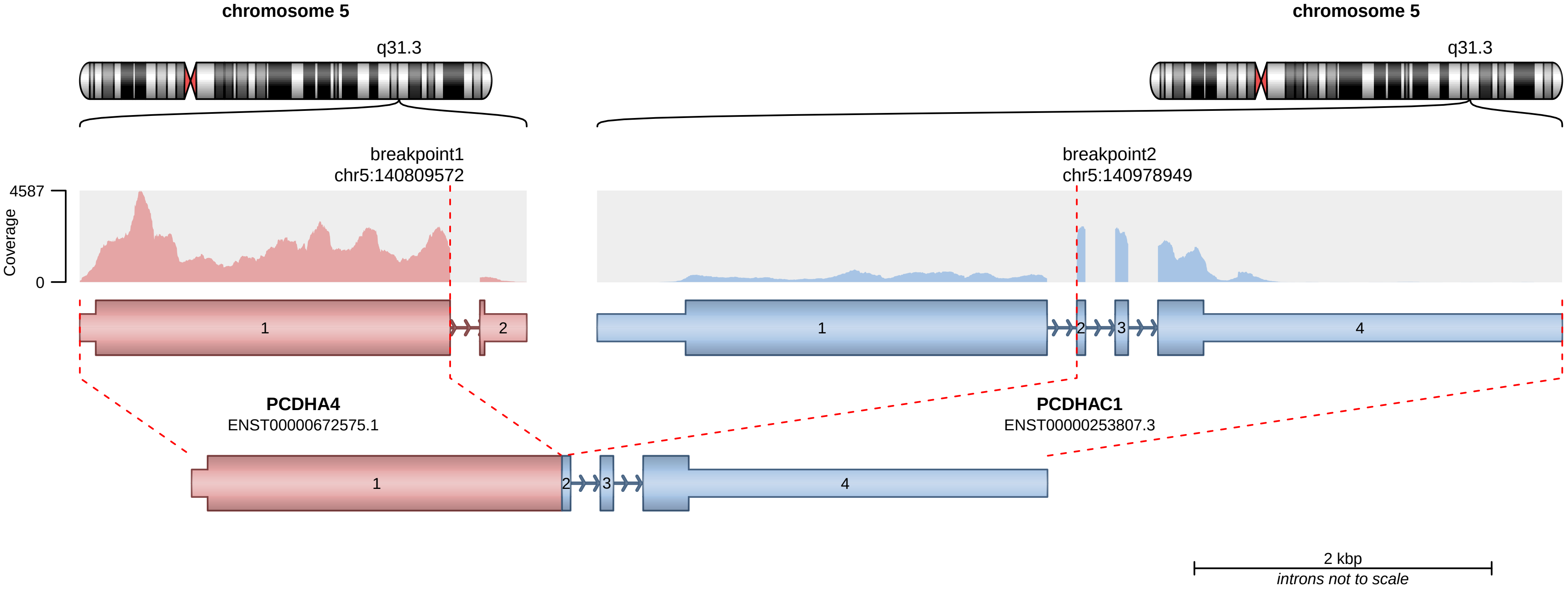
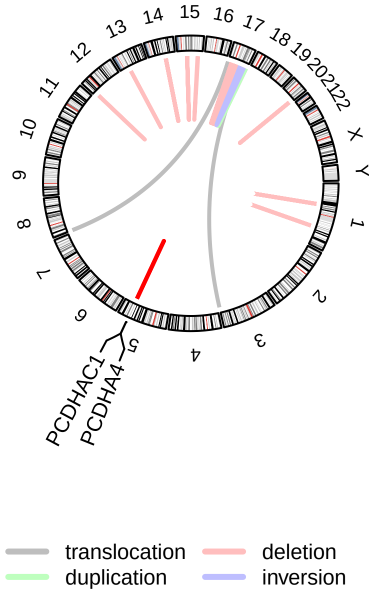
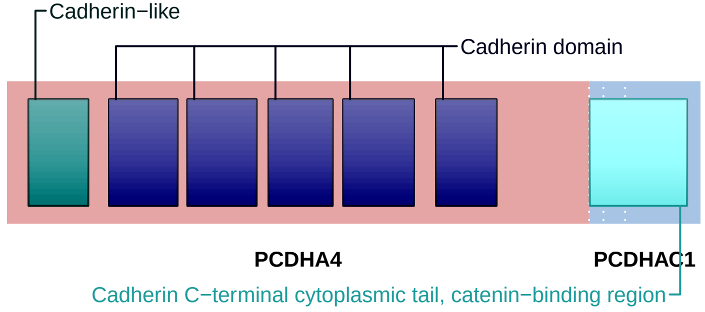


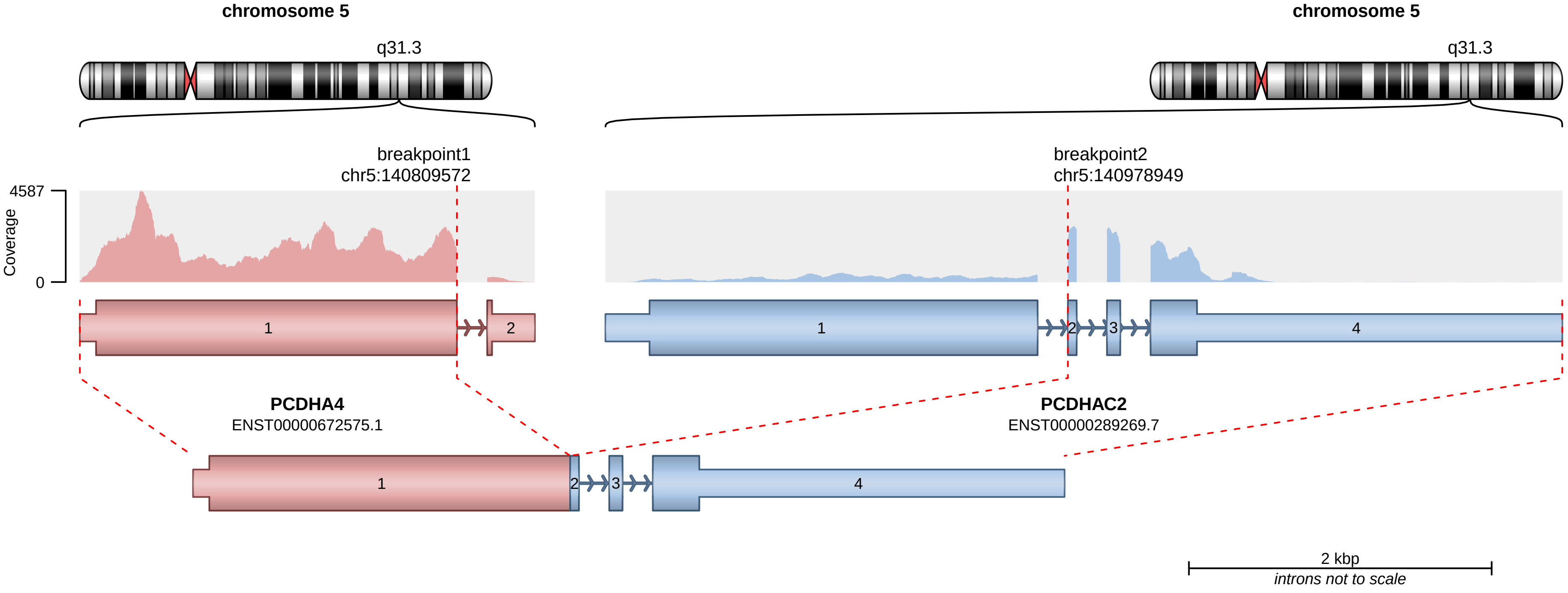


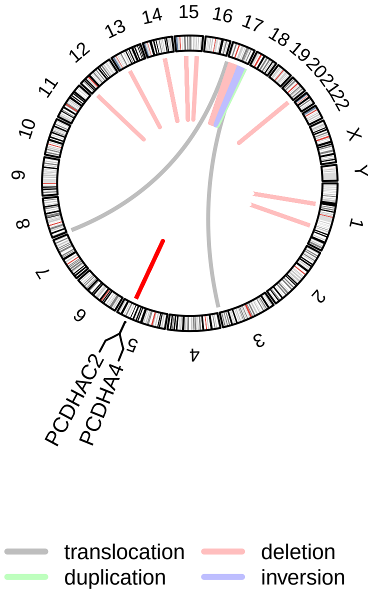
RETAINED PROTEIN DOMAINS
reading frame unclear

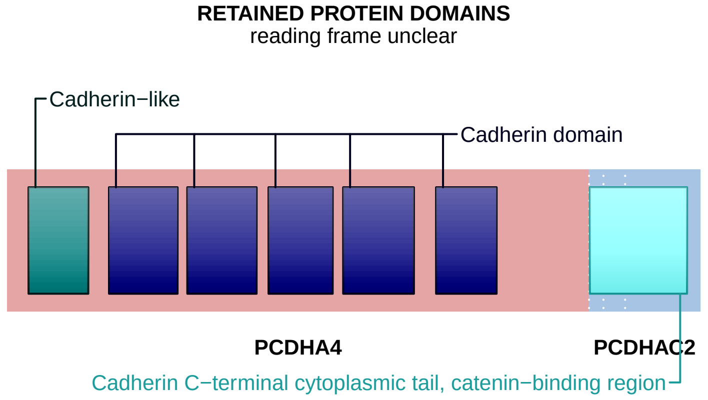


SUPPORTING READ COUNT

Split reads = 513
Discordant mates = 4

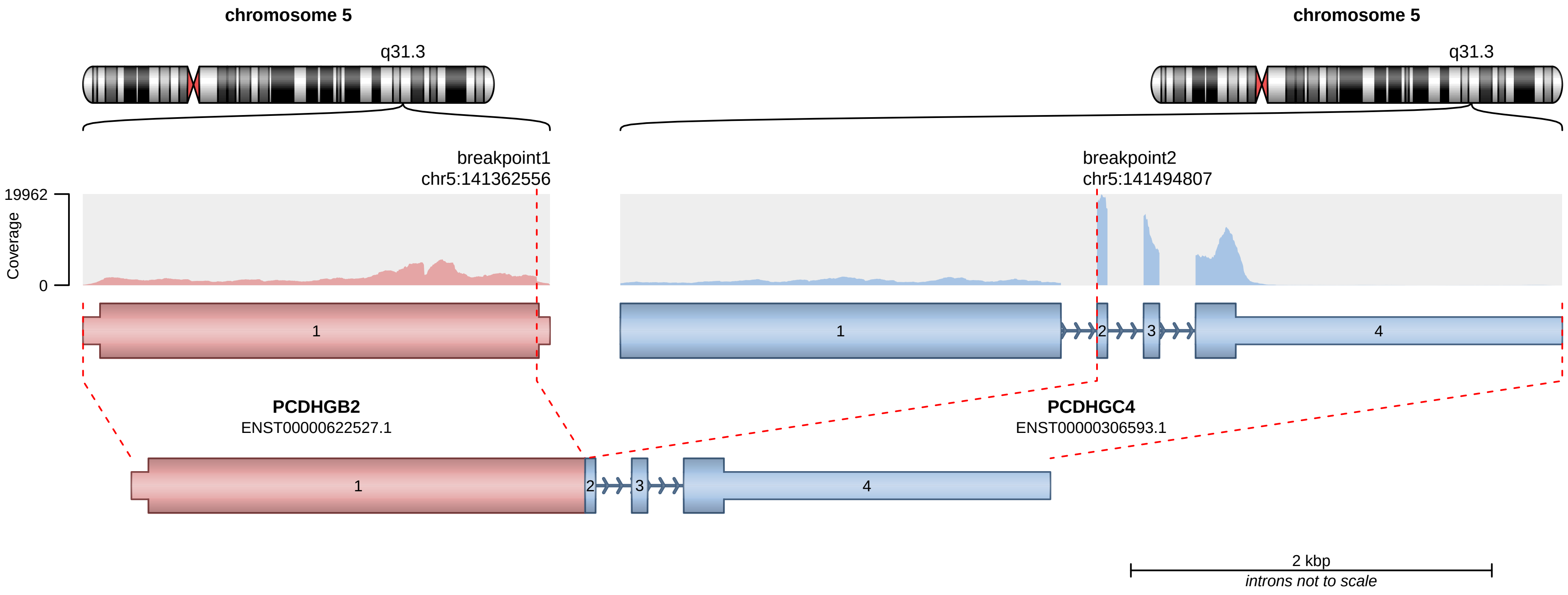


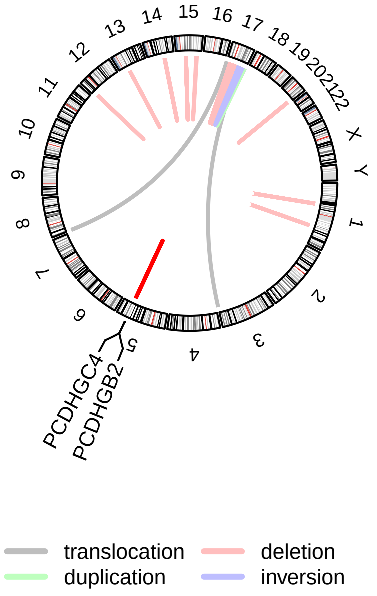




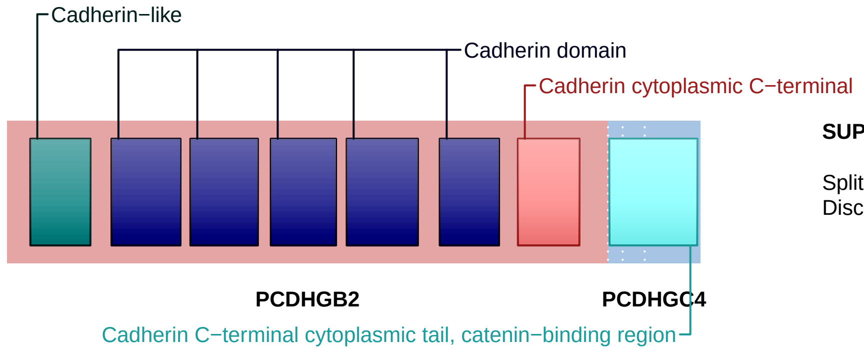
SUPPORTING READ COUNT

Split reads = 513
Discordant mates = 4



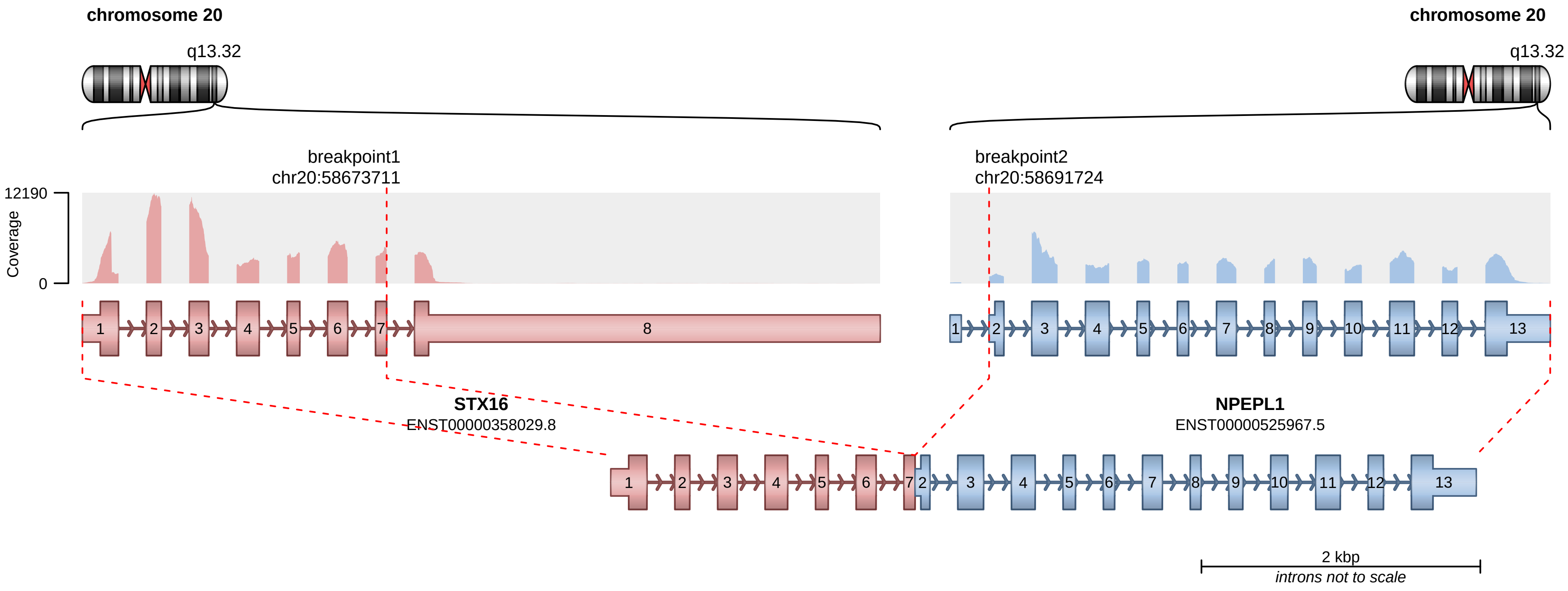


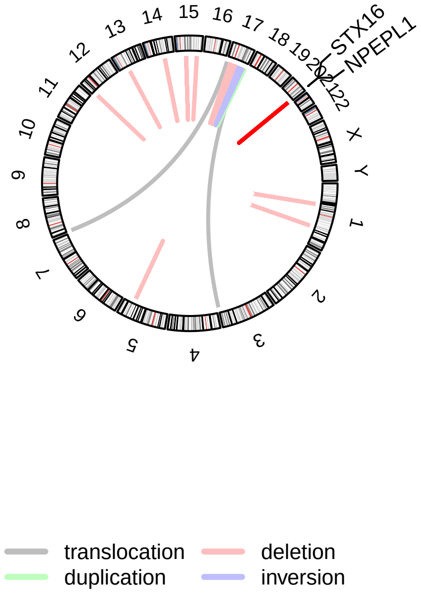
RETAINED PROTEIN DOMAINS
reading frame unclear

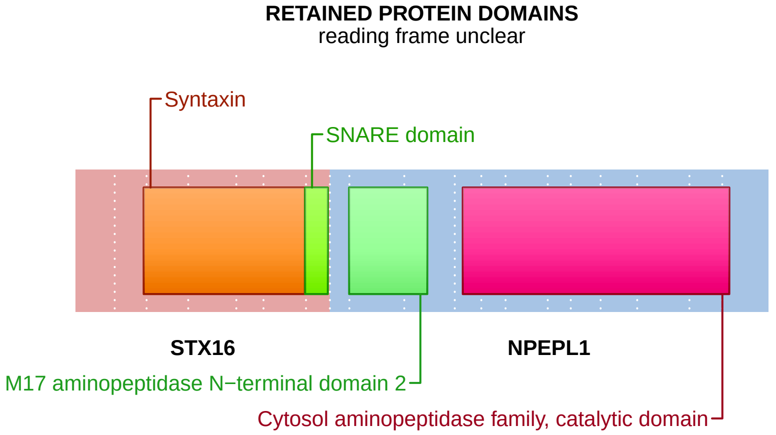


SUPPORTING READ COUNT

Split reads = 372
Discordant mates = 2

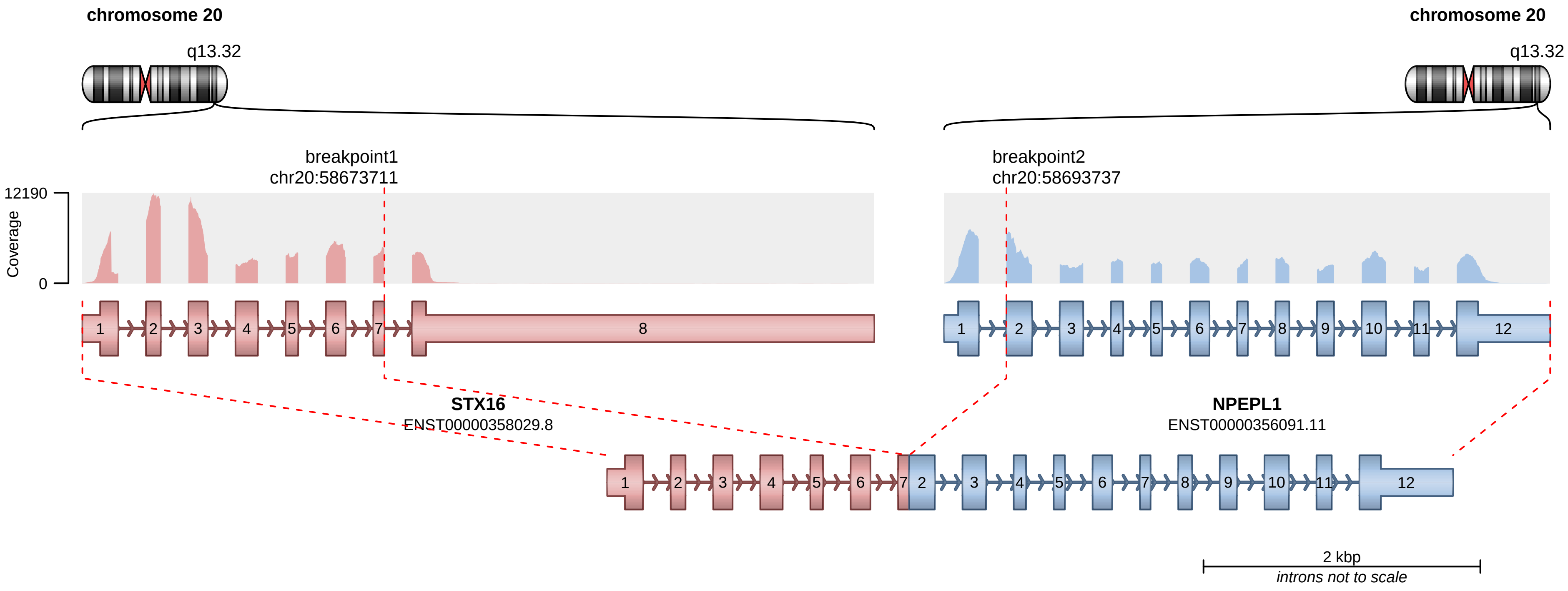


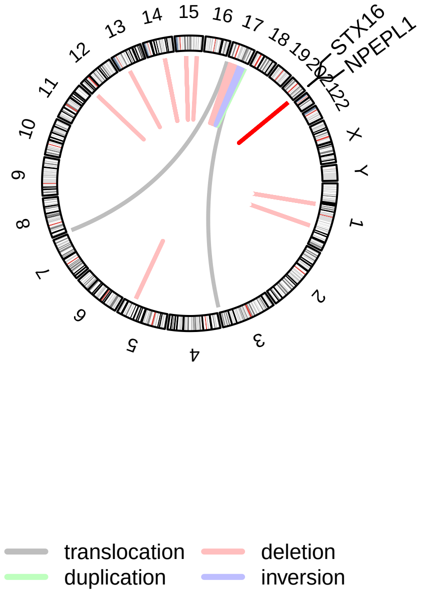


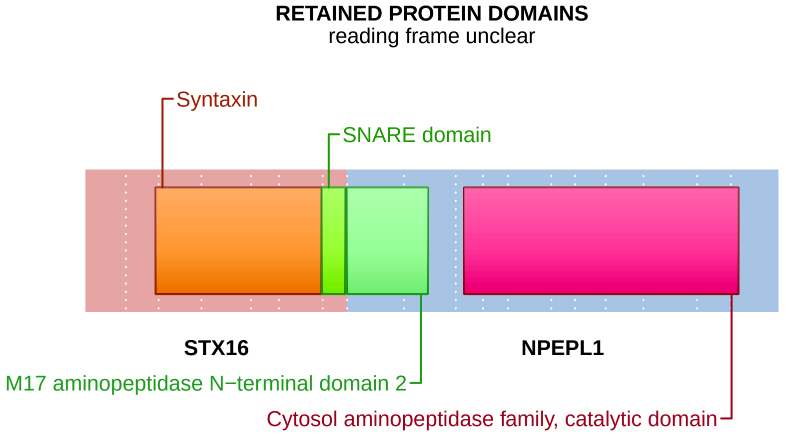


SUPPORTING READ COUNT

Split reads = 264
Discordant mates = 7

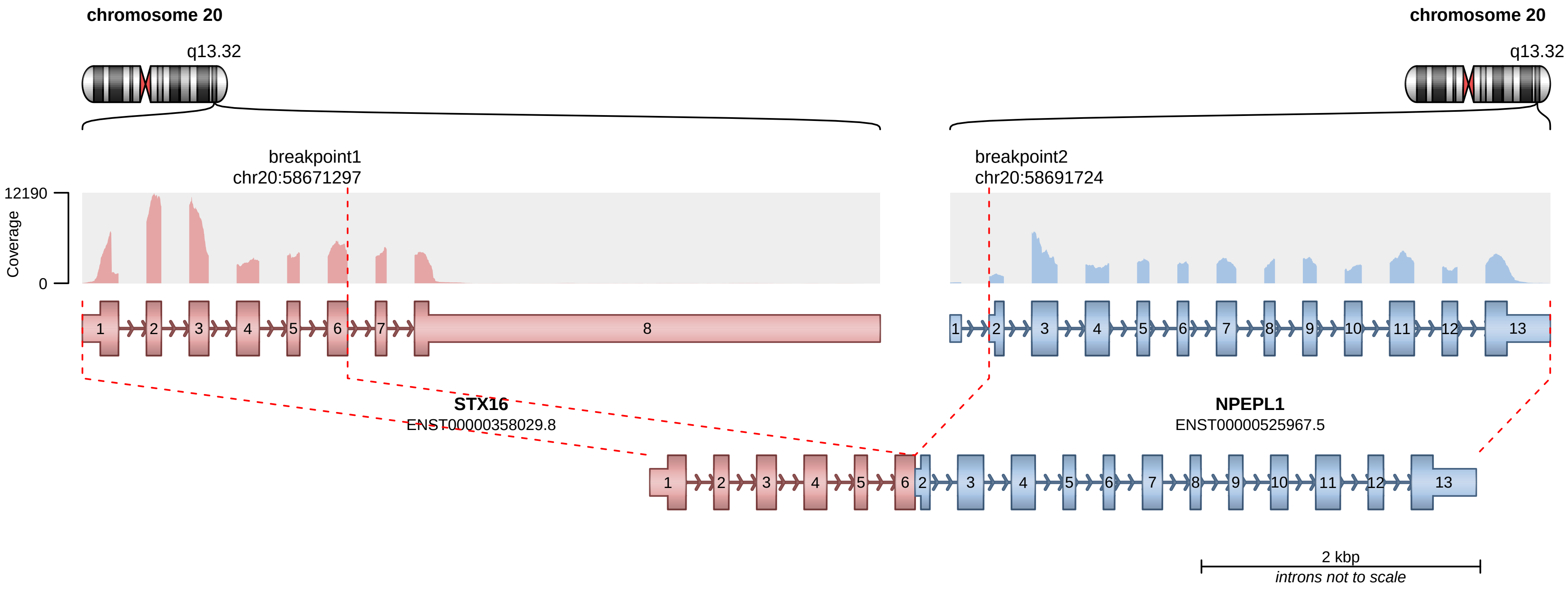


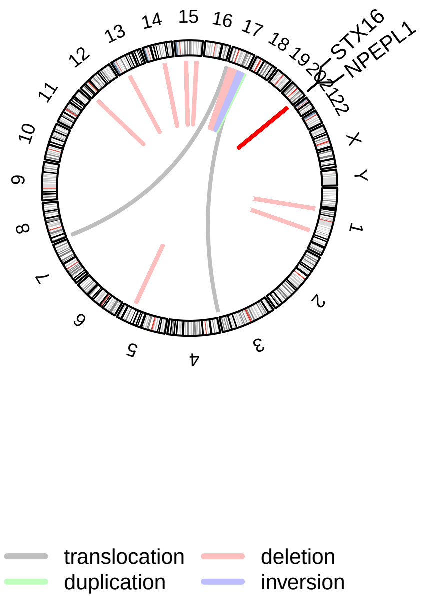


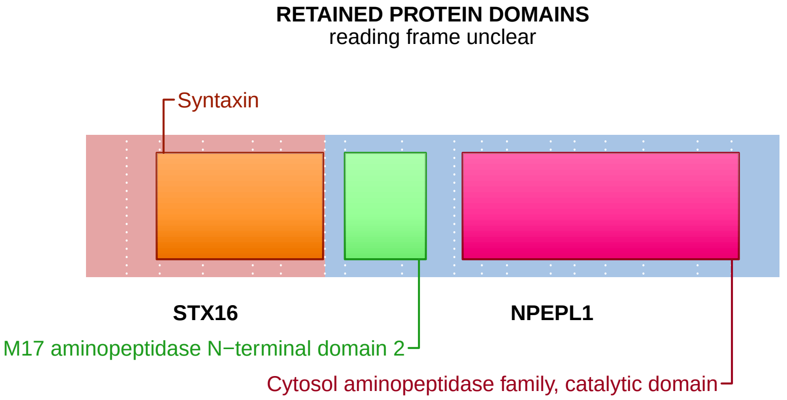


SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

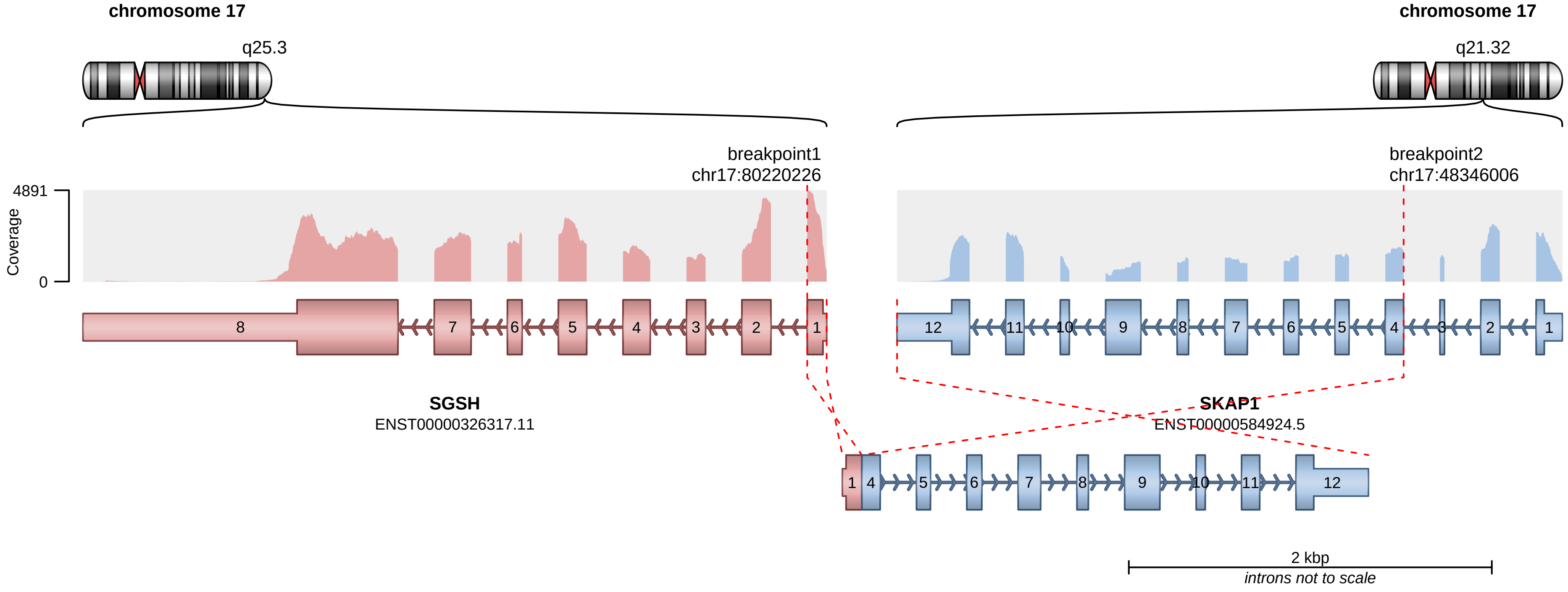


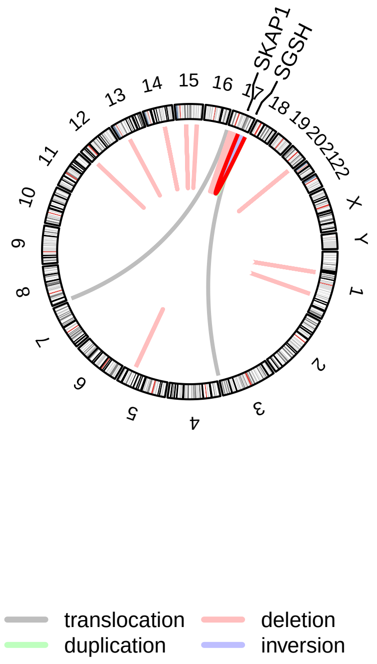




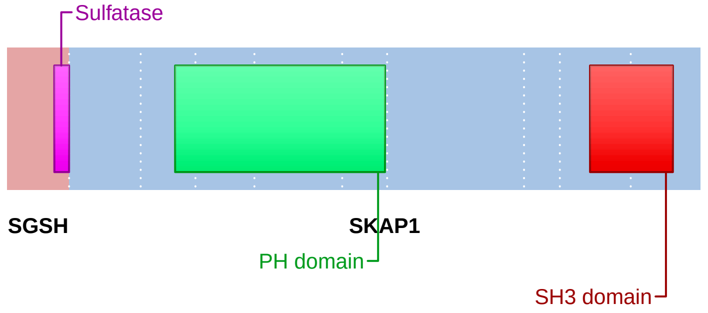
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0



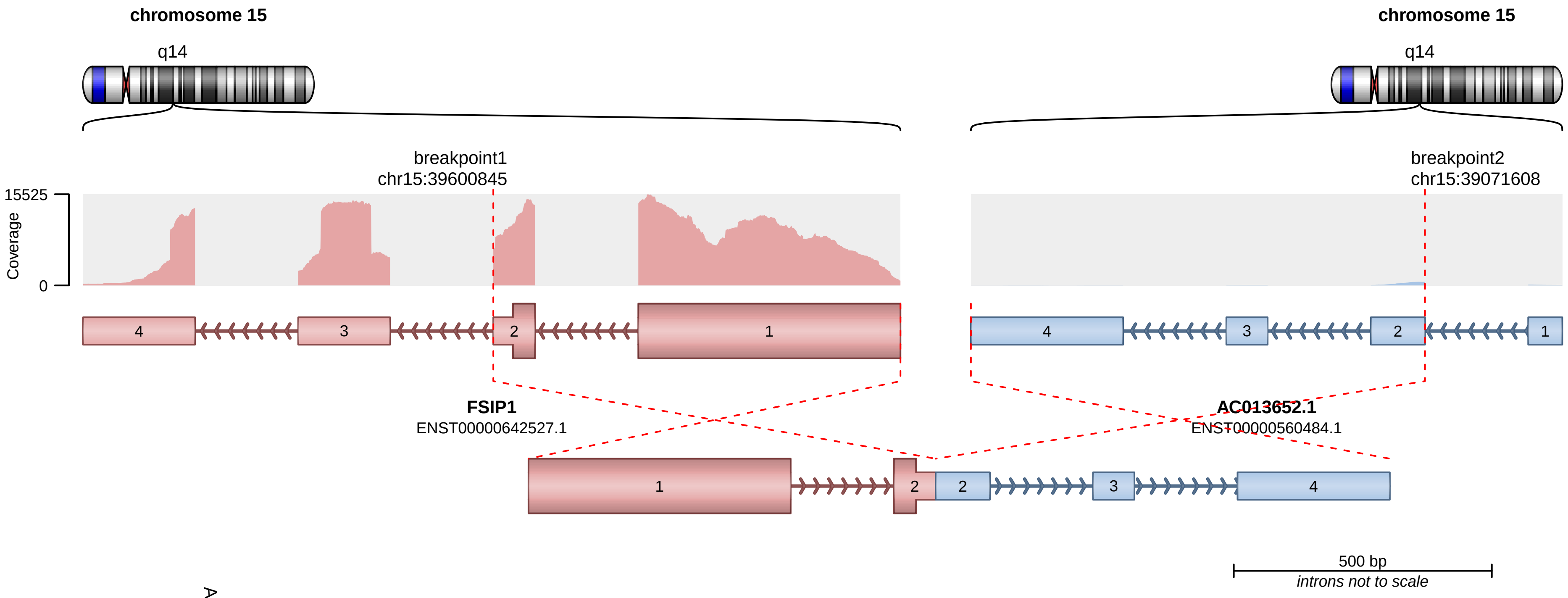


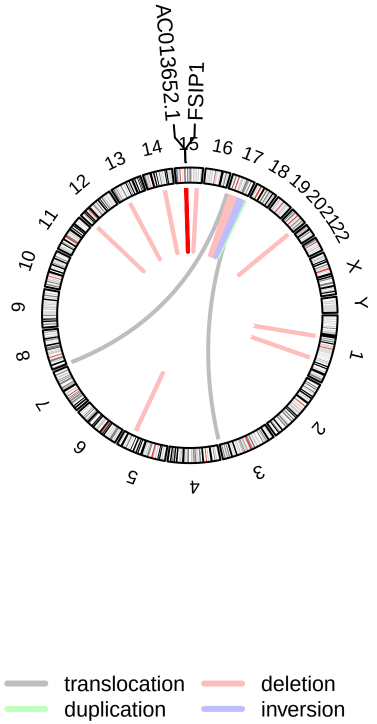
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 264
Discordant mates = 0

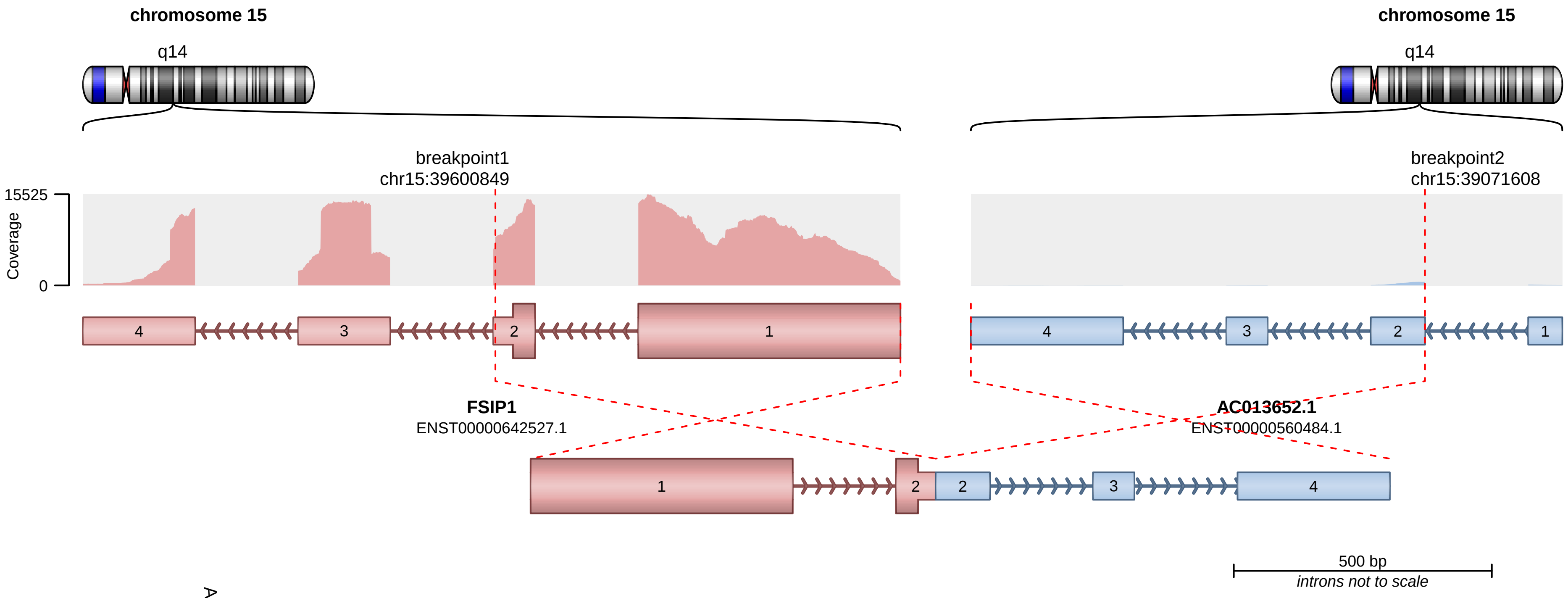


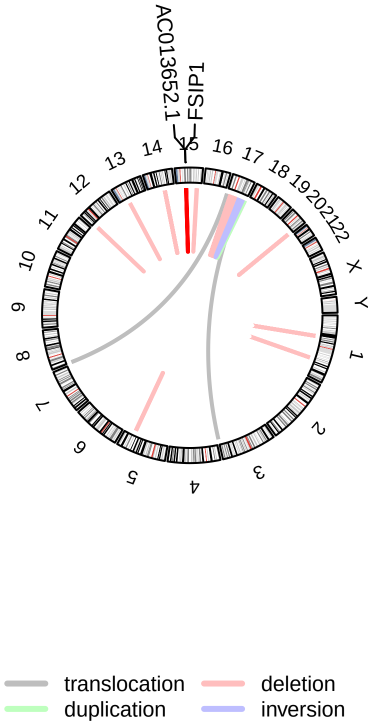


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 204
Discordant mates = 14

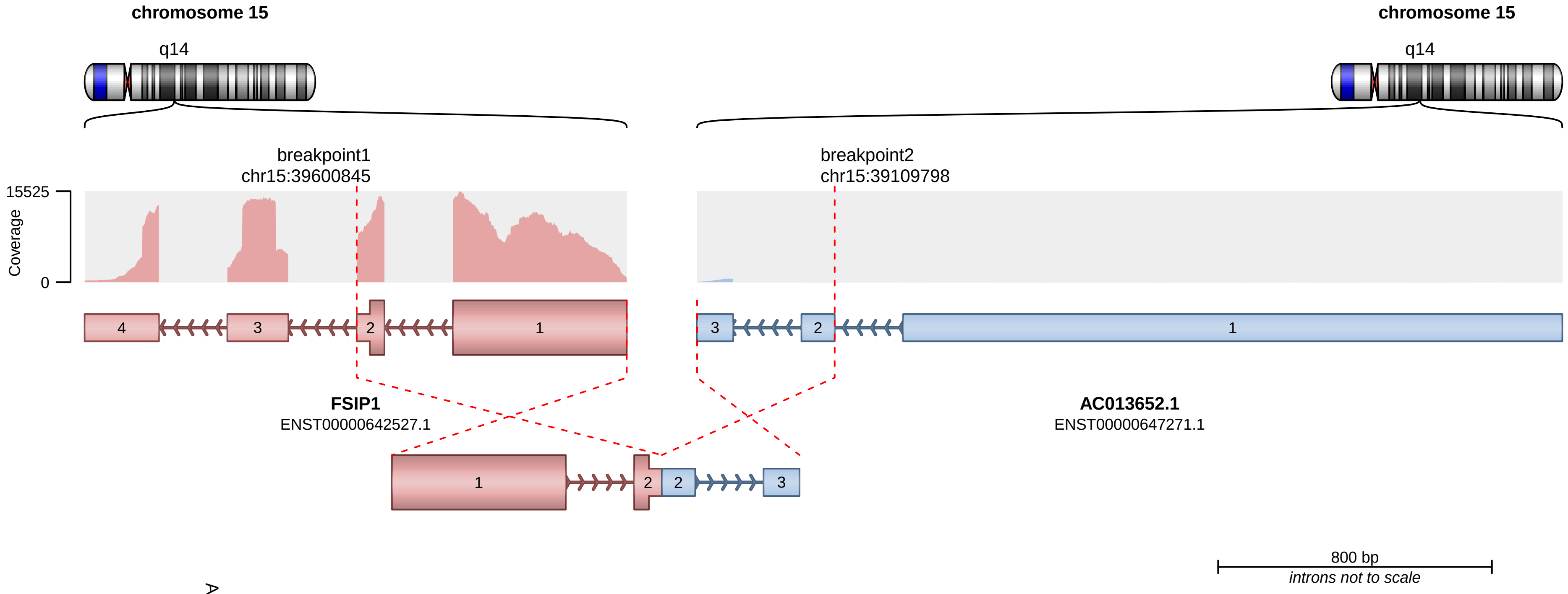


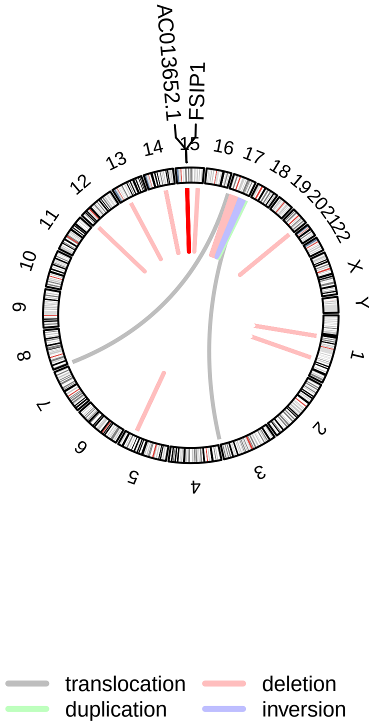


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 160
Discordant mates = 14

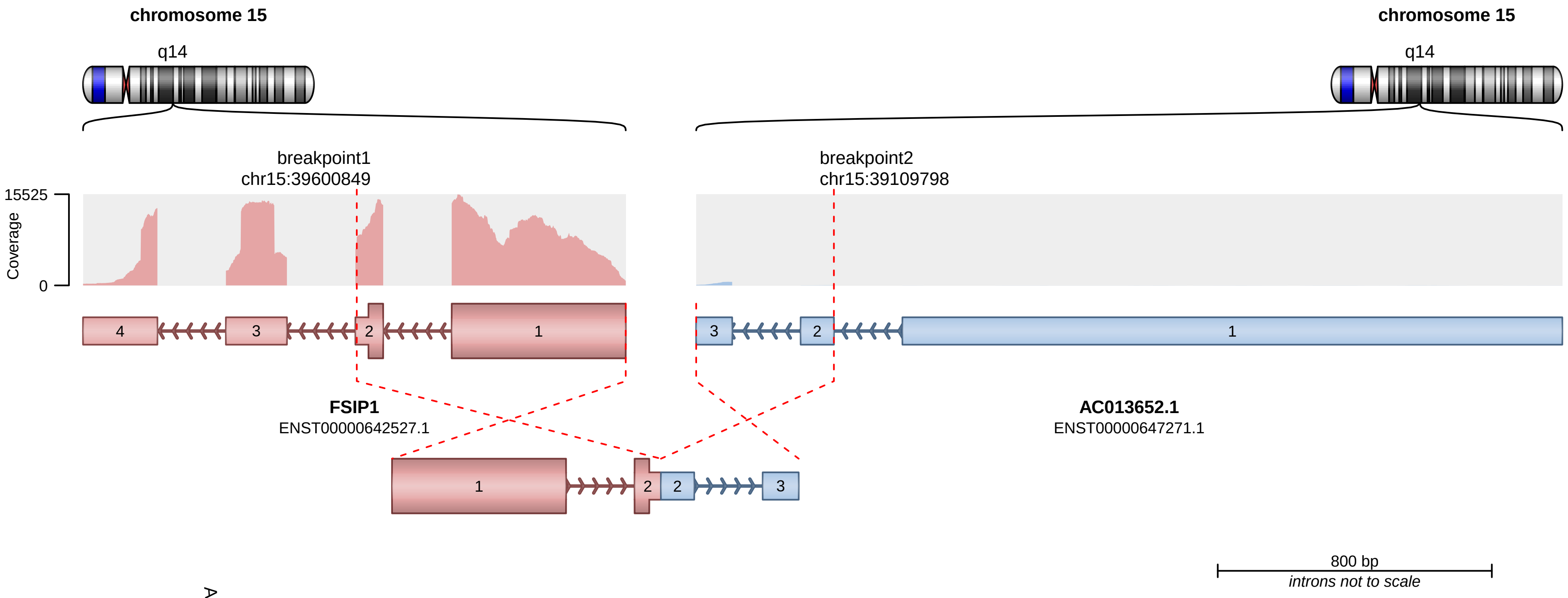


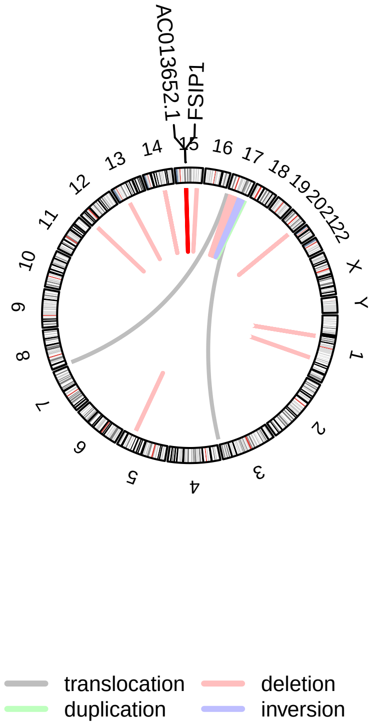


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 15

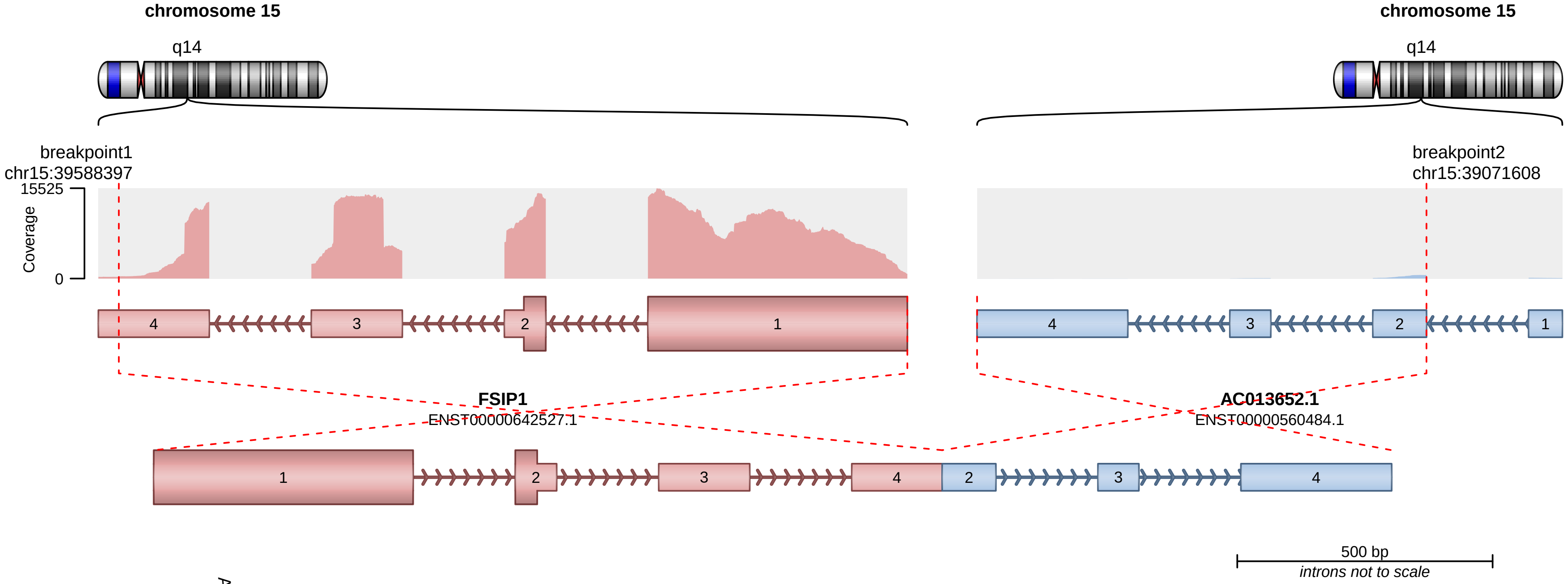


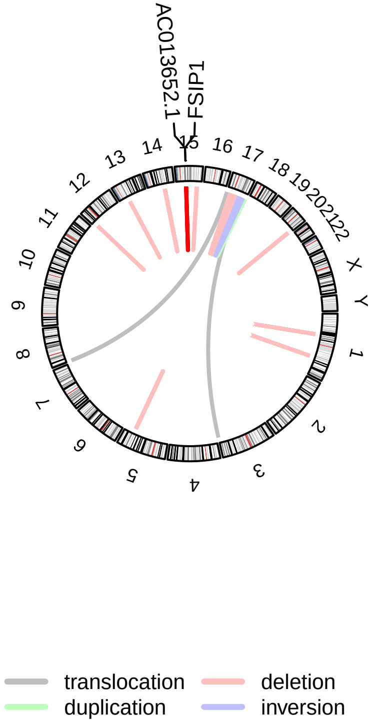


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 15

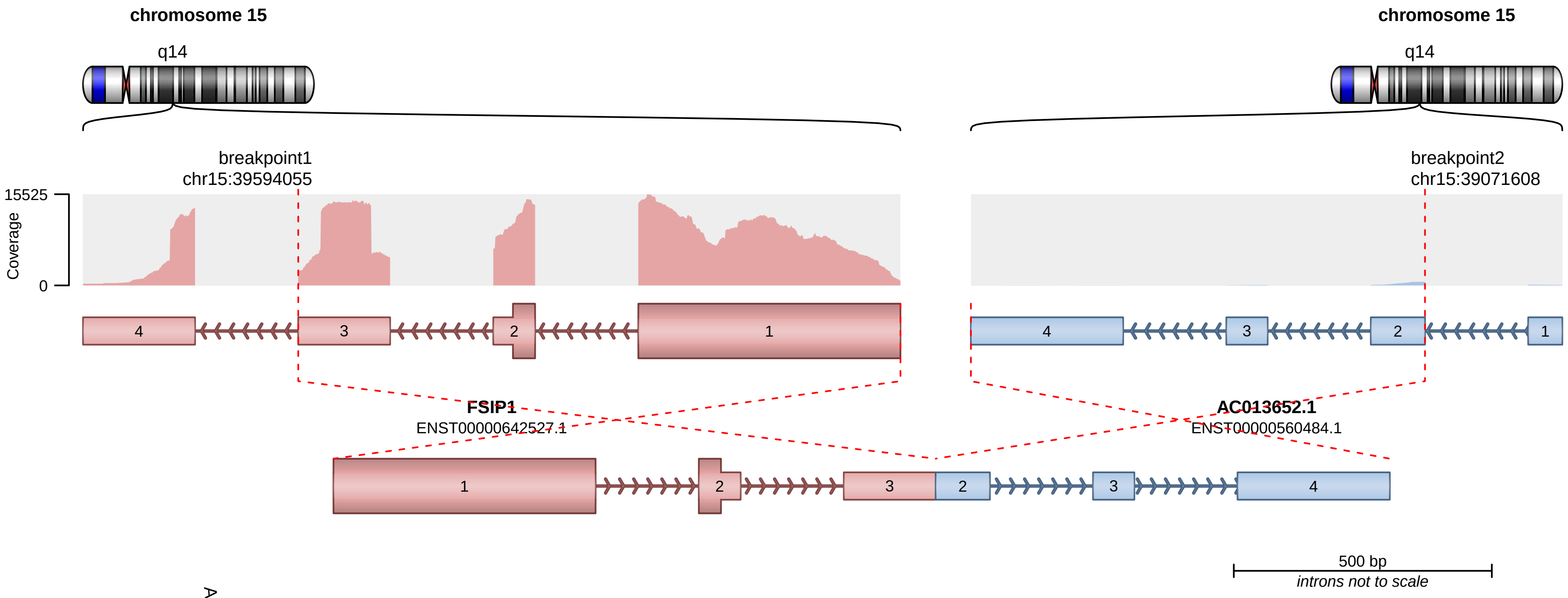


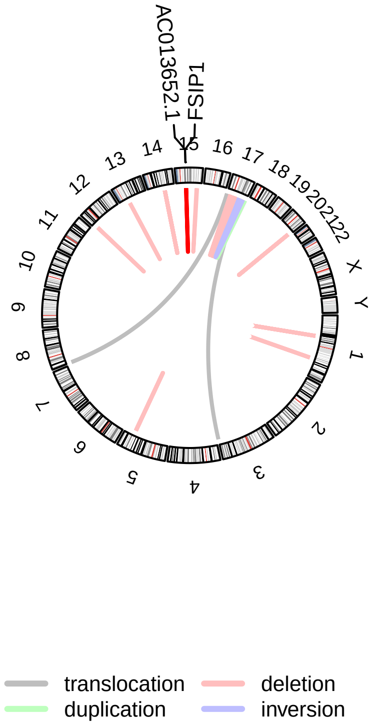


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 14

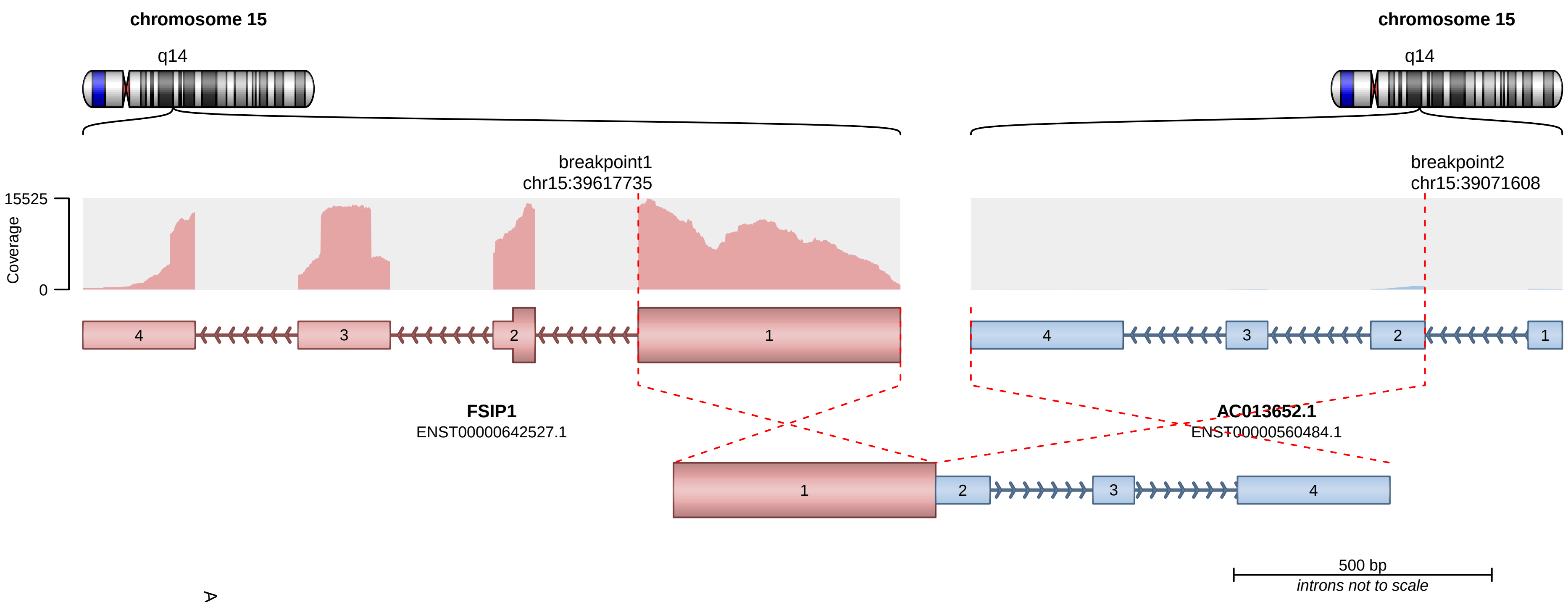


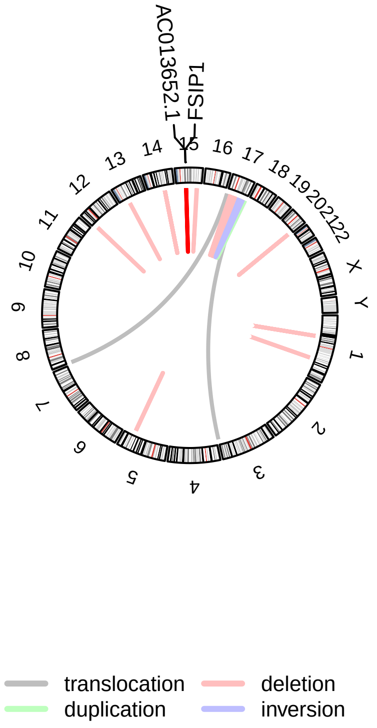


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 14

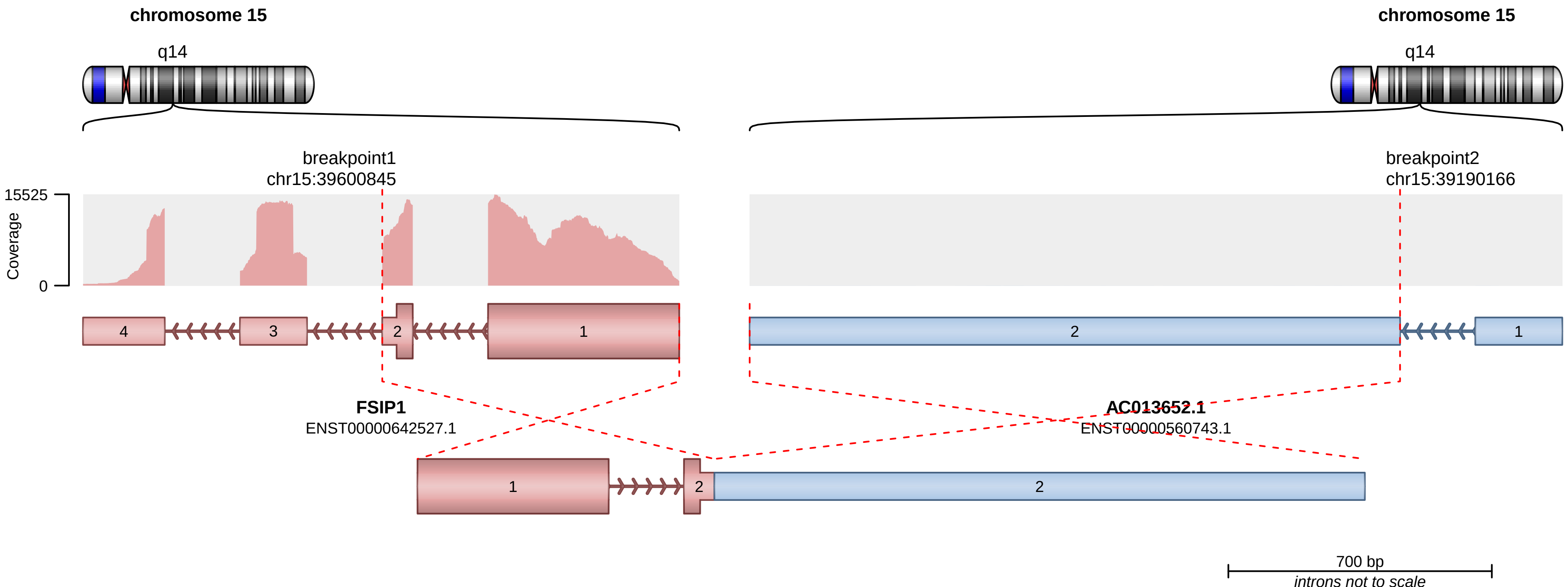


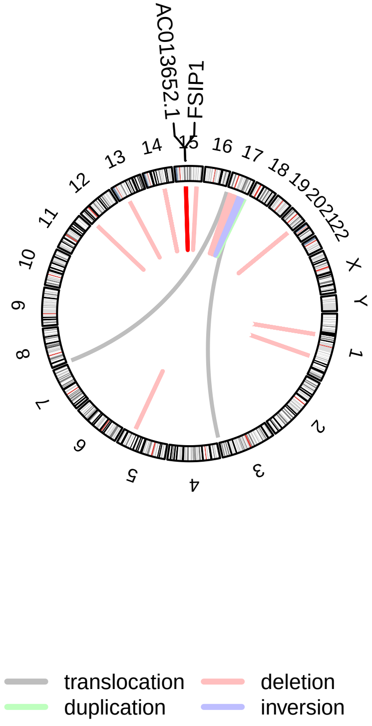


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 4

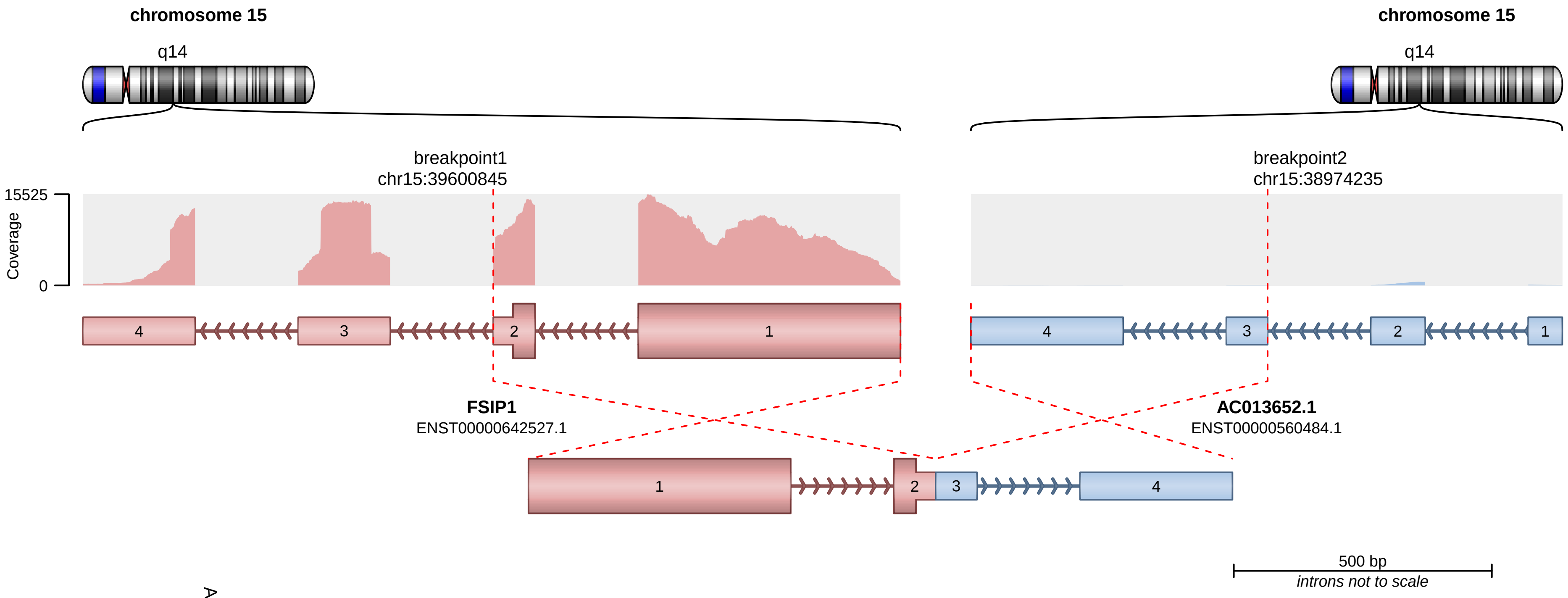


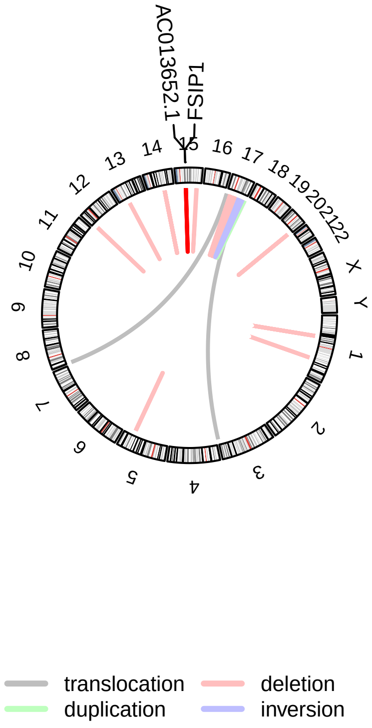


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 15

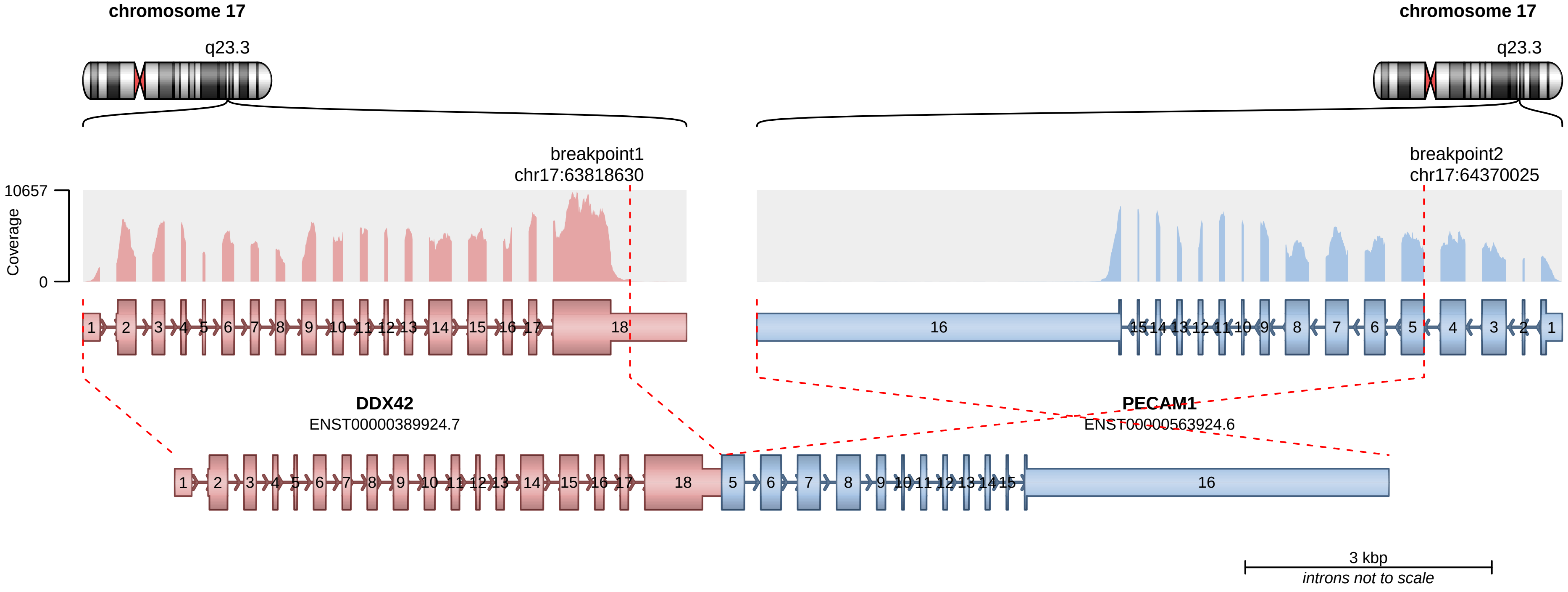


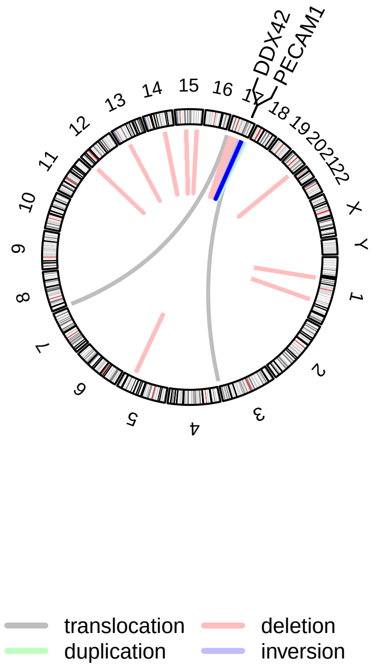


No protein domains retained in fusion.

SUPPORTING READ COUNT

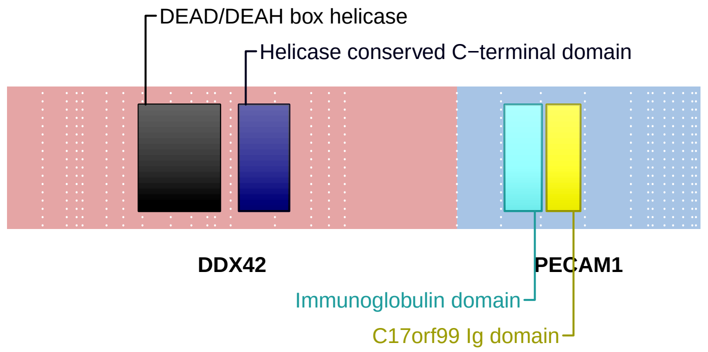
Split reads = 1
Discordant mates = 0





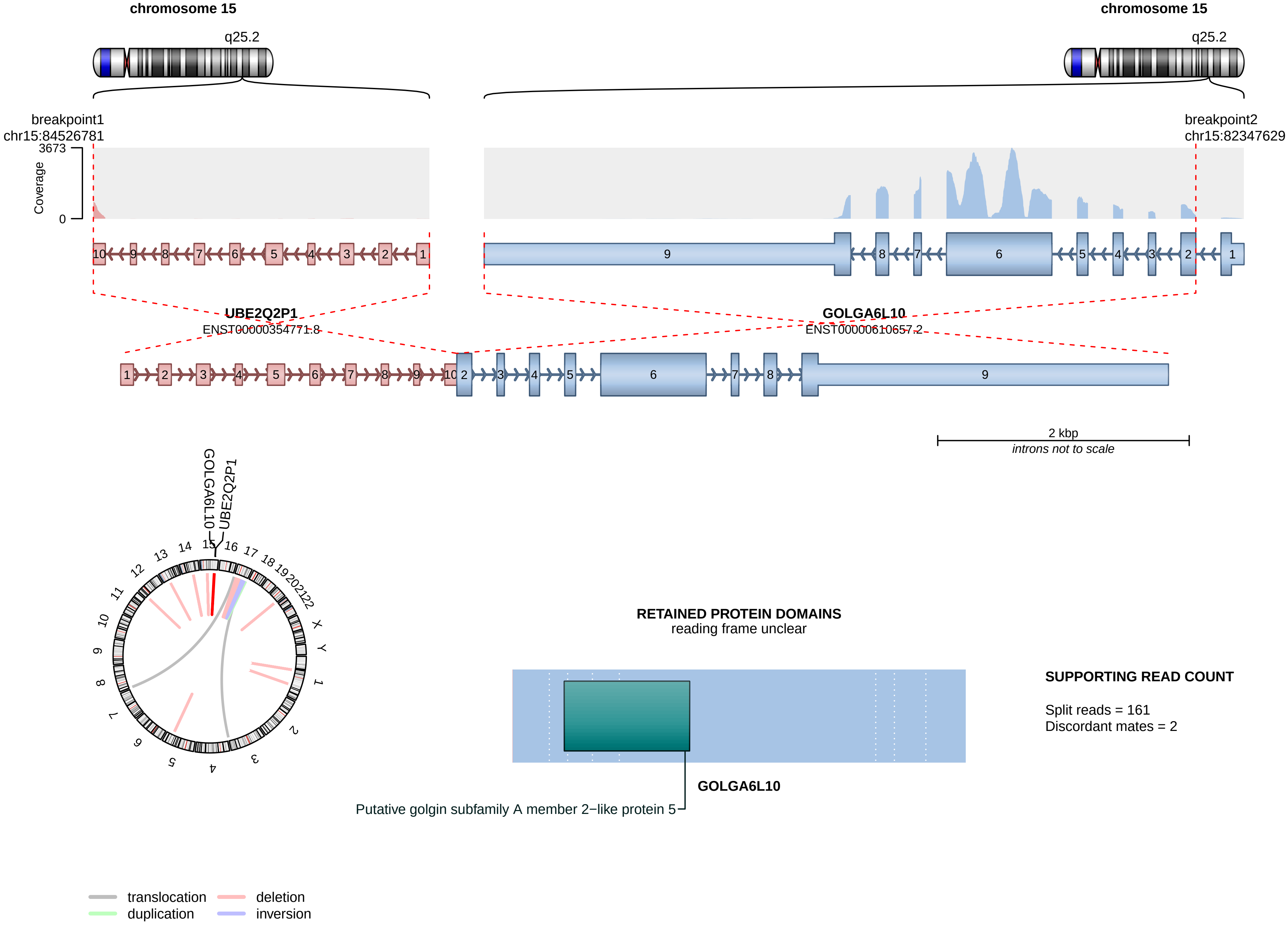
RETAINED PROTEIN DOMAINS

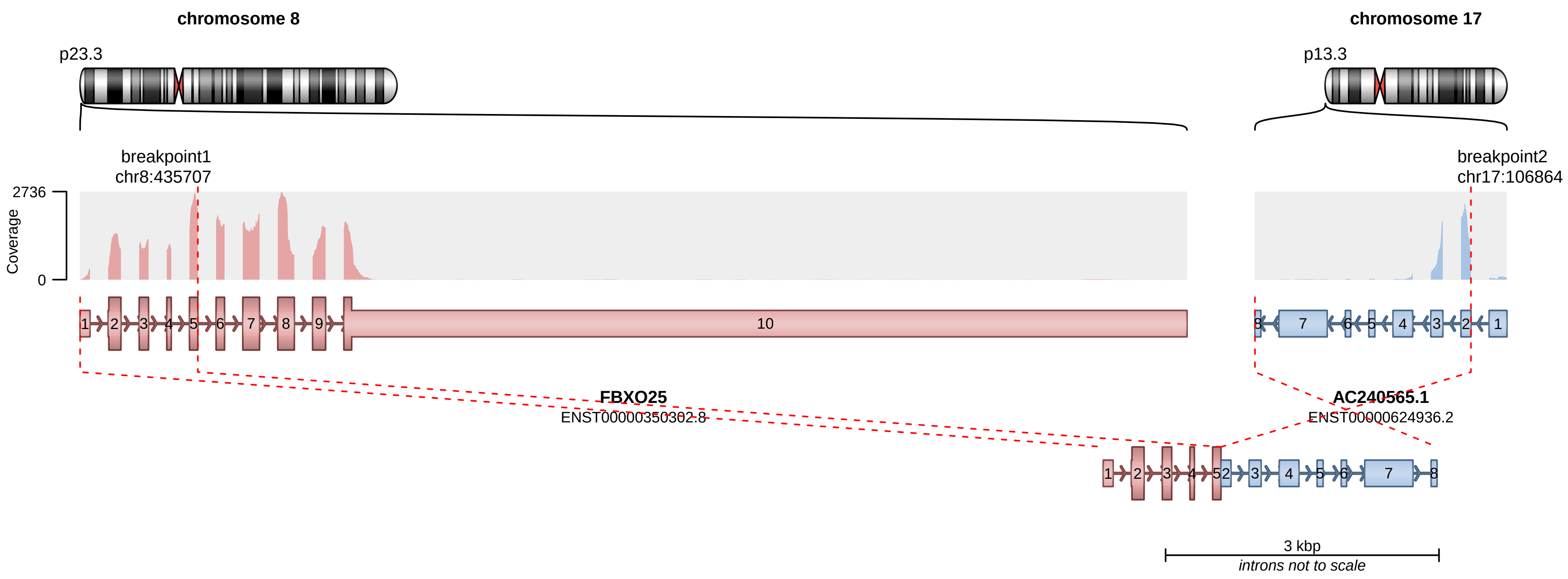
reading frame unclear

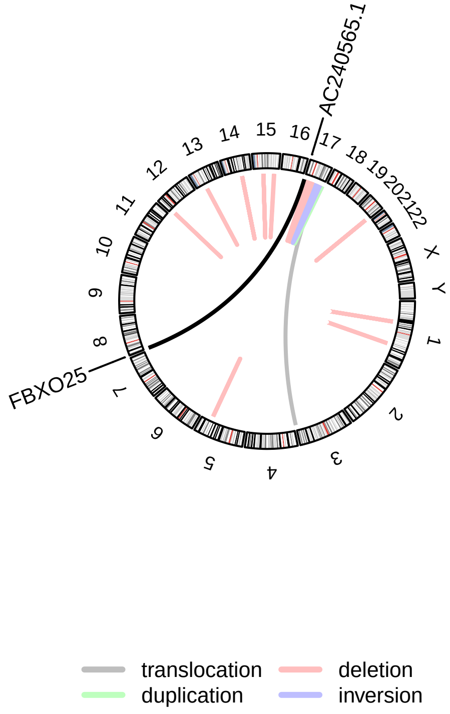


SUPPORTING READ COUNT

Split reads = 165
Discordant mates = 10


chromosome 15
q25.2
chromosome 15
q25.2
breakpoint1
chr15:84526781
breakpoint2
chr15:82347629
3673
Coverage
0
10 9 8 7 6 5 4 3 2 1
9 8 7 6 5 4 3 2 1
UBE2Q2P1
ENST00000354771.8
GOLGA6L10
ENST00000610657.2
1 2 3 4 5 6 7 8 9 10
2 3 4 5 6 7 8 9
2 kbp
introns not to scale
GOLGA6L10
UBE2Q2P1
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y
RETAINED PROTEIN DOMAINS
reading frame unclear
GOLGA6L10
Putative golgin subfamily A member 2−like protein 5
SUPPORTING READ COUNT
Split reads = 161
Discordant mates = 2
translocation
duplication
deletion
inversion

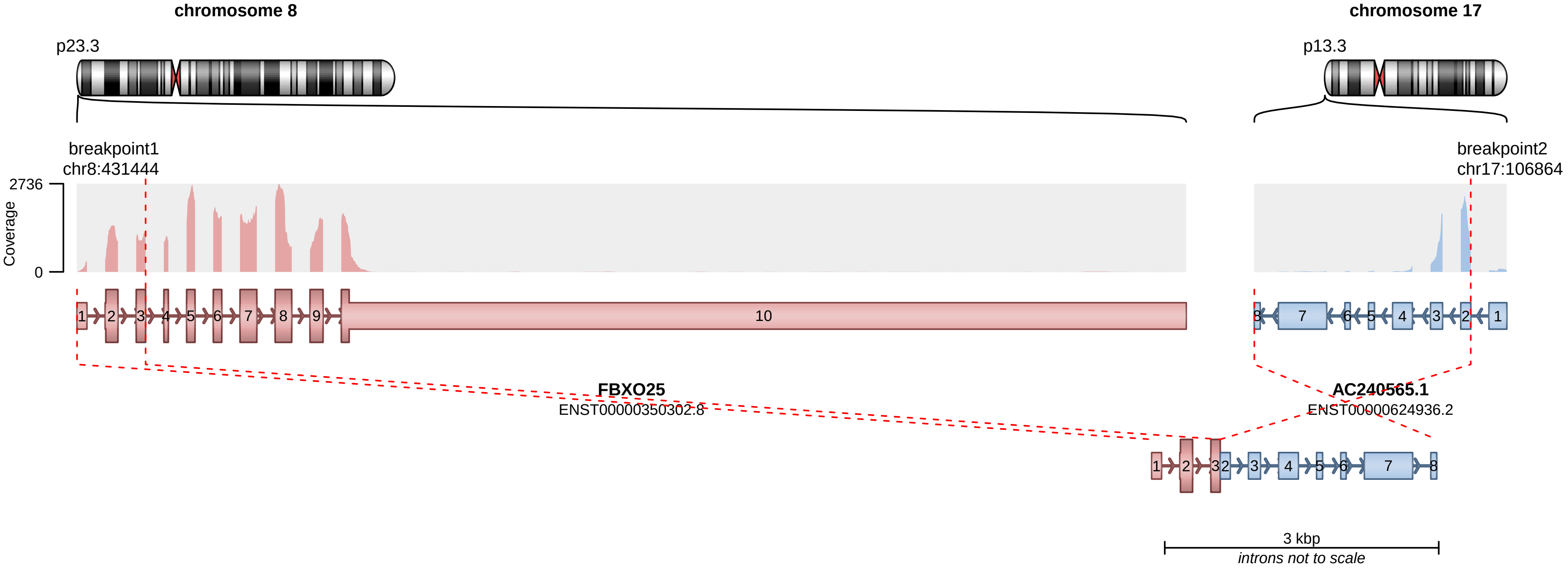


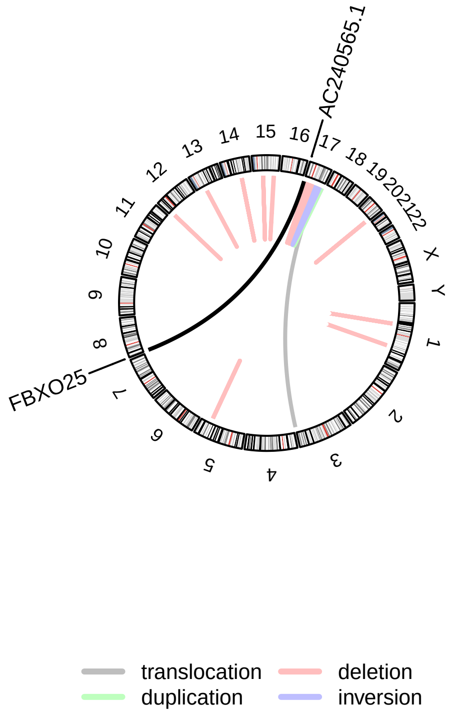


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 158
Discordant mates = 0

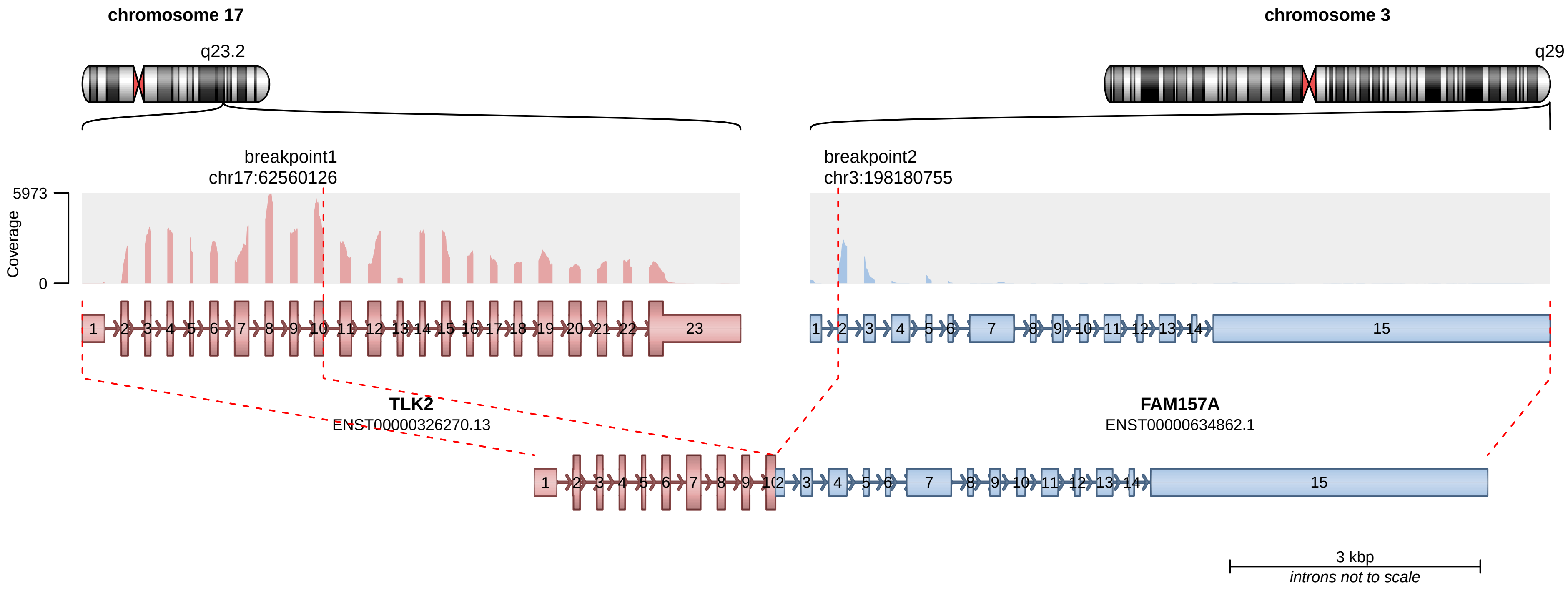


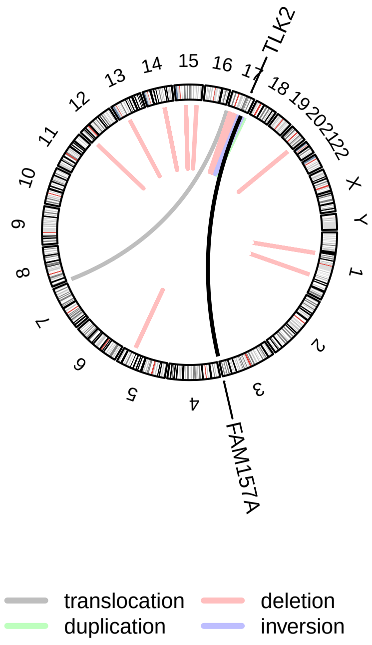


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

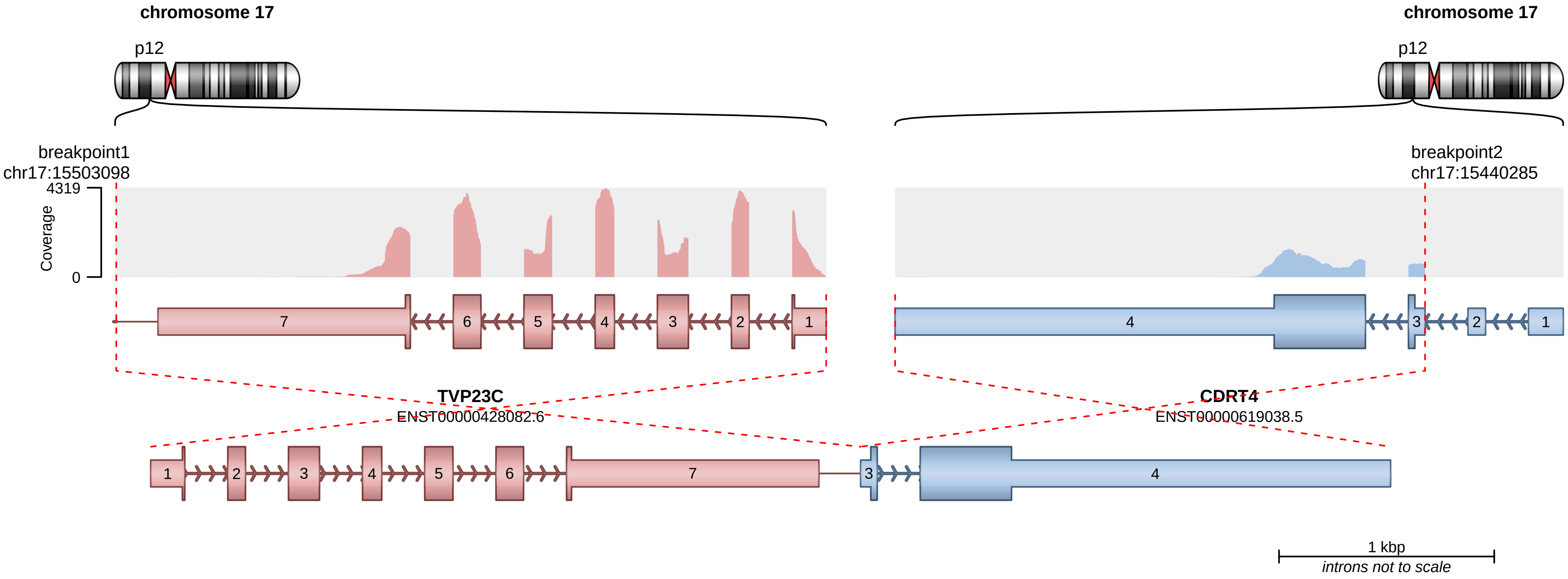


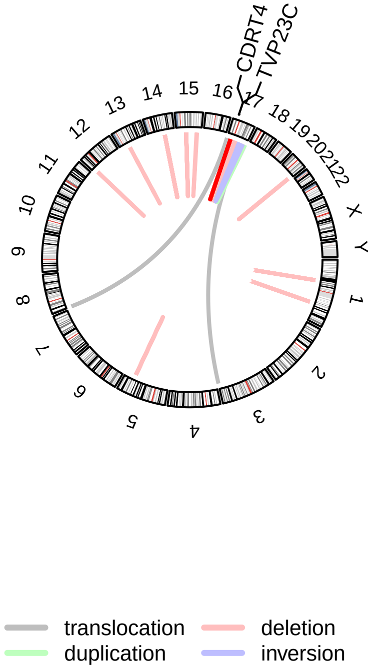


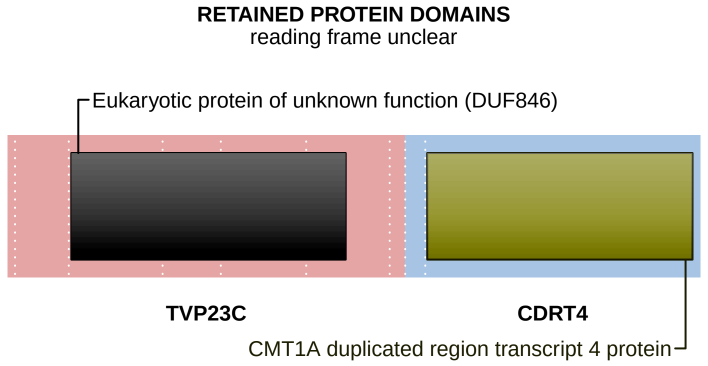
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 122
Discordant mates = 1

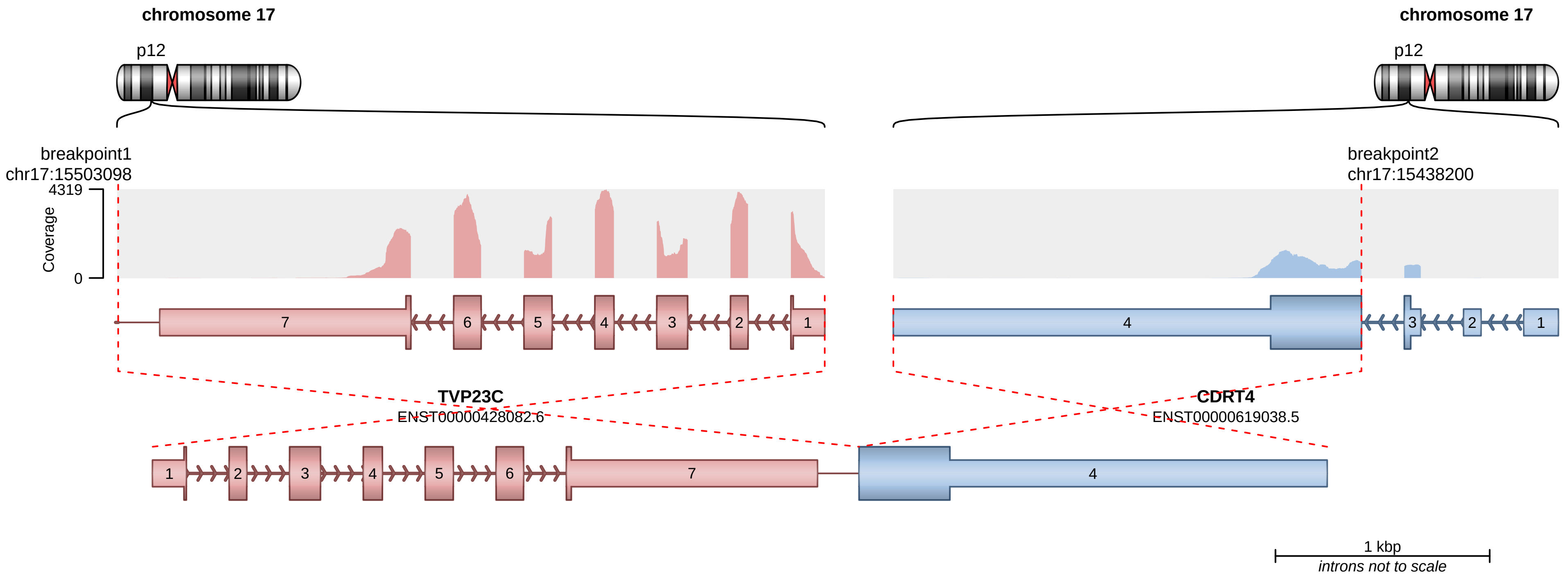


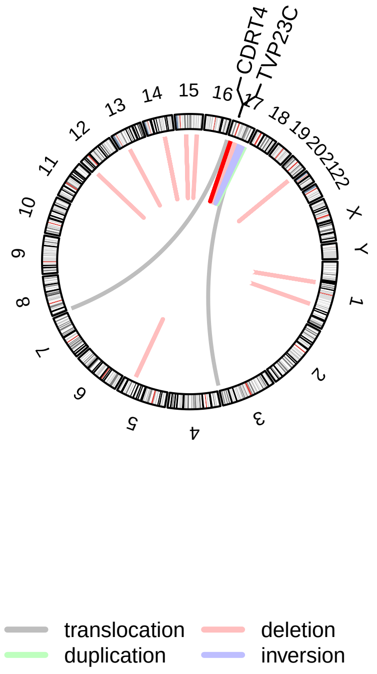




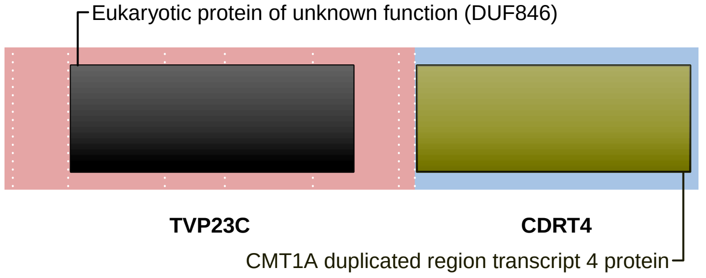
SUPPORTING READ COUNT

Split reads = 117
Discordant mates = 0



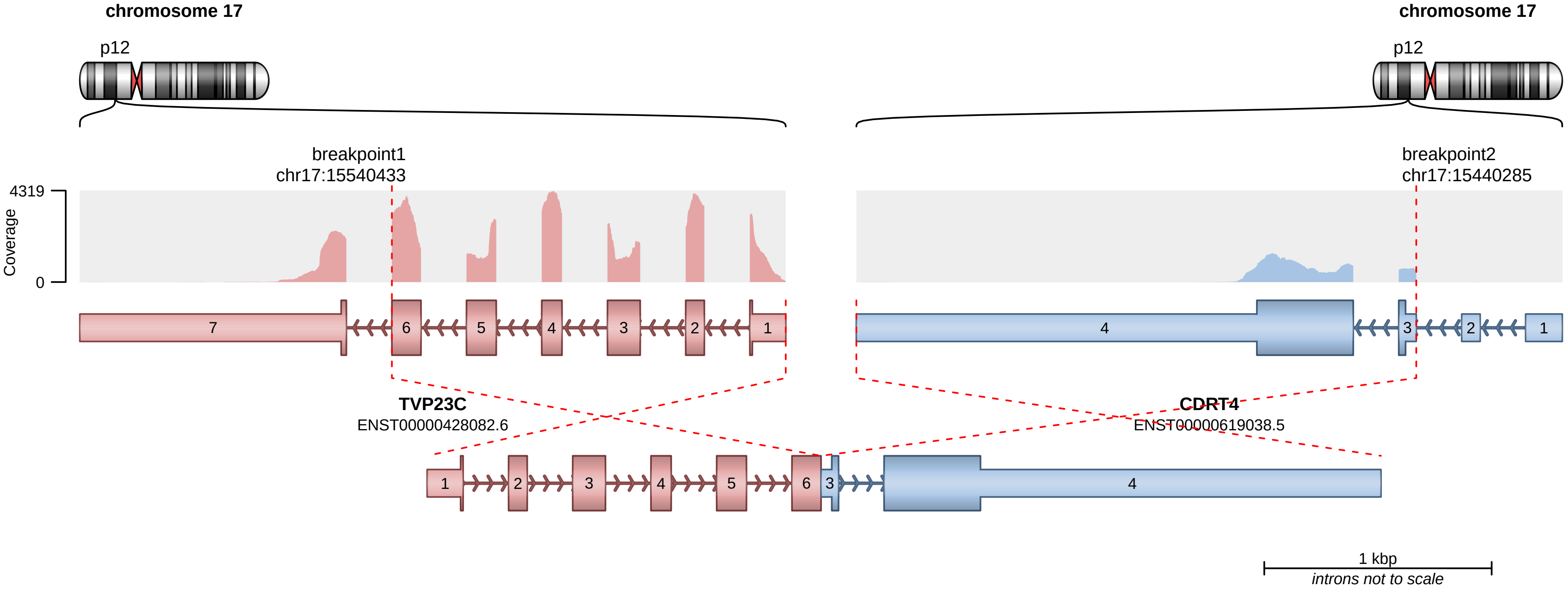


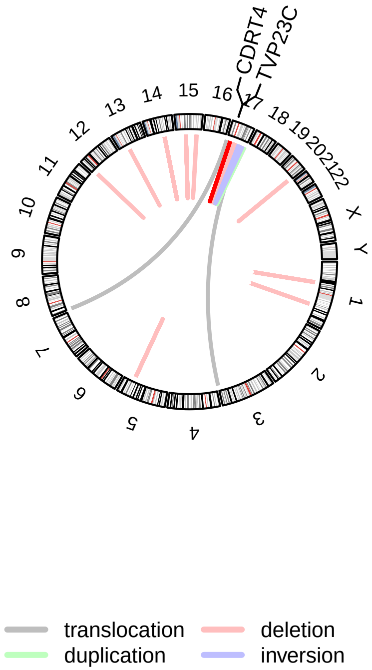
RETAINED PROTEIN DOMAINS
reading frame unclear

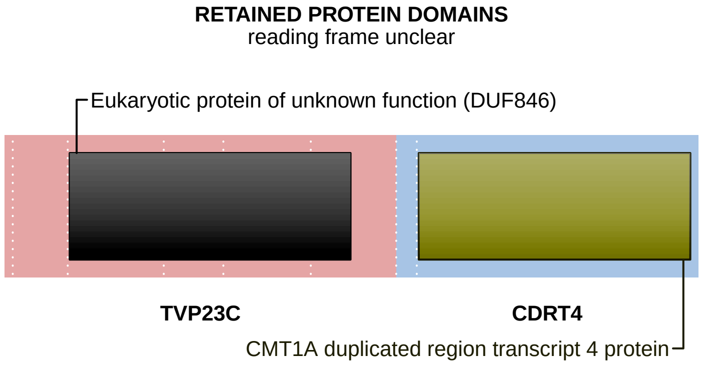


SUPPORTING READ COUNT

Split reads = 44
Discordant mates = 0

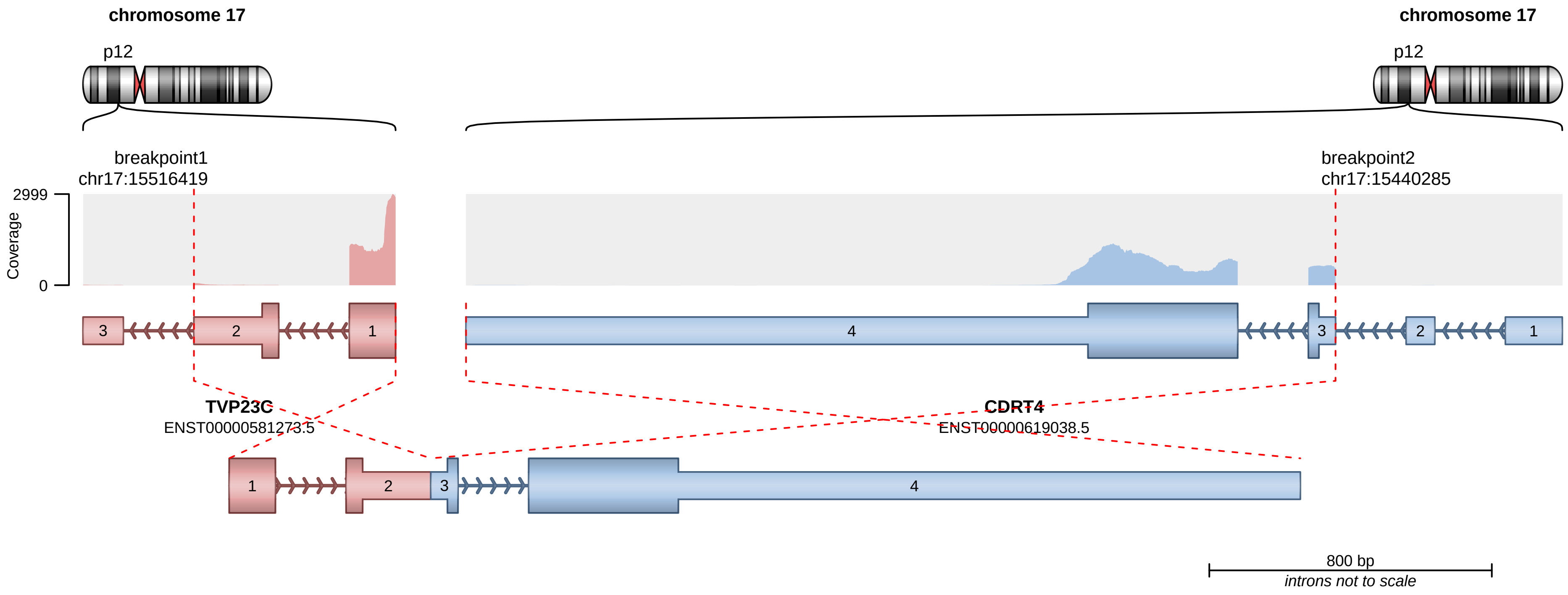


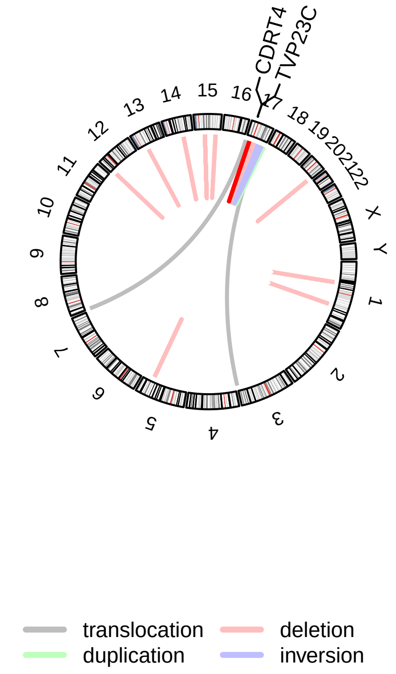


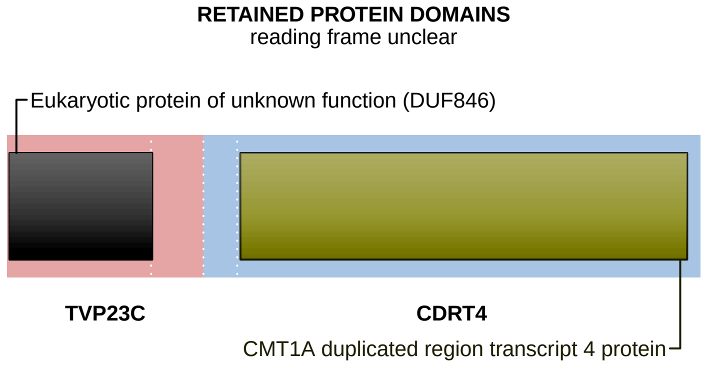


SUPPORTING READ COUNT

Split reads = 39
Discordant mates = 0

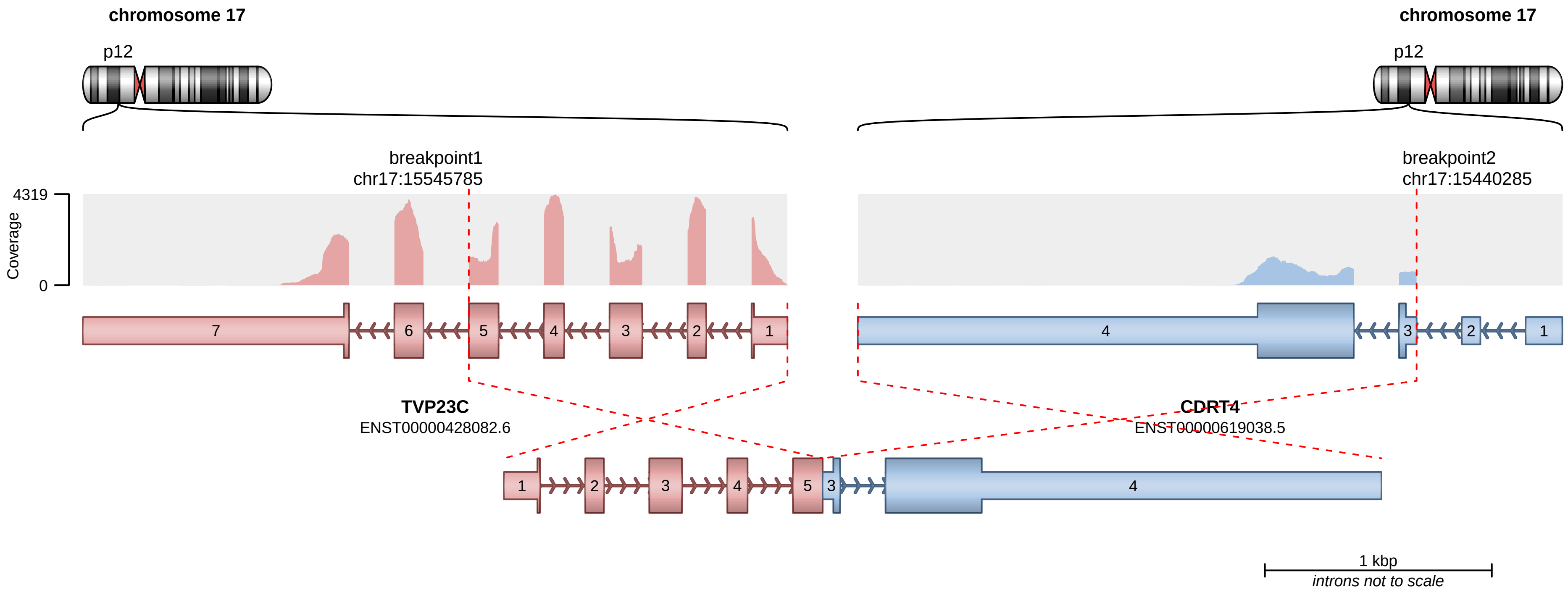


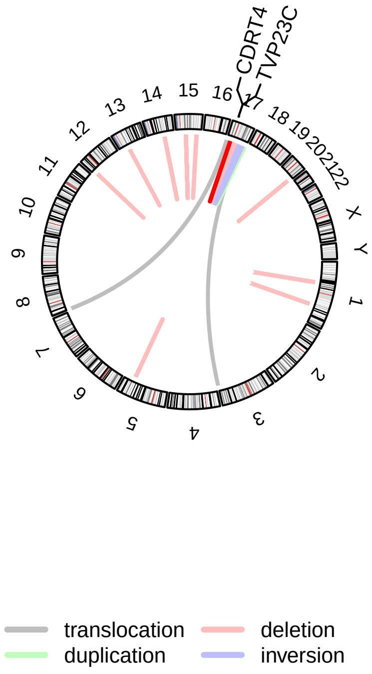




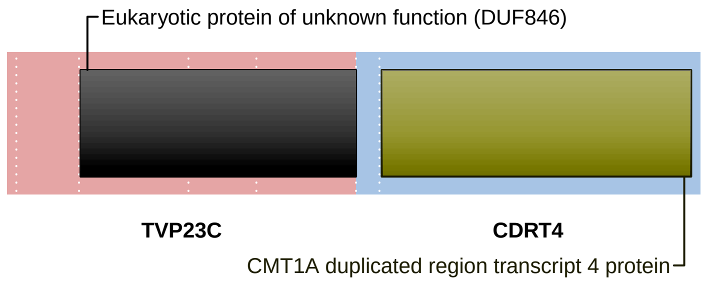
SUPPORTING READ COUNT

Split reads = 17
Discordant mates = 0



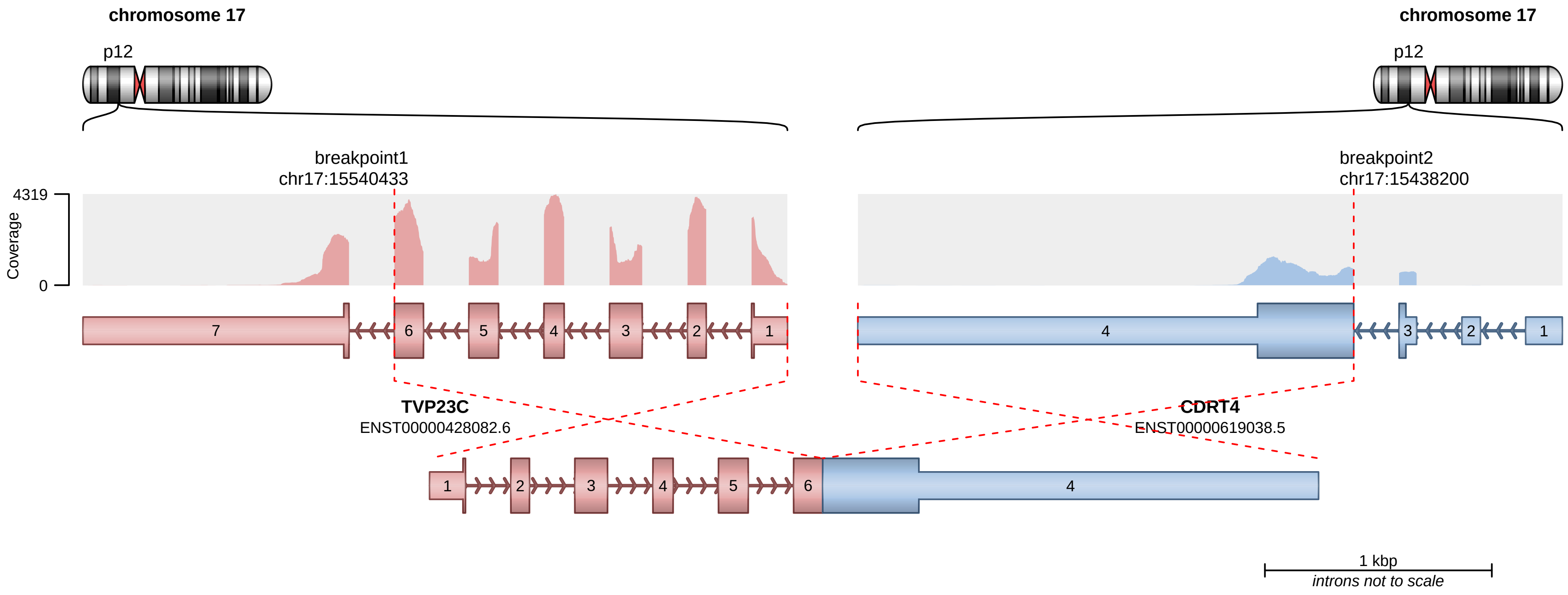


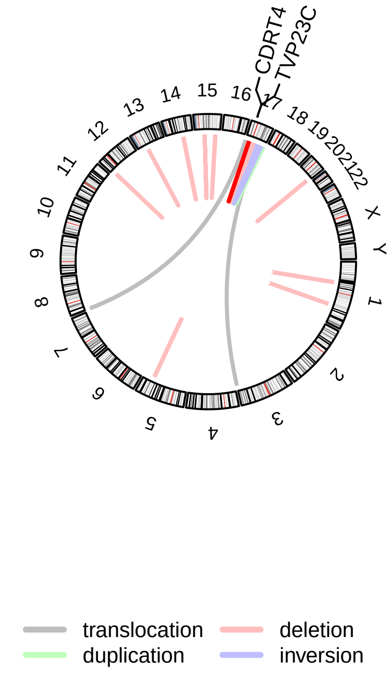
RETAINED PROTEIN DOMAINS
reading frame unclear

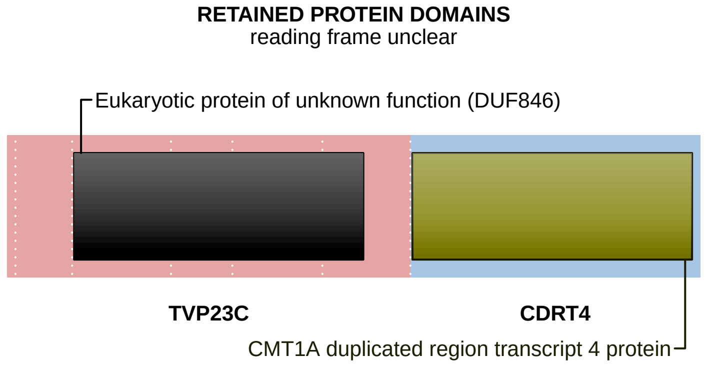


SUPPORTING READ COUNT

Split reads = 9
Discordant mates = 0

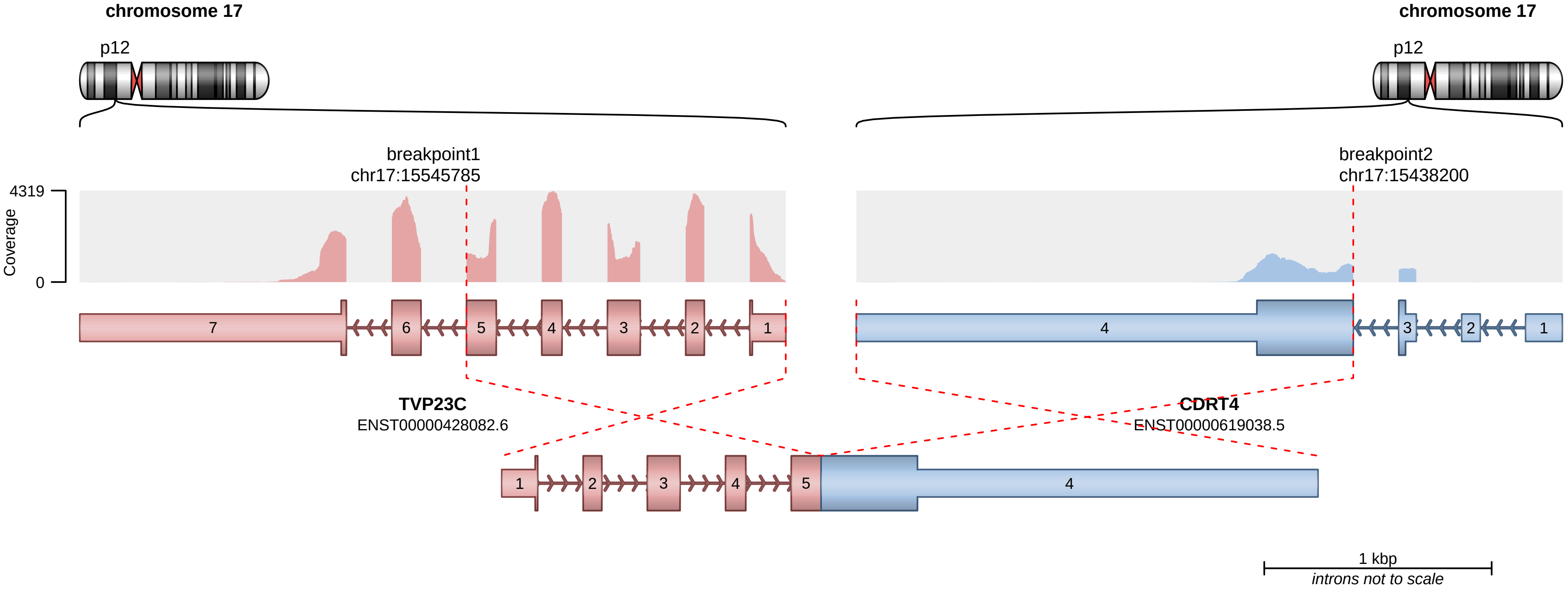


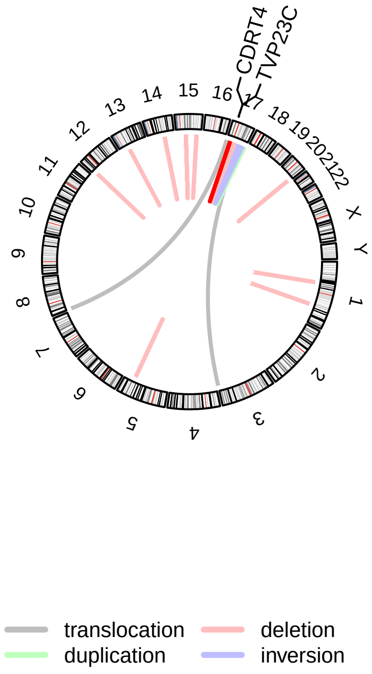


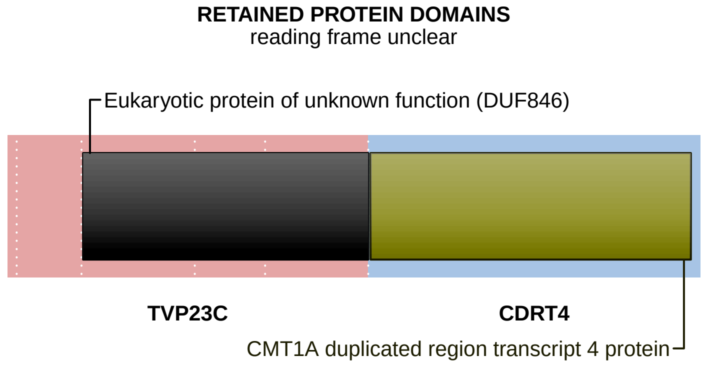


SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0

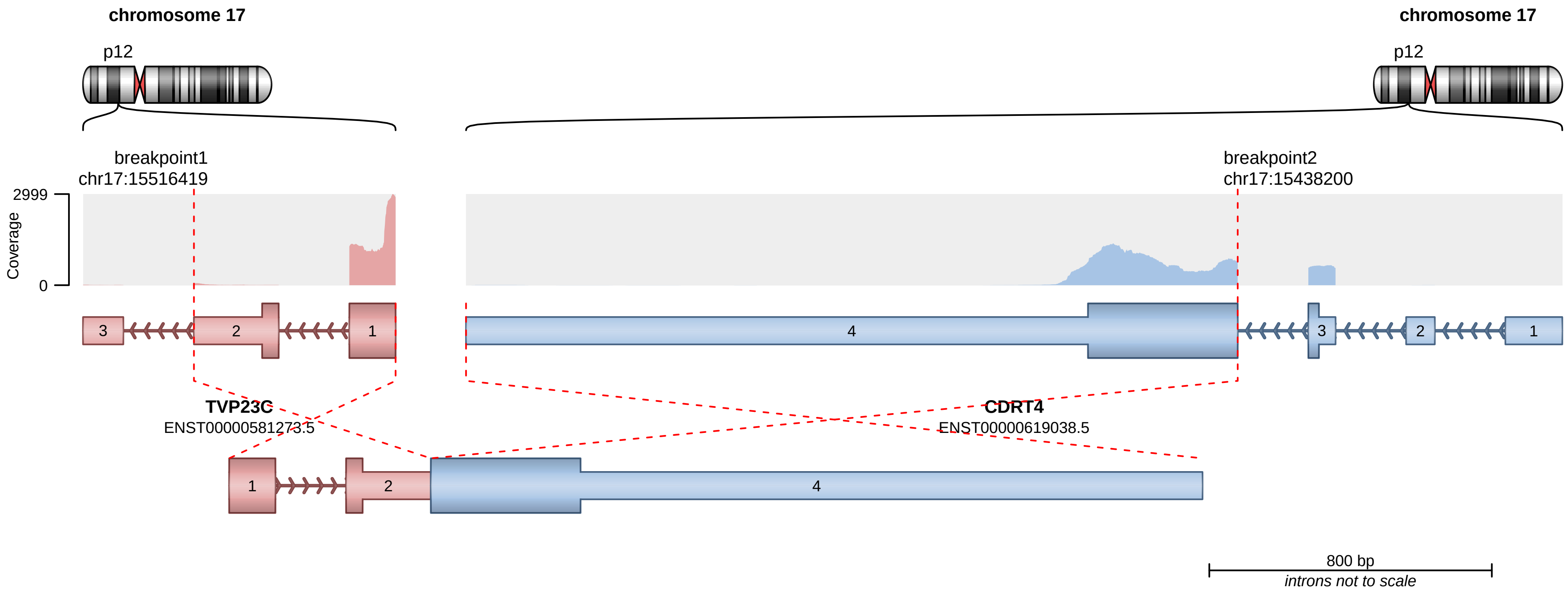


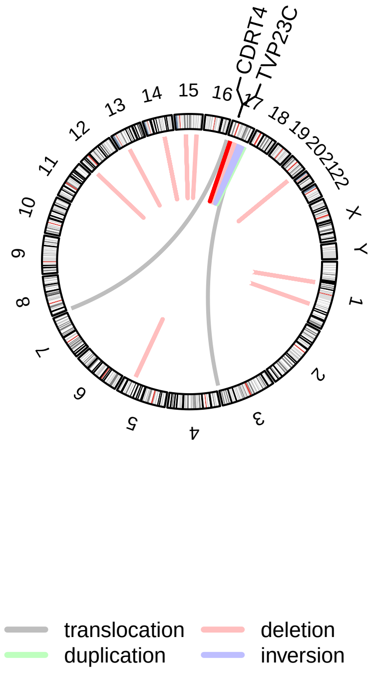




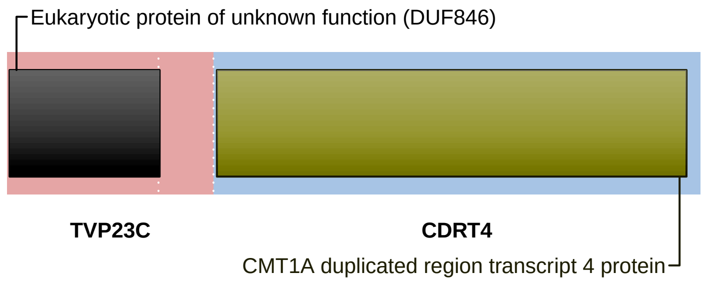
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0



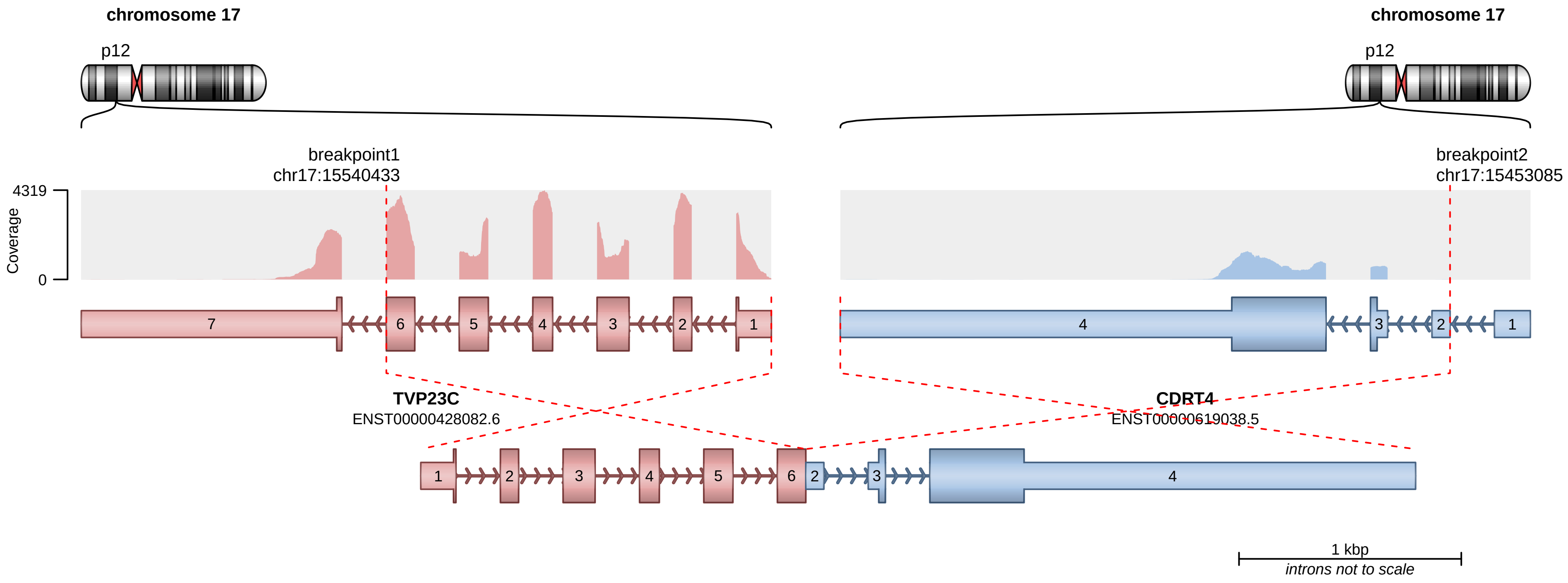


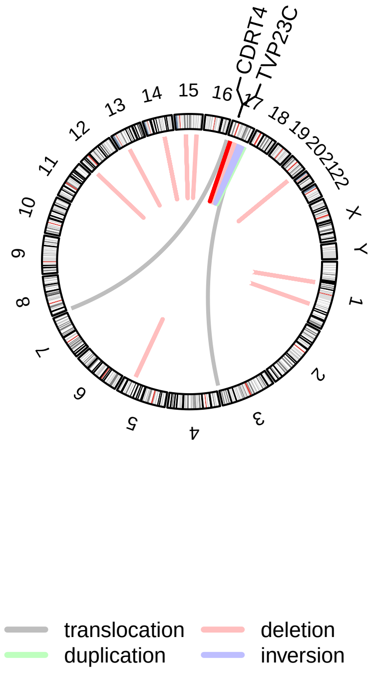
RETAINED PROTEIN DOMAINS
reading frame unclear



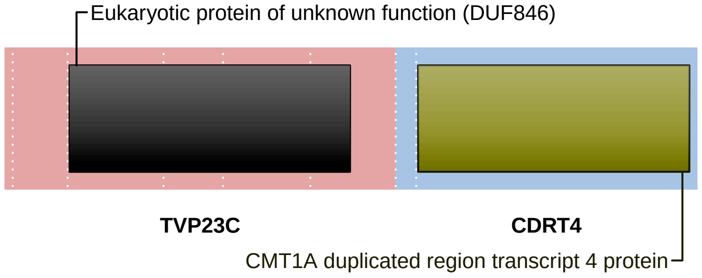
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0



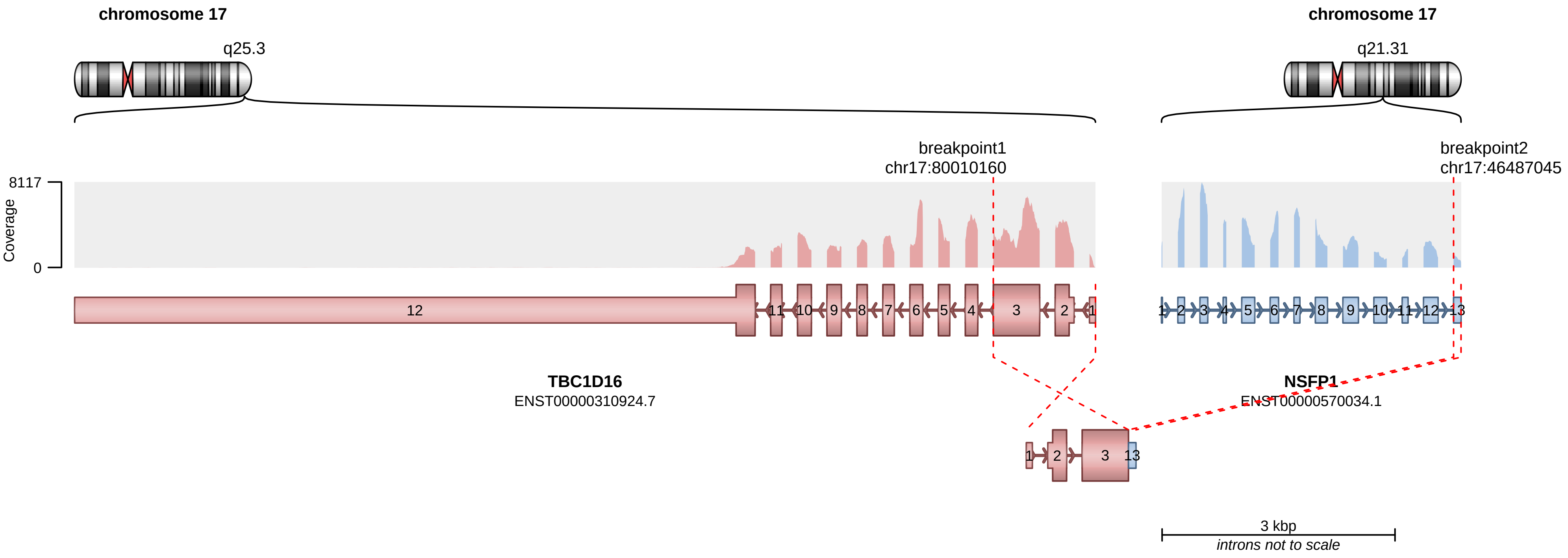


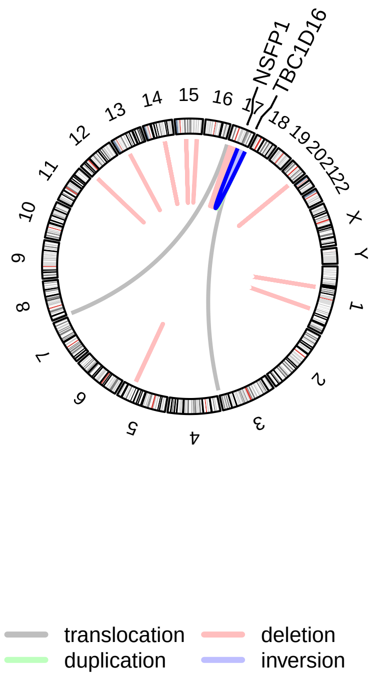
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

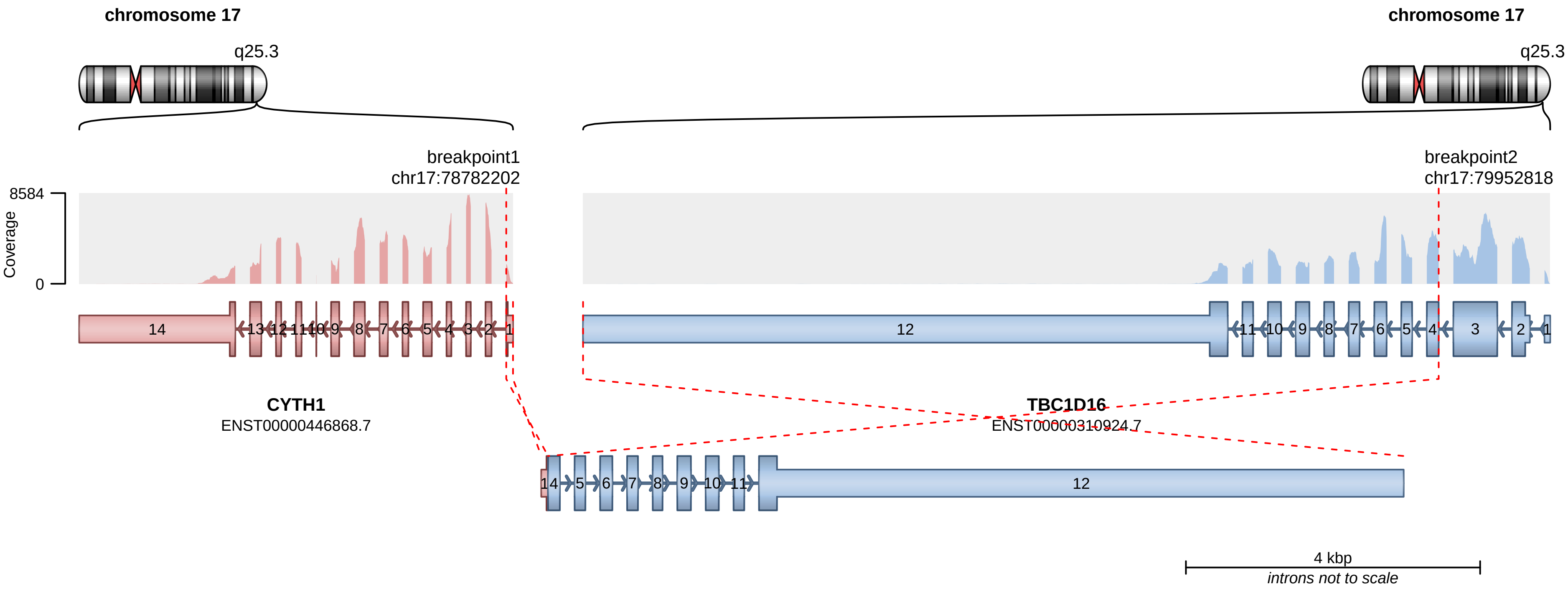


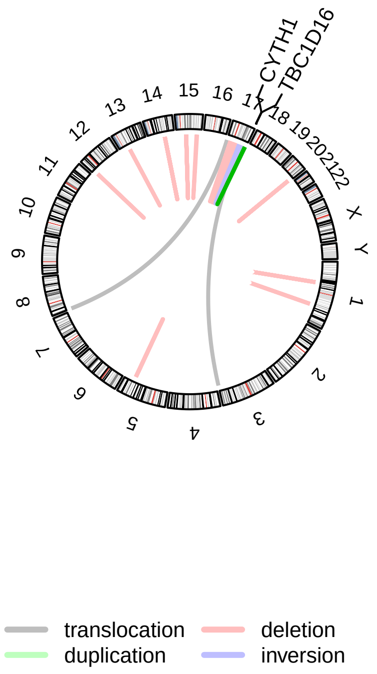


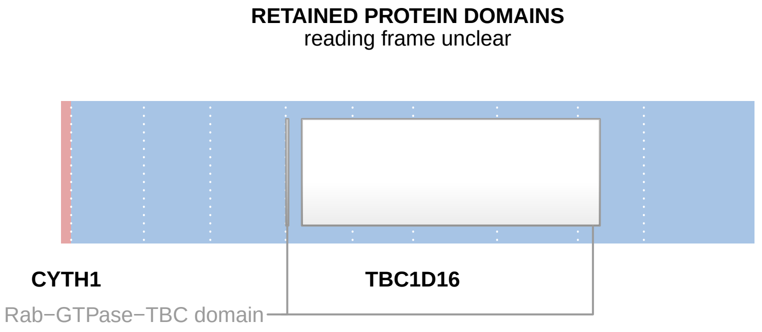
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 89
Discordant mates = 0

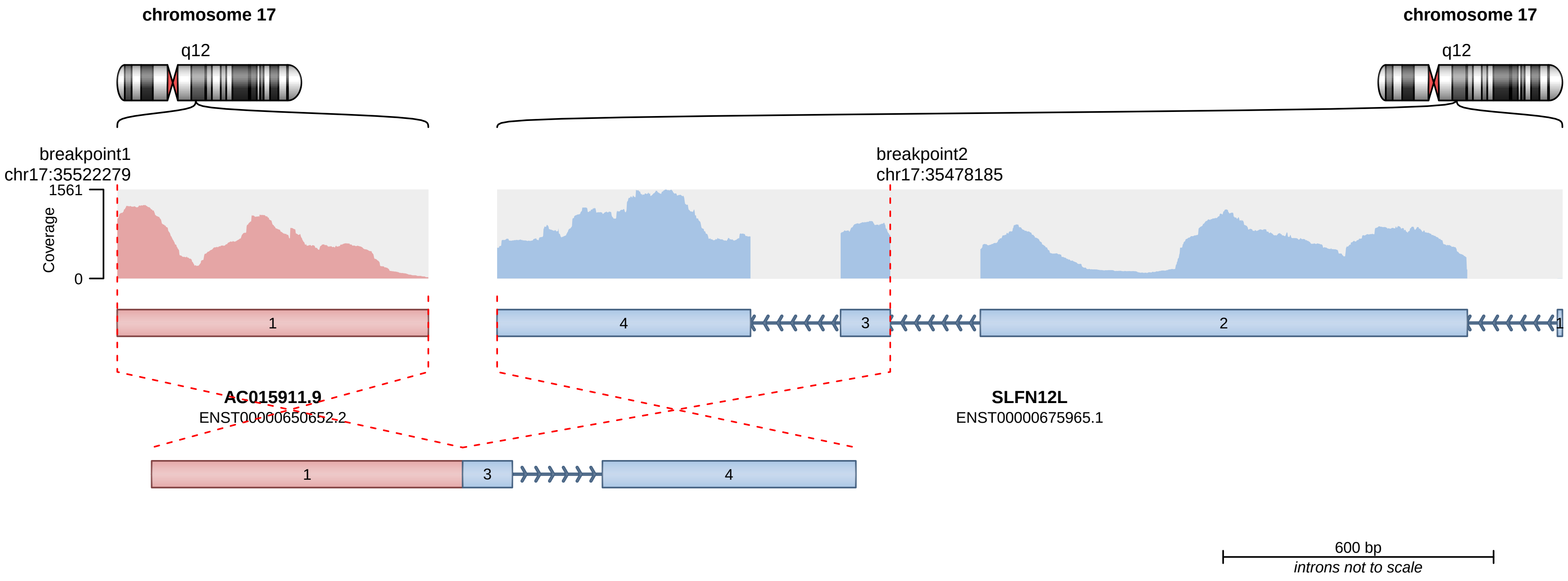


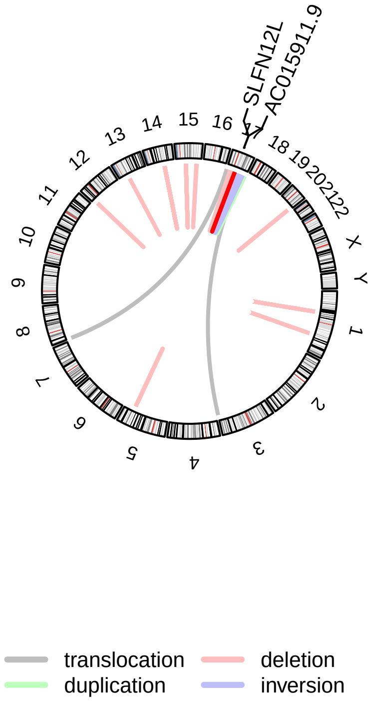




SUPPORTING READ COUNT

Split reads = 81
Discordant mates = 0

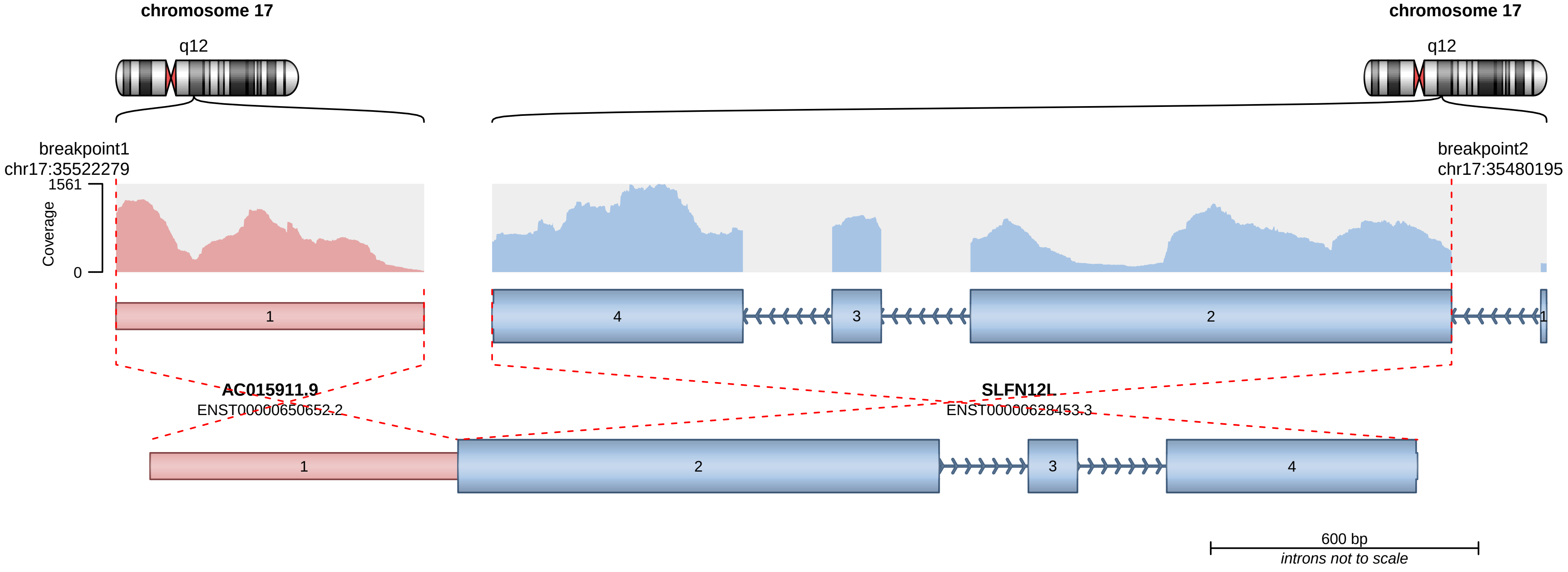


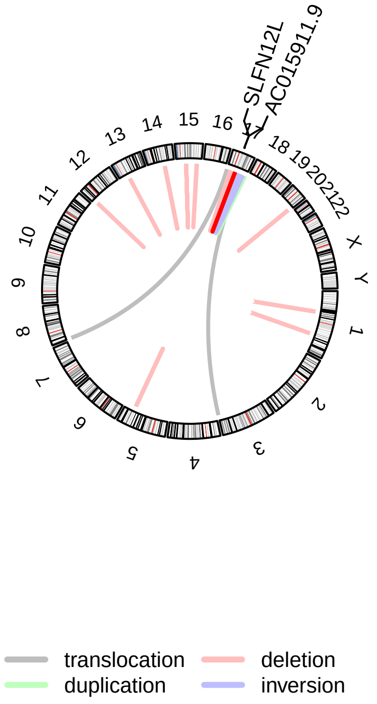


Genes are not protein−coding.

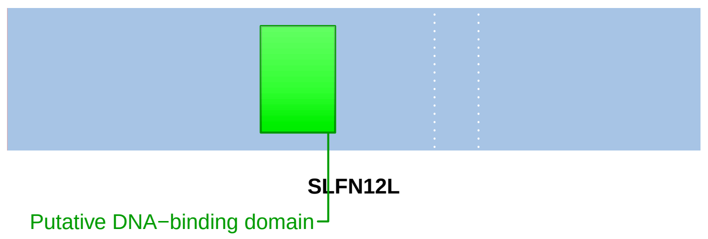
SUPPORTING READ COUNT

Split reads = 70
Discordant mates = 4



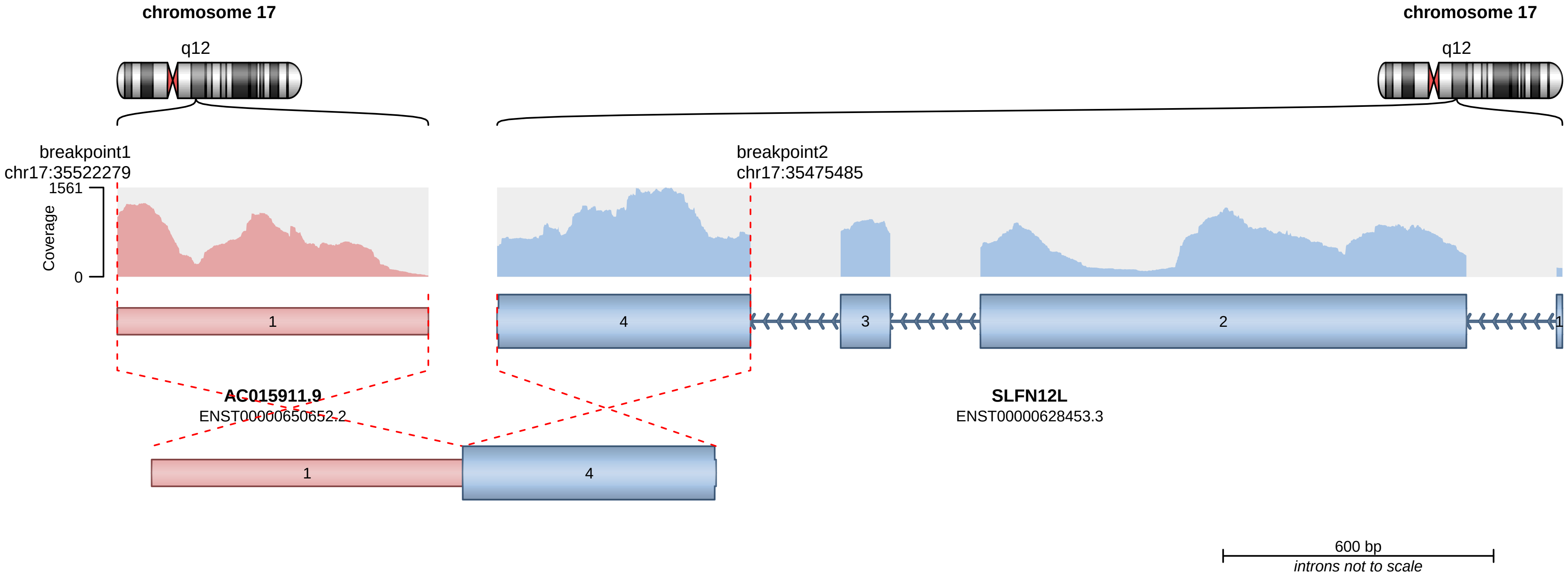


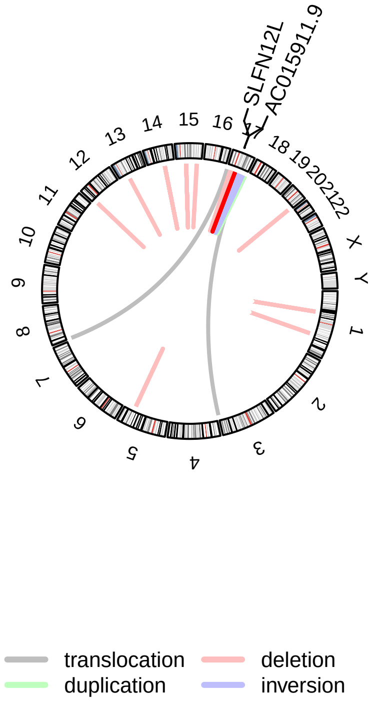
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 65
Discordant mates = 5

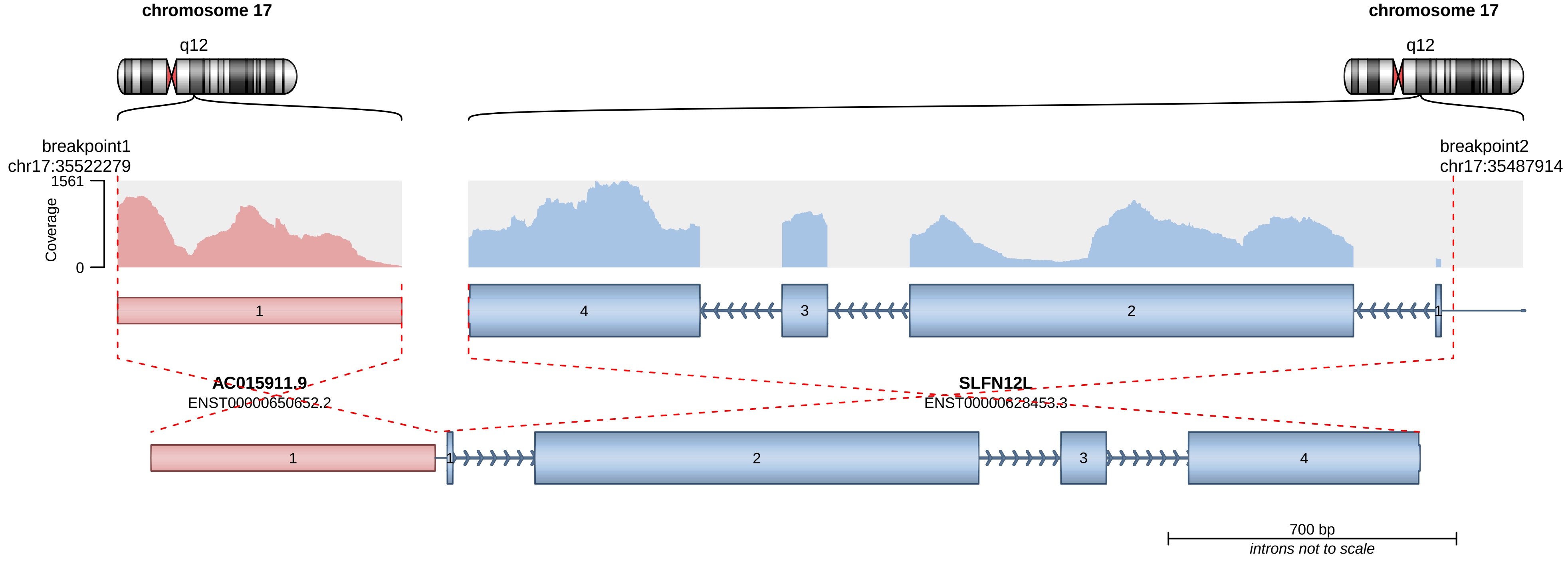


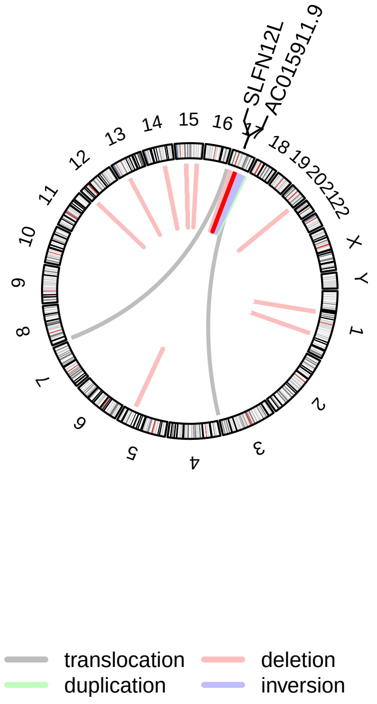


No protein domains retained in fusion.

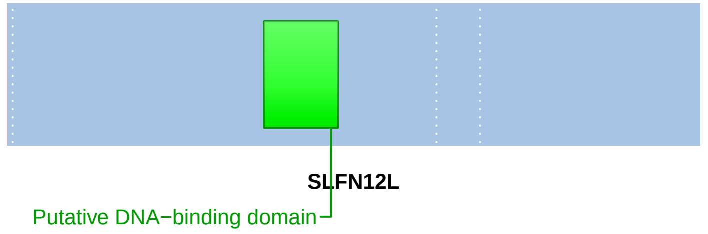
SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 0



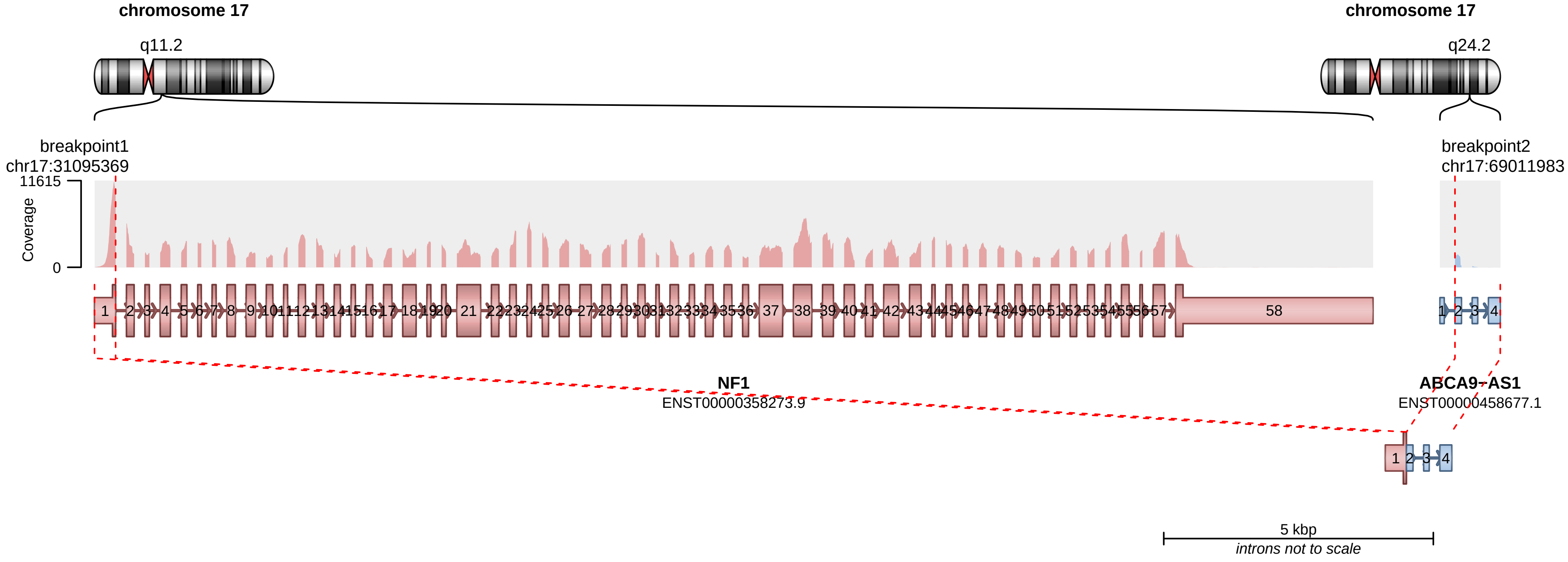


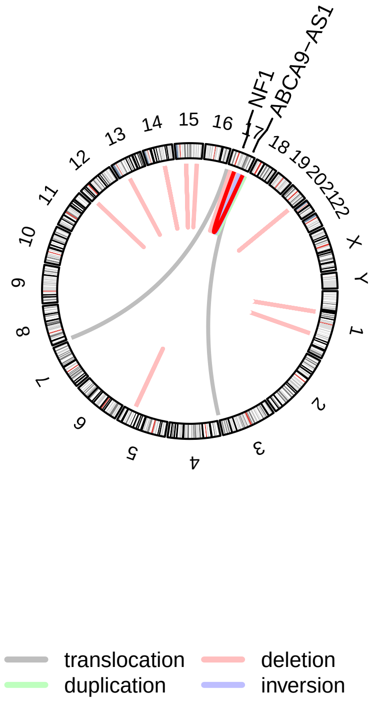
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 5

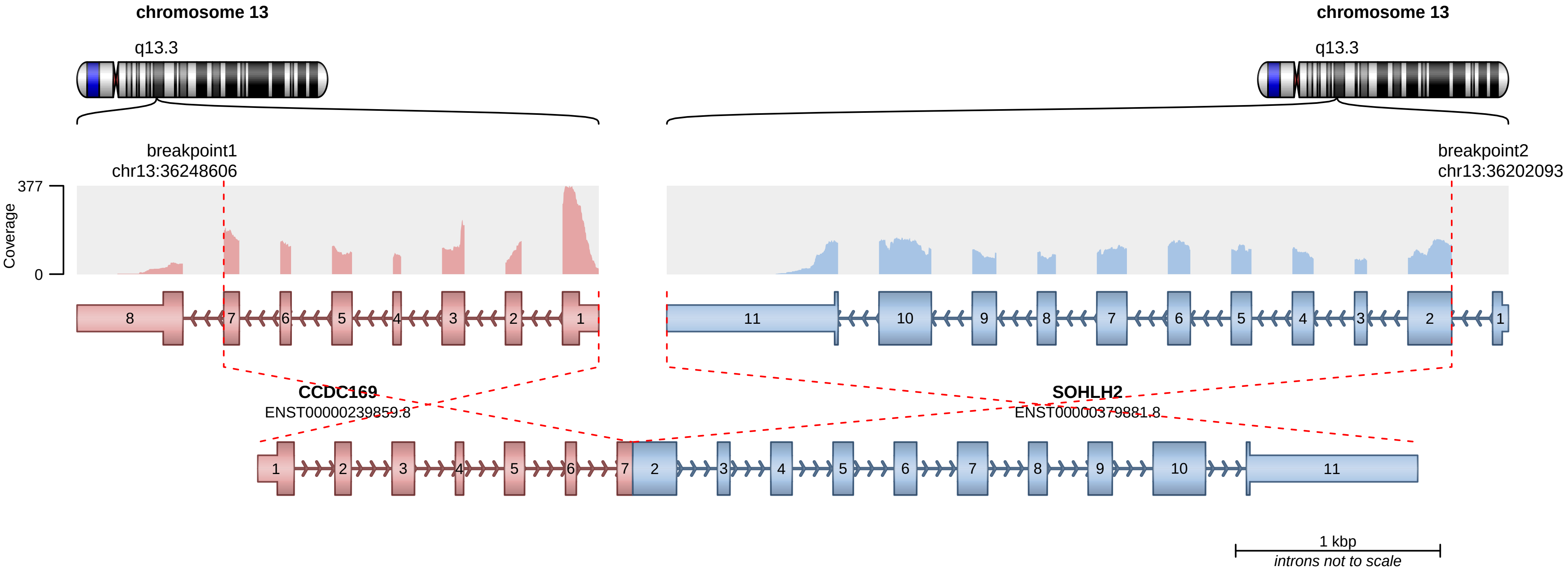


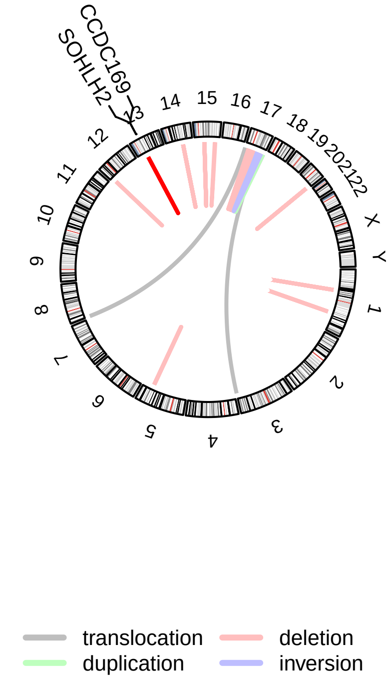


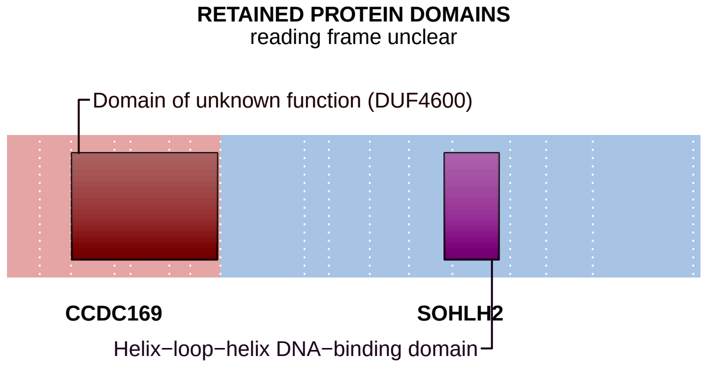
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 62
Discordant mates = 1

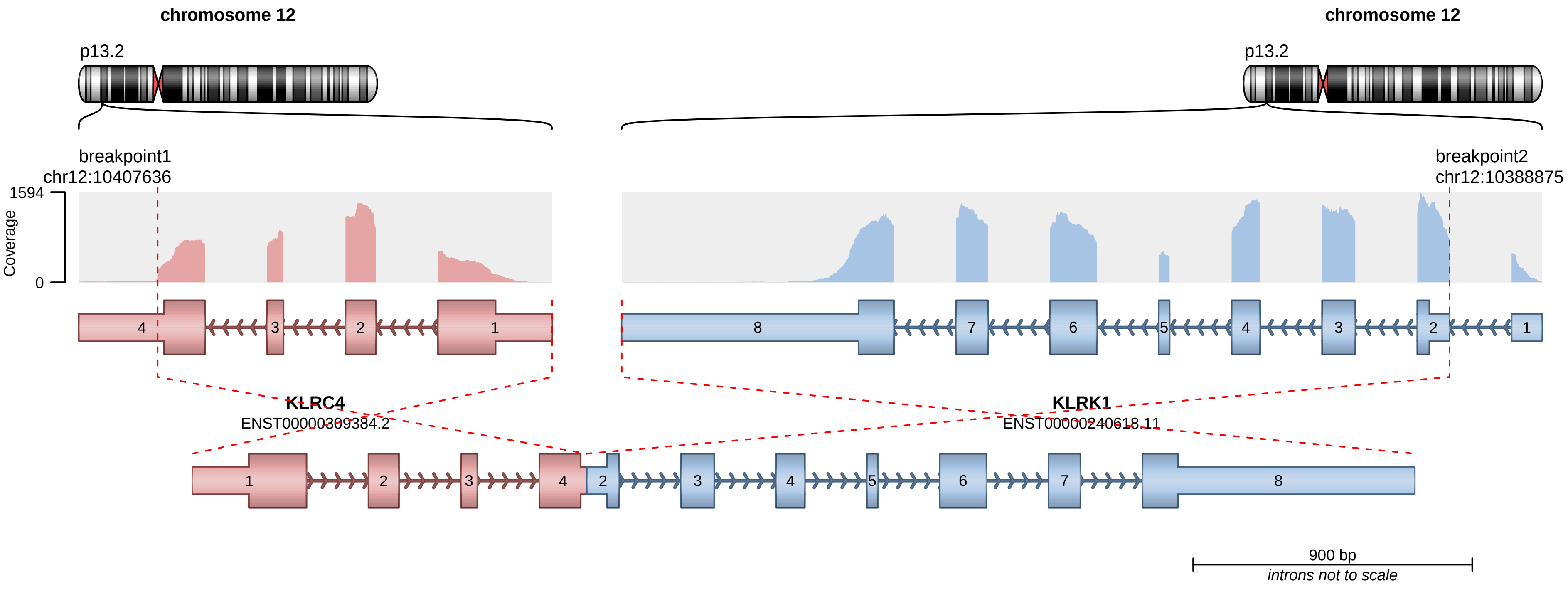


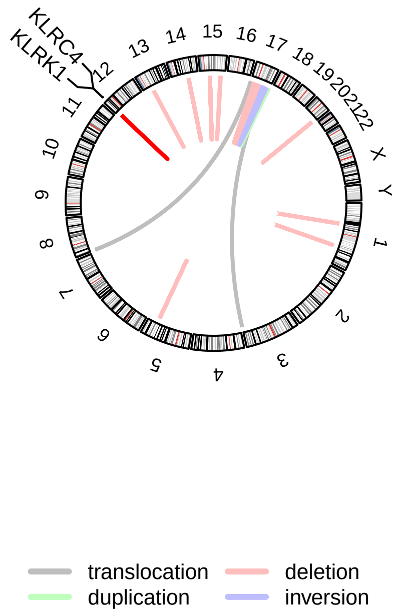




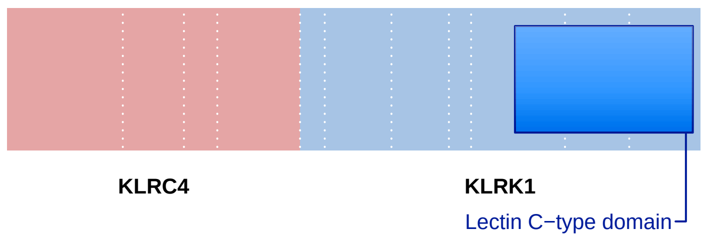
SUPPORTING READ COUNT

Split reads = 49
Discordant mates = 0



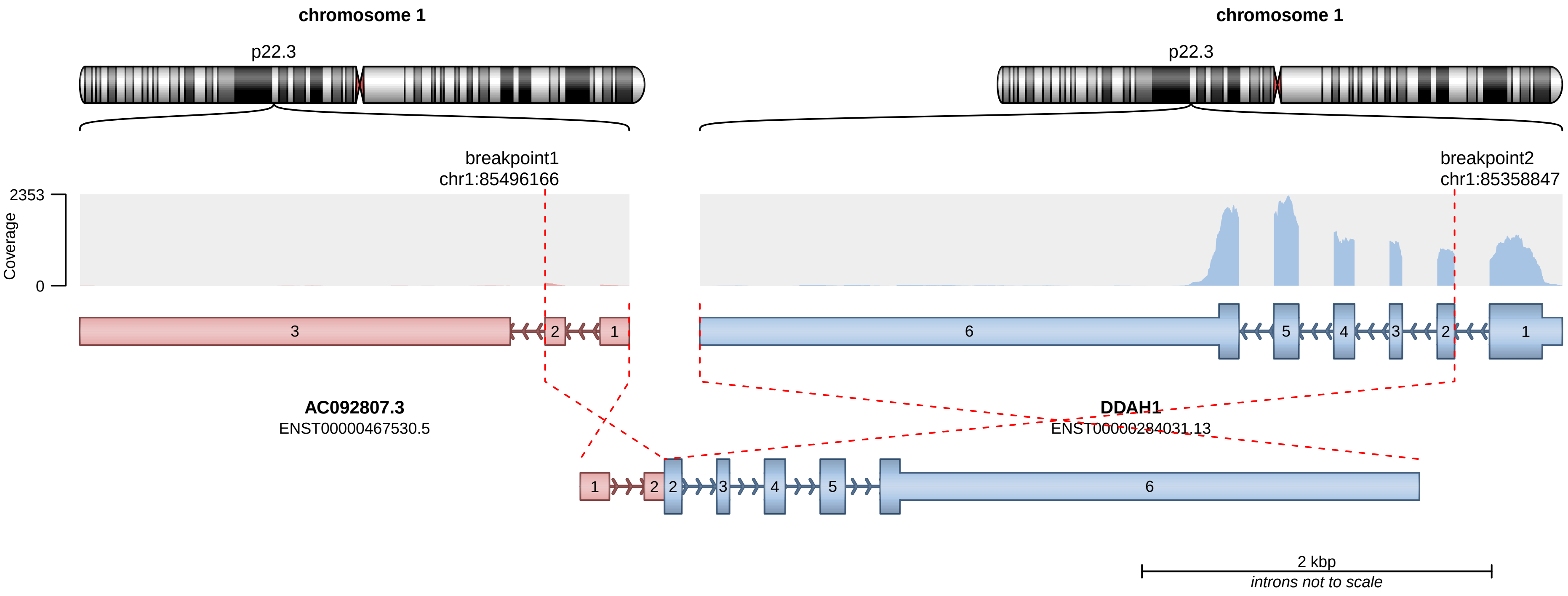


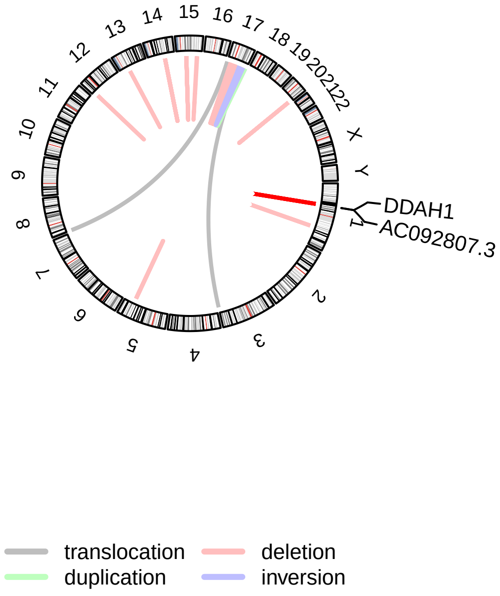
RETAINED PROTEIN DOMAINS
reading frame unclear



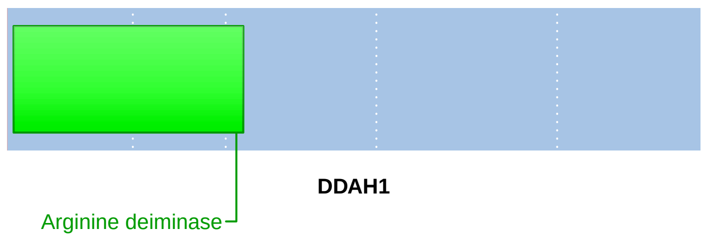
SUPPORTING READ COUNT

Split reads = 43
Discordant mates = 0



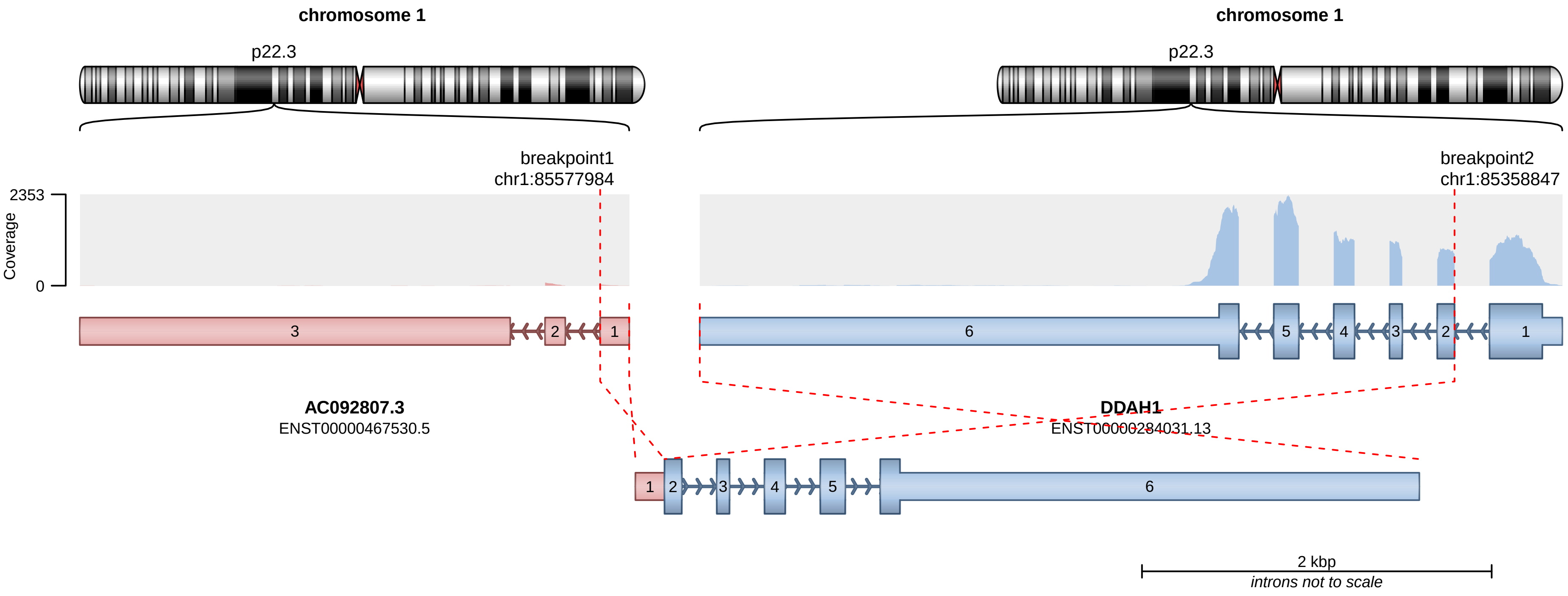


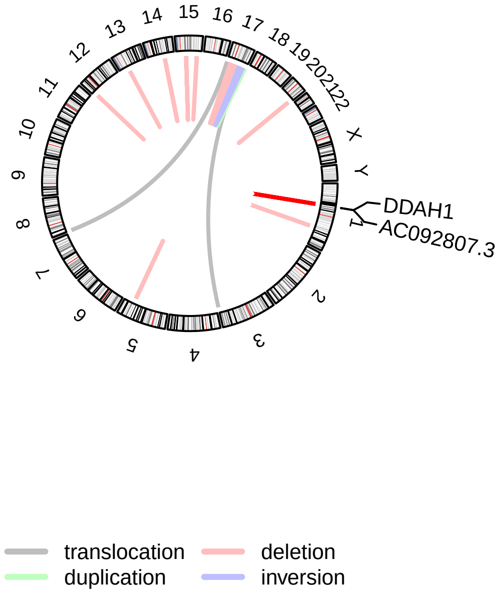
RETAINED PROTEIN DOMAINS
reading frame unclear



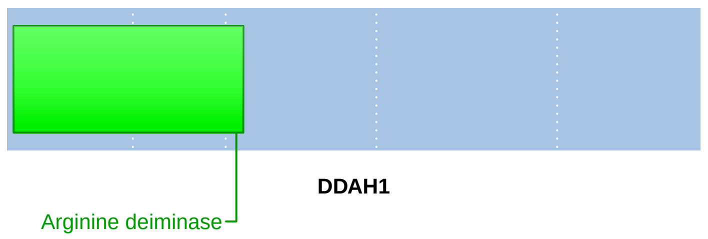
SUPPORTING READ COUNT

Split reads = 31
Discordant mates = 0



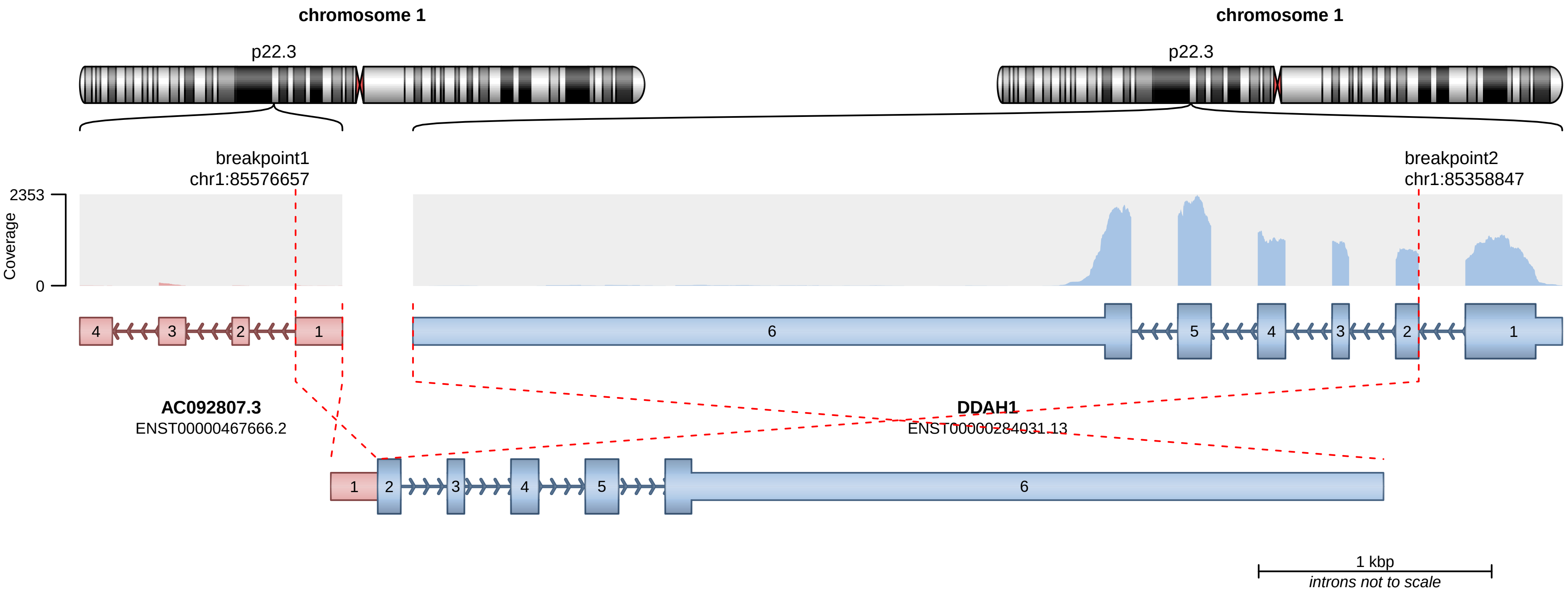


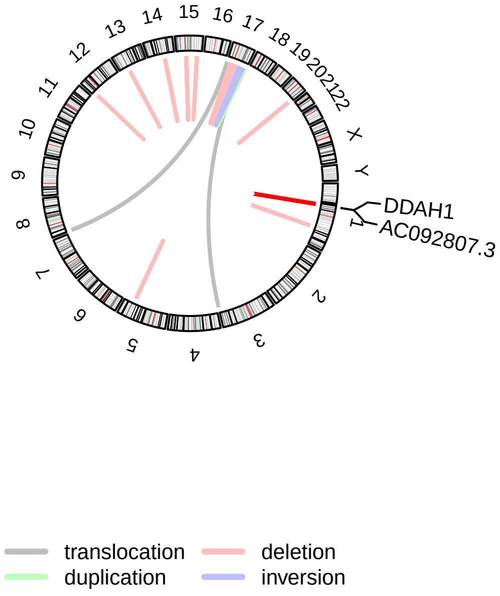
RETAINED PROTEIN DOMAINS
reading frame unclear

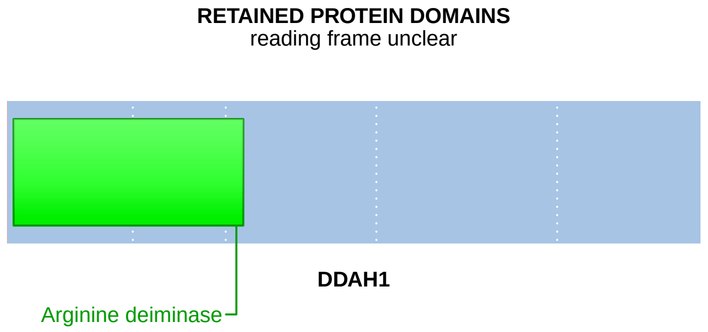


SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 0

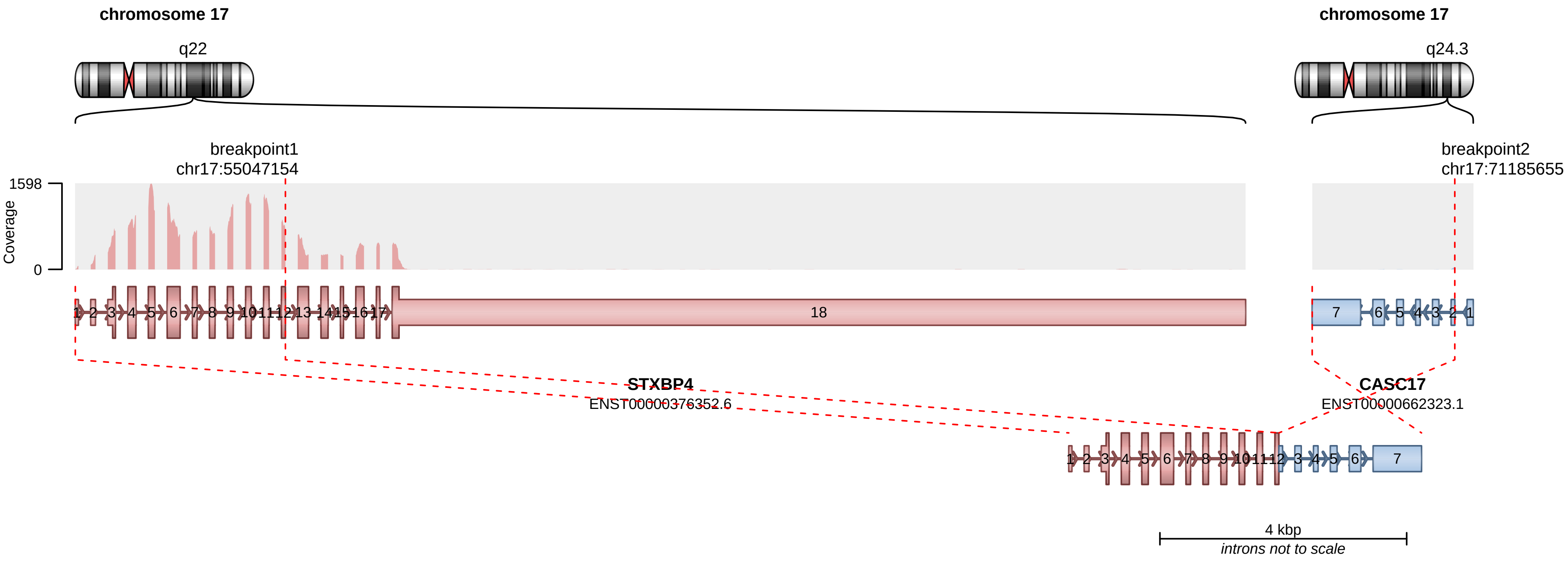


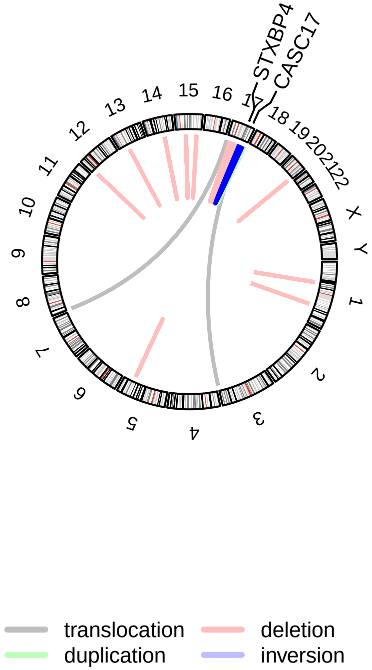




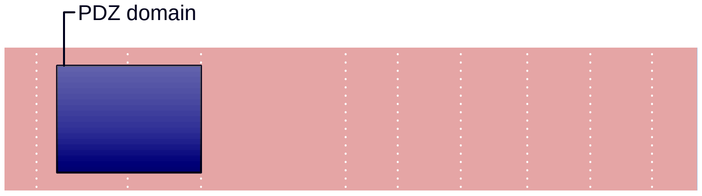
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0





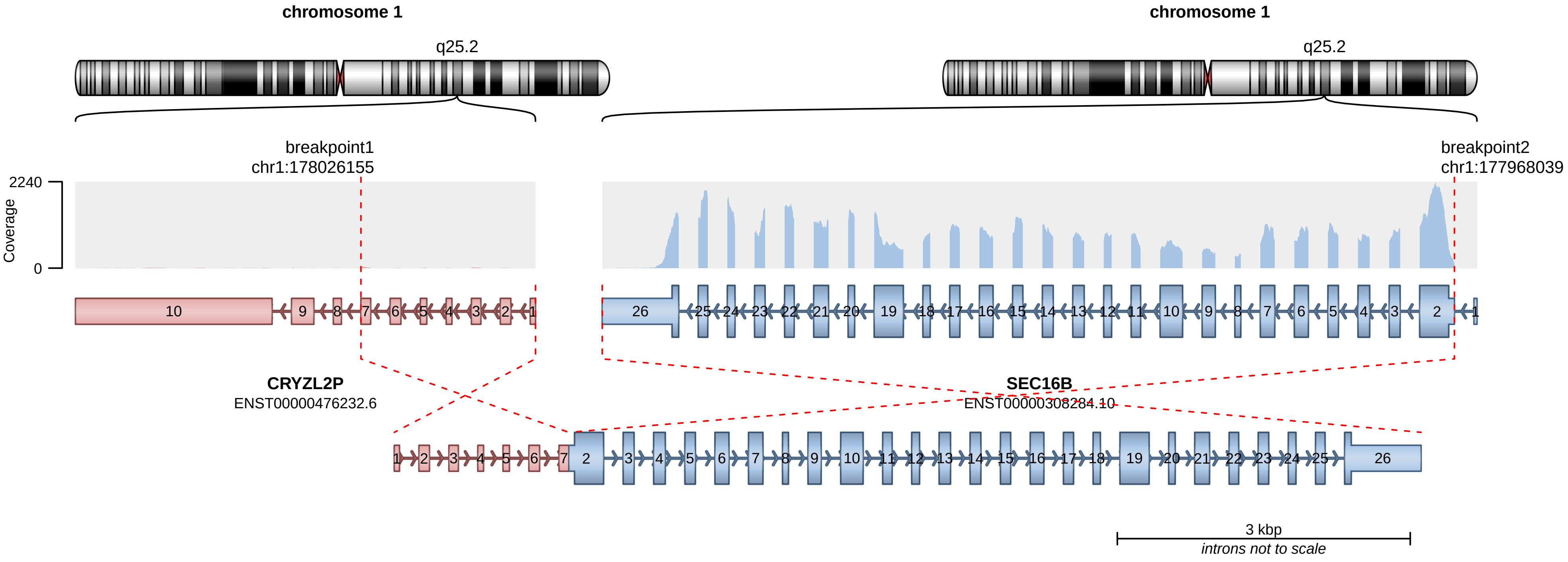
RETAINED PROTEIN DOMAINS
reading frame unclear

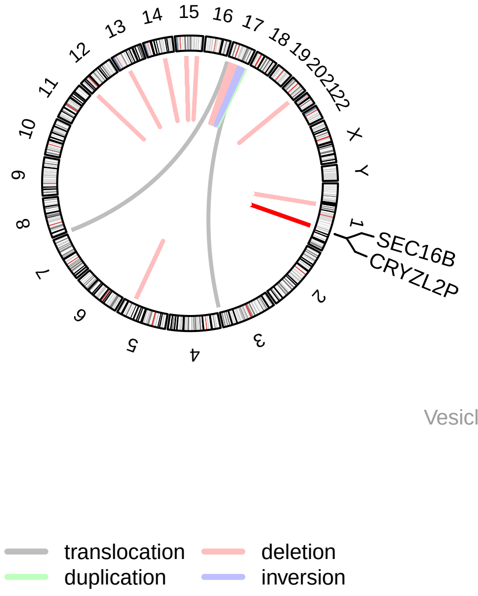


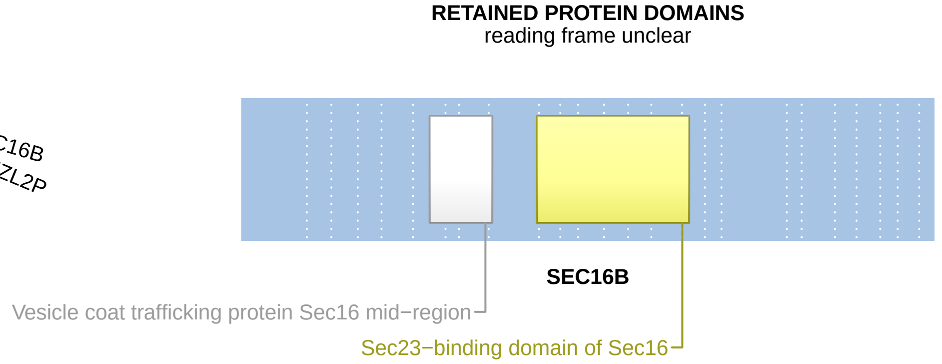
STXBP4

SUPPORTING READ COUNT

Split reads = 26
Discordant mates = 1

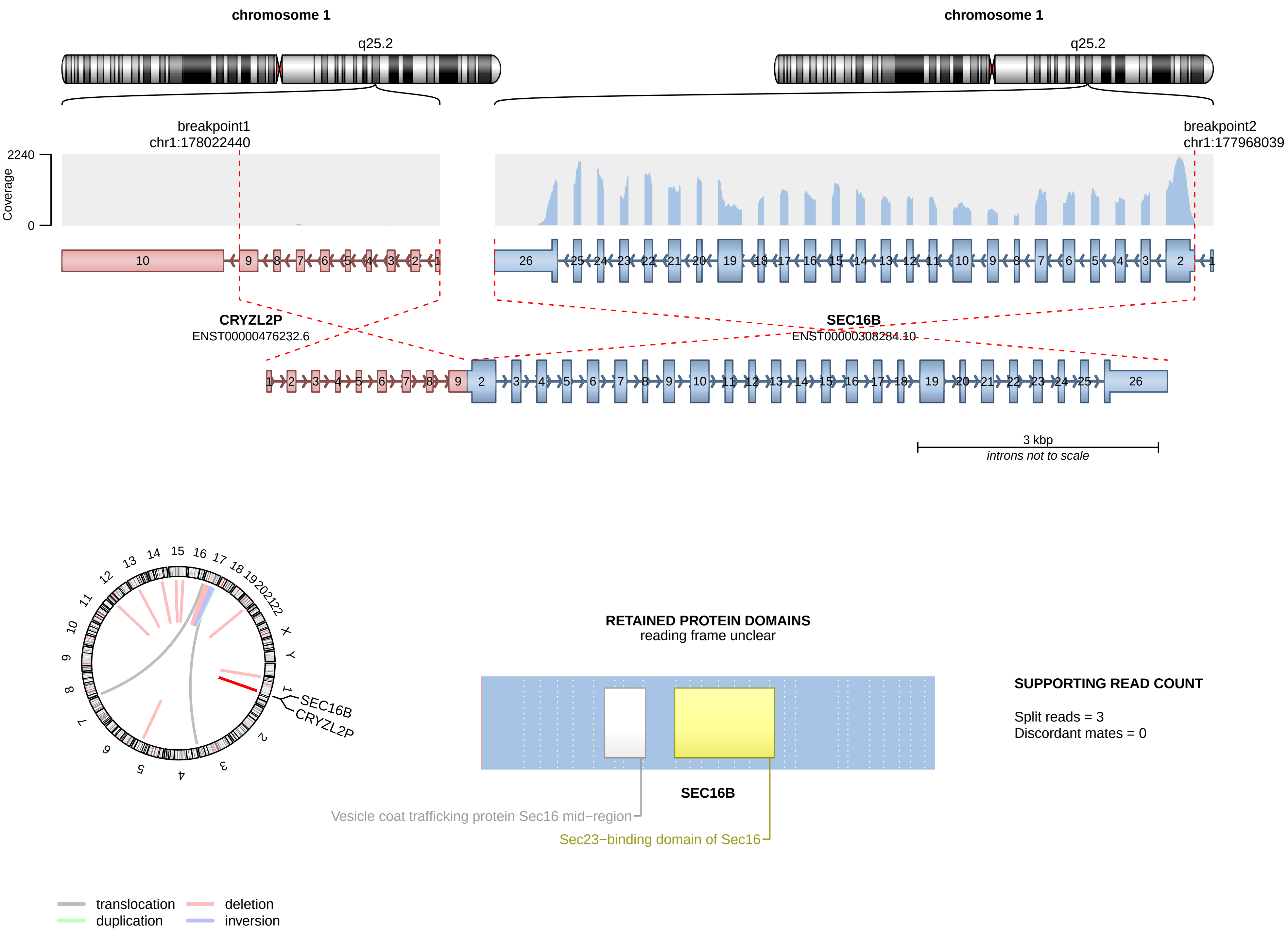






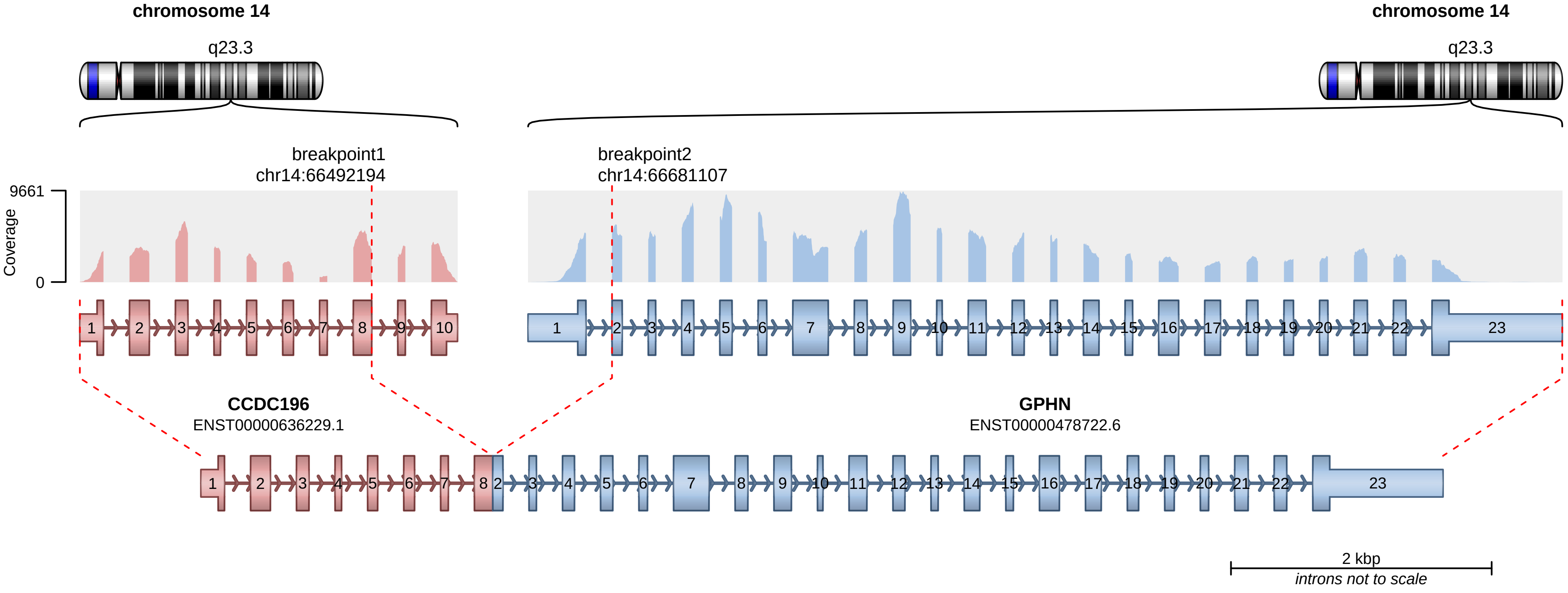
SUPPORTING READ COUNT

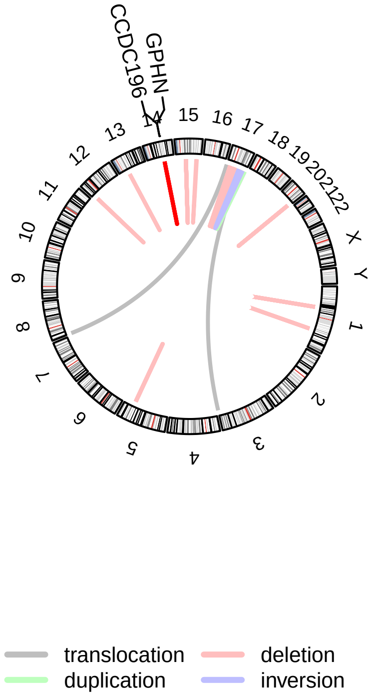
Split reads = 21
Discordant mates = 0



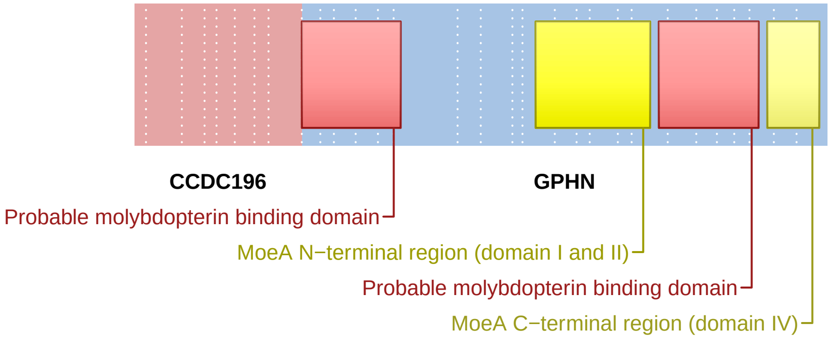
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0



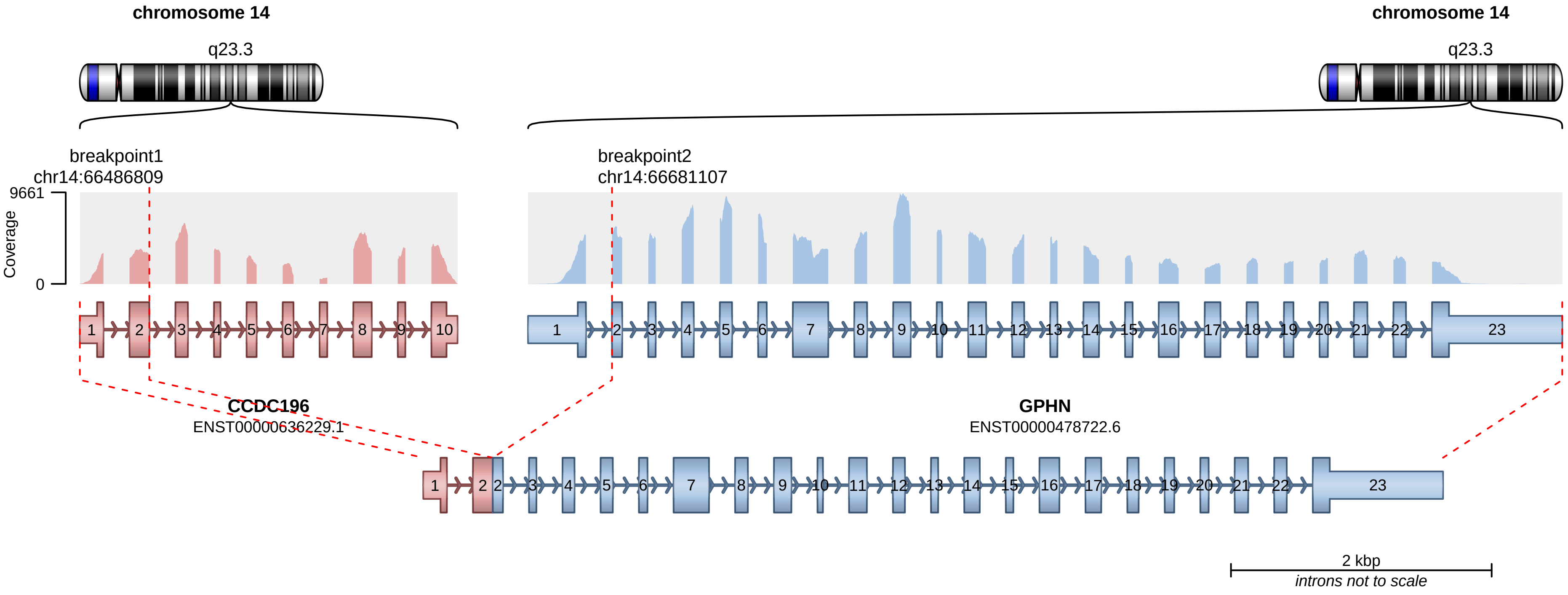


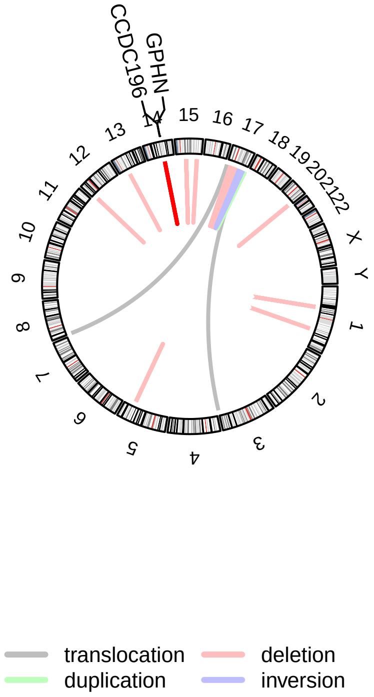
RETAINED PROTEIN DOMAINS
reading frame unclear



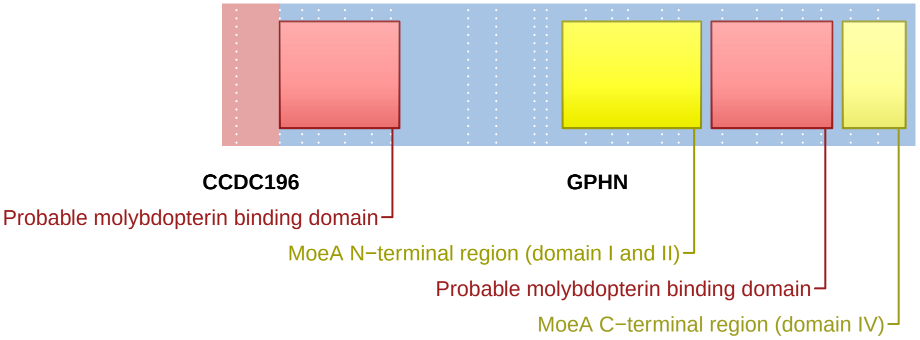
SUPPORTING READ COUNT

Split reads = 14
Discordant mates = 3



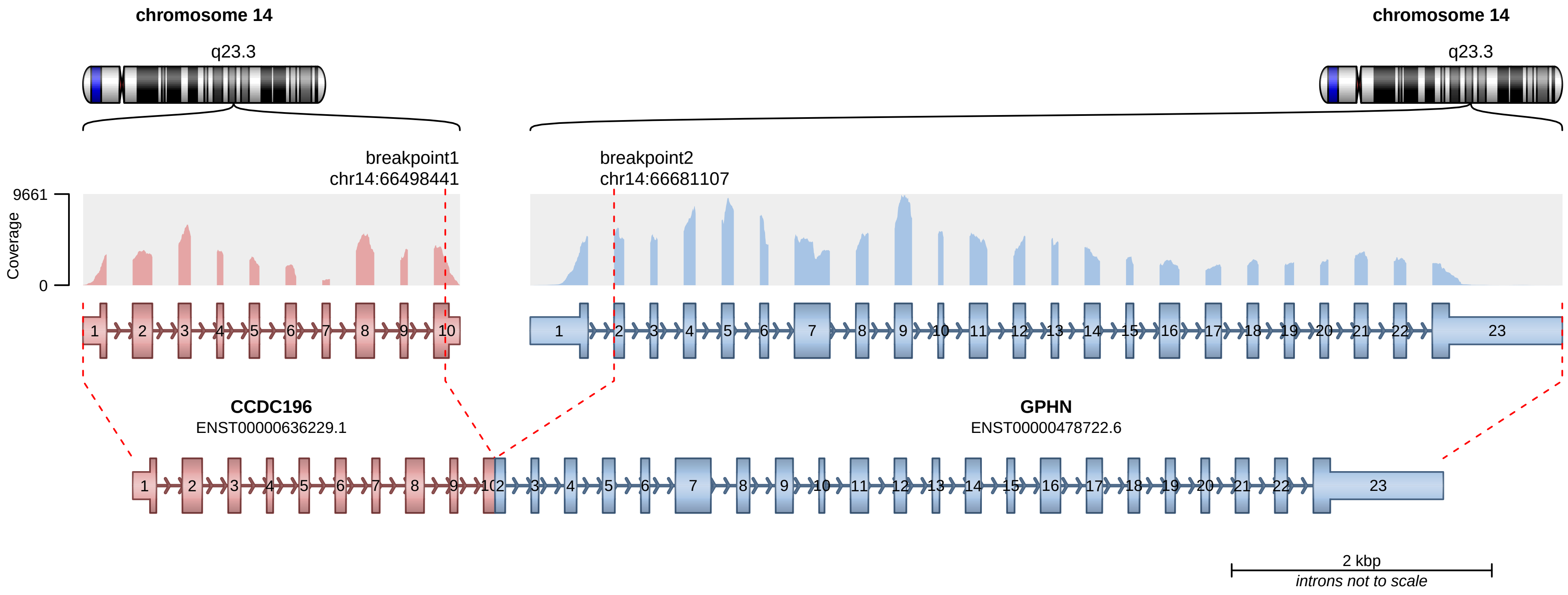


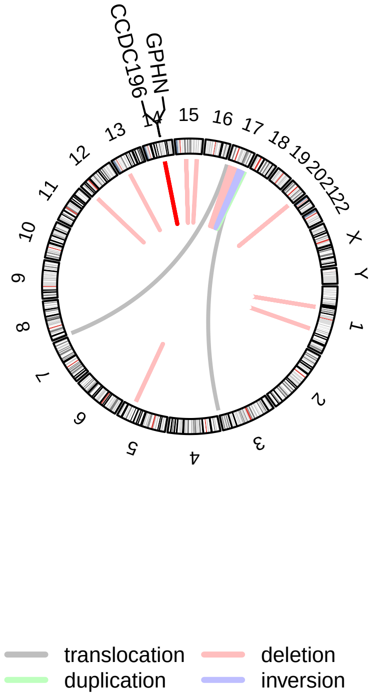
RETAINED PROTEIN DOMAINS
reading frame unclear

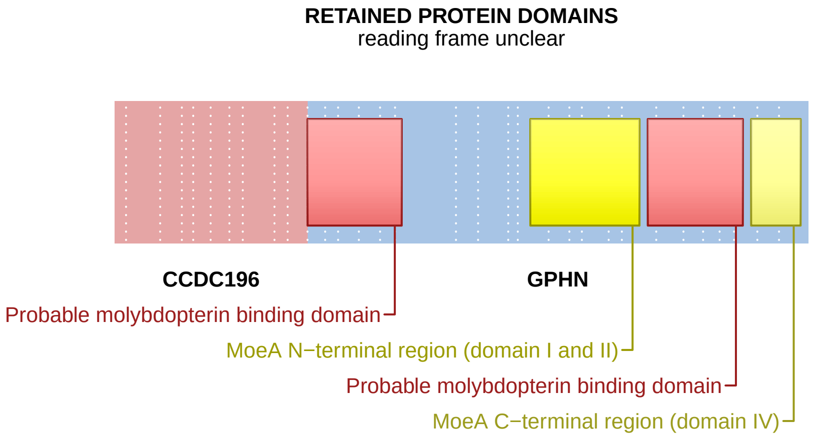


SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 0

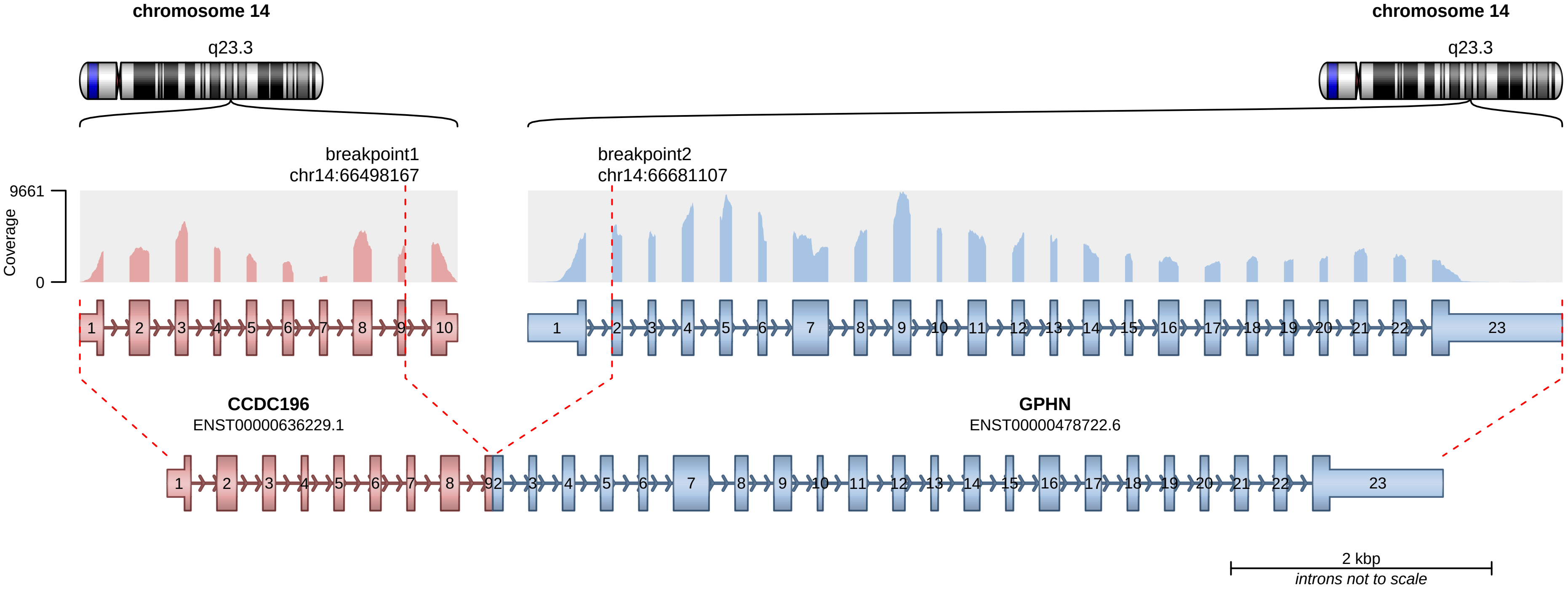


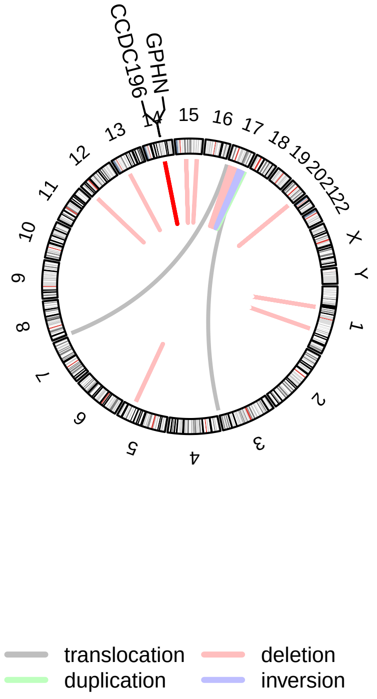




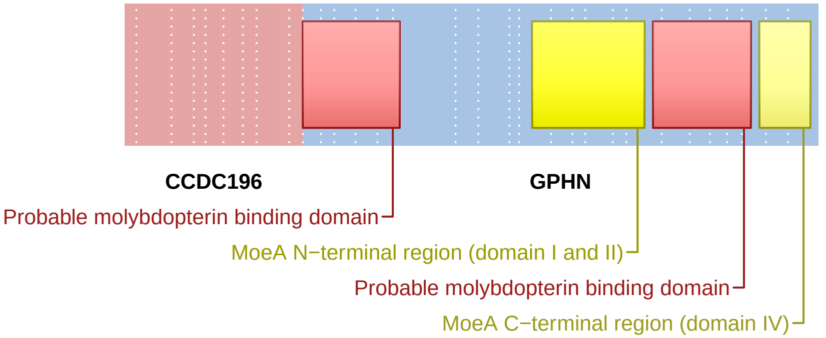
SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 3



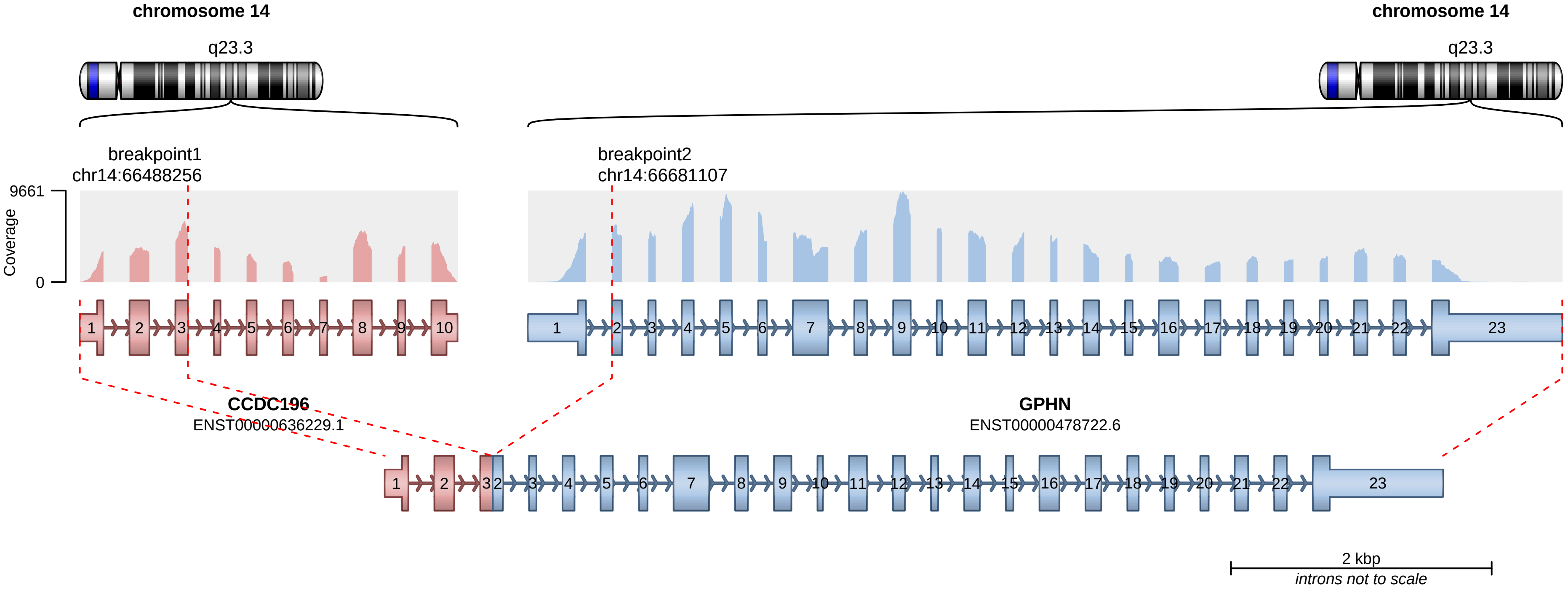


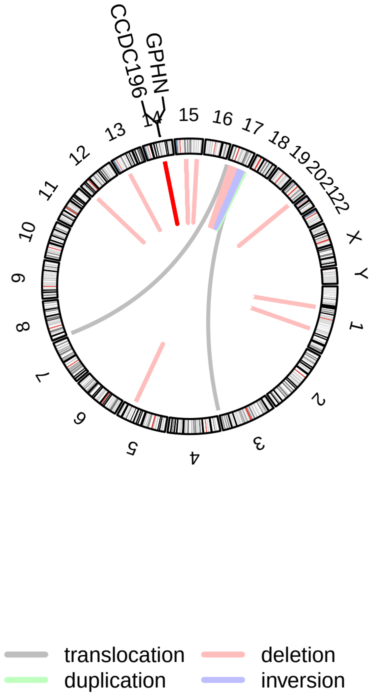
RETAINED PROTEIN DOMAINS
reading frame unclear

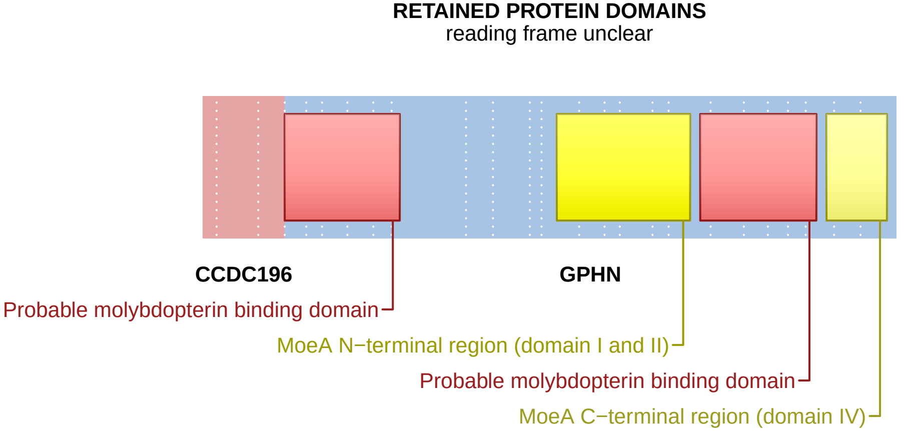


SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 3

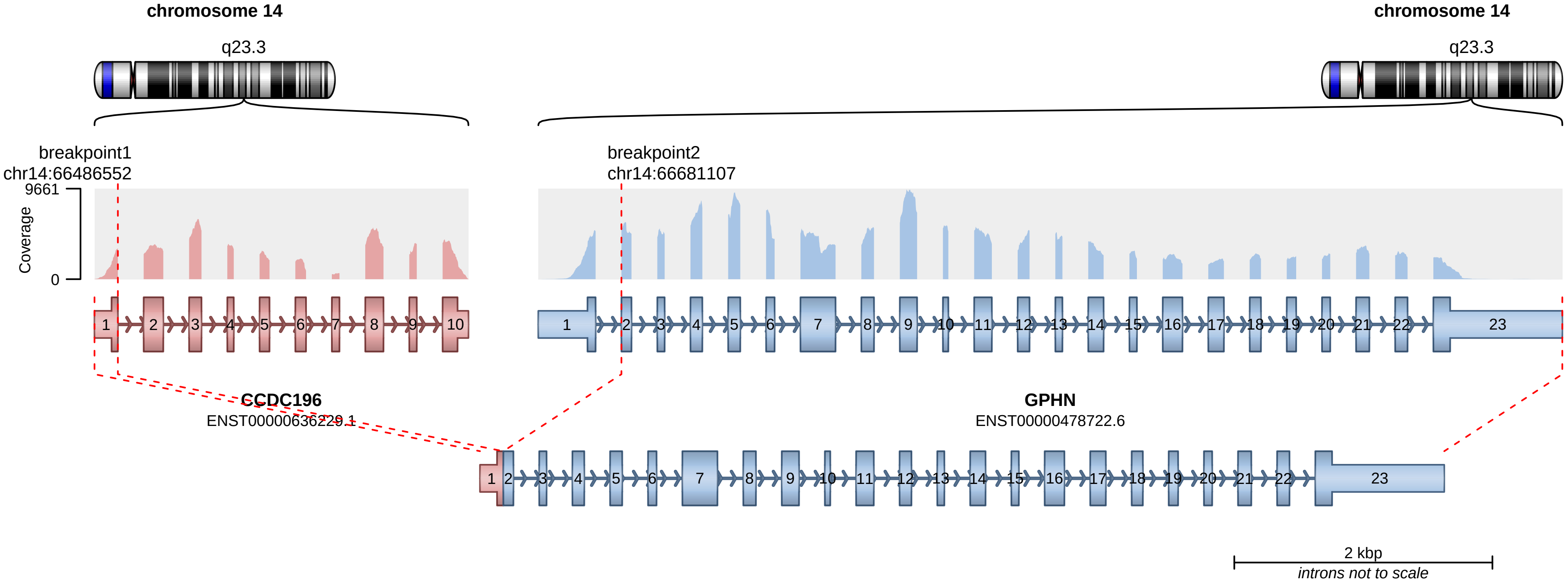


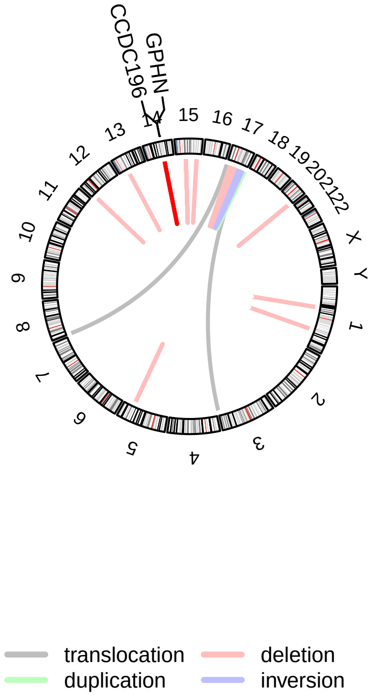


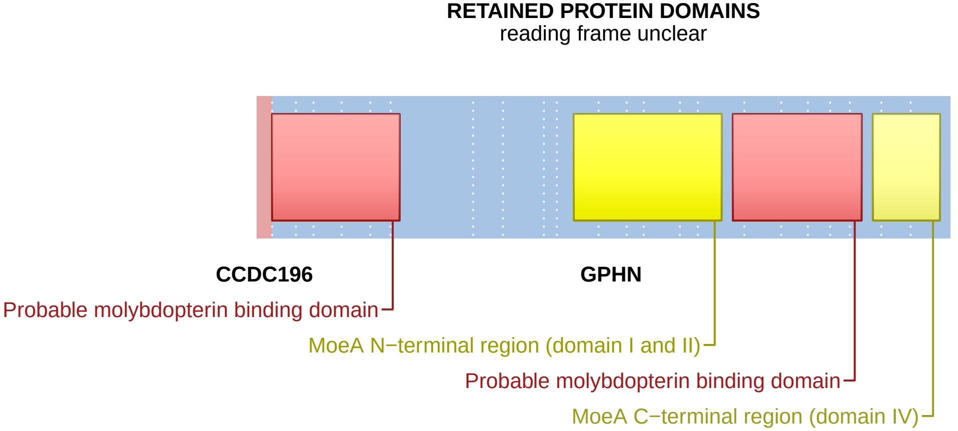


SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 2

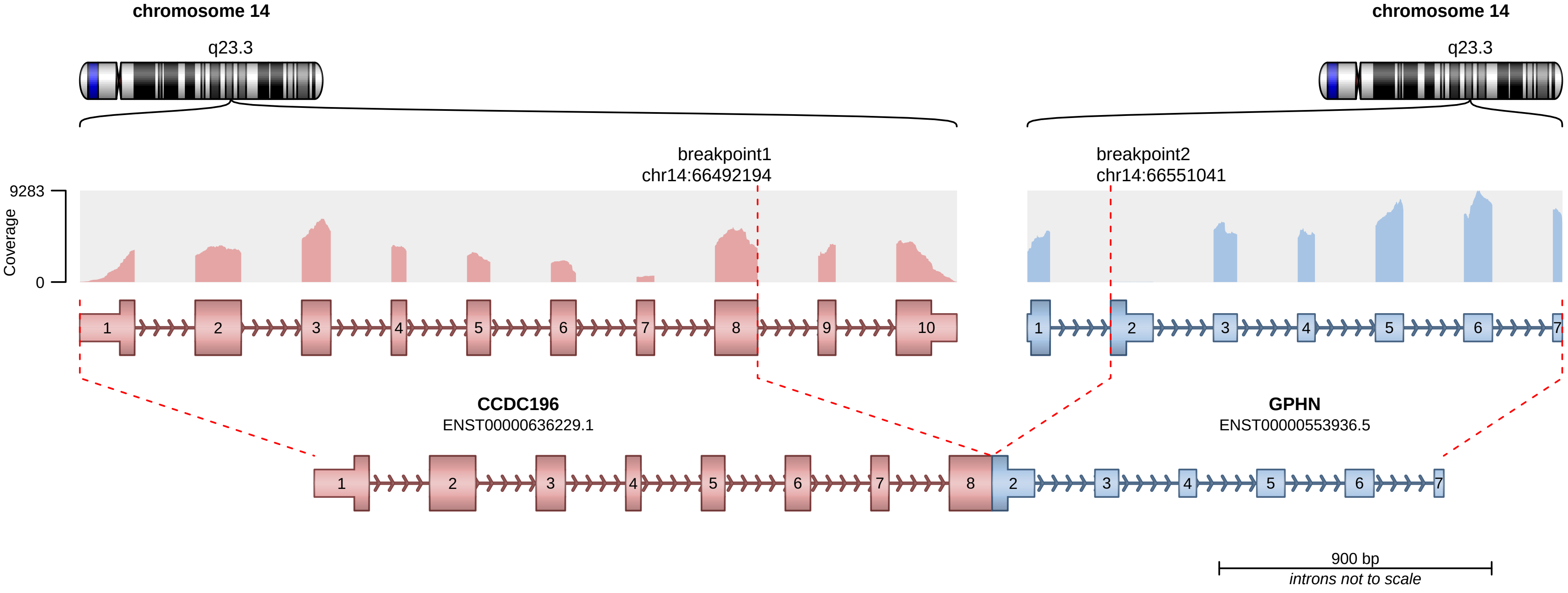


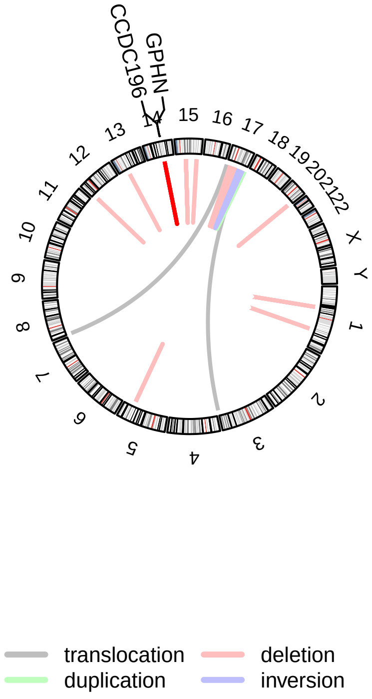




SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

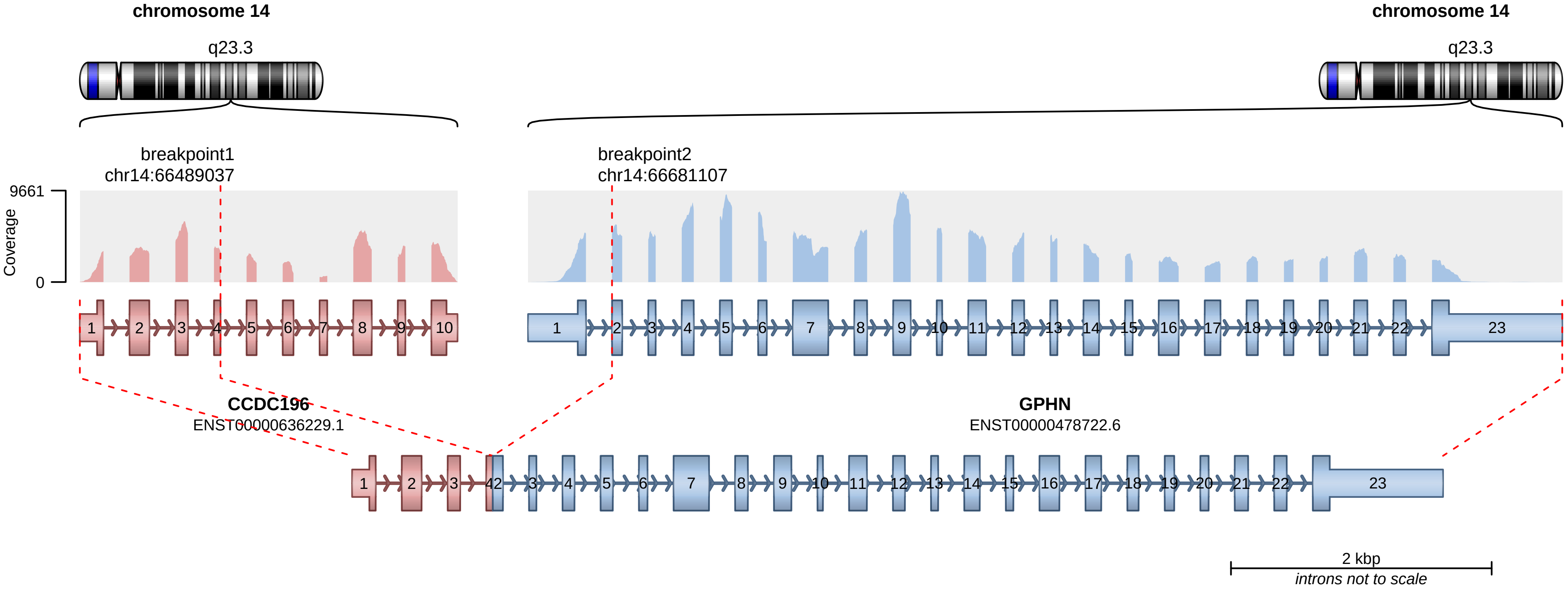


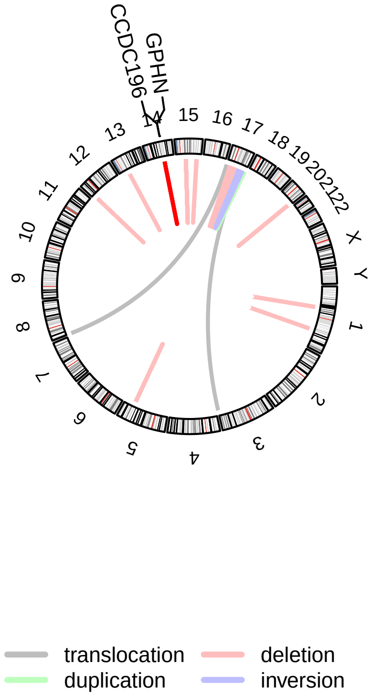


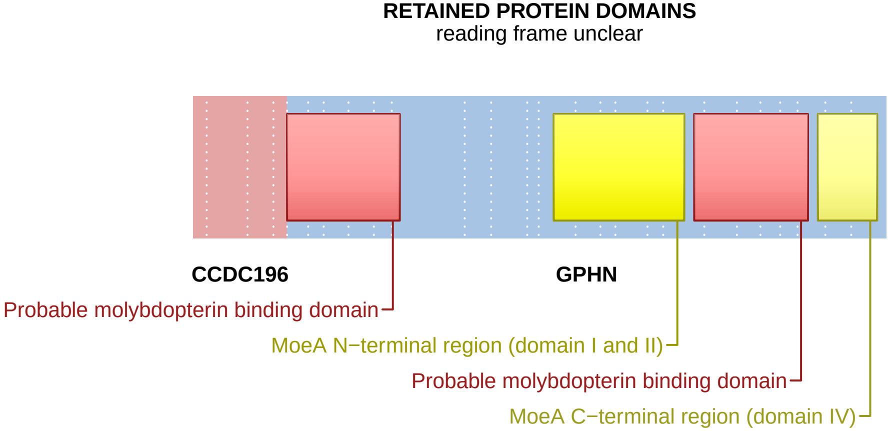
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 3

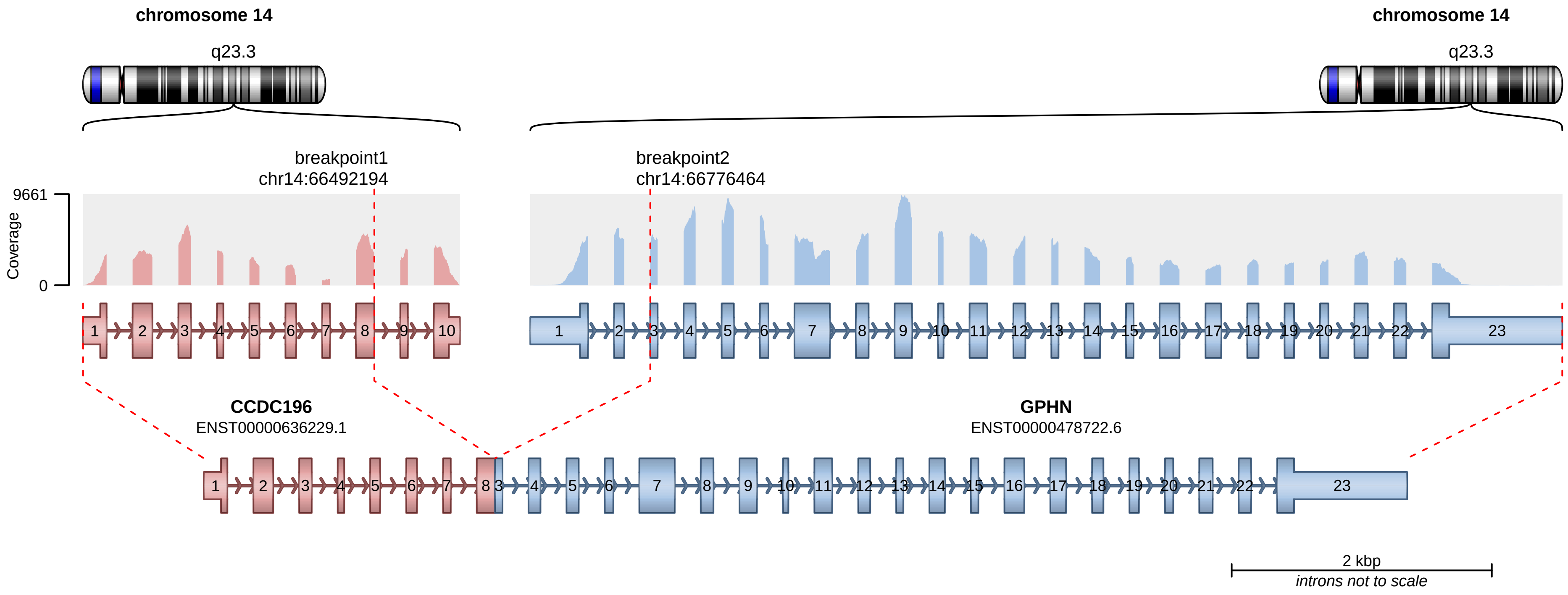


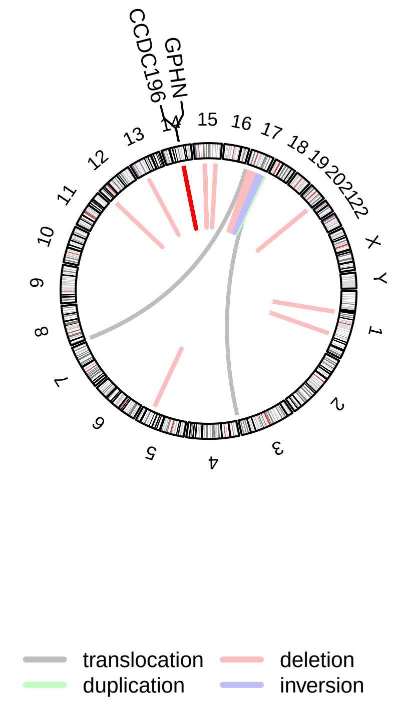


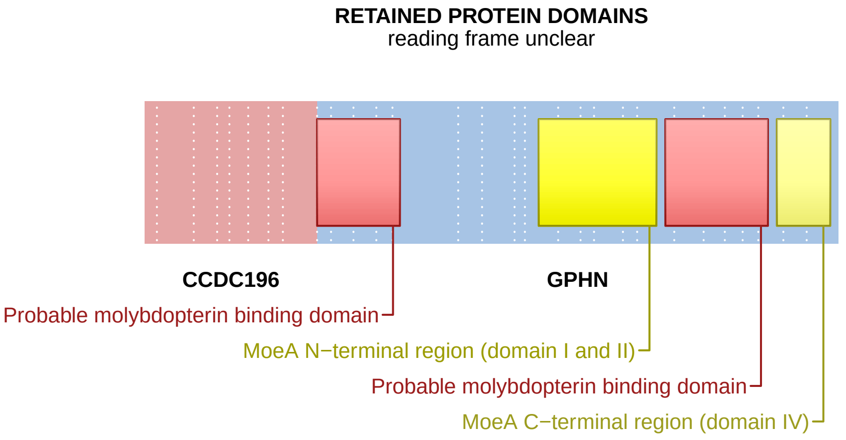


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 2

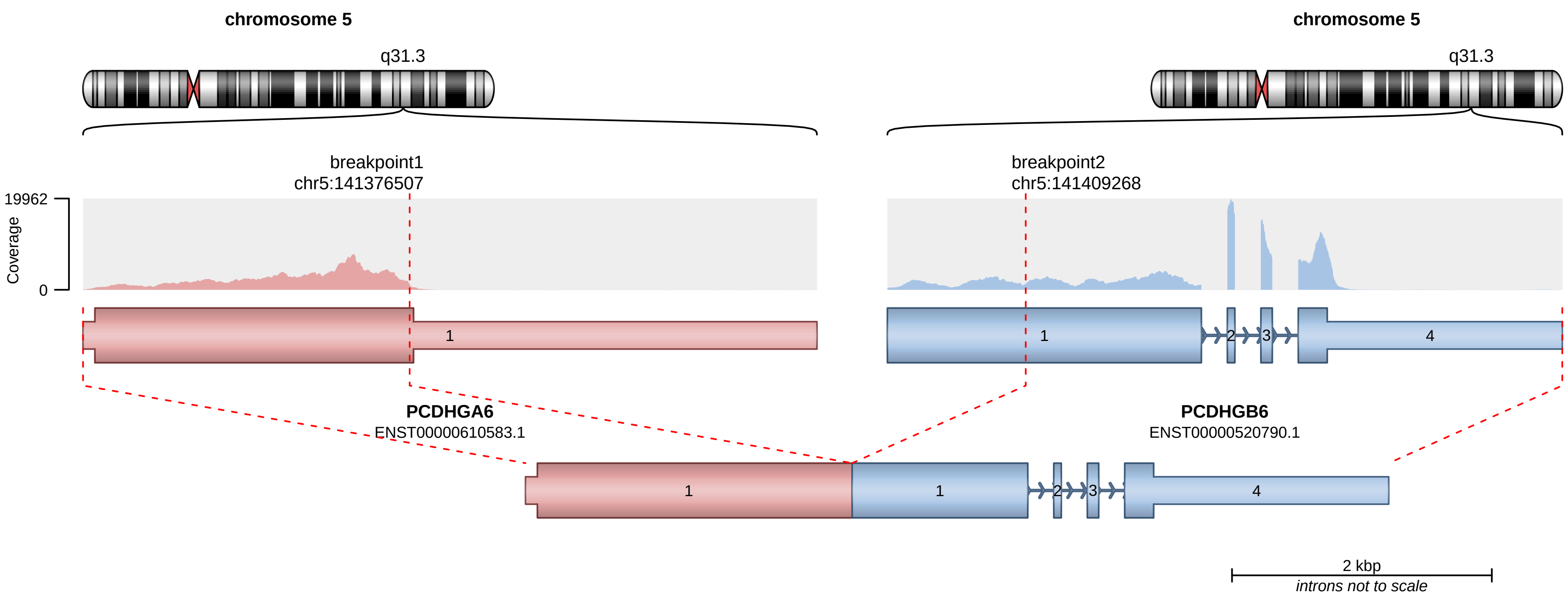


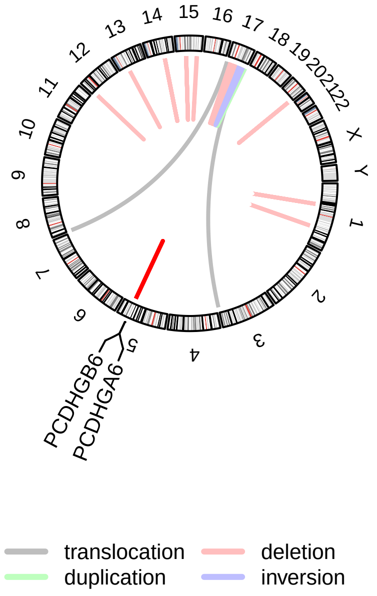




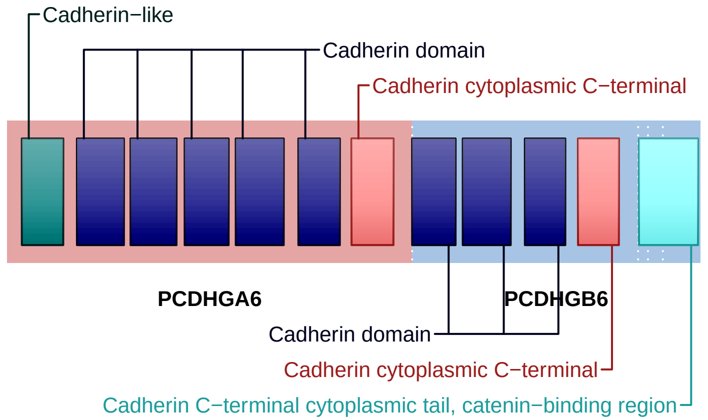
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0





RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 2