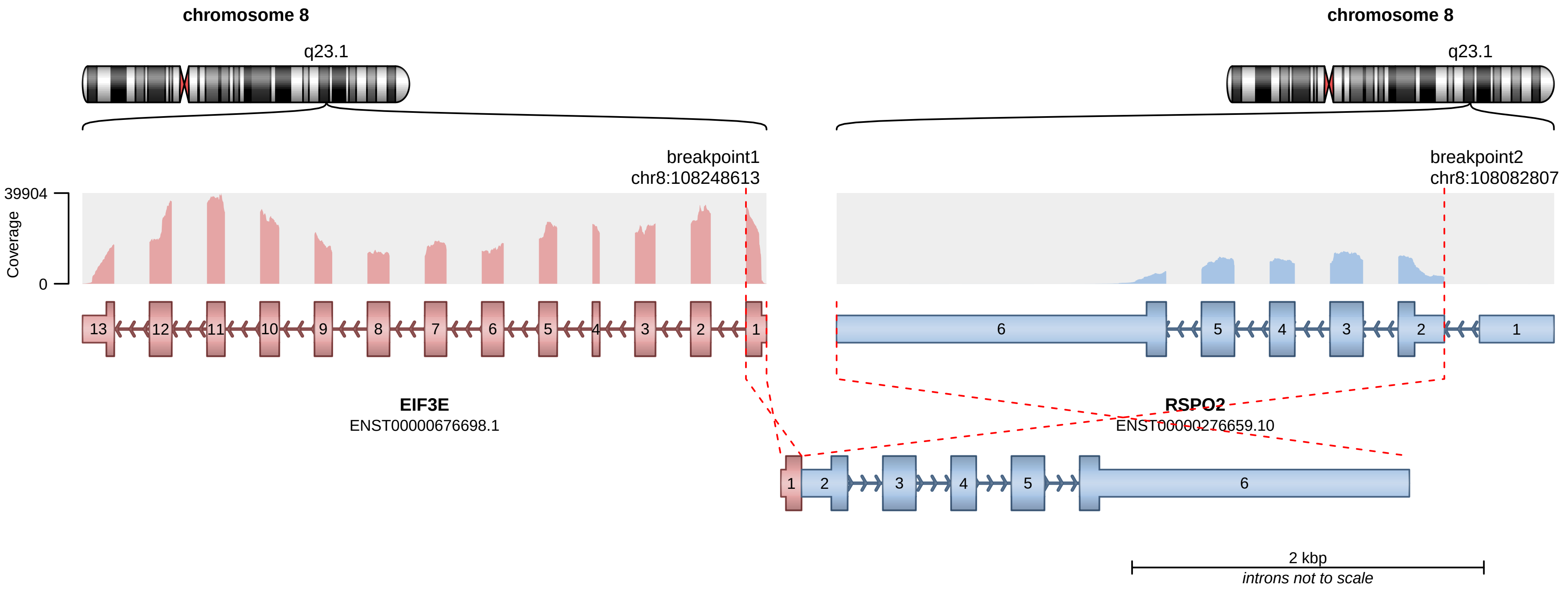
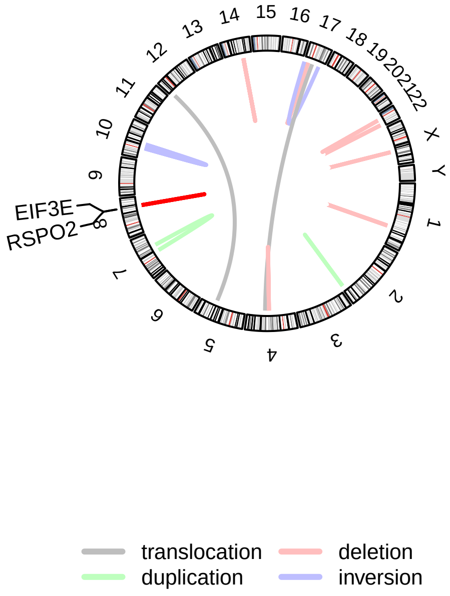
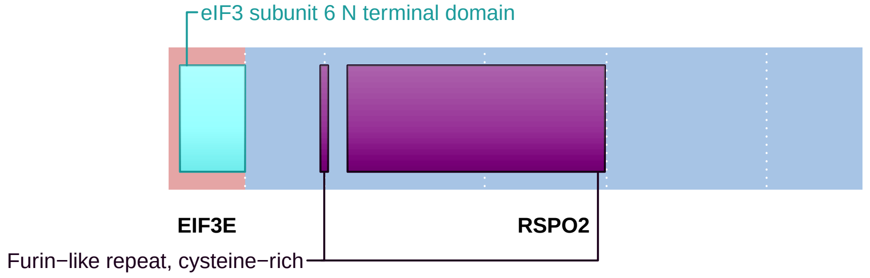


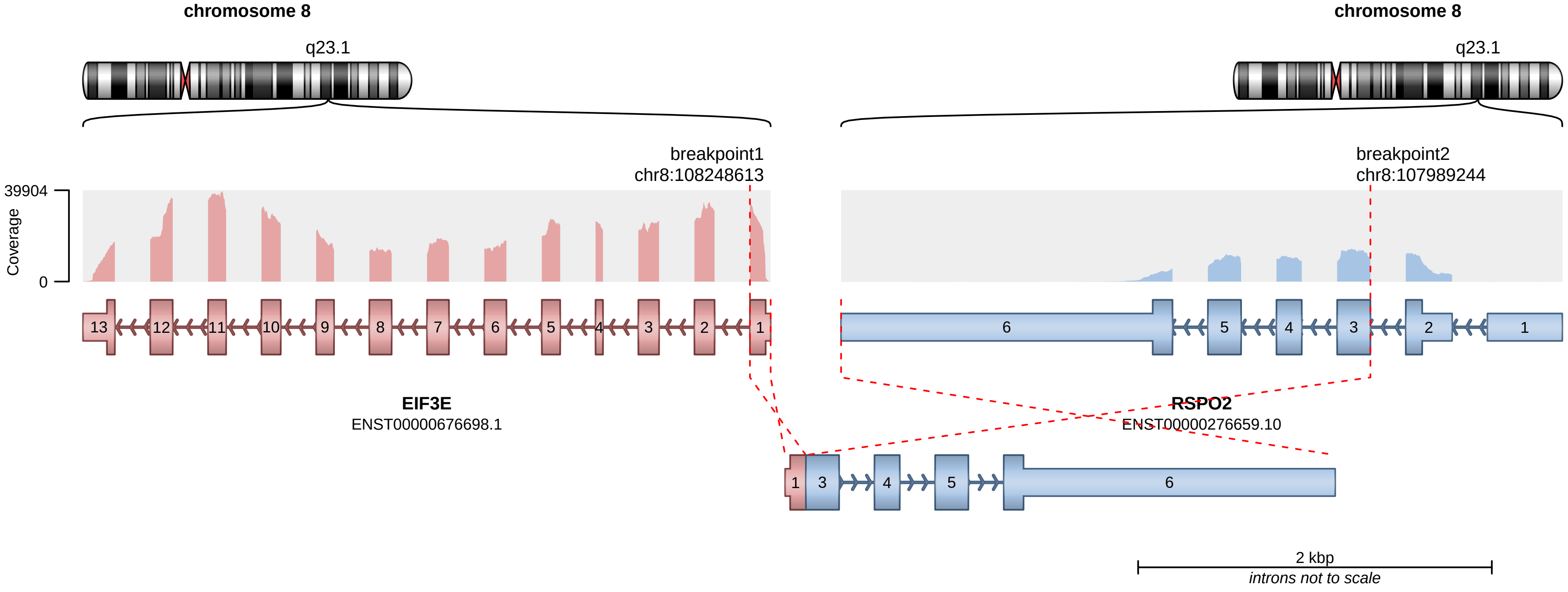


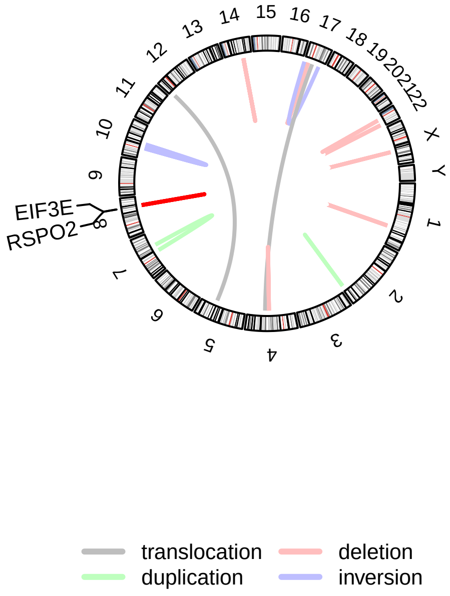
RETAINED PROTEIN DOMAINS
reading frame unclear



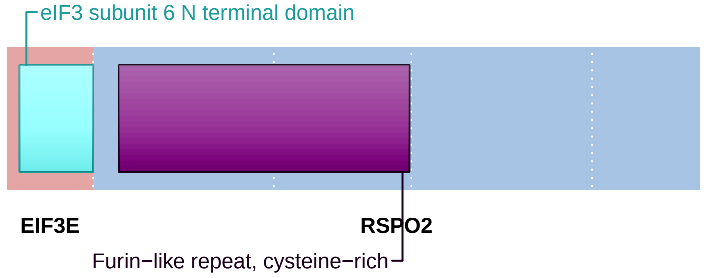
SUPPORTING READ COUNT

Split reads = 1271
Discordant mates = 1



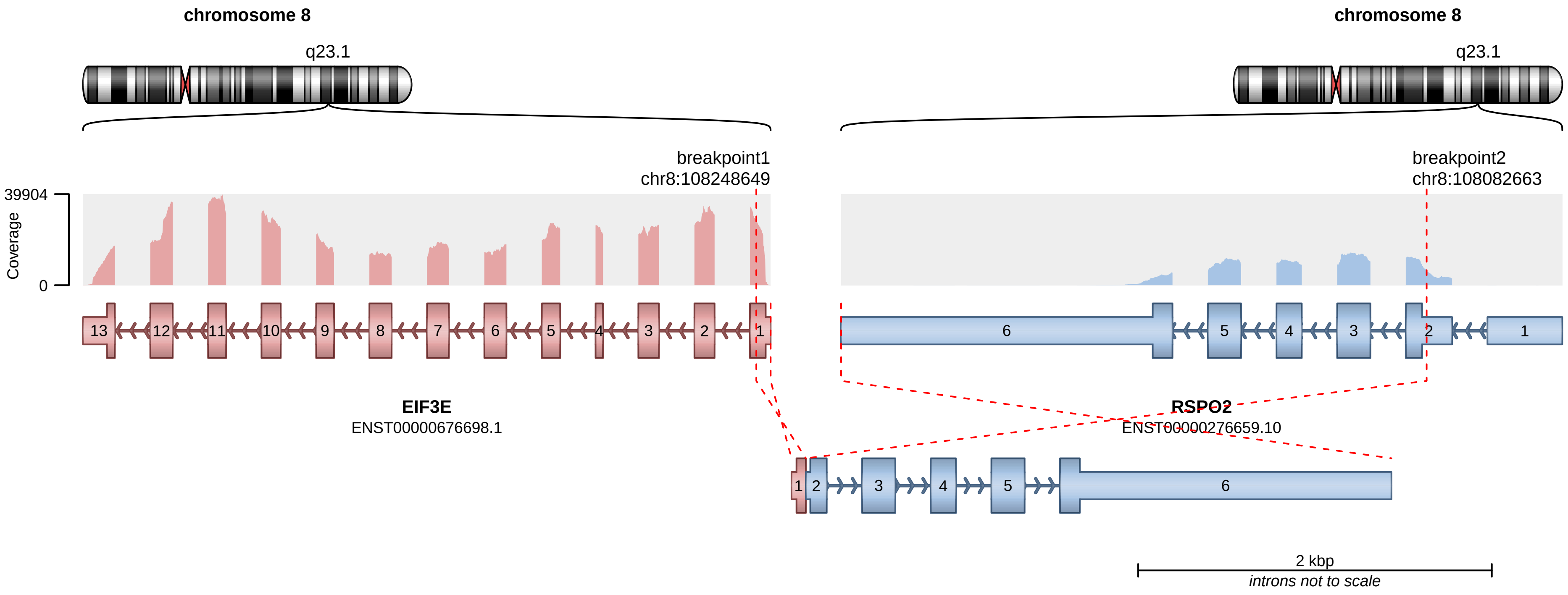


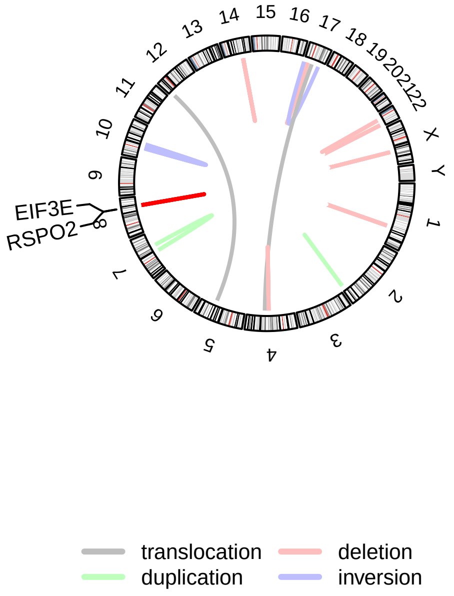
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

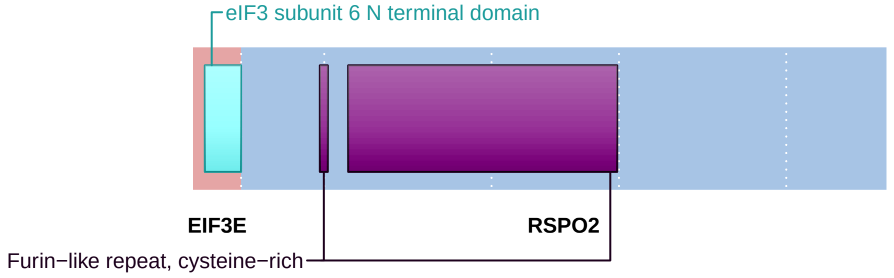
Split reads = 10
Discordant mates = 0





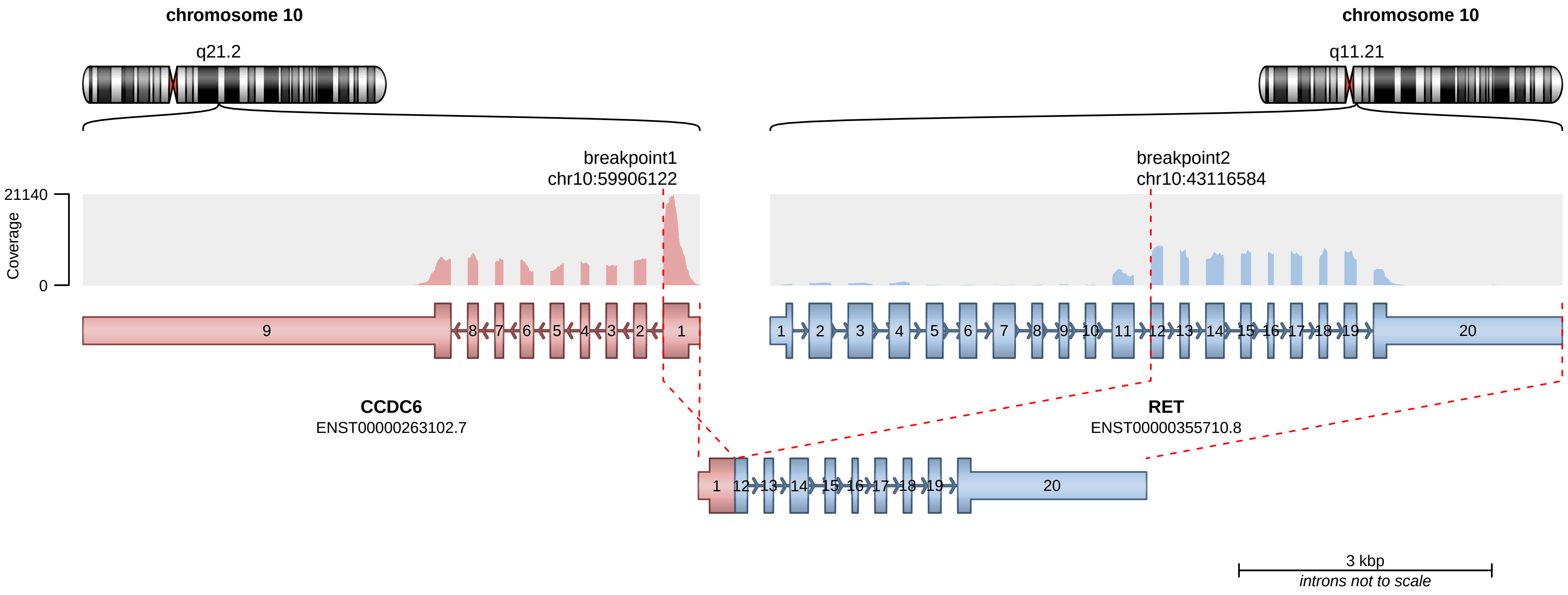
RETAINED PROTEIN DOMAINS

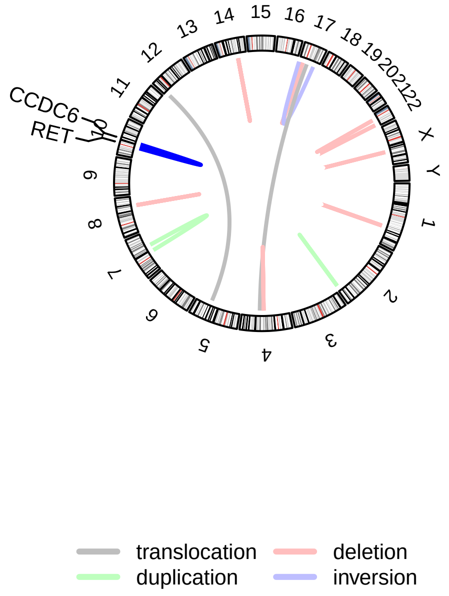
reading frame unclear



SUPPORTING READ COUNT

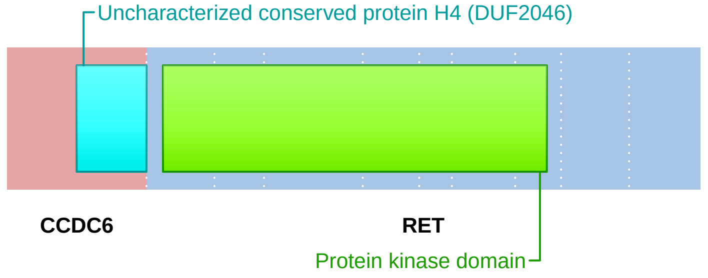
Split reads = 3
Discordant mates = 0





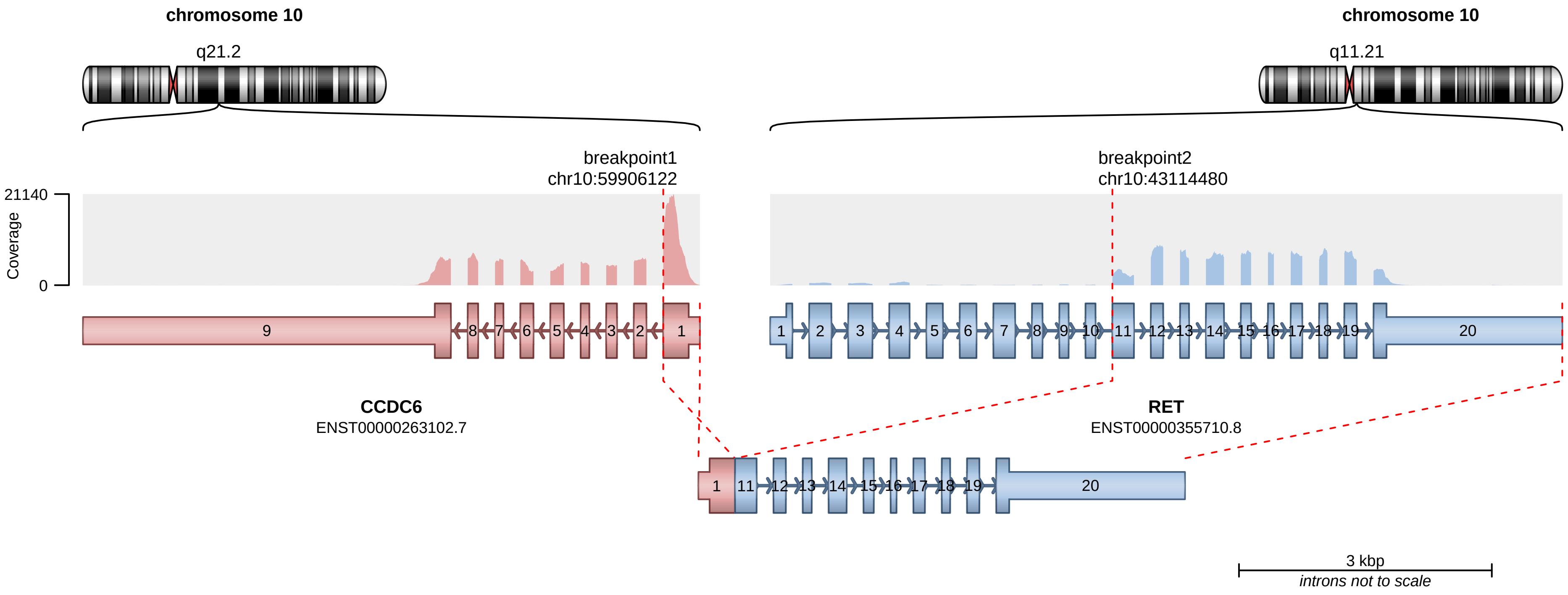
RETAINED PROTEIN DOMAINS

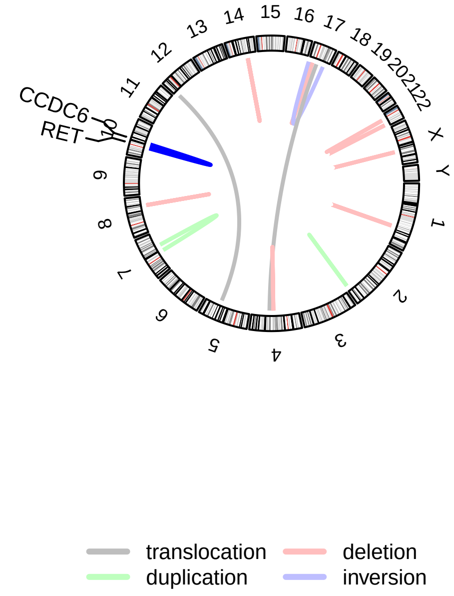
reading frame unclear



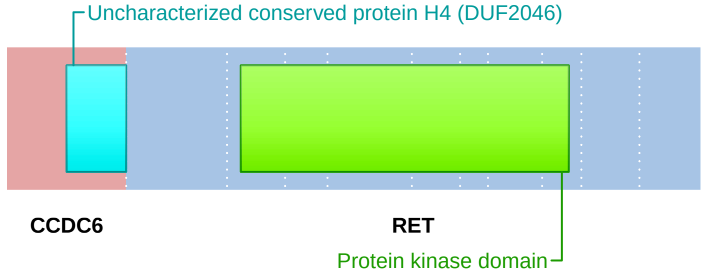
SUPPORTING READ COUNT

Split reads = 1128
Discordant mates = 15



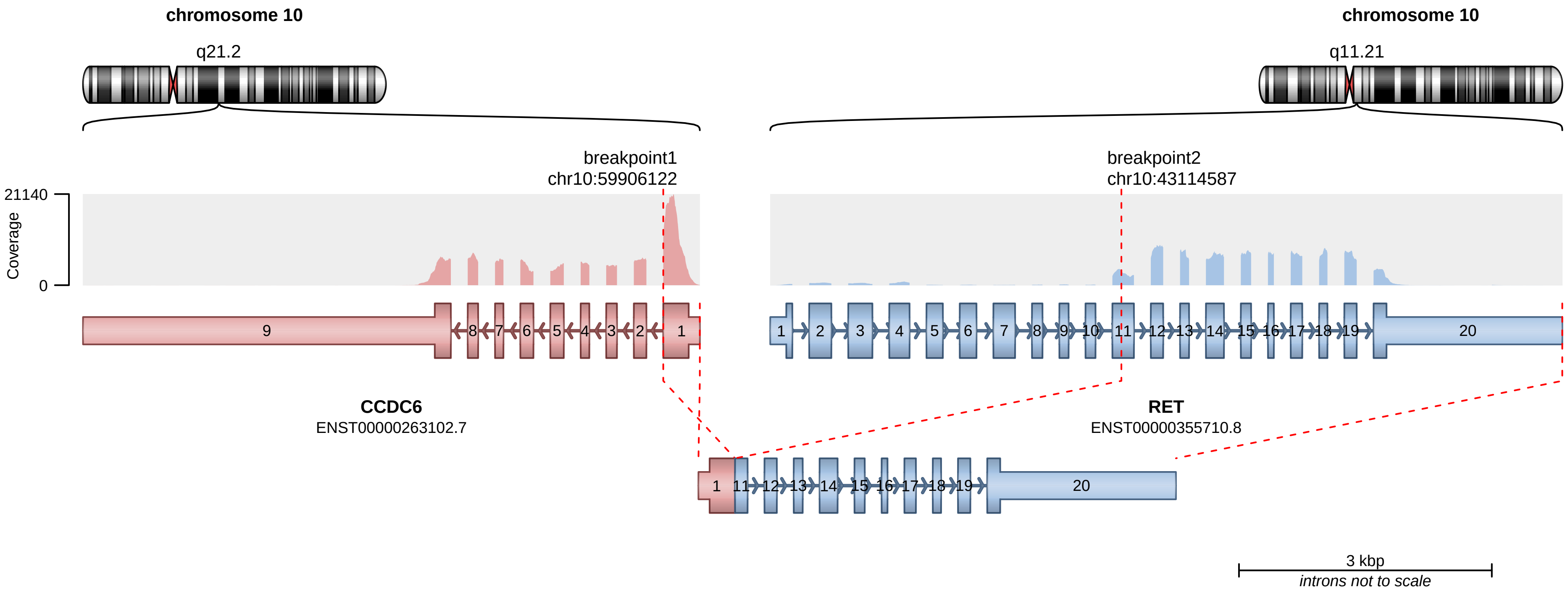


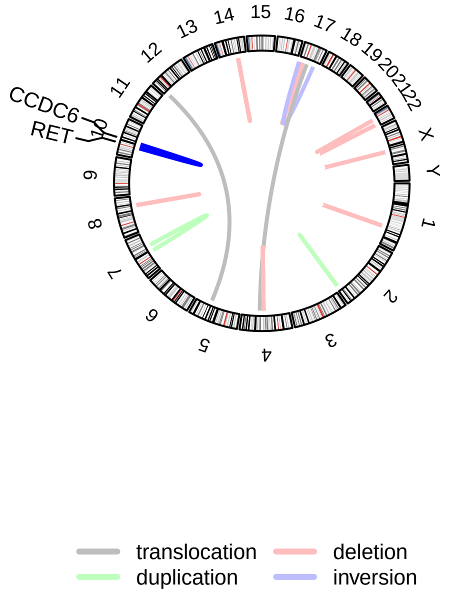
RETAINED PROTEIN DOMAINS
reading frame unclear

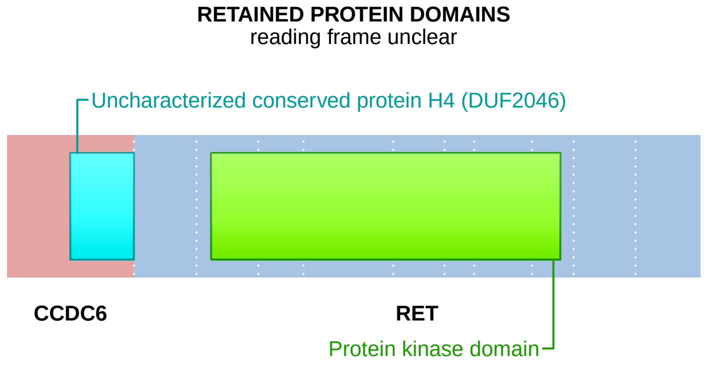


SUPPORTING READ COUNT

Split reads = 332
Discordant mates = 28

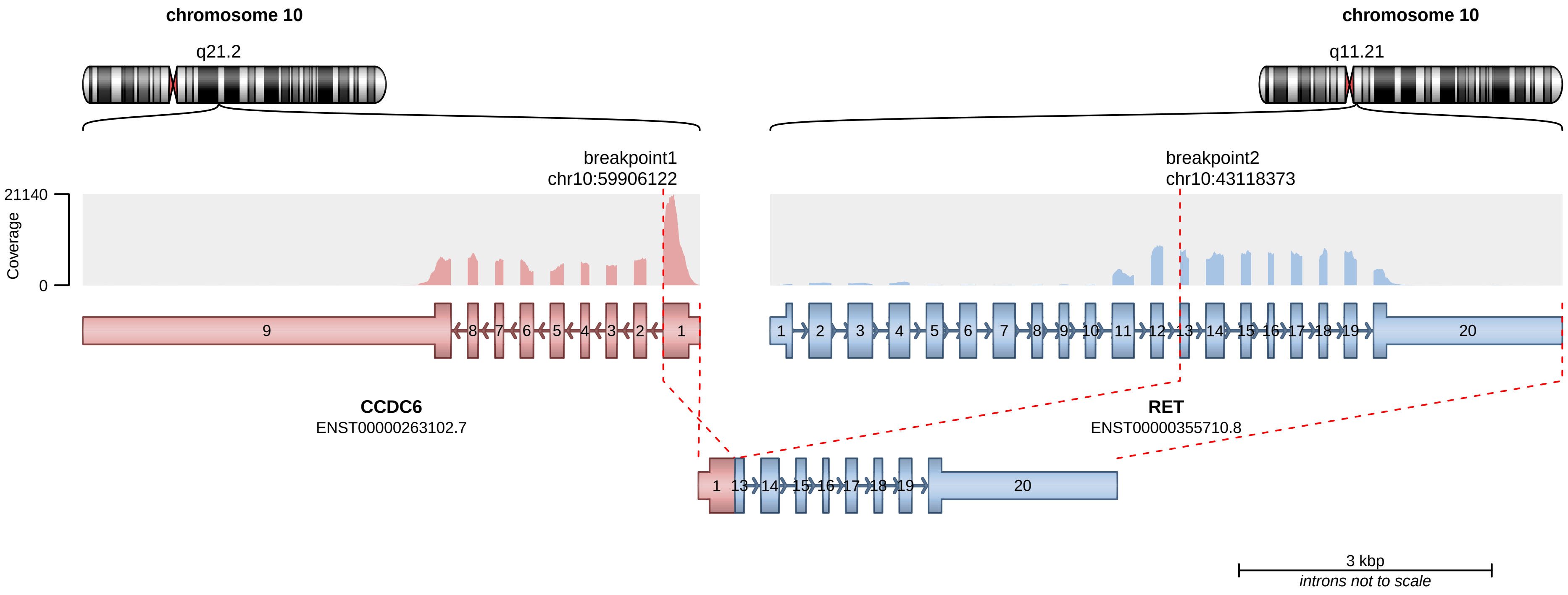


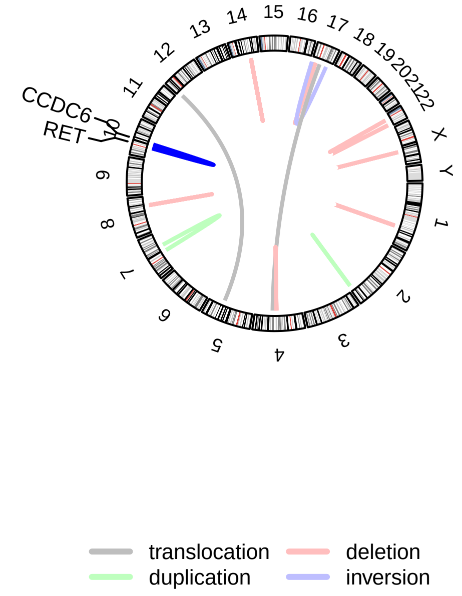


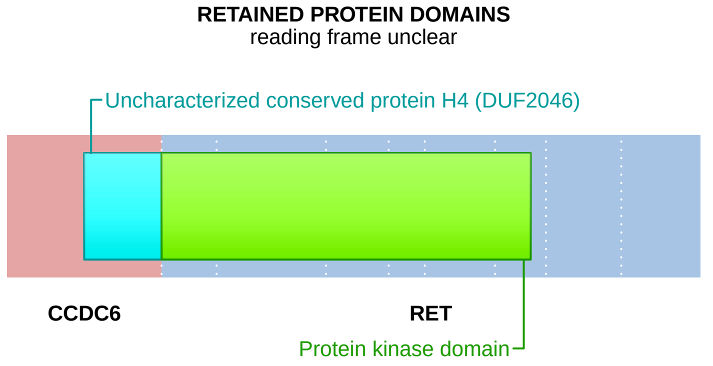


SUPPORTING READ COUNT

Split reads = 26
Discordant mates = 17

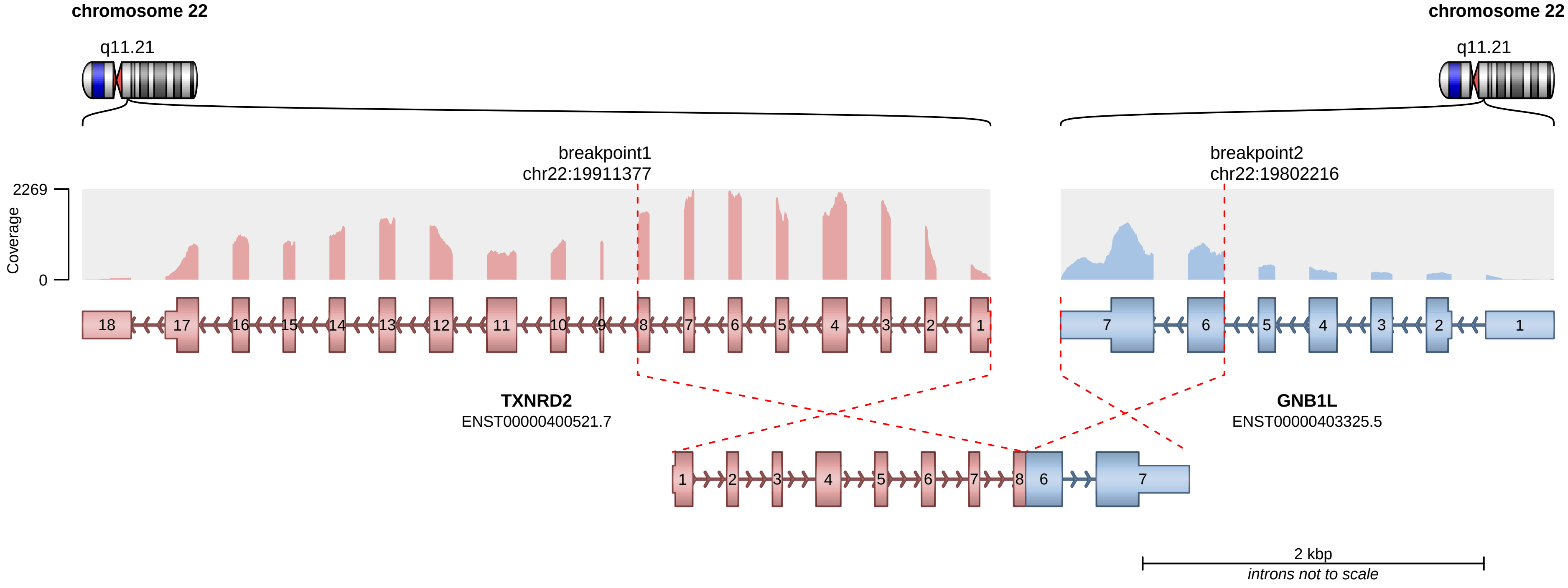


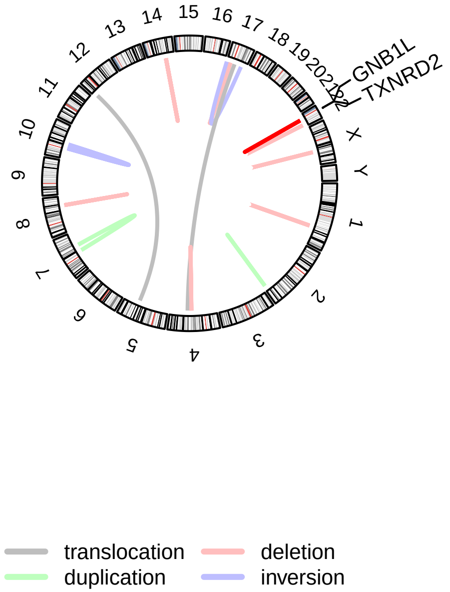


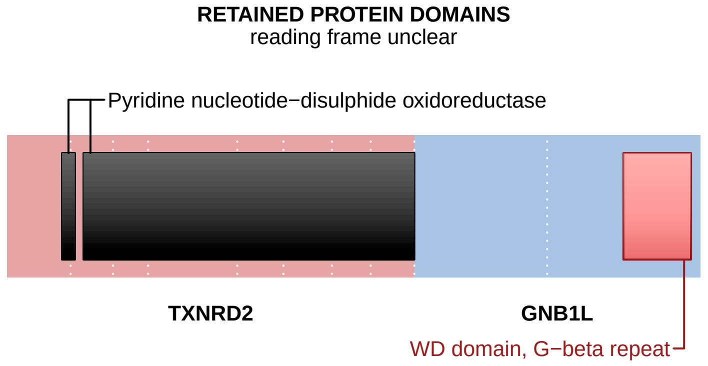


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

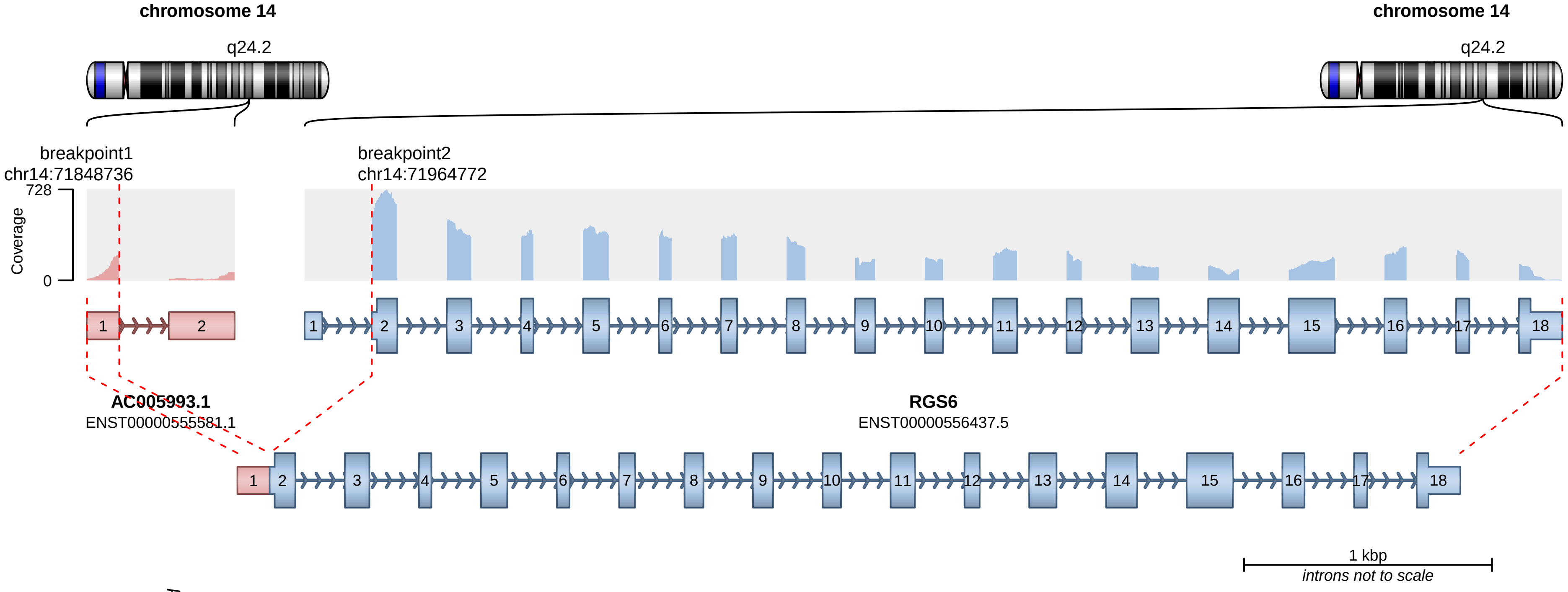


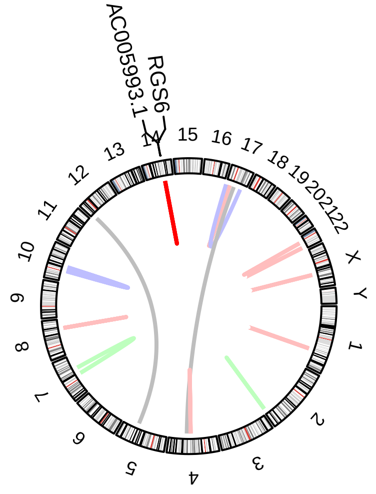




SUPPORTING READ COUNT

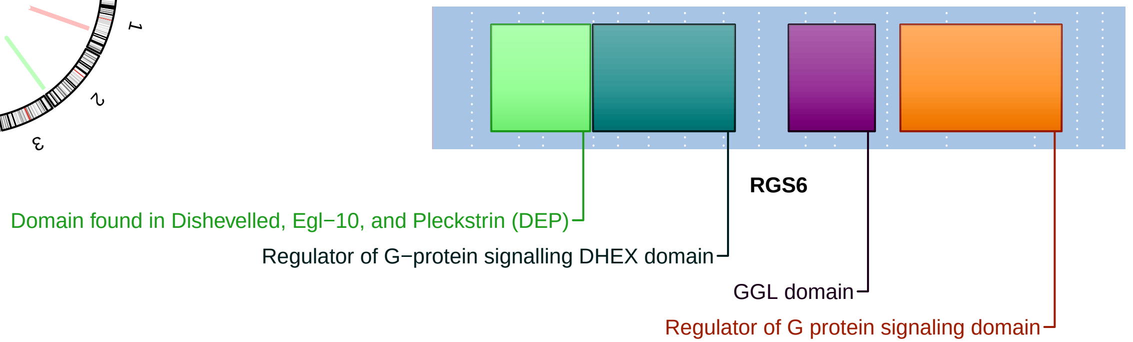
Split reads = 141
Discordant mates = 7





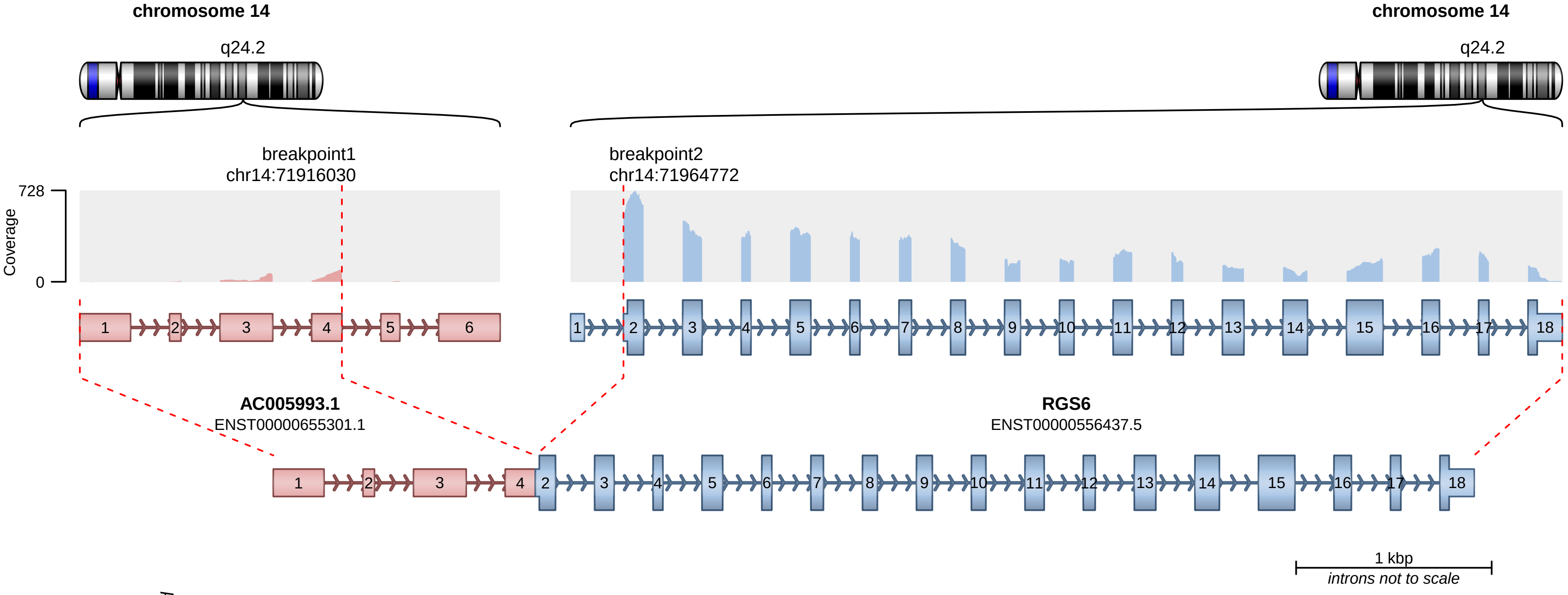
▬ translocation ▬ deletion
▬ duplication ▬ inversion

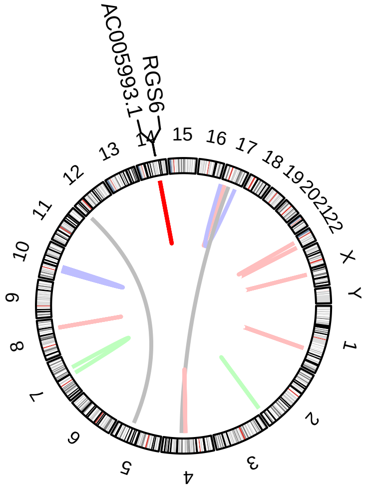
RETAINED PROTEIN DOMAINS
reading frame unclear

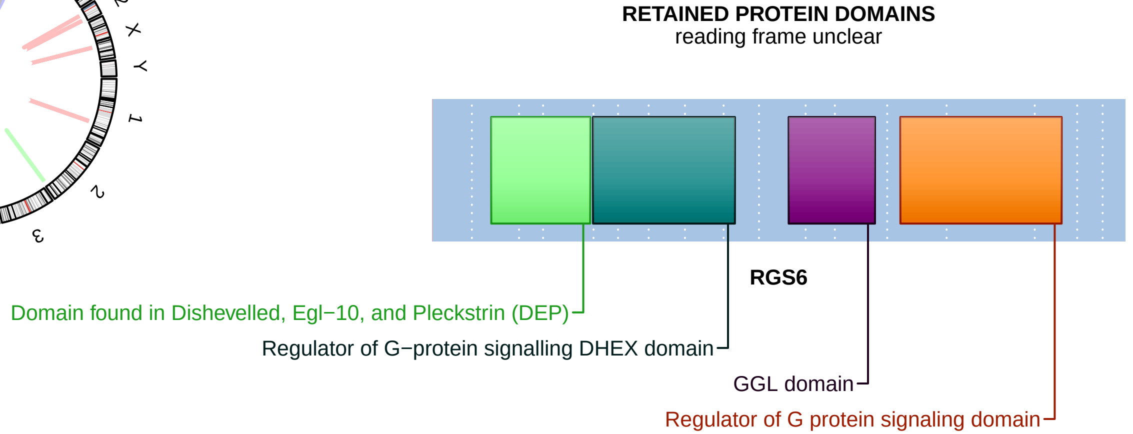


SUPPORTING READ COUNT

Split reads = 85
Discordant mates = 0



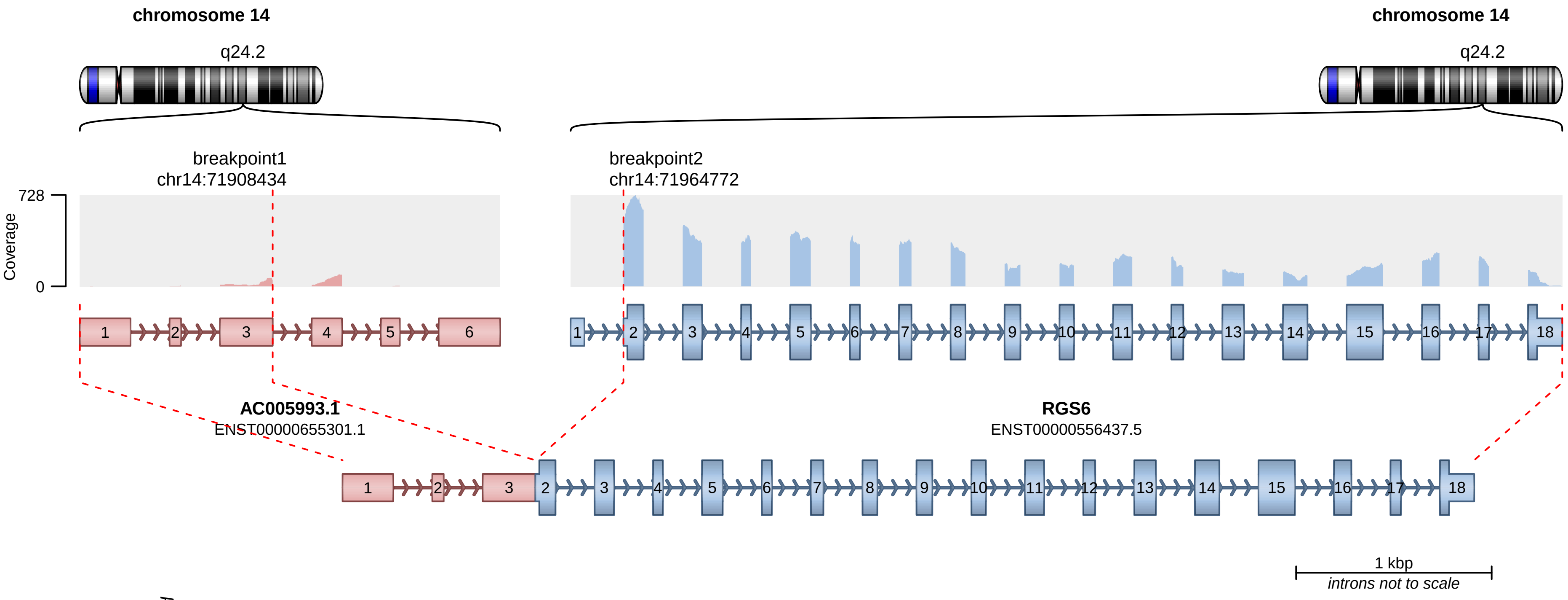


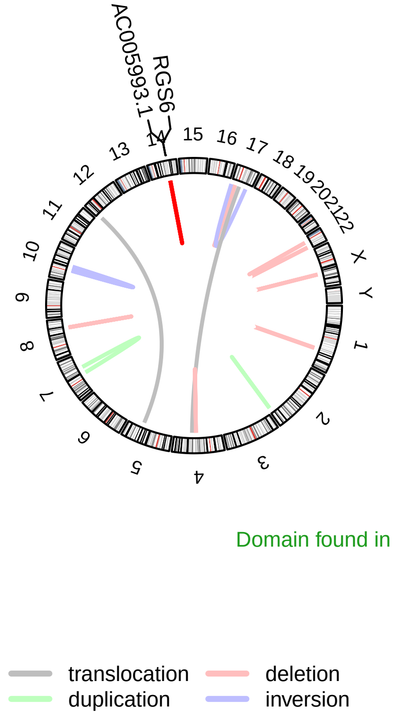

RETAINED PROTEIN DOMAINS
reading frame unclear

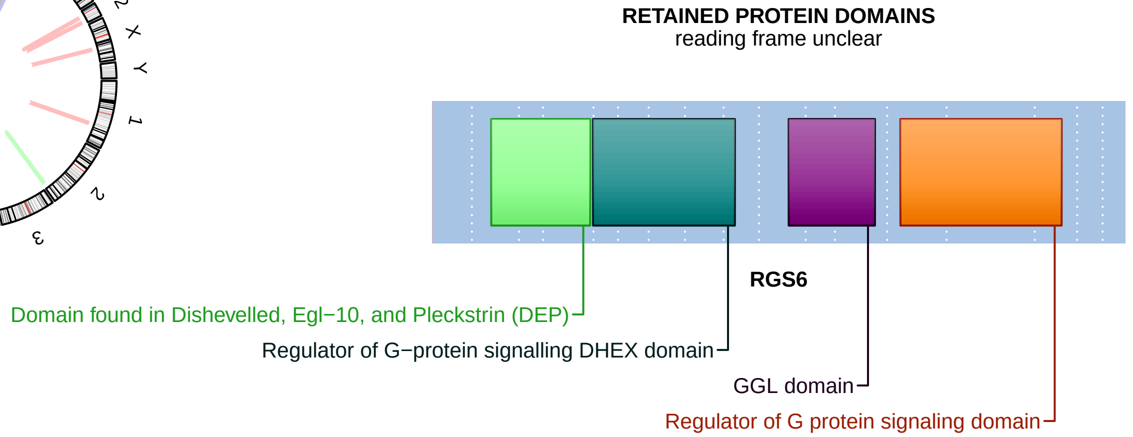
SUPPORTING READ COUNT

Split reads = 43
Discordant mates = 3

— translocation — deletion
— duplication — inversion

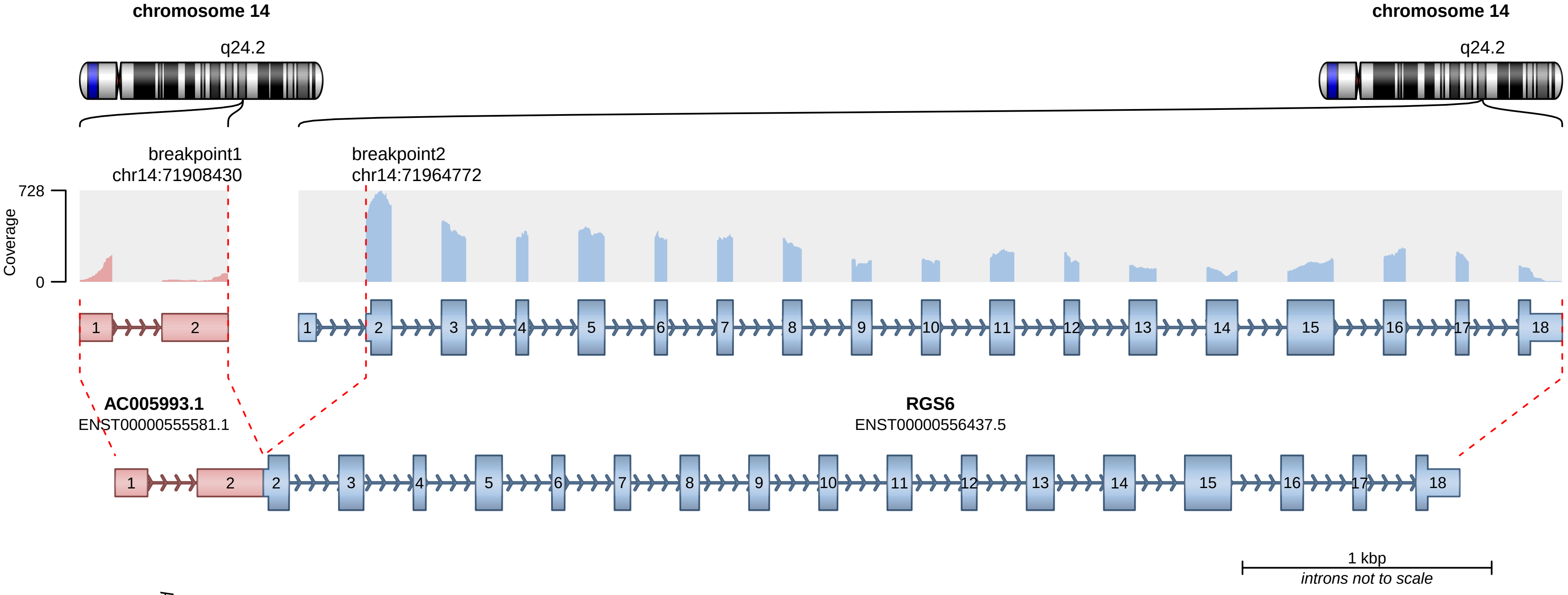


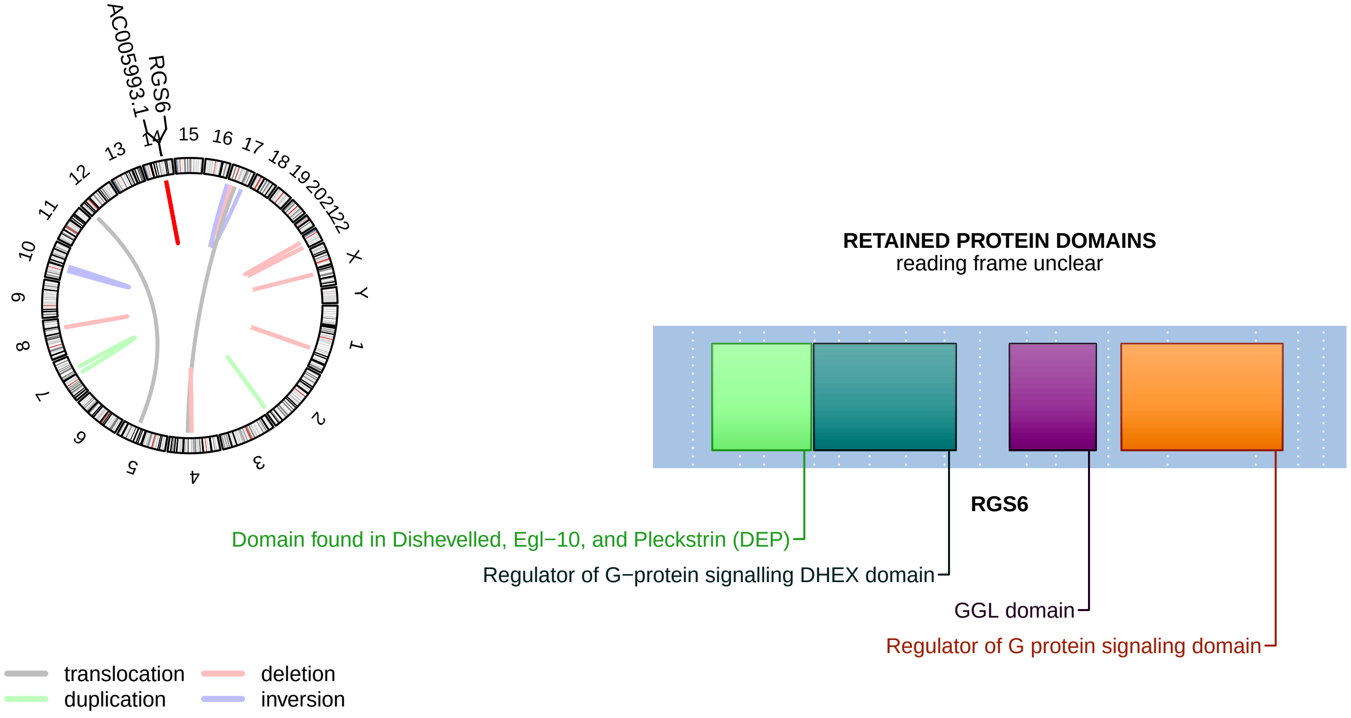




SUPPORTING READ COUNT

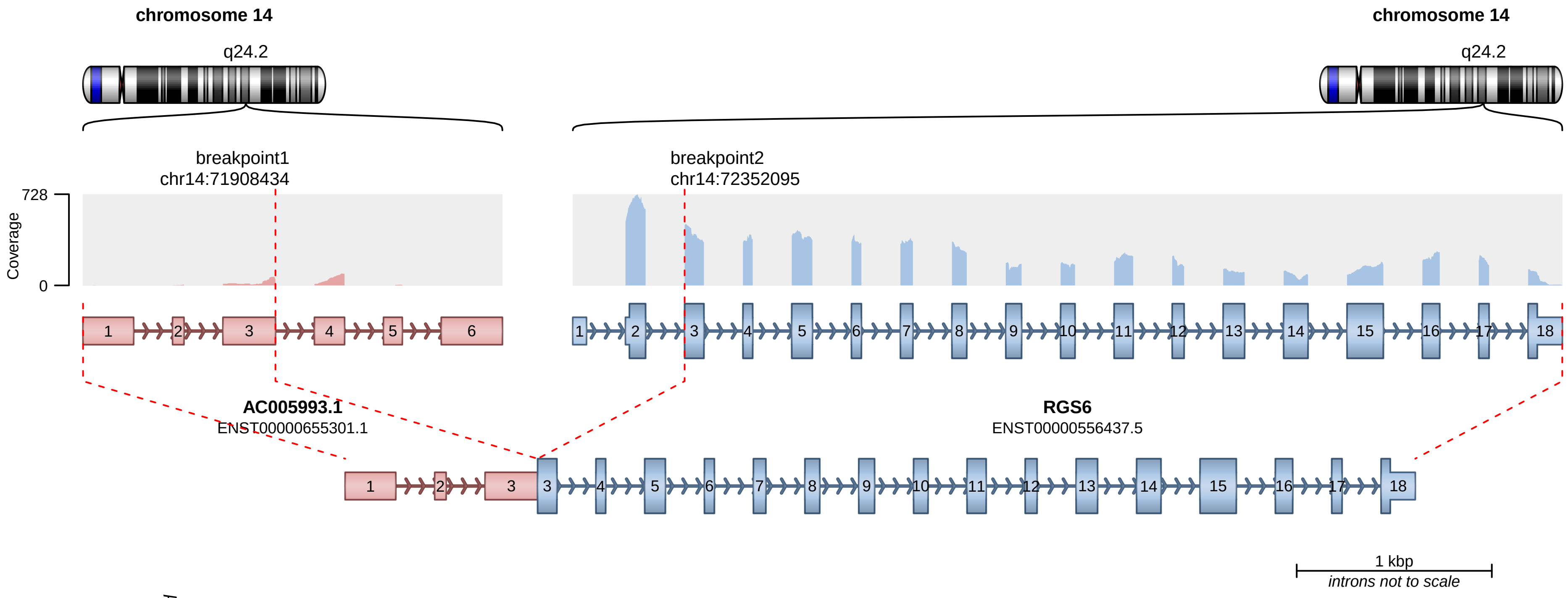
Split reads = 21
Discordant mates = 2

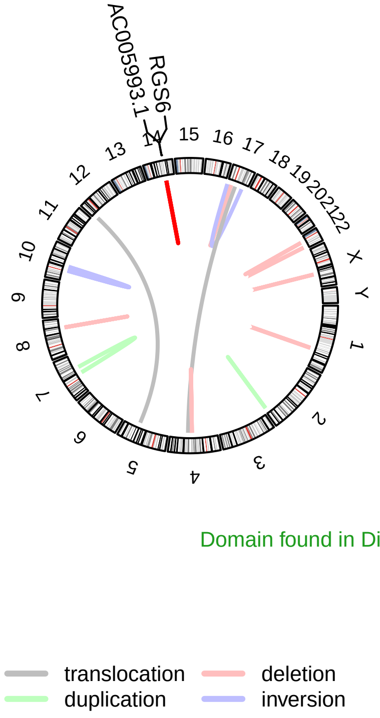


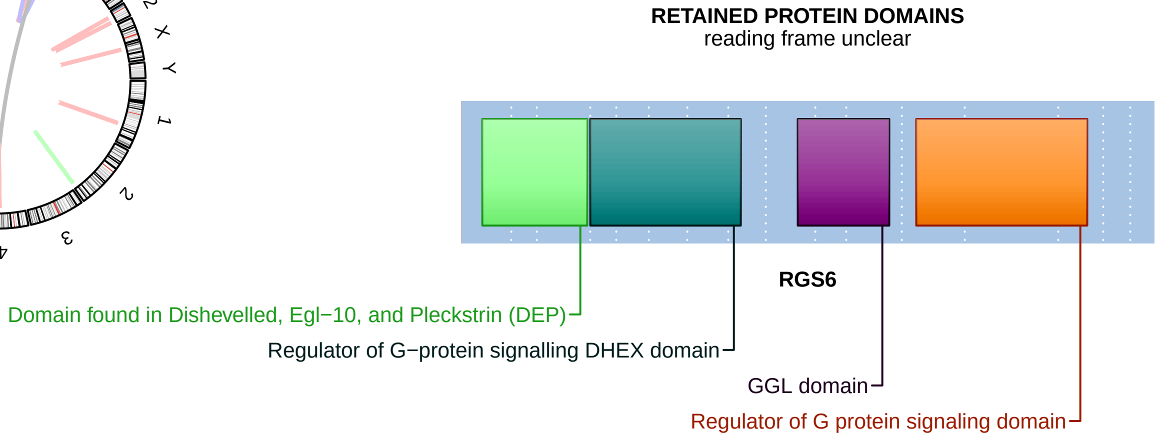


SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 2

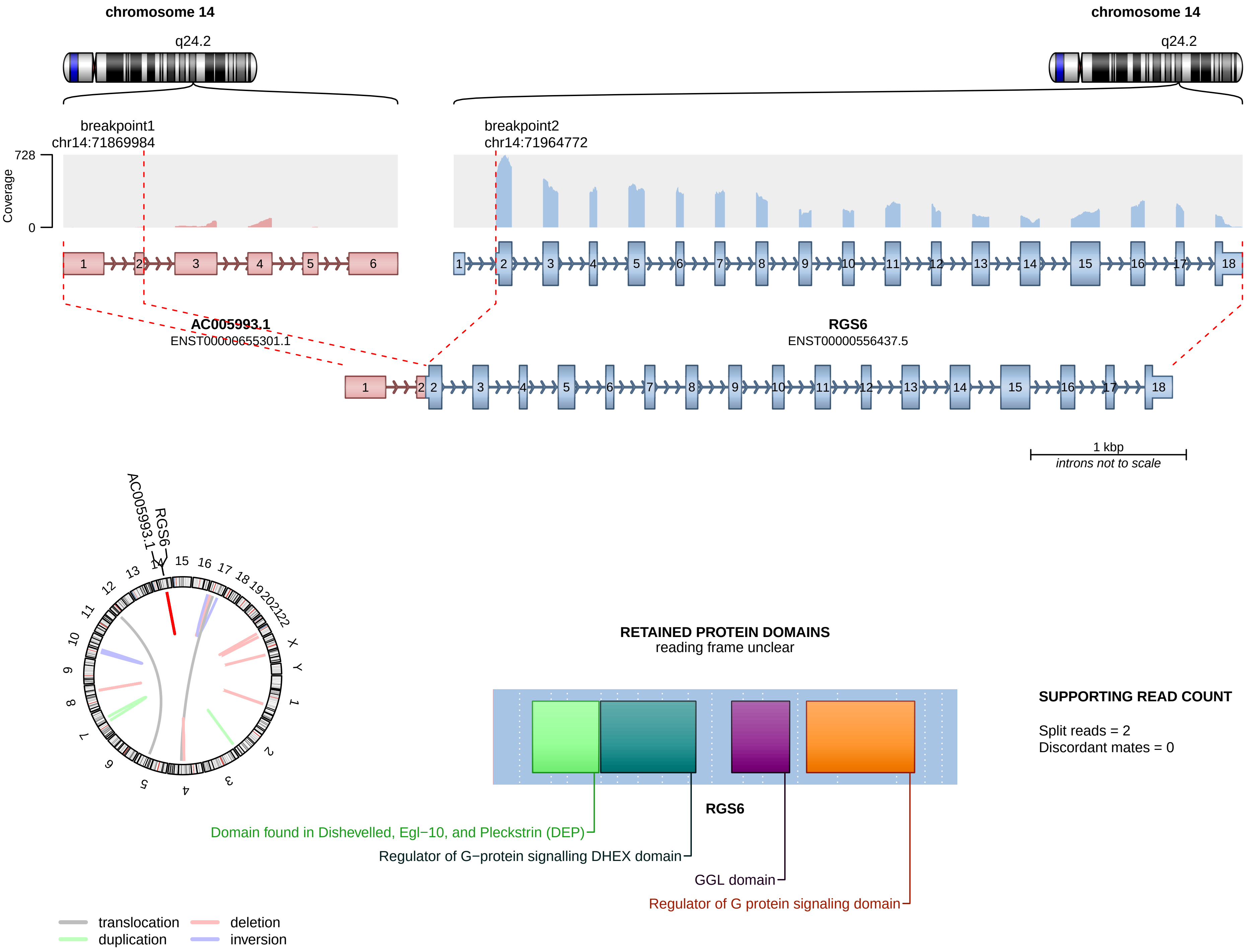


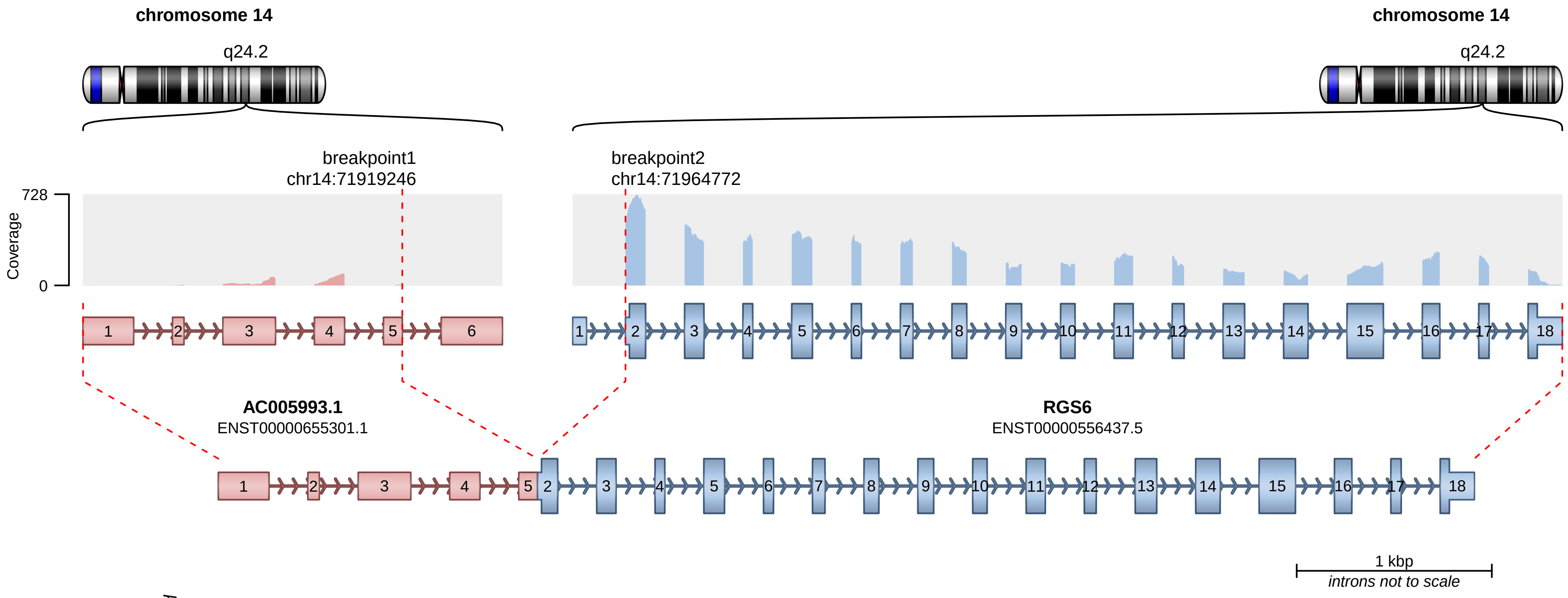


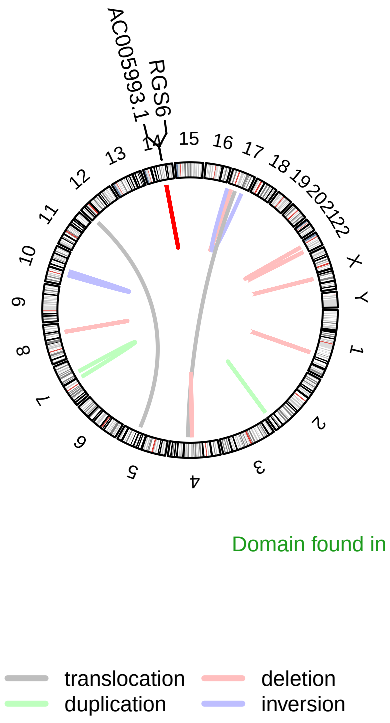


SUPPORTING READ COUNT

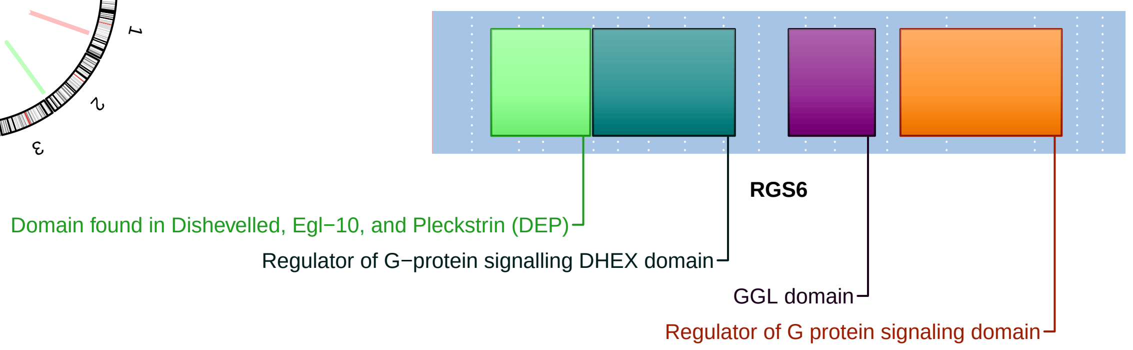
Split reads = 2
Discordant mates = 2


chromosome 14
q24.2
chromosome 14
q24.2
breakpoint1
chr14:71869984
breakpoint2
chr14:71964772
728
Coverage
0
1
2
3
4
5
6
AC005993.1
ENST00000655301.1
RGS6
ENST00000556437.5
1 kbp
introns not to scale
AC005993.1
RGS6
translocation
duplication
deletion
inversion
RETAINED PROTEIN DOMAINS
reading frame unclear
RGS6
Domain found in Dishevelled, Egl−10, and Pleckstrin (DEP)
Regulator of G−protein signalling DHEX domain
GGL domain
Regulator of G protein signaling domain
SUPPORTING READ COUNT
Split reads = 2
Discordant mates = 0



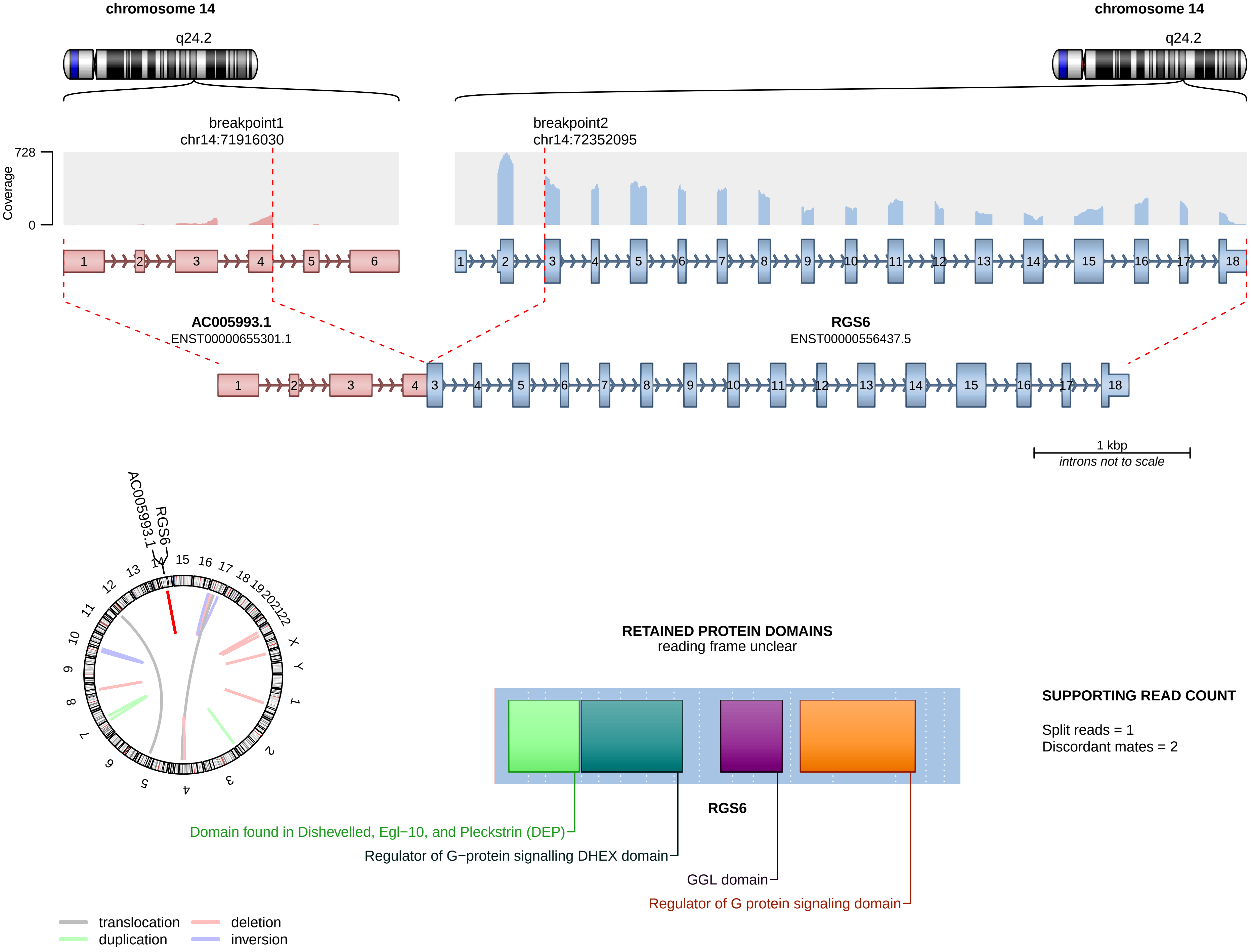


RETAINED PROTEIN DOMAINS
reading frame unclear



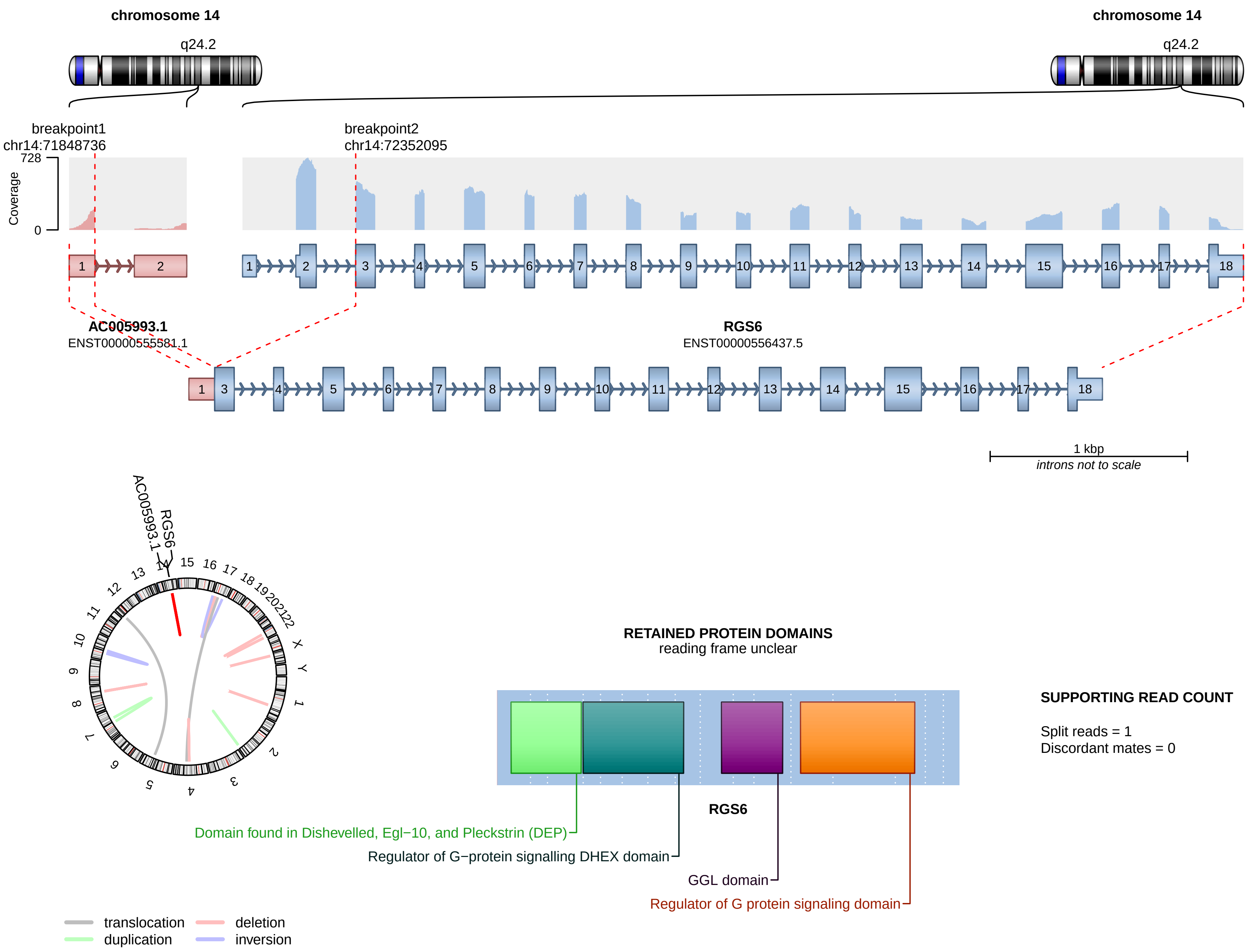
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 3



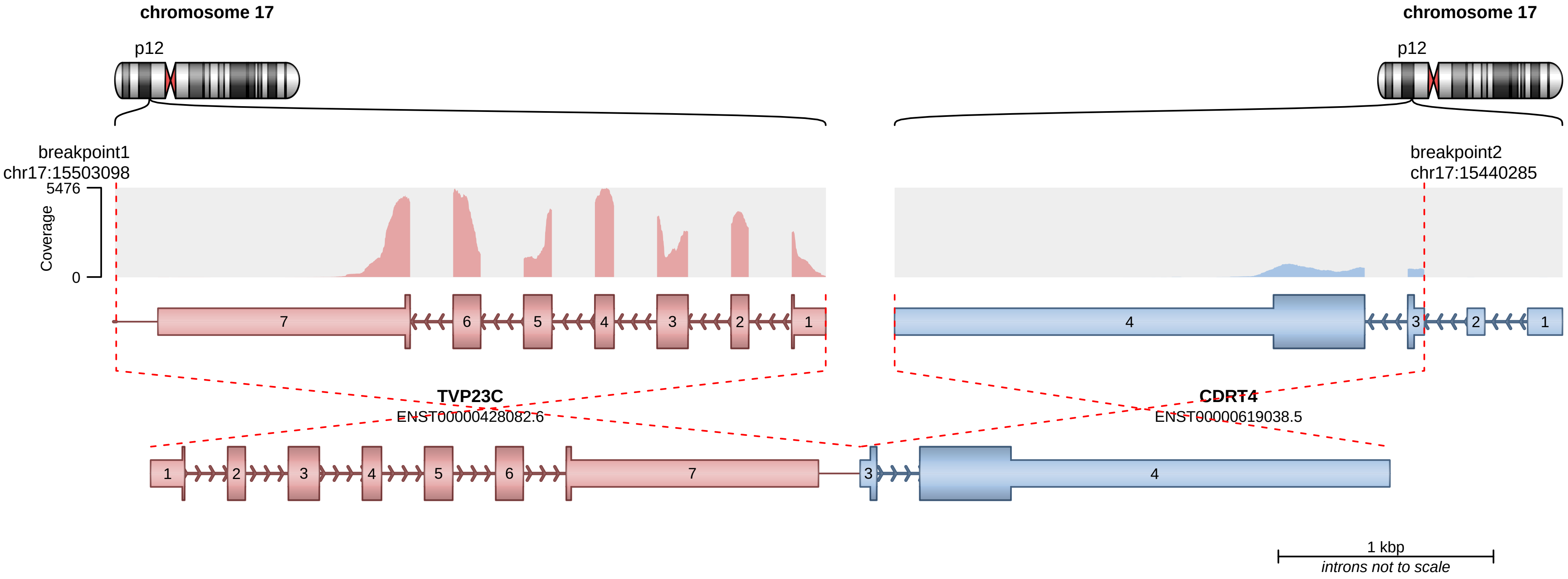
SUPPORTING READ COUNT

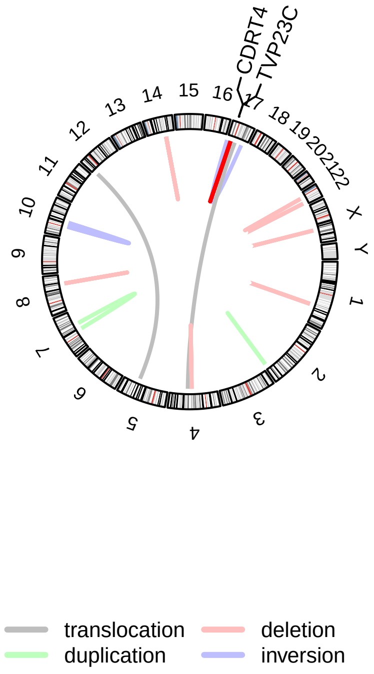
Split reads = 1
Discordant mates = 2

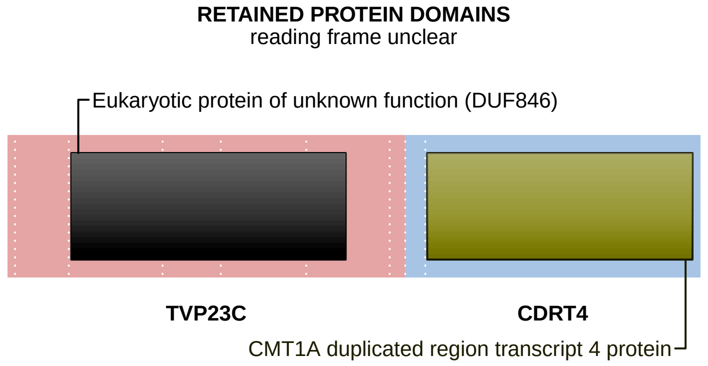


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

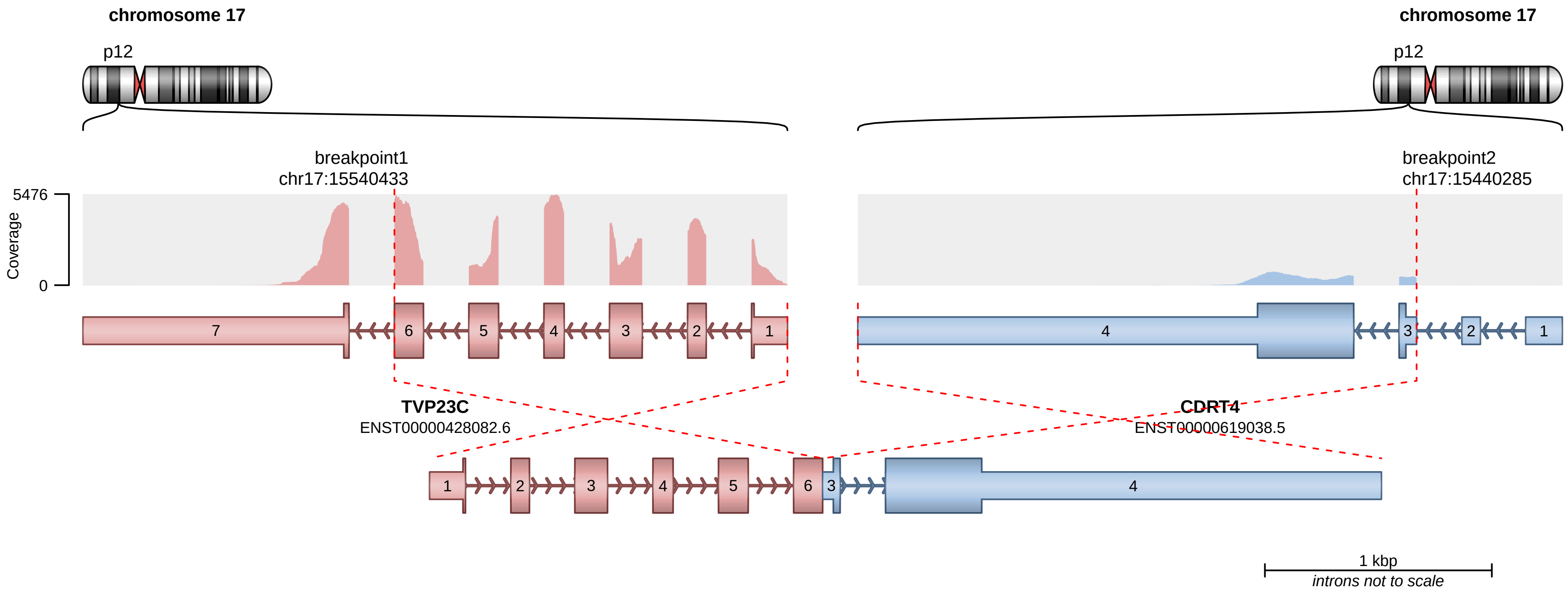


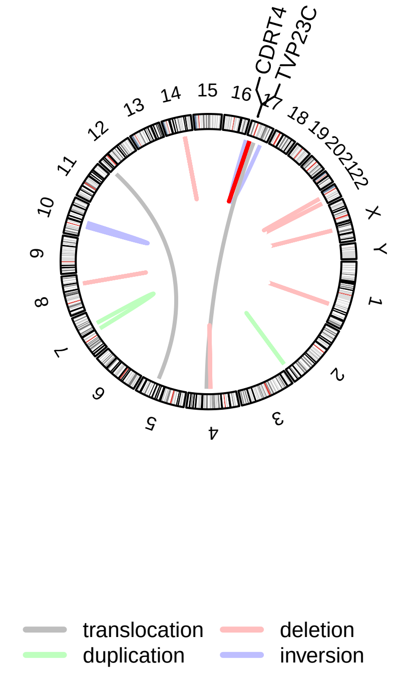


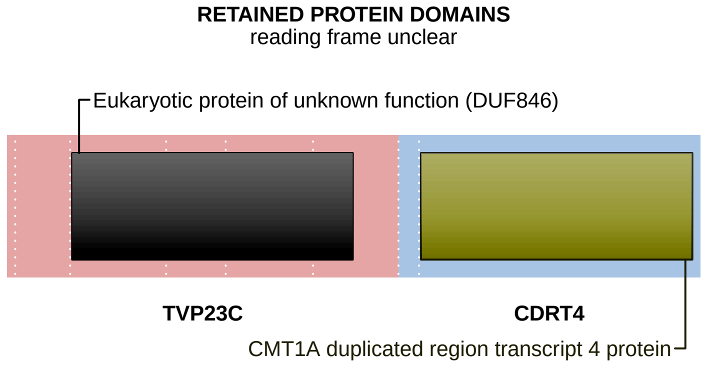


SUPPORTING READ COUNT

Split reads = 68
Discordant mates = 5

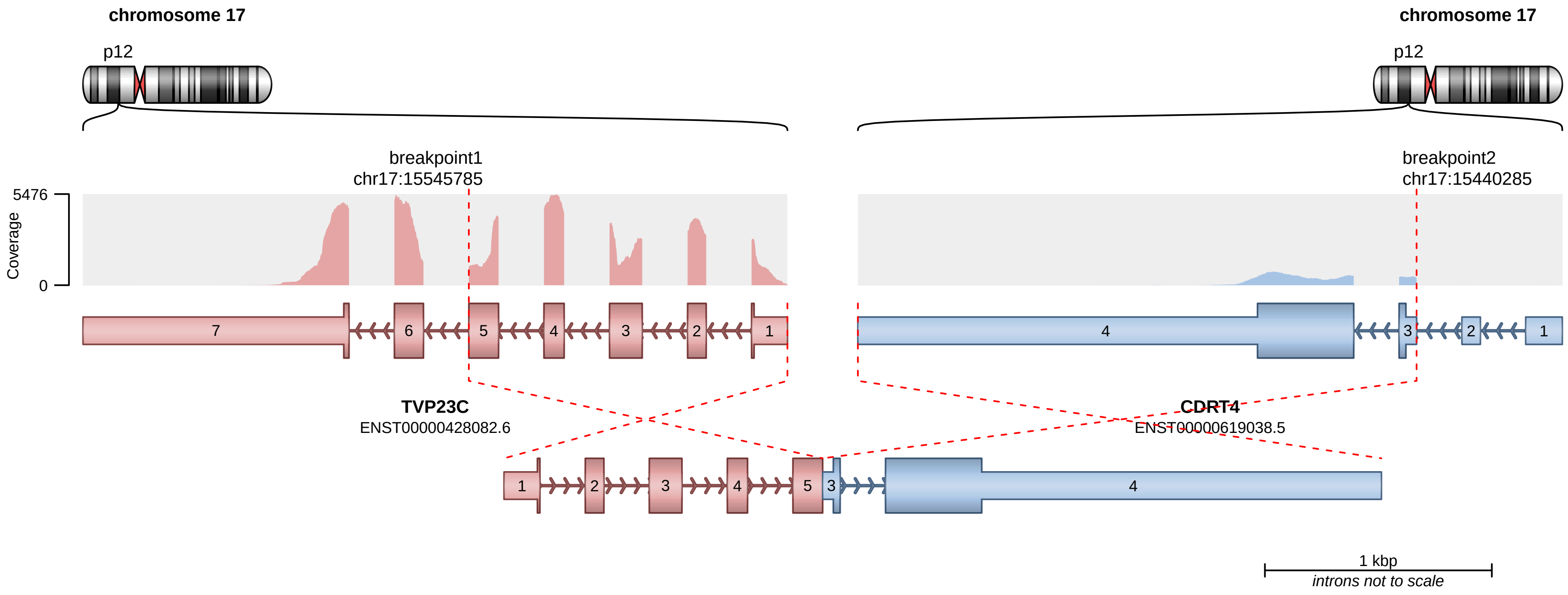


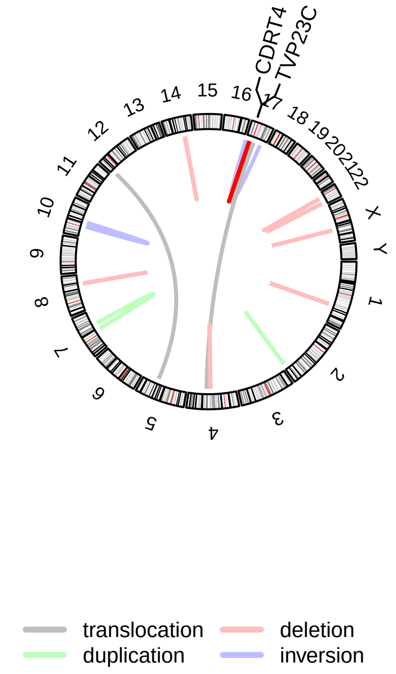


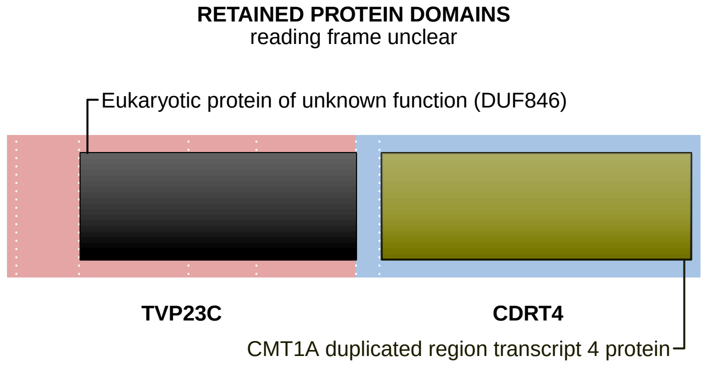


SUPPORTING READ COUNT

Split reads = 38
Discordant mates = 1

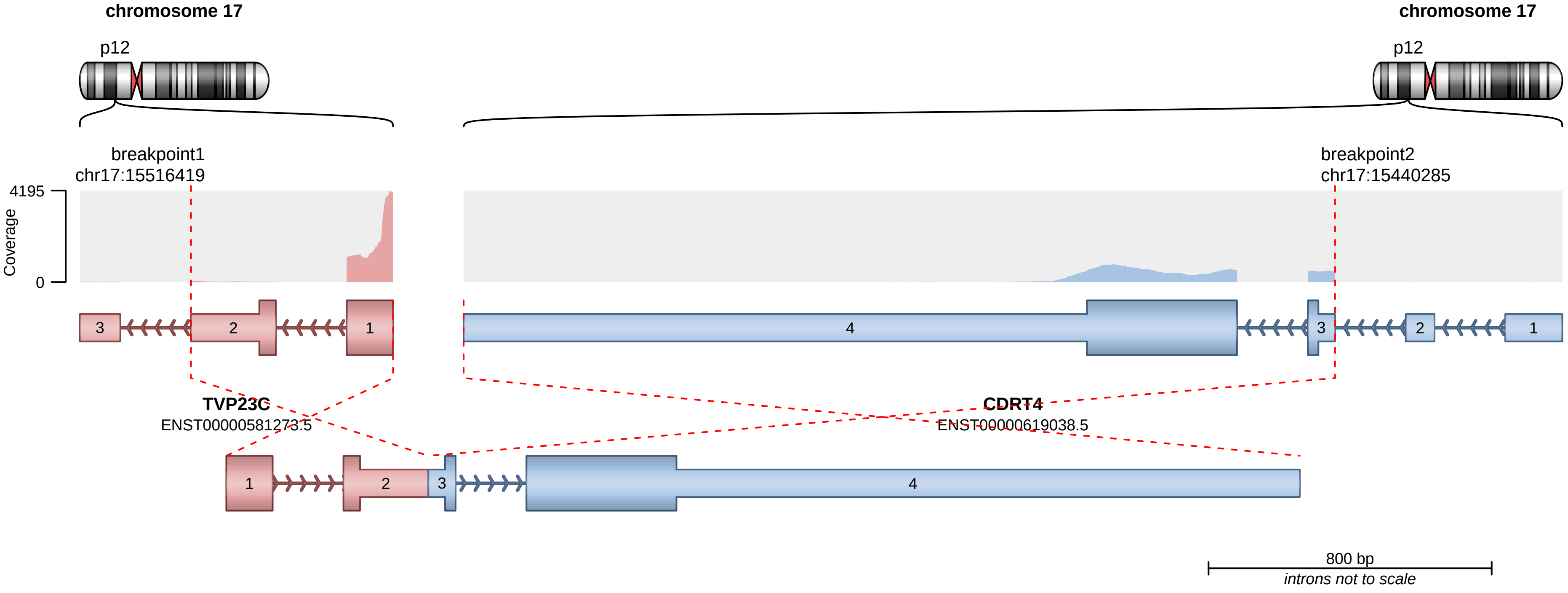


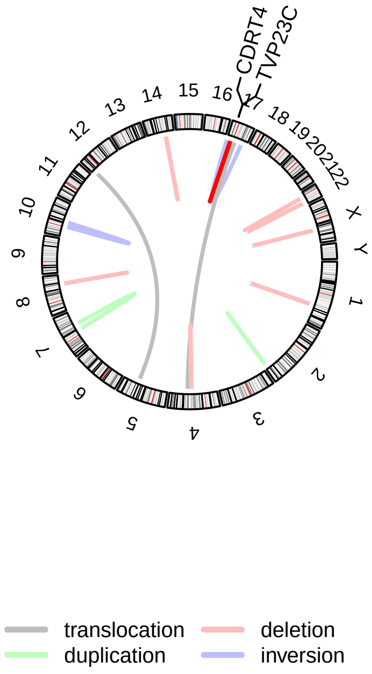


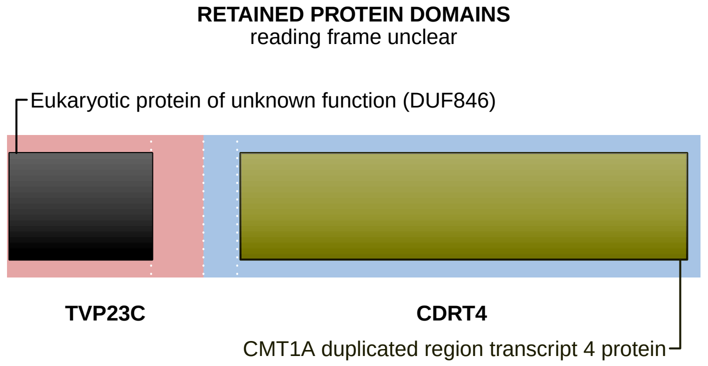


SUPPORTING READ COUNT

Split reads = 27
Discordant mates = 1

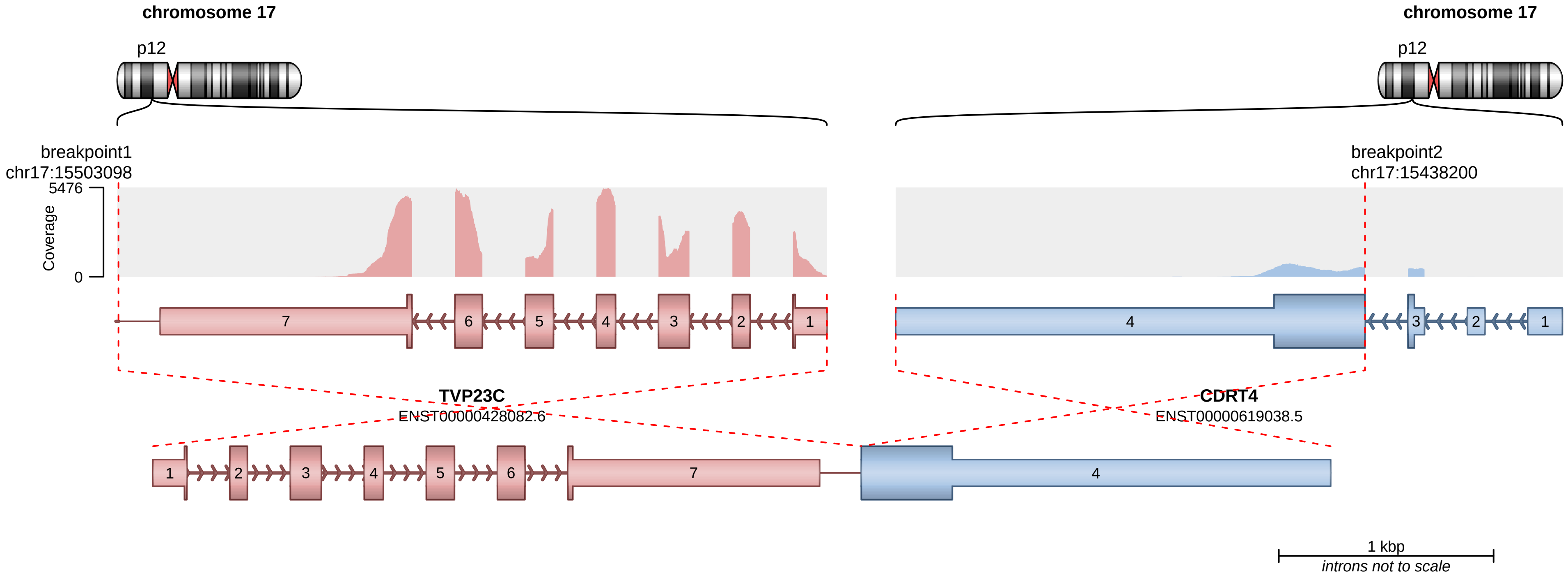


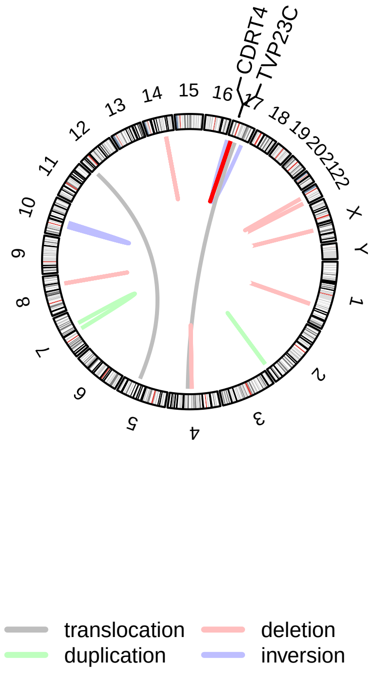


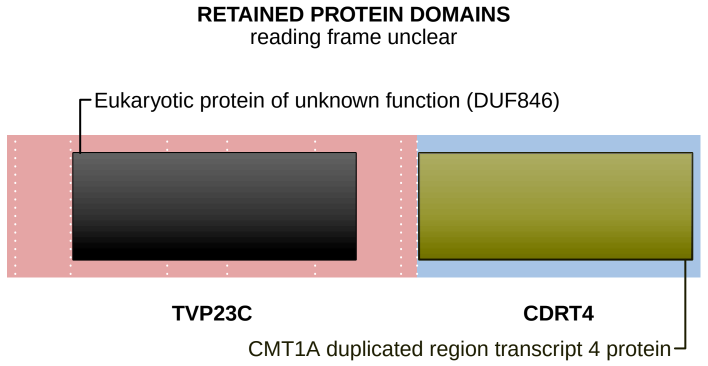


SUPPORTING READ COUNT

Split reads = 13
Discordant mates = 2

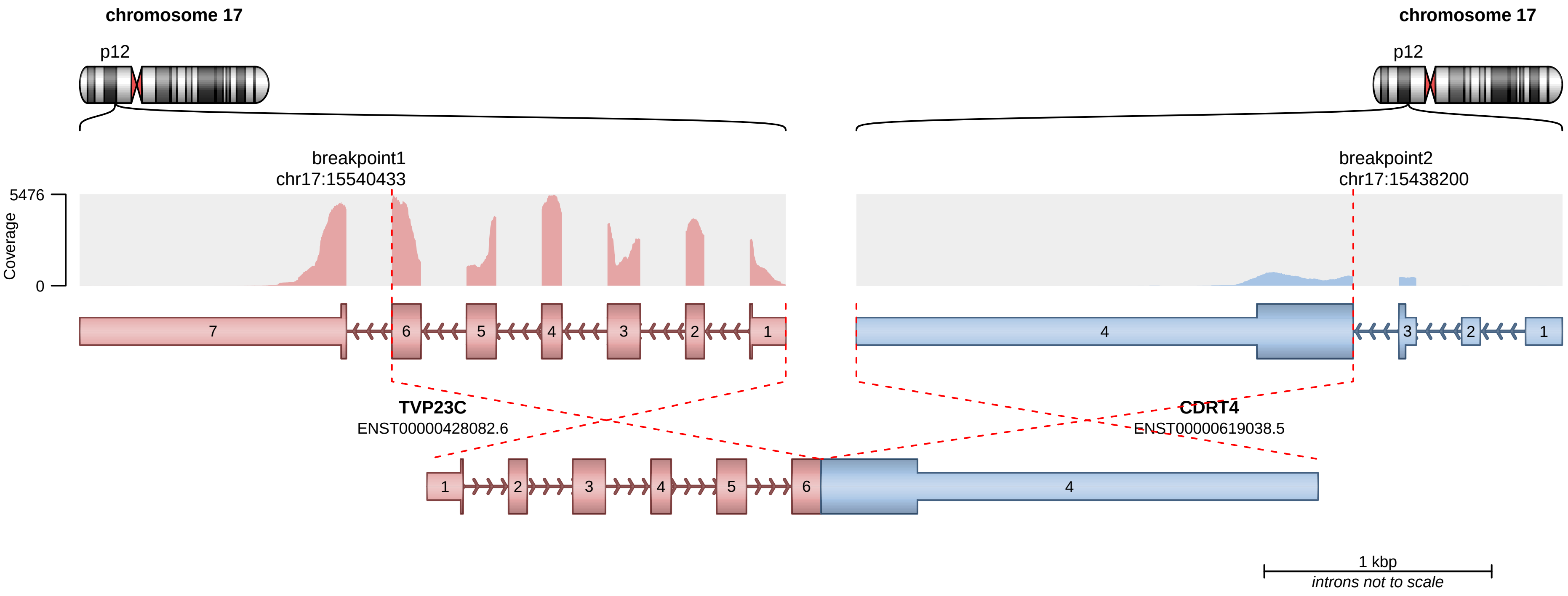


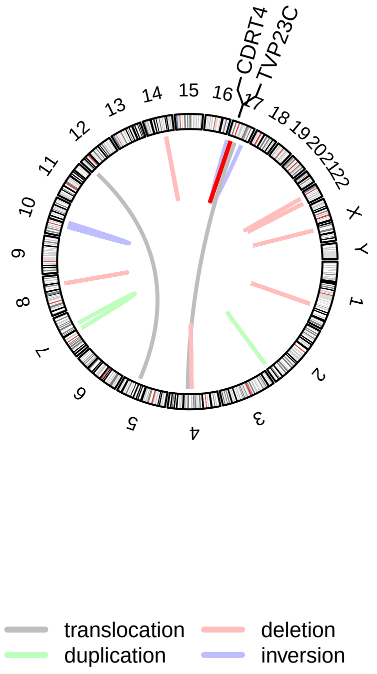




SUPPORTING READ COUNT

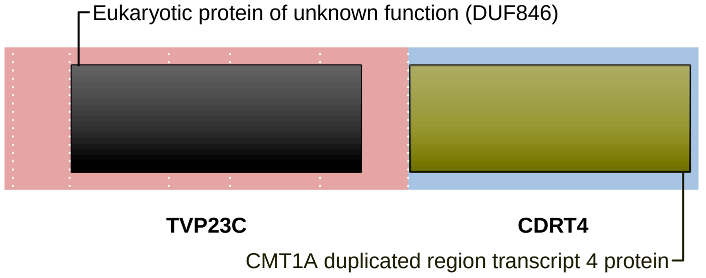
Split reads = 13
Discordant mates = 0





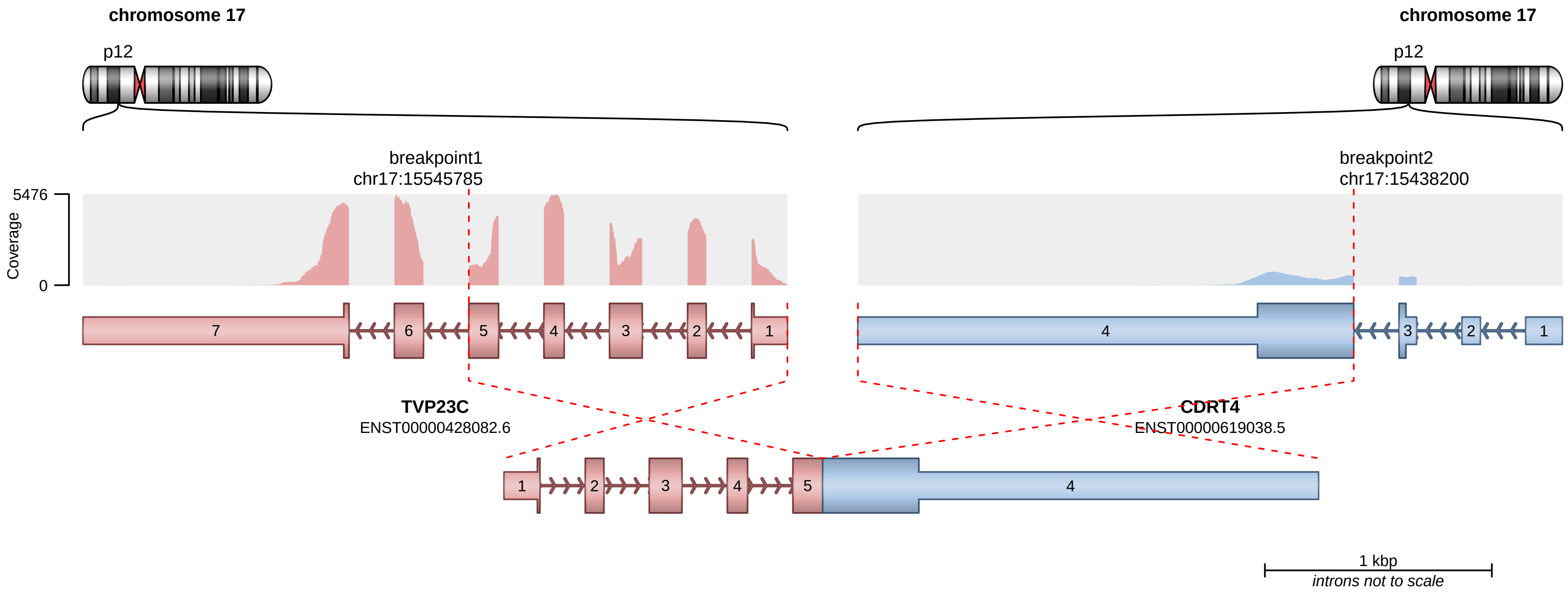
RETAINED PROTEIN DOMAINS

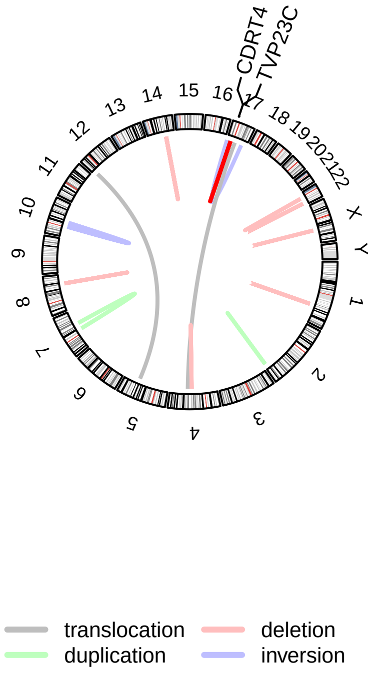
reading frame unclear

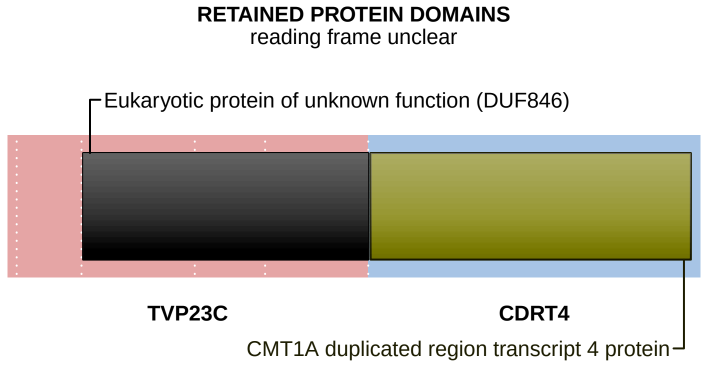


SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 0

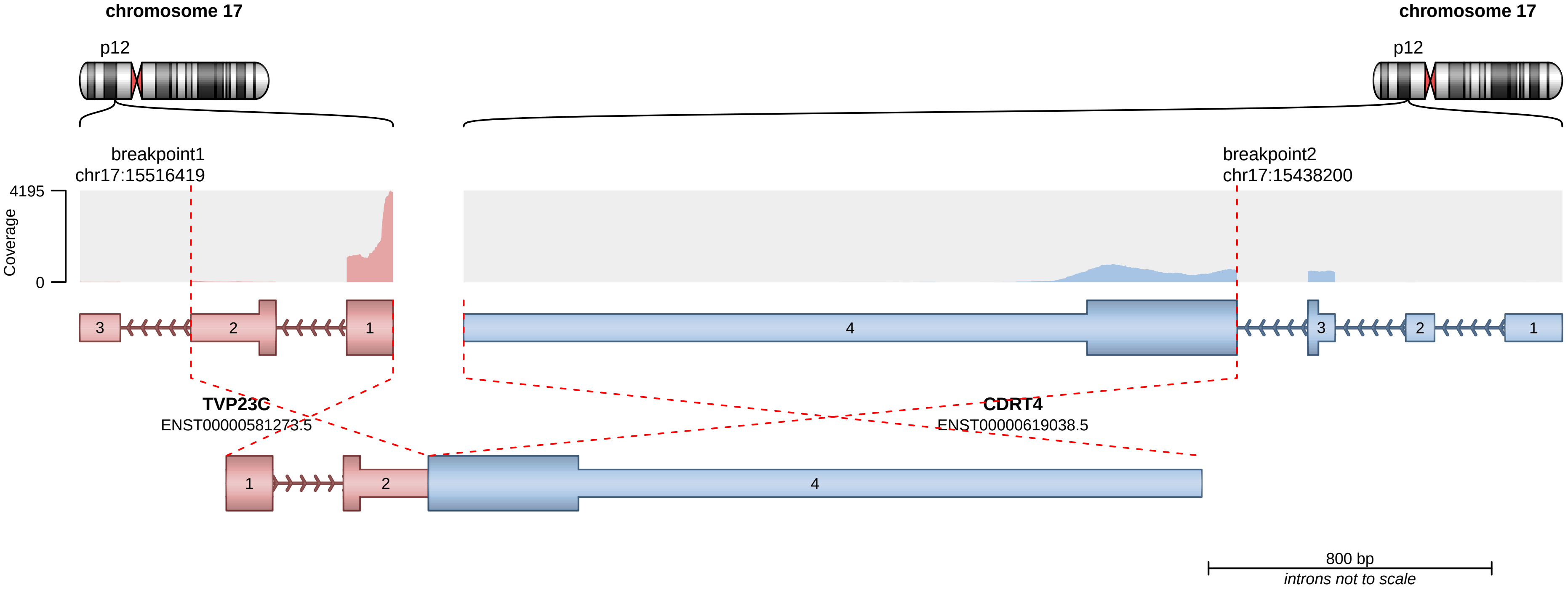


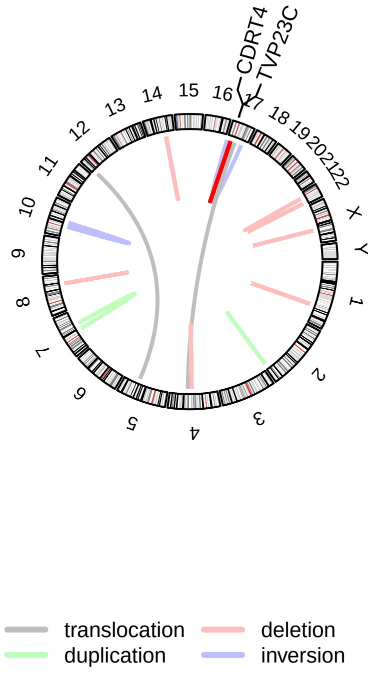


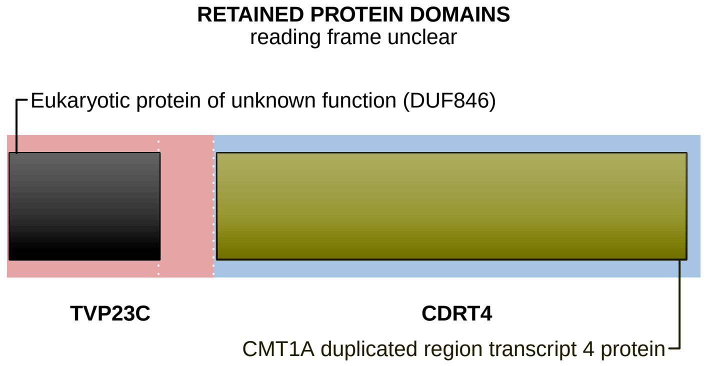


SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

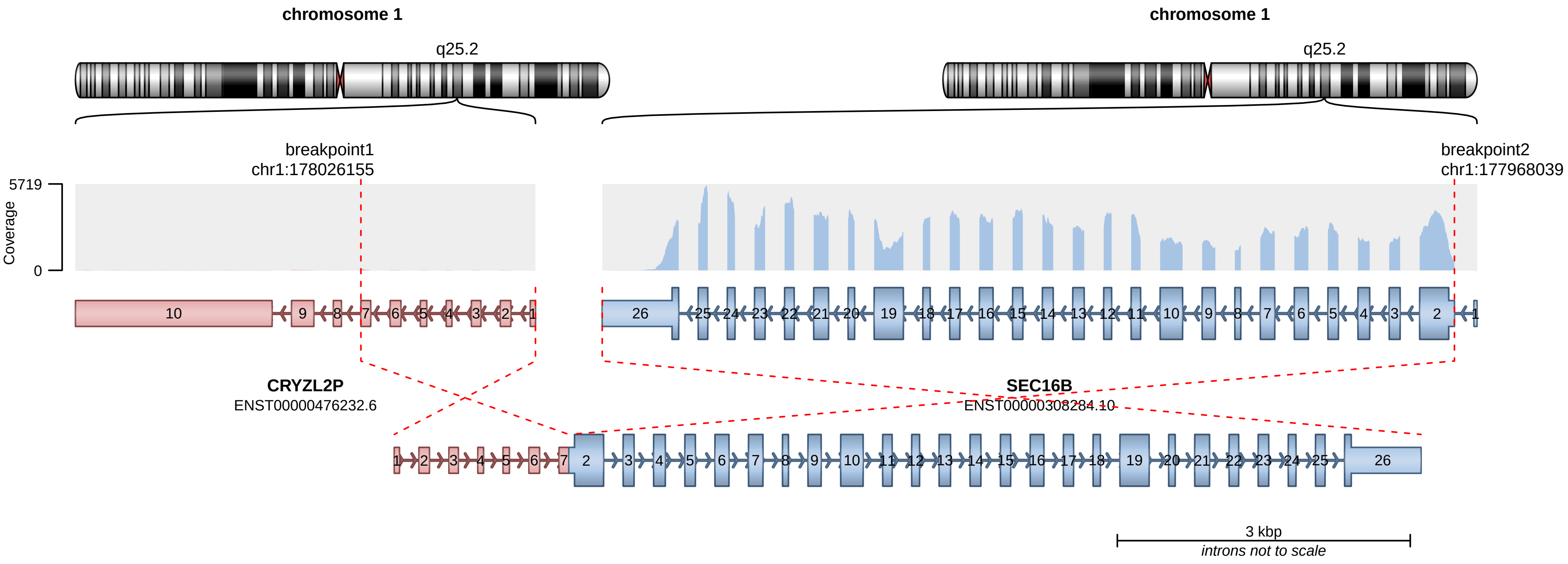


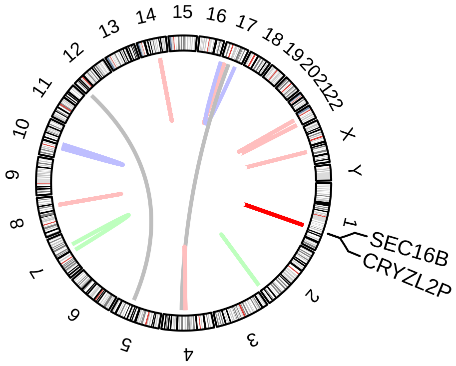


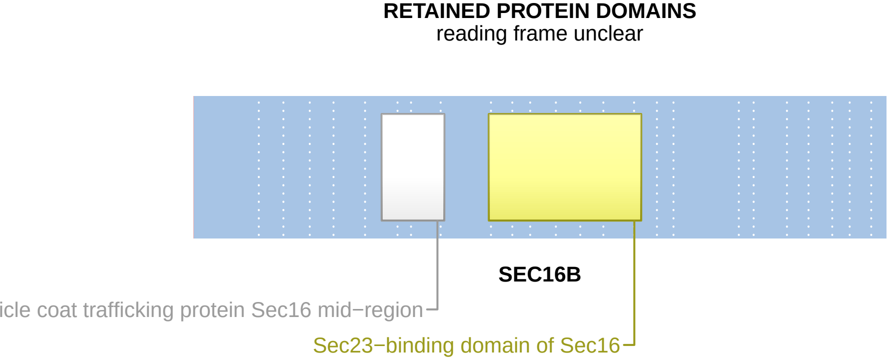


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



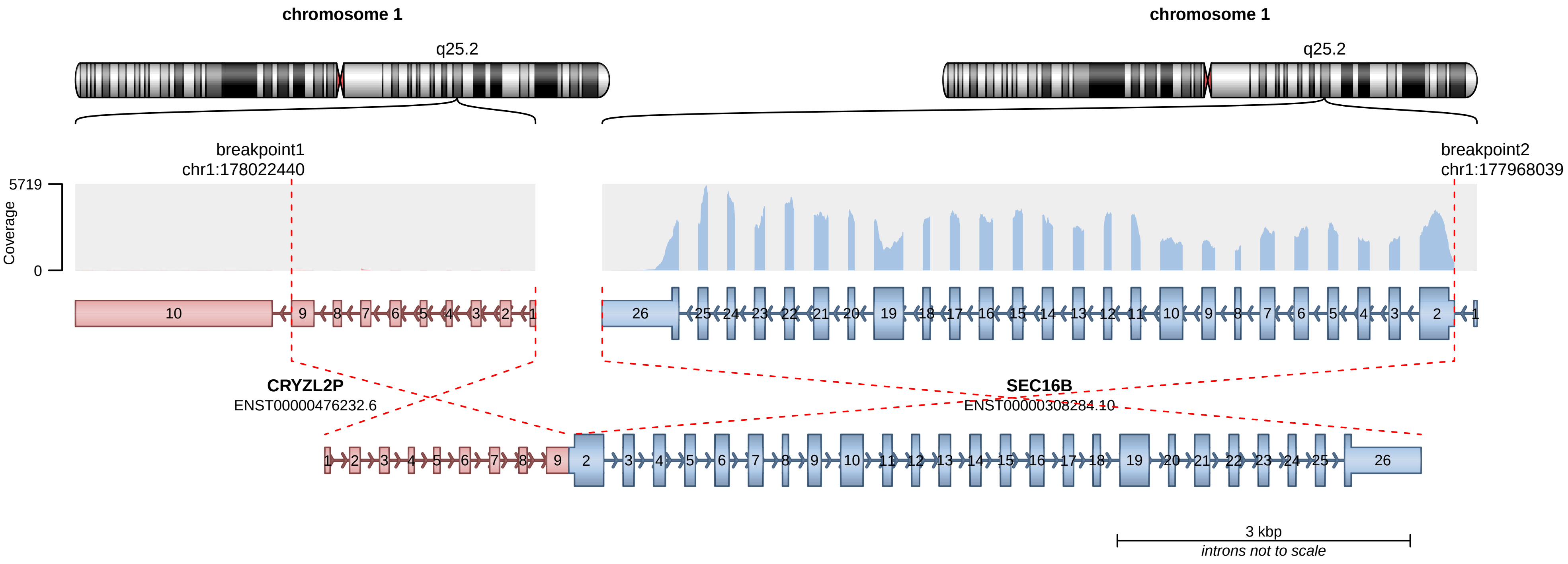


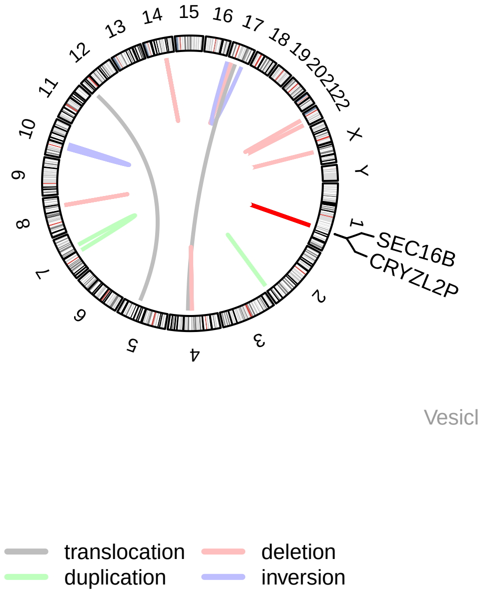


SUPPORTING READ COUNT

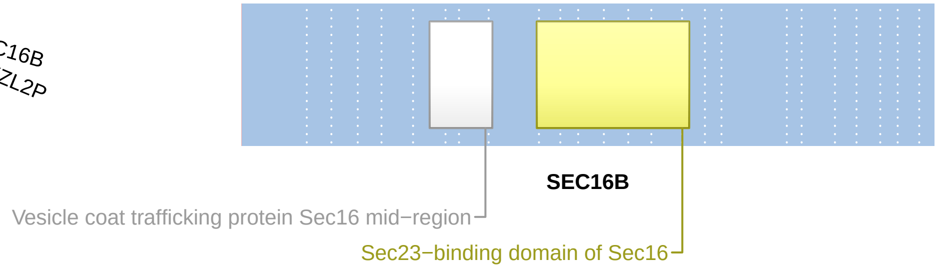
Split reads = 58
Discordant mates = 1

translocation   deletion
duplication   inversion



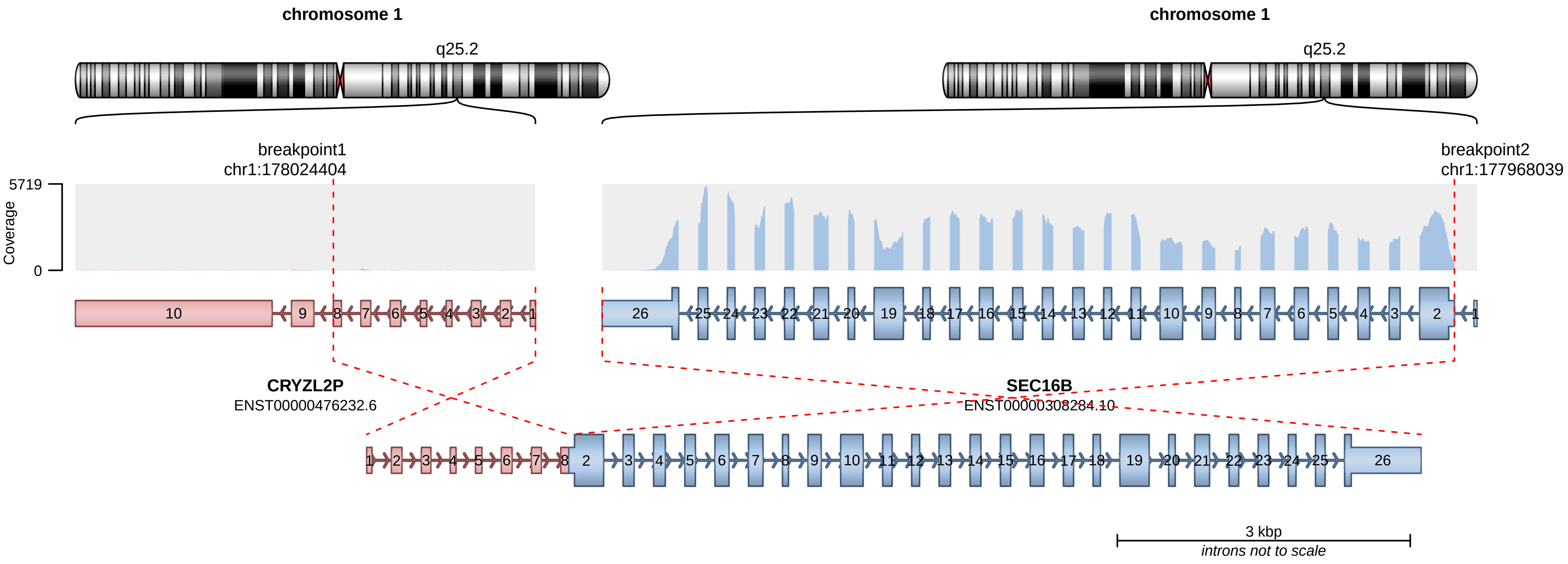


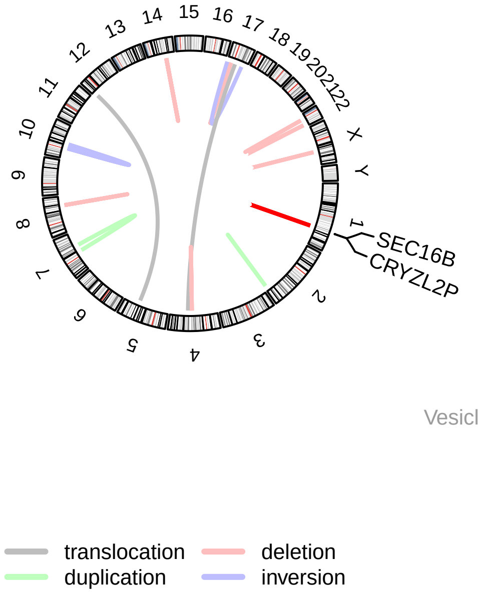
RETAINED PROTEIN DOMAINS
reading frame unclear

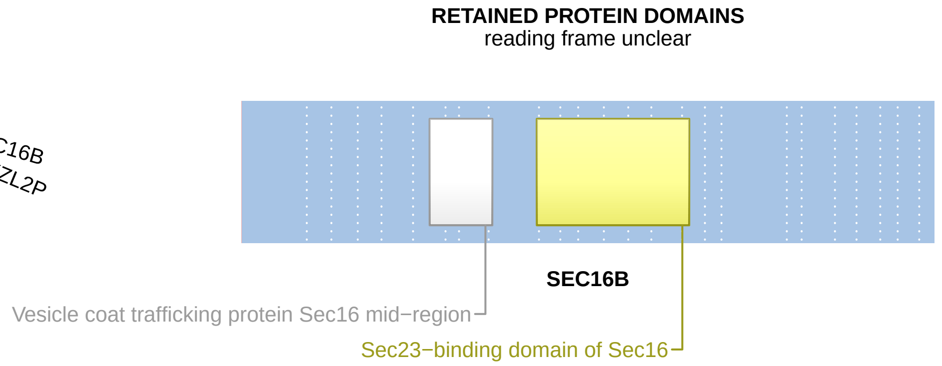


SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 1

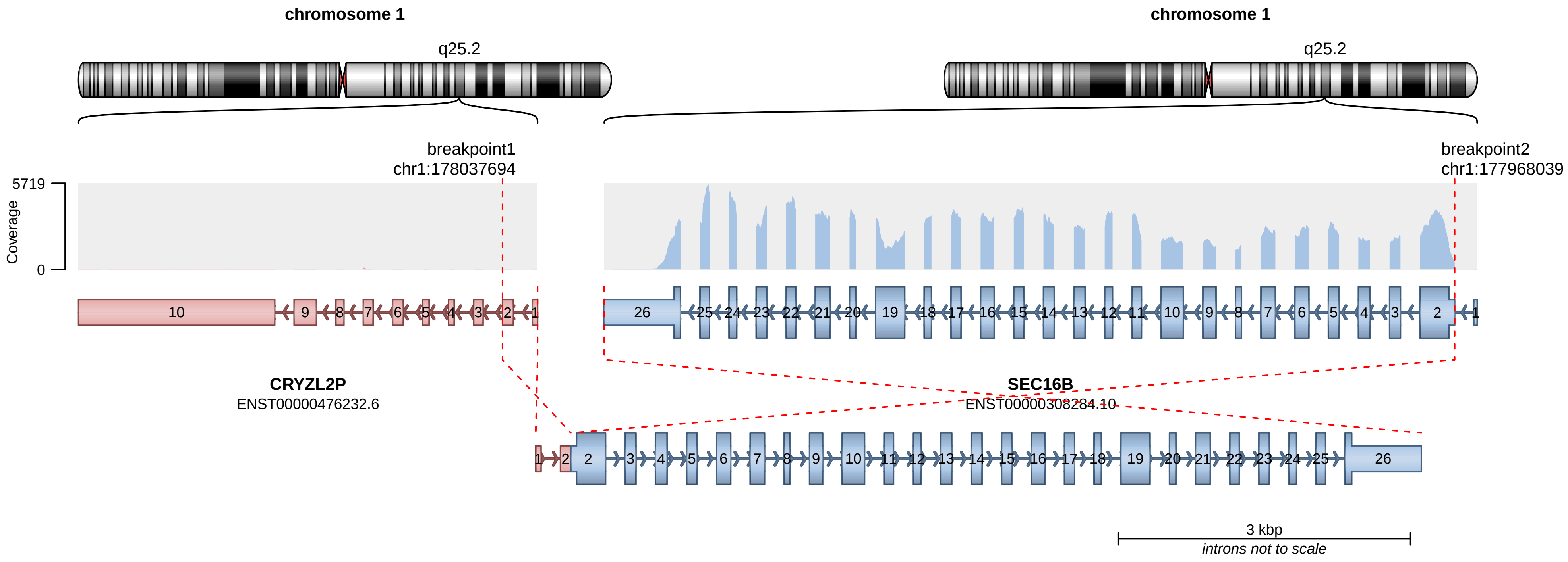


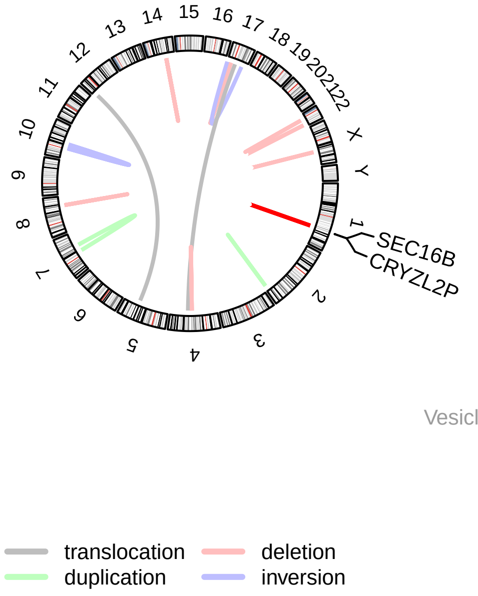


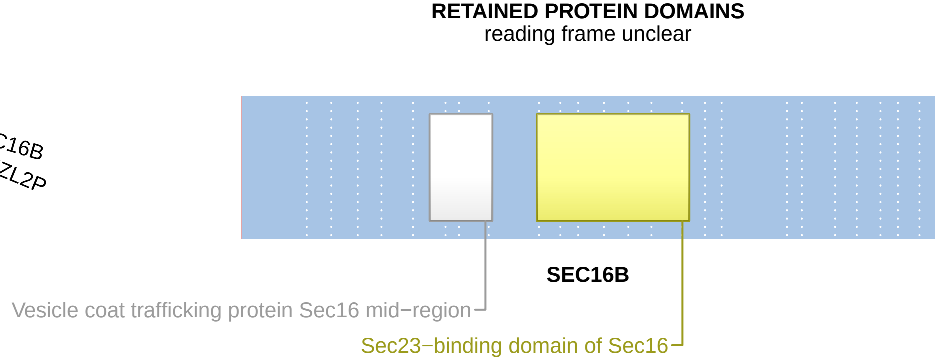


SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 1

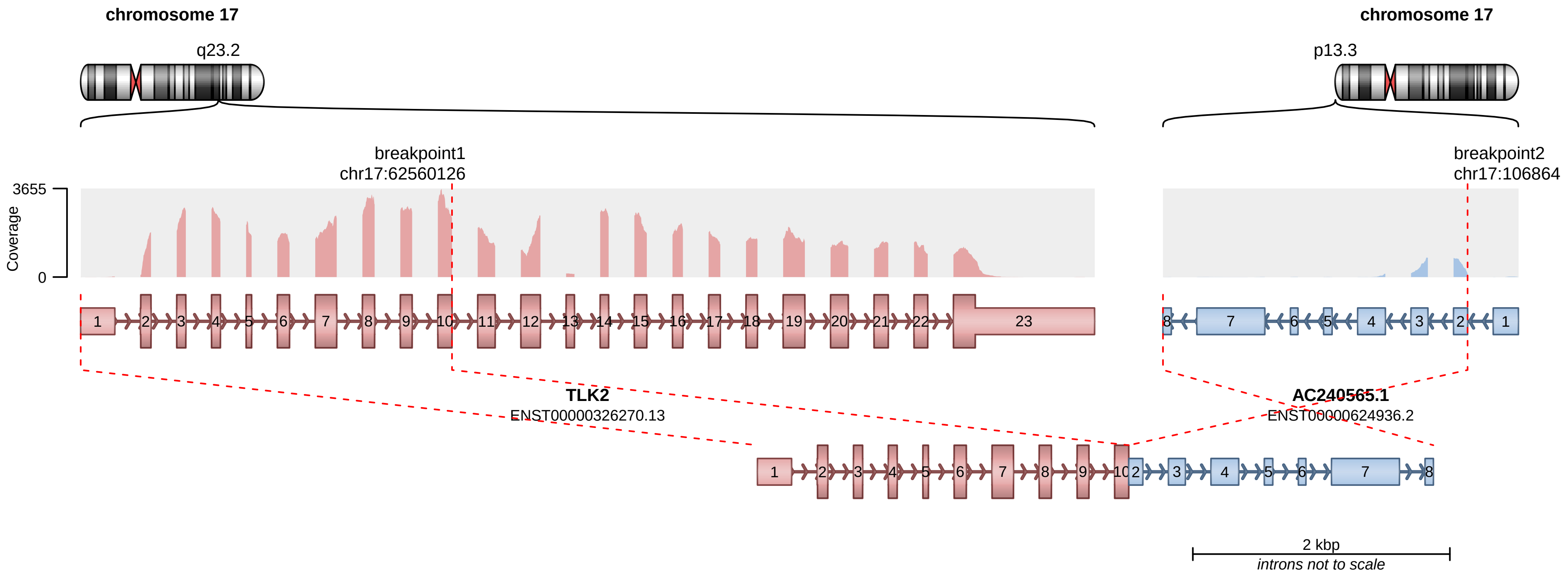


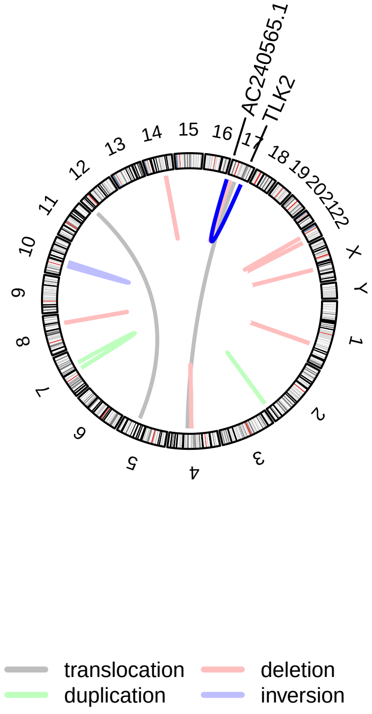




SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

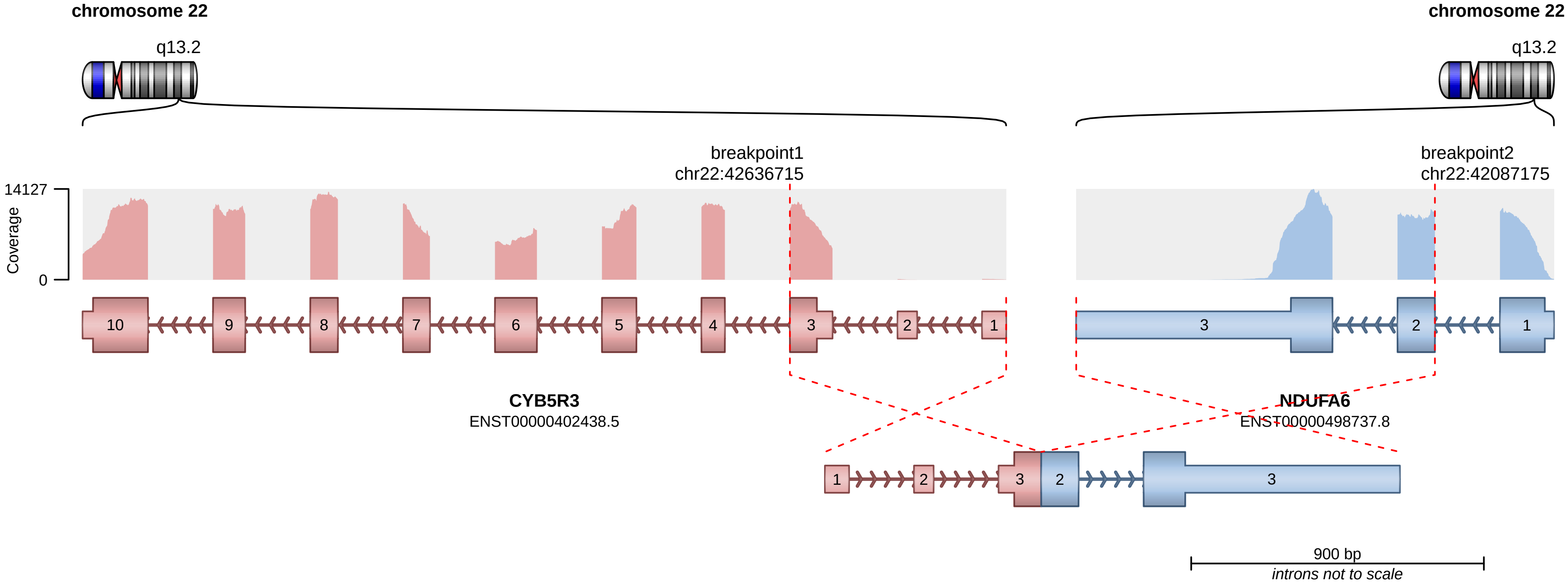


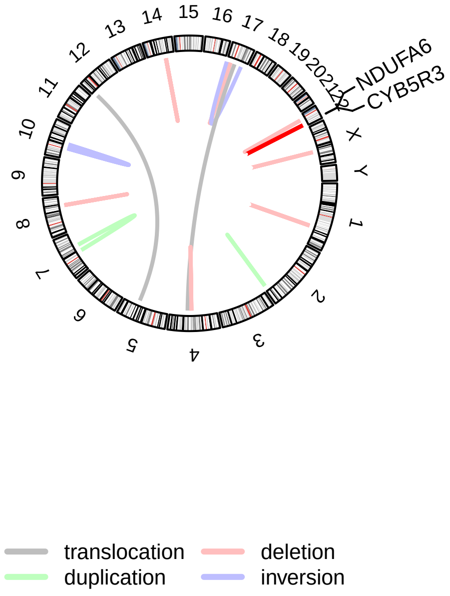


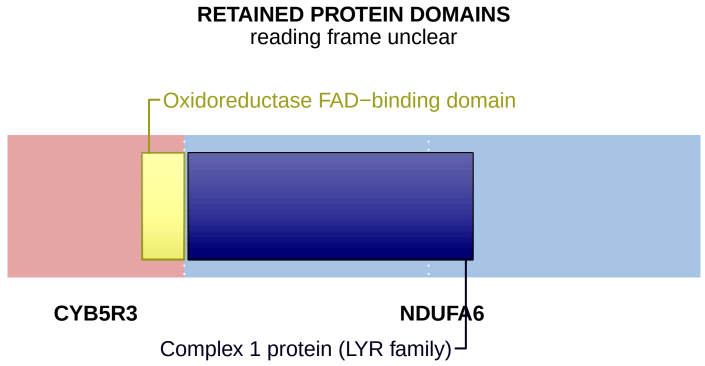
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 56
Discordant mates = 0

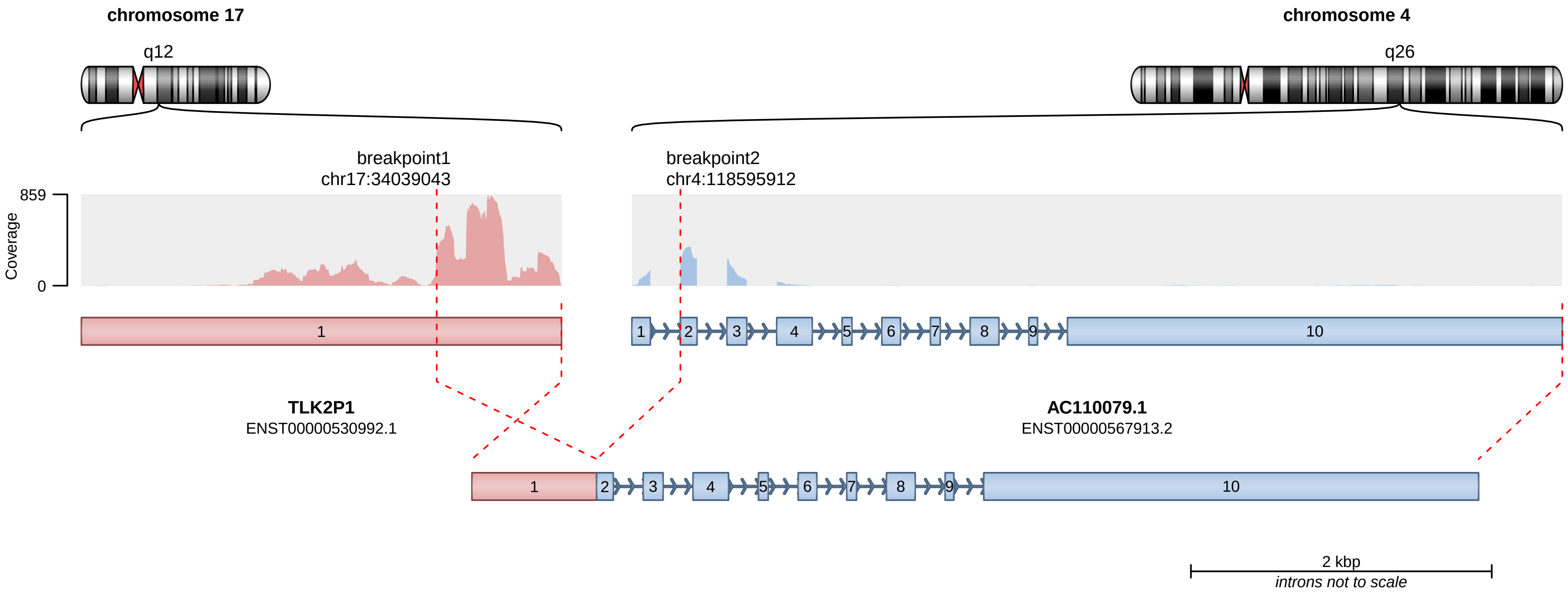


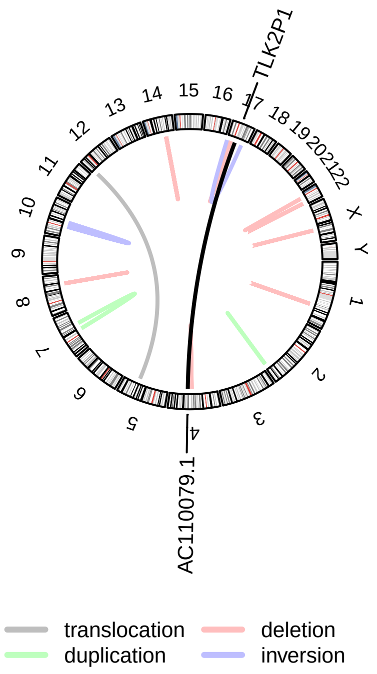




SUPPORTING READ COUNT

Split reads = 44
Discordant mates = 2

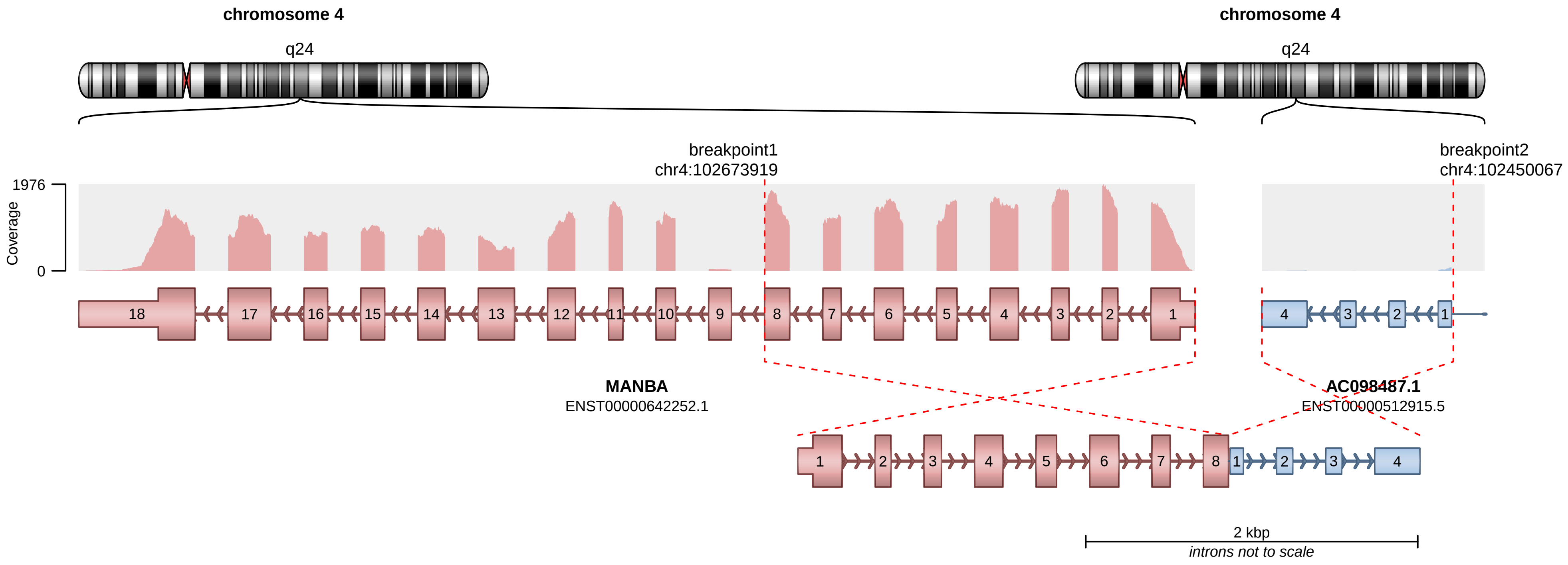


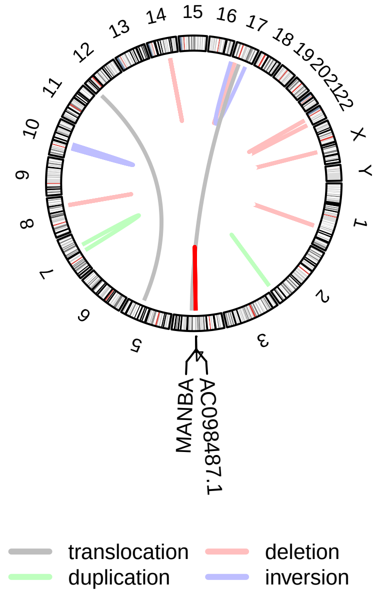


Genes are not protein−coding.

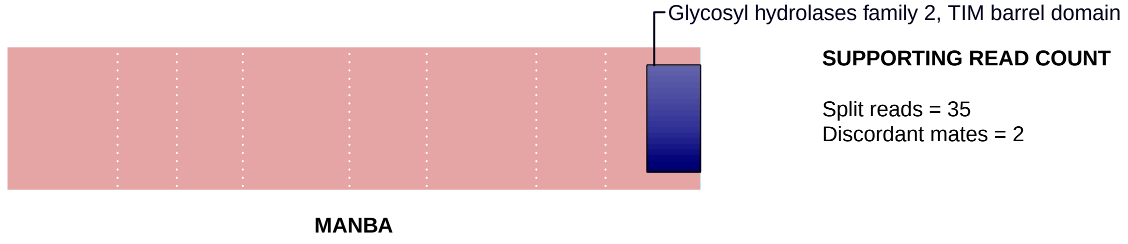
SUPPORTING READ COUNT

Split reads = 44
Discordant mates = 1



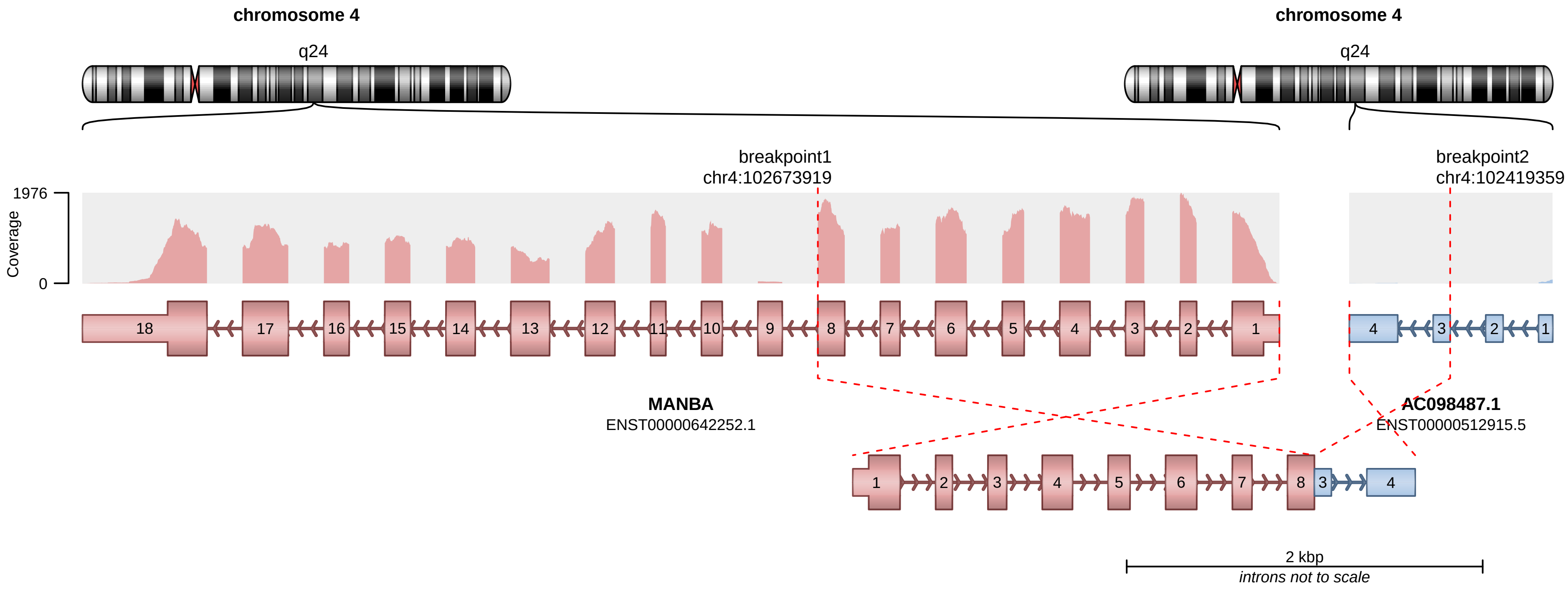


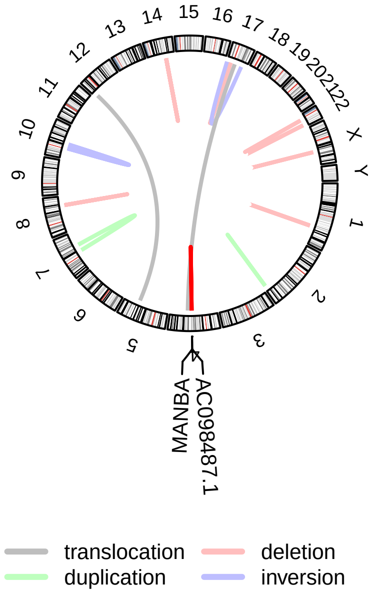
RETAINED PROTEIN DOMAINS
reading frame unclear

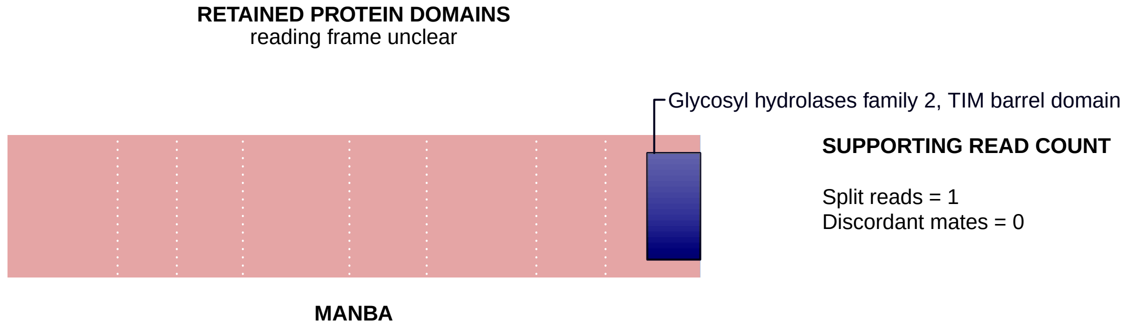


SUPPORTING READ COUNT

Split reads = 35
Discordant mates = 2

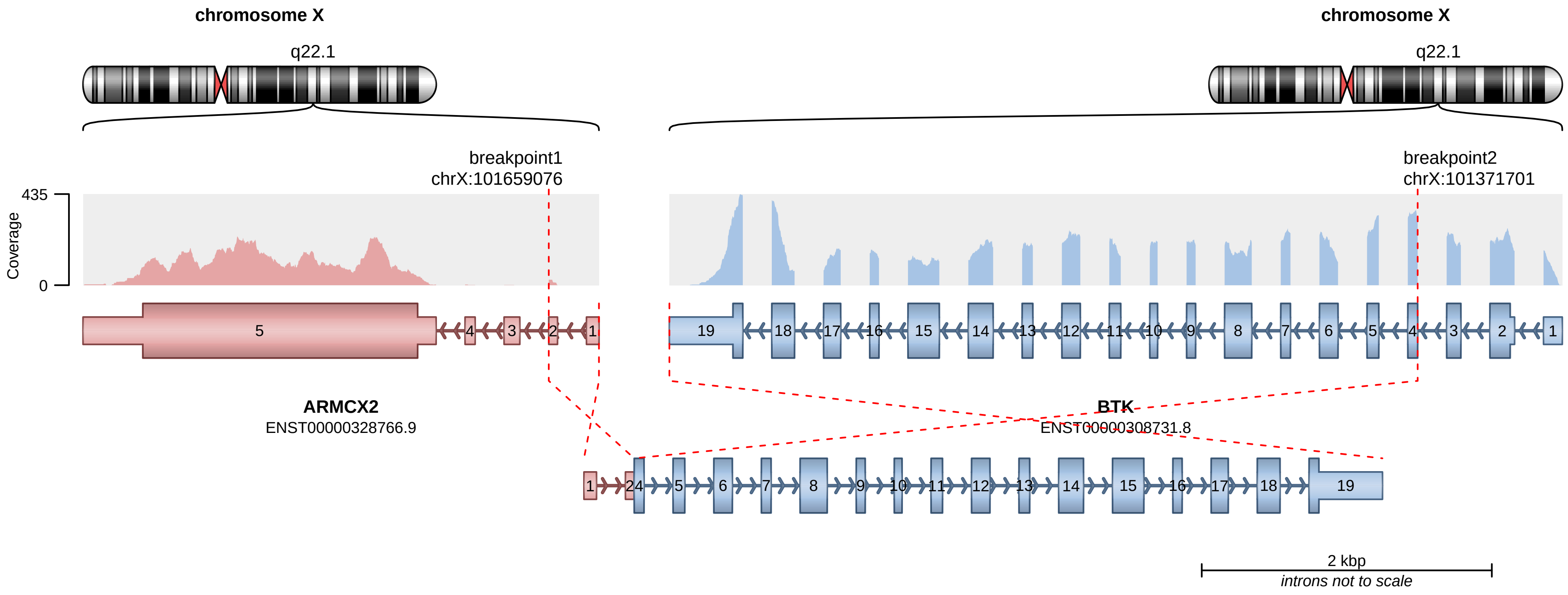


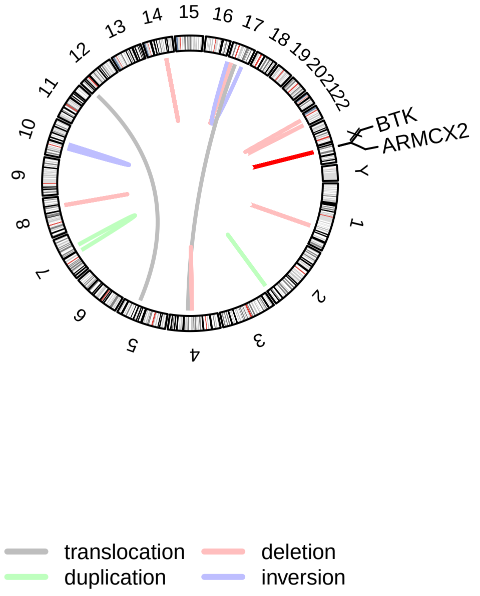


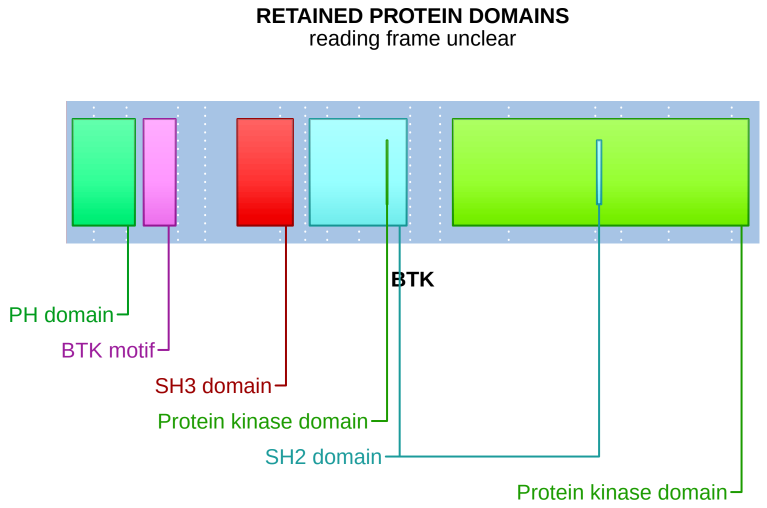


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

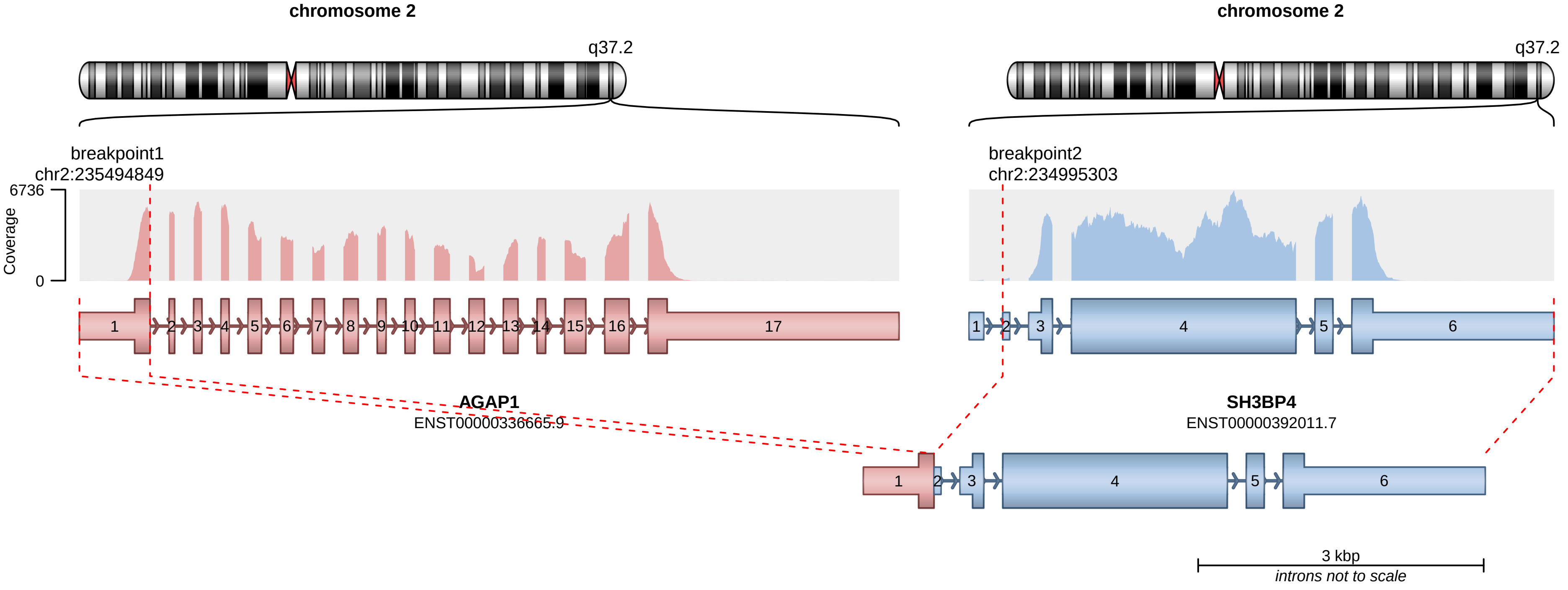


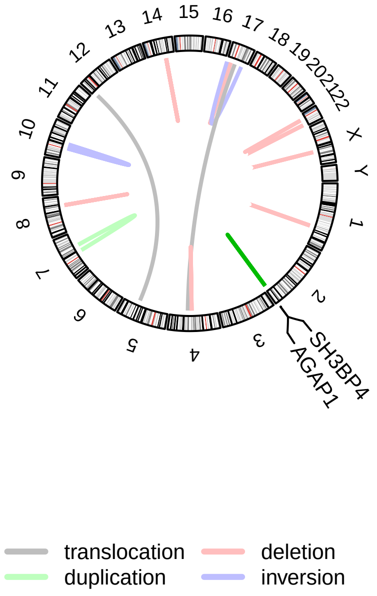


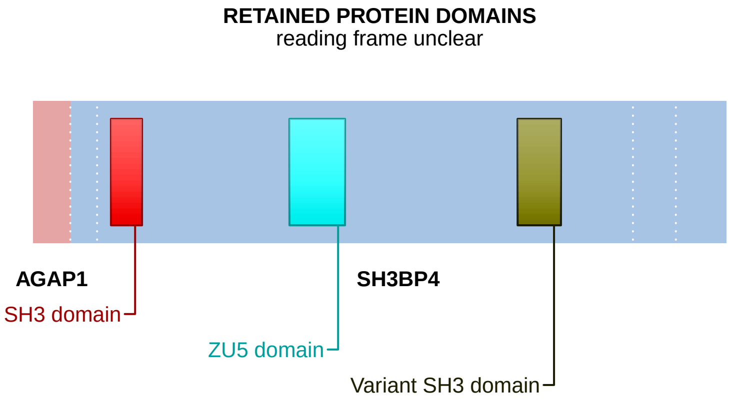


SUPPORTING READ COUNT

Split reads = 20
Discordant mates = 0

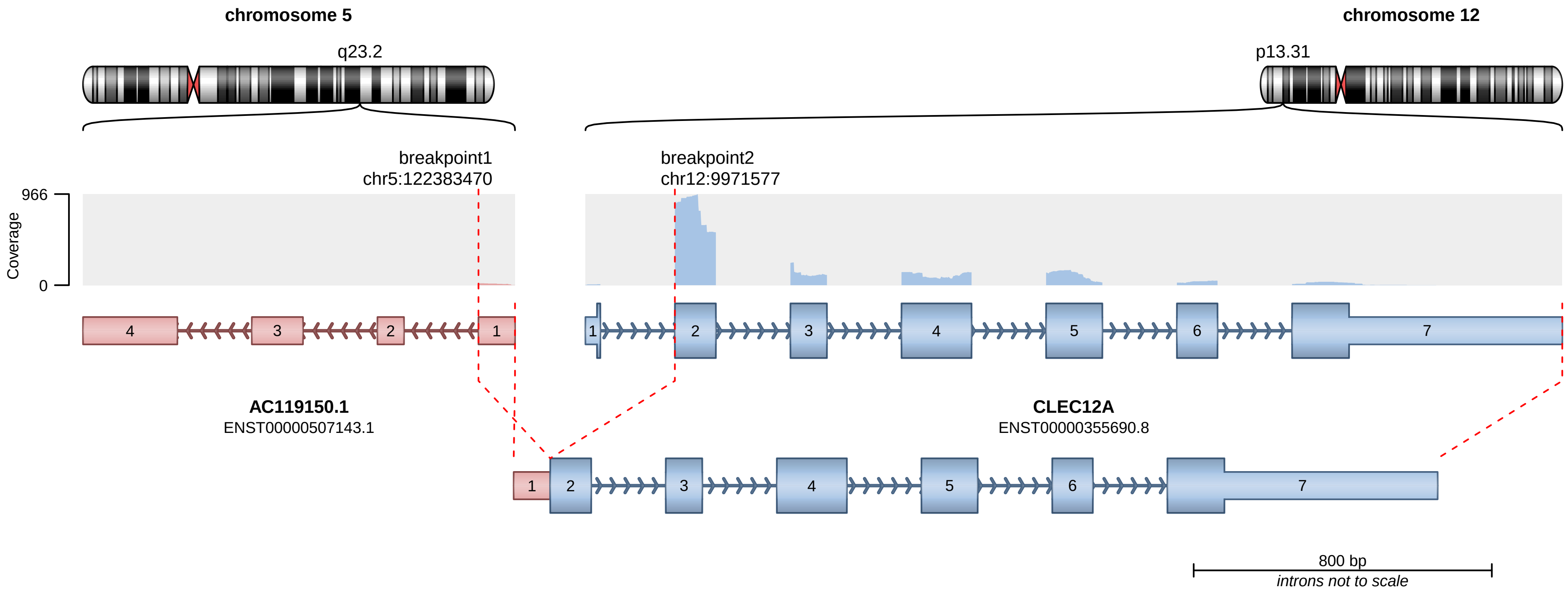


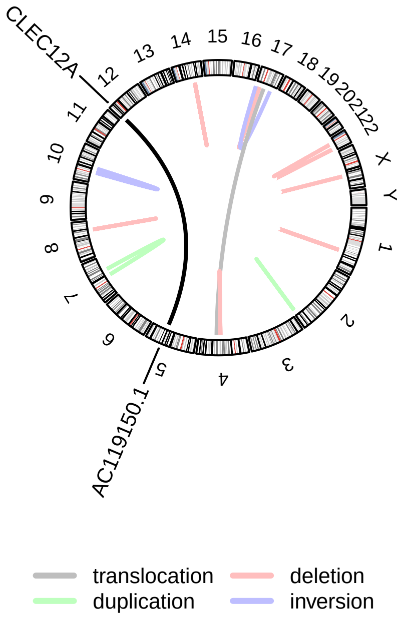




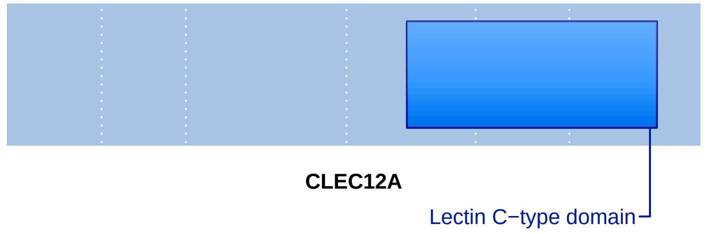
SUPPORTING READ COUNT

Split reads = 15
Discordant mates = 1



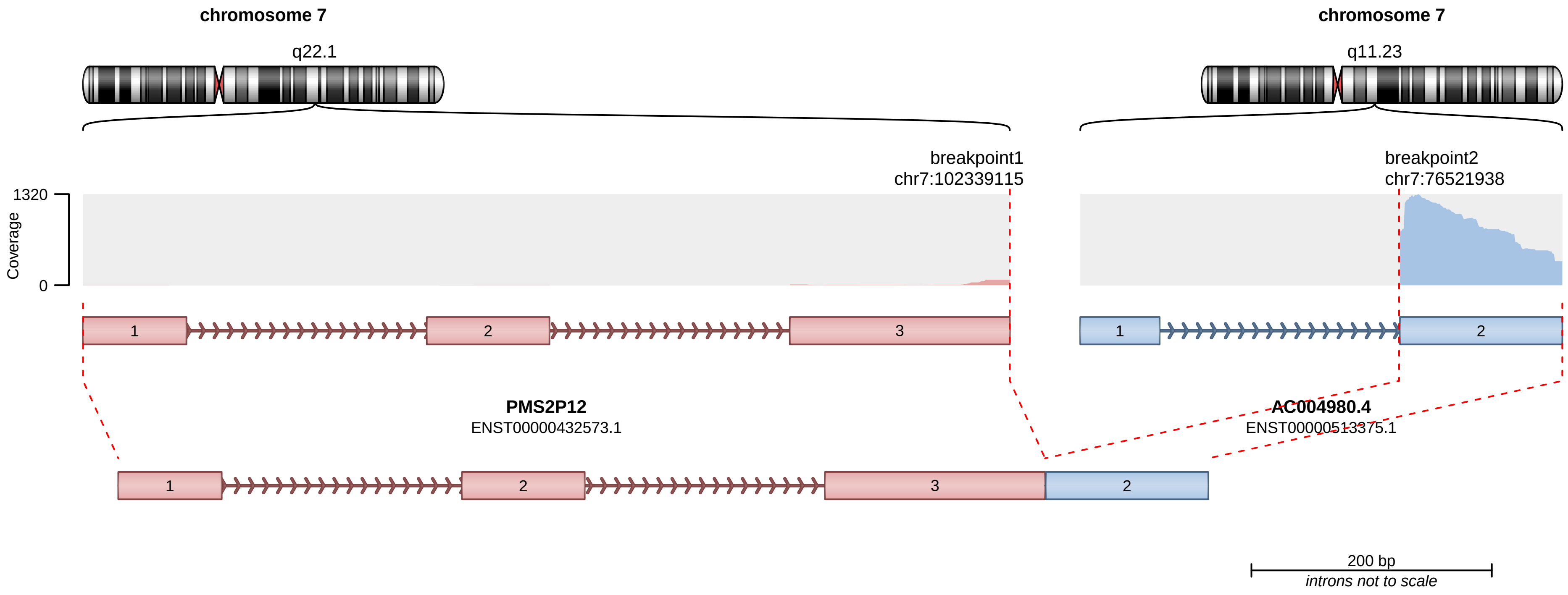


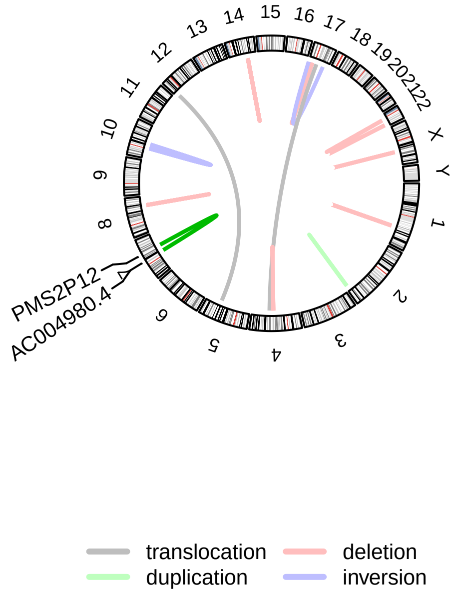
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 14
Discordant mates = 0

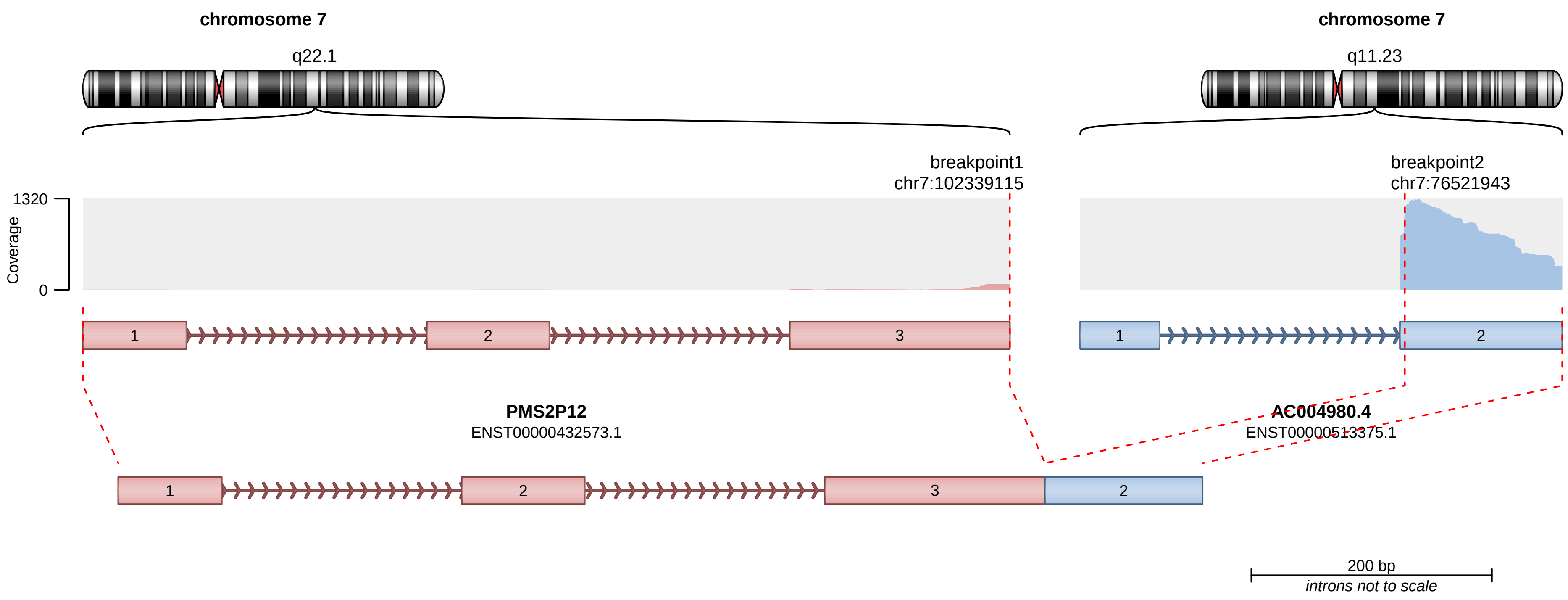


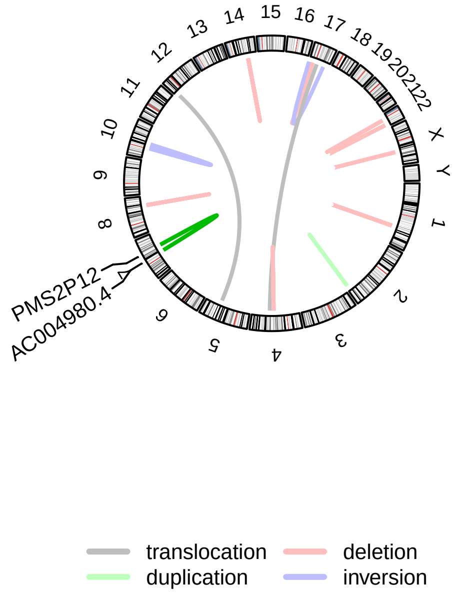


Genes are not protein−coding.

SUPPORTING READ COUNT

Split reads = 9
Discordant mates = 0





Genes are not protein−coding.

SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 0