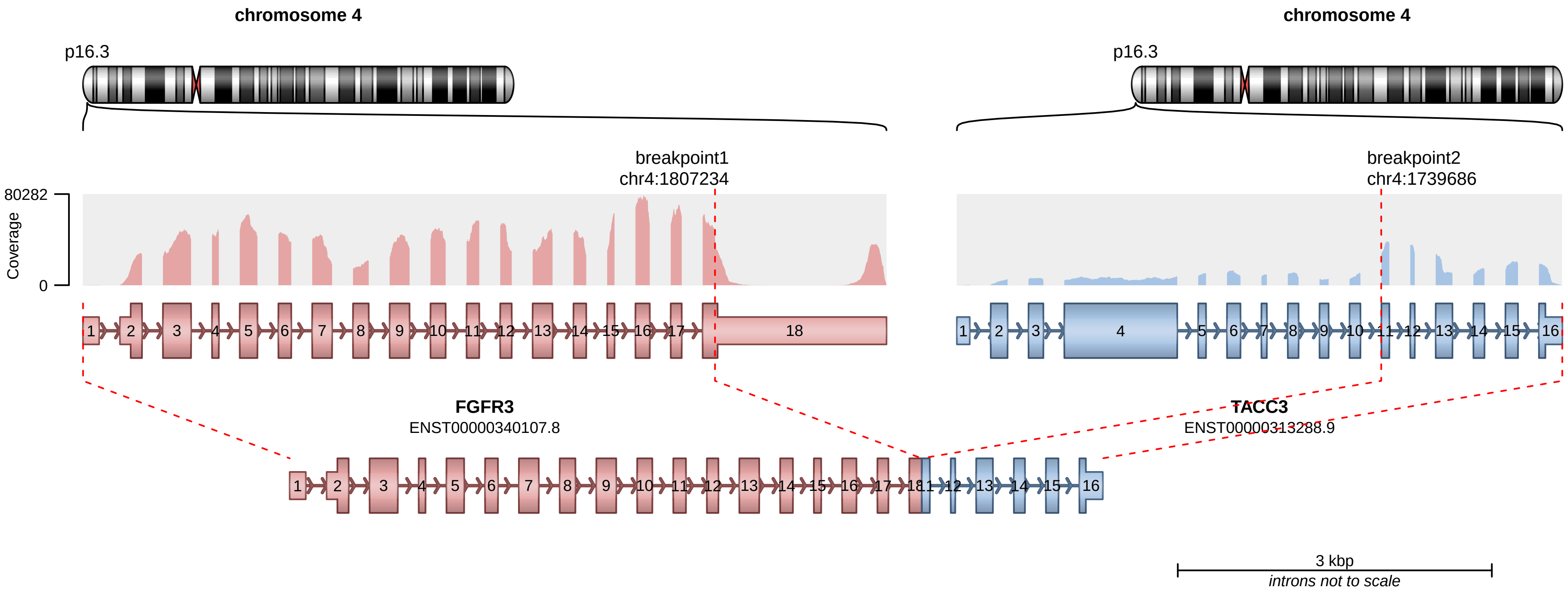
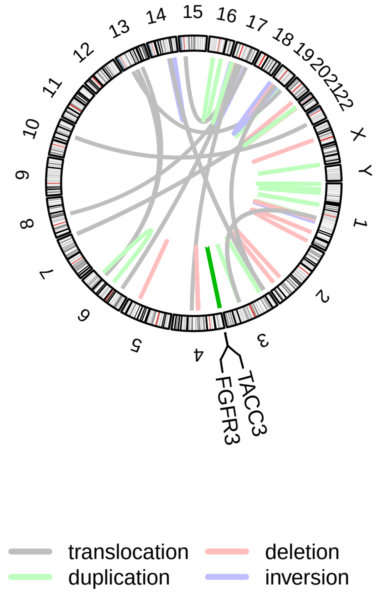
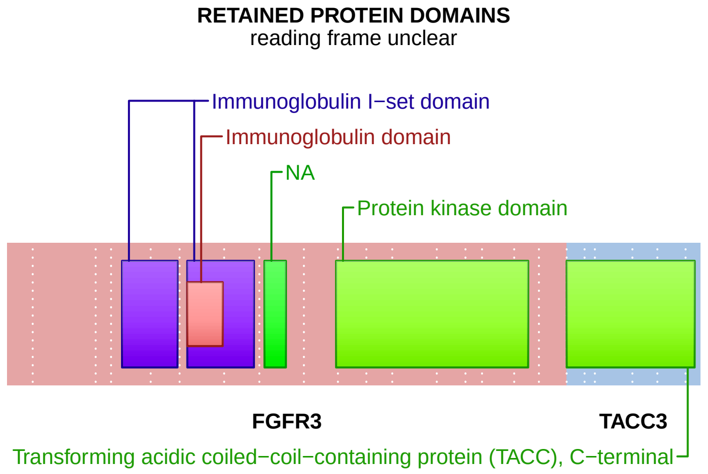
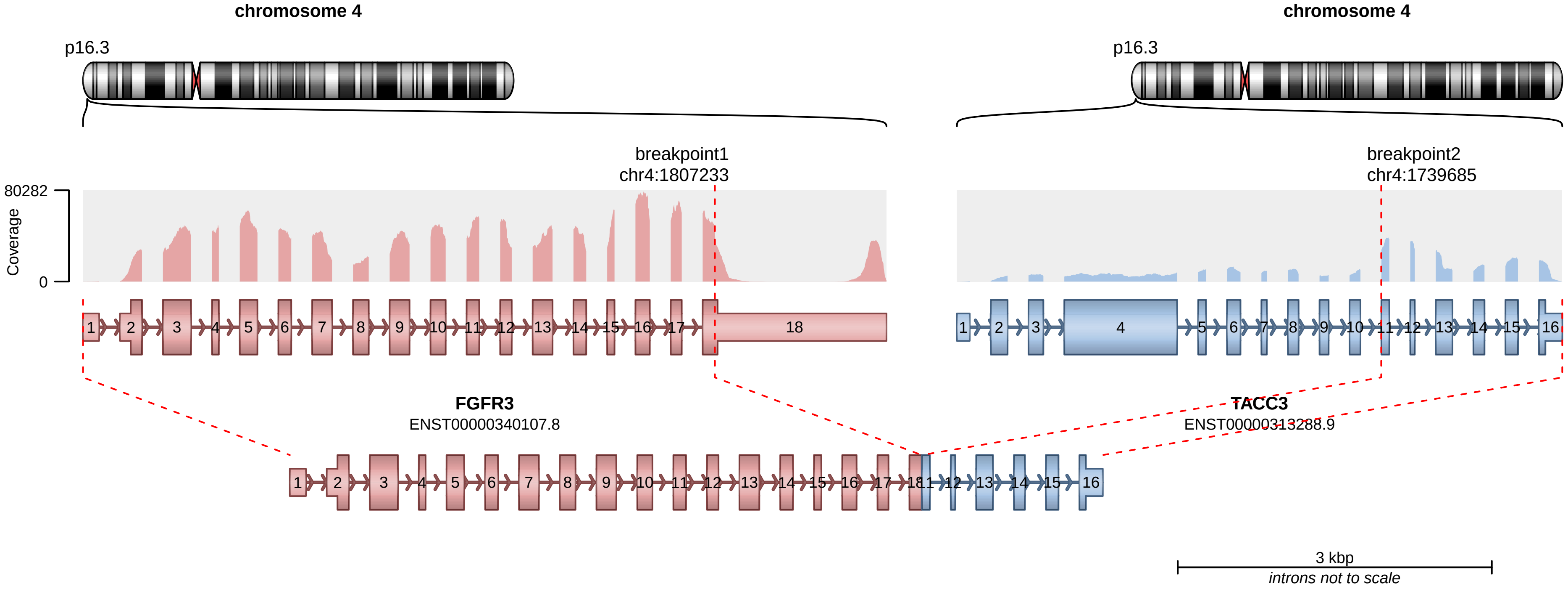


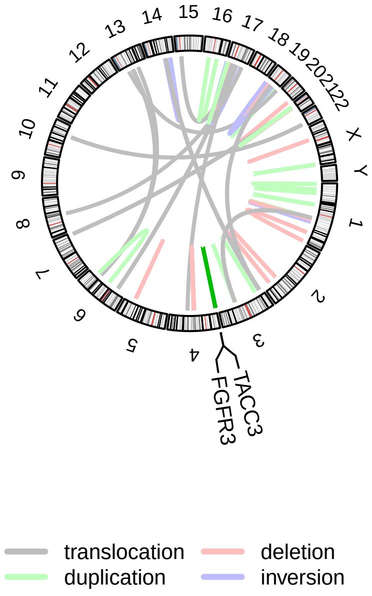




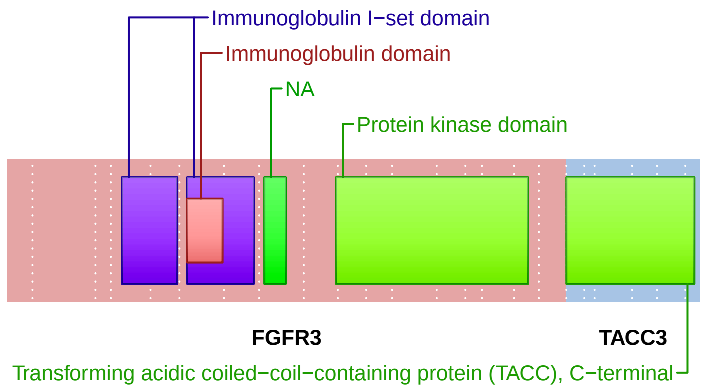
SUPPORTING READ COUNT

Split reads = 2298
Discordant mates = 65



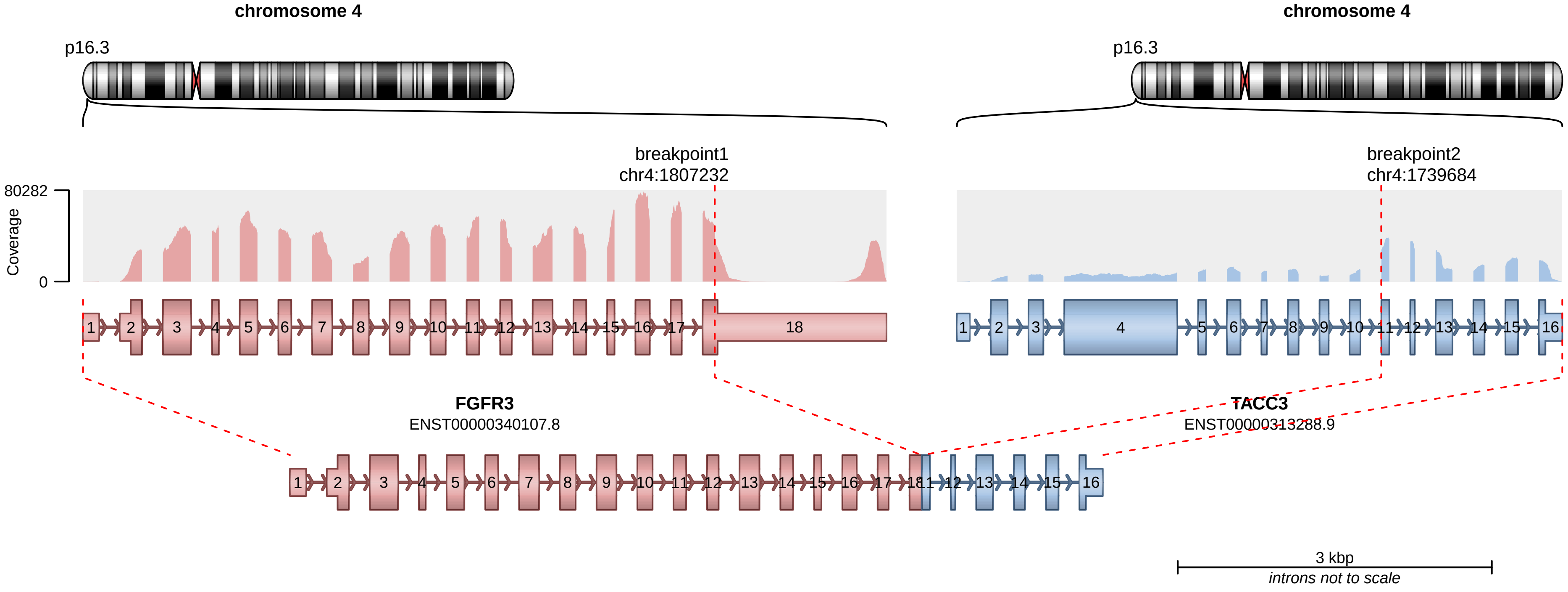


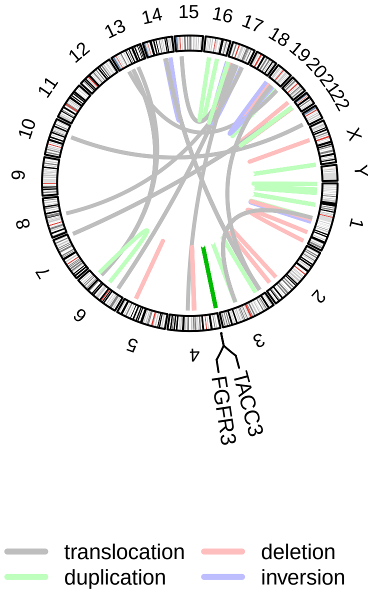
RETAINED PROTEIN DOMAINS
reading frame unclear

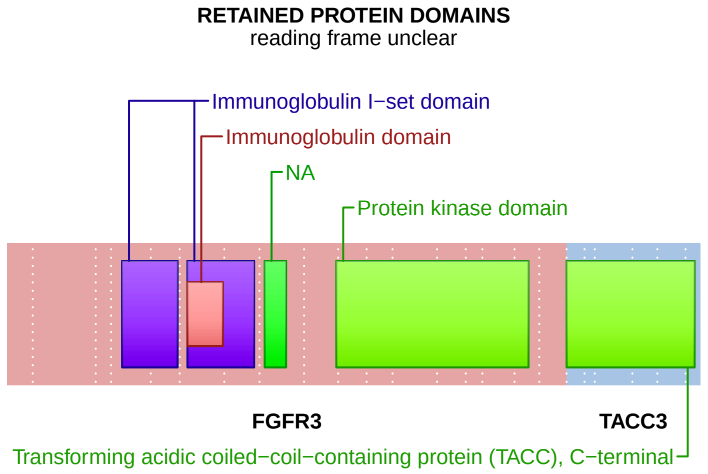


SUPPORTING READ COUNT

Split reads = 26
Discordant mates = 65

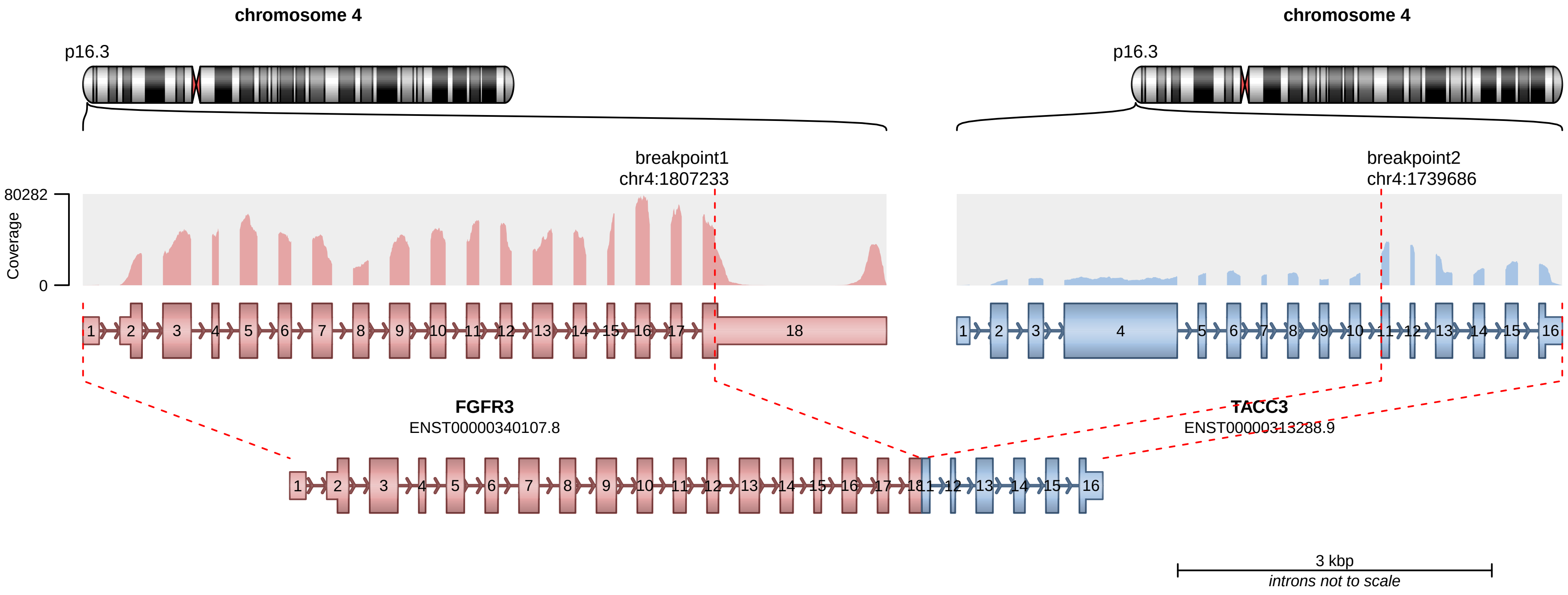


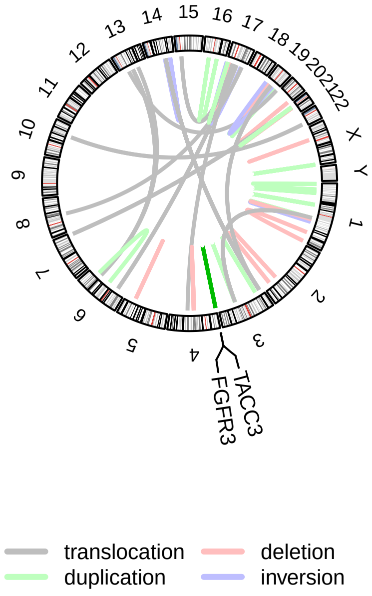




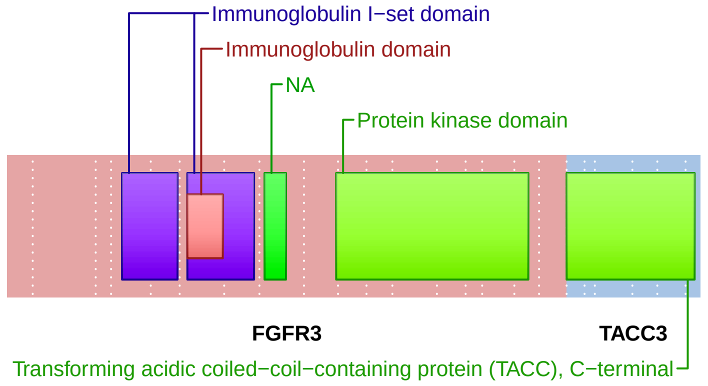
SUPPORTING READ COUNT

Split reads = 26
Discordant mates = 65



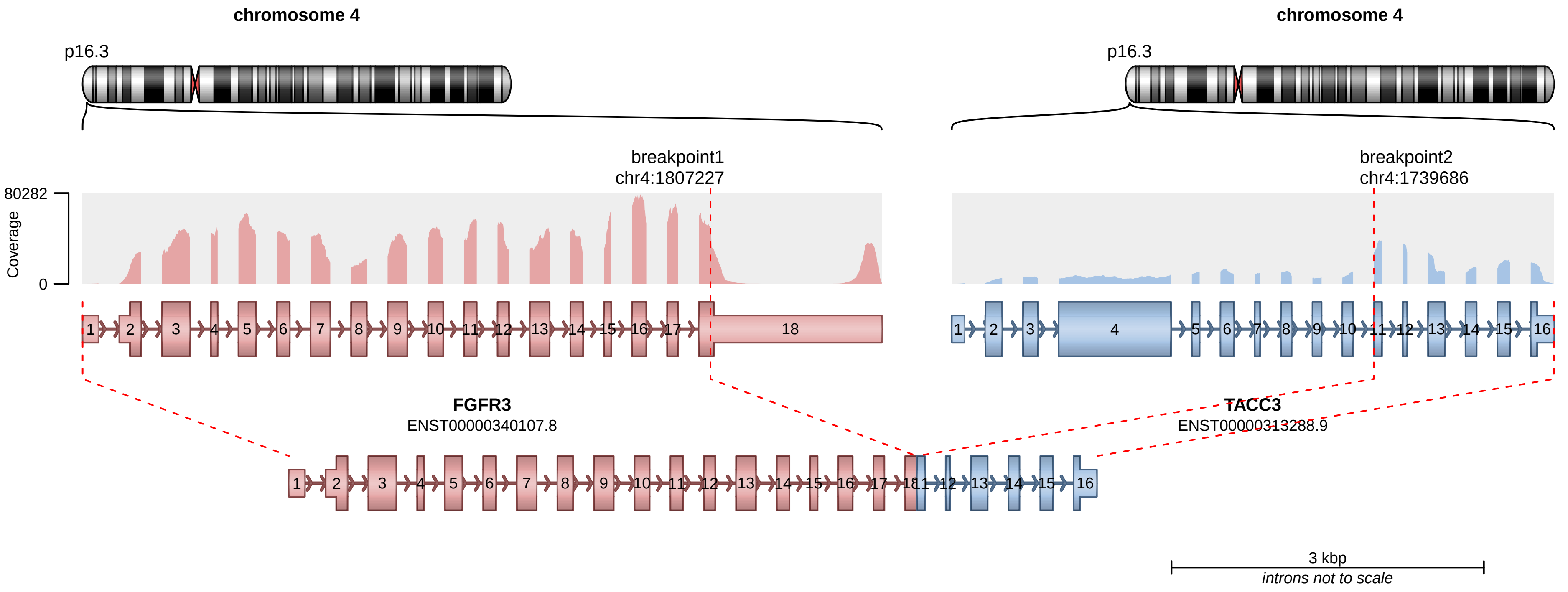


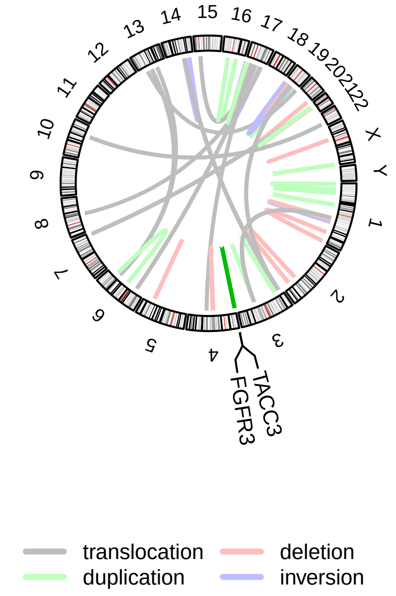
RETAINED PROTEIN DOMAINS
reading frame unclear



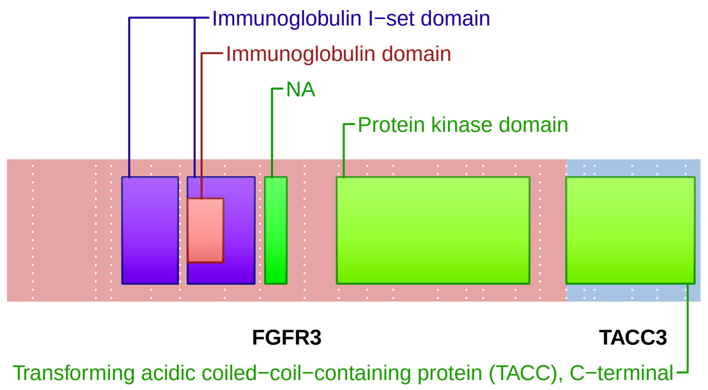
SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 65



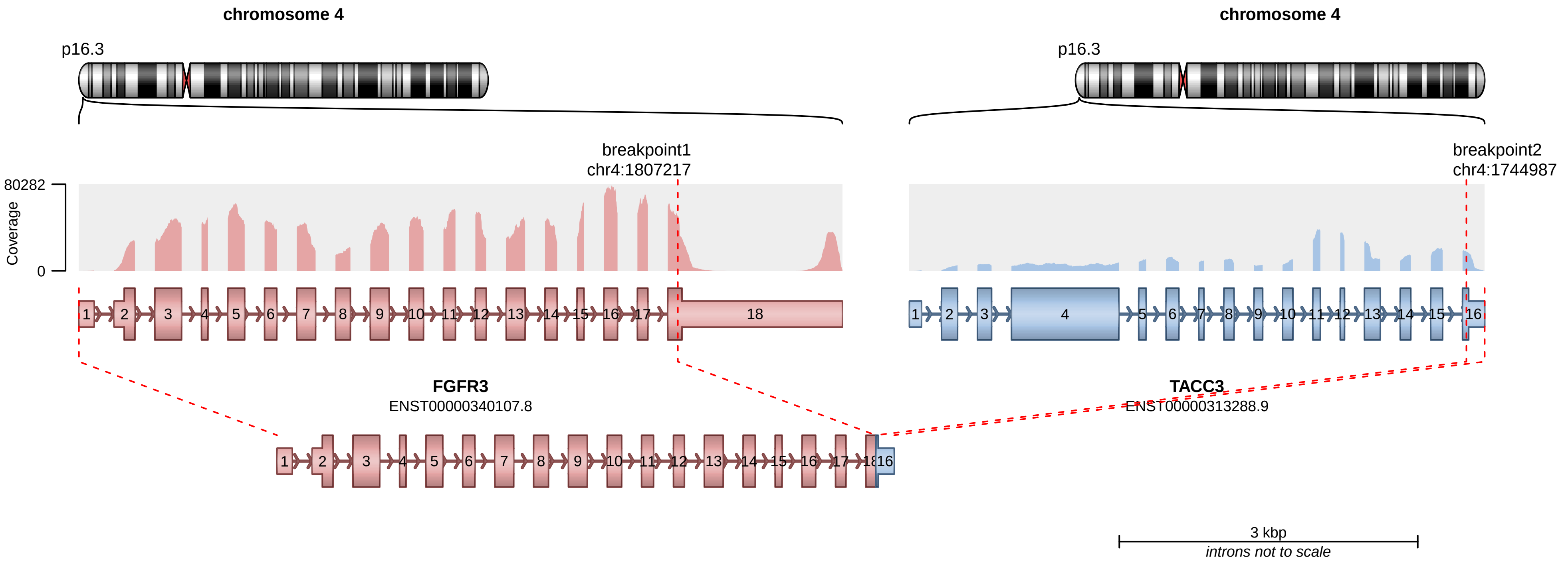


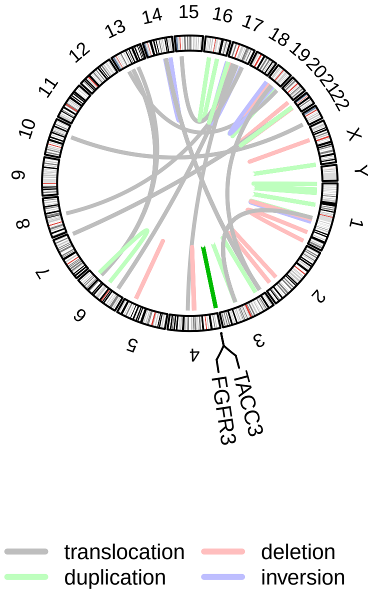
RETAINED PROTEIN DOMAINS
reading frame unclear



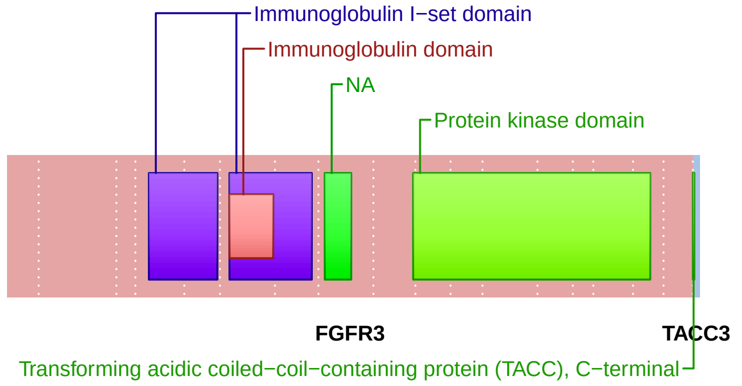
SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 58



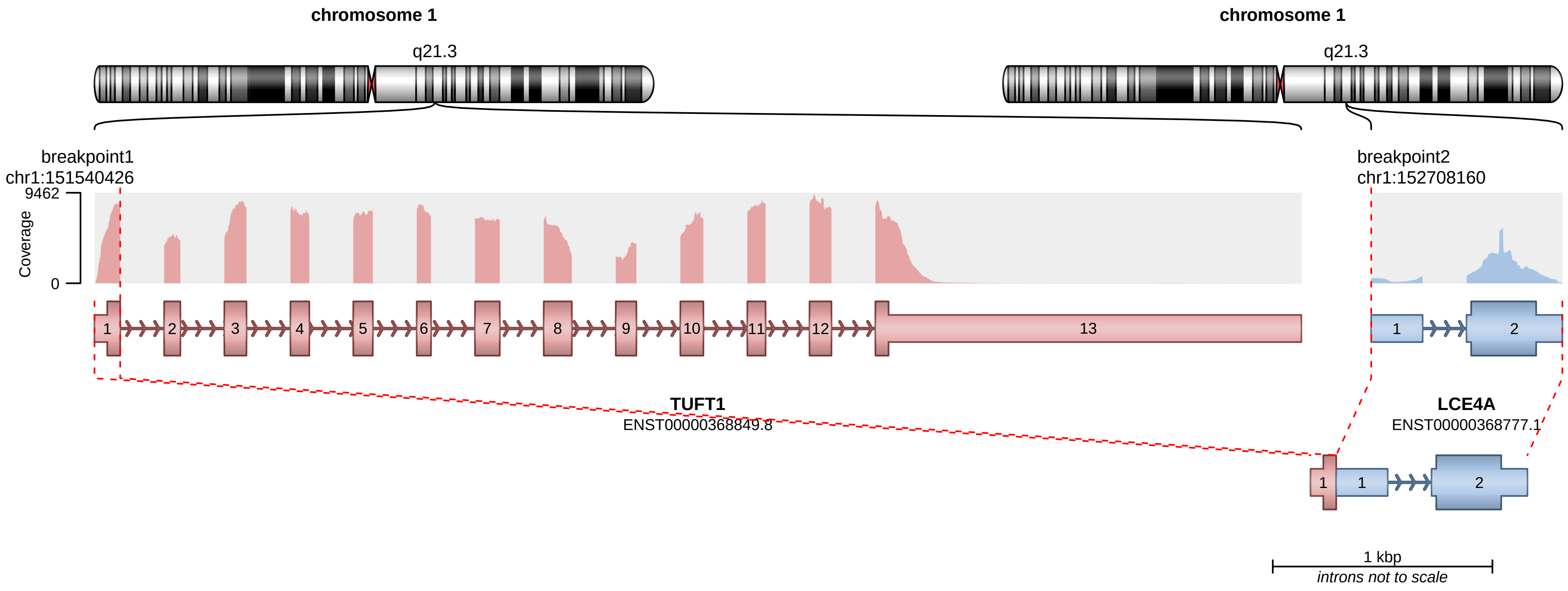


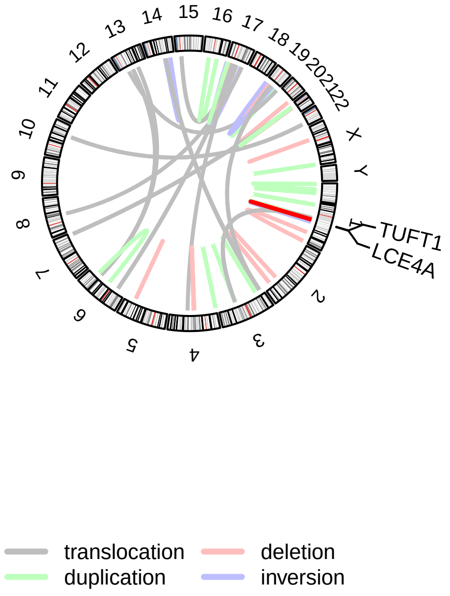
RETAINED PROTEIN DOMAINS
reading frame unclear



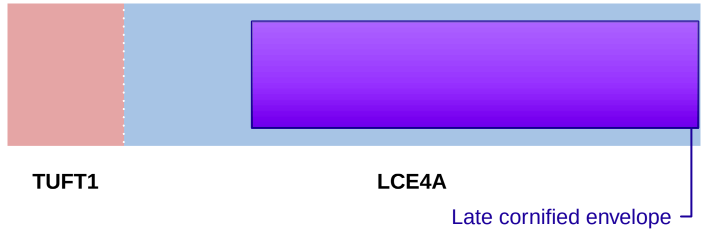
SUPPORTING READ COUNT

Split reads = 19
Discordant mates = 0



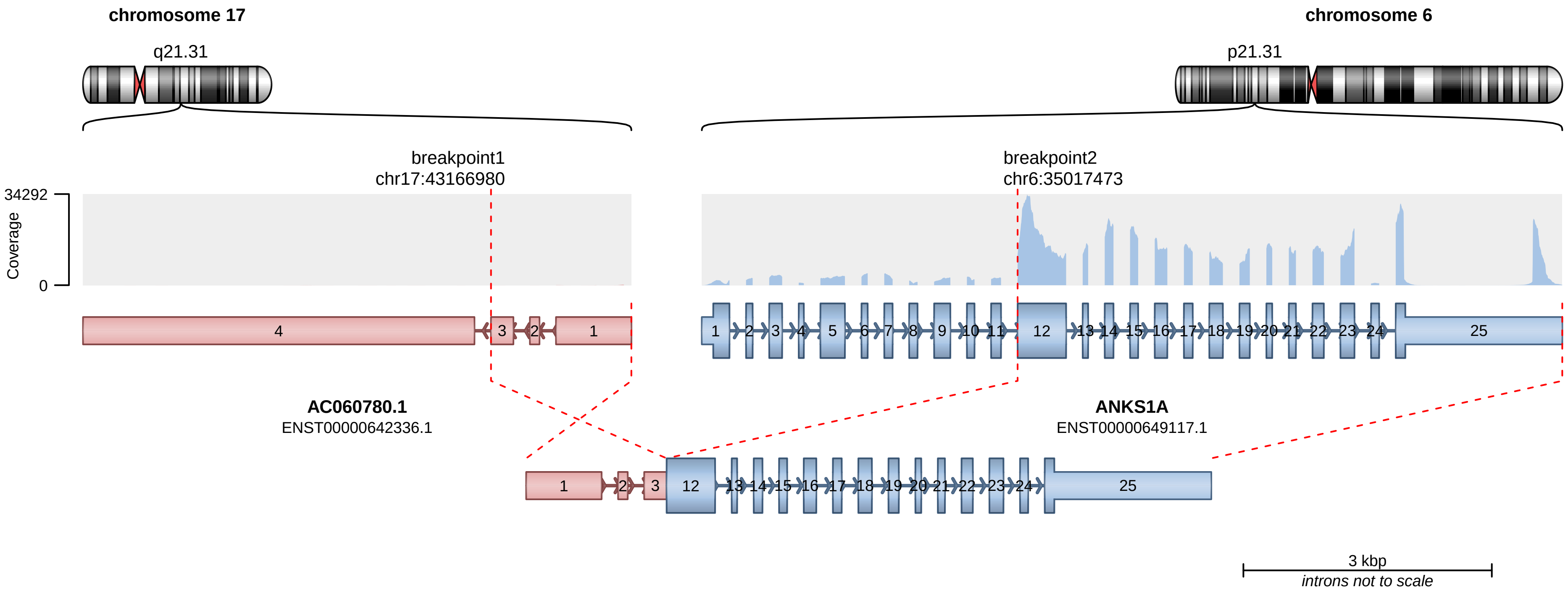


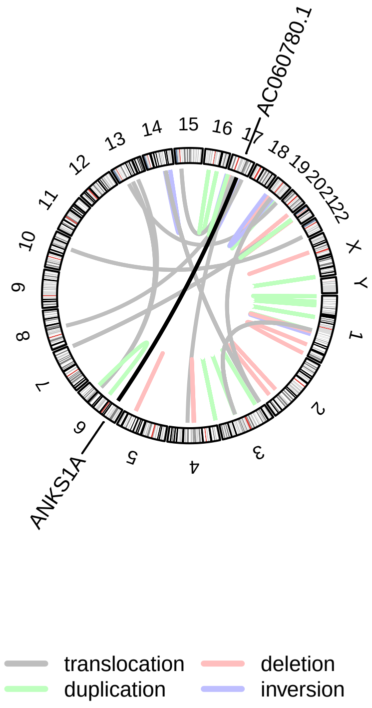
RETAINED PROTEIN DOMAINS
reading frame unclear

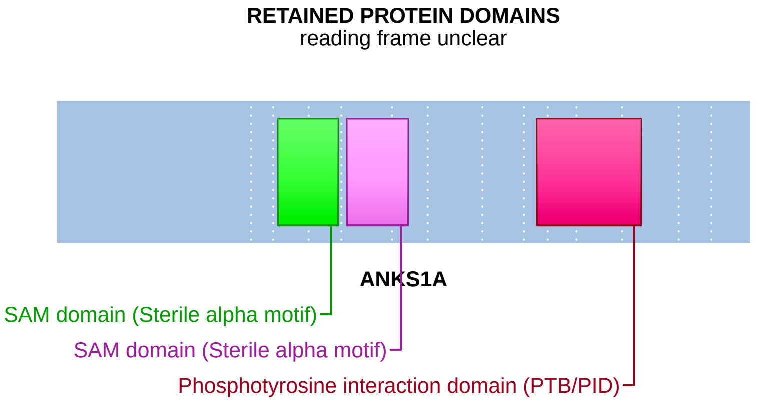


SUPPORTING READ COUNT

Split reads = 430
Discordant mates = 0

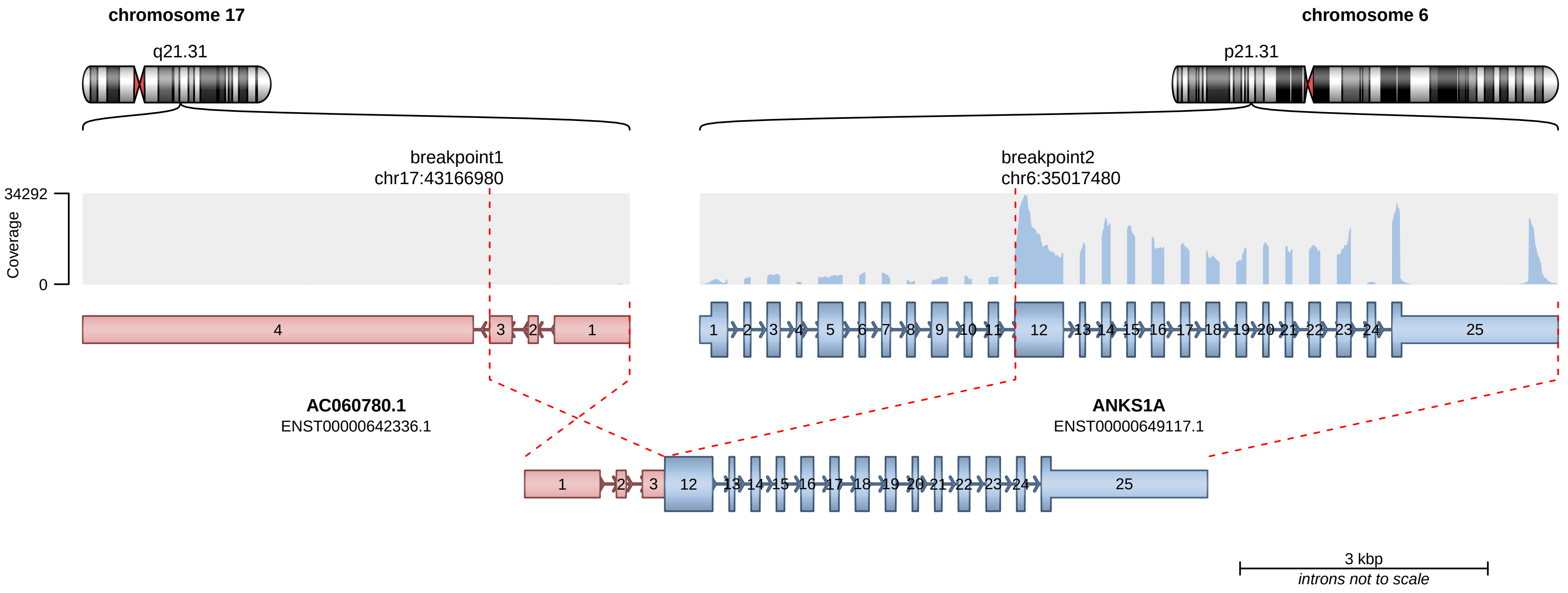


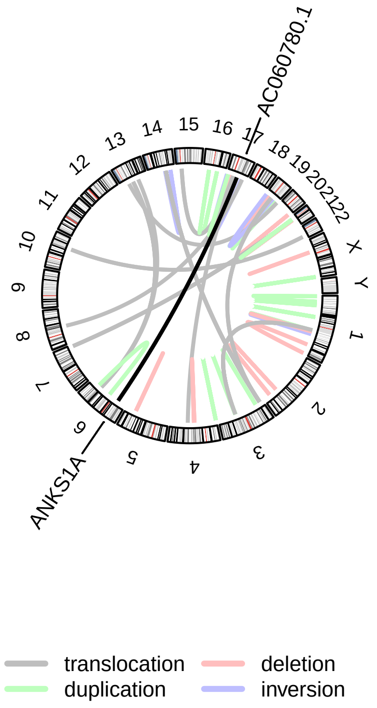


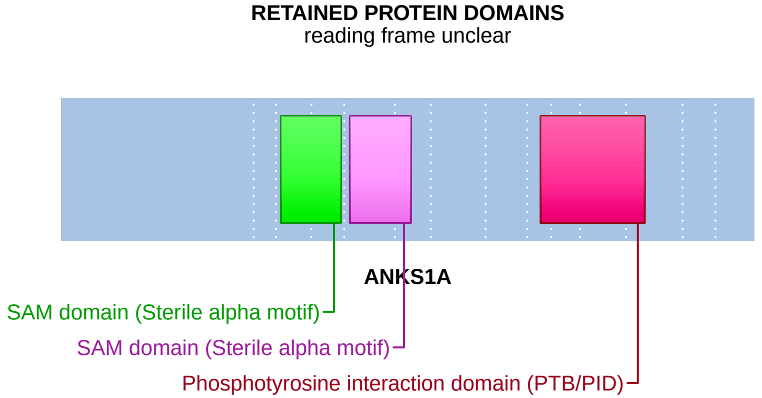


SUPPORTING READ COUNT

Split reads = 298
Discordant mates = 0

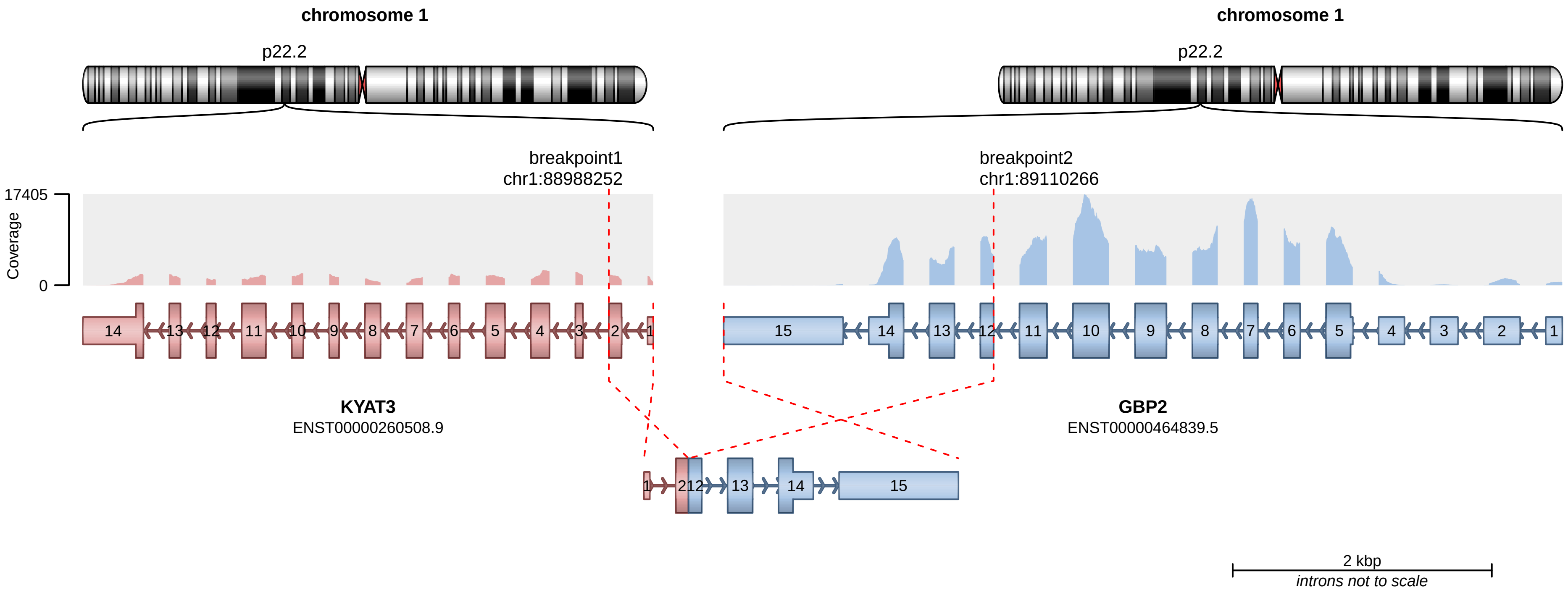


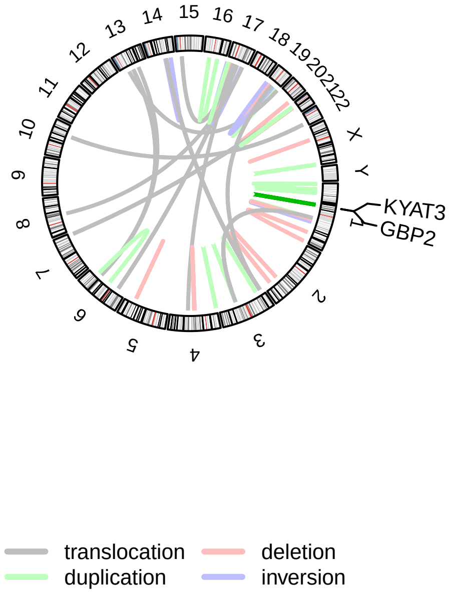


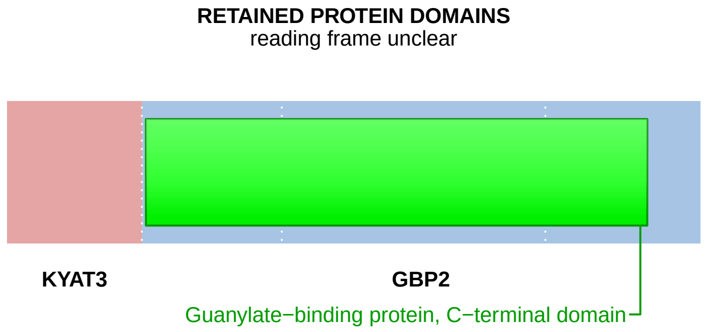


SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 0

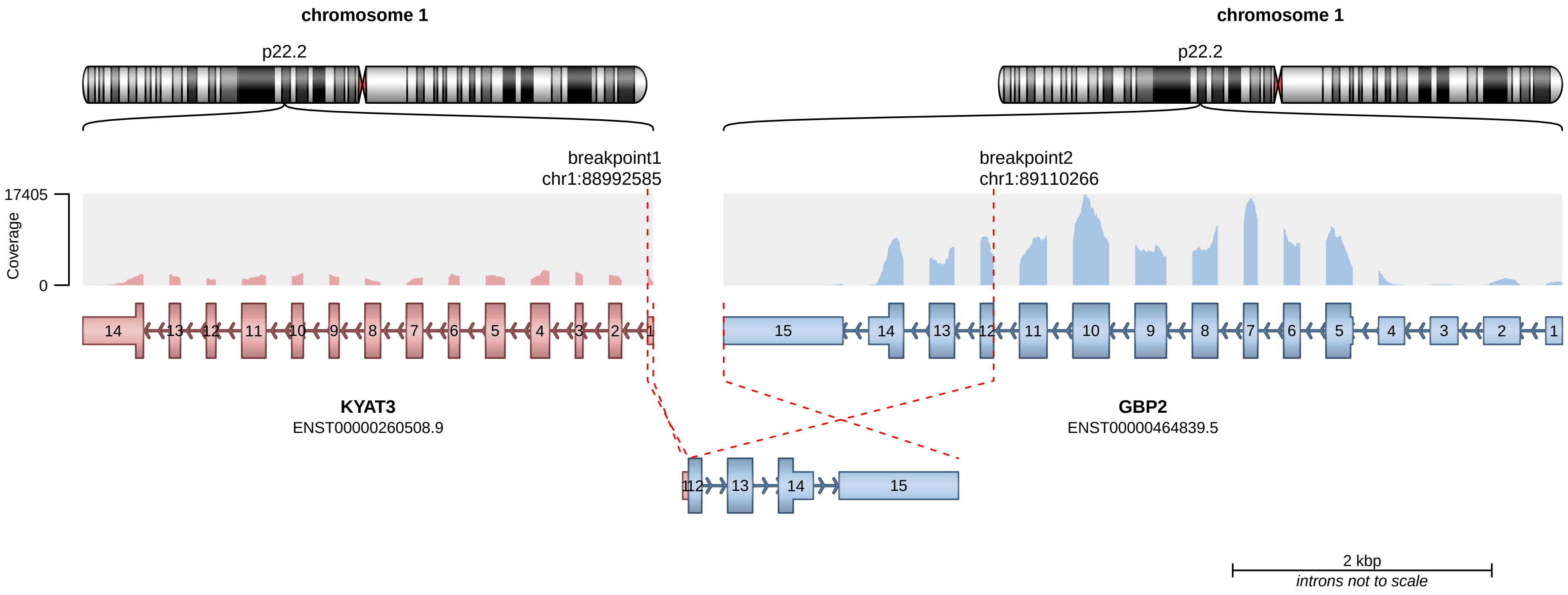


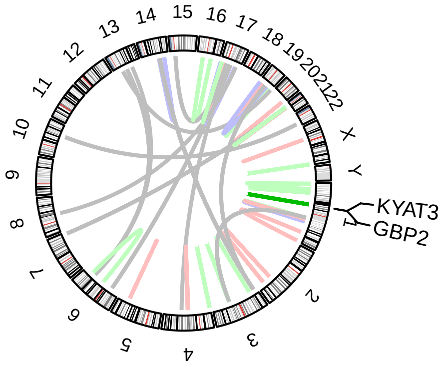




SUPPORTING READ COUNT

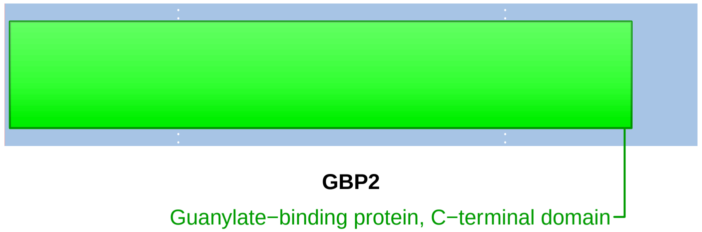
Split reads = 180
Discordant mates = 1





RETAINED PROTEIN DOMAINS

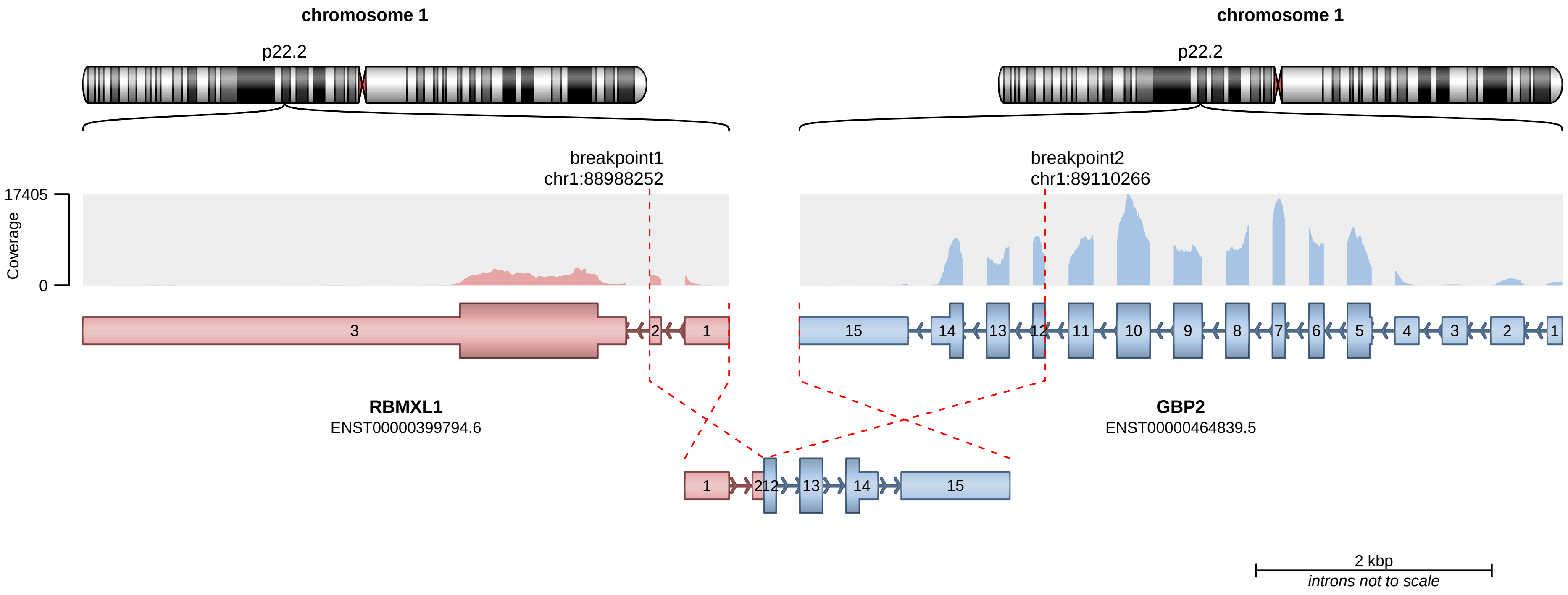
reading frame unclear

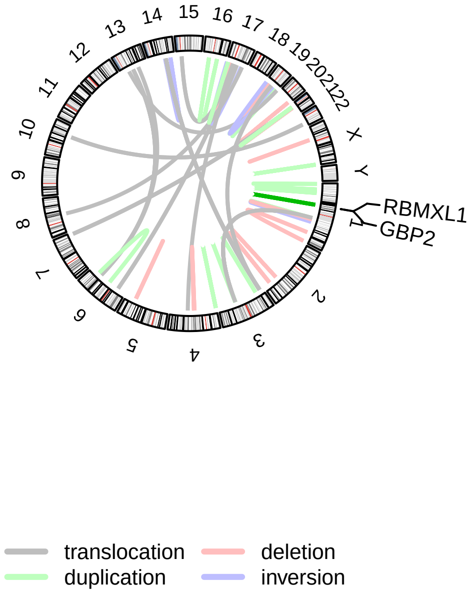


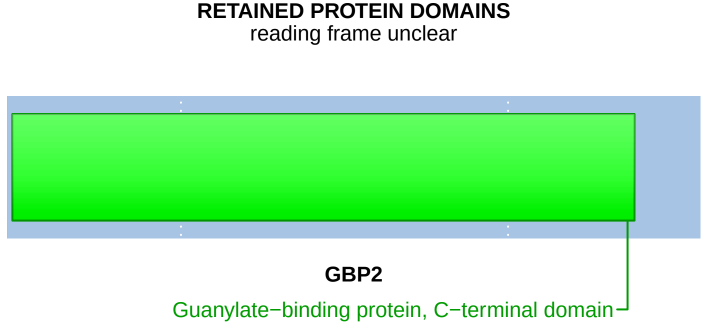
SUPPORTING READ COUNT

Split reads = 17
Discordant mates = 0

▬ translocation ▬ deletion
▬ duplication ▬ inversion

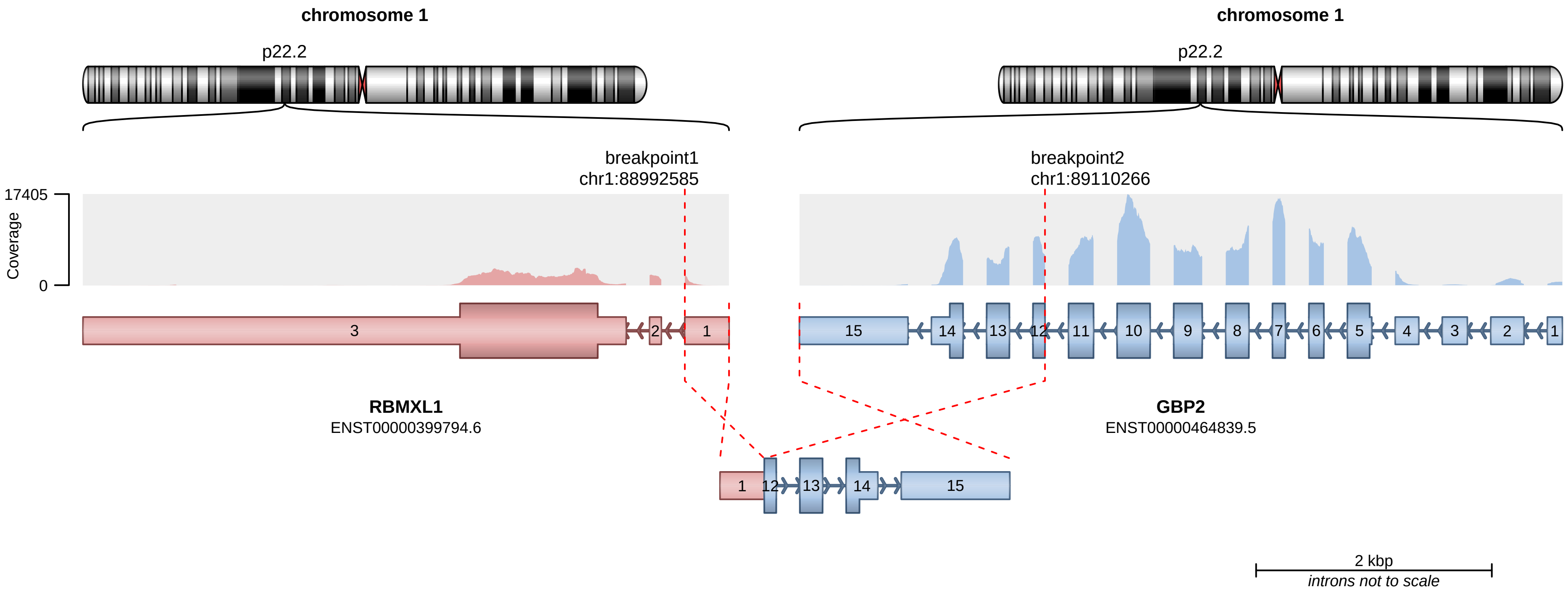


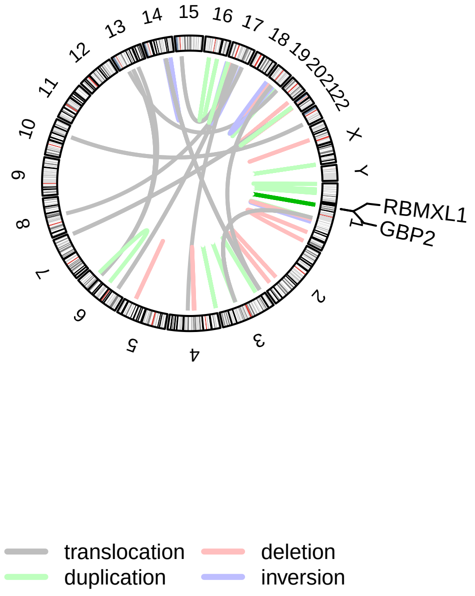




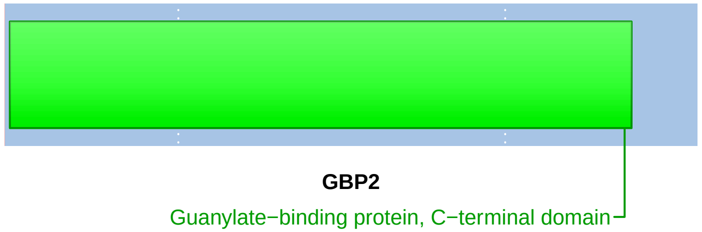
SUPPORTING READ COUNT

Split reads = 180
Discordant mates = 1



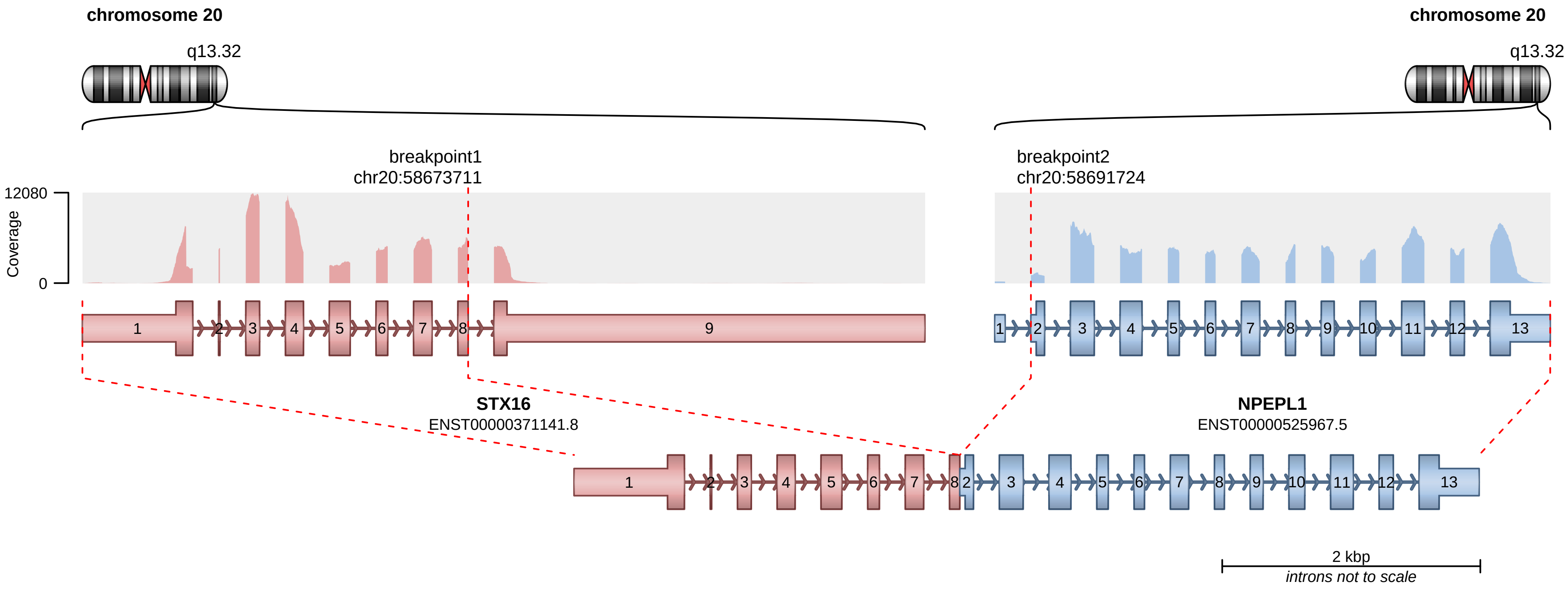


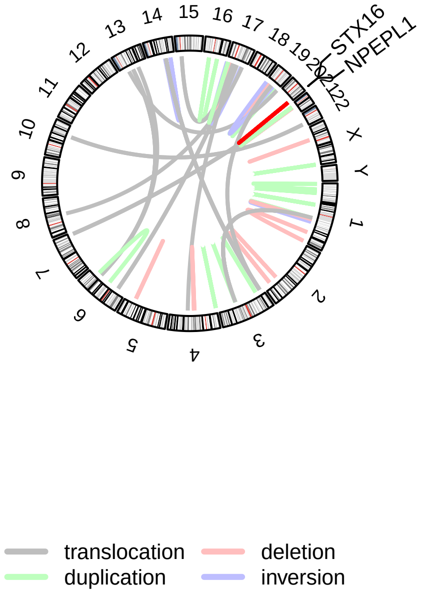
RETAINED PROTEIN DOMAINS
reading frame unclear

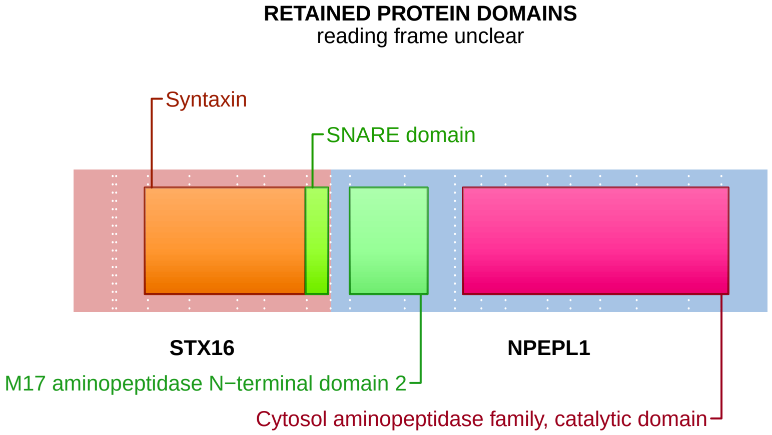


SUPPORTING READ COUNT

Split reads = 17
Discordant mates = 0

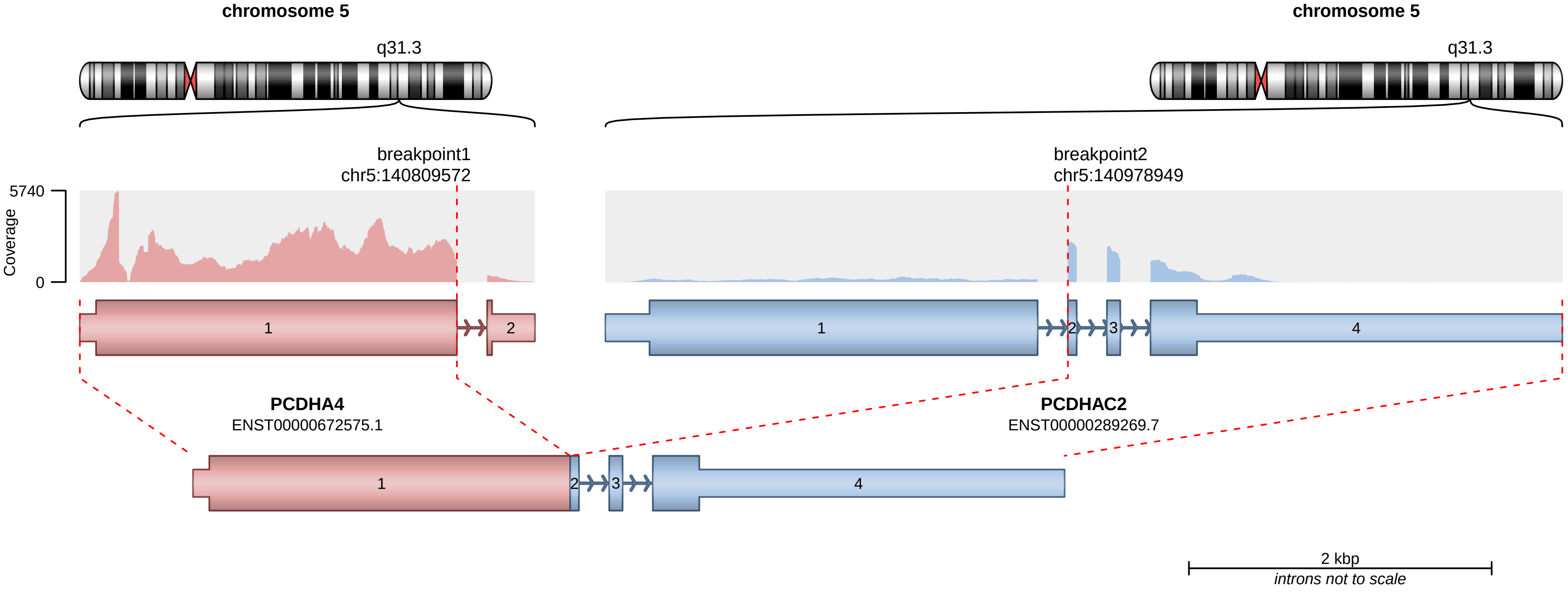


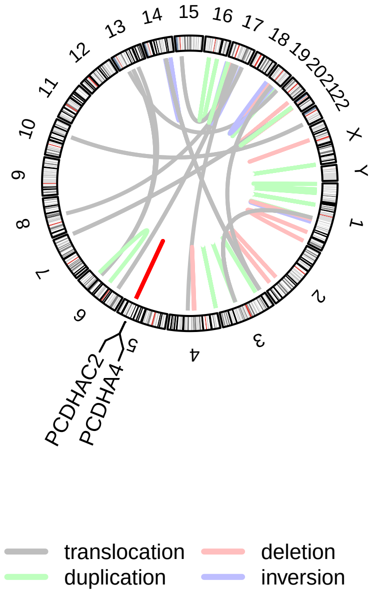


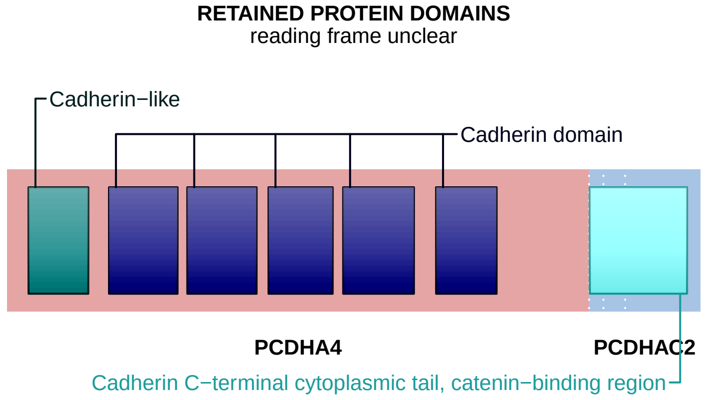


SUPPORTING READ COUNT

Split reads = 166
Discordant mates = 7

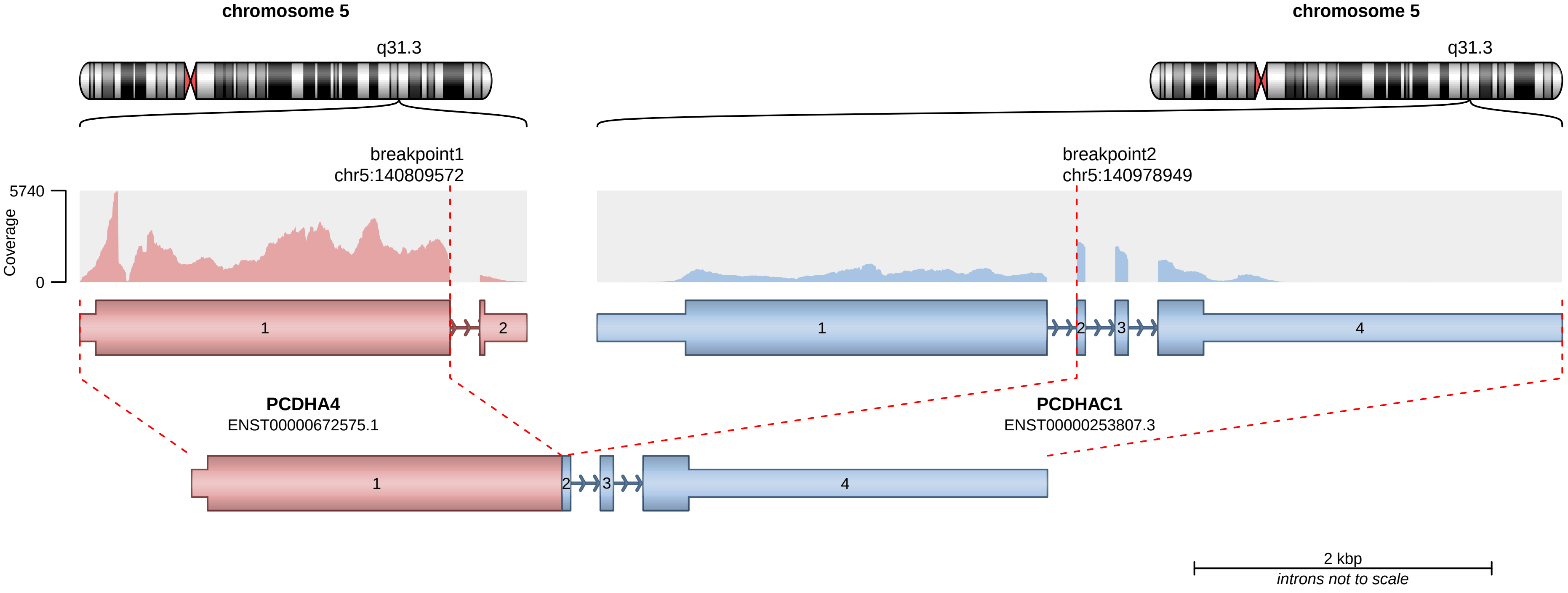


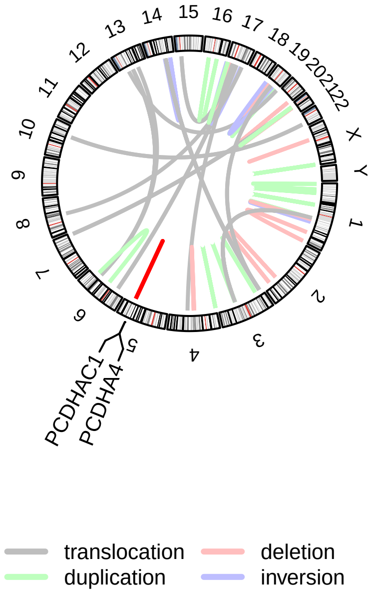


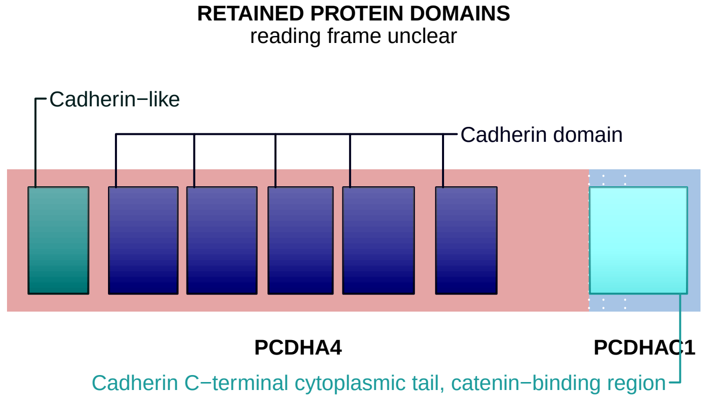


SUPPORTING READ COUNT

Split reads = 156
Discordant mates = 0

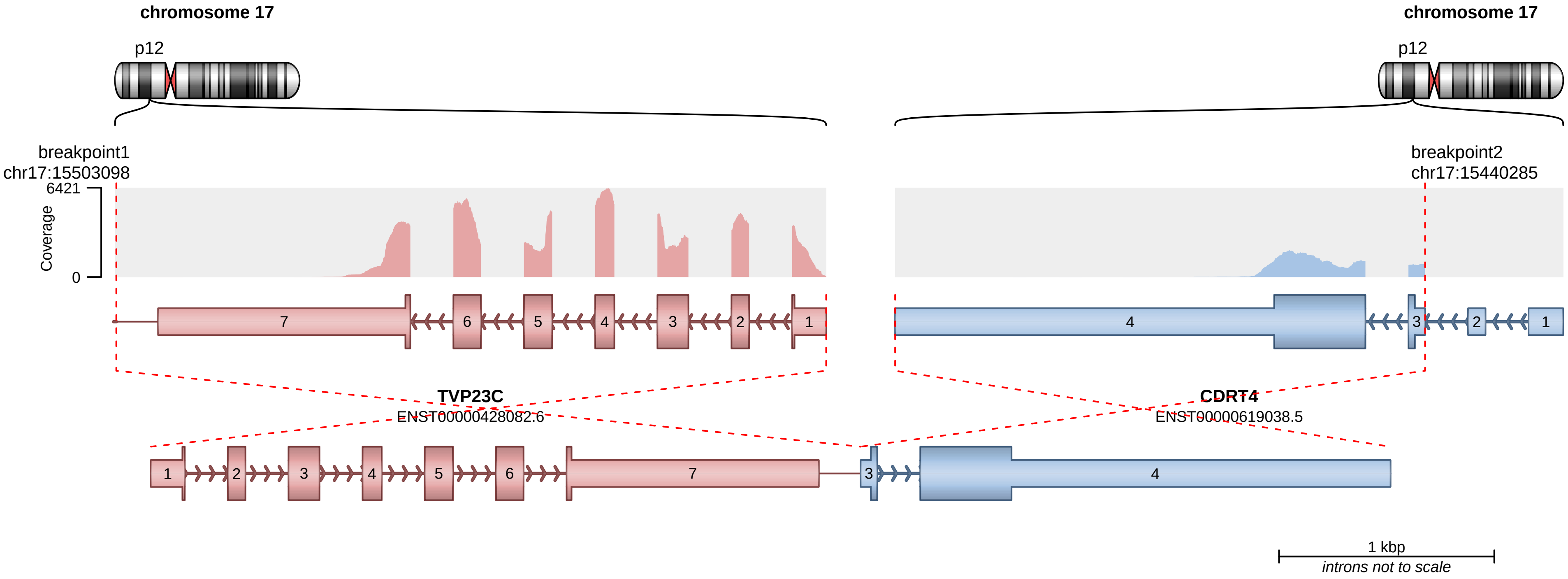


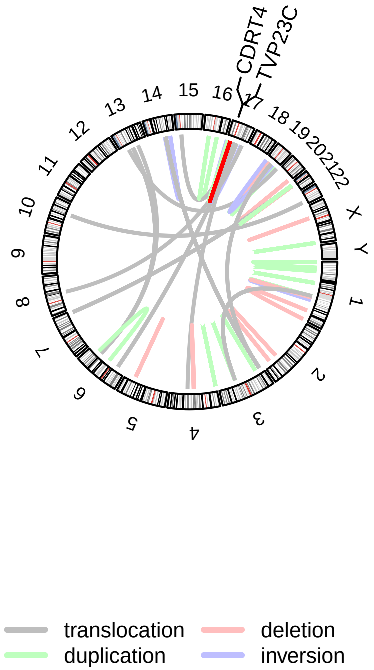




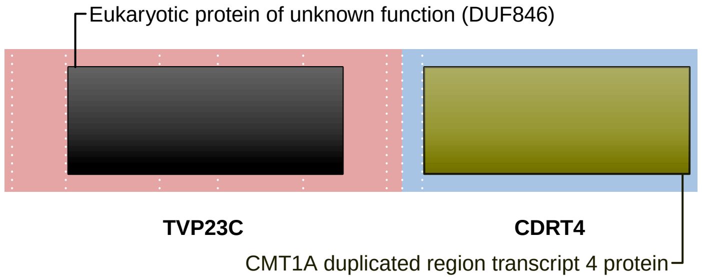
SUPPORTING READ COUNT

Split reads = 155
Discordant mates = 0



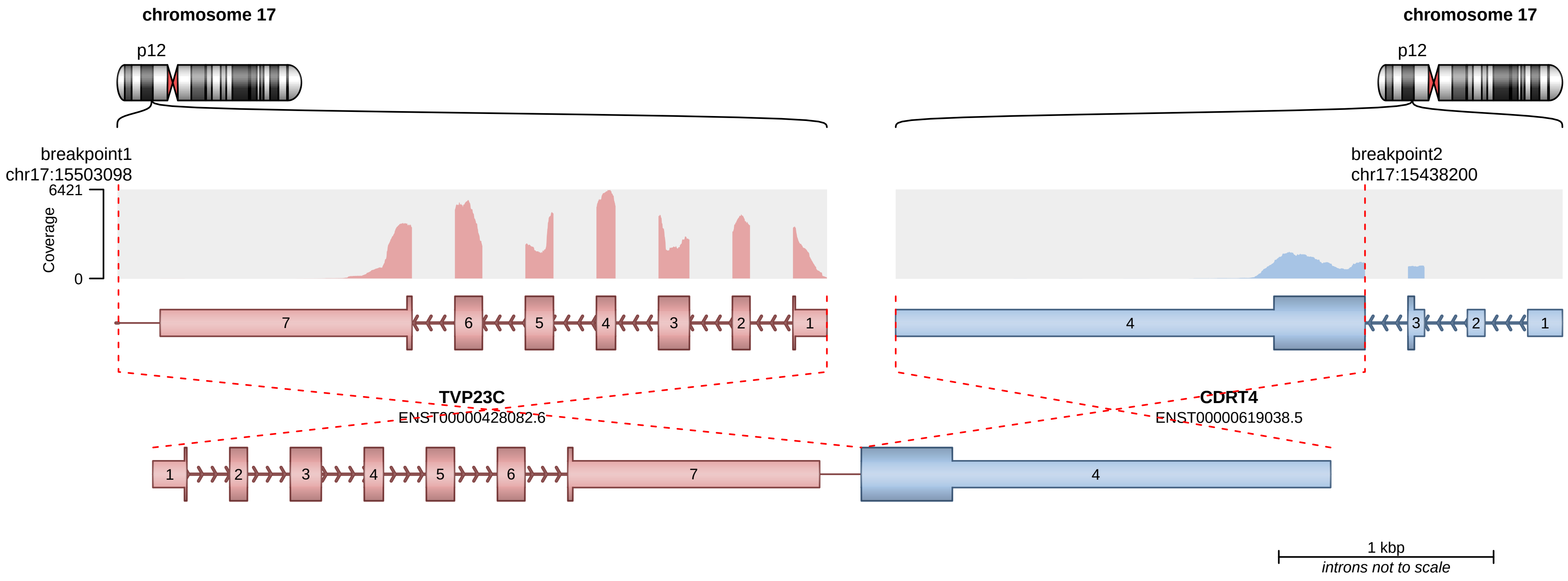


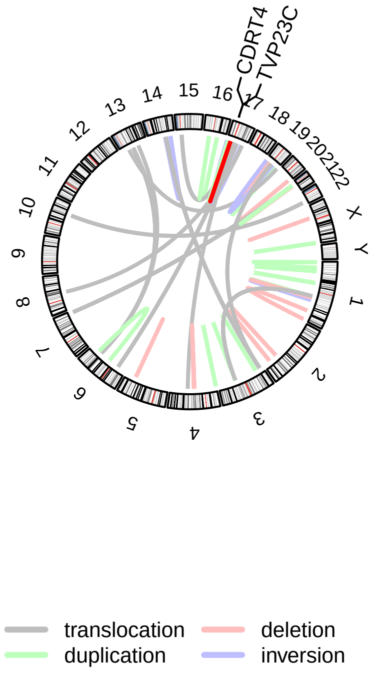
RETAINED PROTEIN DOMAINS
reading frame unclear



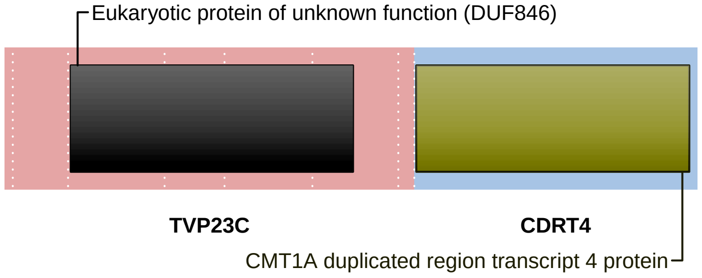
SUPPORTING READ COUNT

Split reads = 134
Discordant mates = 1



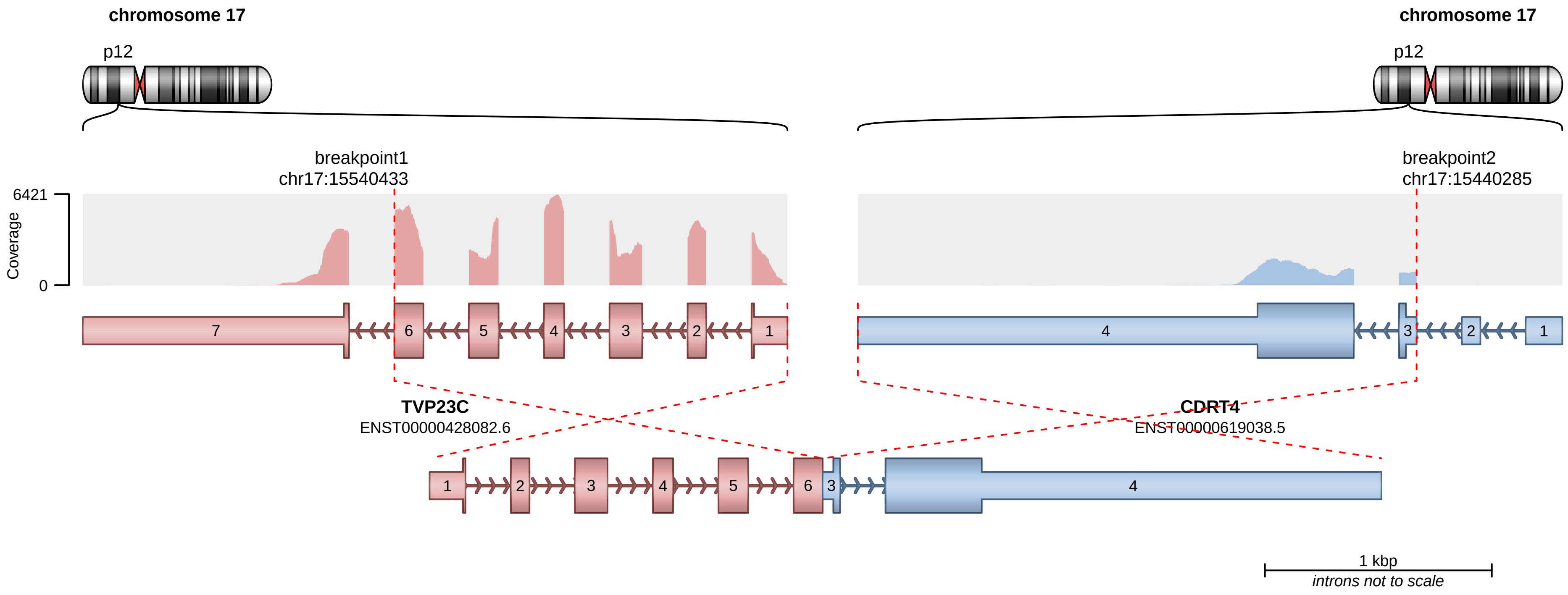


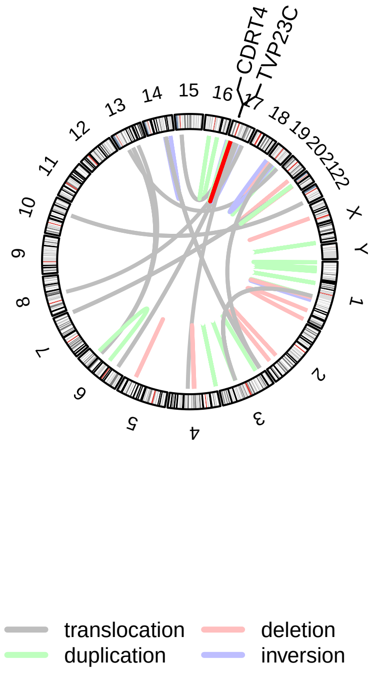
RETAINED PROTEIN DOMAINS
reading frame unclear

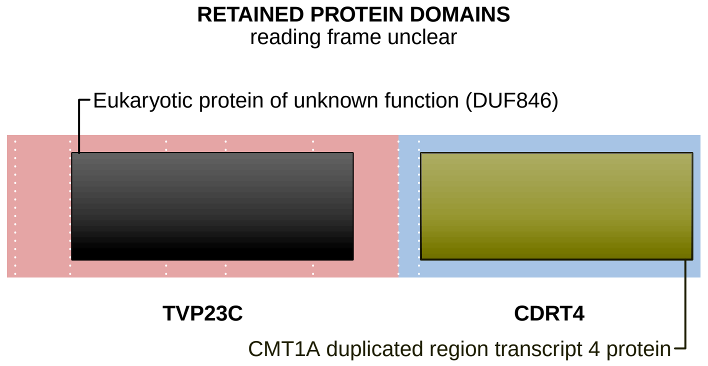


SUPPORTING READ COUNT

Split reads = 56
Discordant mates = 1

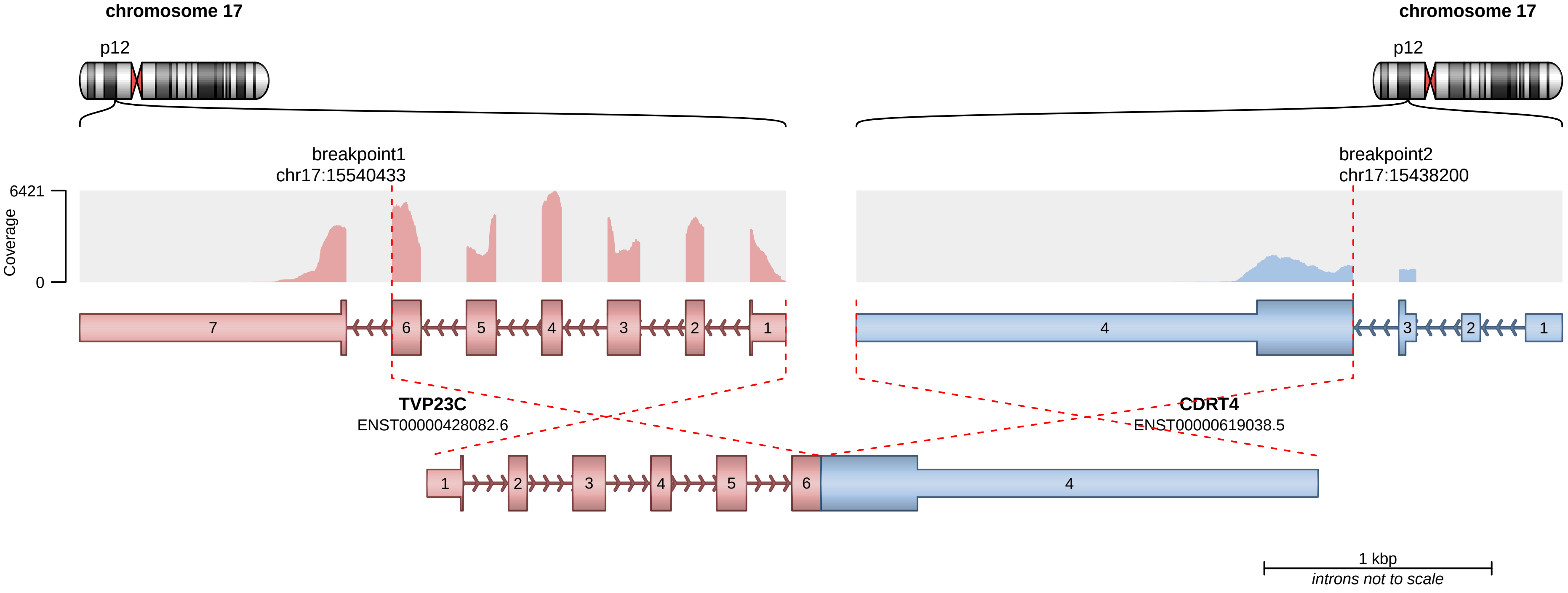


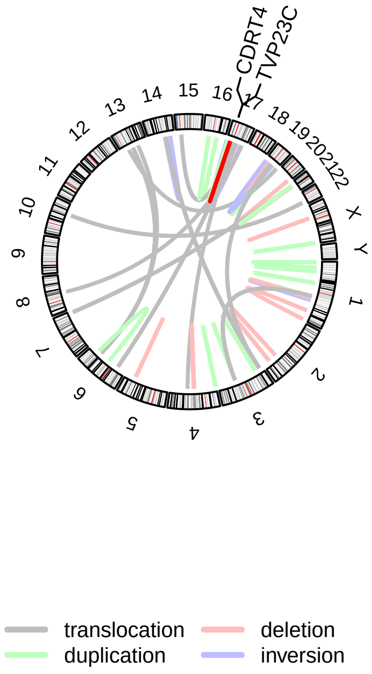




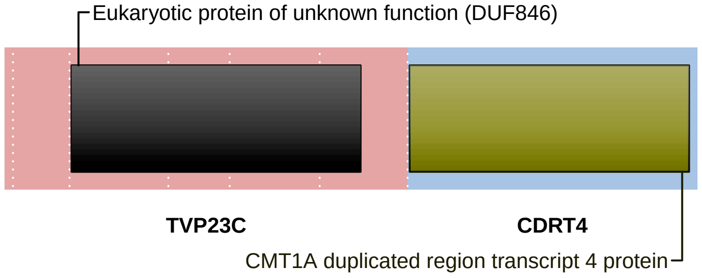
SUPPORTING READ COUNT

Split reads = 36
Discordant mates = 1



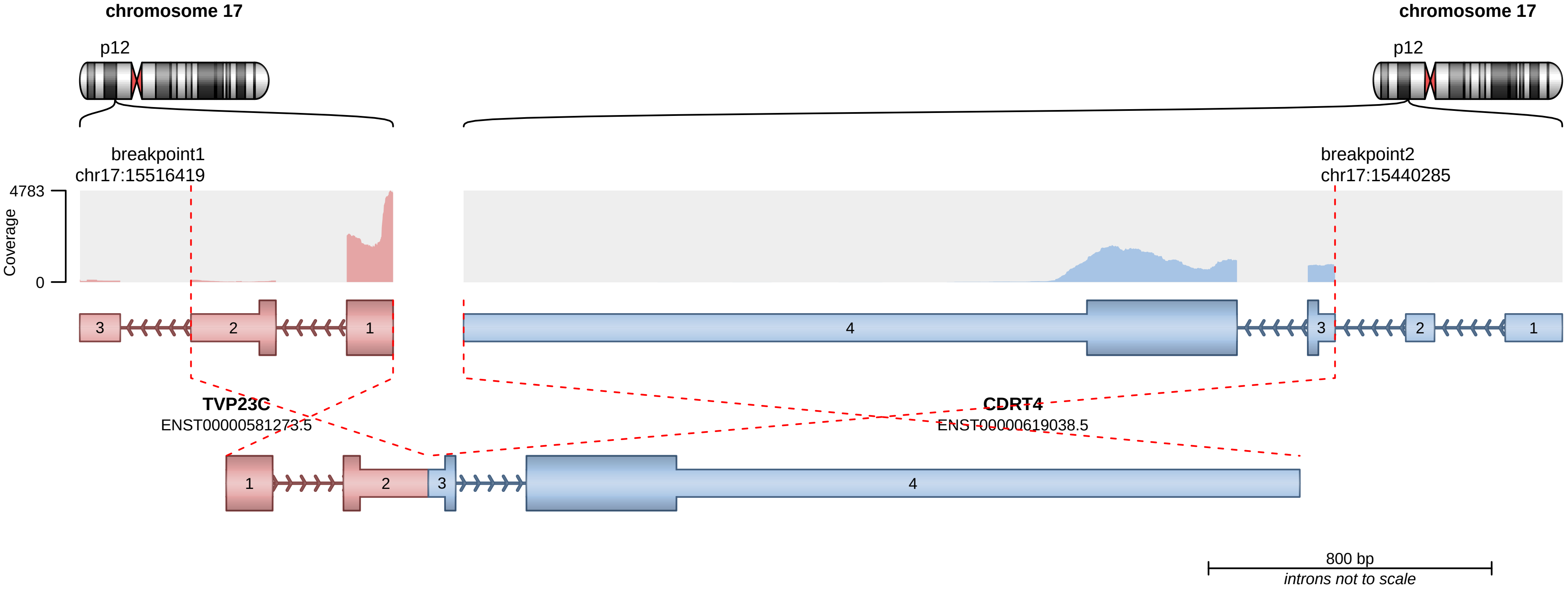


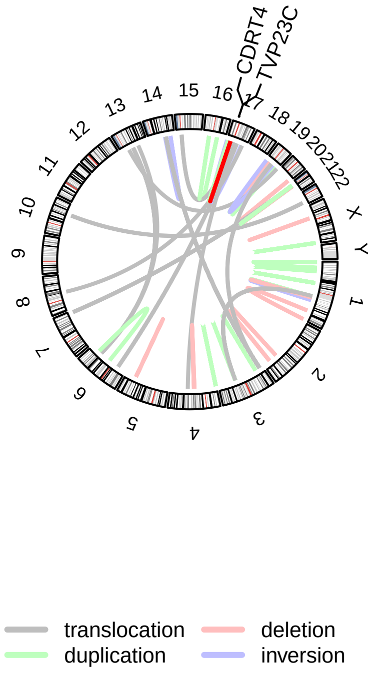
RETAINED PROTEIN DOMAINS
reading frame unclear



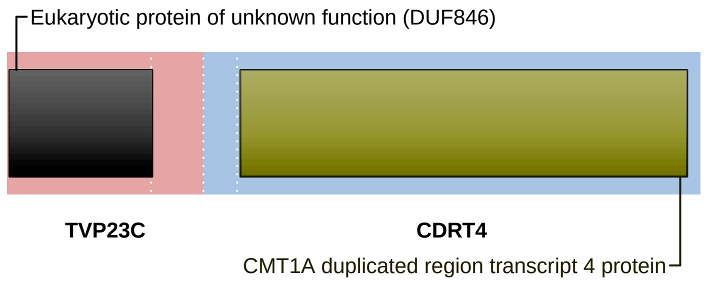
SUPPORTING READ COUNT

Split reads = 13
Discordant mates = 1



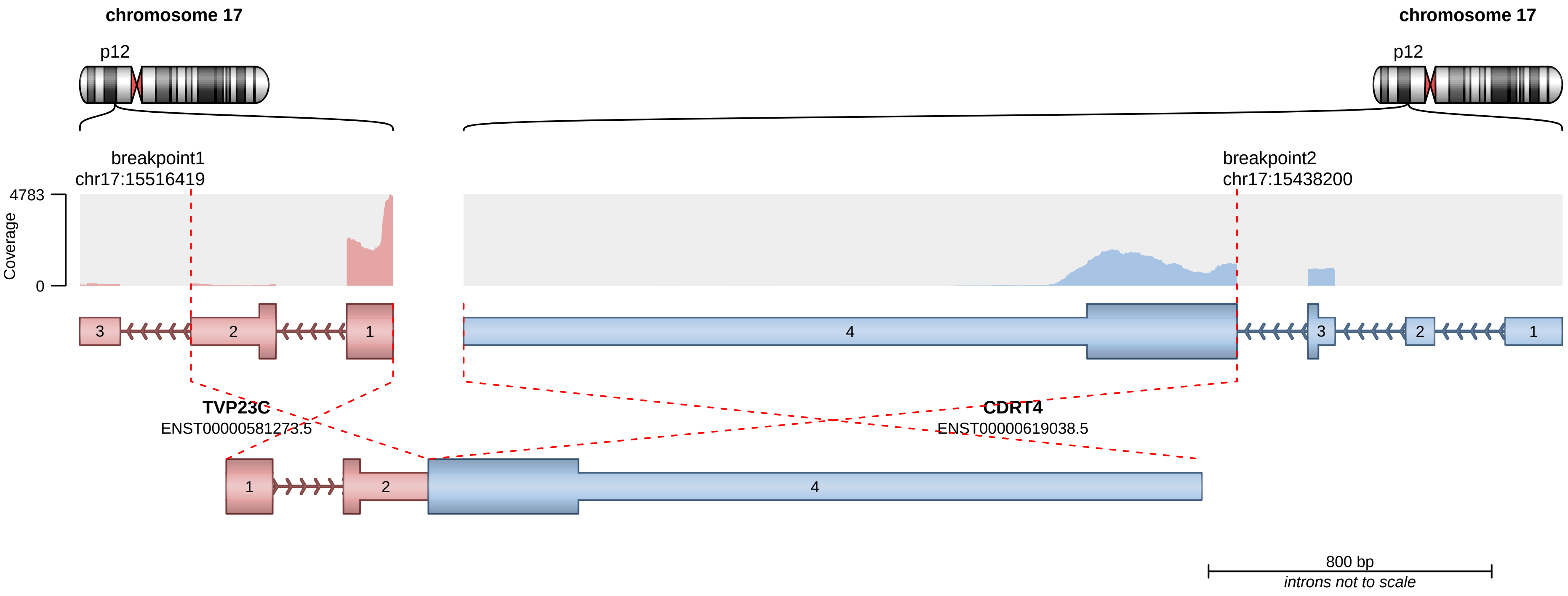


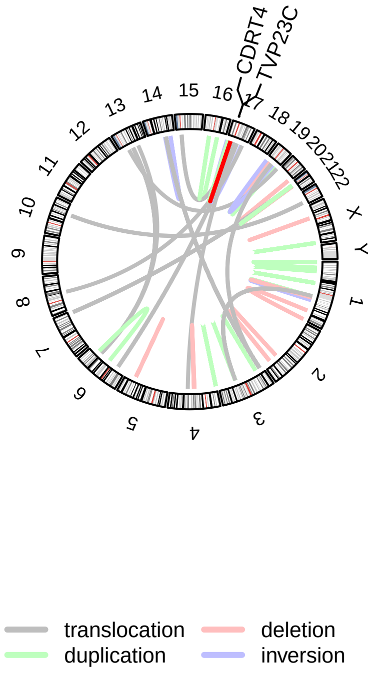
RETAINED PROTEIN DOMAINS
reading frame unclear



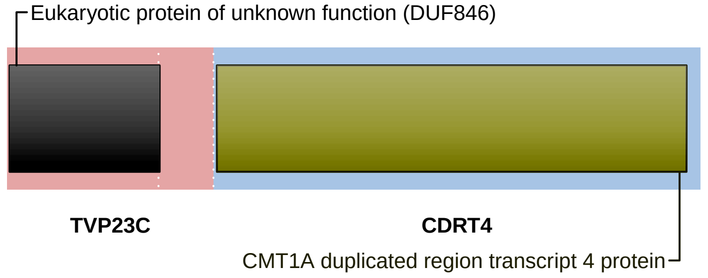
SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 1



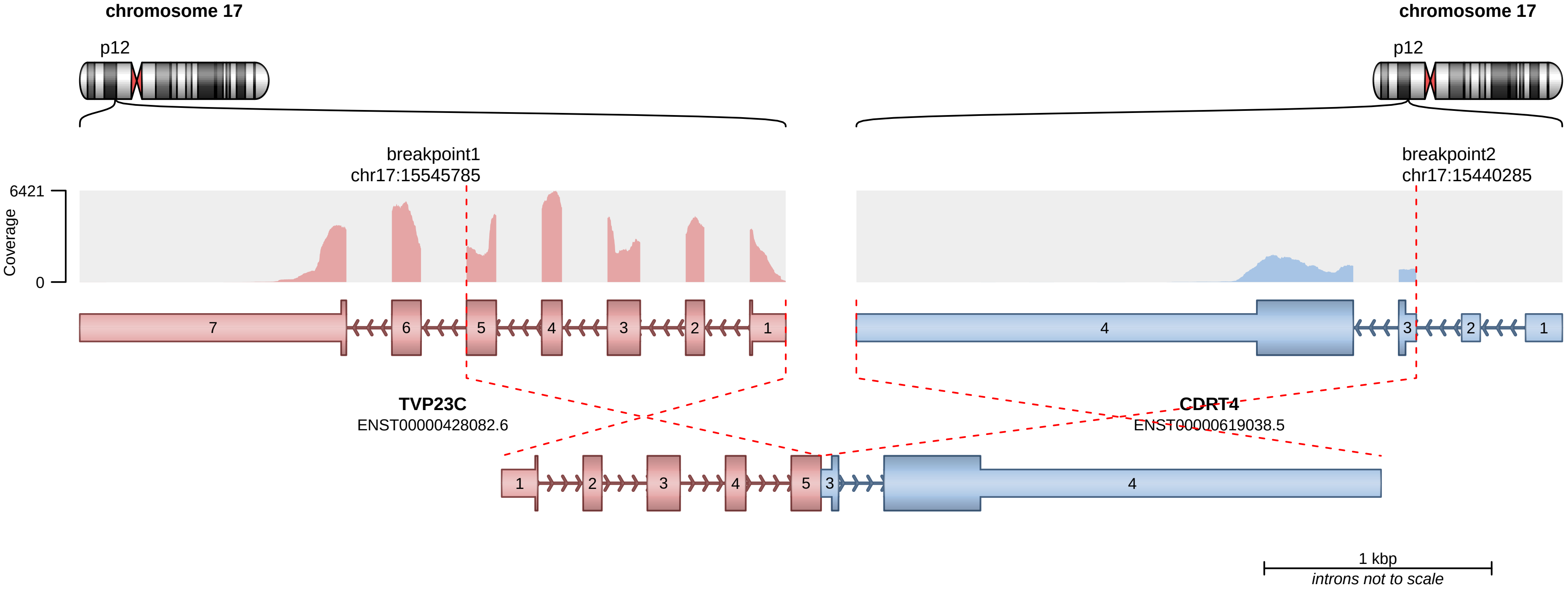


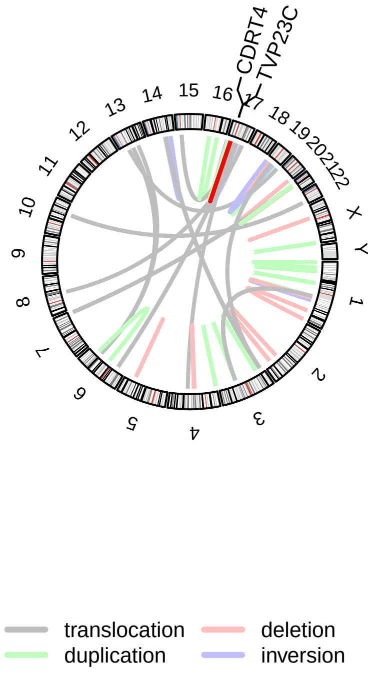
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

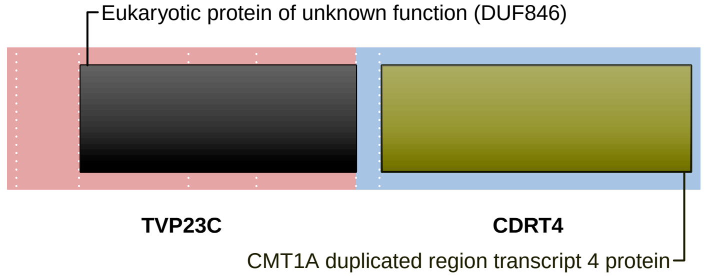
Split reads = 4
Discordant mates = 1





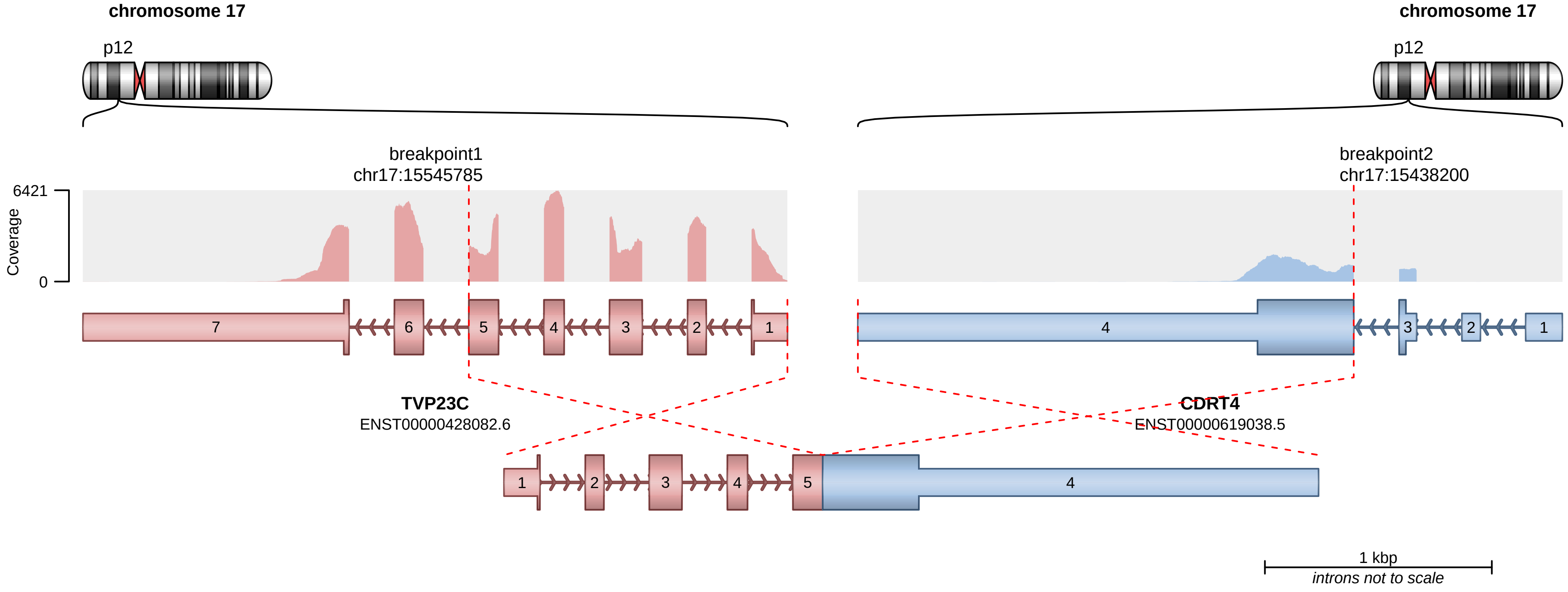
RETAINED PROTEIN DOMAINS

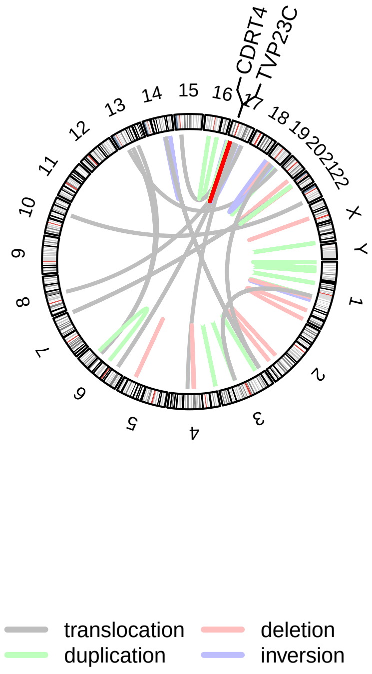
reading frame unclear



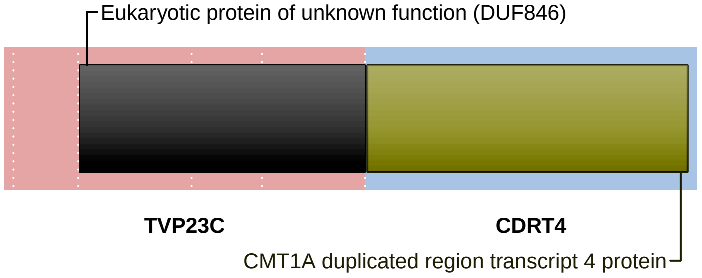
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 1



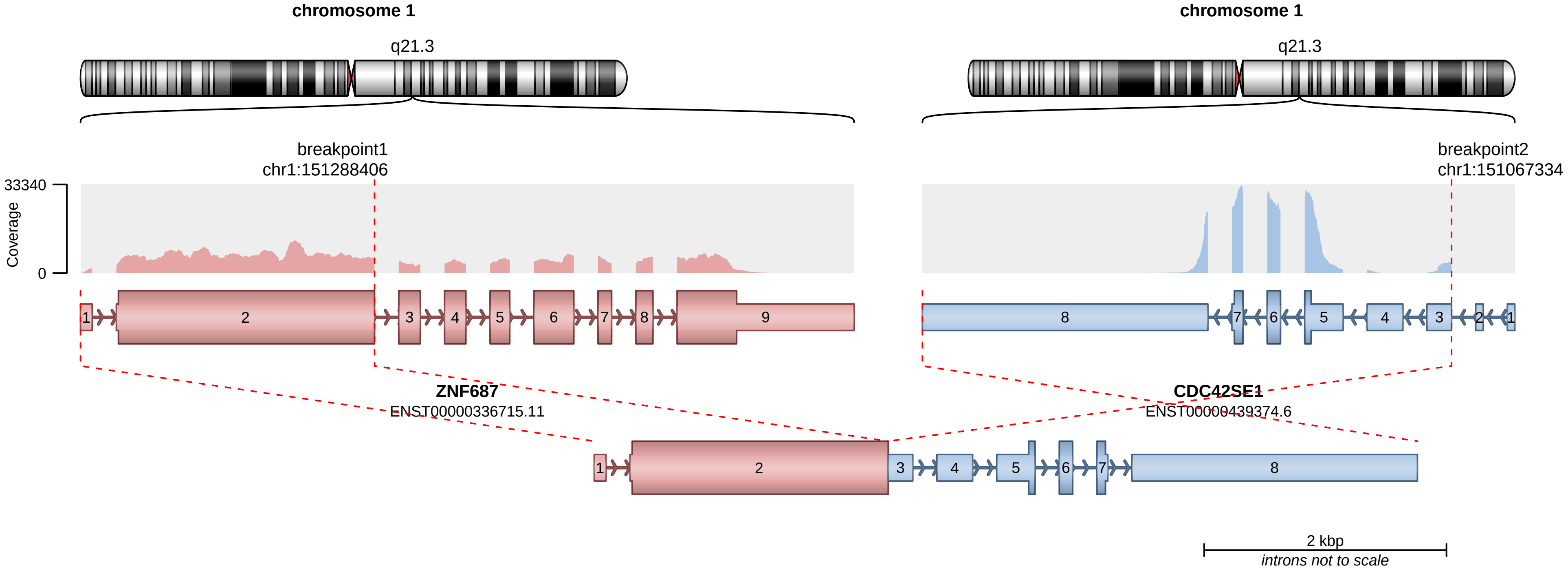


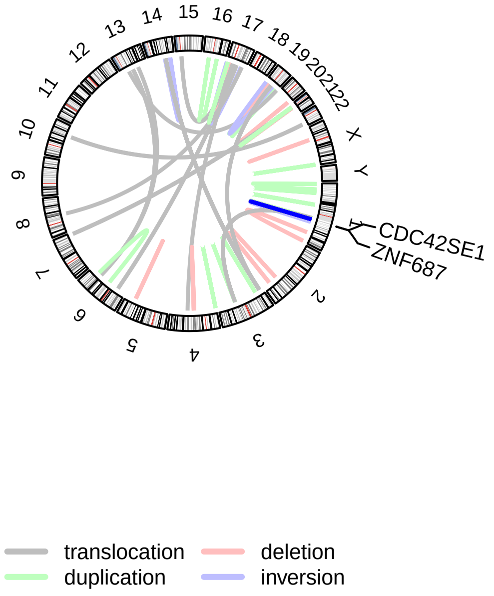
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

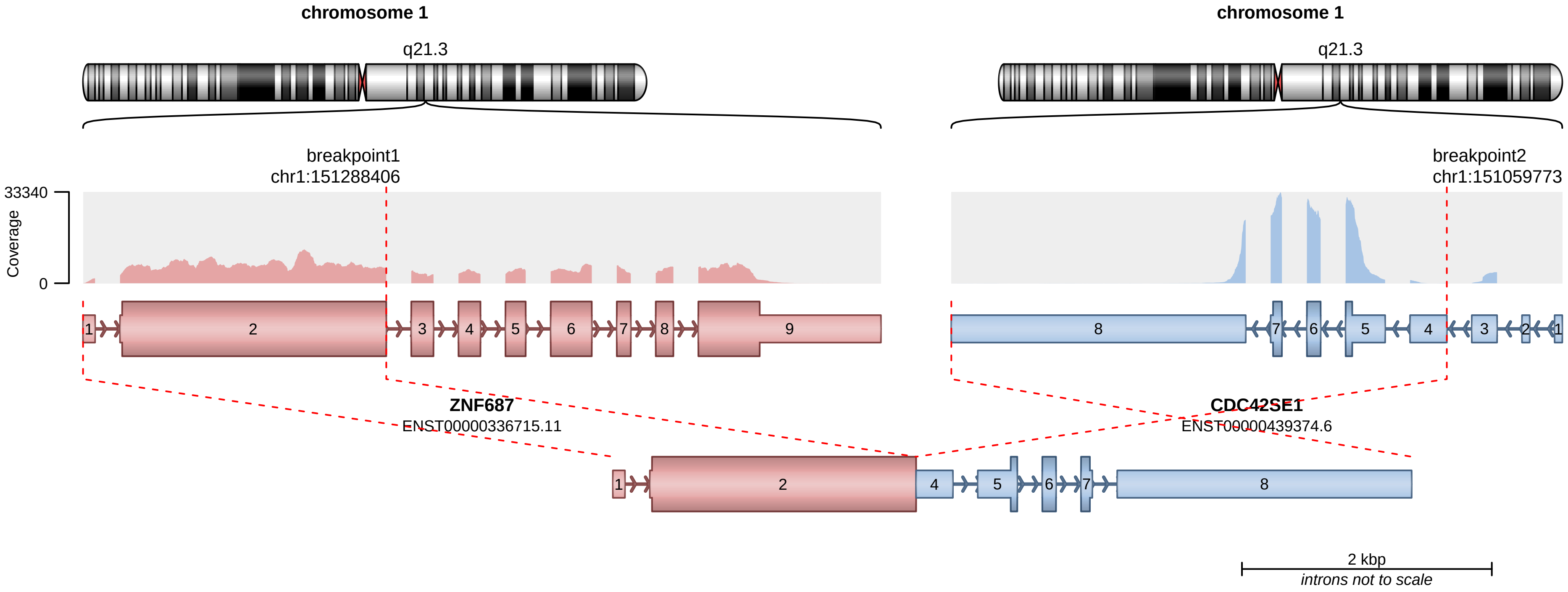


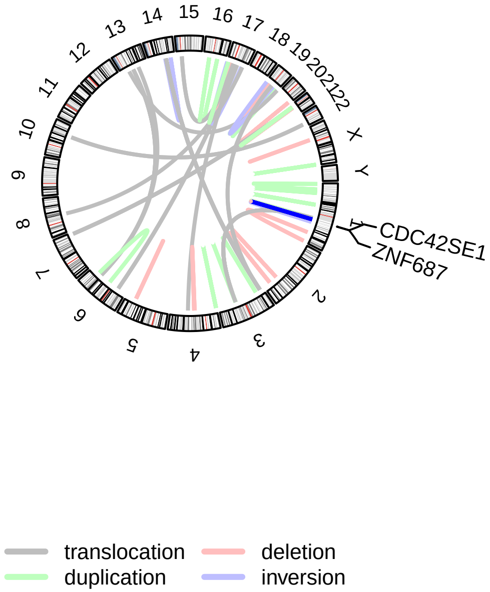


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 121
Discordant mates = 7

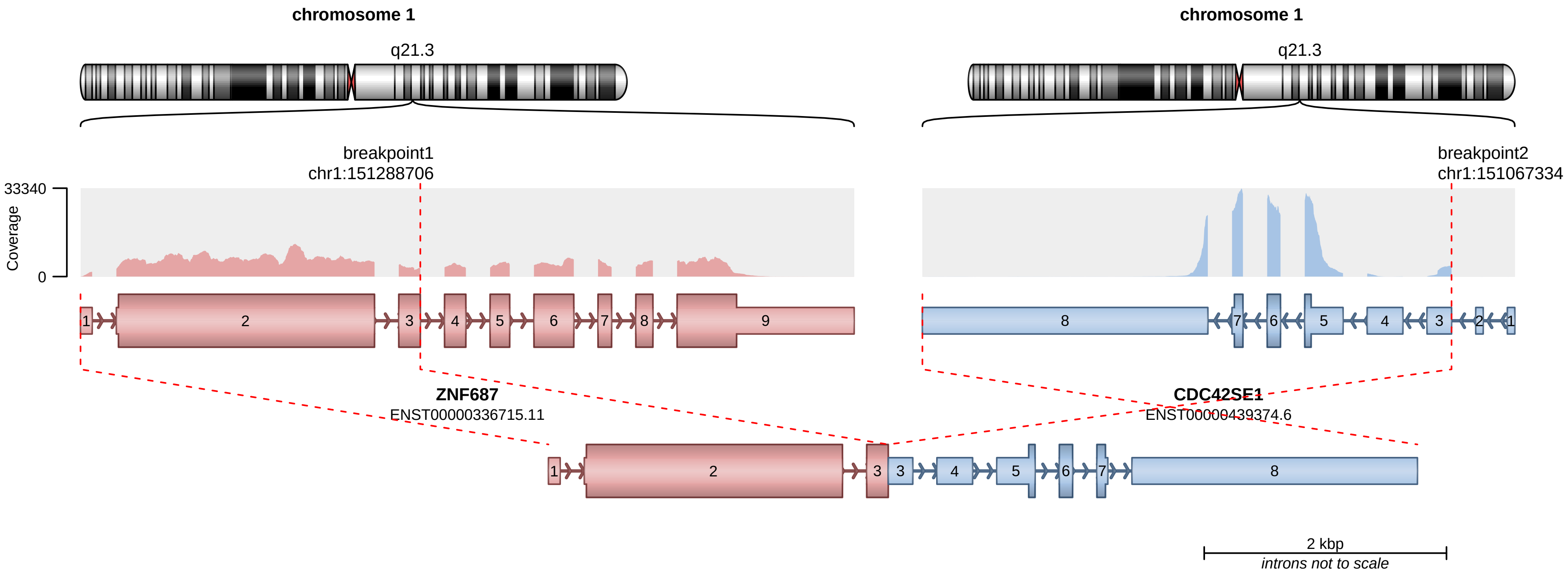


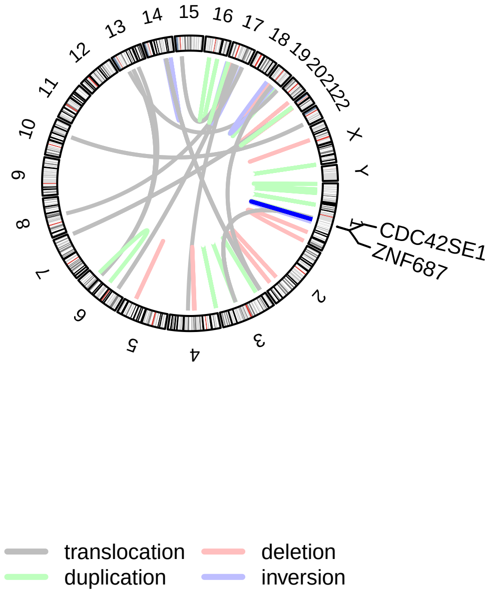


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 24
Discordant mates = 1

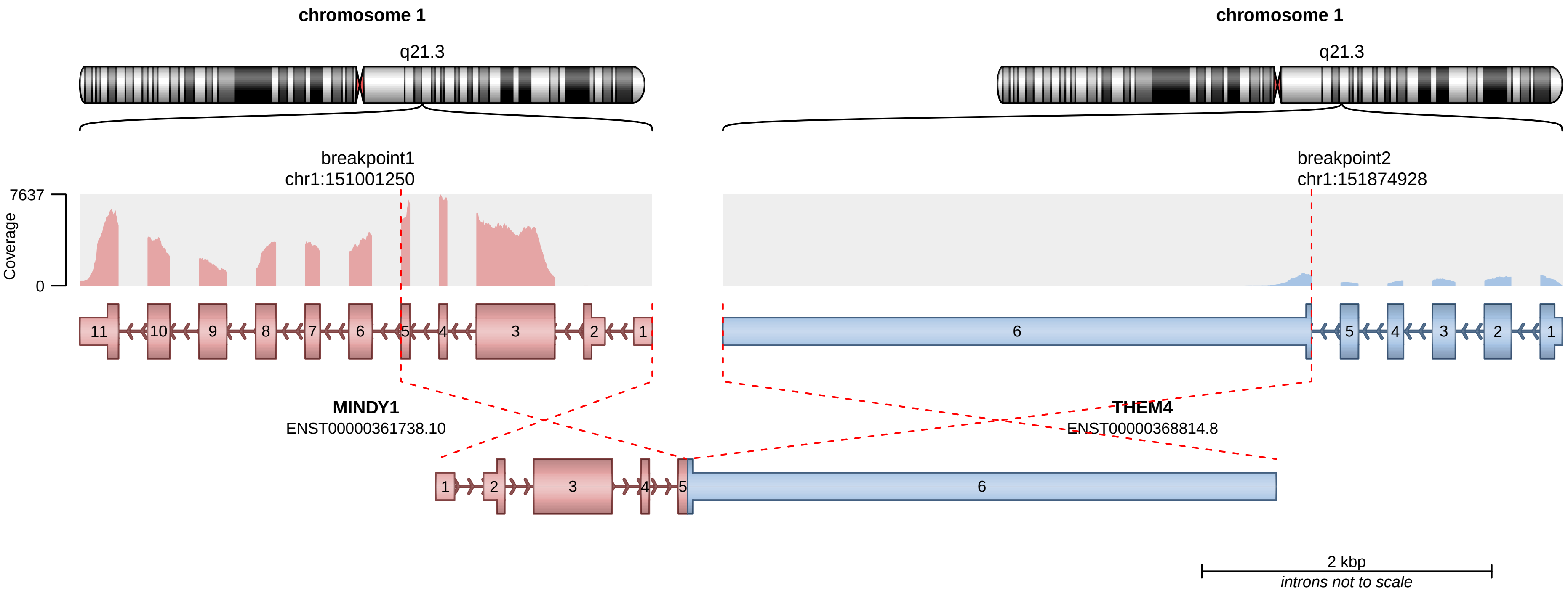


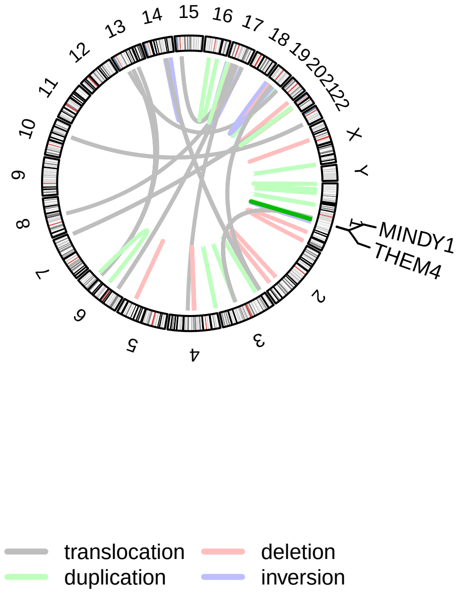


No protein domains retained in fusion.

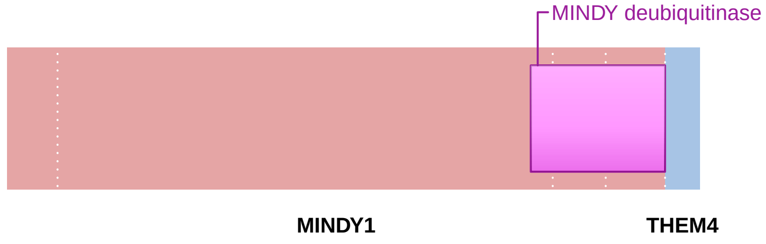
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 8



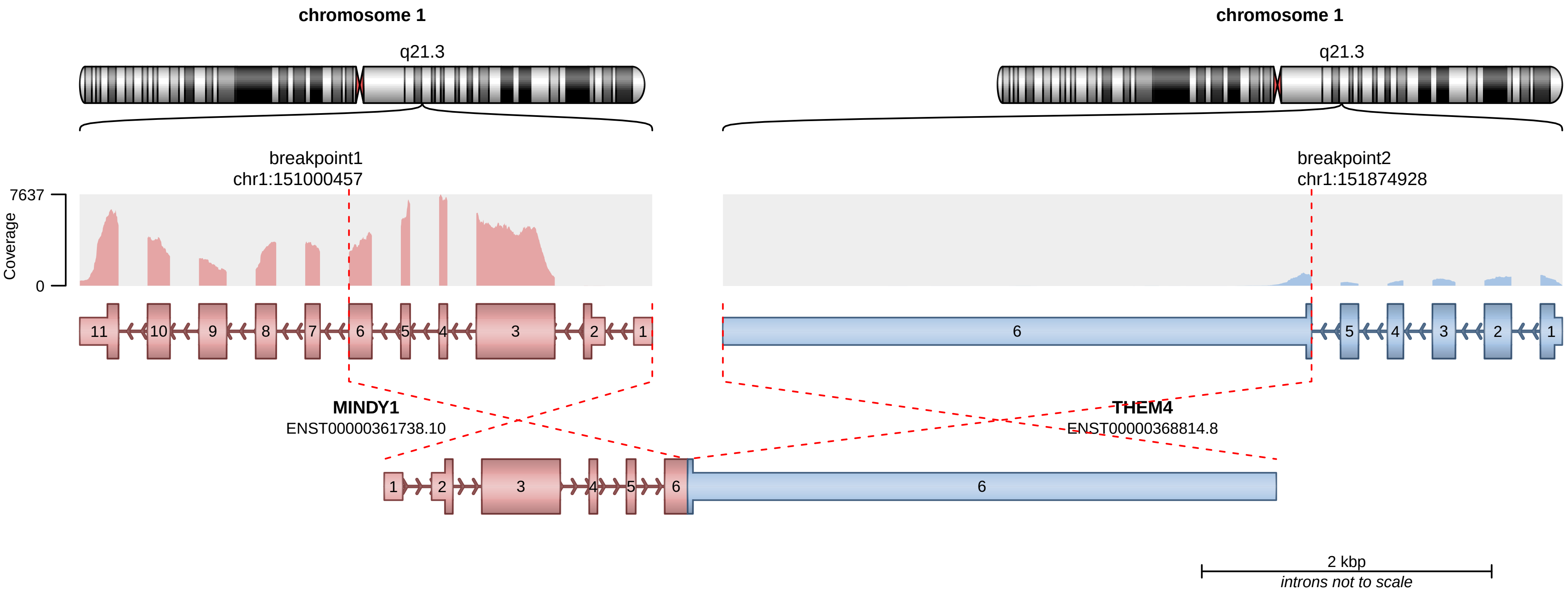


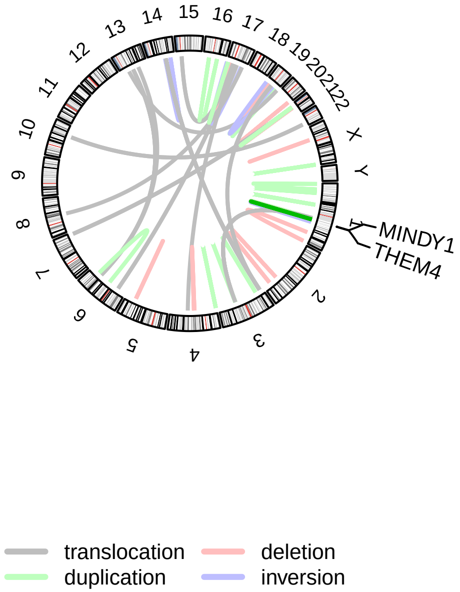
RETAINED PROTEIN DOMAINS
reading frame unclear

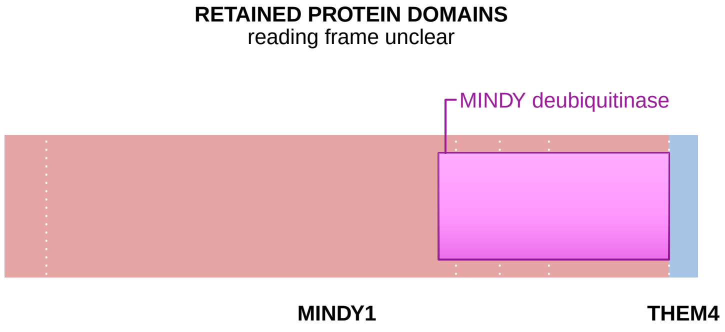


SUPPORTING READ COUNT

Split reads = 110
Discordant mates = 3

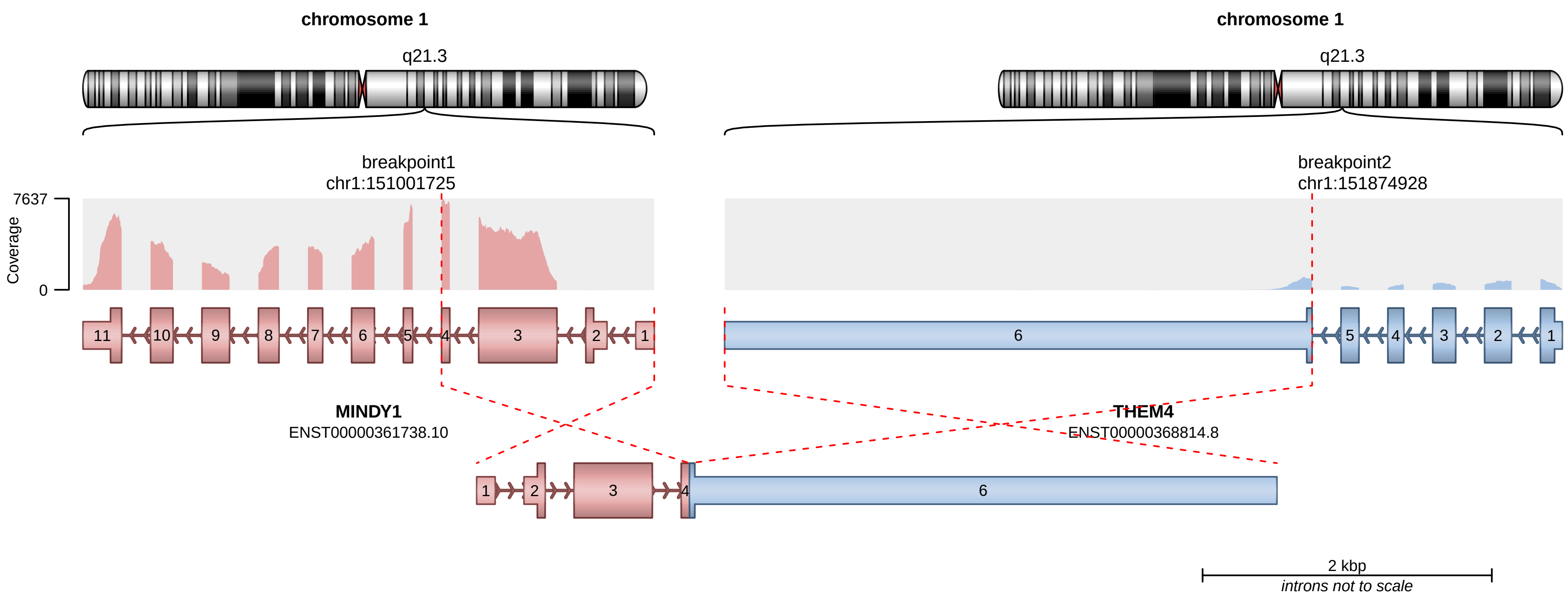


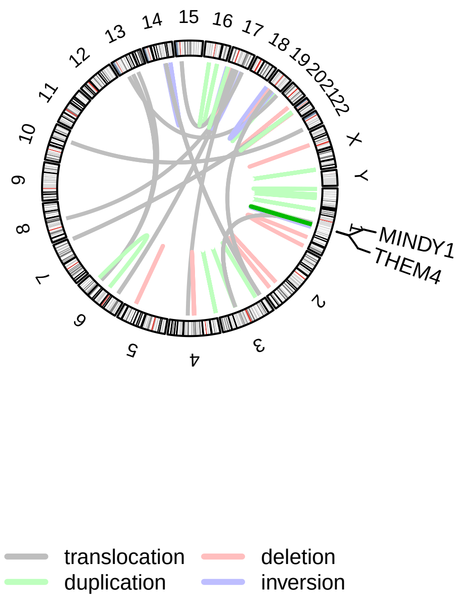


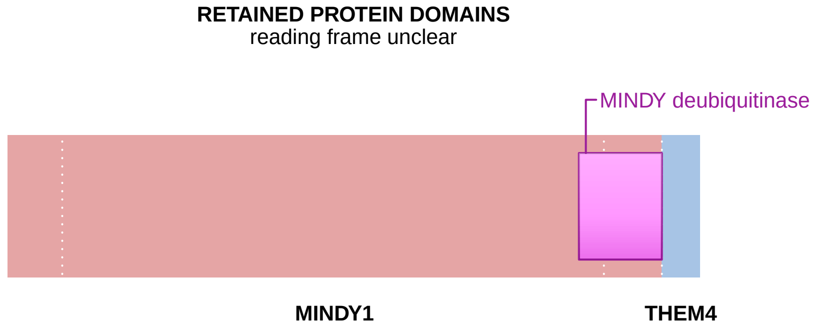


SUPPORTING READ COUNT

Split reads = 101
Discordant mates = 10

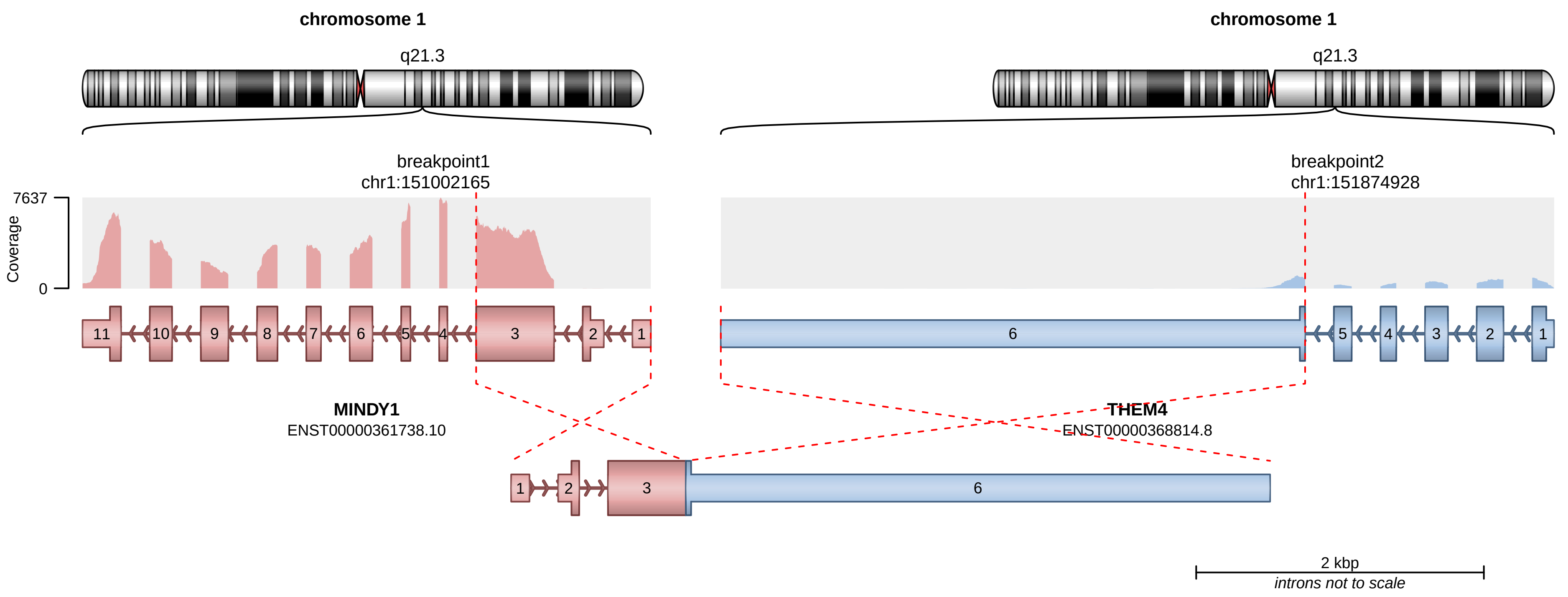


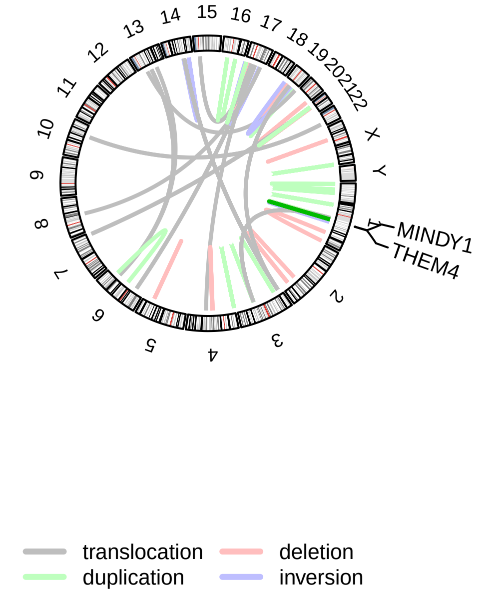




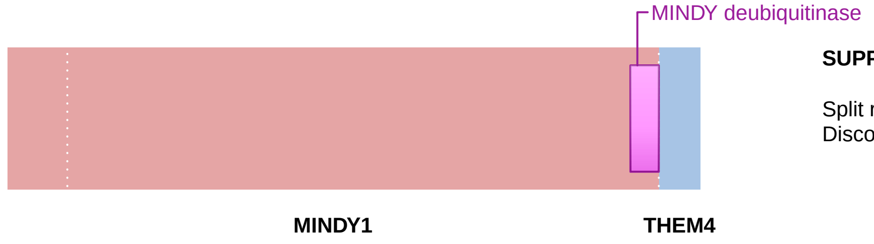
SUPPORTING READ COUNT

Split reads = 33
Discordant mates = 2



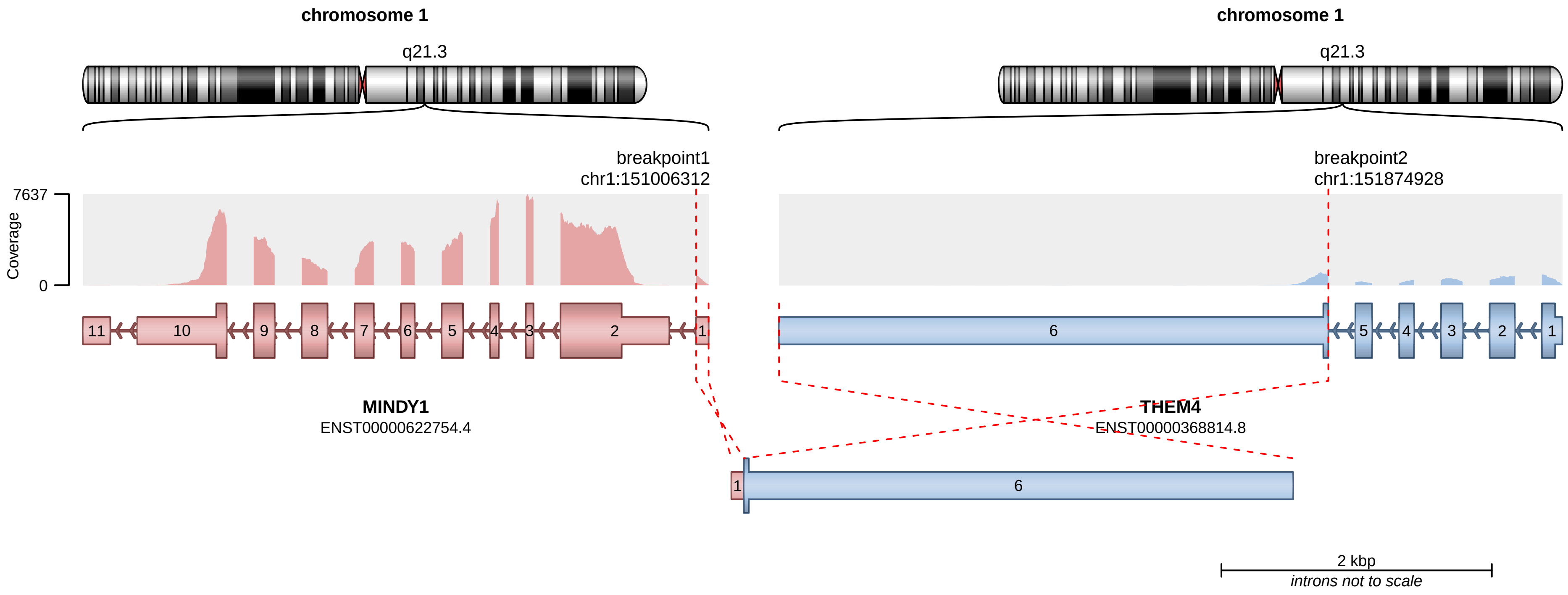


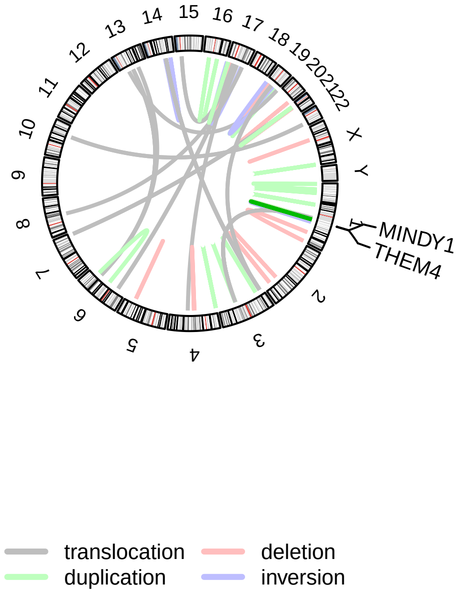
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 0

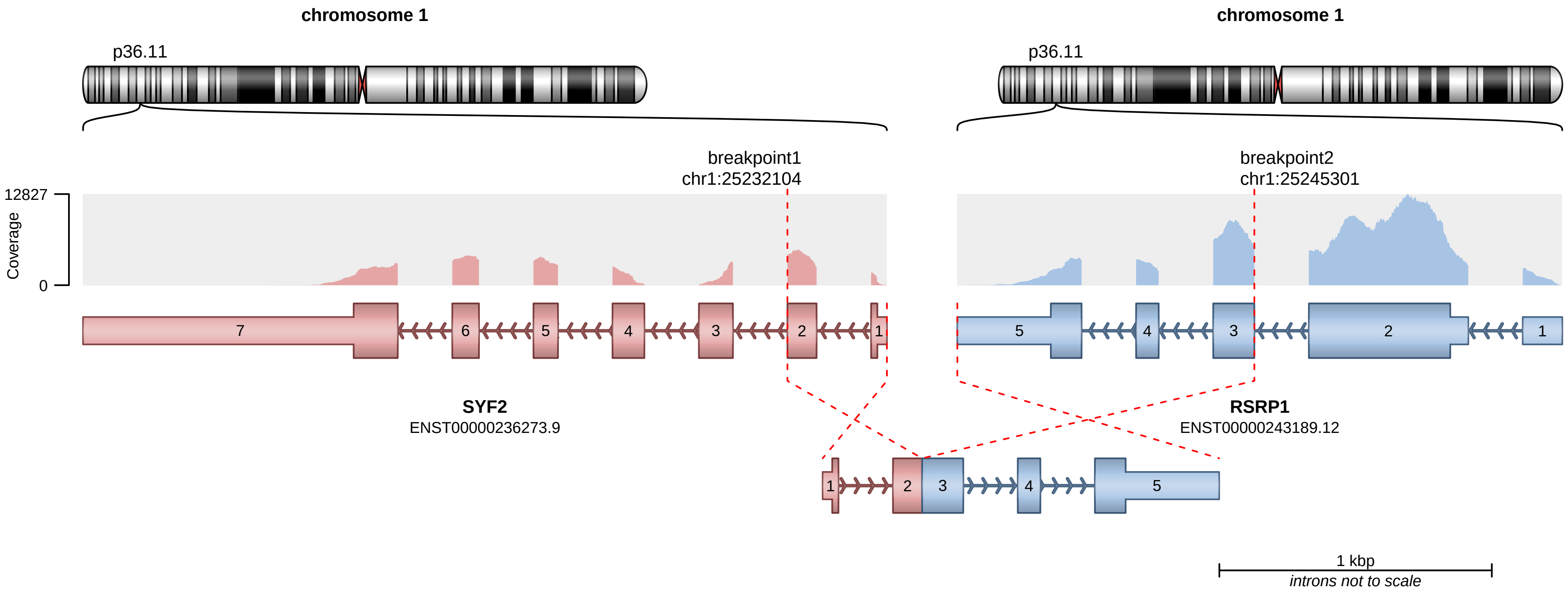


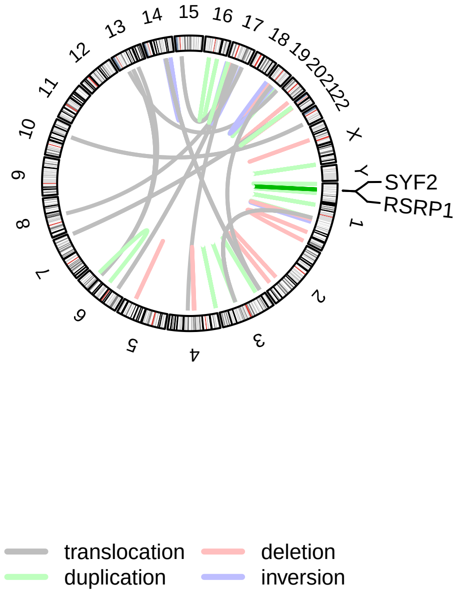


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

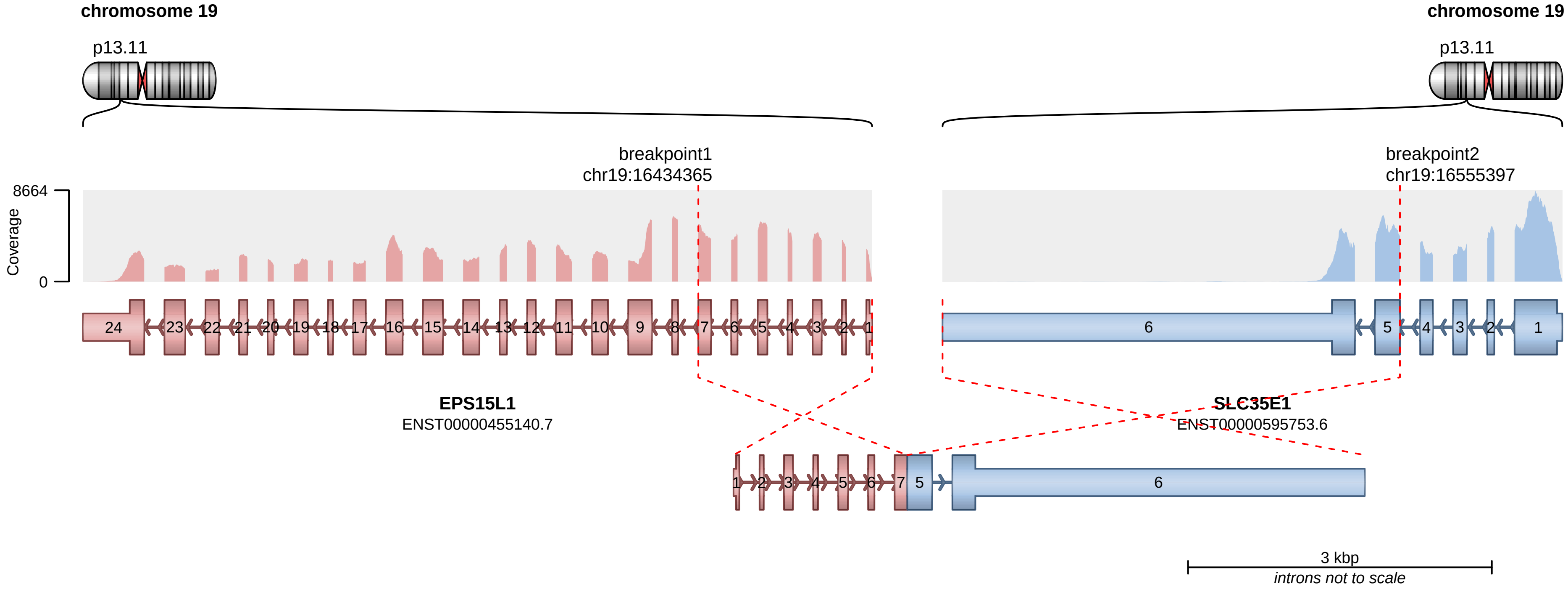


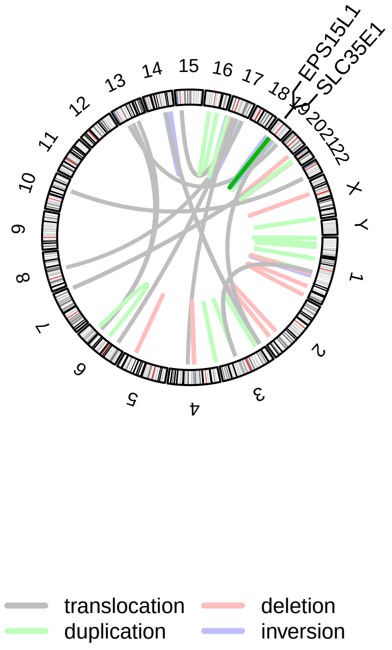


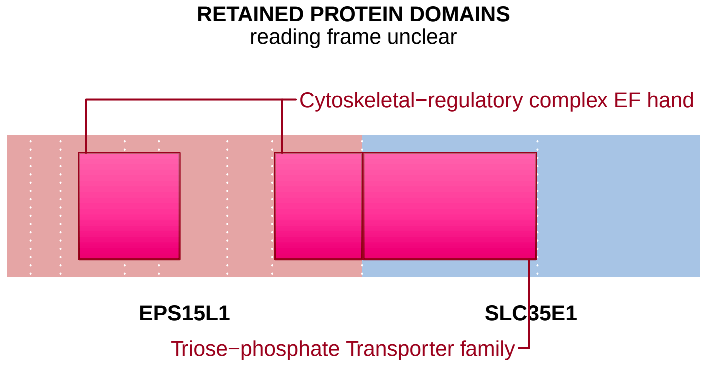
RETAINED PROTEIN DOMAINS
reading frame unclear

SUPPORTING READ COUNT

Split reads = 99
Discordant mates = 0

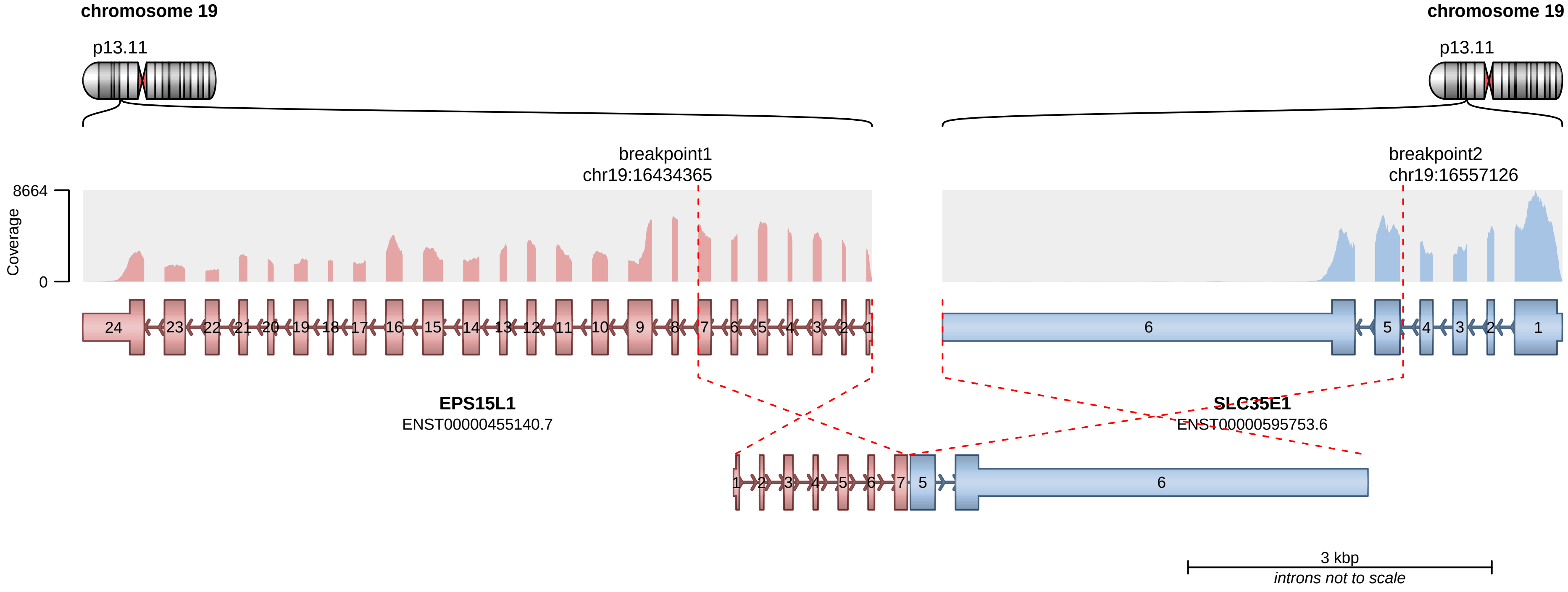


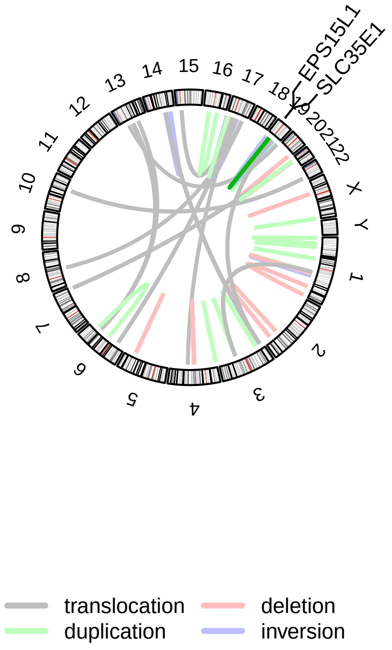




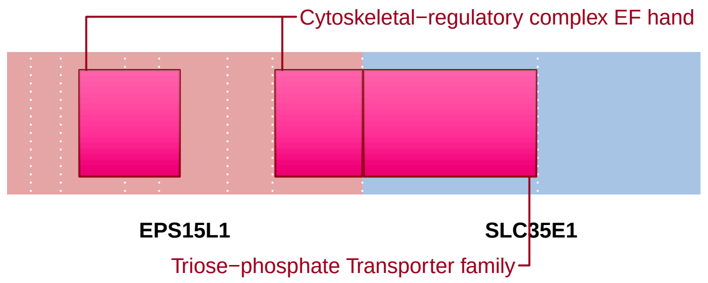
SUPPORTING READ COUNT

Split reads = 96
Discordant mates = 1



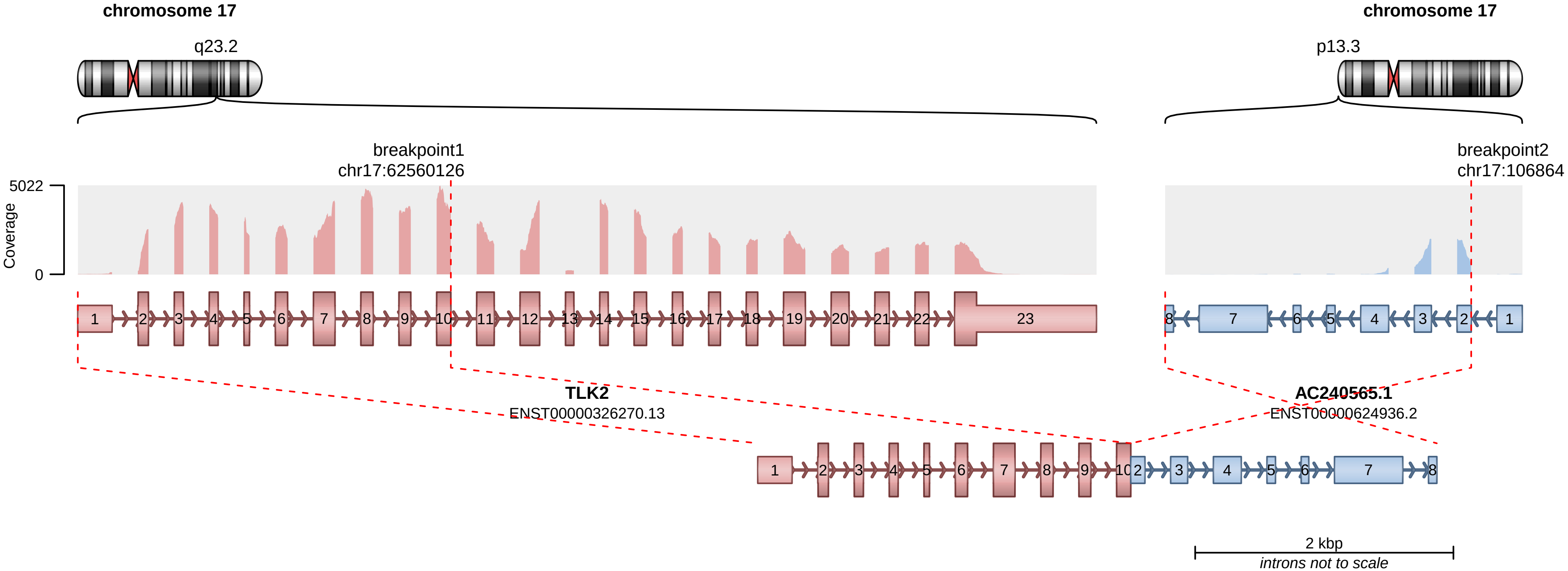


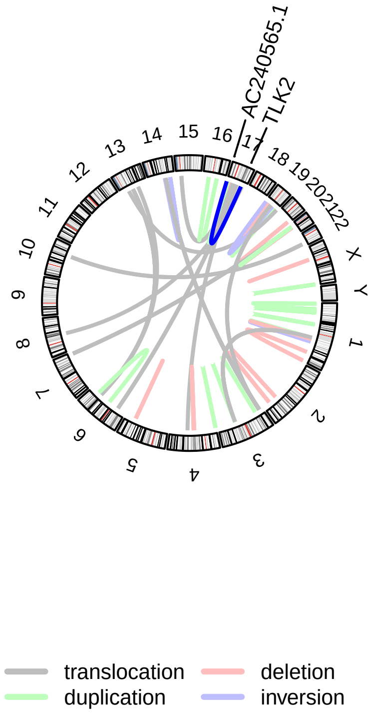
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 1

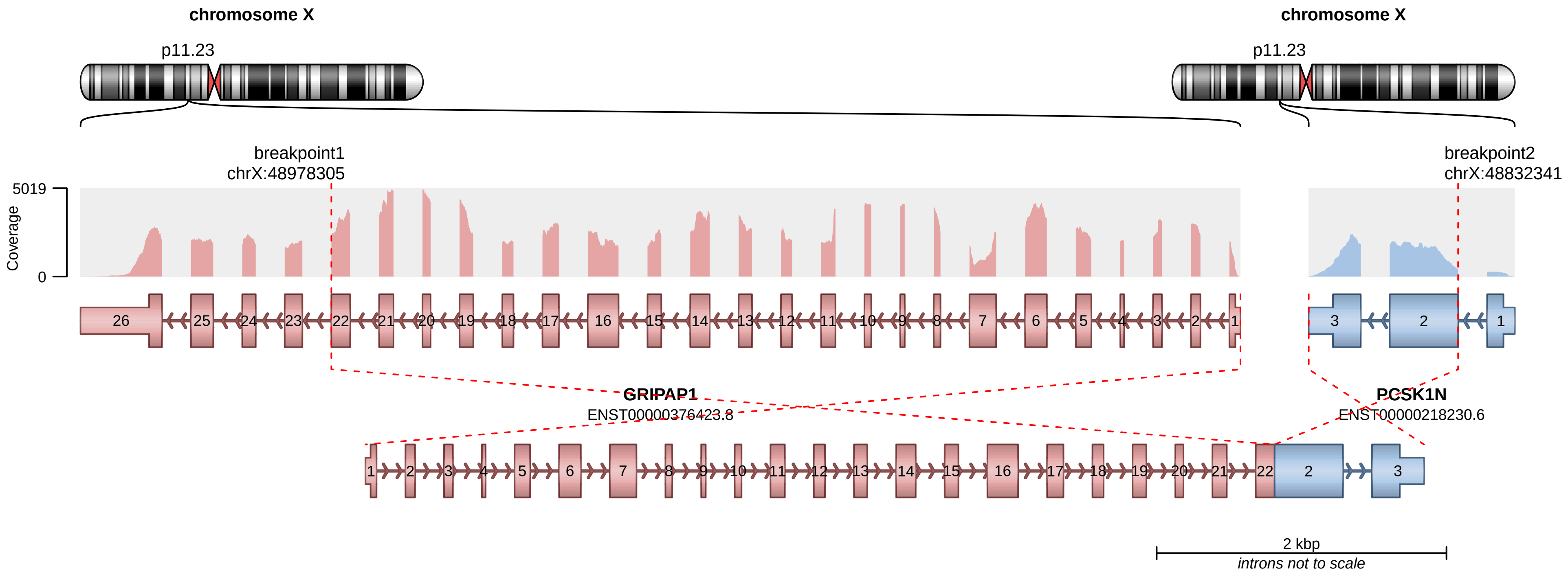


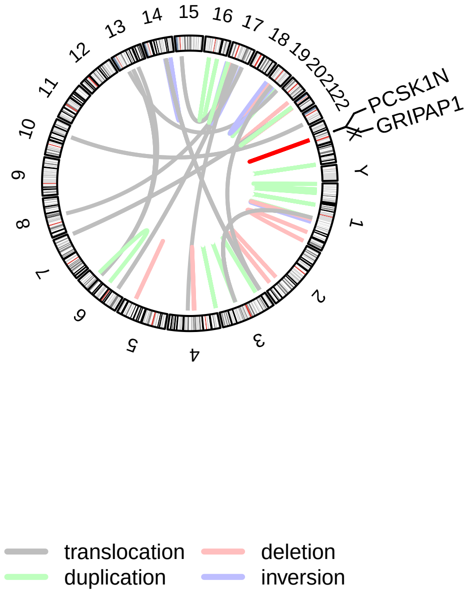


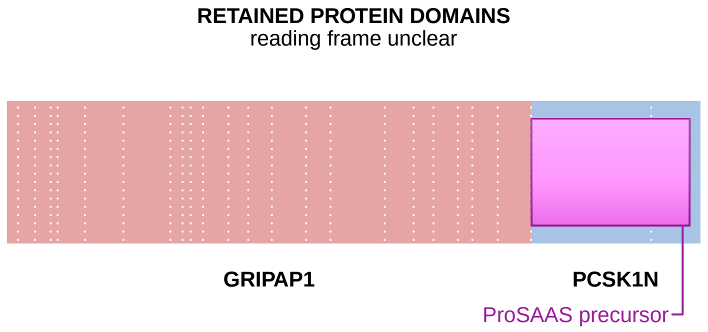
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 88
Discordant mates = 1

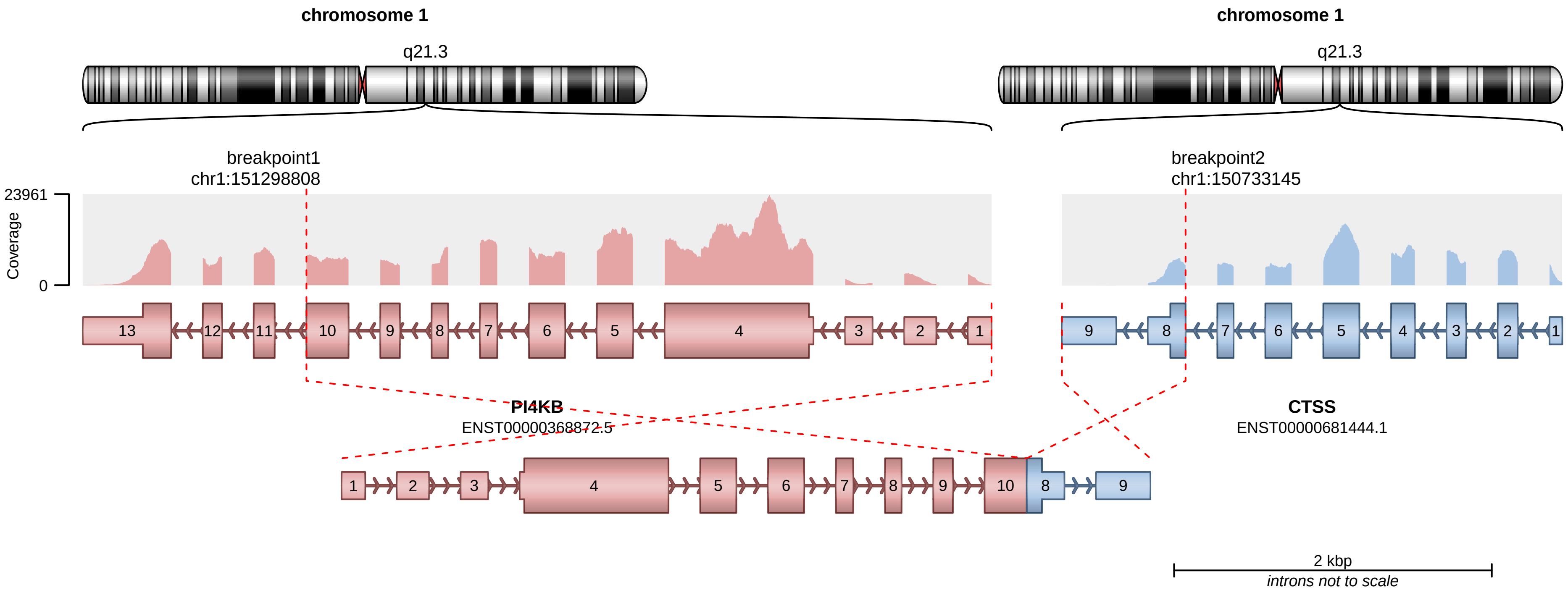


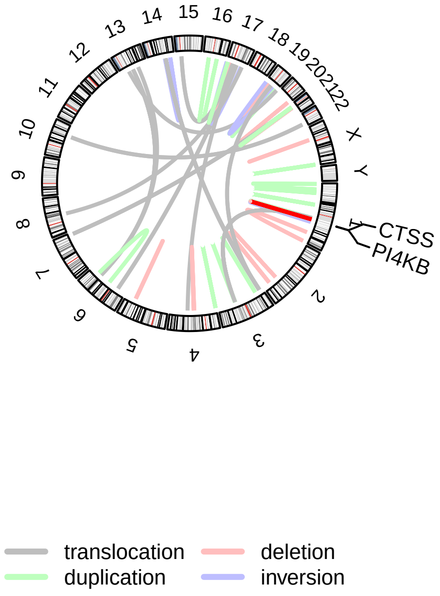




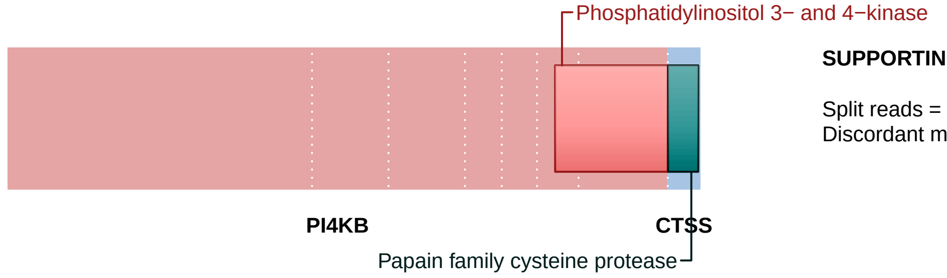
SUPPORTING READ COUNT

Split reads = 85
Discordant mates = 4



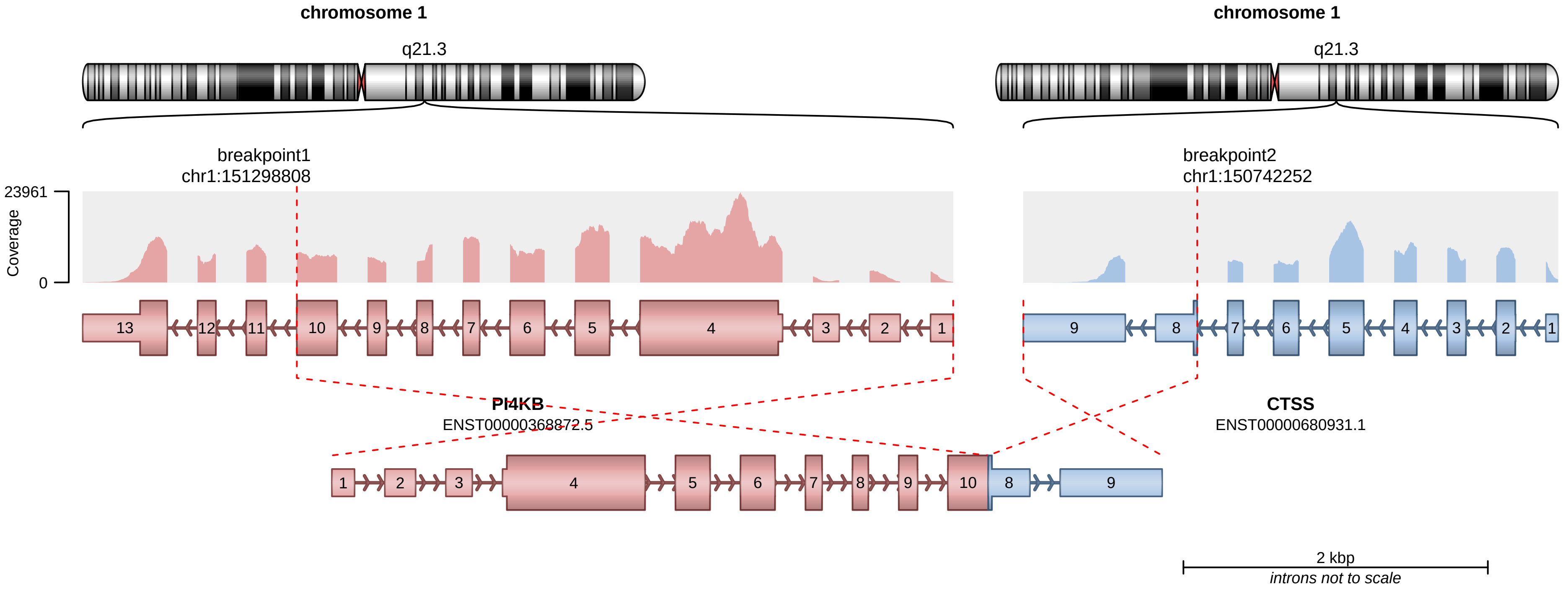


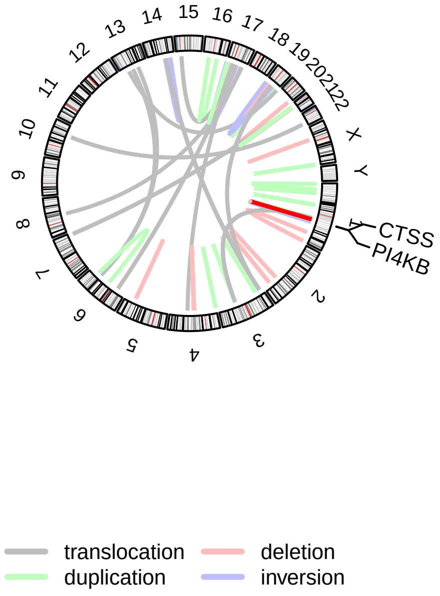
RETAINED PROTEIN DOMAINS
reading frame unclear

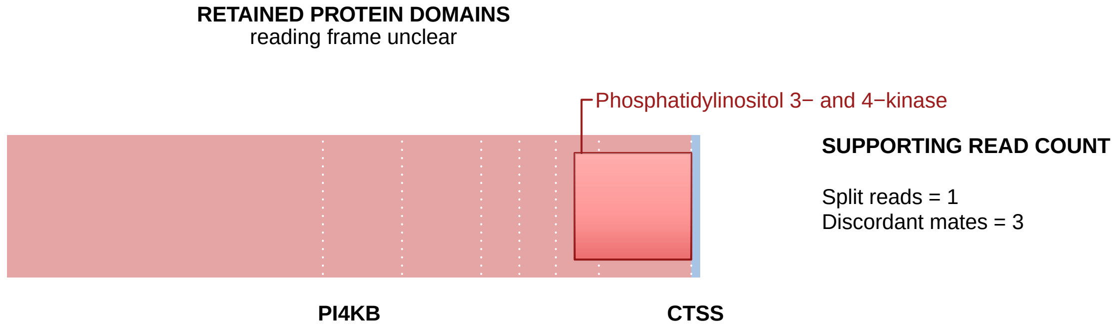


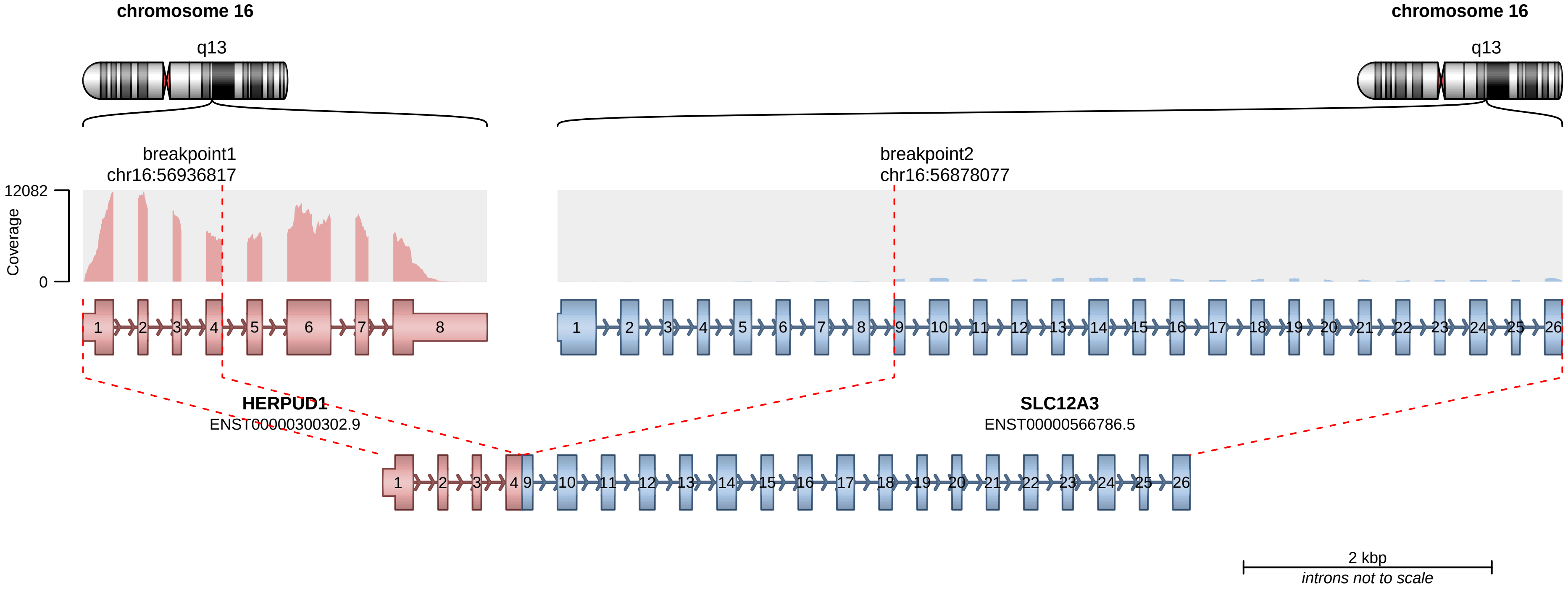
SUPPORTING READ COUNT

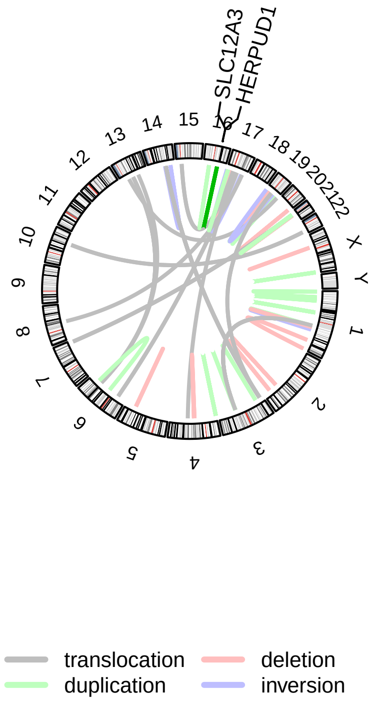
Split reads = 83
Discordant mates = 3


chromosome 1
q21.3
chromosome 1
q21.3
breakpoint1
chr1:151298808
breakpoint2
chr1:150742252
23961
Coverage
0
13
12
11
10
9
8
7
6
5
4
3
2
1
9
8
7
6
5
4
3
2
1
PI4KB
ENST00000368872.5
CTSS
ENST00000680931.1
1
2
3
4
5
6
7
8
9
10
8
9
2 kbp
introns not to scale

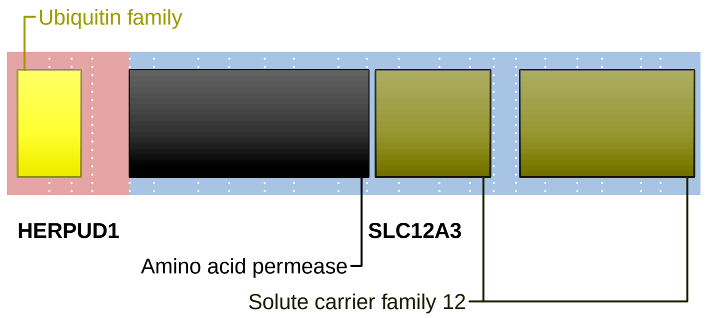

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
X
Y
CTSS
PI4KB
translocation
duplication
deletion
inversion


RETAINED PROTEIN DOMAINS
reading frame unclear
Phosphatidylinositol 3− and 4−kinase
SUPPORTING READ COUNT
Split reads = 1
Discordant mates = 3
PI4KB
CTSS



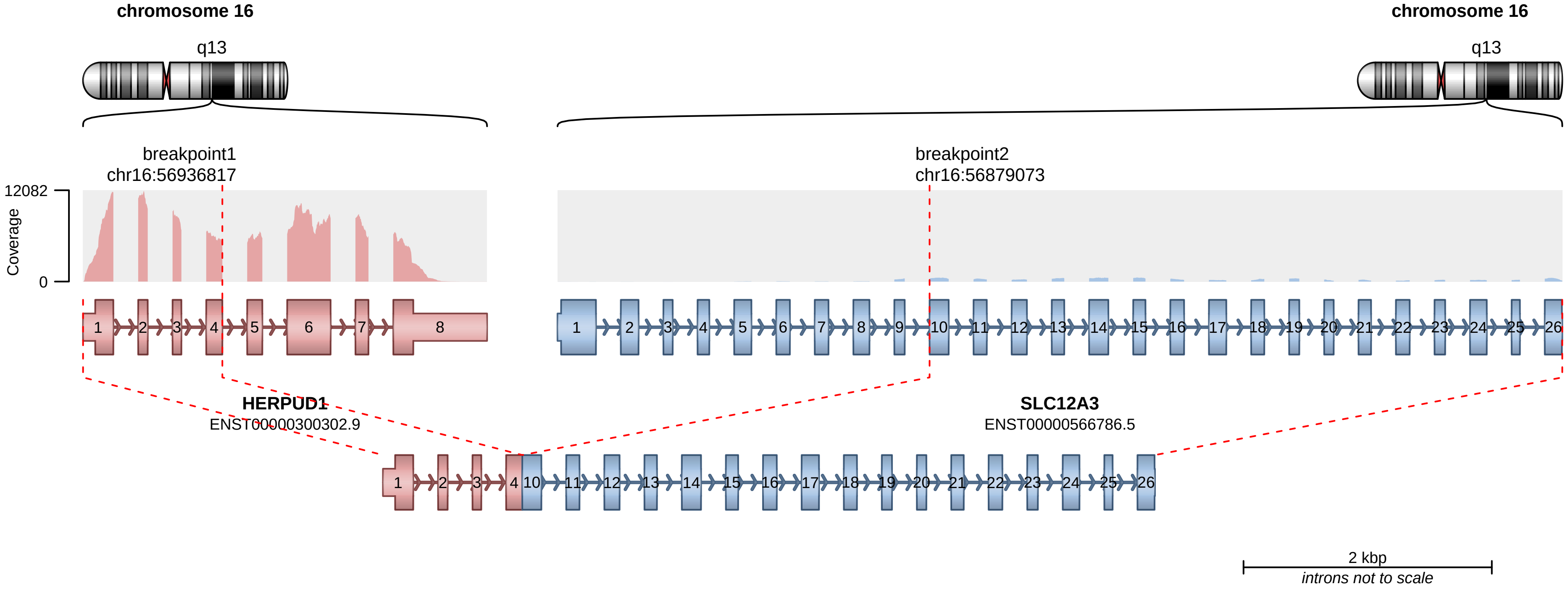


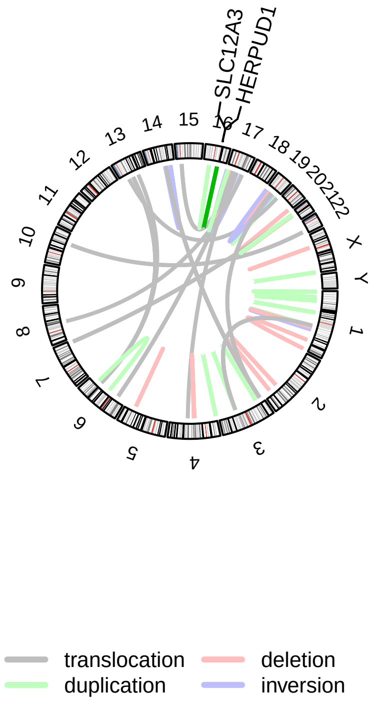
RETAINED PROTEIN DOMAINS
reading frame unclear



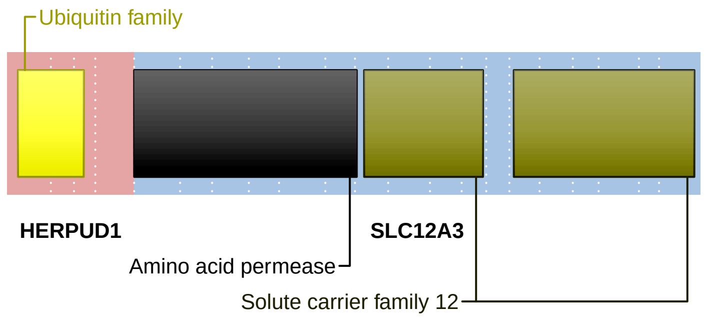
SUPPORTING READ COUNT

Split reads = 78
Discordant mates = 6



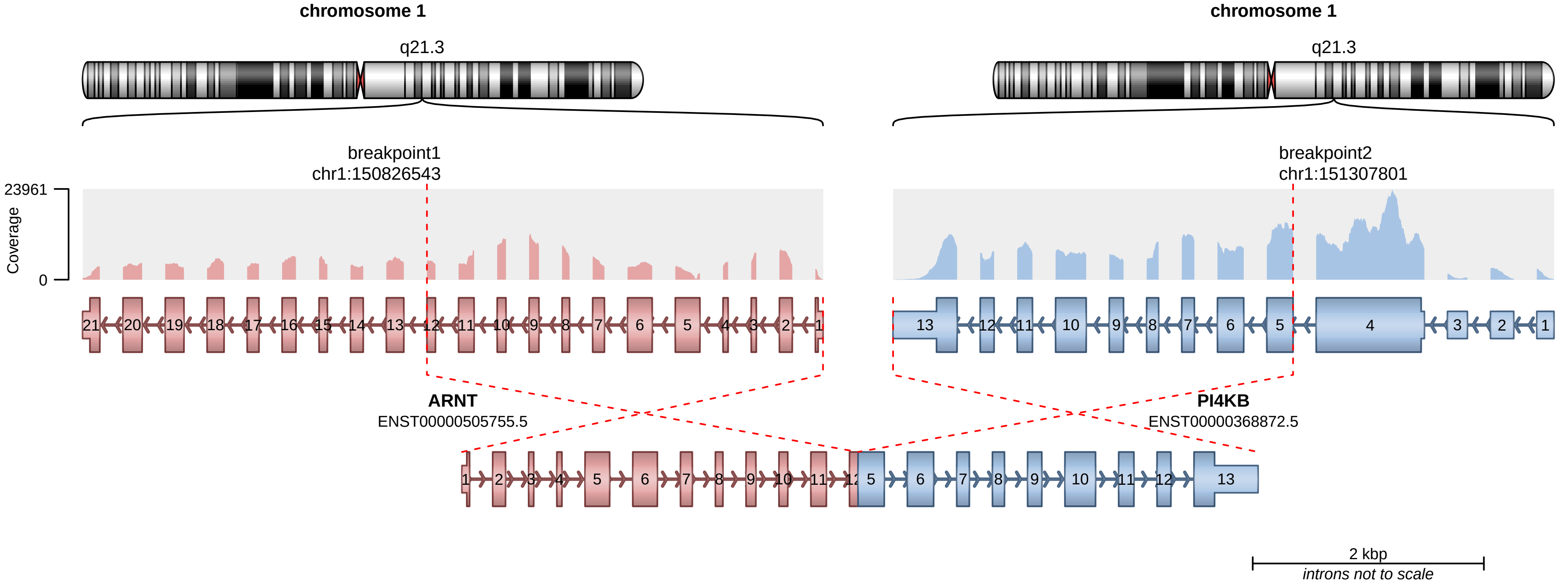


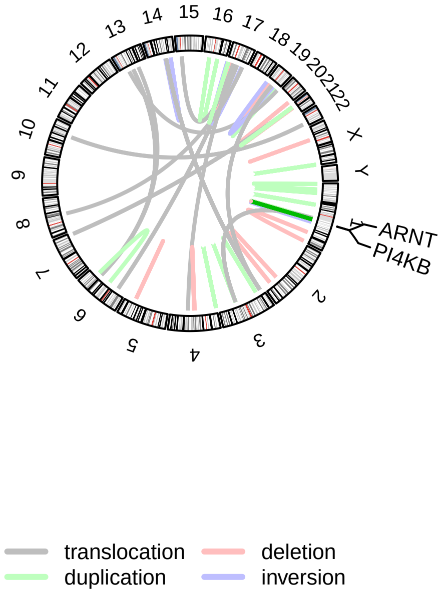
RETAINED PROTEIN DOMAINS
reading frame unclear



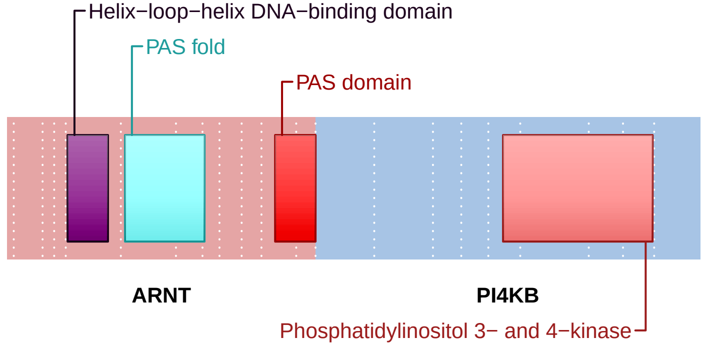
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0



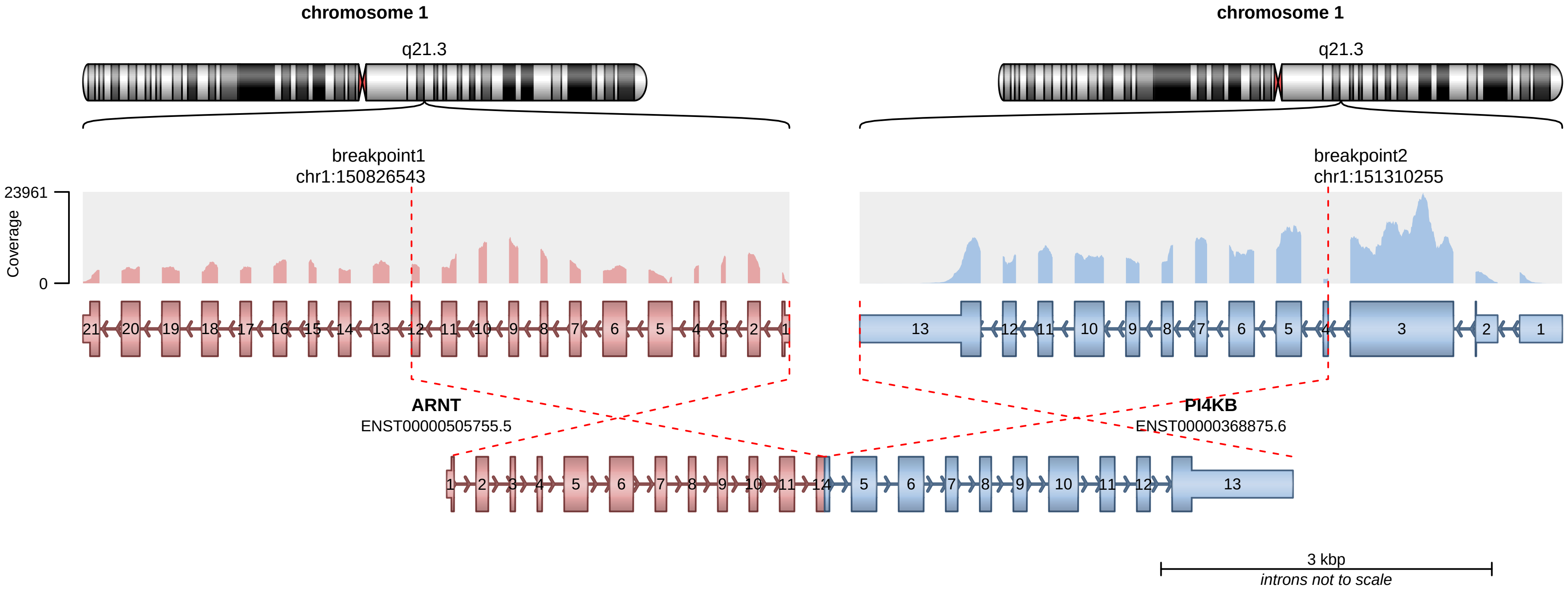


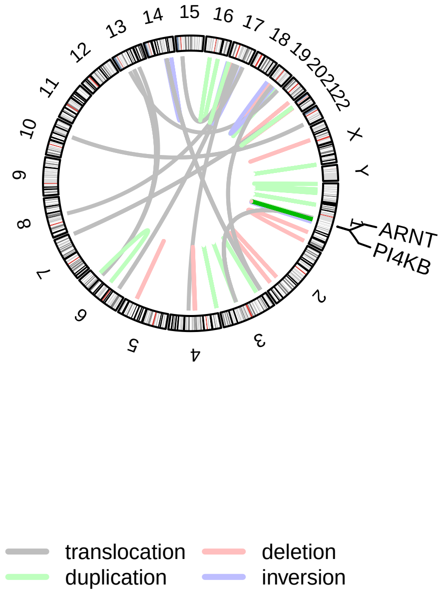
RETAINED PROTEIN DOMAINS
reading frame unclear

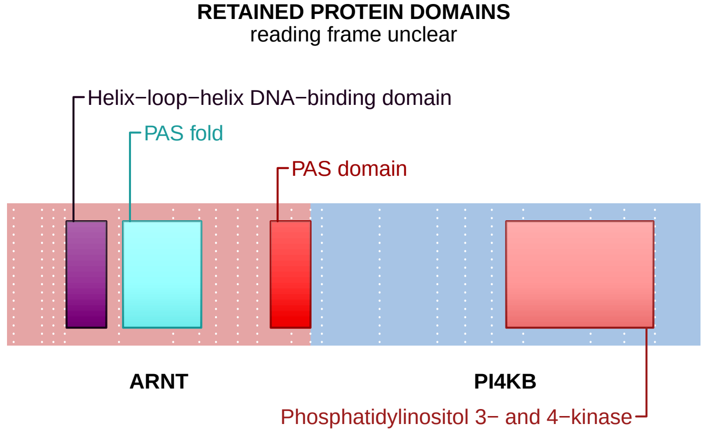


SUPPORTING READ COUNT

Split reads = 74
Discordant mates = 7

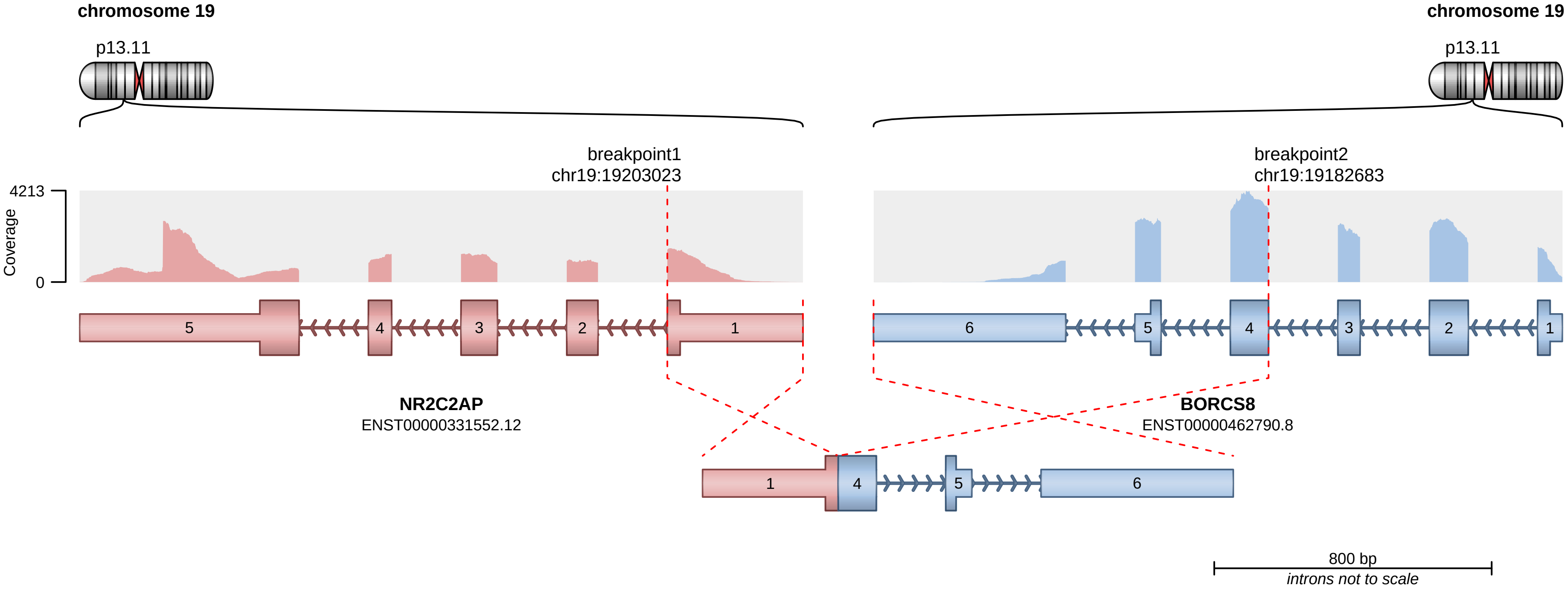


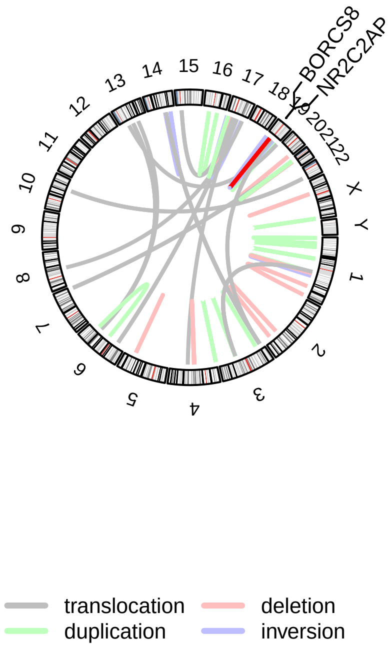


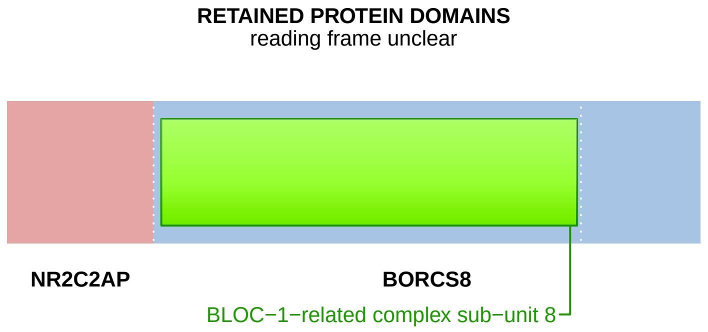


SUPPORTING READ COUNT

Split reads = 37
Discordant mates = 8

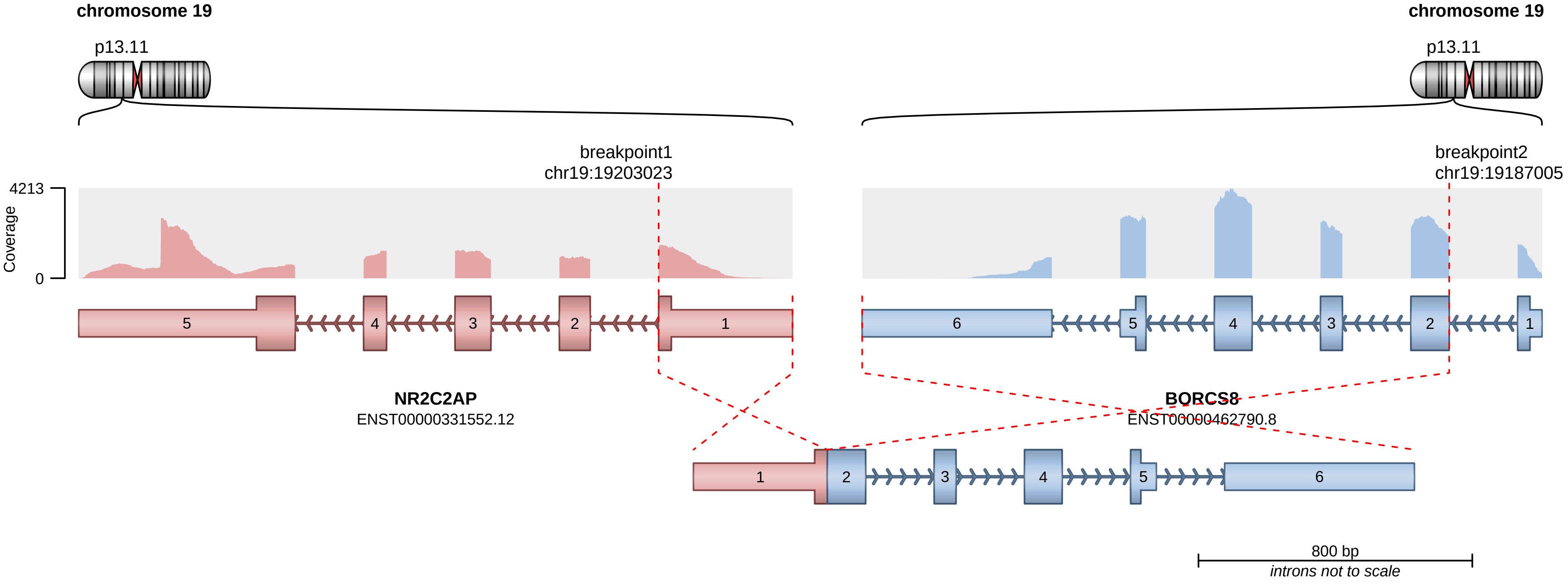


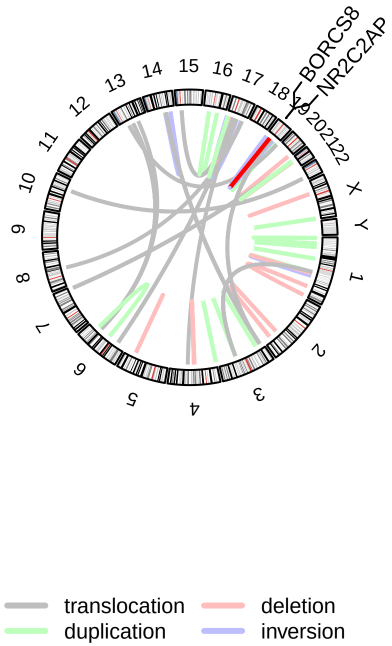


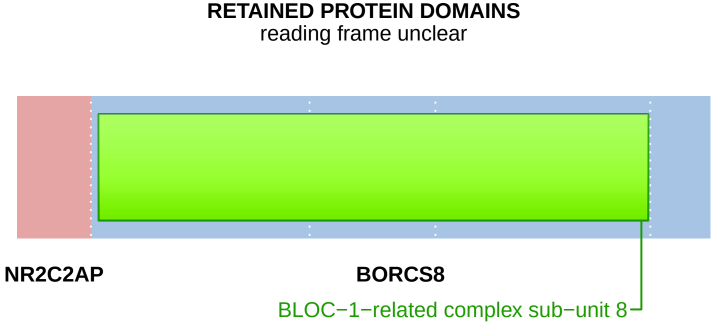


SUPPORTING READ COUNT

Split reads = 68
Discordant mates = 2

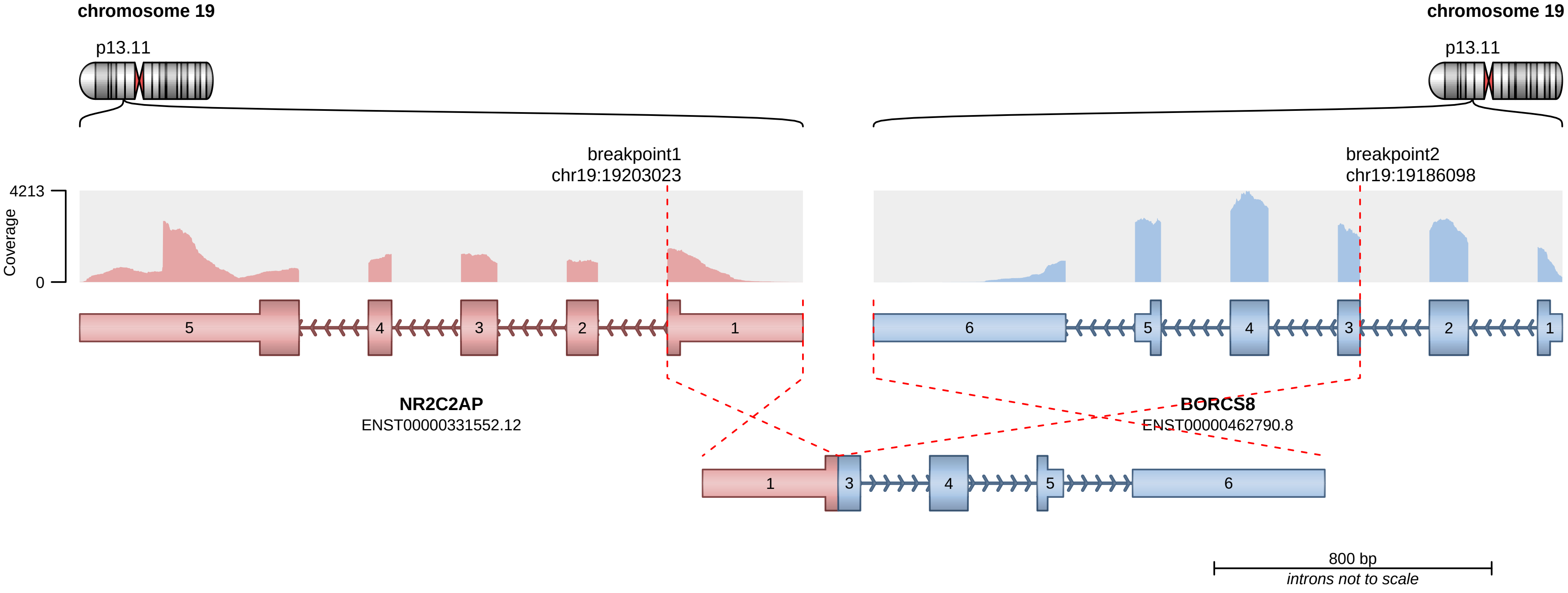


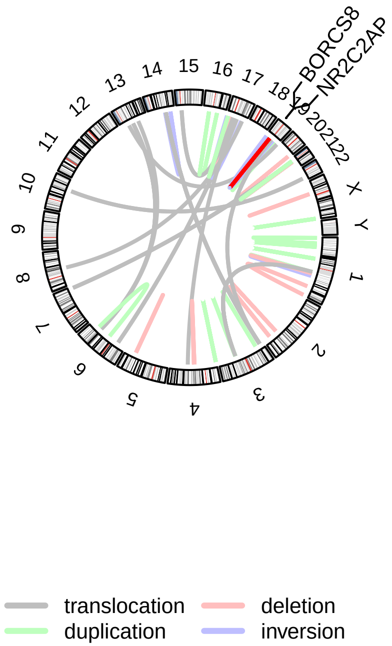


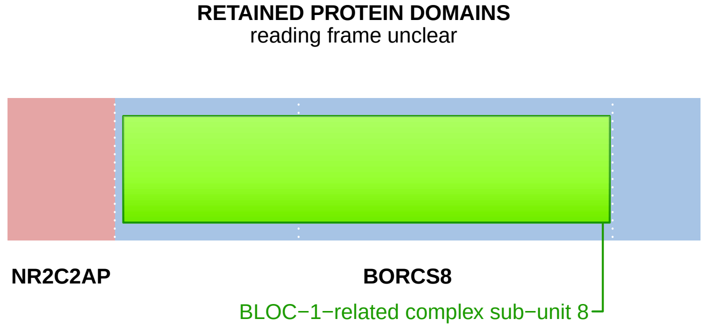


SUPPORTING READ COUNT

Split reads = 38
Discordant mates = 6

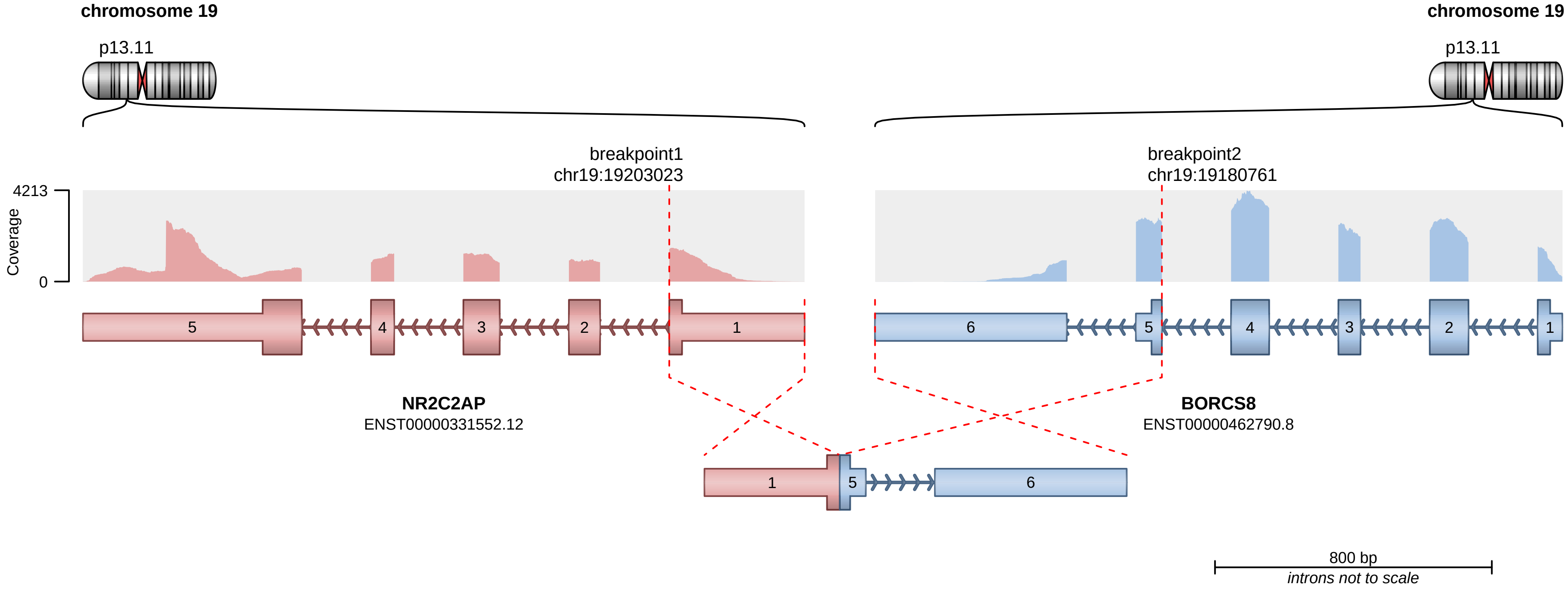


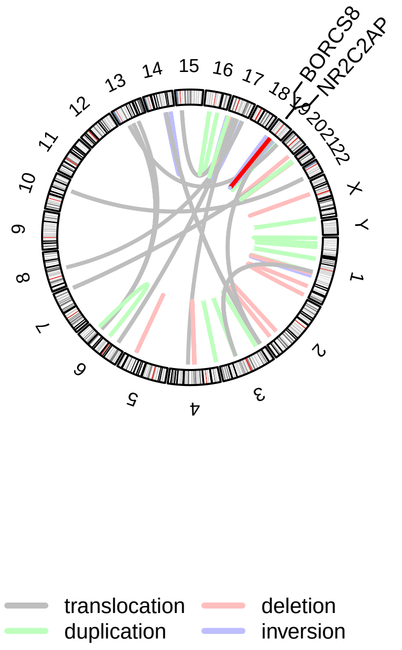




SUPPORTING READ COUNT

Split reads = 23
Discordant mates = 5

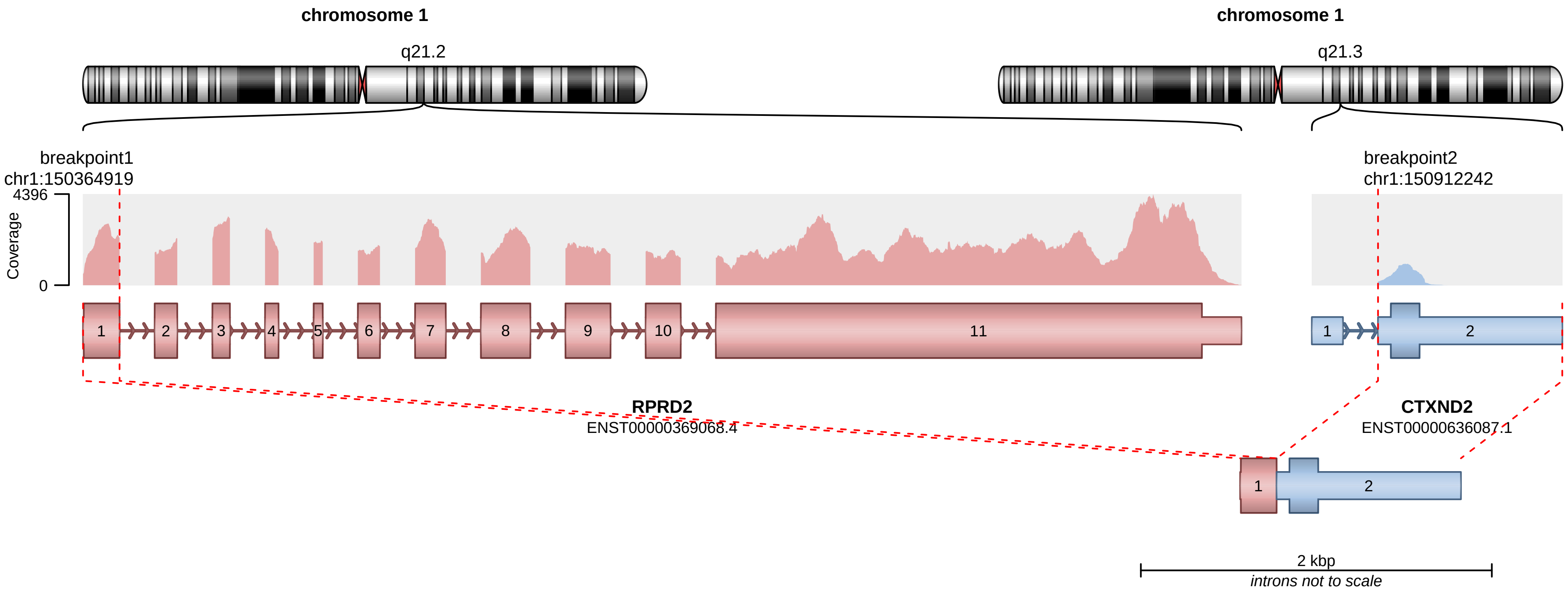


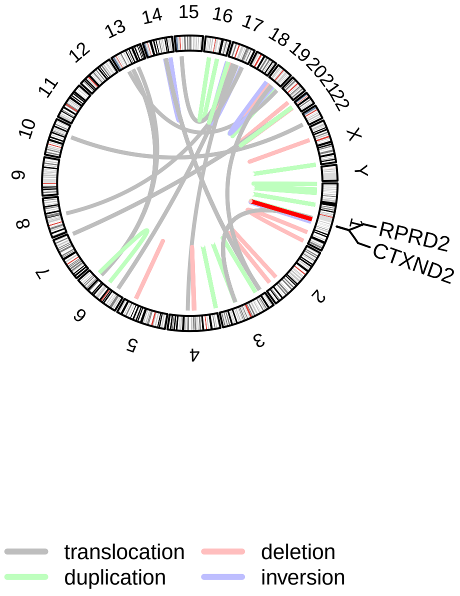


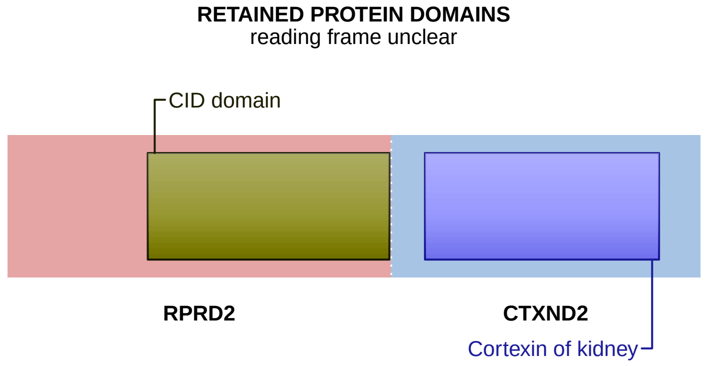
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

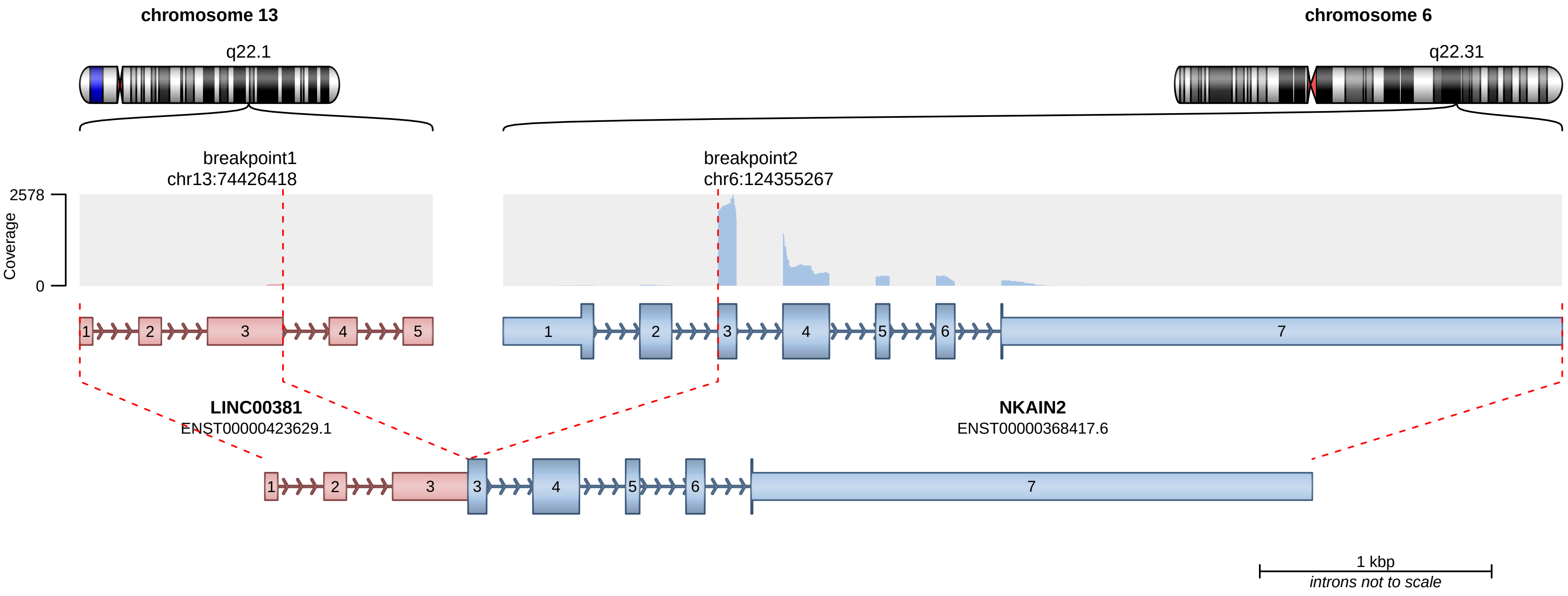


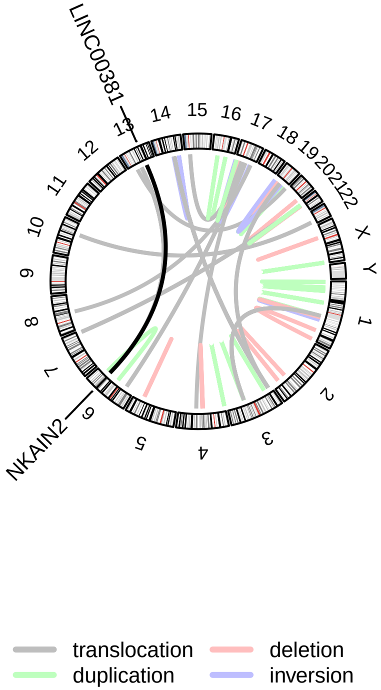




SUPPORTING READ COUNT

Split reads = 65
Discordant mates = 5



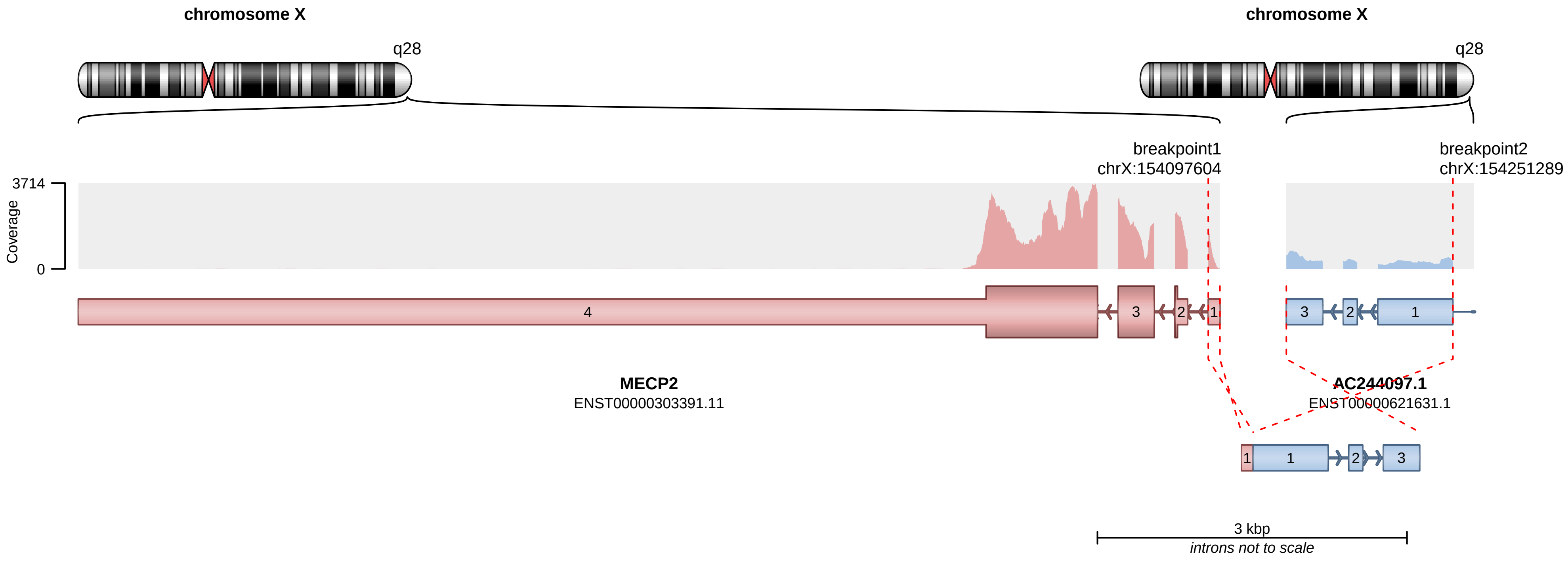


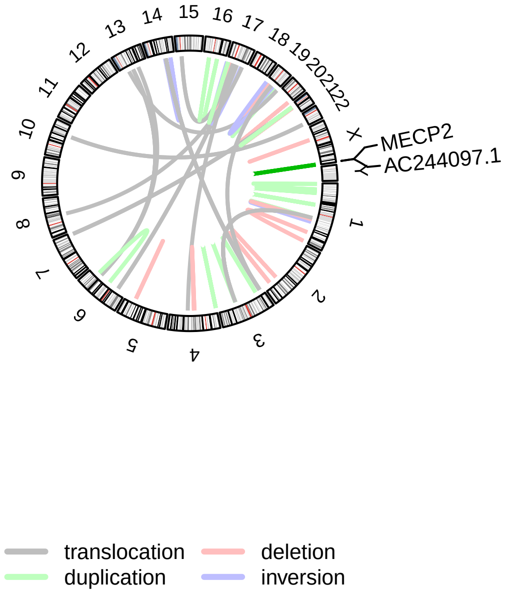
RETAINED PROTEIN DOMAINS

reading frame unclear

SUPPORTING READ COUNT

Split reads = 65
Discordant mates = 0

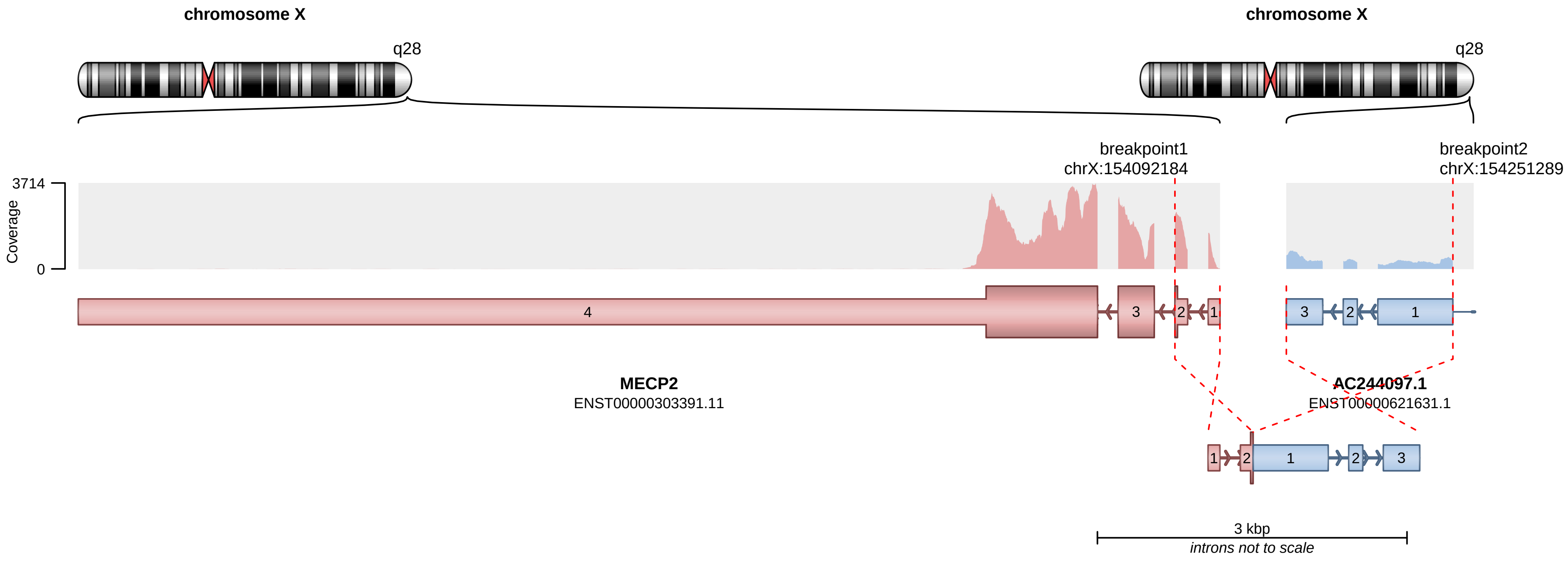


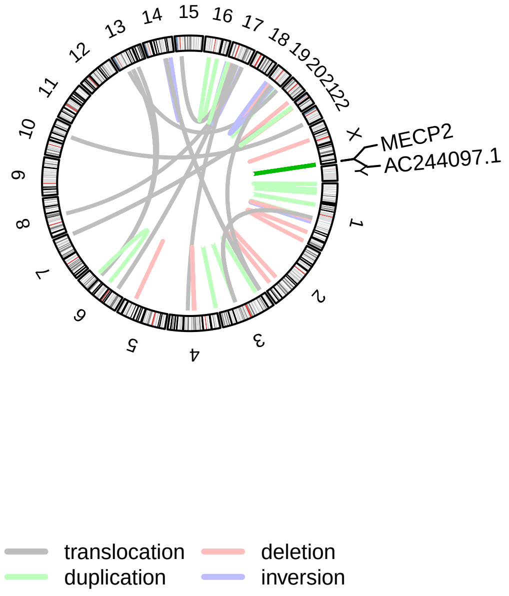


No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 53
Discordant mates = 0

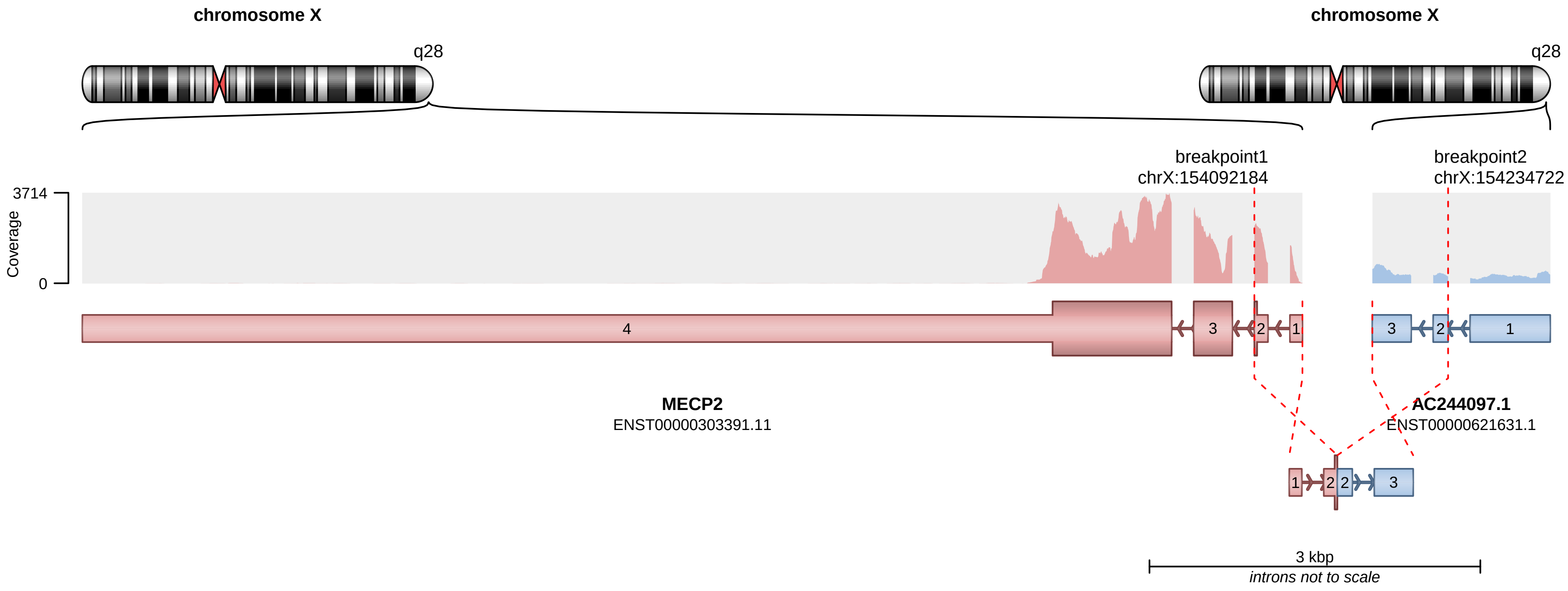


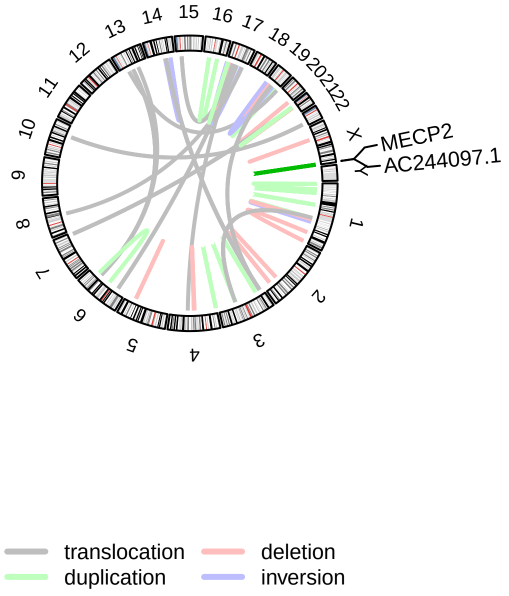


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 33
Discordant mates = 3

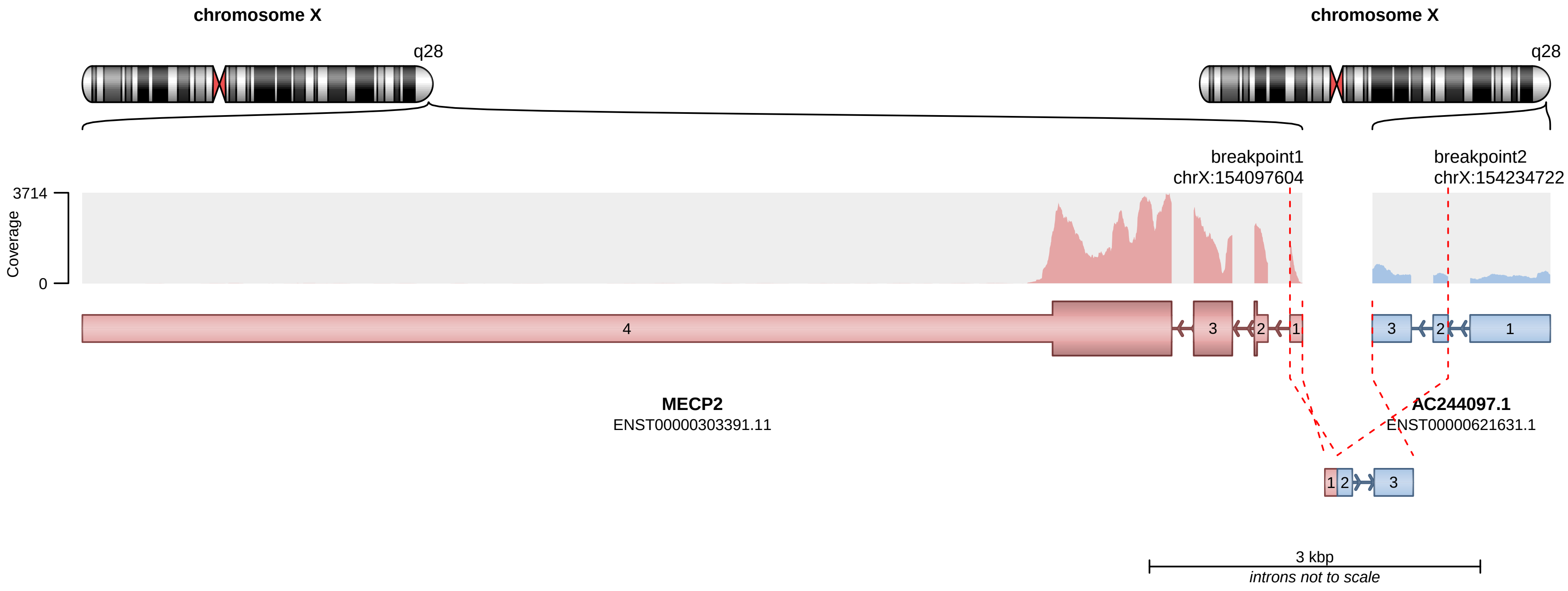


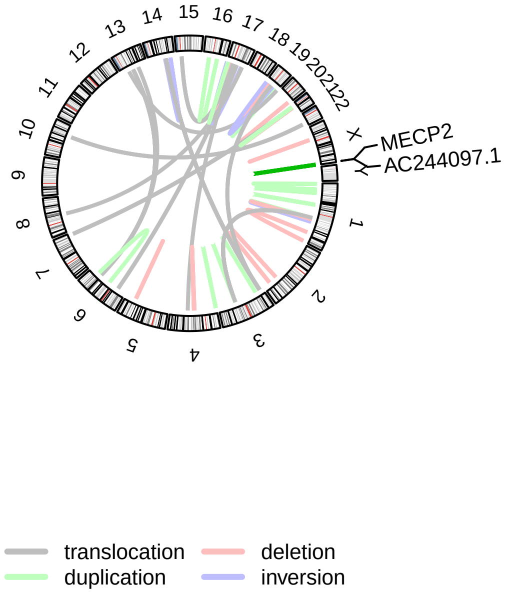


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 2

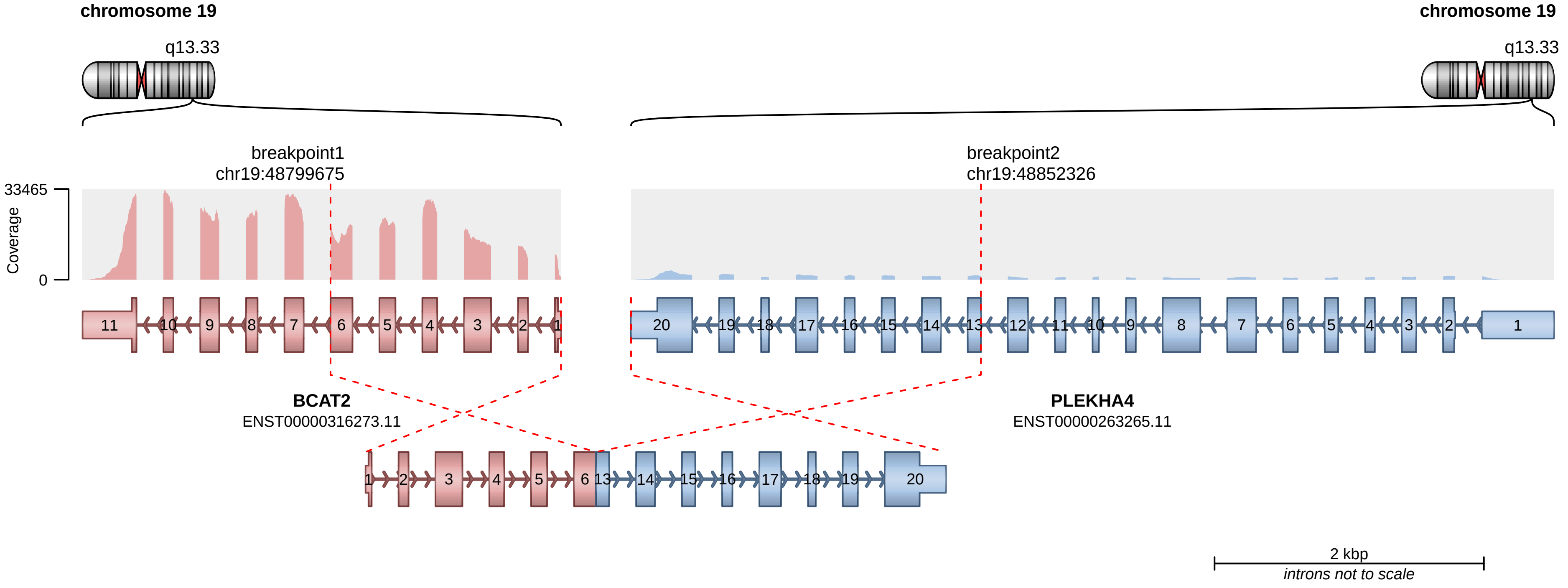


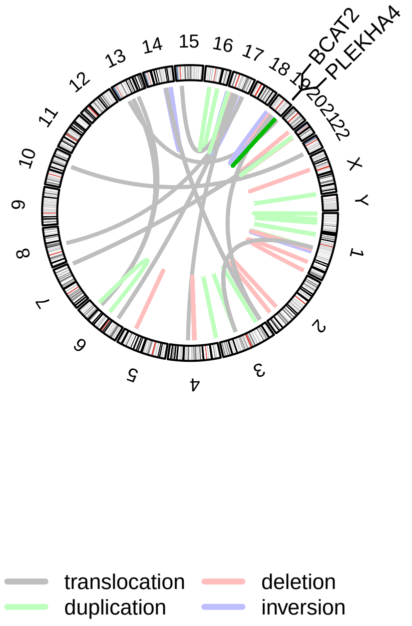


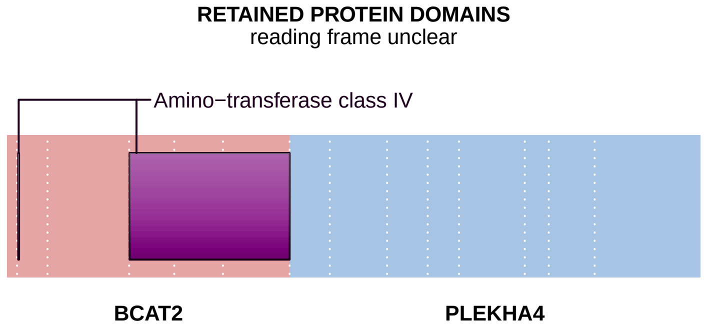
No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 0

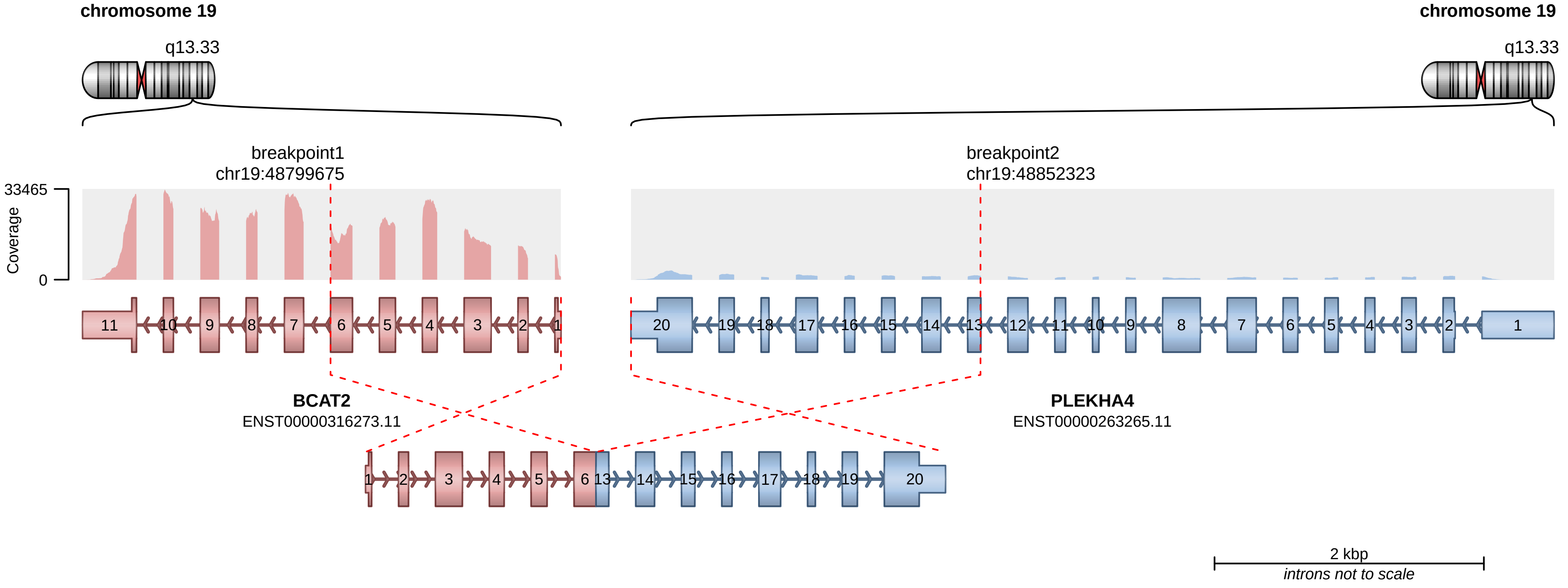


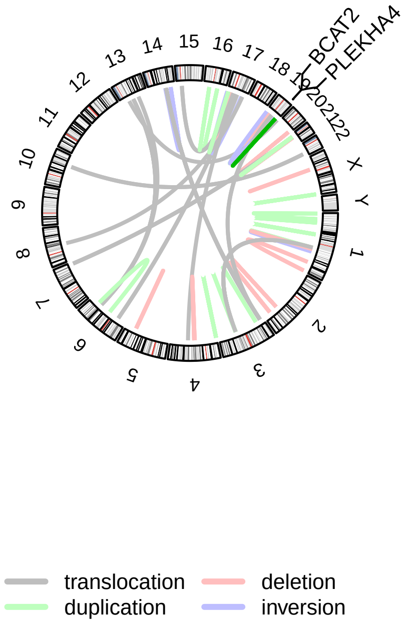




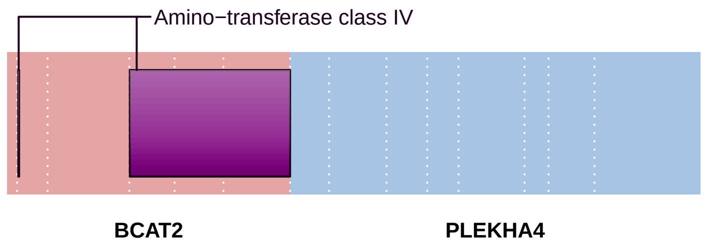
SUPPORTING READ COUNT

Split reads = 51
Discordant mates = 2



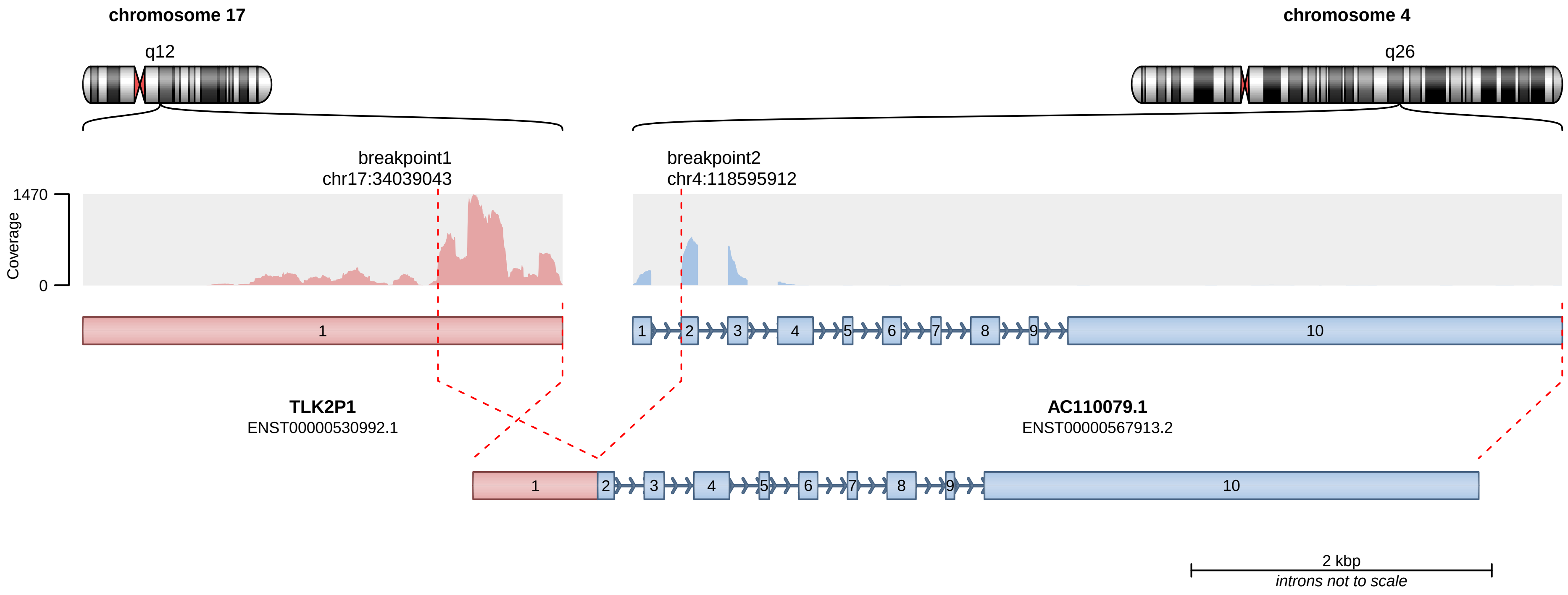


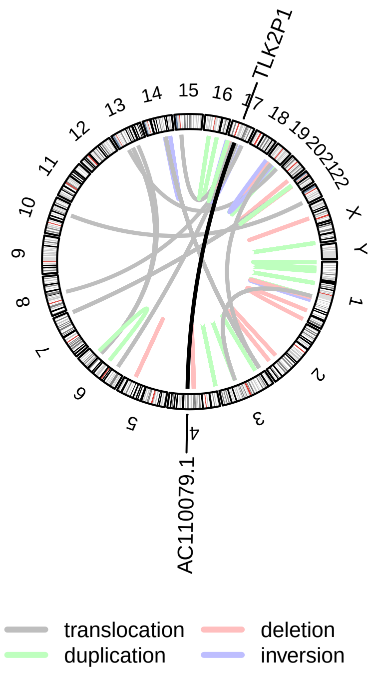
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 2

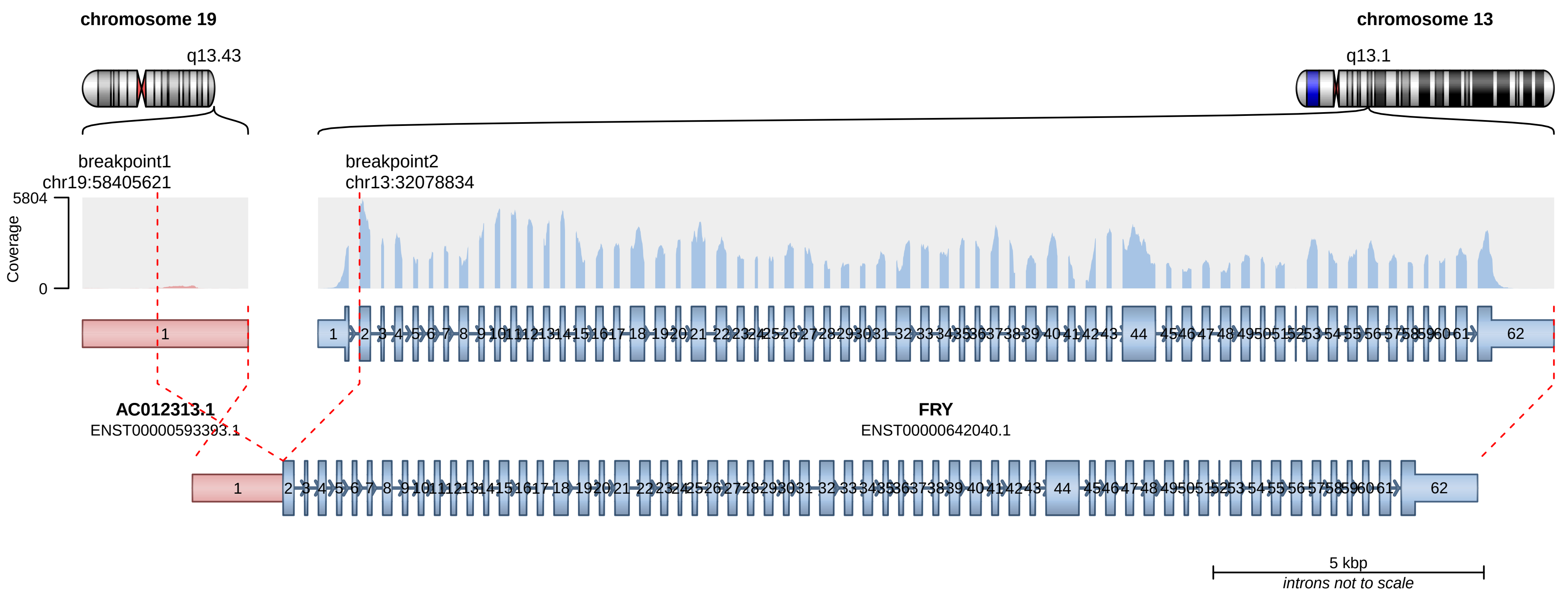


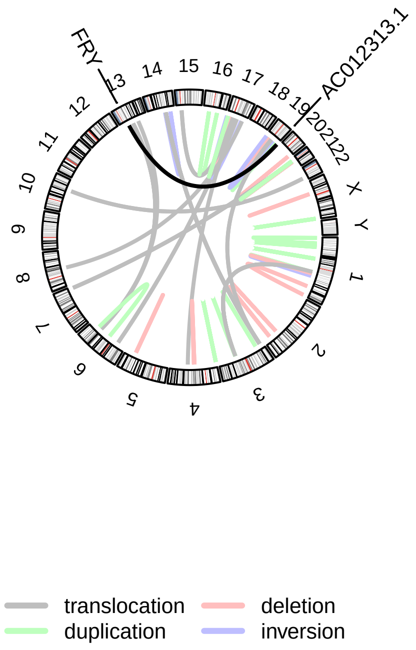


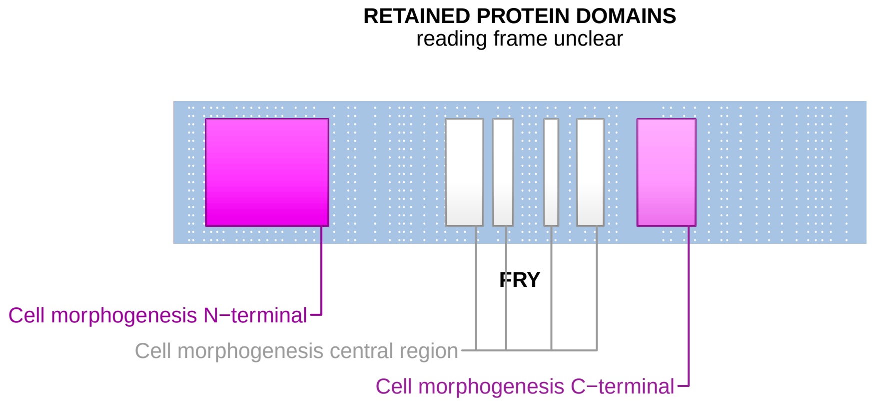
Genes are not protein−coding.

SUPPORTING READ COUNT

Split reads = 51
Discordant mates = 0

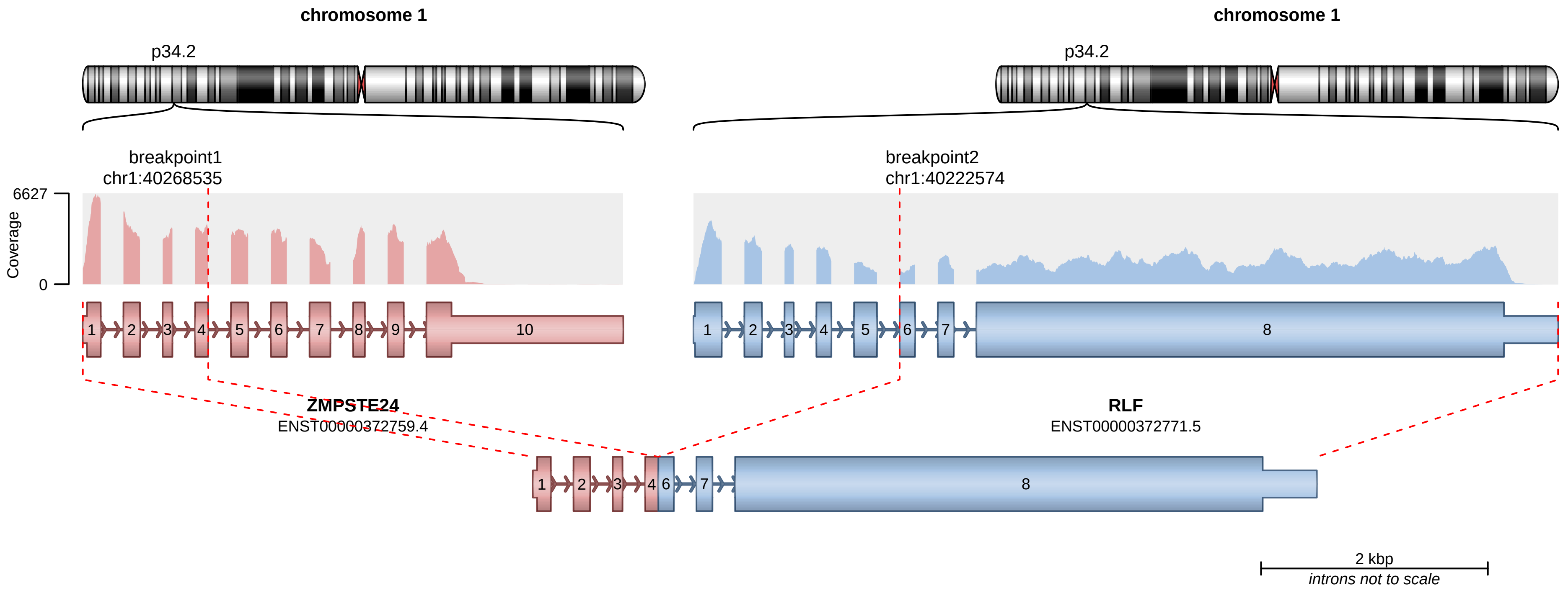


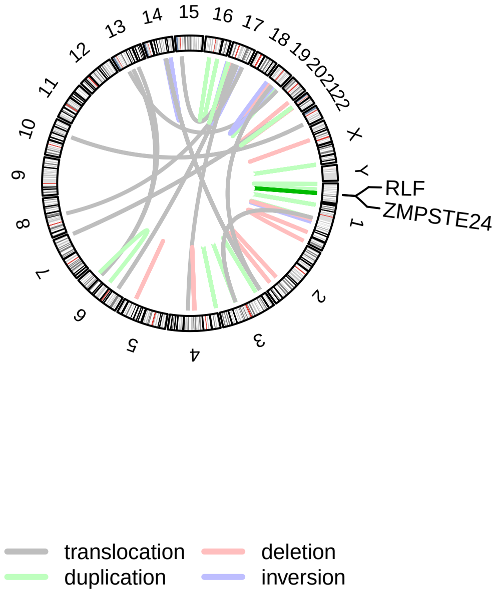




SUPPORTING READ COUNT

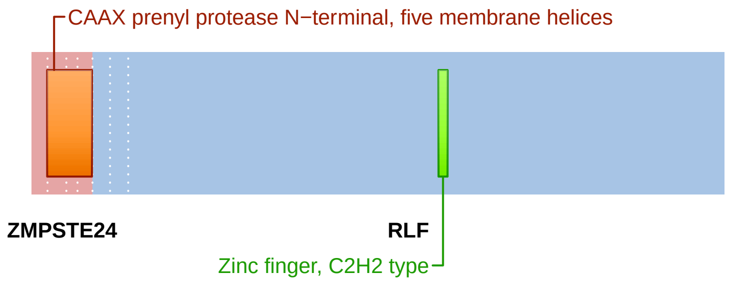
Split reads = 48
Discordant mates = 0





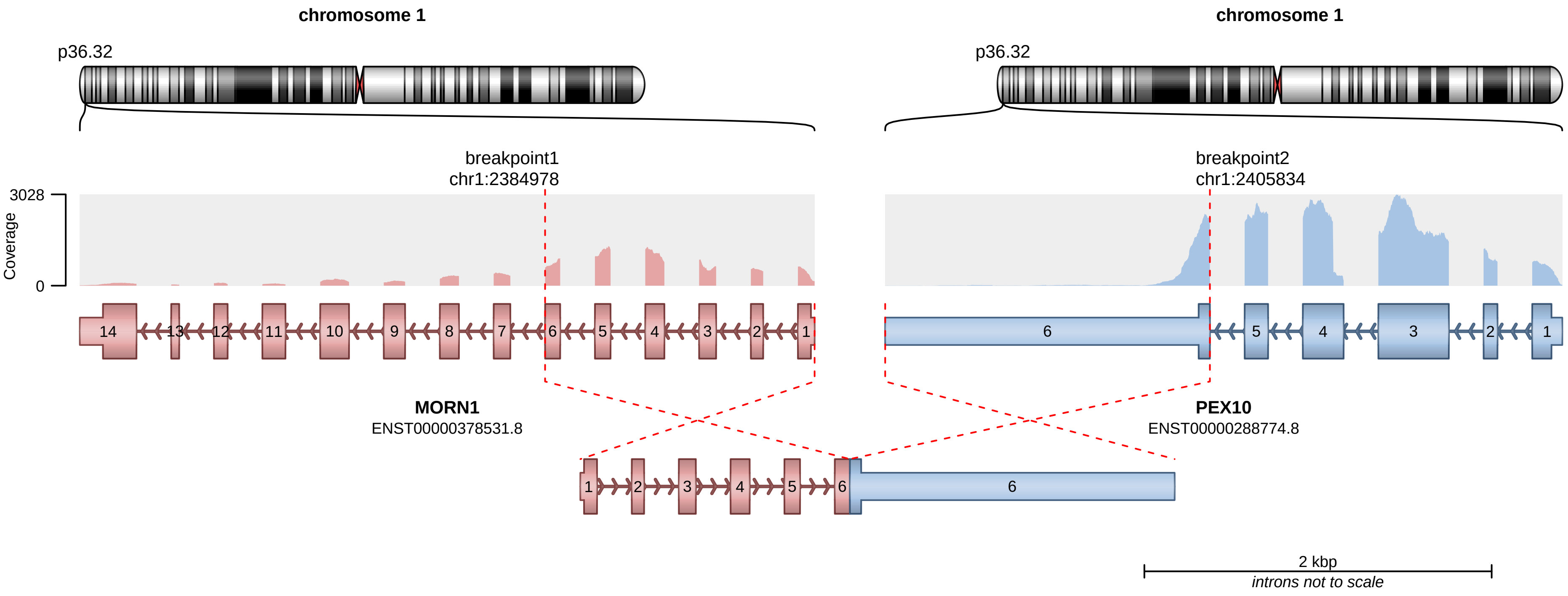
RETAINED PROTEIN DOMAINS

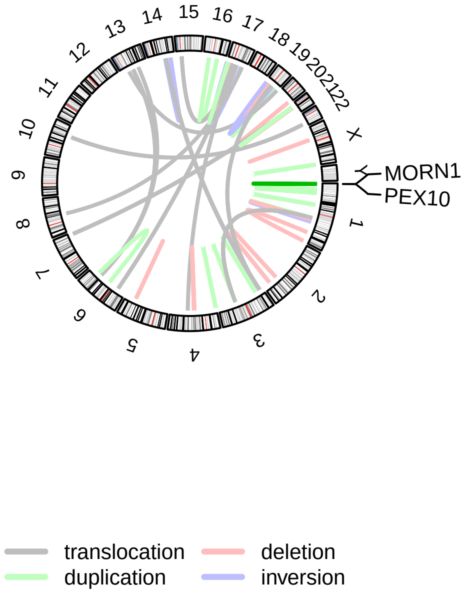
reading frame unclear

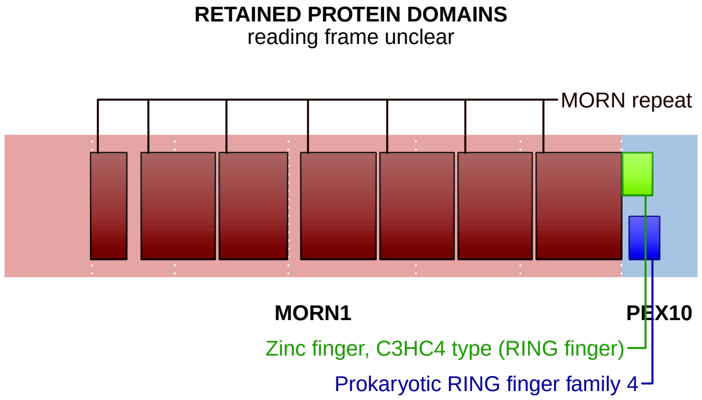


SUPPORTING READ COUNT

Split reads = 42
Discordant mates = 4

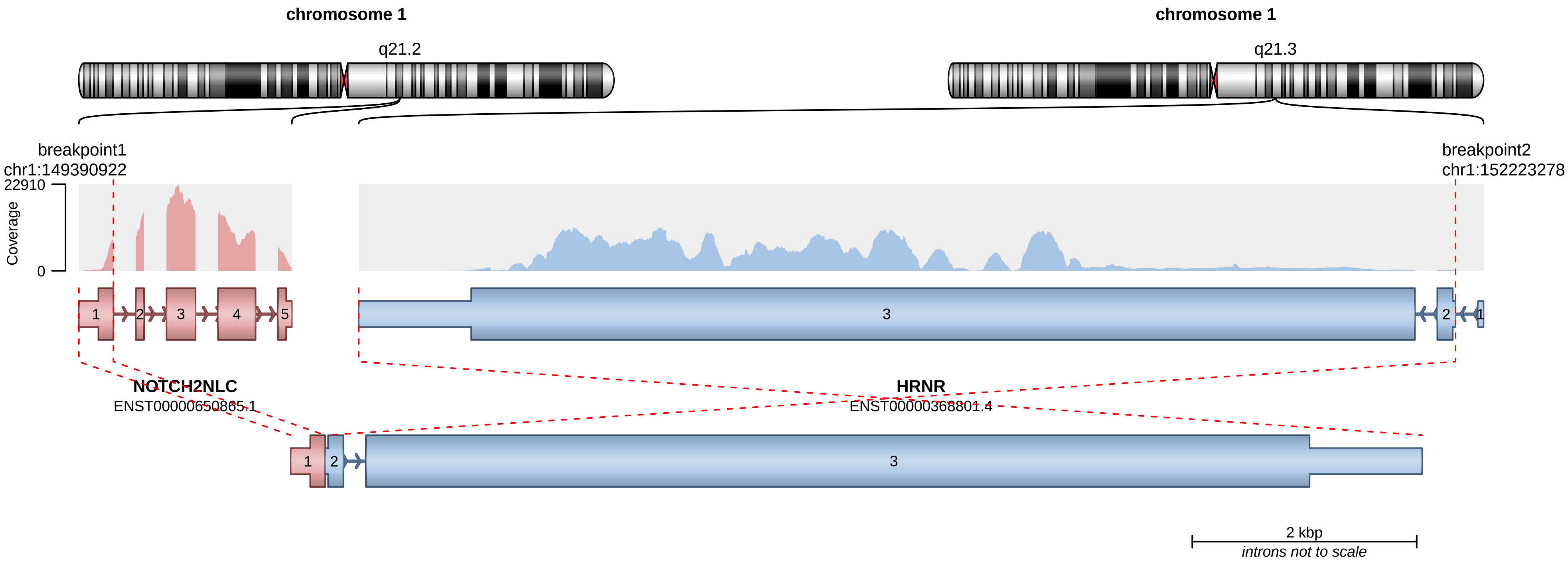


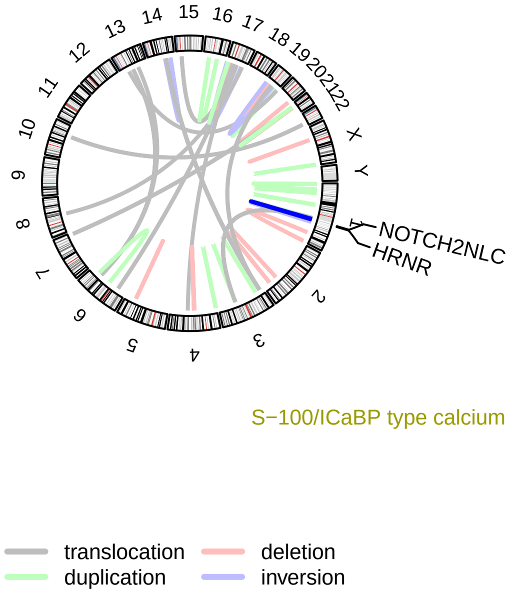


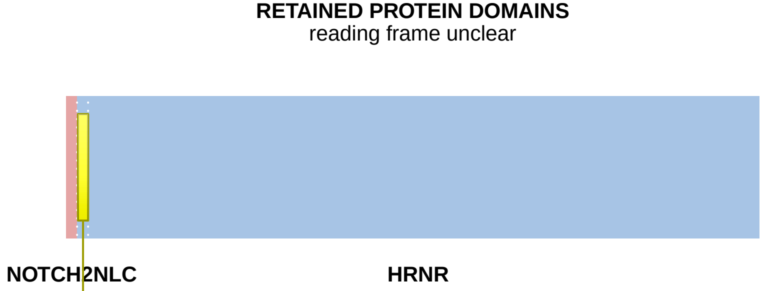


SUPPORTING READ COUNT

Split reads = 41
Discordant mates = 0

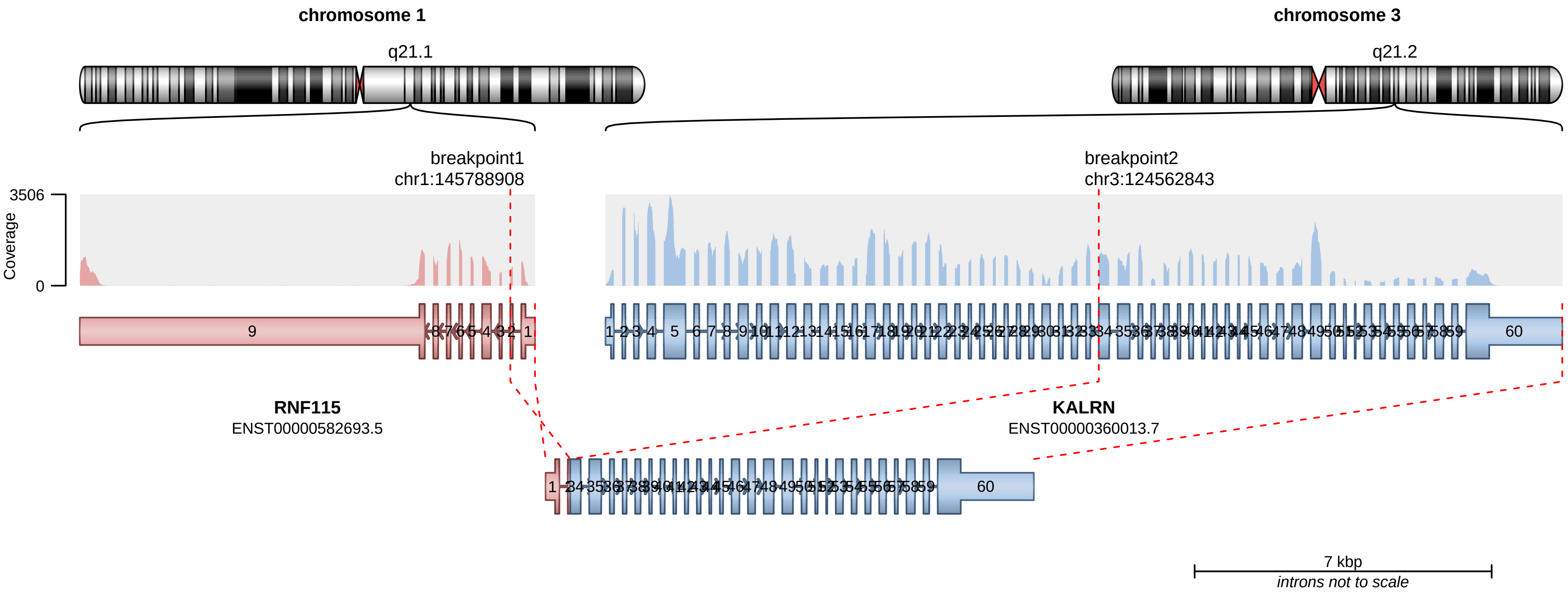


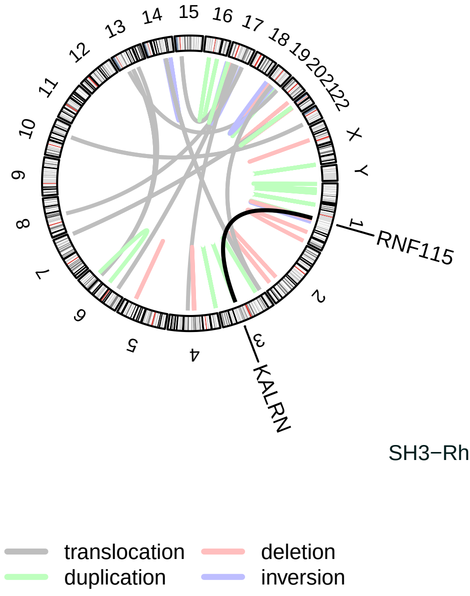


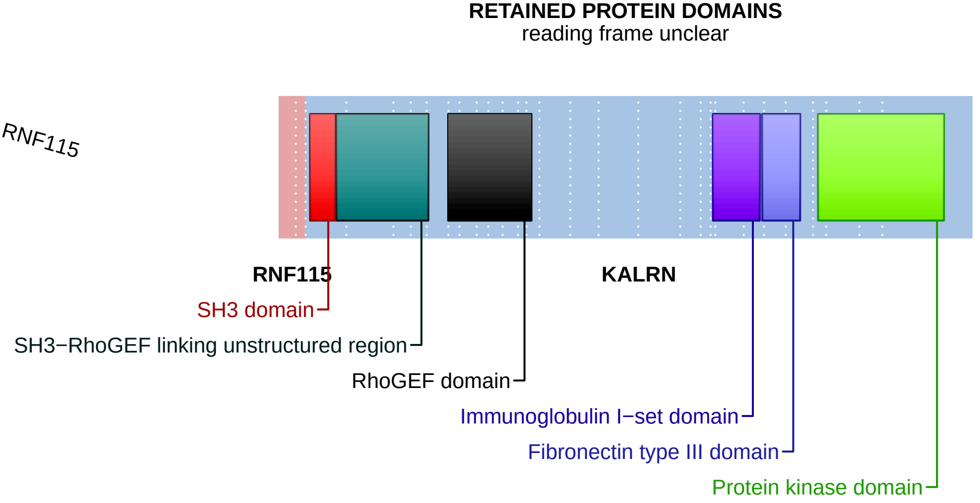


SUPPORTING READ COUNT

Split reads = 40
Discordant mates = 0

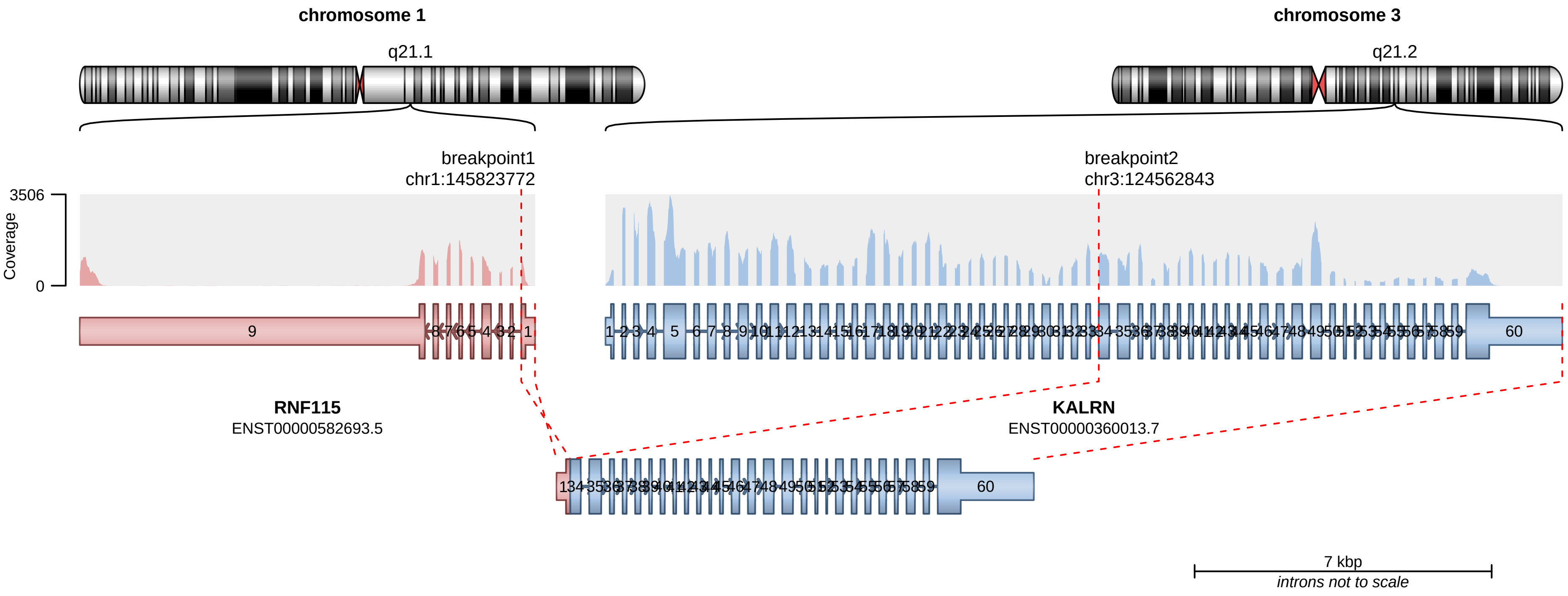


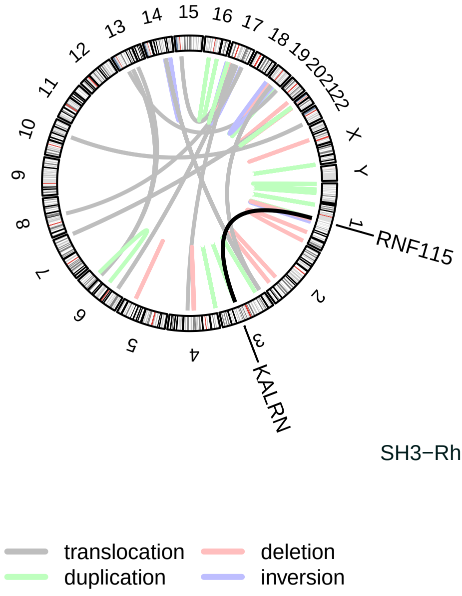


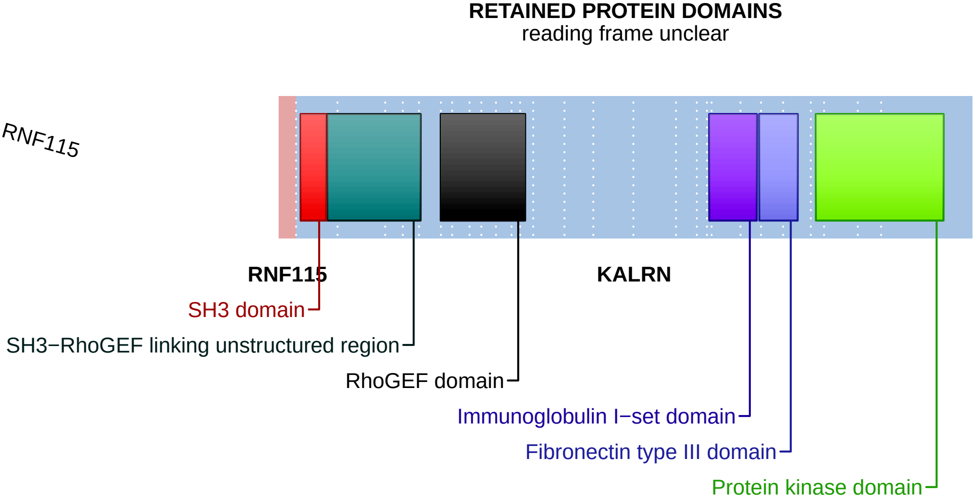


SUPPORTING READ COUNT

Split reads = 38
Discordant mates = 1

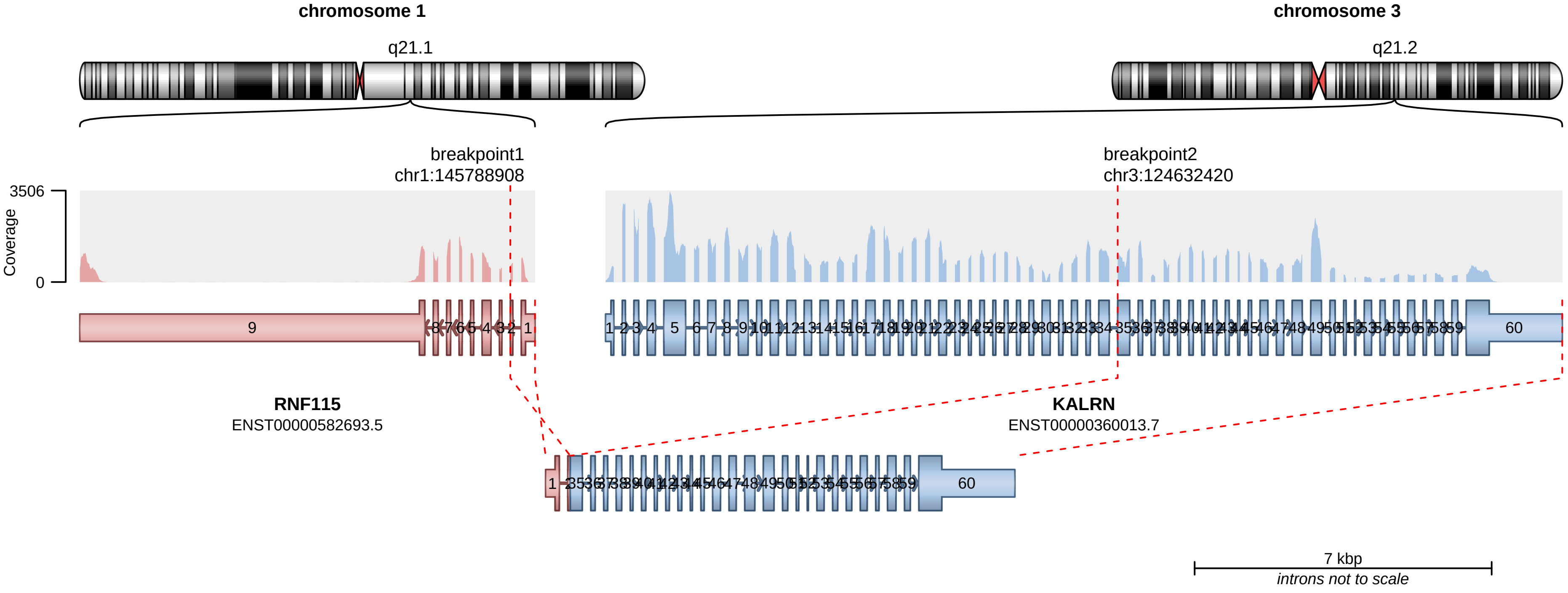


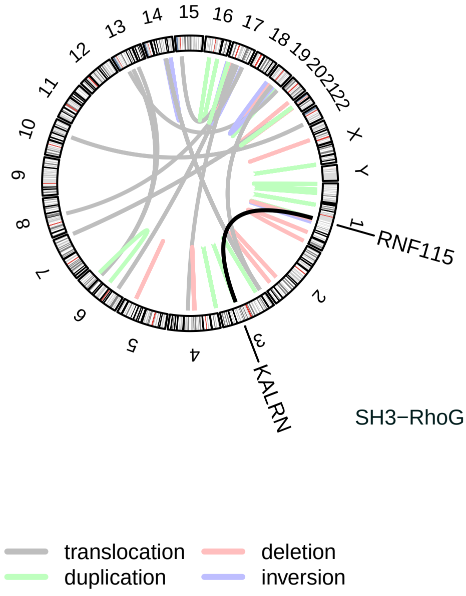




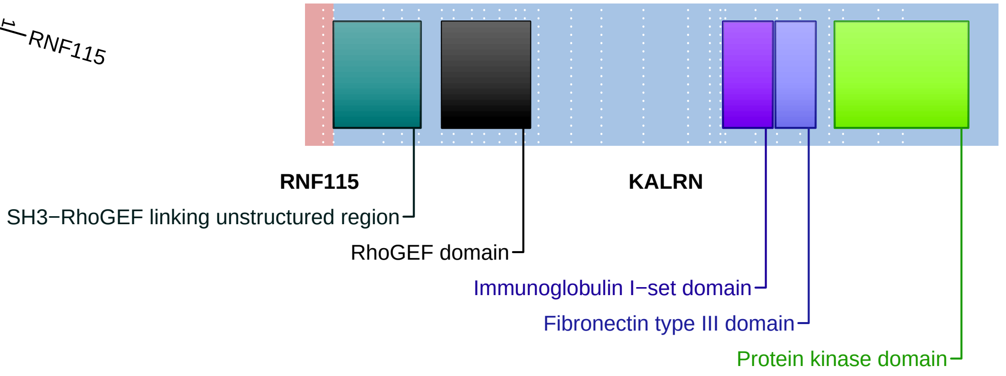
SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 1



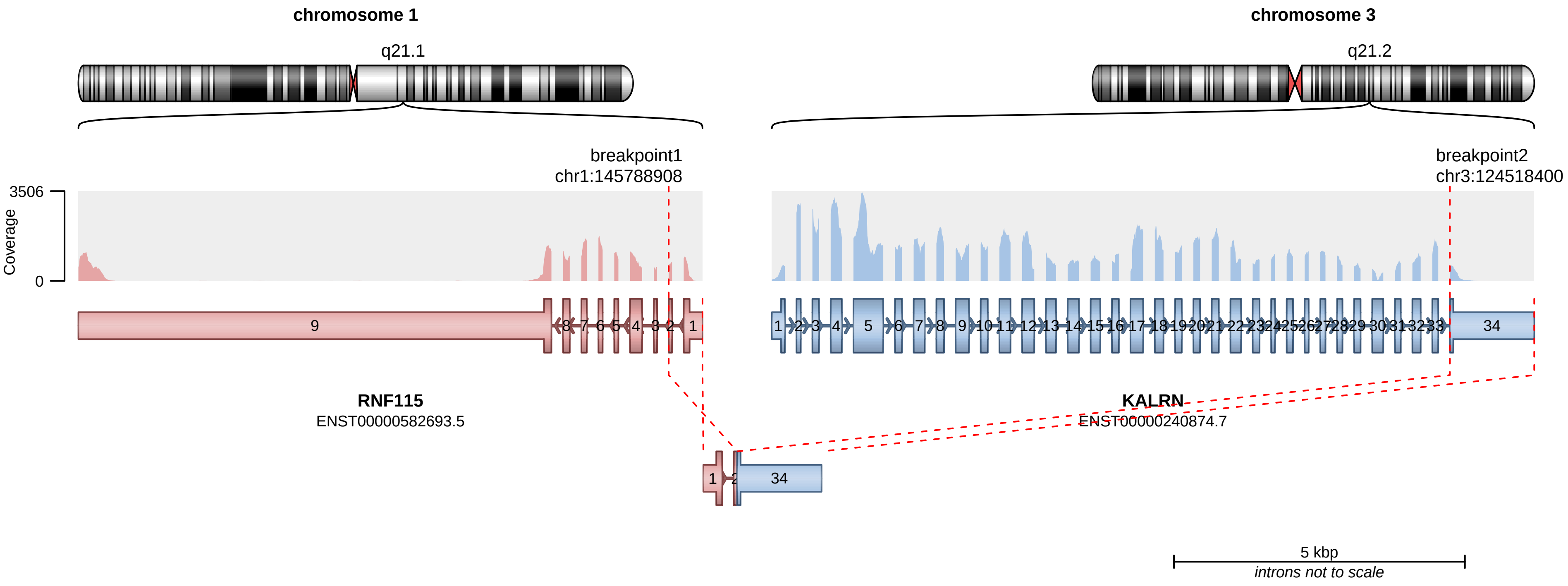


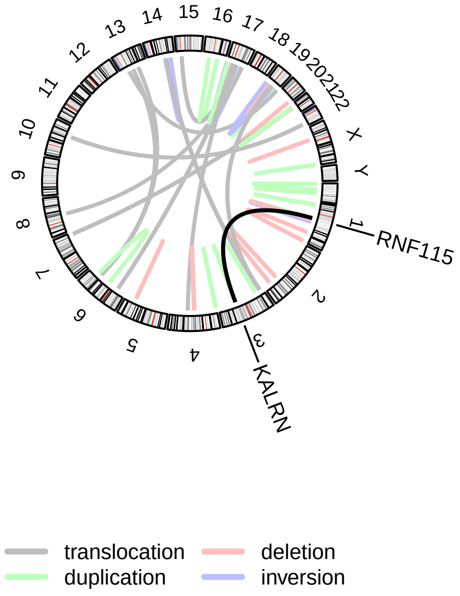
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

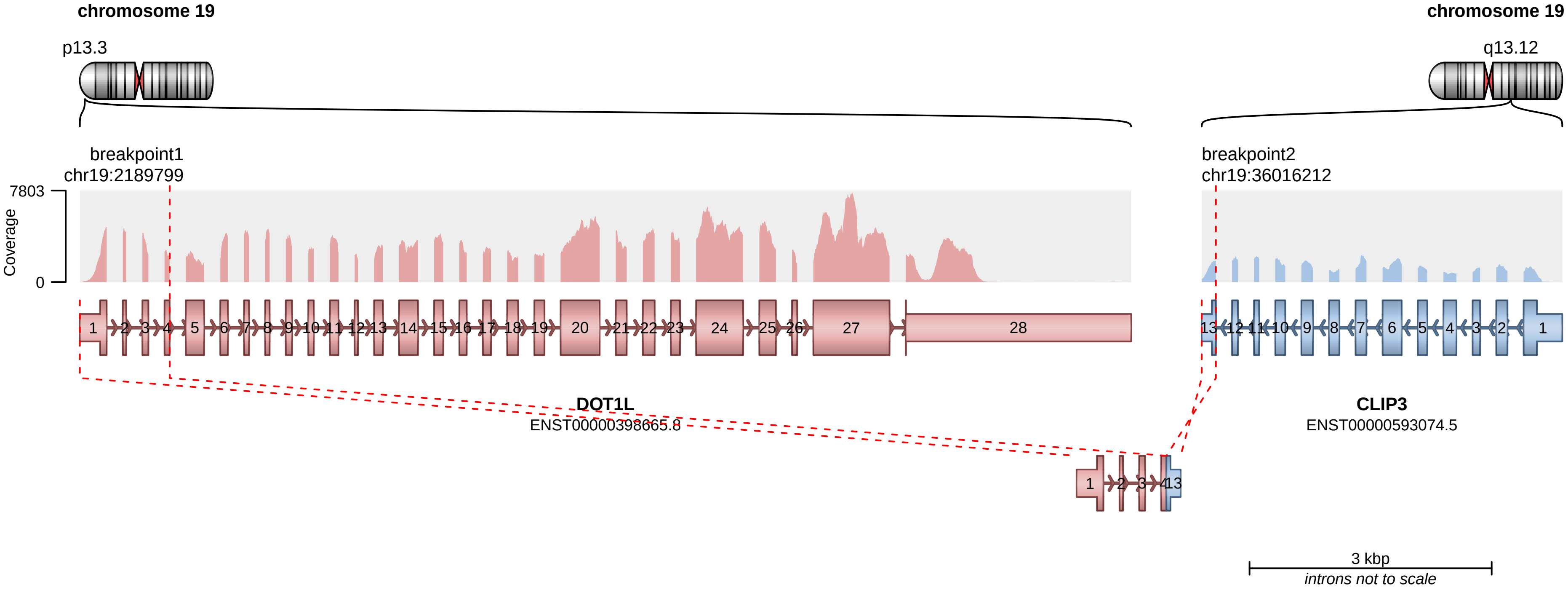


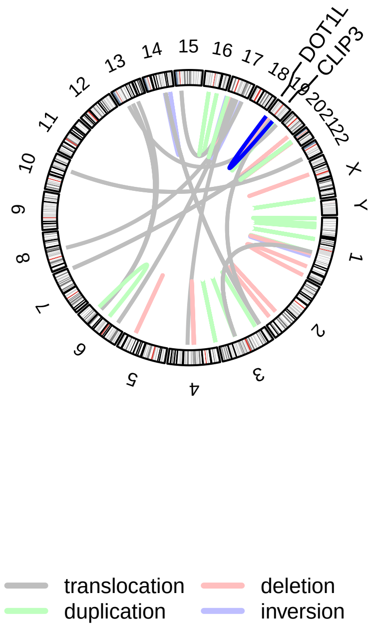


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

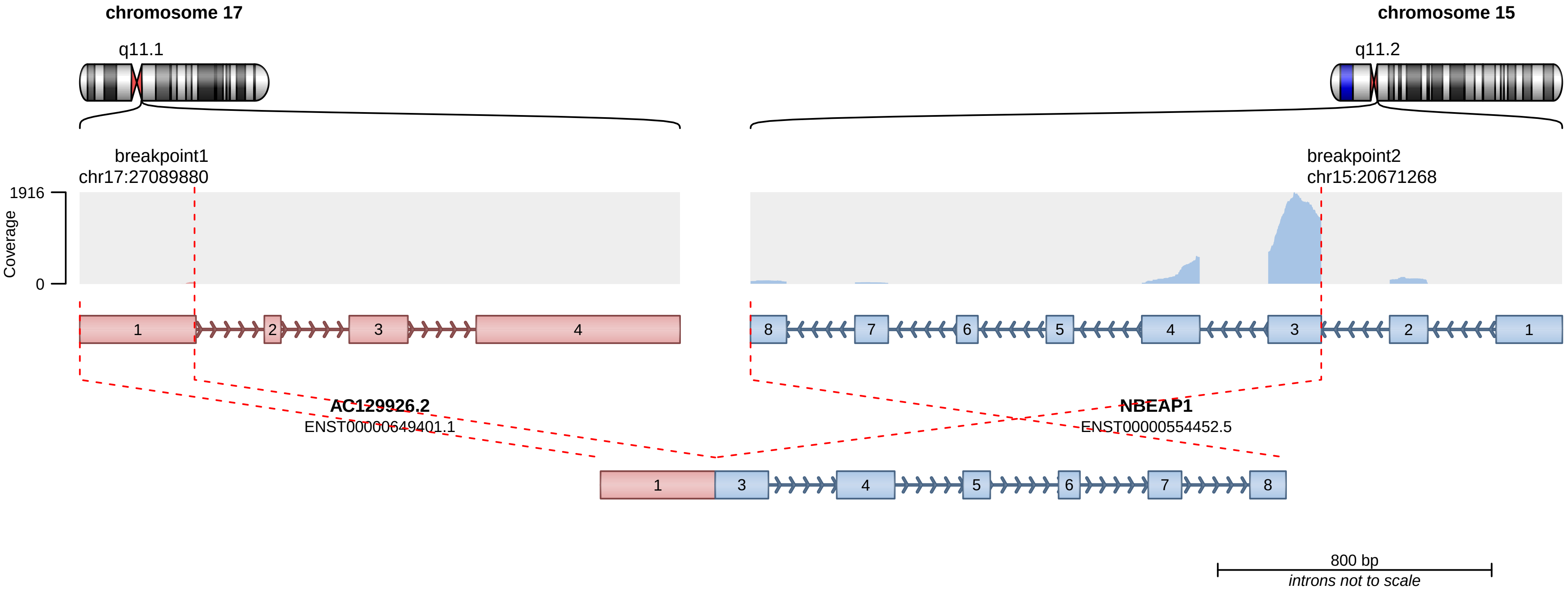


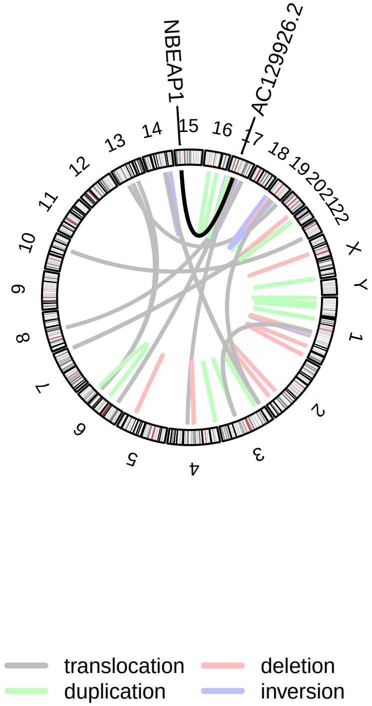


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 36
Discordant mates = 1

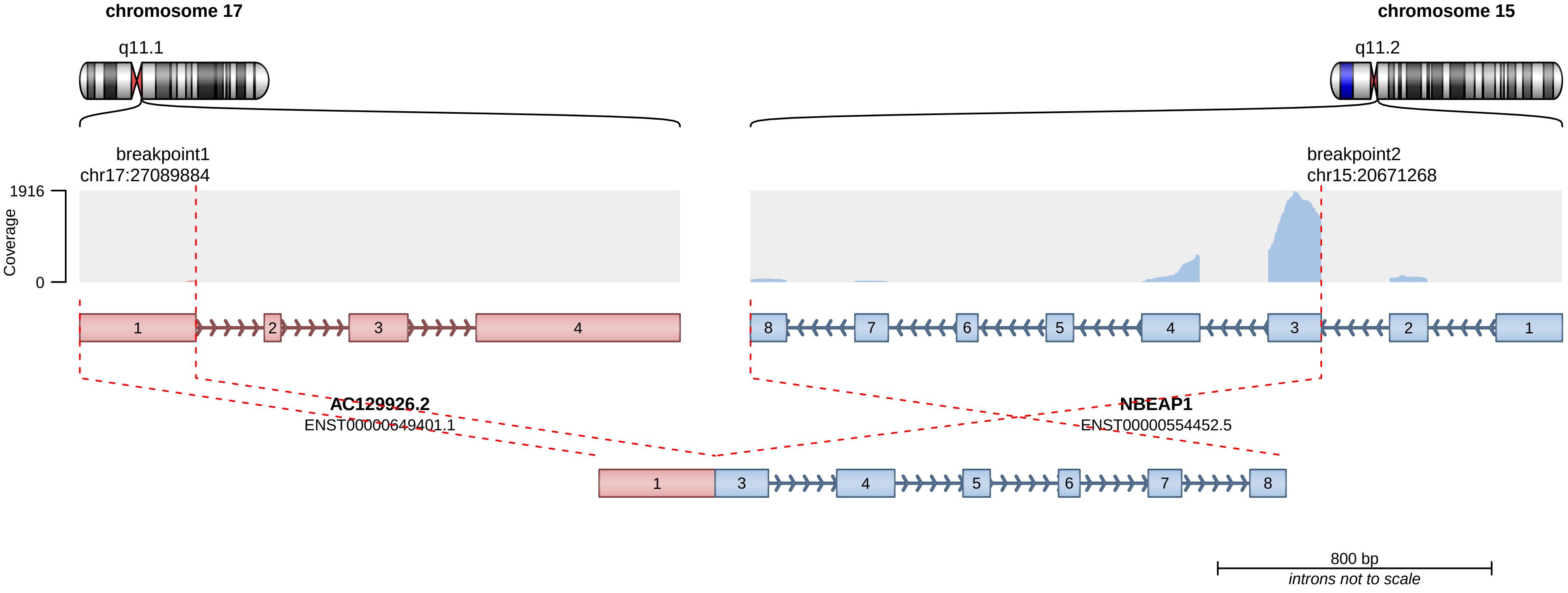


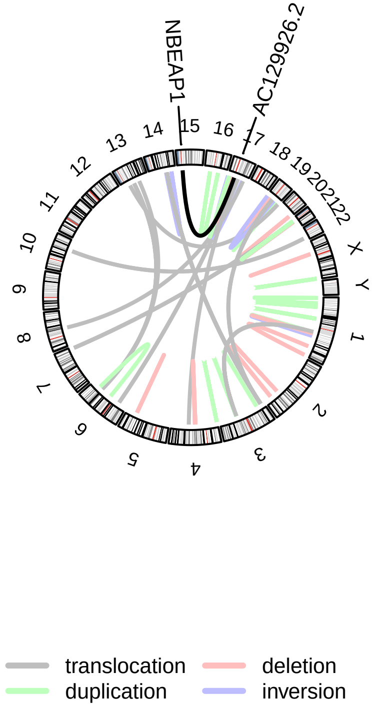


Genes are not protein−coding.

SUPPORTING READ COUNT

Split reads = 30
Discordant mates = 0

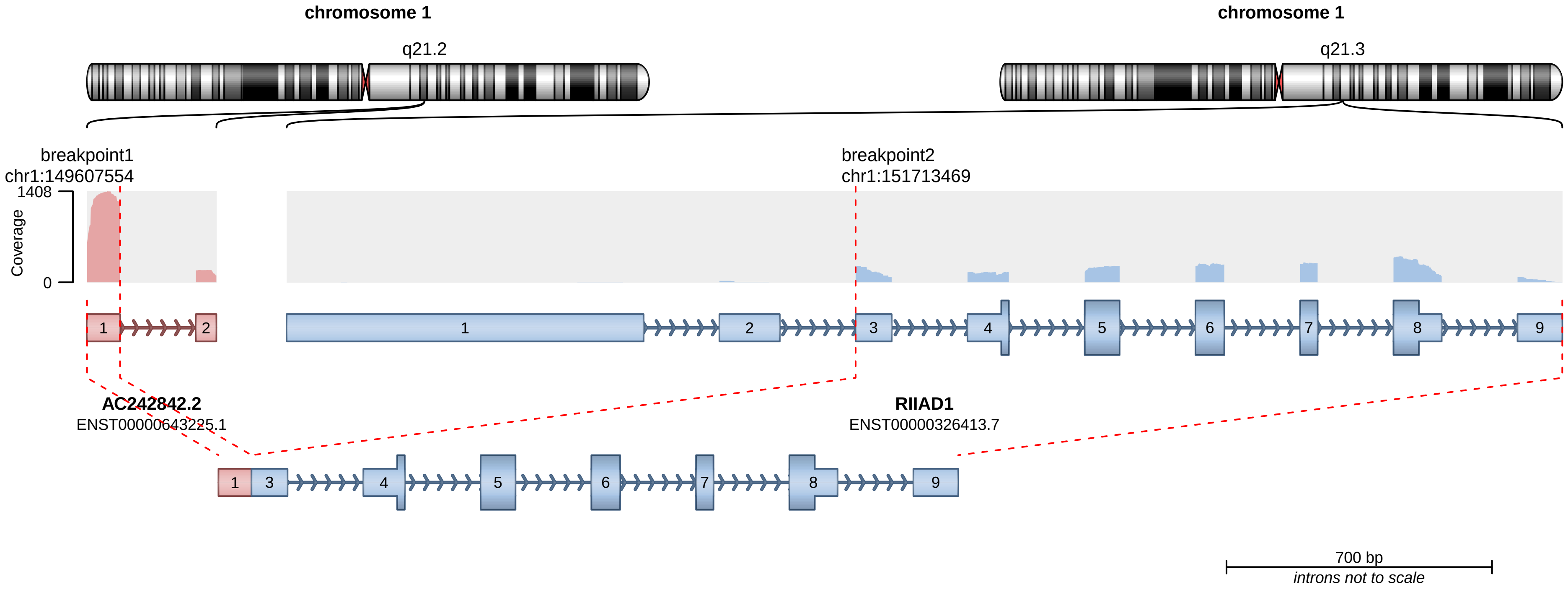


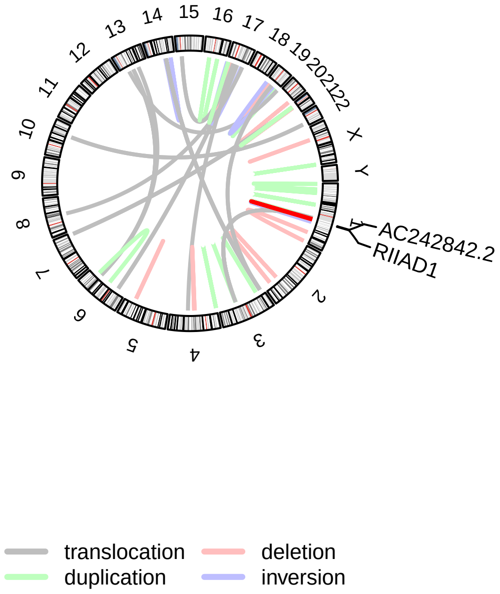


Genes are not protein−coding.

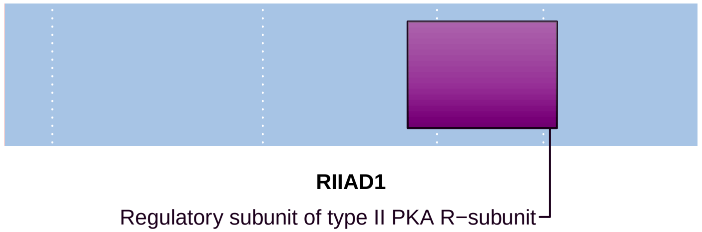
SUPPORTING READ COUNT

Split reads = 23
Discordant mates = 0



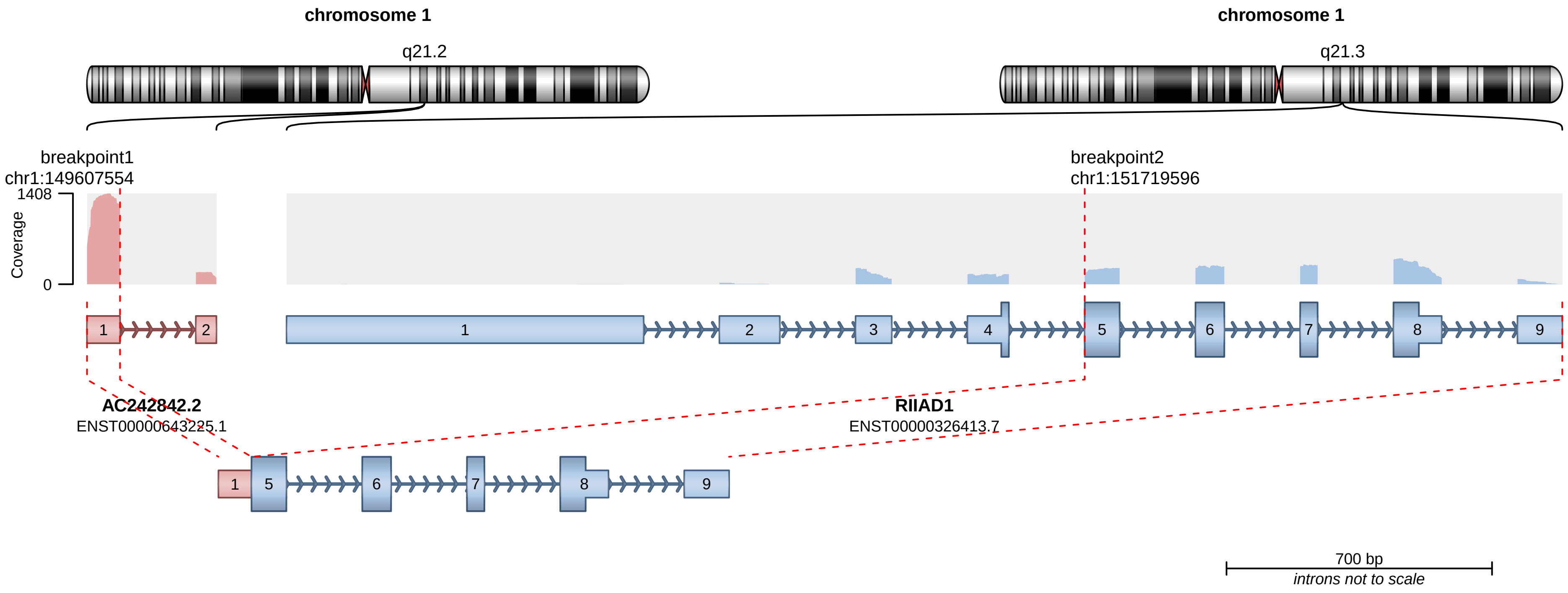


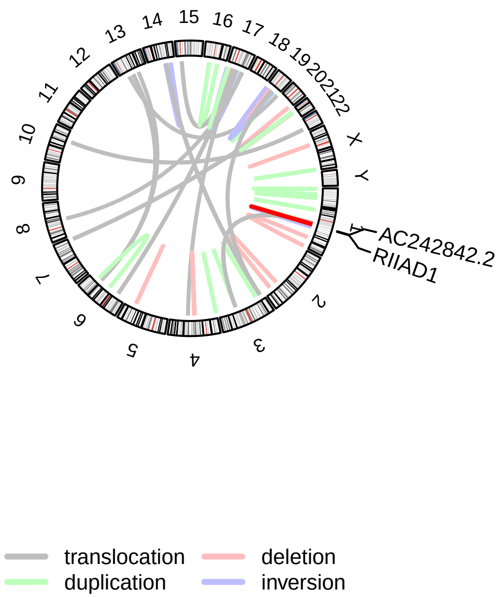
RETAINED PROTEIN DOMAINS
reading frame unclear

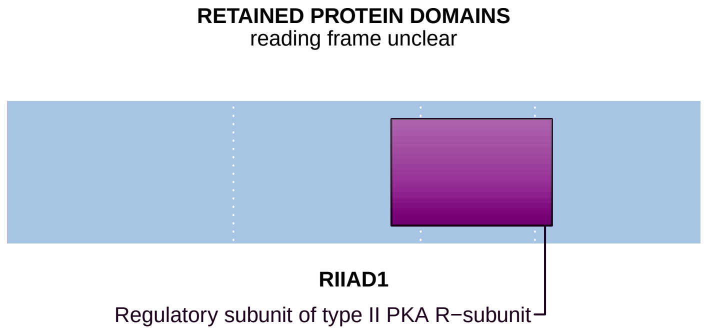


SUPPORTING READ COUNT

Split reads = 27
Discordant mates = 0

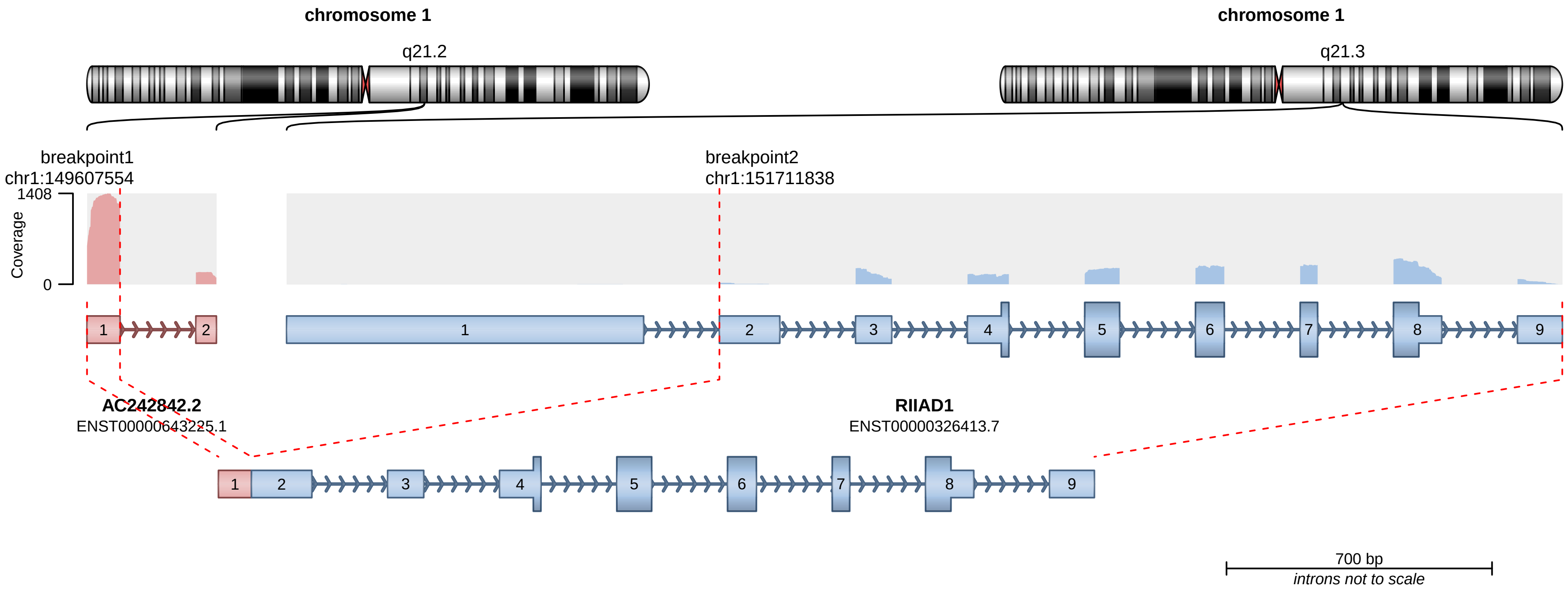


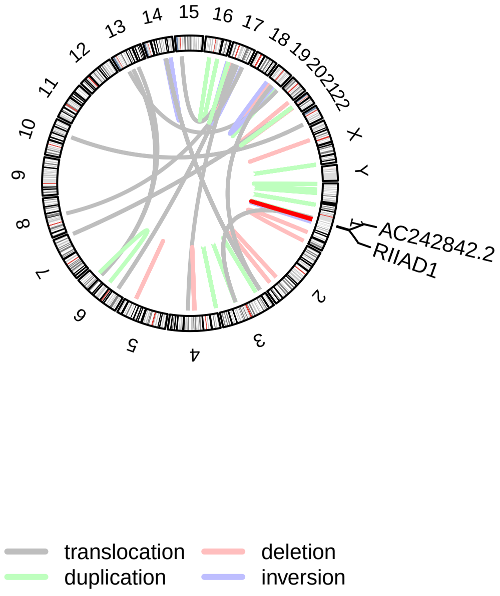


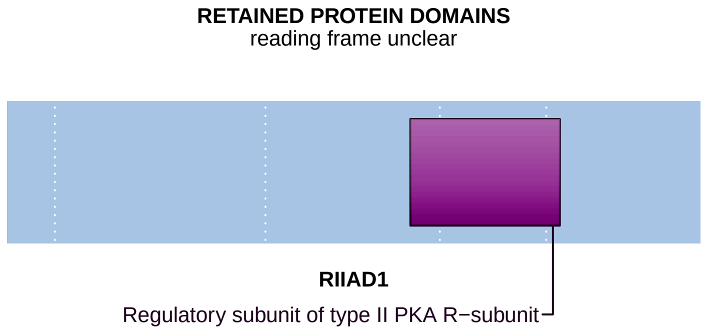


SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

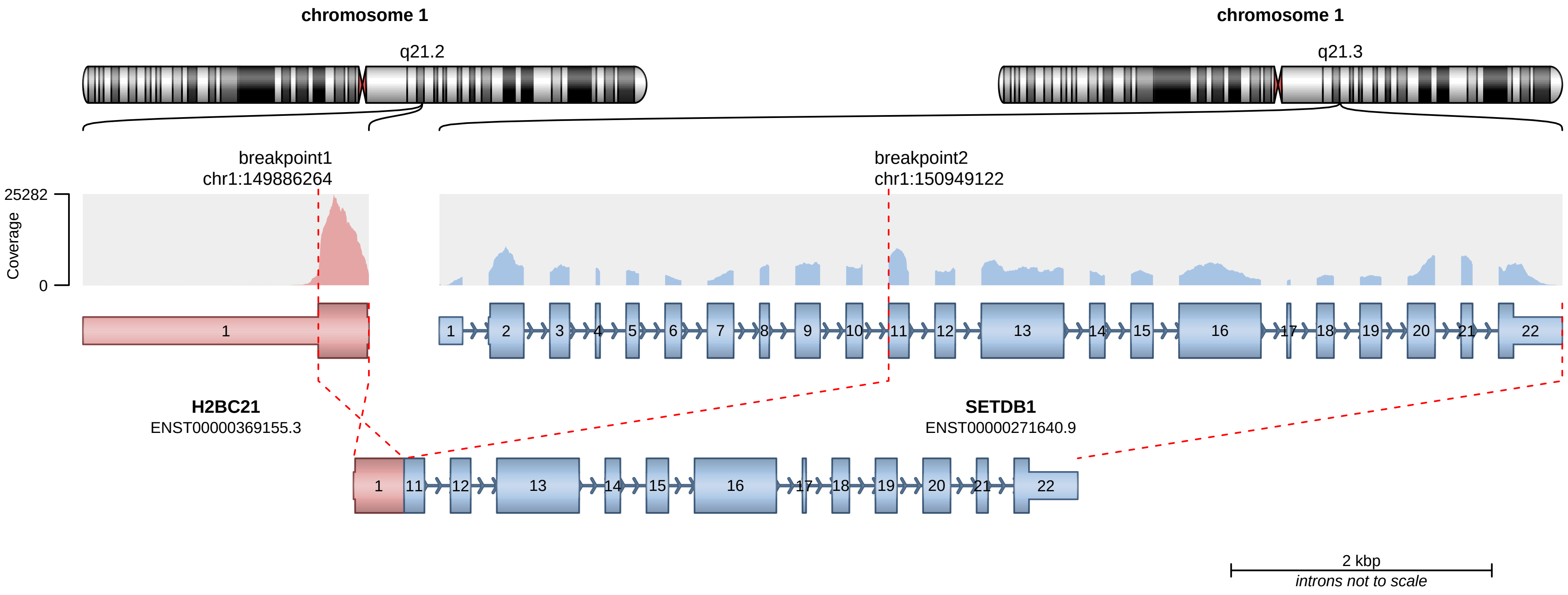


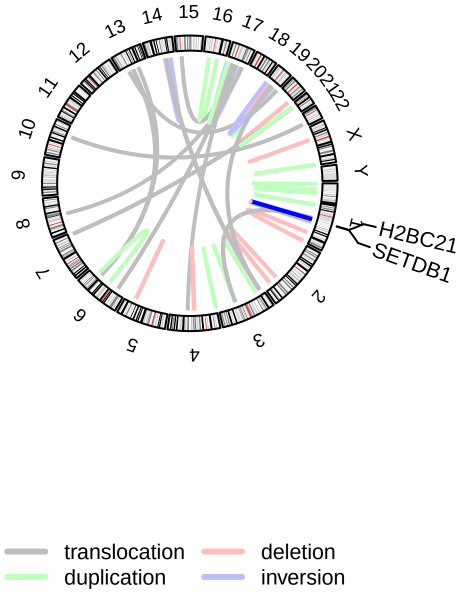


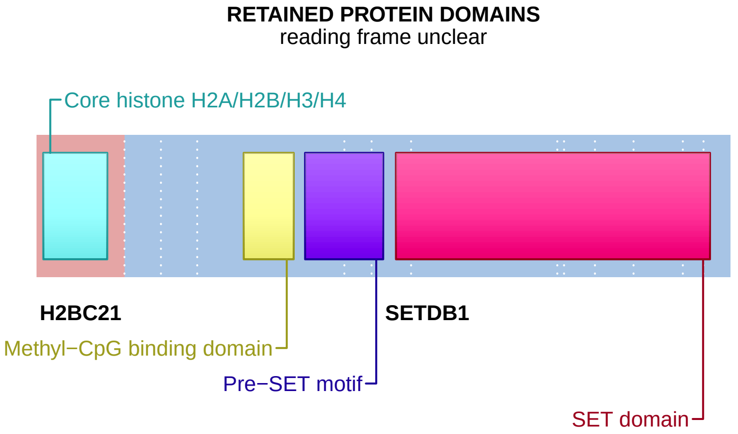


SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

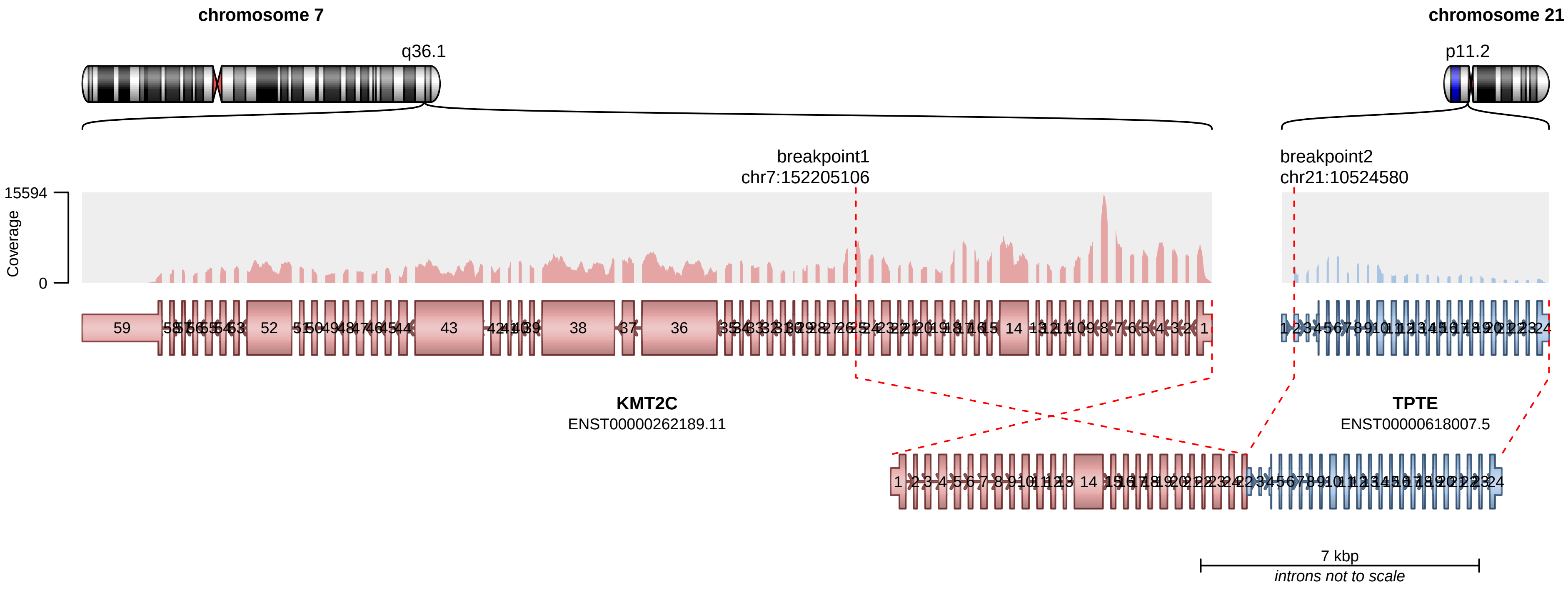


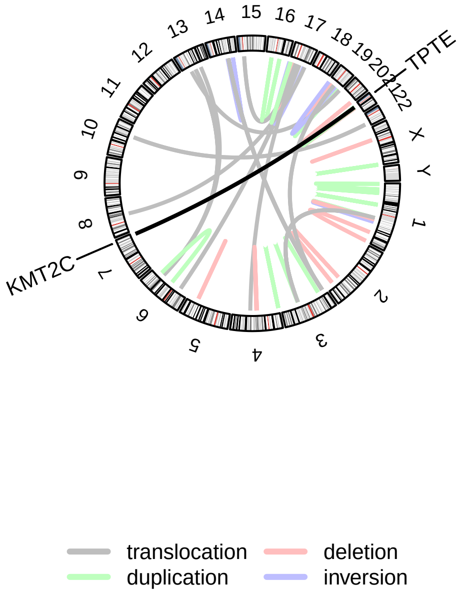


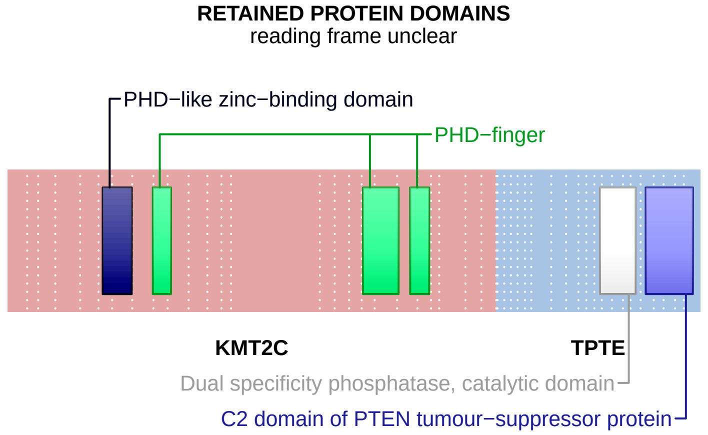


SUPPORTING READ COUNT

Split reads = 27
Discordant mates = 0

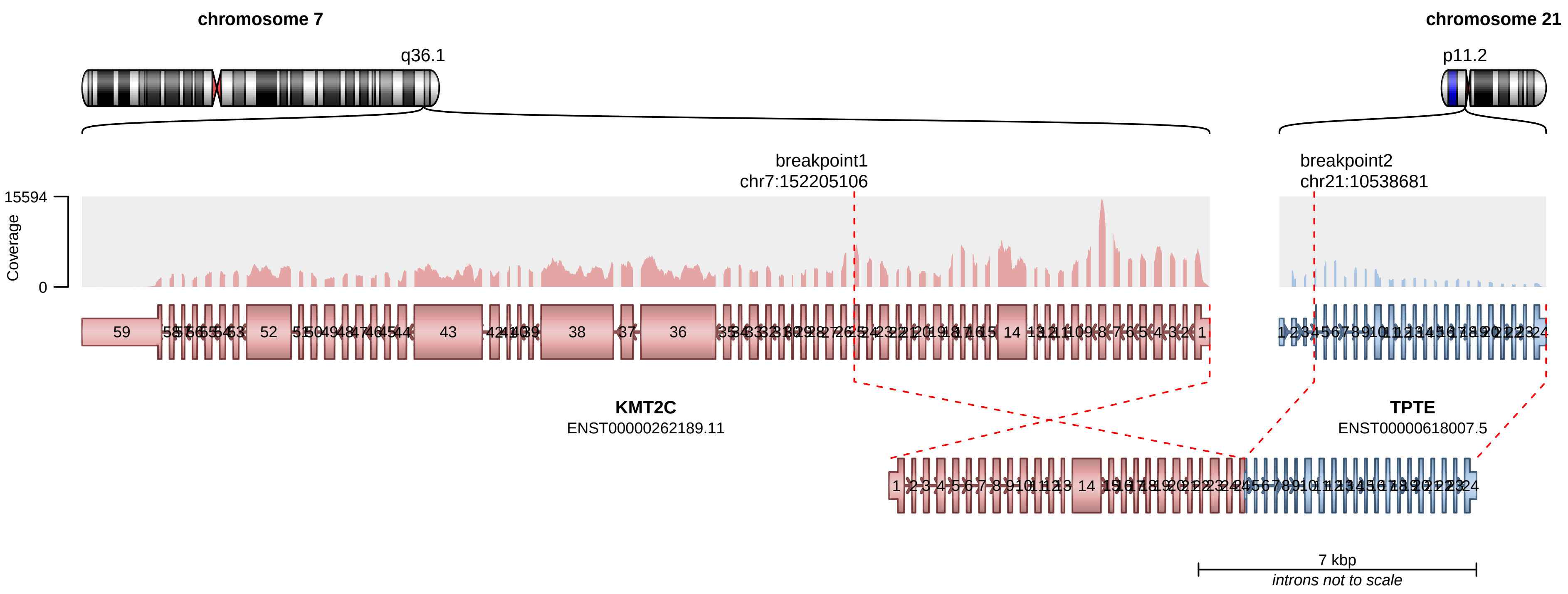


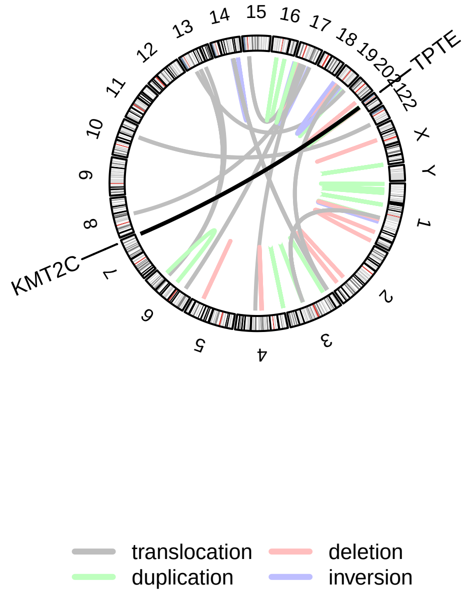


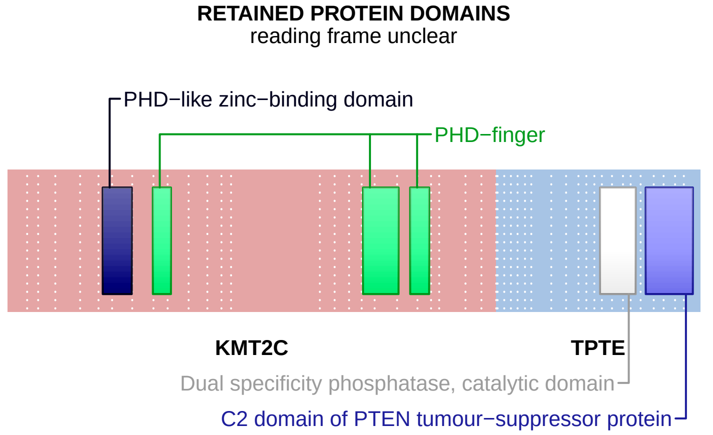


SUPPORTING READ COUNT

Split reads = 26
Discordant mates = 2

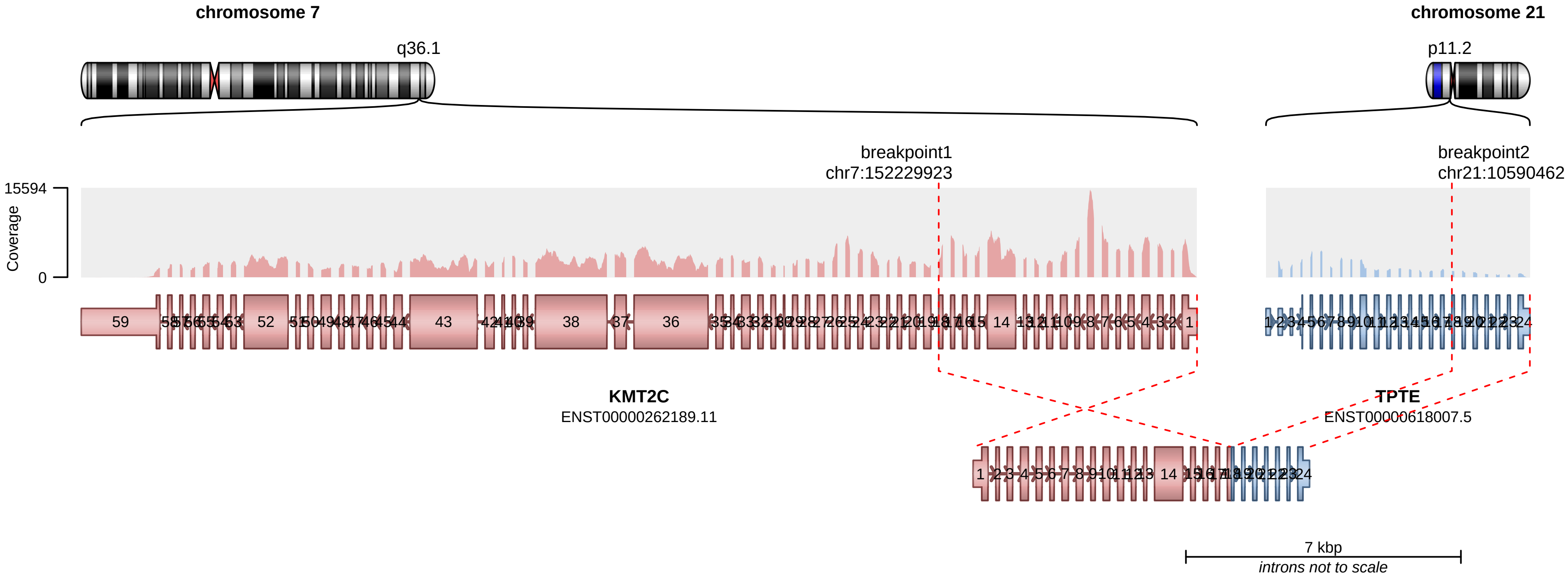


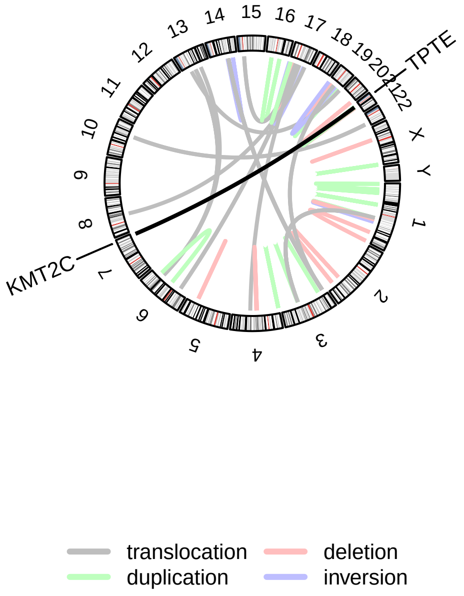


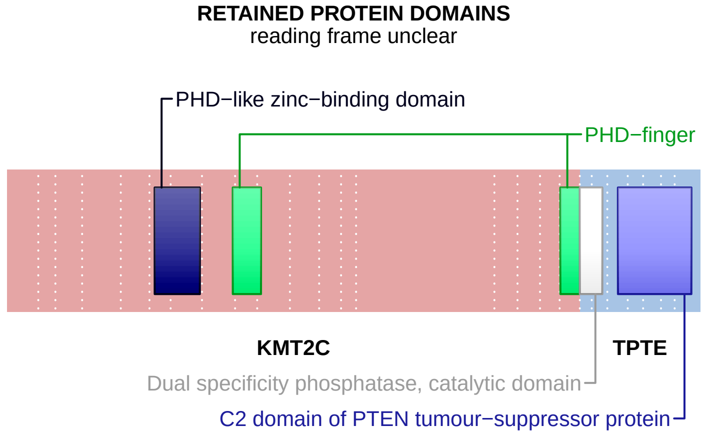


SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

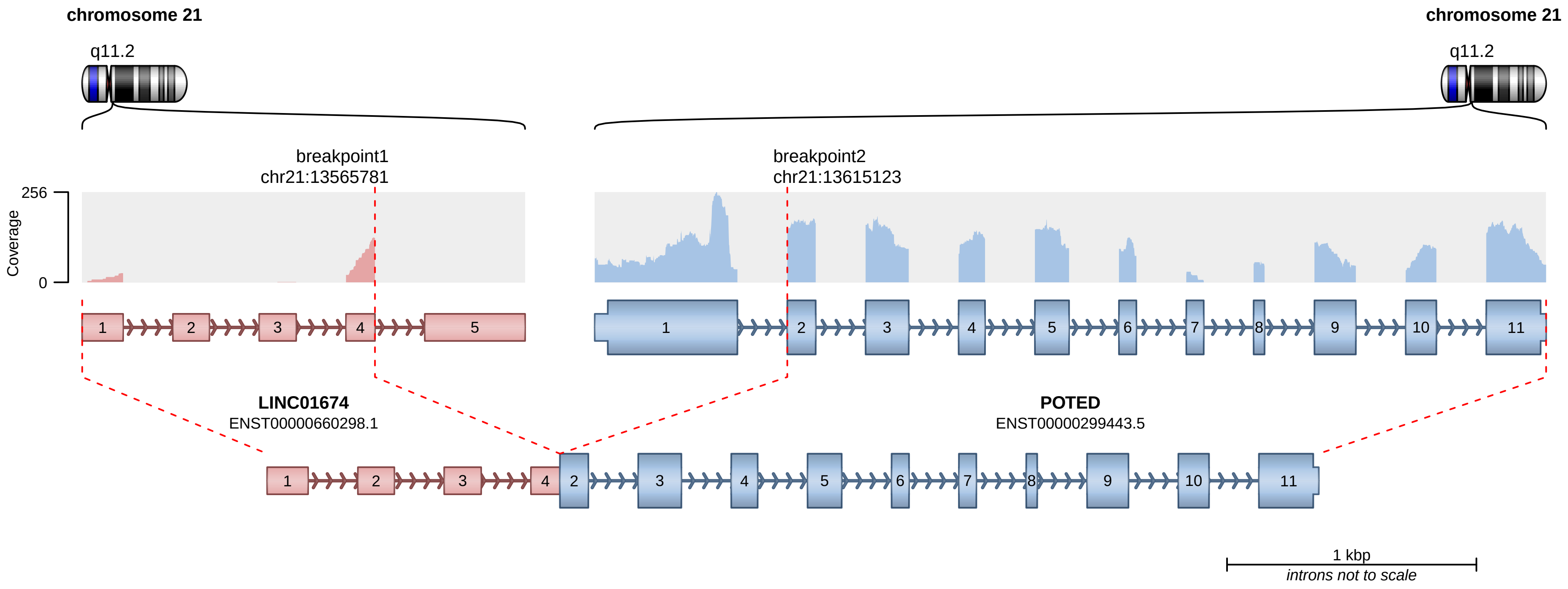


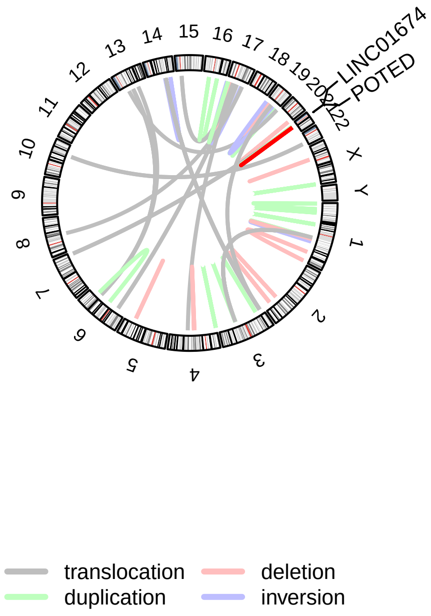


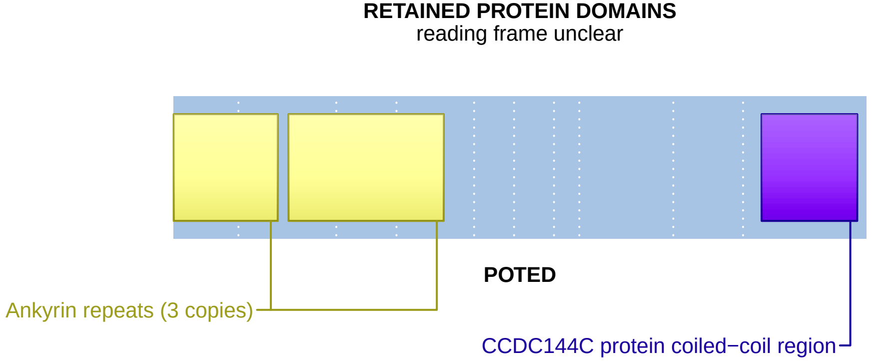


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

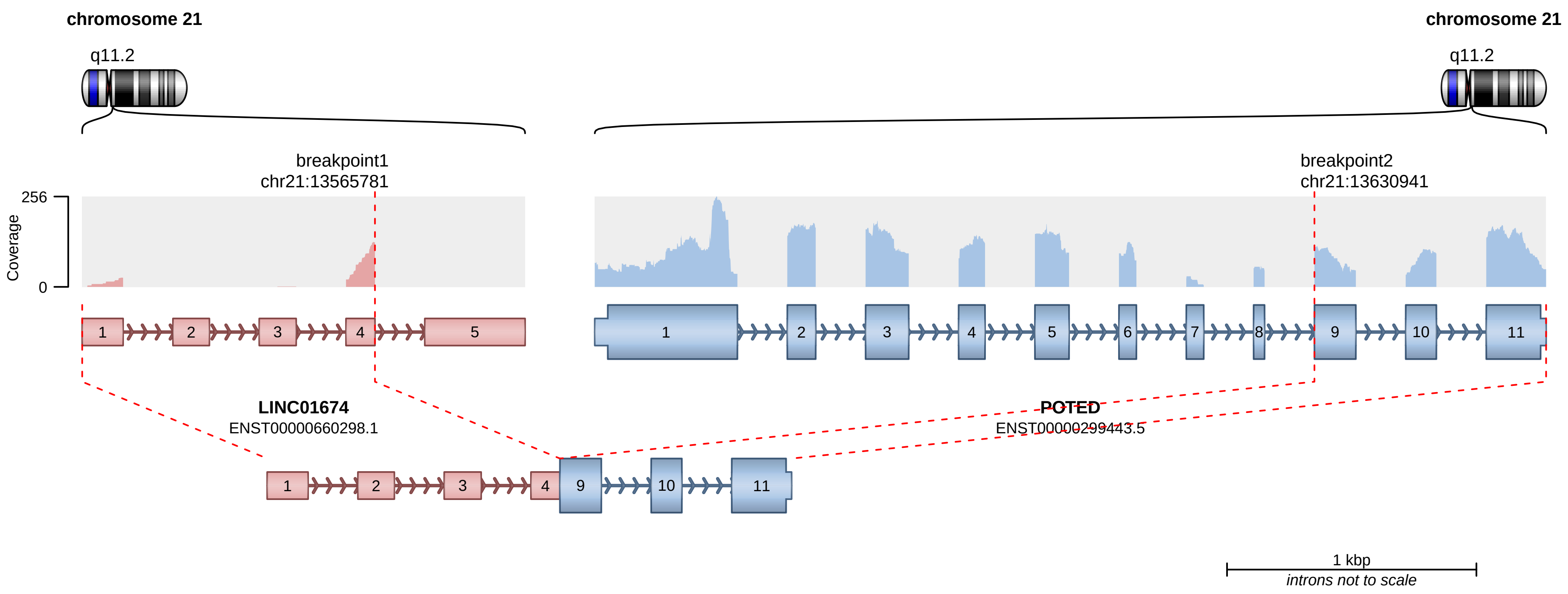


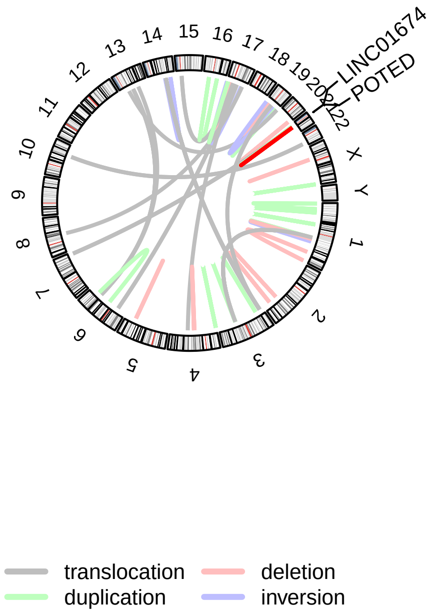




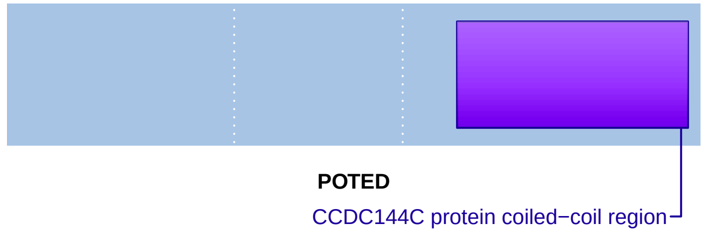
SUPPORTING READ COUNT

Split reads = 26
Discordant mates = 1



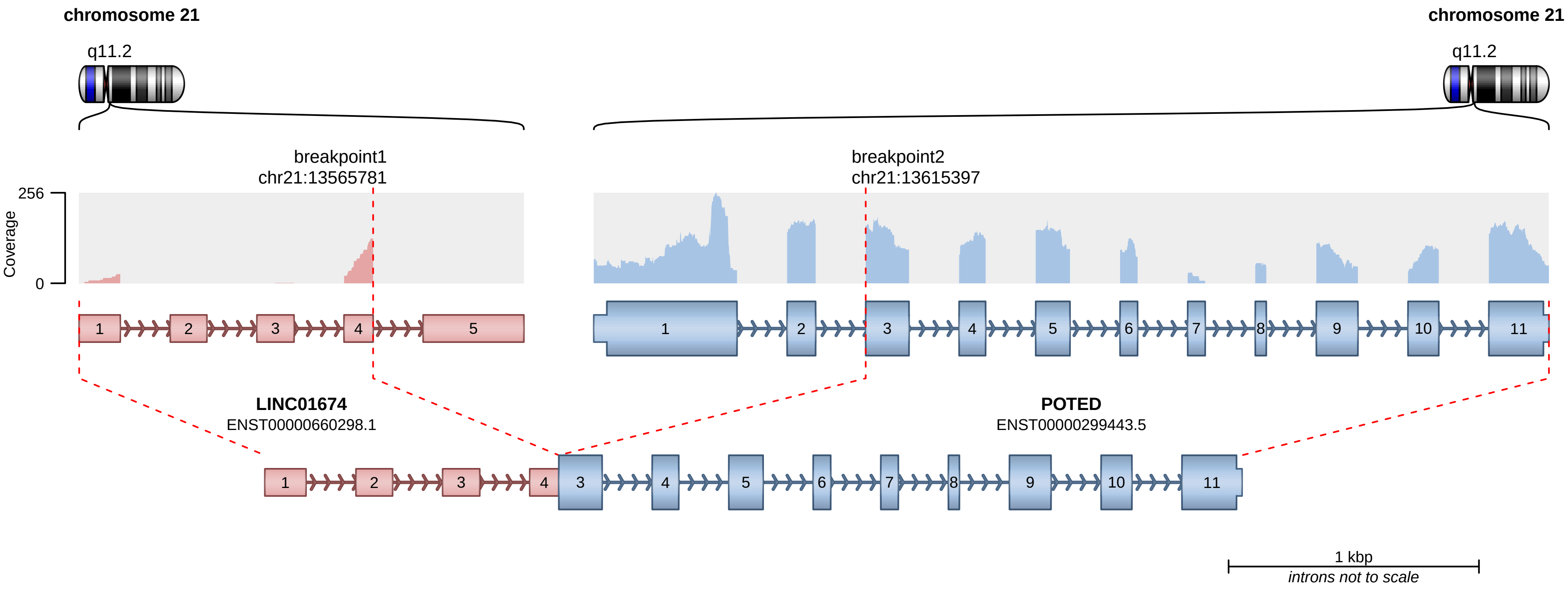


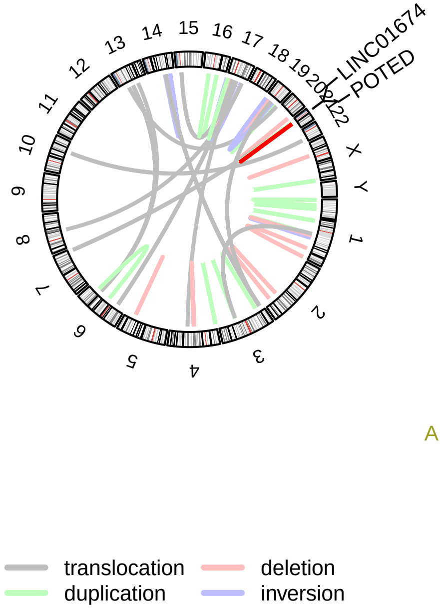
RETAINED PROTEIN DOMAINS
reading frame unclear

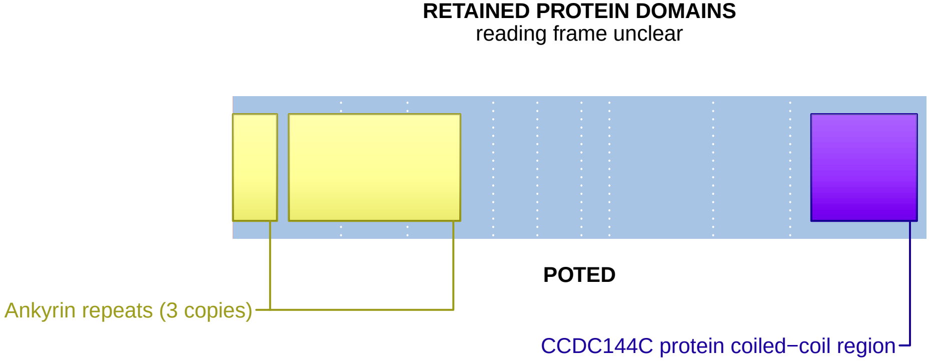


SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 0

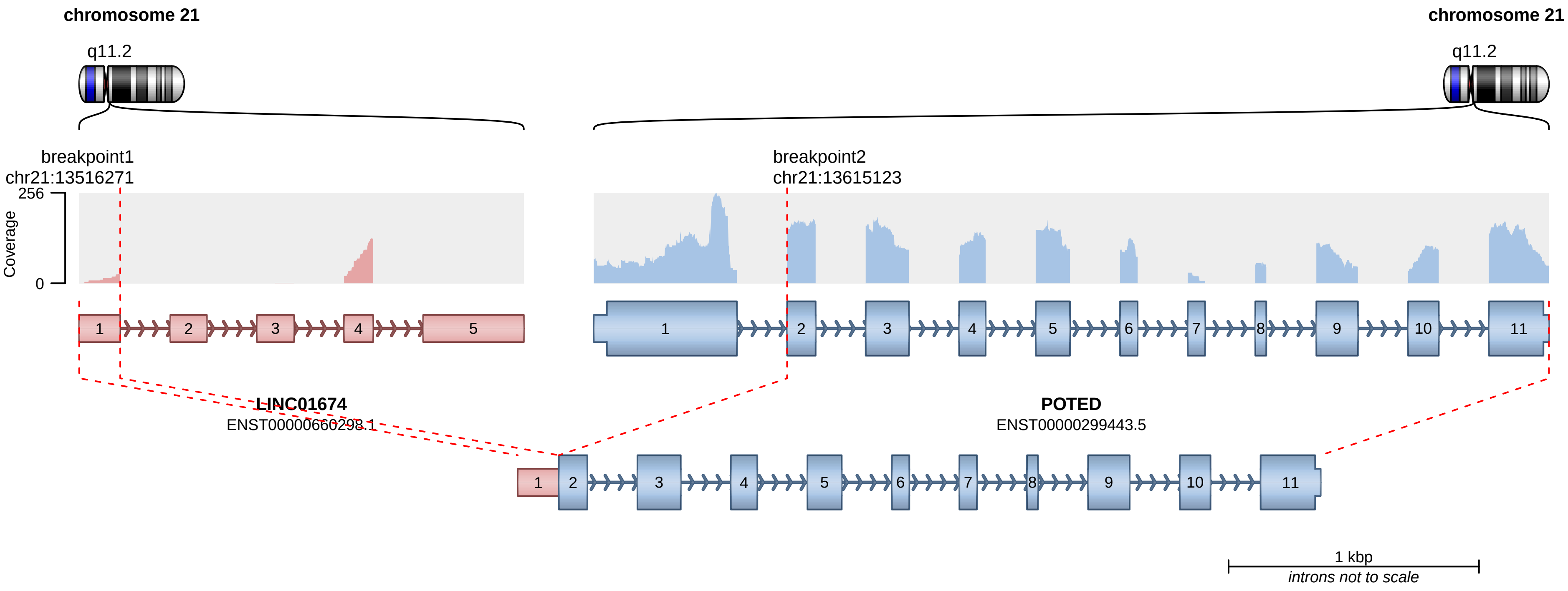


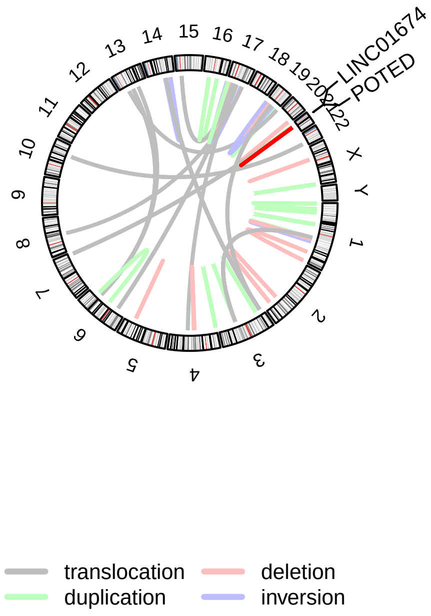




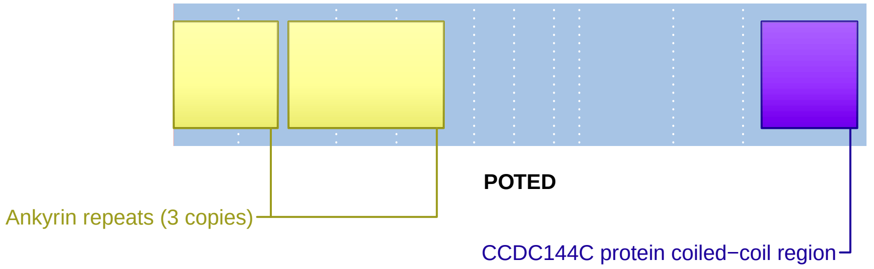
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 1



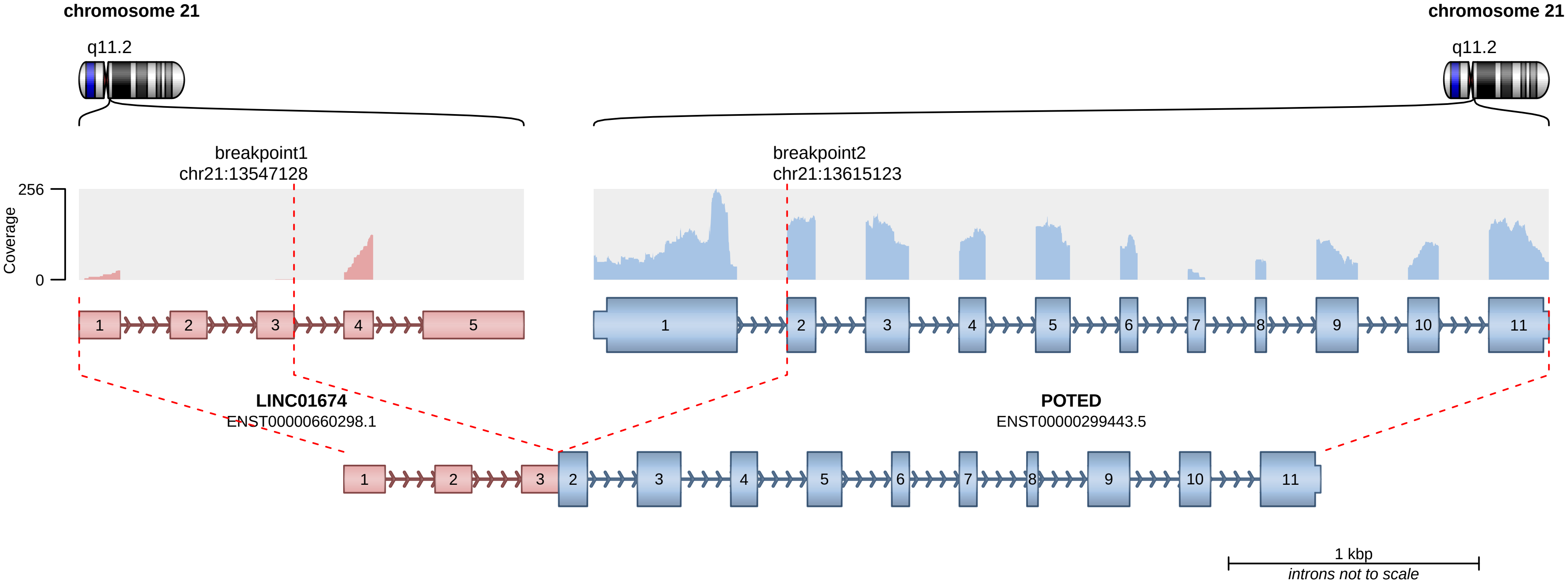


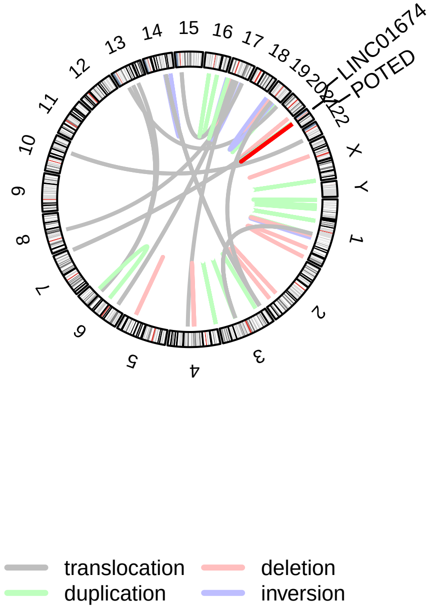
RETAINED PROTEIN DOMAINS
reading frame unclear

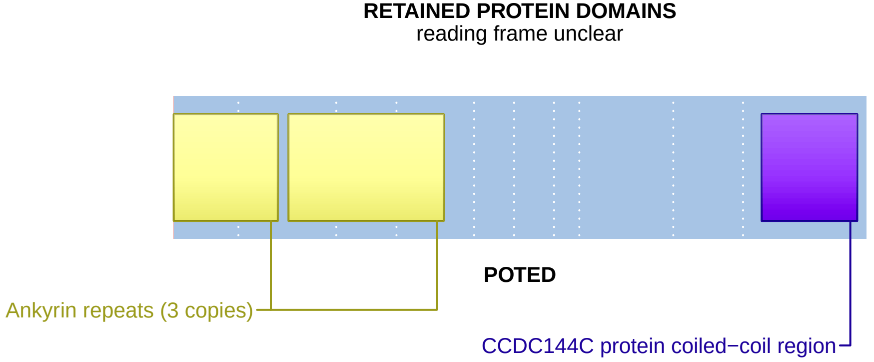


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

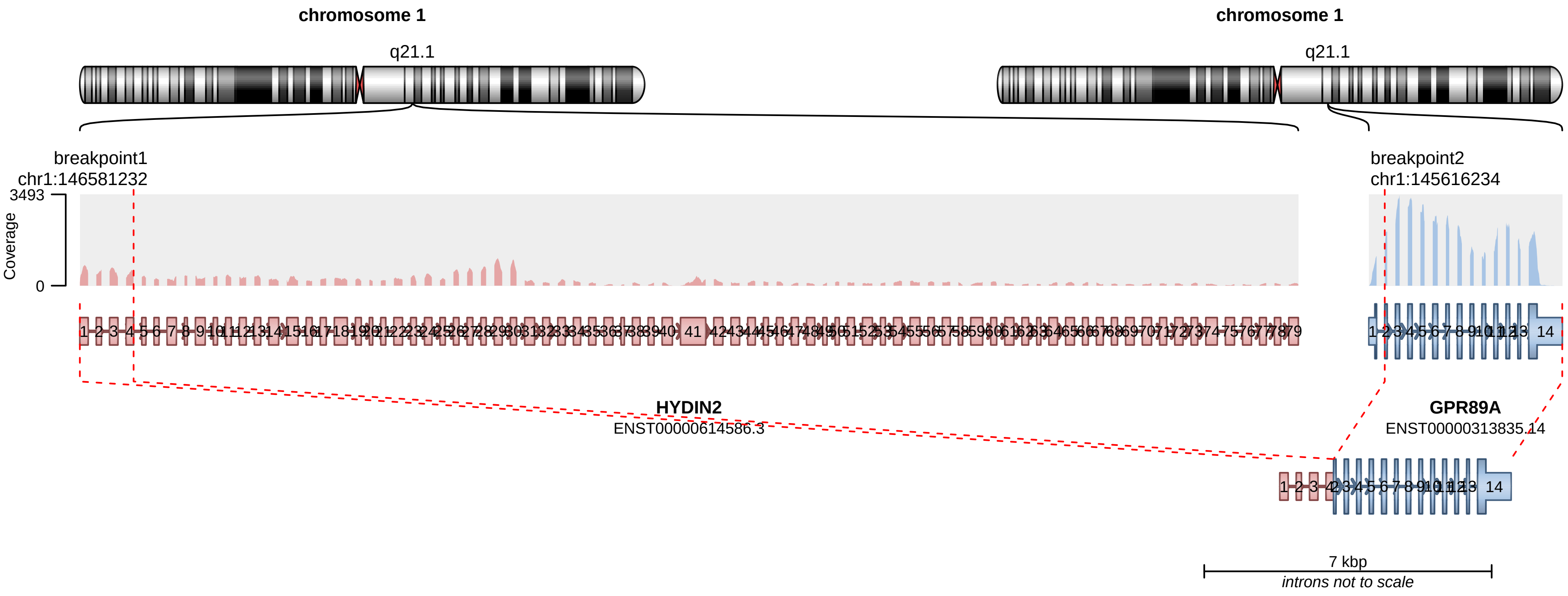


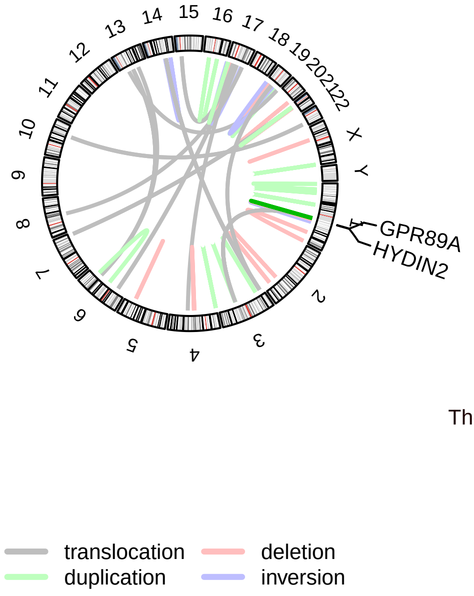


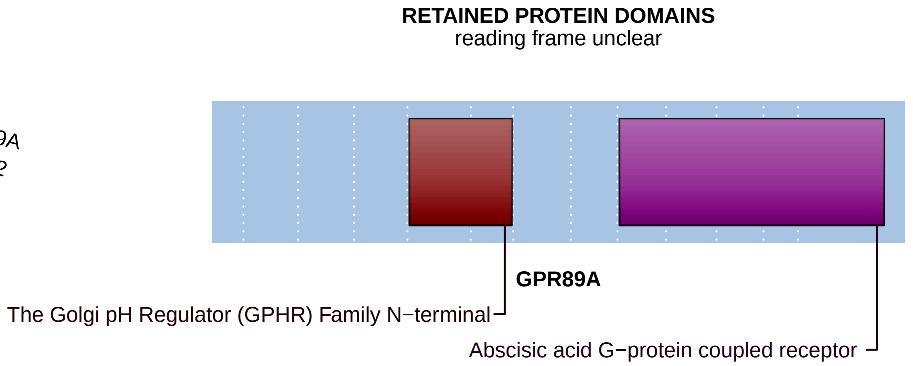


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

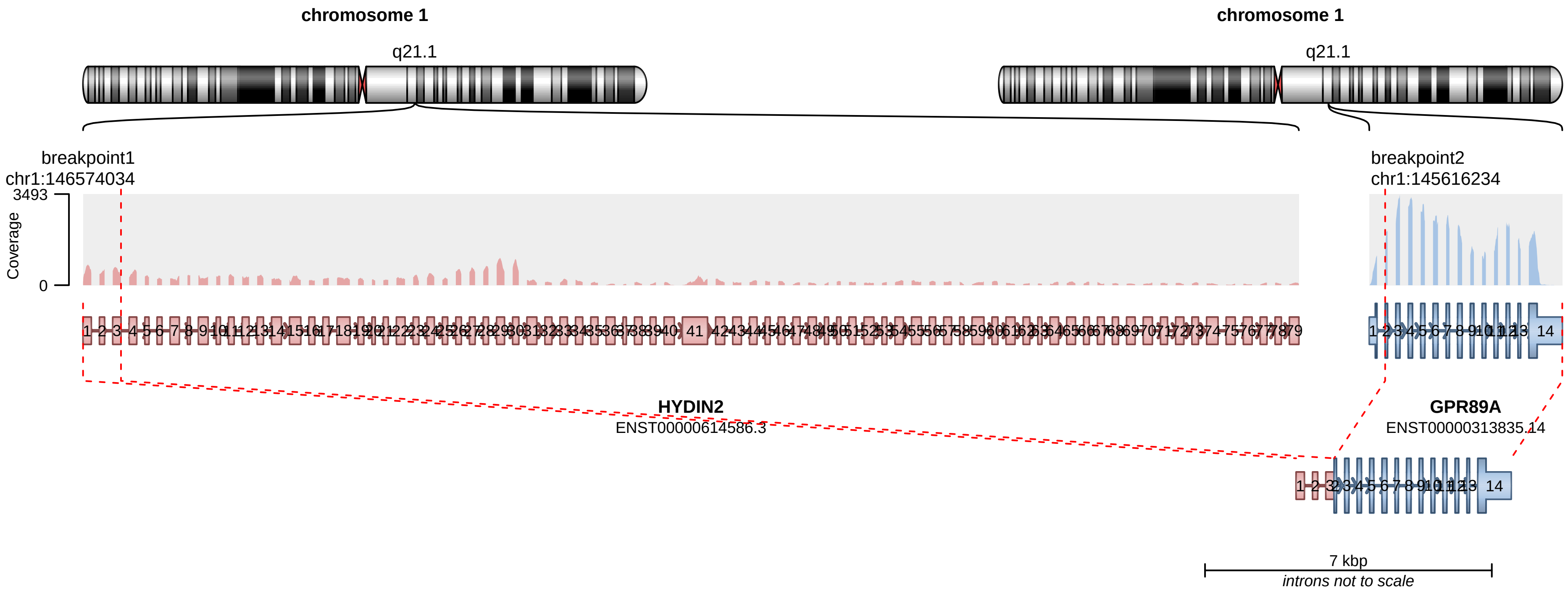


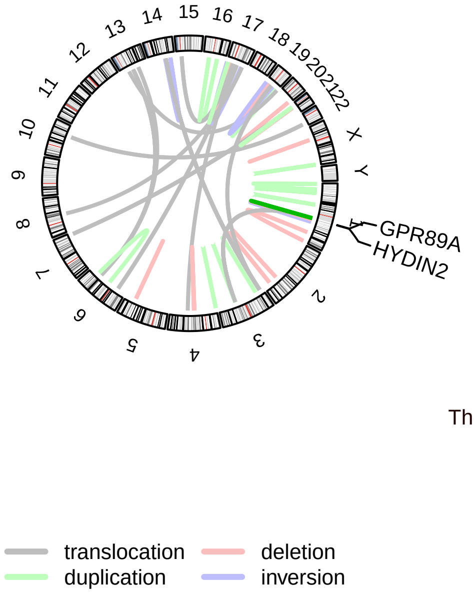




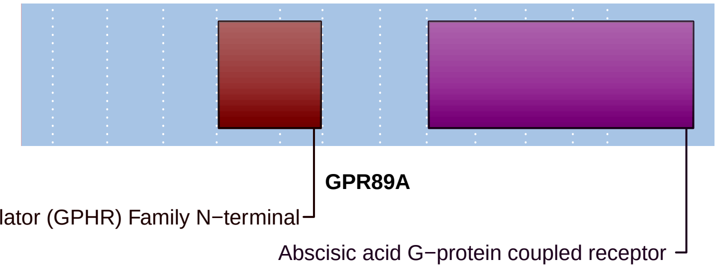
SUPPORTING READ COUNT

Split reads = 25
Discordant mates = 2



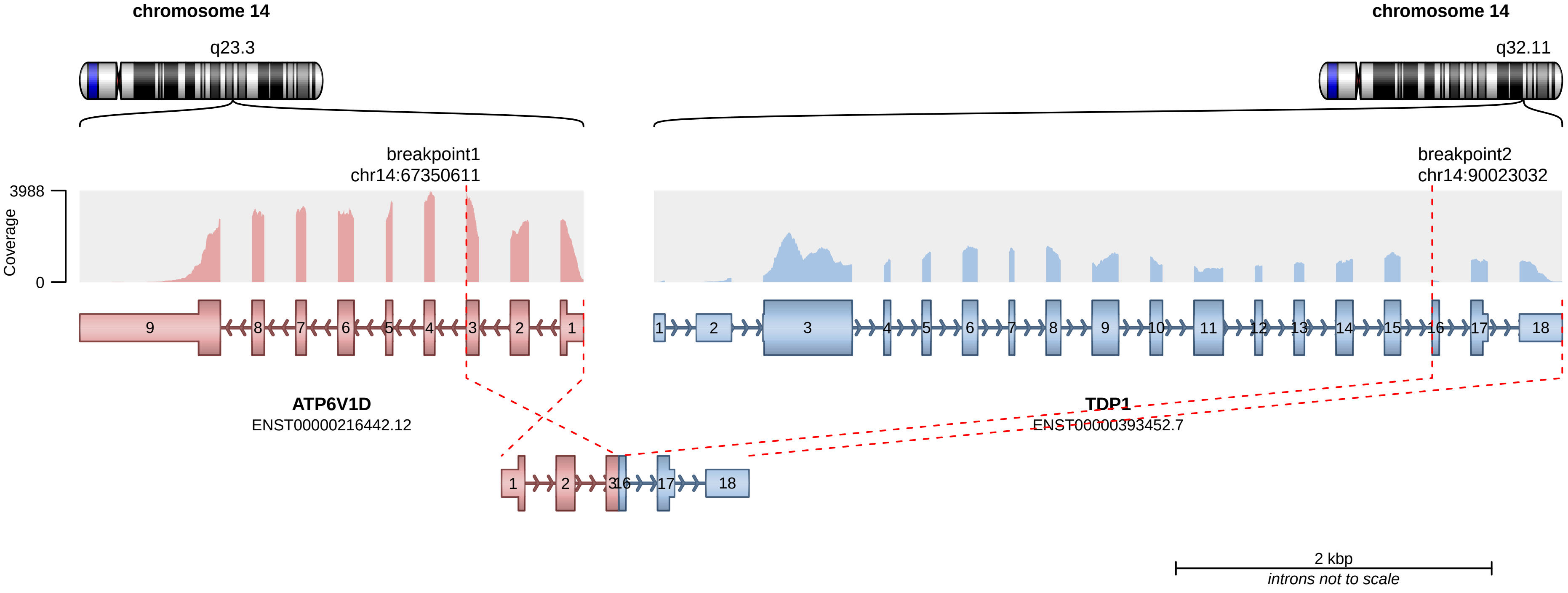


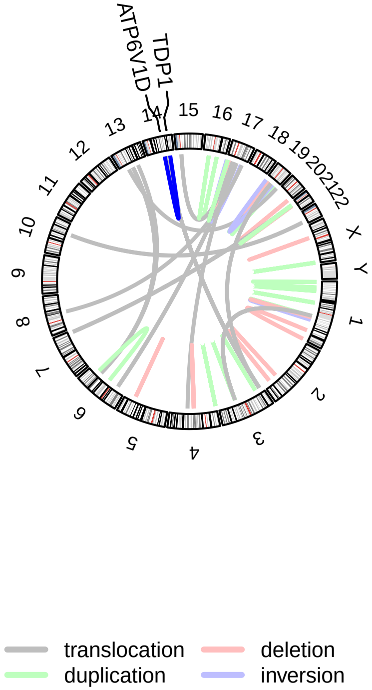
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

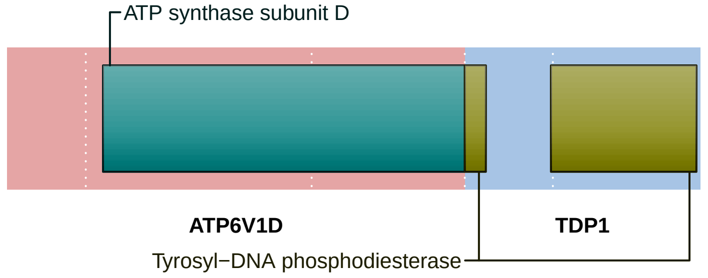
Split reads = 2
Discordant mates = 0





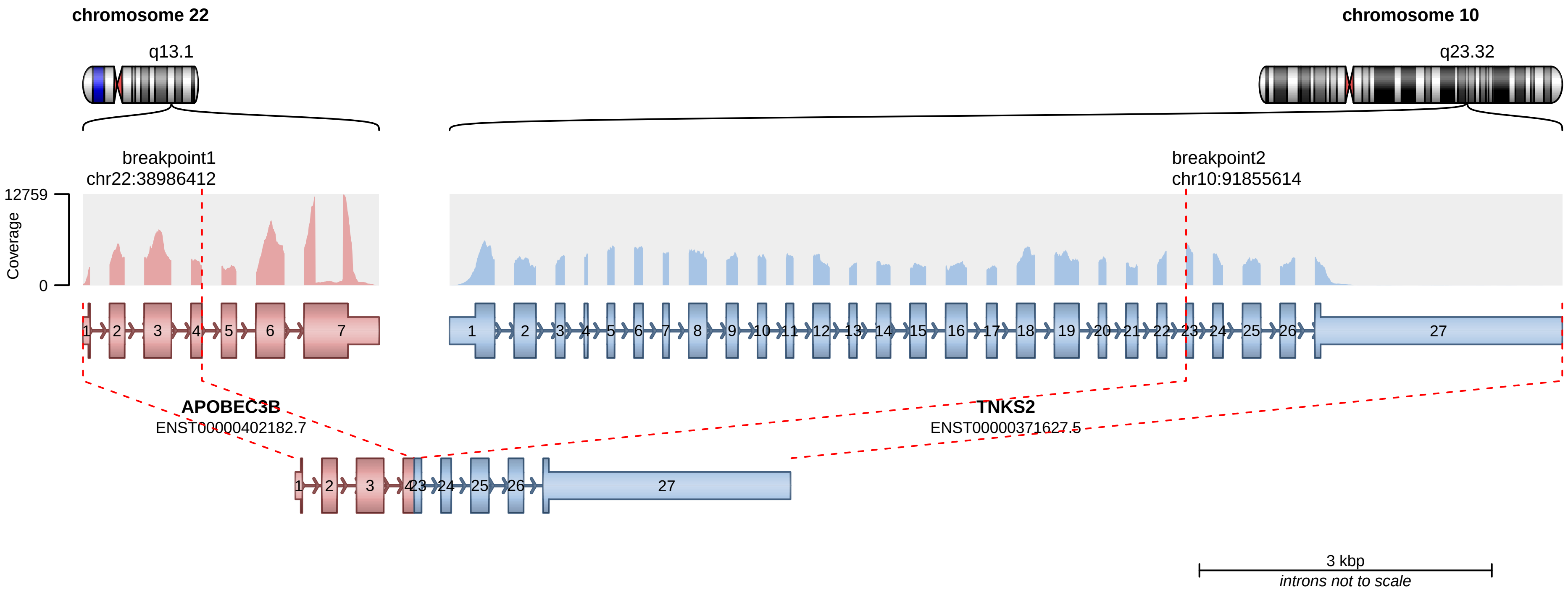
RETAINED PROTEIN DOMAINS

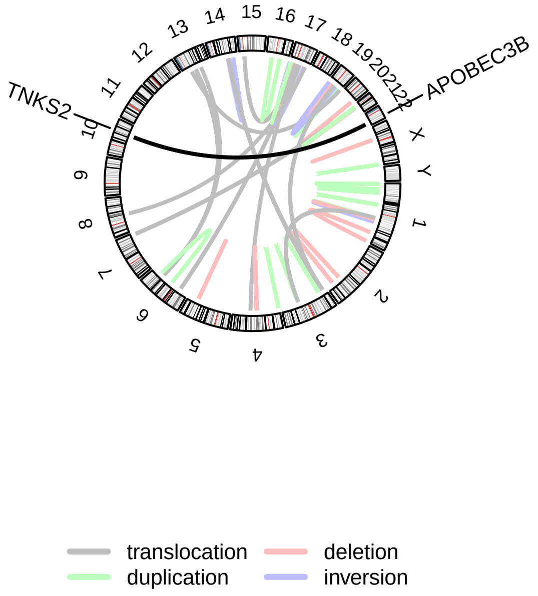
reading frame unclear

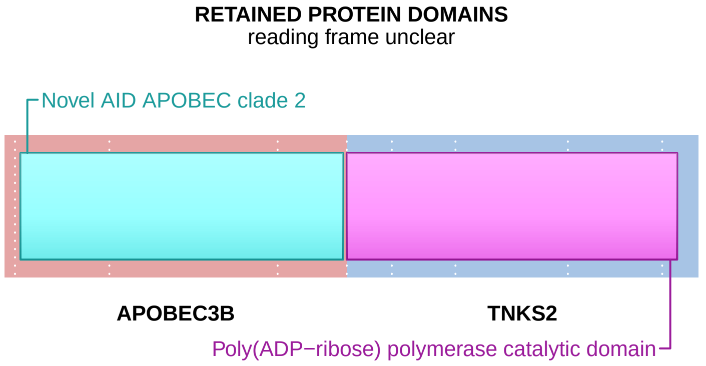


SUPPORTING READ COUNT

Split reads = 23
Discordant mates = 0

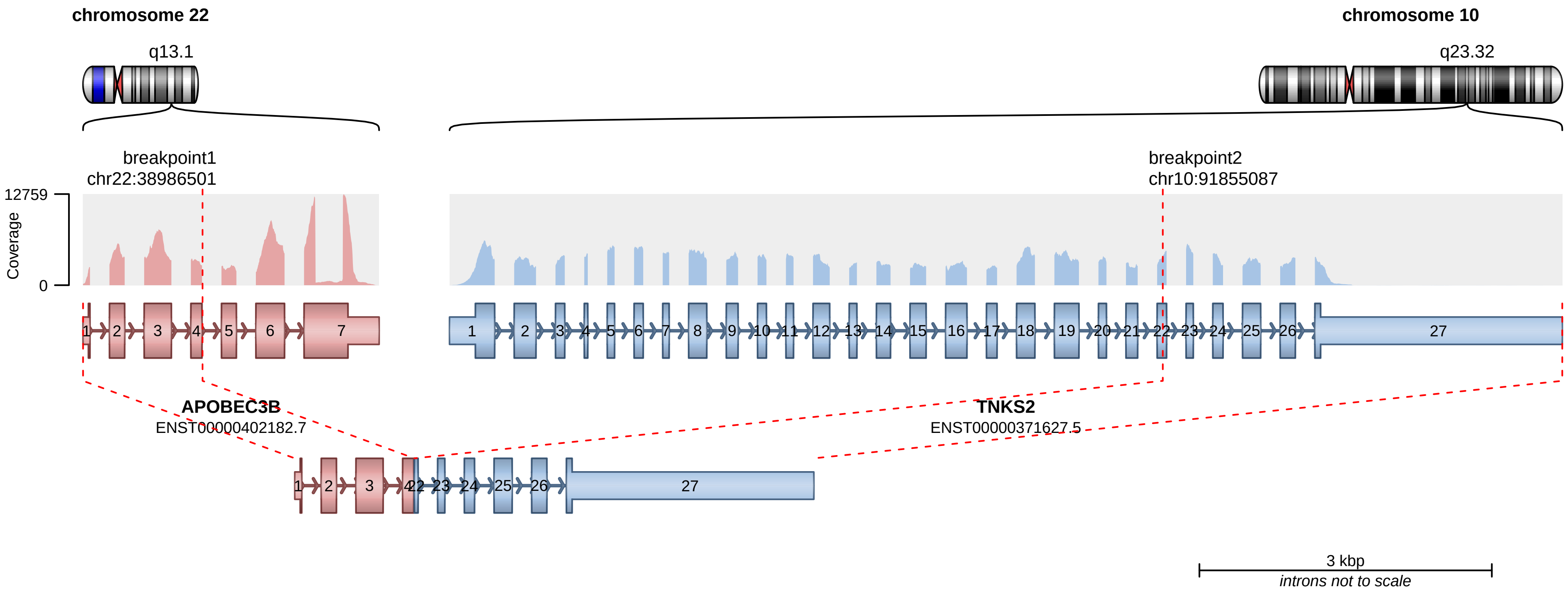


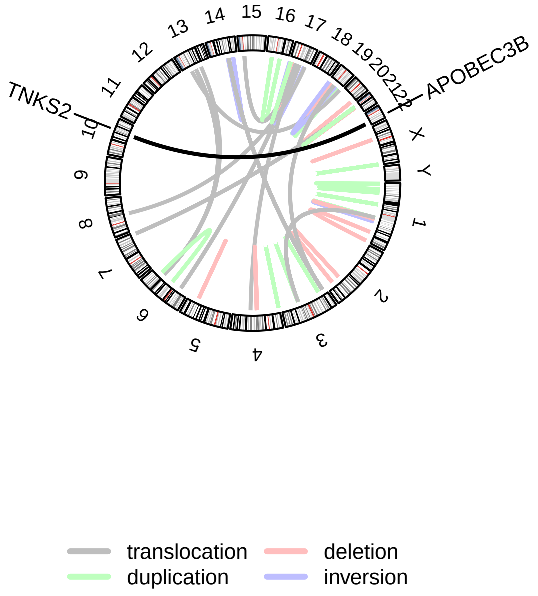




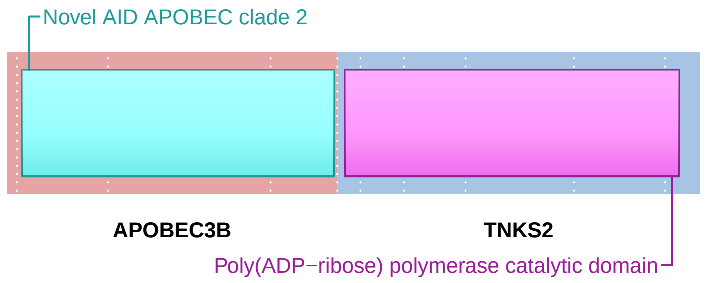
SUPPORTING READ COUNT

Split reads = 22
Discordant mates = 0



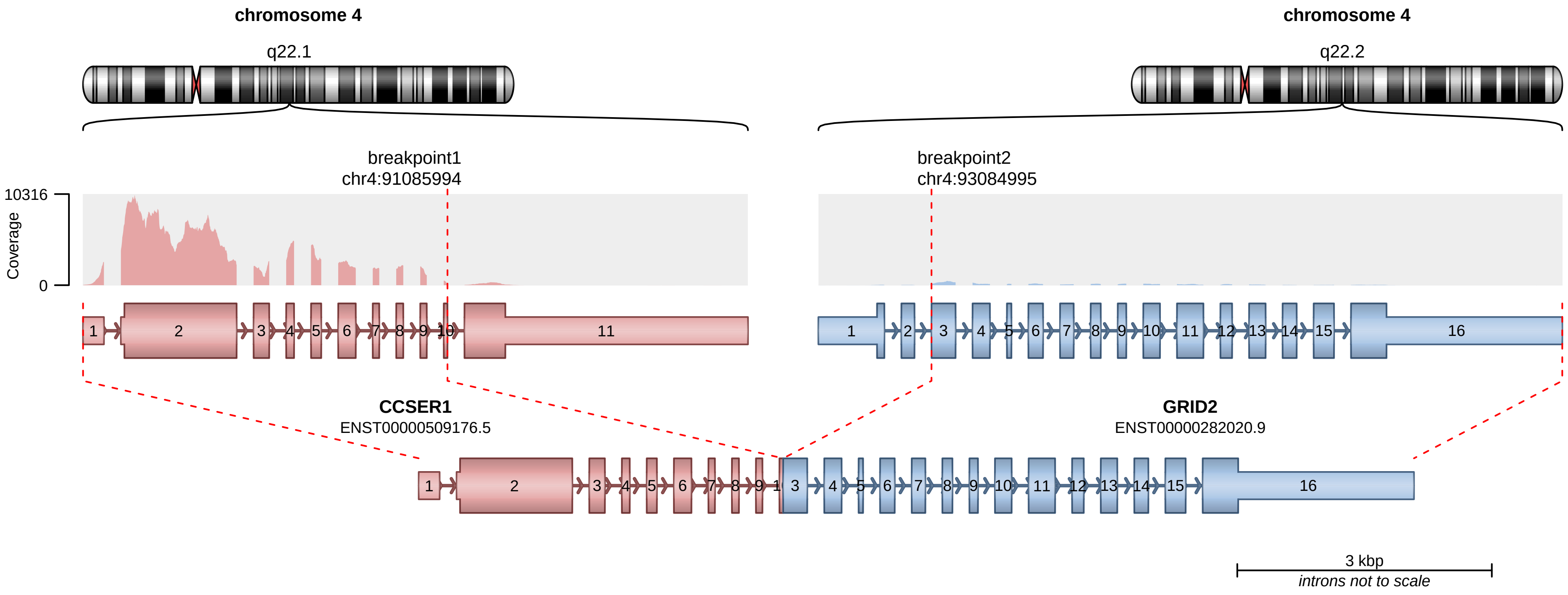


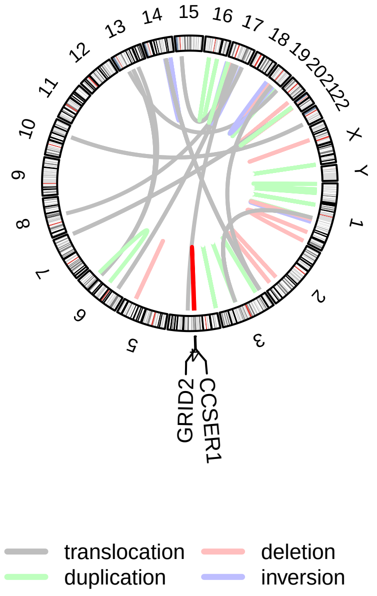
RETAINED PROTEIN DOMAINS
reading frame unclear

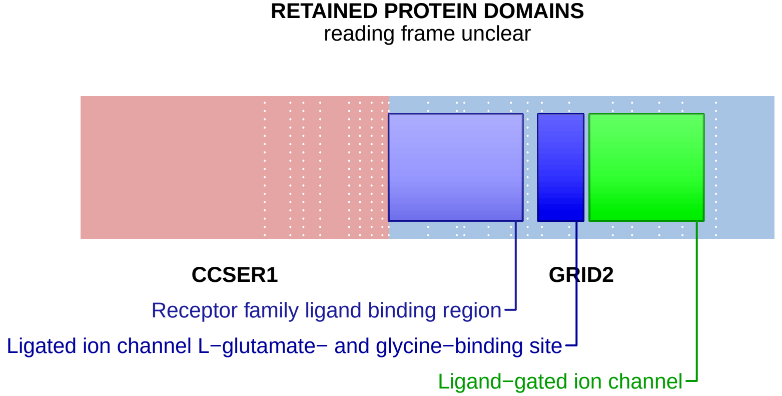


SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 1

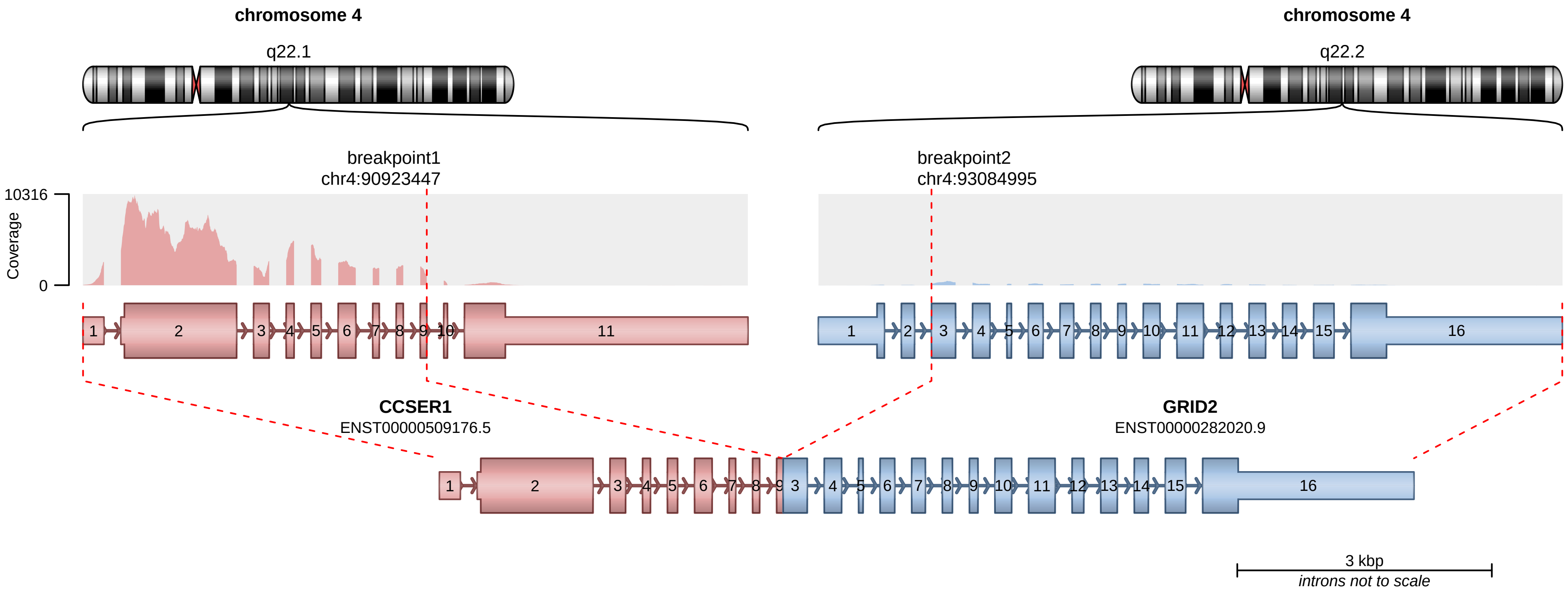


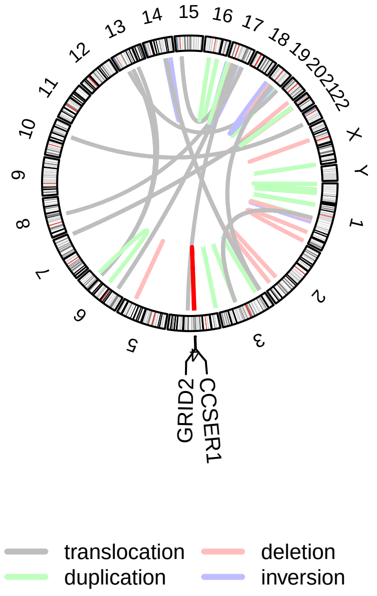


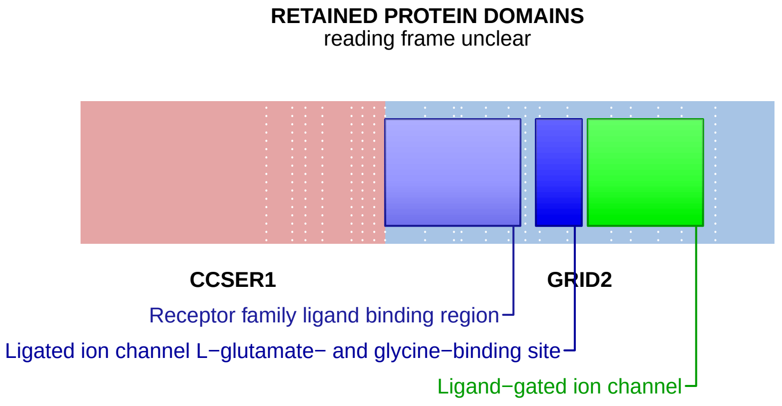


SUPPORTING READ COUNT

Split reads = 21
Discordant mates = 1

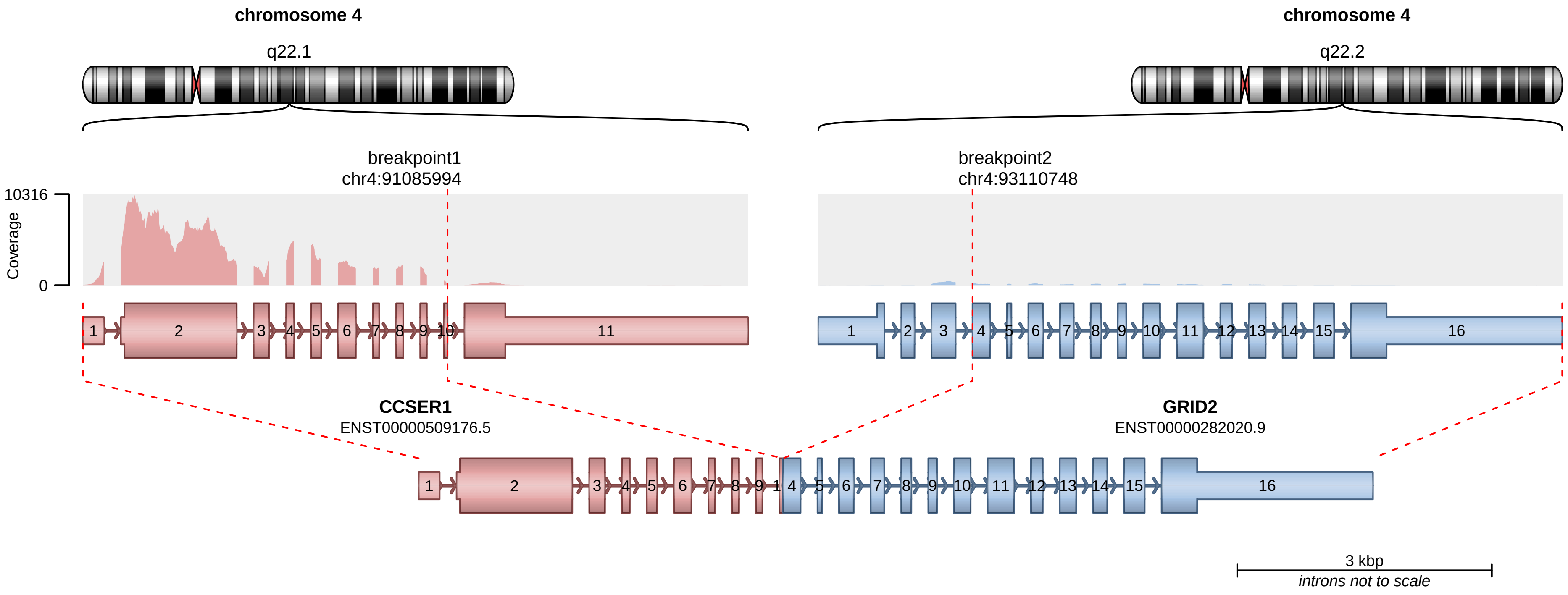


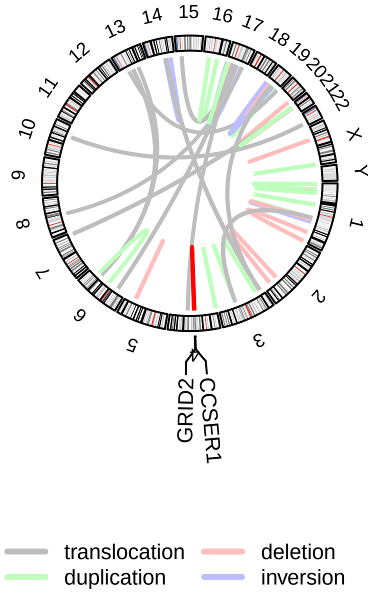


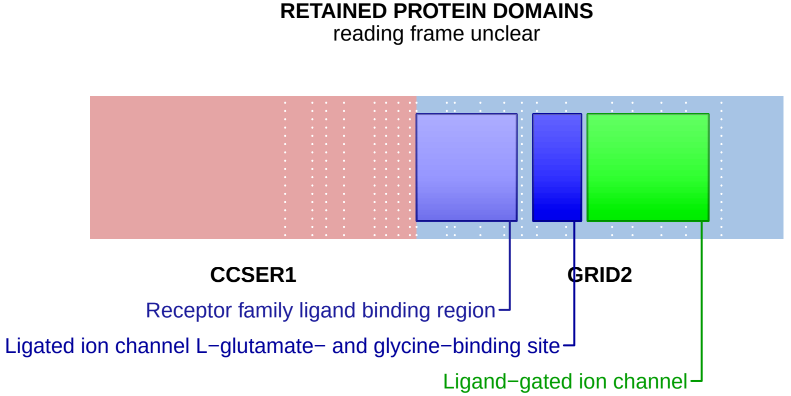


SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 1

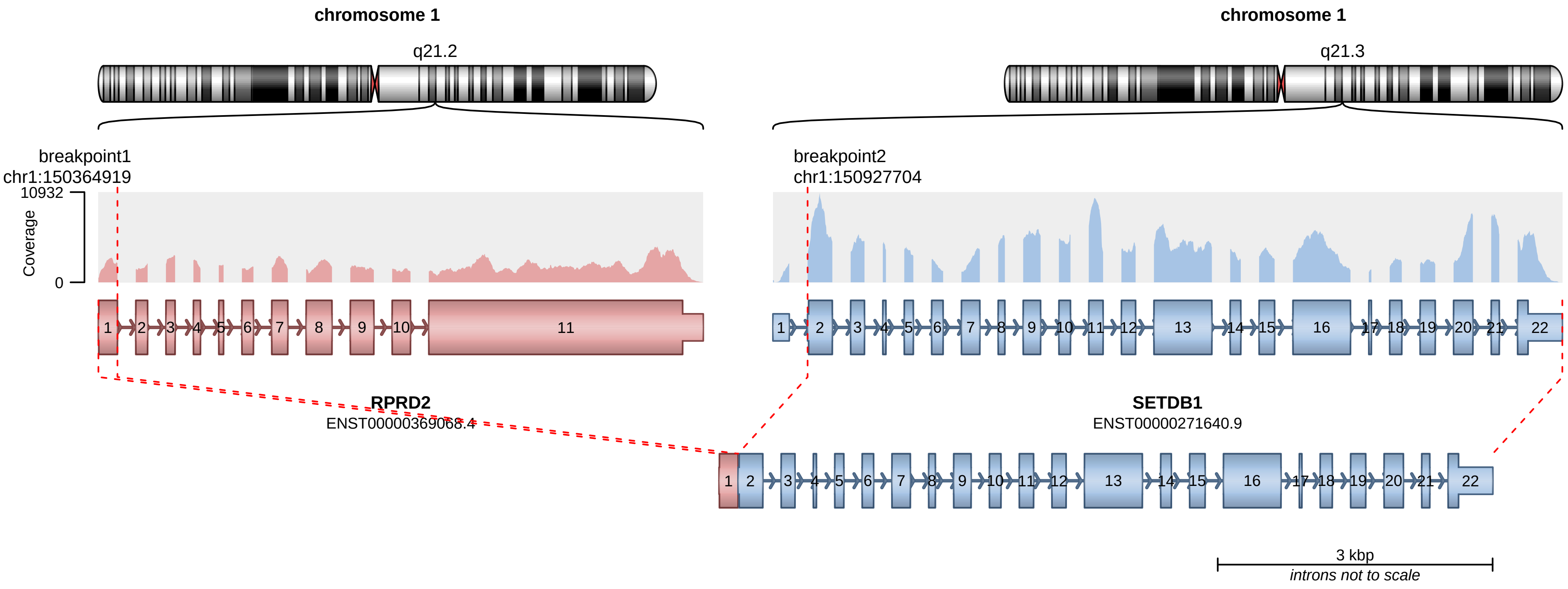


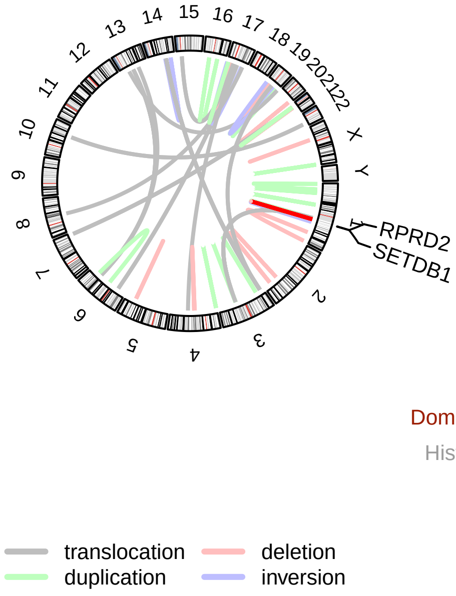


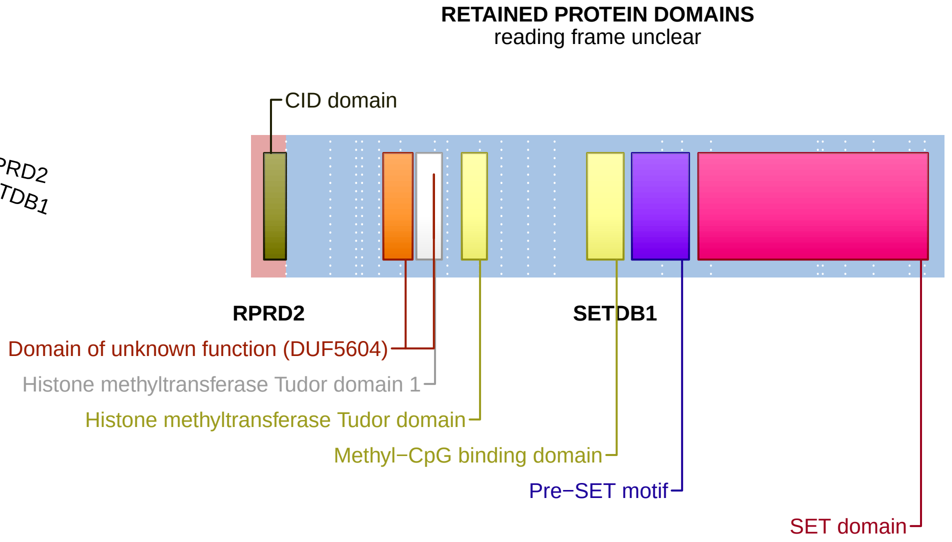


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

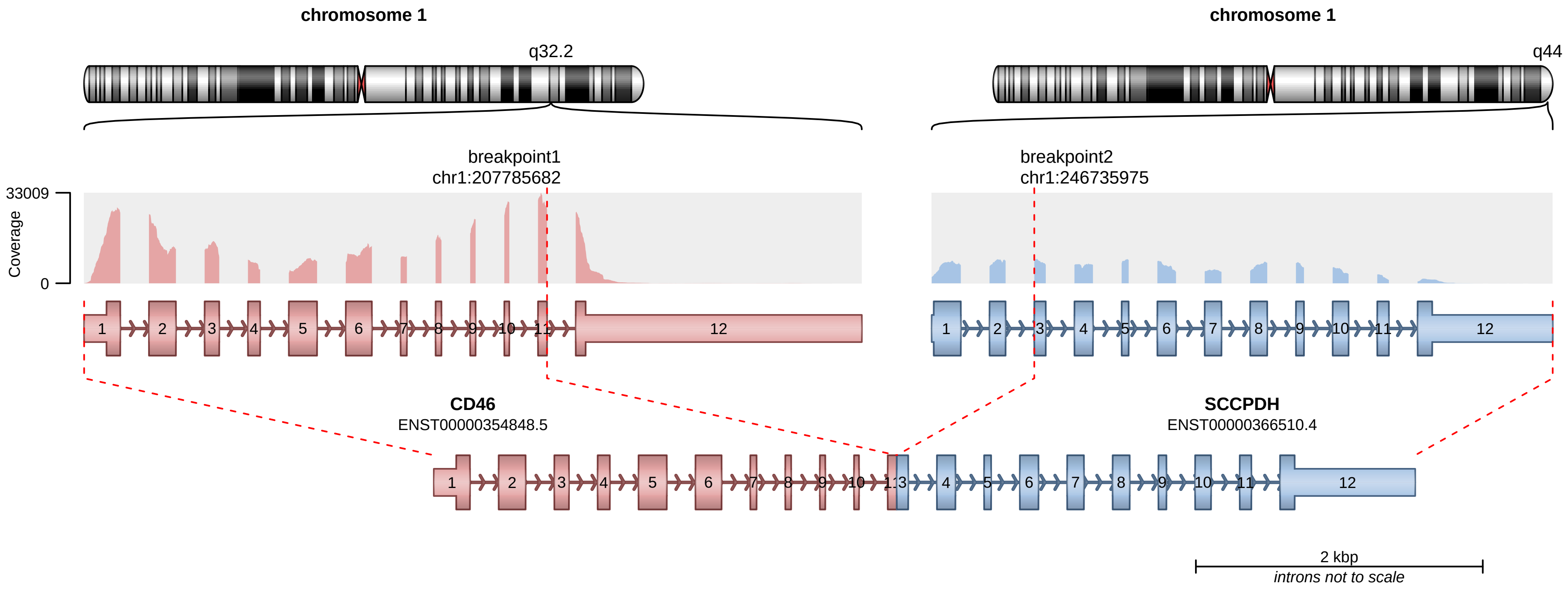


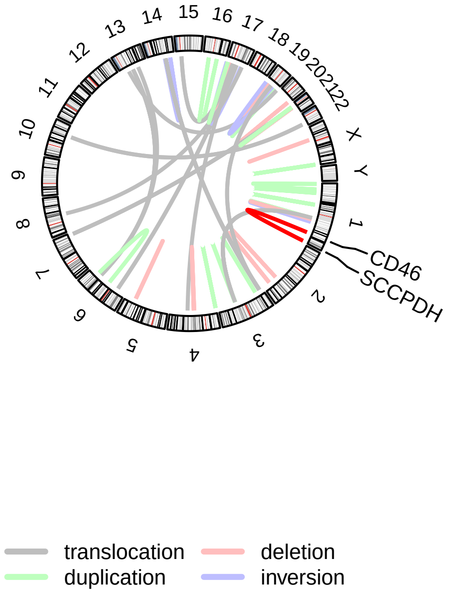


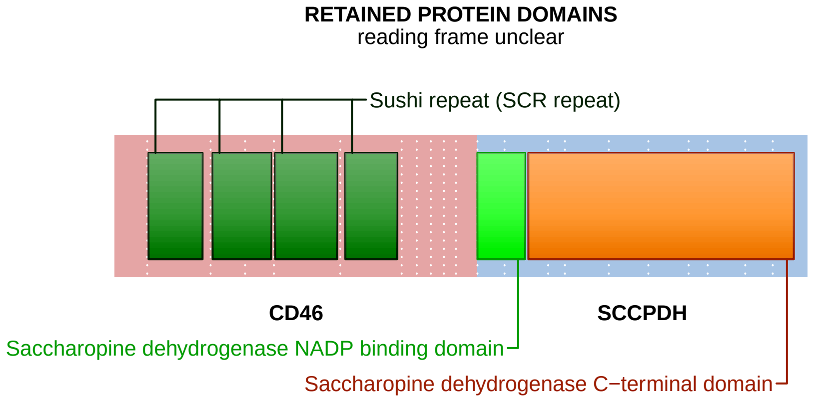


SUPPORTING READ COUNT

Split reads = 21
Discordant mates = 1

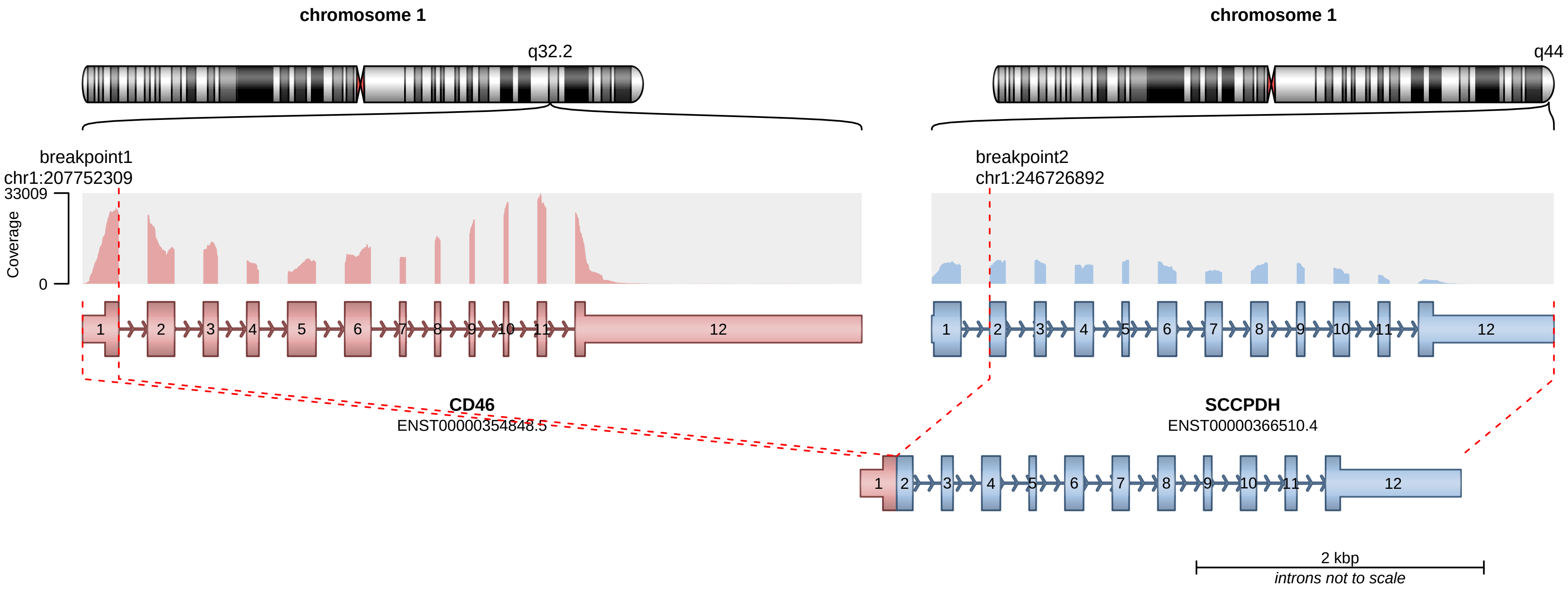


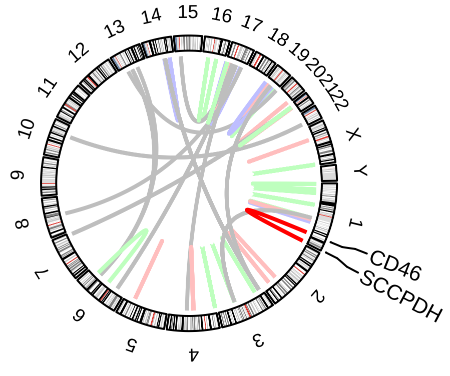


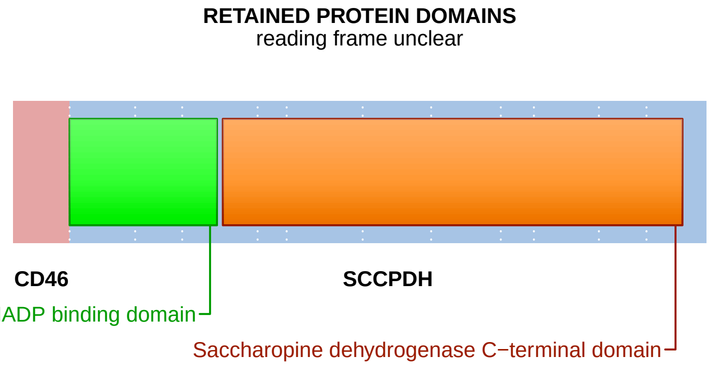


SUPPORTING READ COUNT

Split reads = 21
Discordant mates = 0



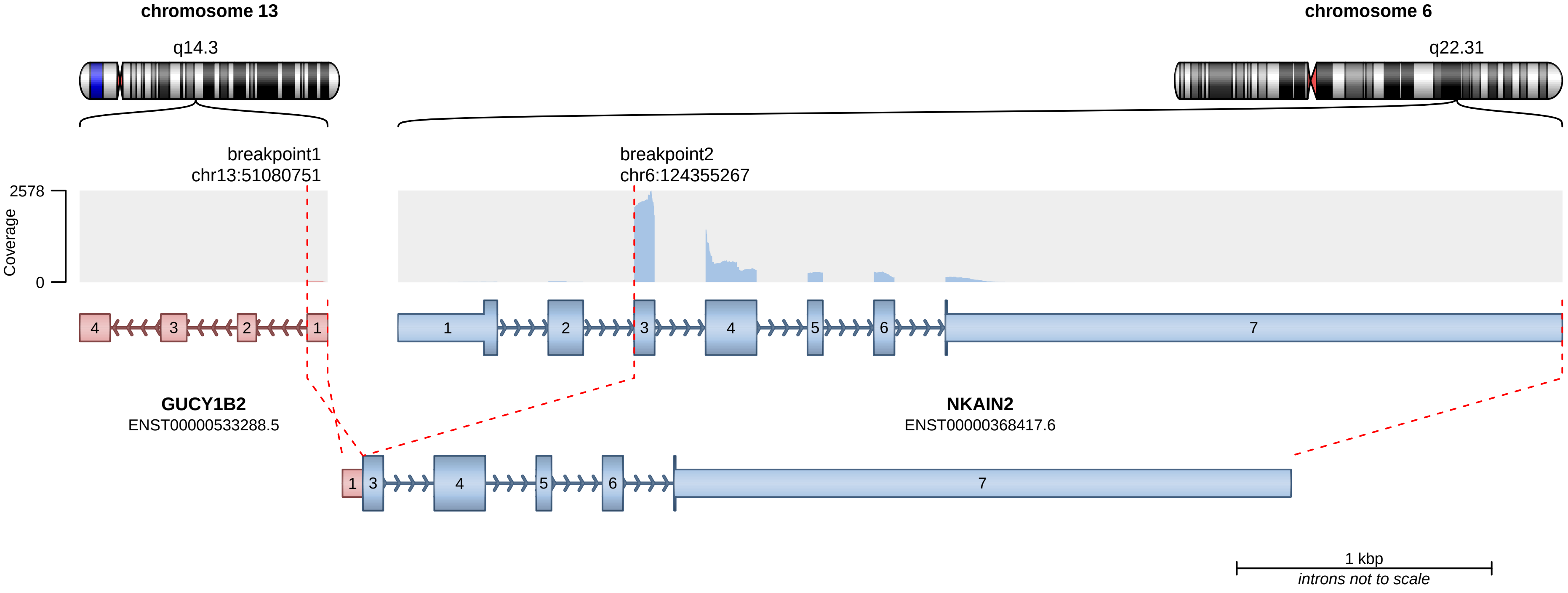


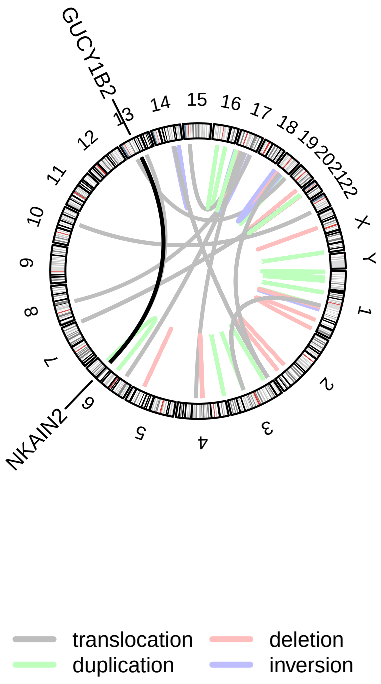


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

translocation
duplication
deletion
inversion

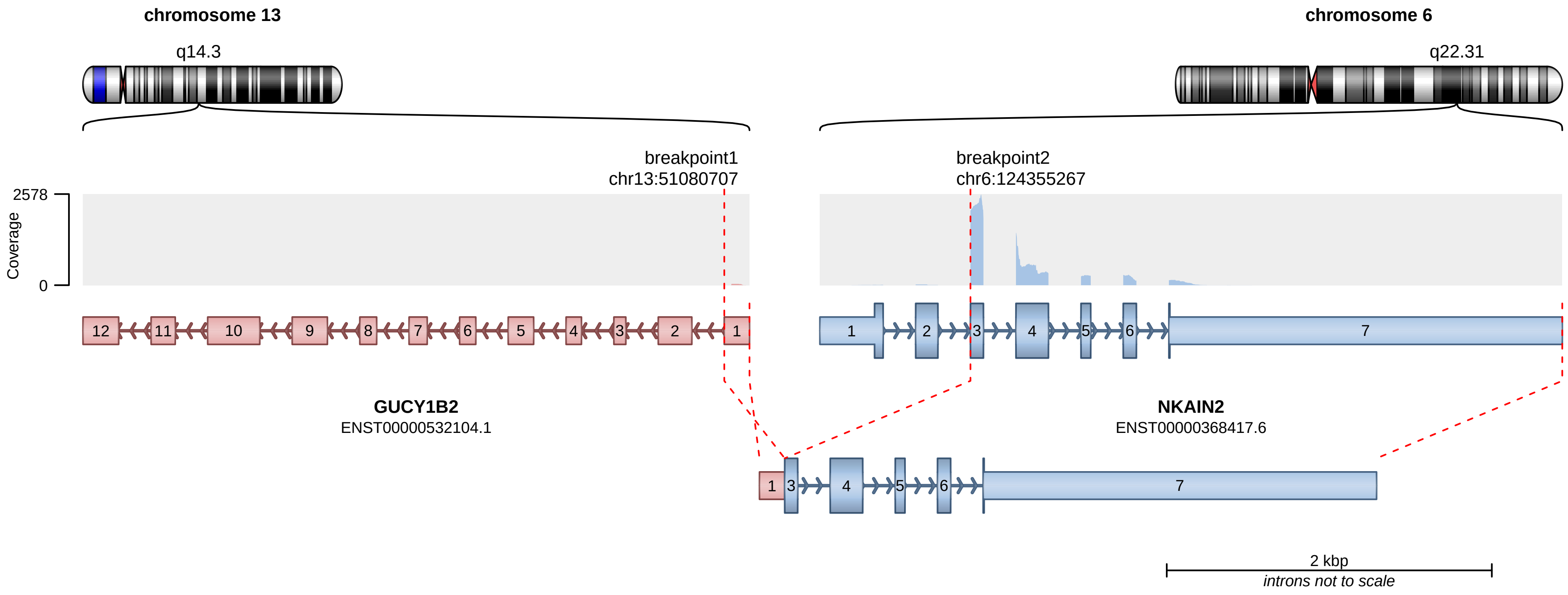


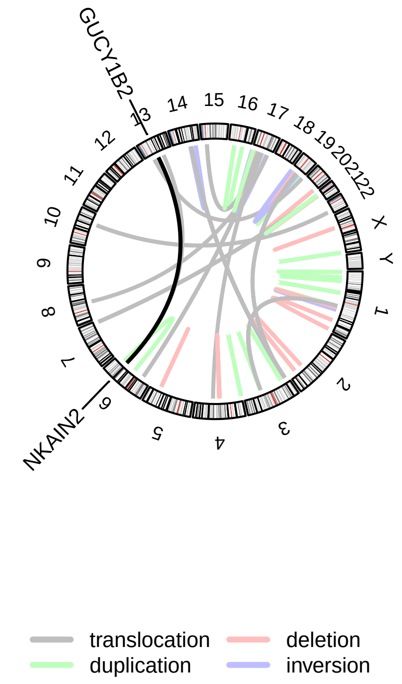


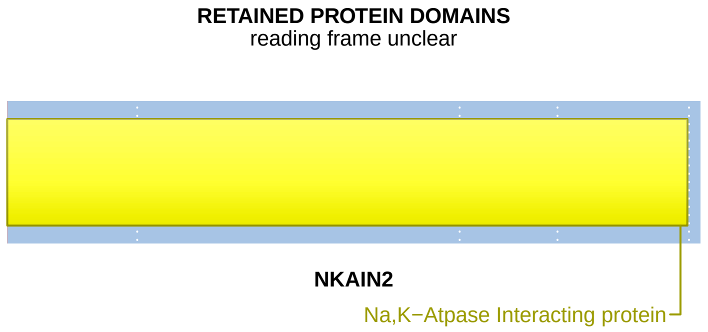
RETAINED PROTEIN DOMAINS
reading frame unclear

SUPPORTING READ COUNT

Split reads = 21
Discordant mates = 0

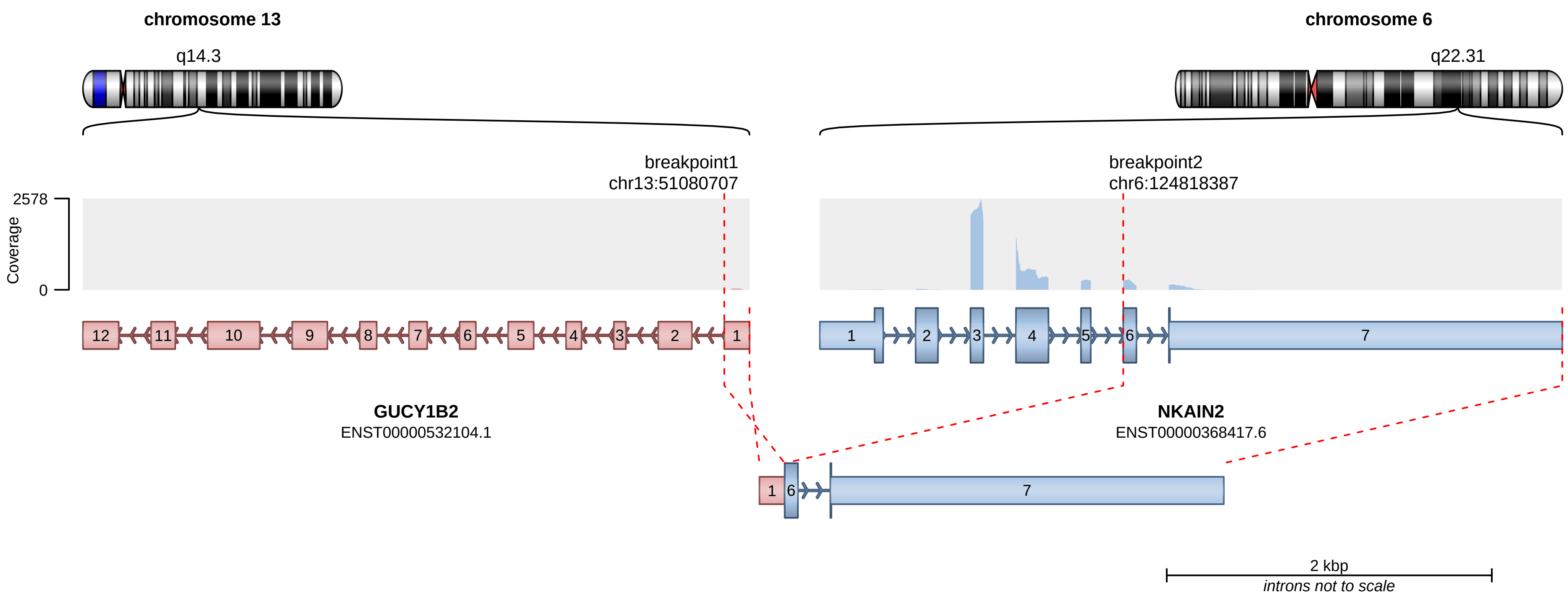


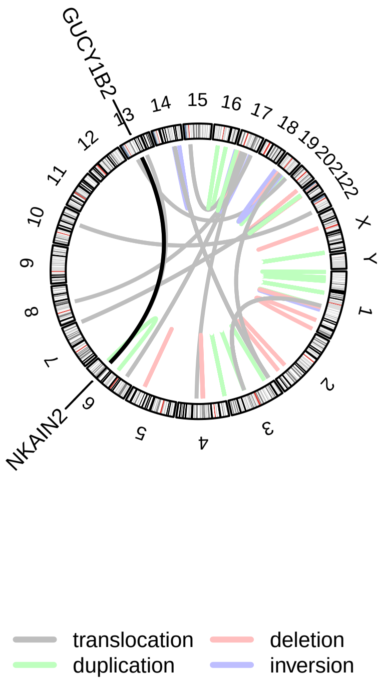


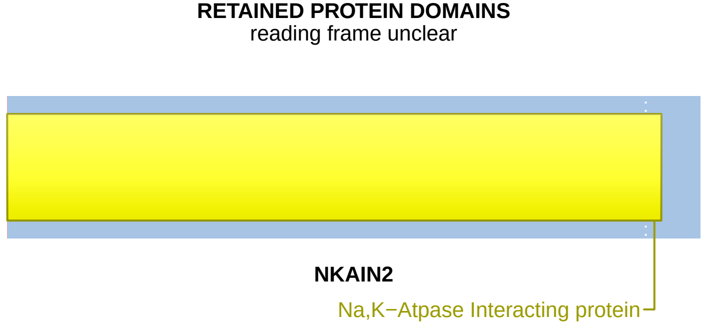


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

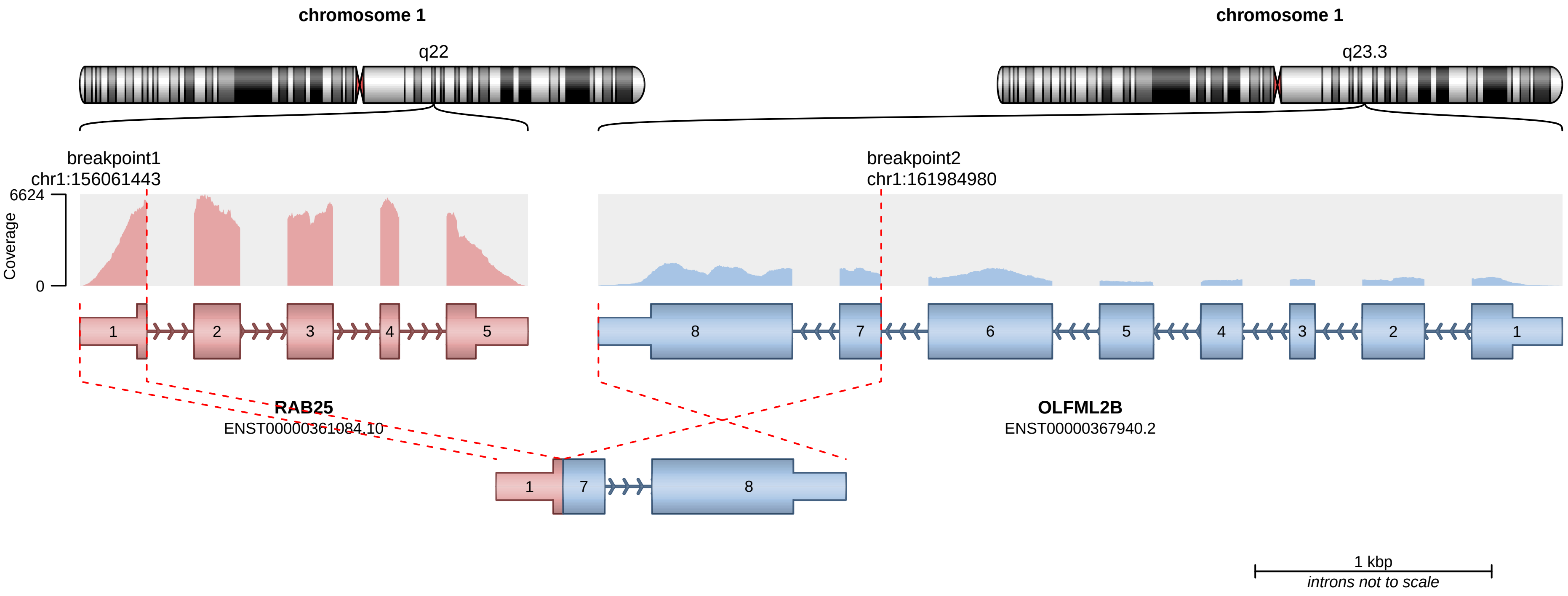


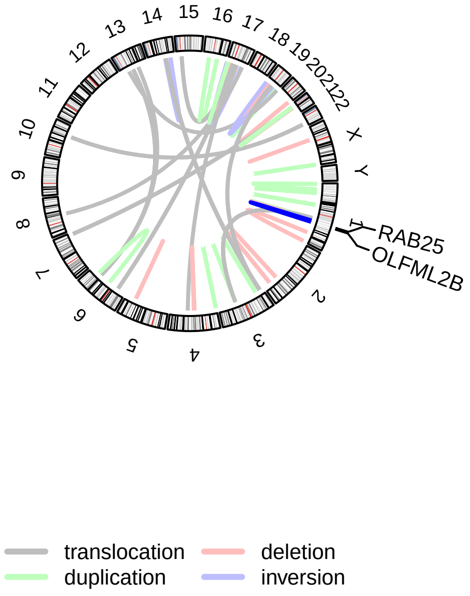


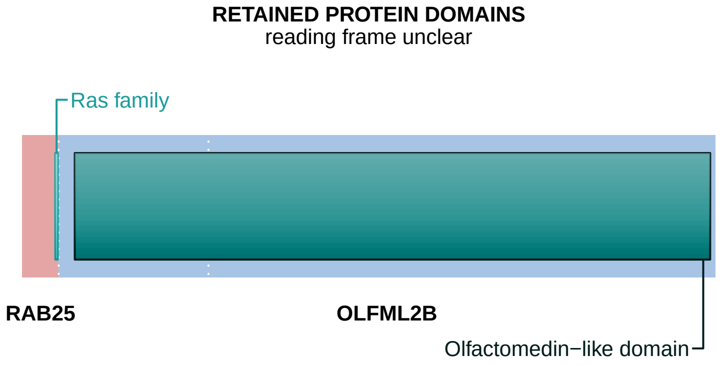


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

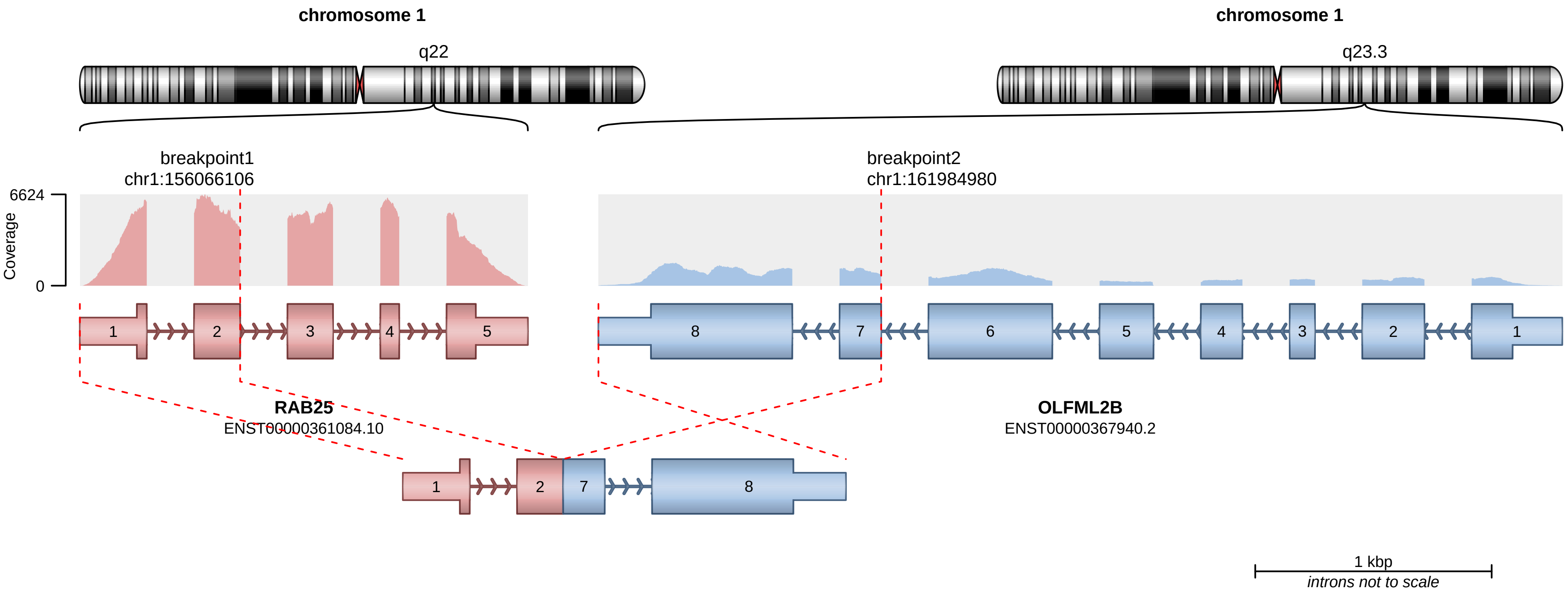


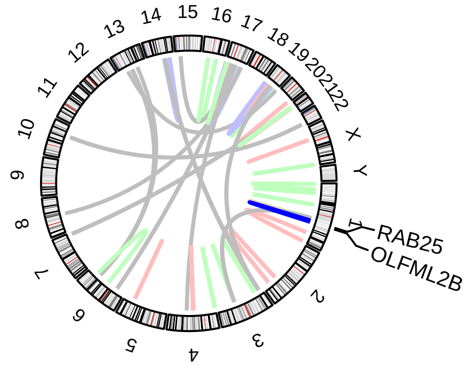


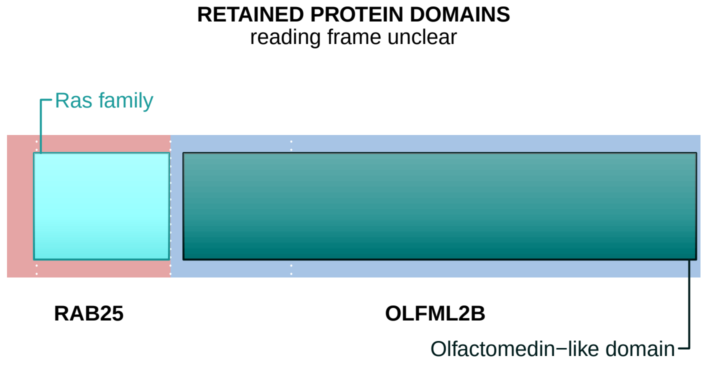


SUPPORTING READ COUNT

Split reads = 19
Discordant mates = 0



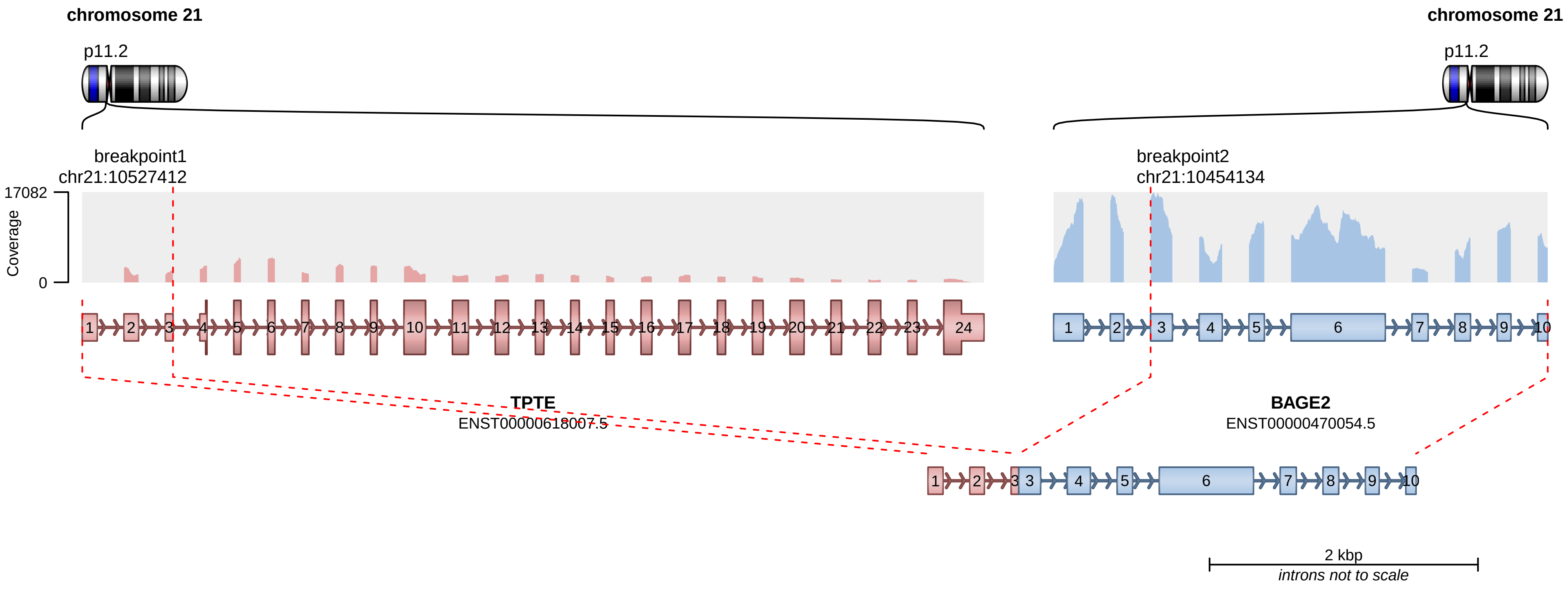


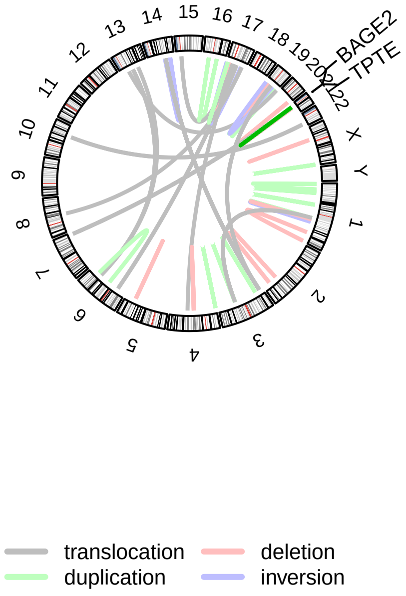


SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 0

translocation
duplication
deletion
inversion

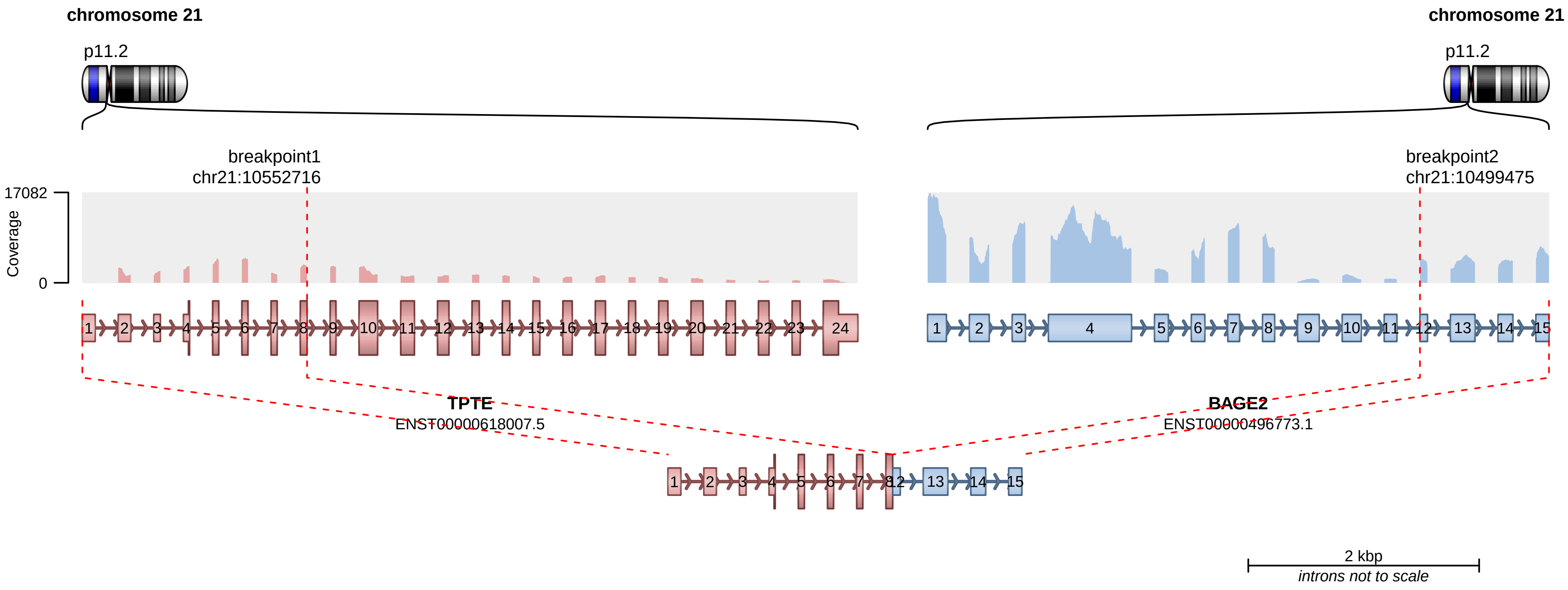


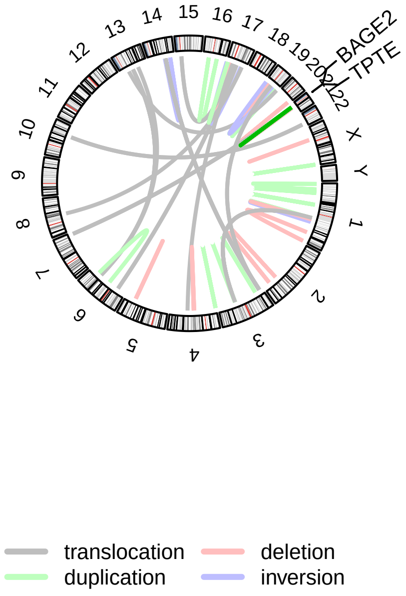


No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 18
Discordant mates = 2

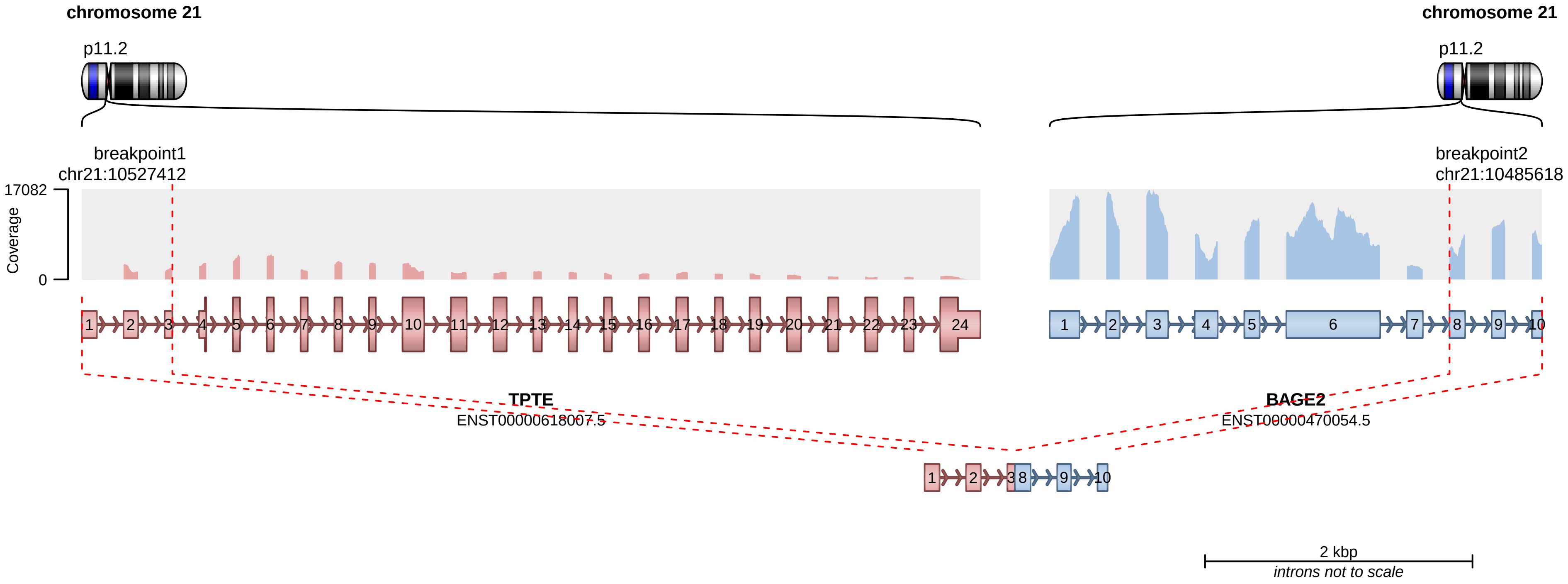


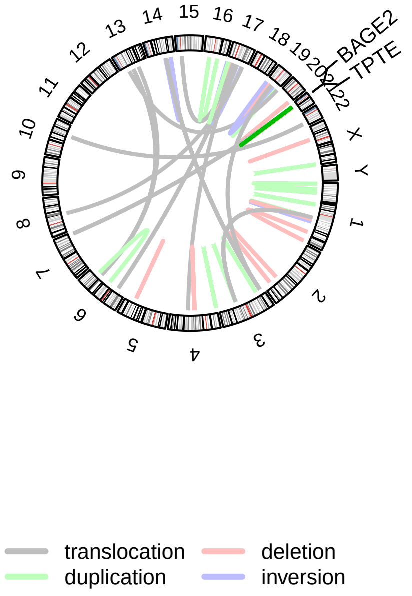


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 11
Discordant mates = 1

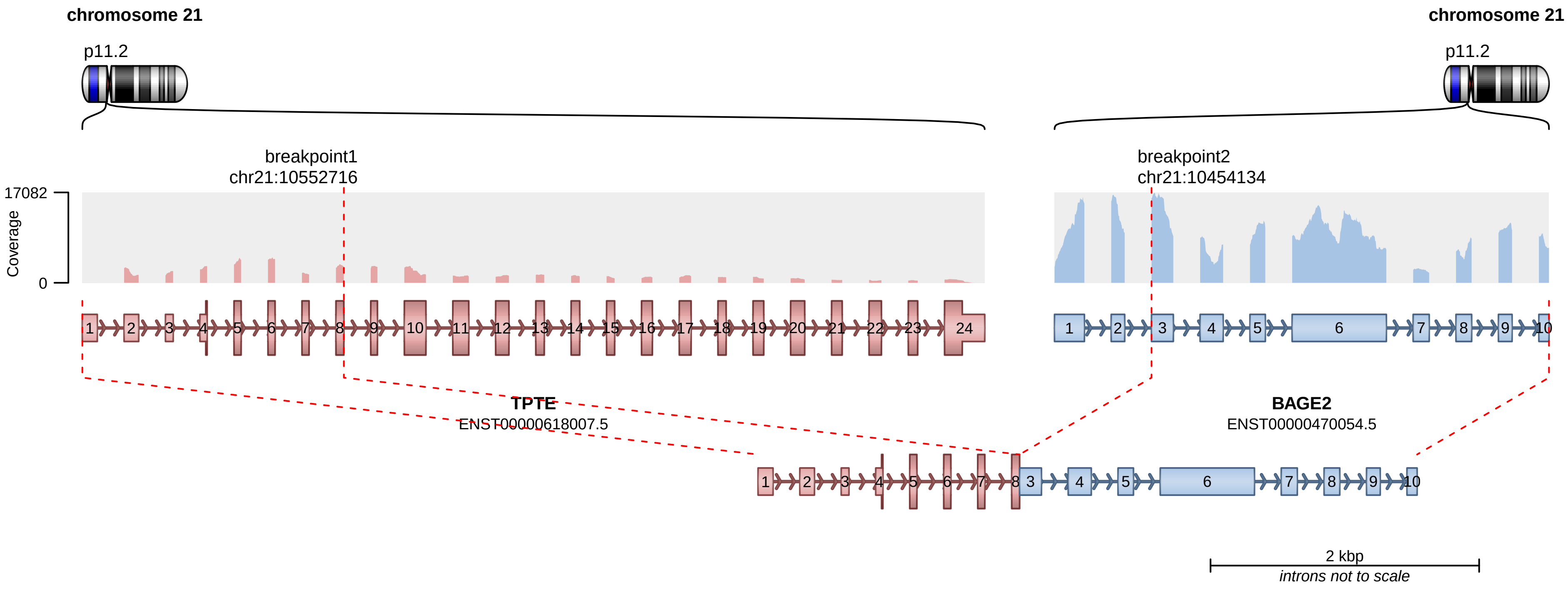


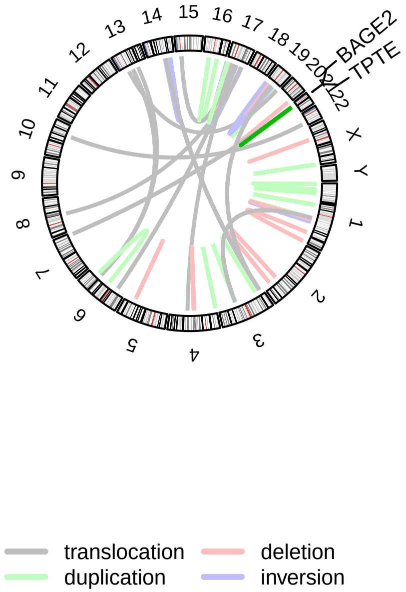


No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 11
Discordant mates = 1

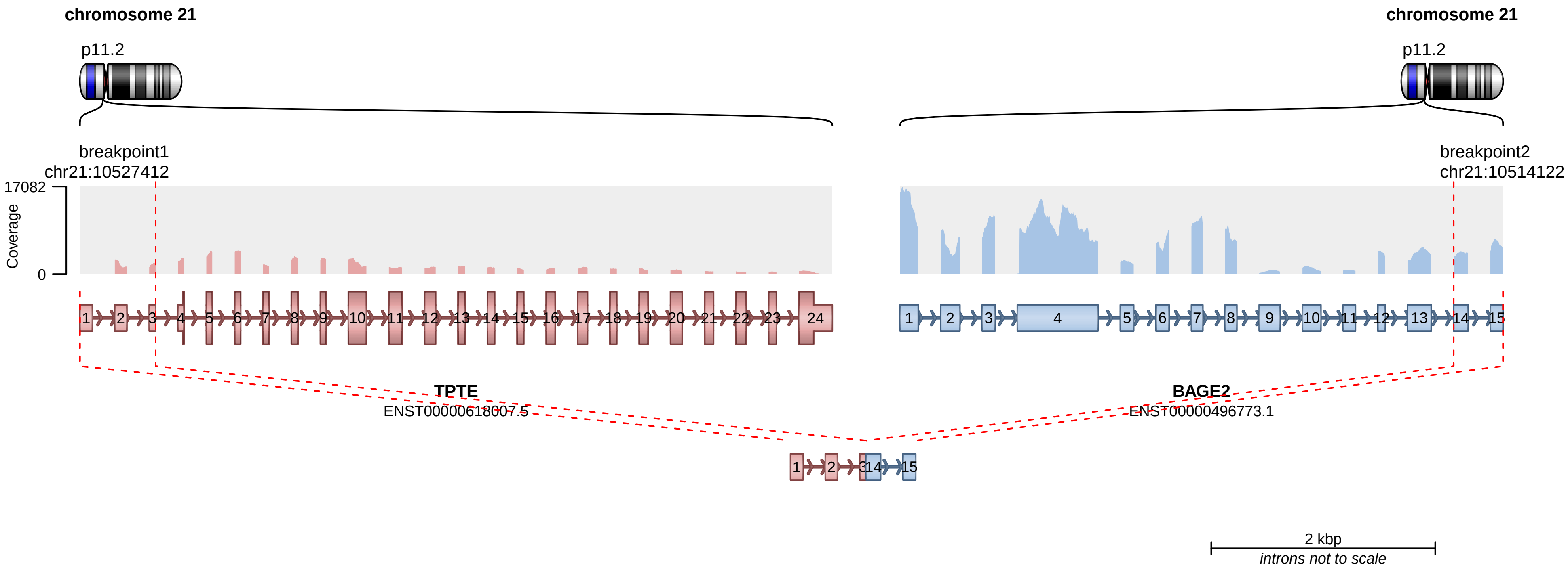


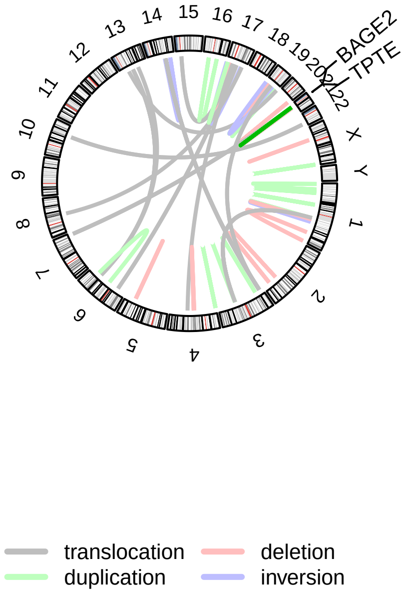


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 3

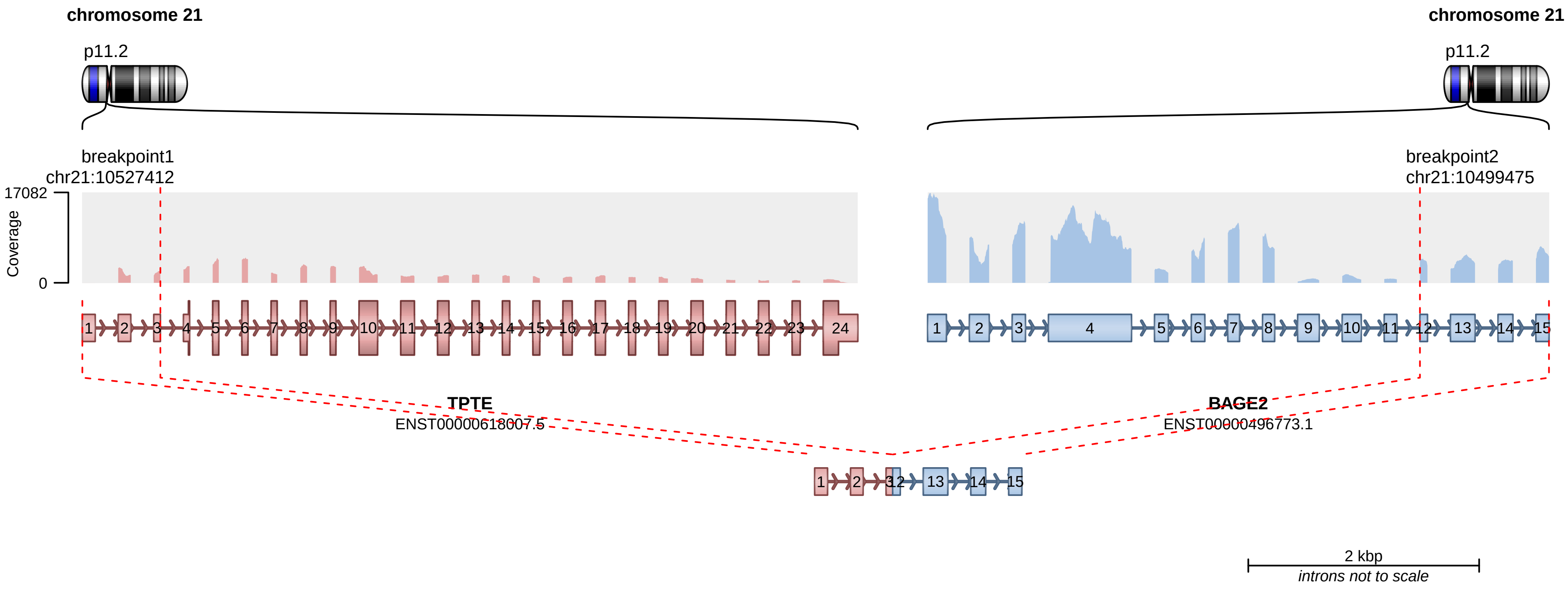


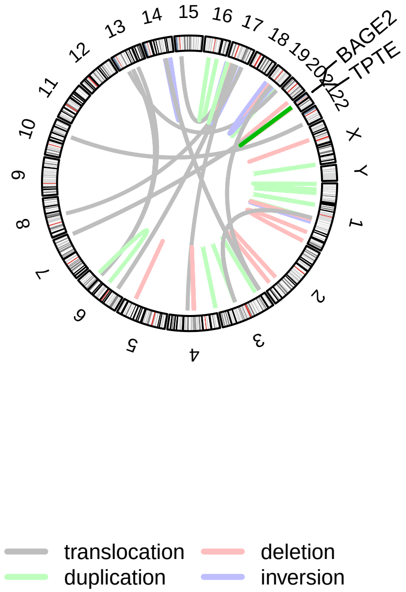


No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 1

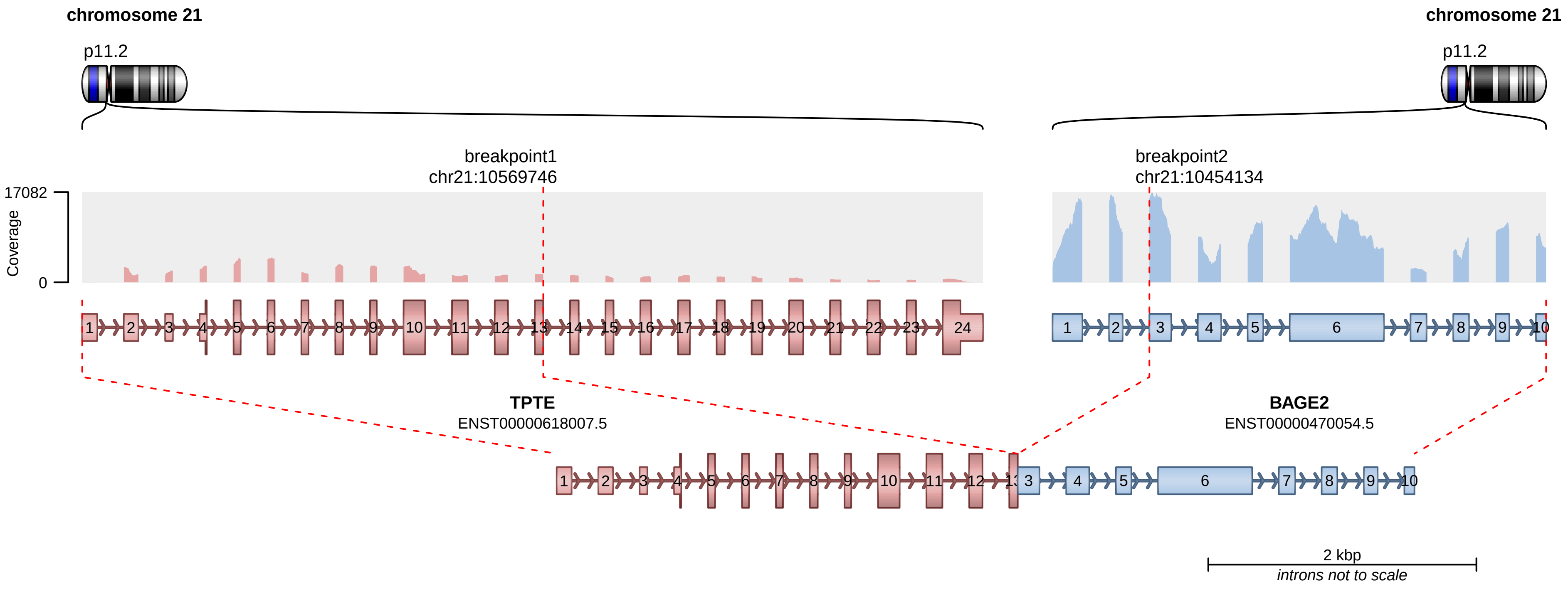


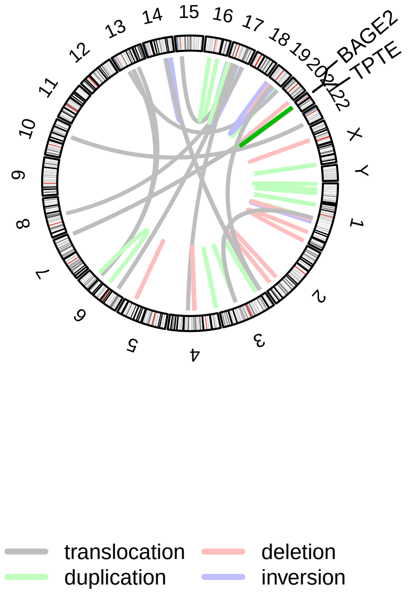


No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 9
Discordant mates = 1

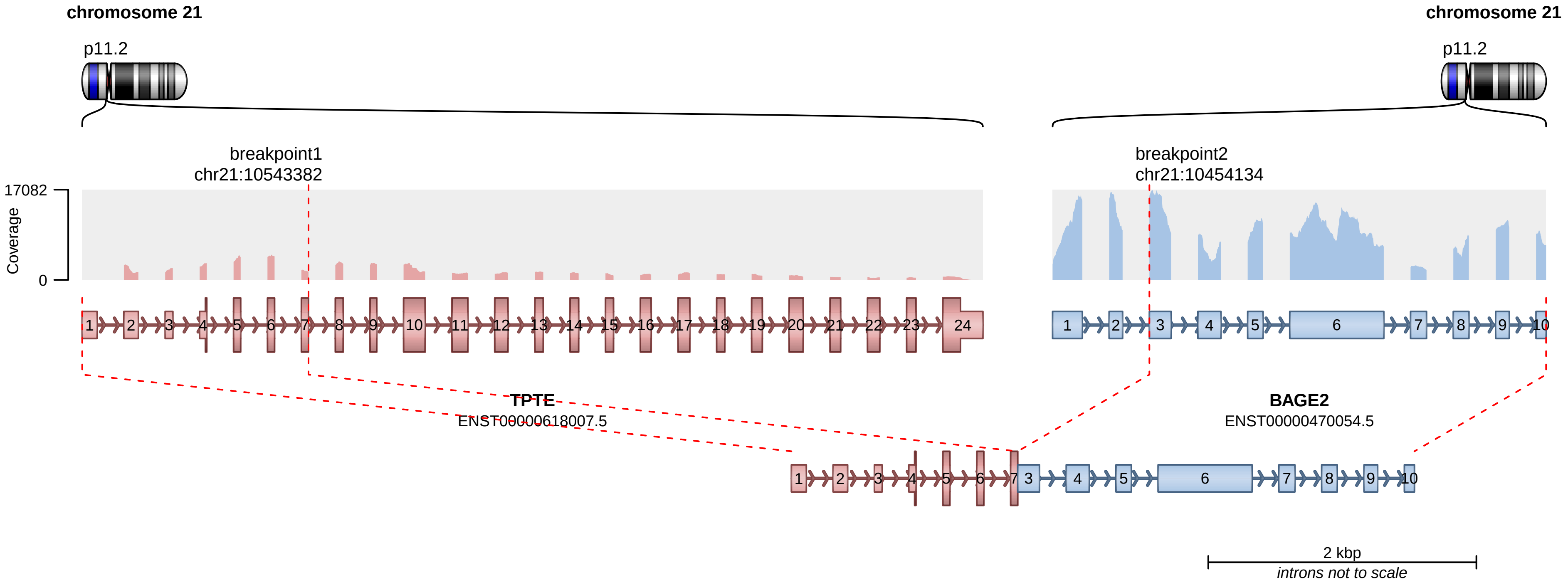


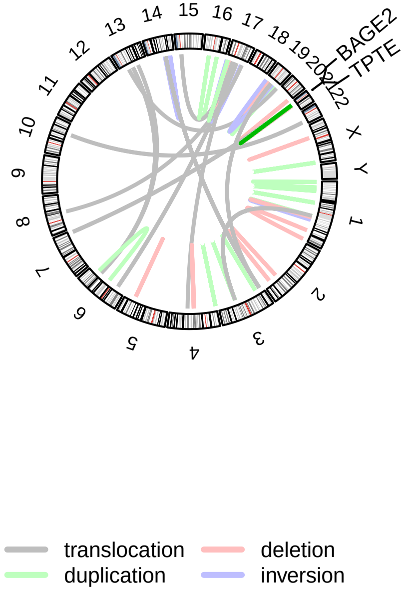


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 3

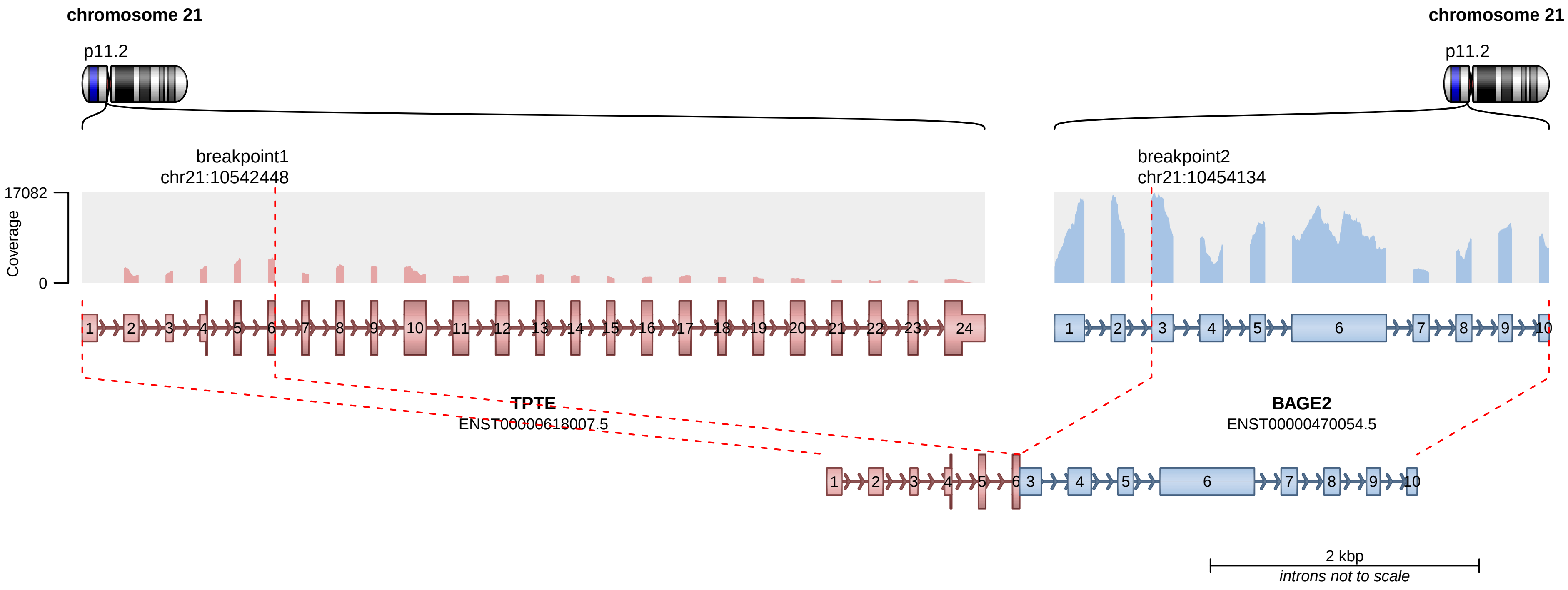


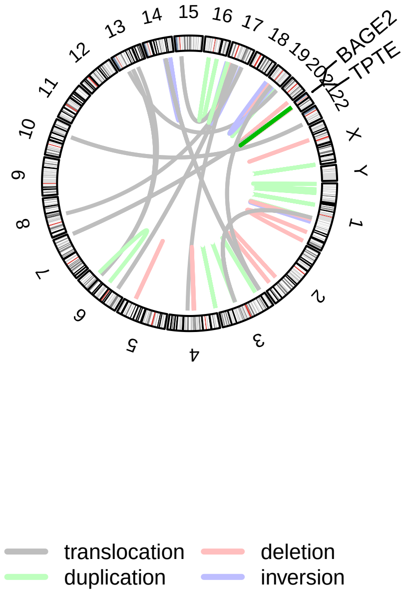


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 3

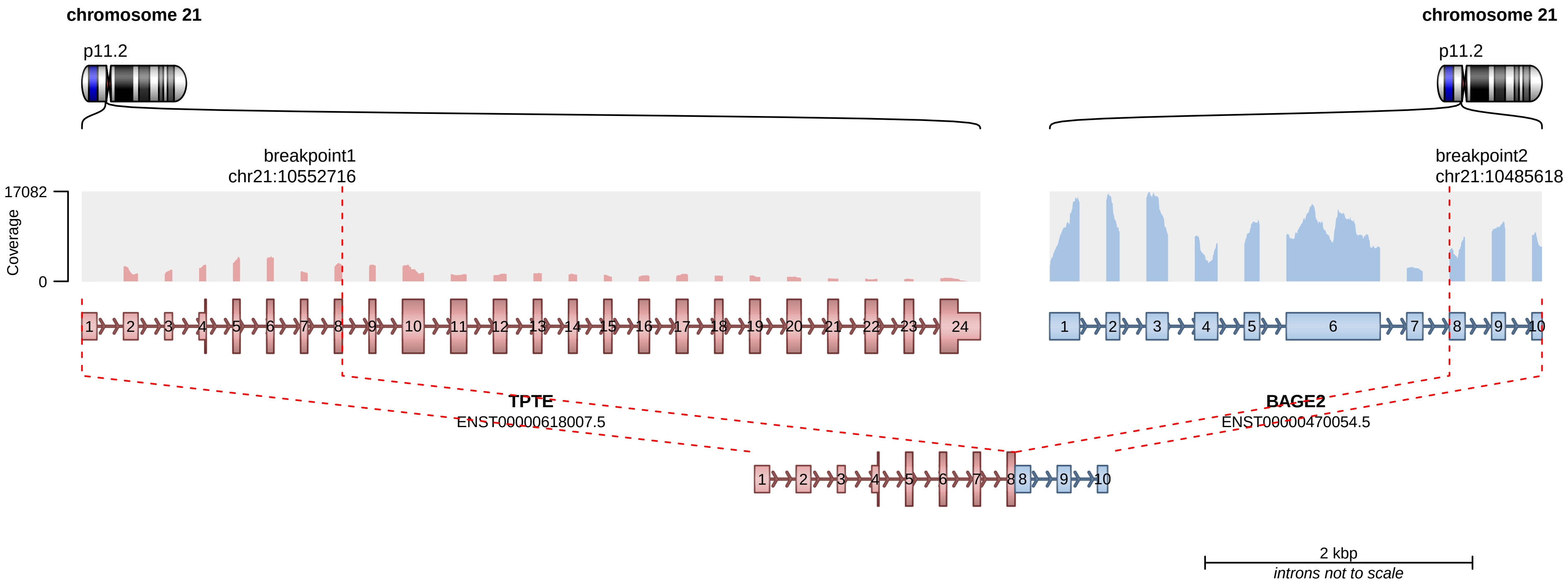


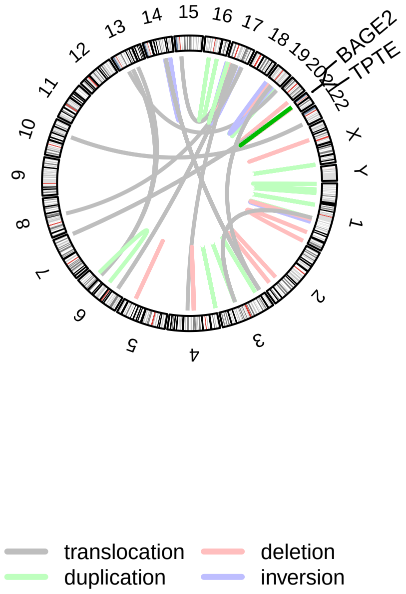


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 3

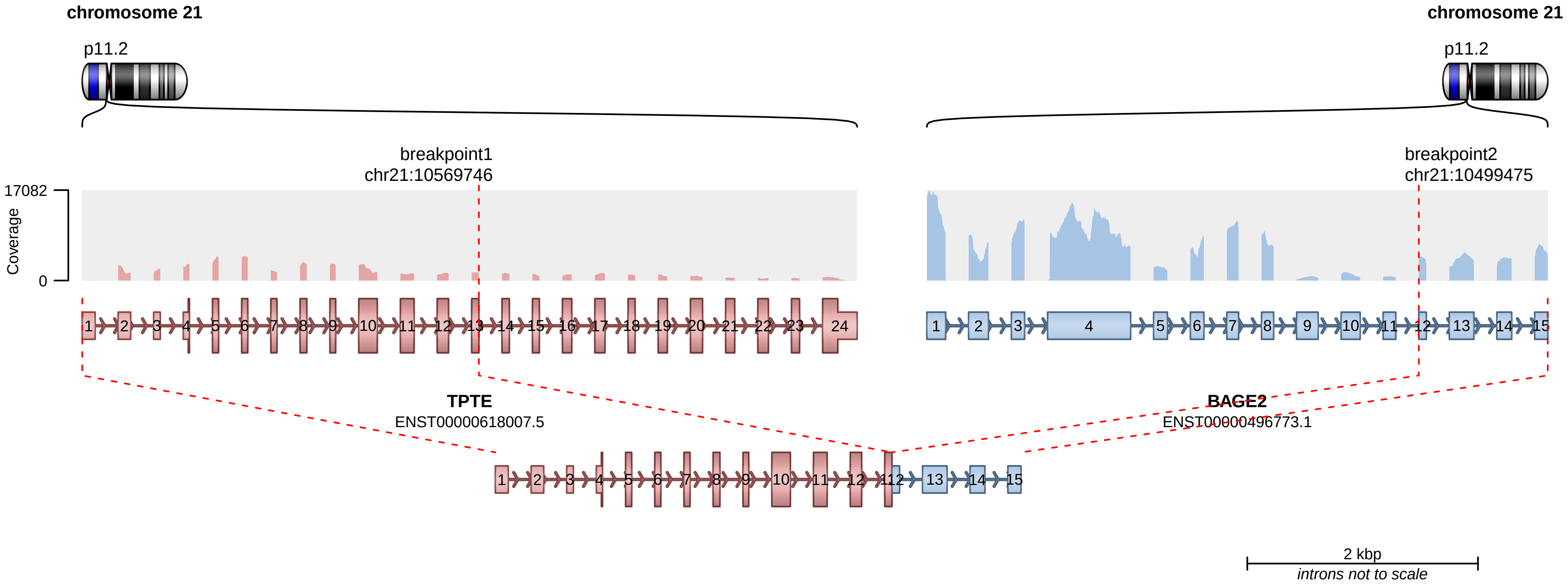


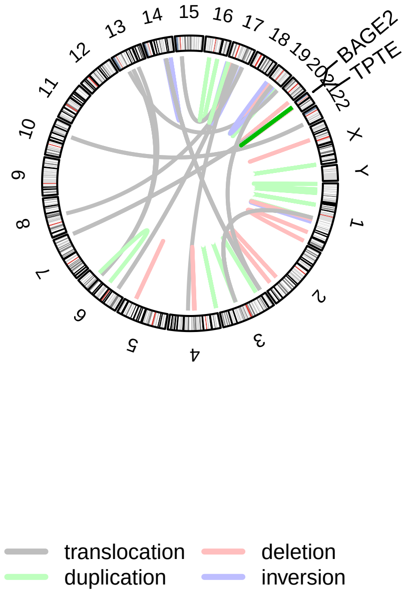


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 2

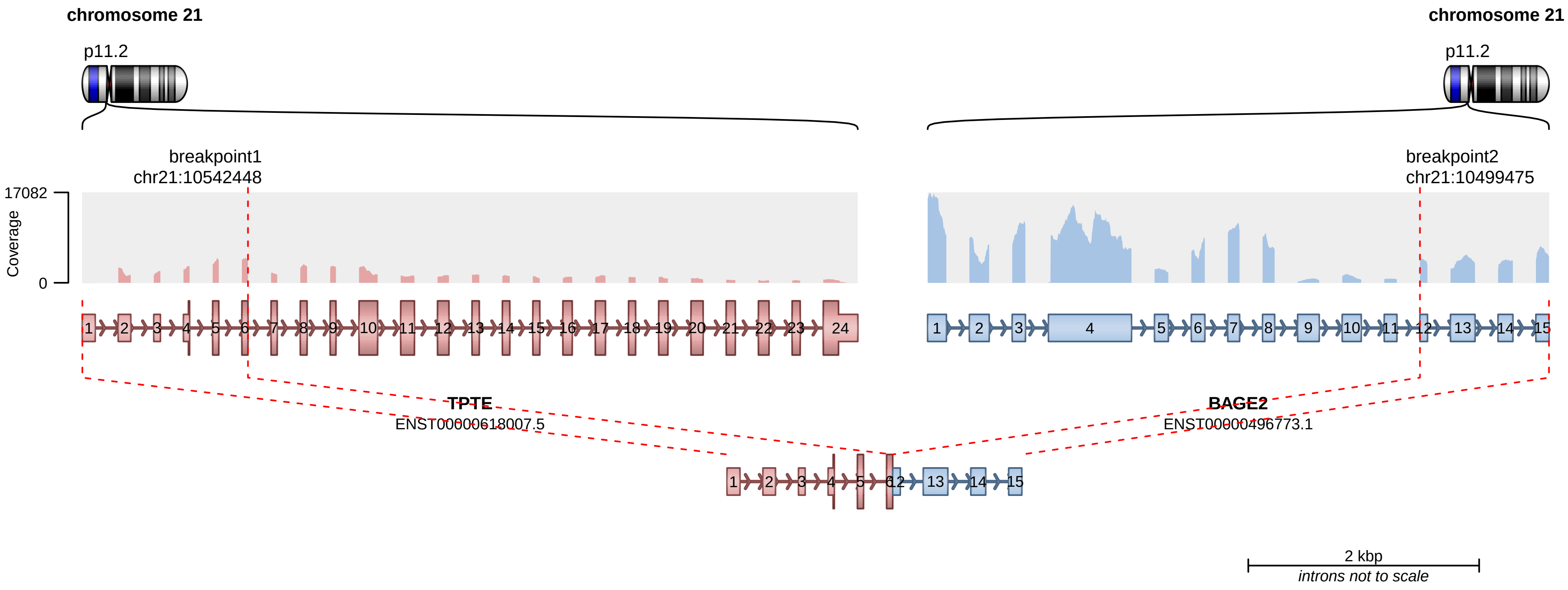


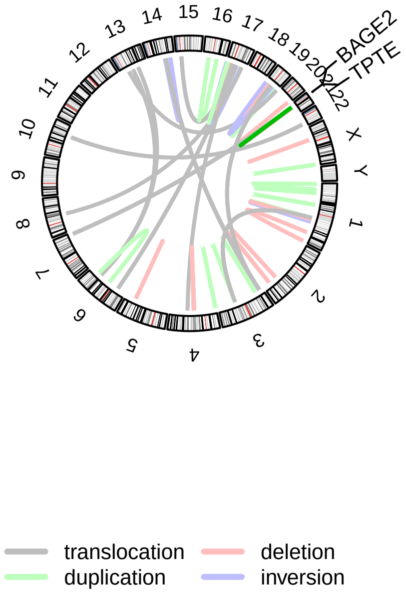


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 1

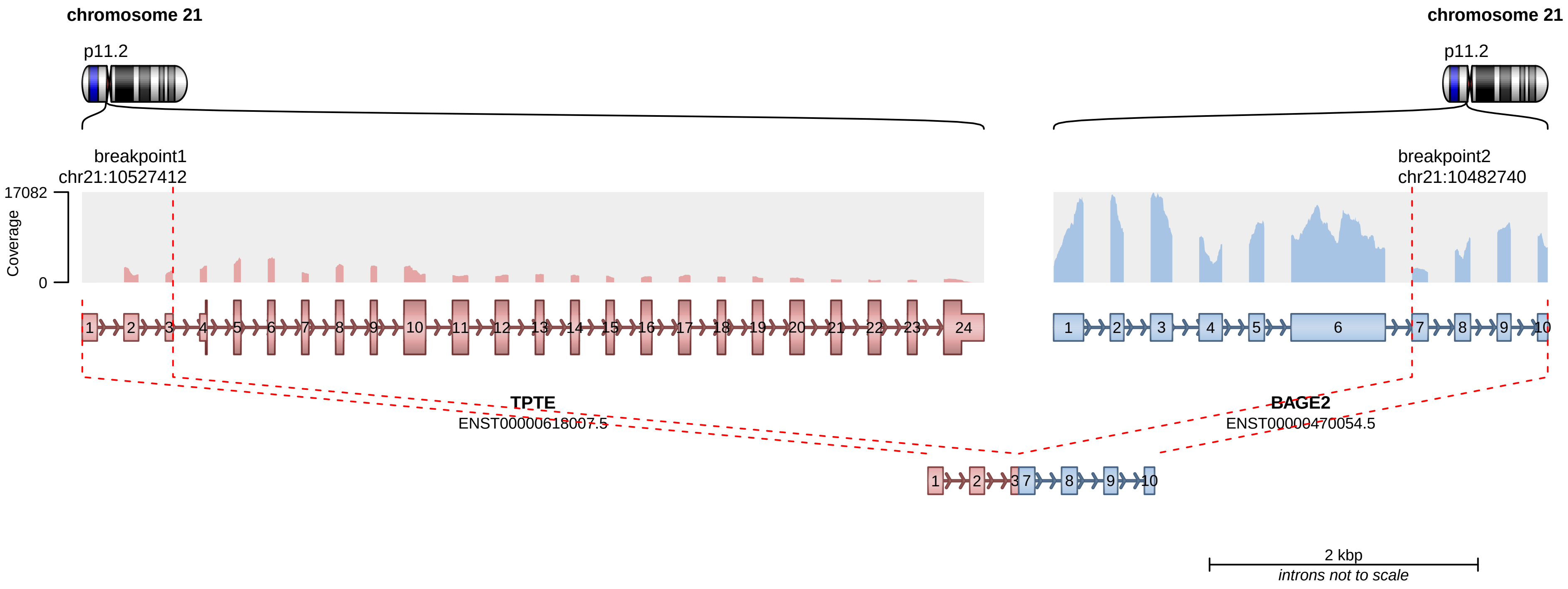


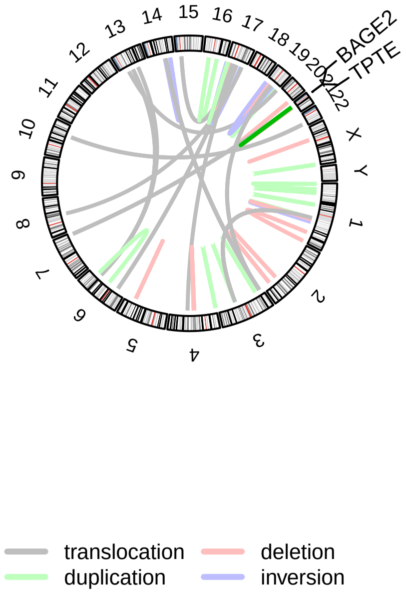


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 1

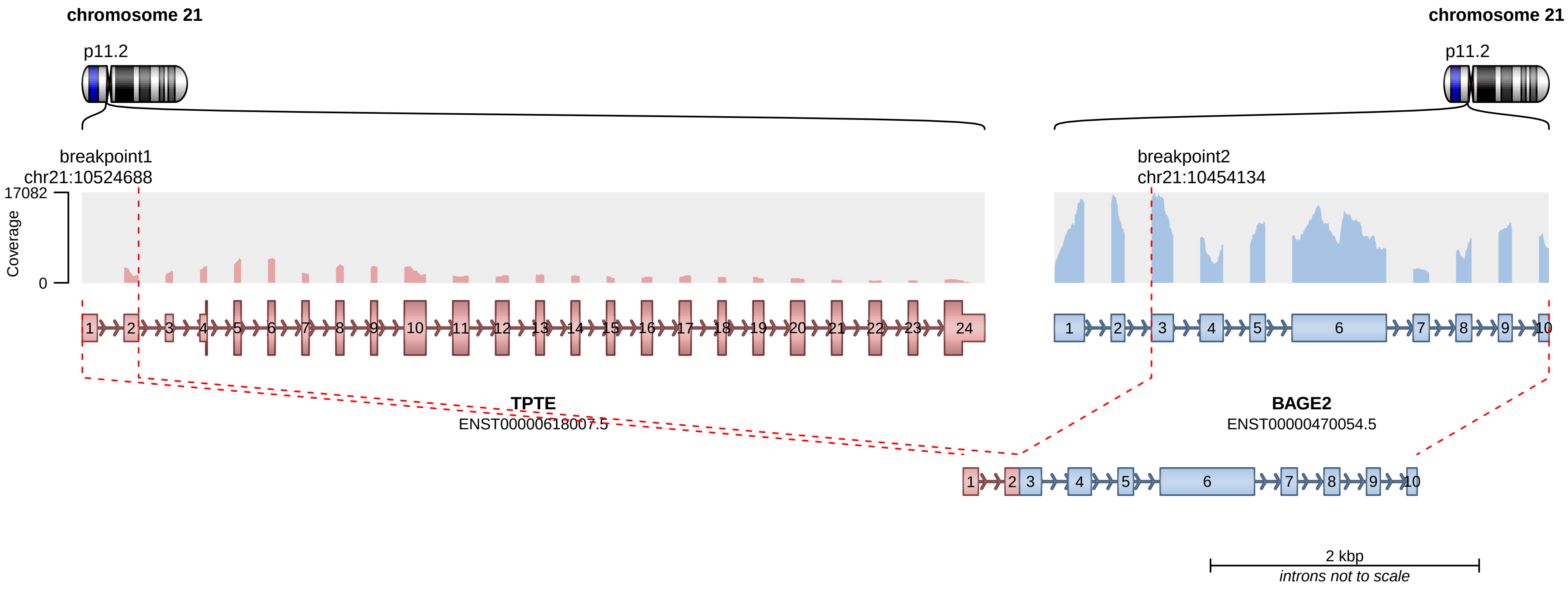


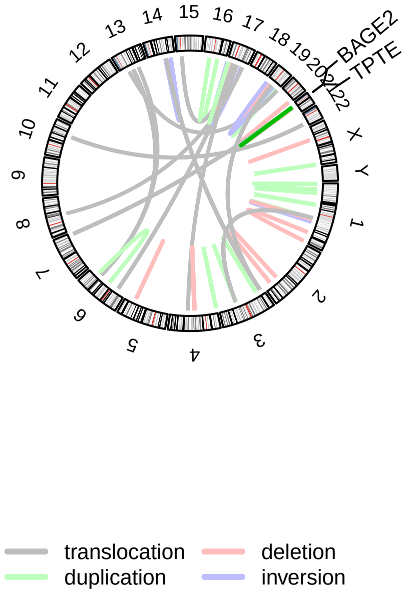


No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 1

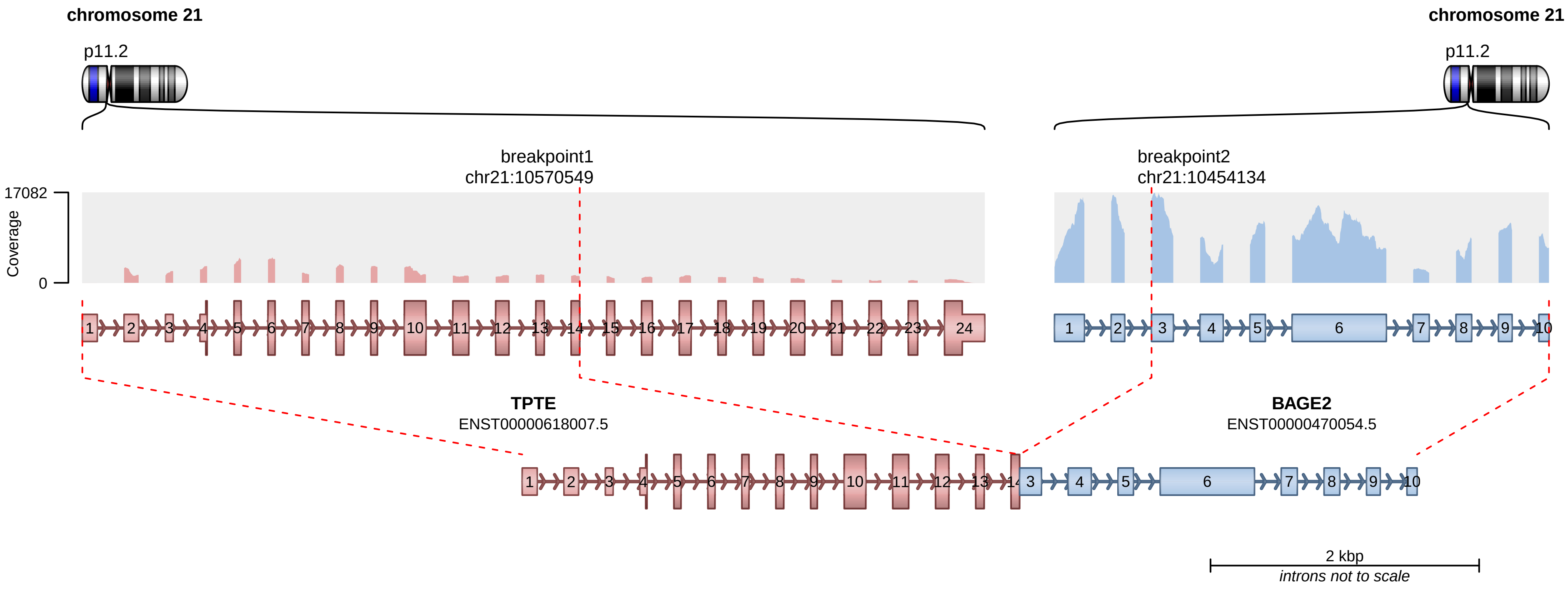


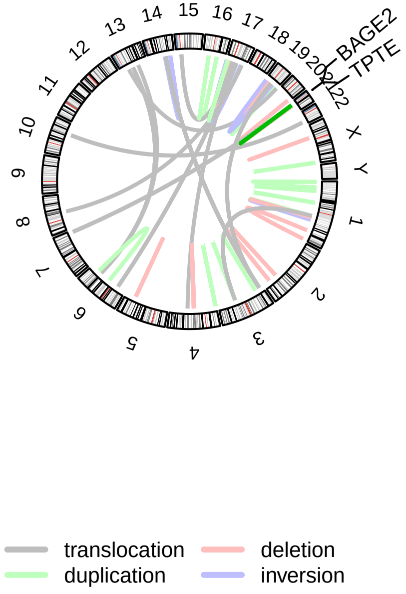


No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

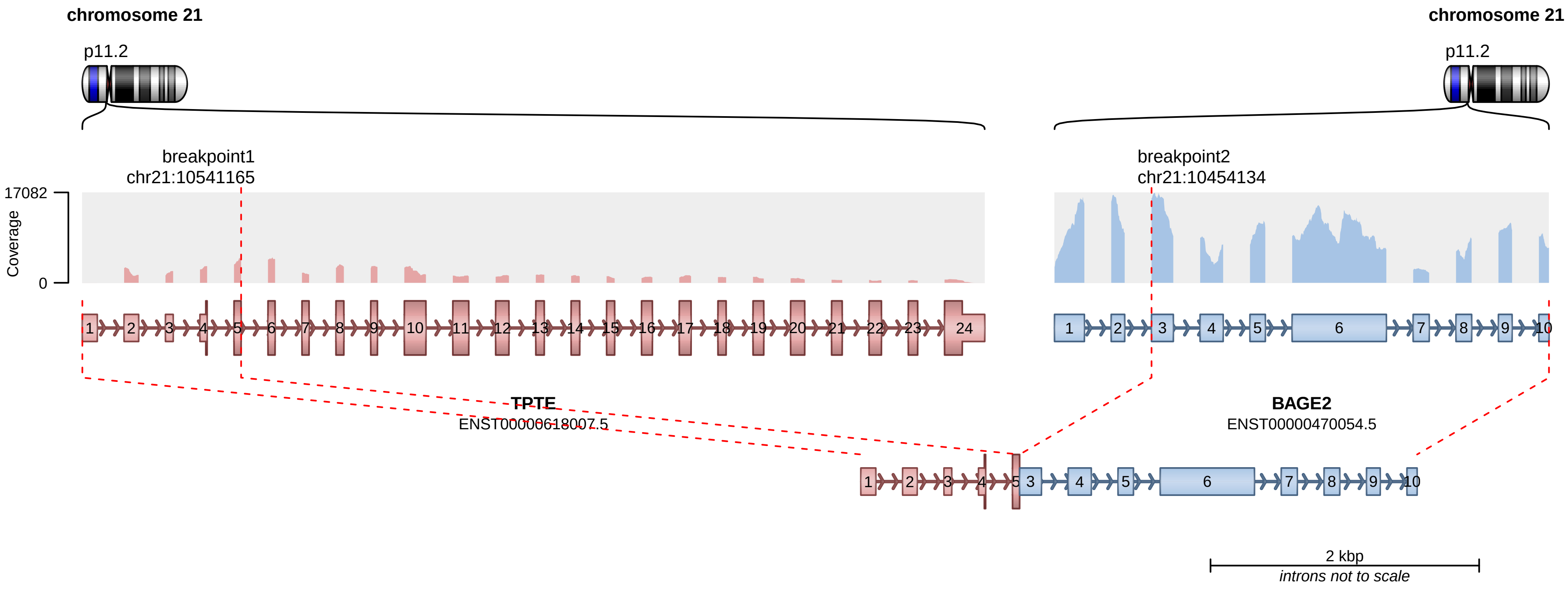


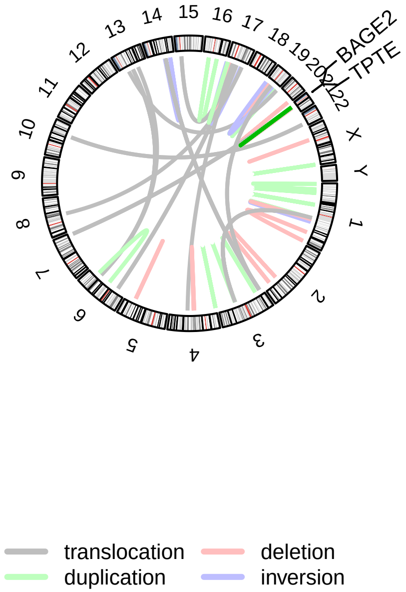


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 3

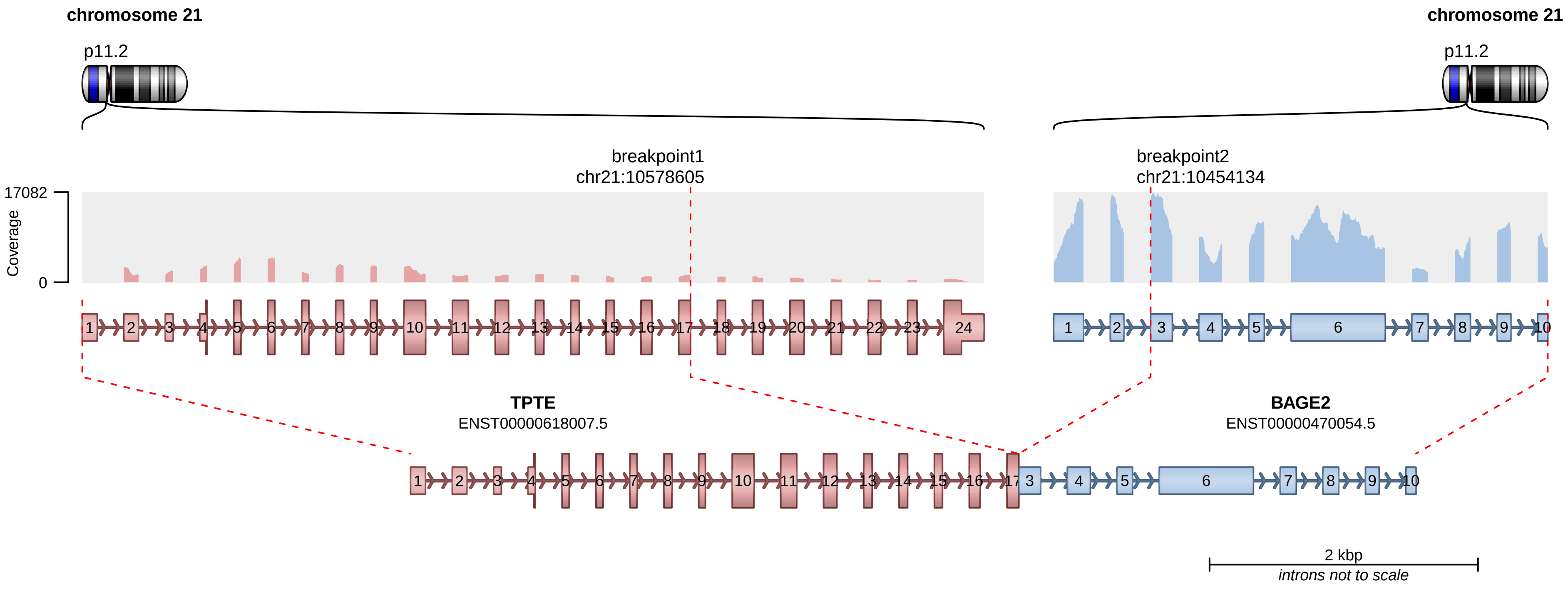


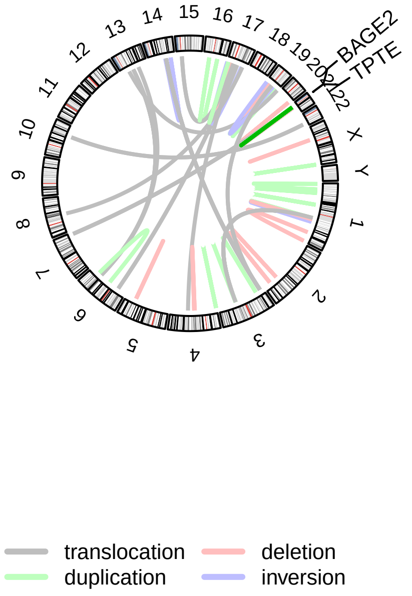


No protein domains retained in fusion.

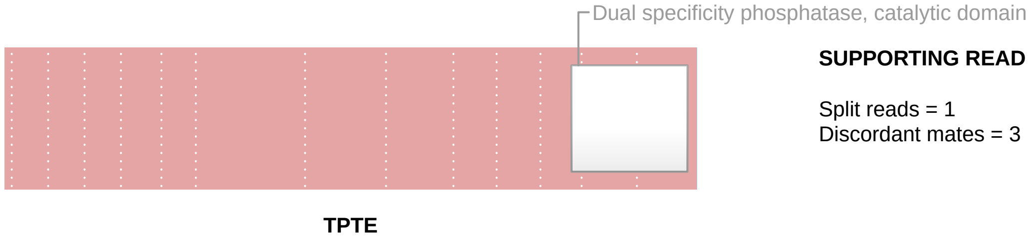
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 3



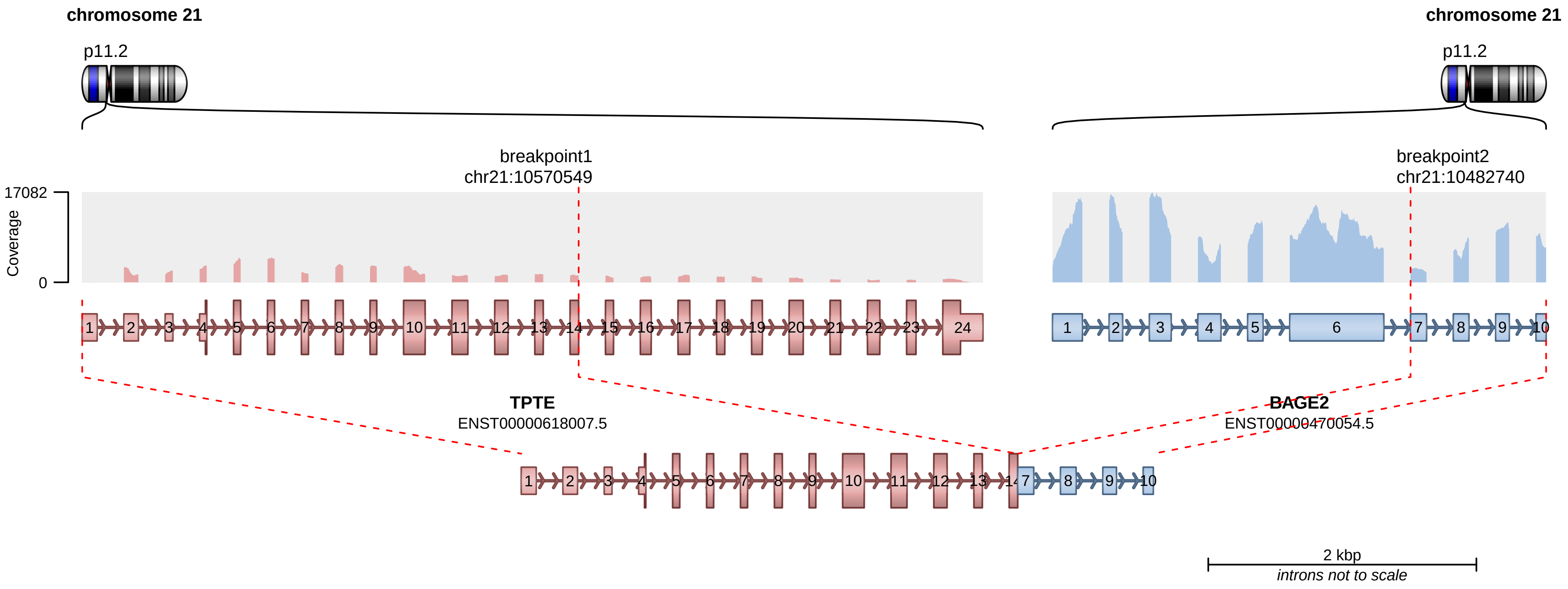


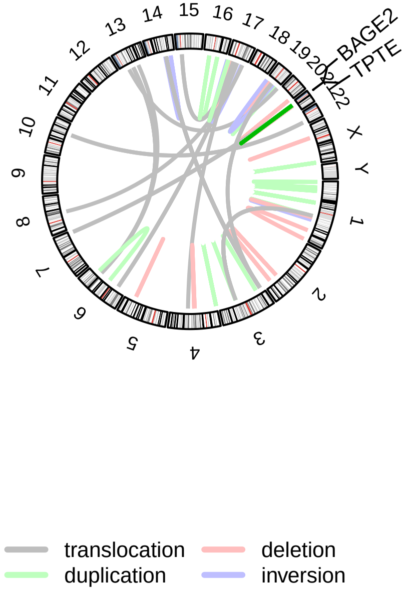
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 3

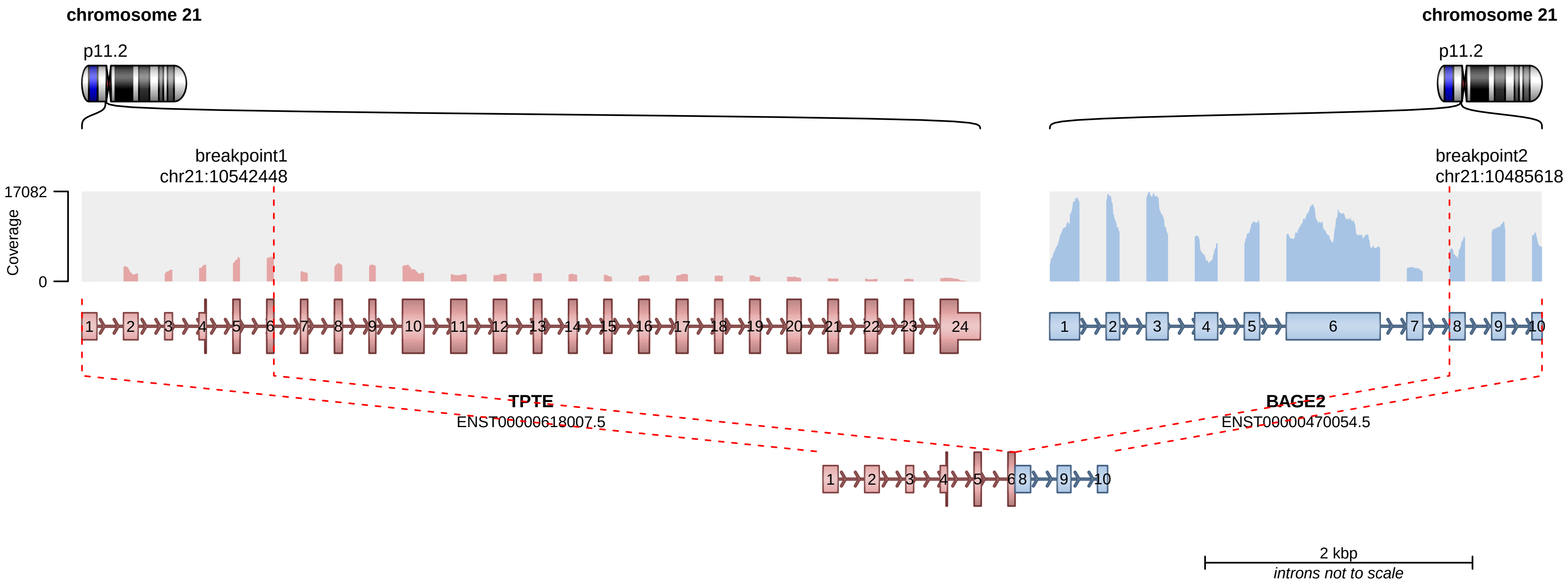


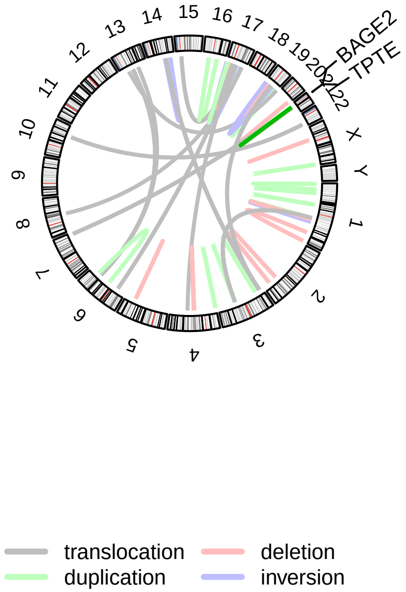


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 2

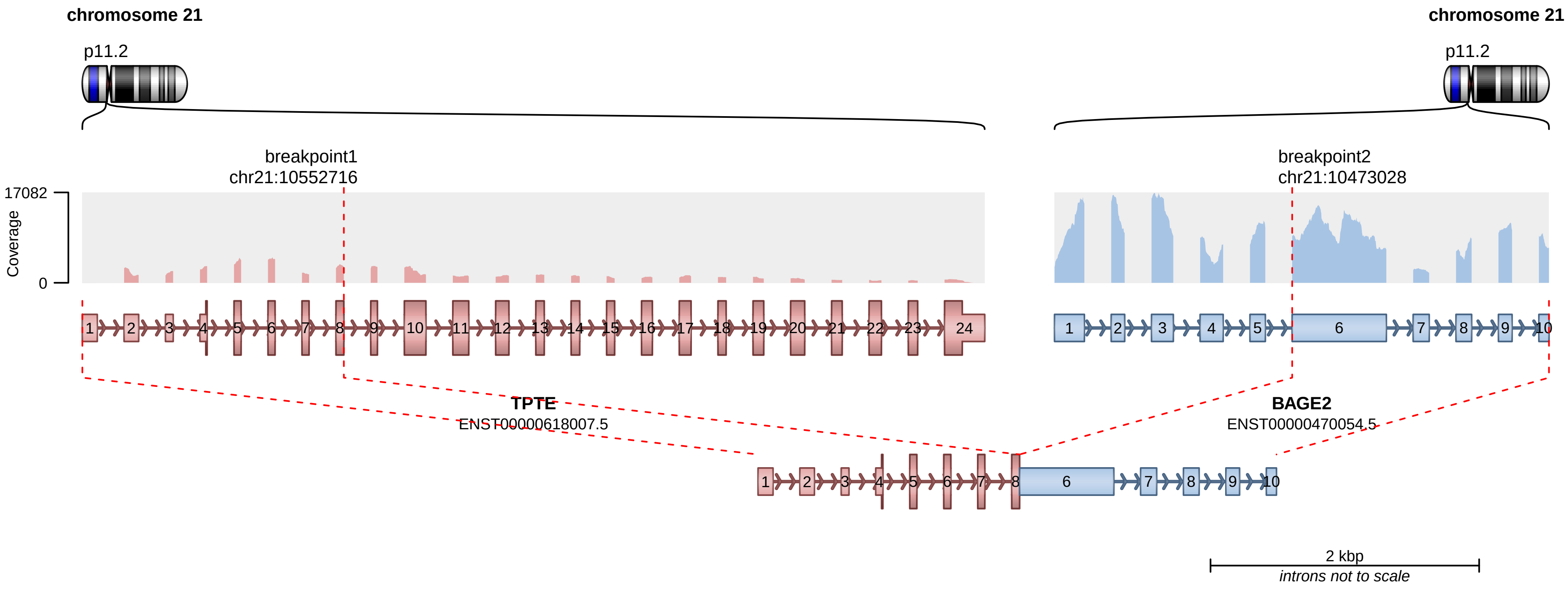


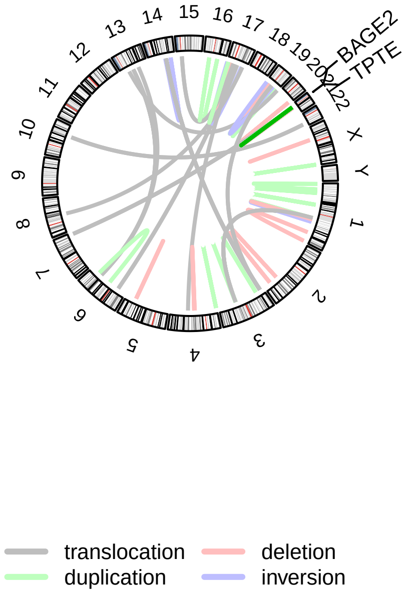


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 2

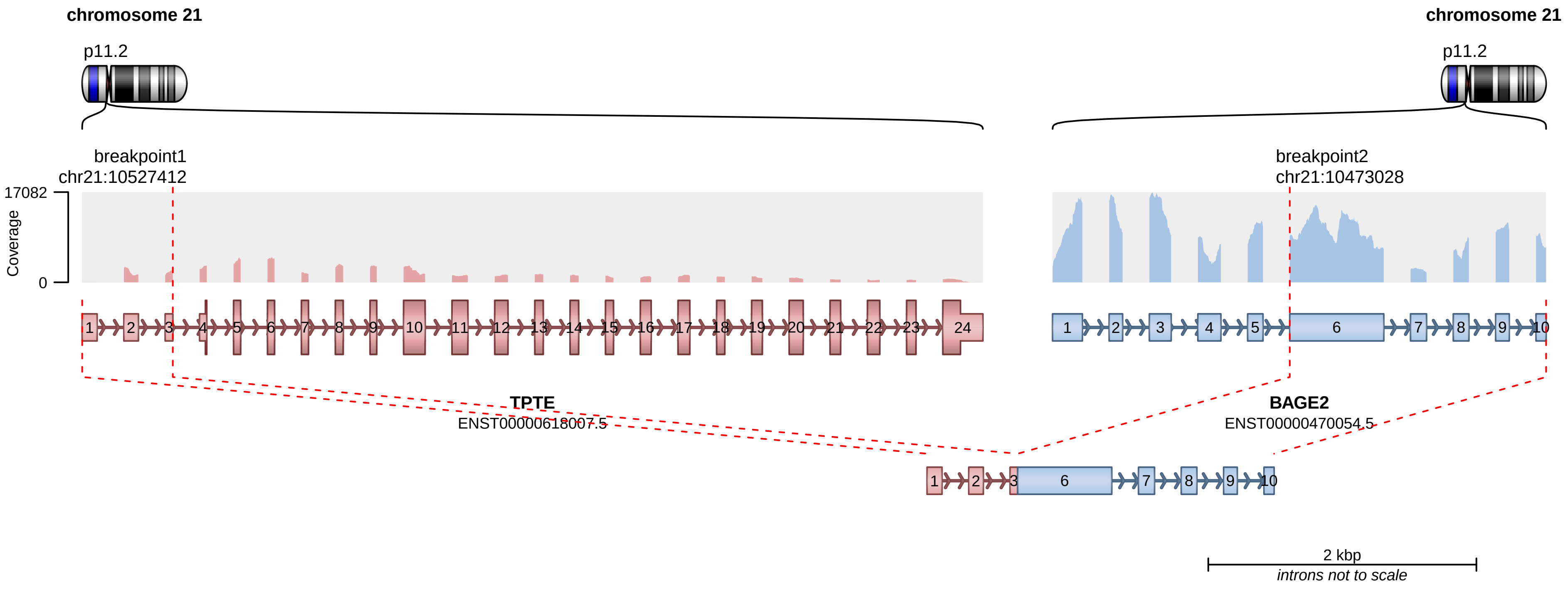


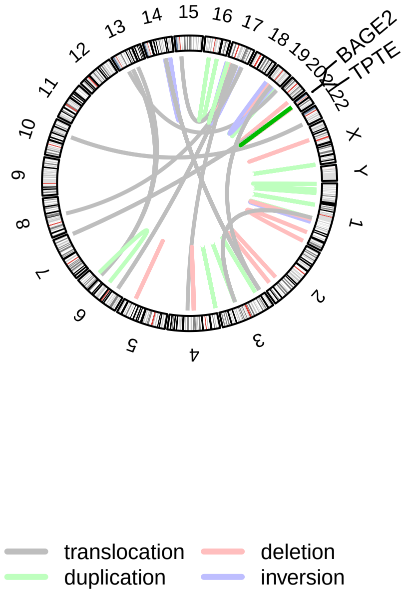


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 2

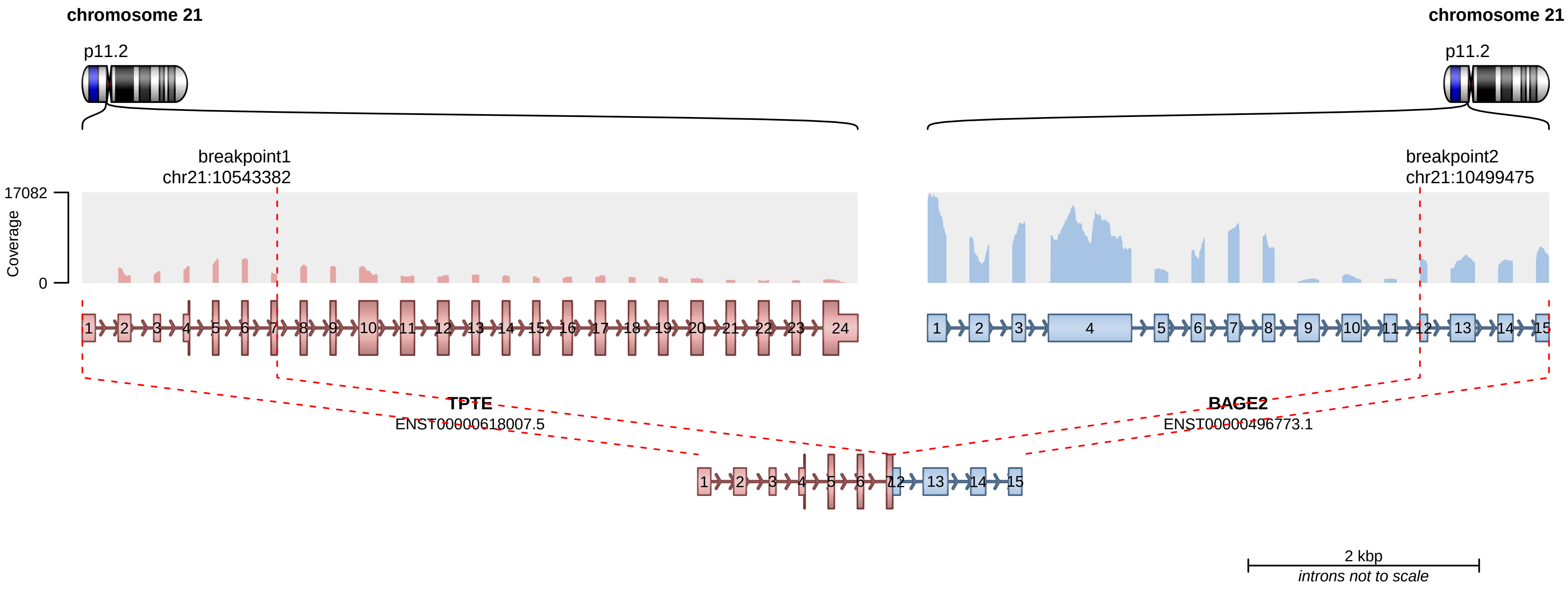


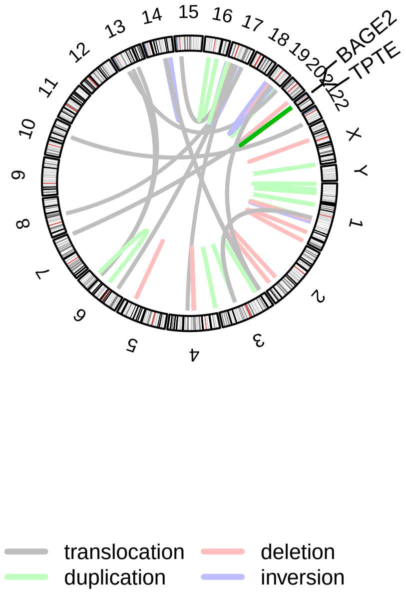


No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

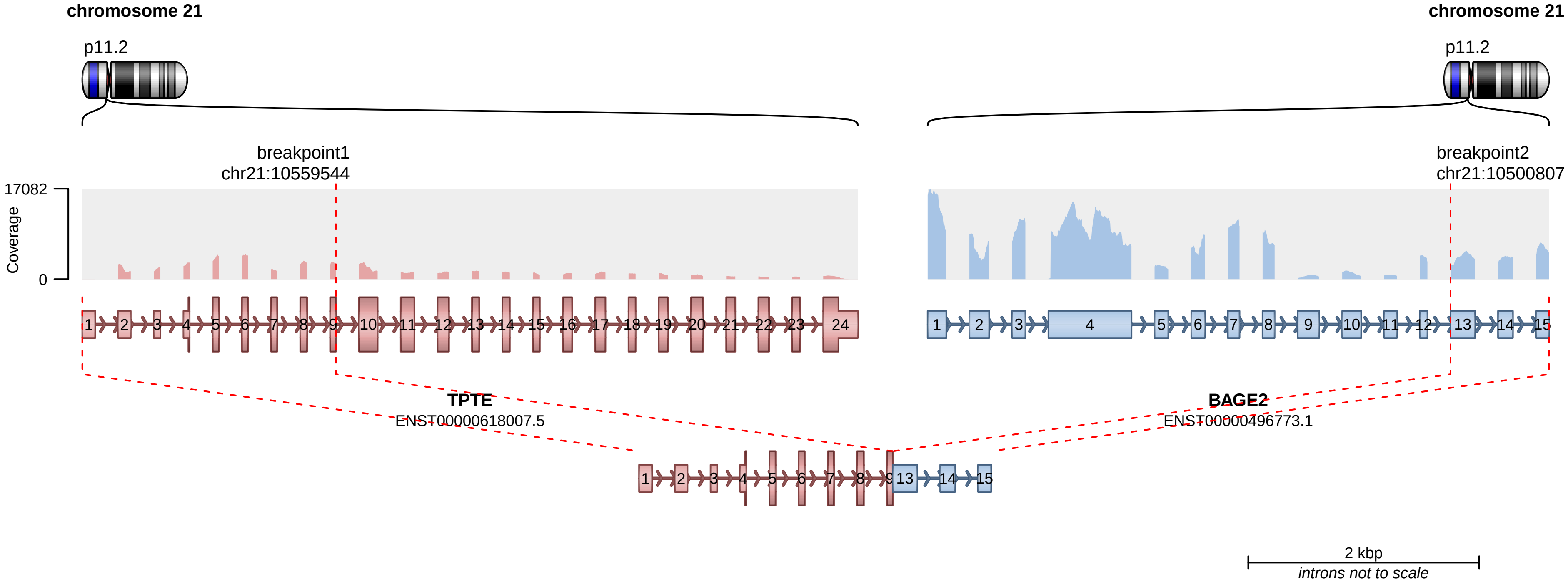


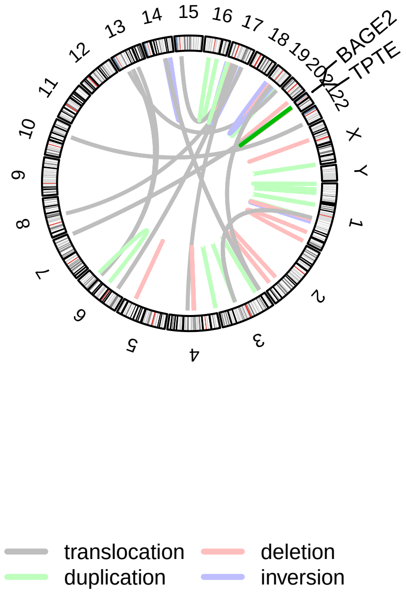


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

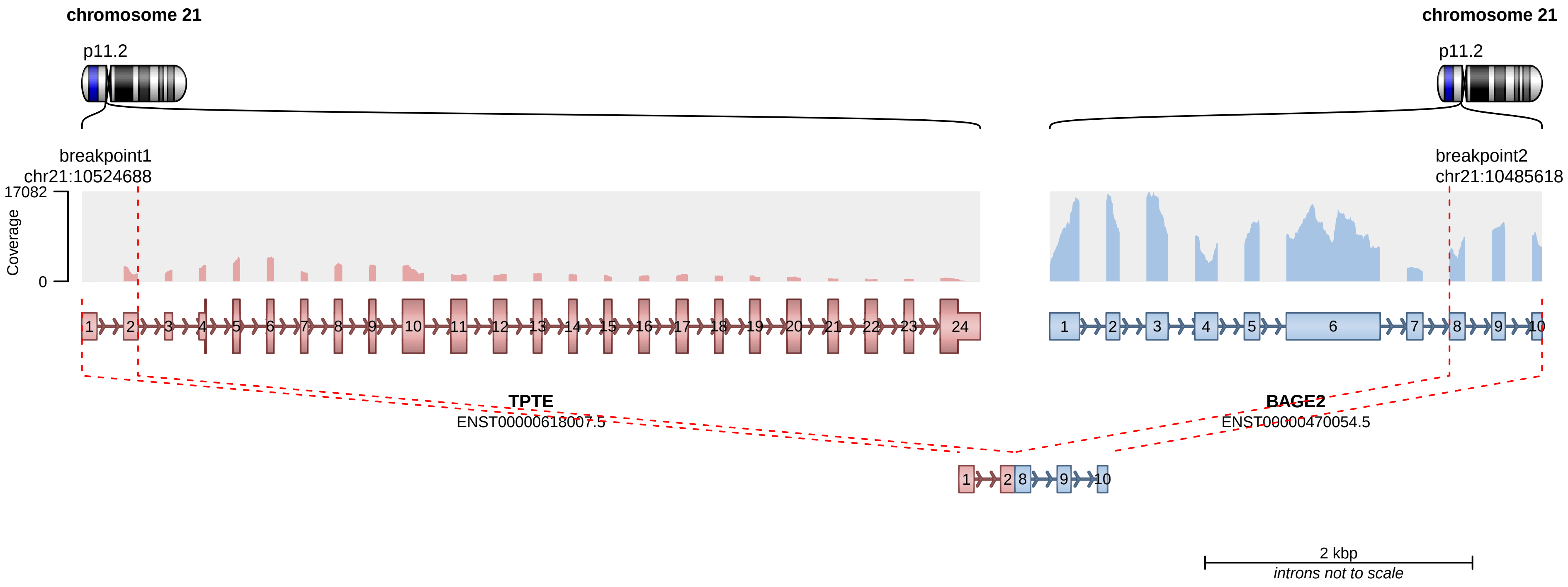


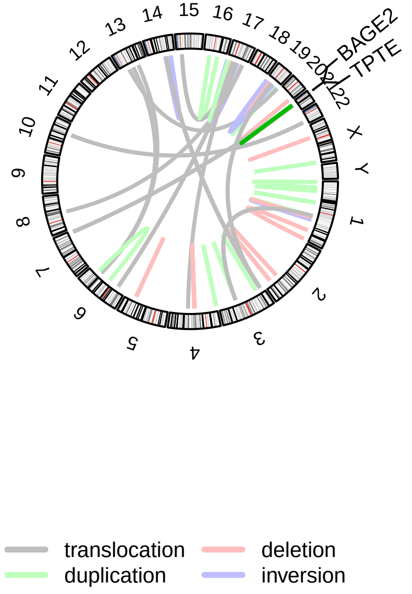


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

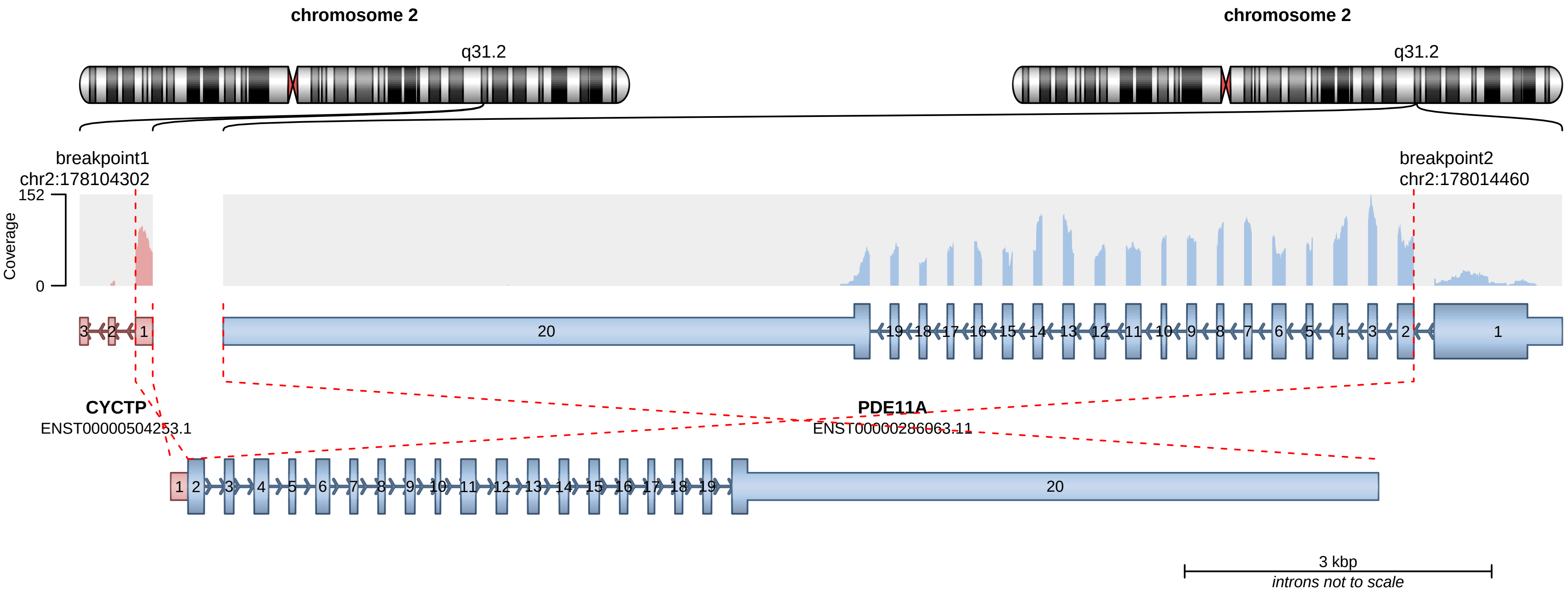


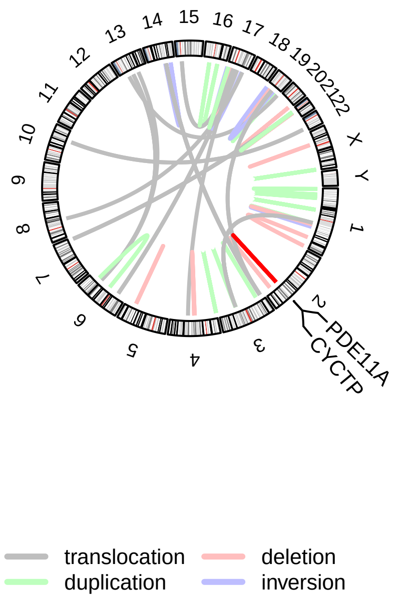


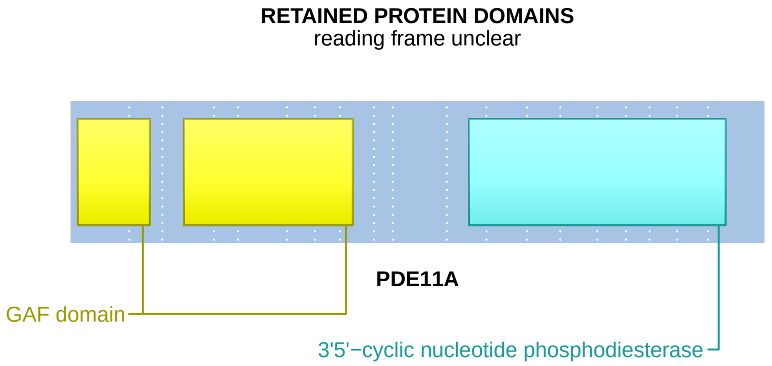
No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

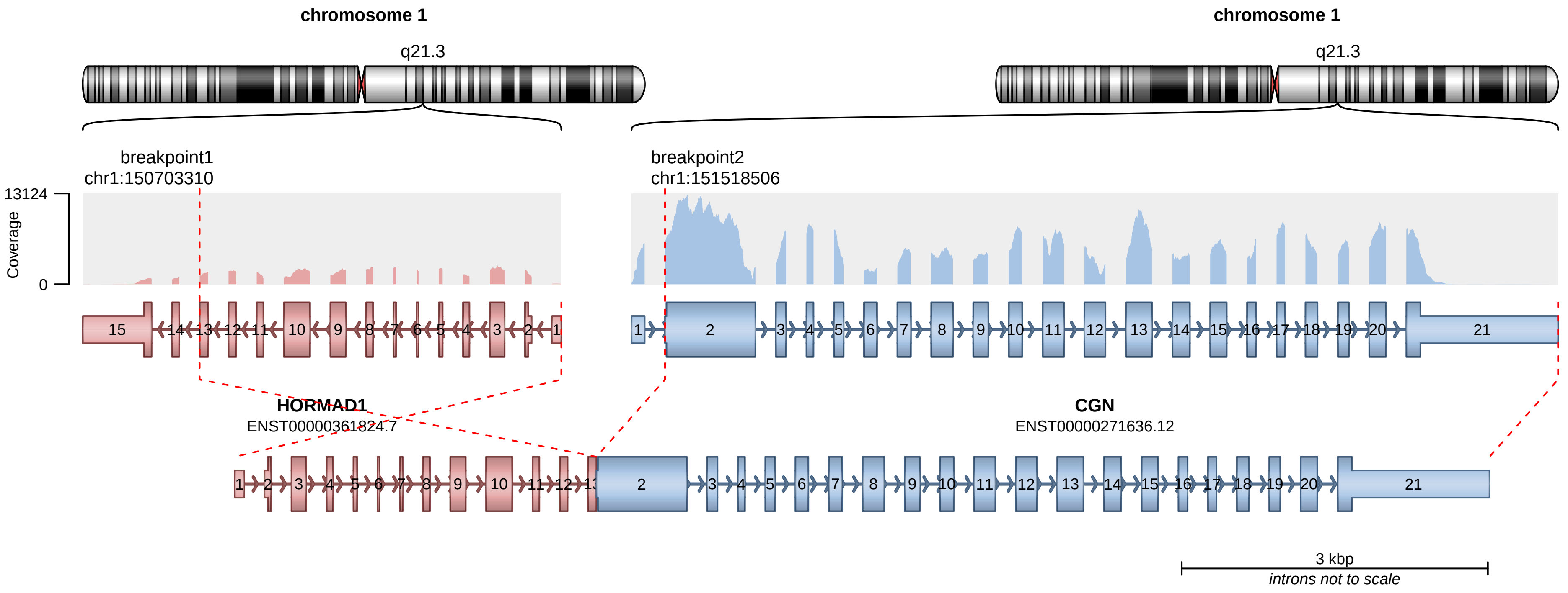


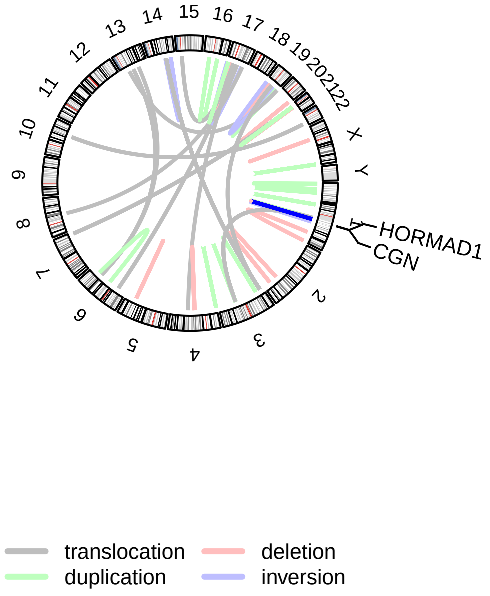


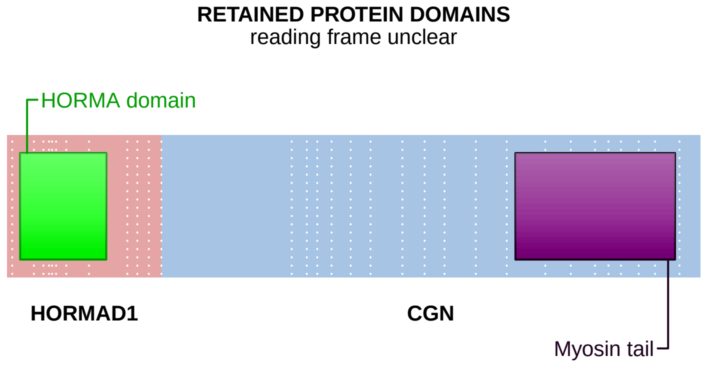


SUPPORTING READ COUNT

Split reads = 16
Discordant mates = 0

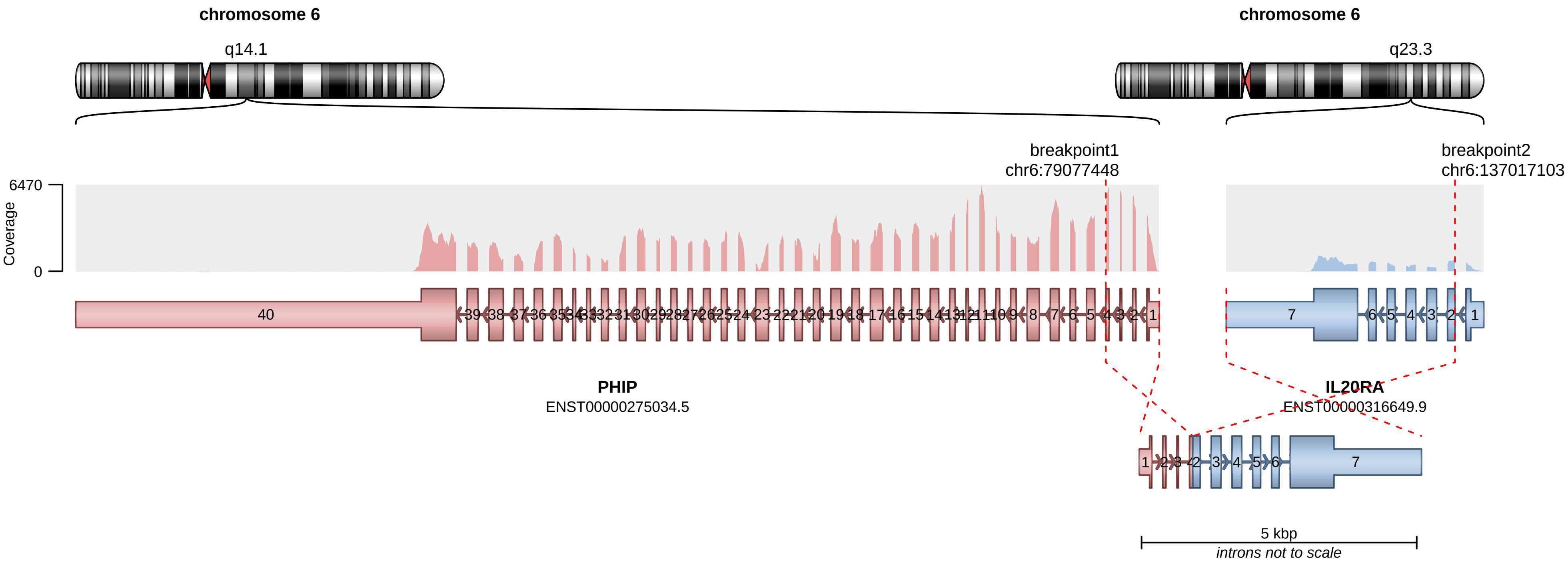


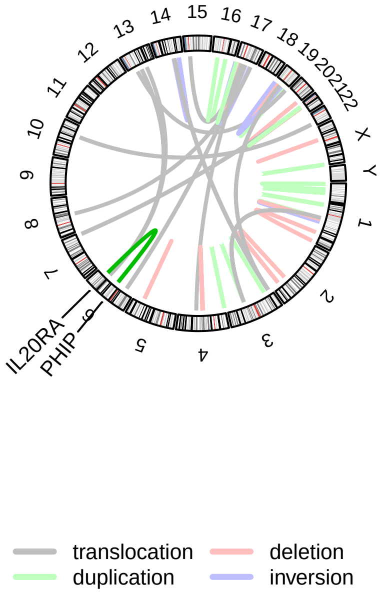


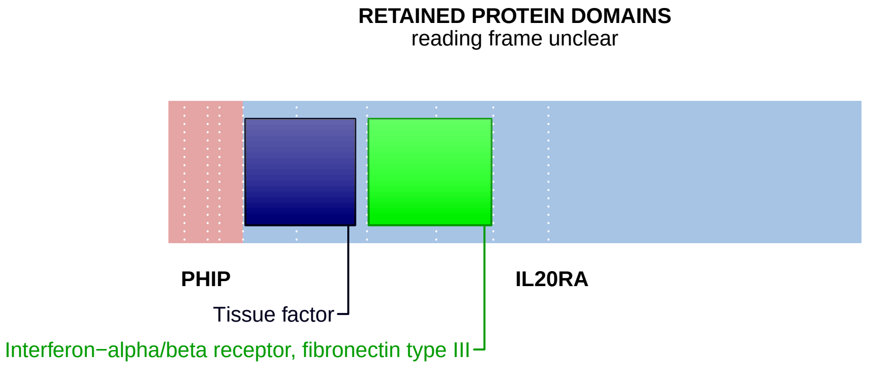


SUPPORTING READ COUNT

Split reads = 15
Discordant mates = 0

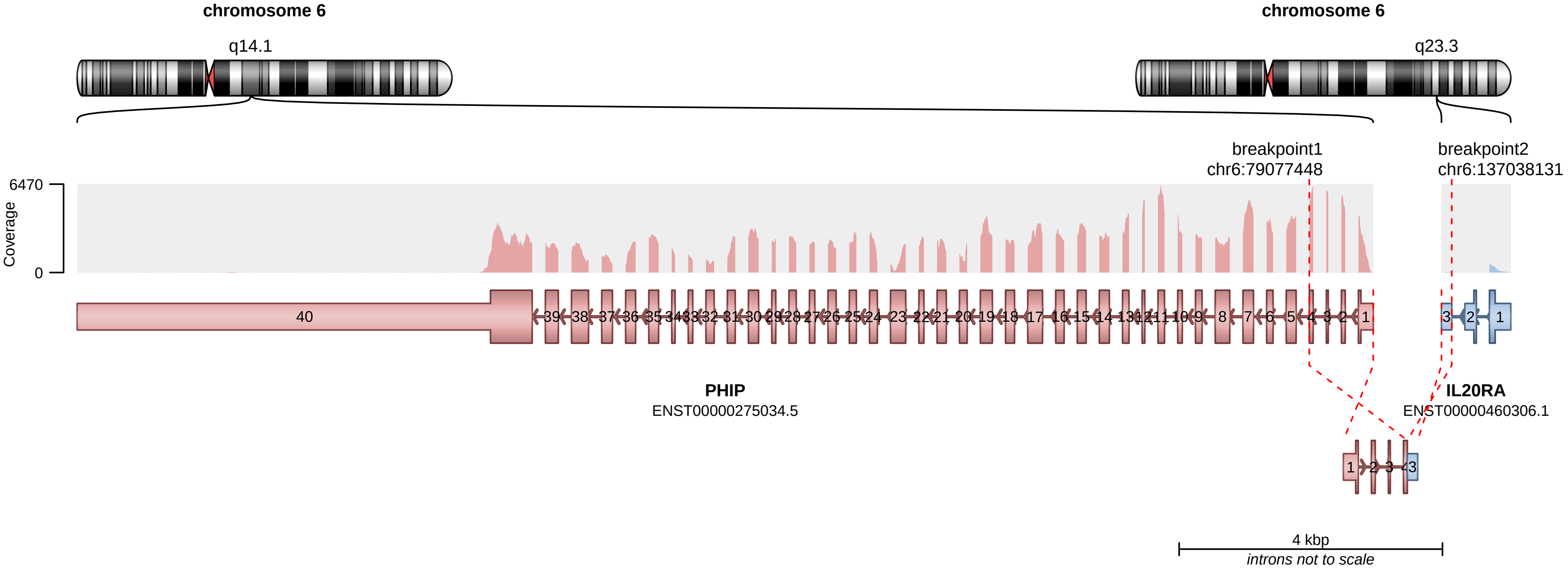


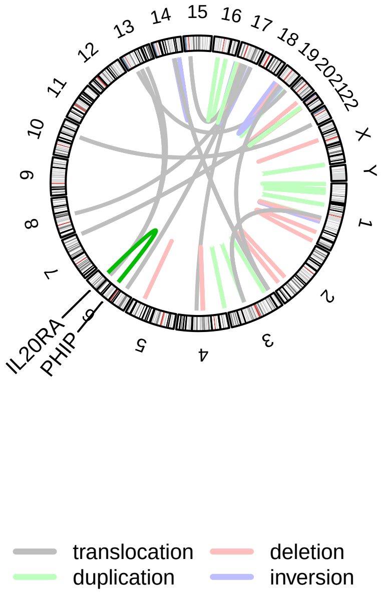




SUPPORTING READ COUNT

Split reads = 15
Discordant mates = 0

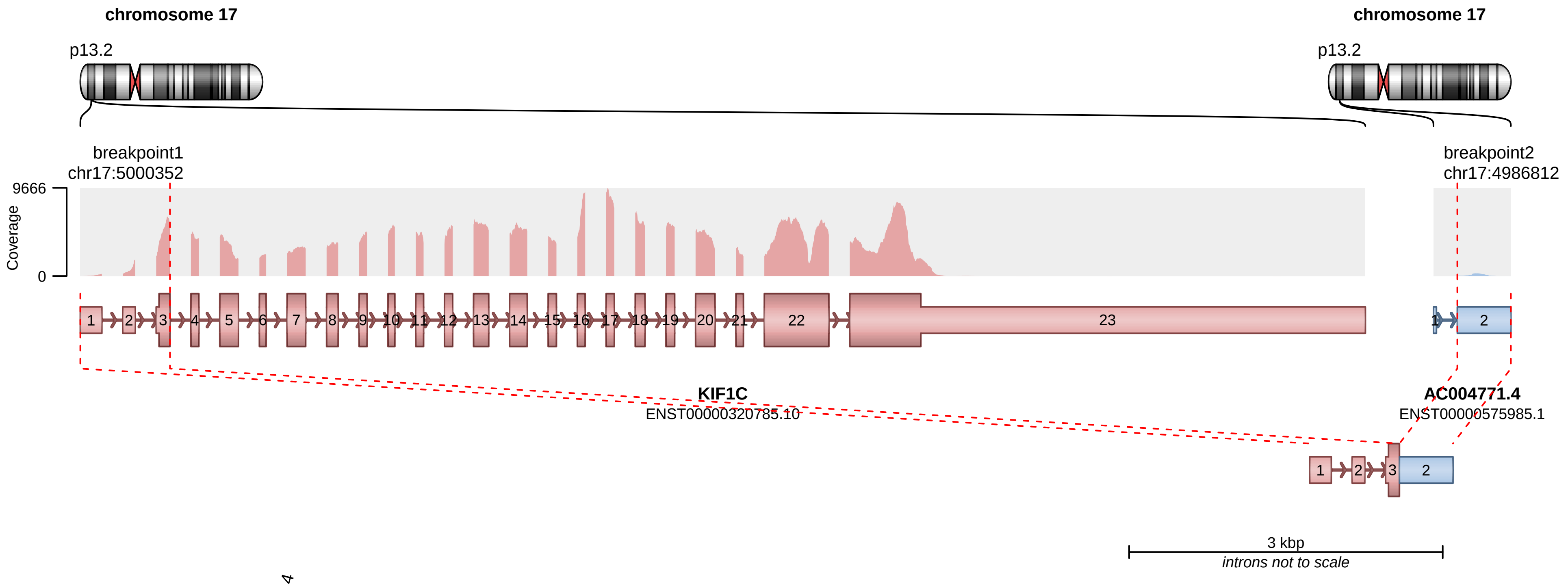


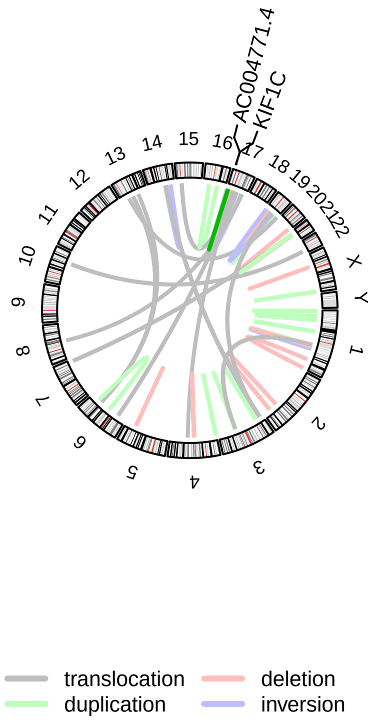


No protein domains retained in fusion.

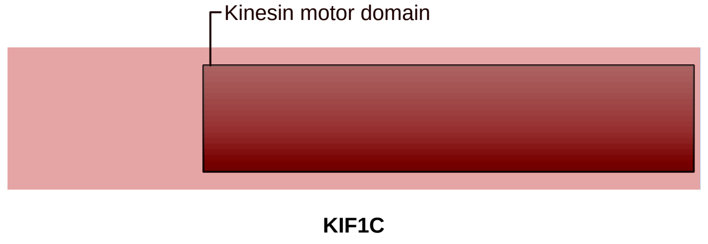
SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 1



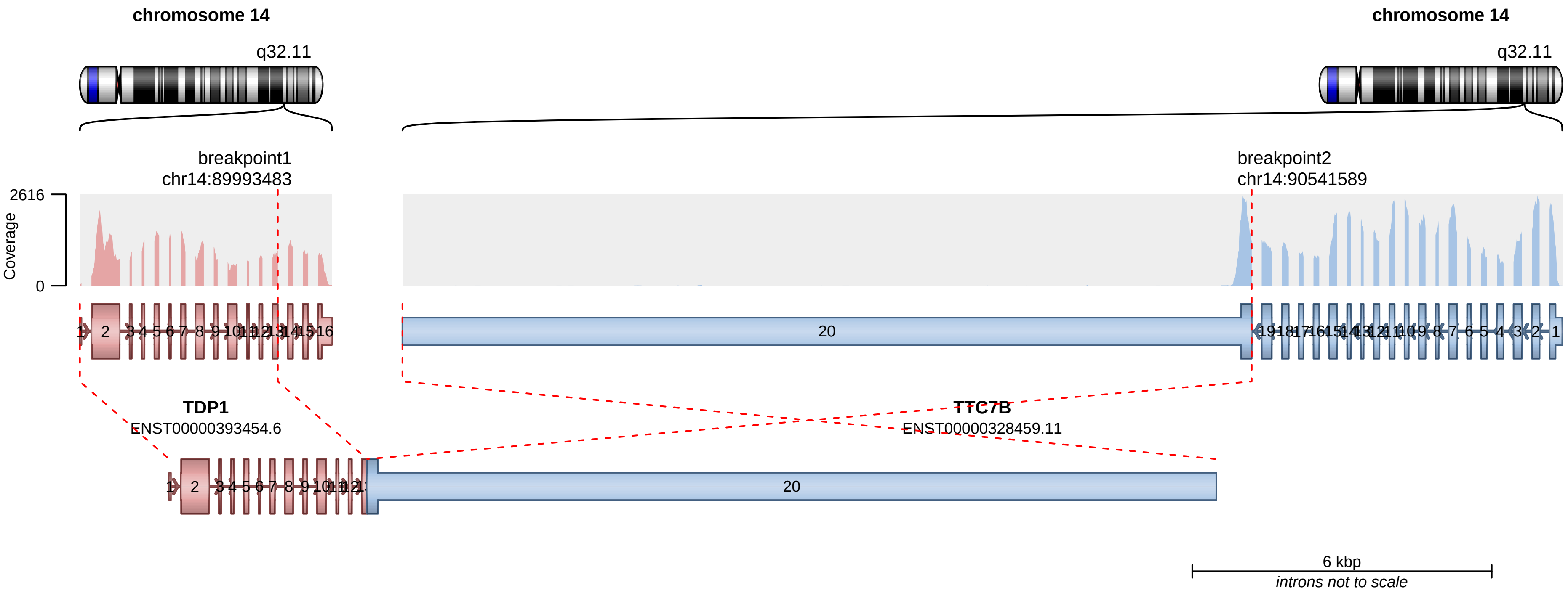


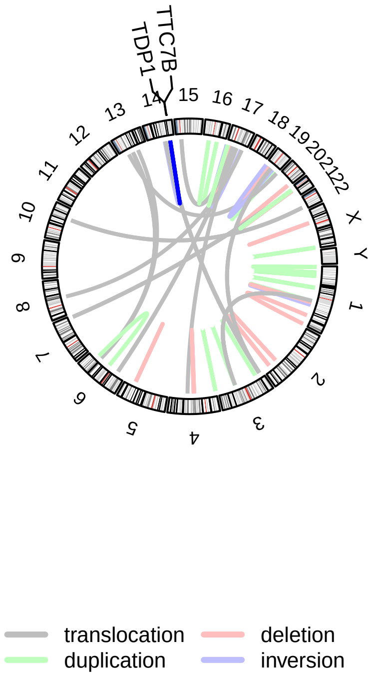
RETAINED PROTEIN DOMAINS
reading frame unclear



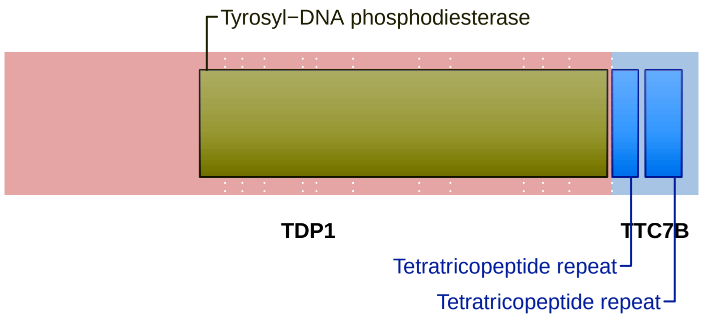
SUPPORTING READ COUNT

Split reads = 14
Discordant mates = 0



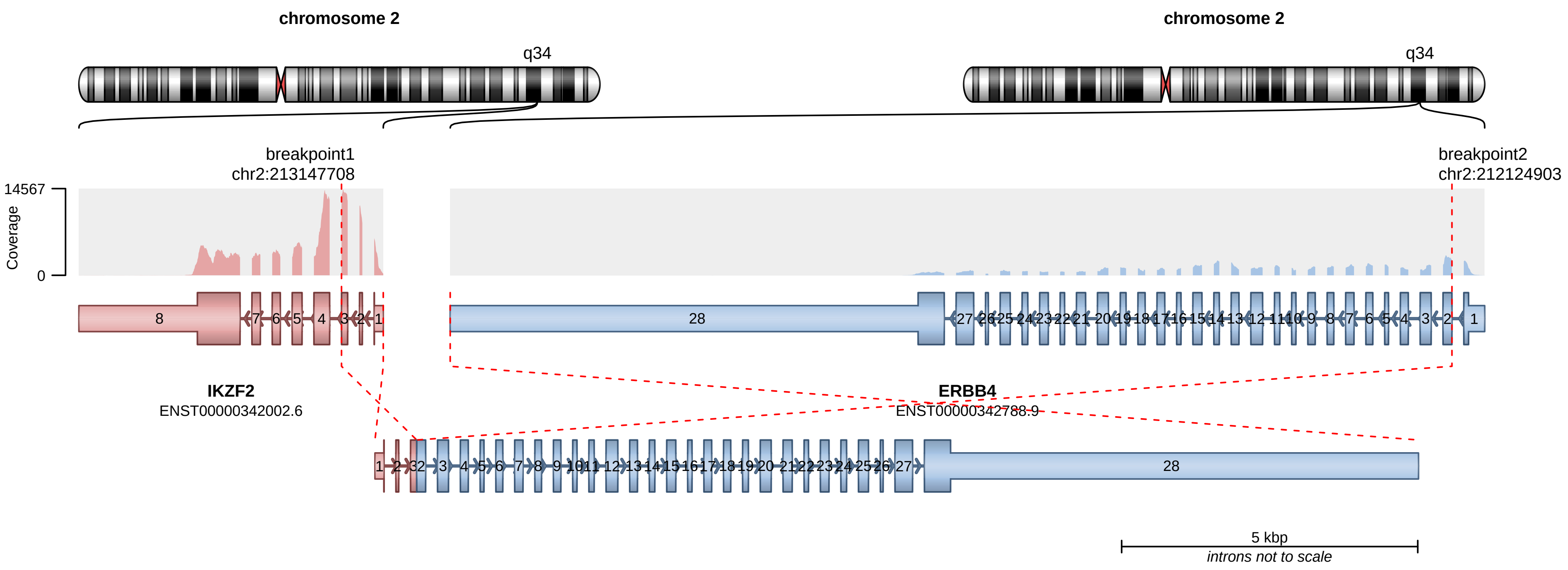


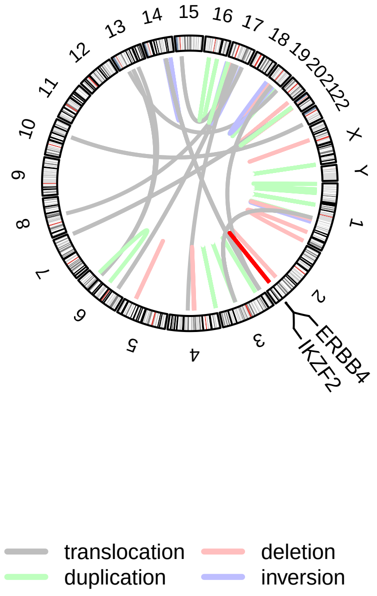
RETAINED PROTEIN DOMAINS
reading frame unclear

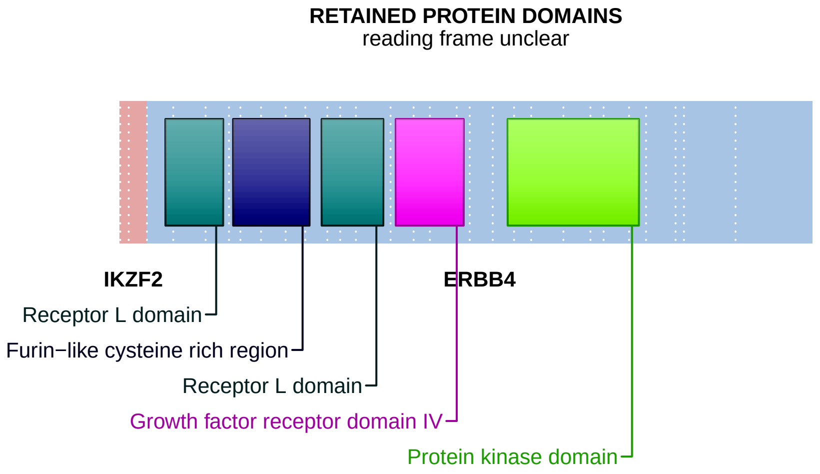


SUPPORTING READ COUNT

Split reads = 13
Discordant mates = 1

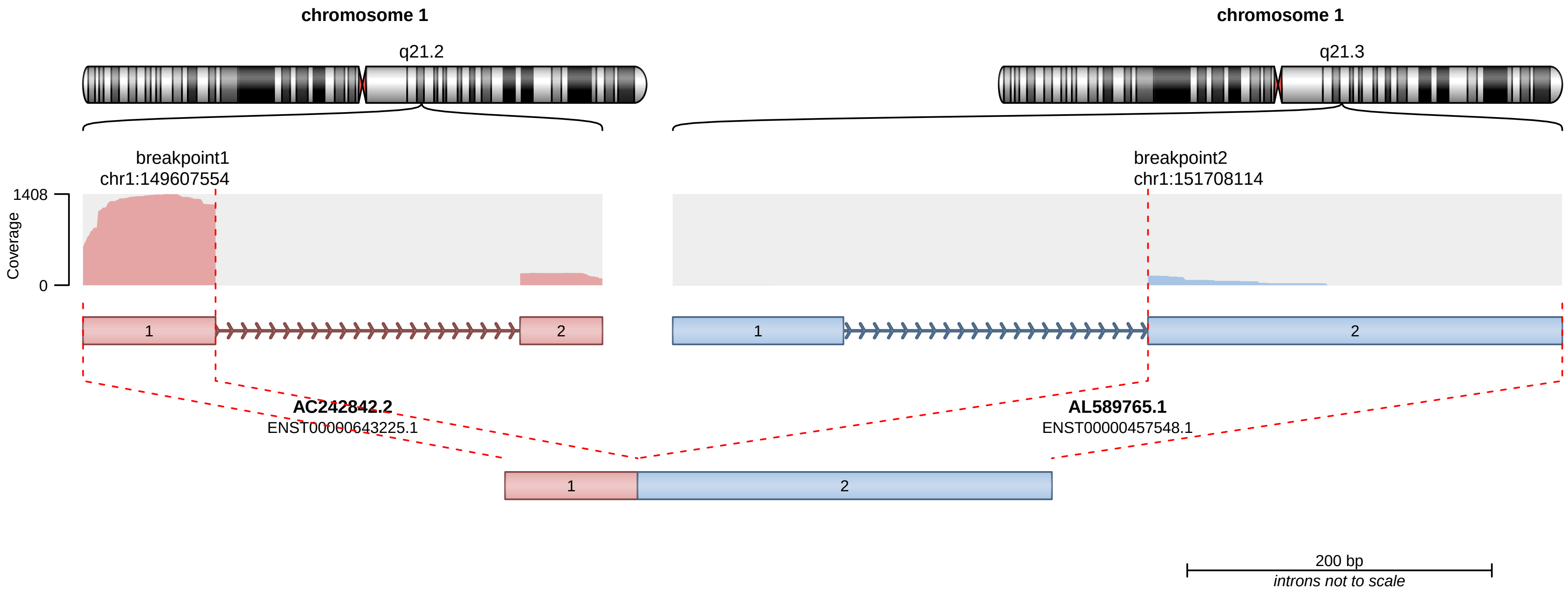


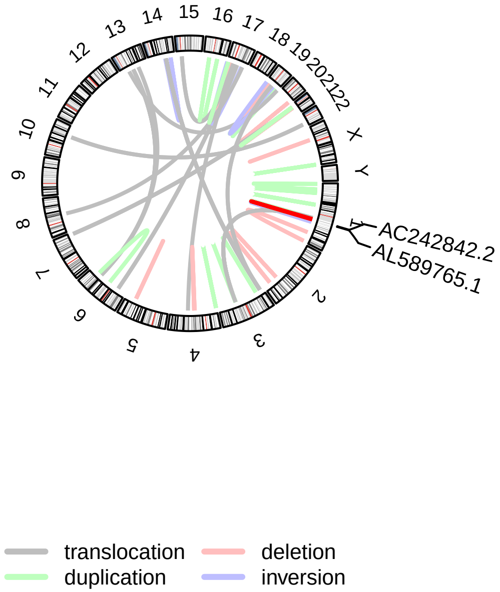




SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 1

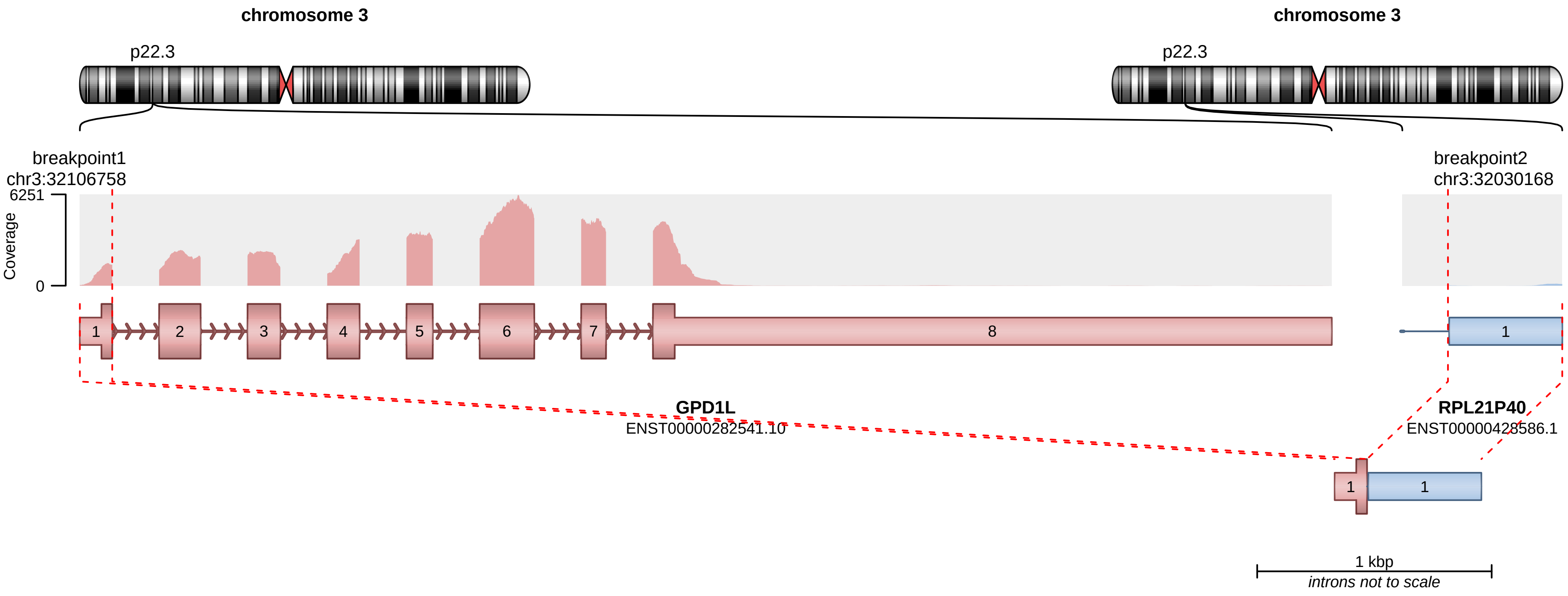


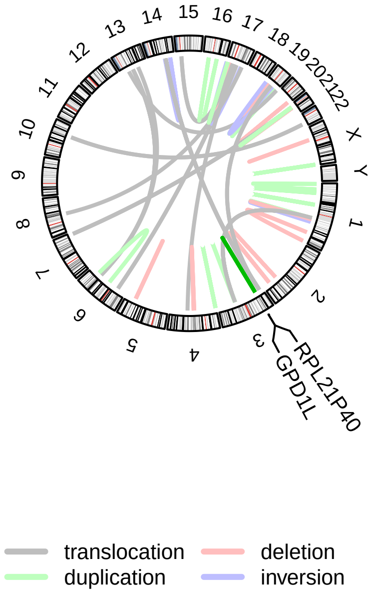


Genes are not protein−coding.

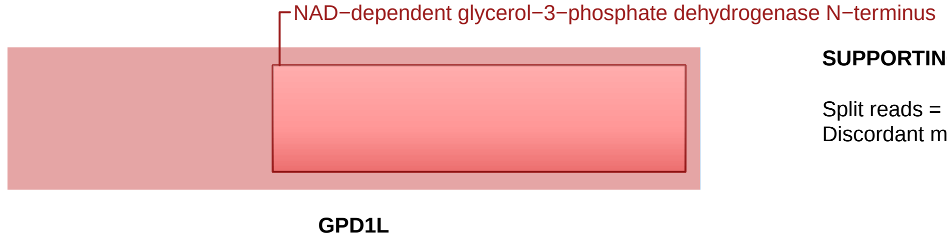
SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 0



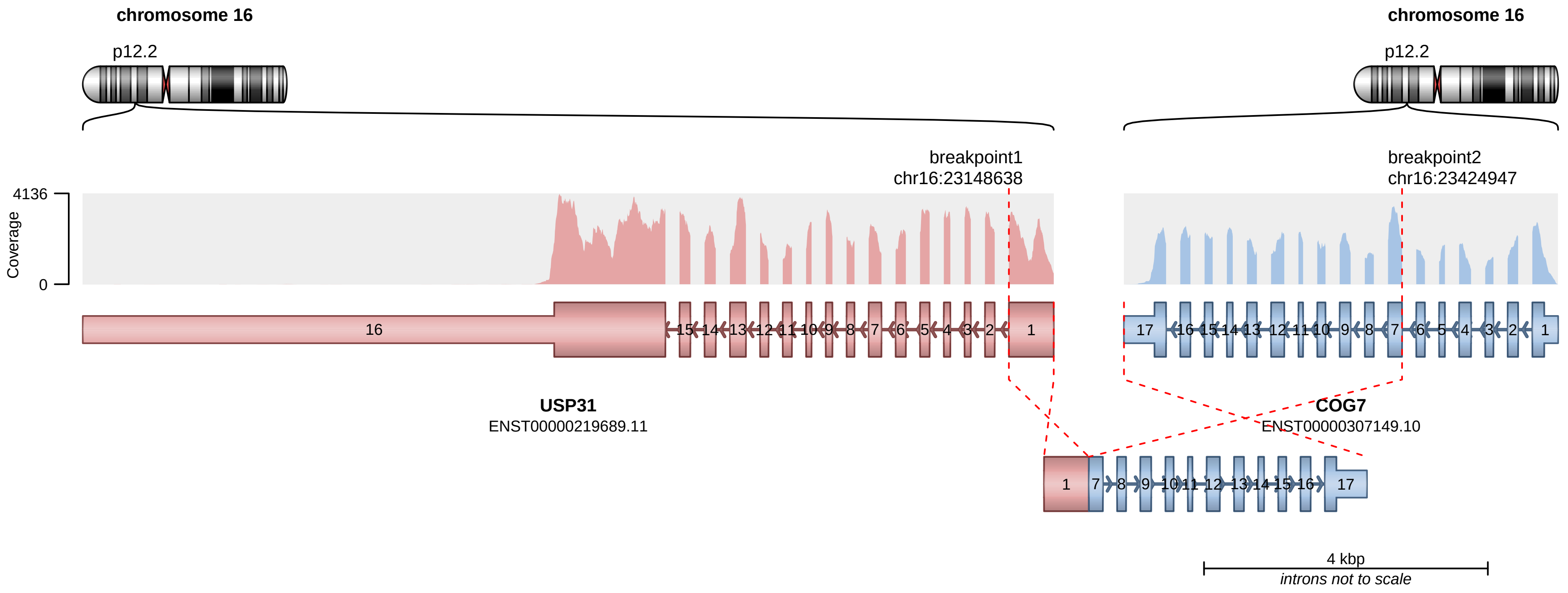


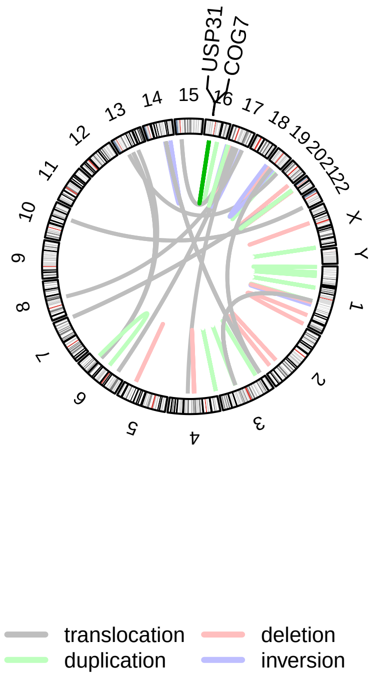
RETAINED PROTEIN DOMAINS
reading frame unclear

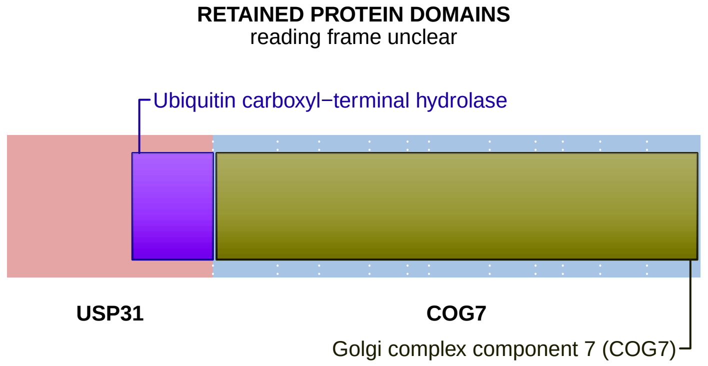


SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 0

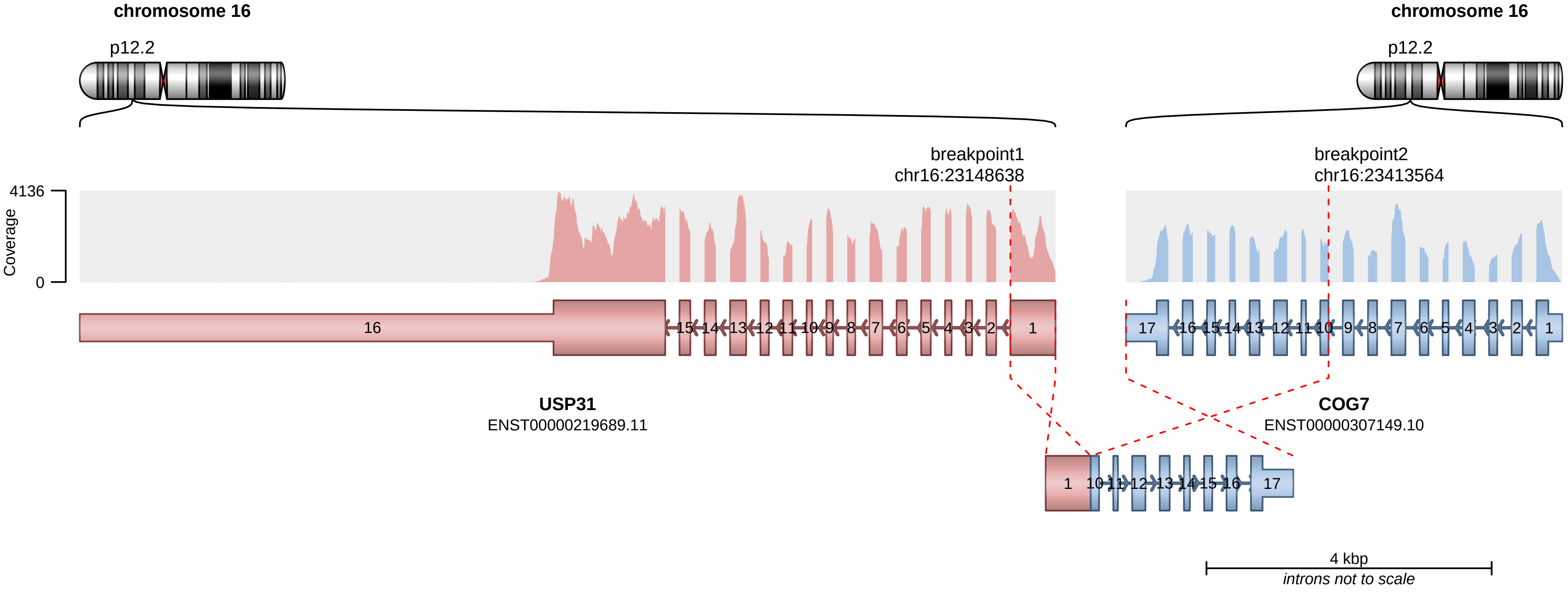


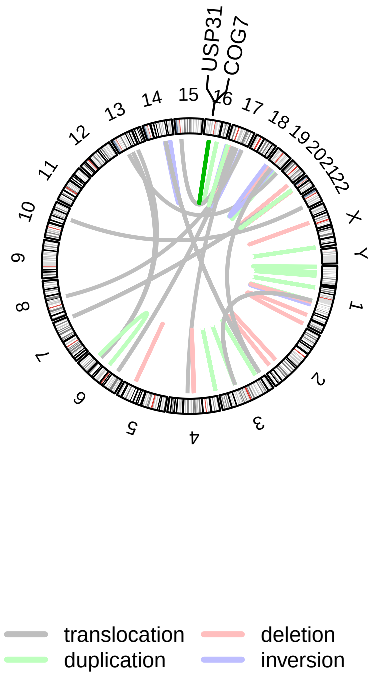


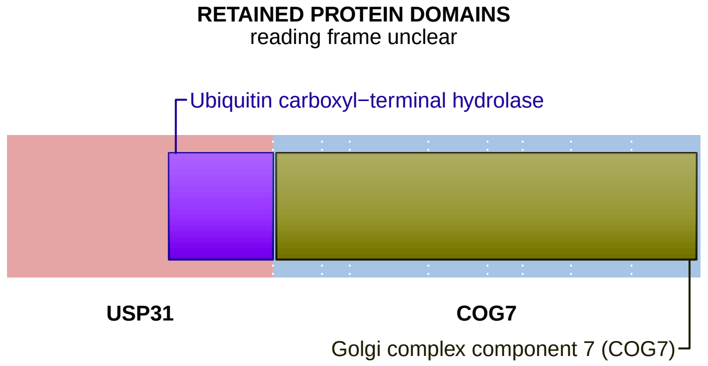


SUPPORTING READ COUNT

Split reads = 11
Discordant mates = 2

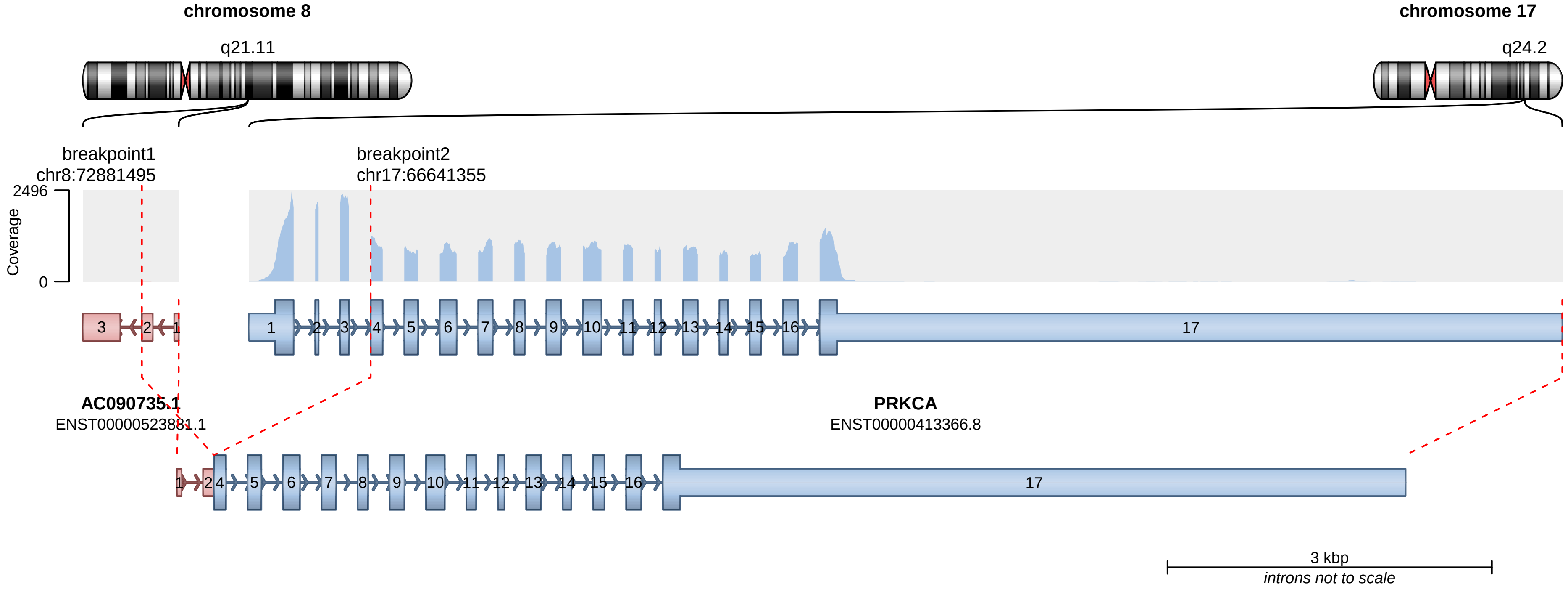


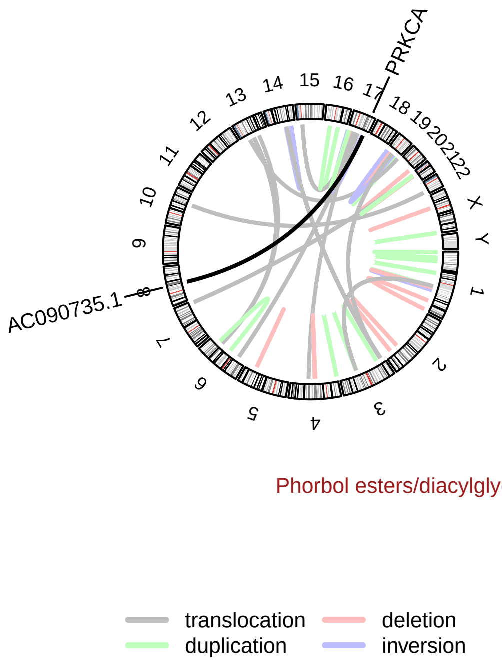


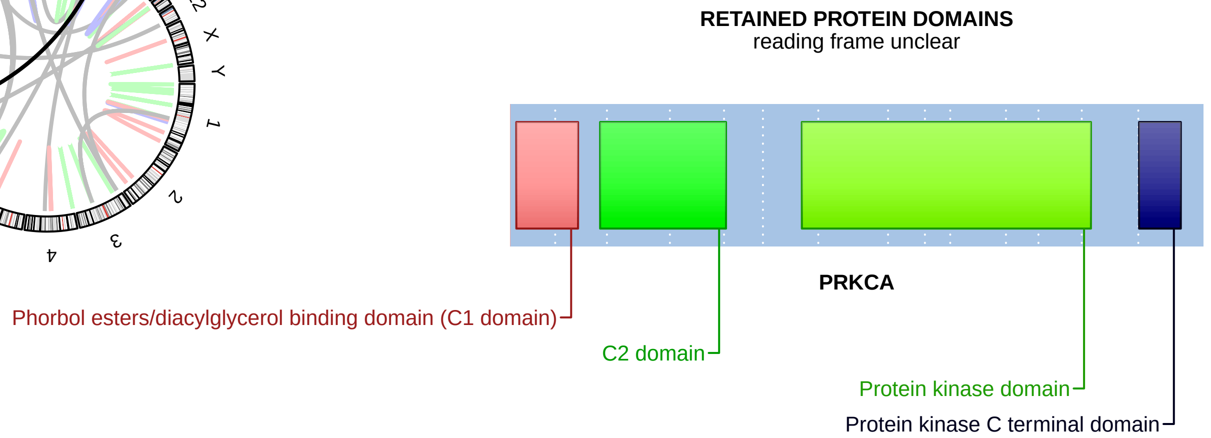


SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

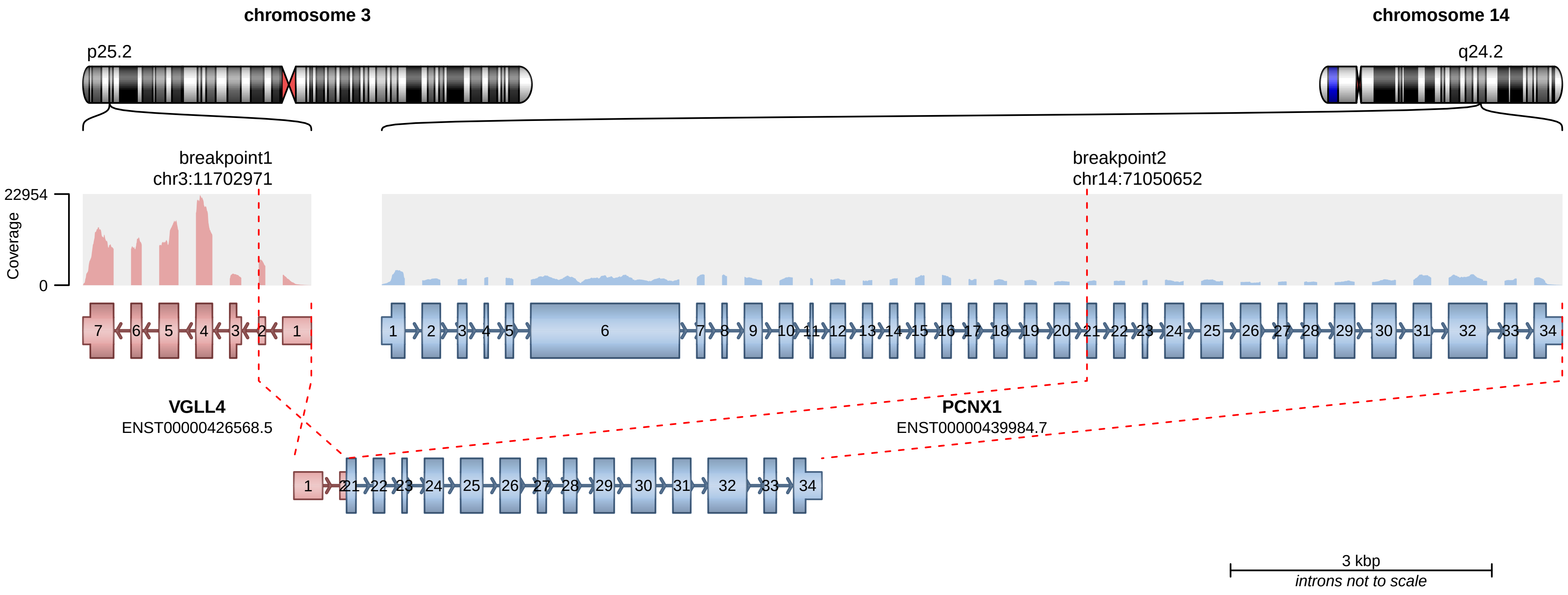


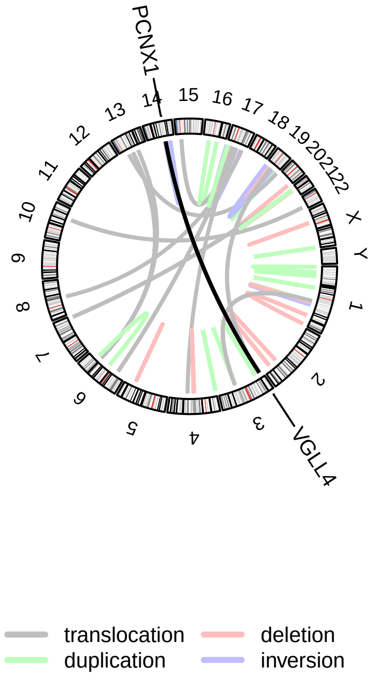




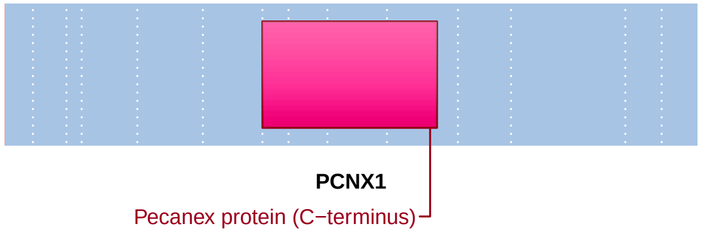
SUPPORTING READ COUNT

Split reads = 11
Discordant mates = 0



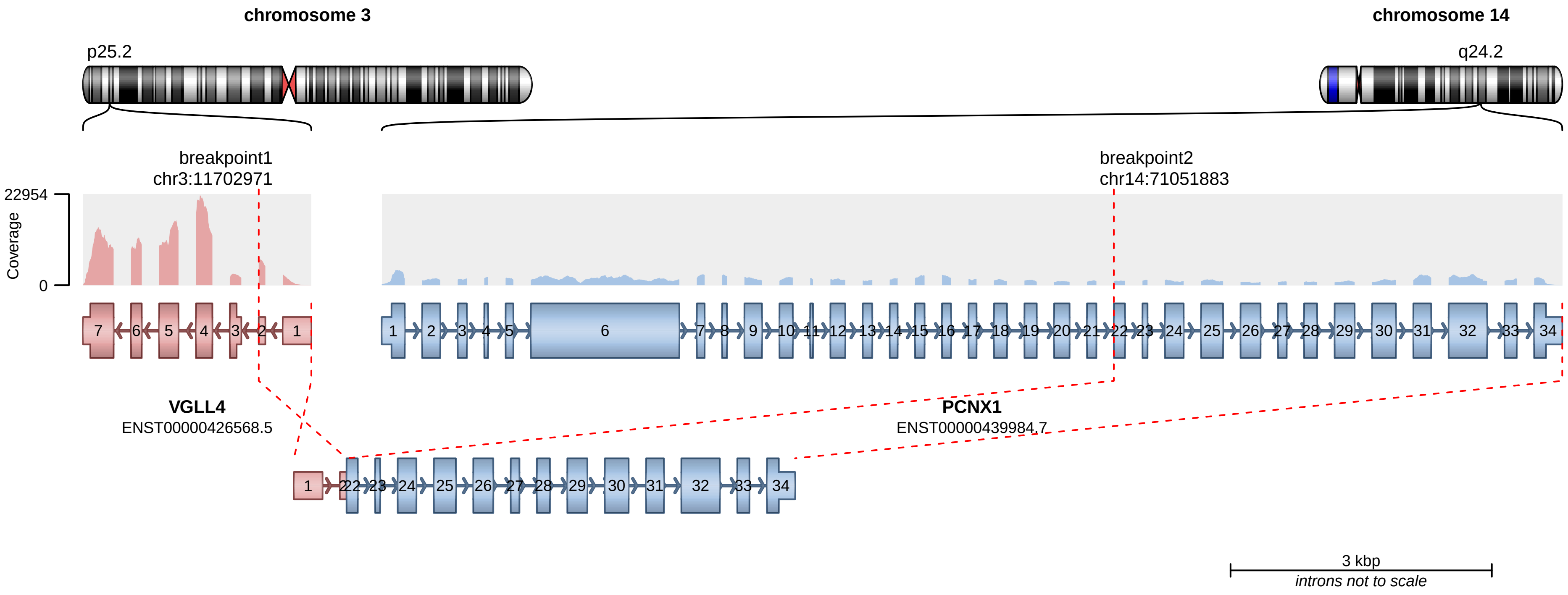


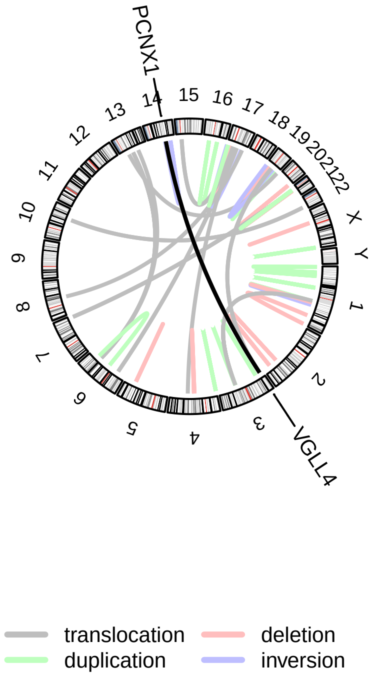
RETAINED PROTEIN DOMAINS
reading frame unclear



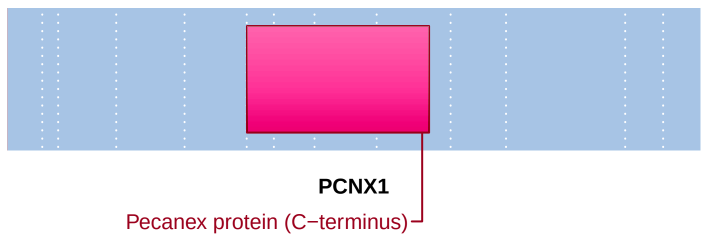
SUPPORTING READ COUNT

Split reads = 11
Discordant mates = 0



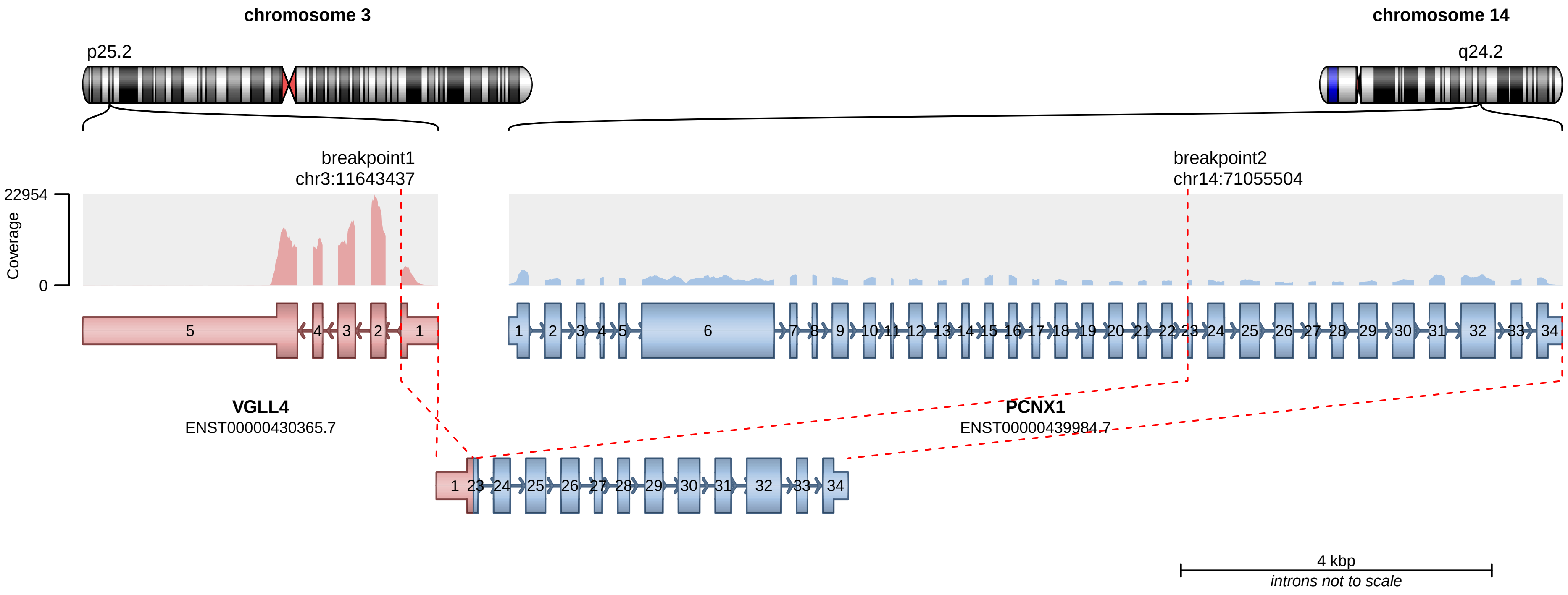


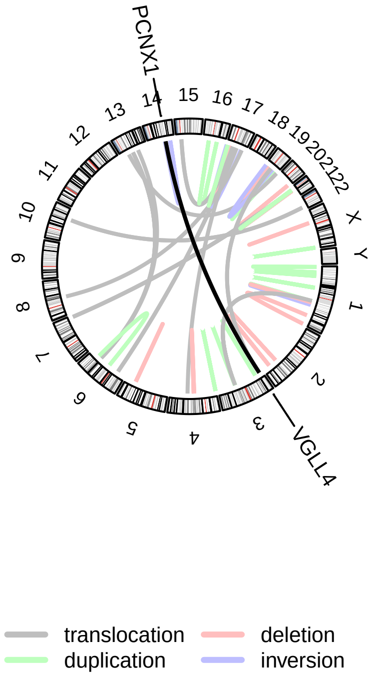
RETAINED PROTEIN DOMAINS
reading frame unclear



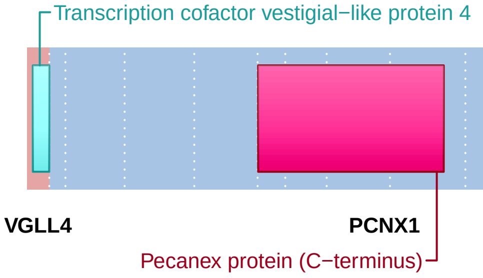
SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 0



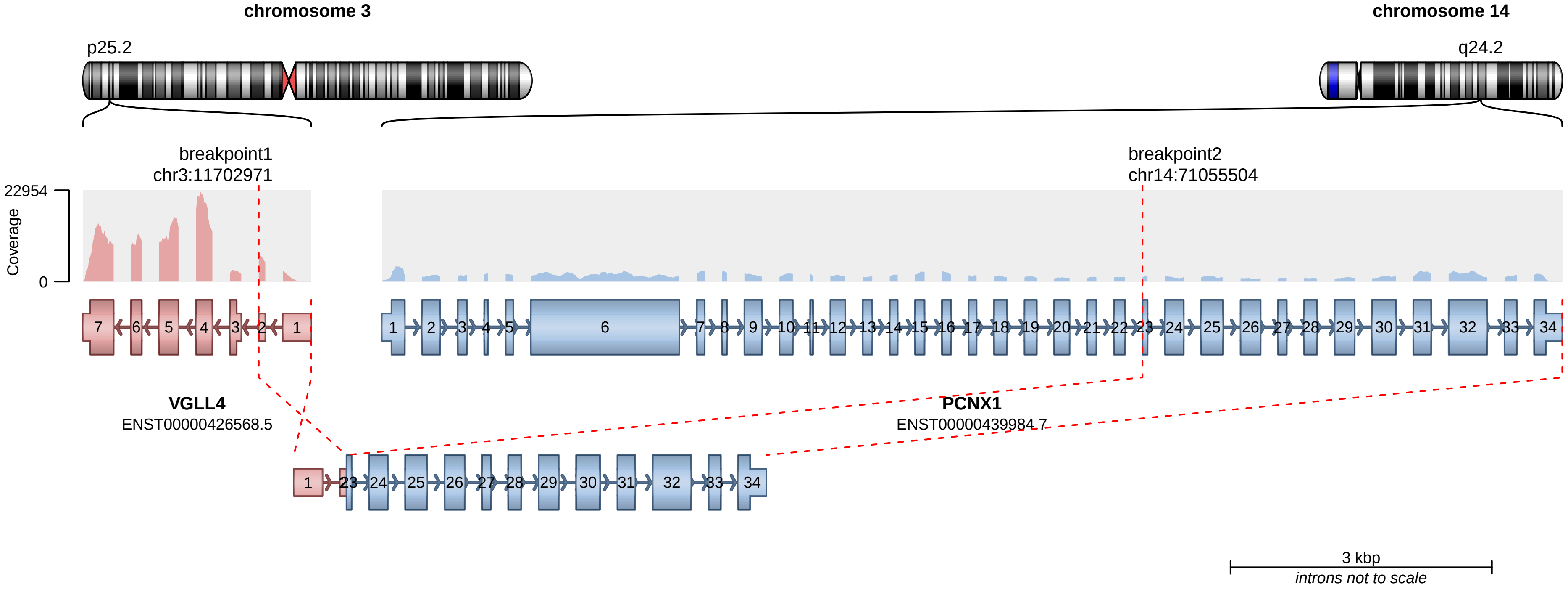


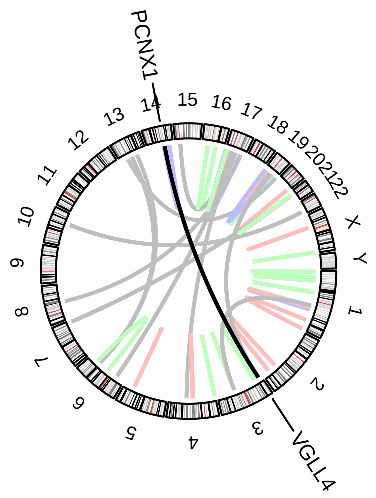
RETAINED PROTEIN DOMAINS
reading frame unclear

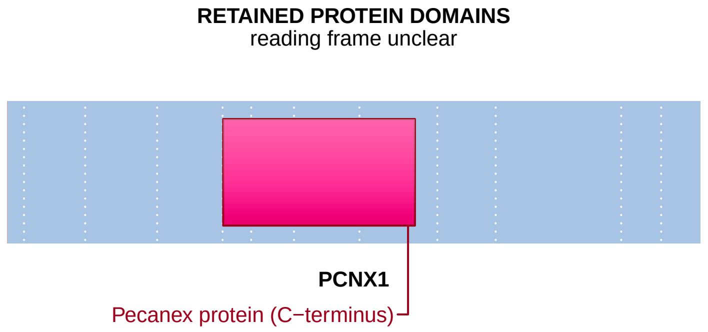


SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

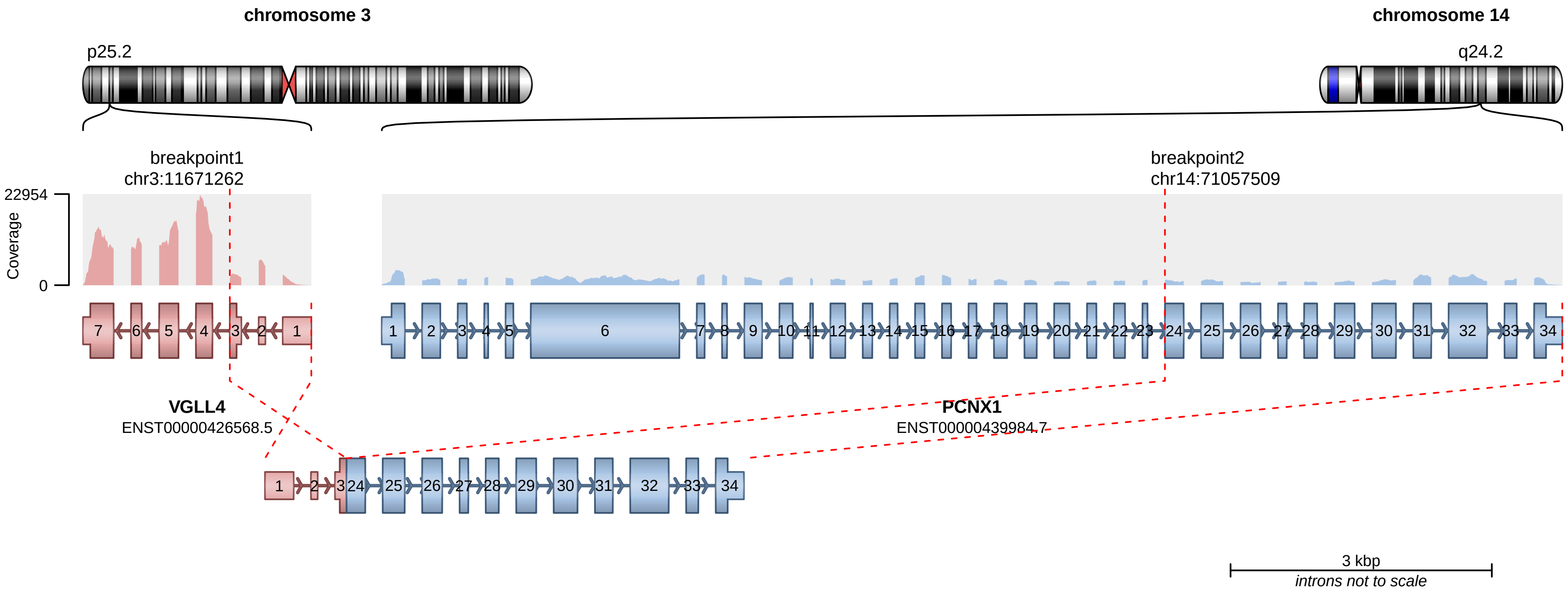


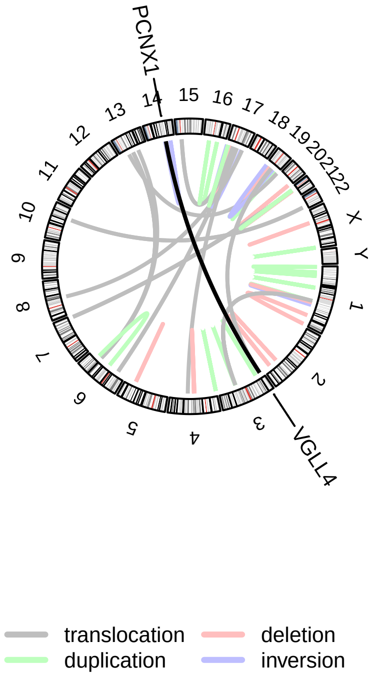




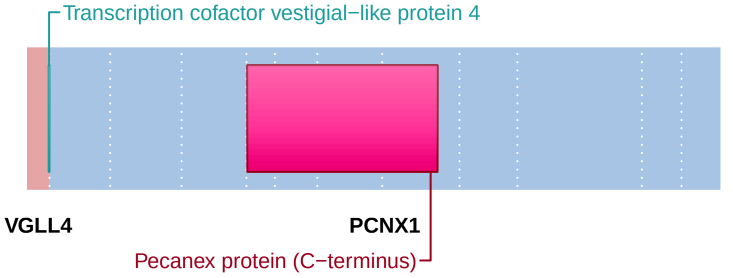
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0



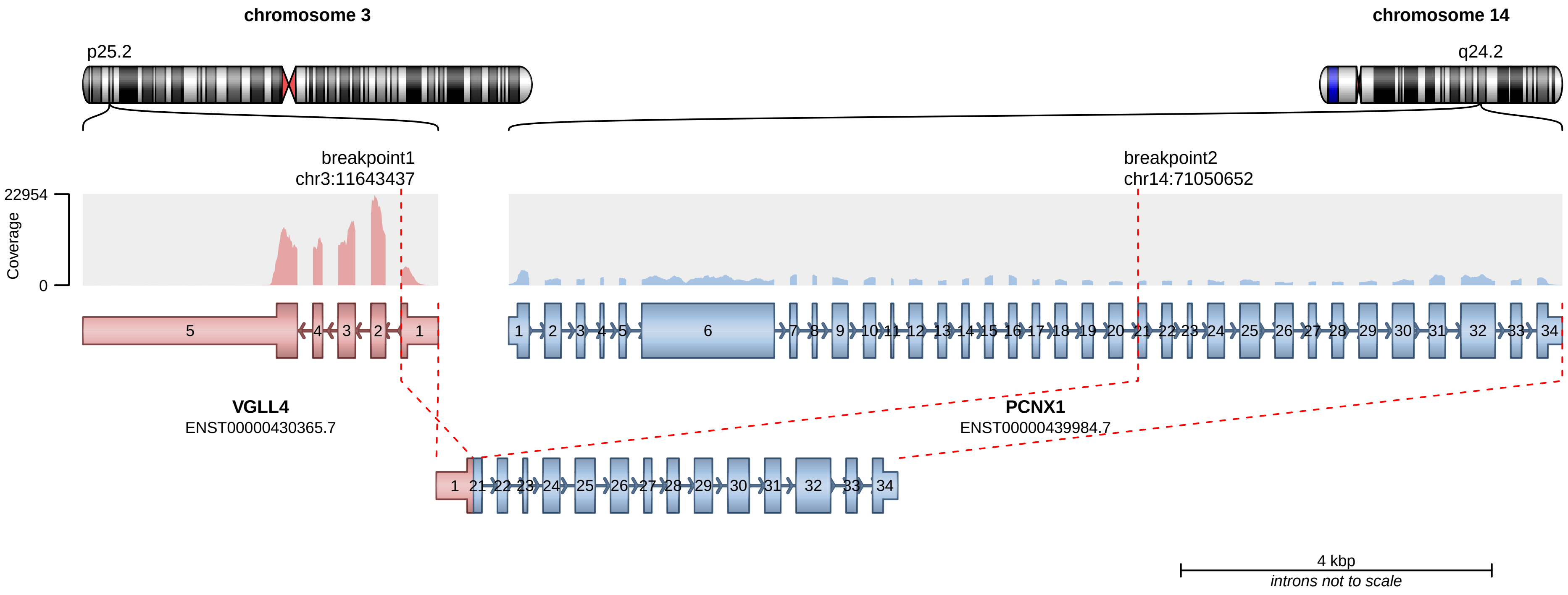


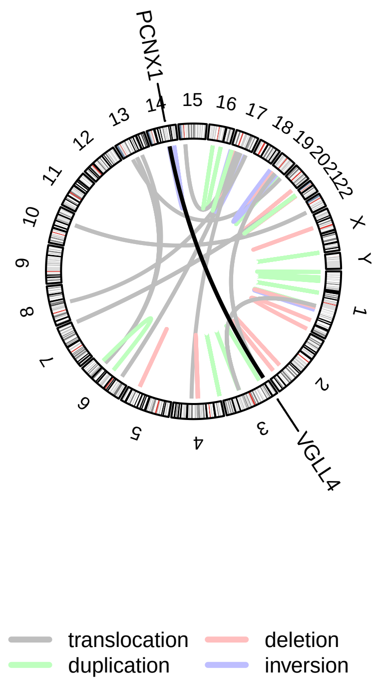
RETAINED PROTEIN DOMAINS
reading frame unclear

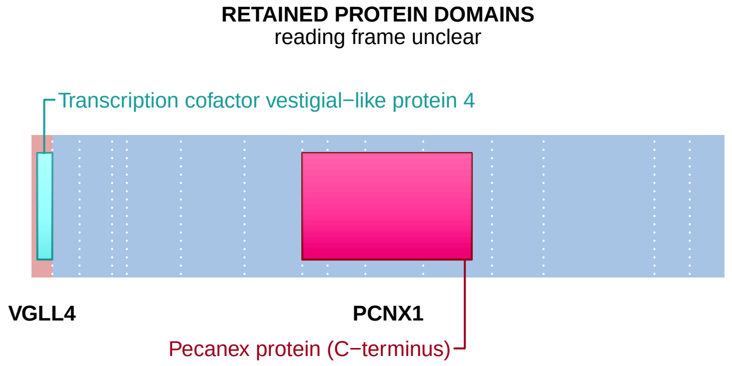


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

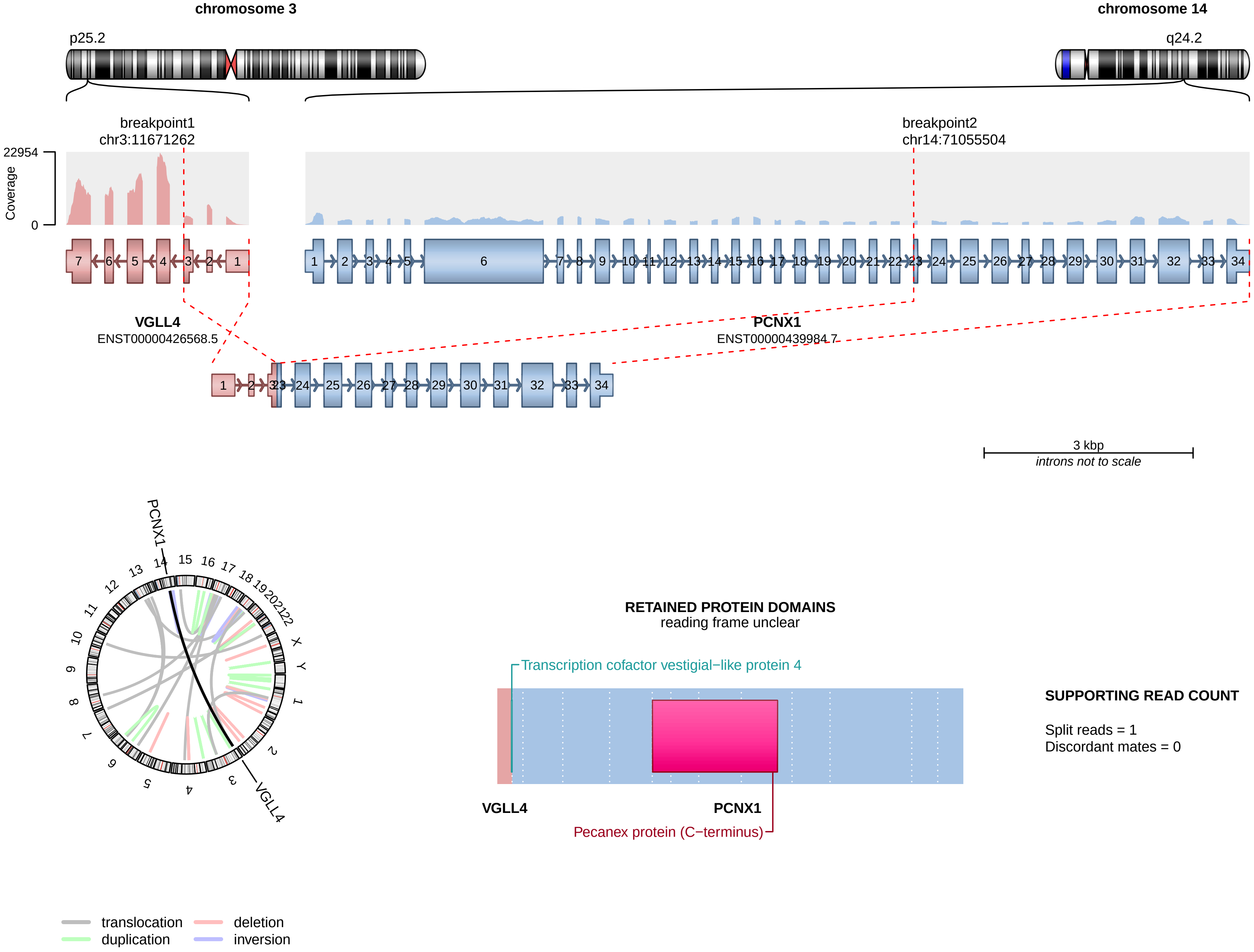


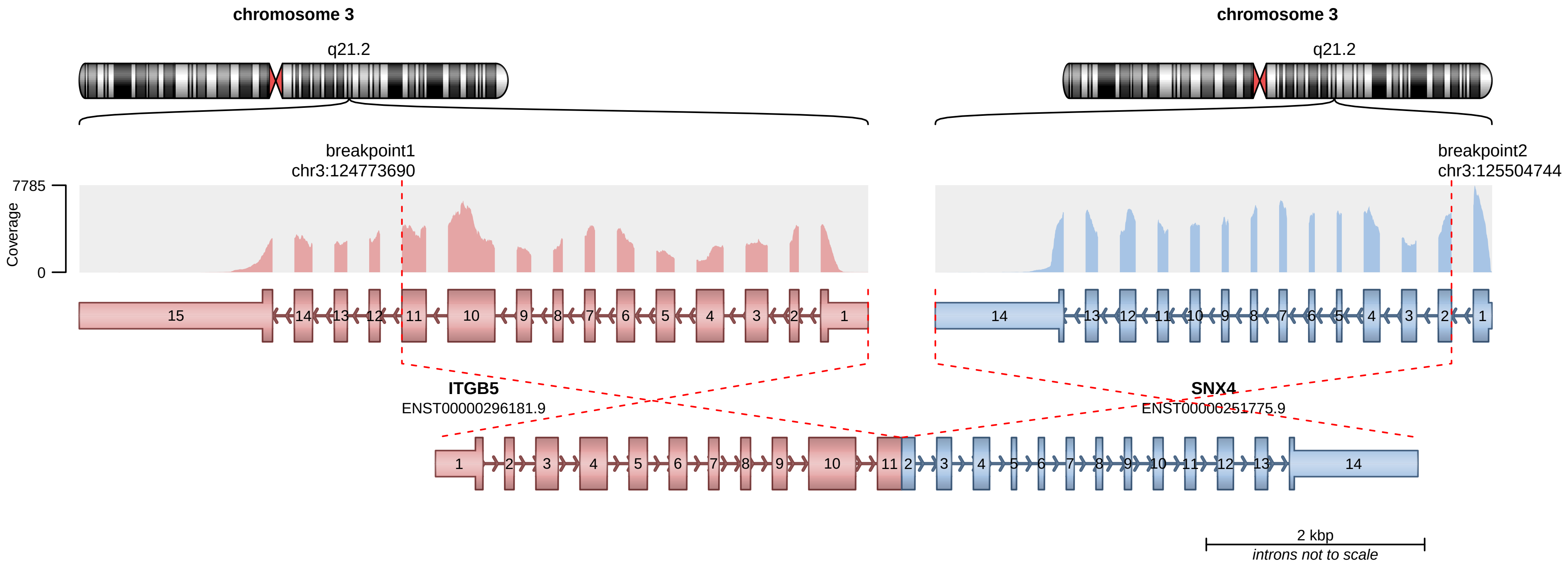


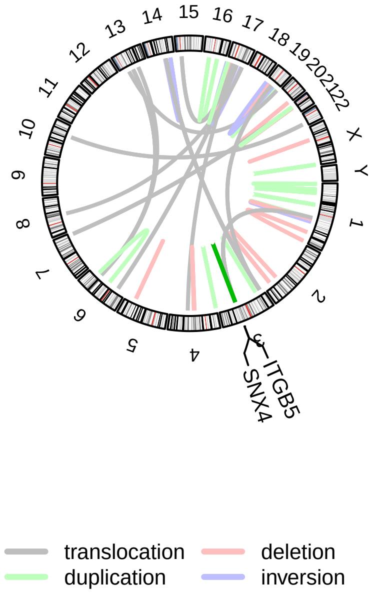


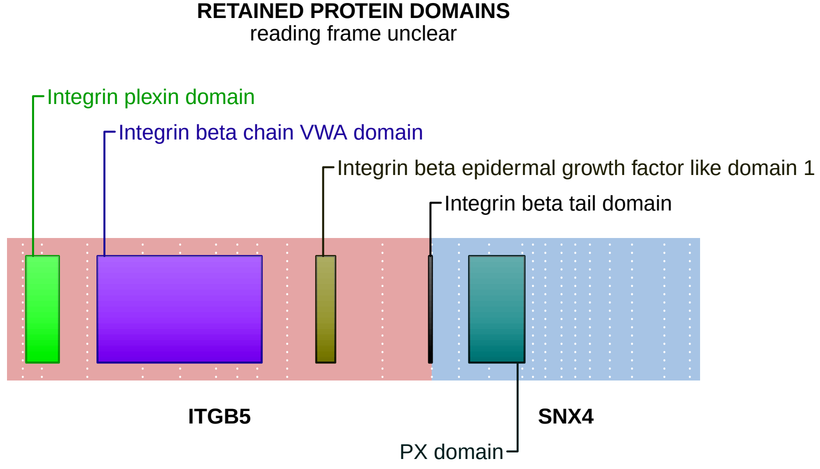
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0


chromosome 3
chromosome 14
p25.2
q24.2
breakpoint1
chr3:11671262
breakpoint2
chr14:71055504
22954
Coverage
0
VGLL4
ENST00000426568.5
PCNX1
ENST00000439984.7
3 kbp
introns not to scale
PCNX1
VGLL4
translocation
duplication
deletion
inversion
RETAINED PROTEIN DOMAINS
reading frame unclear
Transcription cofactor vestigial−like protein 4
VGLL4
PCNX1
Pecanex protein (C−terminus)
SUPPORTING READ COUNT
Split reads = 1
Discordant mates = 0

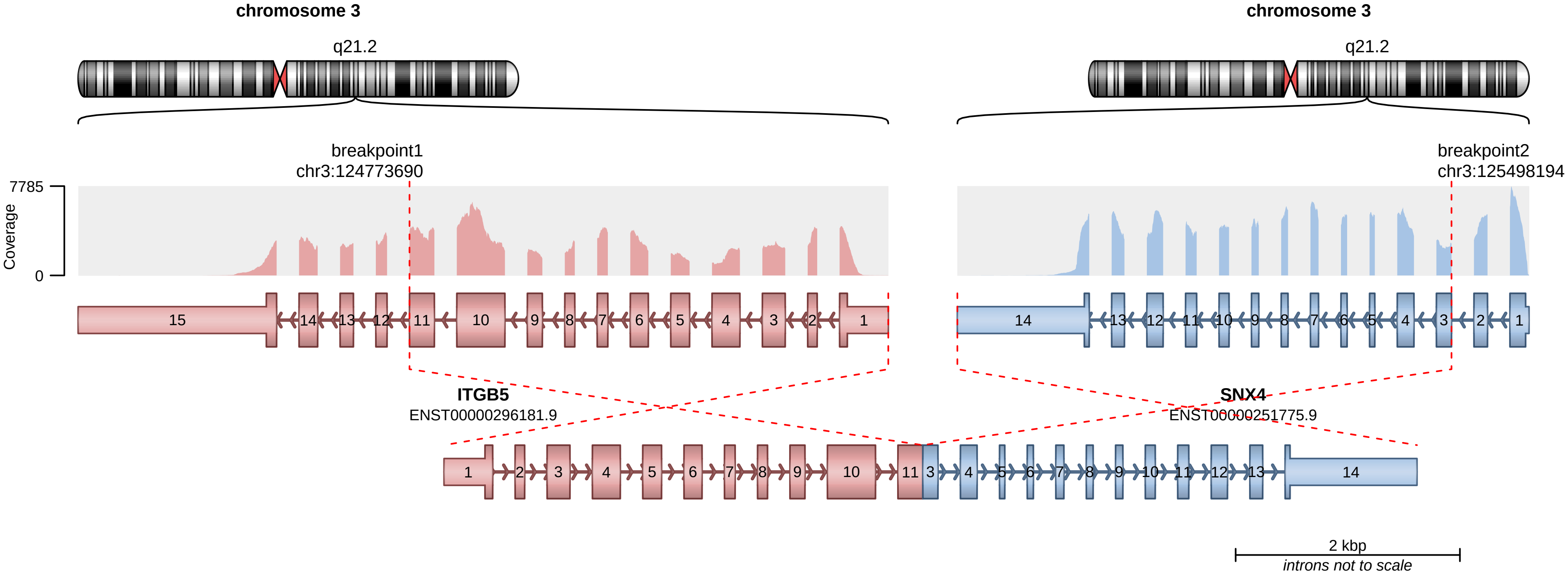


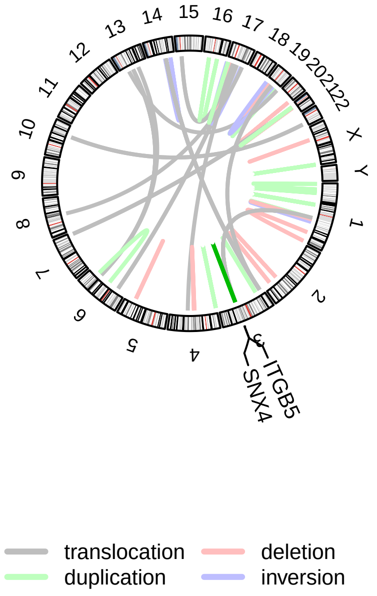




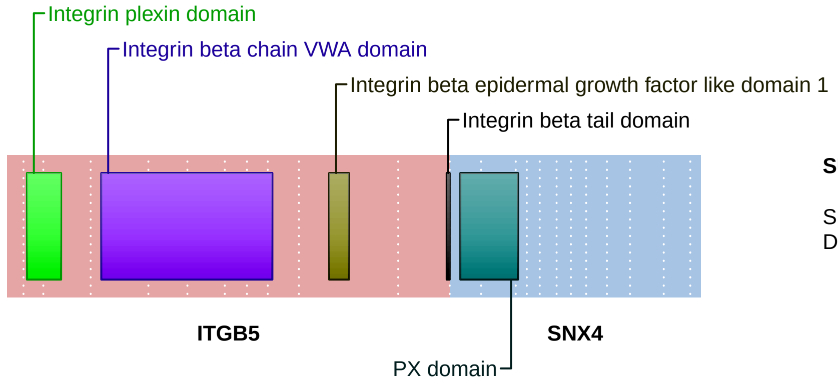
SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 0



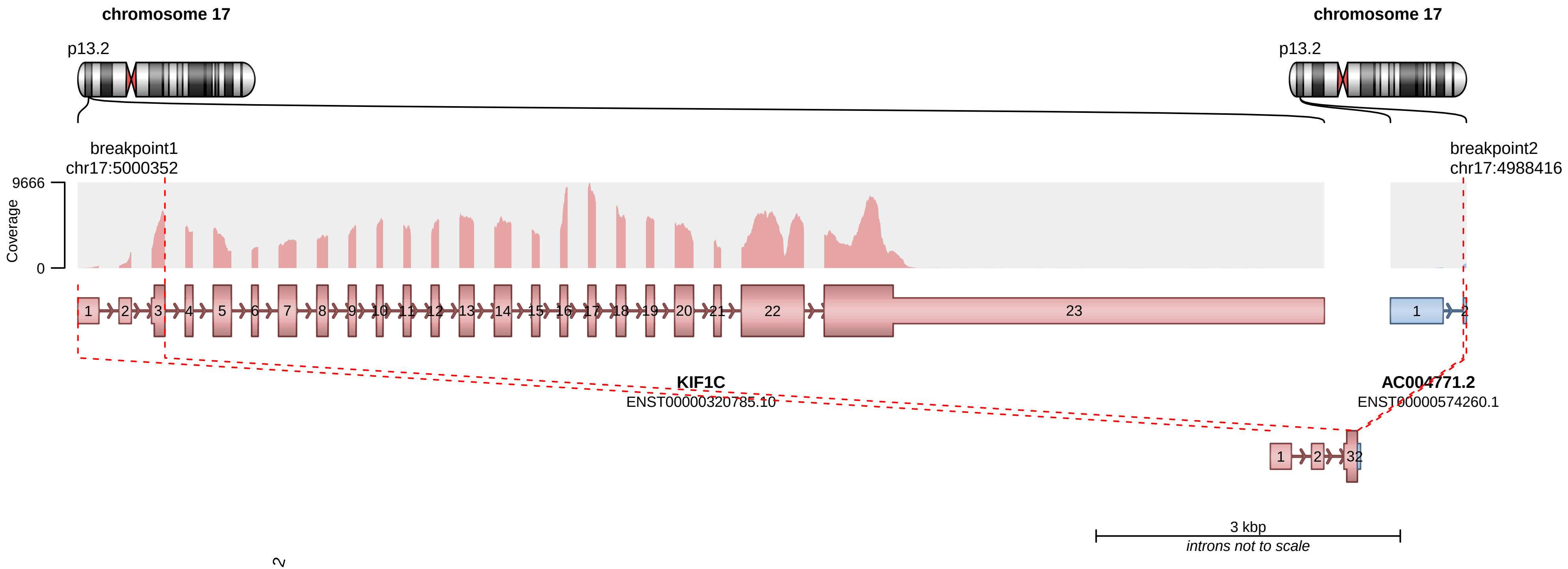


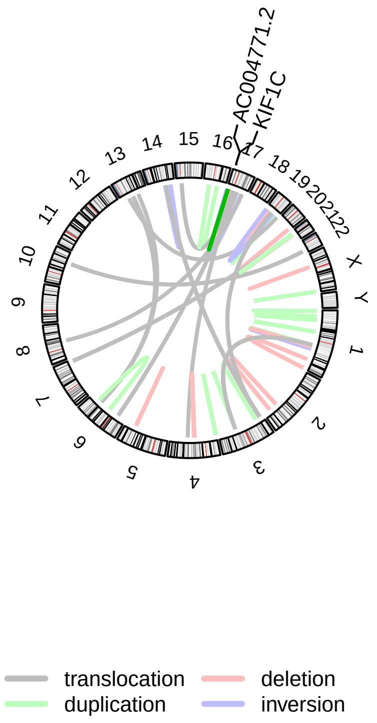
RETAINED PROTEIN DOMAINS
reading frame unclear



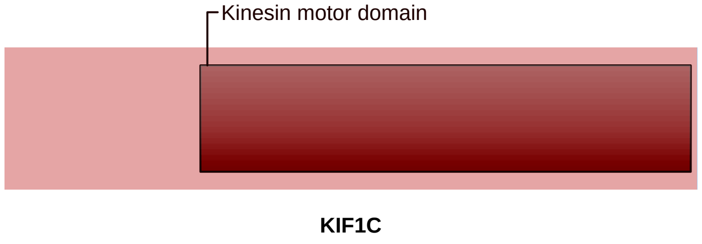
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0



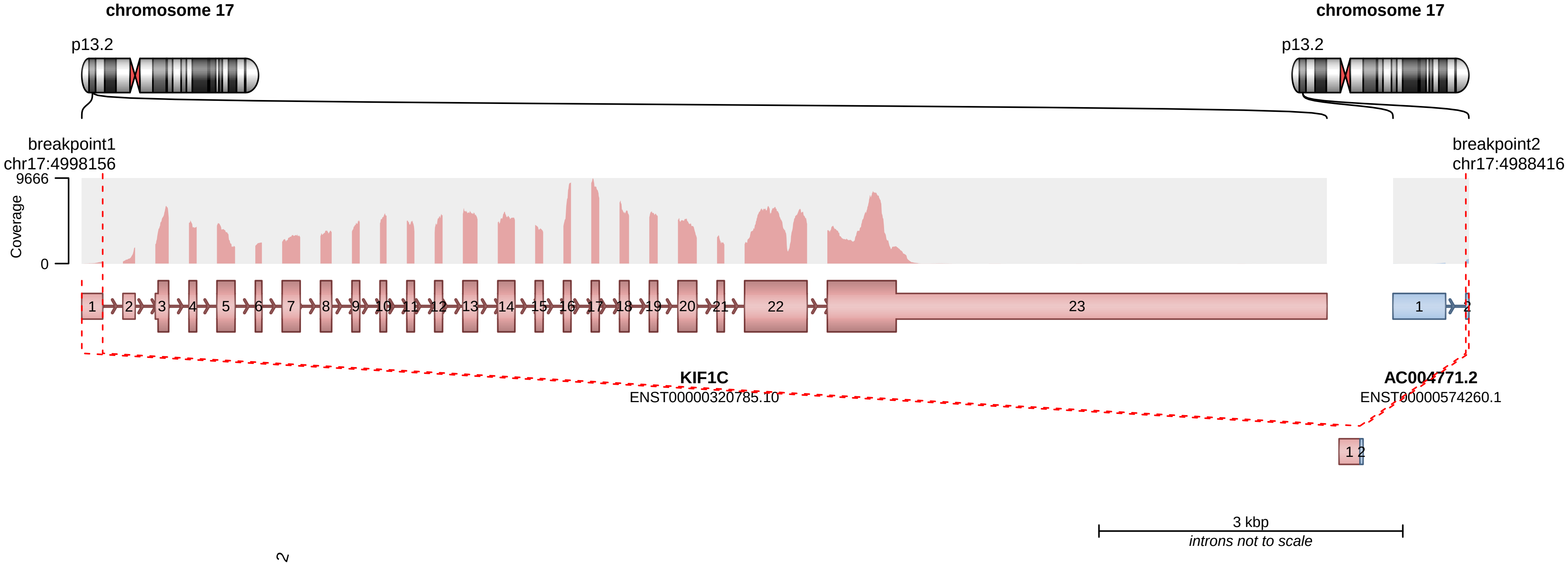


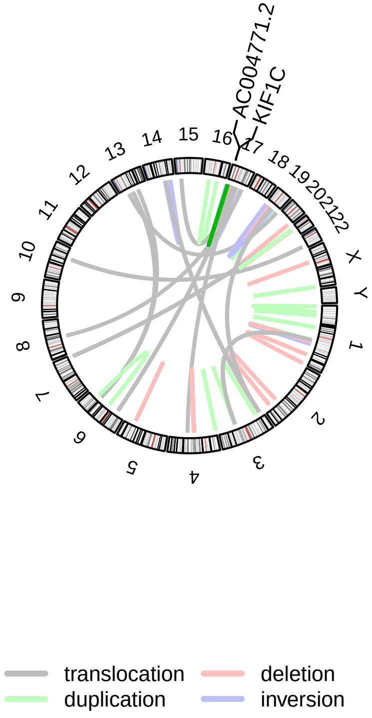
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 0

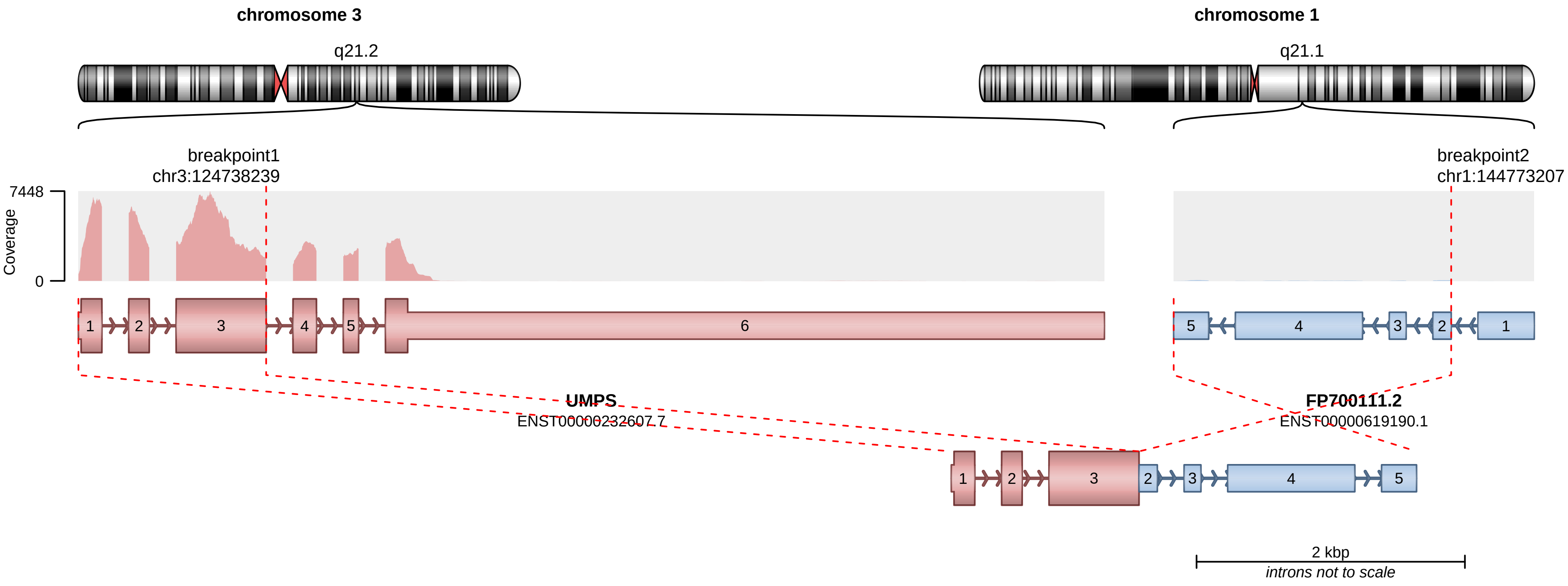


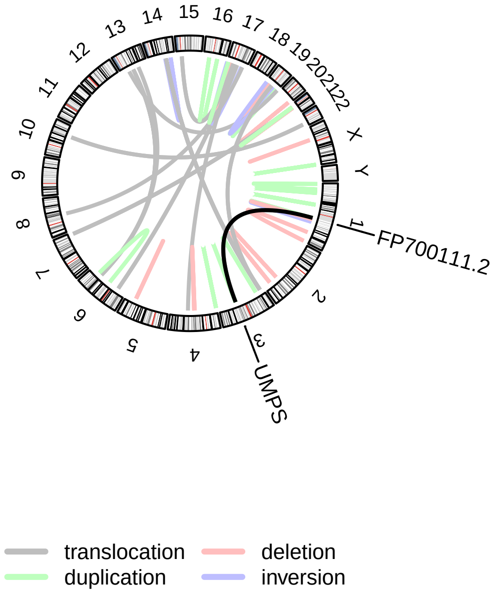


No coding regions retained in fusion transcript.

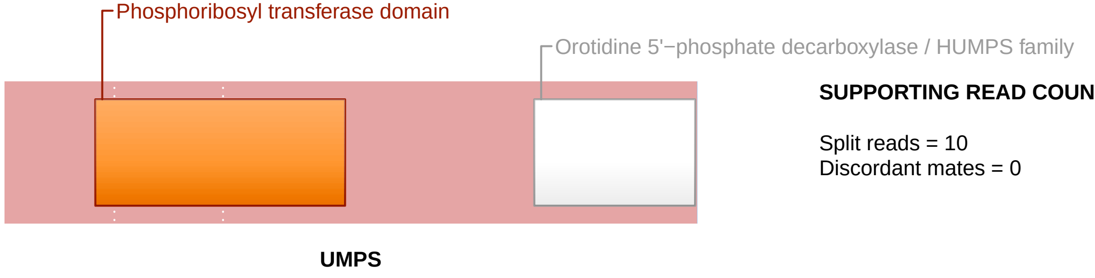
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0



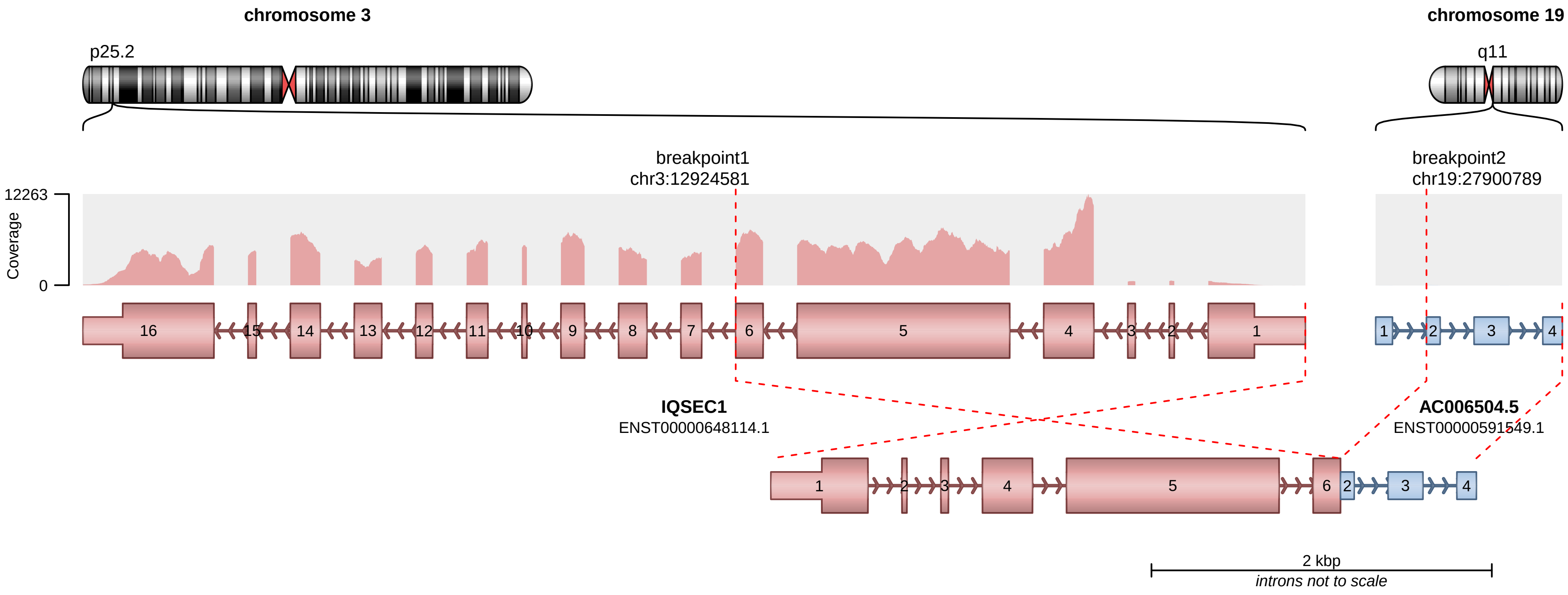


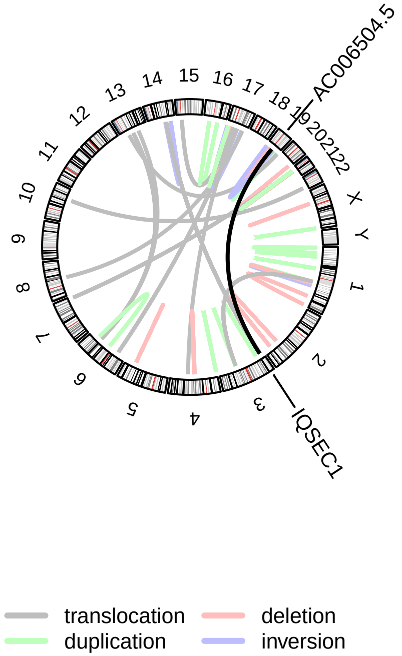
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 0



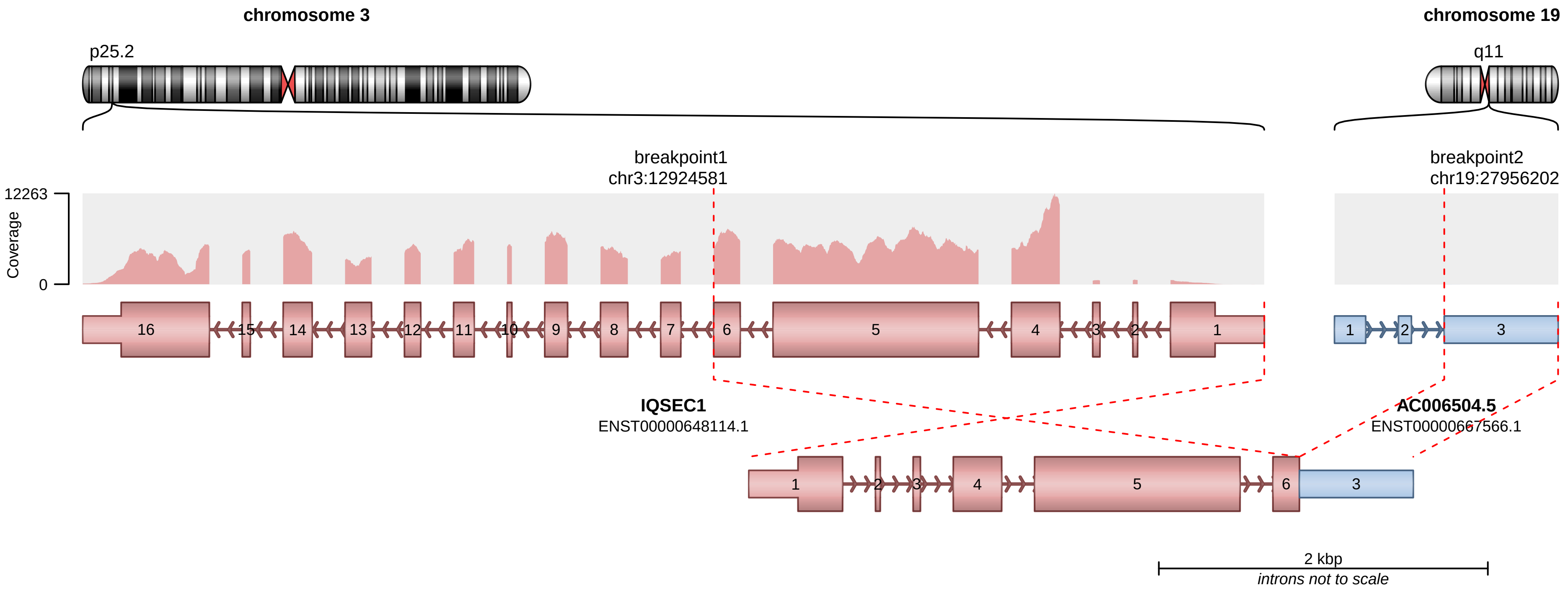


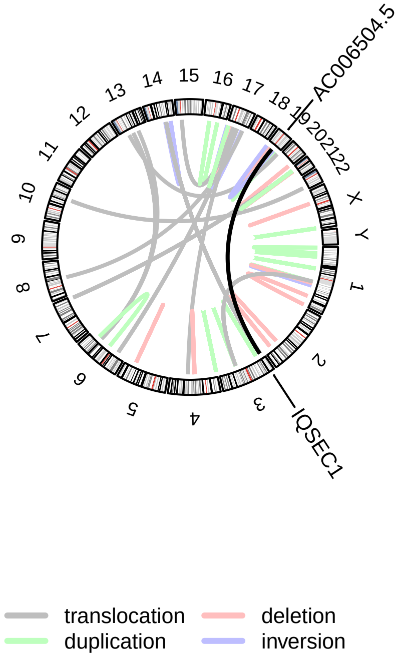
RETAINED PROTEIN DOMAINS
reading frame unclear

IQSEC1

SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 1





RETAINED PROTEIN DOMAINS
reading frame unclear

IQSEC1

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0