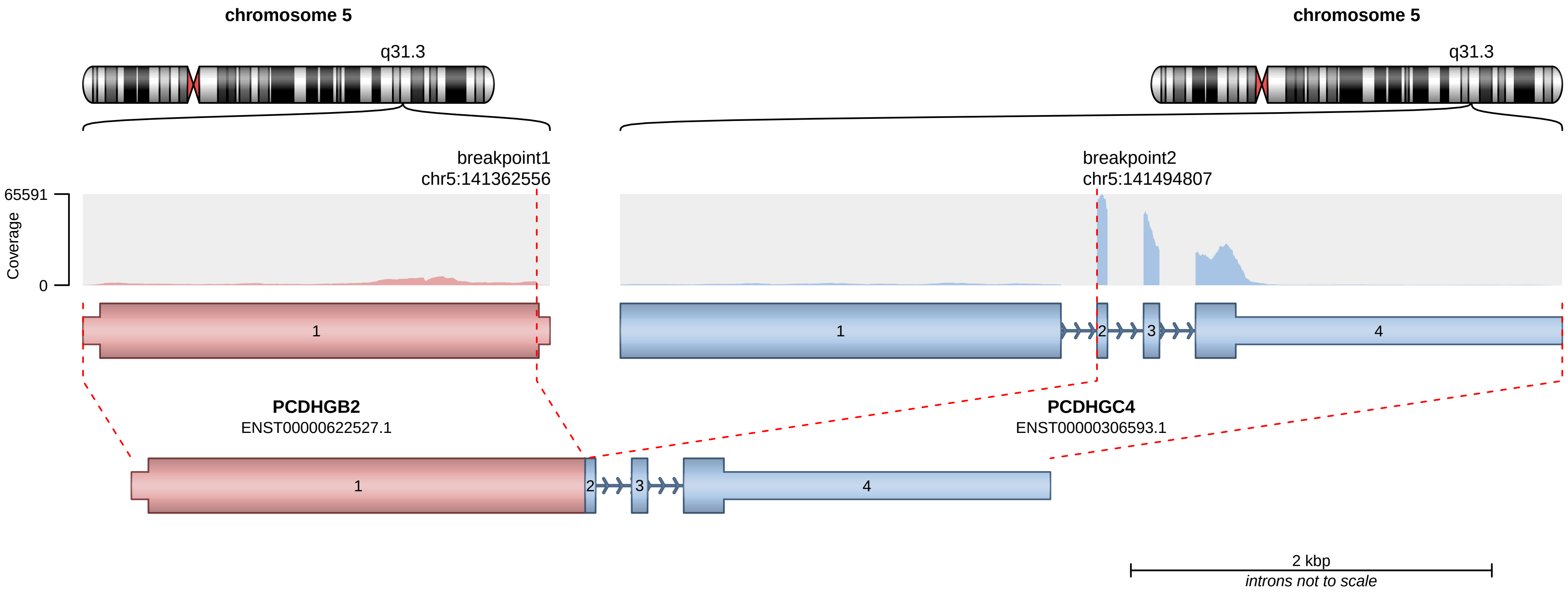
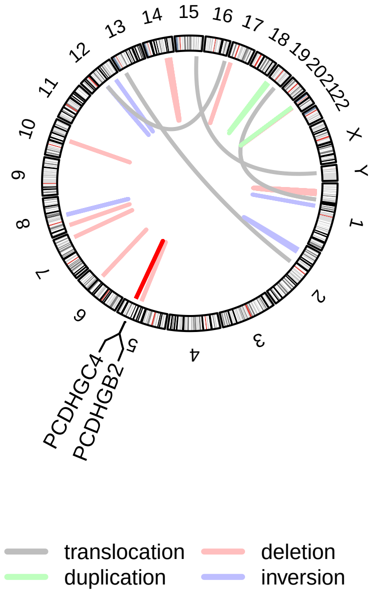
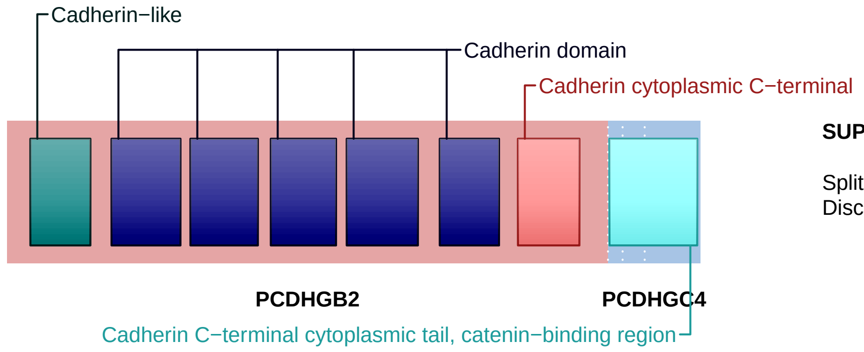


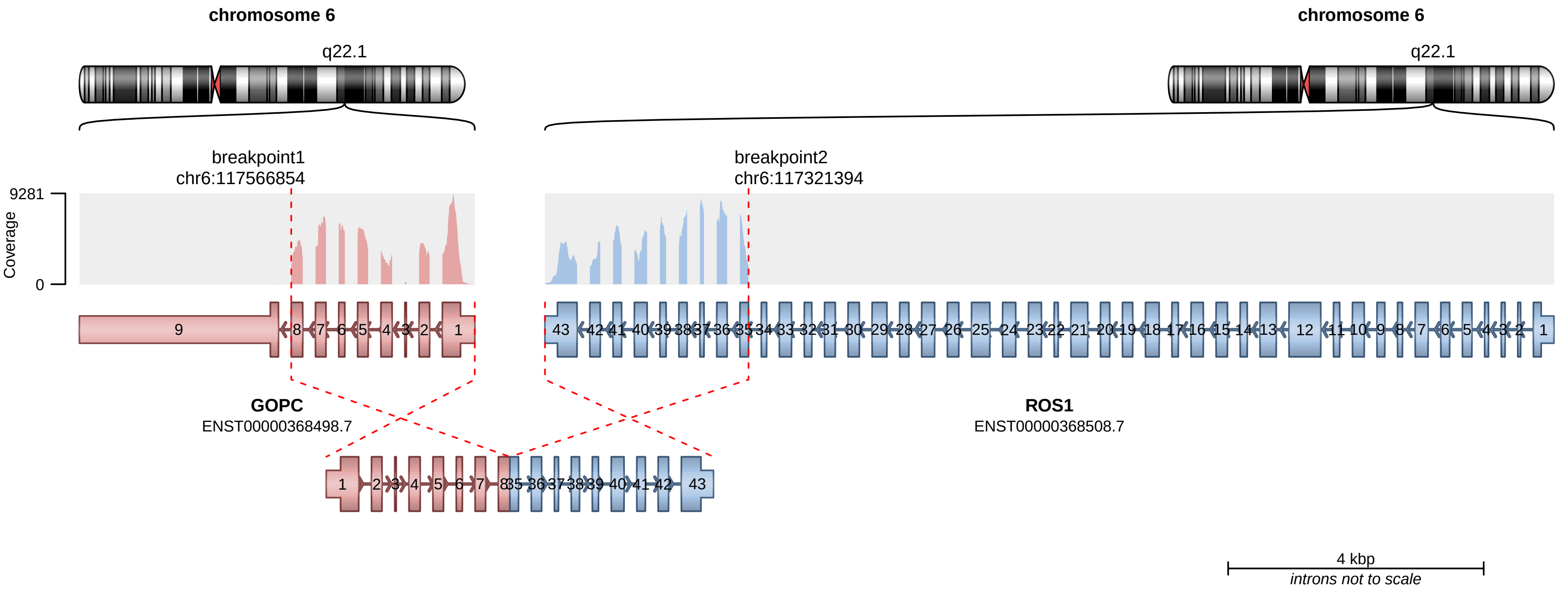


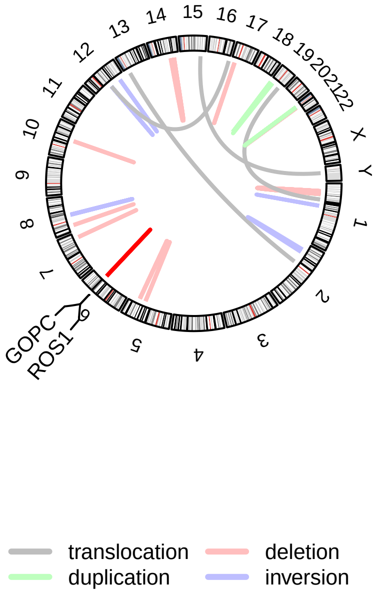
RETAINED PROTEIN DOMAINS
reading frame unclear

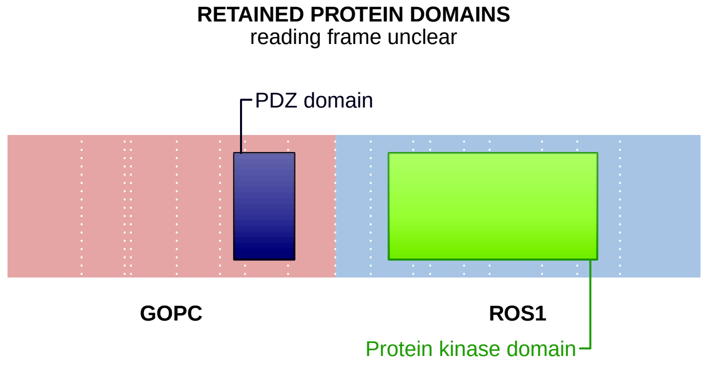


SUPPORTING READ COUNT

Split reads = 928
Discordant mates = 8

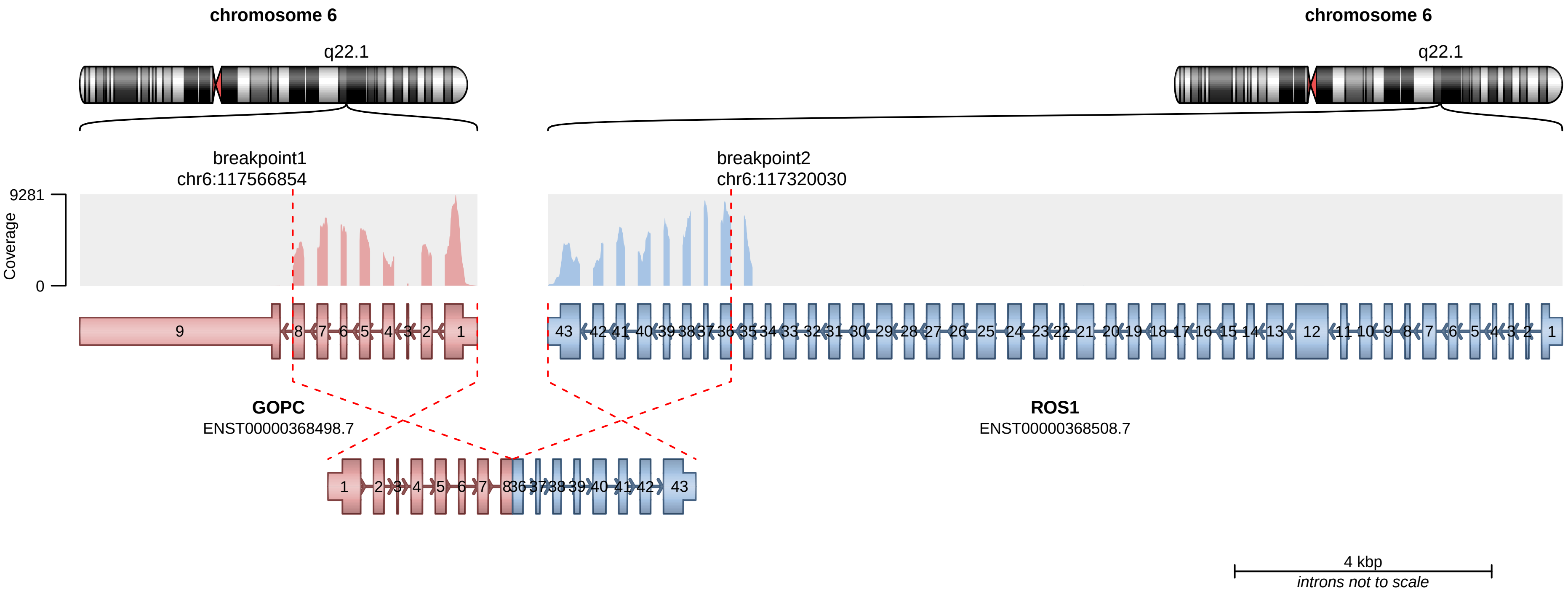


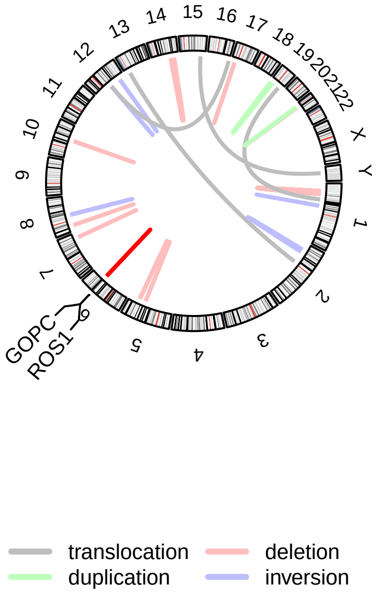


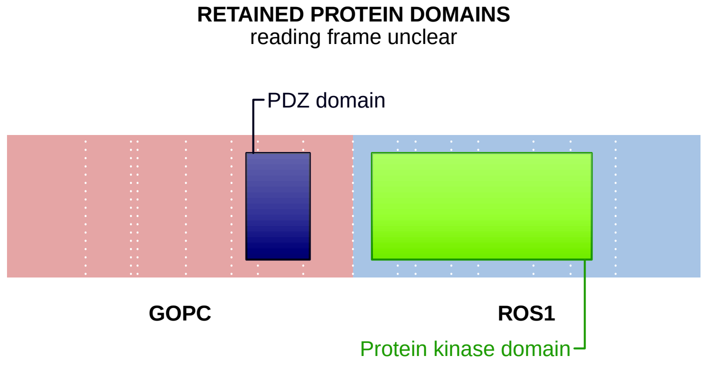


SUPPORTING READ COUNT

Split reads = 805
Discordant mates = 9

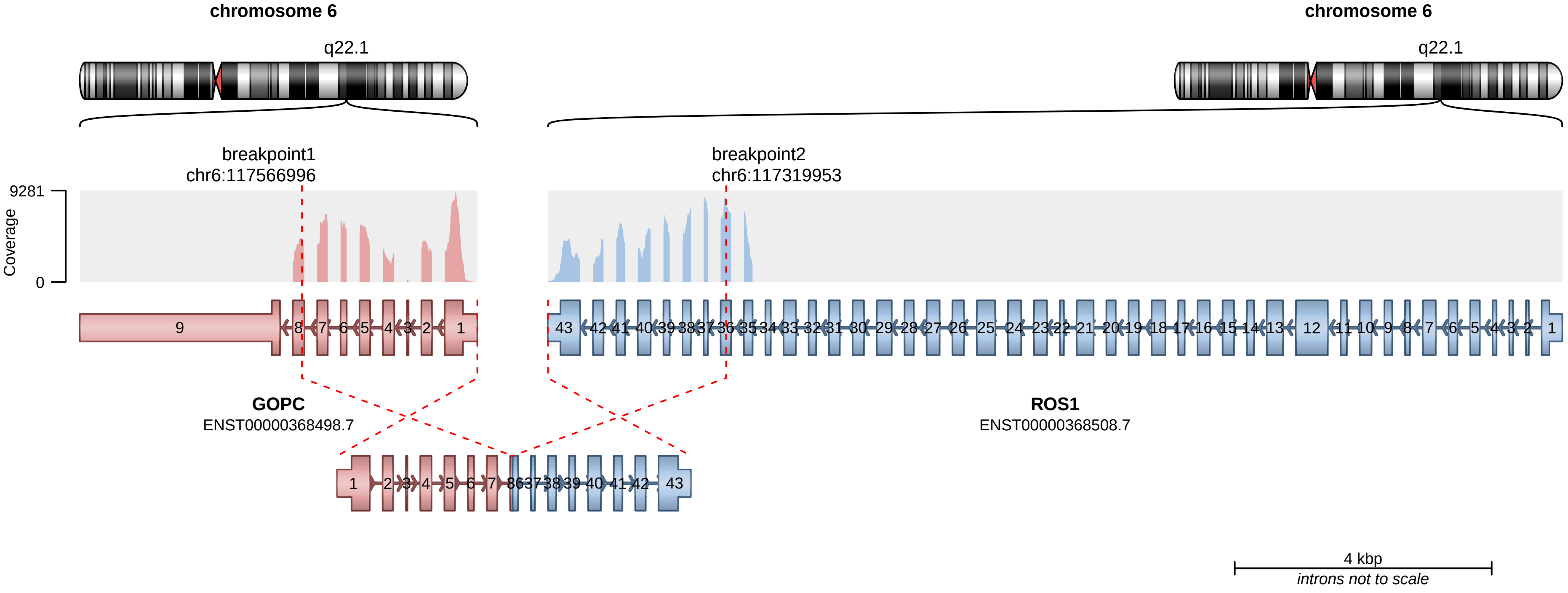


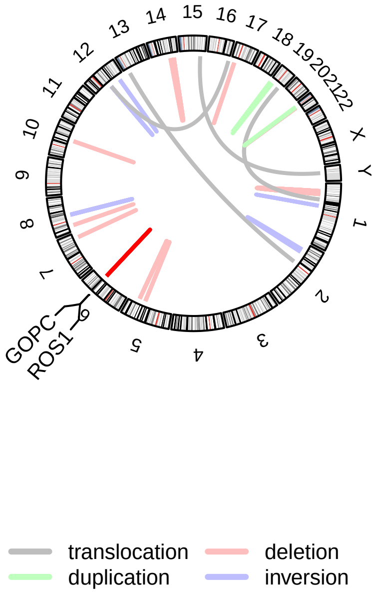




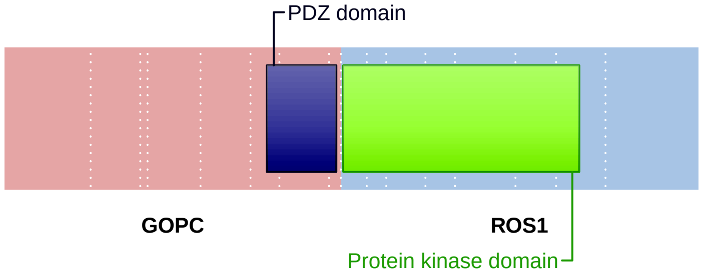
SUPPORTING READ COUNT

Split reads = 21
Discordant mates = 0



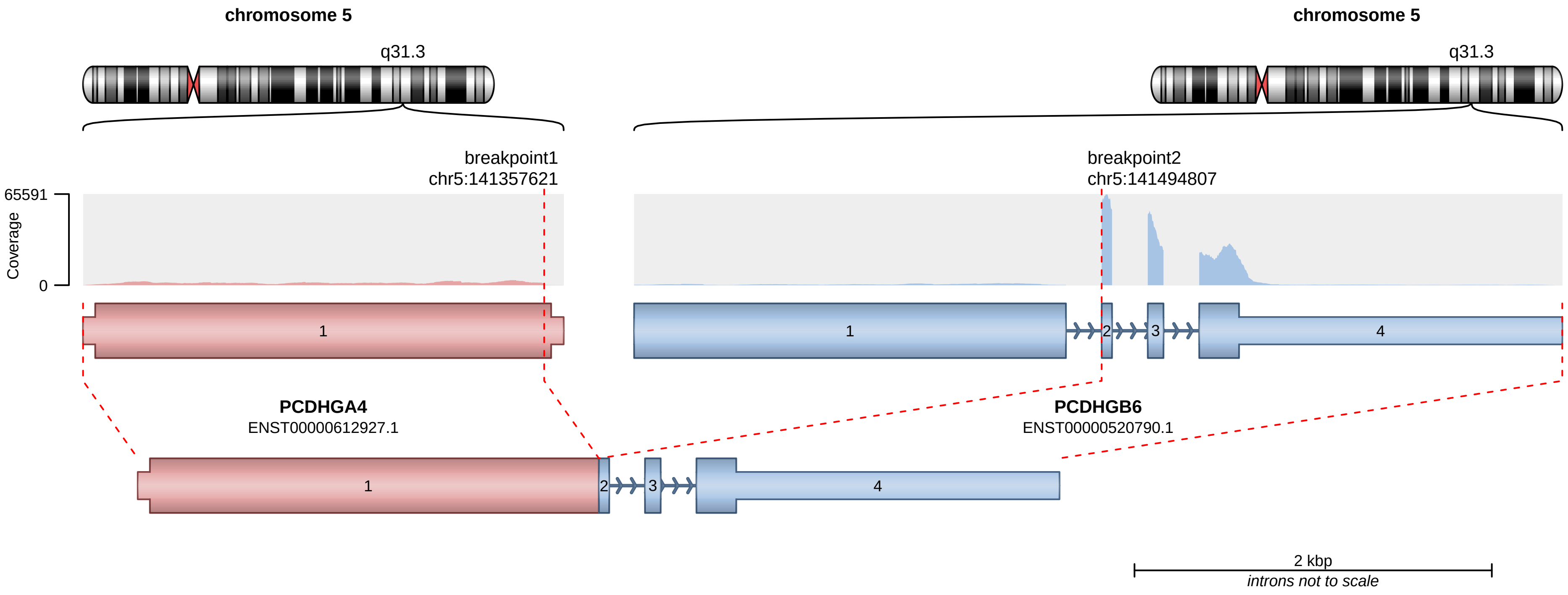


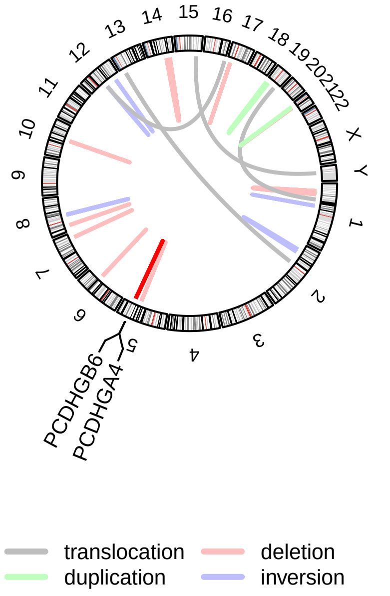
RETAINED PROTEIN DOMAINS
reading frame unclear

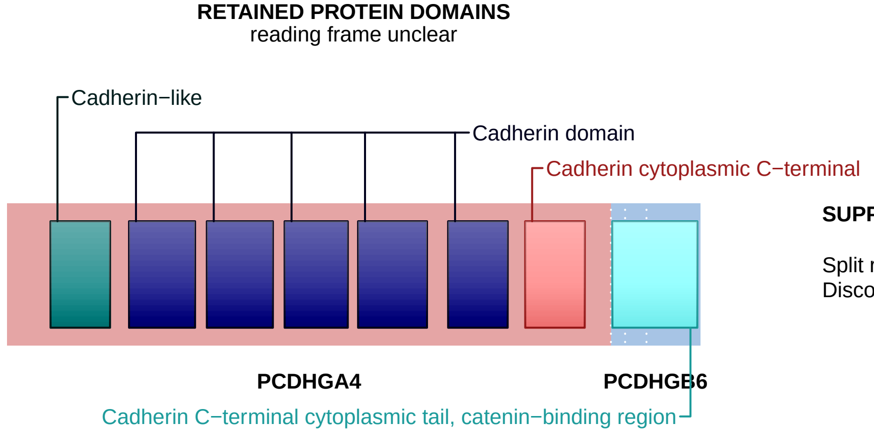


SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

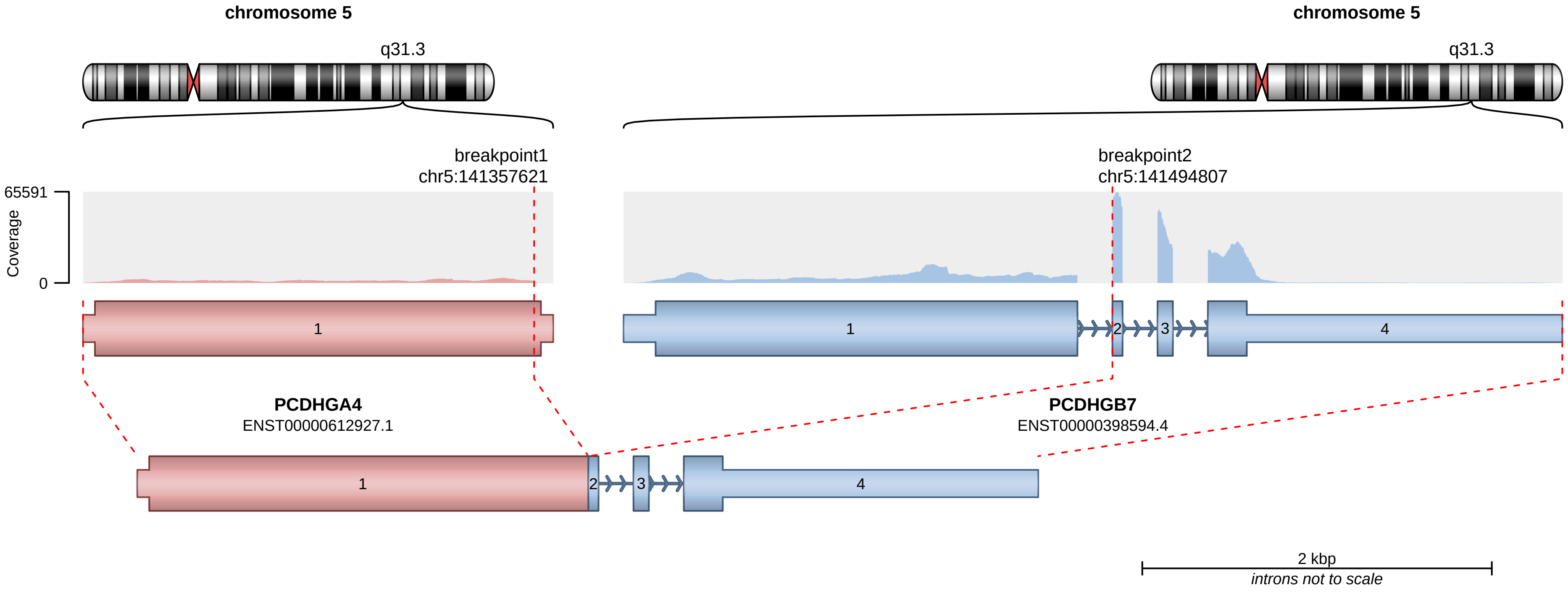


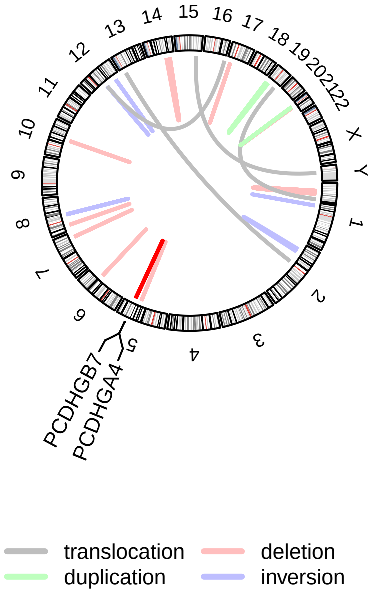


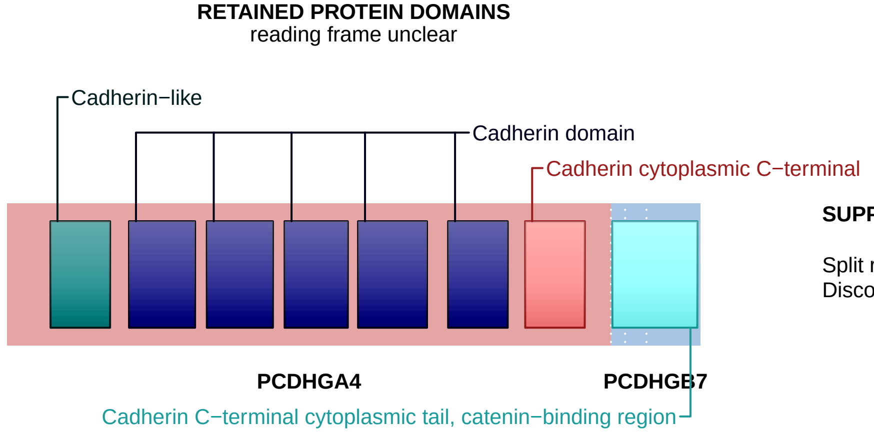


SUPPORTING READ COUNT

Split reads = 533
Discordant mates = 6

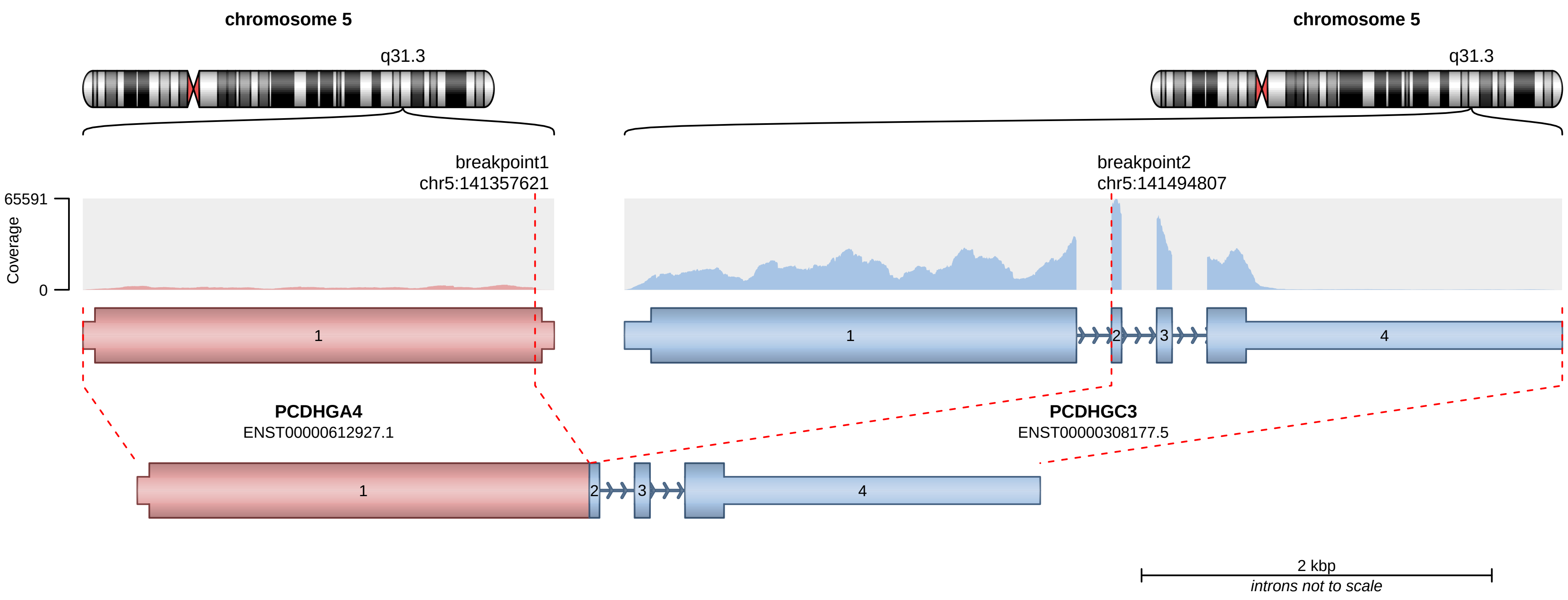


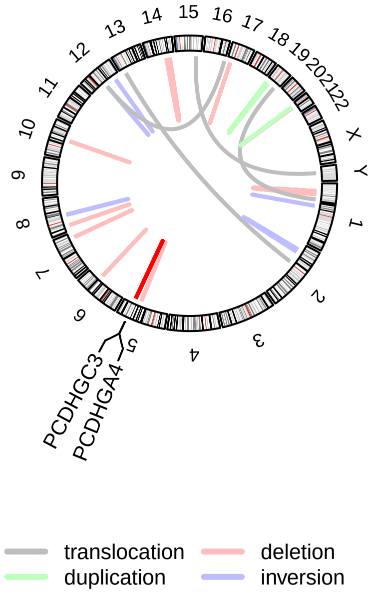


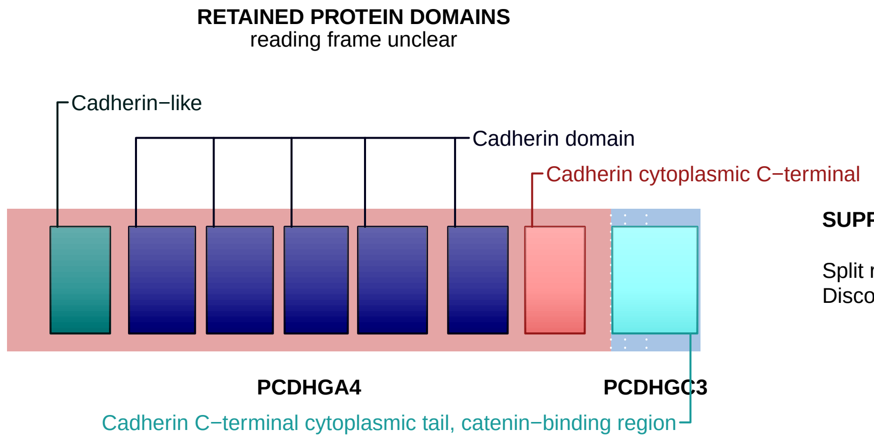


SUPPORTING READ COUNT

Split reads = 533
Discordant mates = 6

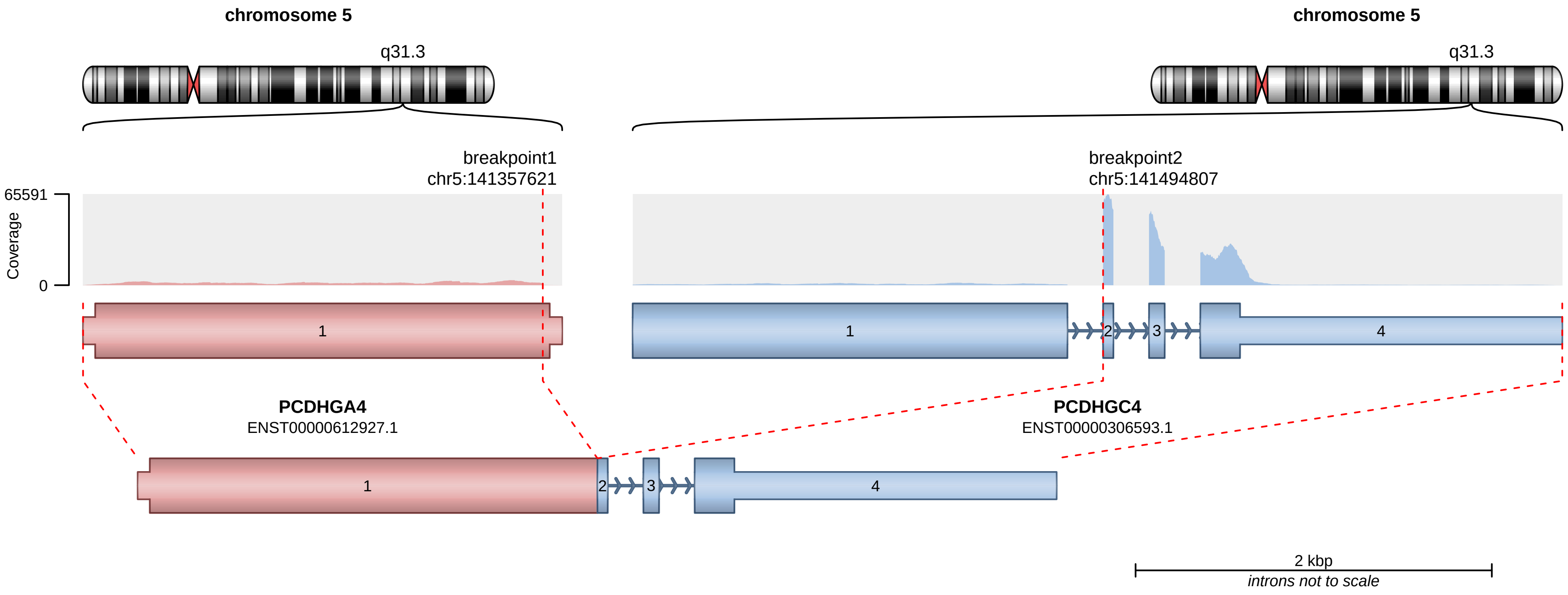


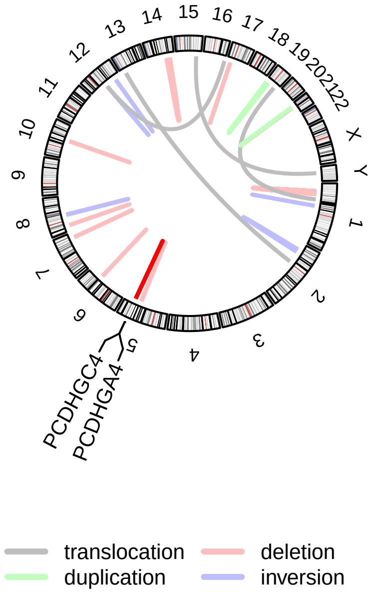


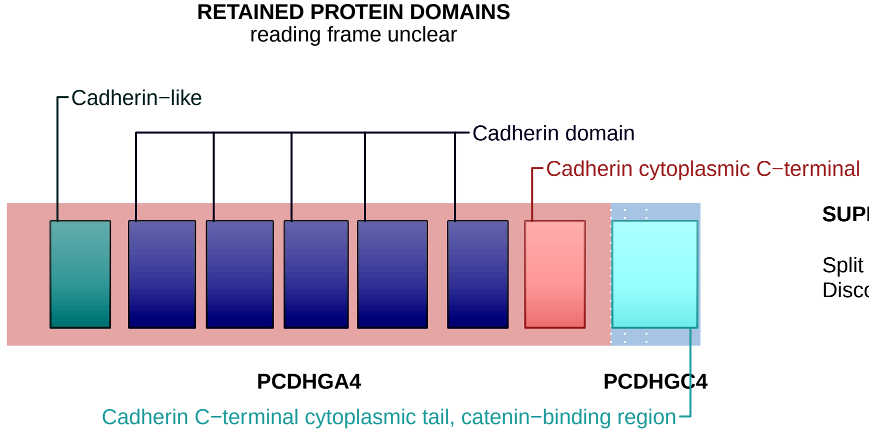


SUPPORTING READ COUNT

Split reads = 533
Discordant mates = 6

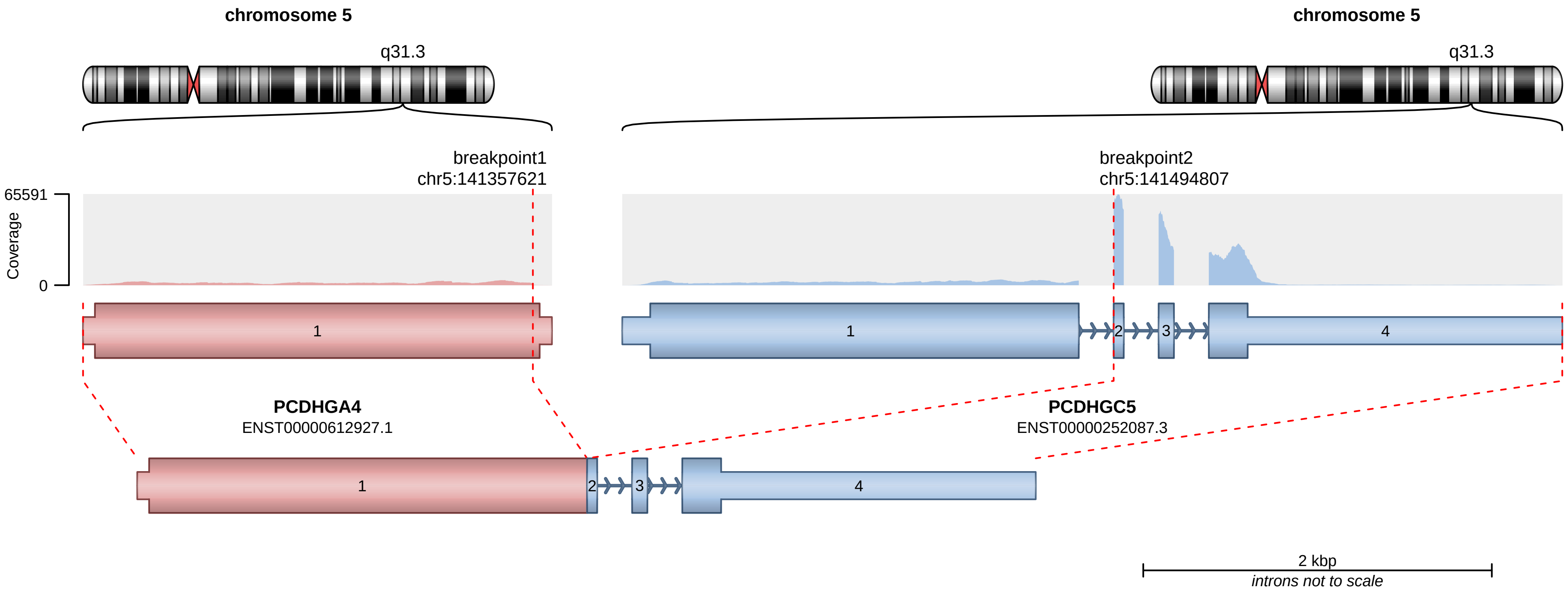


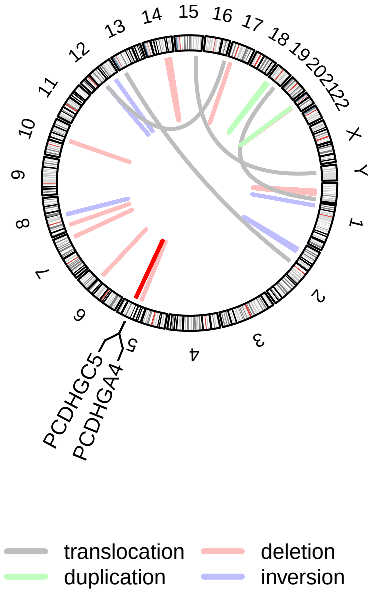




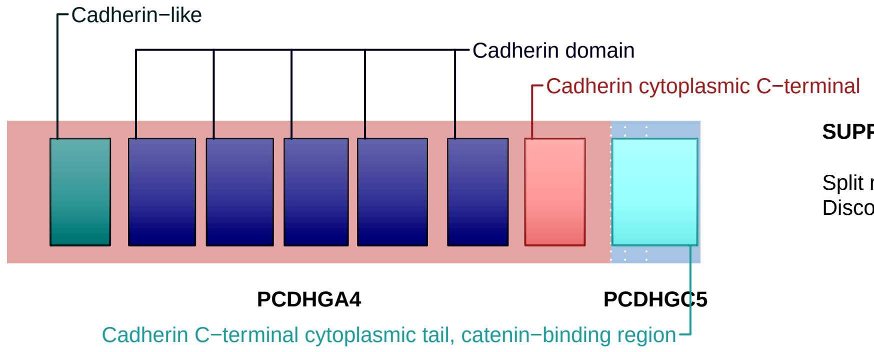
SUPPORTING READ COUNT

Split reads = 533
Discordant mates = 6



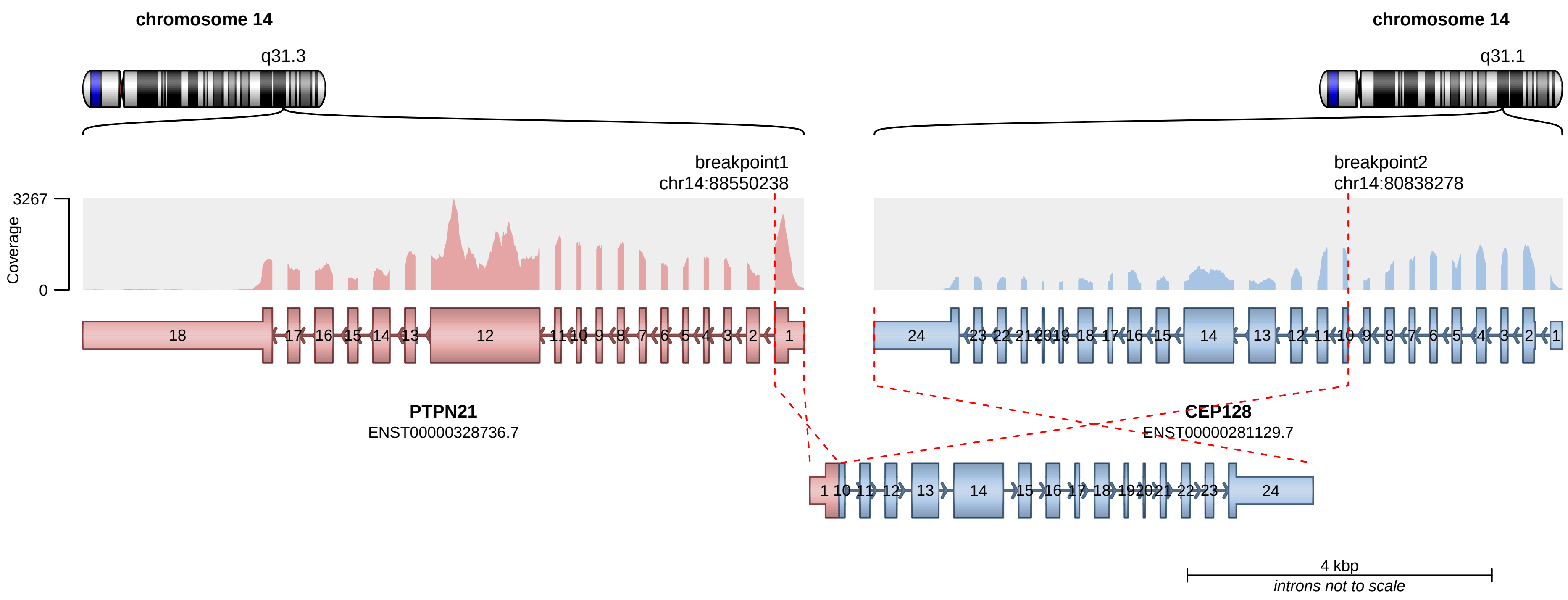


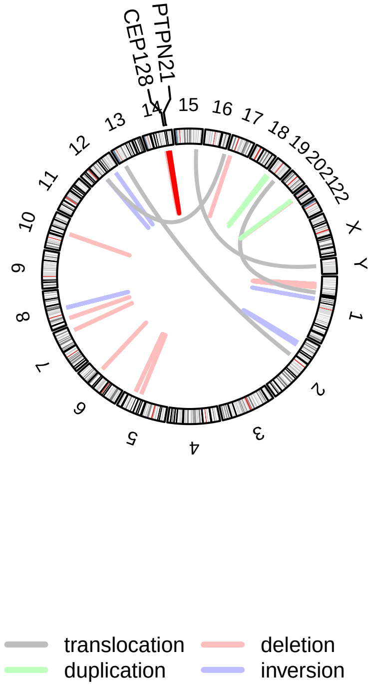
RETAINED PROTEIN DOMAINS
reading frame unclear

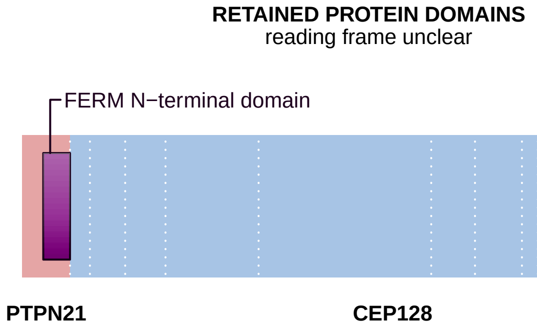


SUPPORTING READ COUNT

Split reads = 533
Discordant mates = 6

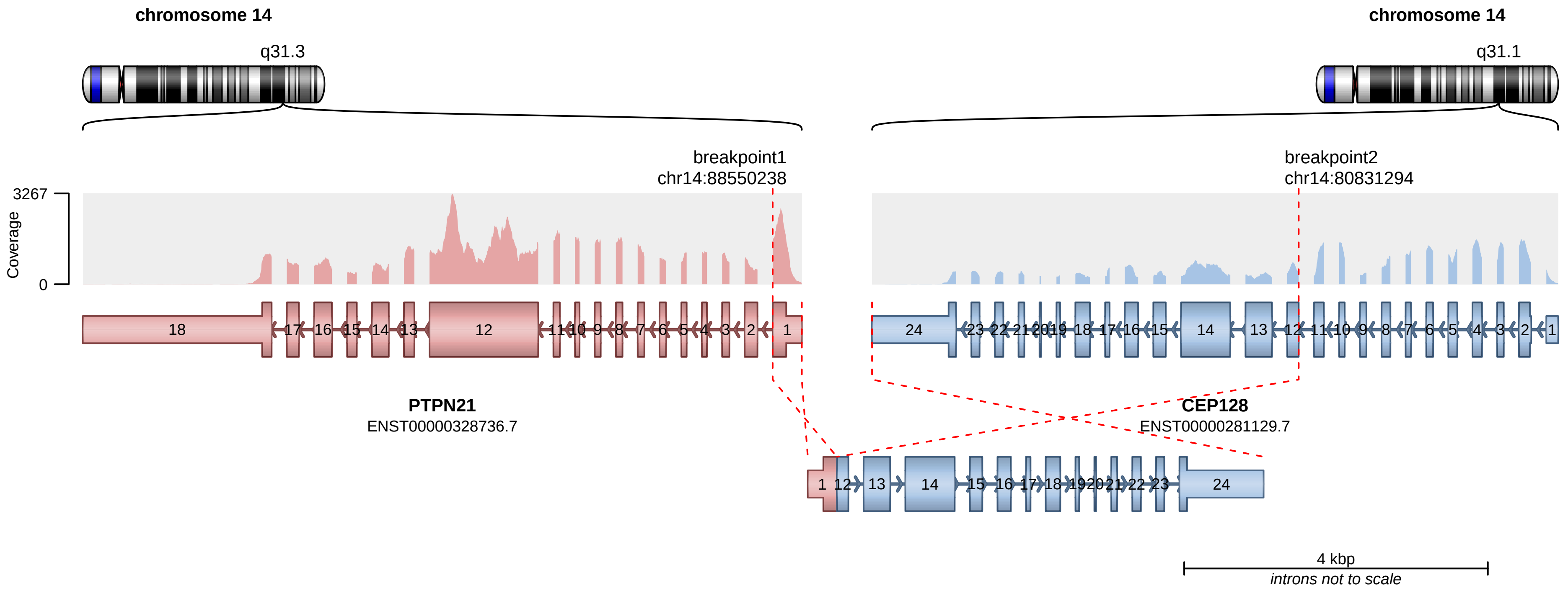


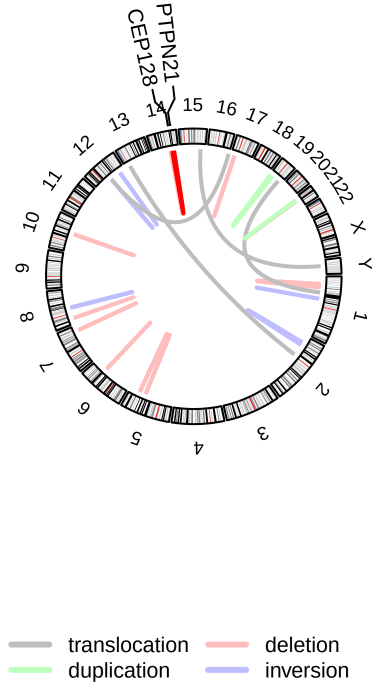




SUPPORTING READ COUNT

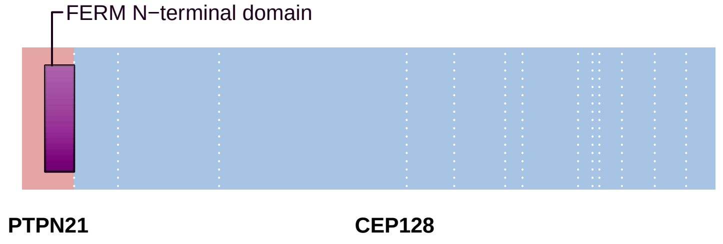
Split reads = 350
Discordant mates = 13





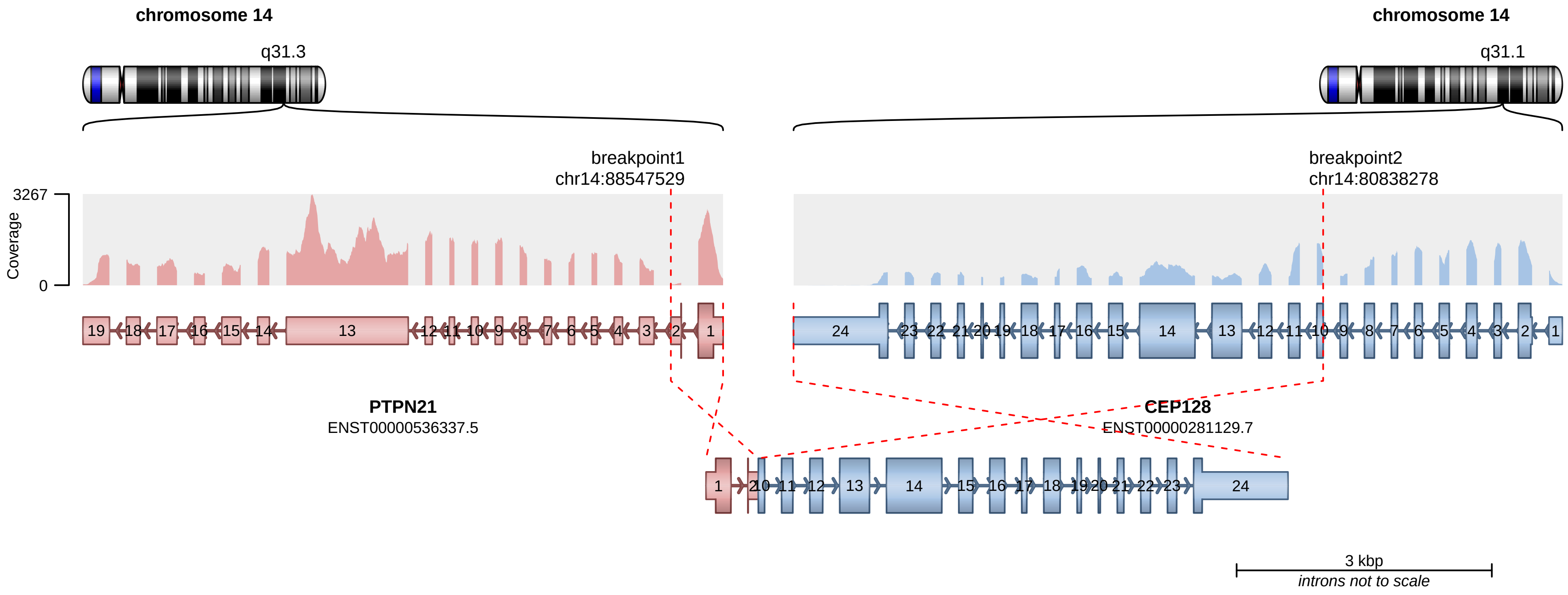
RETAINED PROTEIN DOMAINS

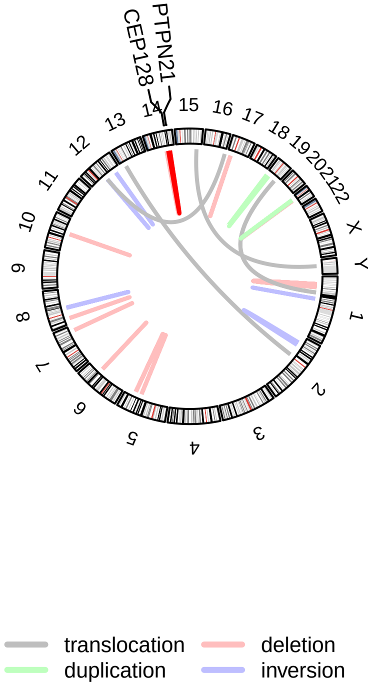
reading frame unclear

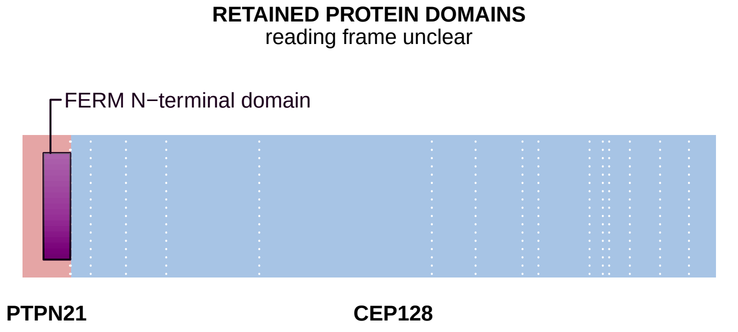


SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 0

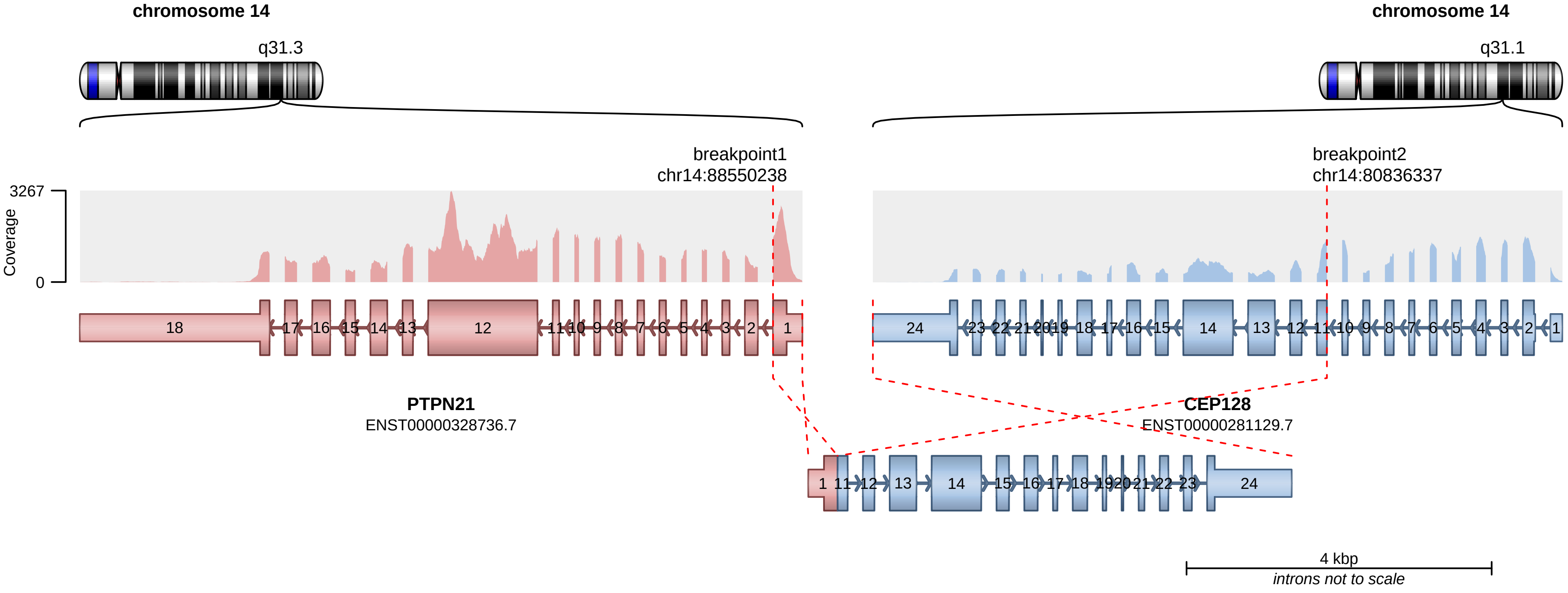


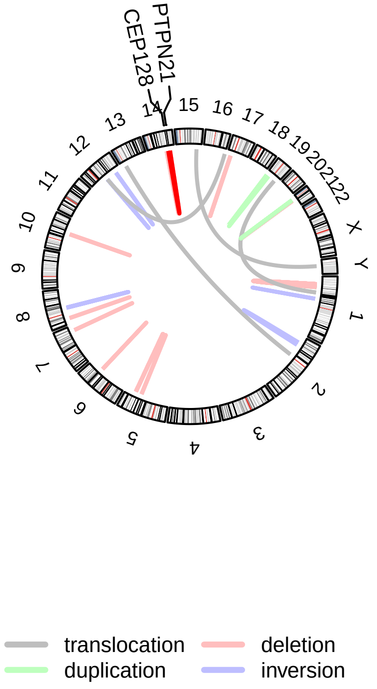




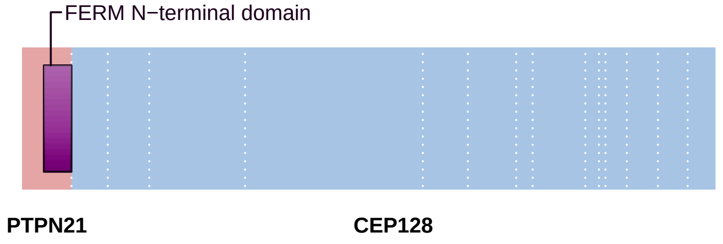
SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 14



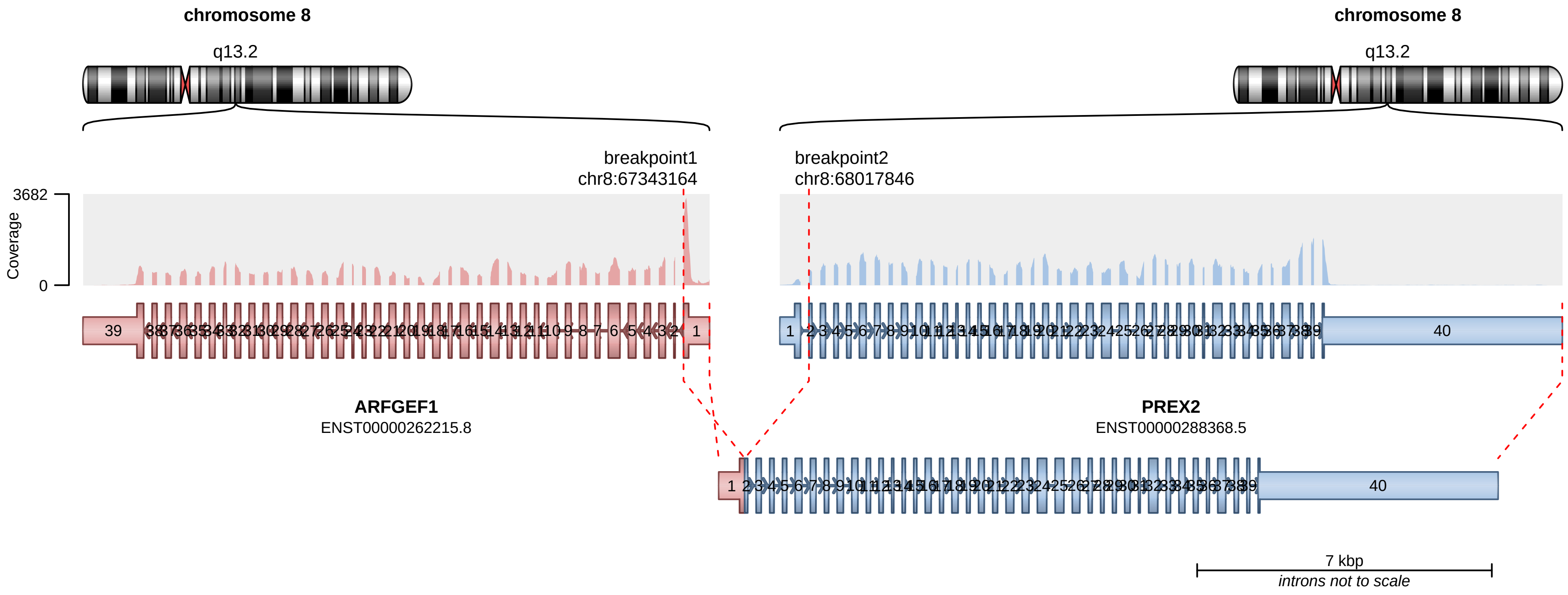


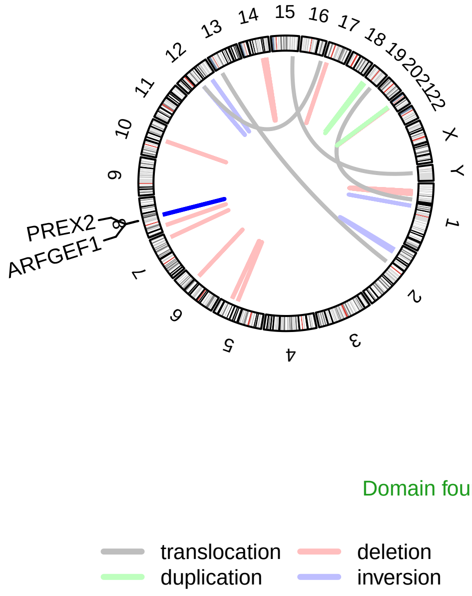
RETAINED PROTEIN DOMAINS
reading frame unclear



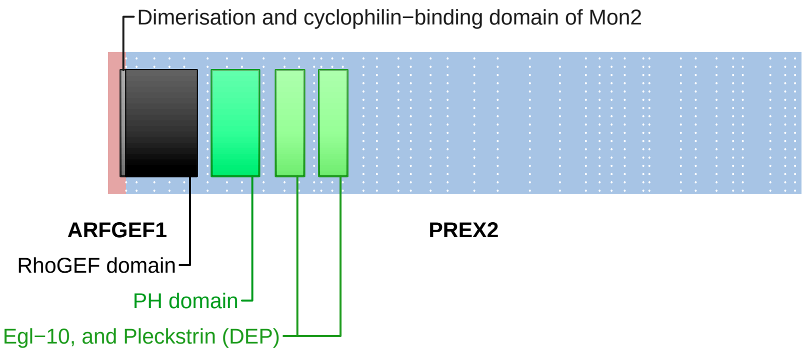
SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0



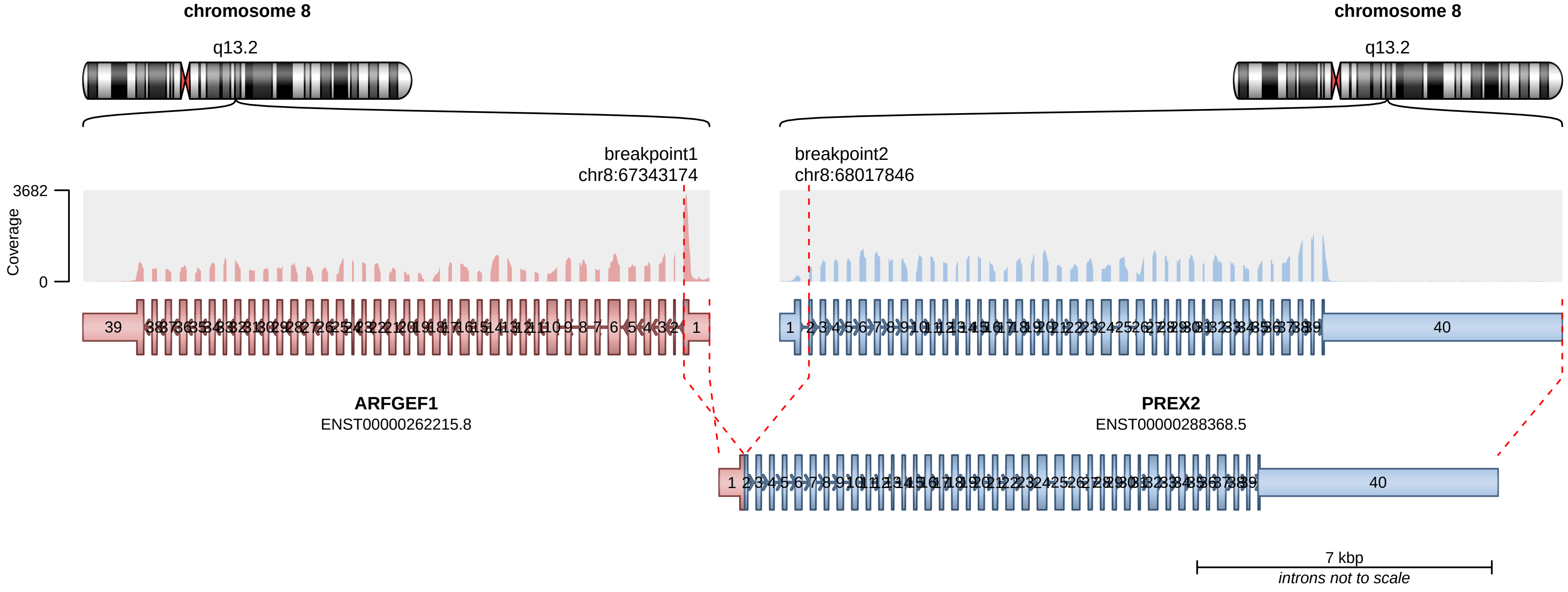


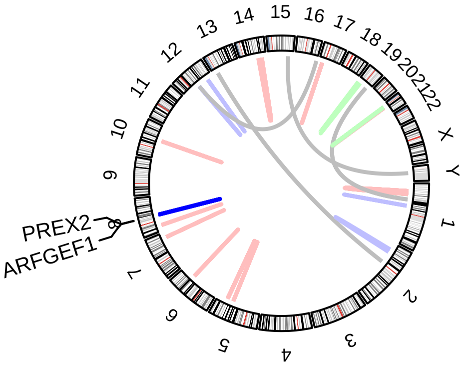
RETAINED PROTEIN DOMAINS
reading frame unclear



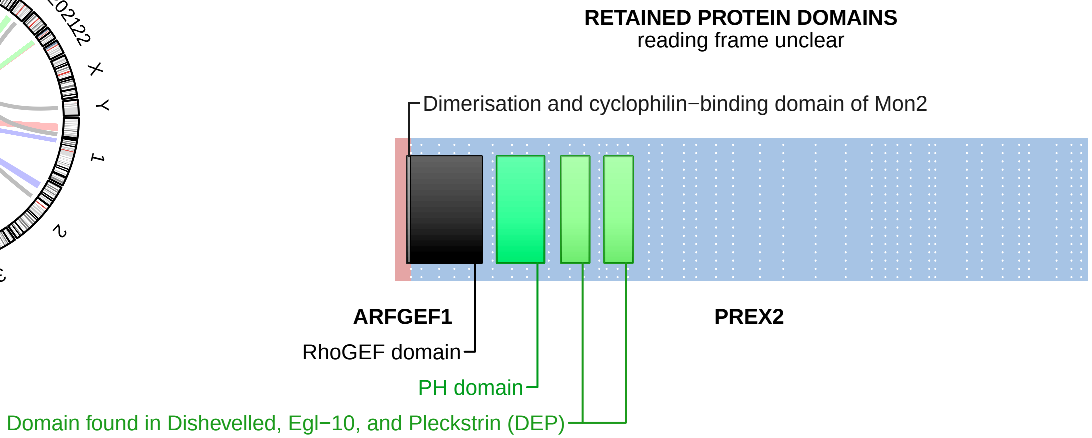
SUPPORTING READ COUNT

Split reads = 205
Discordant mates = 3



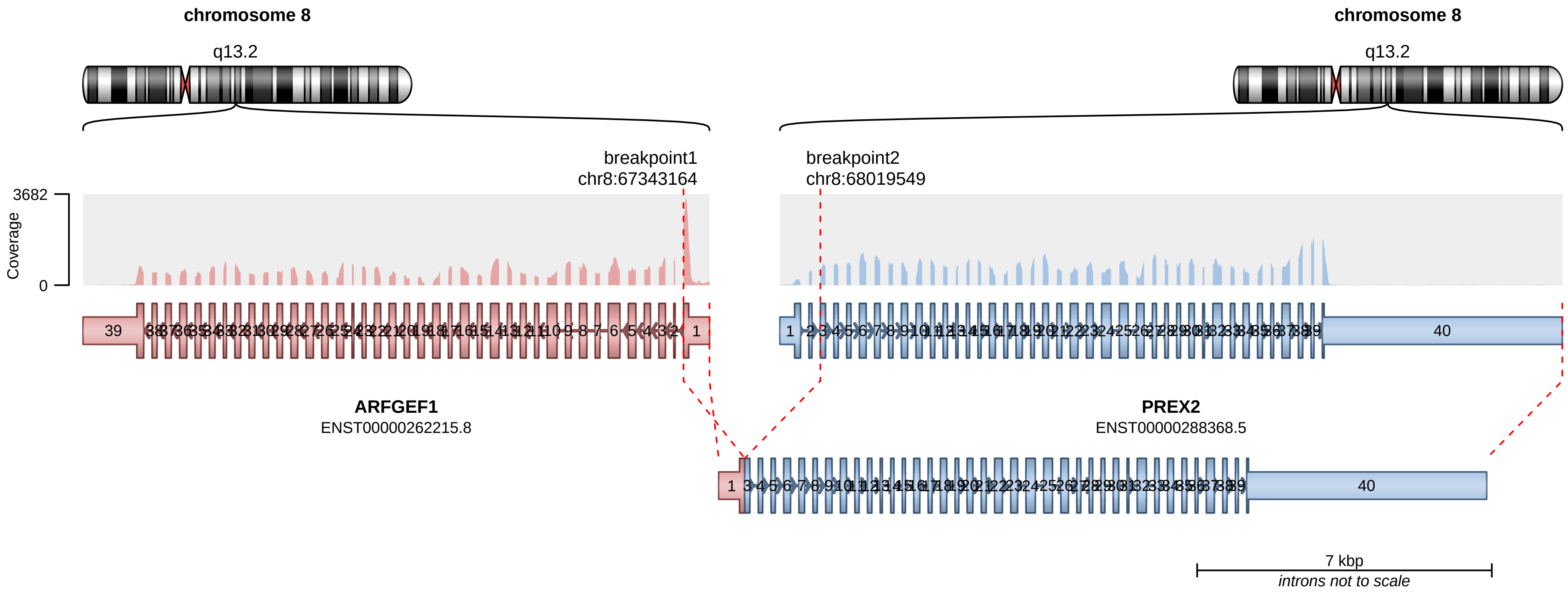


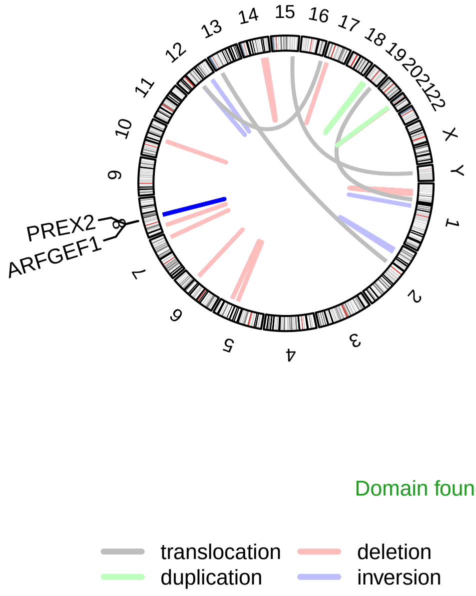
translocation
deletion
duplication
inversion



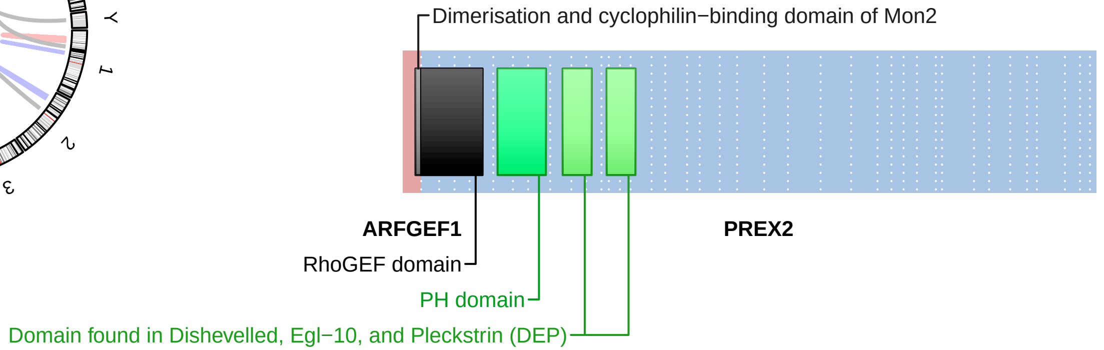
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 1



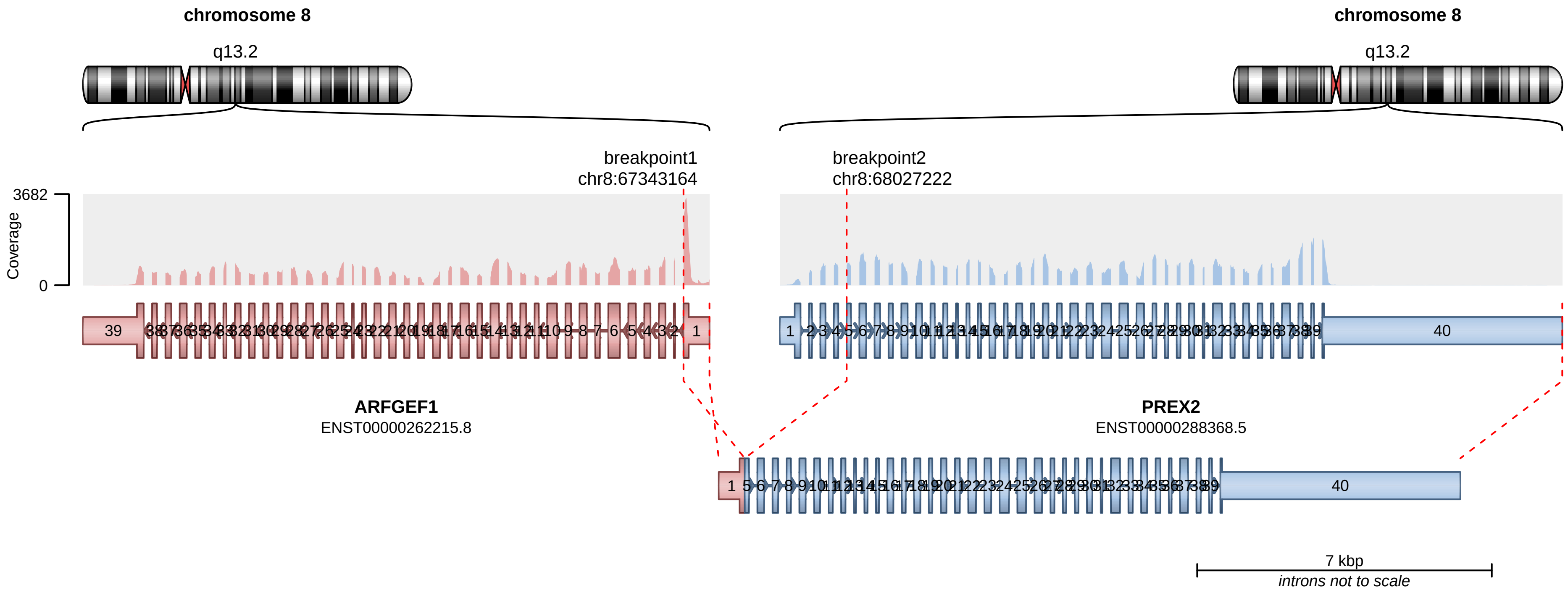


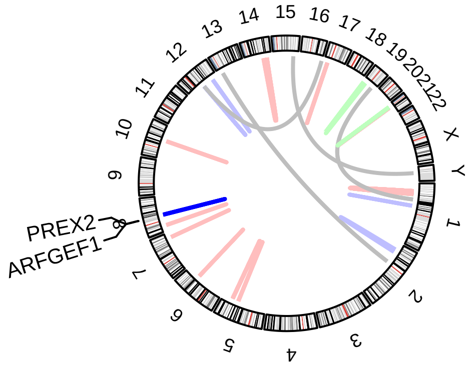
RETAINED PROTEIN DOMAINS
reading frame unclear



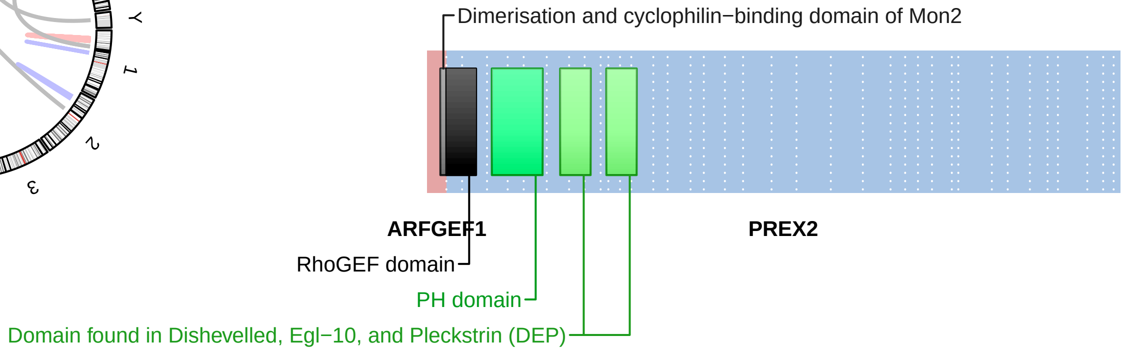
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 3





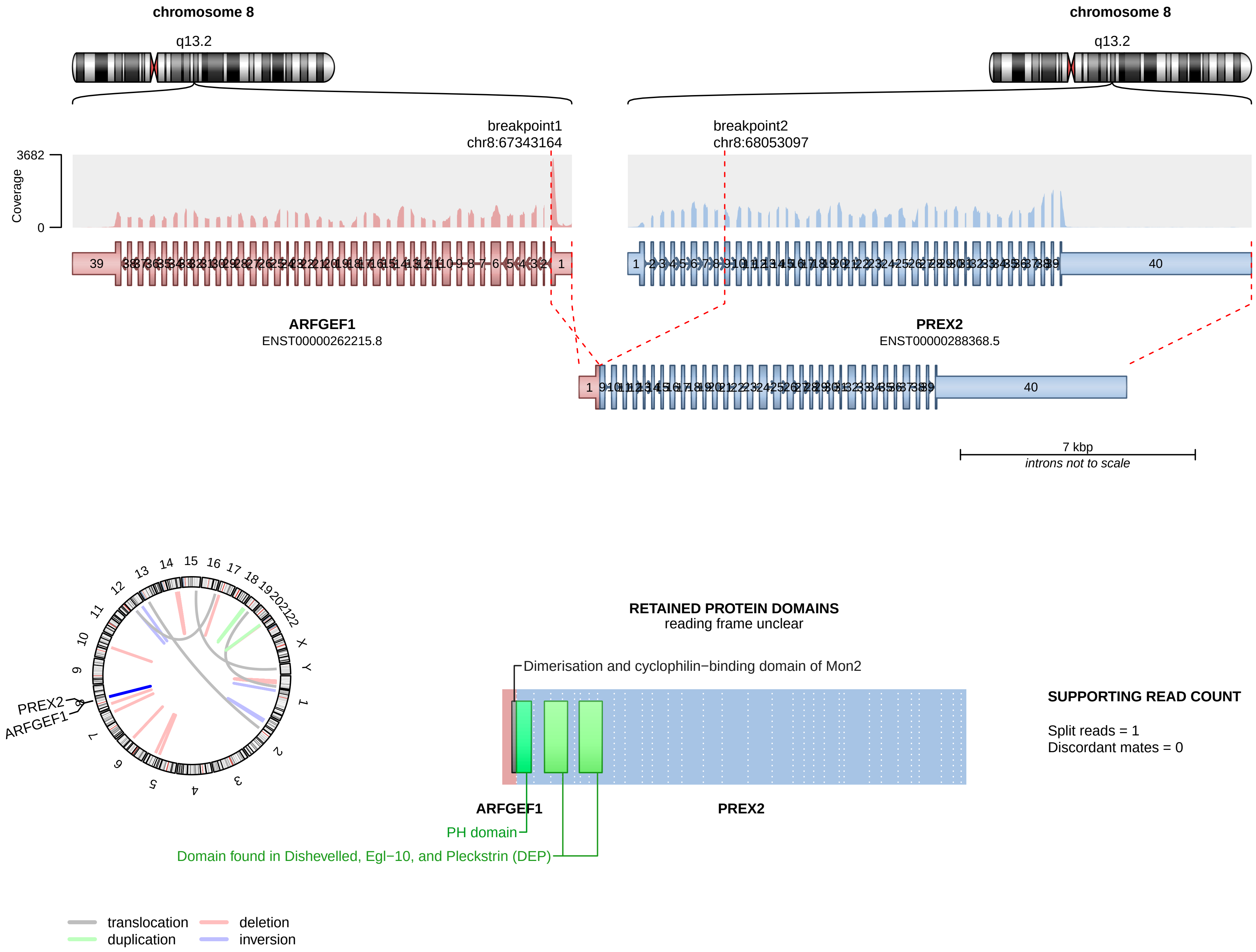
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

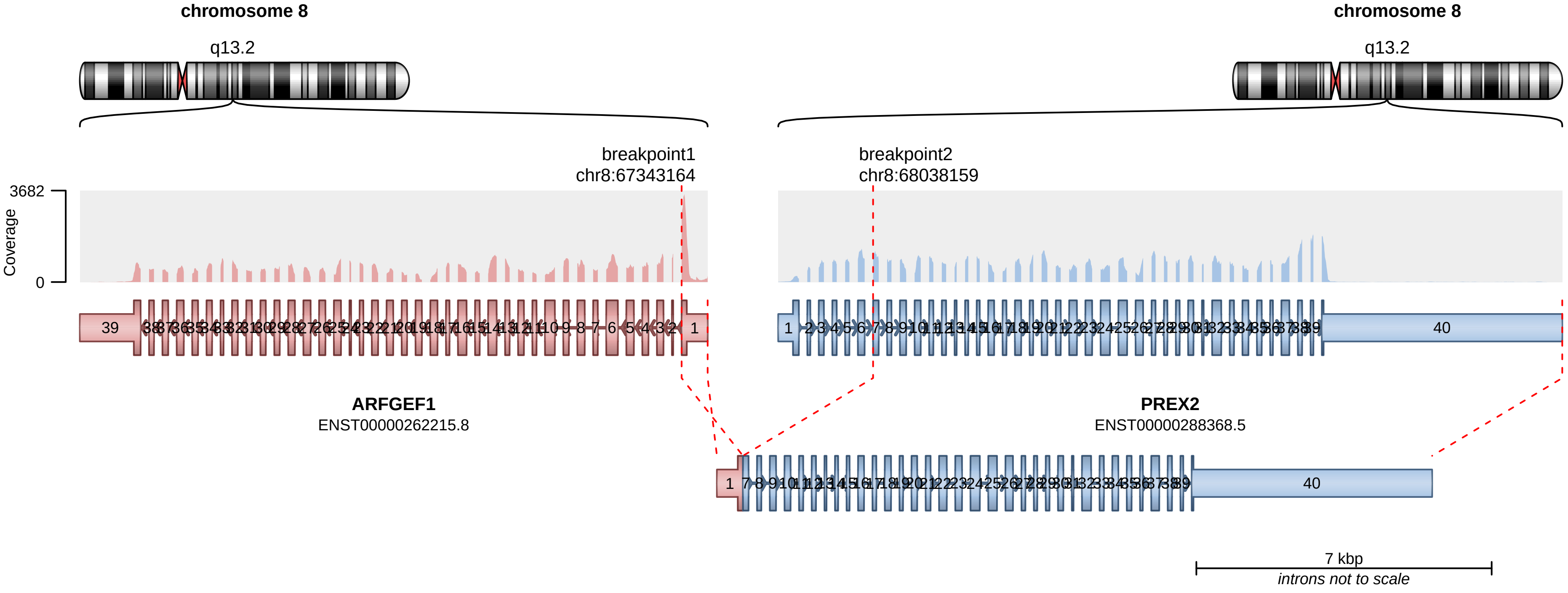
Split reads = 1
Discordant mates = 1

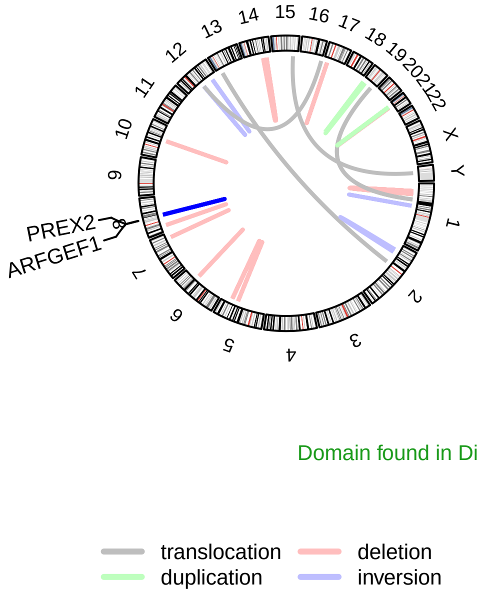
translocation
duplication
deletion
inversion



SUPPORTING READ COUNT

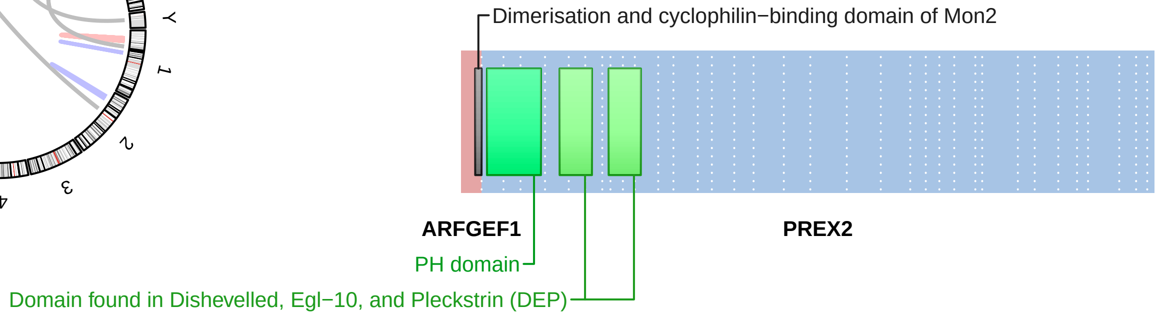
Split reads = 1
Discordant mates = 0





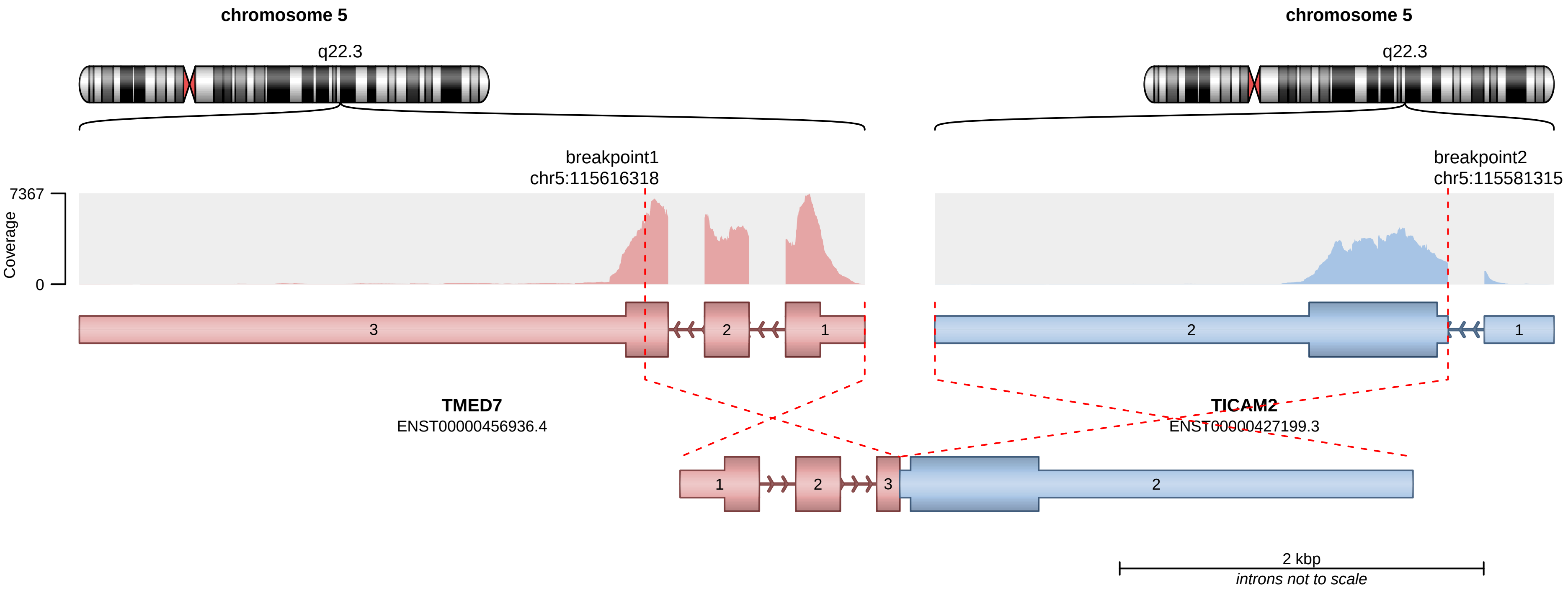
RETAINED PROTEIN DOMAINS

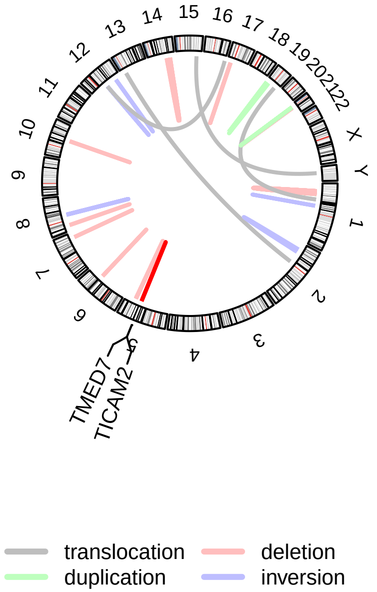
reading frame unclear



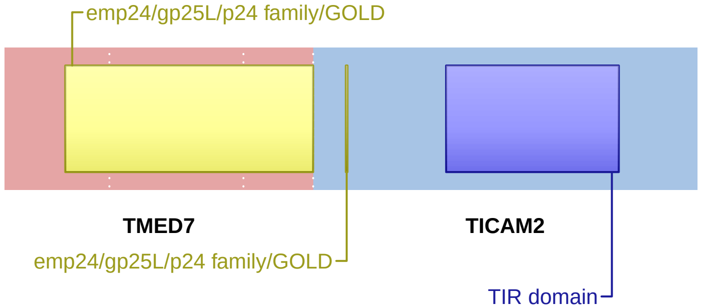
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



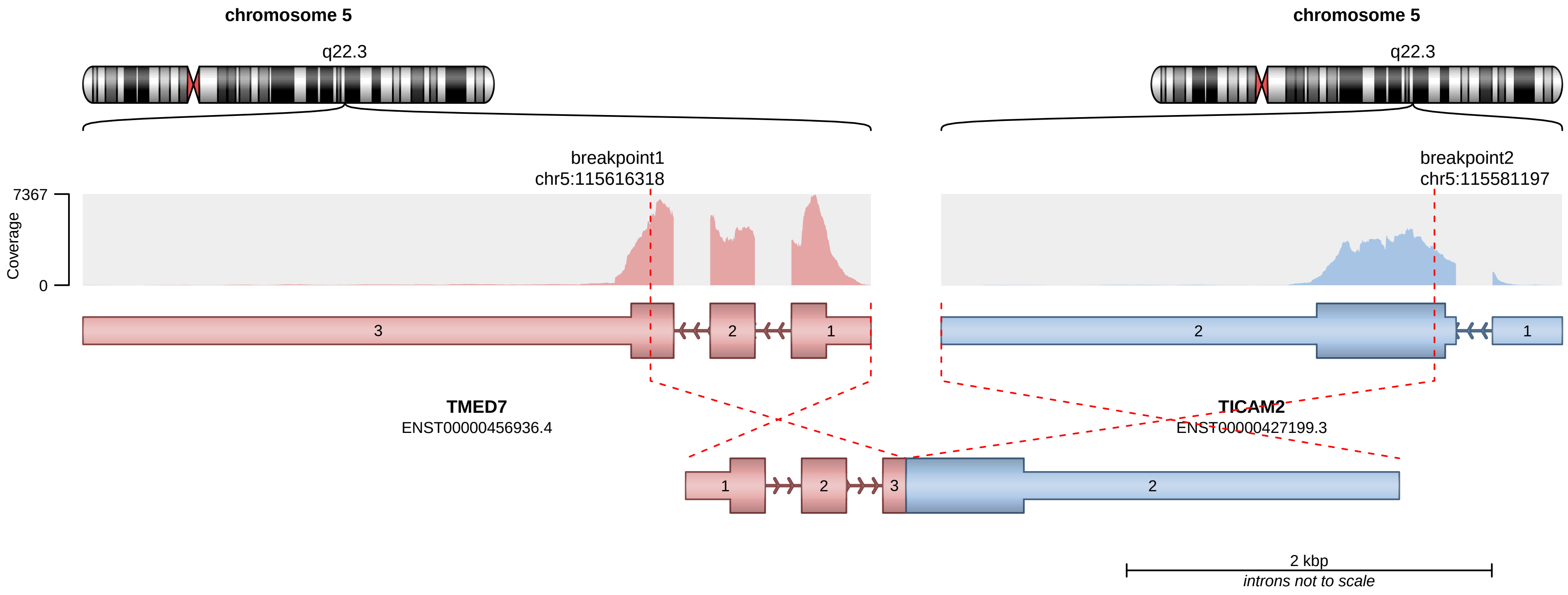


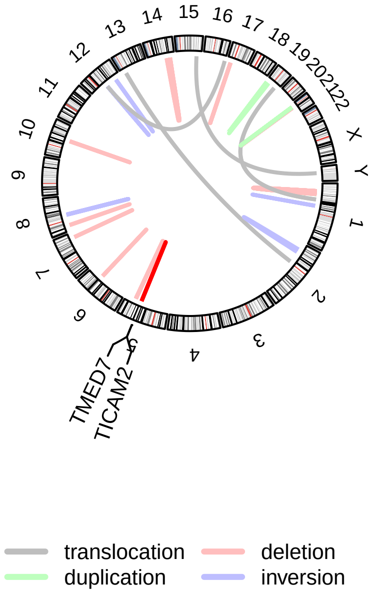
RETAINED PROTEIN DOMAINS
reading frame unclear

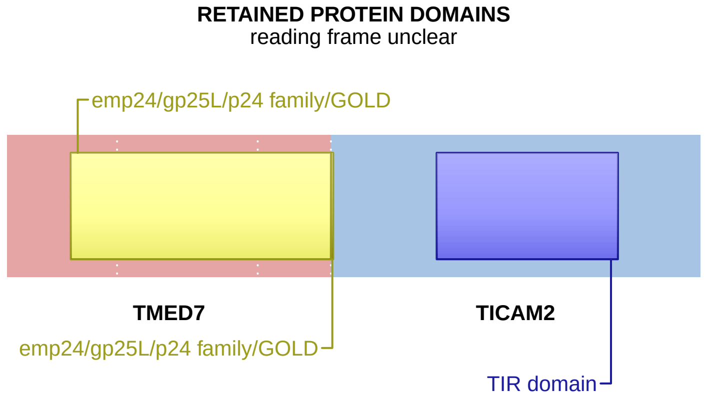


SUPPORTING READ COUNT

Split reads = 153
Discordant mates = 9

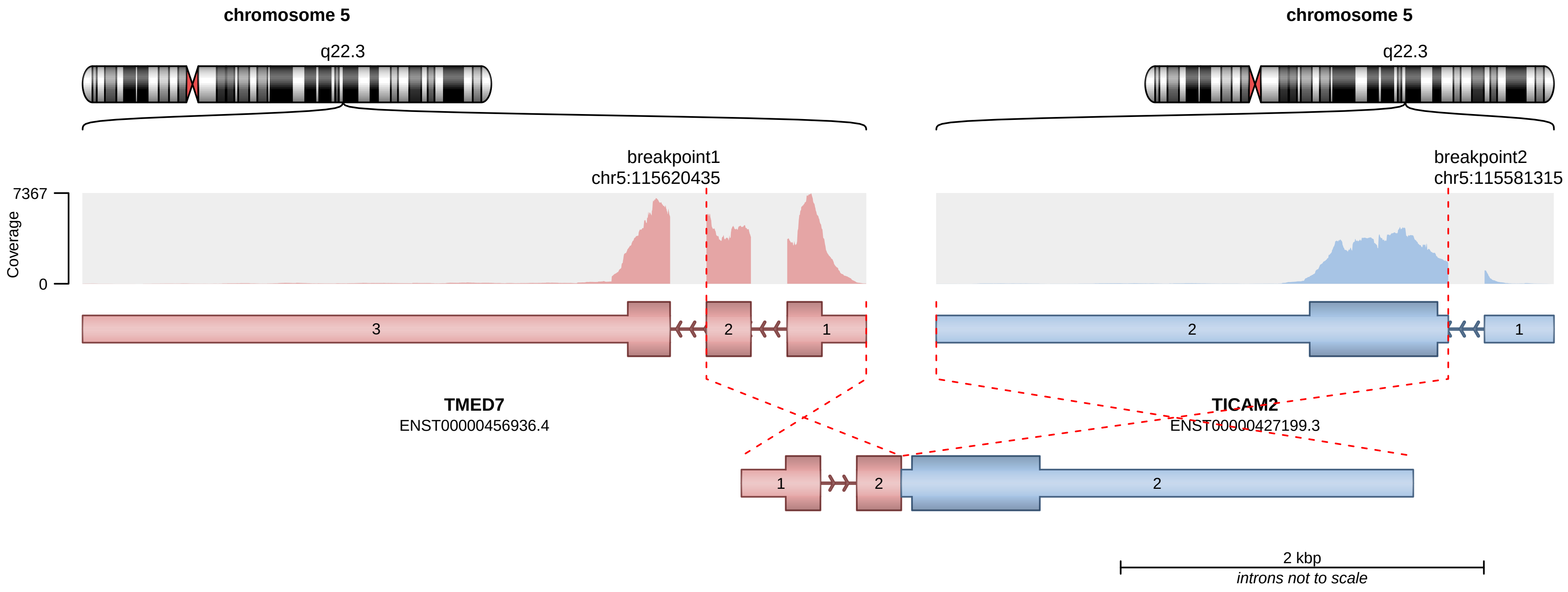


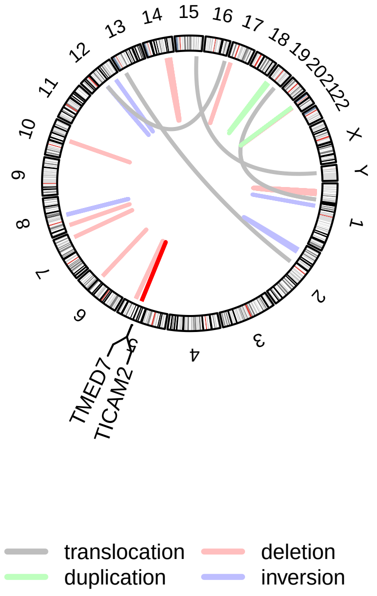




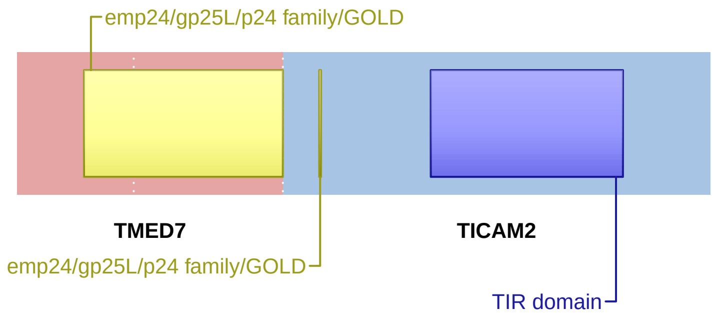
SUPPORTING READ COUNT

Split reads = 20
Discordant mates = 1



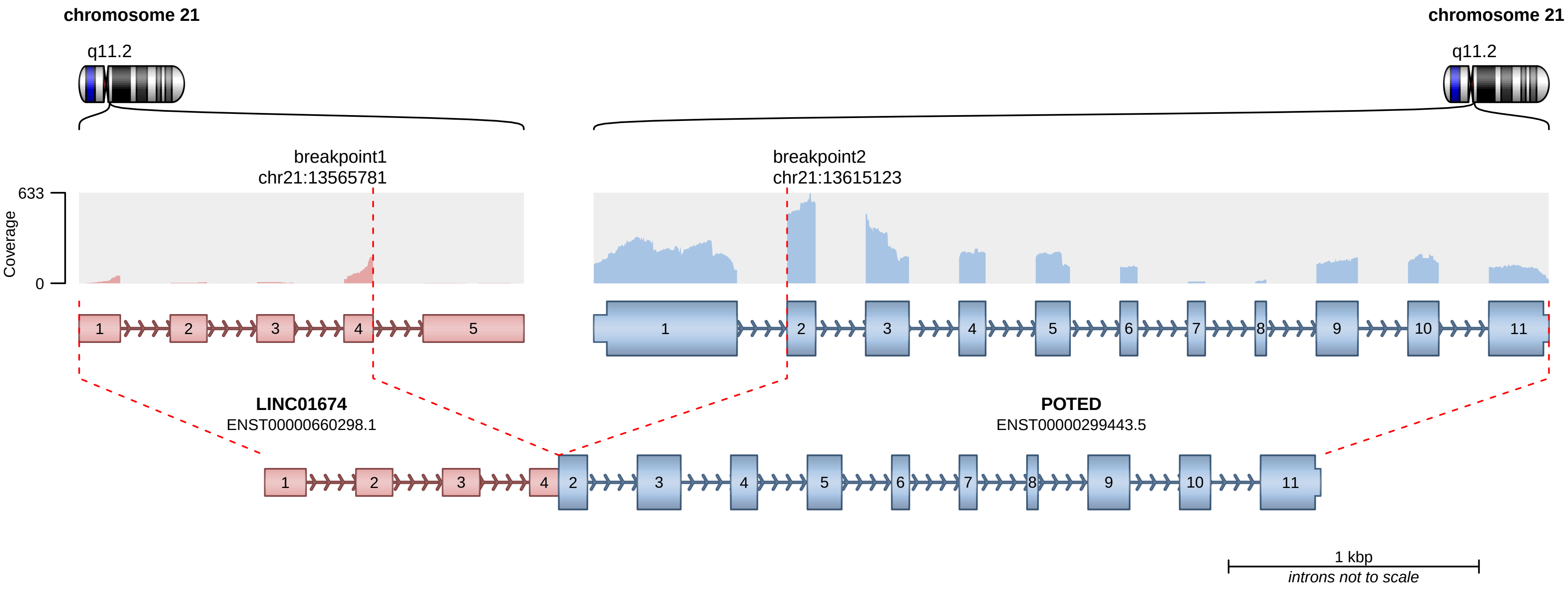


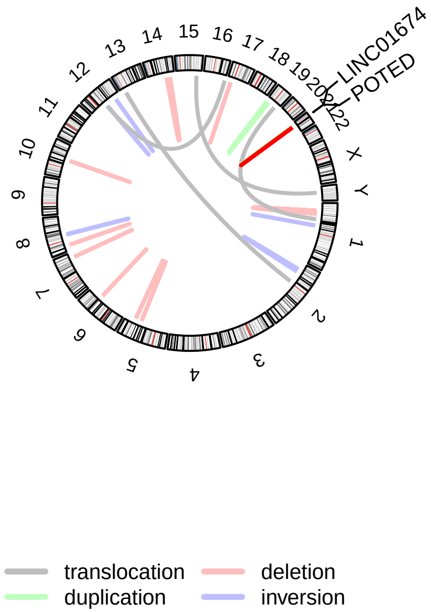
RETAINED PROTEIN DOMAINS
reading frame unclear

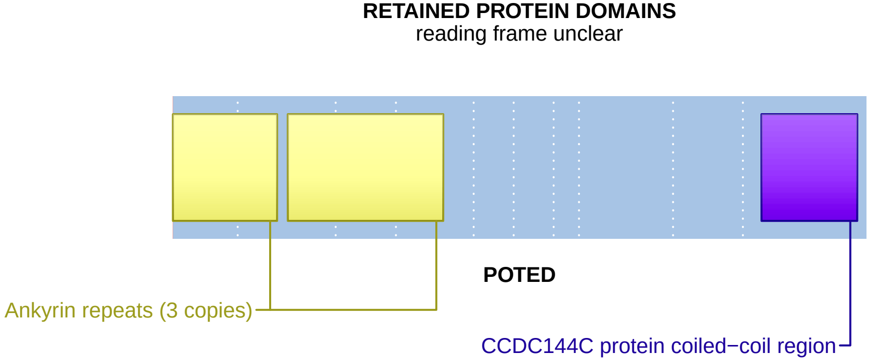


SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 1

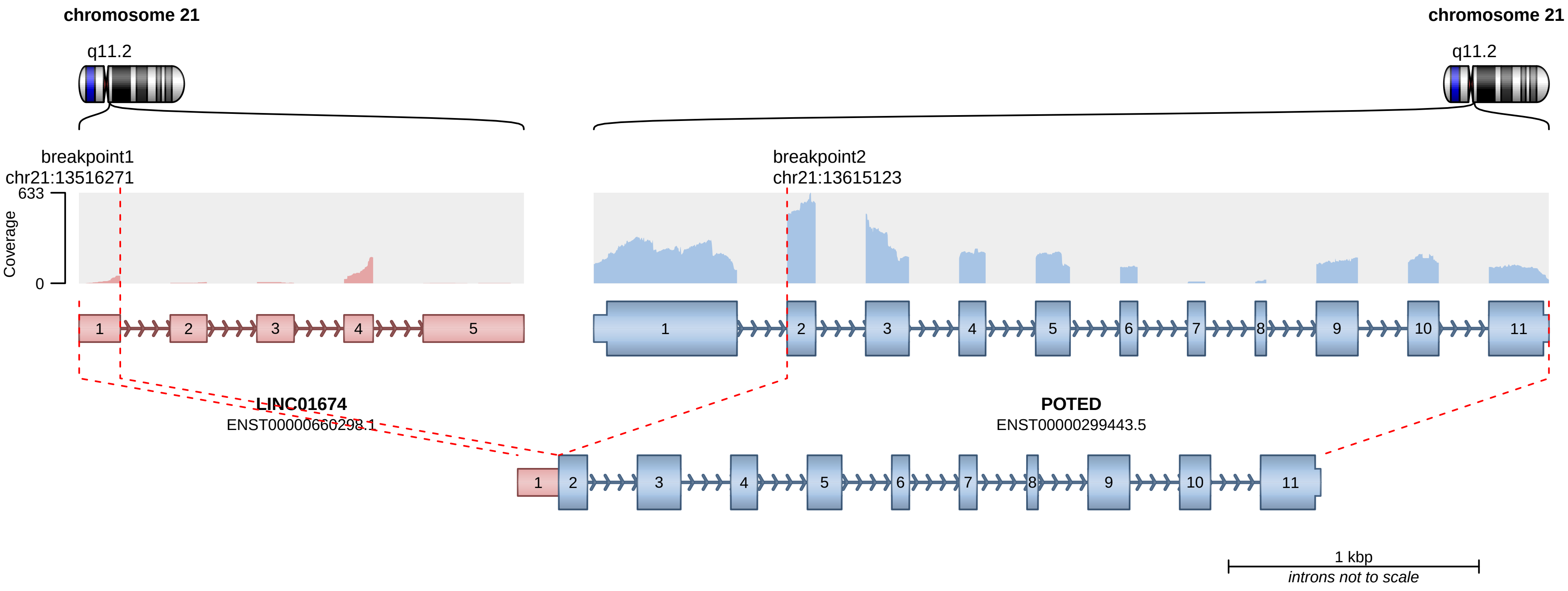


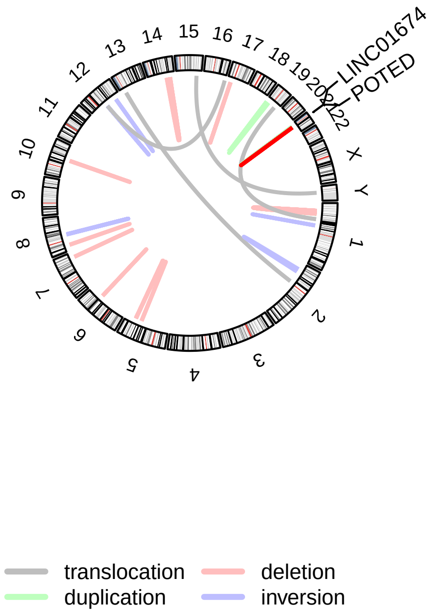


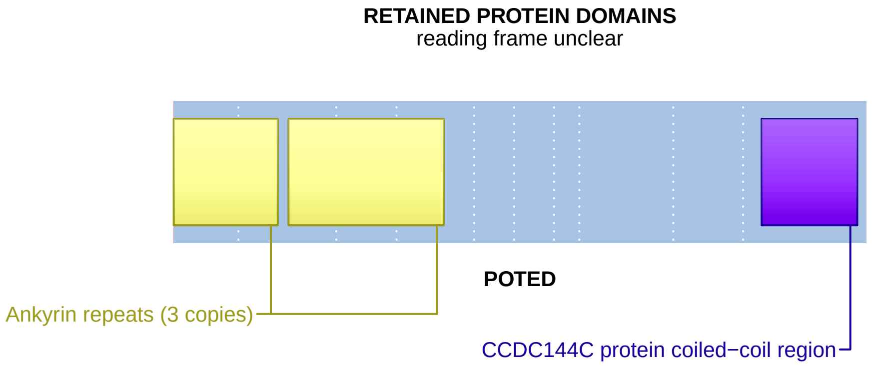


SUPPORTING READ COUNT

Split reads = 74
Discordant mates = 1

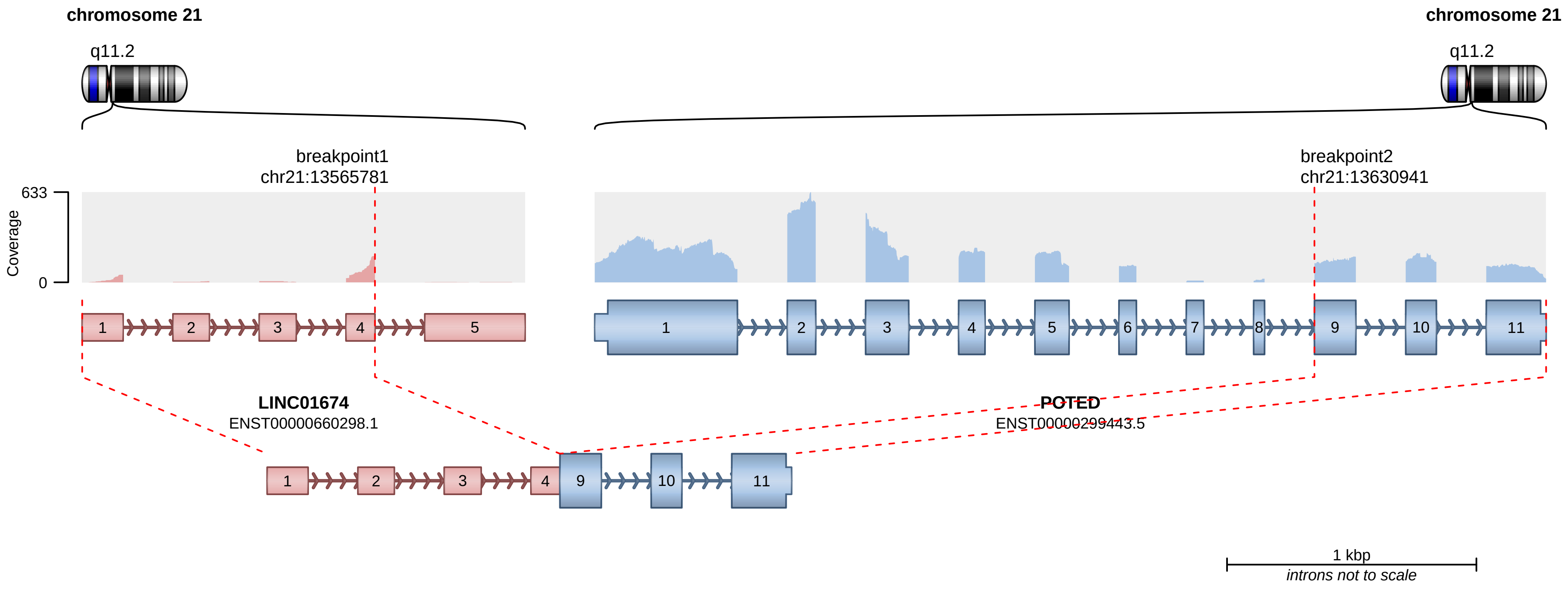


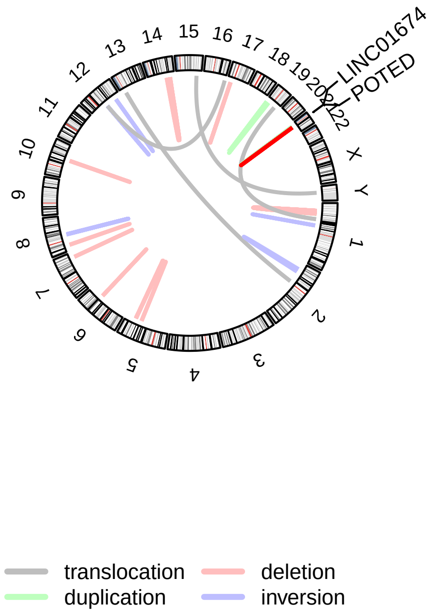




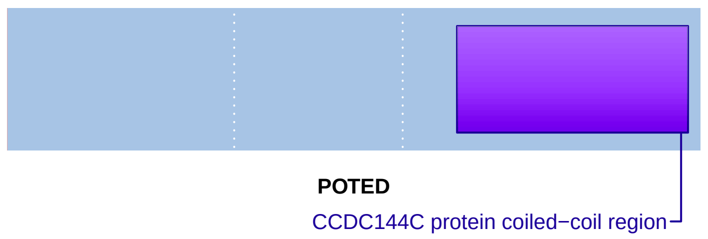
SUPPORTING READ COUNT

Split reads = 11
Discordant mates = 0



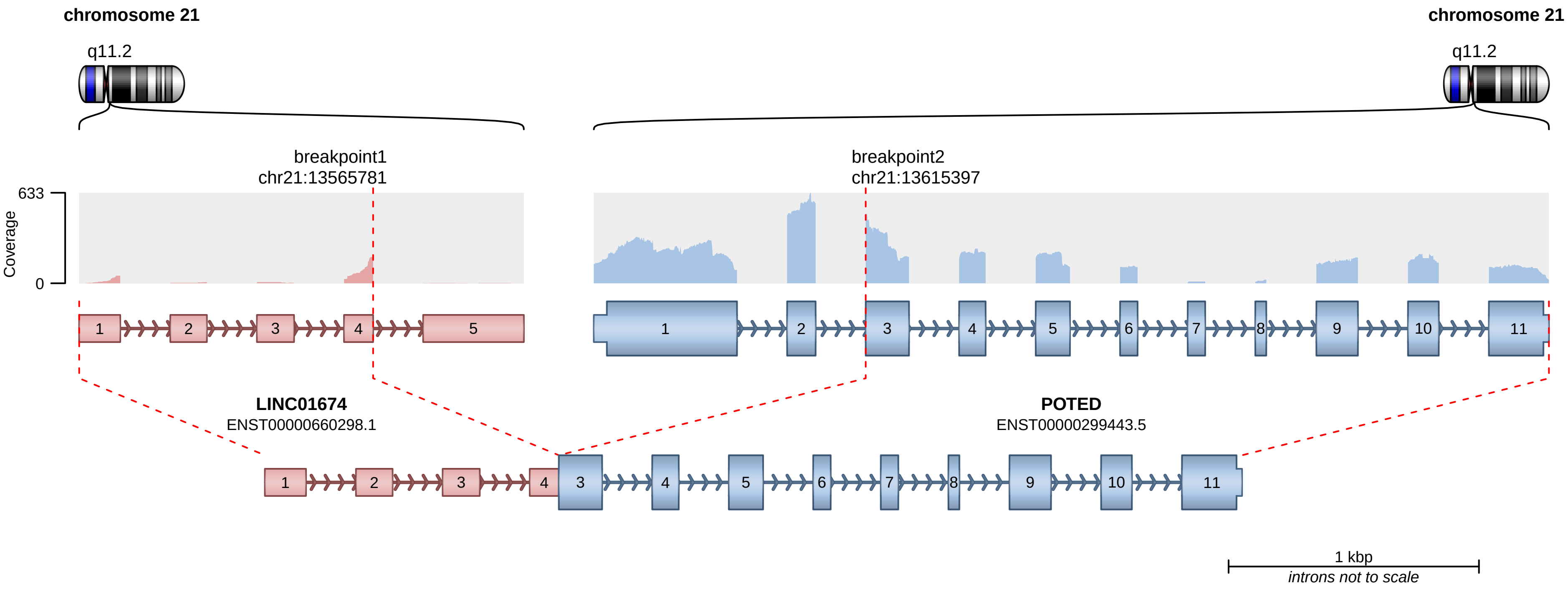


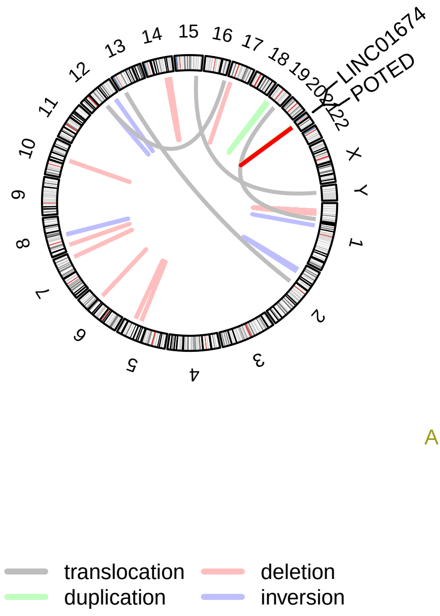
RETAINED PROTEIN DOMAINS
reading frame unclear



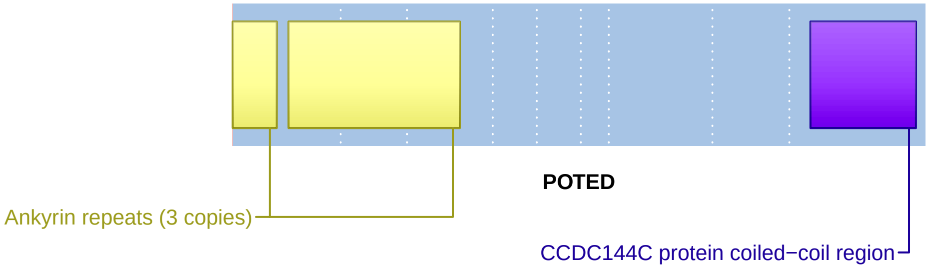
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0



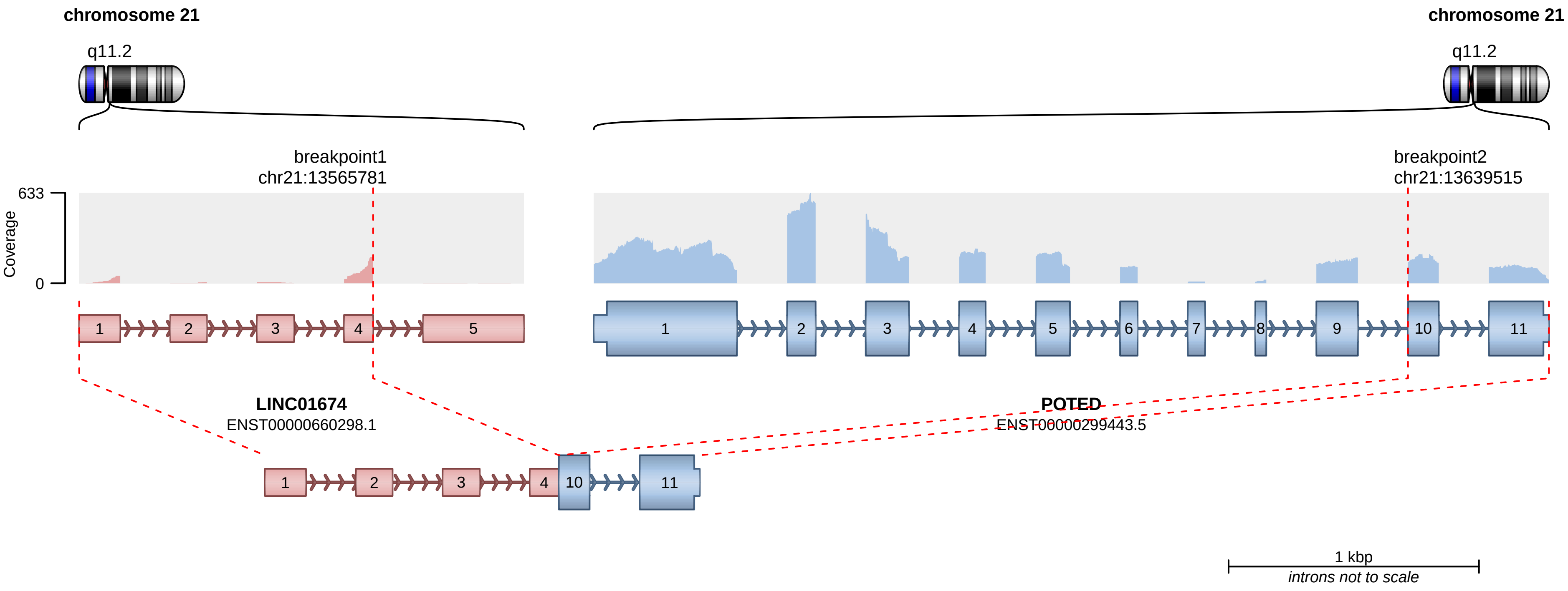


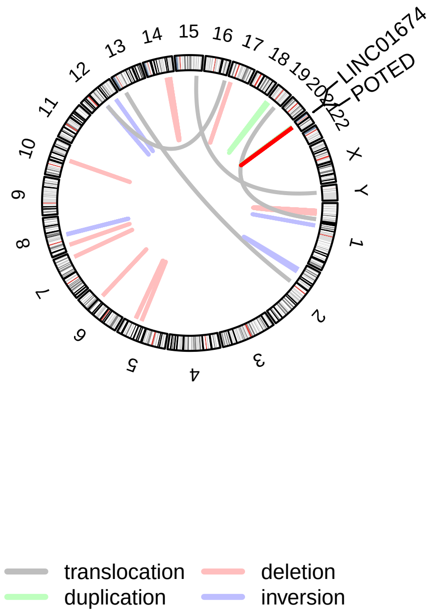
RETAINED PROTEIN DOMAINS
reading frame unclear



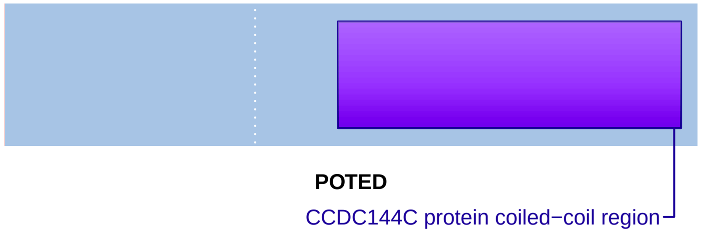
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1



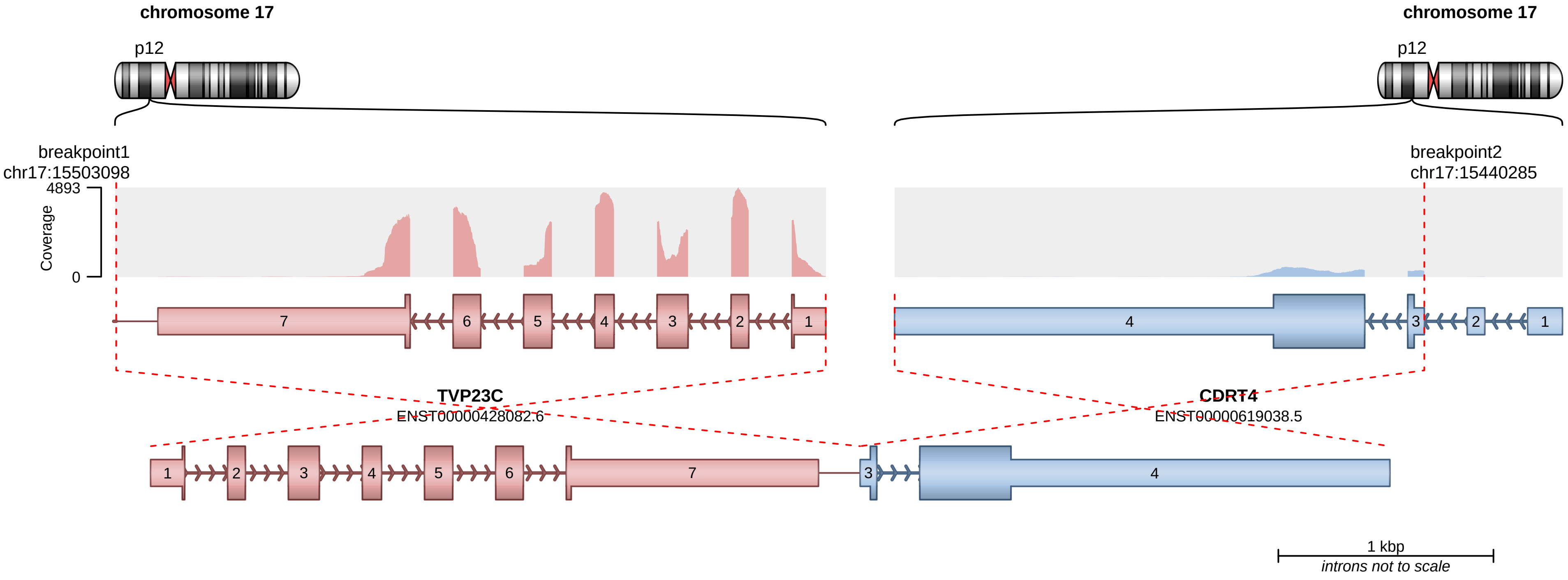


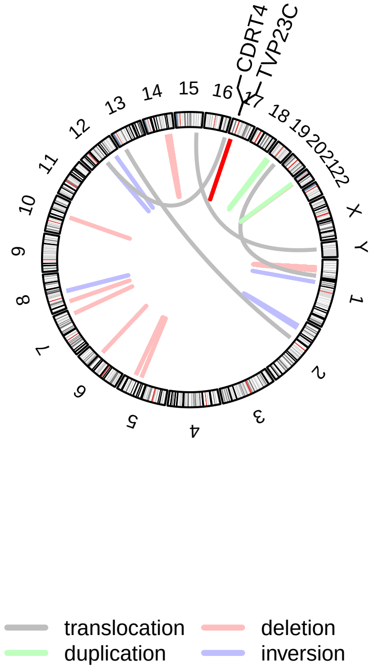
RETAINED PROTEIN DOMAINS
reading frame unclear

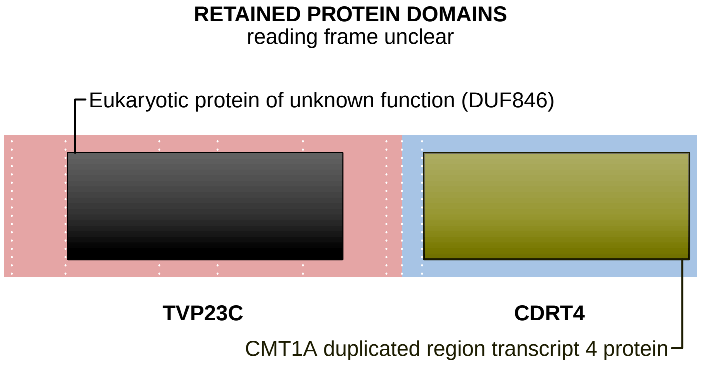


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

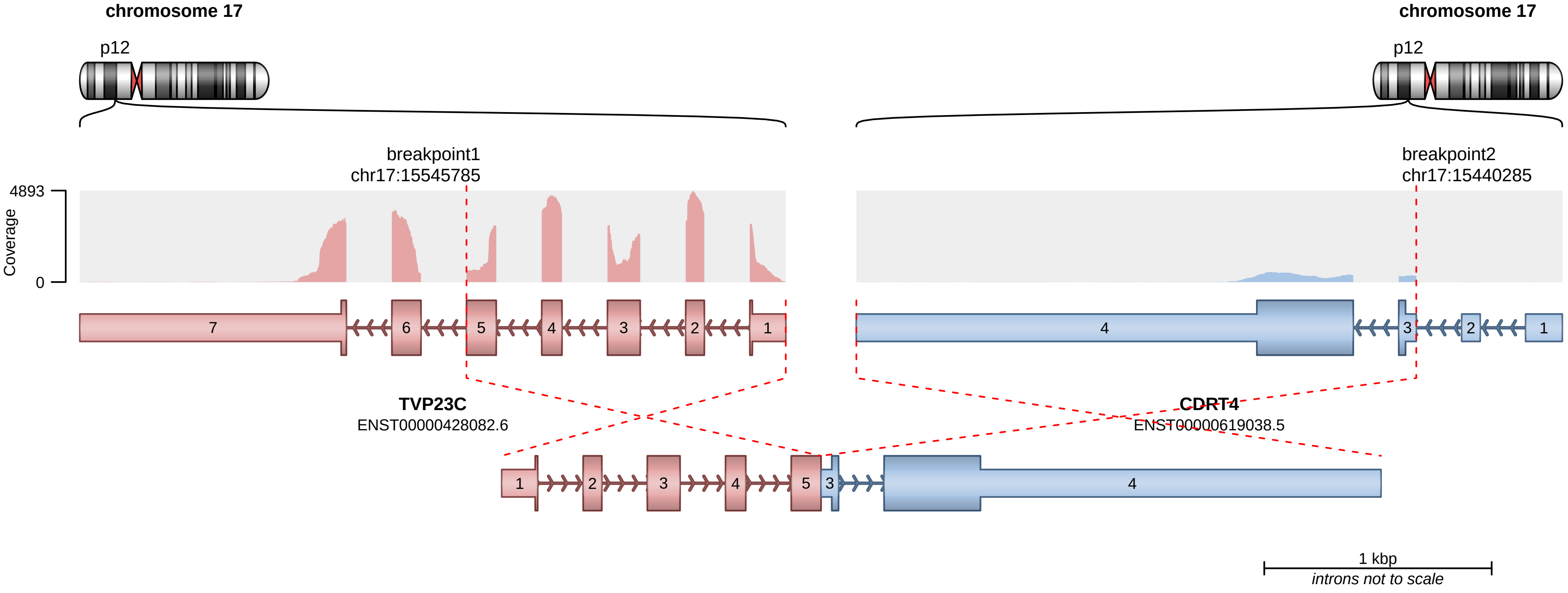


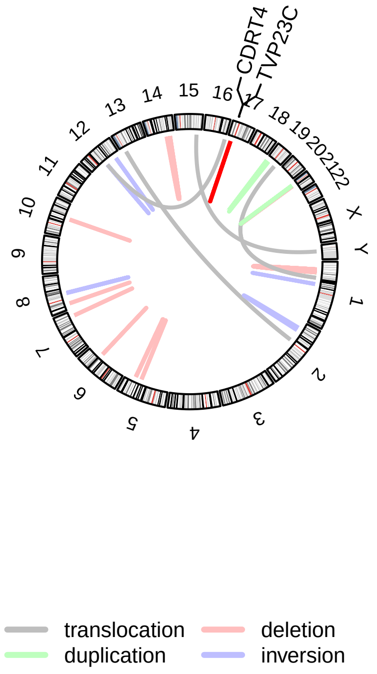




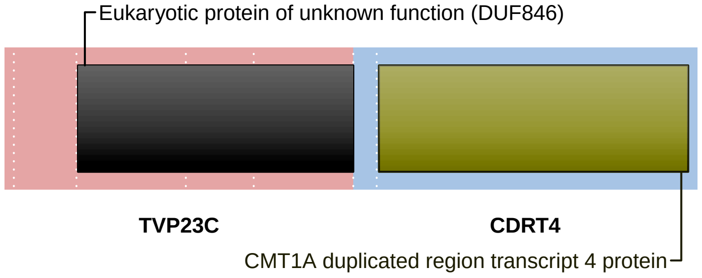
SUPPORTING READ COUNT

Split reads = 71
Discordant mates = 0



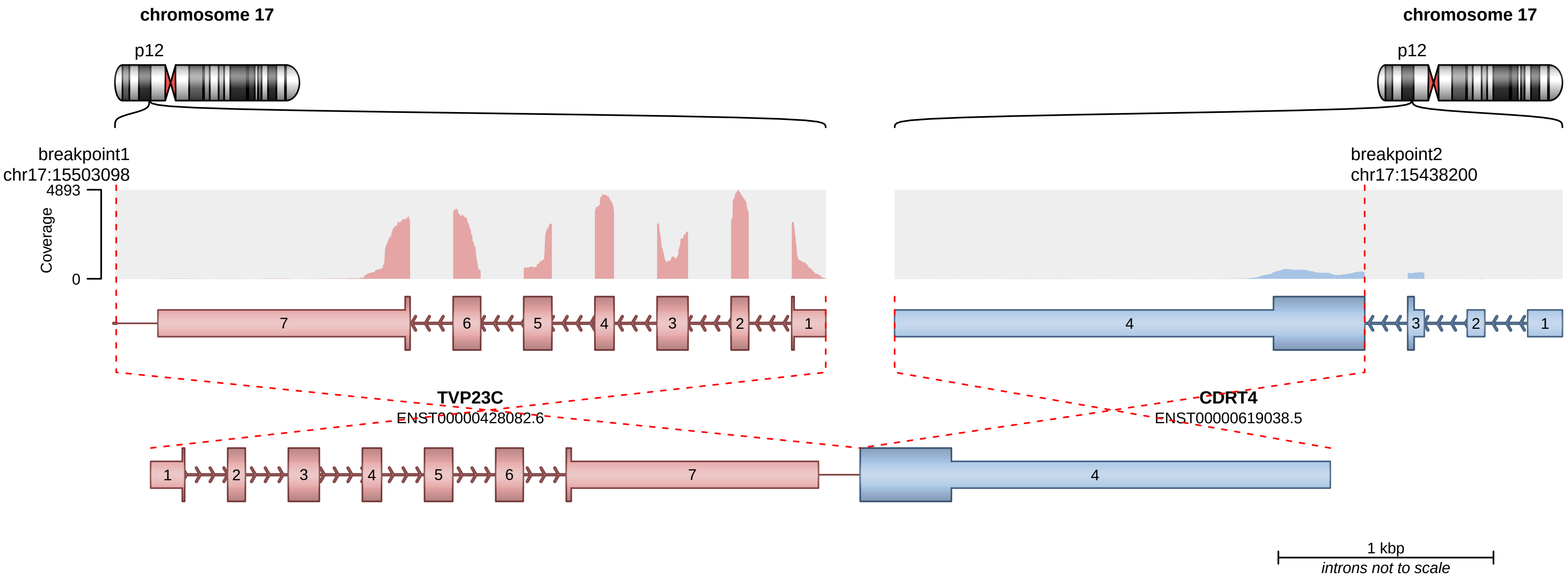


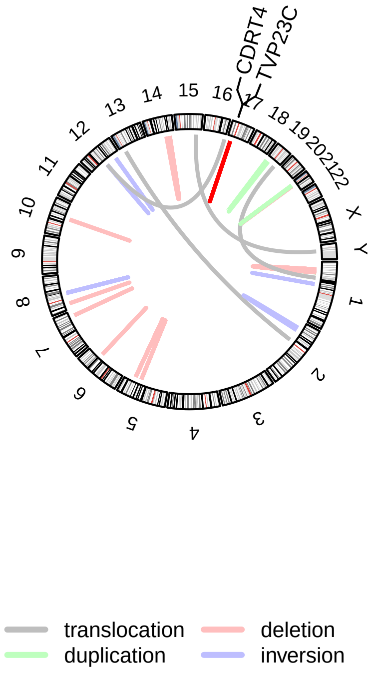
RETAINED PROTEIN DOMAINS
reading frame unclear



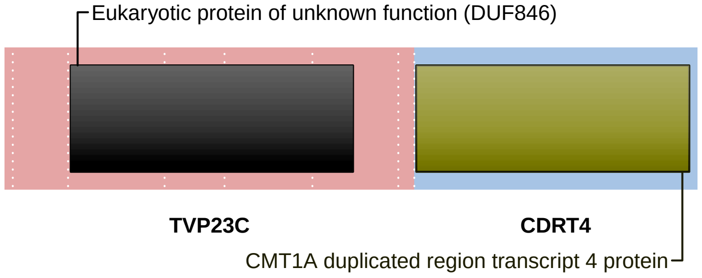
SUPPORTING READ COUNT

Split reads = 55
Discordant mates = 0



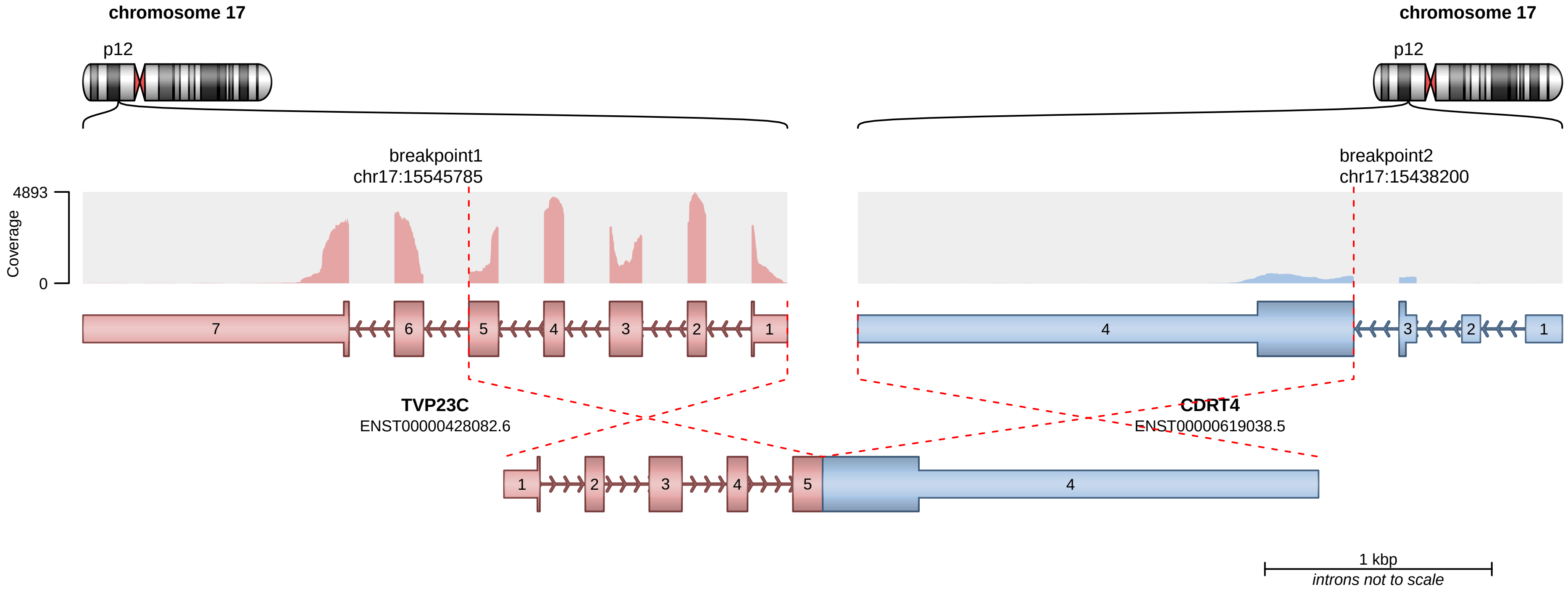


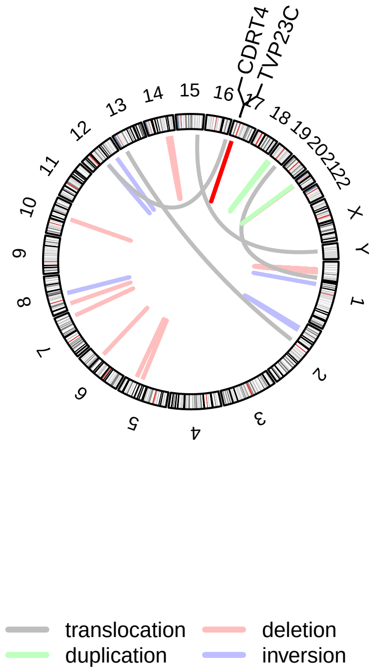
RETAINED PROTEIN DOMAINS
reading frame unclear



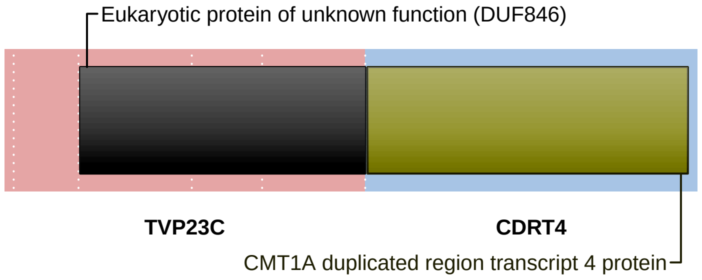
SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 0



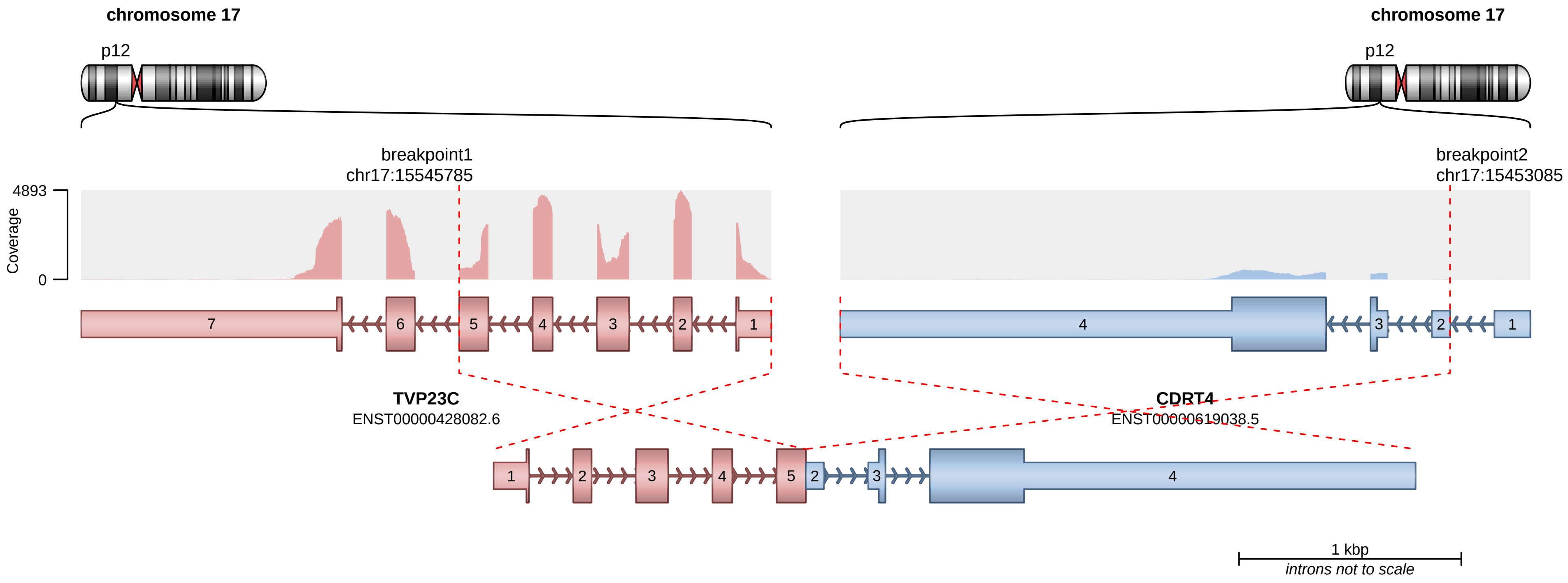


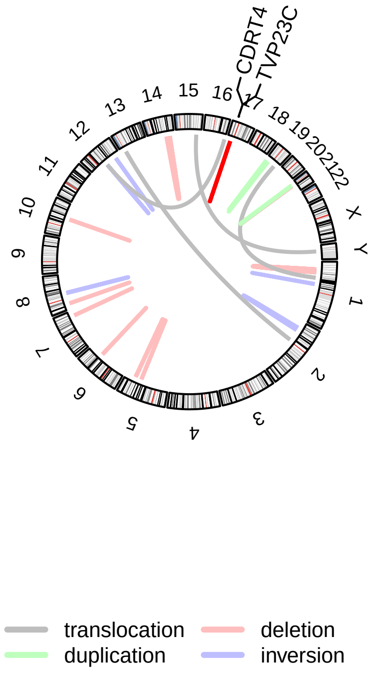
RETAINED PROTEIN DOMAINS
reading frame unclear



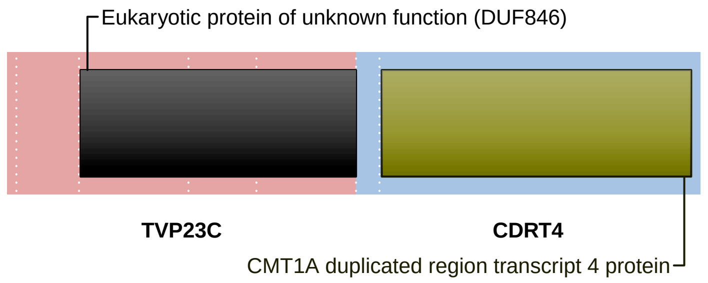
SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 0



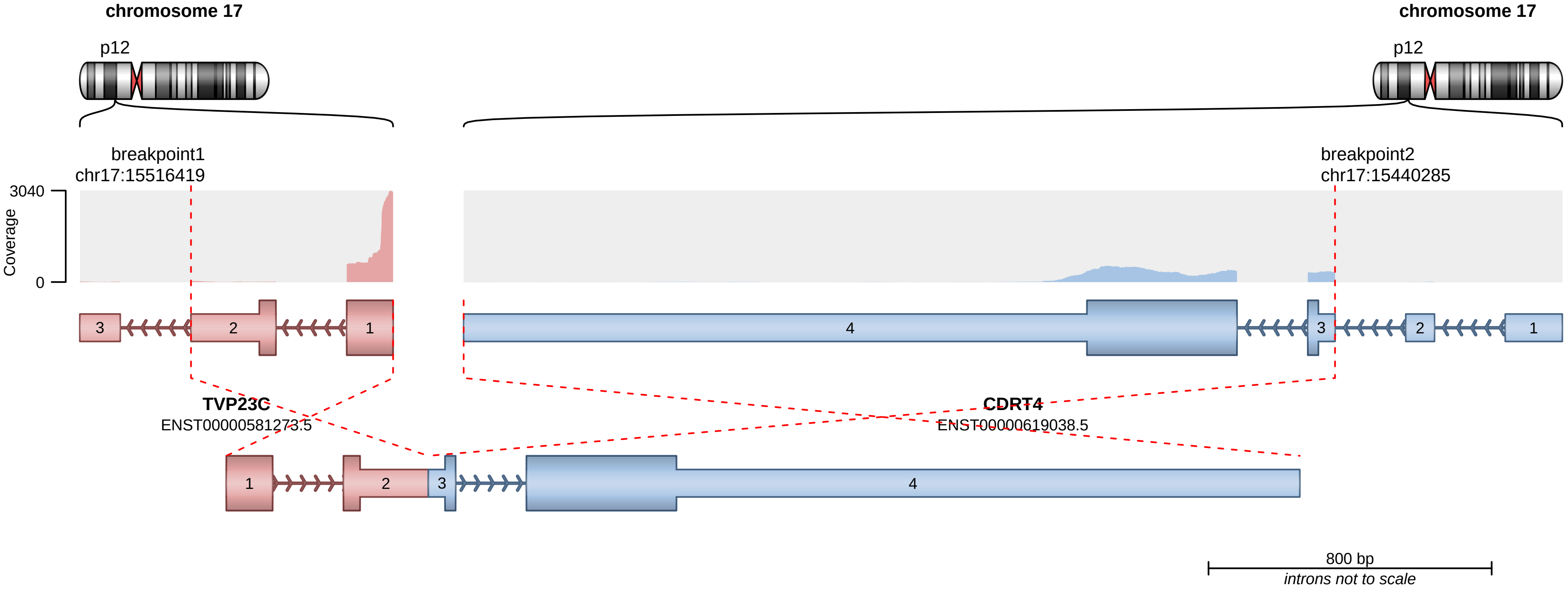


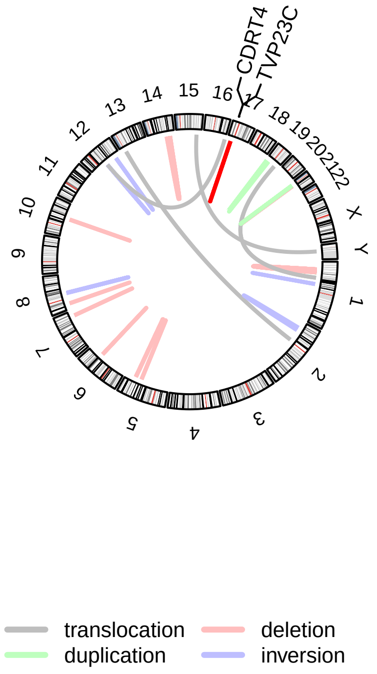
RETAINED PROTEIN DOMAINS
reading frame unclear



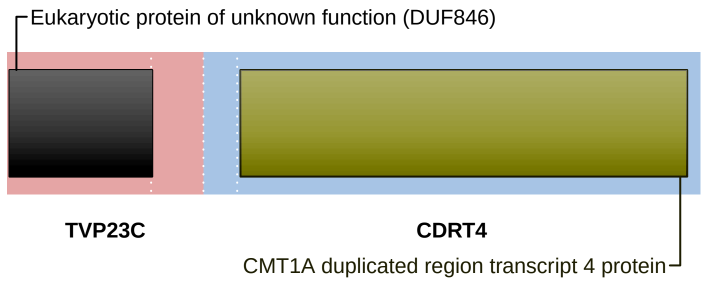
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0



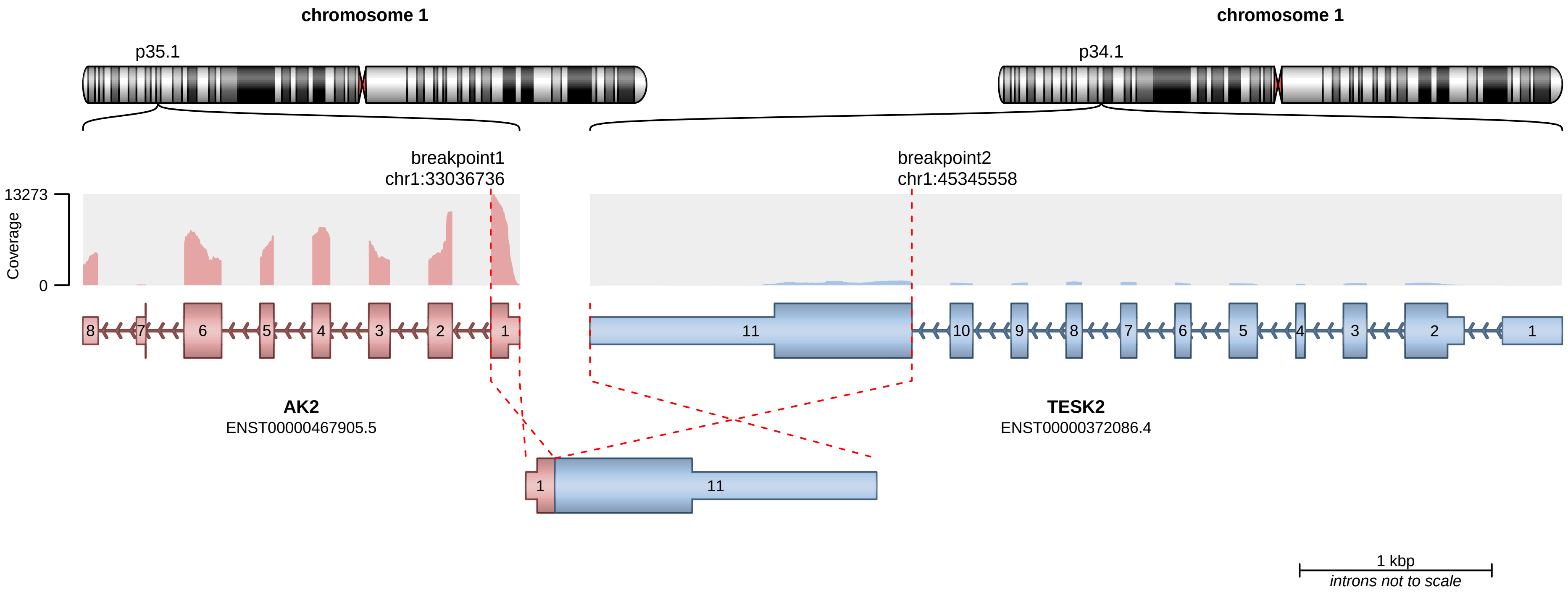


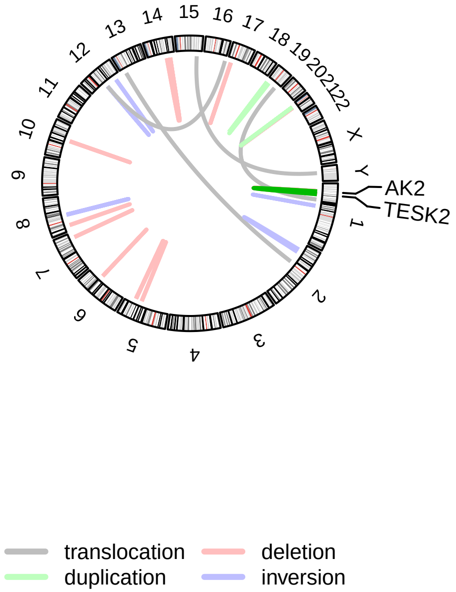
RETAINED PROTEIN DOMAINS
reading frame unclear



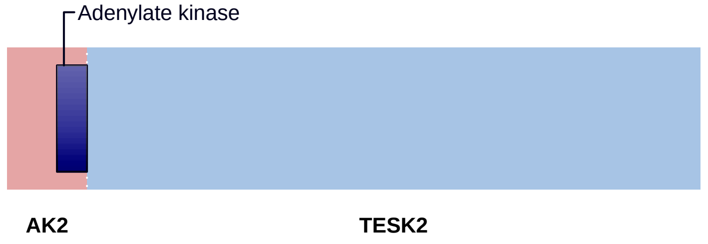
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



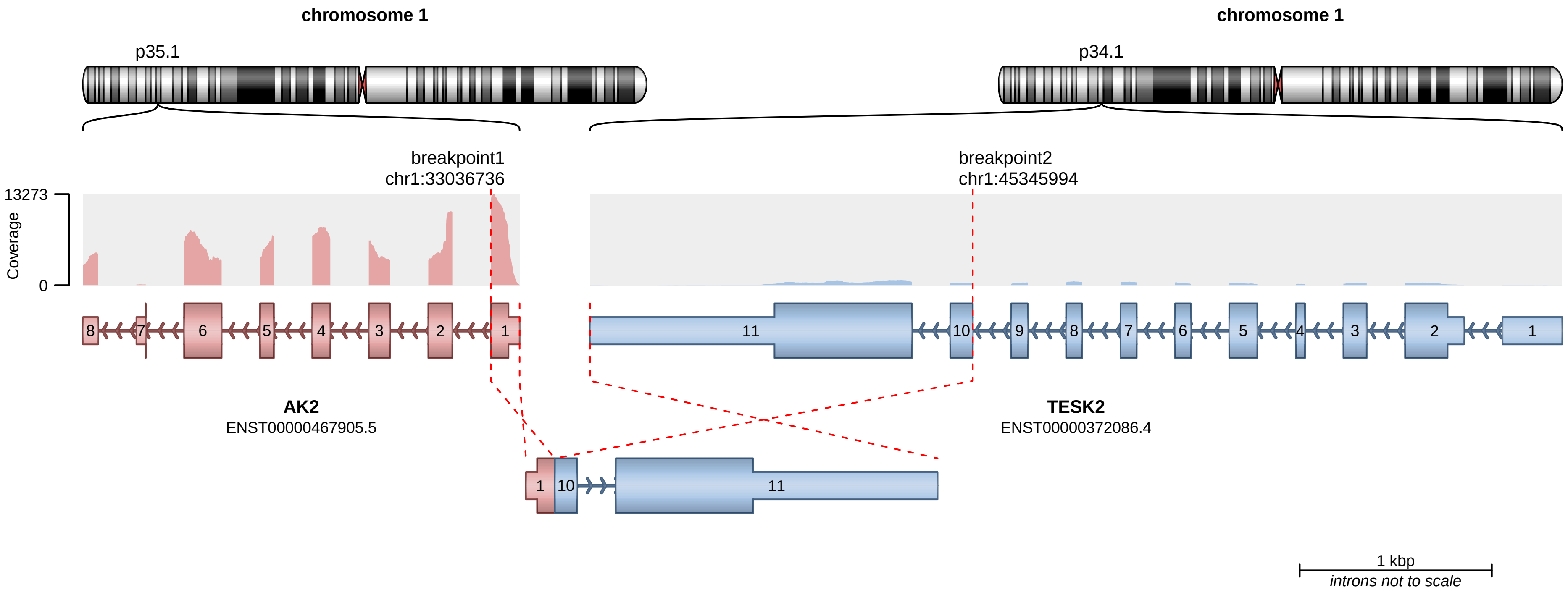


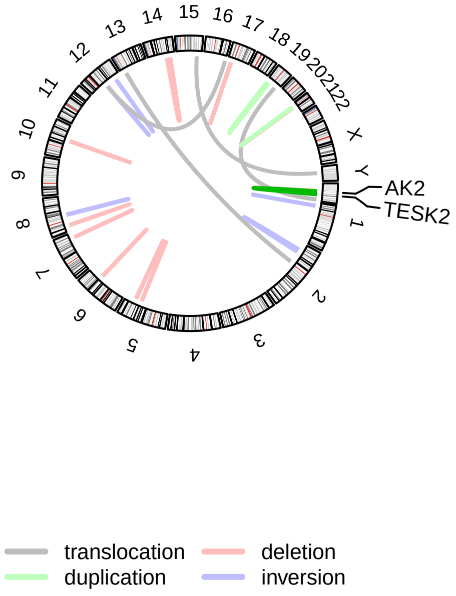
RETAINED PROTEIN DOMAINS
reading frame unclear



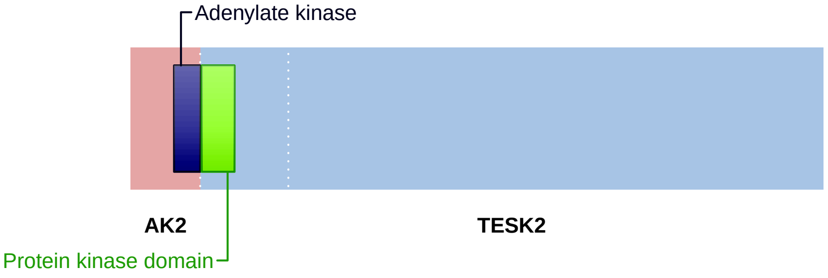
SUPPORTING READ COUNT

Split reads = 51
Discordant mates = 0



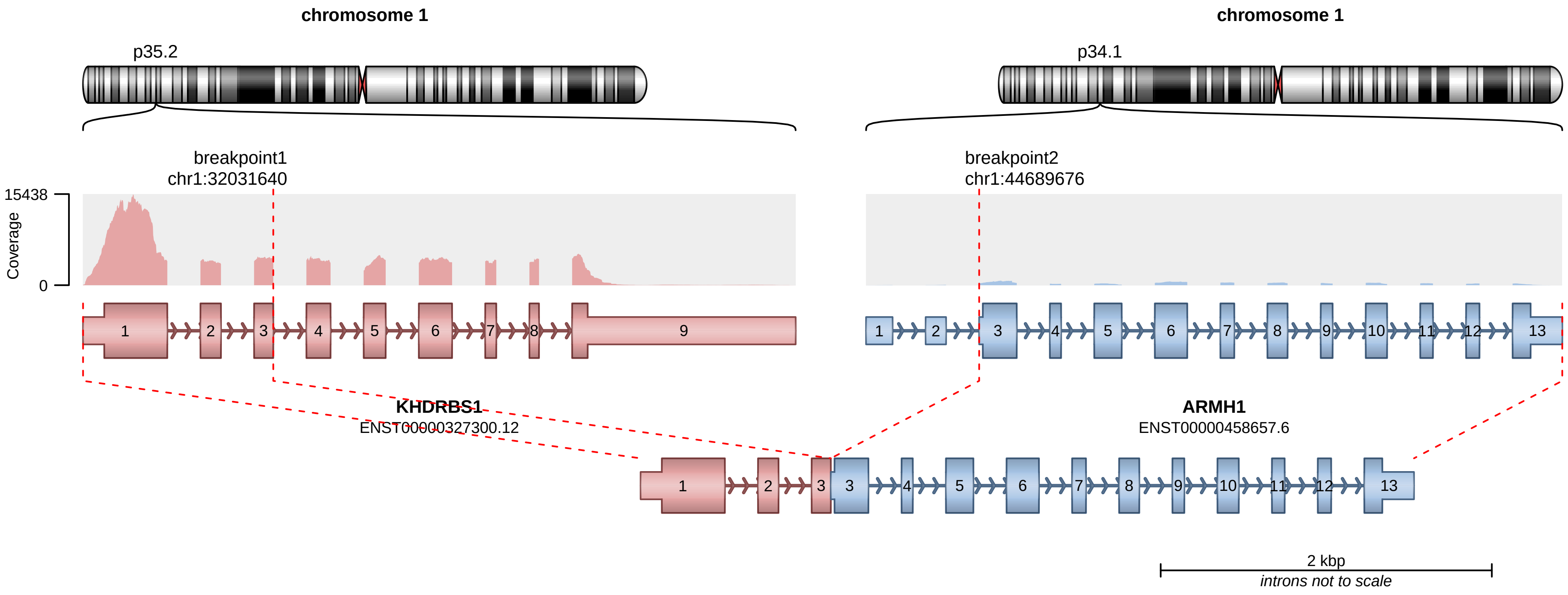


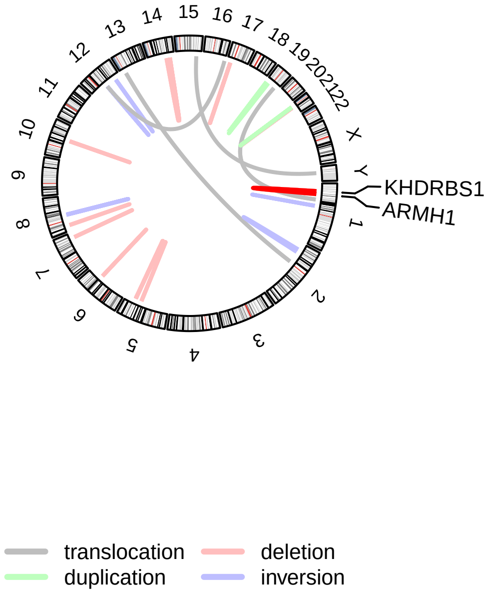
RETAINED PROTEIN DOMAINS
reading frame unclear

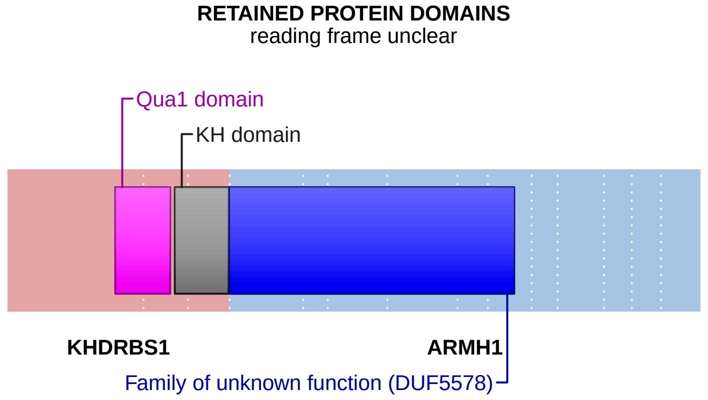


SUPPORTING READ COUNT

Split reads = 20
Discordant mates = 0

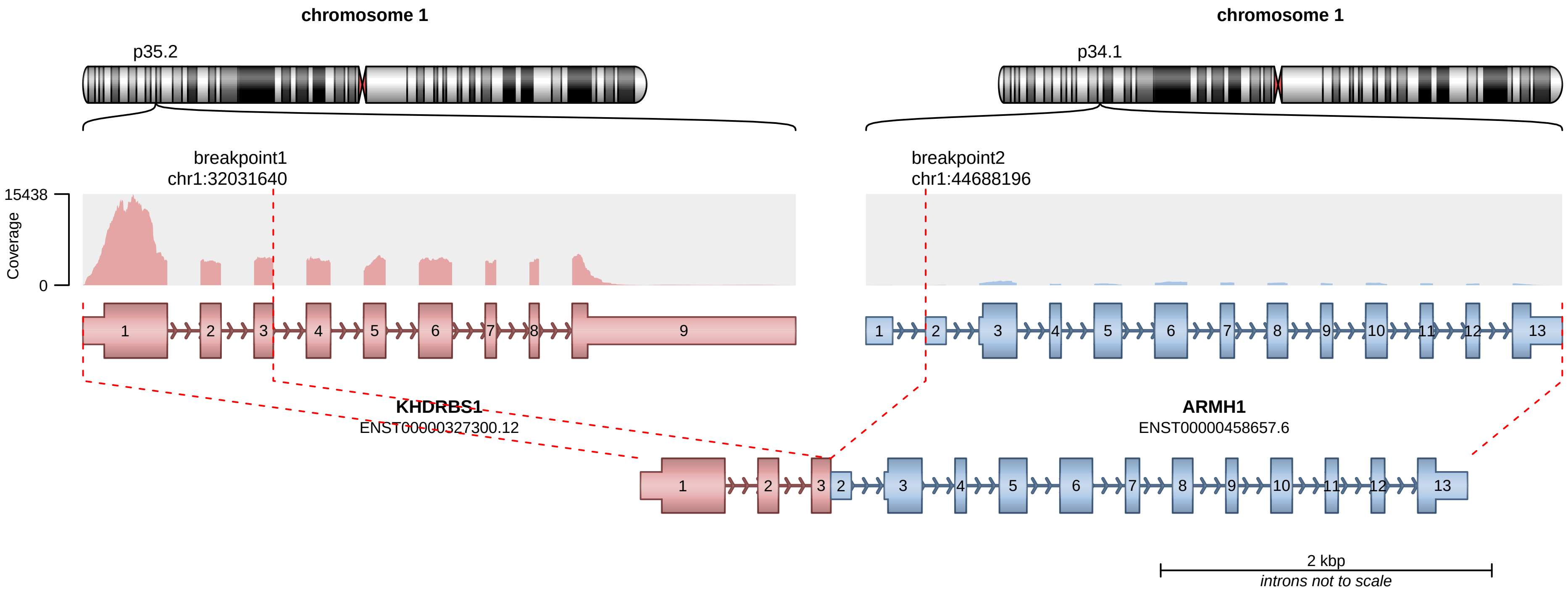


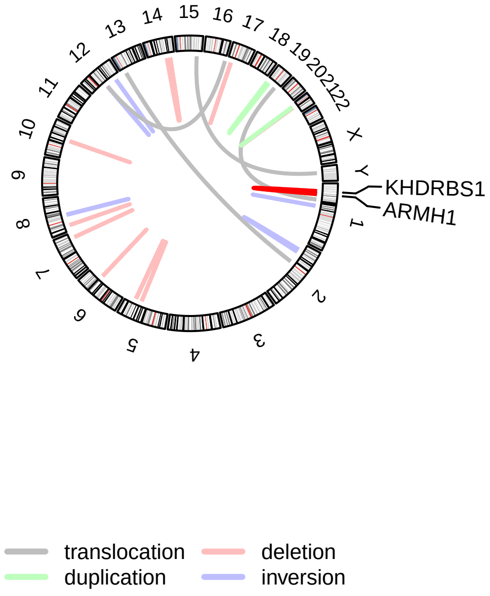




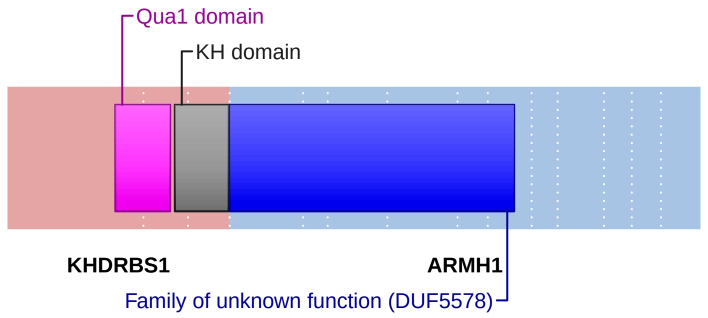
SUPPORTING READ COUNT

Split reads = 50
Discordant mates = 1



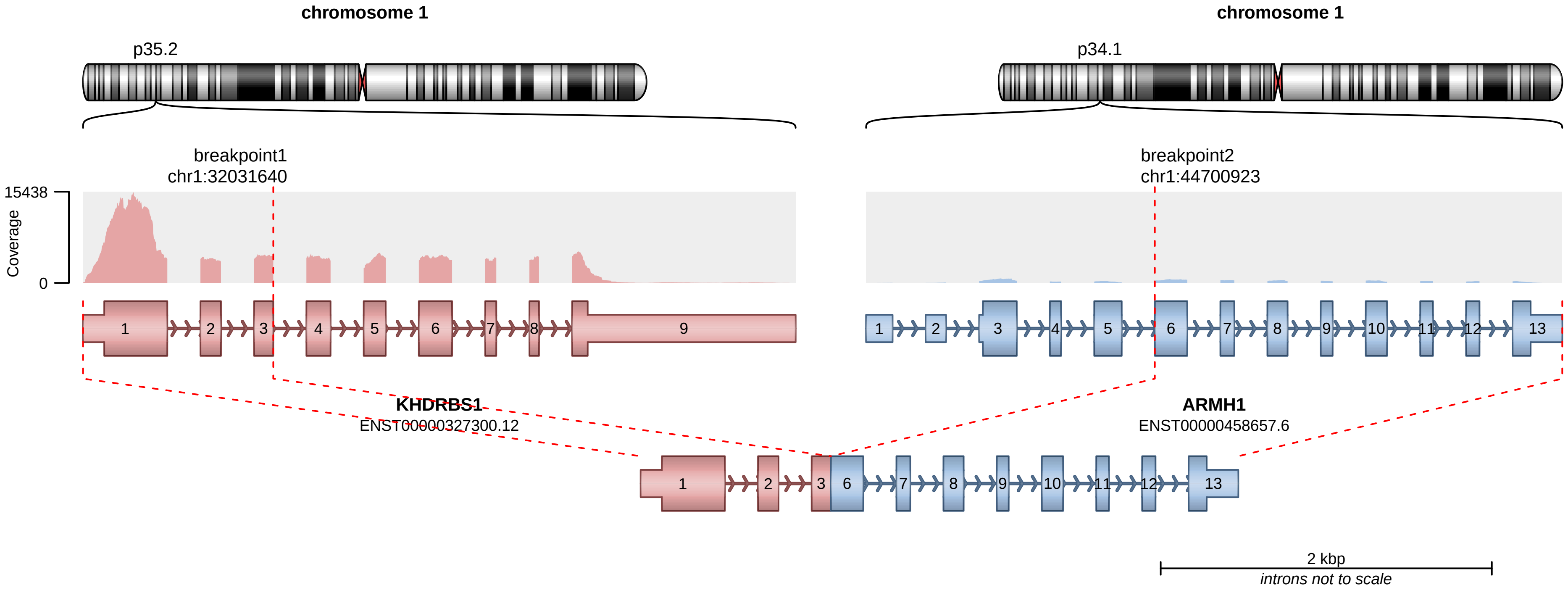


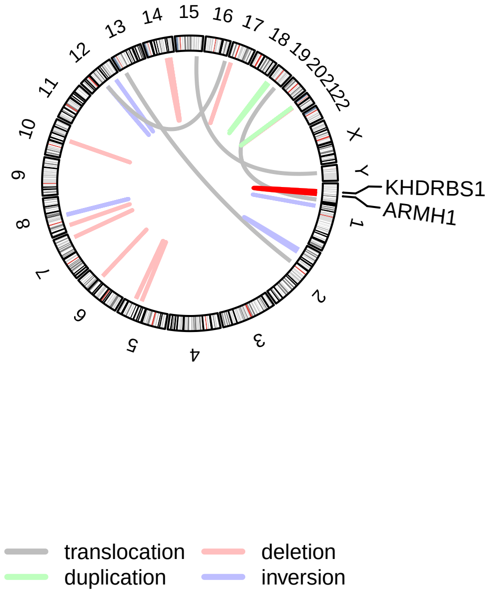
RETAINED PROTEIN DOMAINS
reading frame unclear

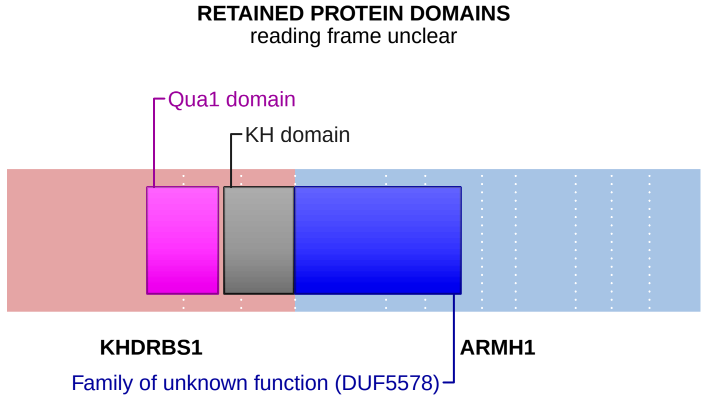


SUPPORTING READ COUNT

Split reads = 14
Discordant mates = 2

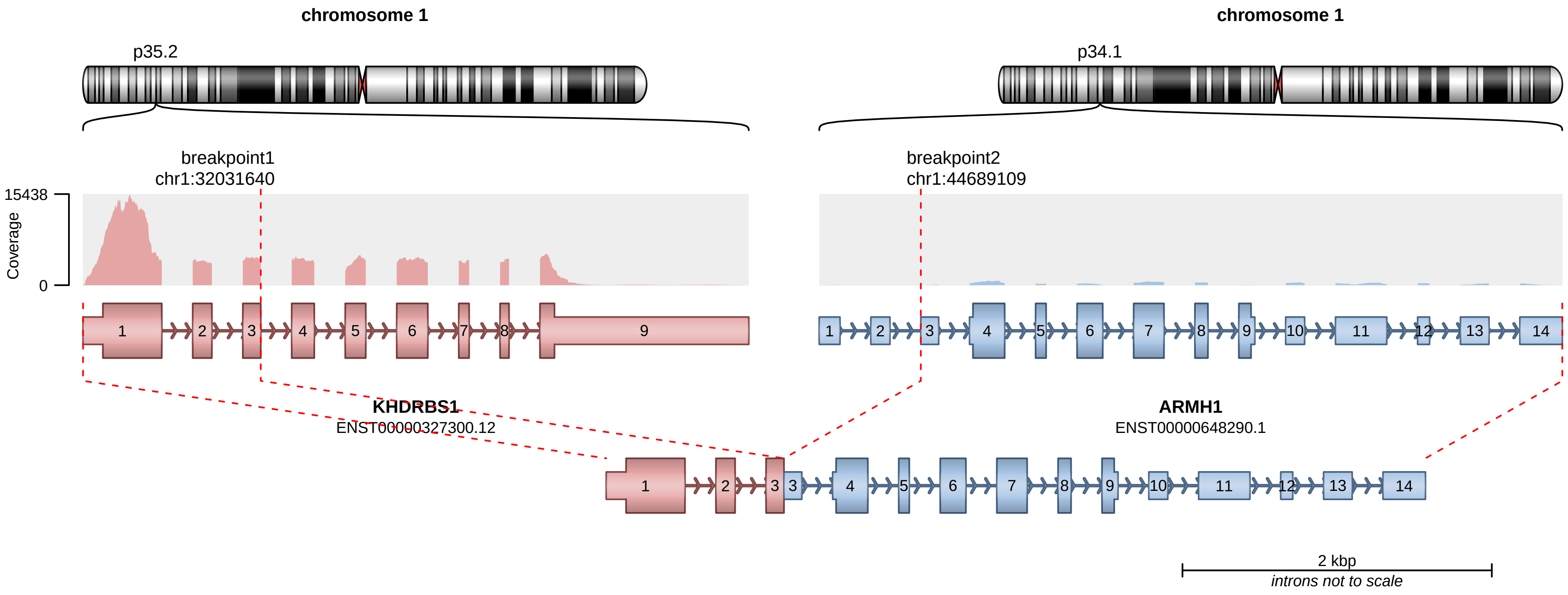


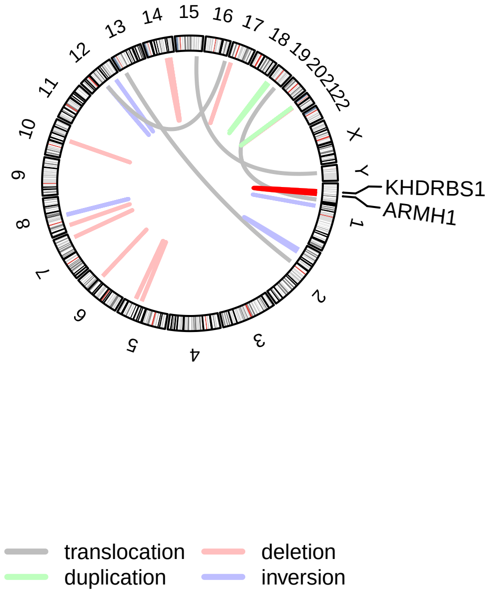


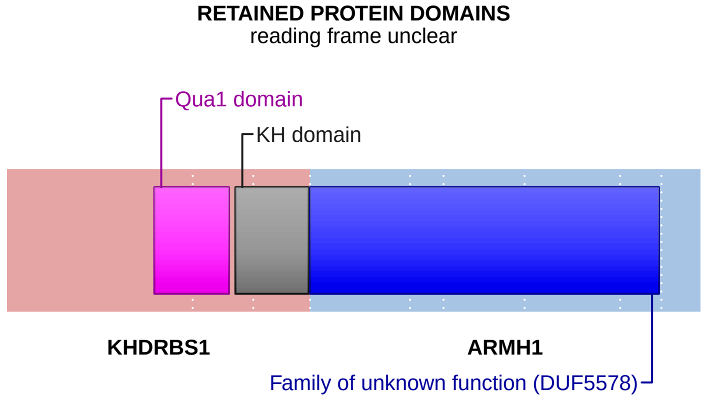


SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 0

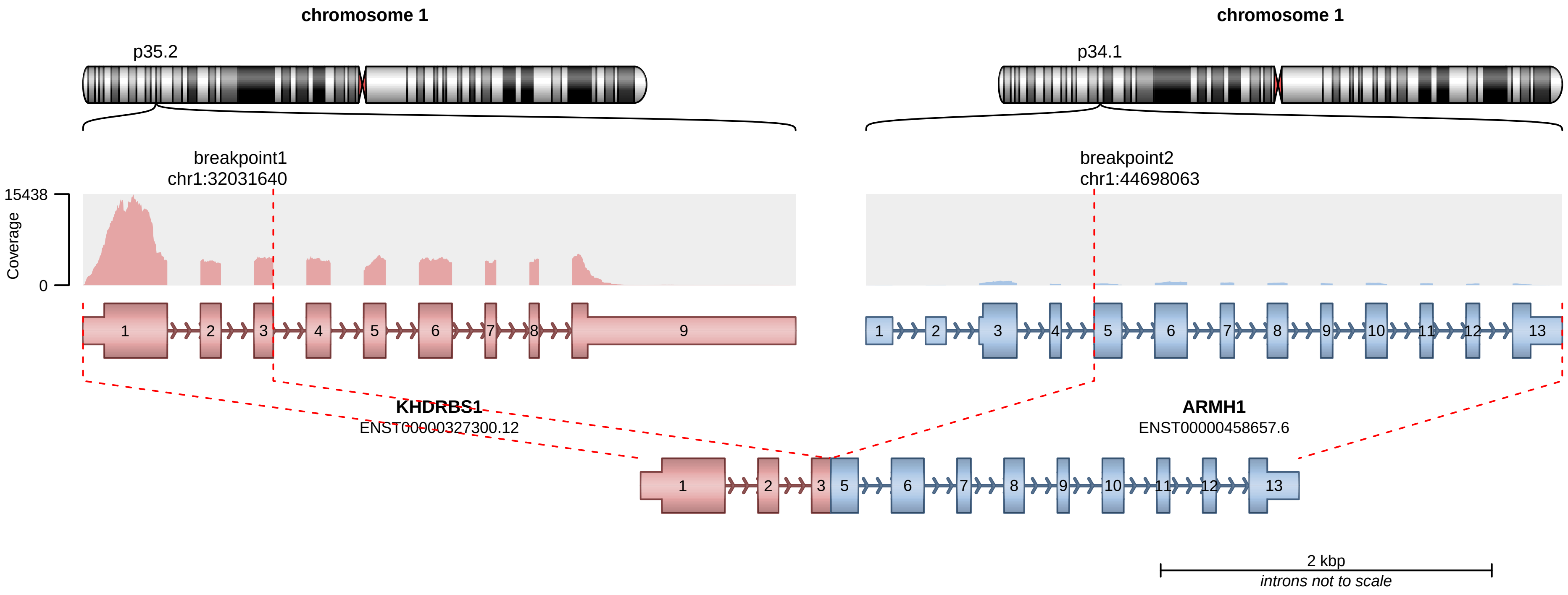


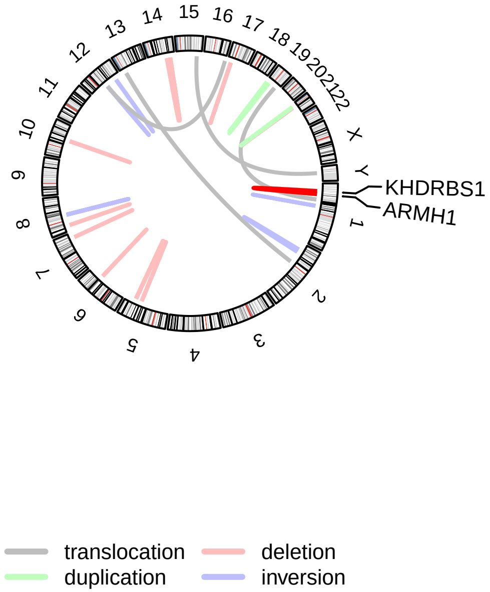


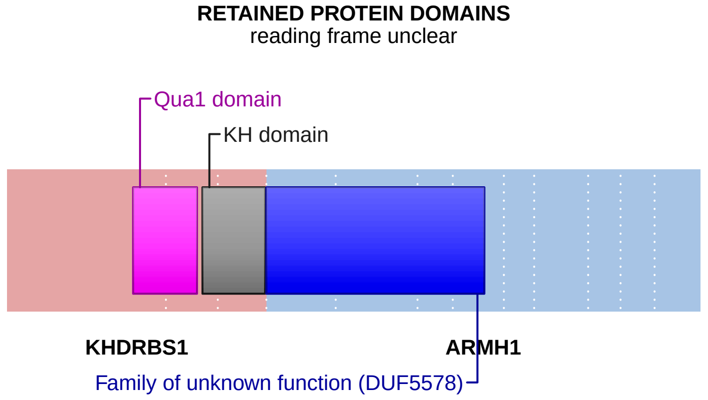


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 2

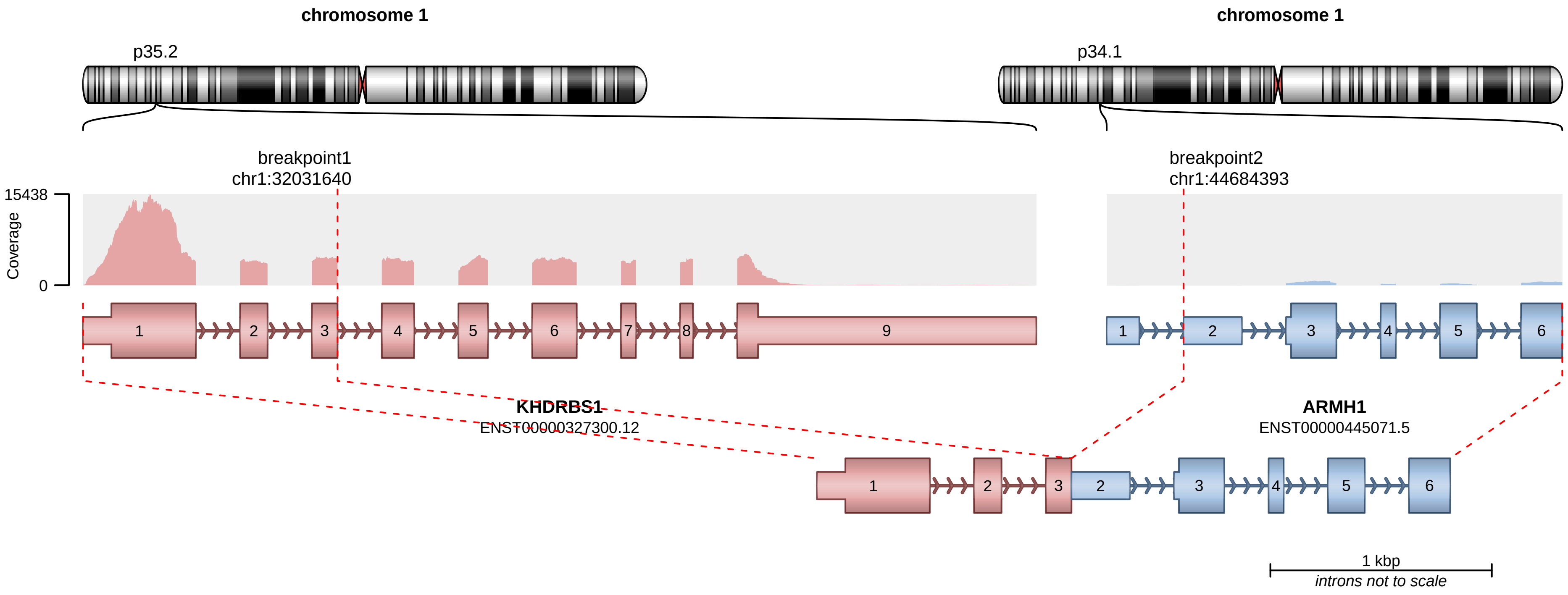


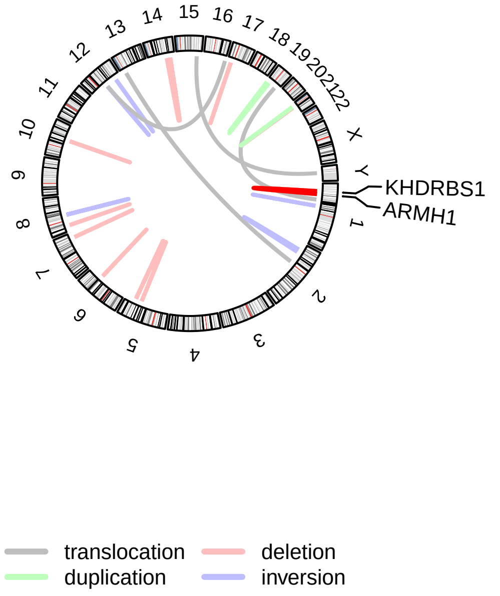


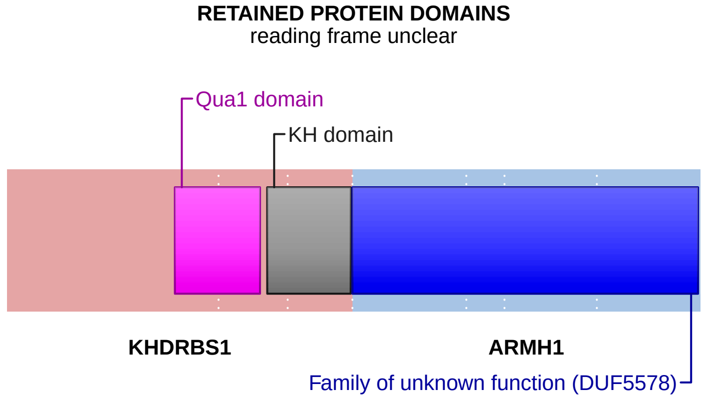


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

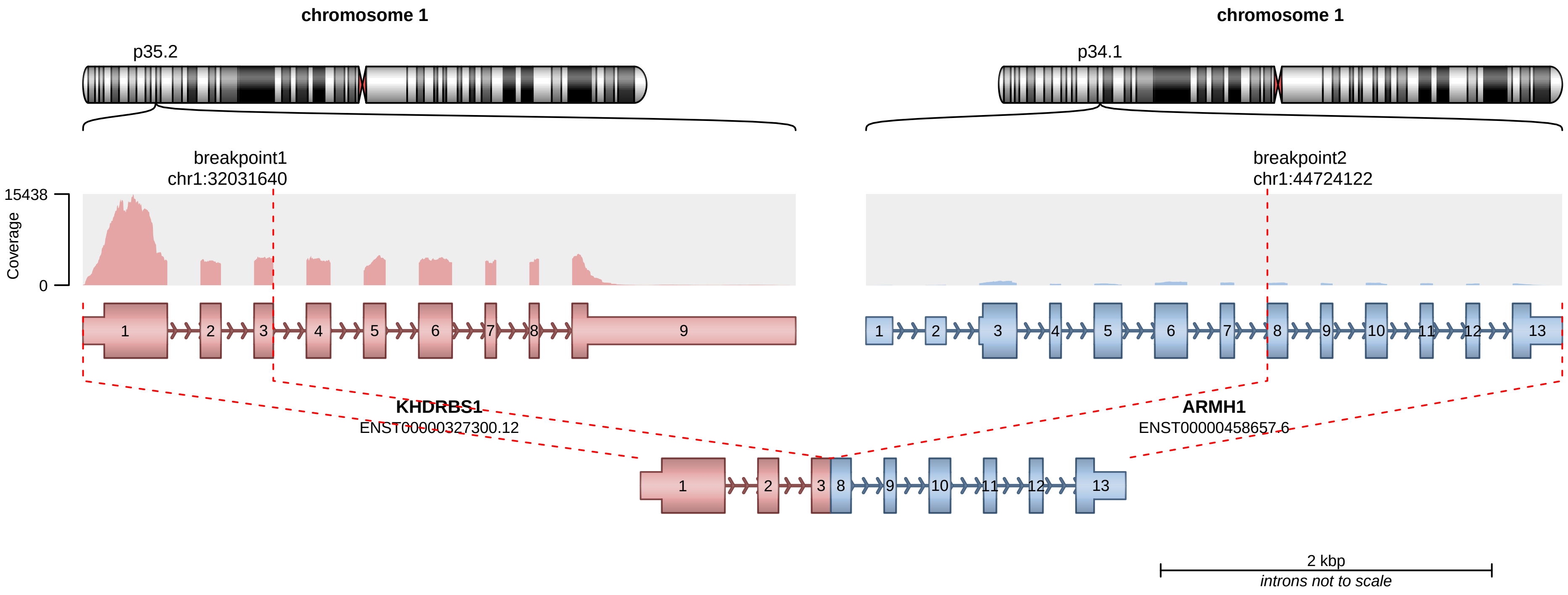


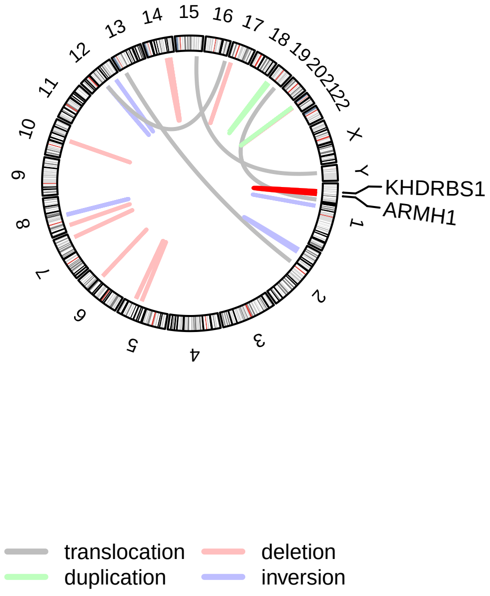


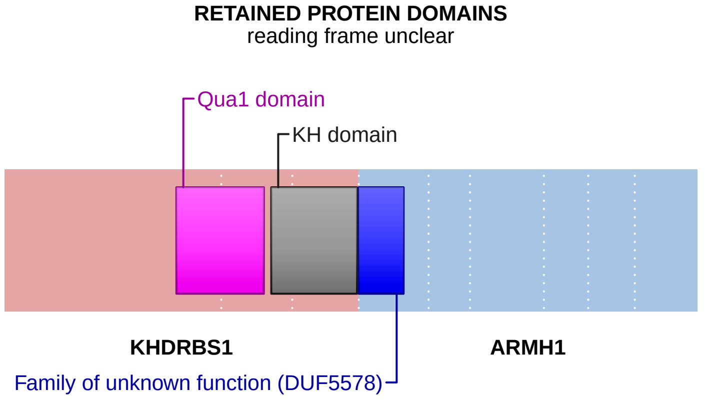


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 2

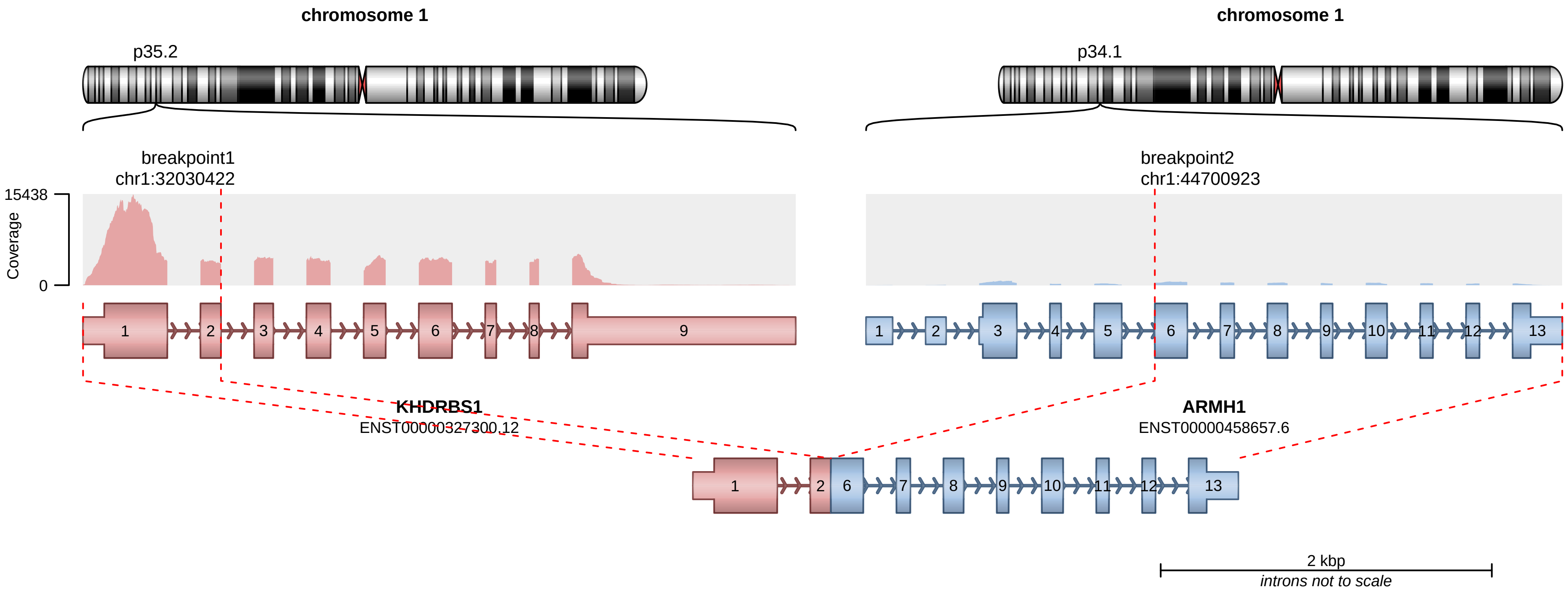


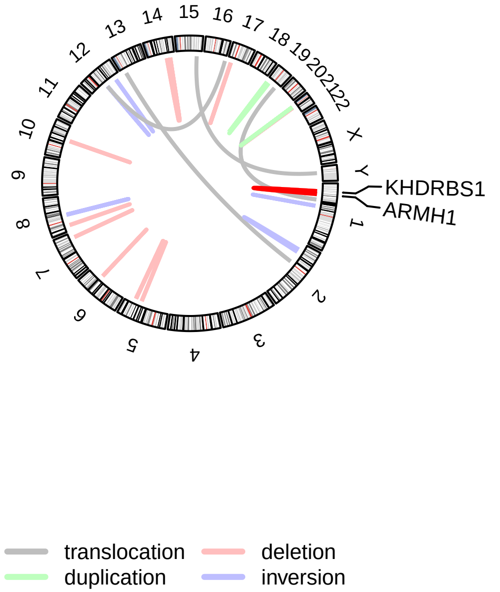


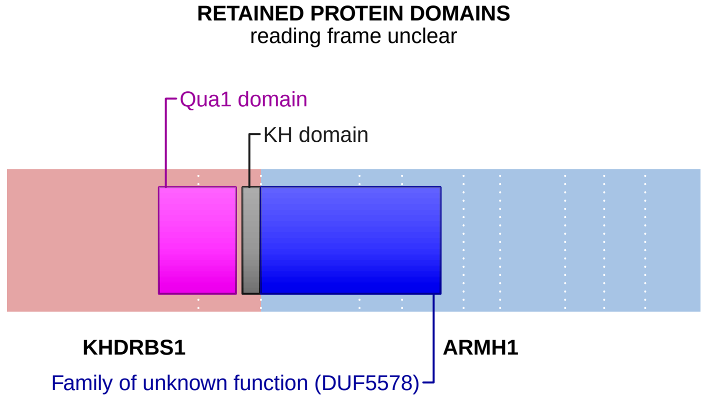


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

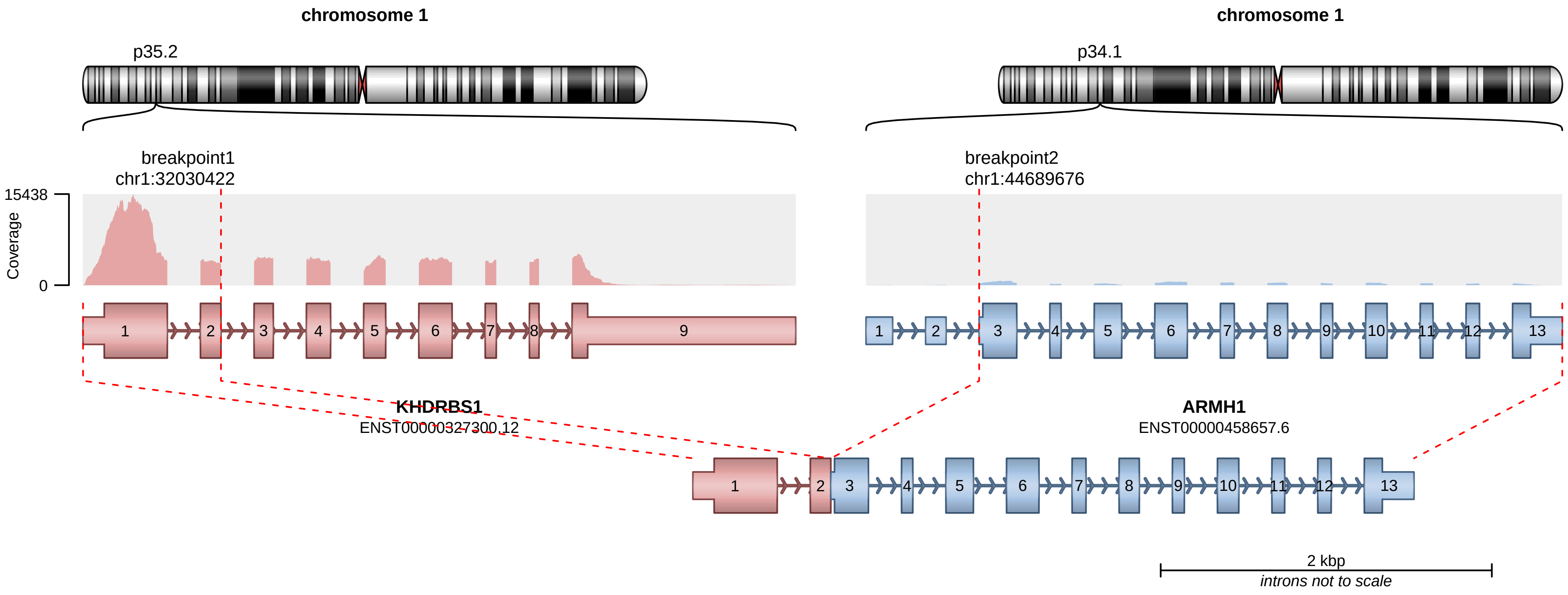


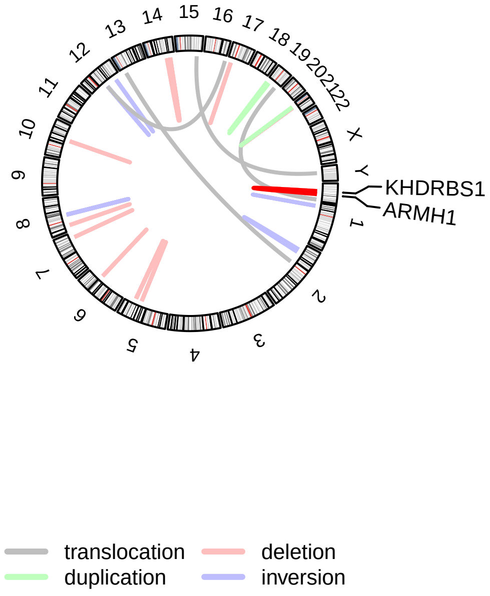


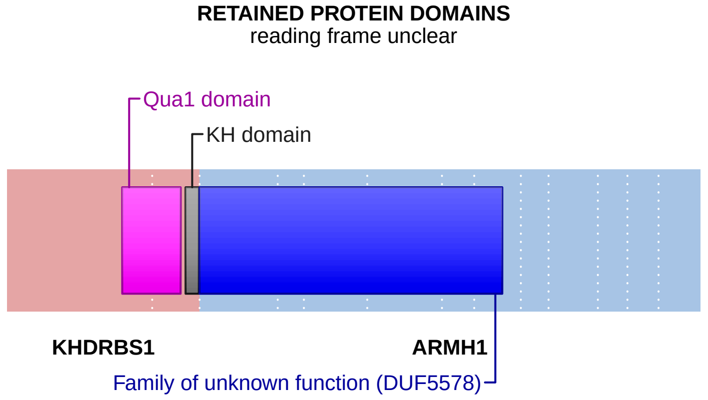


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

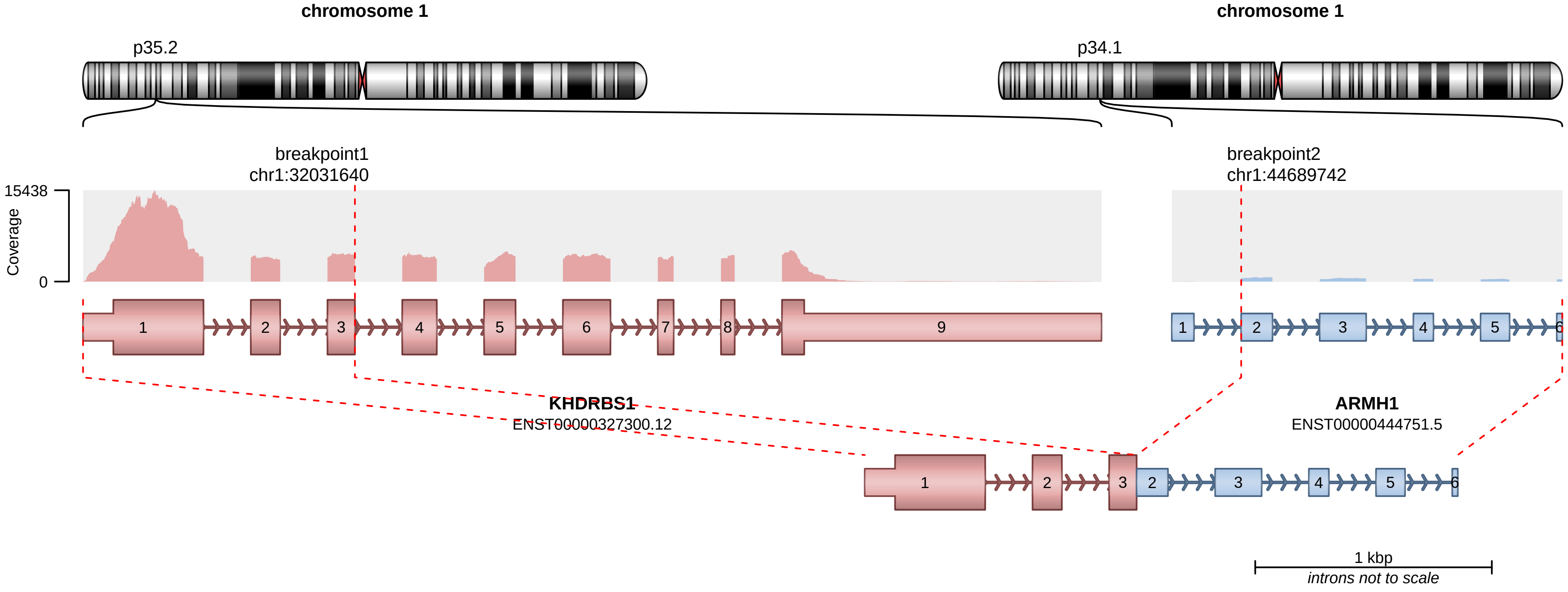


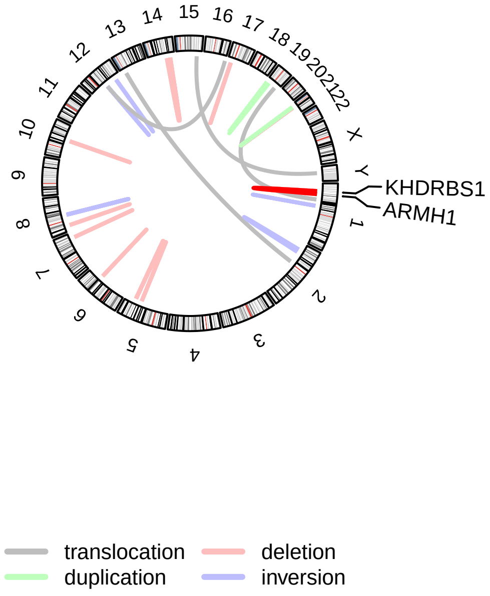




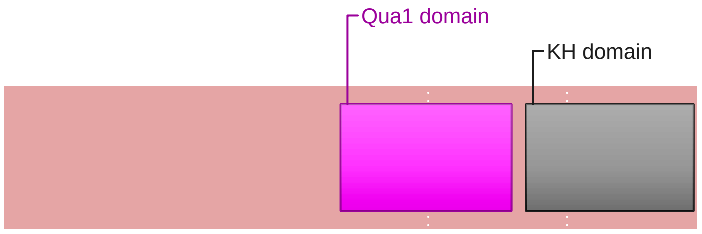
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0





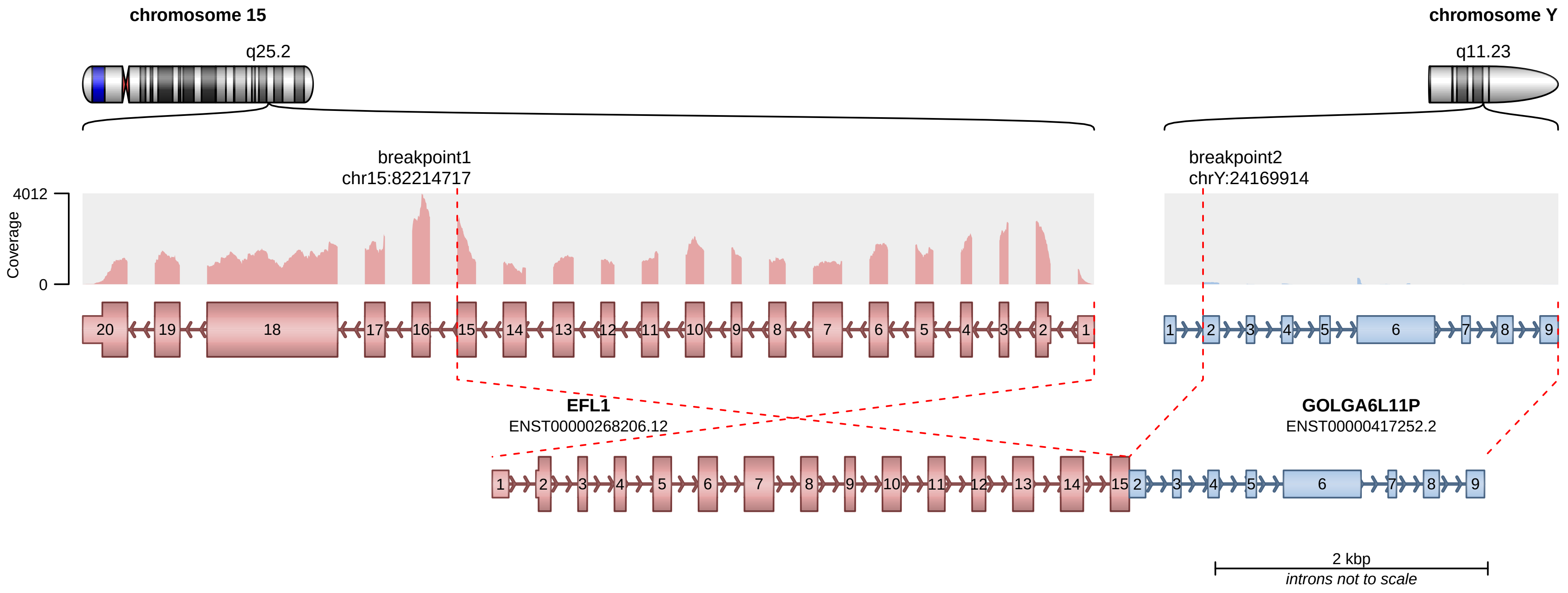
RETAINED PROTEIN DOMAINS
reading frame unclear

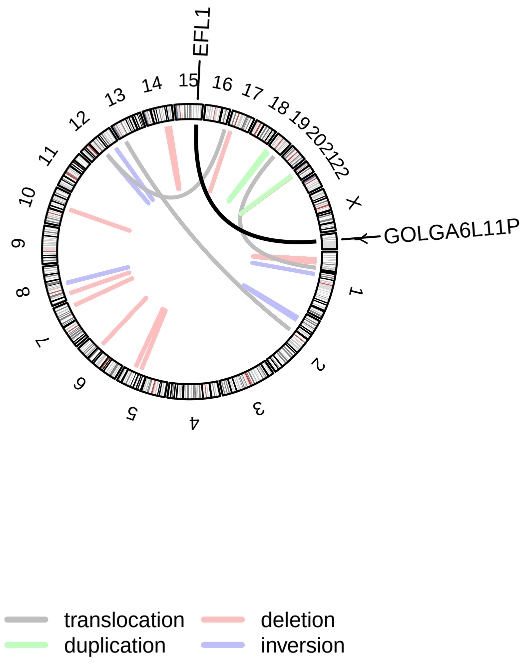


KHDRBS1

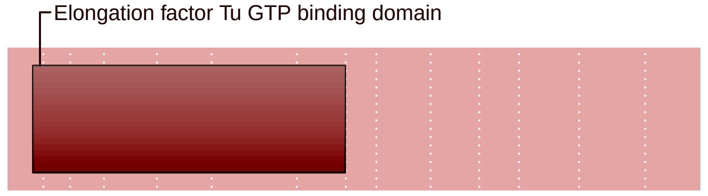
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0





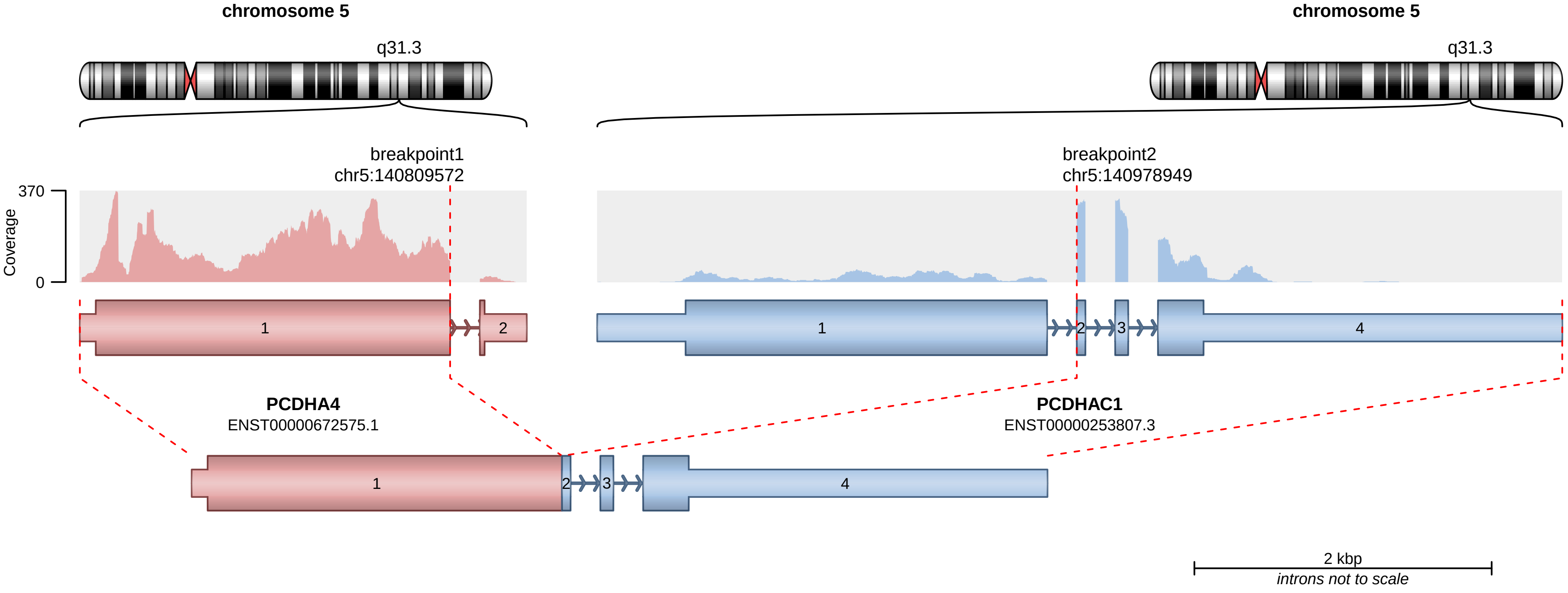
RETAINED PROTEIN DOMAINS
reading frame unclear

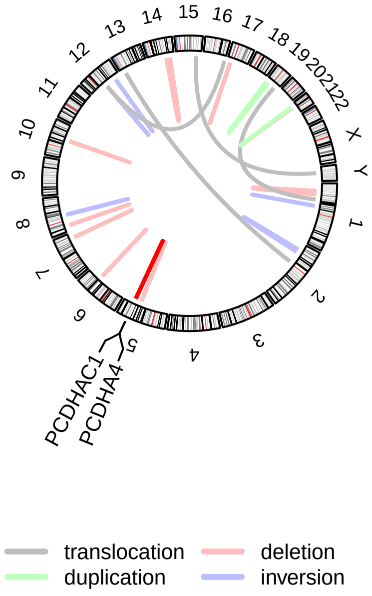


EFL1

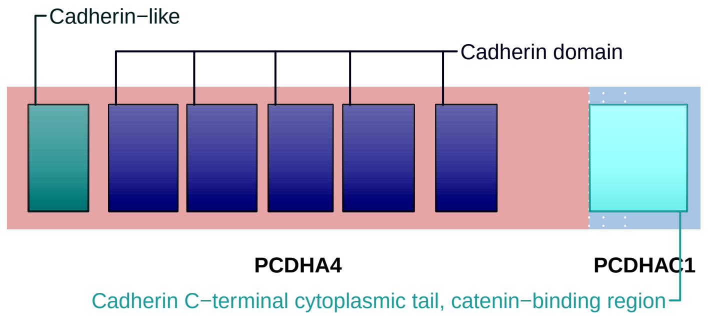
SUPPORTING READ COUNT

Split reads = 33
Discordant mates = 0



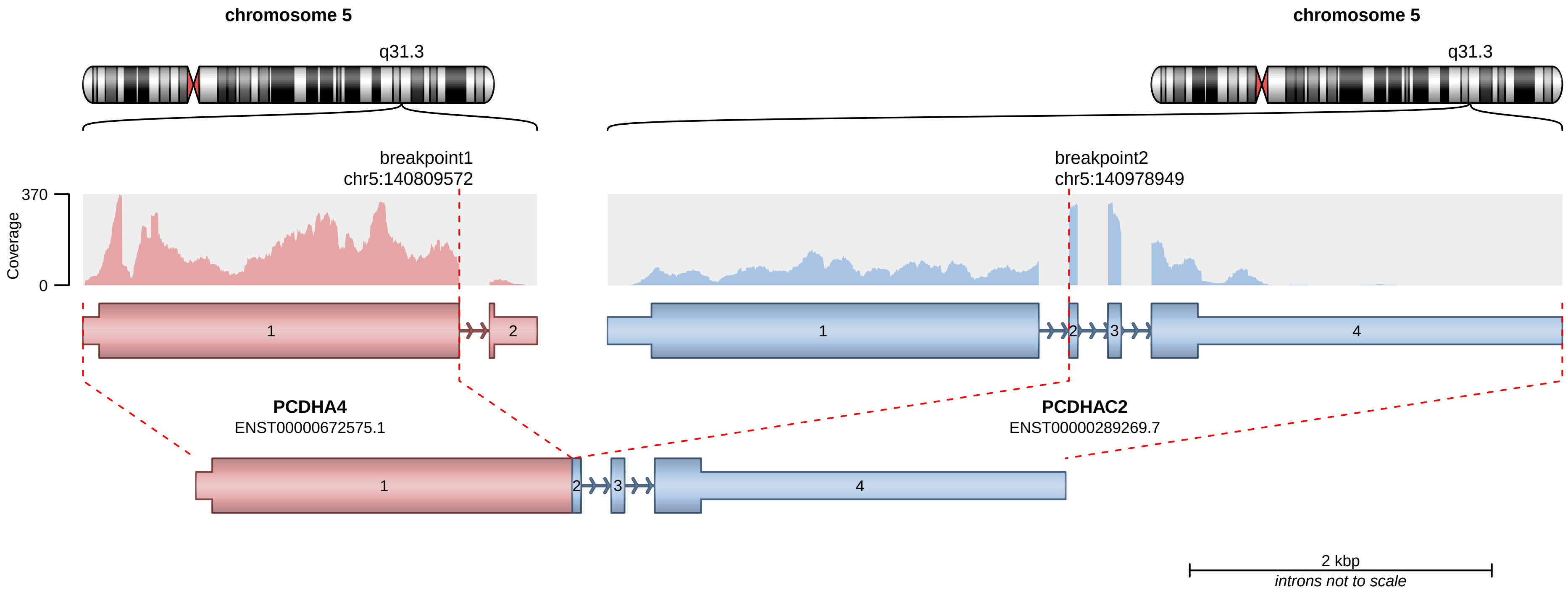


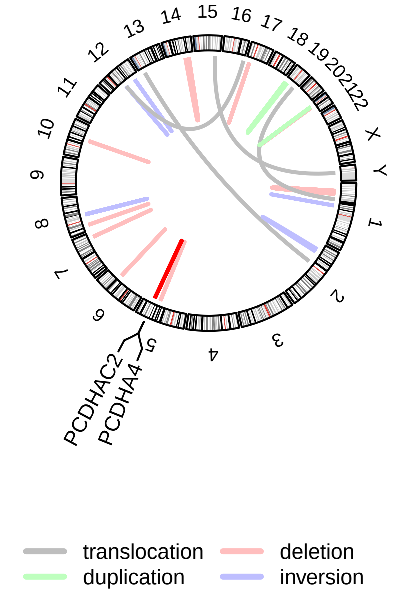
RETAINED PROTEIN DOMAINS
reading frame unclear

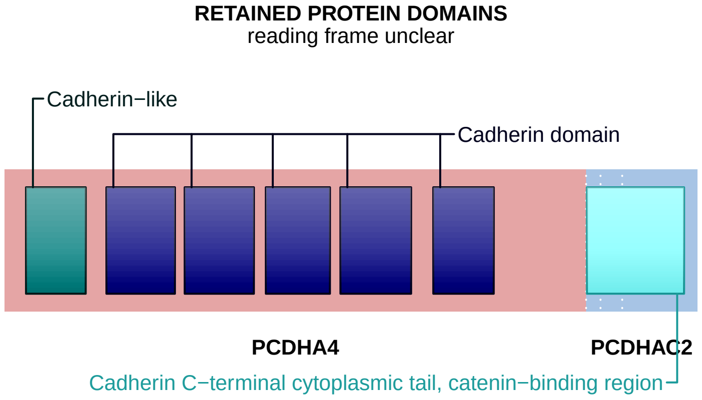


SUPPORTING READ COUNT

Split reads = 32
Discordant mates = 0

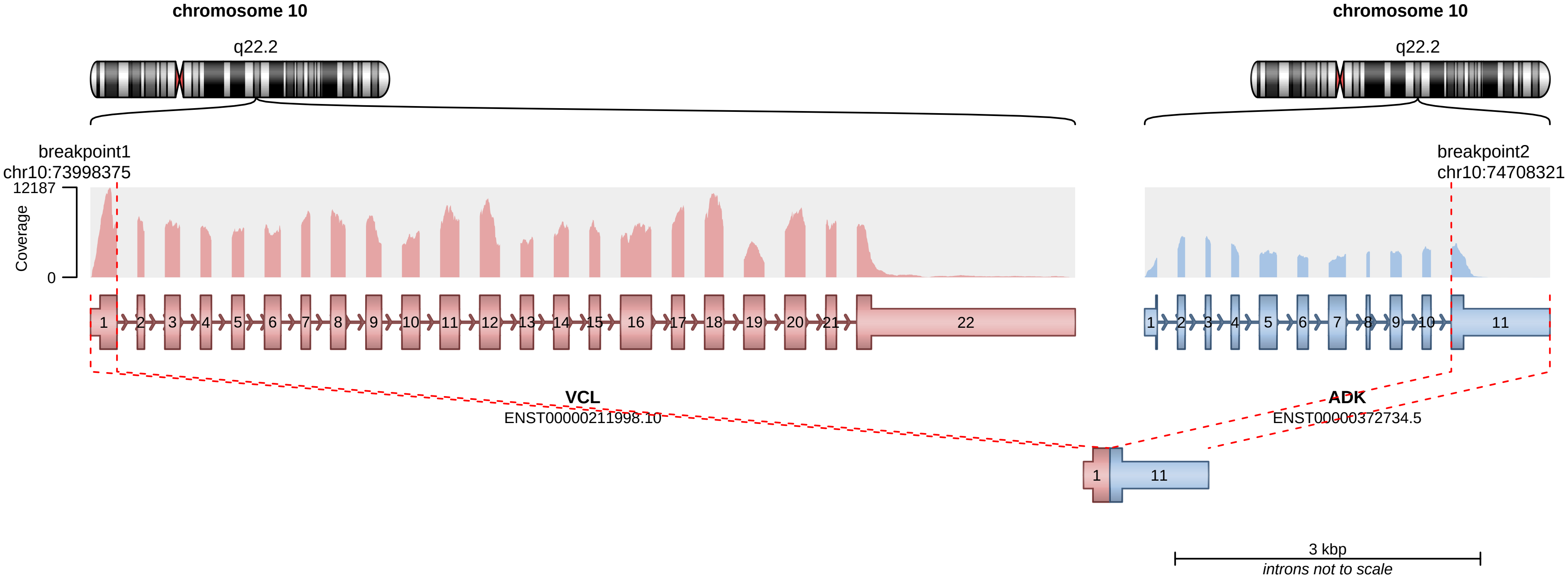


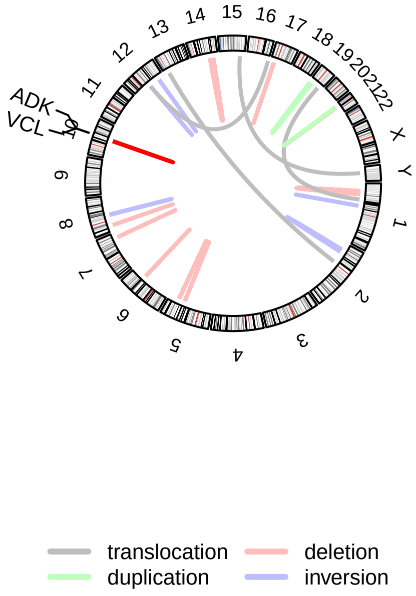




SUPPORTING READ COUNT

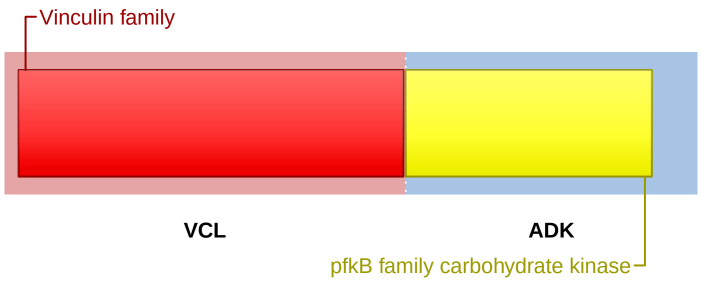
Split reads = 32
Discordant mates = 0





RETAINED PROTEIN DOMAINS

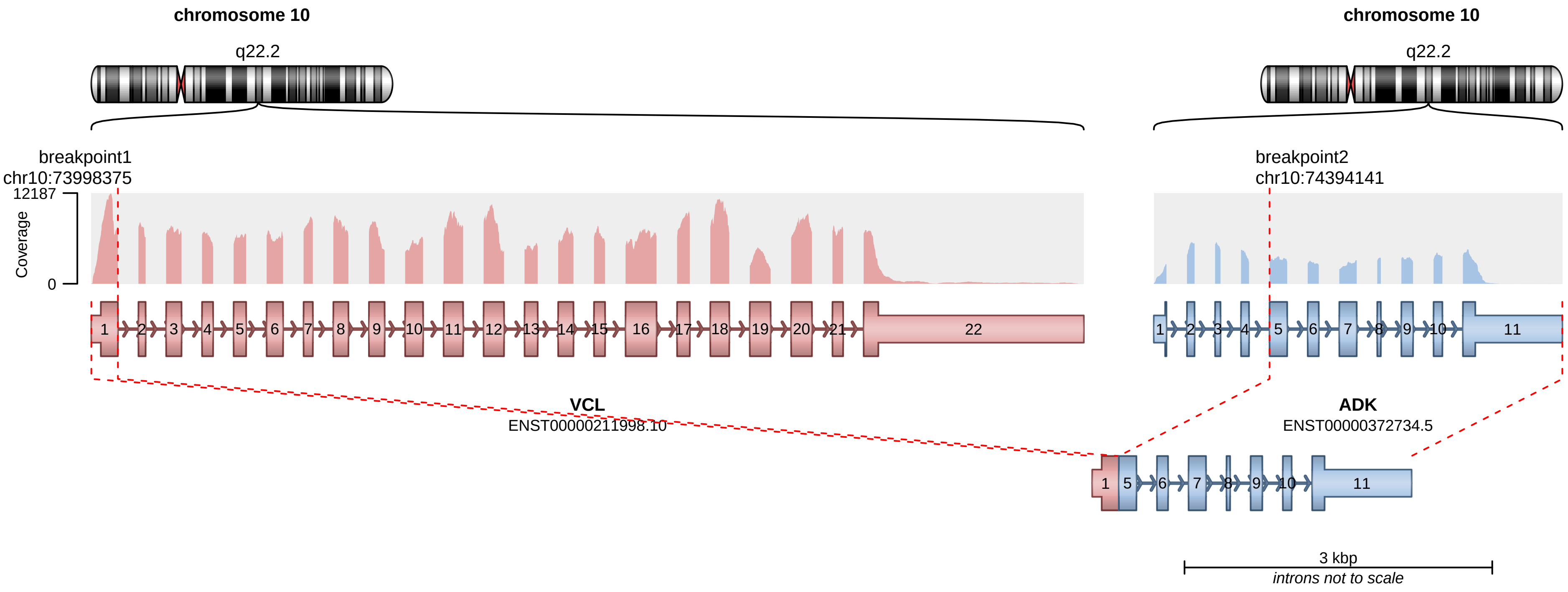
reading frame unclear

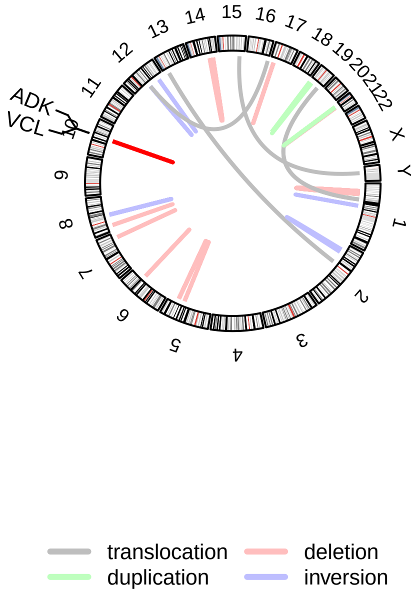


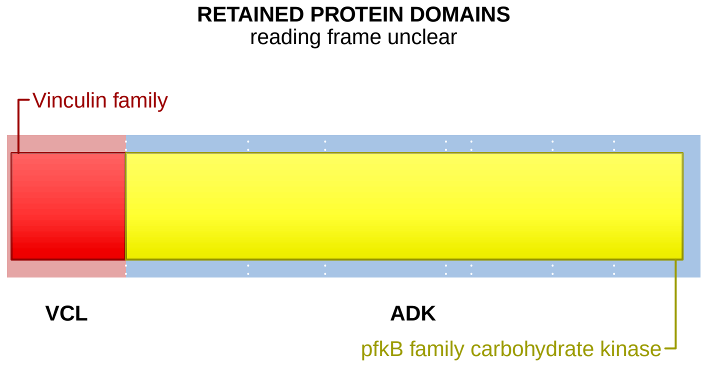
SUPPORTING READ COUNT

Split reads = 28

Discordant mates = 1



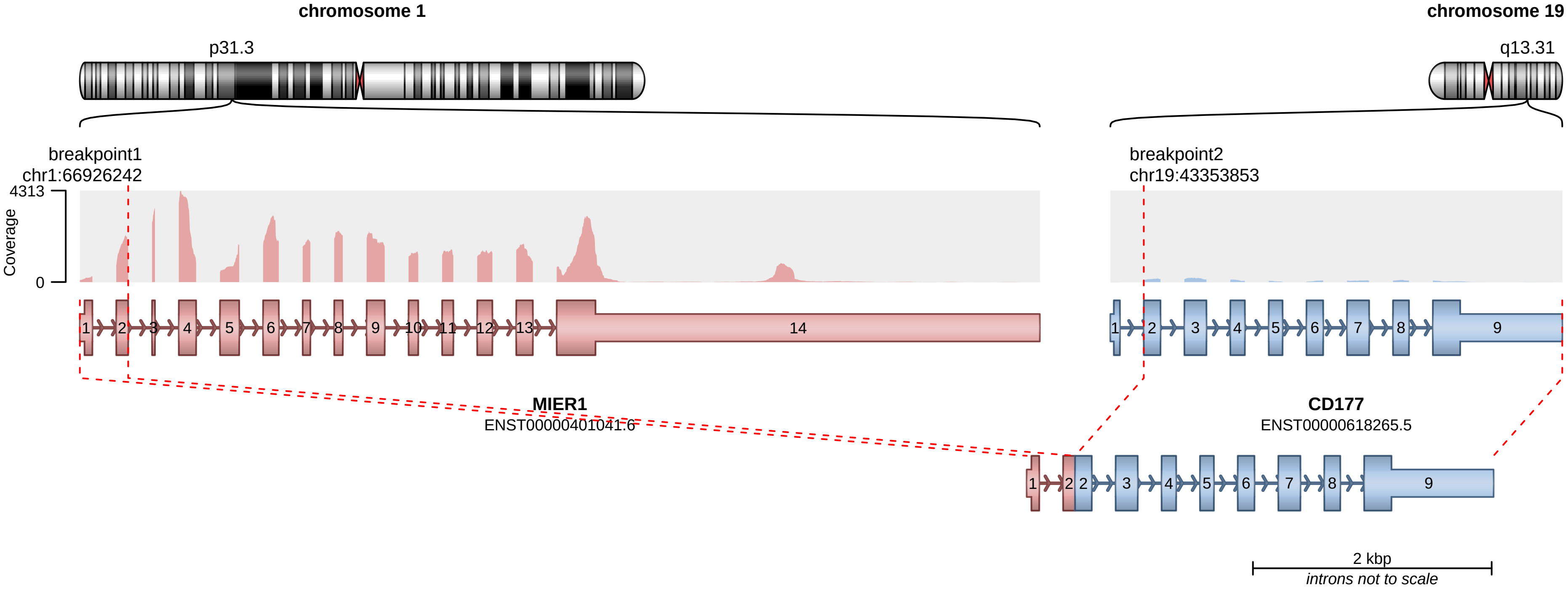


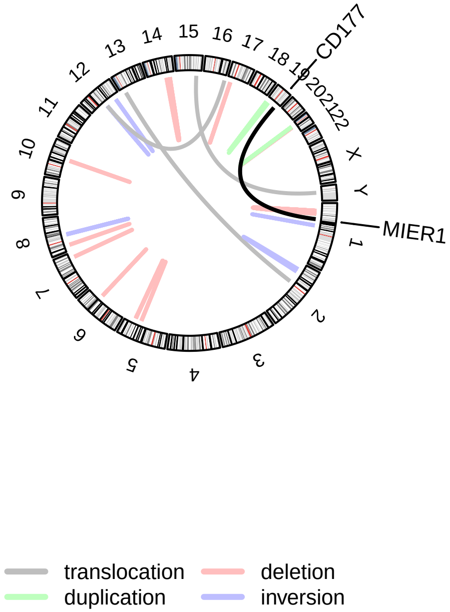


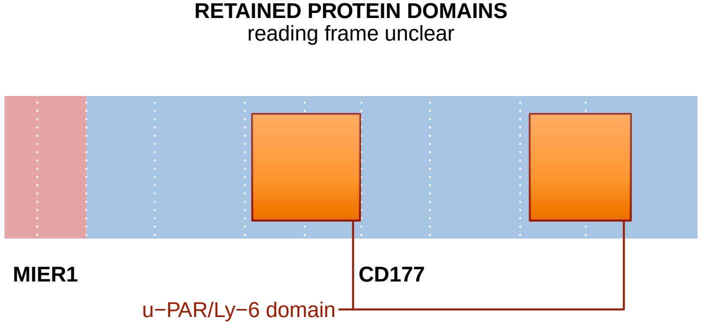
RETAINED PROTEIN DOMAINS
reading frame unclear

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

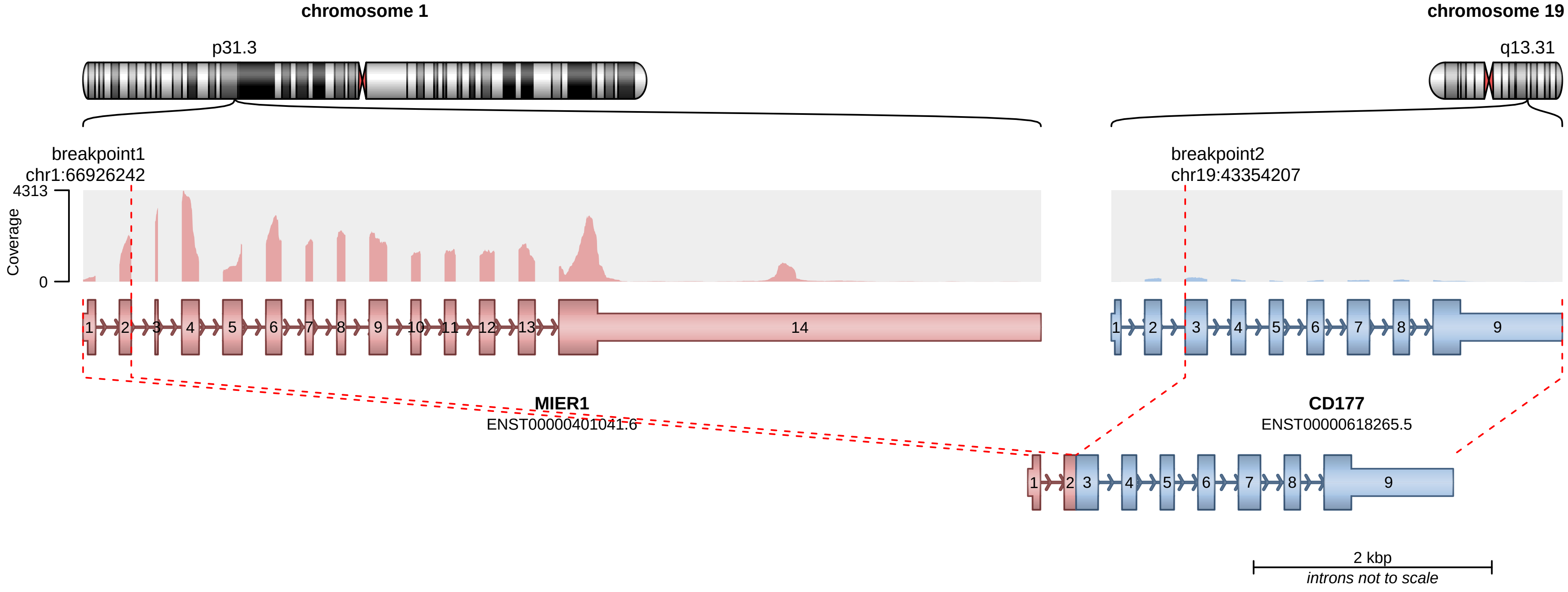


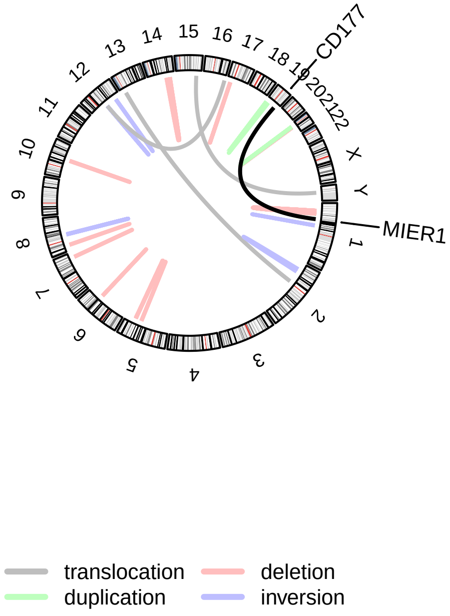




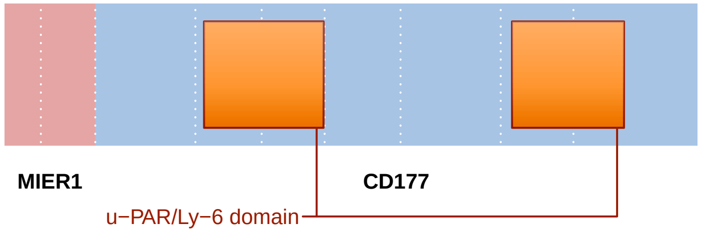
SUPPORTING READ COUNT

Split reads = 24
Discordant mates = 1



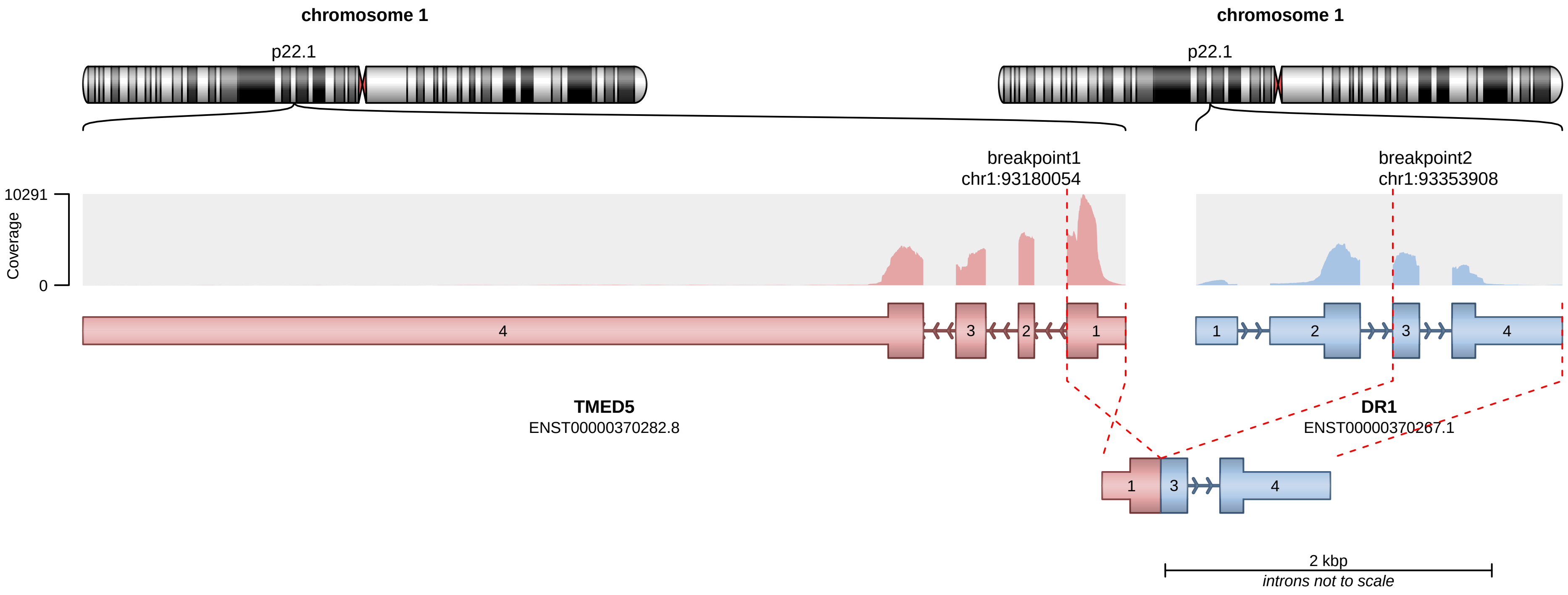


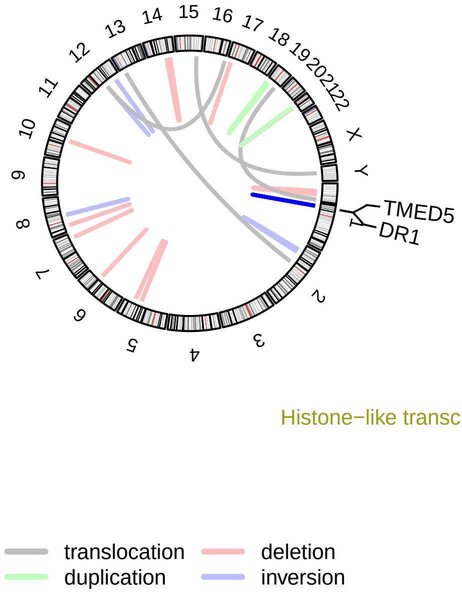
RETAINED PROTEIN DOMAINS
reading frame unclear

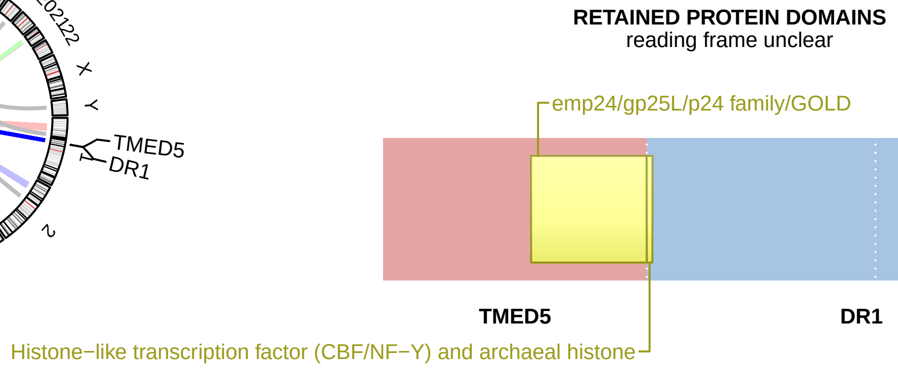


SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

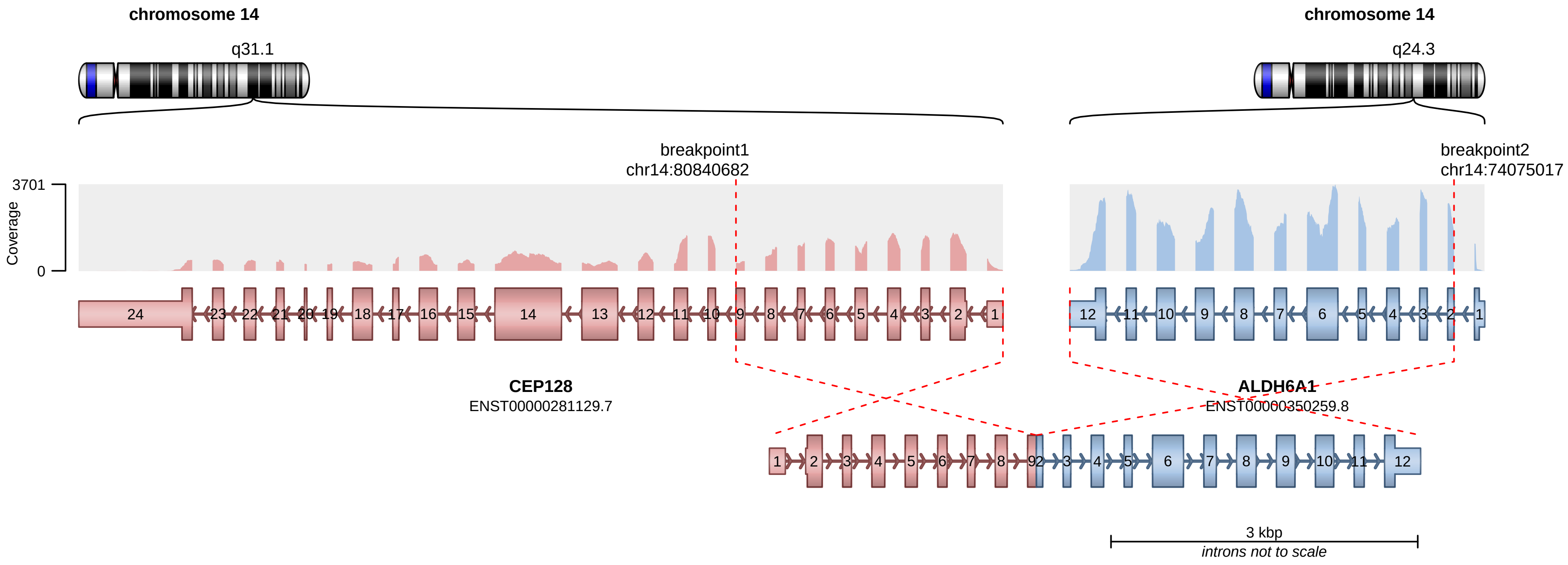


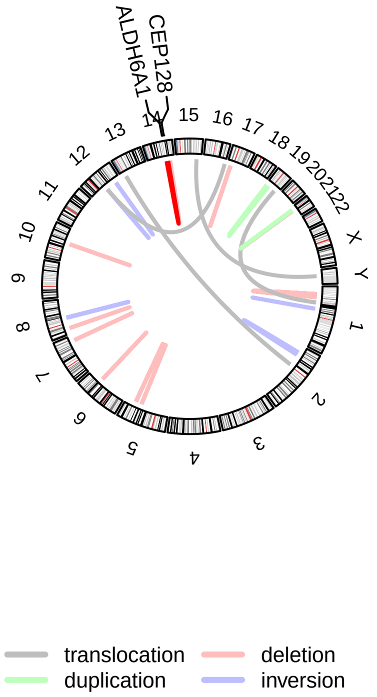




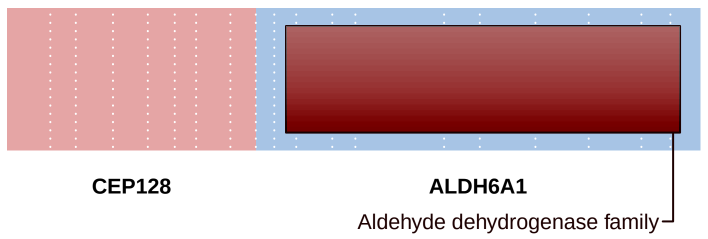
SUPPORTING READ COUNT

Split reads = 22
Discordant mates = 1



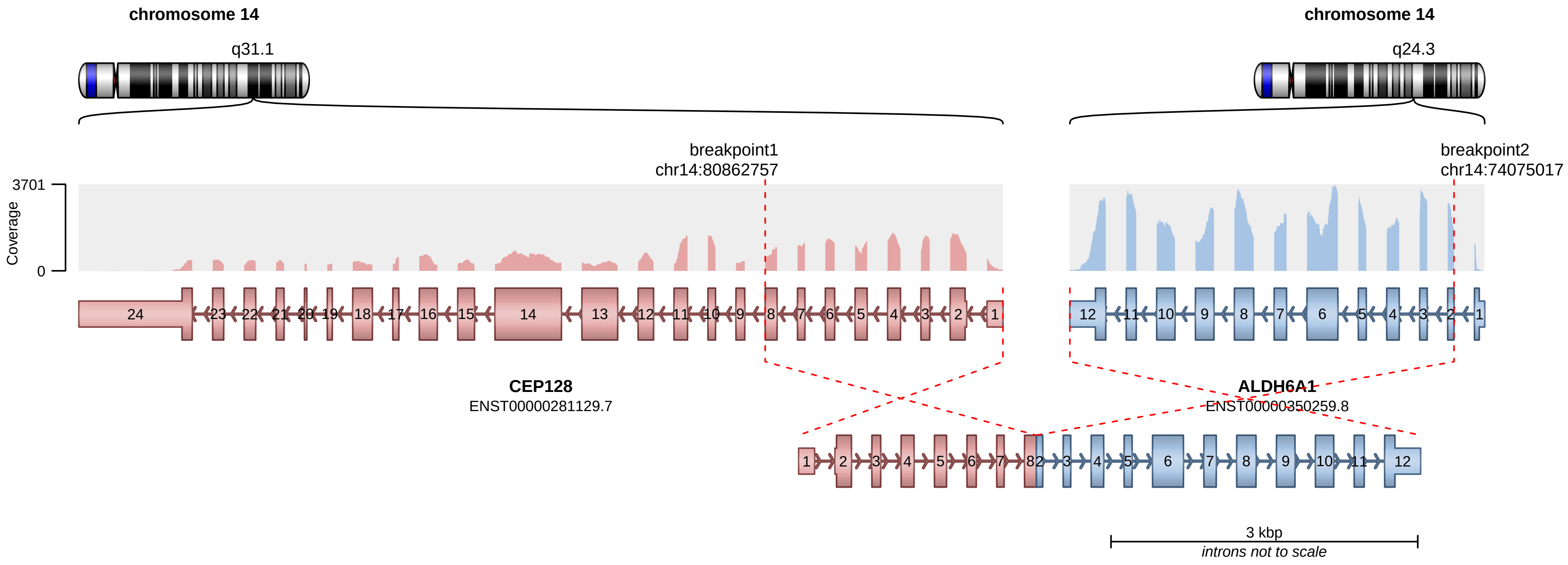


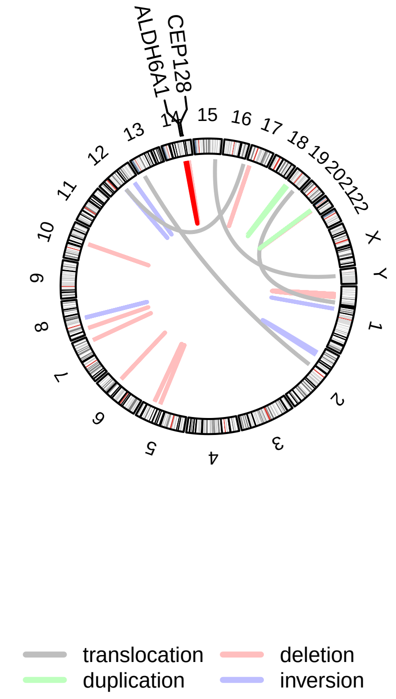
RETAINED PROTEIN DOMAINS
reading frame unclear



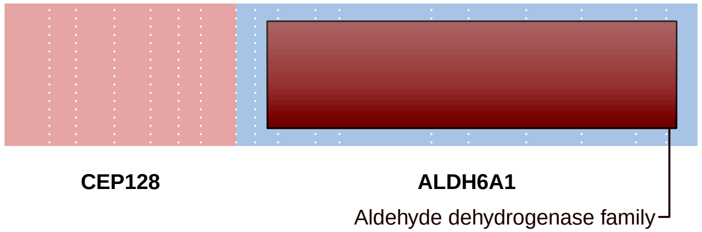
SUPPORTING READ COUNT

Split reads = 21
Discordant mates = 0



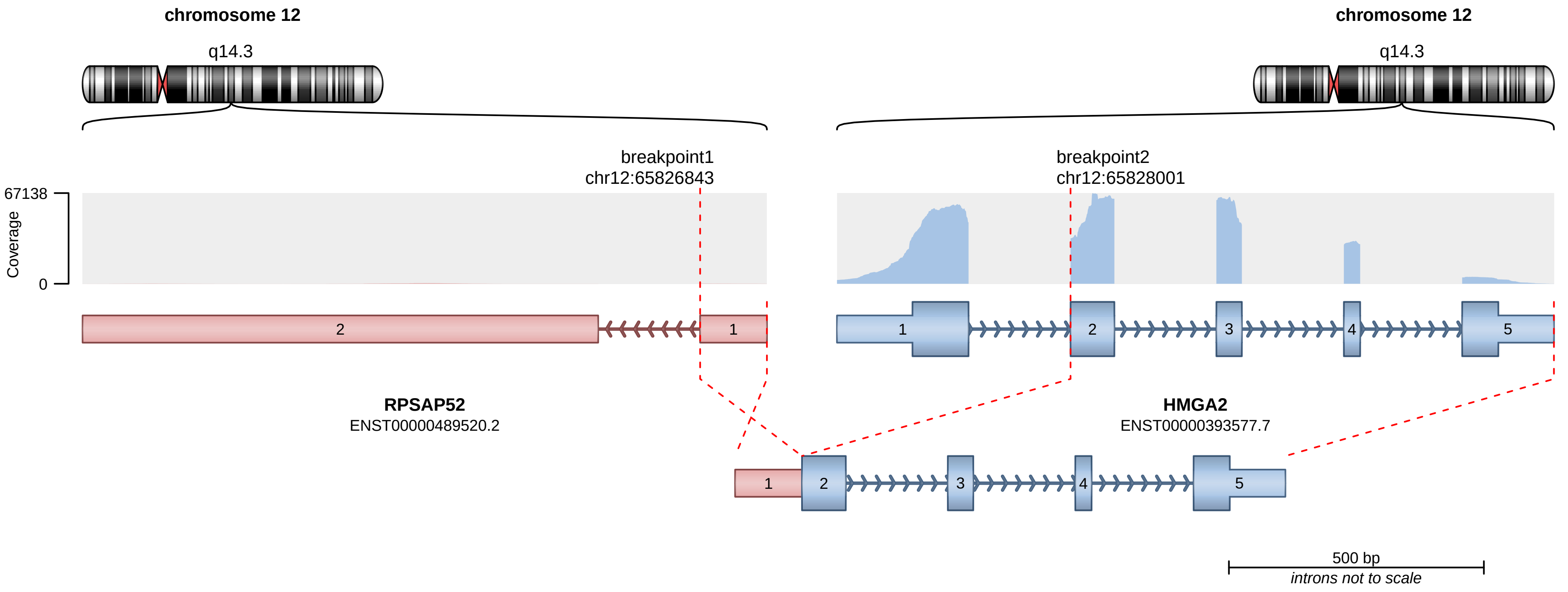


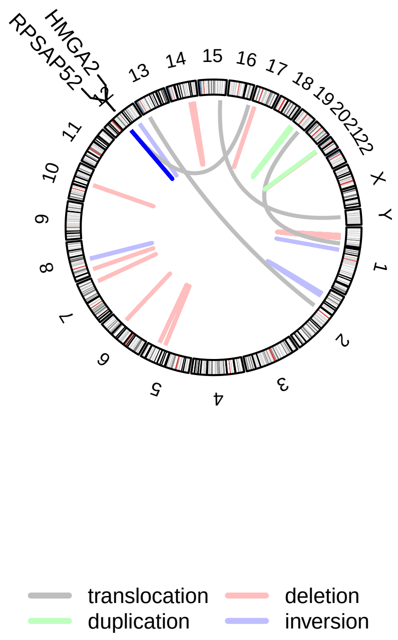
RETAINED PROTEIN DOMAINS
reading frame unclear



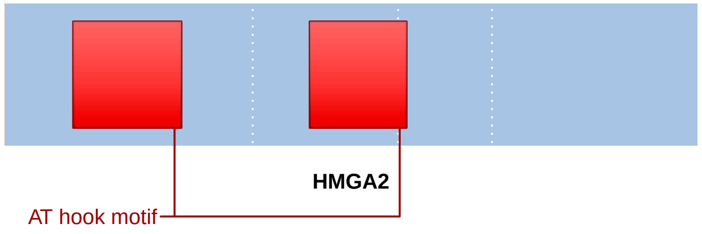
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



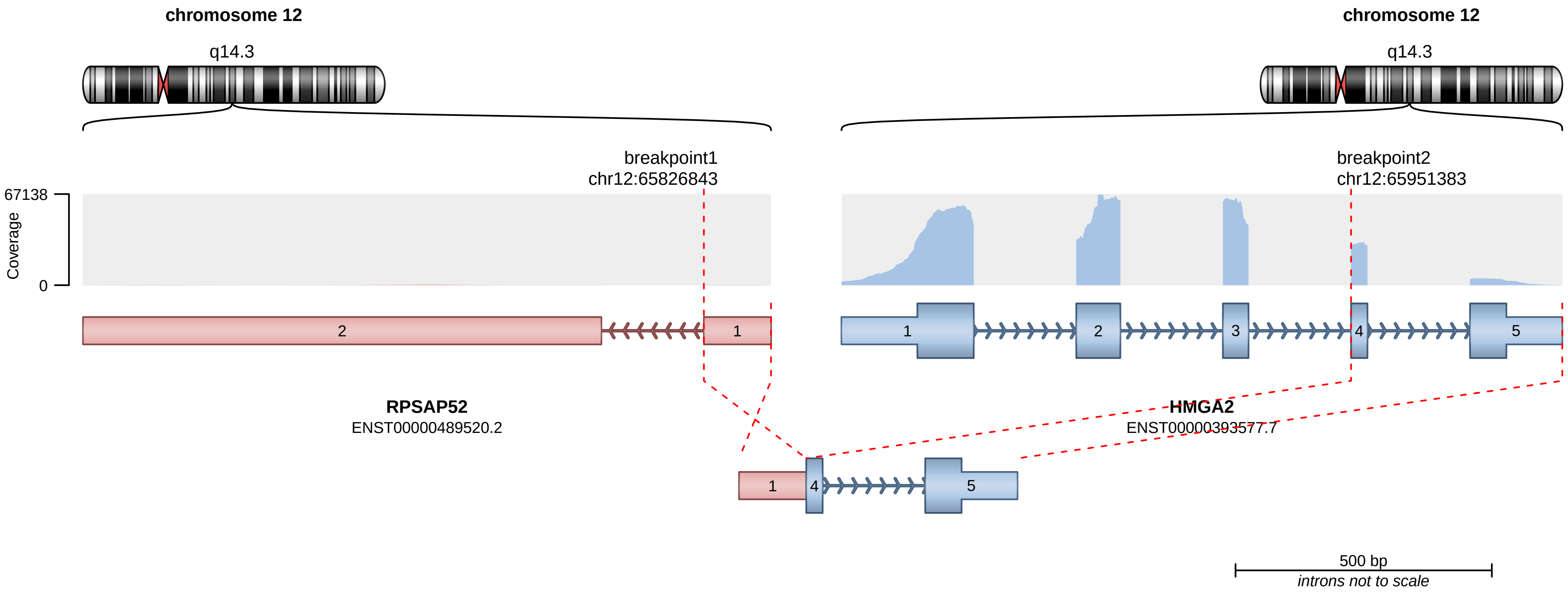


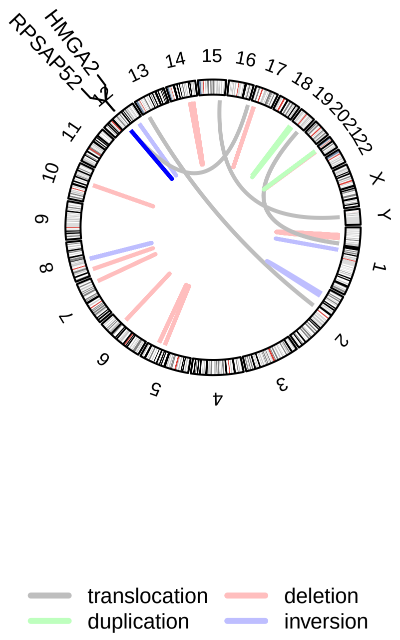
RETAINED PROTEIN DOMAINS
reading frame unclear



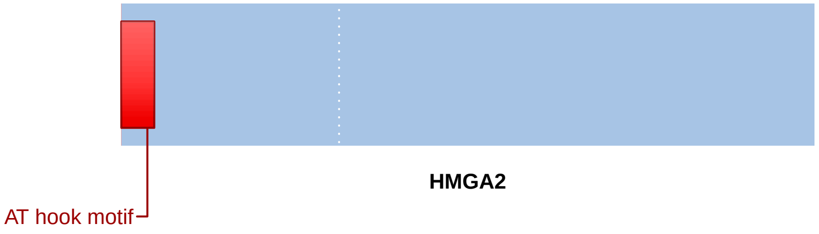
SUPPORTING READ COUNT

Split reads = 20
Discordant mates = 0



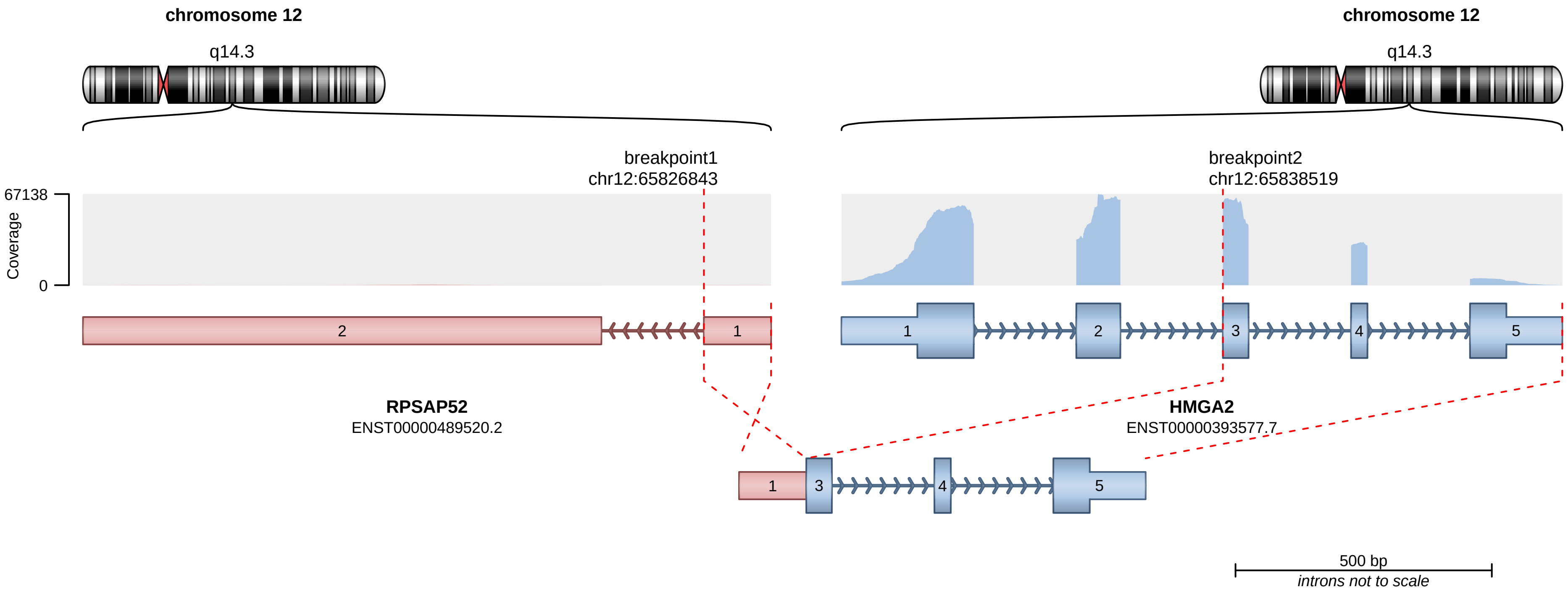


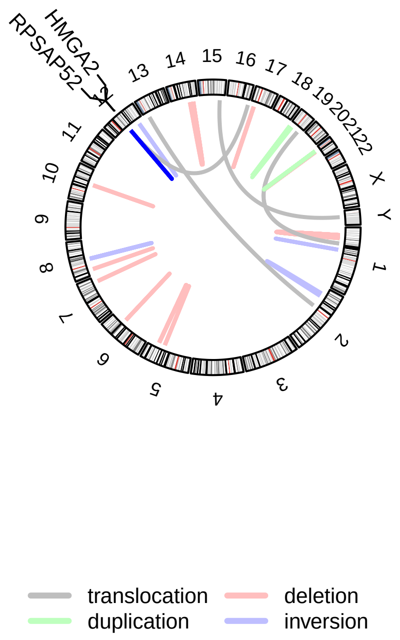
RETAINED PROTEIN DOMAINS
reading frame unclear

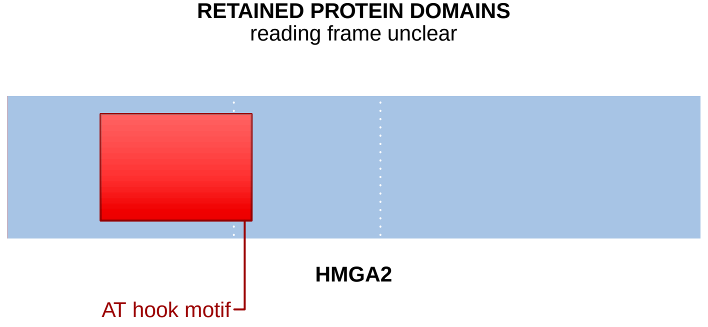


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

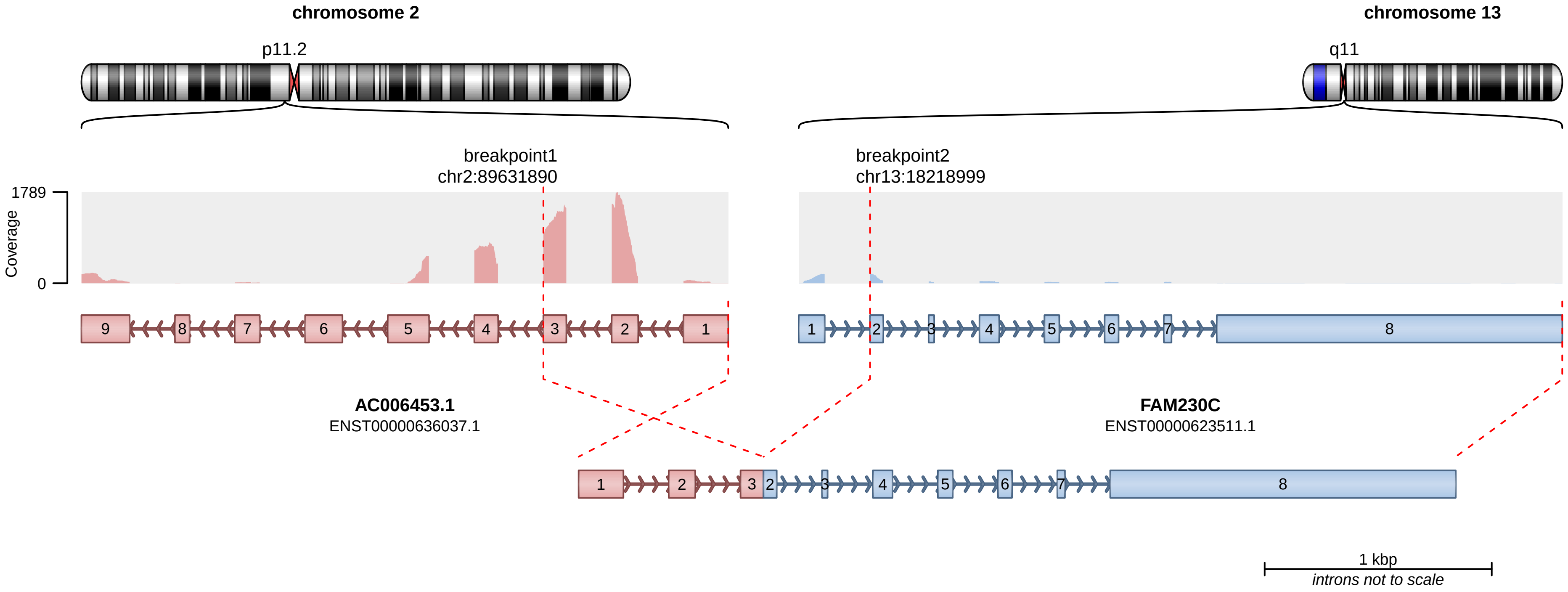


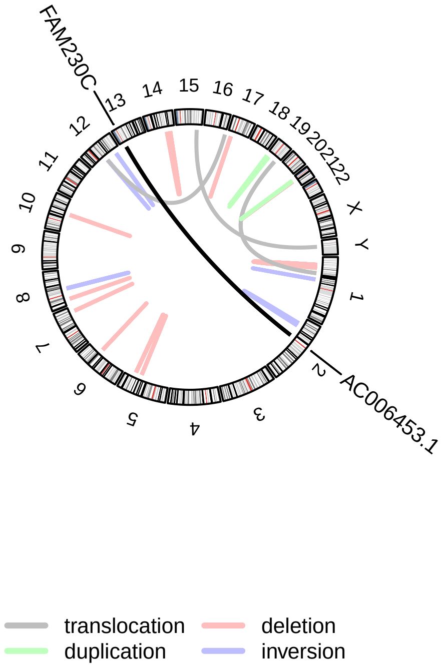




SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

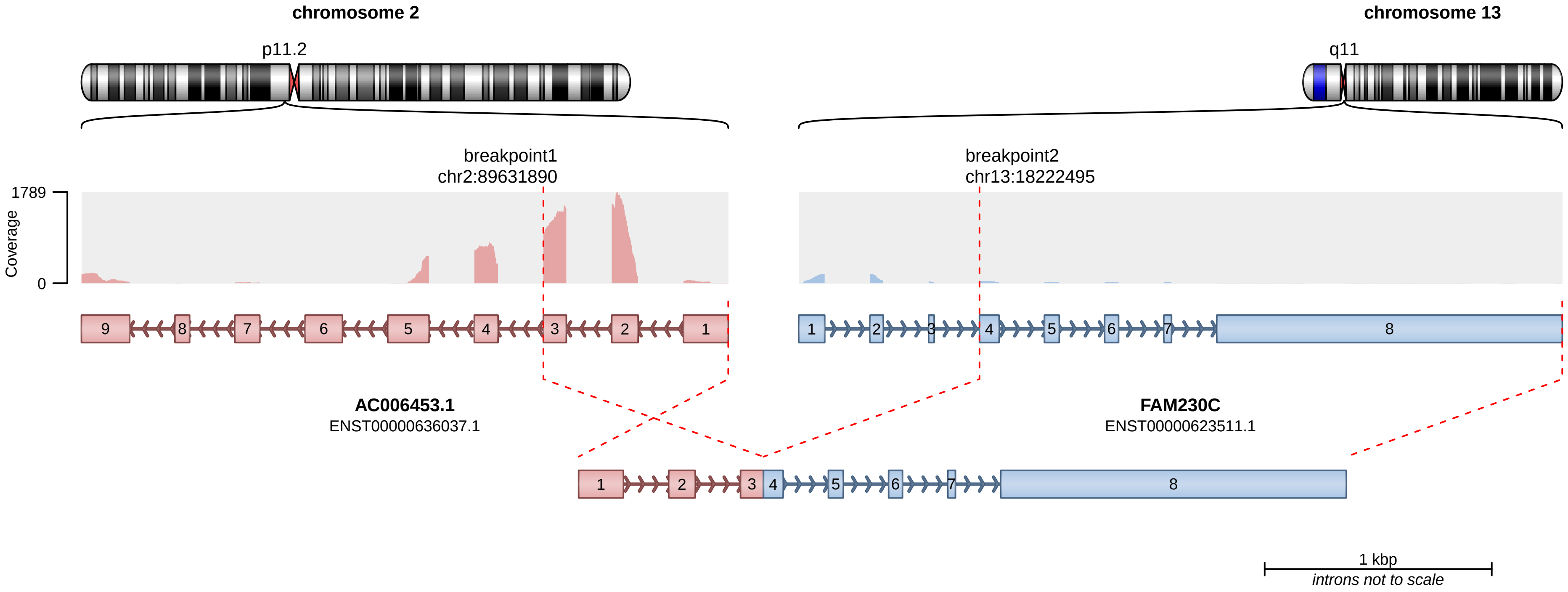


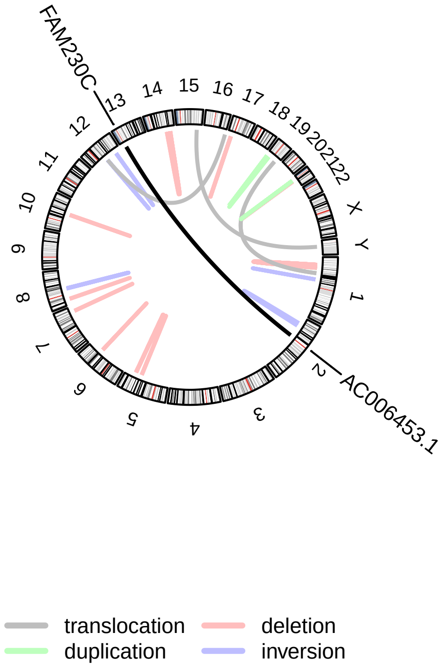


Genes are not protein−coding.

SUPPORTING READ COUNT

Split reads = 18
Discordant mates = 0

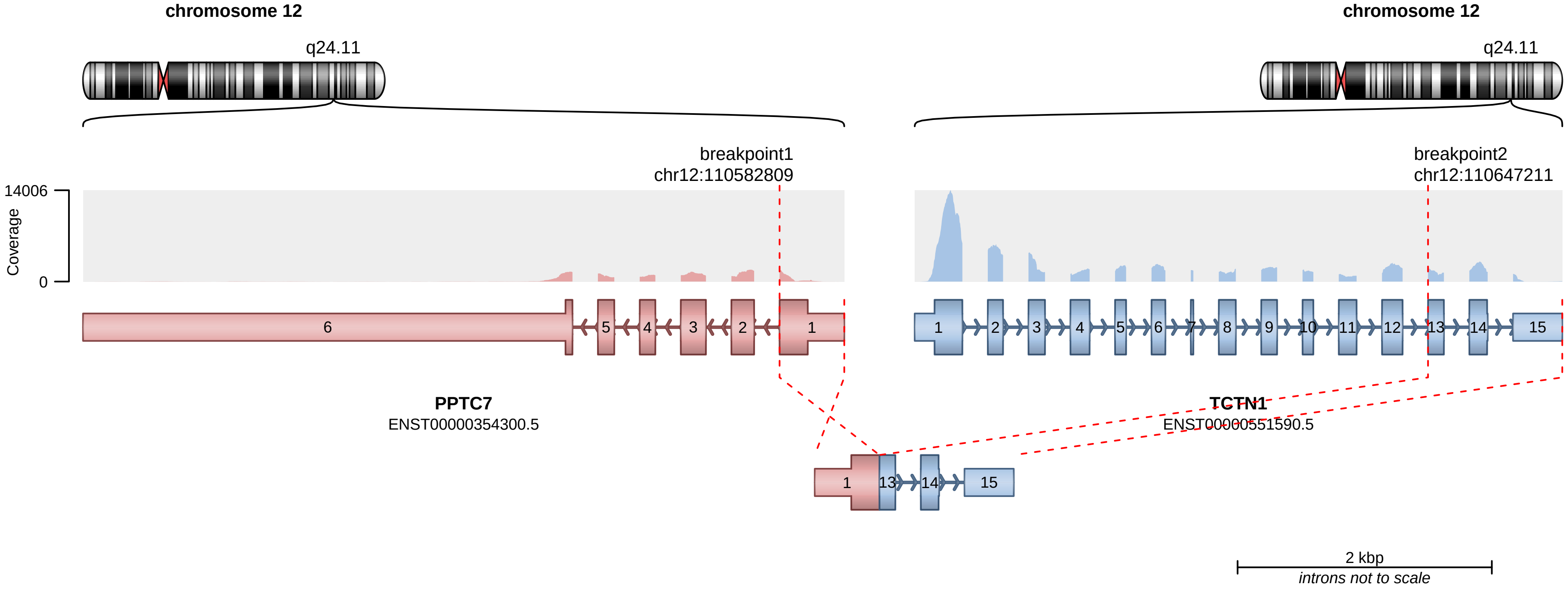


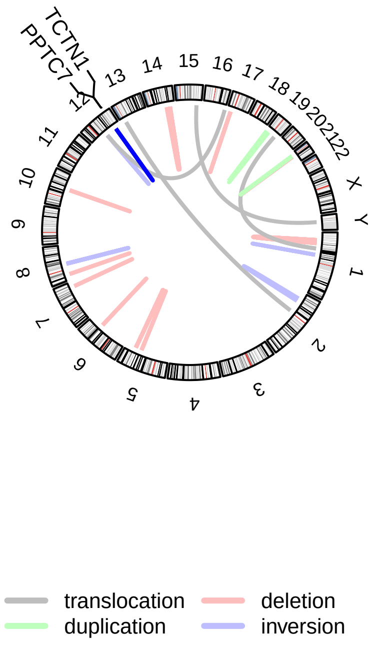


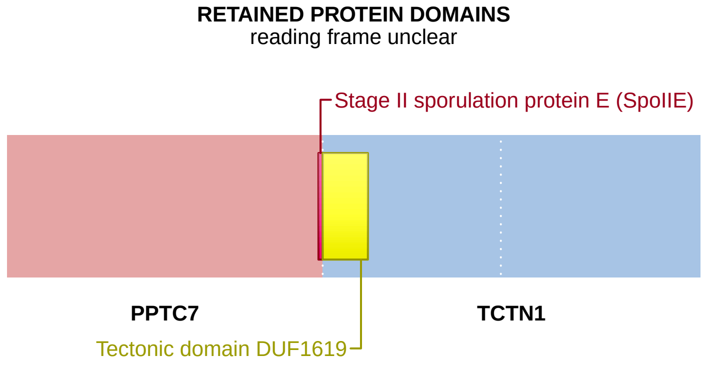
Genes are not protein−coding.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

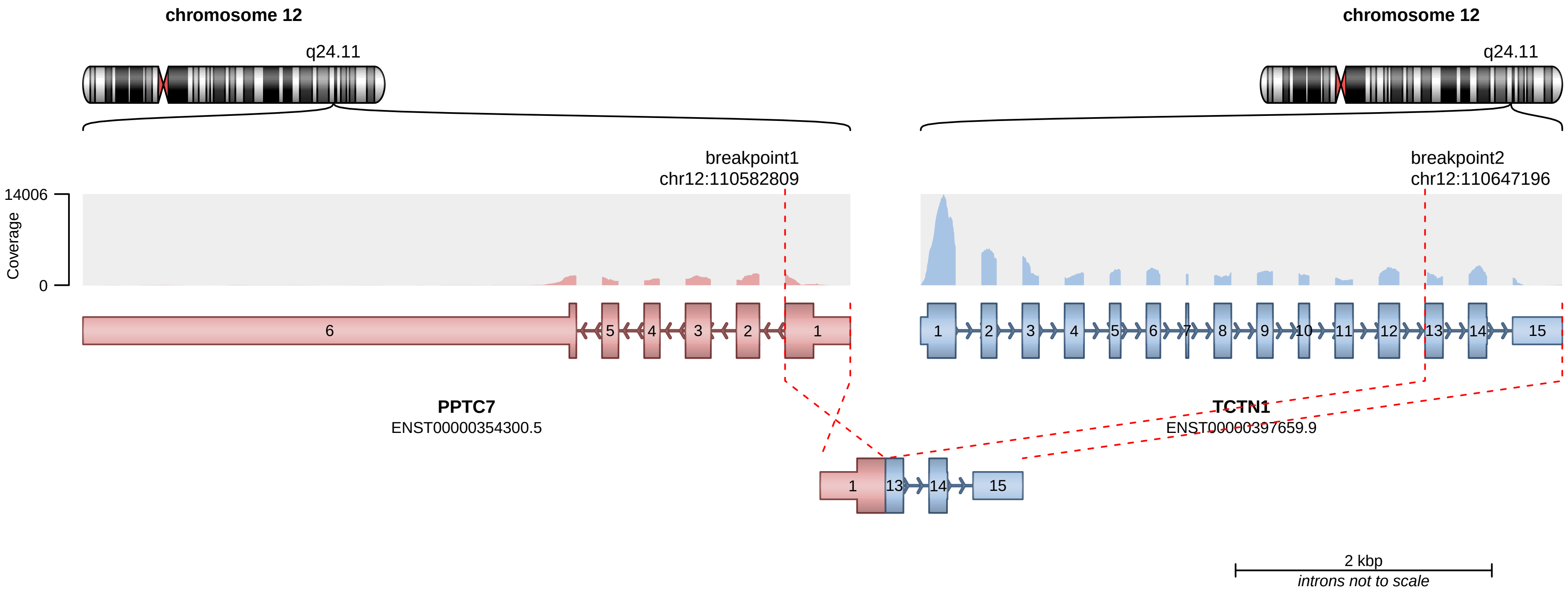


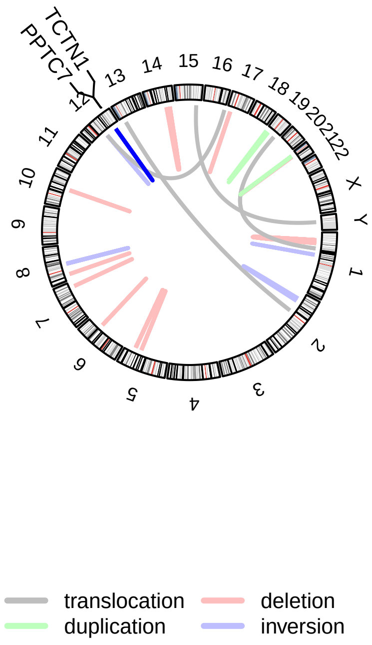


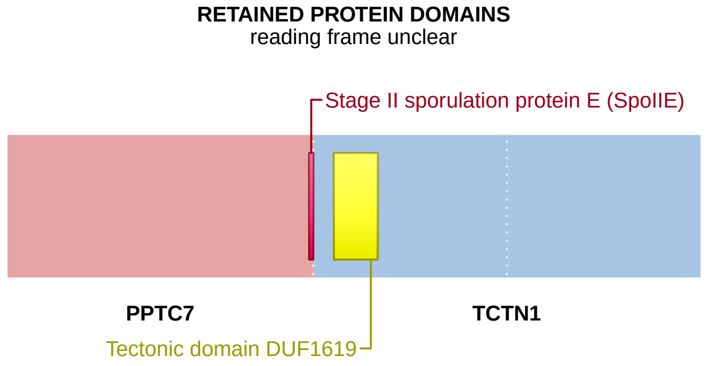


SUPPORTING READ COUNT

Split reads = 16
Discordant mates = 0

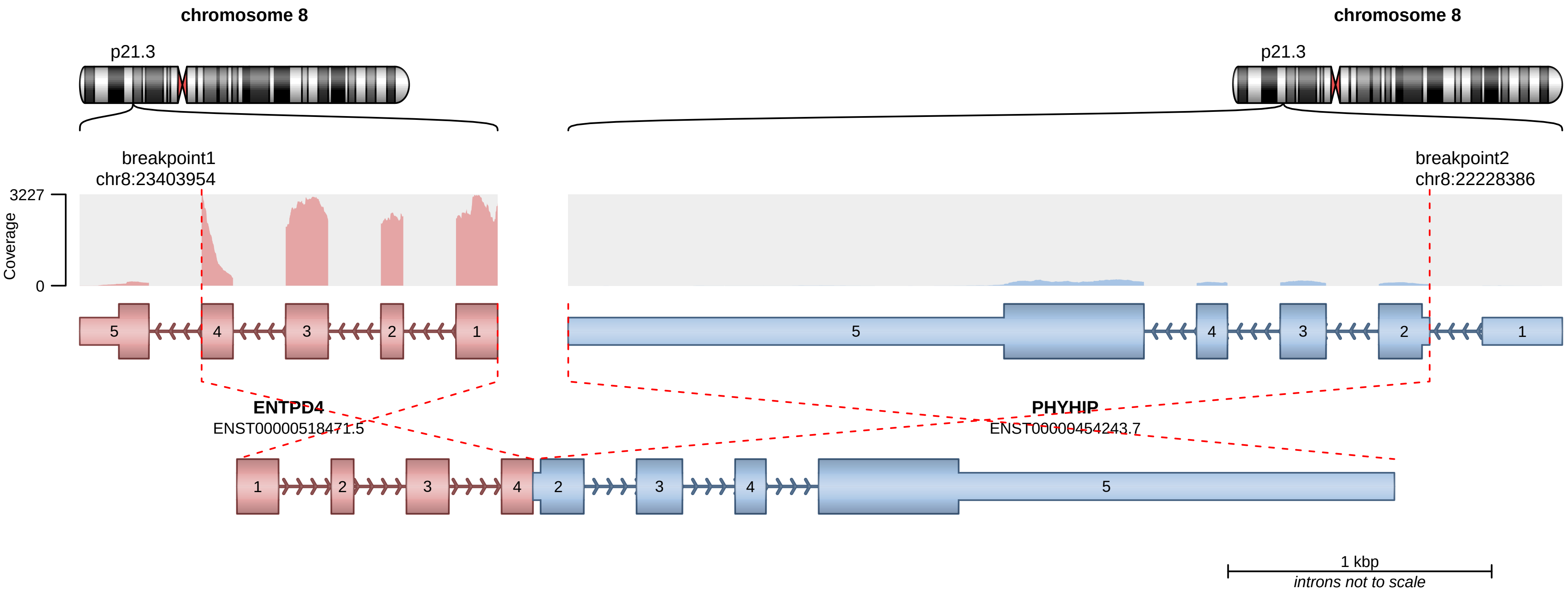


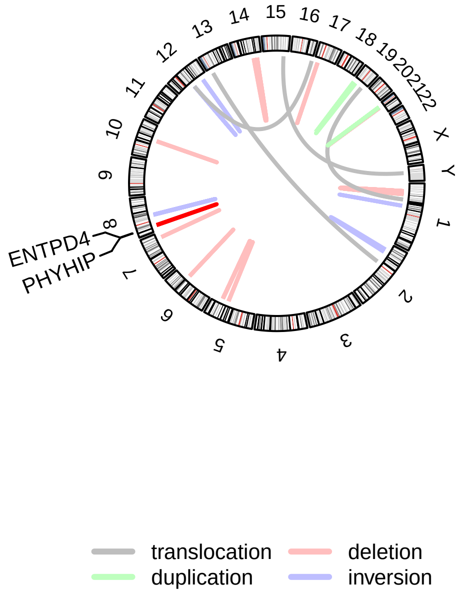




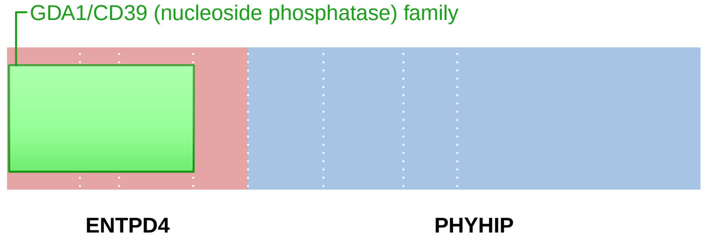
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0



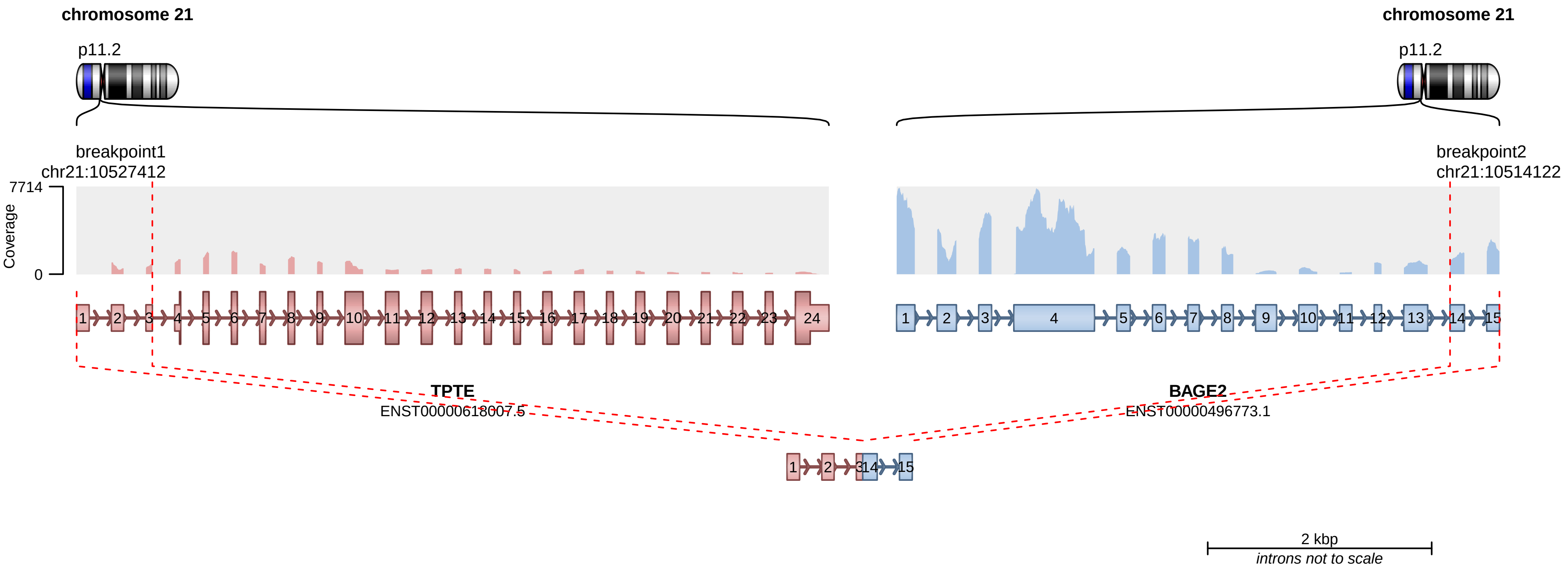


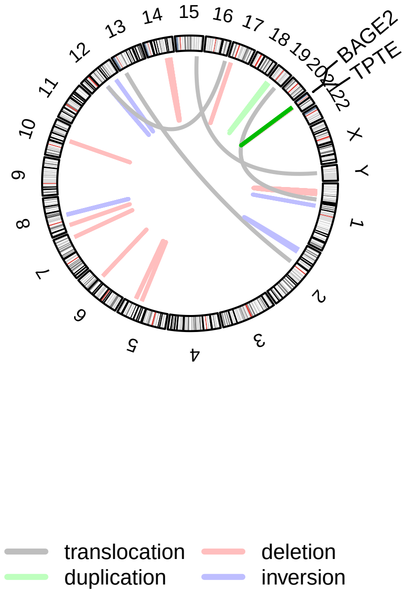
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 0

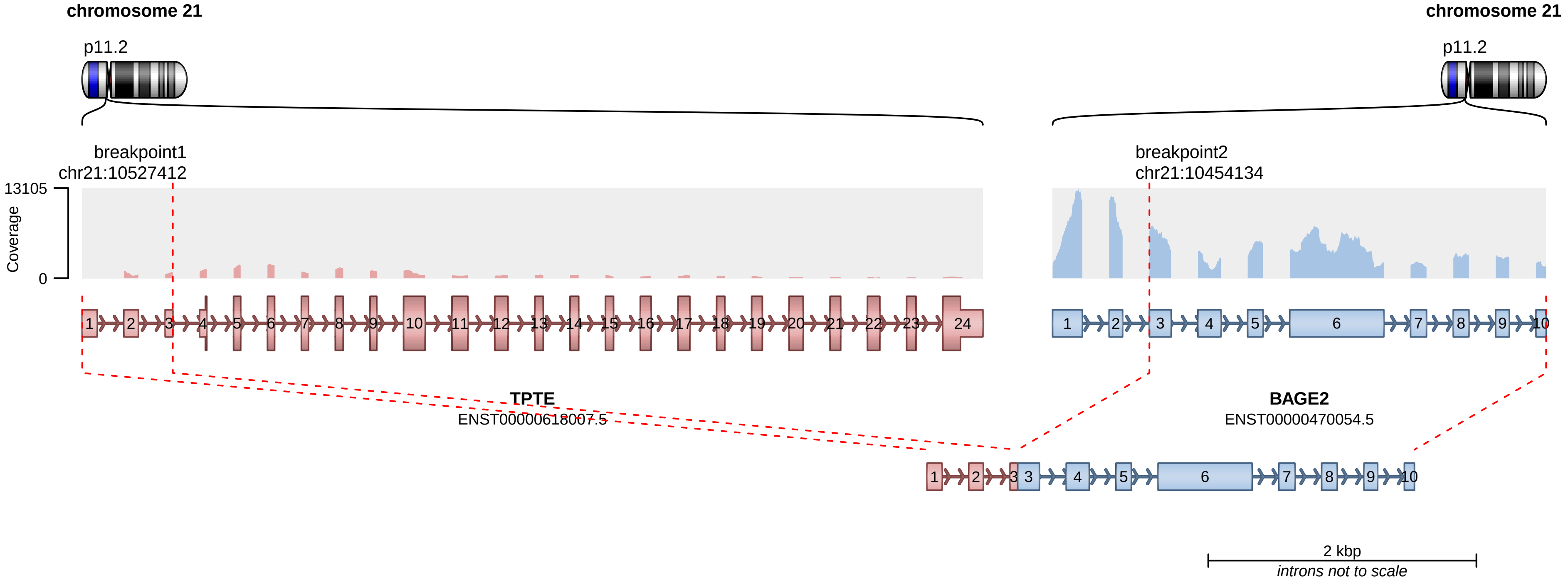


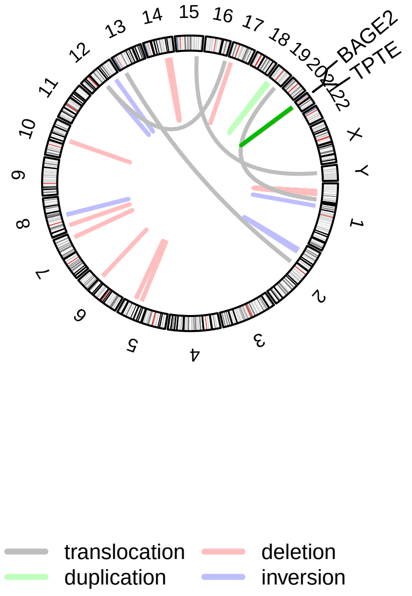


No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 0

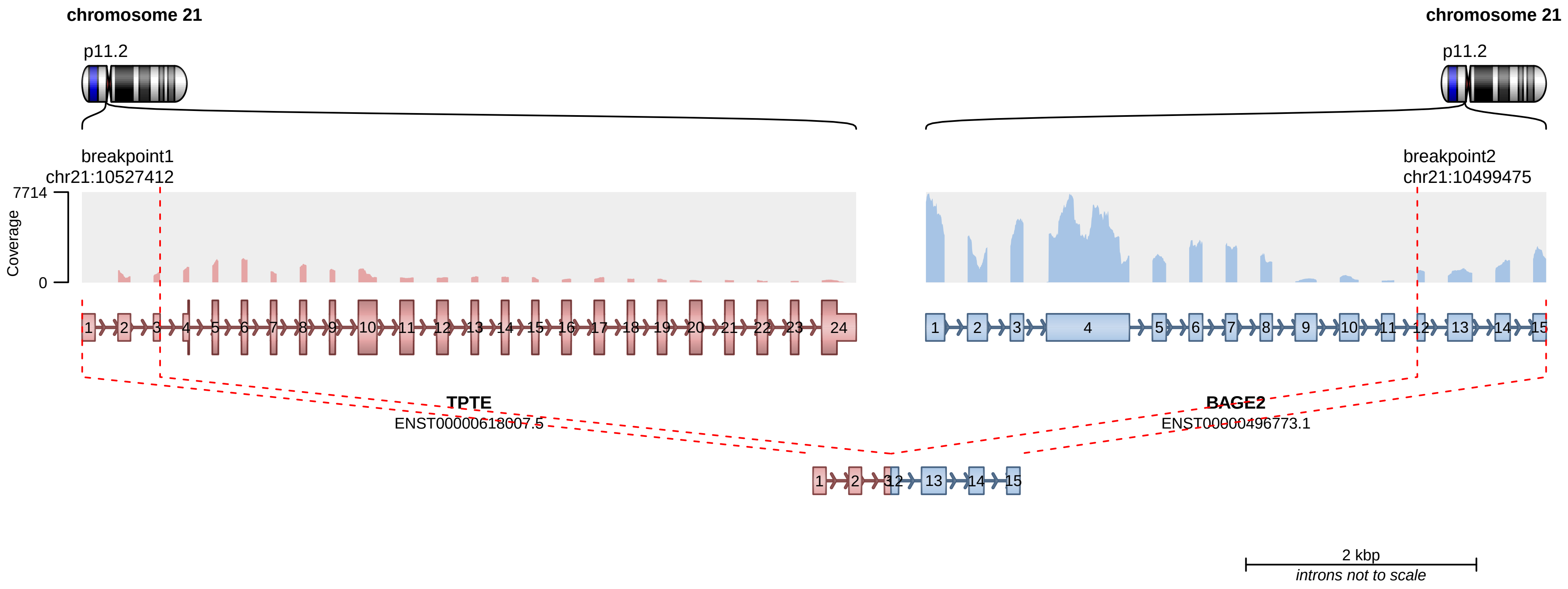


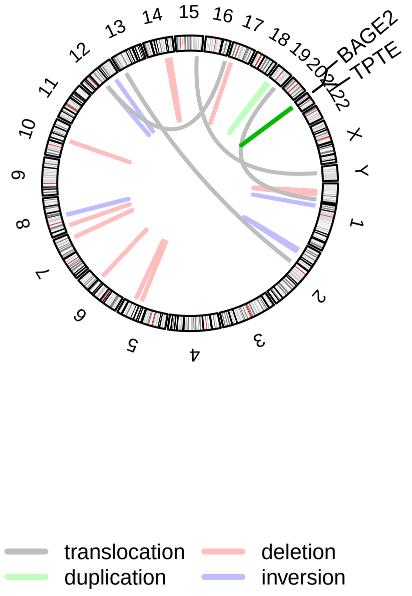


No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 1

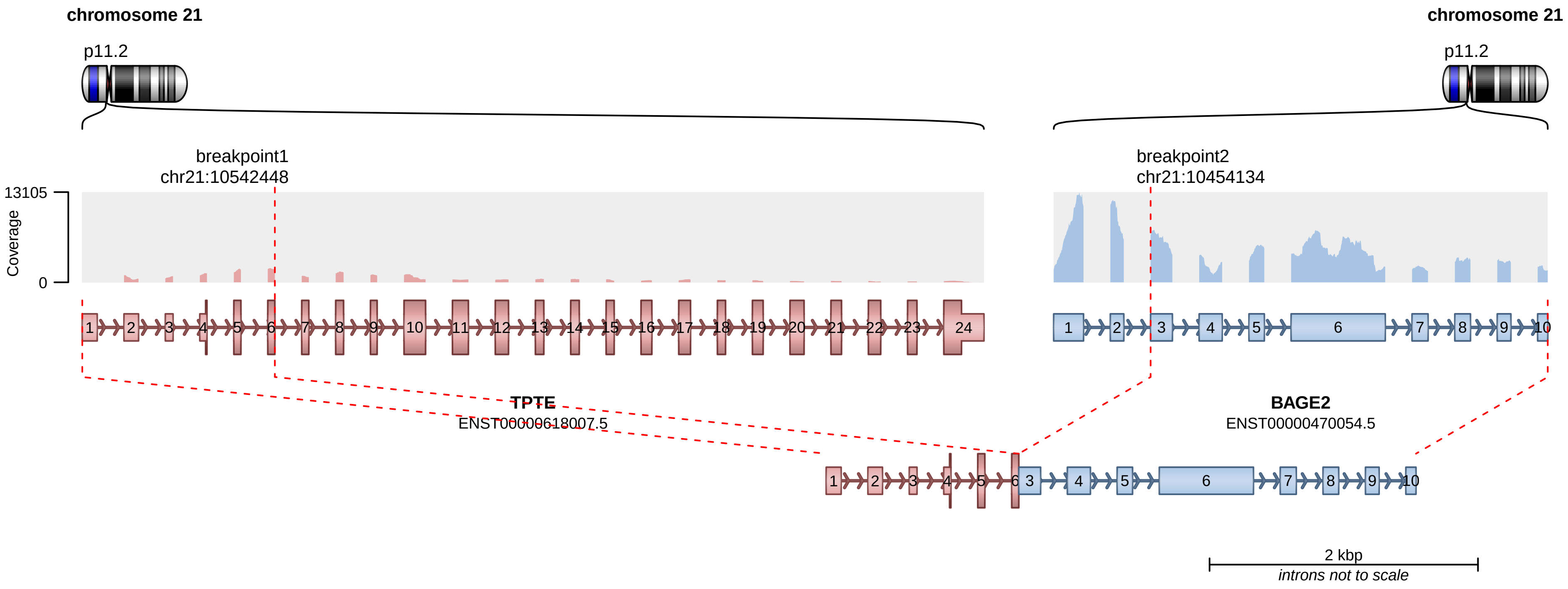


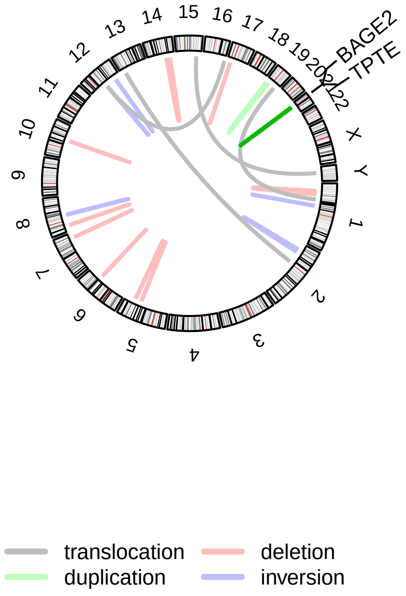


No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0

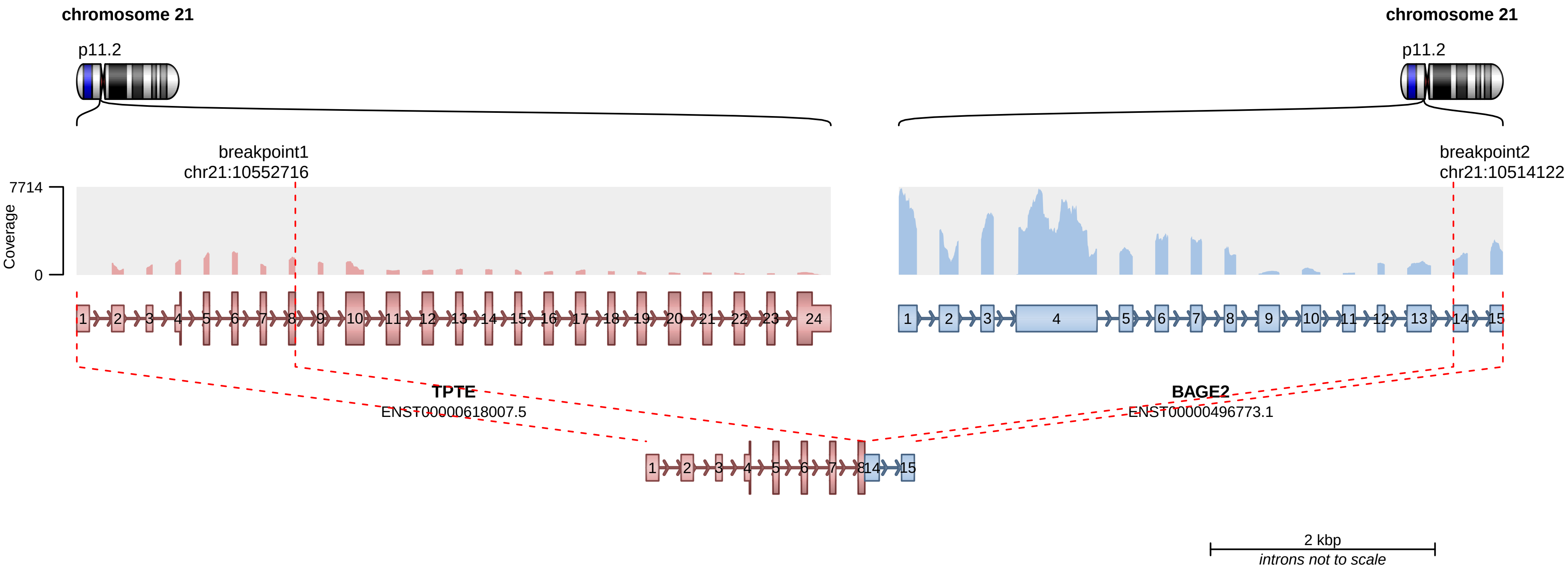


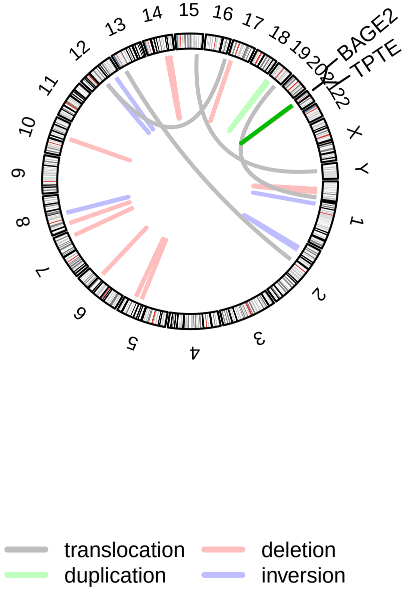


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 1

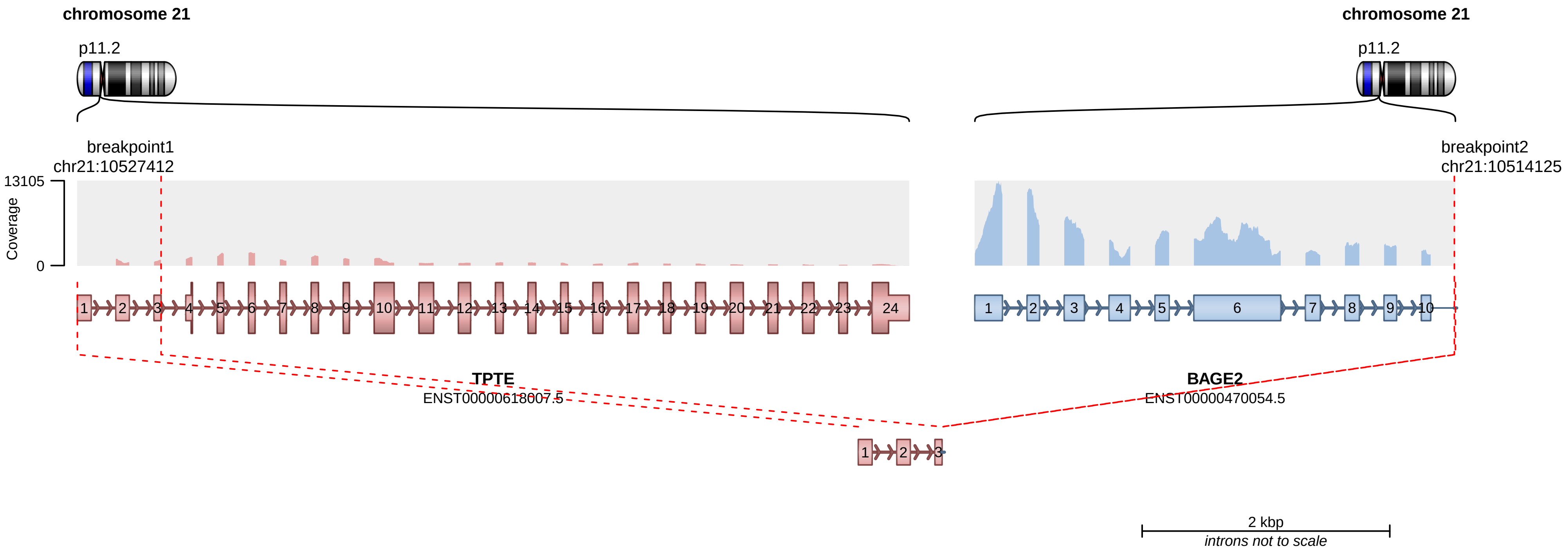


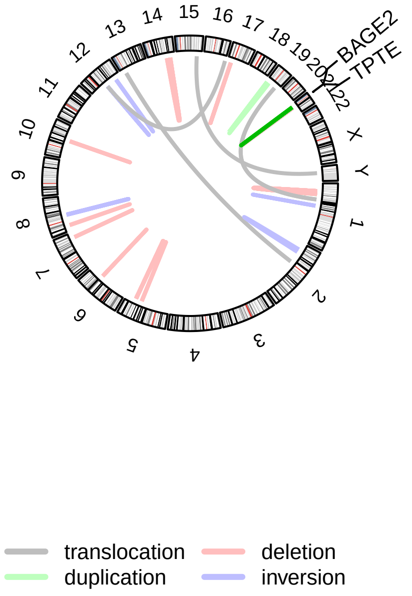


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

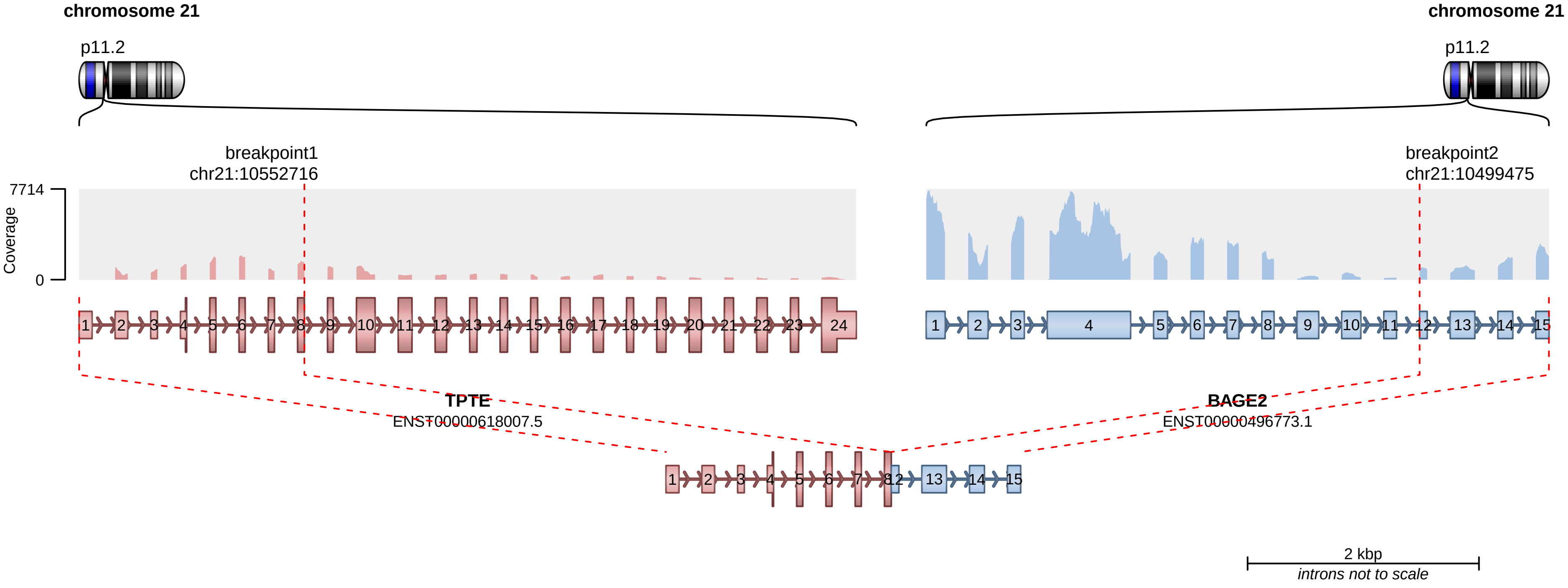


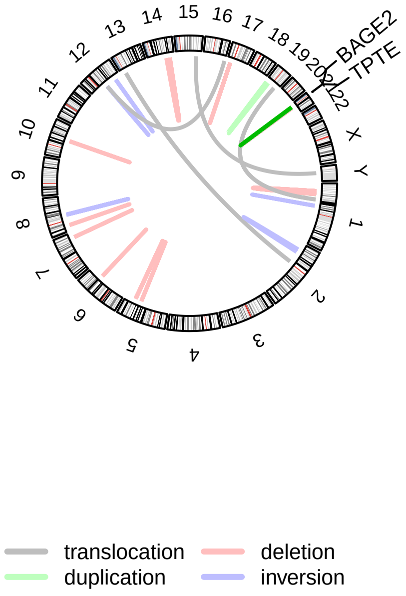


No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

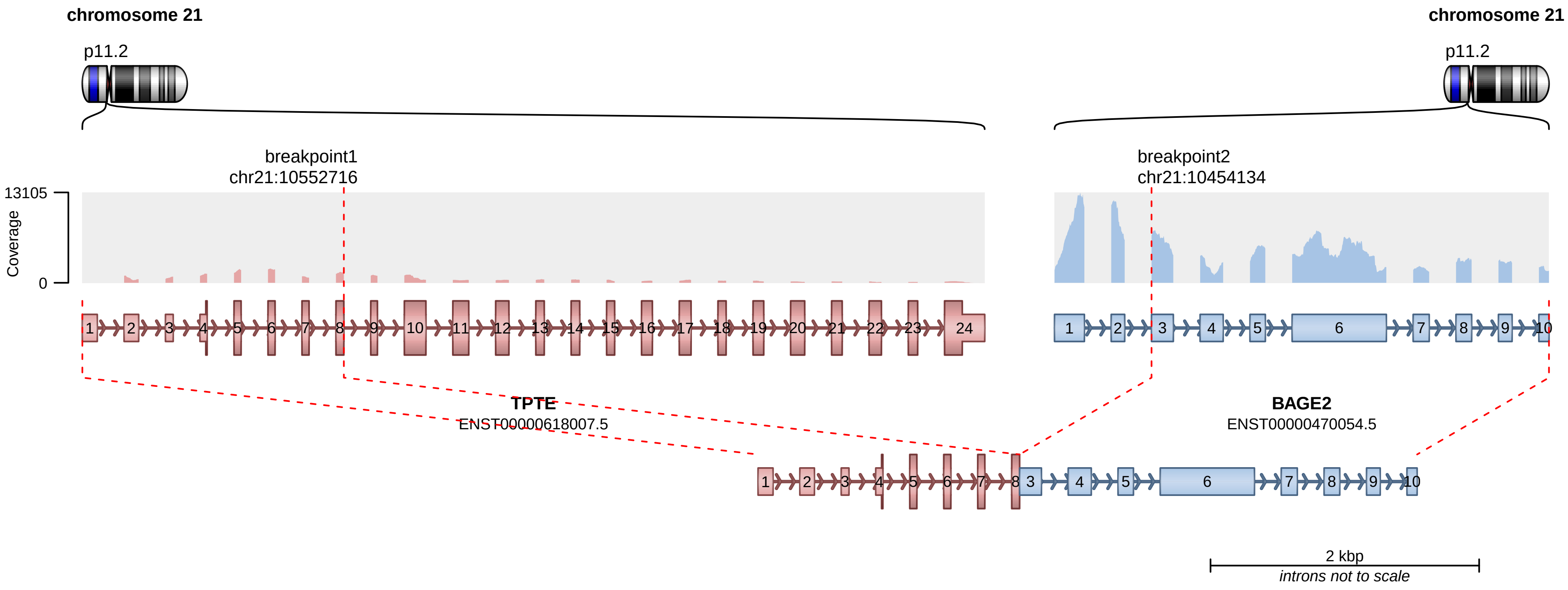


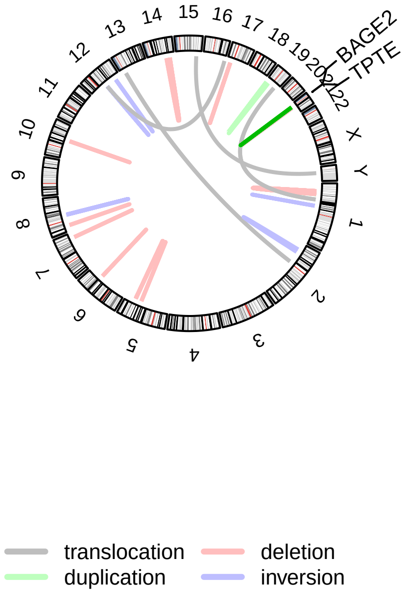


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

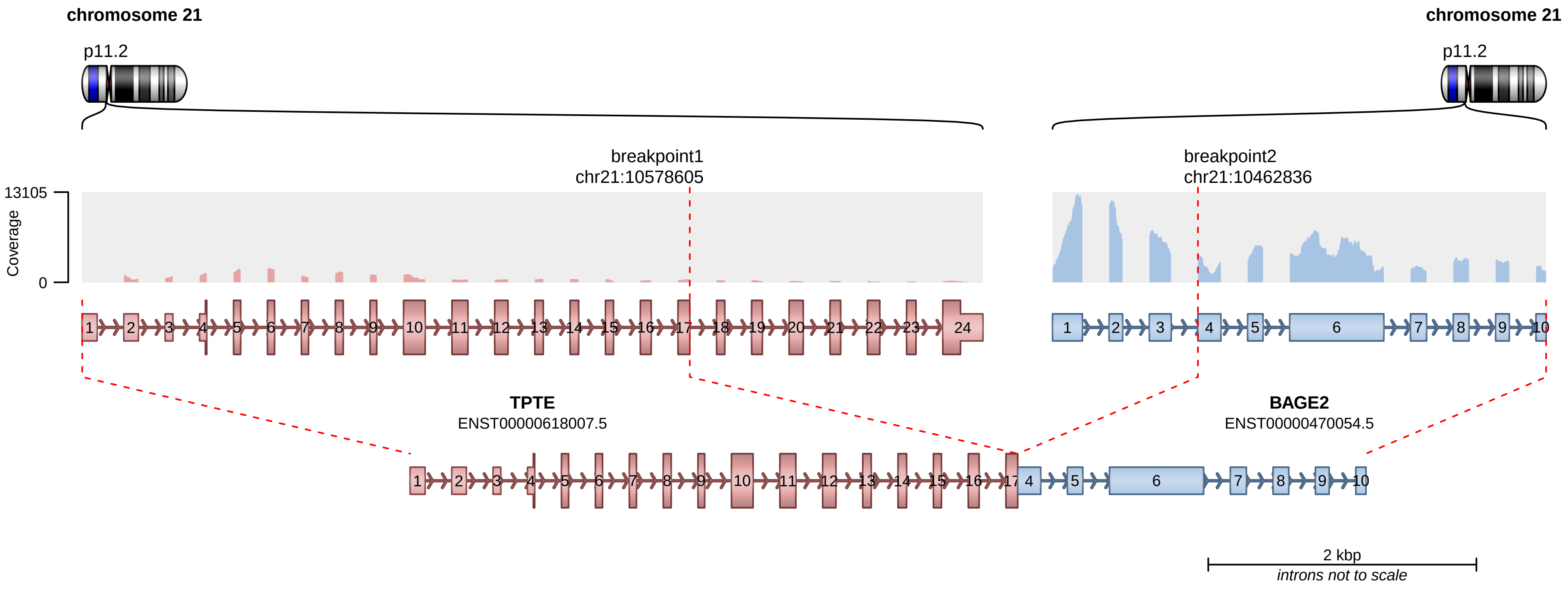


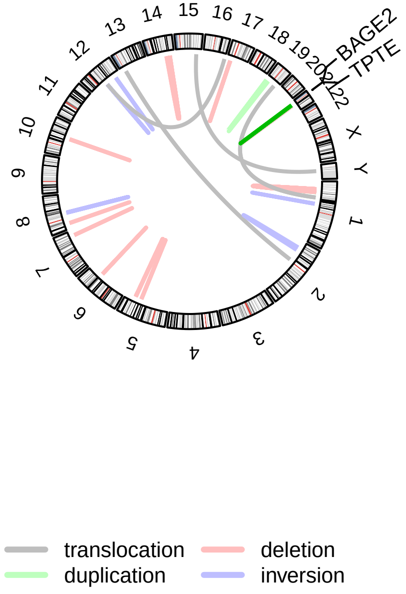


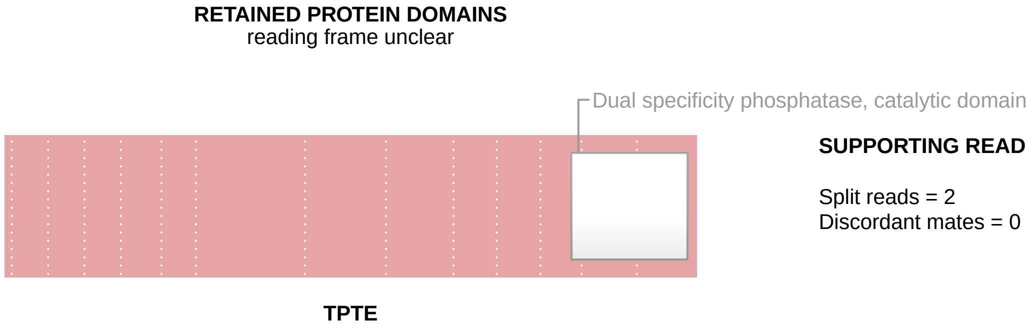
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 1

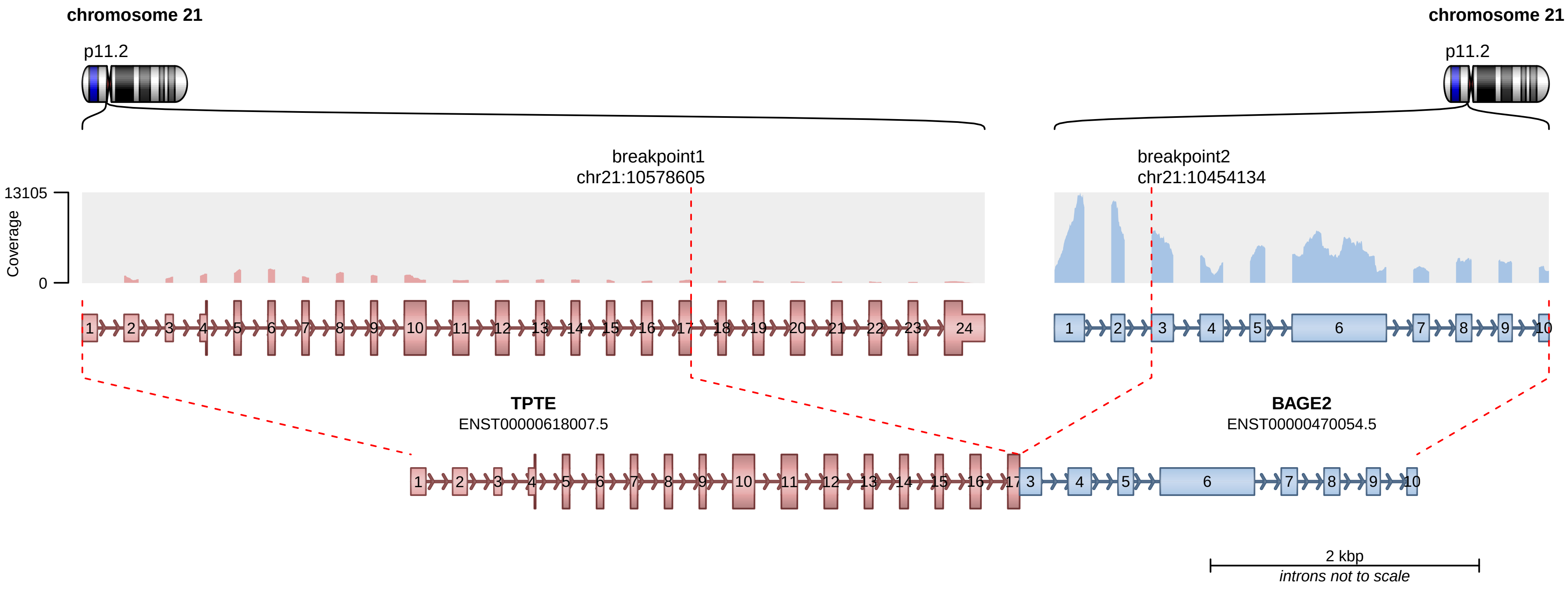


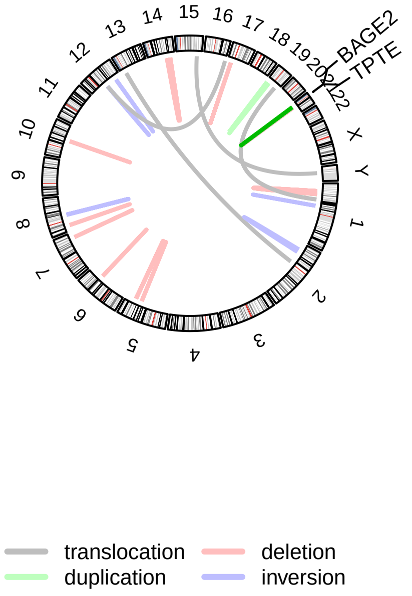




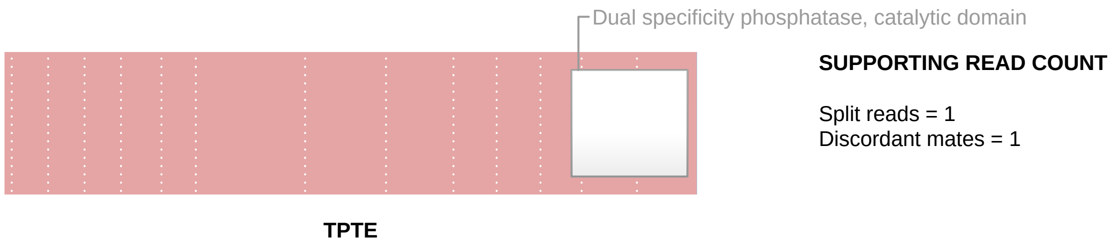
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0



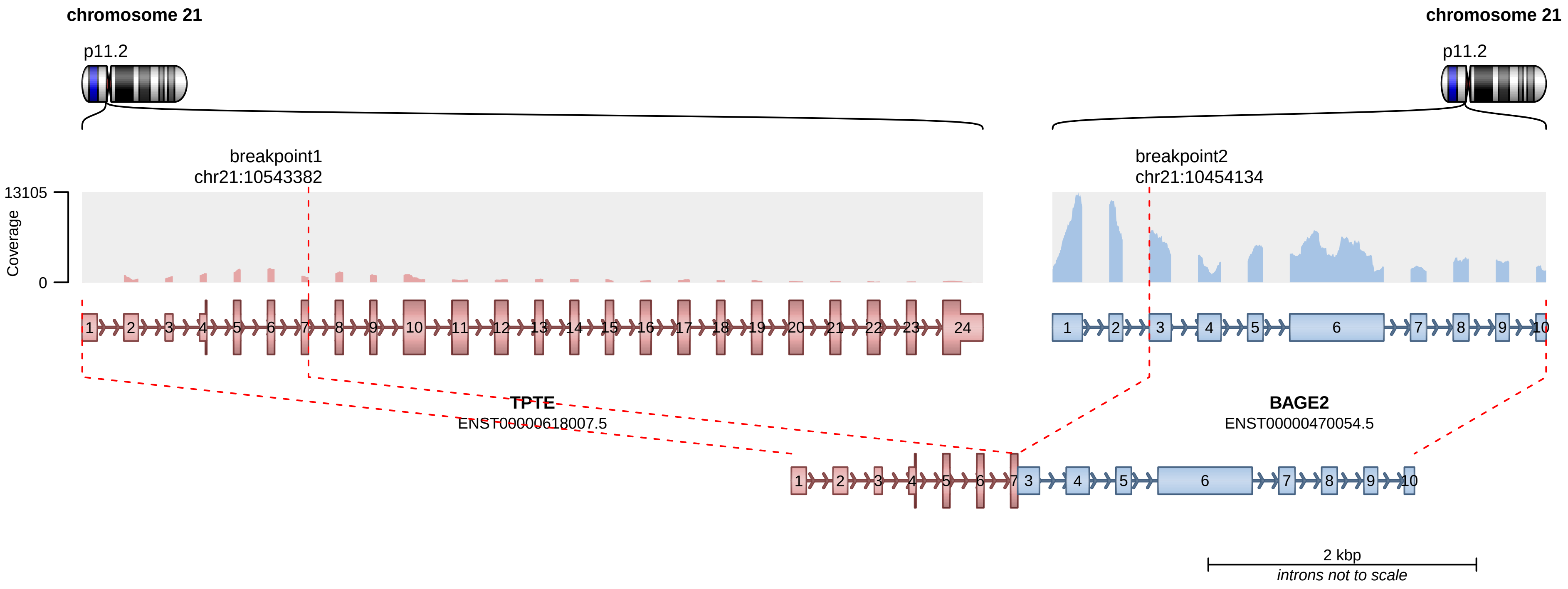


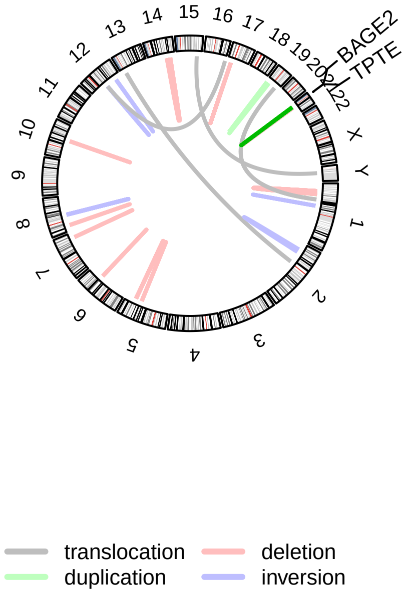
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

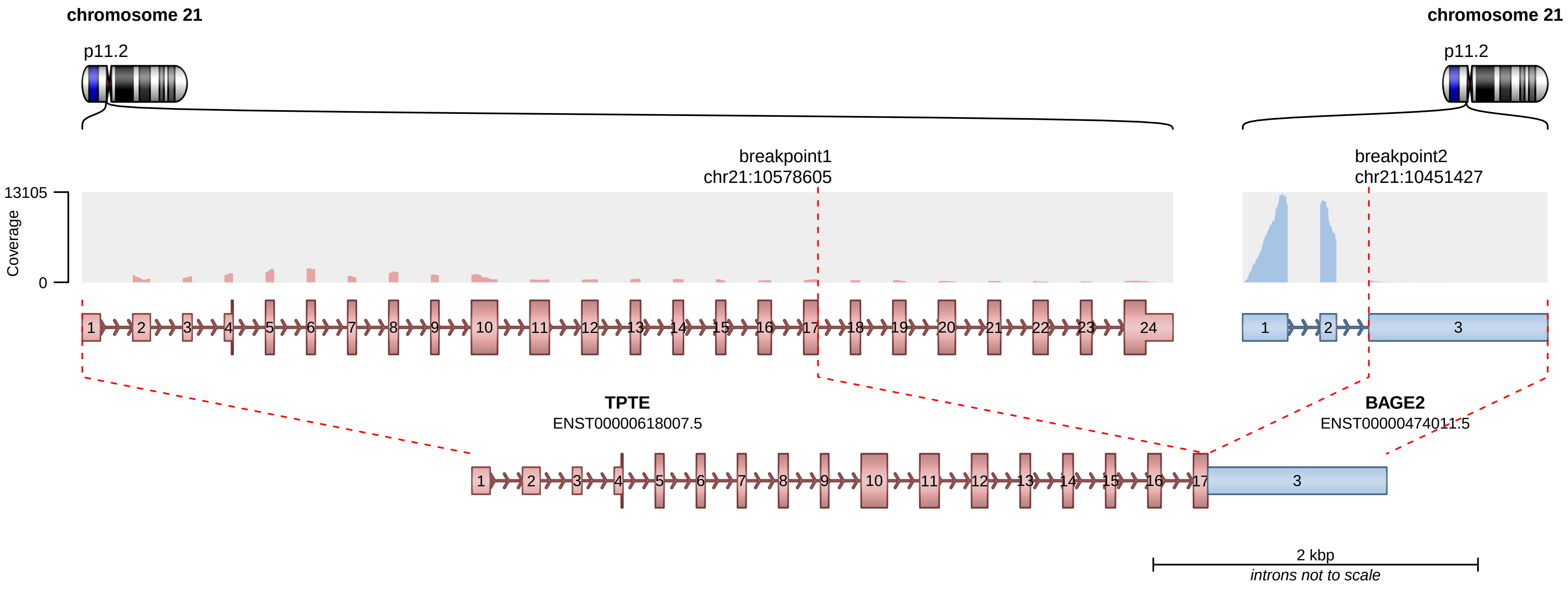


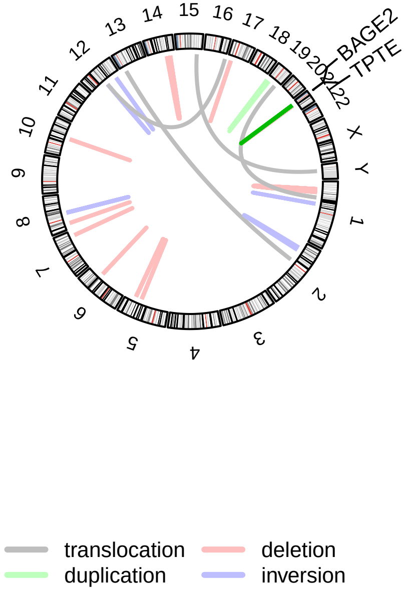


No protein domains retained in fusion.

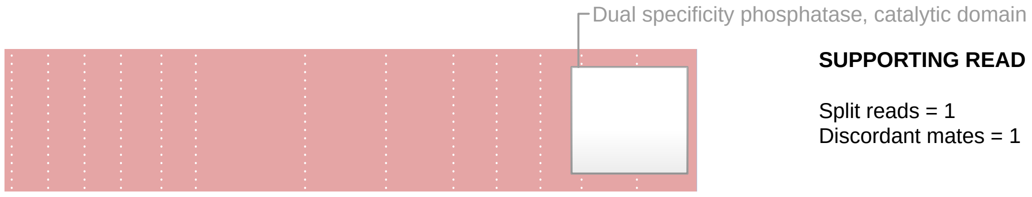
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1





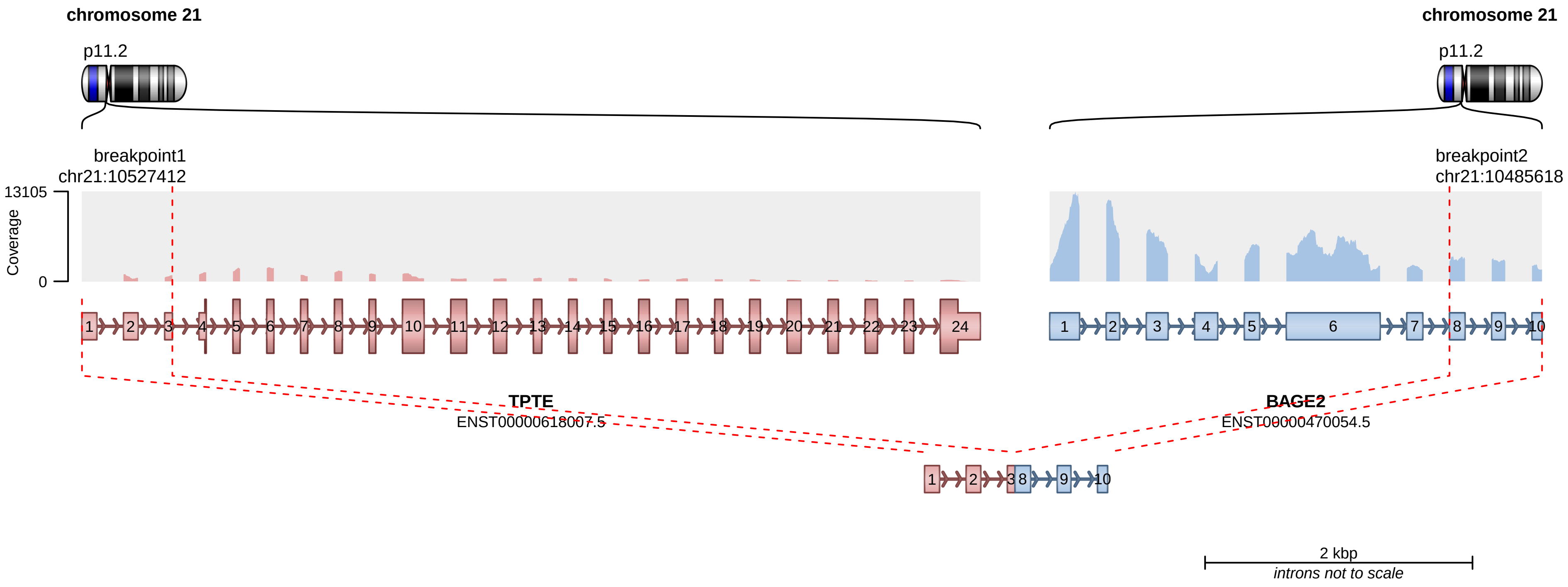
RETAINED PROTEIN DOMAINS
reading frame unclear

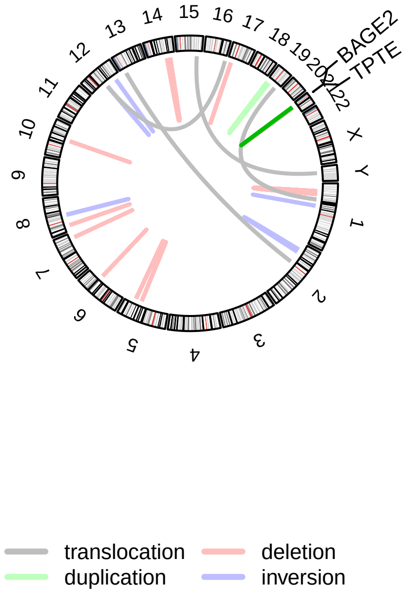


TPTE

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

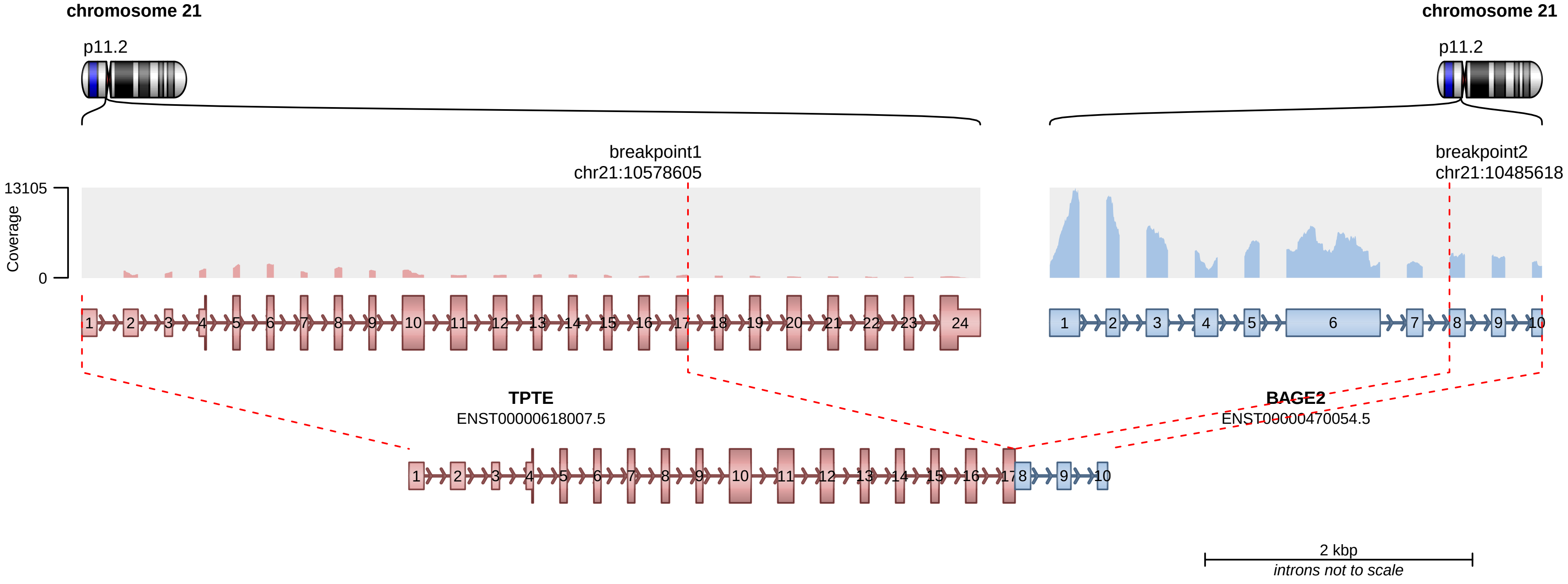


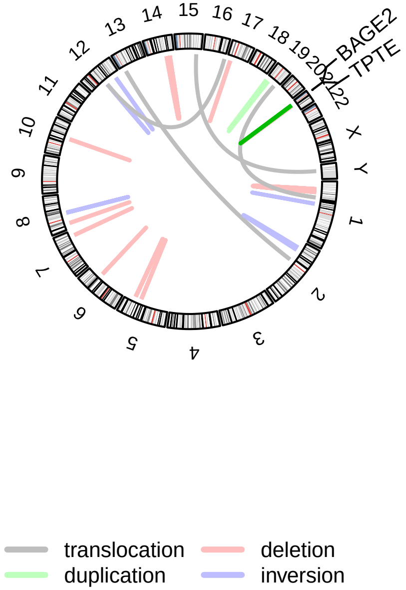


No coding regions retained in fusion transcript.

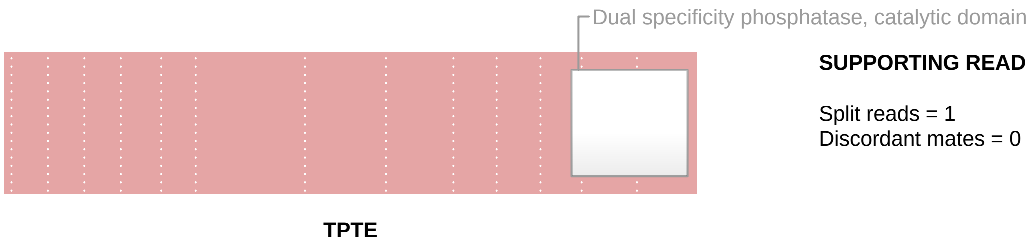
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



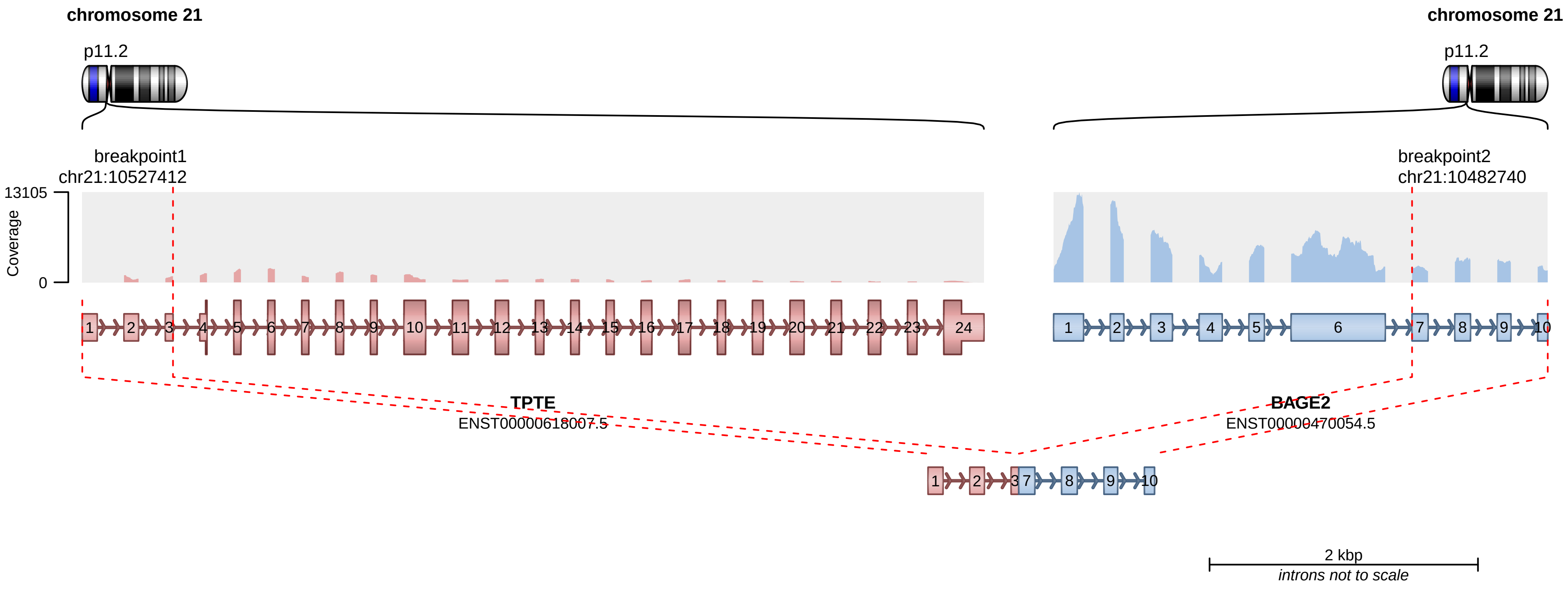


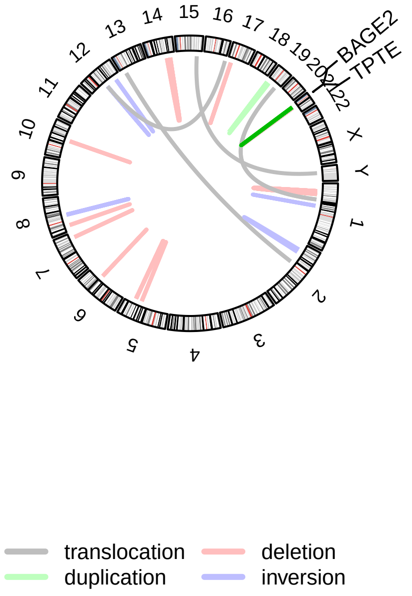
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

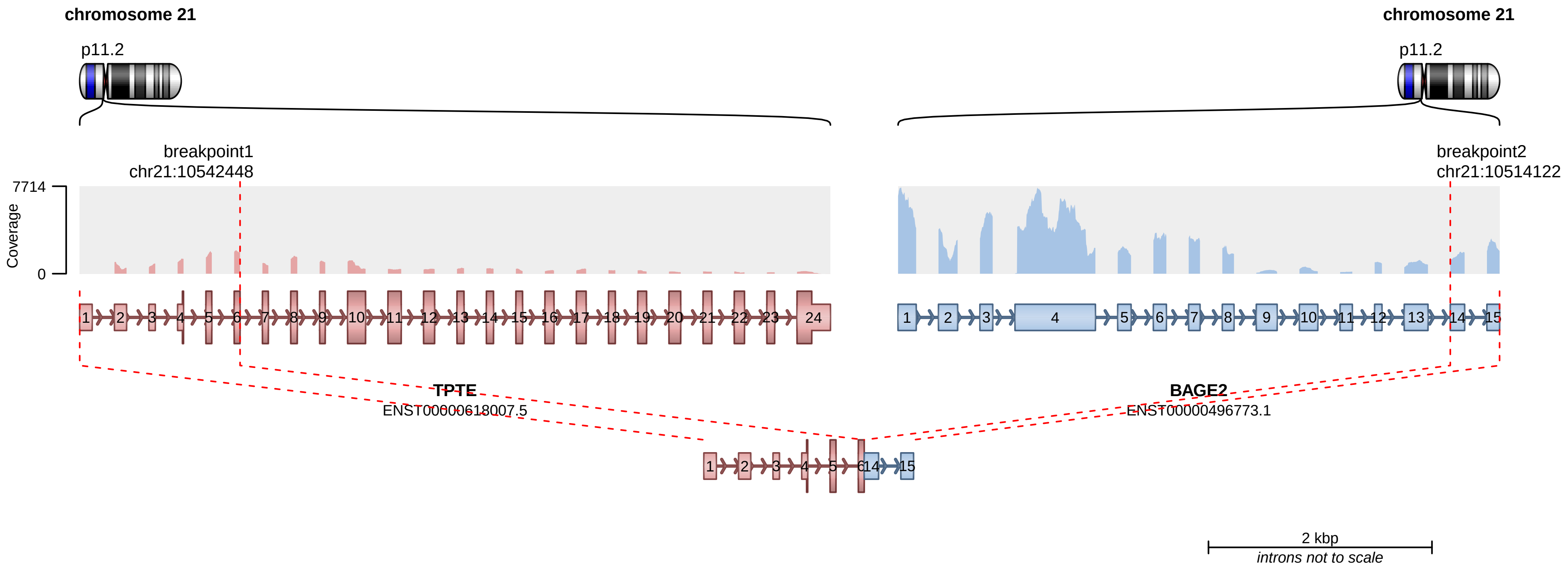


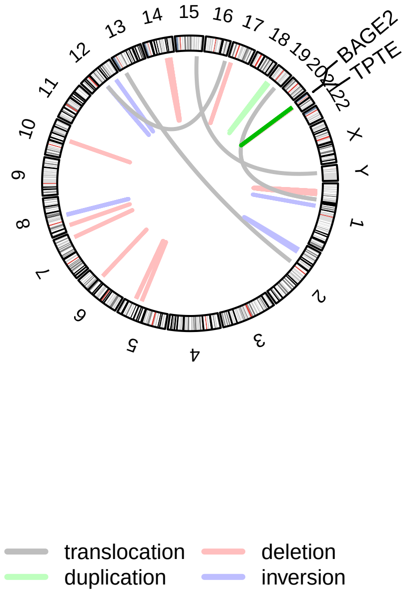


No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

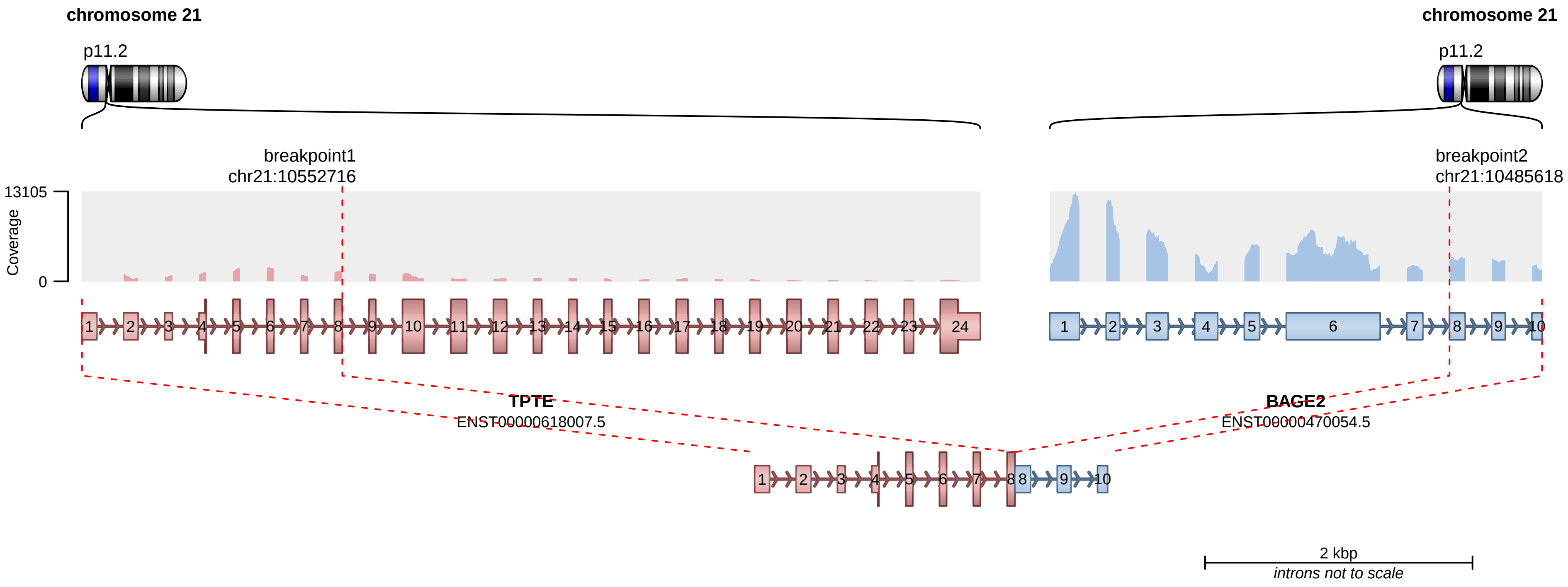


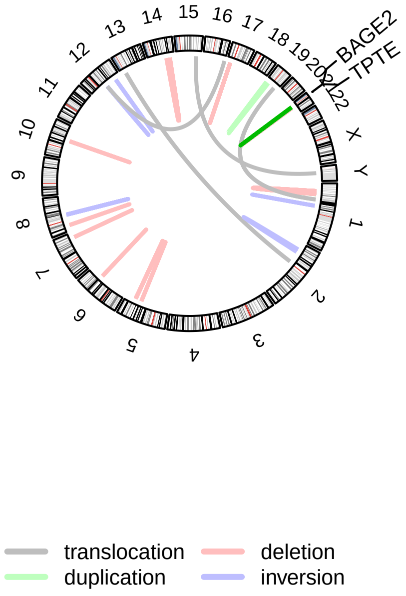


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

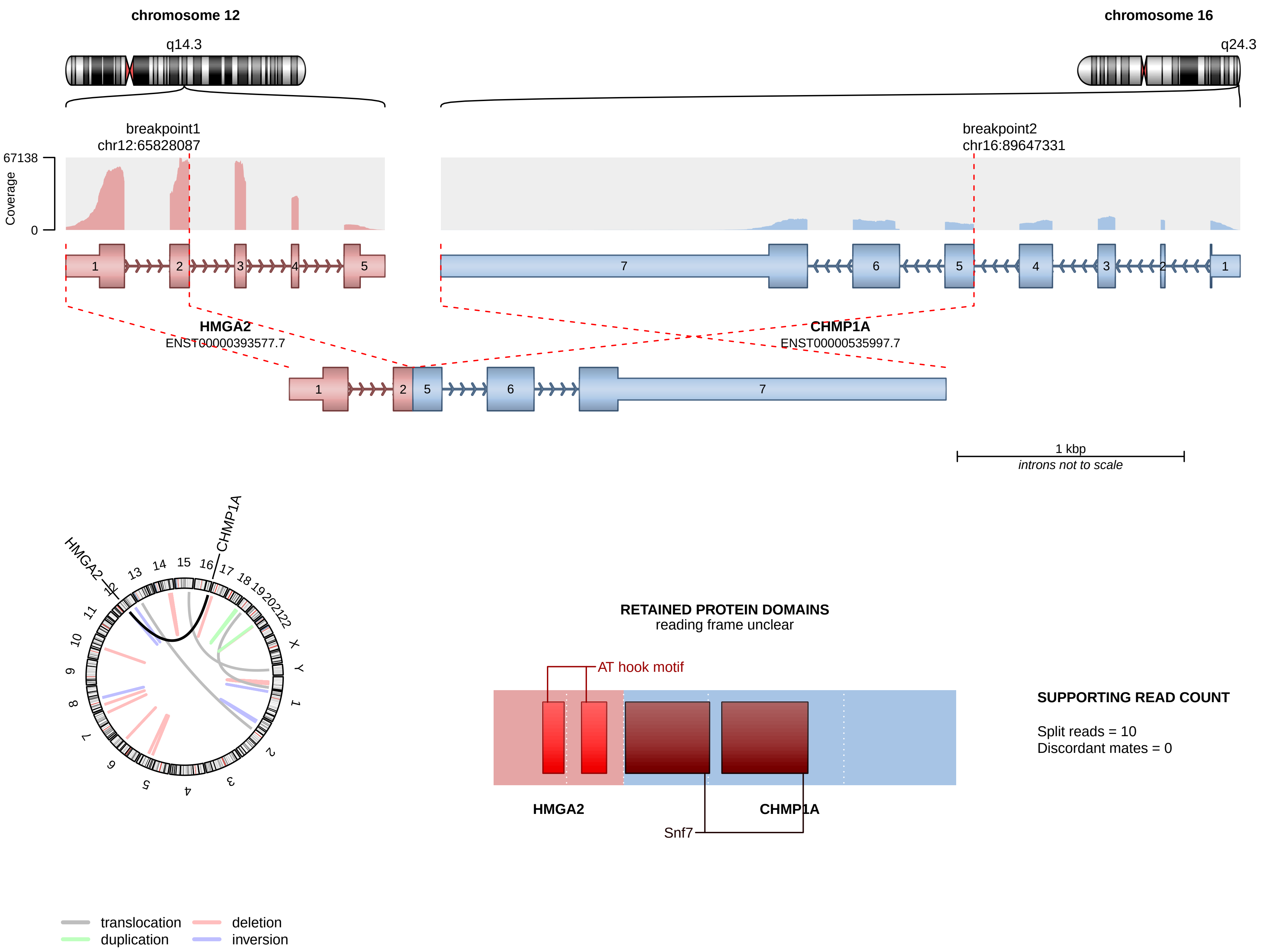


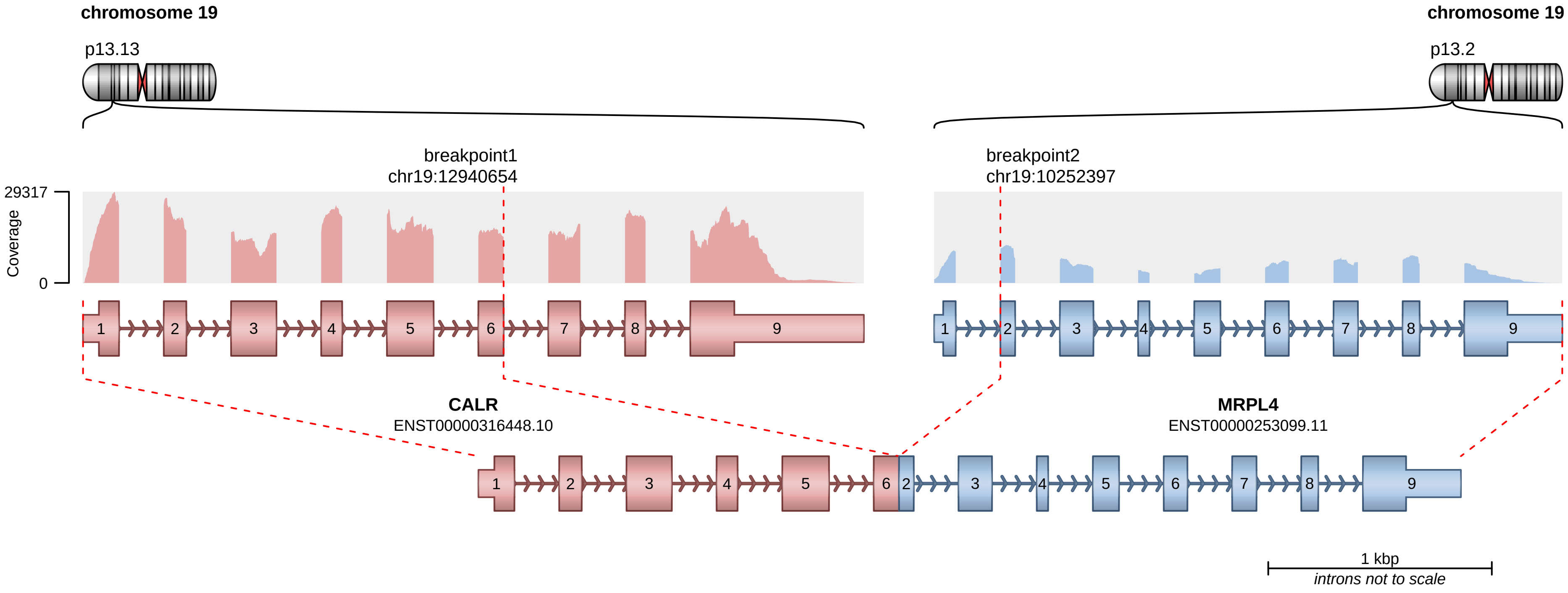


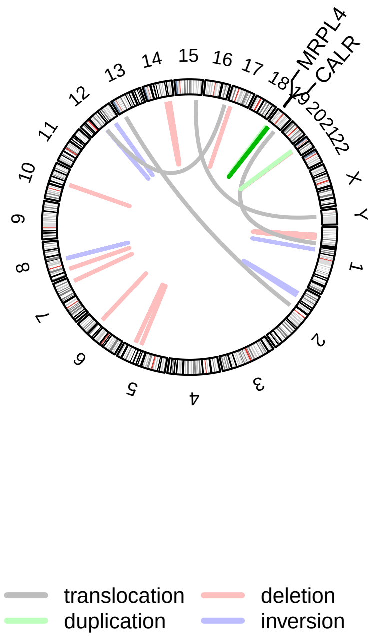
No protein domains retained in fusion.

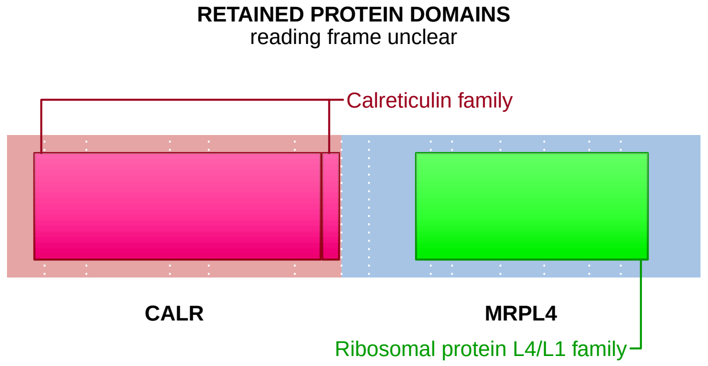
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0


chromosome 12
q14.3
chromosome 16
q24.3
breakpoint1
chr12:65828087
breakpoint2
chr16:89647331
67138
Coverage
0
1
2
3
4
5
7
6
5
4
3
2
1
HMGA2
ENST00000393577.7
CHMP1A
ENST00000535997.7
1
2
5
6
7
1 kbp
introns not to scale
HMGA2
CHMP1A
12
13
14
15
16
17
18
19
20
21
22
X
Y
1
2
3
4
5
6
7
8
9
10
11
RETAINED PROTEIN DOMAINS
reading frame unclear
AT hook motif
HMGA2
CHMP1A
Snf7
SUPPORTING READ COUNT
Split reads = 10
Discordant mates = 0
translocation
deletion
duplication
inversion

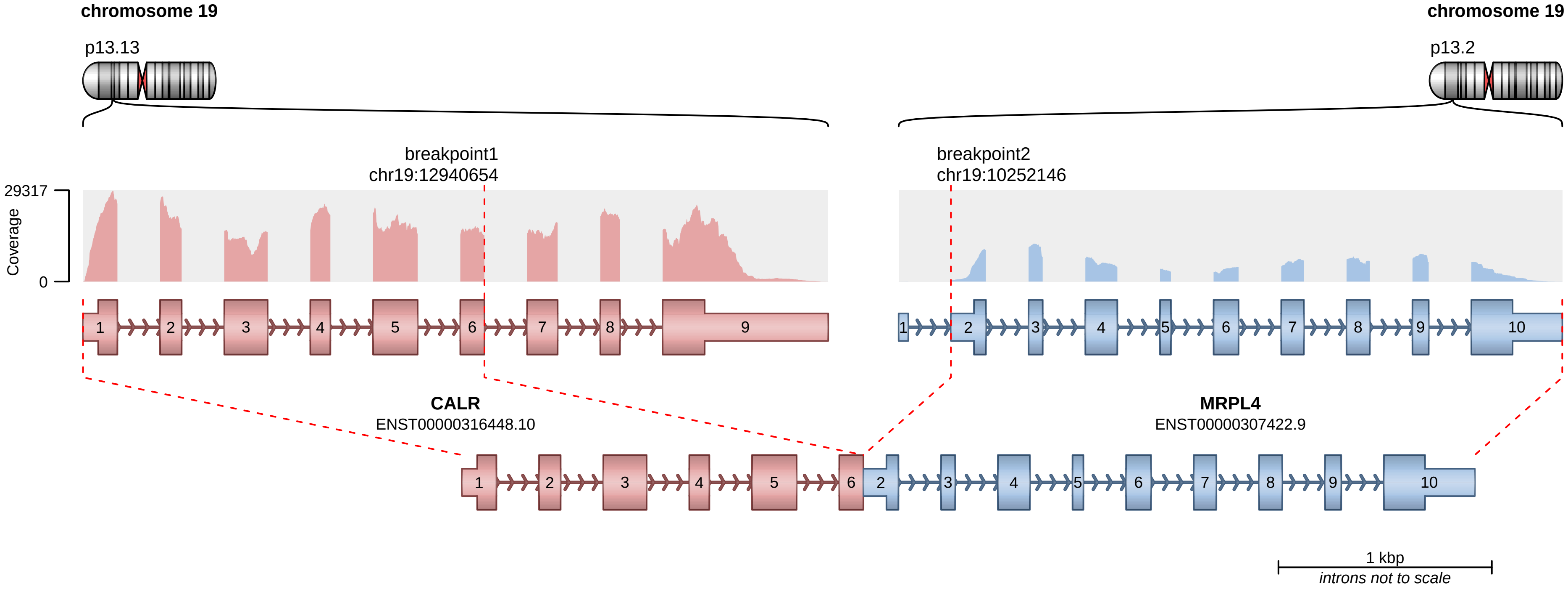


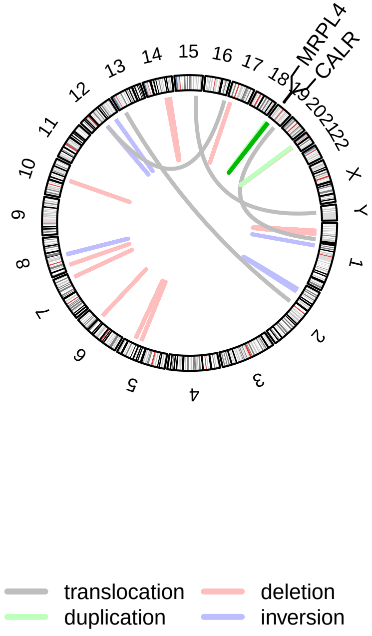




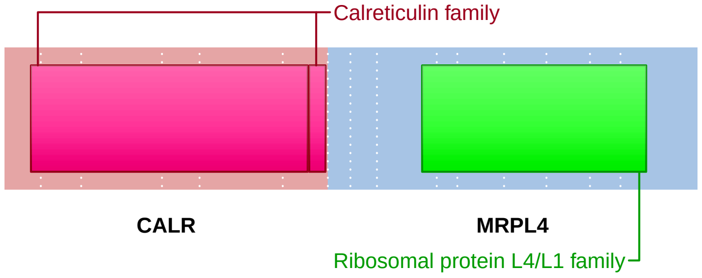
SUPPORTING READ COUNT

Split reads = 9
Discordant mates = 0



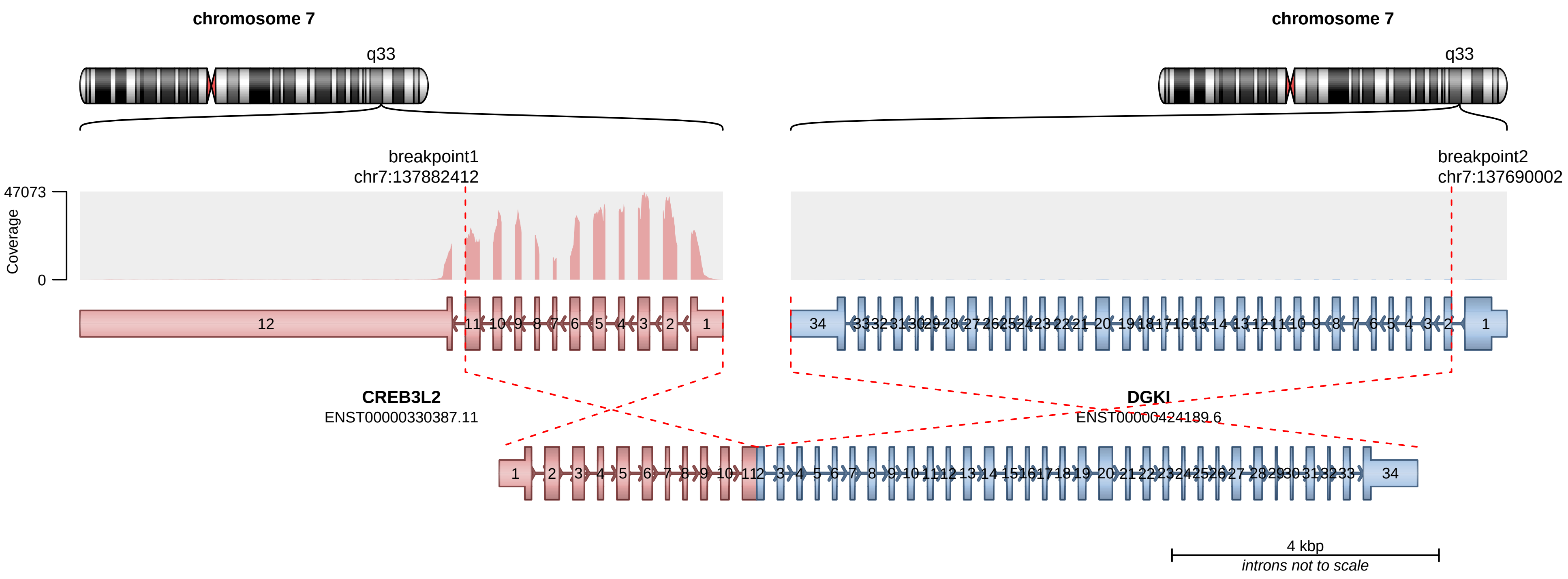


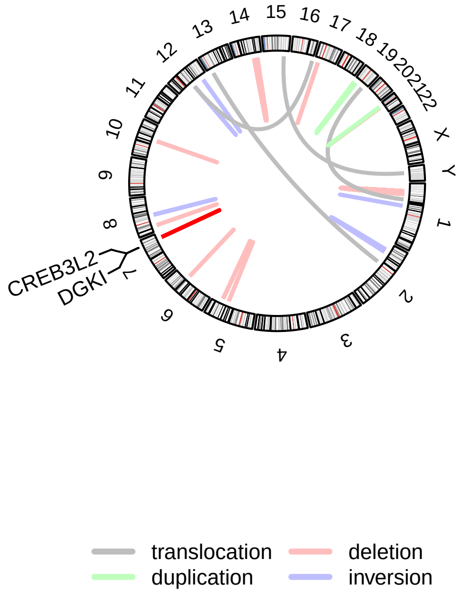
RETAINED PROTEIN DOMAINS
reading frame unclear

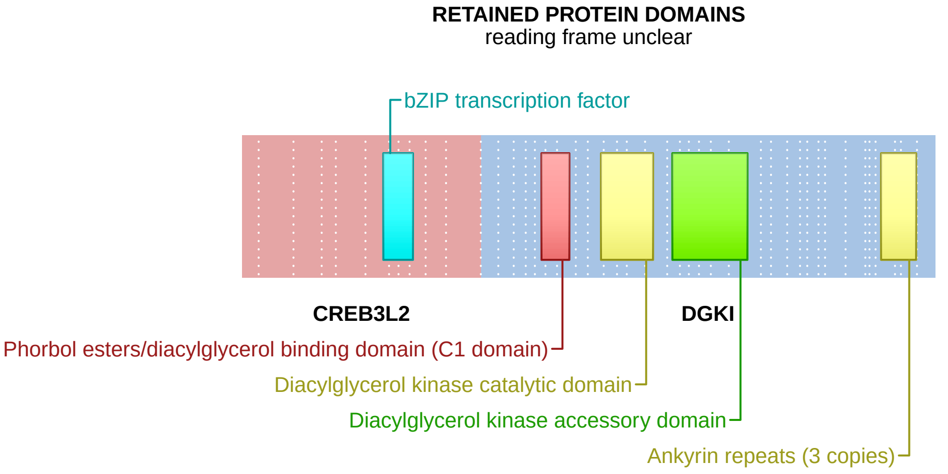


SUPPORTING READ COUNT

Split reads = 9
Discordant mates = 0

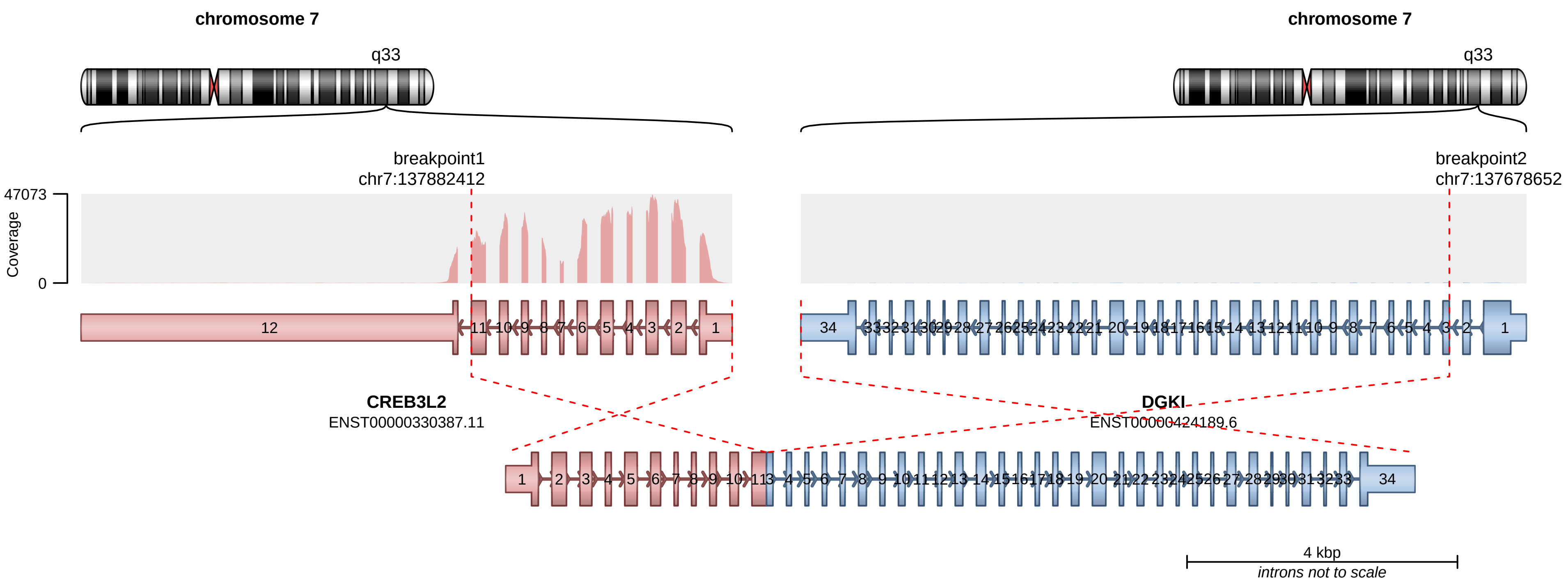


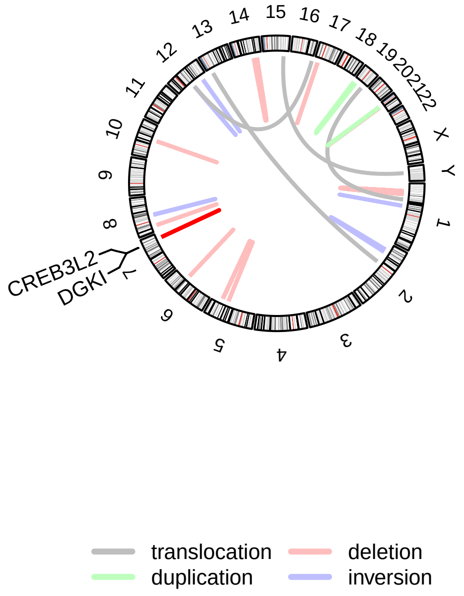


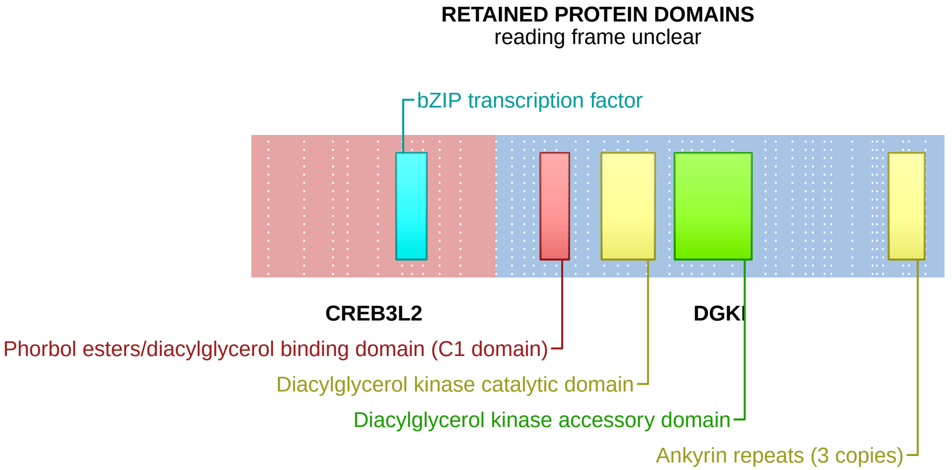


SUPPORTING READ COUNT

Split reads = 9
Discordant mates = 0

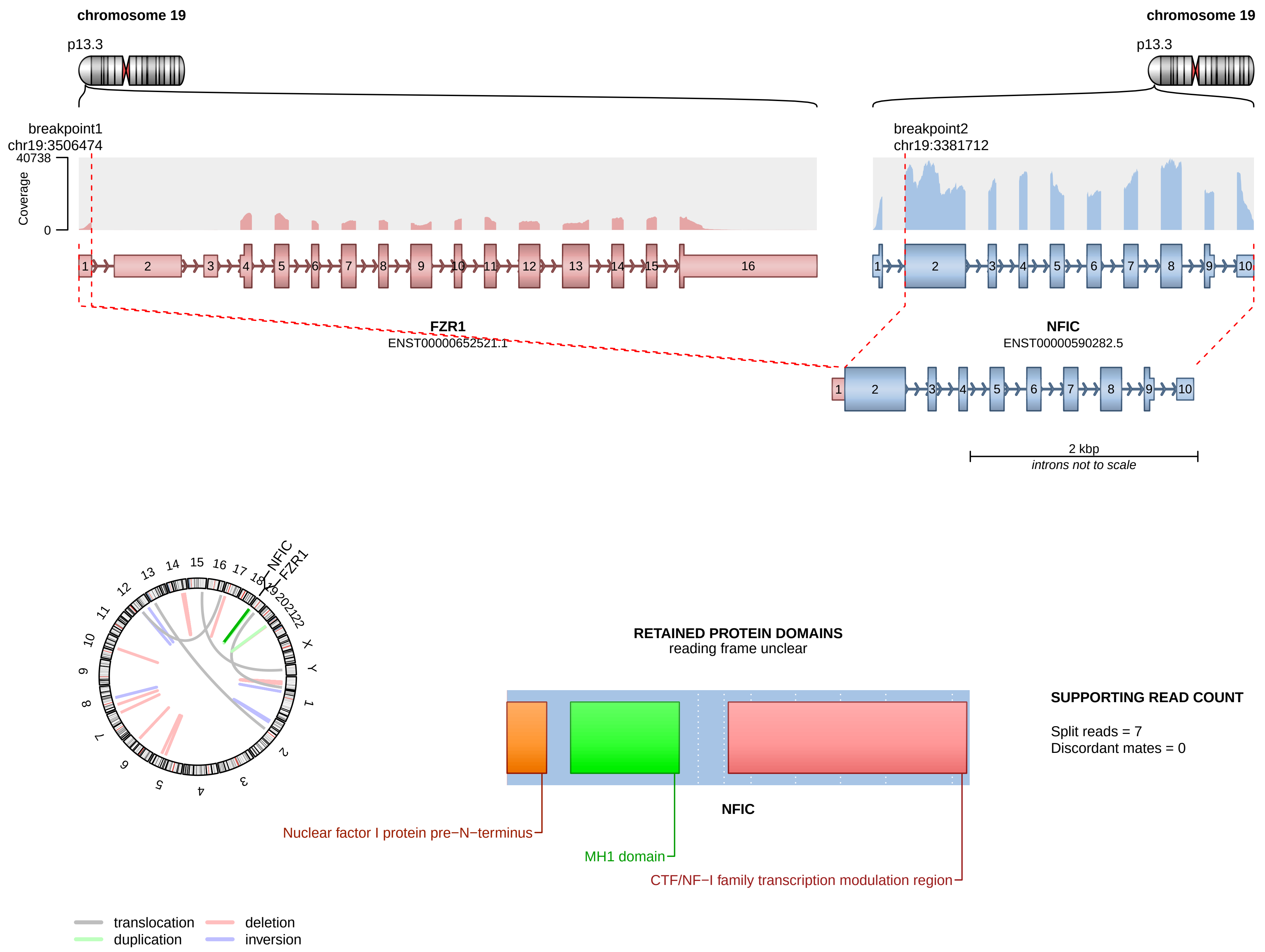






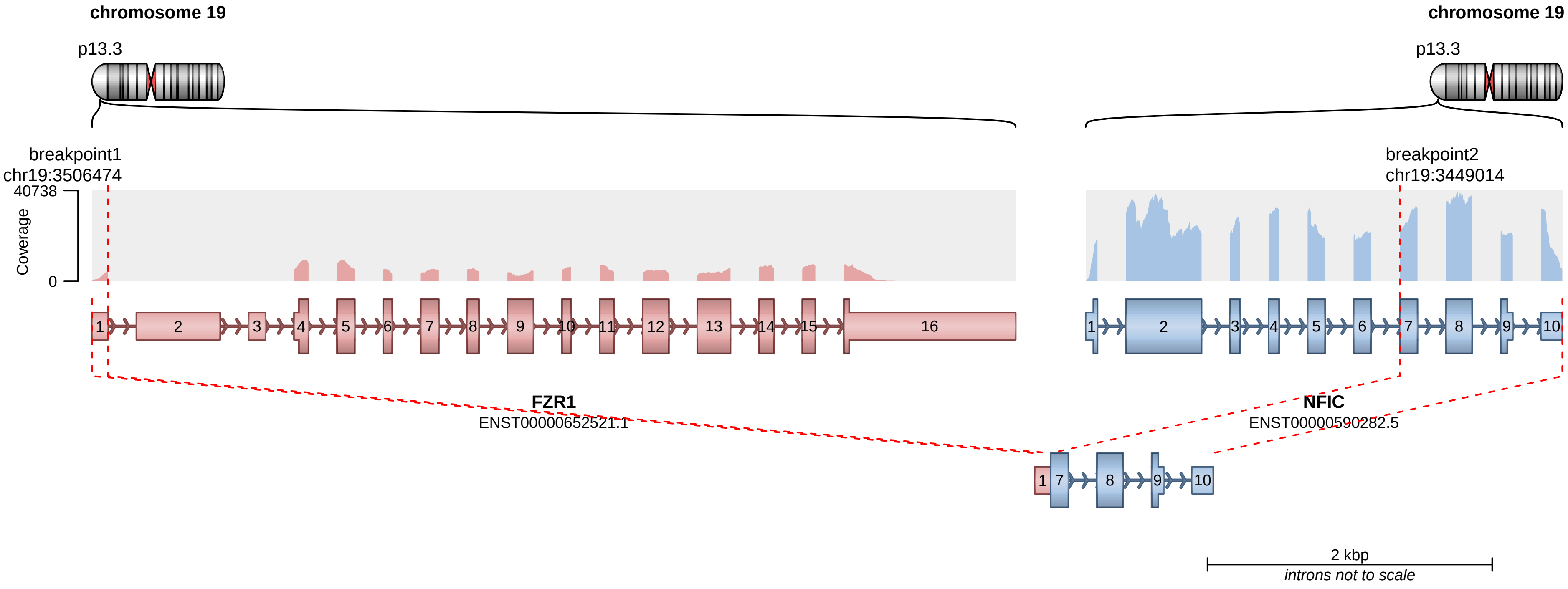
SUPPORTING READ COUNT

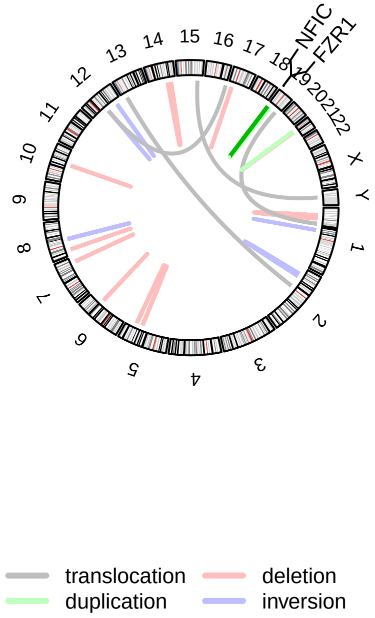
Split reads = 1
Discordant mates = 0



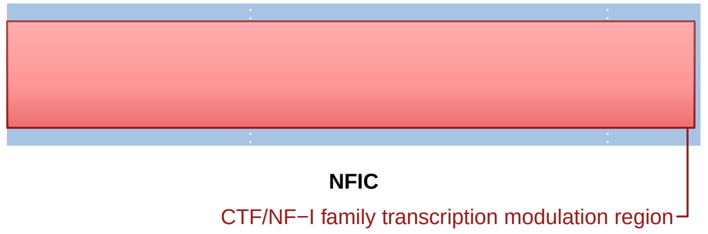
SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 0



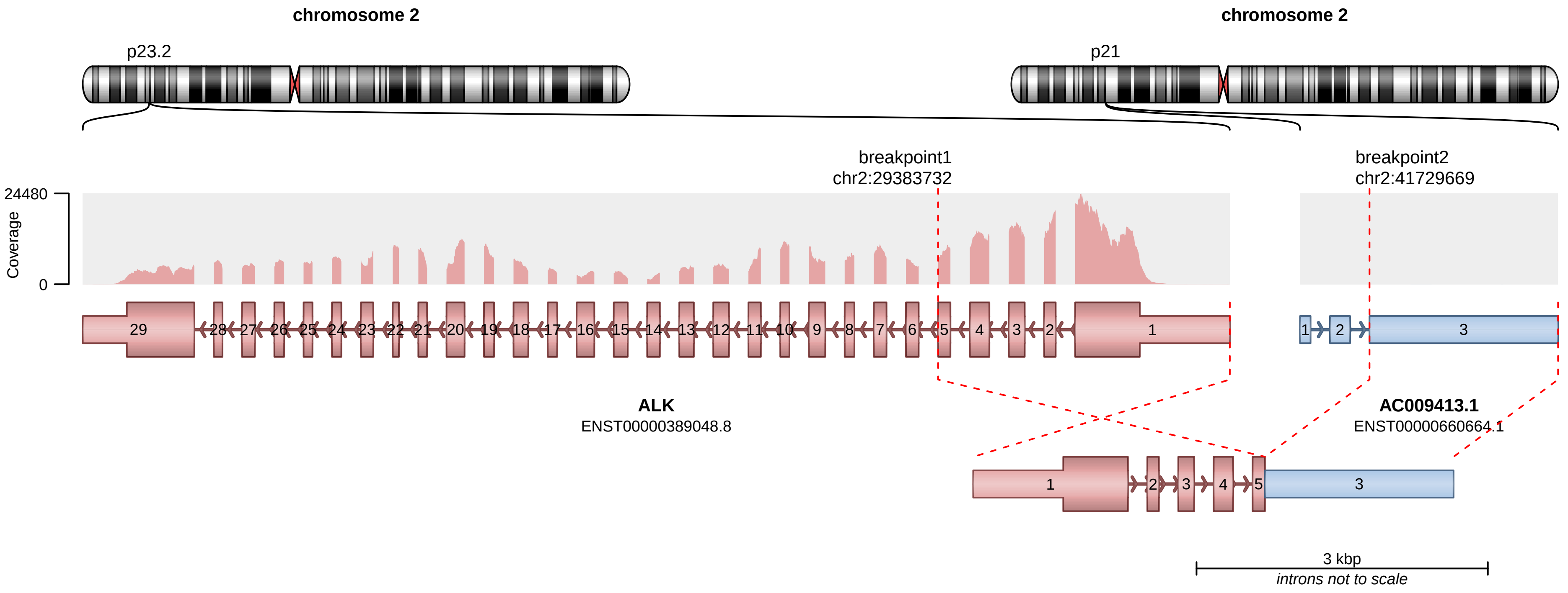


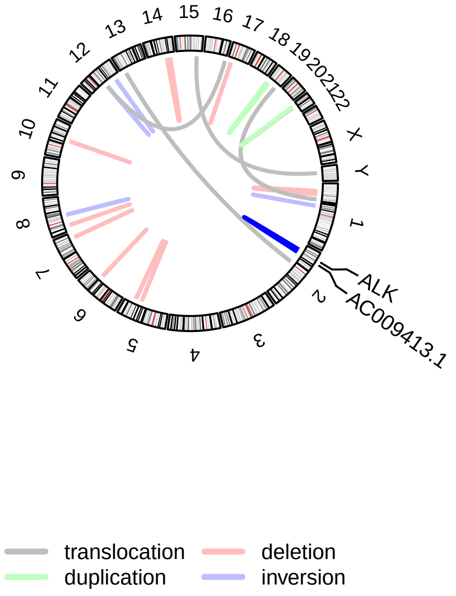
RETAINED PROTEIN DOMAINS
reading frame unclear

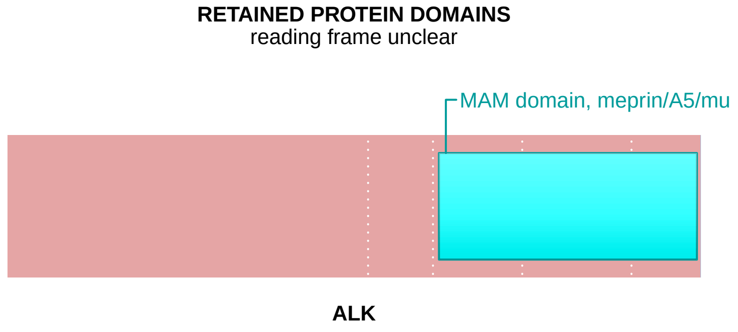


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0







SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0