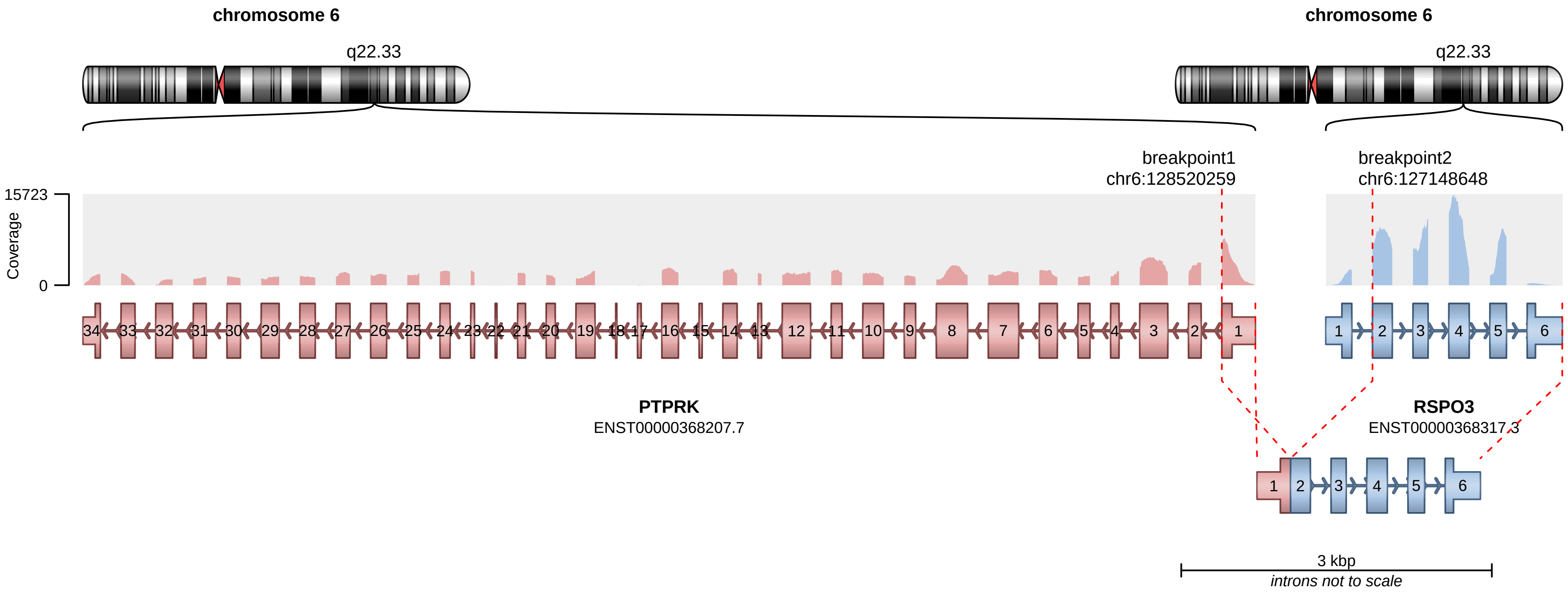
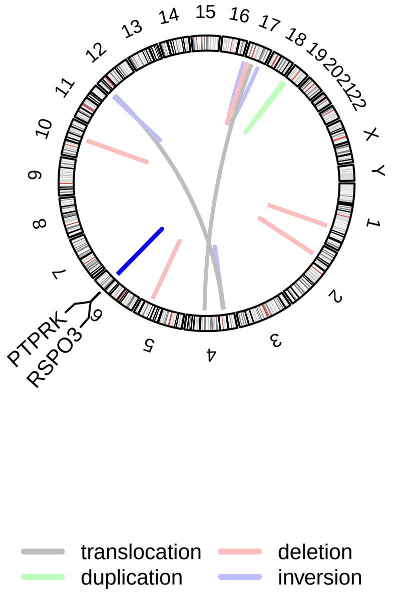
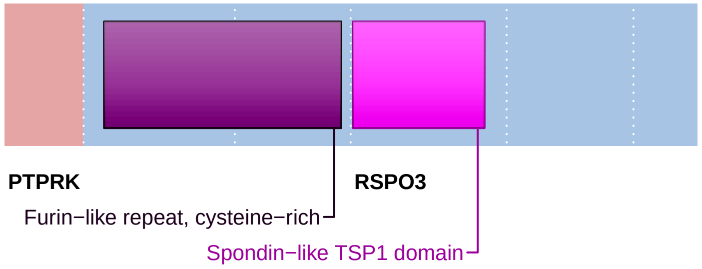


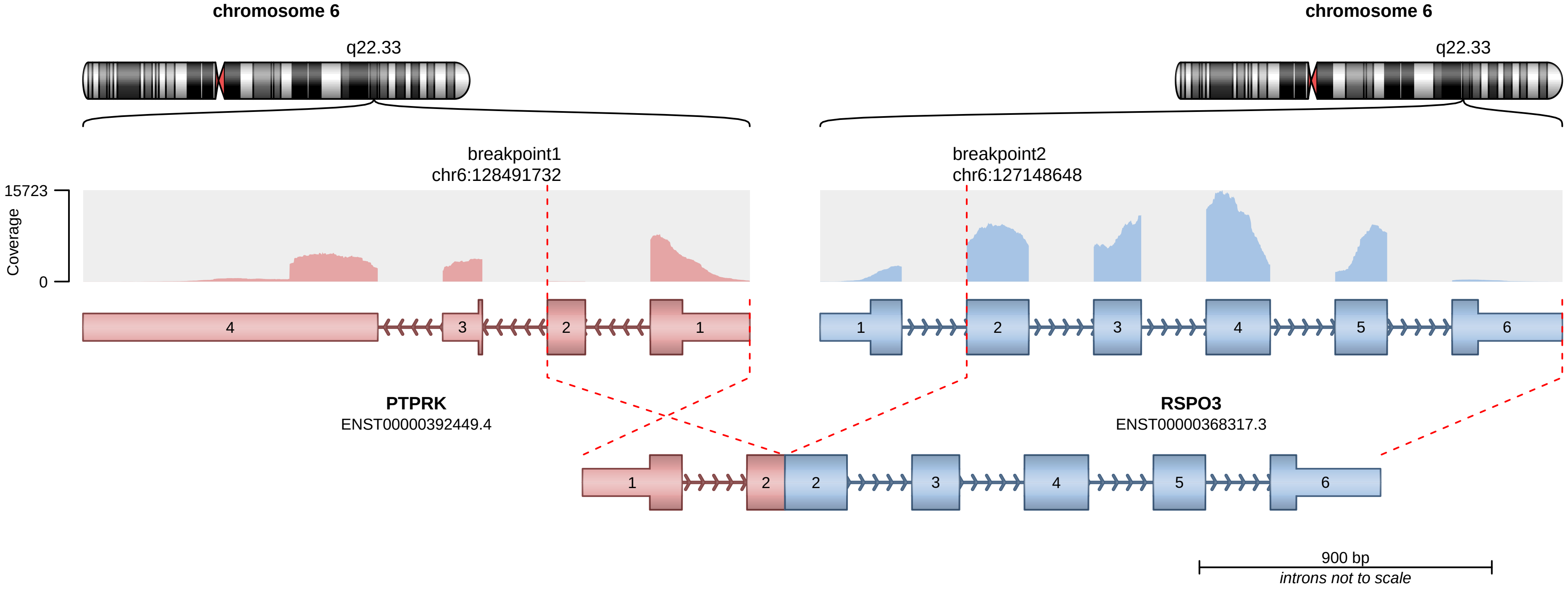


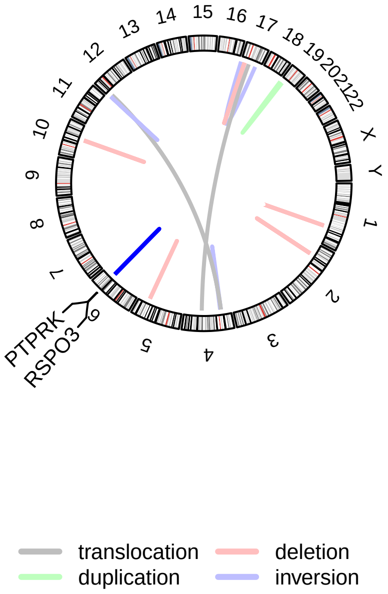
RETAINED PROTEIN DOMAINS
reading frame unclear

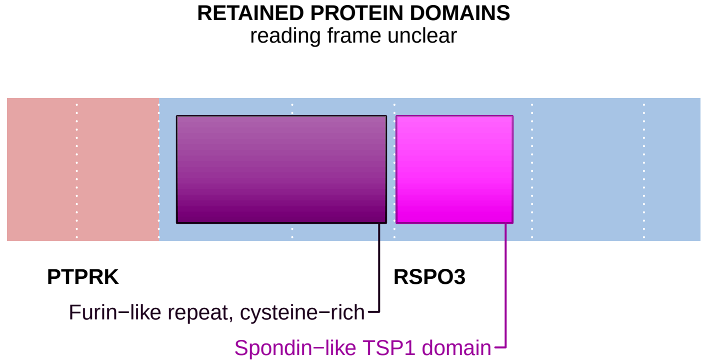


SUPPORTING READ COUNT

Split reads = 1422
Discordant mates = 18

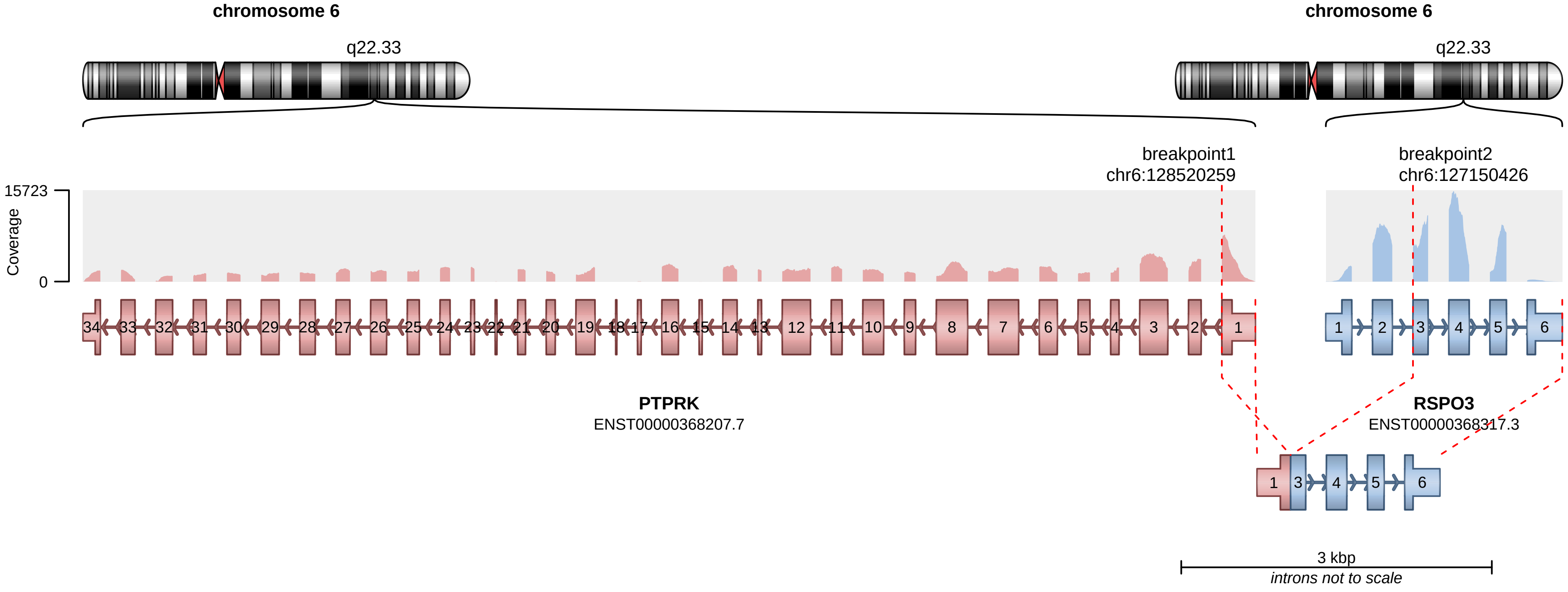


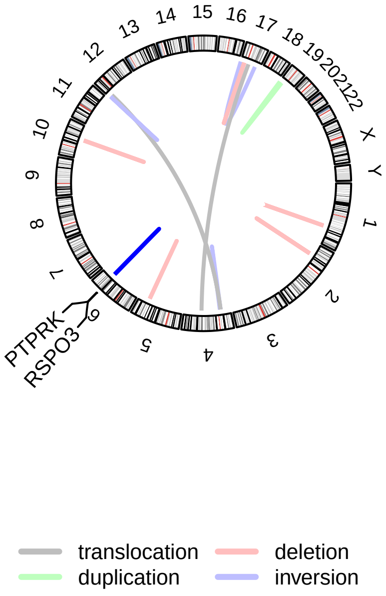


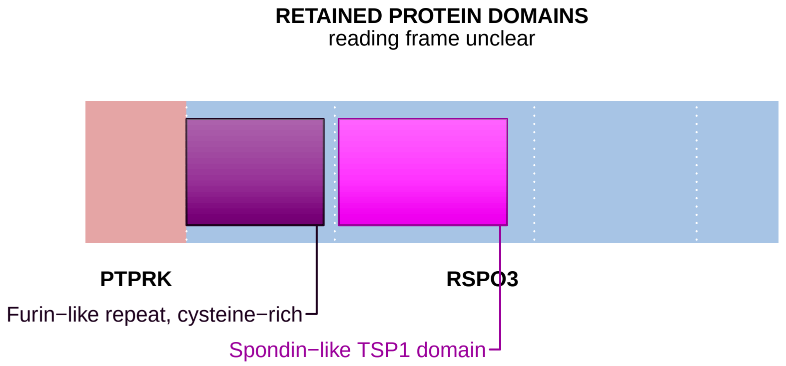


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 18

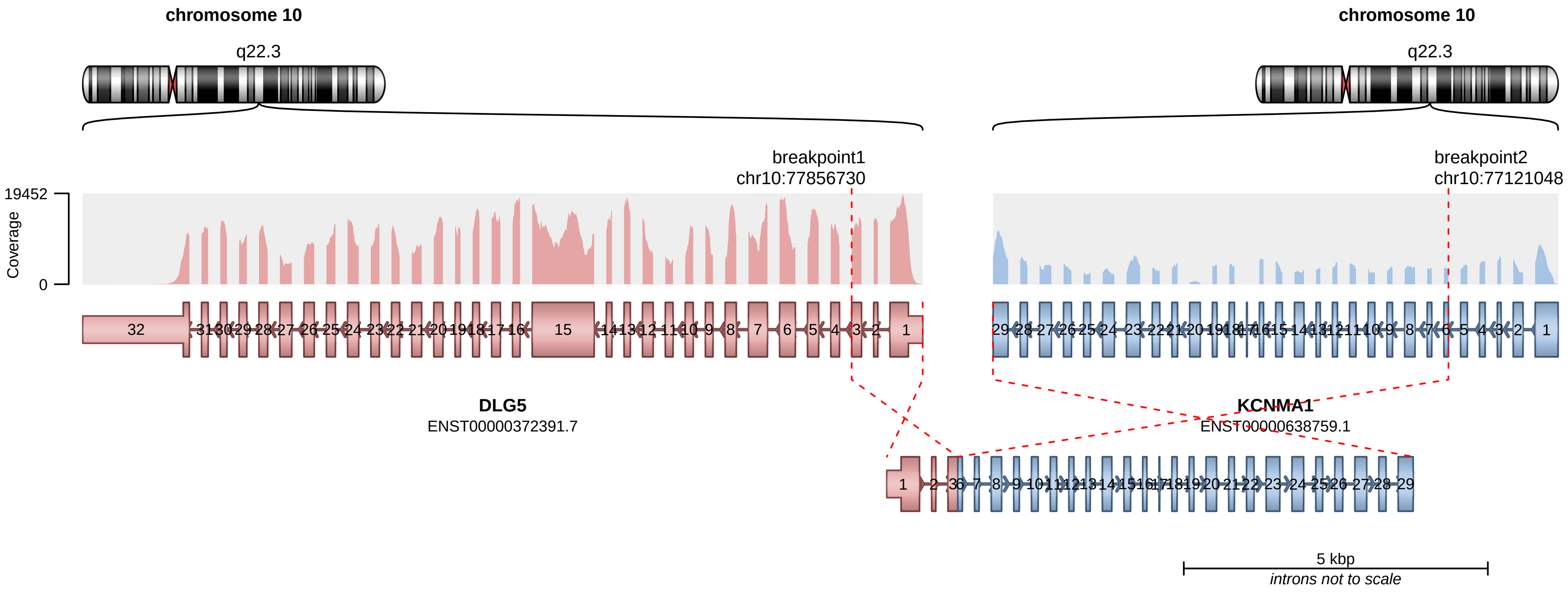


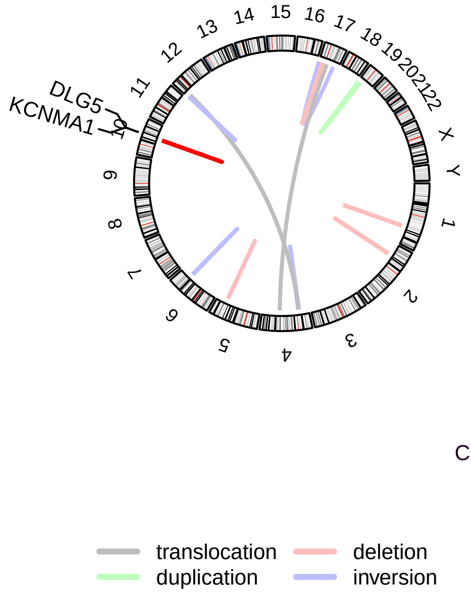


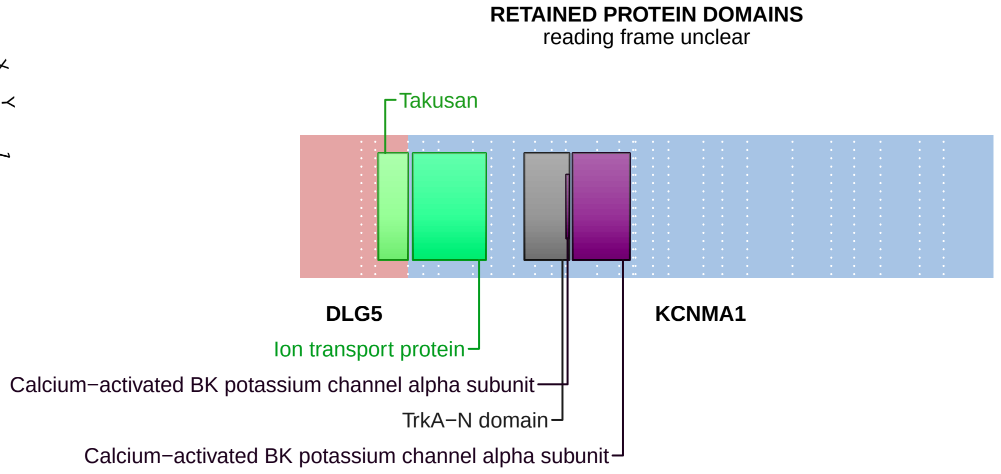


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

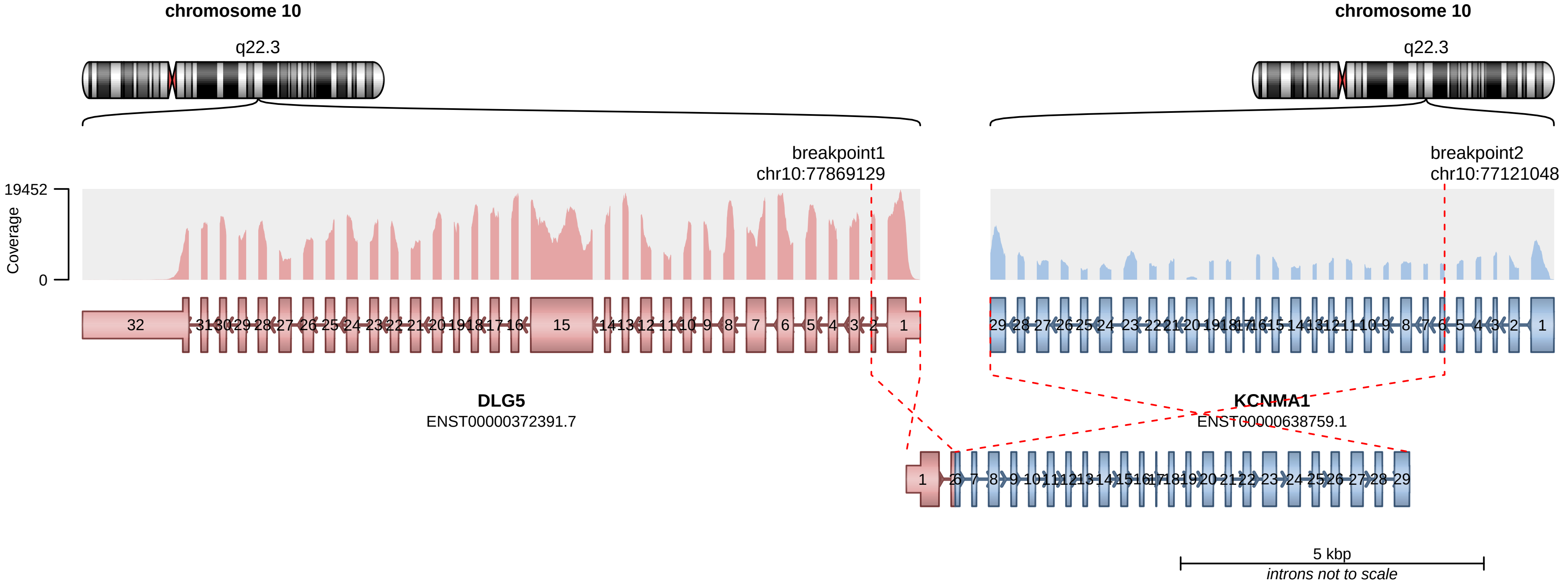


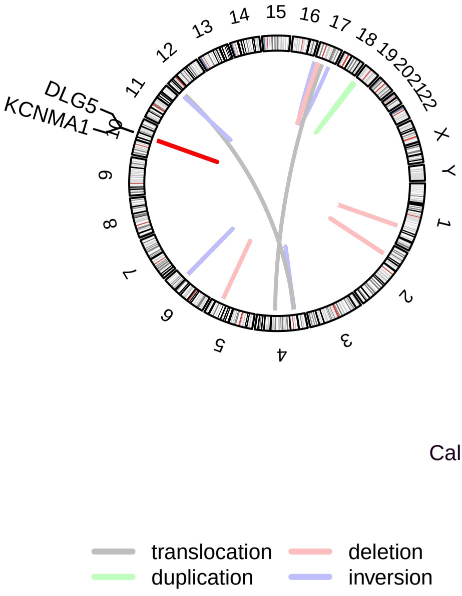


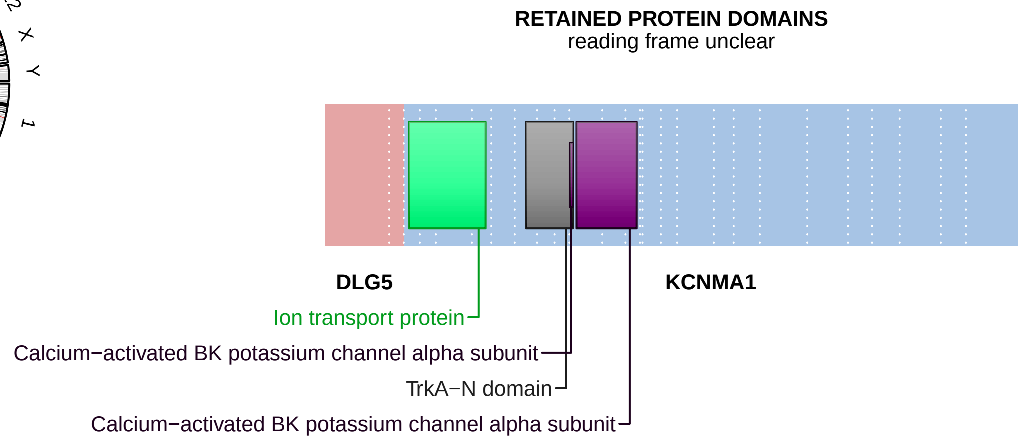


SUPPORTING READ COUNT

Split reads = 138
Discordant mates = 21

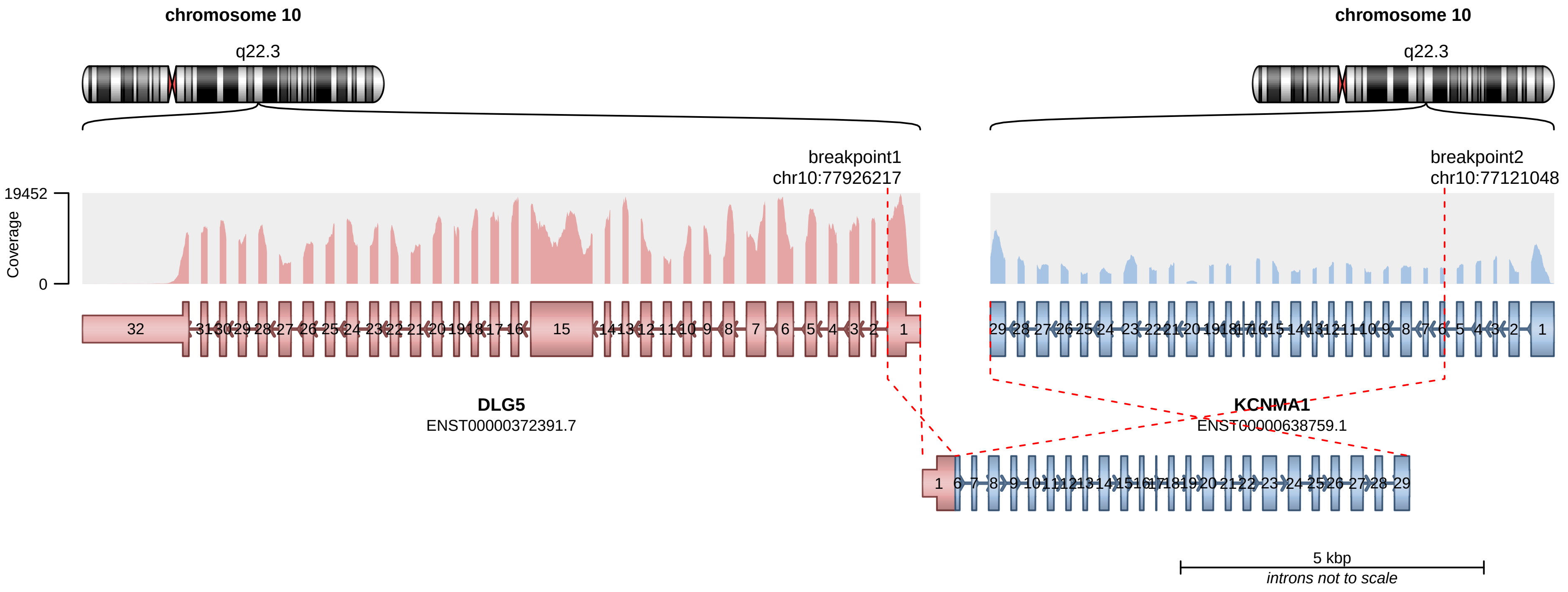


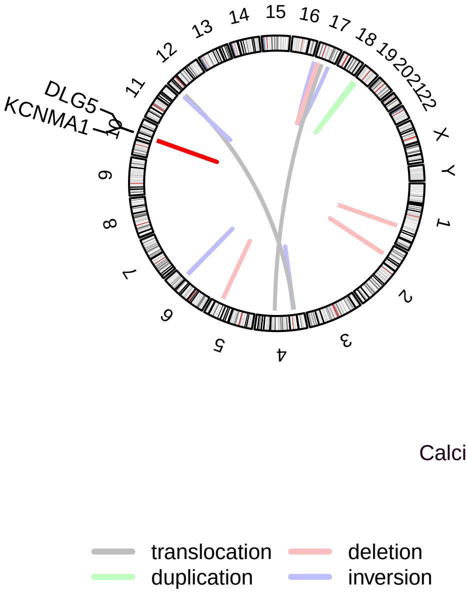


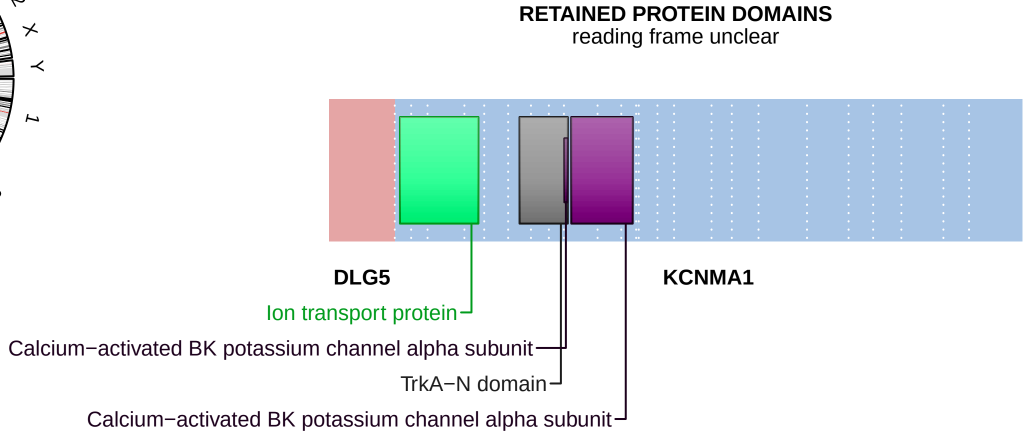

RETAINED PROTEIN DOMAINS
reading frame unclear

SUPPORTING READ COUNT

Split reads = 23
Discordant mates = 2

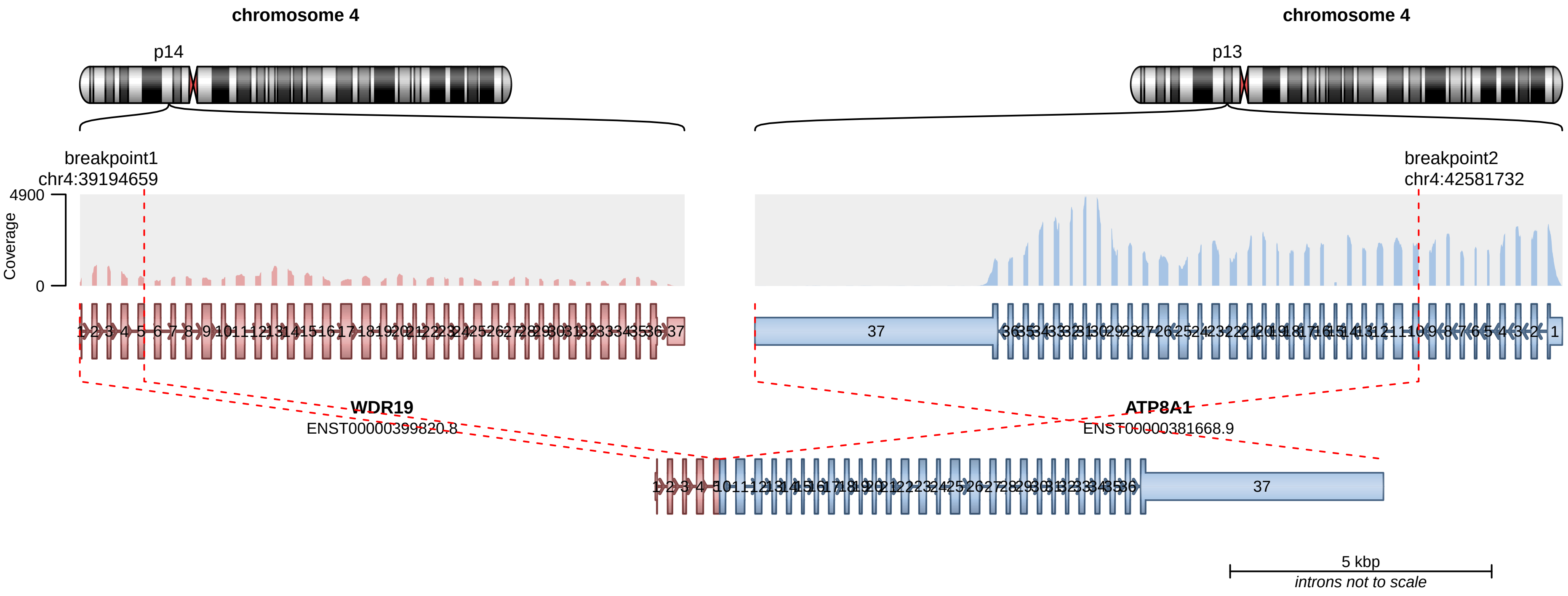


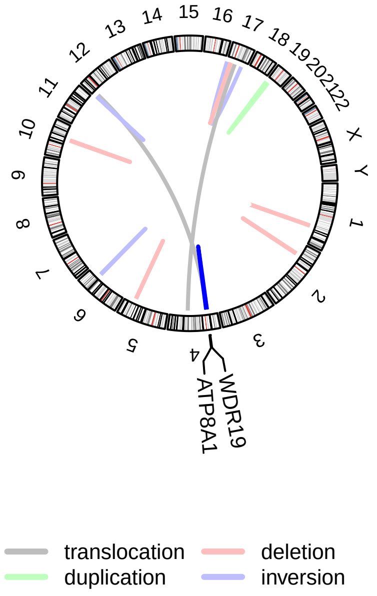




SUPPORTING READ COUNT

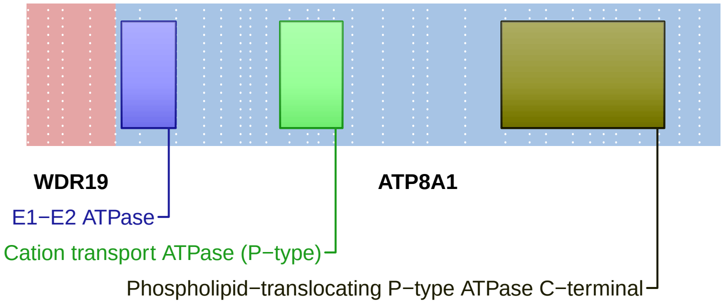
Split reads = 3
Discordant mates = 1





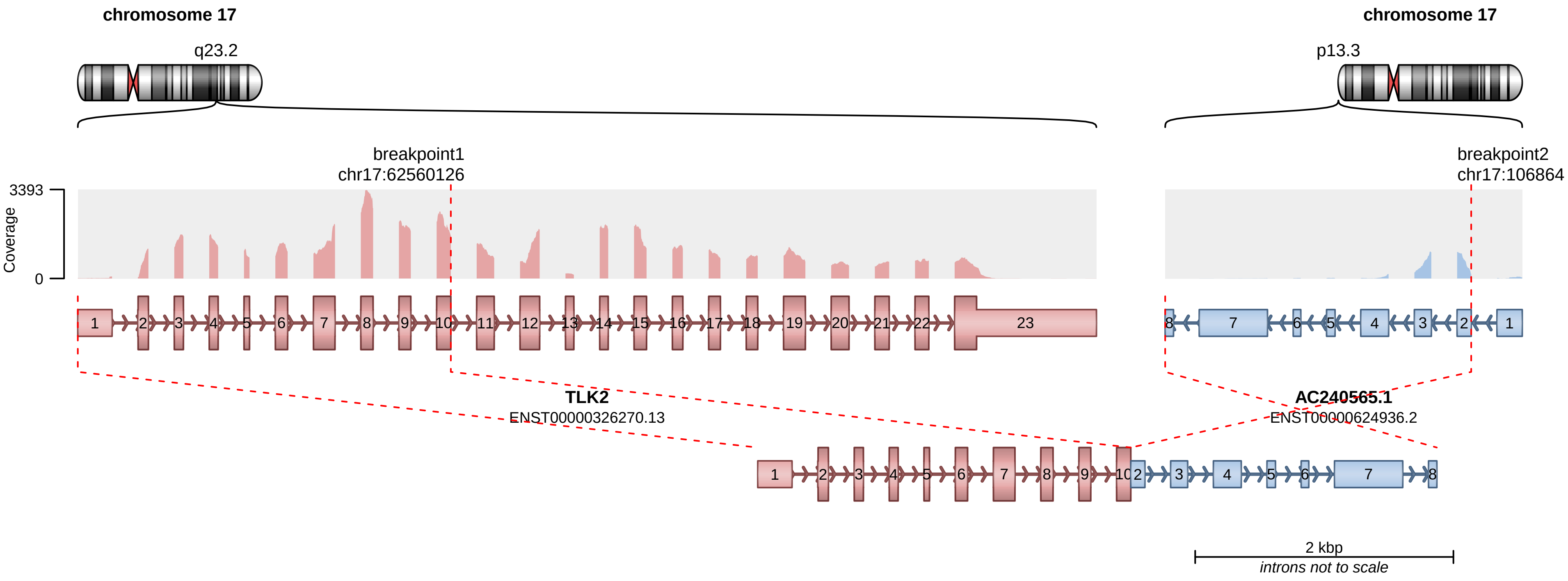
RETAINED PROTEIN DOMAINS

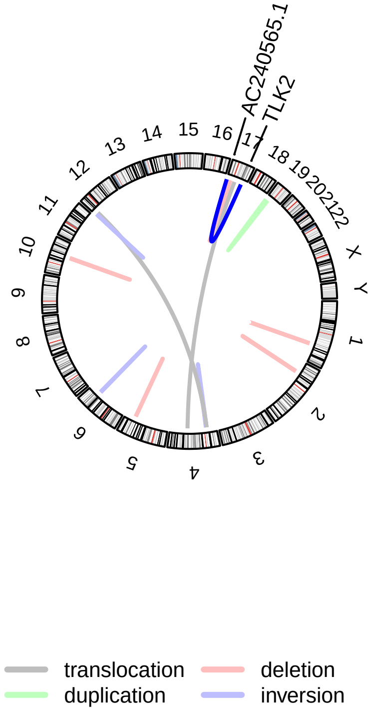
reading frame unclear



SUPPORTING READ COUNT

Split reads = 60
Discordant mates = 0

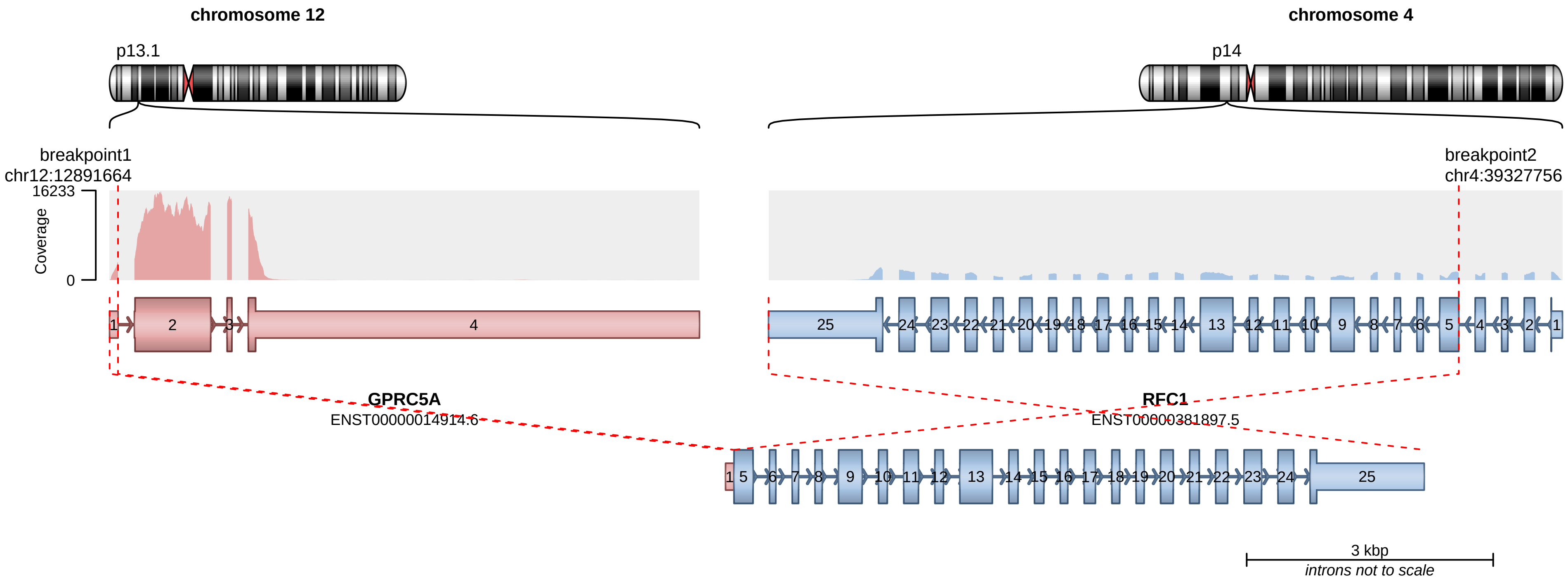


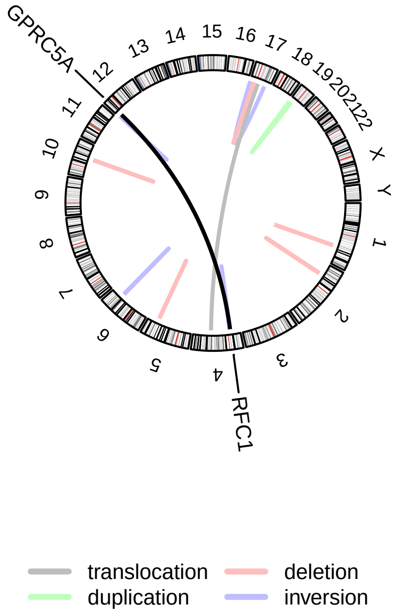


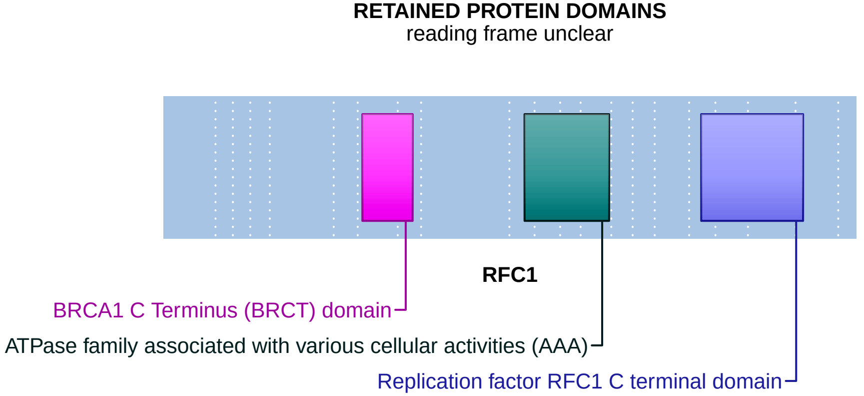
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 59
Discordant mates = 0

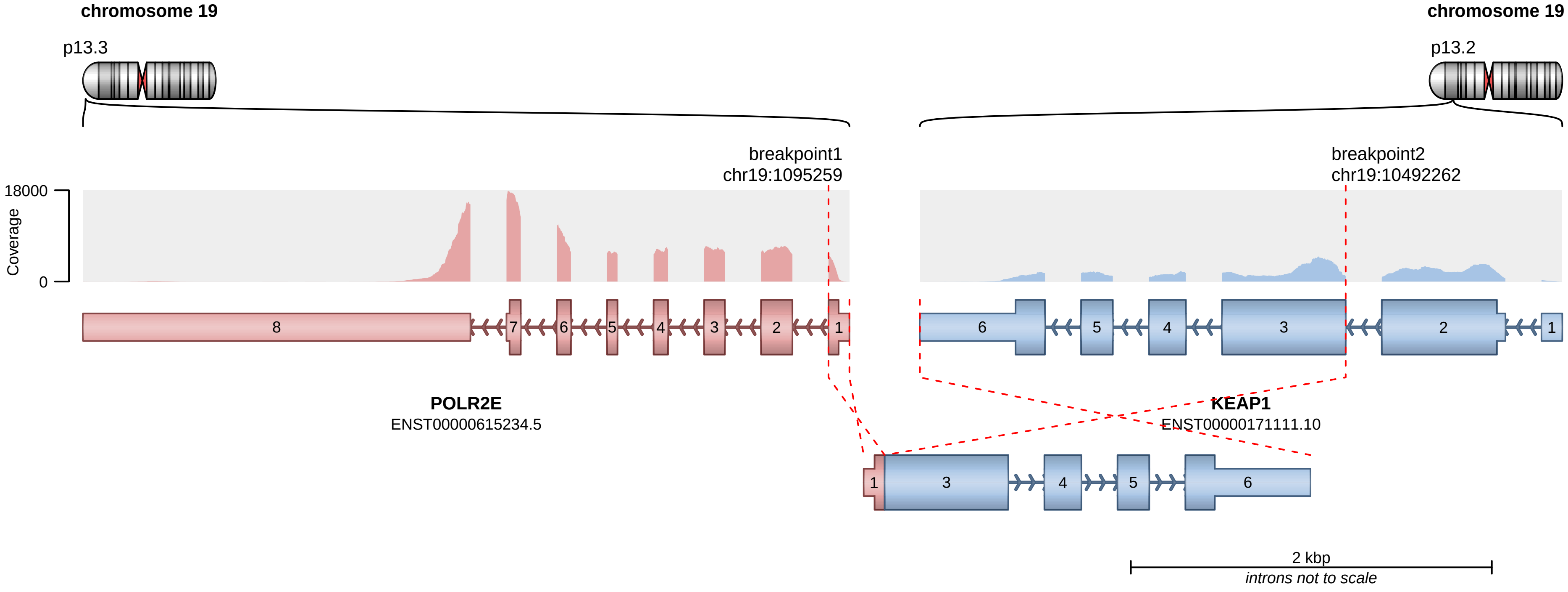


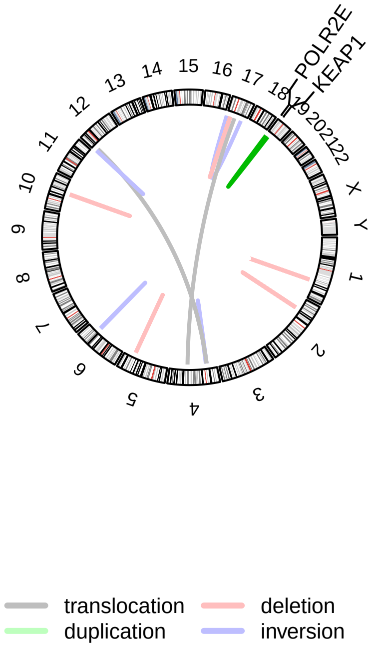


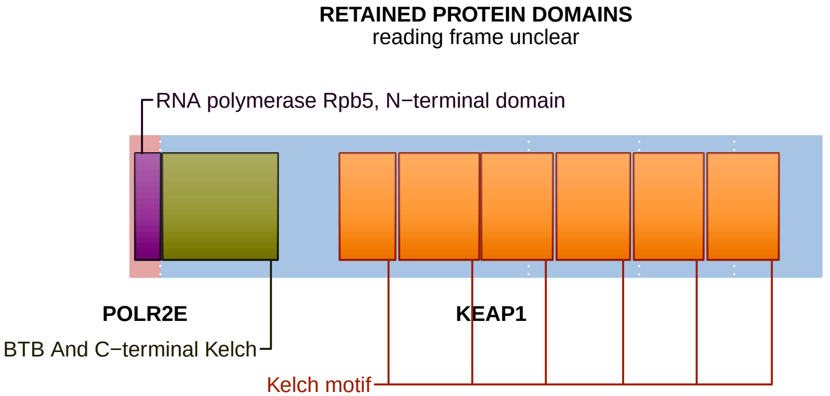


SUPPORTING READ COUNT

Split reads = 55
Discordant mates = 0

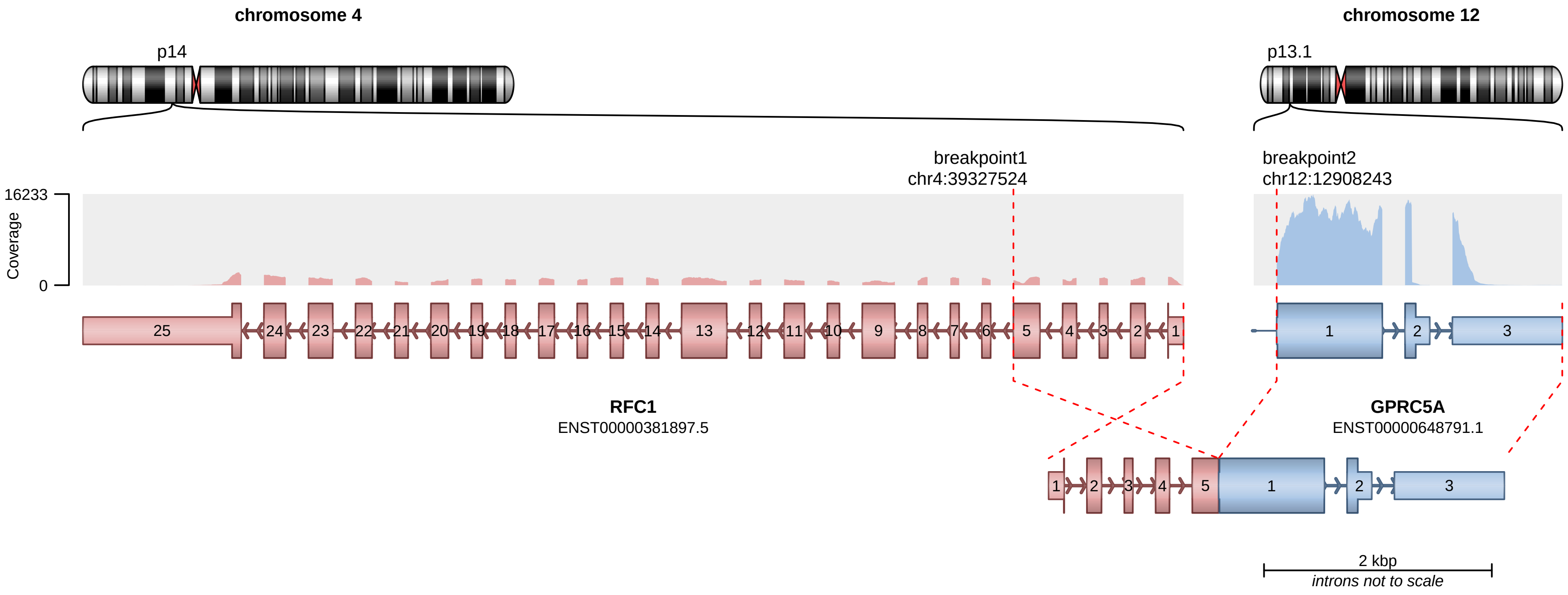


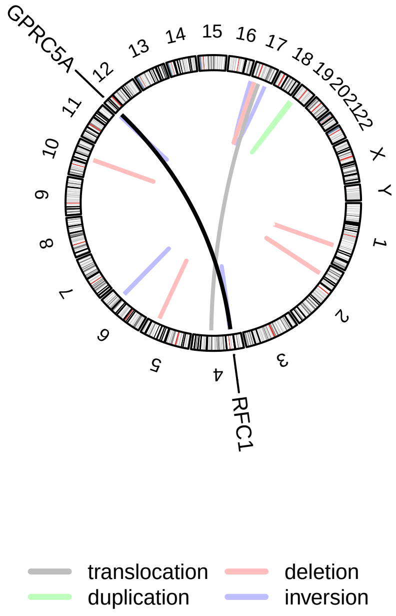


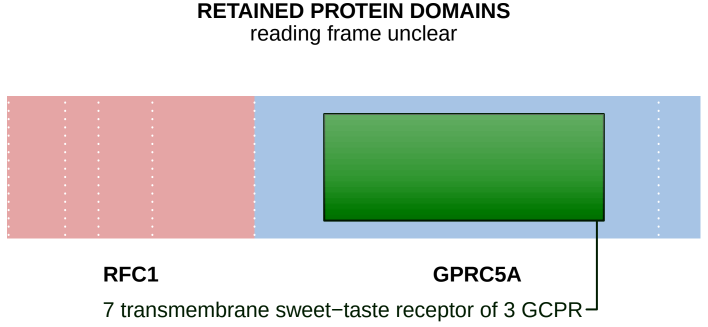


SUPPORTING READ COUNT

Split reads = 50
Discordant mates = 0

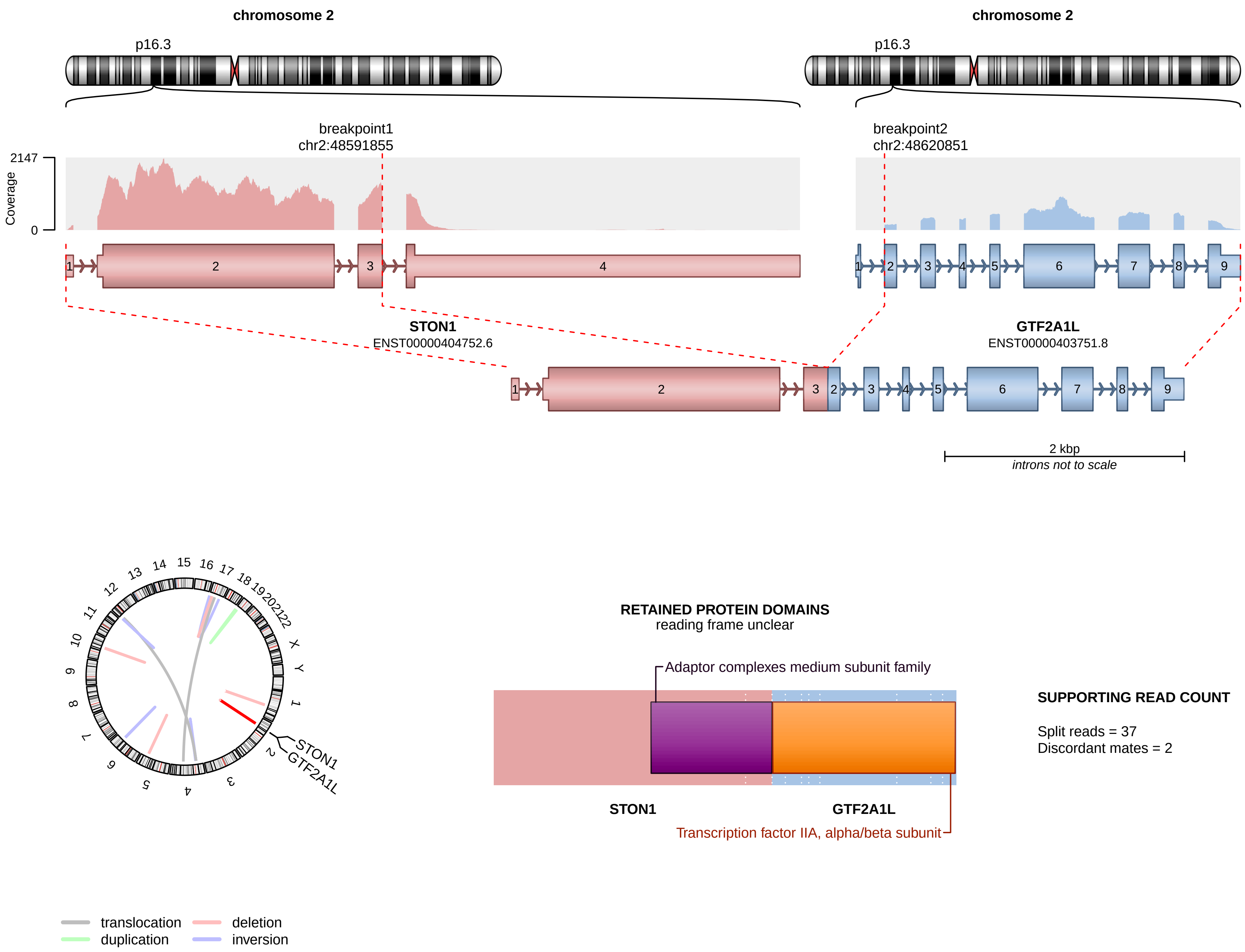


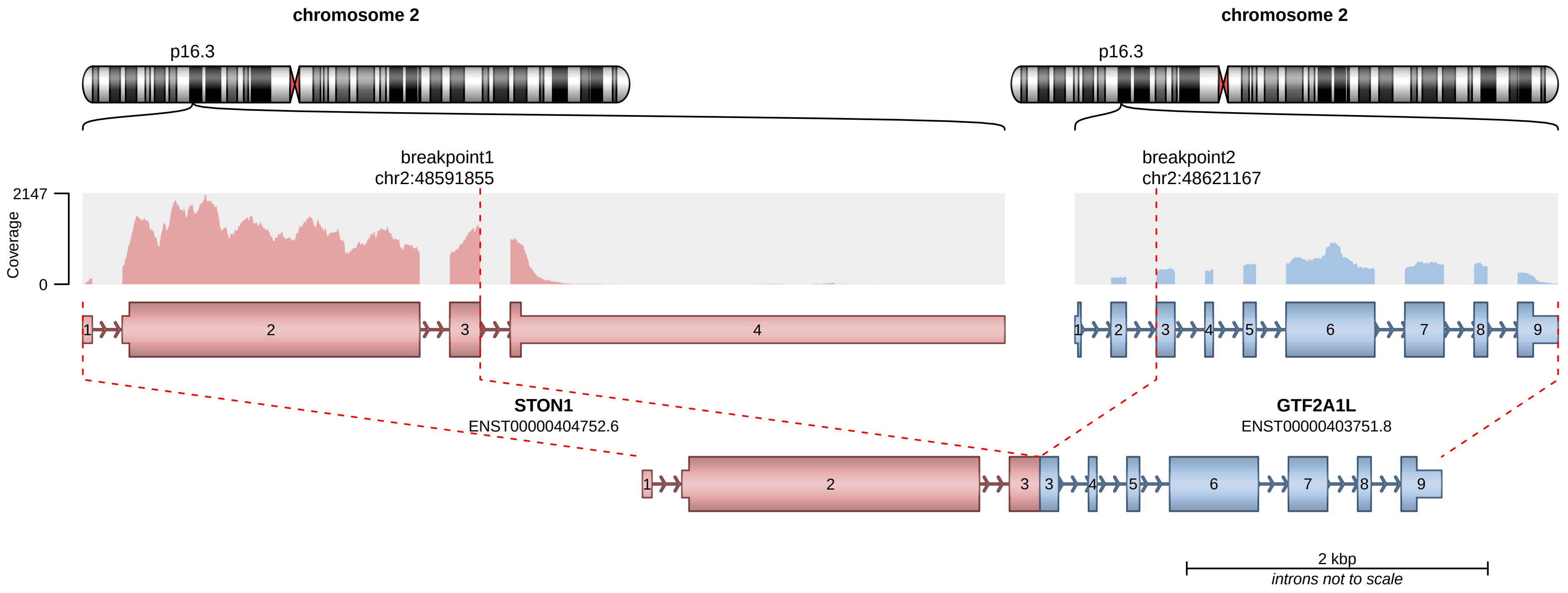


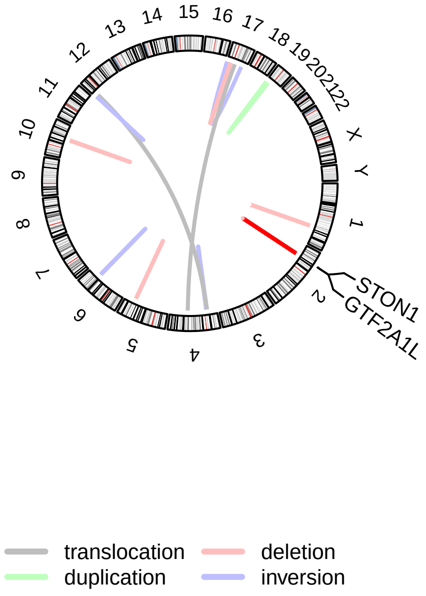


SUPPORTING READ COUNT

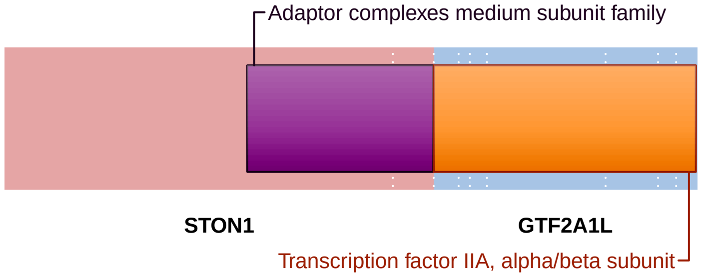
Split reads = 42
Discordant mates = 0


chromosome 2
p16.3
chromosome 2
p16.3
breakpoint1
chr2:48591855
breakpoint2
chr2:48620851
2147
Coverage
0
1
2
3
4
1
2
3
4
5
6
7
8
9
STON1
ENST00000404752.6
GTF2A1L
ENST00000403751.8
1
2
3
2
3
4
5
6
7
8
9
2 kbp
introns not to scale
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
X
Y
STON1
GTF2A1L
RETAINED PROTEIN DOMAINS
reading frame unclear
Adaptor complexes medium subunit family
STON1
GTF2A1L
Transcription factor IIA, alpha/beta subunit
SUPPORTING READ COUNT
Split reads = 37
Discordant mates = 2
translocation
deletion
duplication
inversion



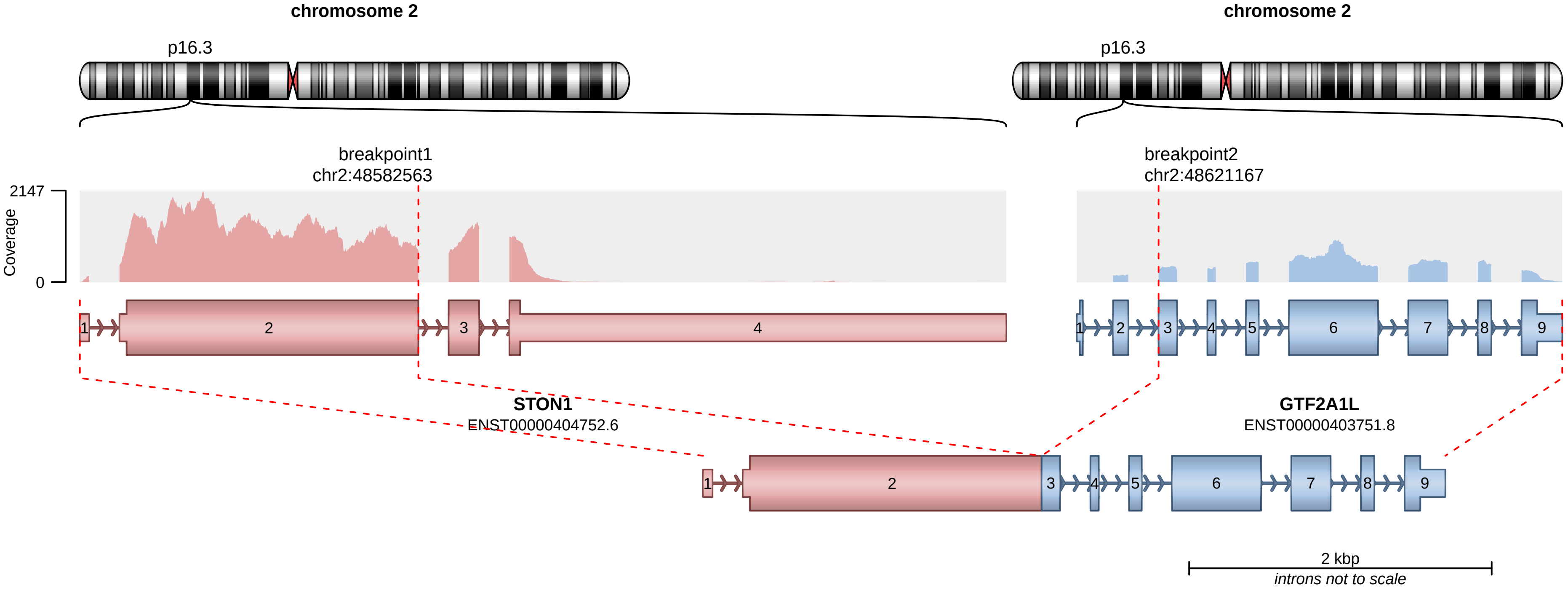


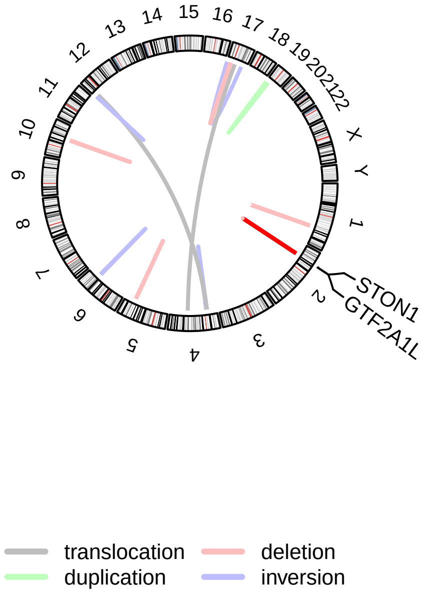
RETAINED PROTEIN DOMAINS
reading frame unclear

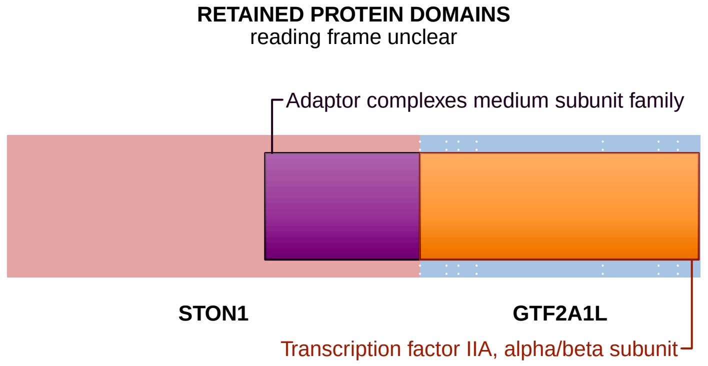


SUPPORTING READ COUNT

Split reads = 25
Discordant mates = 2

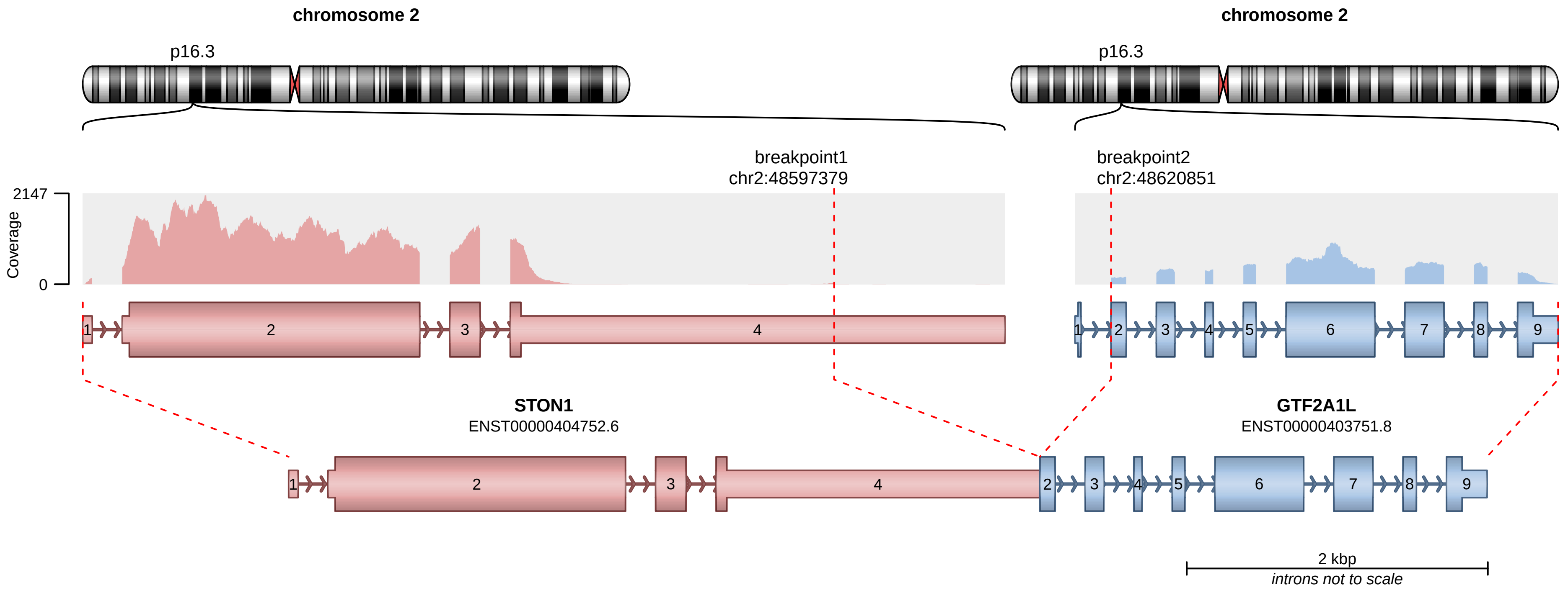


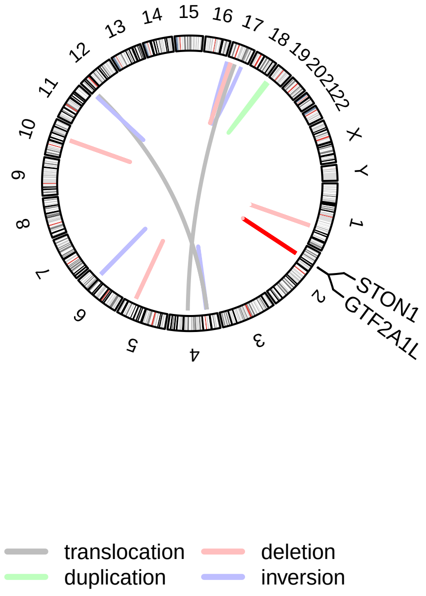


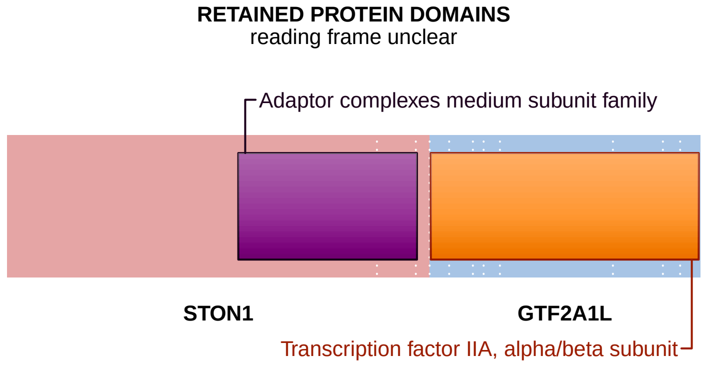


SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 0

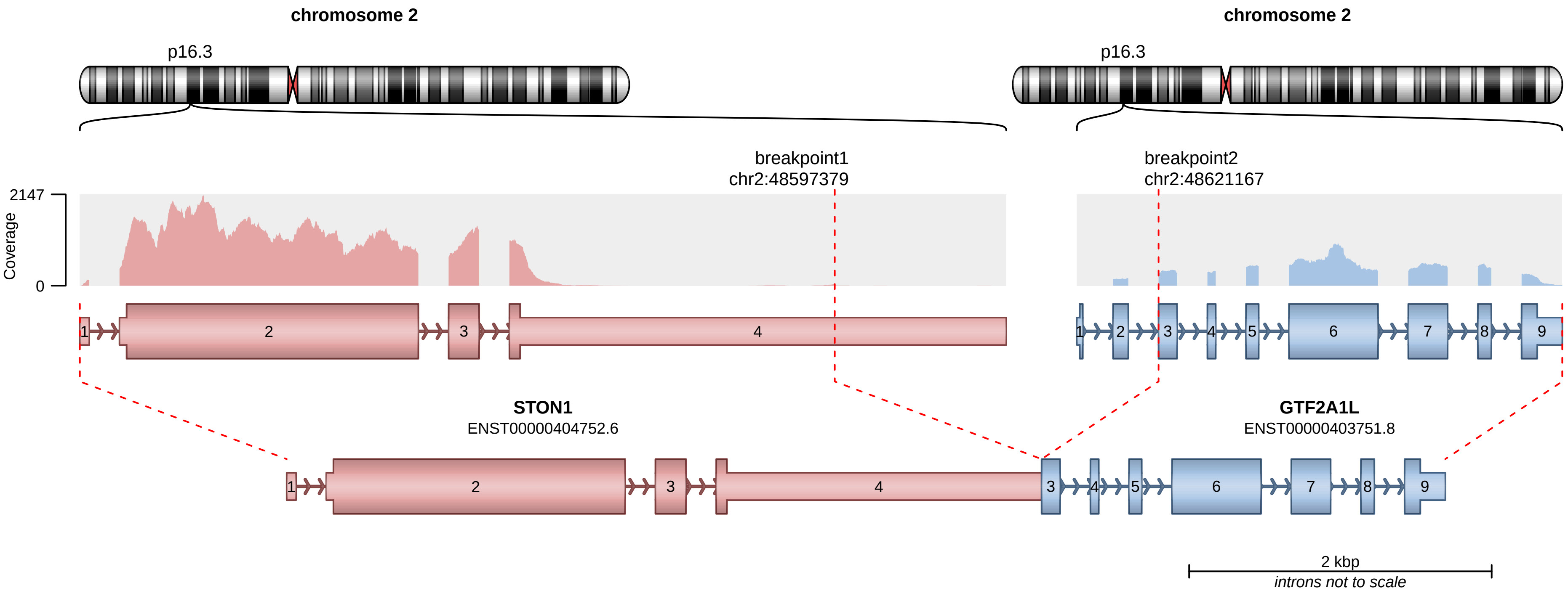


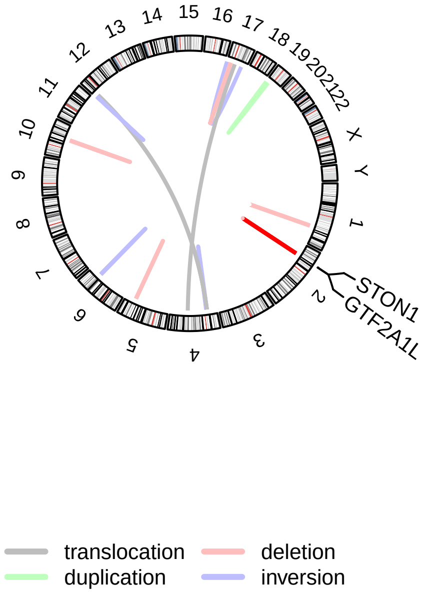




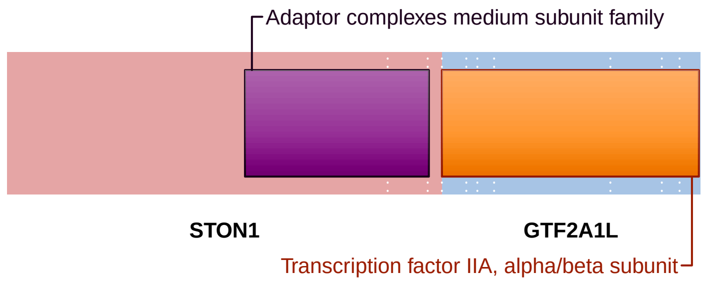
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 2



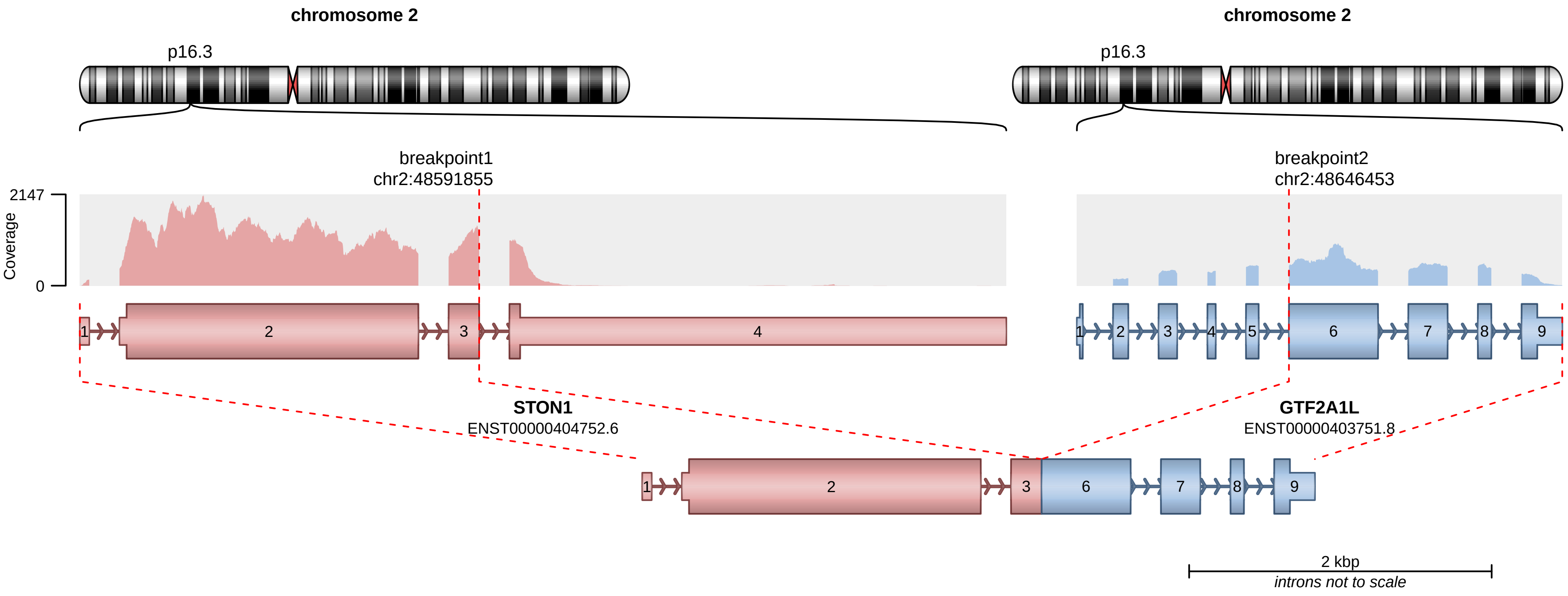


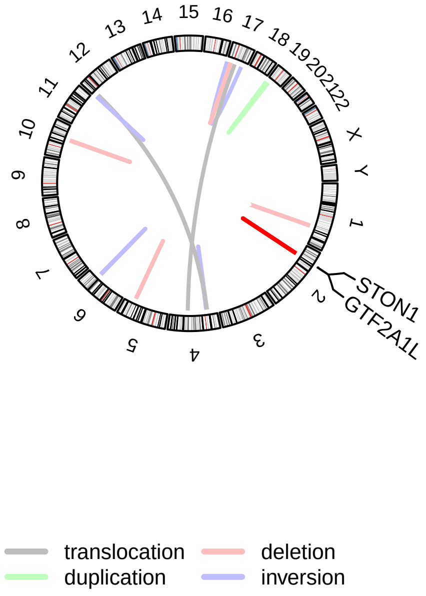
RETAINED PROTEIN DOMAINS
reading frame unclear

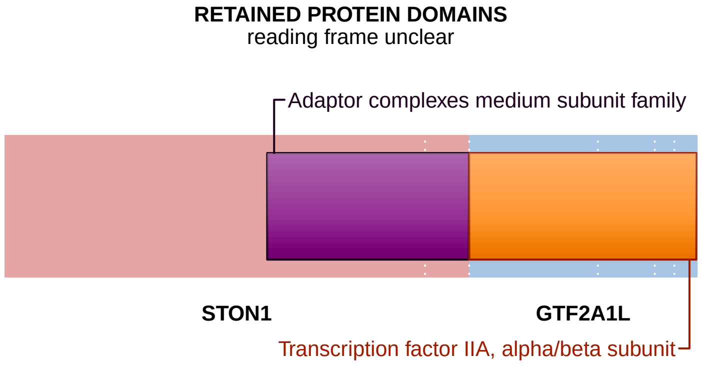


SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 2

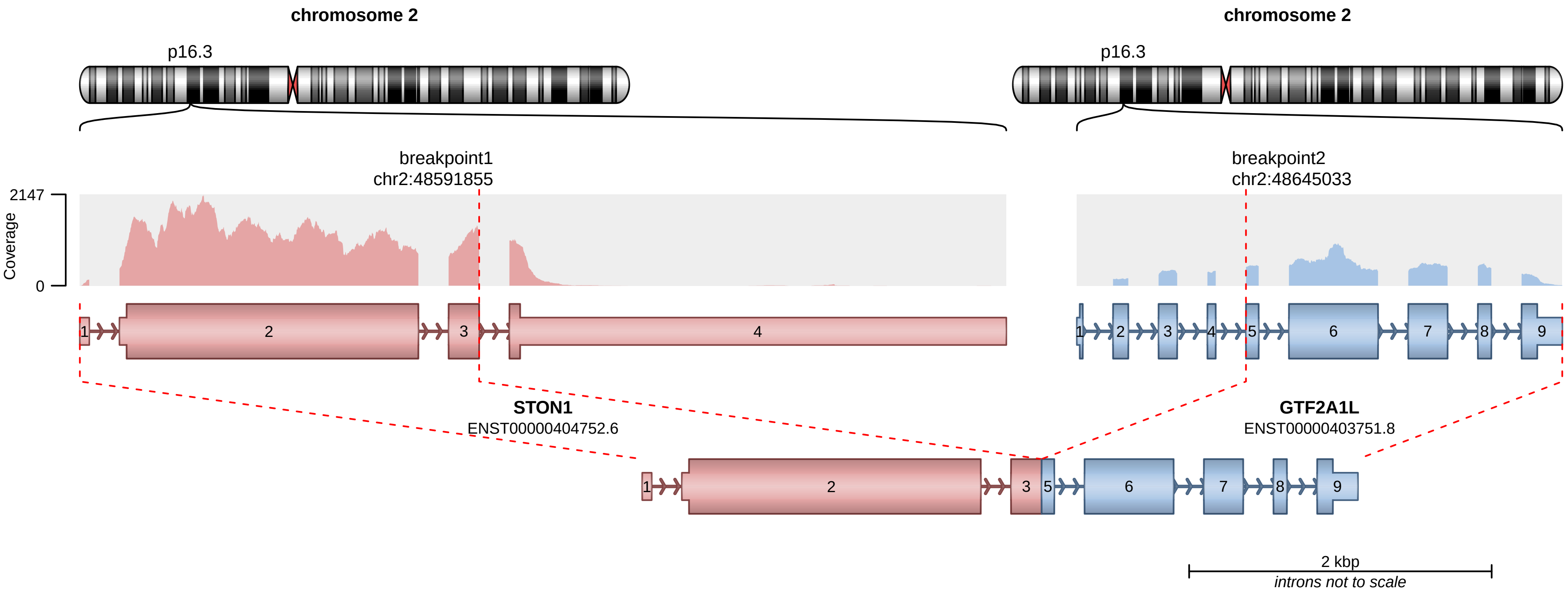


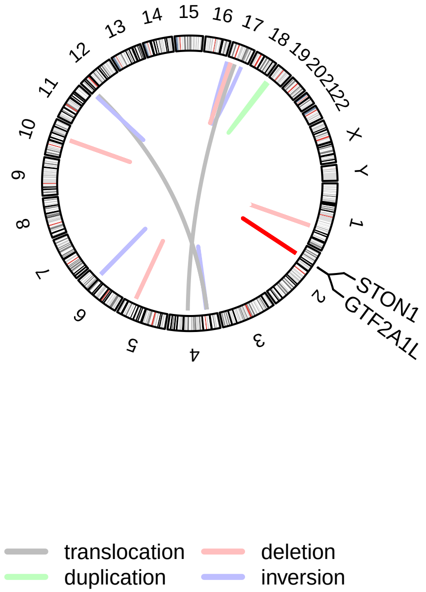


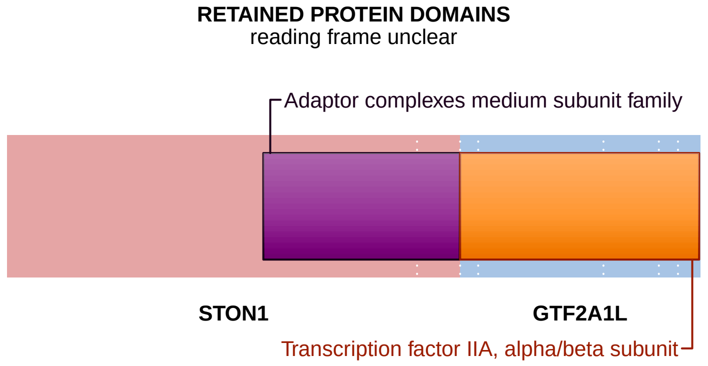


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 1

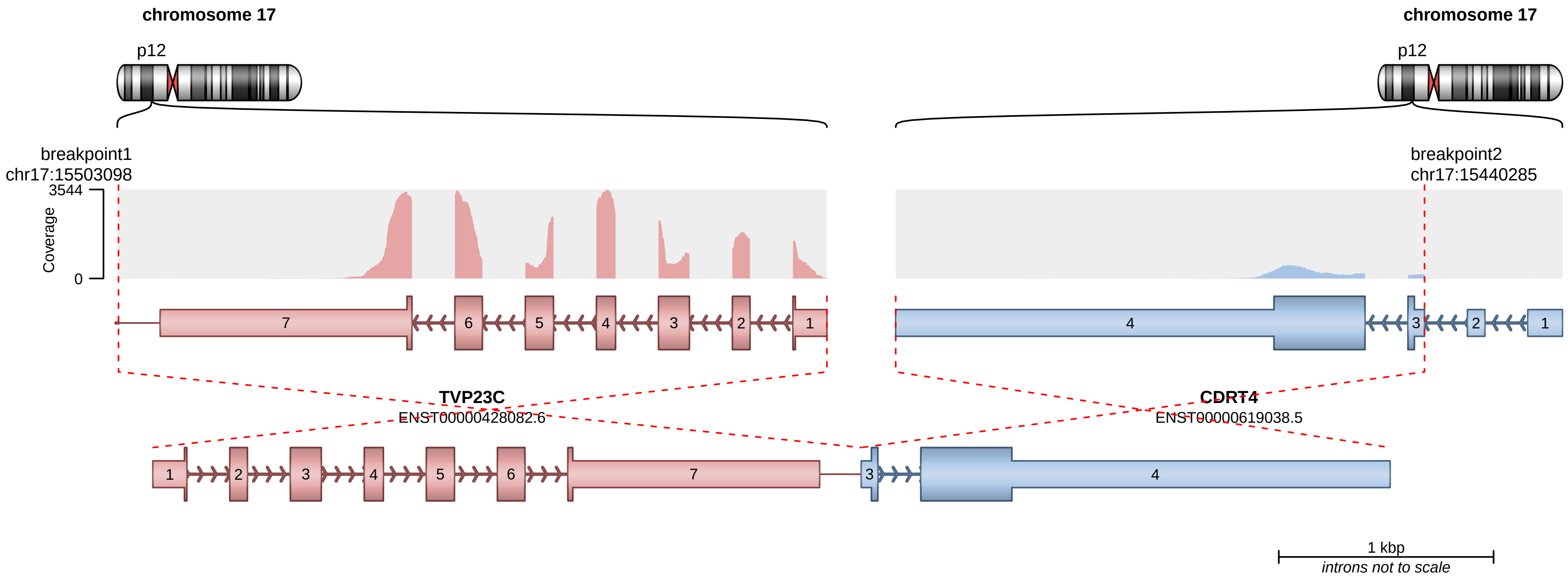


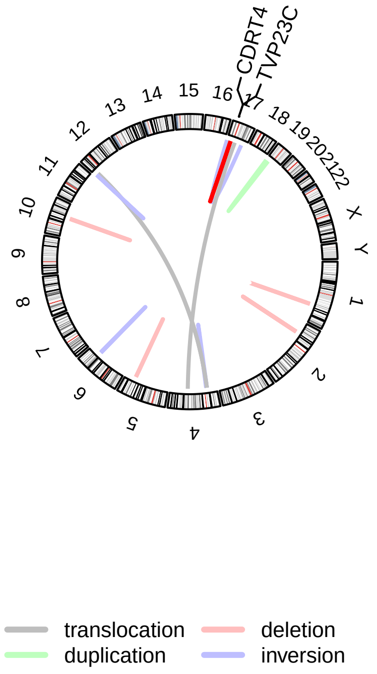


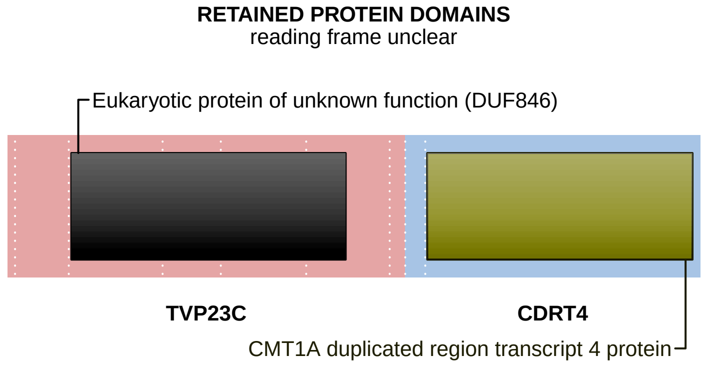


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

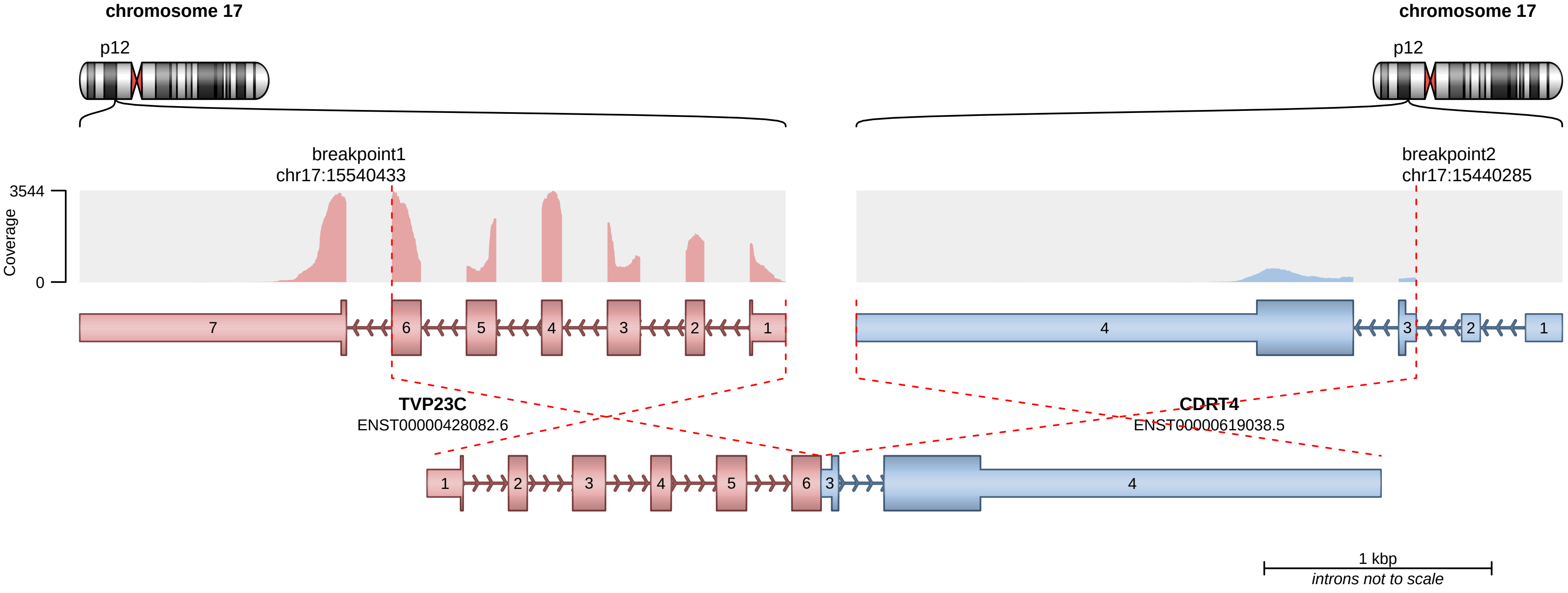


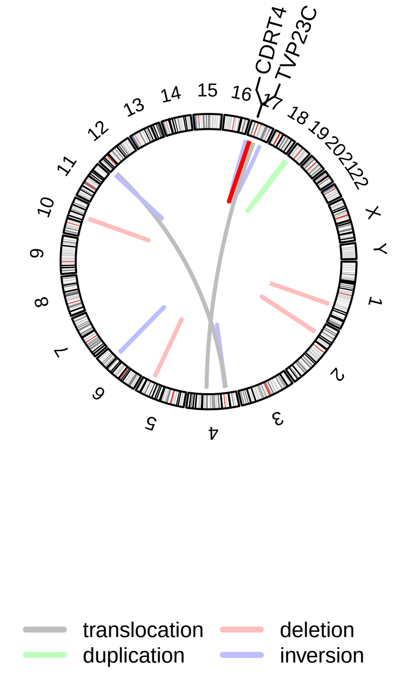


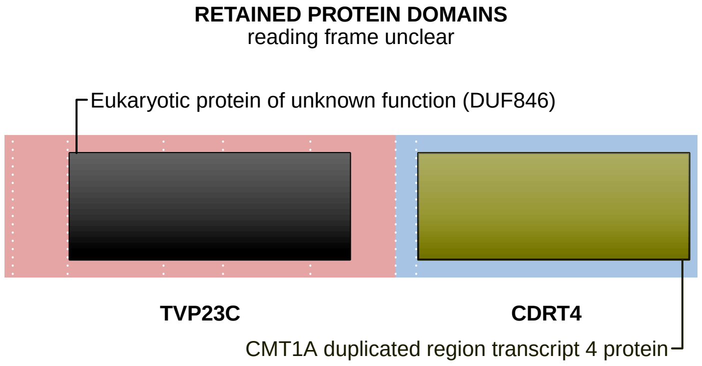


SUPPORTING READ COUNT

Split reads = 33
Discordant mates = 1

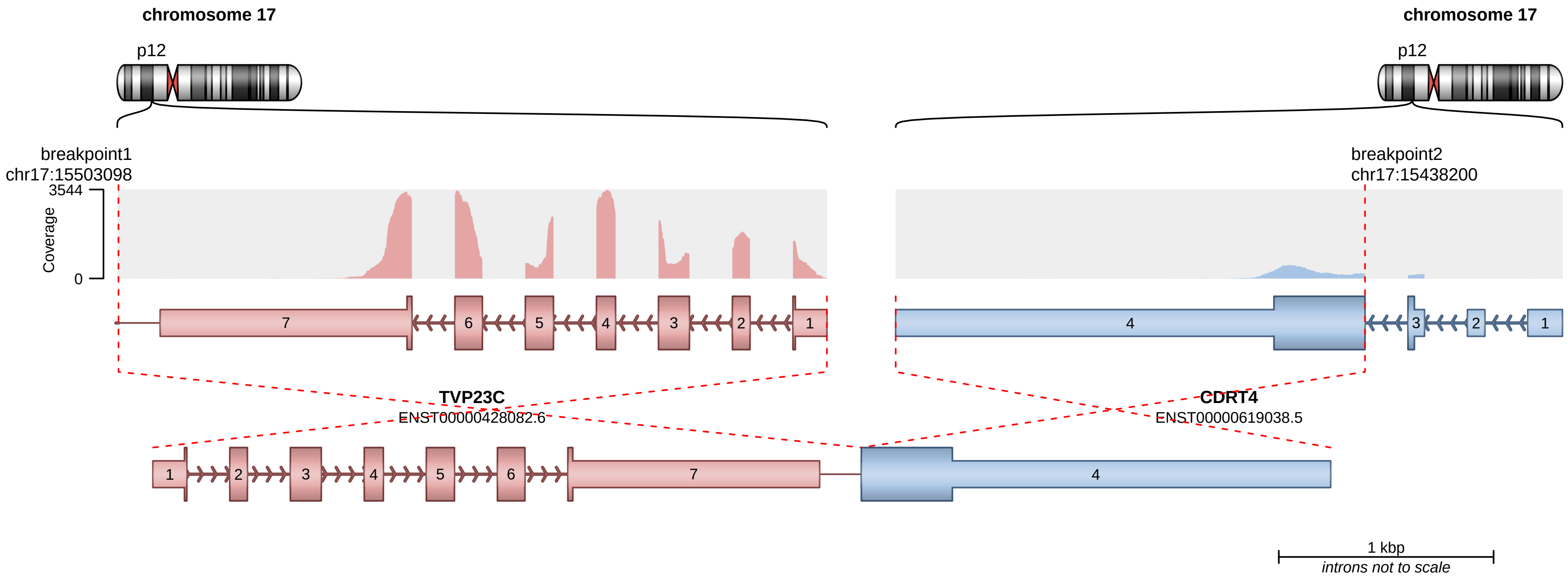


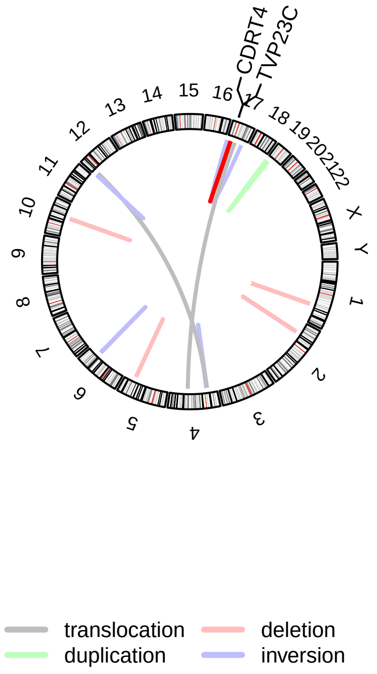




SUPPORTING READ COUNT

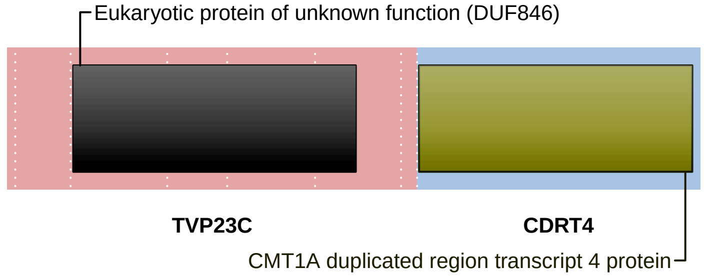
Split reads = 11
Discordant mates = 0





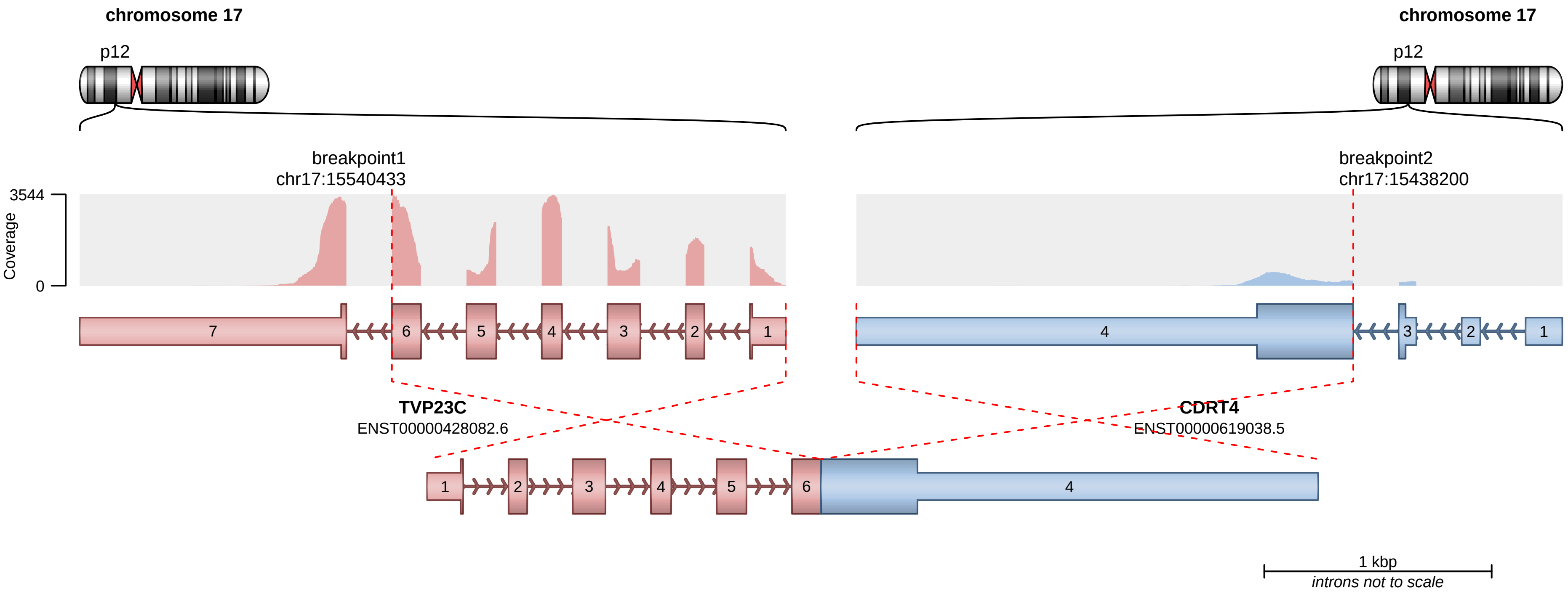
RETAINED PROTEIN DOMAINS

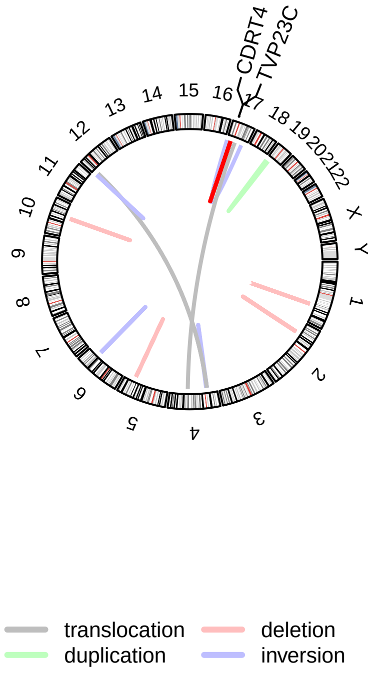
reading frame unclear



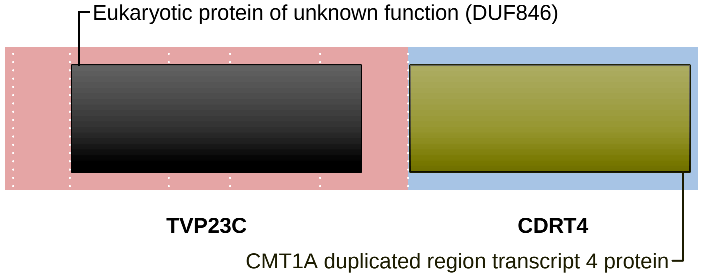
SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 0



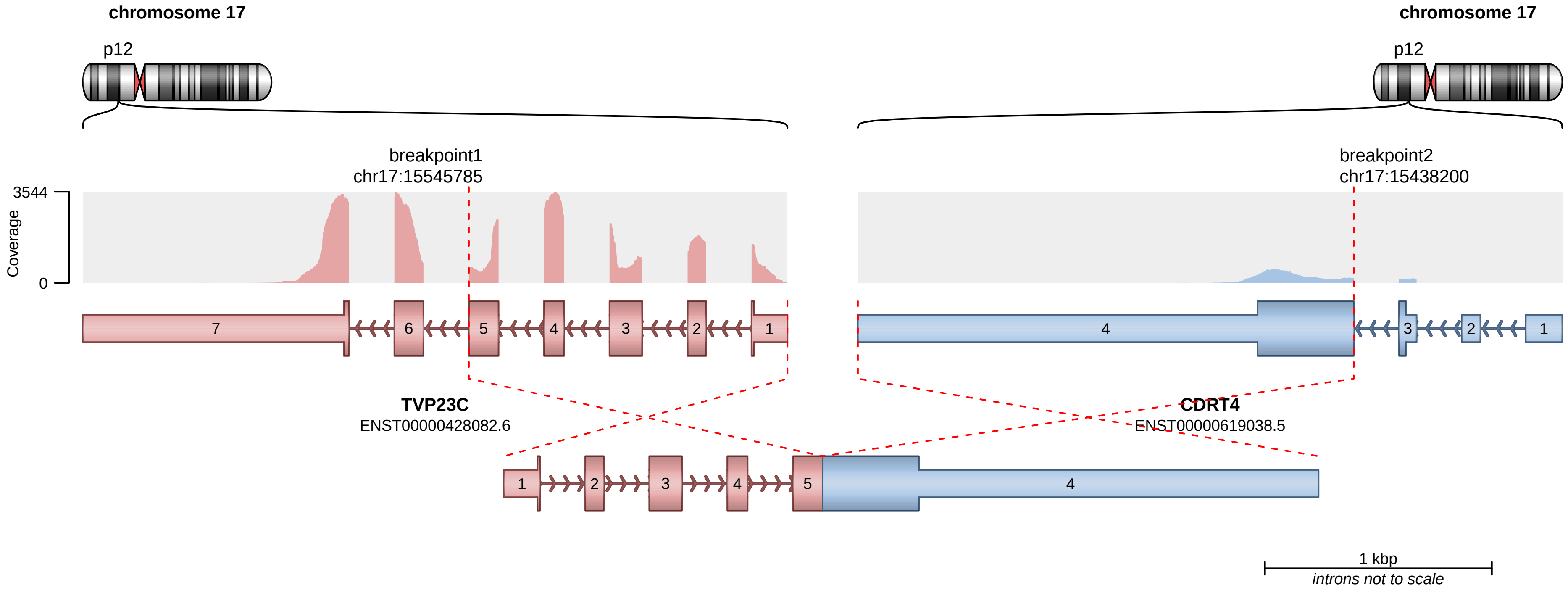


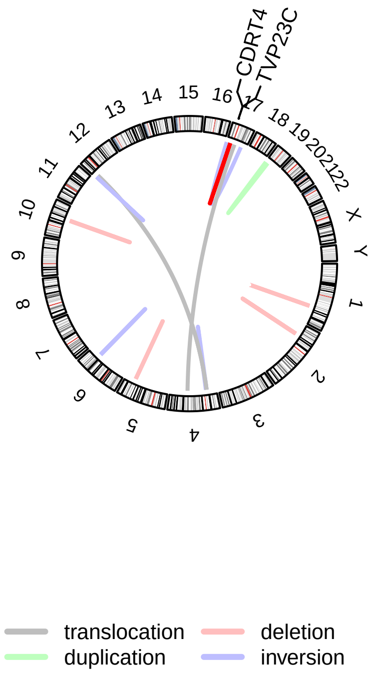
RETAINED PROTEIN DOMAINS
reading frame unclear



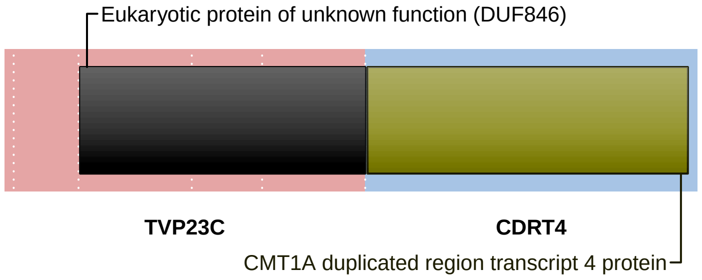
SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0



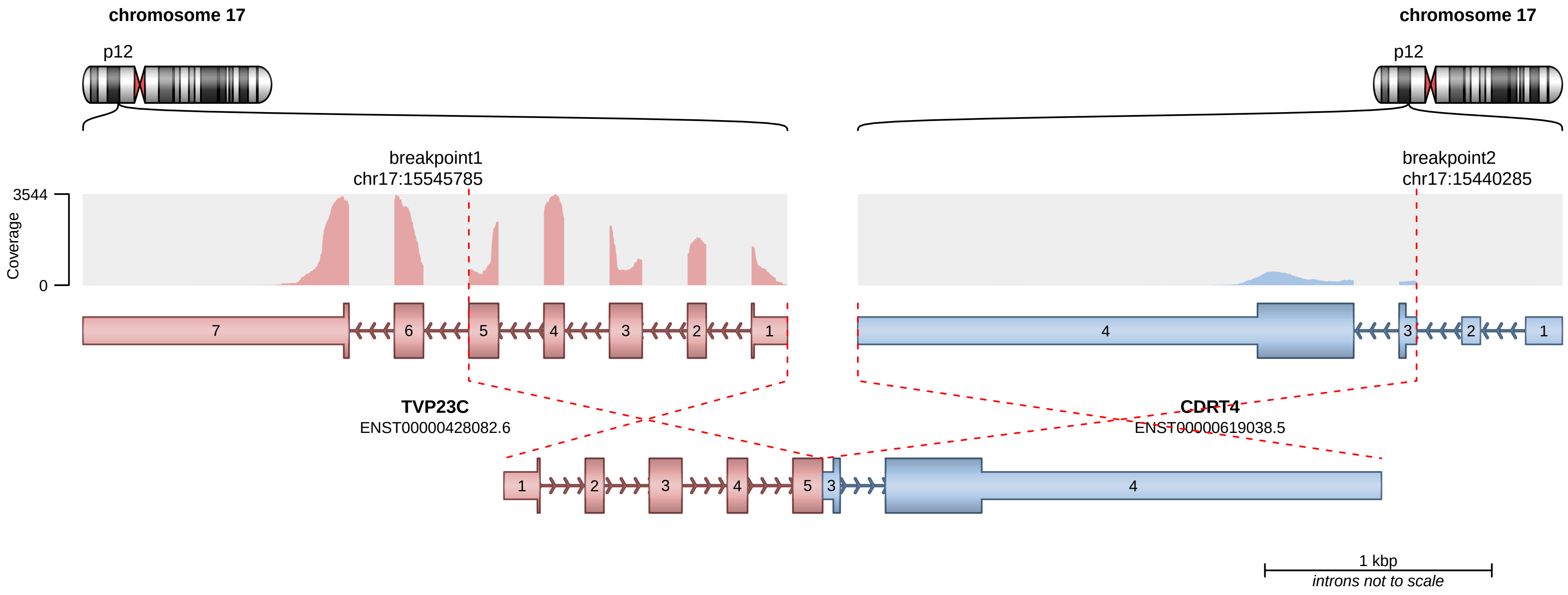


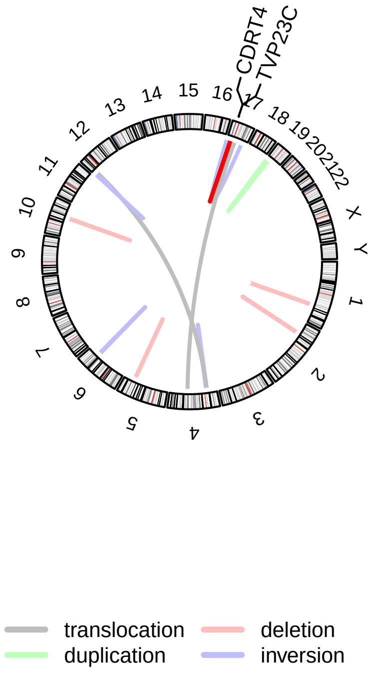
RETAINED PROTEIN DOMAINS
reading frame unclear



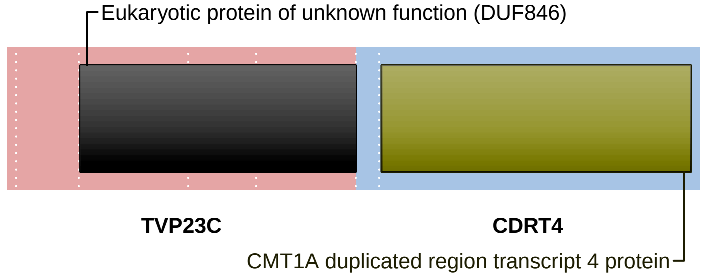
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0



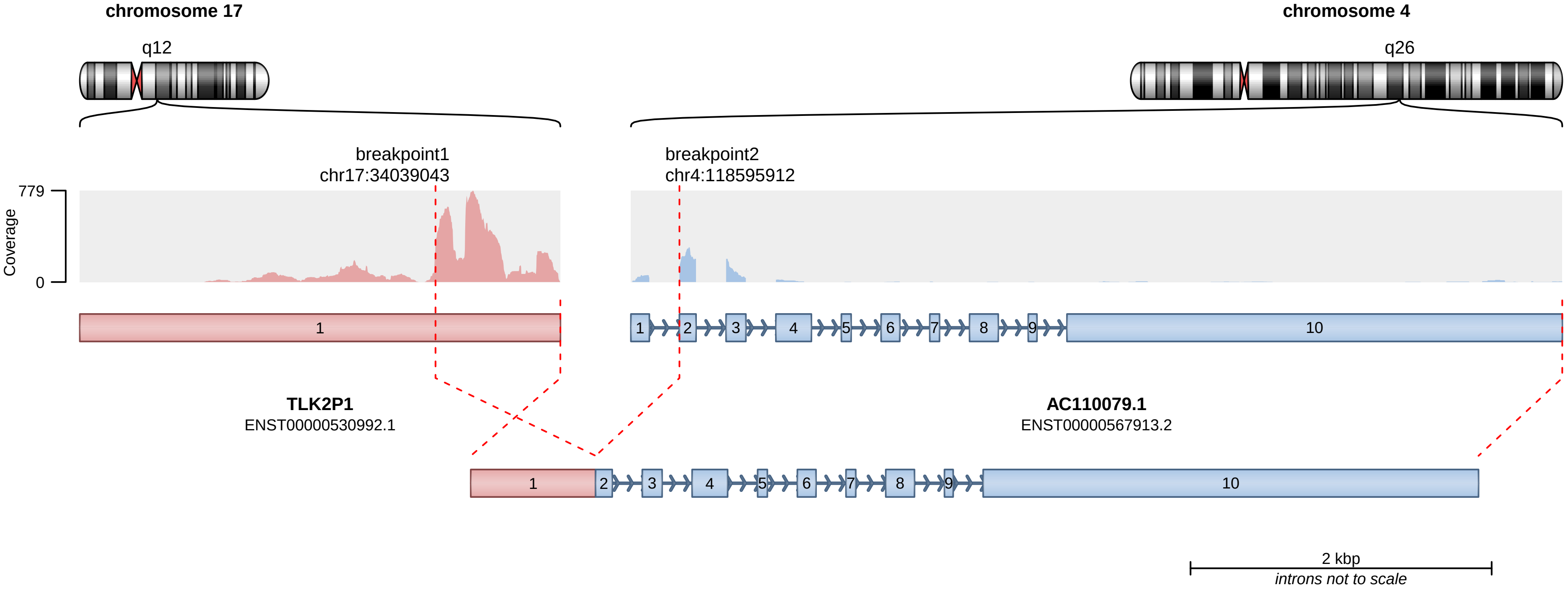


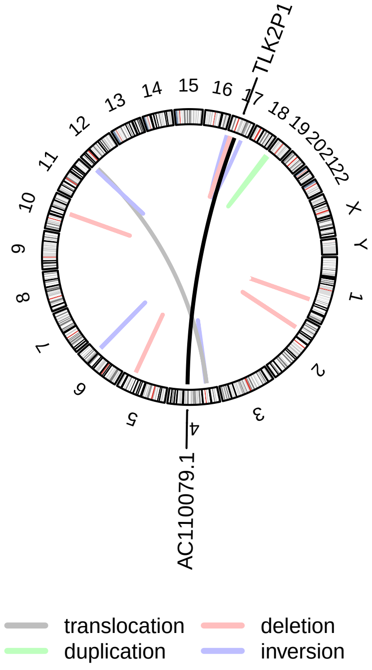
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

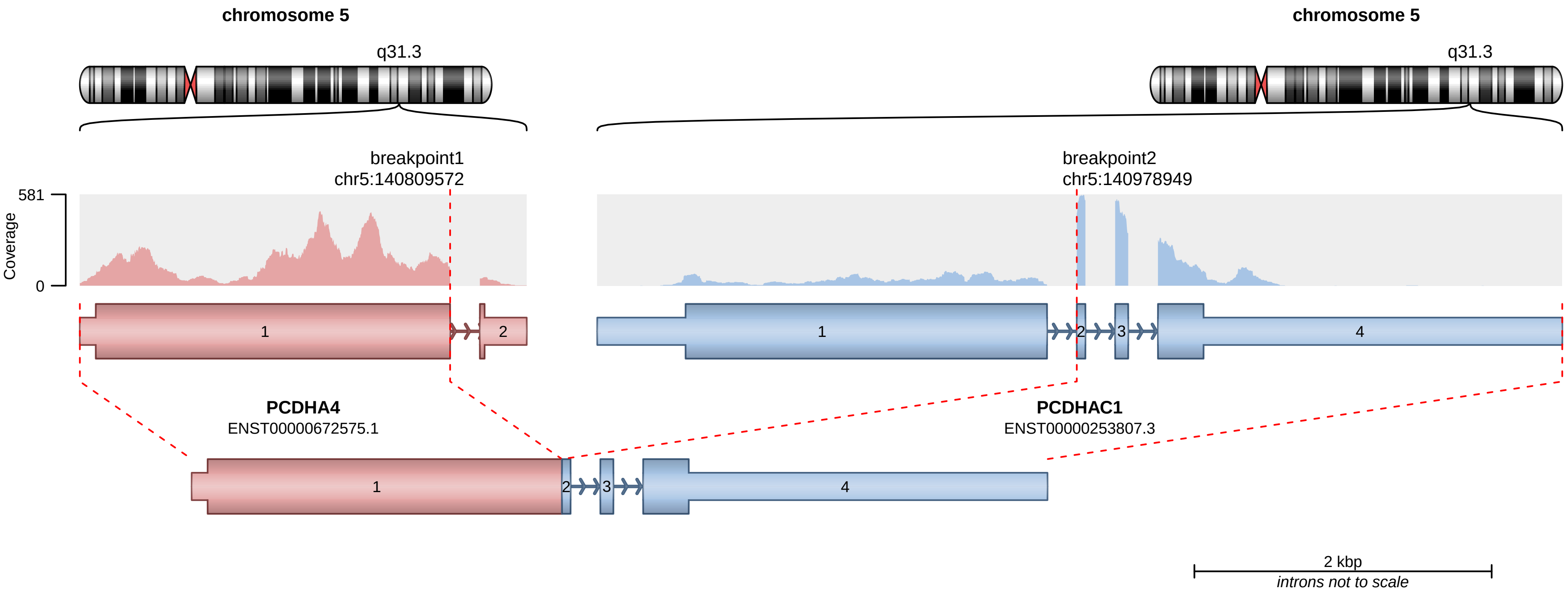


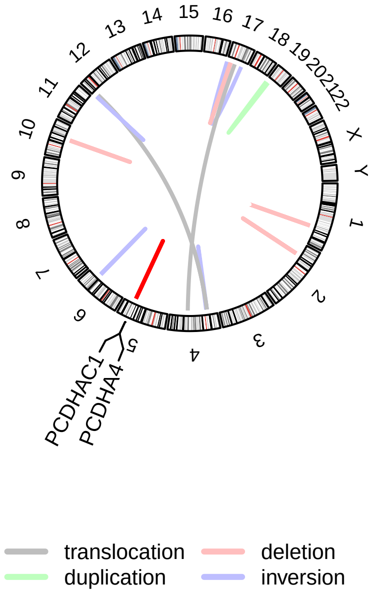


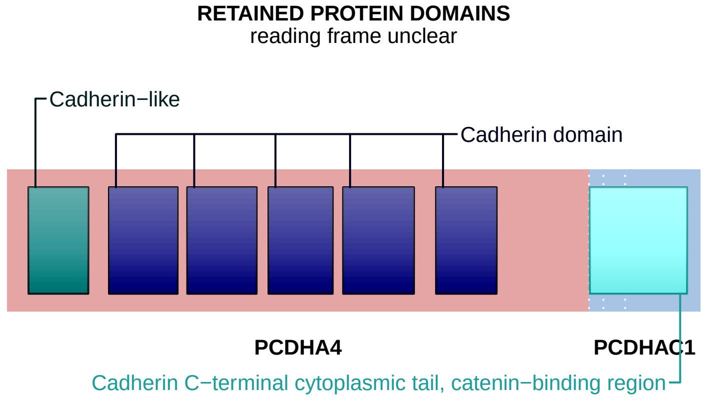
Genes are not protein−coding.

SUPPORTING READ COUNT

Split reads = 29
Discordant mates = 0

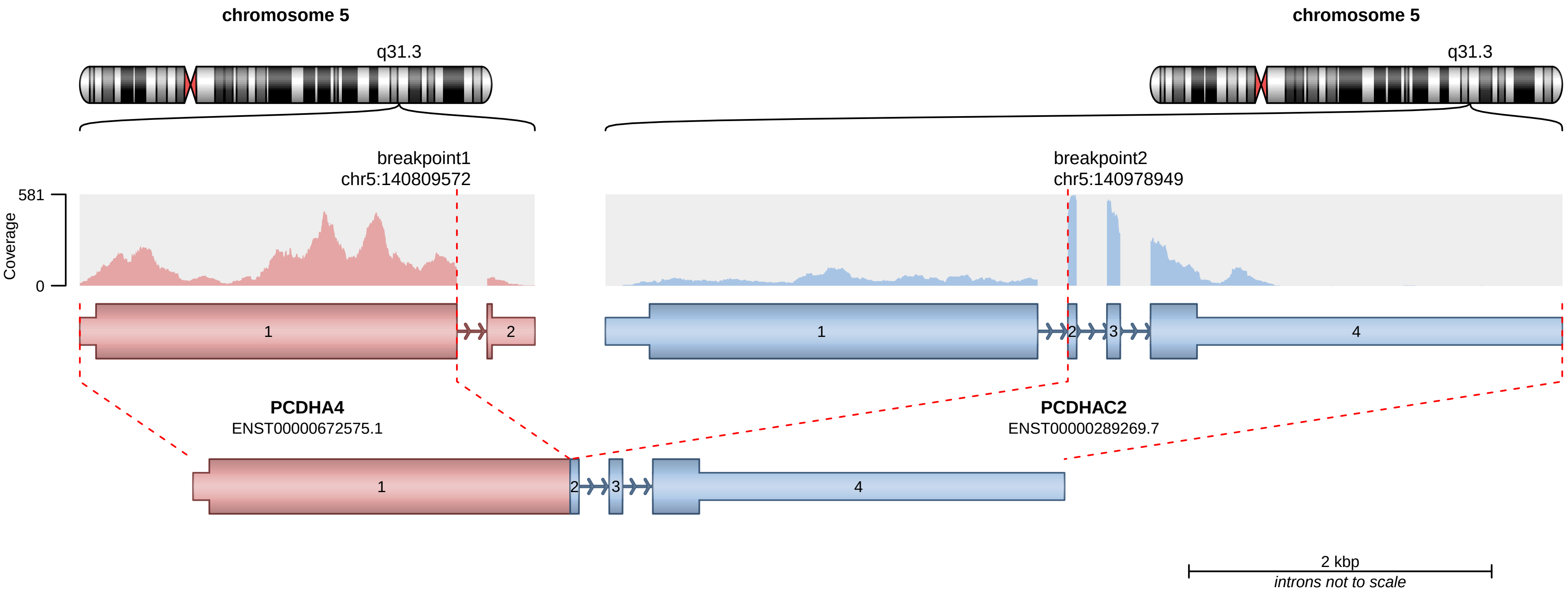


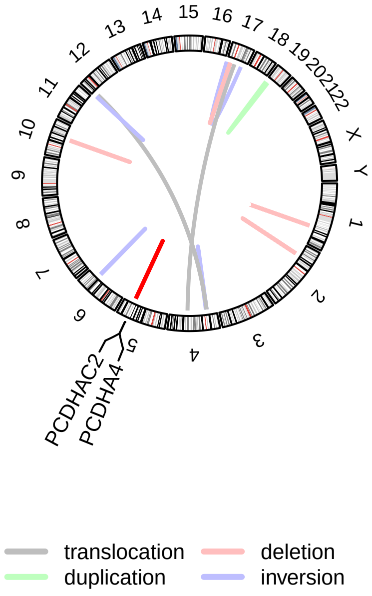




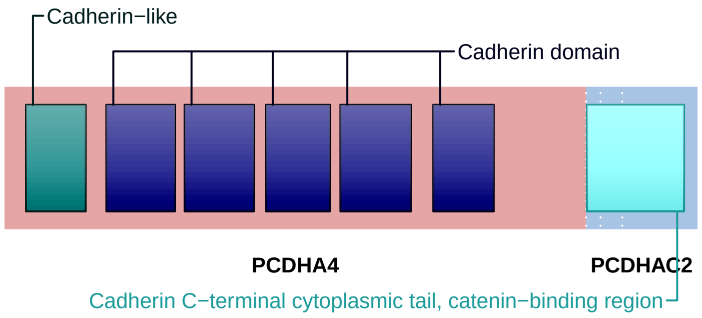
SUPPORTING READ COUNT

Split reads = 27
Discordant mates = 0



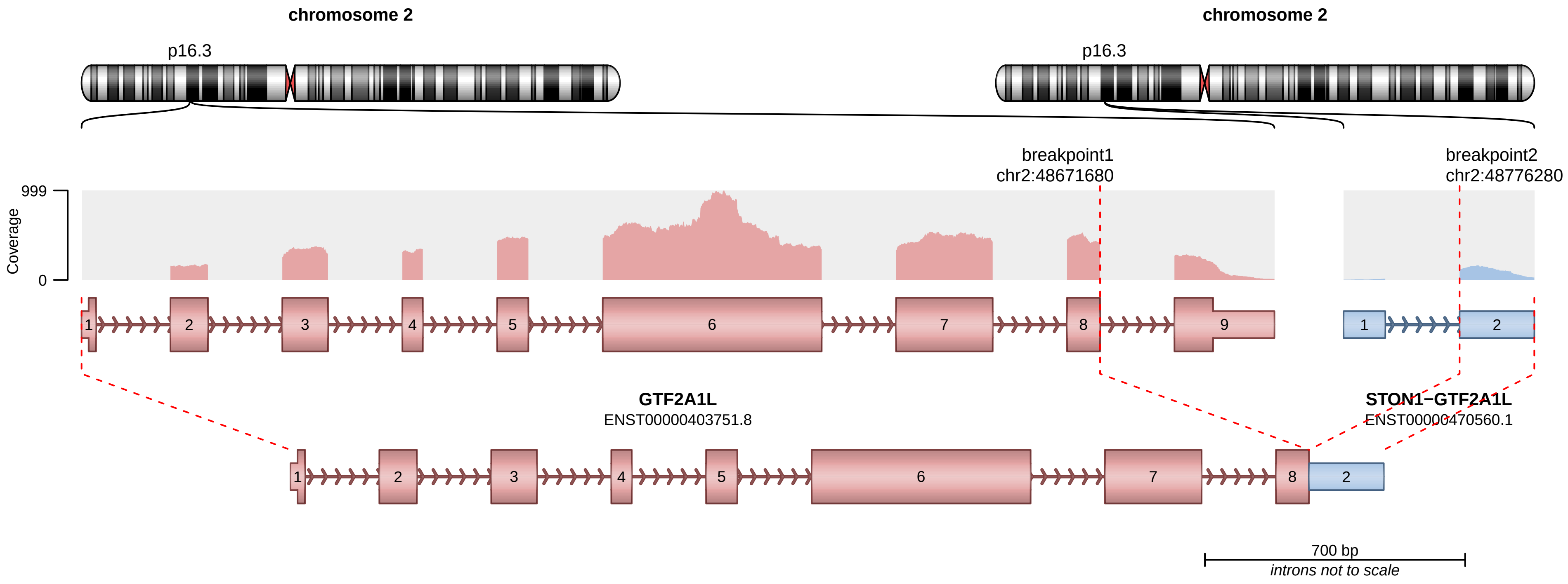


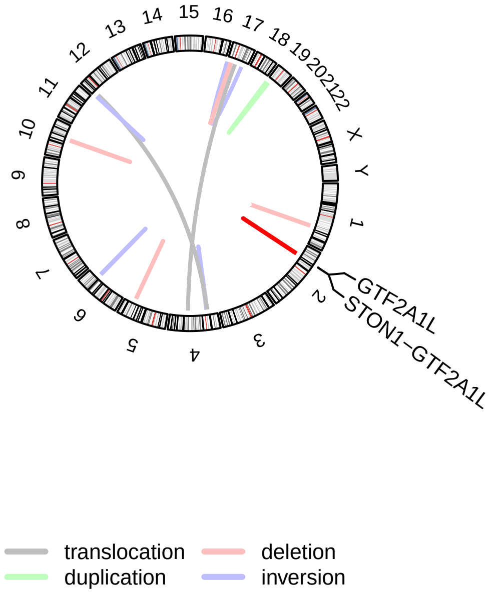
RETAINED PROTEIN DOMAINS
reading frame unclear



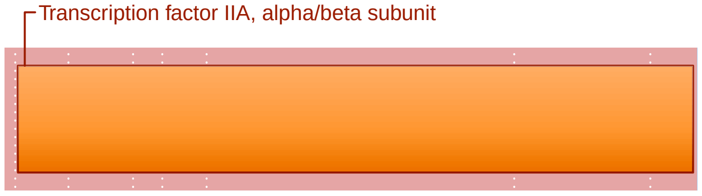
SUPPORTING READ COUNT

Split reads = 27
Discordant mates = 0





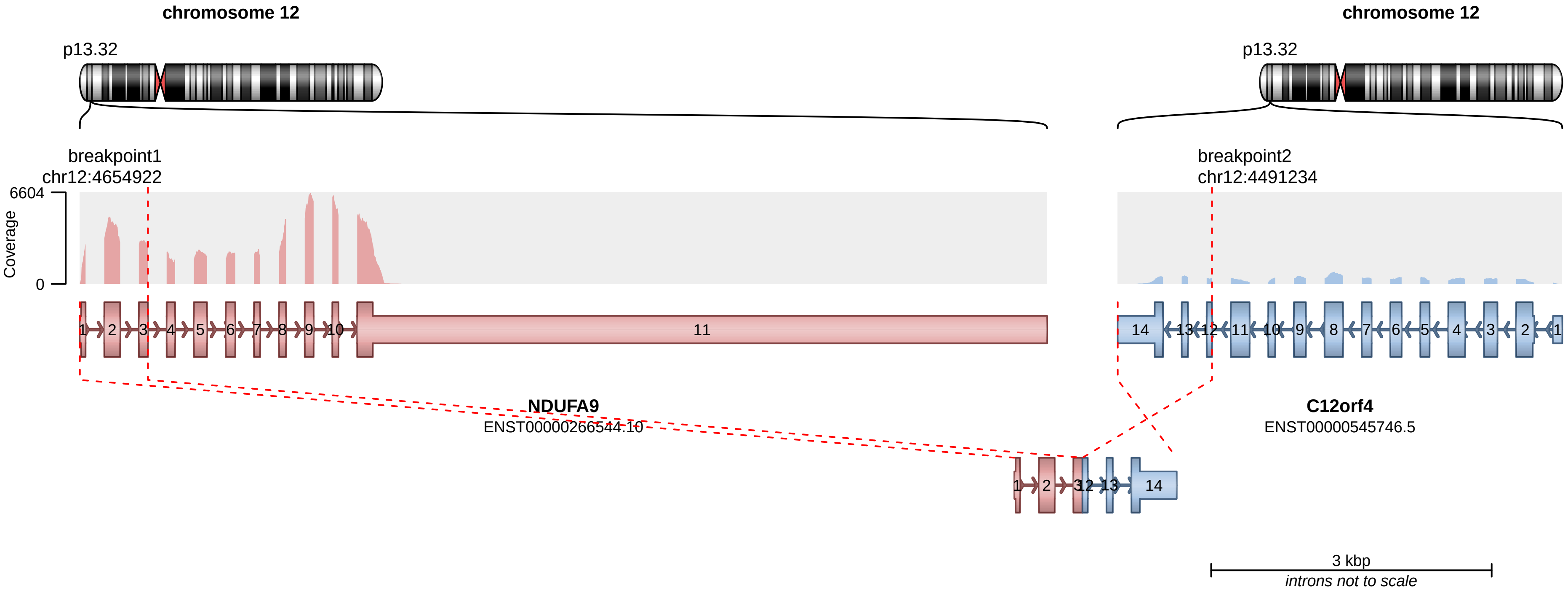
RETAINED PROTEIN DOMAINS
reading frame unclear

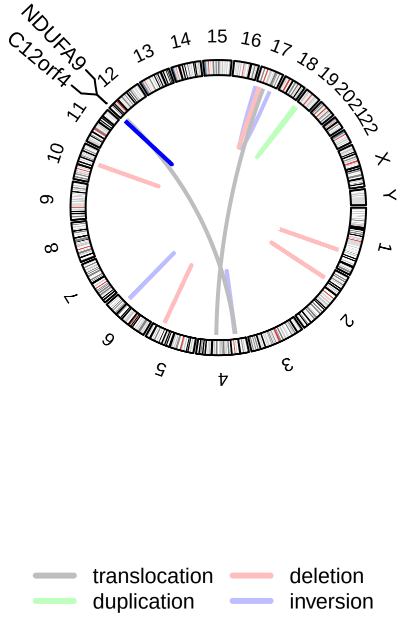


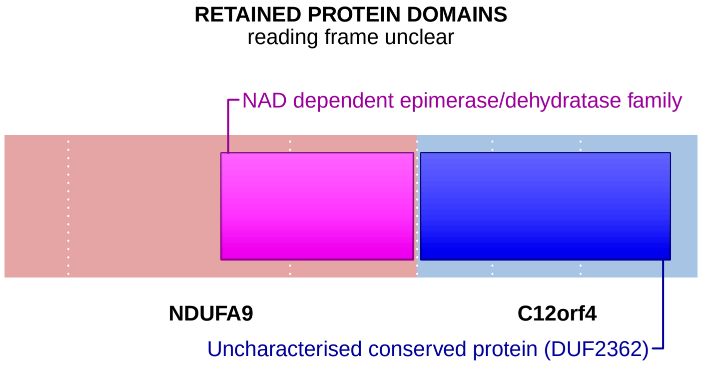
GTF2A1L

SUPPORTING READ COUNT

Split reads = 26
Discordant mates = 0

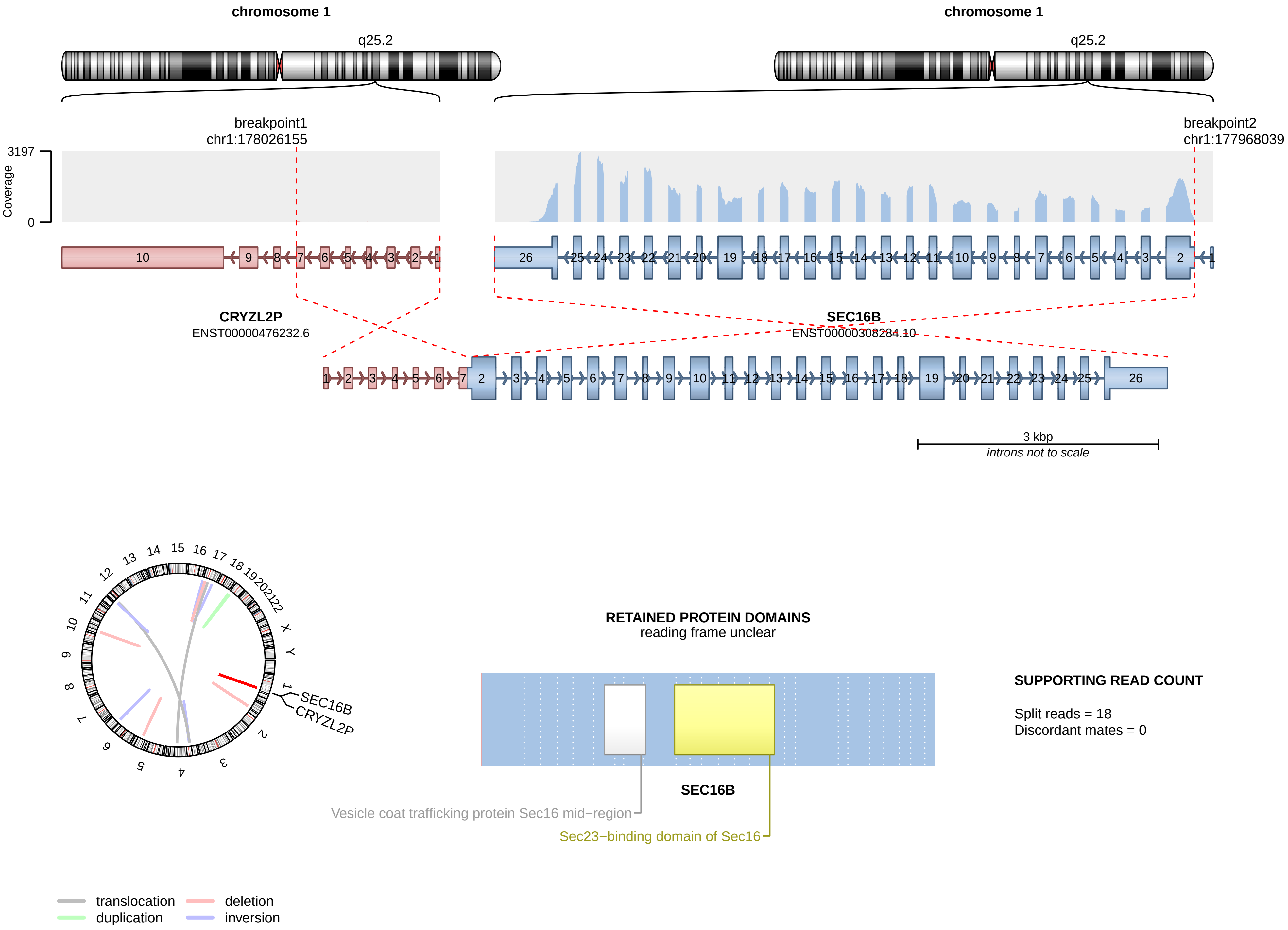


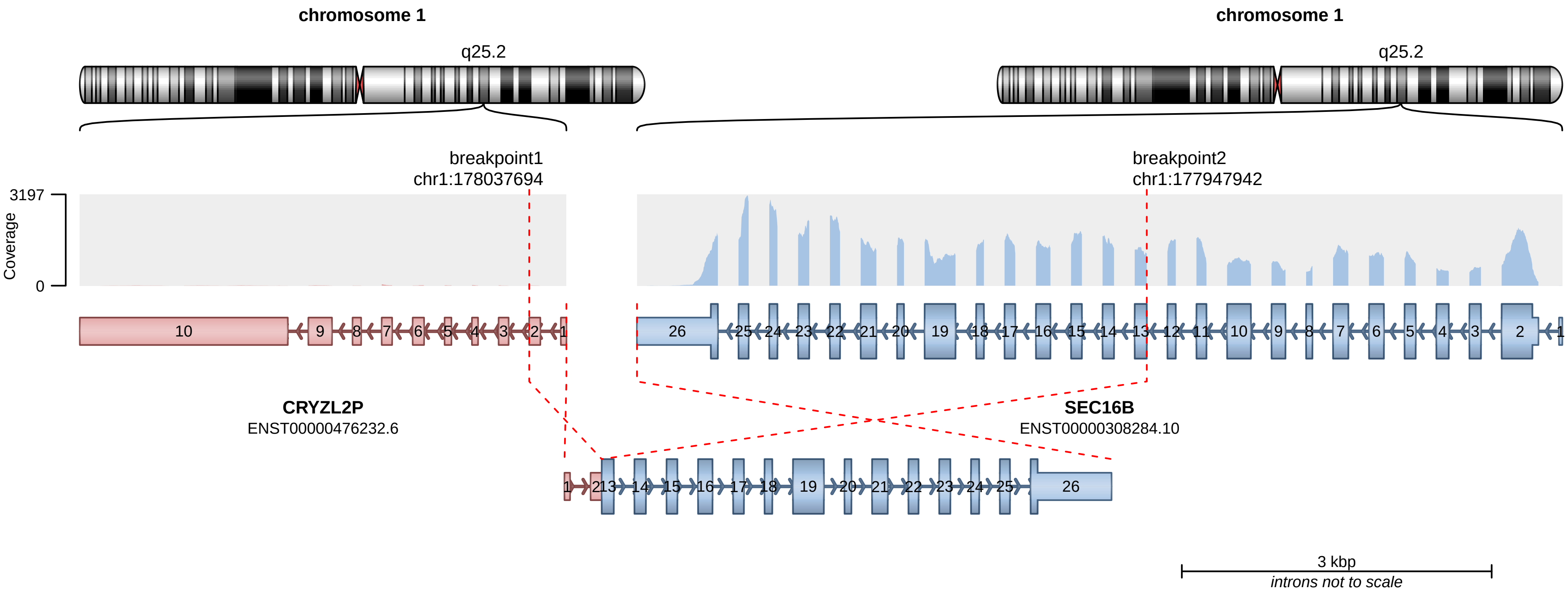


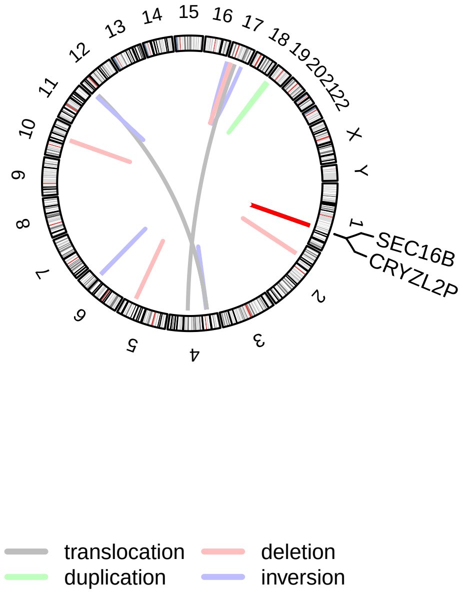


SUPPORTING READ COUNT

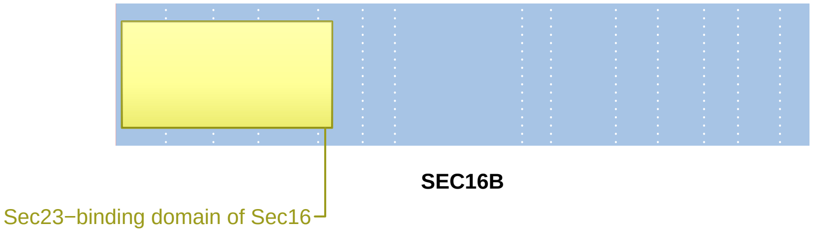
Split reads = 22
Discordant mates = 0


chromosome 1
q25.2
chromosome 1
q25.2
breakpoint1
chr1:178026155
breakpoint2
chr1:177968039
3197
Coverage
0
10
9
8
7
6
5
4
3
2
1
CRYZL2P
ENST00000476232.6
26
25
24
23
22
21
20
19
18
17
16
15
14
13
12
11
10
9
8
7
6
5
4
3
2
1
SEC16B
ENST00000308284.10
1
2
3
4
5
6
7
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
3 kbp
introns not to scale
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
X
Y
SEC16B
CRYZL2P
RETAINED PROTEIN DOMAINS
reading frame unclear
SEC16B
Vesicle coat trafficking protein Sec16 mid−region
Sec23−binding domain of Sec16
SUPPORTING READ COUNT
Split reads = 18
Discordant mates = 0
translocation
duplication
deletion
inversion



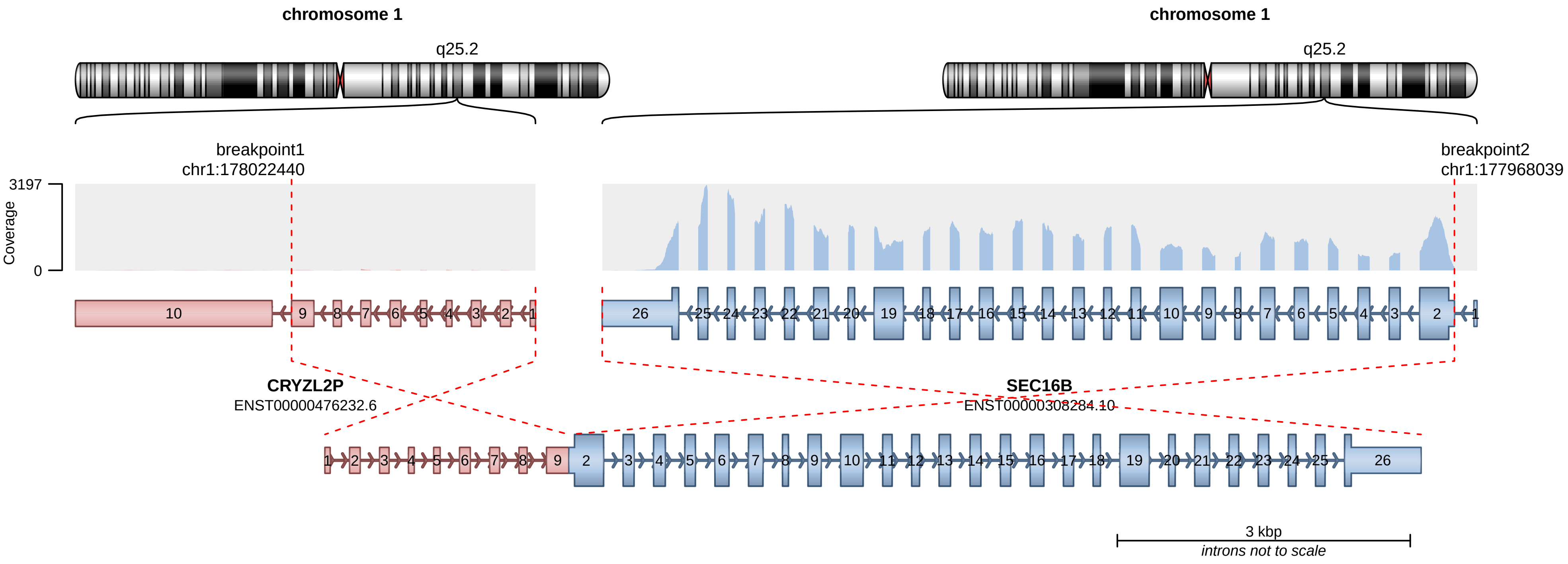


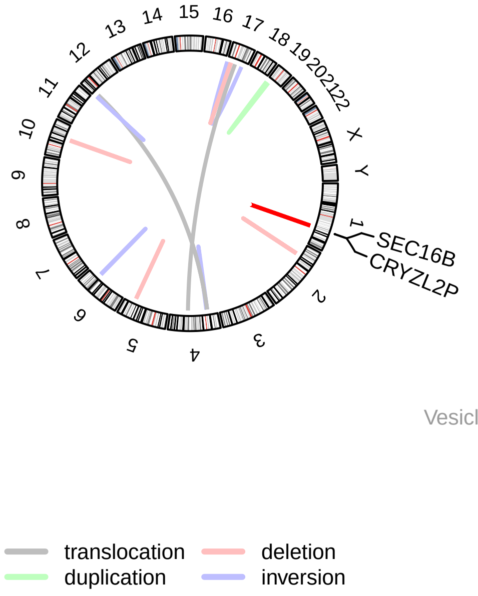
RETAINED PROTEIN DOMAINS
reading frame unclear



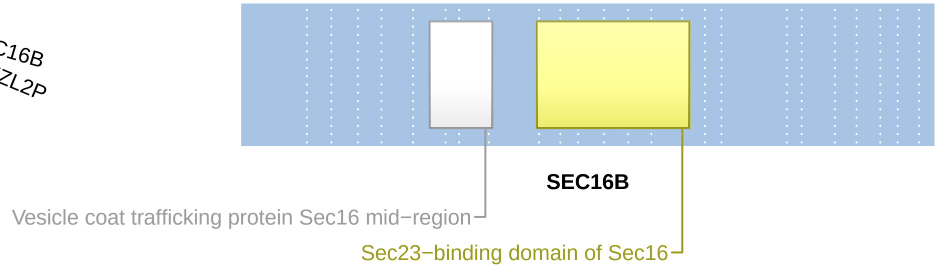
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0





RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0