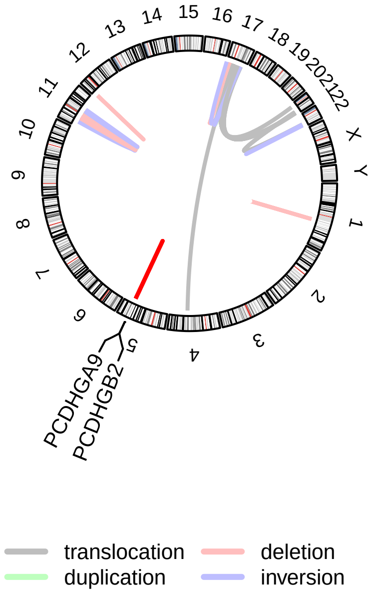


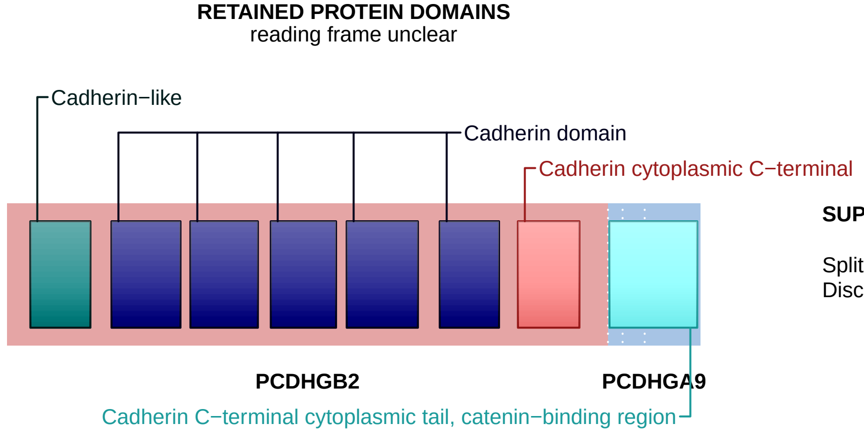


SUPPORTING READ COUNT

Split reads = 140
Discordant mates = 1

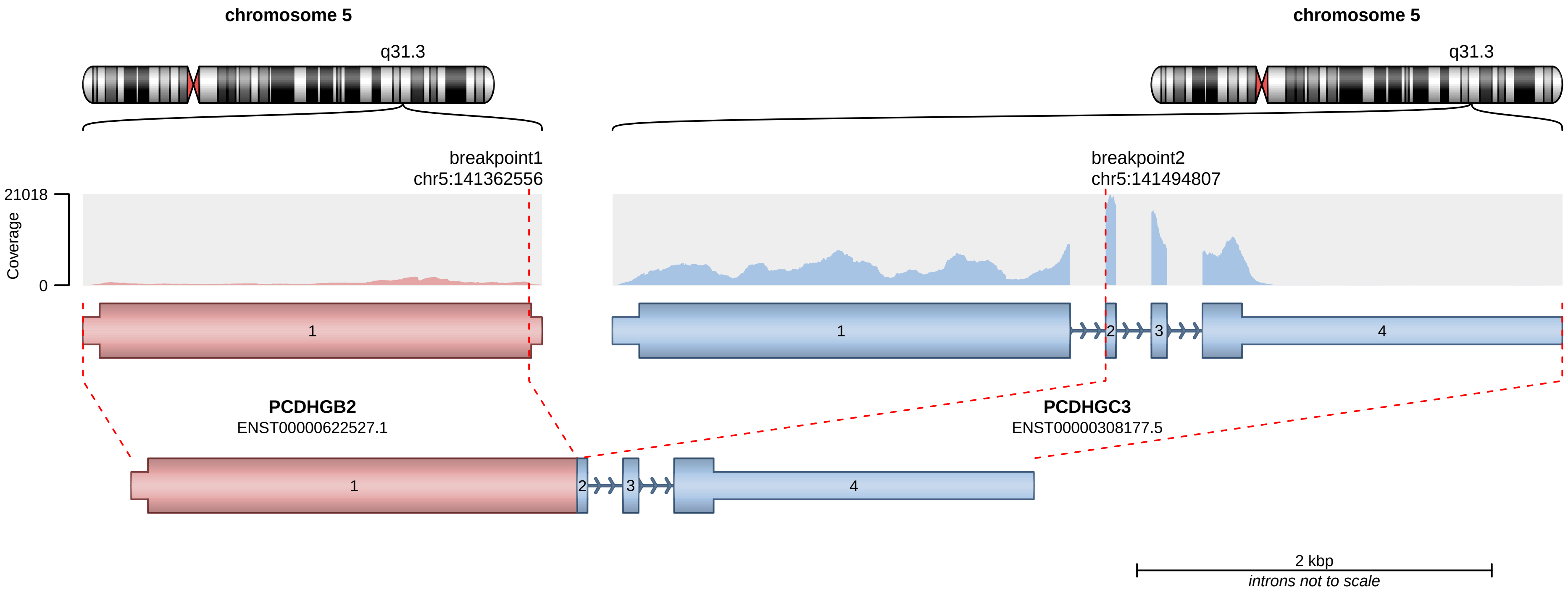


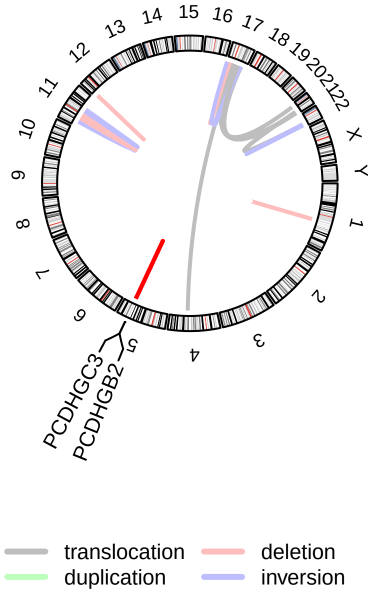




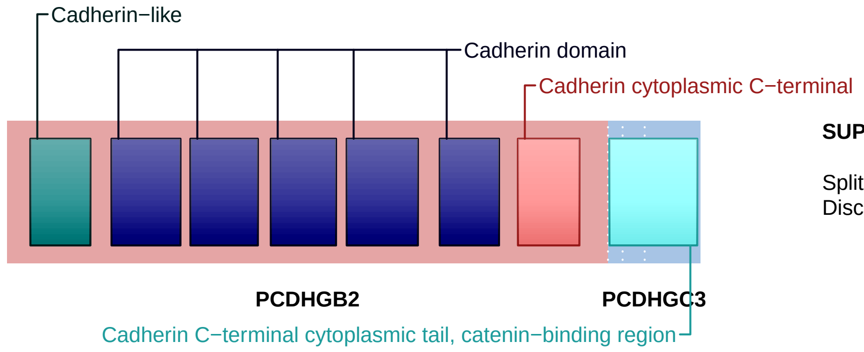
SUPPORTING READ COUNT

Split reads = 140
Discordant mates = 1



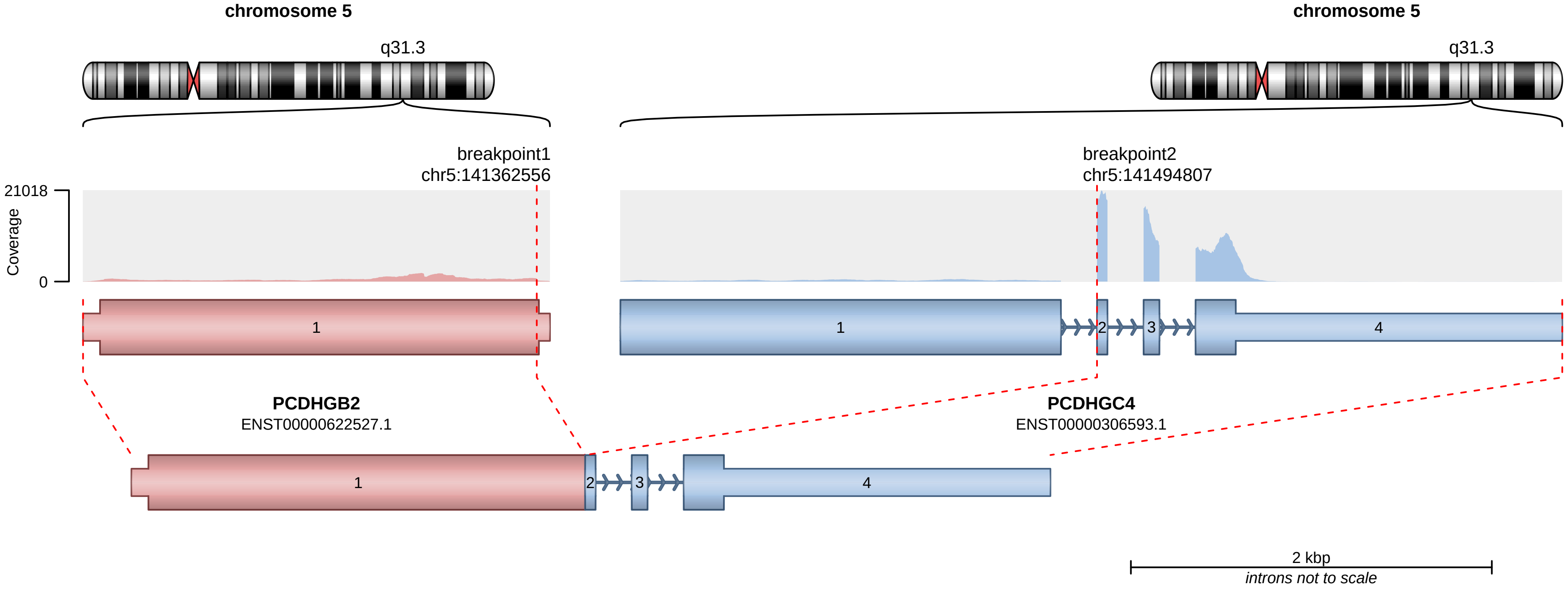


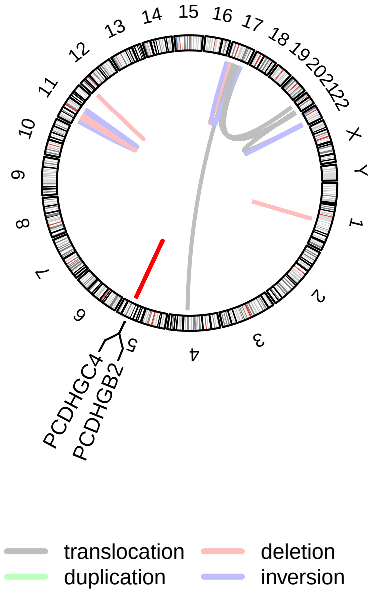
RETAINED PROTEIN DOMAINS
reading frame unclear

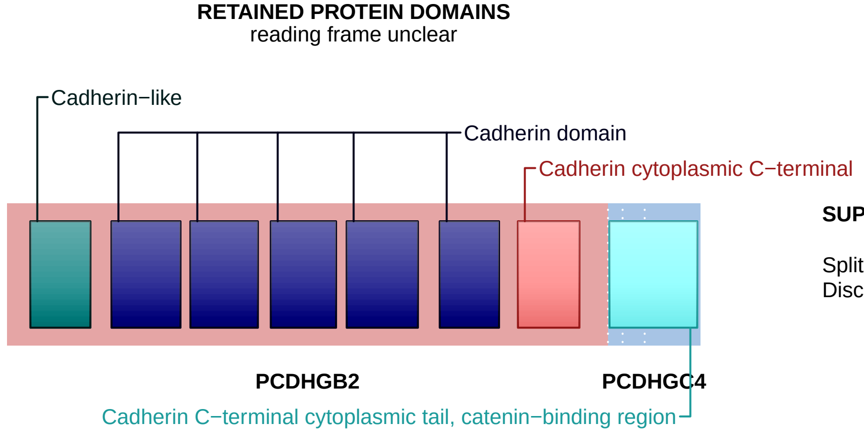


SUPPORTING READ COUNT

Split reads = 140
Discordant mates = 1

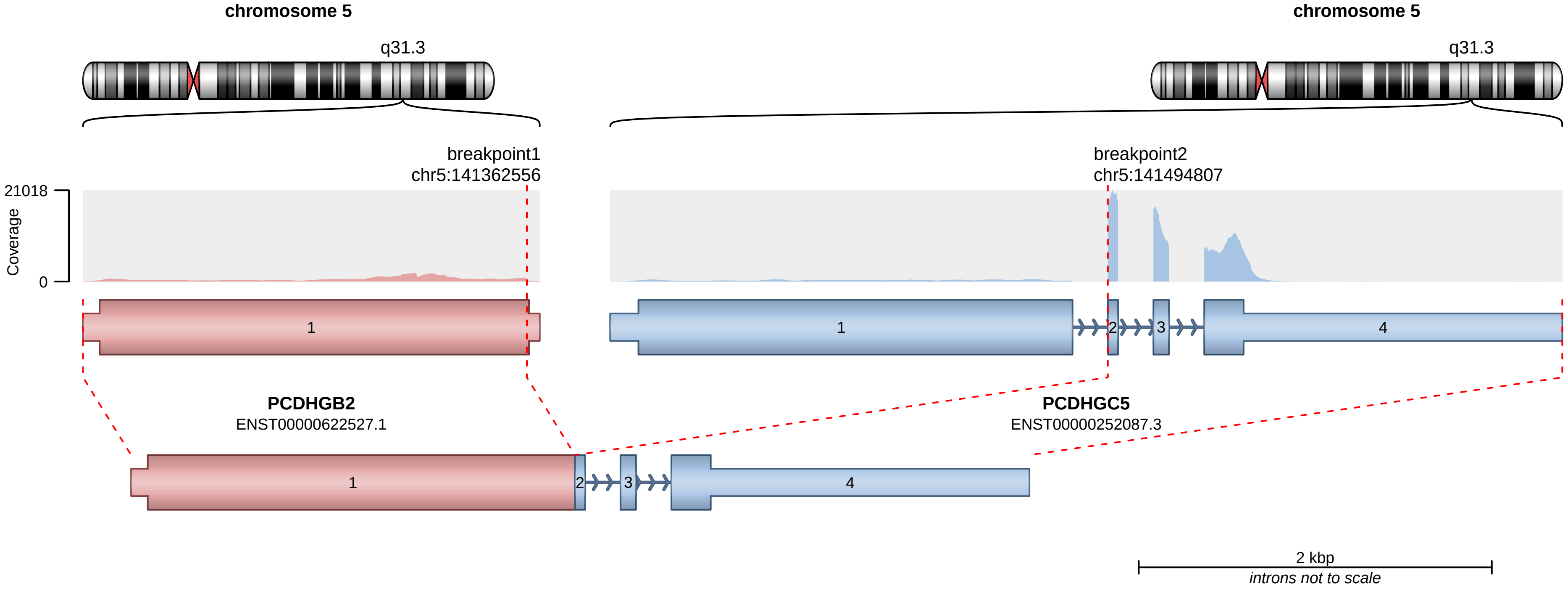


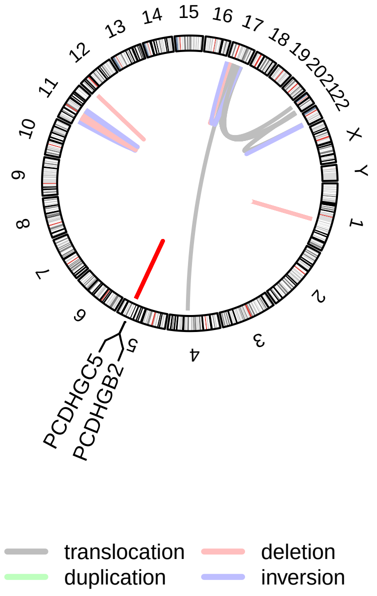


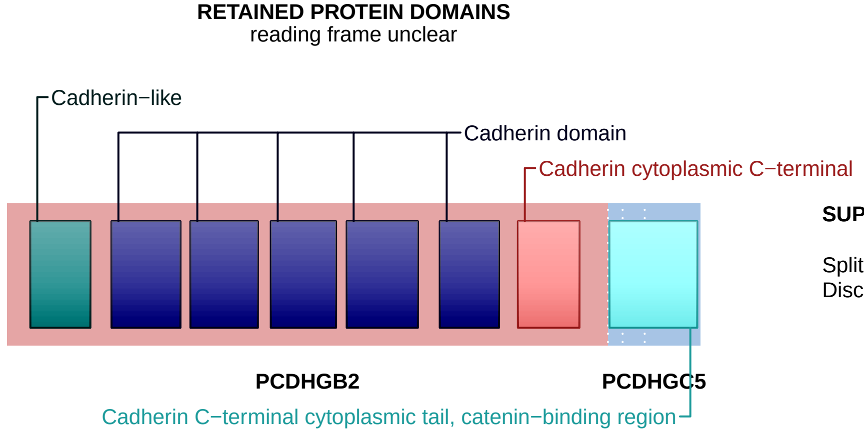


SUPPORTING READ COUNT

Split reads = 140
Discordant mates = 1

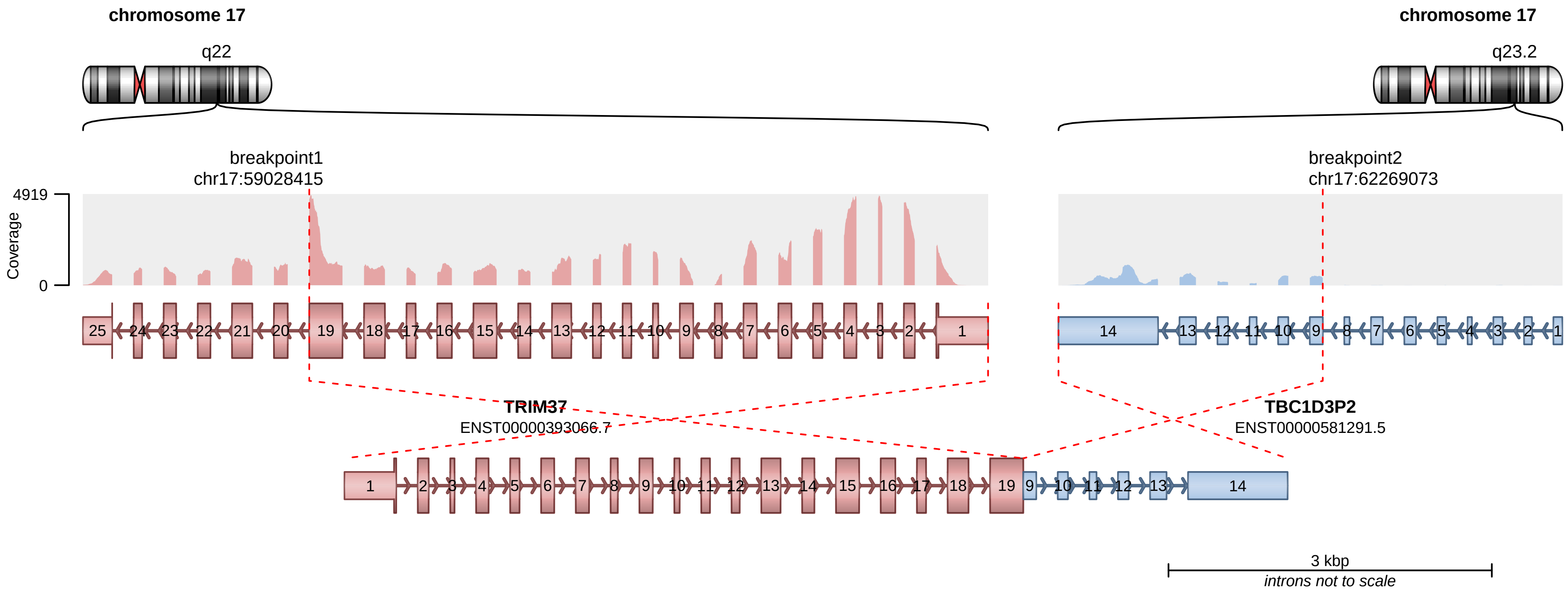


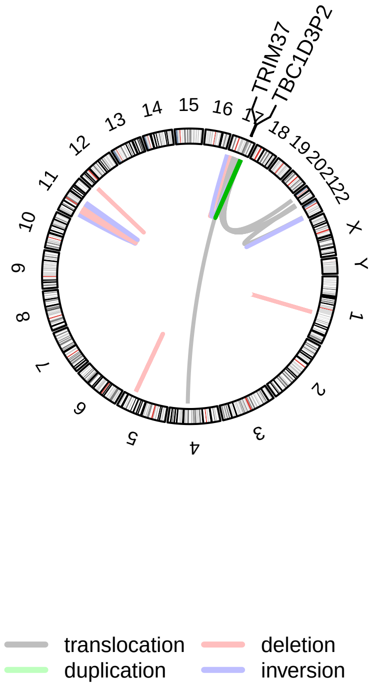




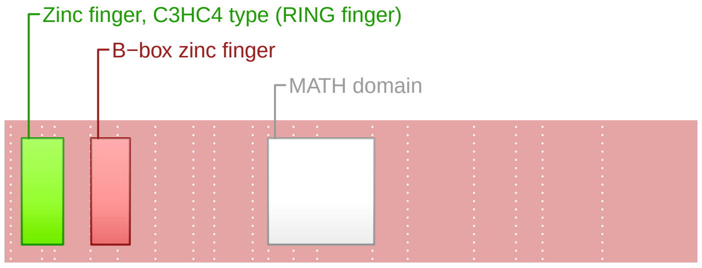
SUPPORTING READ COUNT

Split reads = 140
Discordant mates = 1





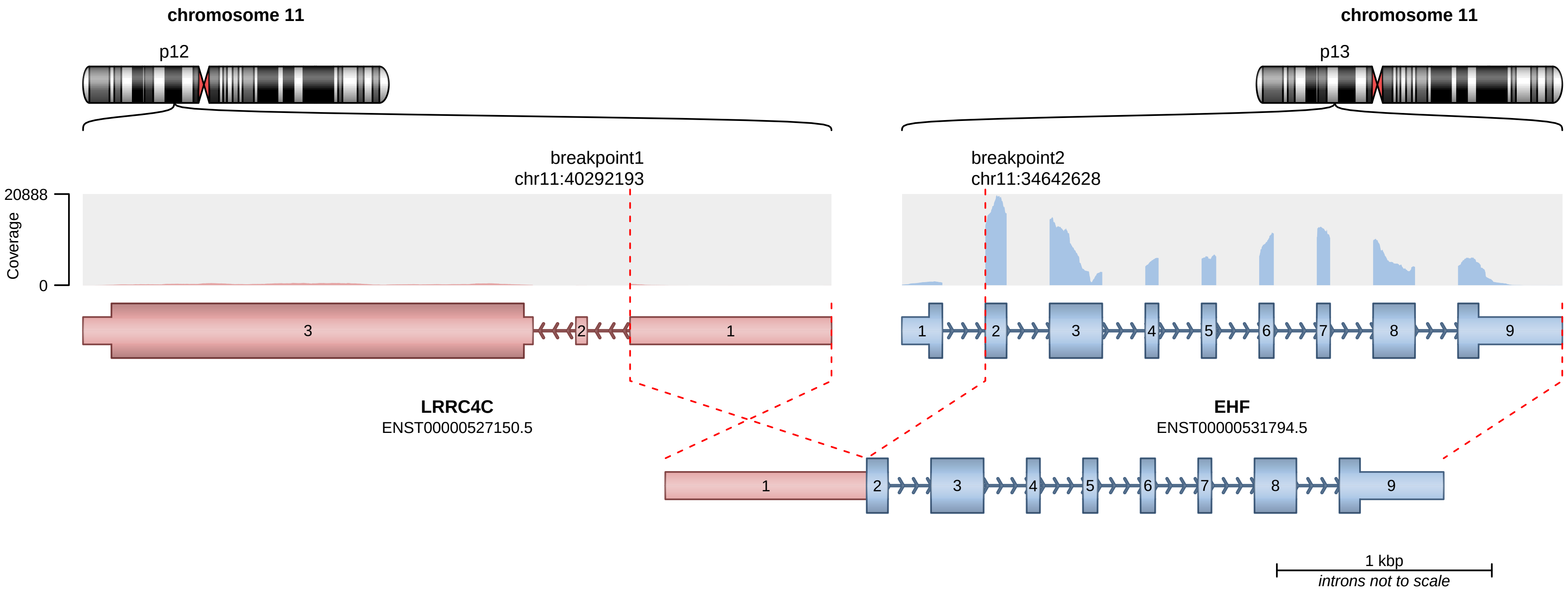
RETAINED PROTEIN DOMAINS
reading frame unclear

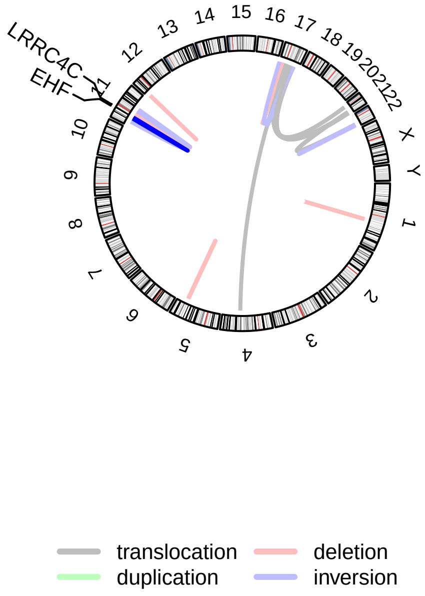


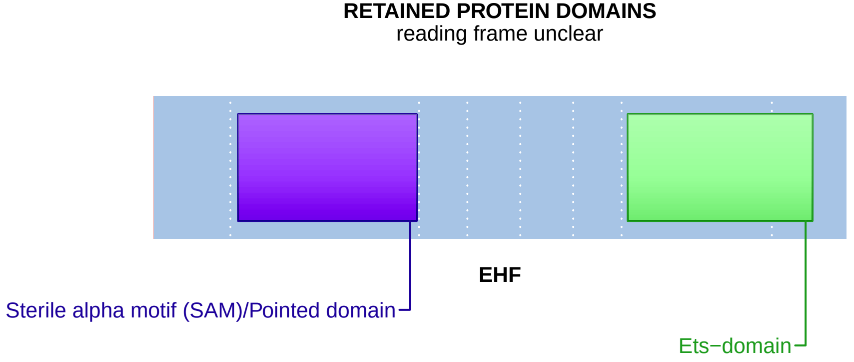
TRIM37

SUPPORTING READ COUNT

Split reads = 135
Discordant mates = 4

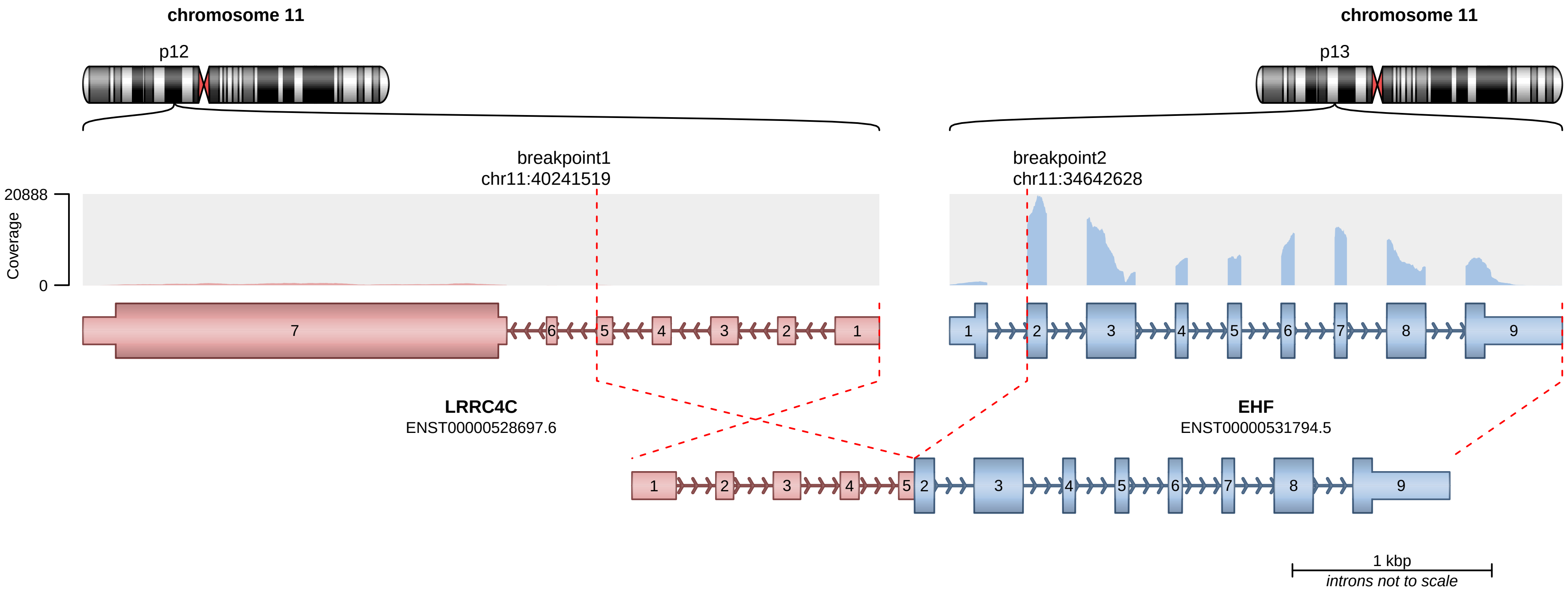


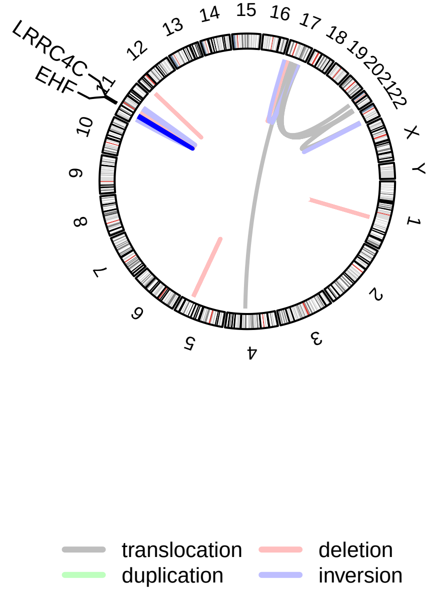


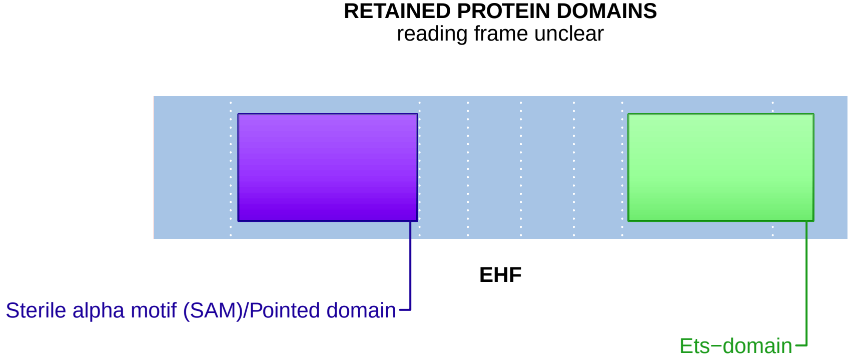


SUPPORTING READ COUNT

Split reads = 125
Discordant mates = 0

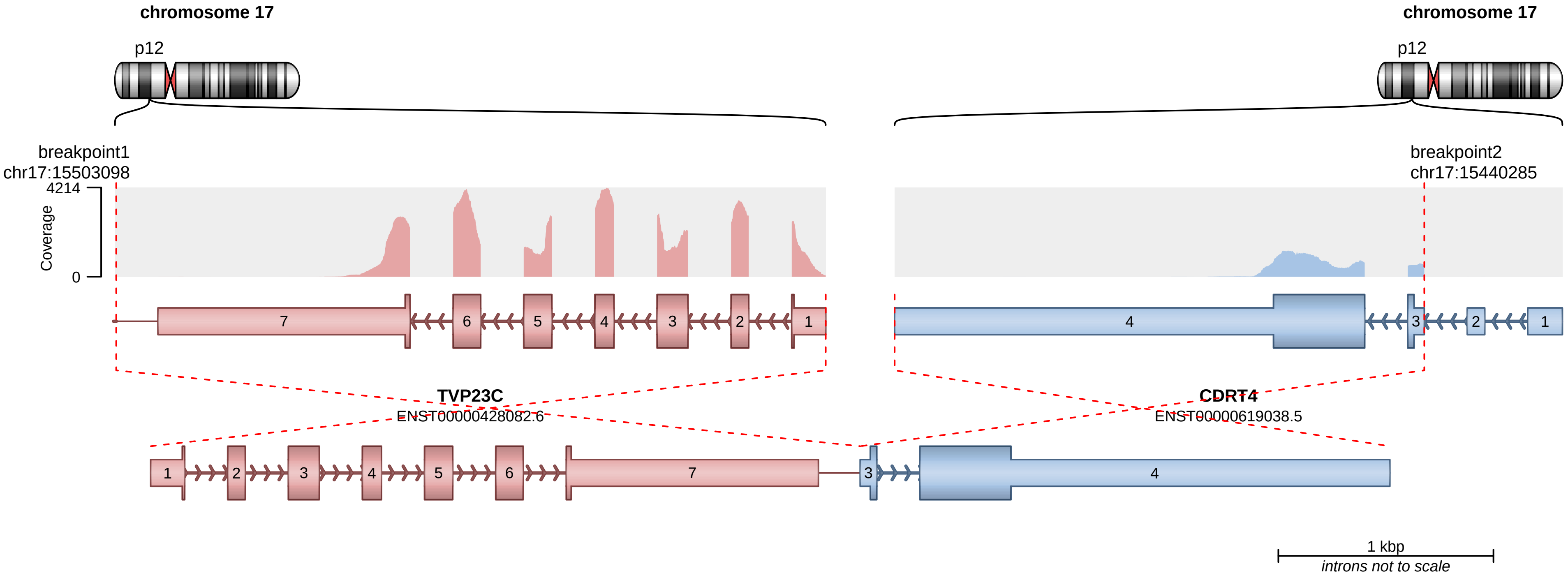


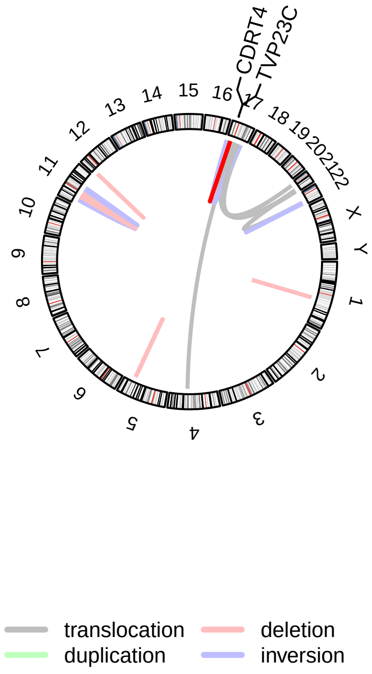


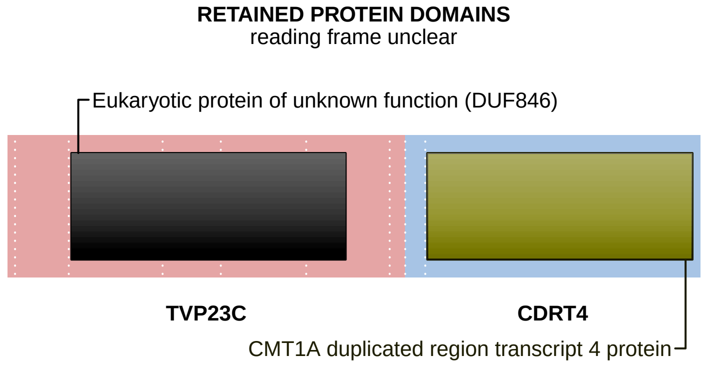


SUPPORTING READ COUNT

Split reads = 27
Discordant mates = 0

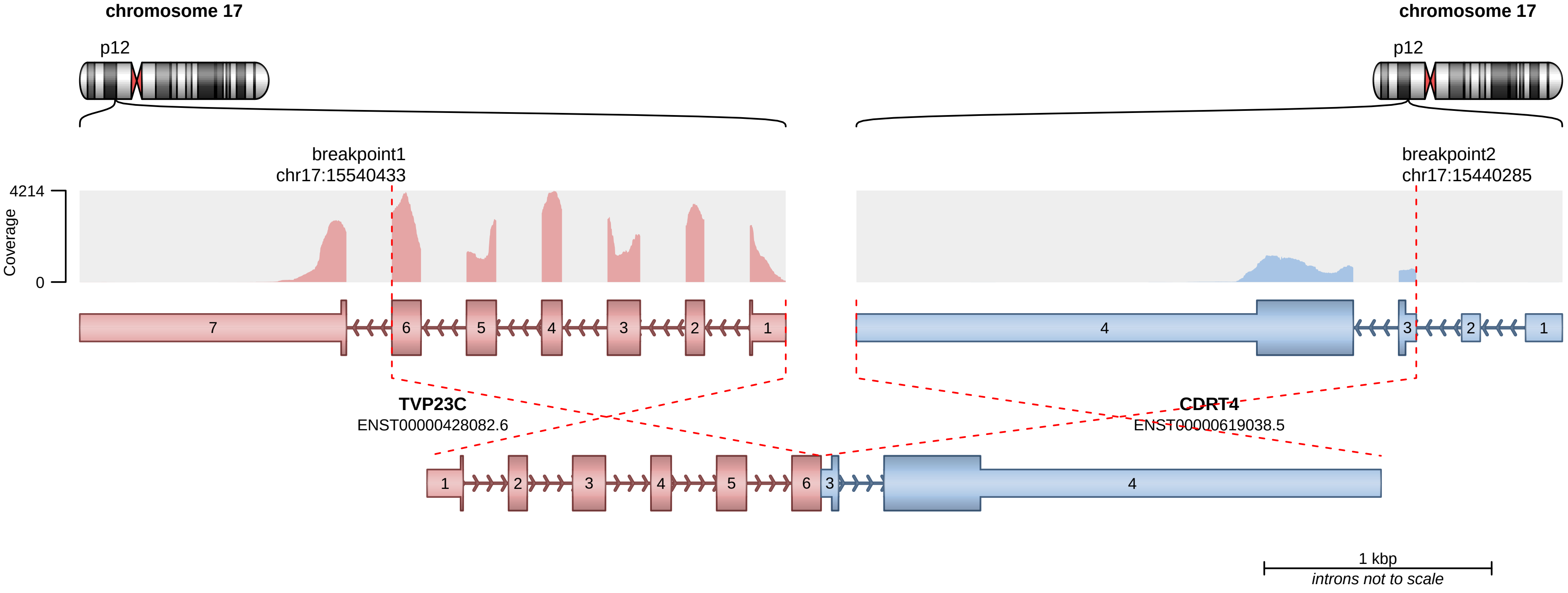


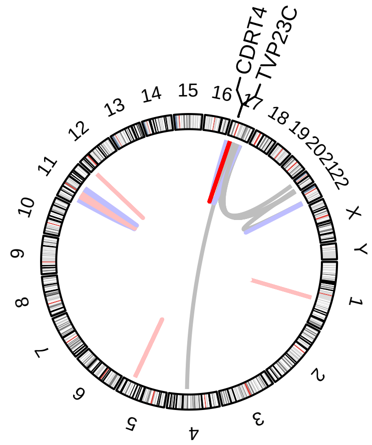




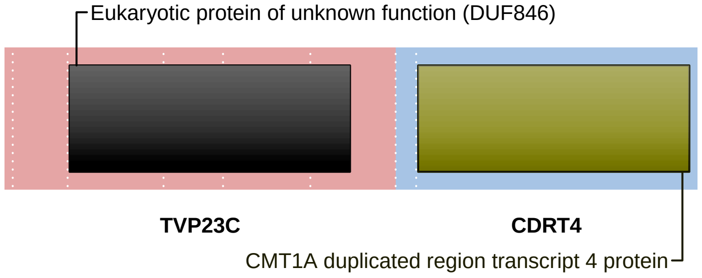
SUPPORTING READ COUNT

Split reads = 114
Discordant mates = 4





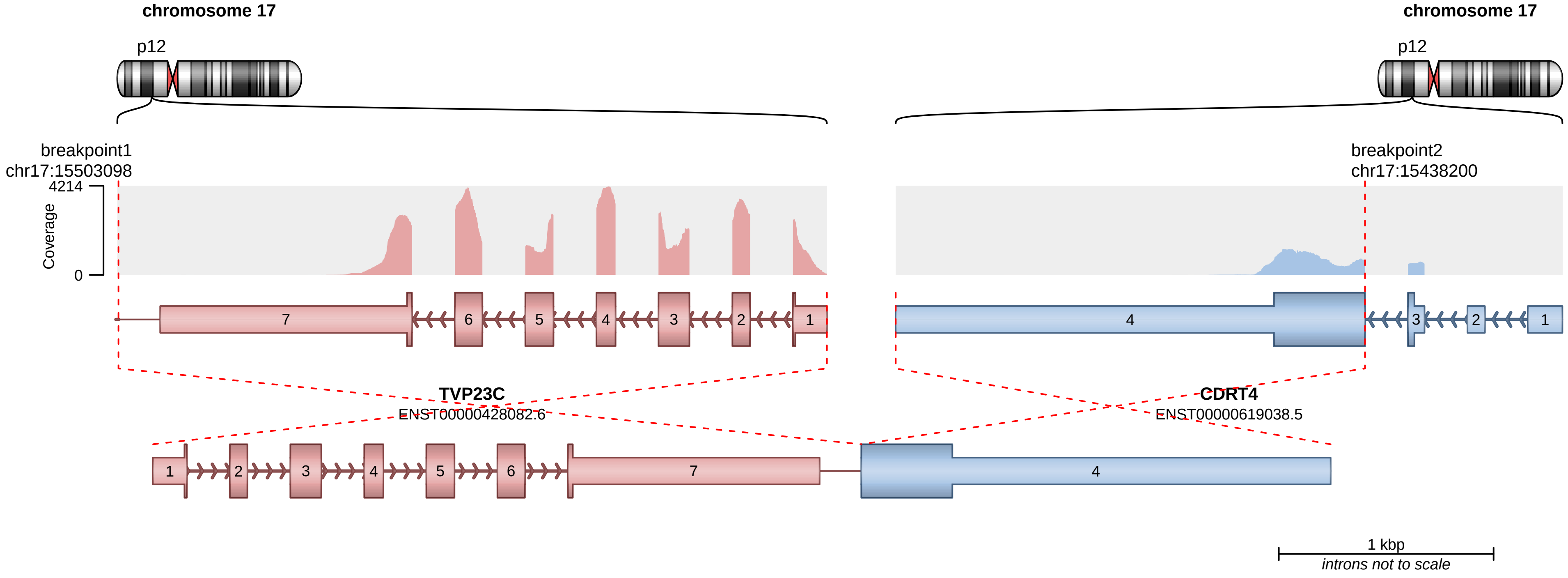
RETAINED PROTEIN DOMAINS
reading frame unclear

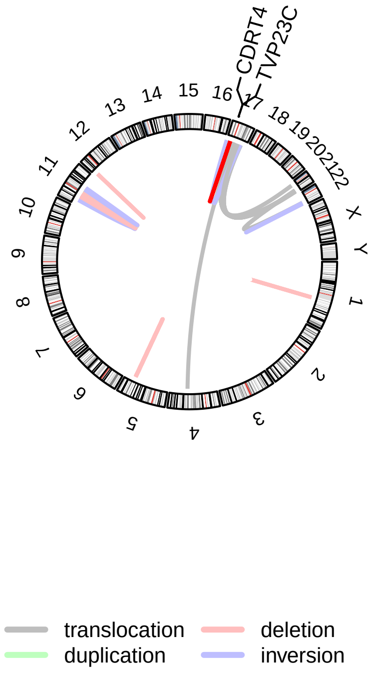


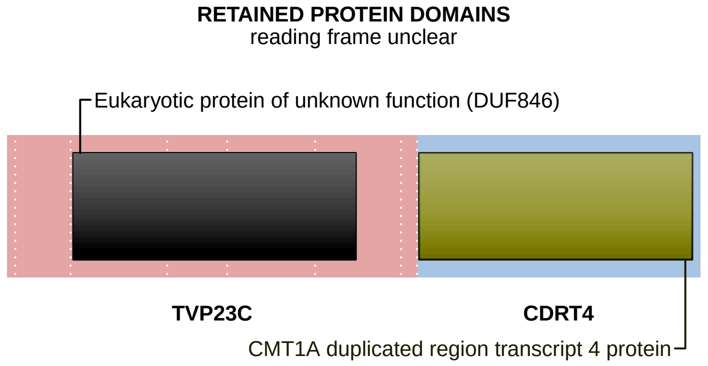
SUPPORTING READ COUNT

Split reads = 42
Discordant mates = 2

▬ translocation ▬ deletion
▬ duplication ▬ inversion

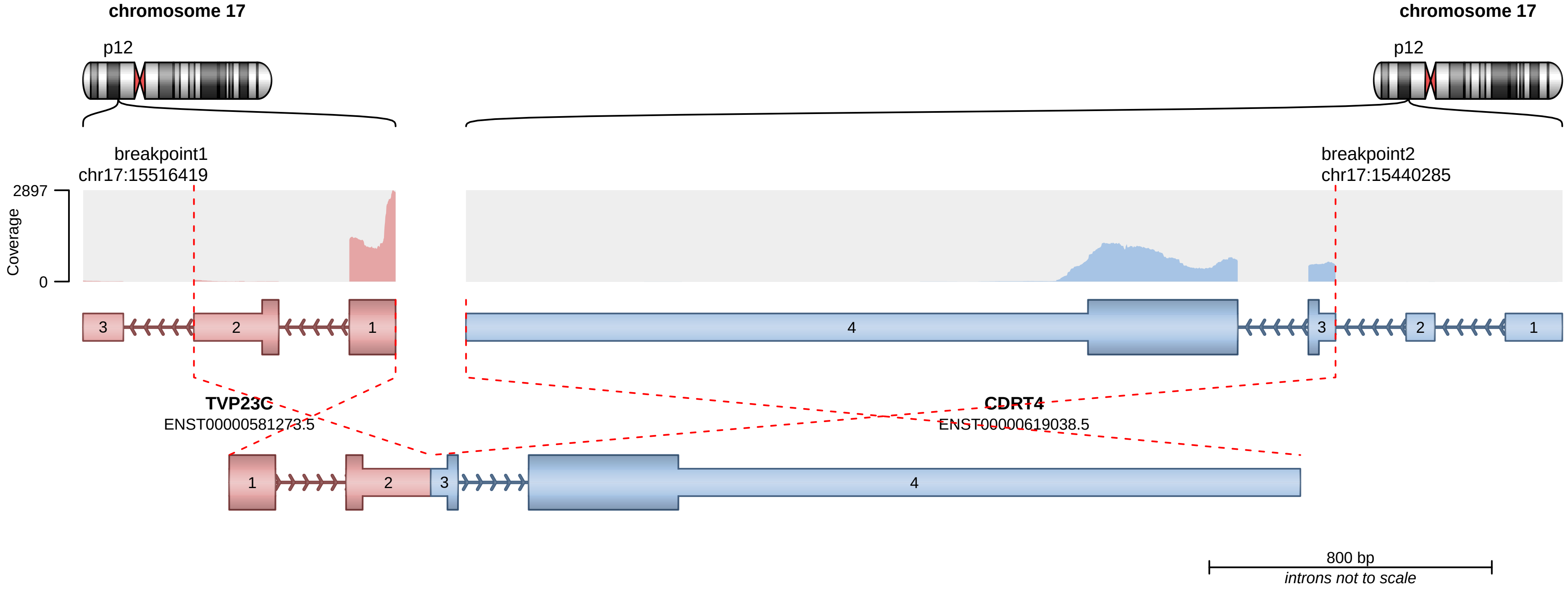


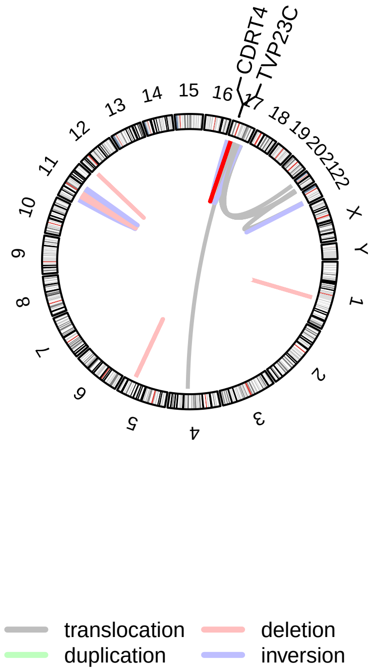


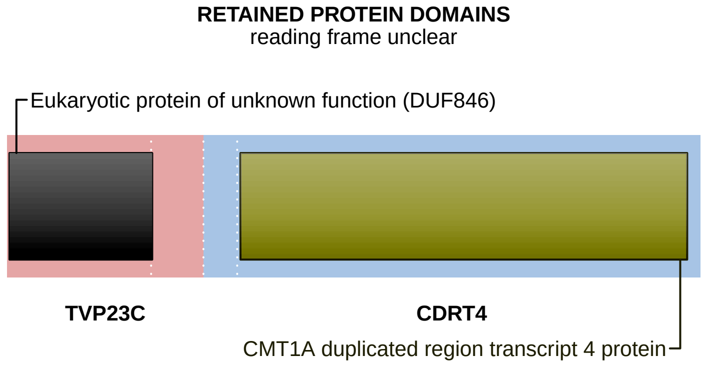


SUPPORTING READ COUNT

Split reads = 37
Discordant mates = 1

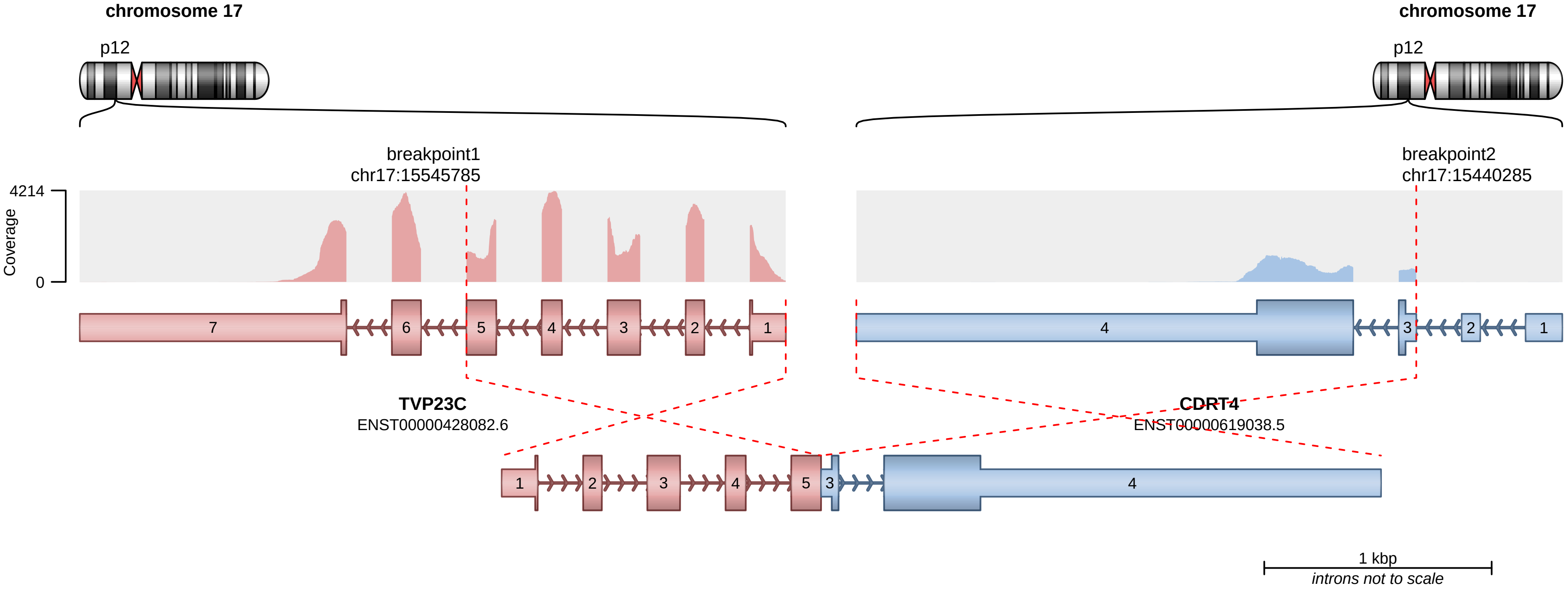


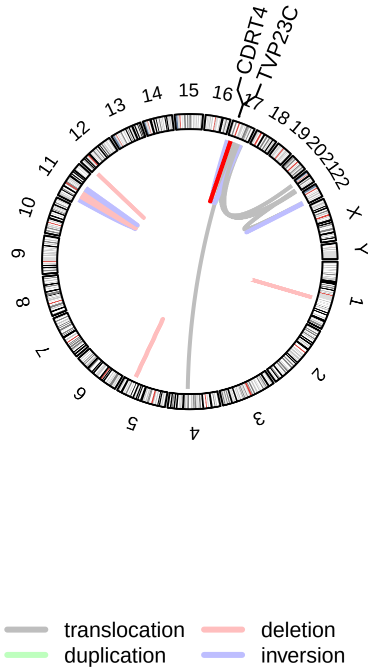




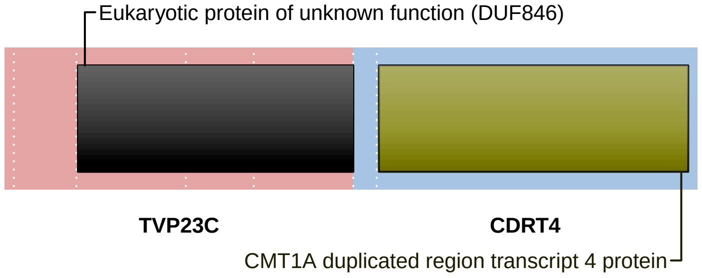
SUPPORTING READ COUNT

Split reads = 9
Discordant mates = 2



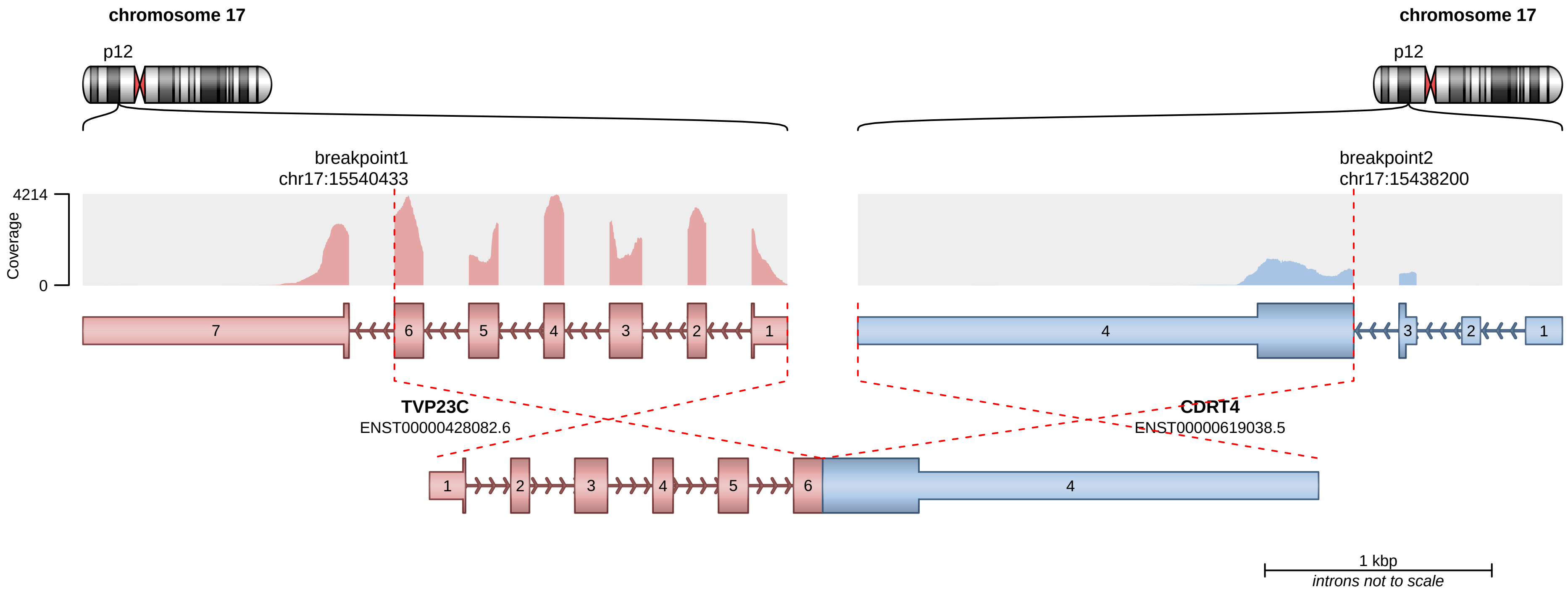


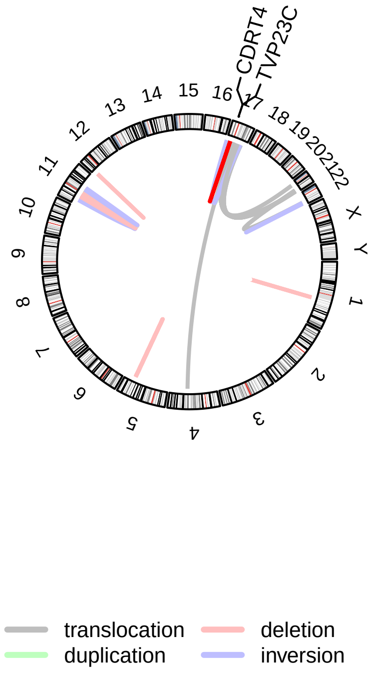
RETAINED PROTEIN DOMAINS
reading frame unclear

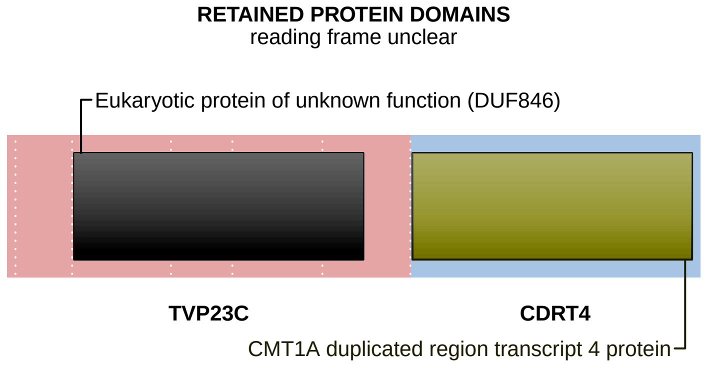


SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 1

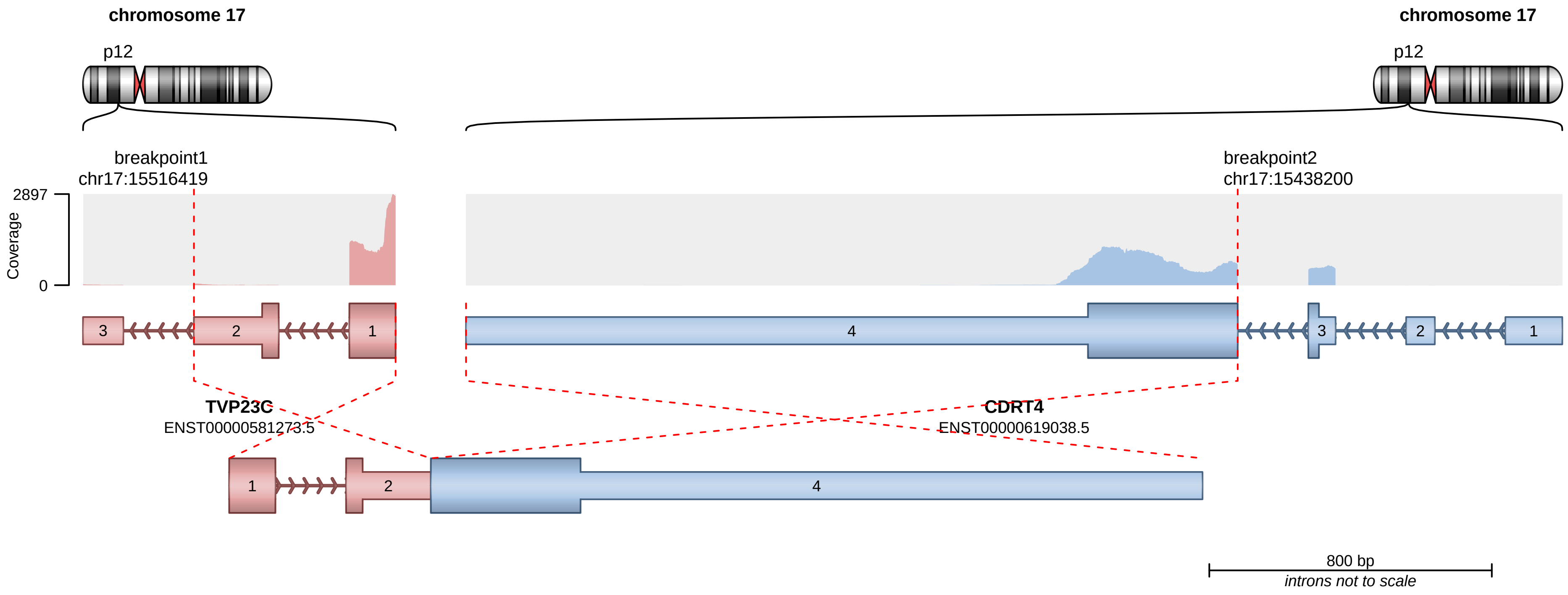


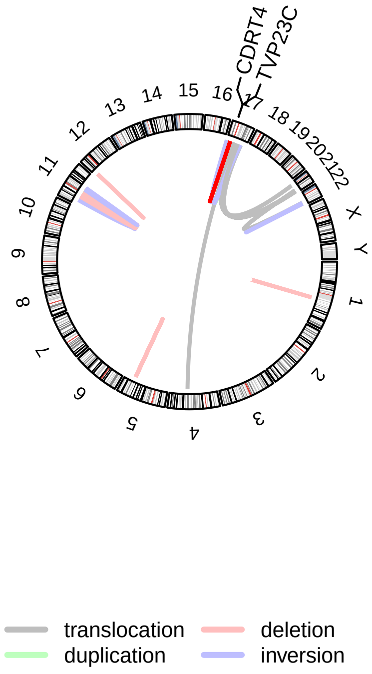


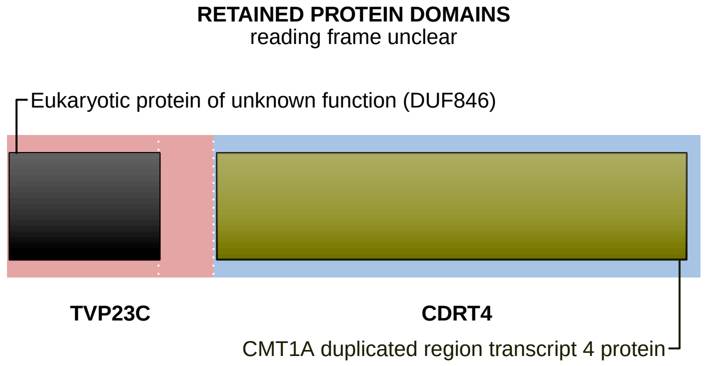


SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 1

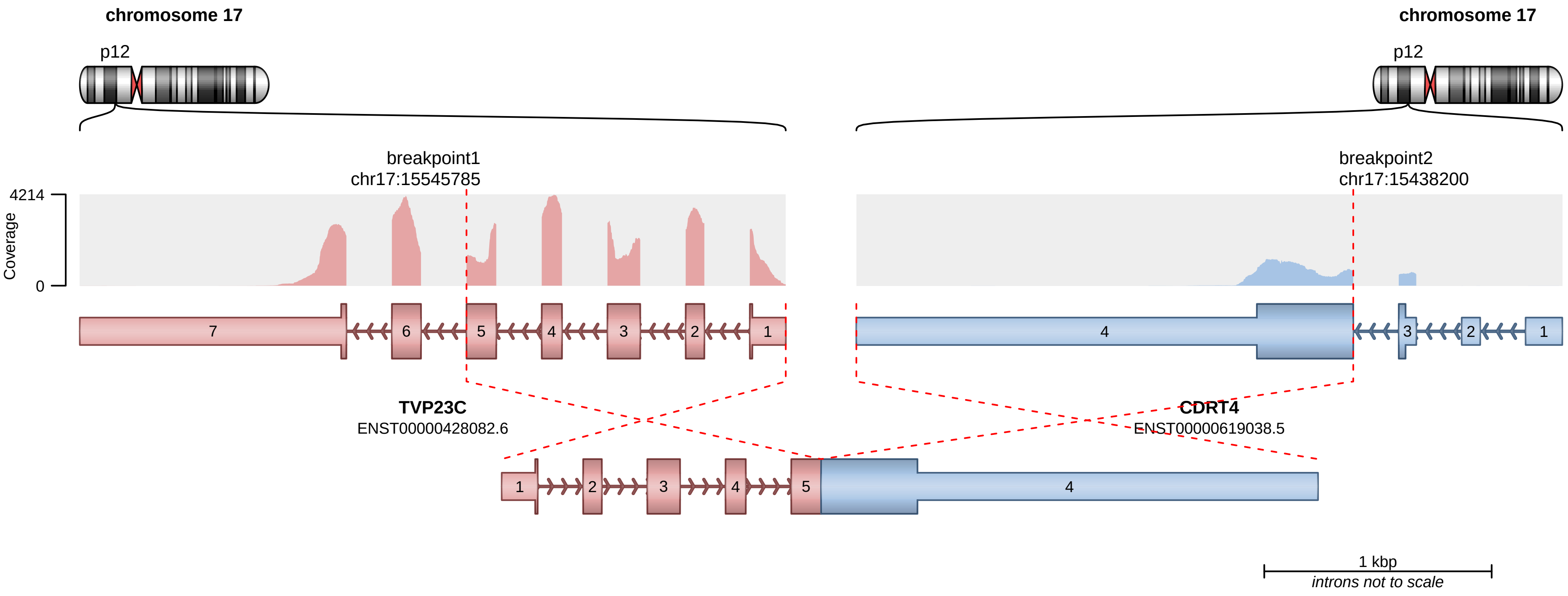


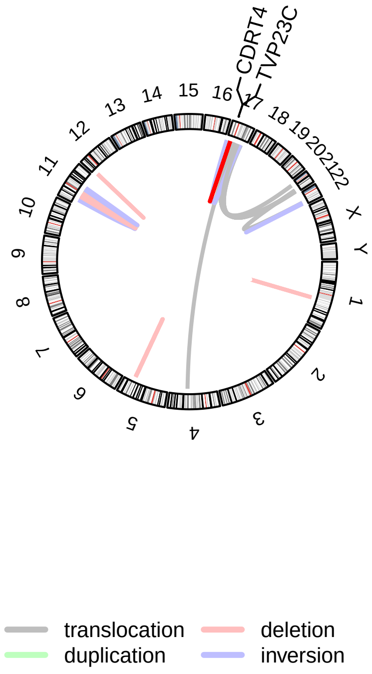




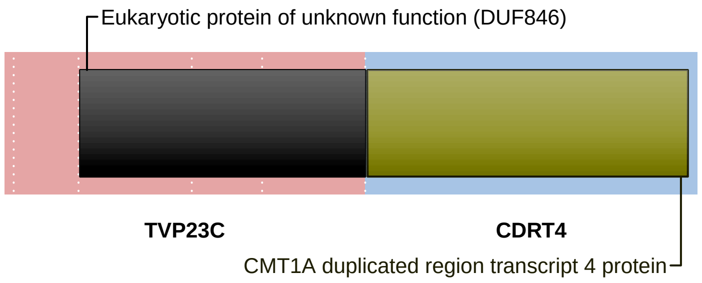
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 1



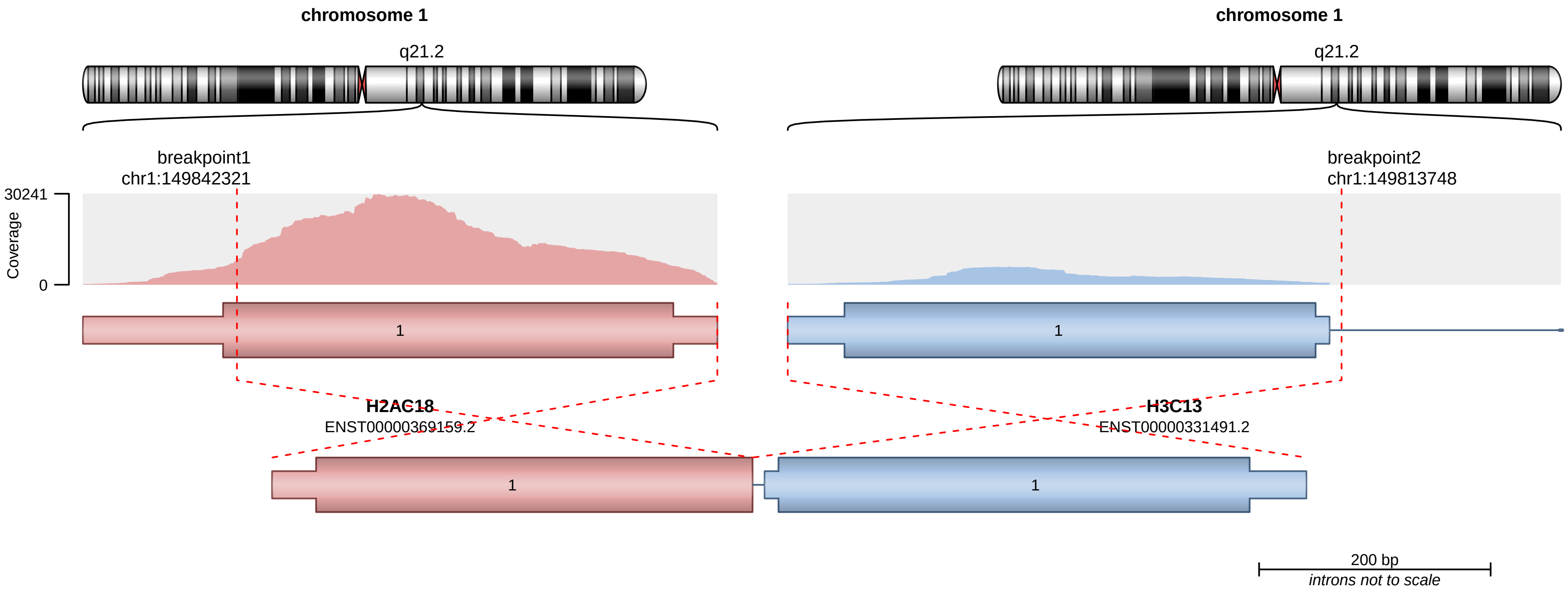


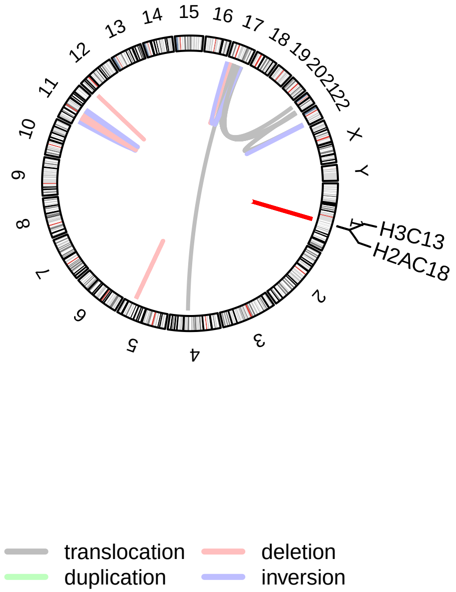
RETAINED PROTEIN DOMAINS
reading frame unclear



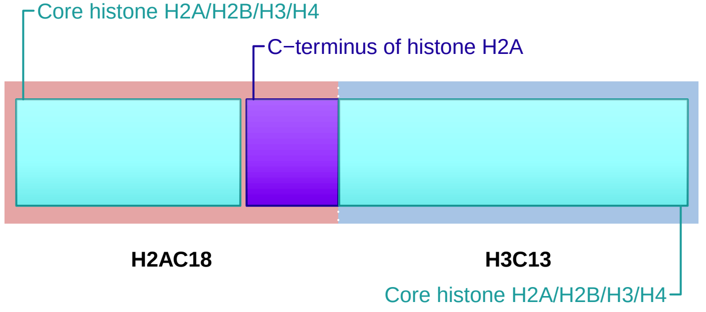
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



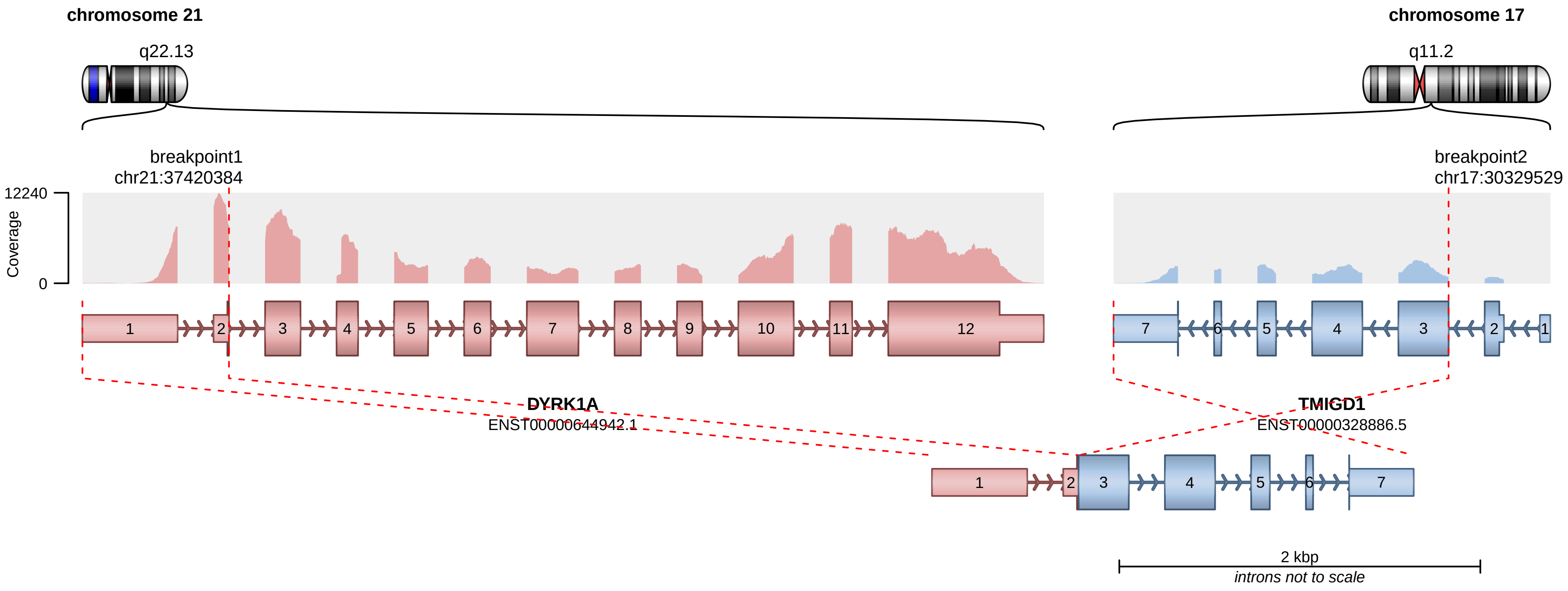


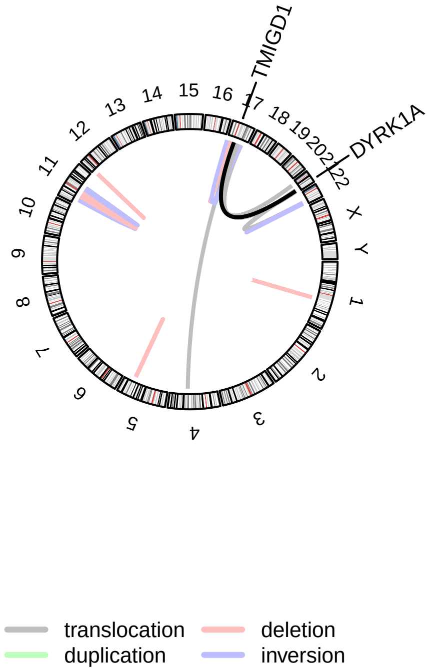
RETAINED PROTEIN DOMAINS
reading frame unclear



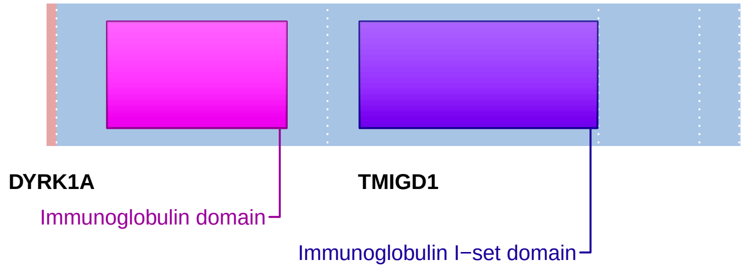
SUPPORTING READ COUNT

Split reads = 112
Discordant mates = 1



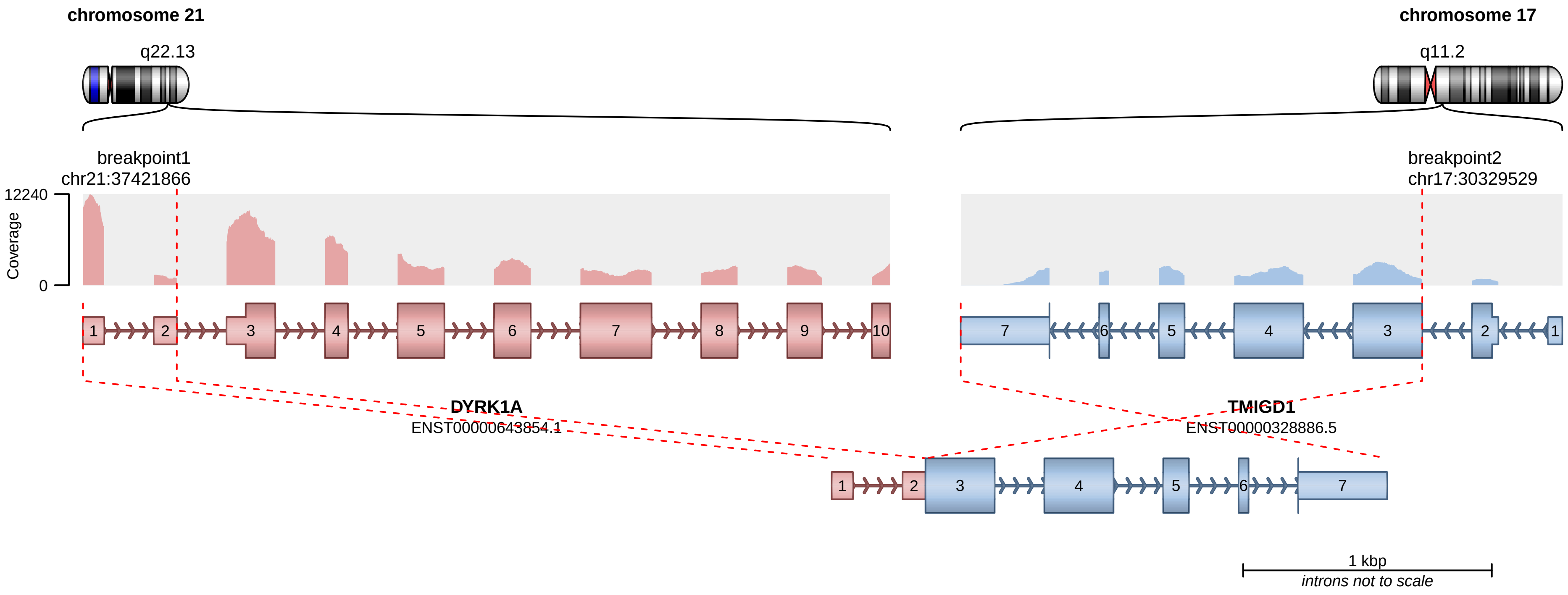


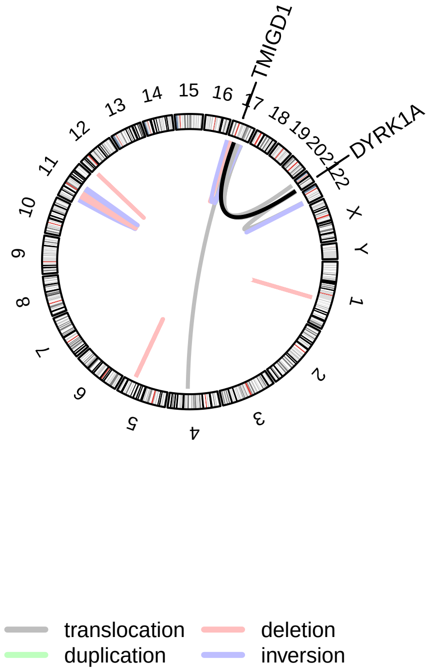
RETAINED PROTEIN DOMAINS
reading frame unclear

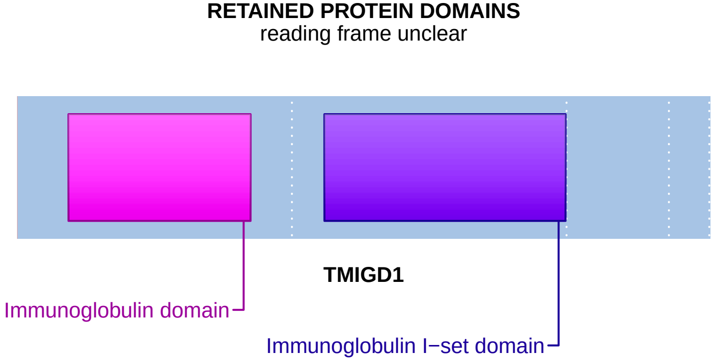


SUPPORTING READ COUNT

Split reads = 103
Discordant mates = 1

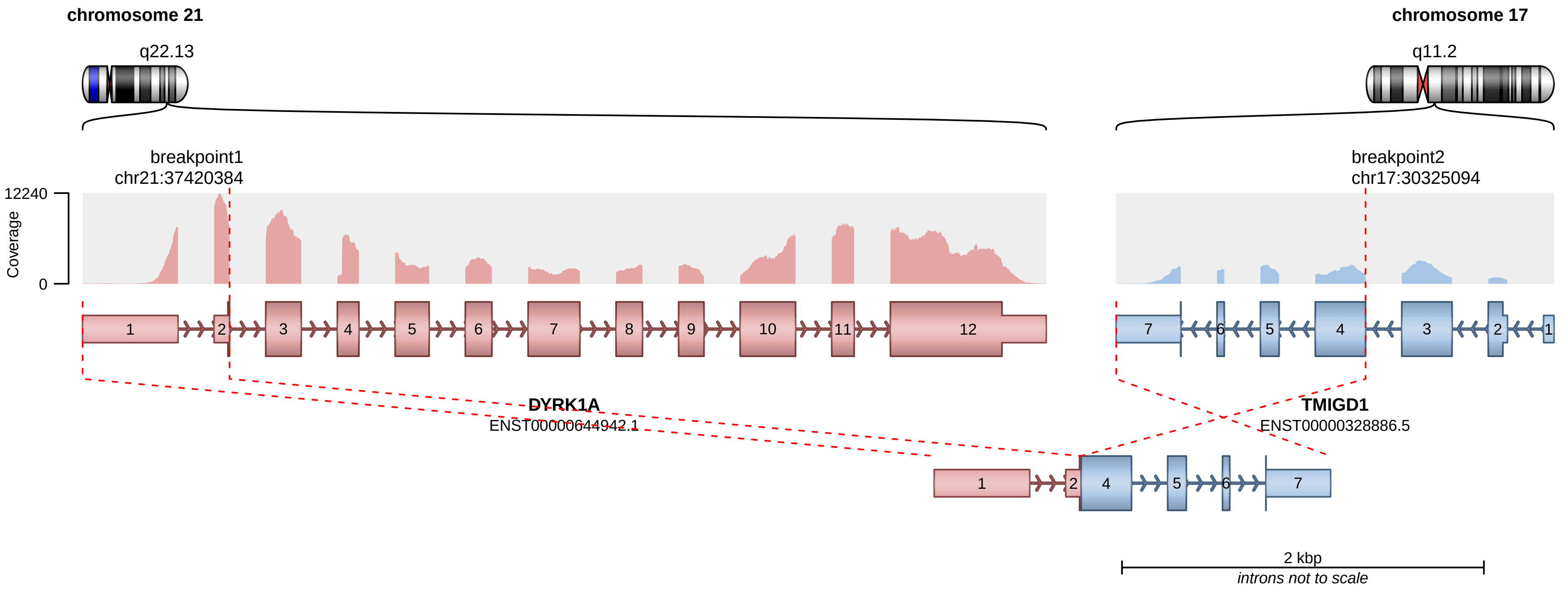


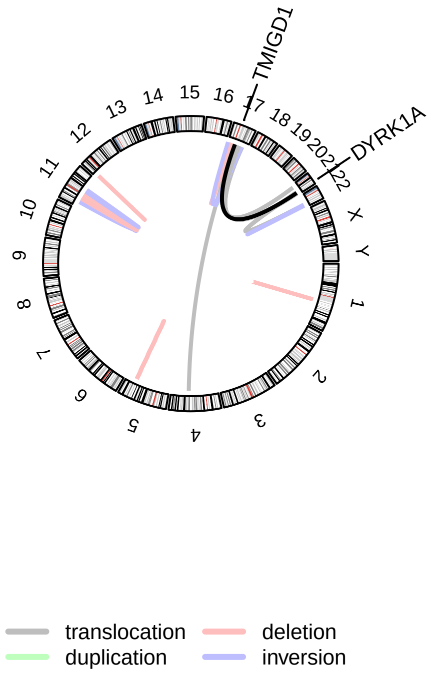


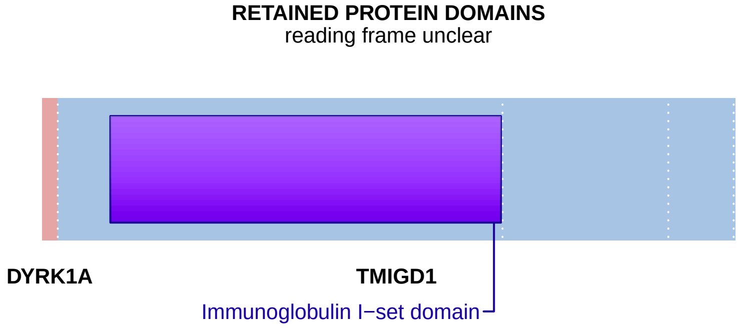


SUPPORTING READ COUNT

Split reads = 22
Discordant mates = 1

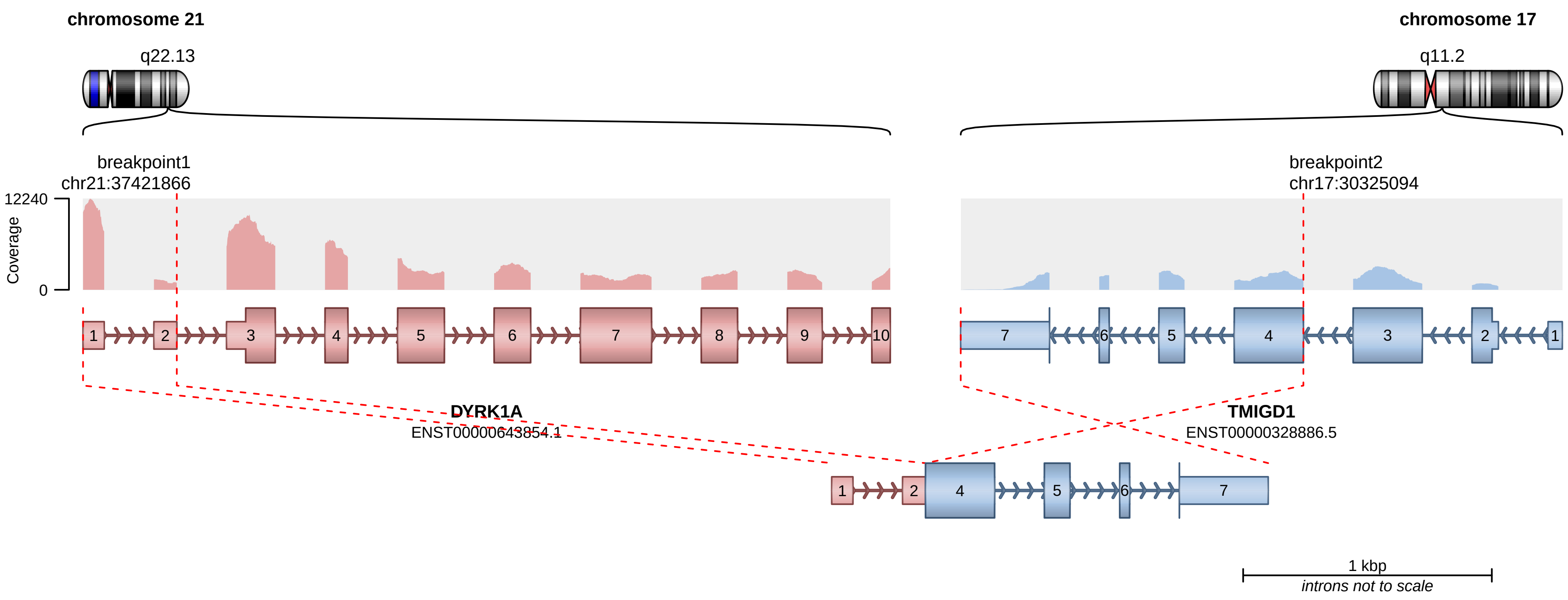


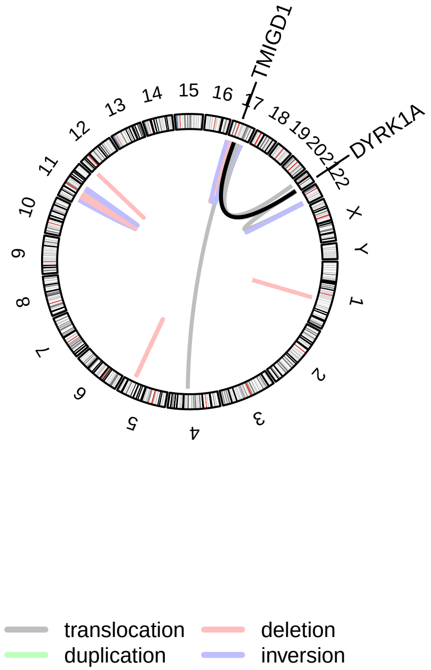


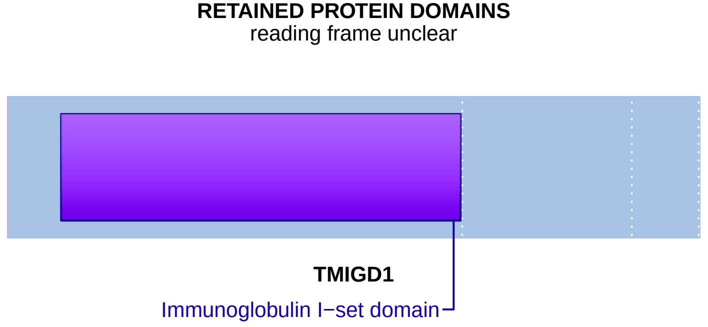


SUPPORTING READ COUNT

Split reads = 20
Discordant mates = 0

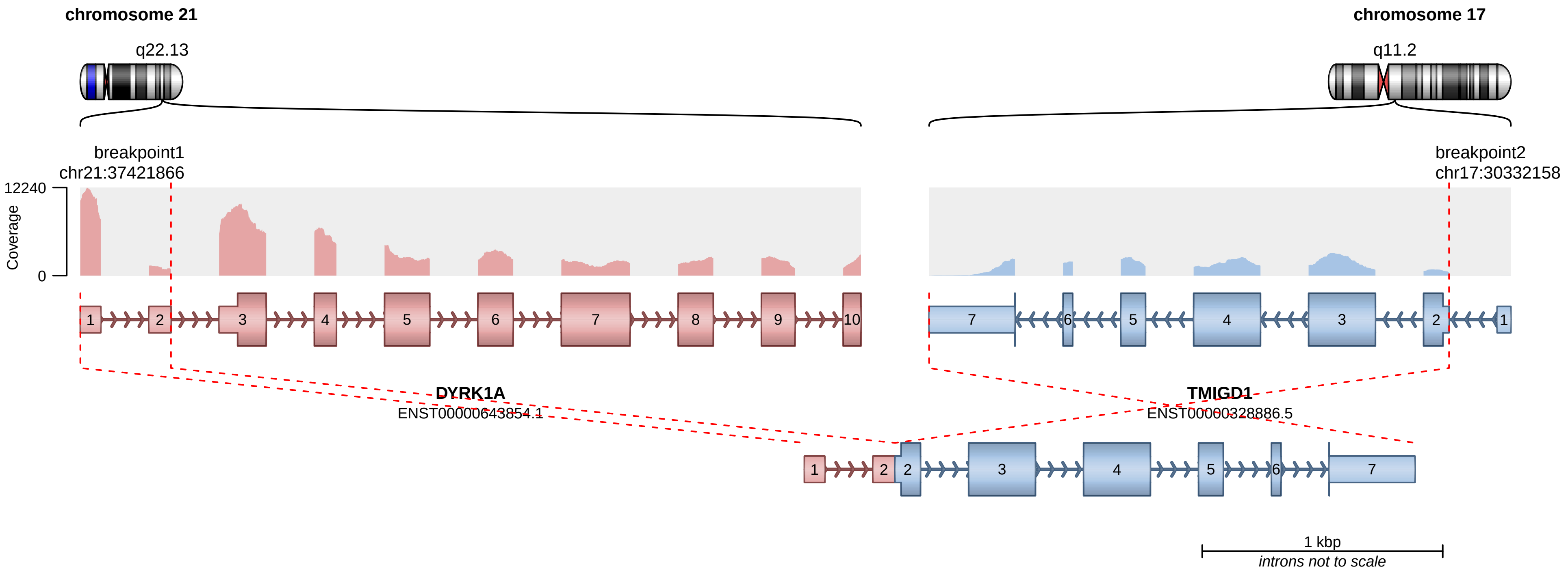


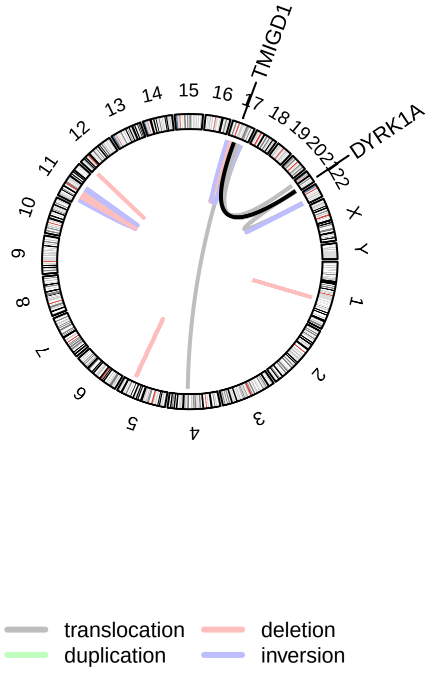




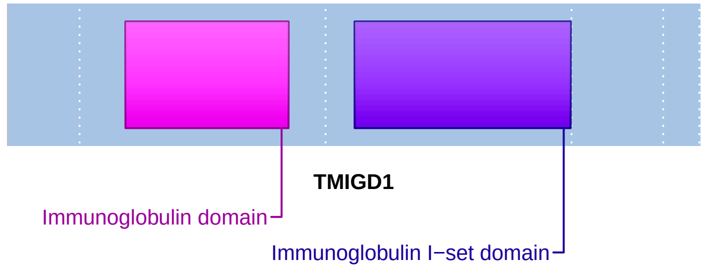
SUPPORTING READ COUNT

Split reads = 17
Discordant mates = 0



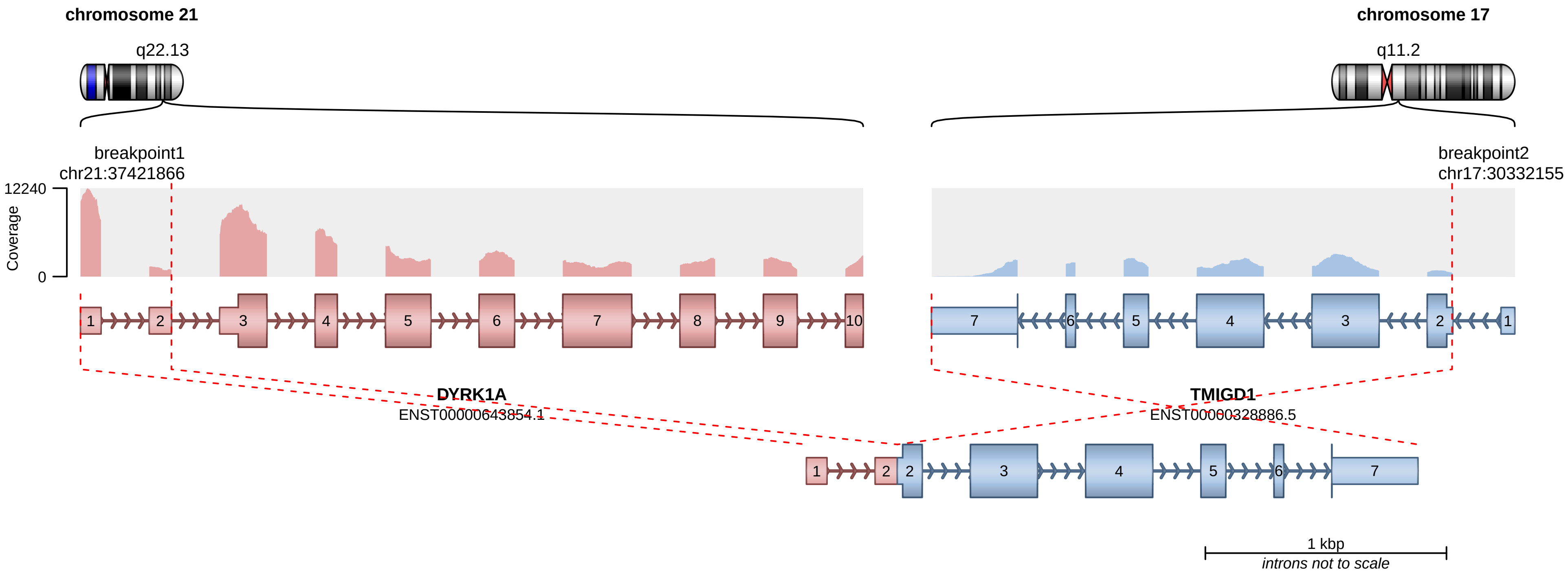


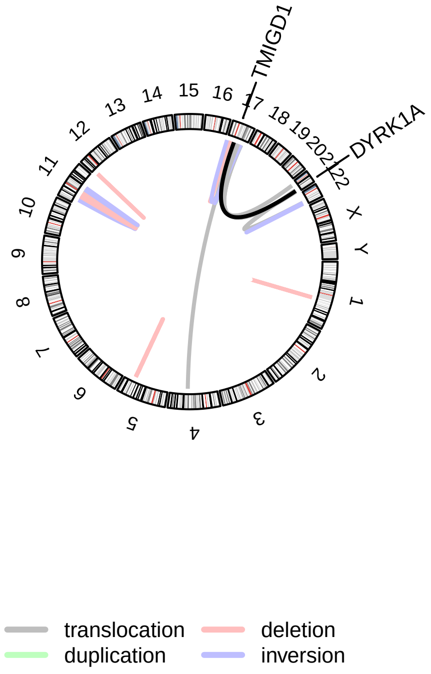
RETAINED PROTEIN DOMAINS
reading frame unclear

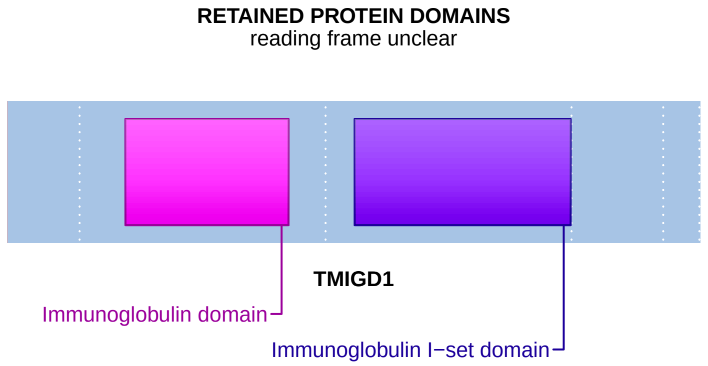


SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 1

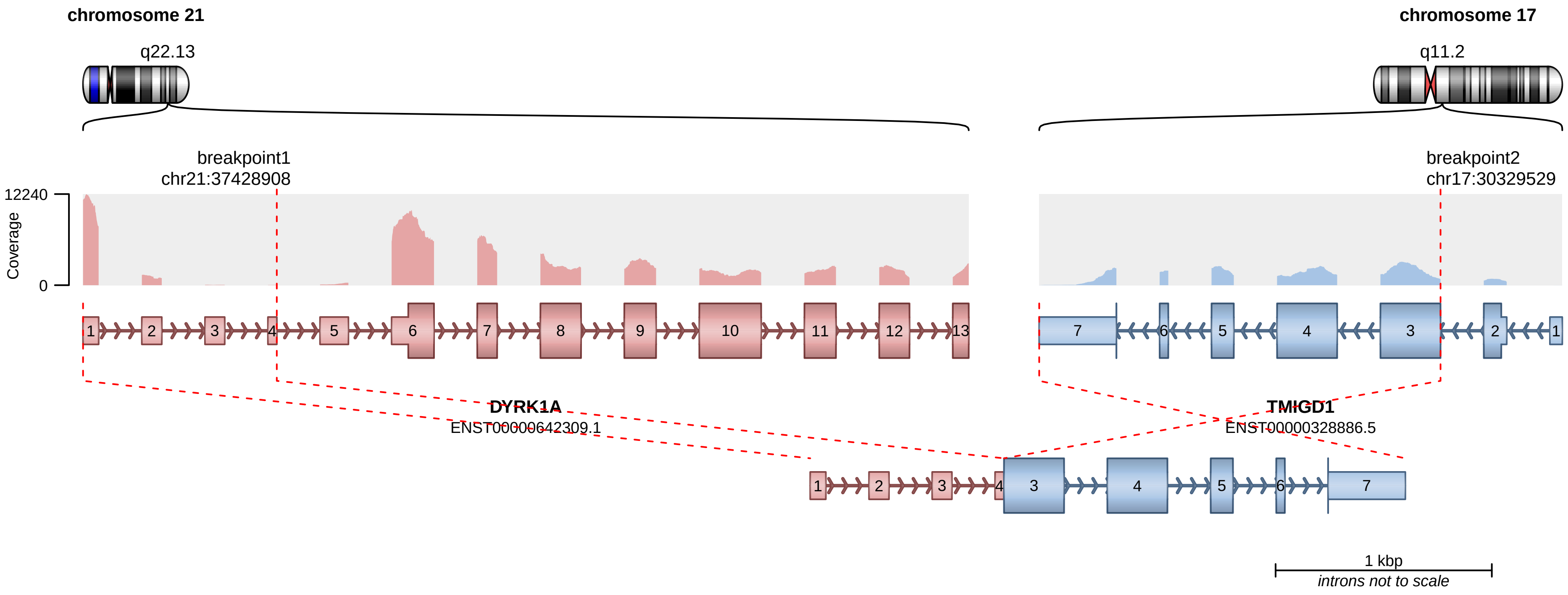


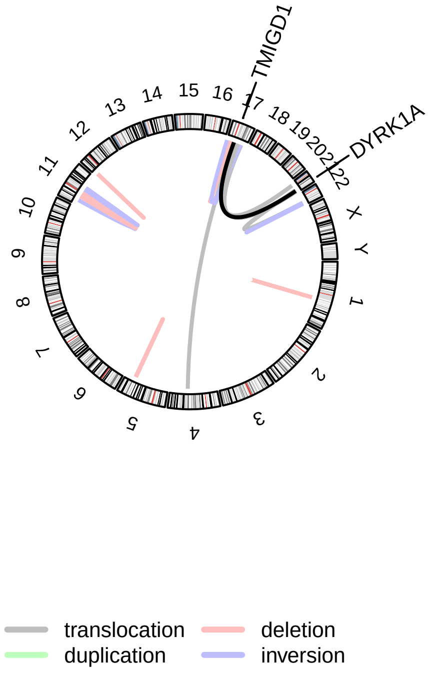




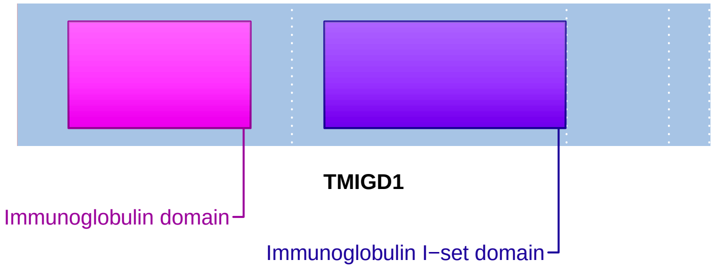
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 1



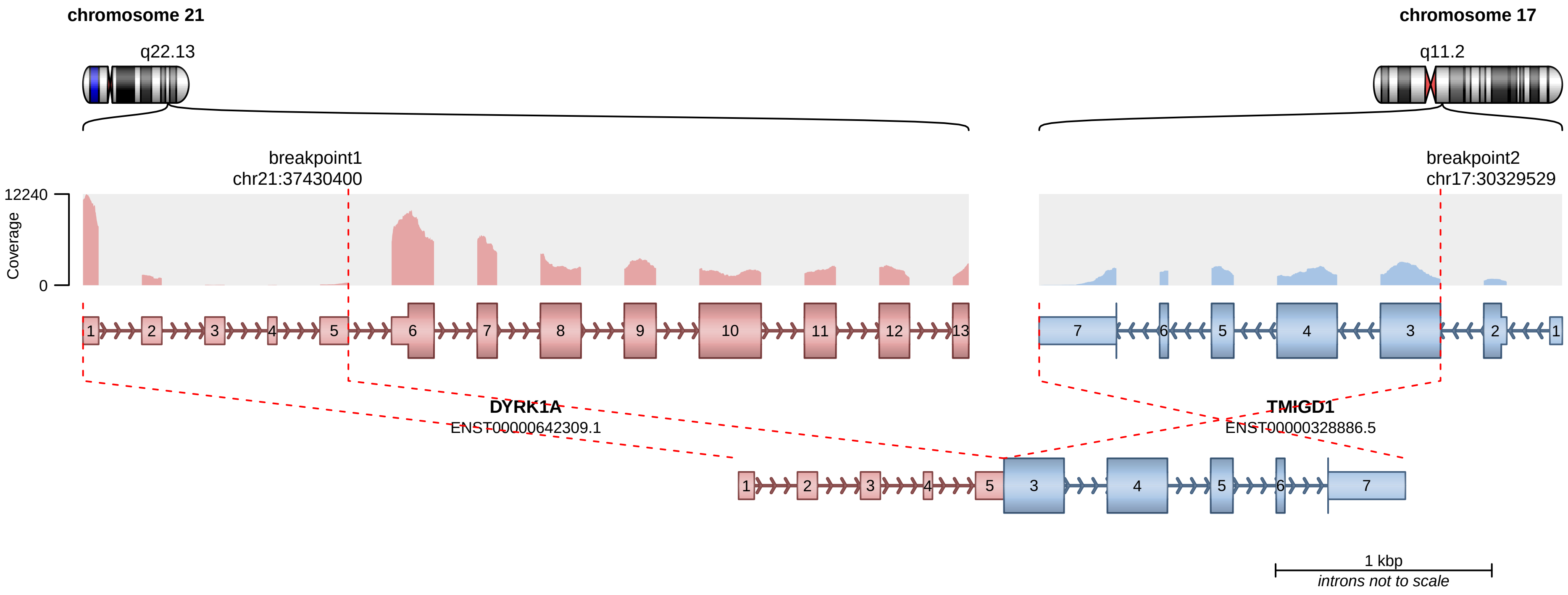


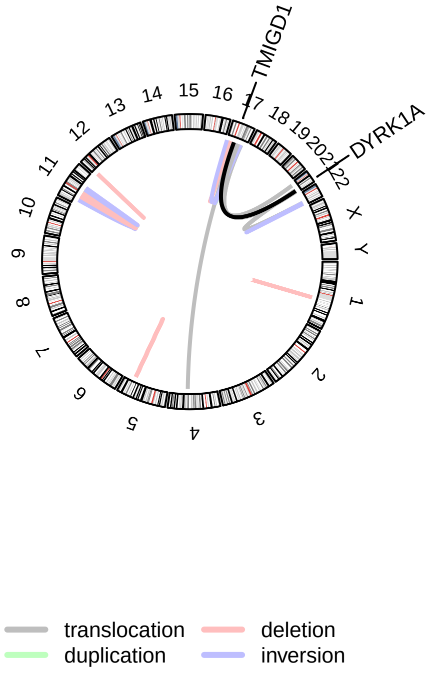
RETAINED PROTEIN DOMAINS
reading frame unclear



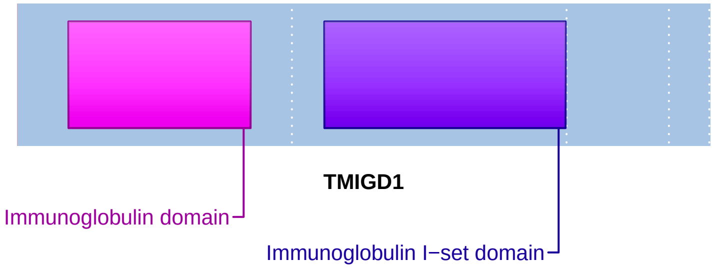
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 1



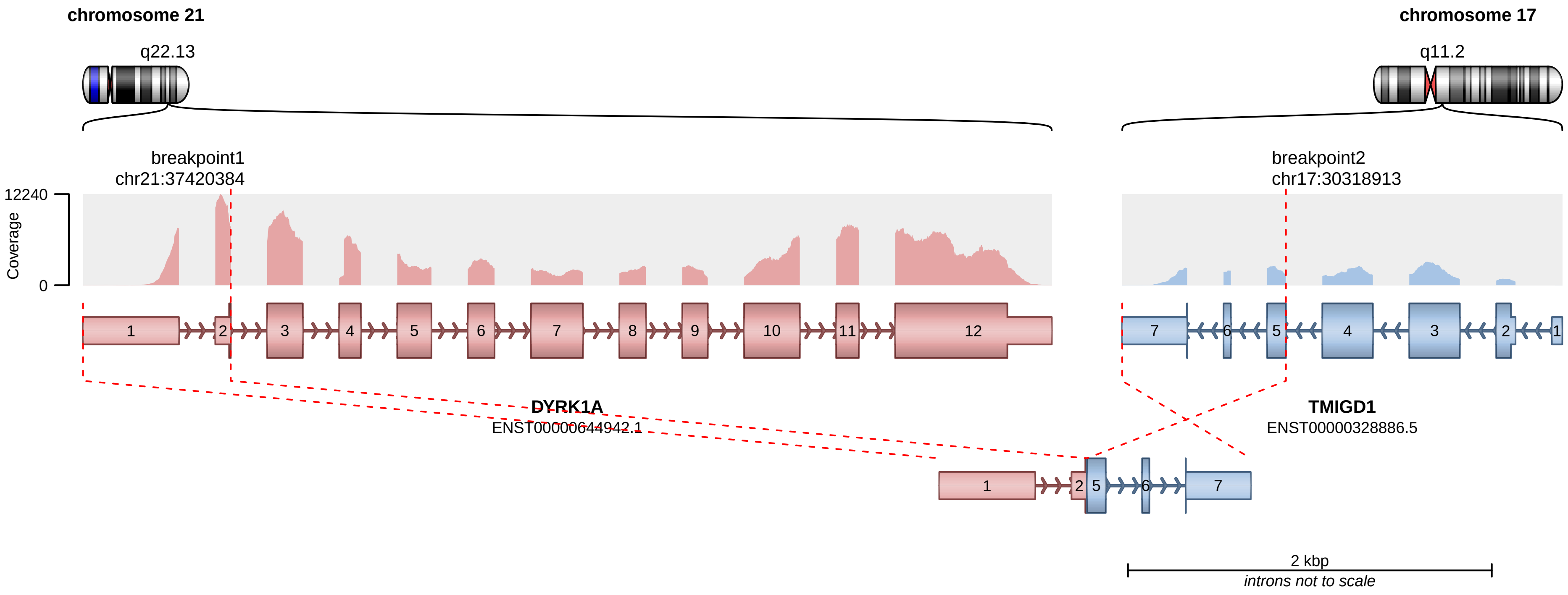


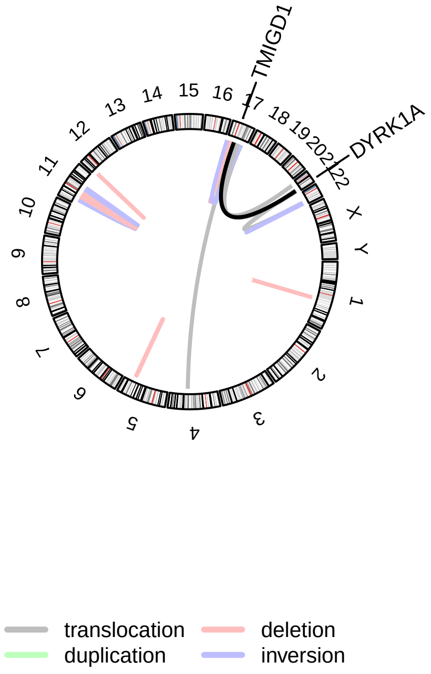
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

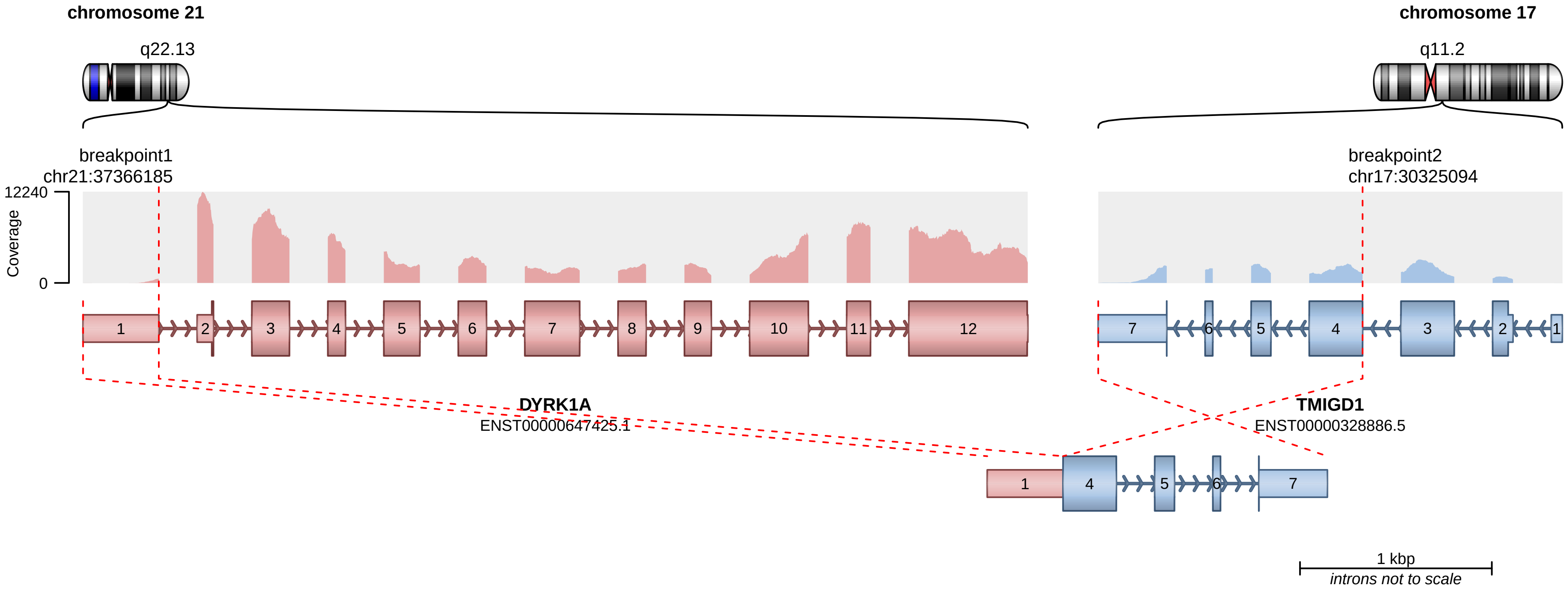


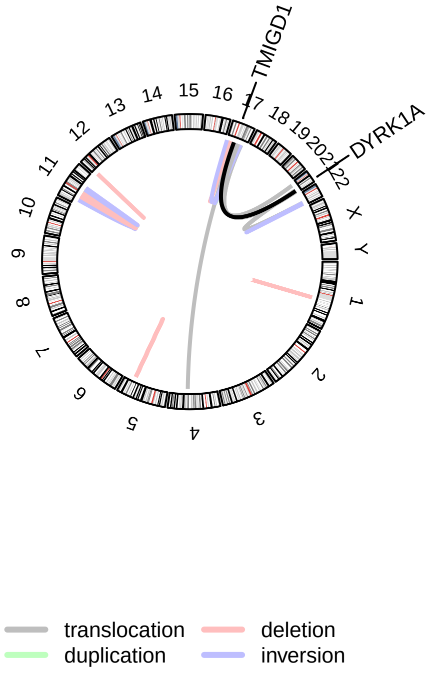


No protein domains retained in fusion.

SUPPORTING READ COUNT

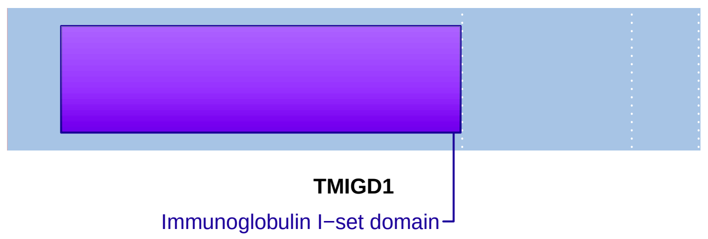
Split reads = 1
Discordant mates = 0





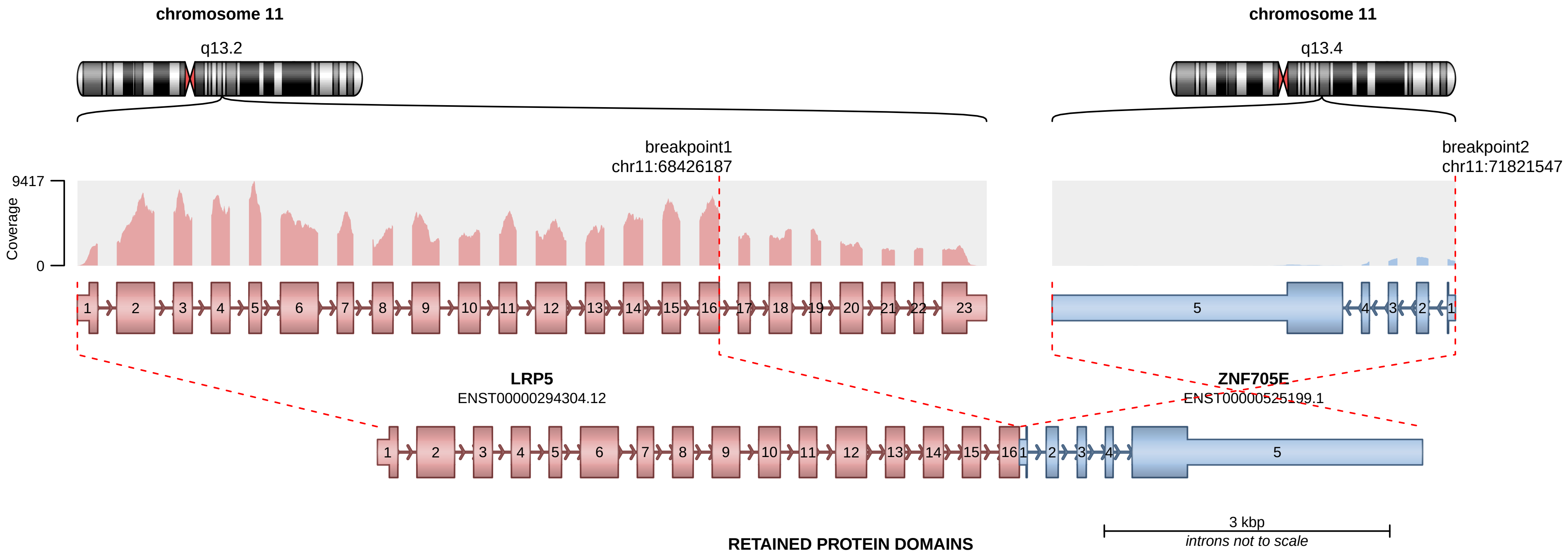
RETAINED PROTEIN DOMAINS

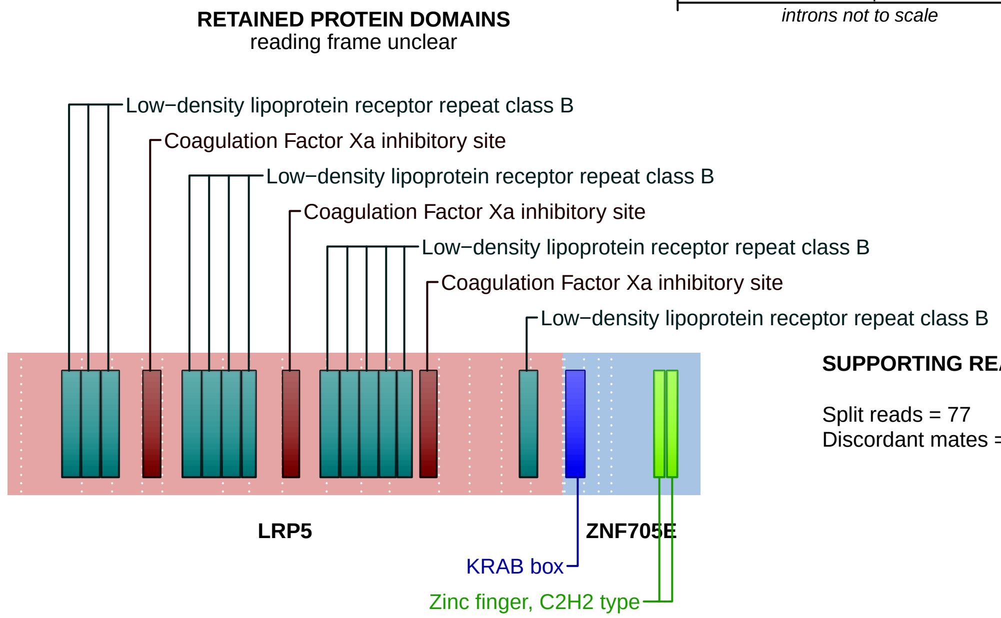
reading frame unclear



SUPPORTING READ COUNT

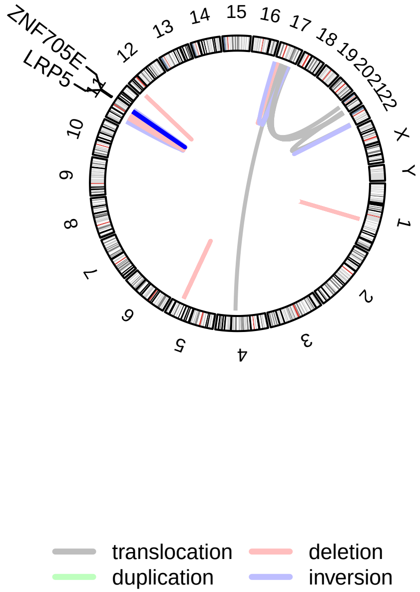
Split reads = 1
Discordant mates = 0

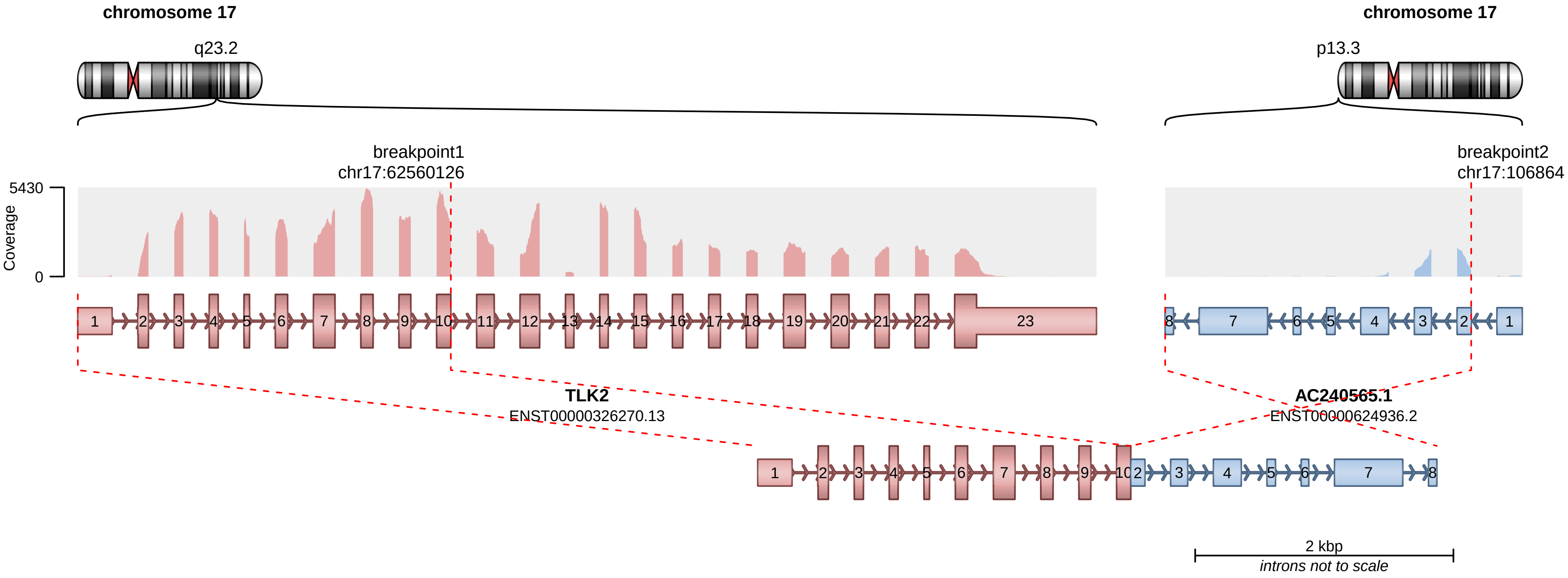


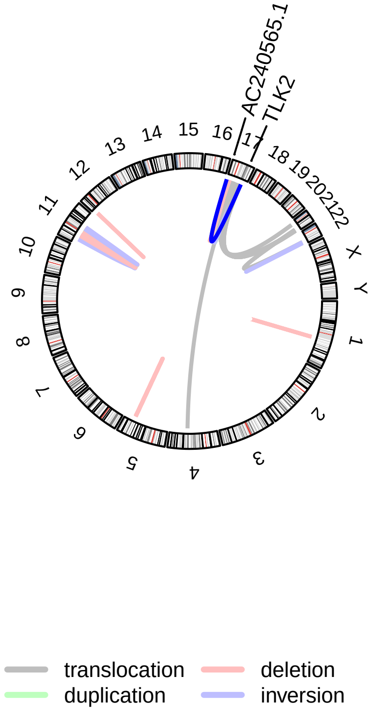


SUPPORTING READ COUNT

Split reads = 77
Discordant mates = 3



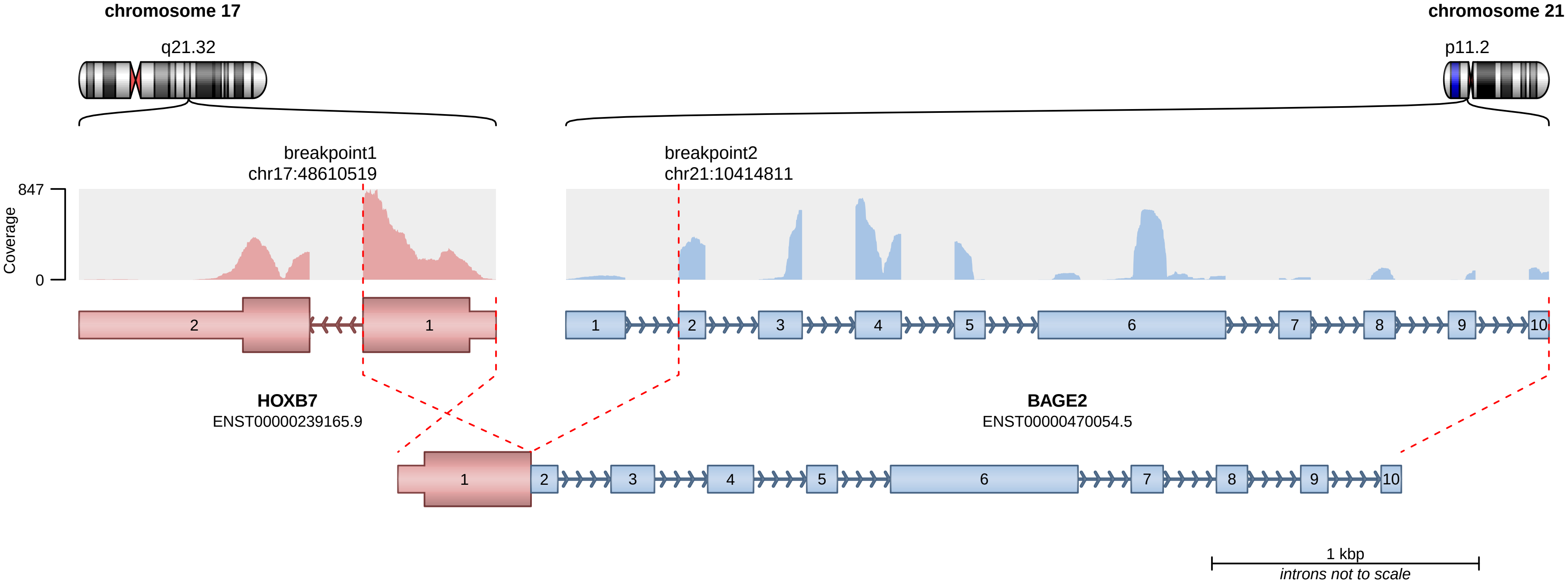


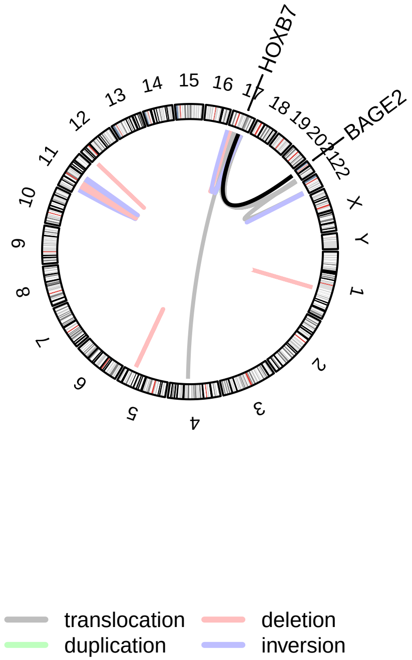


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 75
Discordant mates = 0

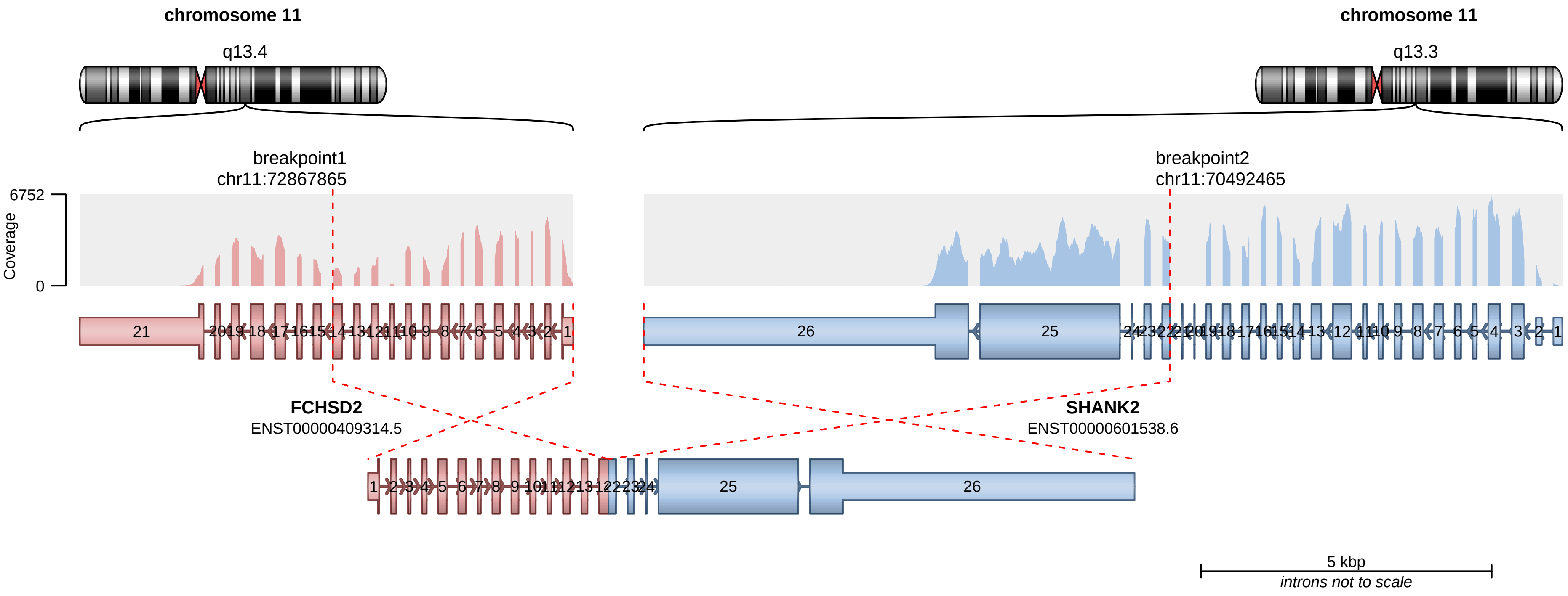


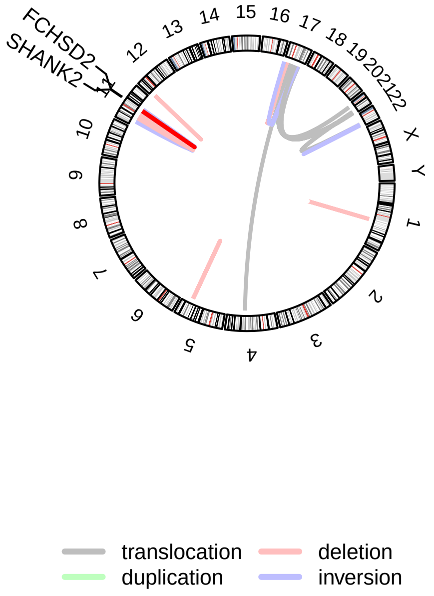


No protein domains retained in fusion.

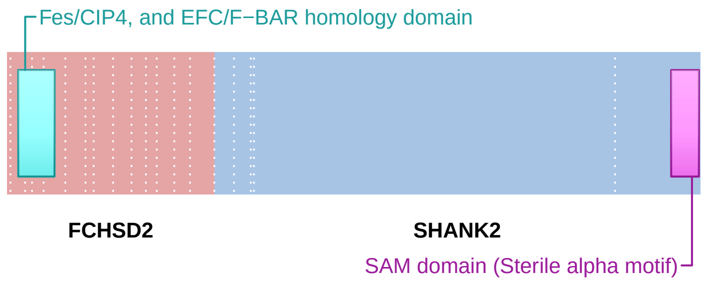
SUPPORTING READ COUNT

Split reads = 69
Discordant mates = 0



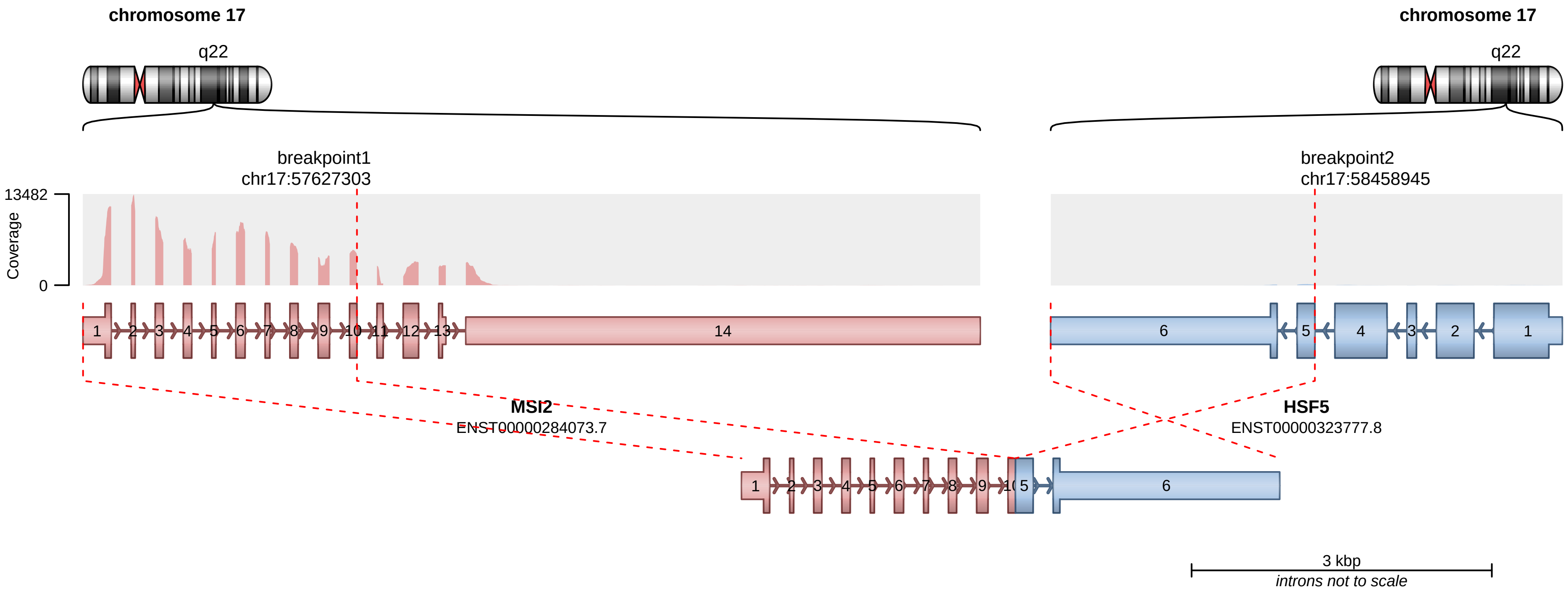


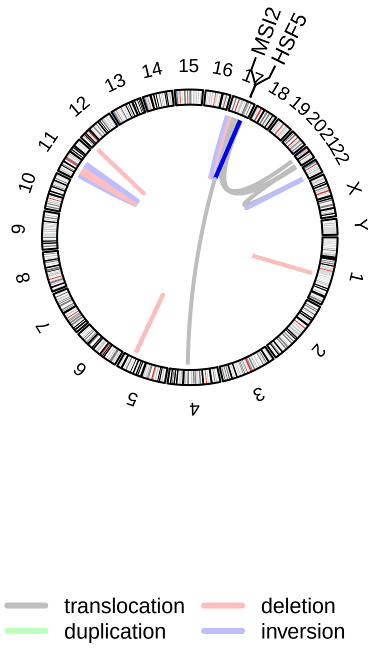
RETAINED PROTEIN DOMAINS
reading frame unclear

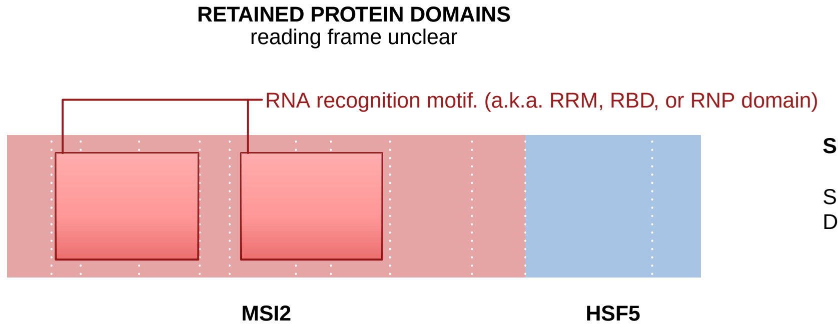


SUPPORTING READ COUNT

Split reads = 62
Discordant mates = 2

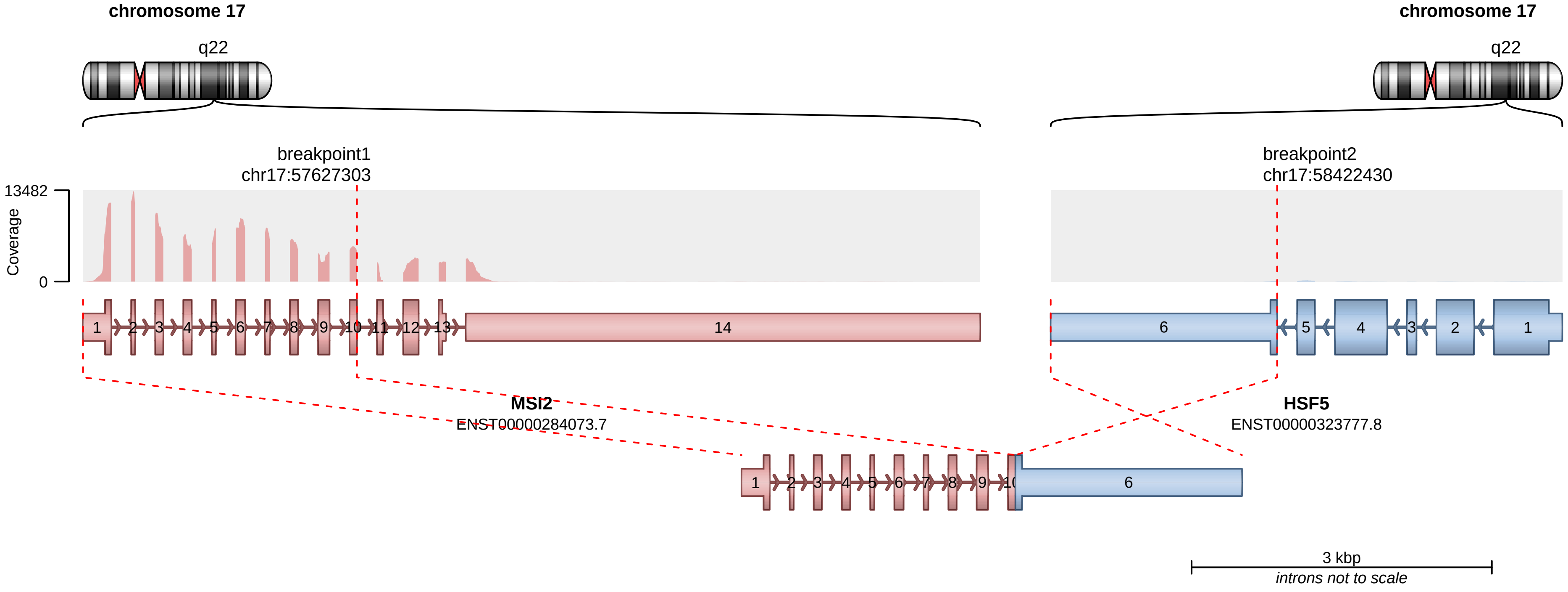


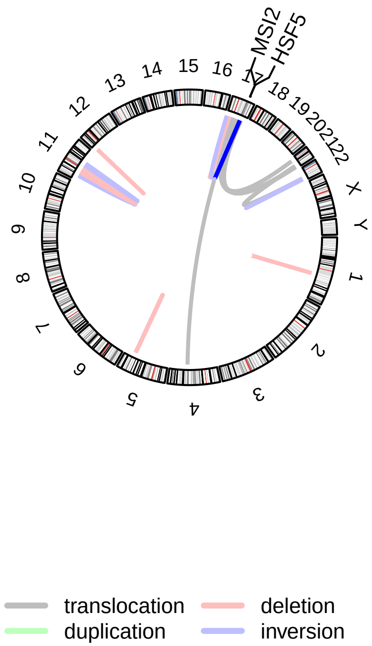


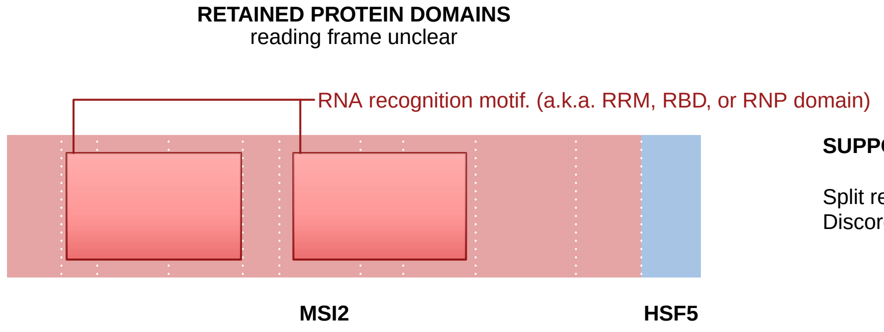


SUPPORTING READ COUNT

Split reads = 57
Discordant mates = 3

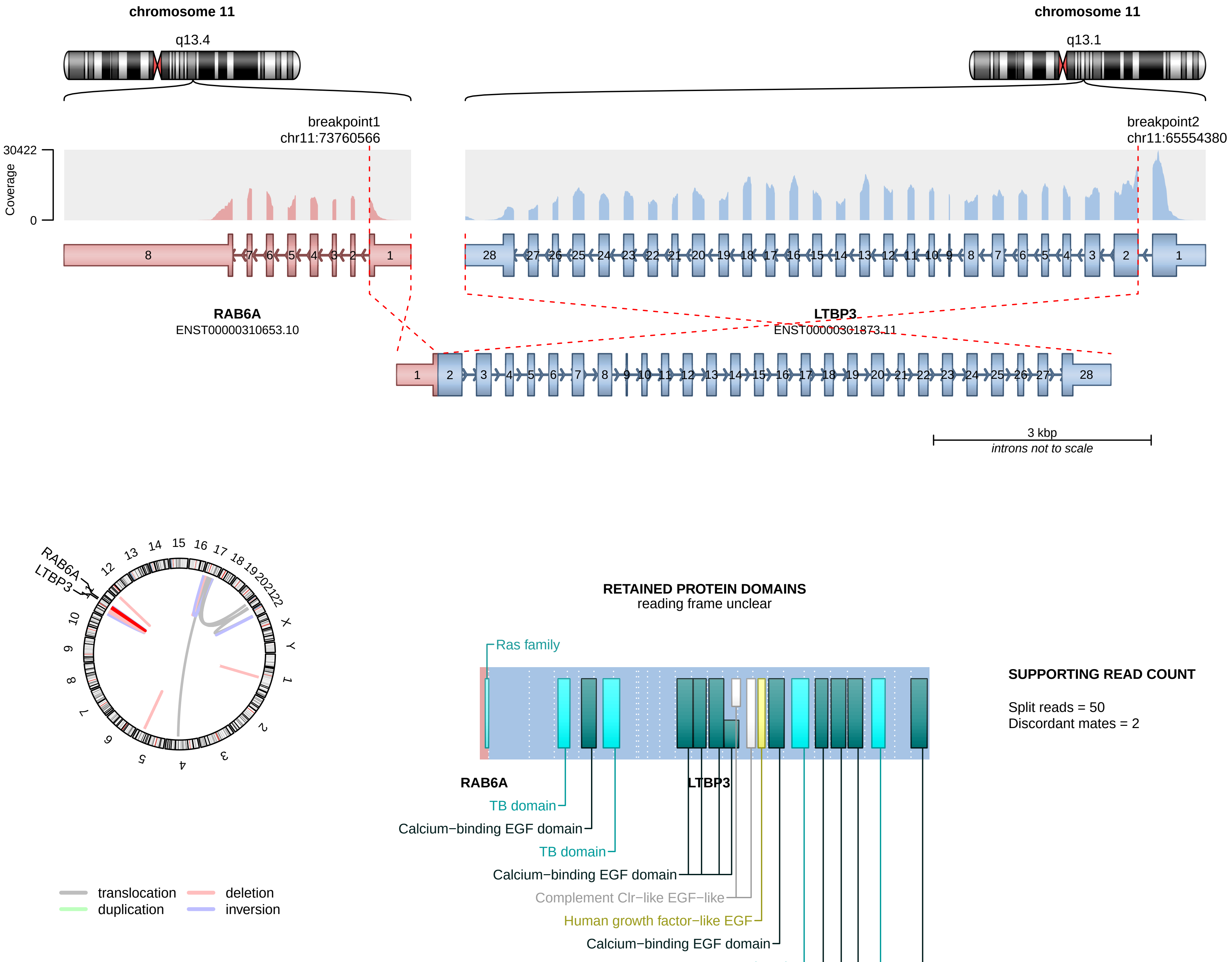






SUPPORTING READ COUNT

Split reads = 21
Discordant mates = 0


chromosome 11
q13.4
chromosome 11
q13.1
breakpoint1
chr11:73760566
breakpoint2
chr11:65554380
30422
Coverage
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7
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28
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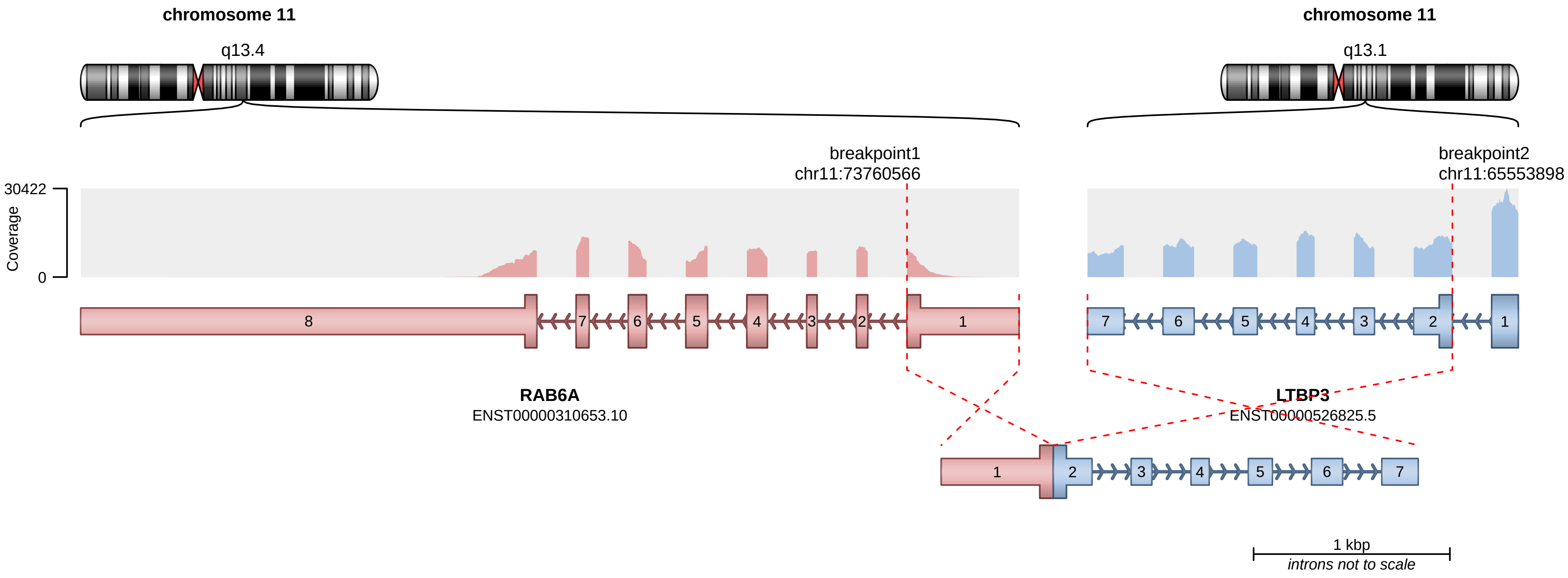
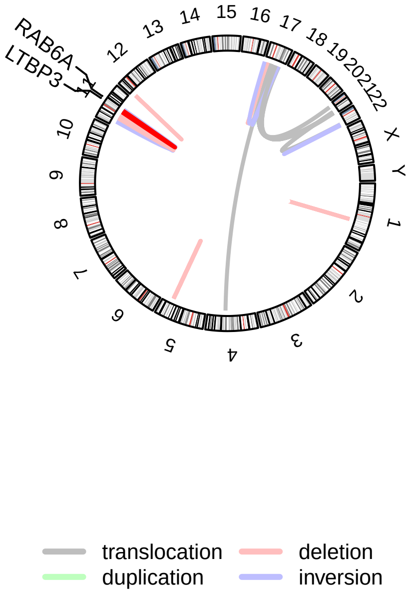
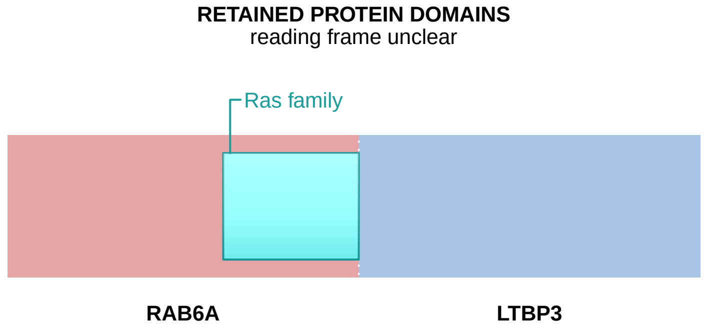
21
20
19
18
17
16
15
14
13
12
11
10
9
RAB6A
ENST00000310653.10
LTBP3
ENST00000301873.11
3 kbp
introns not to scale
RAB6A
LTBP3
12
13
14
15
16
17
18
19
20
21
22
X
Y
1
2
3
4
5
6
7
8
9
10
translocation
deletion
duplication
inversion
RETAINED PROTEIN DOMAINS
reading frame unclear
Ras family
RAB6A
LTBP3
TB domain
Calcium−binding EGF domain
TB domain
Calcium−binding EGF domain
Complement Clr−like EGF−like
Human growth factor−like EGF
Calcium−binding EGF domain
SUPPORTING READ COUNT
Split reads = 50
Discordant mates = 2

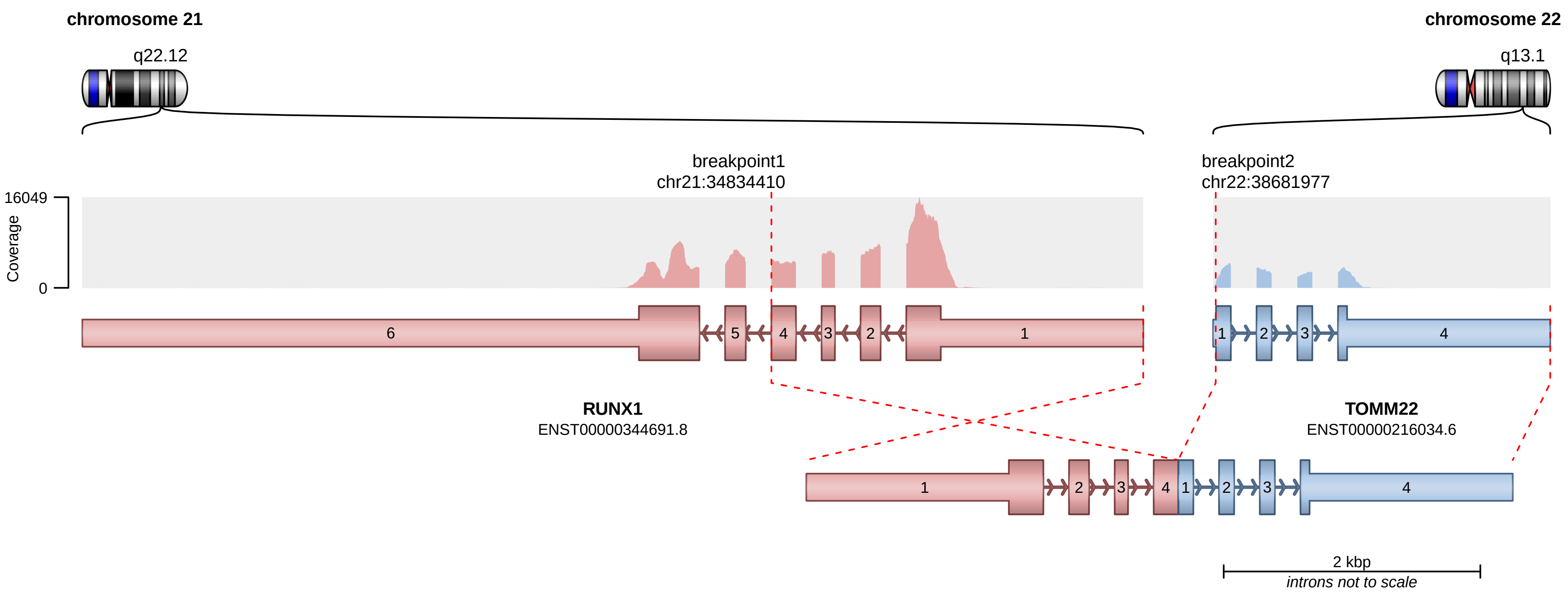


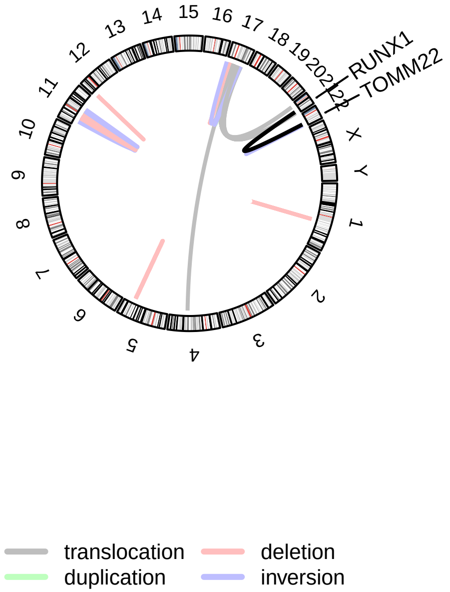


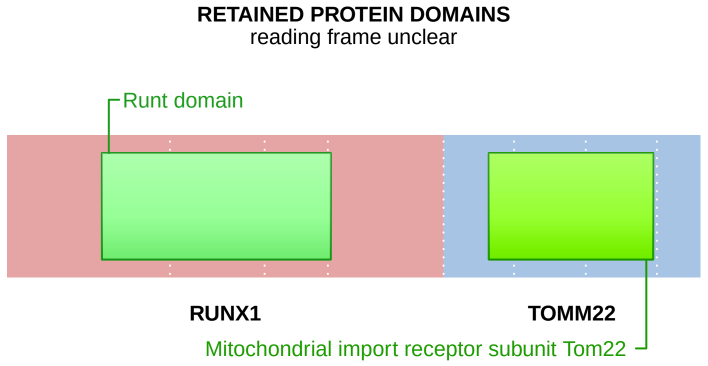


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

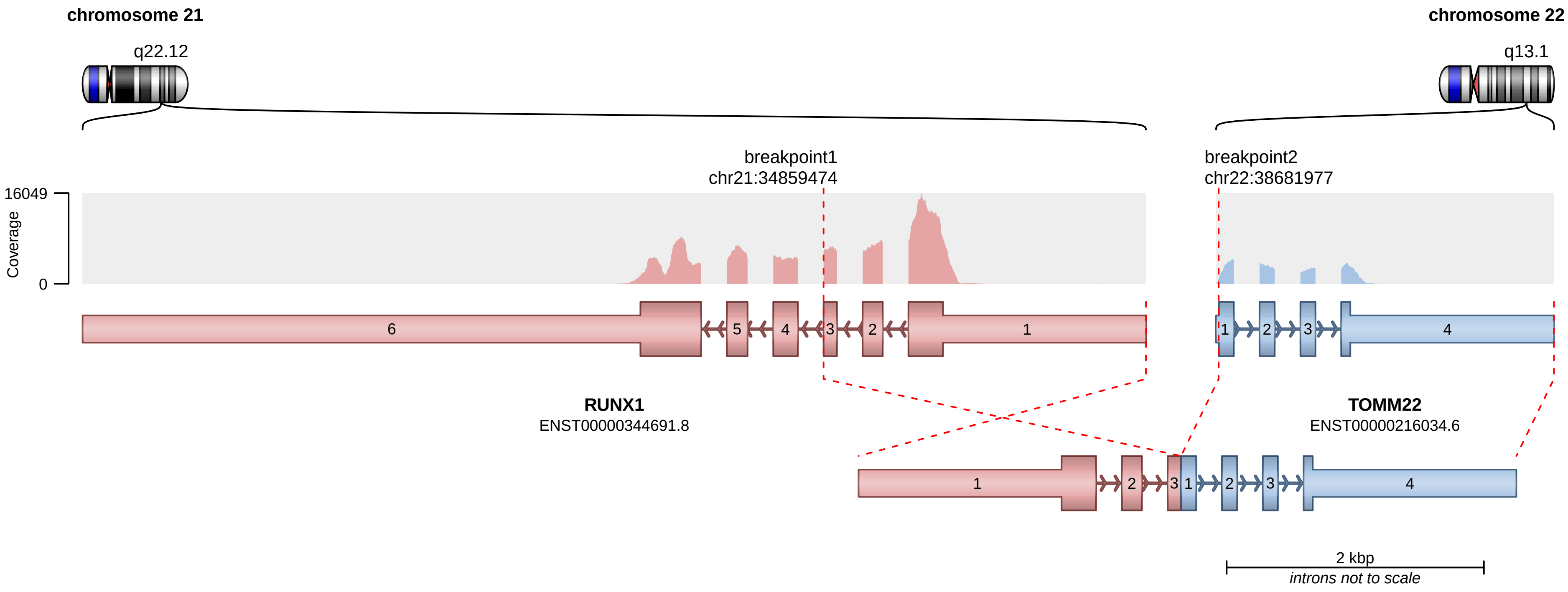


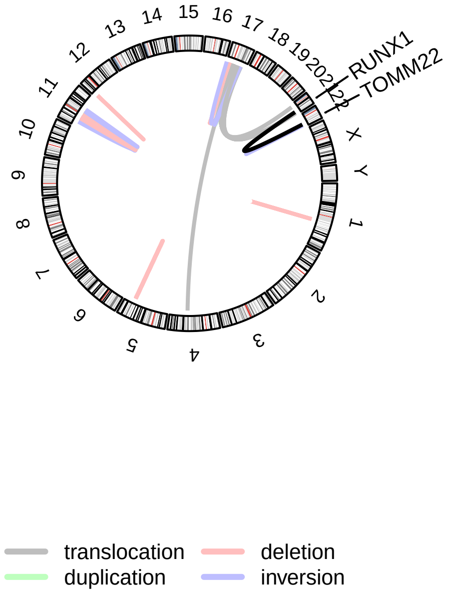




SUPPORTING READ COUNT

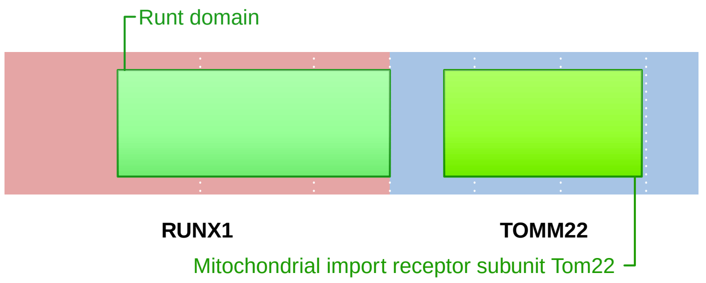
Split reads = 45
Discordant mates = 0





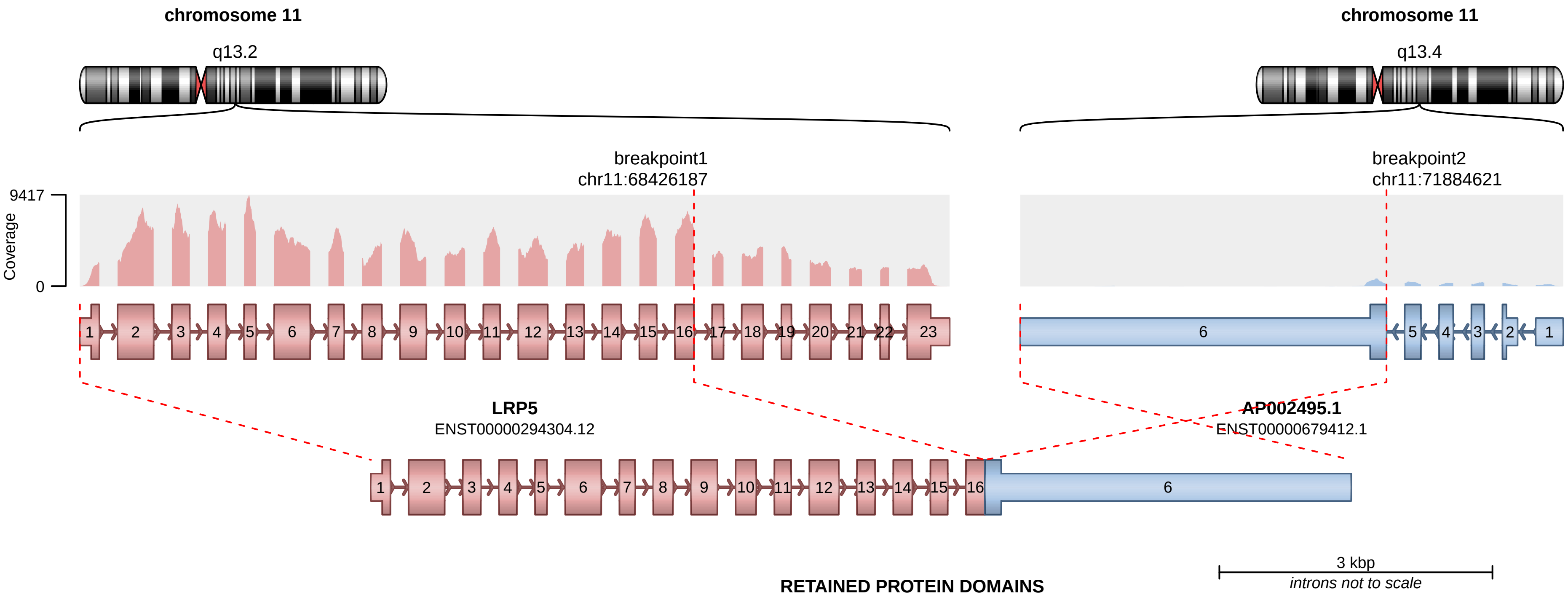
RETAINED PROTEIN DOMAINS

reading frame unclear

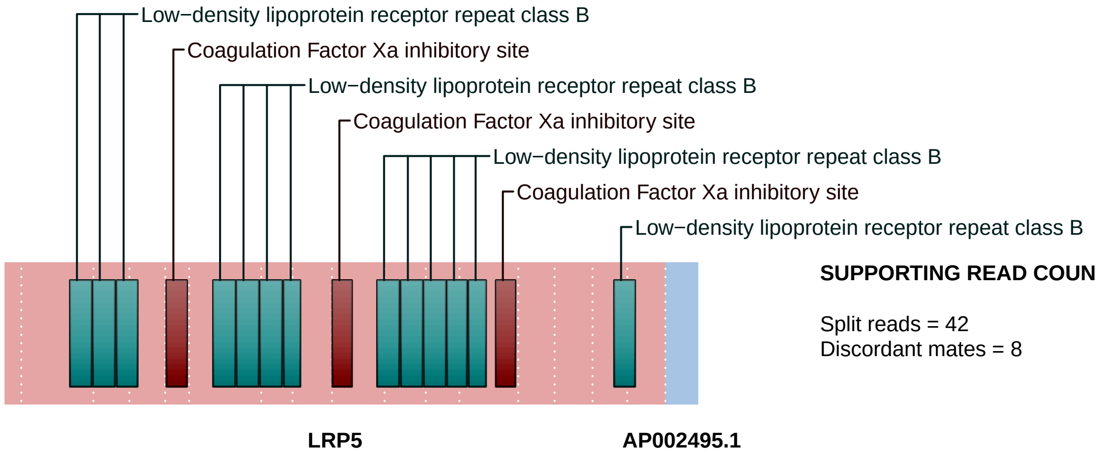


SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 0

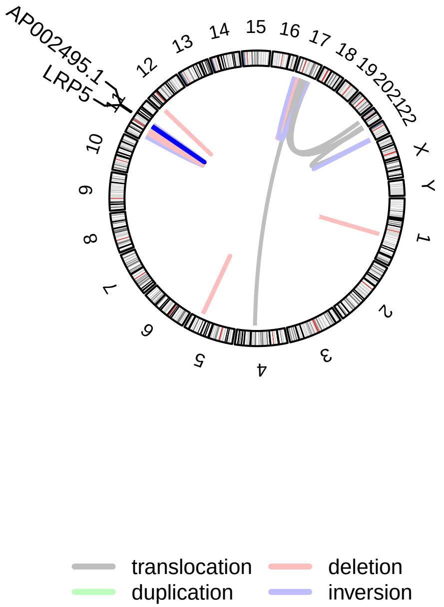


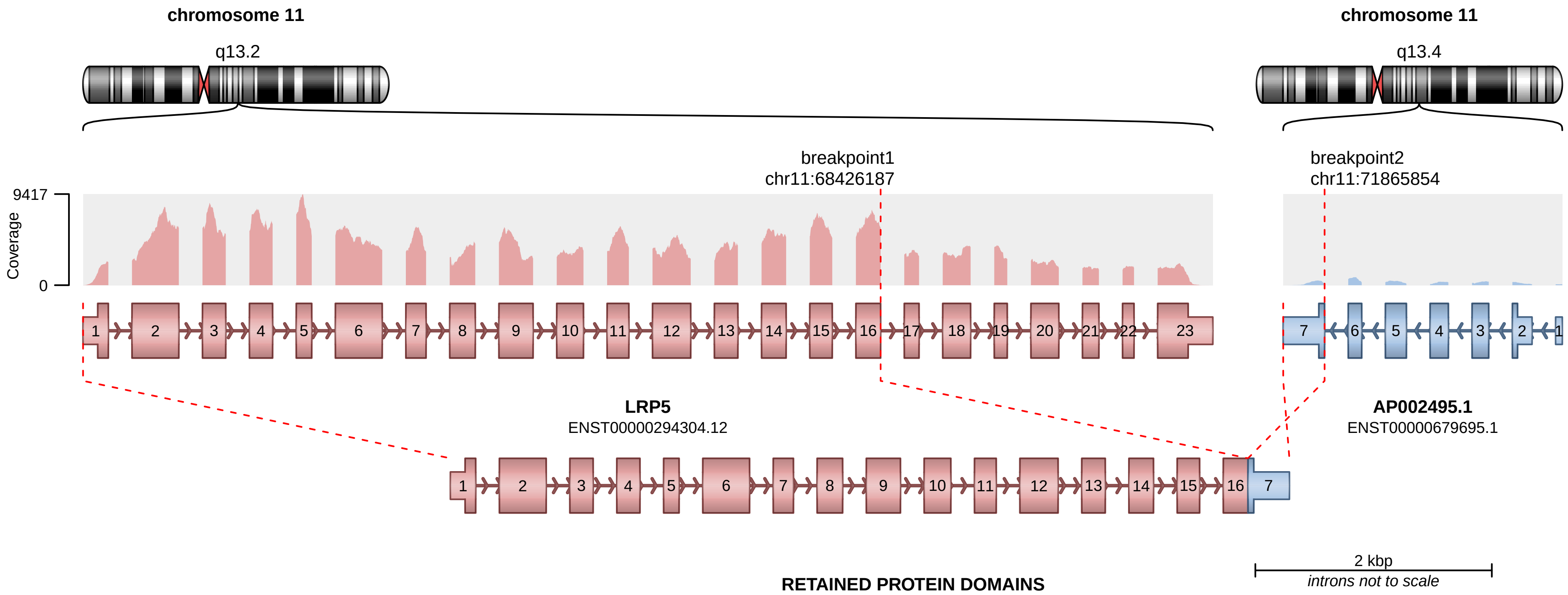
RETAINED PROTEIN DOMAINS
reading frame unclear



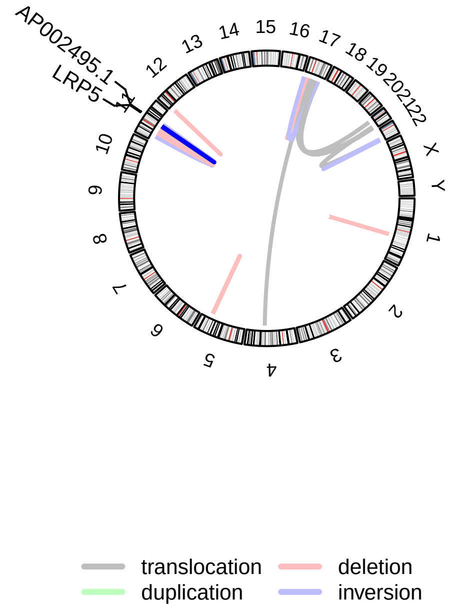
SUPPORTING READ COUNT

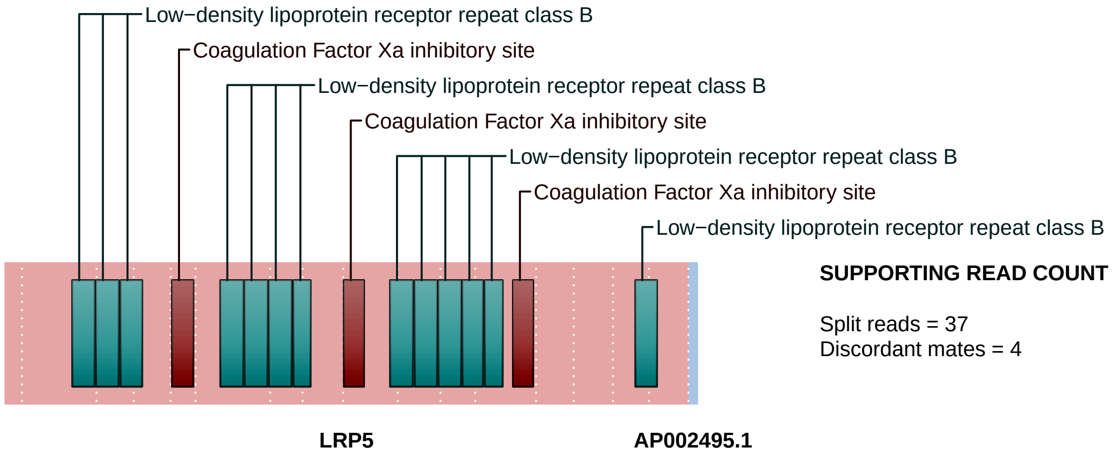
Split reads = 42
Discordant mates = 8





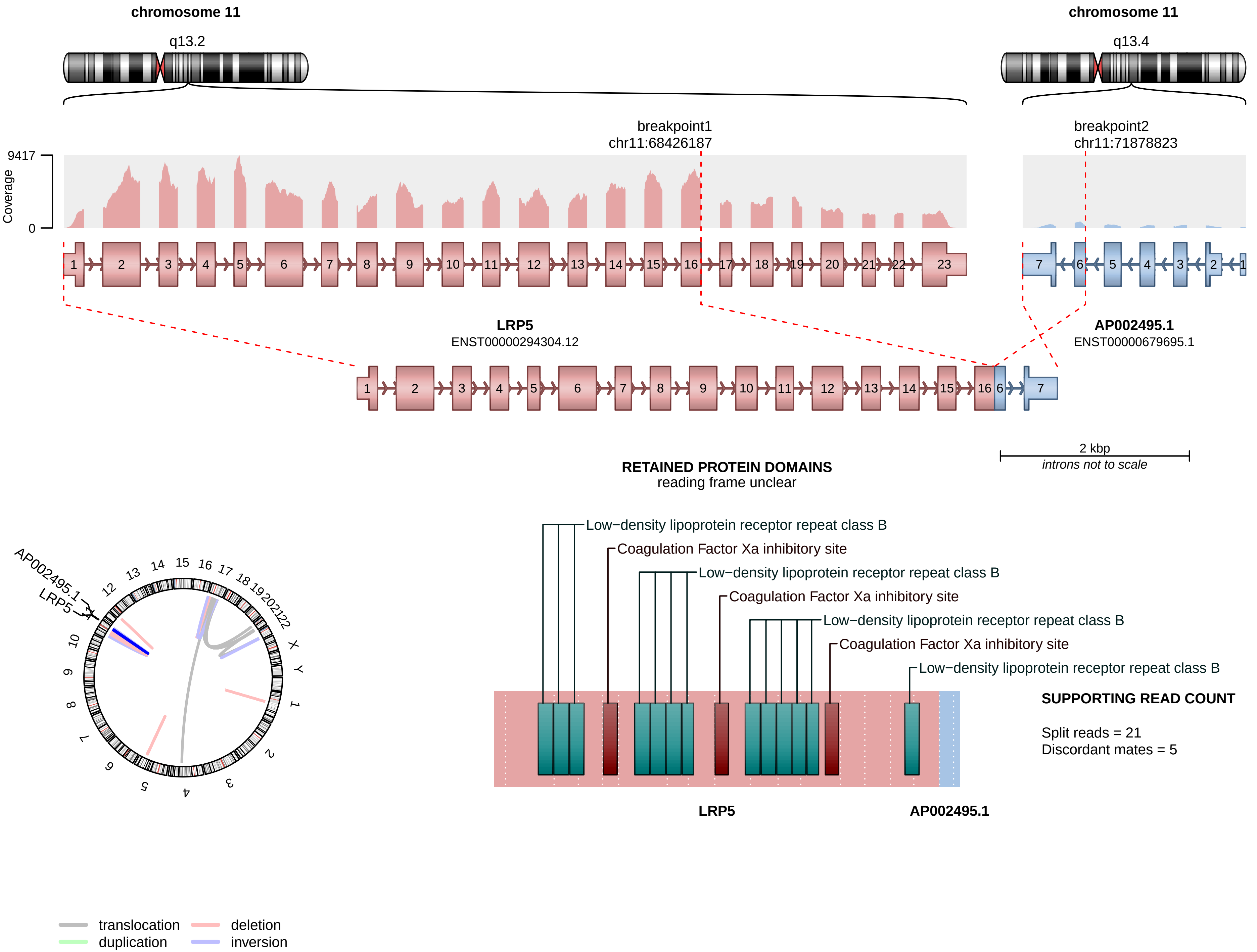
RETAINED PROTEIN DOMAINS
reading frame unclear





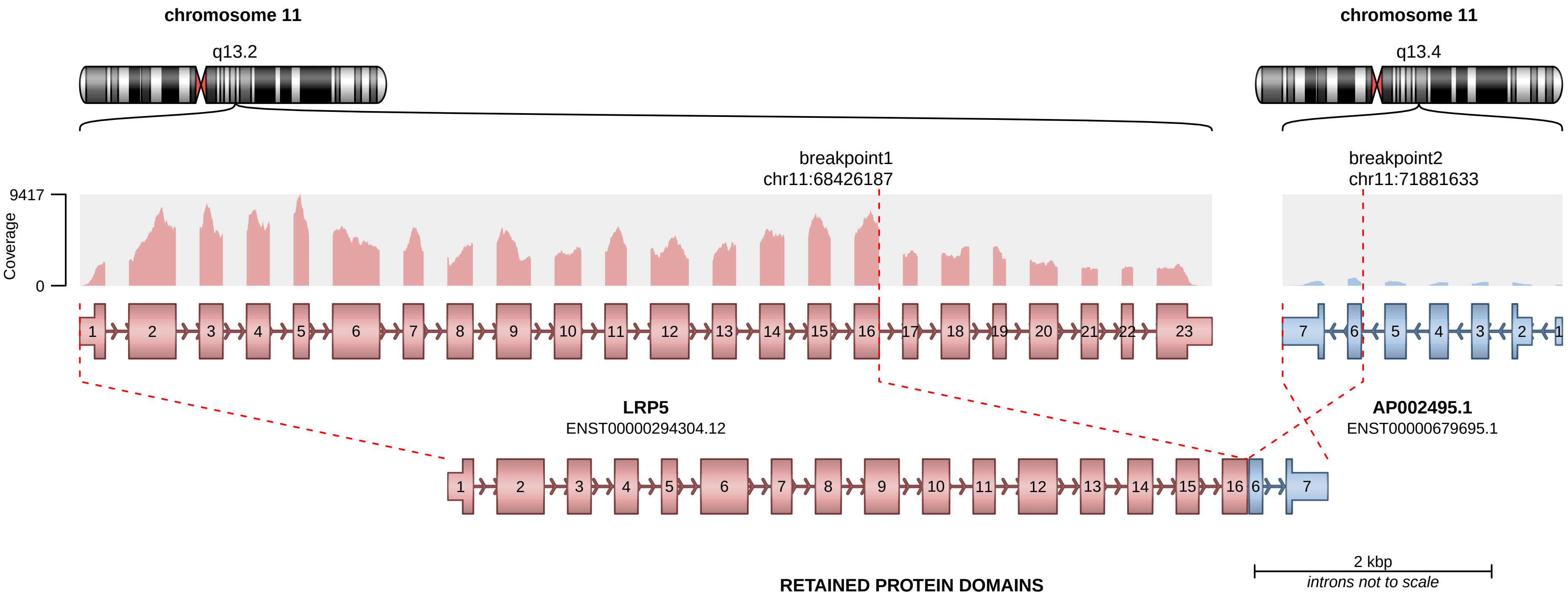
SUPPORTING READ COUNT

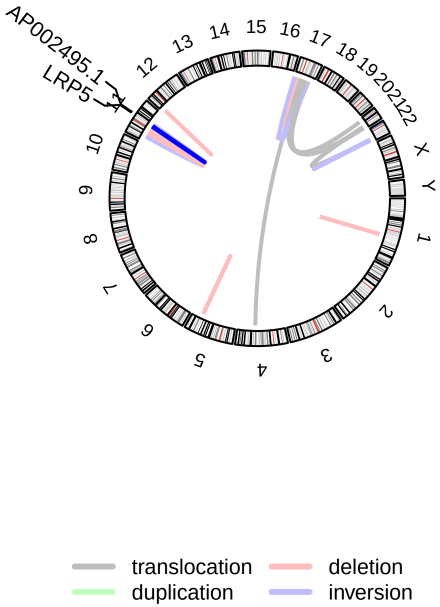
Split reads = 37
Discordant mates = 4



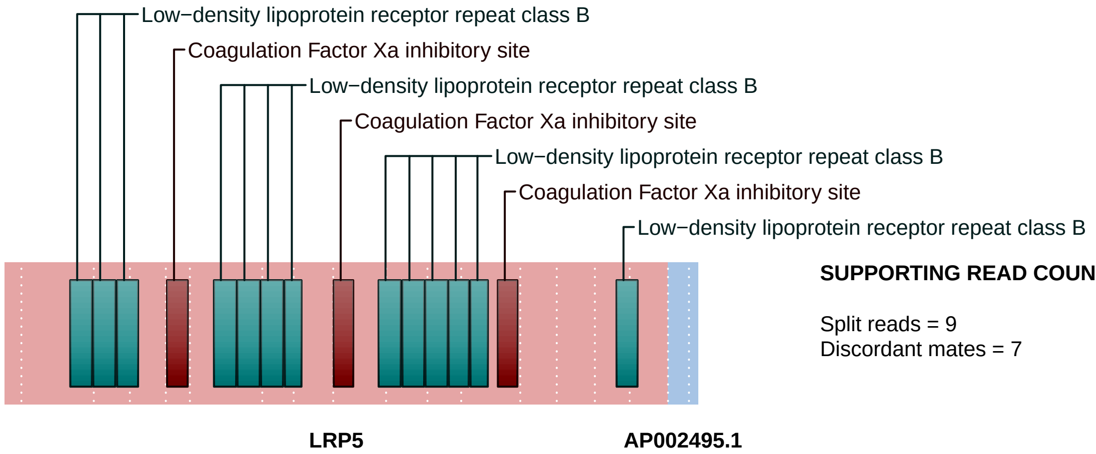
SUPPORTING READ COUNT

Split reads = 21
Discordant mates = 5



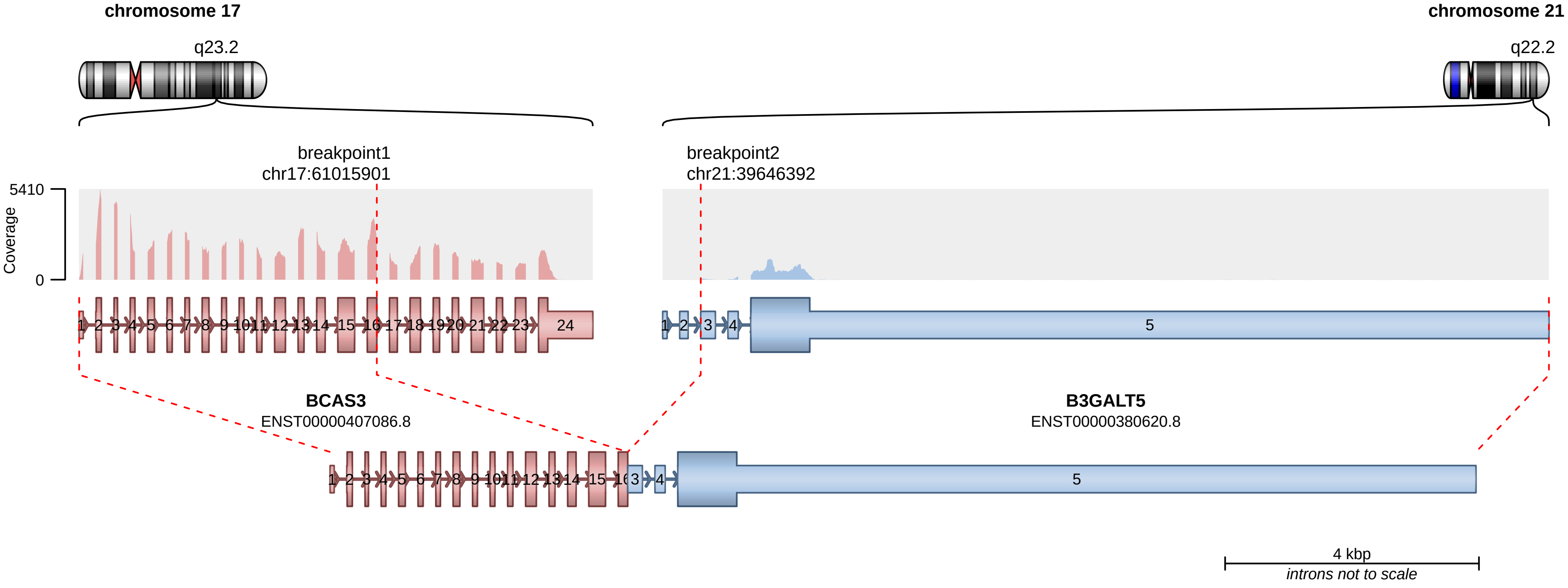


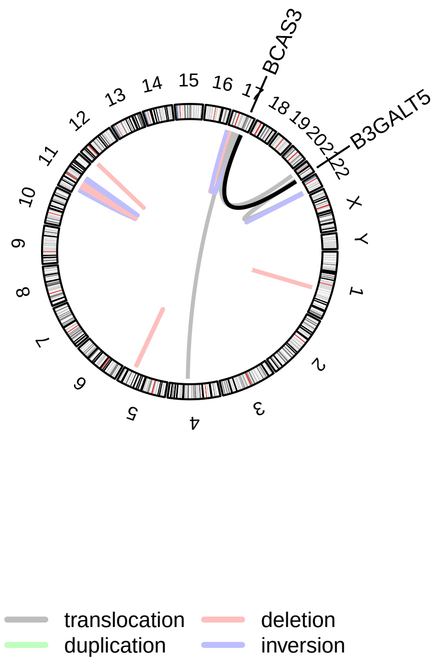
RETAINED PROTEIN DOMAINS
reading frame unclear

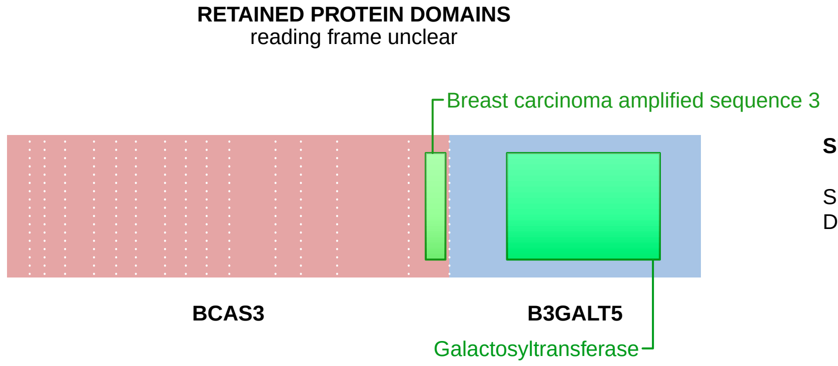


SUPPORTING READ COUNT

Split reads = 9
Discordant mates = 7

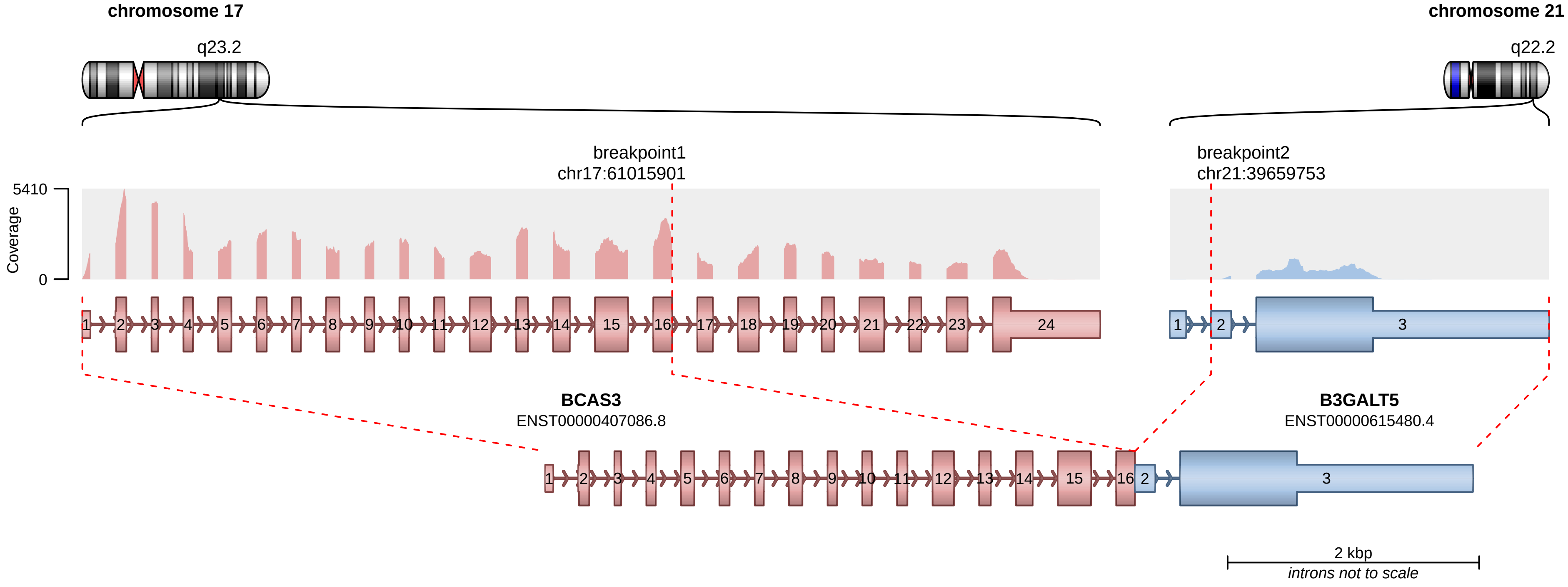


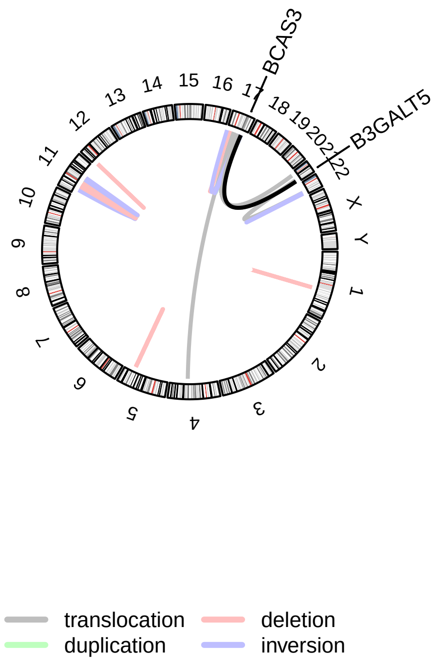




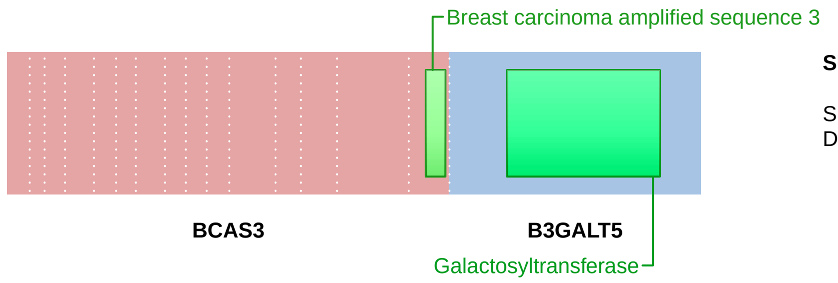
SUPPORTING READ COUNT

Split reads = 42
Discordant mates = 2



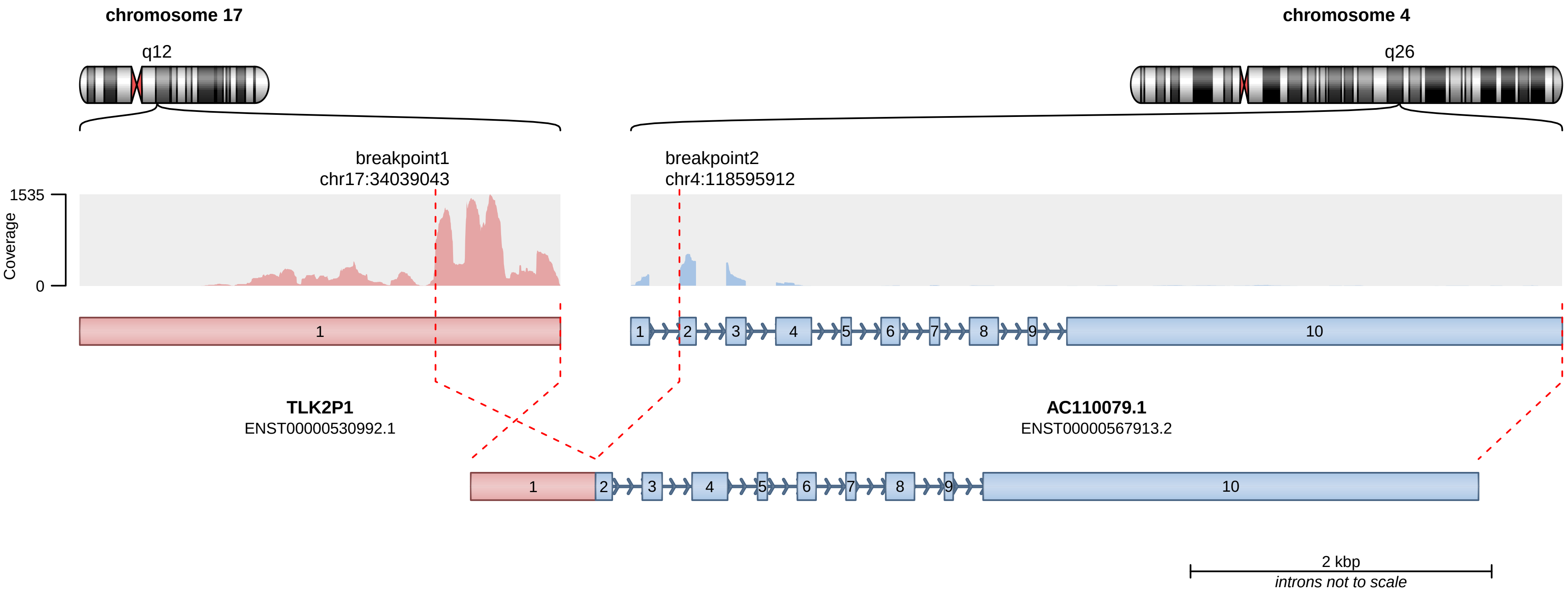


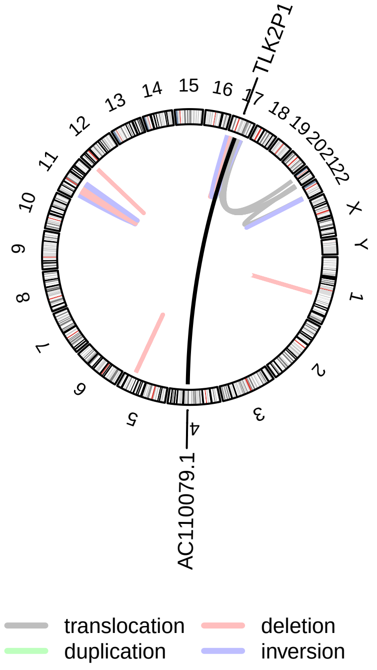
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 0

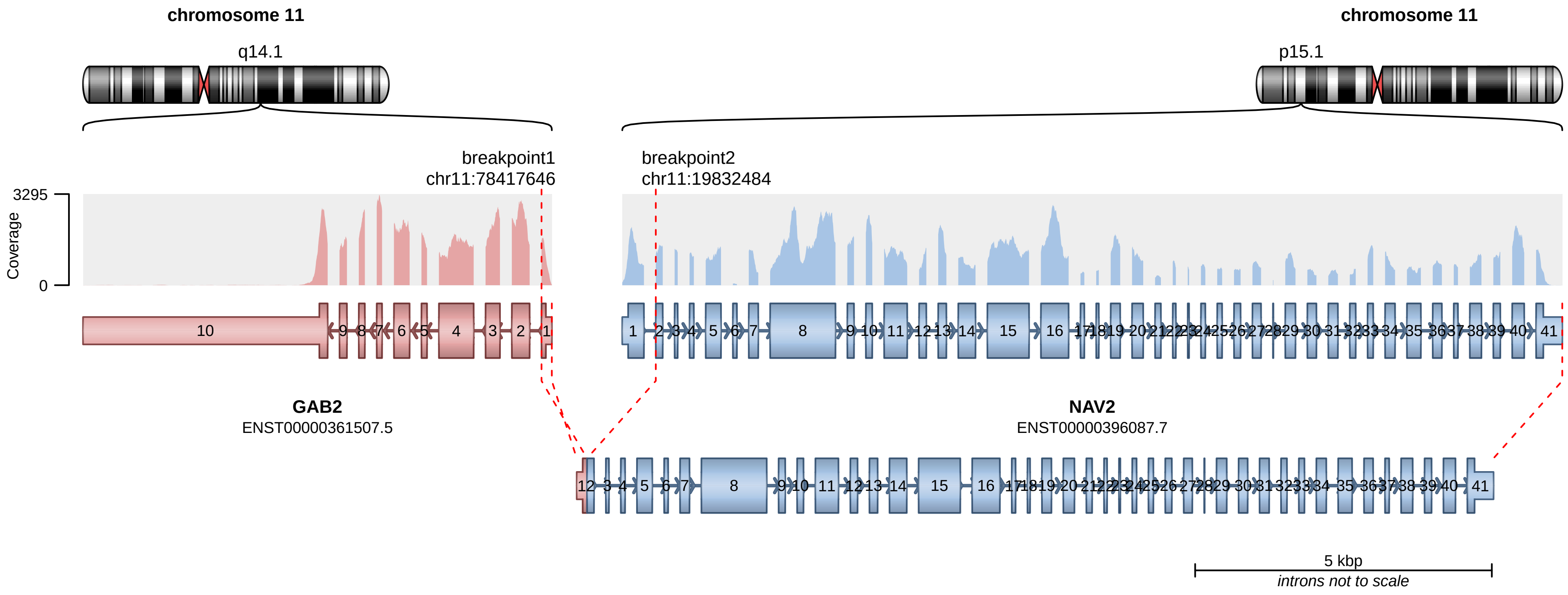


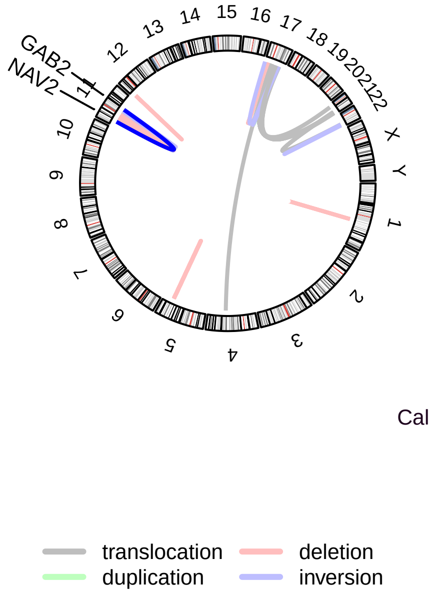


Genes are not protein−coding.

SUPPORTING READ COUNT

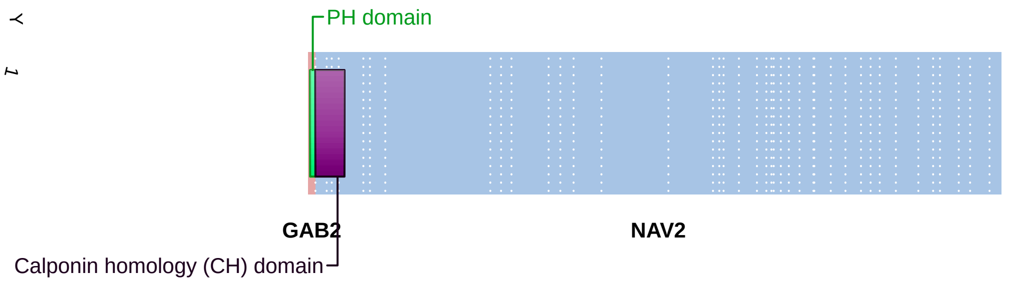
Split reads = 39
Discordant mates = 0





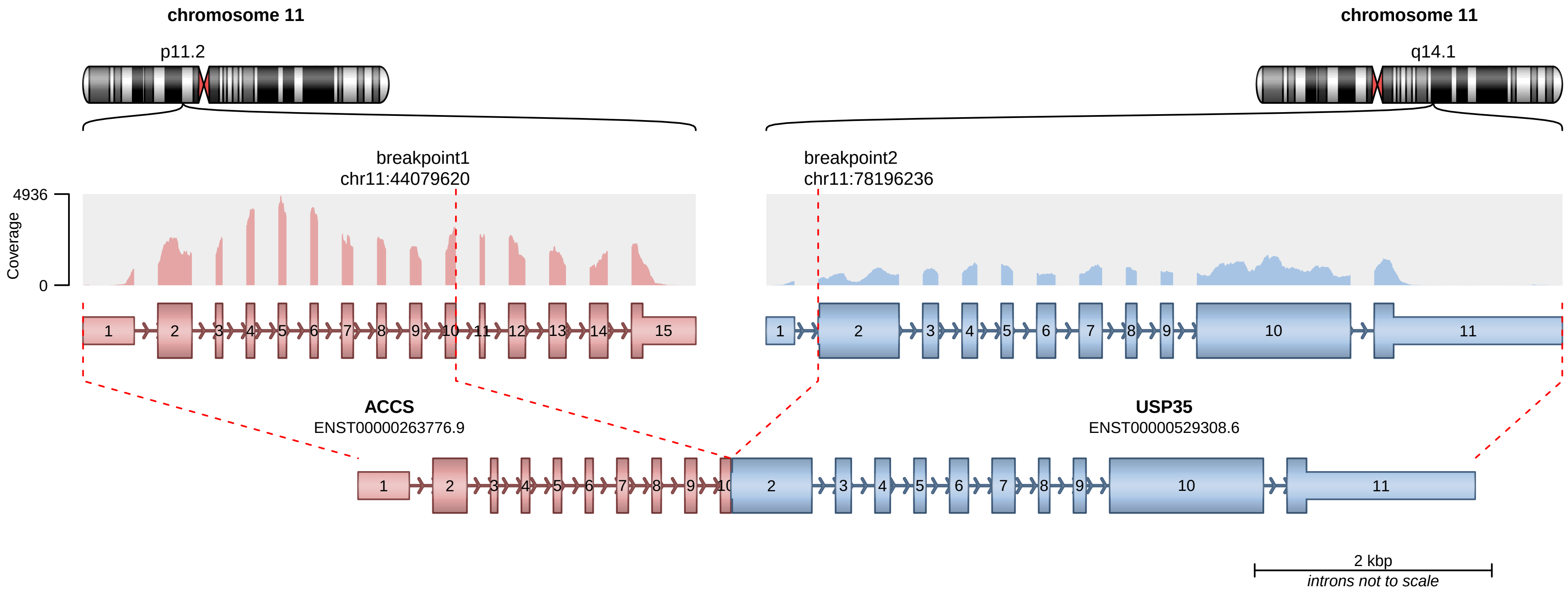
RETAINED PROTEIN DOMAINS

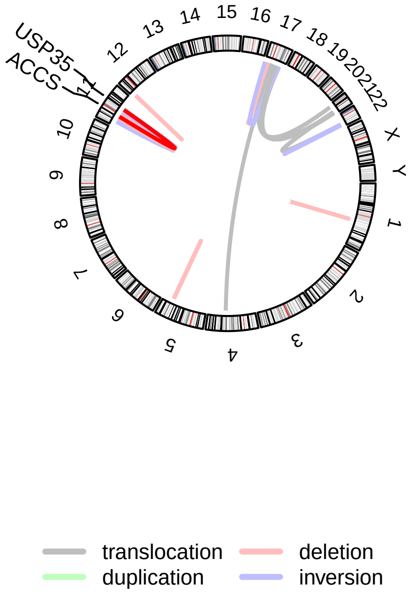
reading frame unclear

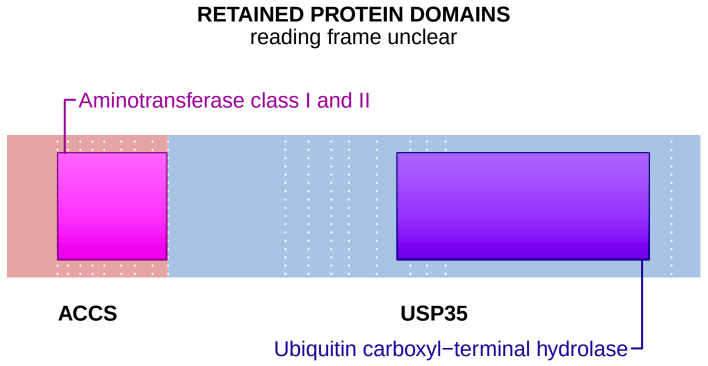


SUPPORTING READ COUNT

Split reads = 25
Discordant mates = 0

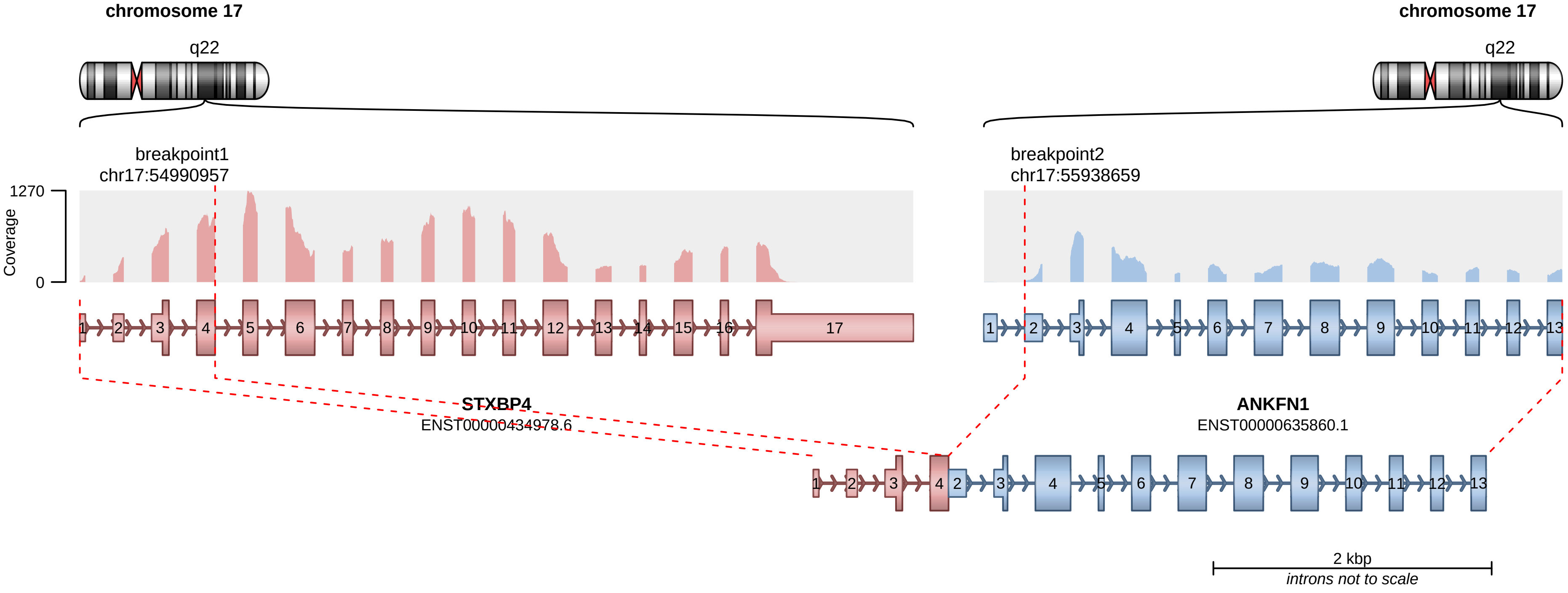


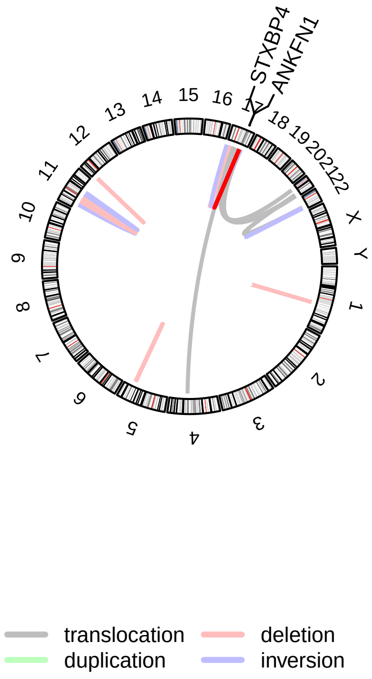




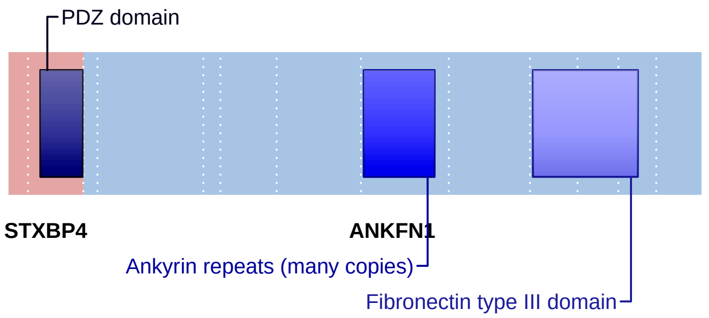
SUPPORTING READ COUNT

Split reads = 20
Discordant mates = 0



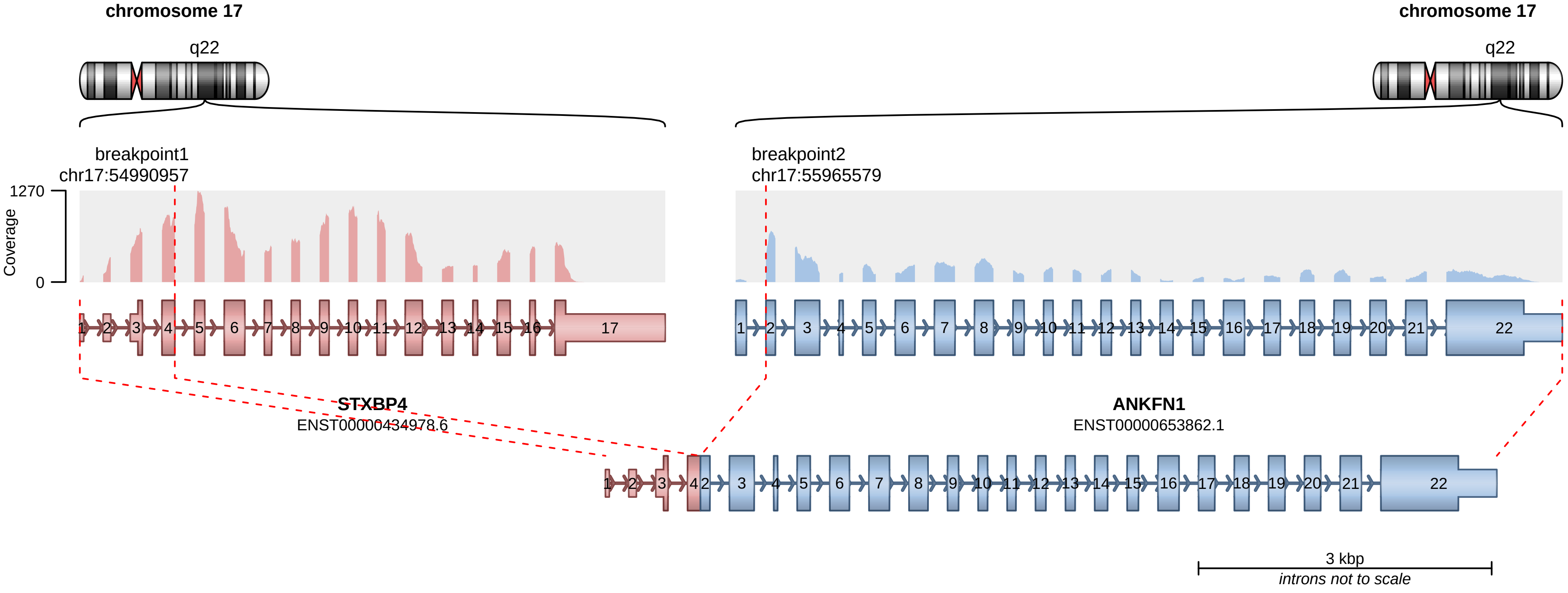


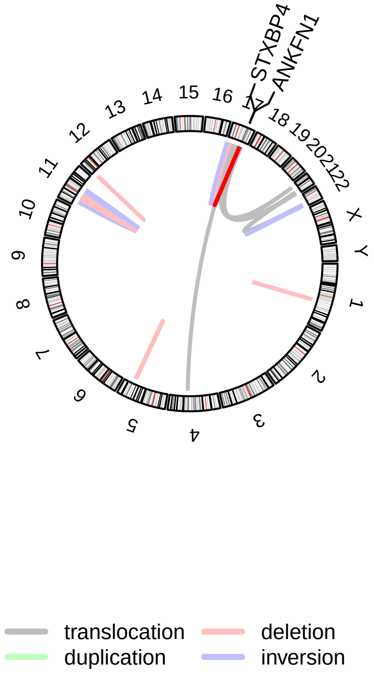
RETAINED PROTEIN DOMAINS
reading frame unclear



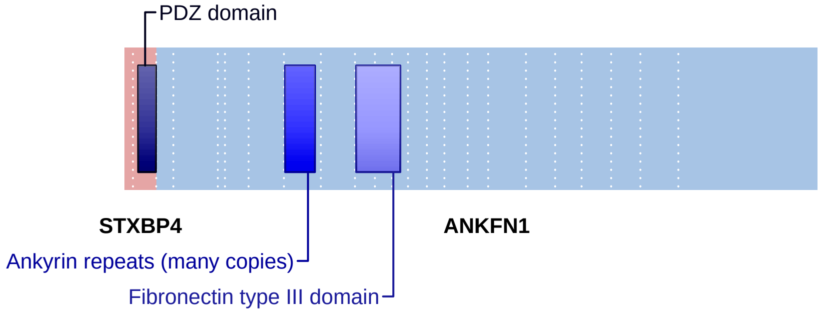
SUPPORTING READ COUNT

Split reads = 19
Discordant mates = 1



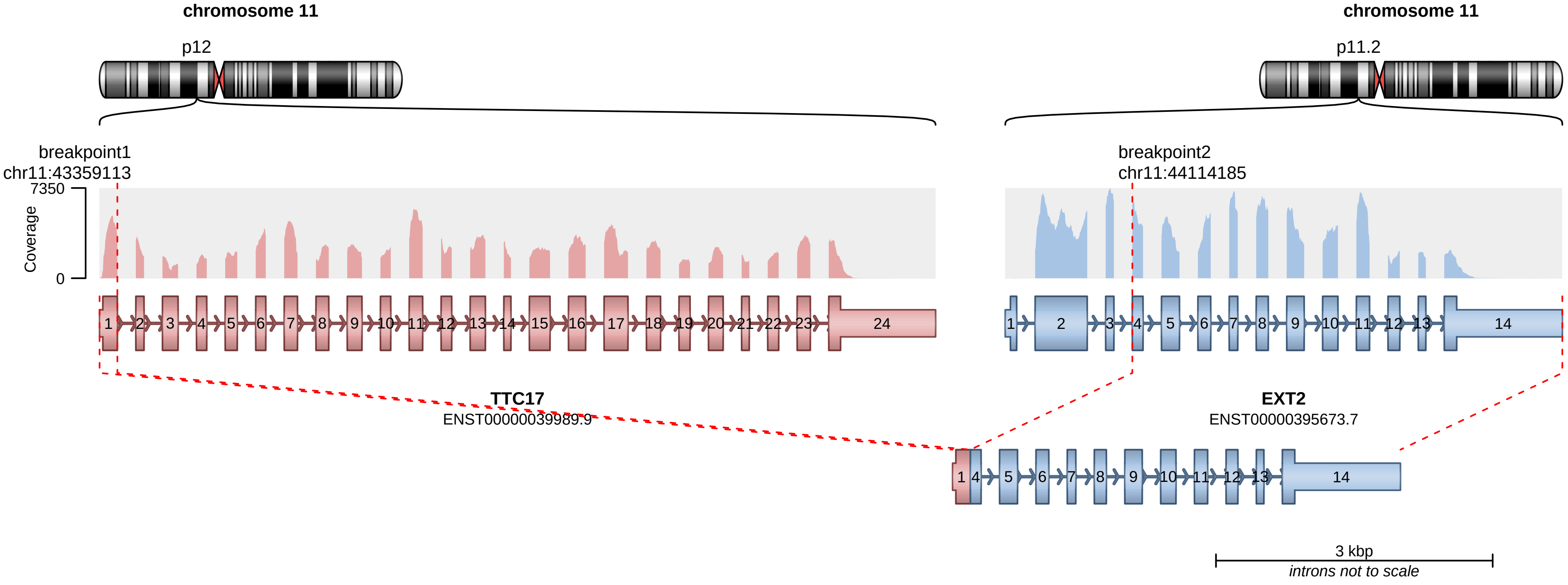


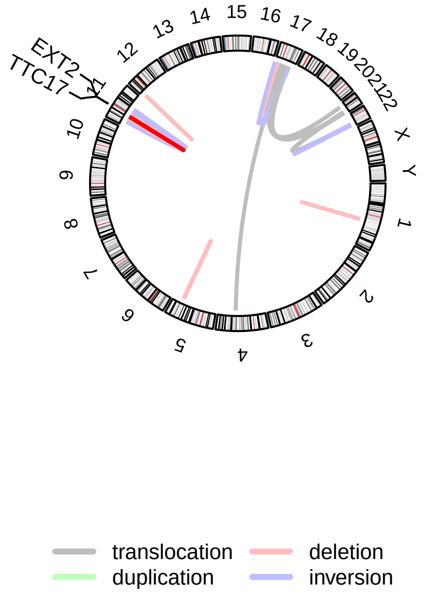
RETAINED PROTEIN DOMAINS
reading frame unclear

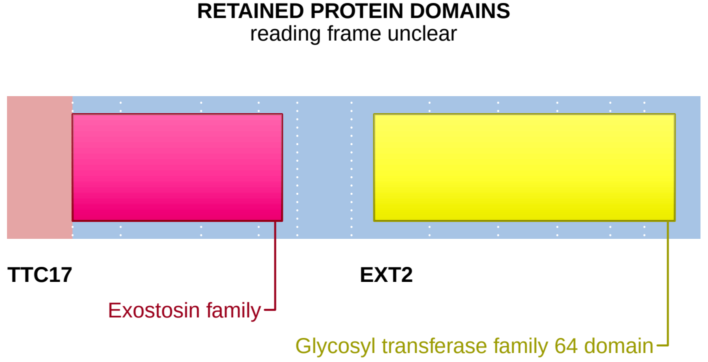


SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 0

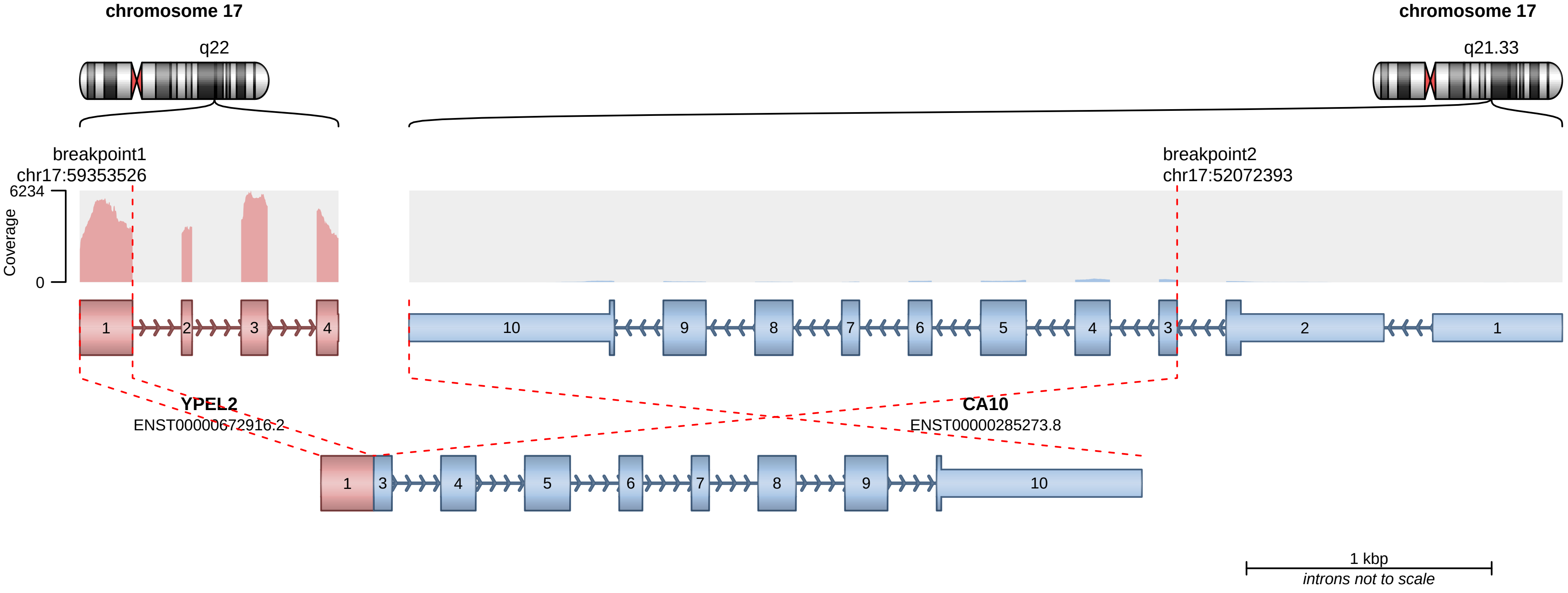


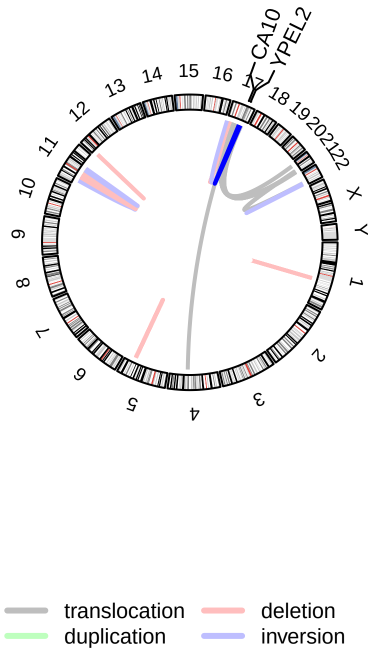




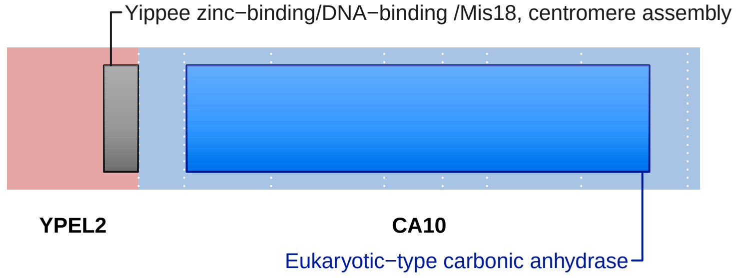
SUPPORTING READ COUNT

Split reads = 18
Discordant mates = 0



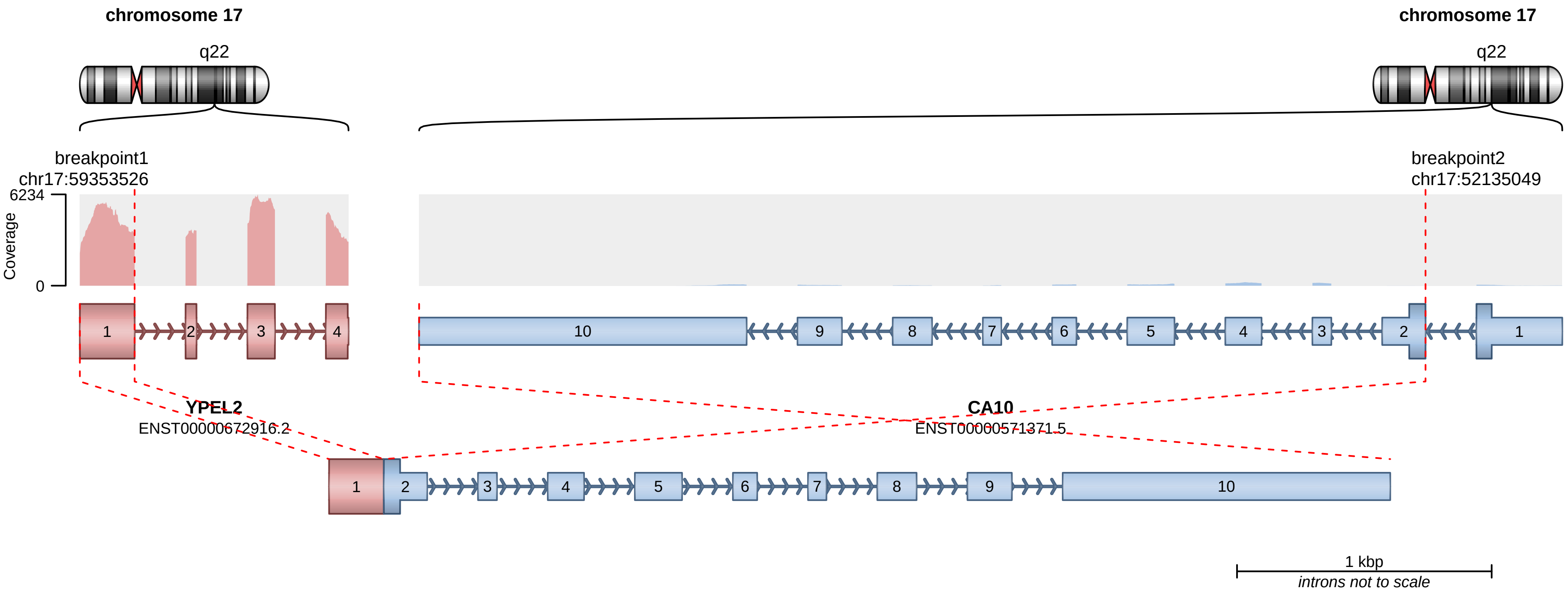


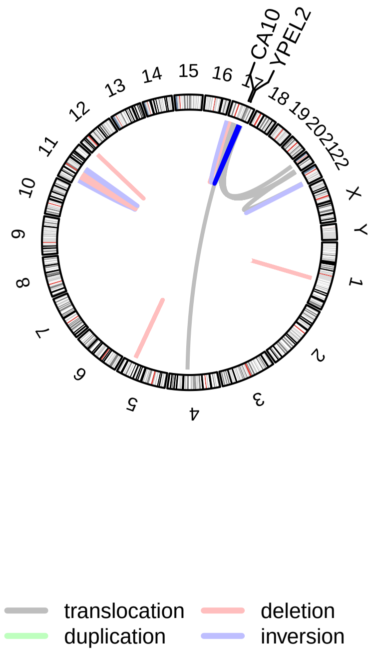
RETAINED PROTEIN DOMAINS
reading frame unclear

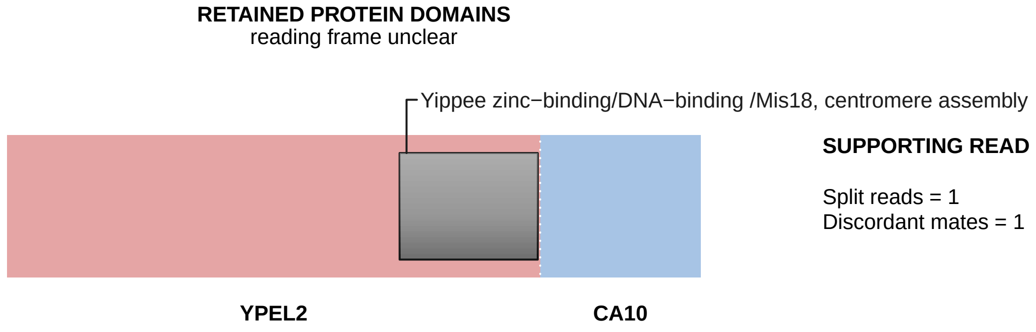


SUPPORTING READ COUNT

Split reads = 17
Discordant mates = 1

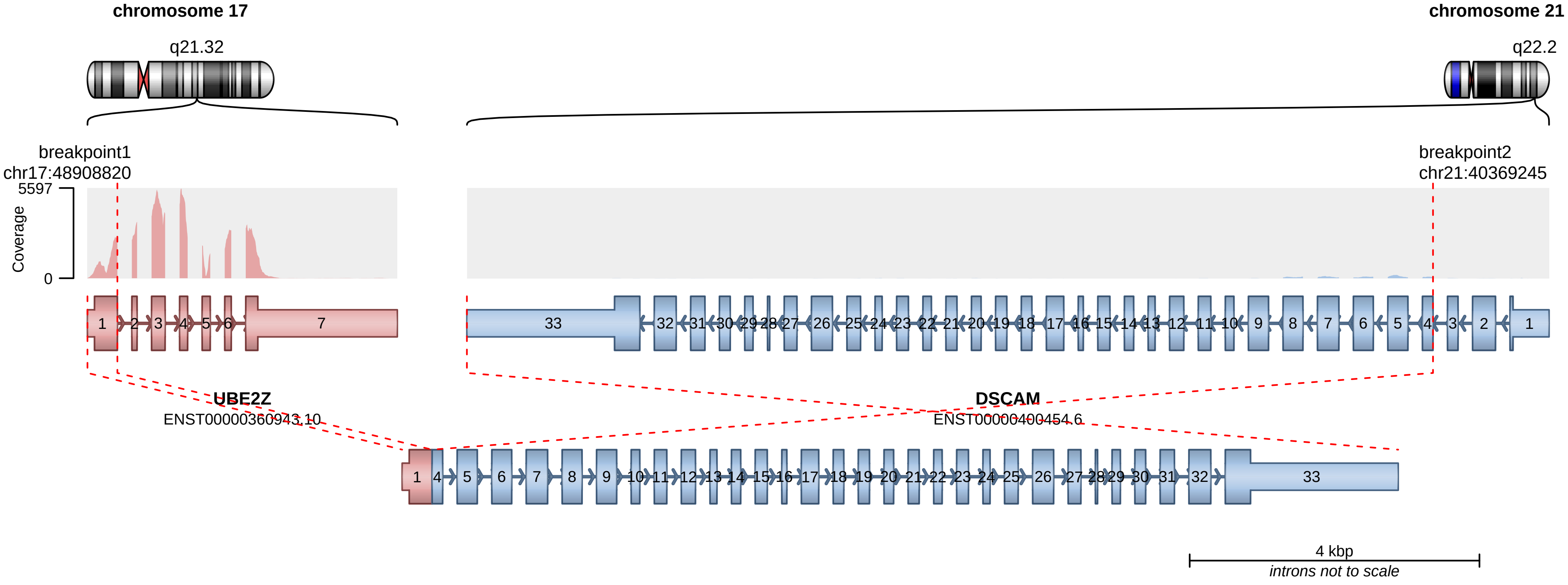


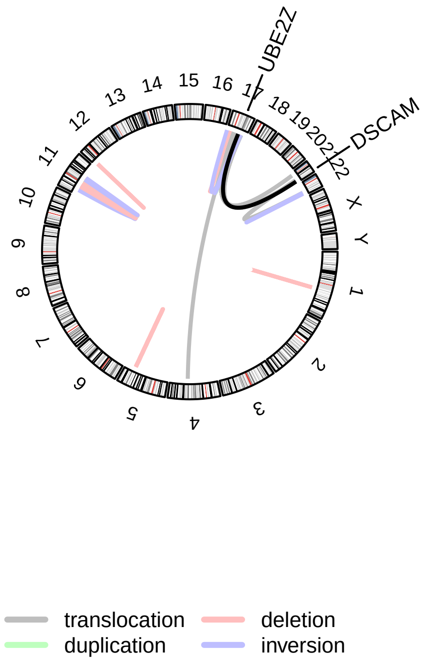




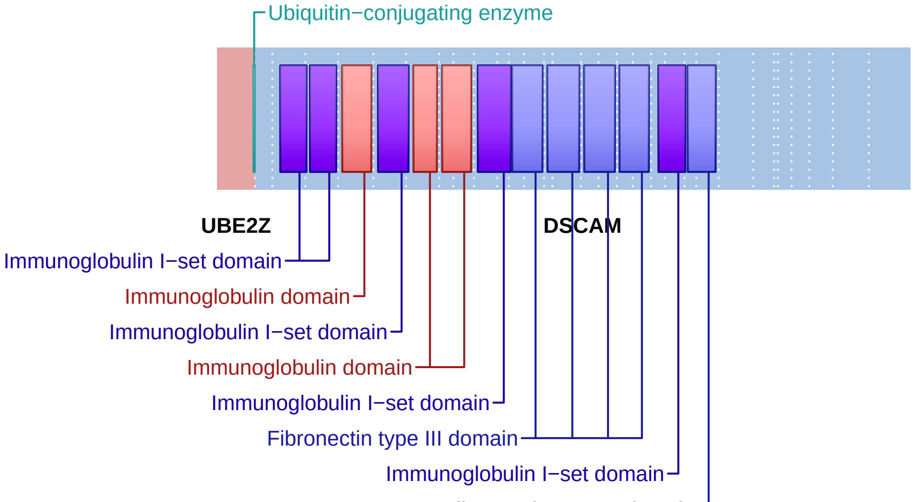
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1



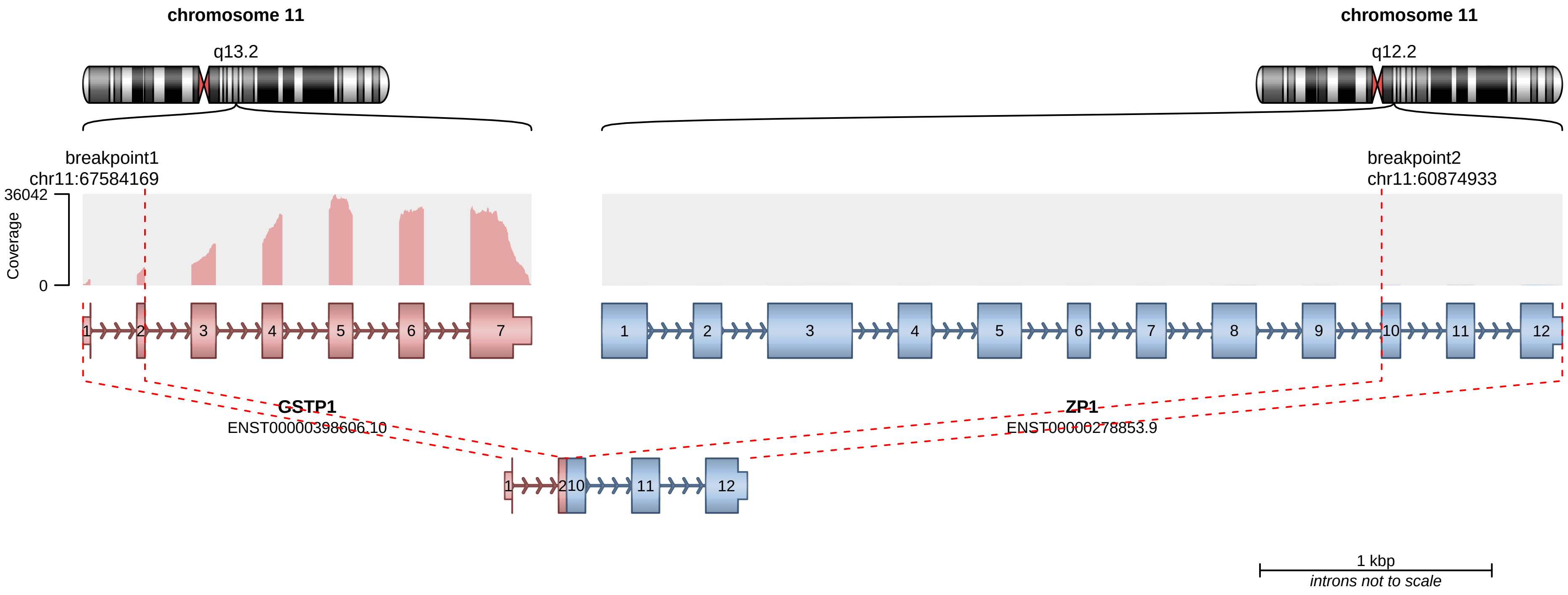


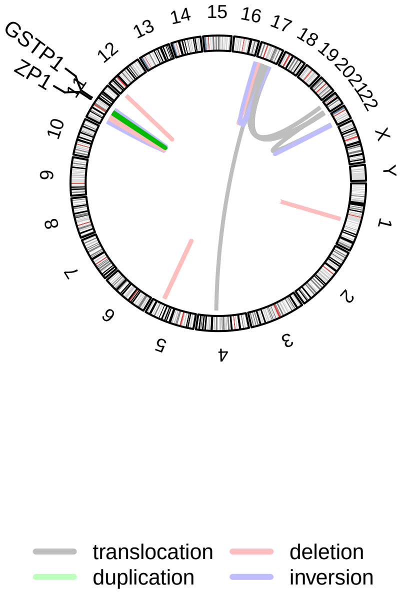
RETAINED PROTEIN DOMAINS
reading frame unclear

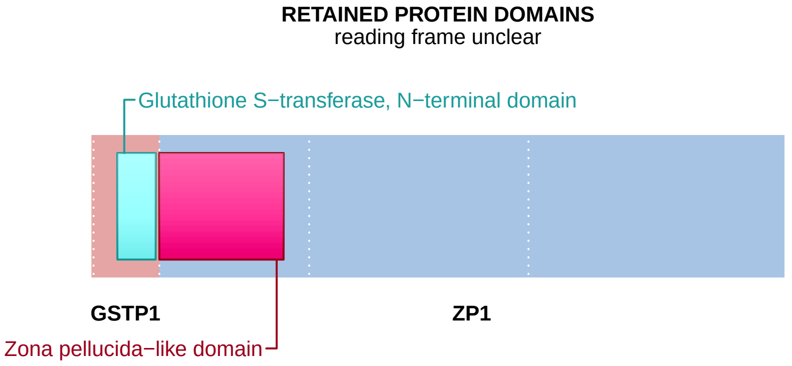


SUPPORTING READ COUNT

Split reads = 16
Discordant mates = 0

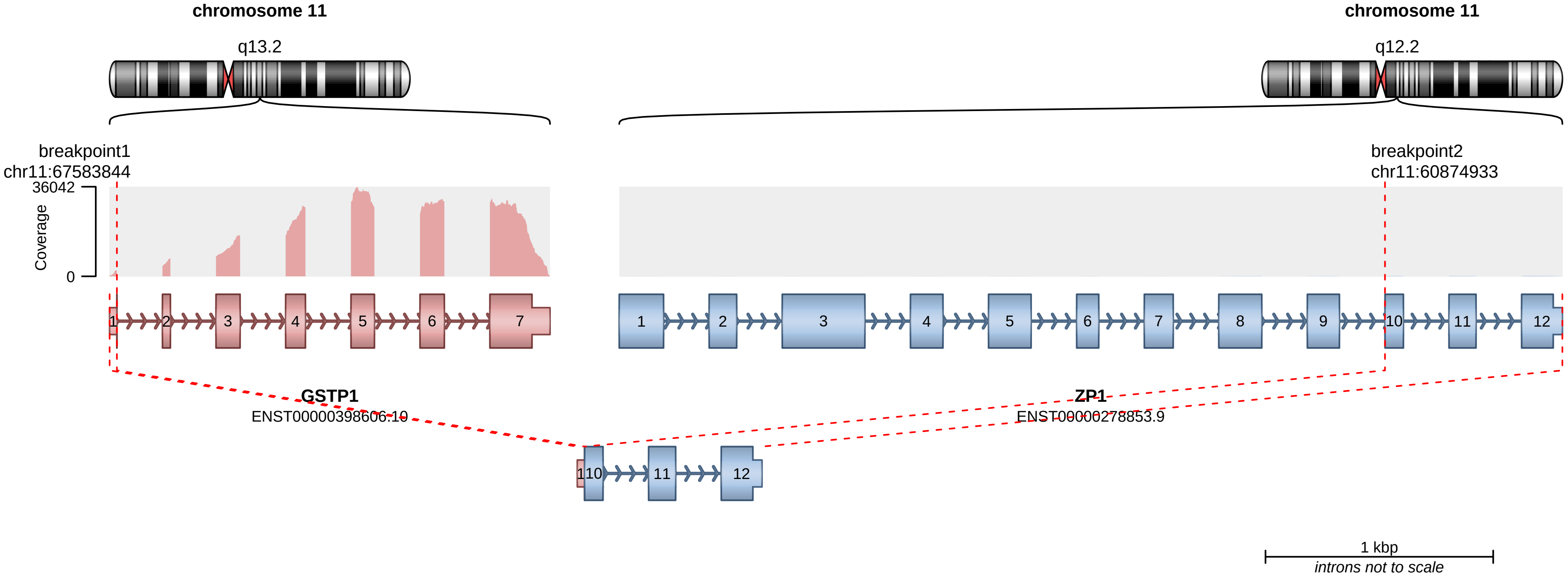


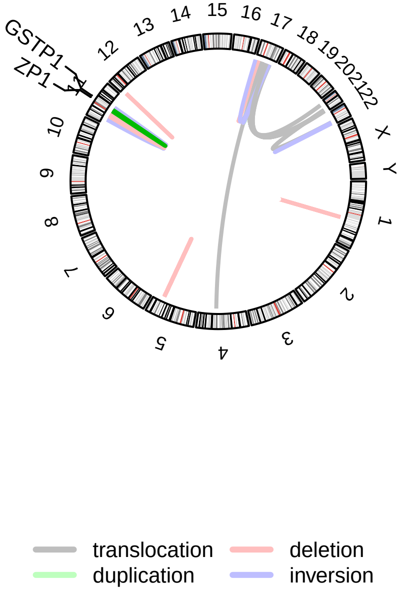


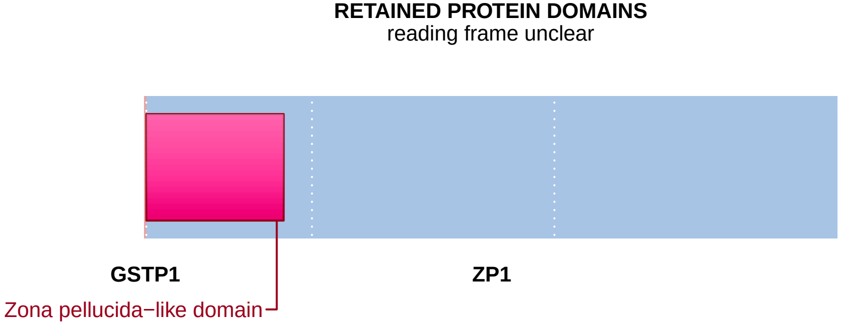


SUPPORTING READ COUNT

Split reads = 13
Discordant mates = 0

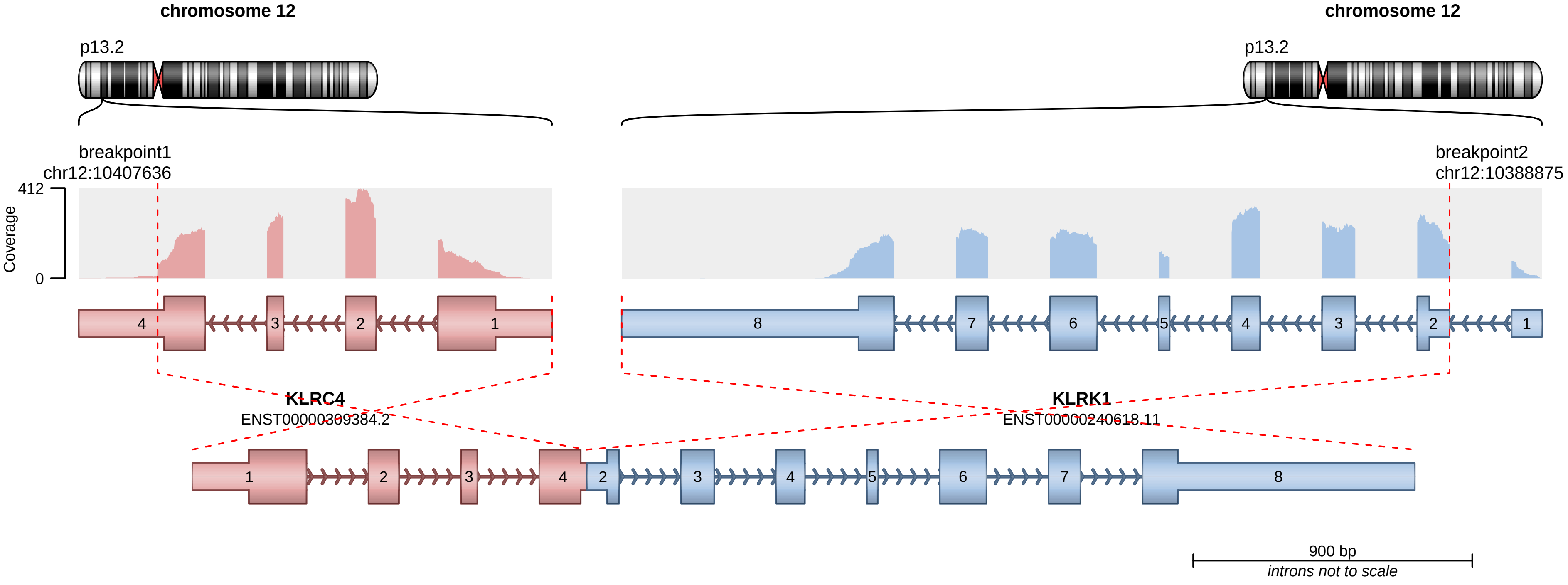


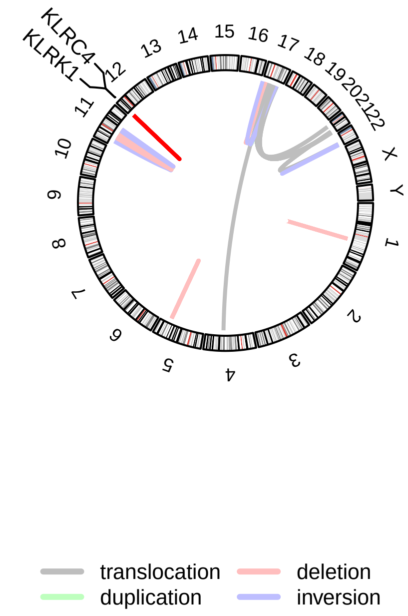




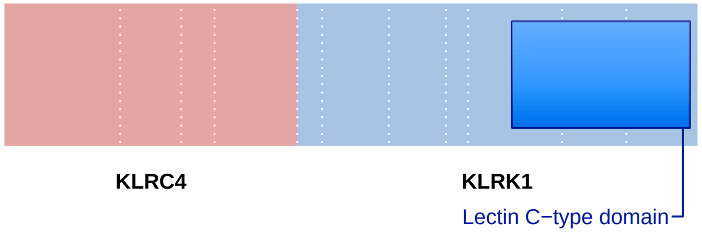
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0



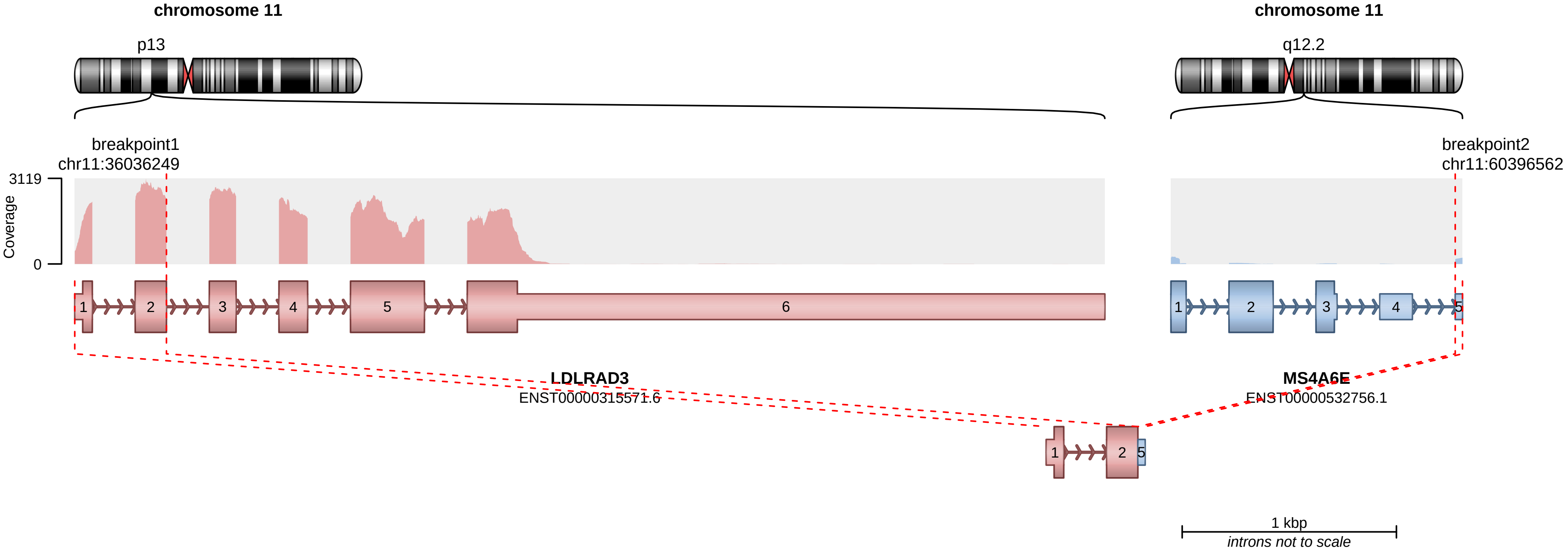


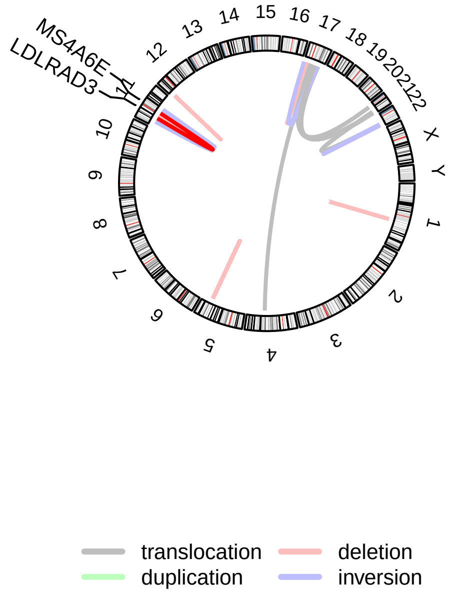
RETAINED PROTEIN DOMAINS
reading frame unclear

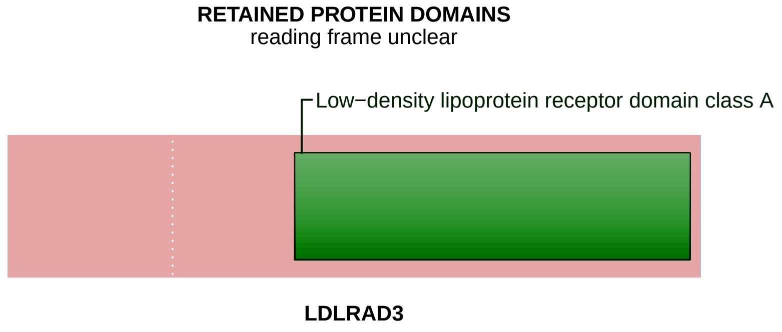


SUPPORTING READ COUNT

Split reads = 13
Discordant mates = 0

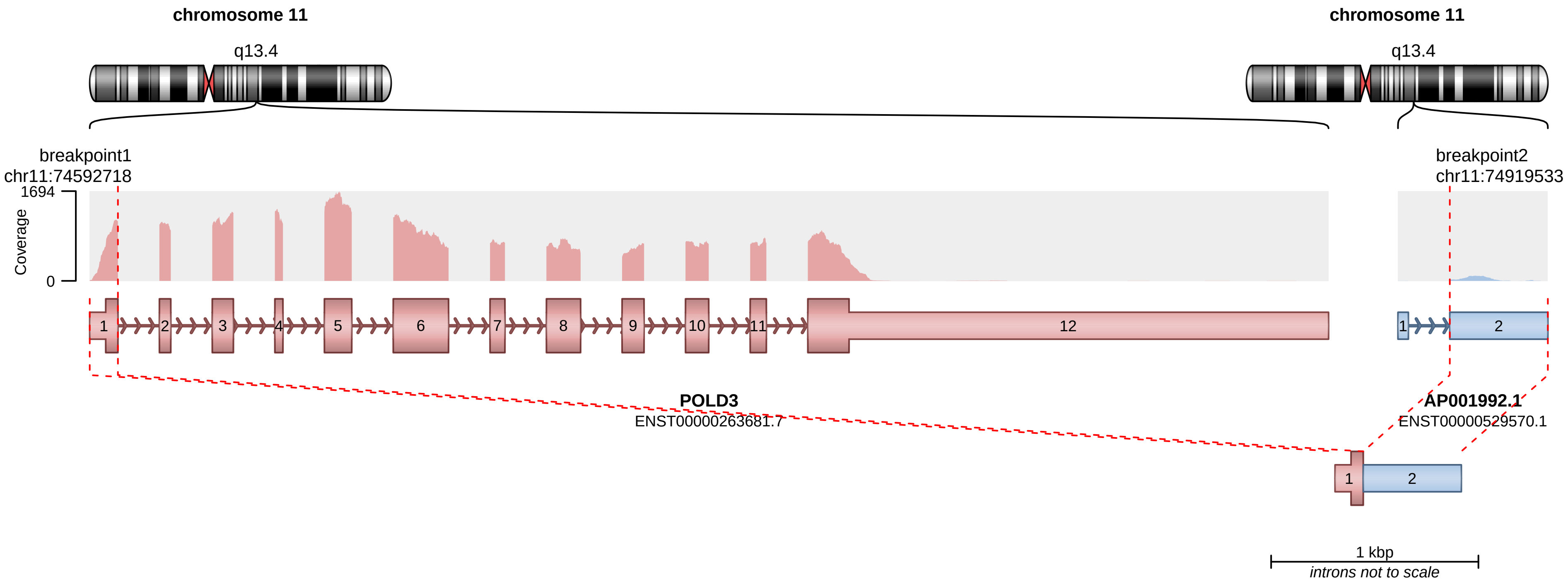


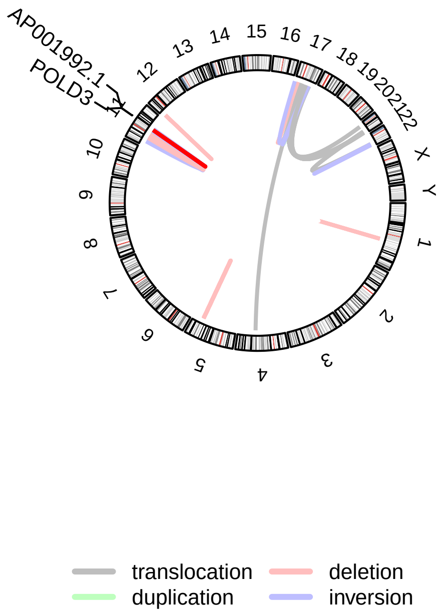




SUPPORTING READ COUNT

Split reads = 13
Discordant mates = 0

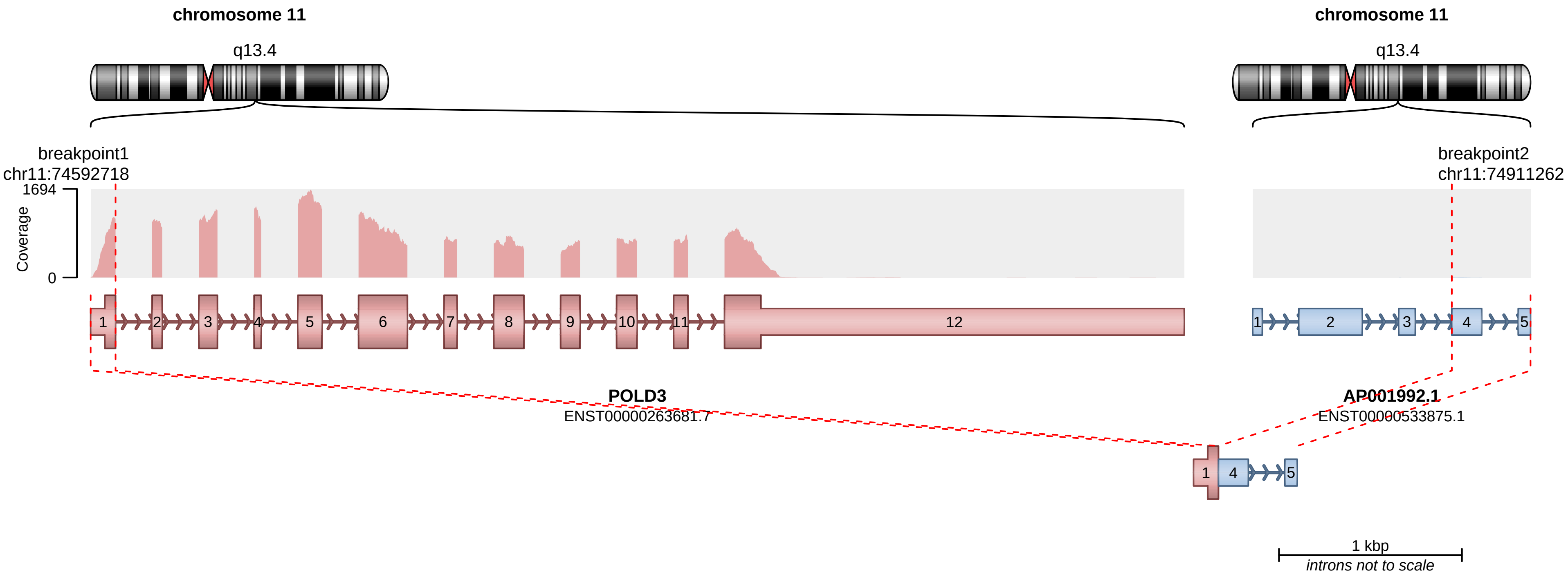


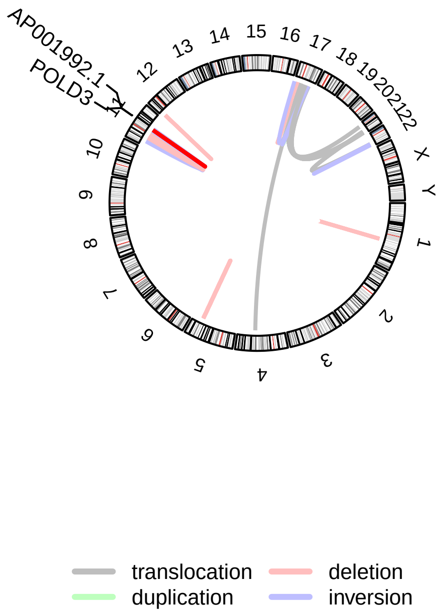


RETAINED PROTEIN DOMAINS
reading frame unclear

SUPPORTING READ COUNT

Split reads = 13
Discordant mates = 0

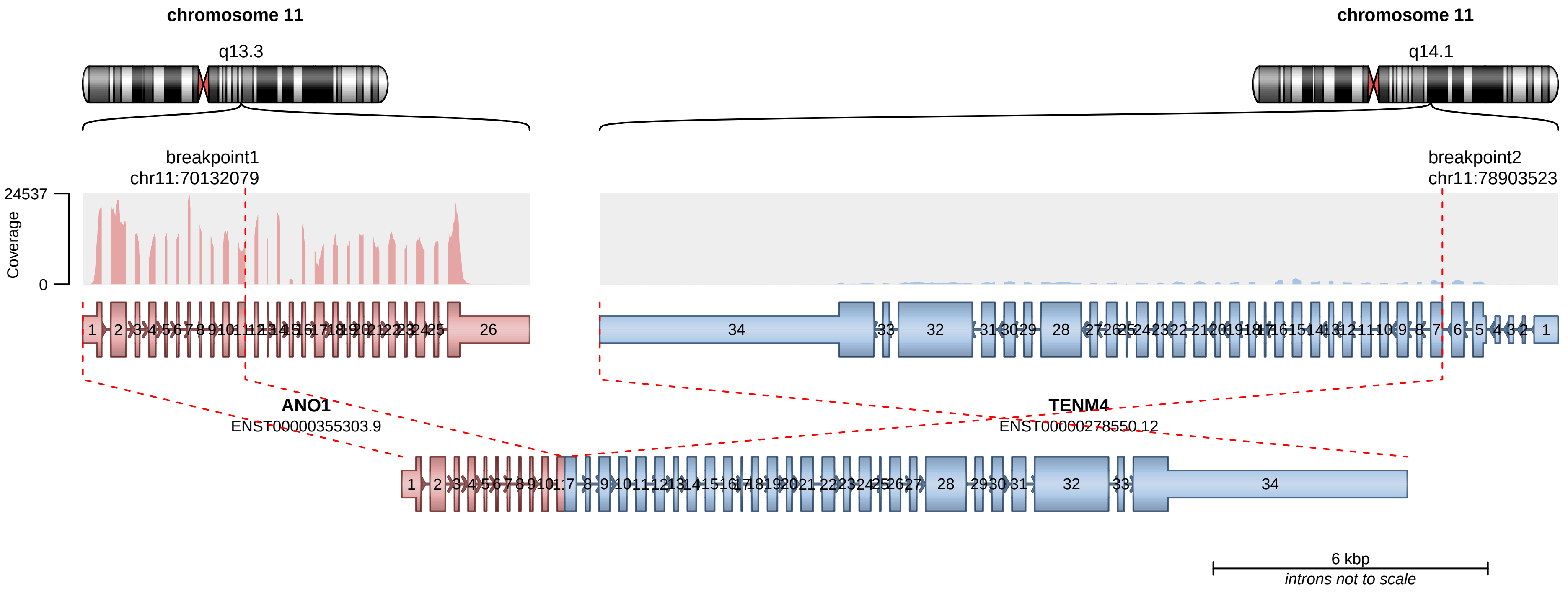


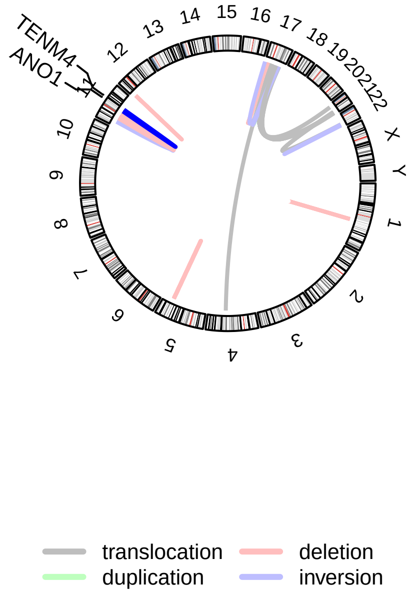


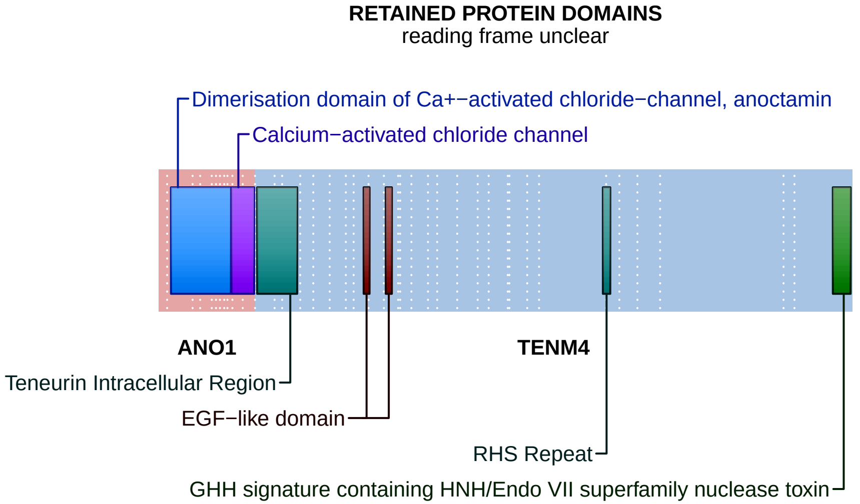
RETAINED PROTEIN DOMAINS
reading frame unclear

SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 0

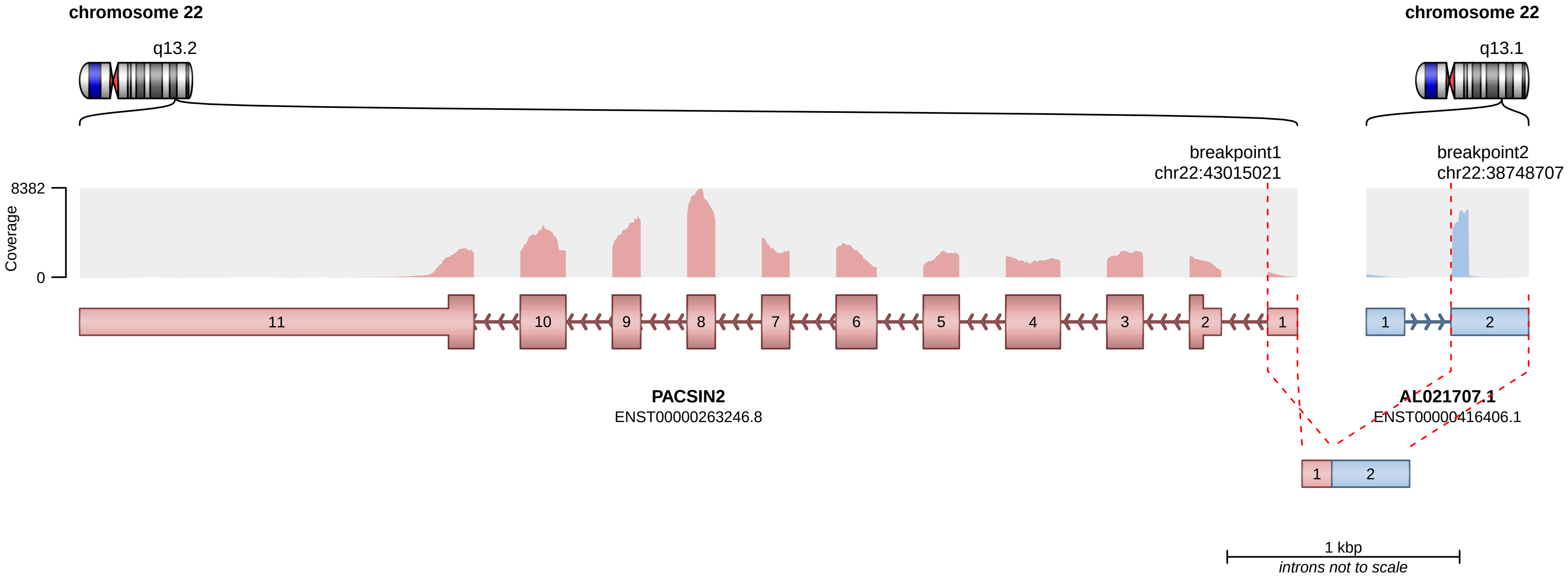


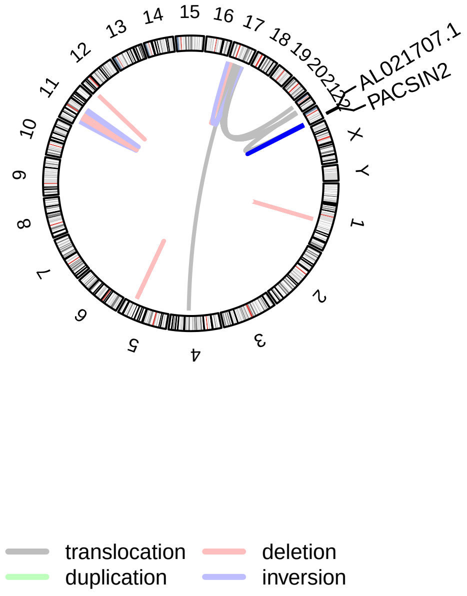




SUPPORTING READ COUNT

Split reads = 9
Discordant mates = 0





No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 9
Discordant mates = 0