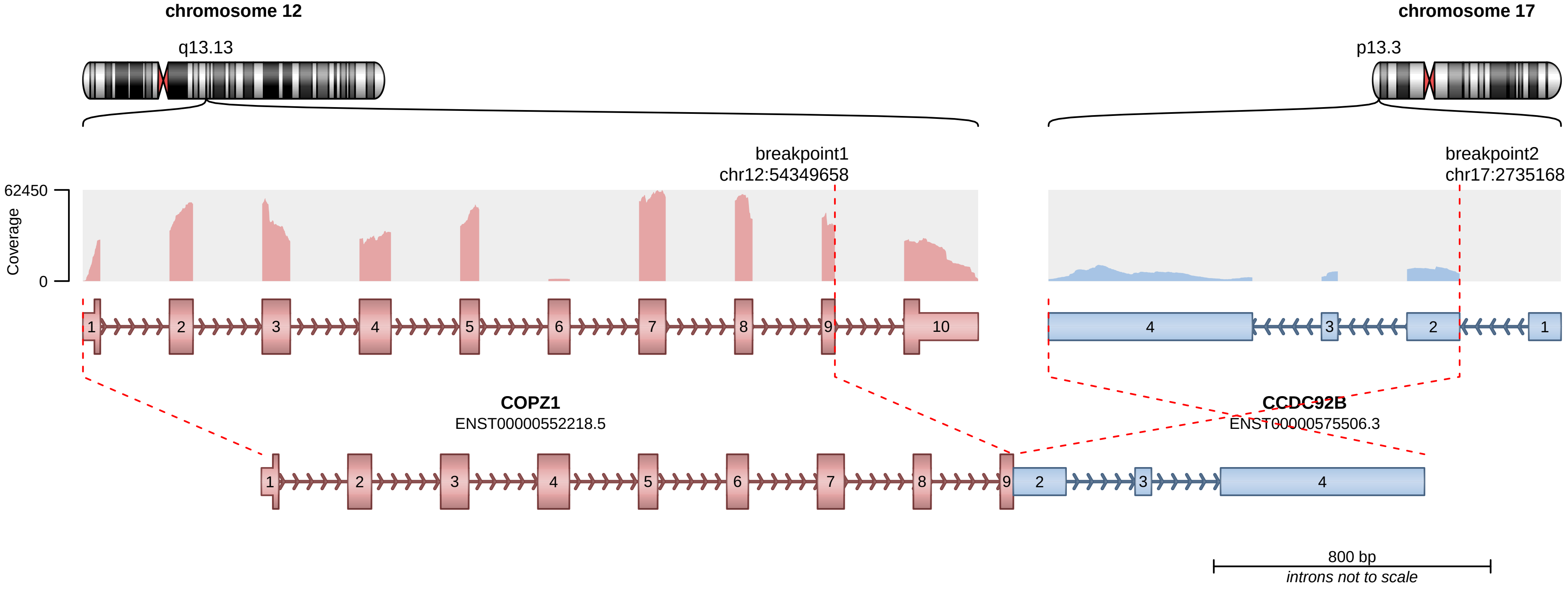
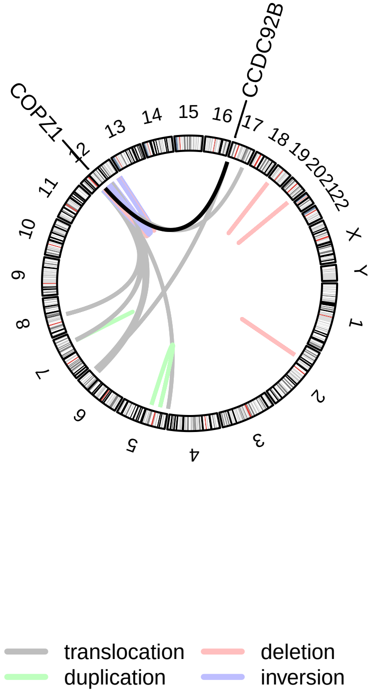
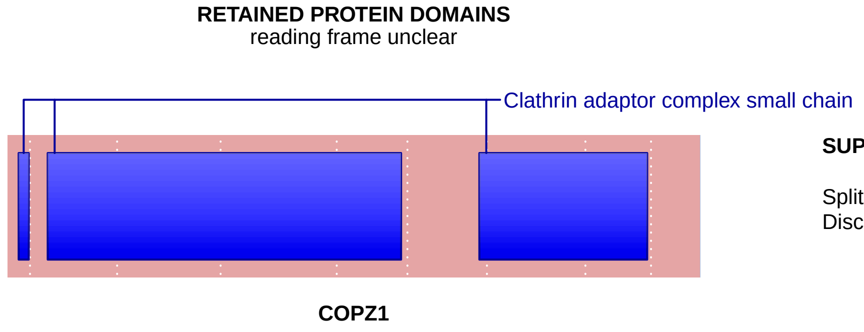
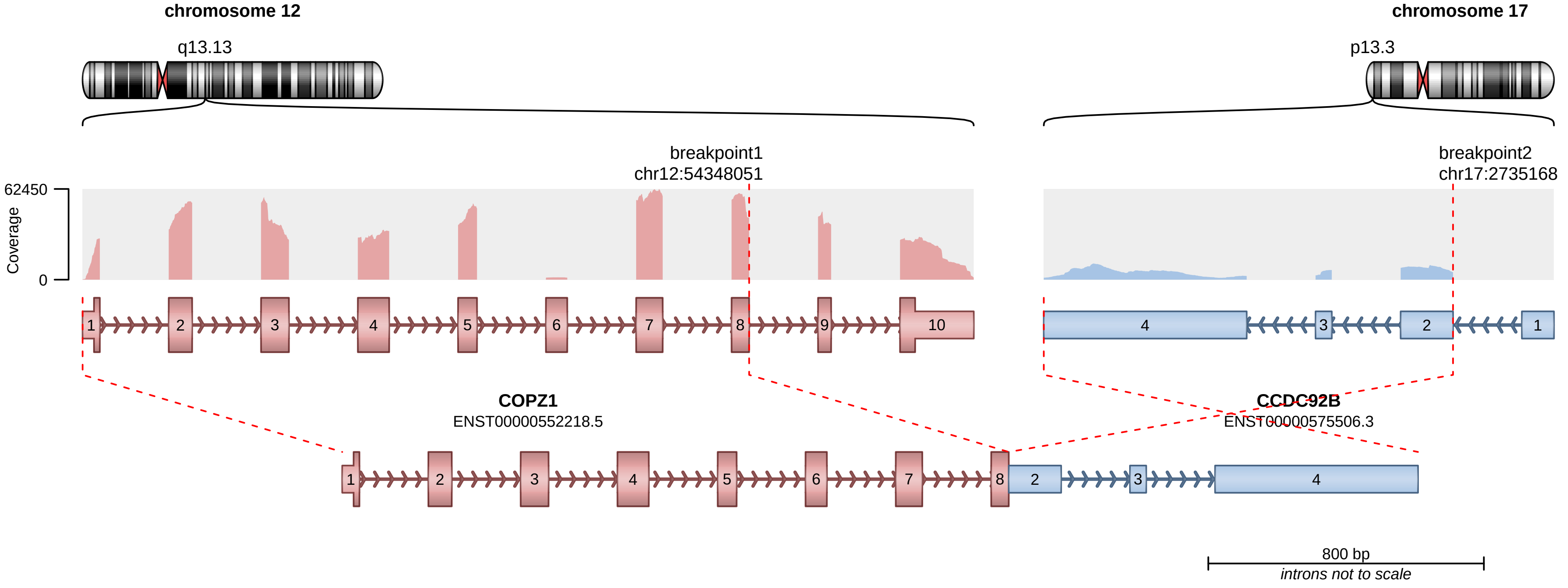


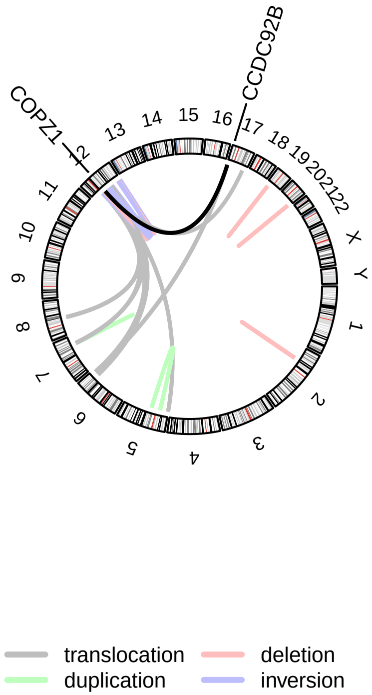


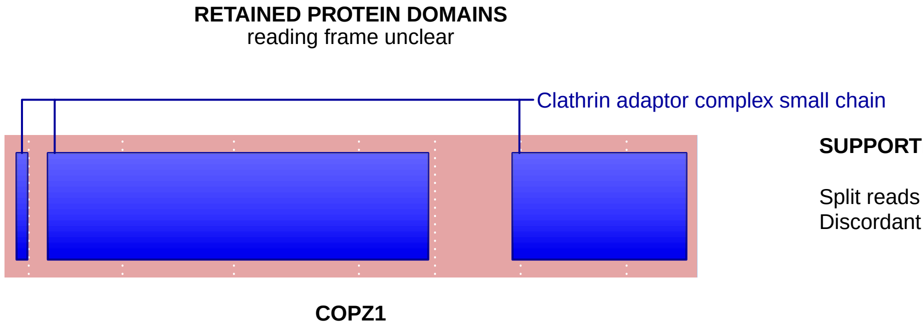


SUPPORTING READ COUNT

Split reads = 2481
Discordant mates = 40

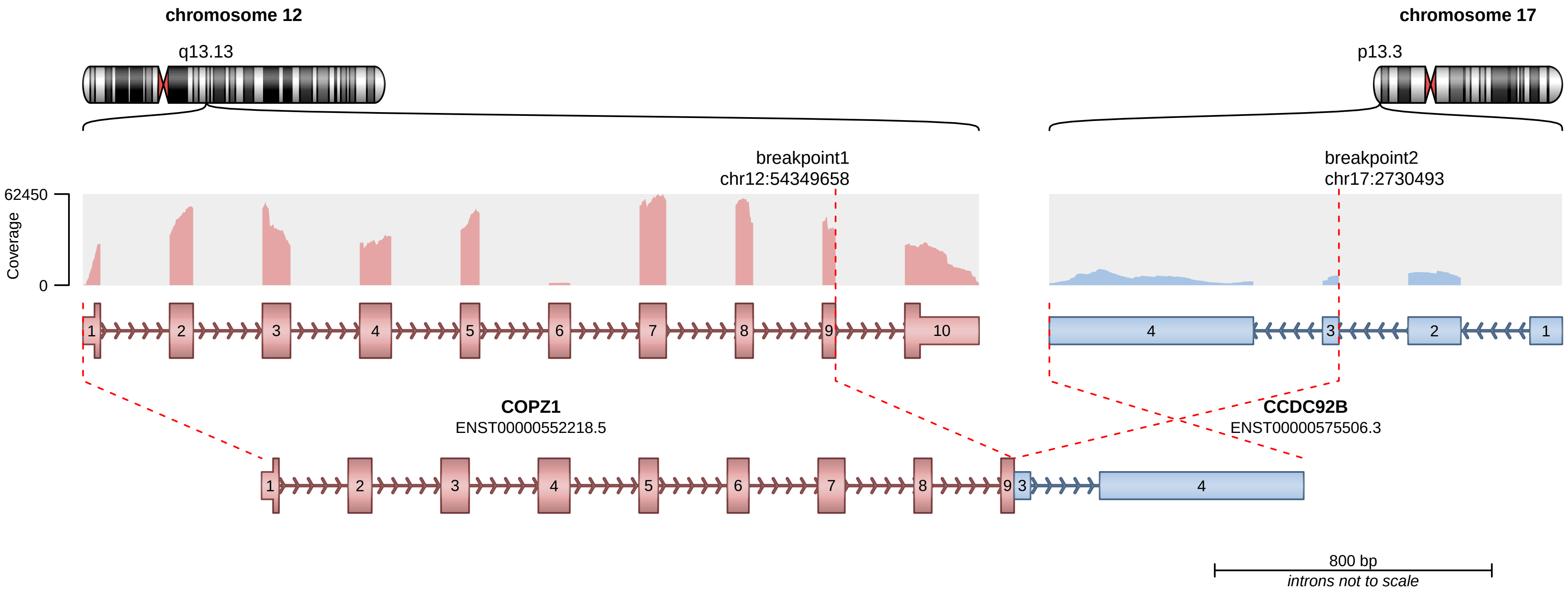


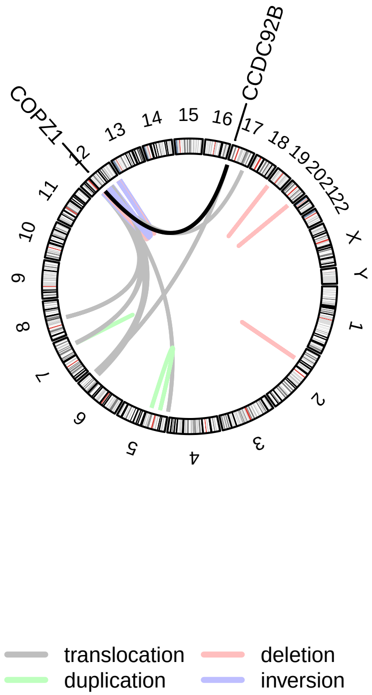


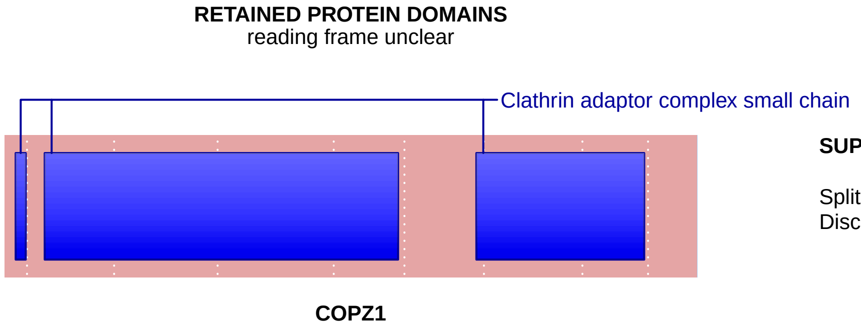


SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 18

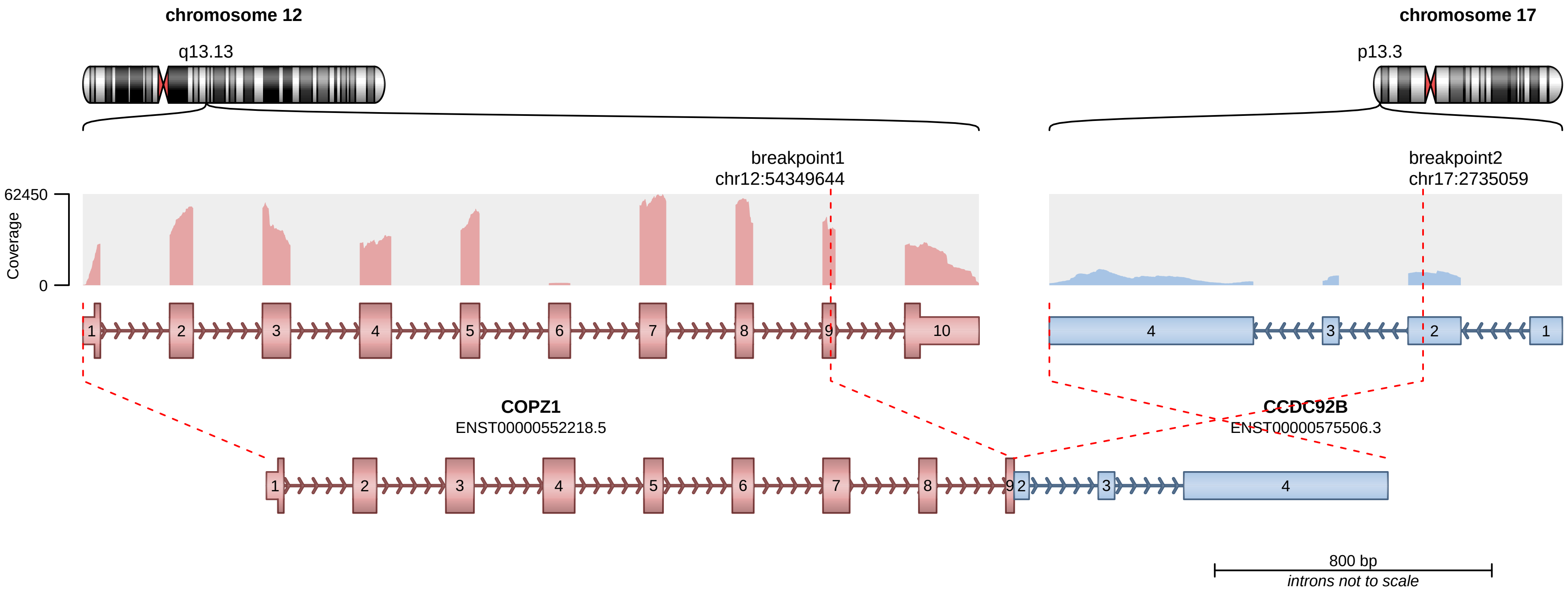


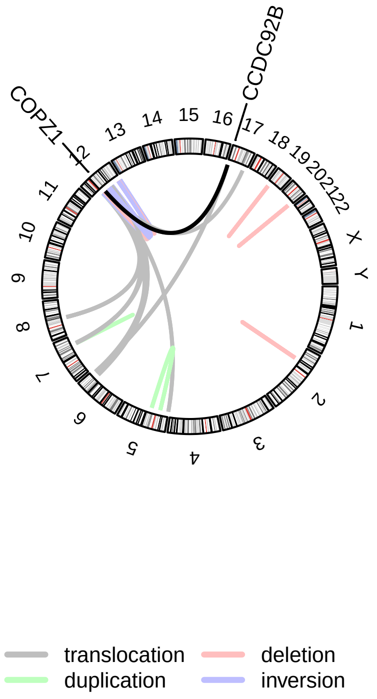


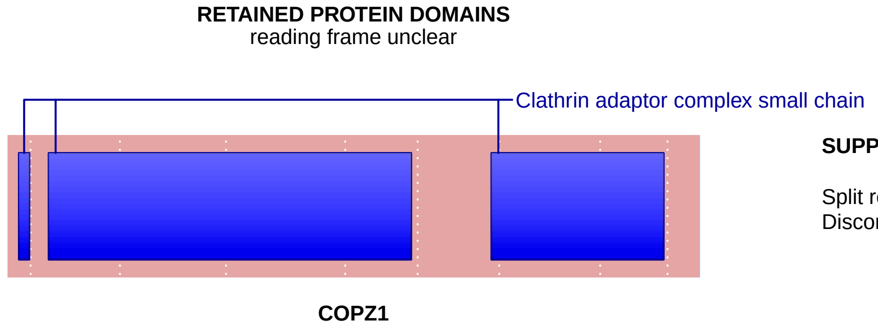


SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

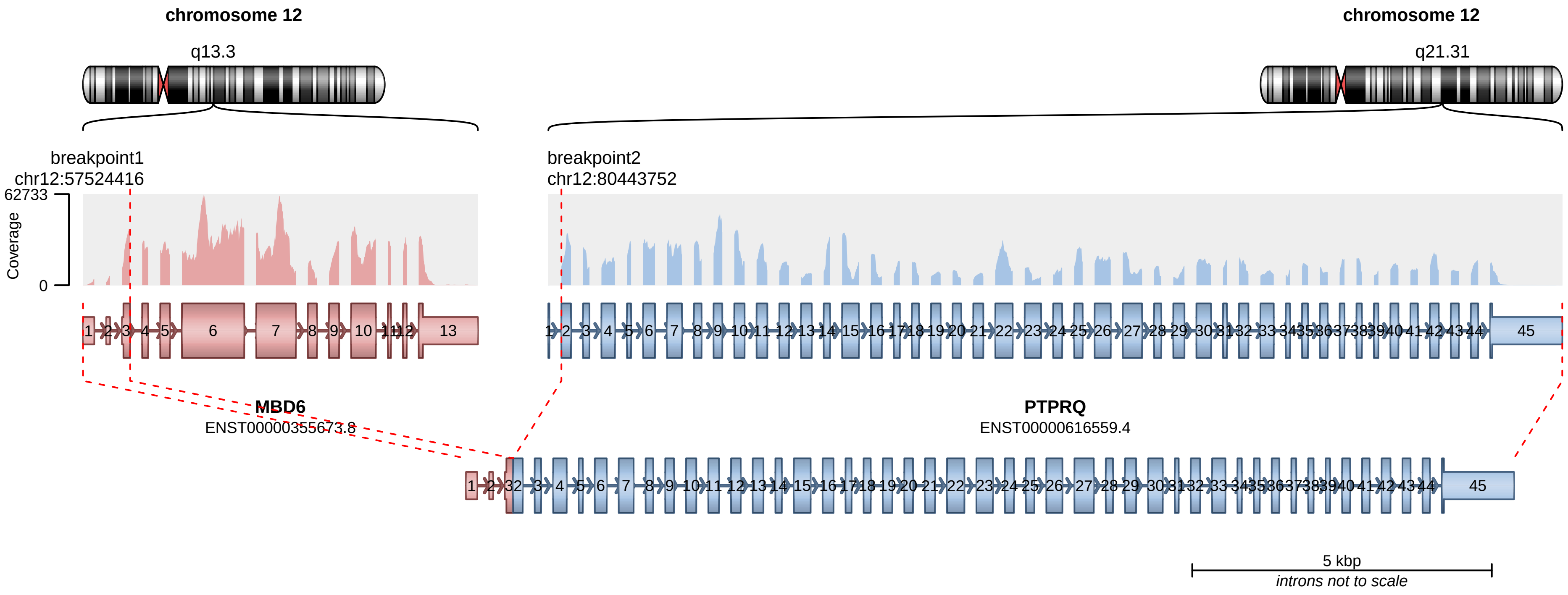


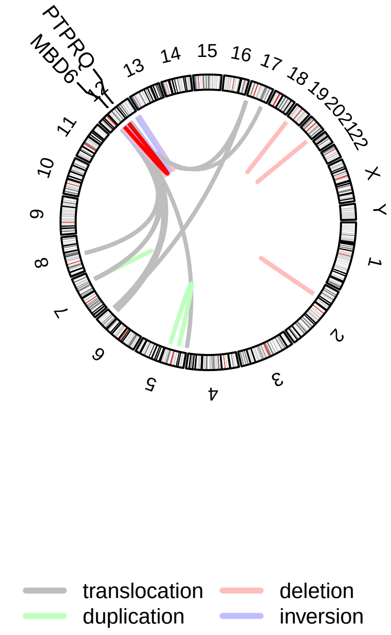




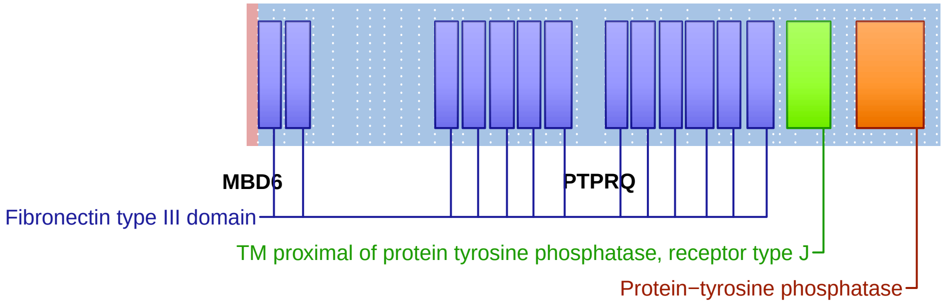
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0



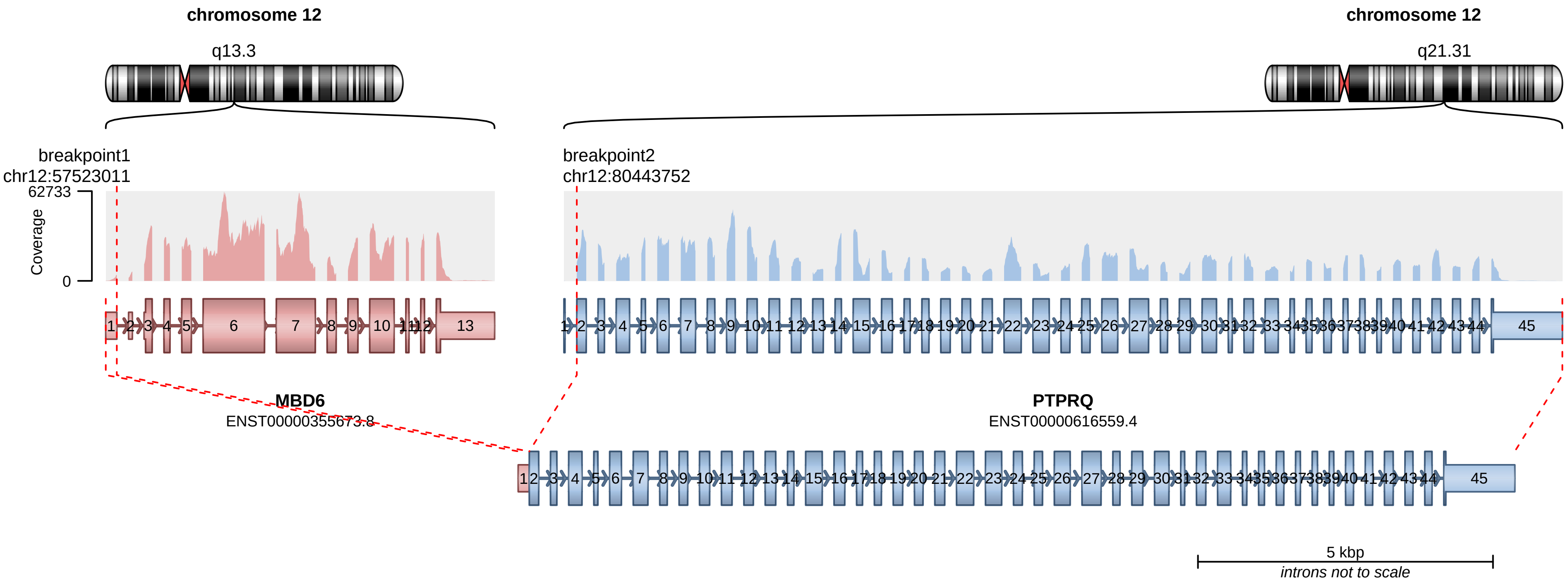


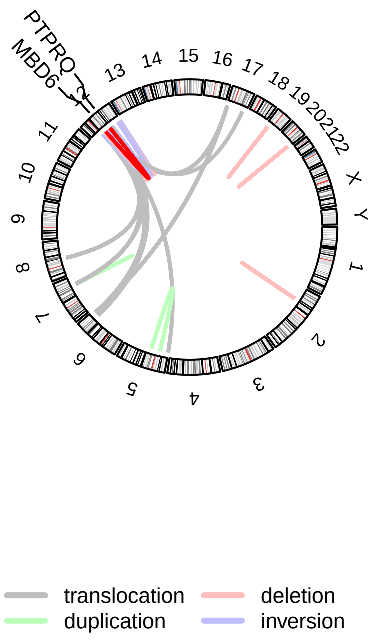
RETAINED PROTEIN DOMAINS
reading frame unclear

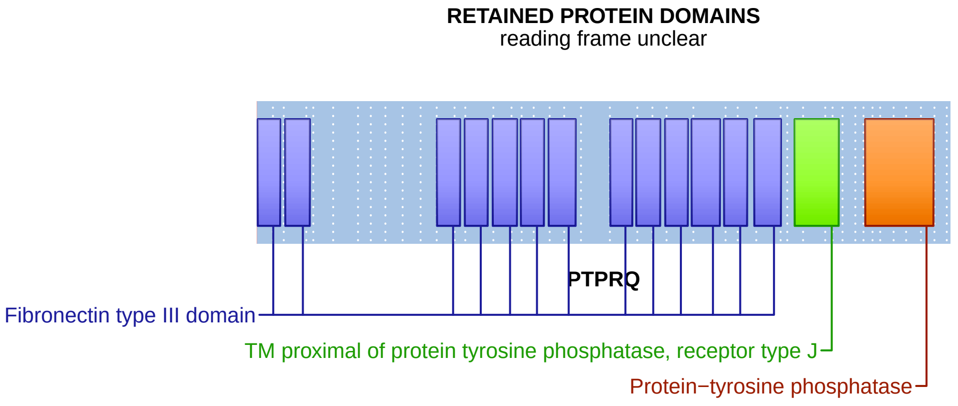


SUPPORTING READ COUNT

Split reads = 1730
Discordant mates = 43

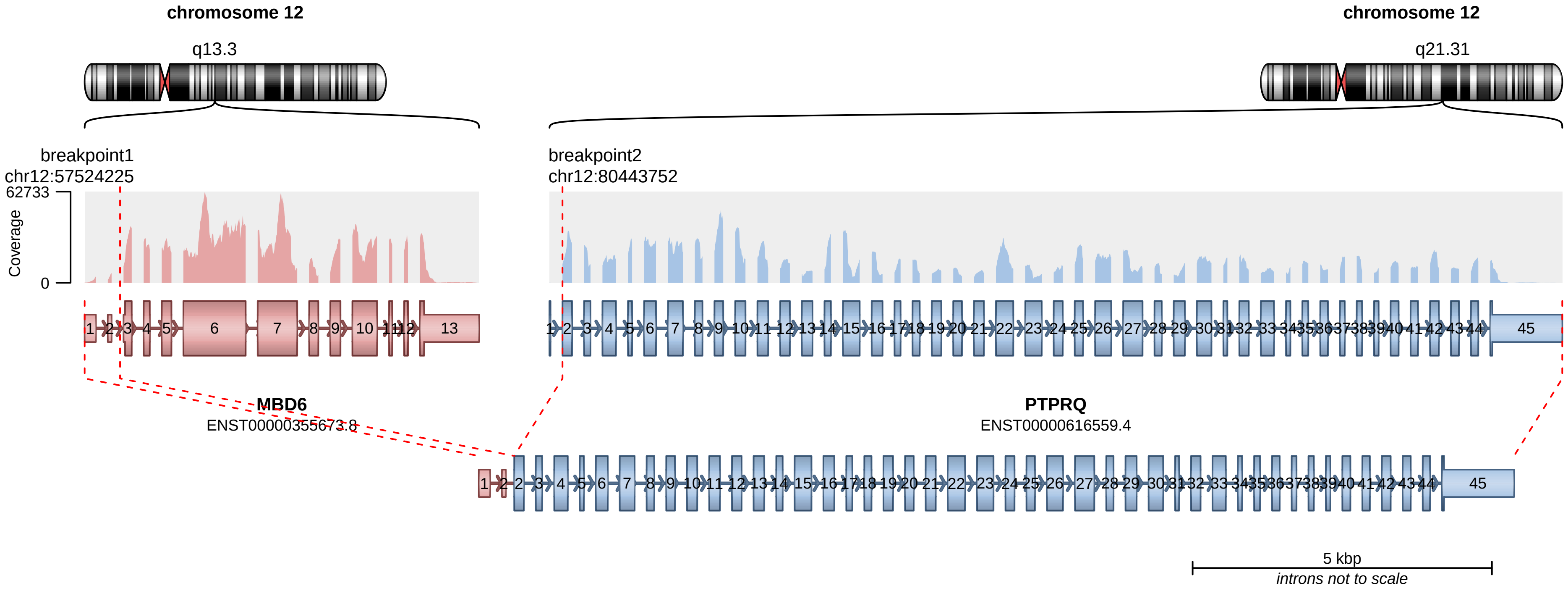


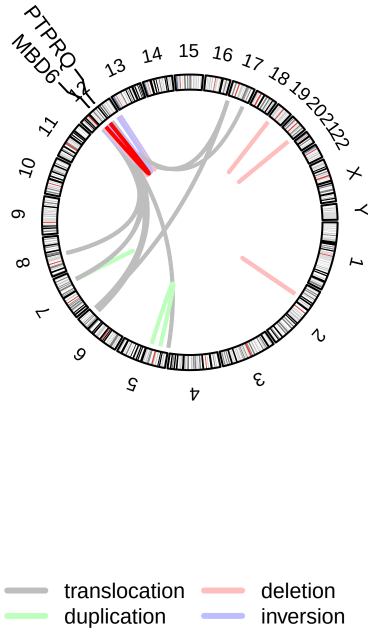


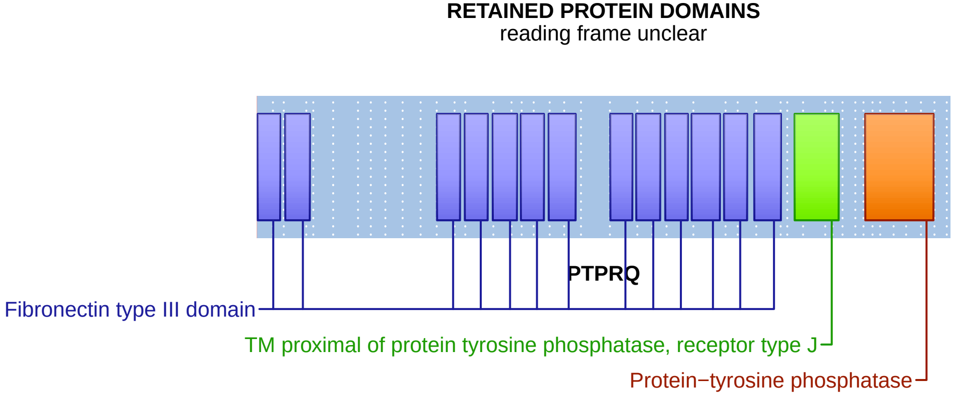


SUPPORTING READ COUNT

Split reads = 1193
Discordant mates = 6

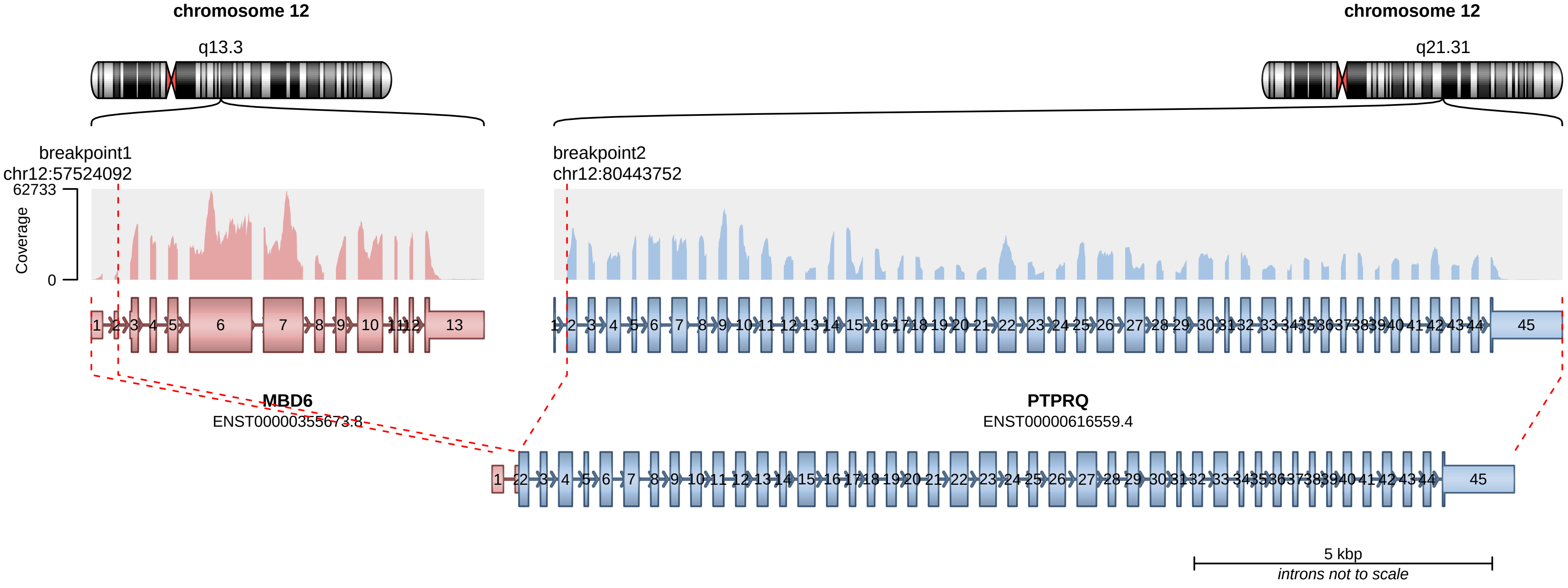


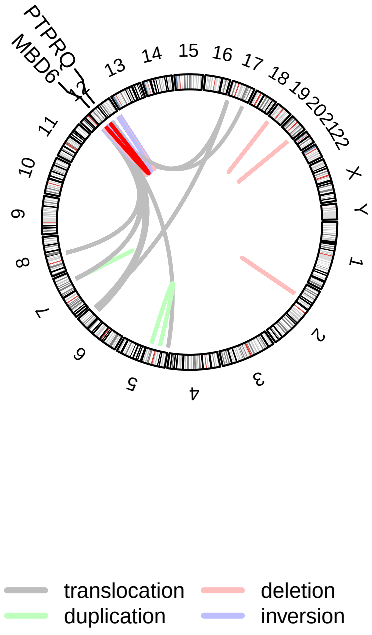


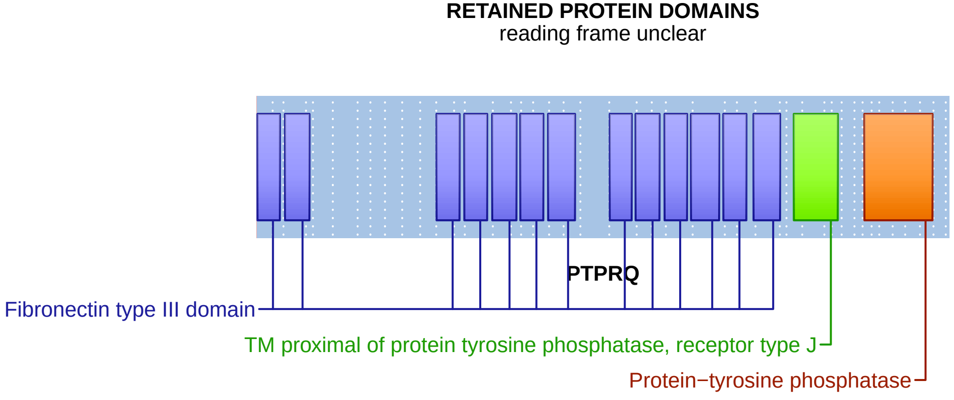


SUPPORTING READ COUNT

Split reads = 967
Discordant mates = 27

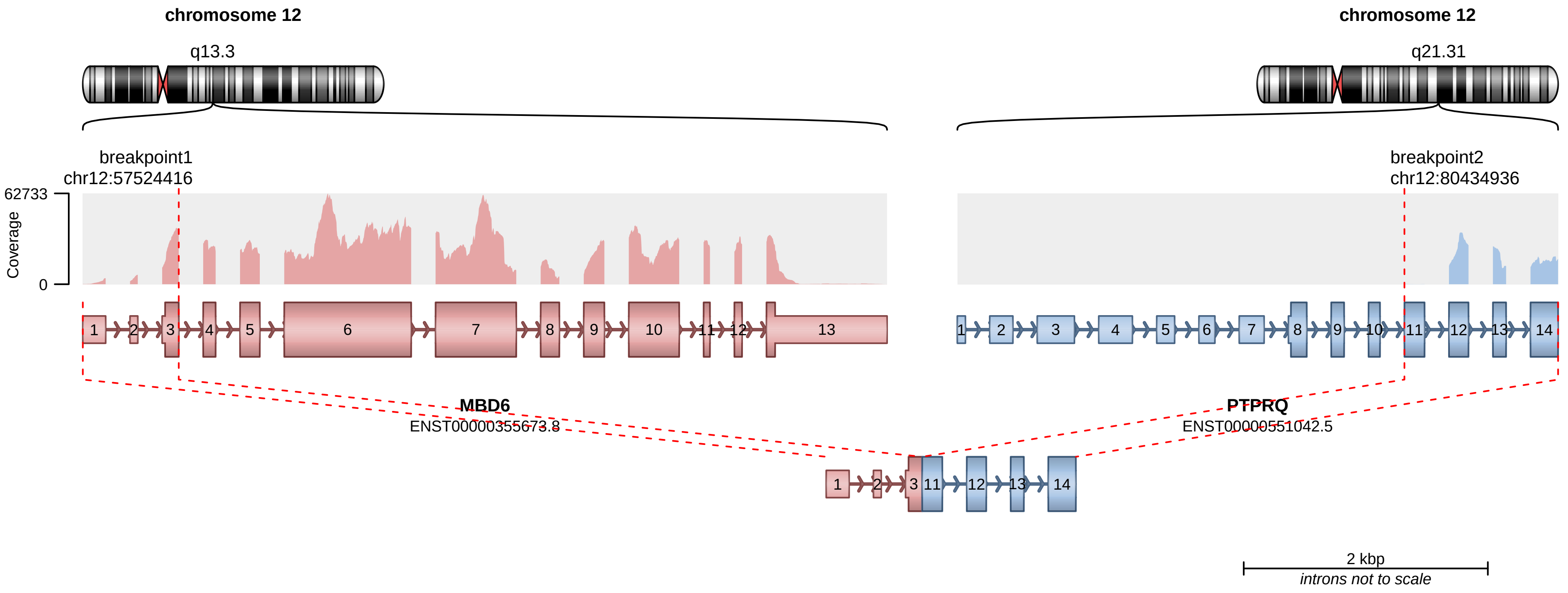


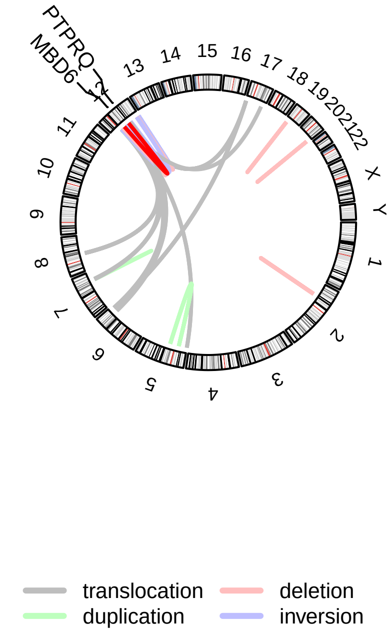




SUPPORTING READ COUNT

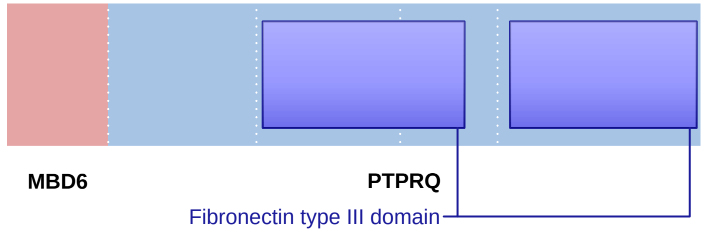
Split reads = 116
Discordant mates = 7





RETAINED PROTEIN DOMAINS

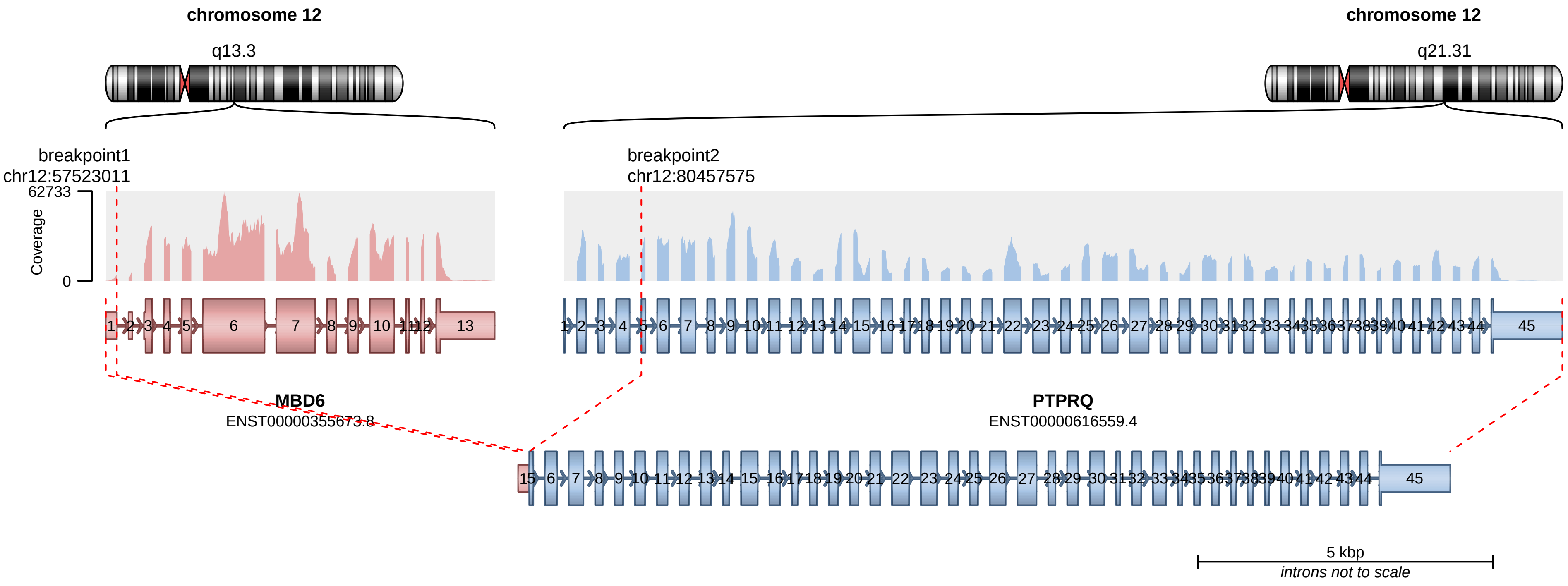
reading frame unclear

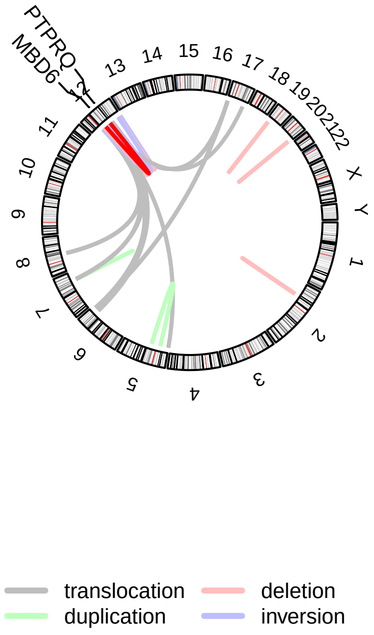


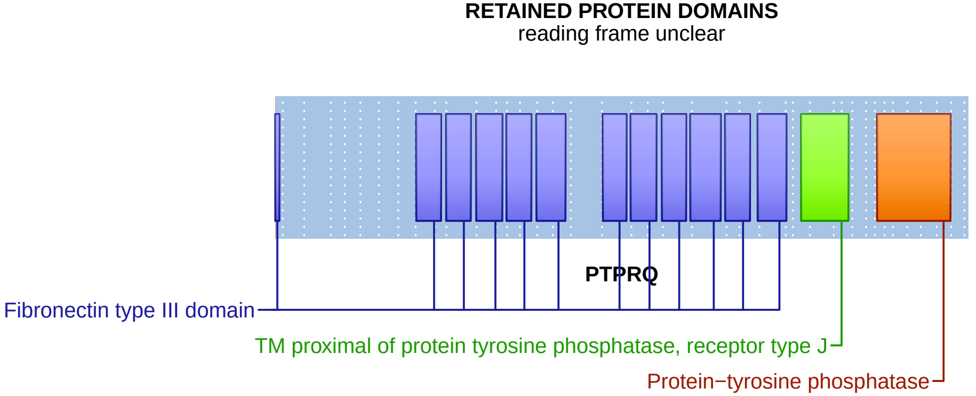
SUPPORTING READ COUNT

Split reads = 64

Discordant mates = 45

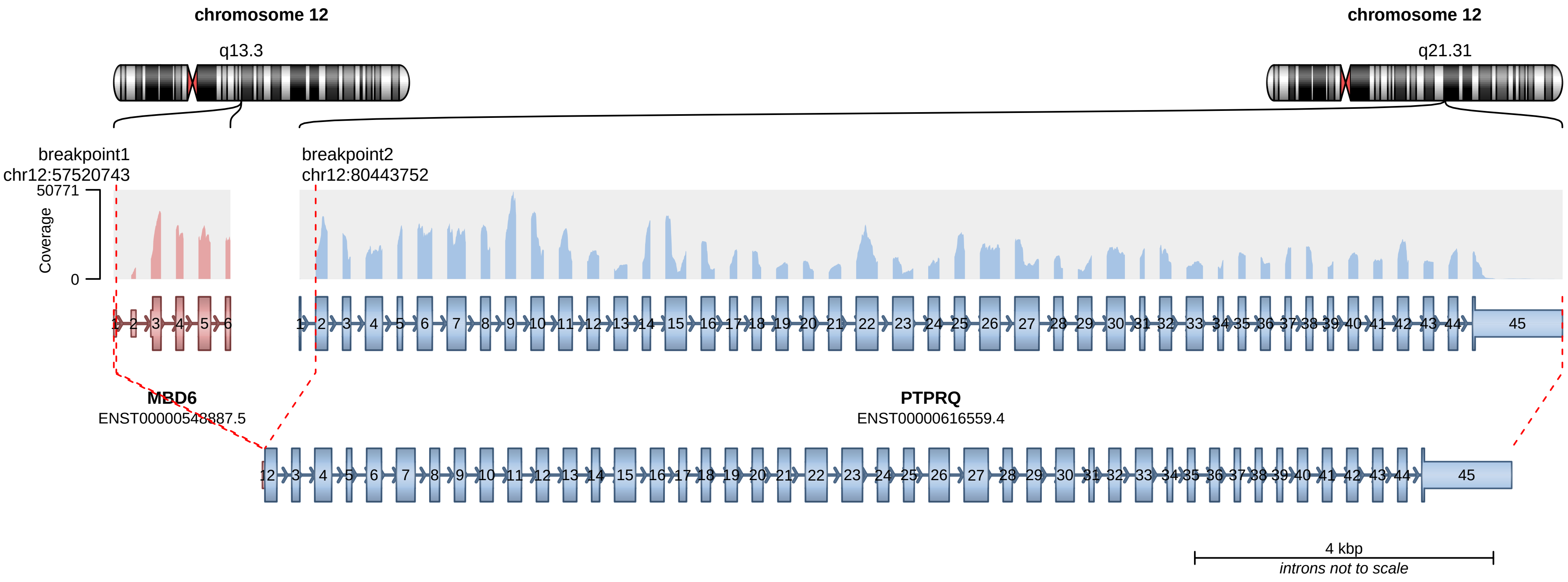


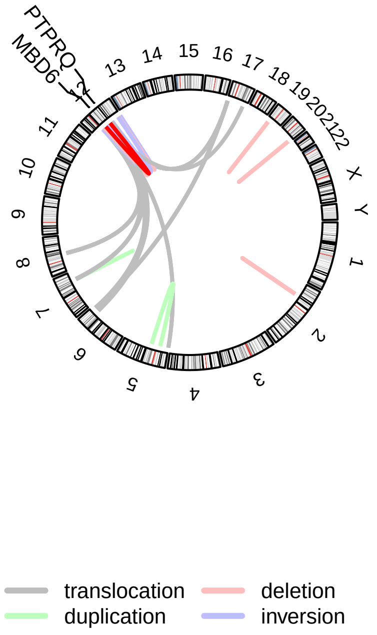


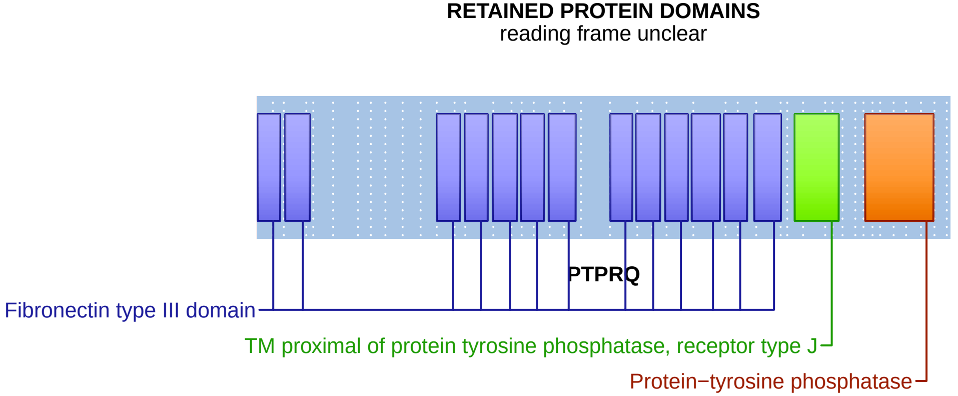


SUPPORTING READ COUNT

Split reads = 39
Discordant mates = 0

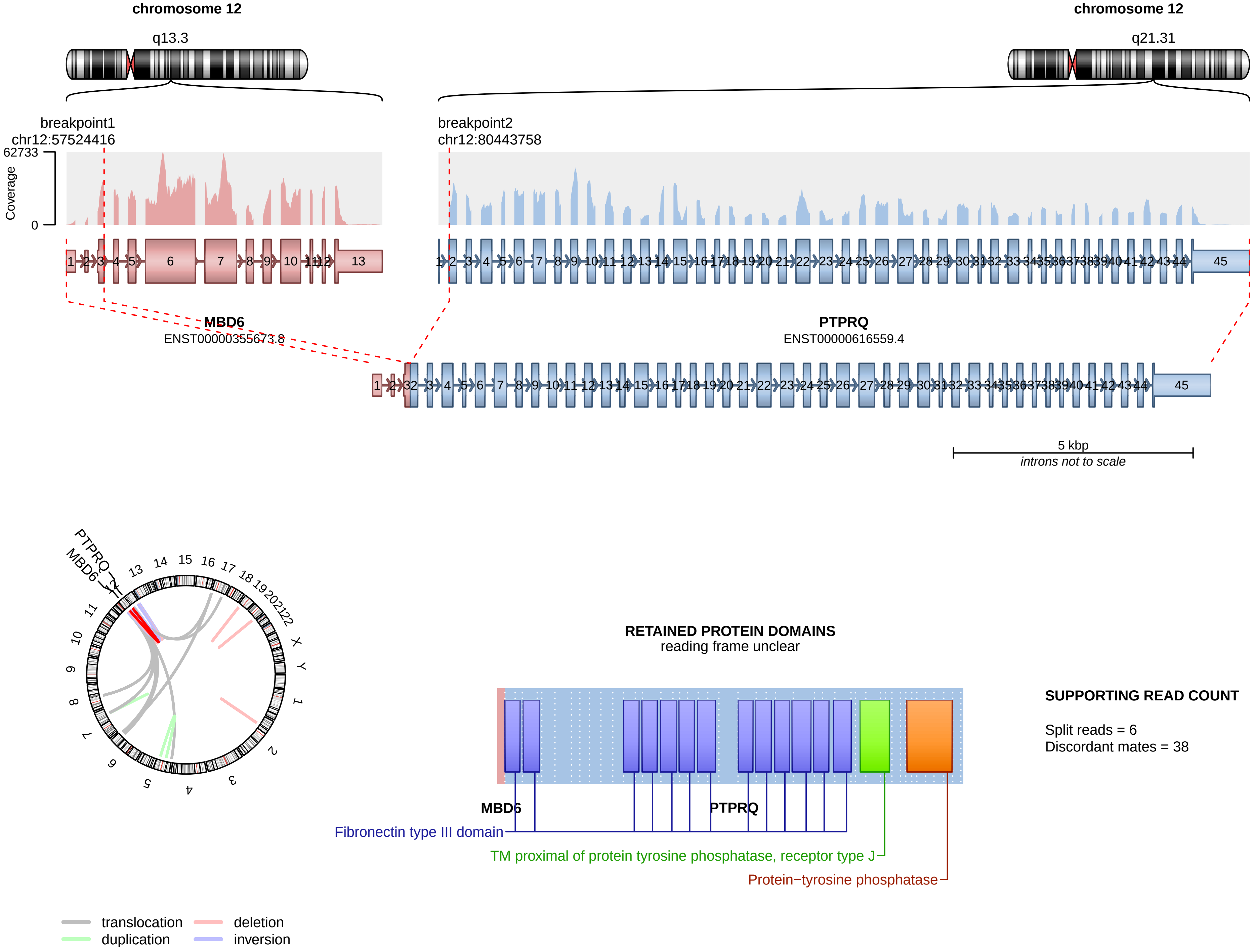






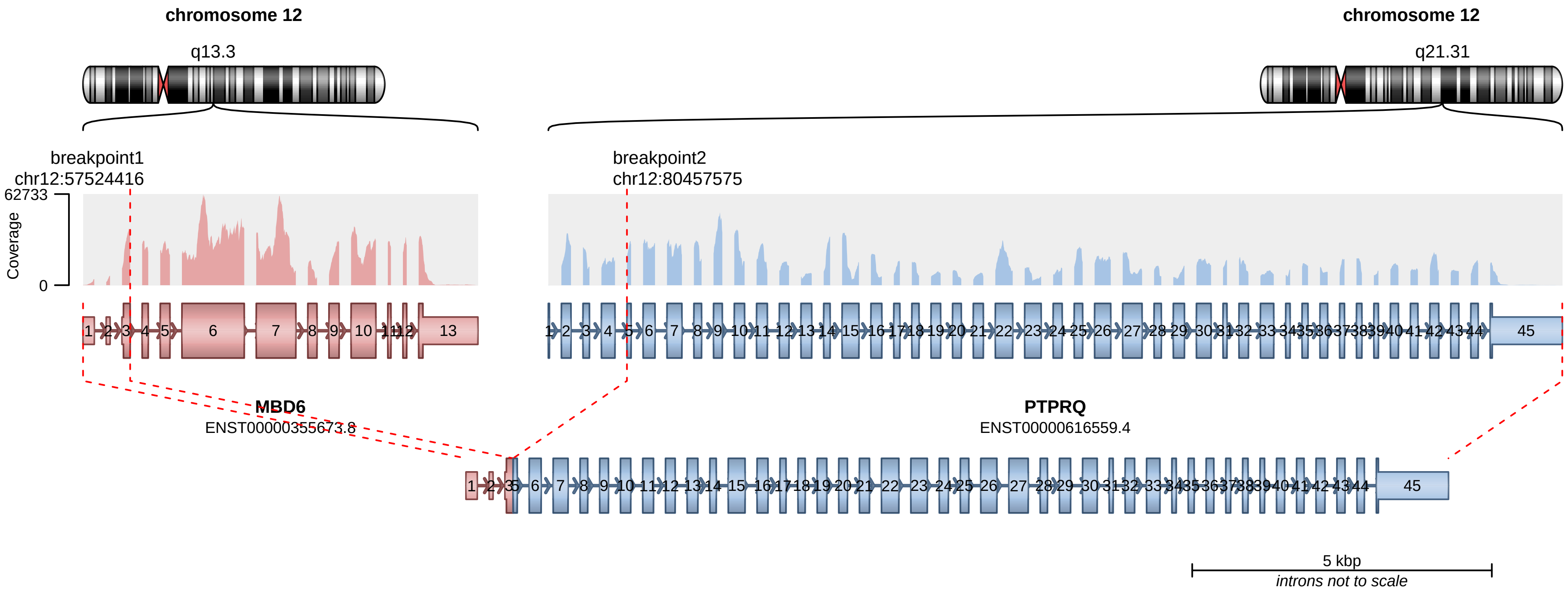
SUPPORTING READ COUNT

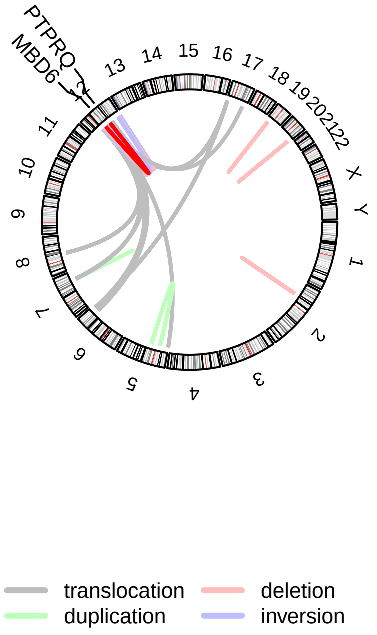
Split reads = 31
Discordant mates = 0

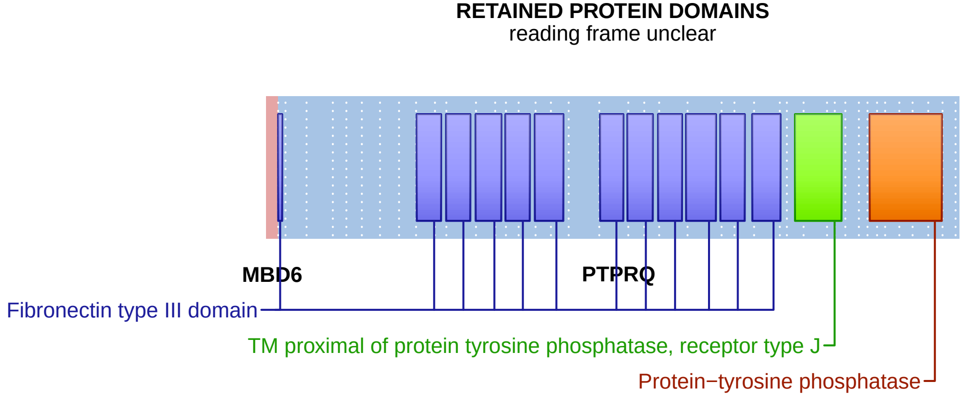


SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 38

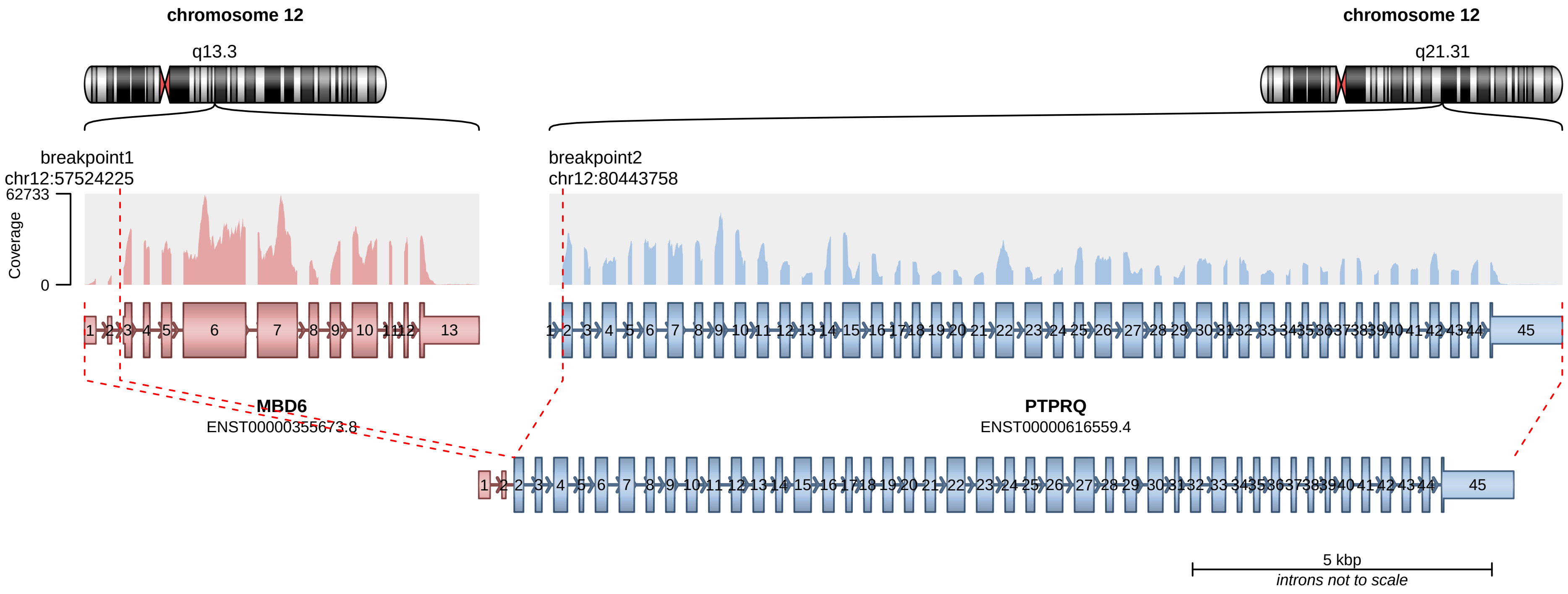


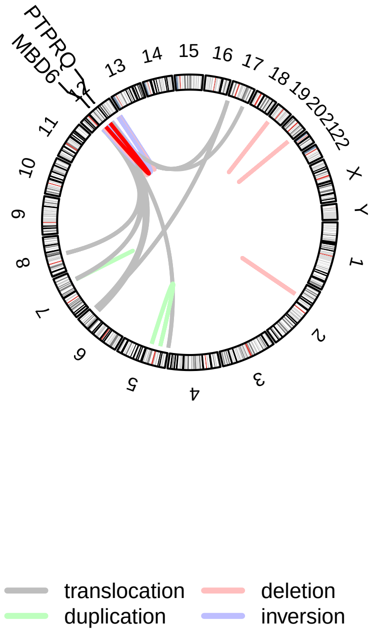


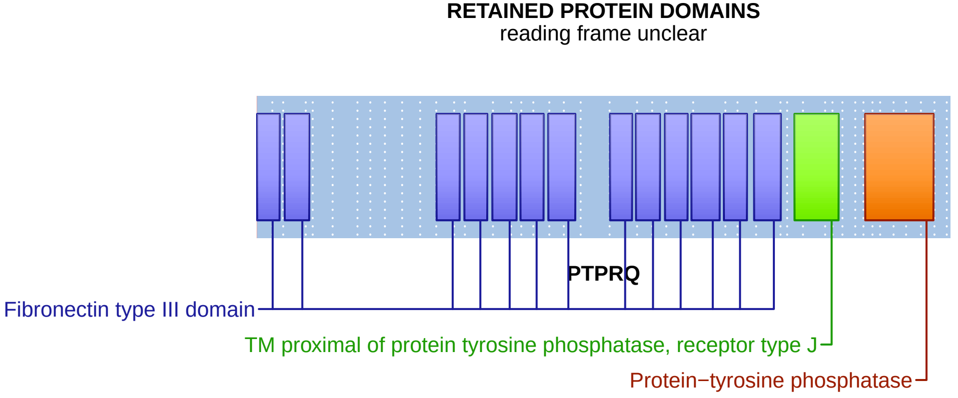


SUPPORTING READ COUNT

Split reads = 9
Discordant mates = 1

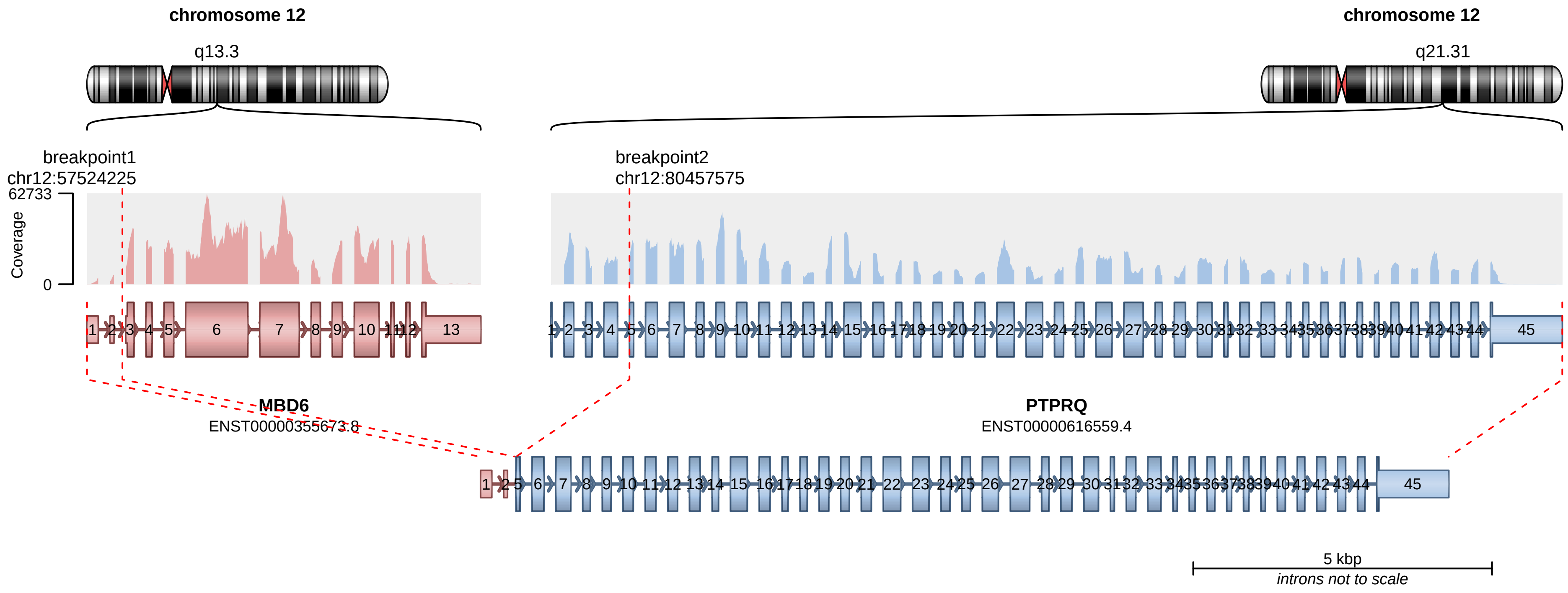


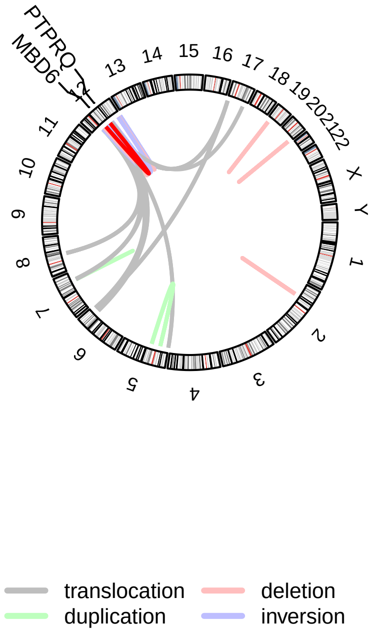




SUPPORTING READ COUNT

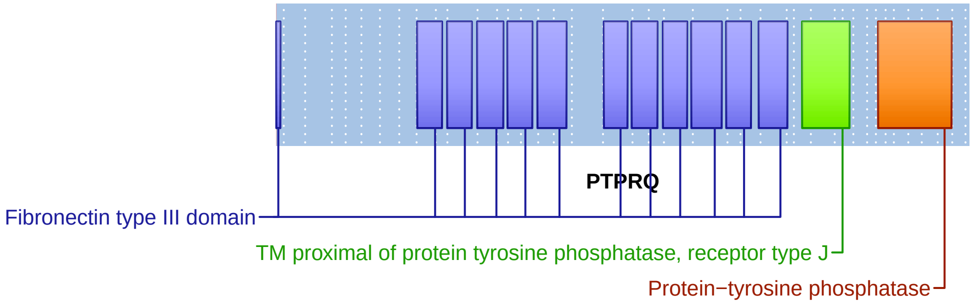
Split reads = 3
Discordant mates = 23





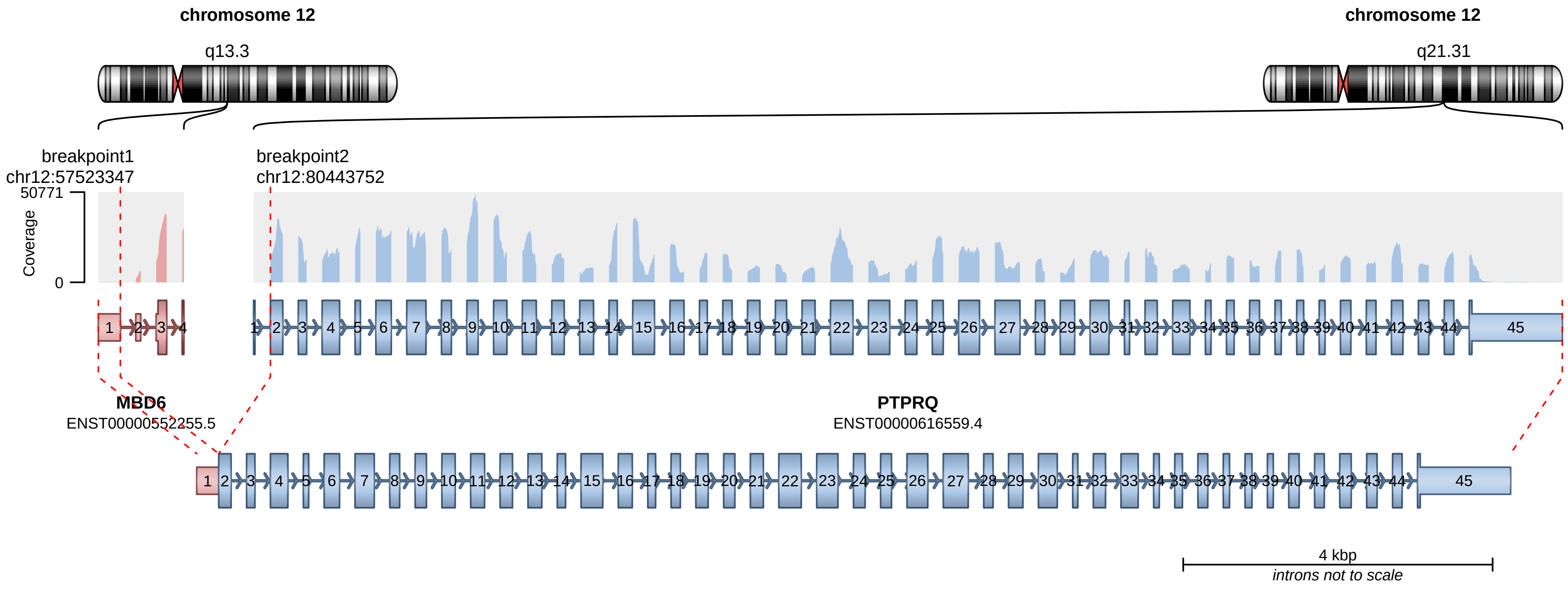
RETAINED PROTEIN DOMAINS

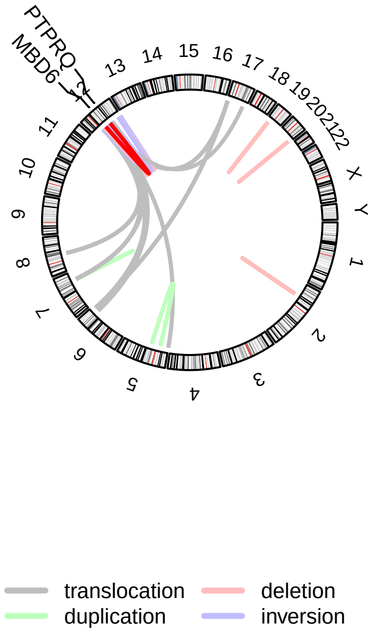
reading frame unclear

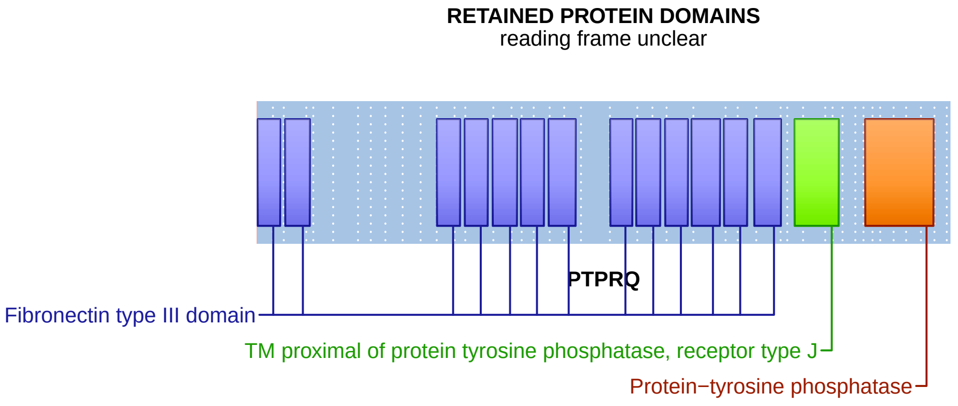


SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 0

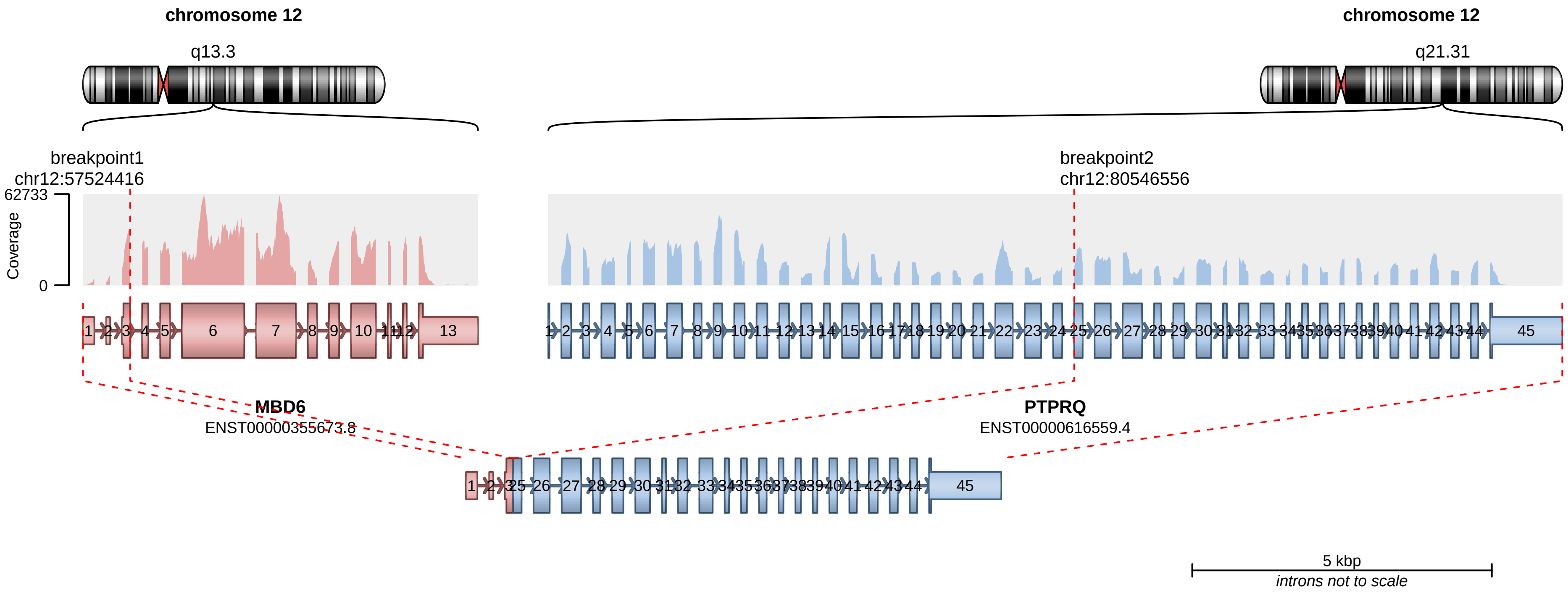


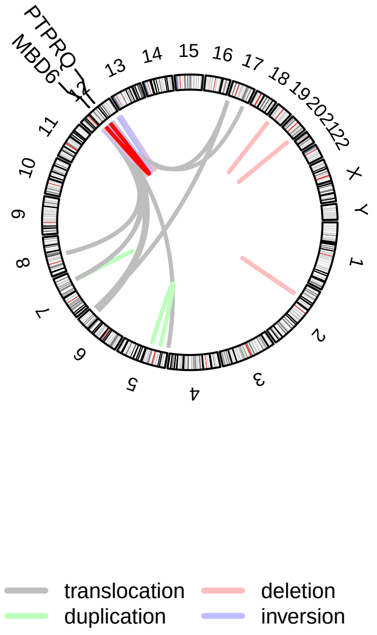


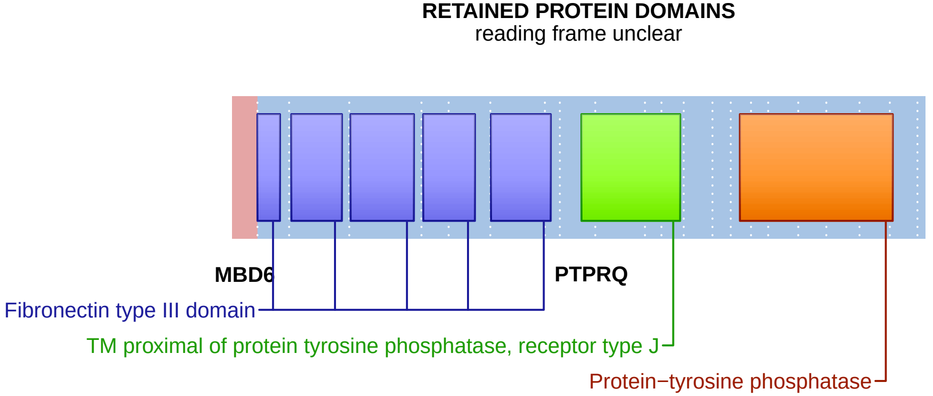


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 6

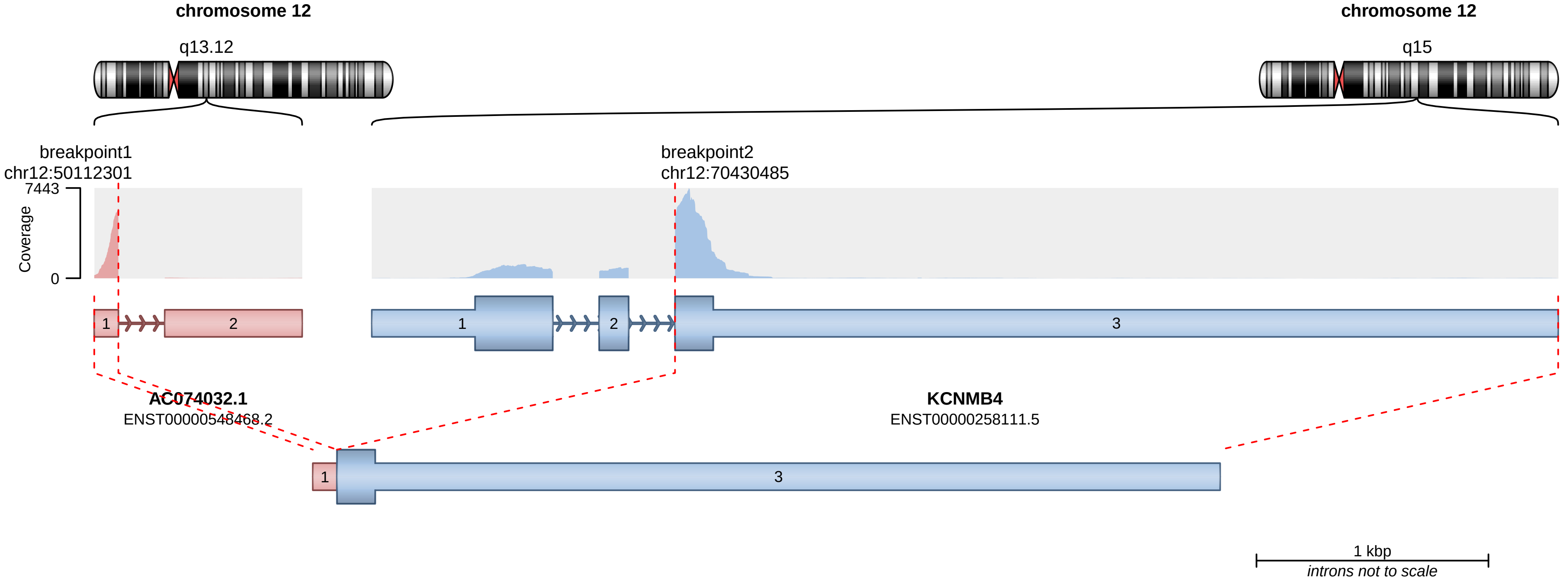


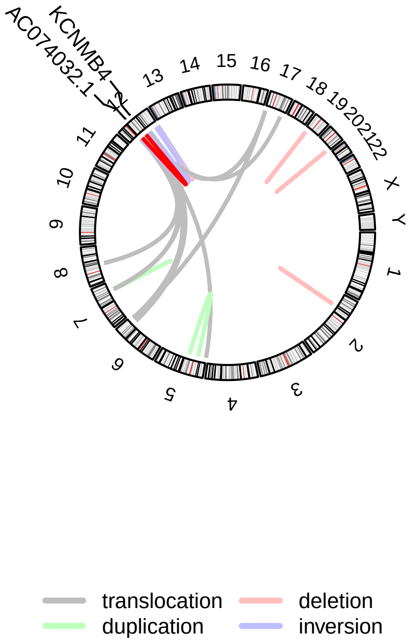


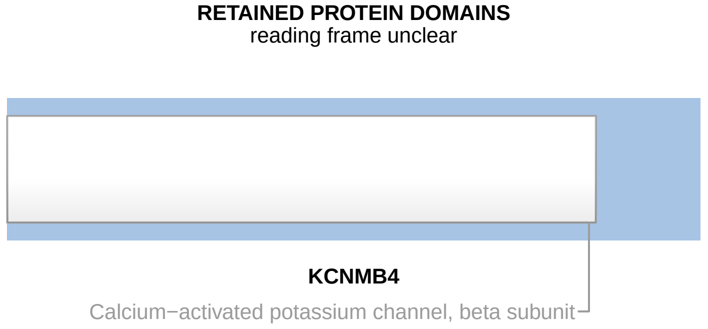


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

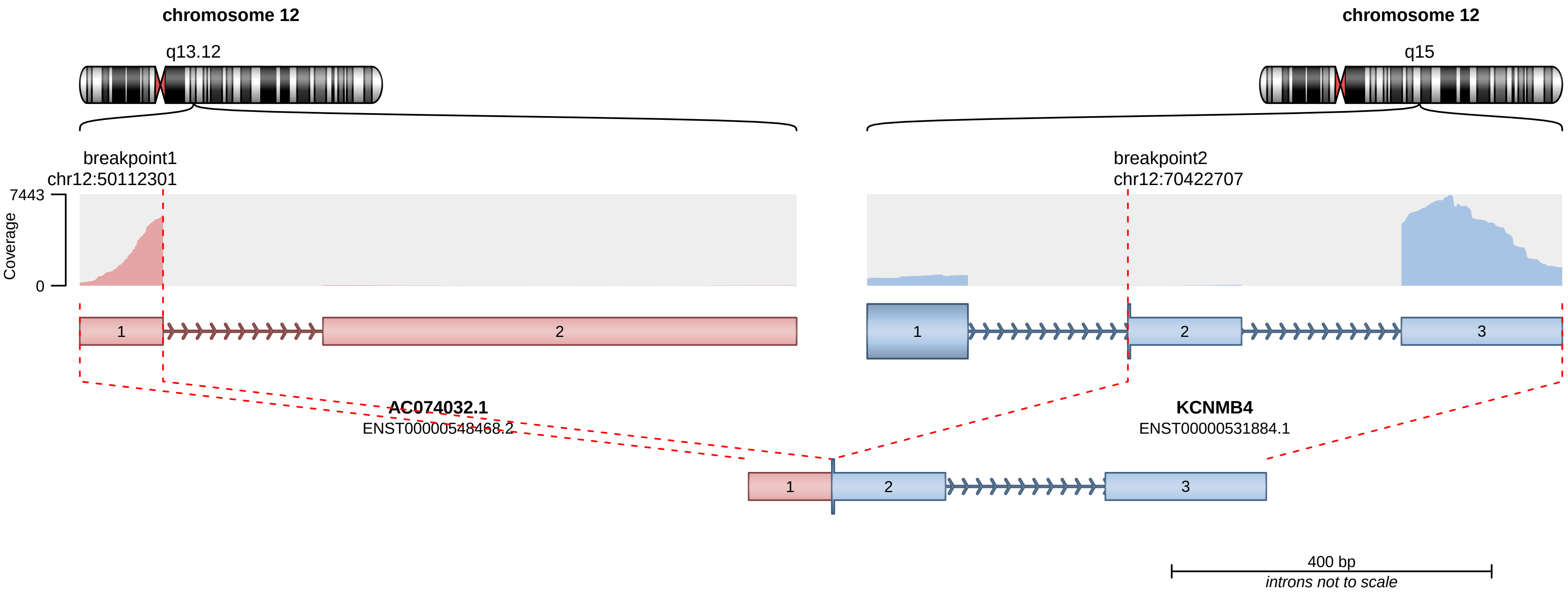


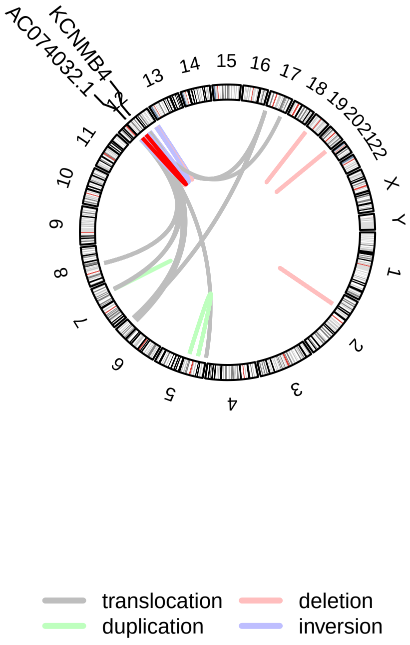




SUPPORTING READ COUNT

Split reads = 1445
Discordant mates = 2

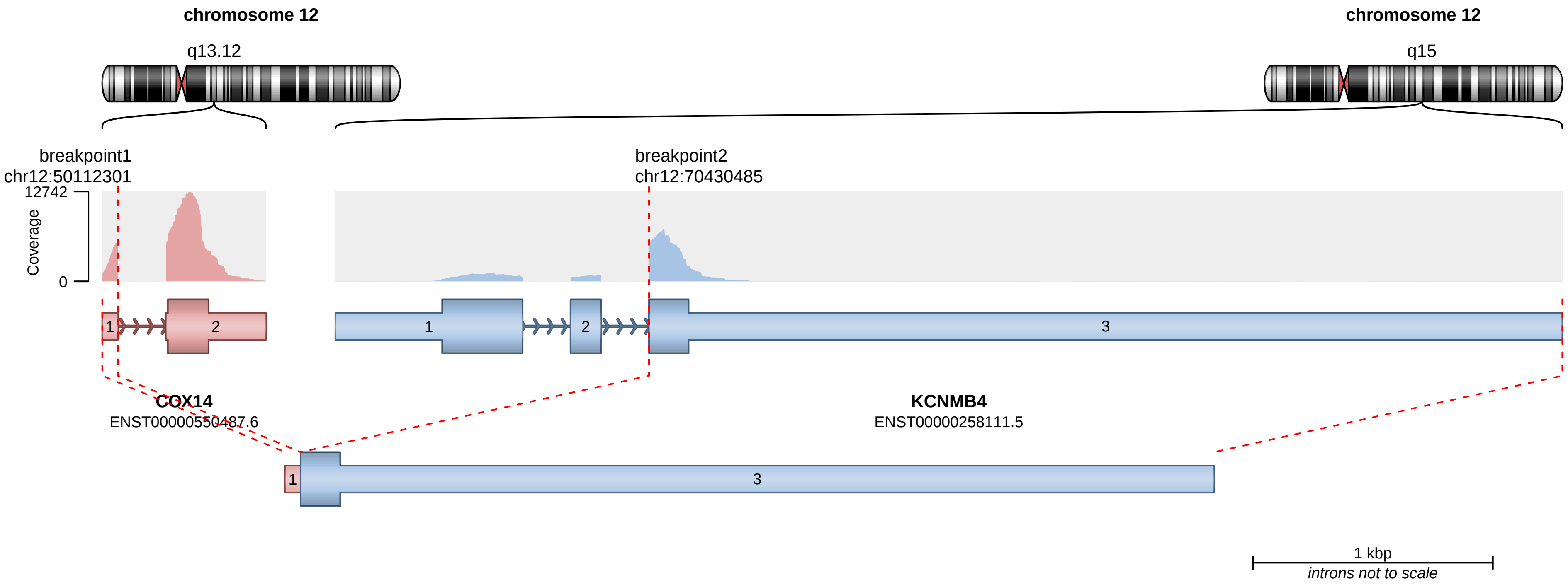


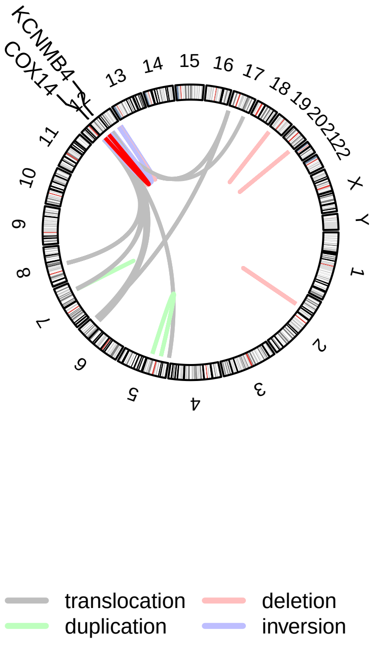


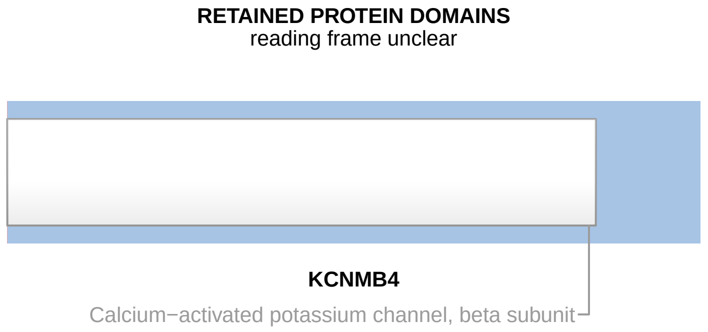
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 2

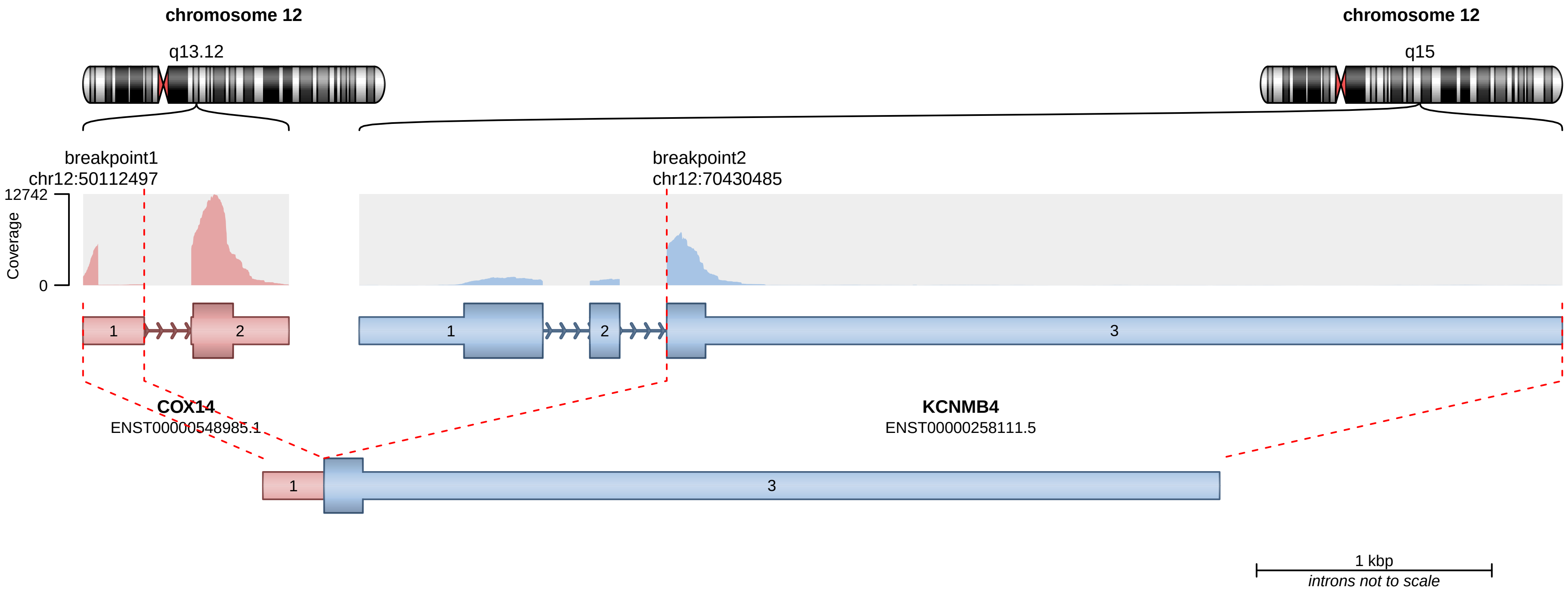


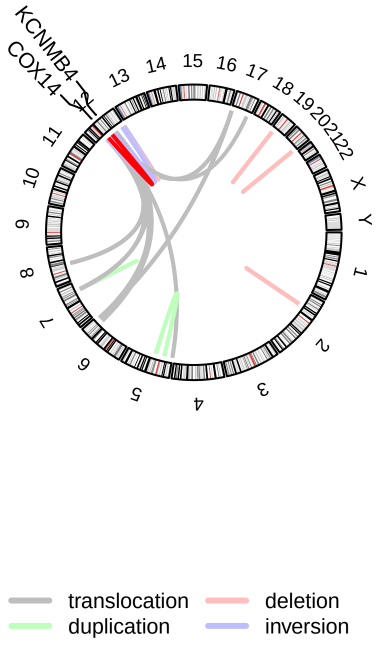




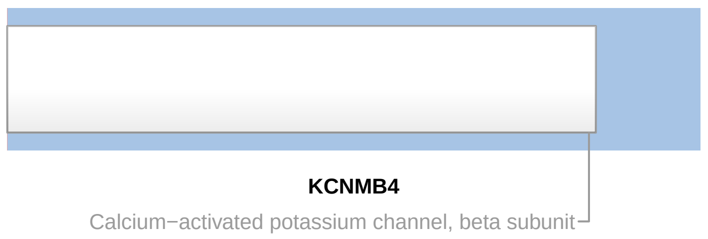
SUPPORTING READ COUNT

Split reads = 1440
Discordant mates = 2



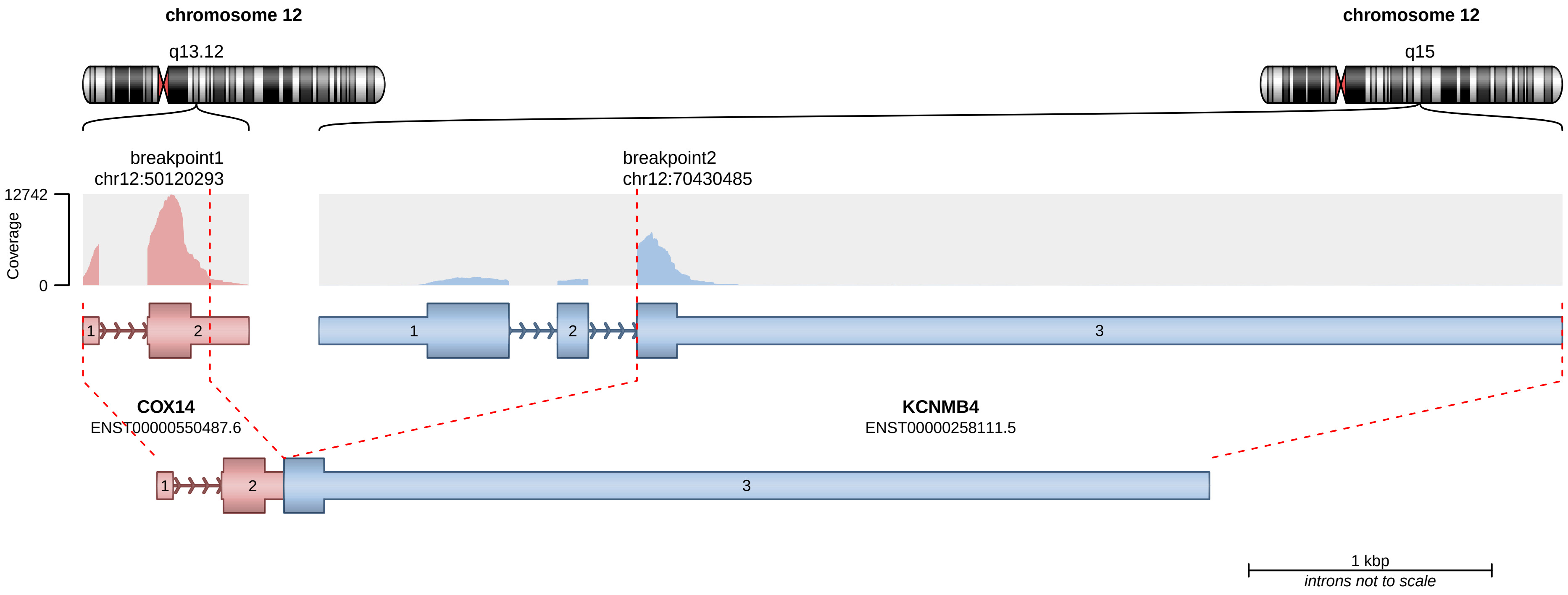


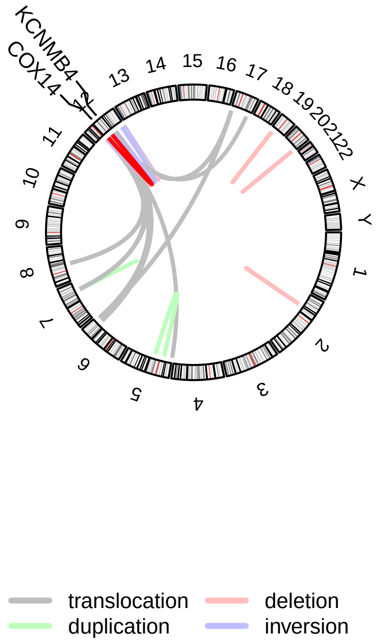
RETAINED PROTEIN DOMAINS
reading frame unclear

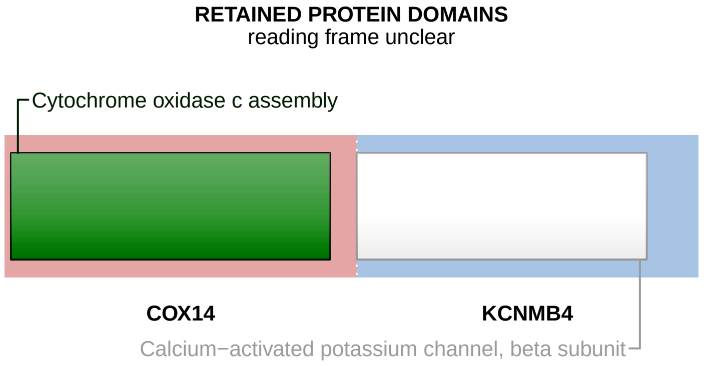


SUPPORTING READ COUNT

Split reads = 14
Discordant mates = 2

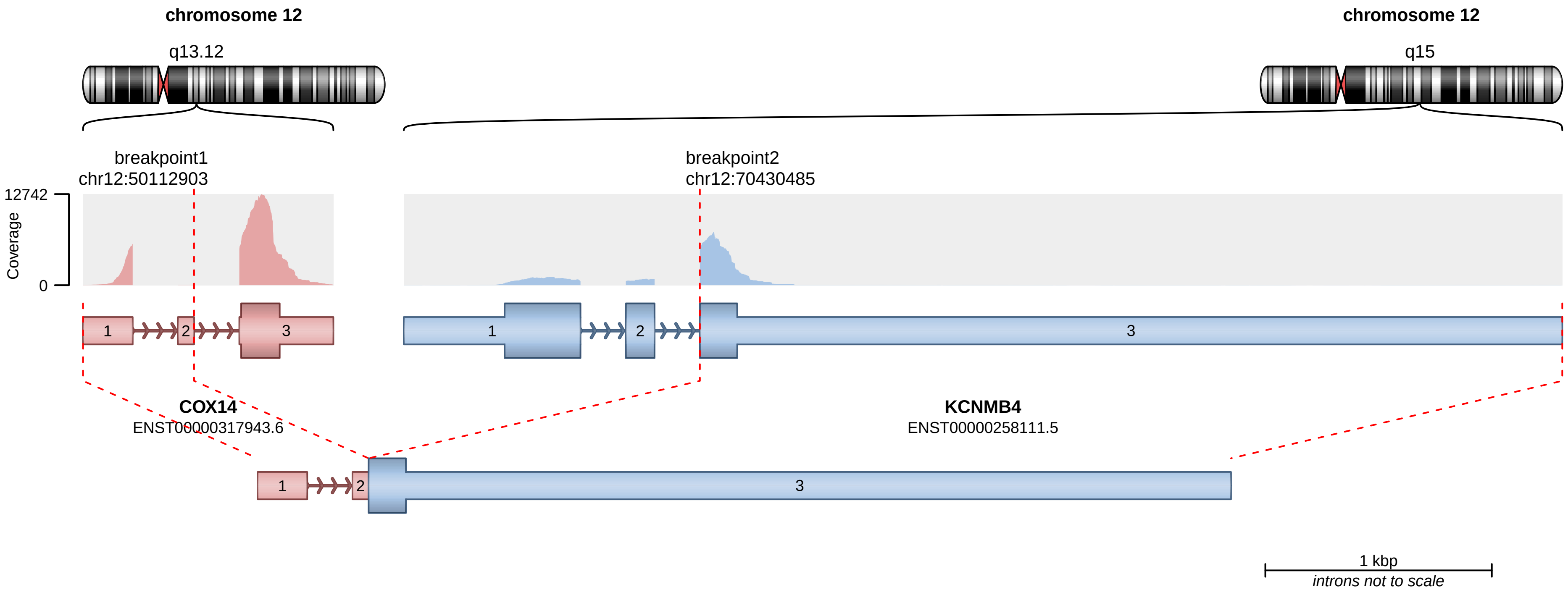


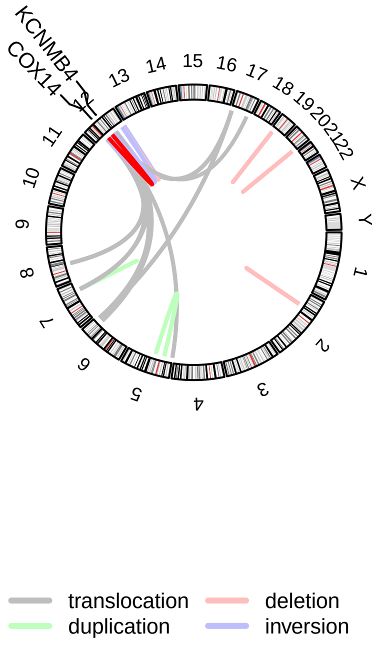




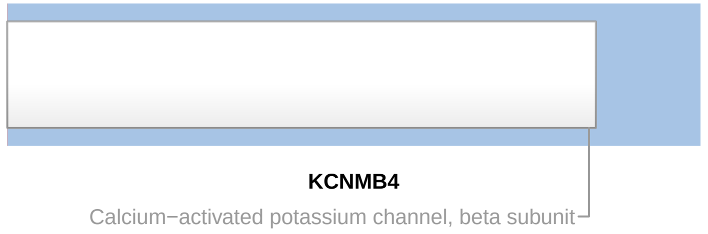
SUPPORTING READ COUNT

Split reads = 13
Discordant mates = 2



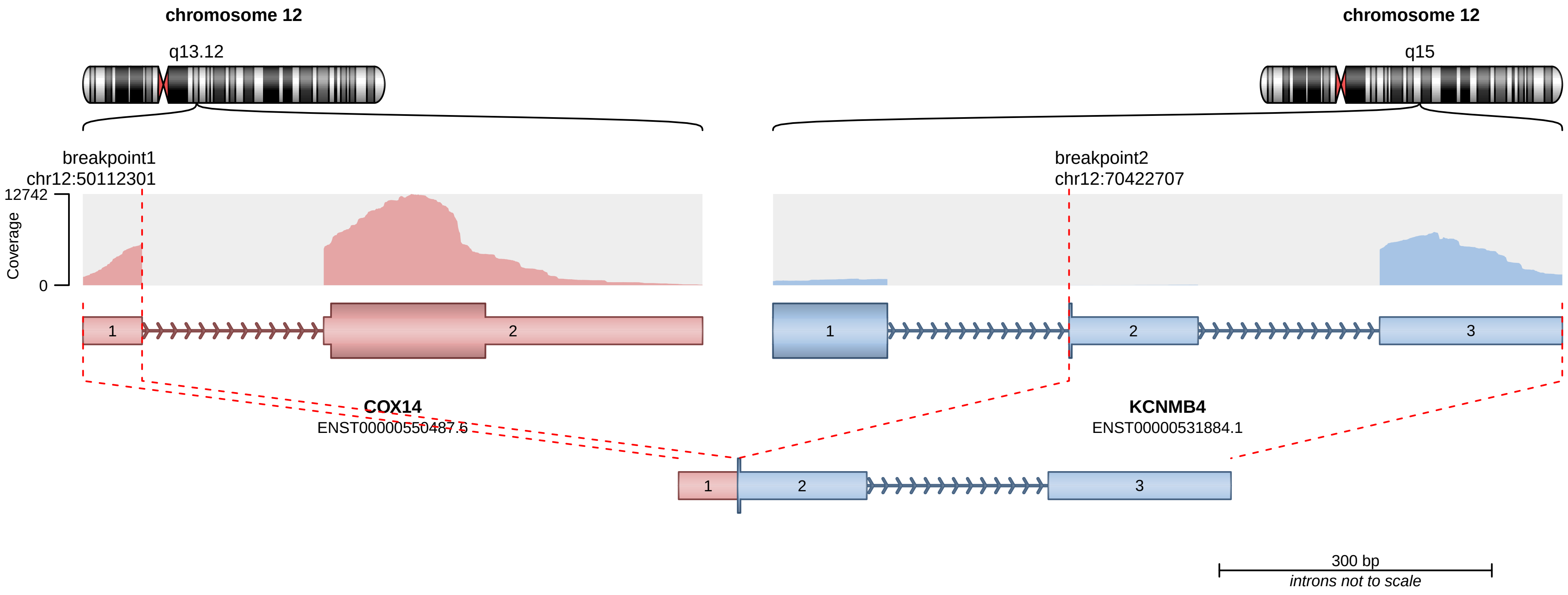


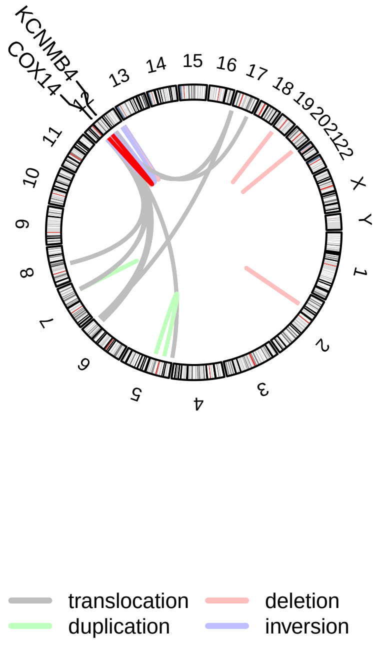
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 2

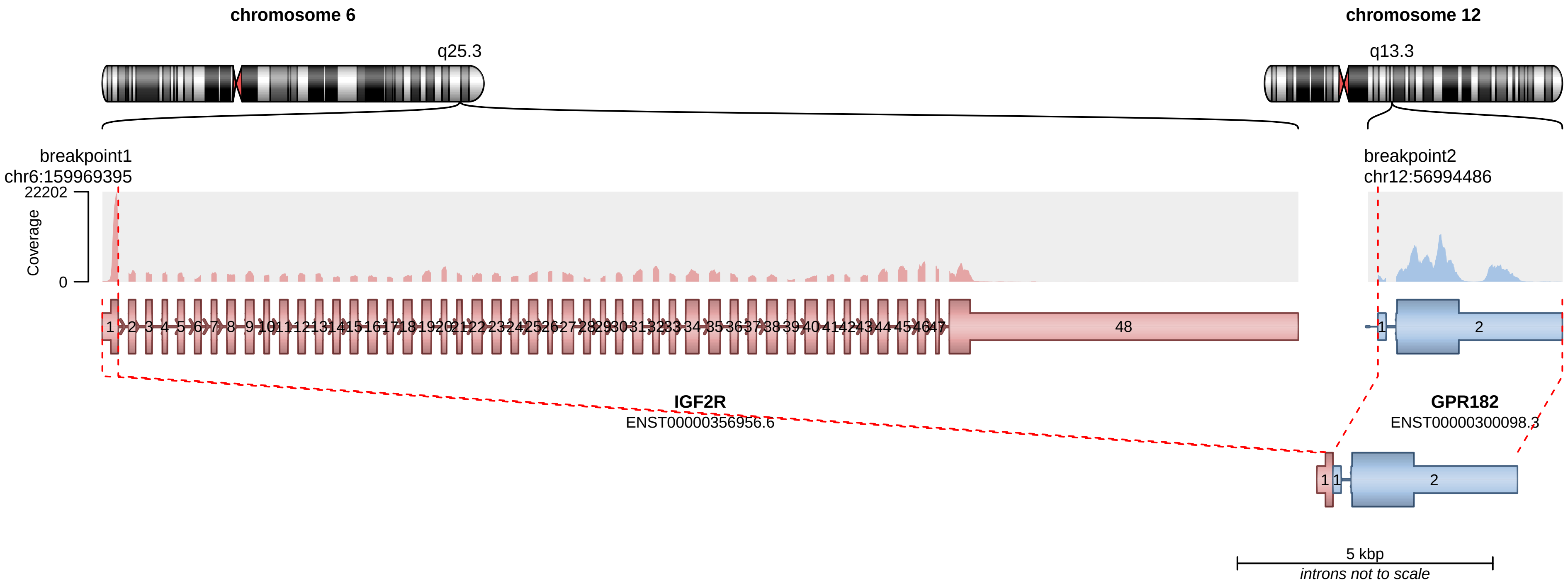


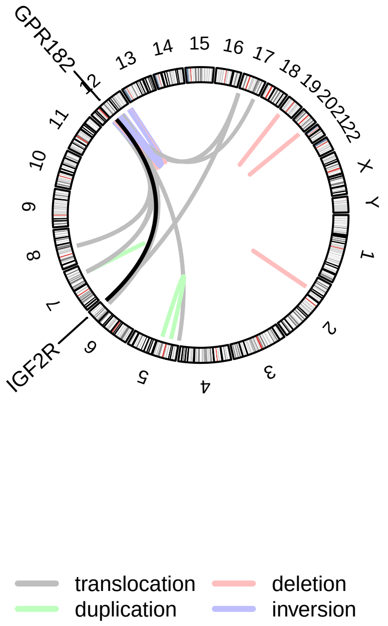


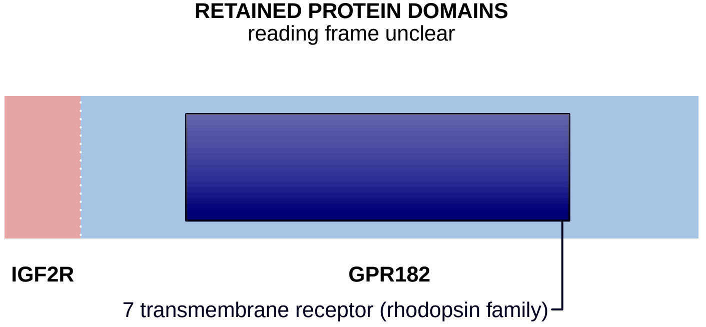
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 2

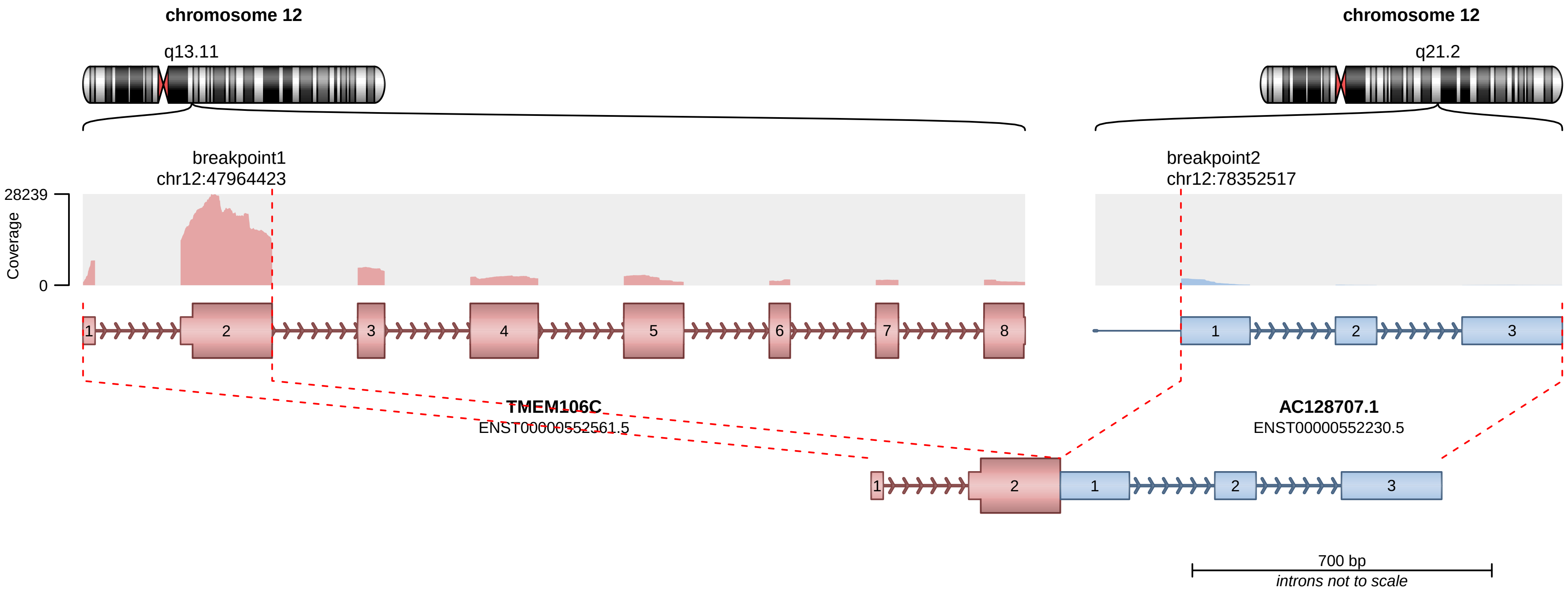


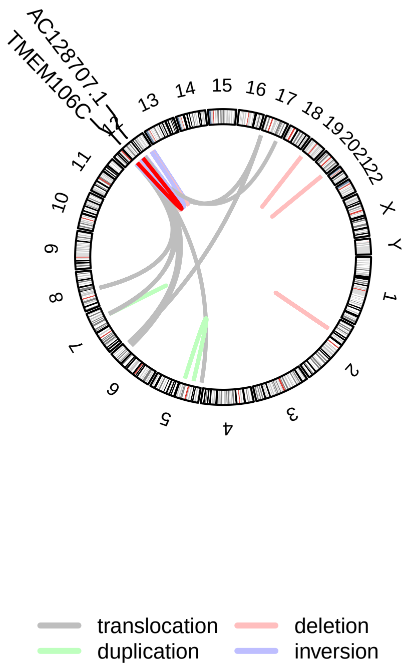




SUPPORTING READ COUNT

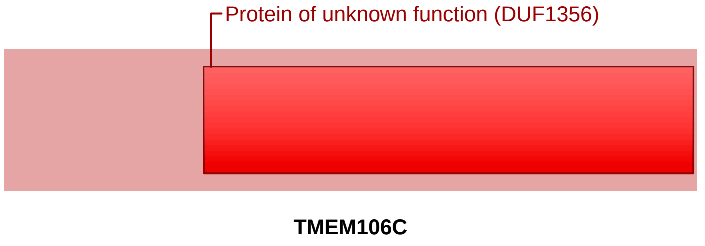
Split reads = 970
Discordant mates = 1





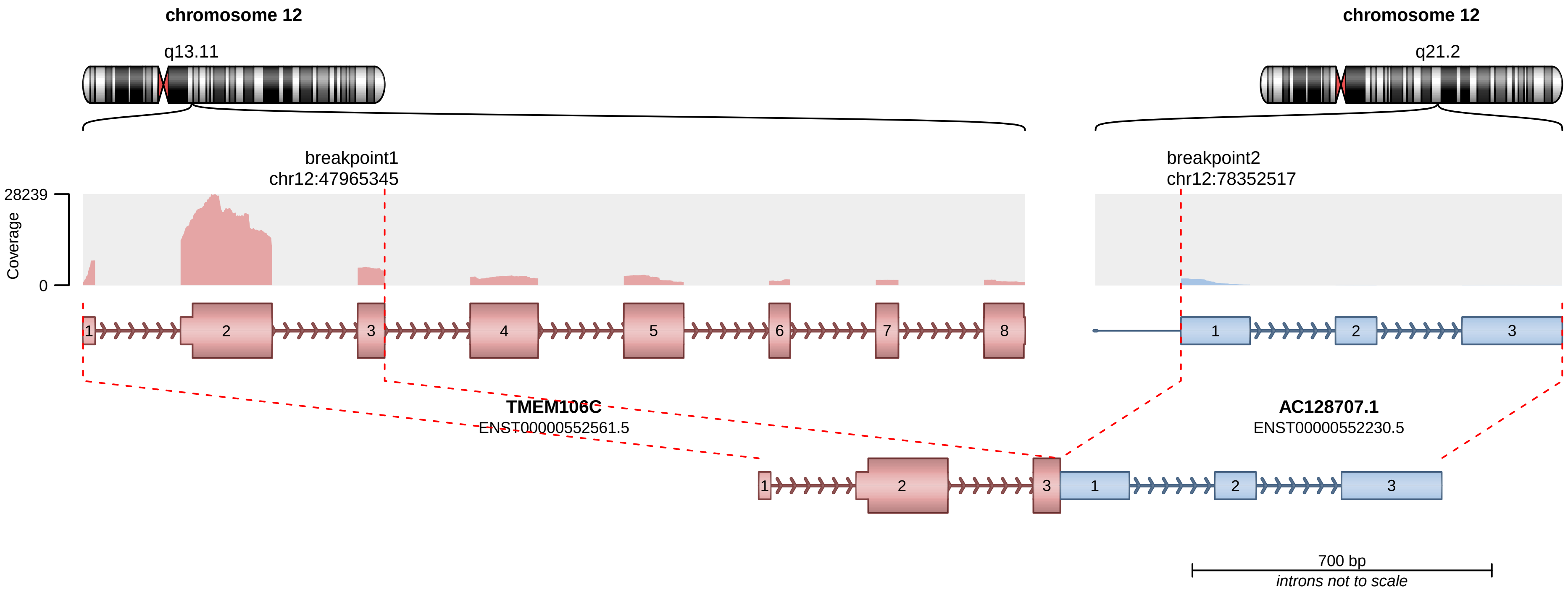
RETAINED PROTEIN DOMAINS

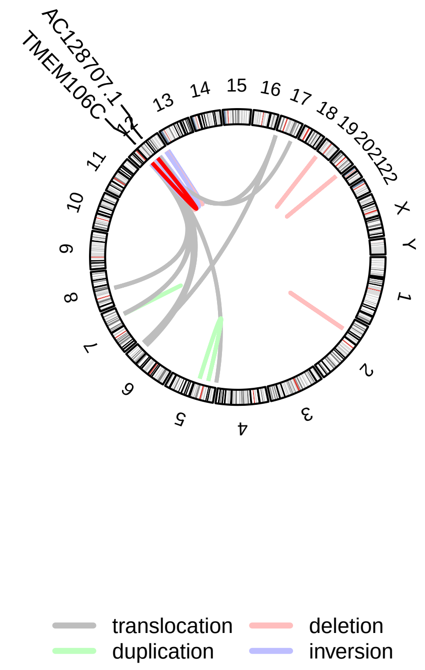
reading frame unclear



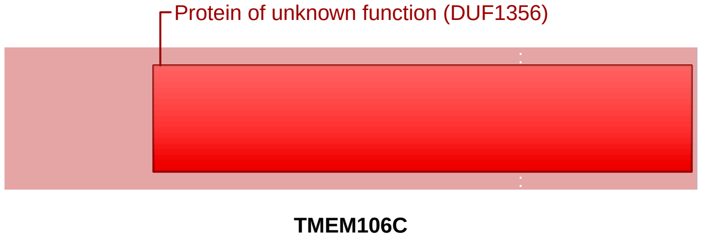
SUPPORTING READ COUNT

Split reads = 826
Discordant mates = 4



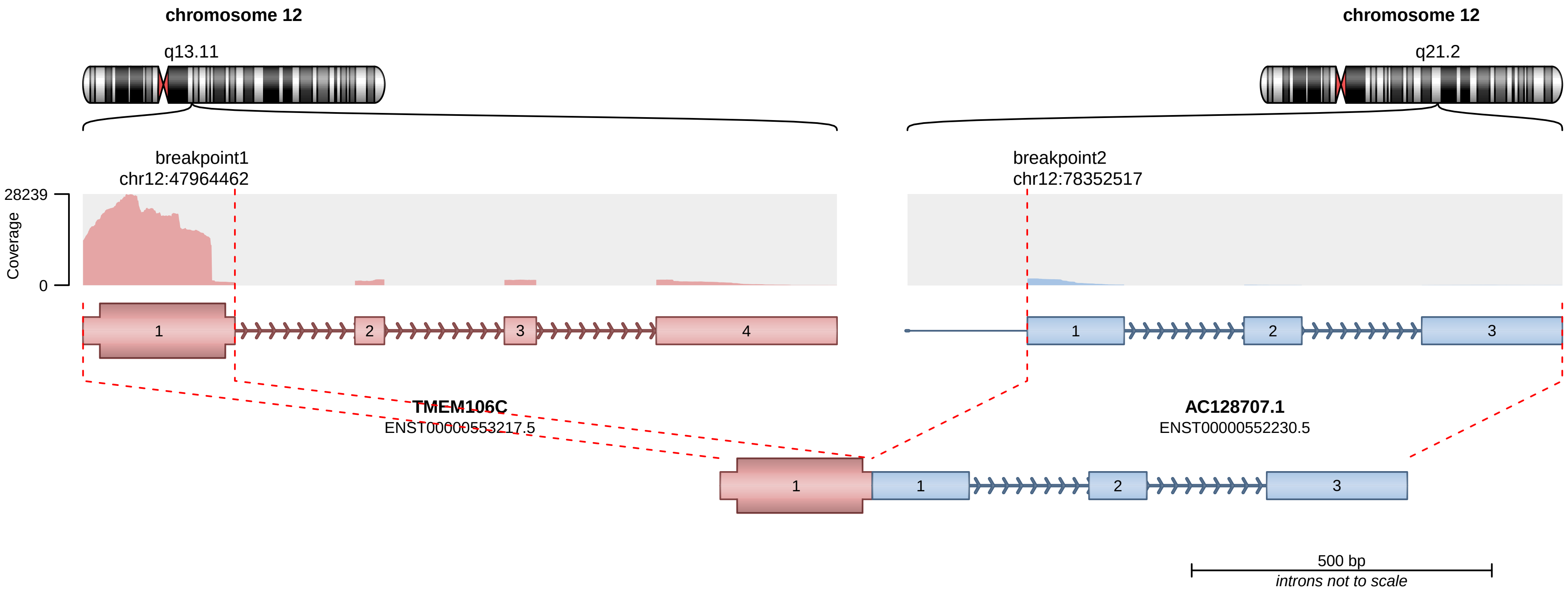


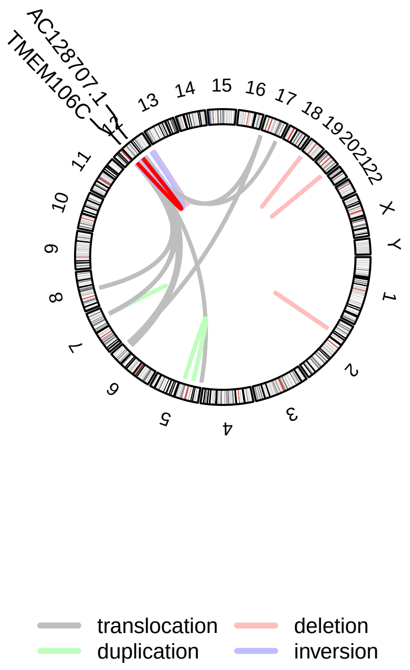
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

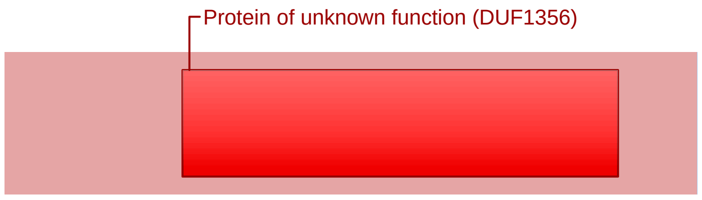
Split reads = 436
Discordant mates = 7





RETAINED PROTEIN DOMAINS

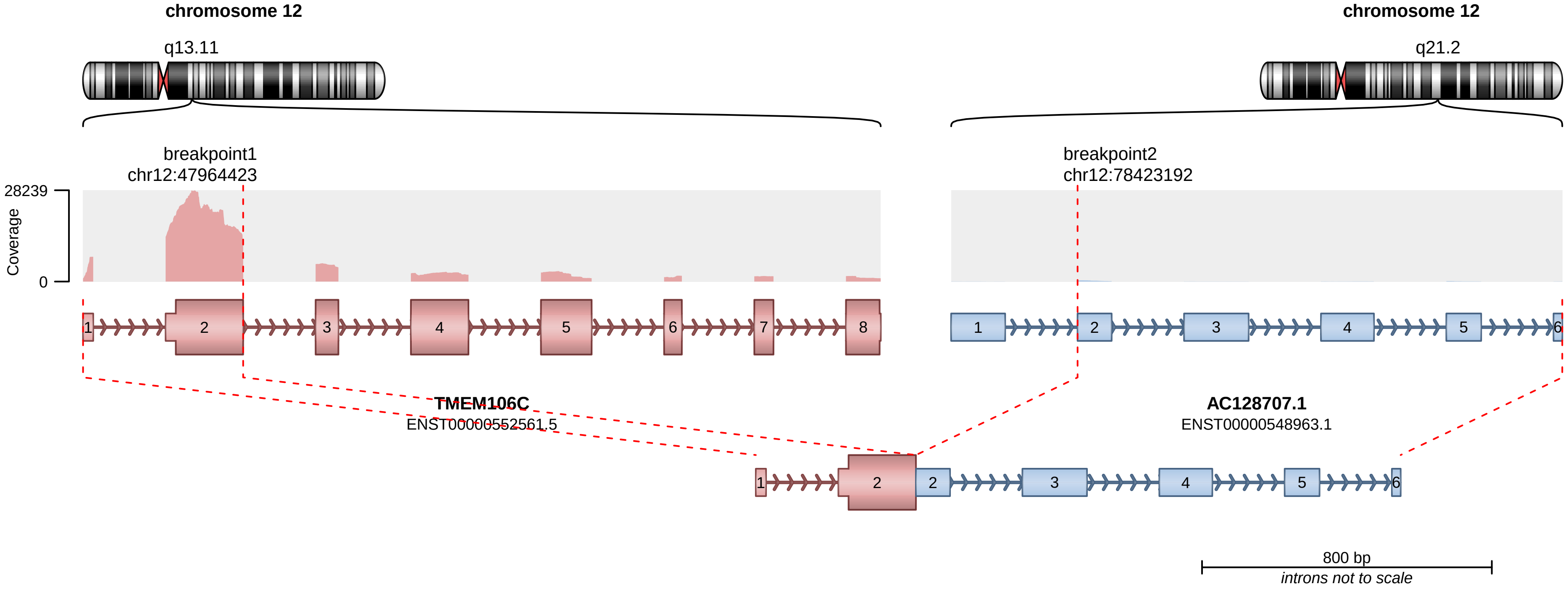
reading frame unclear

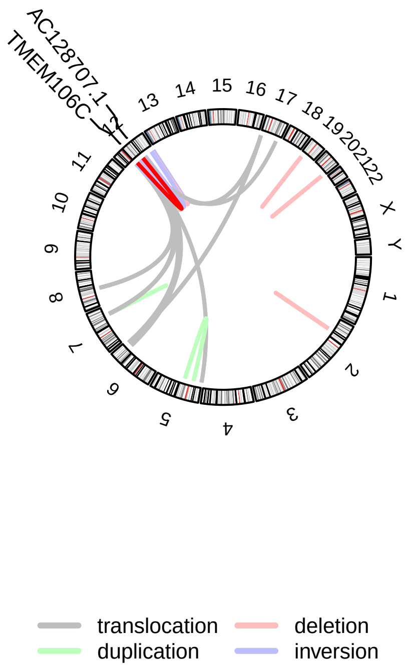


TMEM106C

SUPPORTING READ COUNT

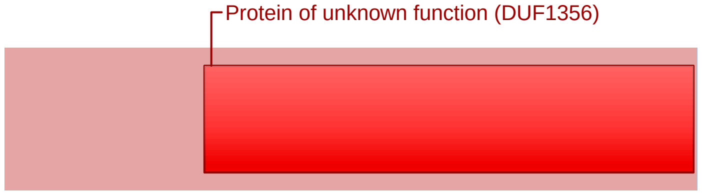
Split reads = 35
Discordant mates = 4





RETAINED PROTEIN DOMAINS

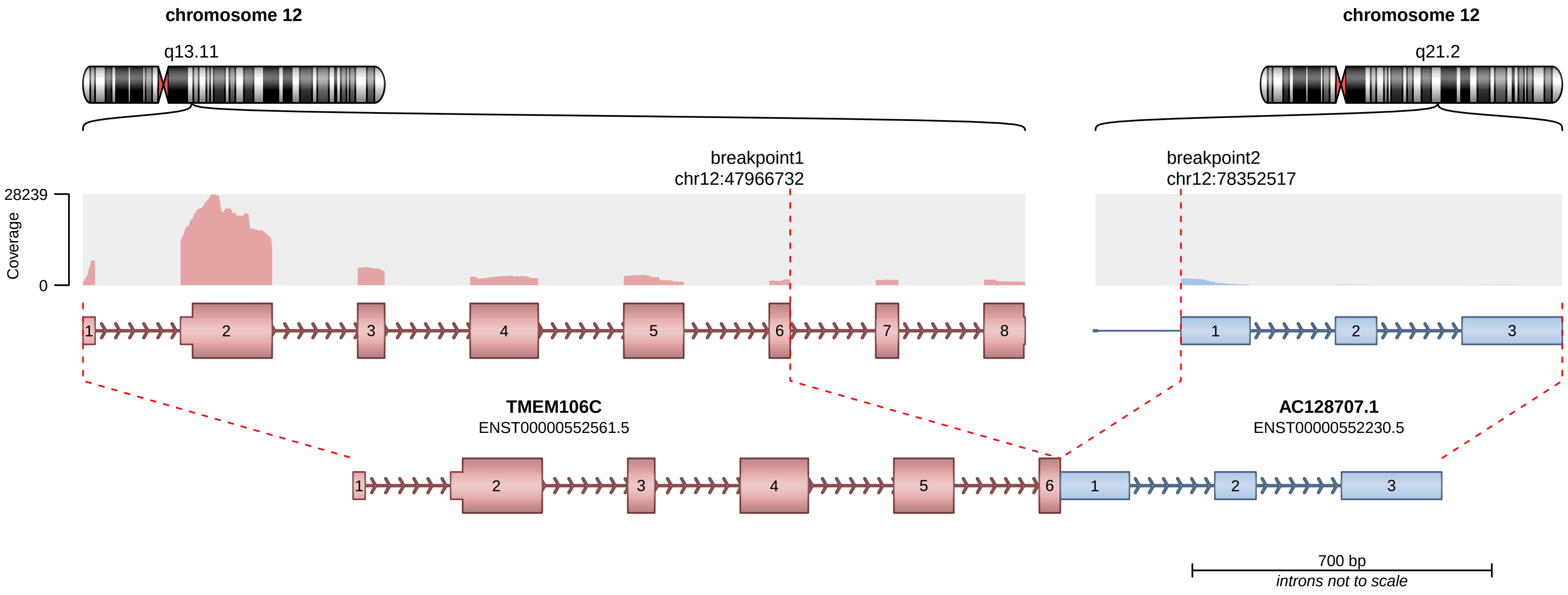
reading frame unclear

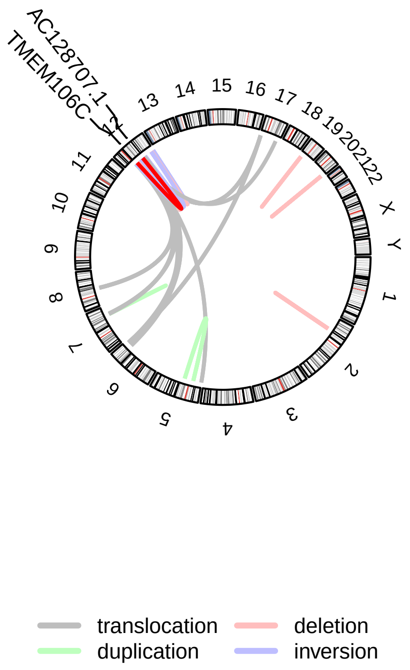


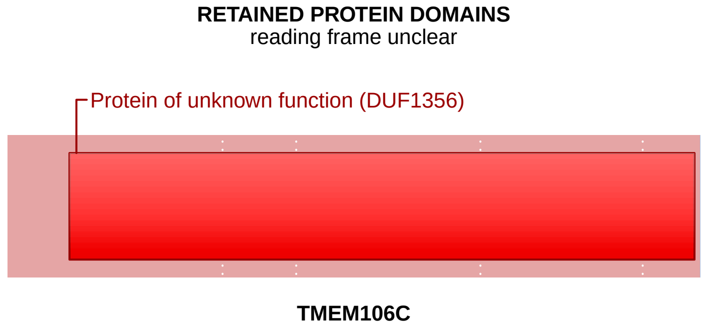
TMEM106C

SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0

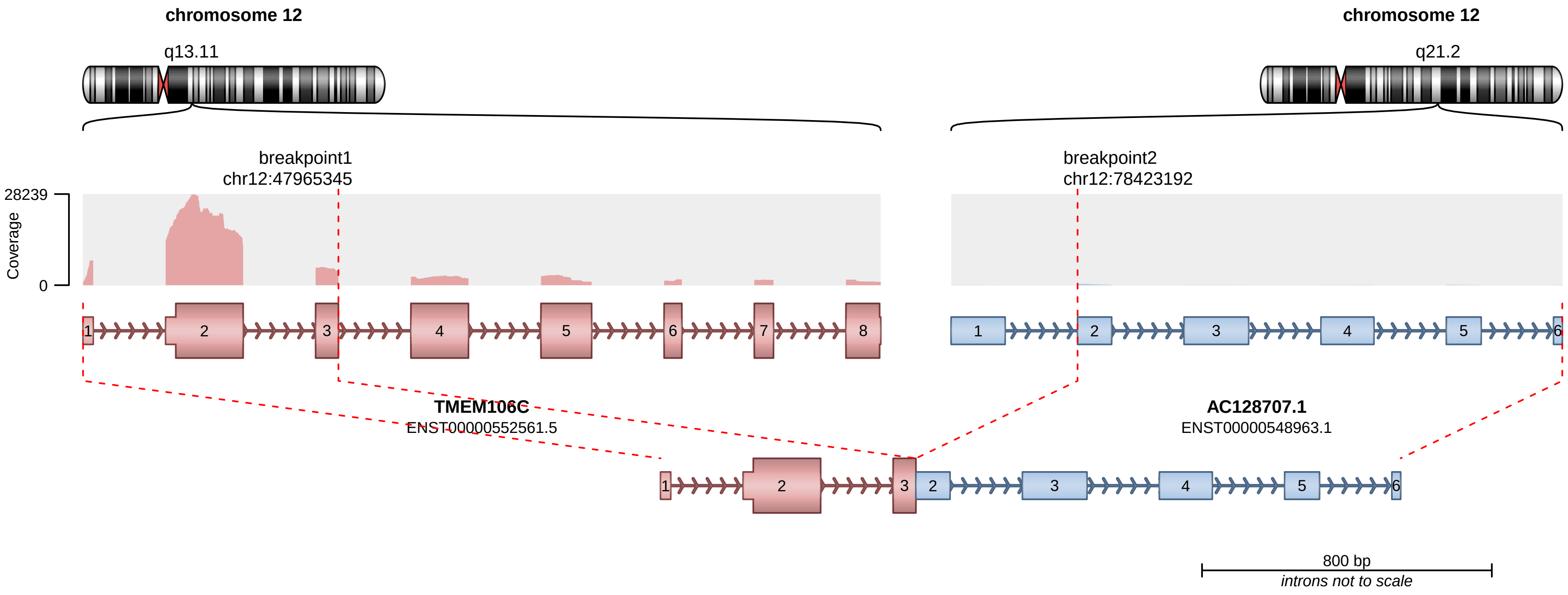


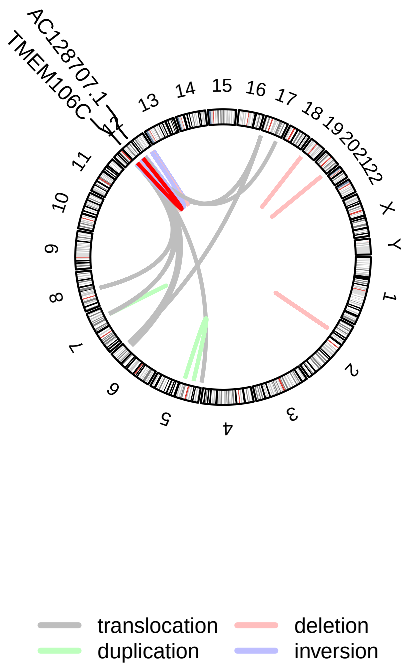




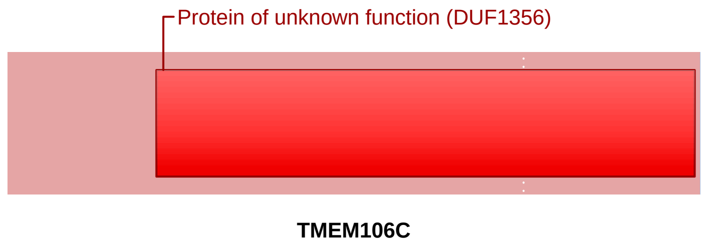
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 7



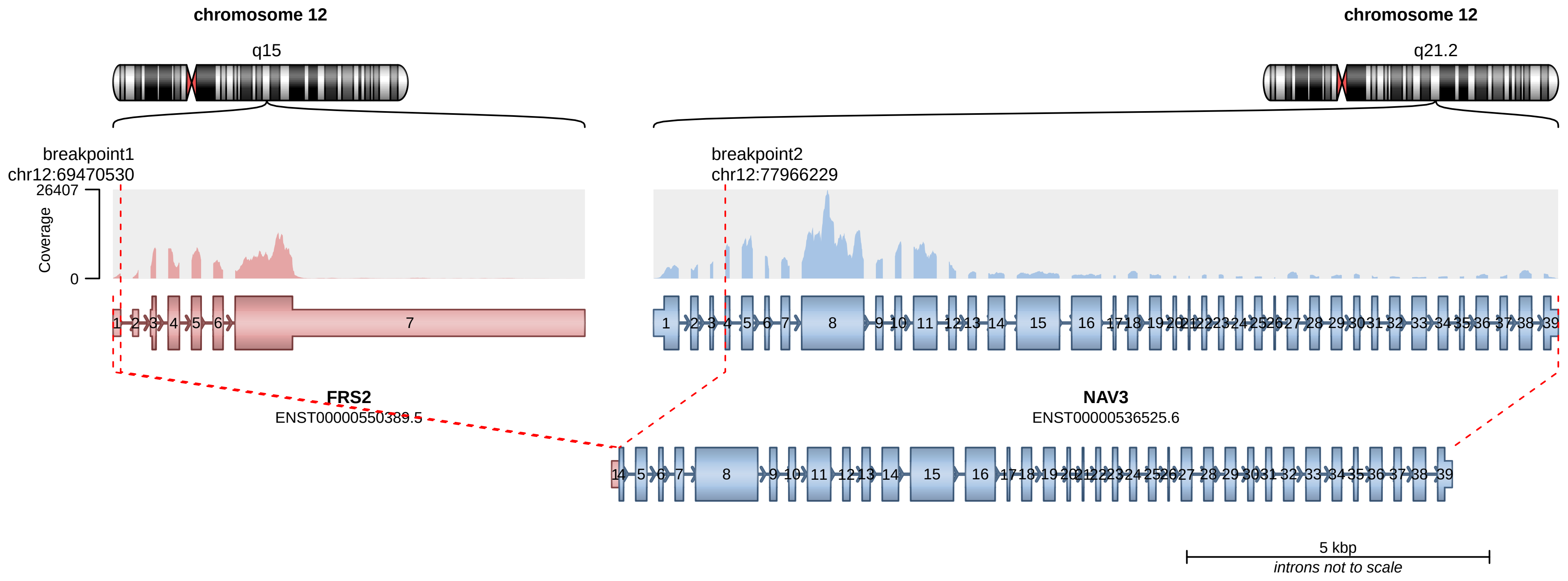


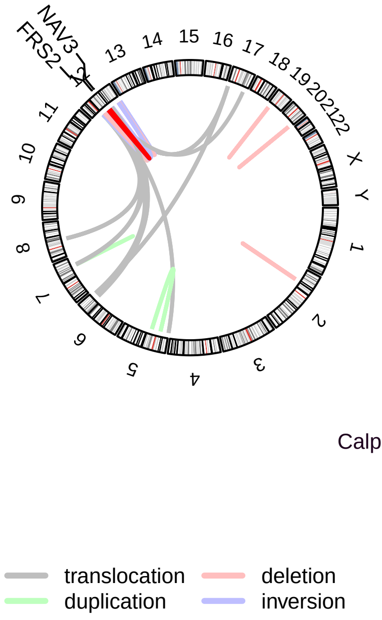
RETAINED PROTEIN DOMAINS
reading frame unclear

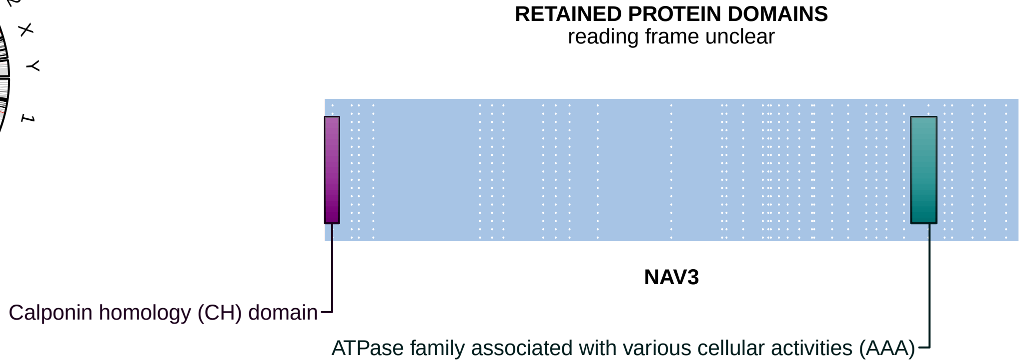


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

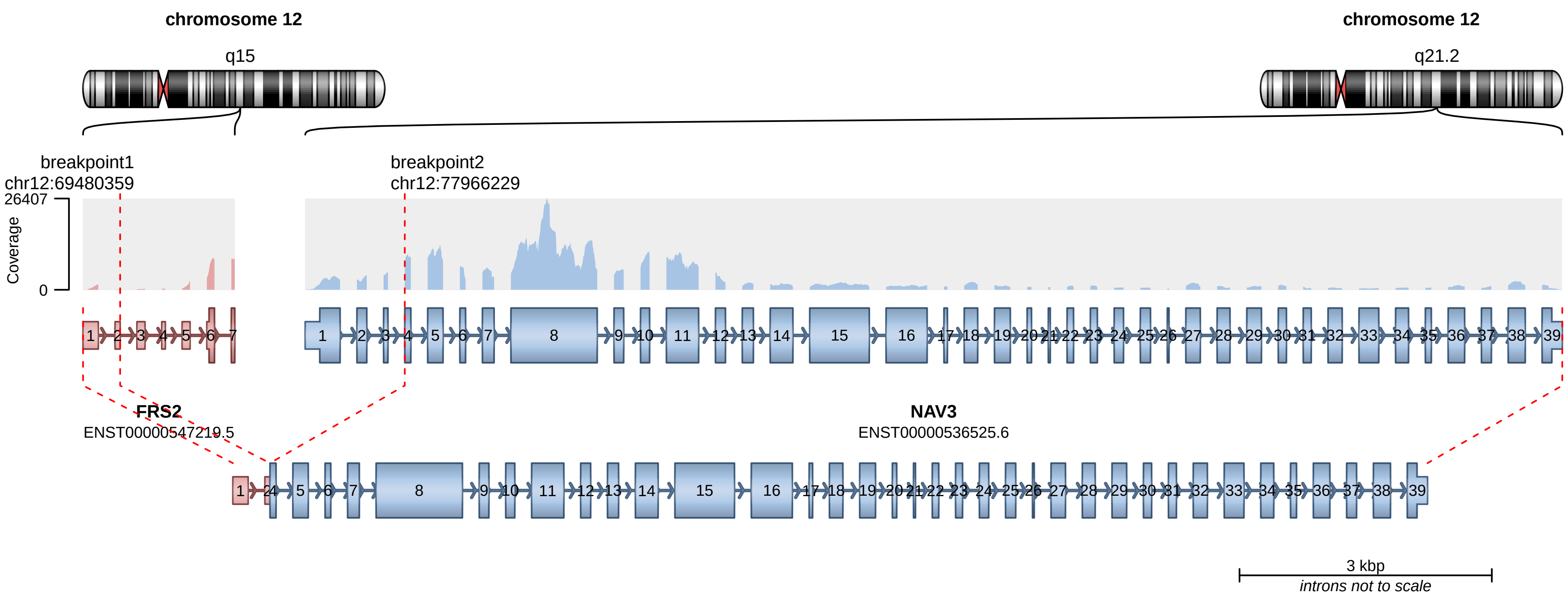


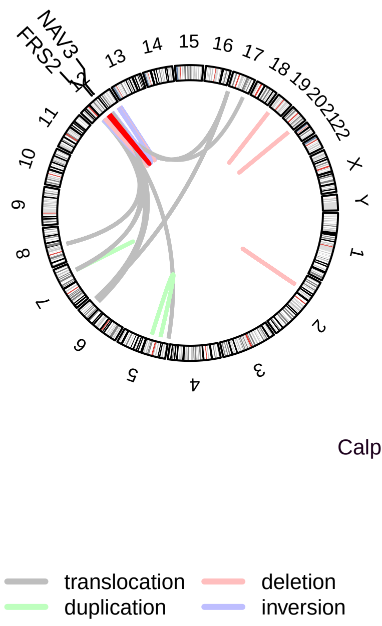


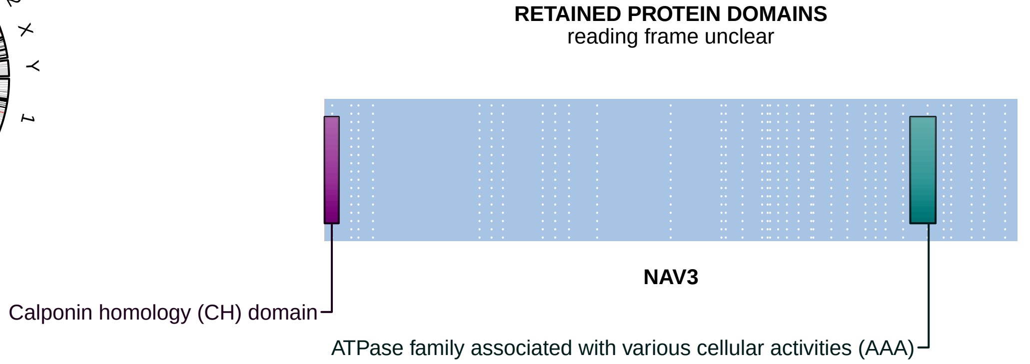


SUPPORTING READ COUNT

Split reads = 645
Discordant mates = 5

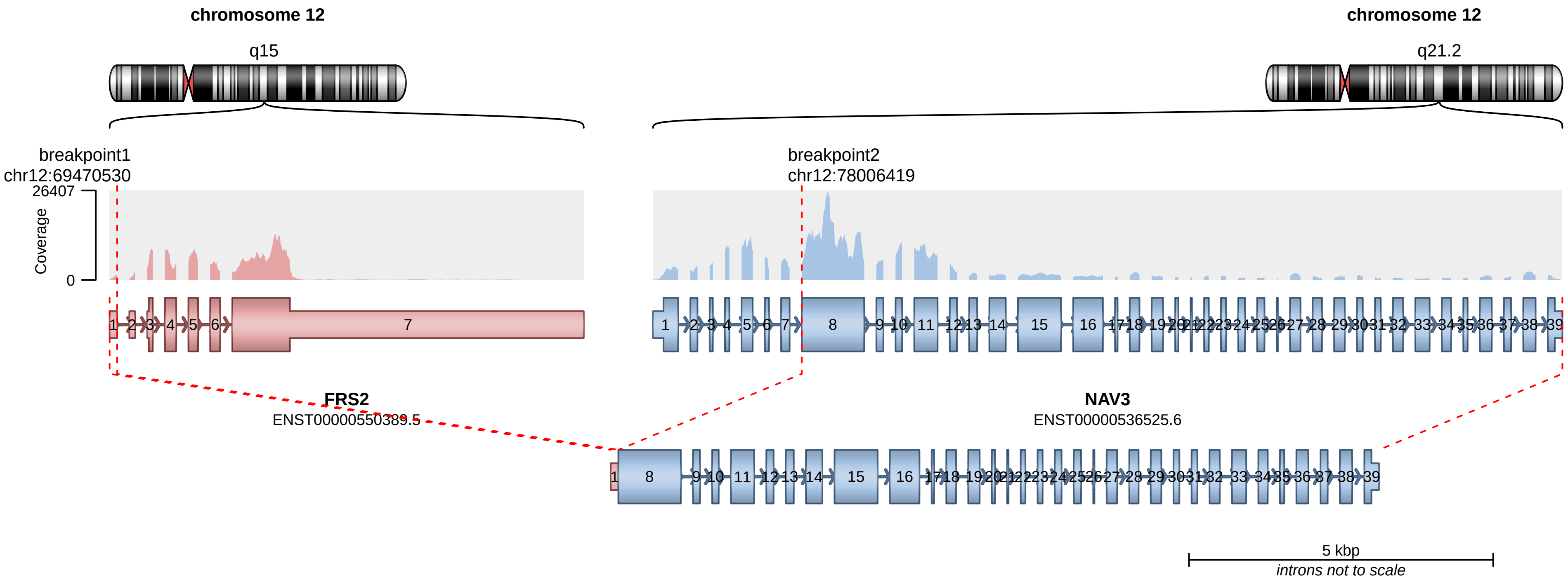


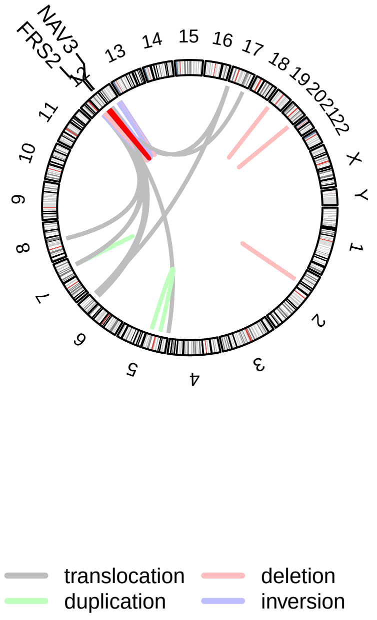




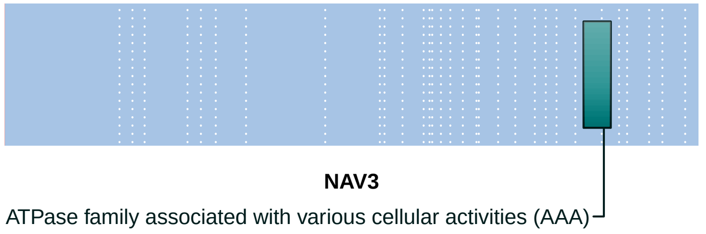
SUPPORTING READ COUNT

Split reads = 29
Discordant mates = 8



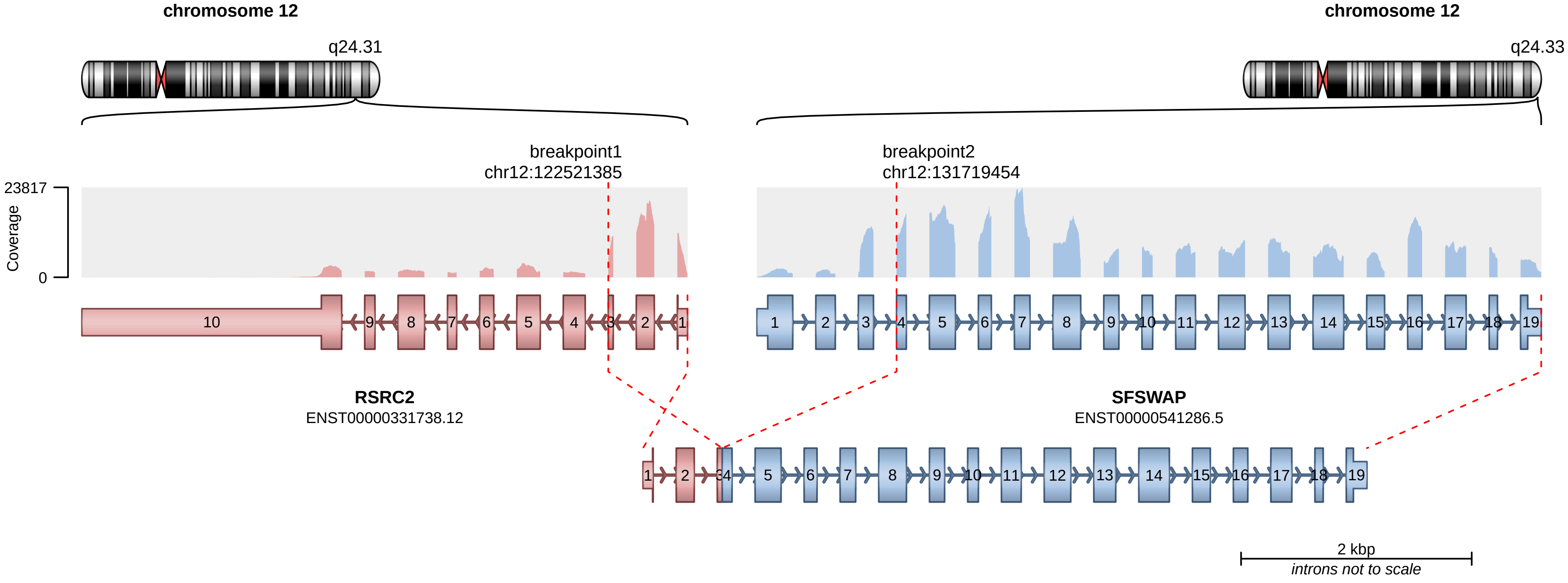


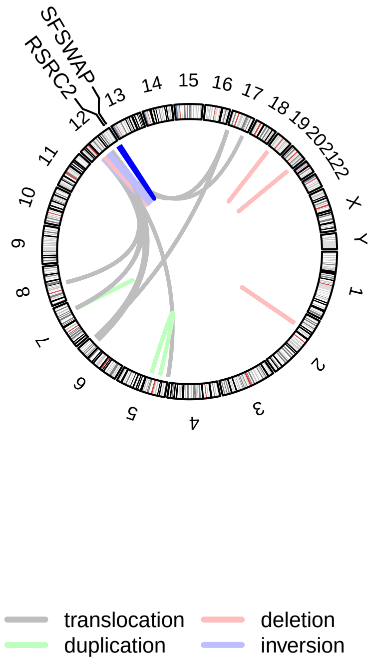
RETAINED PROTEIN DOMAINS
reading frame unclear

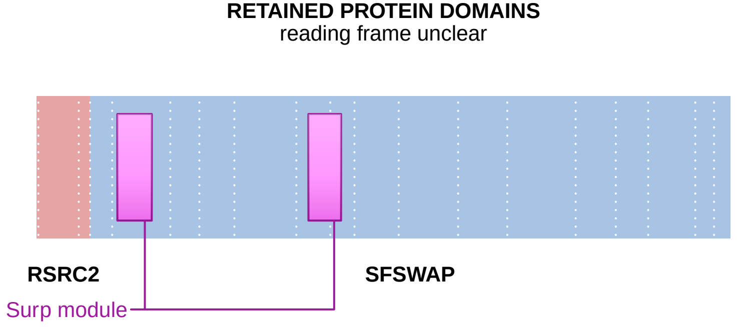


SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

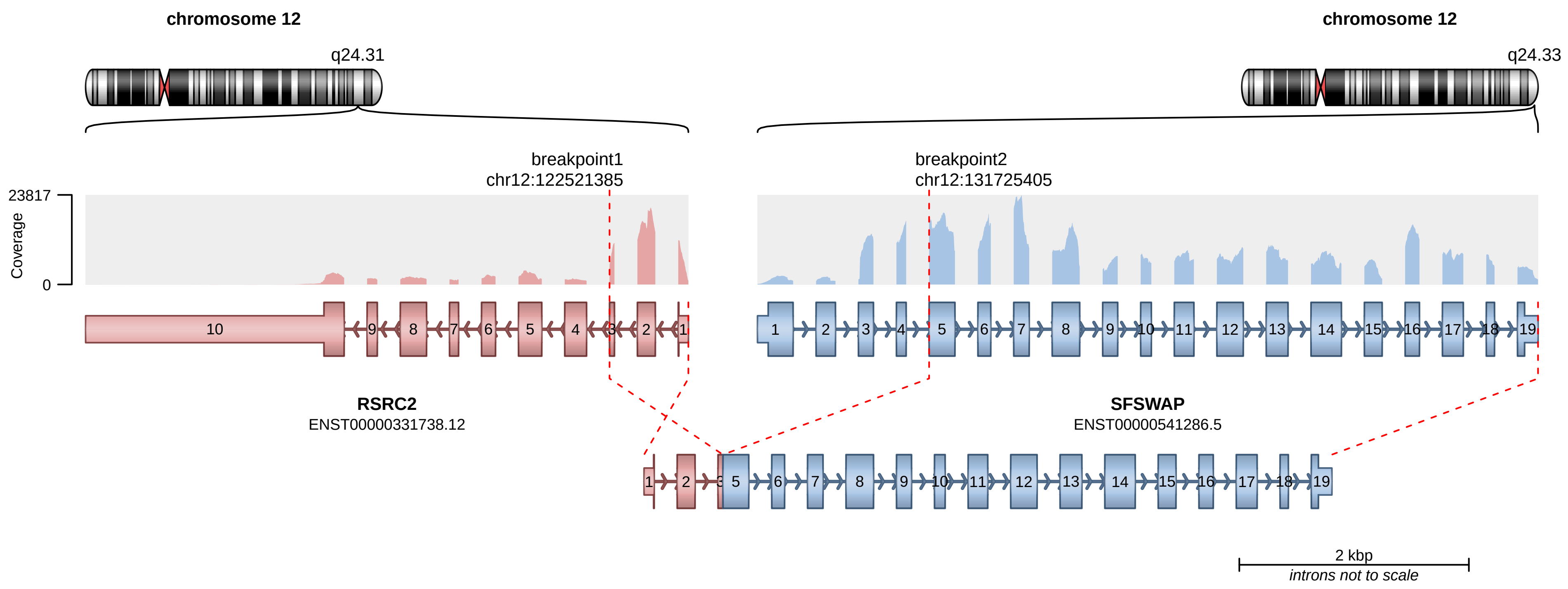


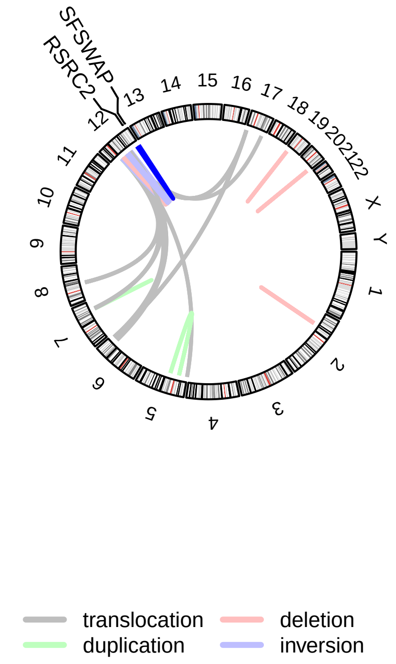




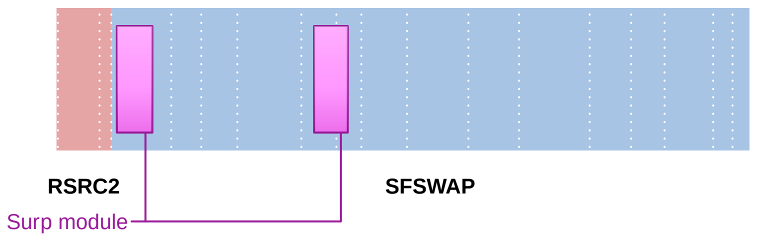
SUPPORTING READ COUNT

Split reads = 551
Discordant mates = 4



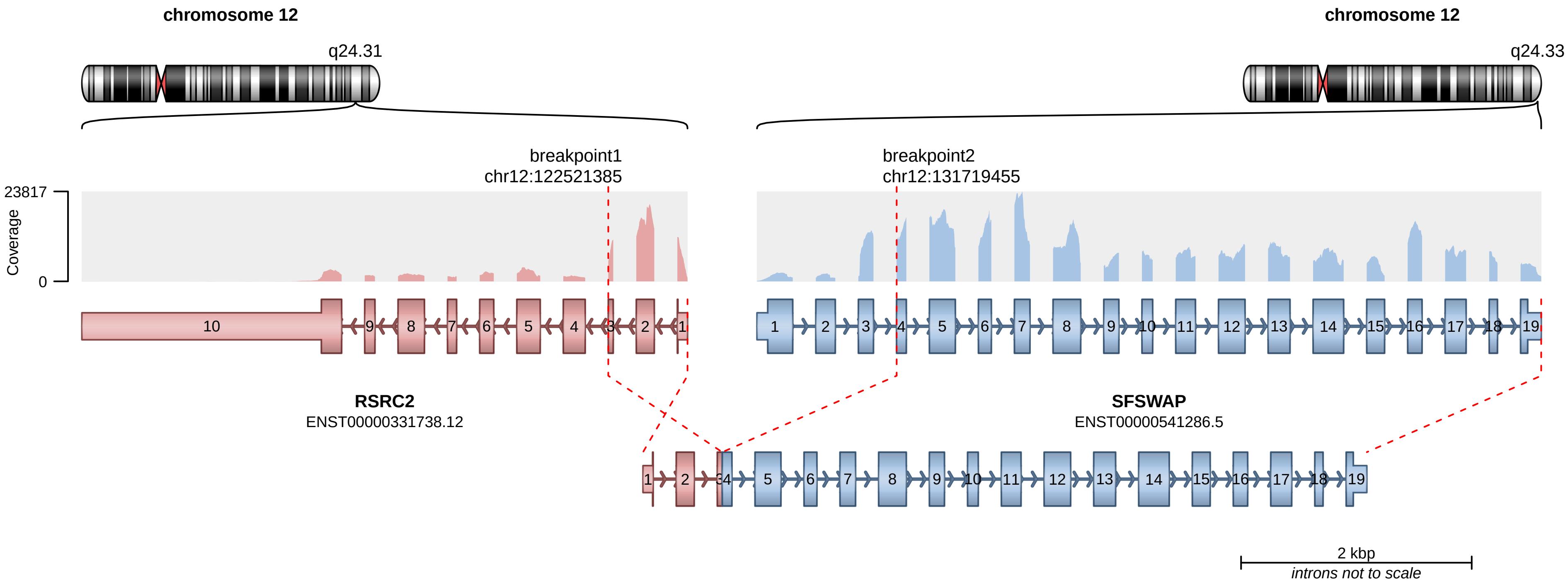


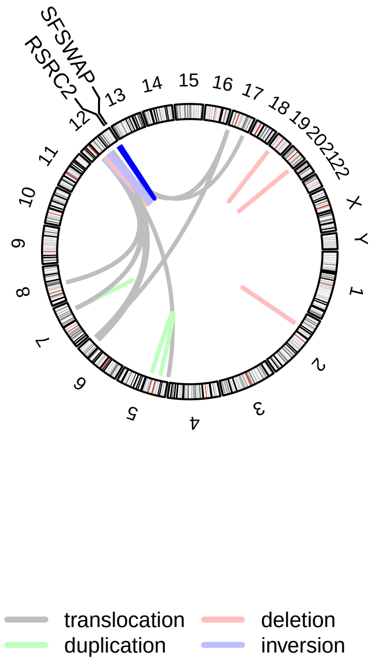
RETAINED PROTEIN DOMAINS
reading frame unclear

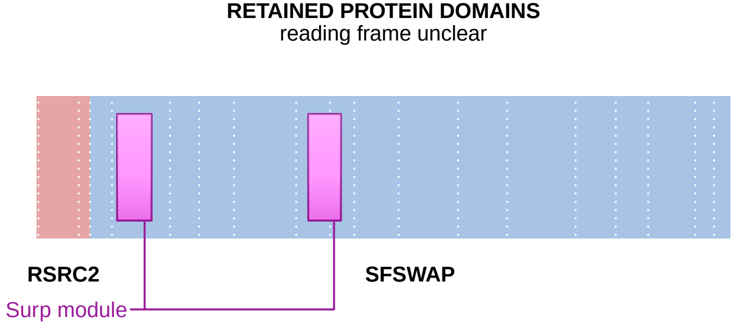


SUPPORTING READ COUNT

Split reads = 114
Discordant mates = 2

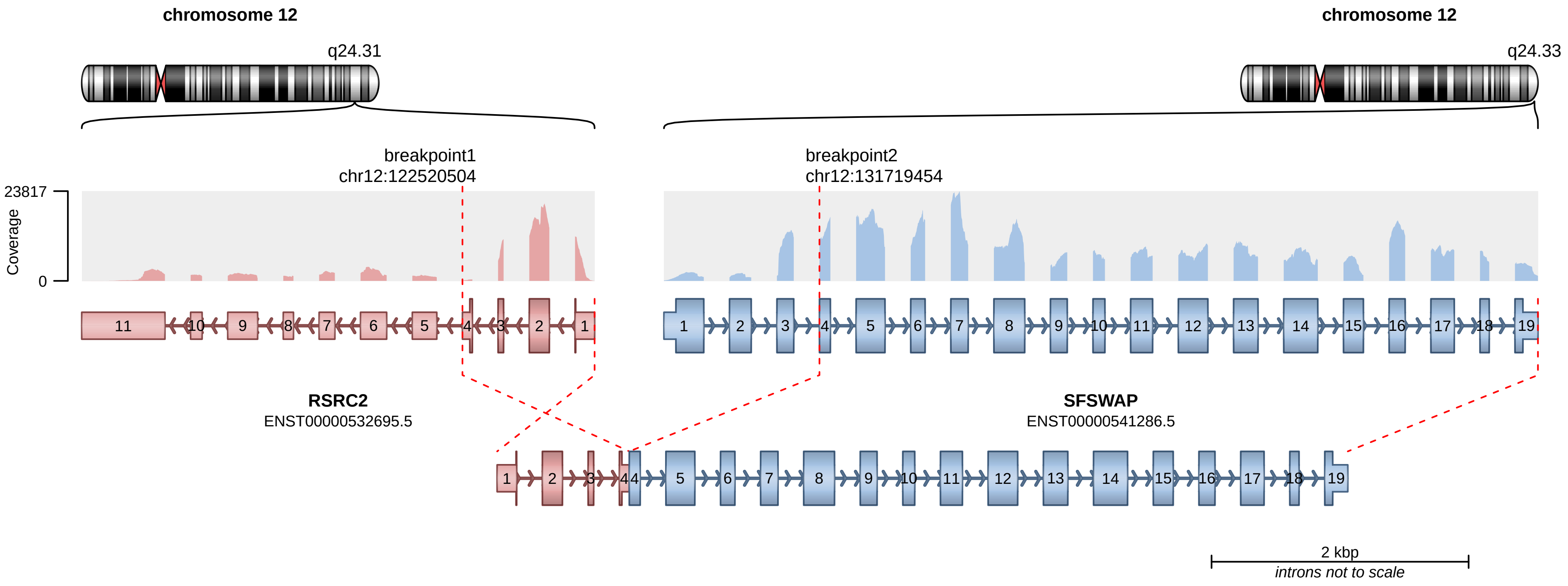


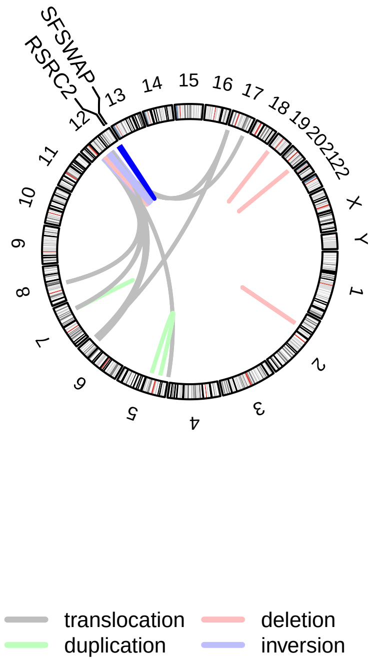




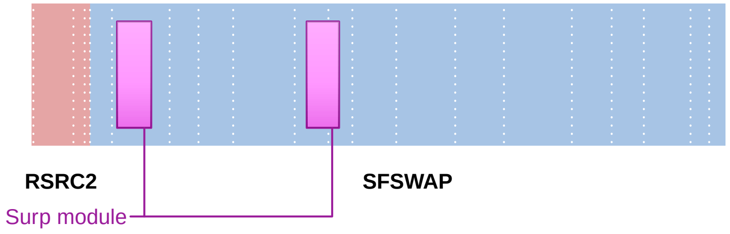
SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 4



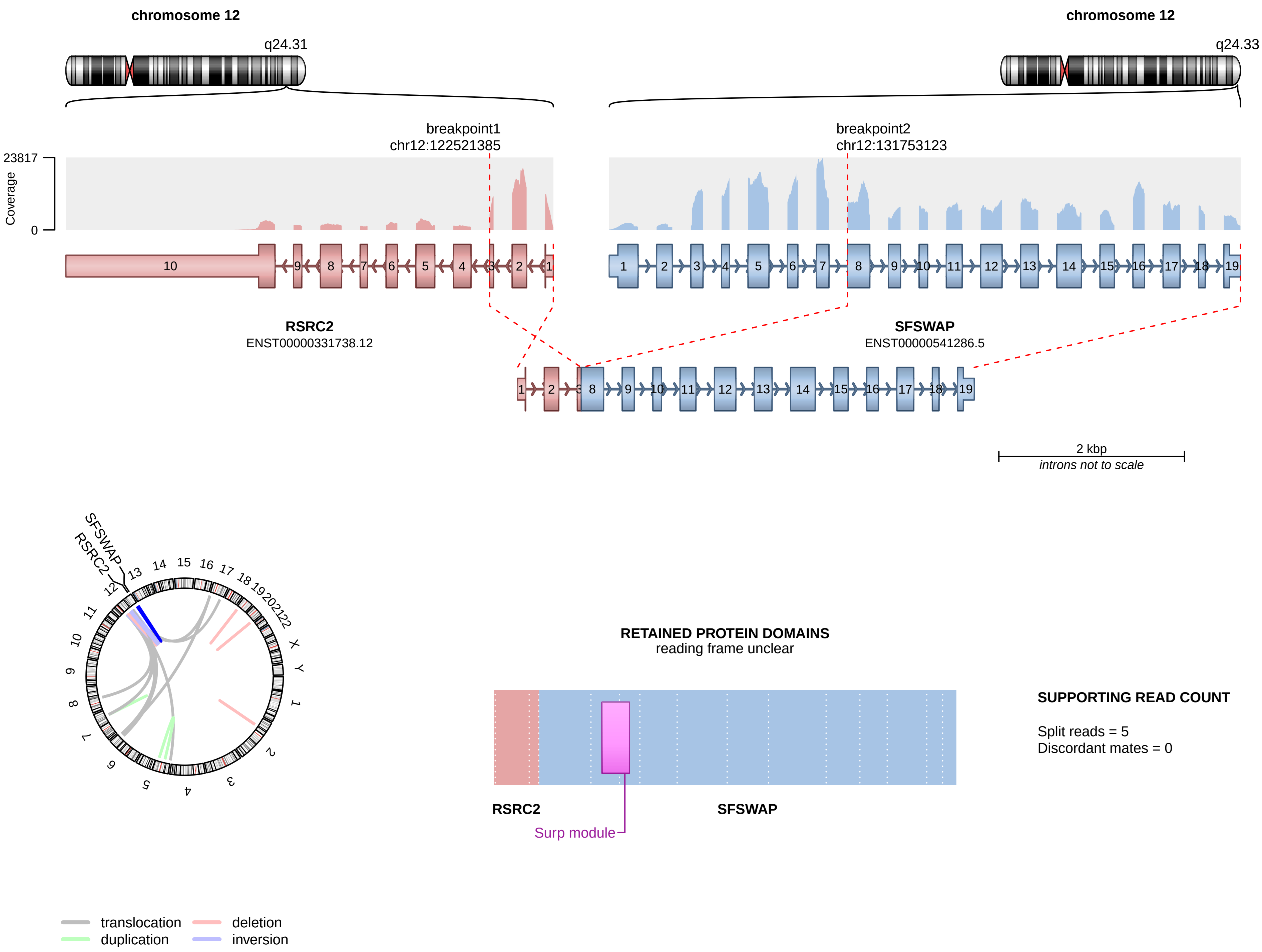


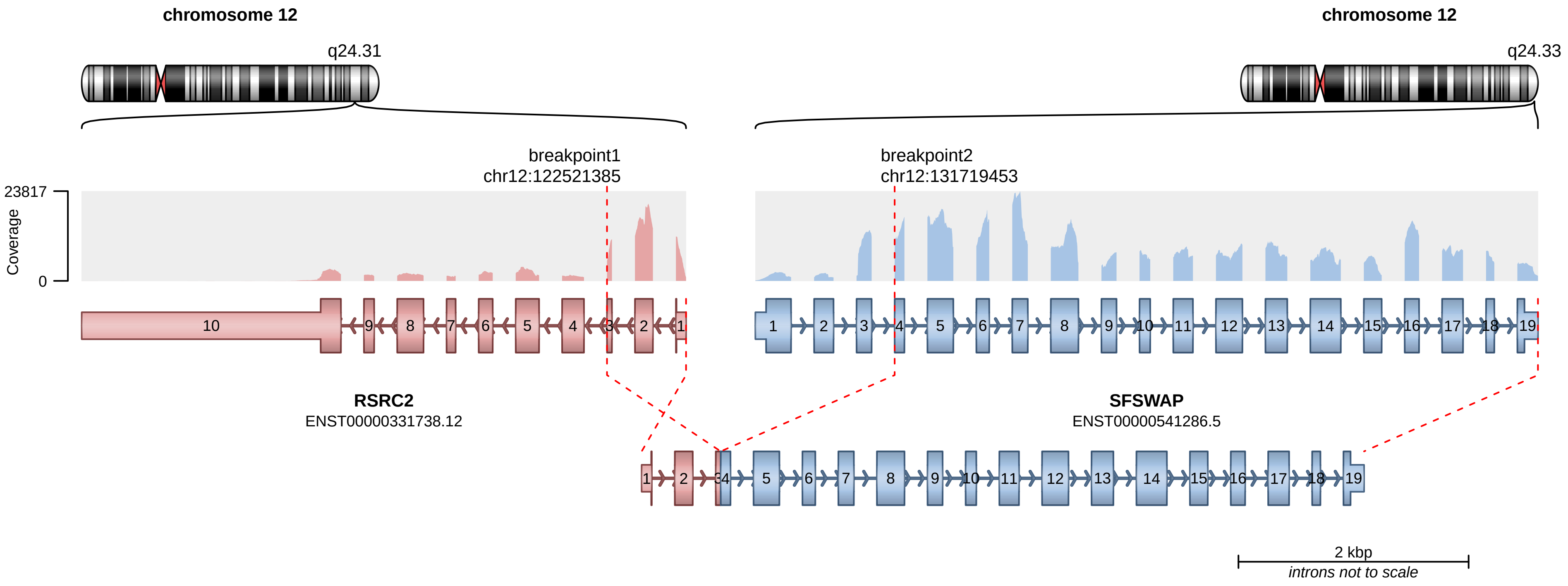
RETAINED PROTEIN DOMAINS
reading frame unclear

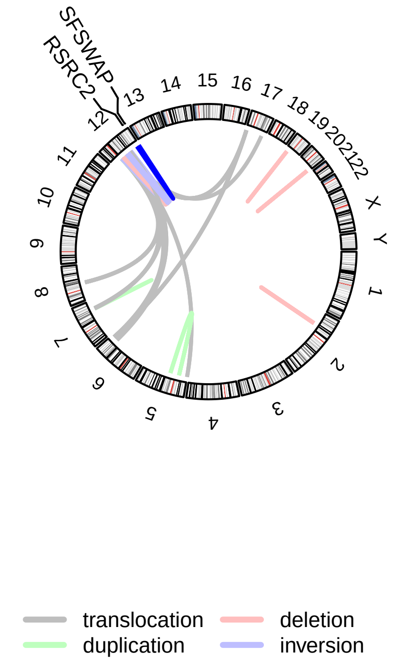


SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 4

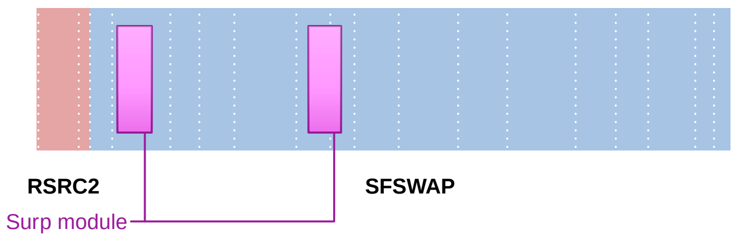

chromosome 12
q24.31
chromosome 12
q24.33
breakpoint1
chr12:122521385
breakpoint2
chr12:131753123
Coverage
23817
0
10
9
8
7
6
5
4
3
2
1
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
RSRC2
ENST00000331738.12
SFSWAP
ENST00000541286.5
1
2
3
8
9
10
11
12
13
14
15
16
17
18
19
2 kbp
introns not to scale
SFSWAP
RSRC2
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y
RETAINED PROTEIN DOMAINS
reading frame unclear
RSRC2
SFSWAP
Surp module
SUPPORTING READ COUNT
Split reads = 5
Discordant mates = 0
translocation
duplication
deletion
inversion





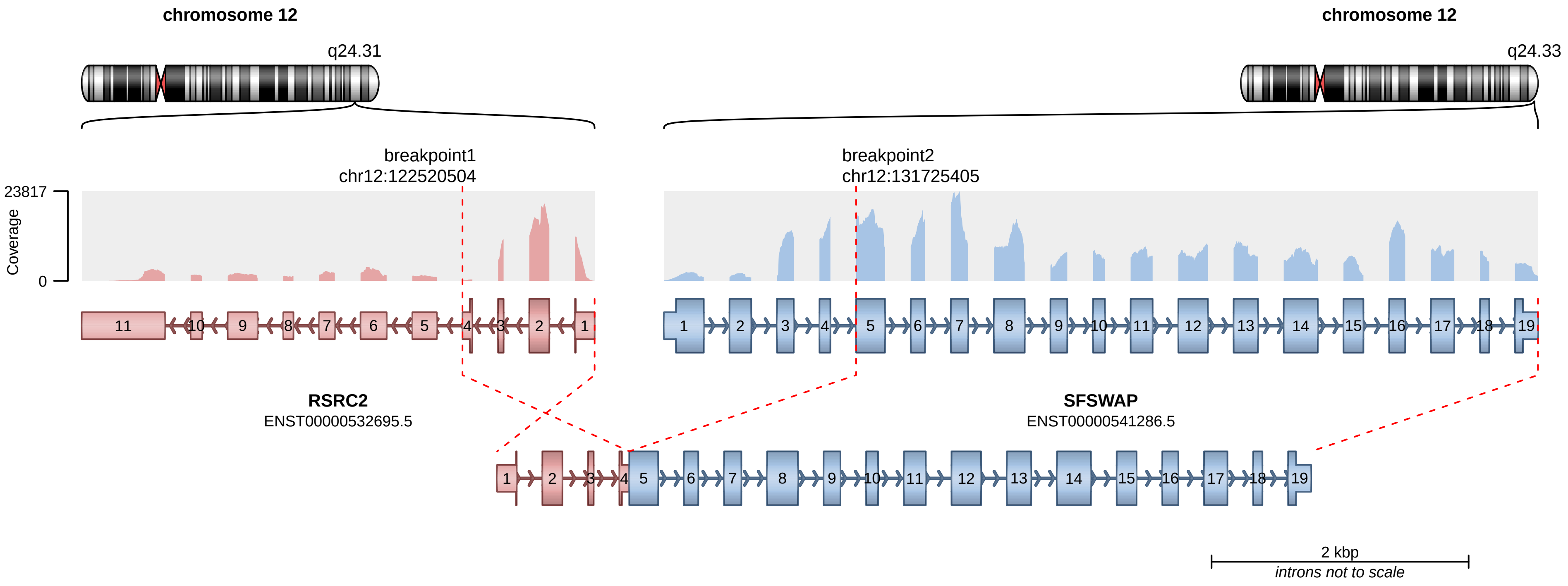
RETAINED PROTEIN DOMAINS

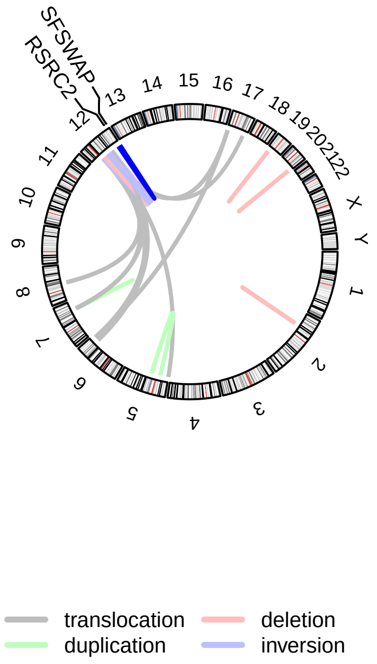
reading frame unclear

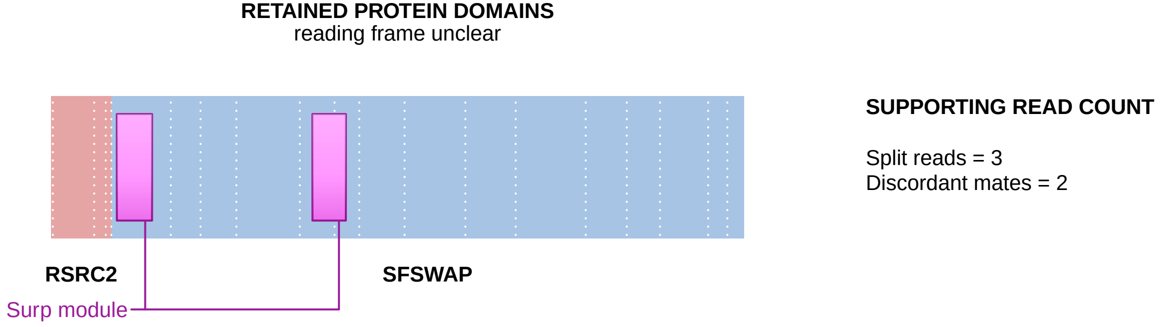


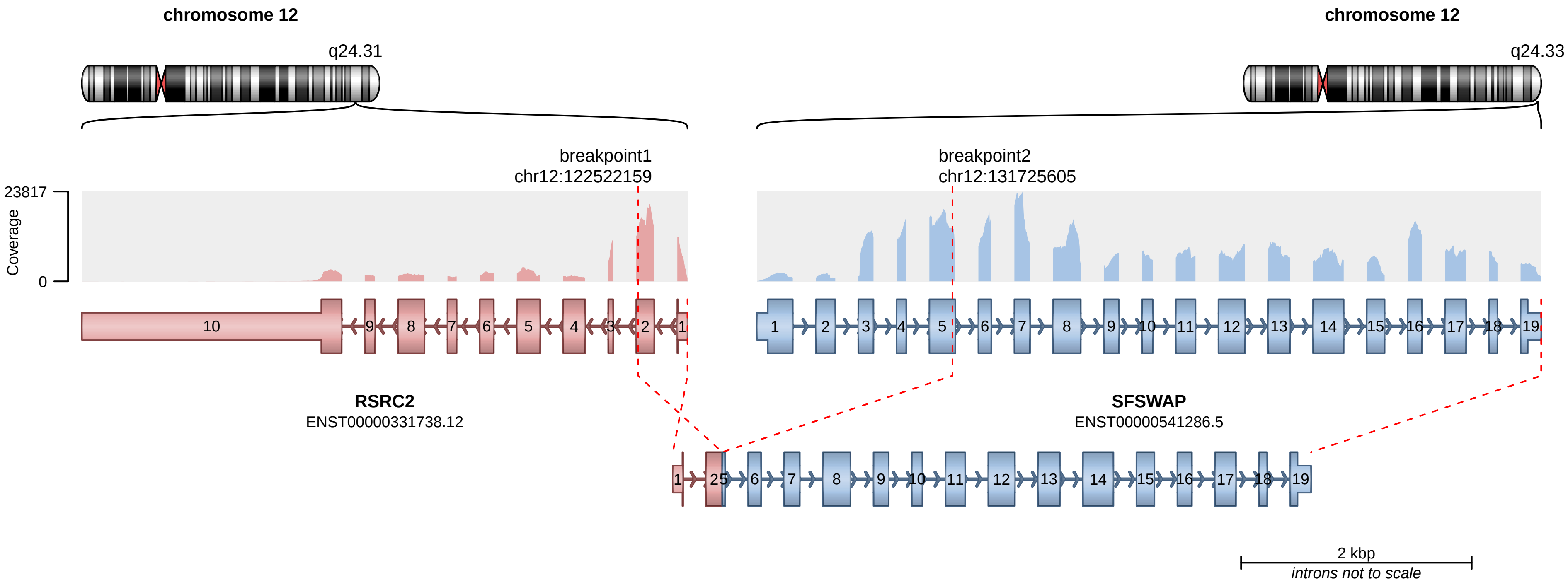
SUPPORTING READ COUNT

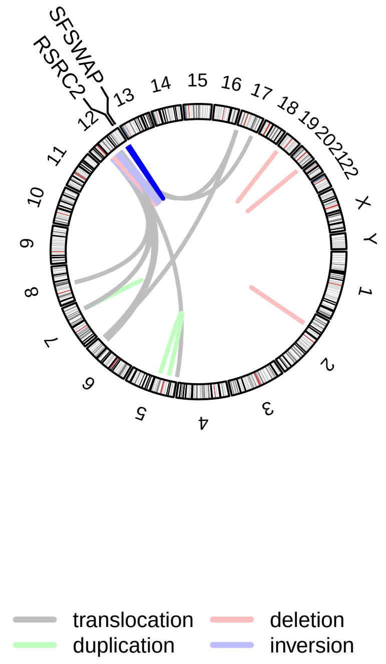
Split reads = 3
Discordant mates = 4


chromosome 12
q24.31
chromosome 12
q24.33
breakpoint1
chr12:122520504
breakpoint2
chr12:131725405
23817
Coverage
0
RSRC2
ENST00000532695.5
SFSWAP
ENST00000541286.5
2 kbp
introns not to scale

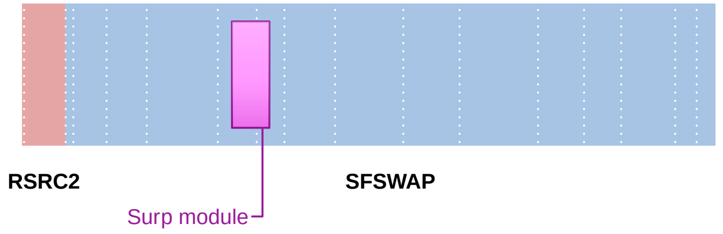

SFSWAP
RSRC2
translocation
duplication
deletion
inversion


RETAINED PROTEIN DOMAINS
reading frame unclear
RSRC2
SFSWAP
Surp module
SUPPORTING READ COUNT
Split reads = 3
Discordant mates = 2



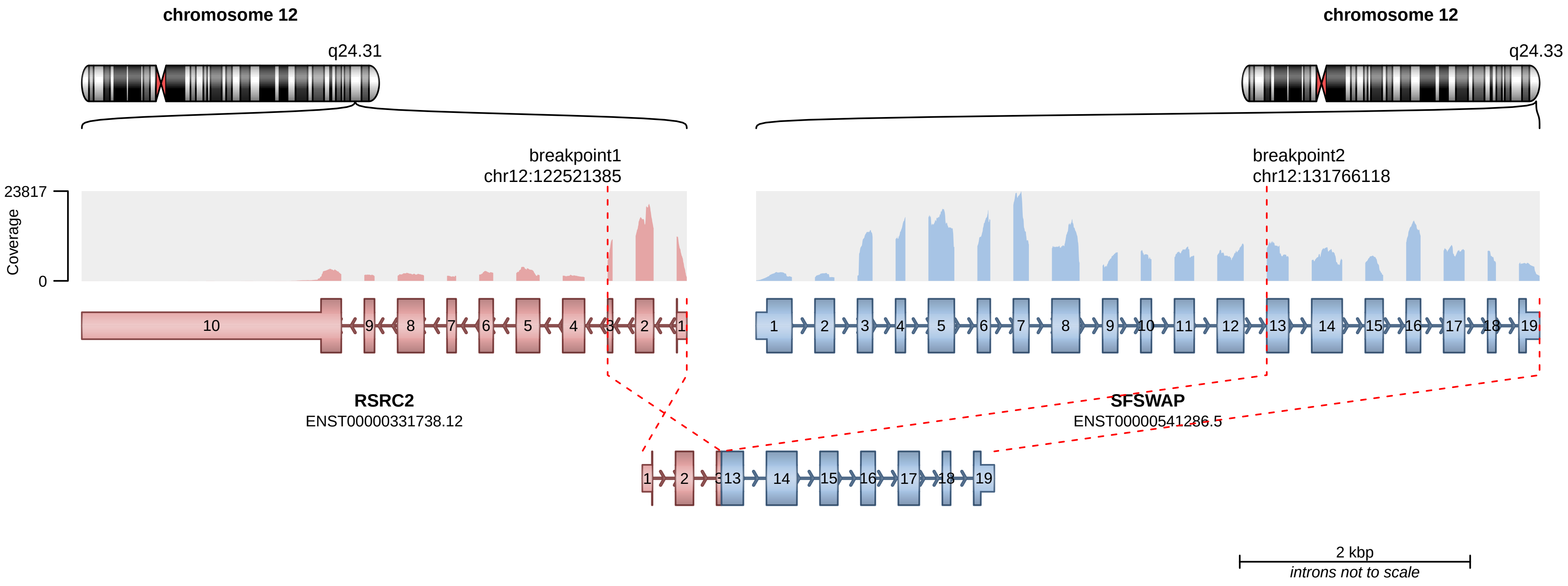


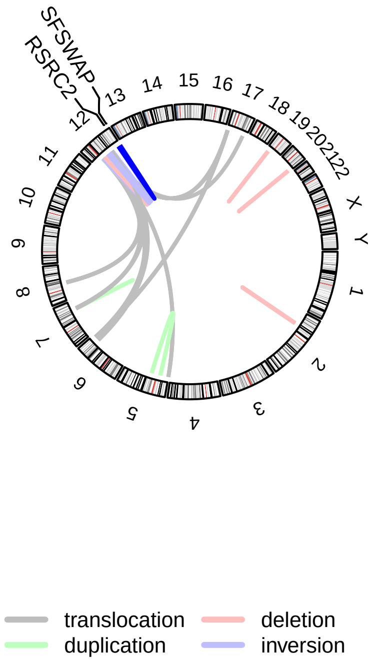
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

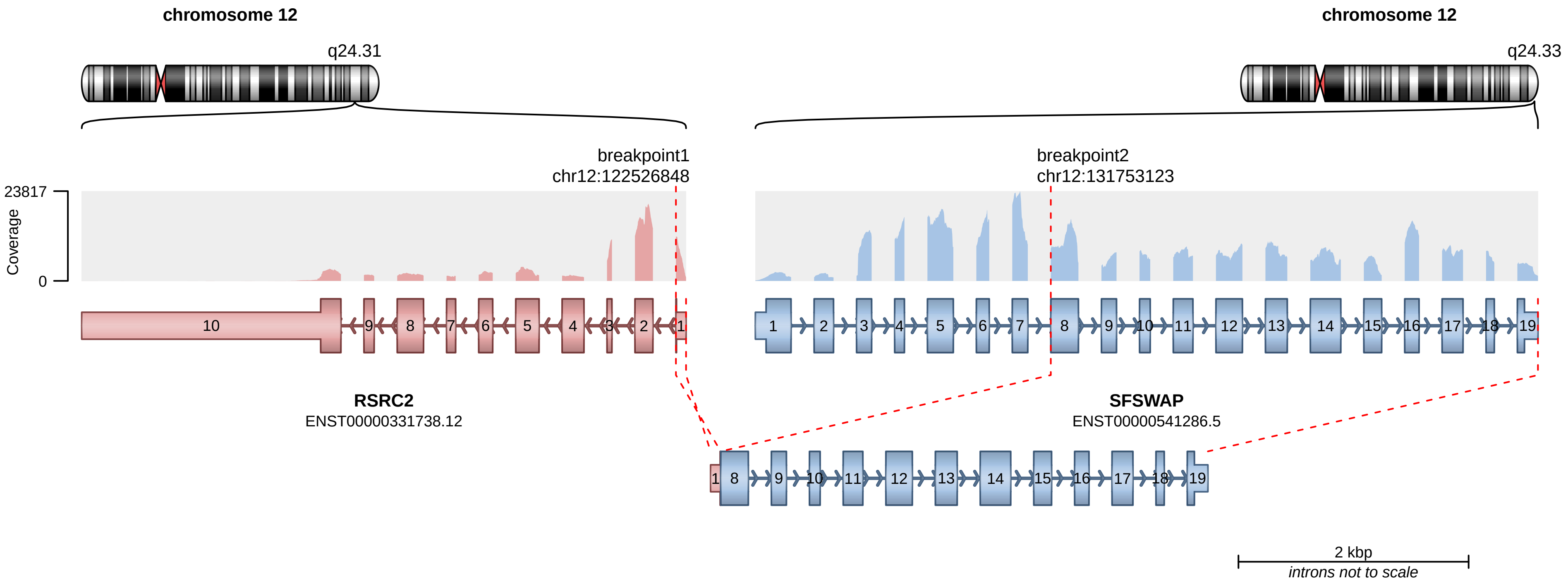


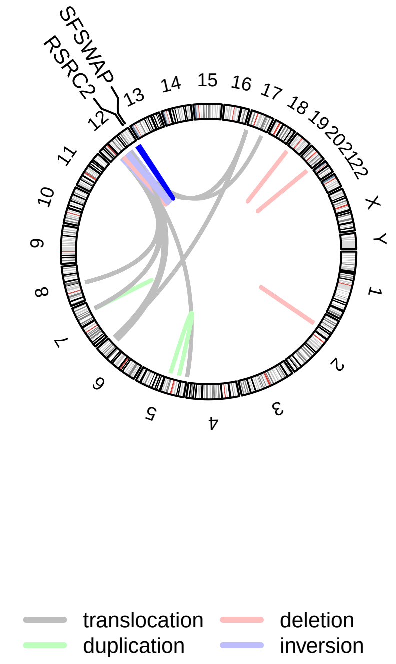


No protein domains retained in fusion.

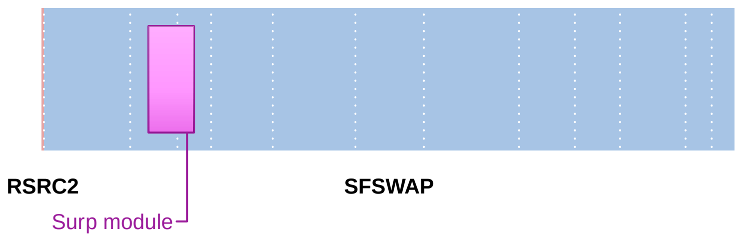
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0



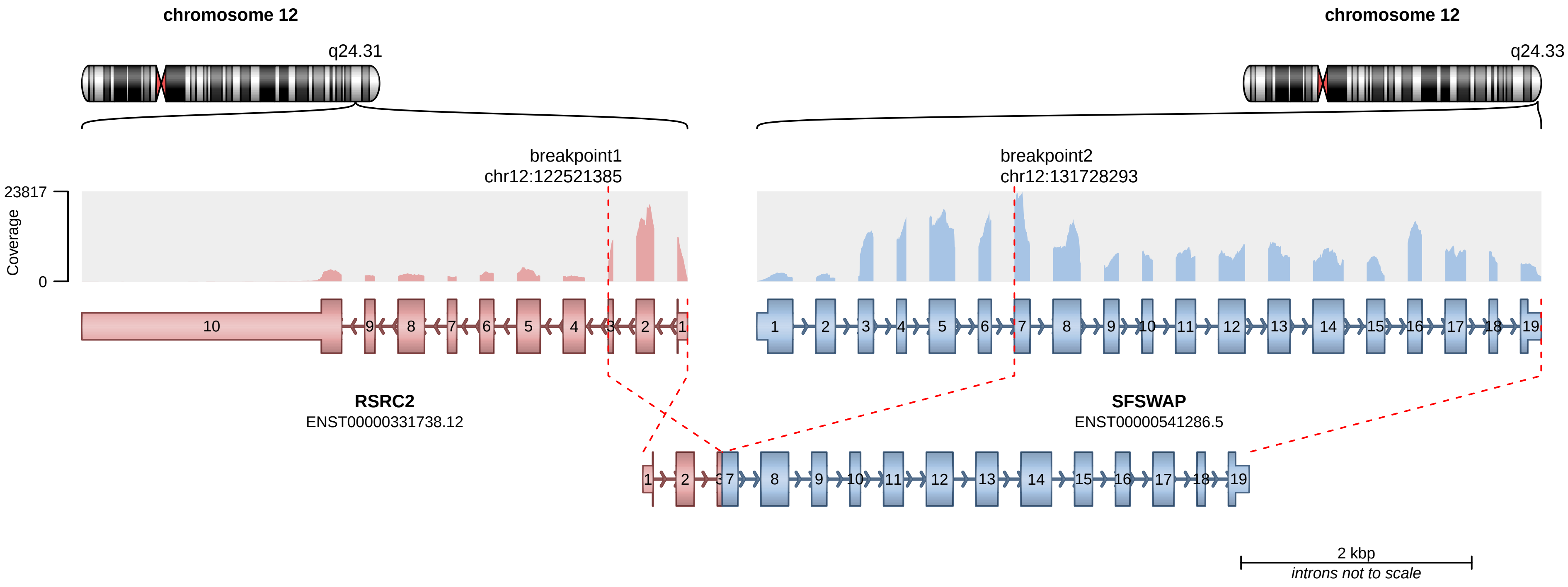


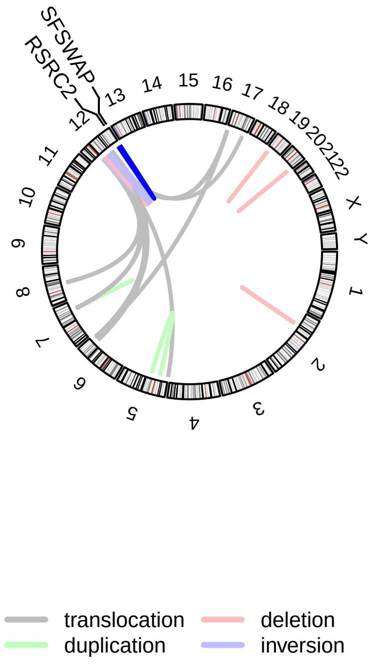
RETAINED PROTEIN DOMAINS
reading frame unclear

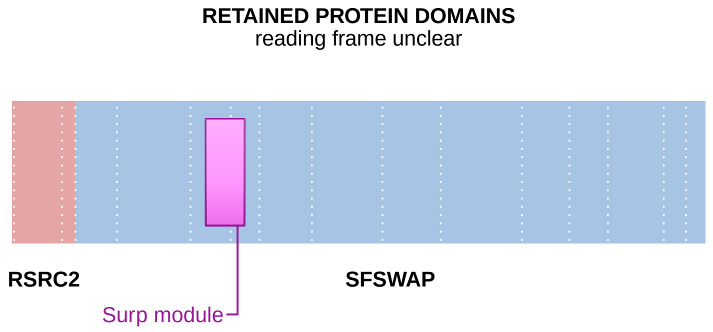


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

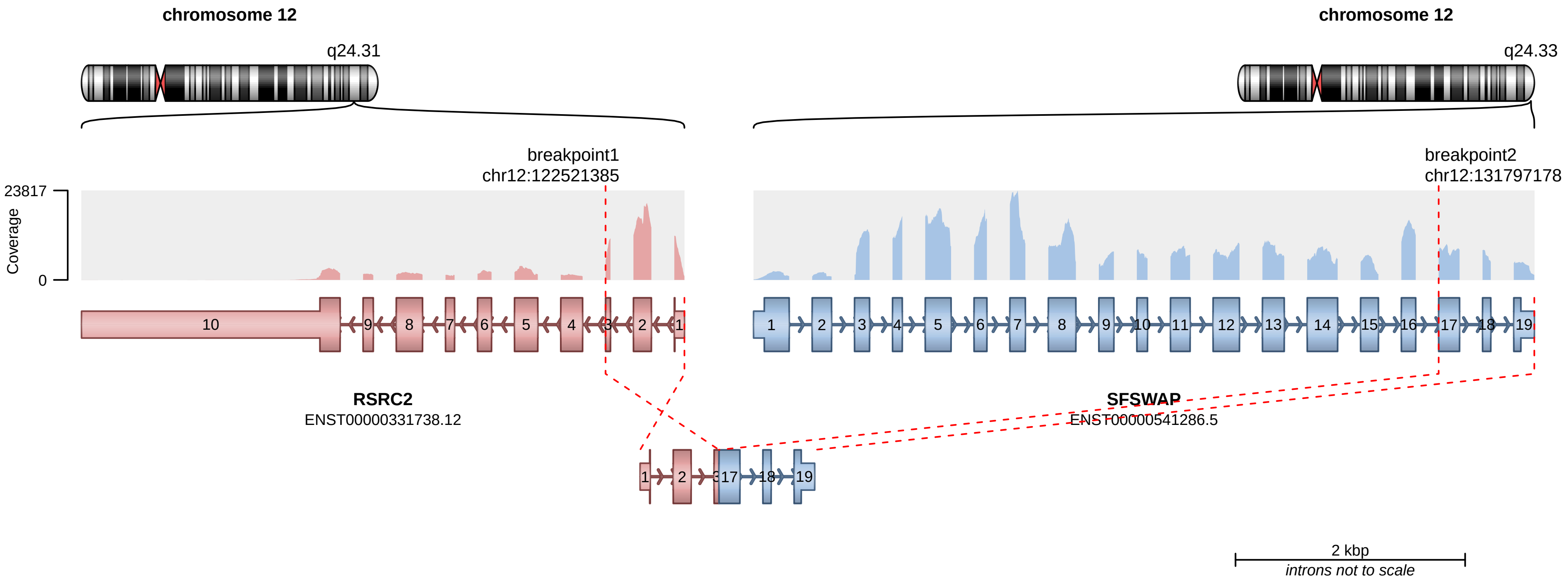


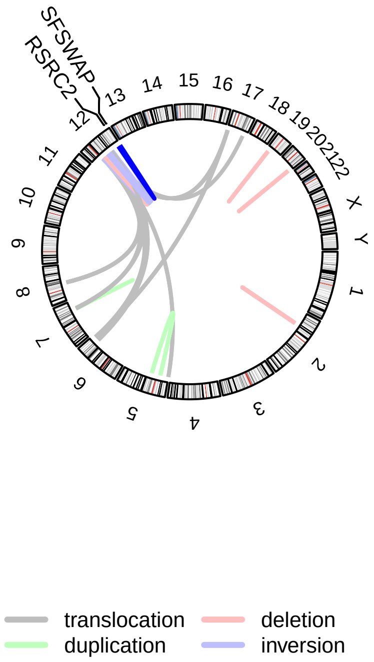




SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

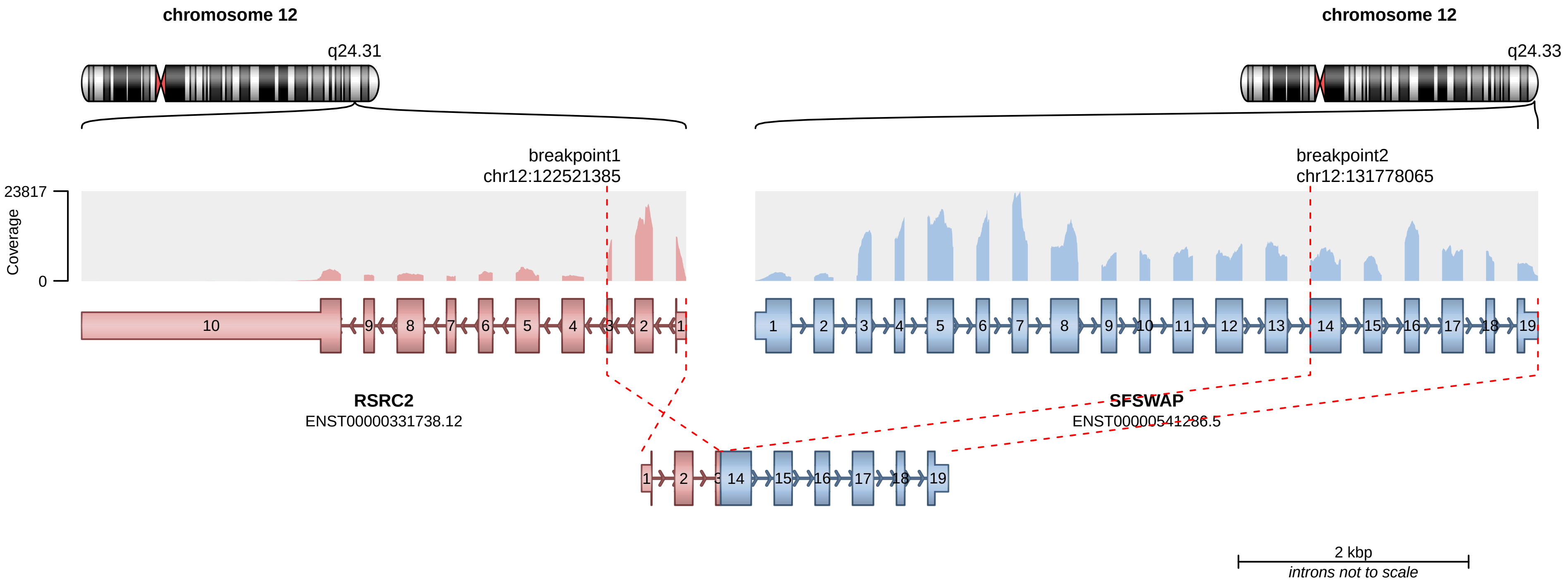


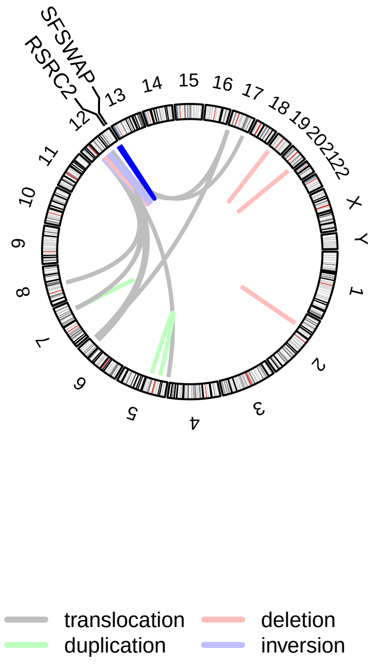


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

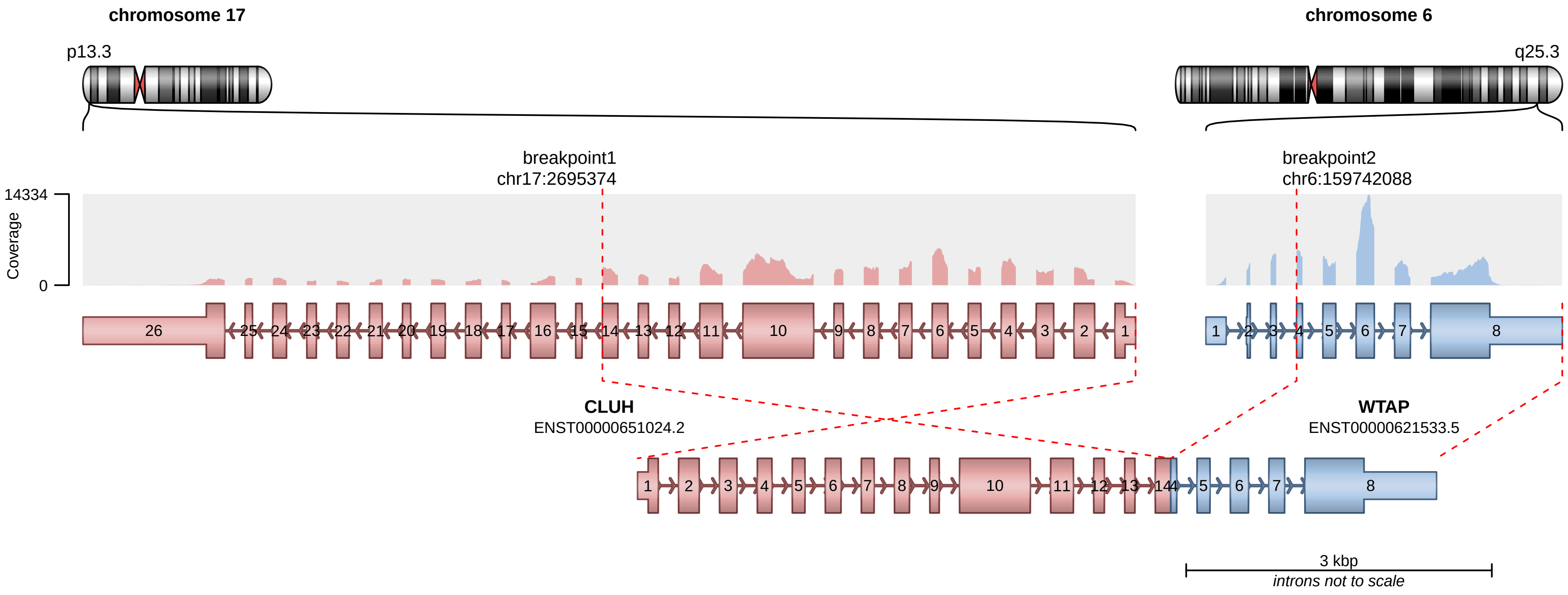


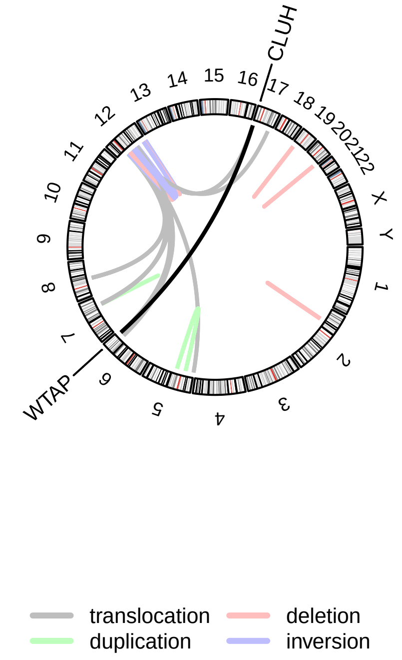


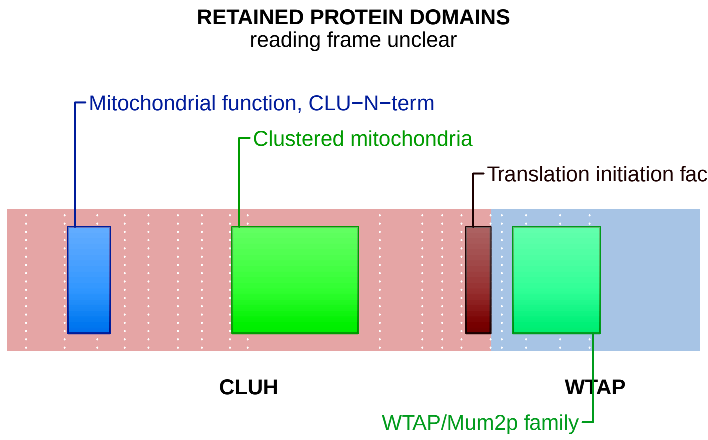
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

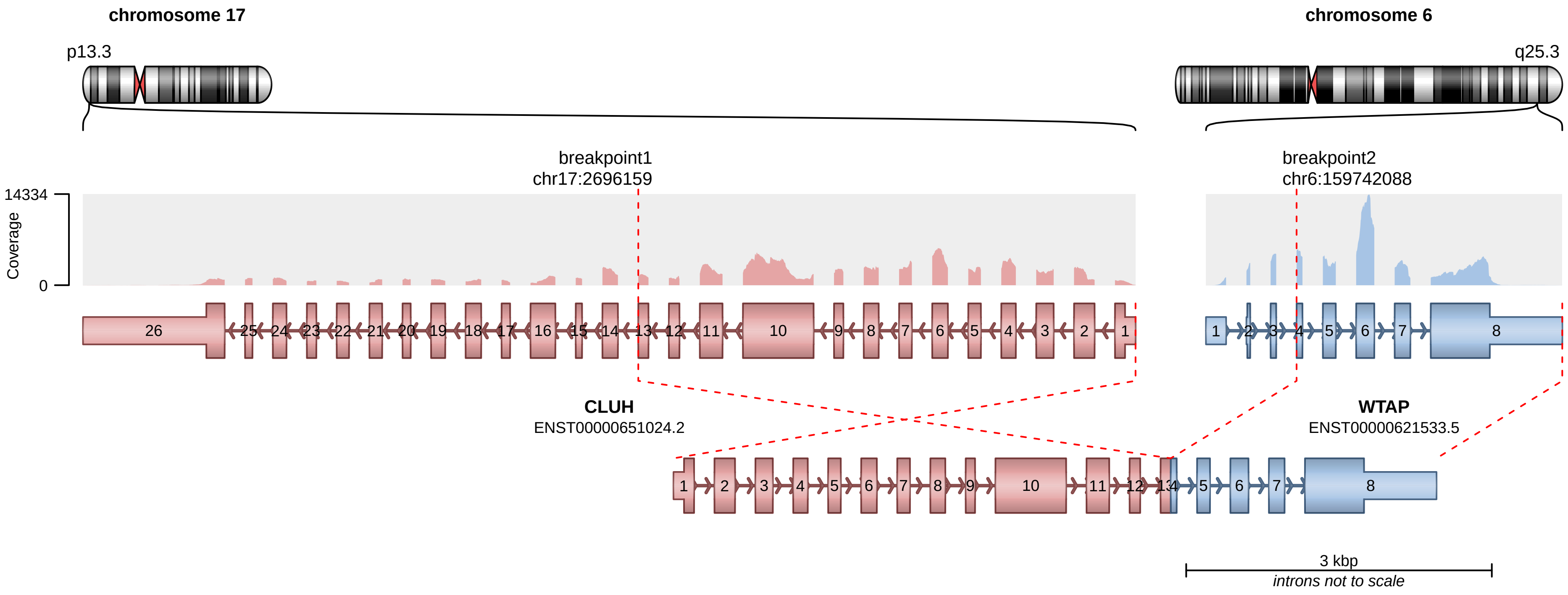


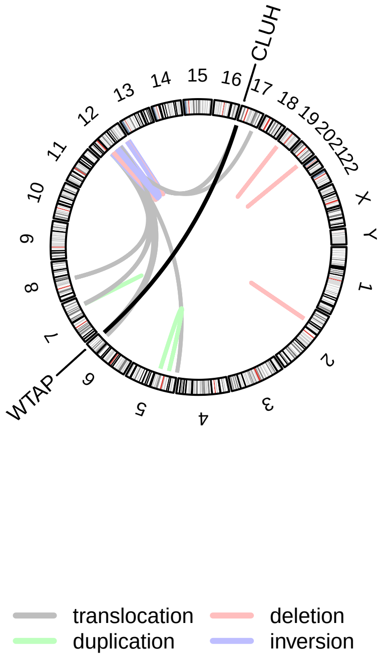


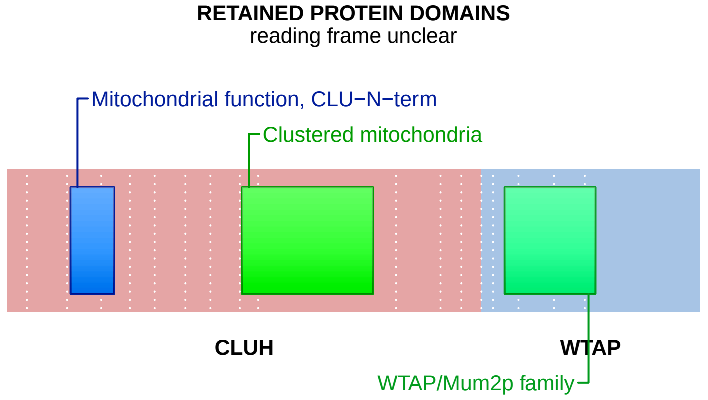


SUPPORTING READ COUNT

Split reads = 455
Discordant mates = 1

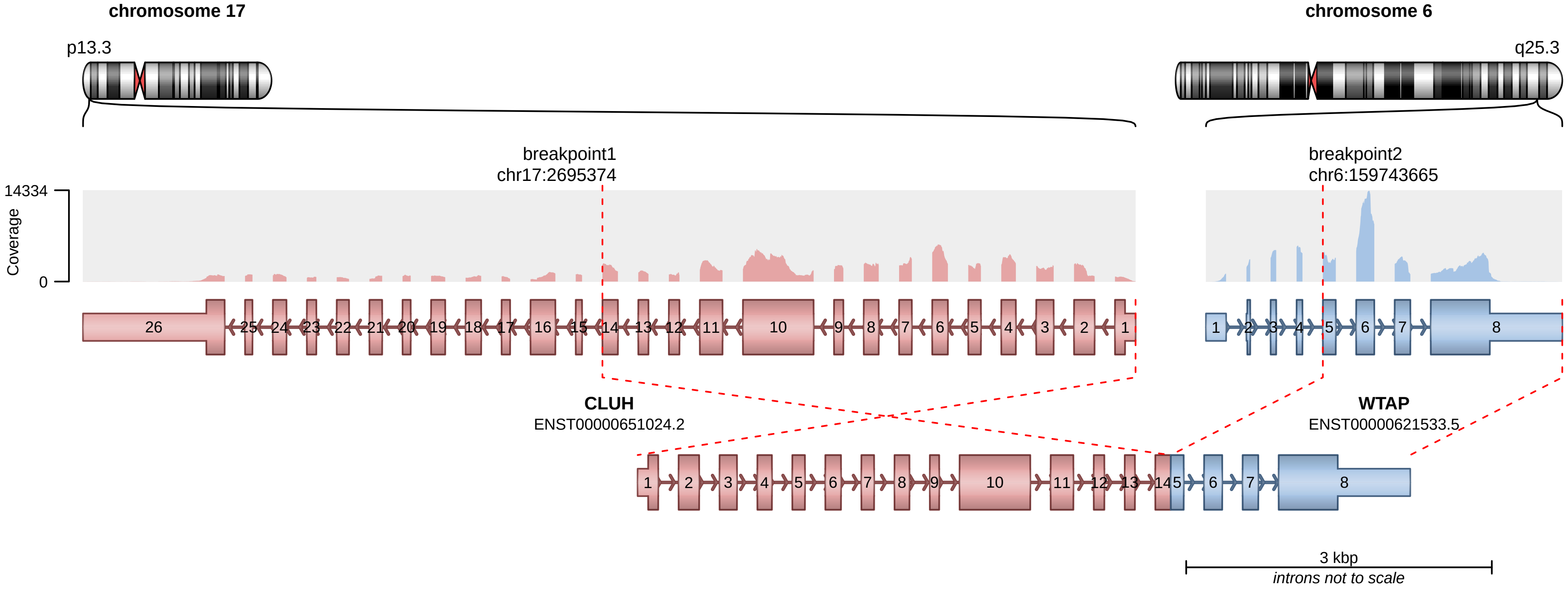


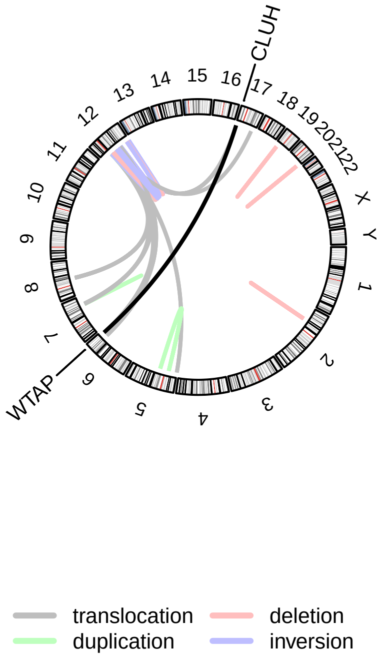


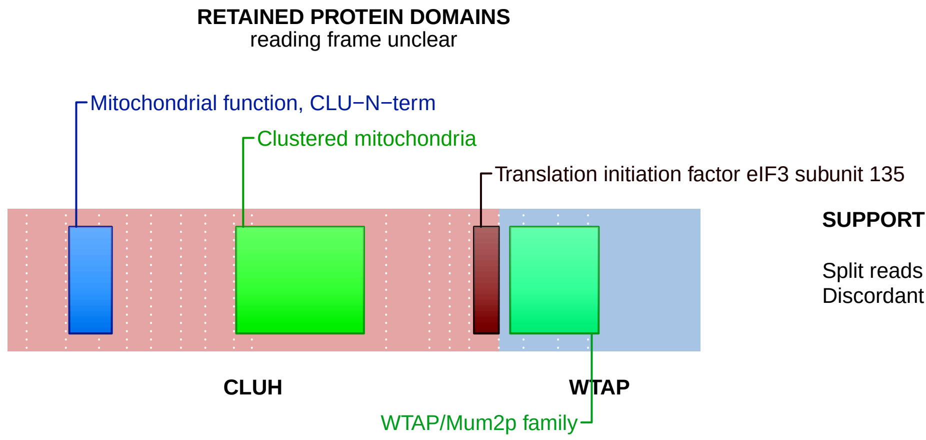


SUPPORTING READ COUNT

Split reads = 30
Discordant mates = 0

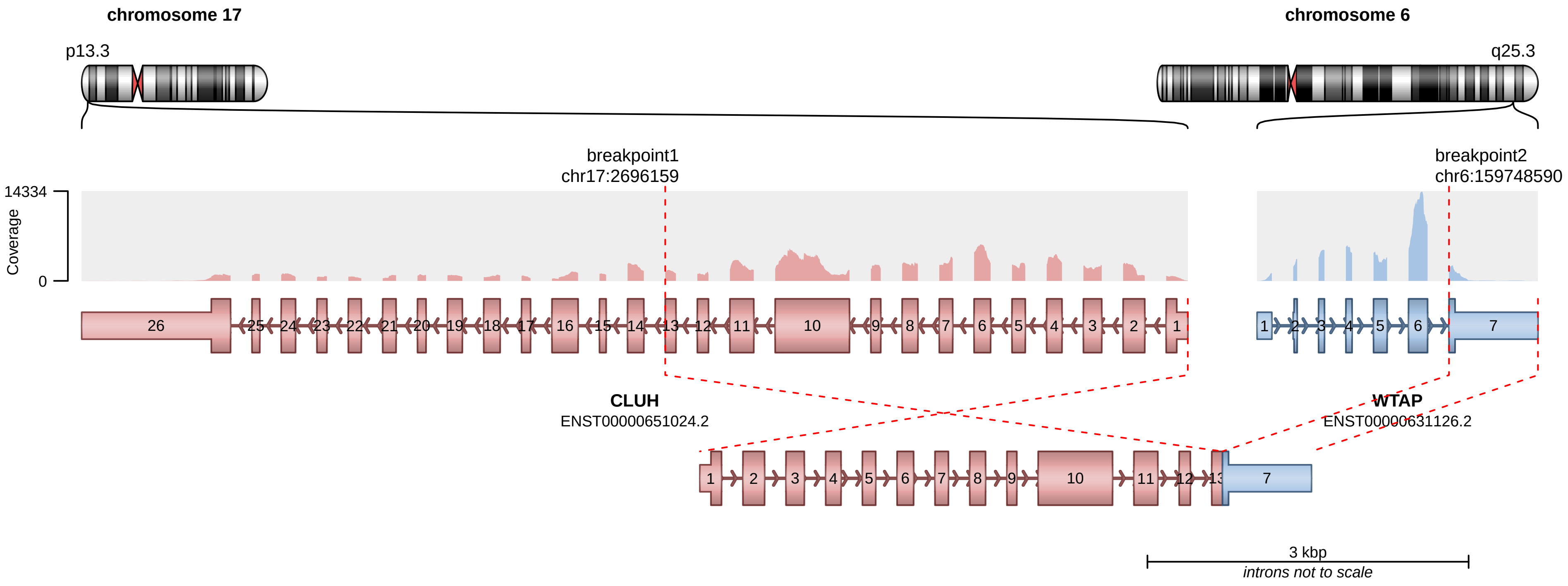


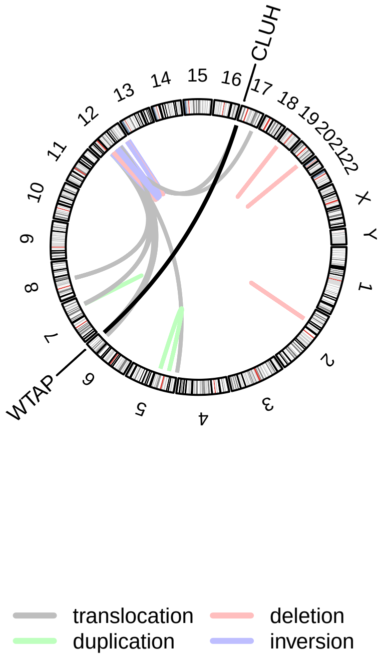




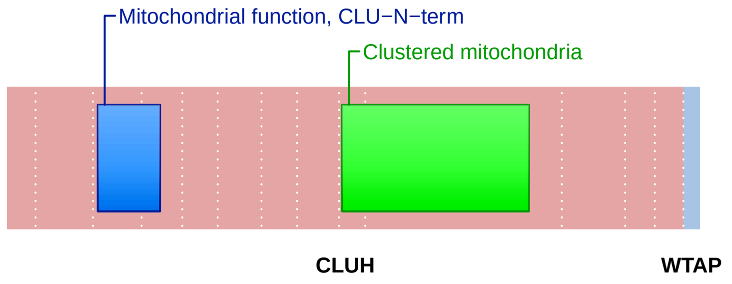
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0



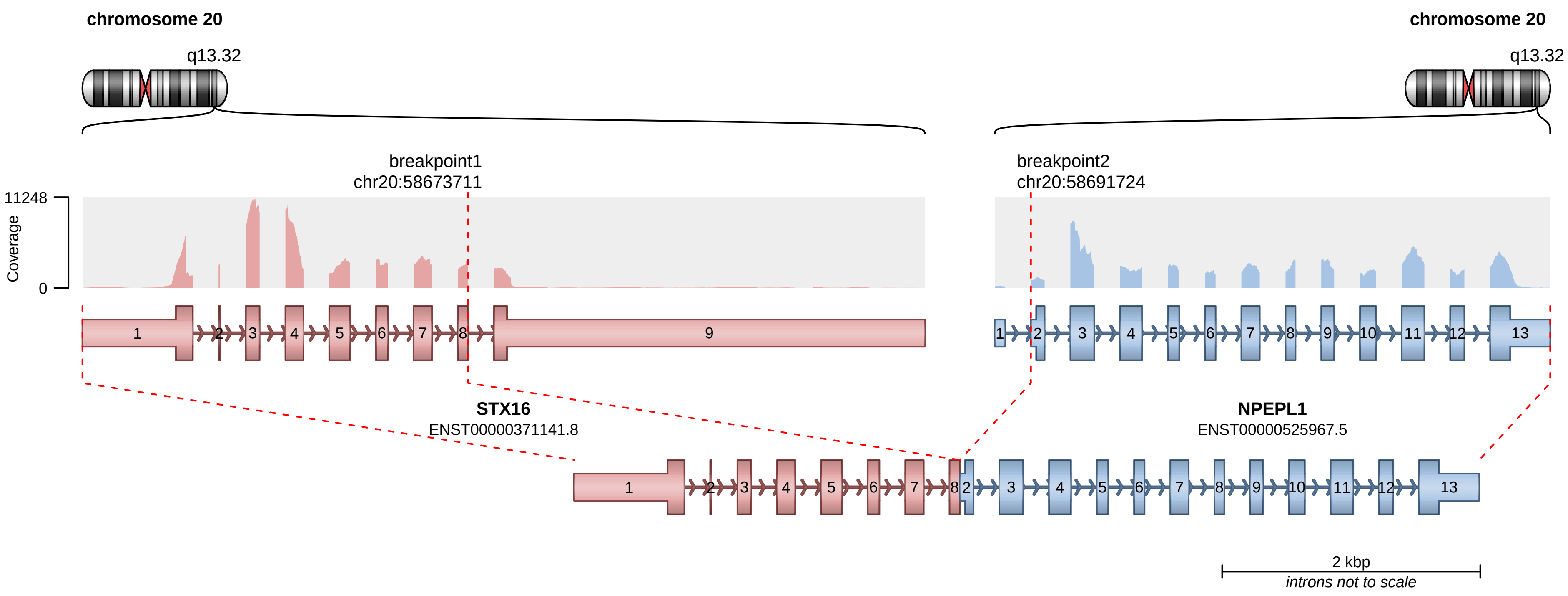


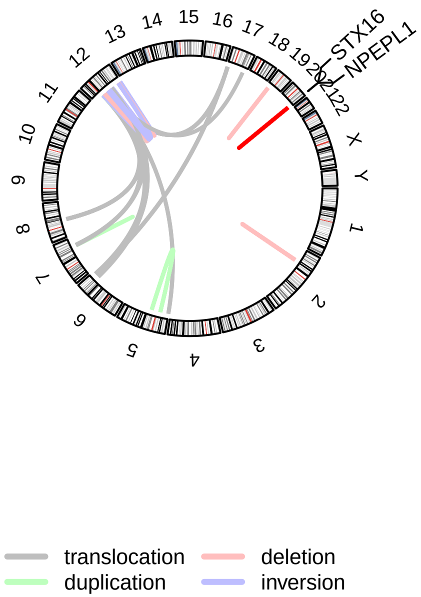
RETAINED PROTEIN DOMAINS
reading frame unclear

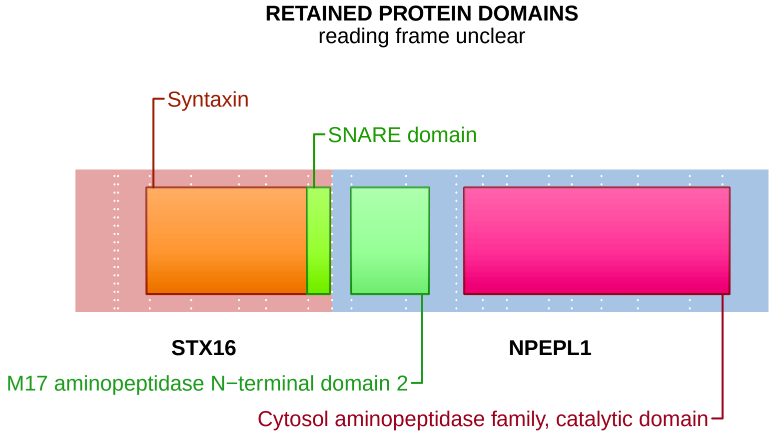


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

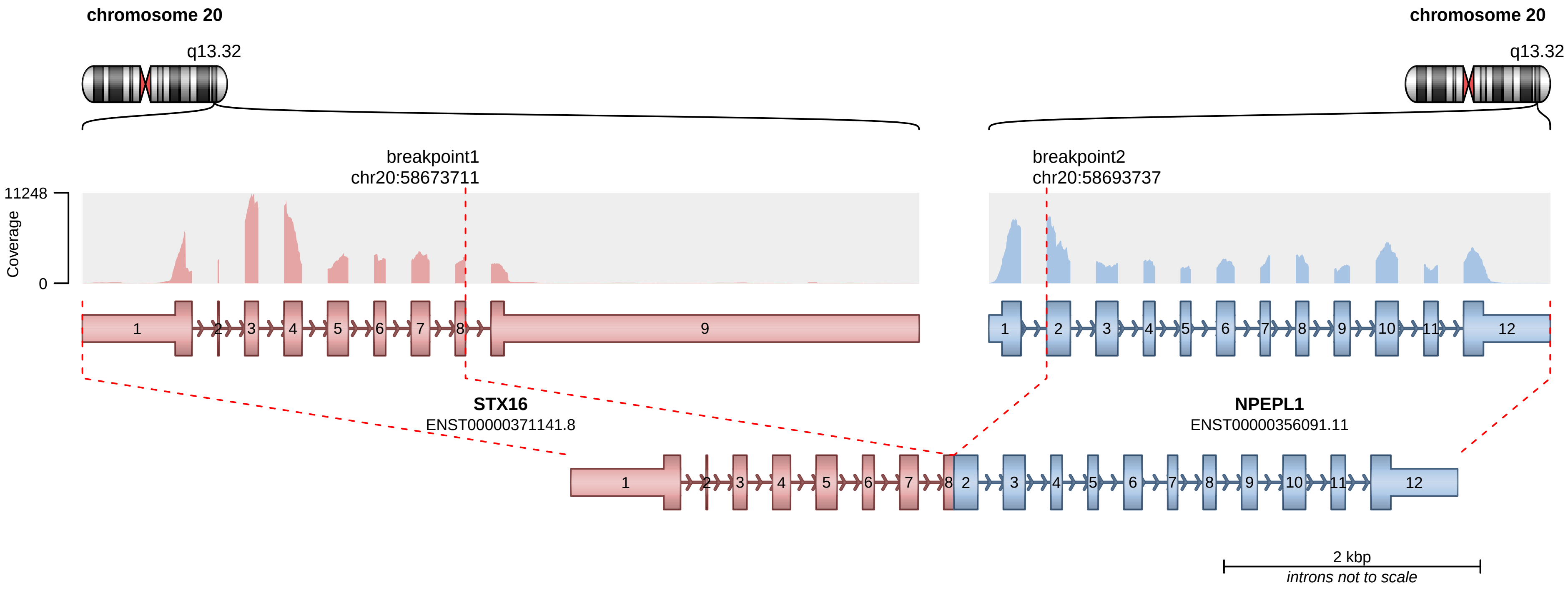


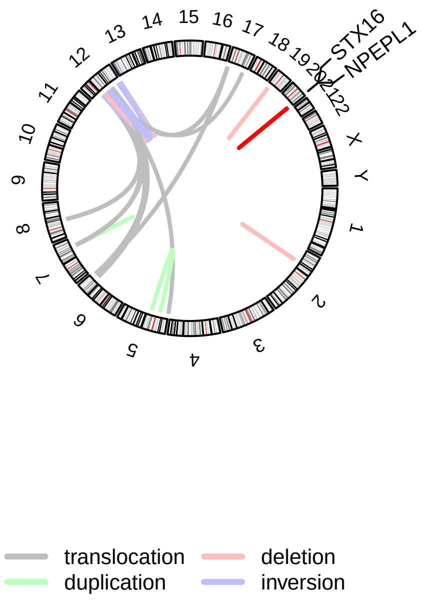


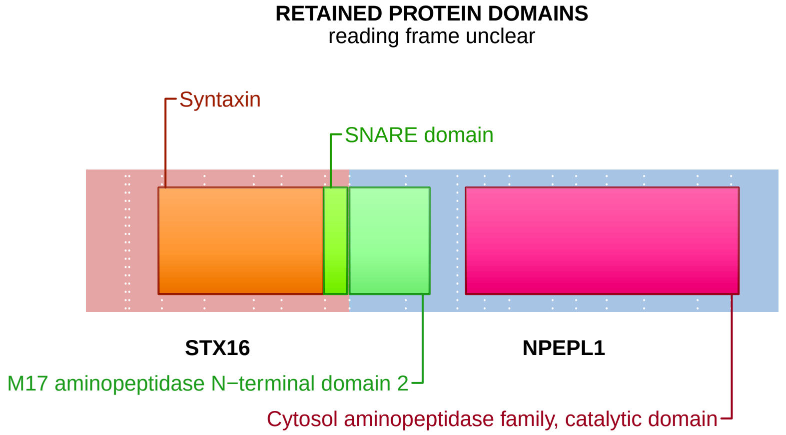


SUPPORTING READ COUNT

Split reads = 182
Discordant mates = 4

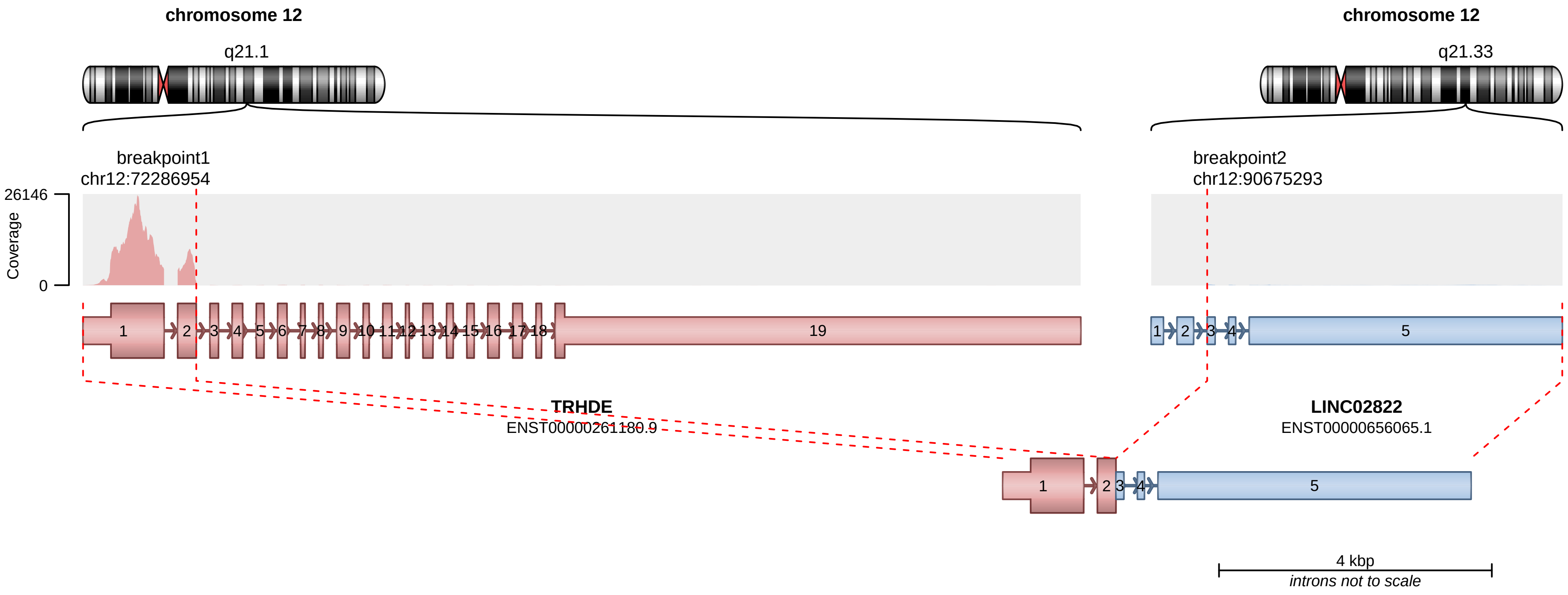


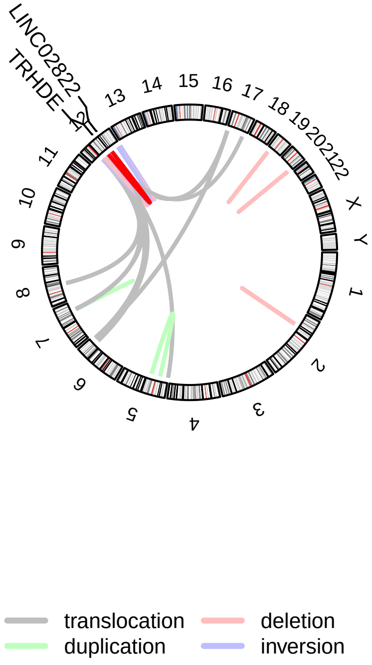


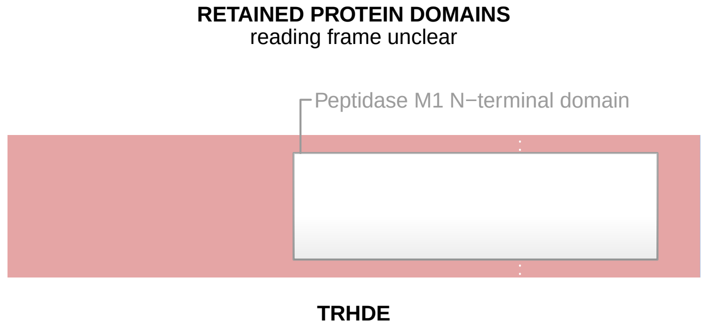


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

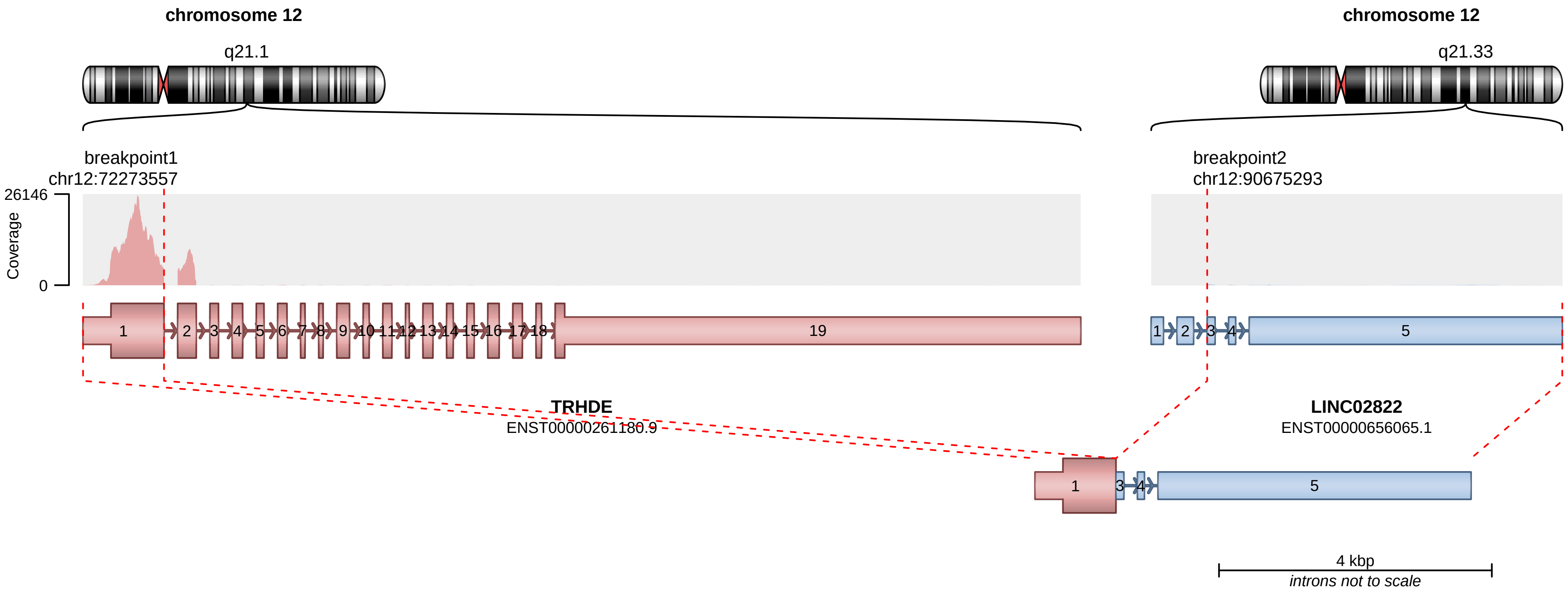


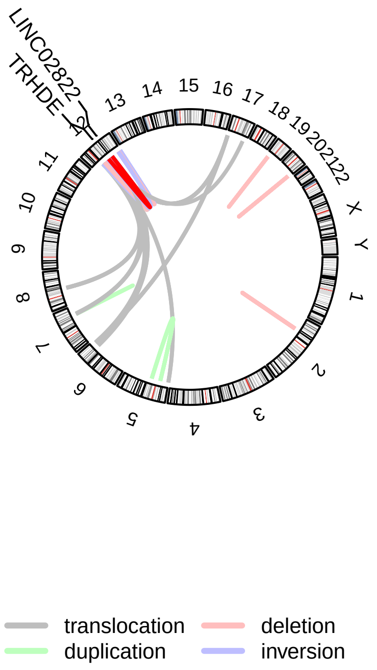




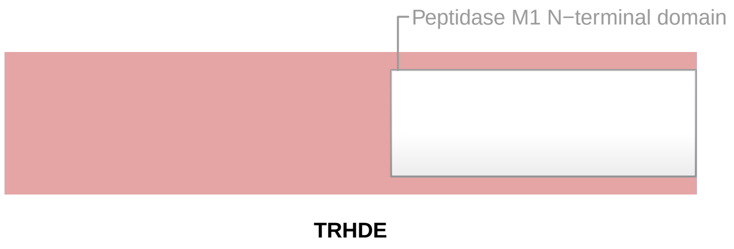
SUPPORTING READ COUNT

Split reads = 178
Discordant mates = 4



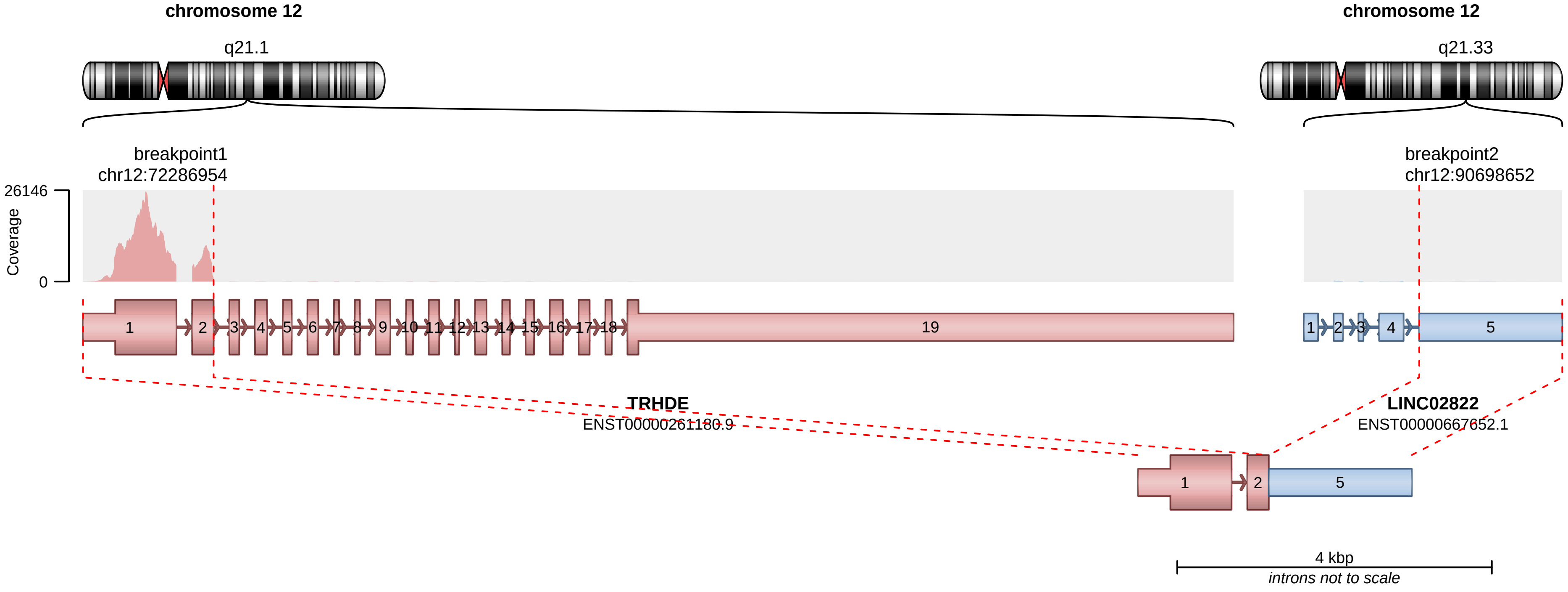


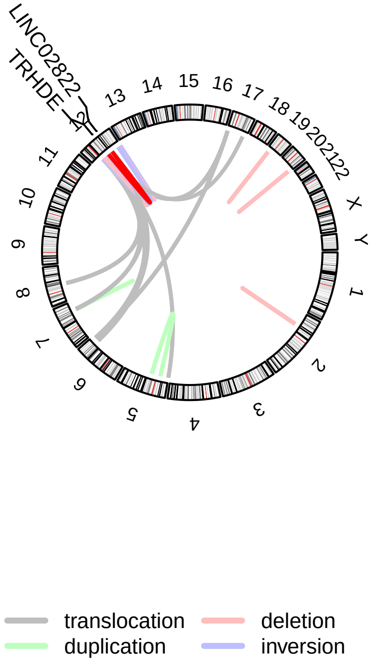
RETAINED PROTEIN DOMAINS
reading frame unclear

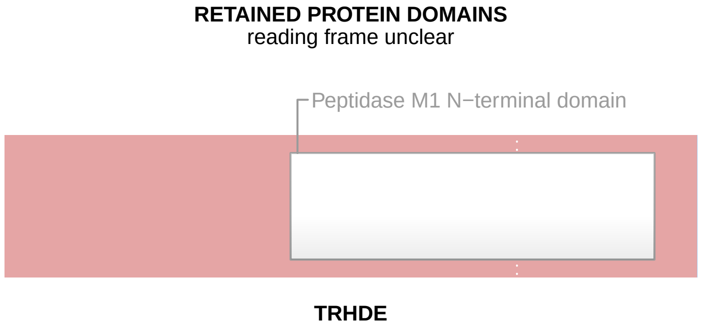


SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 0

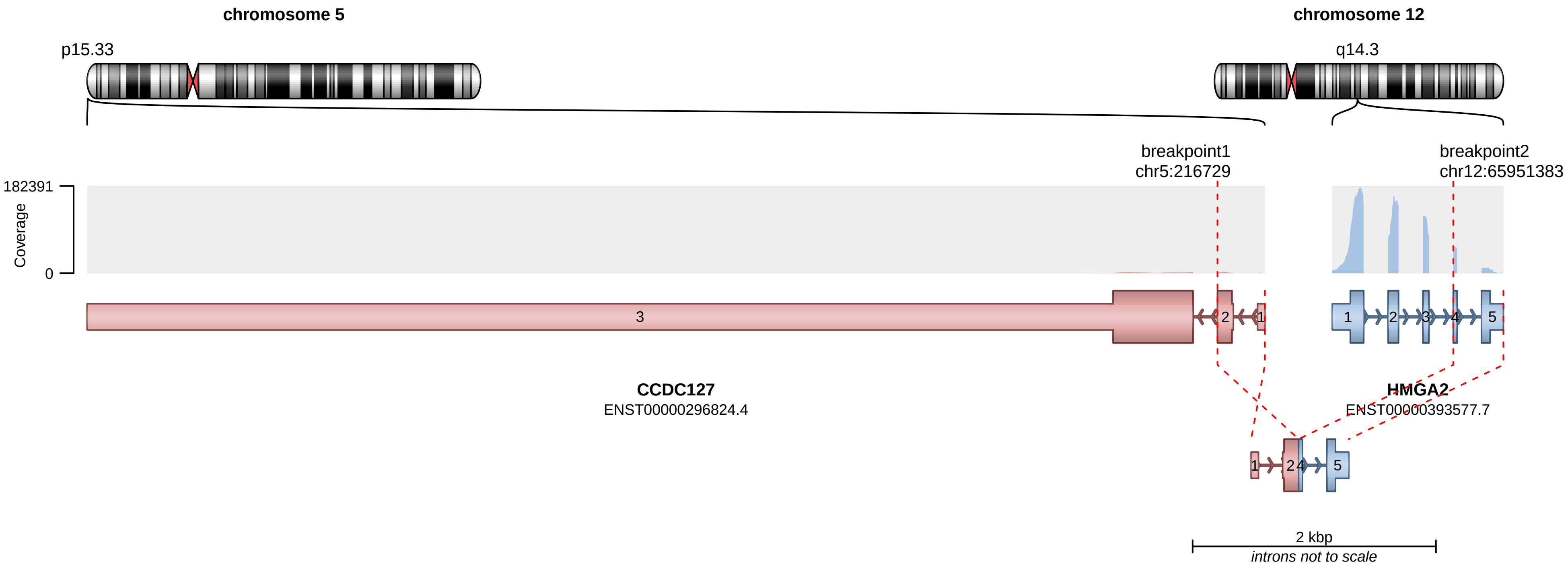


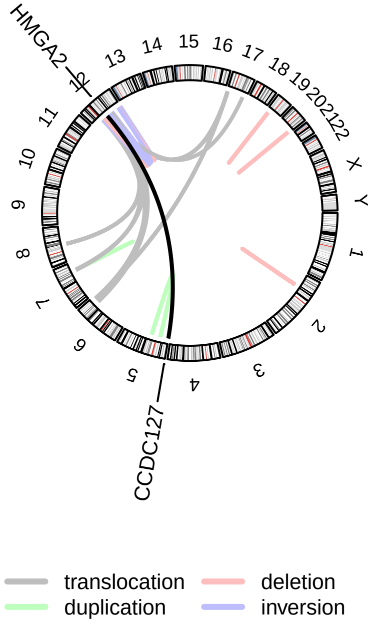


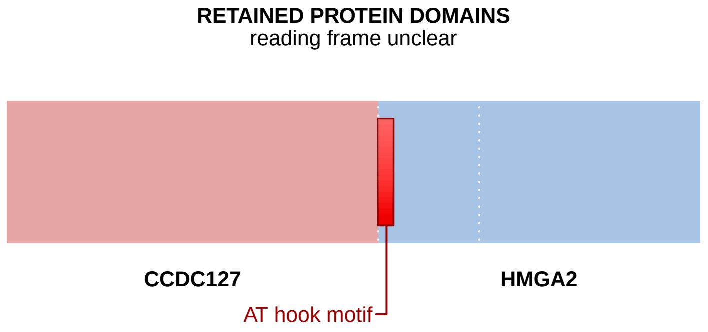

RETAINED PROTEIN DOMAINS
reading frame unclear

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

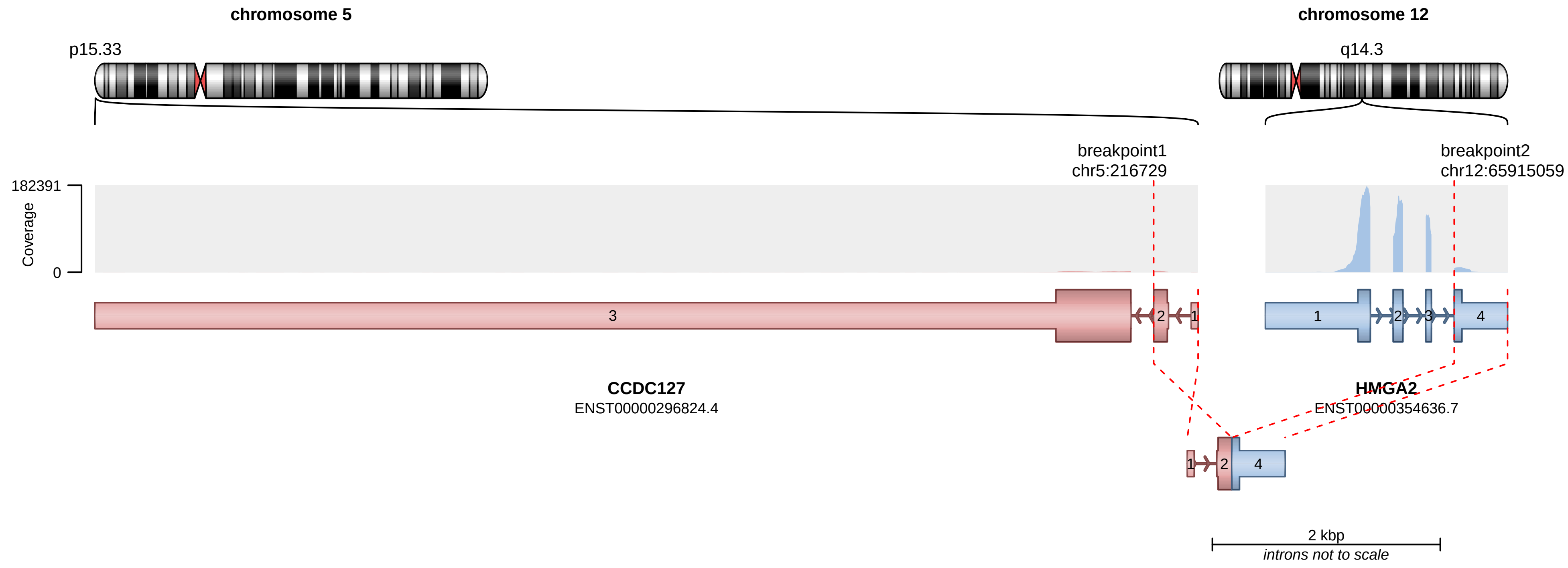


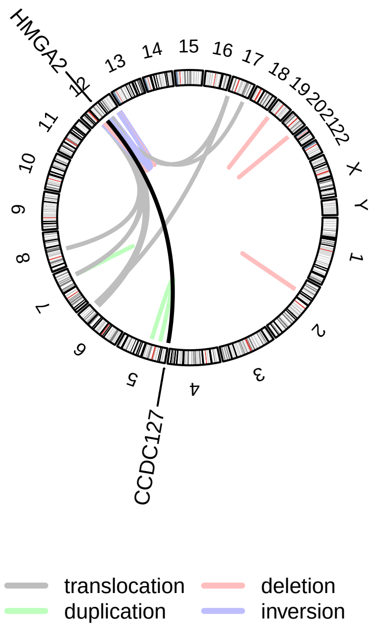




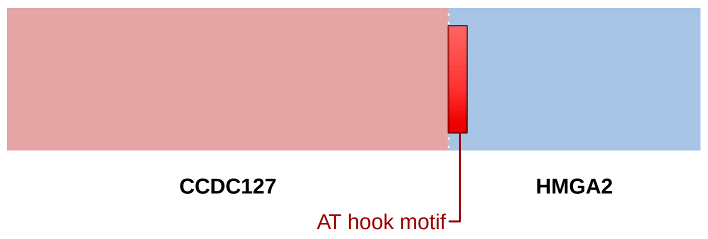
SUPPORTING READ COUNT

Split reads = 177
Discordant mates = 0



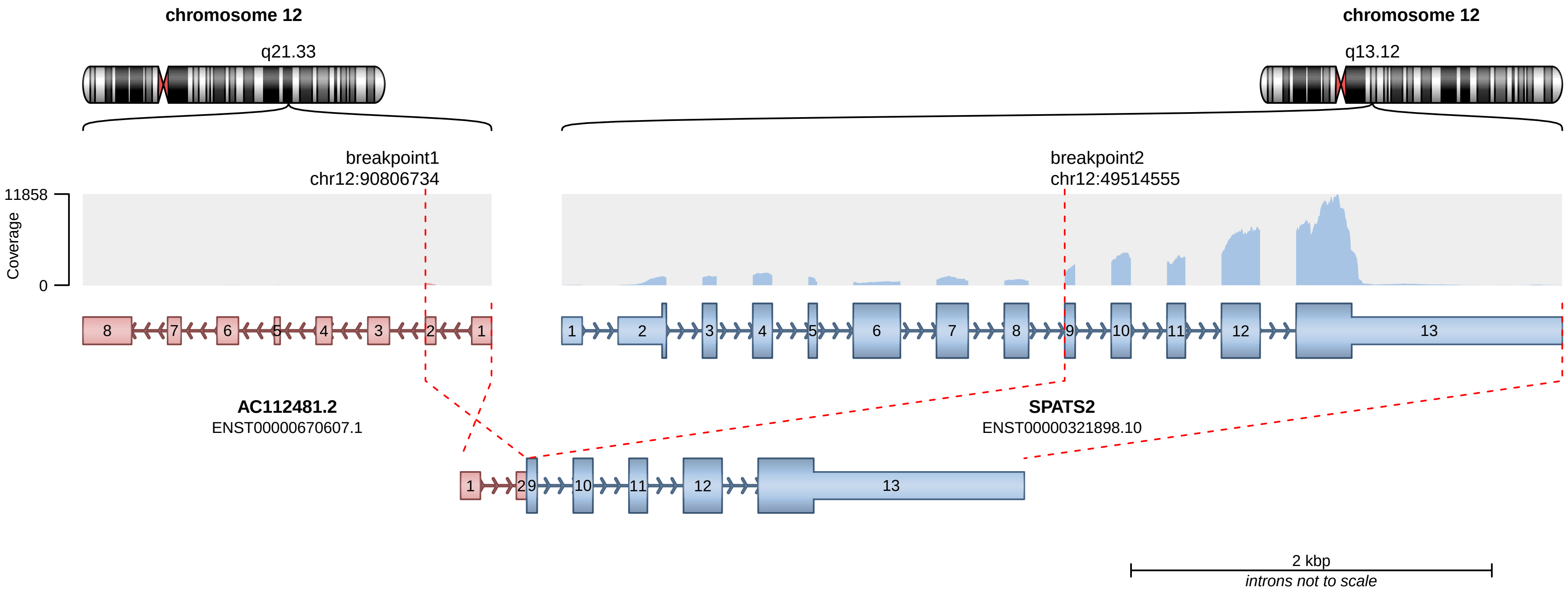


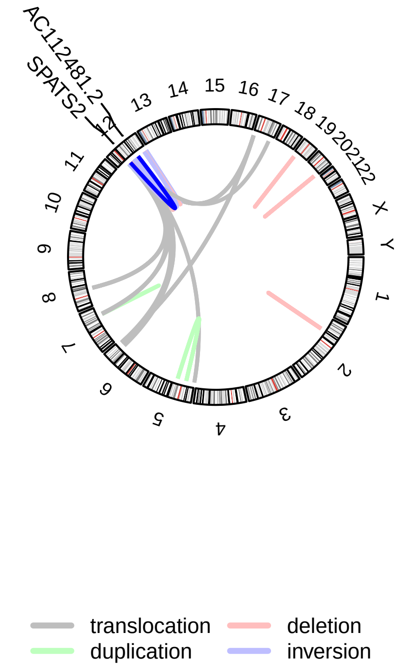
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

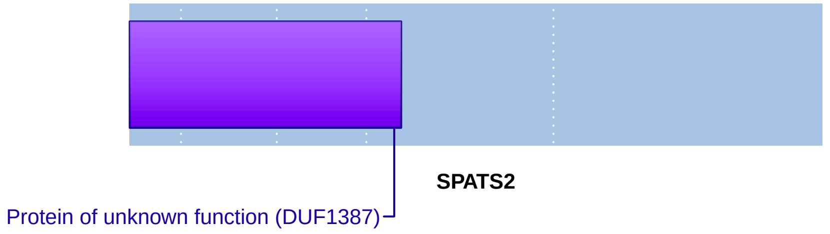
Split reads = 1
Discordant mates = 0





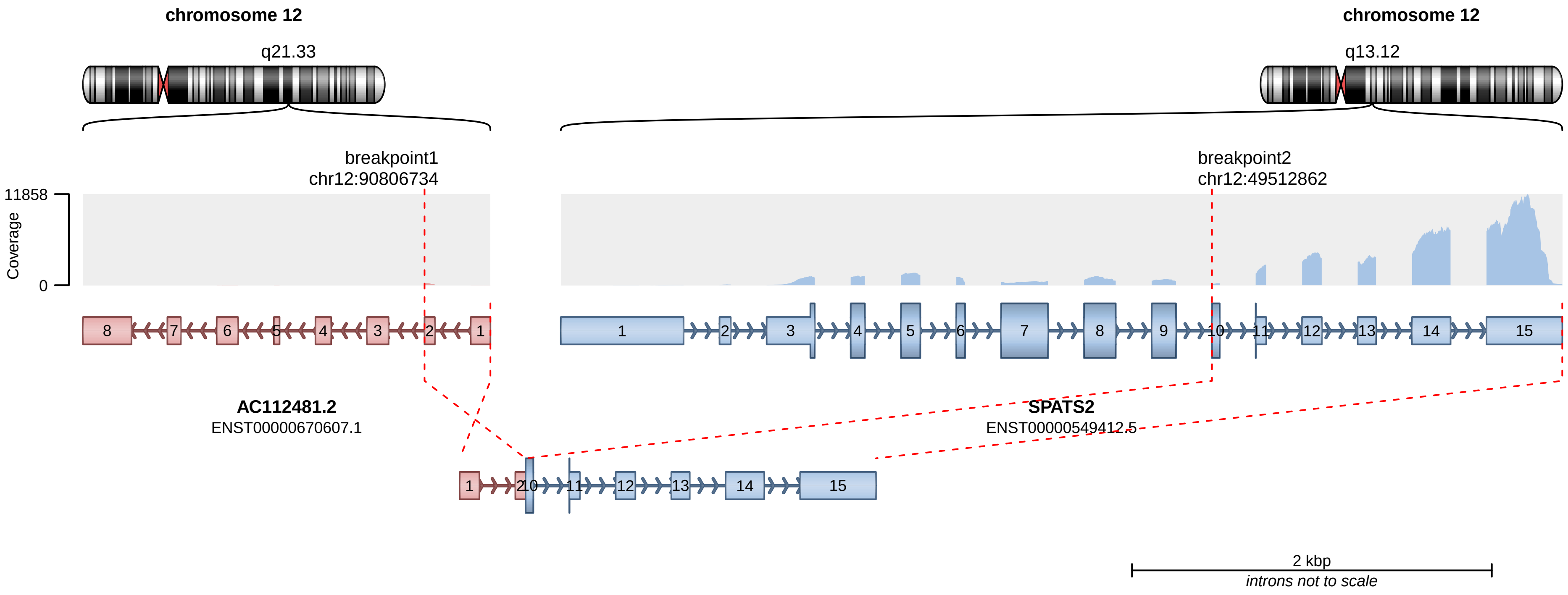
RETAINED PROTEIN DOMAINS

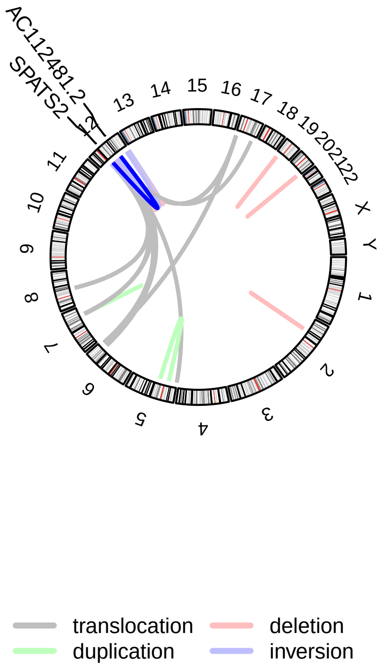
reading frame unclear

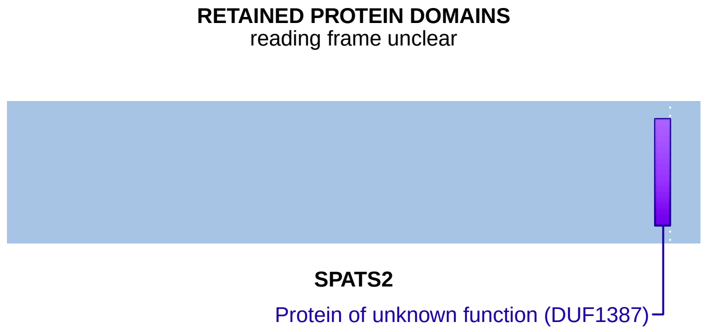


SUPPORTING READ COUNT

Split reads = 167
Discordant mates = 0

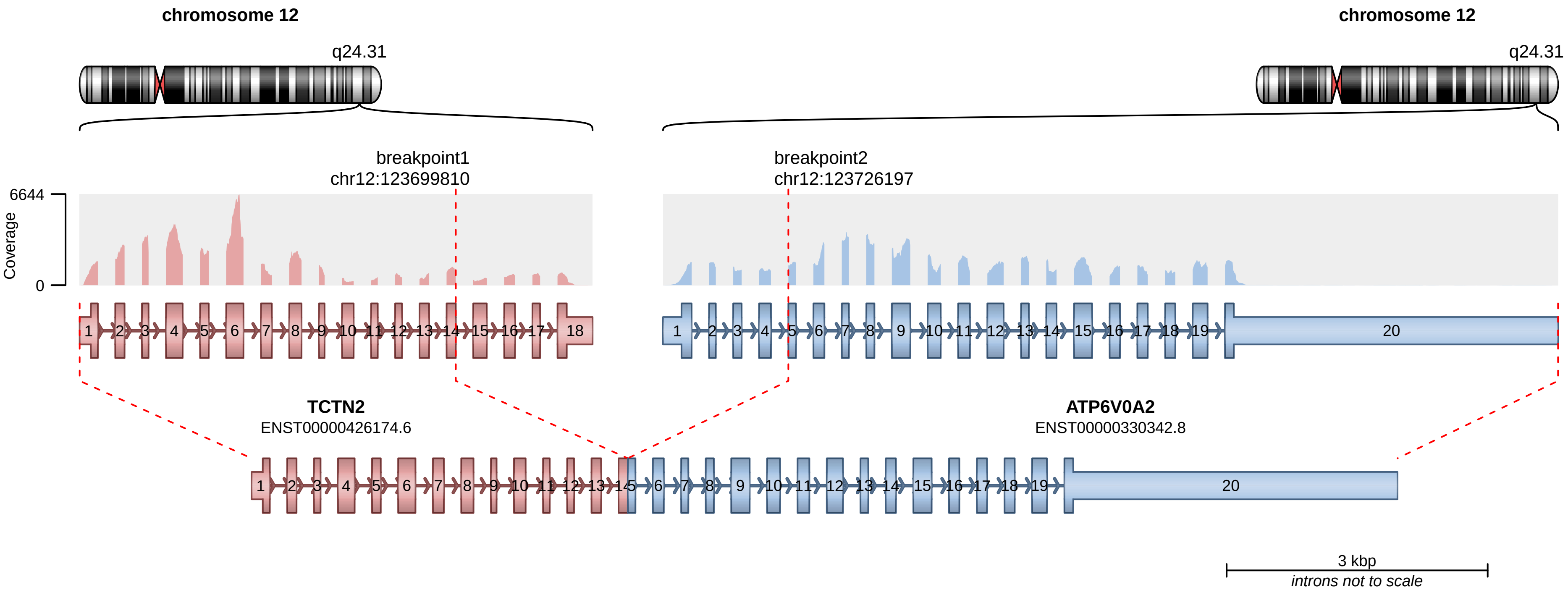


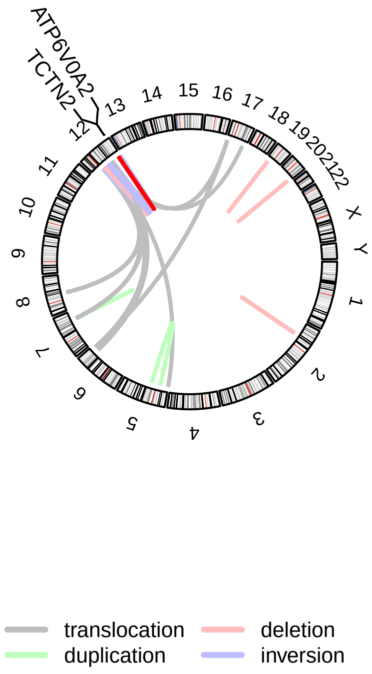


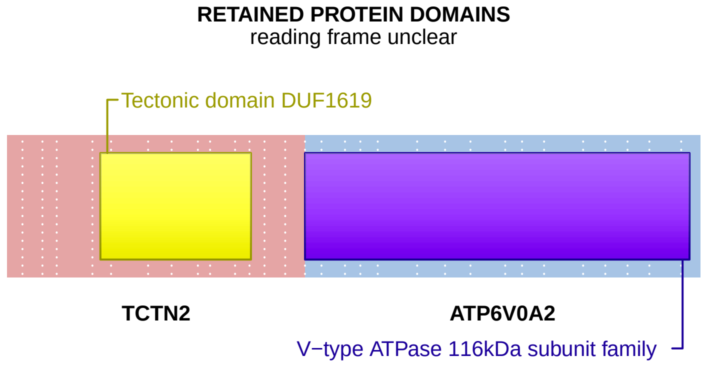


SUPPORTING READ COUNT

Split reads = 30
Discordant mates = 0

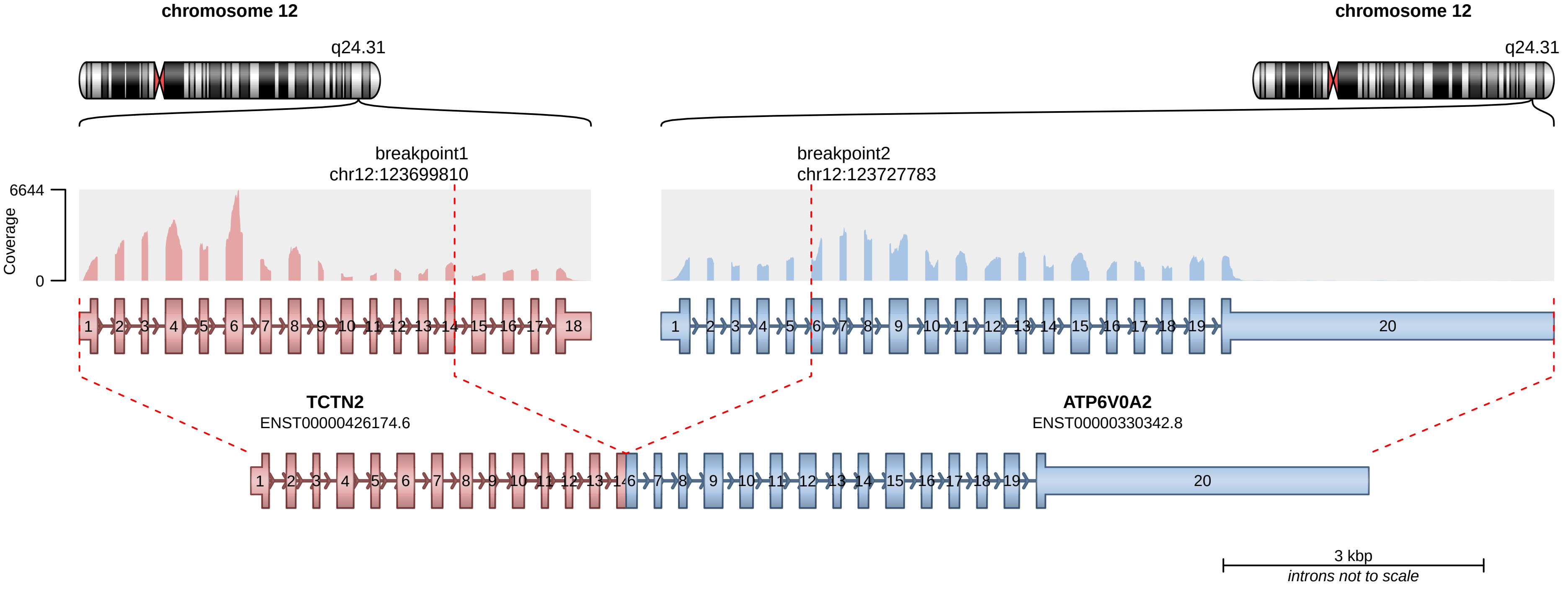


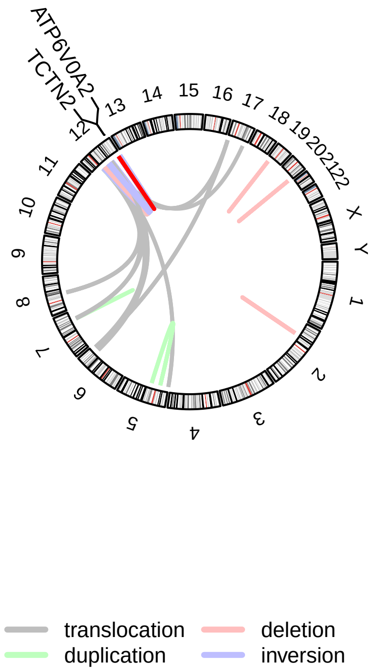


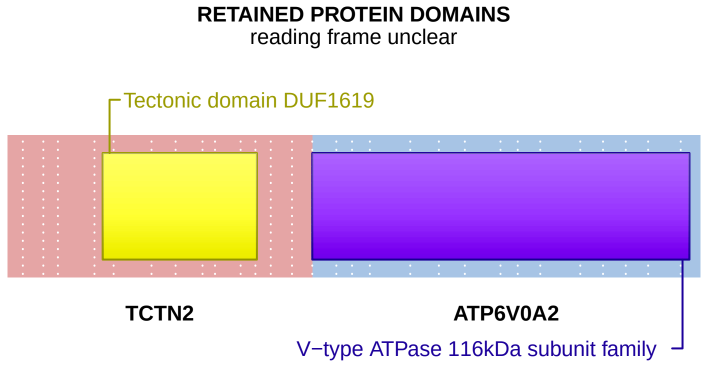


SUPPORTING READ COUNT

Split reads = 159
Discordant mates = 0

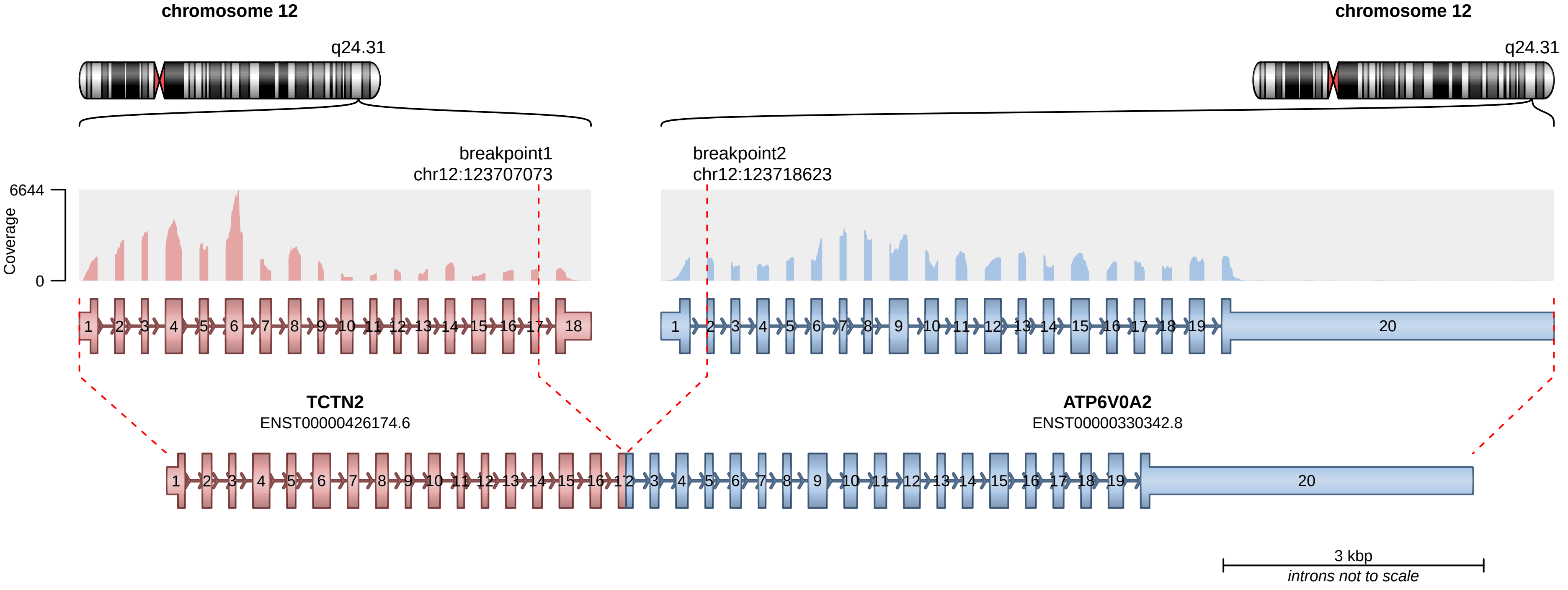


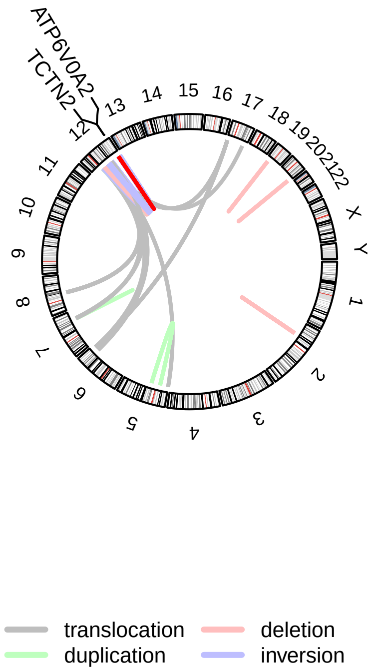


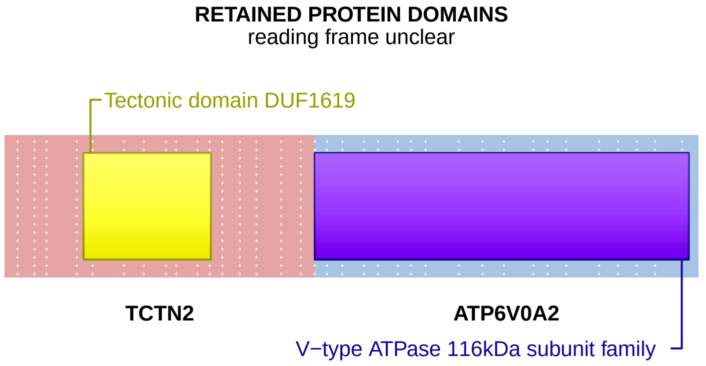


SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 0

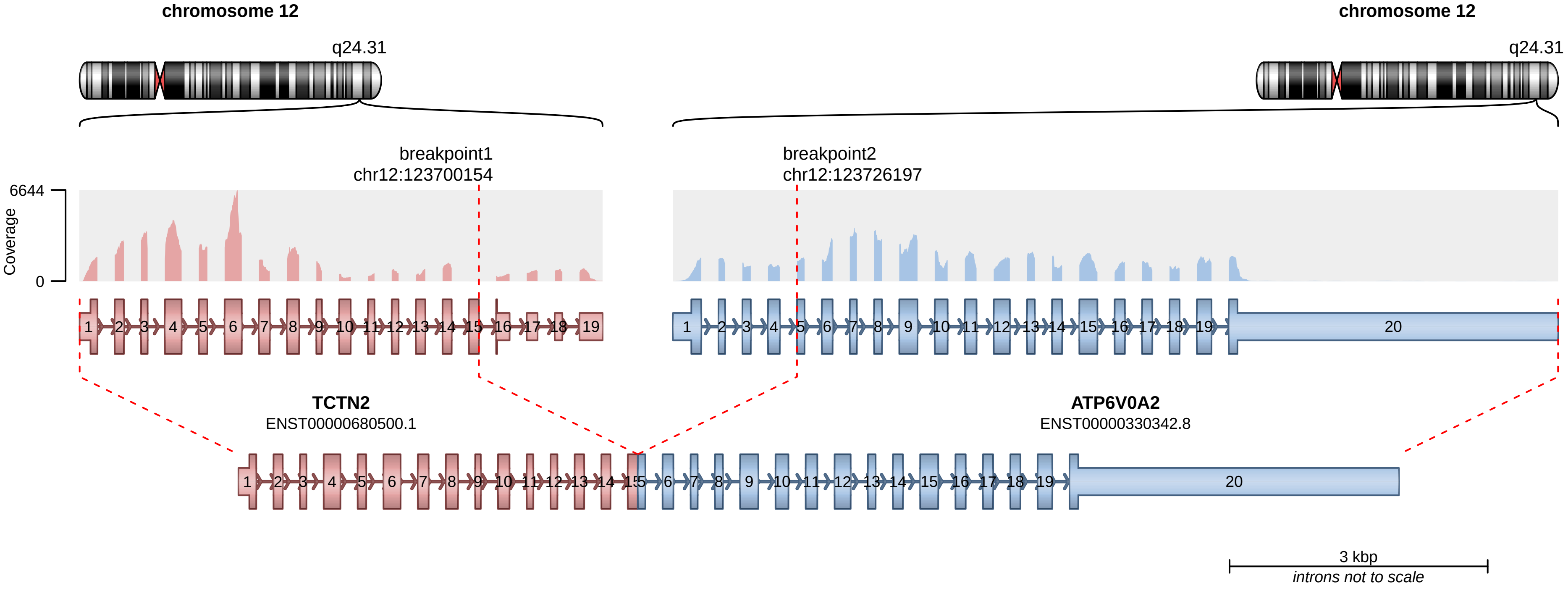


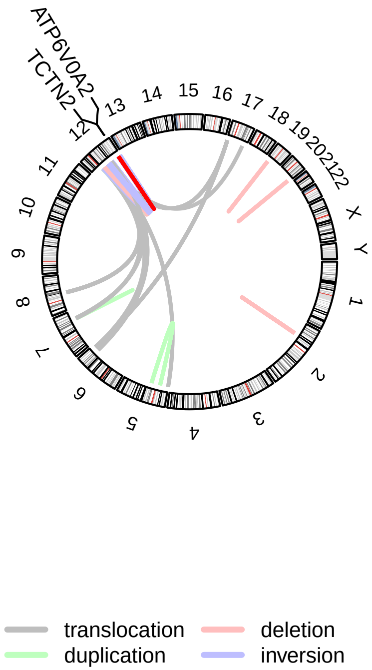


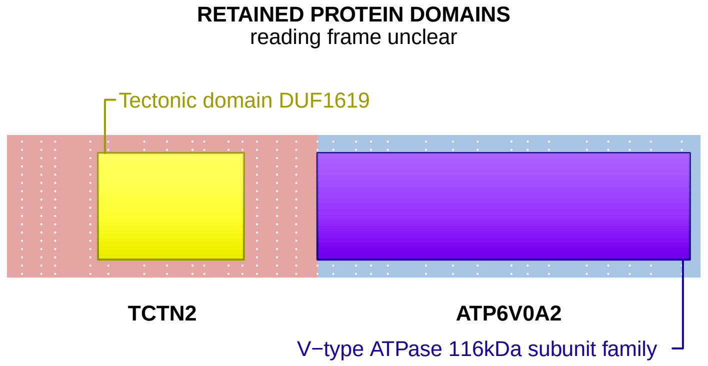


SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 0

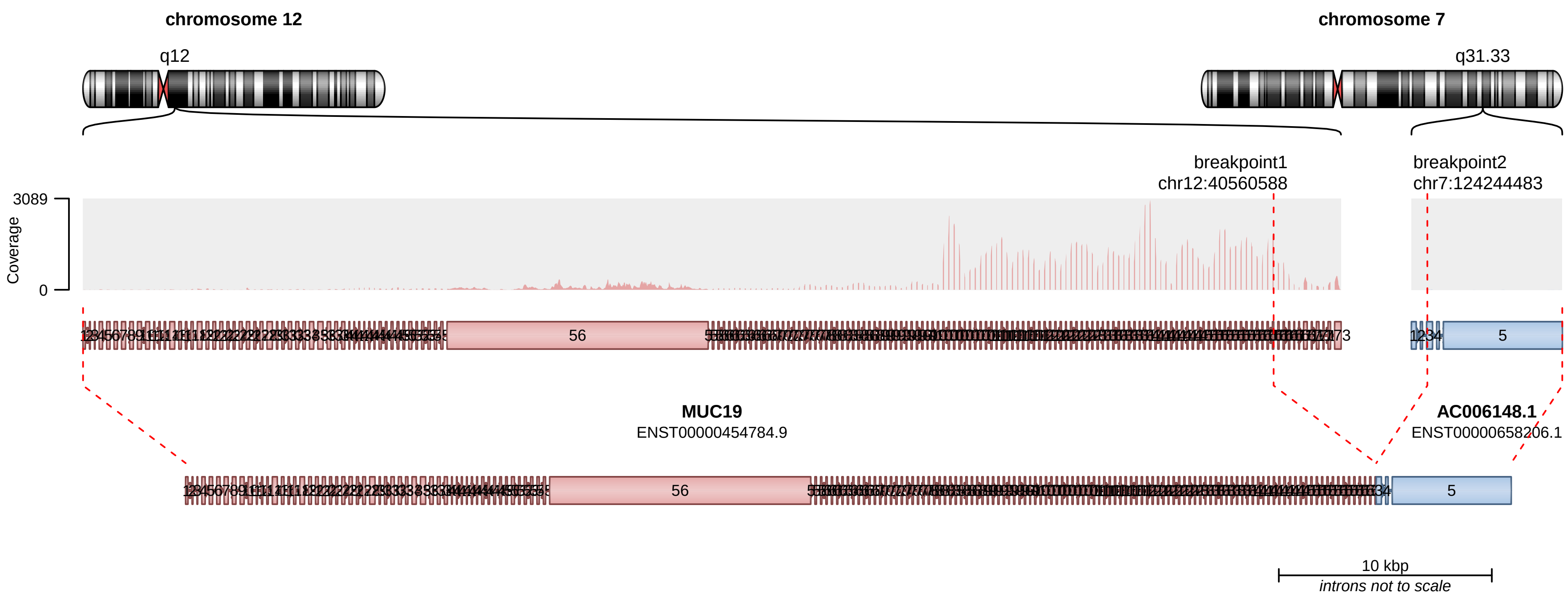


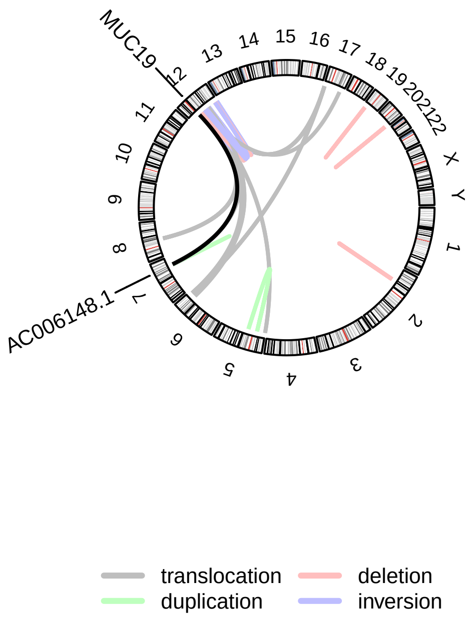




SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

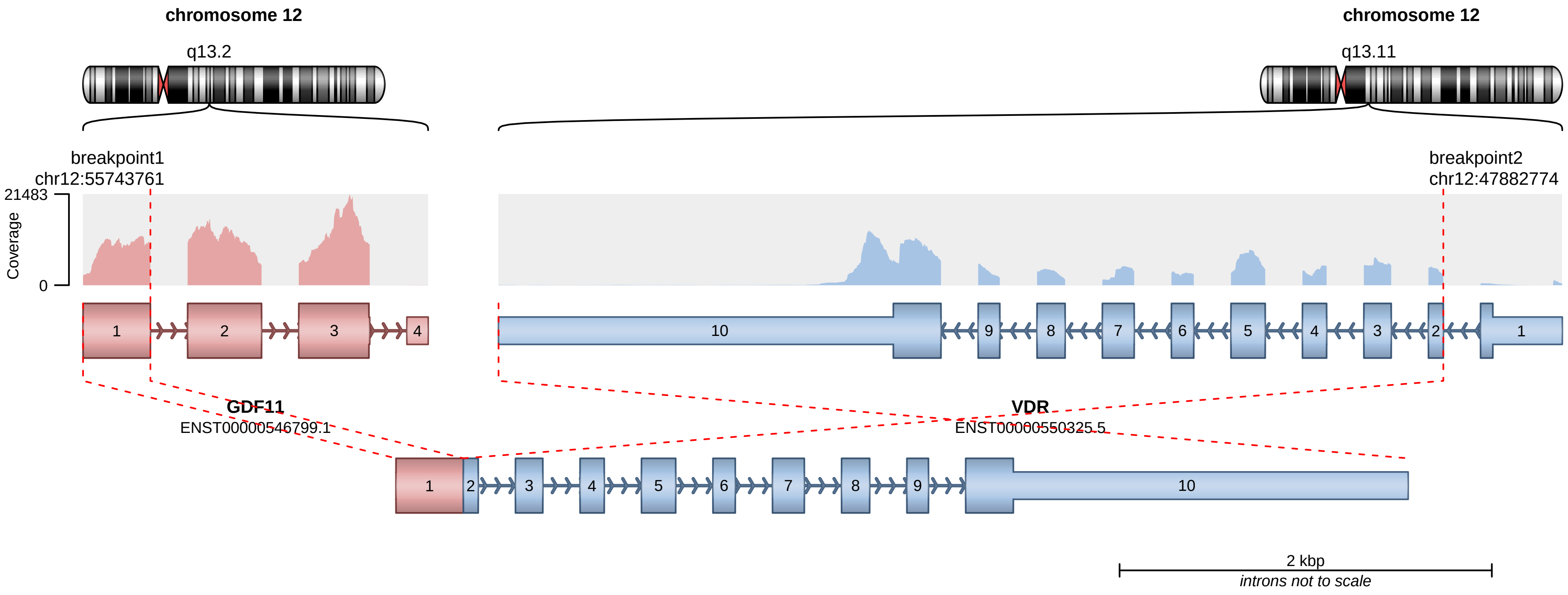


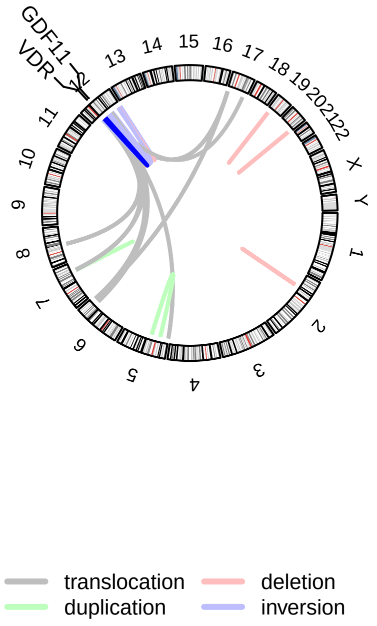


Genes are not protein−coding.

SUPPORTING READ COUNT

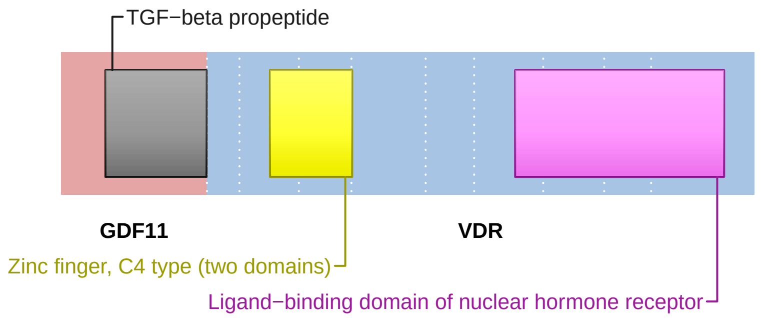
Split reads = 152
Discordant mates = 0





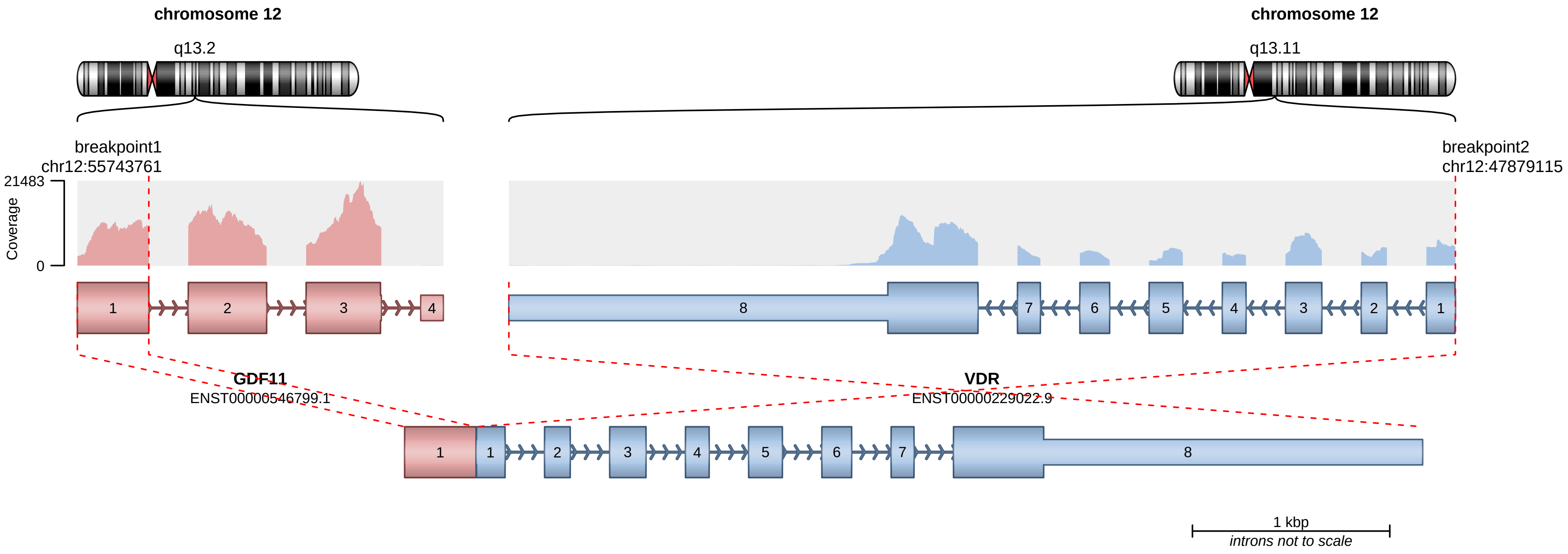
RETAINED PROTEIN DOMAINS

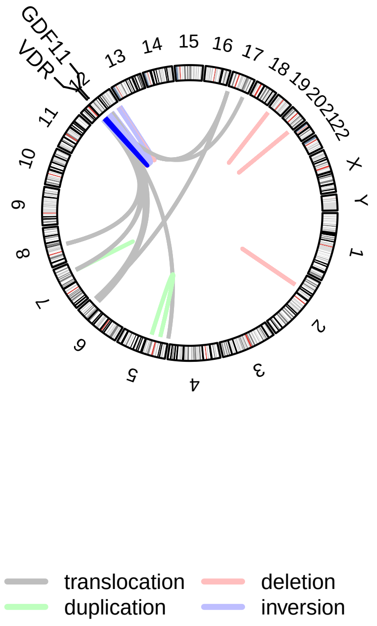
reading frame unclear



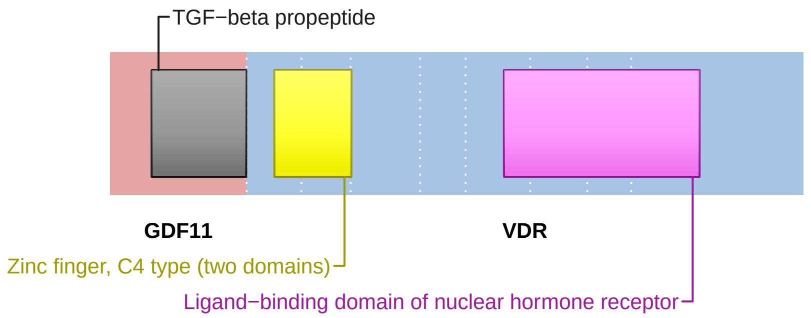
SUPPORTING READ COUNT

Split reads = 129
Discordant mates = 1



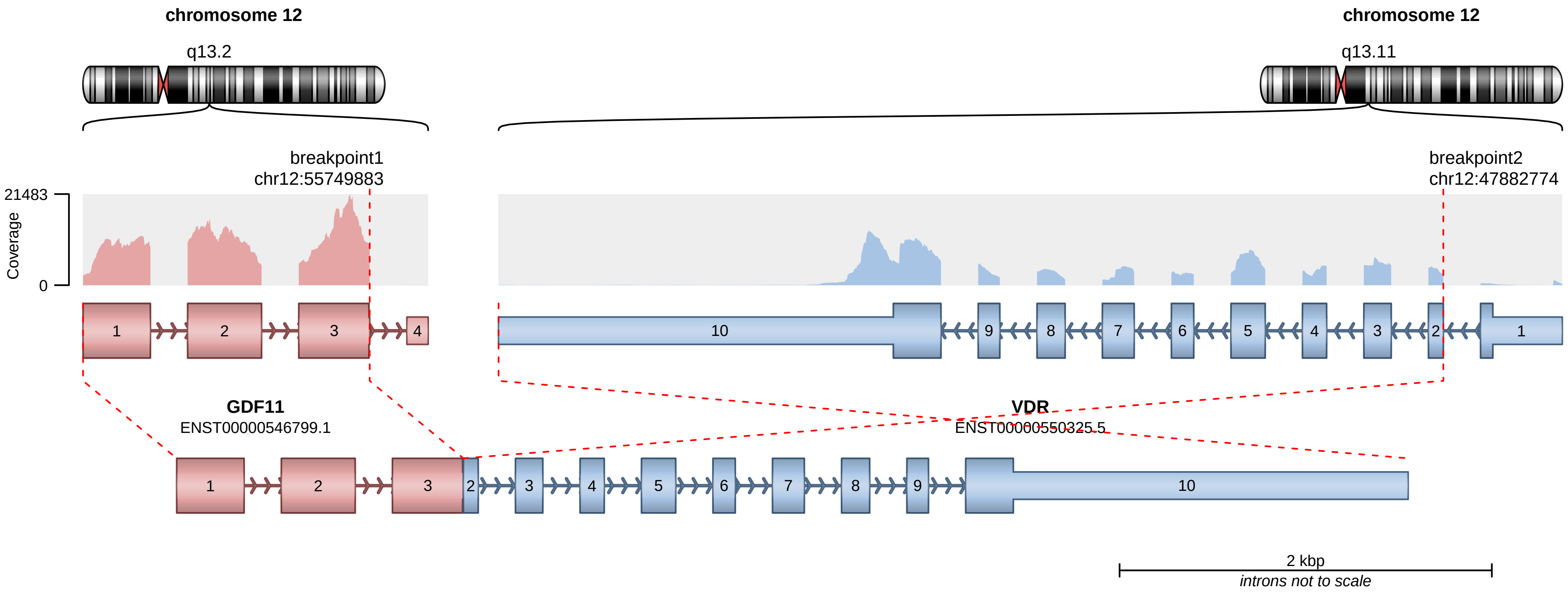


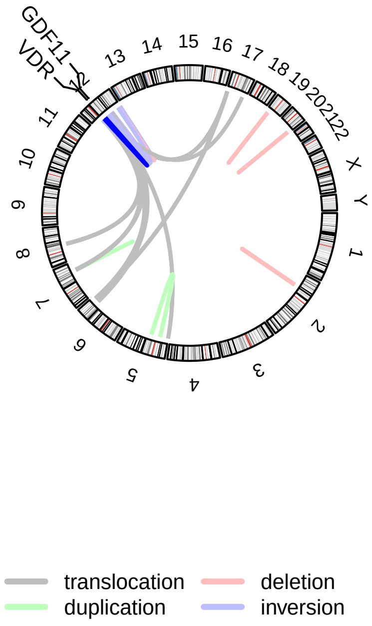
RETAINED PROTEIN DOMAINS
reading frame unclear

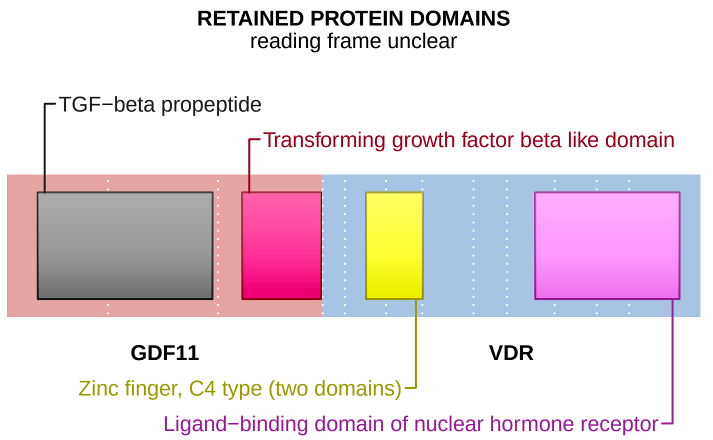


SUPPORTING READ COUNT

Split reads = 25
Discordant mates = 0

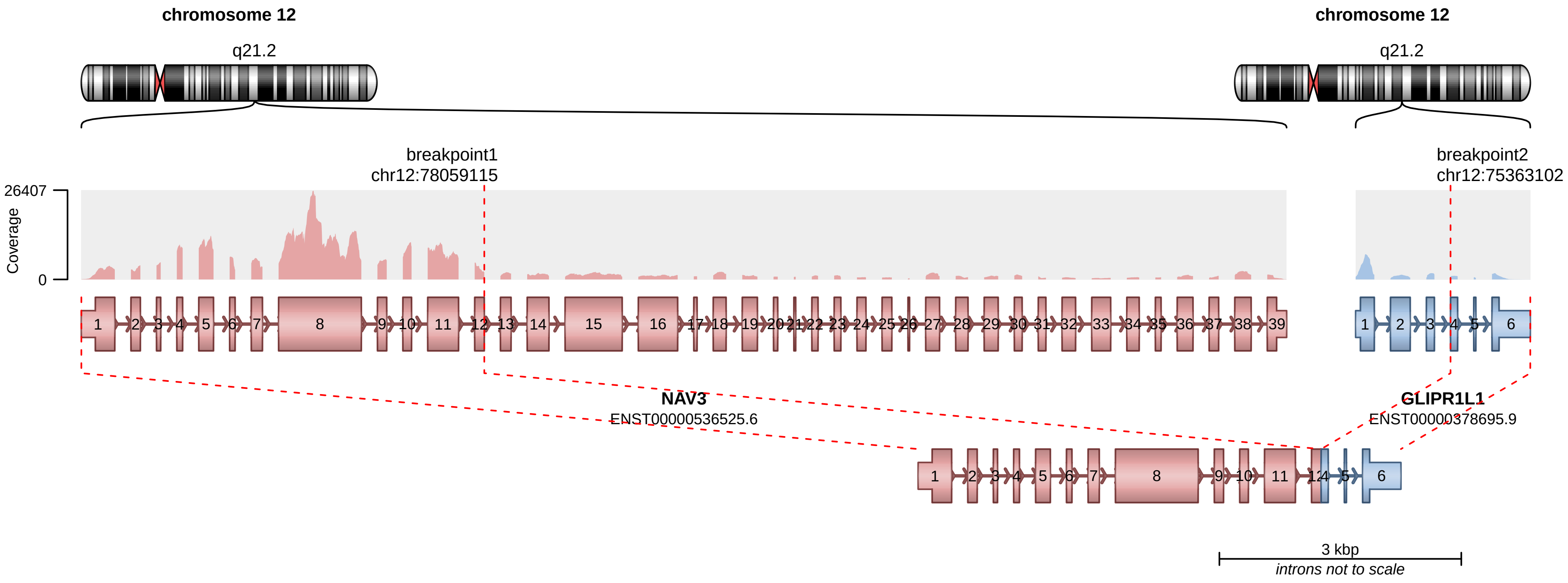


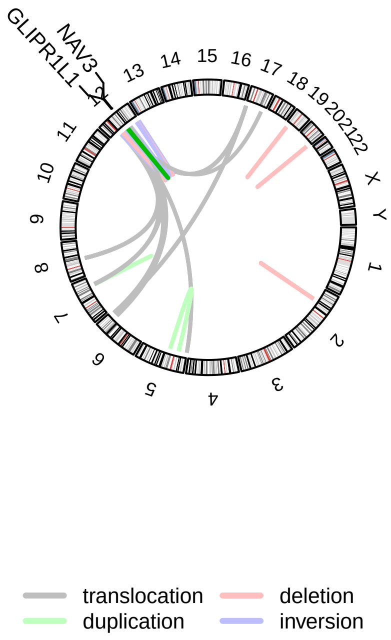




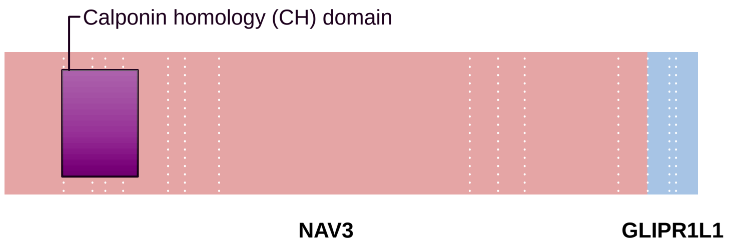
SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 1



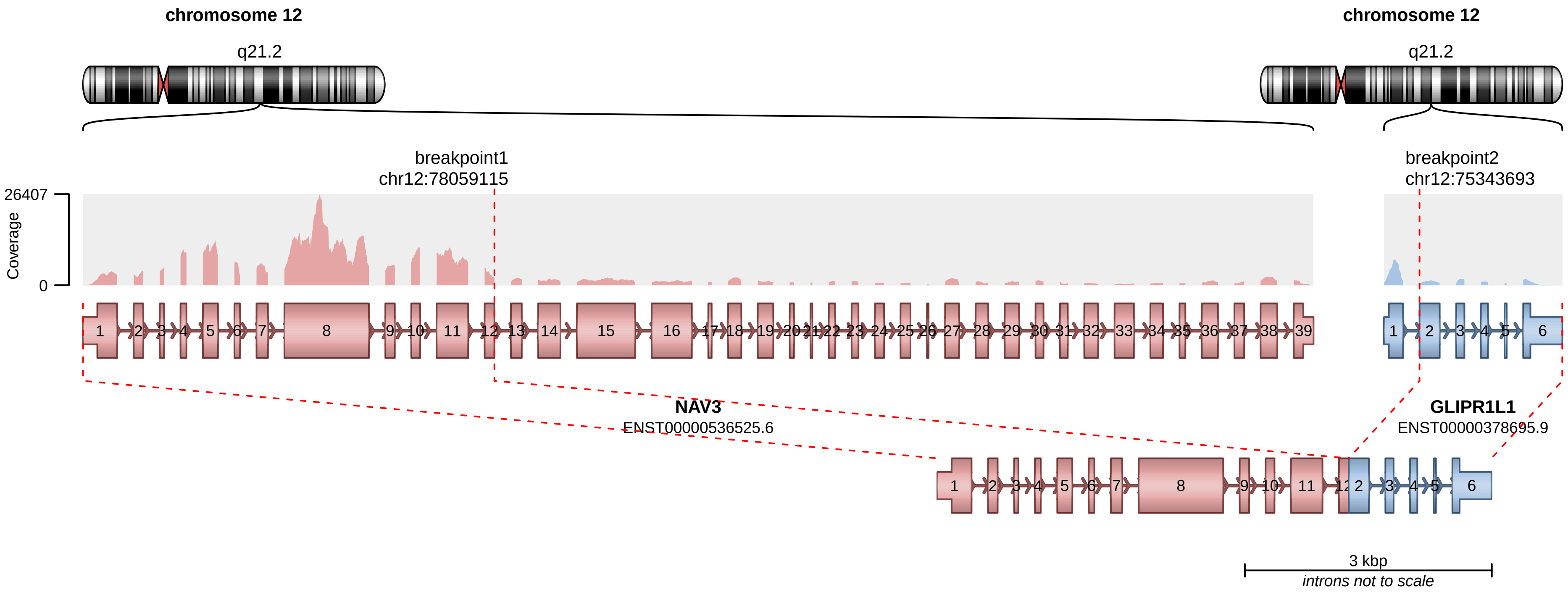


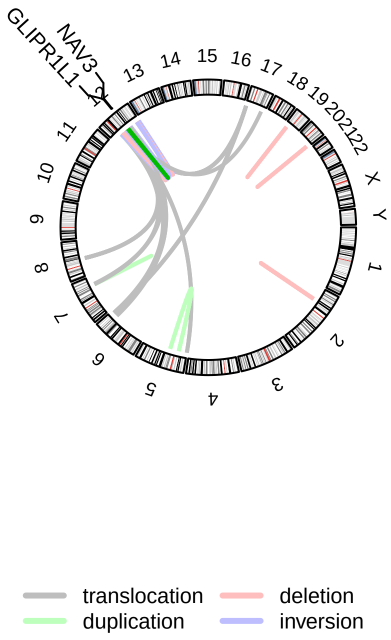
RETAINED PROTEIN DOMAINS
reading frame unclear

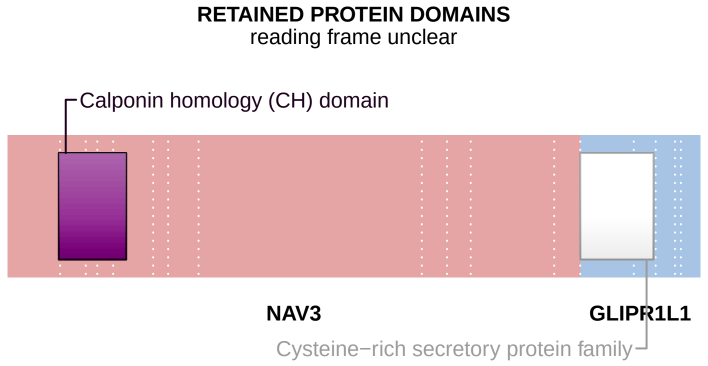


SUPPORTING READ COUNT

Split reads = 118
Discordant mates = 1

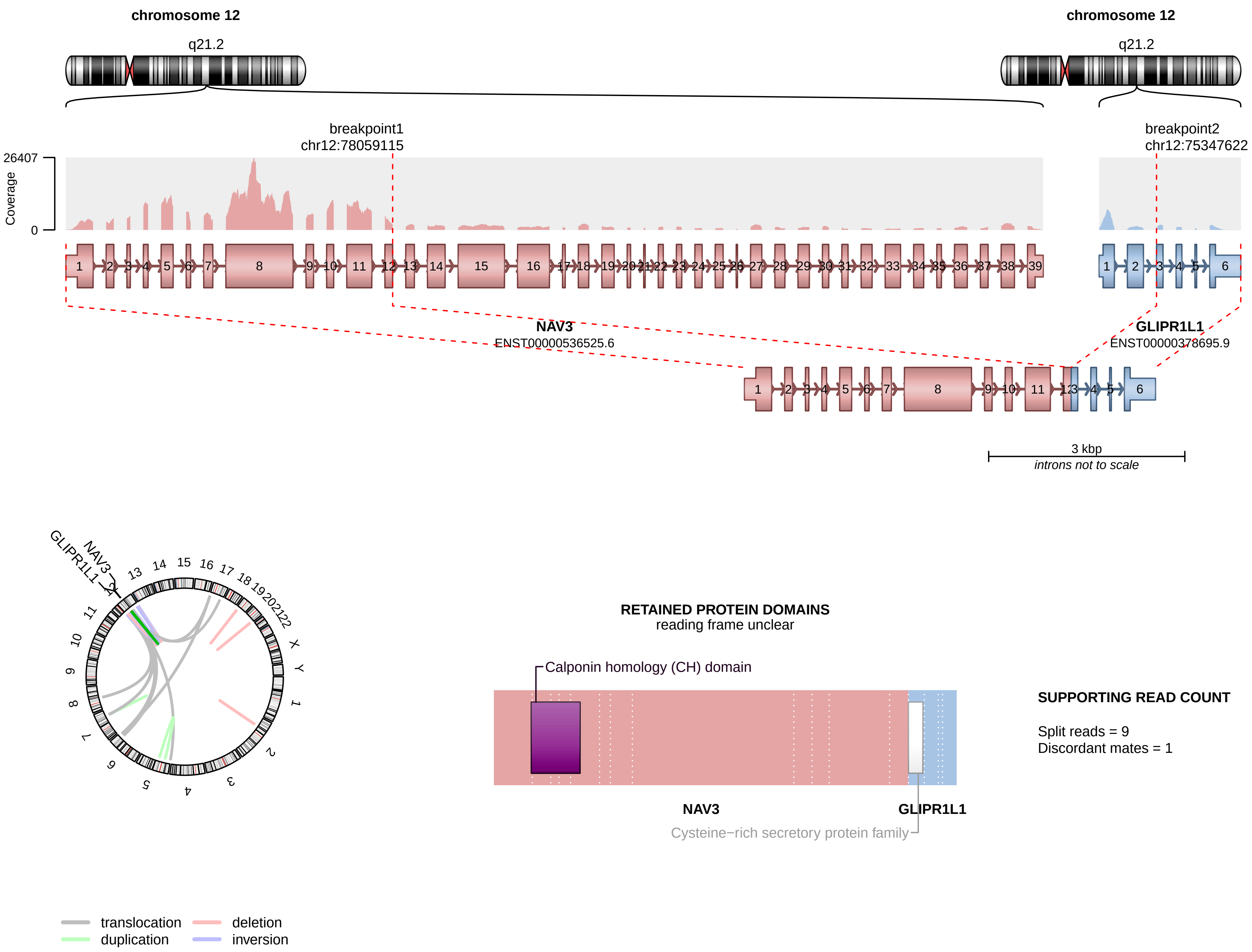


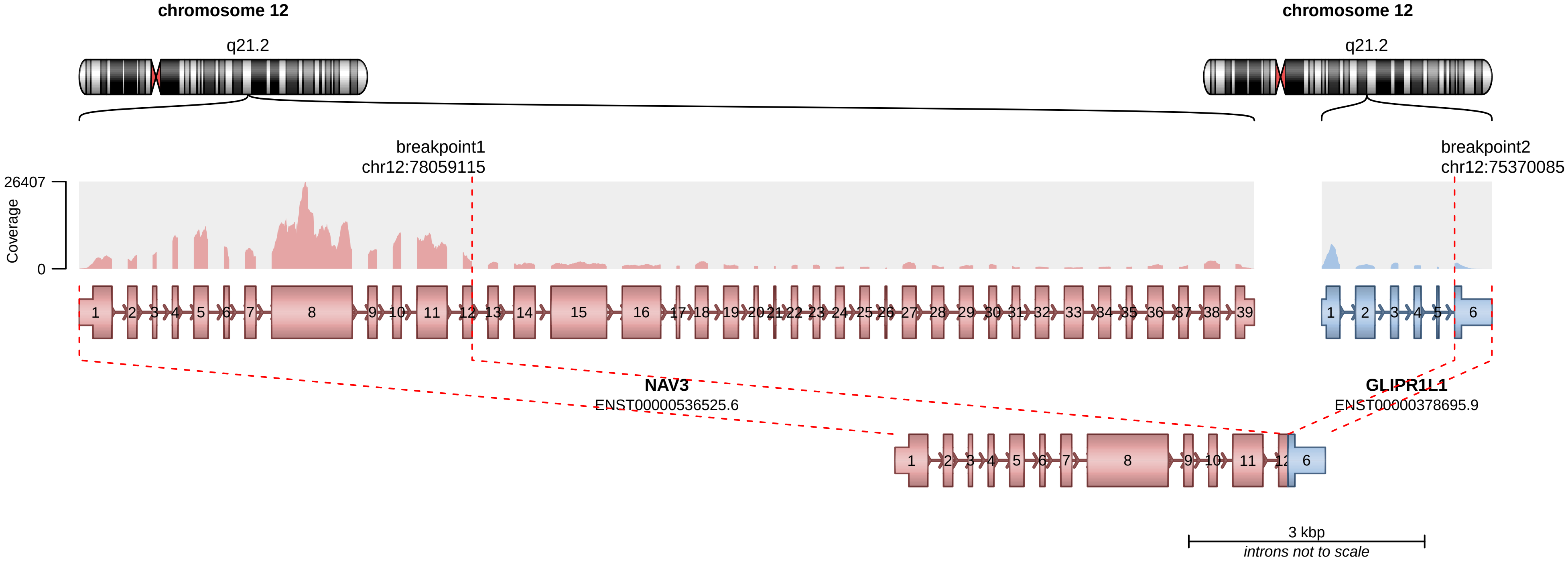


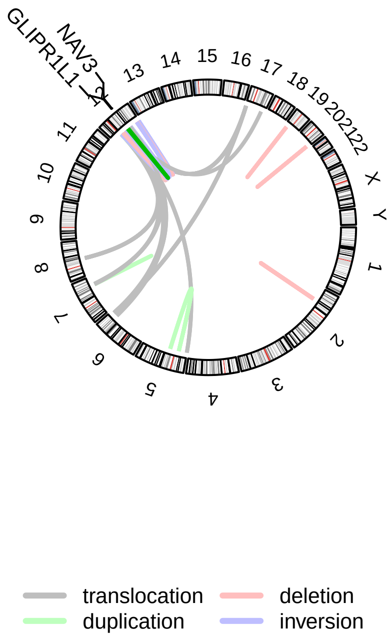


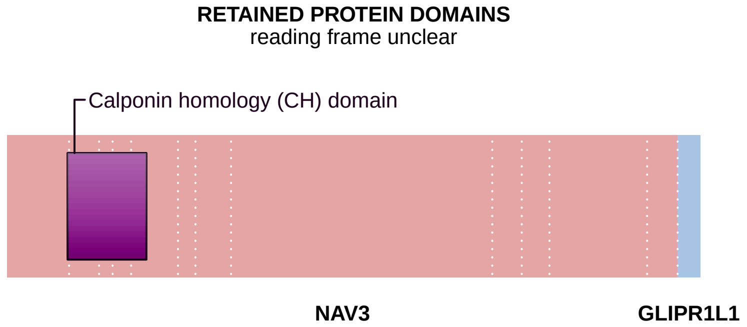
SUPPORTING READ COUNT

Split reads = 80
Discordant mates = 2


chromosome 12
q21.2
chromosome 12
q21.2
breakpoint1
chr12:78059115
breakpoint2
chr12:75347622
26407
Coverage
0
NAV3
ENST00000536525.6
GLIPR1L1
ENST00000378695.9
3 kbp
introns not to scale
NAV3
GLIPR1L1
RETAINED PROTEIN DOMAINS
reading frame unclear
Calponin homology (CH) domain
NAV3
GLIPR1L1
Cysteine−rich secretory protein family
SUPPORTING READ COUNT
Split reads = 9
Discordant mates = 1
translocation
deletion
duplication
inversion

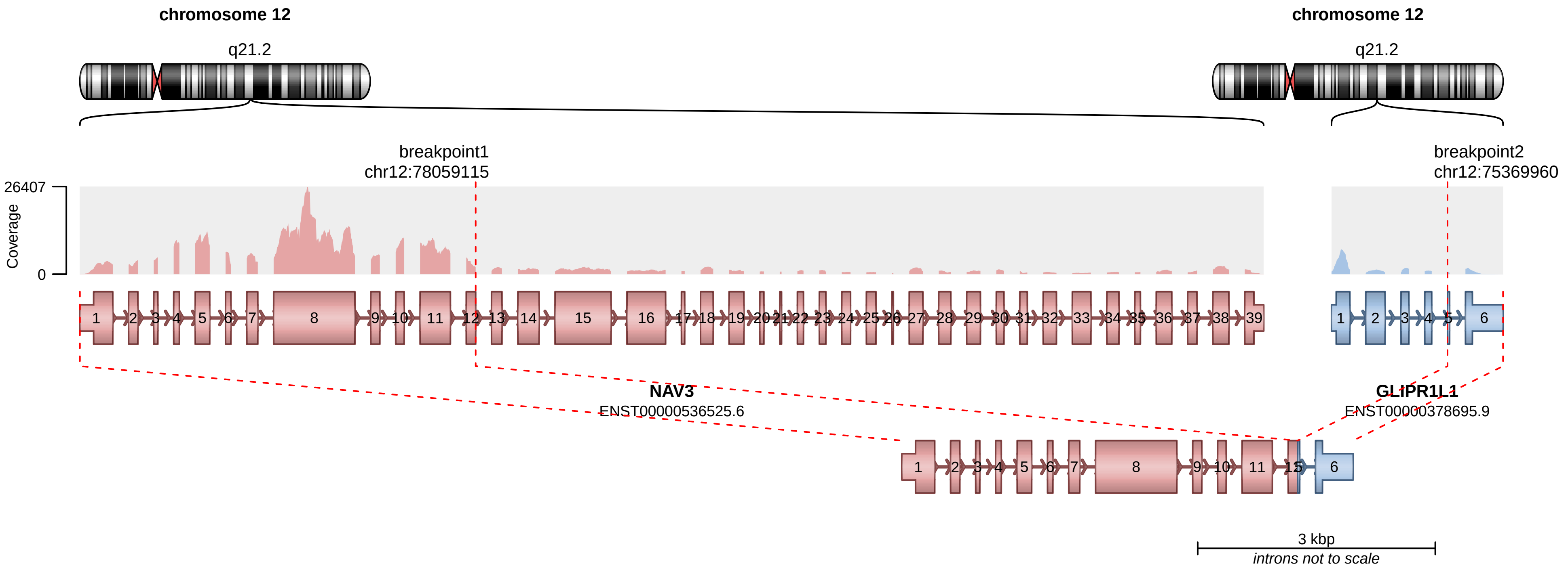


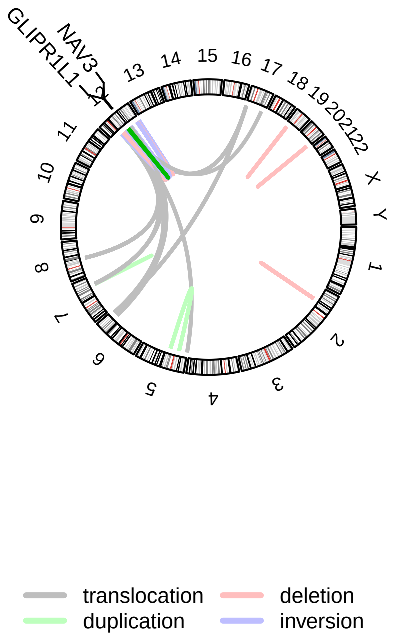


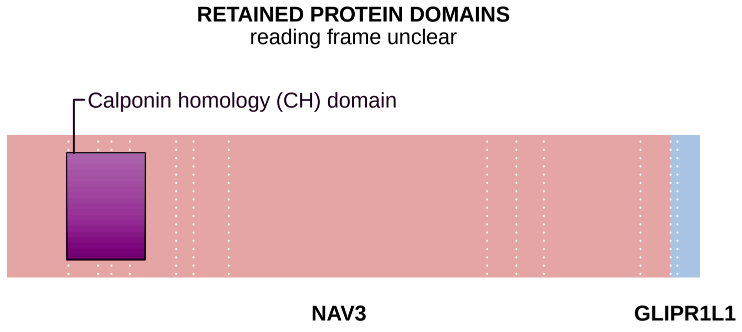


SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 0

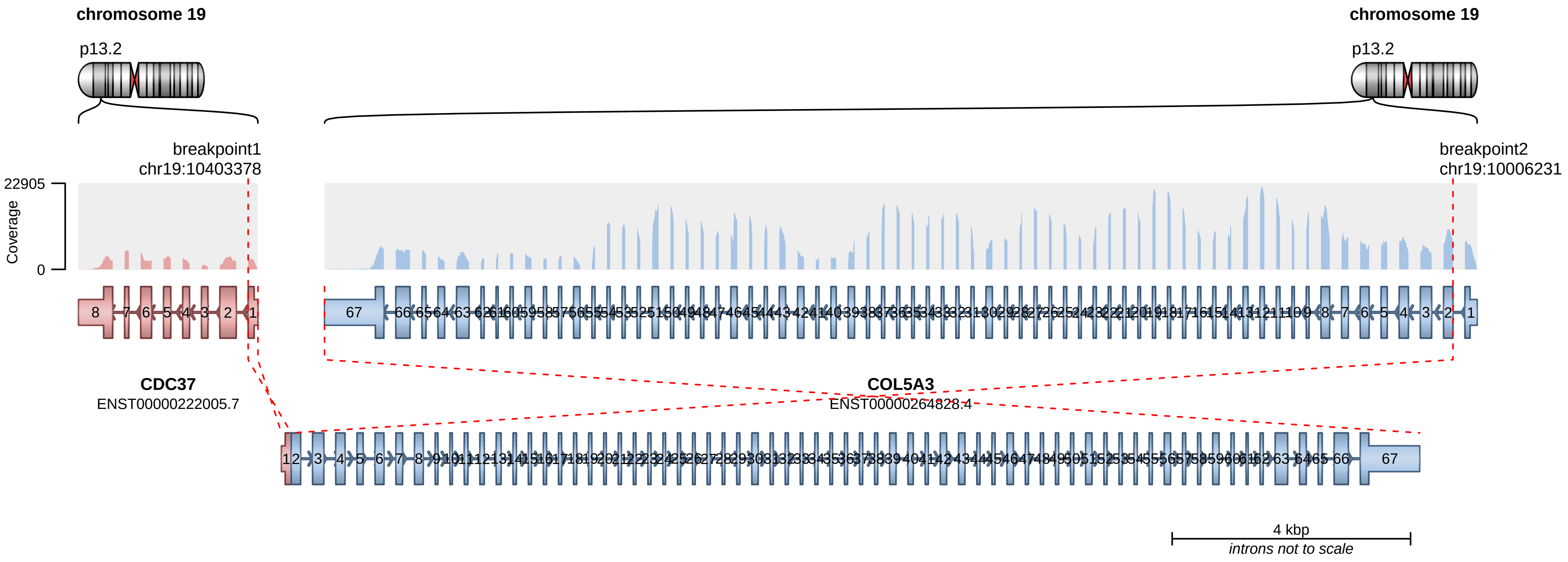


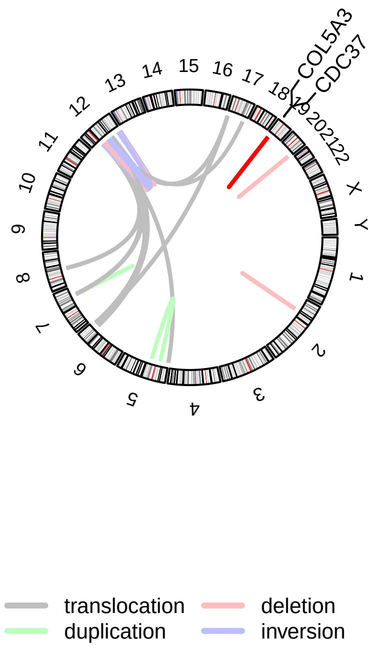




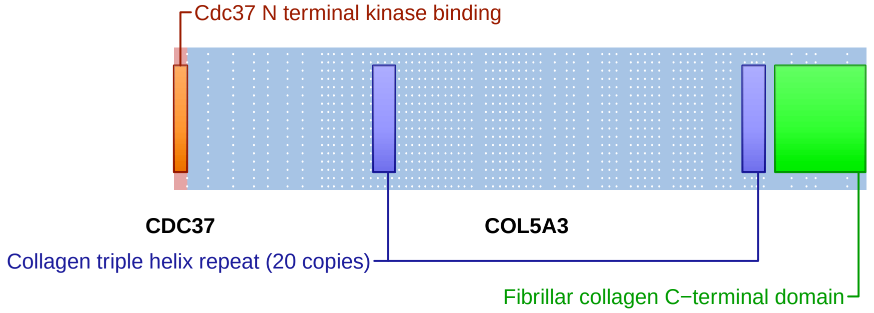
SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 0



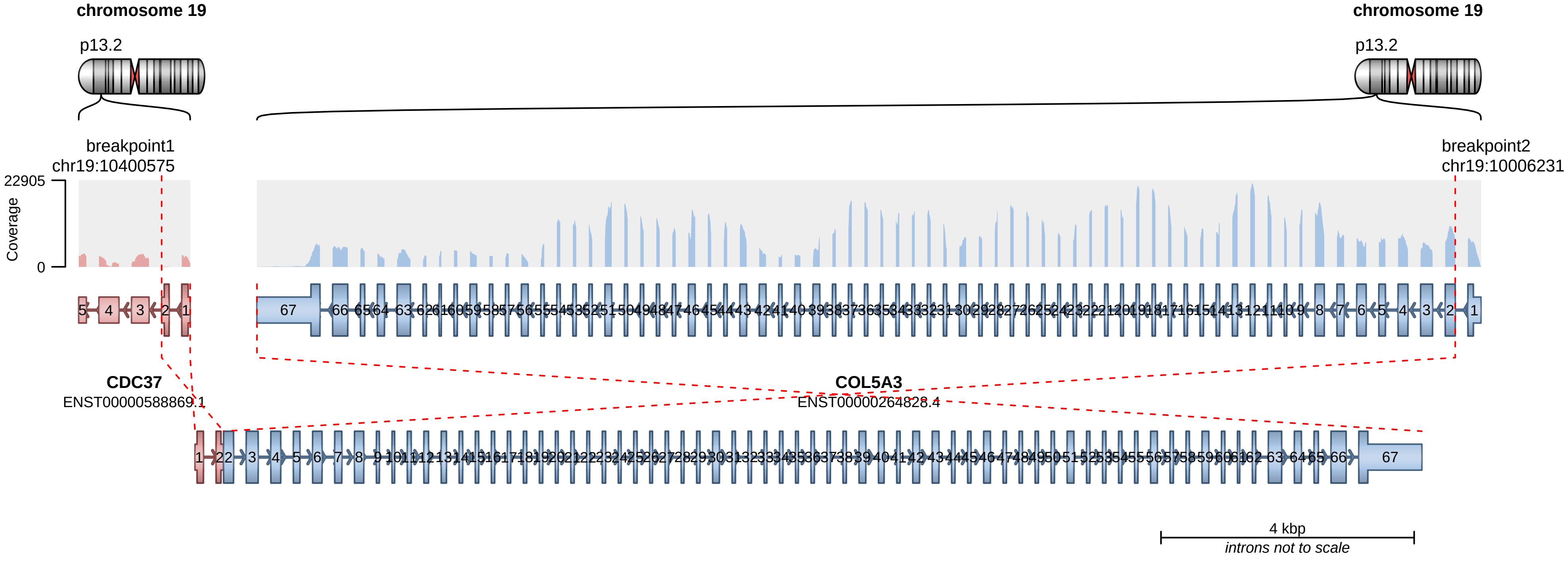


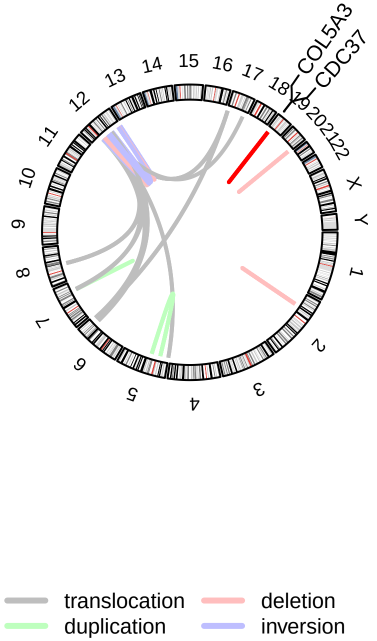
RETAINED PROTEIN DOMAINS
reading frame unclear

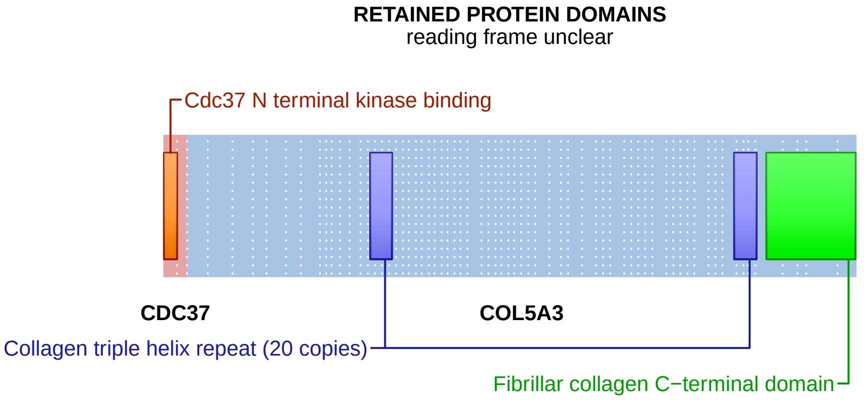


SUPPORTING READ COUNT

Split reads = 97
Discordant mates = 0

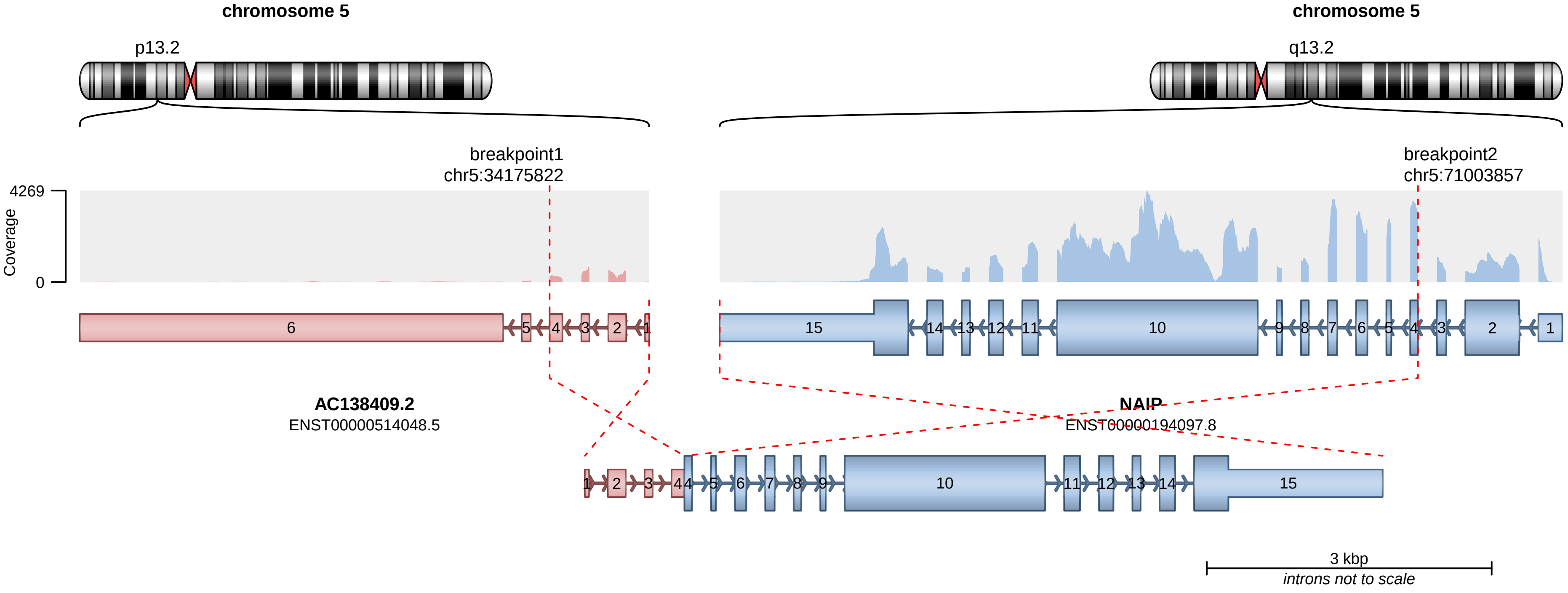


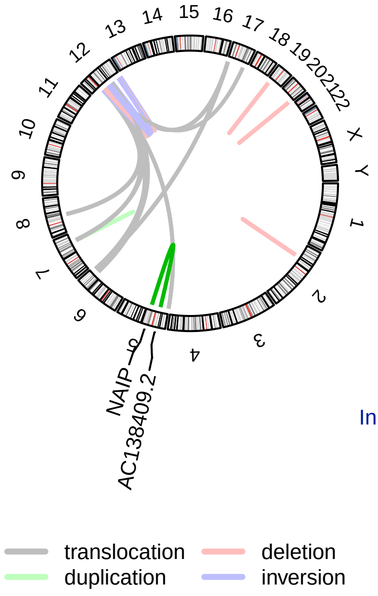




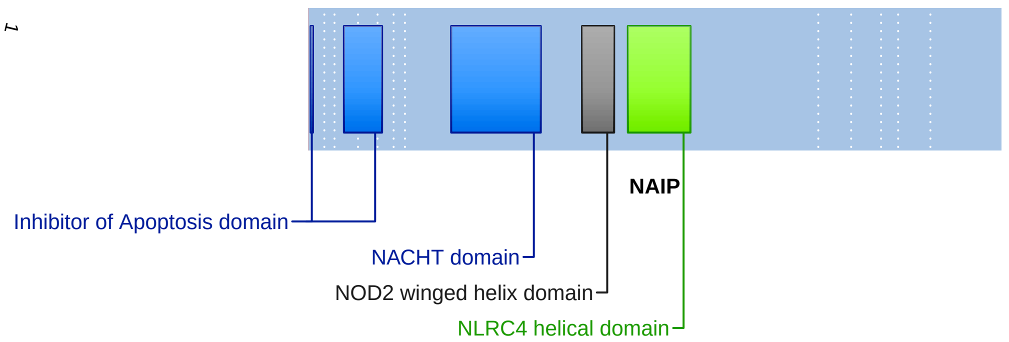
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



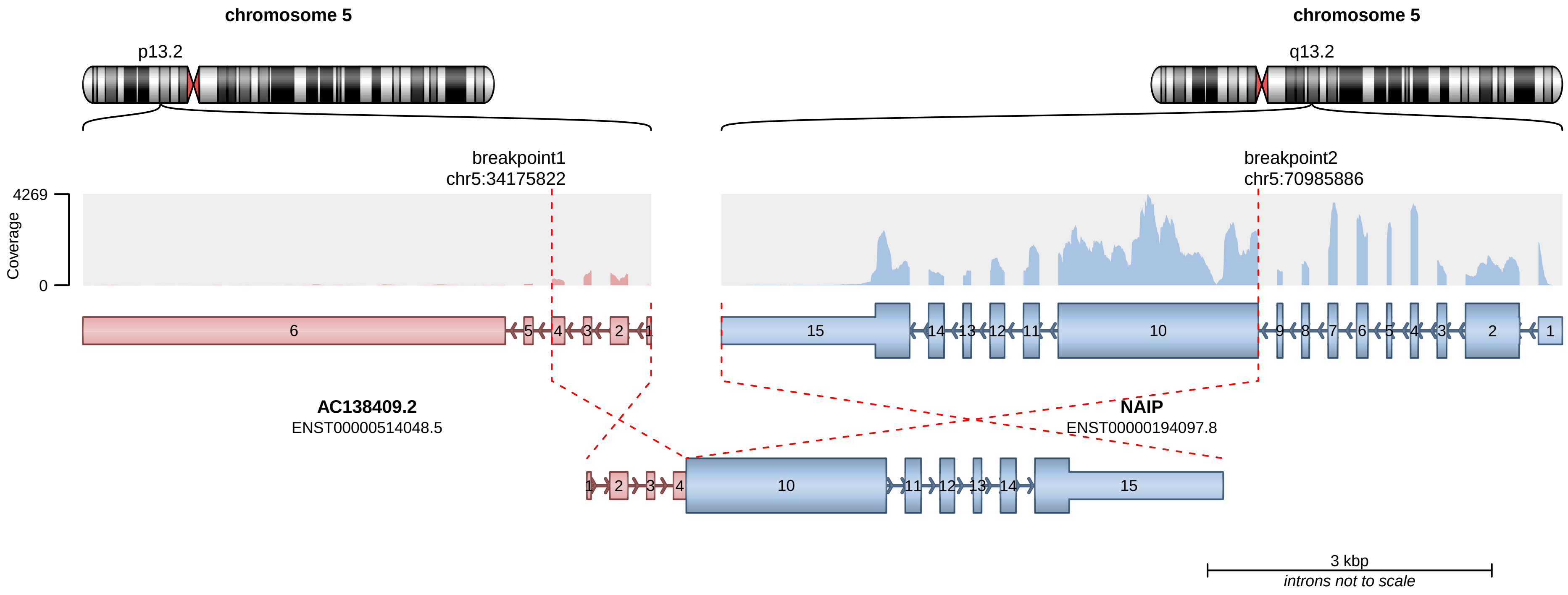


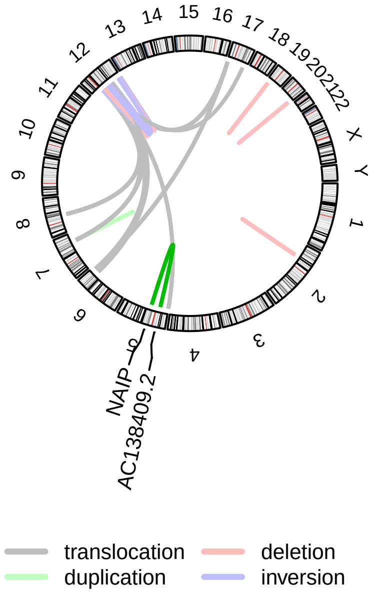
RETAINED PROTEIN DOMAINS
reading frame unclear



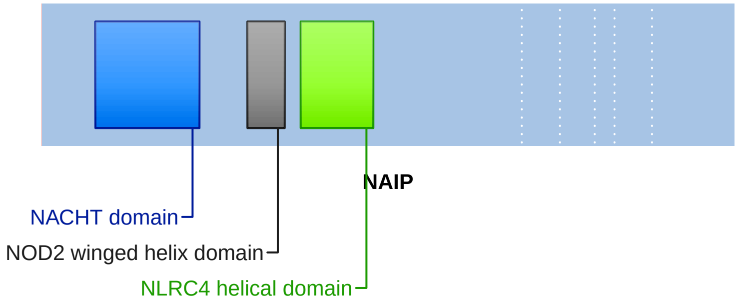
SUPPORTING READ COUNT

Split reads = 94
Discordant mates = 0



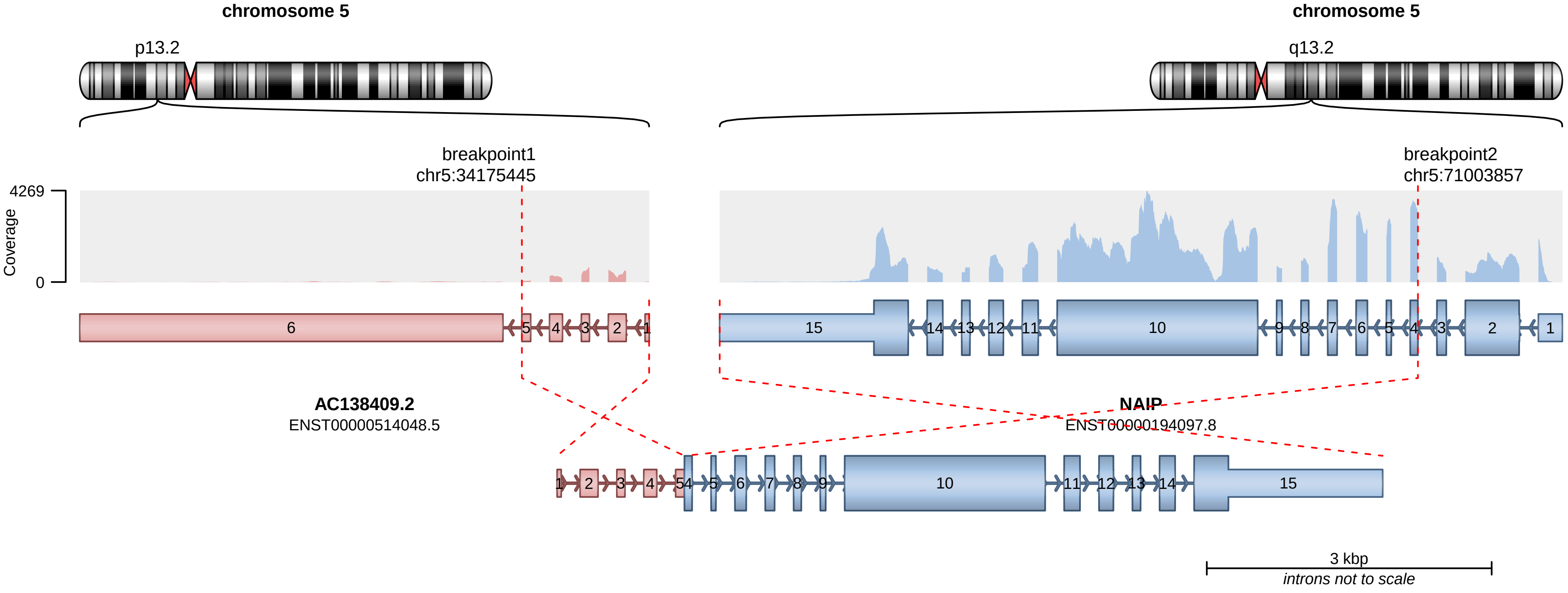


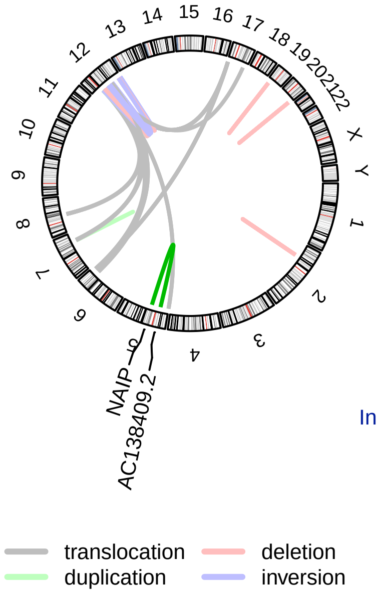
RETAINED PROTEIN DOMAINS
reading frame unclear

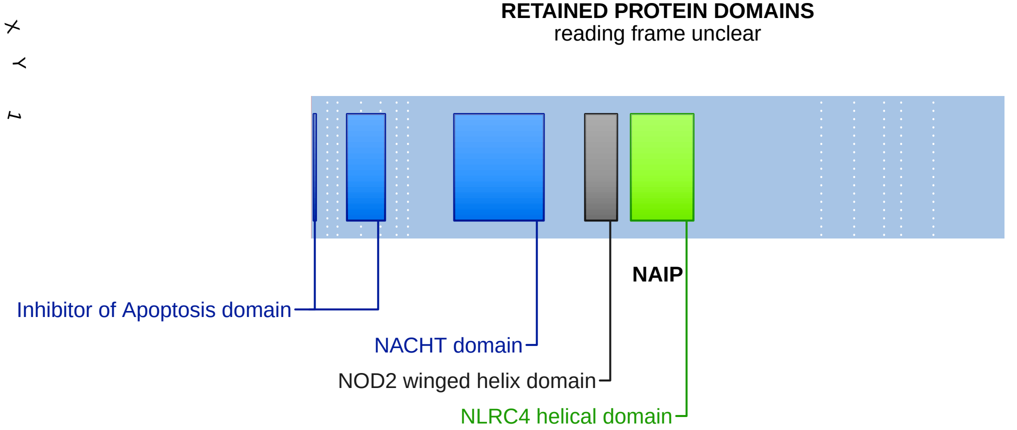


SUPPORTING READ COUNT

Split reads = 15
Discordant mates = 0

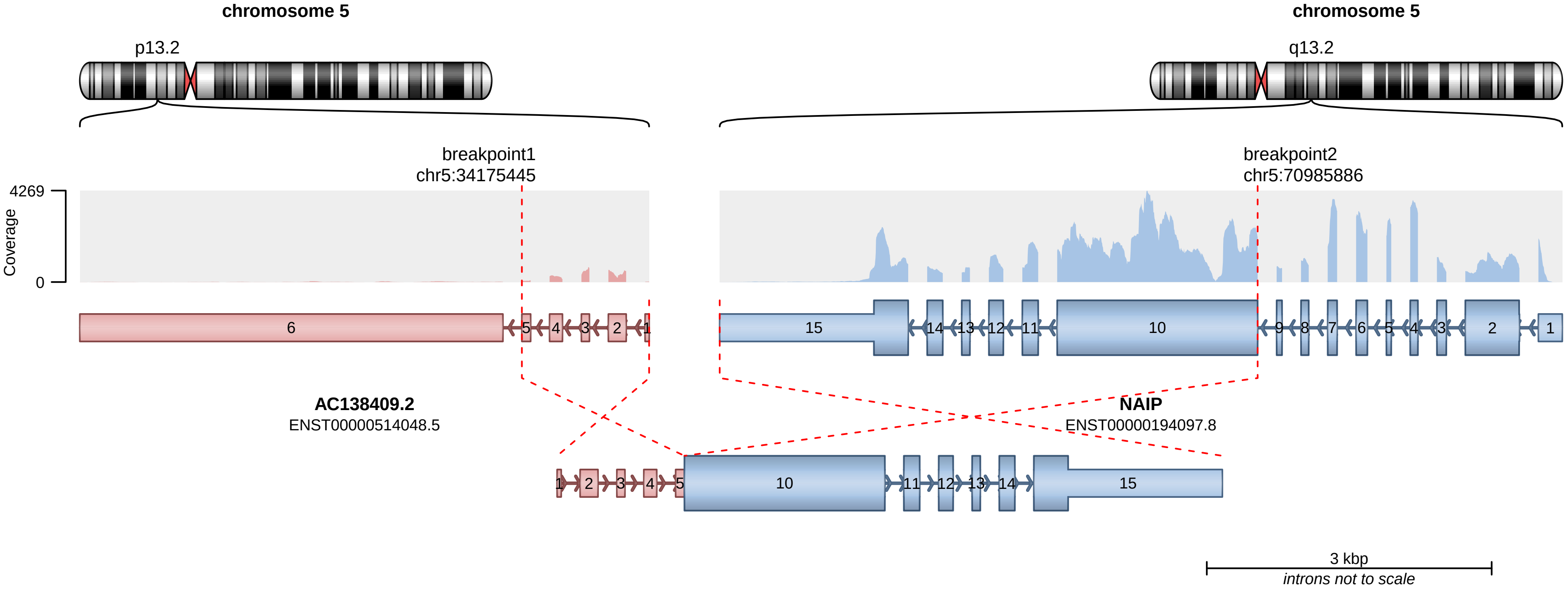


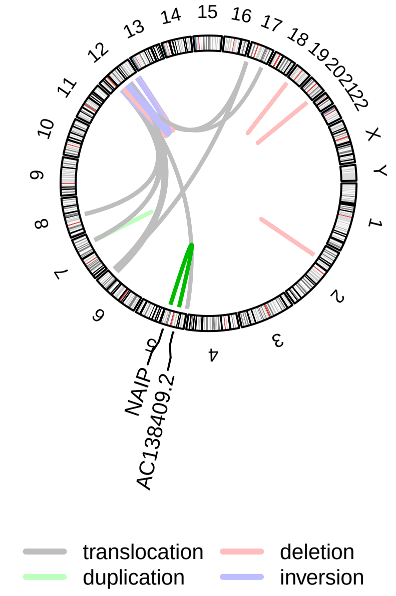




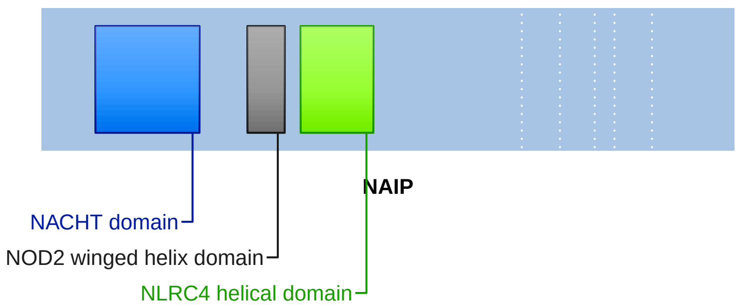
SUPPORTING READ COUNT

Split reads = 13
Discordant mates = 0



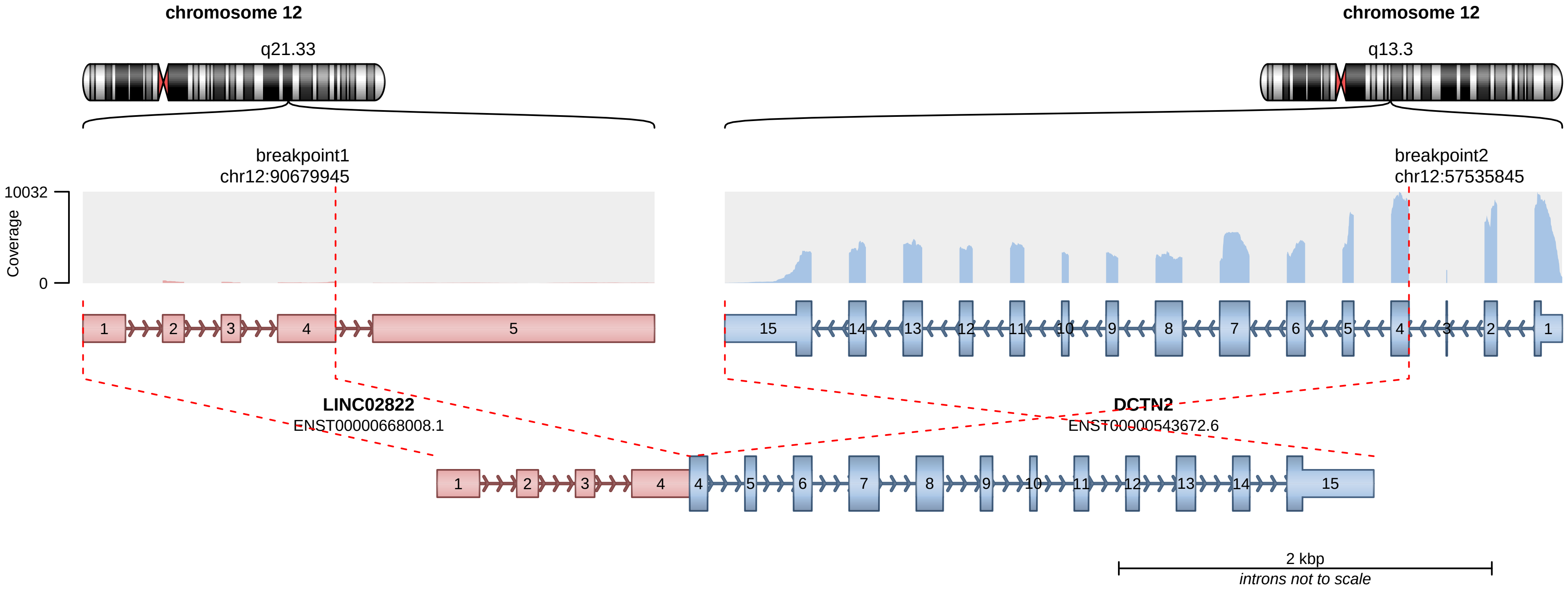


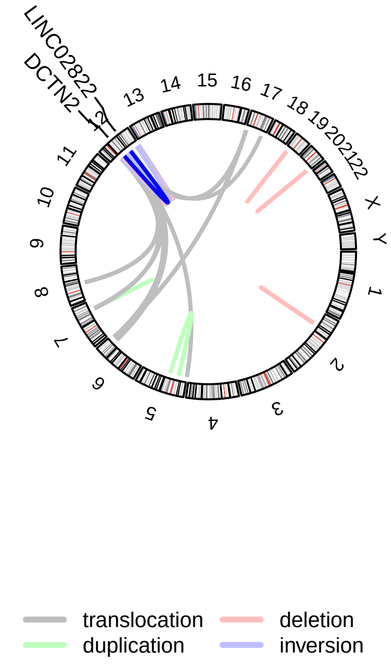
RETAINED PROTEIN DOMAINS
reading frame unclear



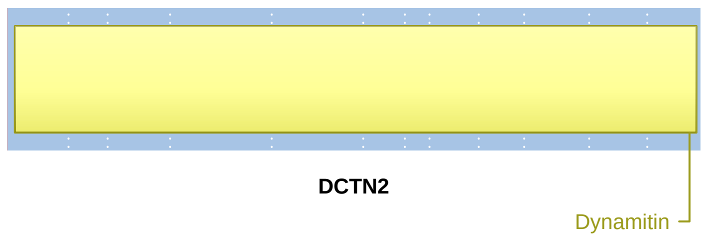
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



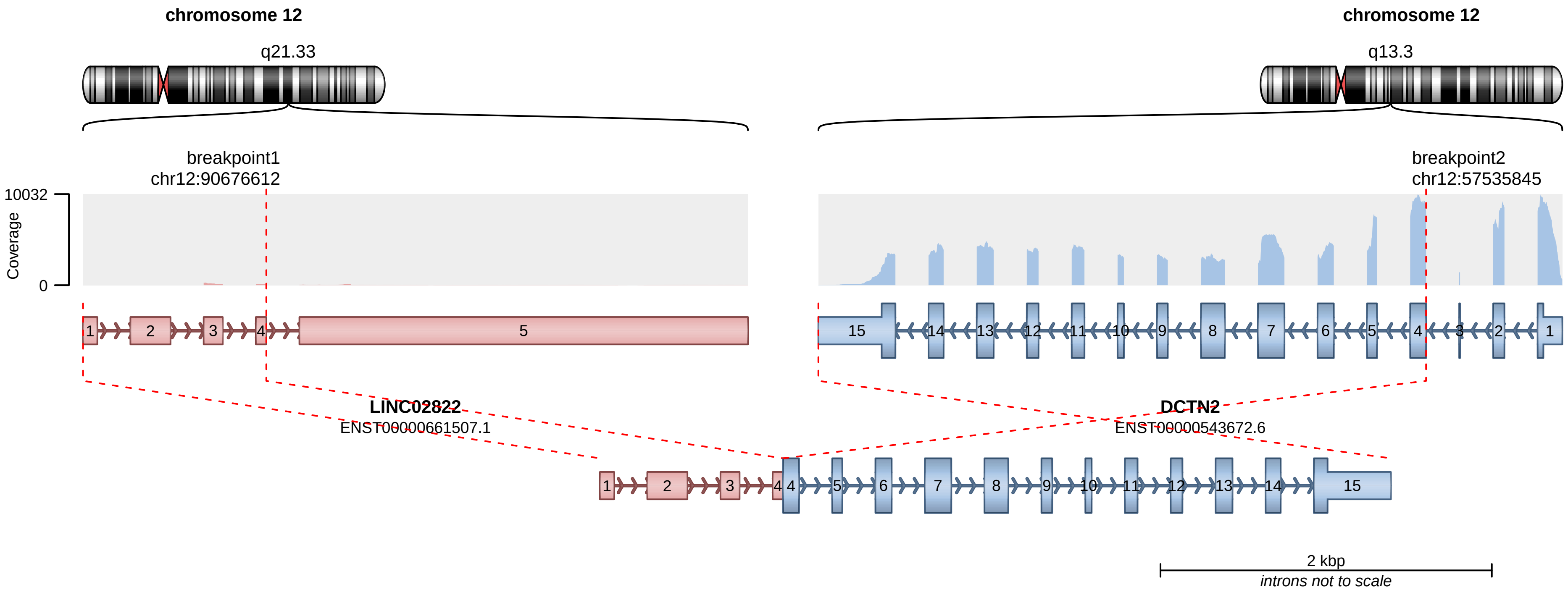


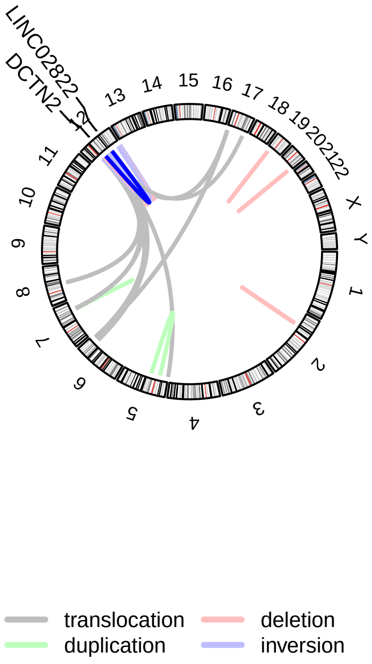
RETAINED PROTEIN DOMAINS
reading frame unclear



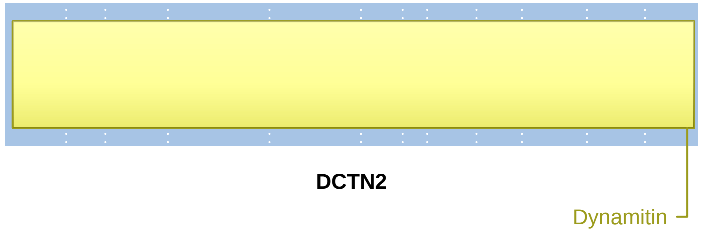
SUPPORTING READ COUNT

Split reads = 85
Discordant mates = 0



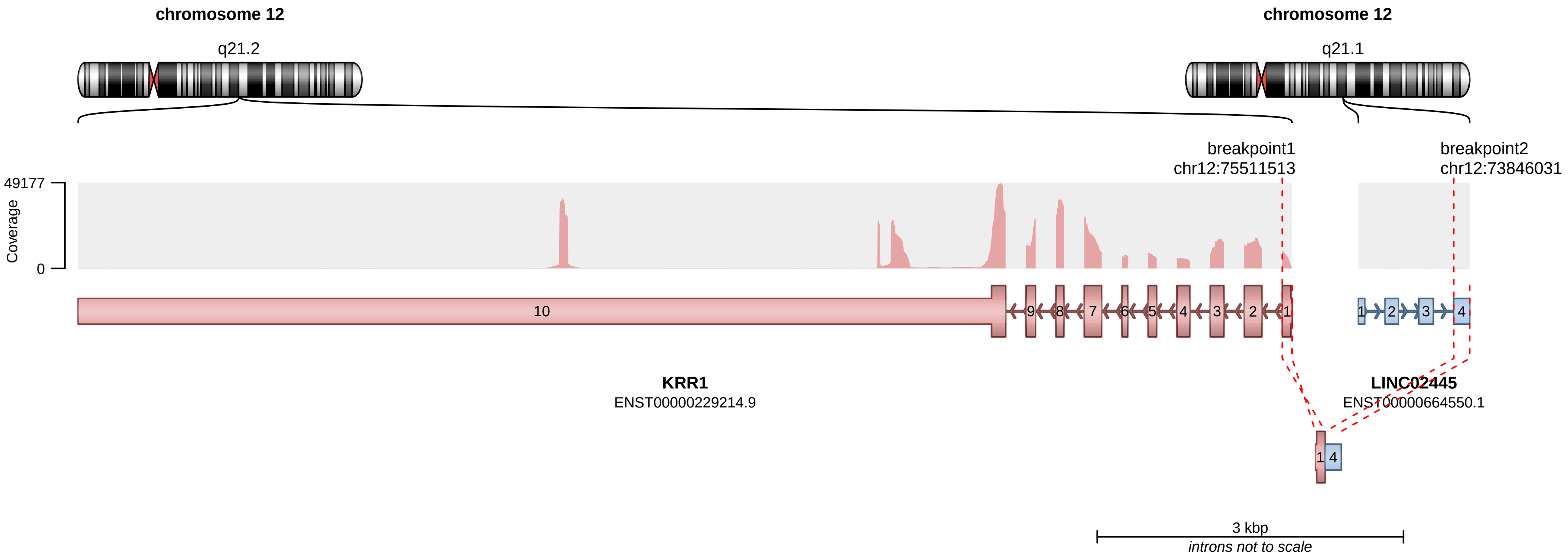


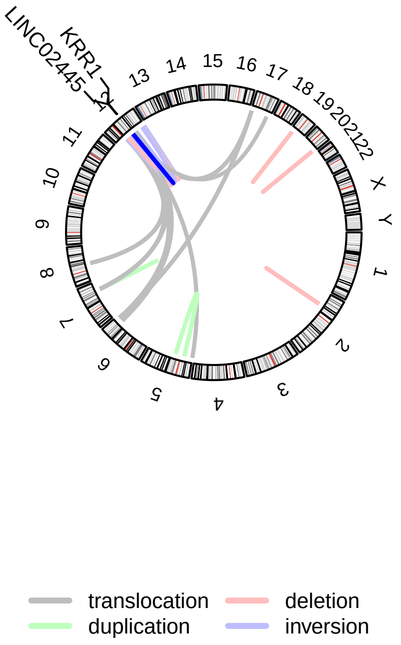
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

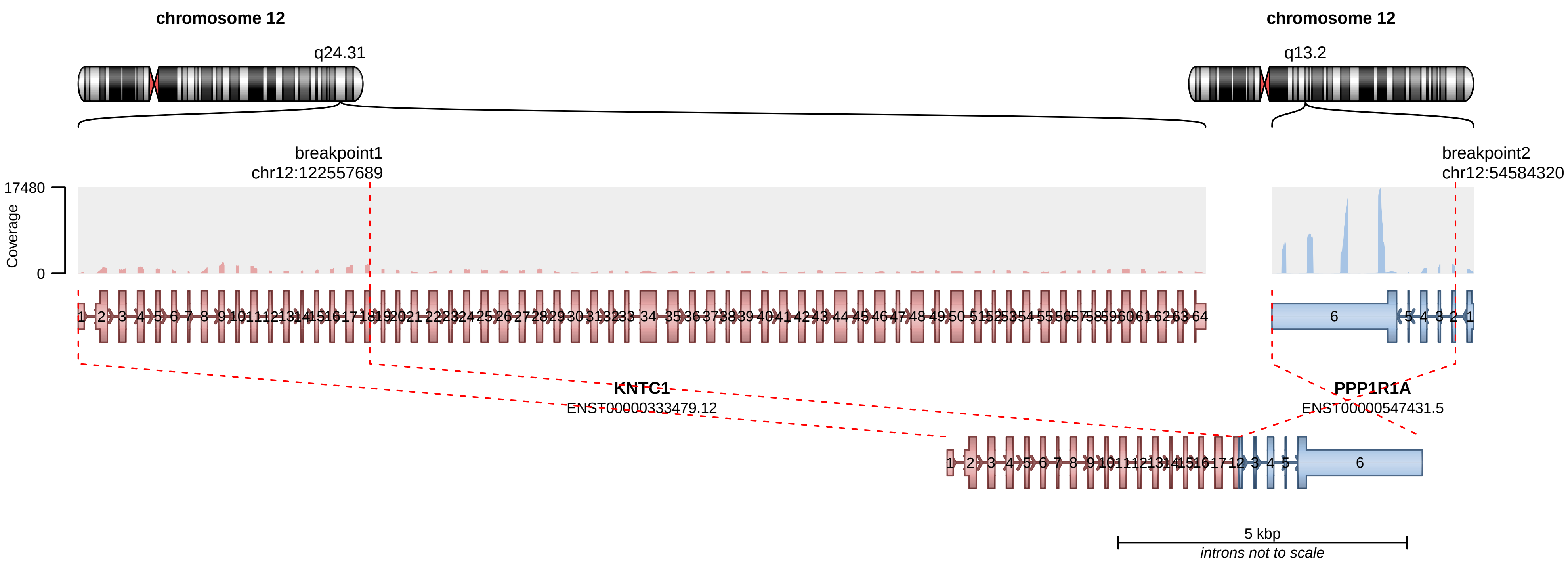


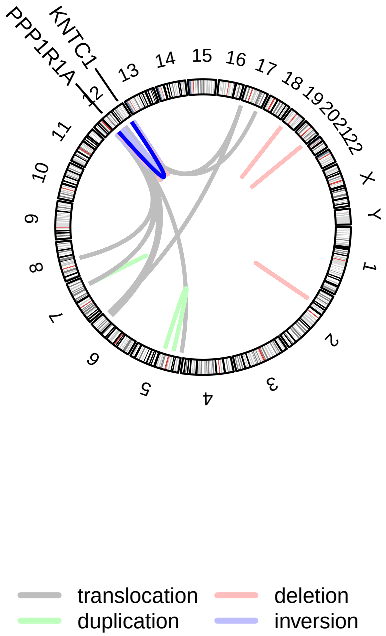


No protein domains retained in fusion.

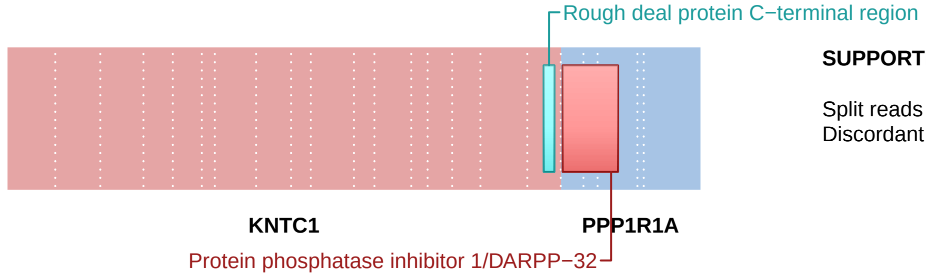
SUPPORTING READ COUNT

Split reads = 81
Discordant mates = 0



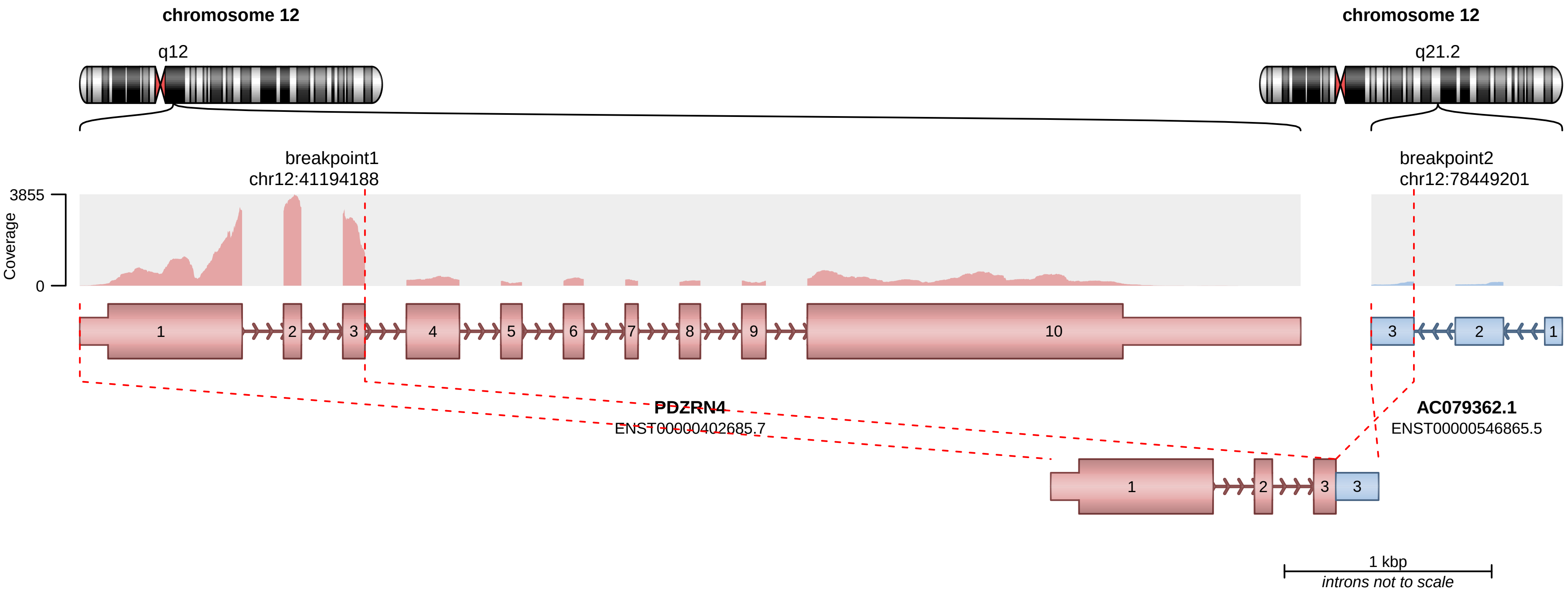


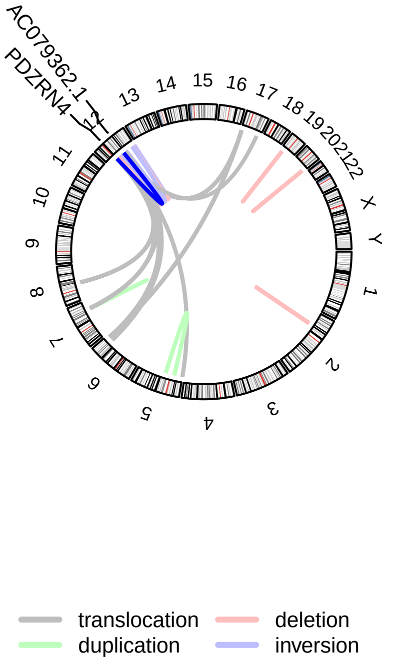
RETAINED PROTEIN DOMAINS
reading frame unclear



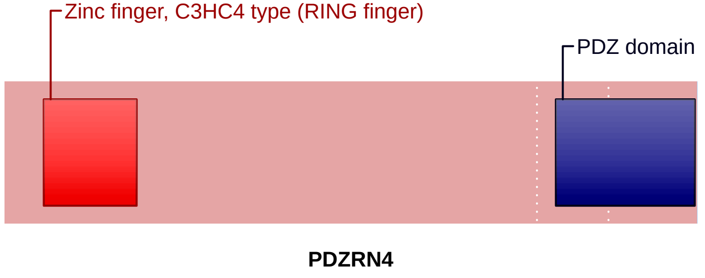
SUPPORTING READ COUNT

Split reads = 77
Discordant mates = 0



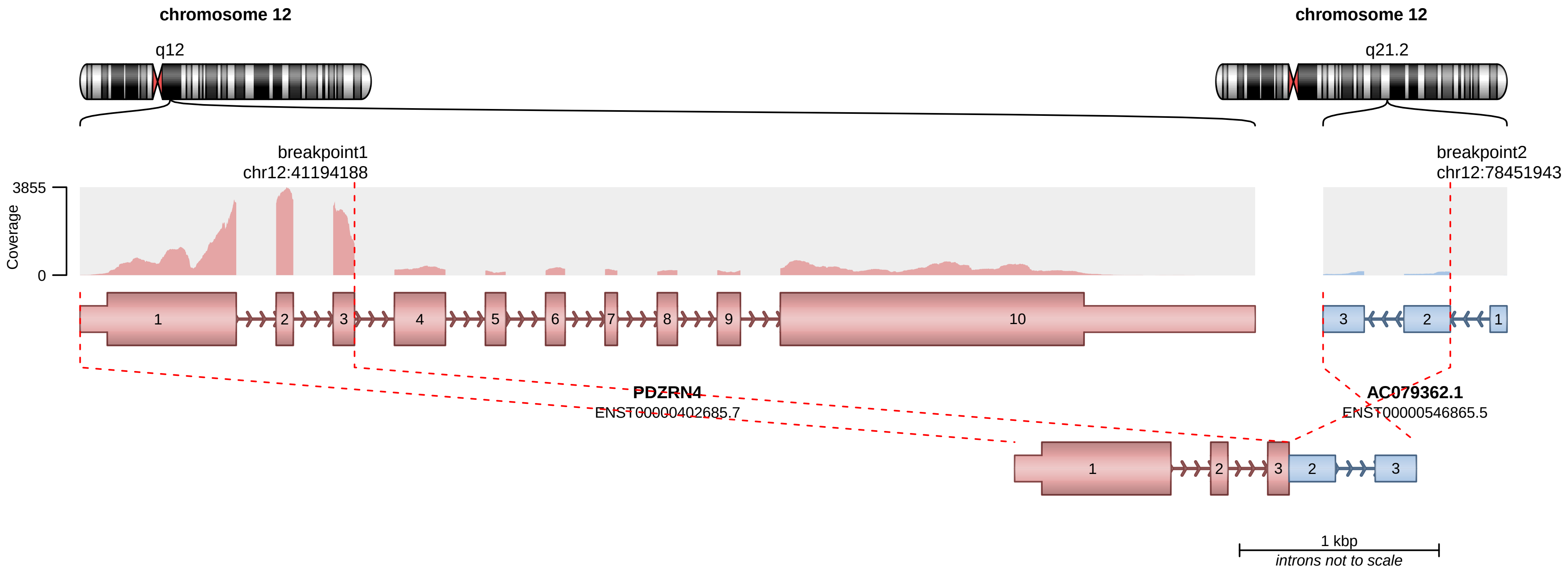


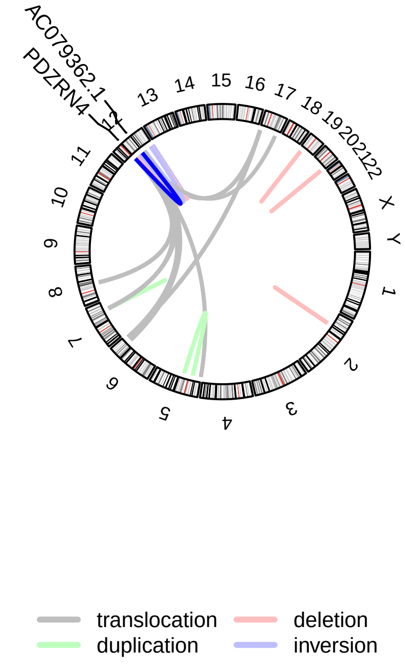
RETAINED PROTEIN DOMAINS
reading frame unclear

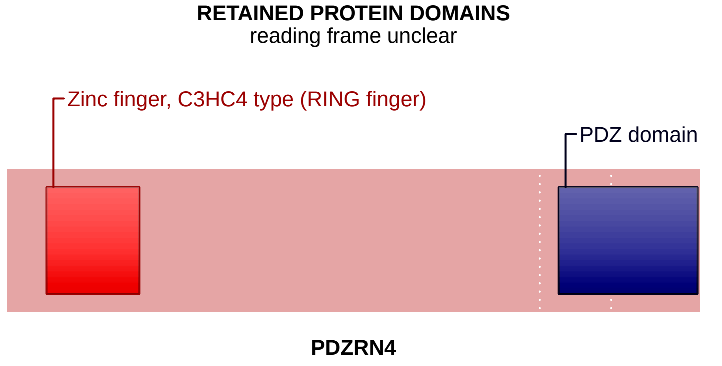


SUPPORTING READ COUNT

Split reads = 63
Discordant mates = 2

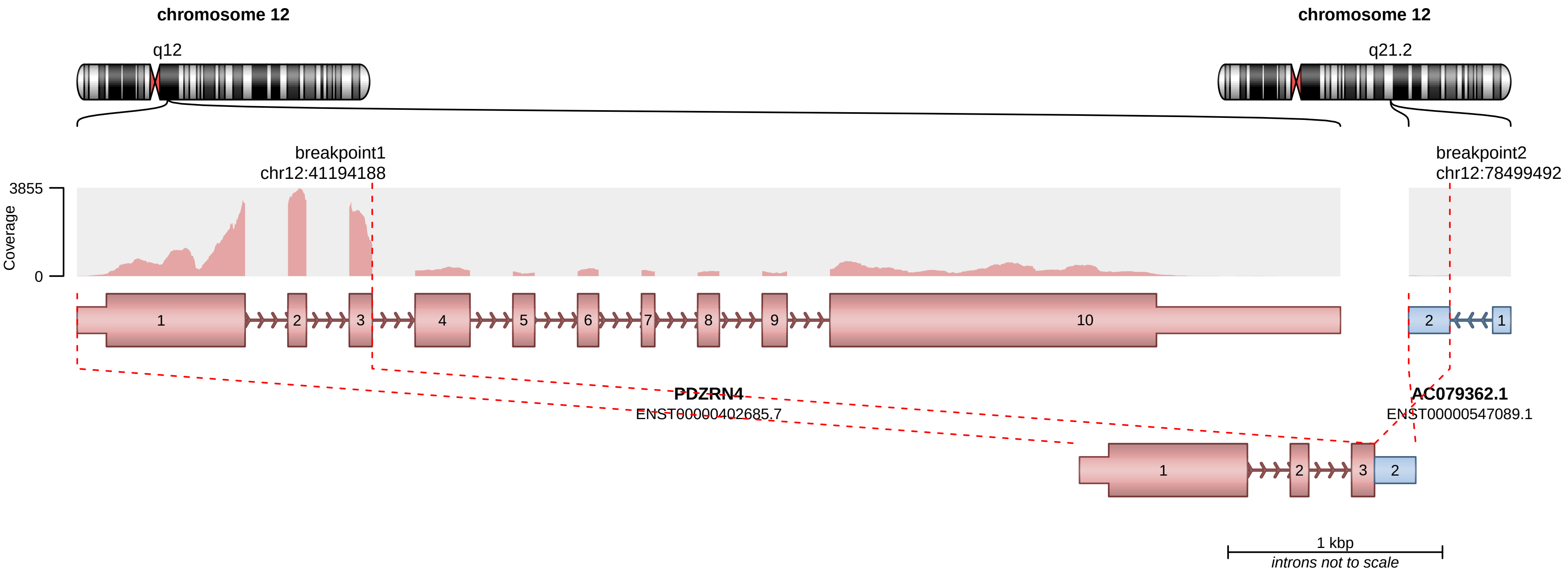


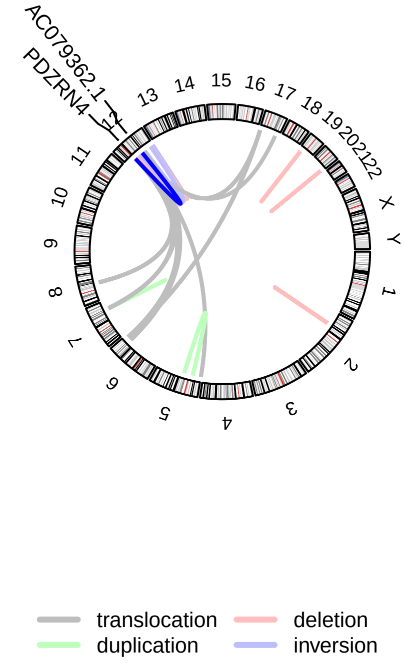


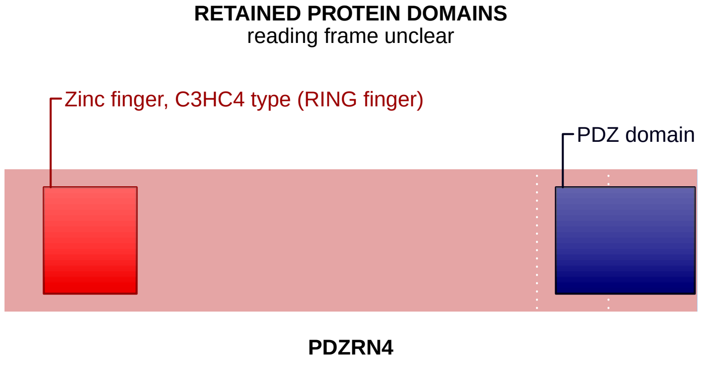


SUPPORTING READ COUNT

Split reads = 52
Discordant mates = 2

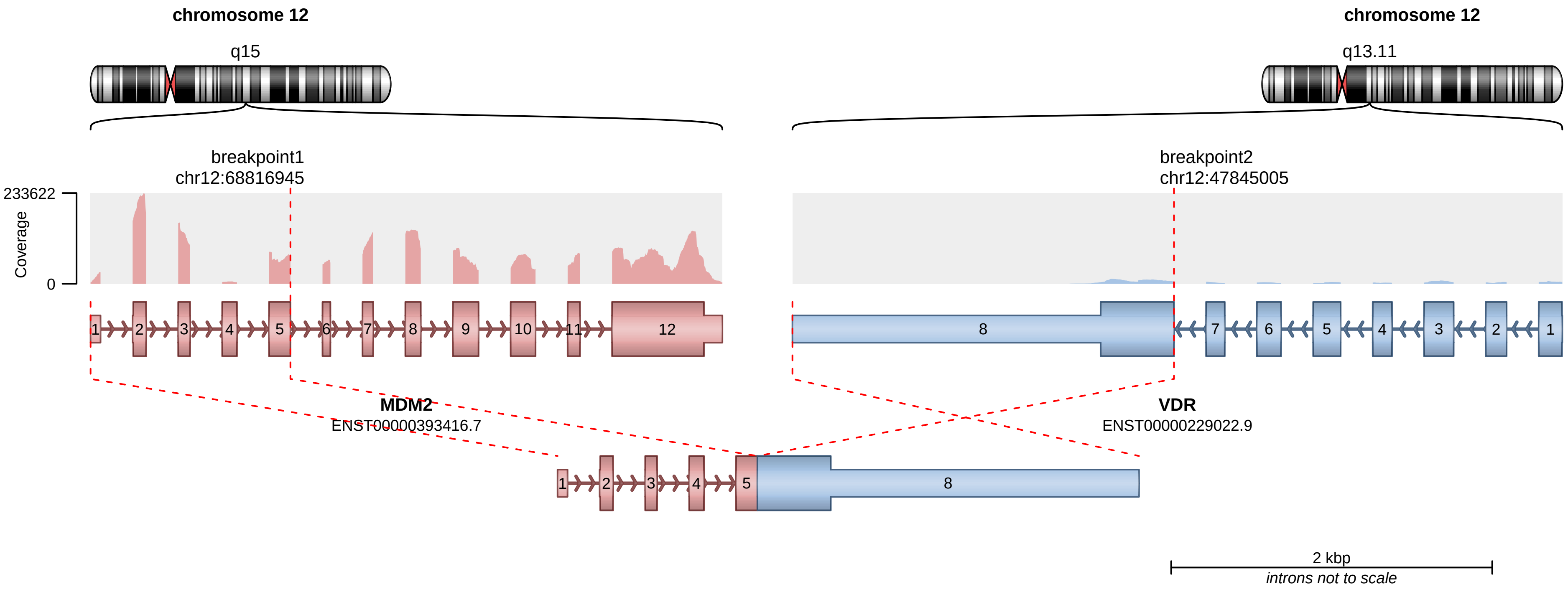


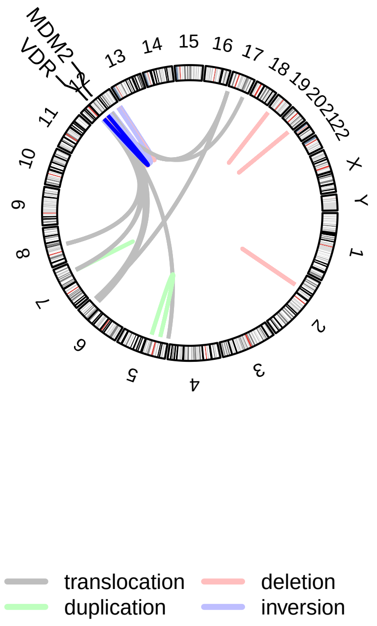




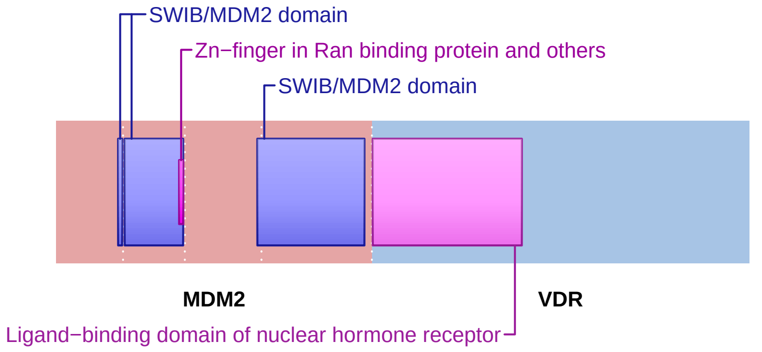
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 3



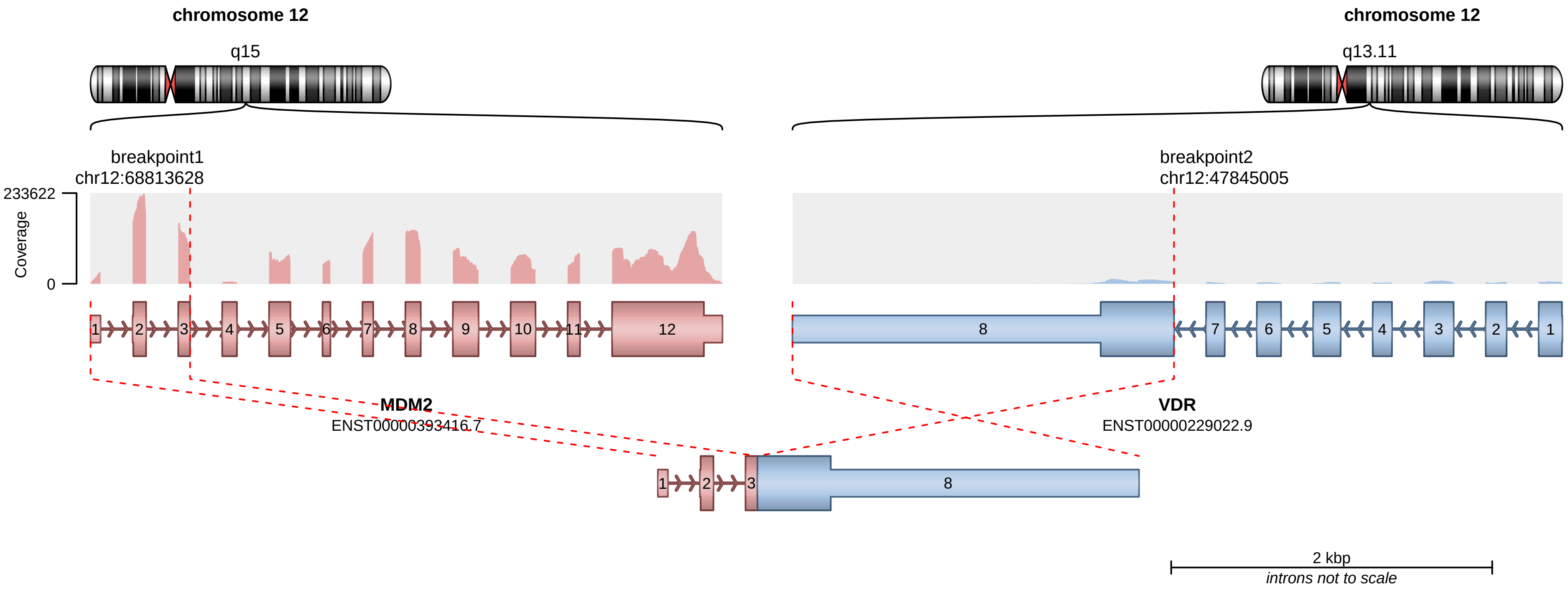


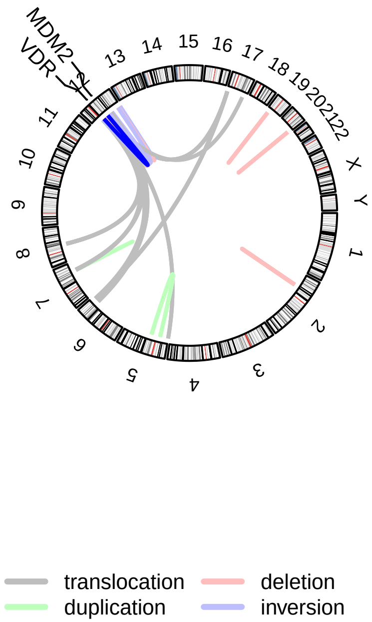
RETAINED PROTEIN DOMAINS
reading frame unclear

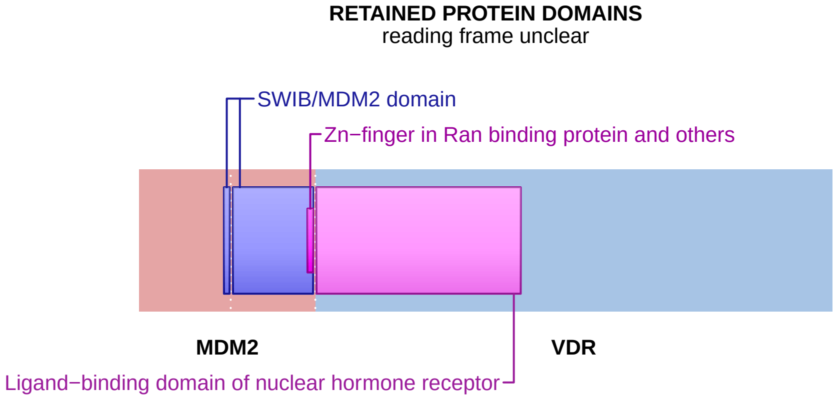


SUPPORTING READ COUNT

Split reads = 48
Discordant mates = 0

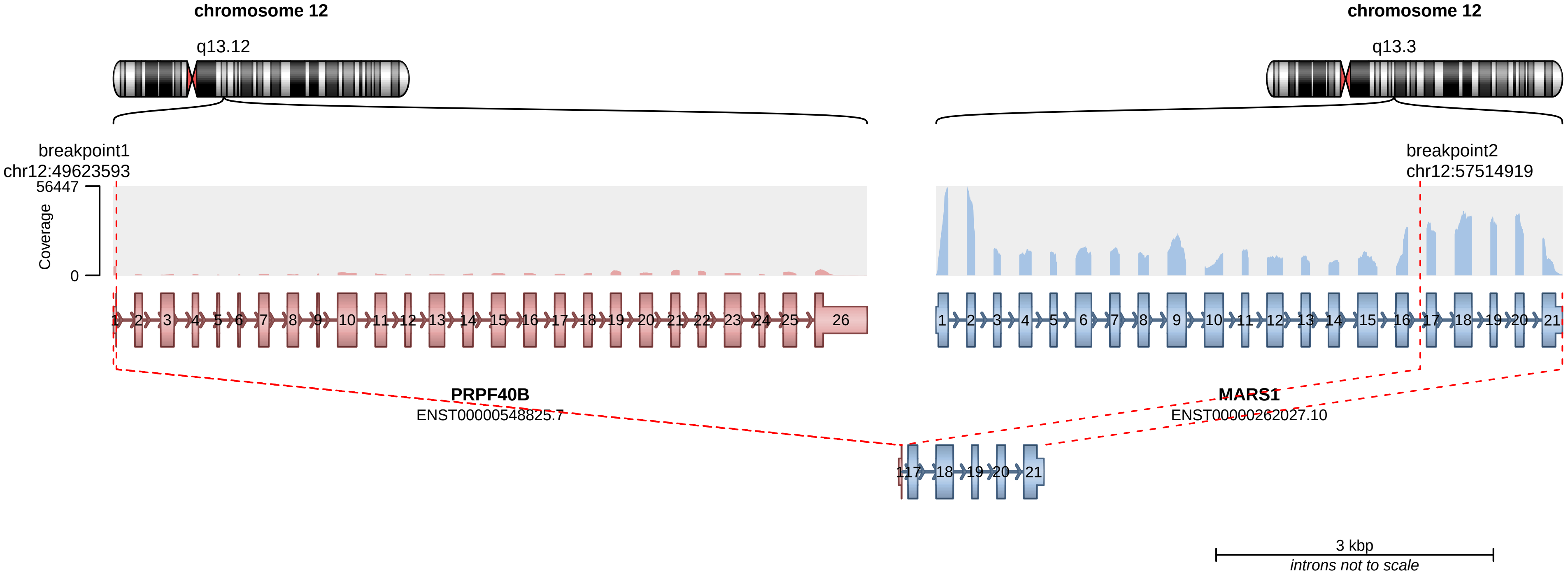


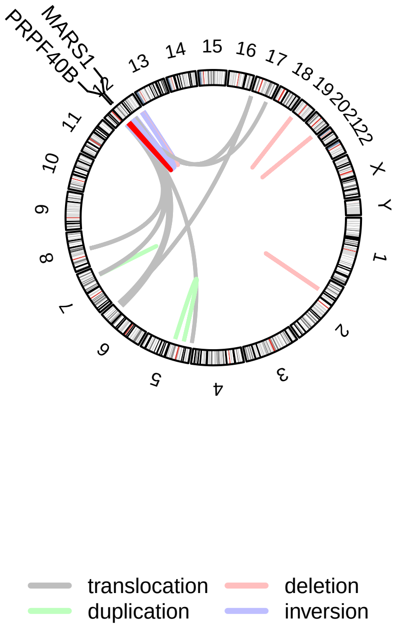


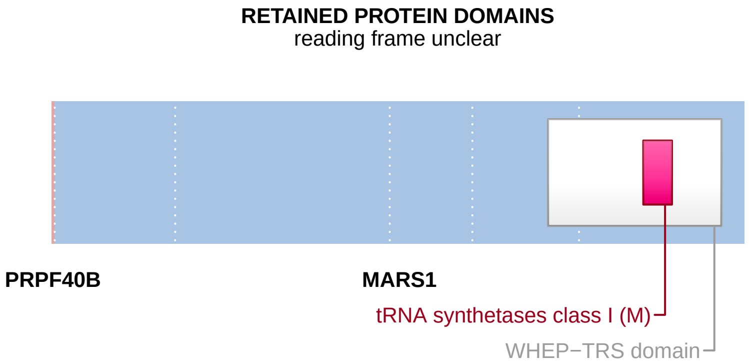


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

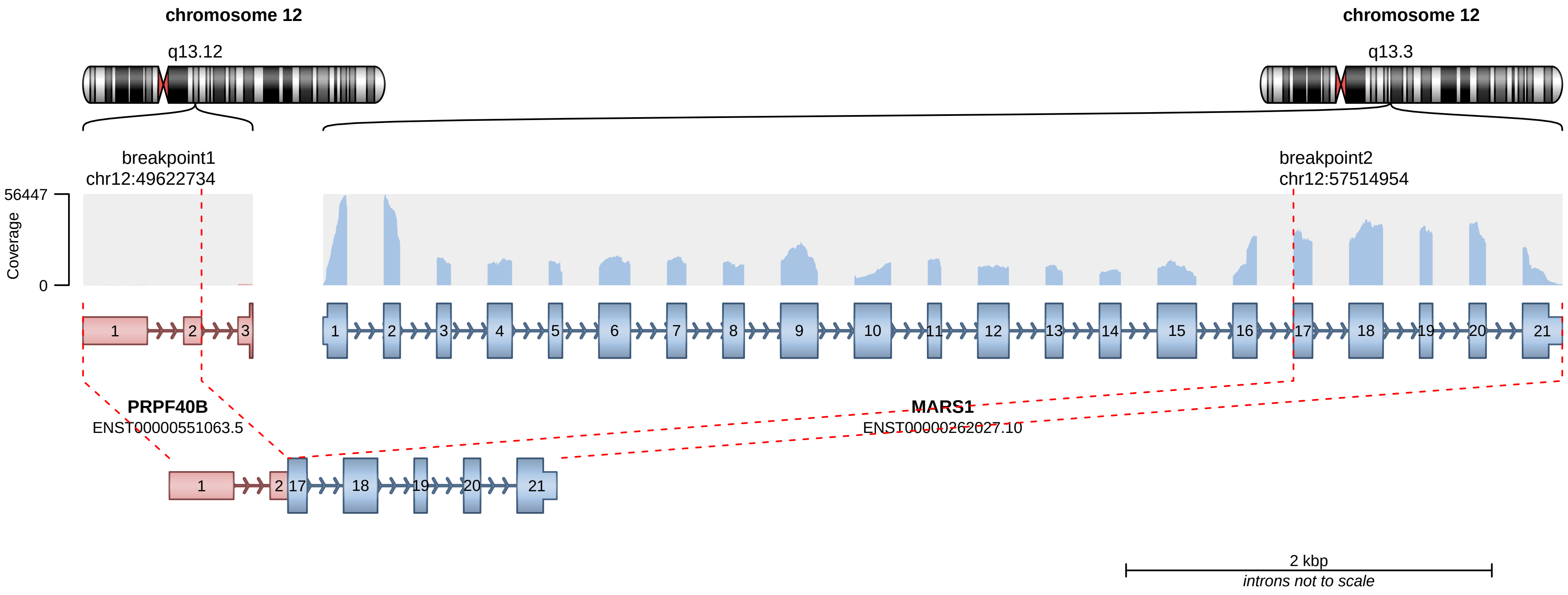


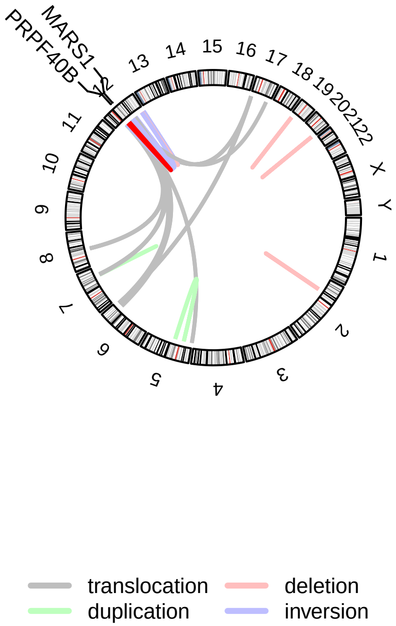


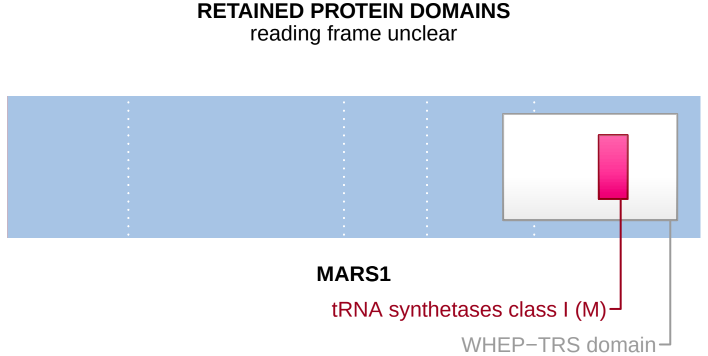


SUPPORTING READ COUNT

Split reads = 46
Discordant mates = 1

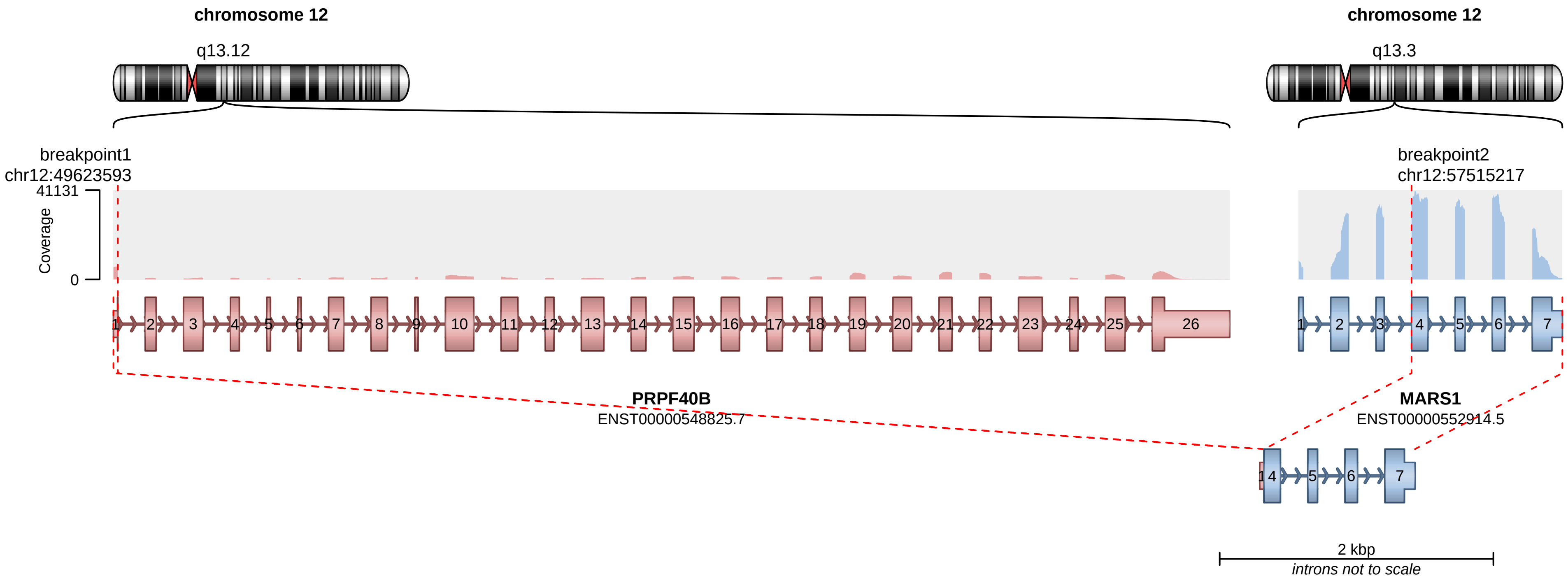


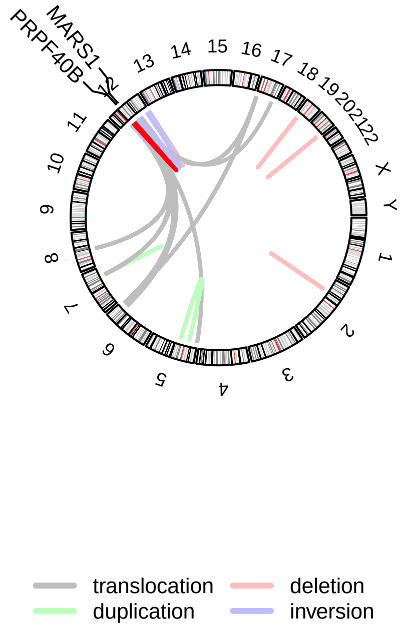


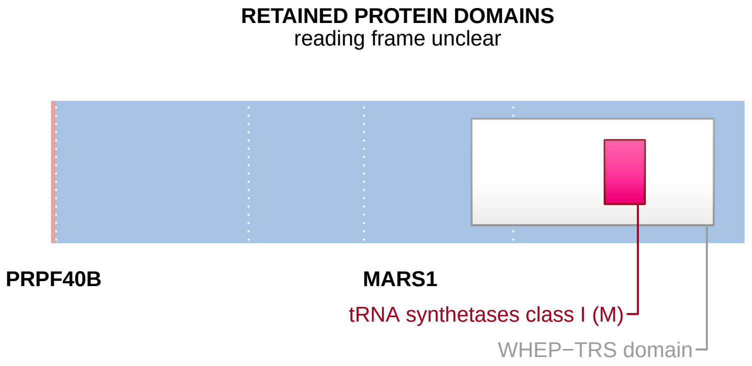


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

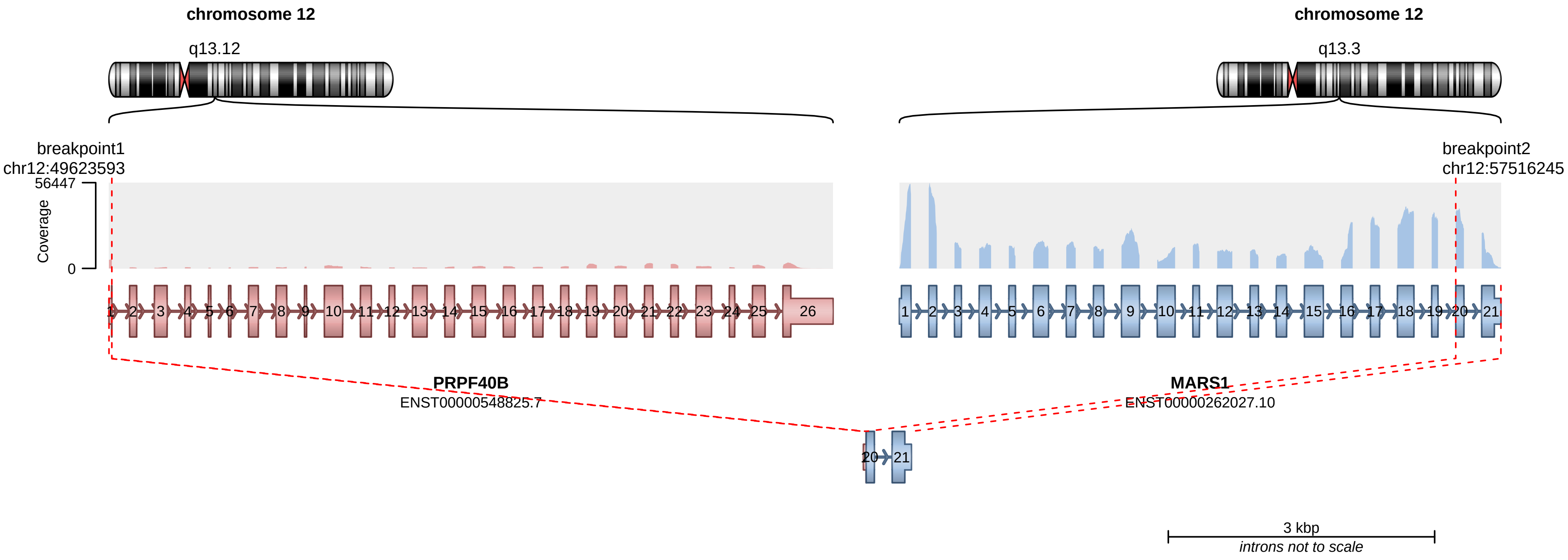


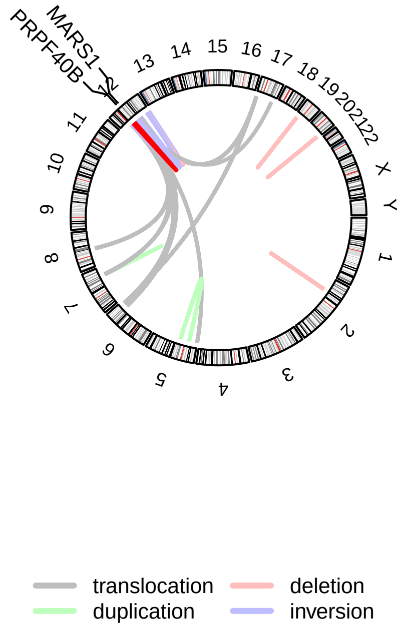


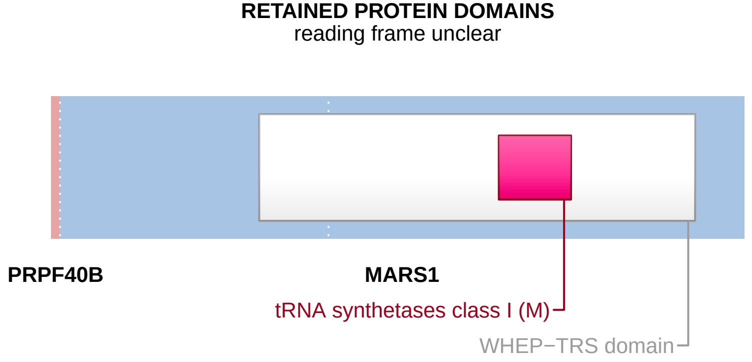


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

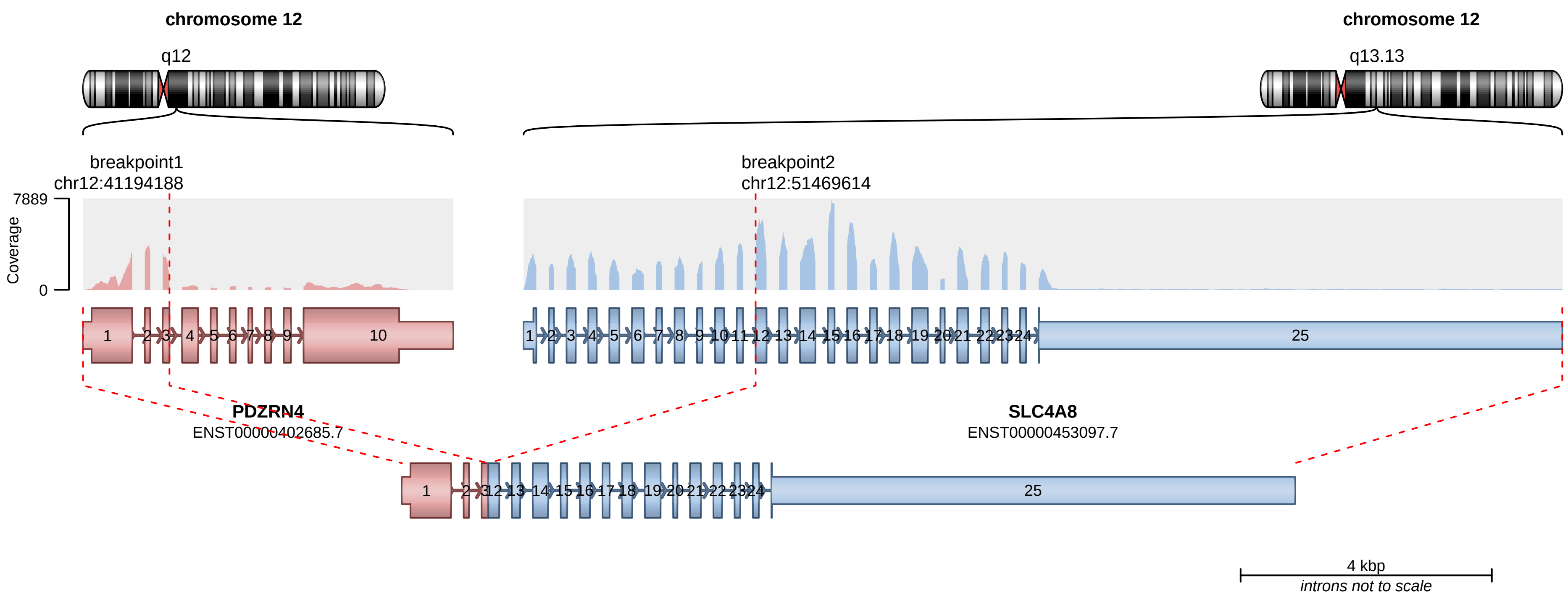


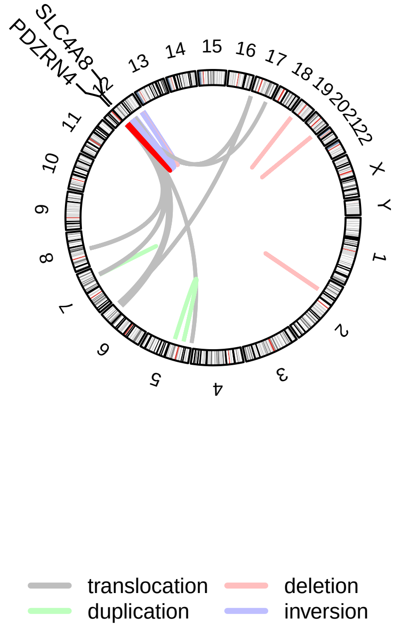


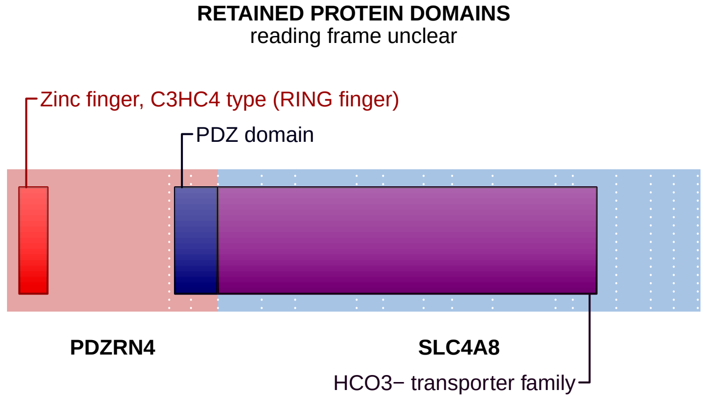


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

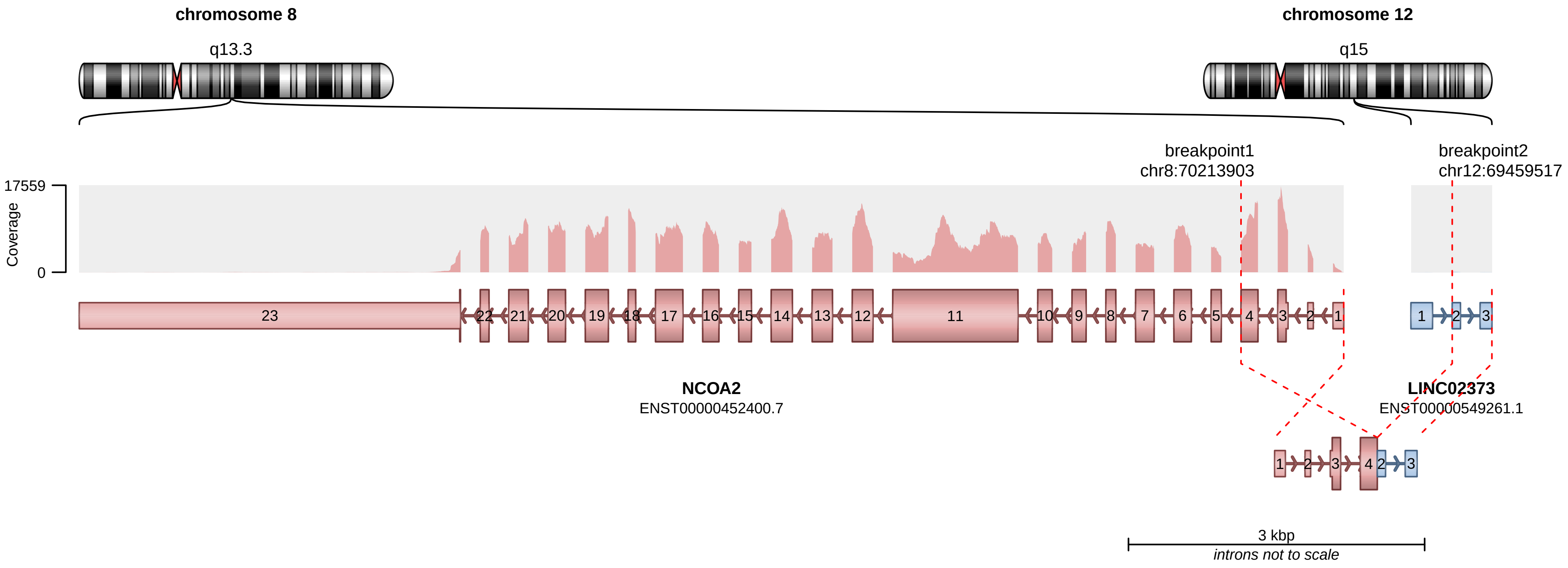


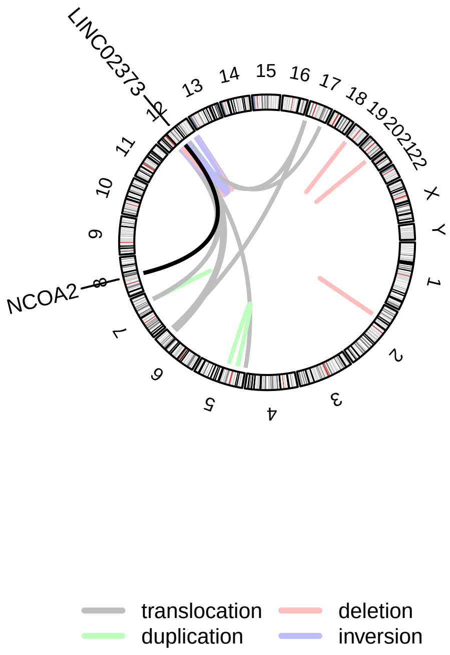




SUPPORTING READ COUNT

Split reads = 41
Discordant mates = 0

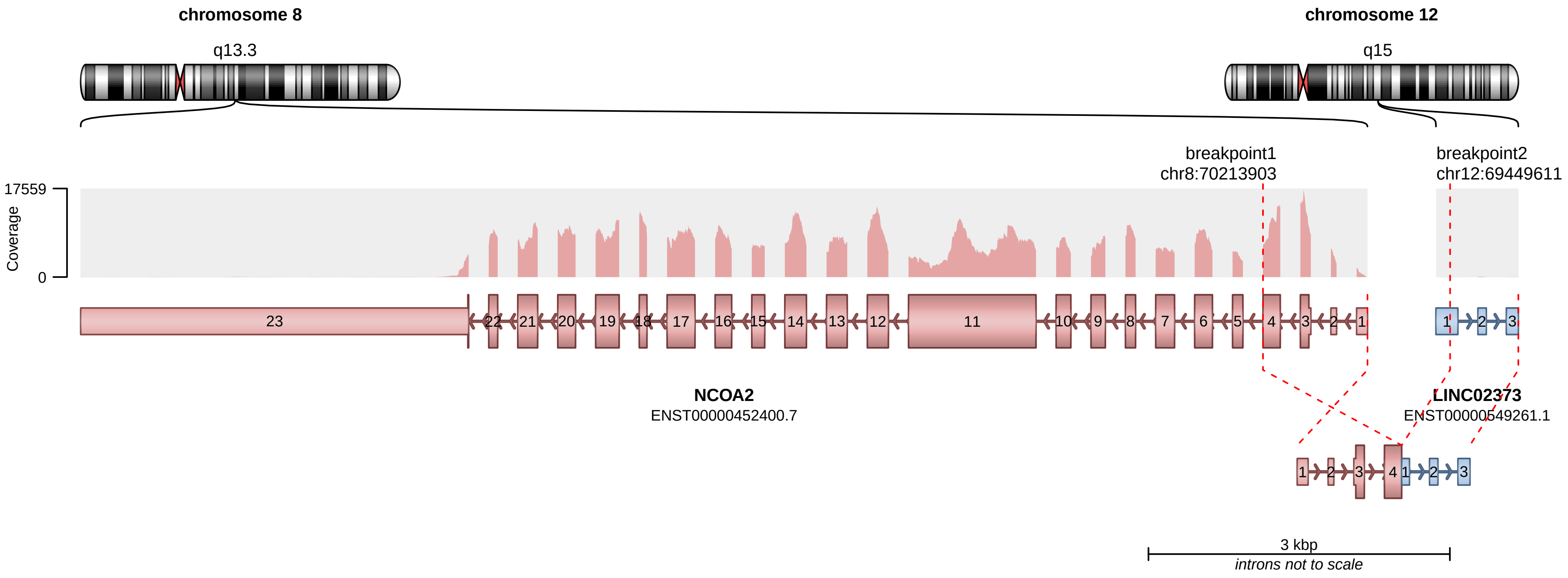


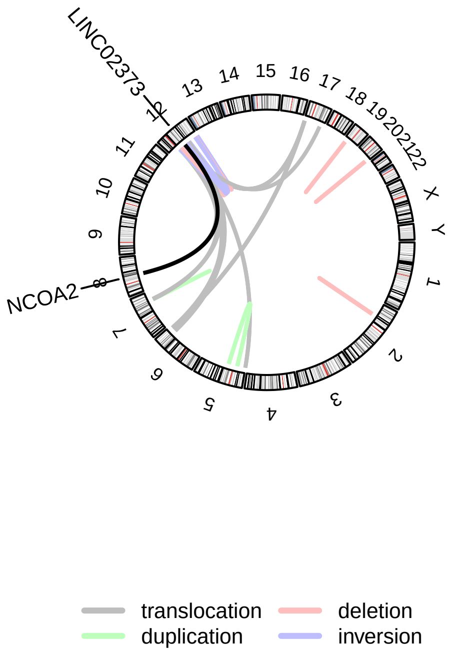


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 34
Discordant mates = 1

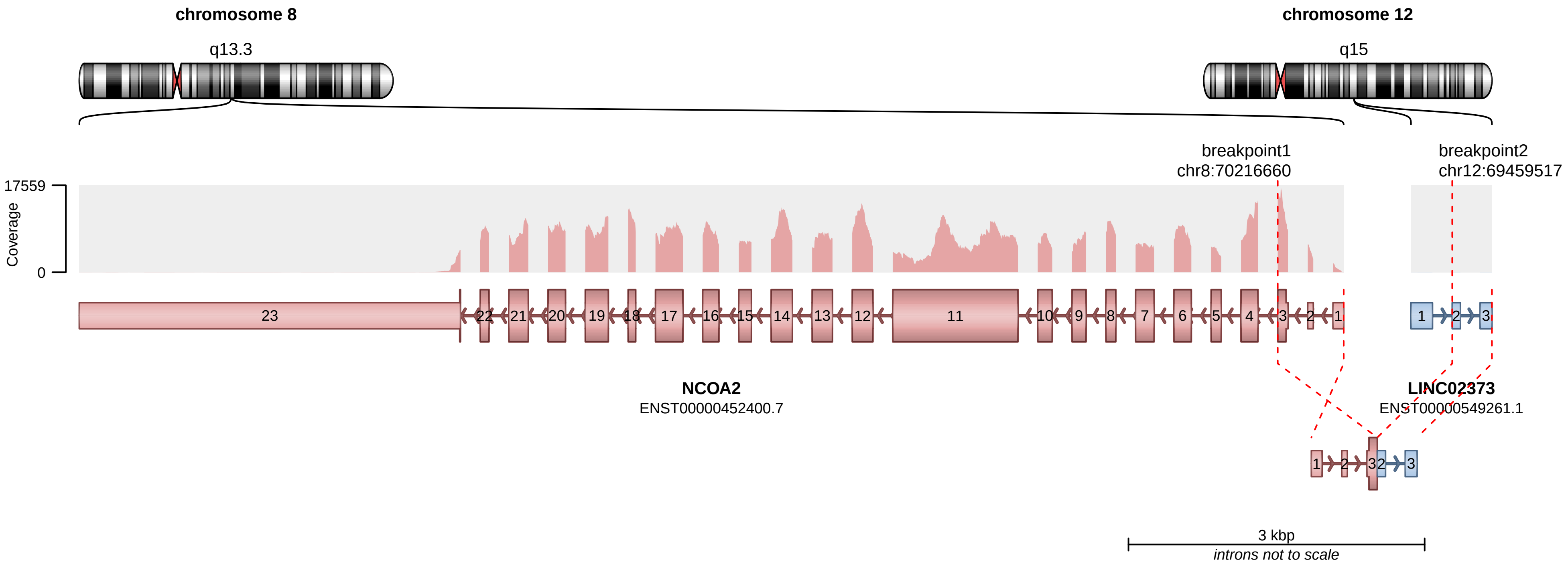


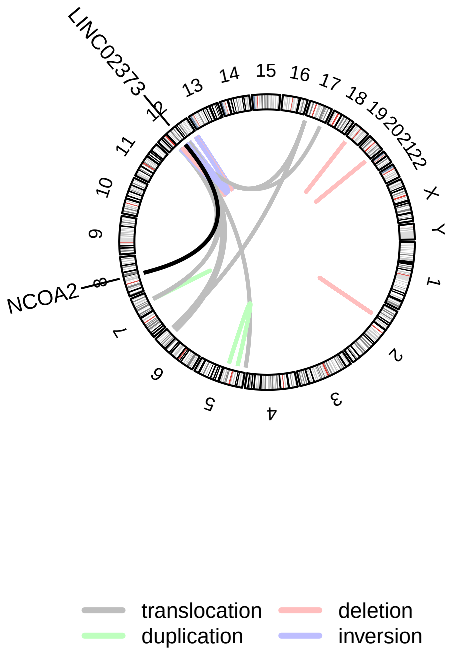


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 9
Discordant mates = 1

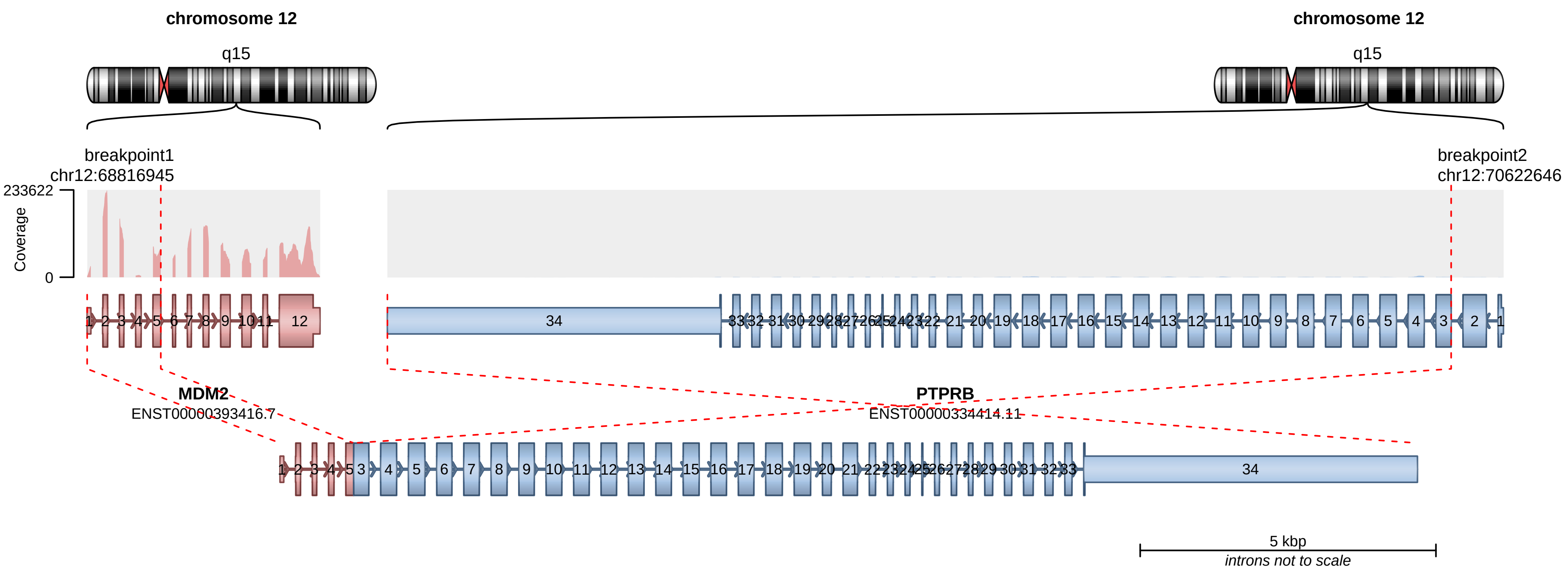


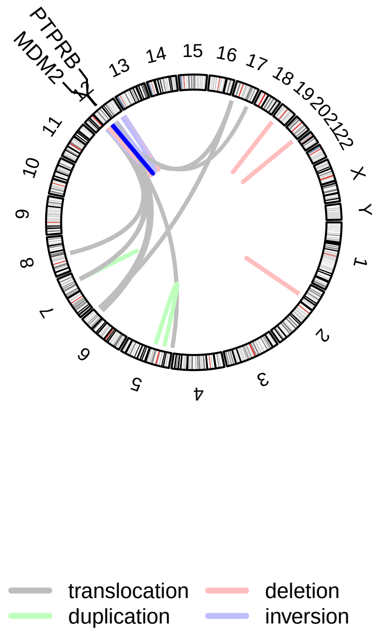


No protein domains retained in fusion.

SUPPORTING READ COUNT

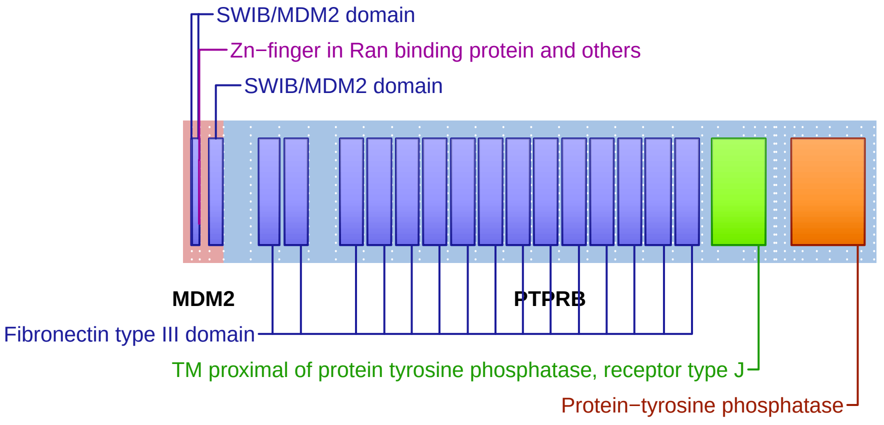
Split reads = 2
Discordant mates = 0





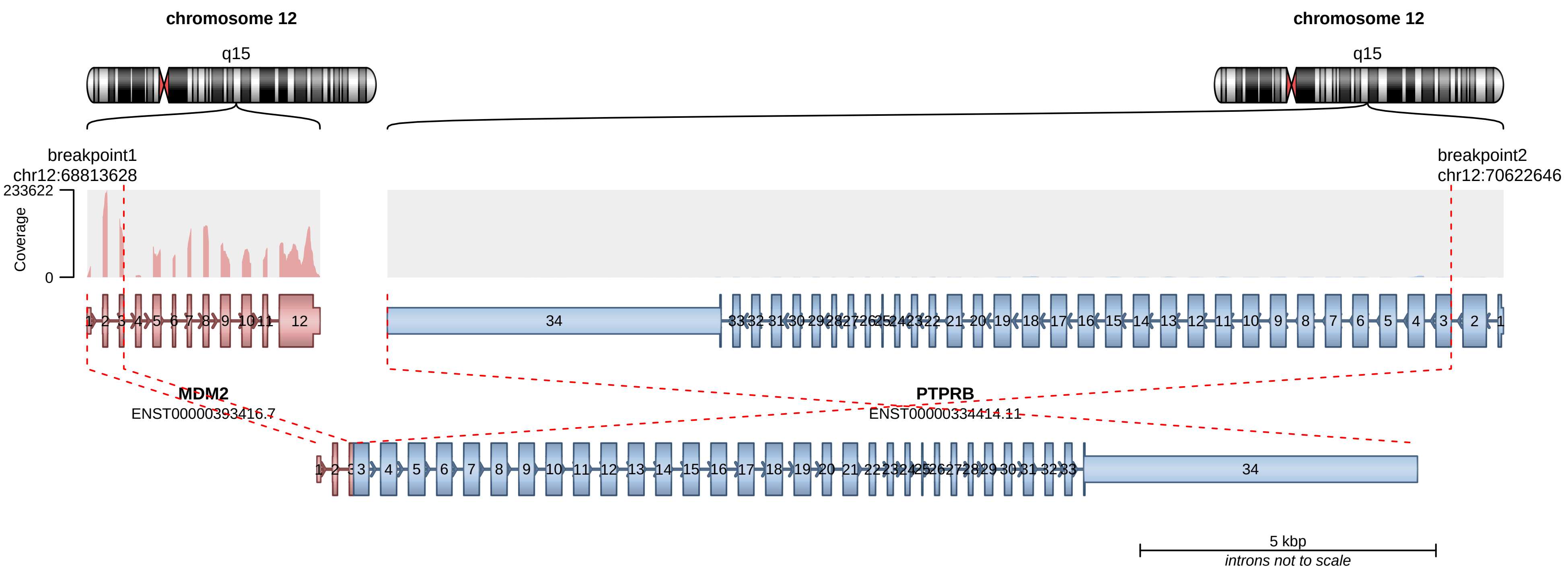
RETAINED PROTEIN DOMAINS

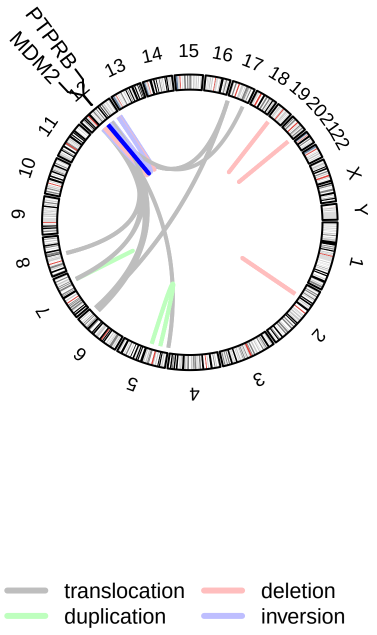
reading frame unclear

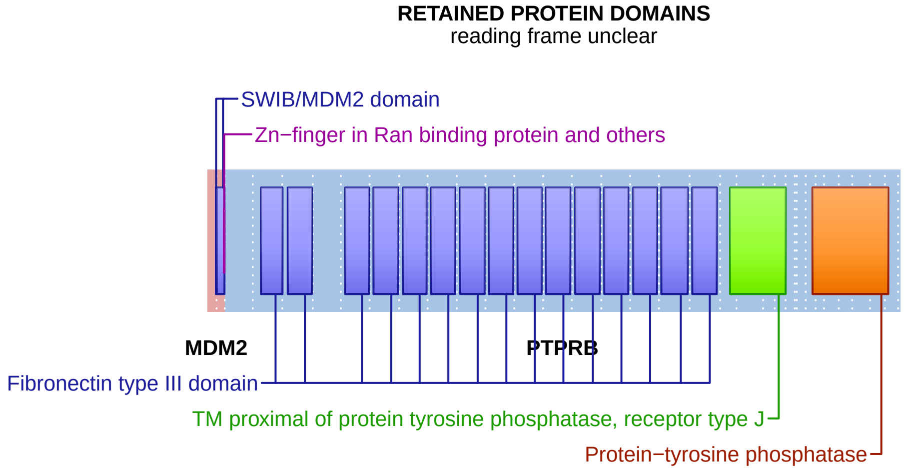


SUPPORTING READ COUNT

Split reads = 31
Discordant mates = 2

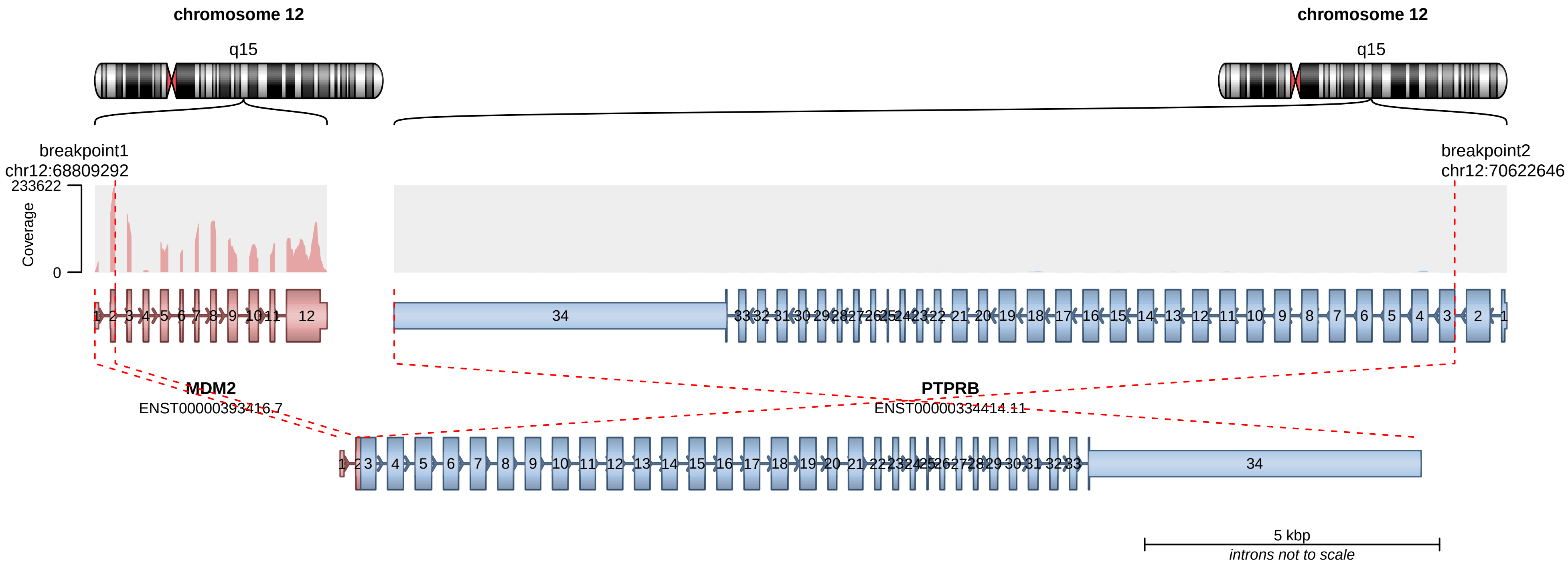


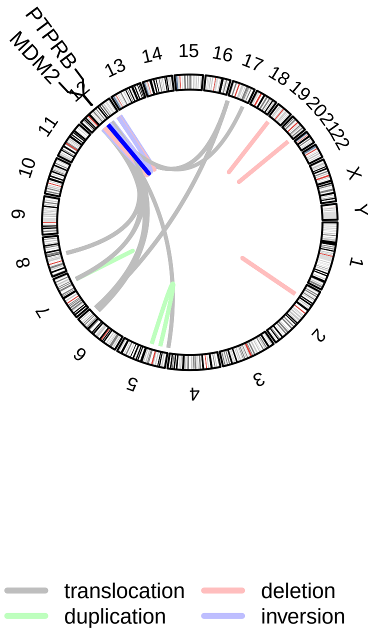




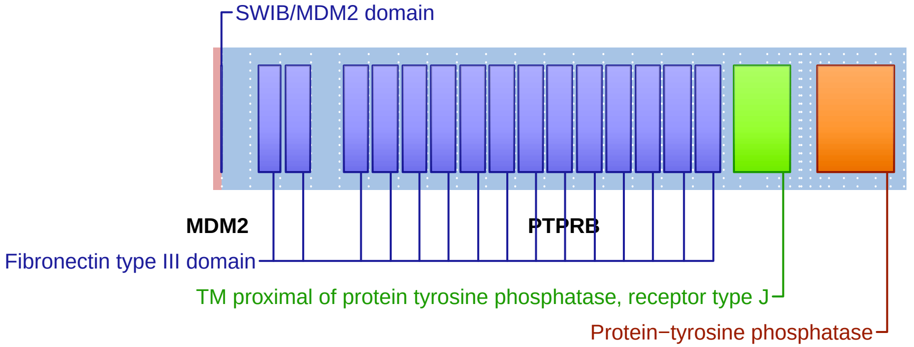
SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 1



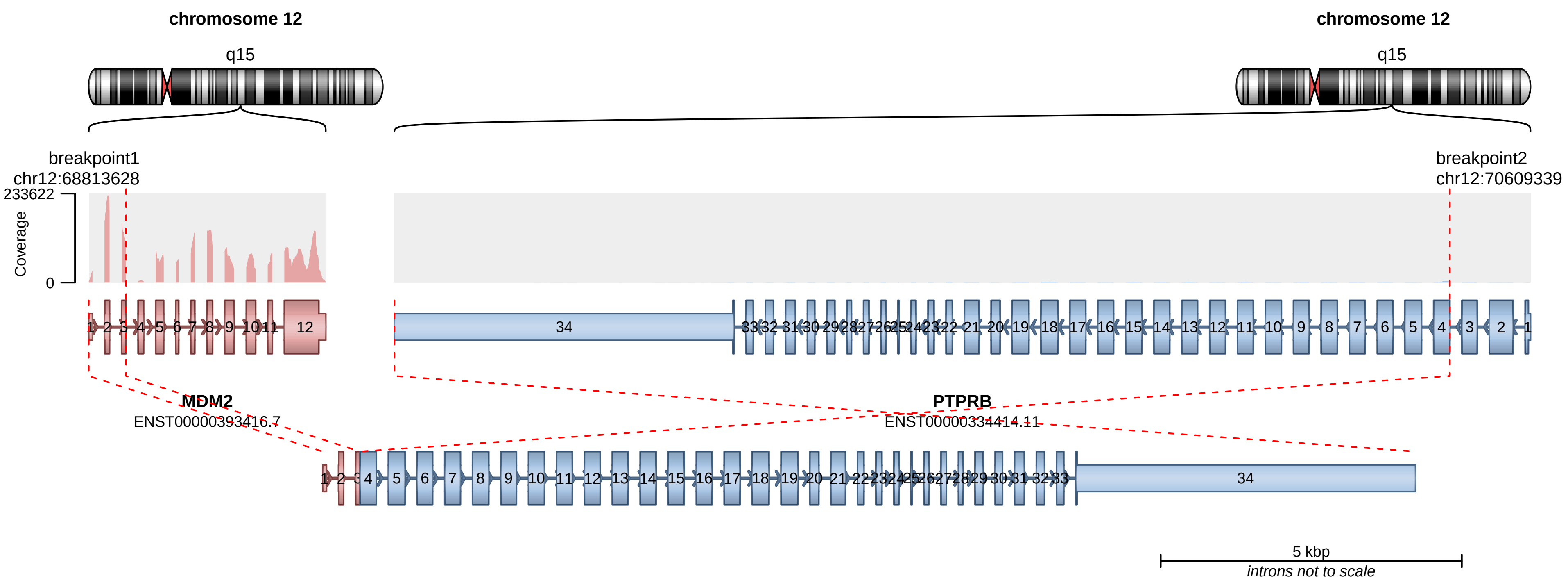


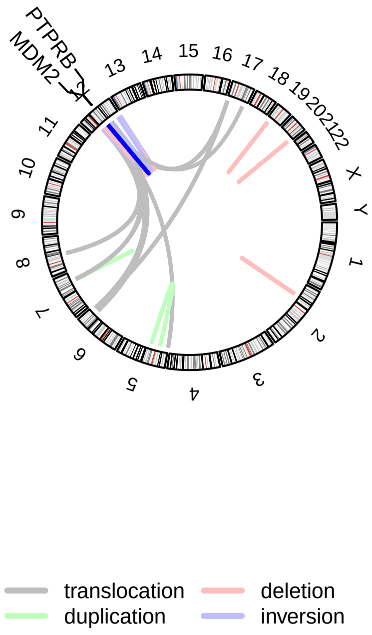
RETAINED PROTEIN DOMAINS
reading frame unclear



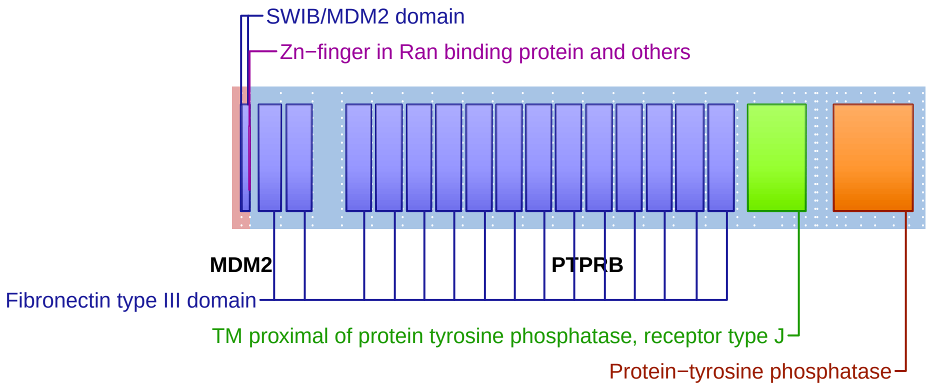
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1



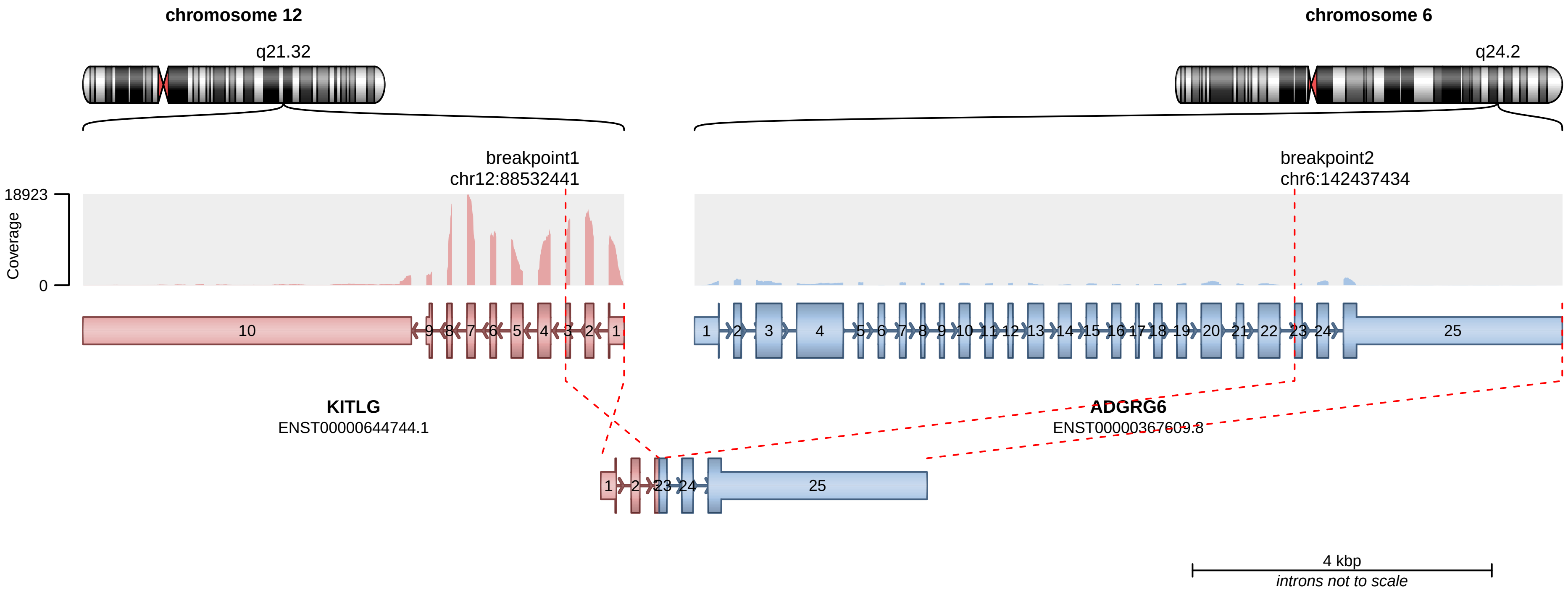


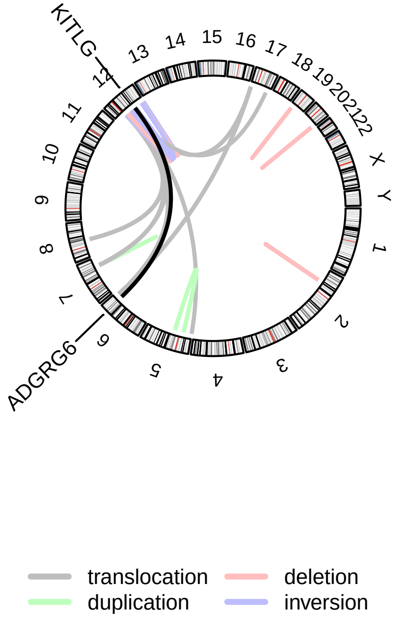
RETAINED PROTEIN DOMAINS
reading frame unclear

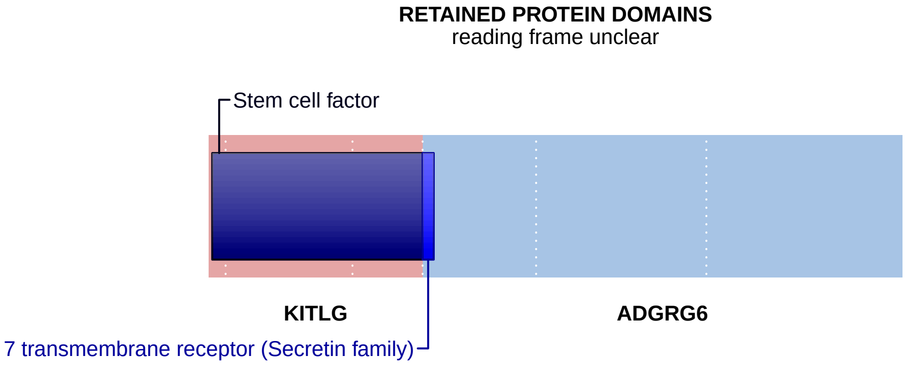


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

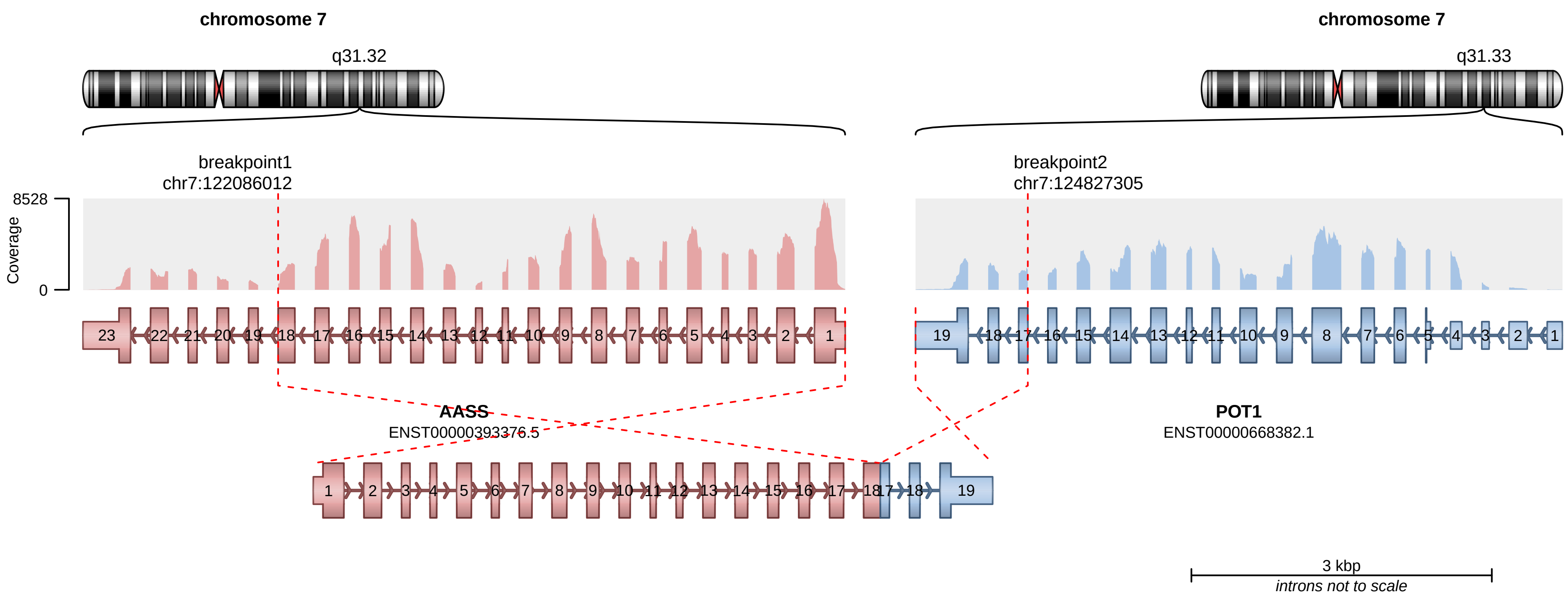


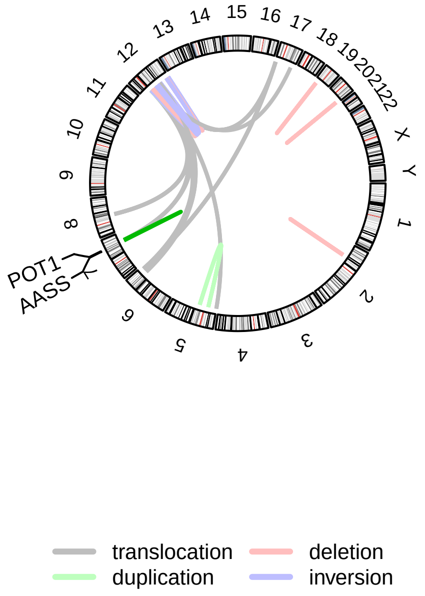


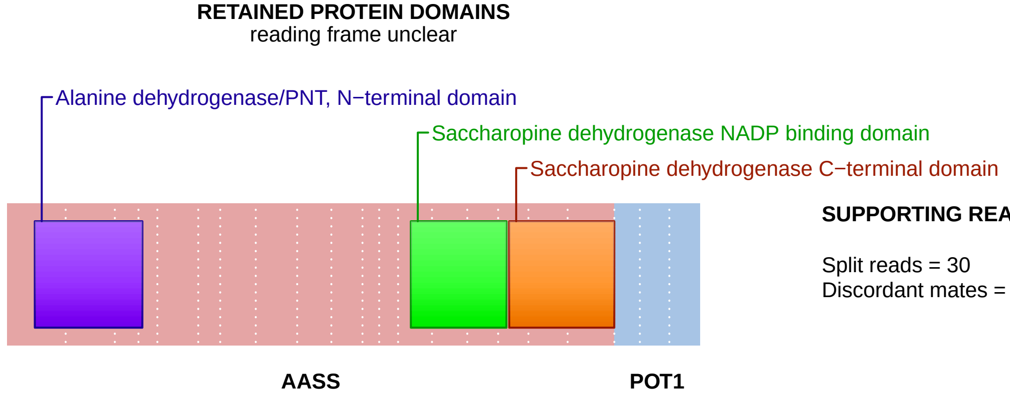


SUPPORTING READ COUNT

Split reads = 31
Discordant mates = 1

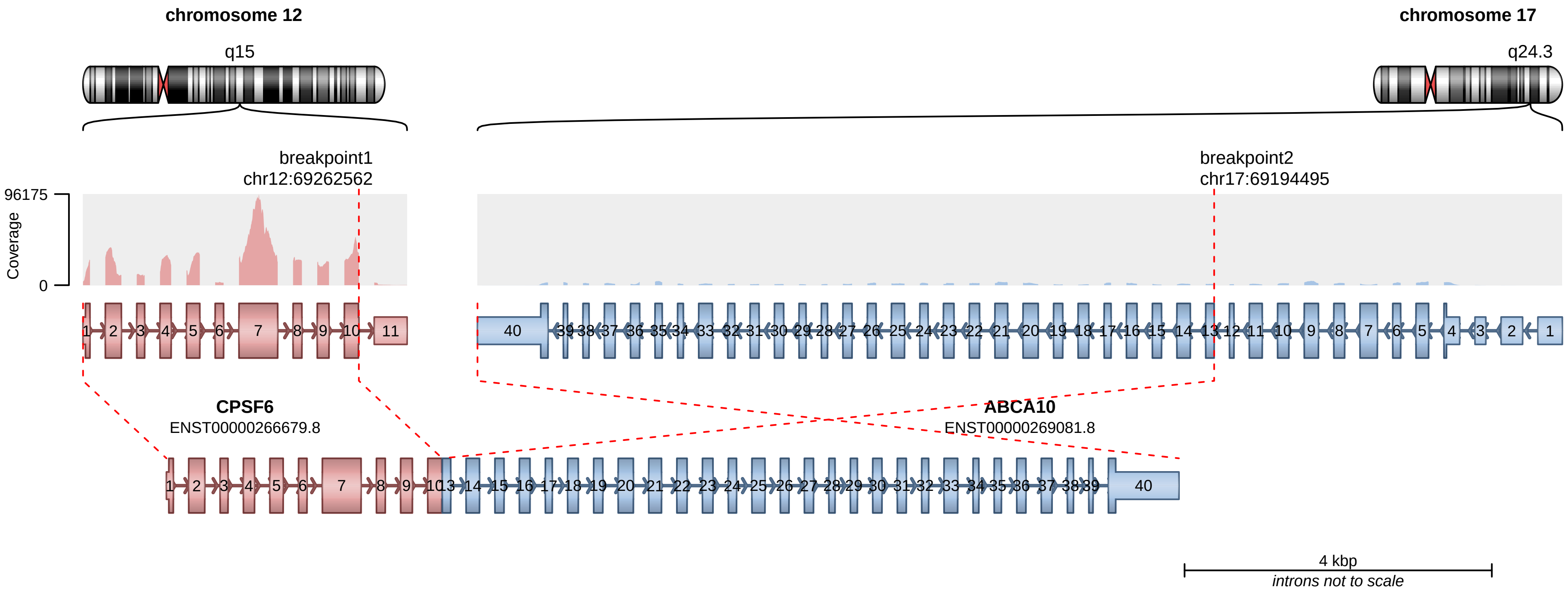


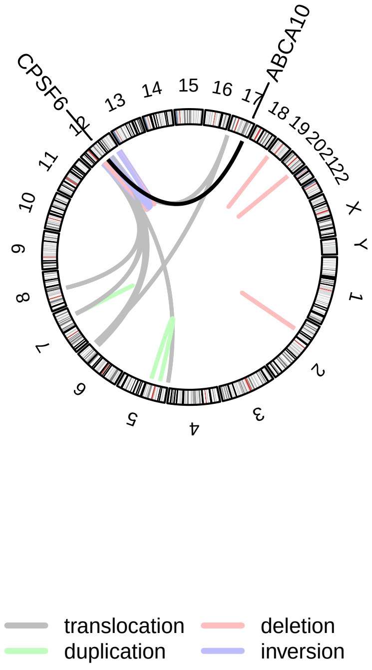




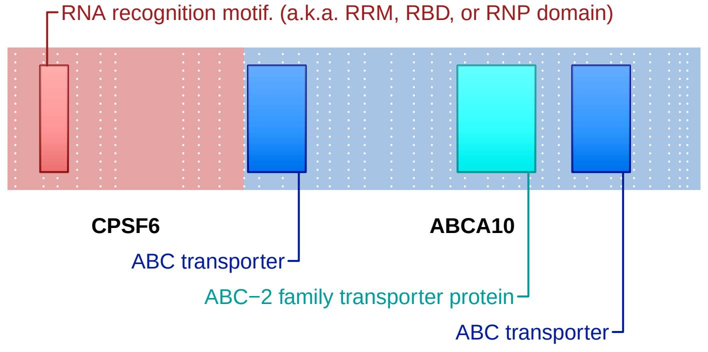
SUPPORTING READ COUNT

Split reads = 30
Discordant mates = 0



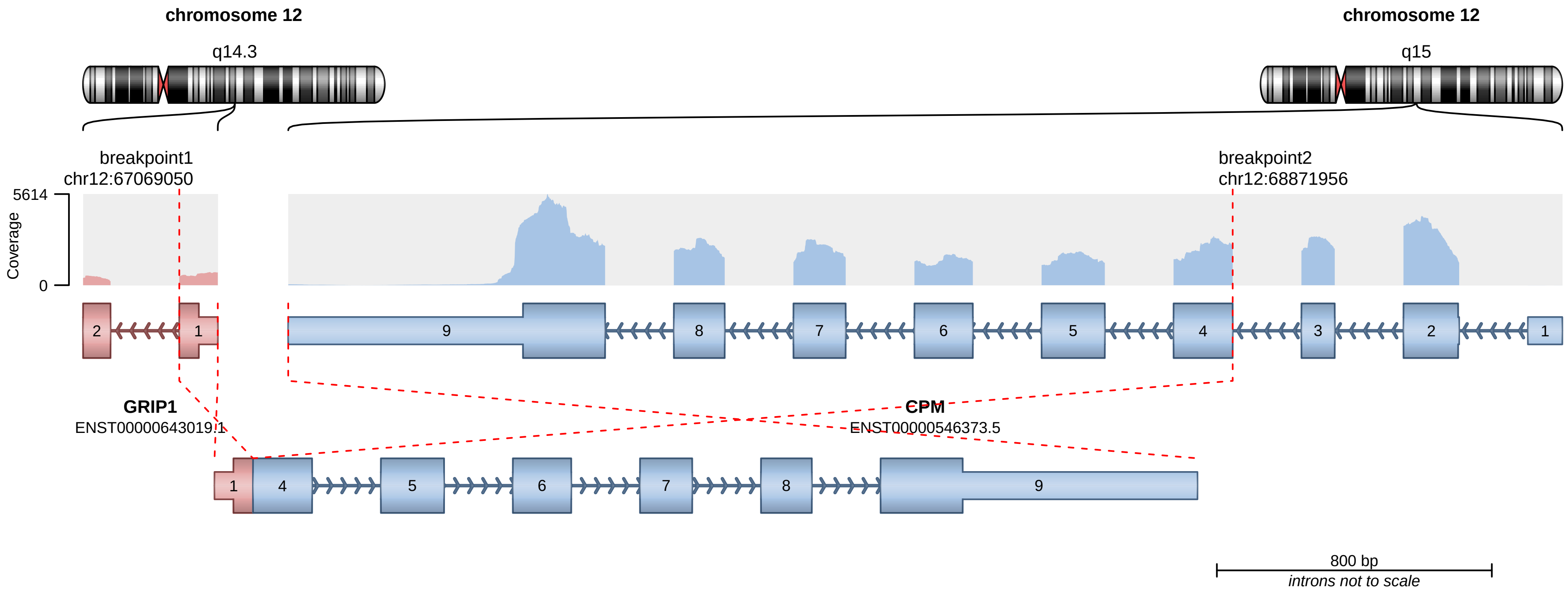


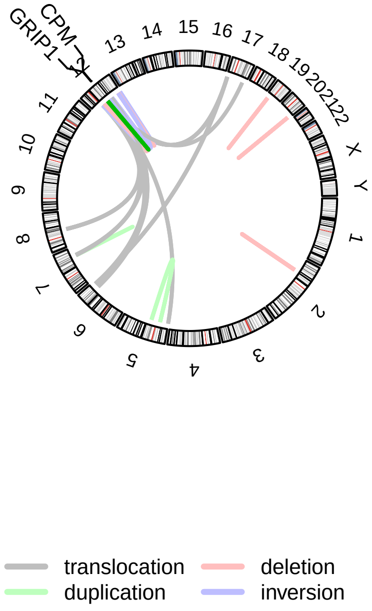
RETAINED PROTEIN DOMAINS
reading frame unclear

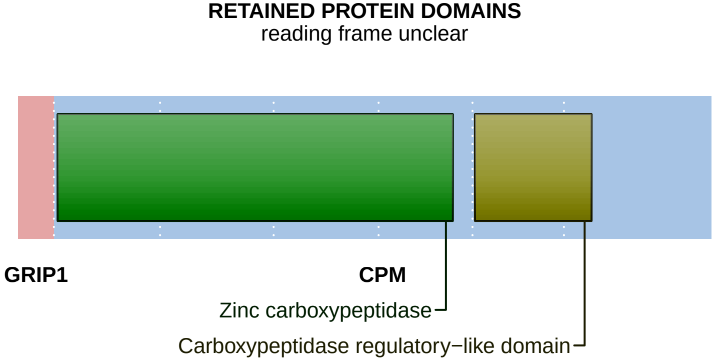


SUPPORTING READ COUNT

Split reads = 24
Discordant mates = 0

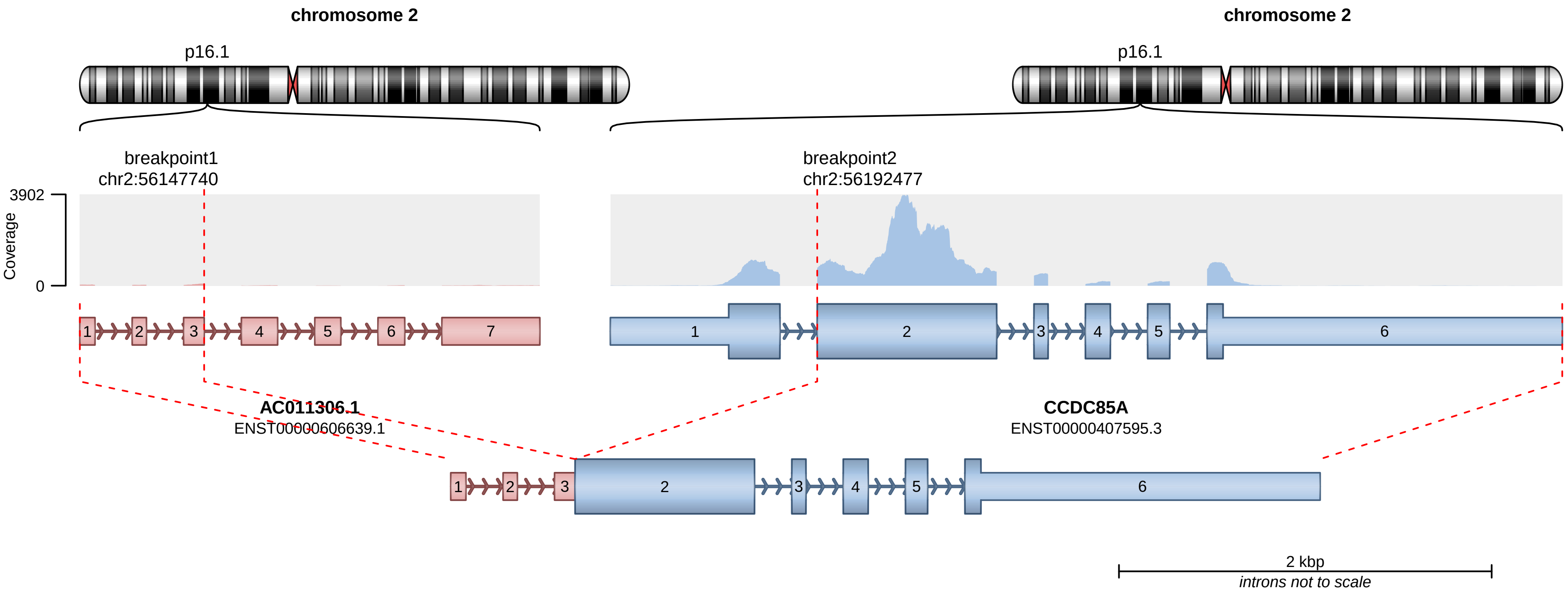


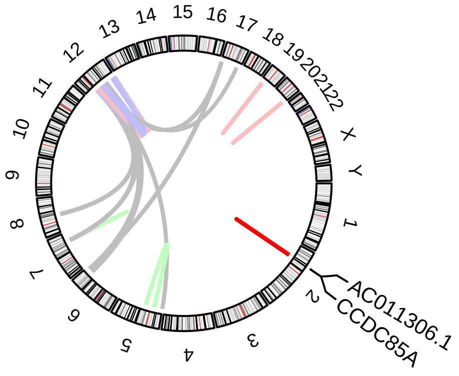




SUPPORTING READ COUNT

Split reads = 22
Discordant mates = 0

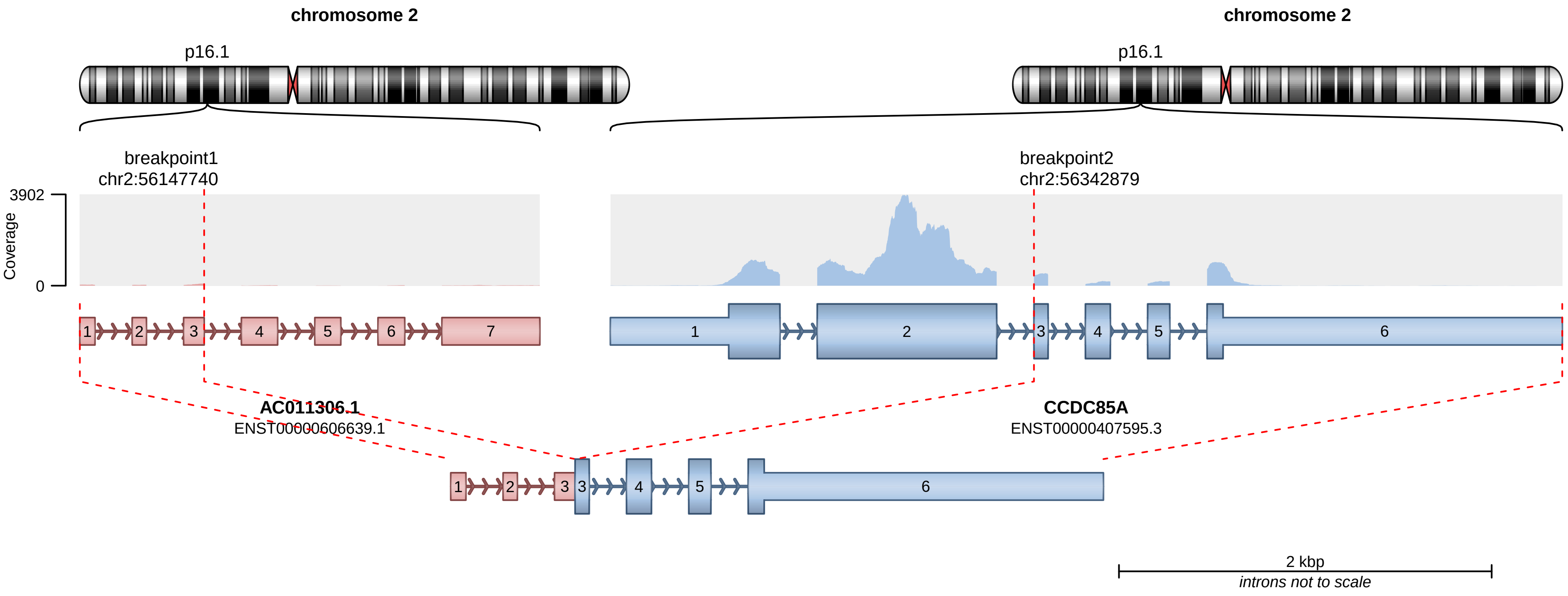


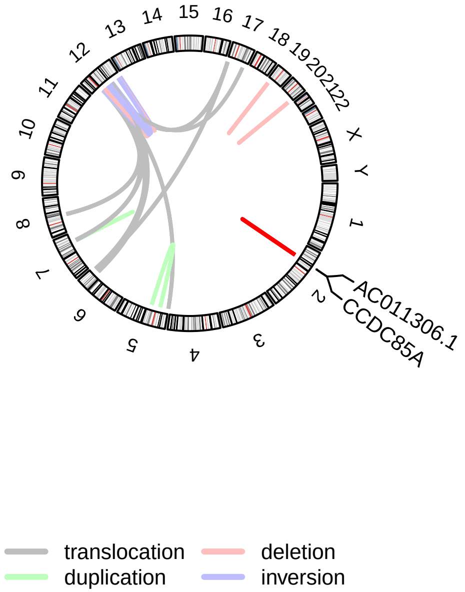


RETAINED PROTEIN DOMAINS
reading frame unclear

SUPPORTING READ COUNT

Split reads = 21
Discordant mates = 0

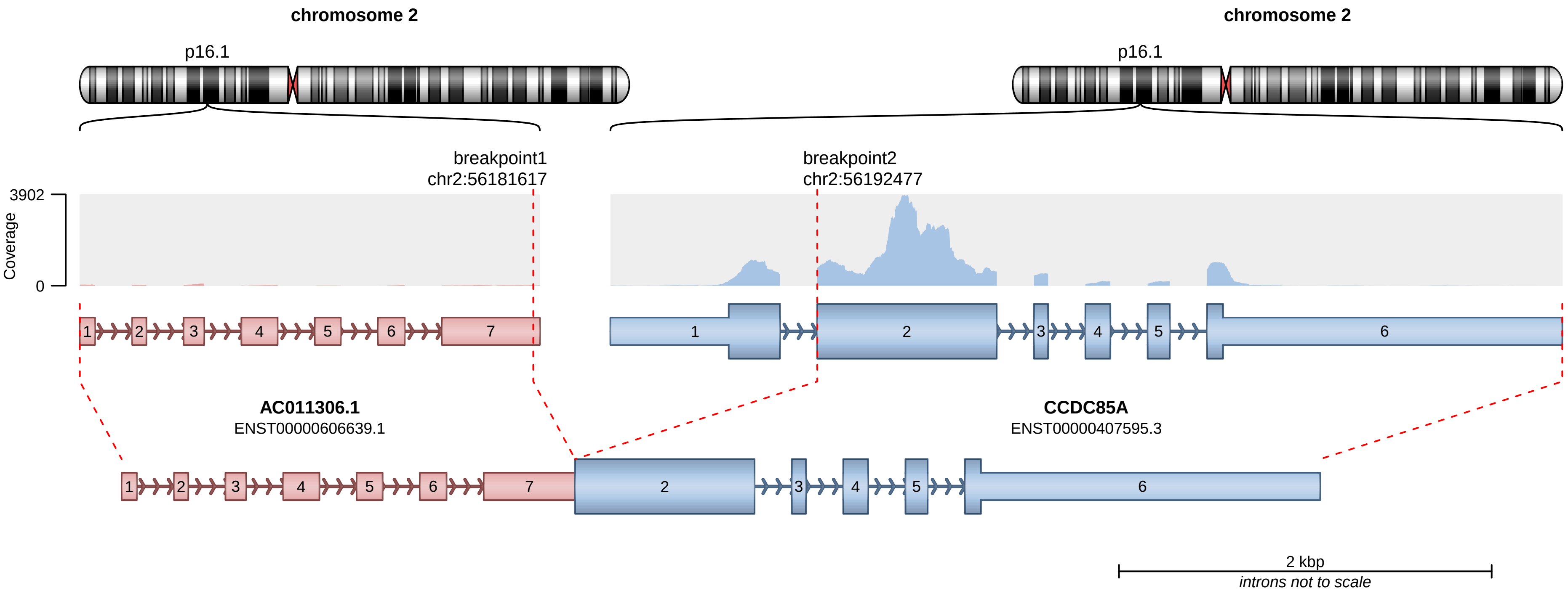


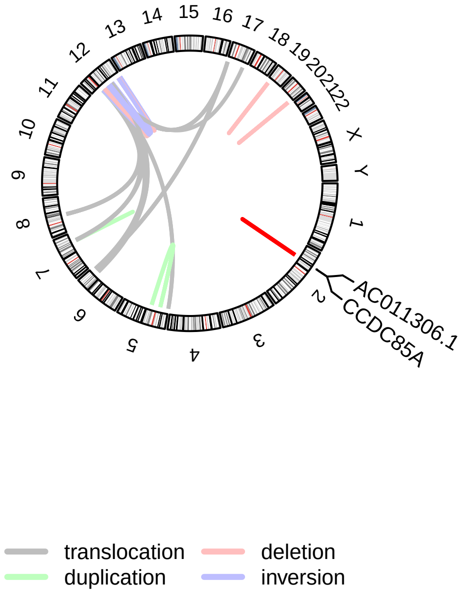


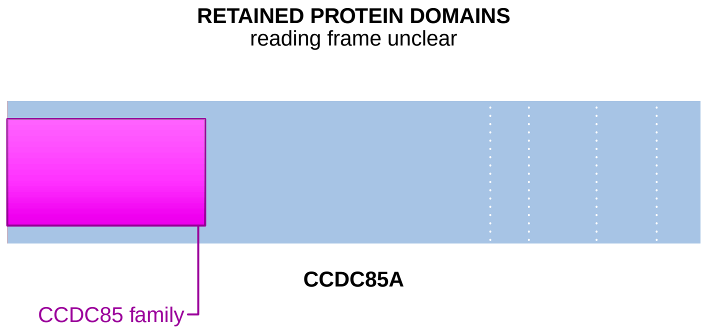
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 15
Discordant mates = 0

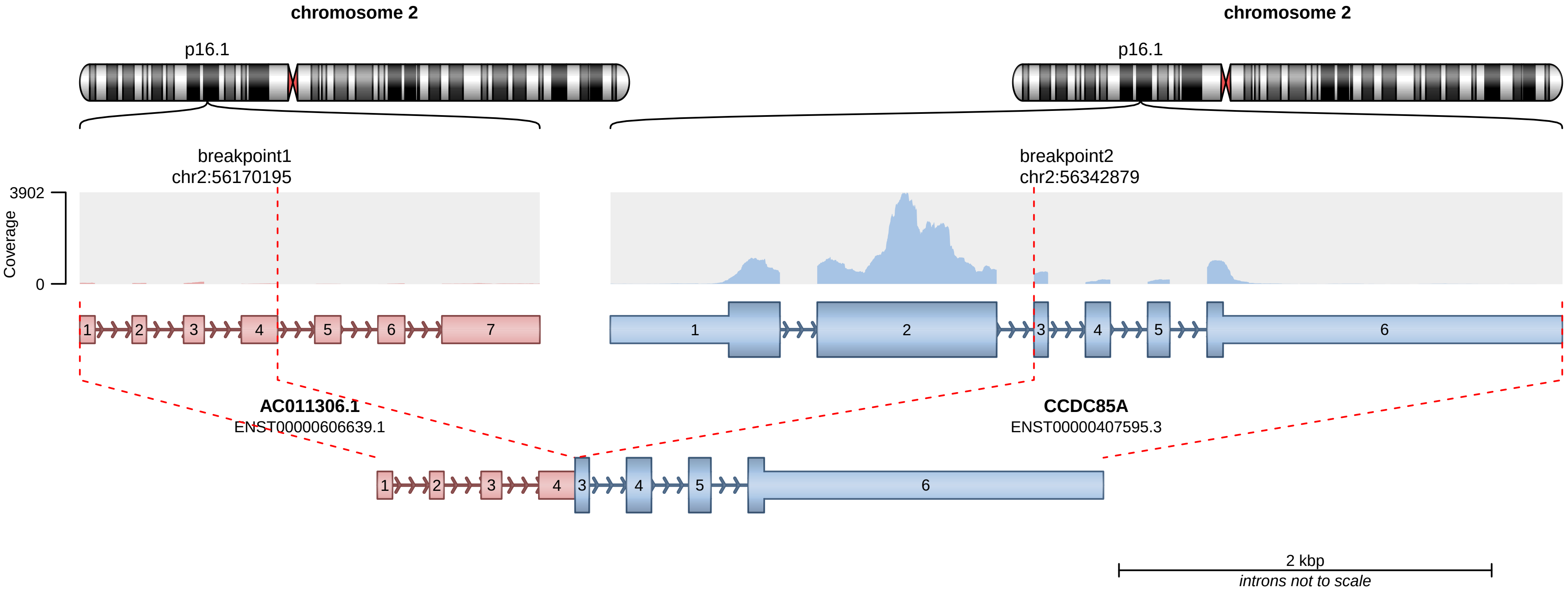


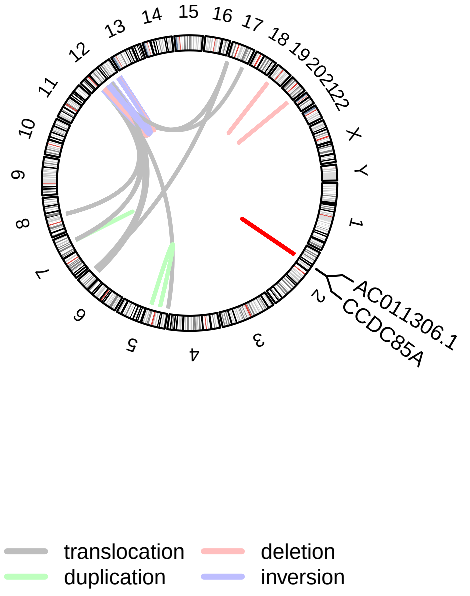




SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0

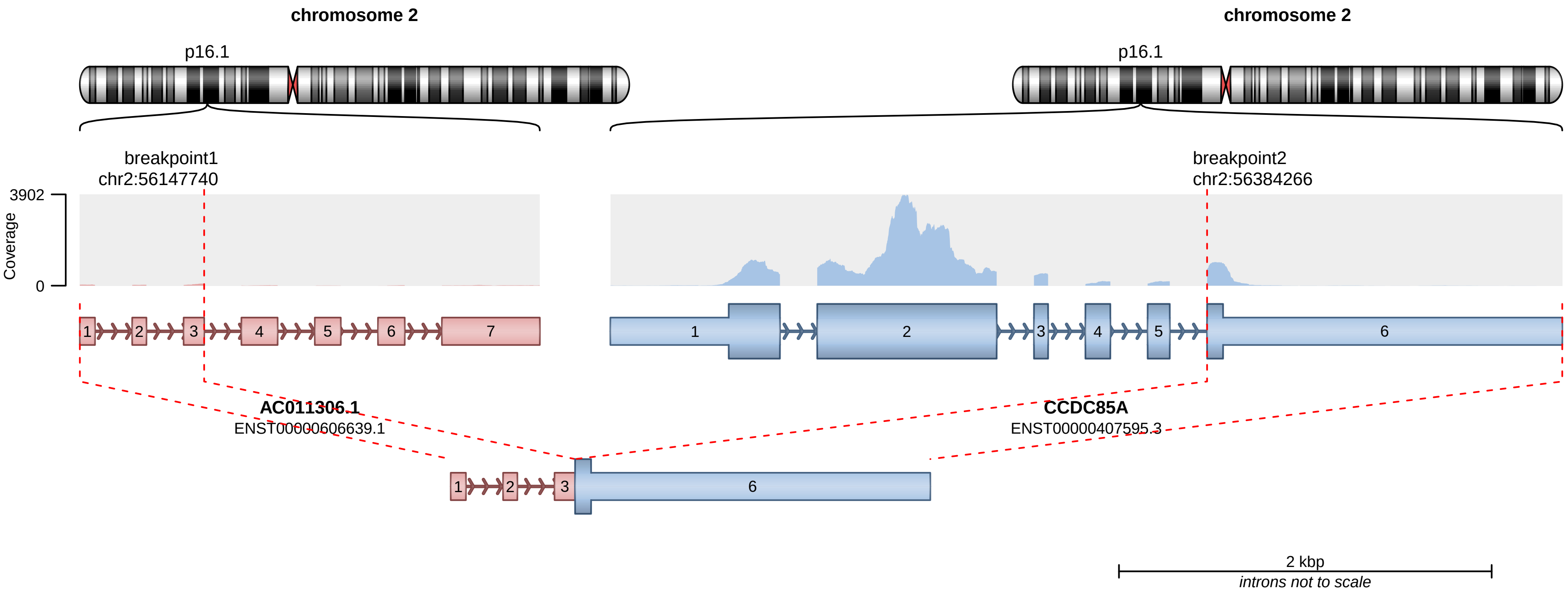


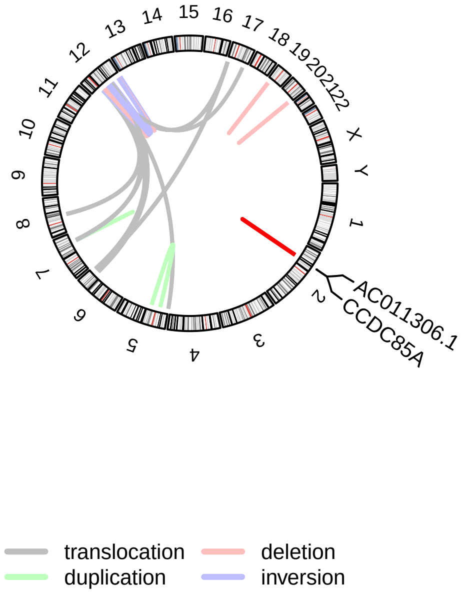


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

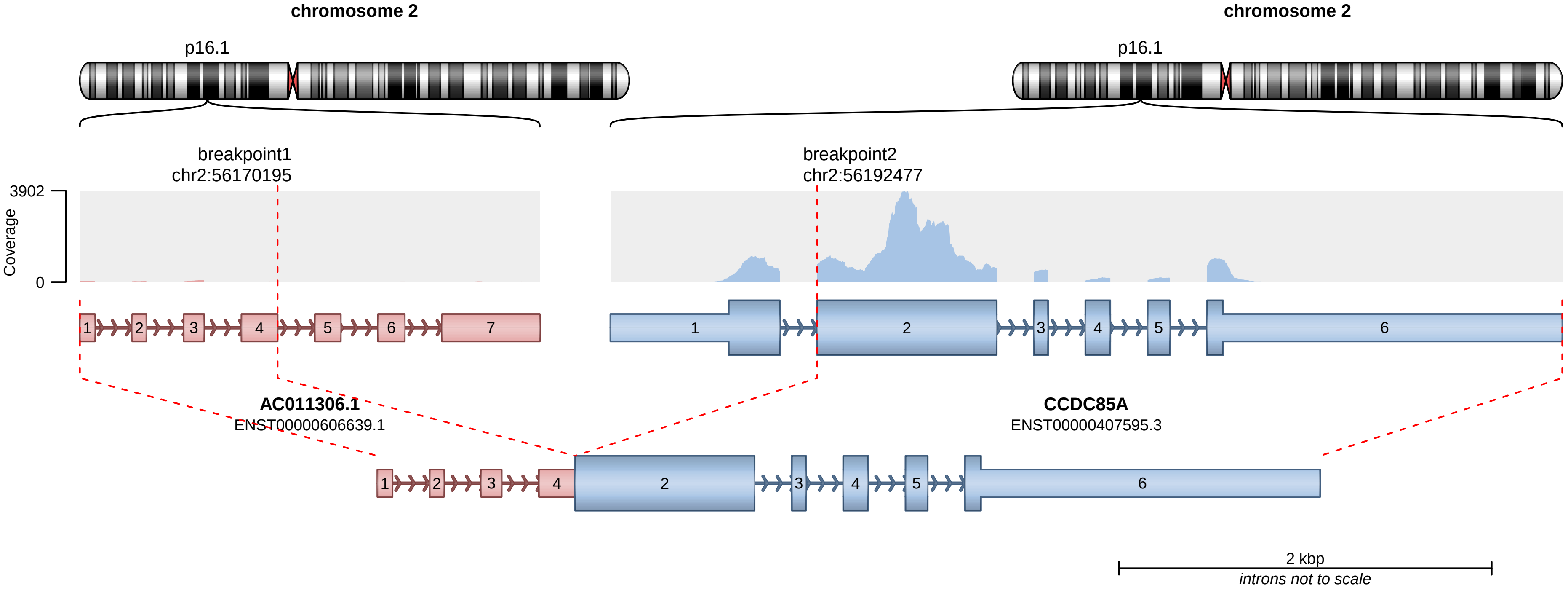


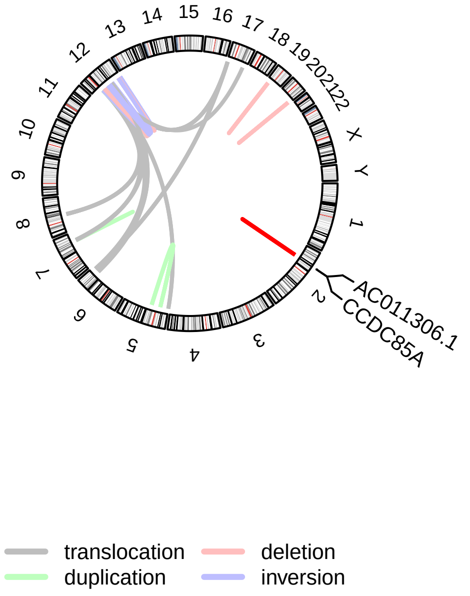


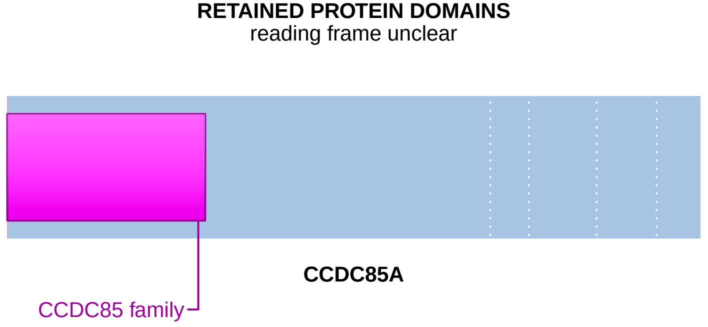
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

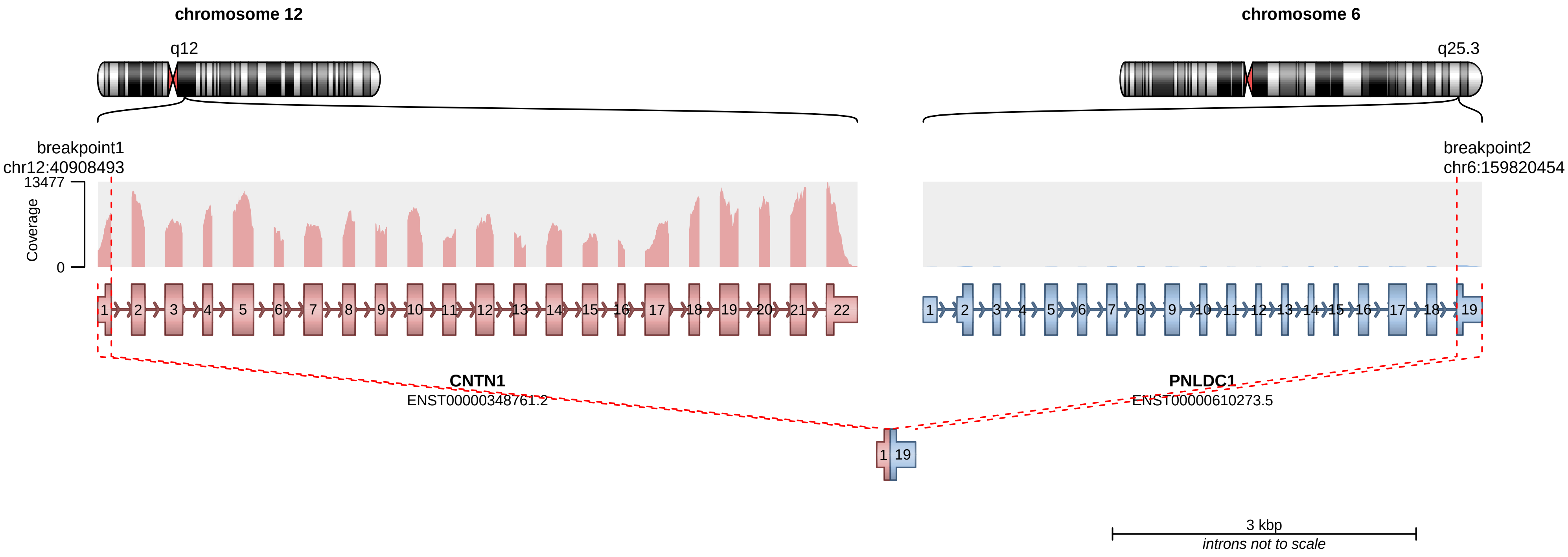


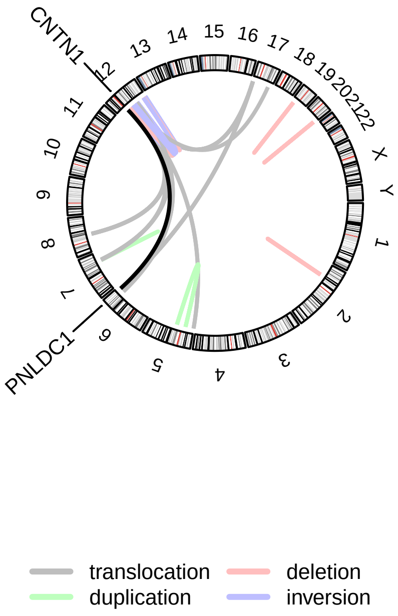




SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

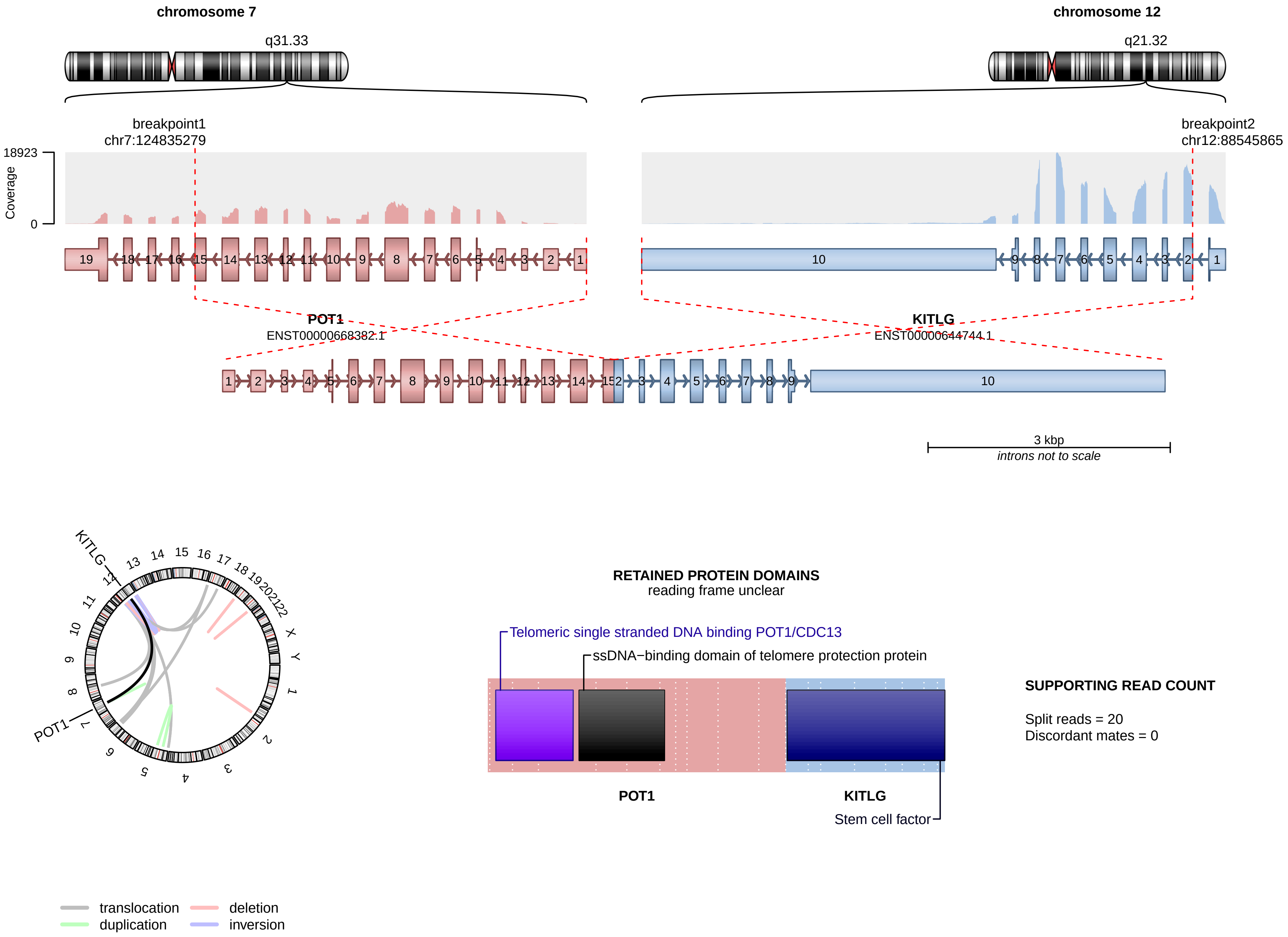


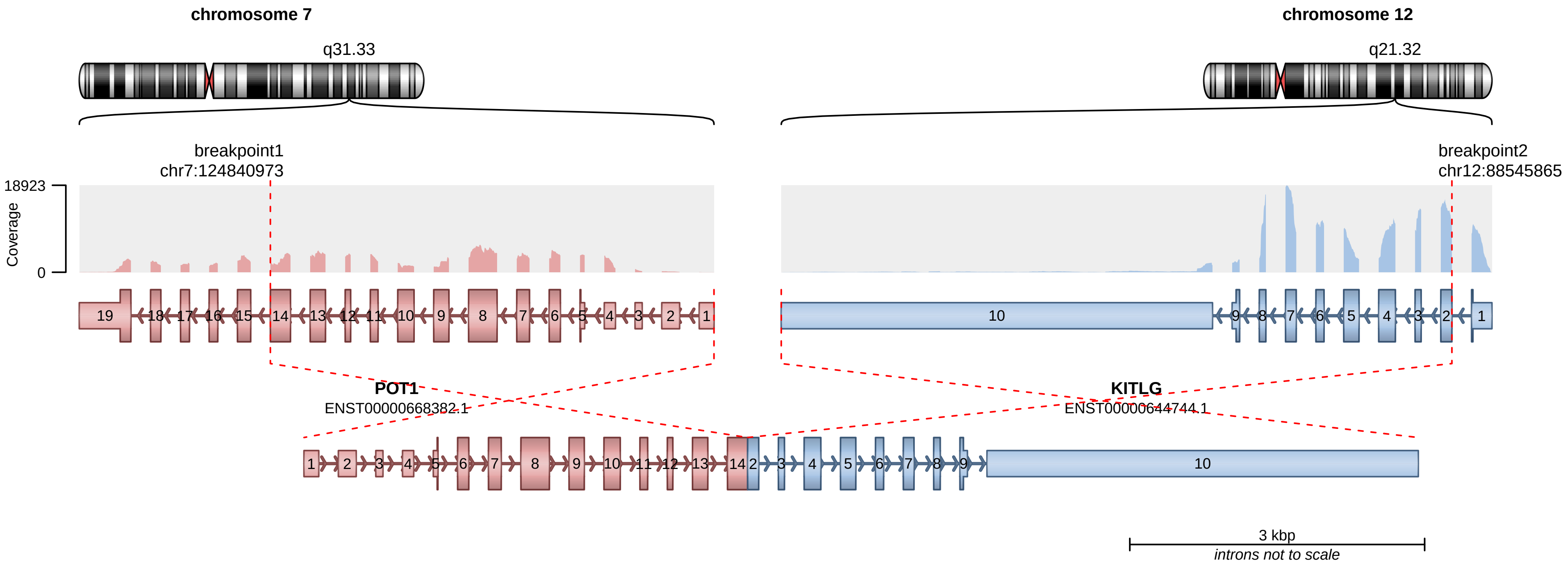


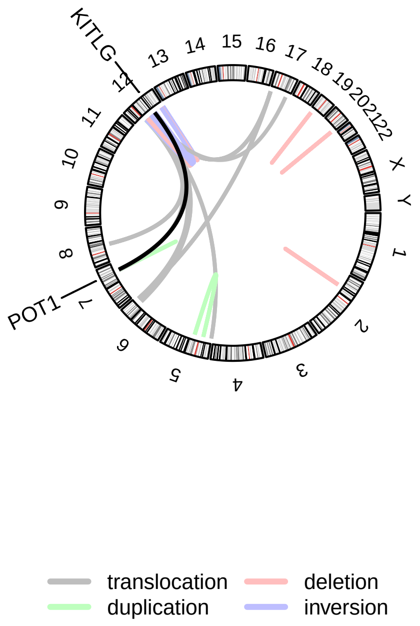
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 21
Discordant mates = 0

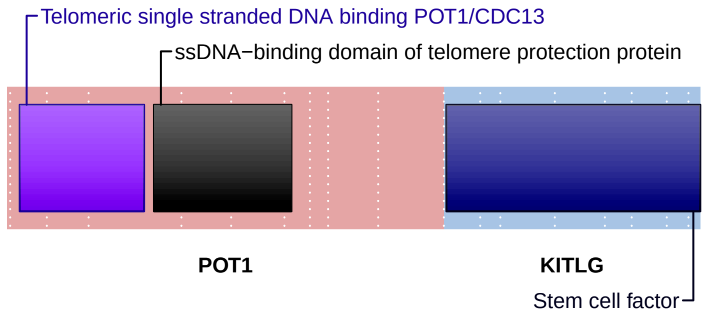

chromosome 7
q31.33
chromosome 12
q21.32
breakpoint1
chr7:124835279
breakpoint2
chr12:88545865
18923
Coverage
0
19 18 17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1
10 9 8 7 6 5 4 3 2 1
POT1
ENST00000668382.1
KITLG
ENST00000644744.1
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 2 3 4 5 6 7 8 9 10
3 kbp
introns not to scale
KITLG
POT1
13 14 15 16 17 18 19 20 21 22 X Y 1 2 3 4 5 6 7 8 9 10 11 12
RETAINED PROTEIN DOMAINS
reading frame unclear
Telomeric single stranded DNA binding POT1/CDC13
ssDNA−binding domain of telomere protection protein
POT1
KITLG
Stem cell factor
SUPPORTING READ COUNT
Split reads = 20
Discordant mates = 0
translocation
duplication
deletion
inversion





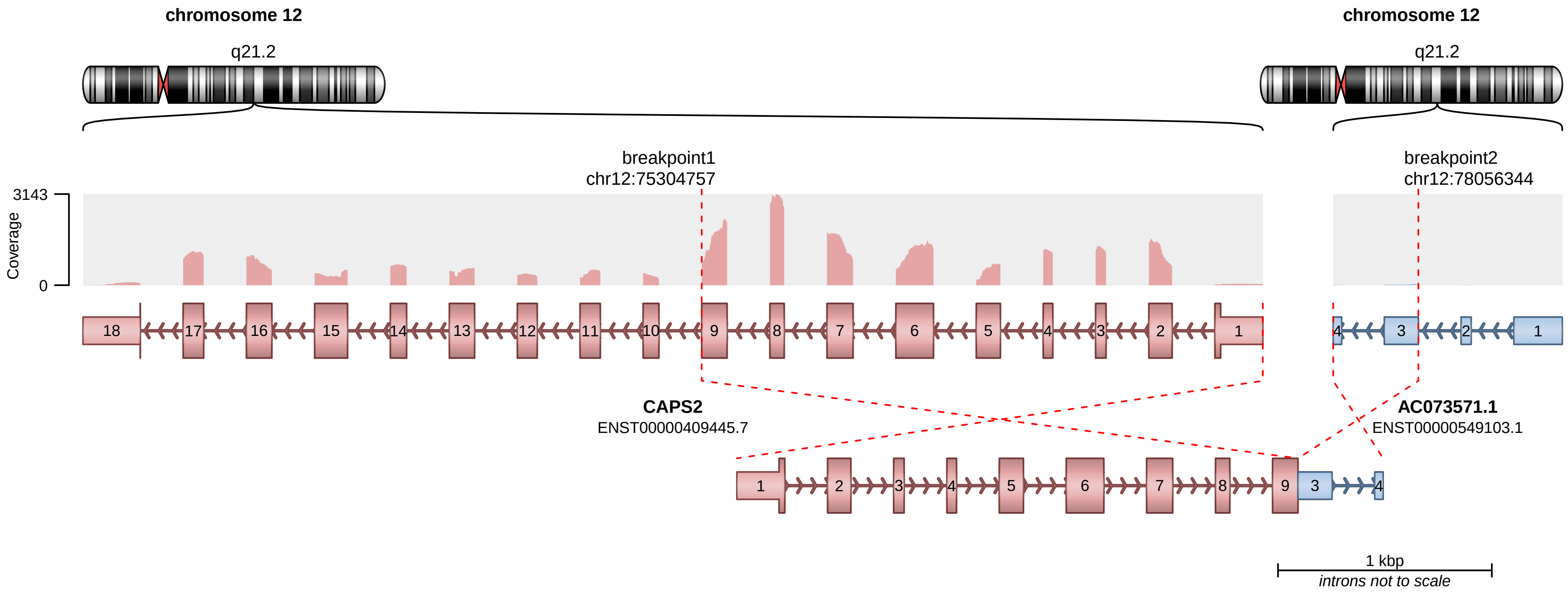
RETAINED PROTEIN DOMAINS

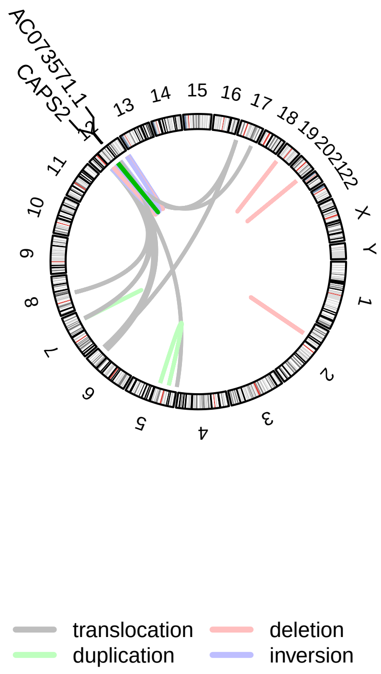
reading frame unclear



SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

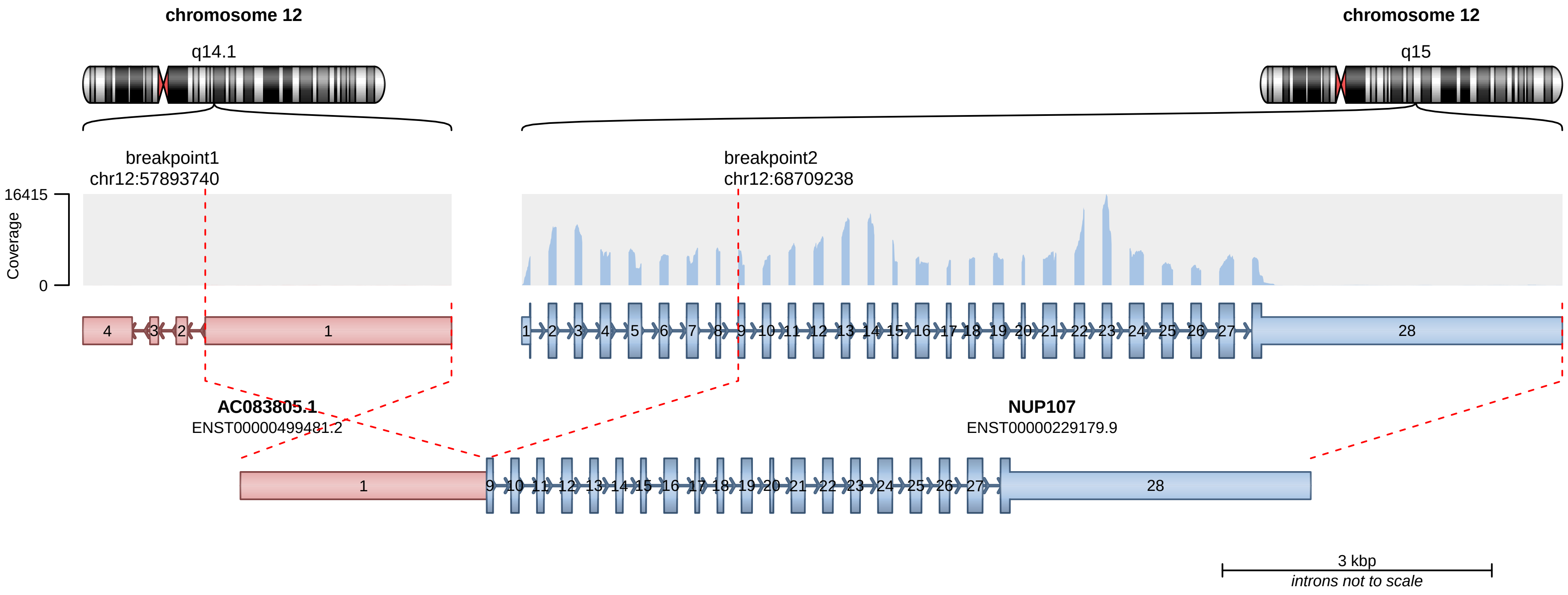


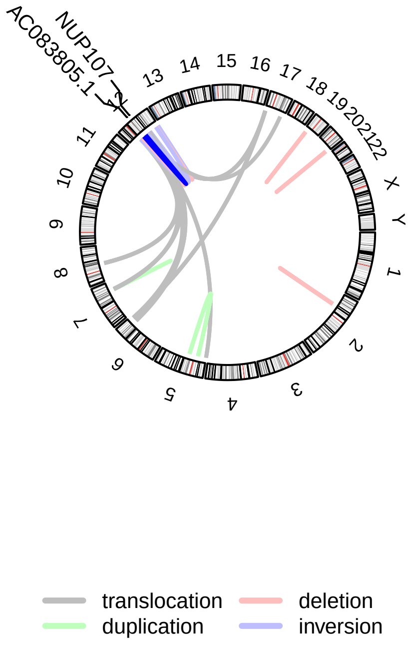


No protein domains retained in fusion.

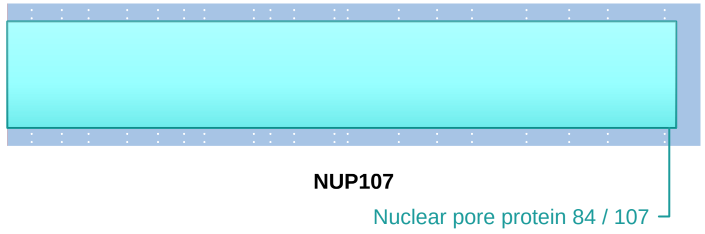
SUPPORTING READ COUNT

Split reads = 19
Discordant mates = 0



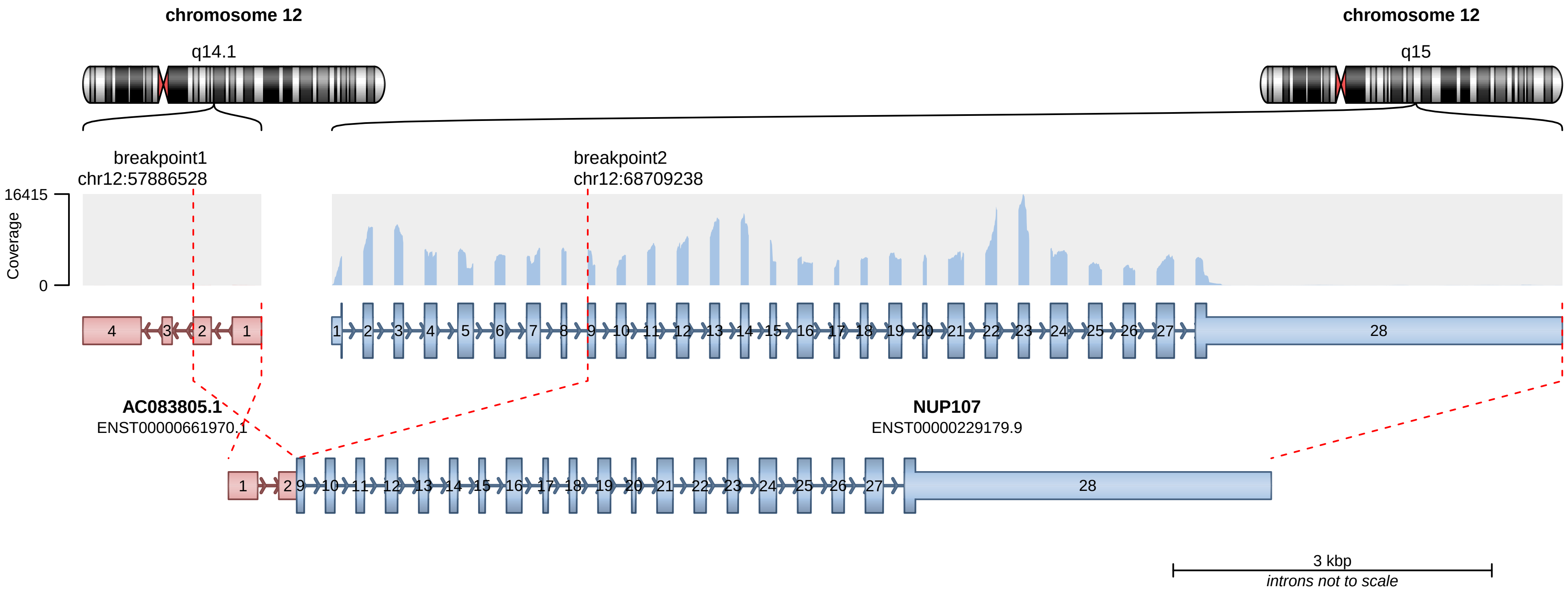


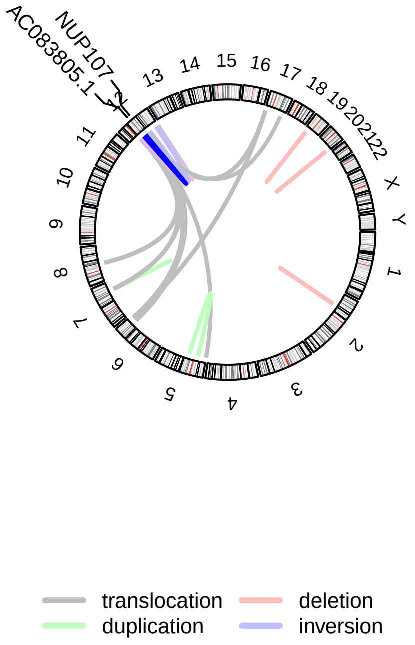
RETAINED PROTEIN DOMAINS
reading frame unclear



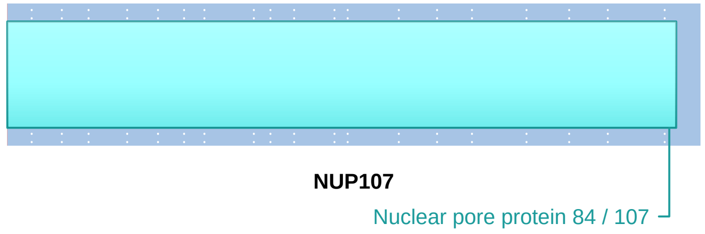
SUPPORTING READ COUNT

Split reads = 17
Discordant mates = 0



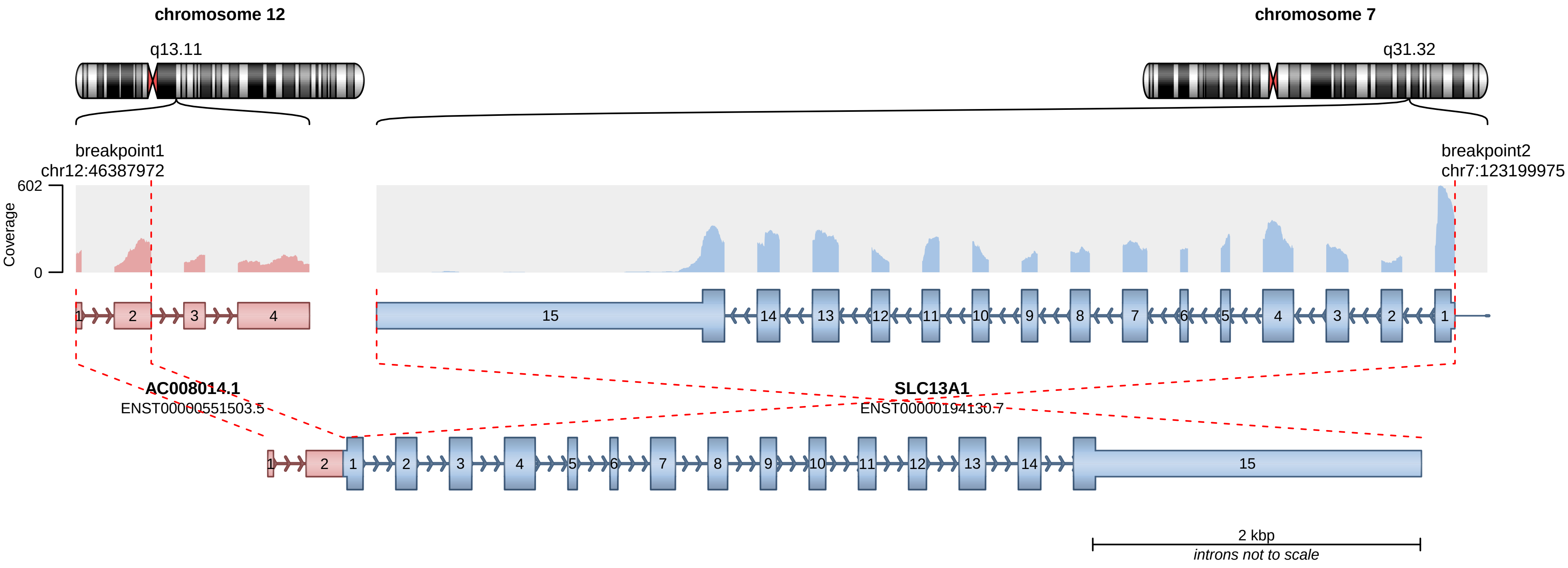


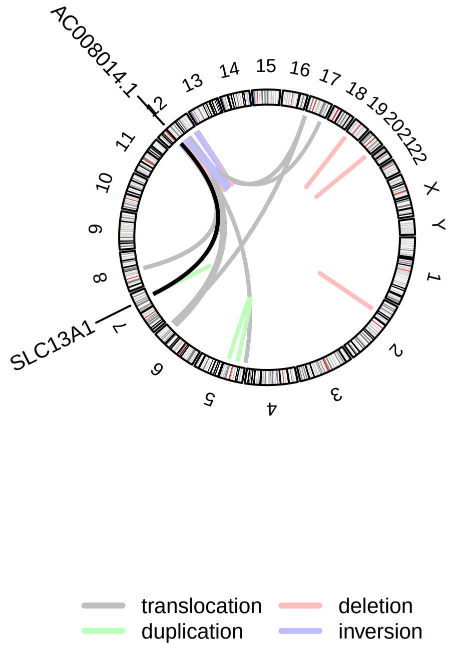
RETAINED PROTEIN DOMAINS
reading frame unclear

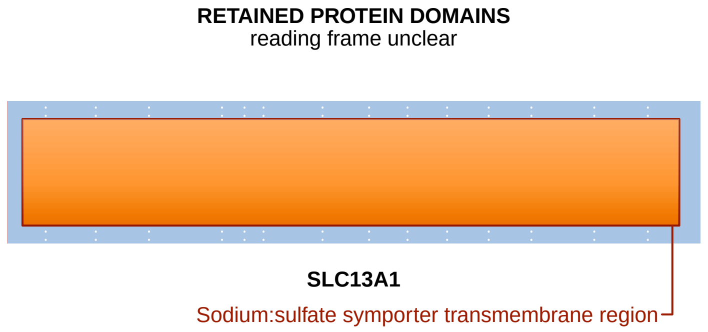


SUPPORTING READ COUNT

Split reads = 9
Discordant mates = 0

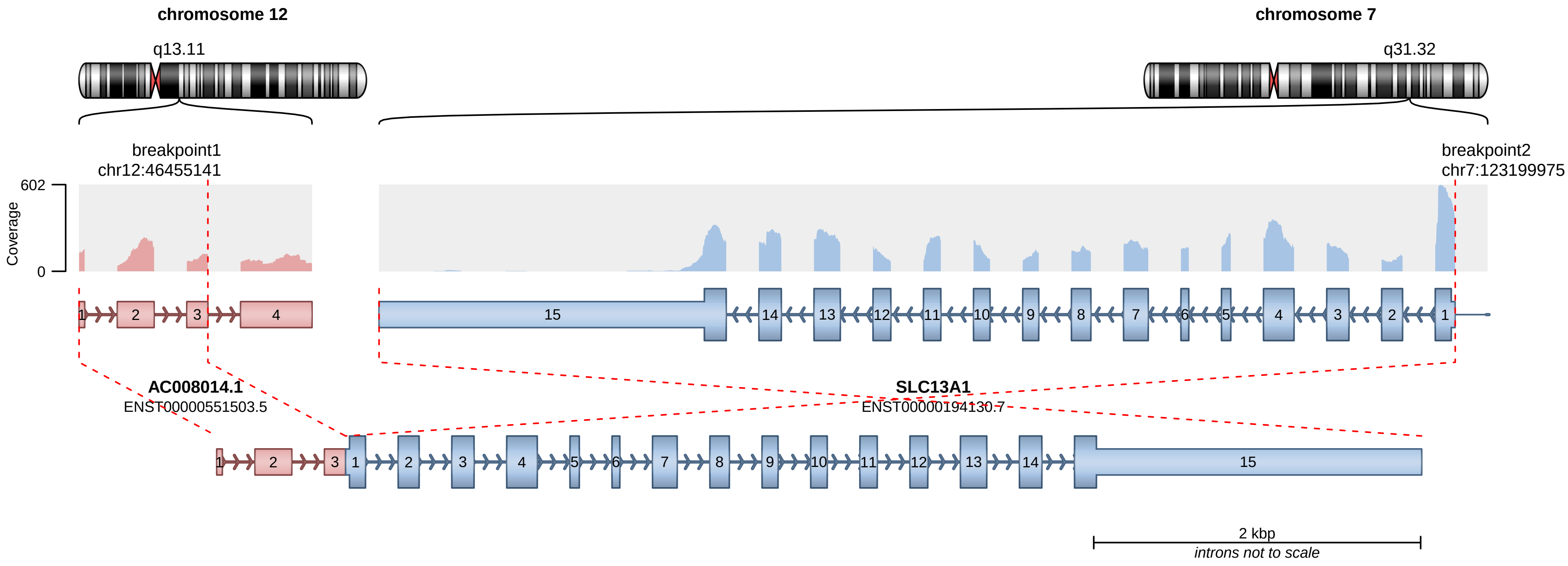


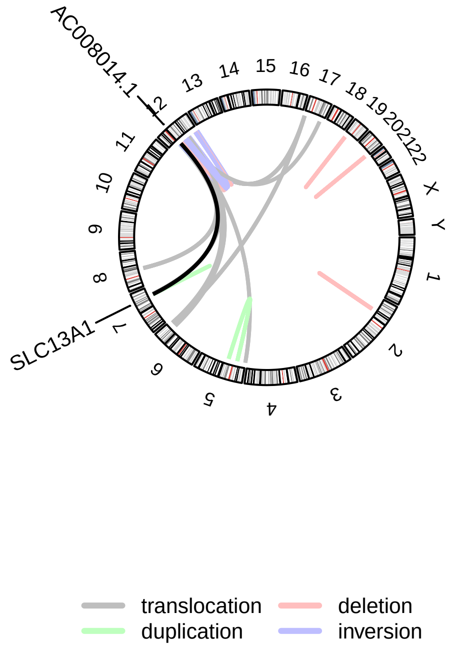


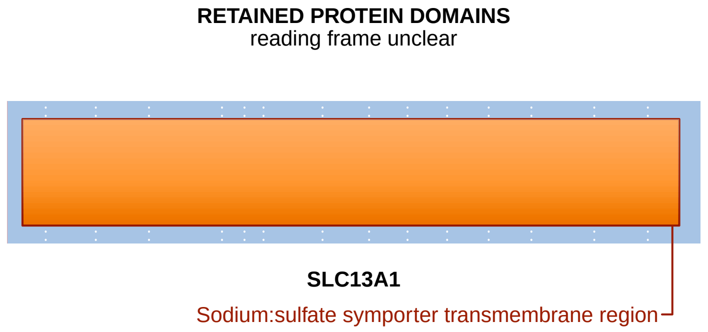


SUPPORTING READ COUNT

Split reads = 15
Discordant mates = 0

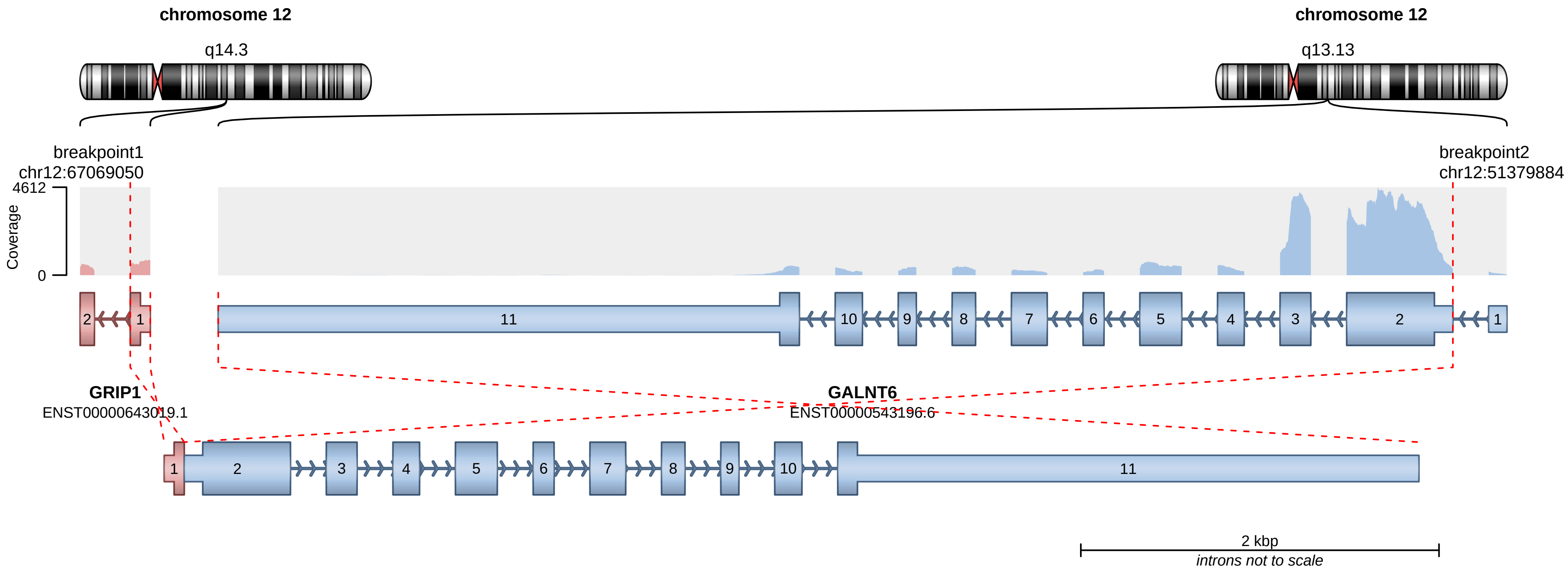


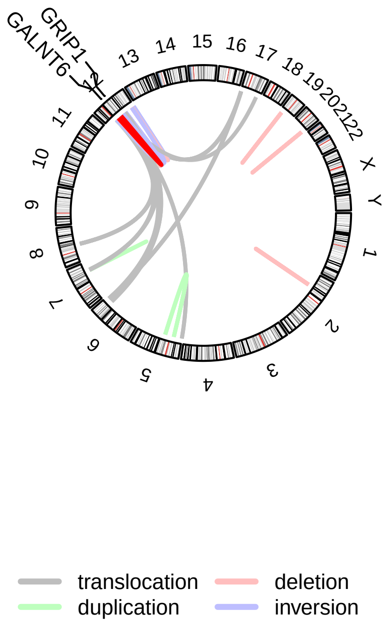




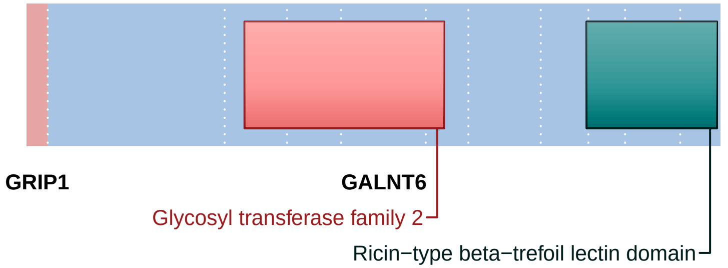
SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 0



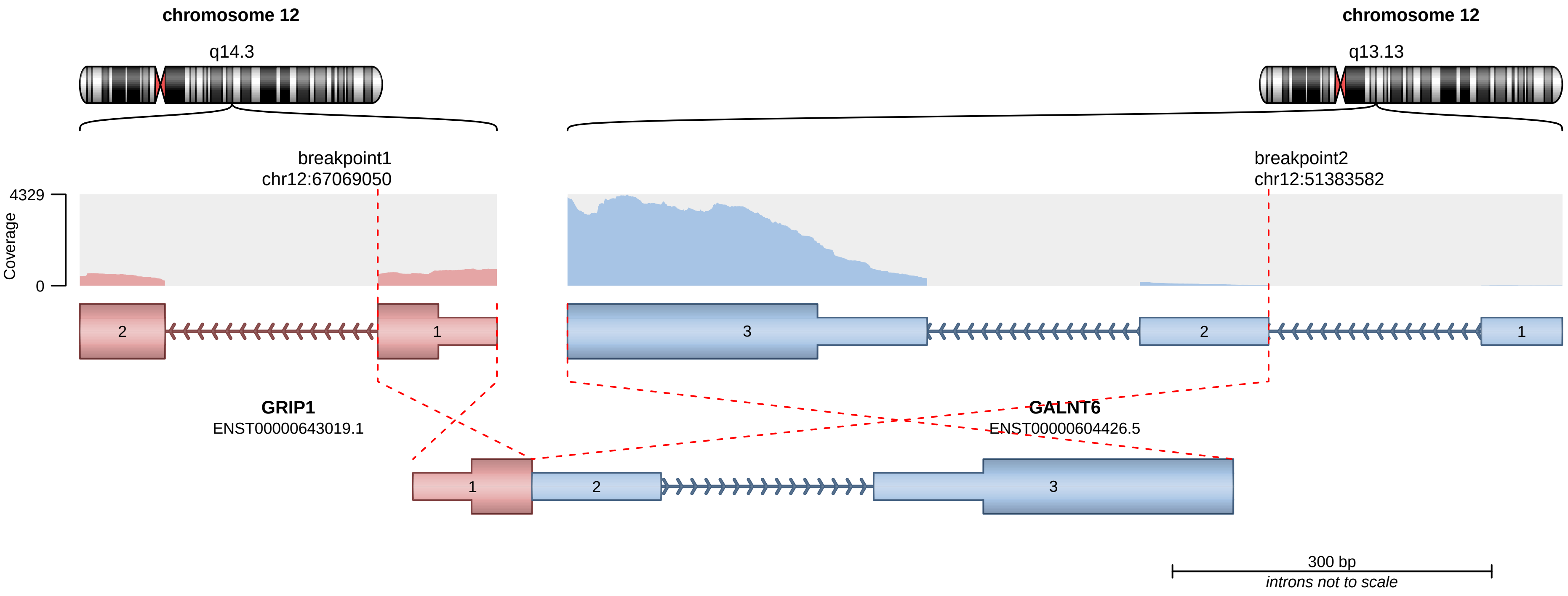


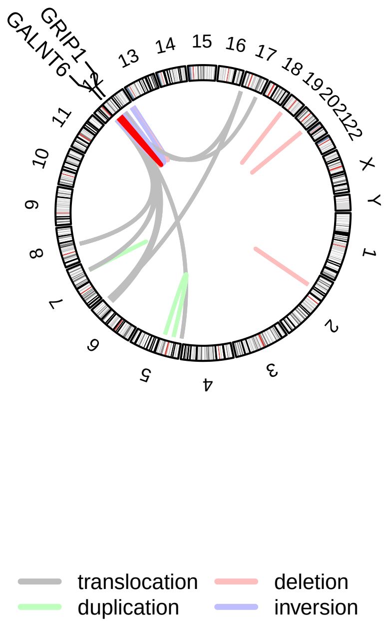
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 13
Discordant mates = 1

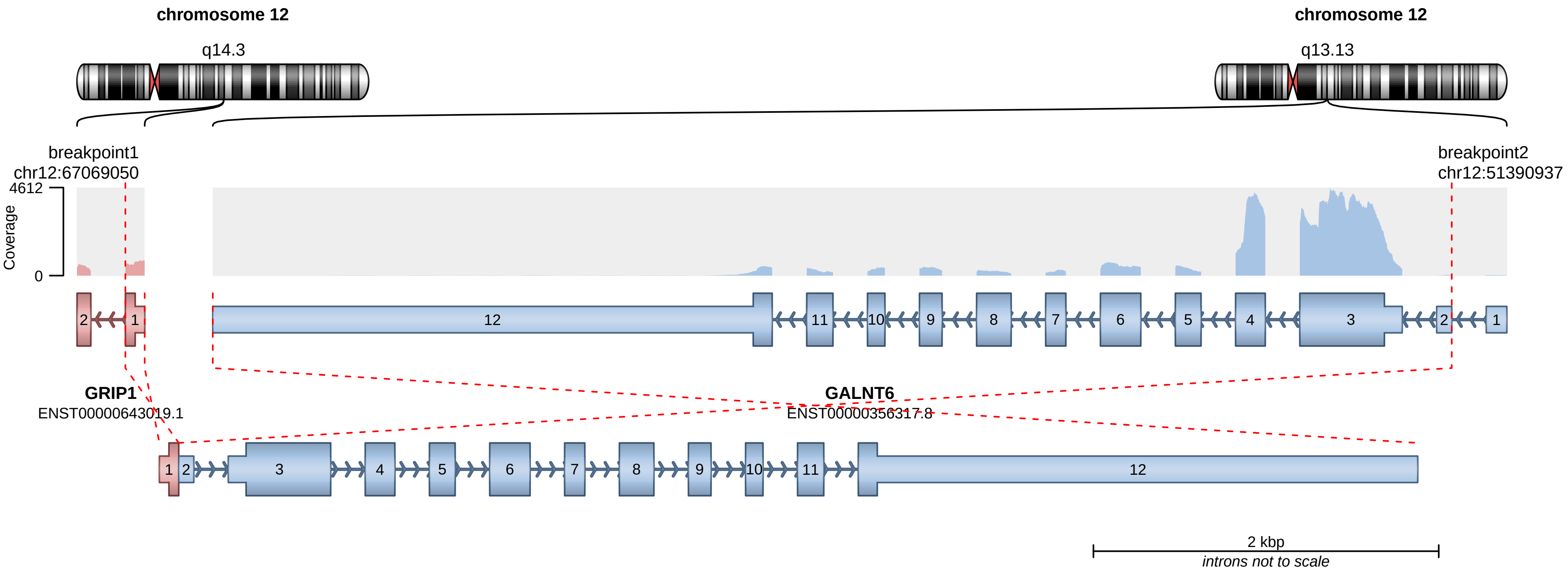


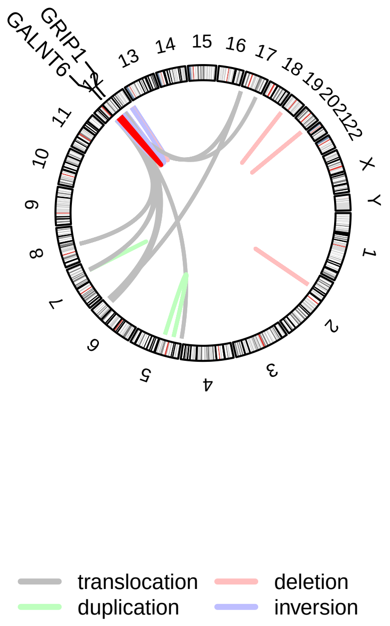


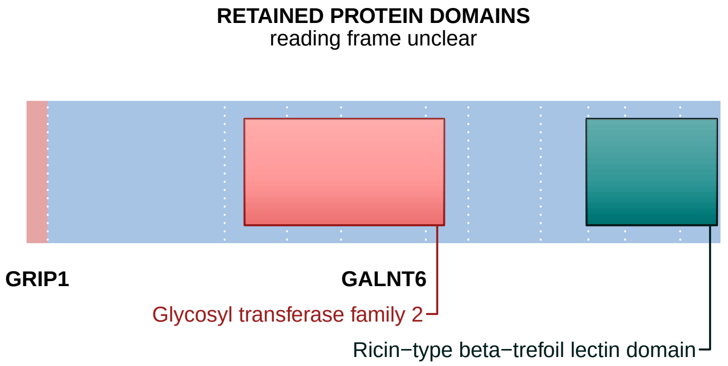
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 1

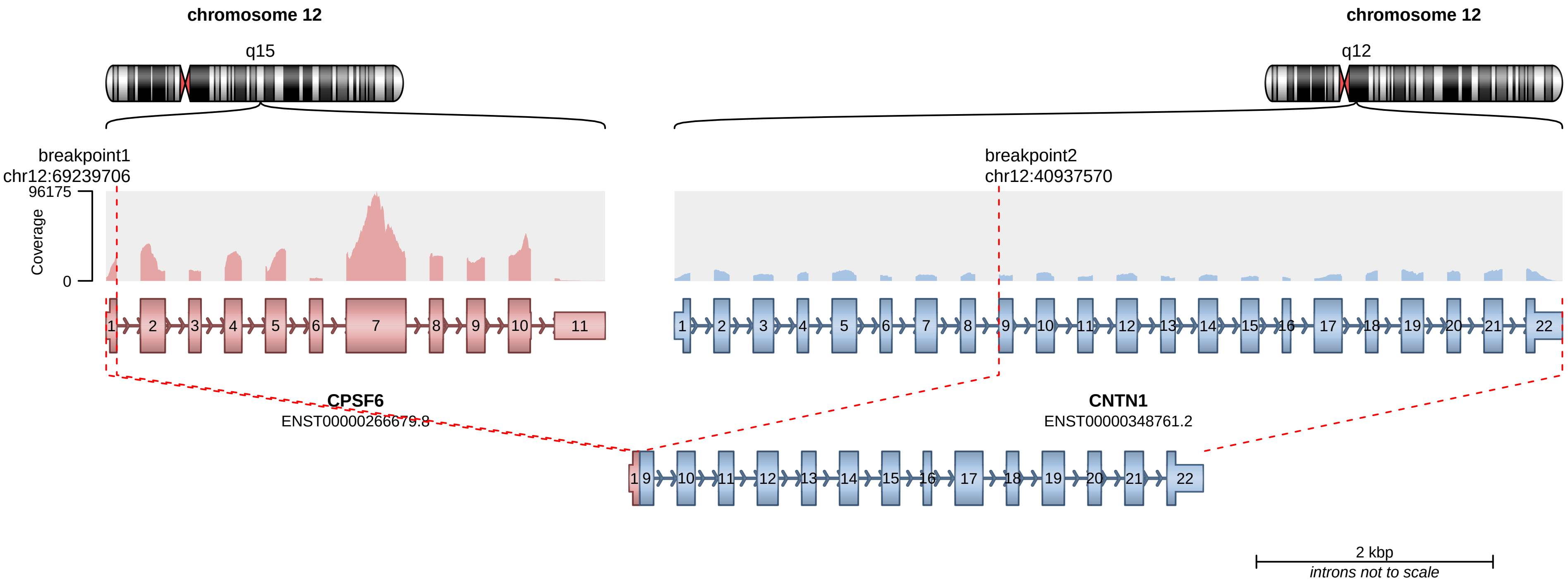


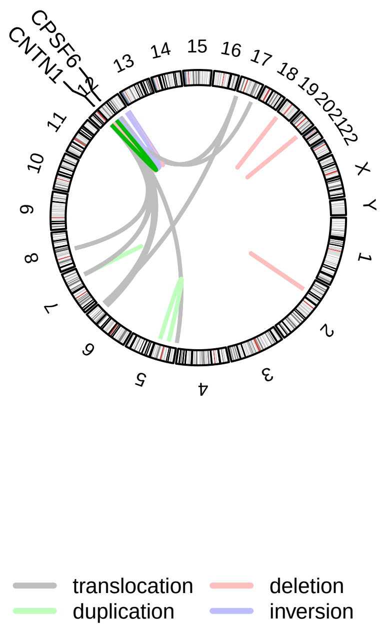


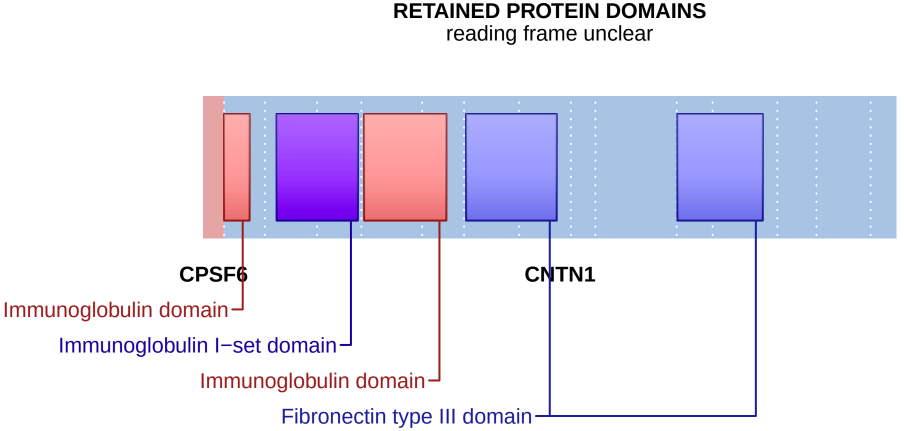


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

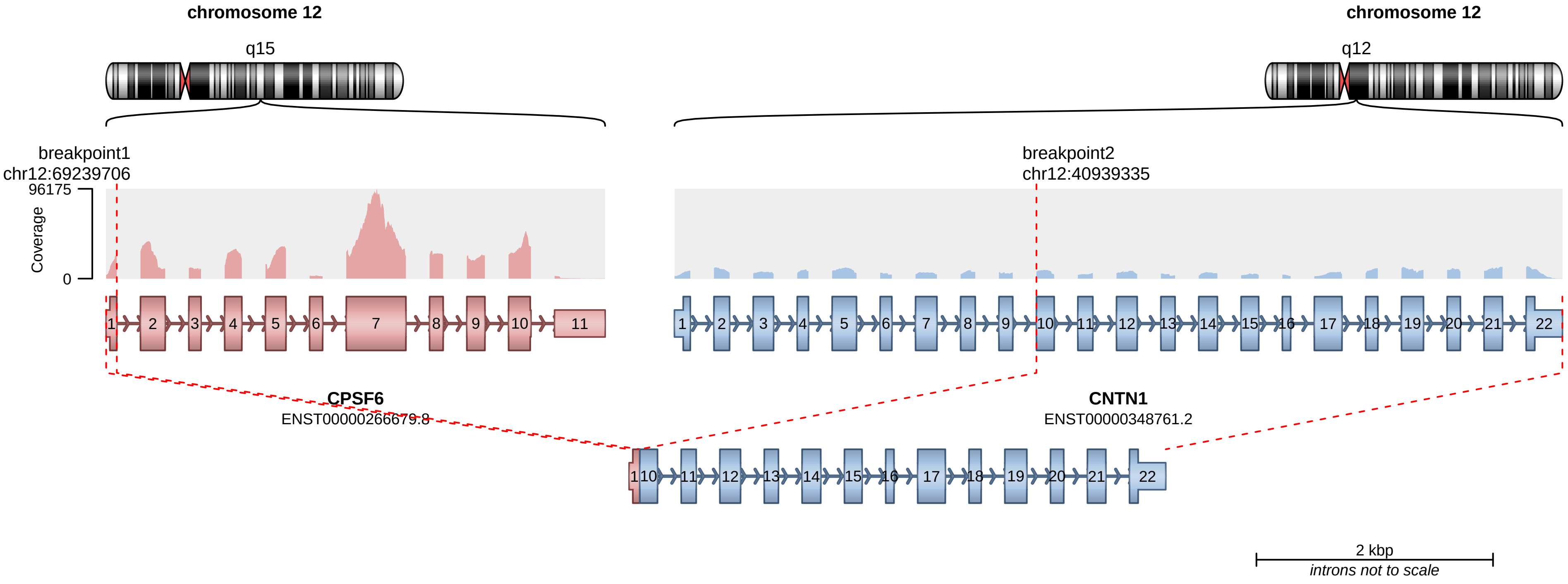


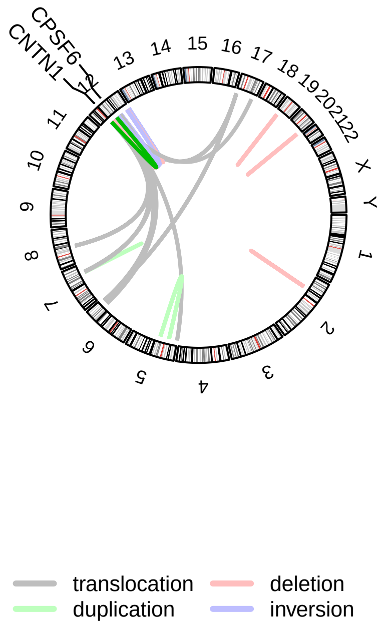


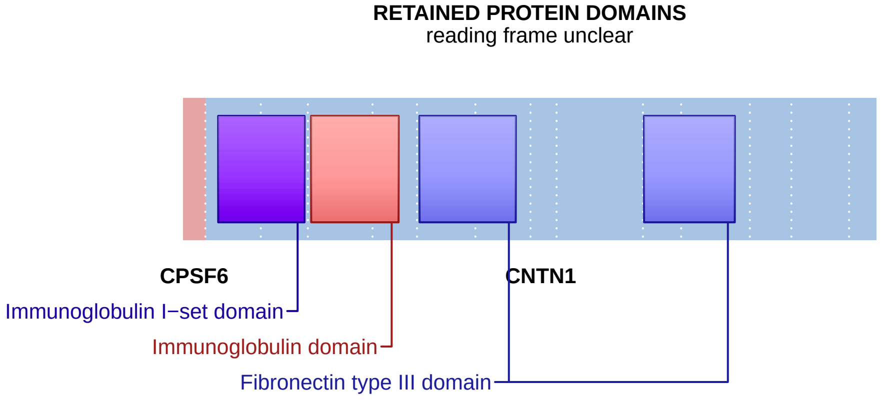


SUPPORTING READ COUNT

Split reads = 13
Discordant mates = 0

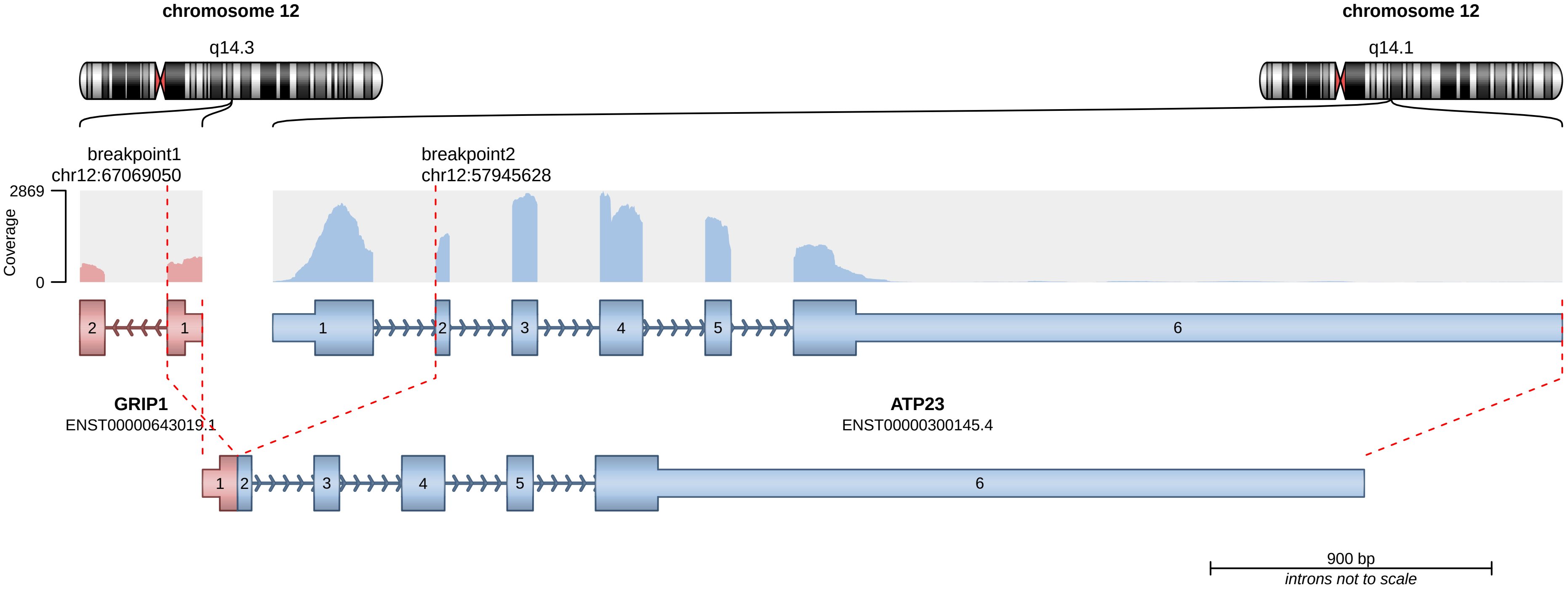


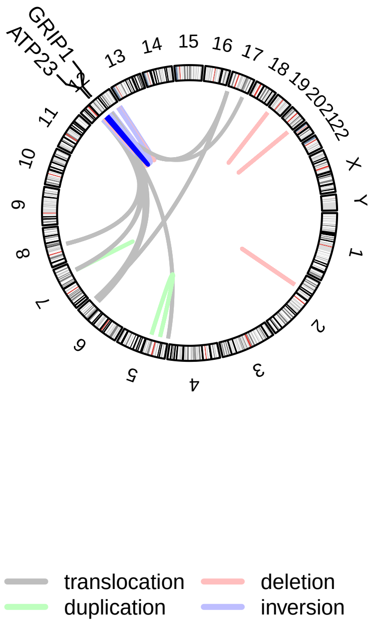




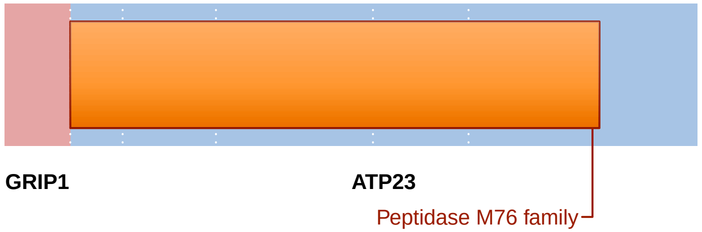
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0



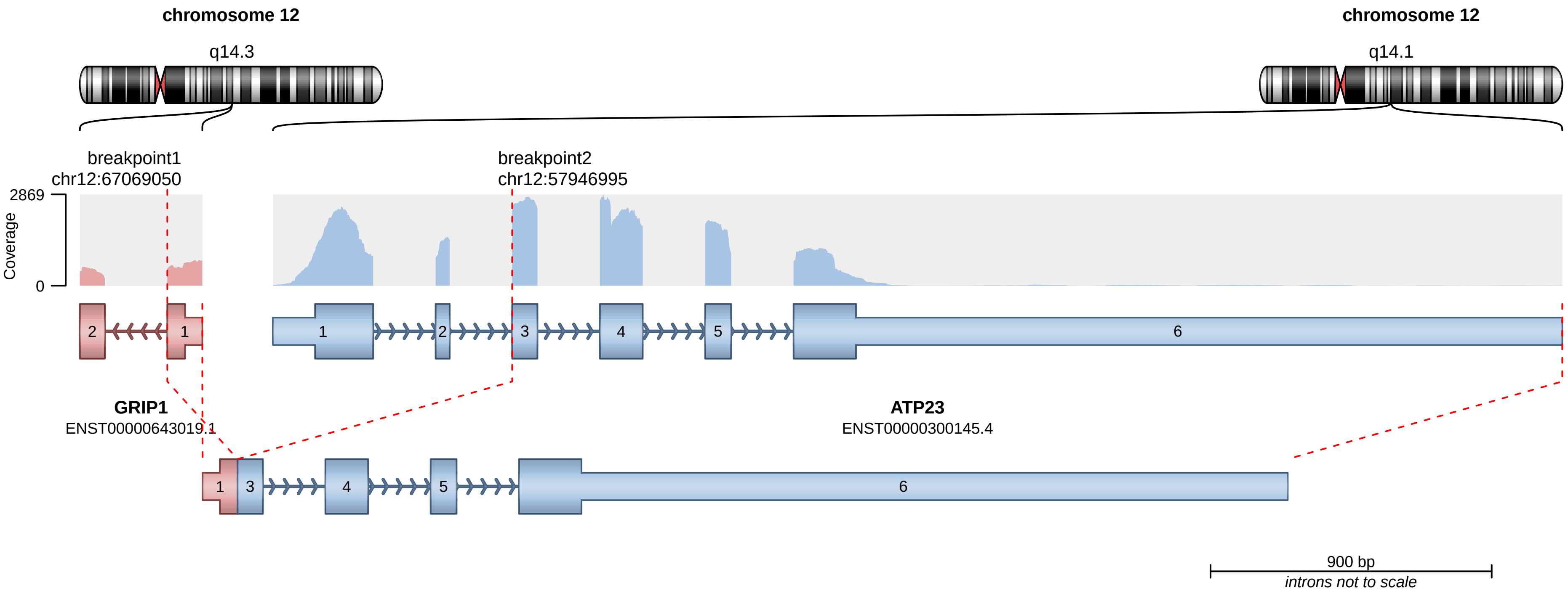


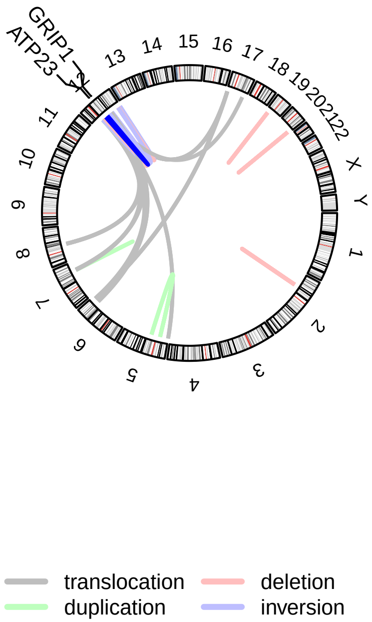
RETAINED PROTEIN DOMAINS
reading frame unclear

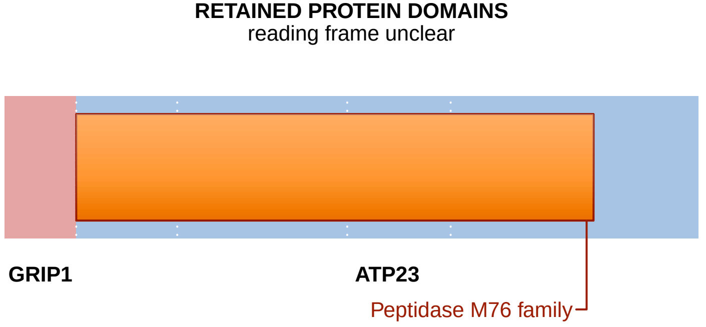


SUPPORTING READ COUNT

Split reads = 13
Discordant mates = 0

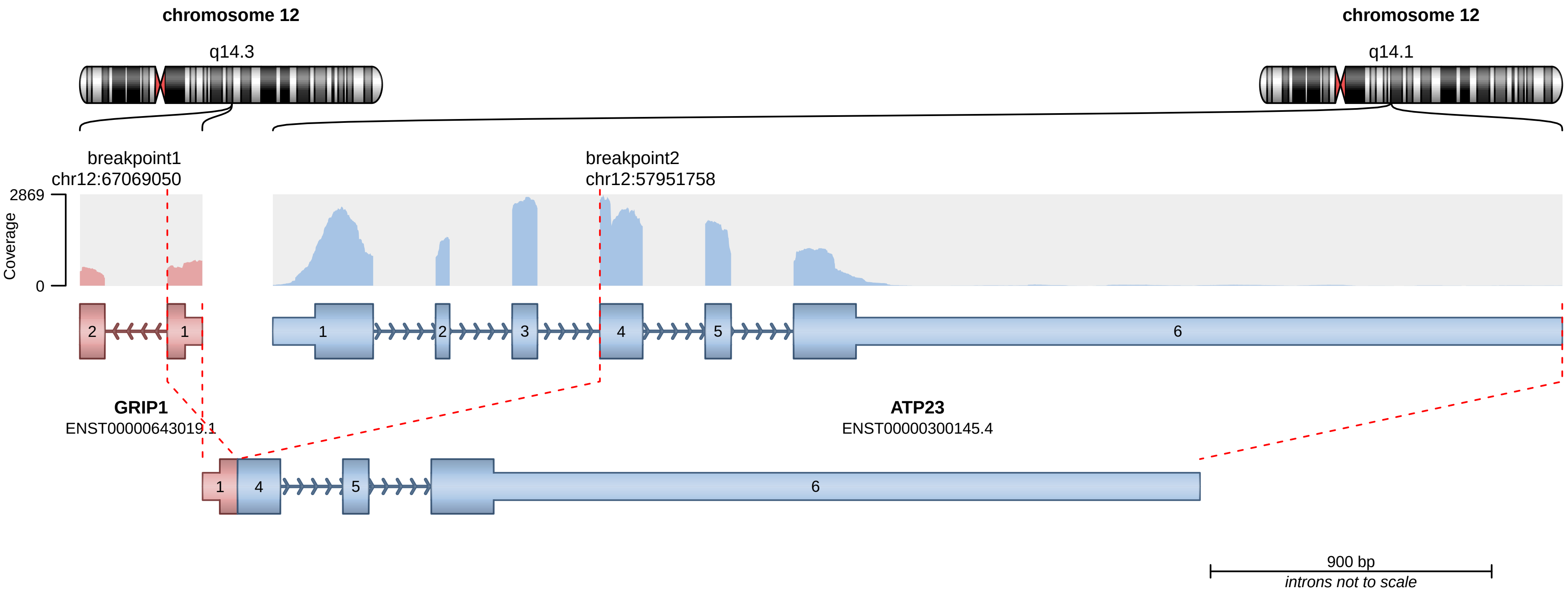


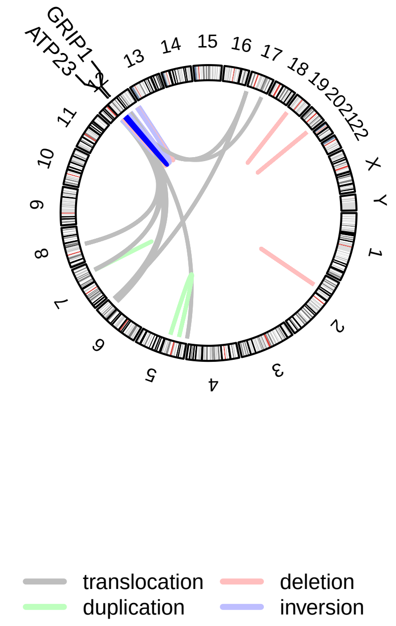




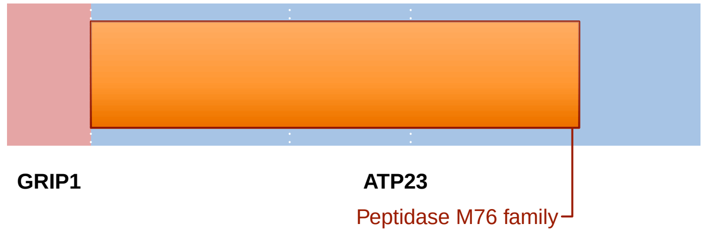
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0



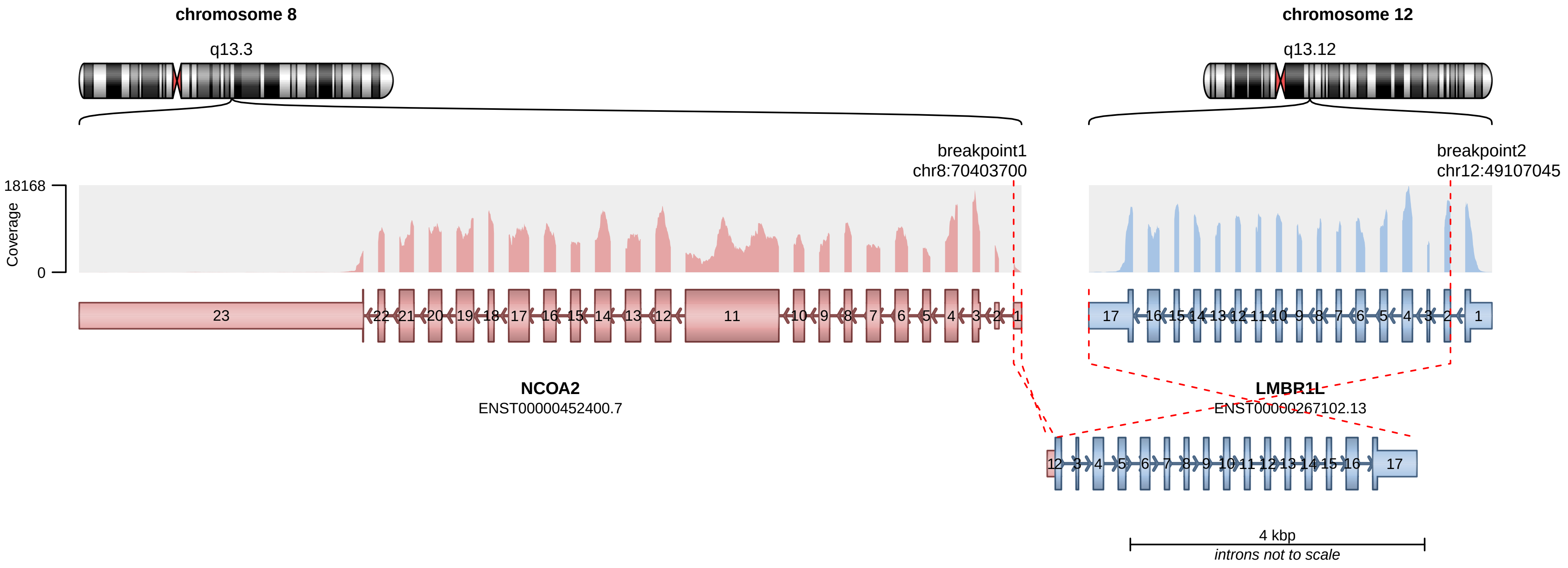


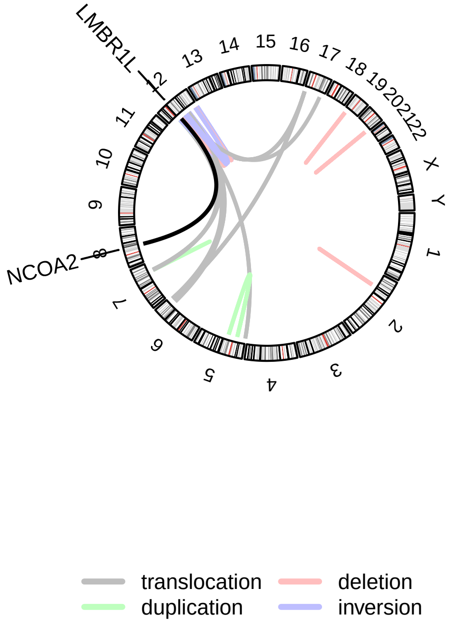
RETAINED PROTEIN DOMAINS
reading frame unclear

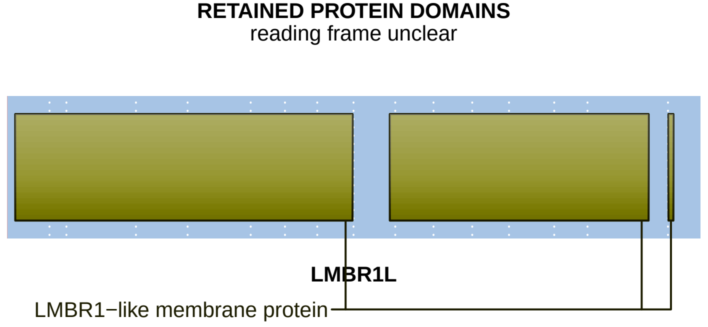


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

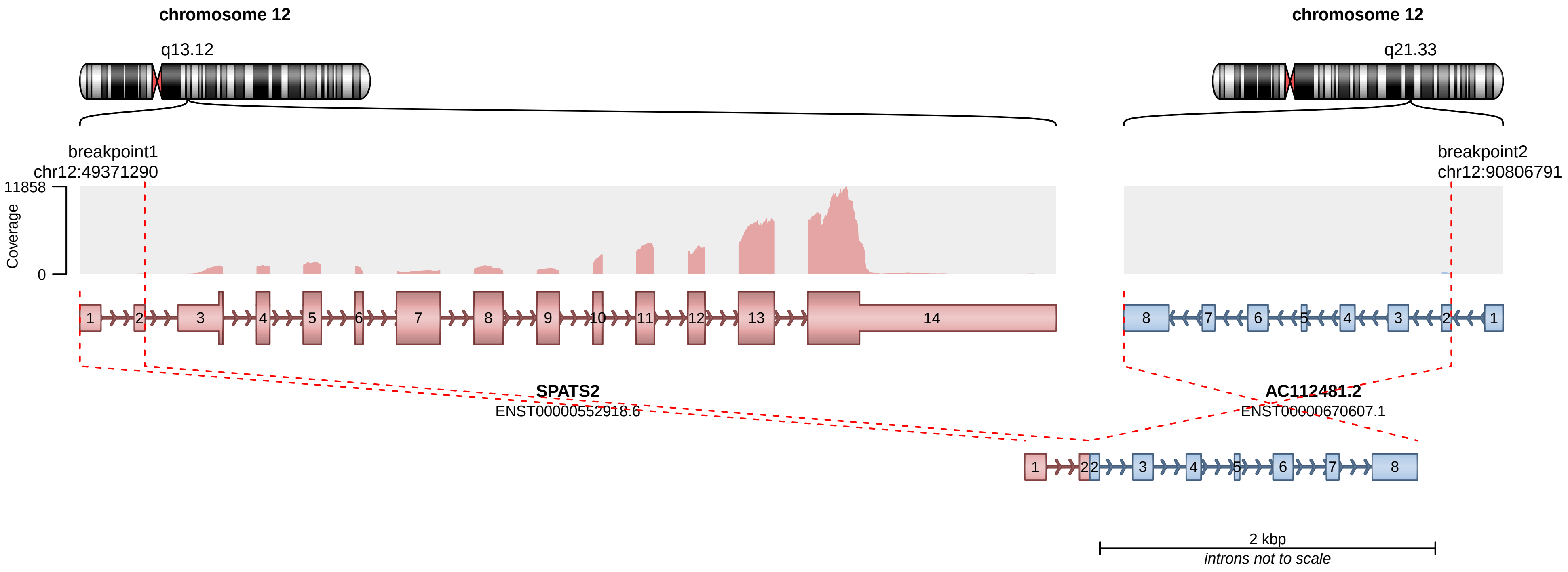


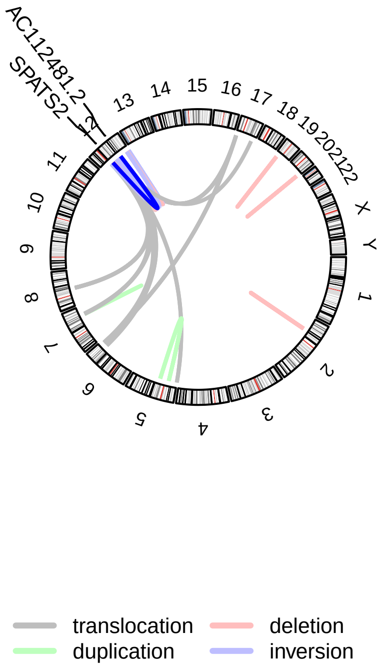




SUPPORTING READ COUNT

Split reads = 13
Discordant mates = 0

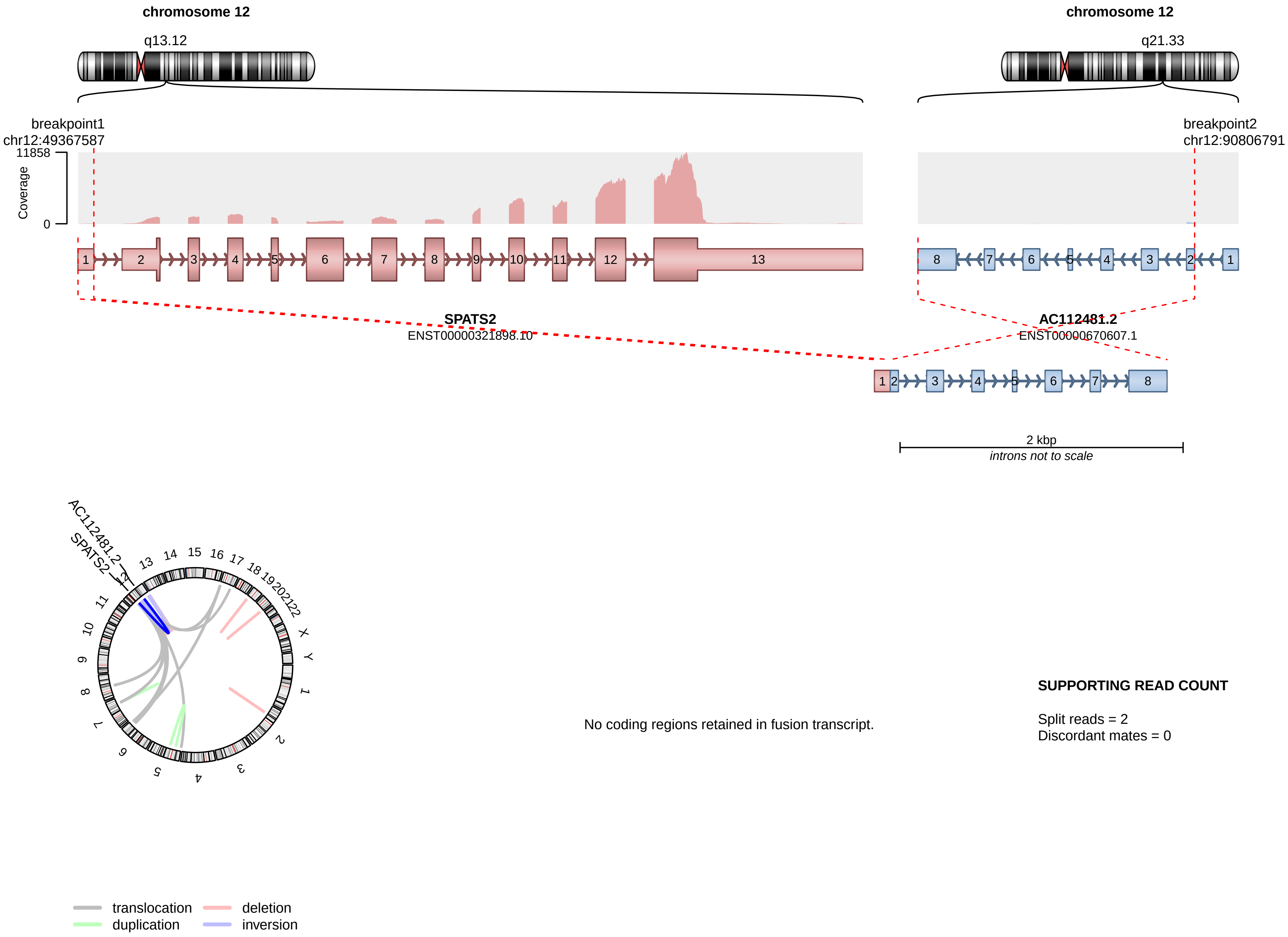




No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

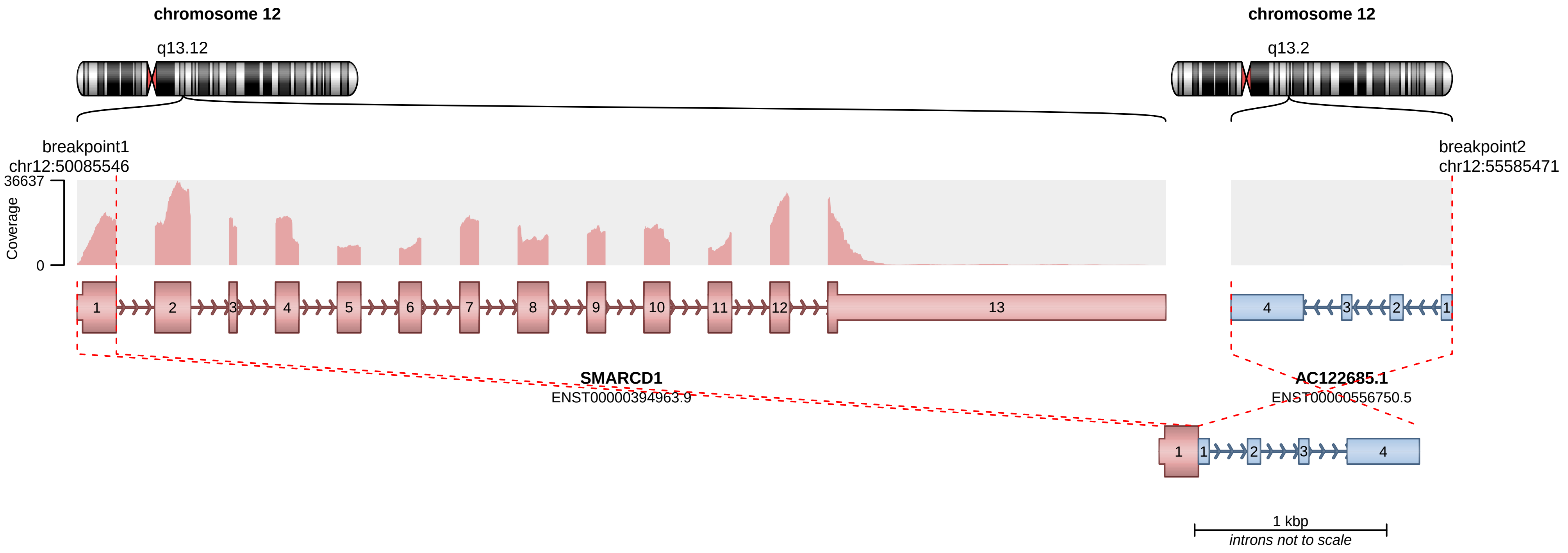
Split reads = 12
Discordant mates = 0

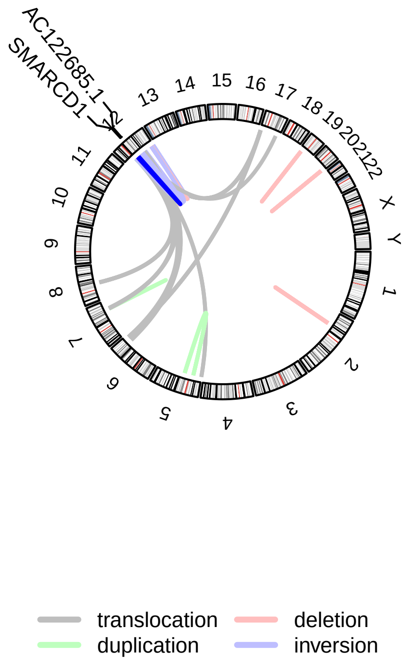


No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

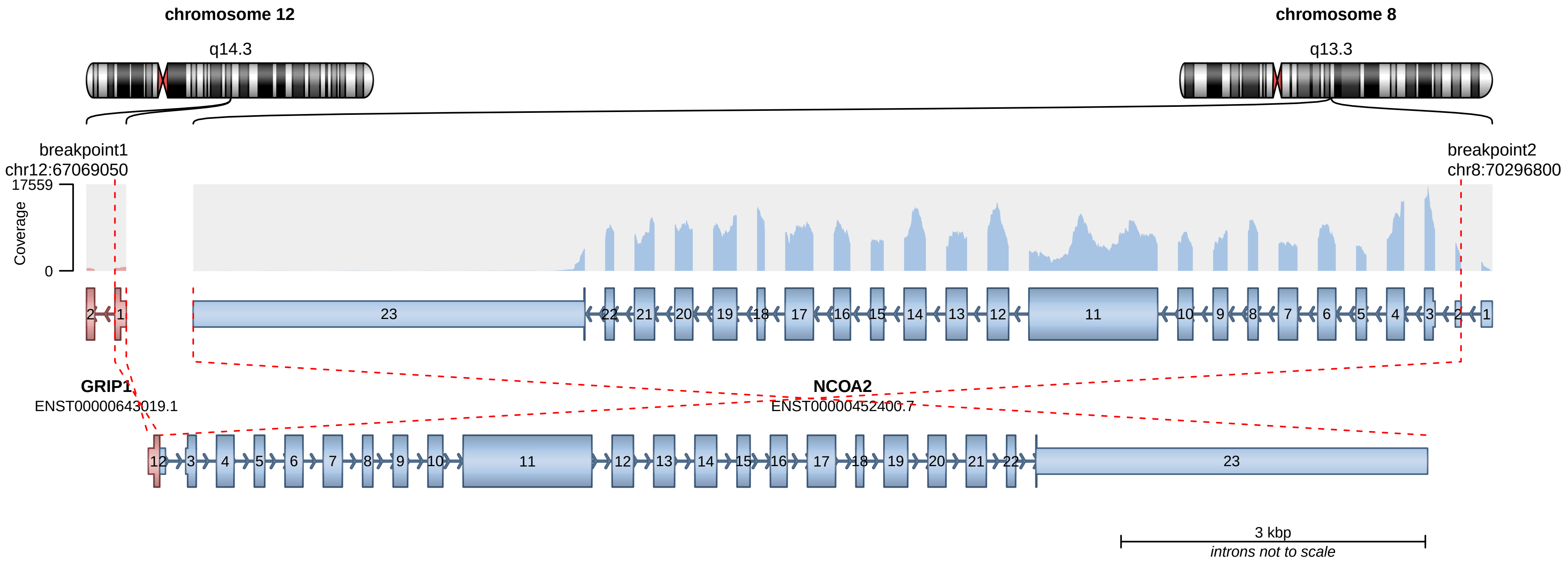


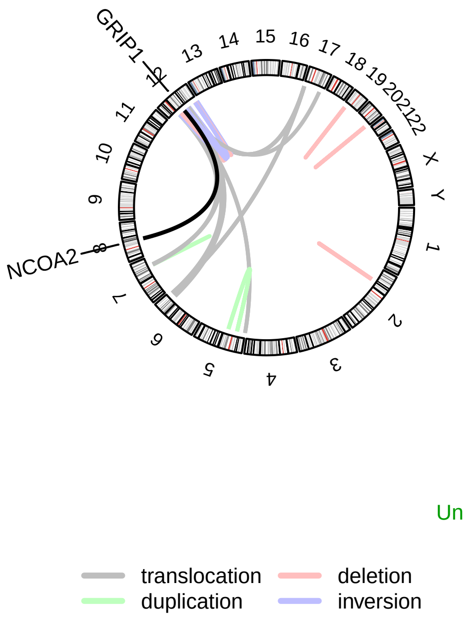


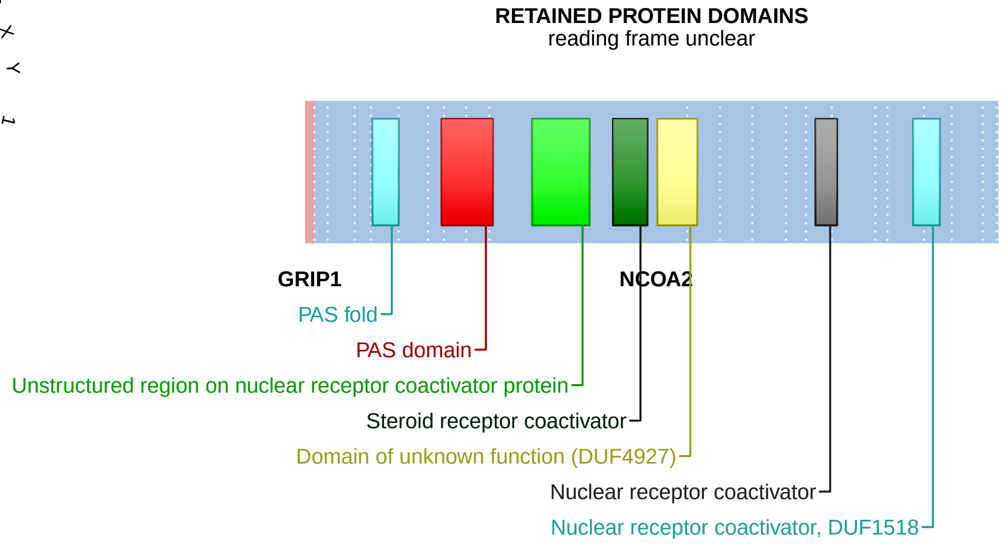
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 11
Discordant mates = 0

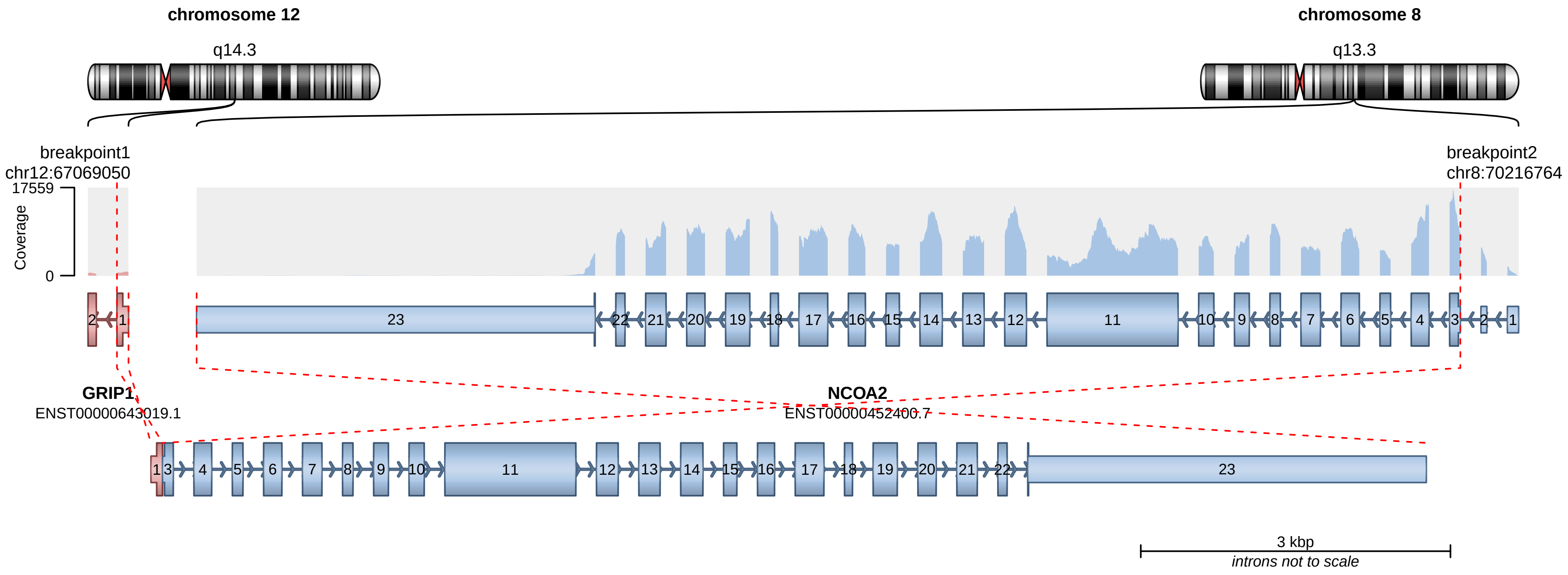


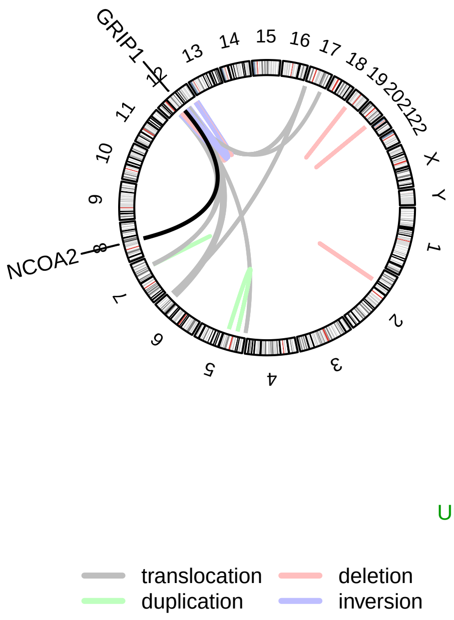


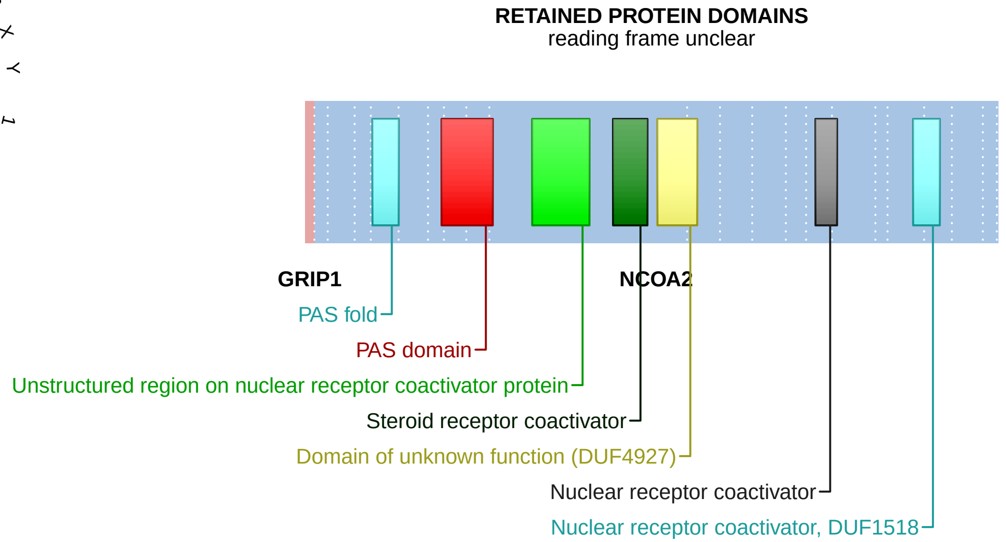


SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 1

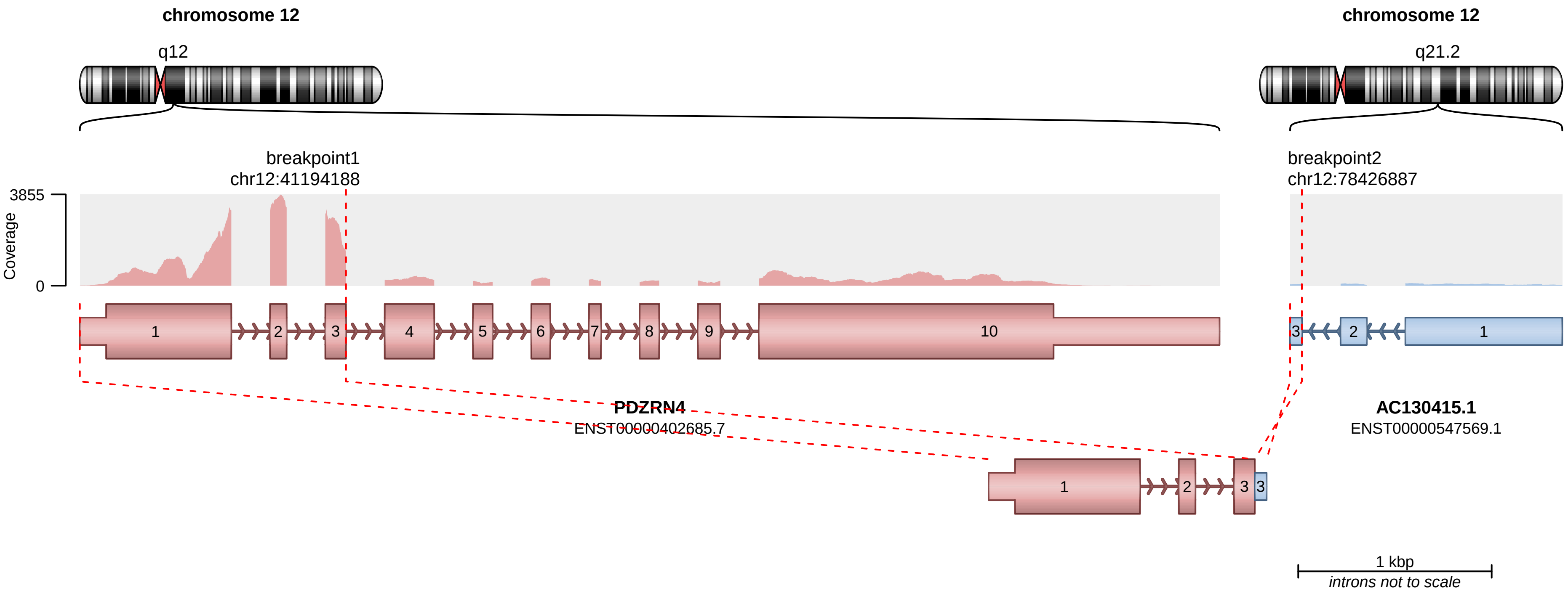


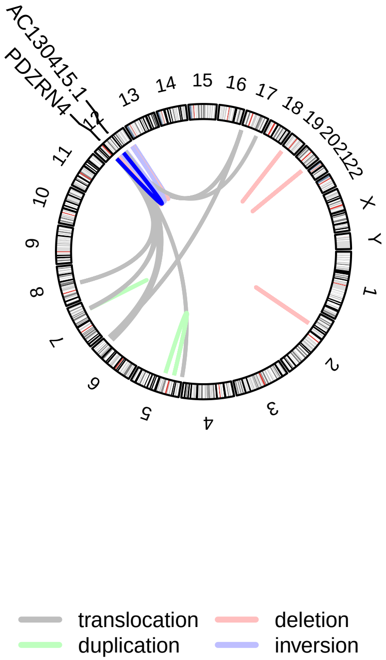




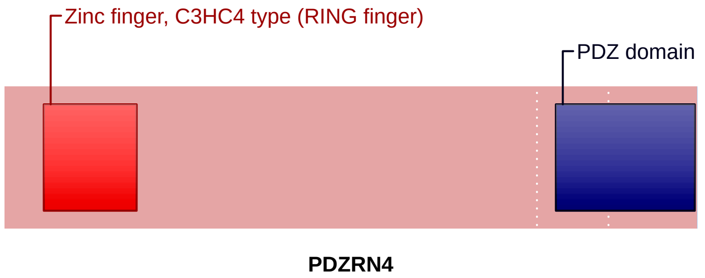
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 1



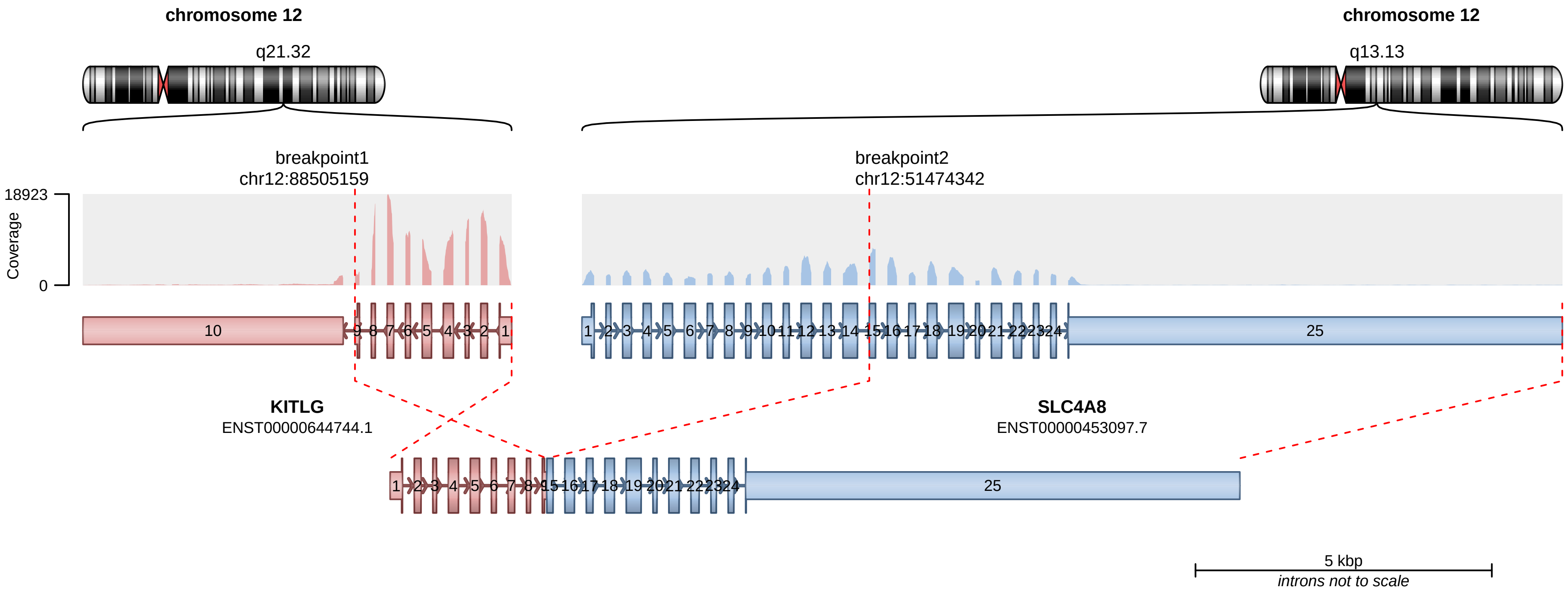


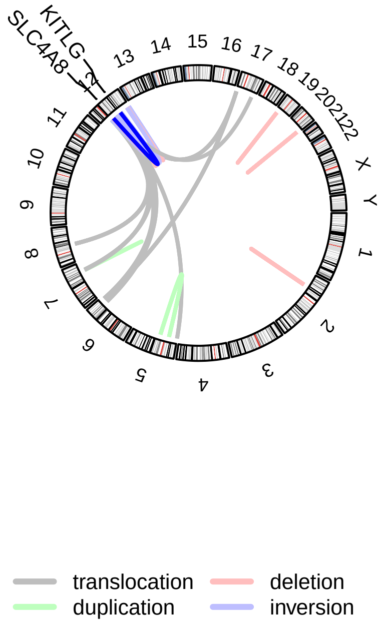
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

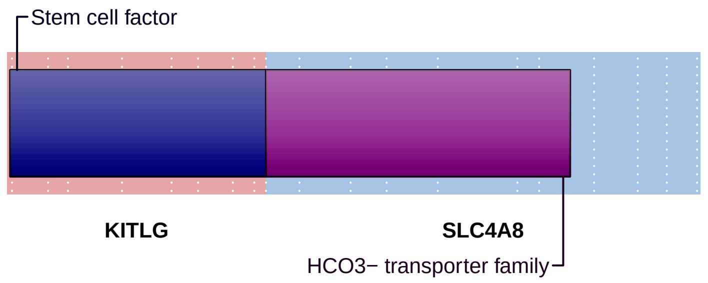
Split reads = 9
Discordant mates = 0





RETAINED PROTEIN DOMAINS

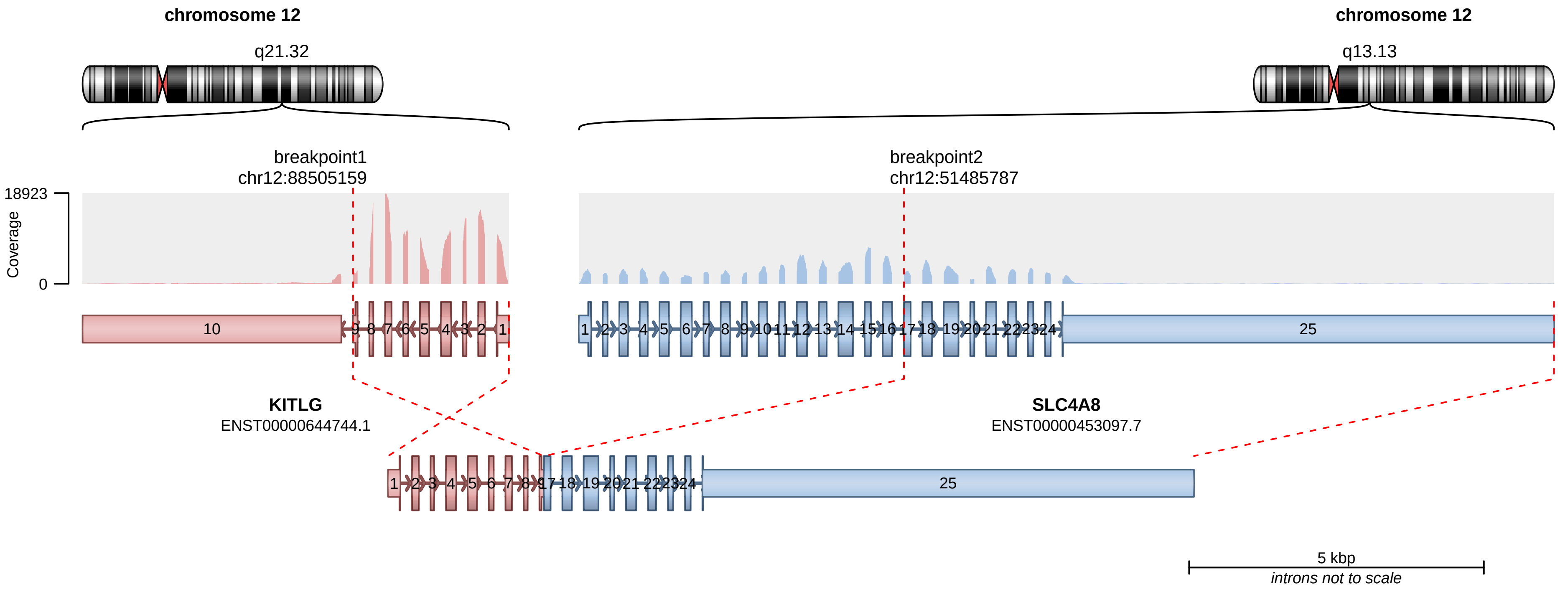
reading frame unclear

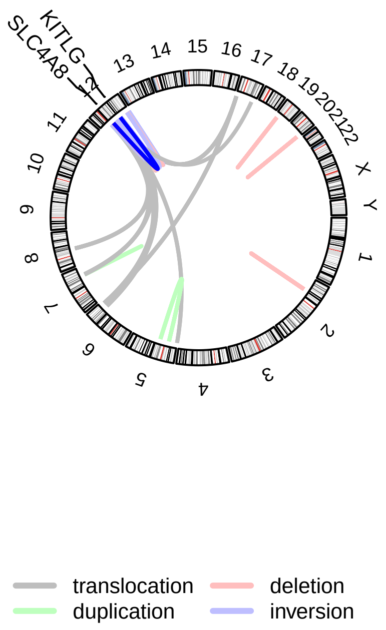


SUPPORTING READ COUNT

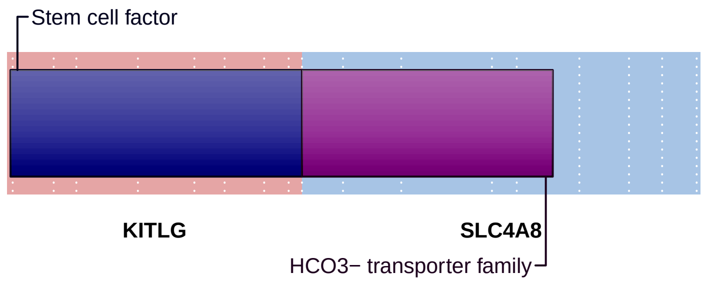
Split reads = 8

Discordant mates = 0



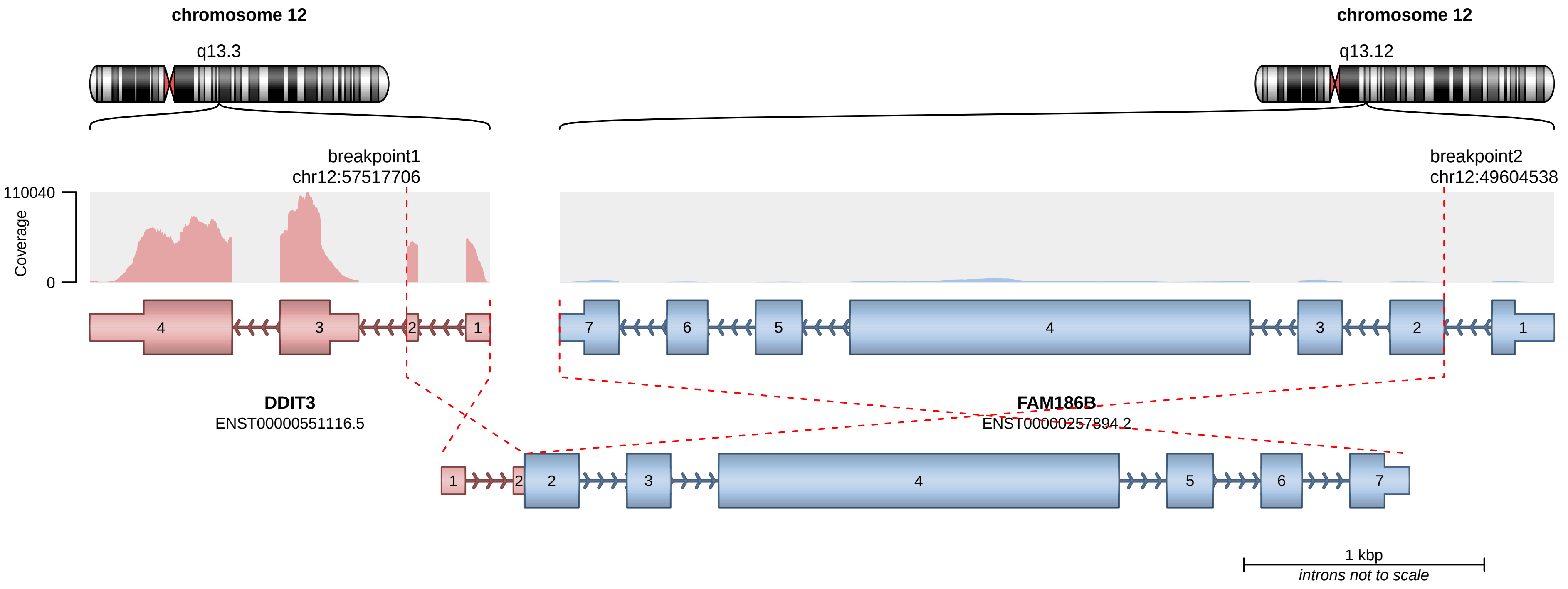


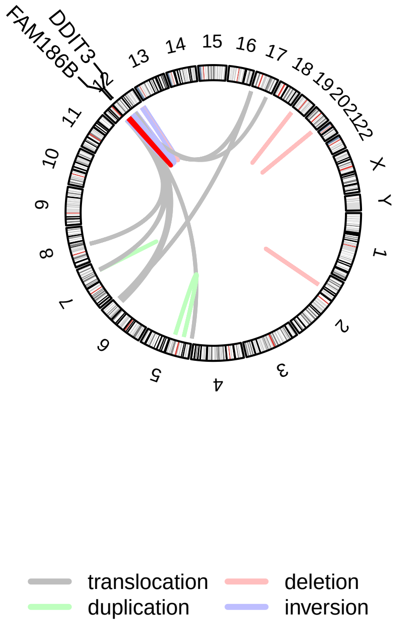
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

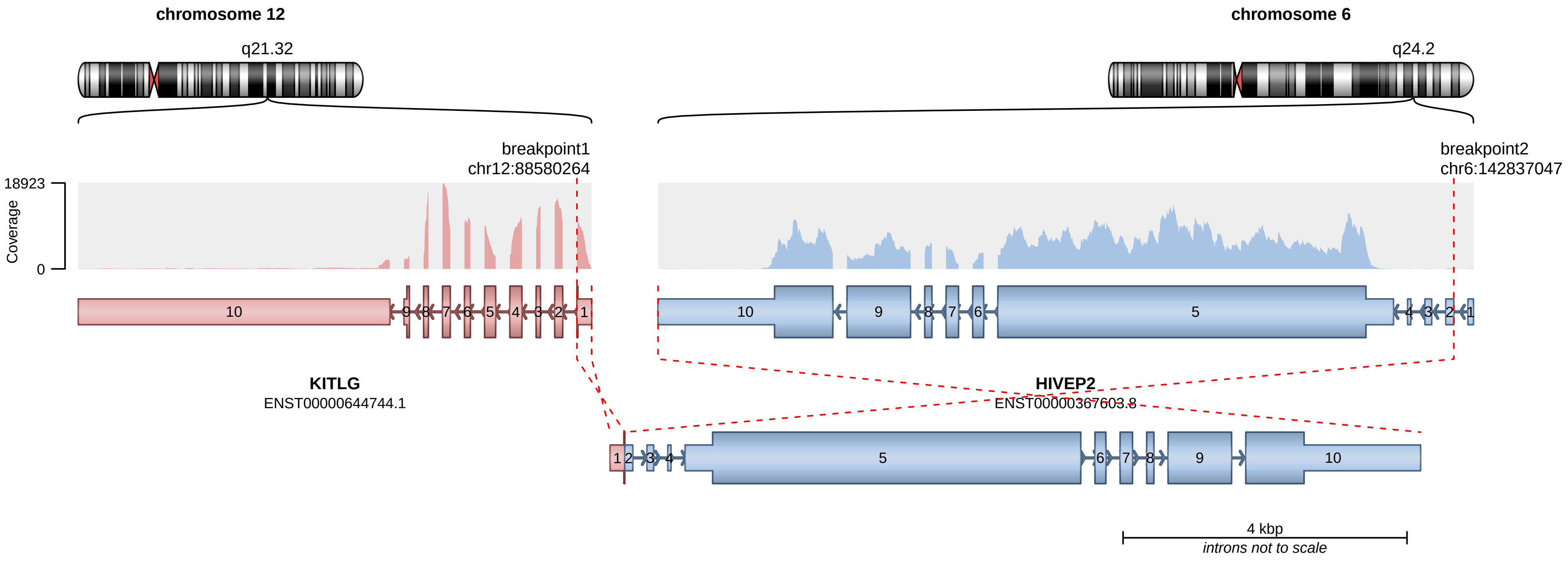


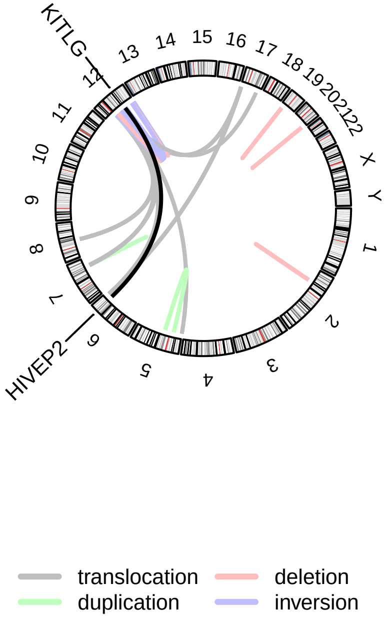


No protein domains retained in fusion.

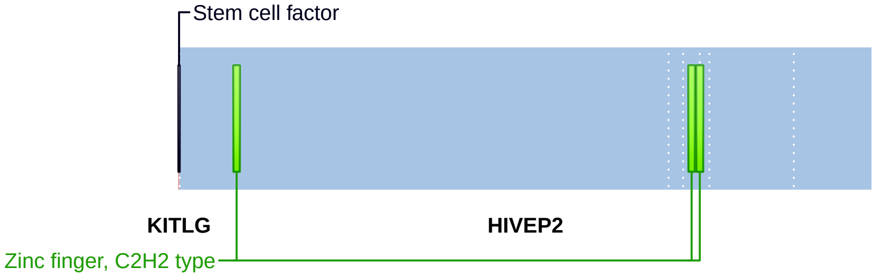
SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 0



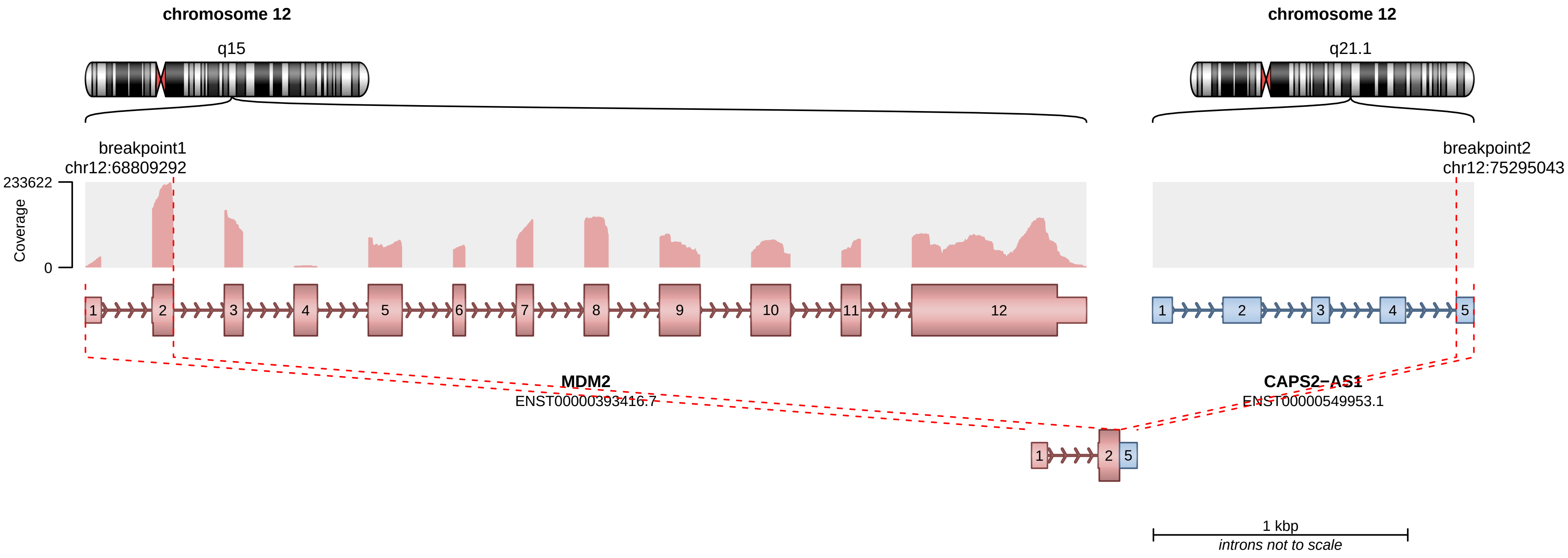


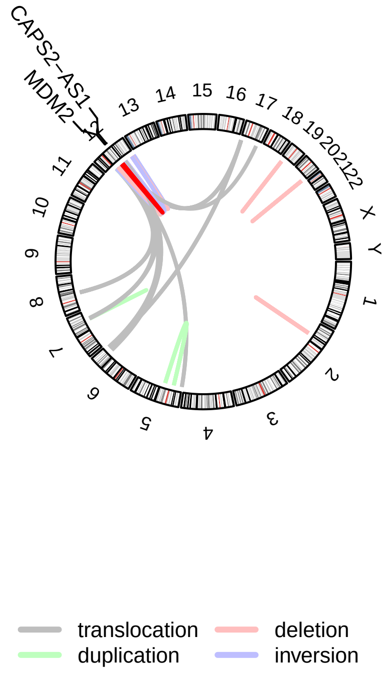
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 0

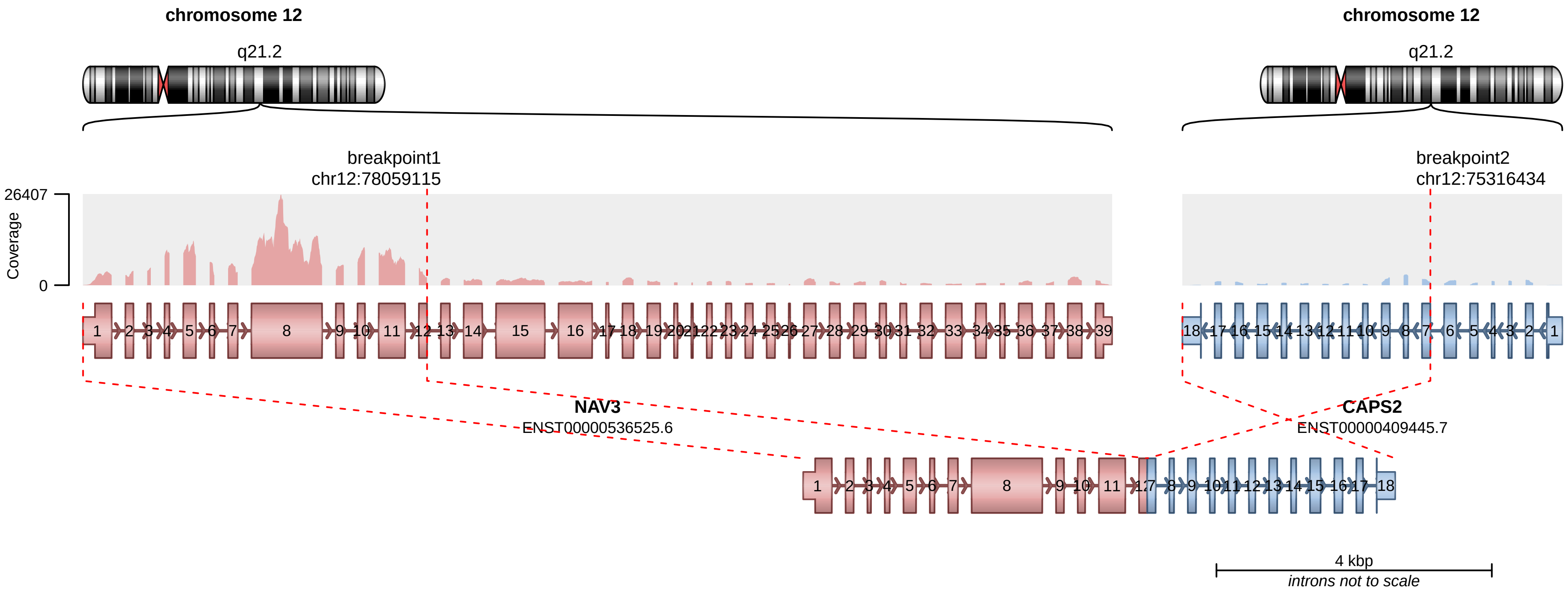


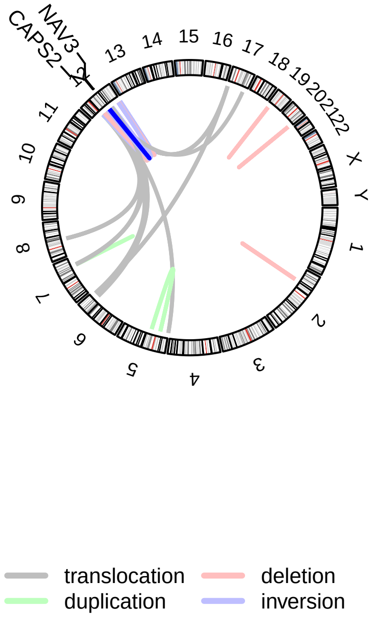


RETAINED PROTEIN DOMAINS
reading frame unclear

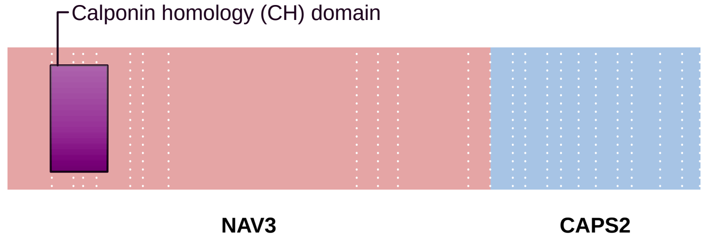
SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 0



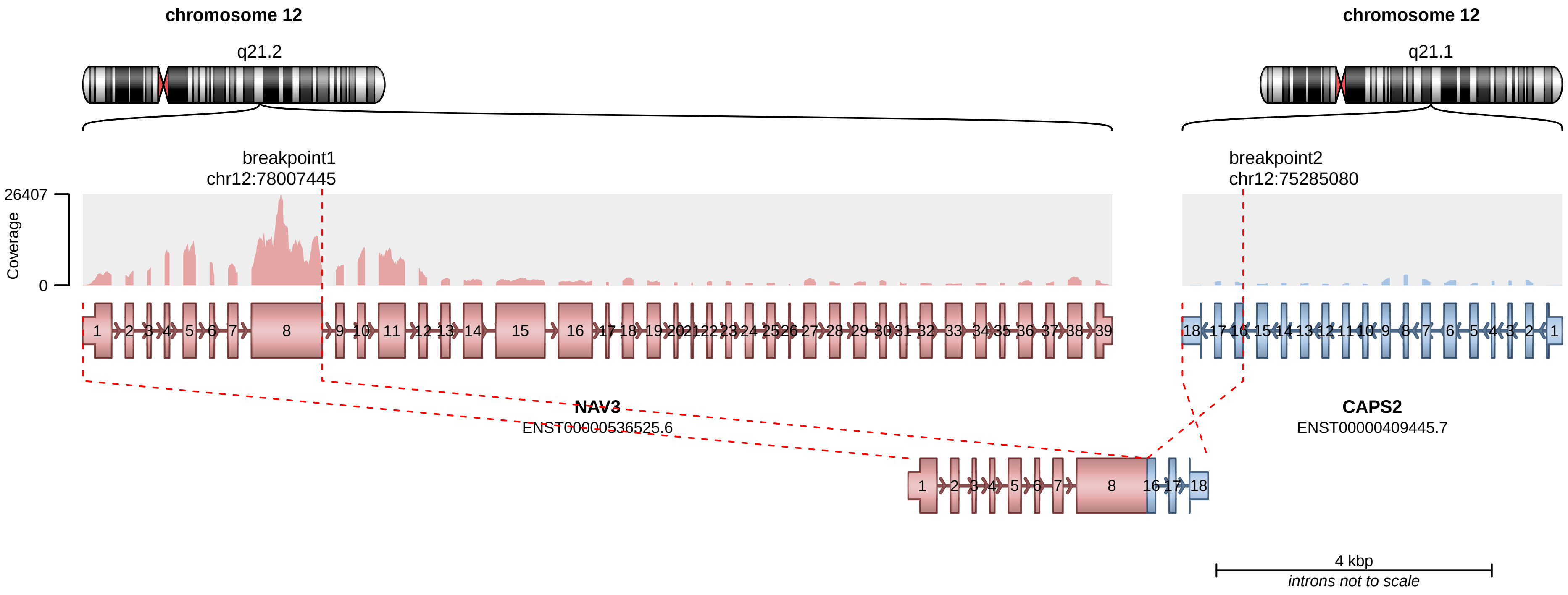


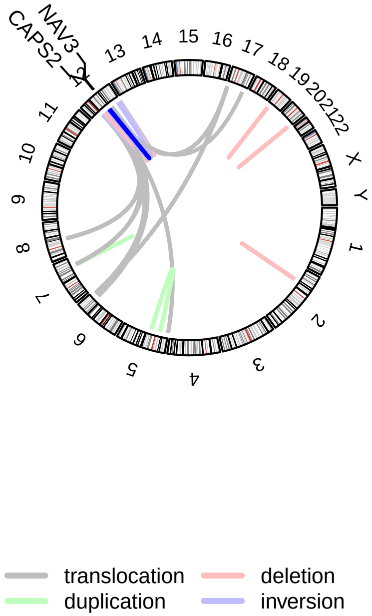
RETAINED PROTEIN DOMAINS
reading frame unclear

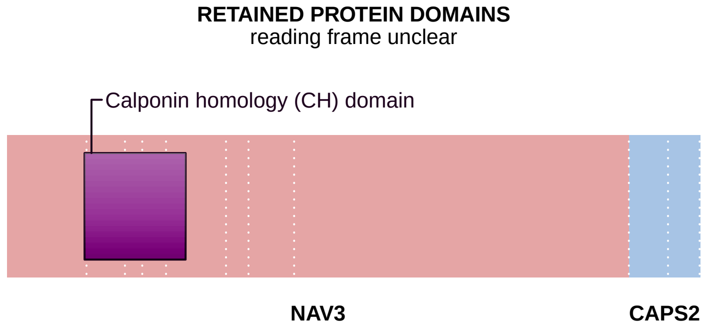


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

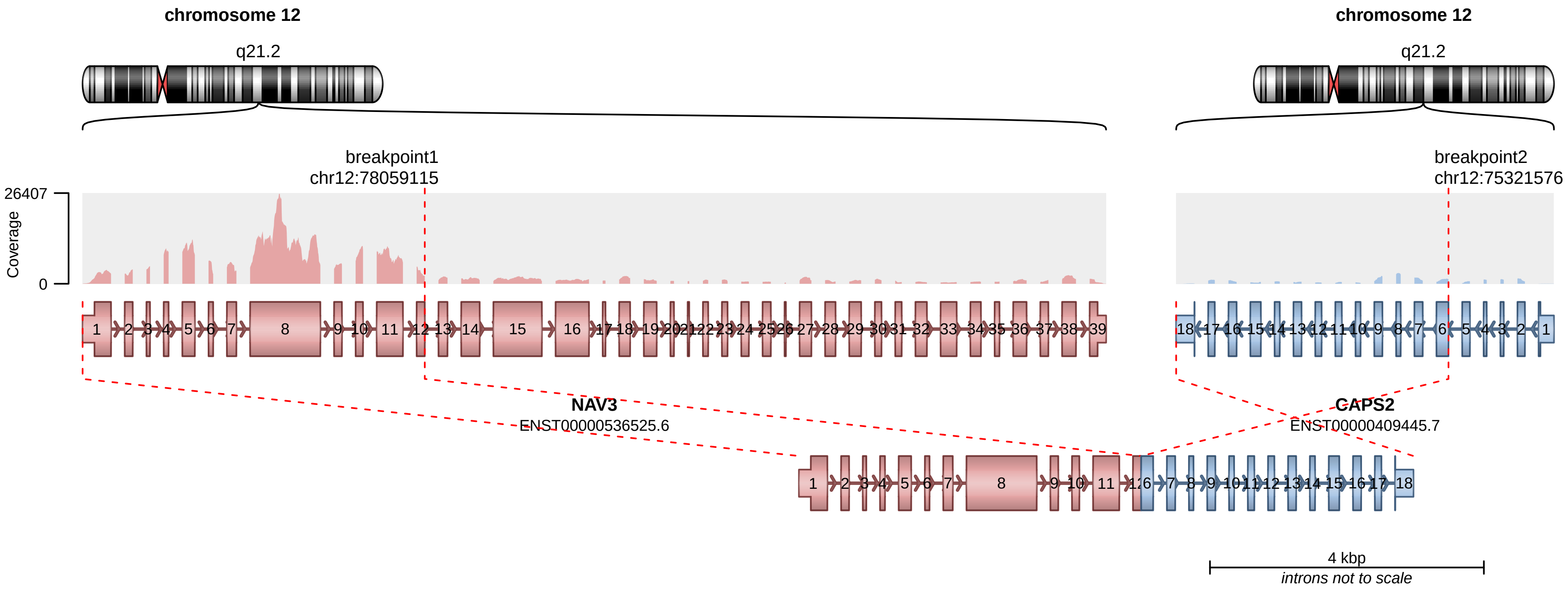


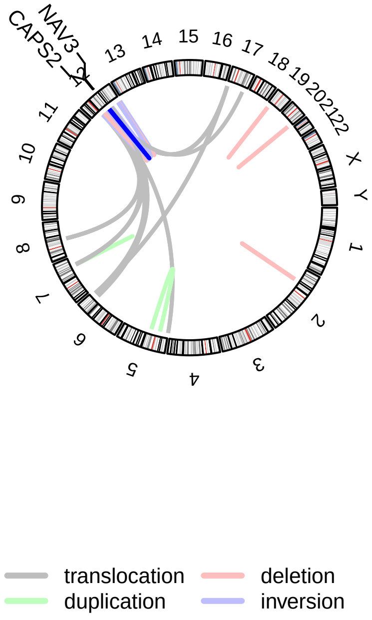




SUPPORTING READ COUNT

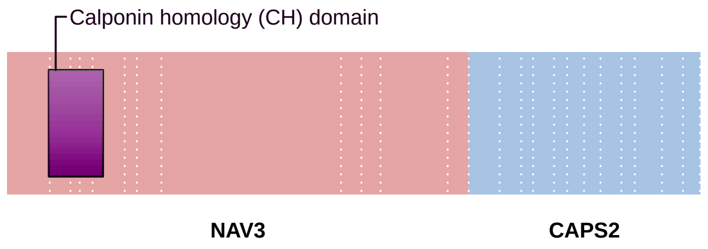
Split reads = 1
Discordant mates = 0





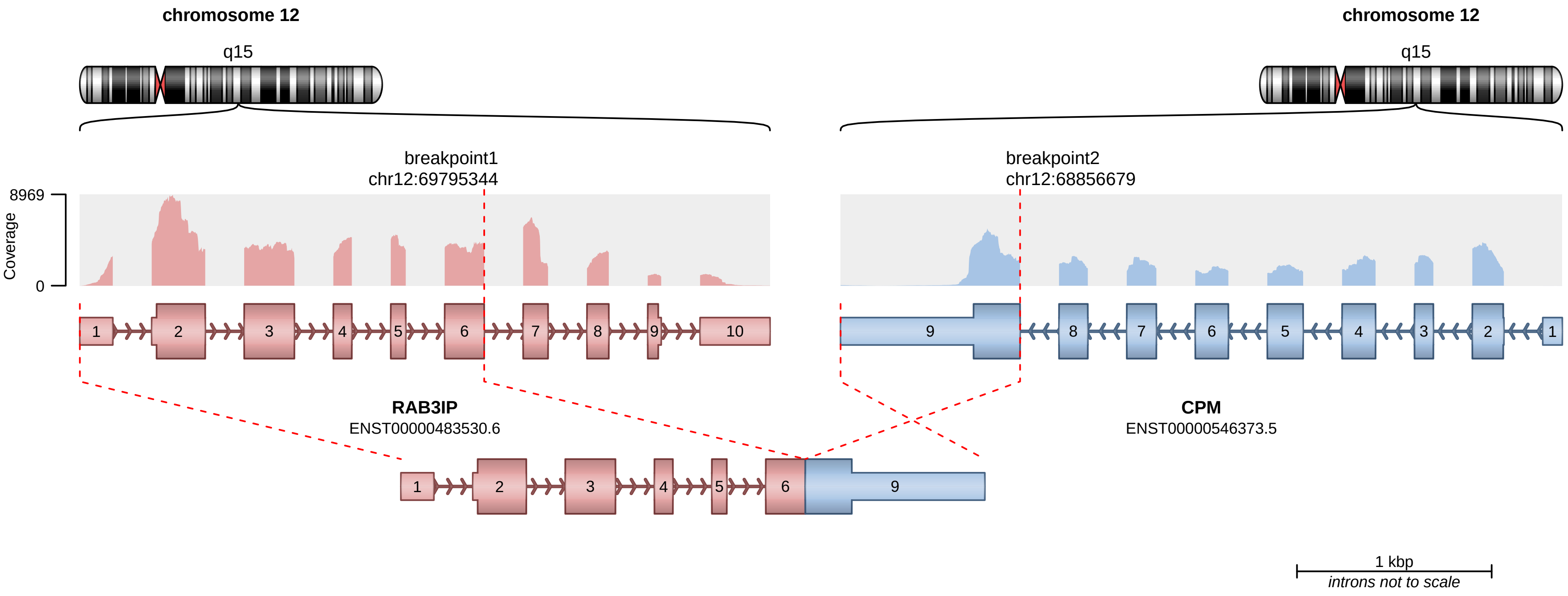
RETAINED PROTEIN DOMAINS

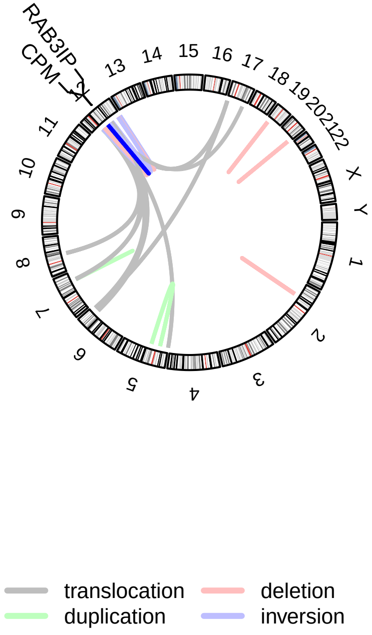
reading frame unclear



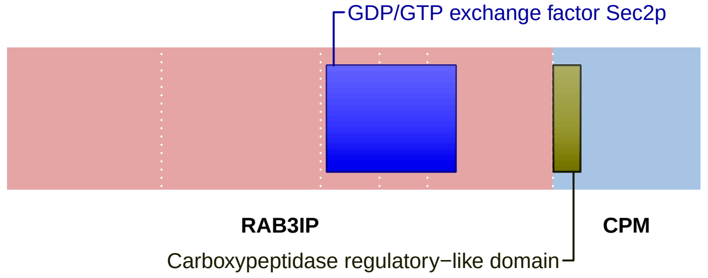
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0





RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0