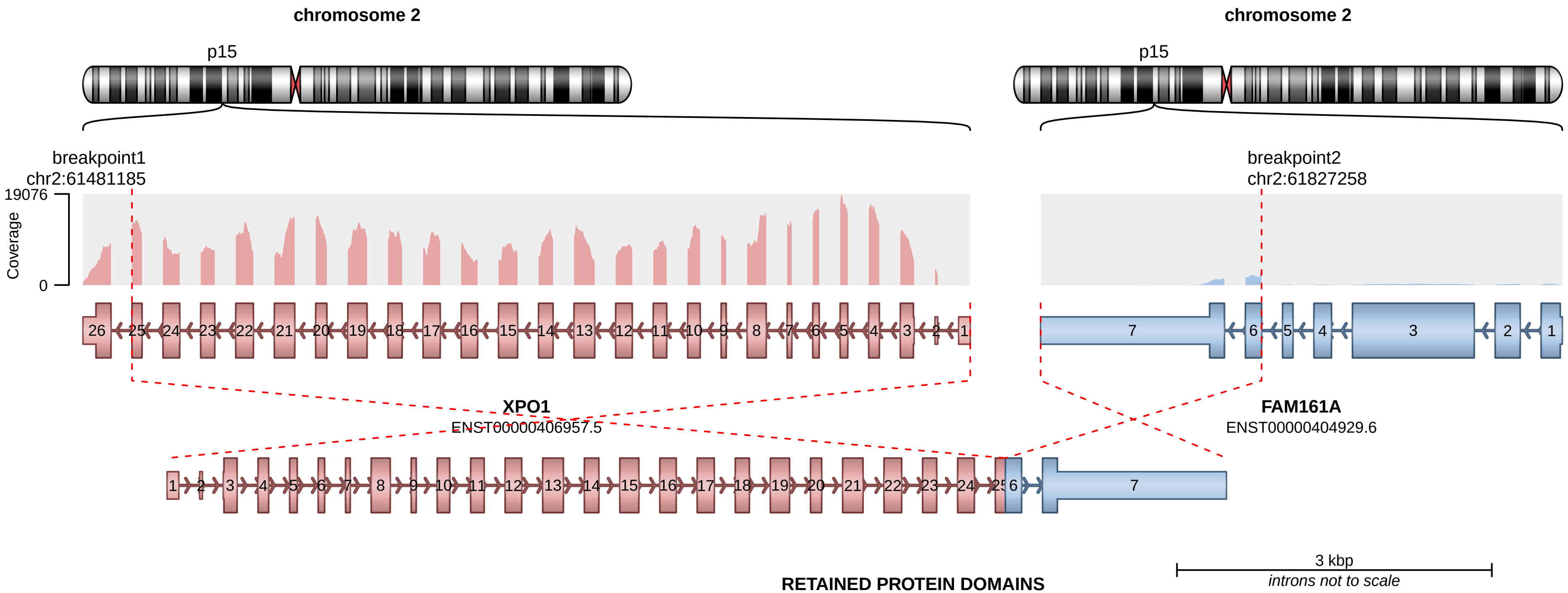
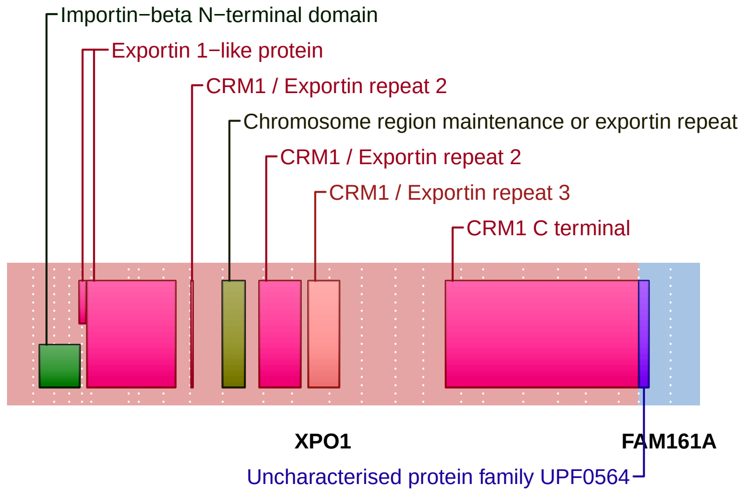
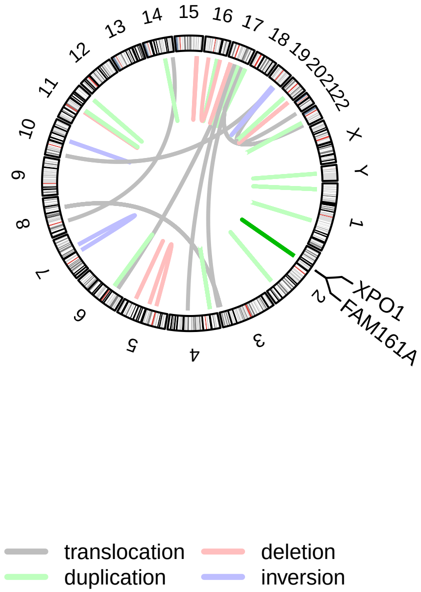


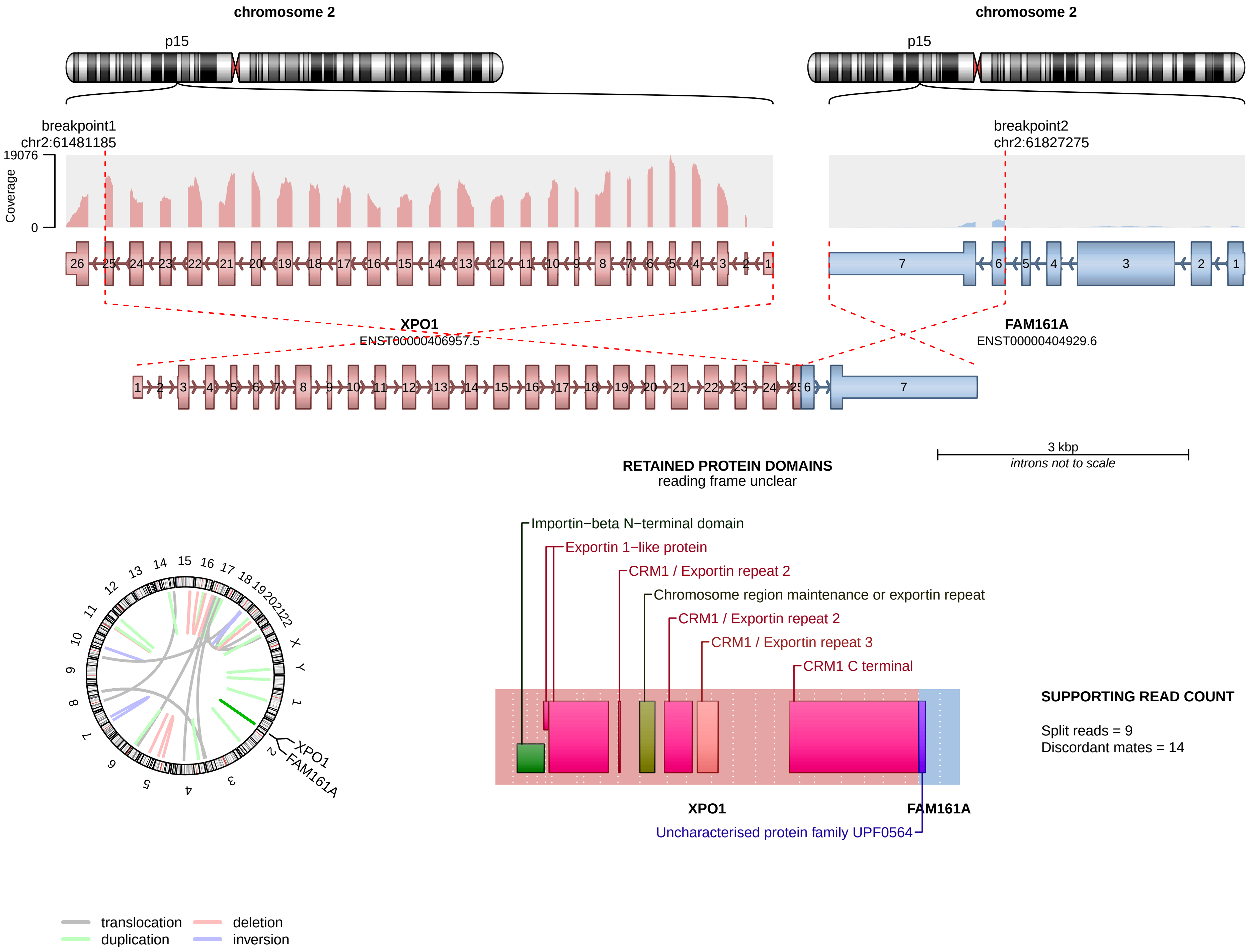
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

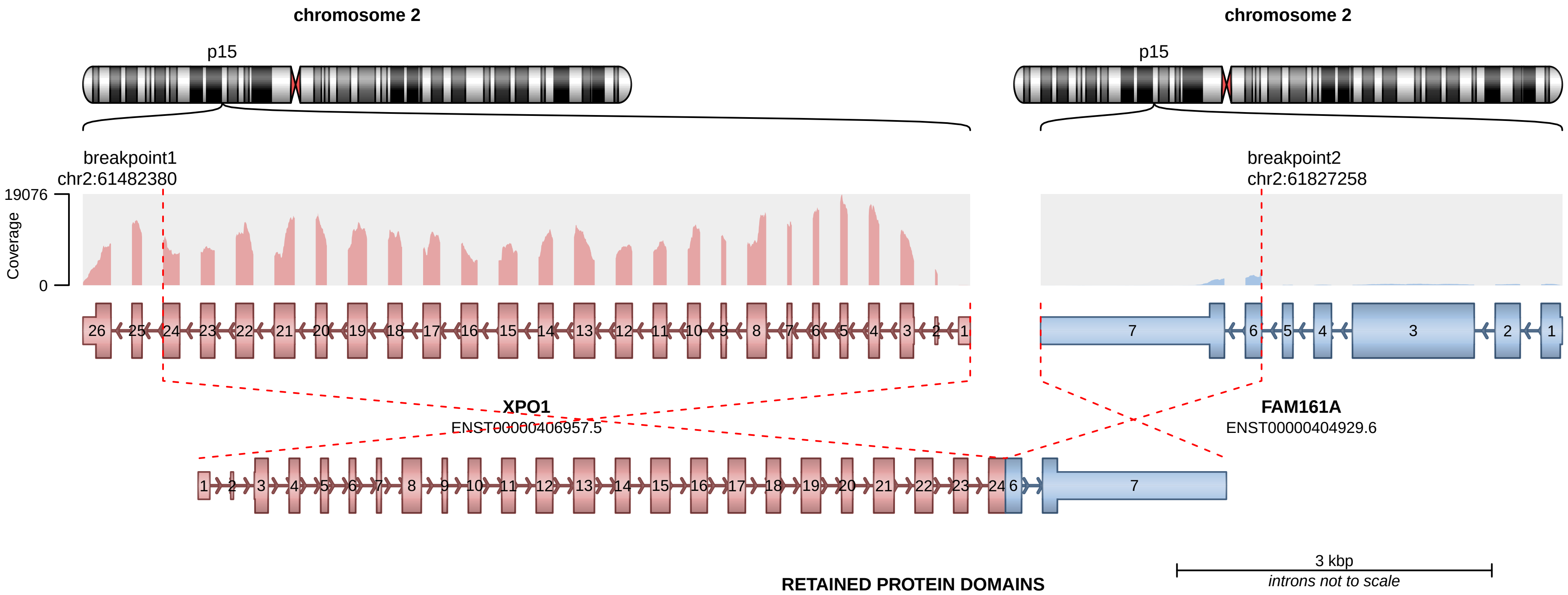
Split reads = 1407
Discordant mates = 11



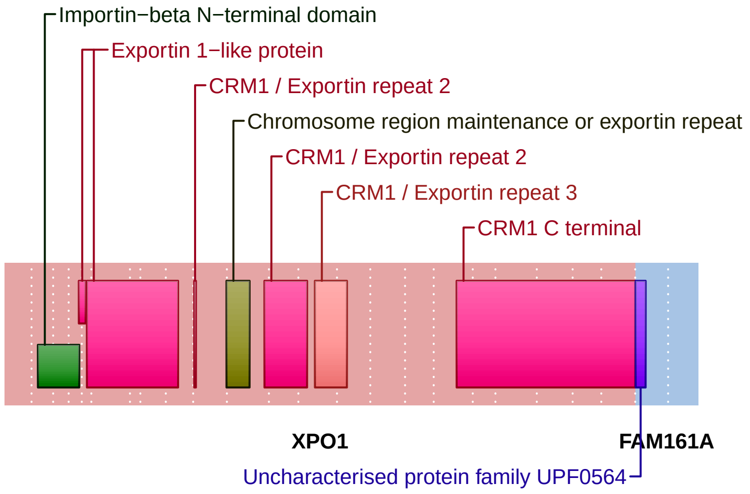


SUPPORTING READ COUNT

Split reads = 9
Discordant mates = 14

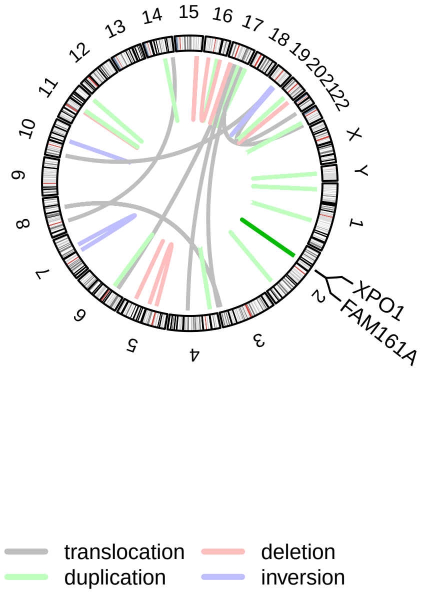


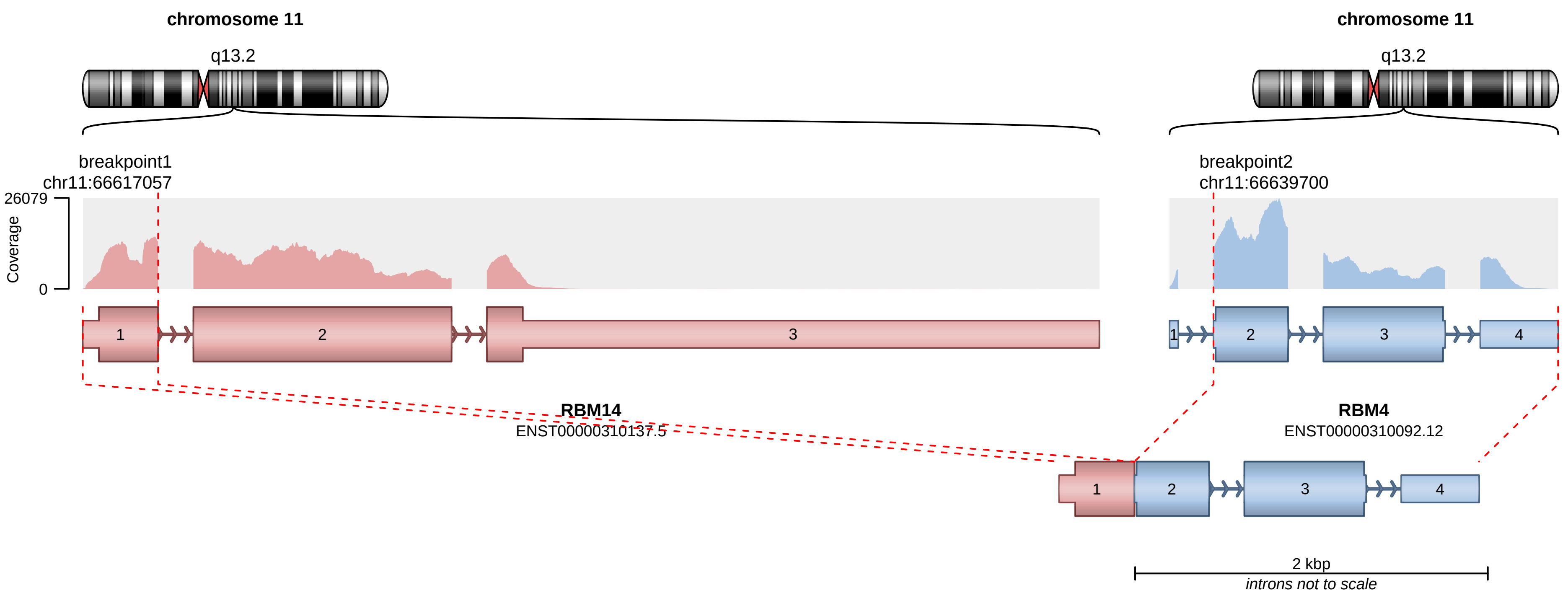
RETAINED PROTEIN DOMAINS
reading frame unclear

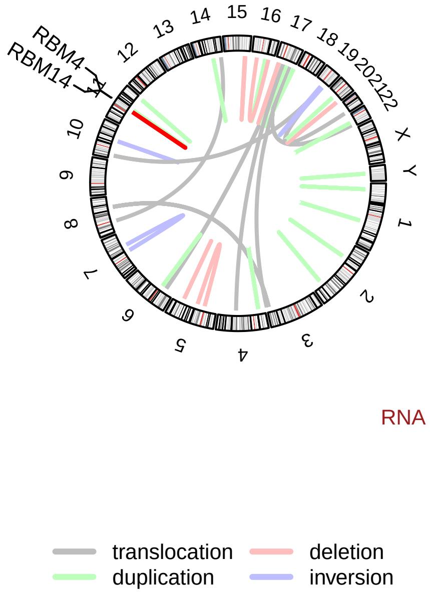


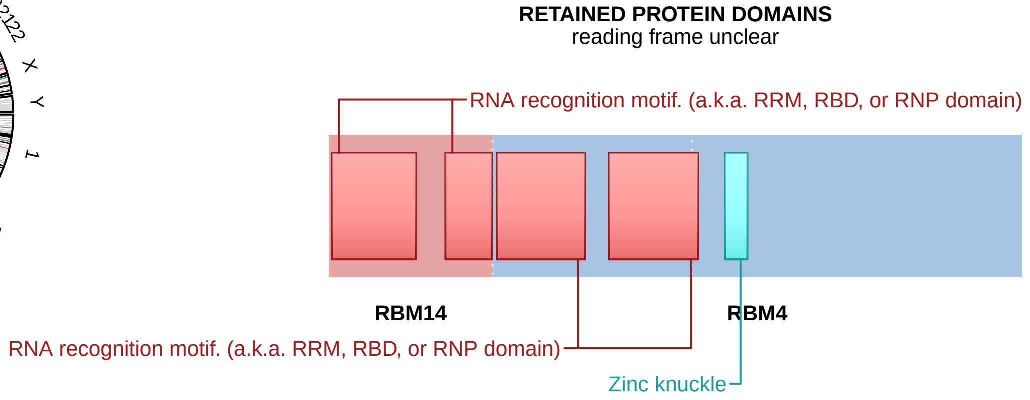
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 2



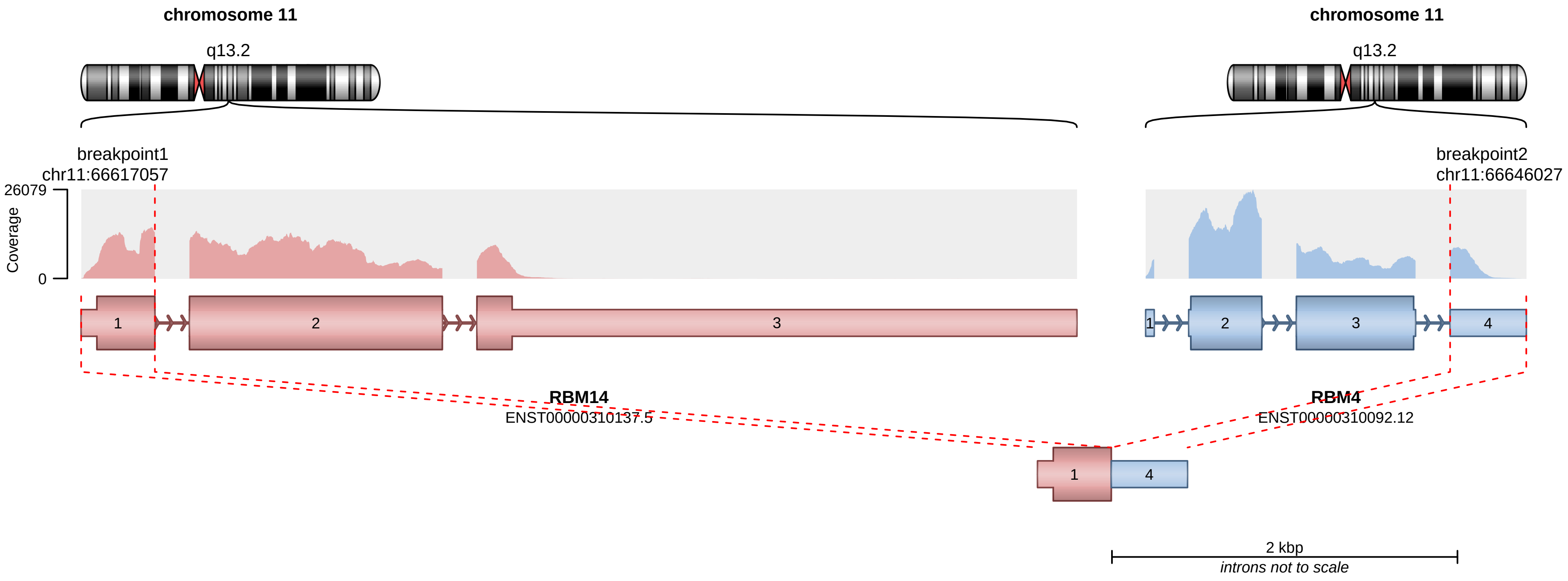


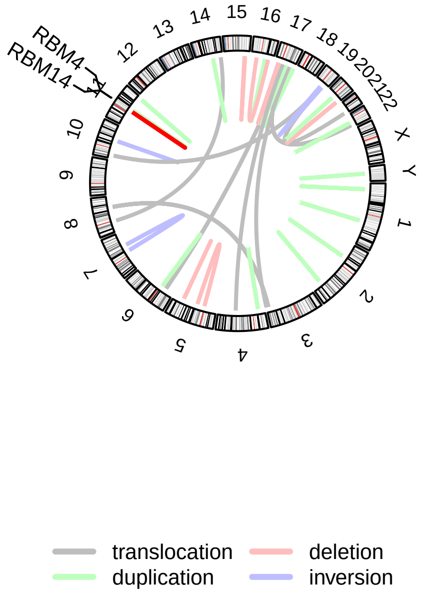




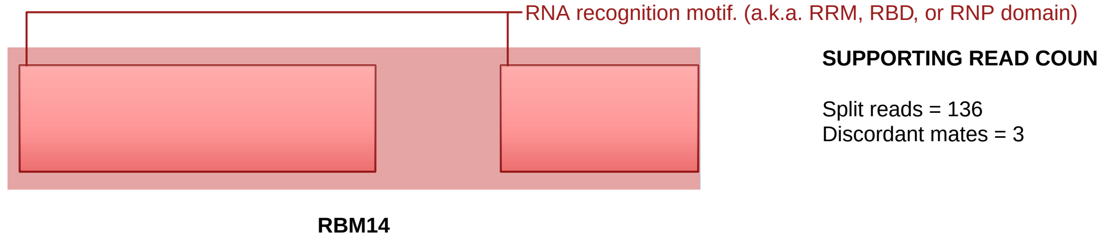
SUPPORTING READ COUNT

Split reads = 795
Discordant mates = 10



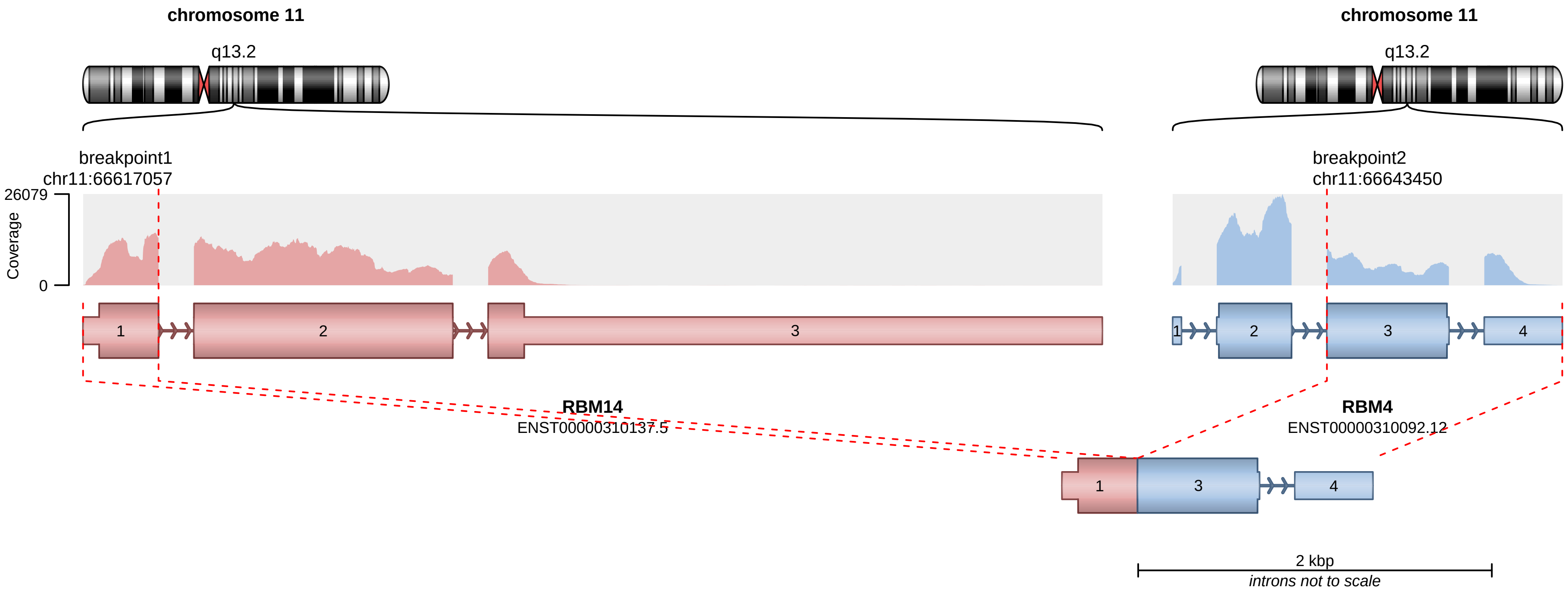


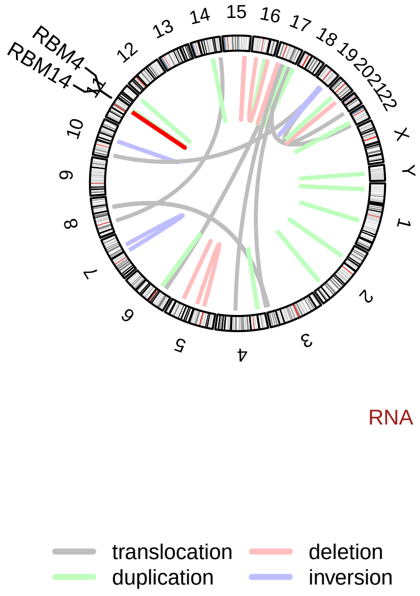
RETAINED PROTEIN DOMAINS
reading frame unclear

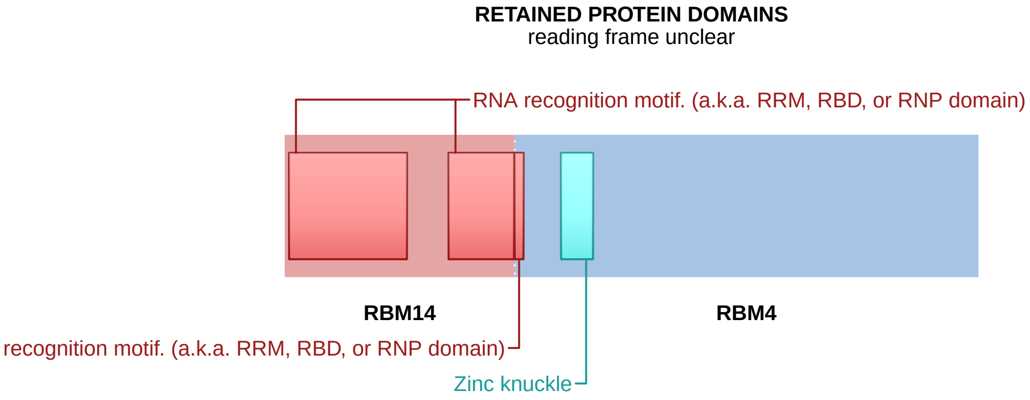


SUPPORTING READ COUNT

Split reads = 136
Discordant mates = 3

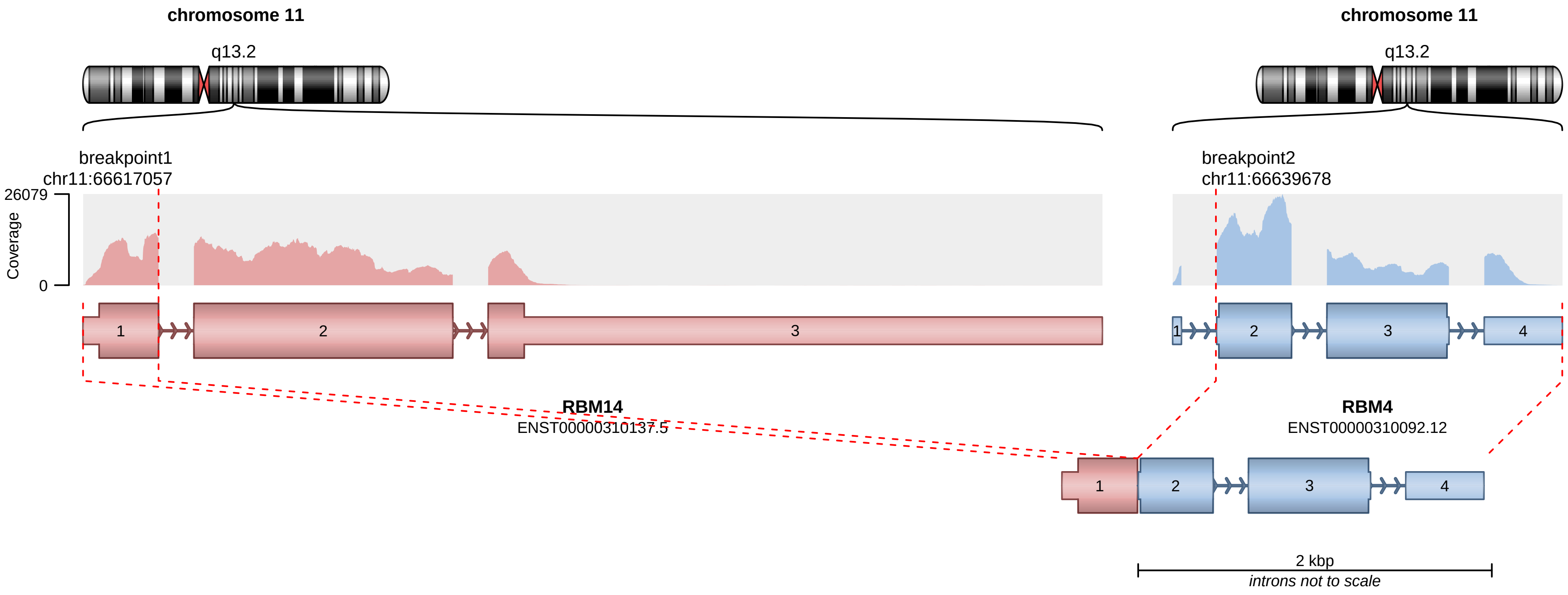


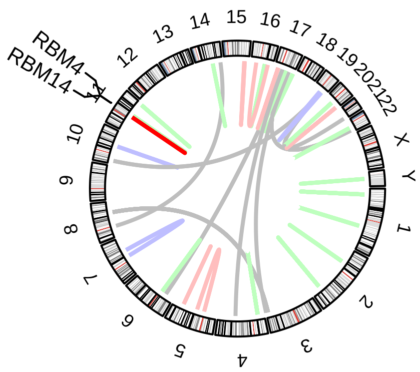


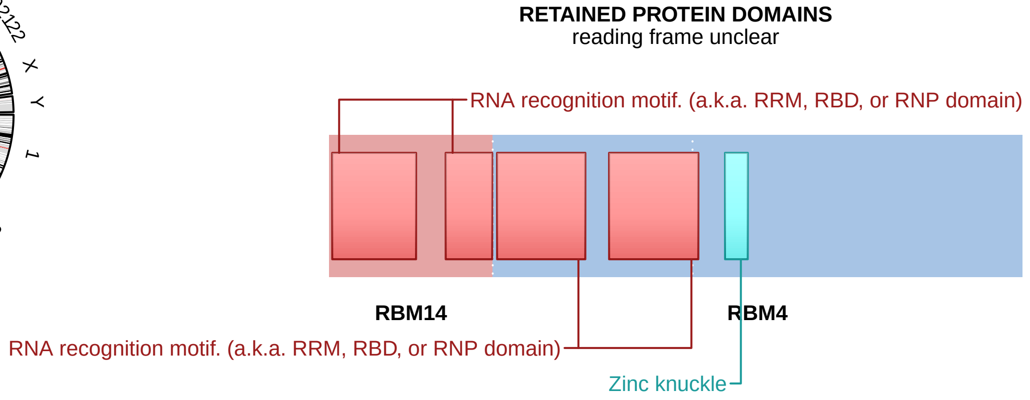


SUPPORTING READ COUNT

Split reads = 43
Discordant mates = 4

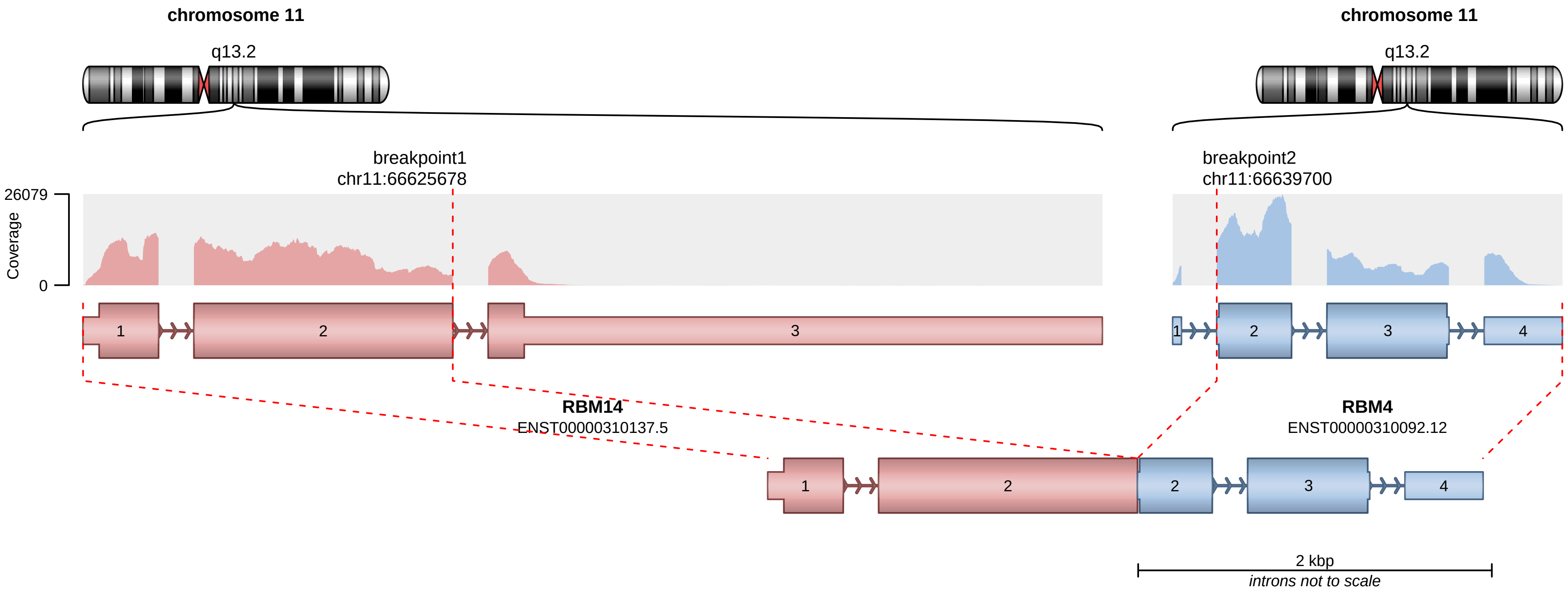


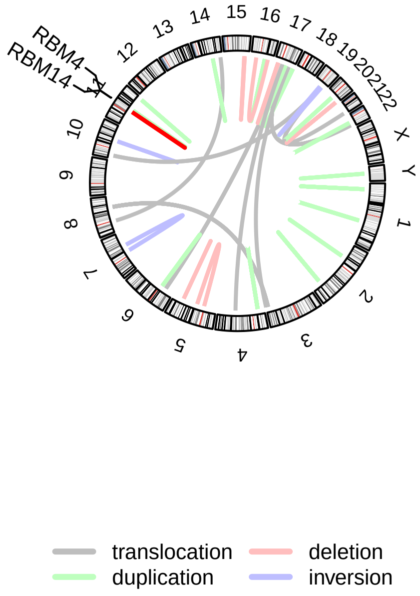


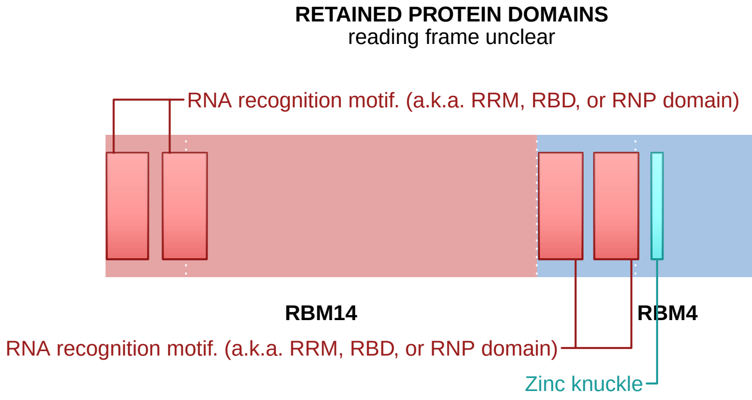


SUPPORTING READ COUNT

Split reads = 13
Discordant mates = 10

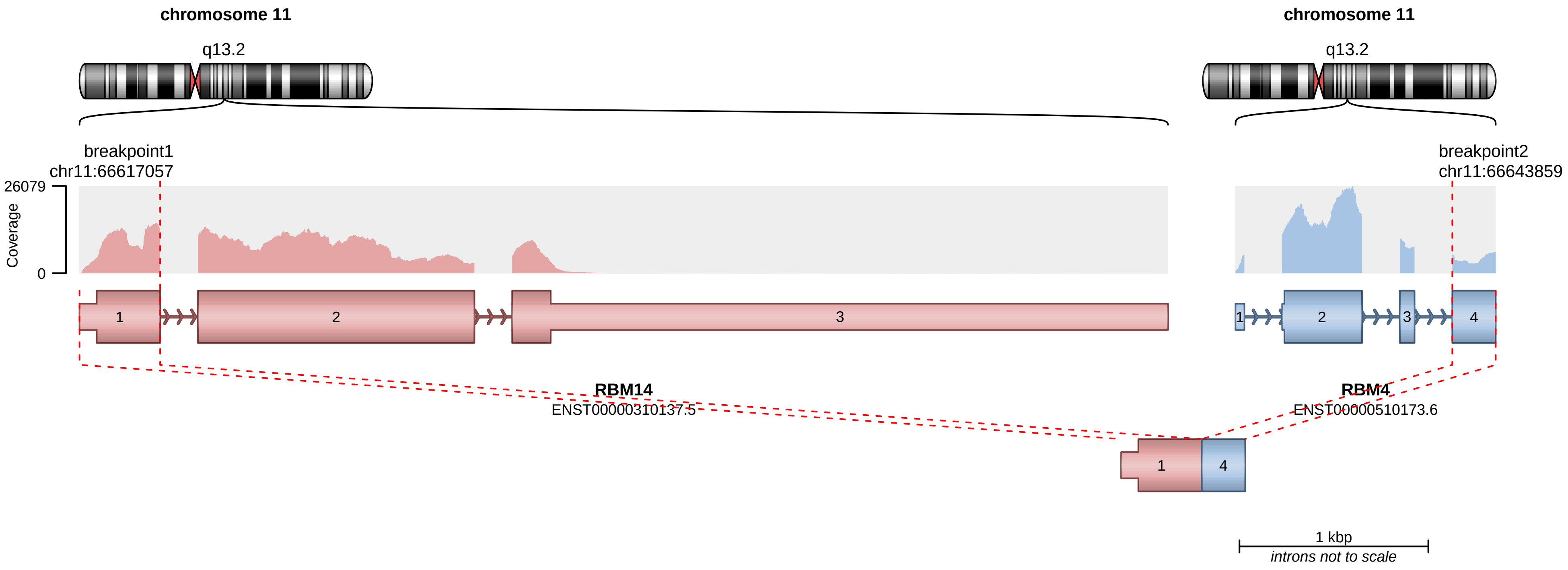


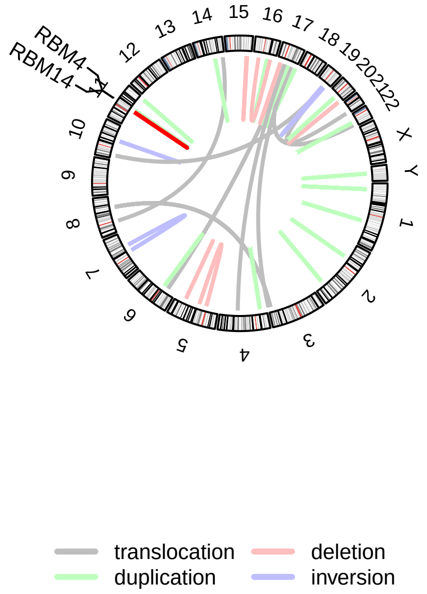




SUPPORTING READ COUNT

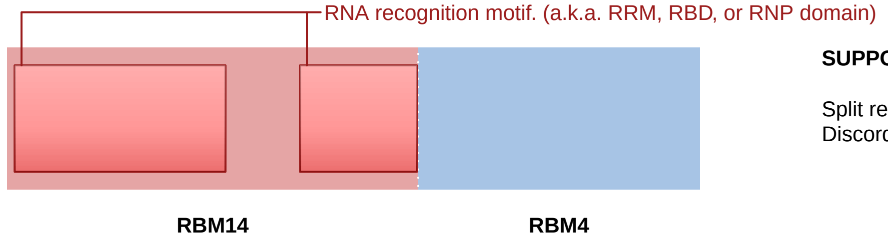
Split reads = 8
Discordant mates = 11





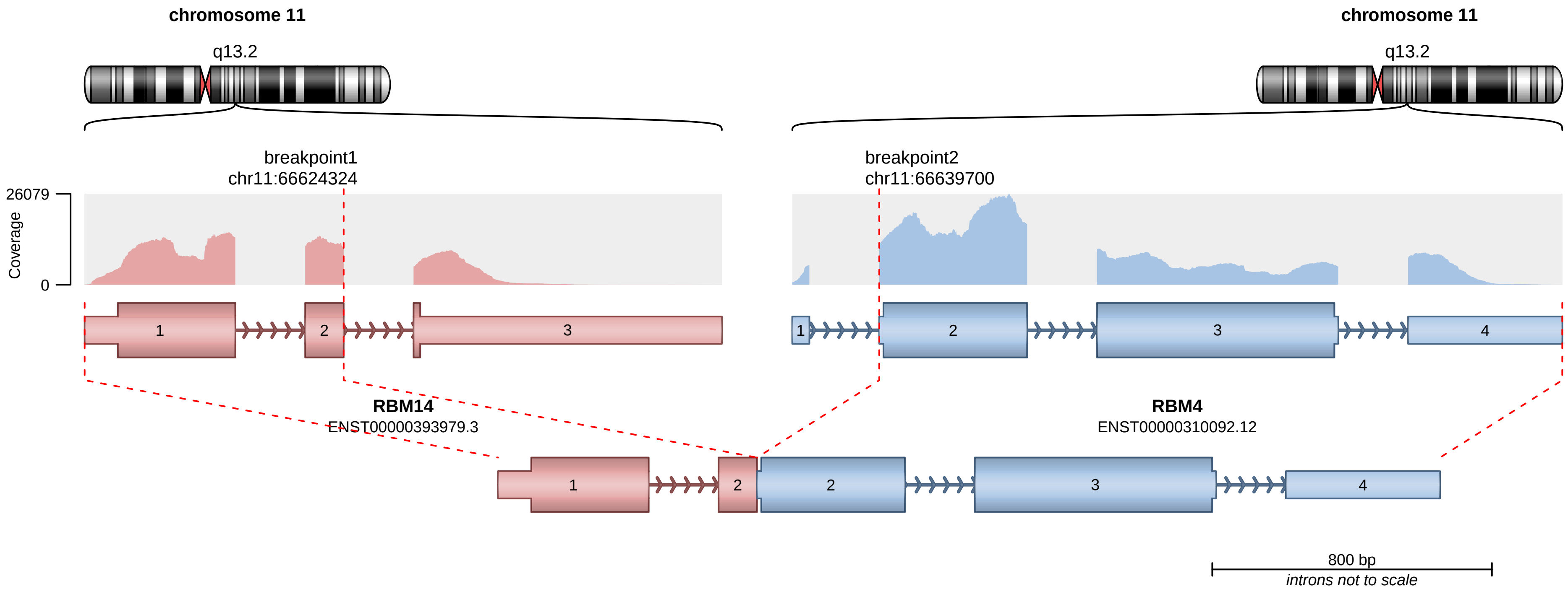
RETAINED PROTEIN DOMAINS

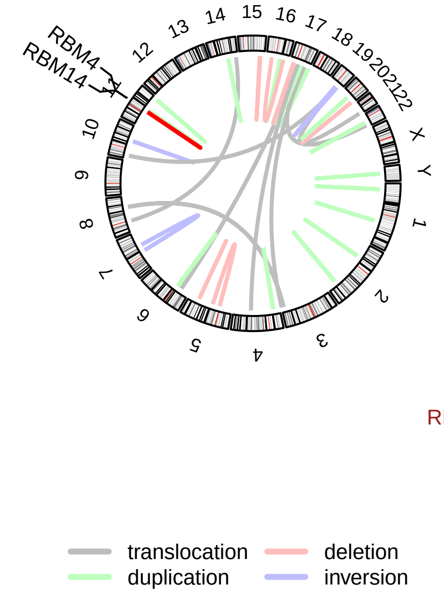
reading frame unclear



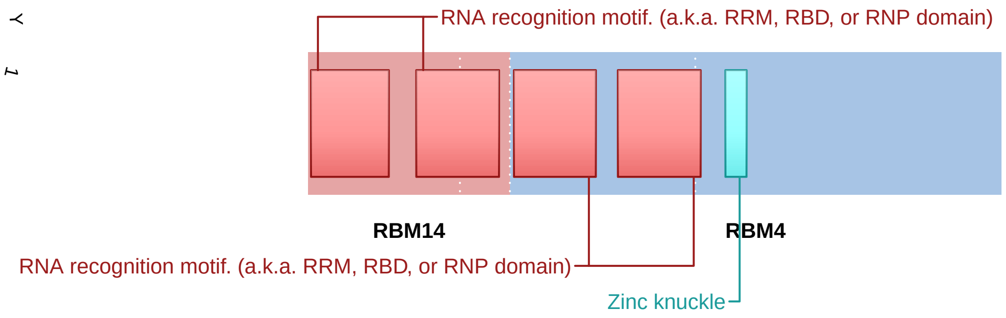
SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 3



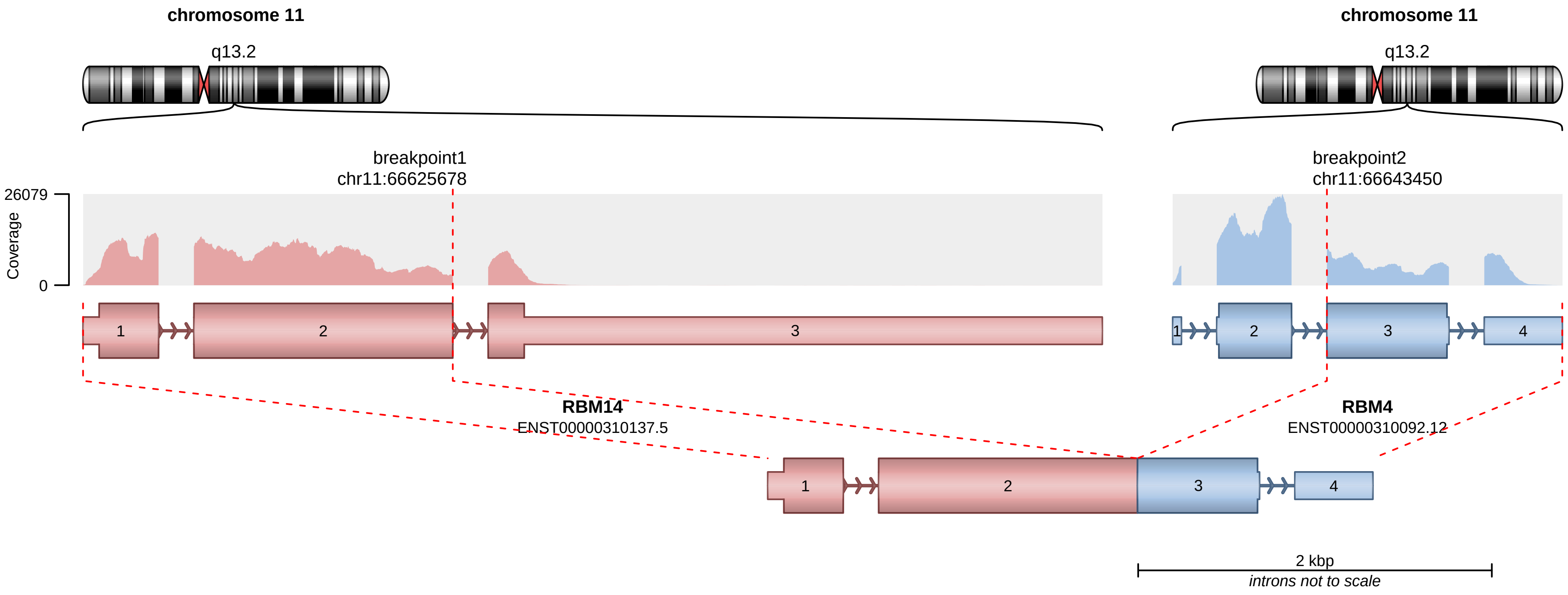


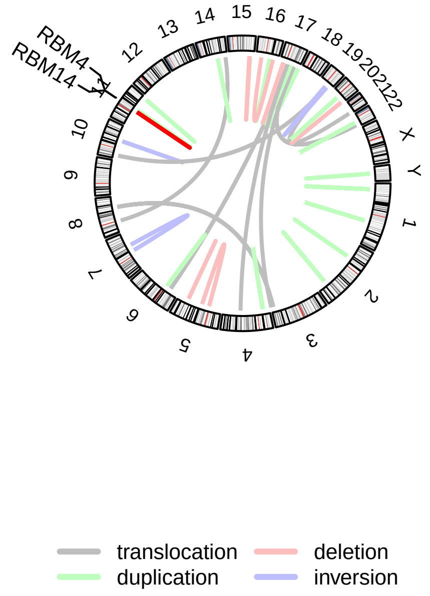
RETAINED PROTEIN DOMAINS
reading frame unclear

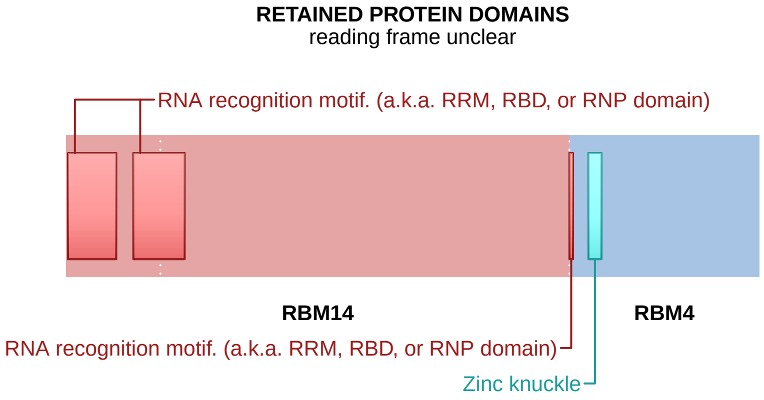


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 10

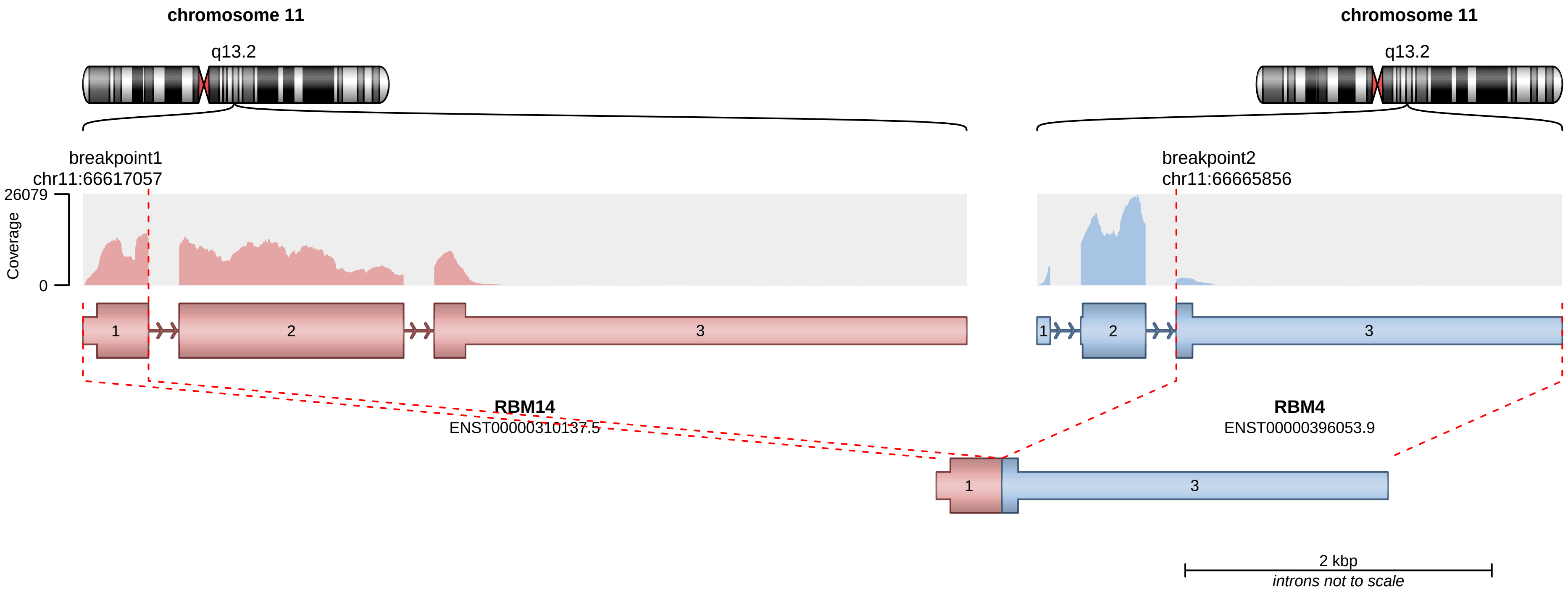


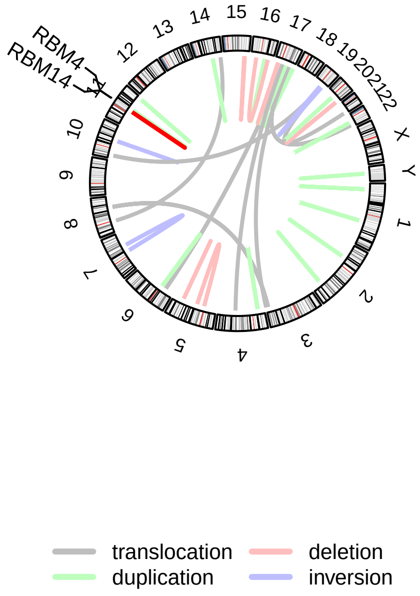




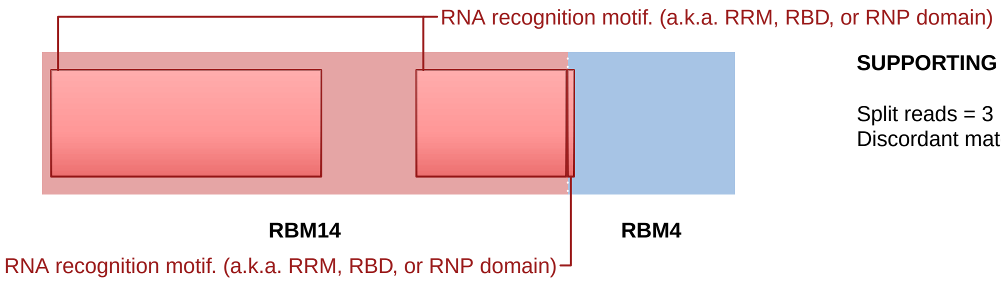
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 4



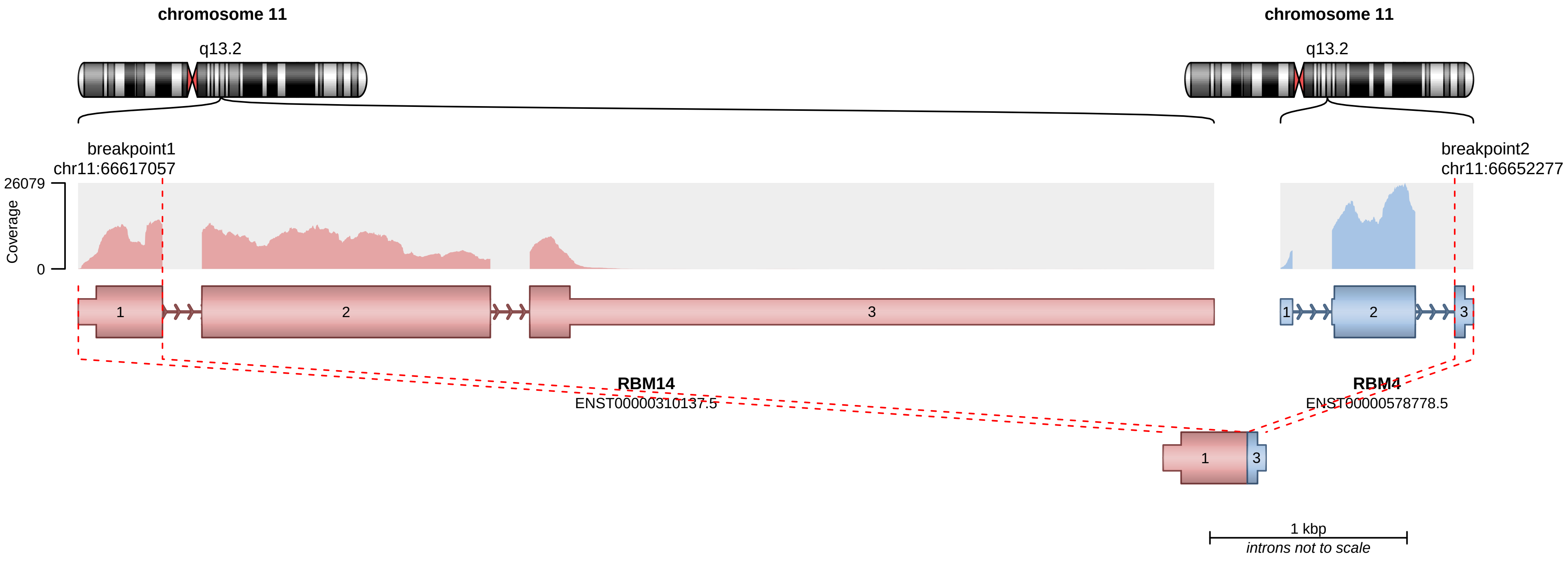


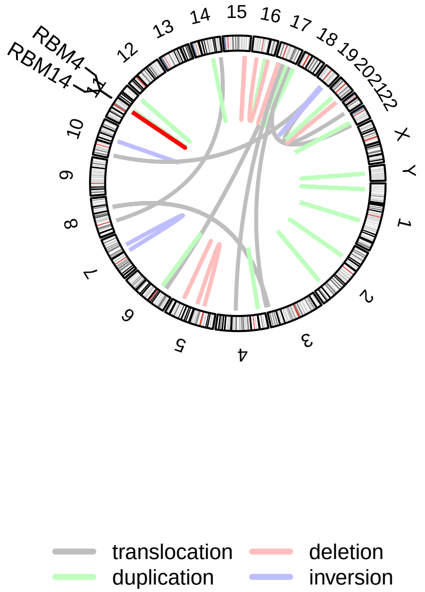
RETAINED PROTEIN DOMAINS
reading frame unclear

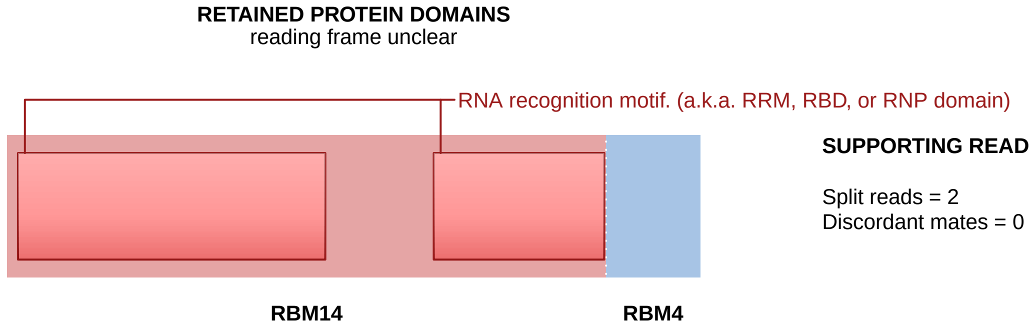


SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

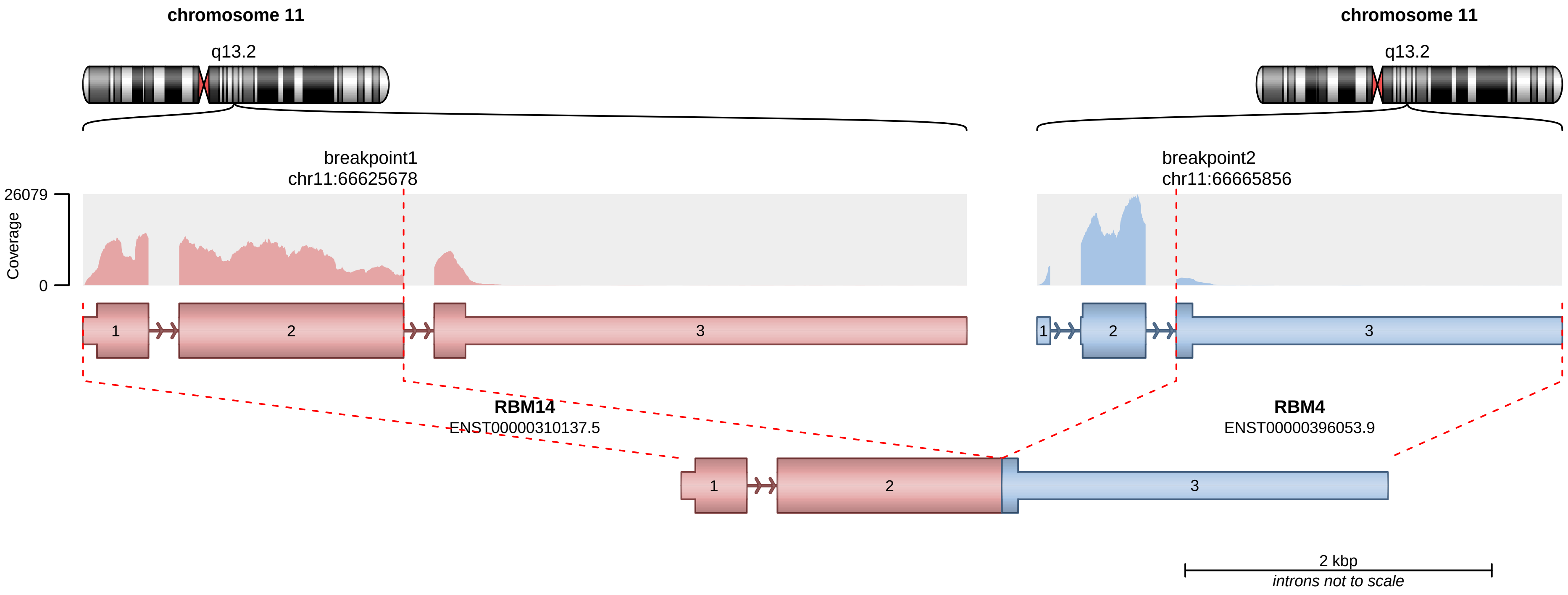


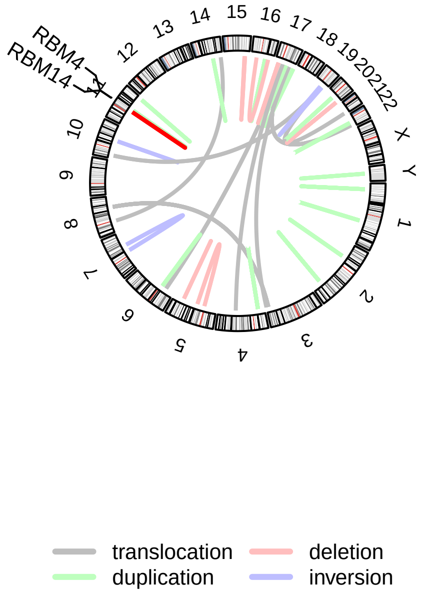


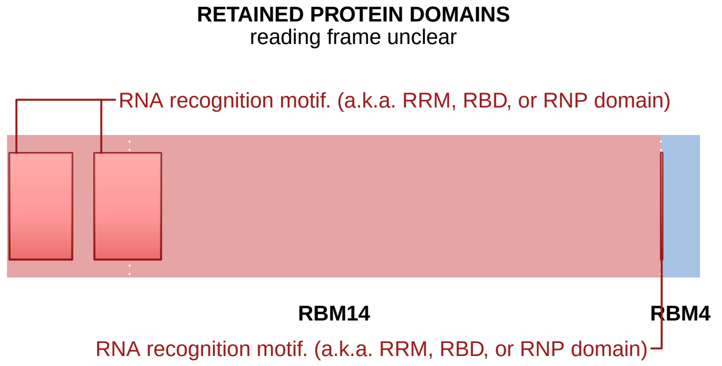


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

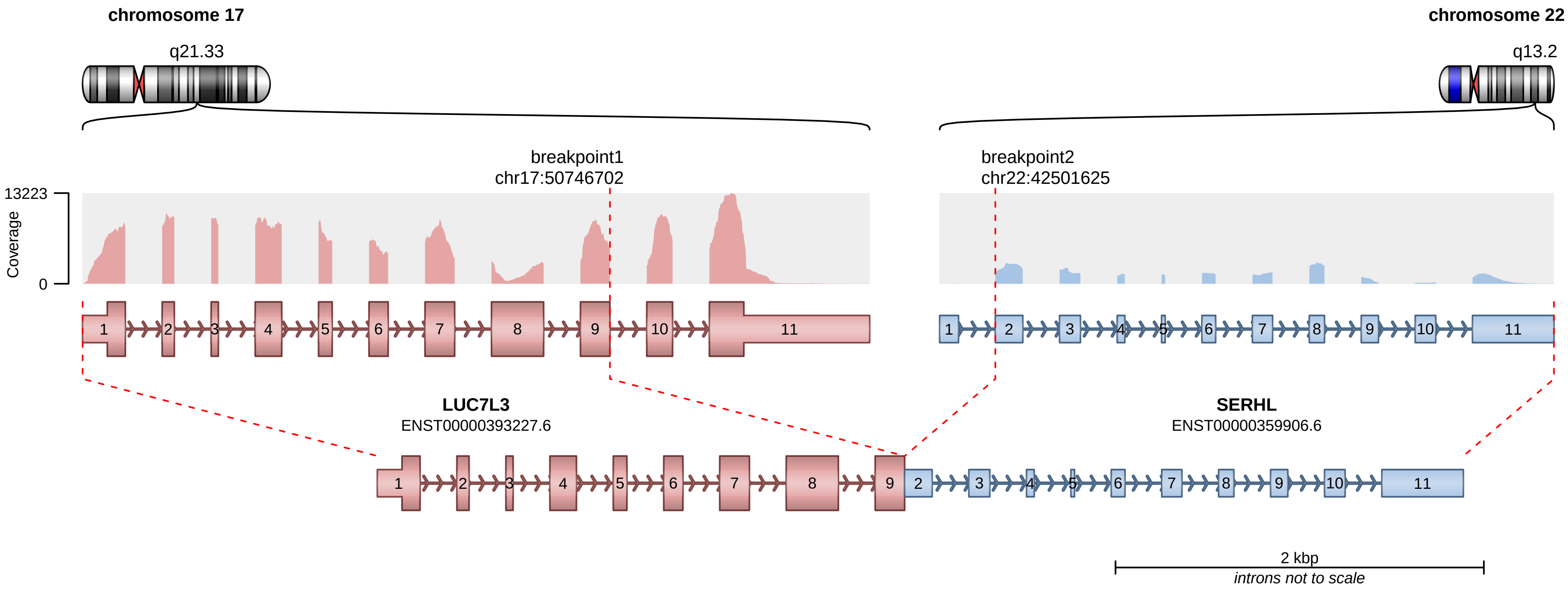


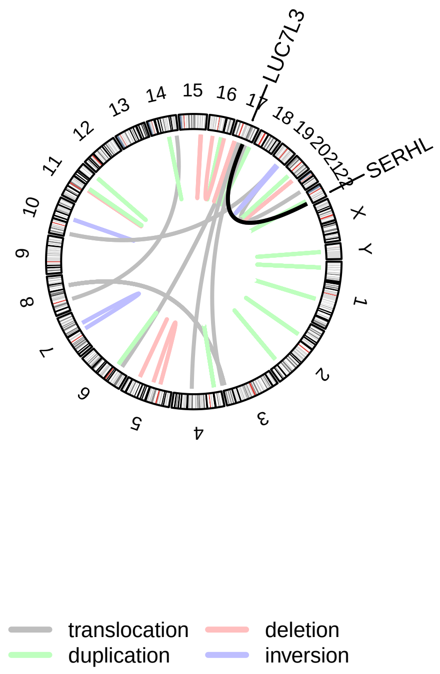




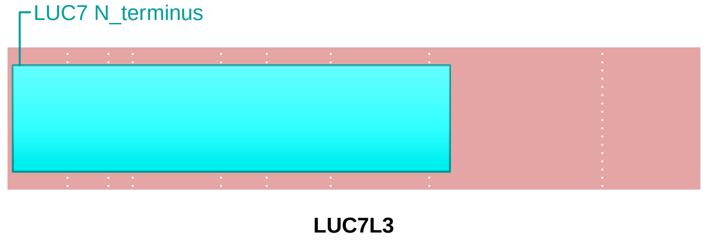
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



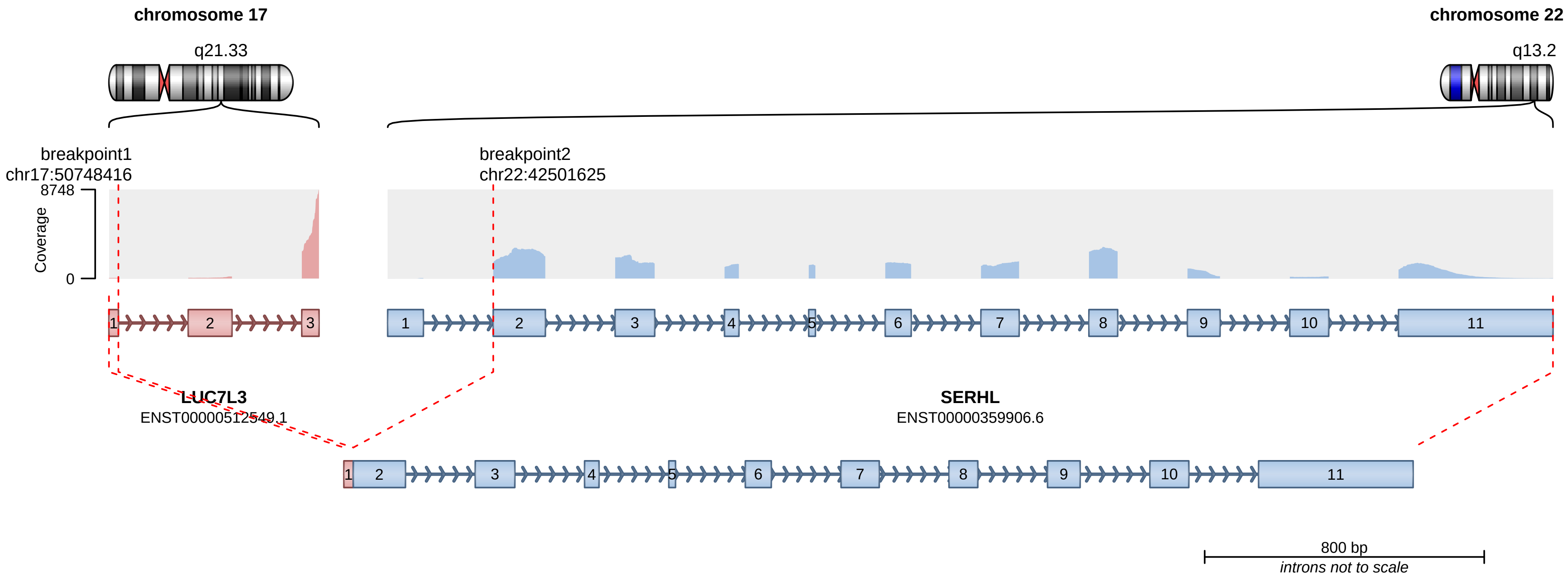


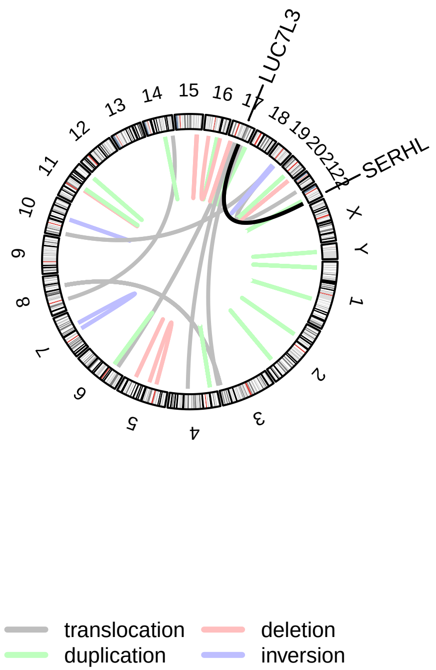
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 551
Discordant mates = 18

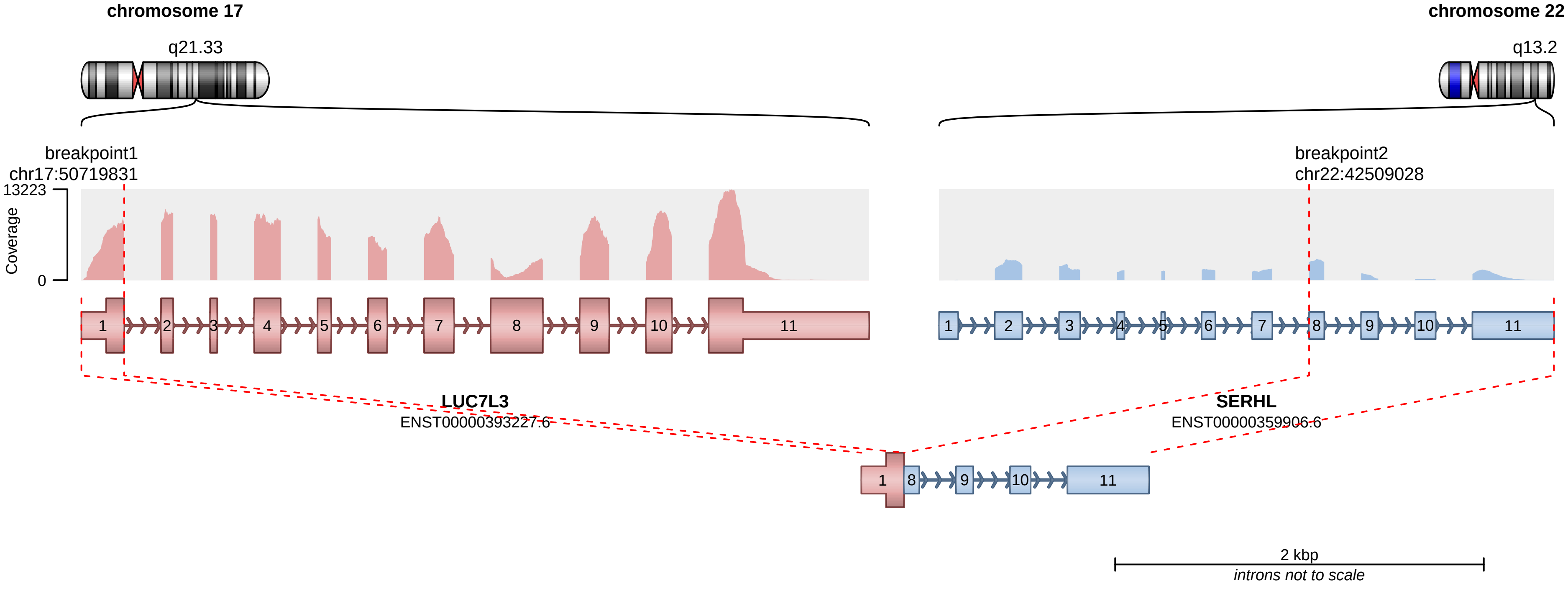


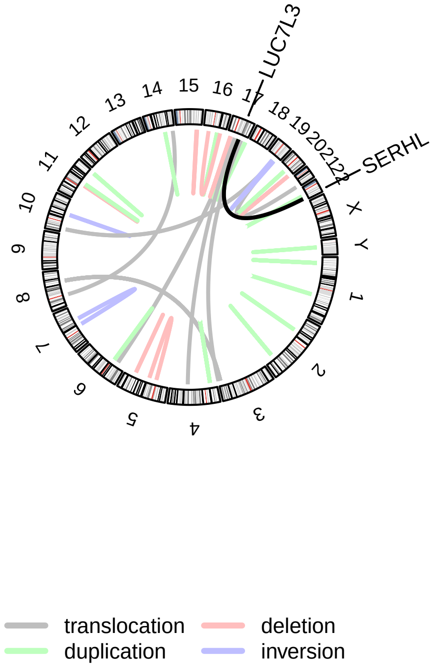


Genes are not protein−coding.

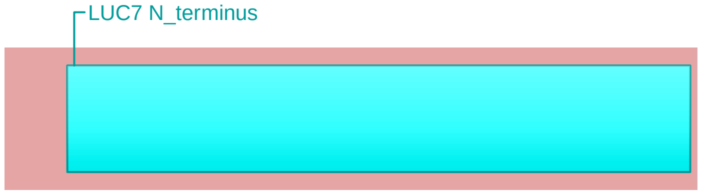
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 18





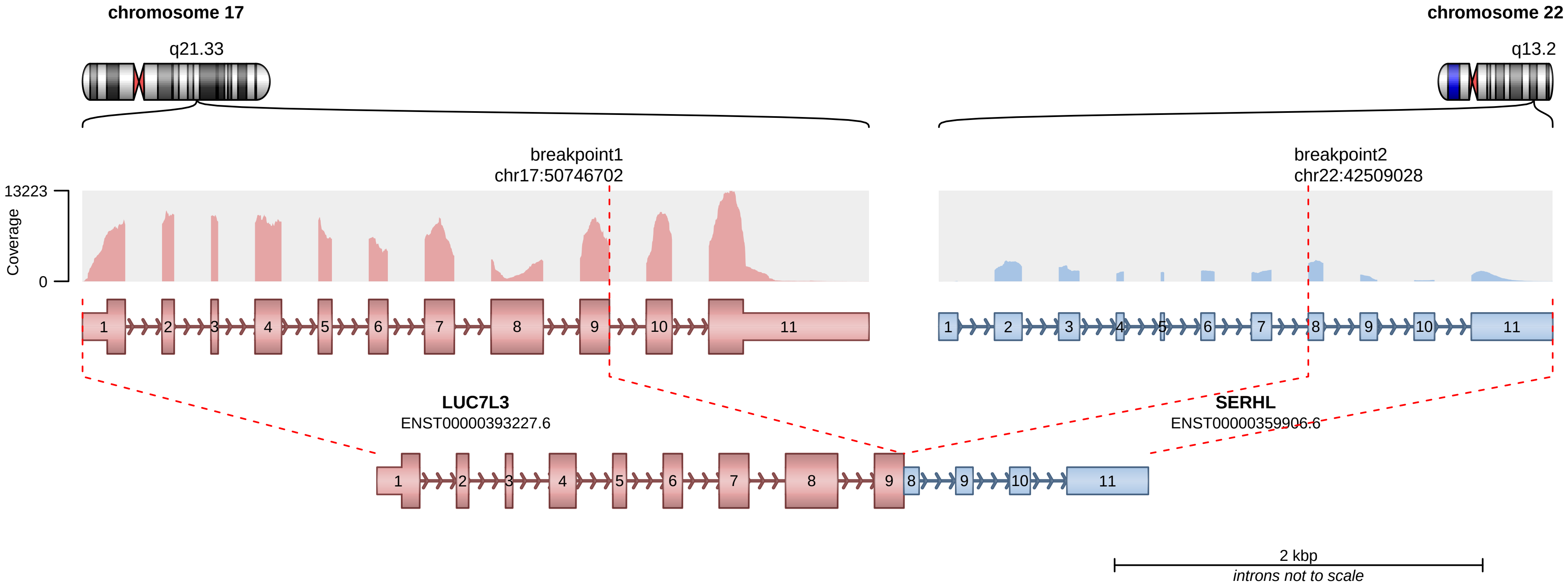
RETAINED PROTEIN DOMAINS
reading frame unclear

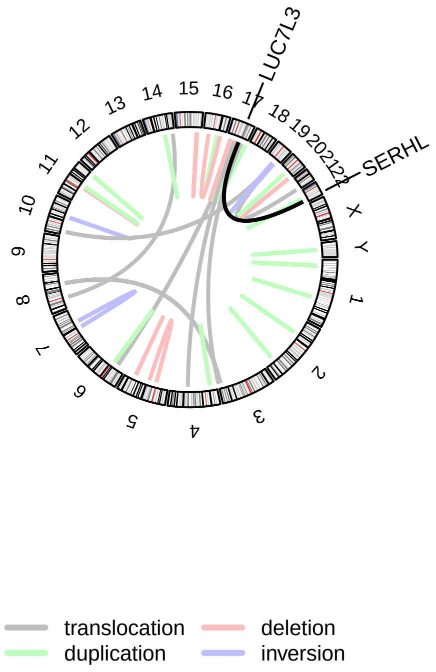


LUC7L3

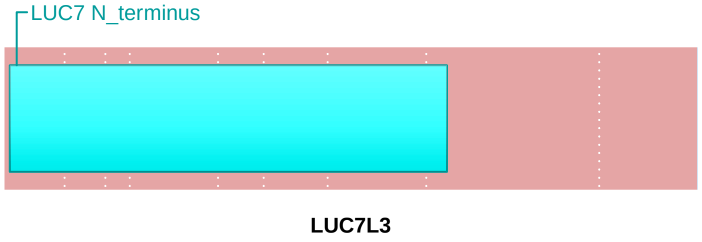
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



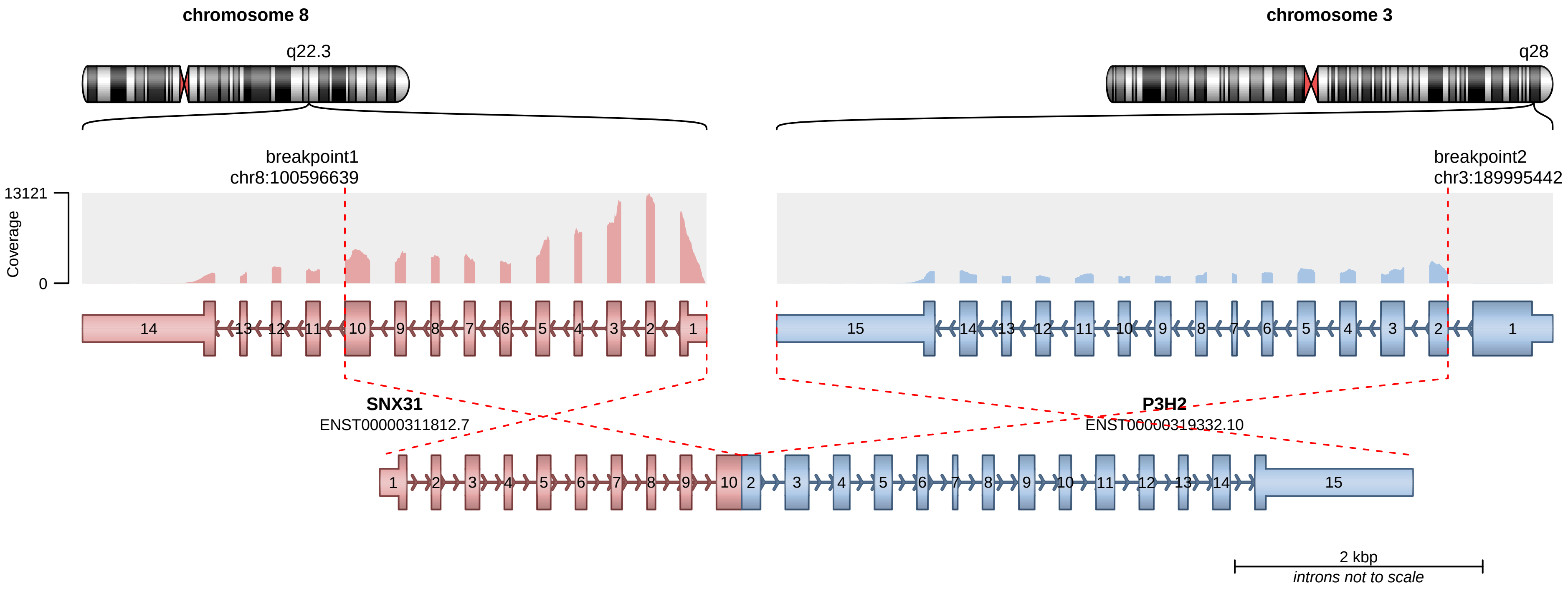


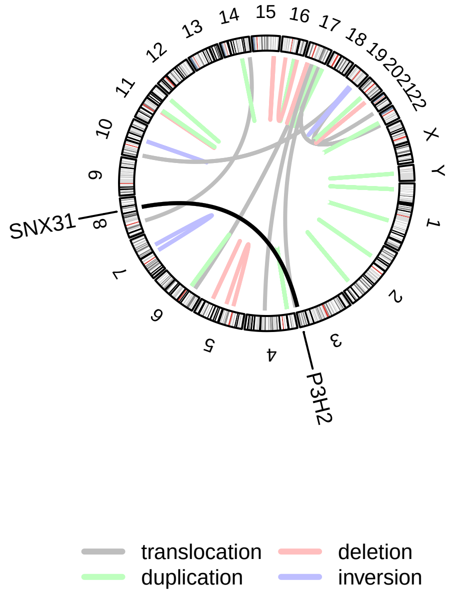
RETAINED PROTEIN DOMAINS
reading frame unclear



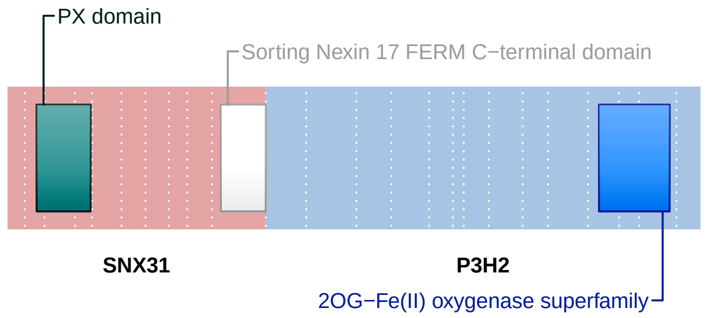
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



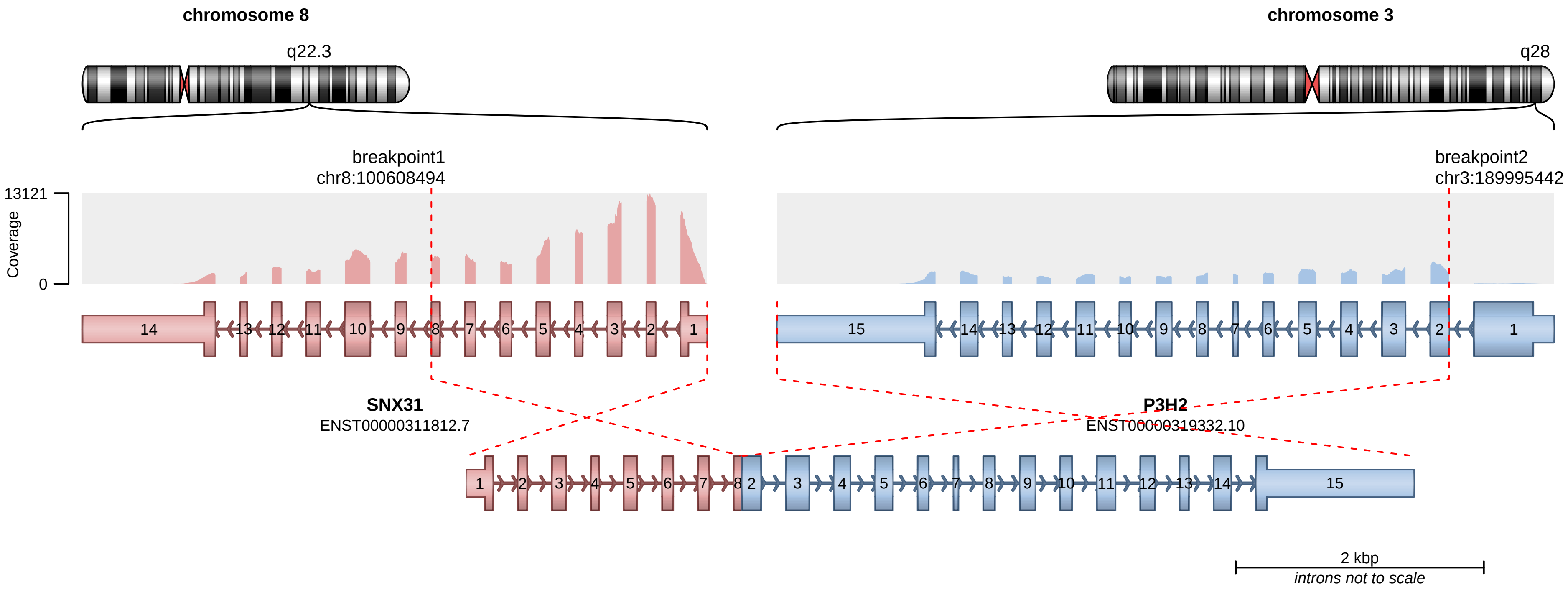


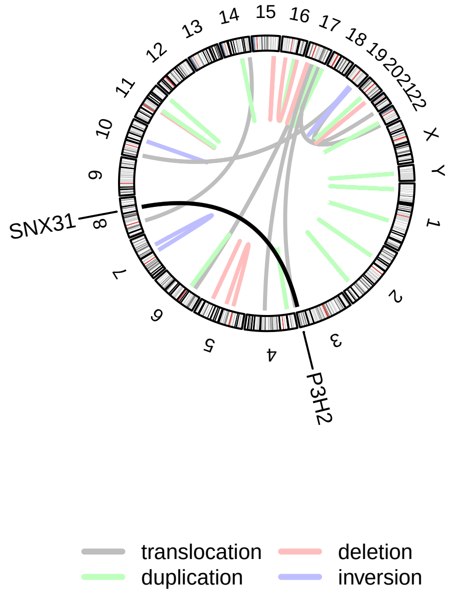
RETAINED PROTEIN DOMAINS
reading frame unclear



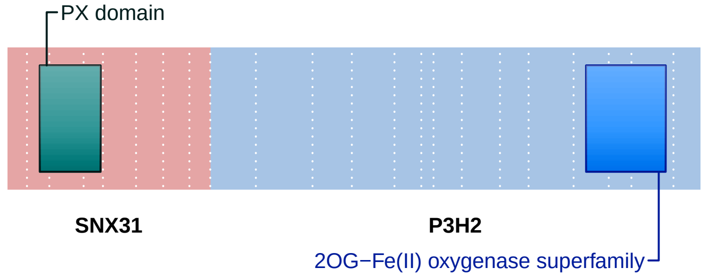
SUPPORTING READ COUNT

Split reads = 520
Discordant mates = 42



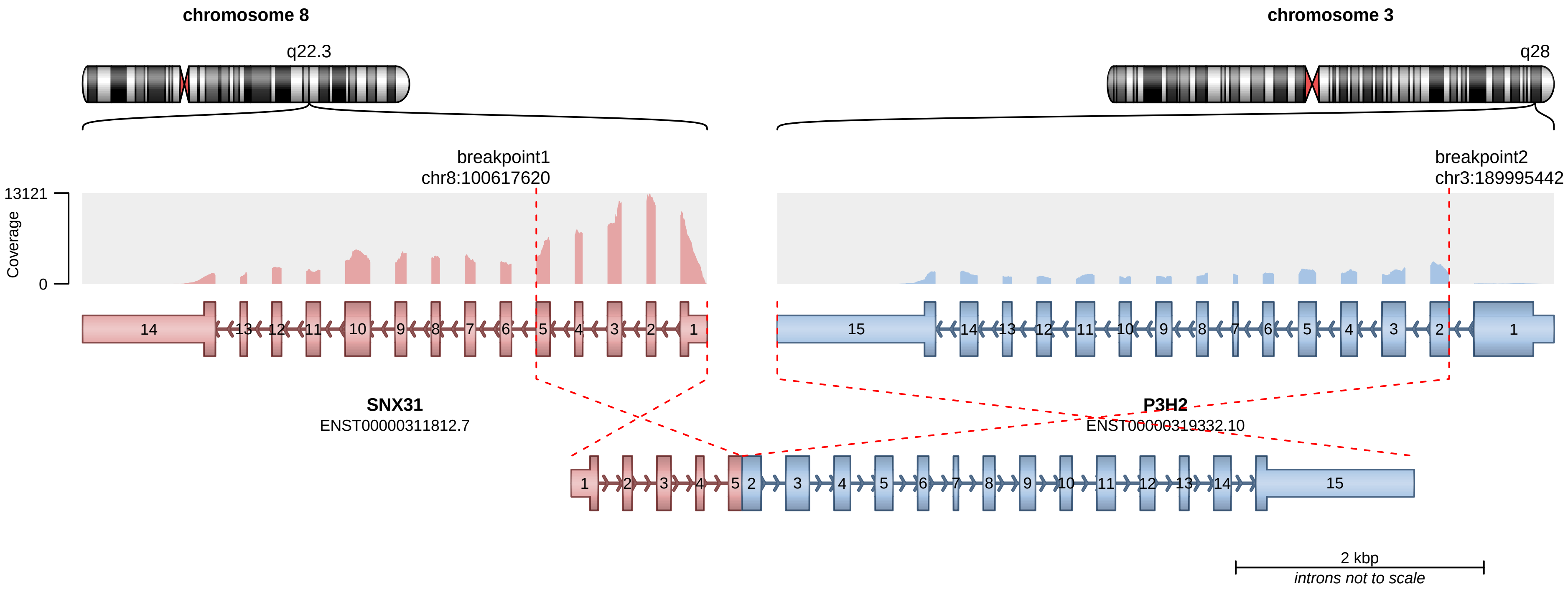


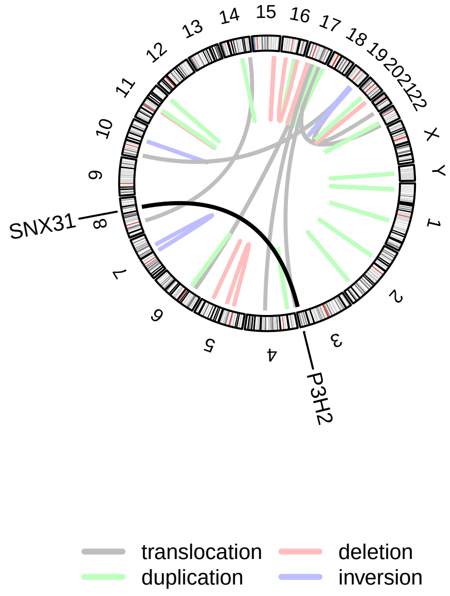
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 34
Discordant mates = 10





RETAINED PROTEIN DOMAINS
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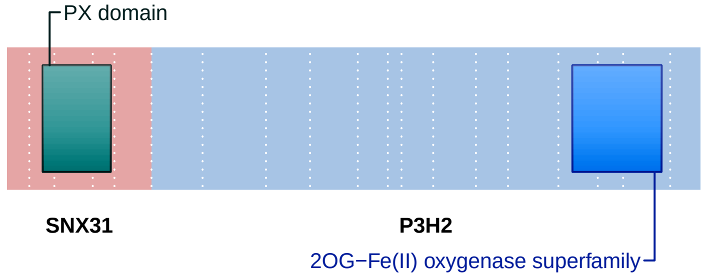
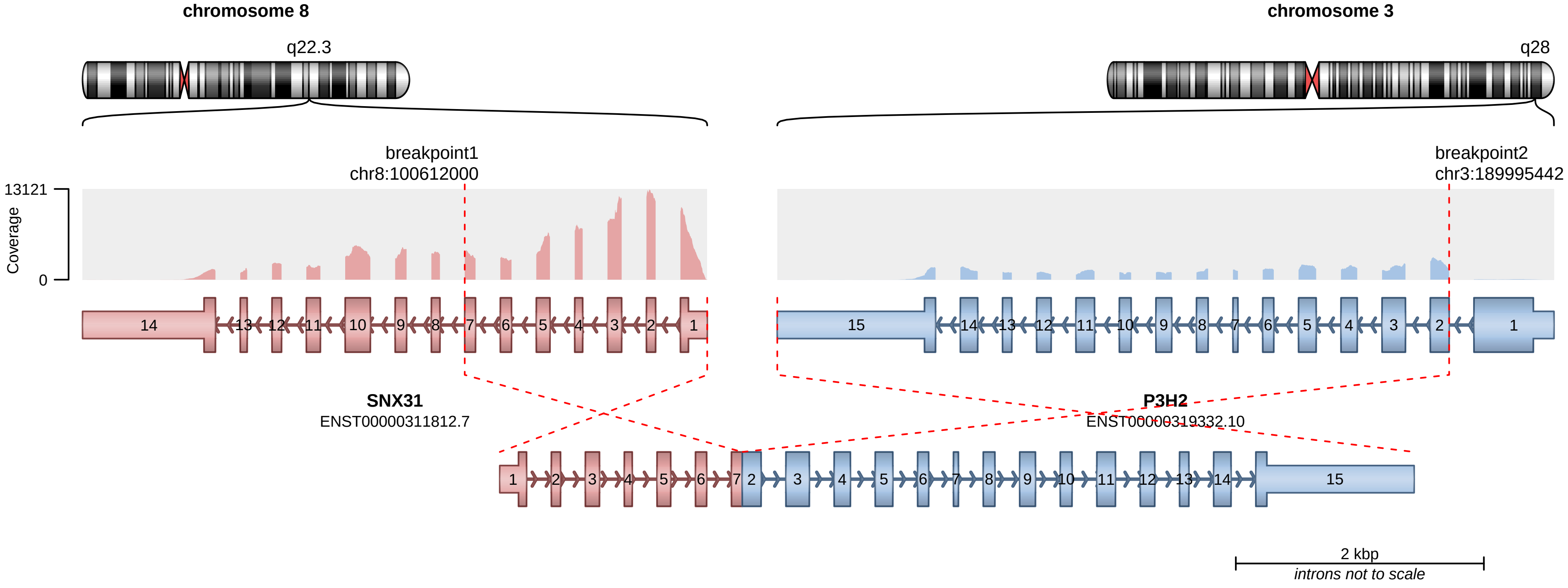
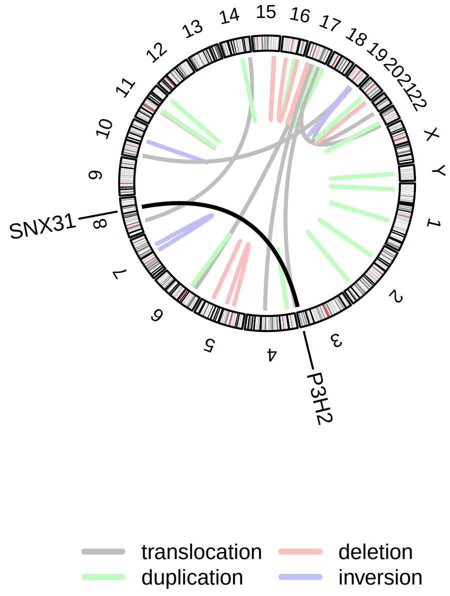
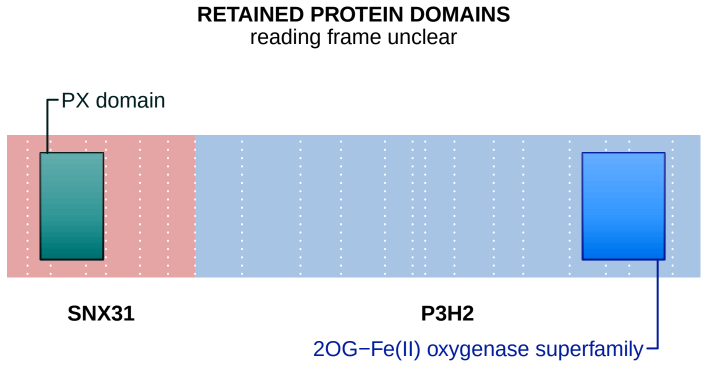


SUPPORTING READ COUNT

Split reads = 34
Discordant mates = 6

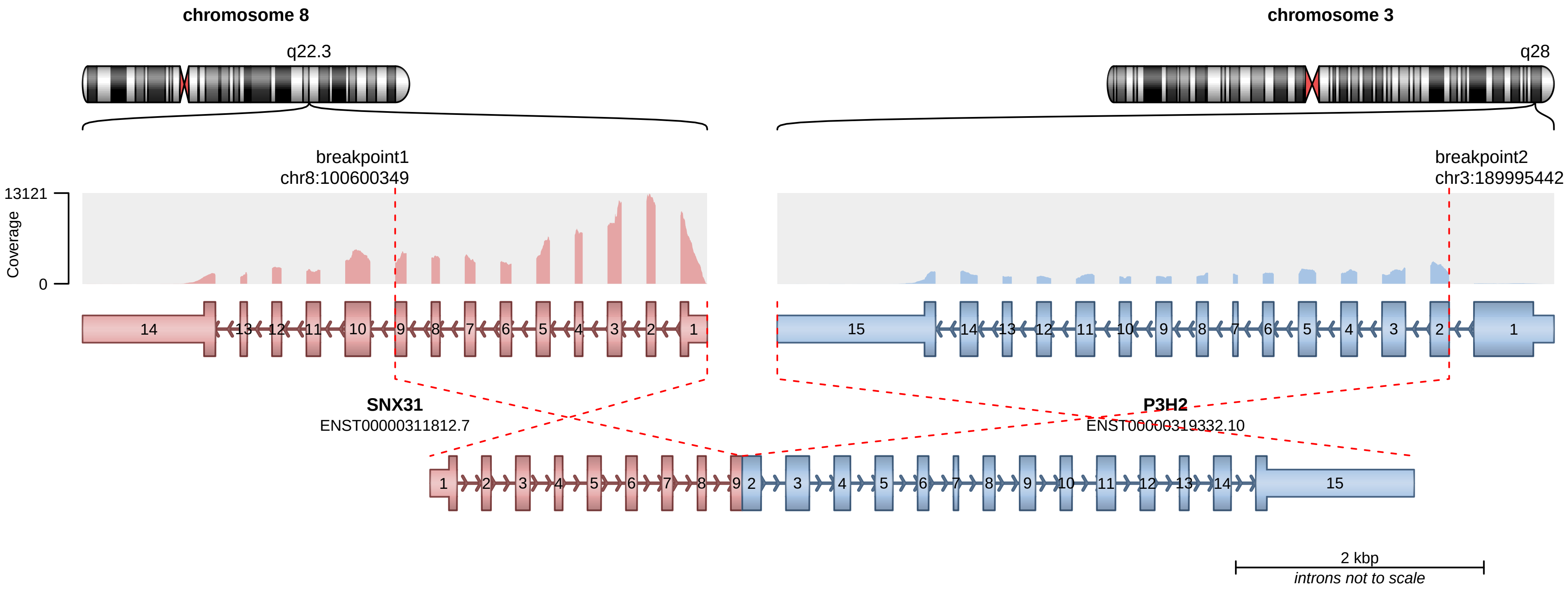


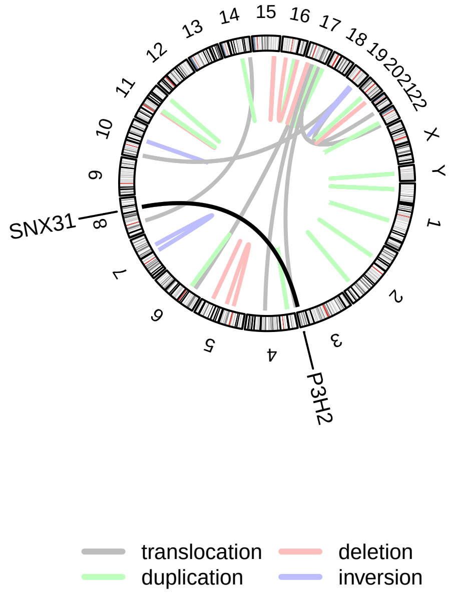




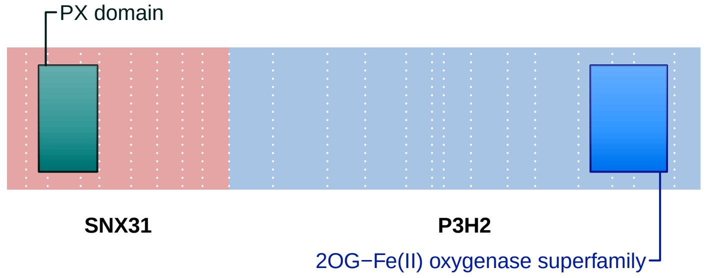
SUPPORTING READ COUNT

Split reads = 31
Discordant mates = 8



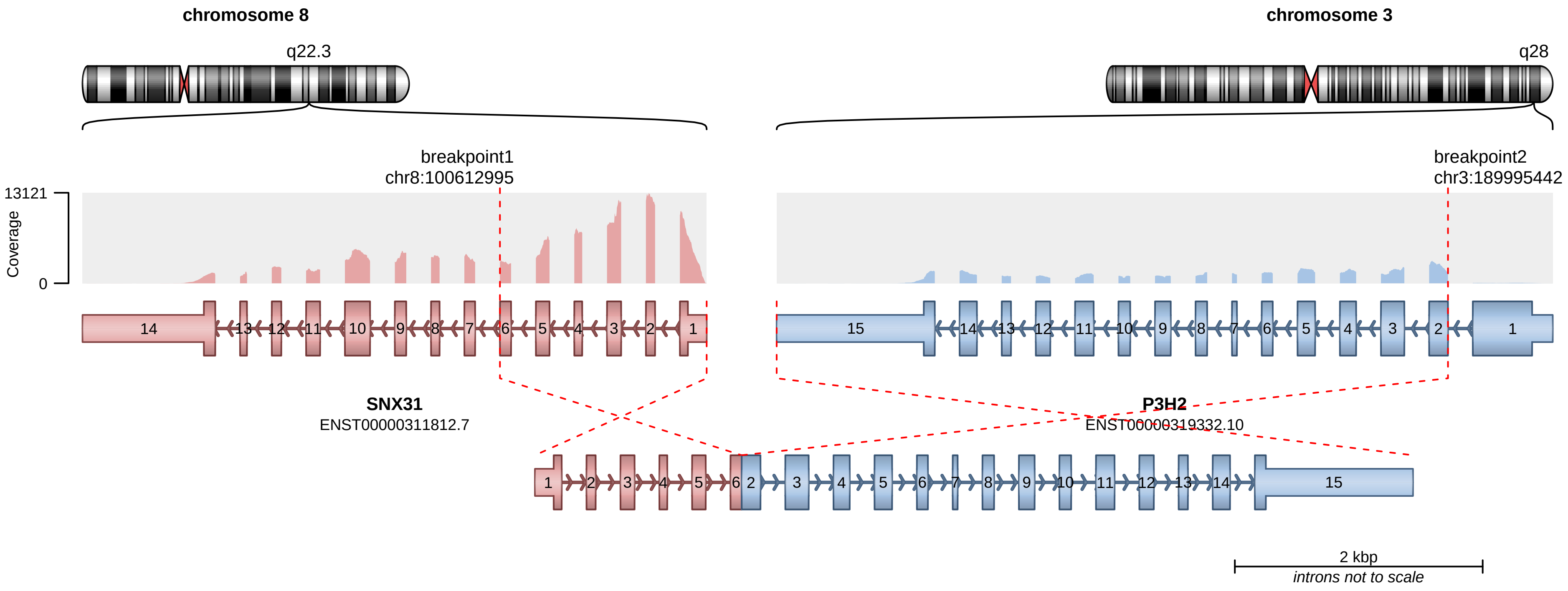


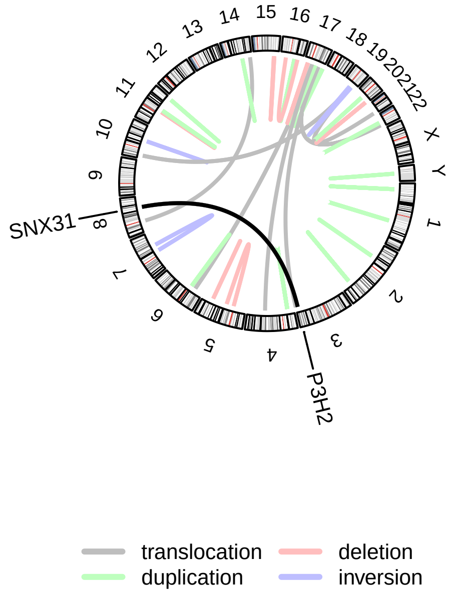
RETAINED PROTEIN DOMAINS
reading frame unclear

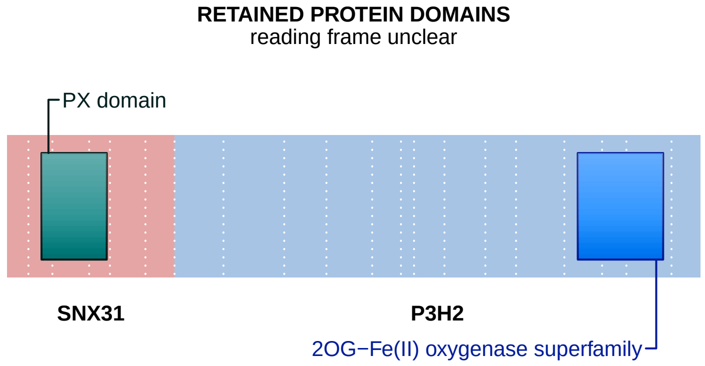


SUPPORTING READ COUNT

Split reads = 24
Discordant mates = 11

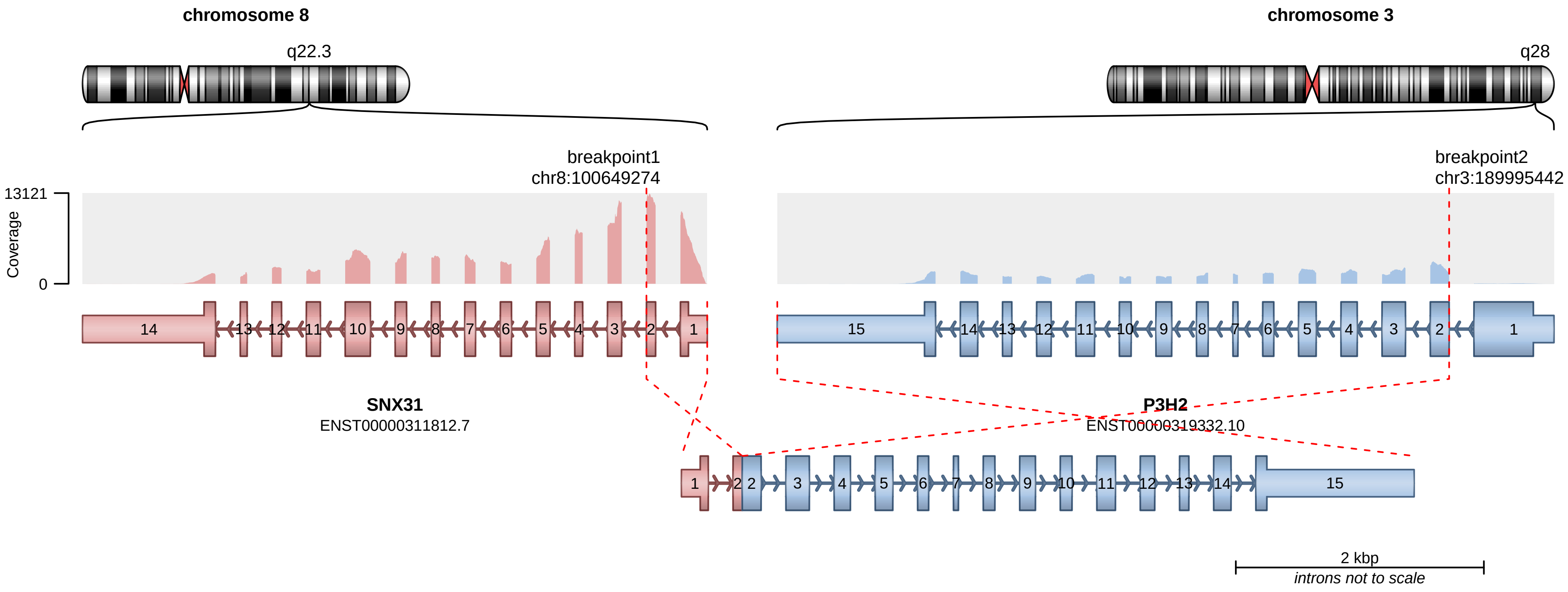


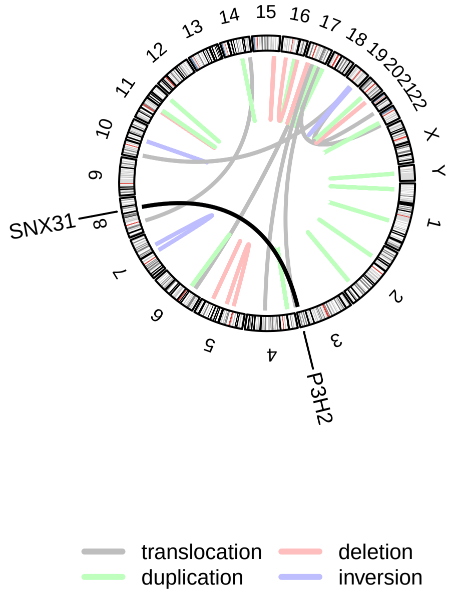




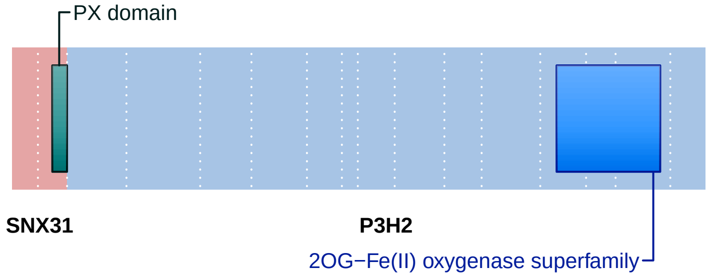
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 6



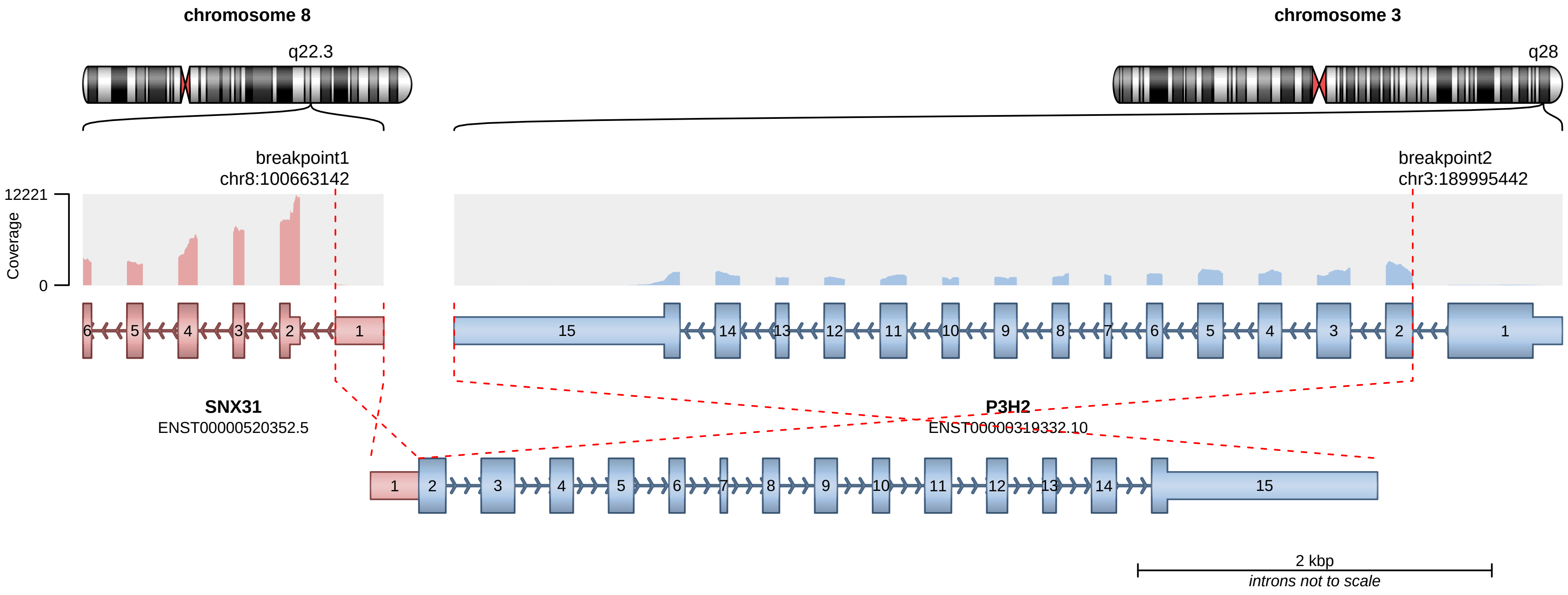


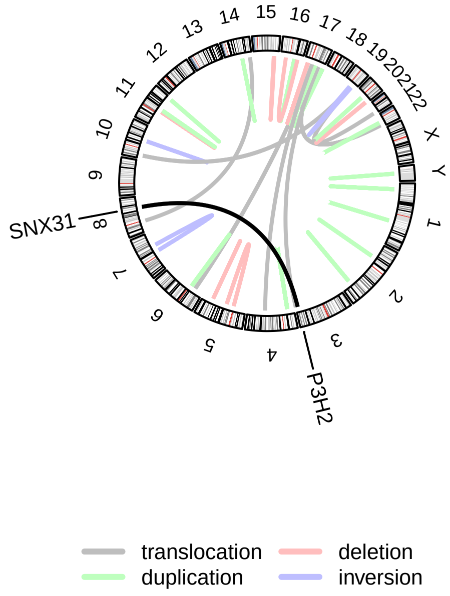
RETAINED PROTEIN DOMAINS
reading frame unclear



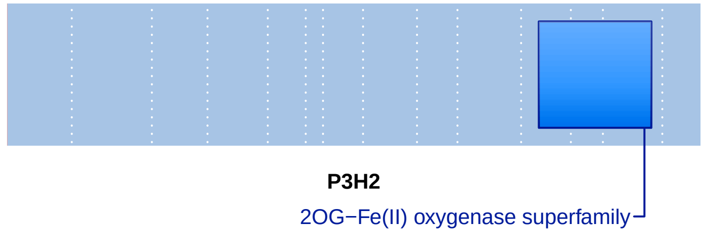
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0



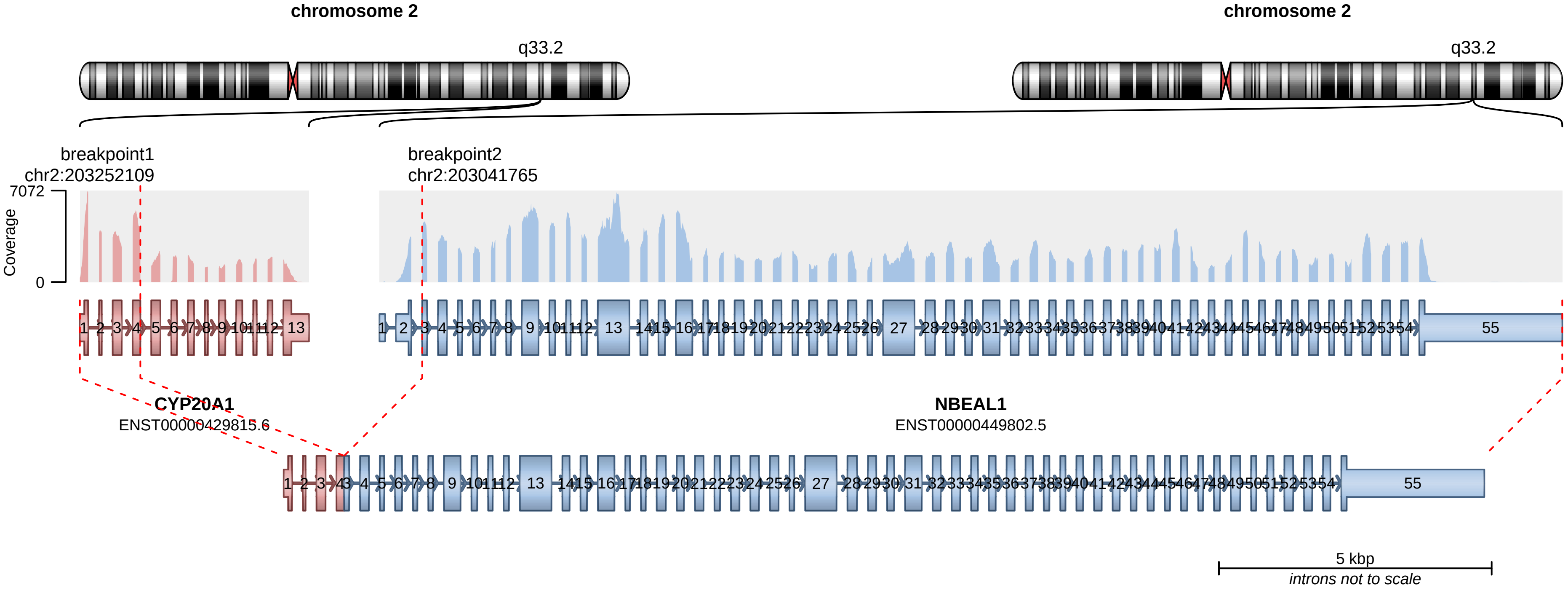


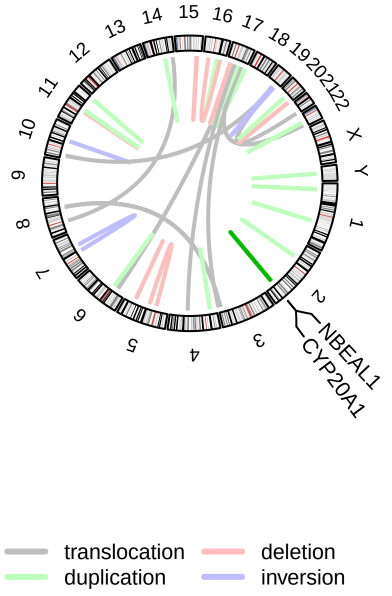
RETAINED PROTEIN DOMAINS
reading frame unclear

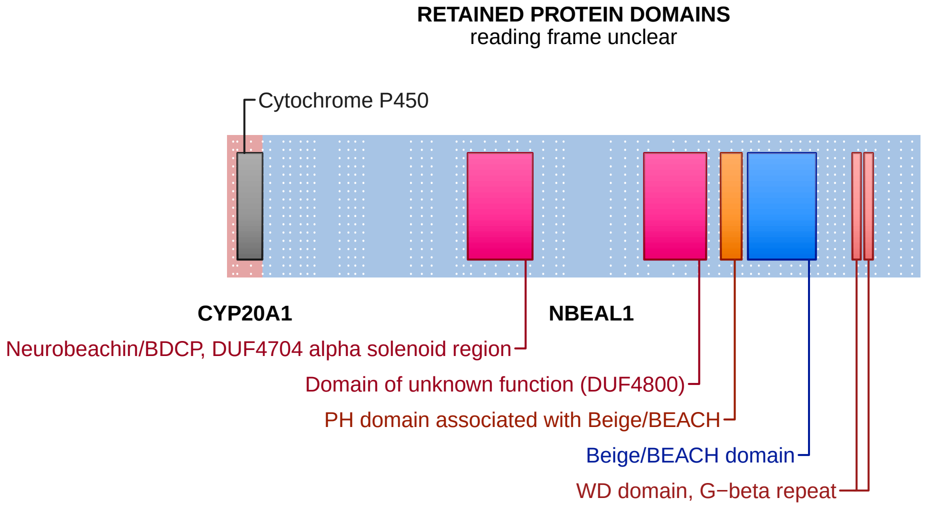


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

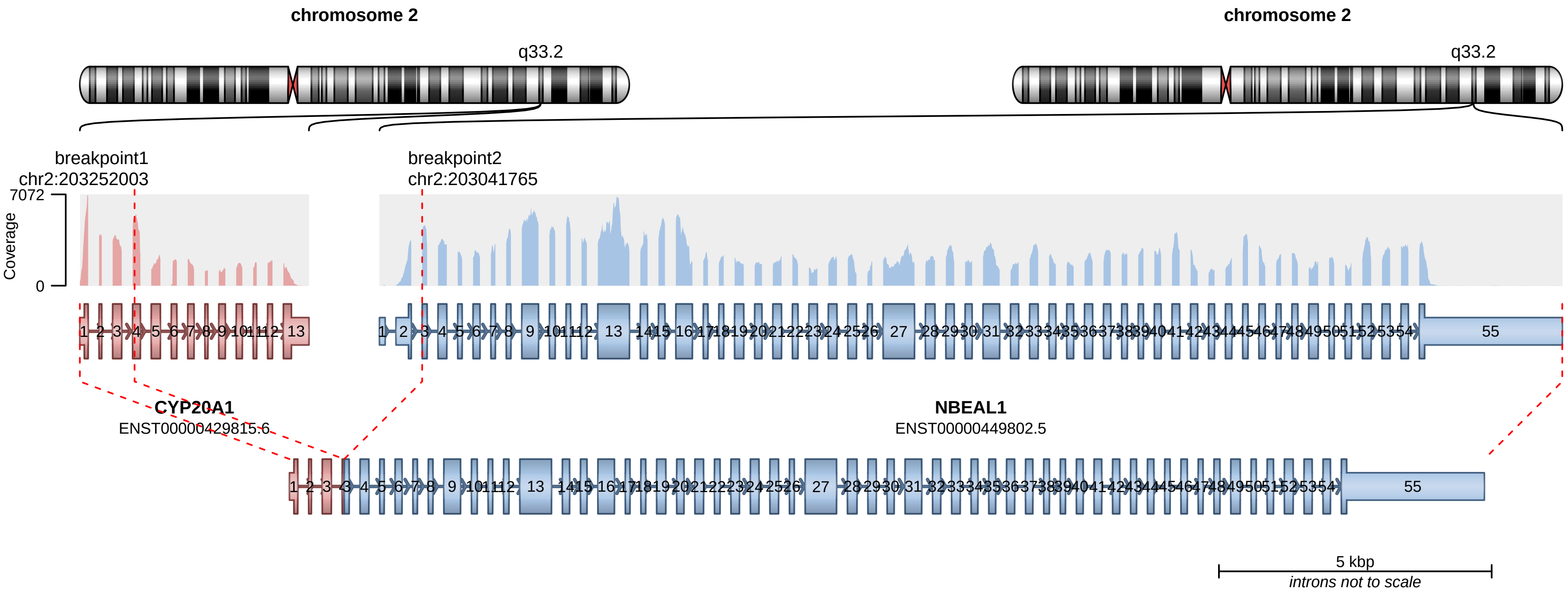


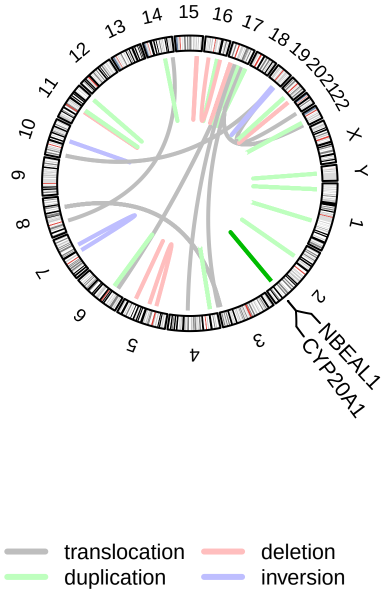


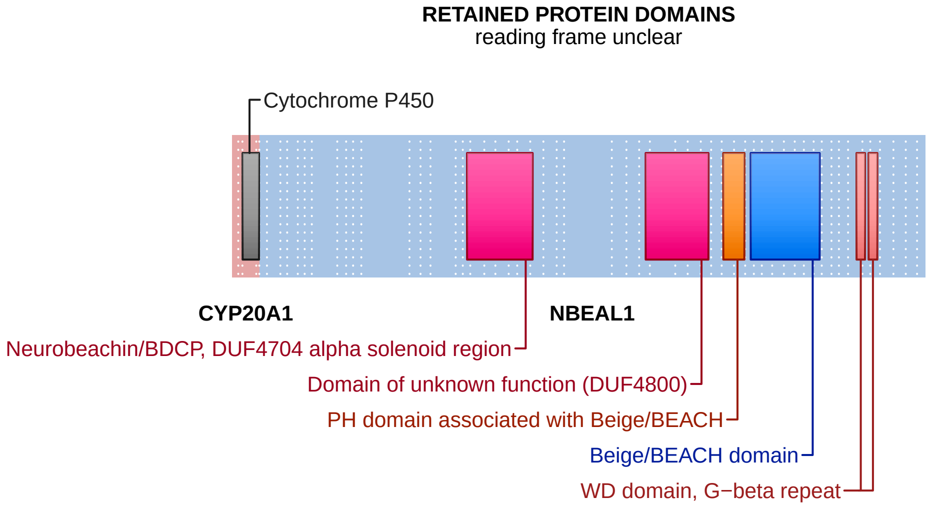


SUPPORTING READ COUNT

Split reads = 493
Discordant mates = 17

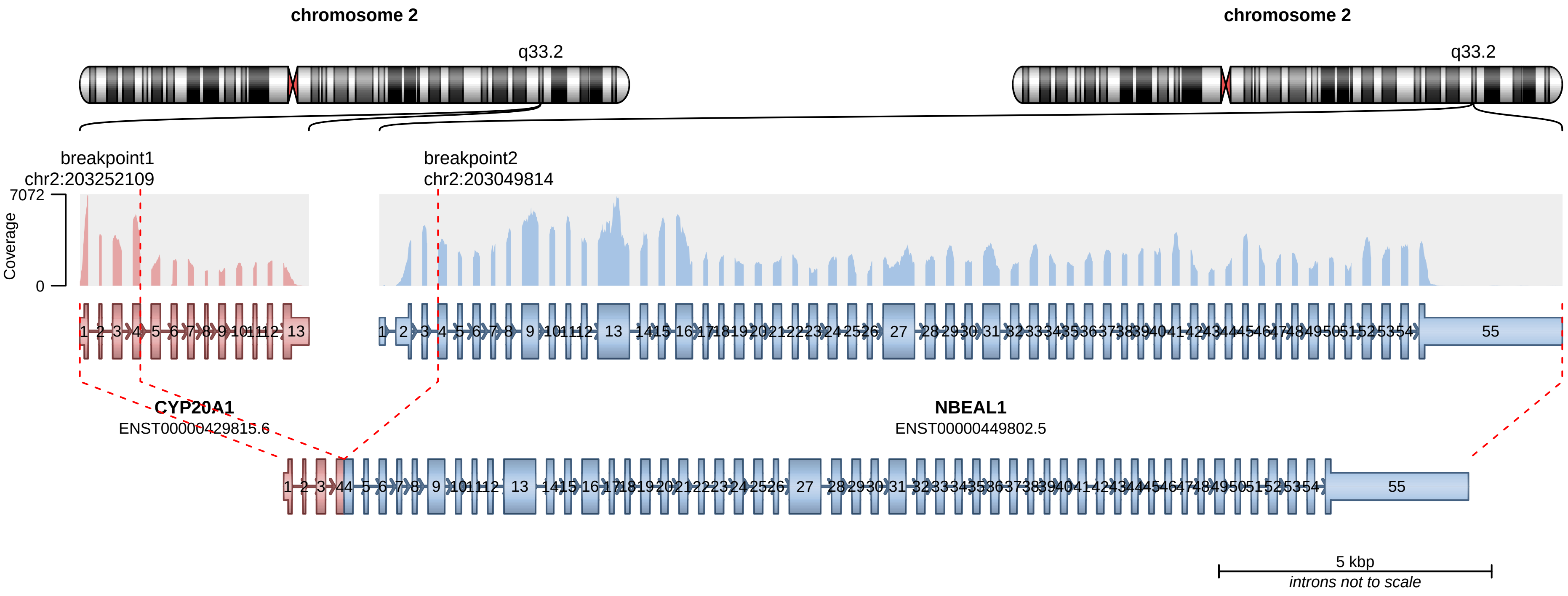


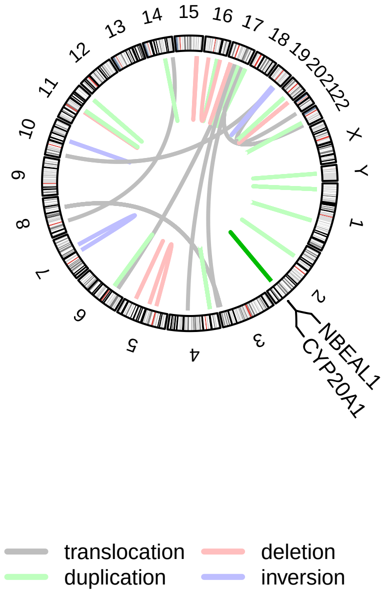




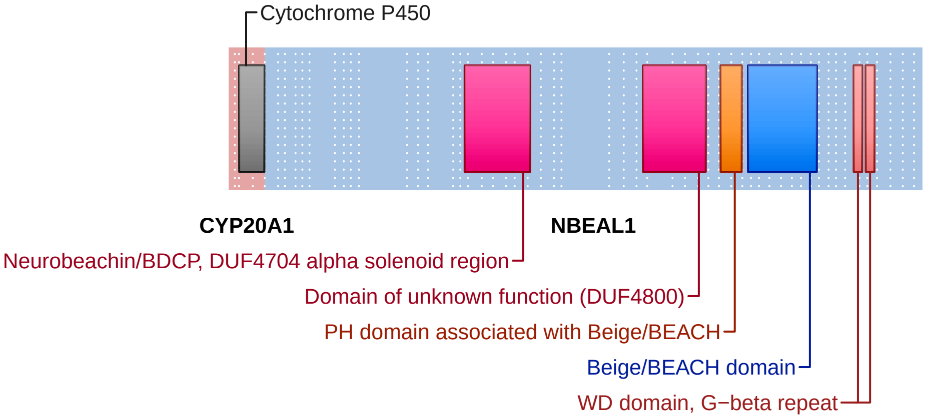
SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 1



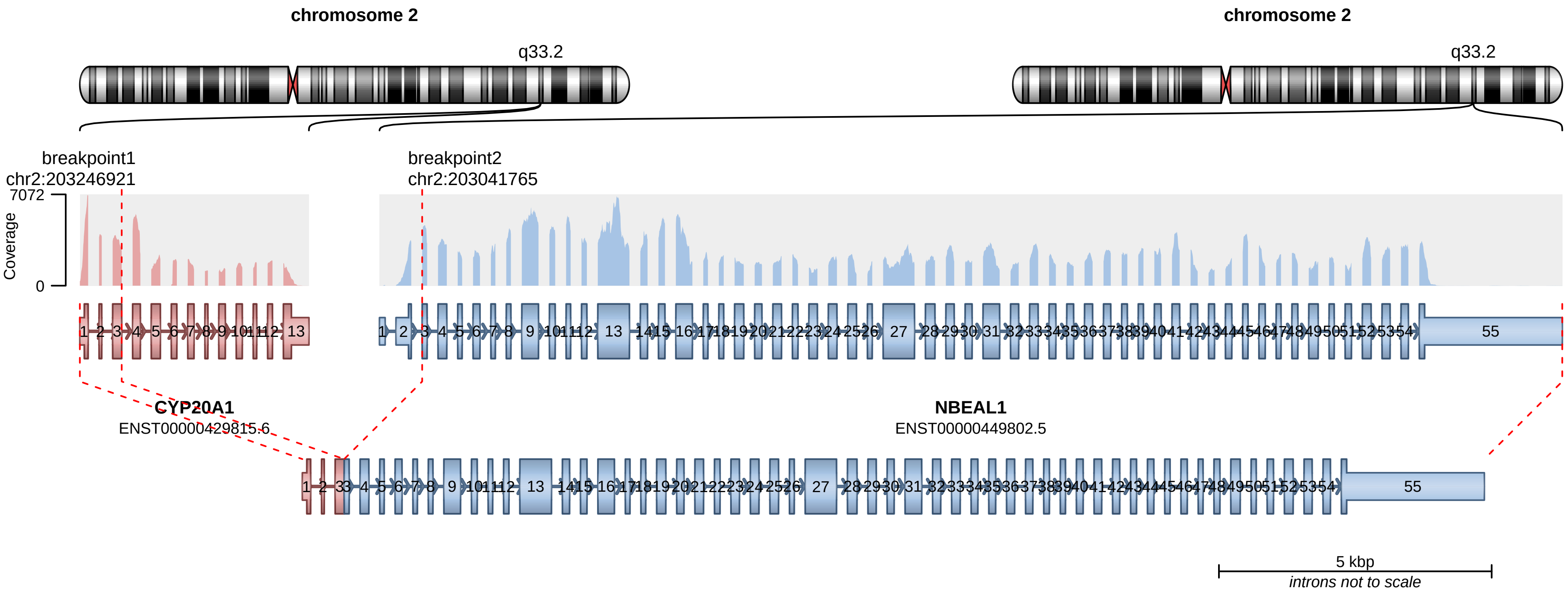


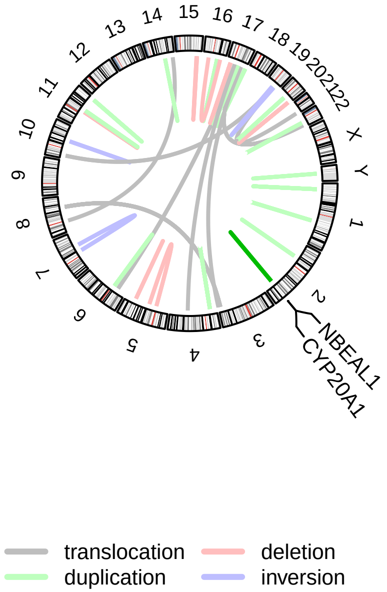
RETAINED PROTEIN DOMAINS
reading frame unclear

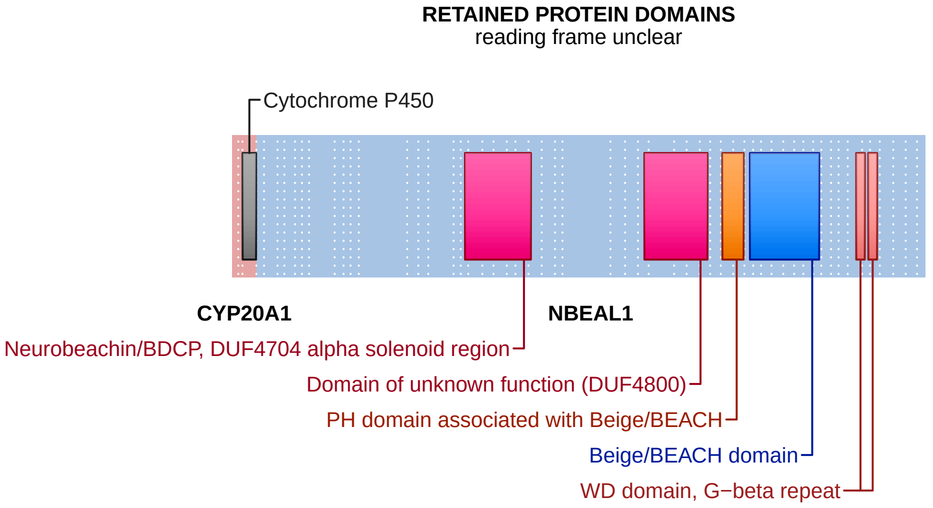


SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 7

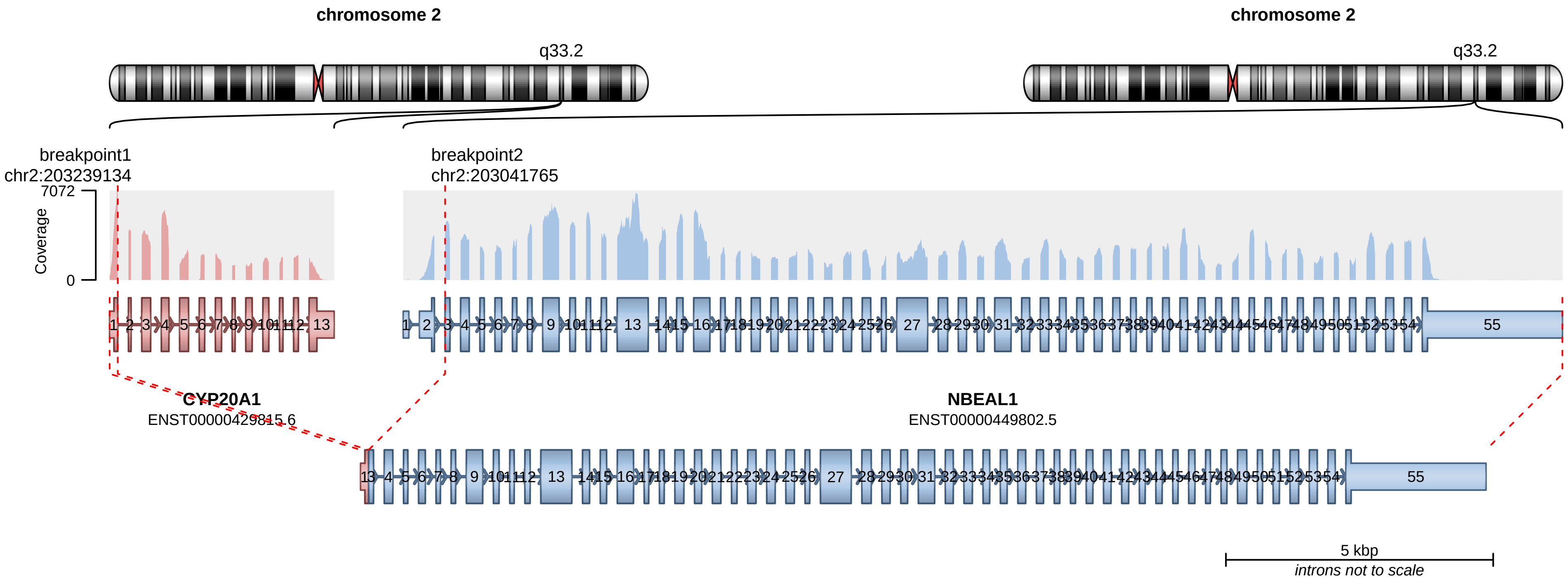


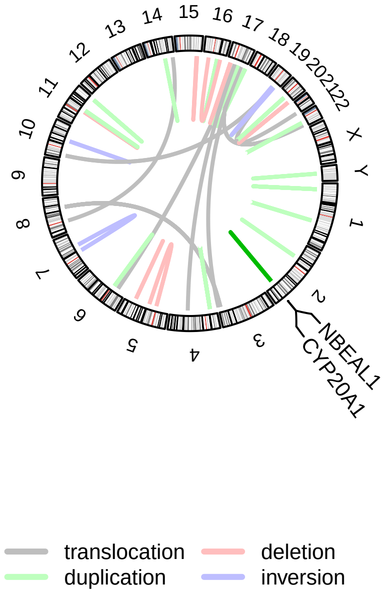


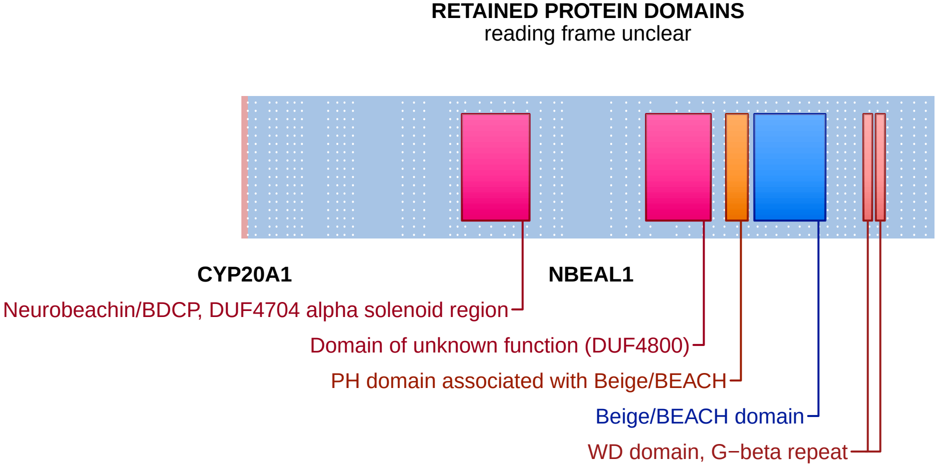


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

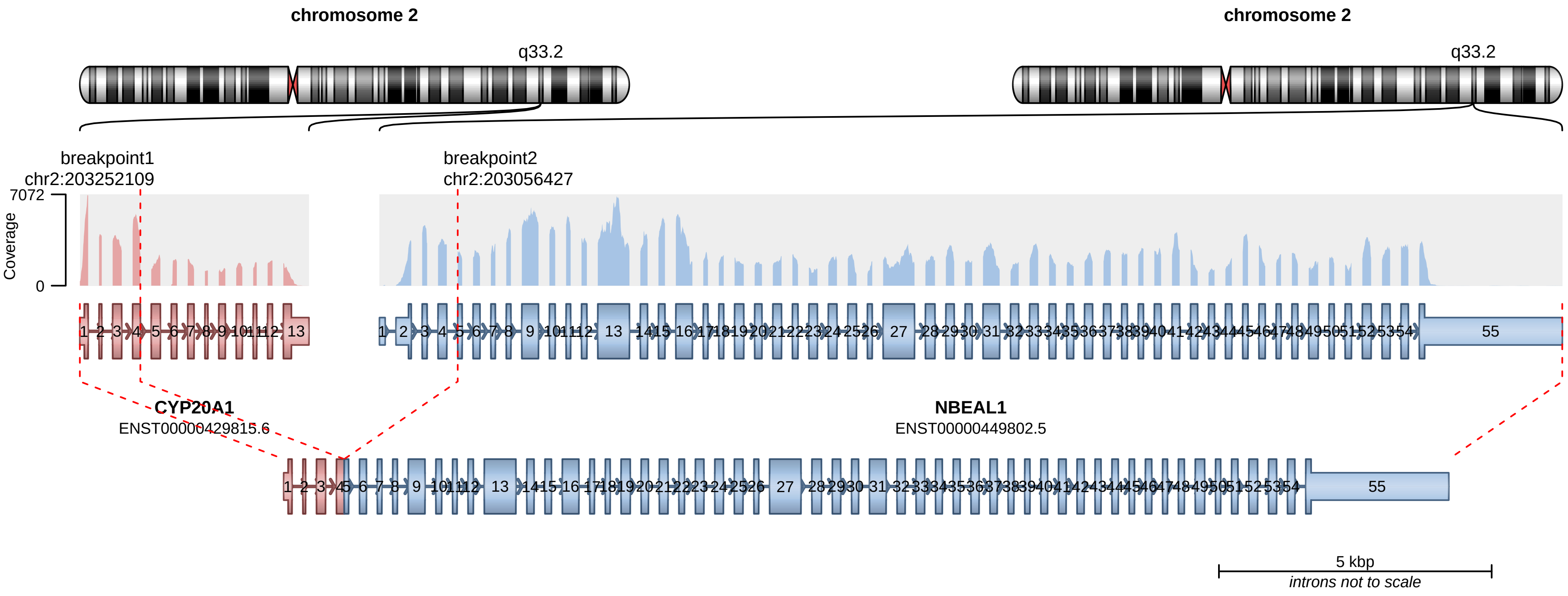


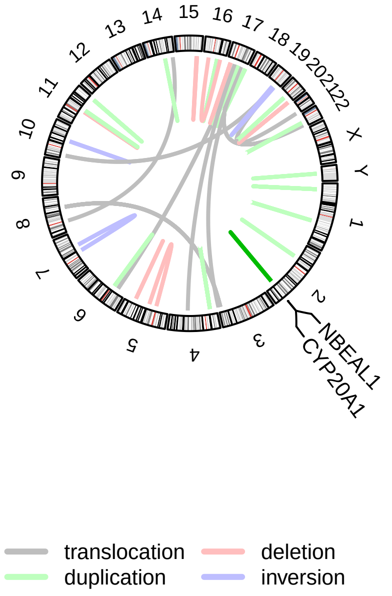




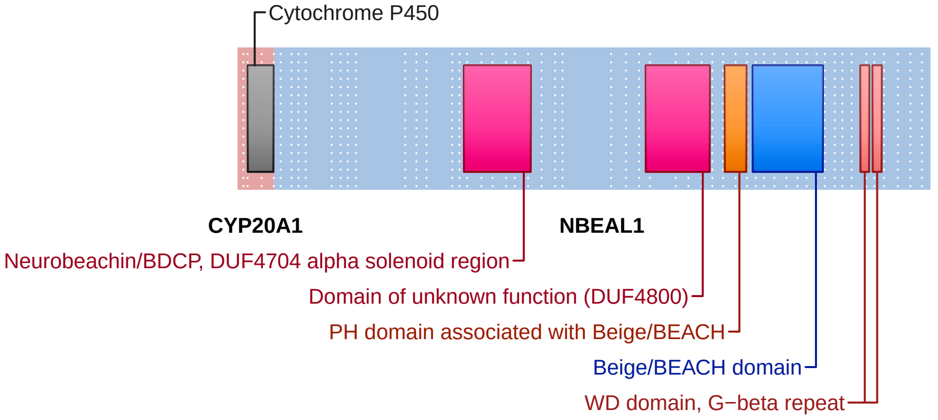
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



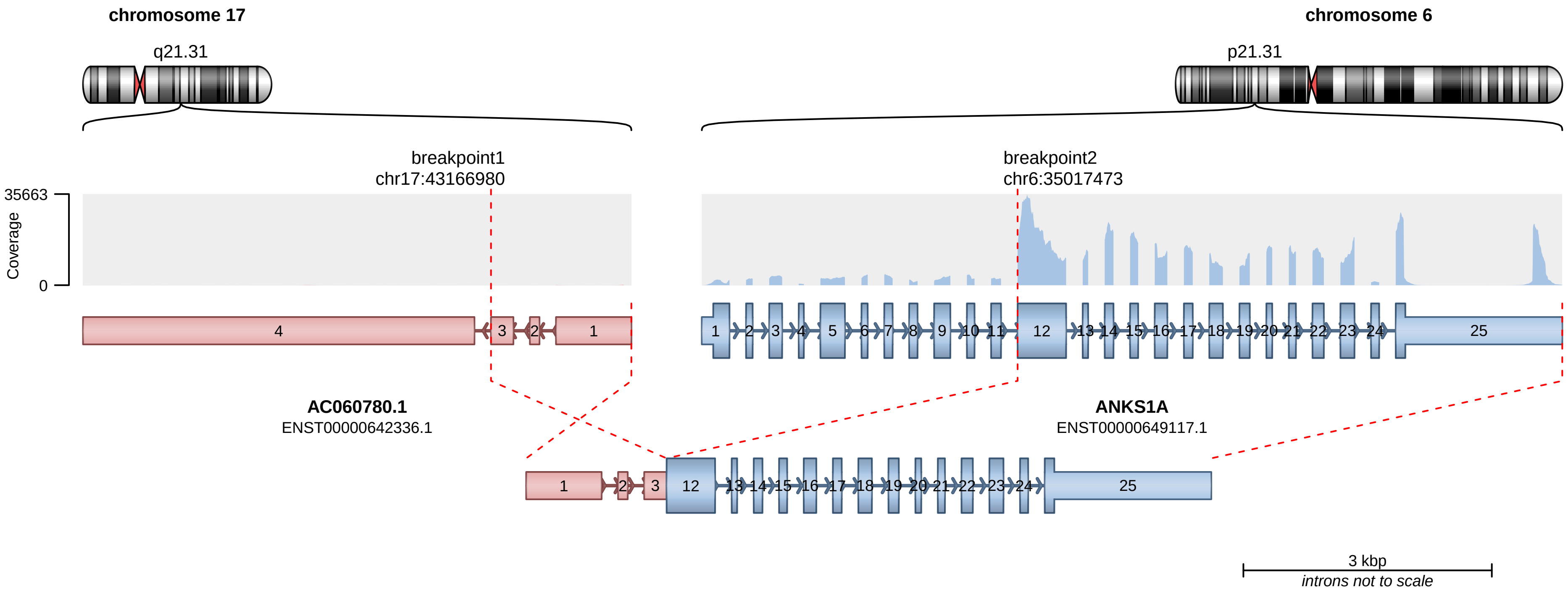


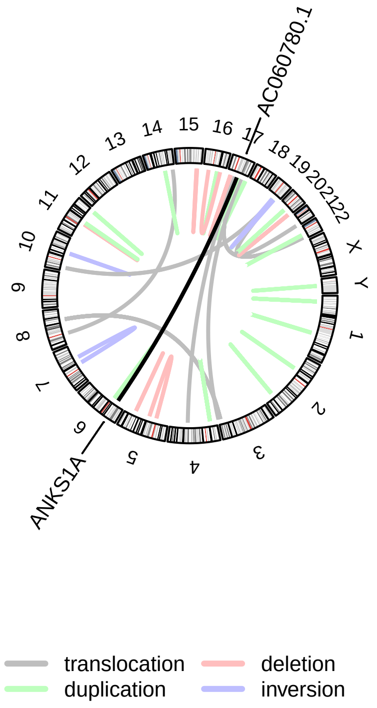
RETAINED PROTEIN DOMAINS
reading frame unclear

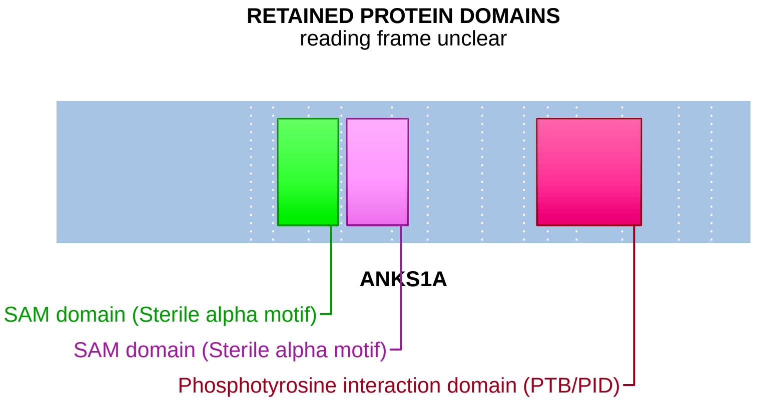


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

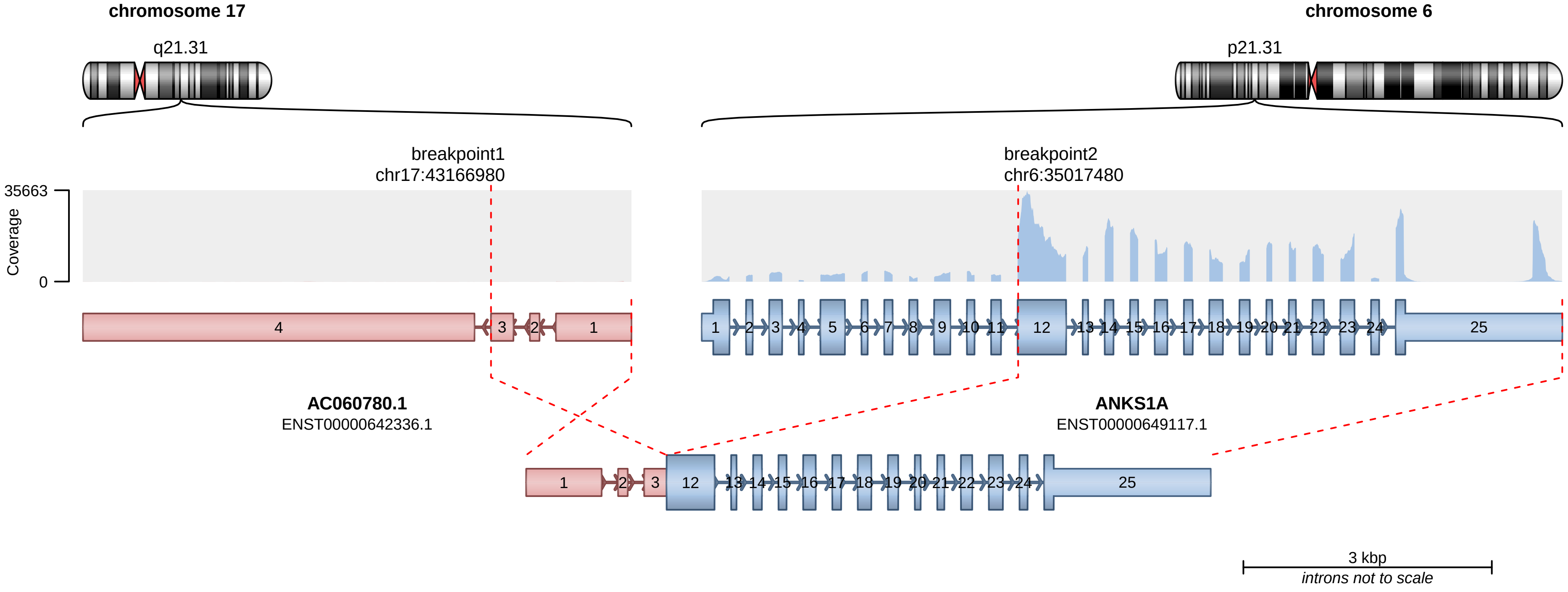


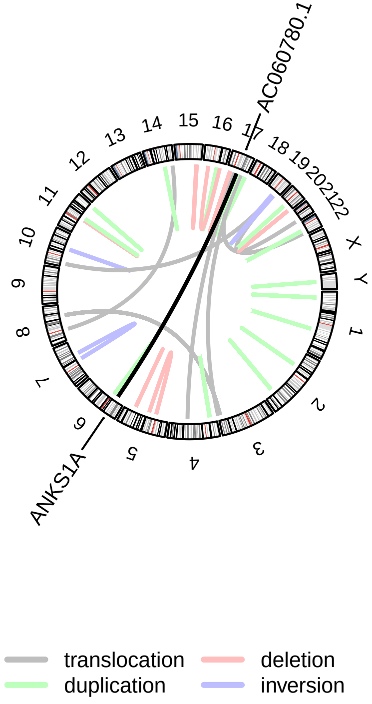


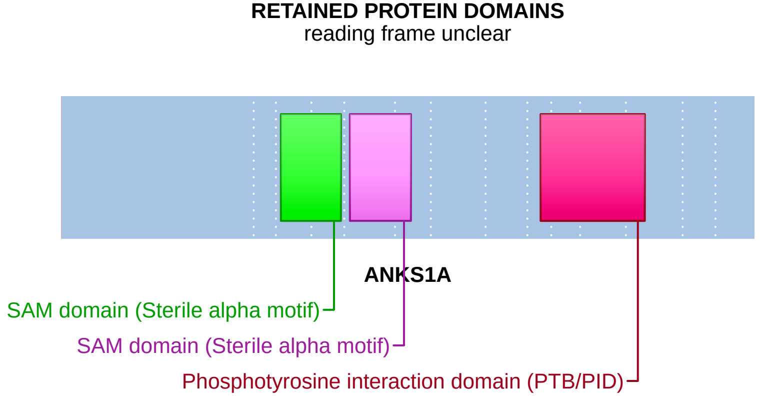


SUPPORTING READ COUNT

Split reads = 409
Discordant mates = 0

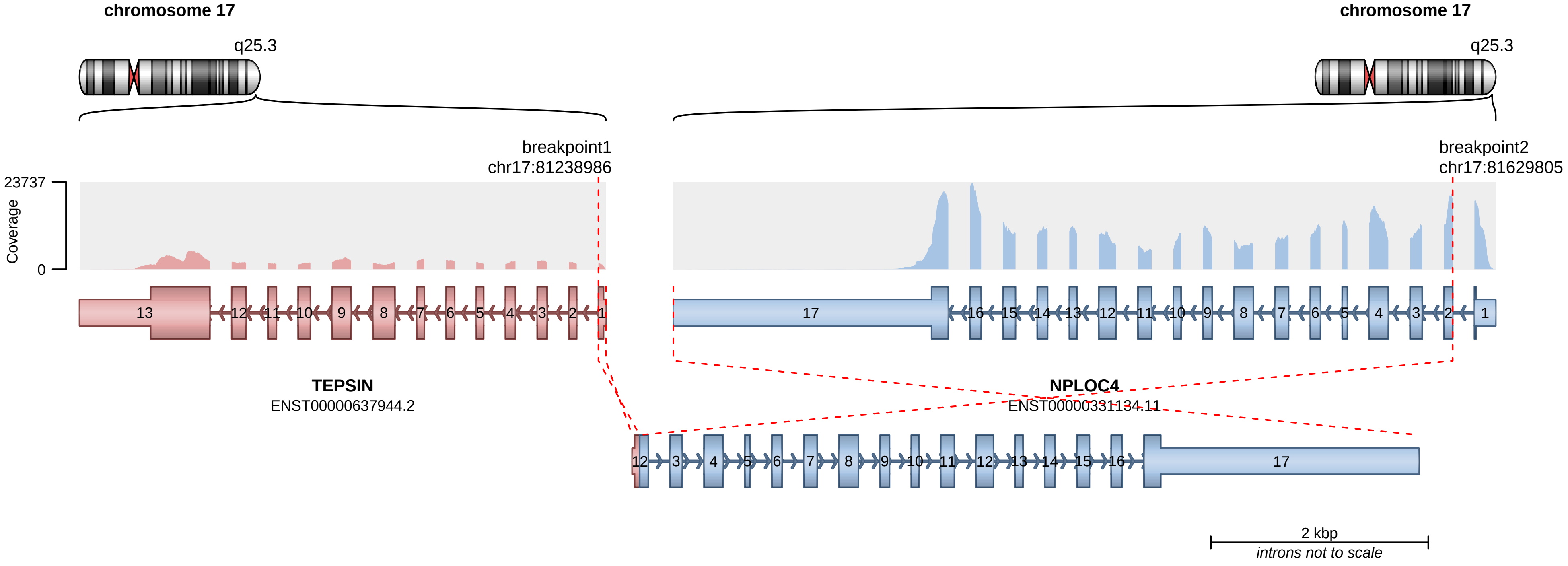


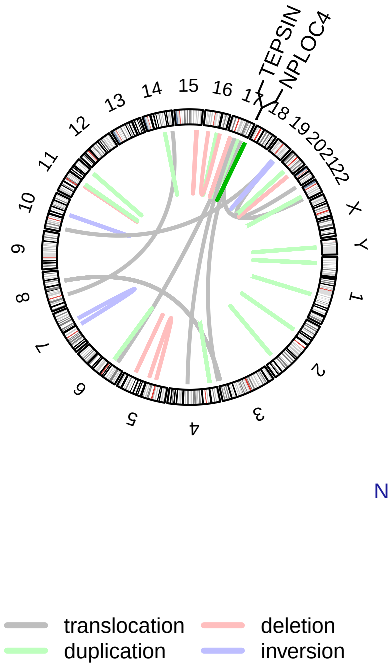




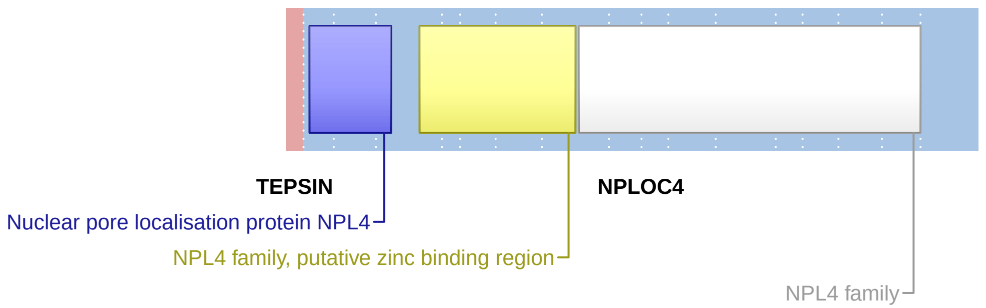
SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 0



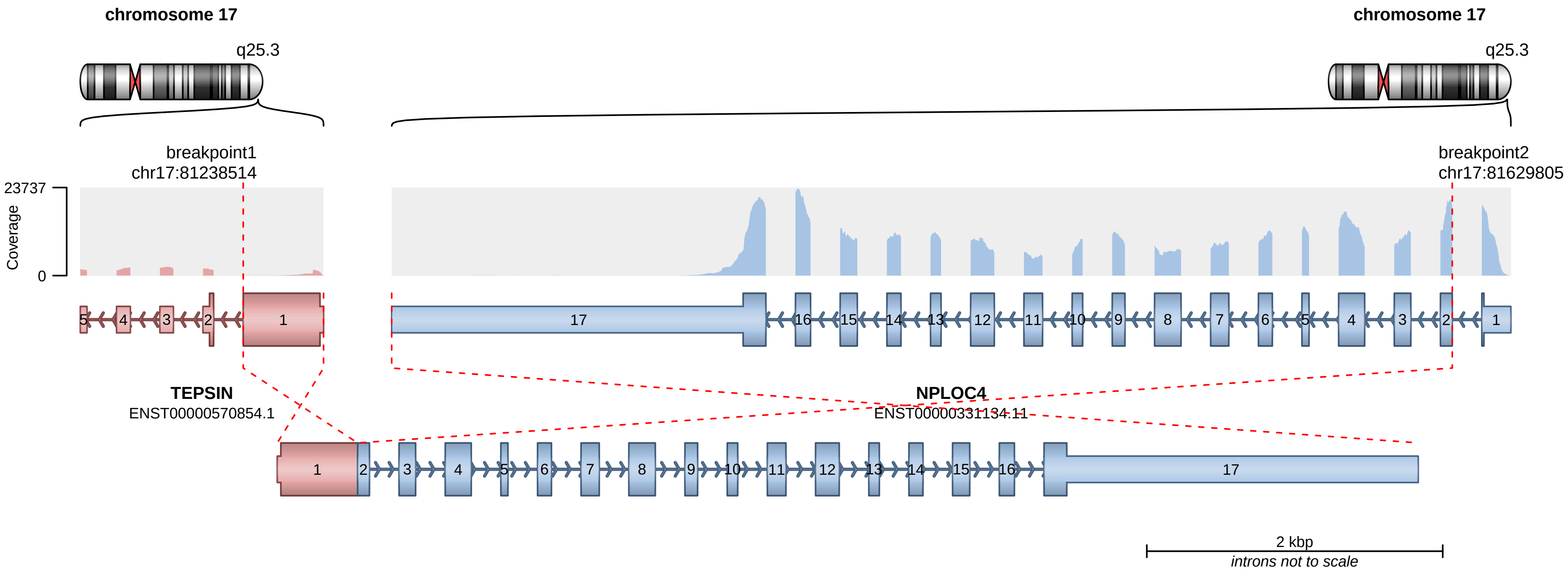


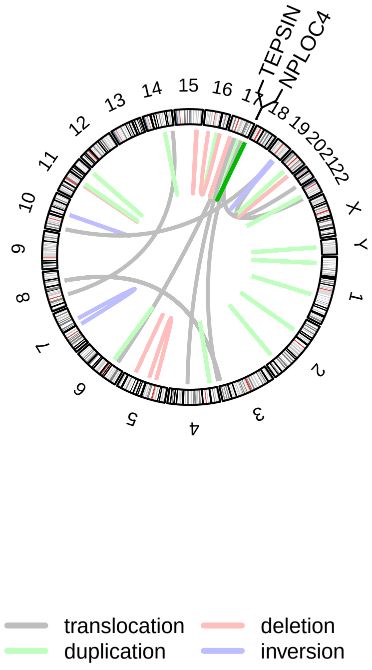
RETAINED PROTEIN DOMAINS
reading frame unclear

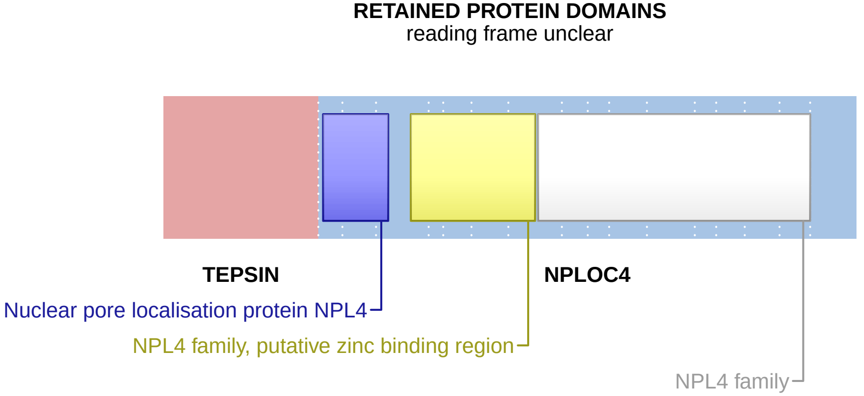


SUPPORTING READ COUNT

Split reads = 377
Discordant mates = 0

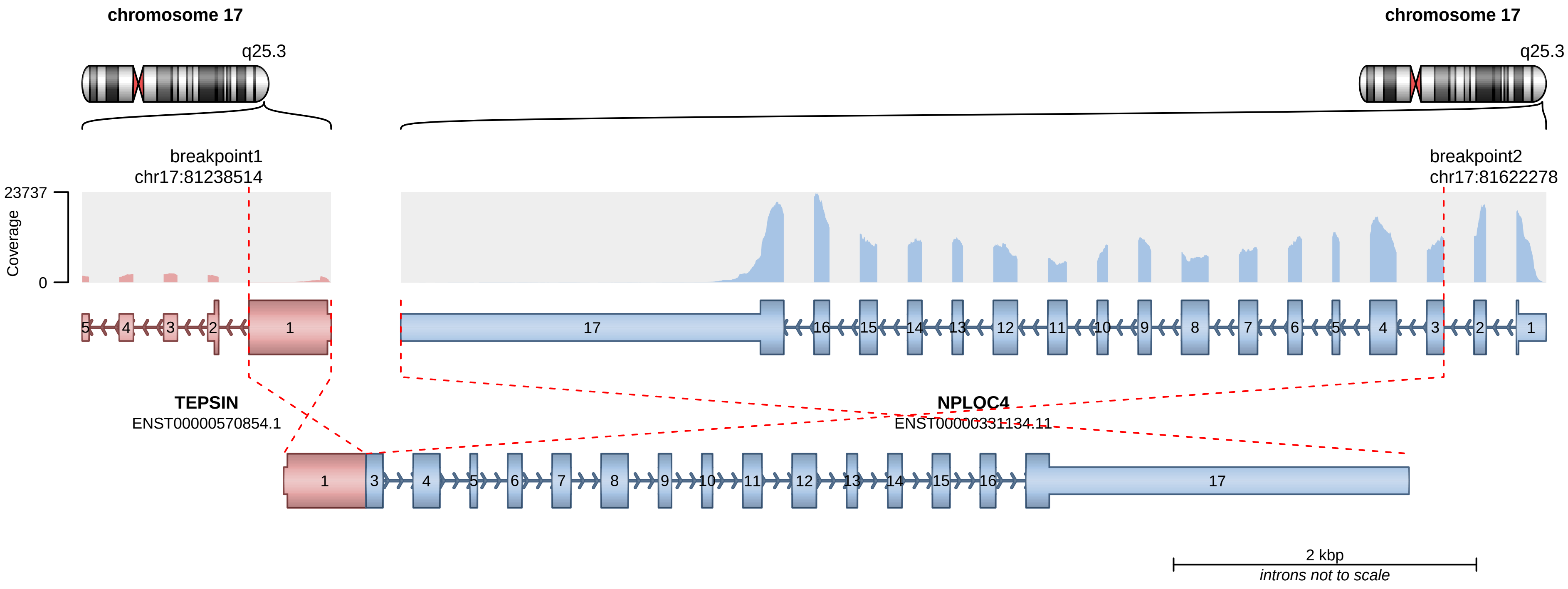


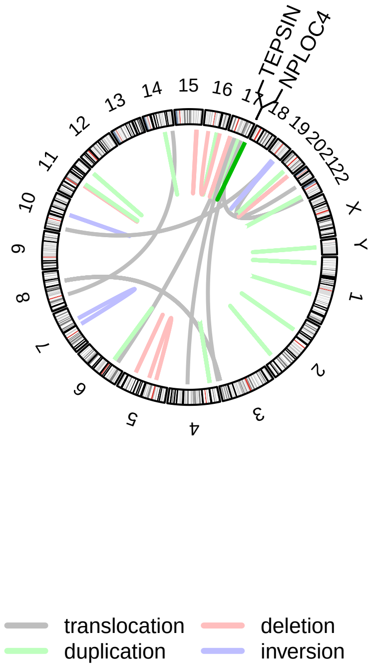


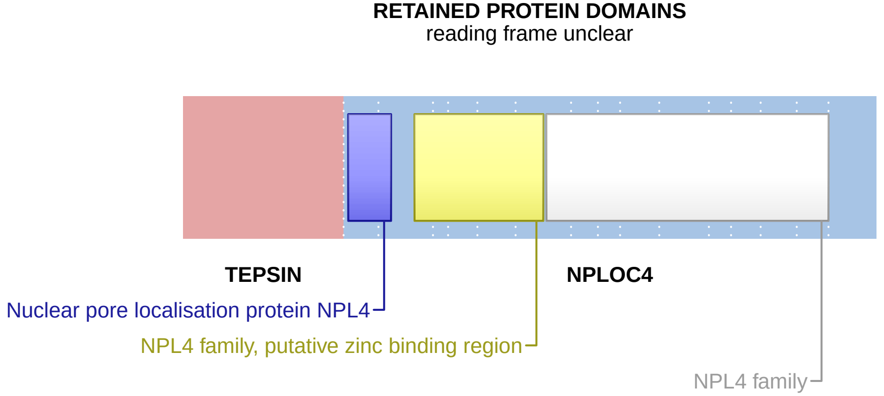


SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0

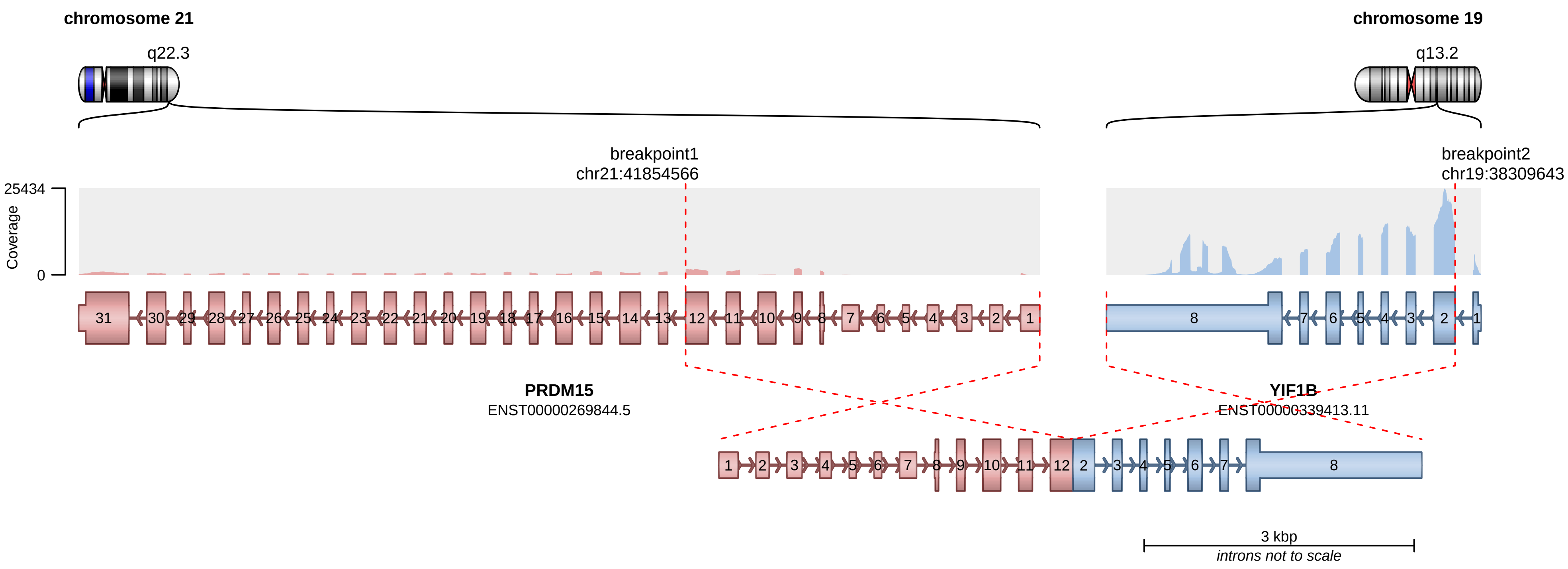


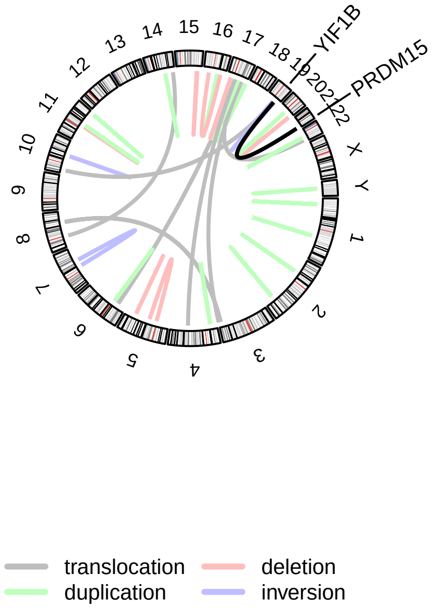




SUPPORTING READ COUNT

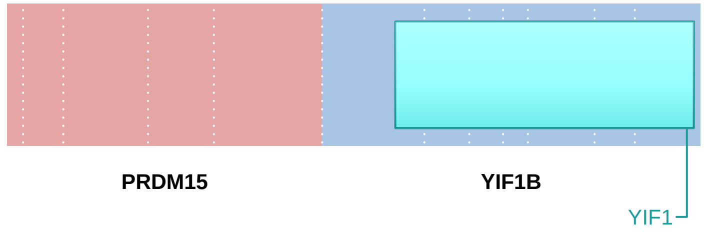
Split reads = 1
Discordant mates = 0





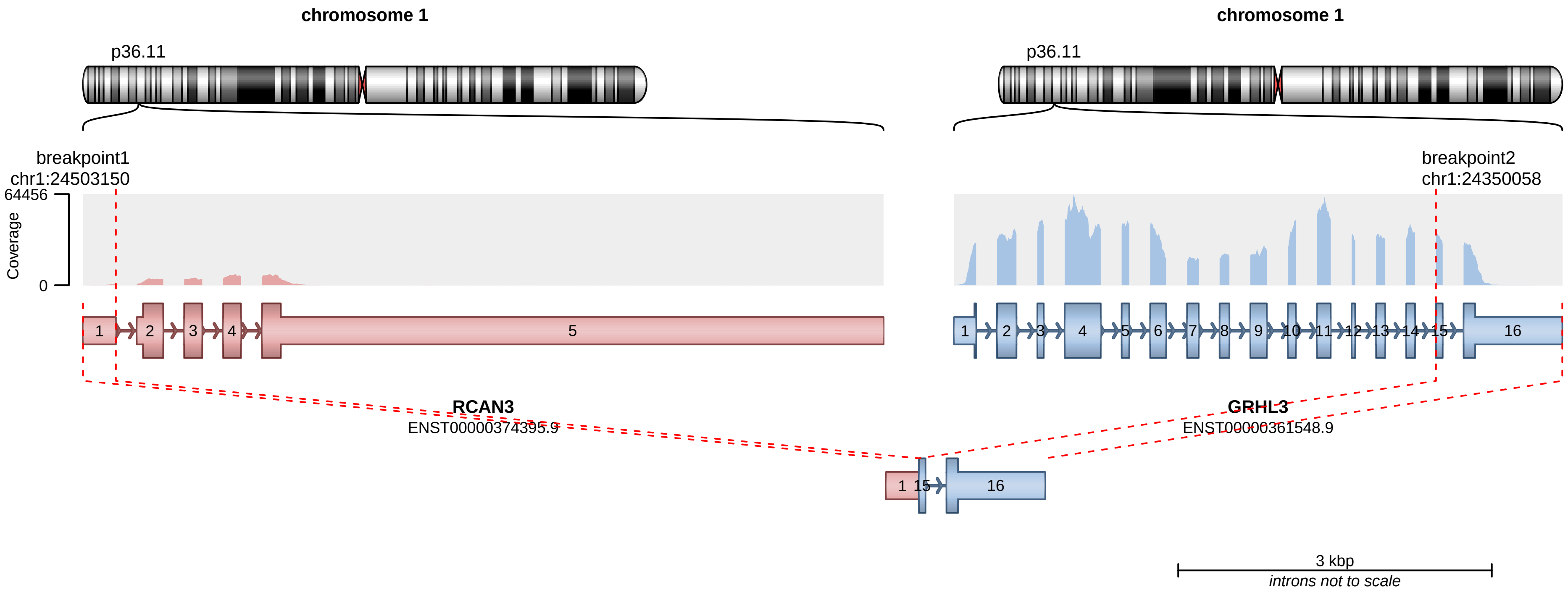
RETAINED PROTEIN DOMAINS

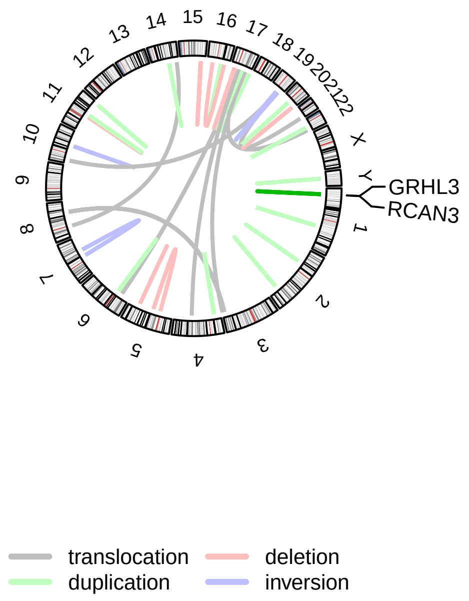
reading frame unclear



SUPPORTING READ COUNT

Split reads = 351
Discordant mates = 8

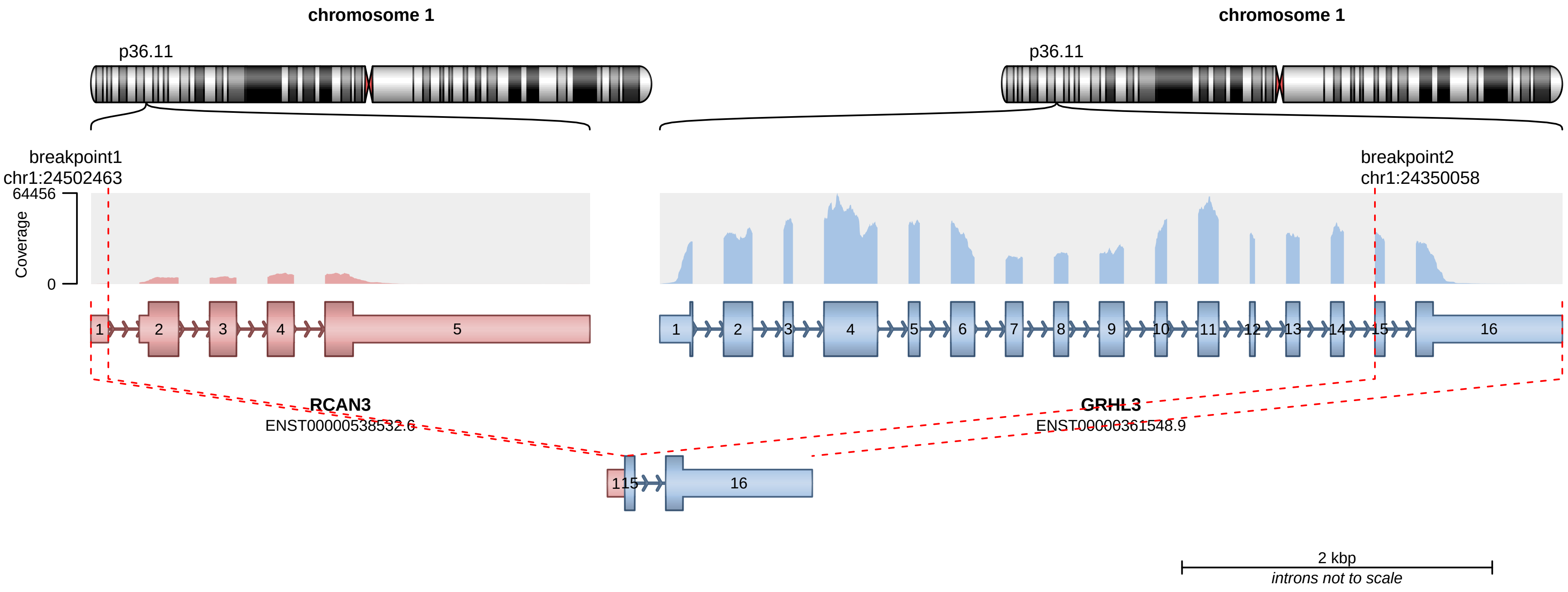


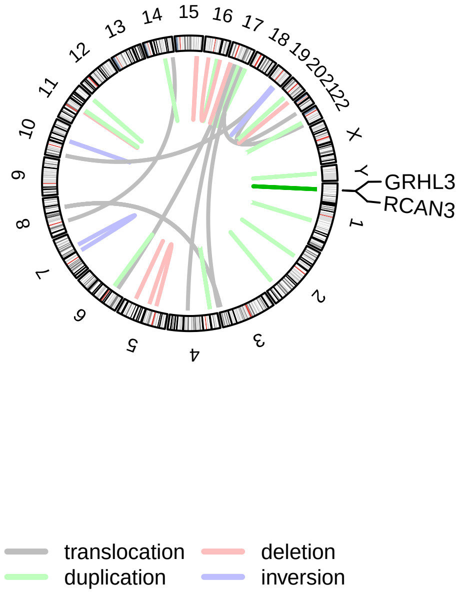


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 338
Discordant mates = 9

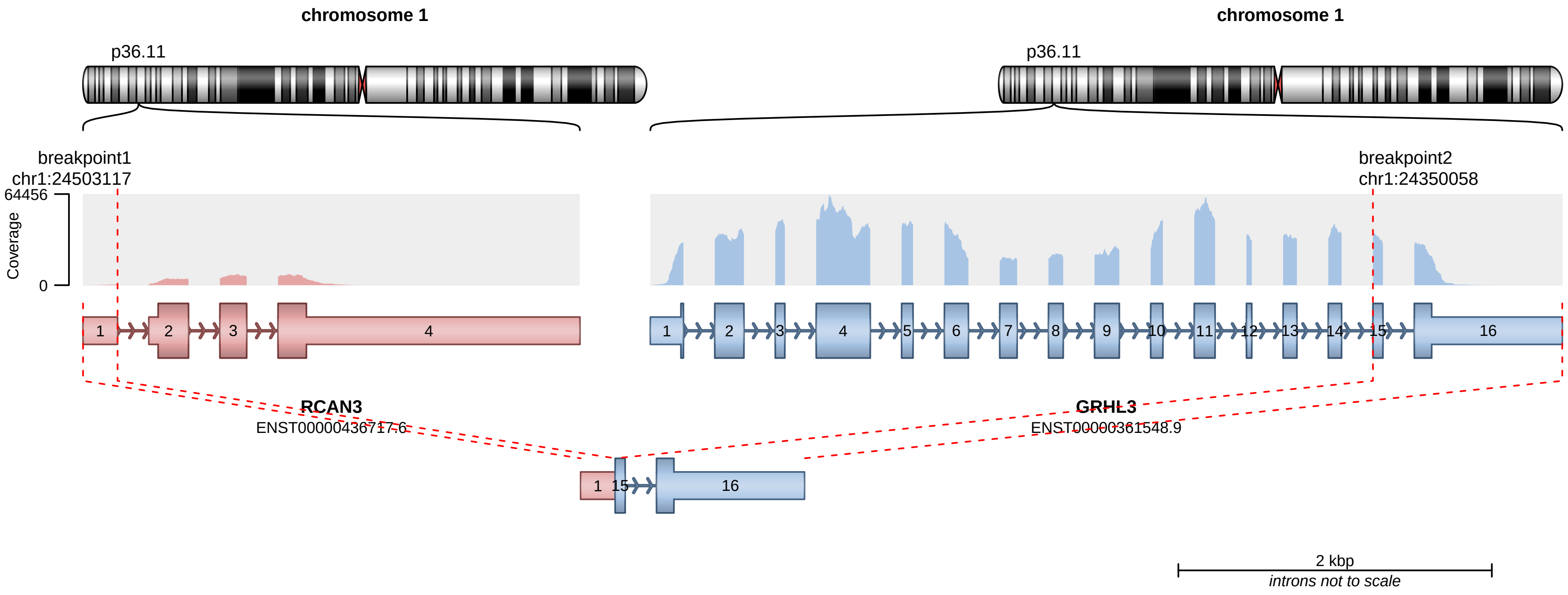


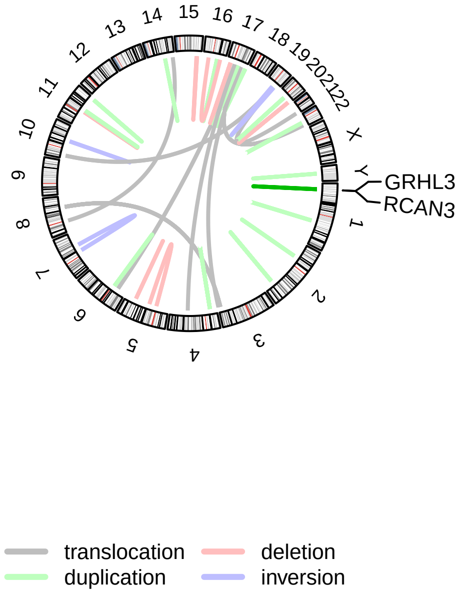


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 153
Discordant mates = 0

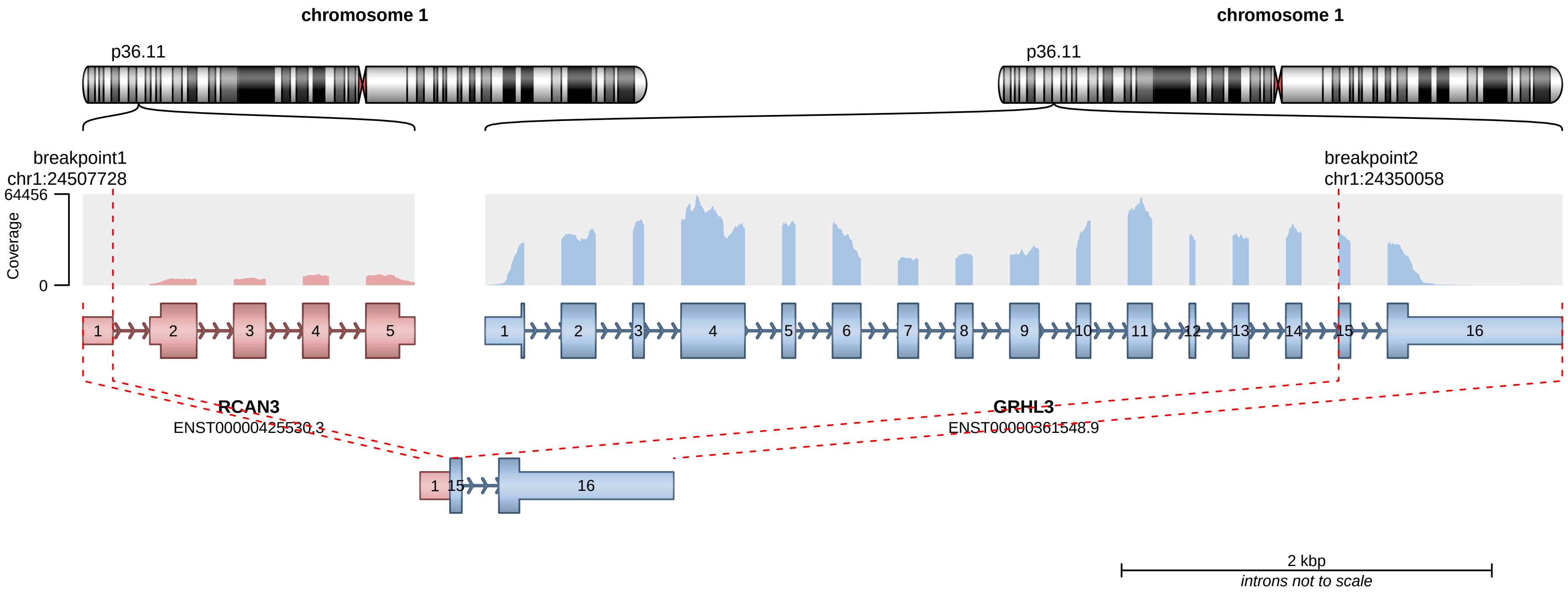


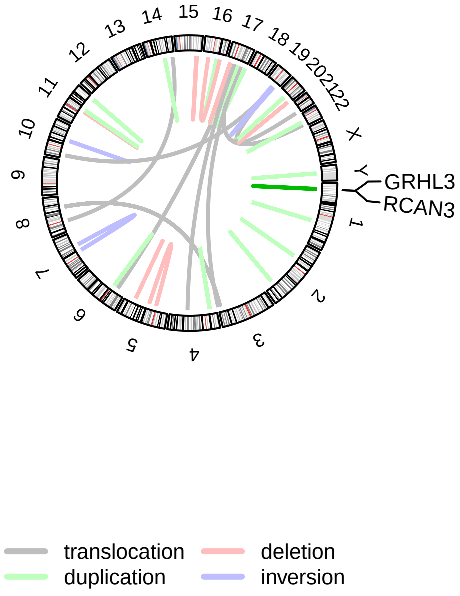


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 57
Discordant mates = 2

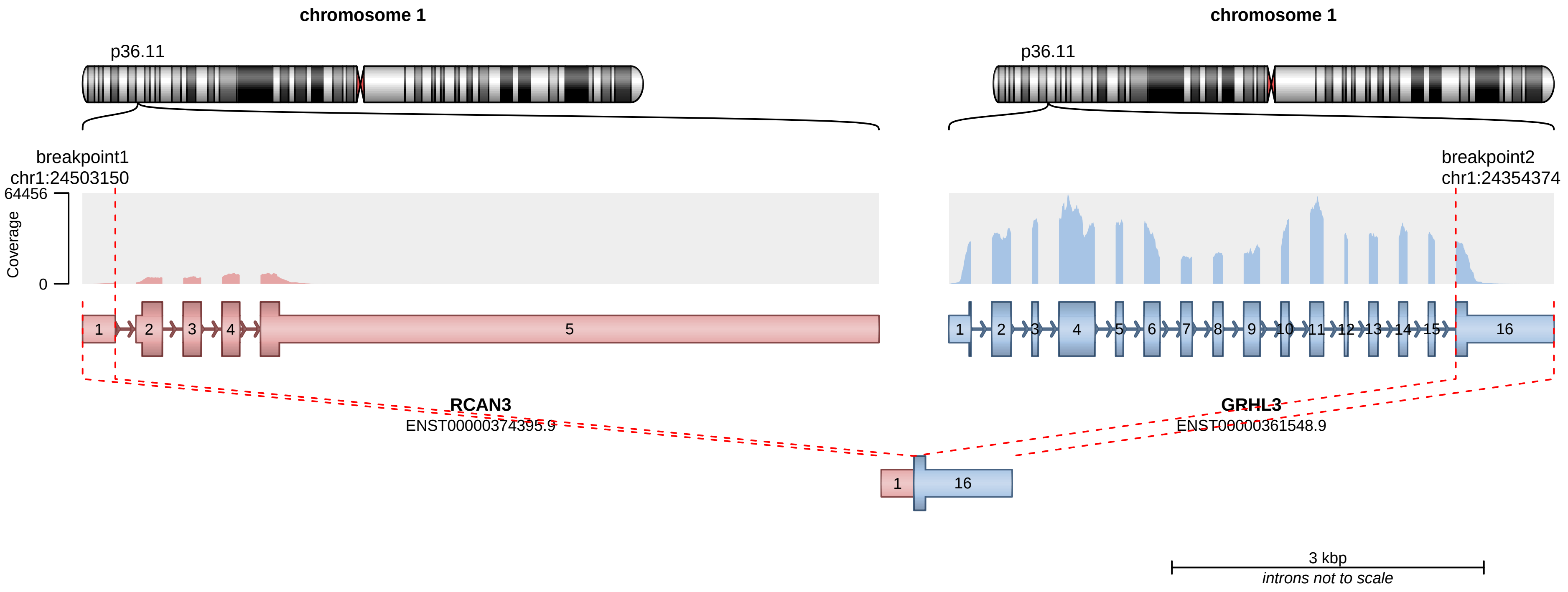


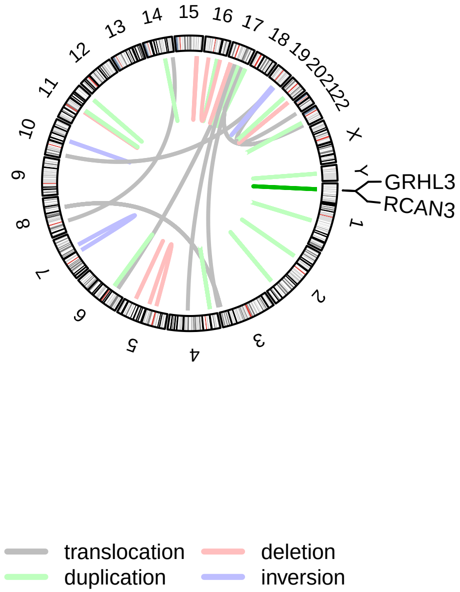


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 9

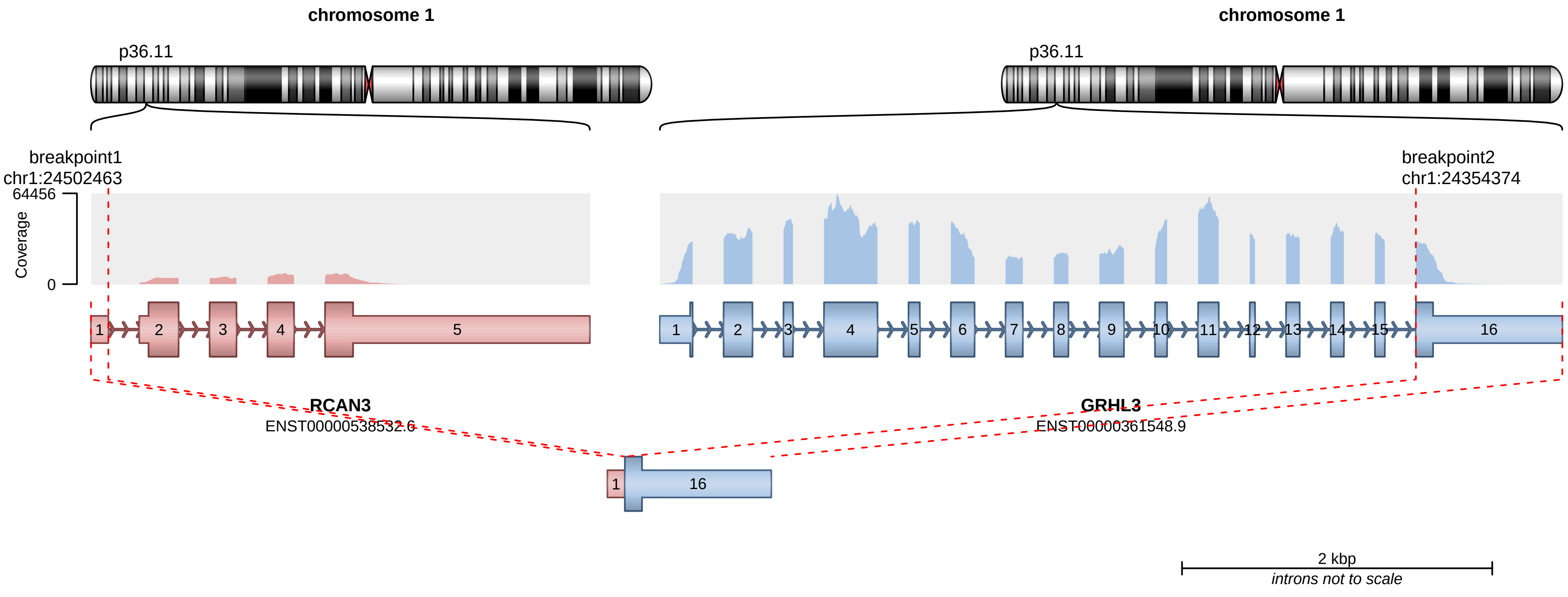


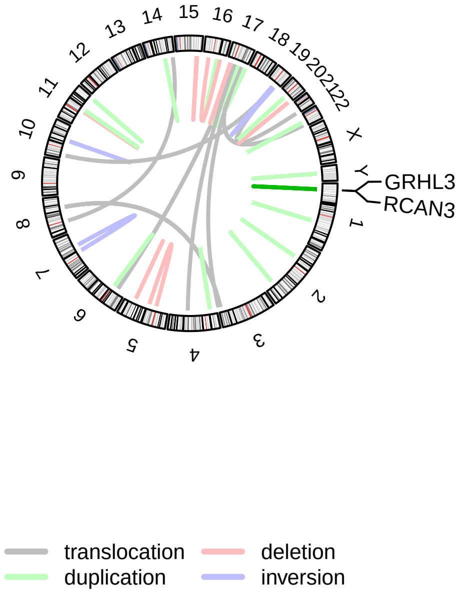


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 2

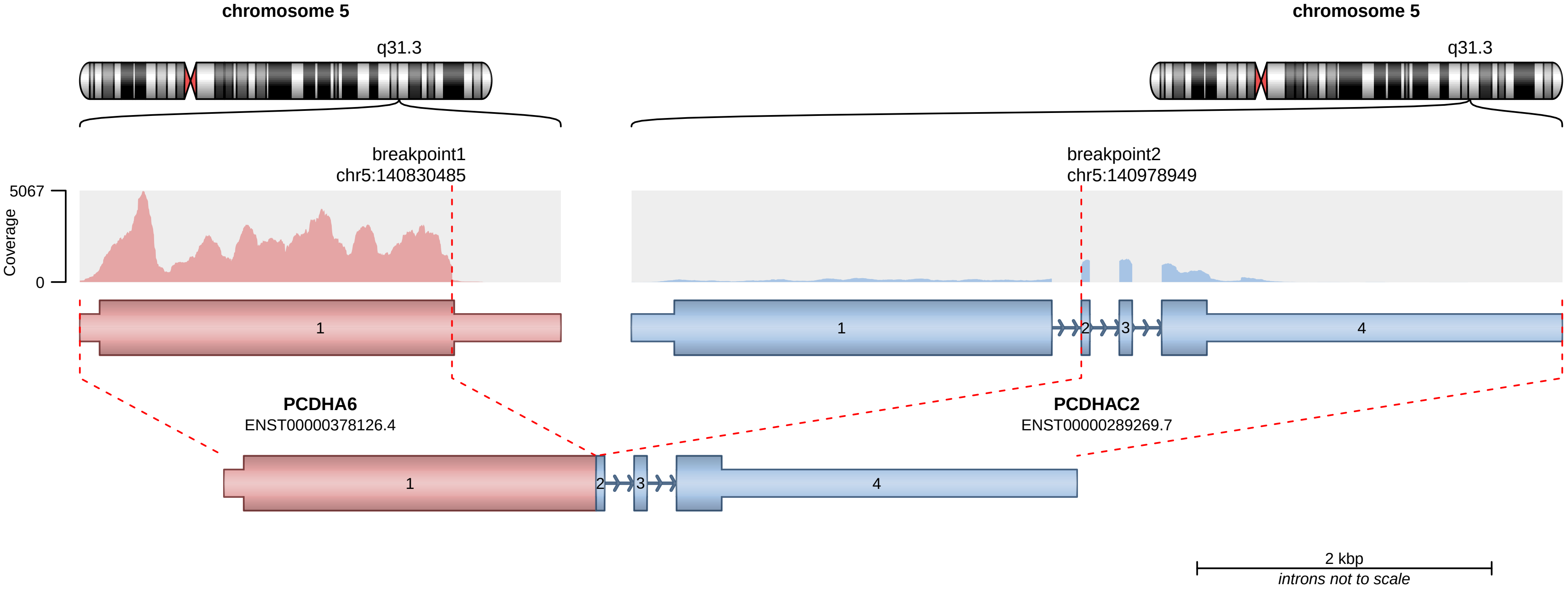


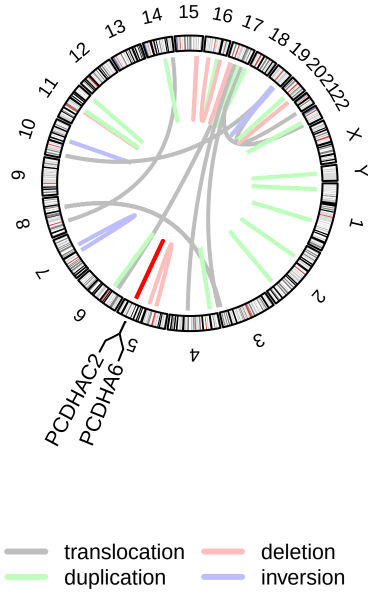


No protein domains retained in fusion.

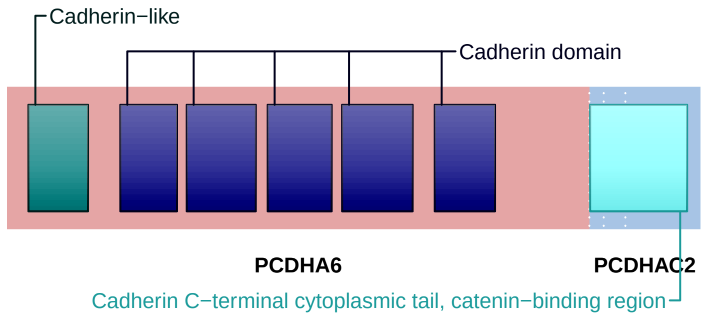
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



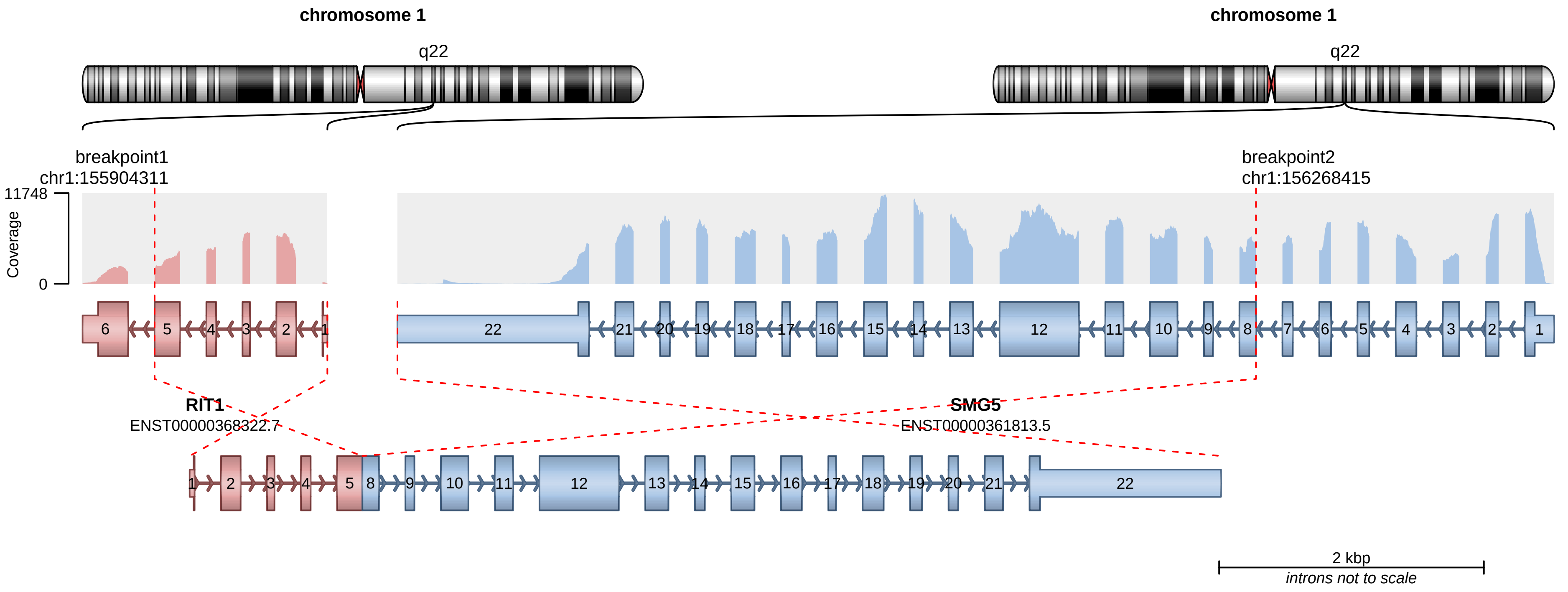


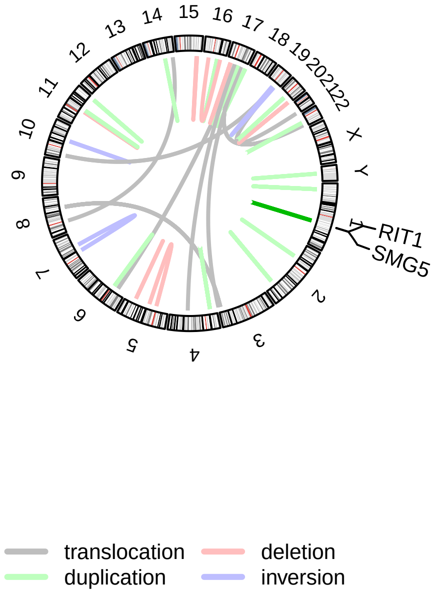
RETAINED PROTEIN DOMAINS
reading frame unclear

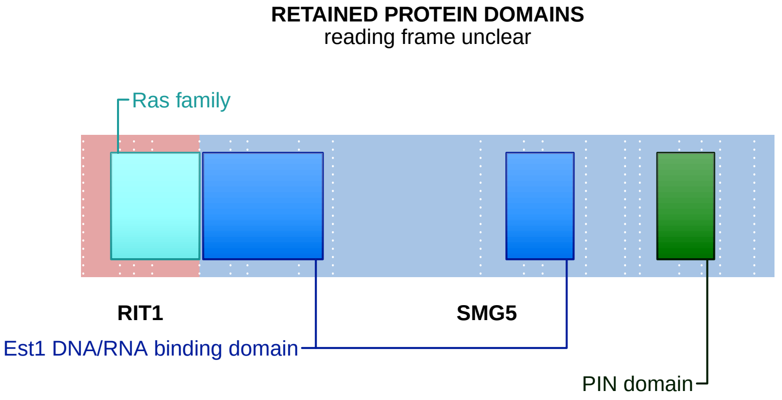


SUPPORTING READ COUNT

Split reads = 329
Discordant mates = 4

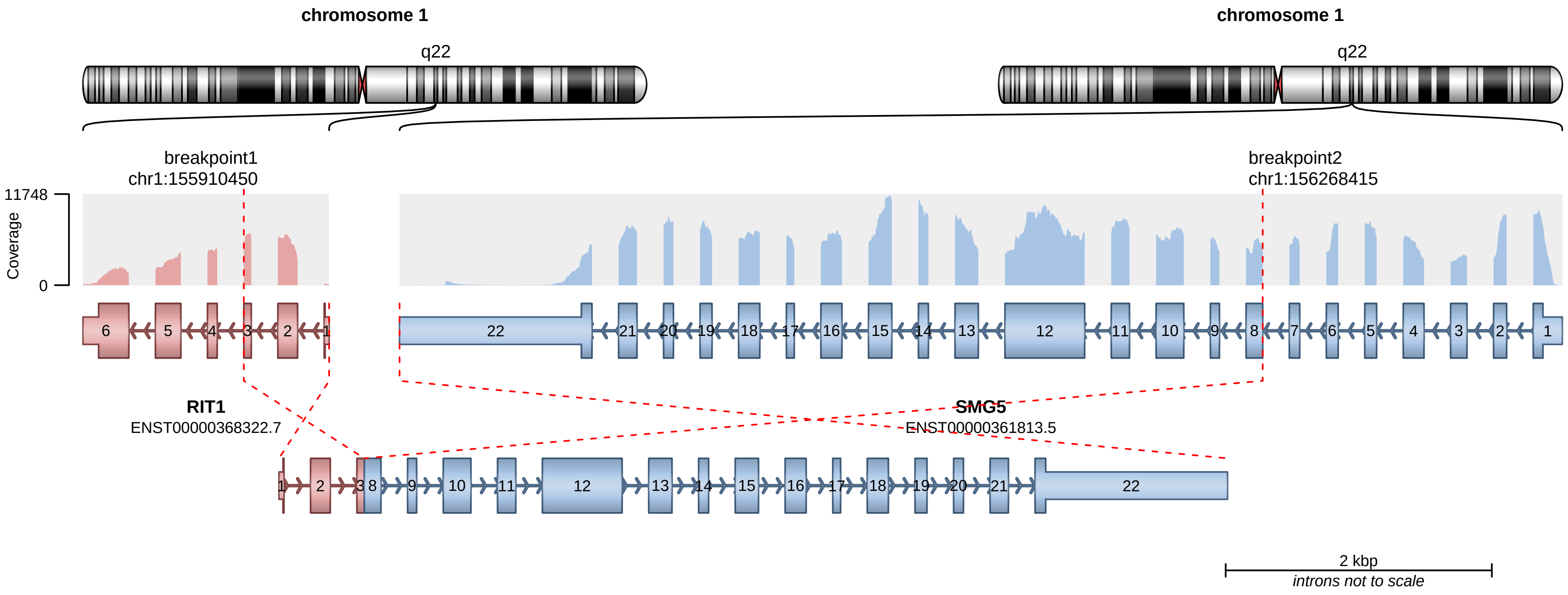


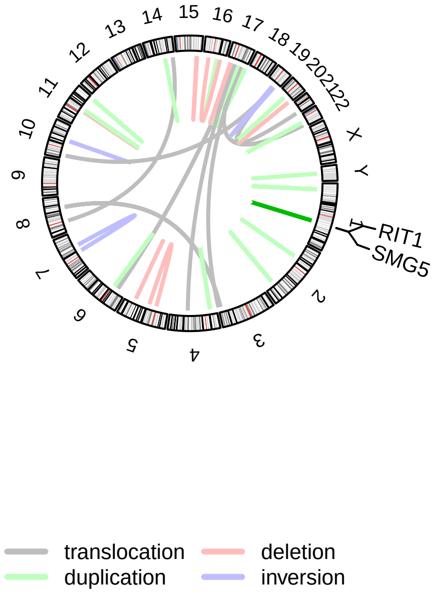




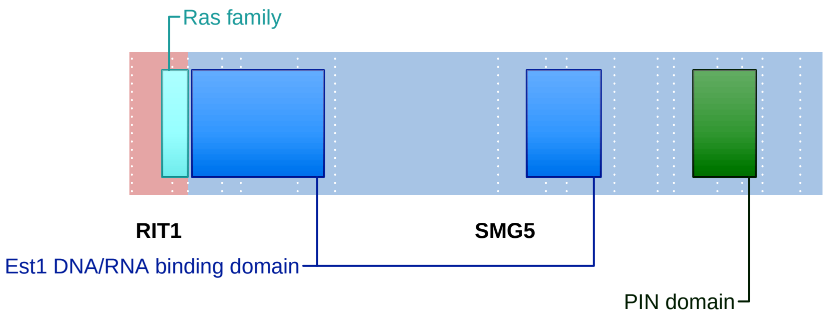
SUPPORTING READ COUNT

Split reads = 297
Discordant mates = 12



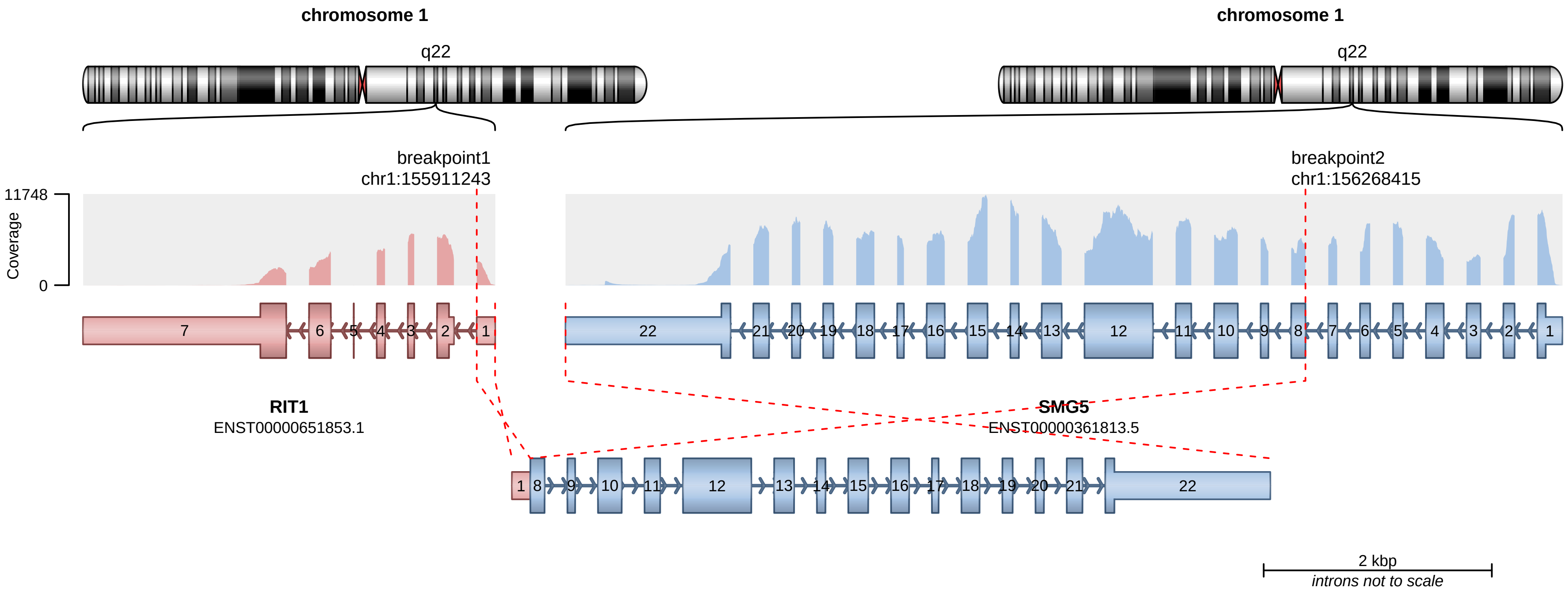


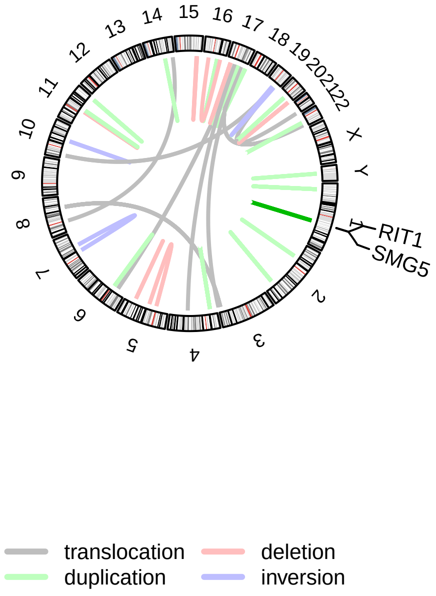
RETAINED PROTEIN DOMAINS
reading frame unclear

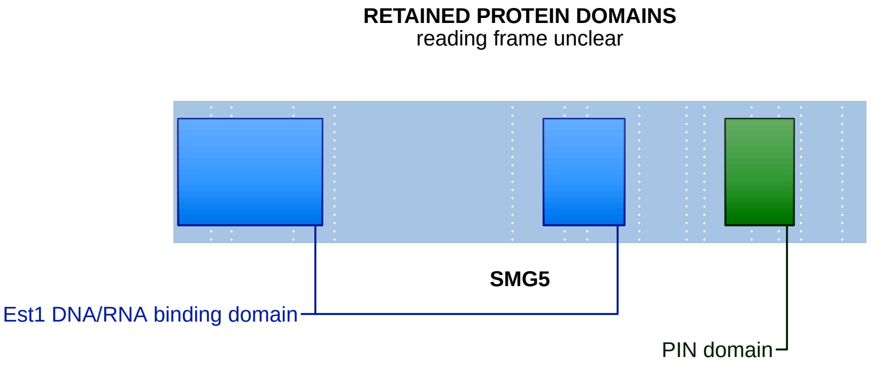


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

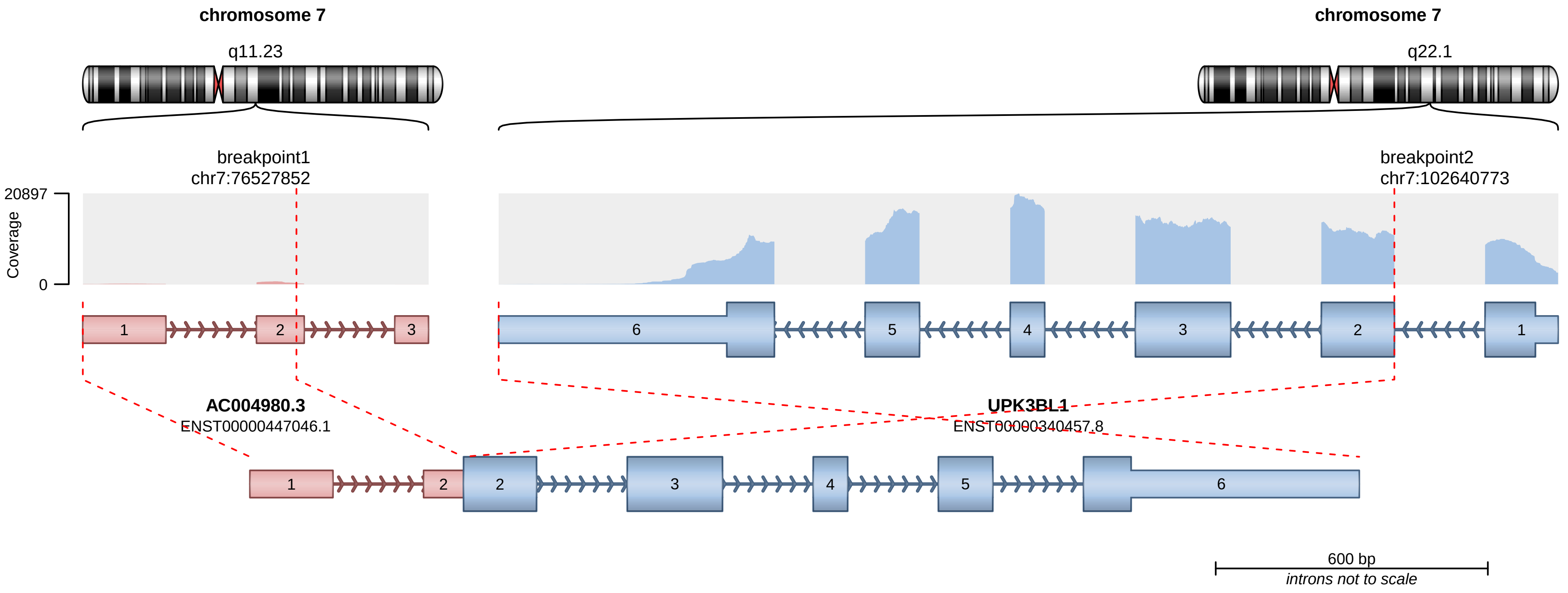


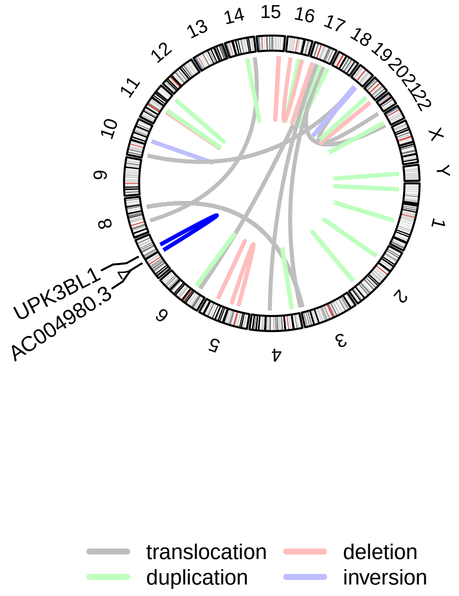




SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

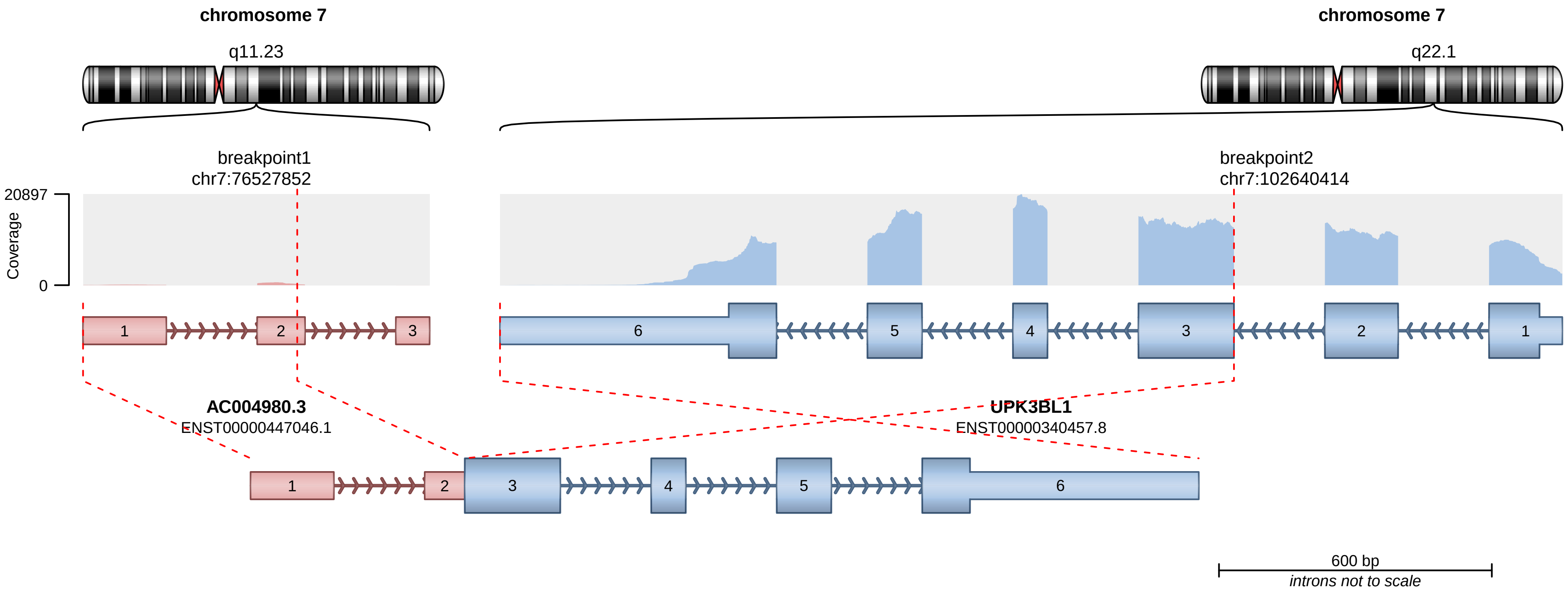


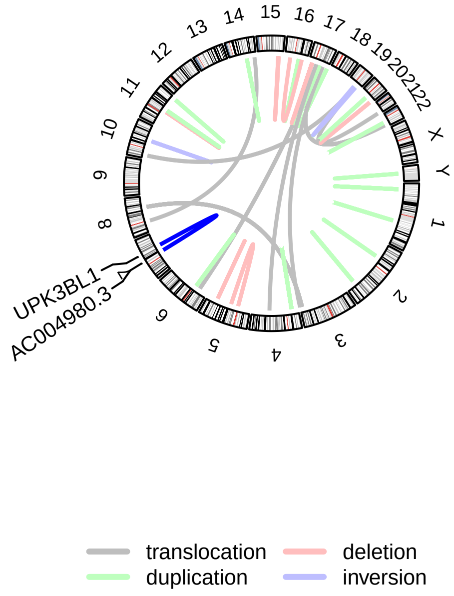


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 259
Discordant mates = 1

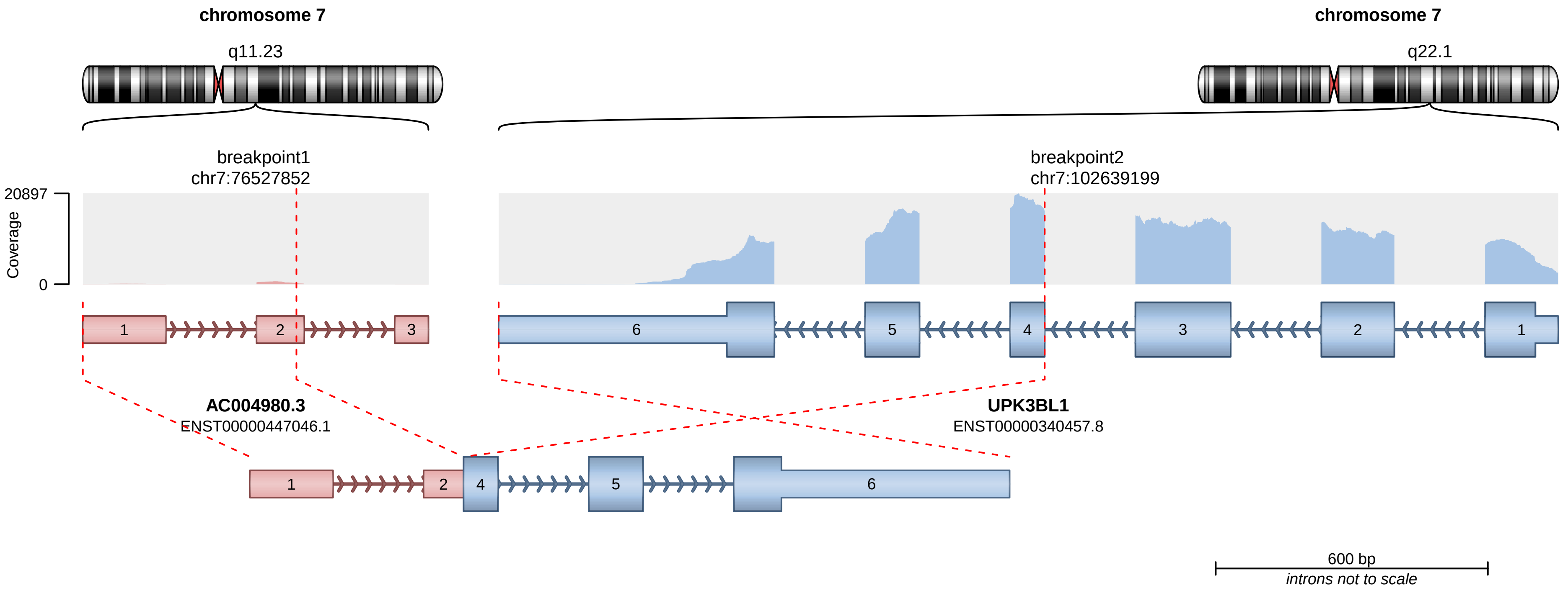


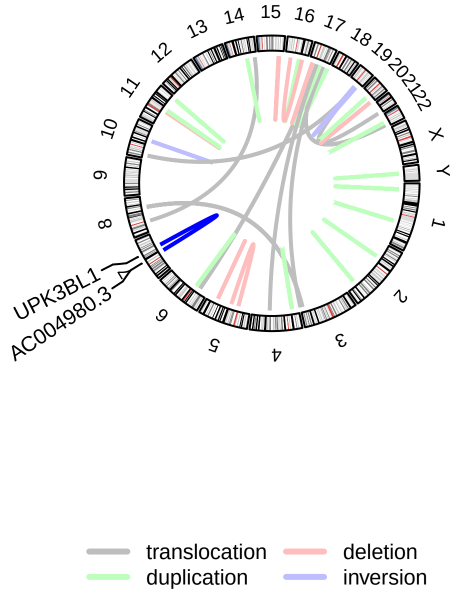


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

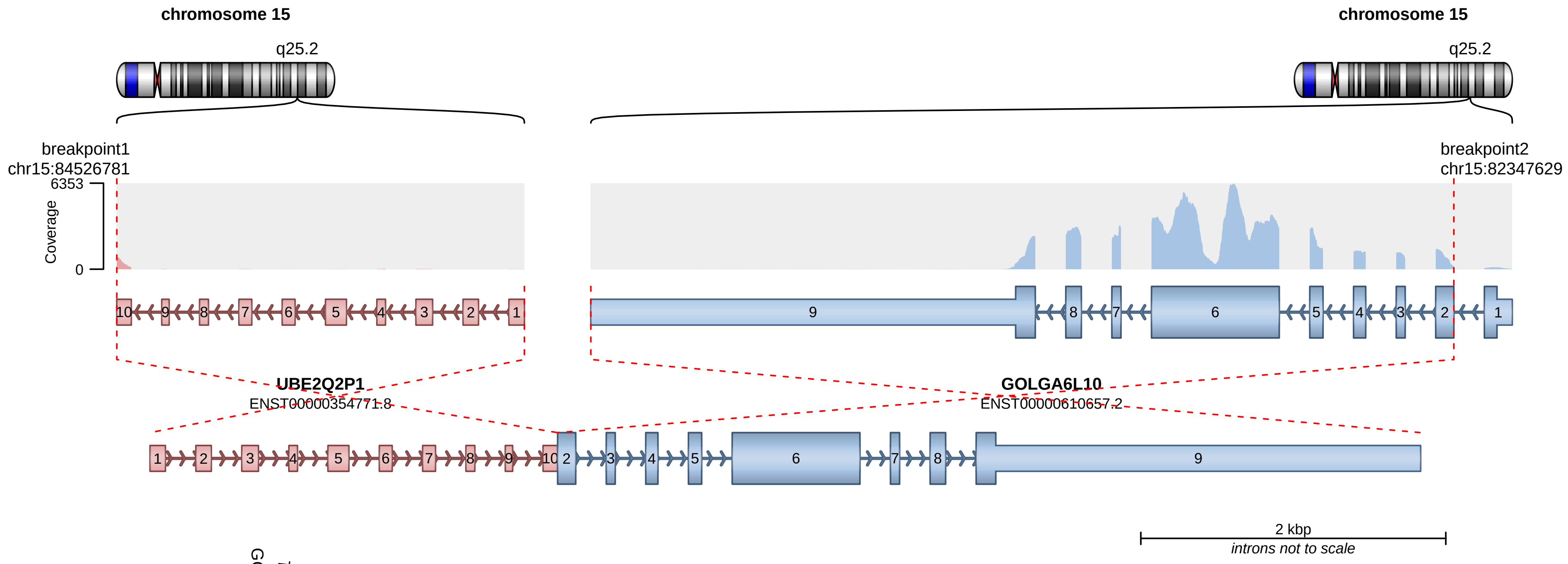


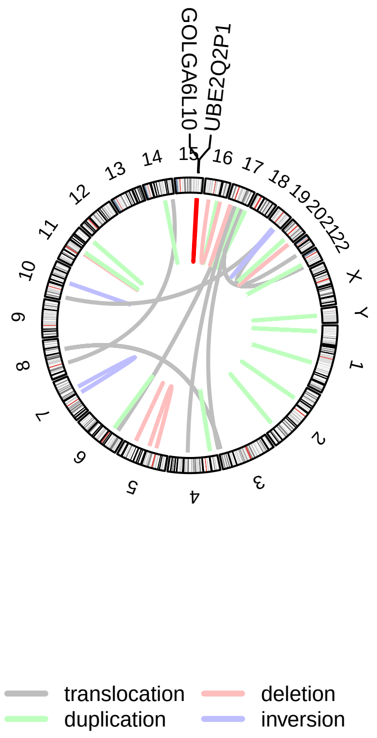


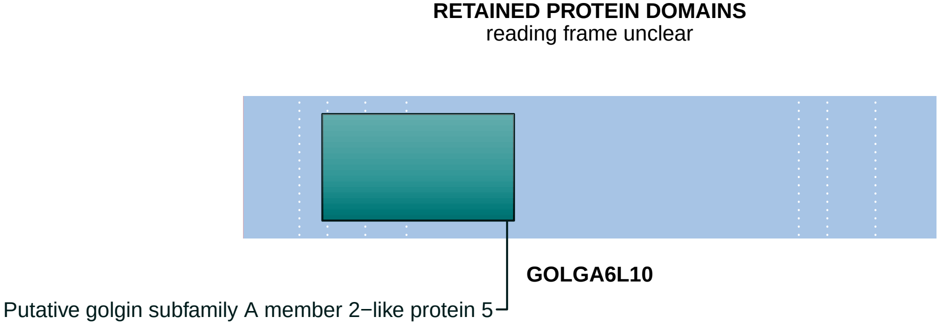
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

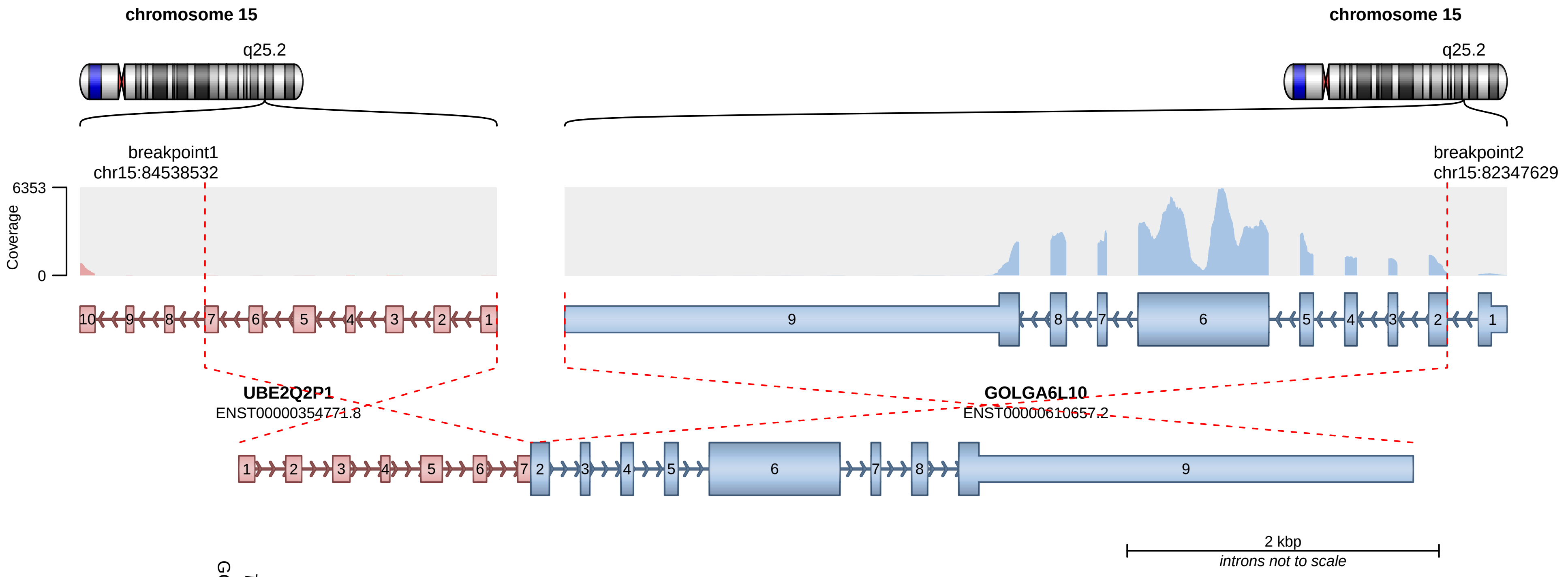


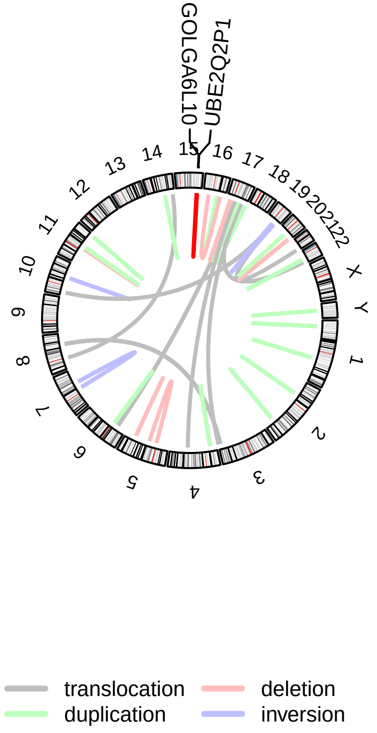




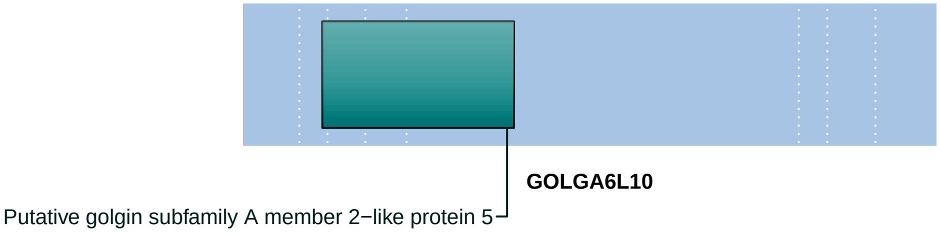
SUPPORTING READ COUNT

Split reads = 212
Discordant mates = 5



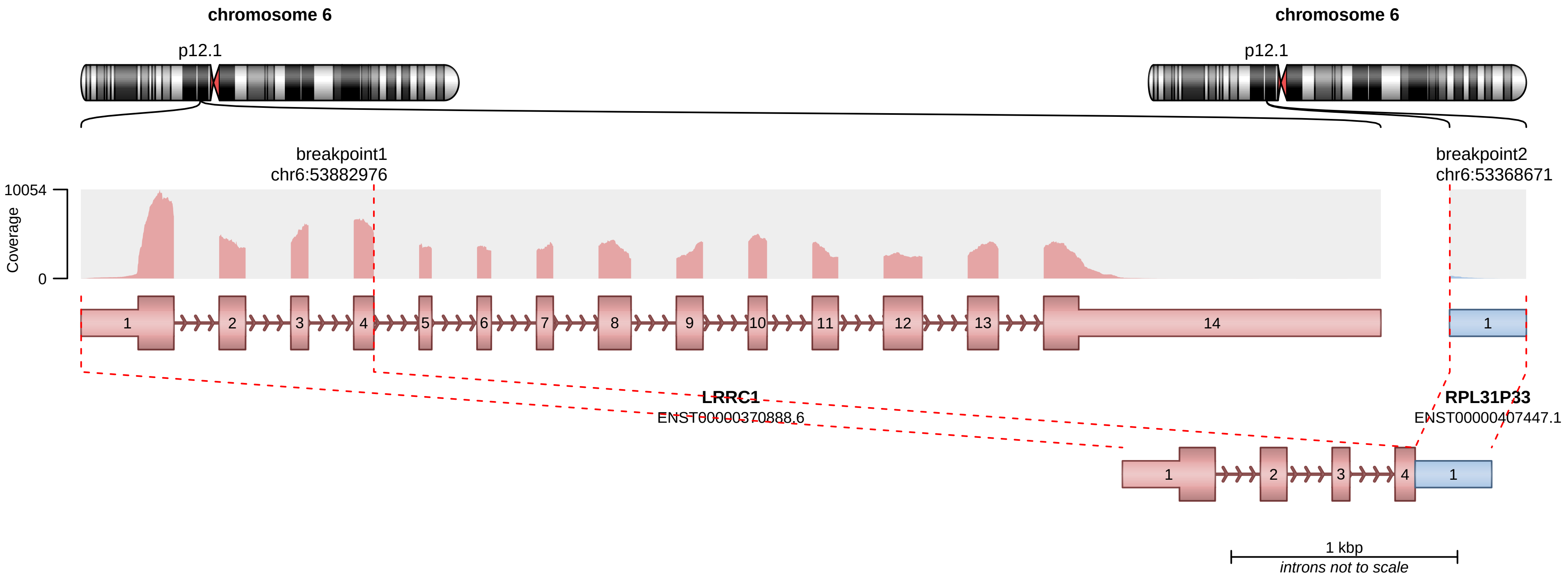


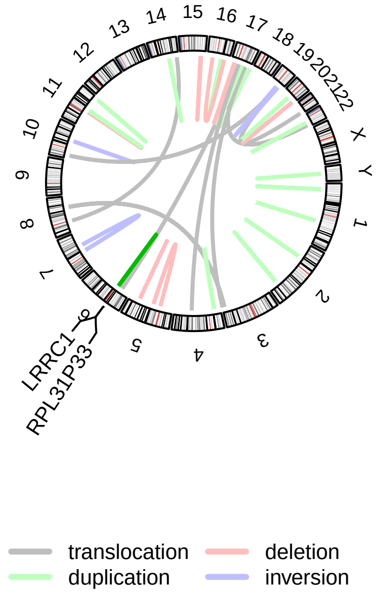
RETAINED PROTEIN DOMAINS
reading frame unclear

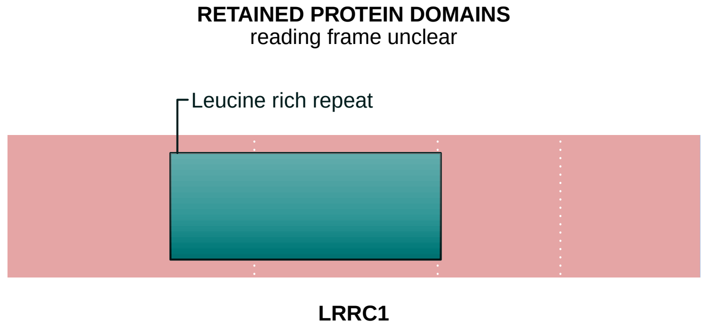


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

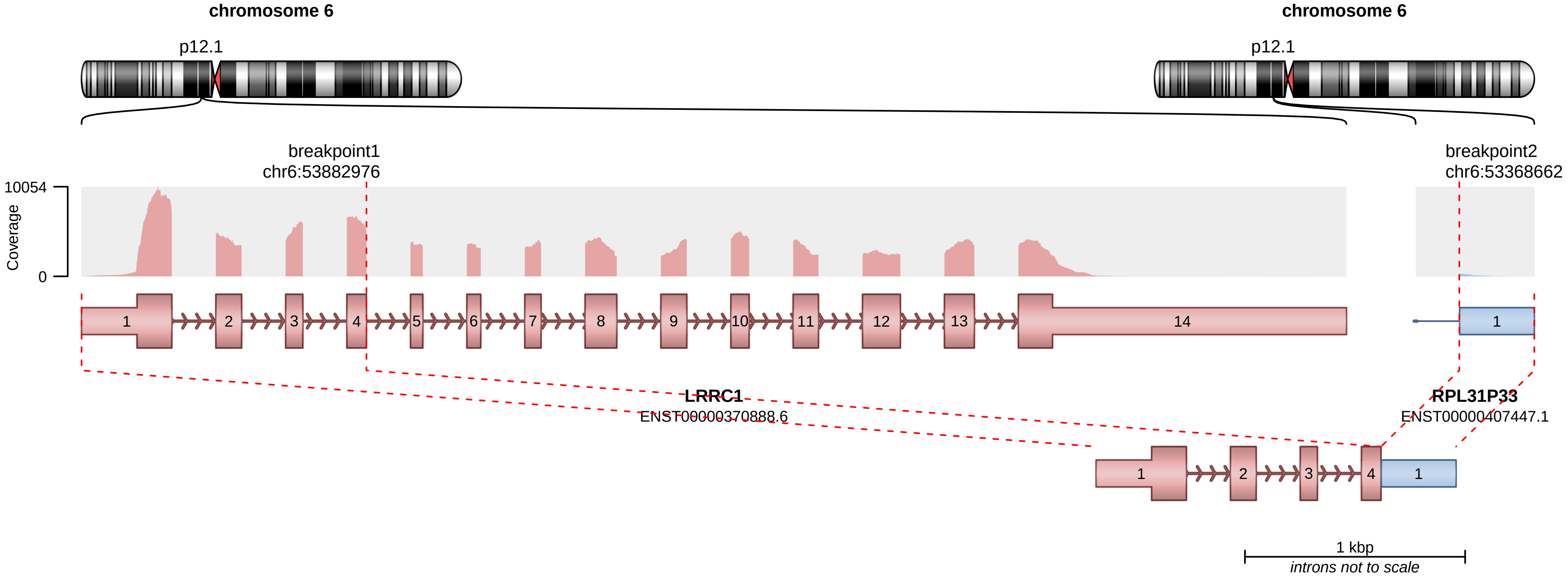


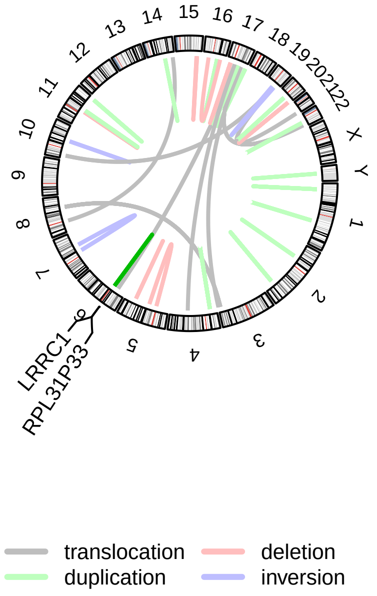




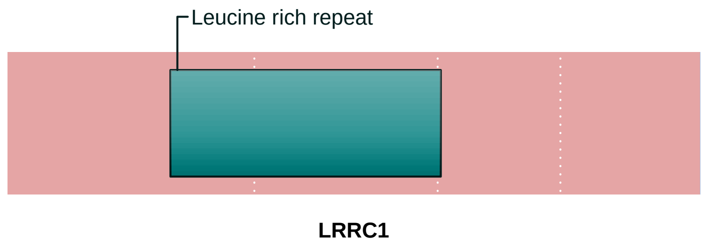
SUPPORTING READ COUNT

Split reads = 161
Discordant mates = 8



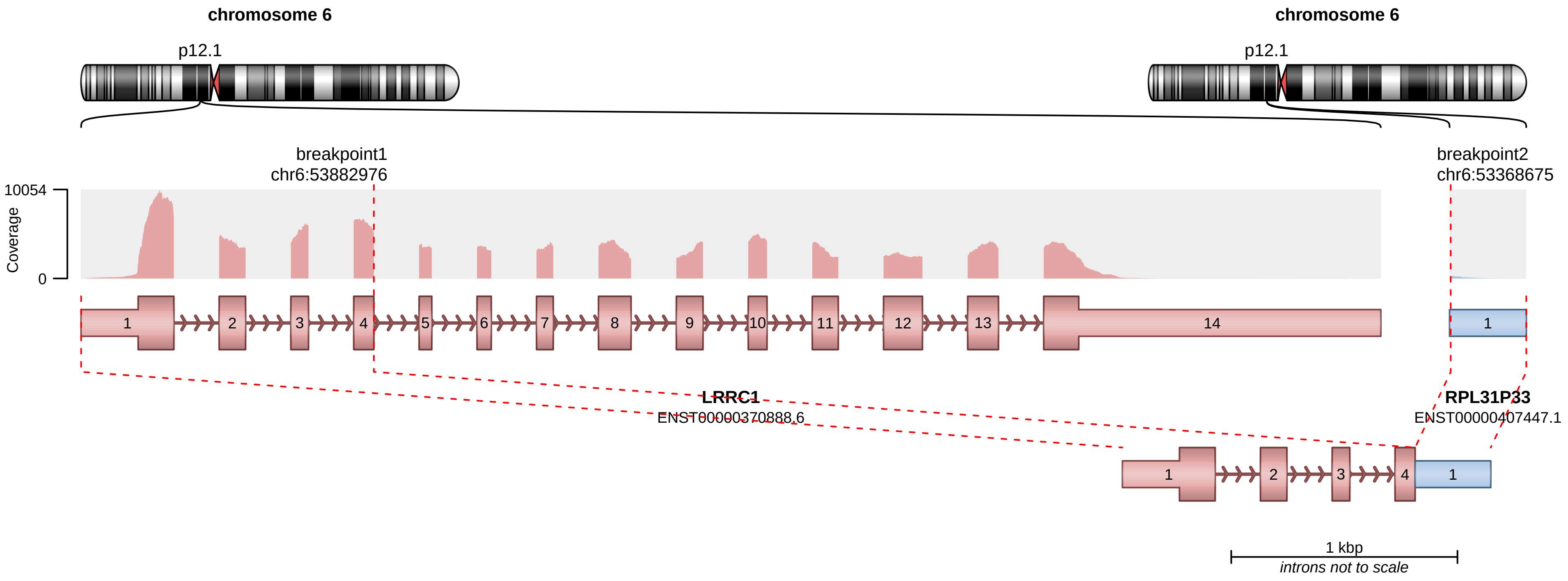


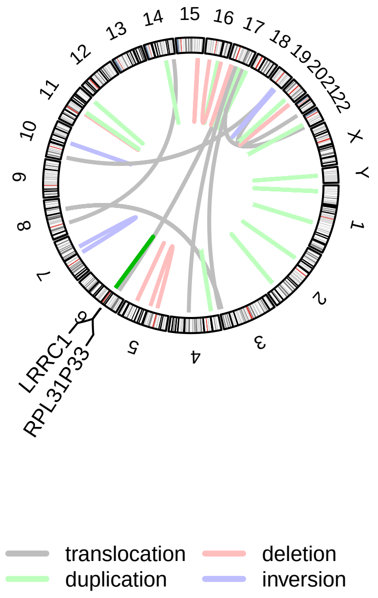
RETAINED PROTEIN DOMAINS
reading frame unclear

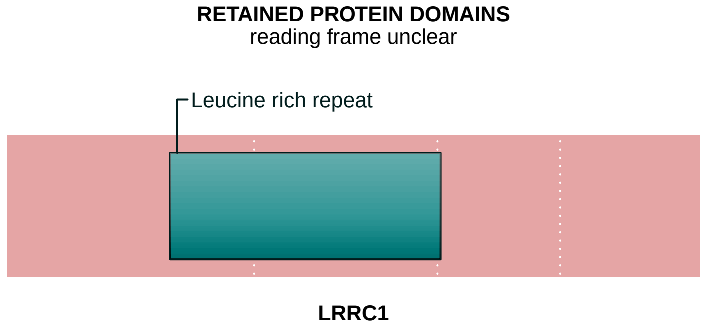


SUPPORTING READ COUNT

Split reads = 21
Discordant mates = 8

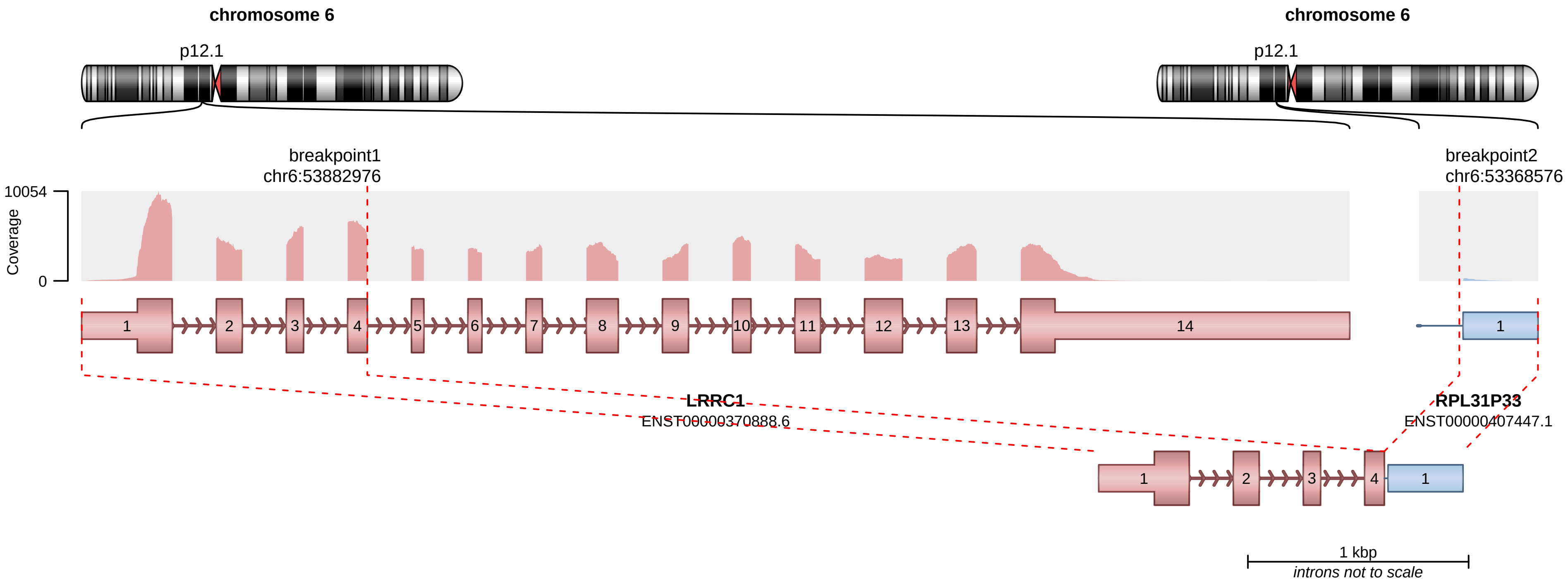


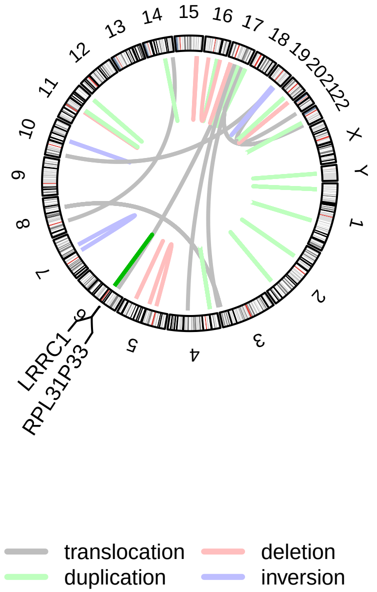




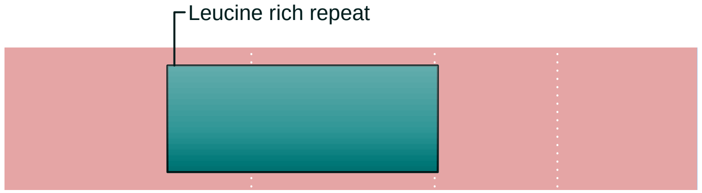
SUPPORTING READ COUNT

Split reads = 14
Discordant mates = 8





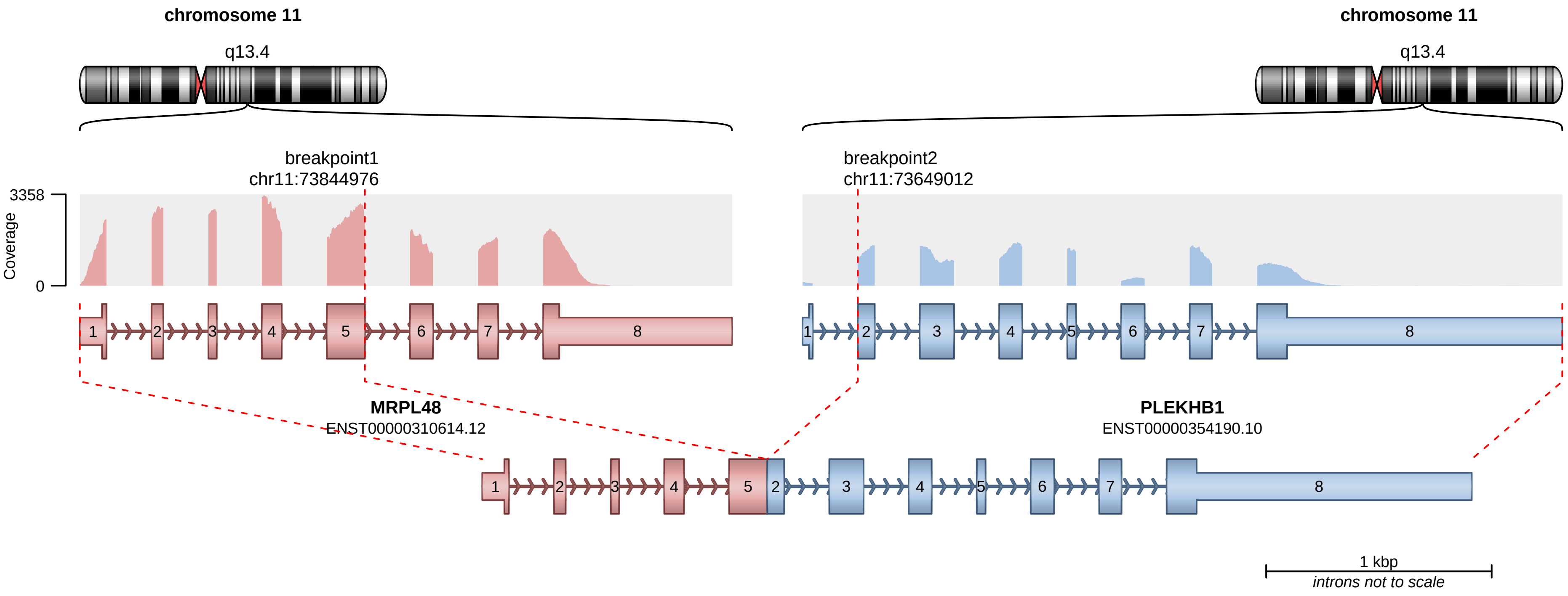
RETAINED PROTEIN DOMAINS
reading frame unclear

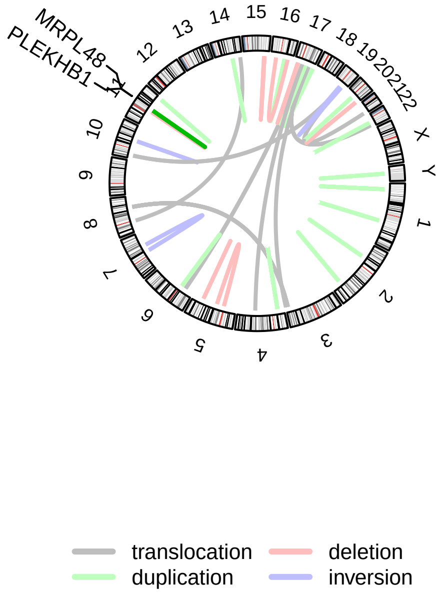


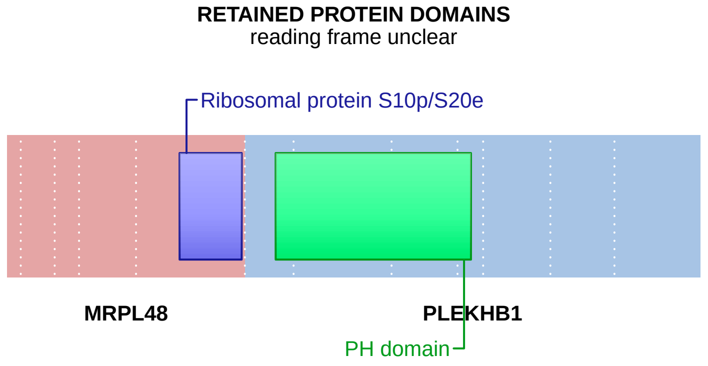
LRRC1

SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 8

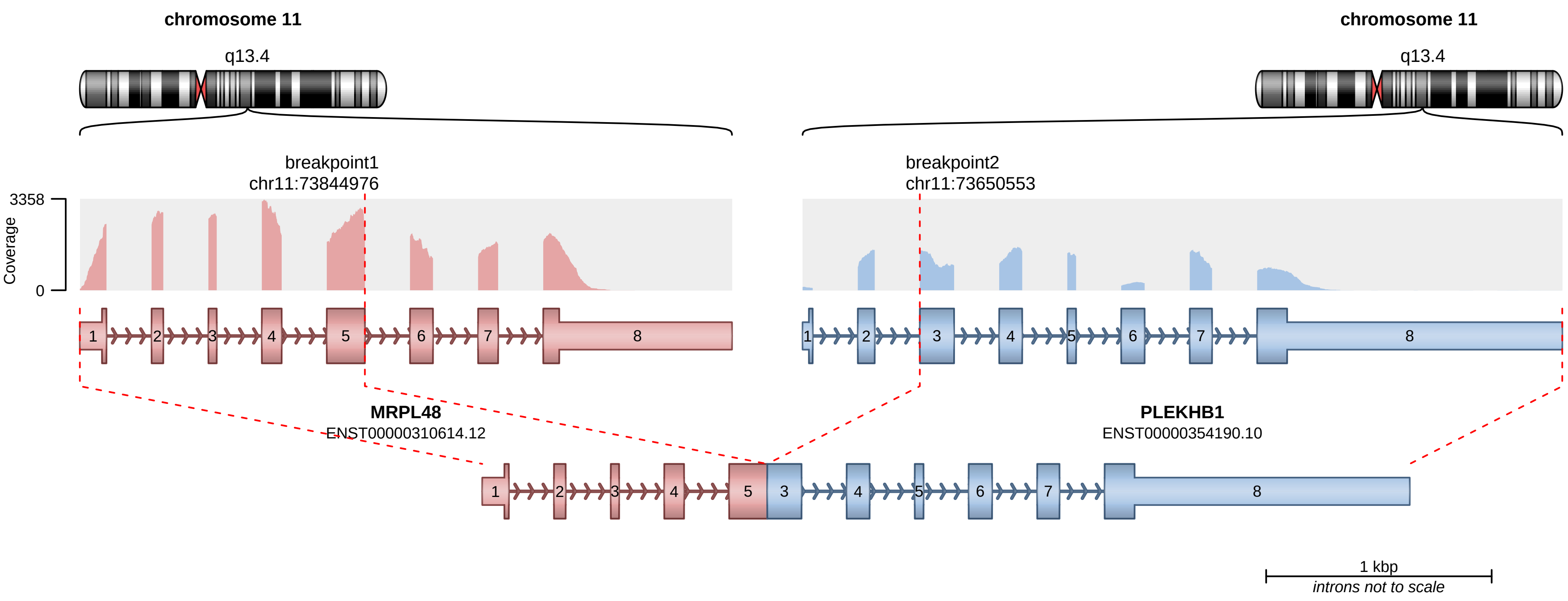


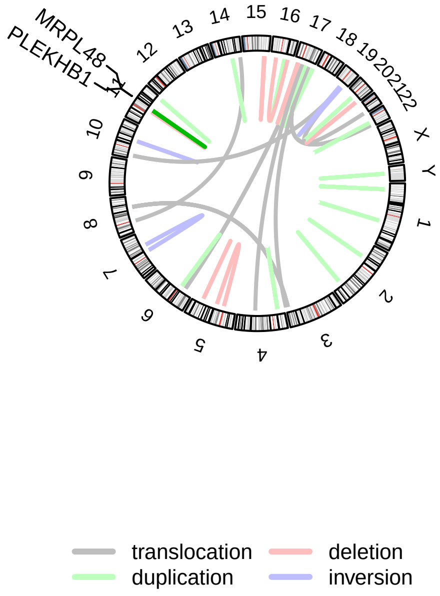




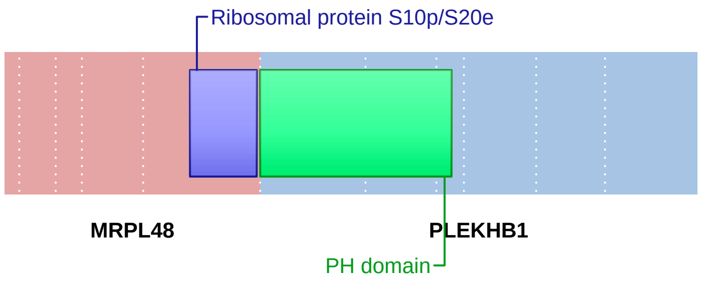
SUPPORTING READ COUNT

Split reads = 150
Discordant mates = 5



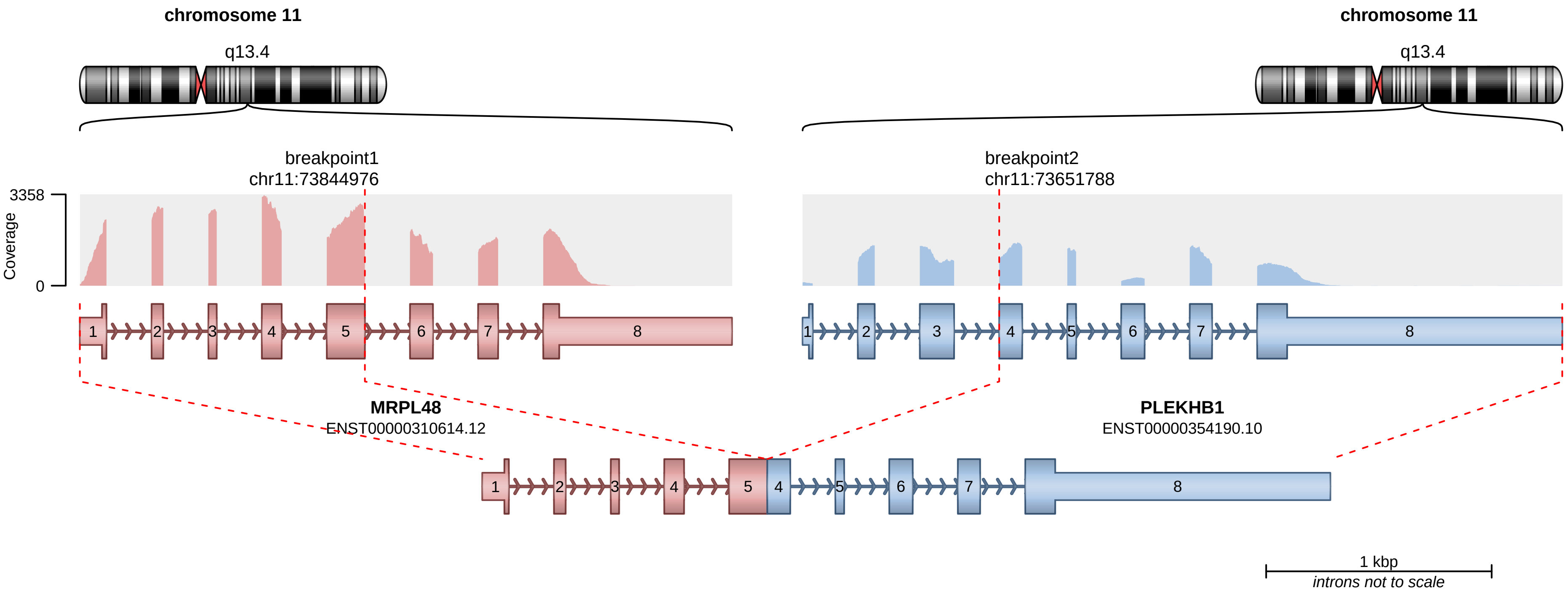


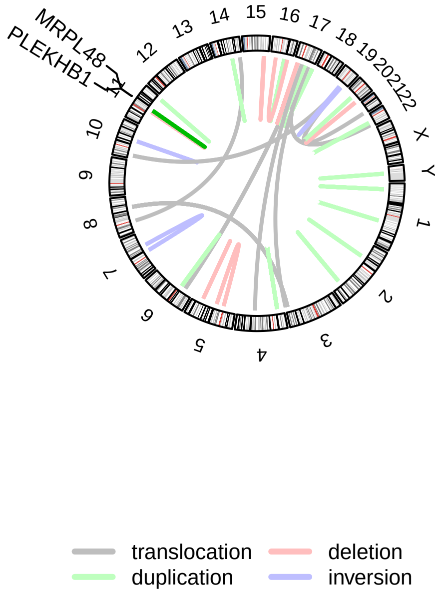
RETAINED PROTEIN DOMAINS
reading frame unclear



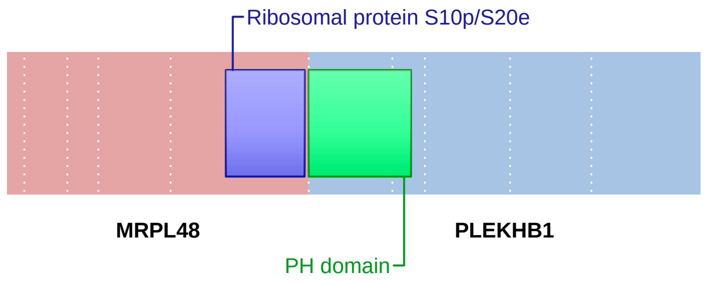
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 2



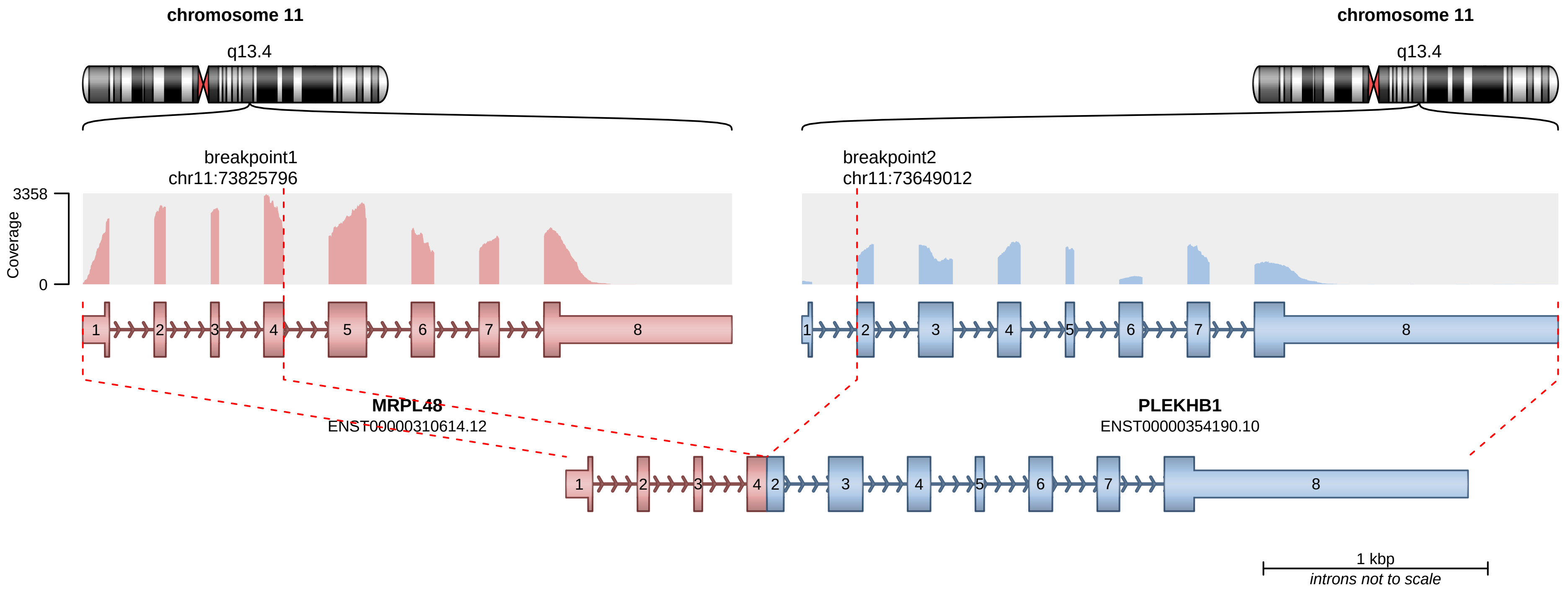


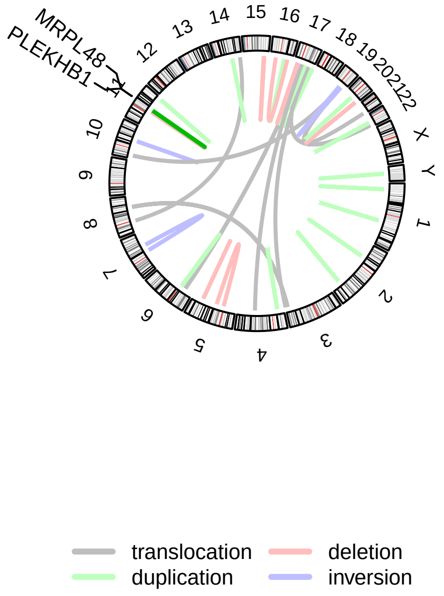
RETAINED PROTEIN DOMAINS
reading frame unclear



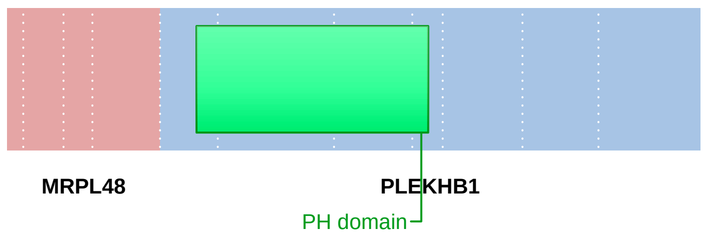
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



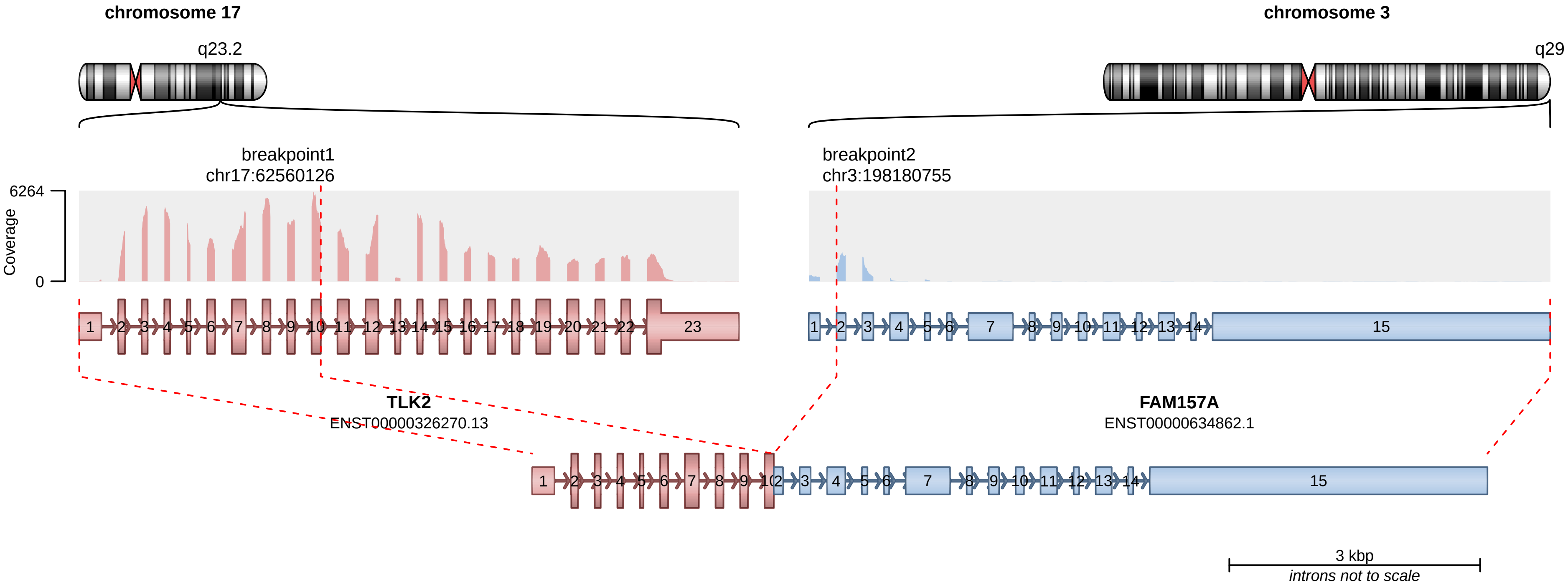


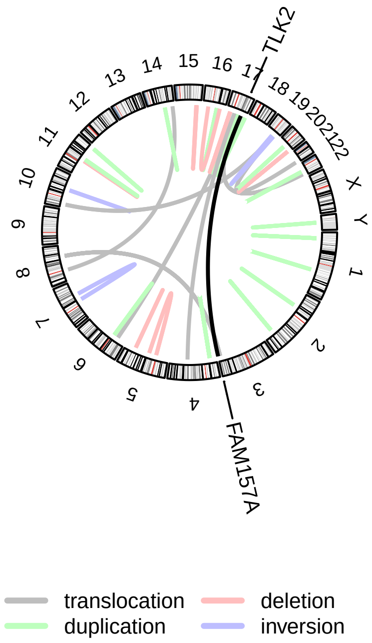
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

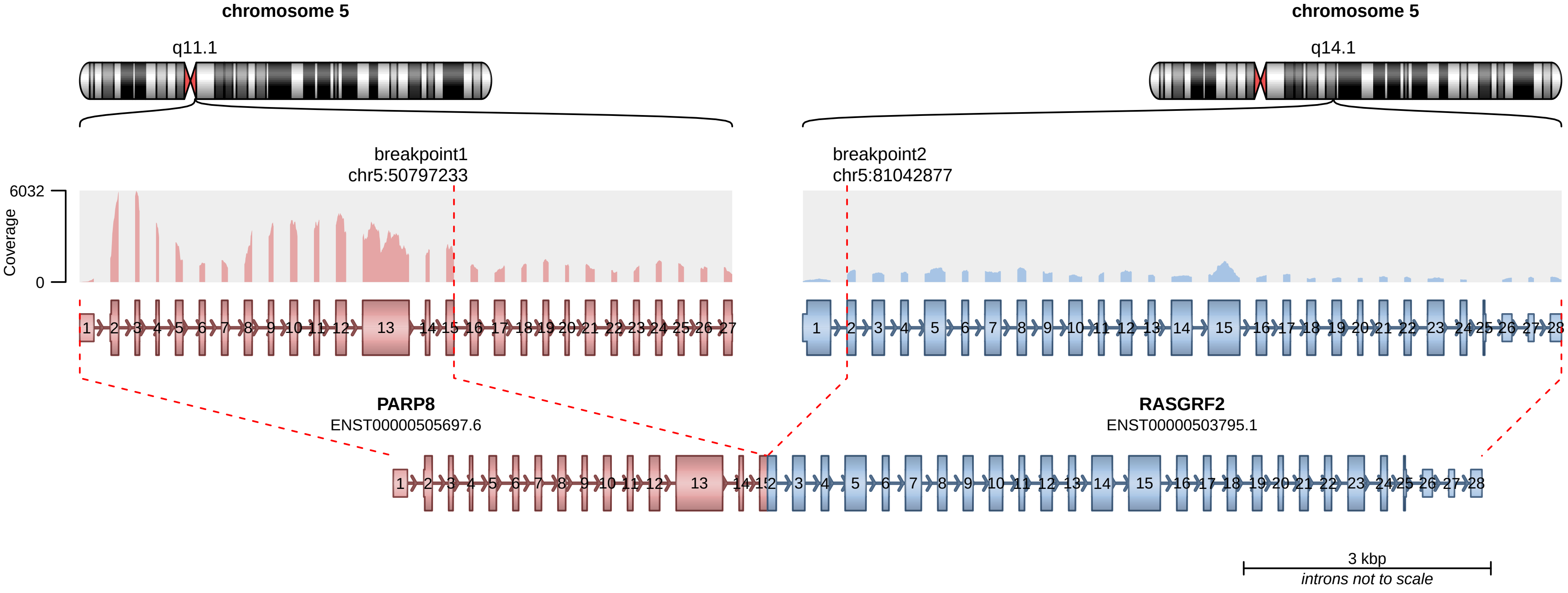


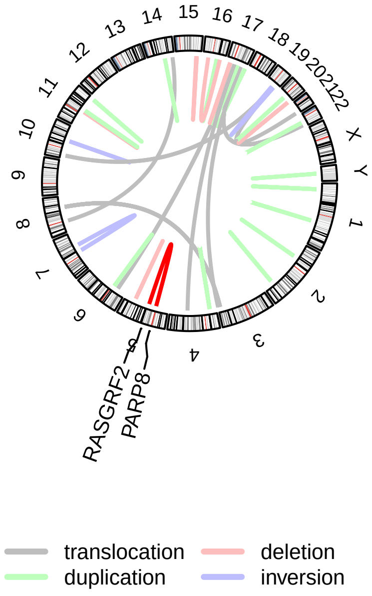


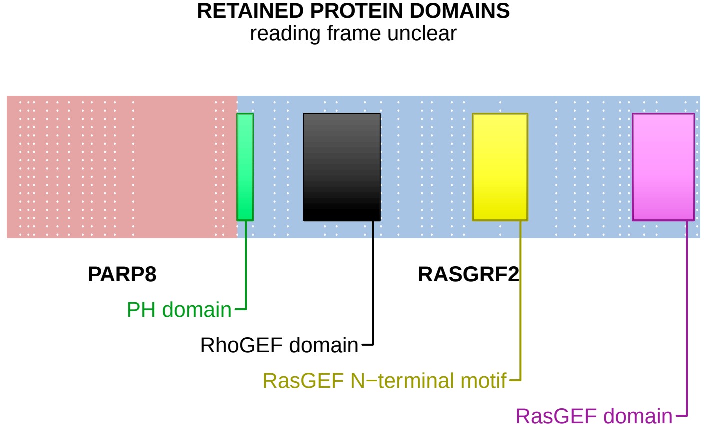
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 138
Discordant mates = 2

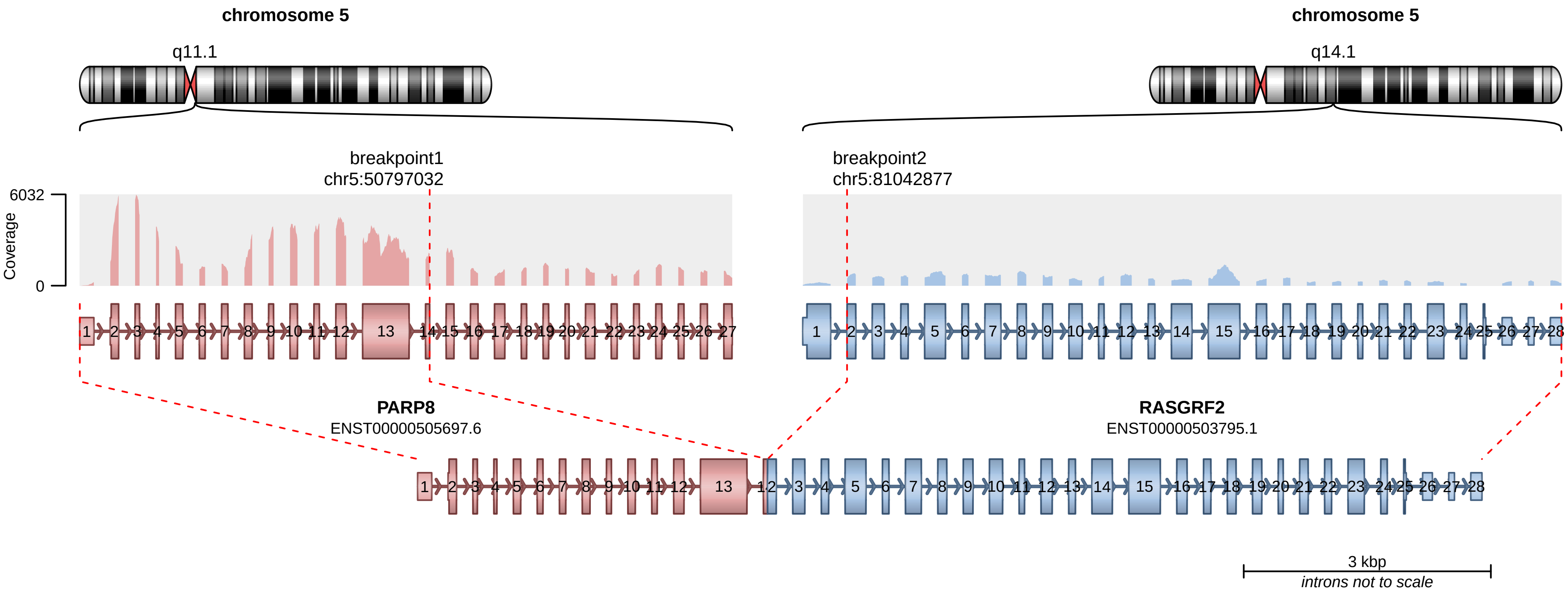


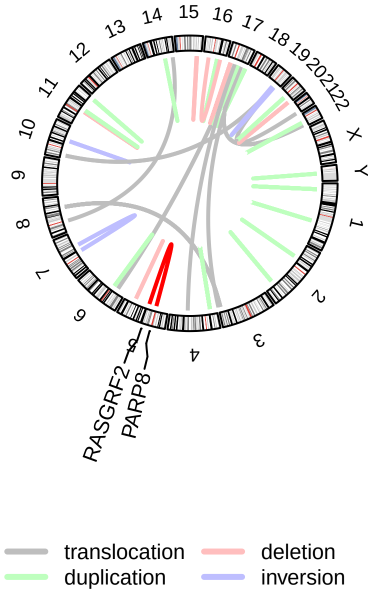




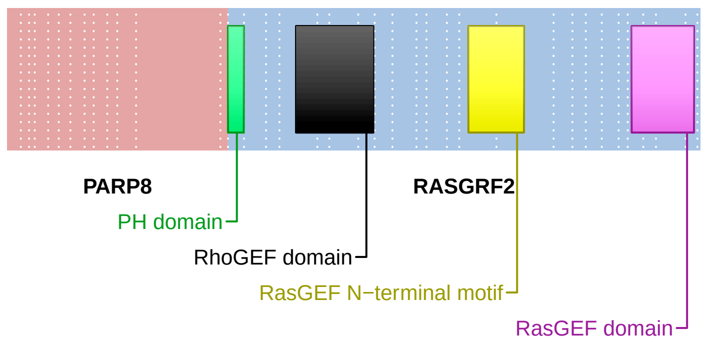
SUPPORTING READ COUNT

Split reads = 121
Discordant mates = 8



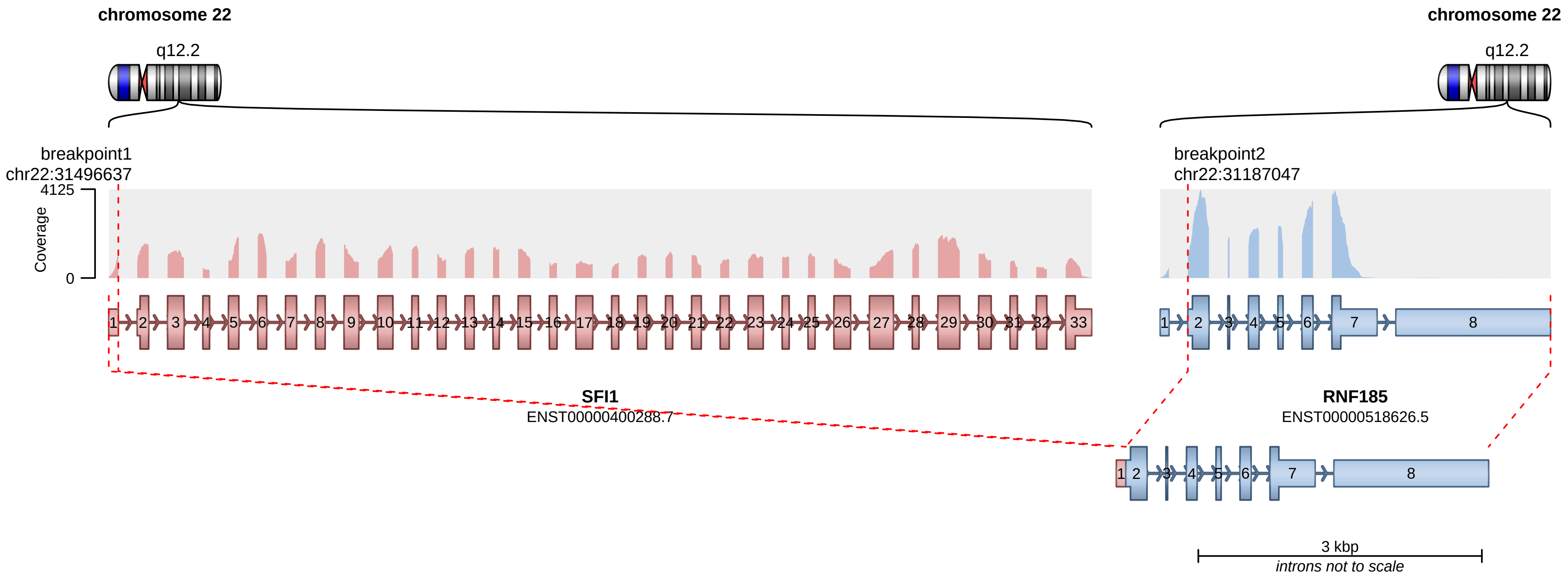


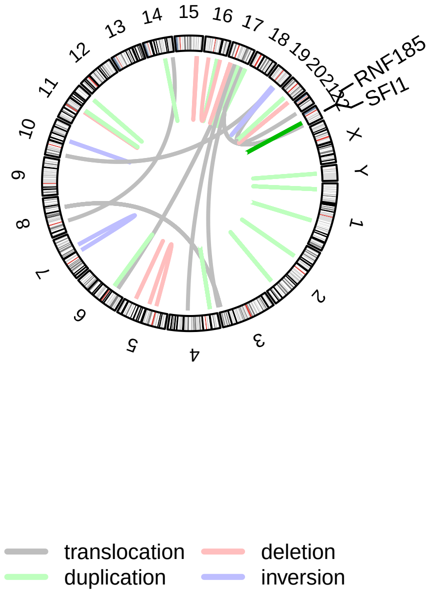
RETAINED PROTEIN DOMAINS
reading frame unclear

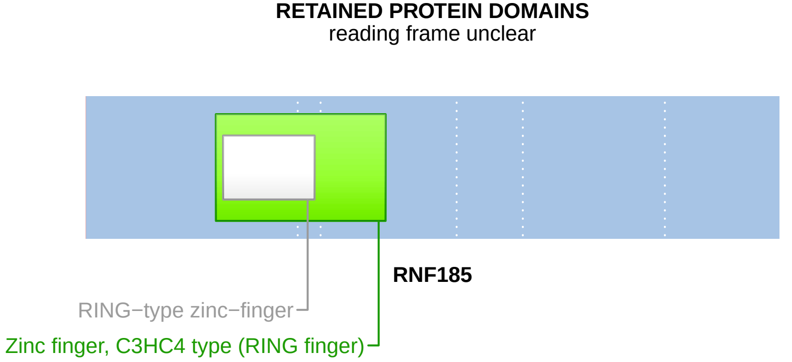


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

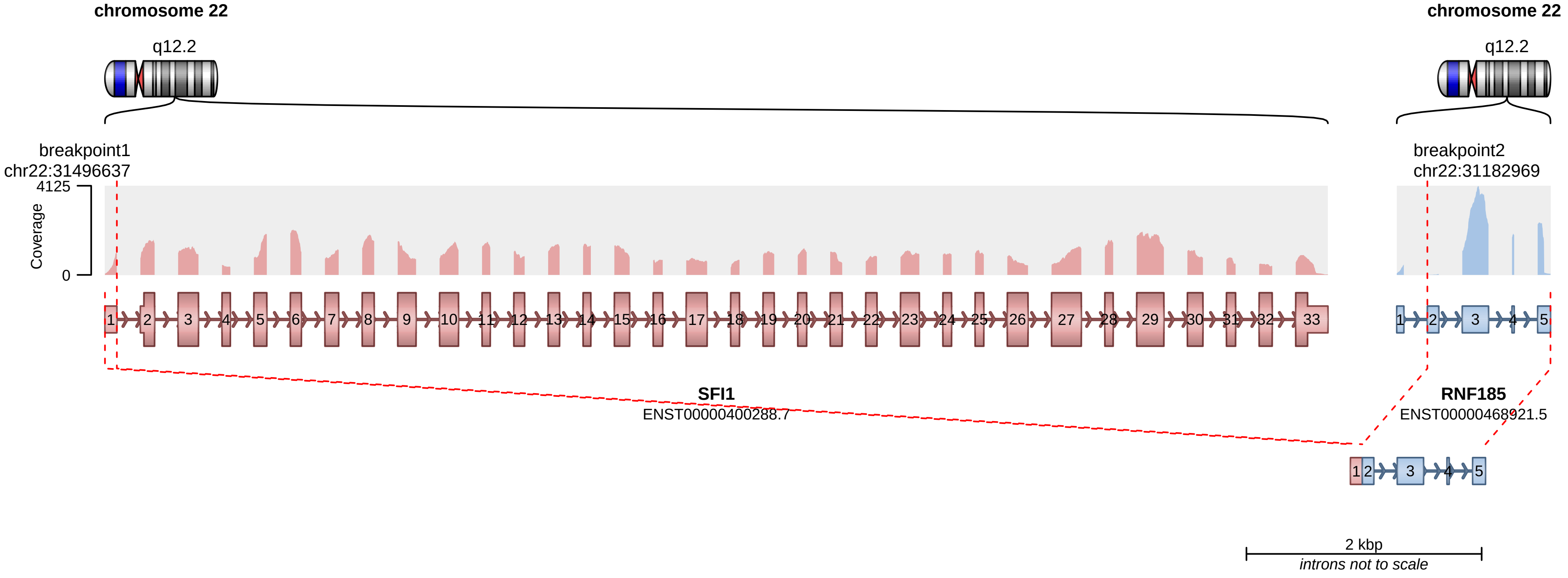


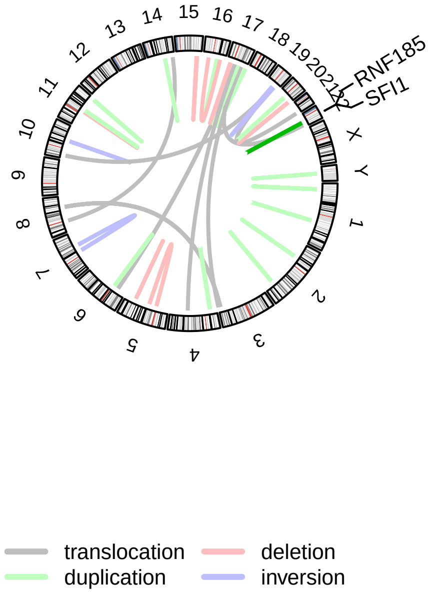




SUPPORTING READ COUNT

Split reads = 118
Discordant mates = 4

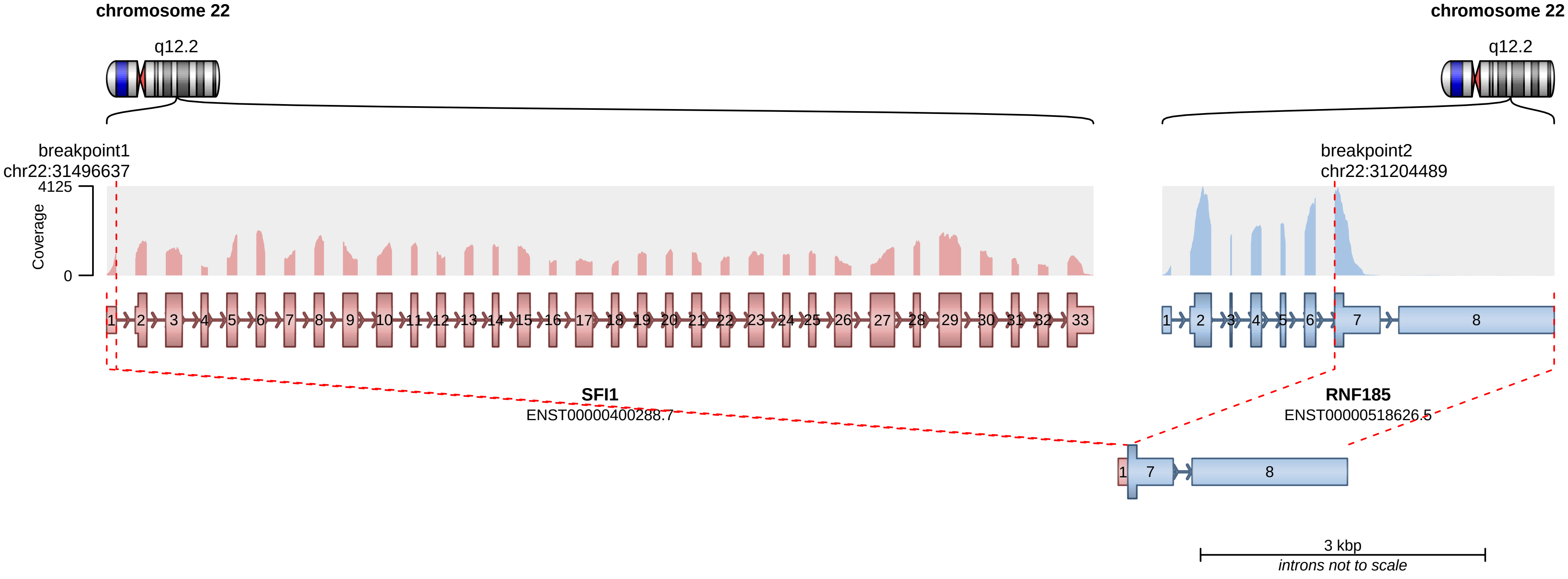


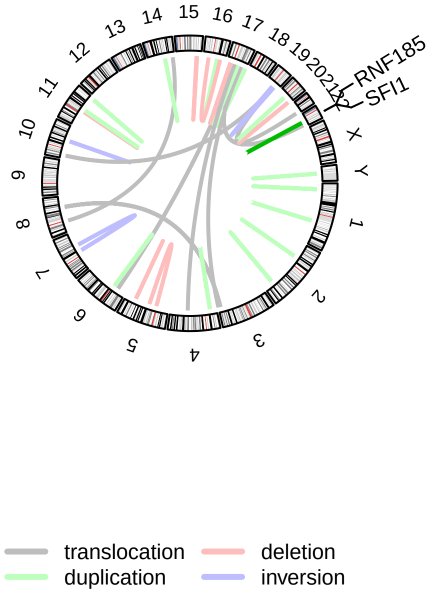


No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 4

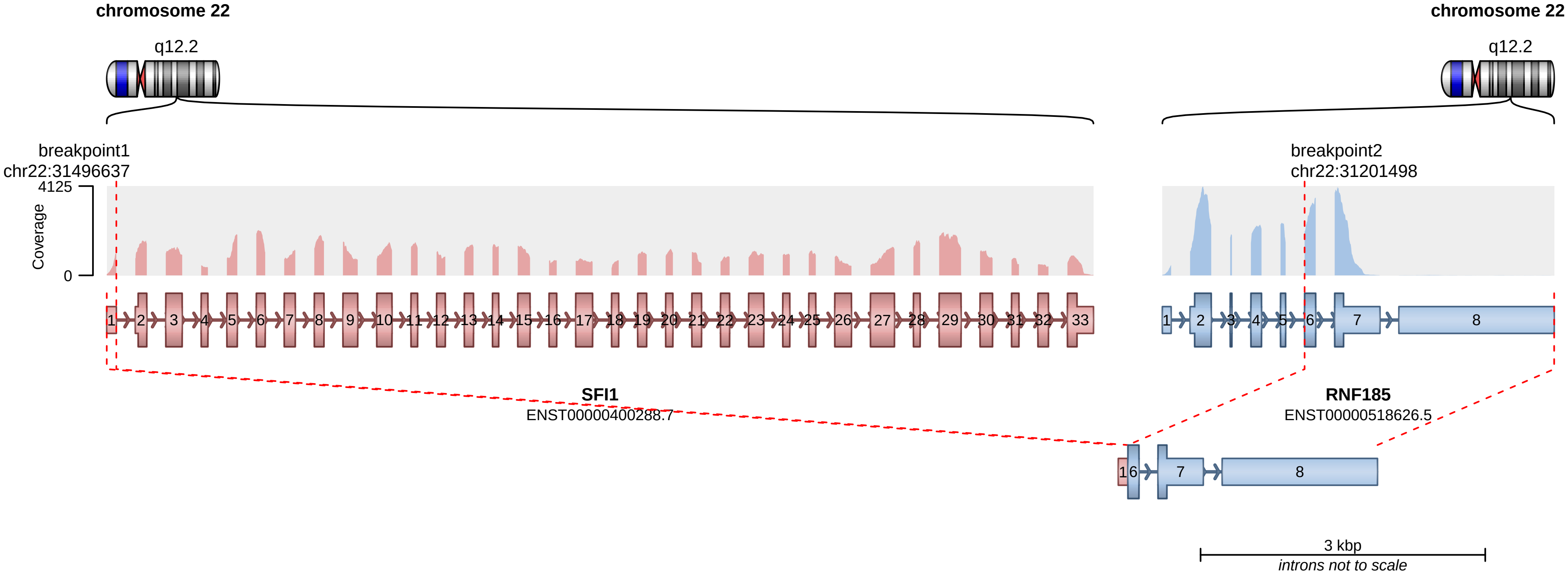


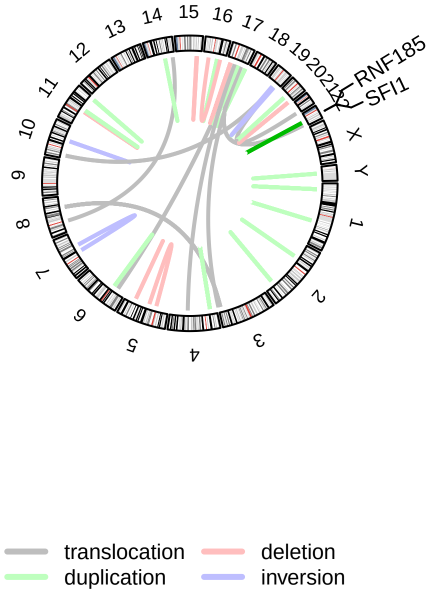


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

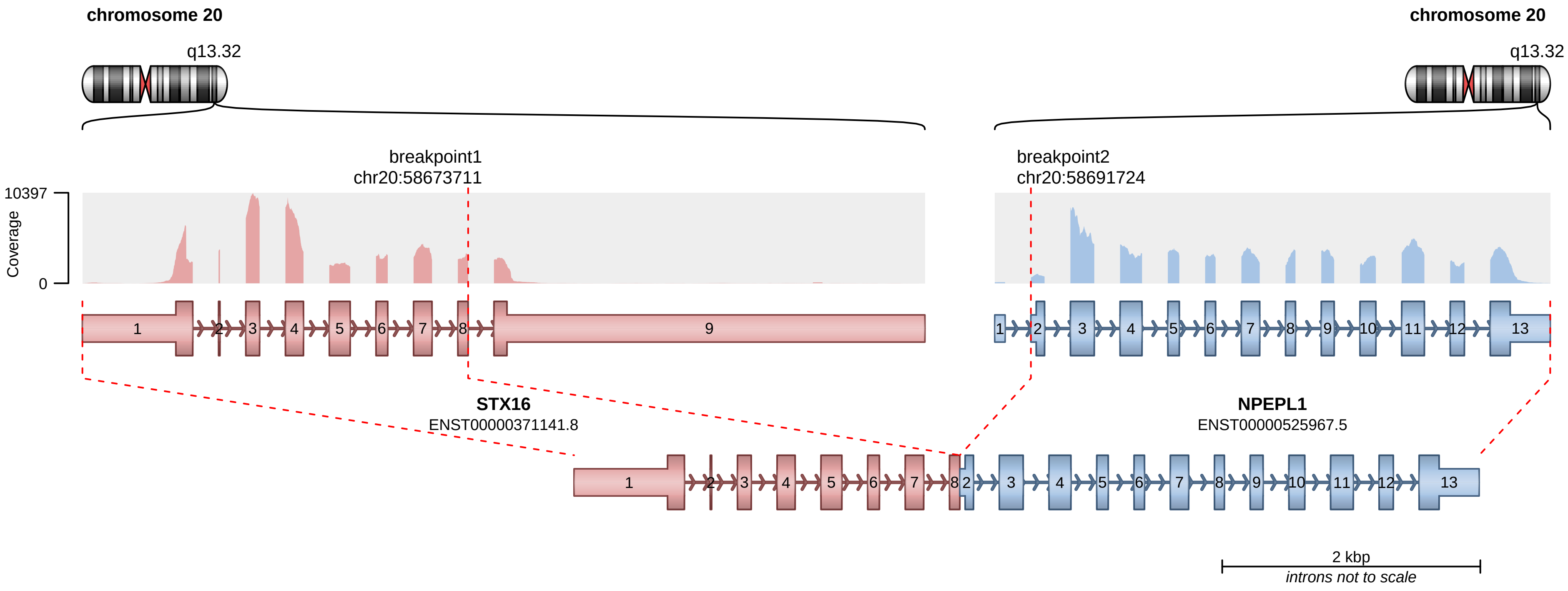


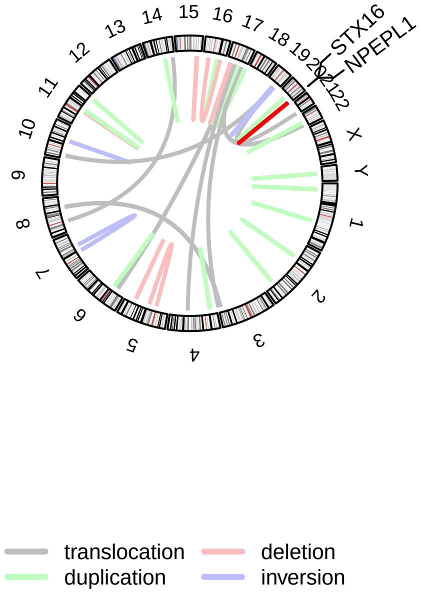


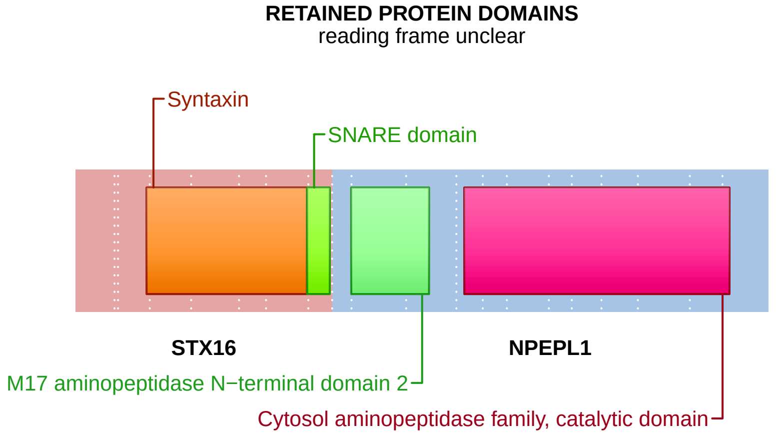
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

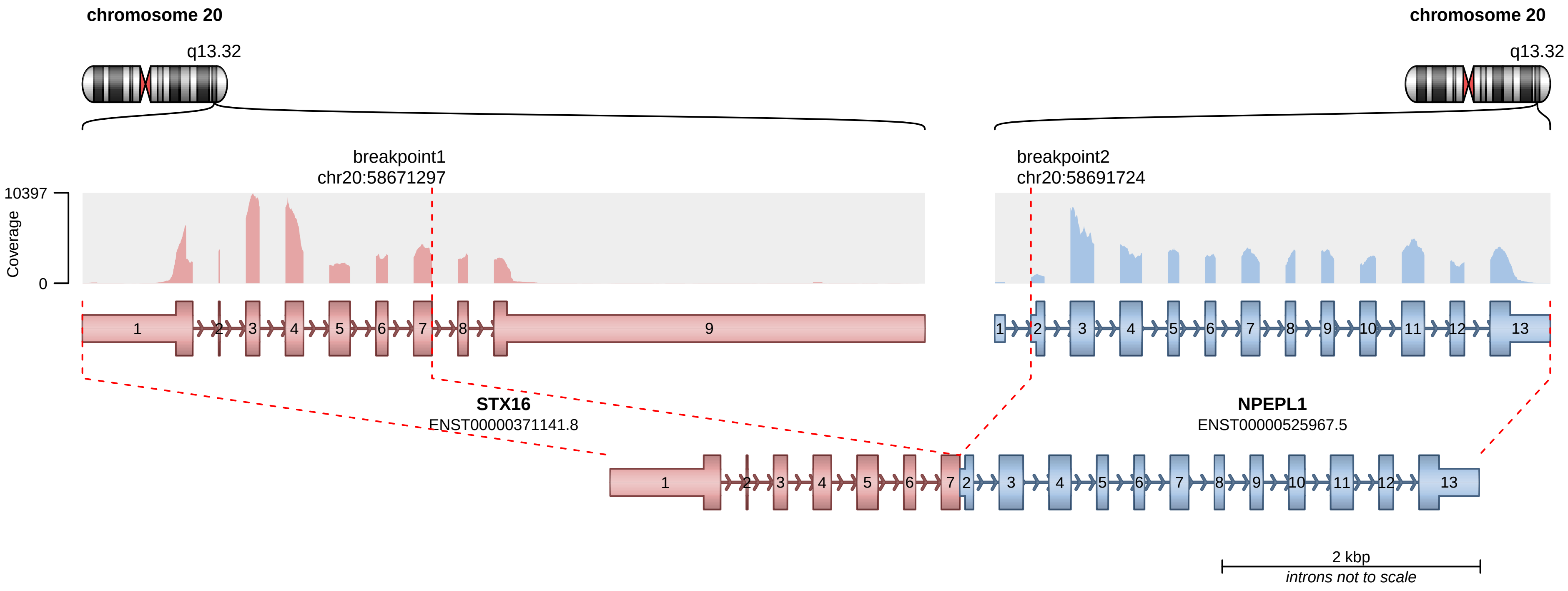


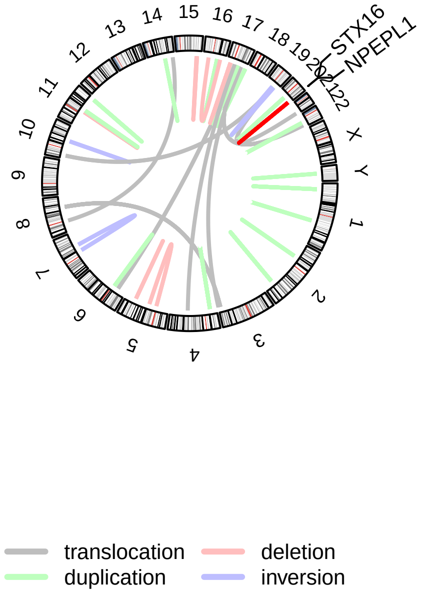


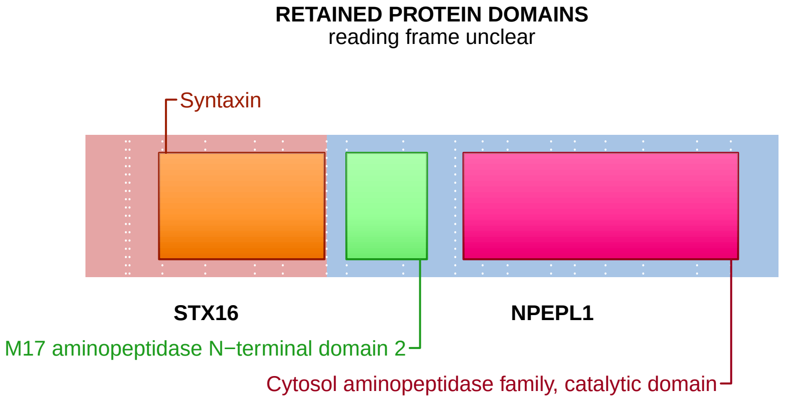


SUPPORTING READ COUNT

Split reads = 116
Discordant mates = 3

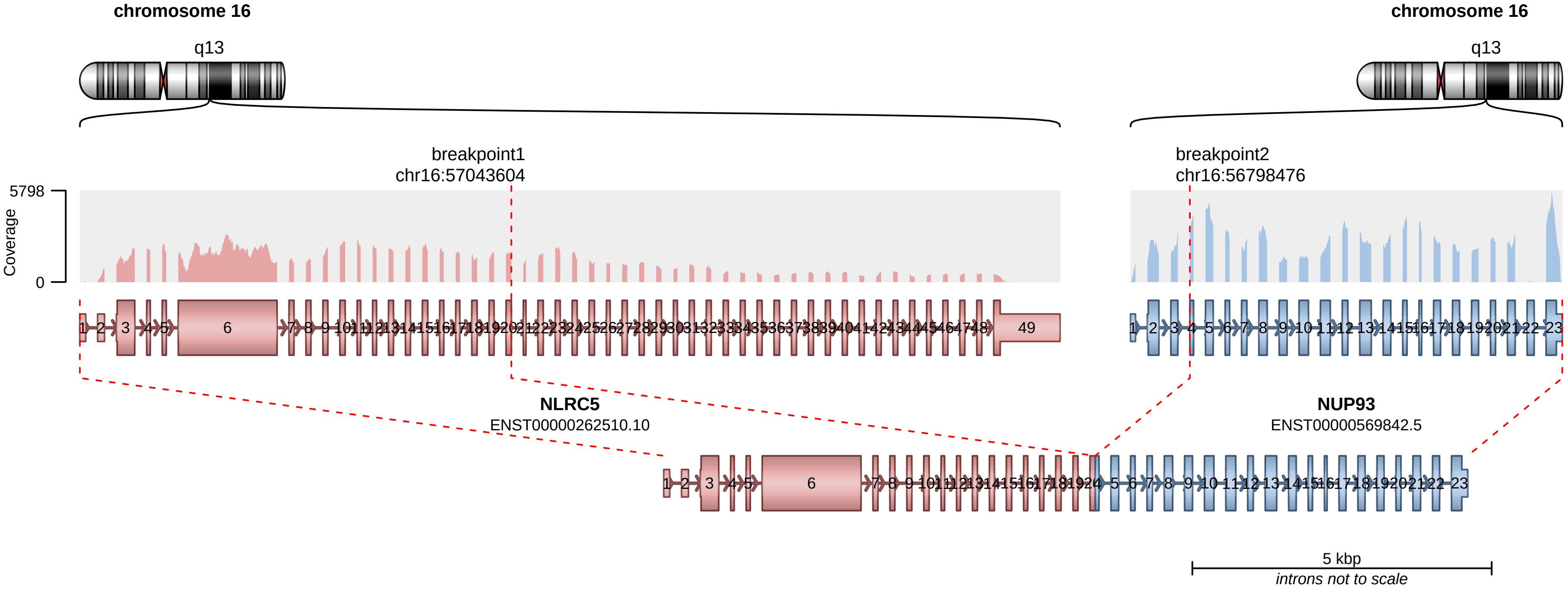


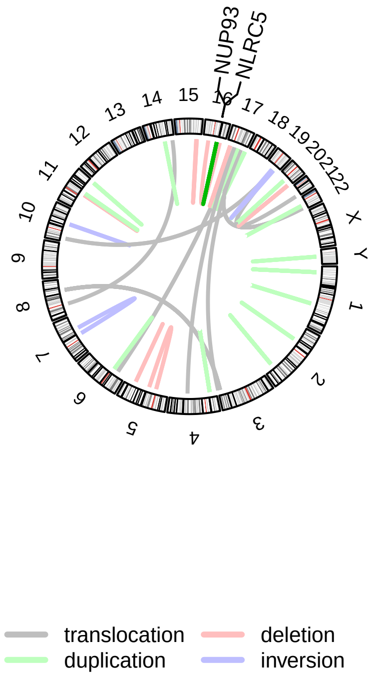


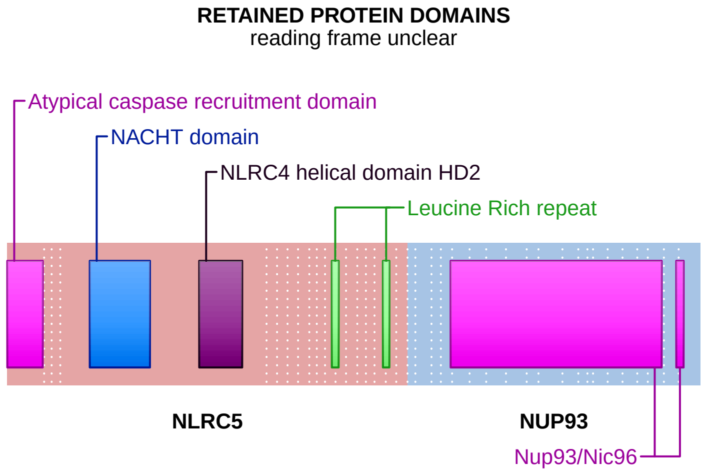


SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

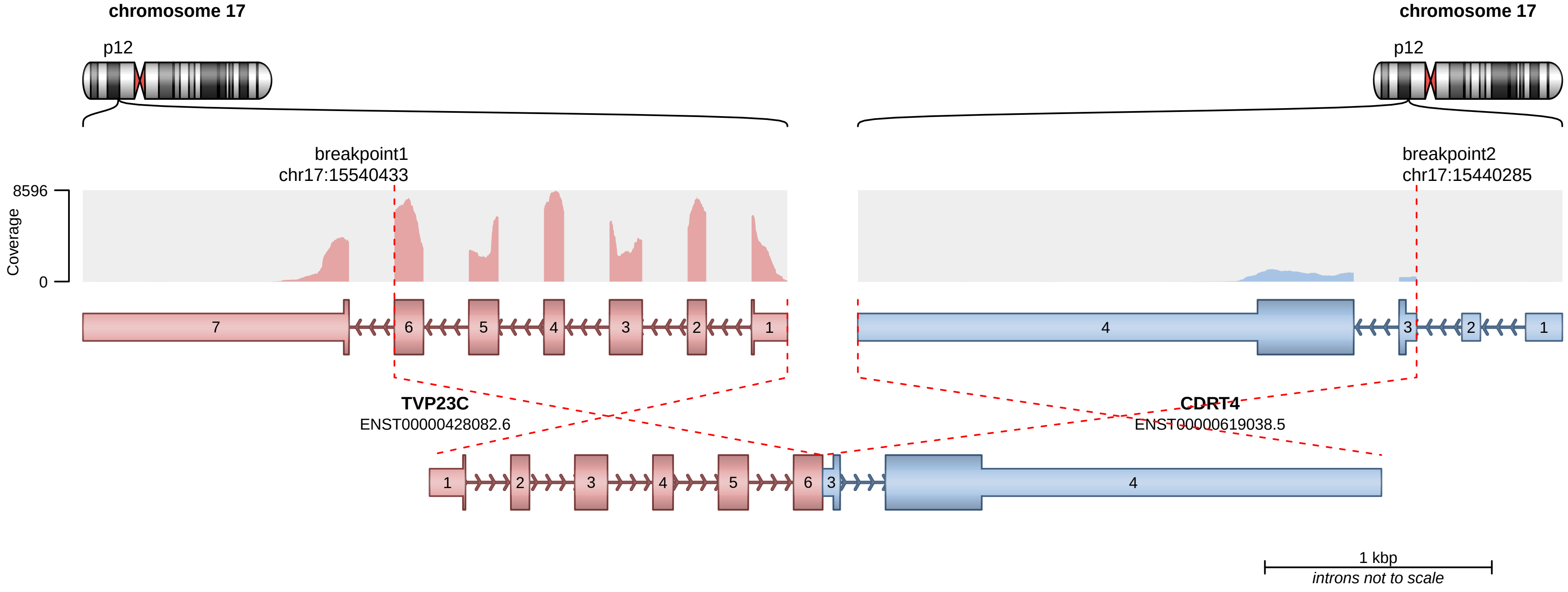


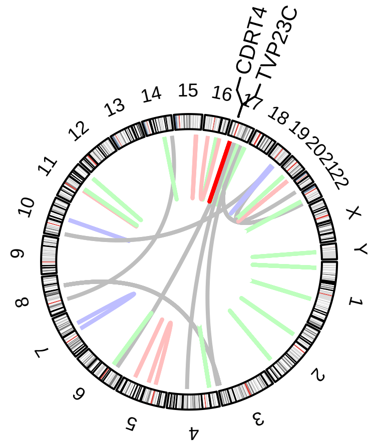




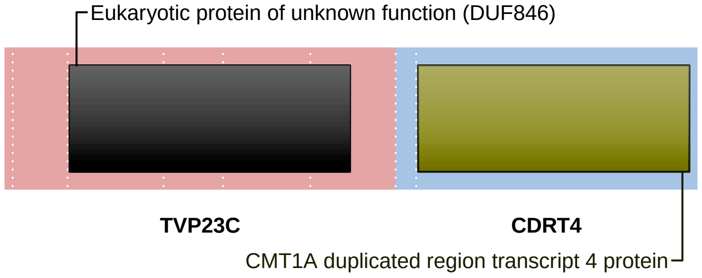
SUPPORTING READ COUNT

Split reads = 96
Discordant mates = 13





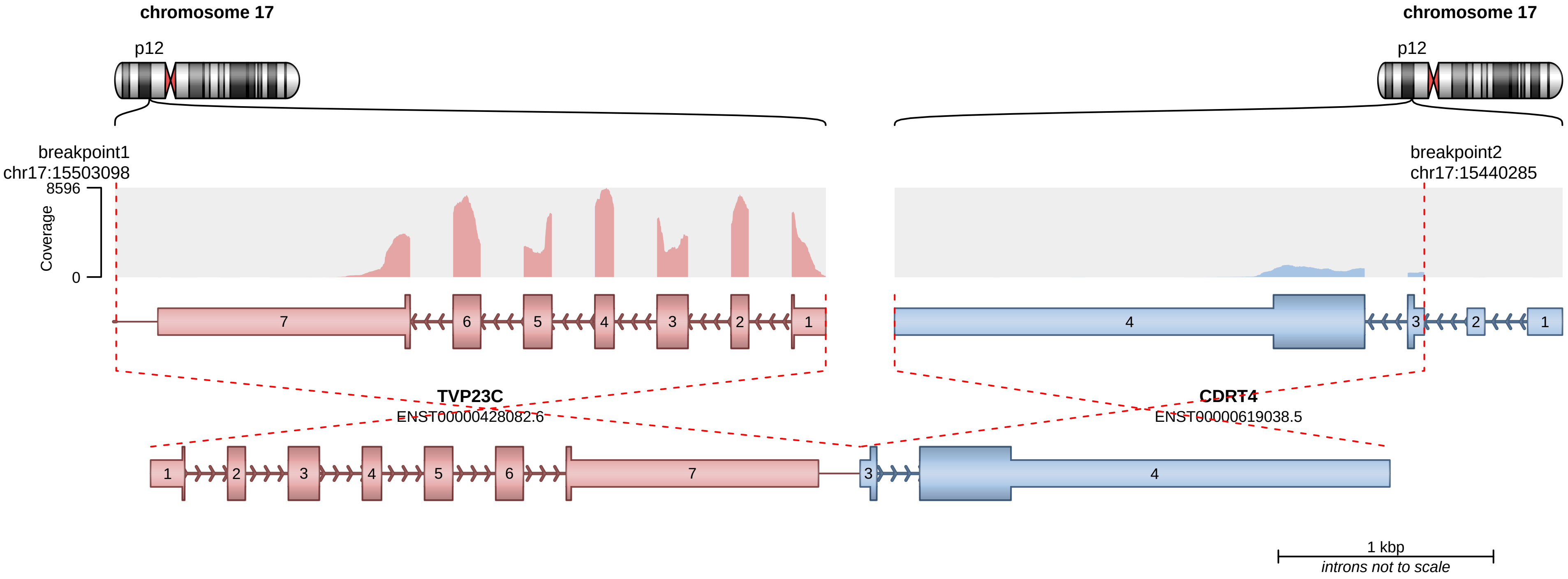
RETAINED PROTEIN DOMAINS
reading frame unclear

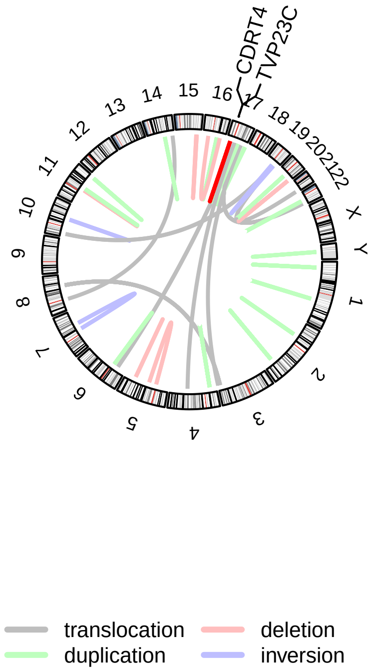


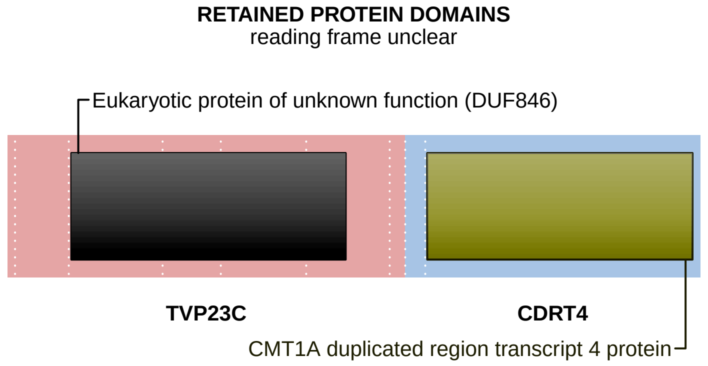
SUPPORTING READ COUNT

Split reads = 96
Discordant mates = 3

translocation
duplication
deletion
inversion

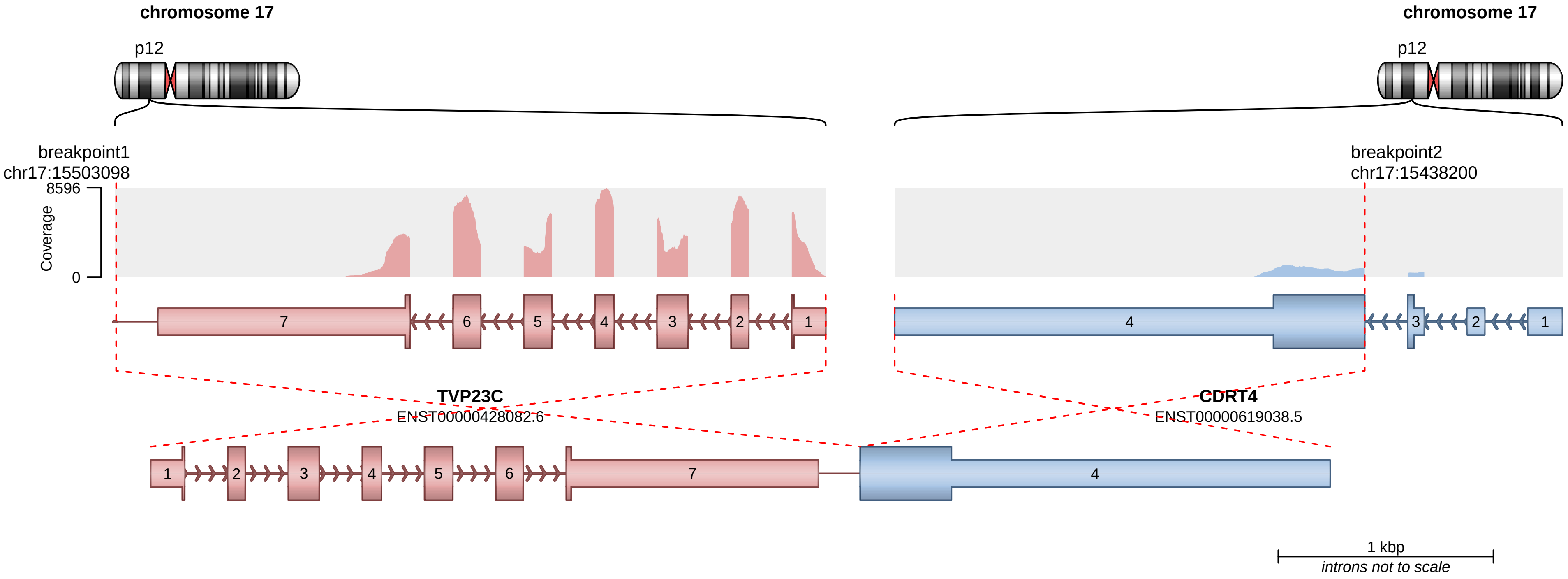


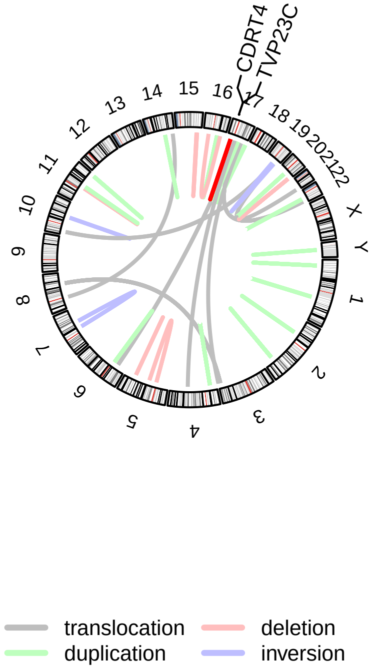


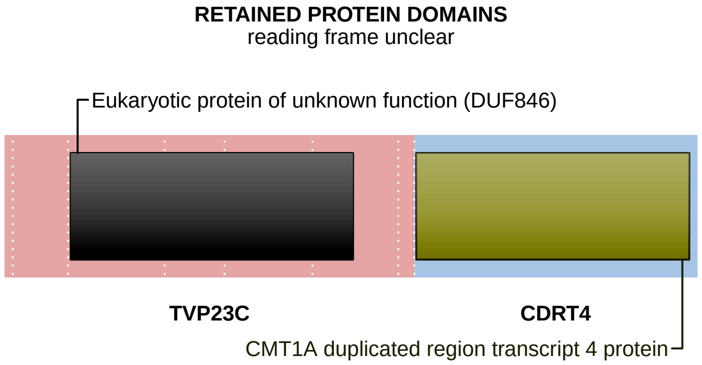


SUPPORTING READ COUNT

Split reads = 77
Discordant mates = 3

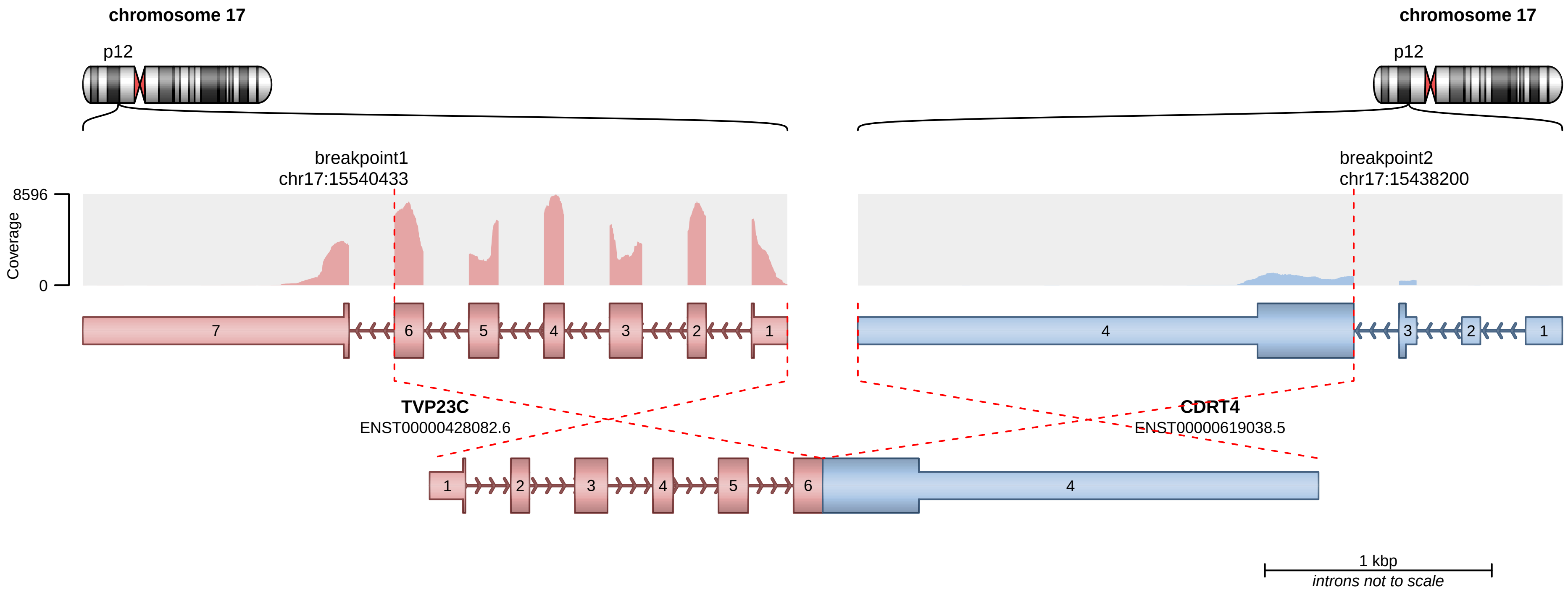


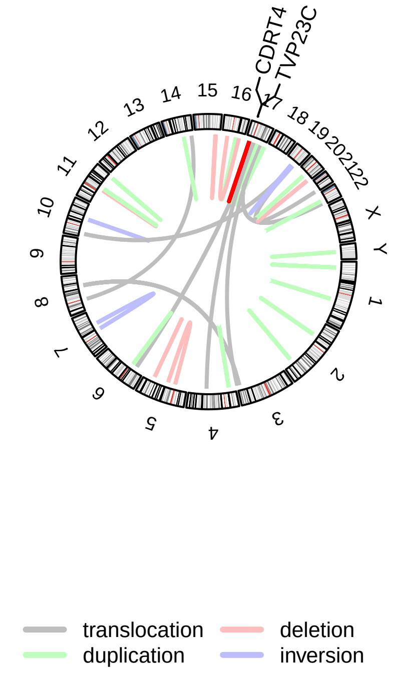




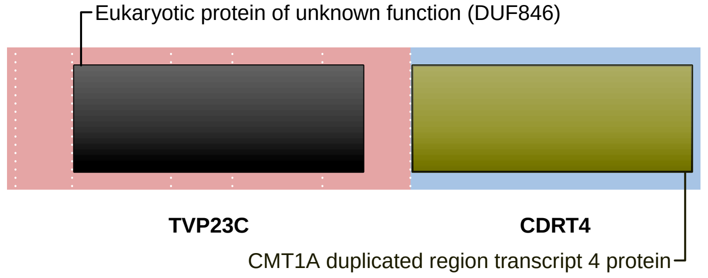
SUPPORTING READ COUNT

Split reads = 73
Discordant mates = 1



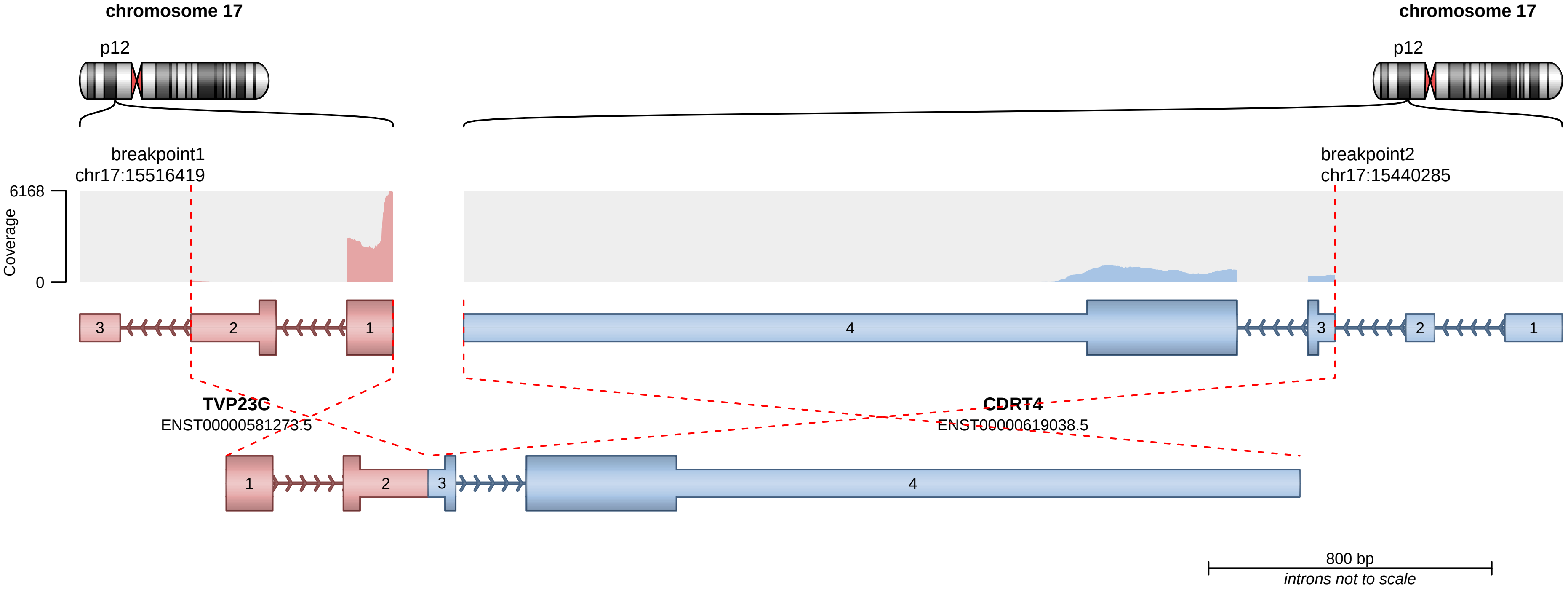


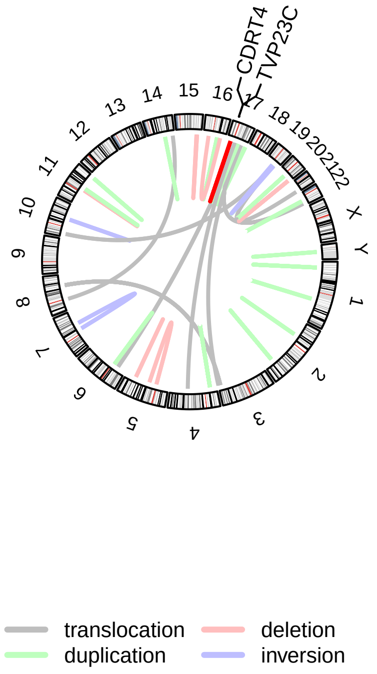
RETAINED PROTEIN DOMAINS
reading frame unclear



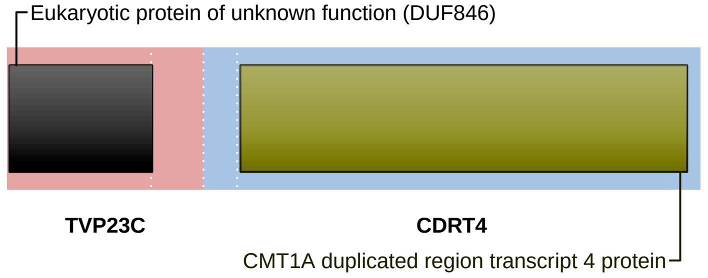
SUPPORTING READ COUNT

Split reads = 59
Discordant mates = 1



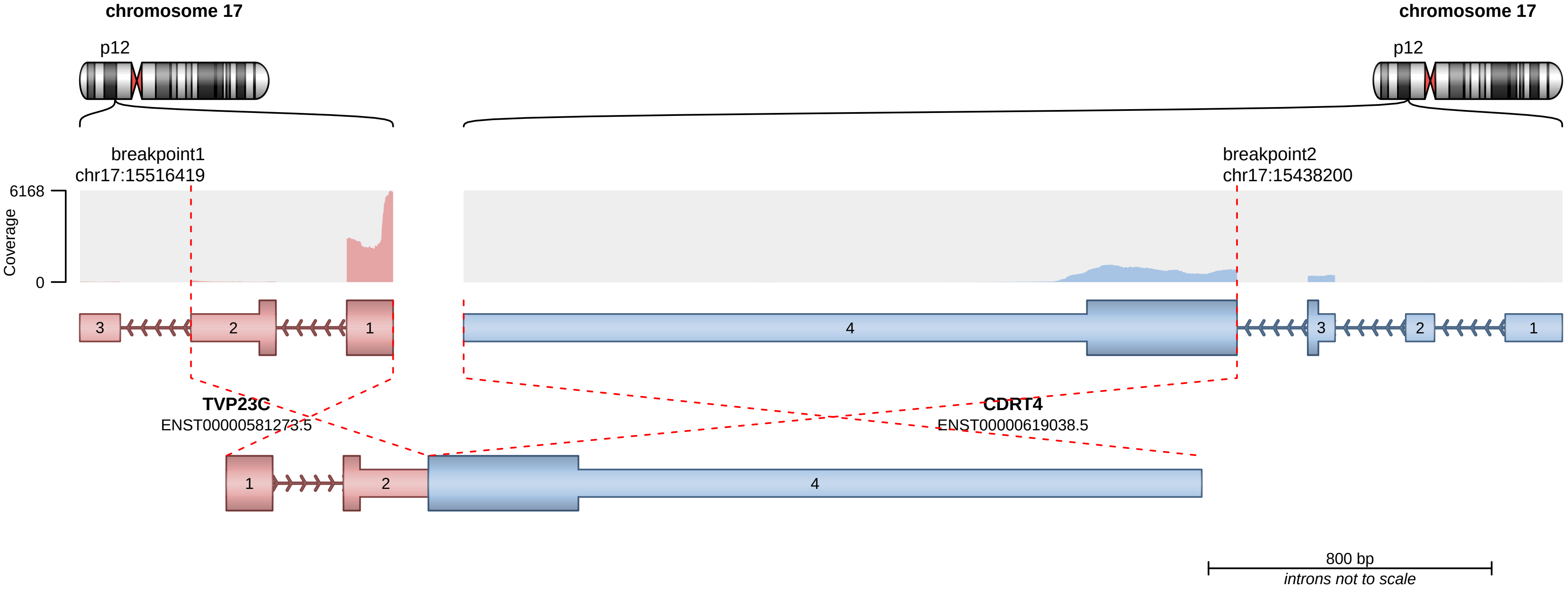


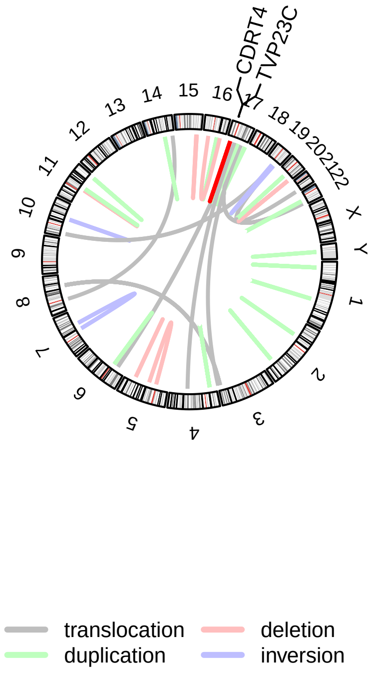
RETAINED PROTEIN DOMAINS
reading frame unclear



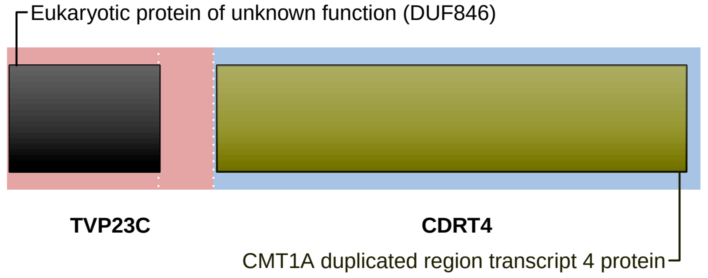
SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 3



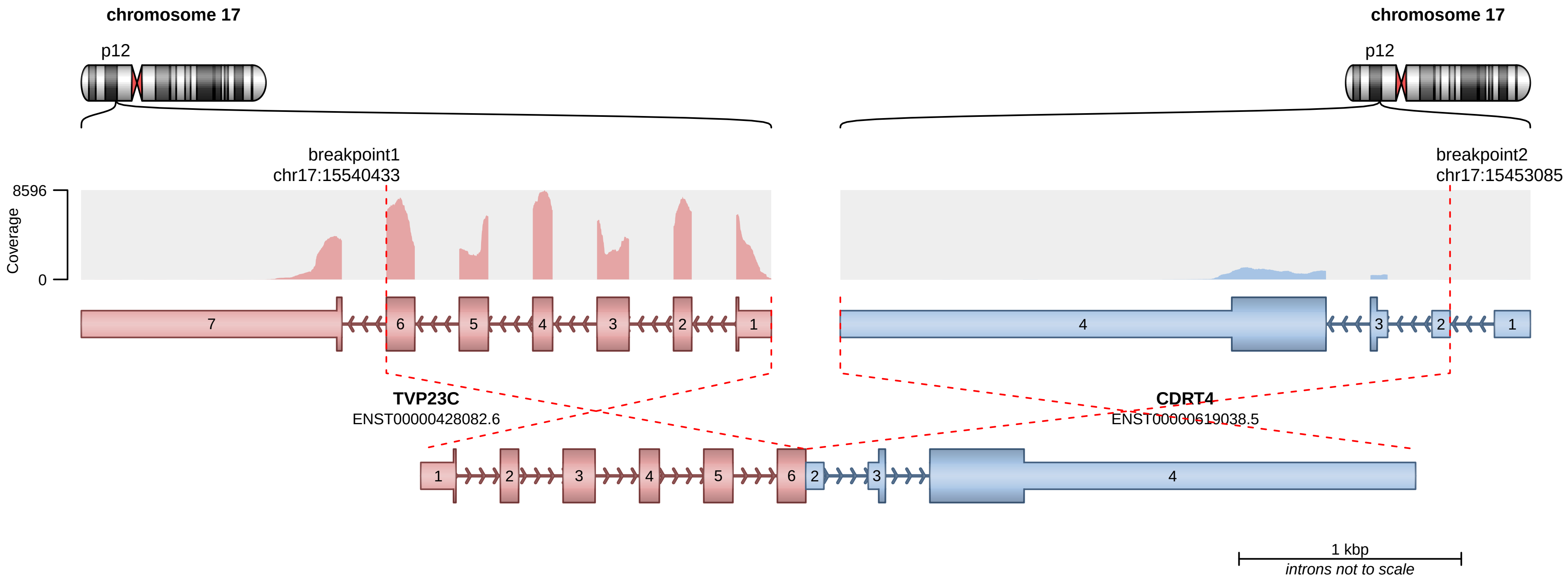


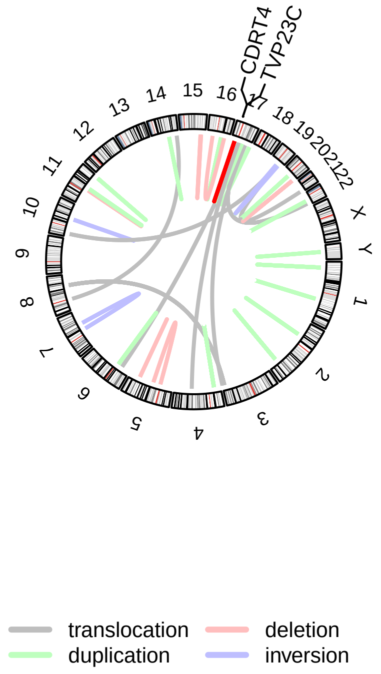
RETAINED PROTEIN DOMAINS
reading frame unclear

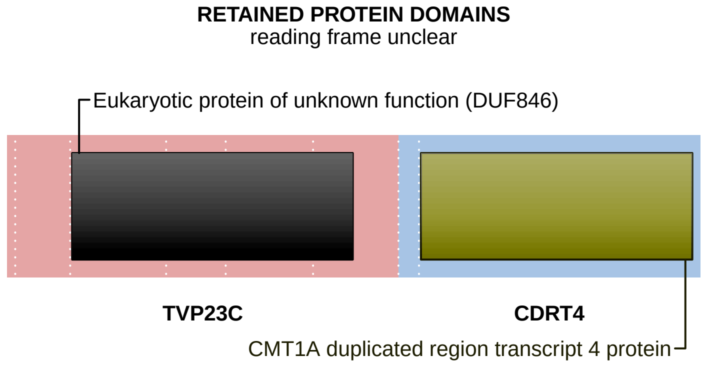


SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 1

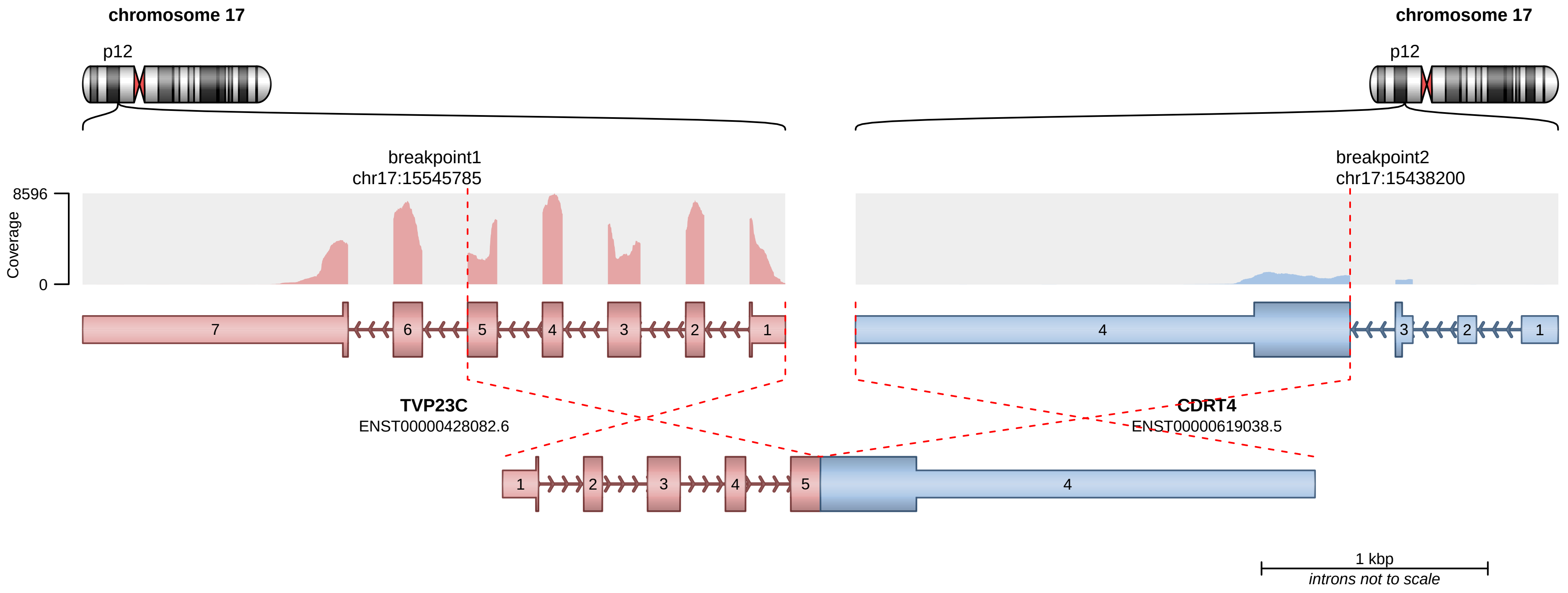


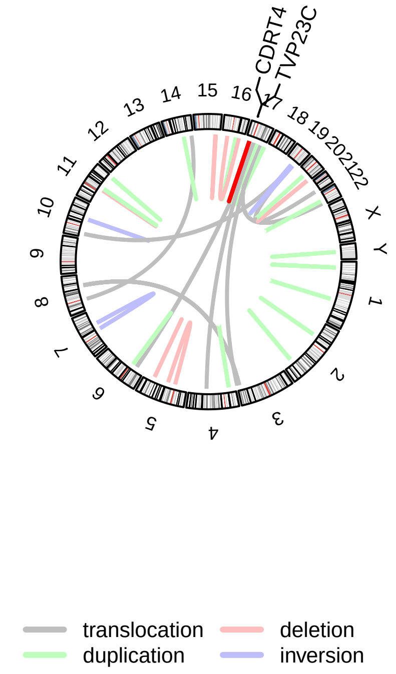




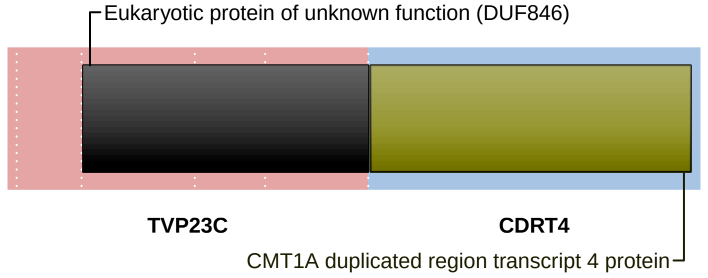
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 3



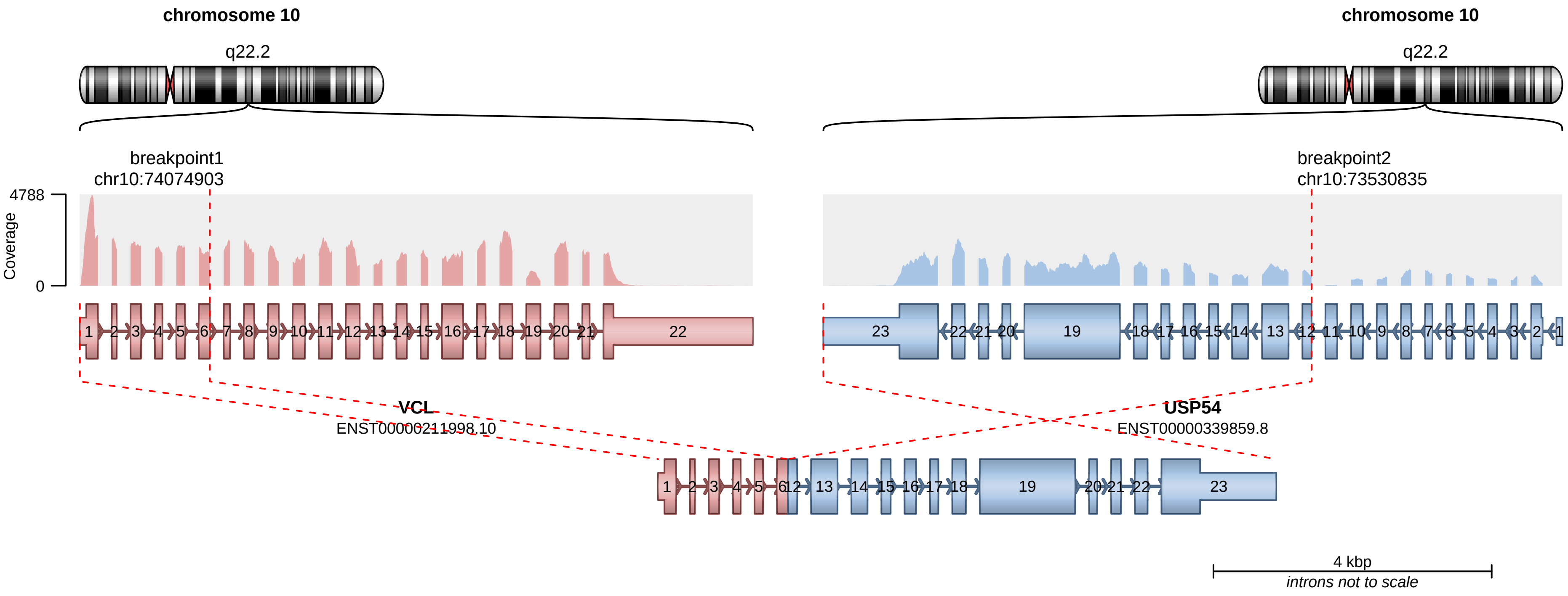


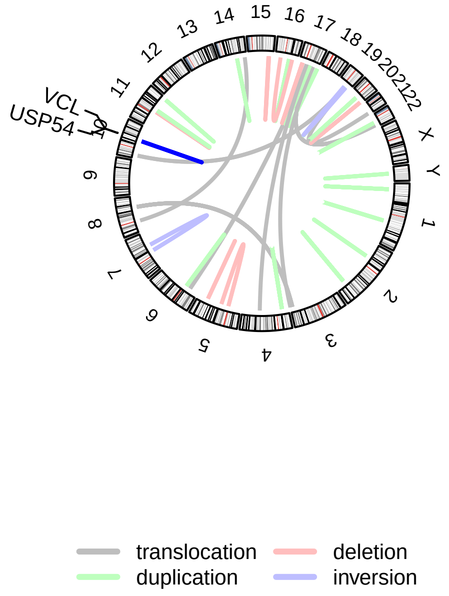
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

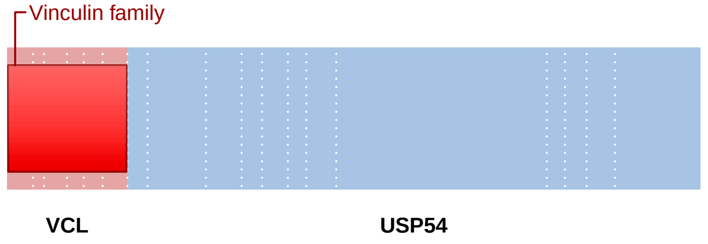
Split reads = 1
Discordant mates = 0





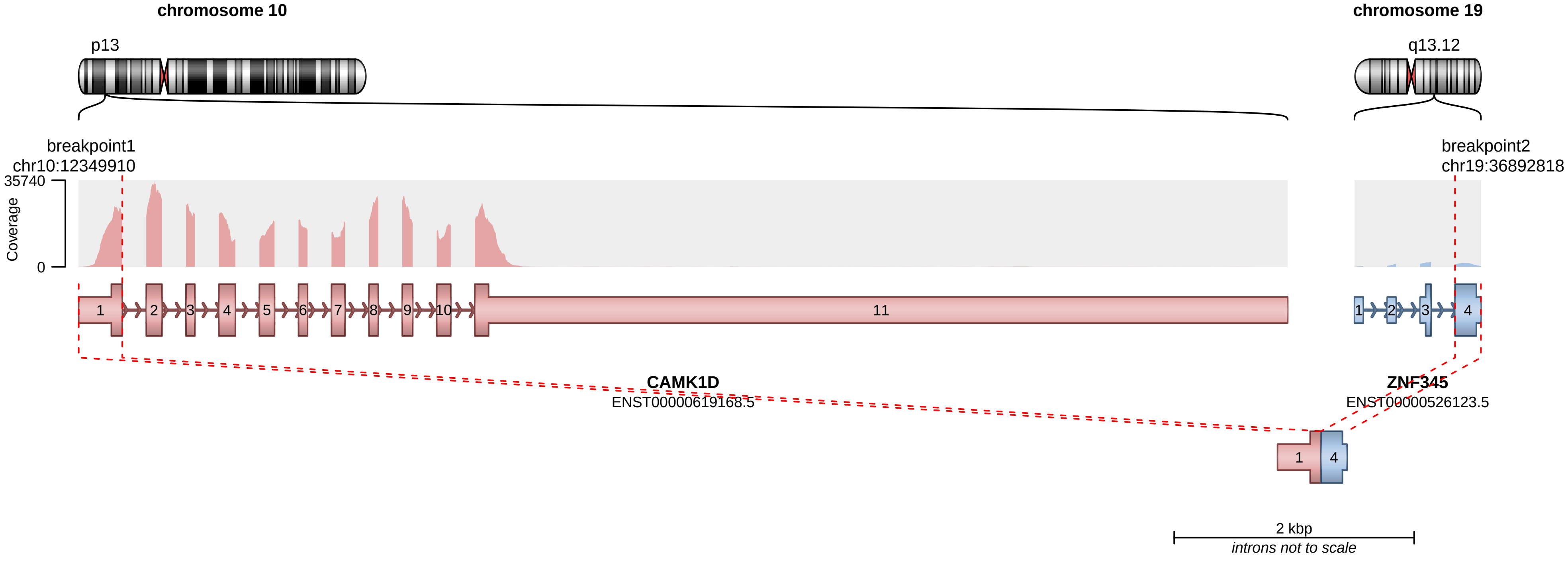
RETAINED PROTEIN DOMAINS

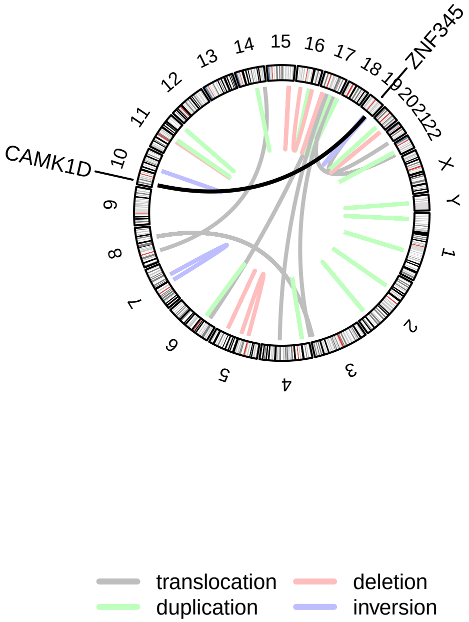
reading frame unclear



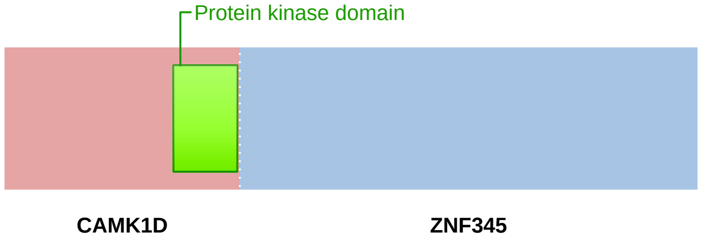
SUPPORTING READ COUNT

Split reads = 91
Discordant mates = 0



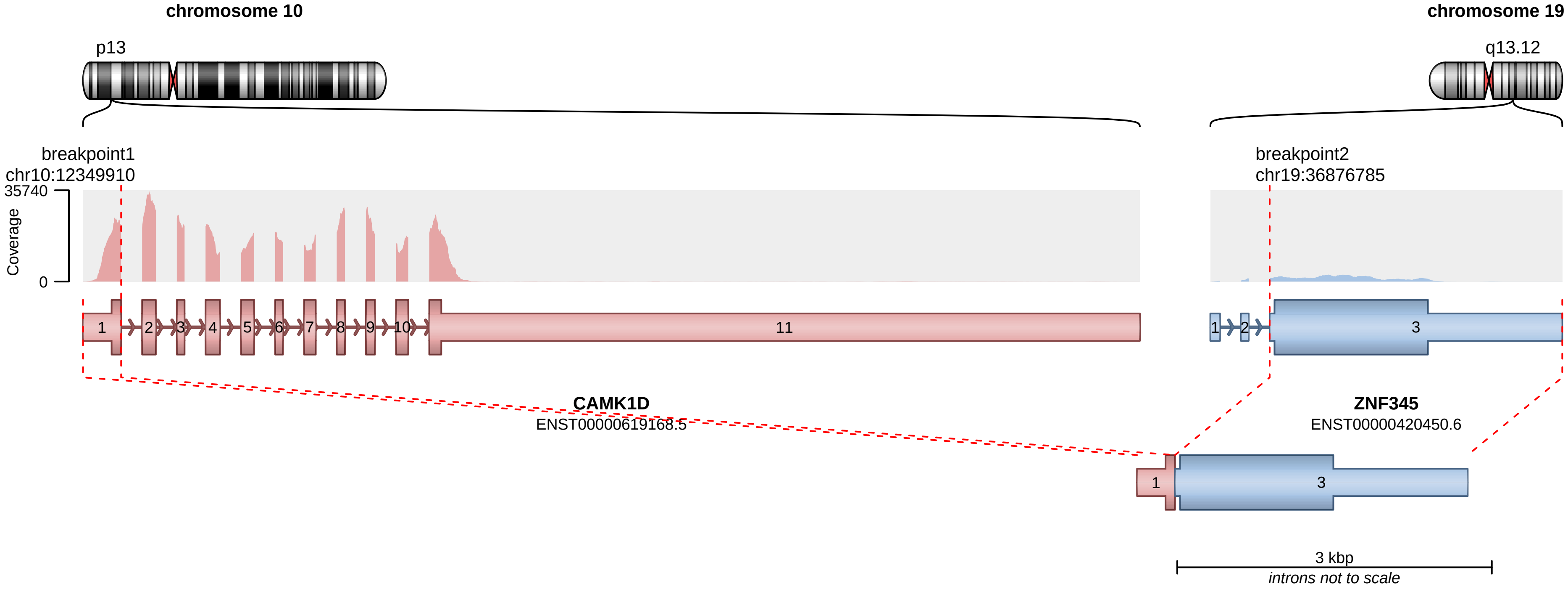


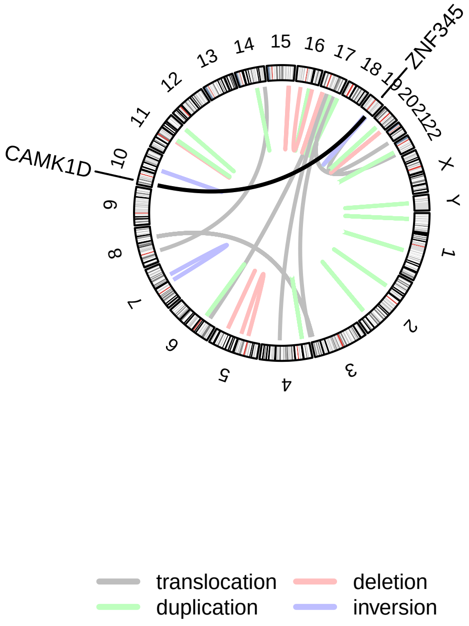
RETAINED PROTEIN DOMAINS
reading frame unclear

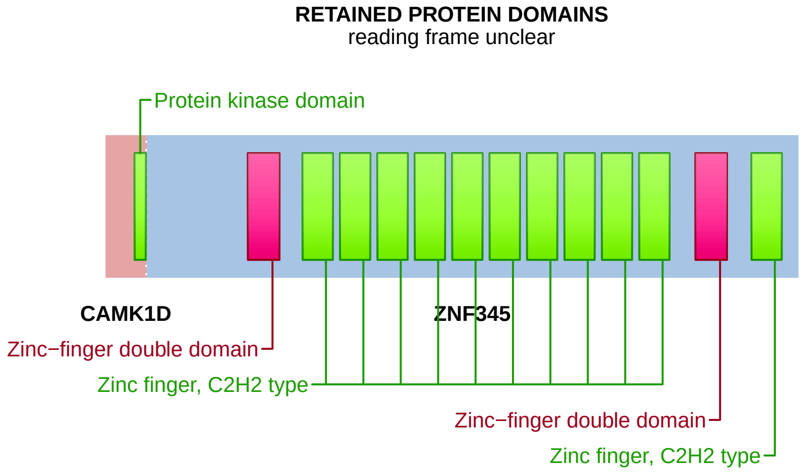


SUPPORTING READ COUNT

Split reads = 87
Discordant mates = 2

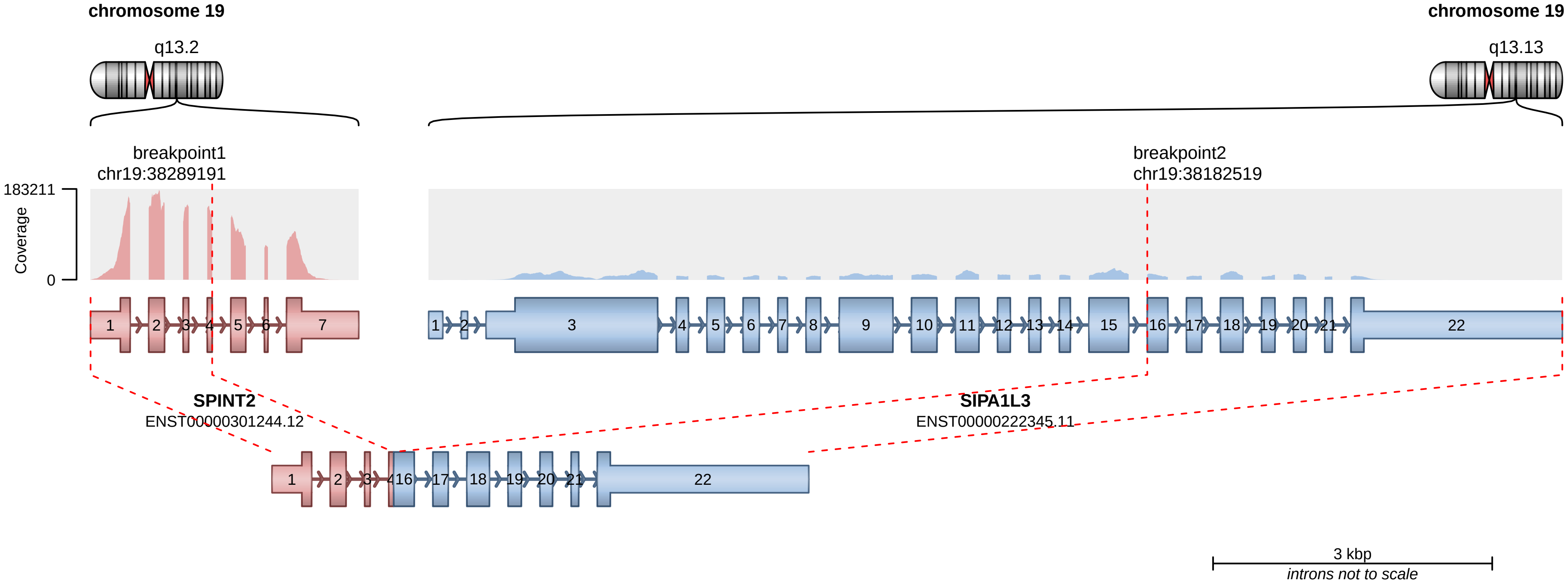


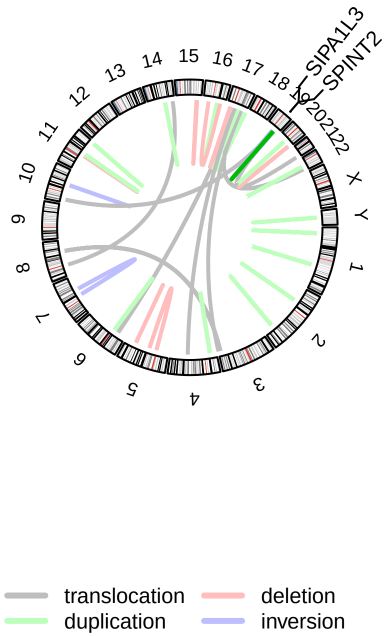


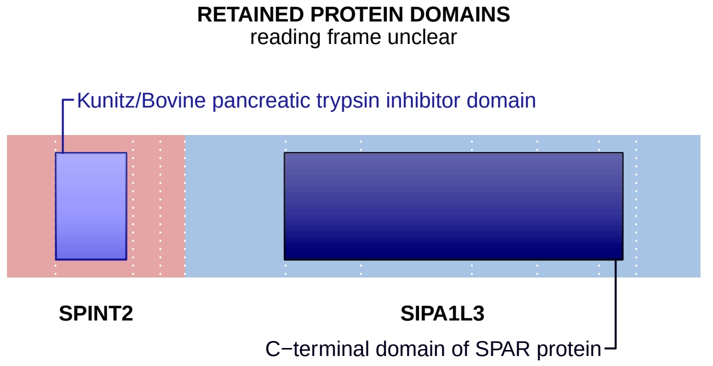


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 2

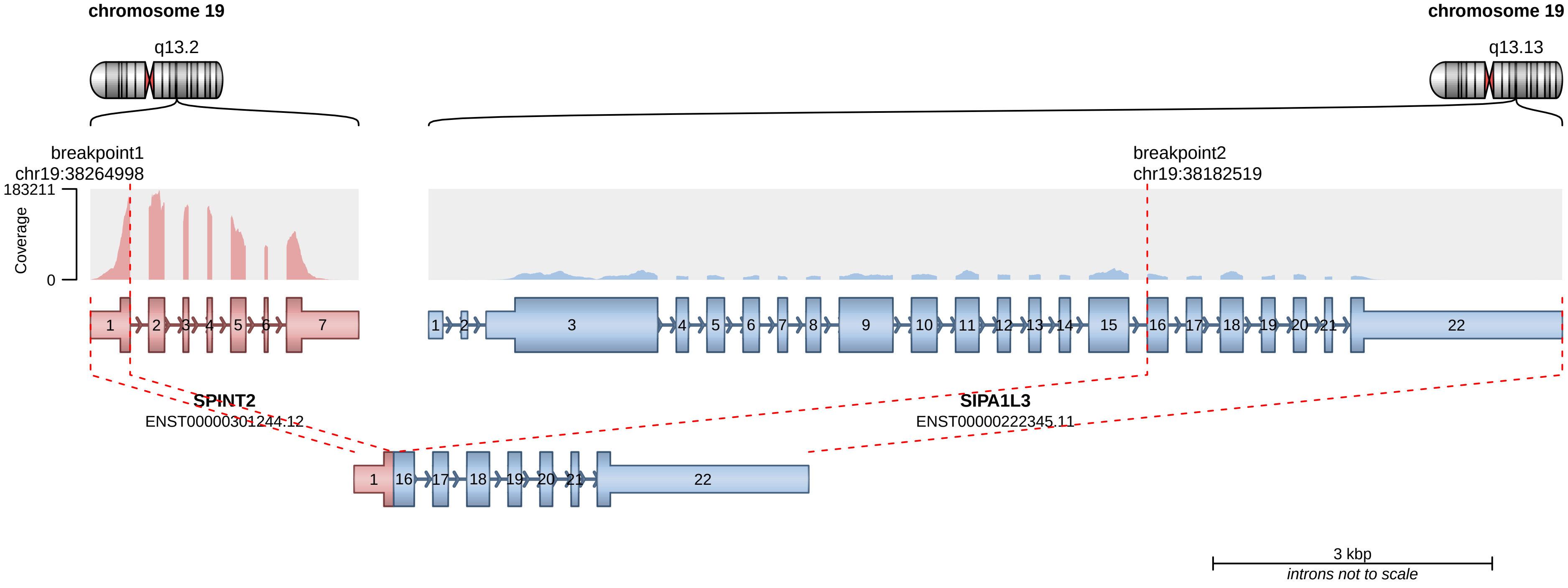


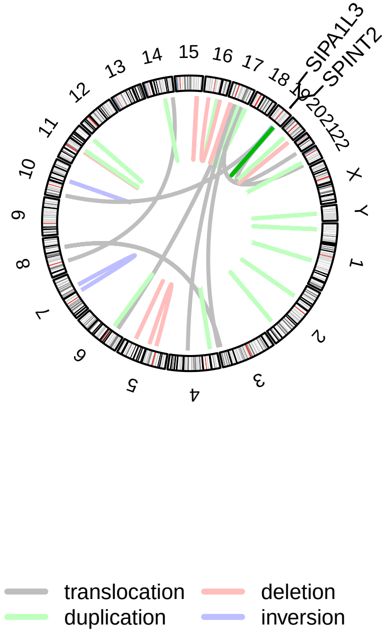


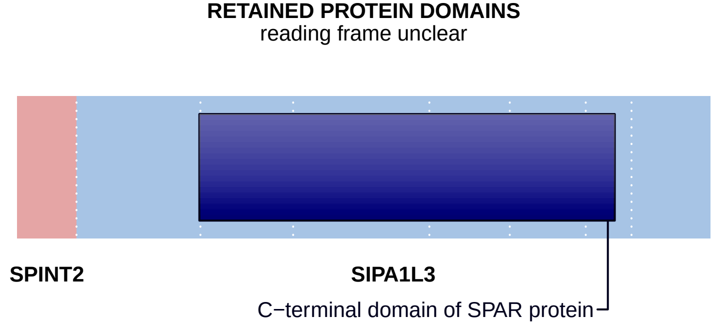


SUPPORTING READ COUNT

Split reads = 85
Discordant mates = 6

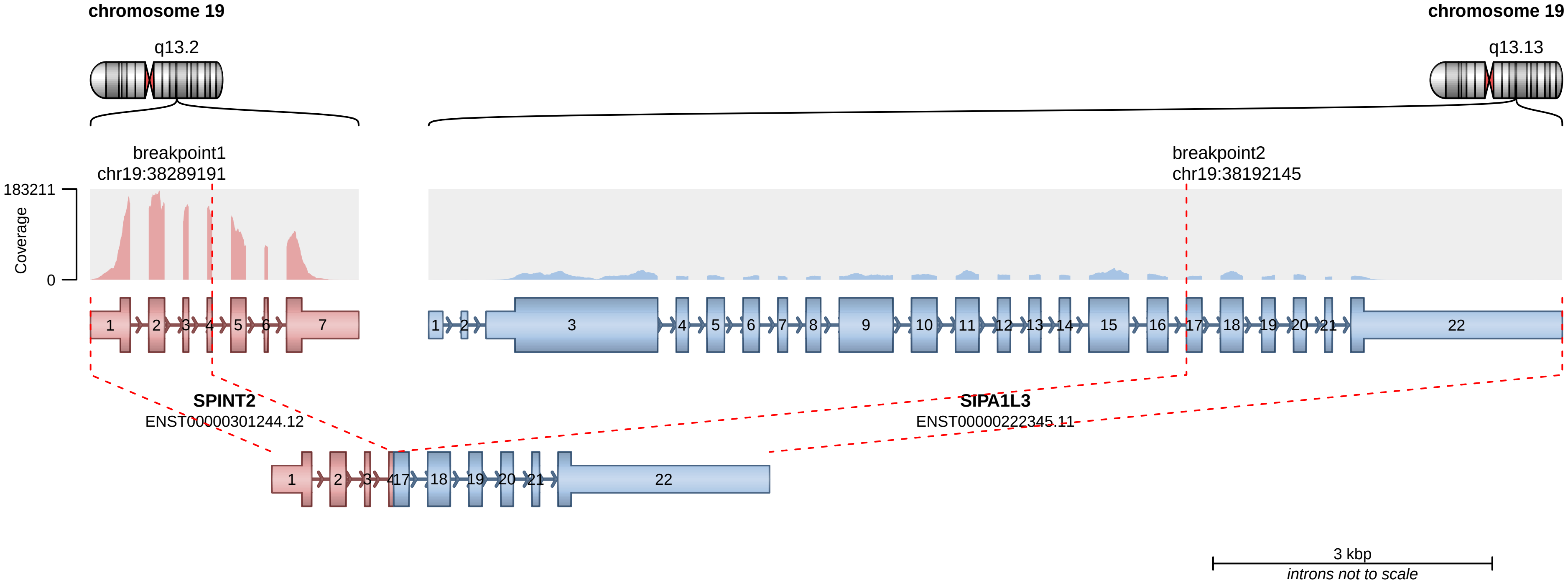


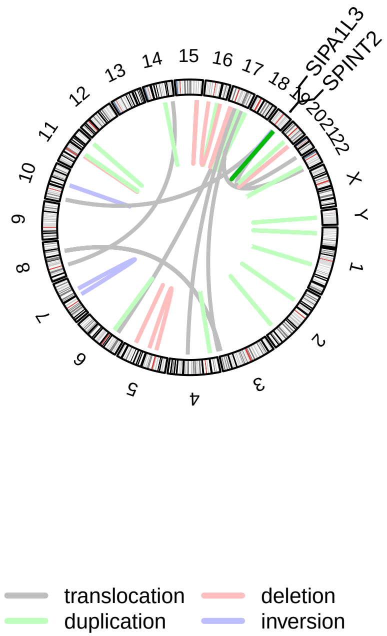


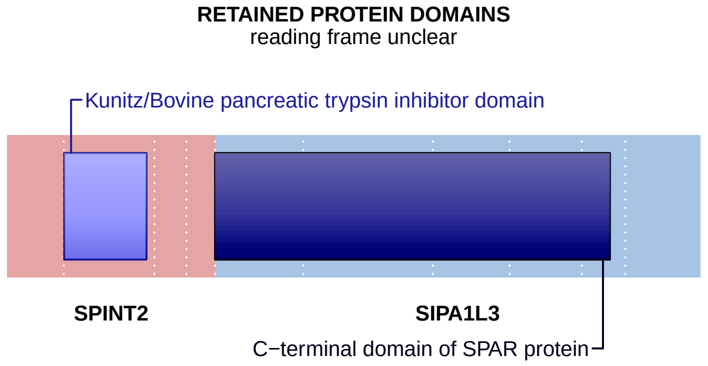


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

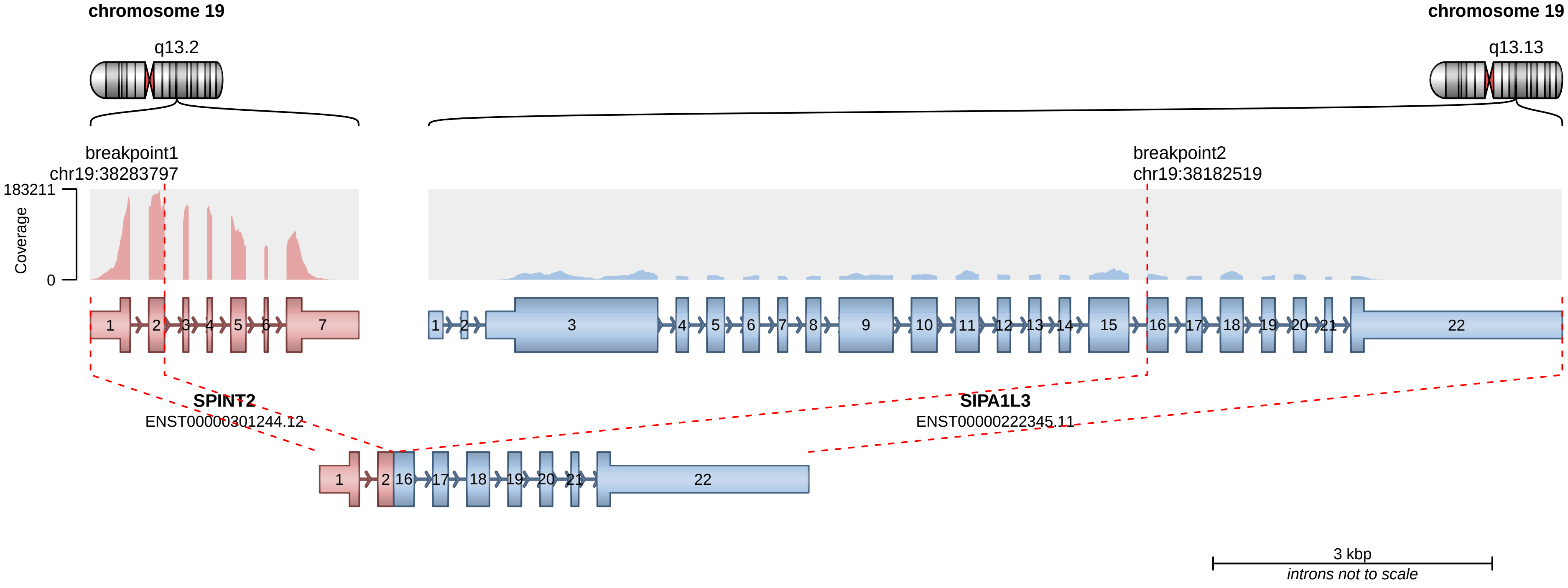


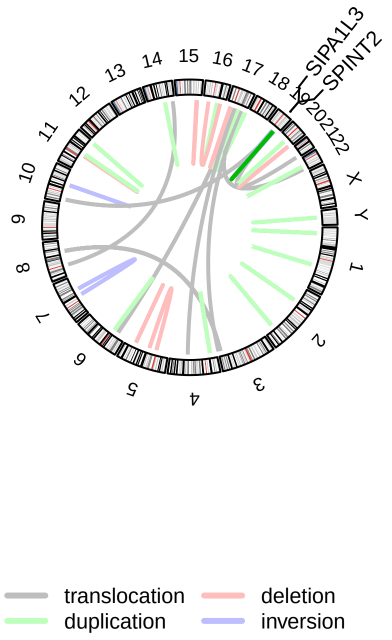


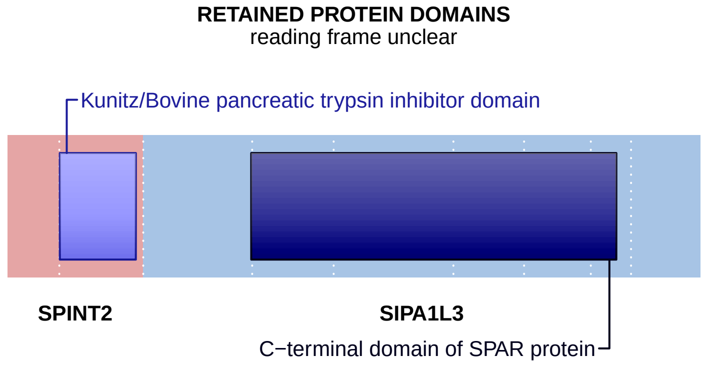


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

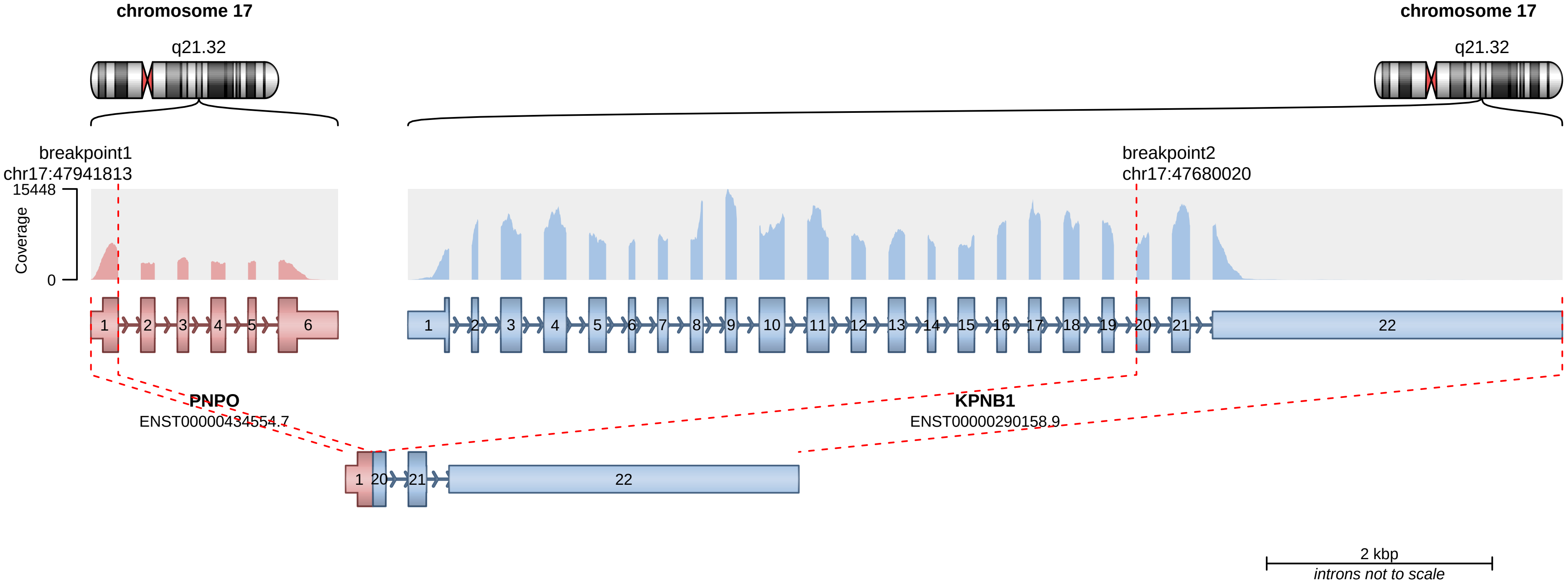


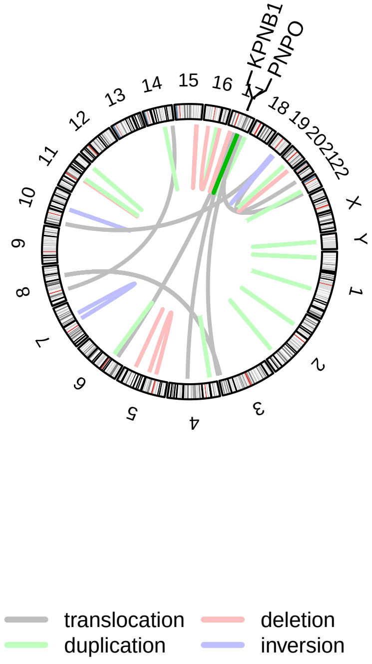




SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

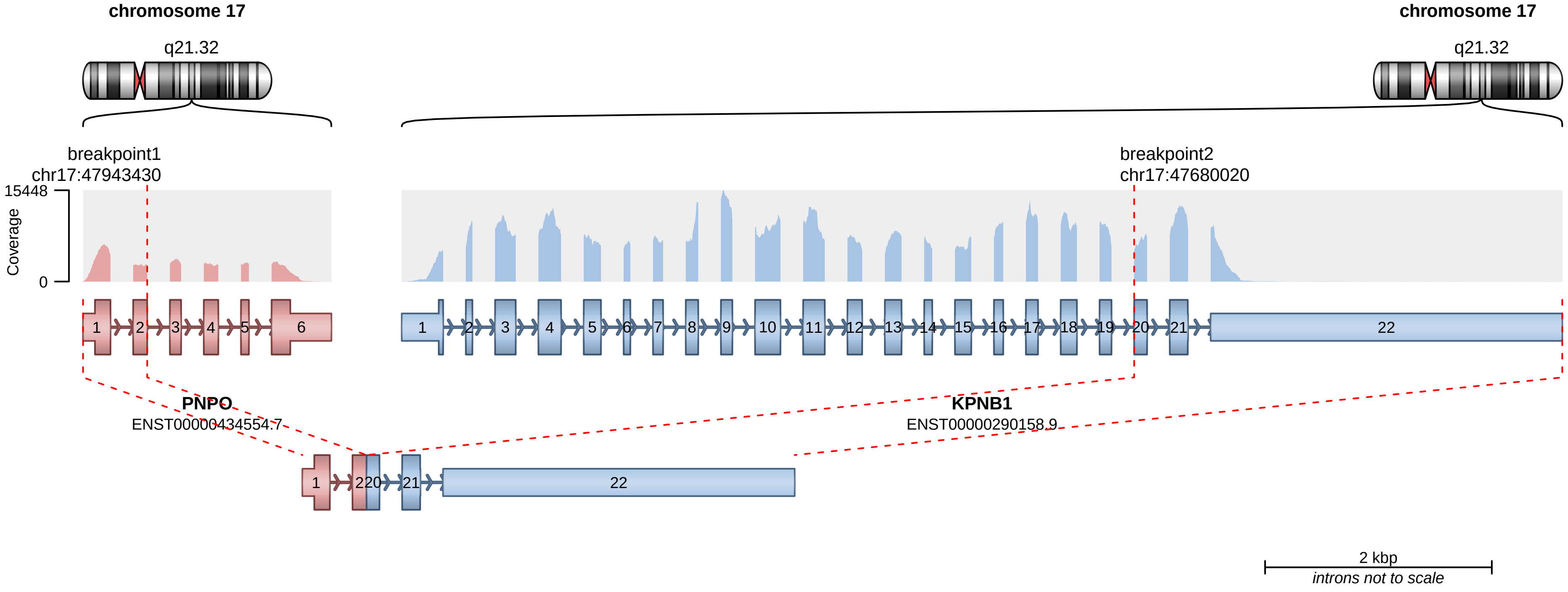


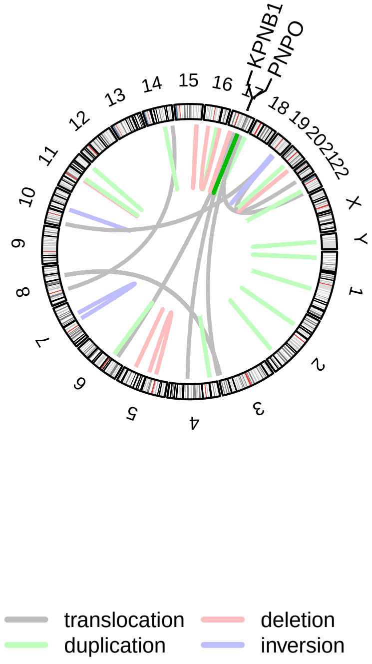


No protein domains retained in fusion.

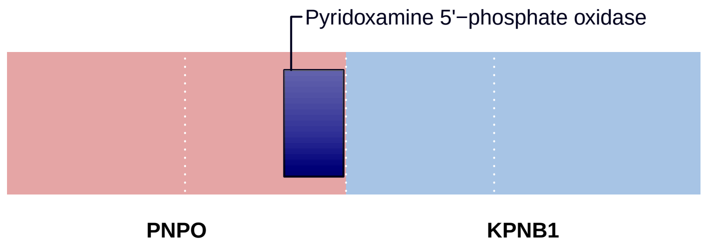
SUPPORTING READ COUNT

Split reads = 84
Discordant mates = 3



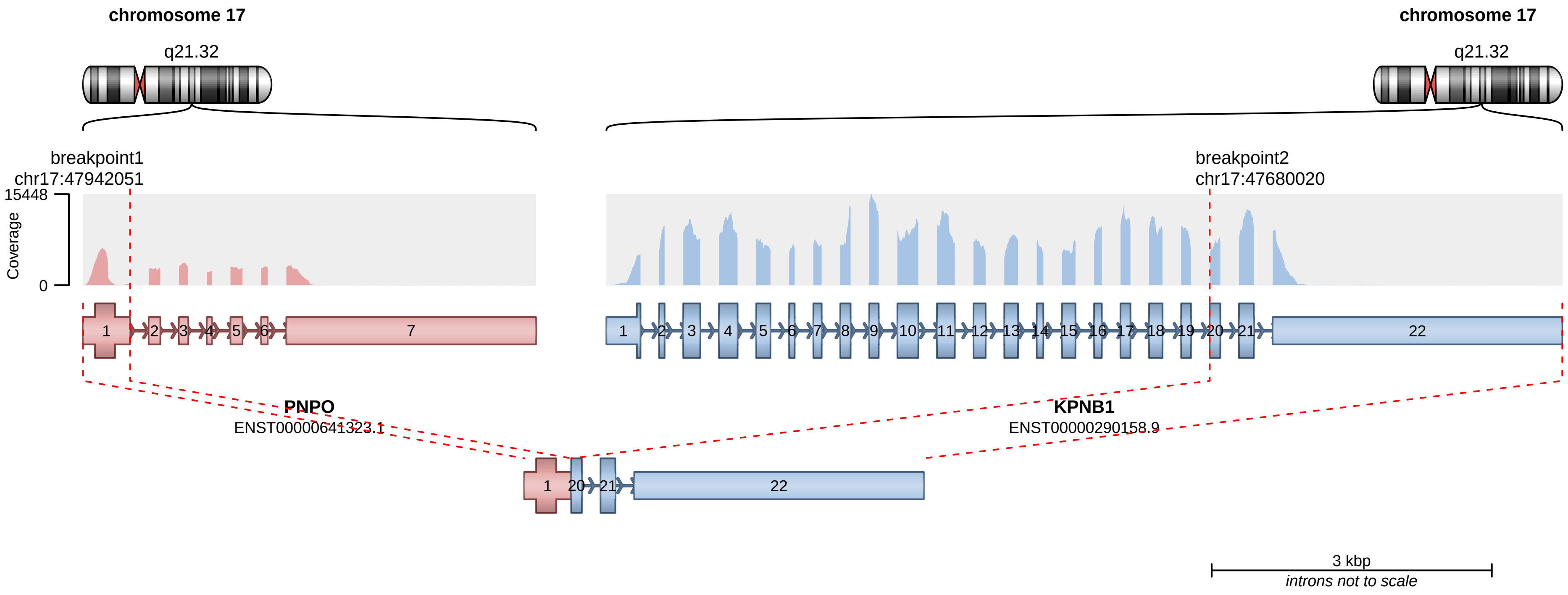


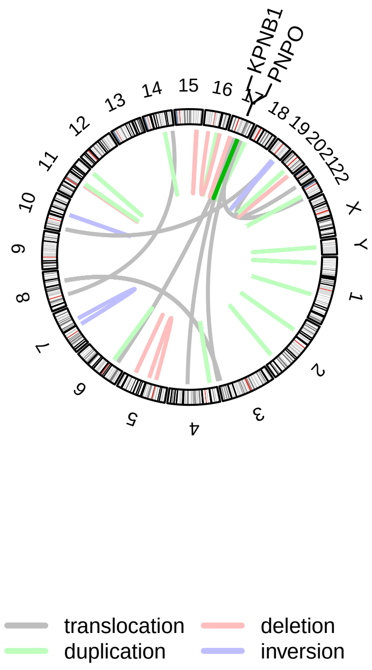
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 33
Discordant mates = 5

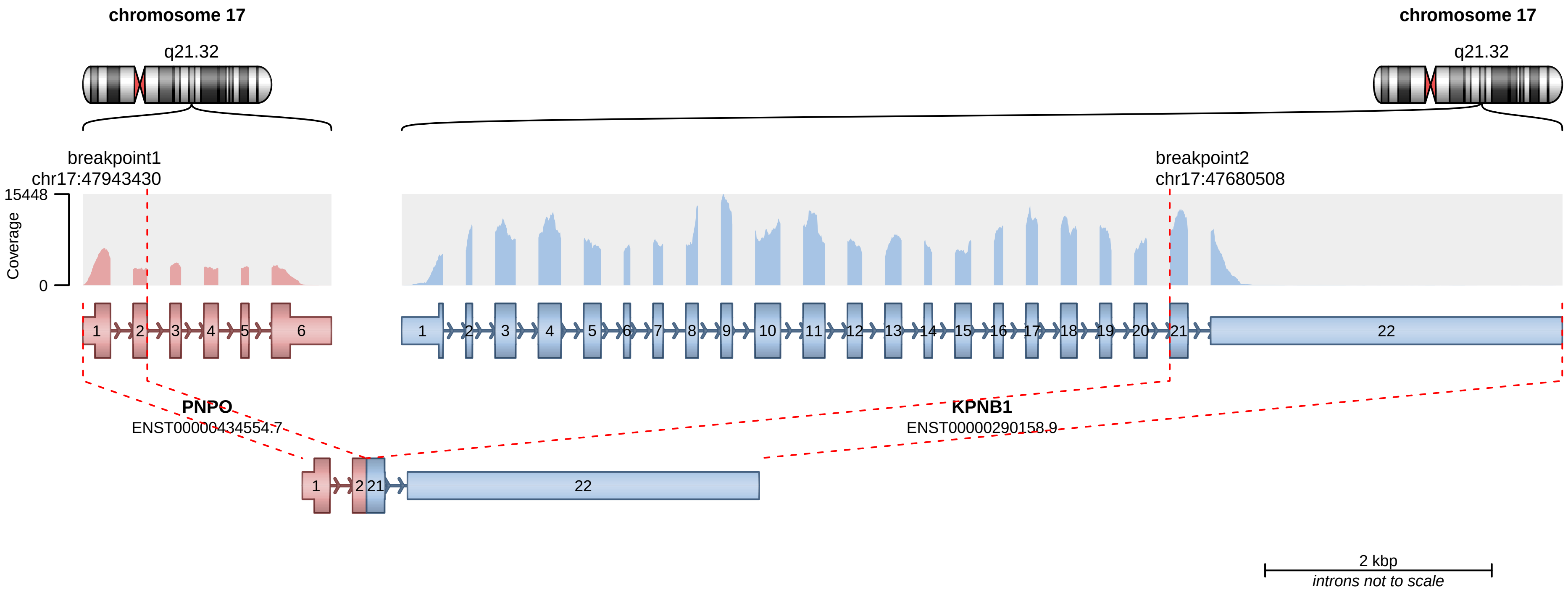


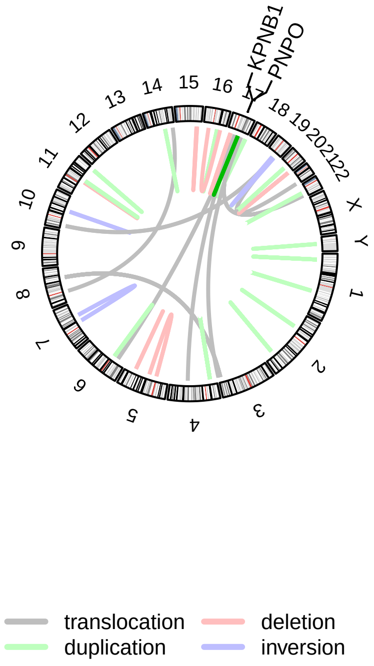


No protein domains retained in fusion.

SUPPORTING READ COUNT

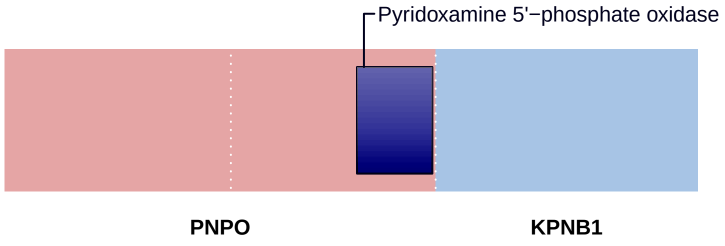
Split reads = 16
Discordant mates = 3





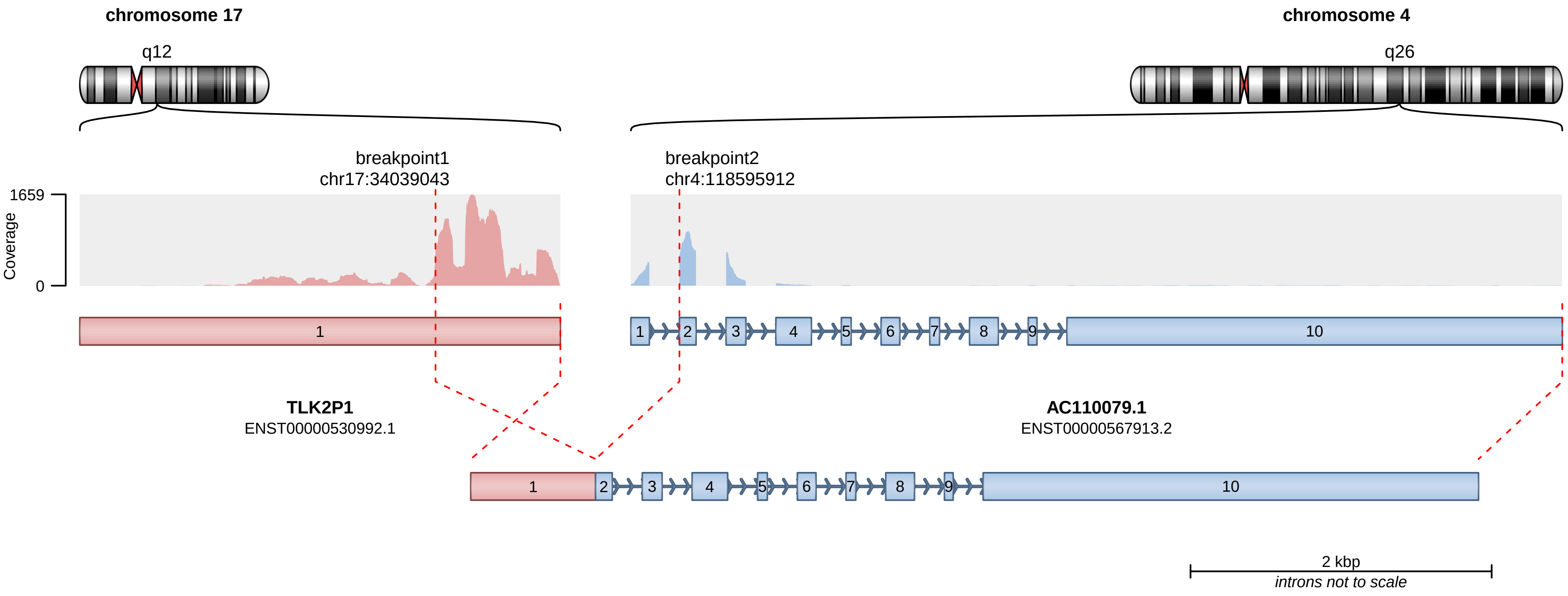
RETAINED PROTEIN DOMAINS

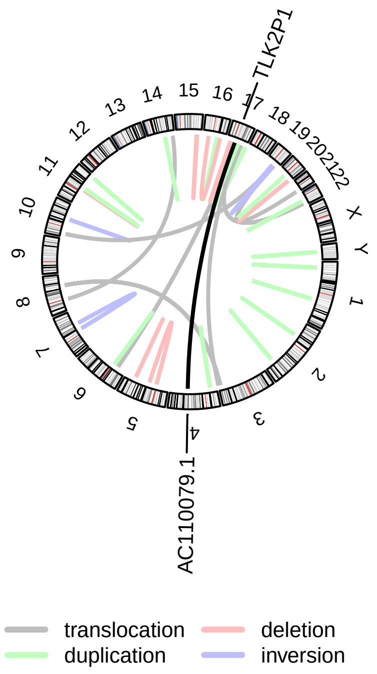
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

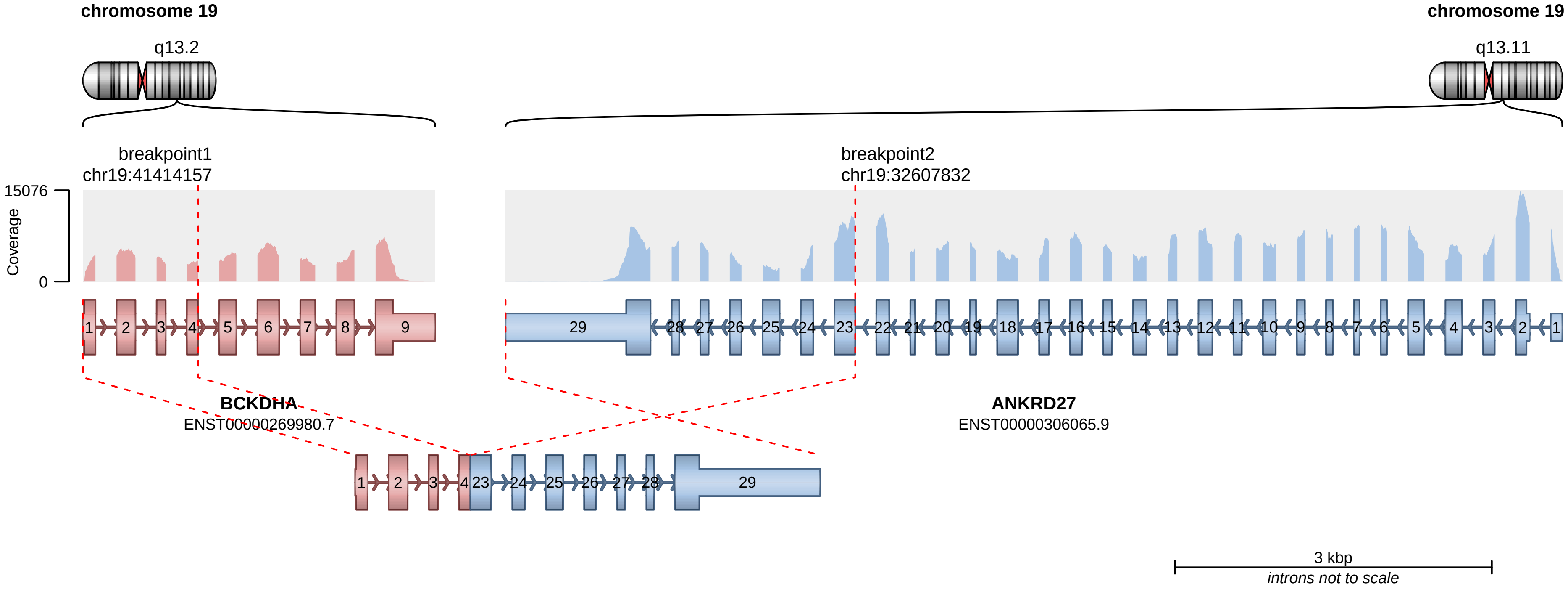


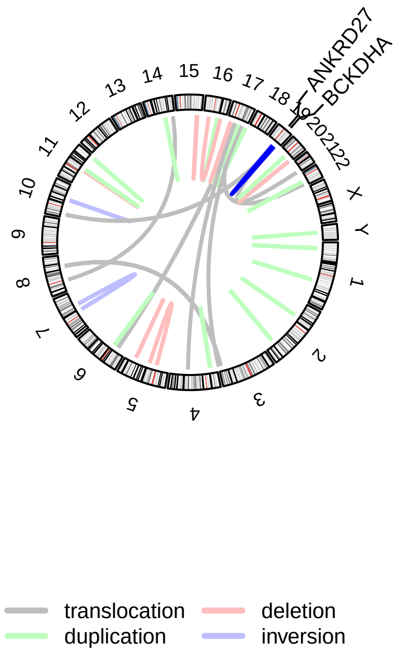


Genes are not protein−coding.

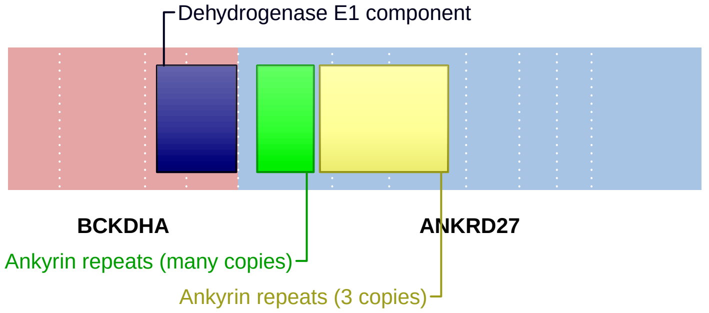
SUPPORTING READ COUNT

Split reads = 83
Discordant mates = 0



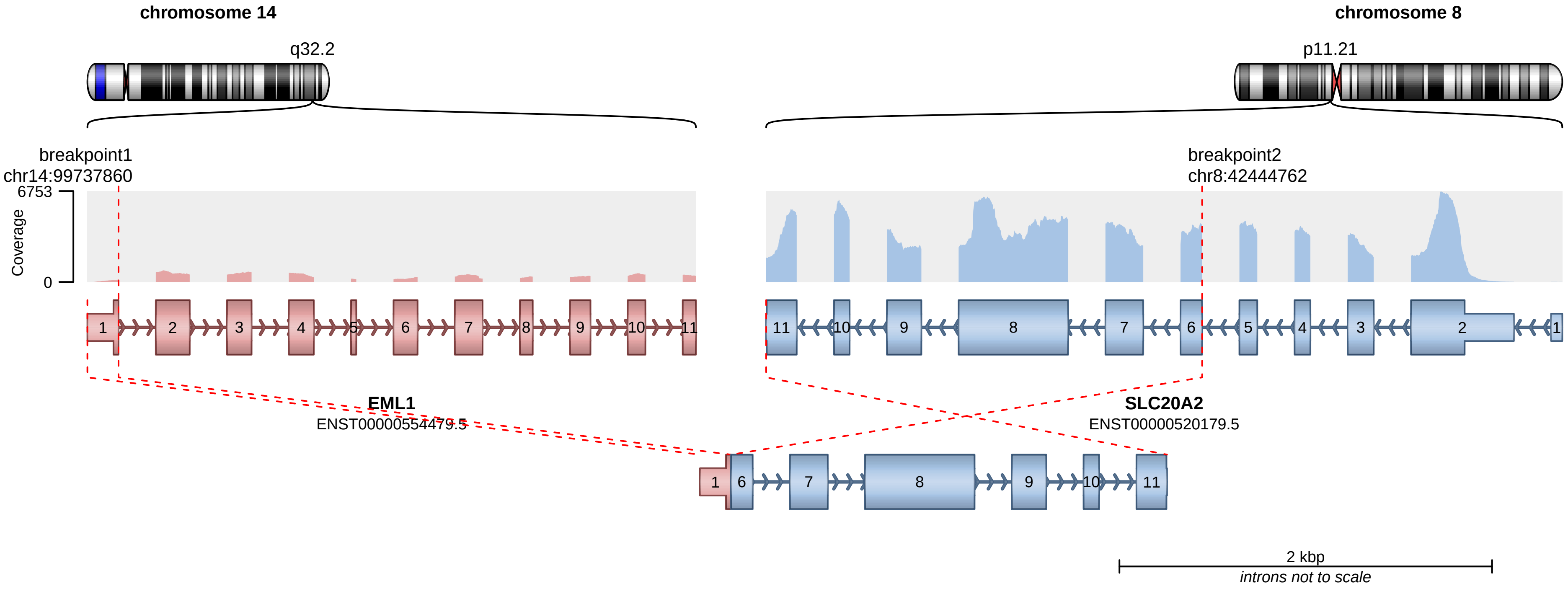


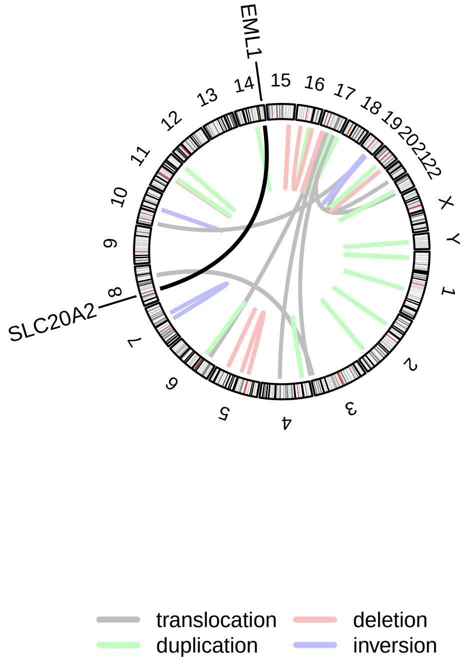
RETAINED PROTEIN DOMAINS
reading frame unclear

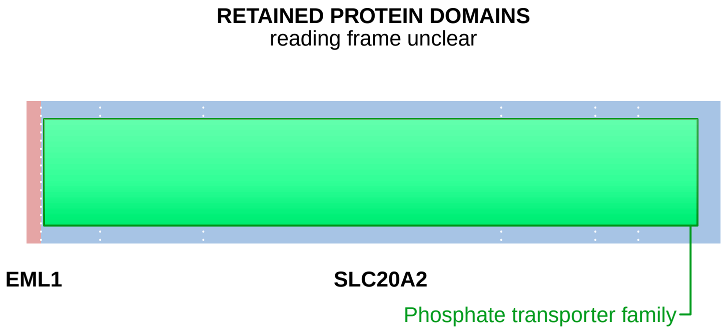


SUPPORTING READ COUNT

Split reads = 66
Discordant mates = 0

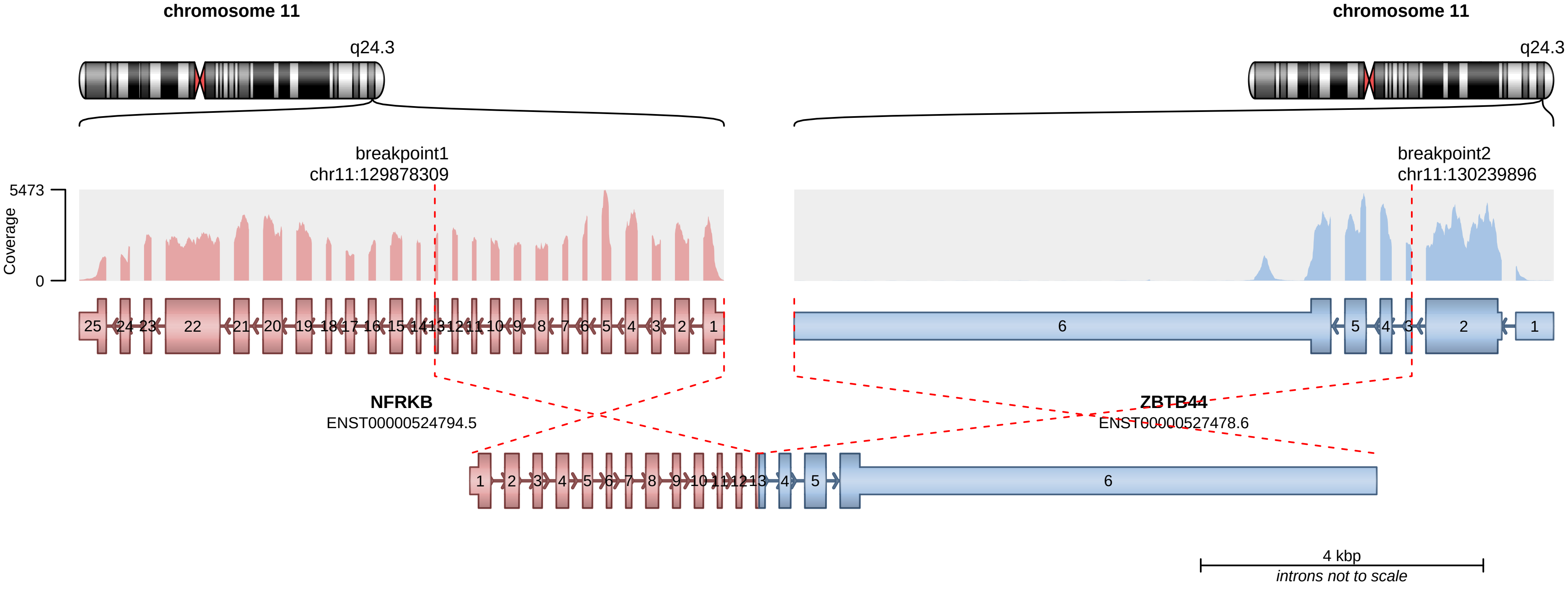


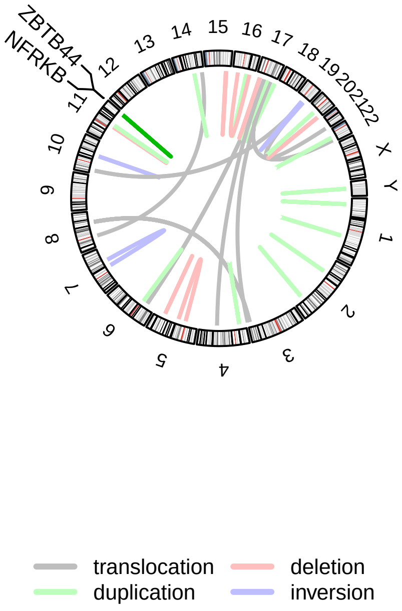


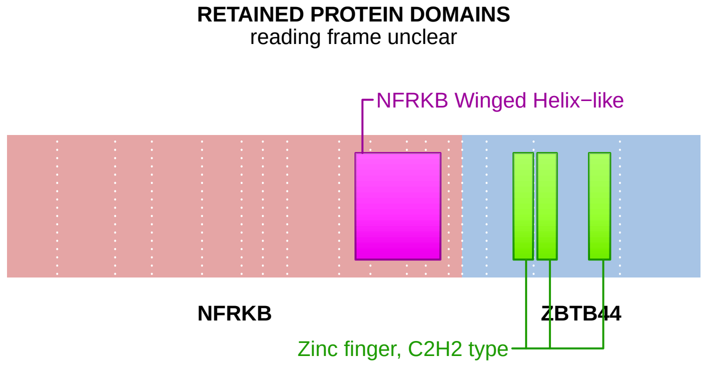


SUPPORTING READ COUNT

Split reads = 62
Discordant mates = 1

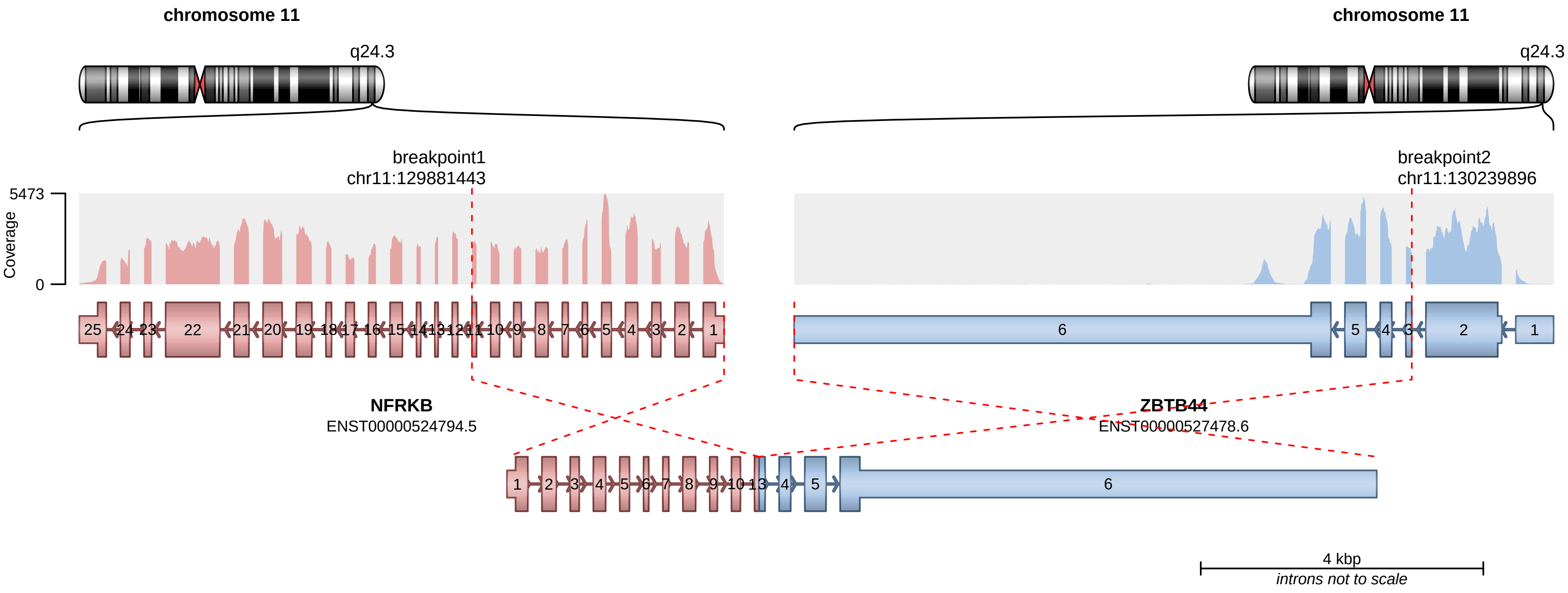


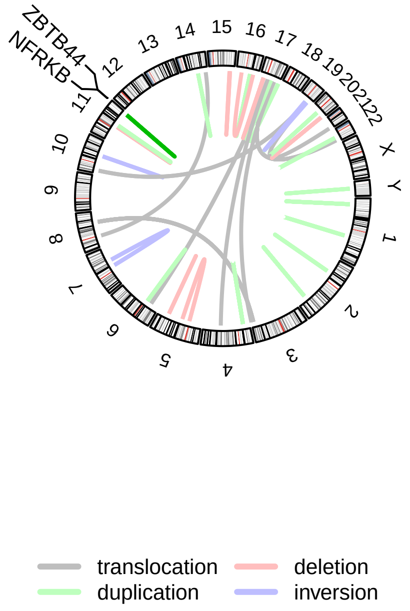


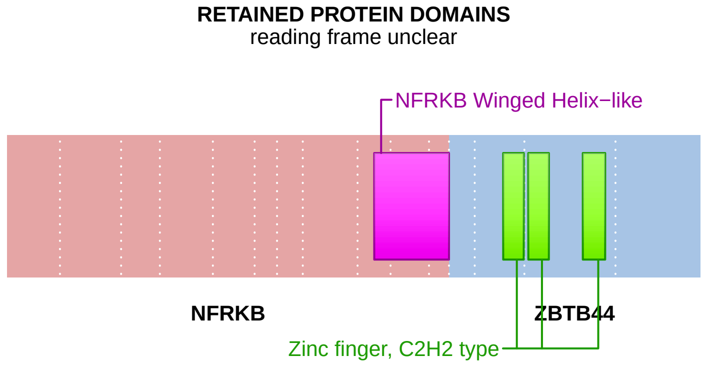


SUPPORTING READ COUNT

Split reads = 55
Discordant mates = 3

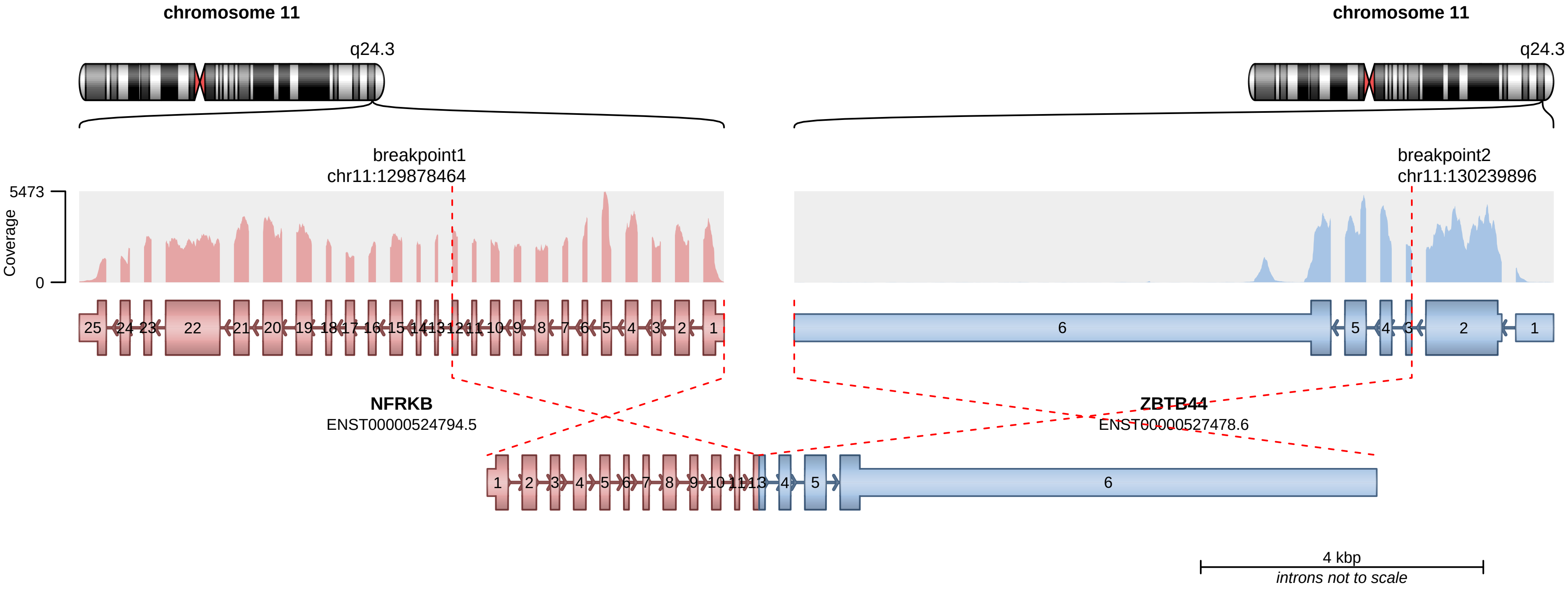


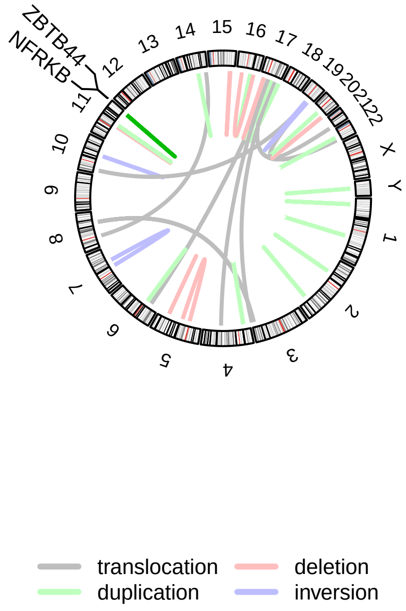




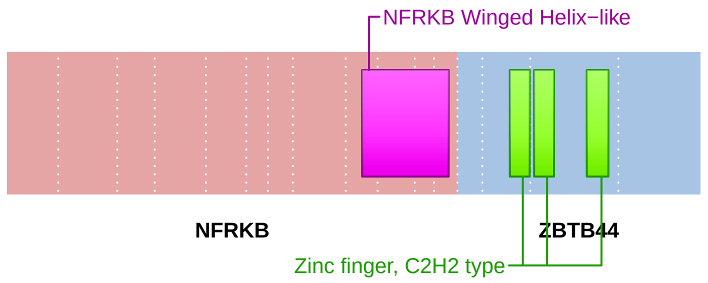
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 1



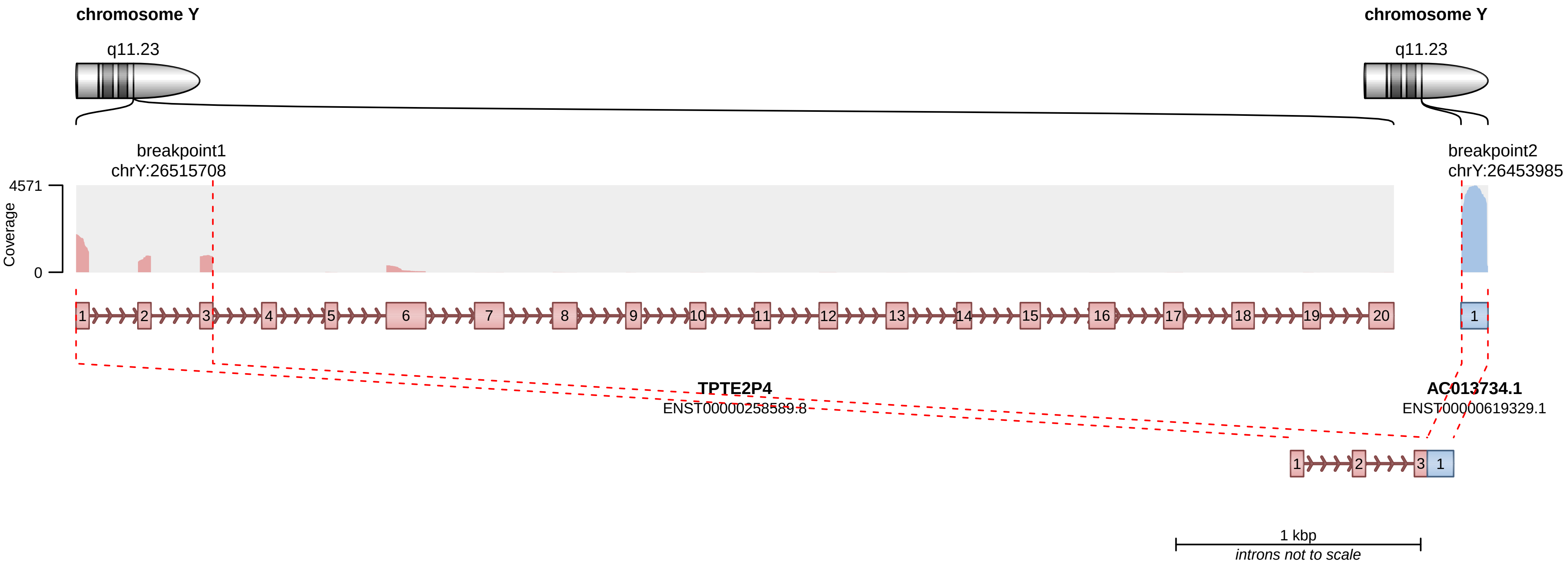


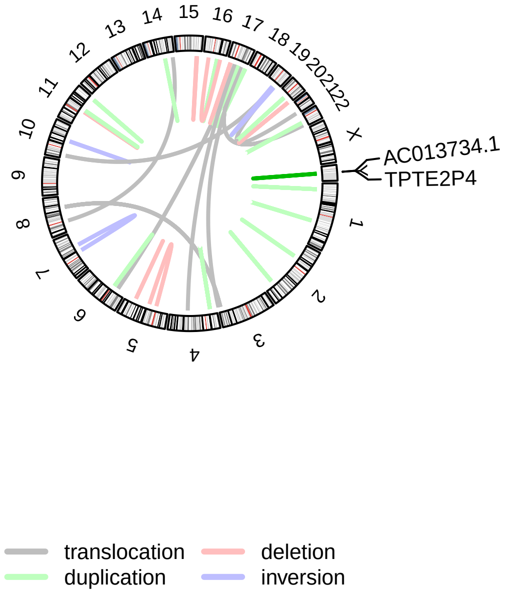
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 2

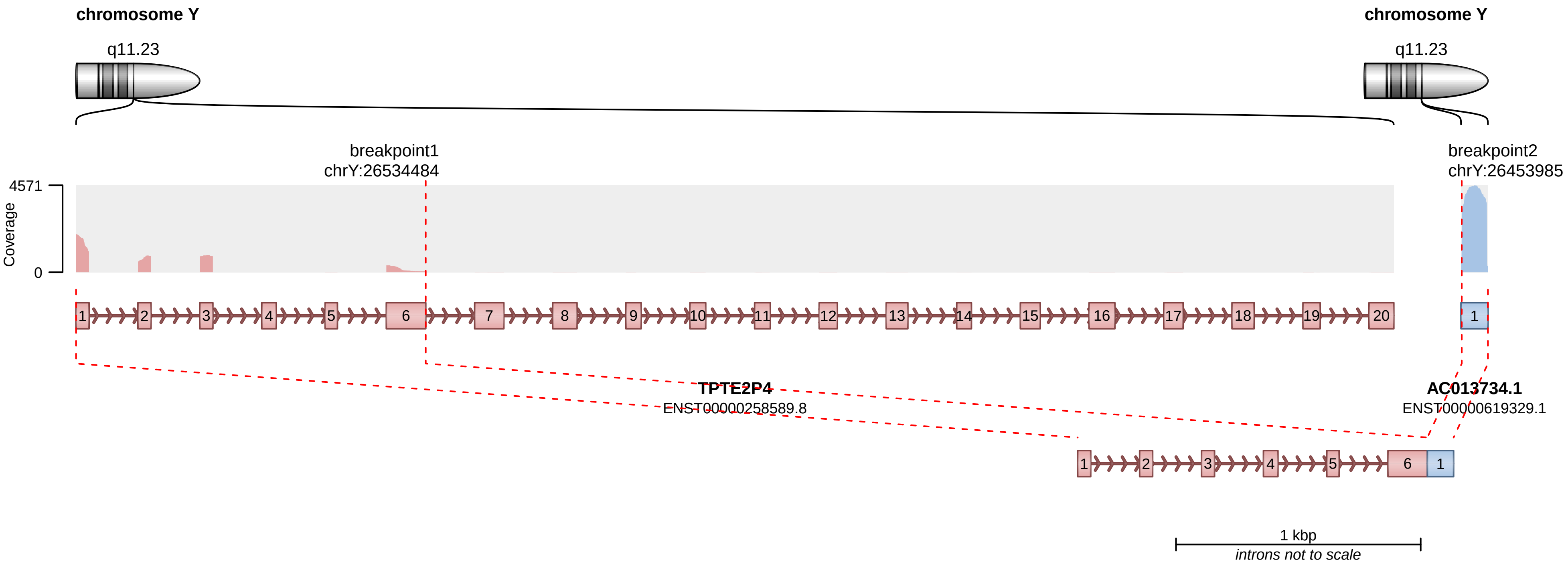


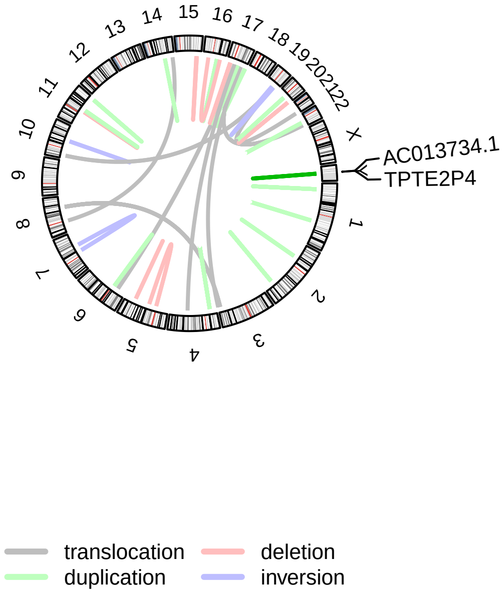


Genes are not protein−coding.

SUPPORTING READ COUNT

Split reads = 23
Discordant mates = 0

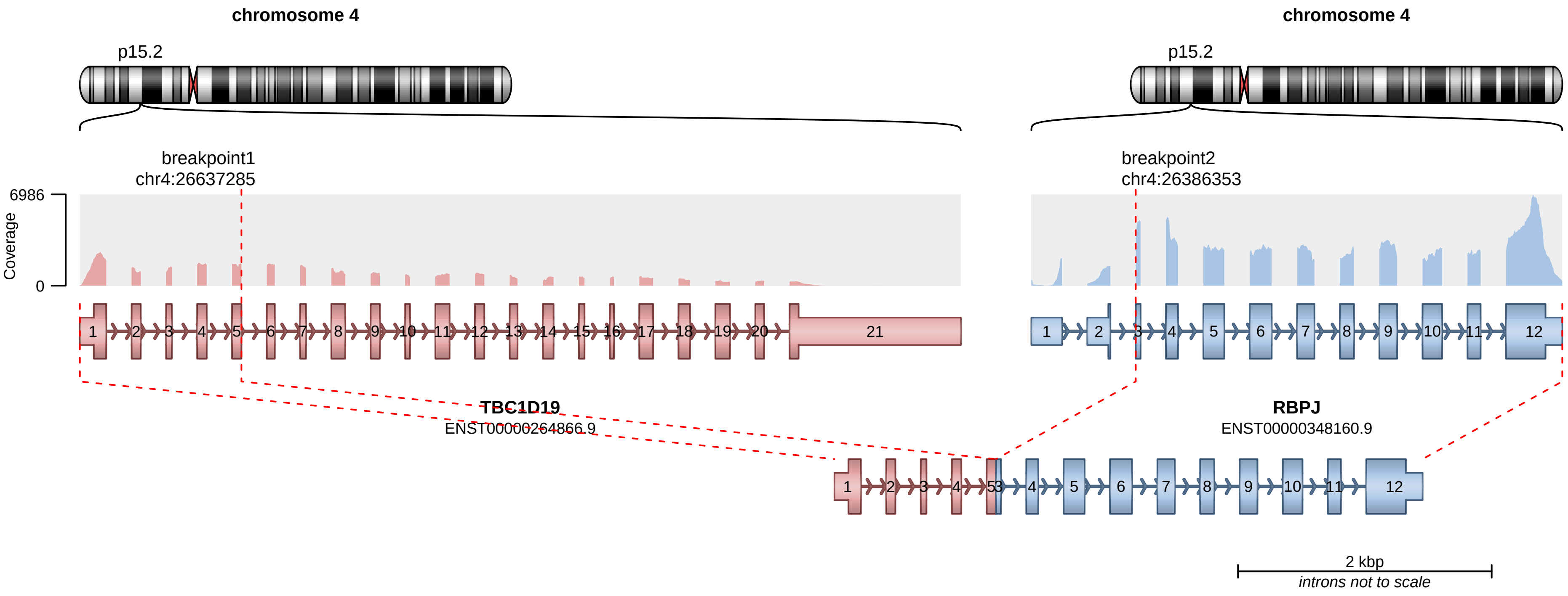


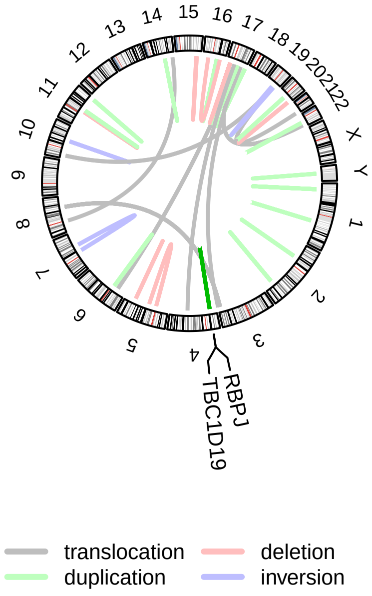


Genes are not protein−coding.

SUPPORTING READ COUNT

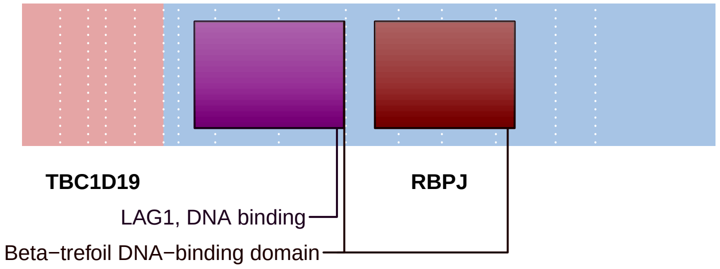
Split reads = 6
Discordant mates = 0





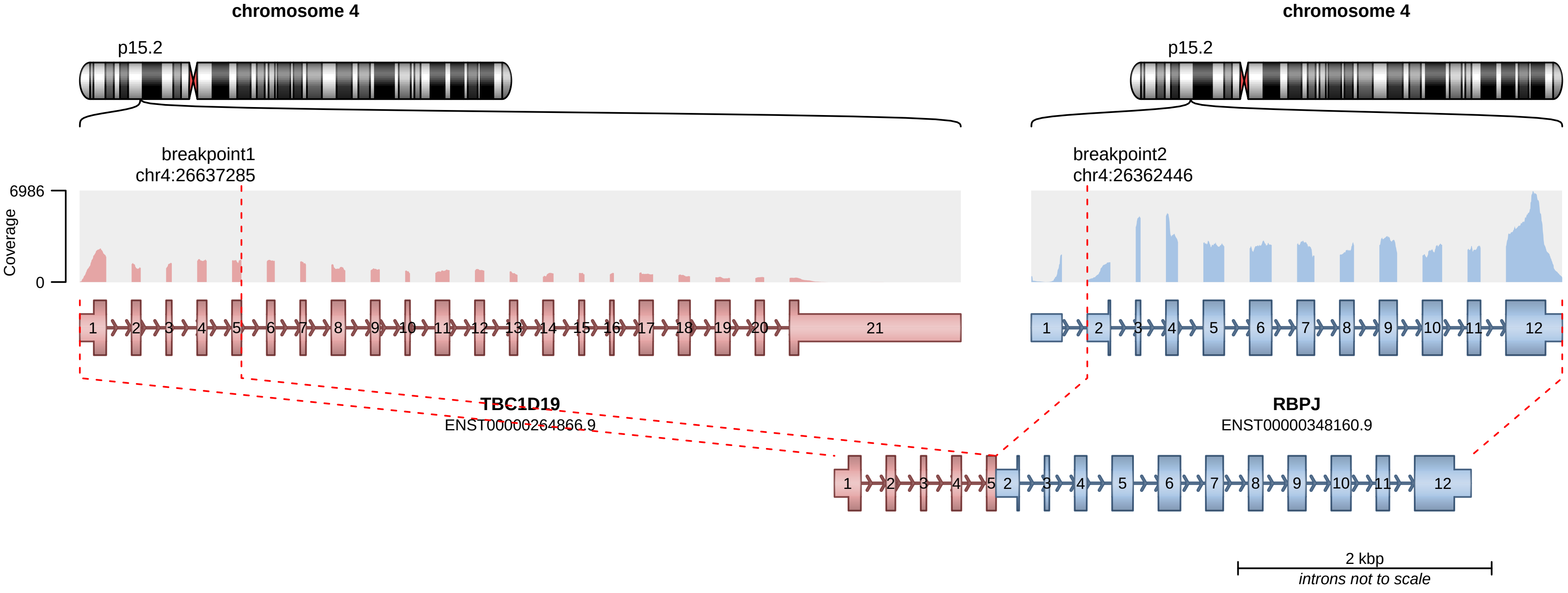
RETAINED PROTEIN DOMAINS

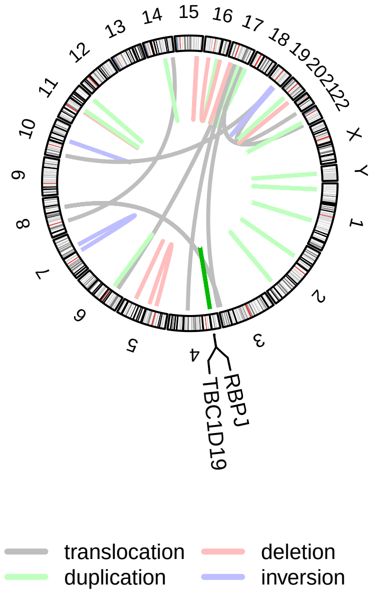
reading frame unclear



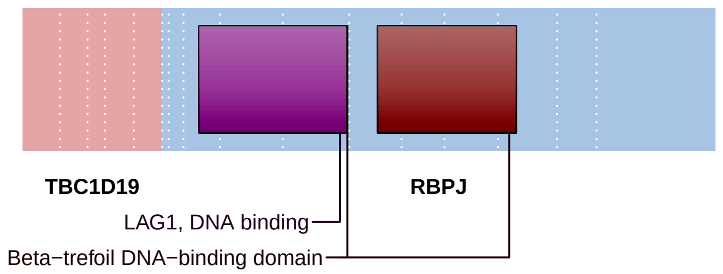
SUPPORTING READ COUNT

Split reads = 21
Discordant mates = 1



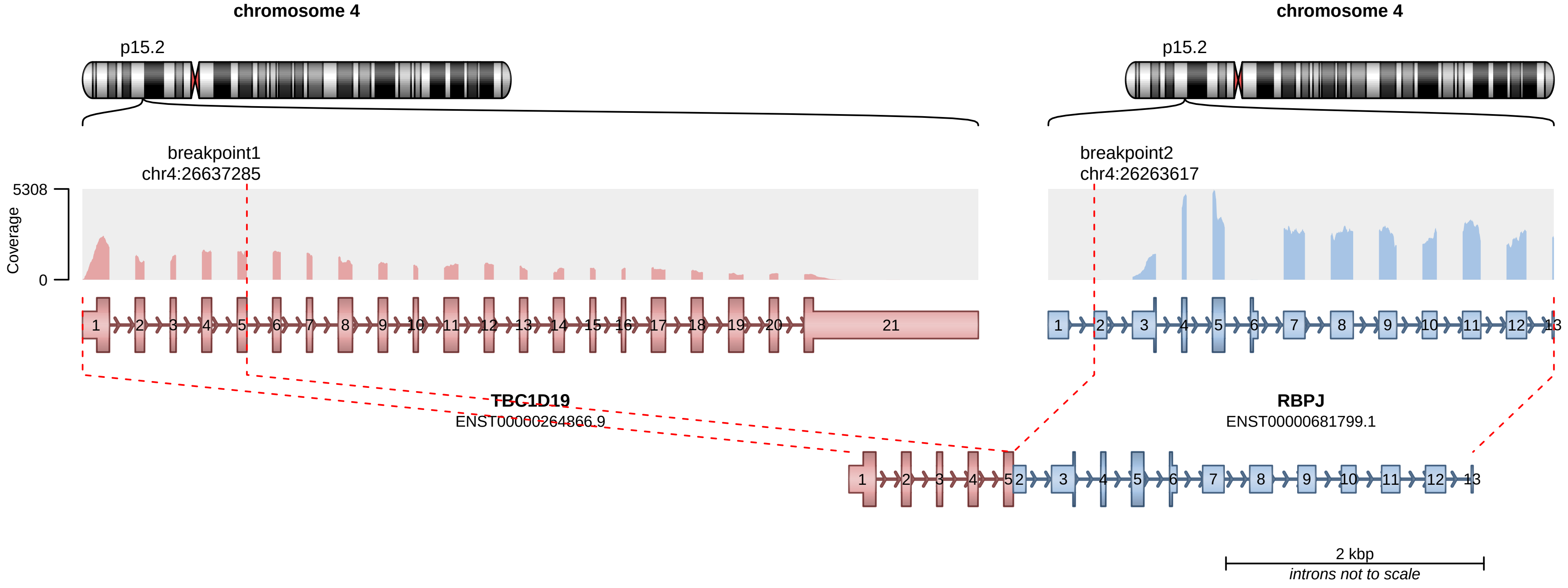


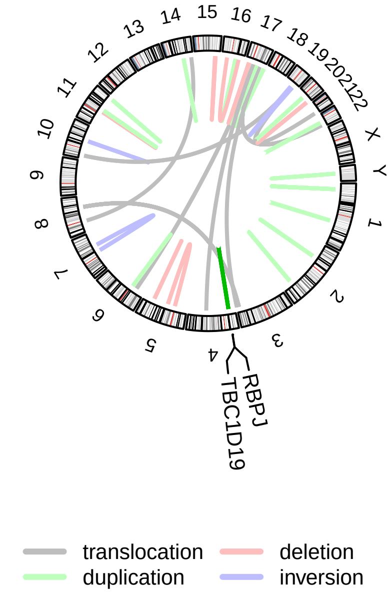
RETAINED PROTEIN DOMAINS
reading frame unclear

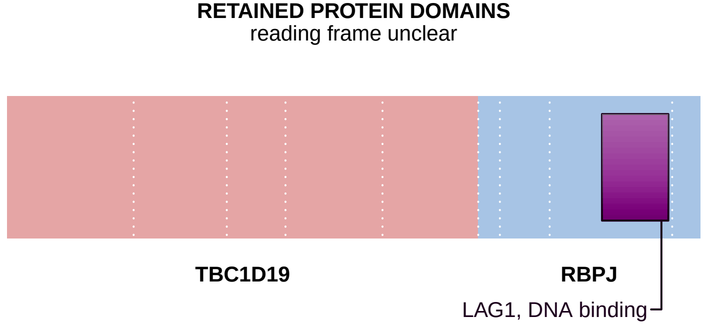


SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 2

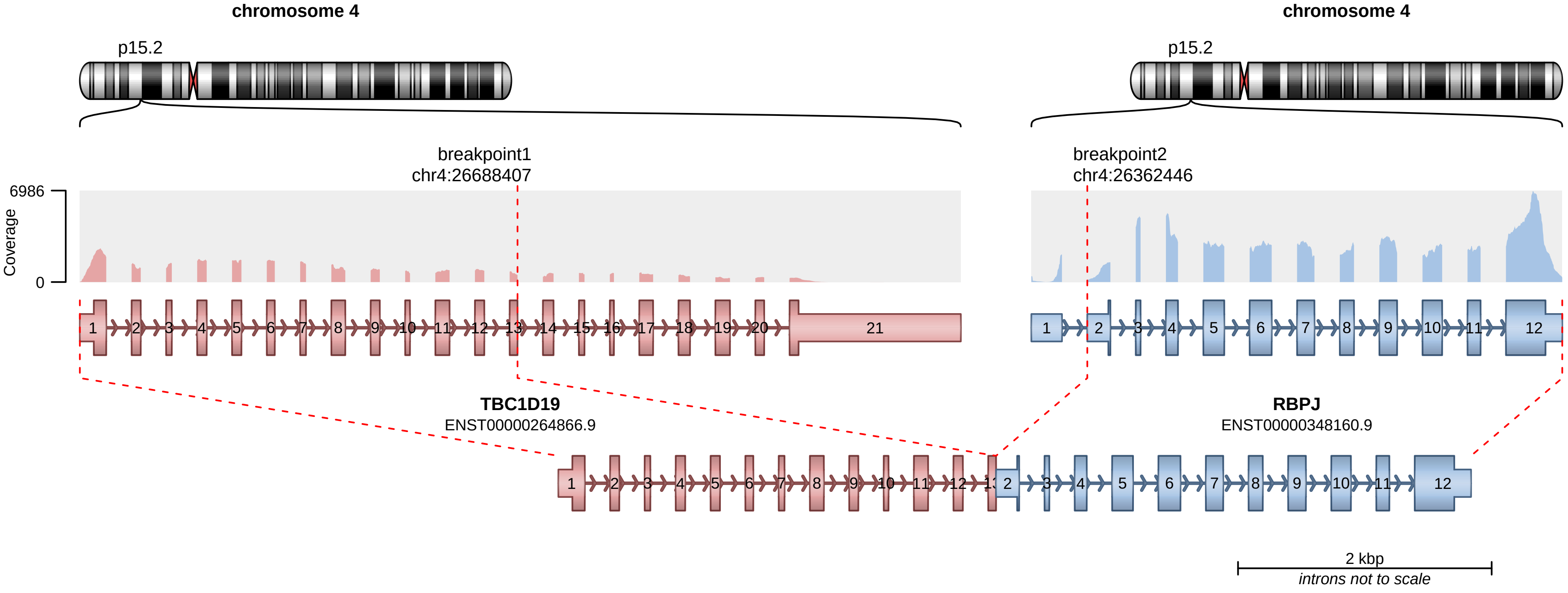


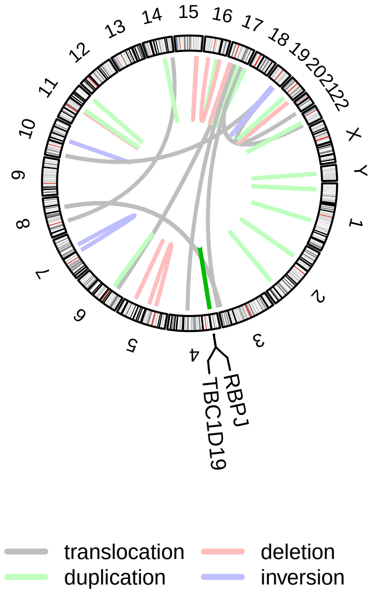


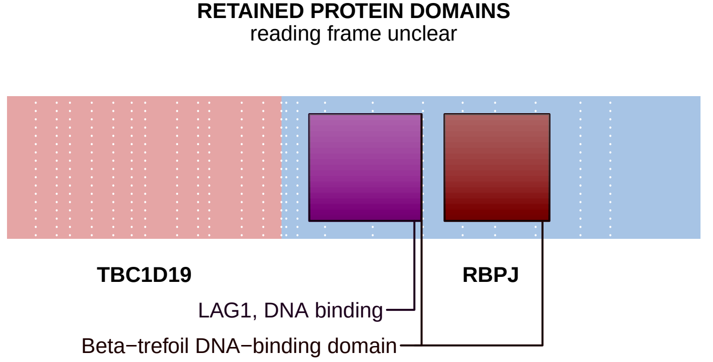


SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 2

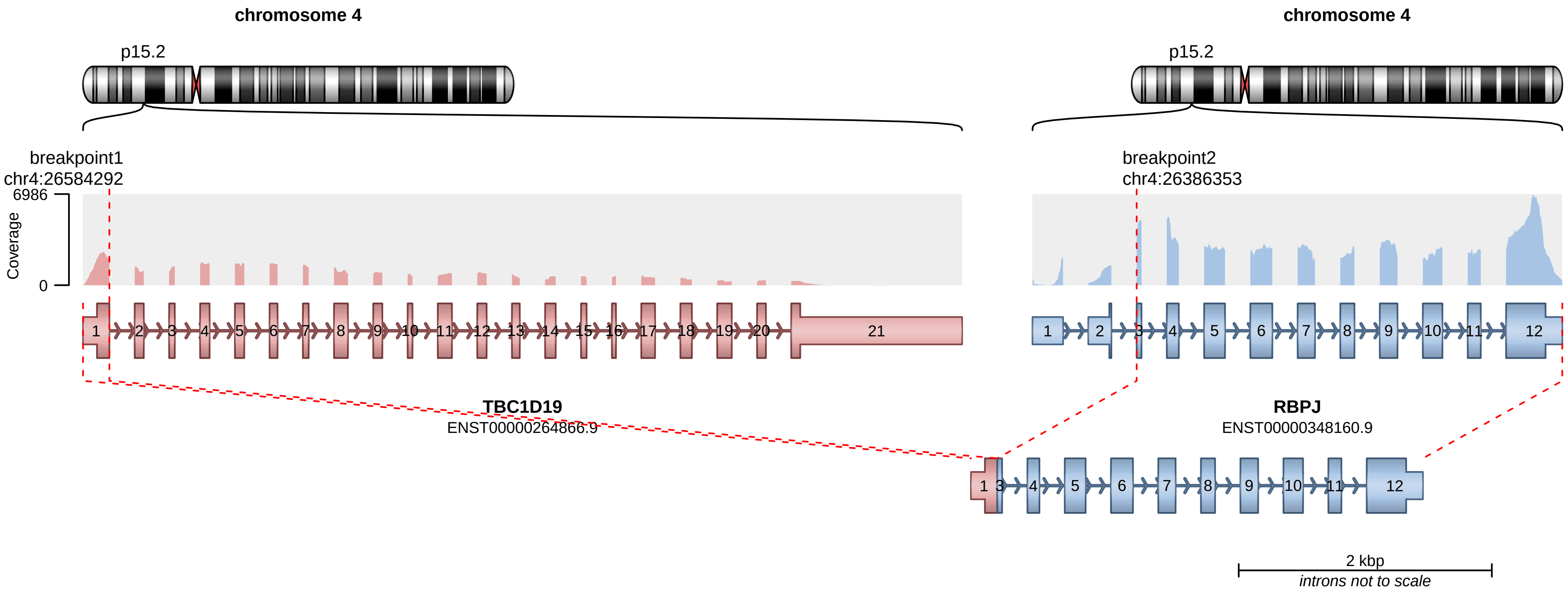


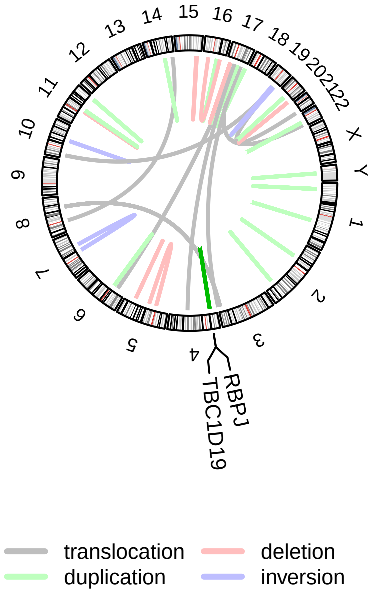




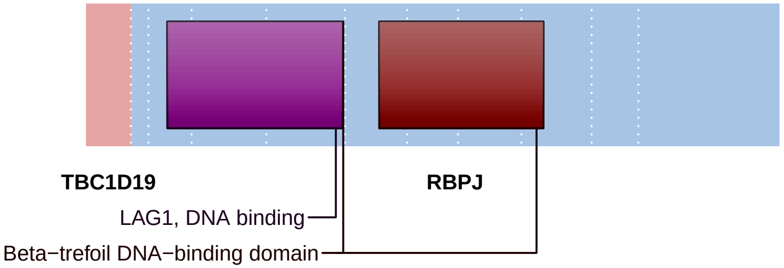
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 2



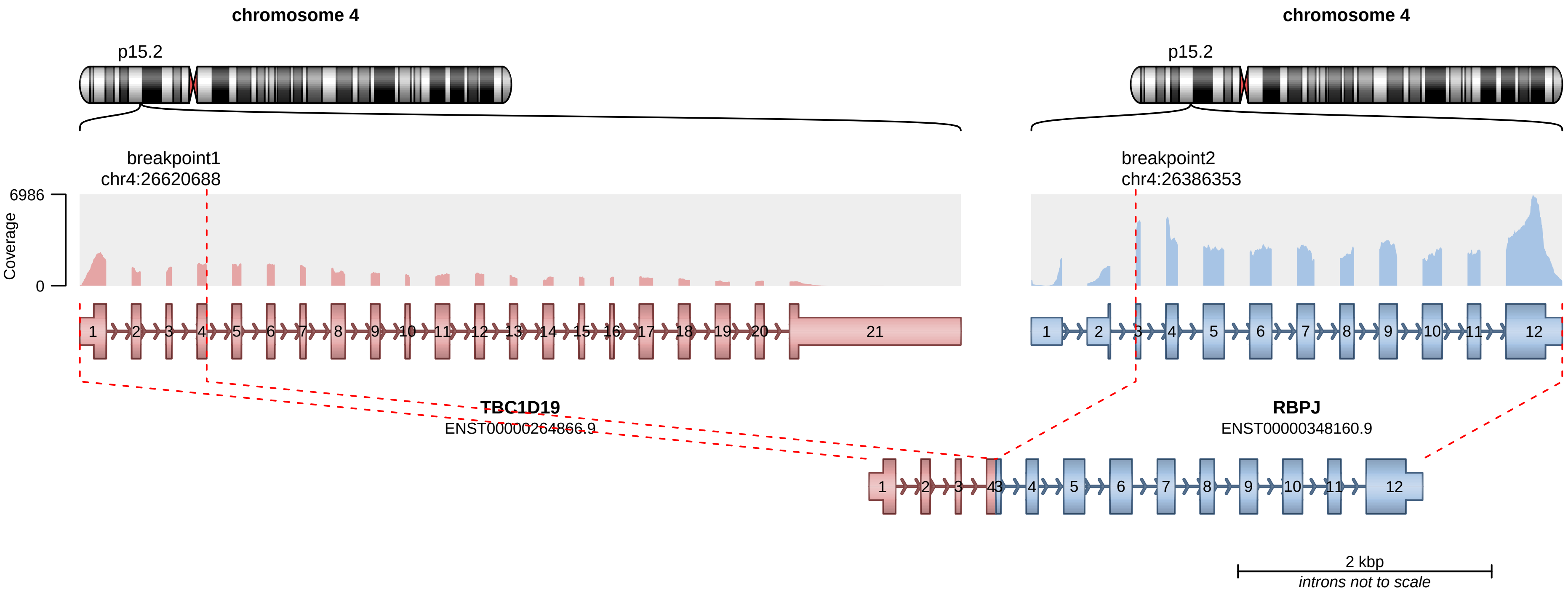


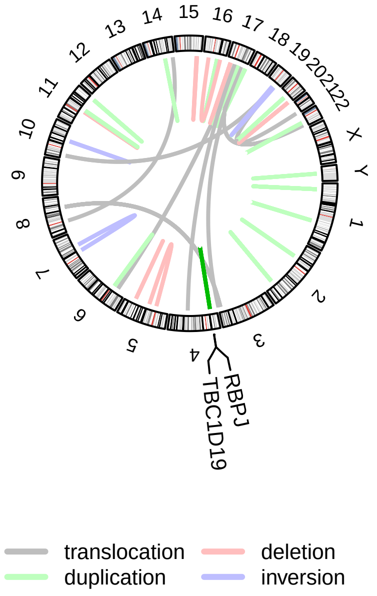
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

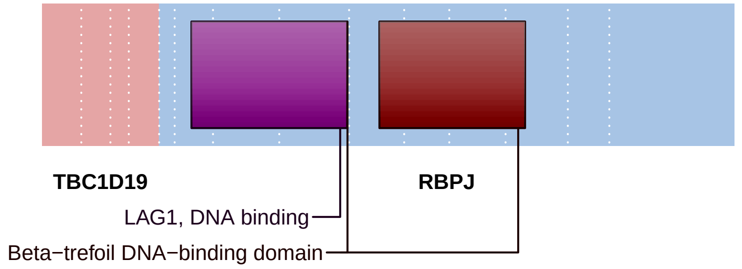
Split reads = 3
Discordant mates = 0





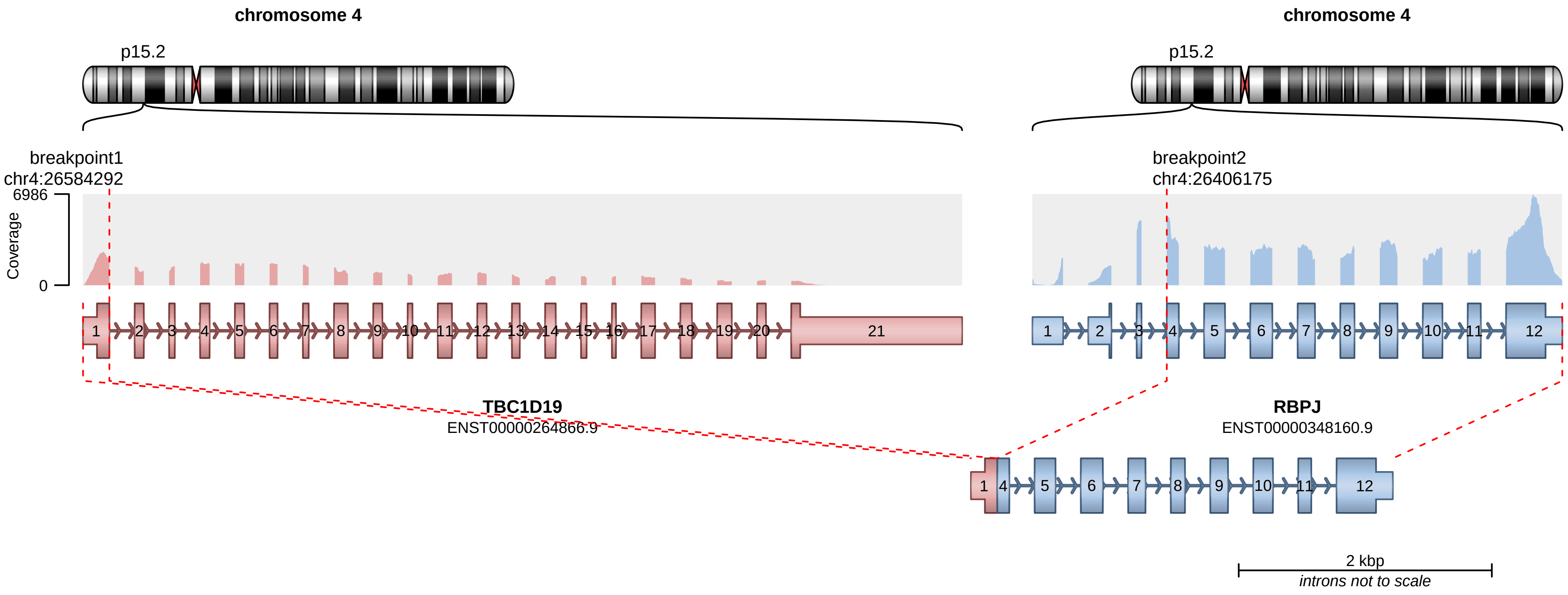
RETAINED PROTEIN DOMAINS

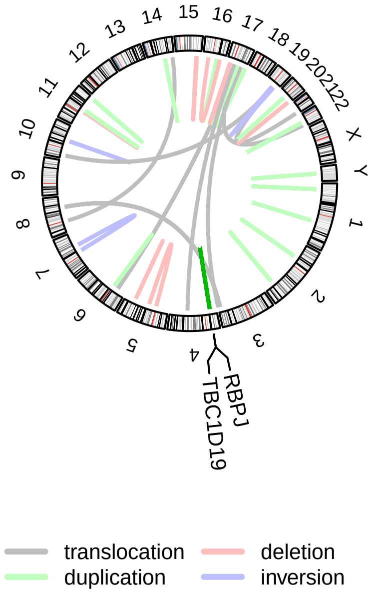
reading frame unclear



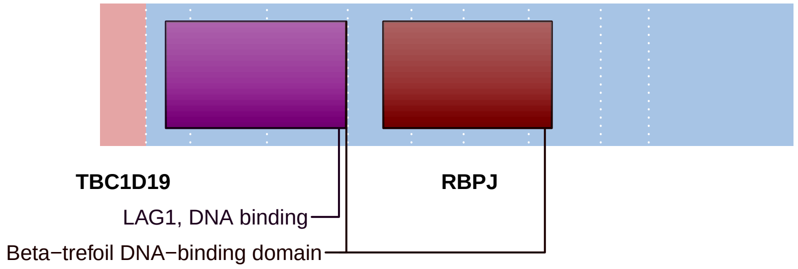
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0



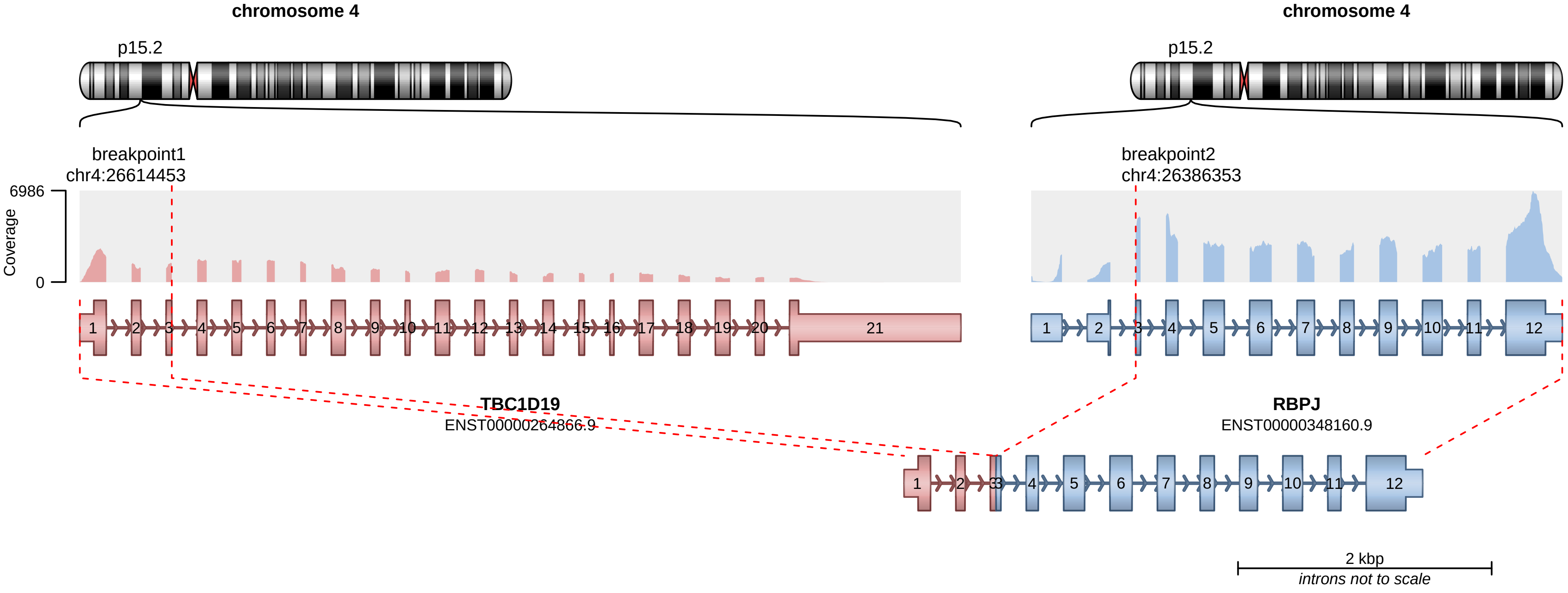


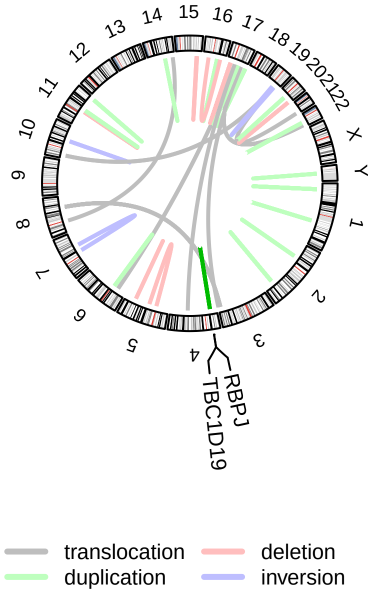
RETAINED PROTEIN DOMAINS
reading frame unclear

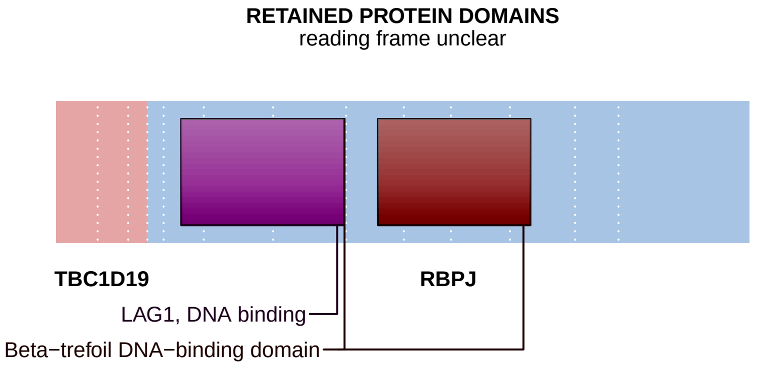


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

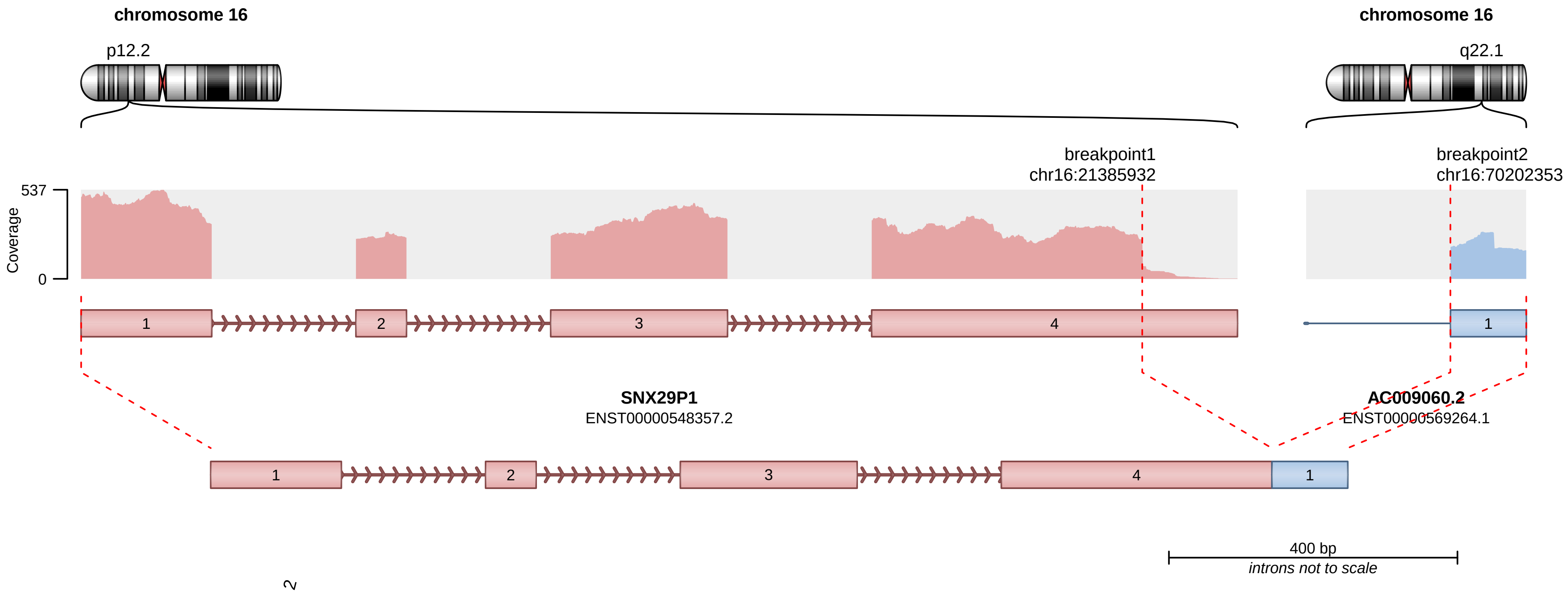


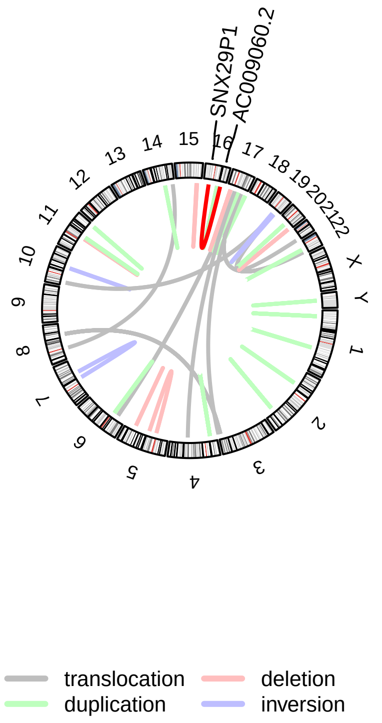




SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

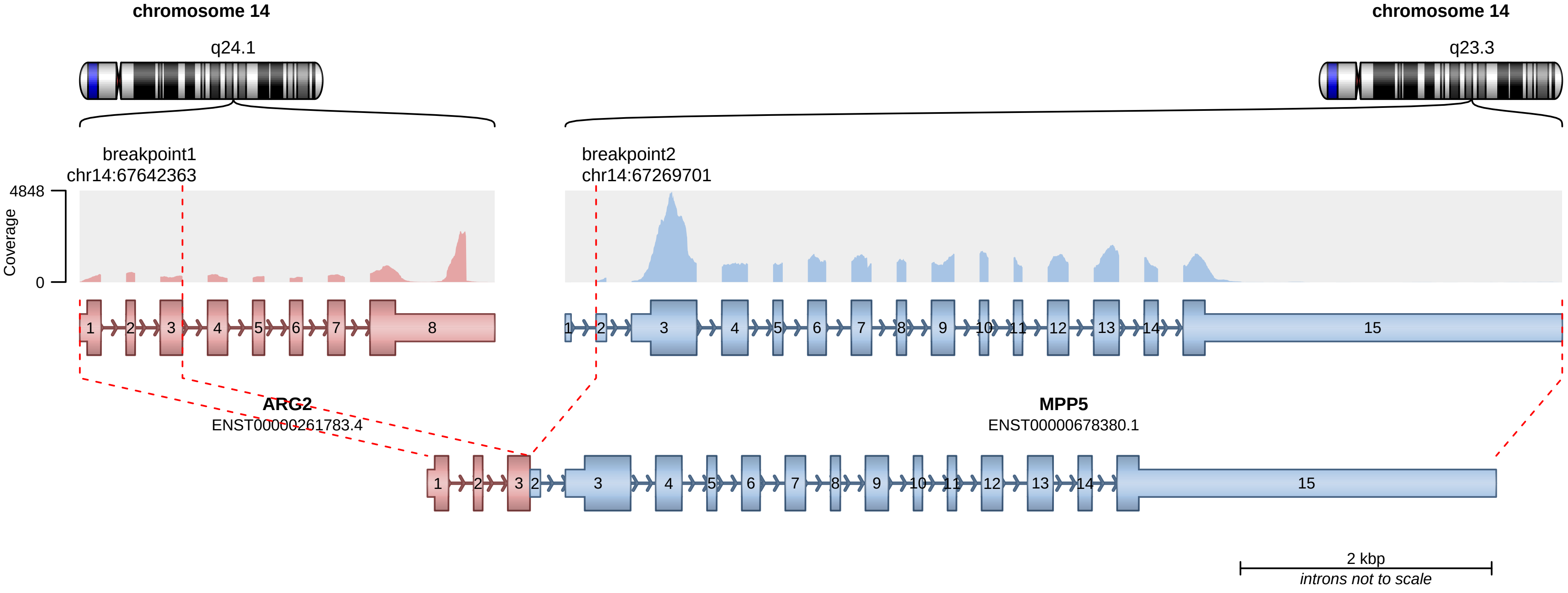


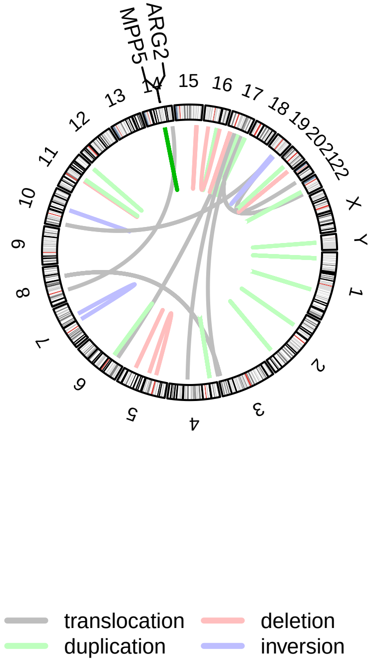


Genes are not protein−coding.

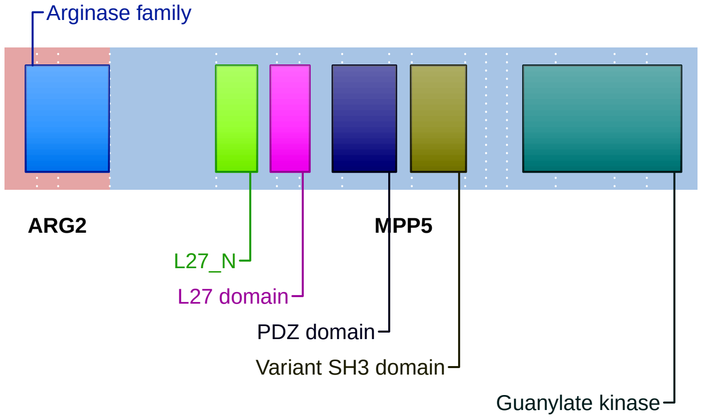
SUPPORTING READ COUNT

Split reads = 19
Discordant mates = 0



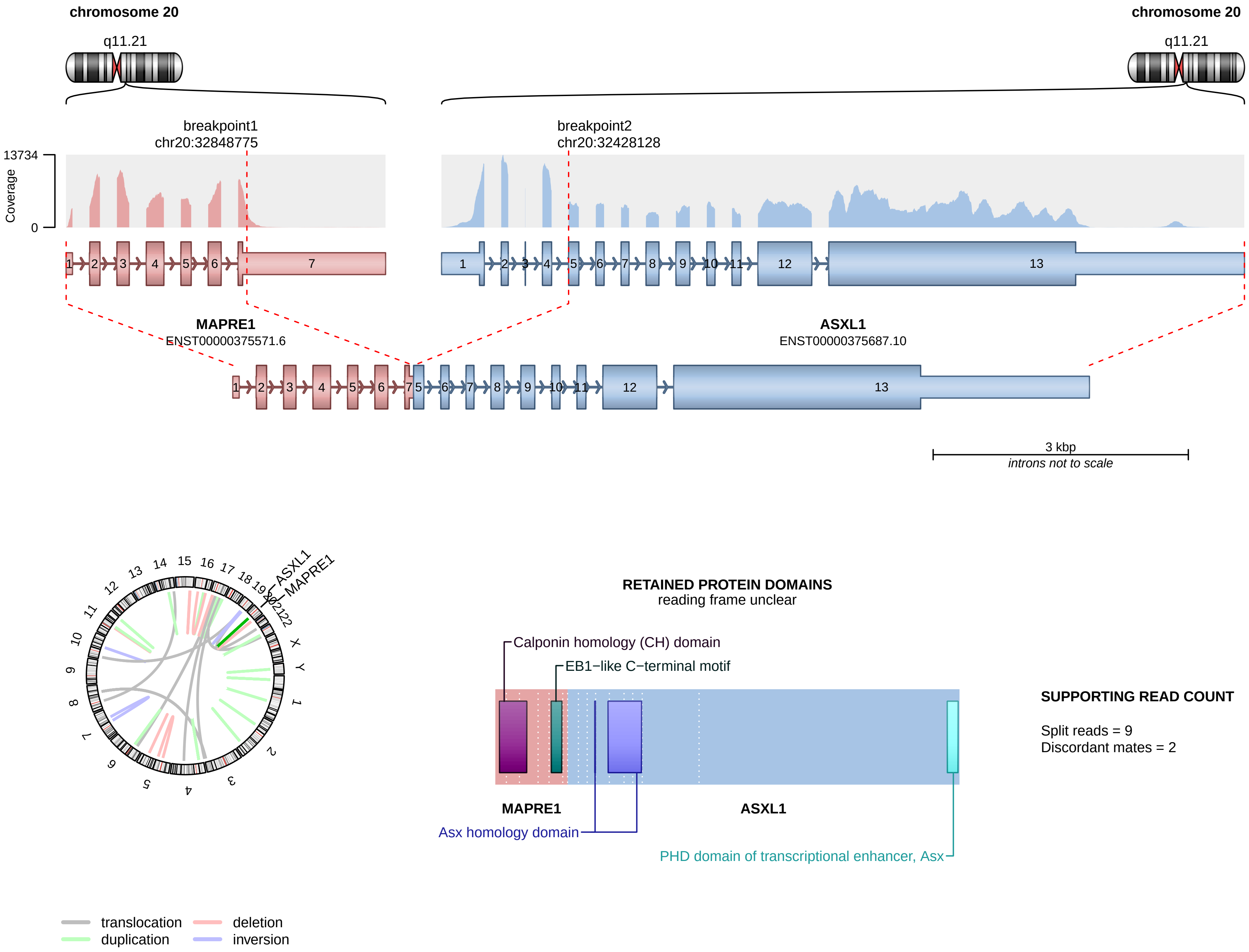


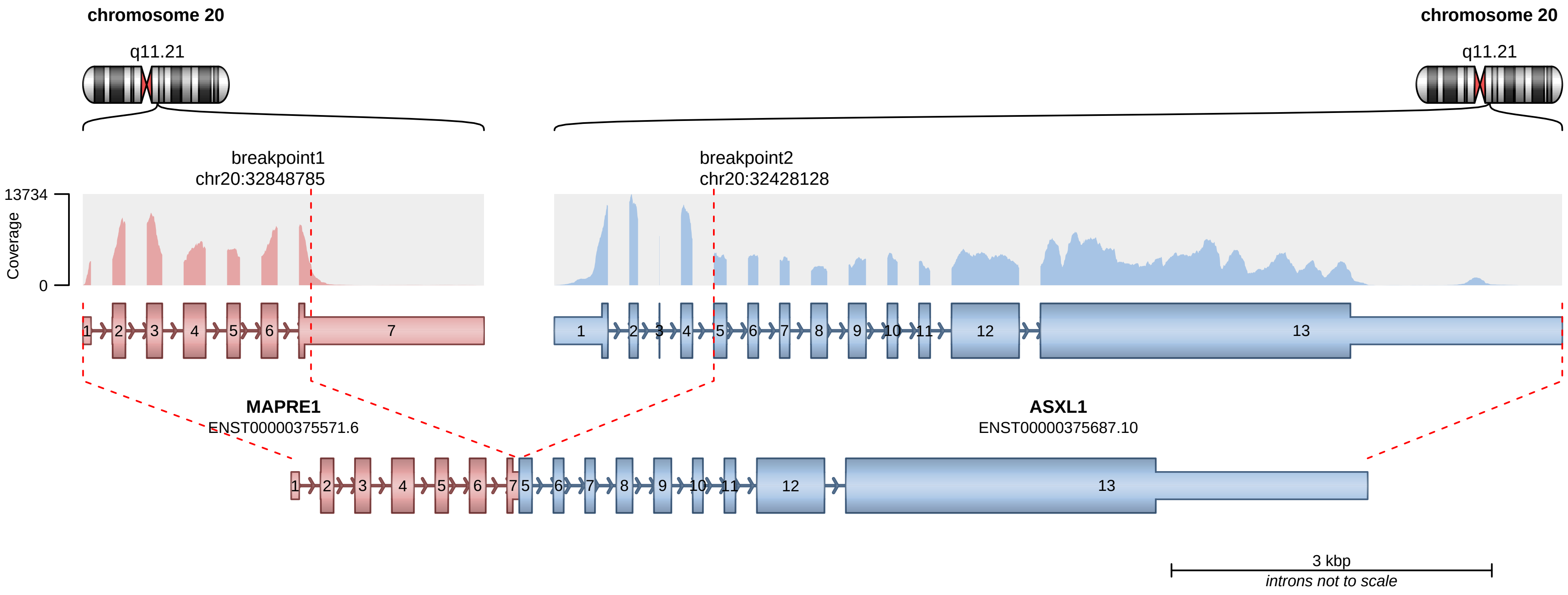
RETAINED PROTEIN DOMAINS
reading frame unclear

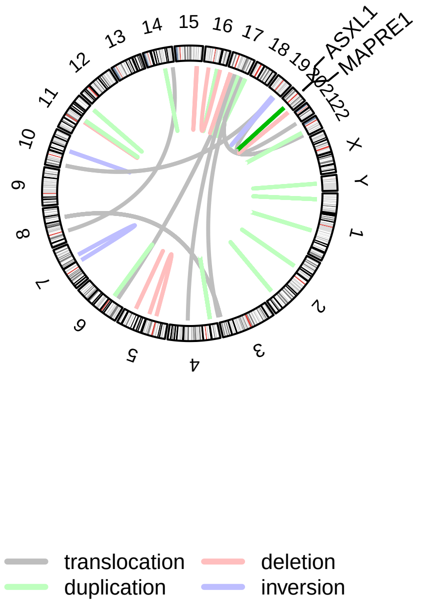


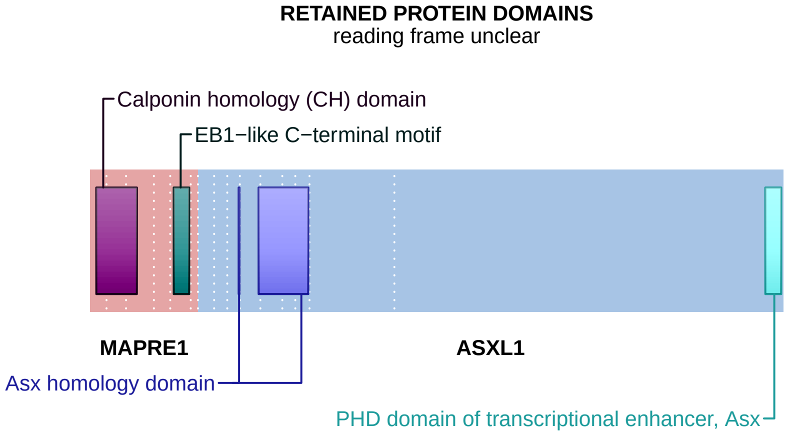
SUPPORTING READ COUNT

Split reads = 17
Discordant mates = 1


chromosome 20
q11.21
chromosome 20
q11.21
breakpoint1
chr20:32848775
breakpoint2
chr20:32428128
Coverage
13734
0
MAPRE1
ENST00000375571.6
ASXL1
ENST00000375687.10
3 kbp
introns not to scale
ASXL1
MAPRE1
RETAINED PROTEIN DOMAINS
reading frame unclear
Calponin homology (CH) domain
EB1−like C−terminal motif
MAPRE1
ASXL1
Asx homology domain
PHD domain of transcriptional enhancer, Asx
SUPPORTING READ COUNT
Split reads = 9
Discordant mates = 2
translocation
deletion
duplication
inversion

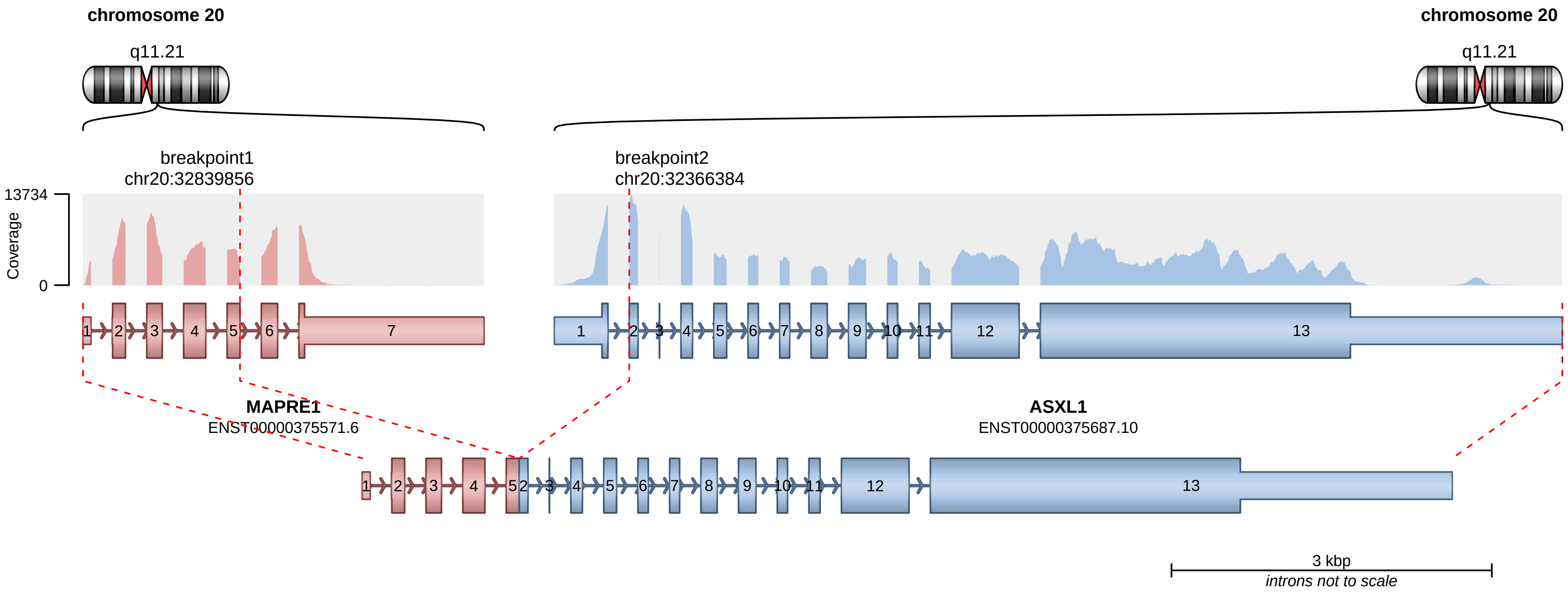


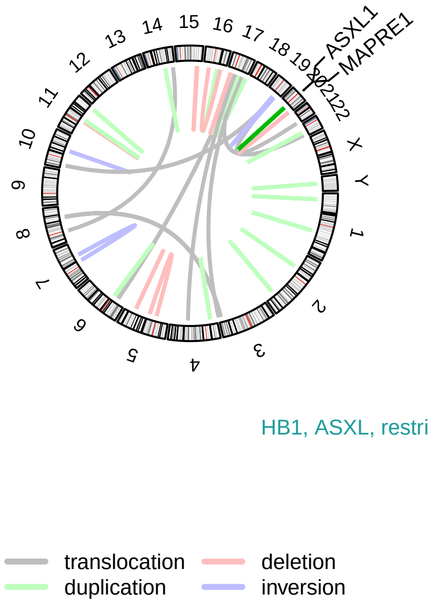




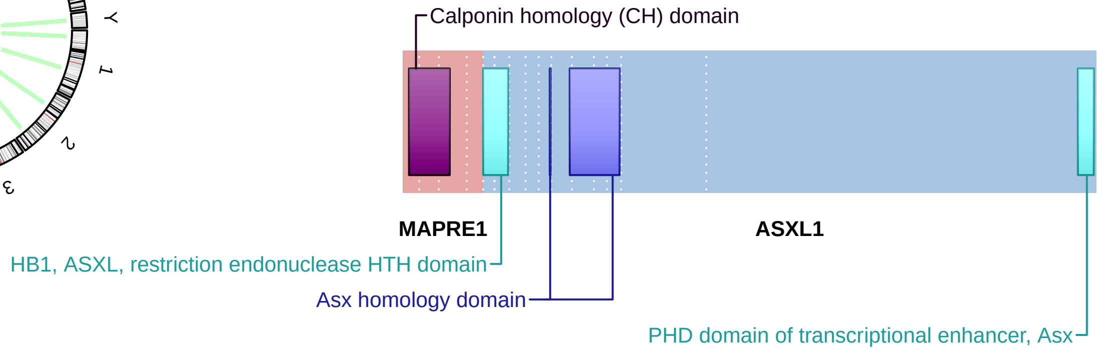
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 2





RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0