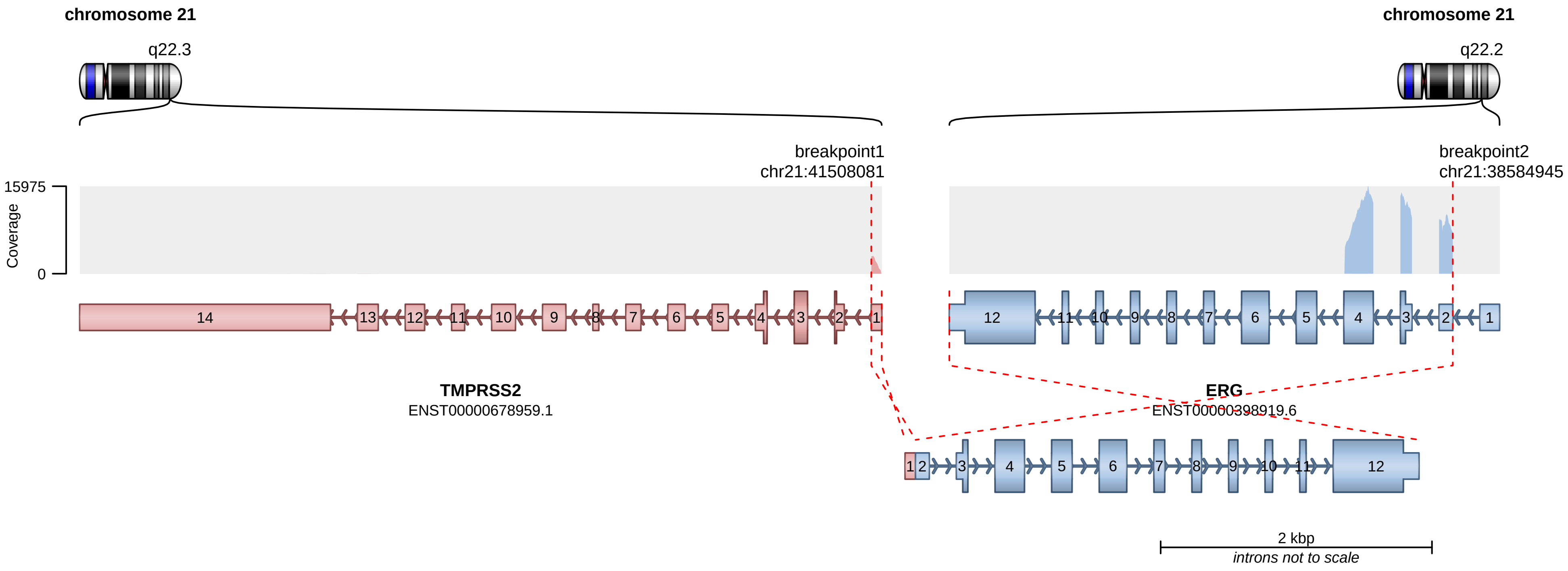
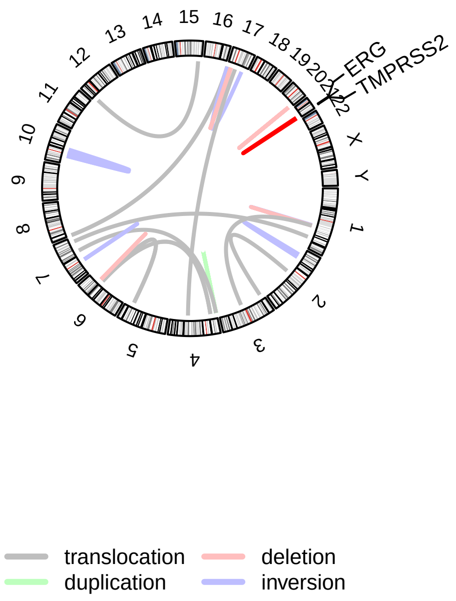
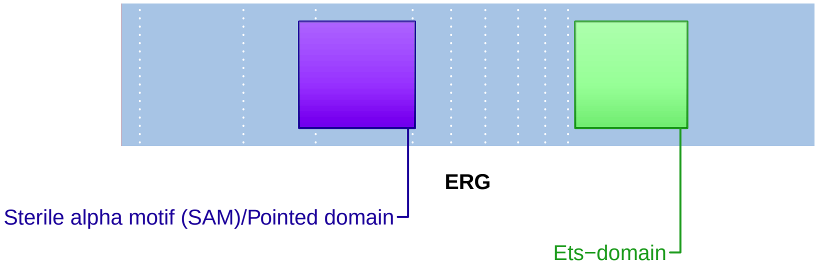


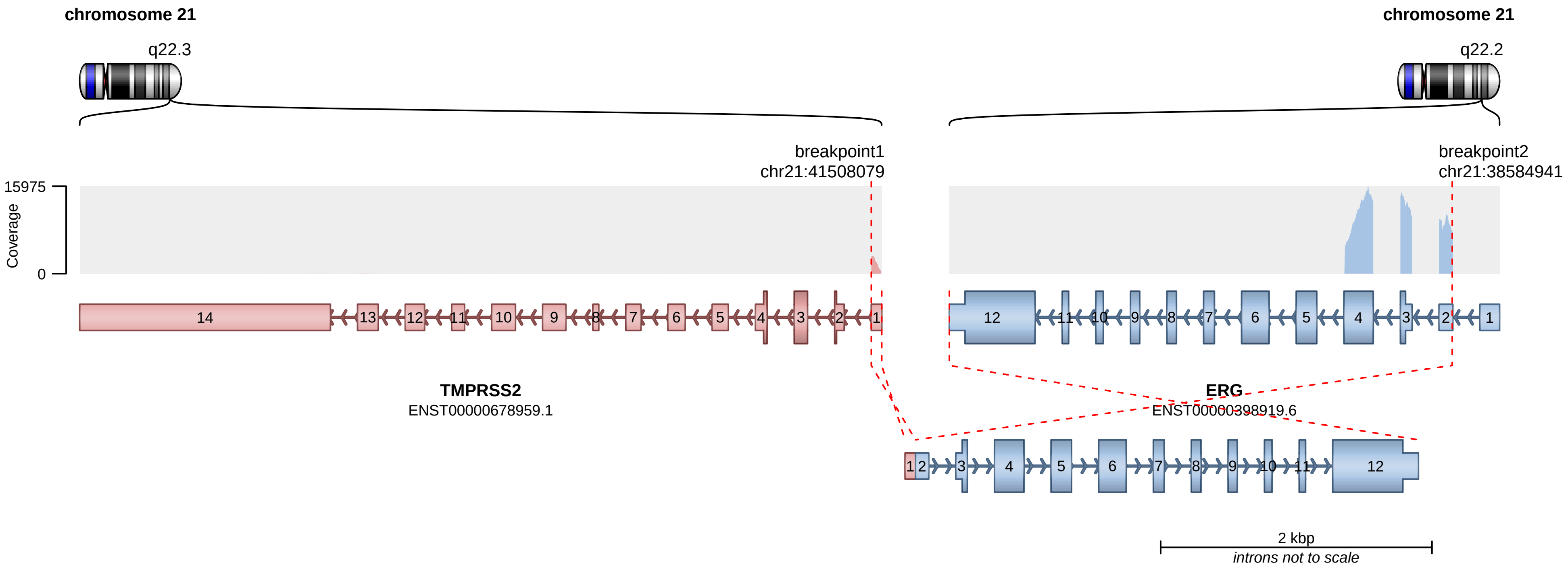


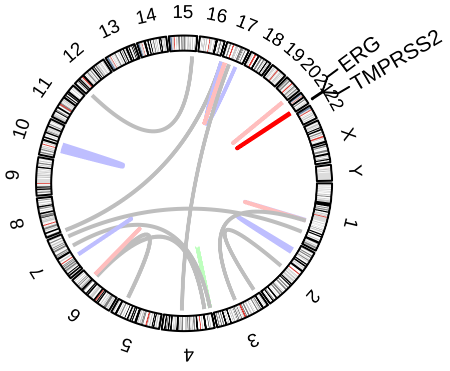
**RETAINED PROTEIN DOMAINS**
reading frame unclear



**SUPPORTING READ COUNT**

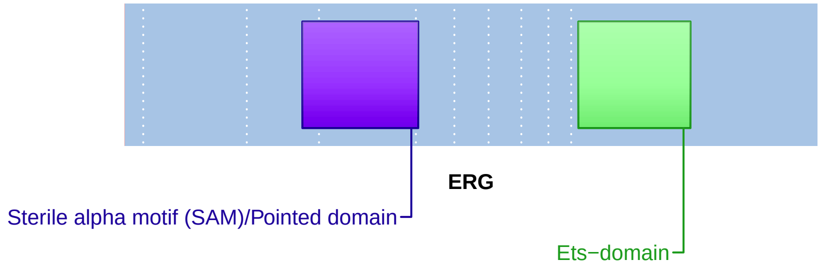
Split reads = 2941
Discordant mates = 0





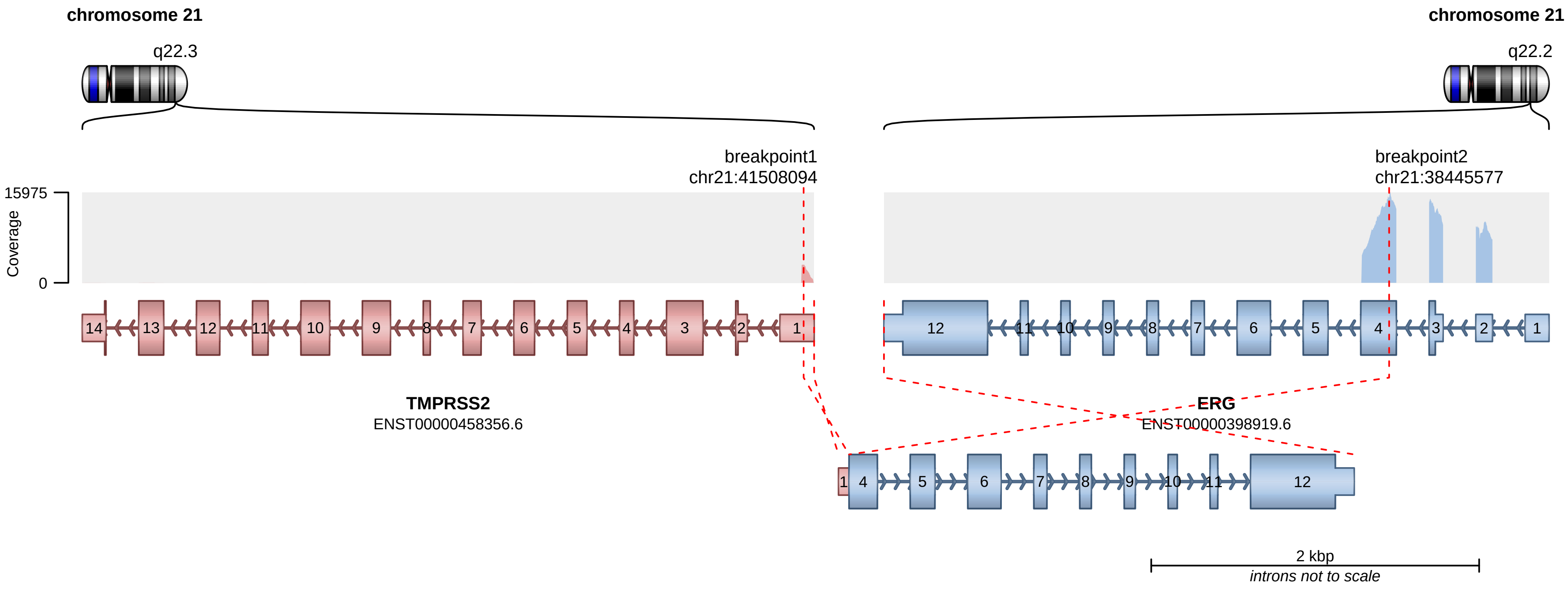
▬ translocation ▬ deletion
▬ duplication ▬ inversion

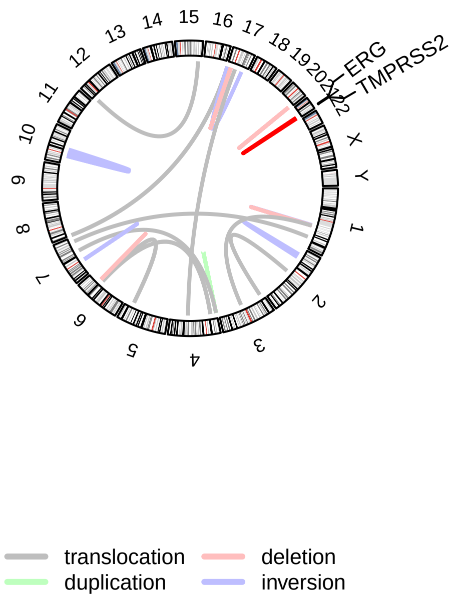
## RETAINED PROTEIN DOMAINS
reading frame unclear

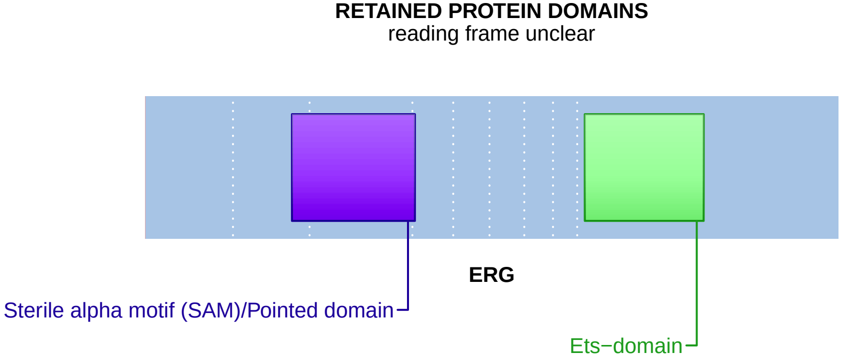


**SUPPORTING READ COUNT**

Split reads = 7
Discordant mates = 0

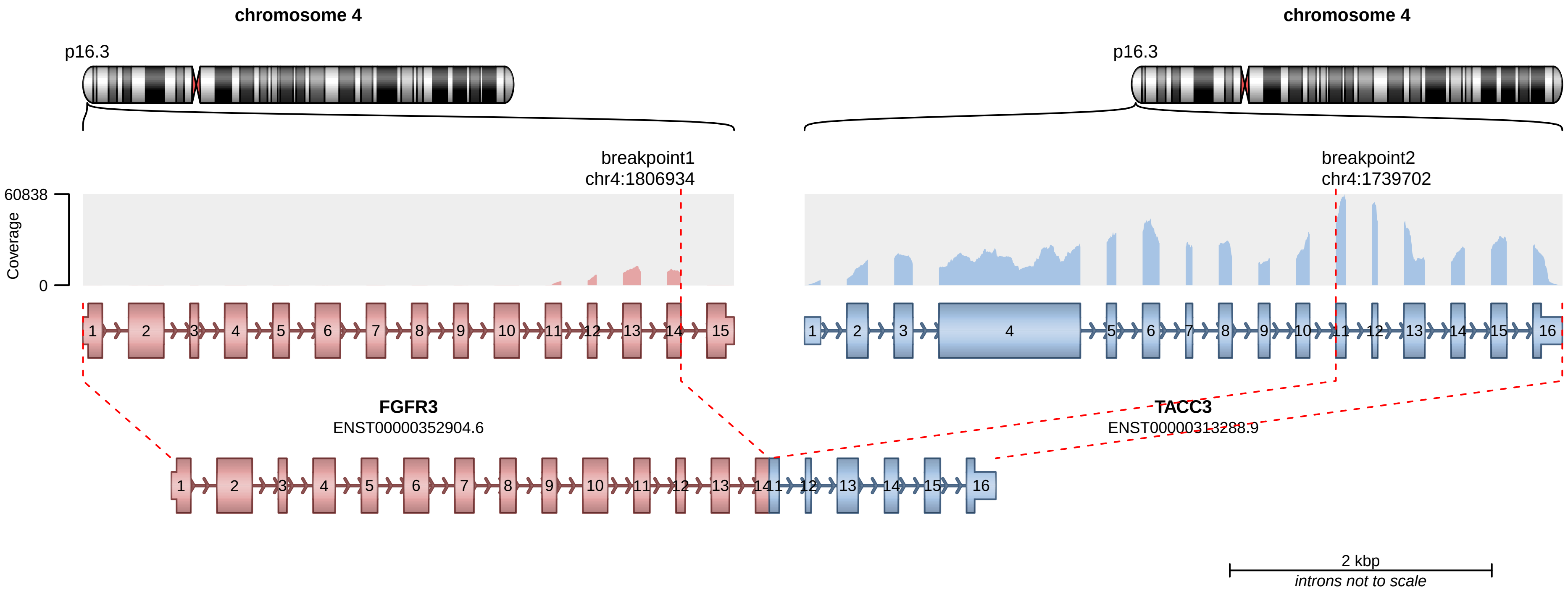


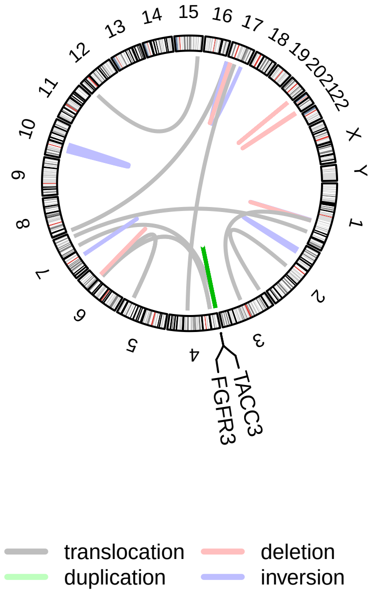


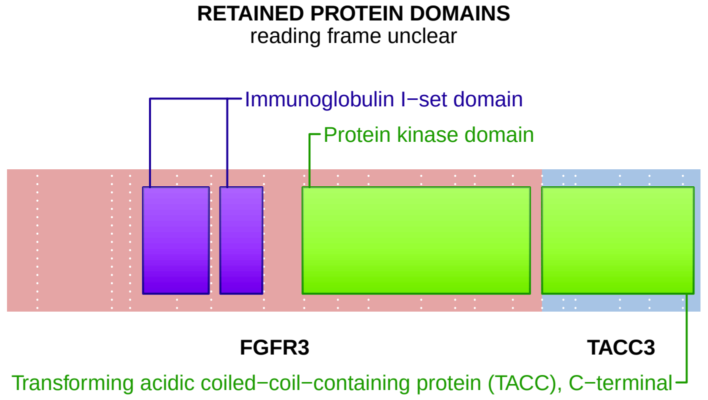


**SUPPORTING READ COUNT**

Split reads = 7
Discordant mates = 0

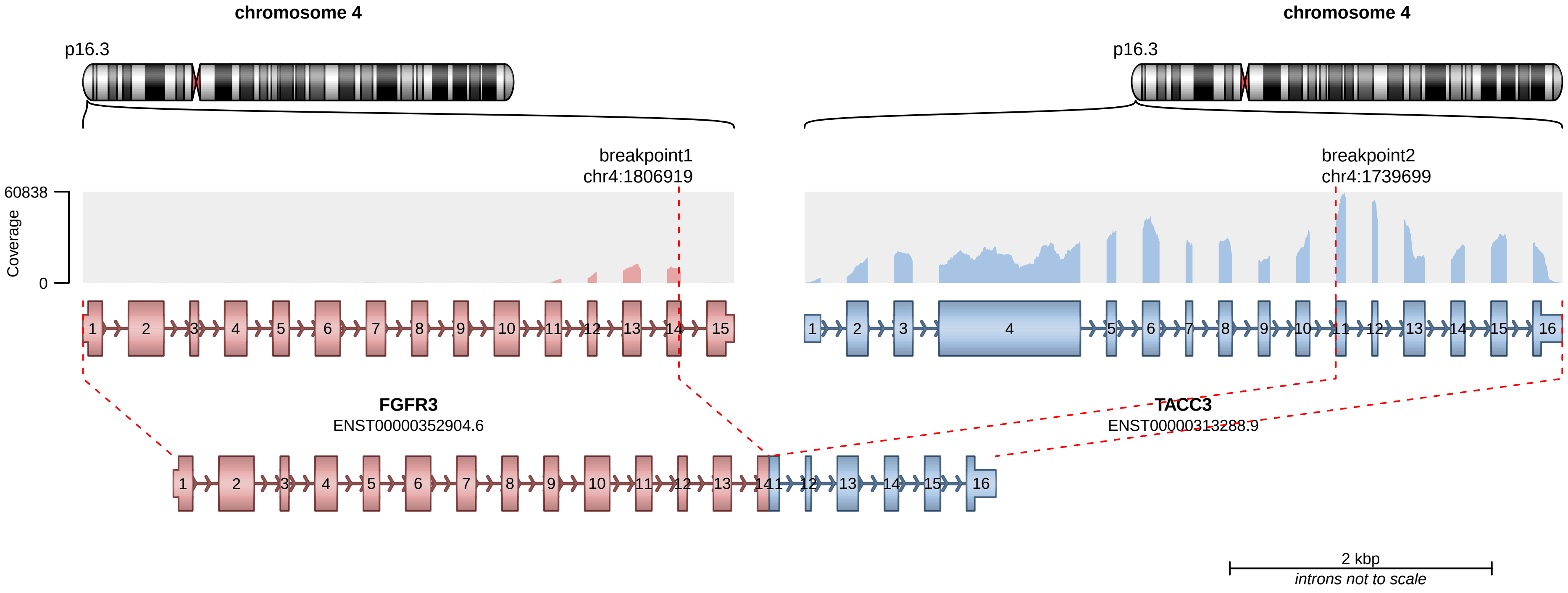


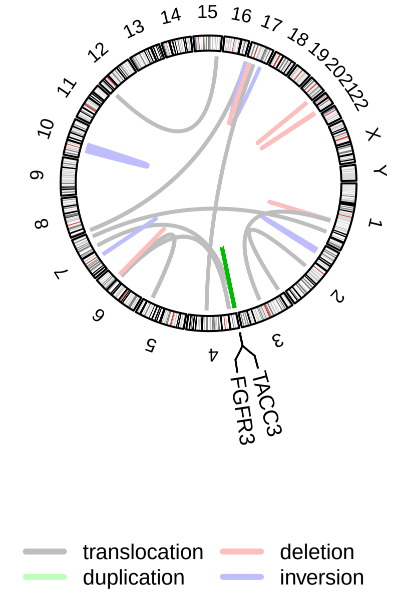


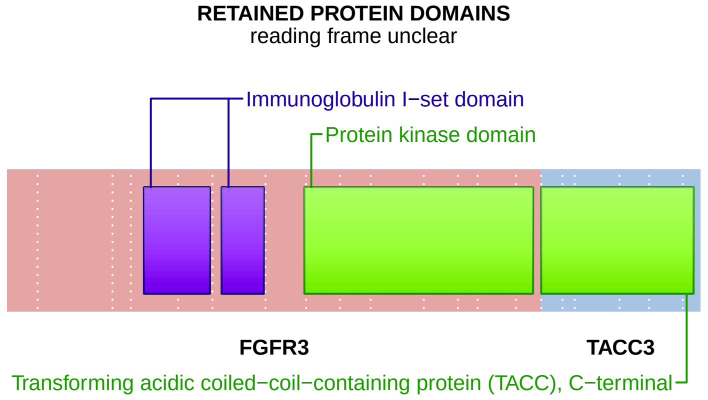


**SUPPORTING READ COUNT**

Split reads = 2765
Discordant mates = 3

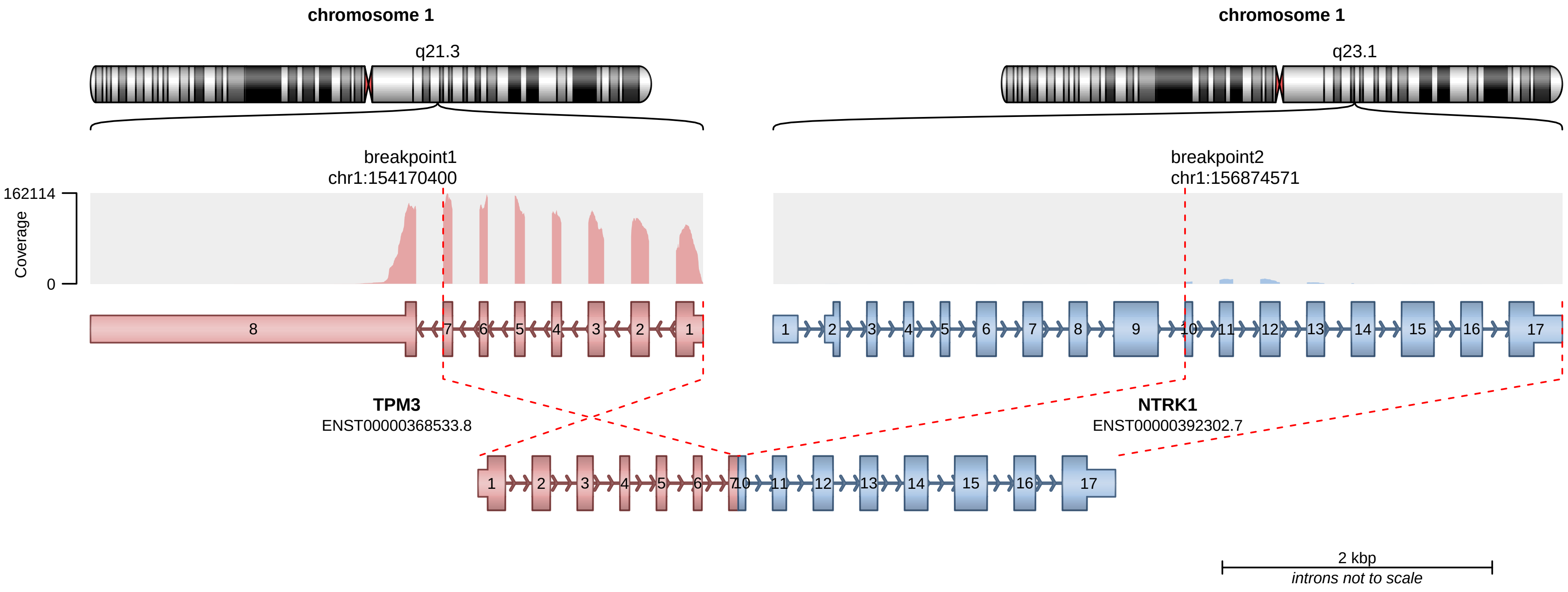


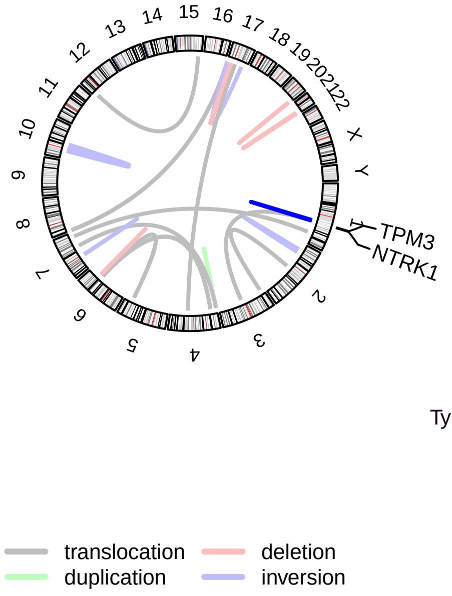


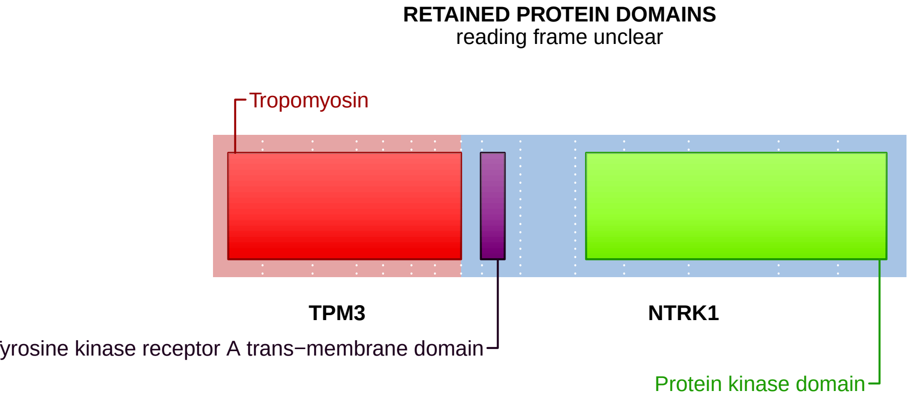


**SUPPORTING READ COUNT**

Split reads = 8
Discordant mates = 3

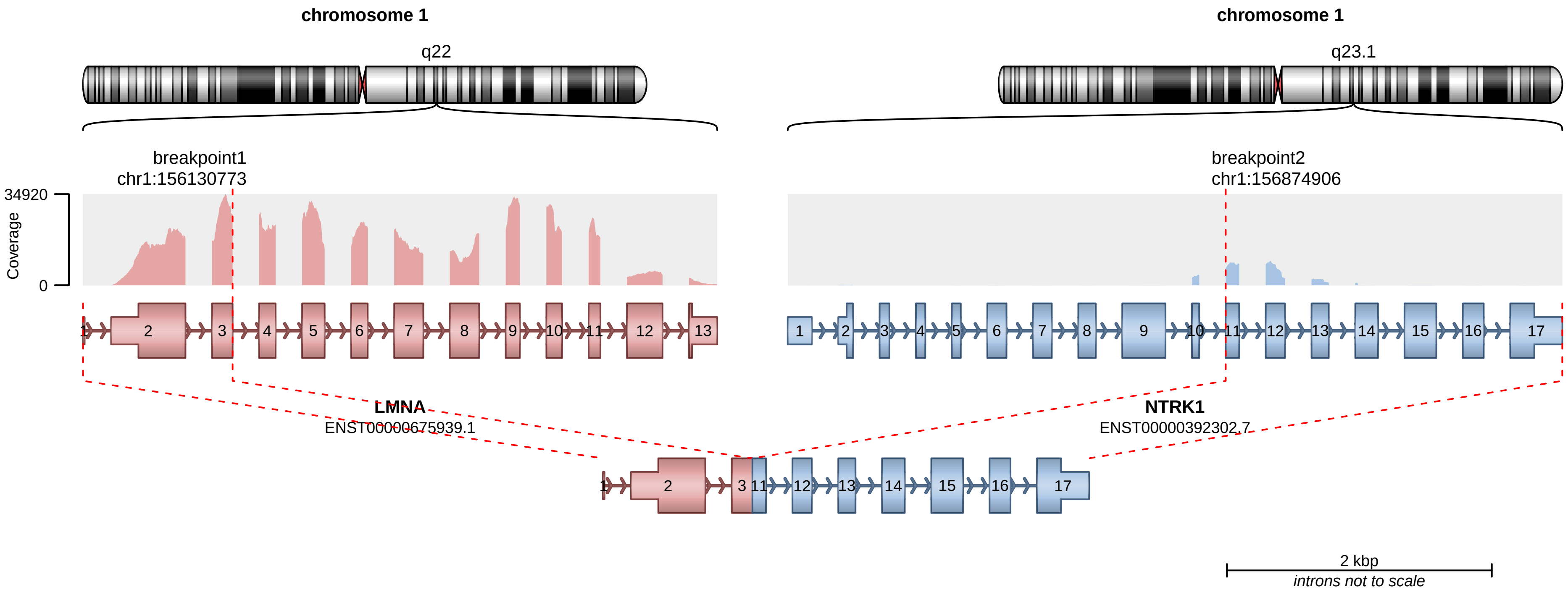


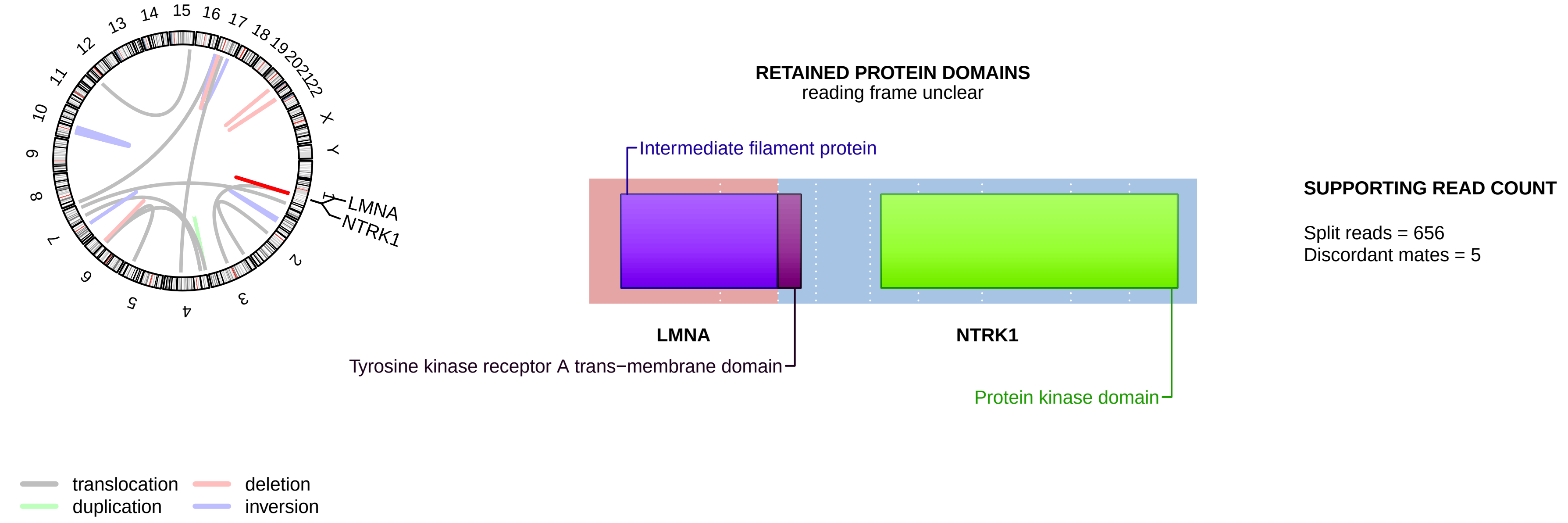


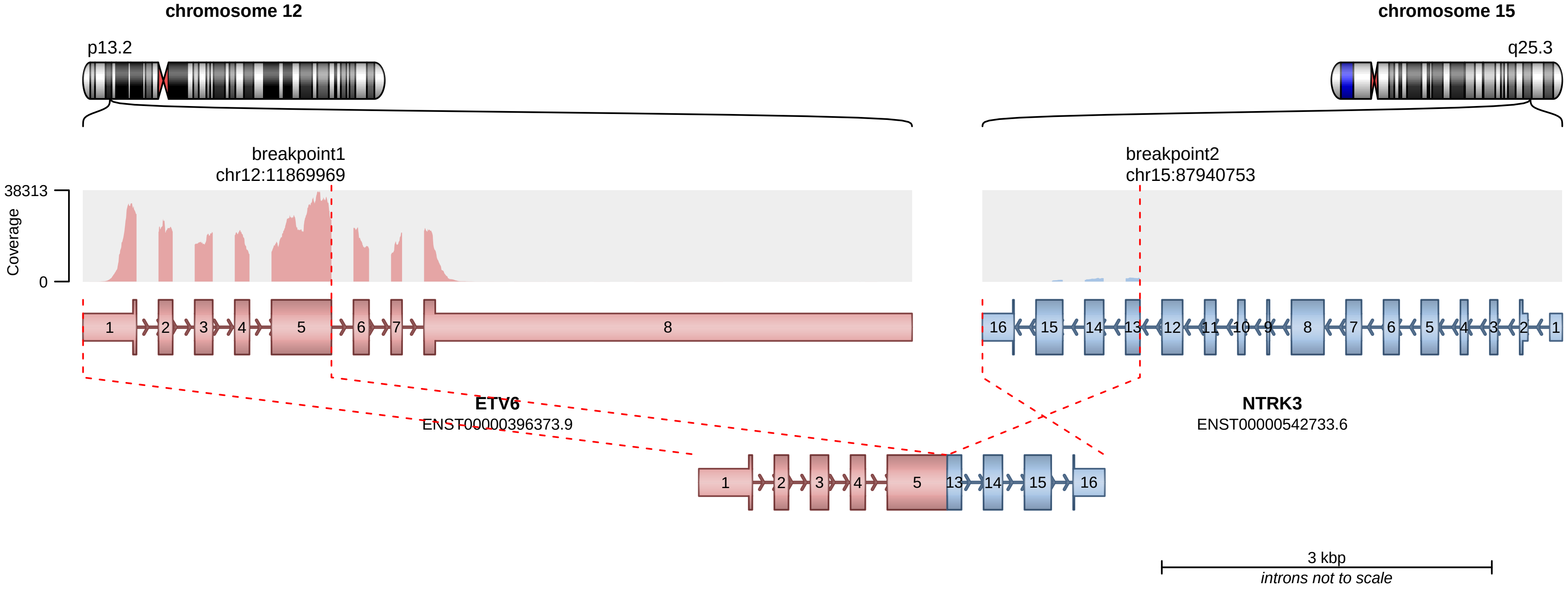


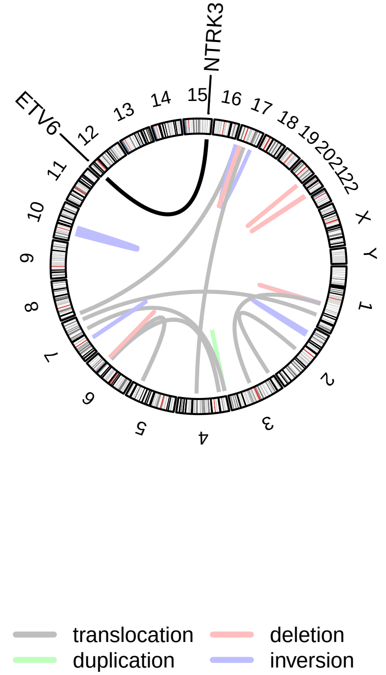
**SUPPORTING READ COUNT**

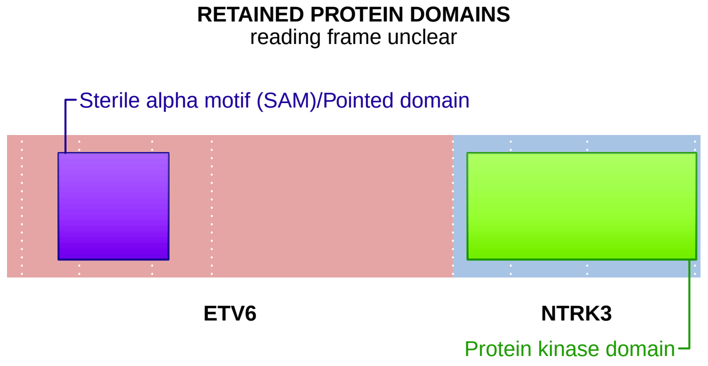
Split reads = 720
Discordant mates = 4


chromosome 1
q22
chromosome 1
q23.1
breakpoint1
chr1:156130773
breakpoint2
chr1:156874906
34920
Coverage
0
1
2
3
4
5
6
7
8
9
10
11
12
13
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
LMNA
ENST00000675939.1
NTRK1
ENST00000392302.7
1
2
3
11
12
13
14
15
16
17
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
LMNA
NTRK1
translocation
deletion
duplication
inversion
RETAINED PROTEIN DOMAINS
reading frame unclear
Intermediate filament protein
LMNA
NTRK1
Tyrosine kinase receptor A trans−membrane domain
Protein kinase domain
SUPPORTING READ COUNT
Split reads = 656
Discordant mates = 5

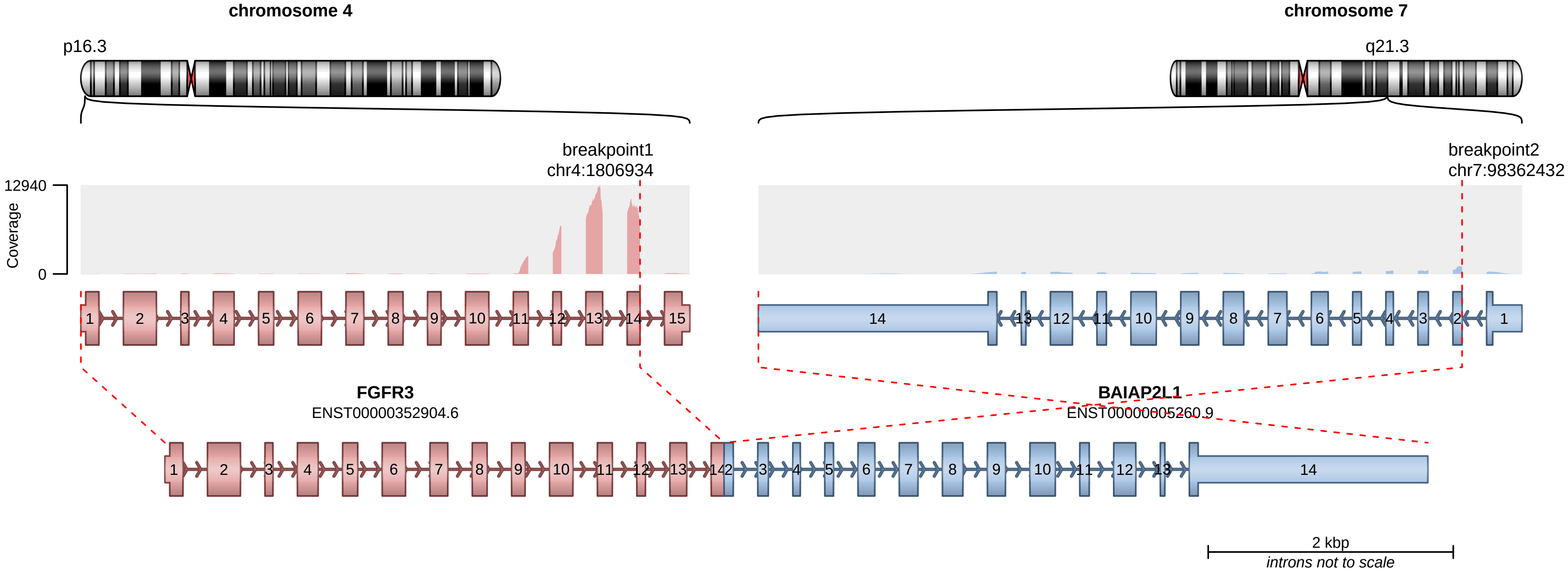


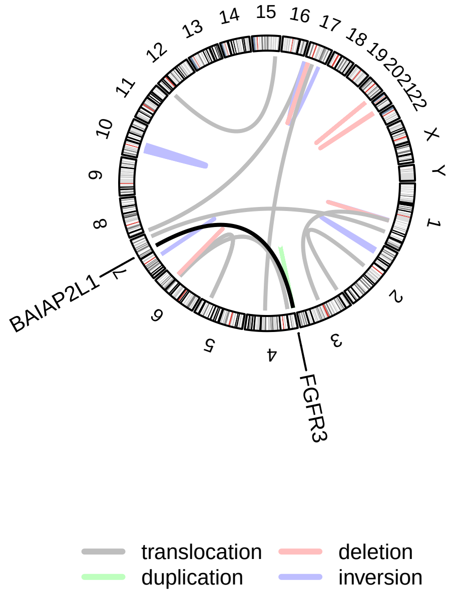


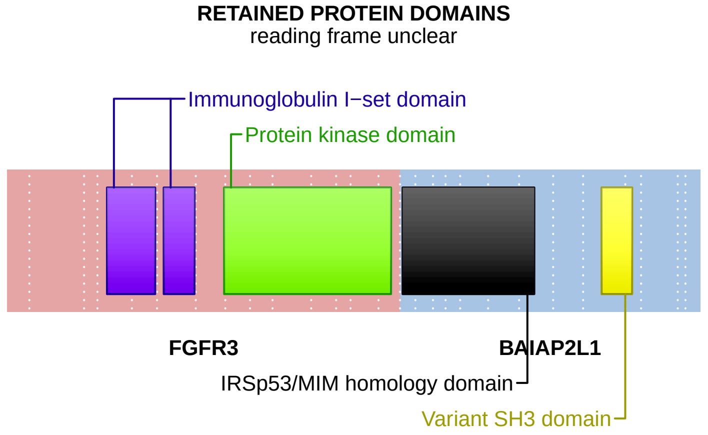


**SUPPORTING READ COUNT**

Split reads = 592
Discordant mates = 5

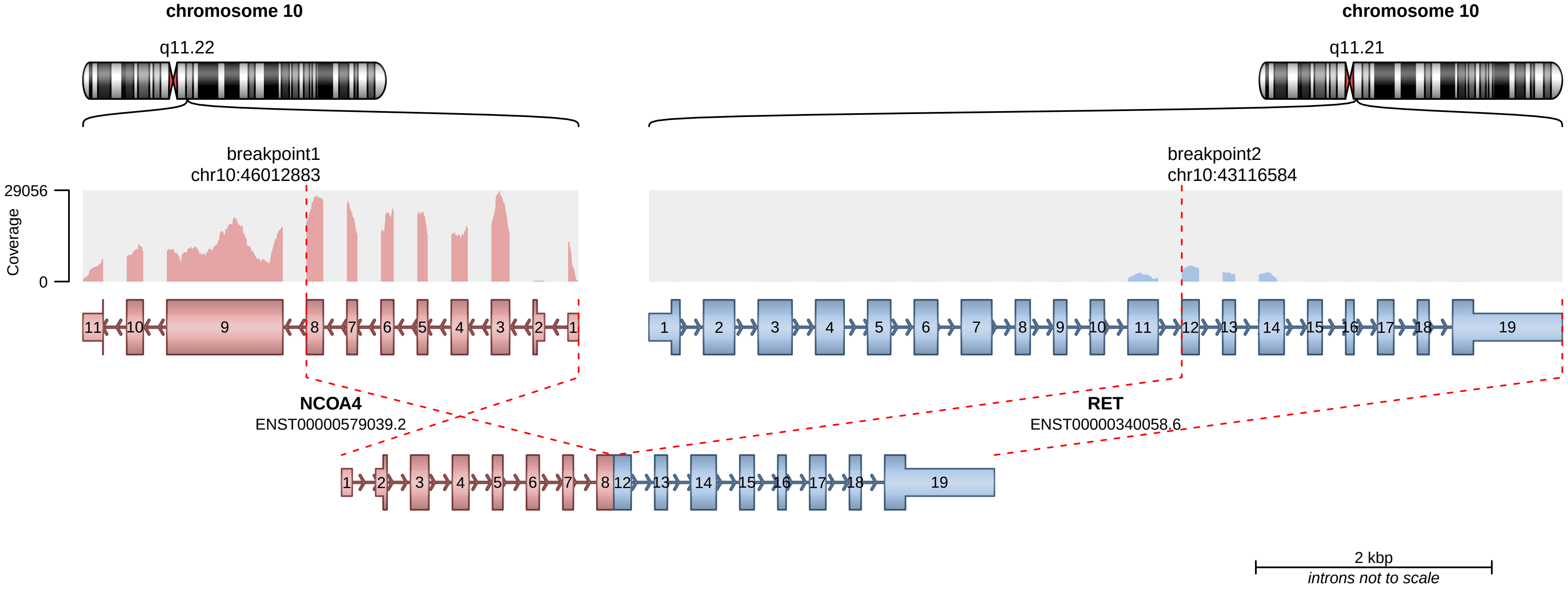


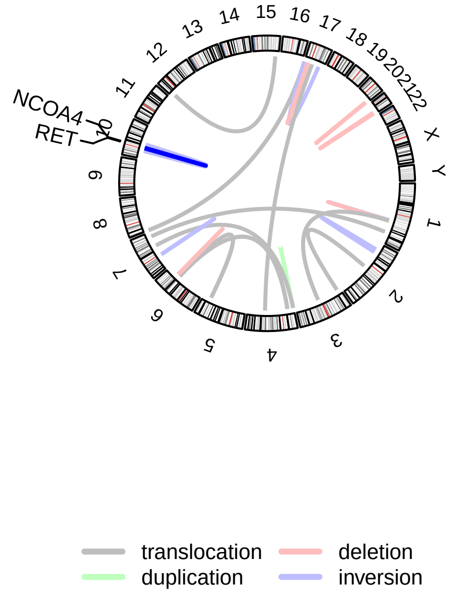




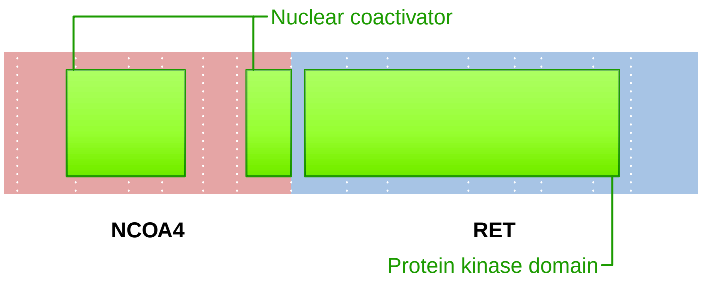
**SUPPORTING READ COUNT**

Split reads = 418
Discordant mates = 2



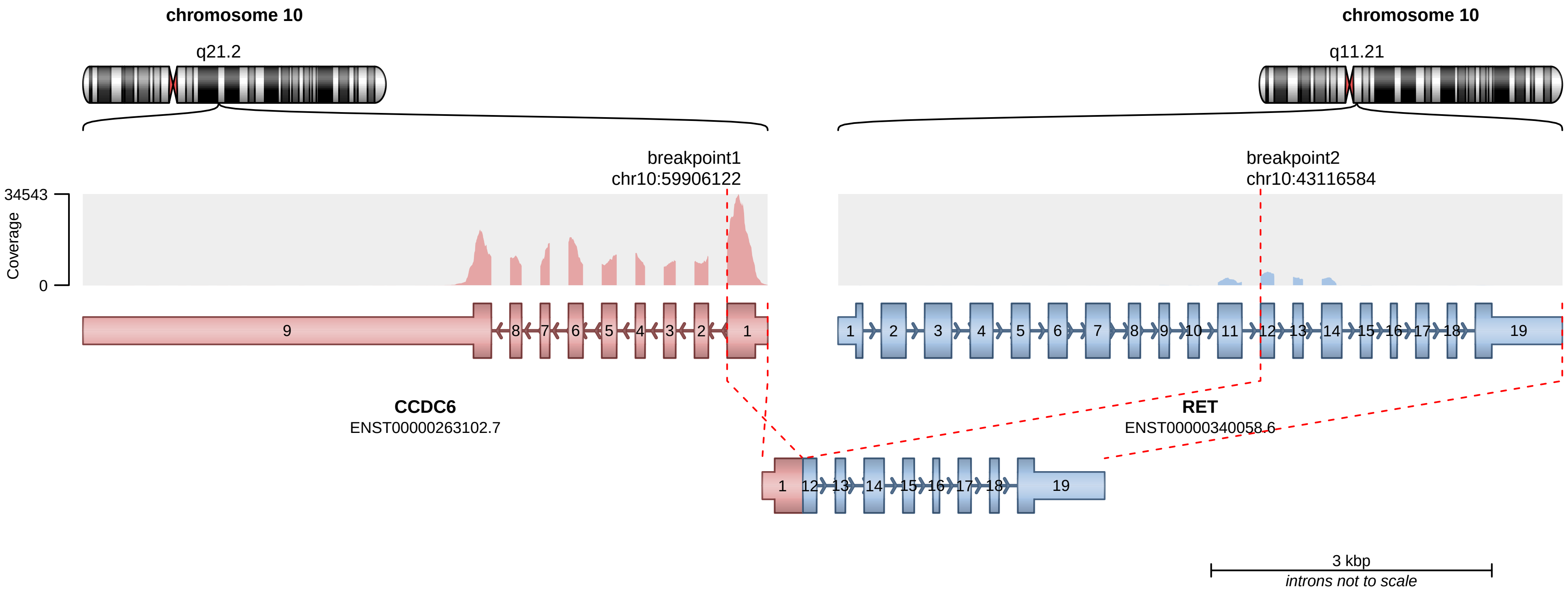


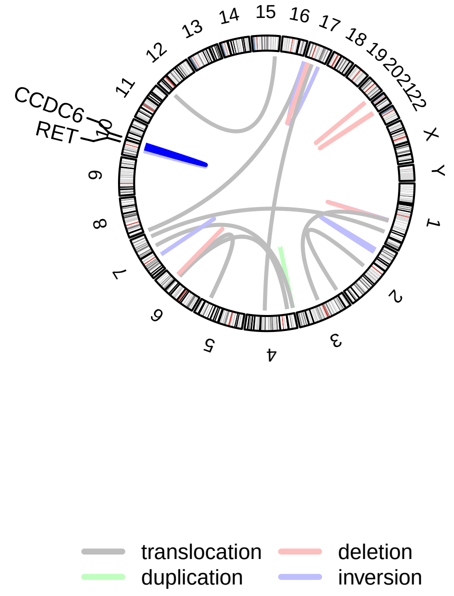
**RETAINED PROTEIN DOMAINS**
reading frame unclear

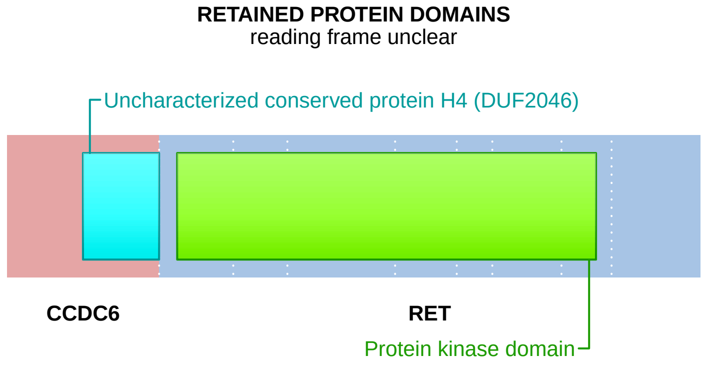


**SUPPORTING READ COUNT**

Split reads = 410
Discordant mates = 4

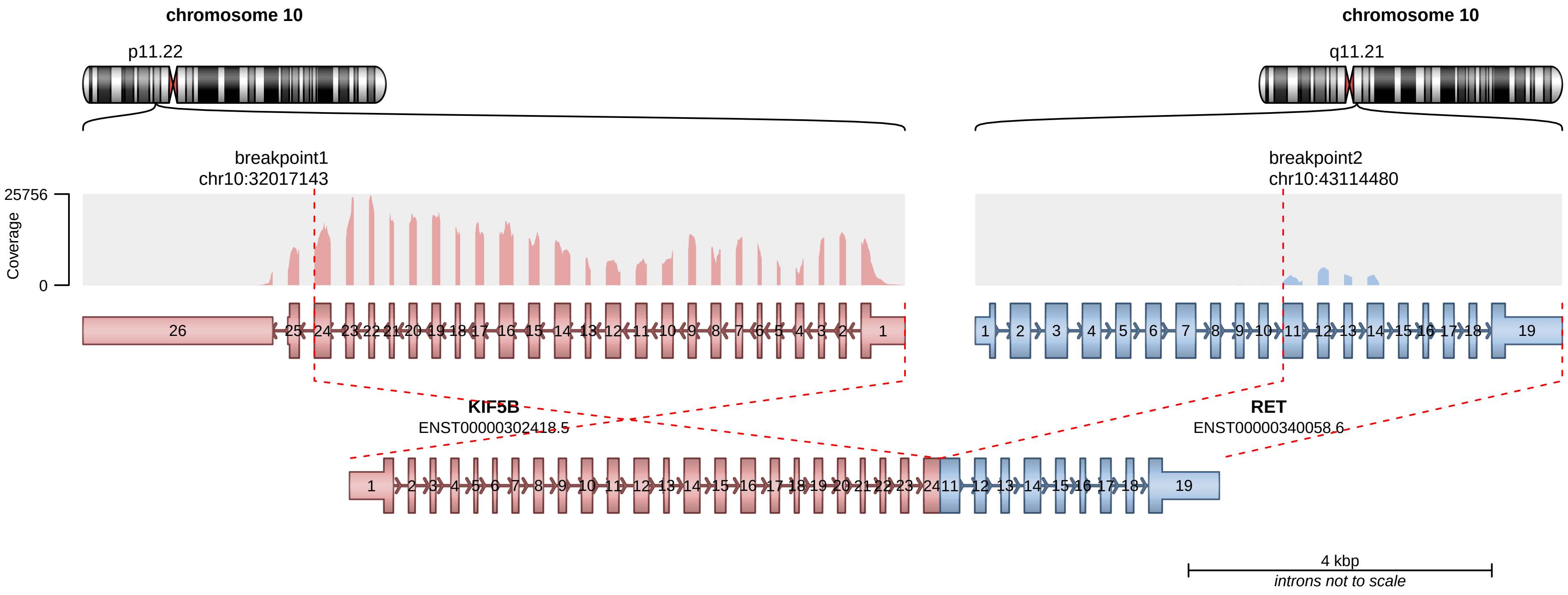


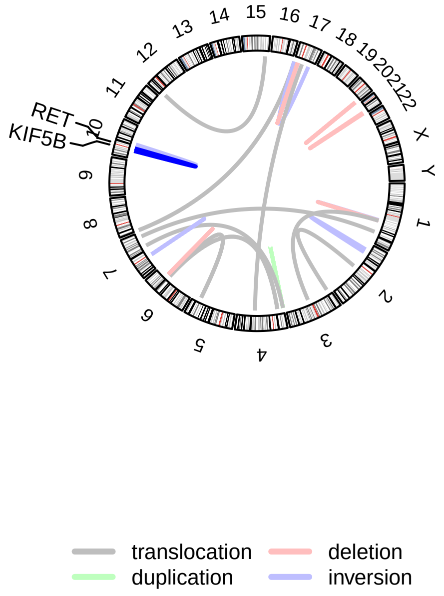




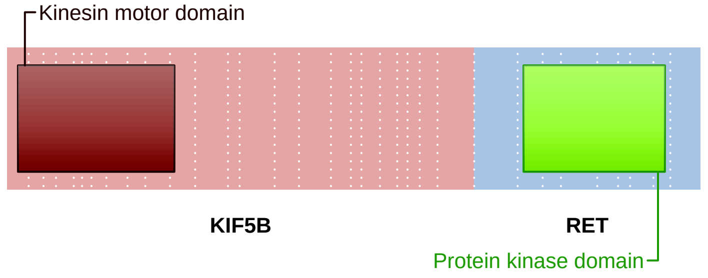
**SUPPORTING READ COUNT**

Split reads = 383
Discordant mates = 3



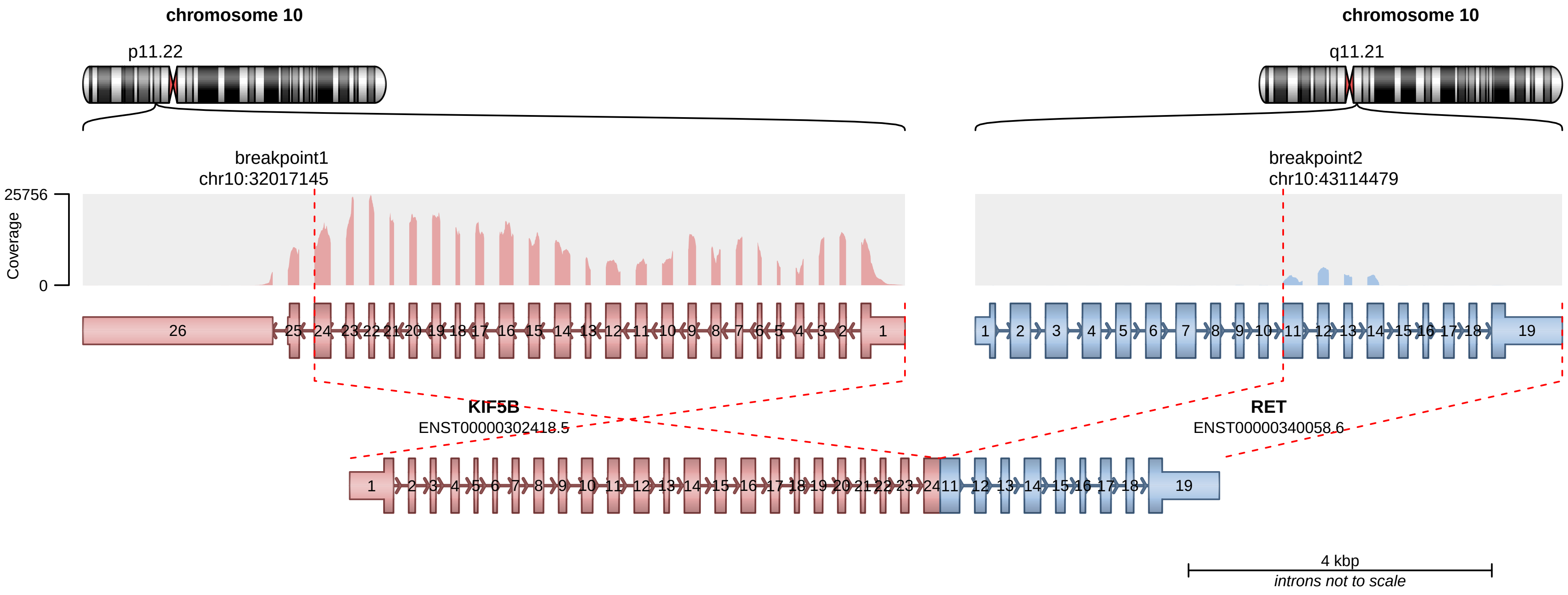


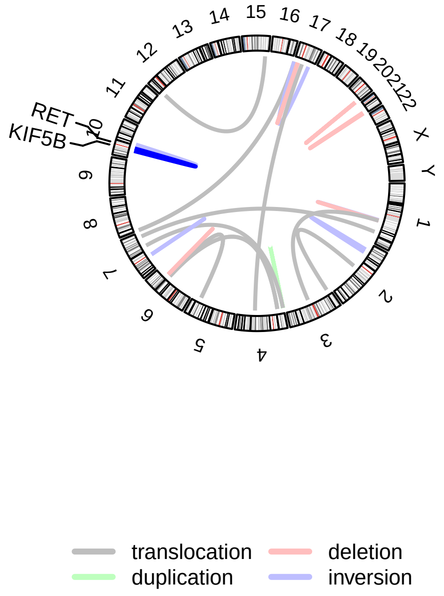
**RETAINED PROTEIN DOMAINS**
reading frame unclear

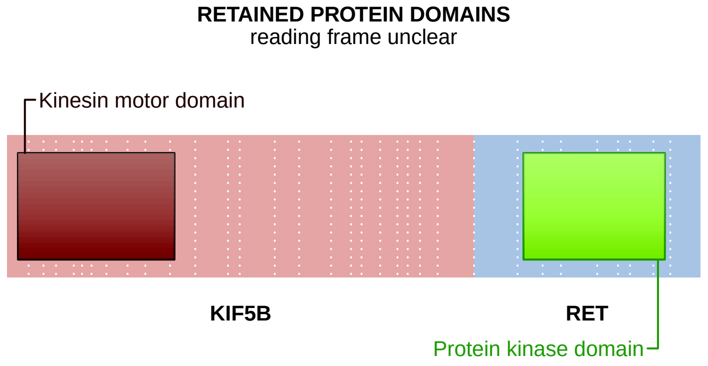


**SUPPORTING READ COUNT**

Split reads = 335
Discordant mates = 5

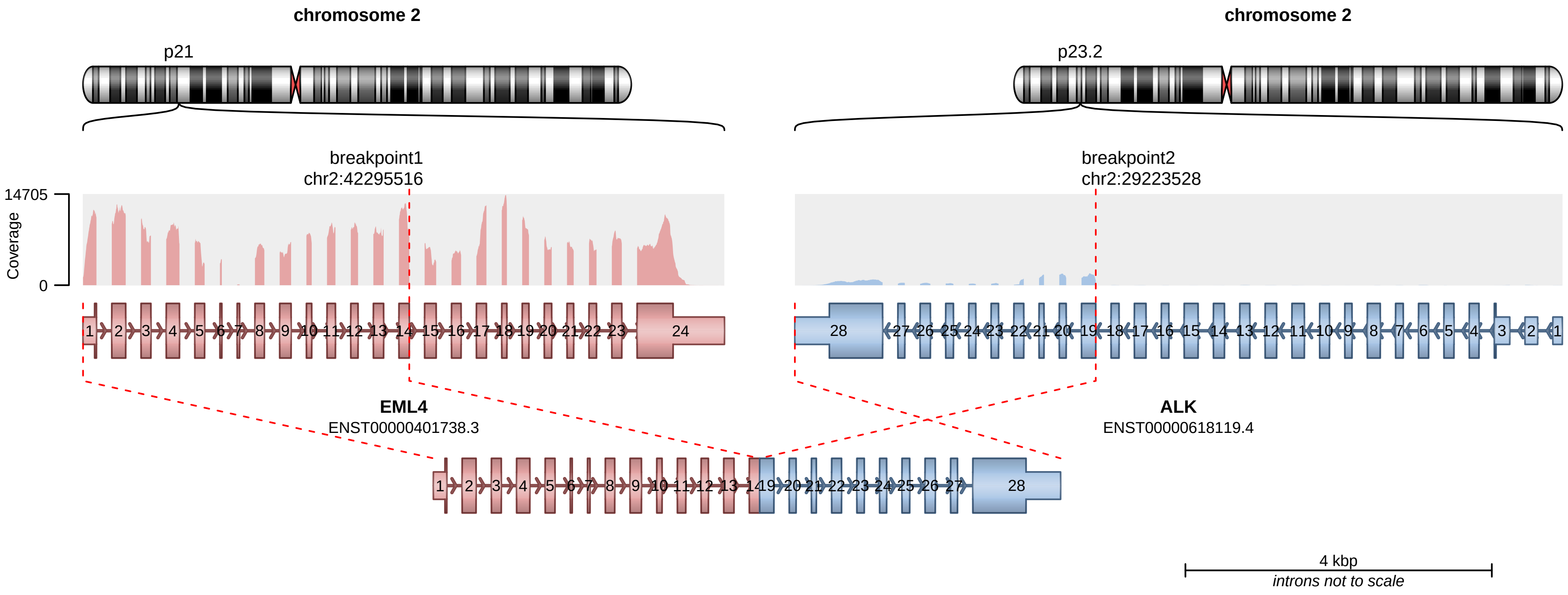


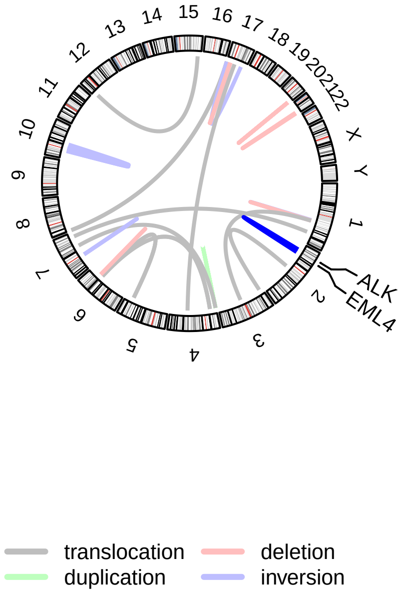


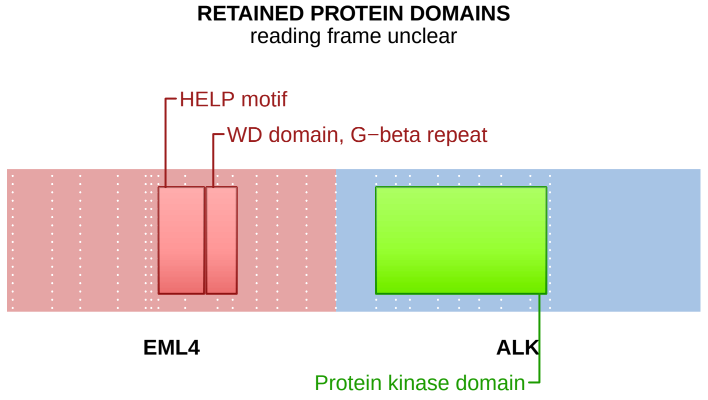


**SUPPORTING READ COUNT**

Split reads = 6
Discordant mates = 5

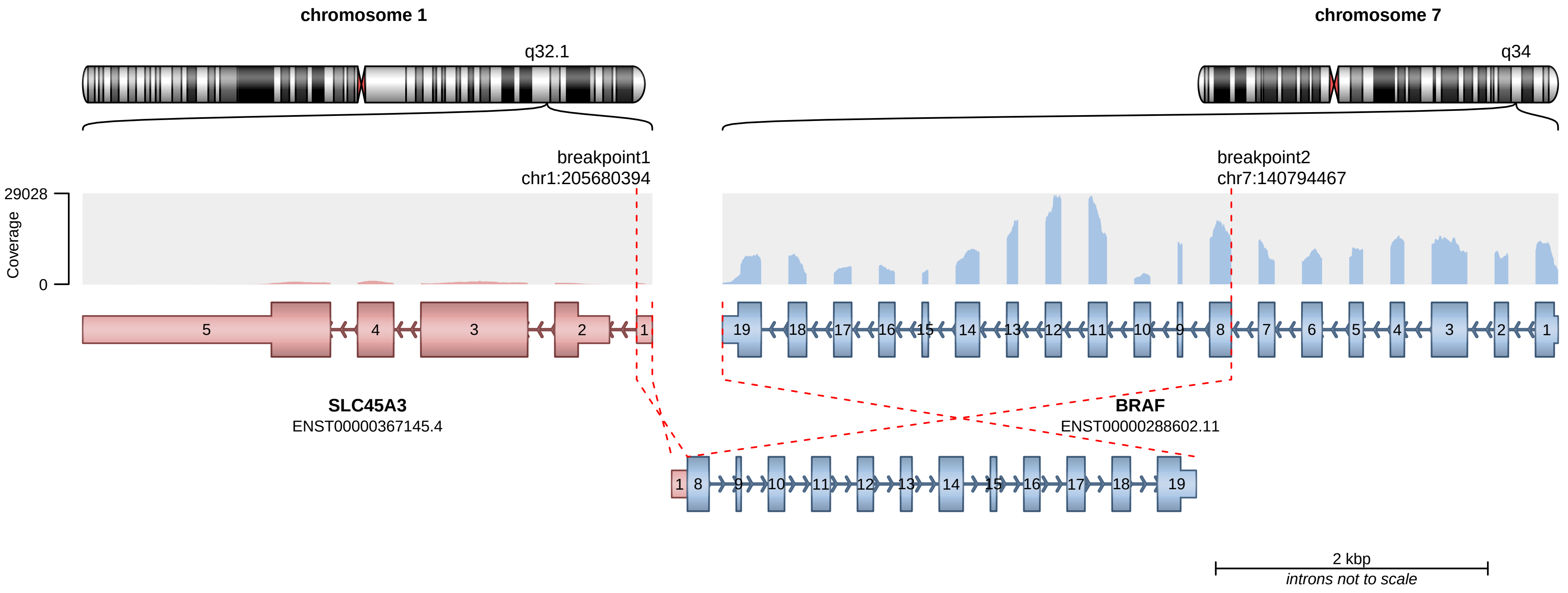


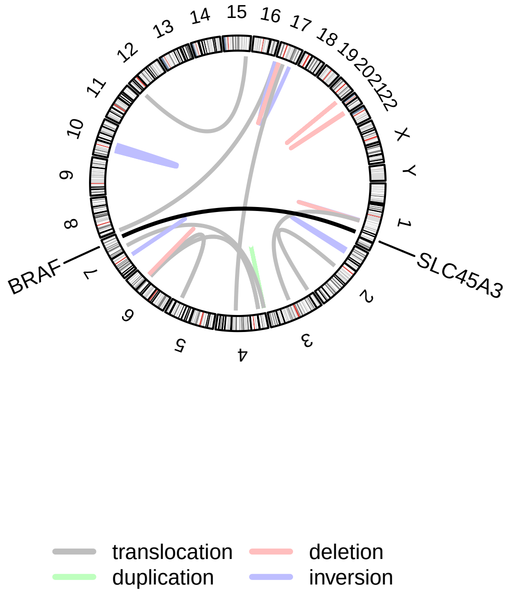


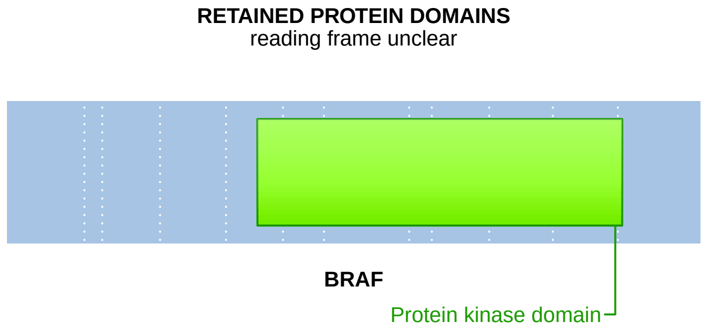


**SUPPORTING READ COUNT**

Split reads = 305
Discordant mates = 0

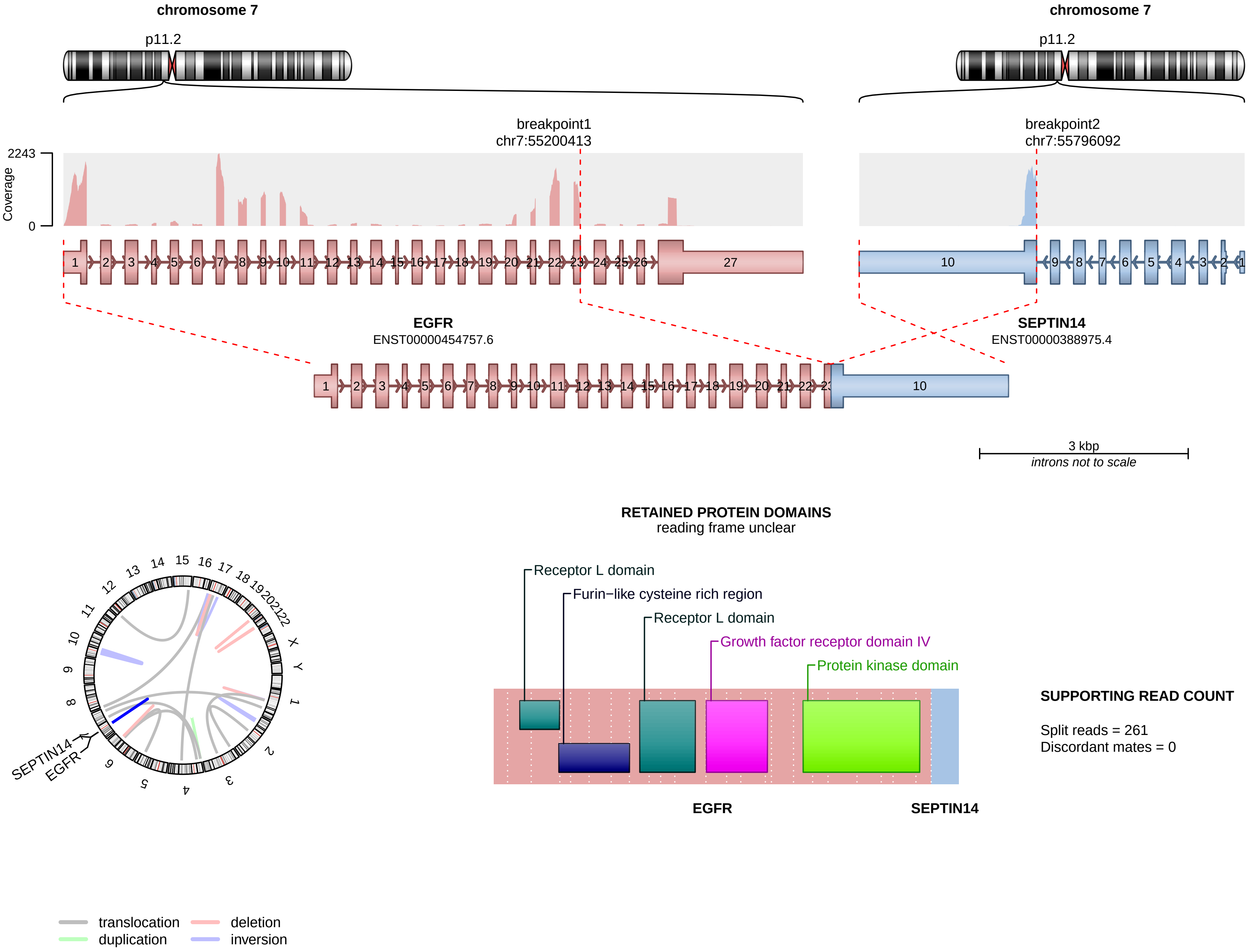


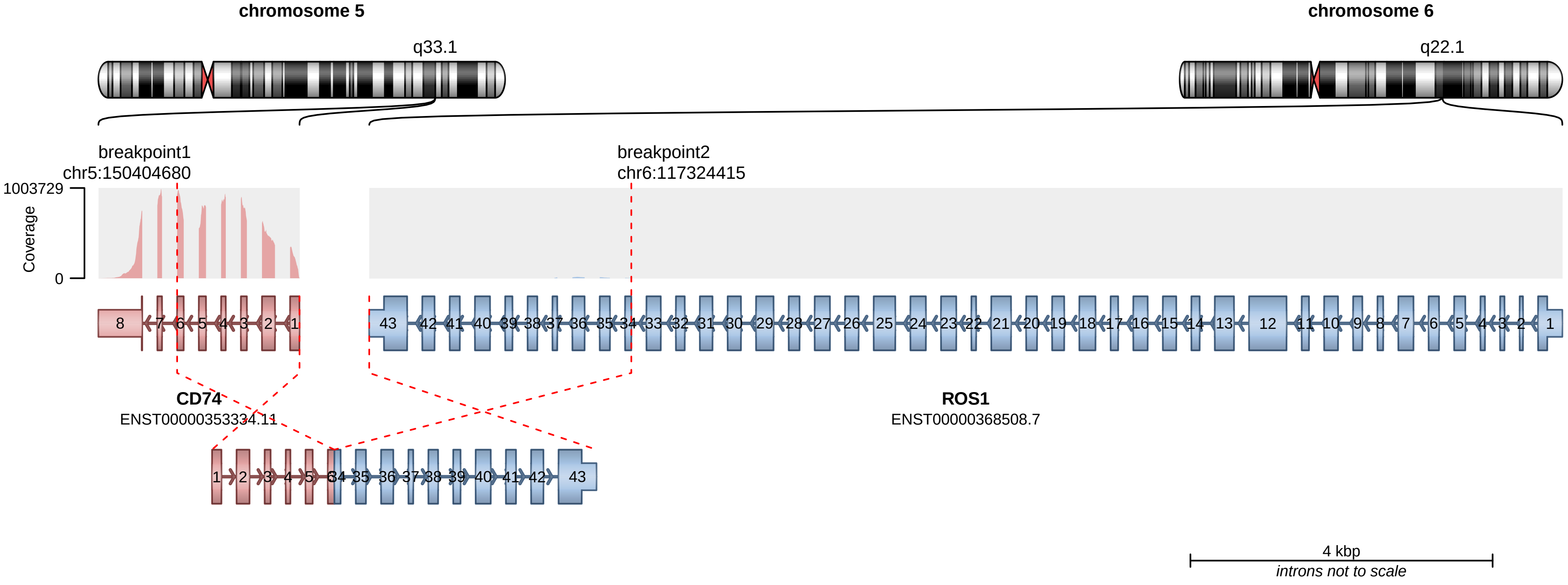


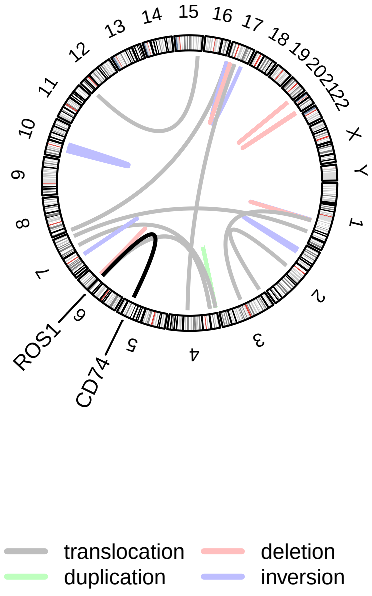


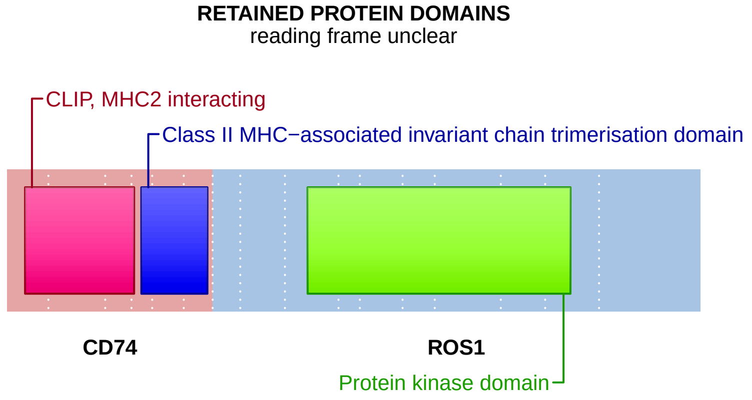
**SUPPORTING READ COUNT**

Split reads = 271
Discordant mates = 0


chromosome 7
p11.2
chromosome 7
p11.2
breakpoint1
chr7:55200413
breakpoint2
chr7:55796092
2243
Coverage
0
1 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 27
10 9 8 7 6 5 4 3 2 1
EGFR
ENST00000454757.6
SEPTIN14
ENST00000388975.4
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23
10
3 kbp
introns not to scale
RETAINED PROTEIN DOMAINS
reading frame unclear
Receptor L domain
Furin−like cysteine rich region
Receptor L domain
Growth factor receptor domain IV
Protein kinase domain
EGFR
SEPTIN14
SUPPORTING READ COUNT
Split reads = 261
Discordant mates = 0
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y
SEPTIN14
EGFR
translocation
duplication
deletion
inversion

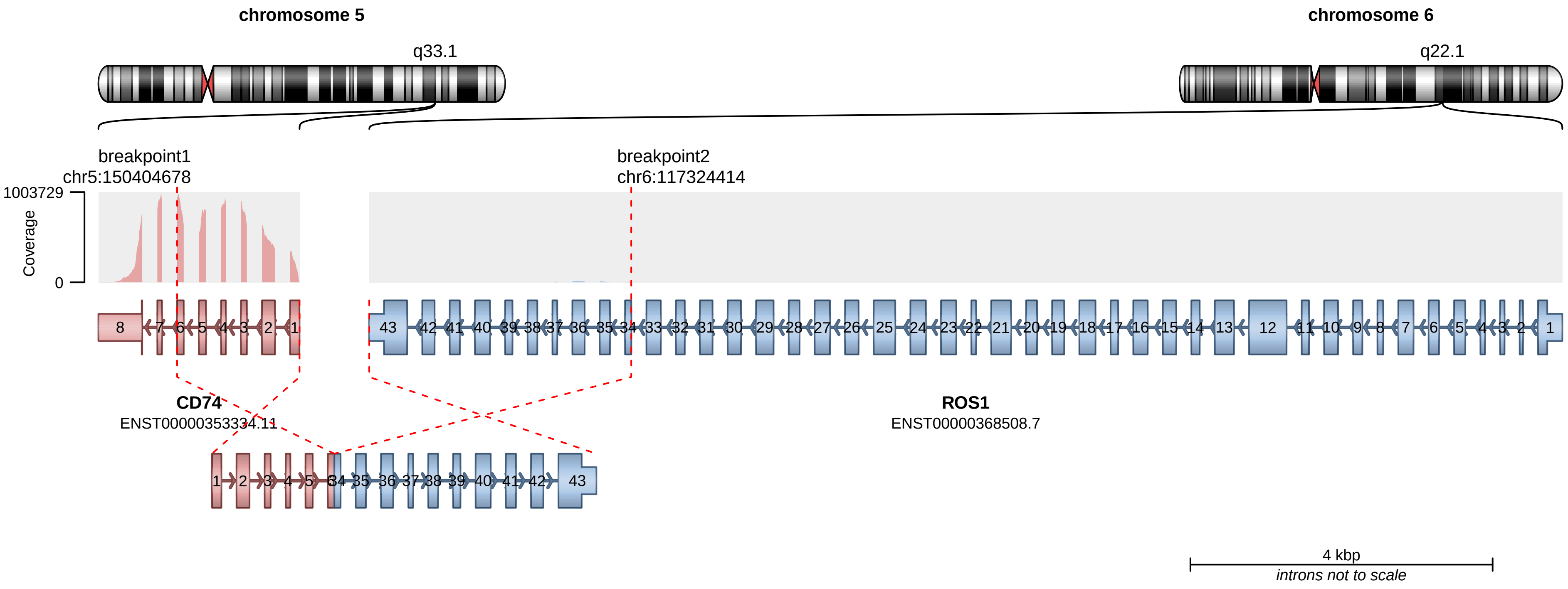


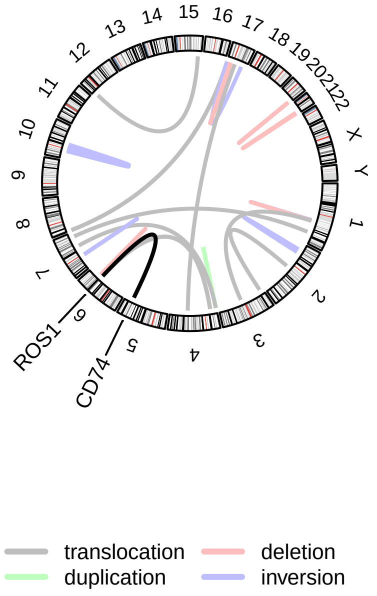




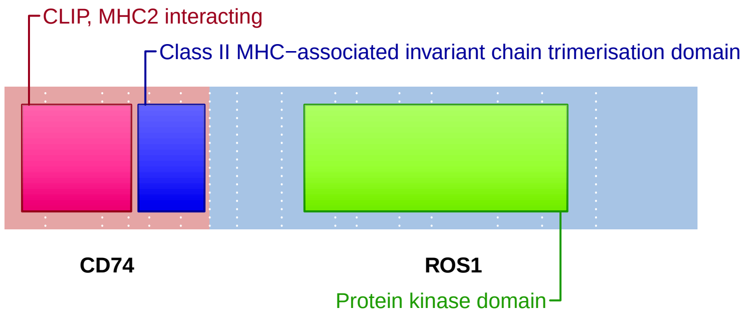
**SUPPORTING READ COUNT**

Split reads = 240
Discordant mates = 3



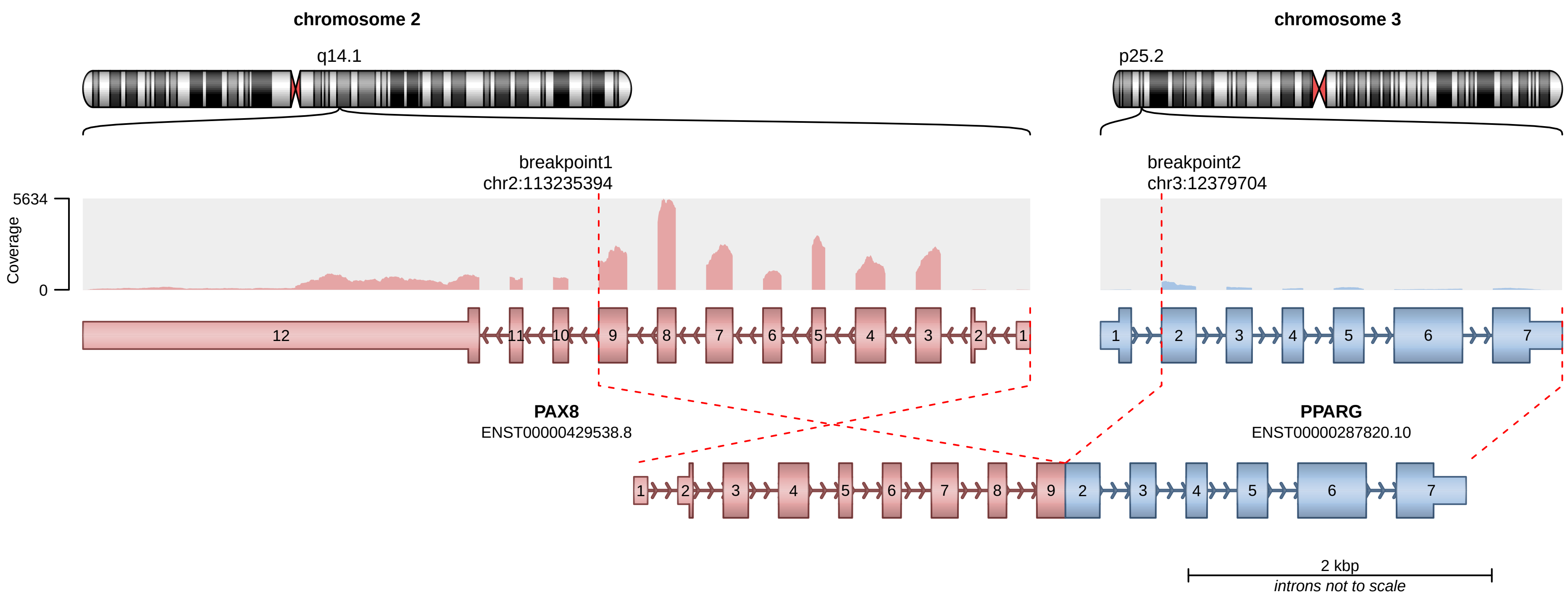


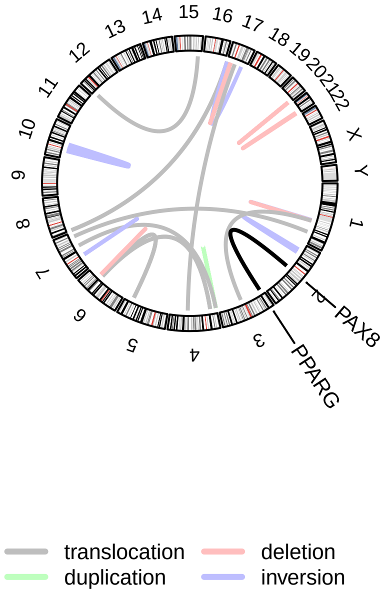
**RETAINED PROTEIN DOMAINS**
reading frame unclear

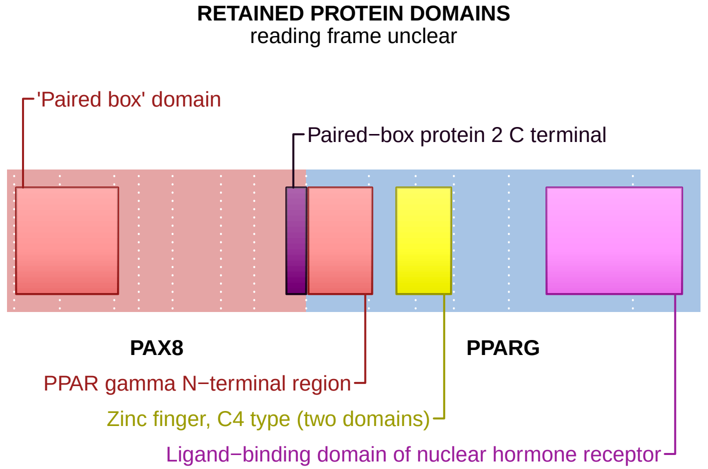


**SUPPORTING READ COUNT**

Split reads = 7
Discordant mates = 3

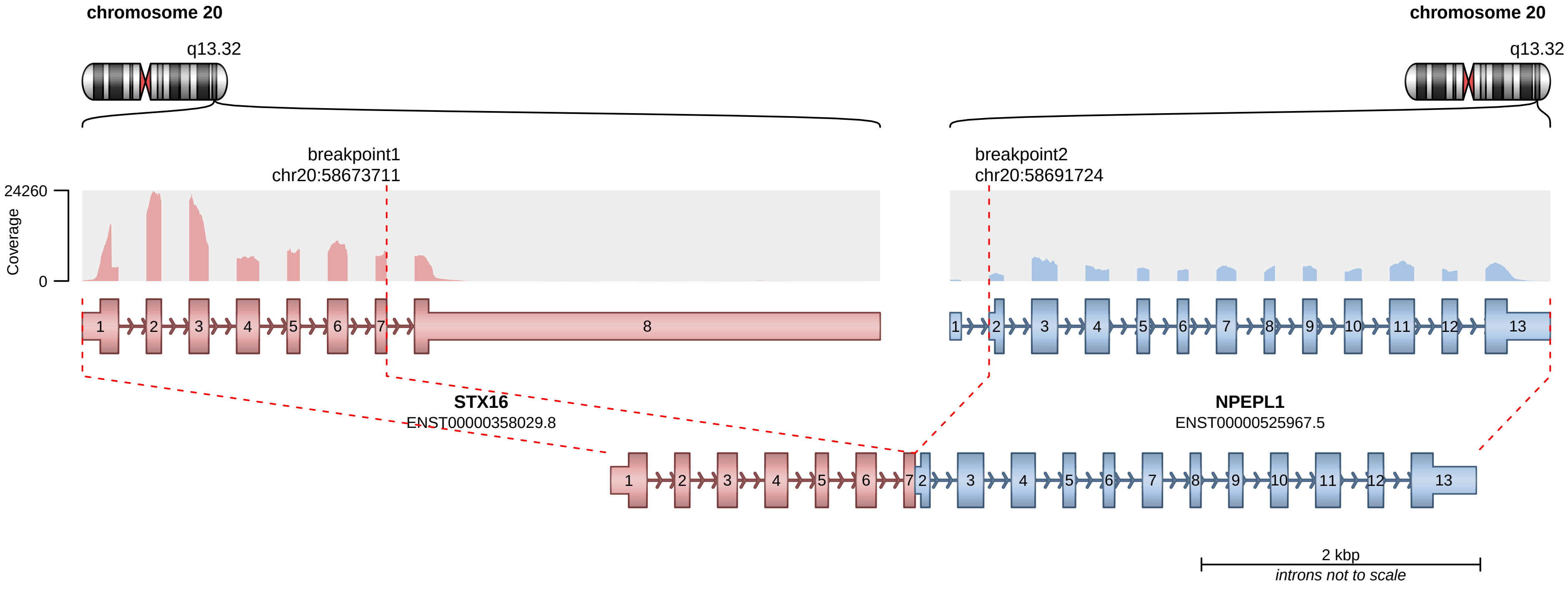


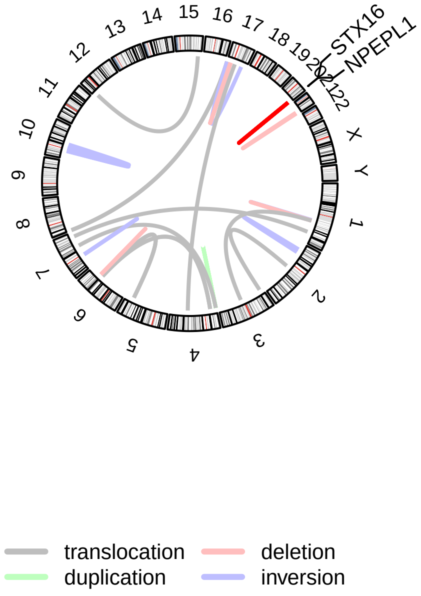


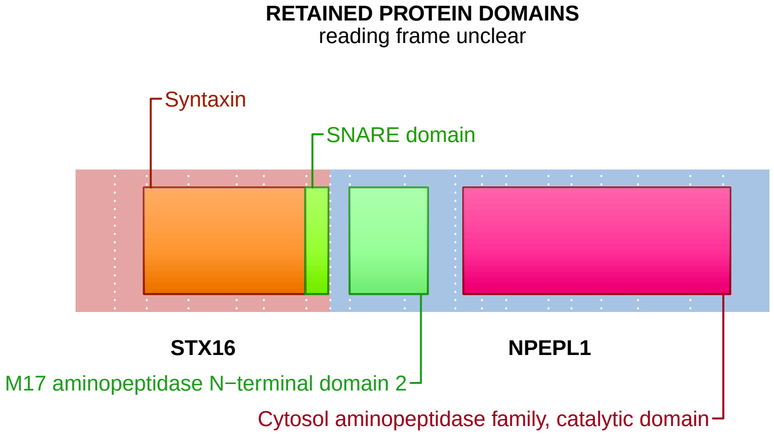


**SUPPORTING READ COUNT**

Split reads = 224
Discordant mates = 0

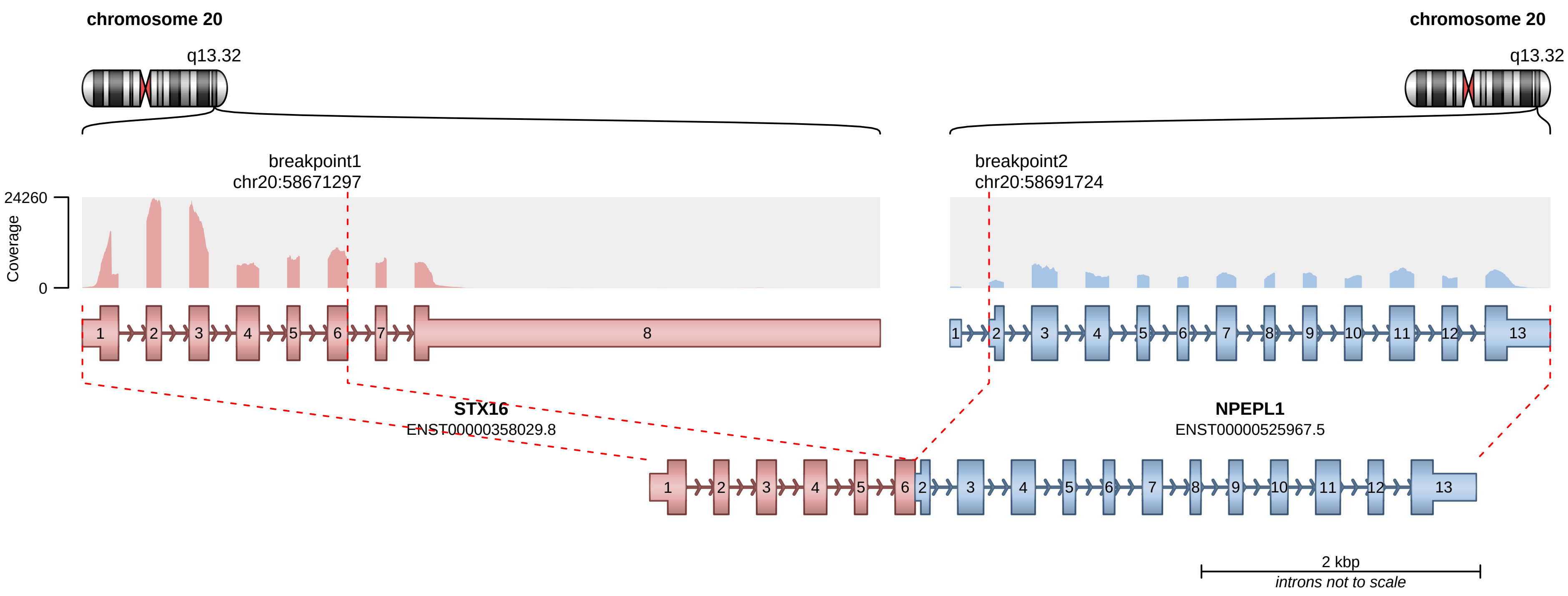


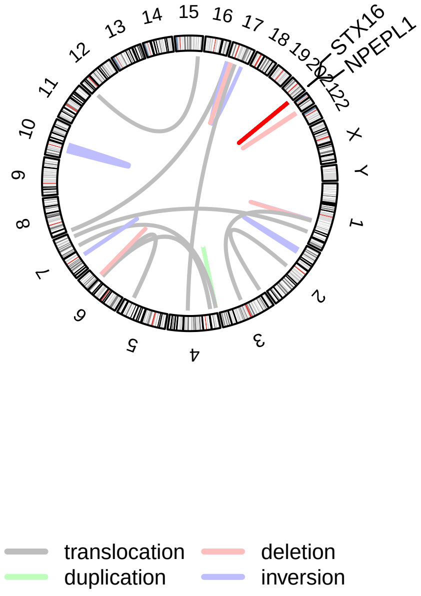


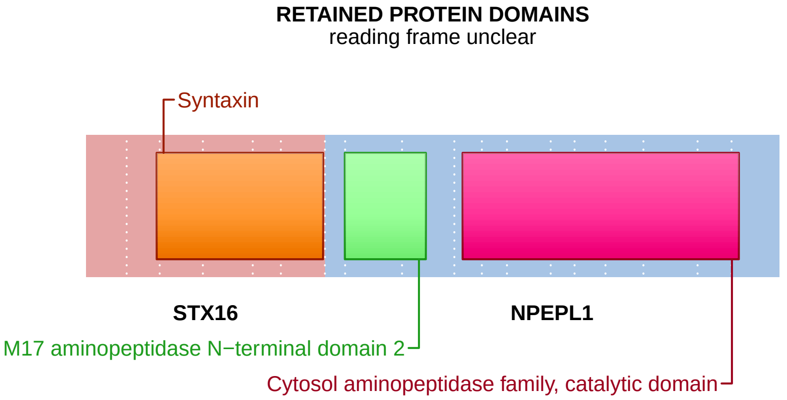

RETAINED PROTEIN DOMAINS
reading frame unclear

**SUPPORTING READ COUNT**

Split reads = 209
Discordant mates = 9

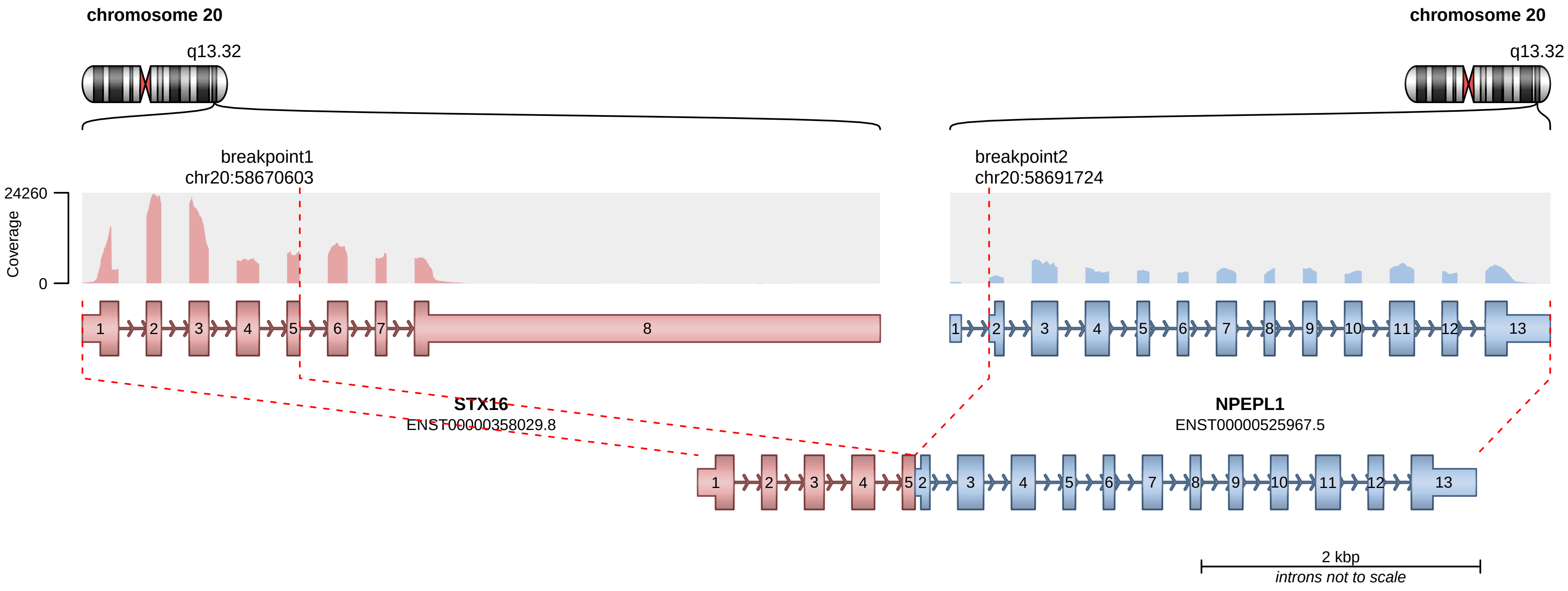


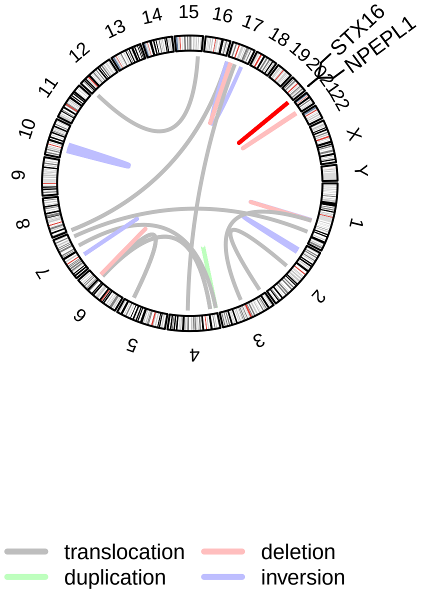




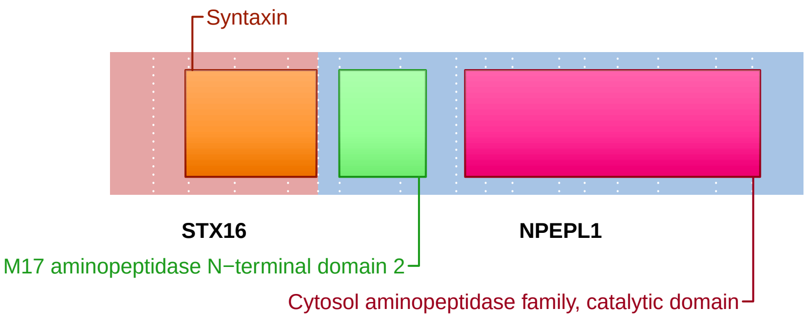
**SUPPORTING READ COUNT**

Split reads = 6
Discordant mates = 1



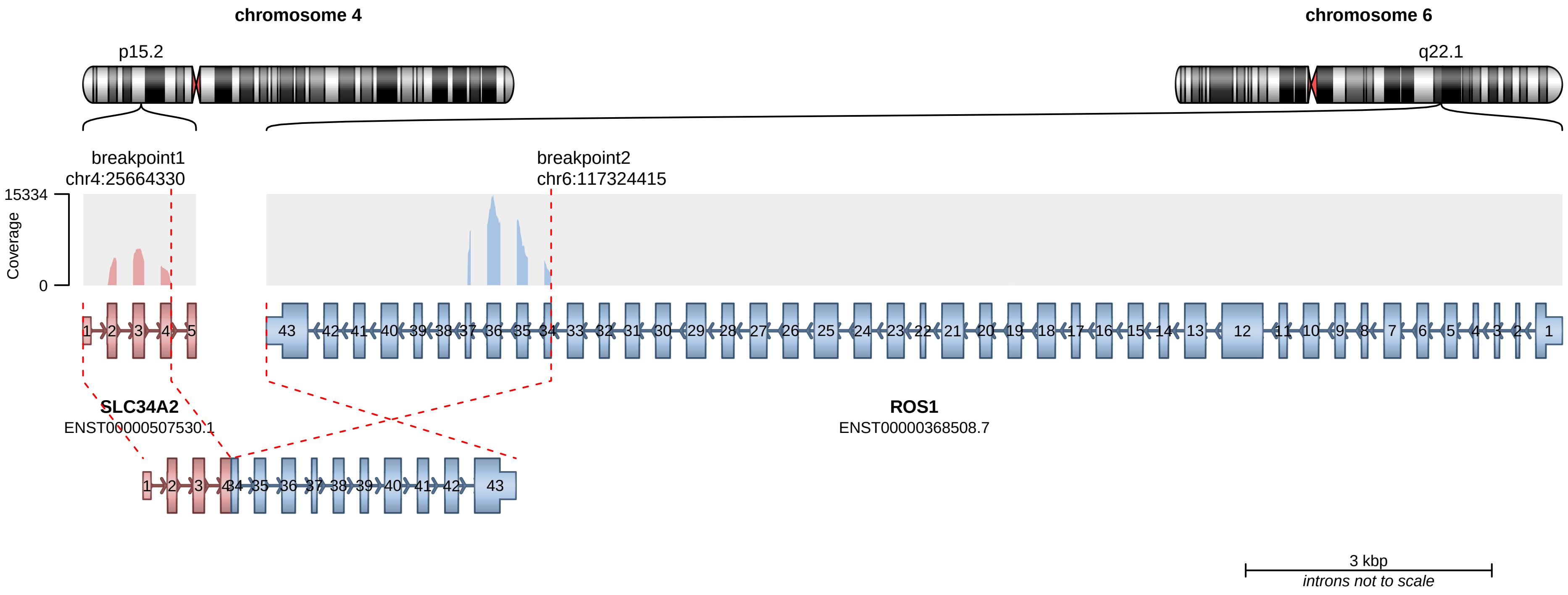


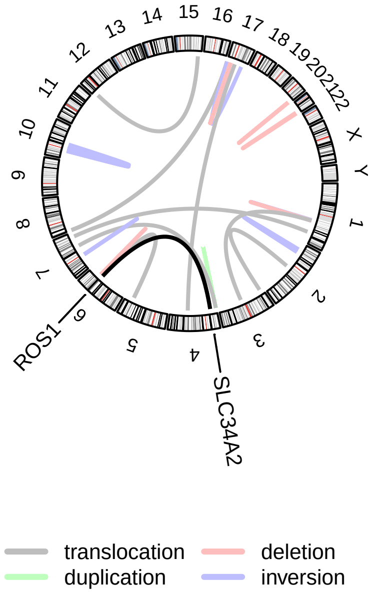
**RETAINED PROTEIN DOMAINS**
reading frame unclear



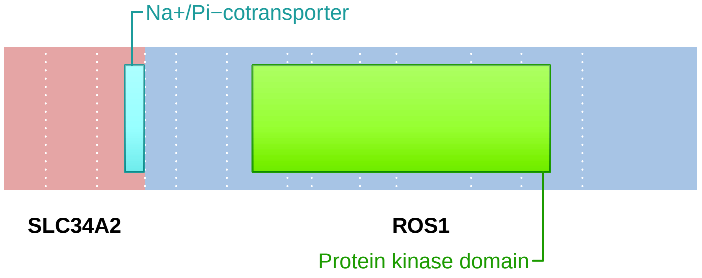
**SUPPORTING READ COUNT**

Split reads = 2
Discordant mates = 0



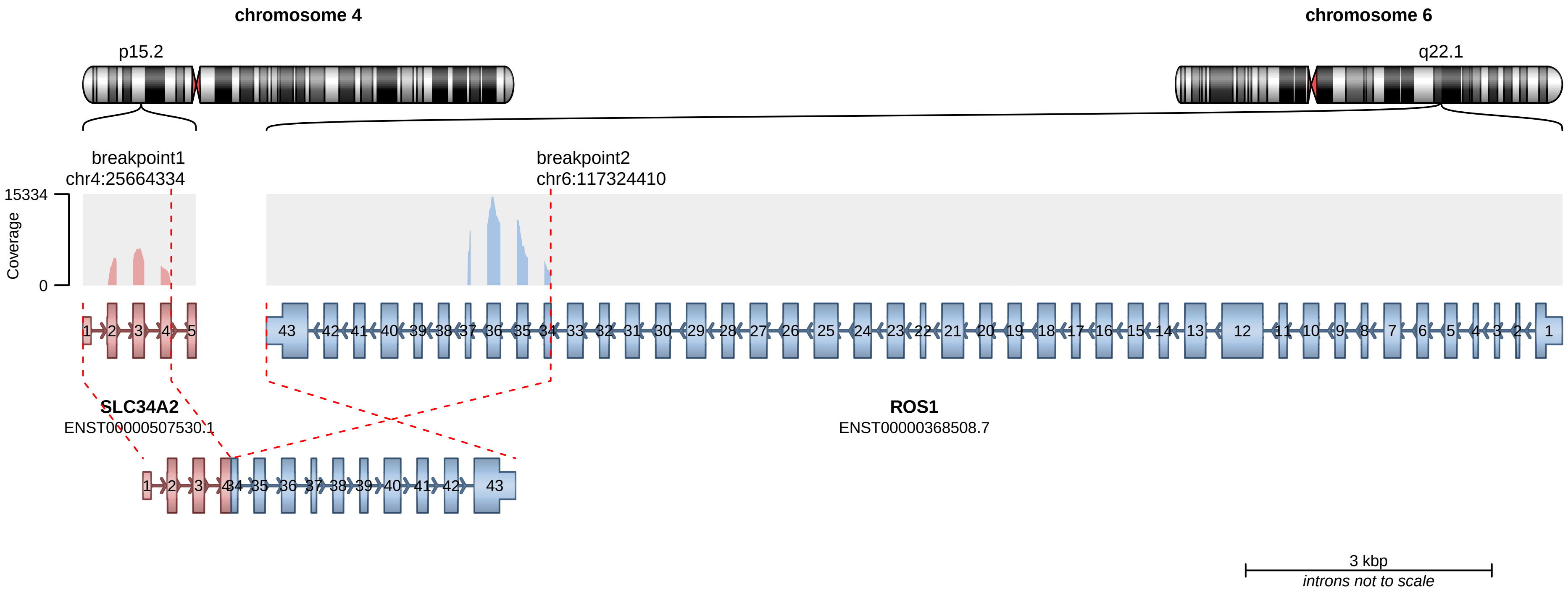


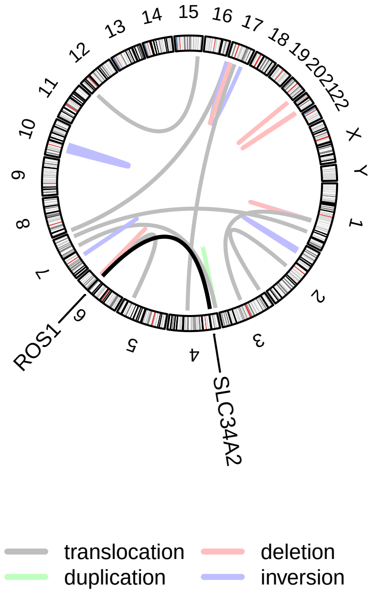
**RETAINED PROTEIN DOMAINS**
reading frame unclear



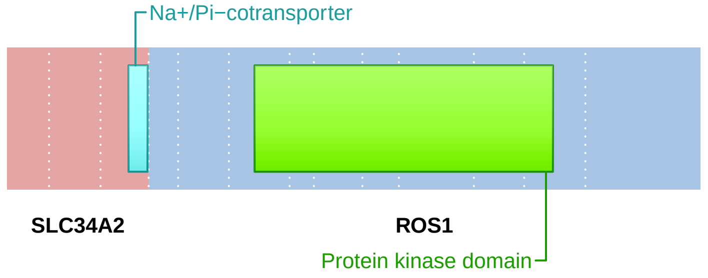
**SUPPORTING READ COUNT**

Split reads = 198
Discordant mates = 5



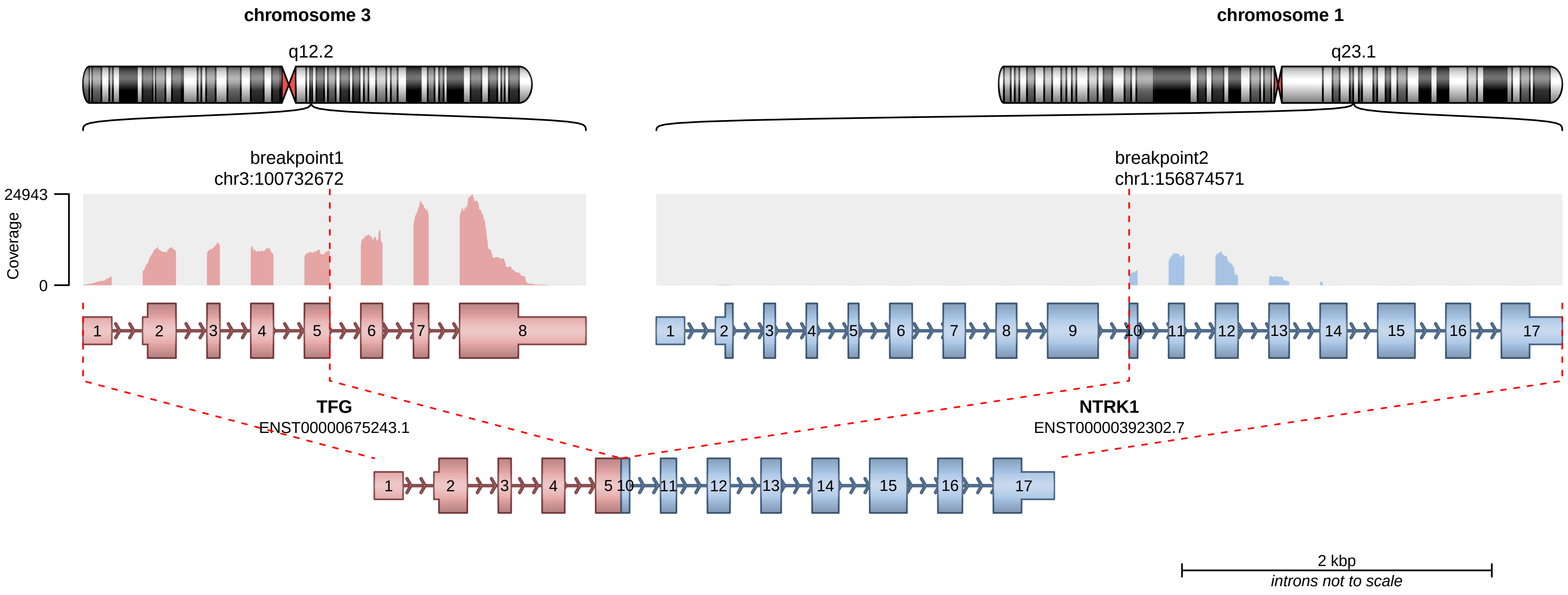


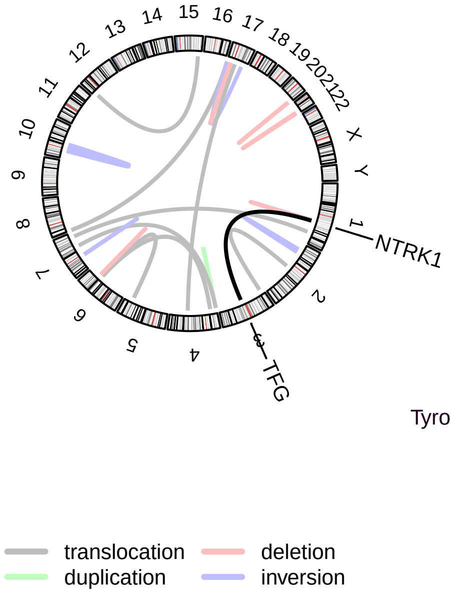
**RETAINED PROTEIN DOMAINS**
reading frame unclear

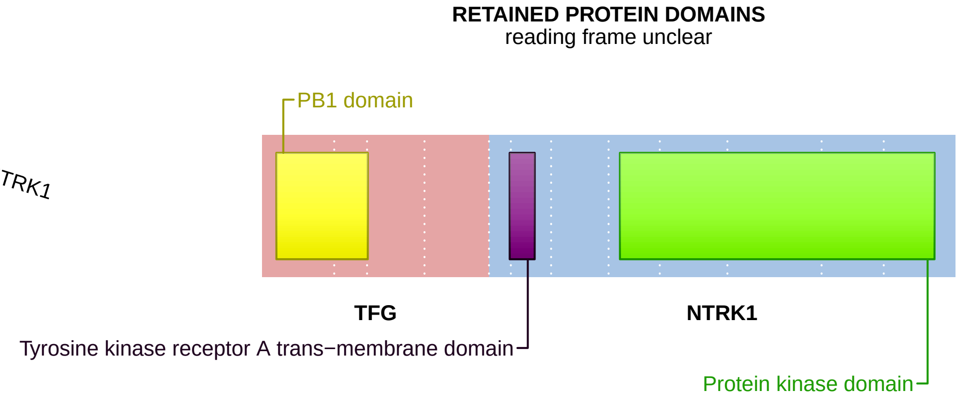


**SUPPORTING READ COUNT**

Split reads = 3
Discordant mates = 1

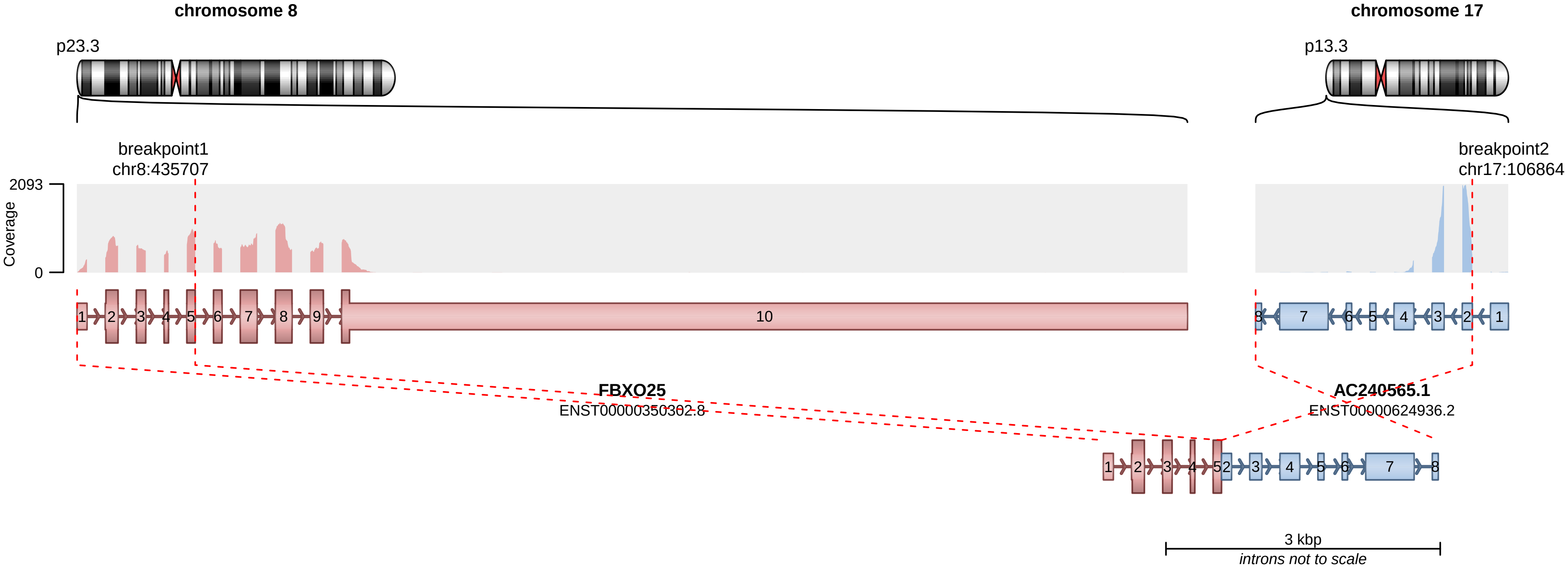


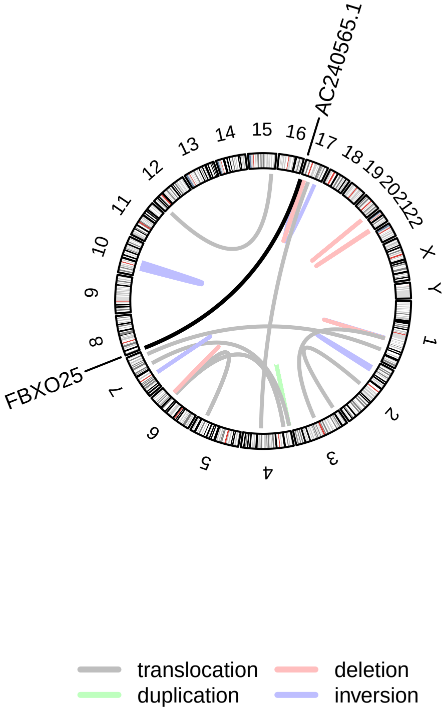




**SUPPORTING READ COUNT**

Split reads = 186
Discordant mates = 2

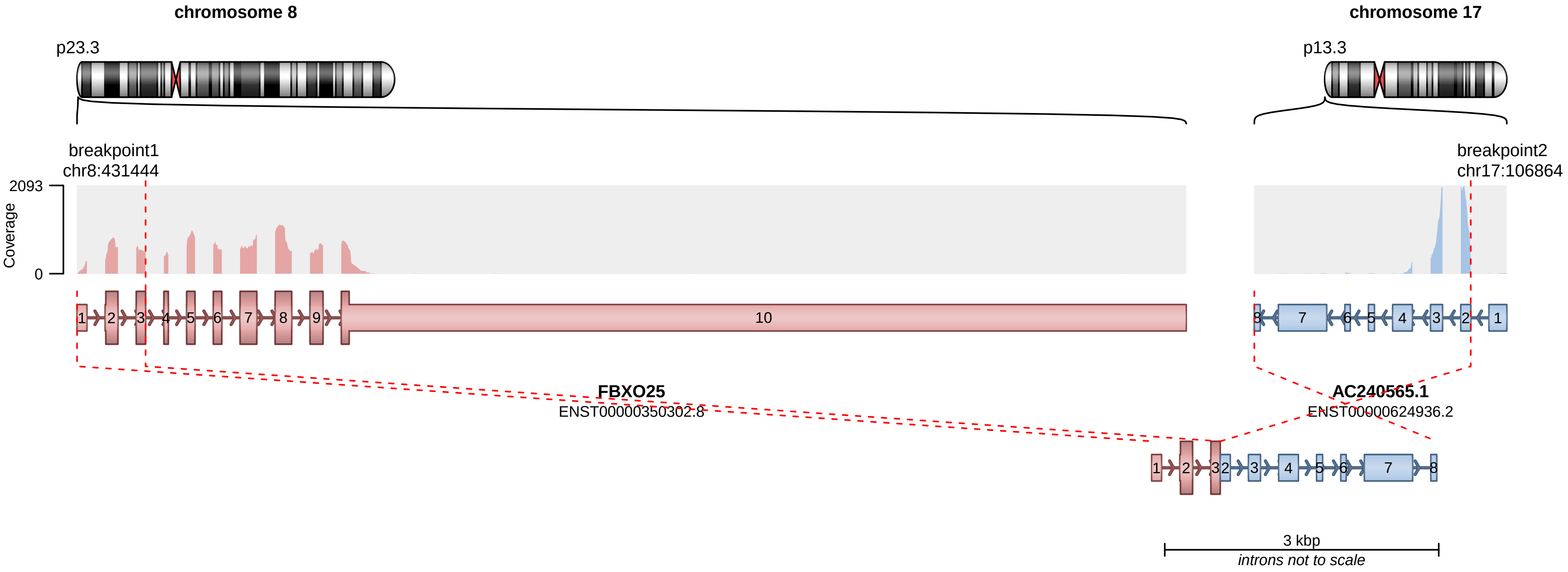


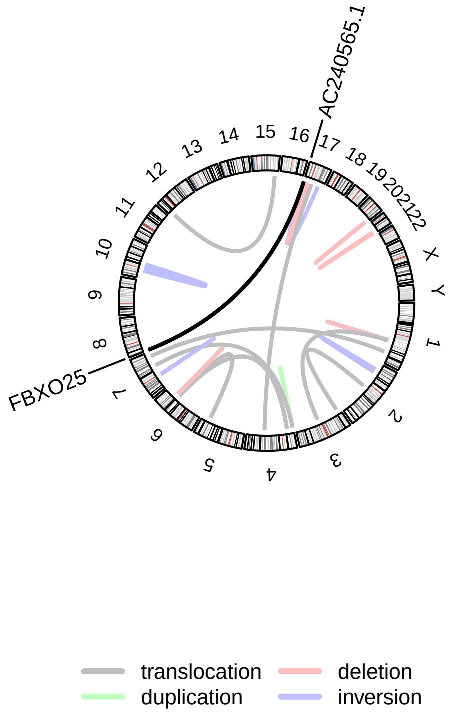


No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 111
Discordant mates = 0

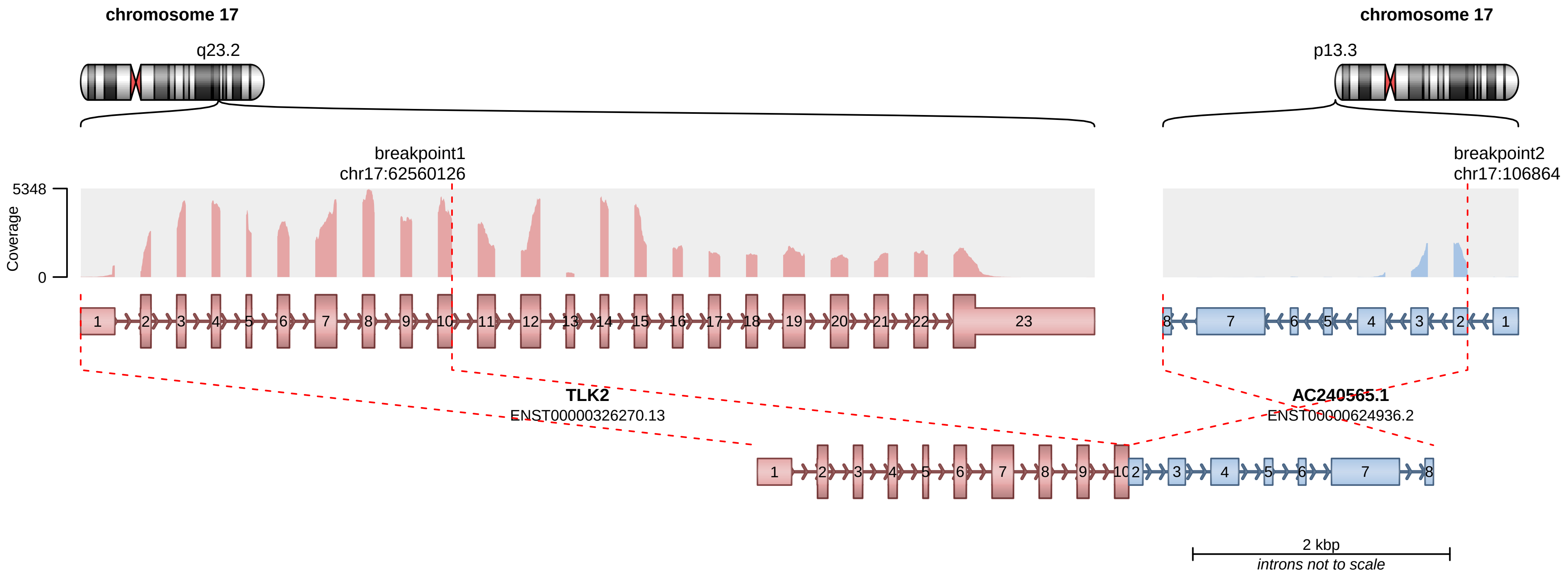


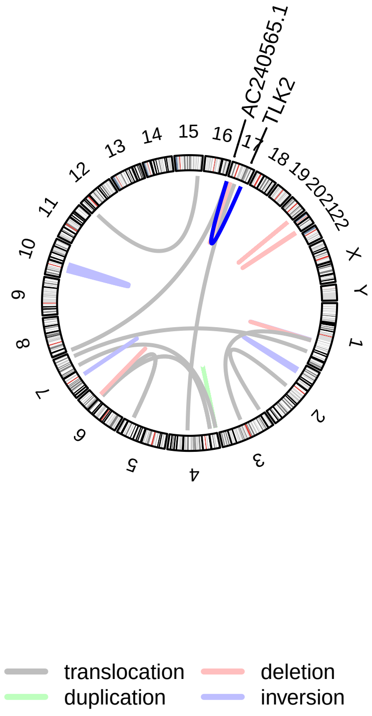


No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 1
Discordant mates = 0

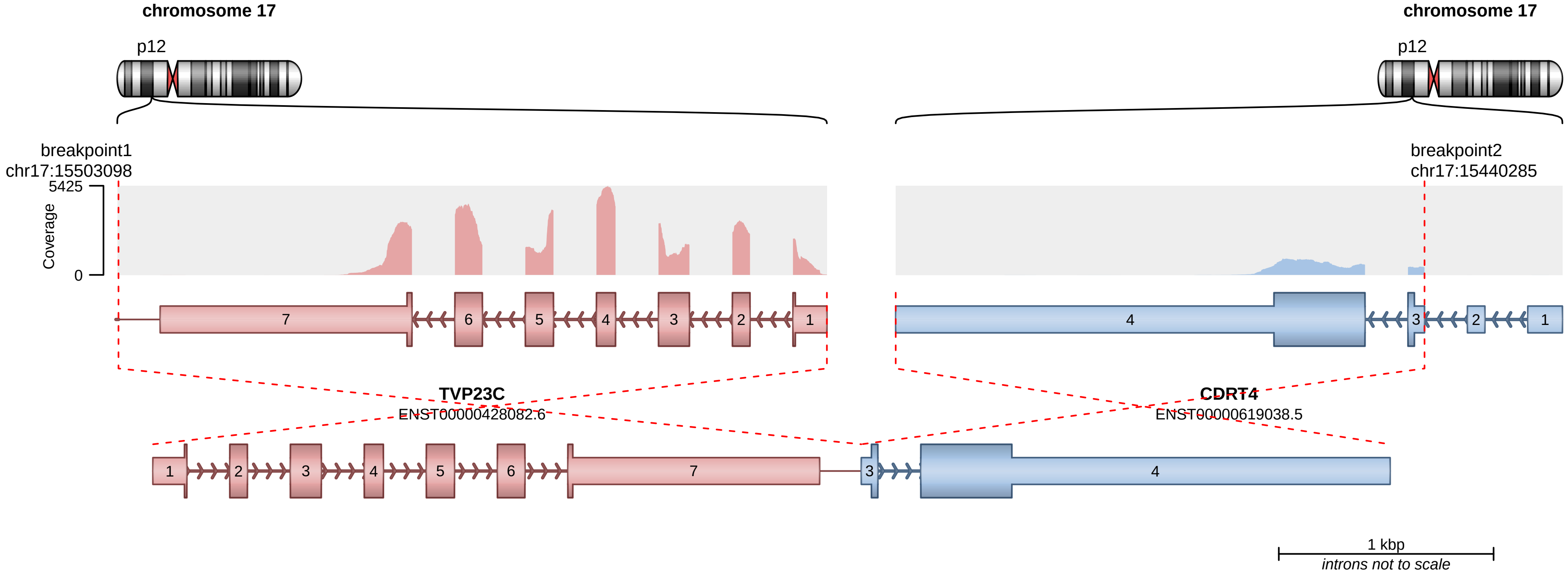


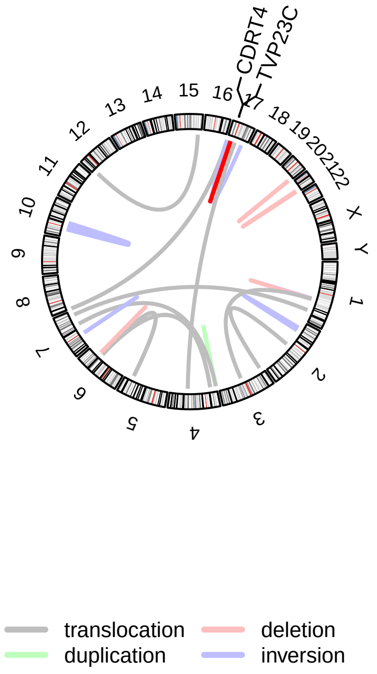


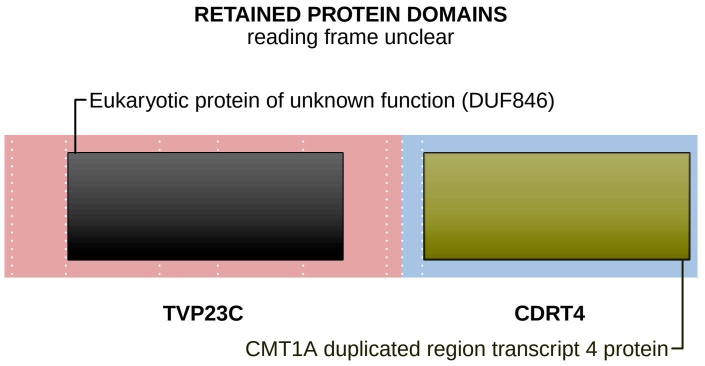
No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 76
Discordant mates = 0

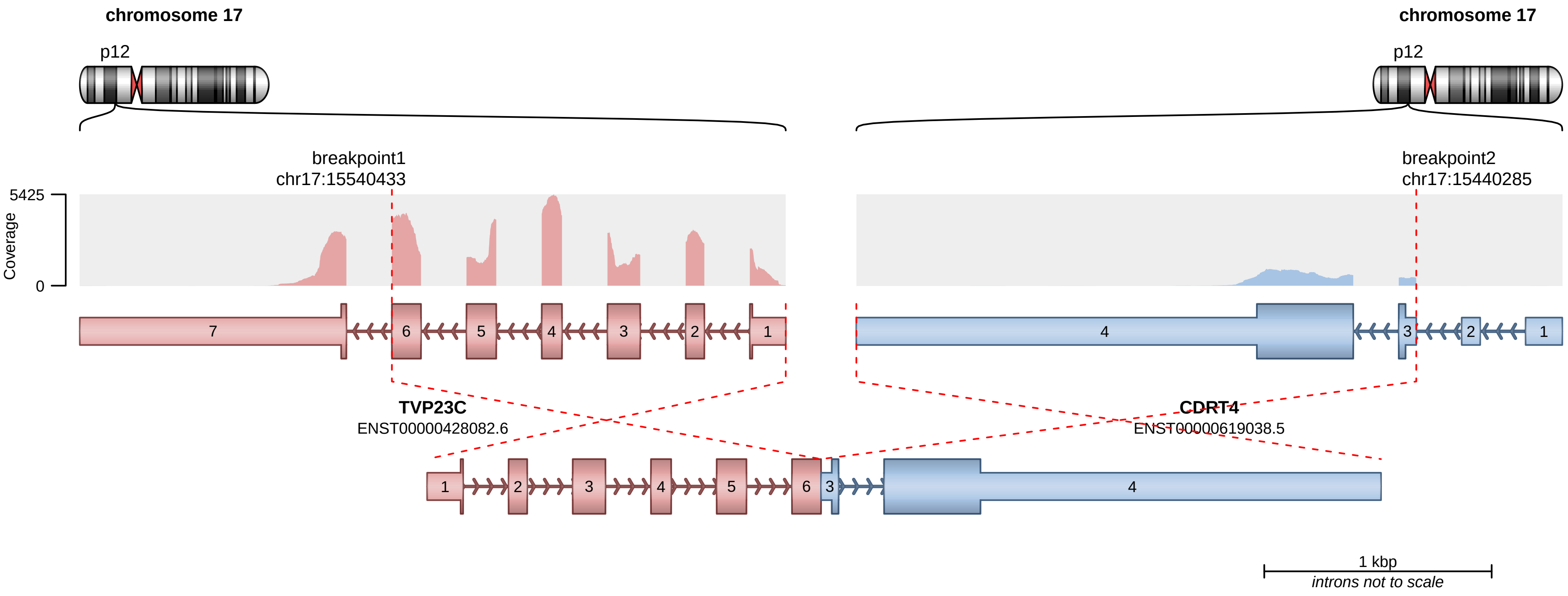


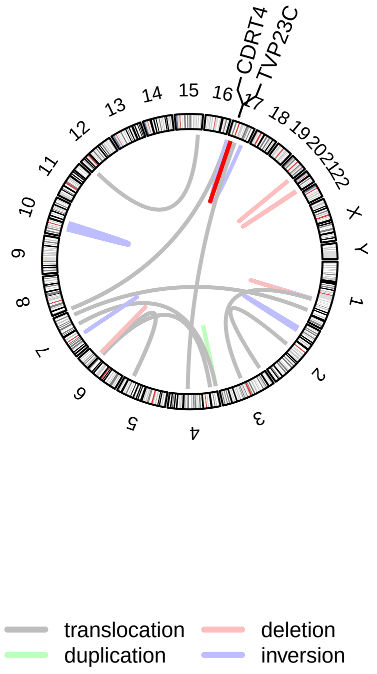


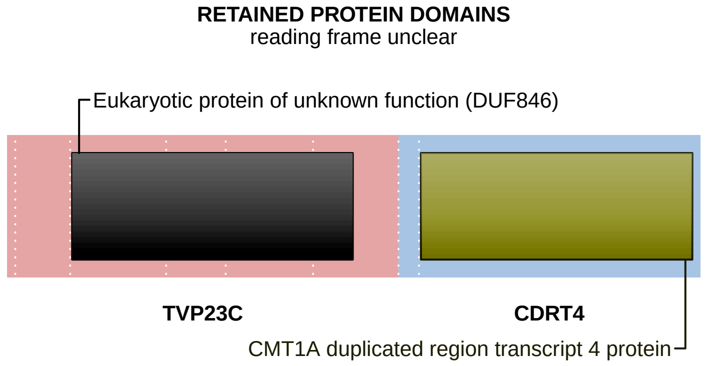


**SUPPORTING READ COUNT**

Split reads = 64
Discordant mates = 2

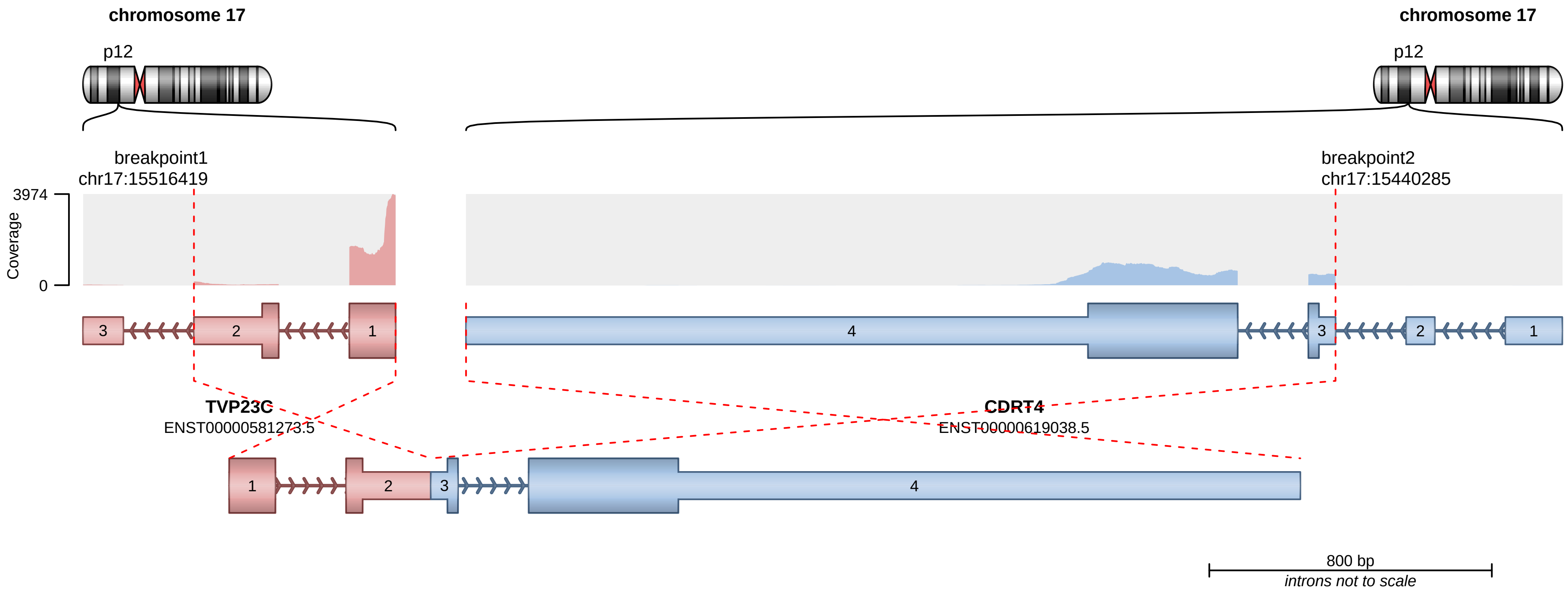


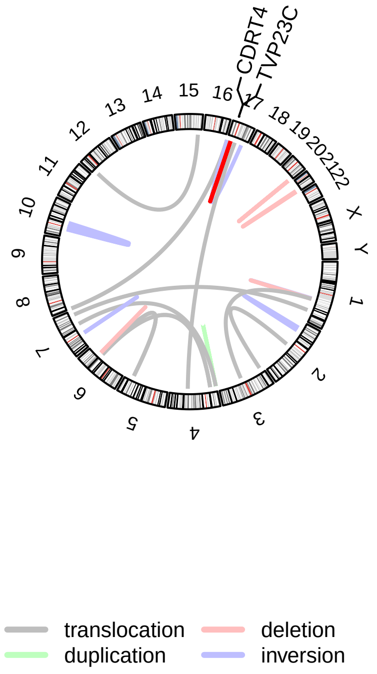


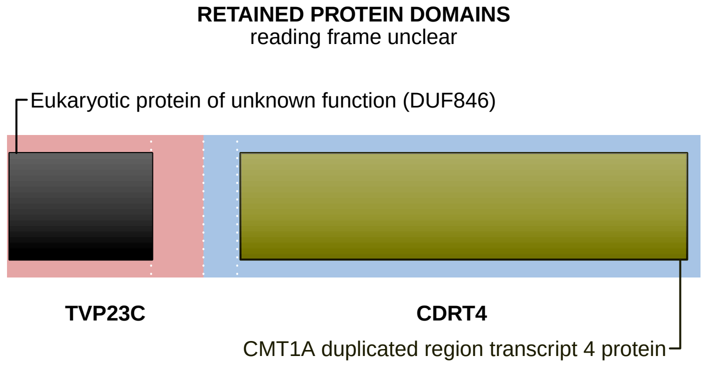


**SUPPORTING READ COUNT**

Split reads = 39
Discordant mates = 1

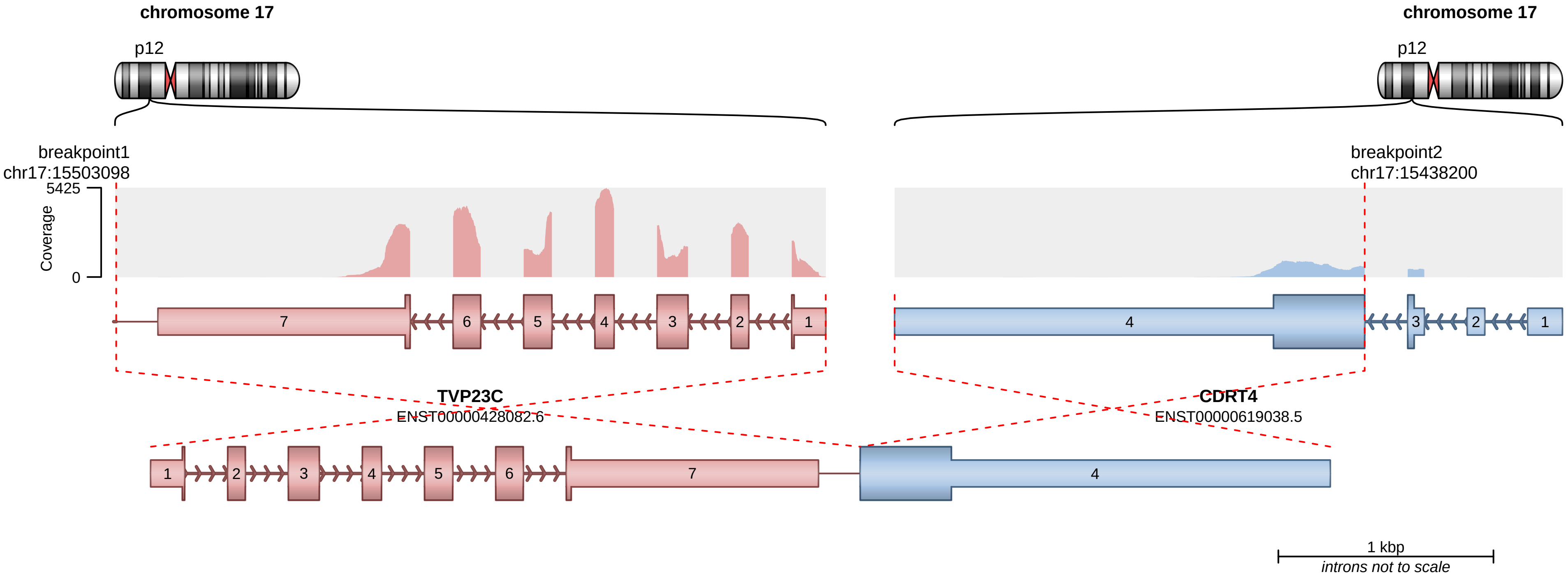


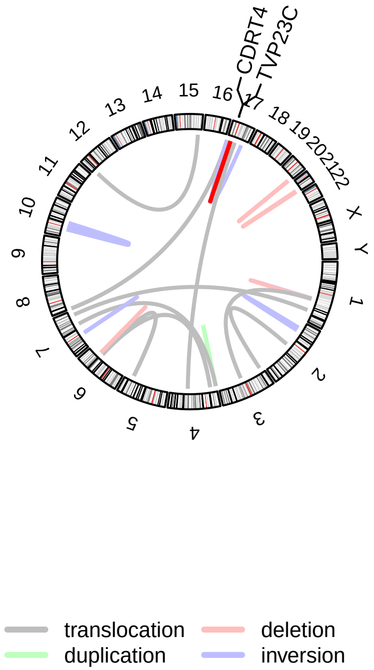




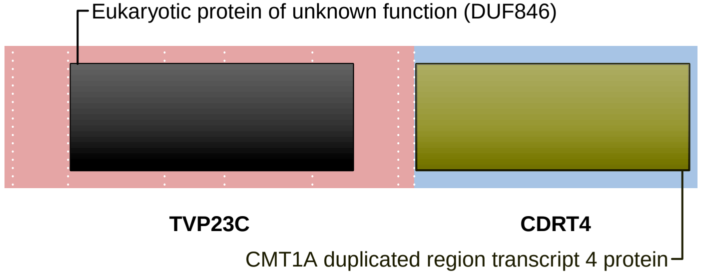
**SUPPORTING READ COUNT**

Split reads = 30
Discordant mates = 1



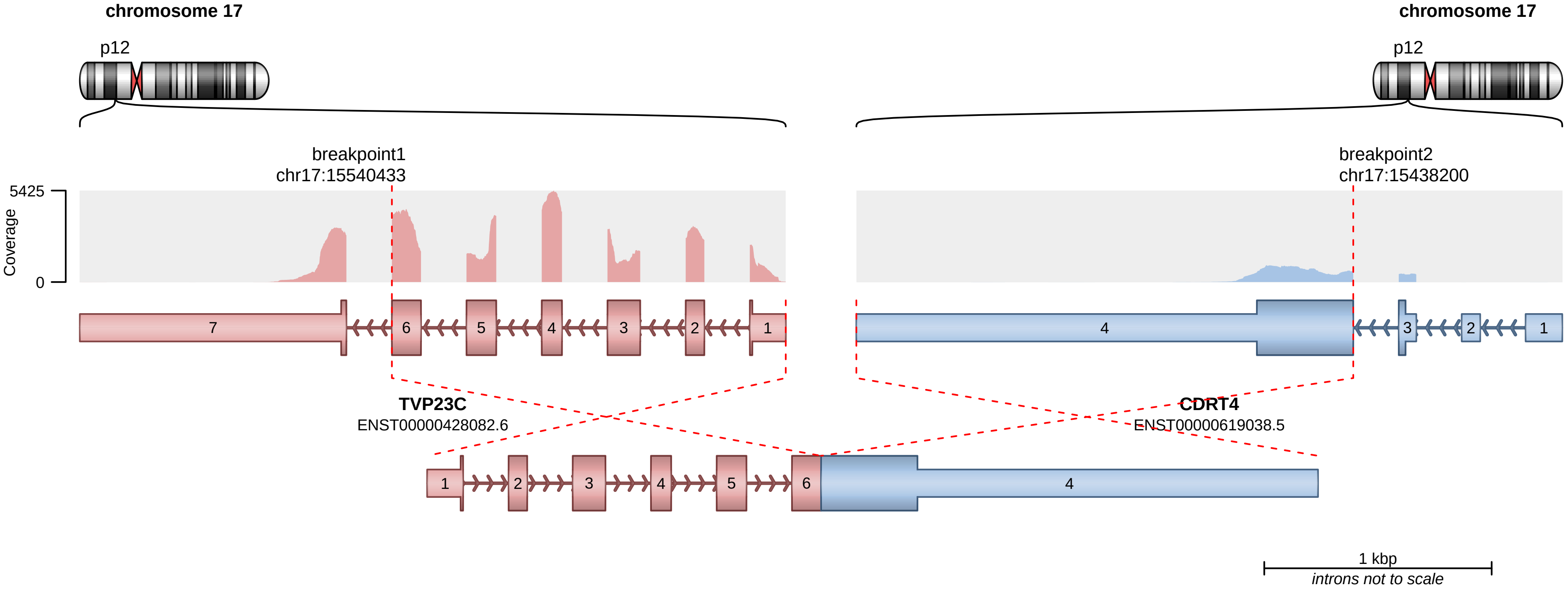


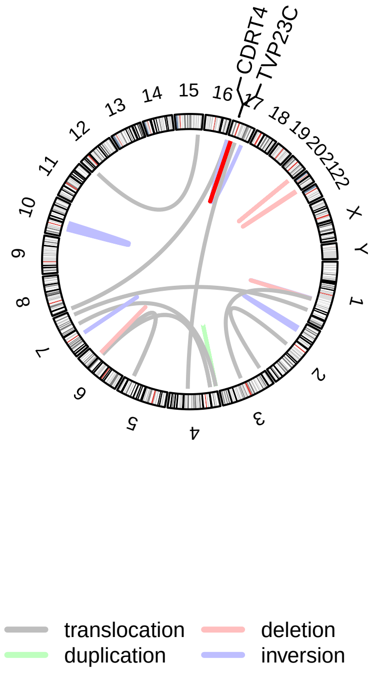
**RETAINED PROTEIN DOMAINS**
reading frame unclear

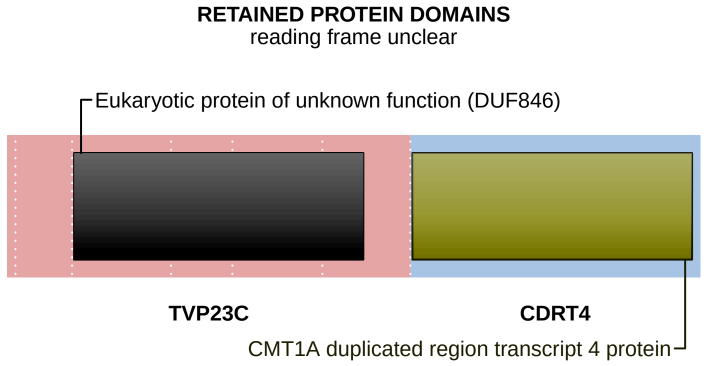


**SUPPORTING READ COUNT**

Split reads = 13
Discordant mates = 0

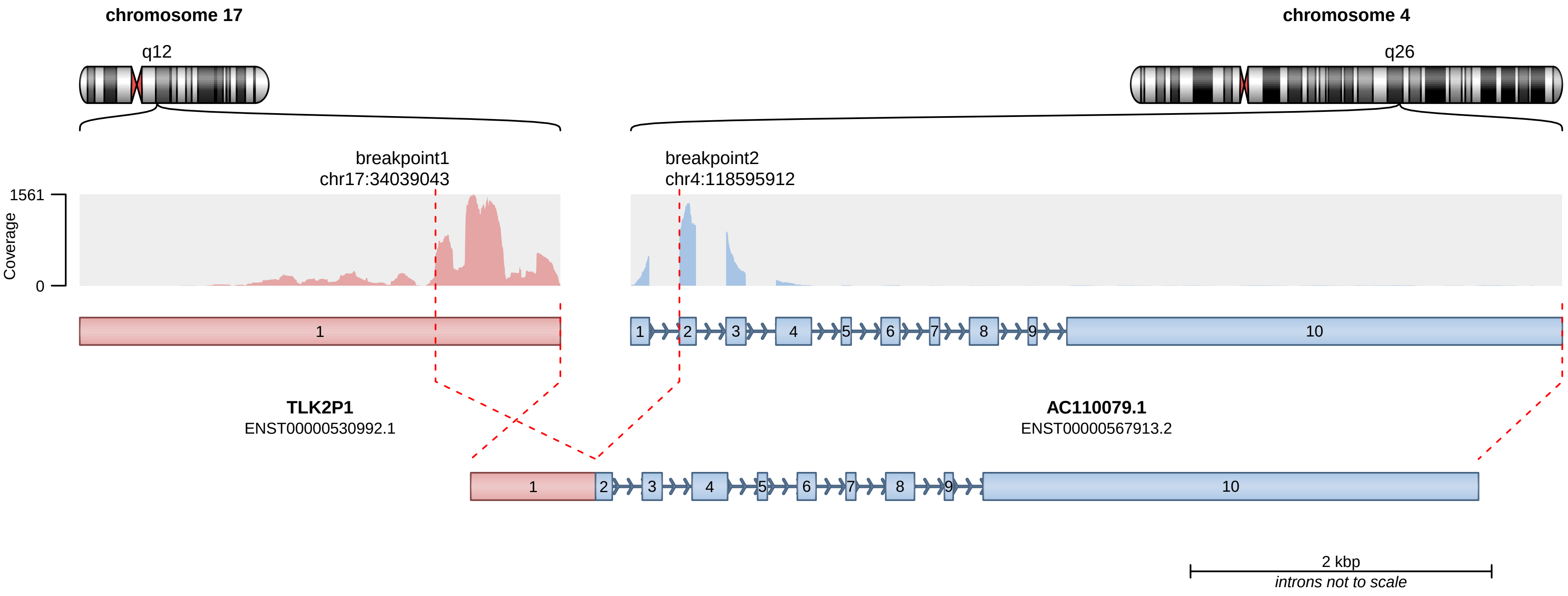


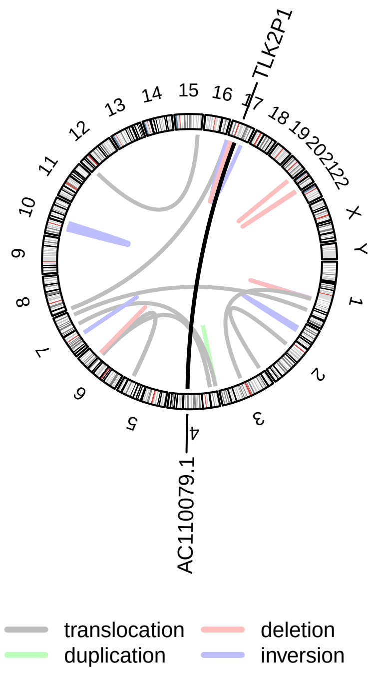




**SUPPORTING READ COUNT**

Split reads = 10
Discordant mates = 0

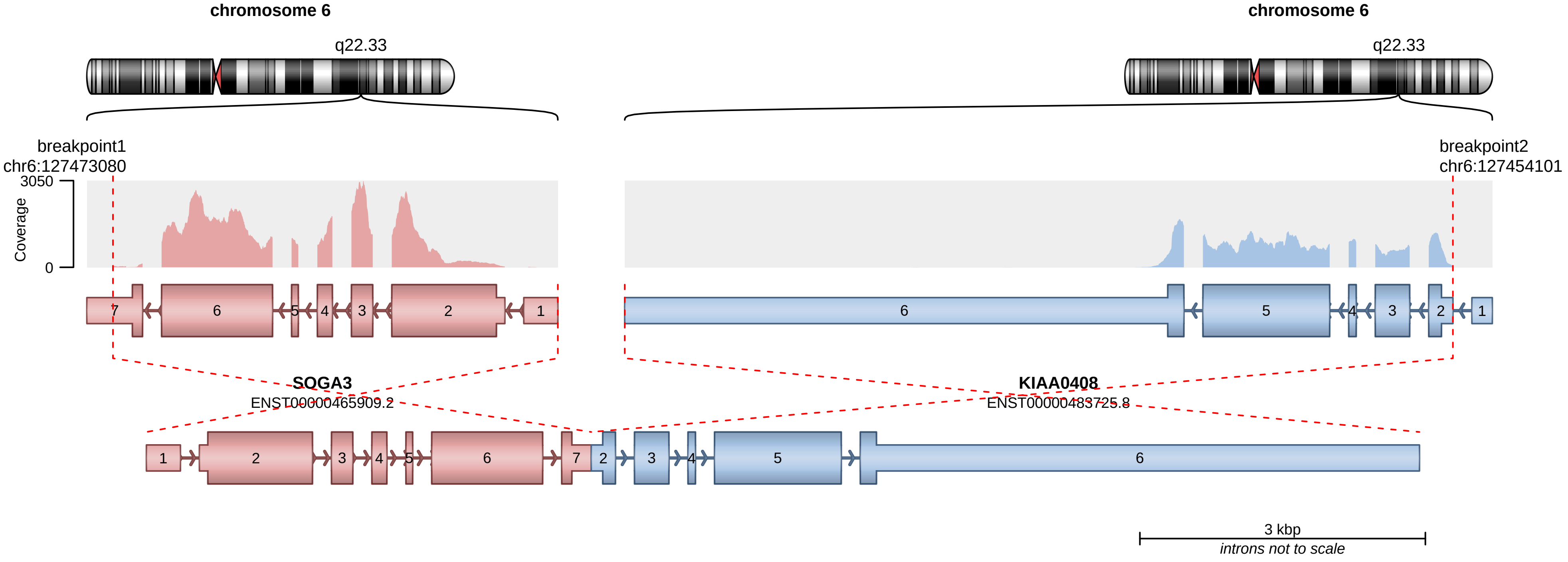


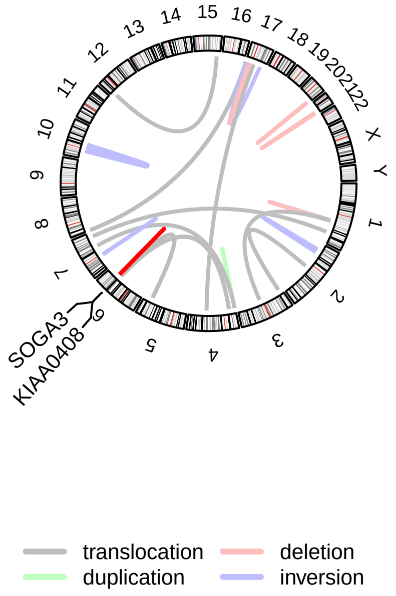


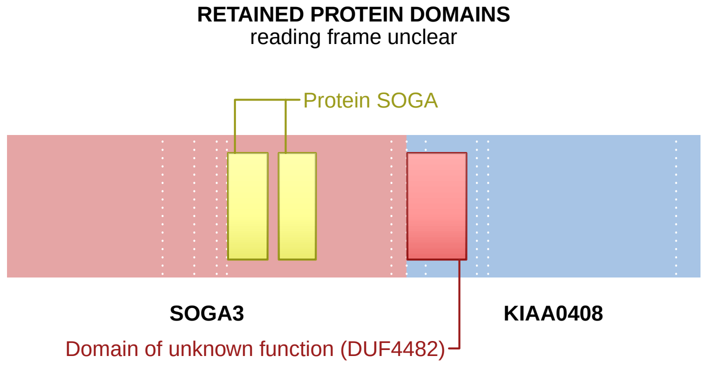
Genes are not protein−coding.

**SUPPORTING READ COUNT**

Split reads = 62
Discordant mates = 0







**SUPPORTING READ COUNT**

Split reads = 19
Discordant mates = 1