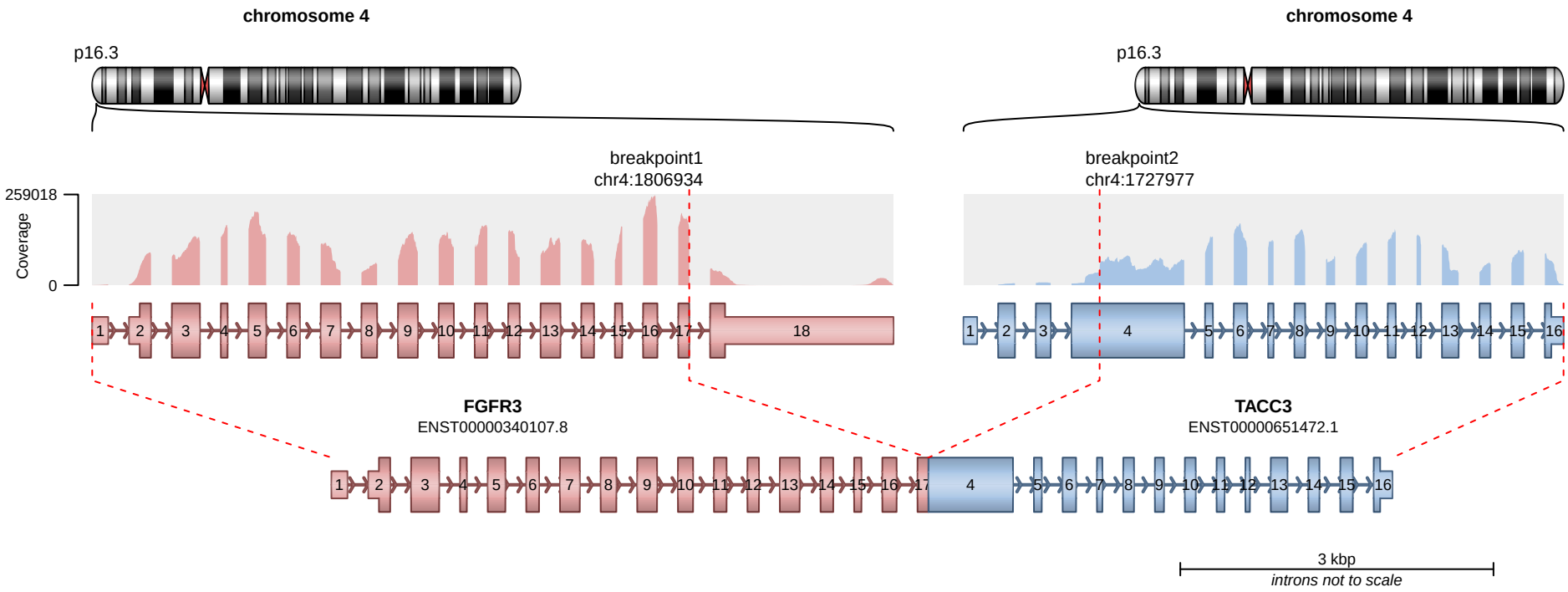
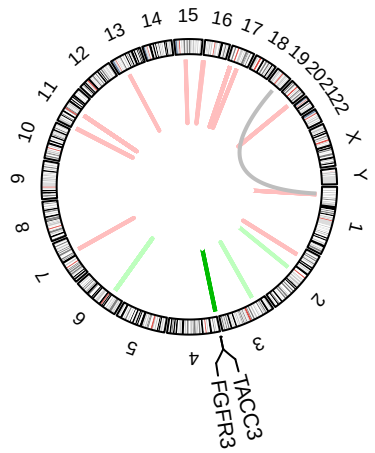
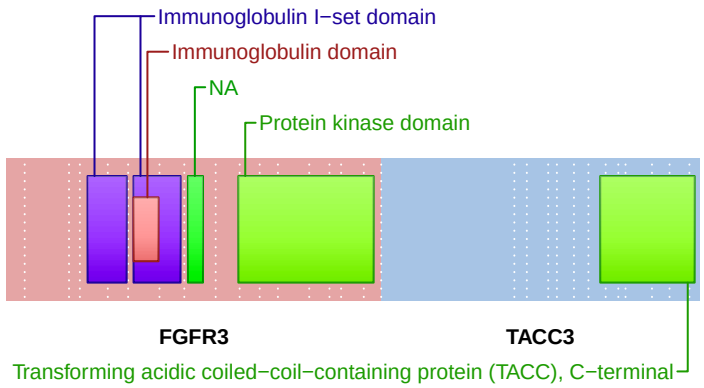




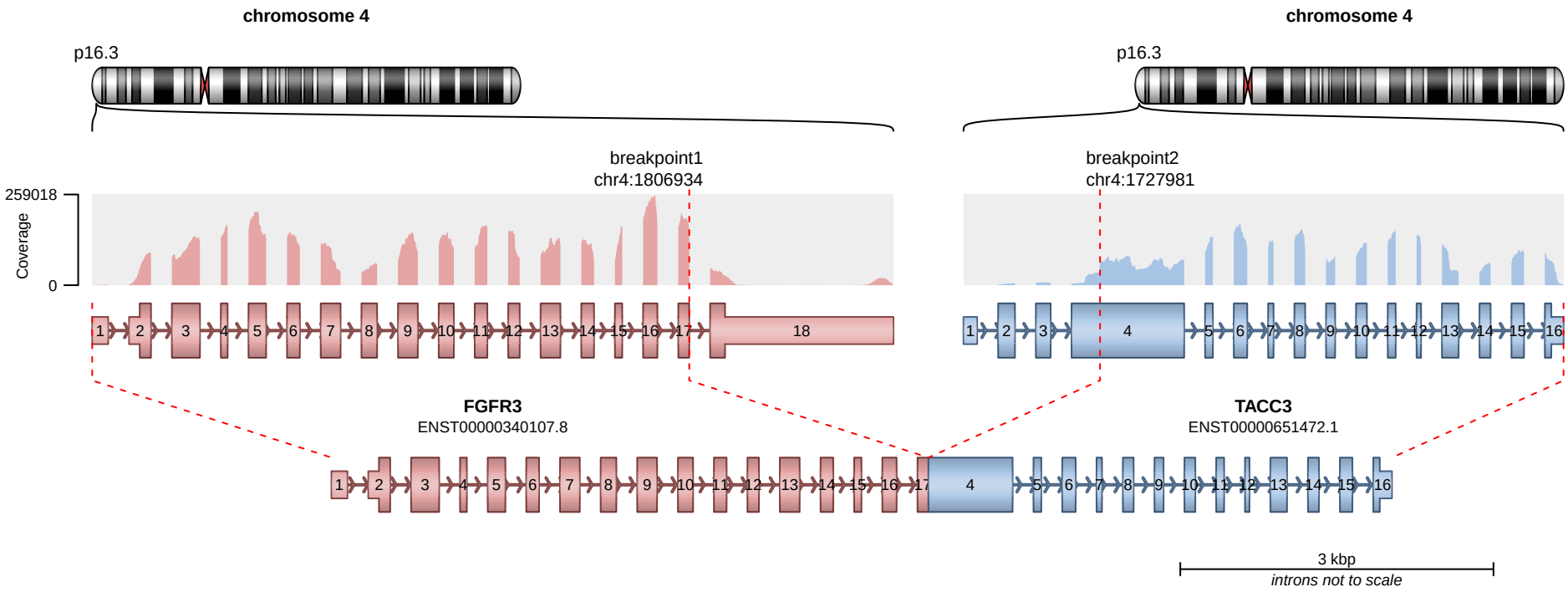
translocation
deletion
duplication
inversion

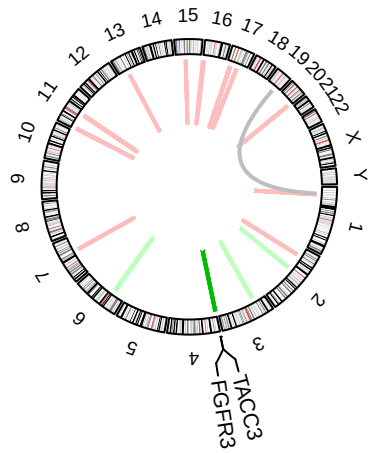
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

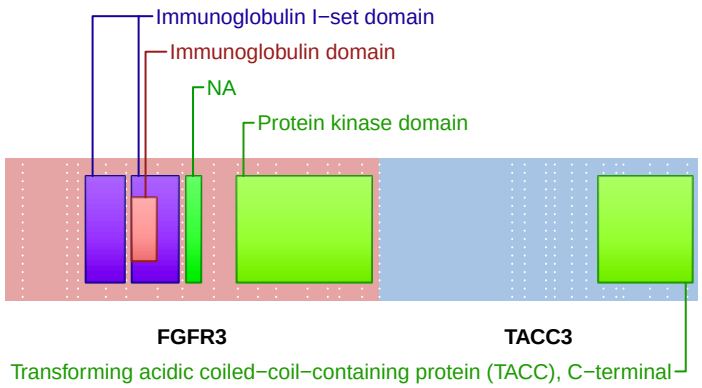
Split reads = 10715
Discordant mates = 59





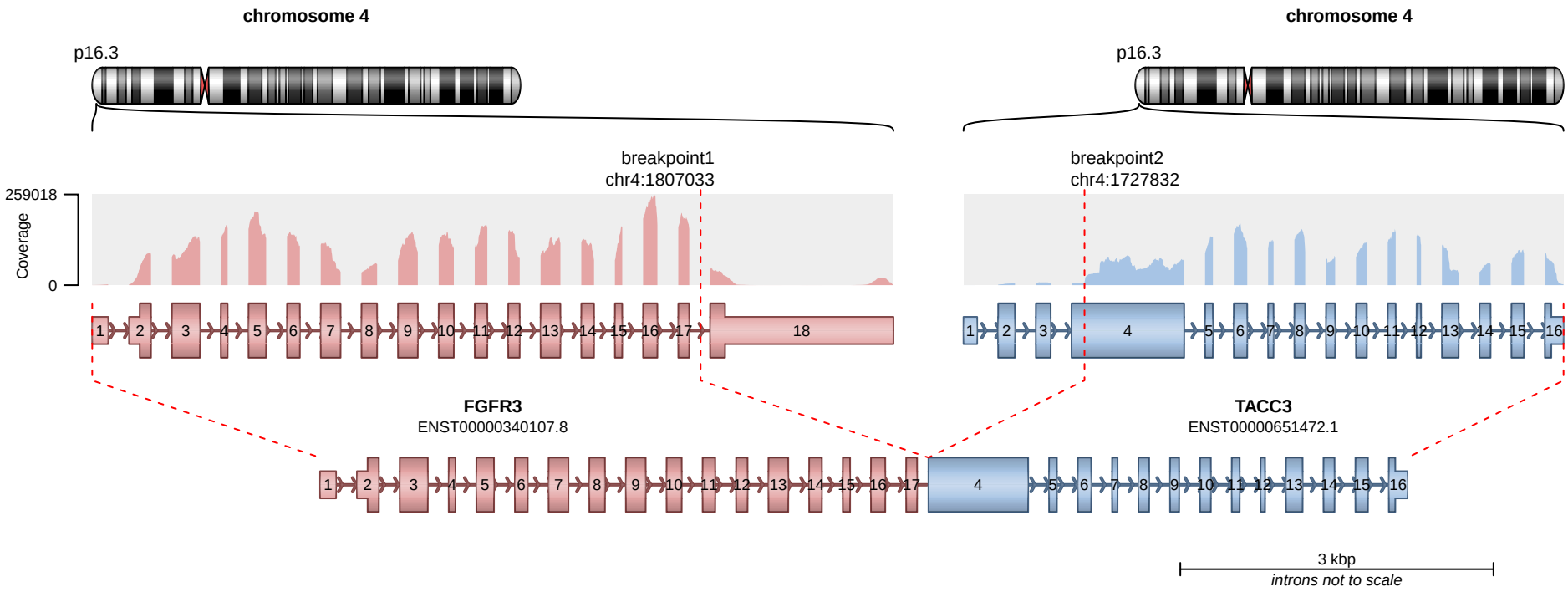
translocation
deletion
duplication
inversion

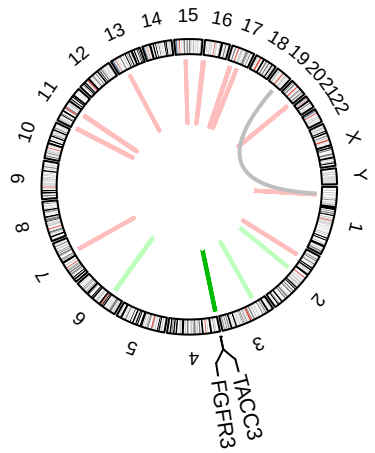
RETAINED PROTEIN DOMAINS
reading frame unclear

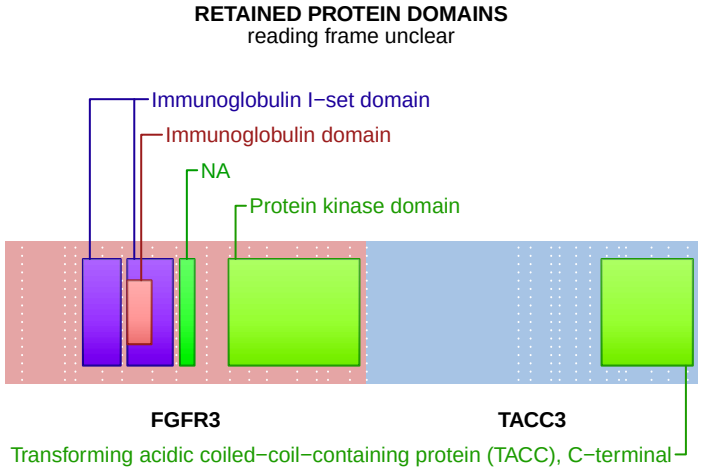


SUPPORTING READ COUNT

Split reads = 2862
Discordant mates = 59



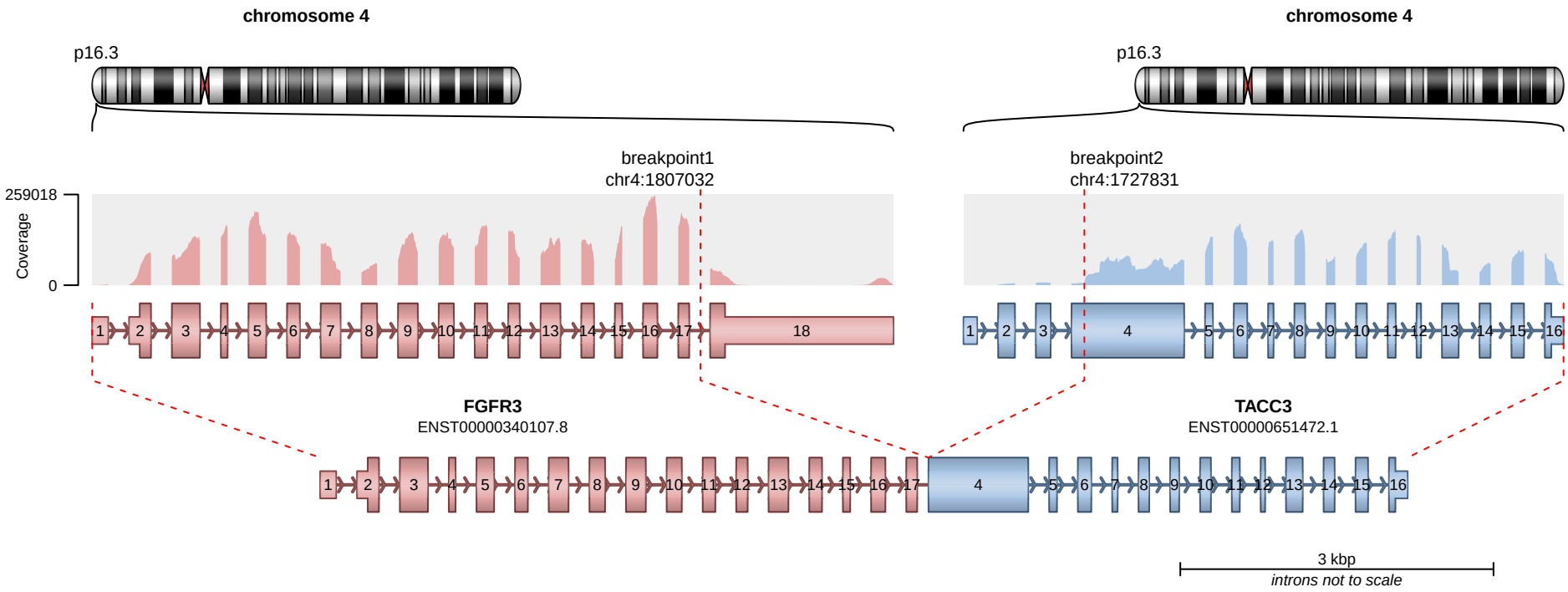


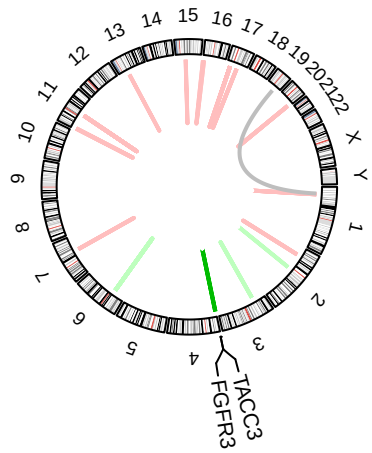


SUPPORTING READ COUNT

Split reads = 749
Discordant mates = 349

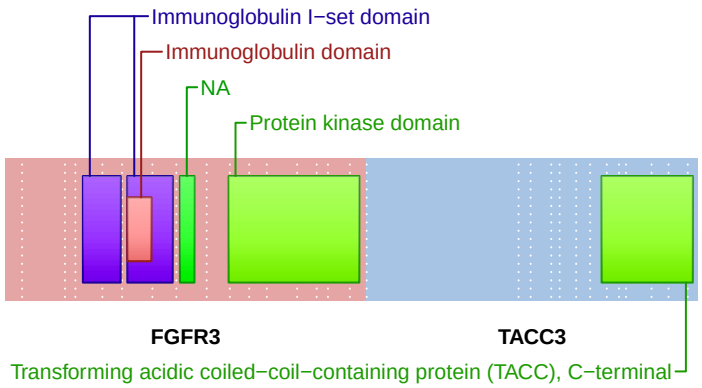
translocation
deletion
duplication
inversion





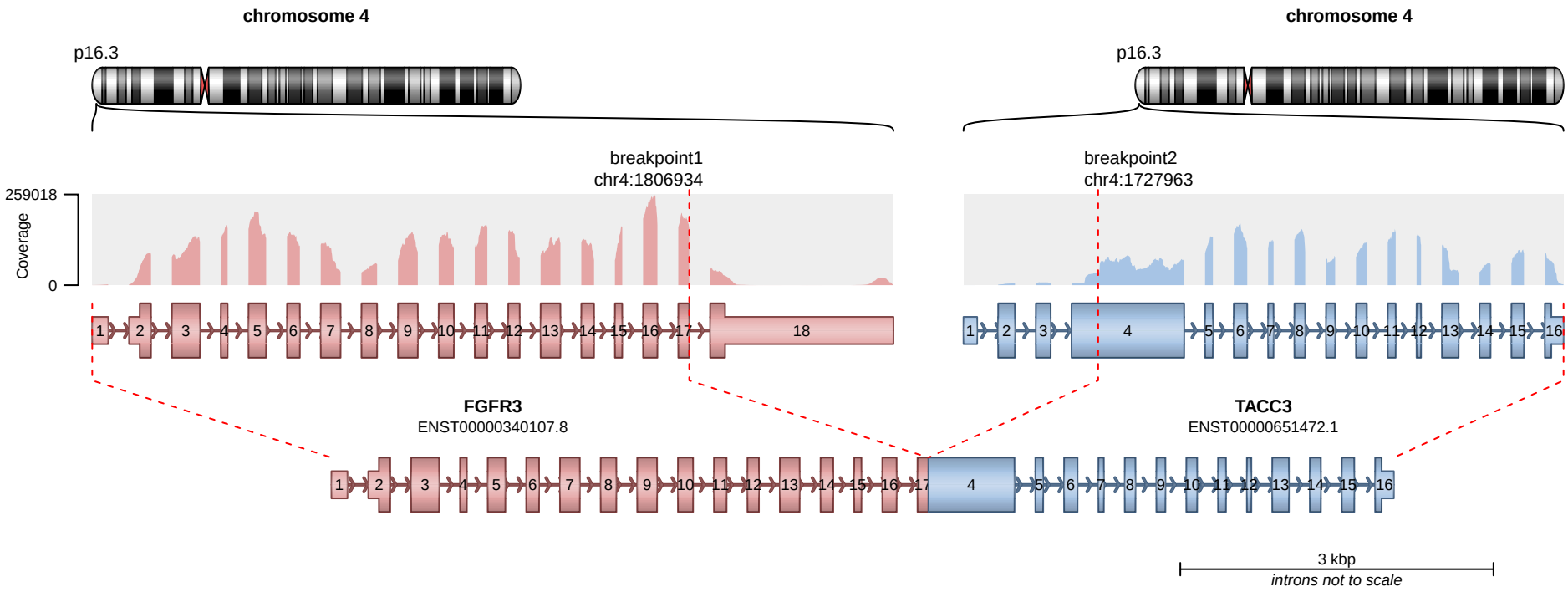
translocation
deletion
duplication
inversion

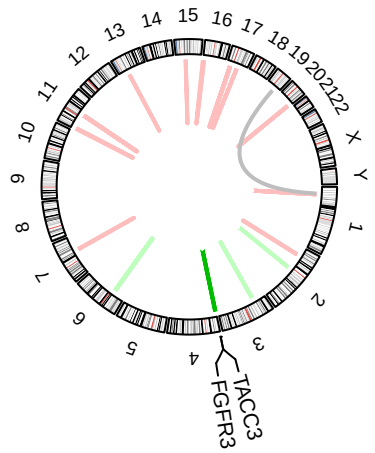
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

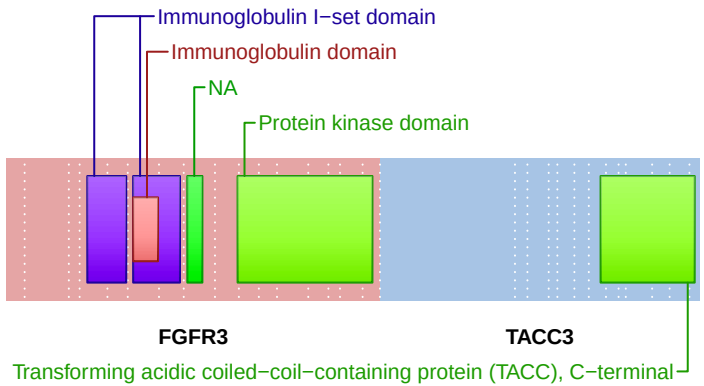
Split reads = 3
Discordant mates = 308





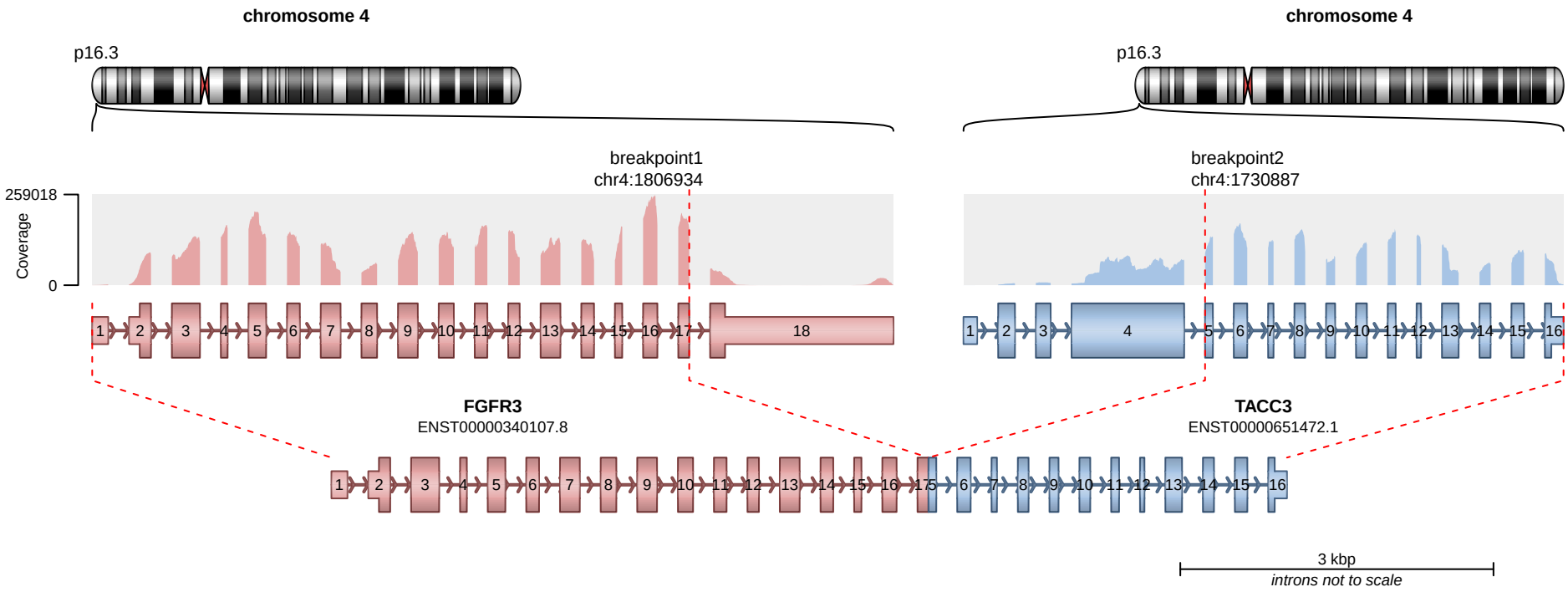
translocation
deletion
duplication
inversion

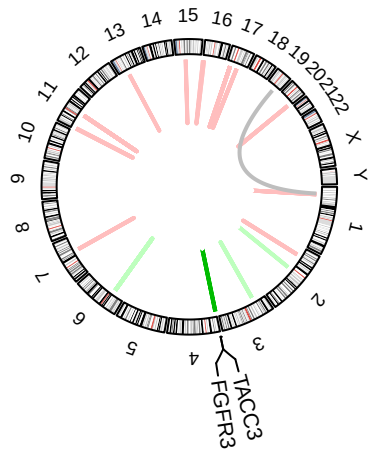
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

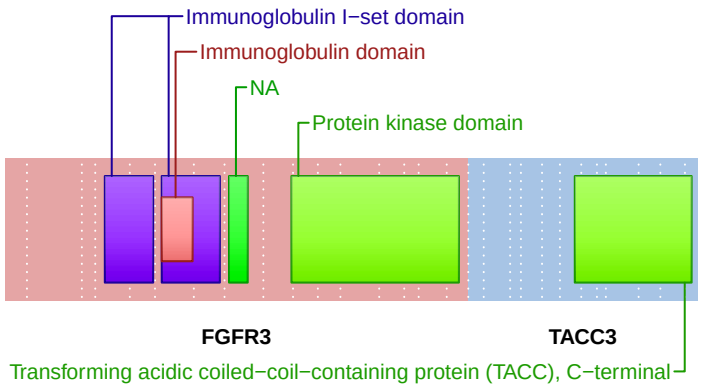
Split reads = 45
Discordant mates = 59





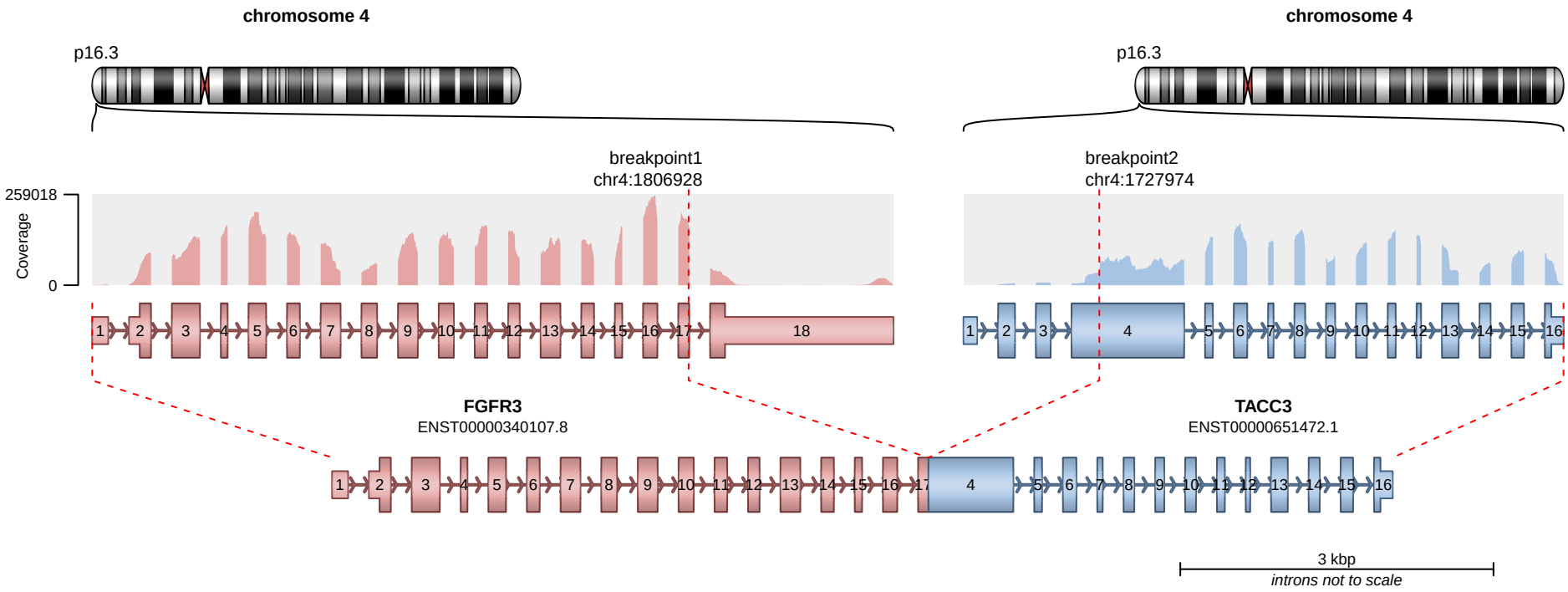
translocation
deletion
duplication
inversion

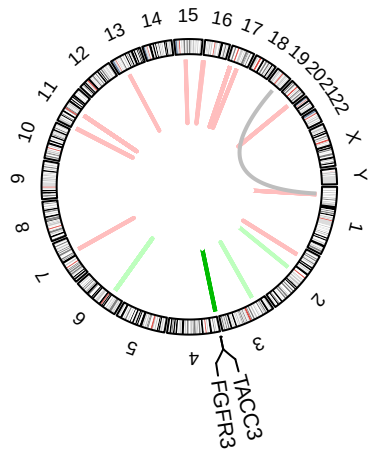
RETAINED PROTEIN DOMAINS
reading frame unclear

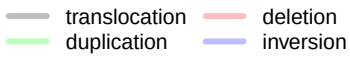


SUPPORTING READ COUNT

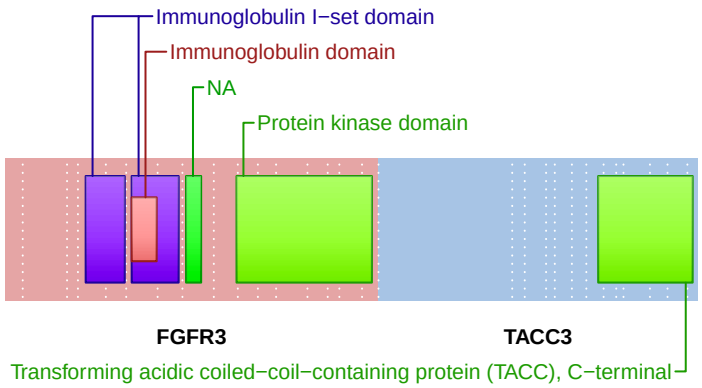
Split reads = 43
Discordant mates = 1





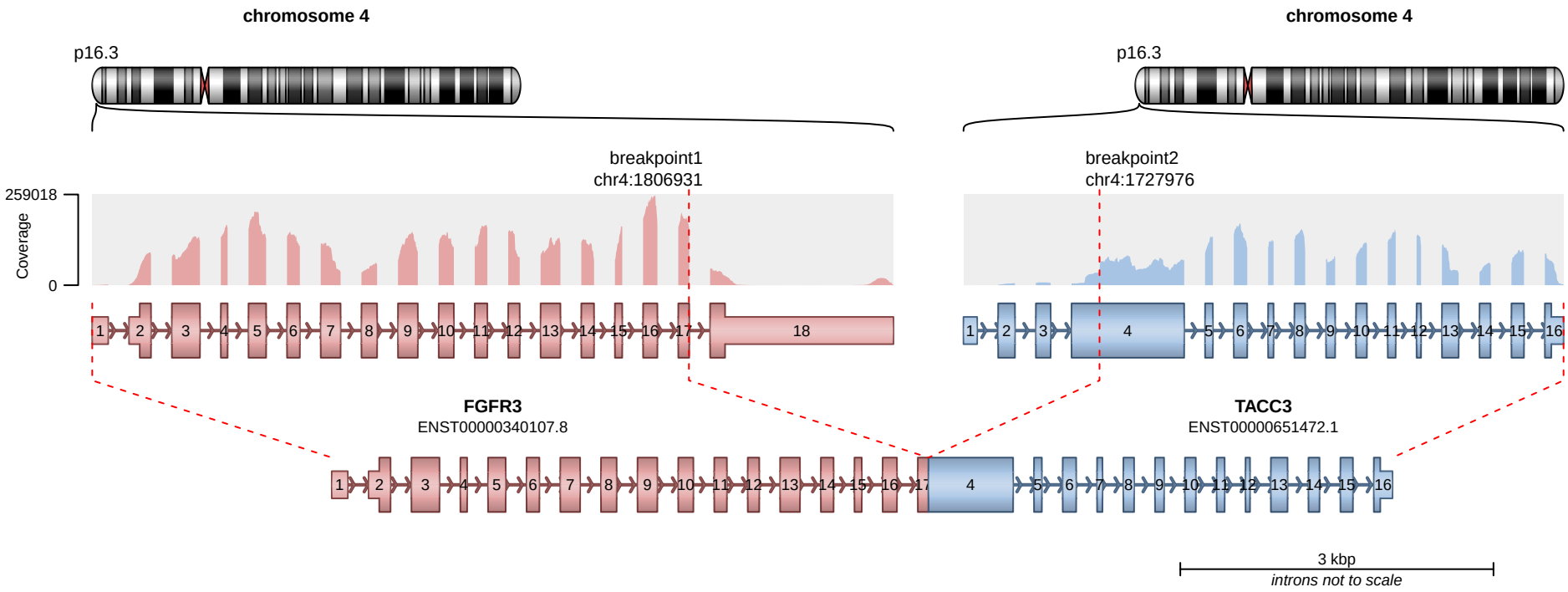


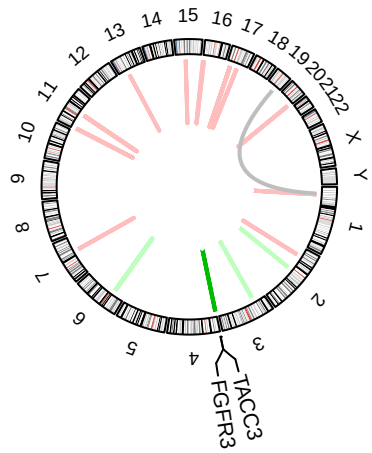
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

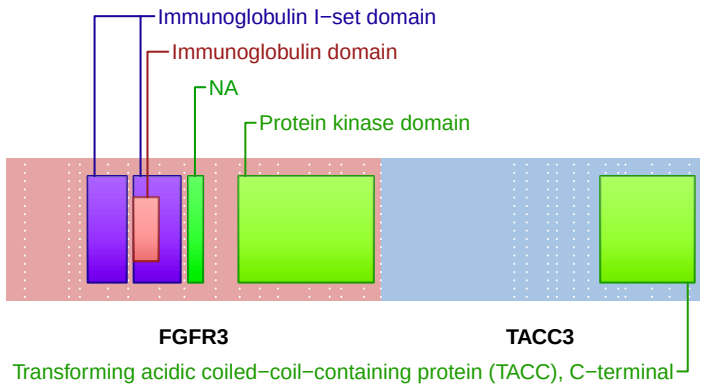
Split reads = 8
Discordant mates = 45





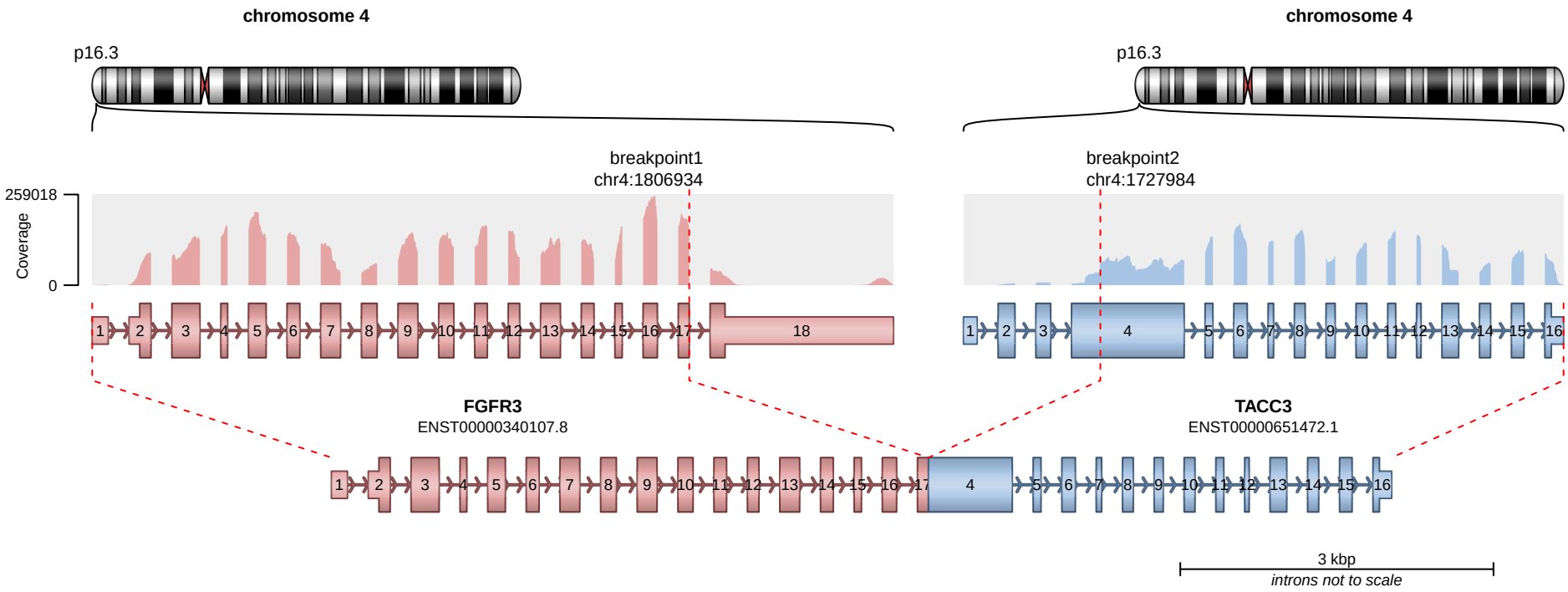
translocation
deletion
duplication
inversion

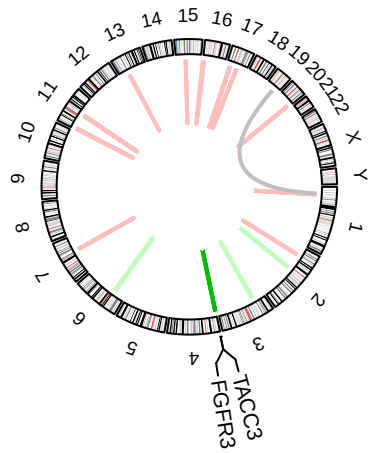
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

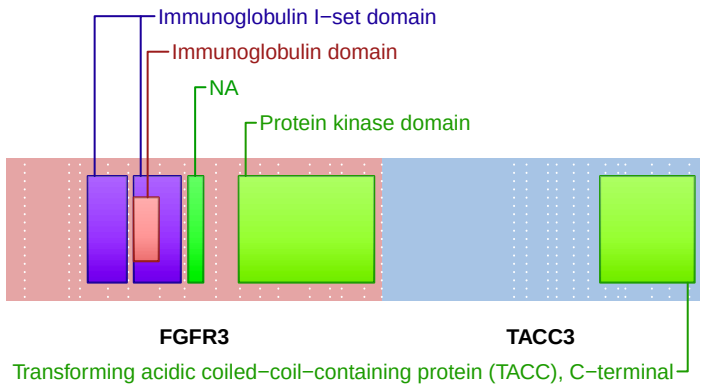
Split reads = 3
Discordant mates = 59





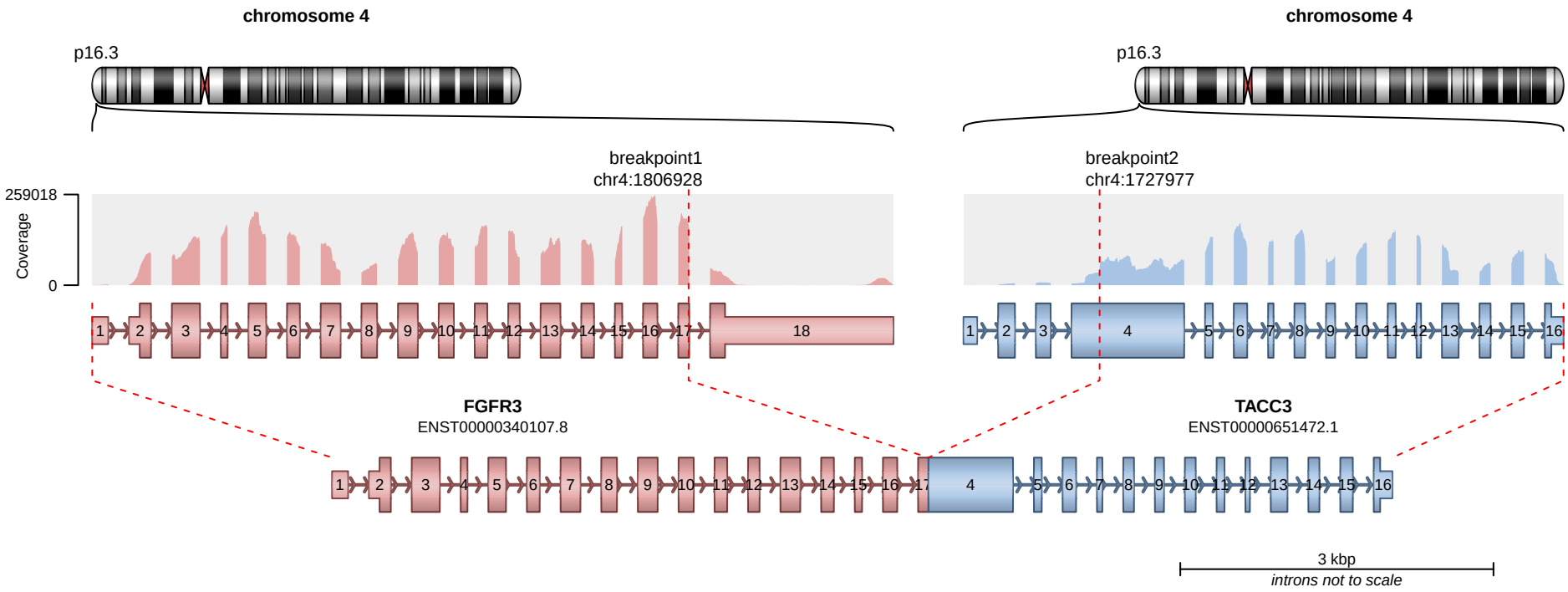
translocation
deletion
duplication
inversion

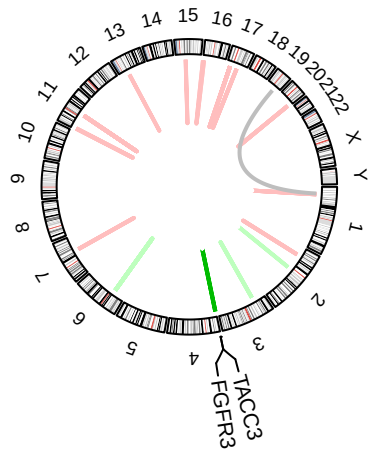
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

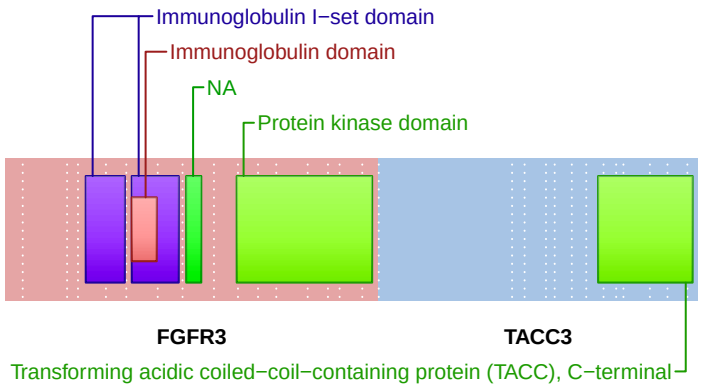
Split reads = 3
Discordant mates = 56





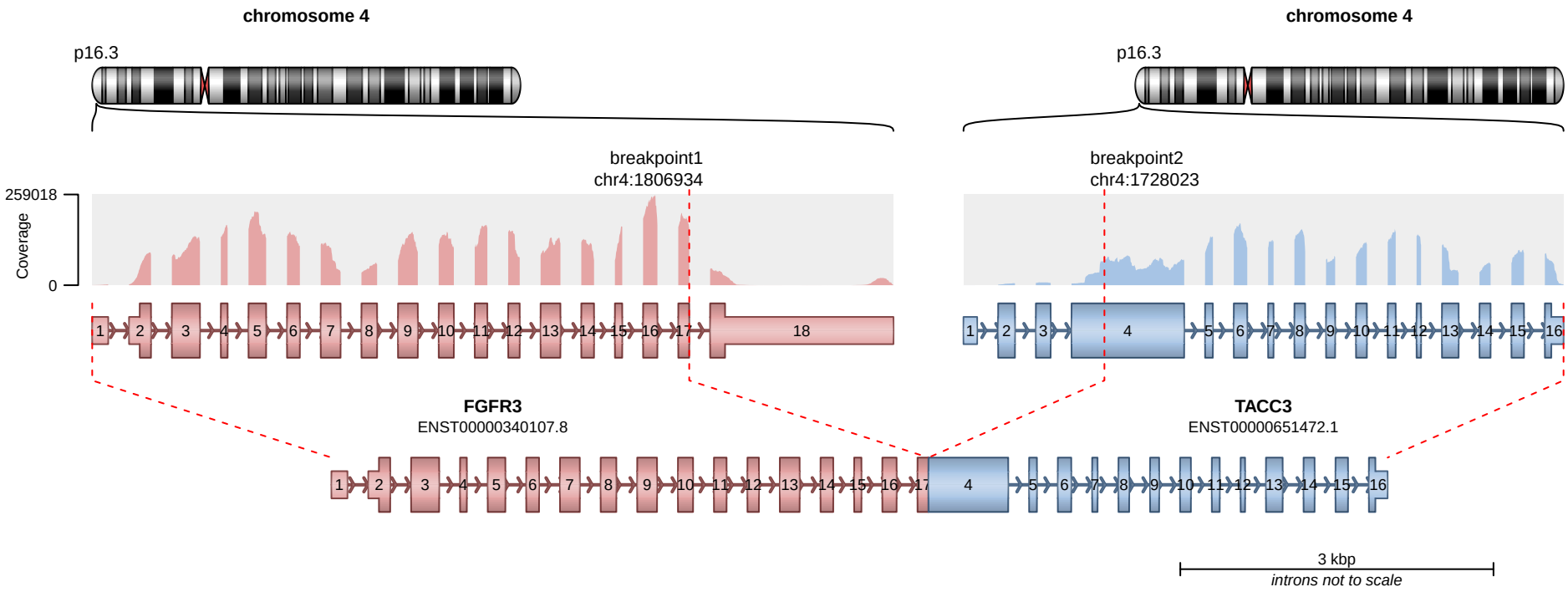
translocation
deletion
duplication
inversion

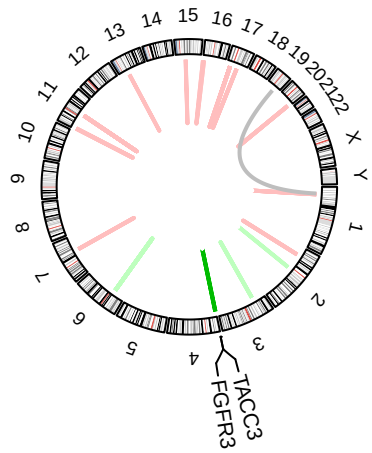
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

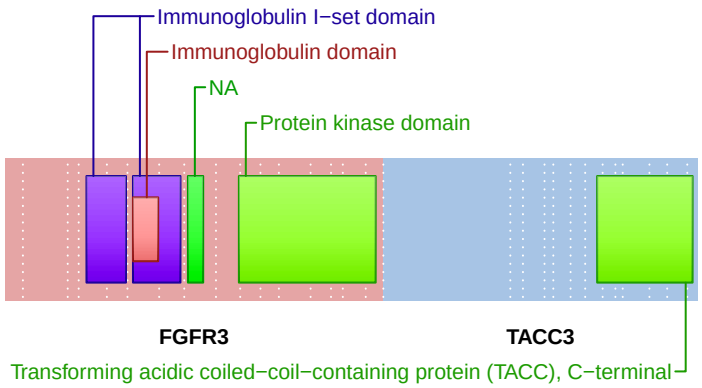
Split reads = 4
Discordant mates = 45





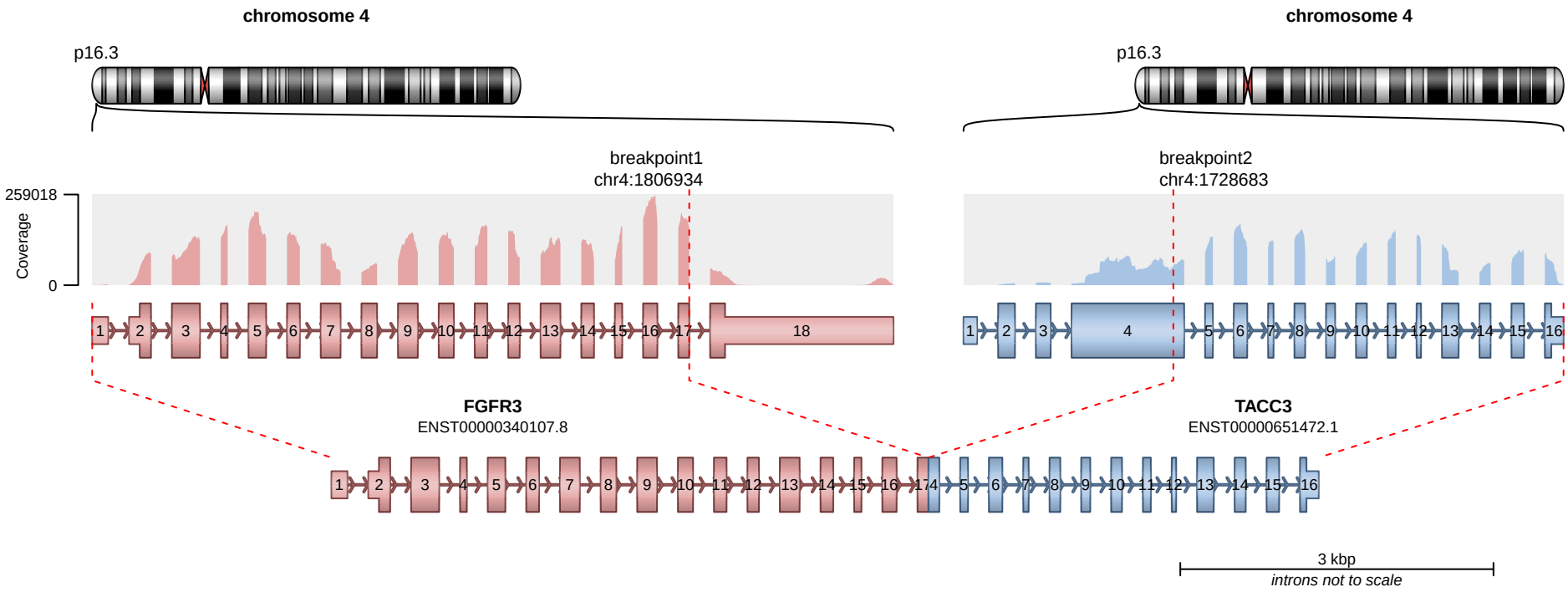
translocation
deletion
duplication
inversion

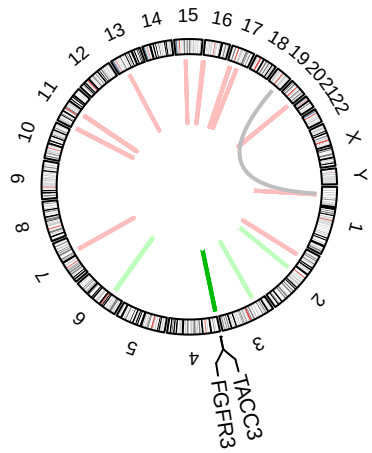
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

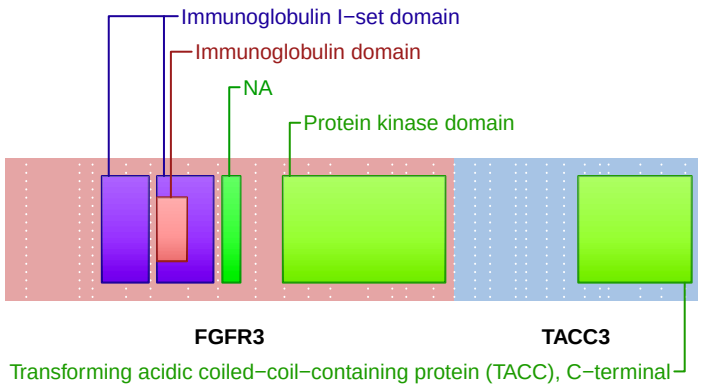
Split reads = 5
Discordant mates = 18





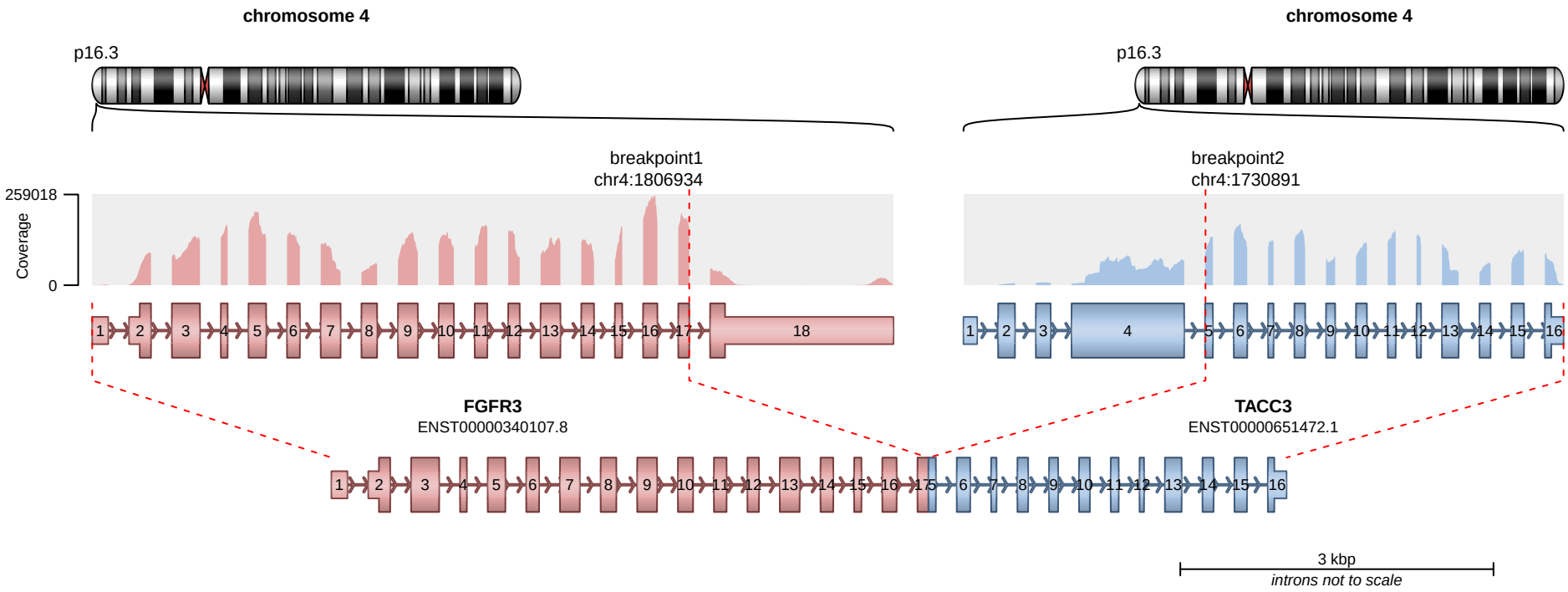
translocation
deletion
duplication
inversion

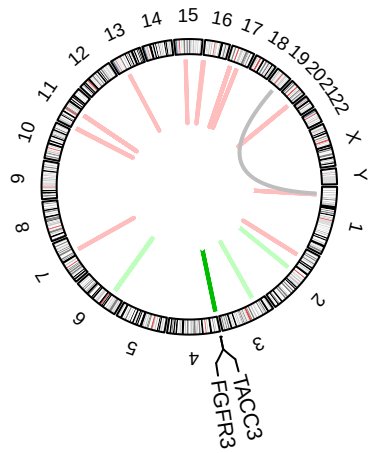
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

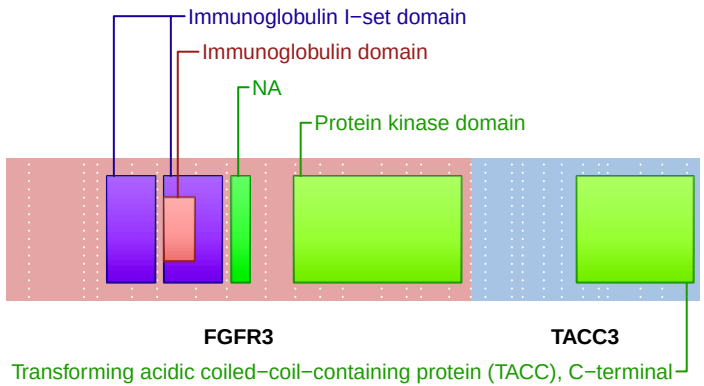
Split reads = 7
Discordant mates = 1





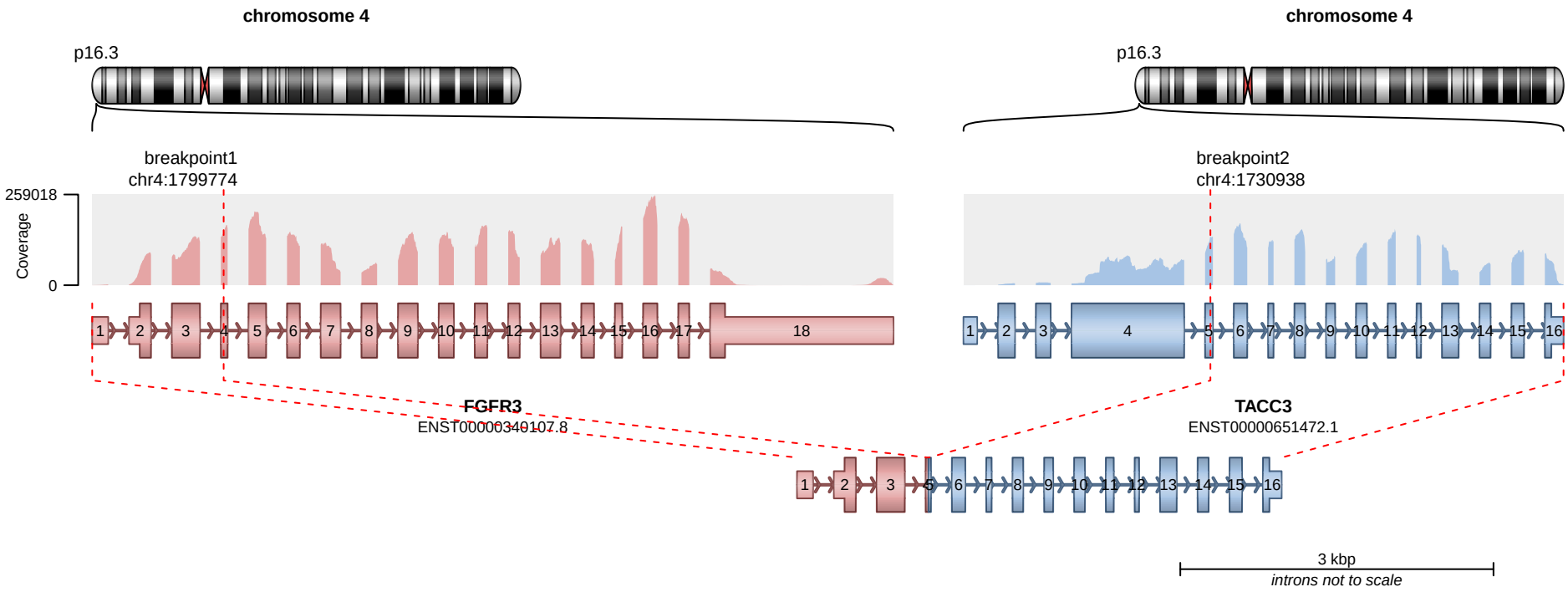
translocation
deletion
duplication
inversion

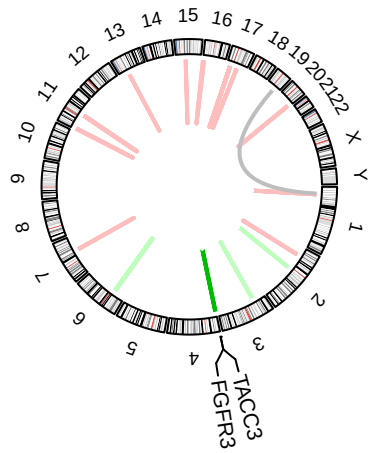
RETAINED PROTEIN DOMAINS
reading frame unclear

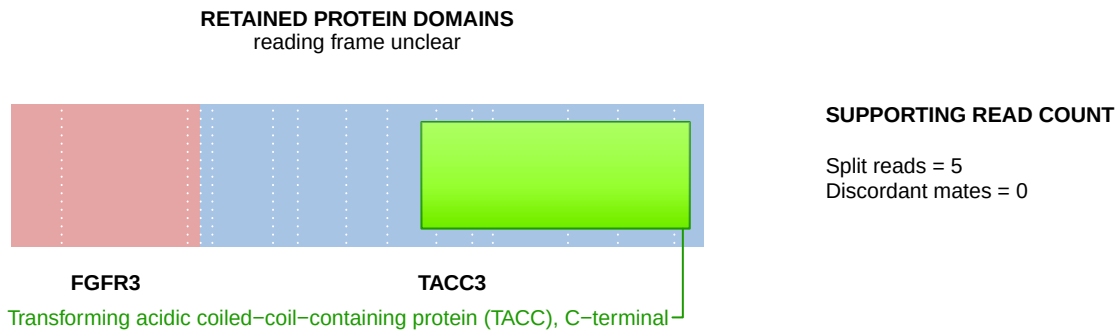


SUPPORTING READ COUNT

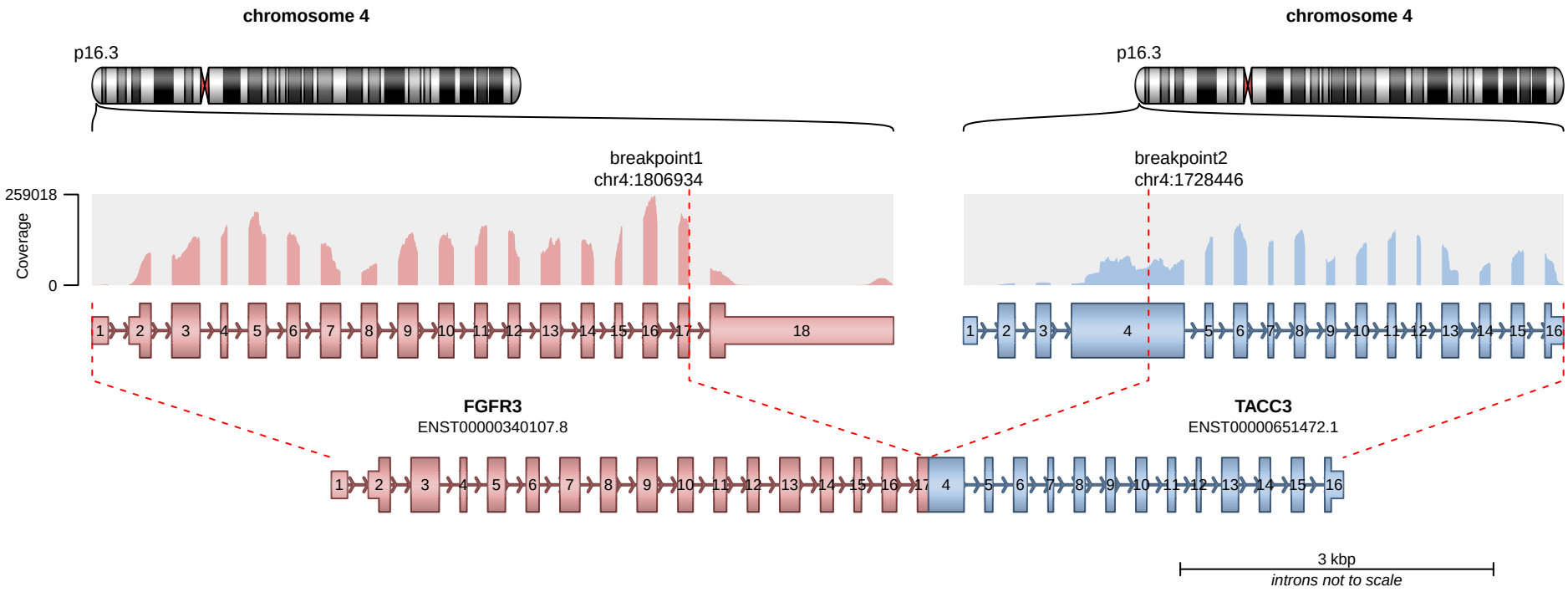
Split reads = 6
Discordant mates = 1

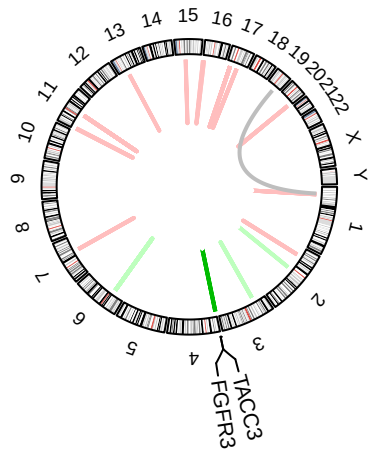




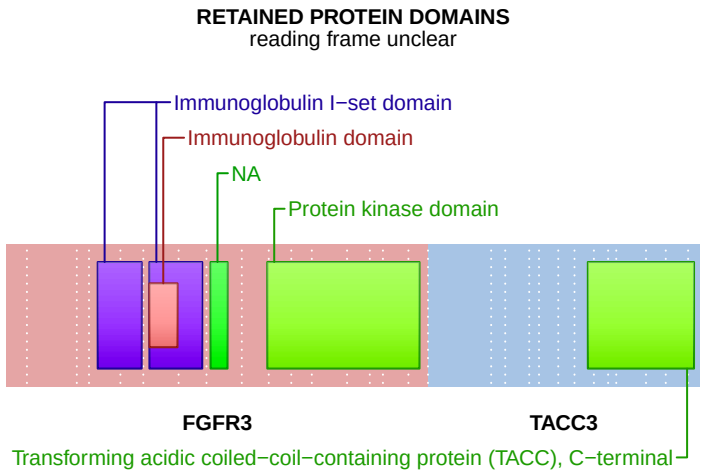


translocation
deletion
duplication
inversion



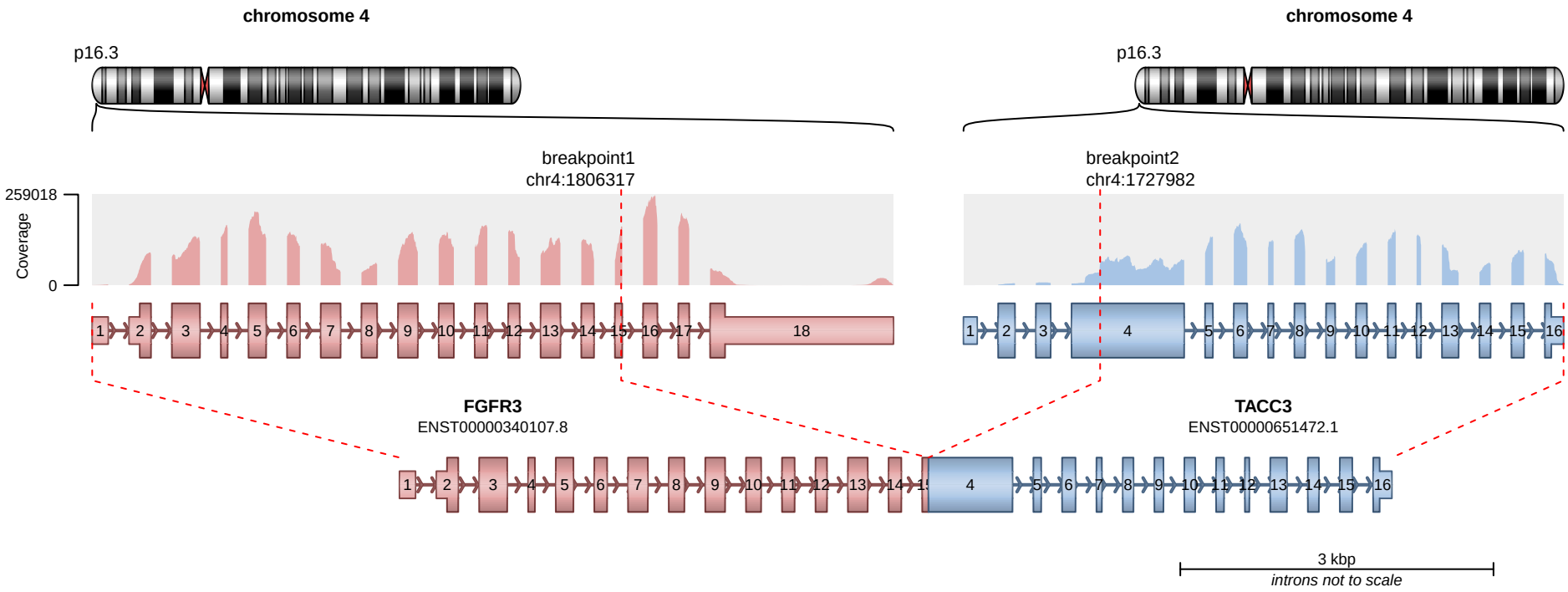


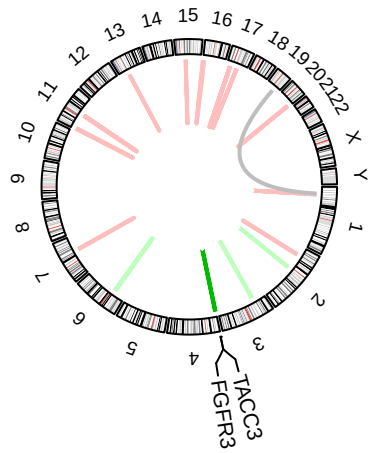
translocation
duplication
deletion
inversion



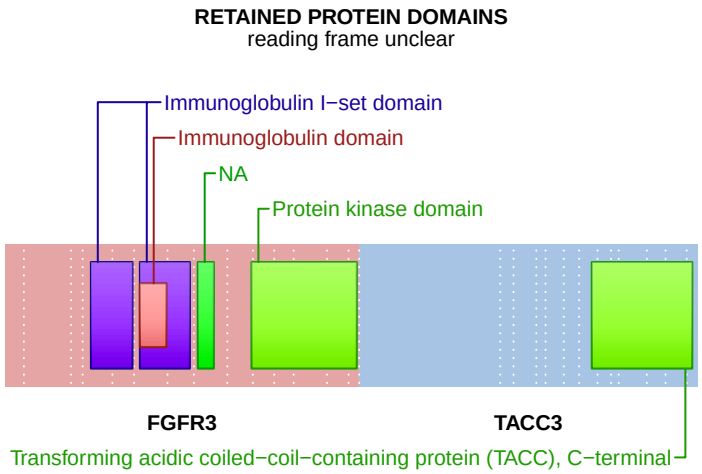
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 1



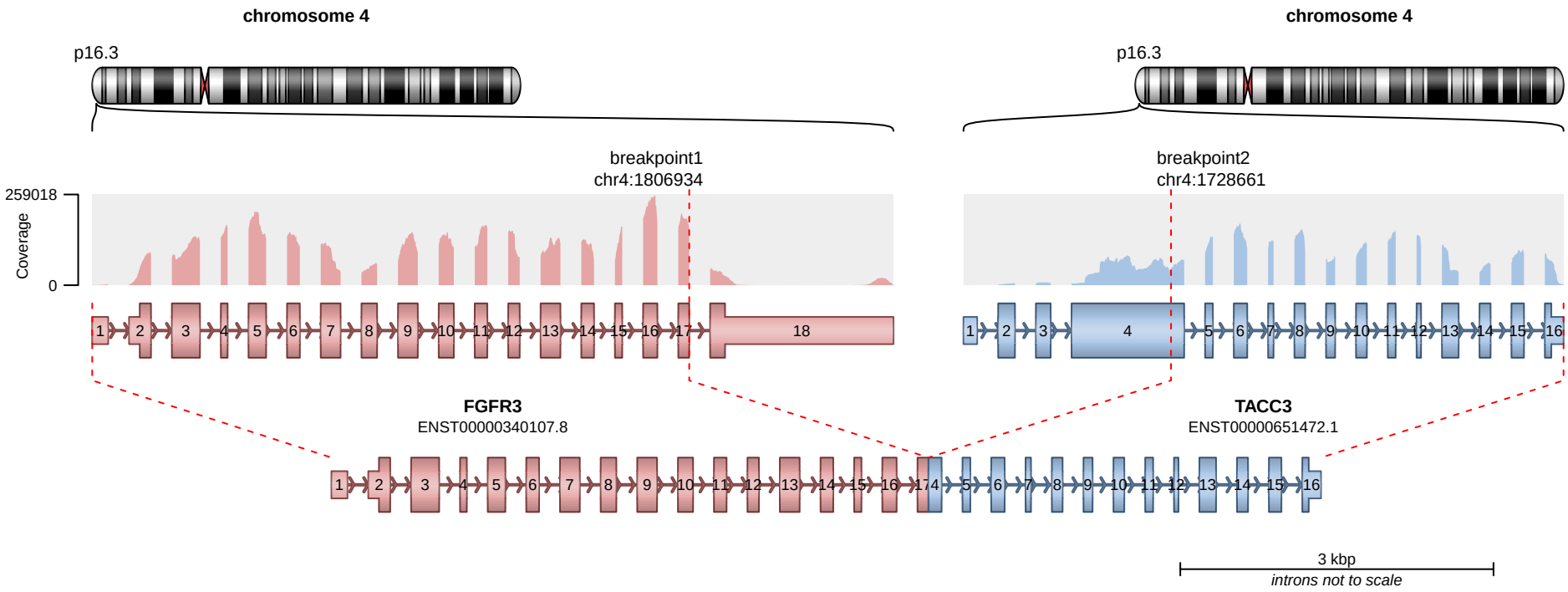


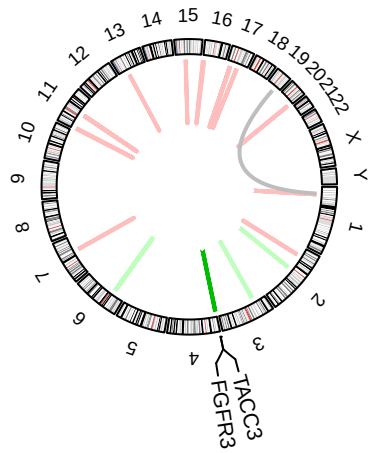
translocation
deletion
duplication
inversion



SUPPORTING READ COUNT

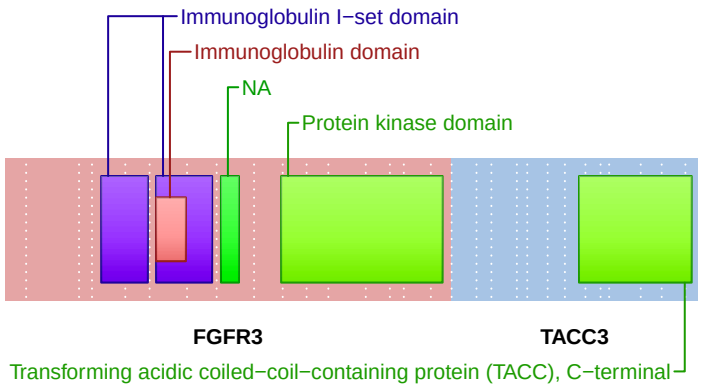
Split reads = 4
Discordant mates = 0





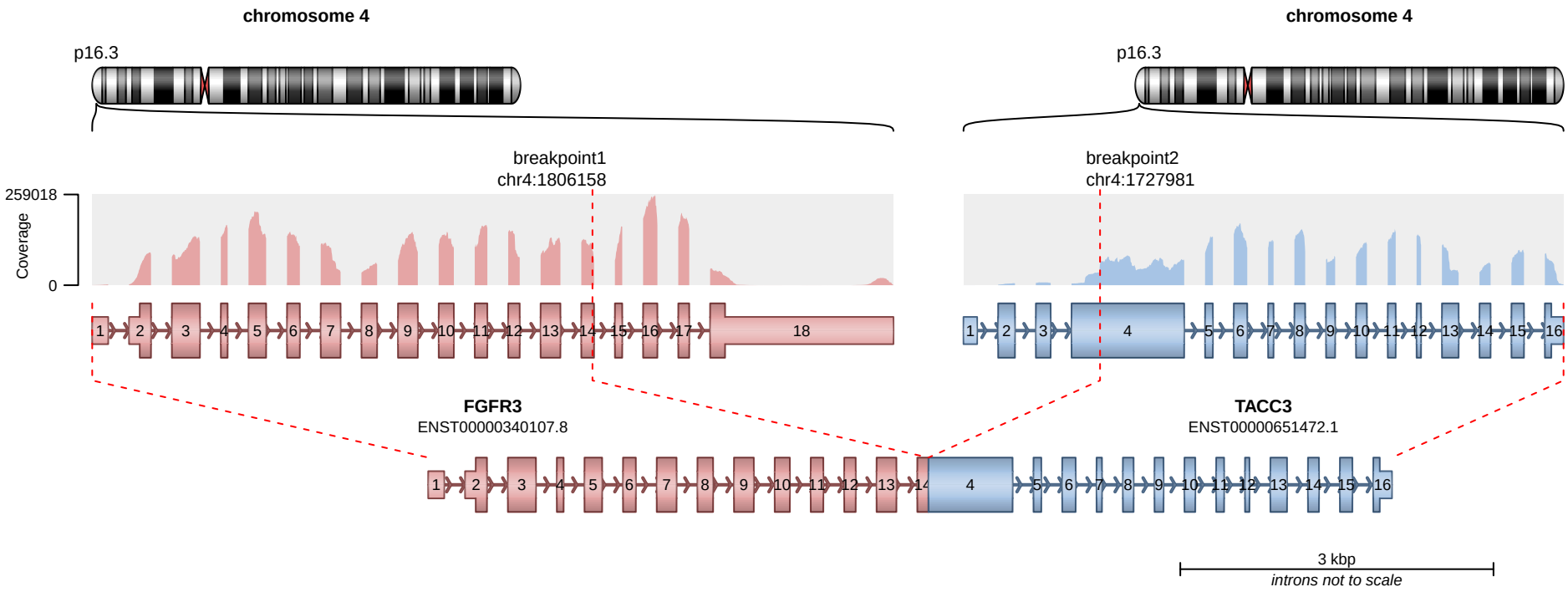
translocation
deletion
duplication
inversion

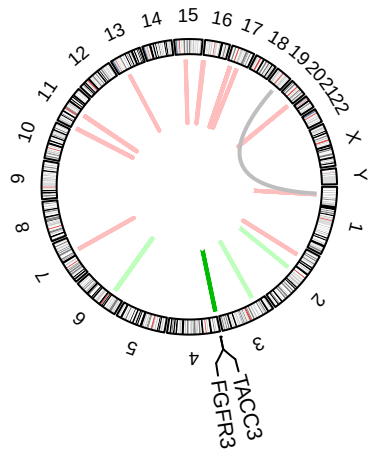
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

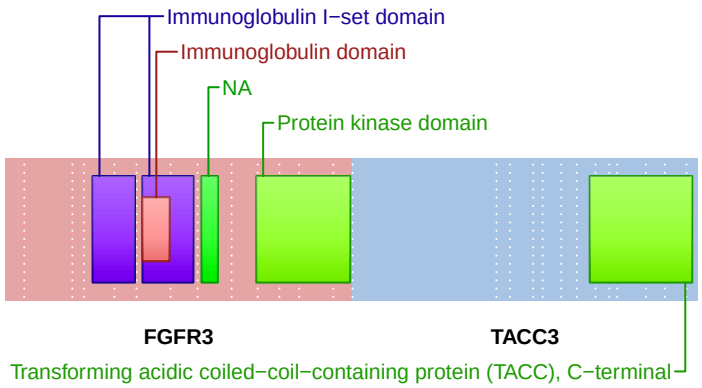
Split reads = 3
Discordant mates = 1





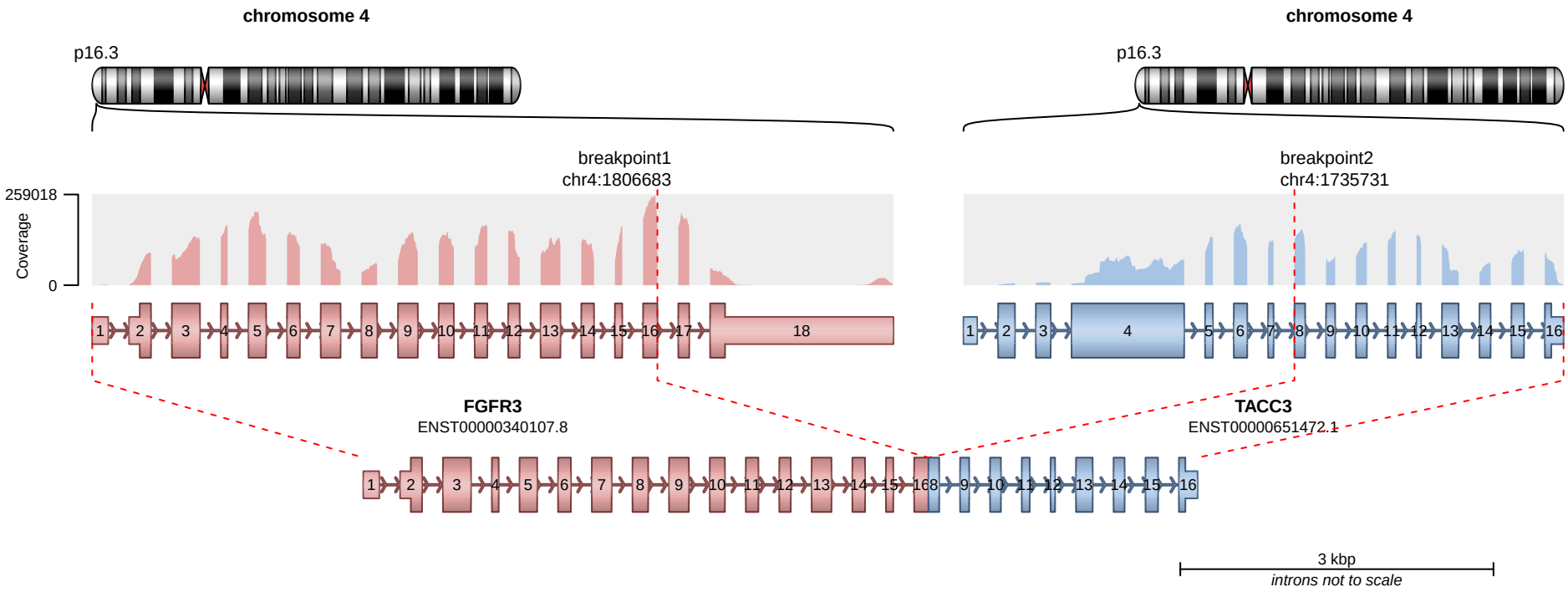
translocation
deletion
duplication
inversion

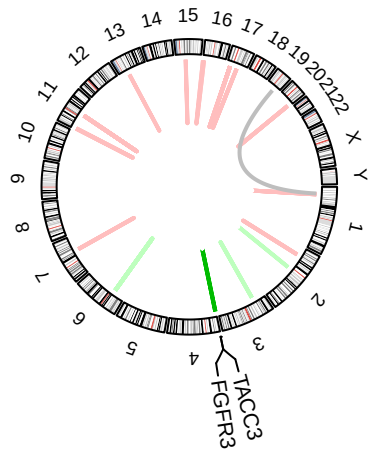
RETAINED PROTEIN DOMAINS
reading frame unclear

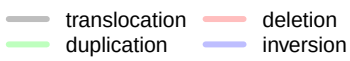


SUPPORTING READ COUNT

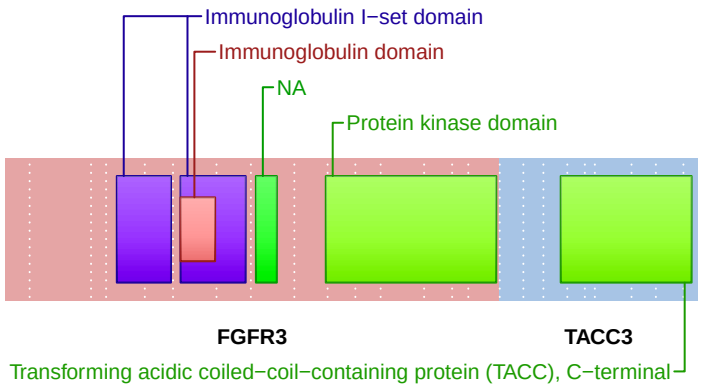
Split reads = 3
Discordant mates = 0





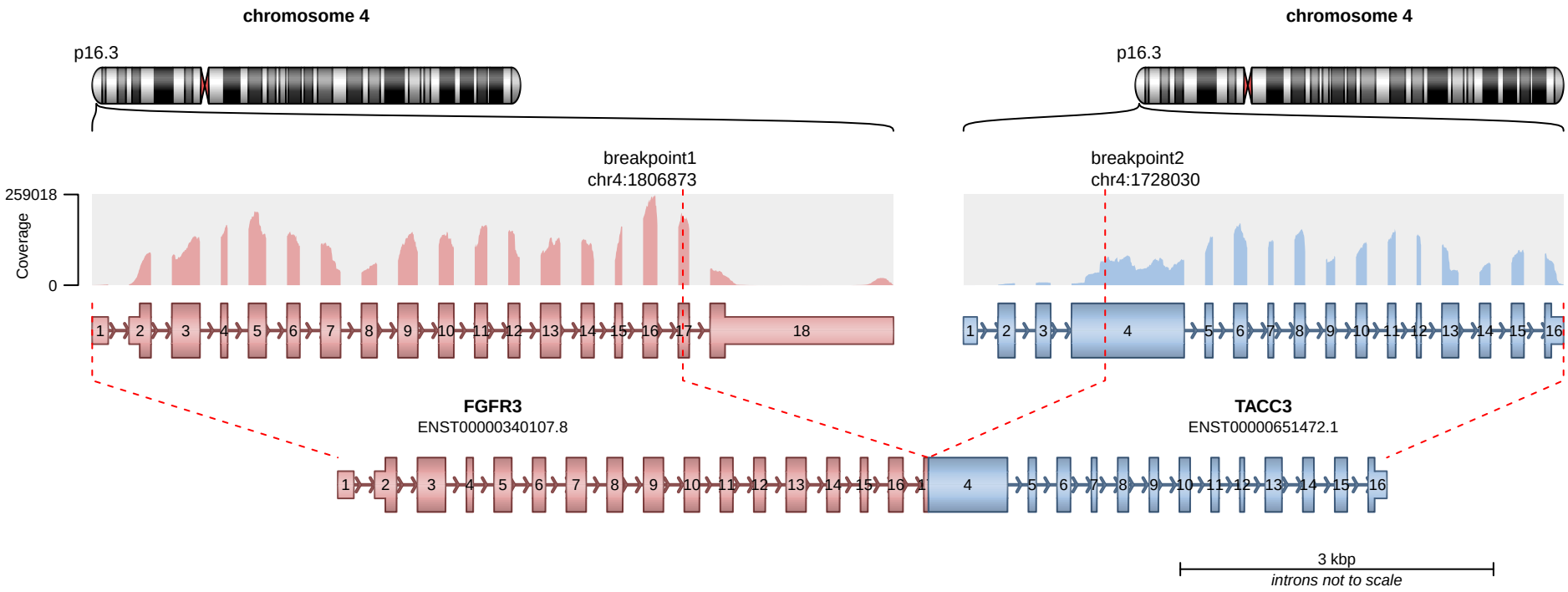


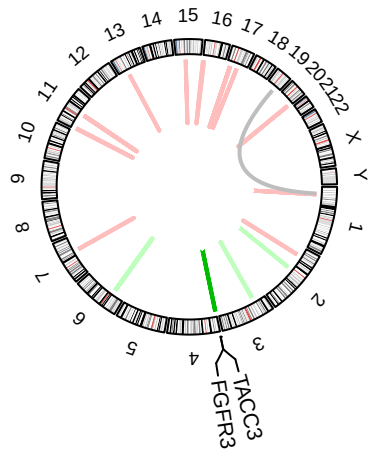
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

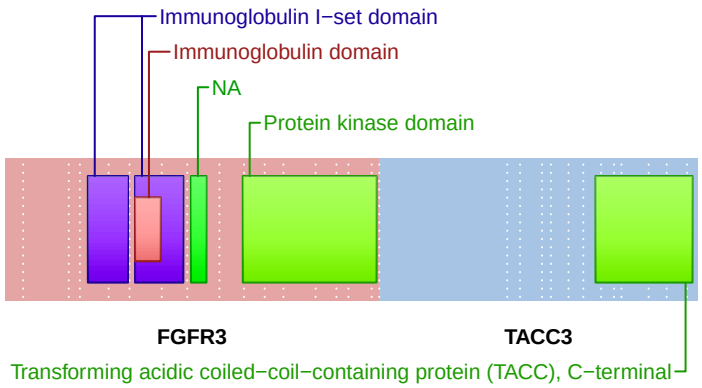
Split reads = 3
Discordant mates = 0





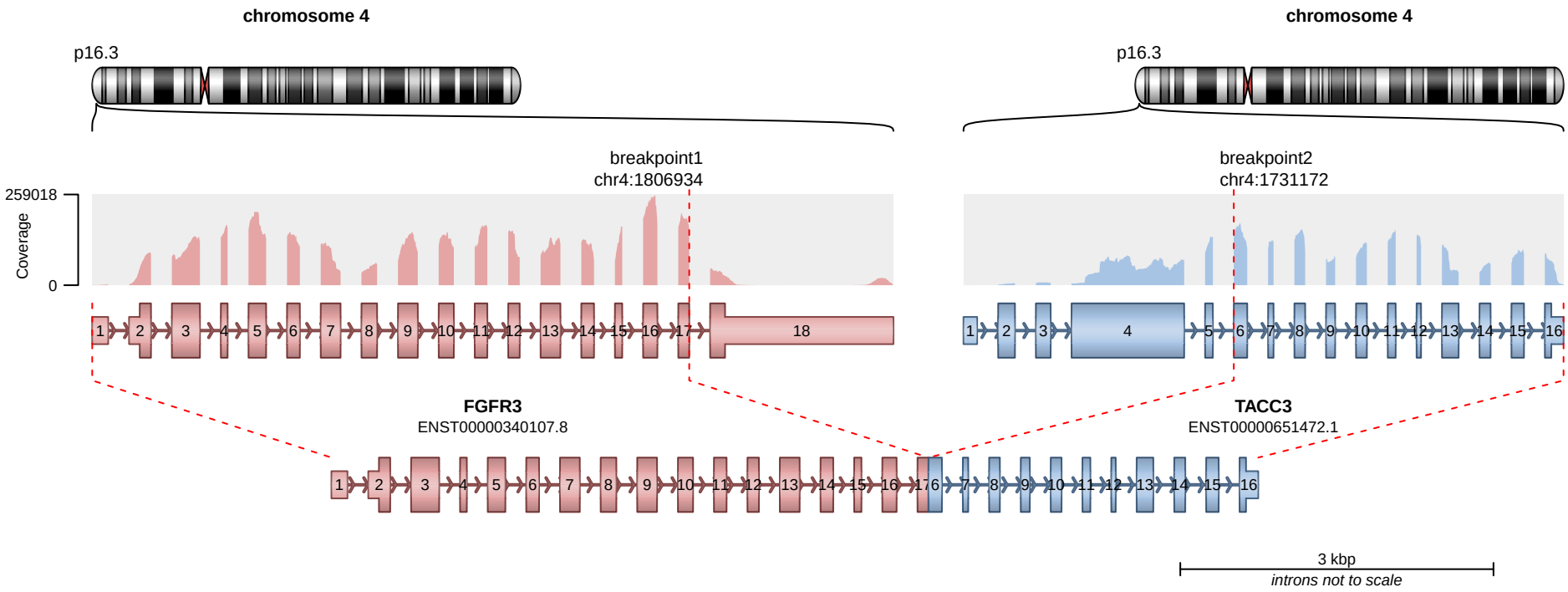
translocation
deletion
duplication
inversion

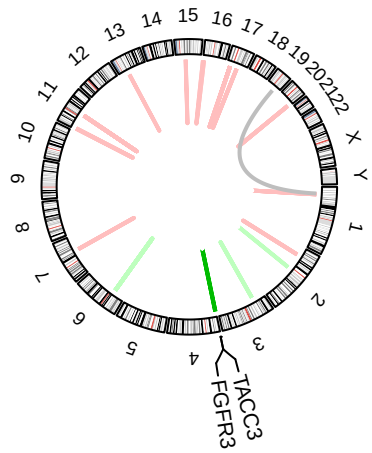
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

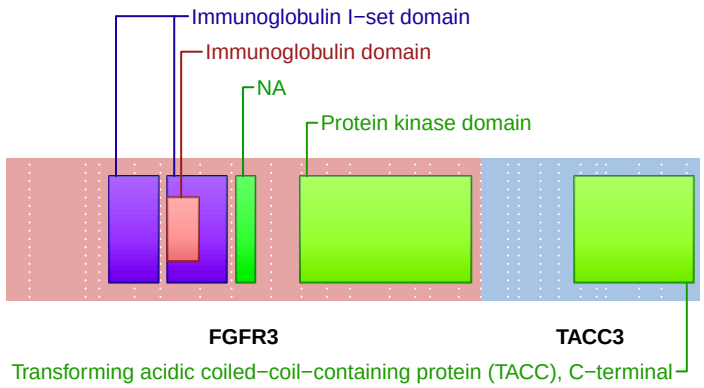
Split reads = 3
Discordant mates = 0





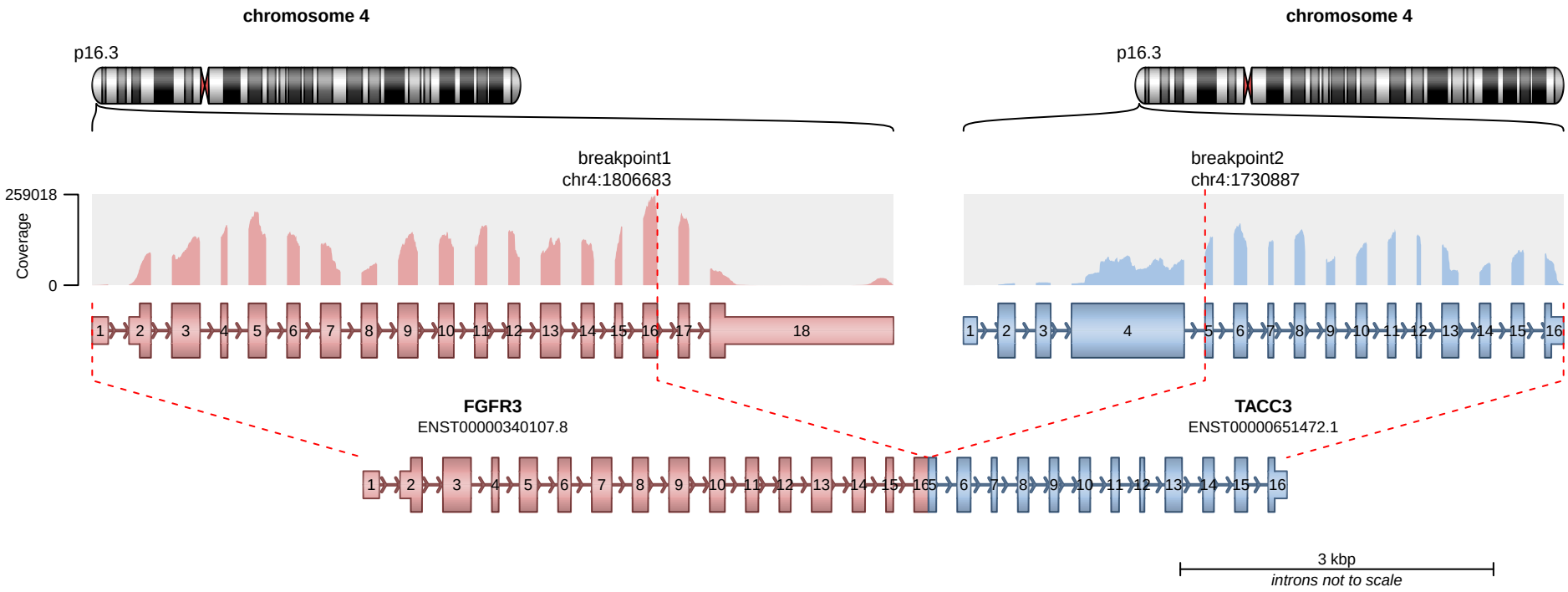
translocation
deletion
duplication
inversion

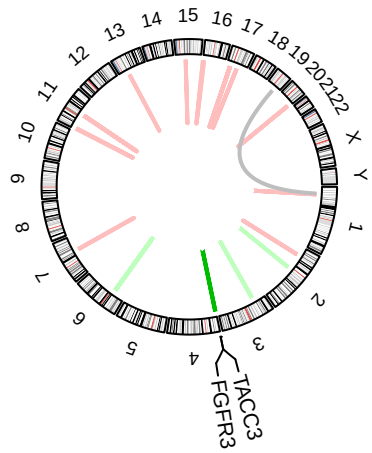
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

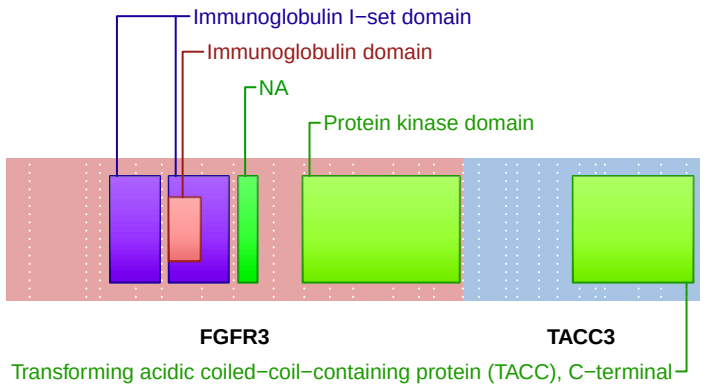
Split reads = 2
Discordant mates = 0





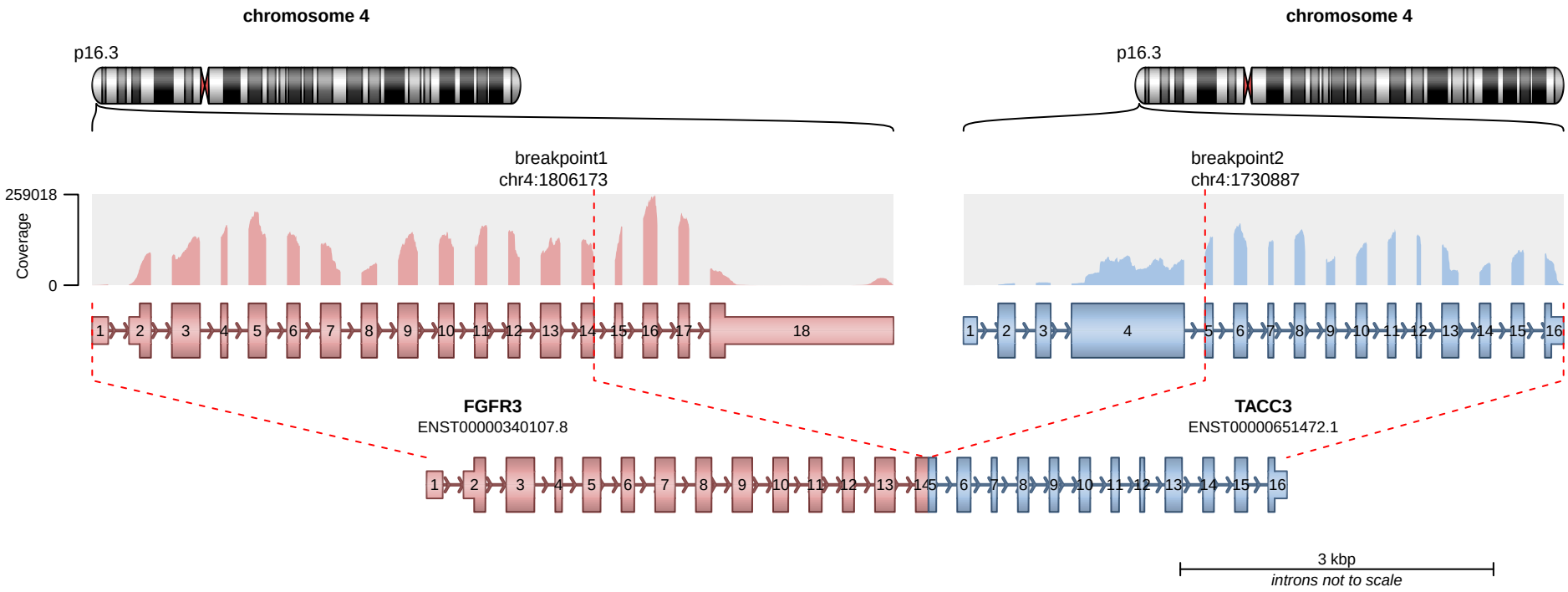
translocation
deletion
duplication
inversion

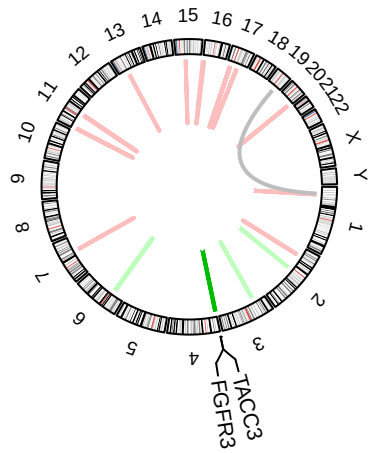
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

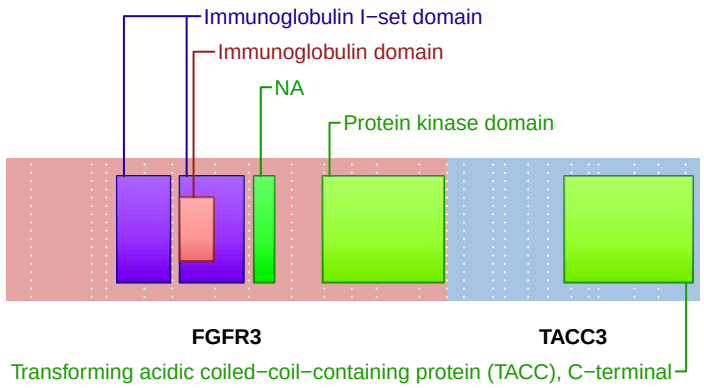
Split reads = 2
Discordant mates = 0





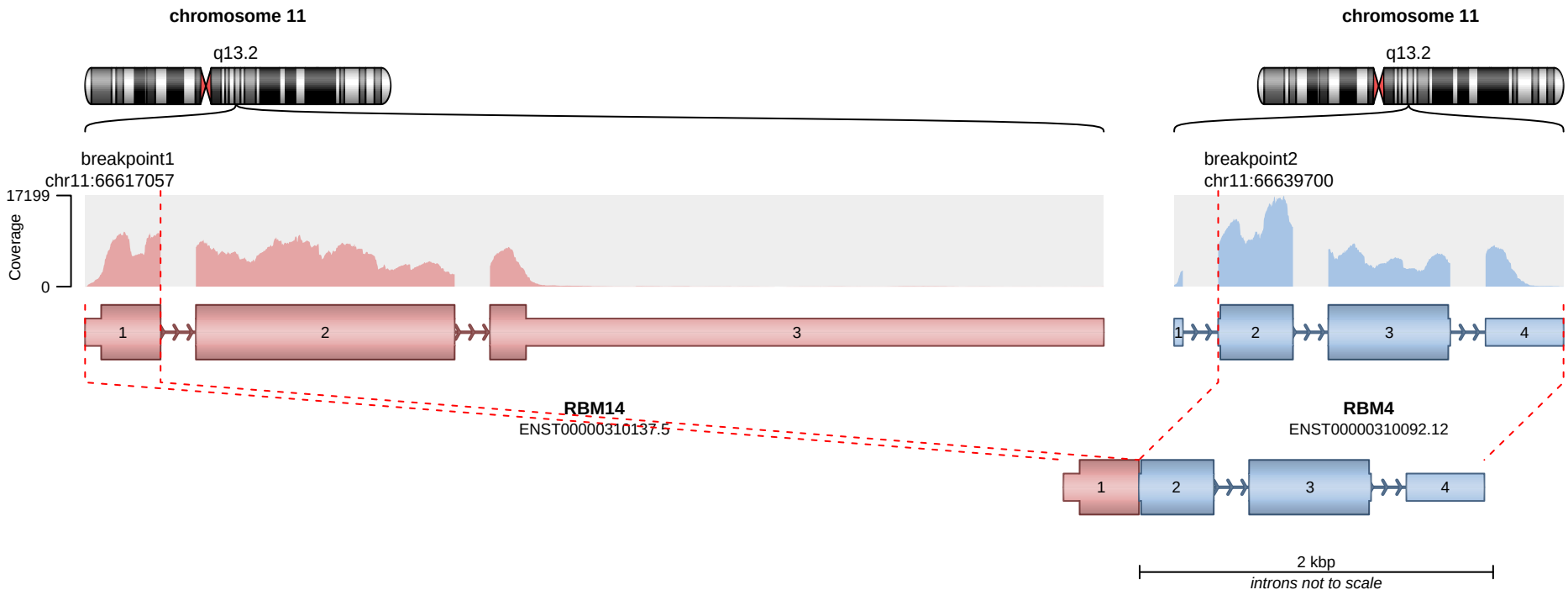
translocation
deletion
duplication
inversion

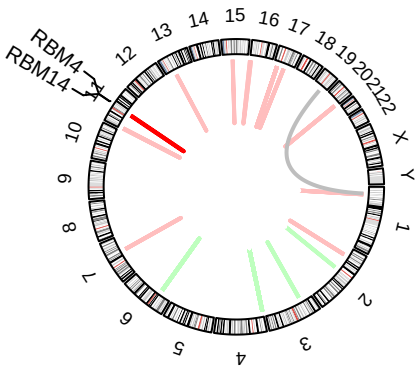
RETAINED PROTEIN DOMAINS
reading frame unclear

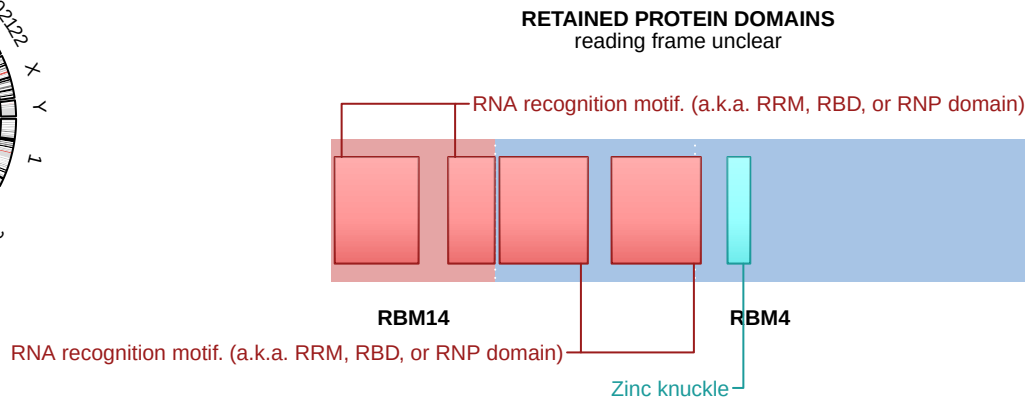


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



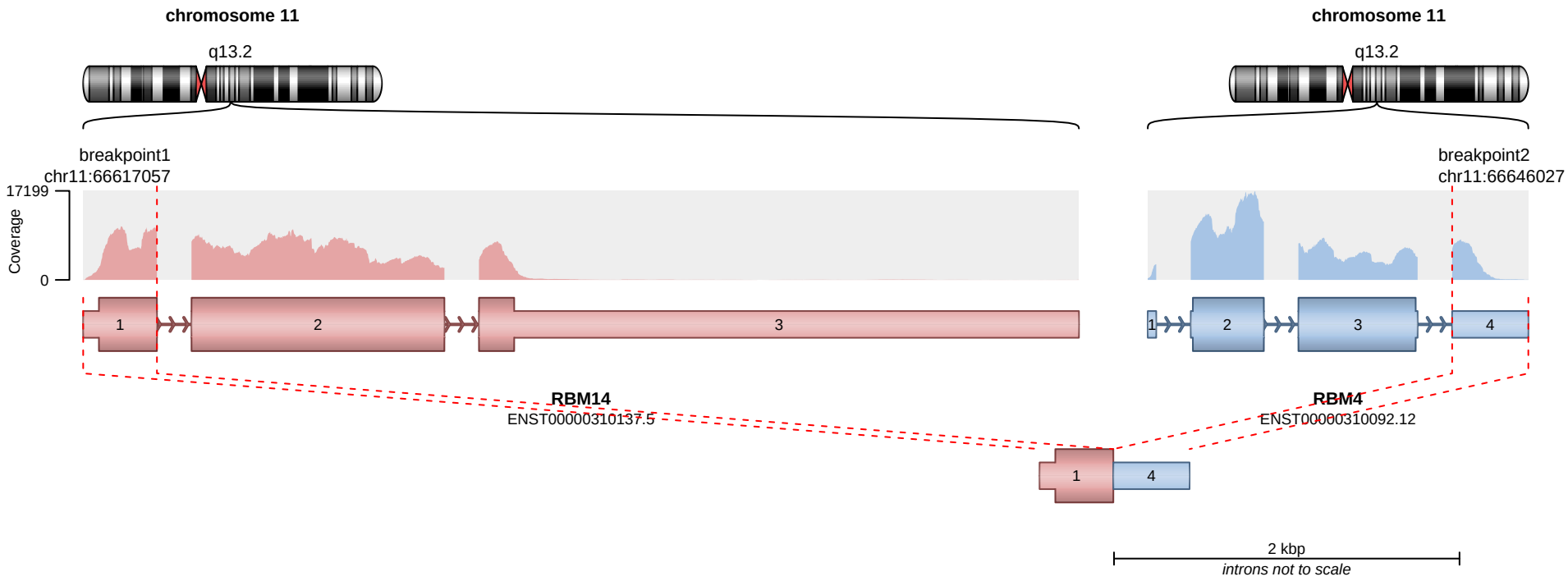


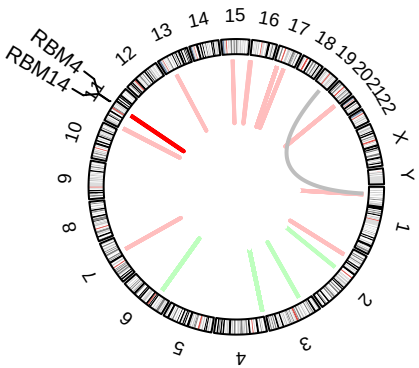


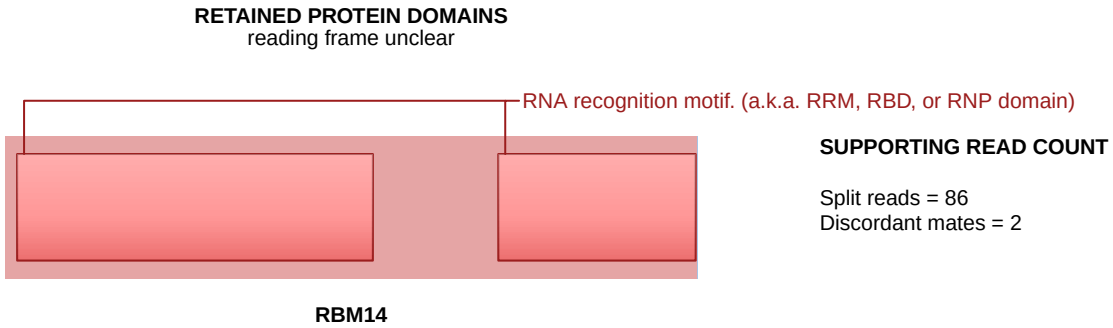
SUPPORTING READ COUNT

Split reads = 732
Discordant mates = 7

translocation
deletion
duplication
inversion



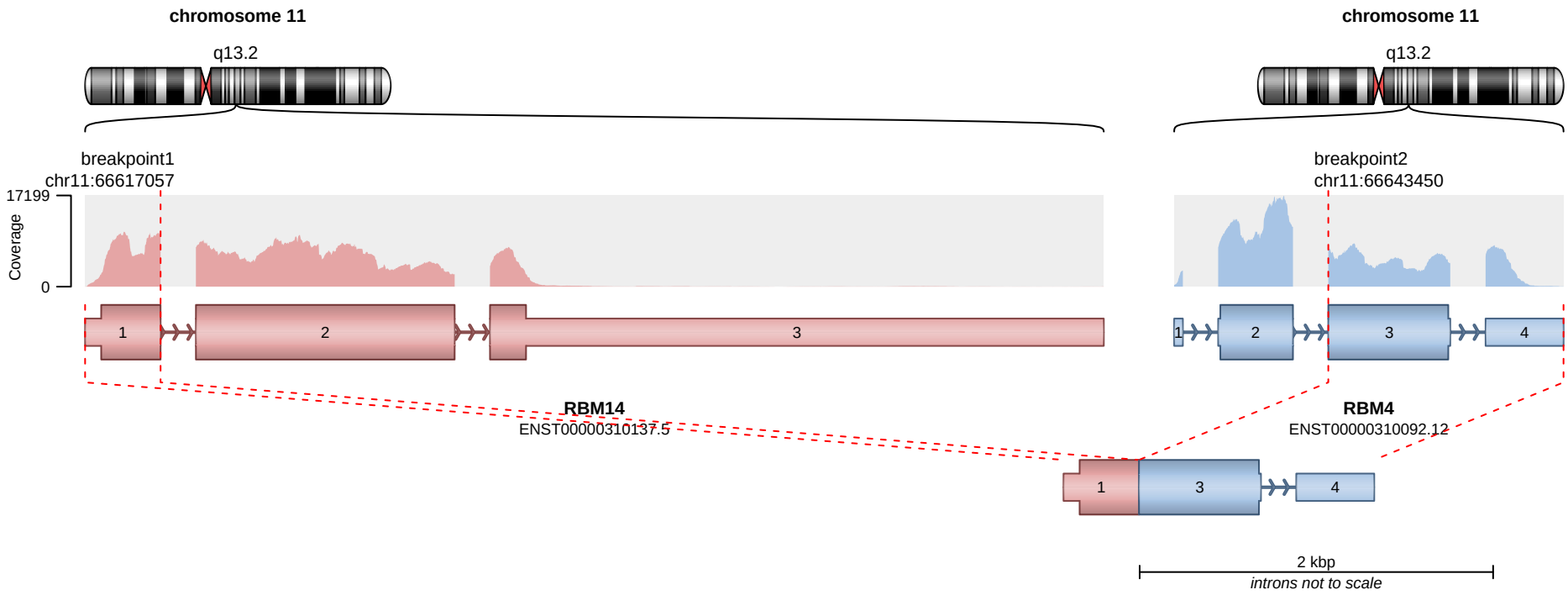


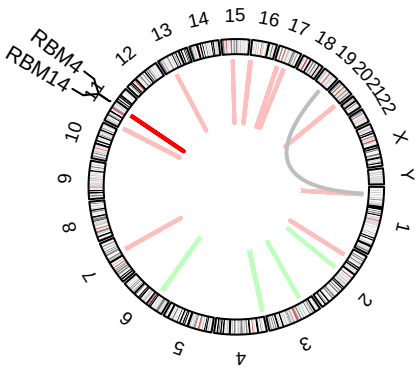


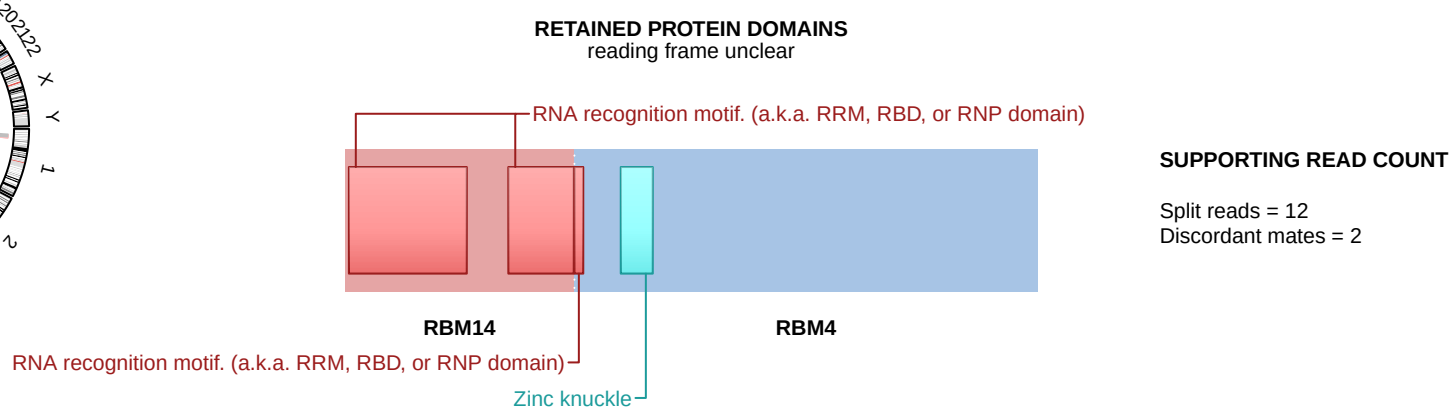
SUPPORTING READ COUNT

Split reads = 86
Discordant mates = 2

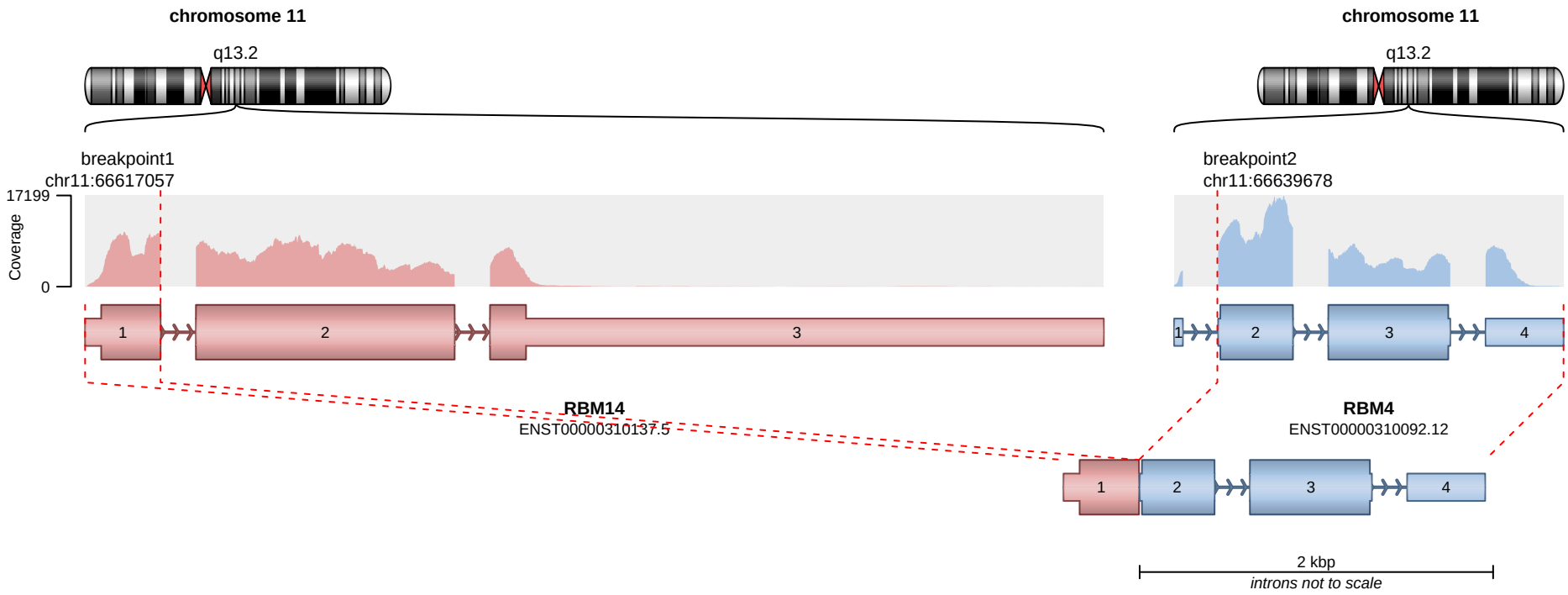
translocation
deletion
duplication
inversion

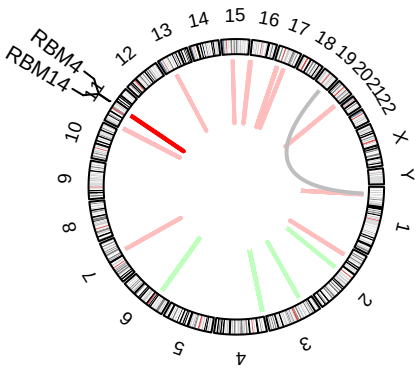


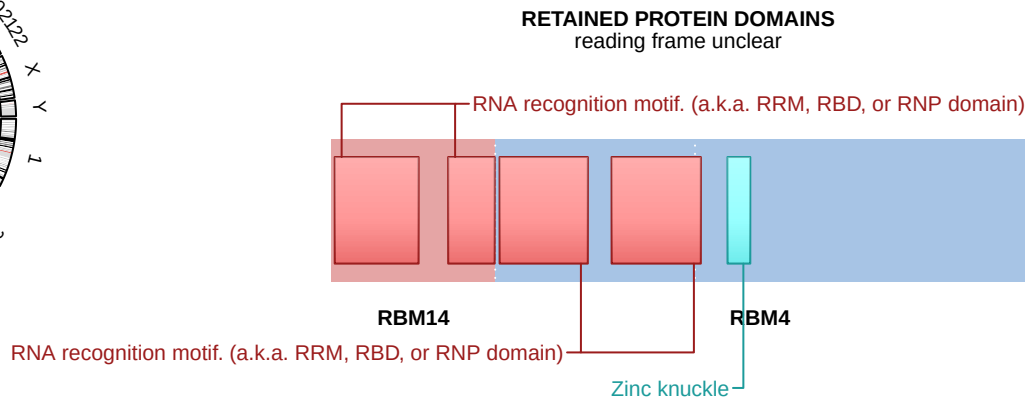




translocation
deletion
duplication
inversion



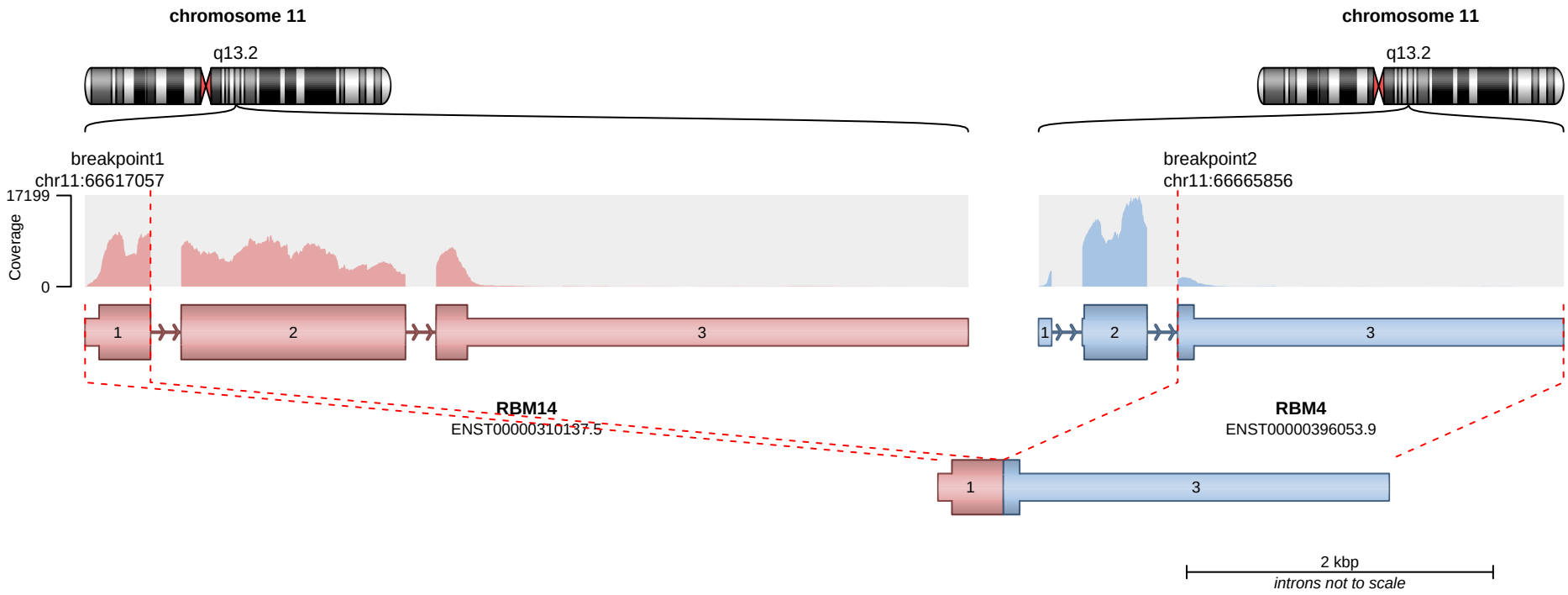


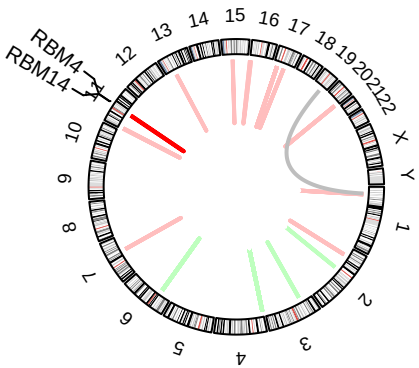


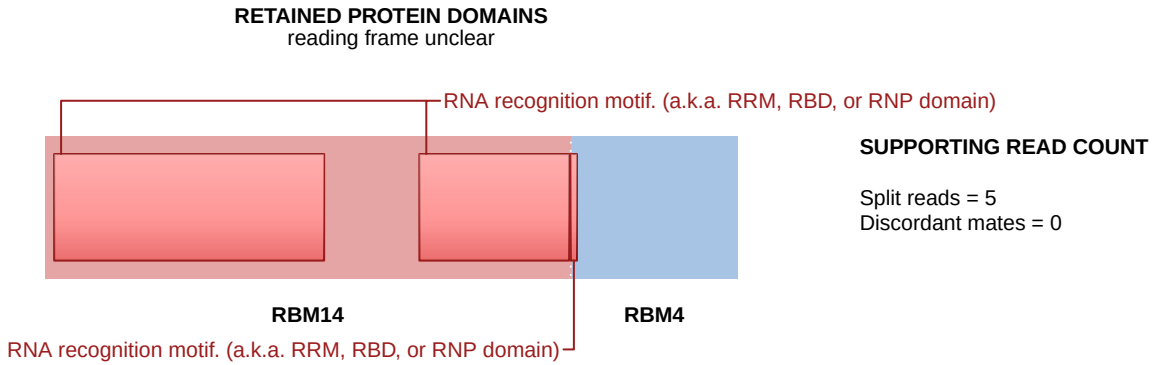
SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 7

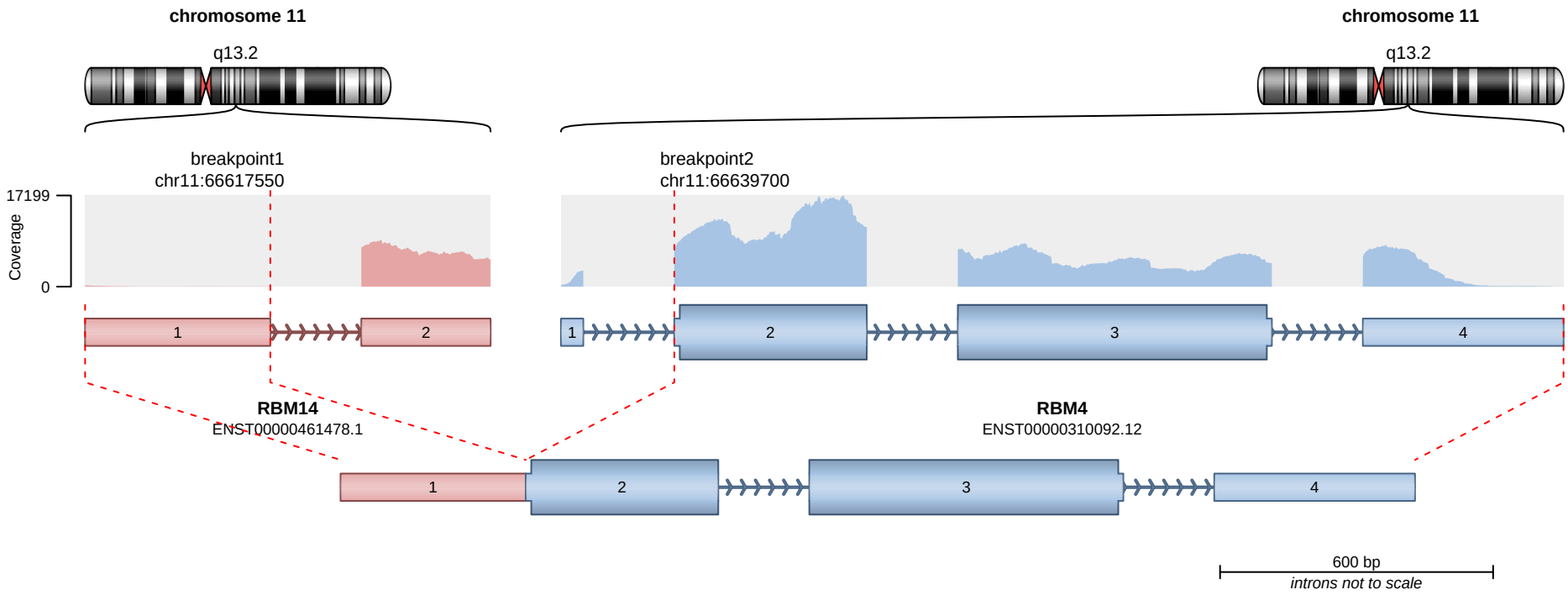
translocation
deletion
duplication
inversion

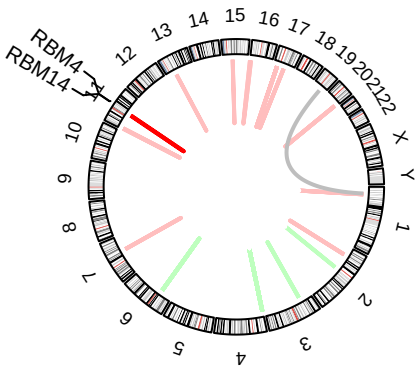


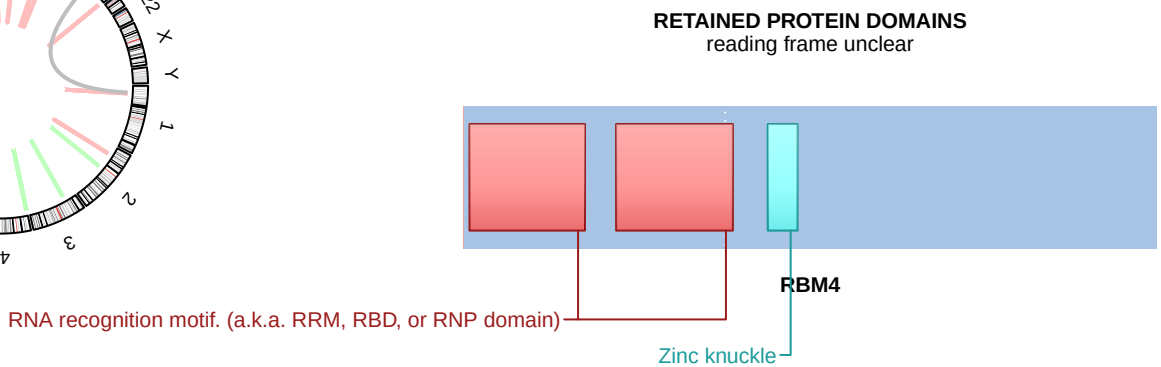




translocation
deletion
duplication
inversion



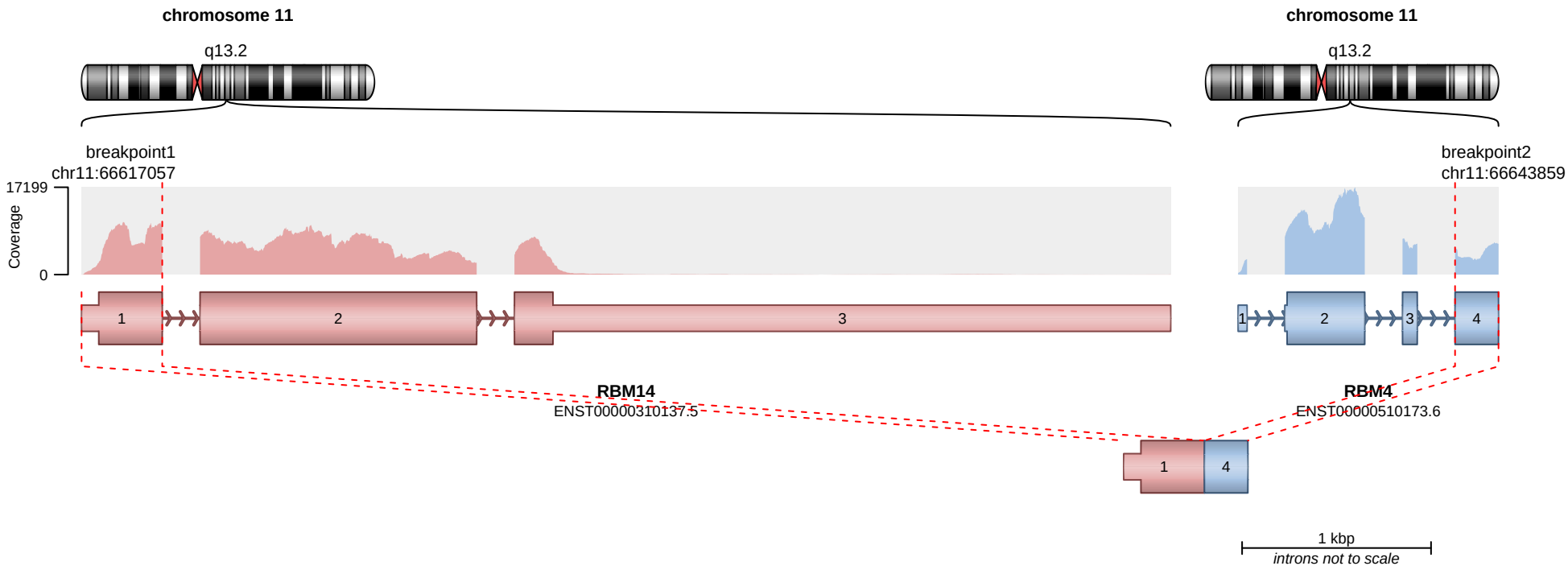


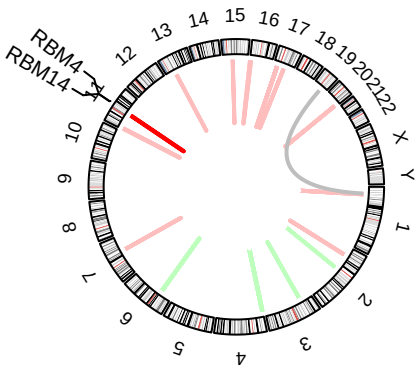


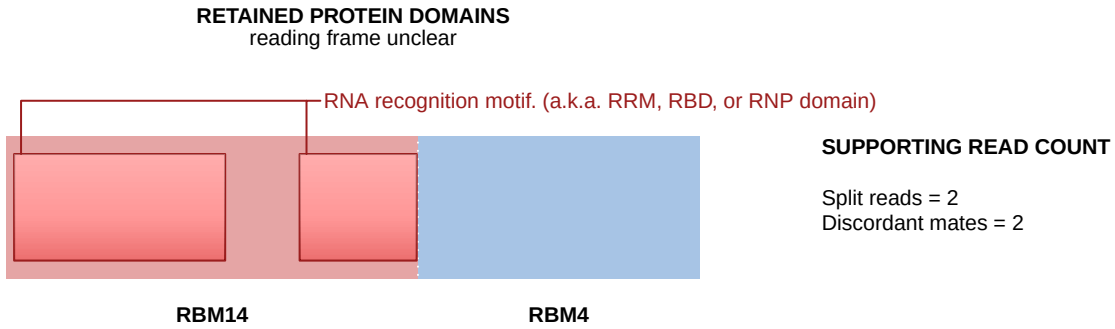
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 7

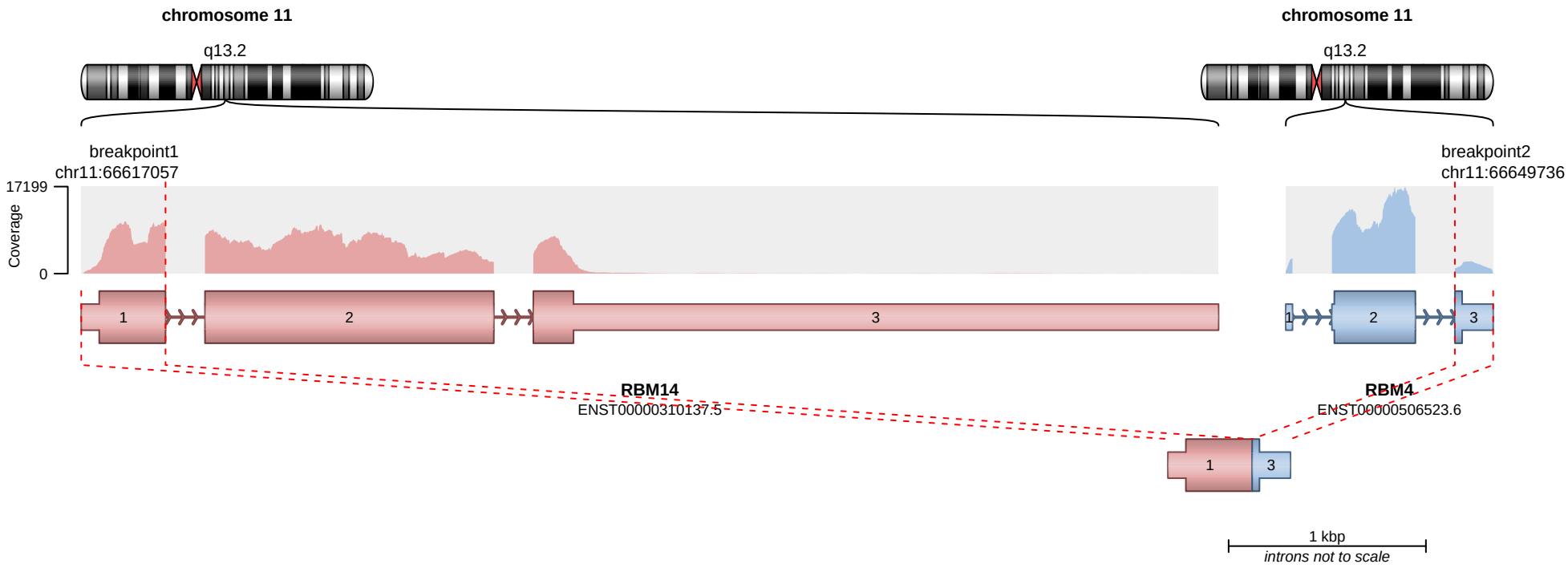
translocation
deletion
duplication
inversion

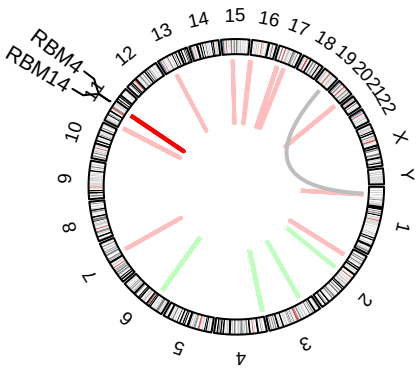


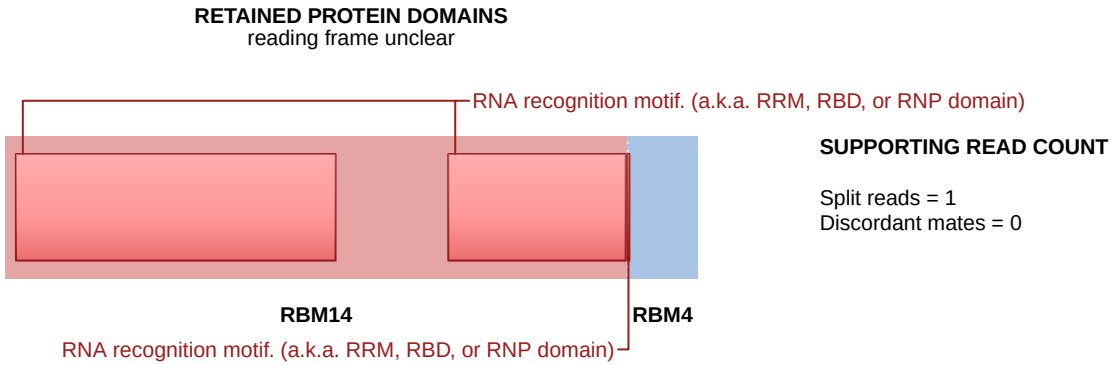




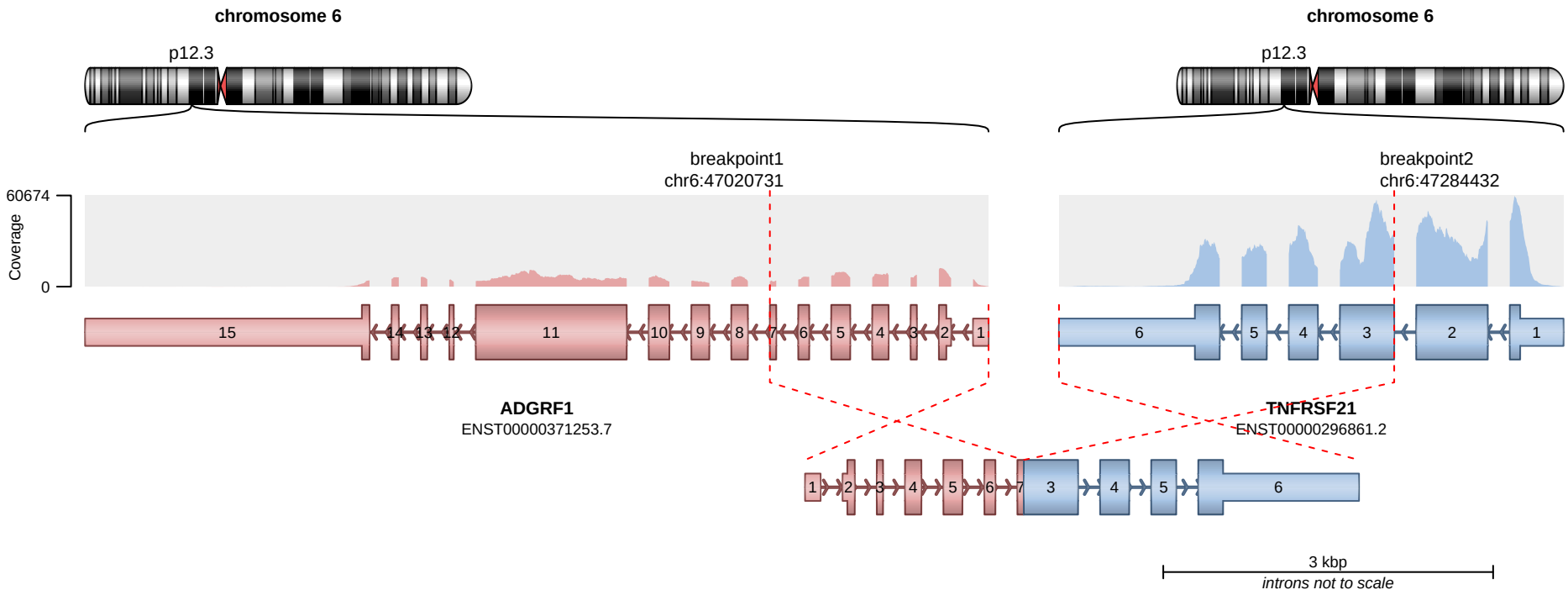
translocation
deletion
duplication
inversion

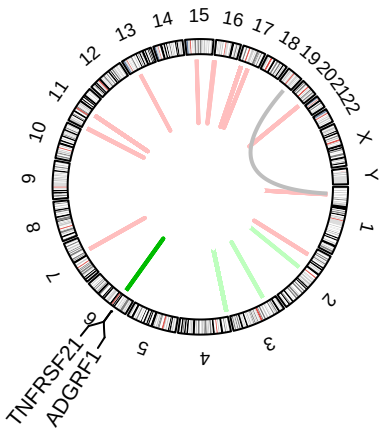


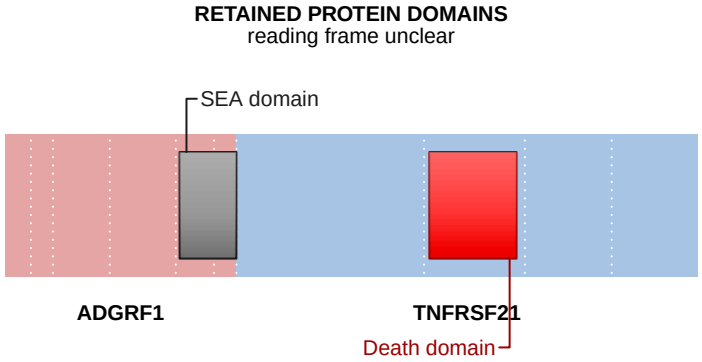




translocation
deletion
duplication
inversion



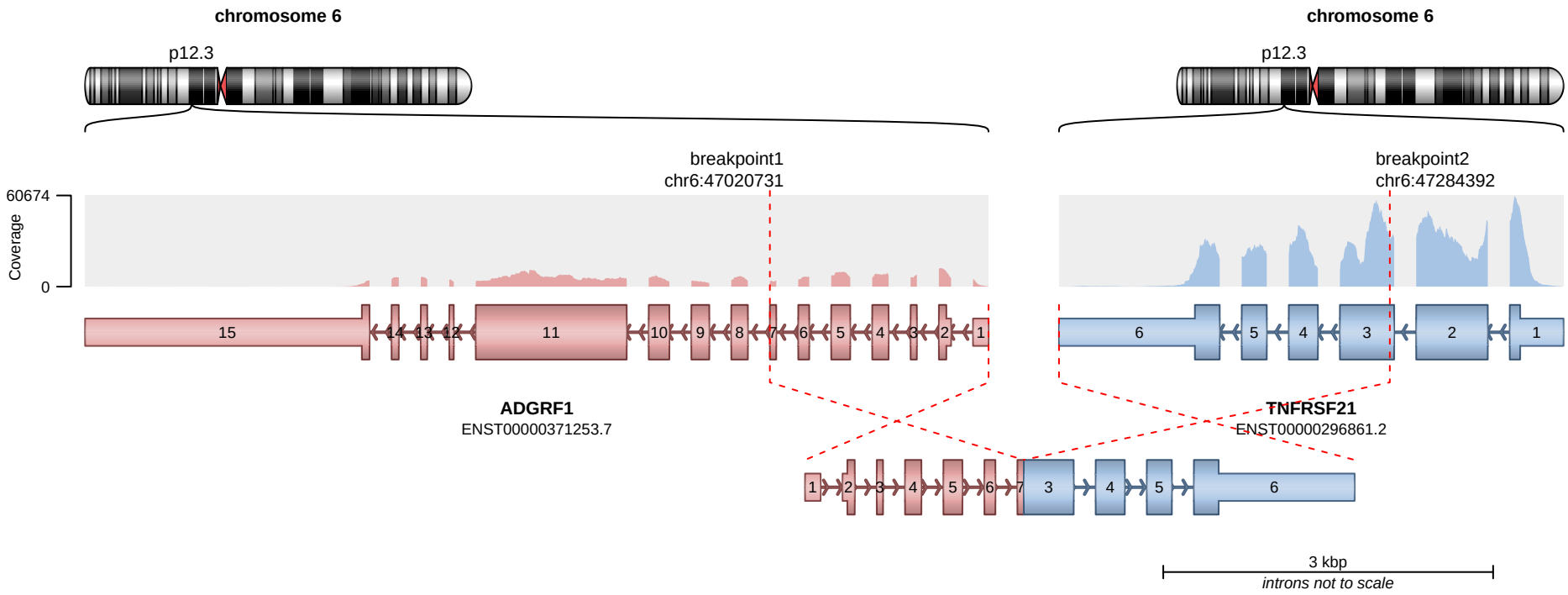


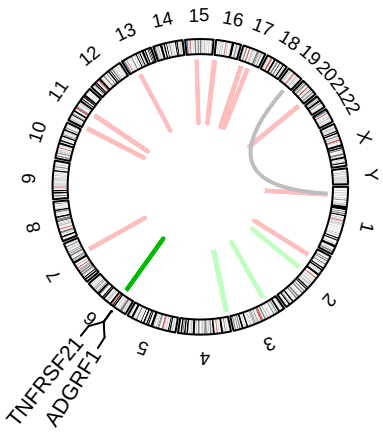


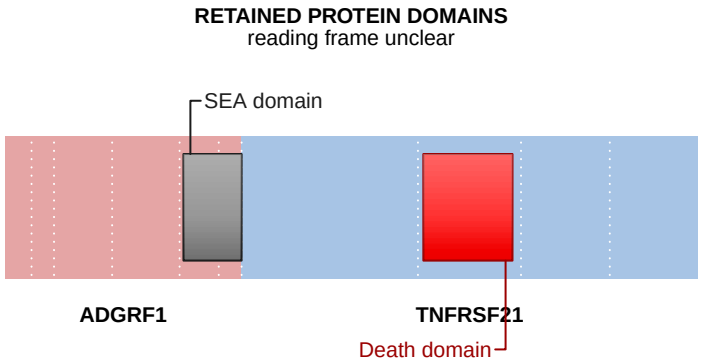
SUPPORTING READ COUNT

Split reads = 574
Discordant mates = 21

translocation
deletion
duplication
inversion



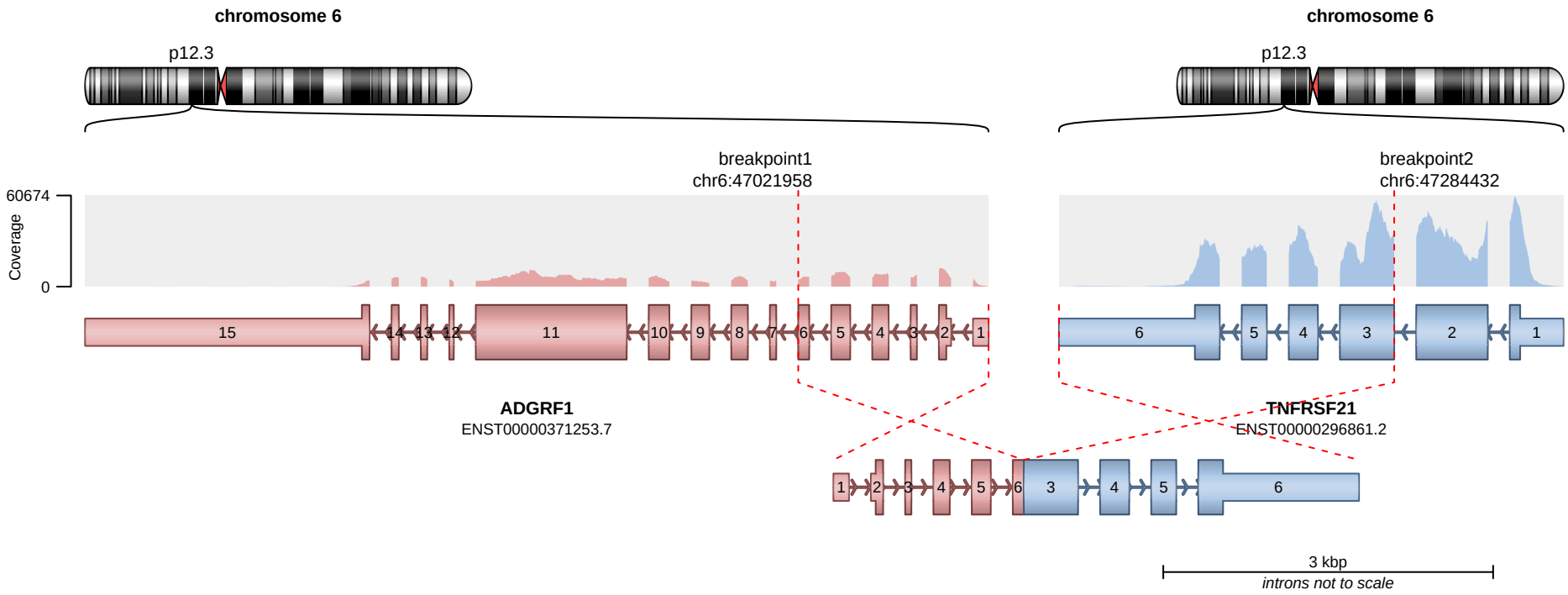


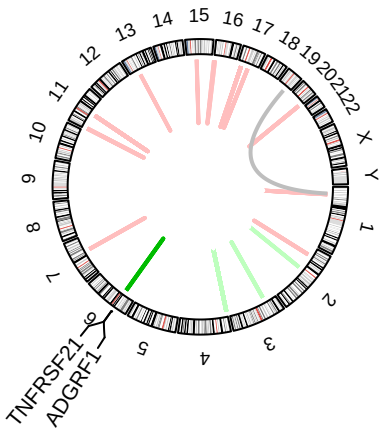


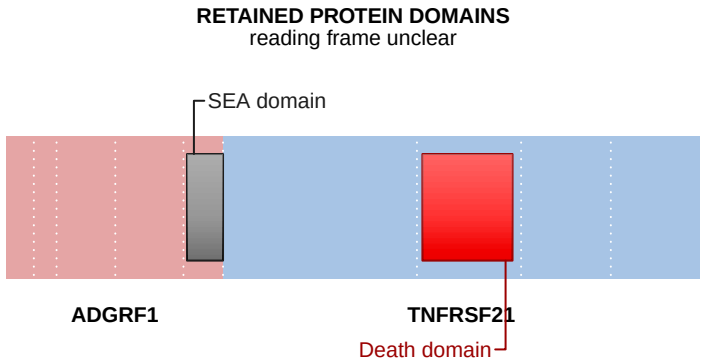
SUPPORTING READ COUNT

Split reads = 121
Discordant mates = 4

translocation
deletion
duplication
inversion



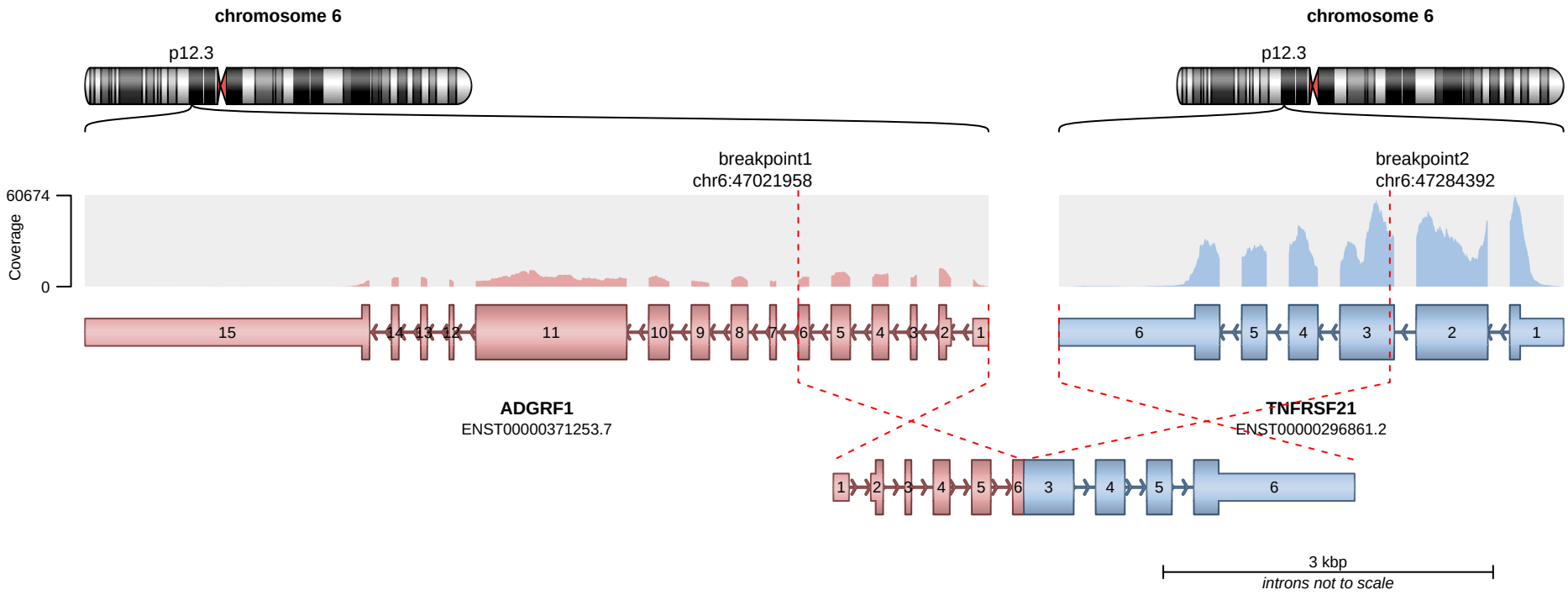


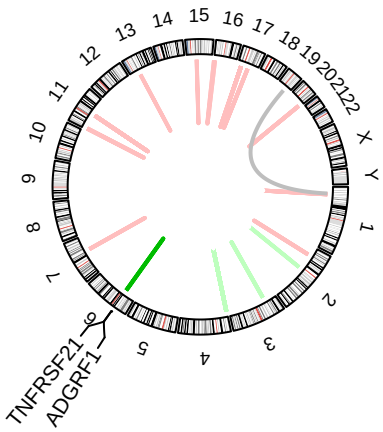


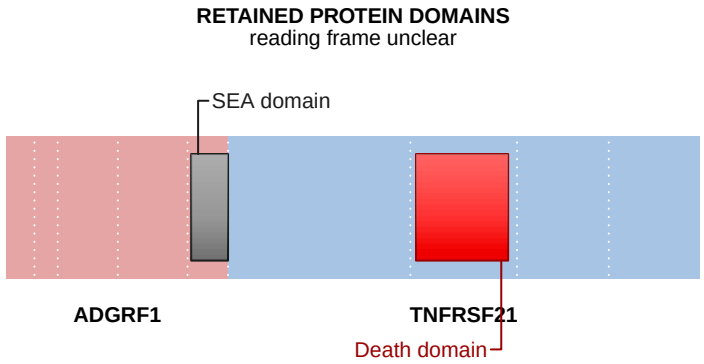
SUPPORTING READ COUNT

Split reads = 86
Discordant mates = 5

translocation
deletion
duplication
inversion



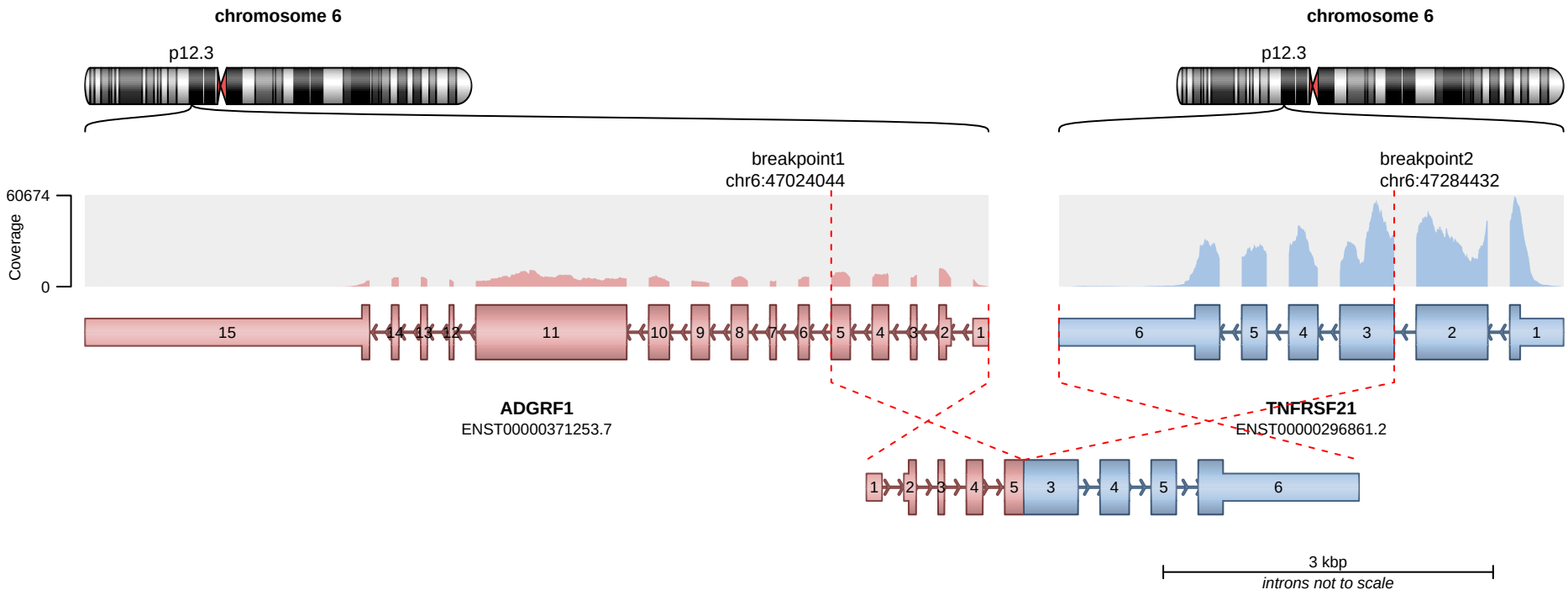


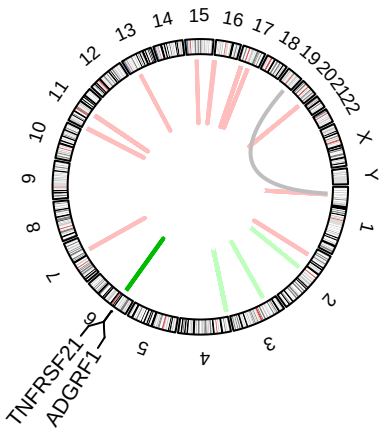


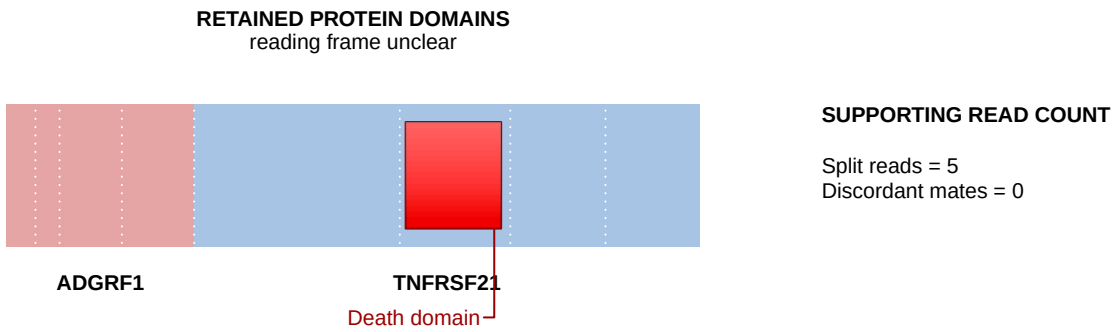
SUPPORTING READ COUNT

Split reads = 13
Discordant mates = 0

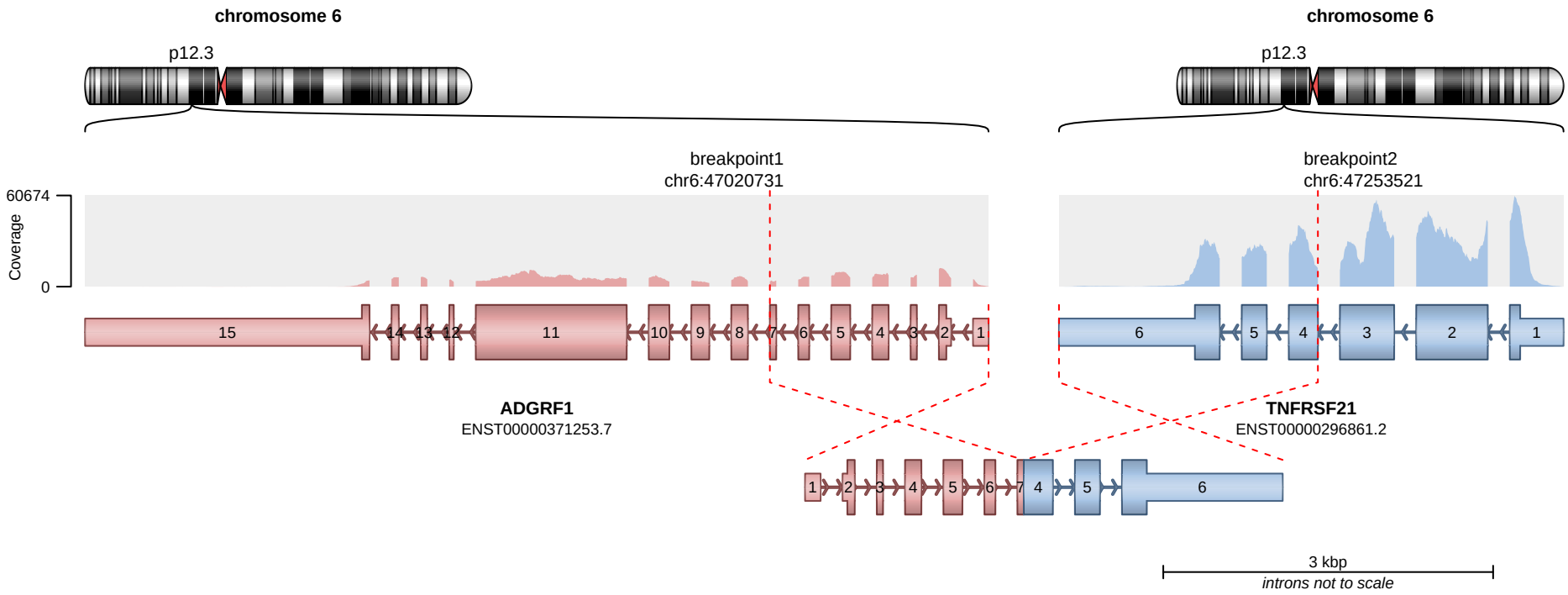
translocation
deletion
duplication
inversion

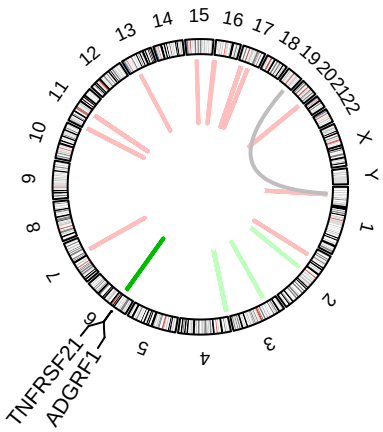


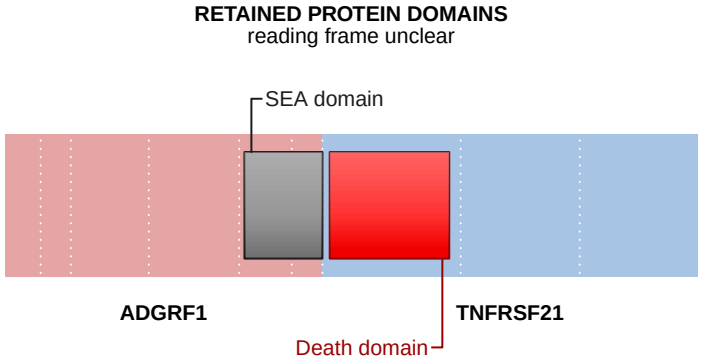




translocation
deletion
duplication
inversion

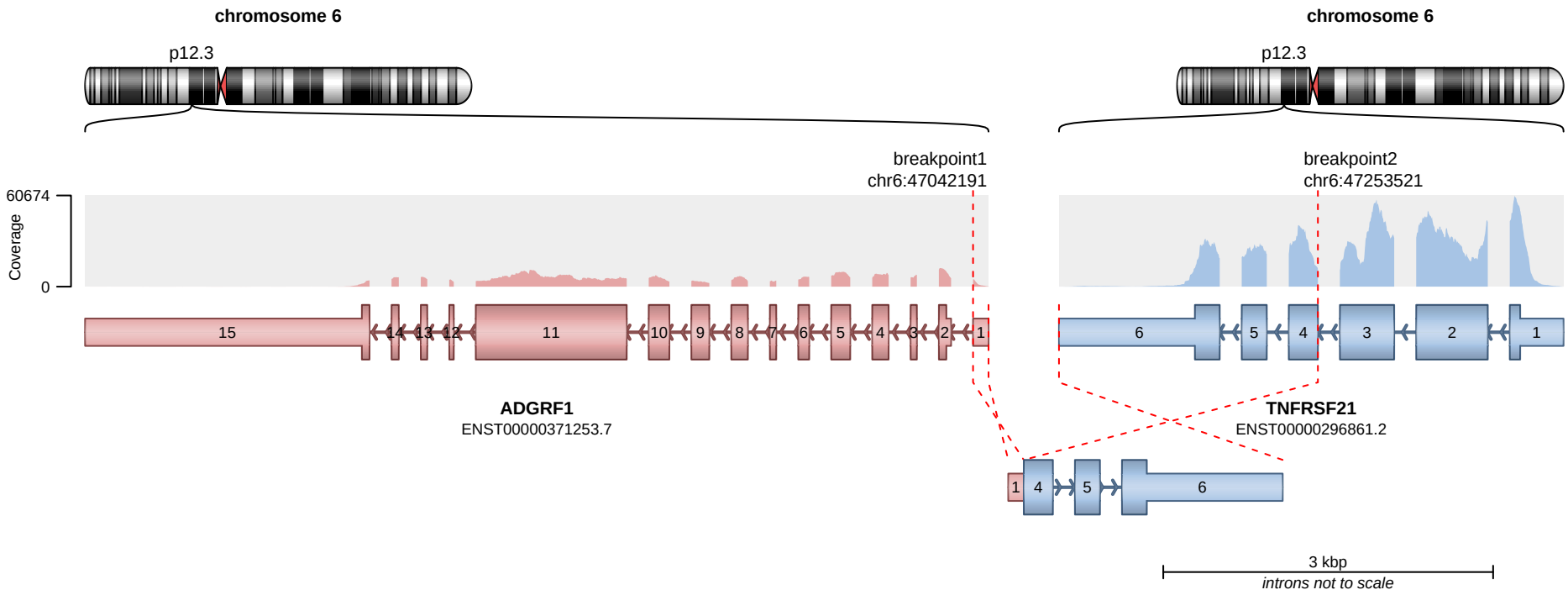


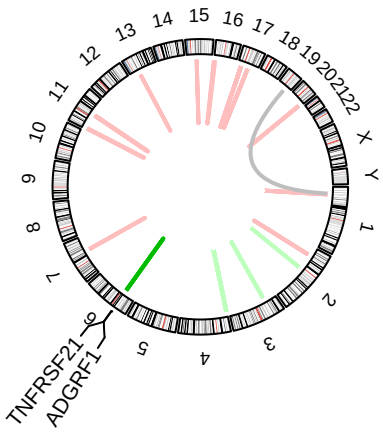


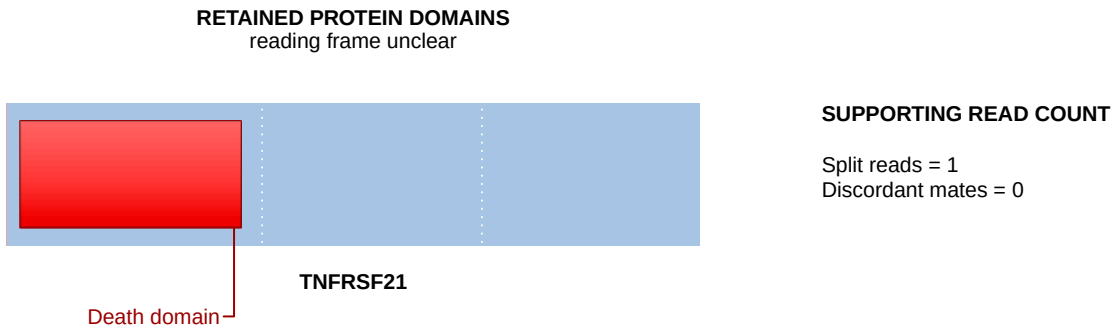


SUPPORTING READ COUNT

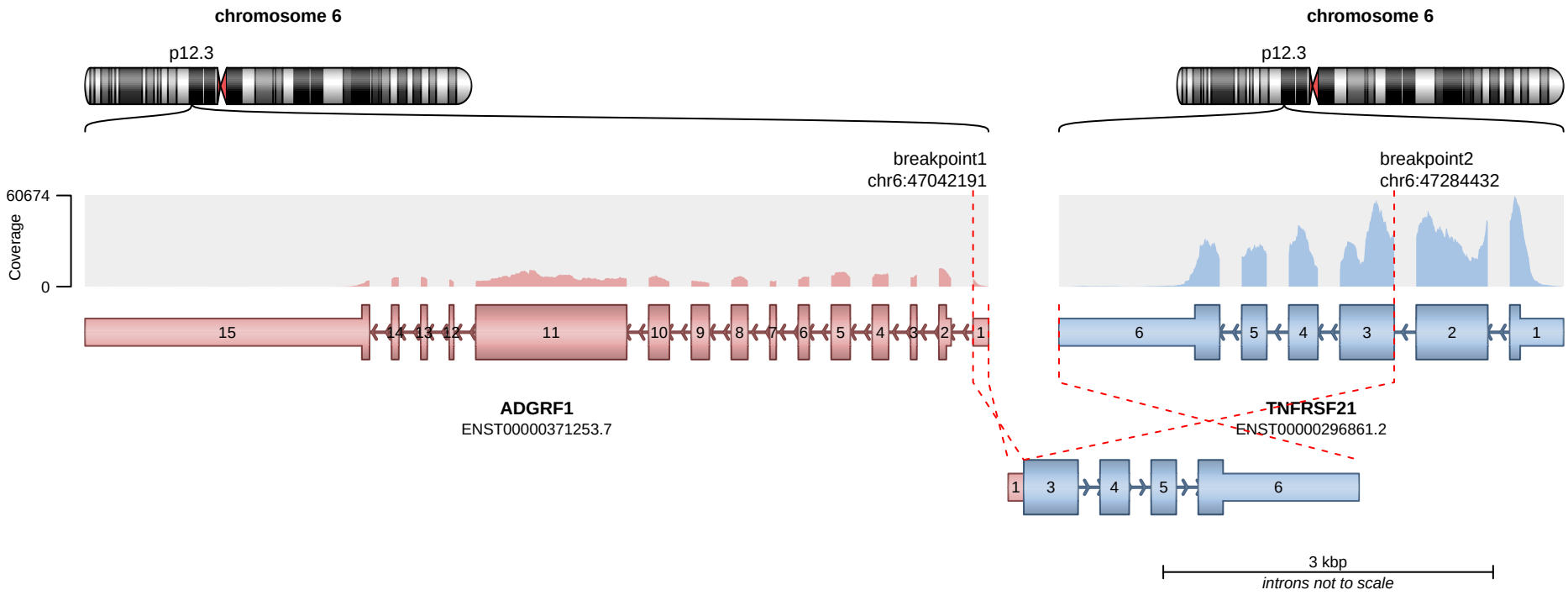
Split reads = 4
Discordant mates = 0

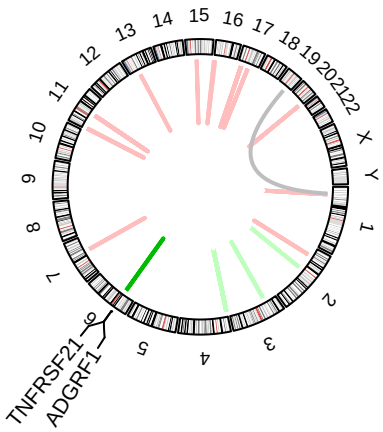






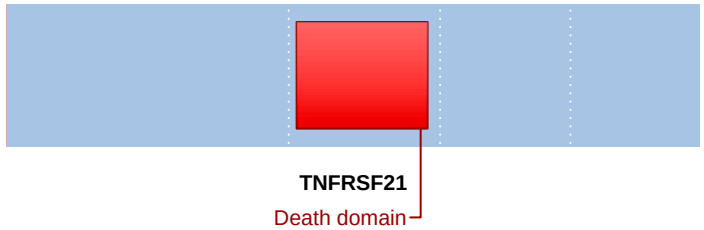
translocation
deletion
duplication
inversion





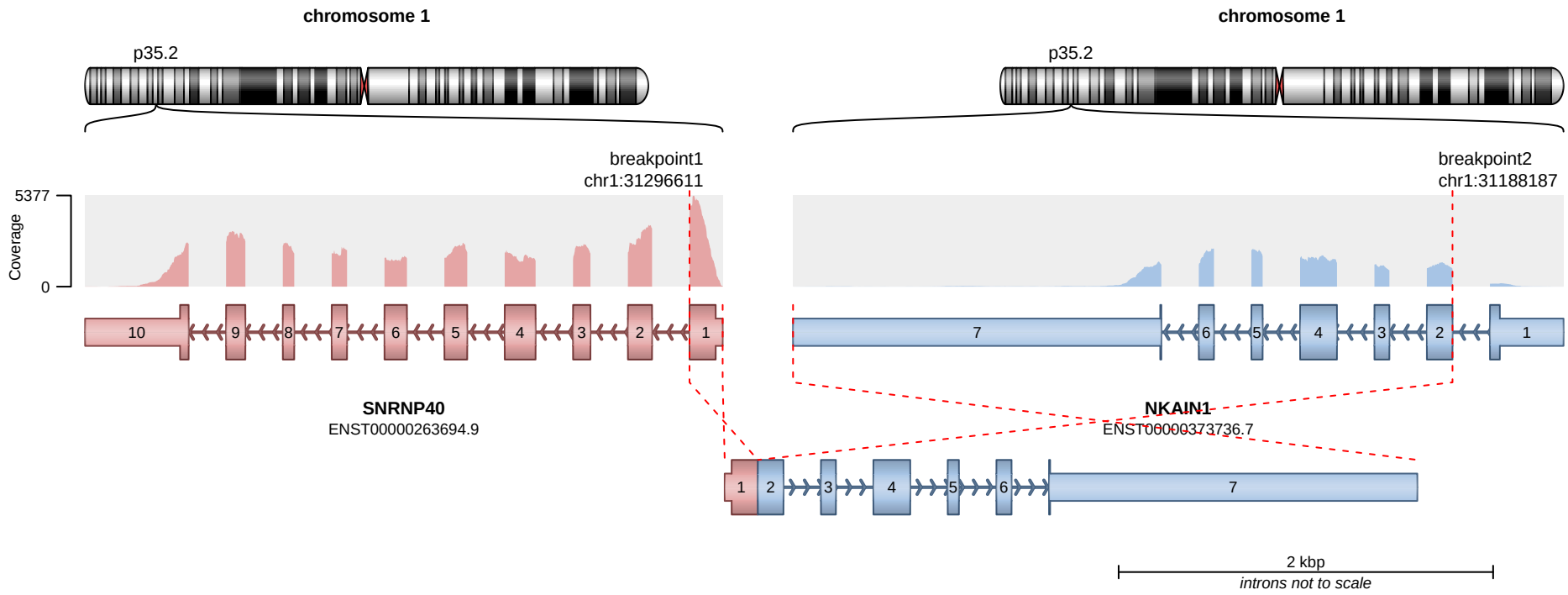
translocation
deletion
duplication
inversion

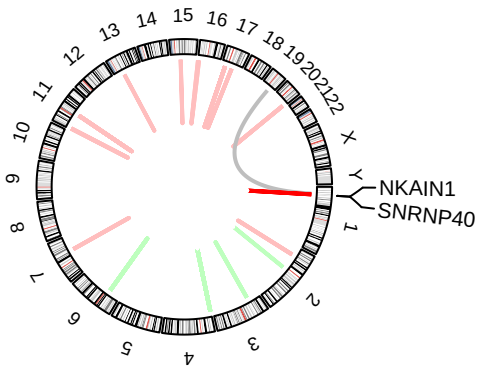
RETAINED PROTEIN DOMAINS
reading frame unclear

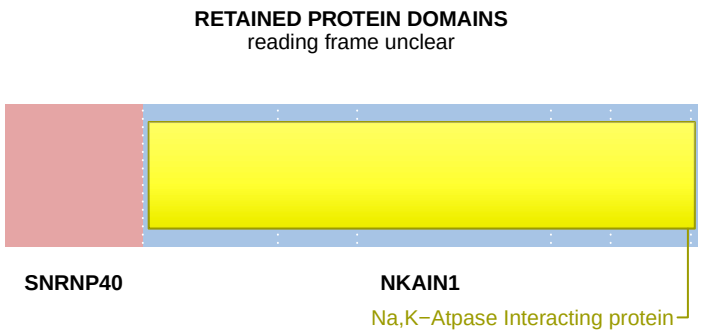


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



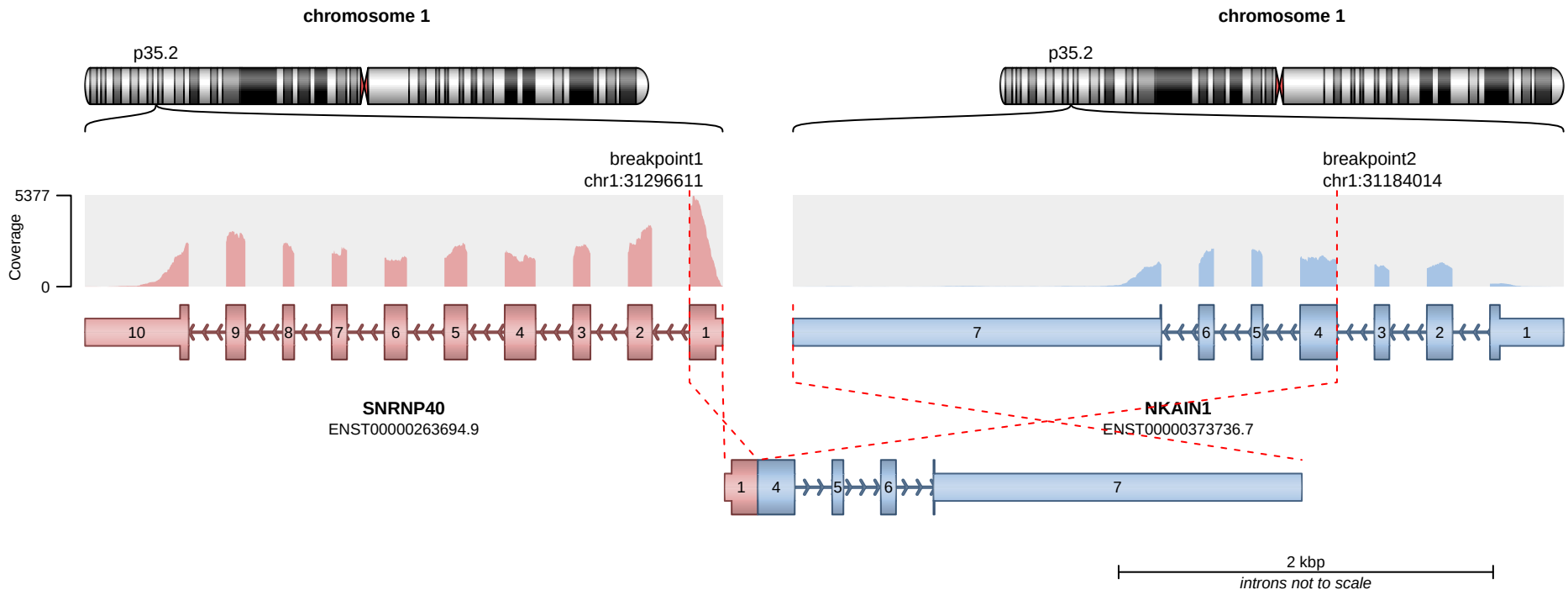


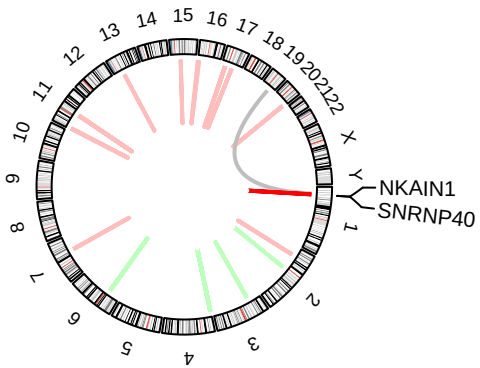


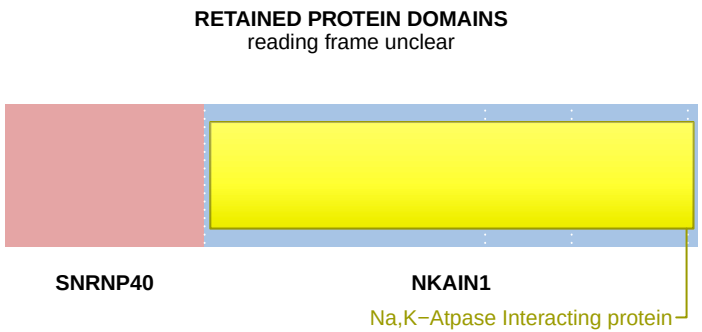
SUPPORTING READ COUNT

Split reads = 319
Discordant mates = 1

translocation
deletion
duplication
inversion



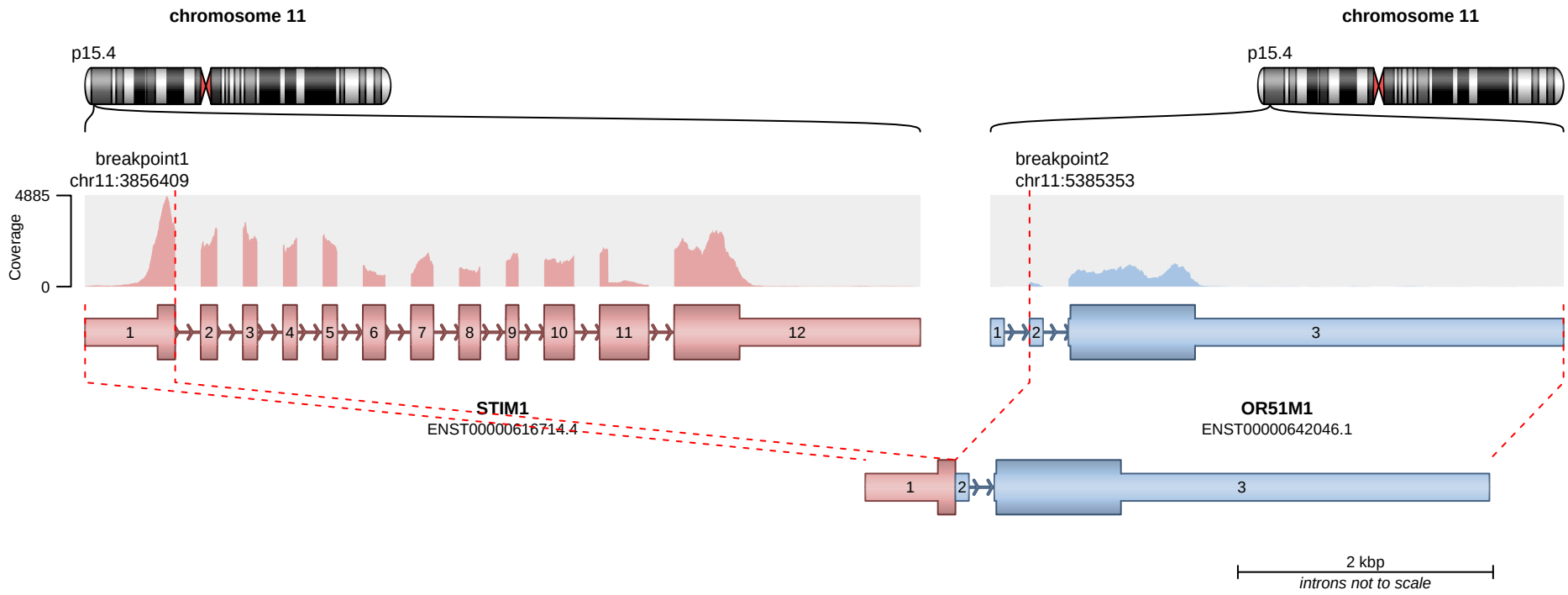


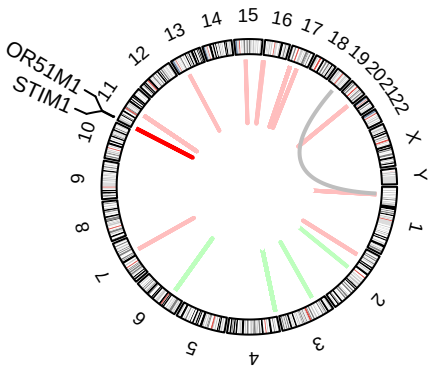


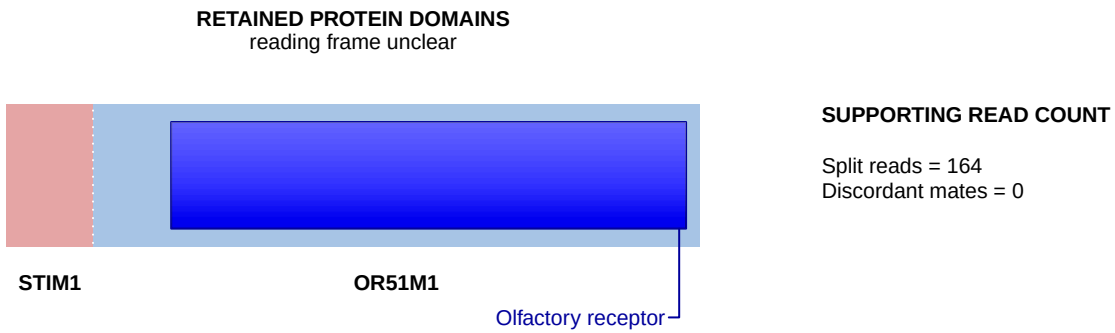
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

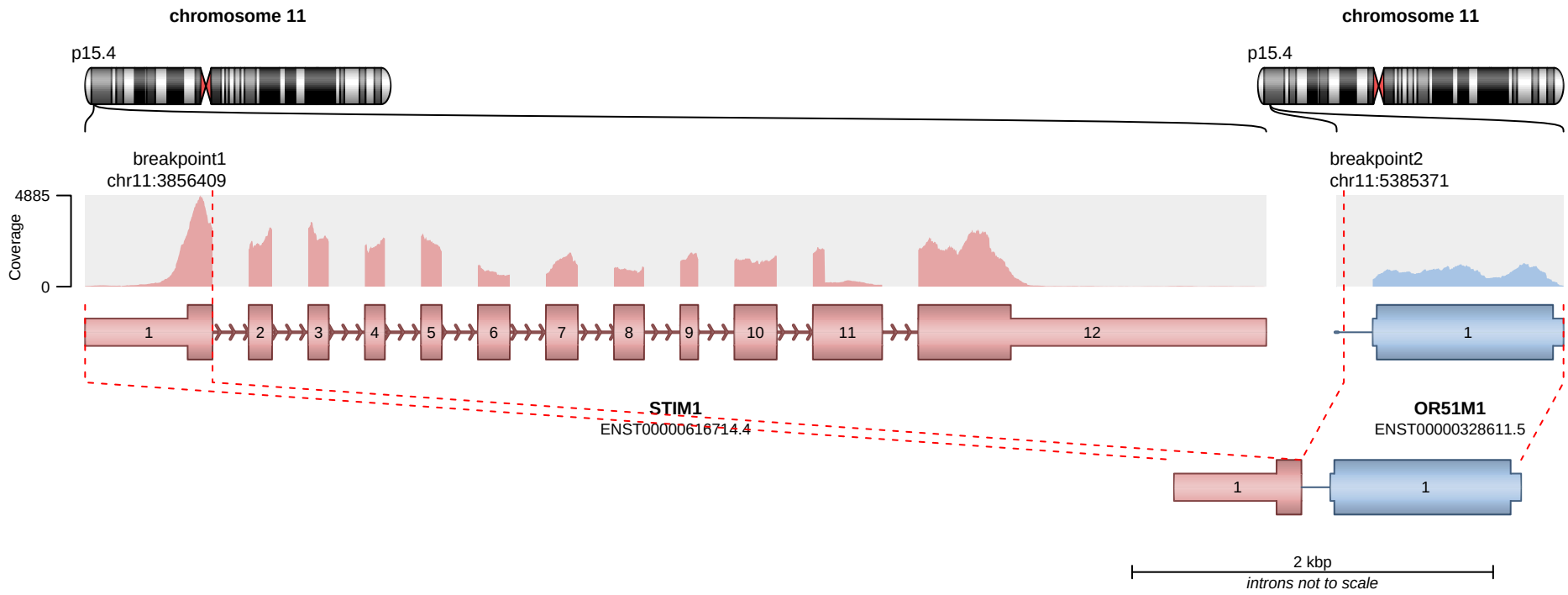
translocation
deletion
duplication
inversion

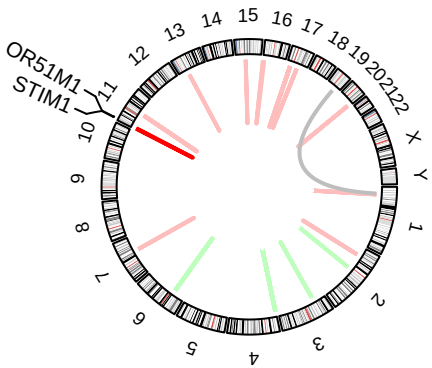




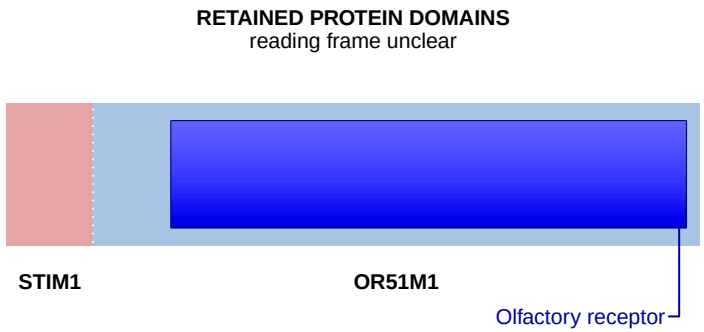


translocation
deletion
duplication
inversion



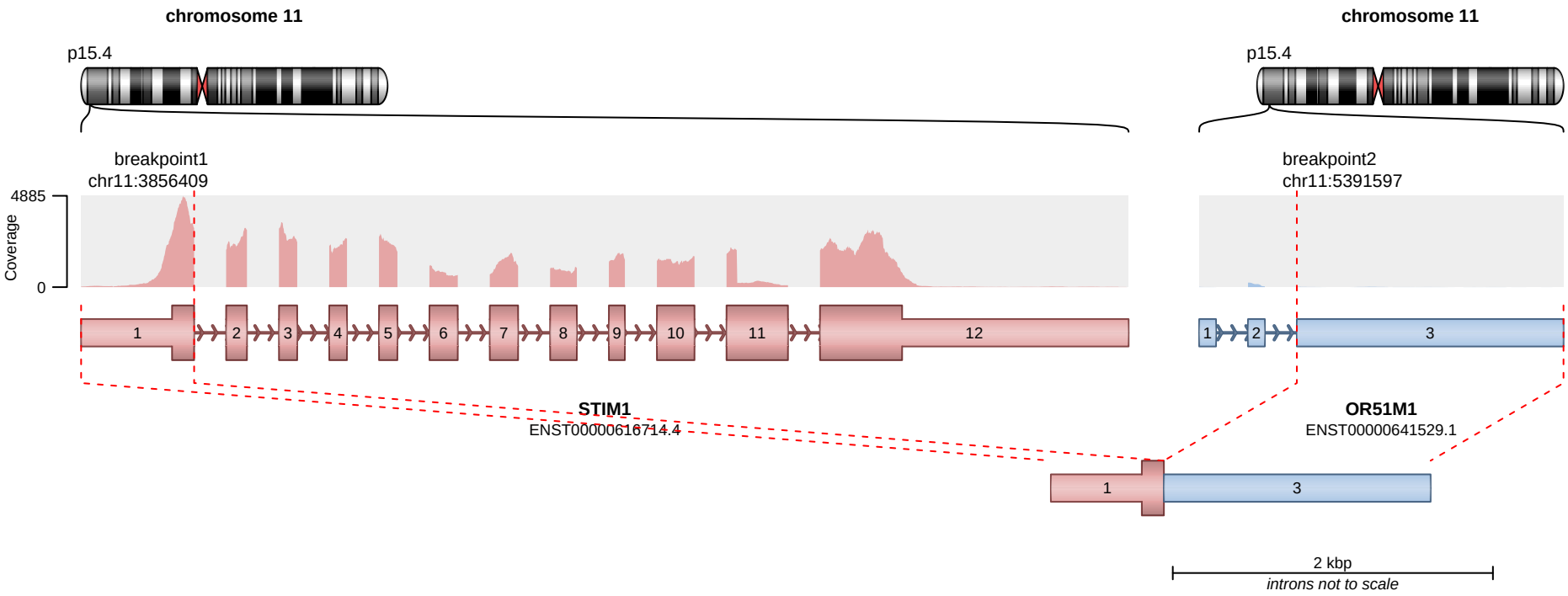


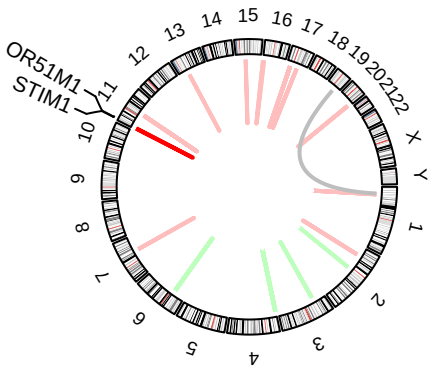
translocation
deletion
duplication
inversion



SUPPORTING READ COUNT

Split reads = 14
Discordant mates = 0



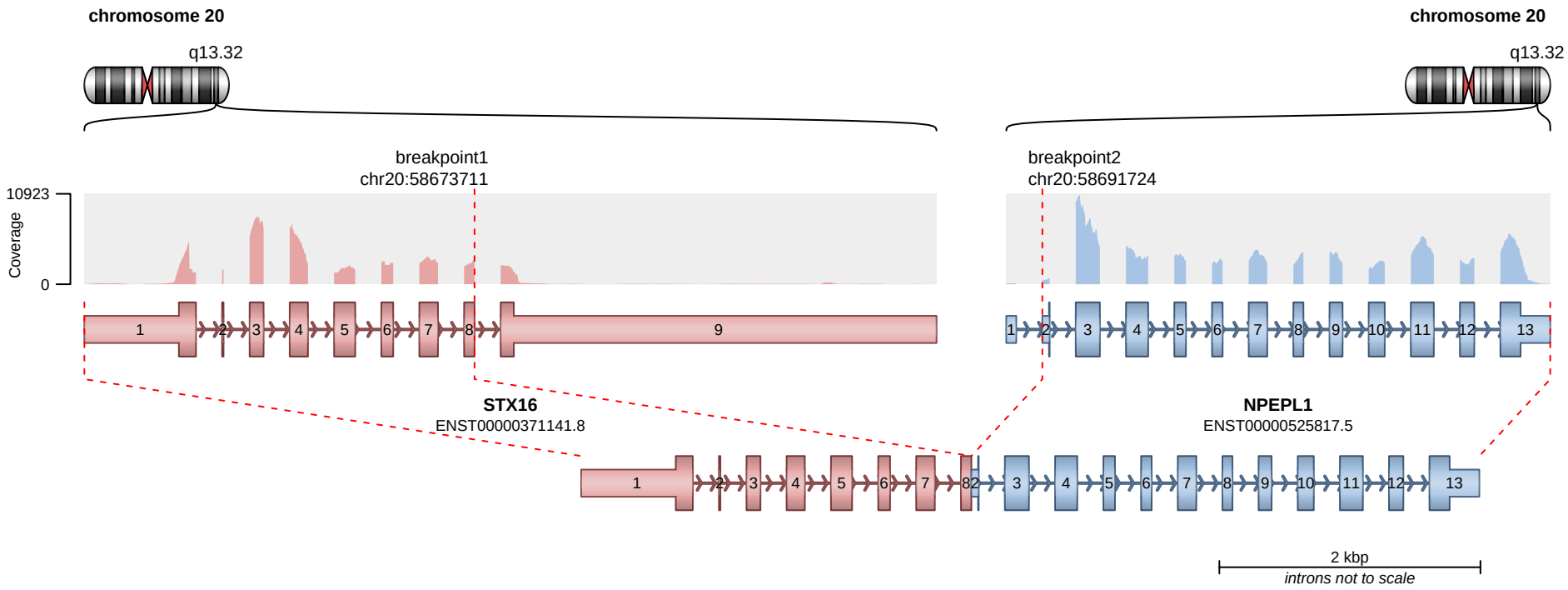


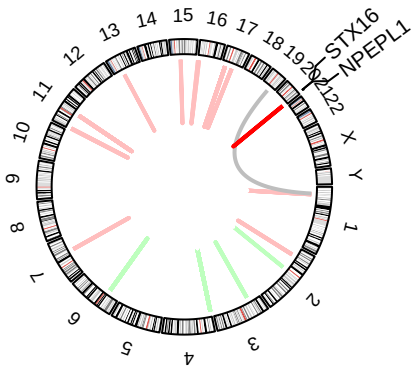
No protein domains retained in fusion.

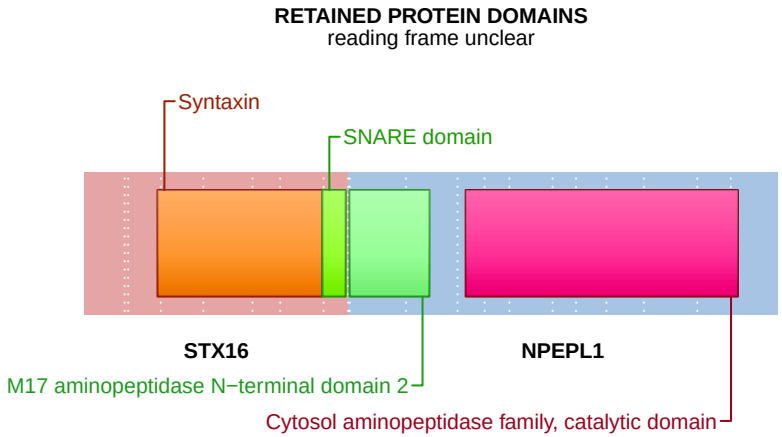
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

translocation
deletion
duplication
inversion



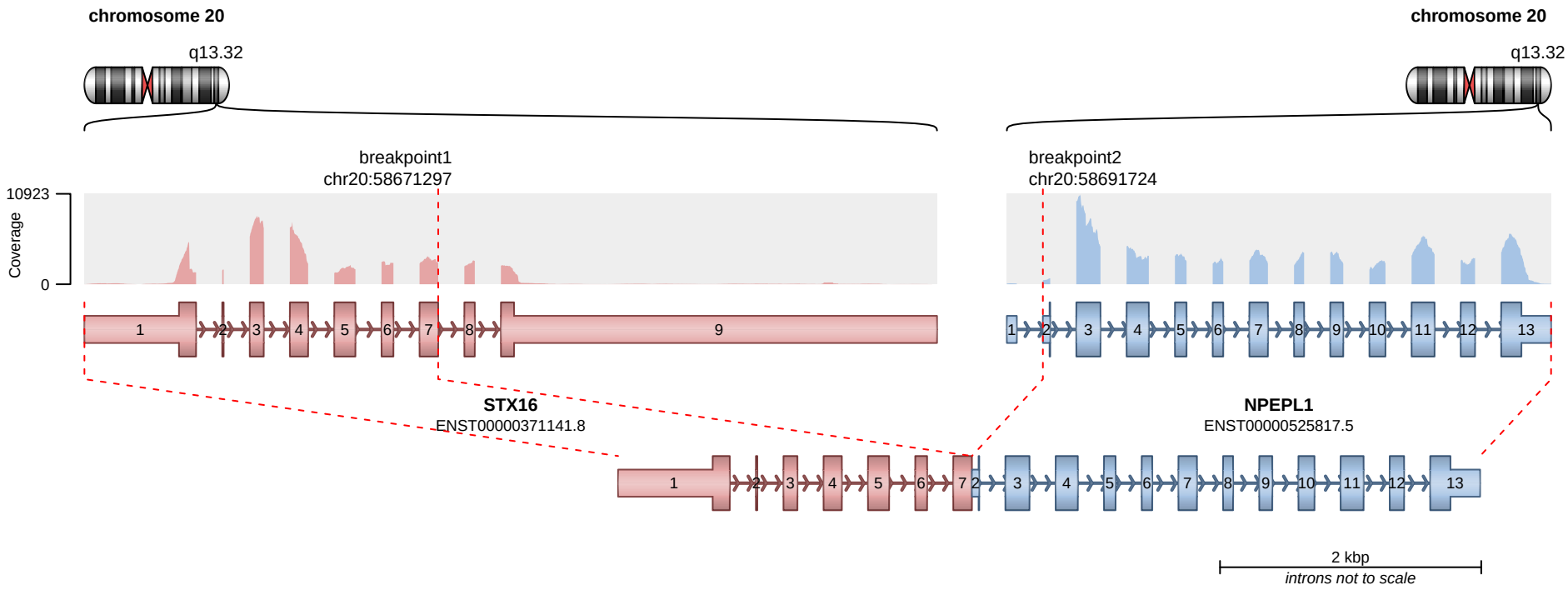


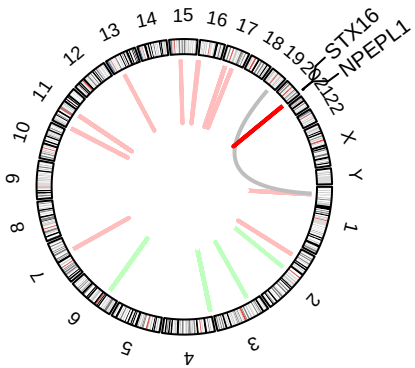


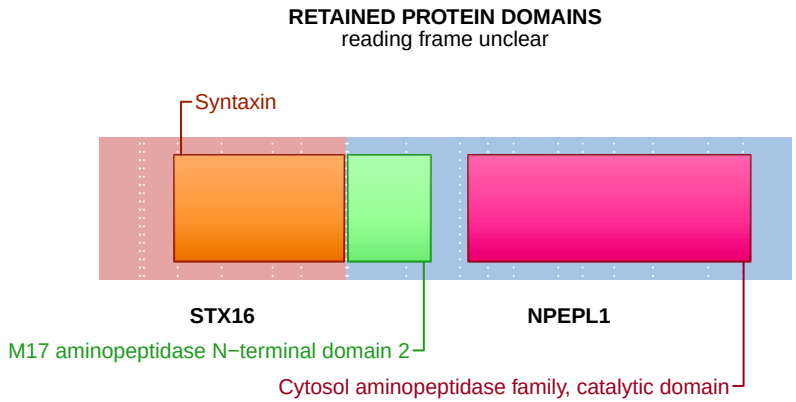
SUPPORTING READ COUNT

Split reads = 154
Discordant mates = 2

translocation
deletion
duplication
inversion



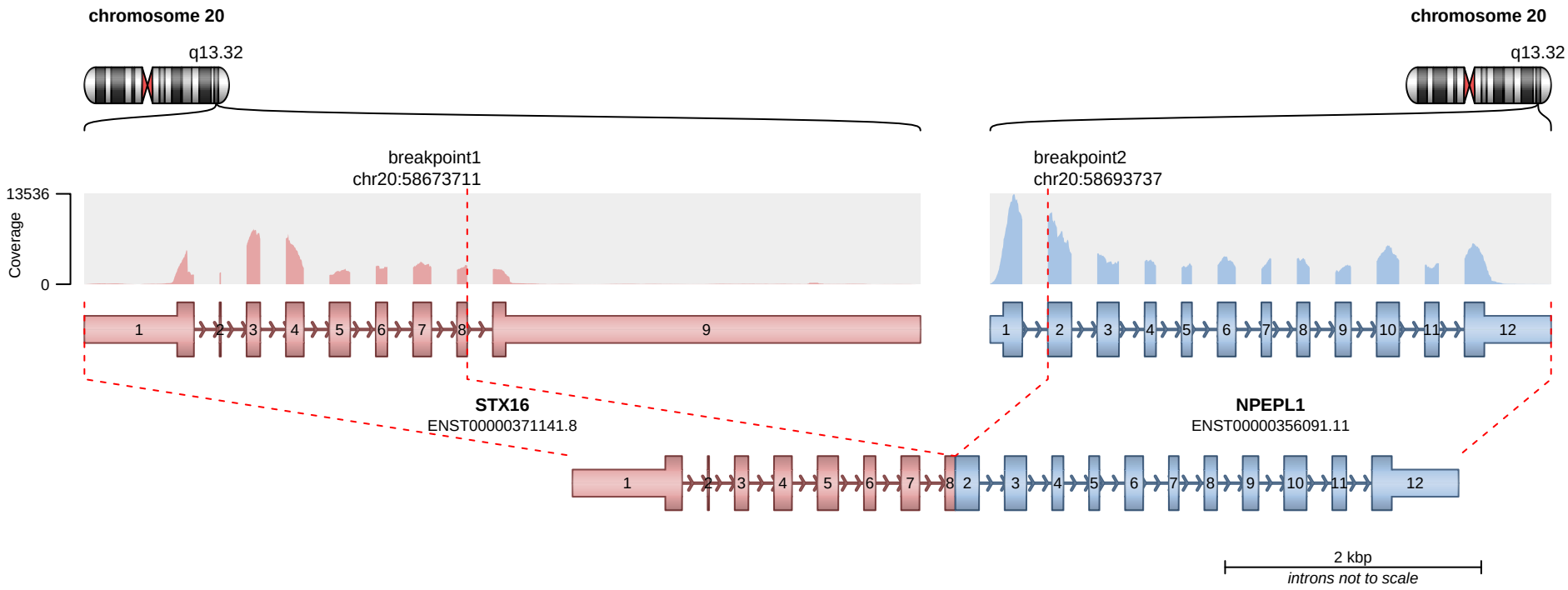


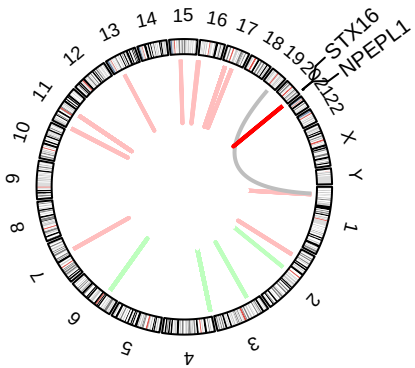


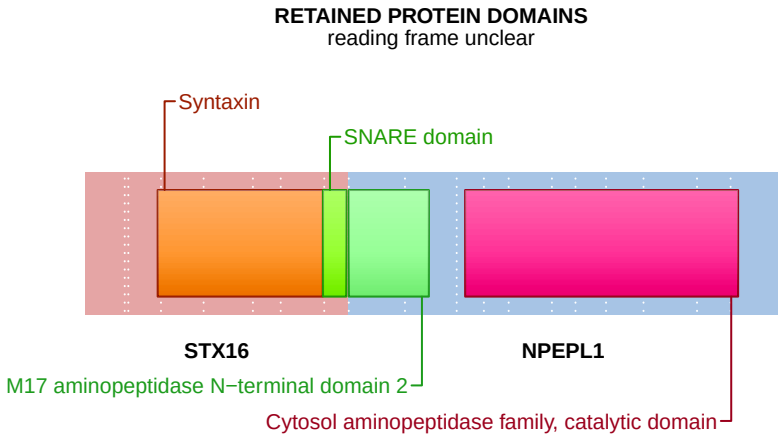
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

translocation
deletion
duplication
inversion



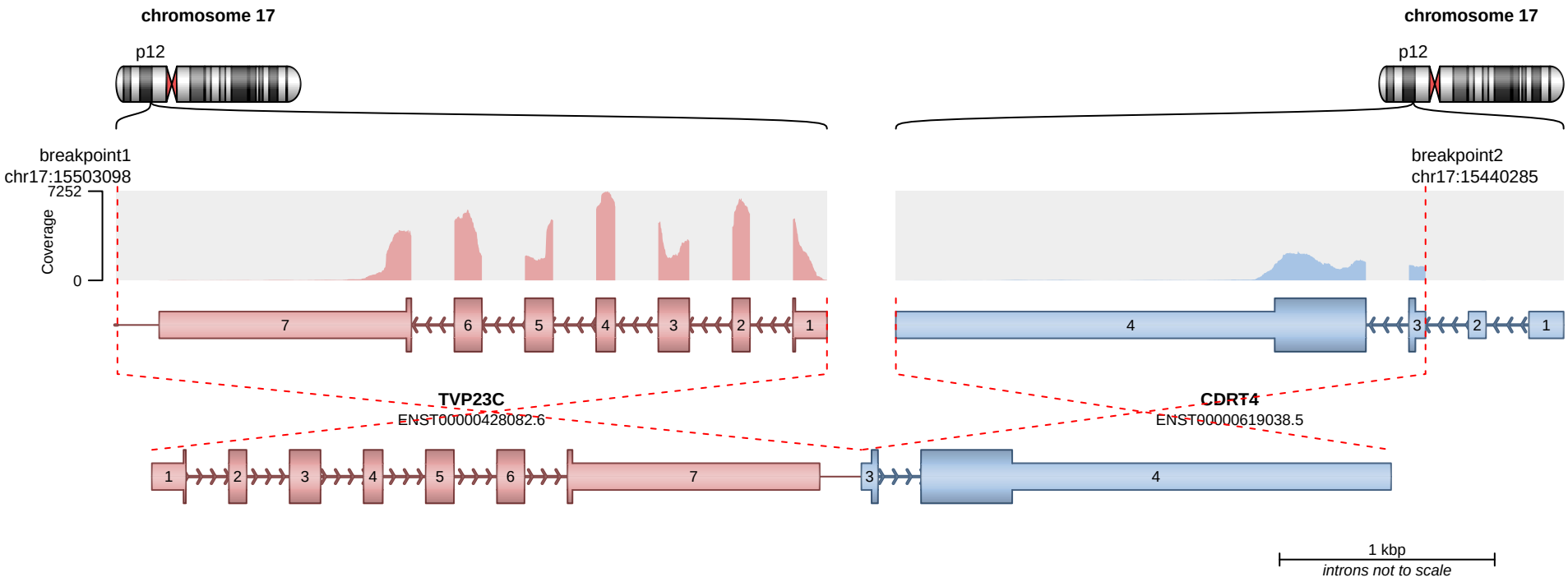


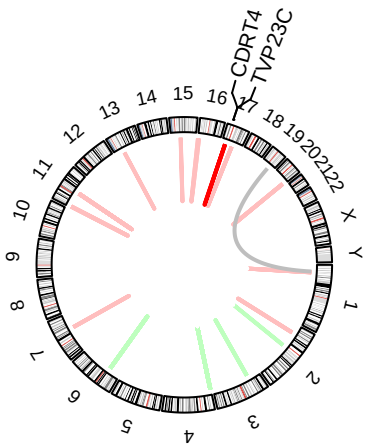


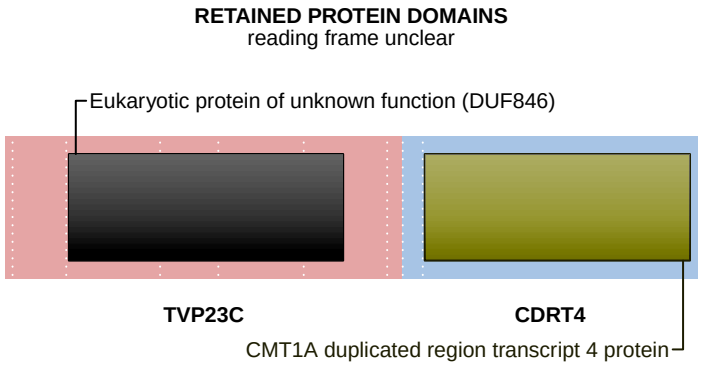
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

translocation
deletion
duplication
inversion



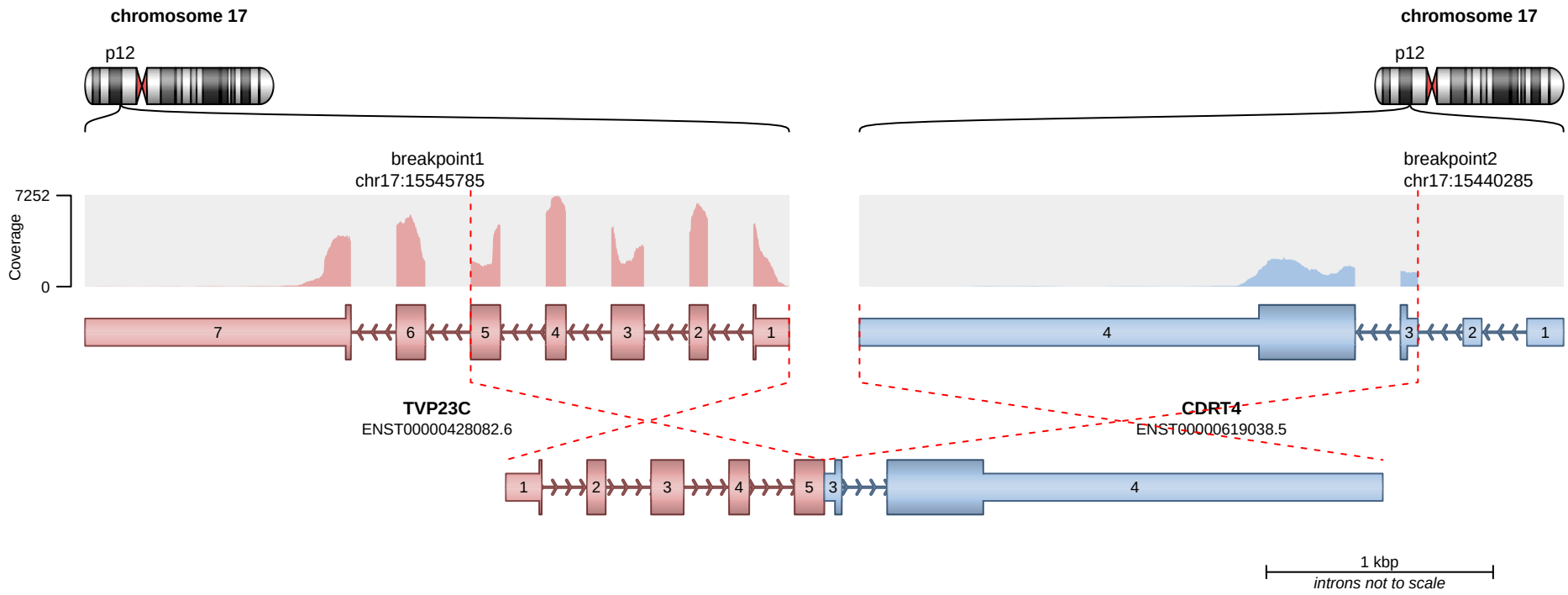


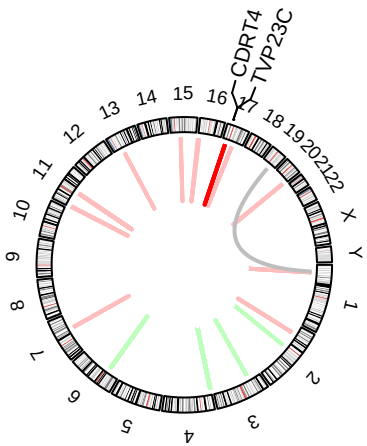


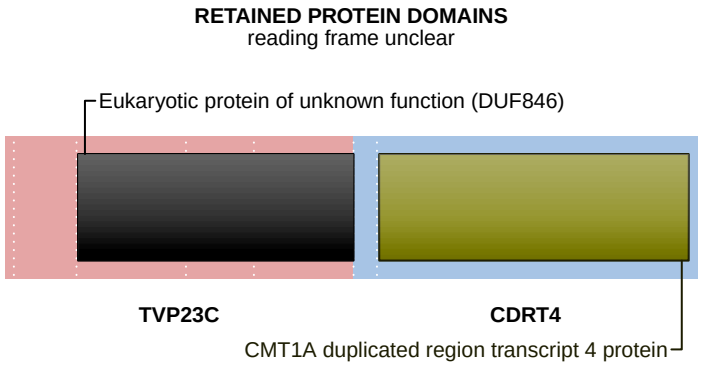
SUPPORTING READ COUNT

Split reads = 153
Discordant mates = 4

translocation
deletion
duplication
inversion



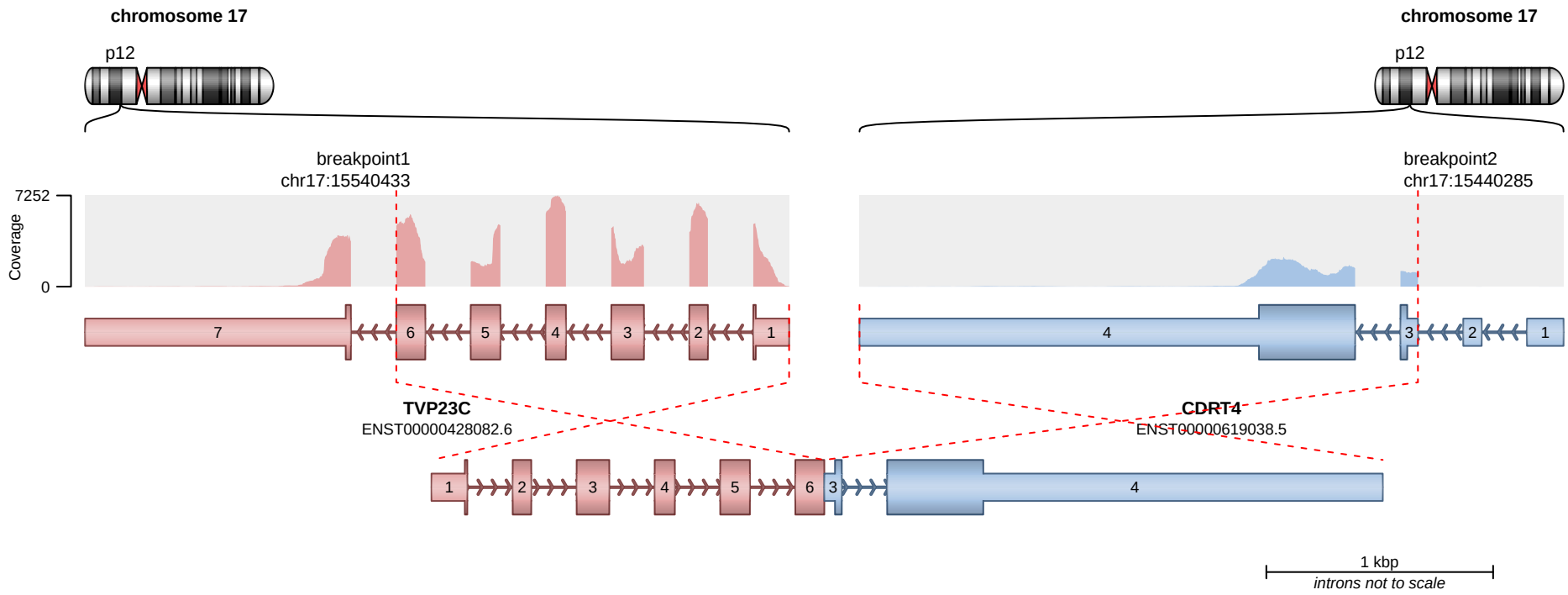


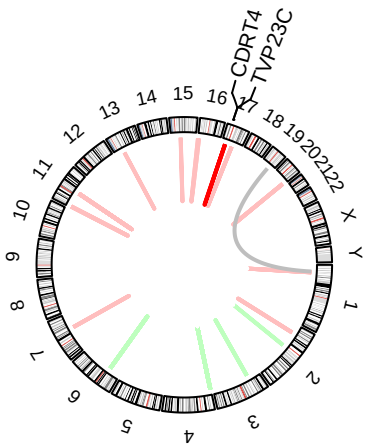


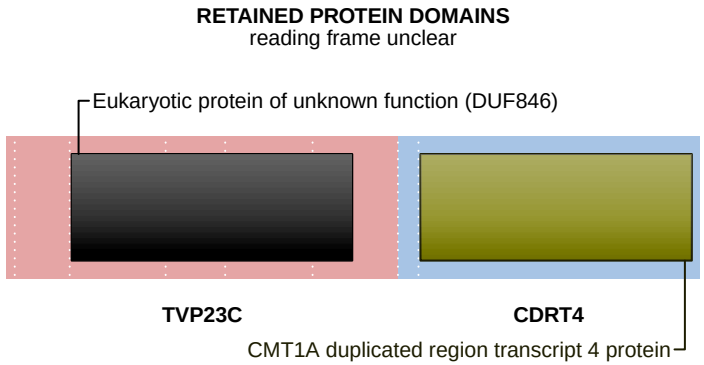
SUPPORTING READ COUNT

Split reads = 118
Discordant mates = 1

translocation
deletion
duplication
inversion



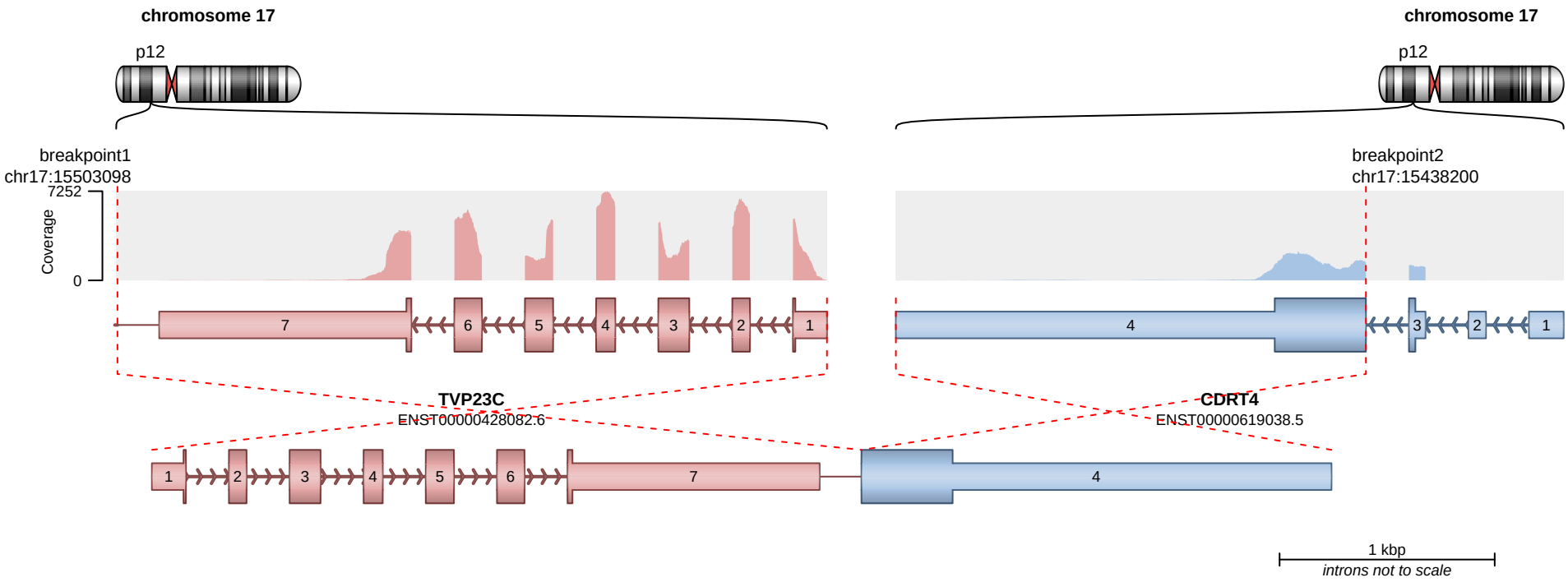


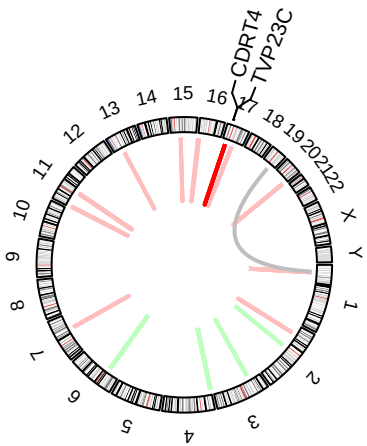


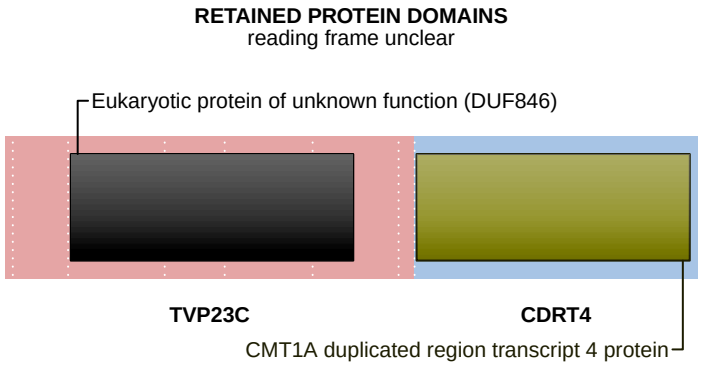
SUPPORTING READ COUNT

Split reads = 79
Discordant mates = 2

translocation
deletion
duplication
inversion



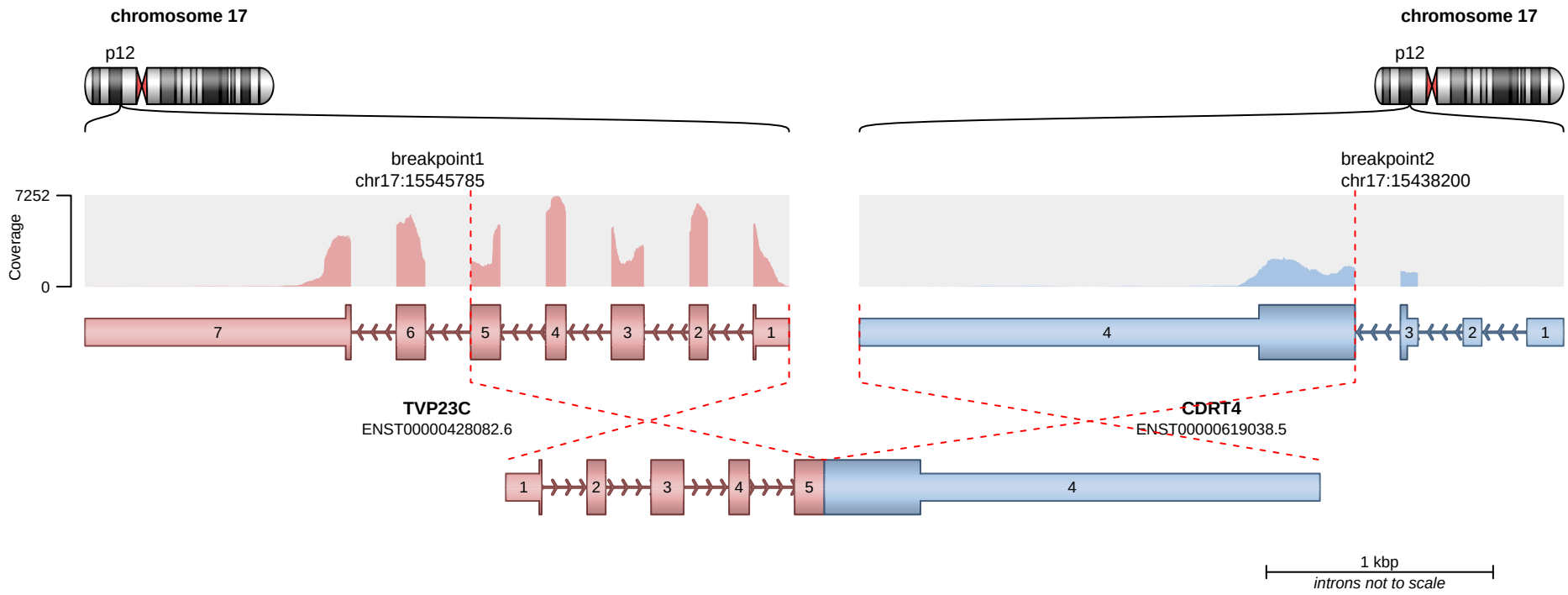


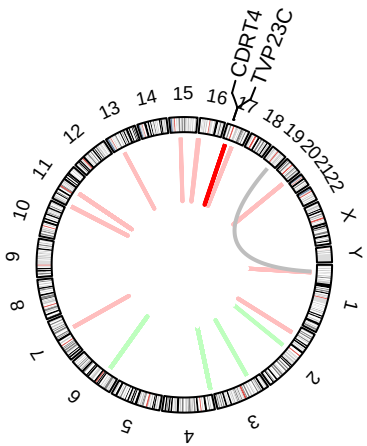


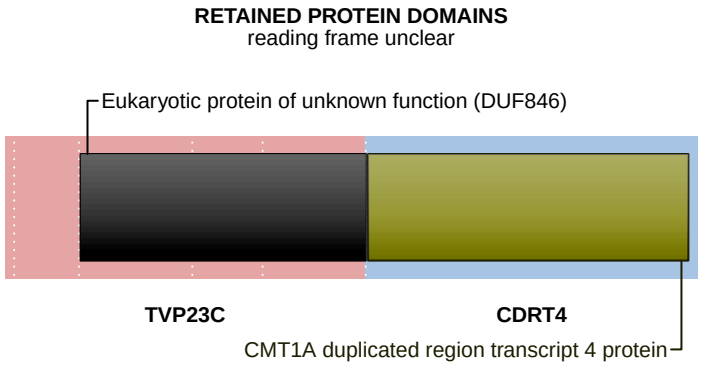
SUPPORTING READ COUNT

Split reads = 41
Discordant mates = 0

translocation
deletion
duplication
inversion



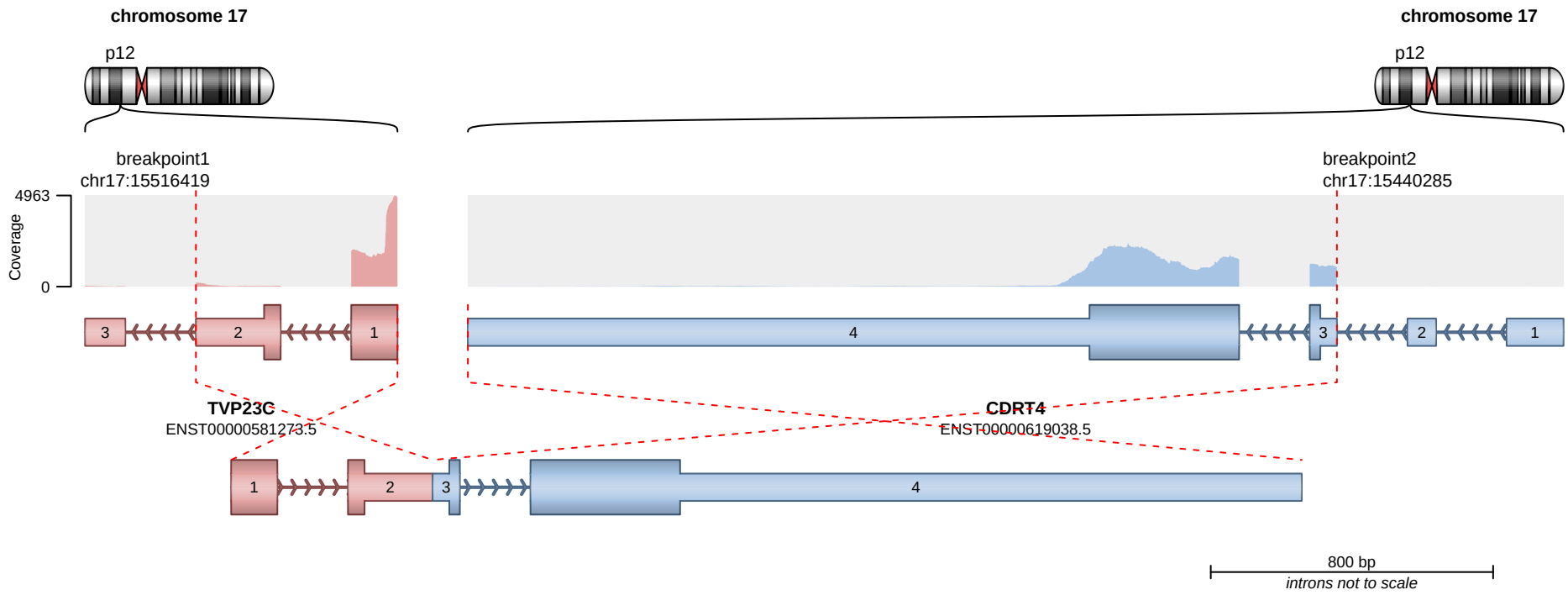


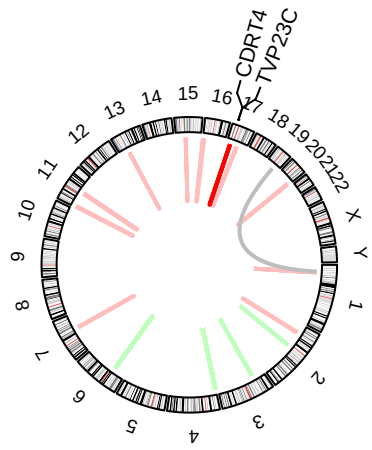


SUPPORTING READ COUNT

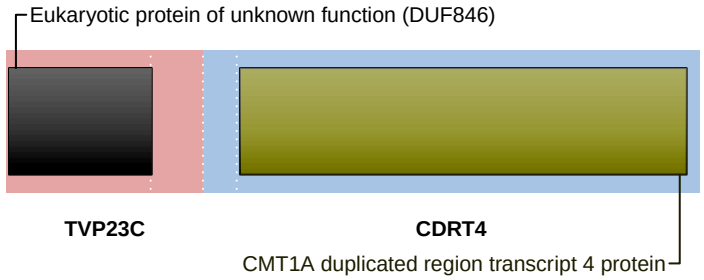
Split reads = 30
Discordant mates = 0

translocation
deletion
duplication
inversion





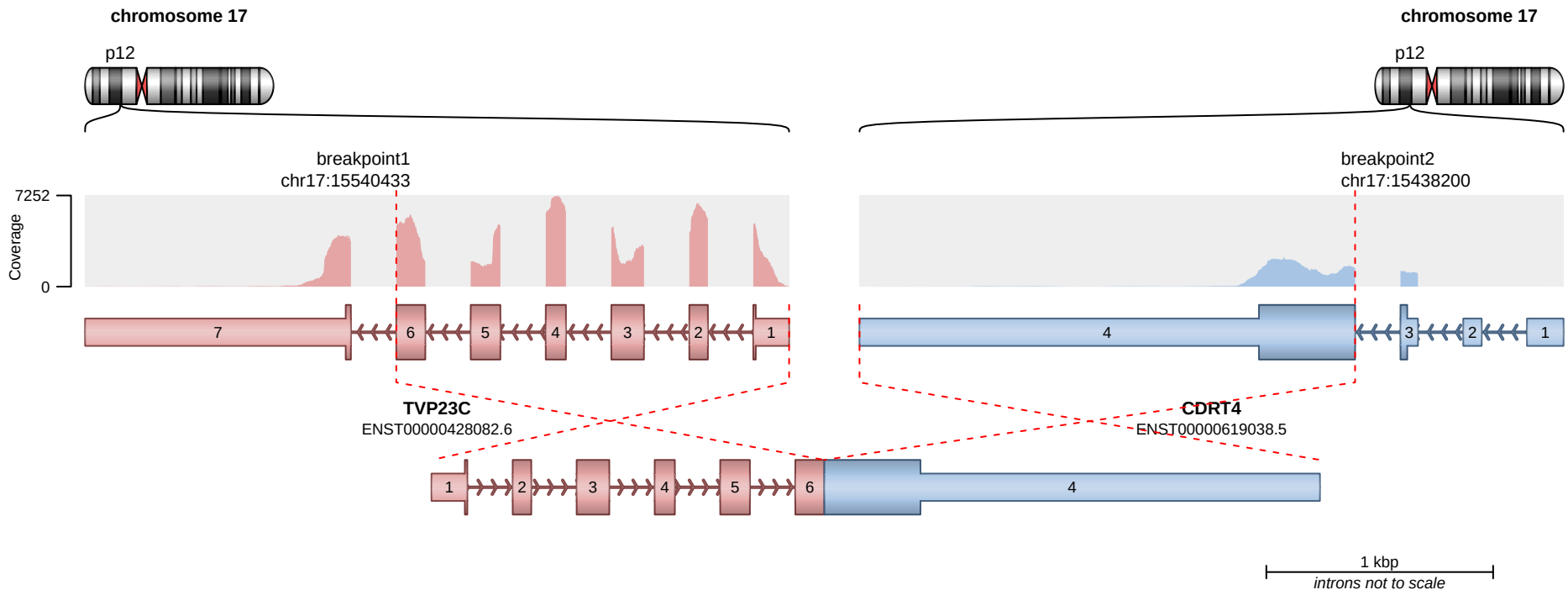
RETAINED PROTEIN DOMAINS
reading frame unclear

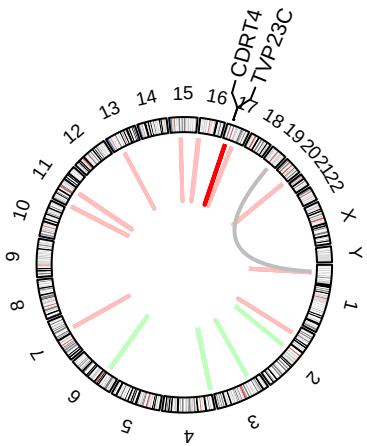


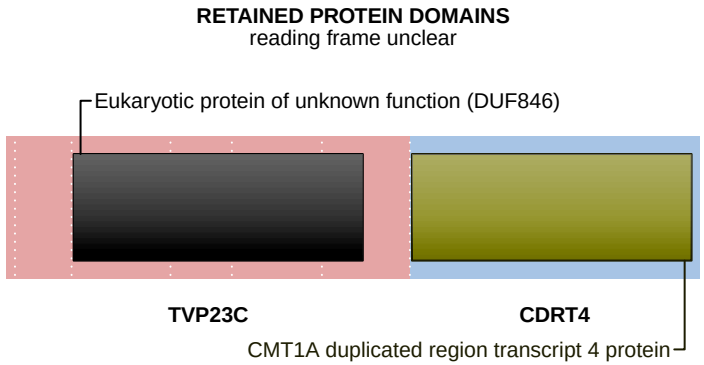
SUPPORTING READ COUNT

Split reads = 23
Discordant mates = 2

translocation
deletion
duplication
inversion



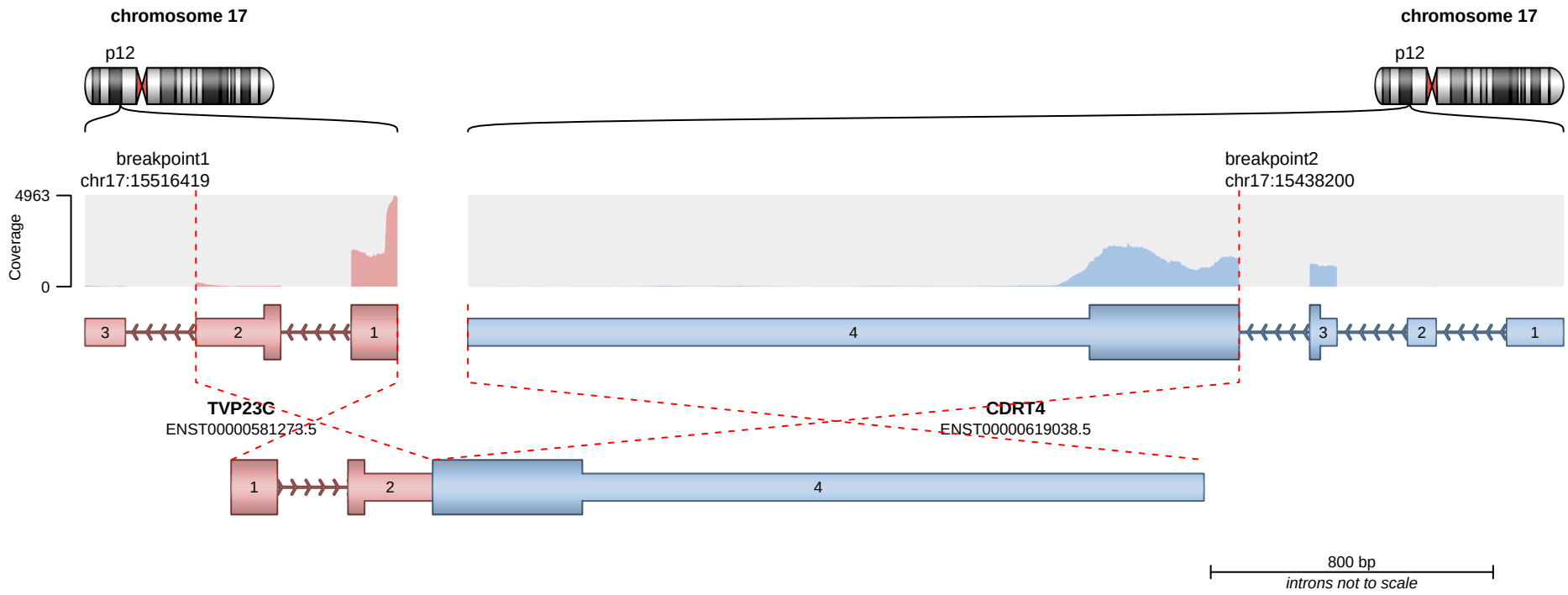


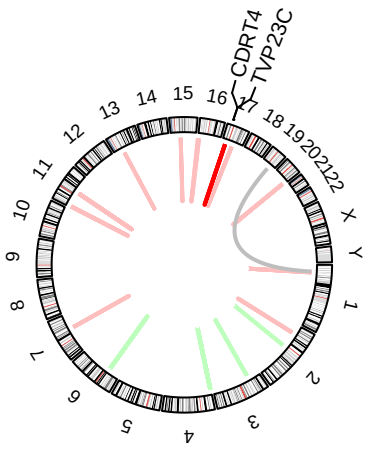


SUPPORTING READ COUNT

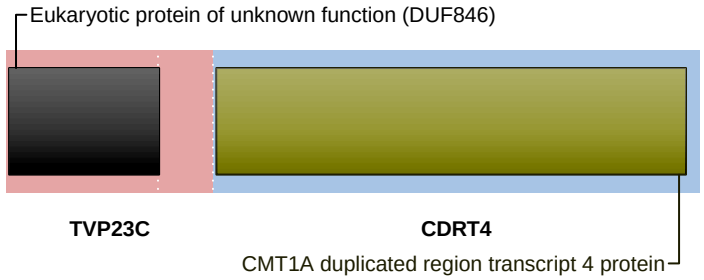
Split reads = 13
Discordant mates = 0

translocation
deletion
duplication
inversion





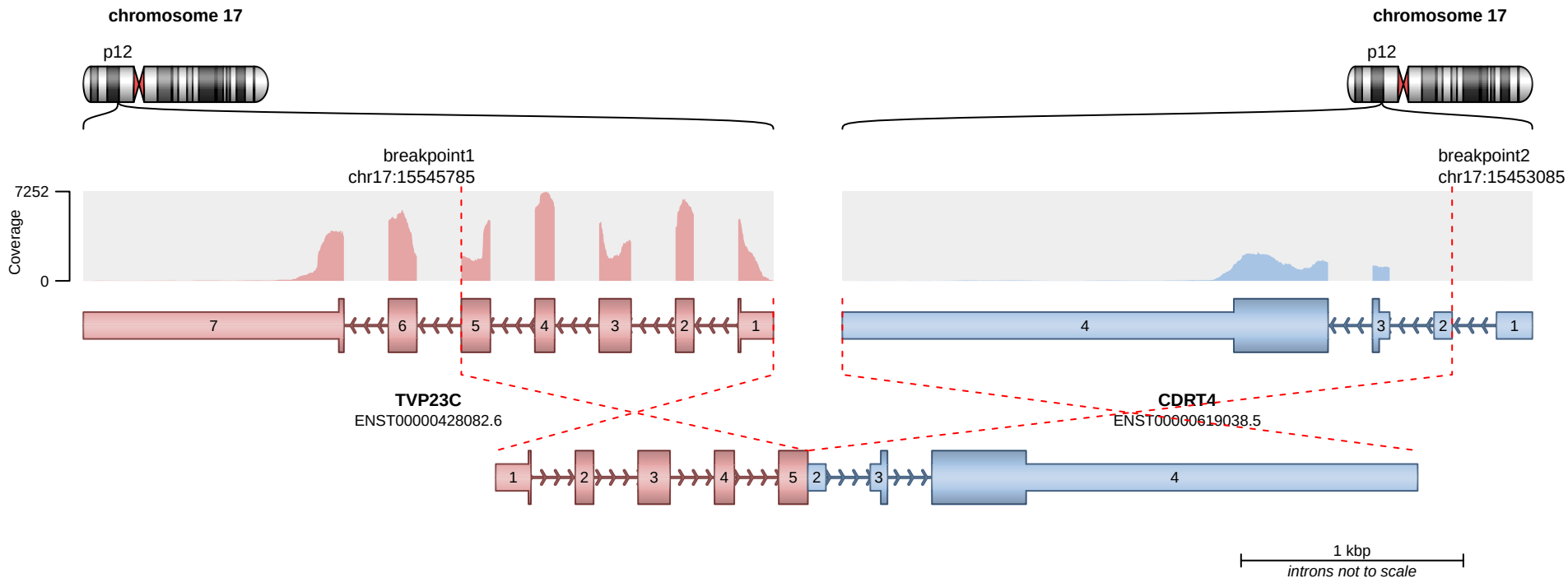
RETAINED PROTEIN DOMAINS
reading frame unclear

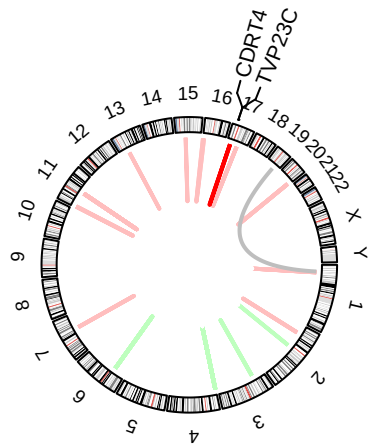


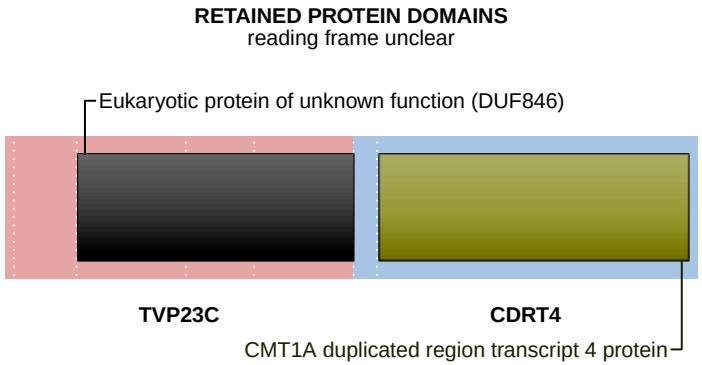
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

translocation
deletion
duplication
inversion



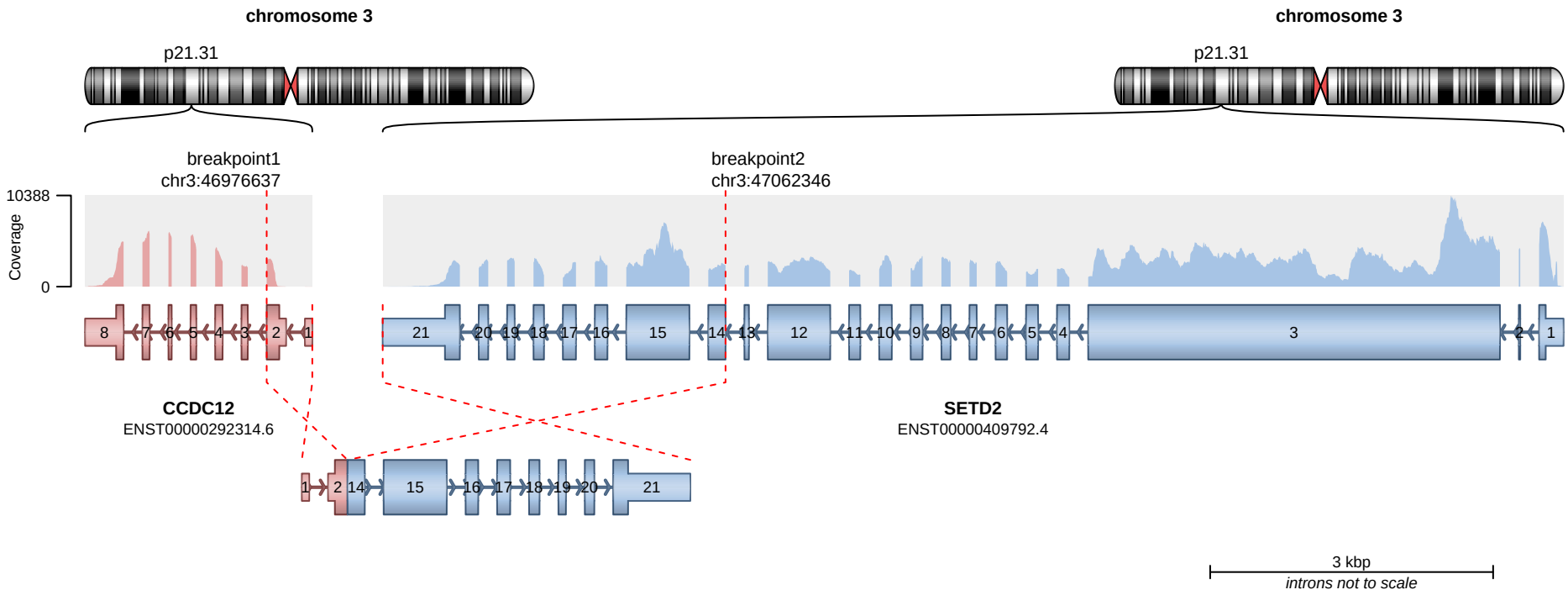


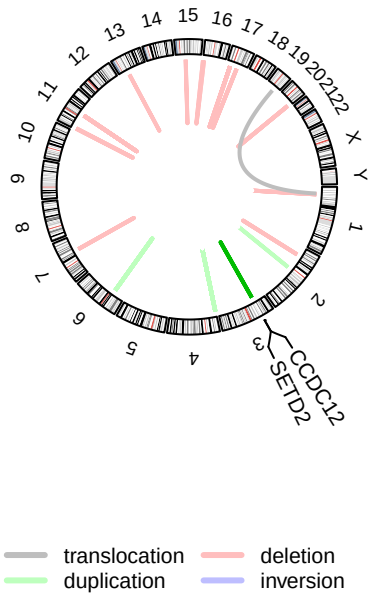


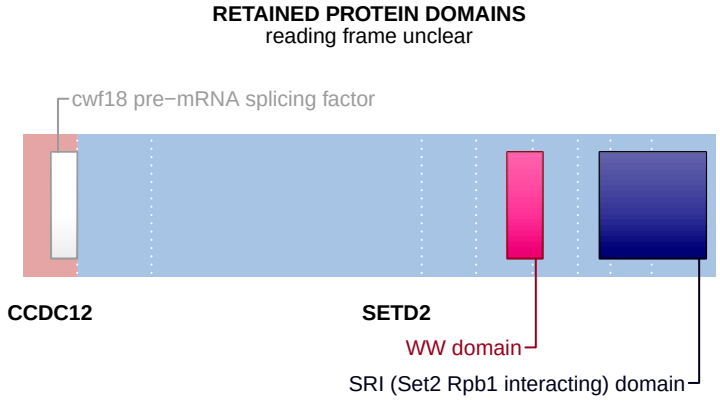
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 1

translocation
deletion
duplication
inversion

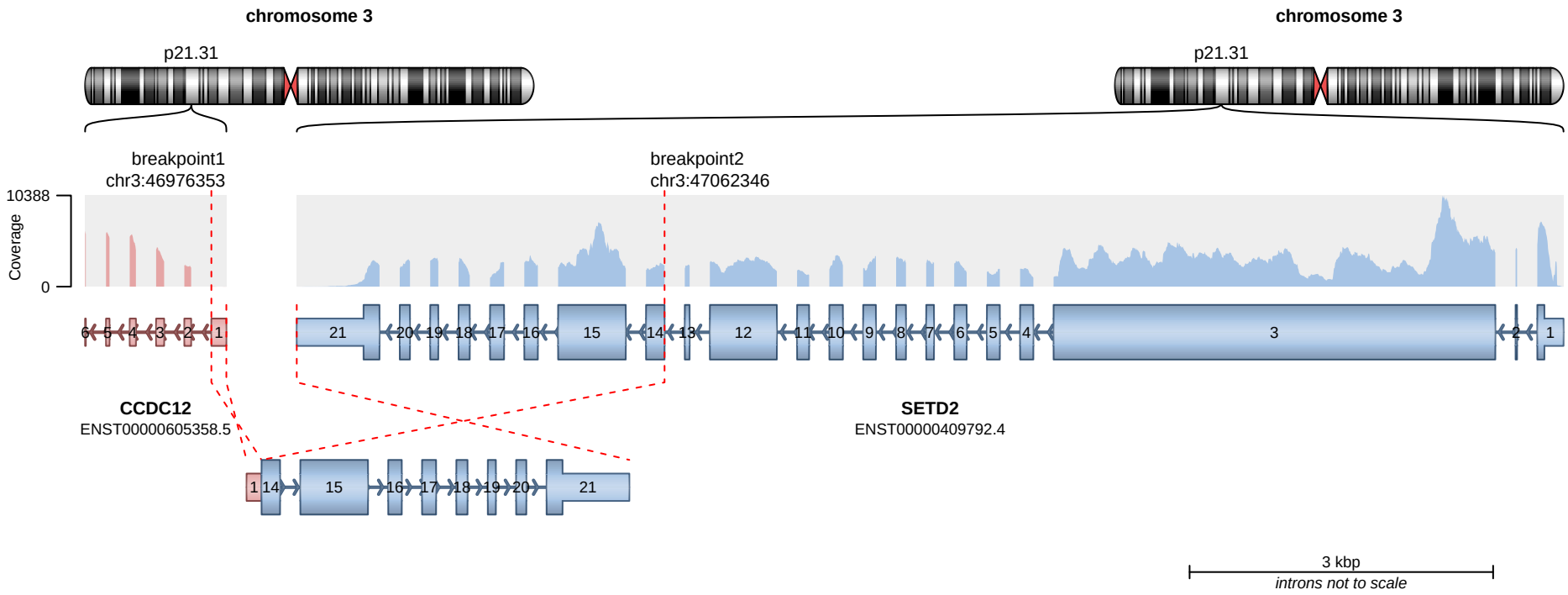


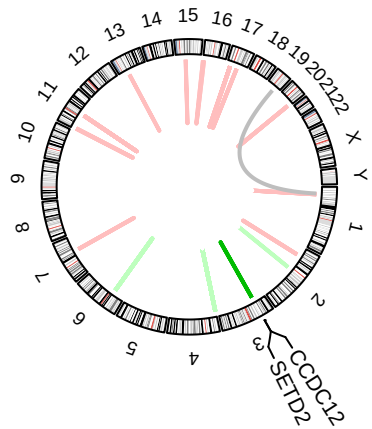


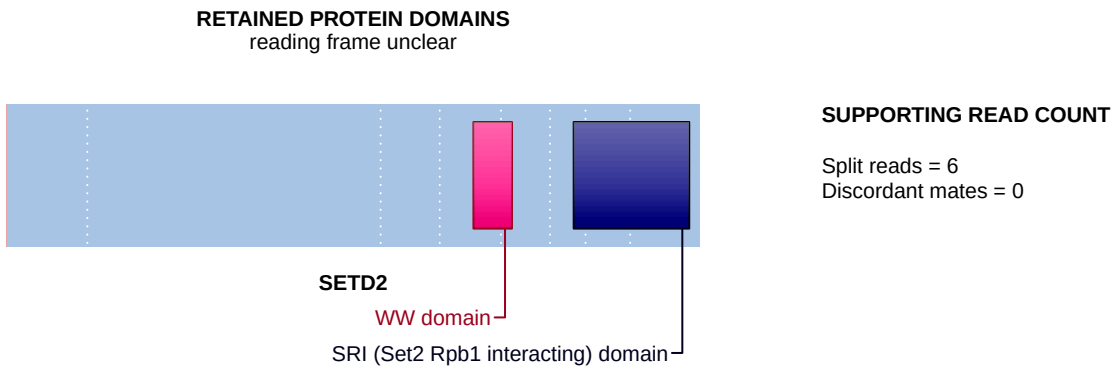


SUPPORTING READ COUNT

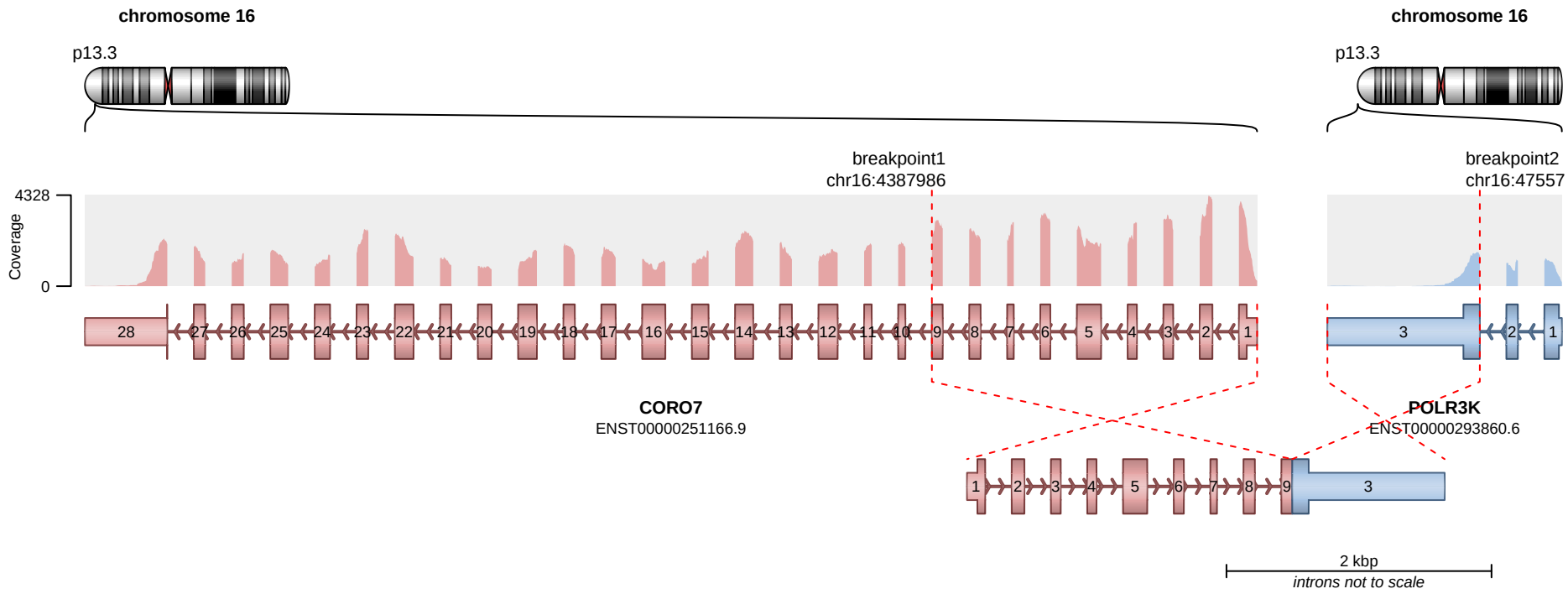
Split reads = 141
Discordant mates = 0

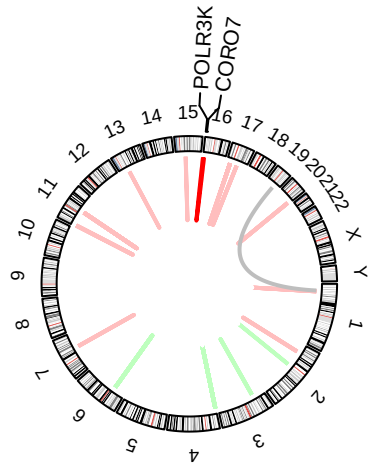


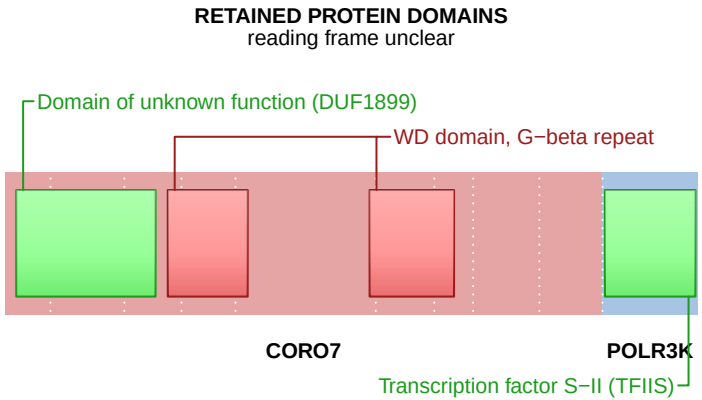




translocation
deletion
duplication
inversion



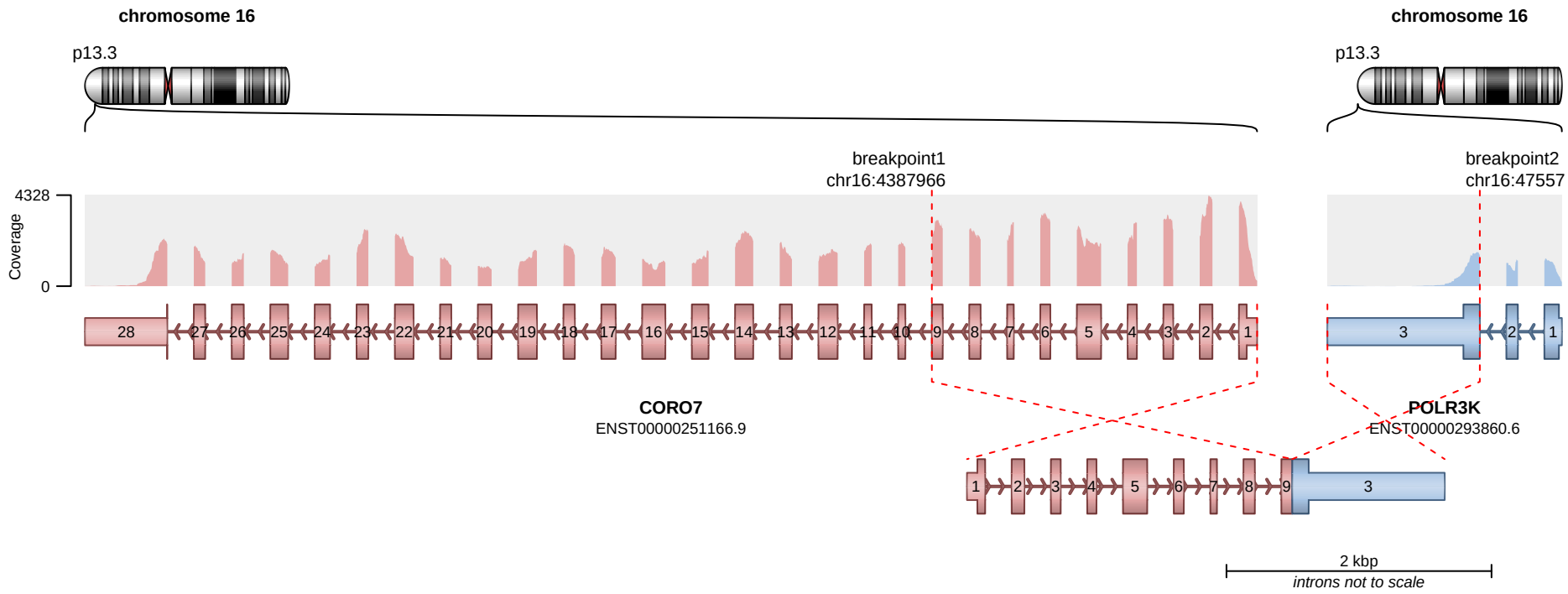


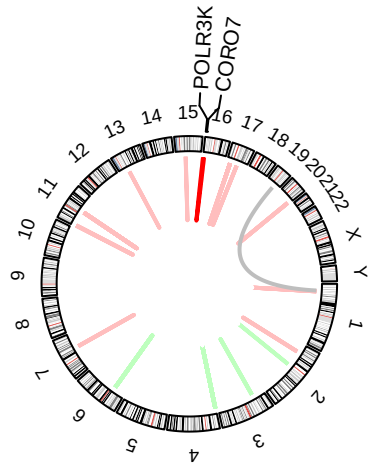


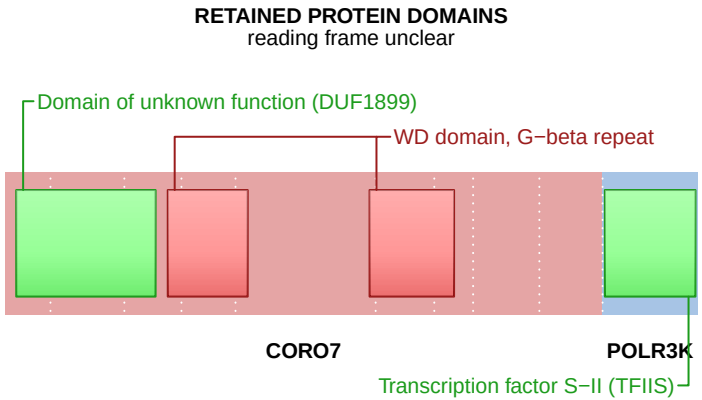
SUPPORTING READ COUNT

Split reads = 135
Discordant mates = 3

translocation
deletion
duplication
inversion



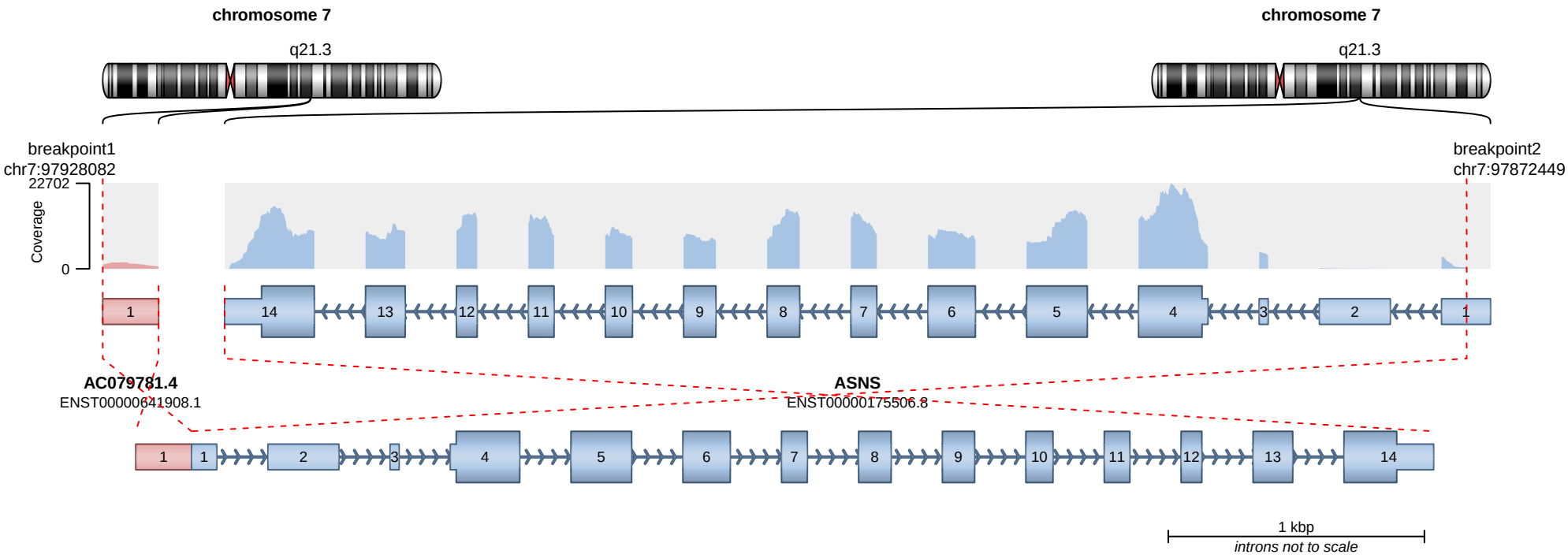


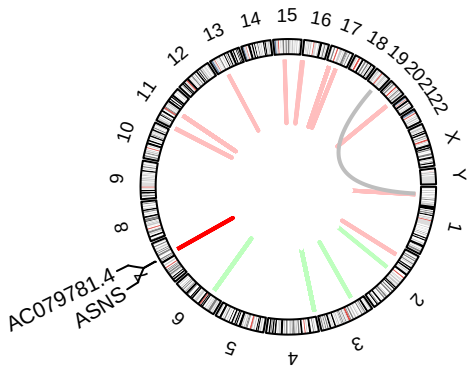


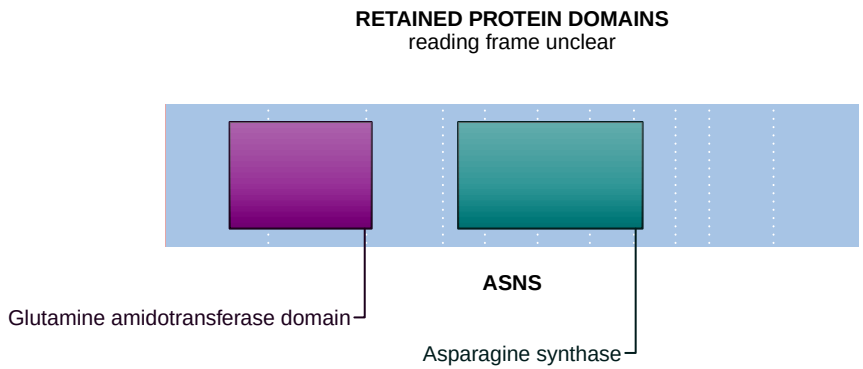
SUPPORTING READ COUNT

Split reads = 27
Discordant mates = 3

translocation
deletion
duplication
inversion



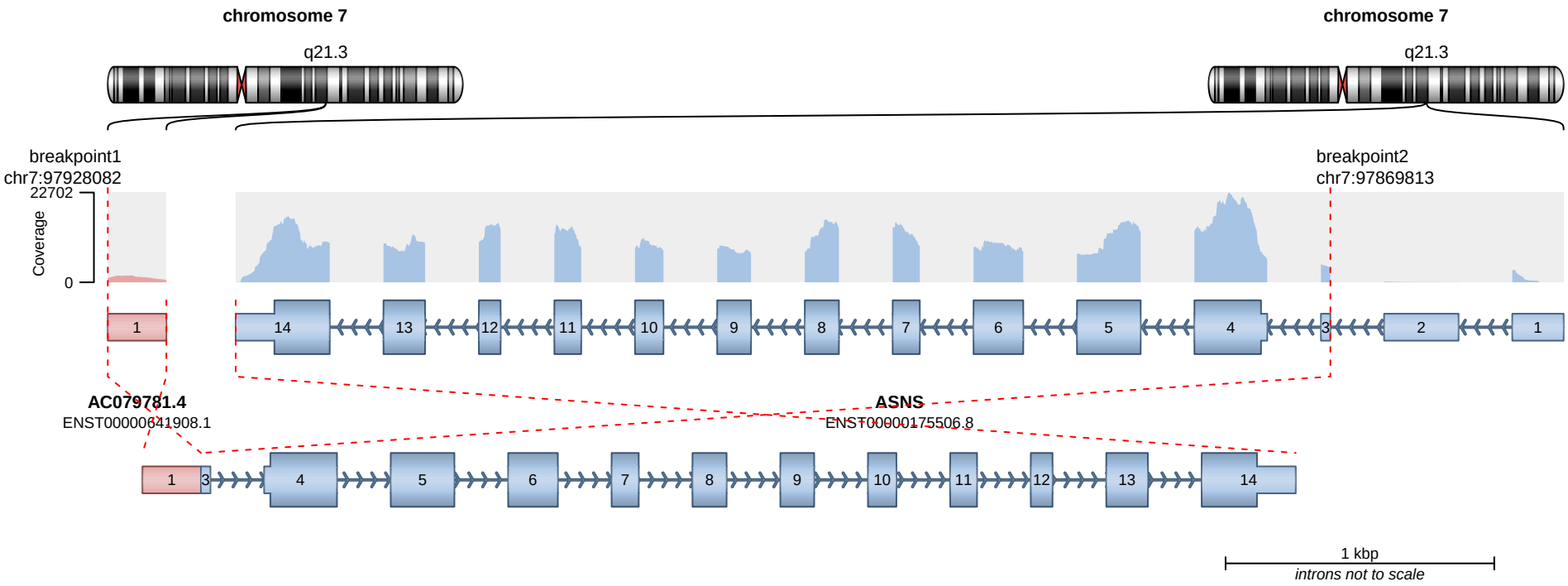


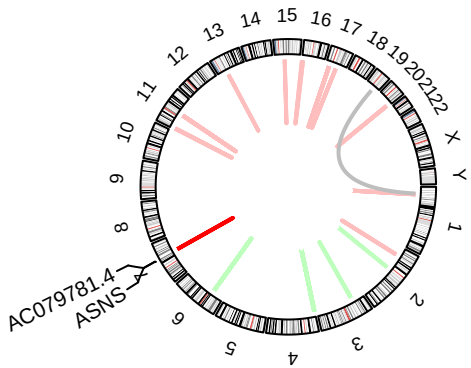


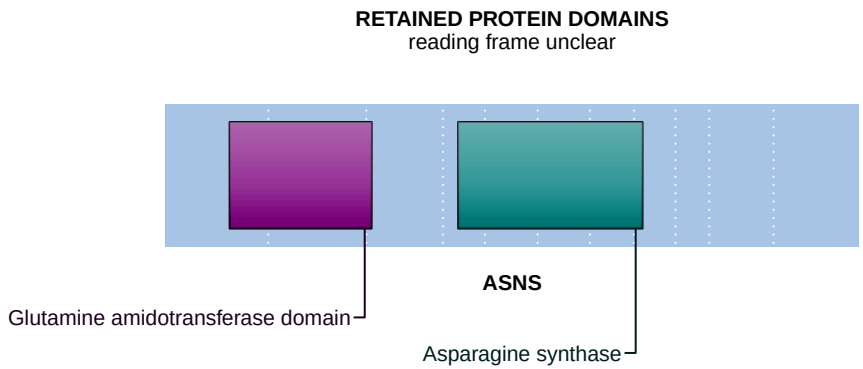
SUPPORTING READ COUNT

Split reads = 130
Discordant mates = 0

translocation
deletion
duplication
inversion



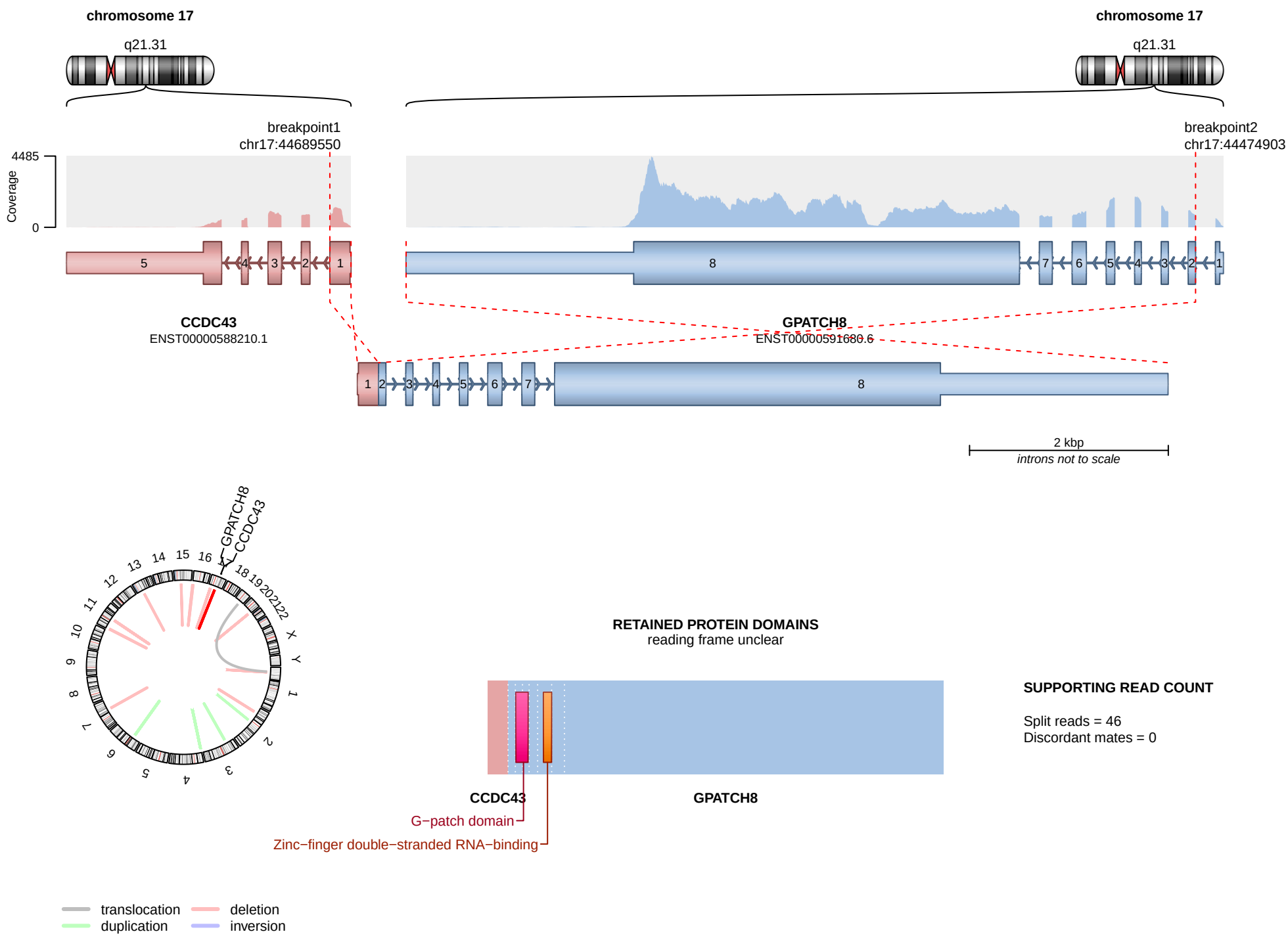


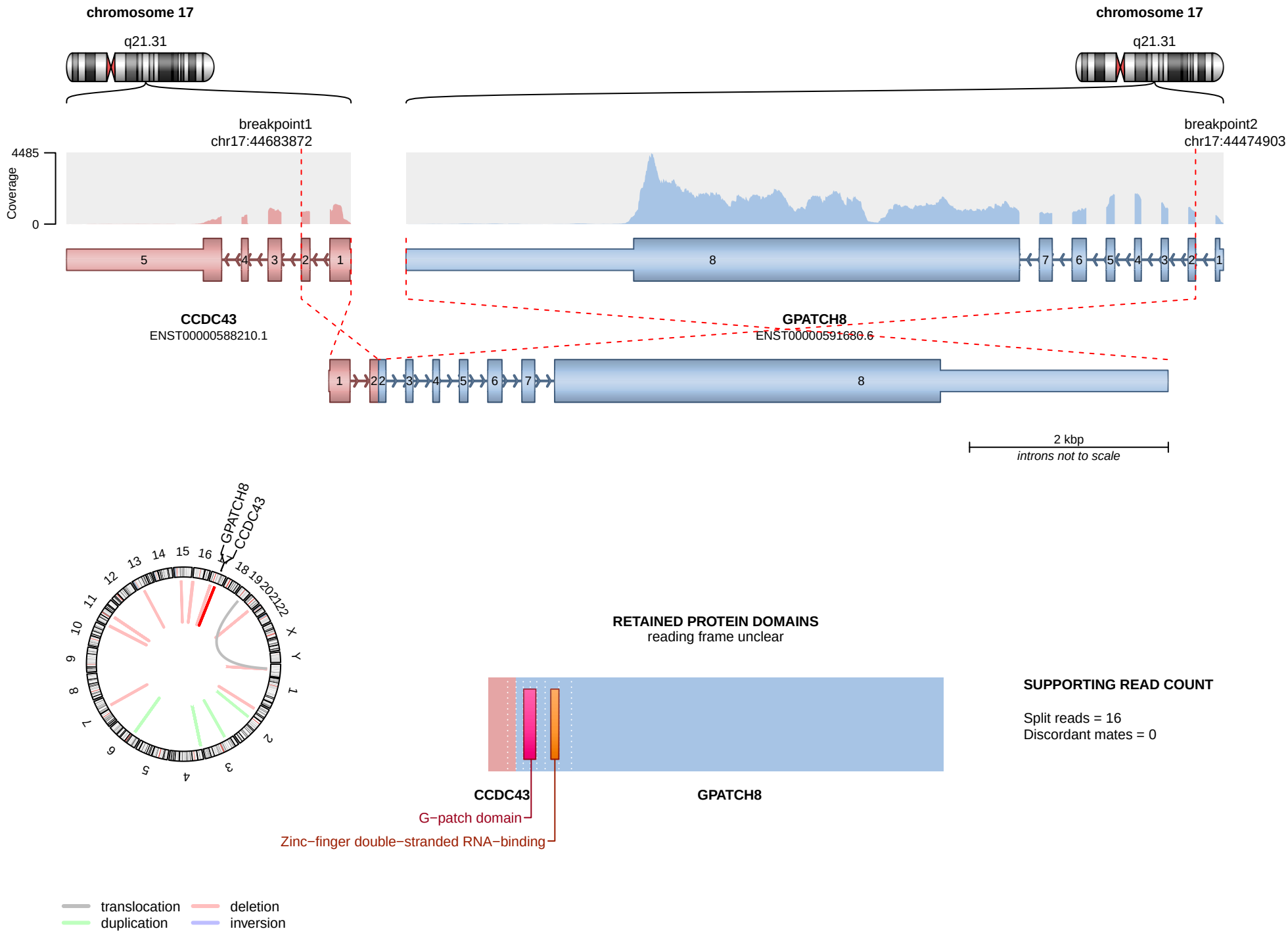


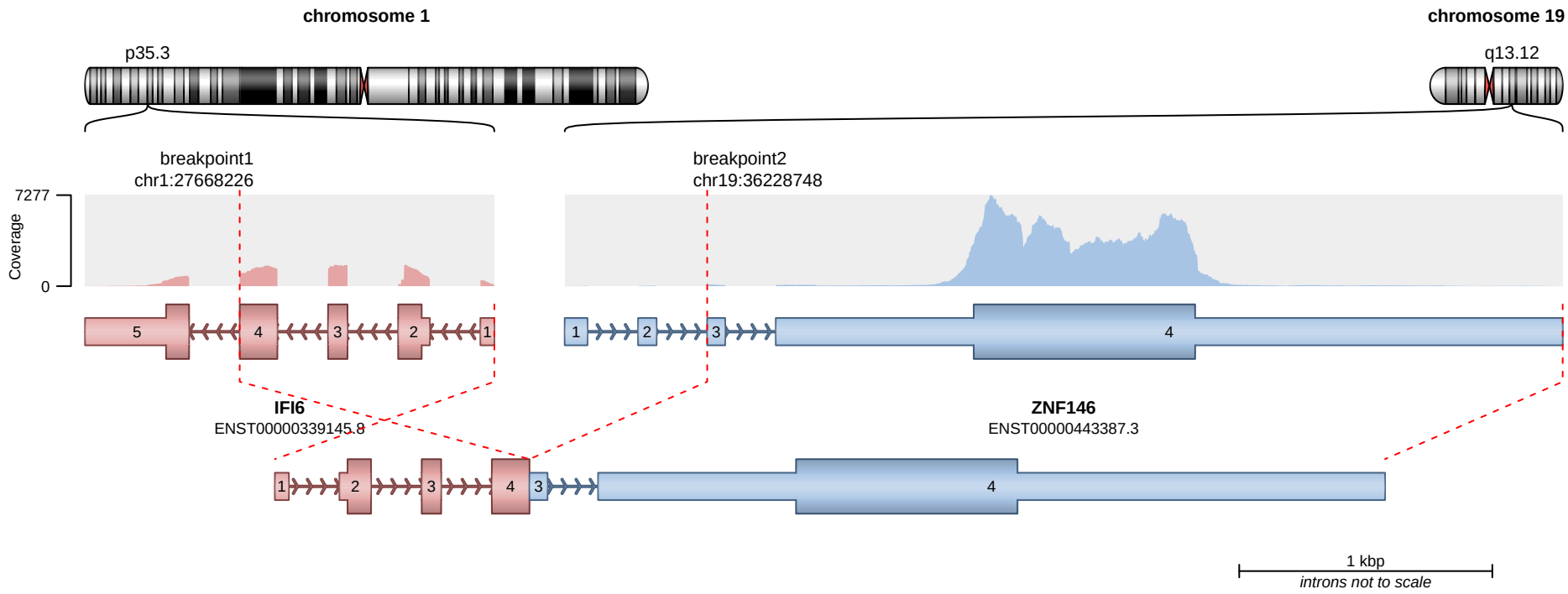
SUPPORTING READ COUNT

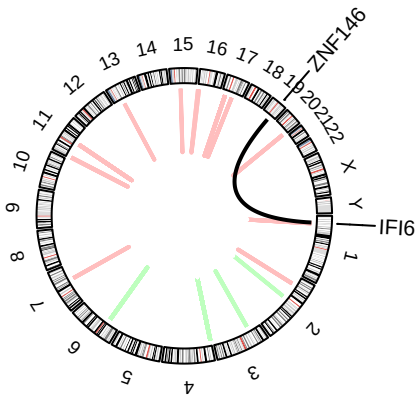
Split reads = 11
Discordant mates = 0

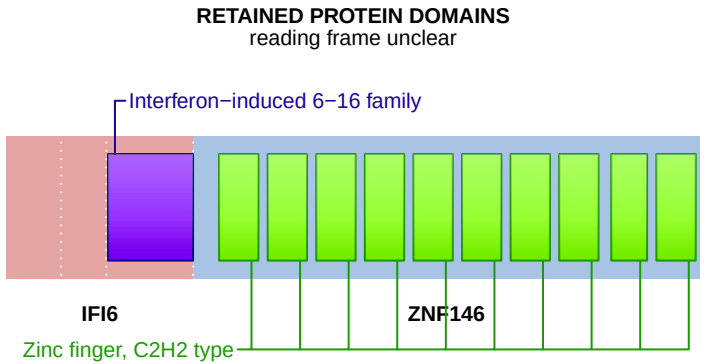
translocation
deletion
duplication
inversion


chromosome 17
q21.31
chromosome 17
q21.31
breakpoint1
chr17:44689550
breakpoint2
chr17:44474903
4485
Coverage
0
CCDC43
ENST00000588210.1
GPATCH8
ENST00000591680.6
2 kbp
introns not to scale
GPATCH8
CCDC43
RETAINED PROTEIN DOMAINS
reading frame unclear
CCDC43
GPATCH8
G−patch domain
Zinc−finger double−stranded RNA−binding
SUPPORTING READ COUNT
Split reads = 46
Discordant mates = 0
translocation
deletion
duplication
inversion


chromosome 17
q21.31
chromosome 17
q21.31
breakpoint1
chr17:44683872
breakpoint2
chr17:44474903
4485
Coverage
0
CCDC43
ENST00000588210.1
GPATCH8
ENST00000591680.6
2 kbp
introns not to scale
GPATCH8
CCDC43
RETAINED PROTEIN DOMAINS
reading frame unclear
CCDC43
GPATCH8
G−patch domain
Zinc−finger double−stranded RNA−binding
SUPPORTING READ COUNT
Split reads = 16
Discordant mates = 0
translocation
deletion
duplication
inversion



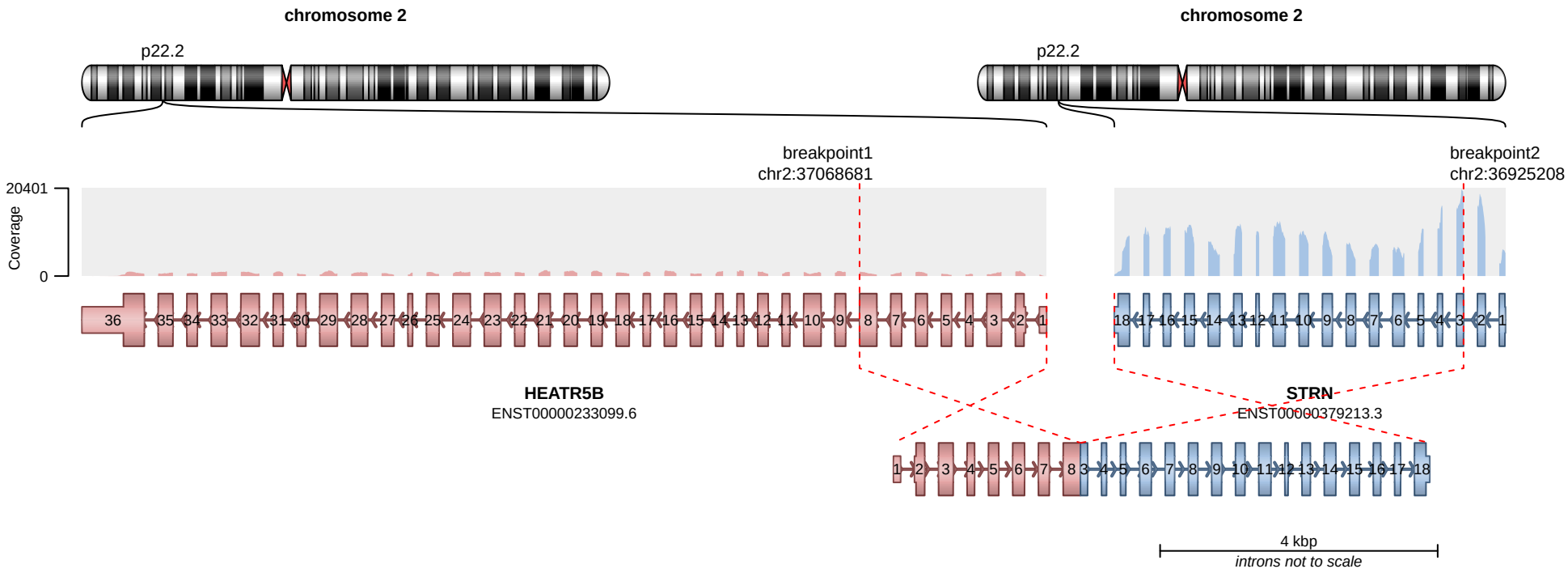


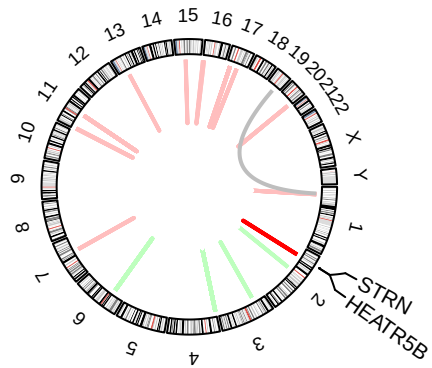


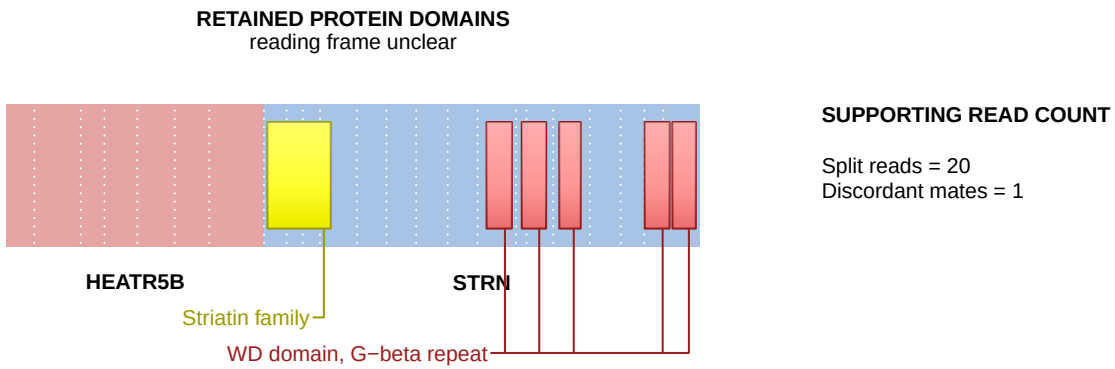
SUPPORTING READ COUNT

Split reads = 29
Discordant mates = 0

translocation
deletion
duplication
inversion



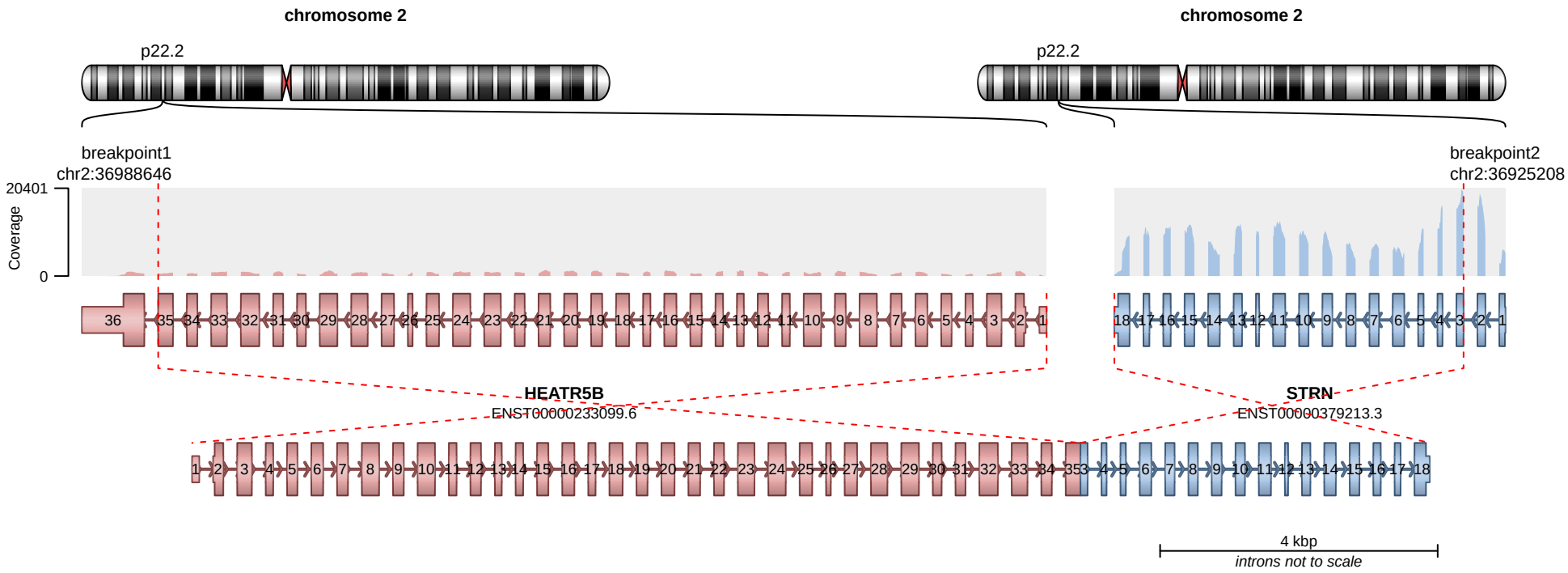


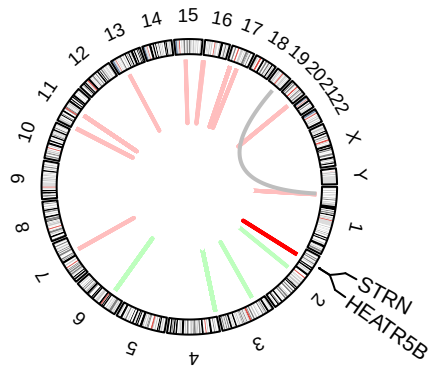


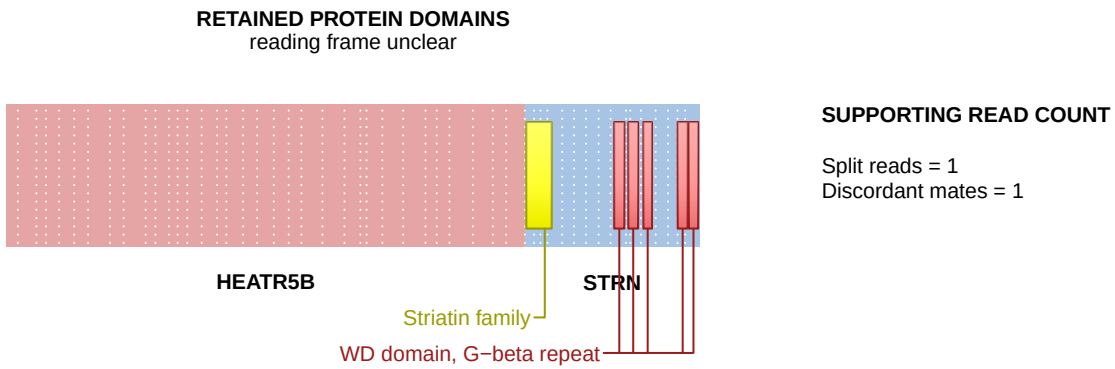
SUPPORTING READ COUNT

Split reads = 20
Discordant mates = 1

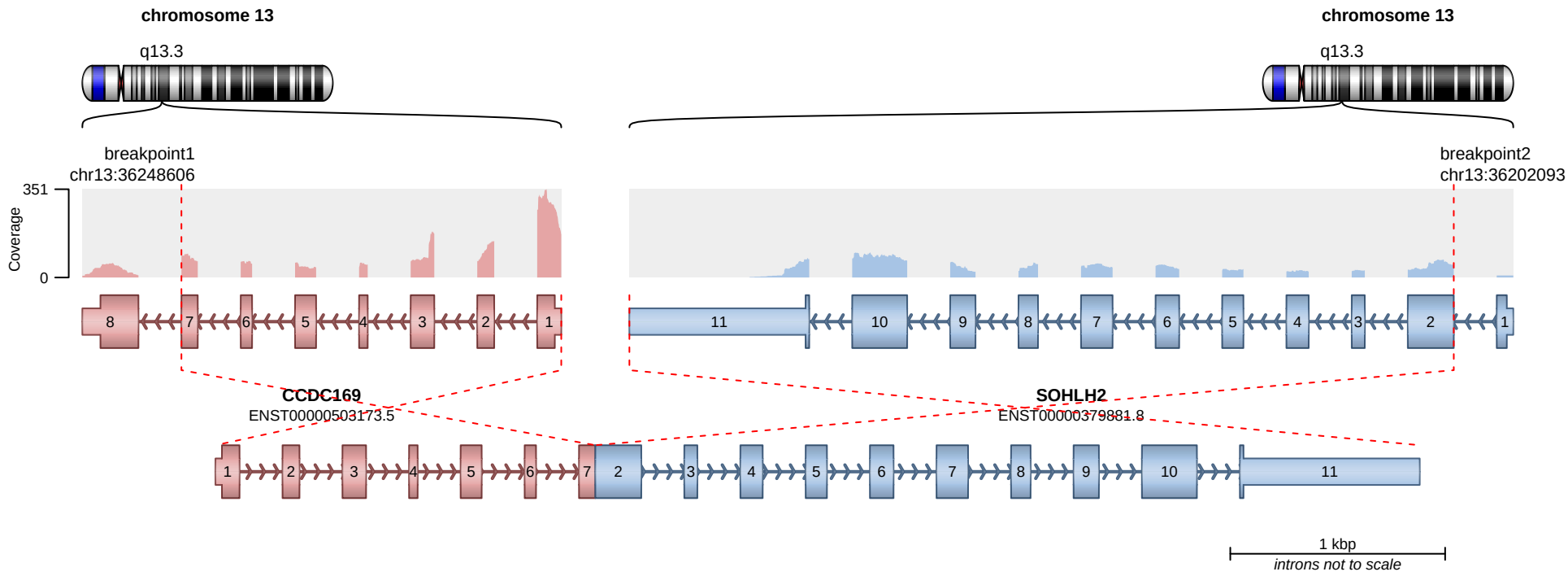
translocation
deletion
duplication
inversion

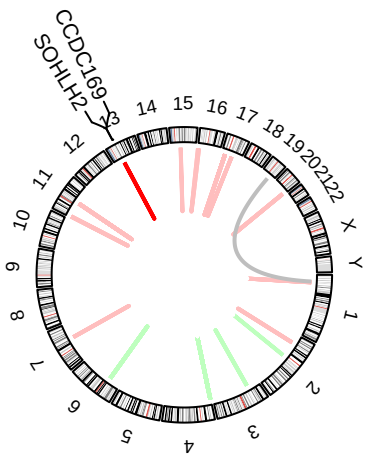


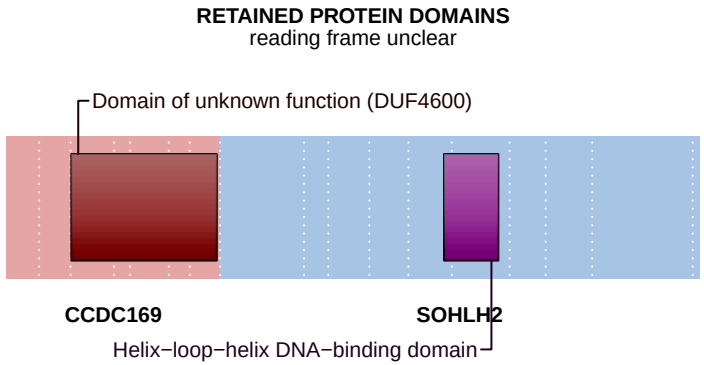




translocation
deletion
duplication
inversion



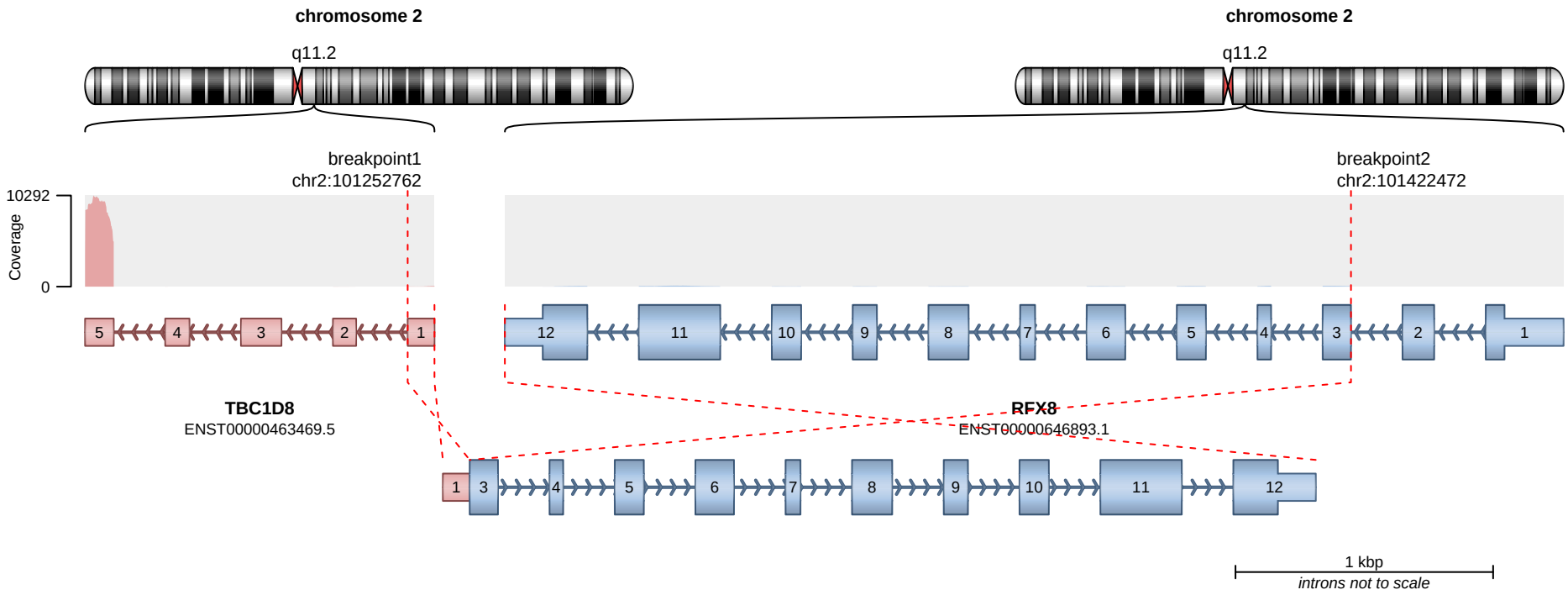


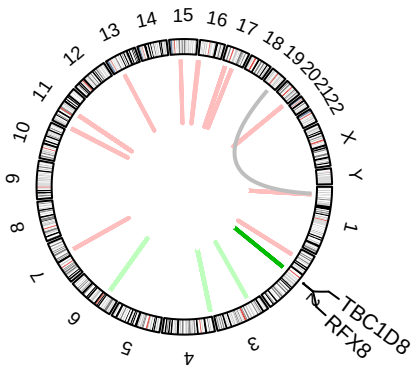


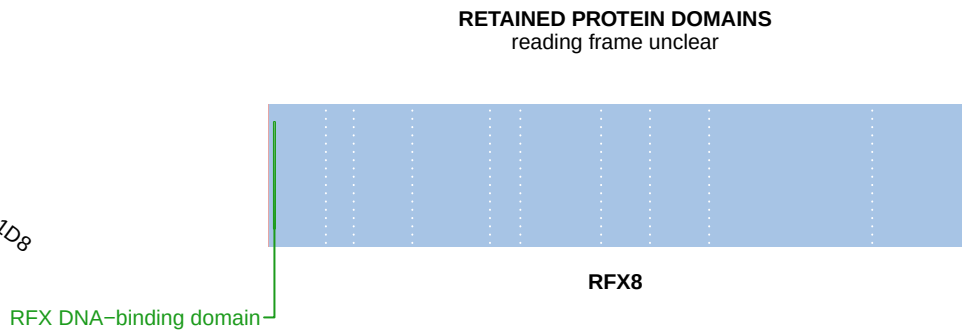
SUPPORTING READ COUNT

Split reads = 20
Discordant mates = 0

translocation
deletion
duplication
inversion



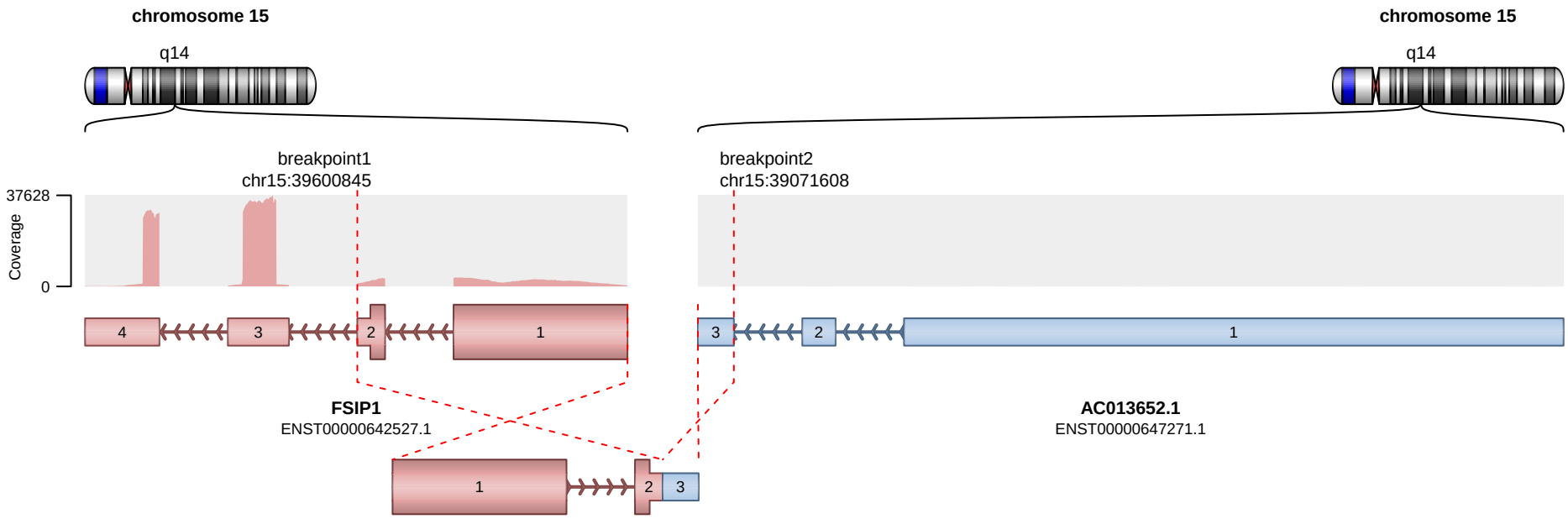


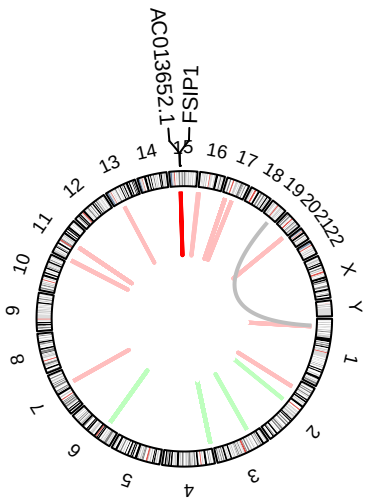


SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 0

translocation
deletion
duplication
inversion





translation
deletion
duplication
inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 0