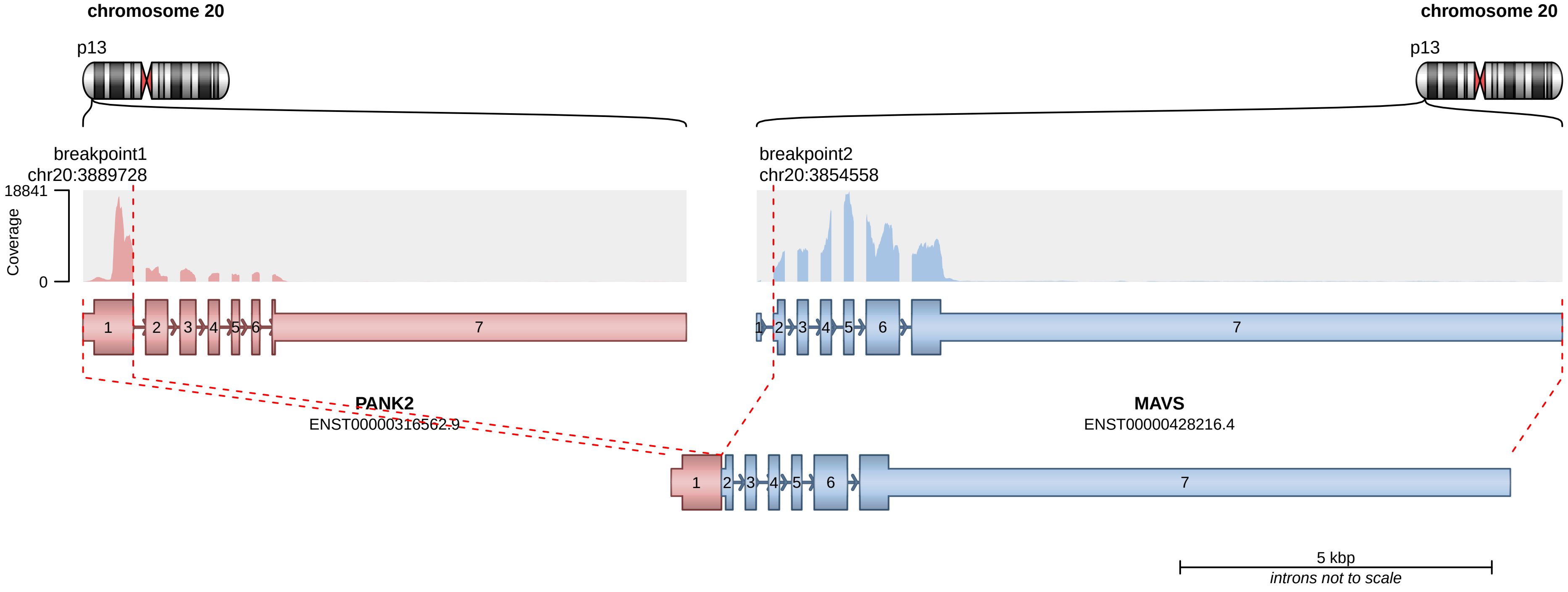
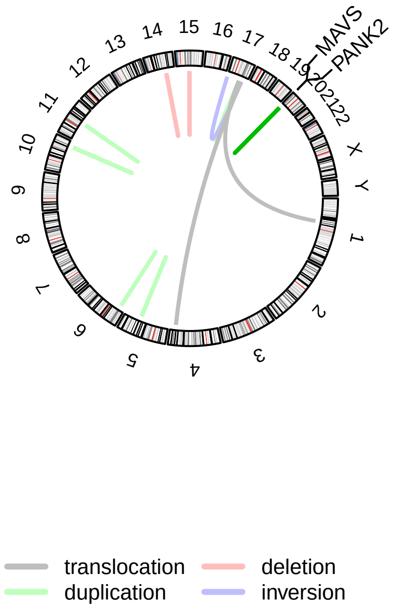
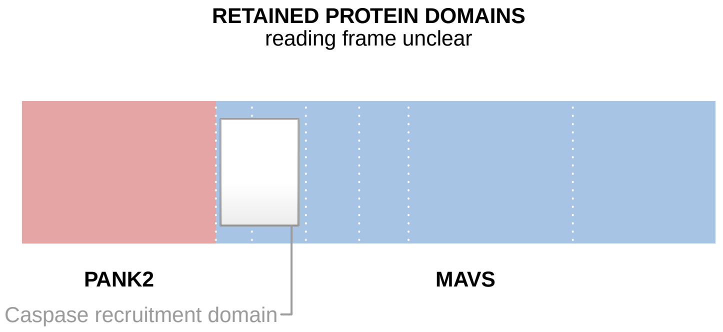
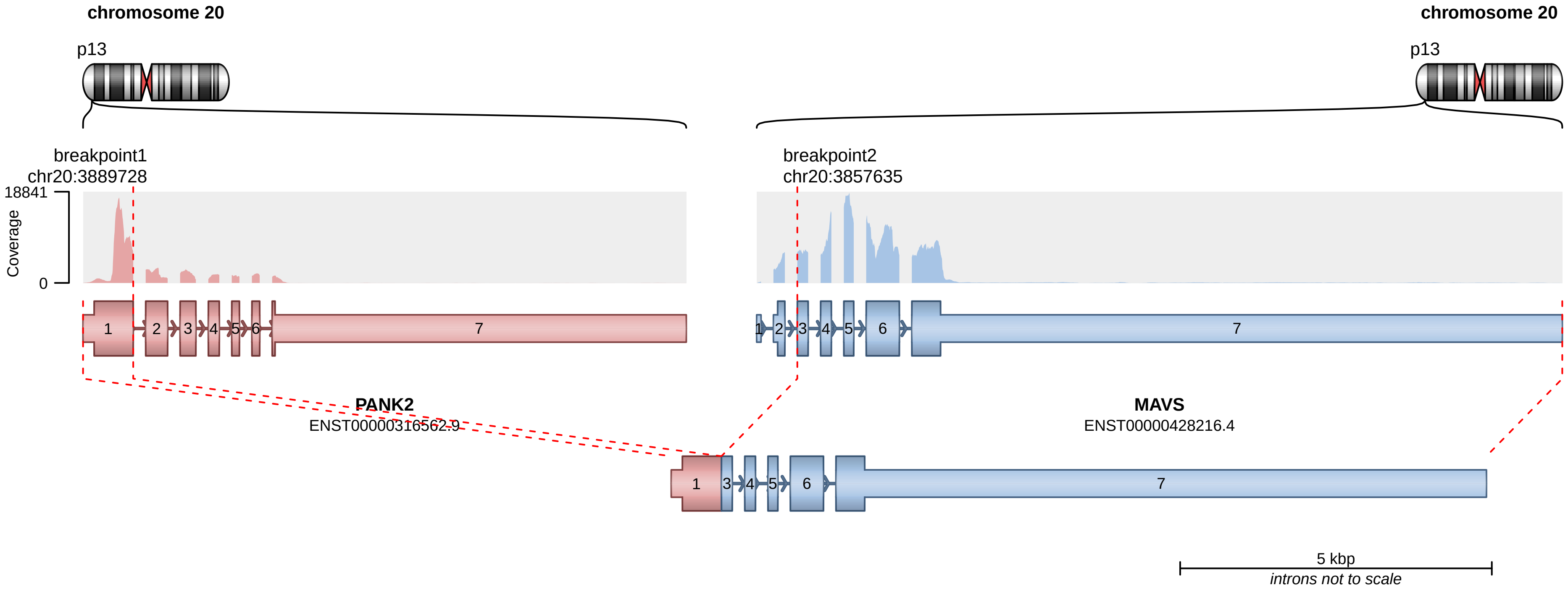


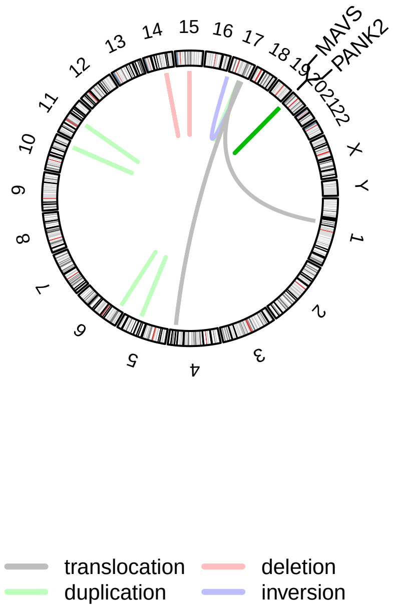




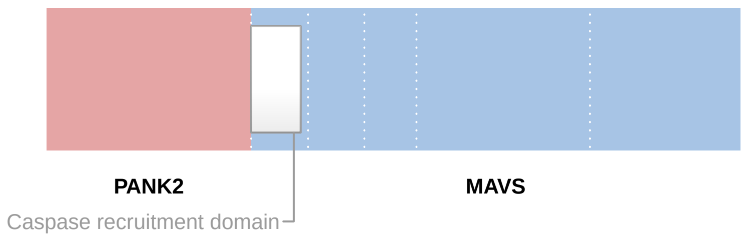
SUPPORTING READ COUNT

Split reads = 1446
Discordant mates = 30



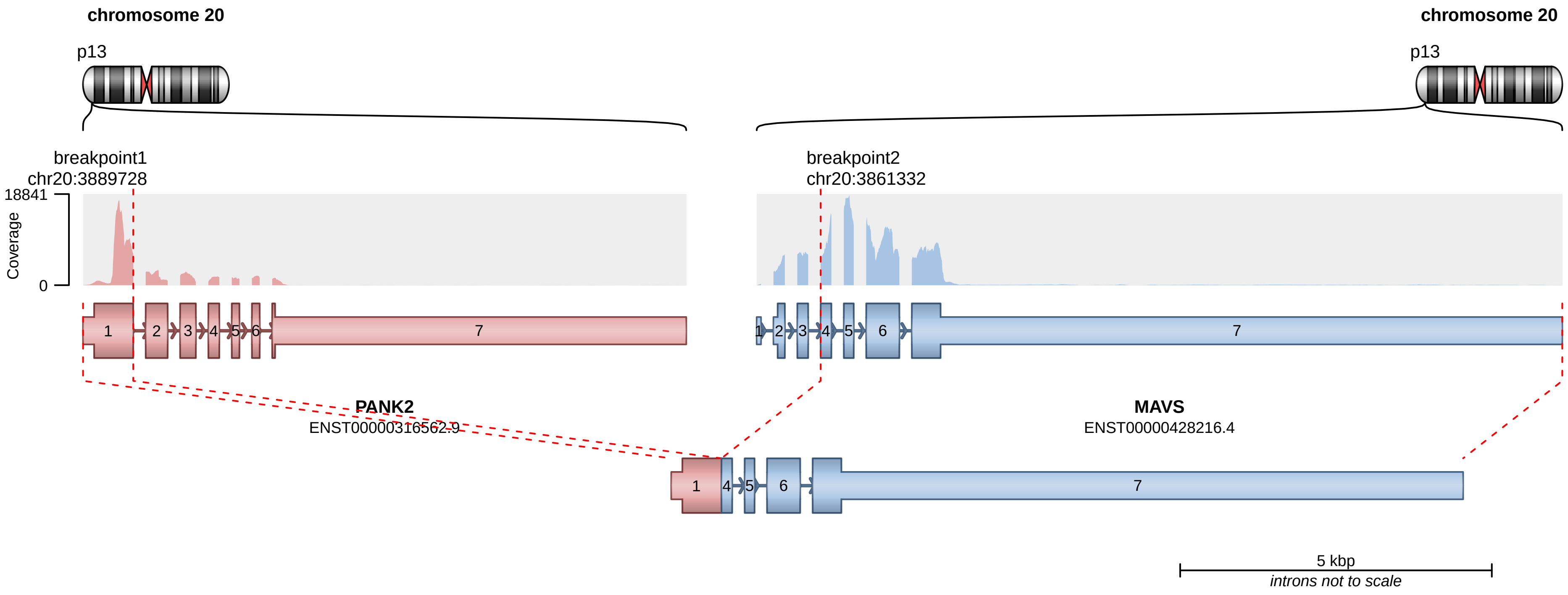


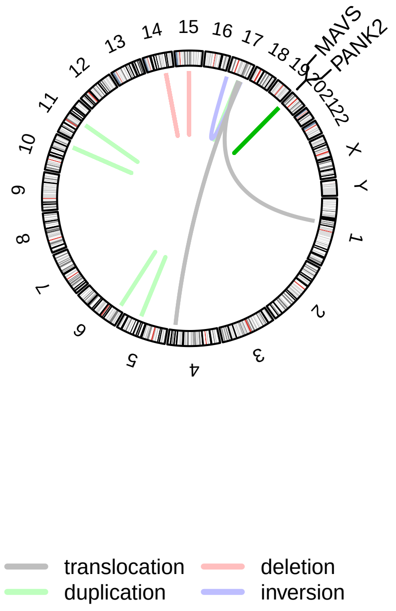
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 68
Discordant mates = 2

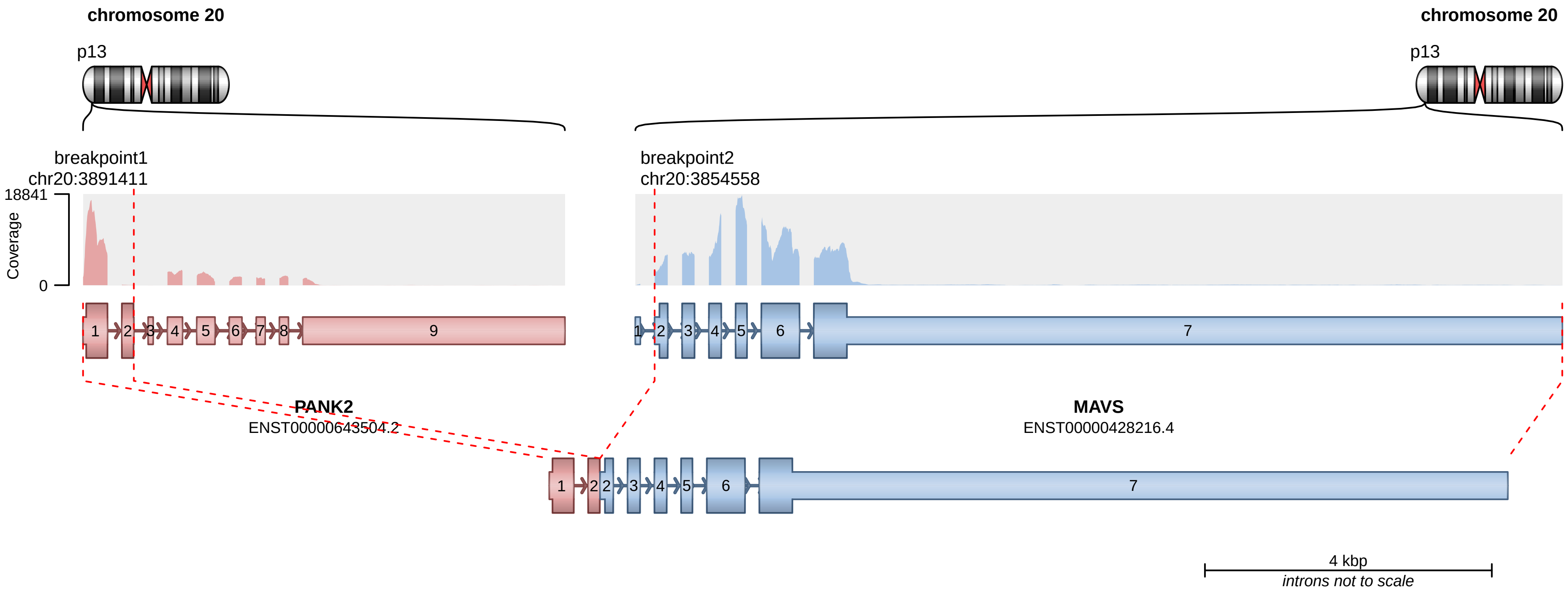


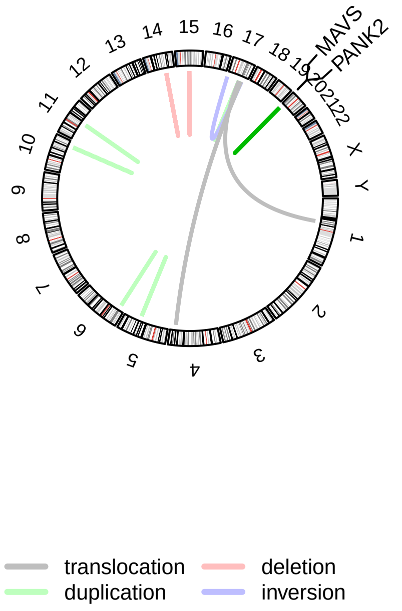


No protein domains retained in fusion.

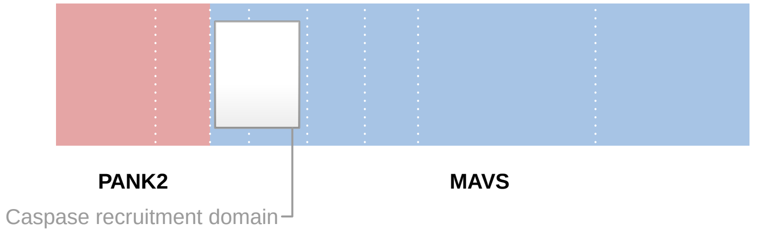
SUPPORTING READ COUNT

Split reads = 18
Discordant mates = 0



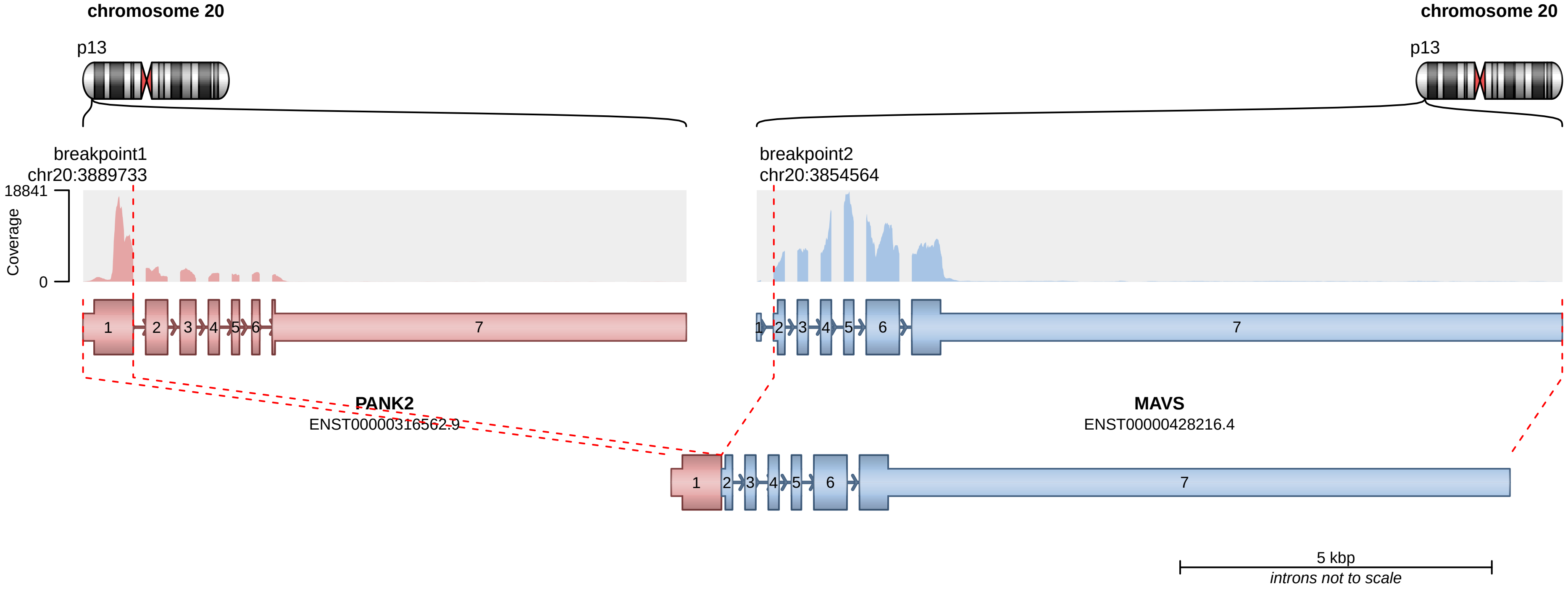


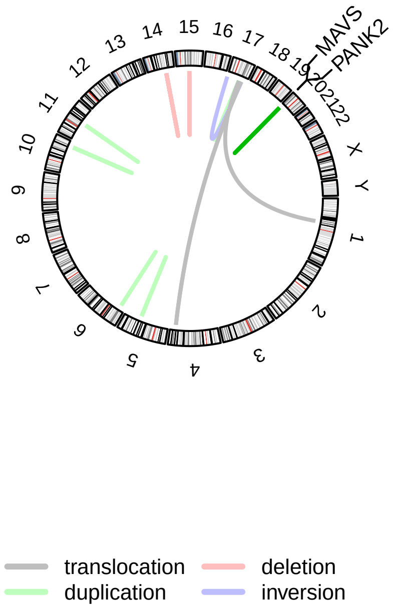
RETAINED PROTEIN DOMAINS
reading frame unclear

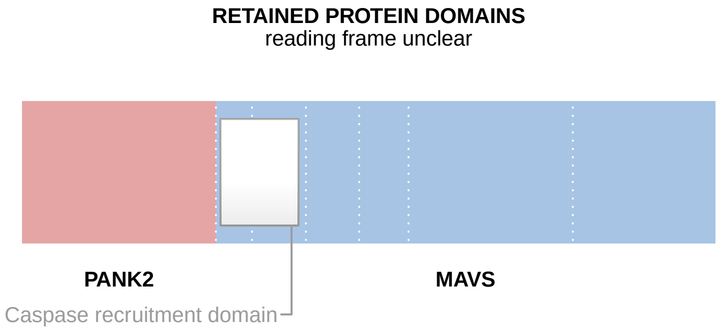


SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 30

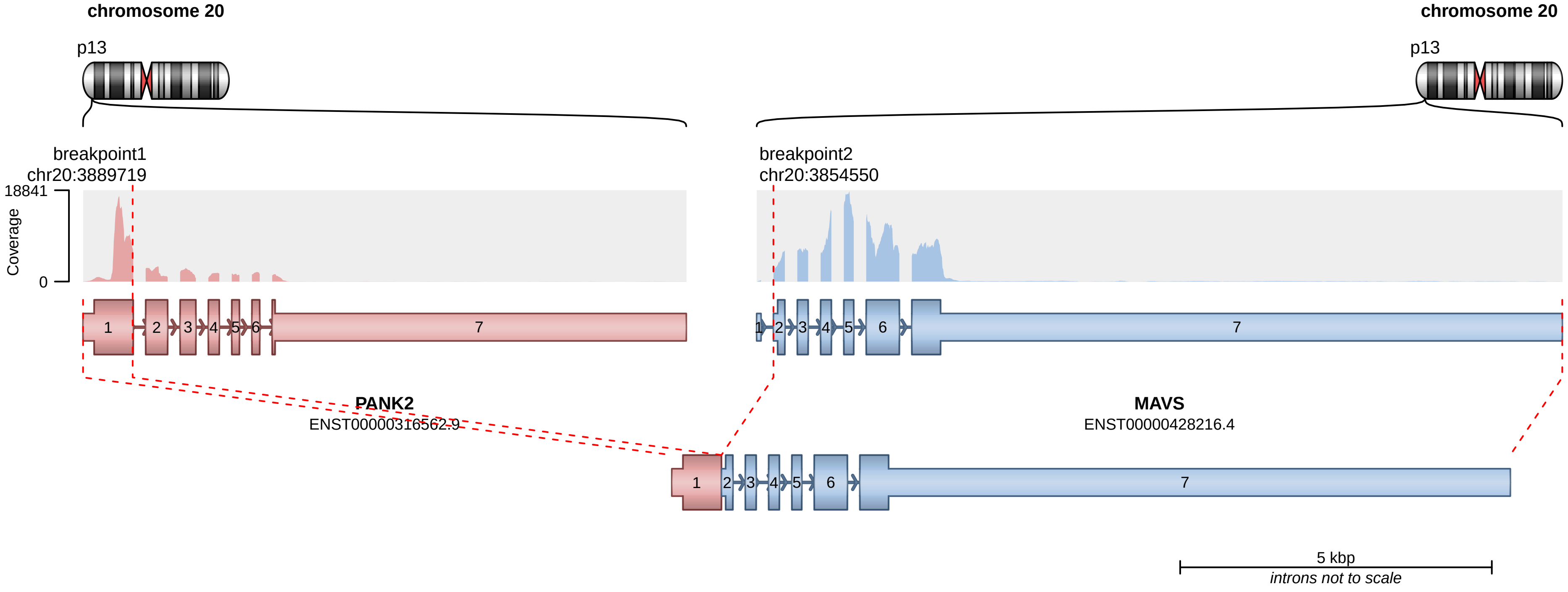


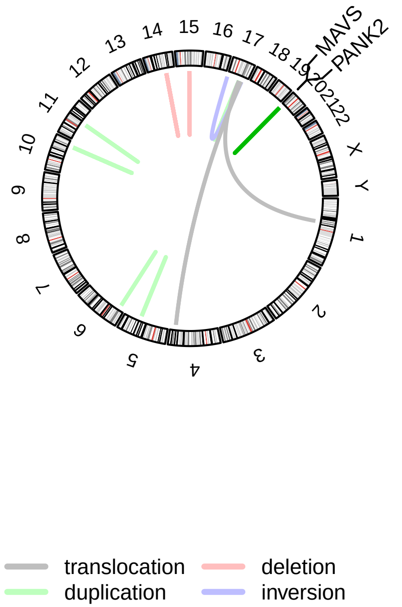


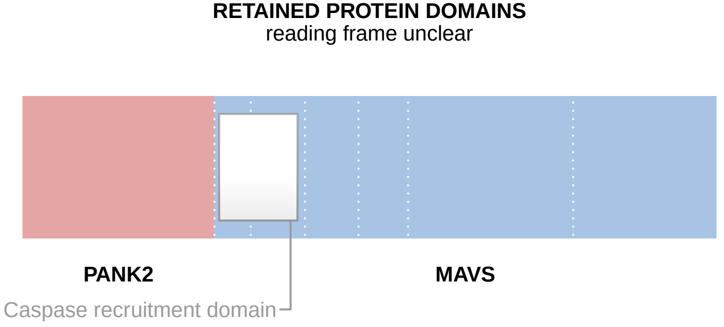


SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 29

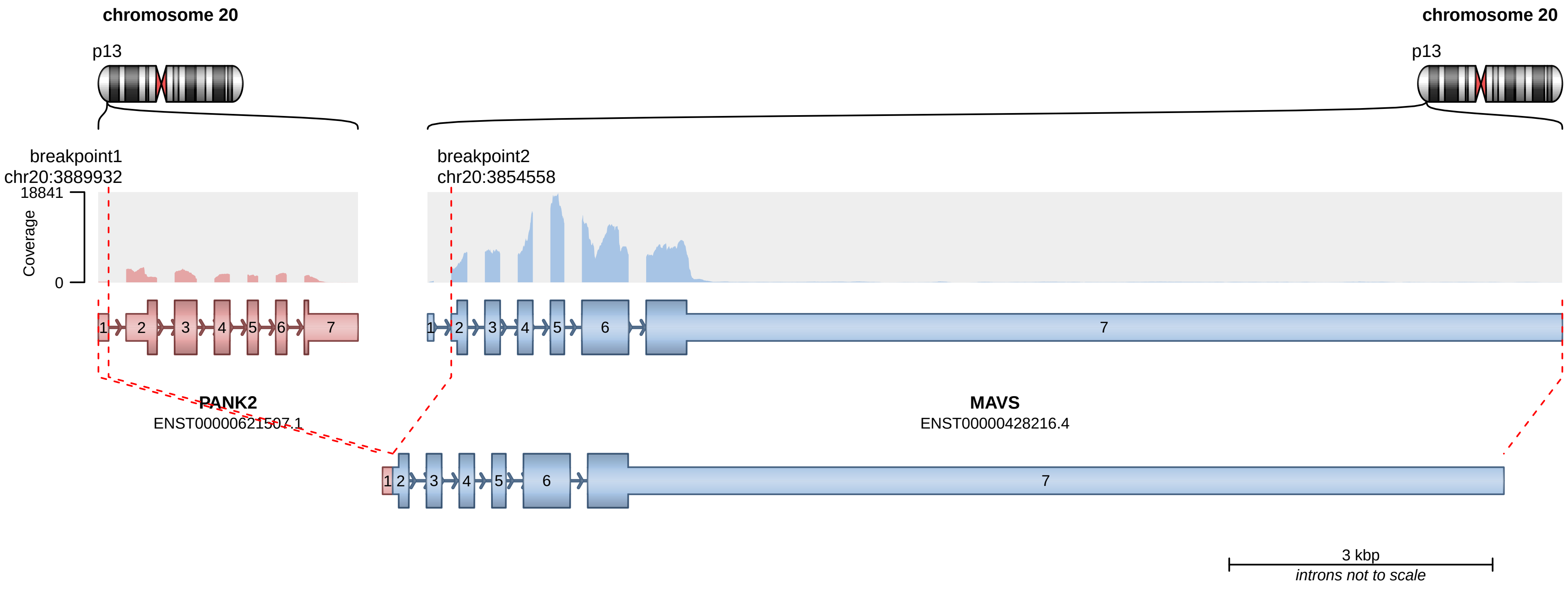


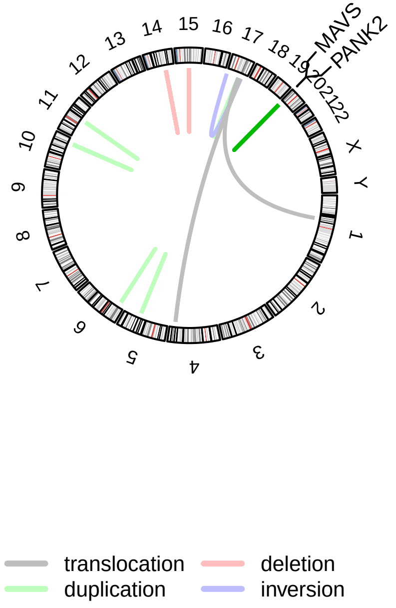




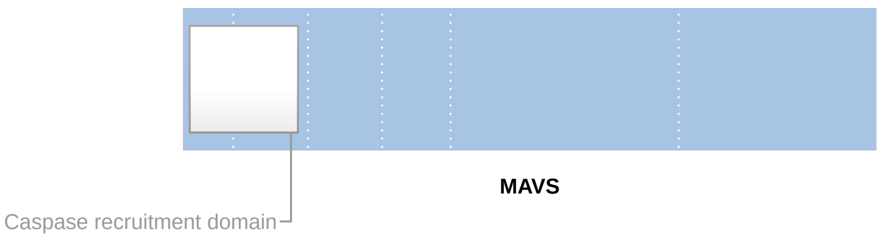
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 28



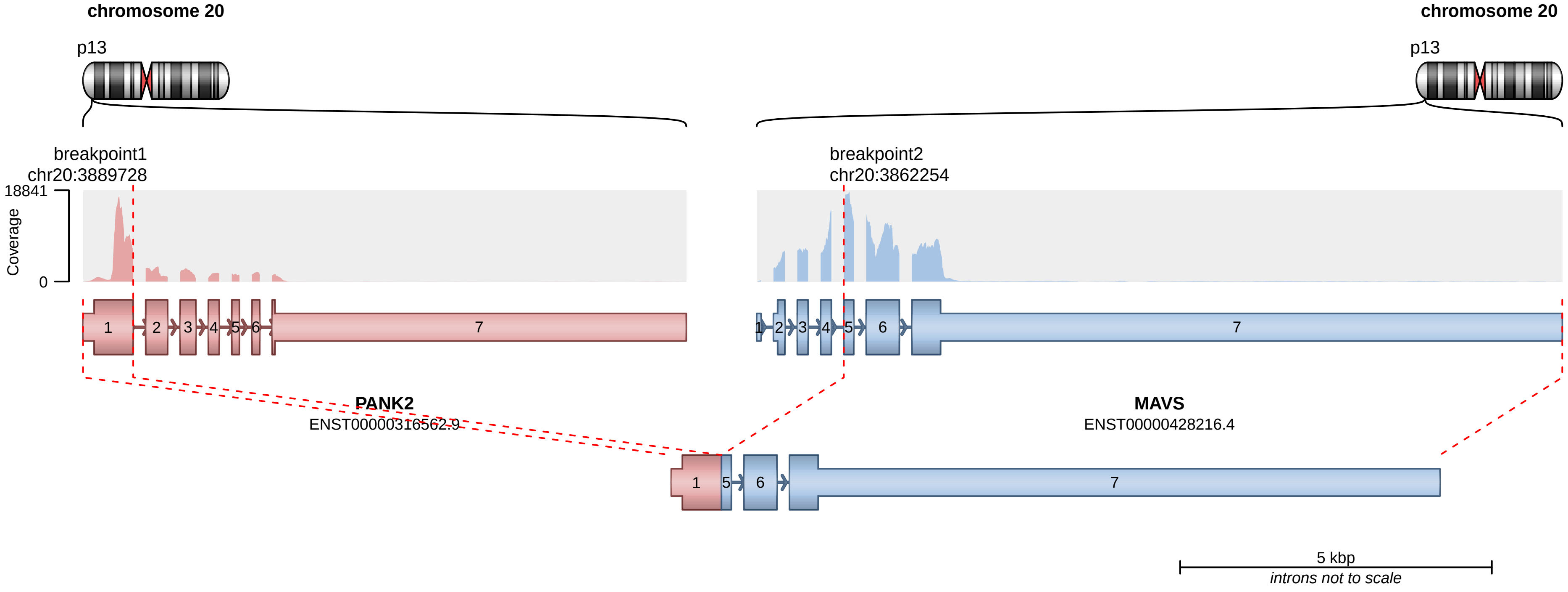


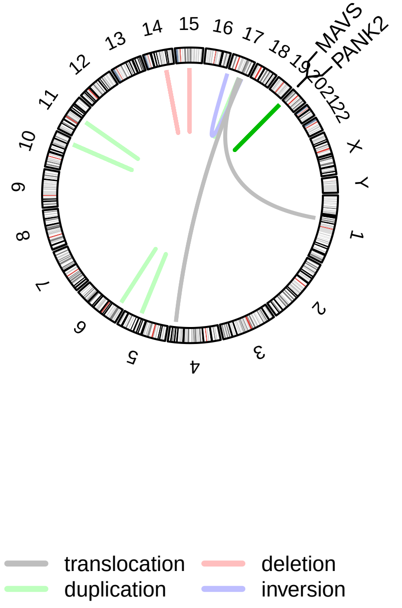
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 30

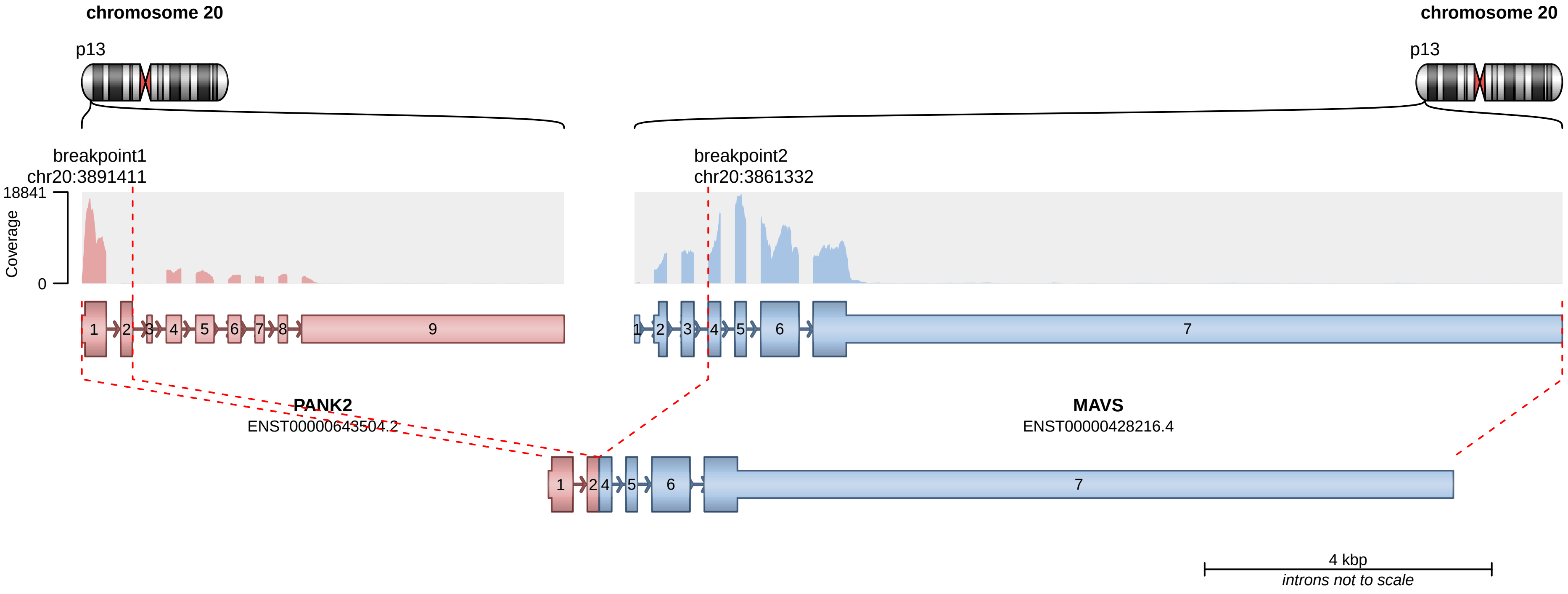


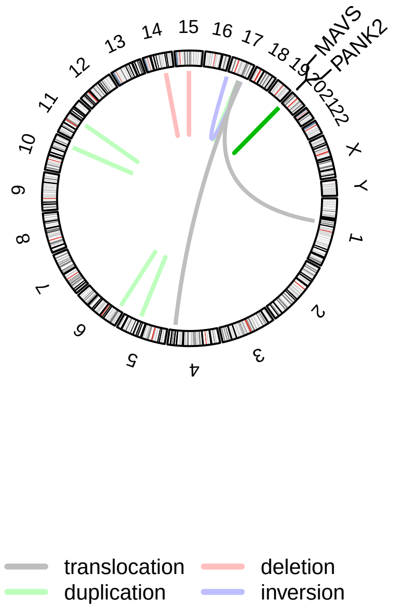


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 0

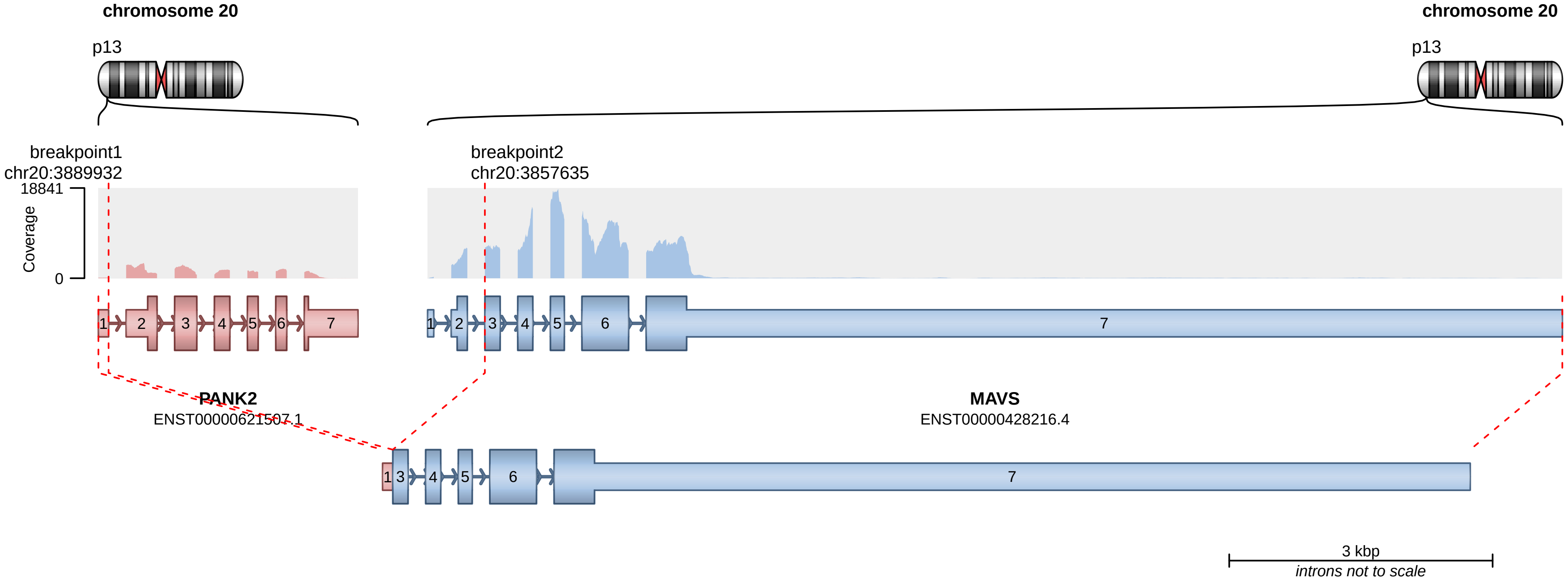


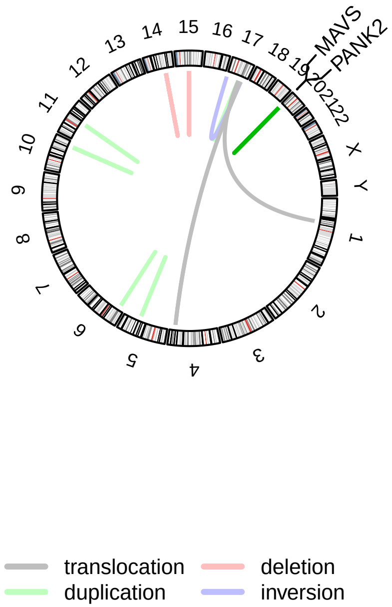


No protein domains retained in fusion.

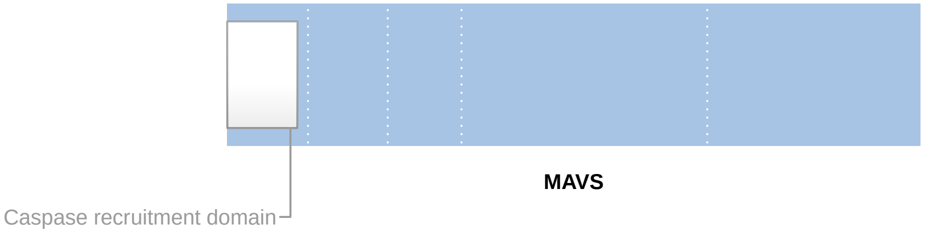
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0



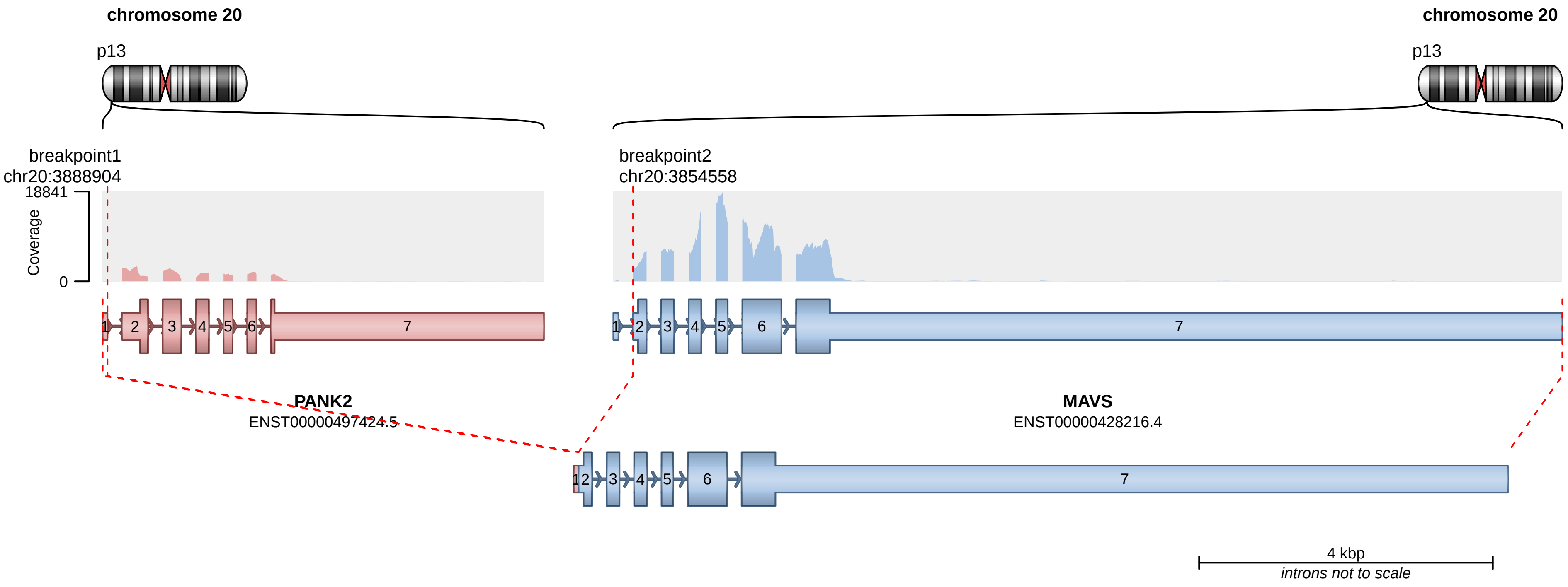


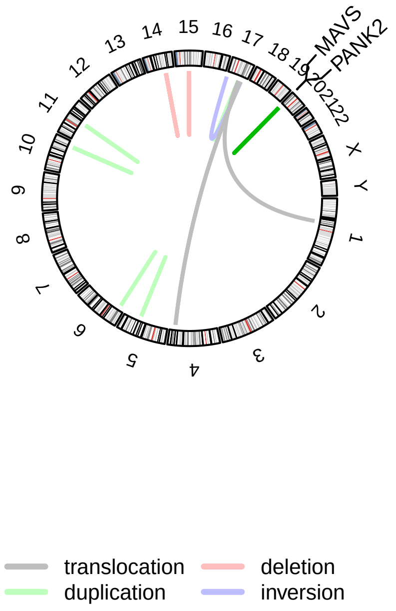
RETAINED PROTEIN DOMAINS
reading frame unclear

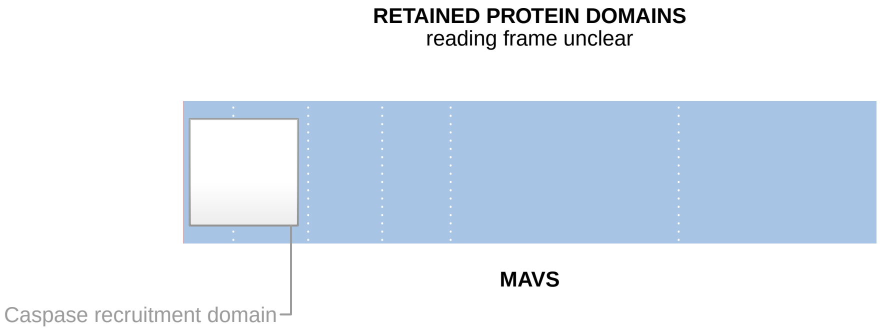


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 2

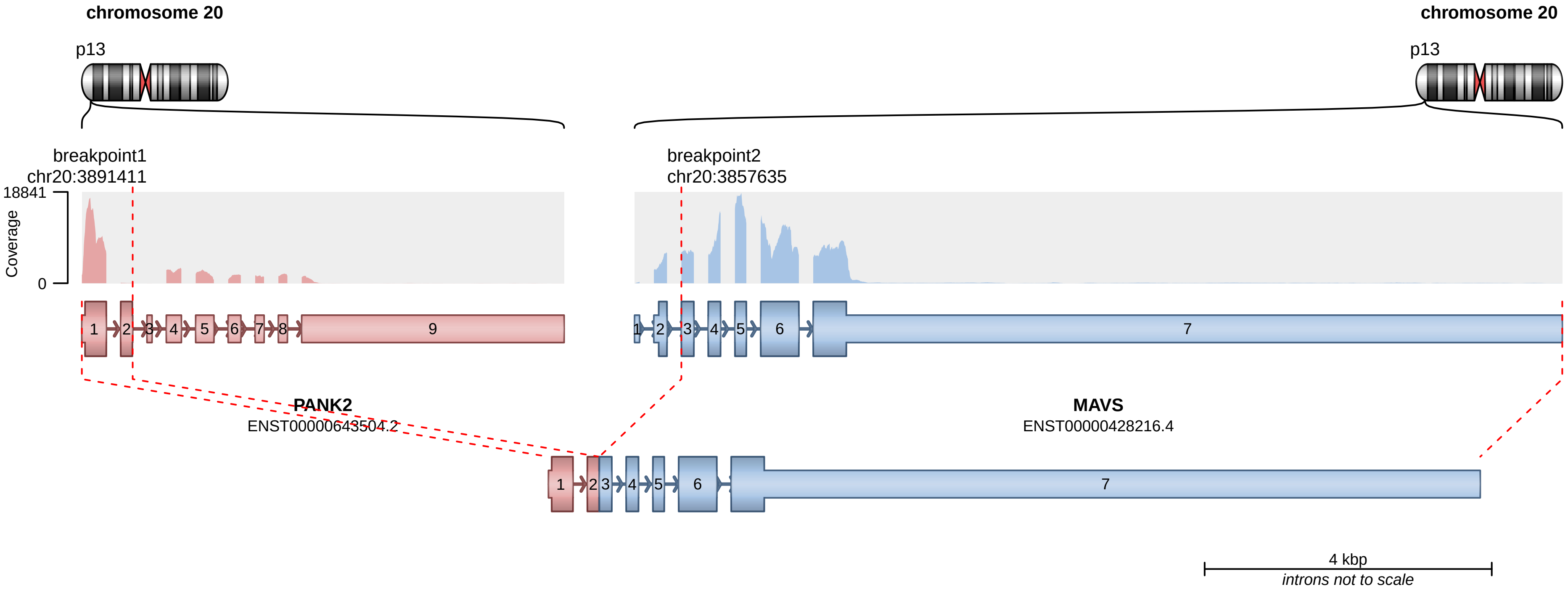


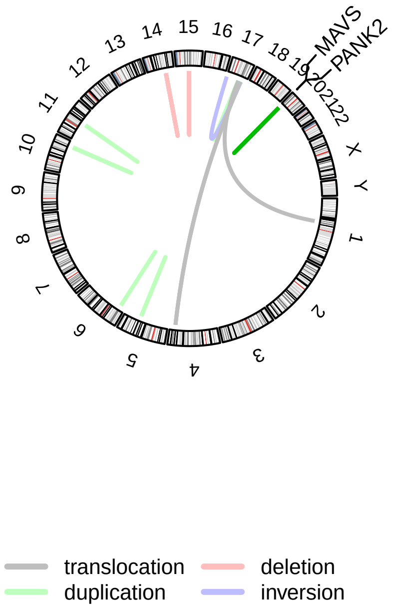




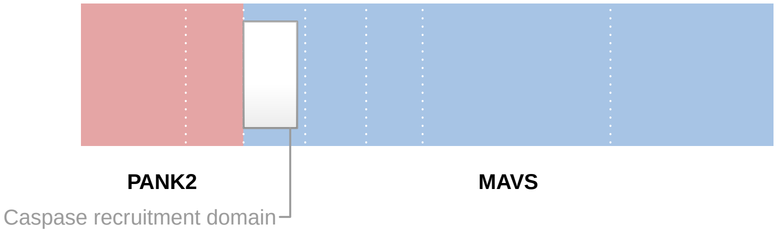
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0



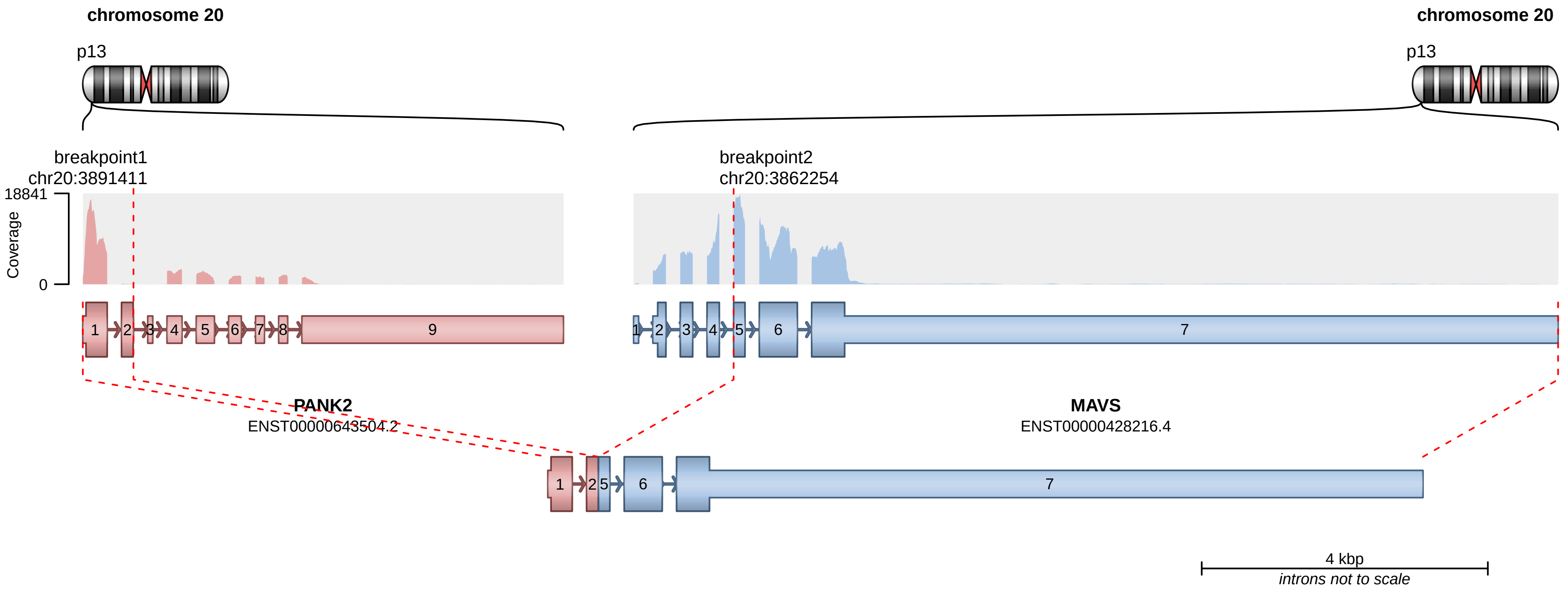


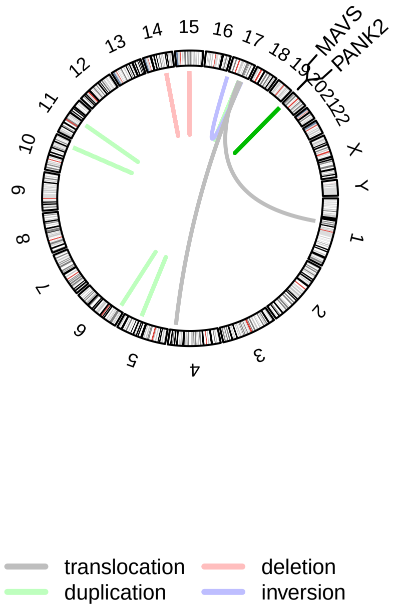
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 2

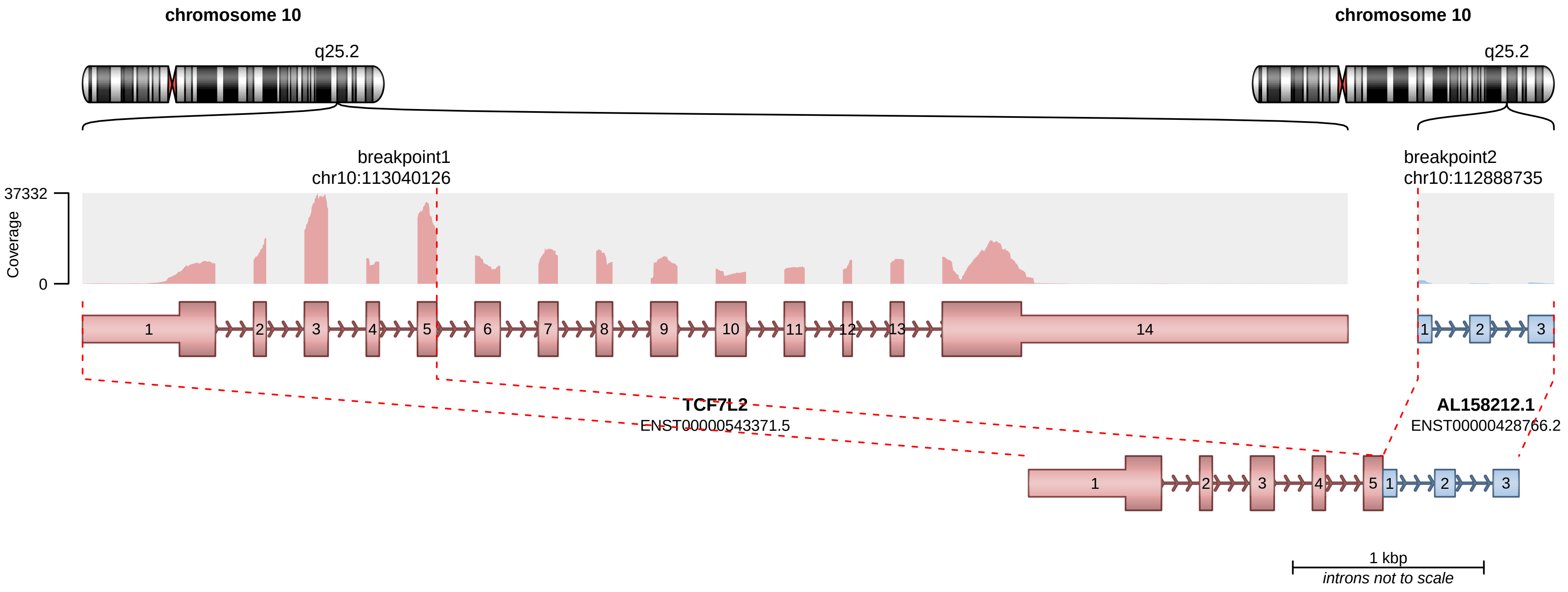


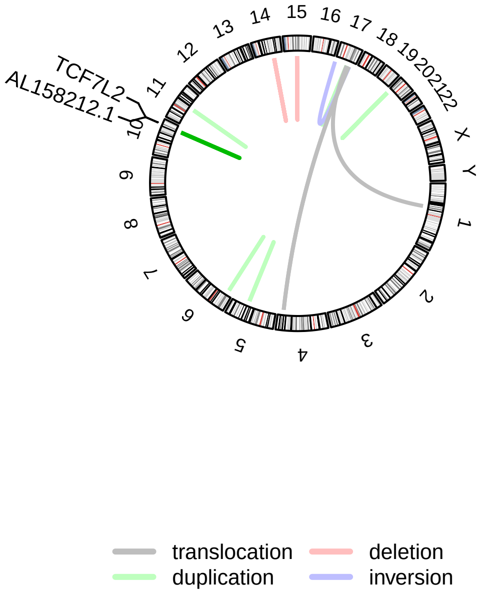


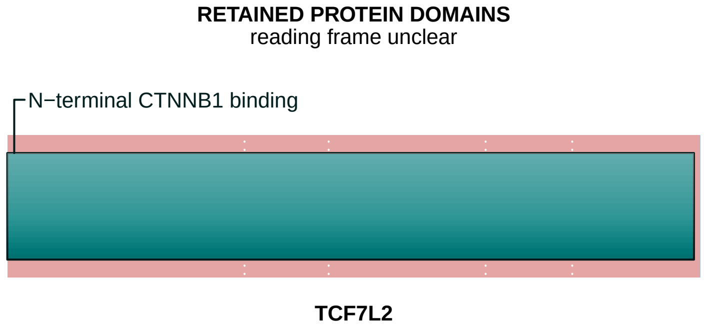
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

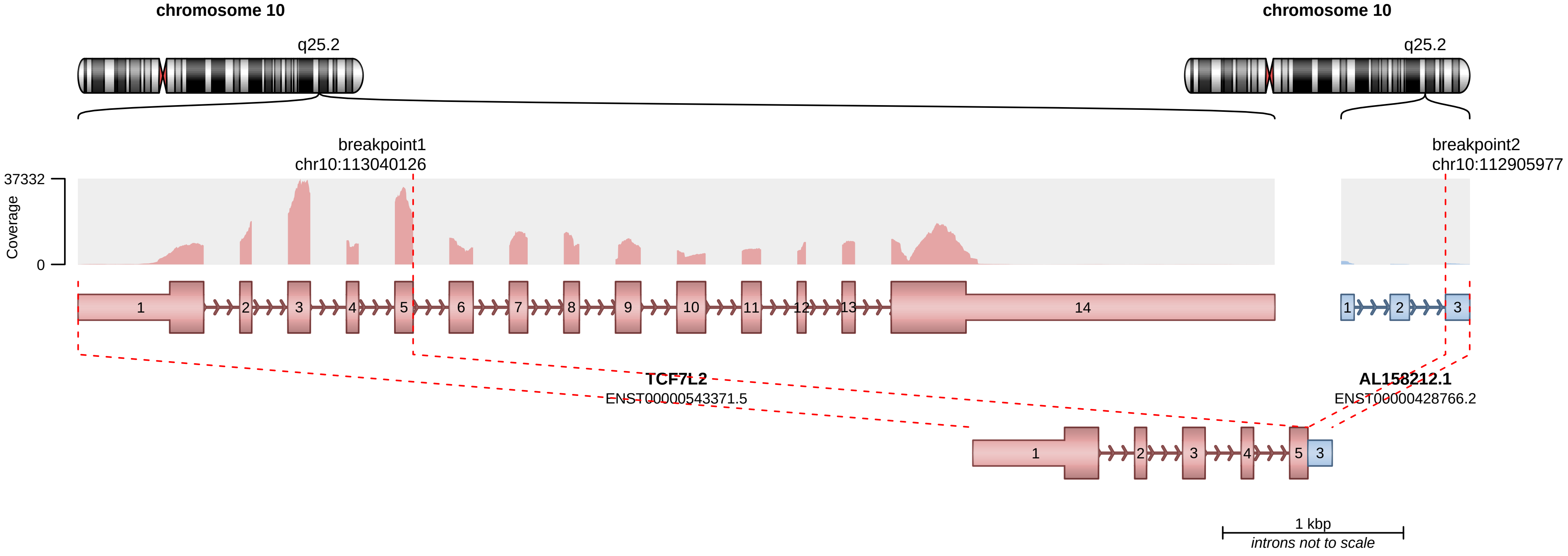


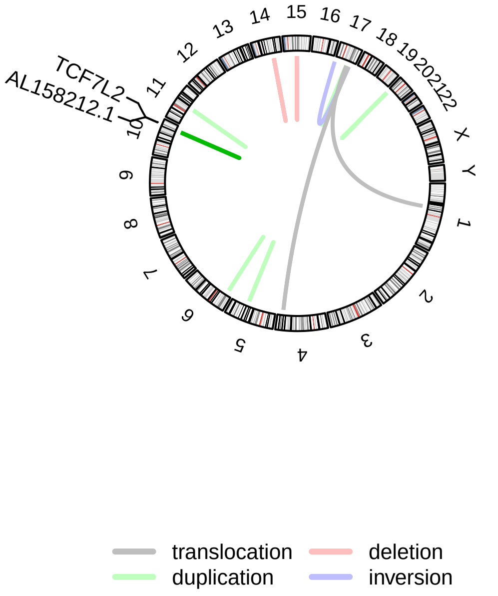




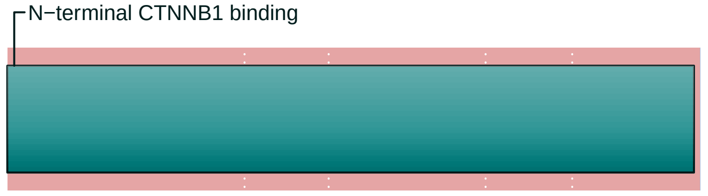
SUPPORTING READ COUNT

Split reads = 827
Discordant mates = 22





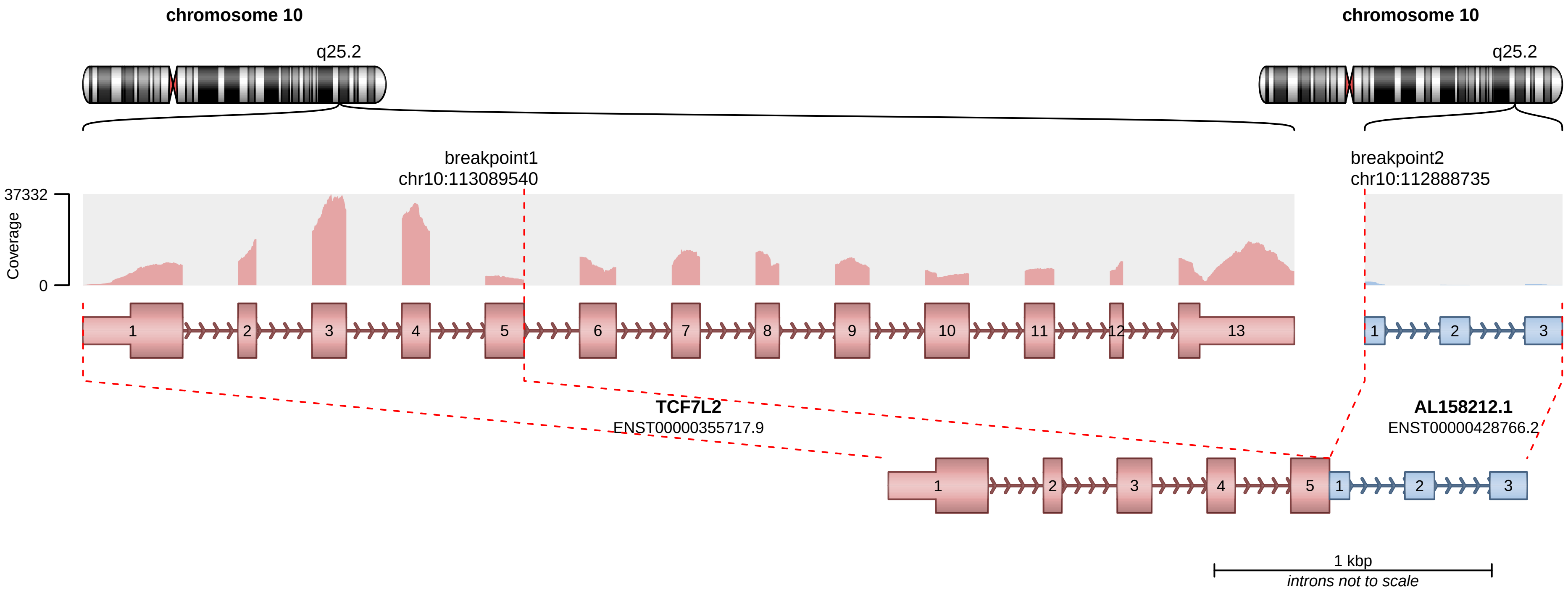
RETAINED PROTEIN DOMAINS
reading frame unclear

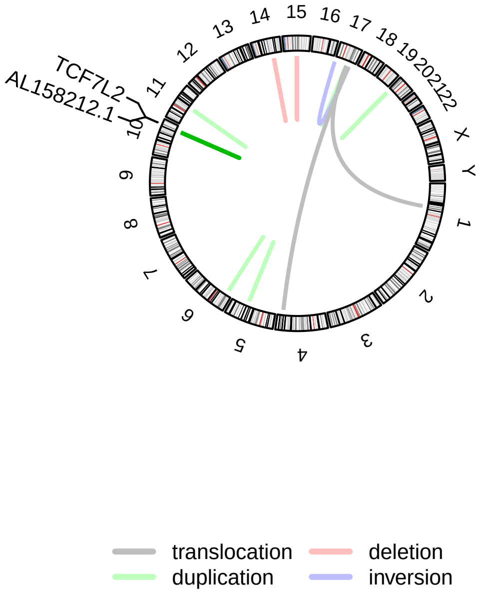


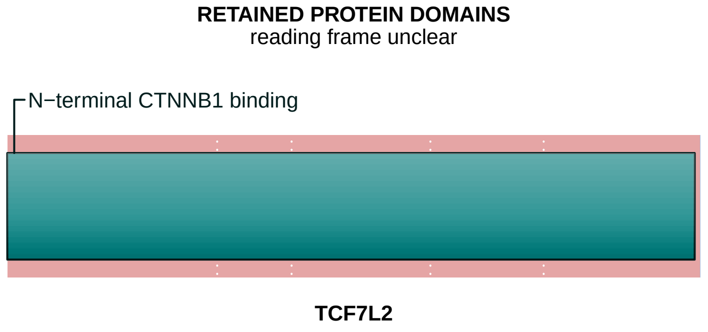
TCF7L2

SUPPORTING READ COUNT

Split reads = 210
Discordant mates = 11

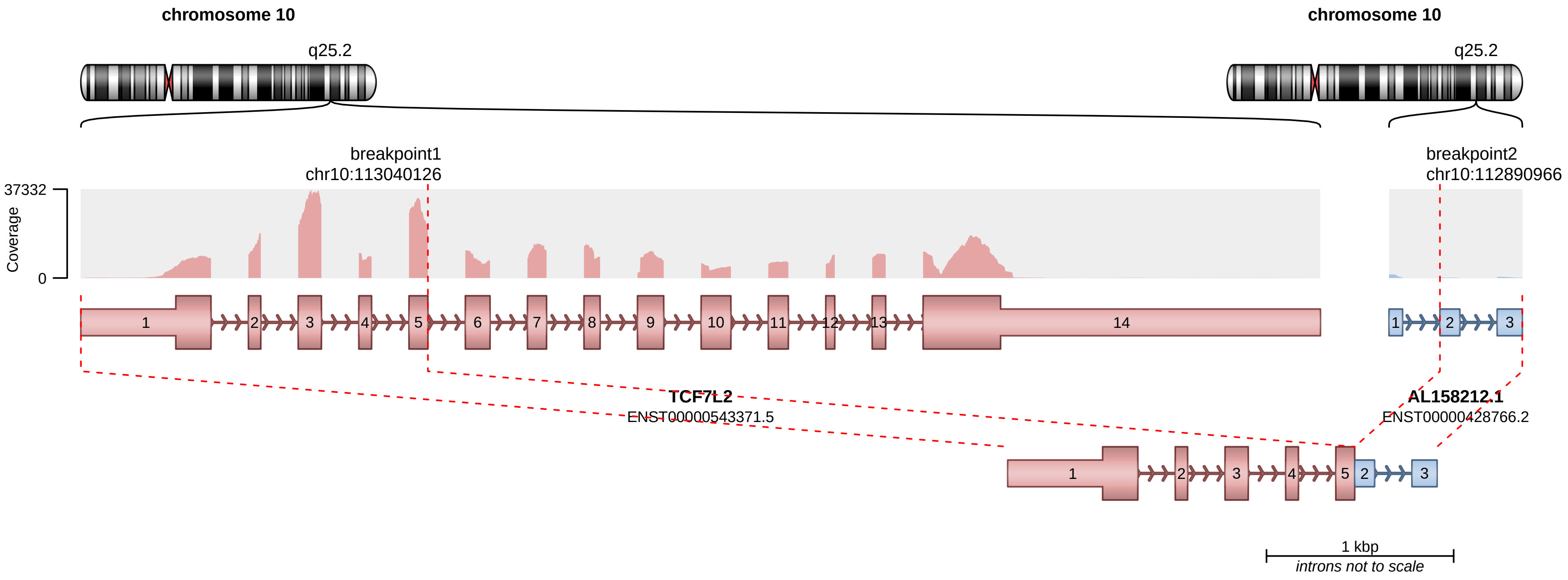


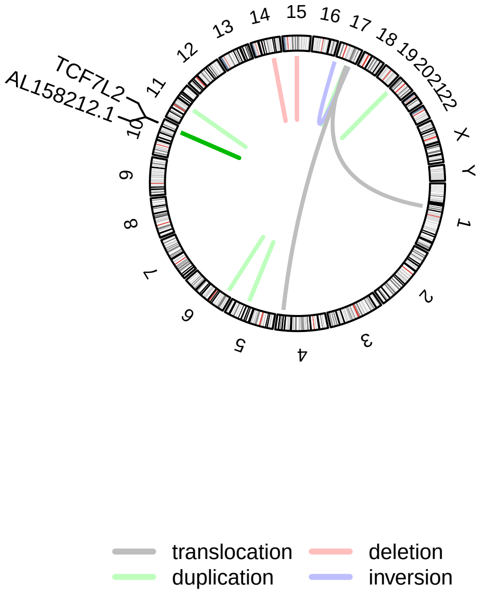




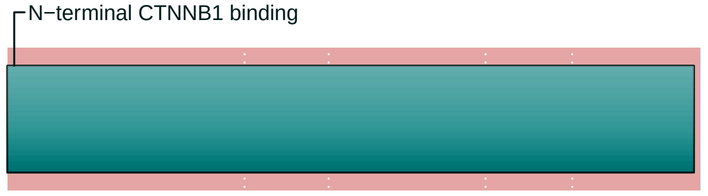
SUPPORTING READ COUNT

Split reads = 139
Discordant mates = 24





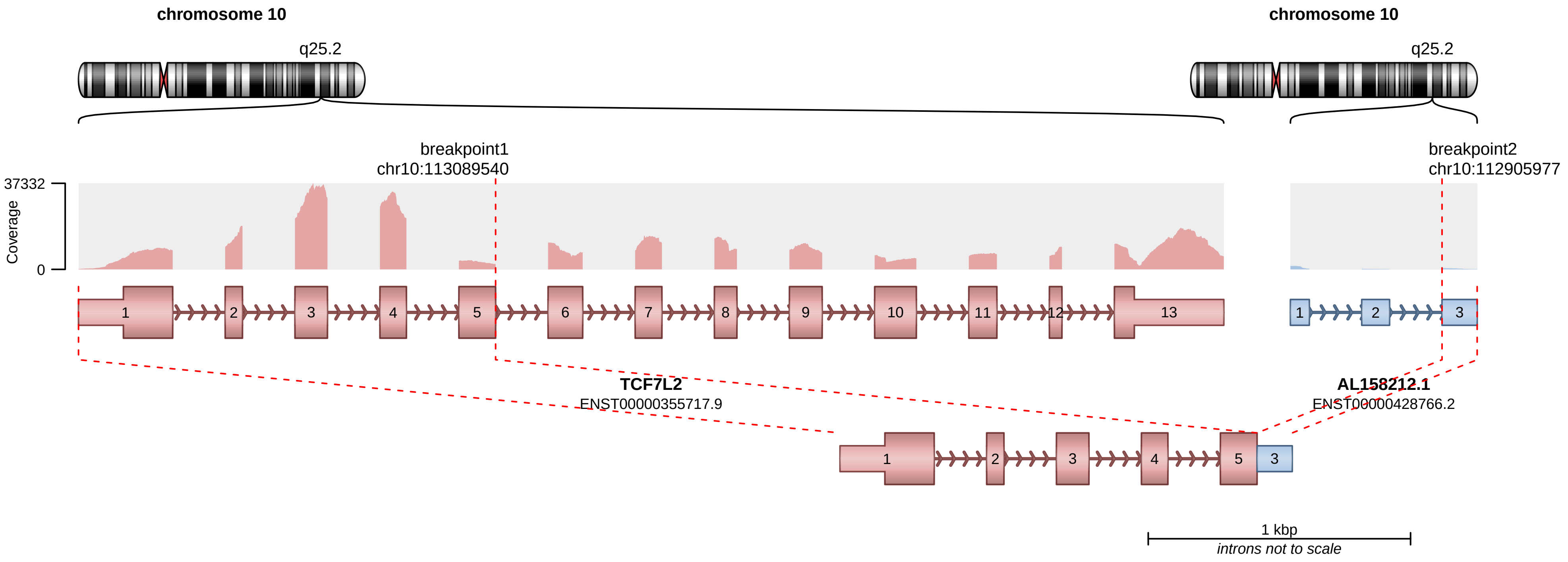
RETAINED PROTEIN DOMAINS
reading frame unclear

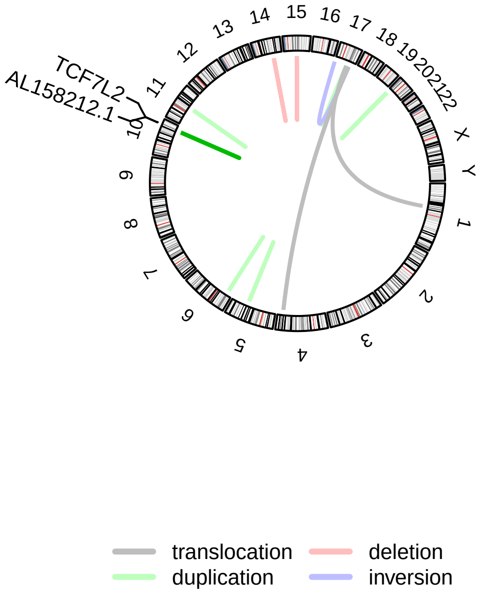


TCF7L2

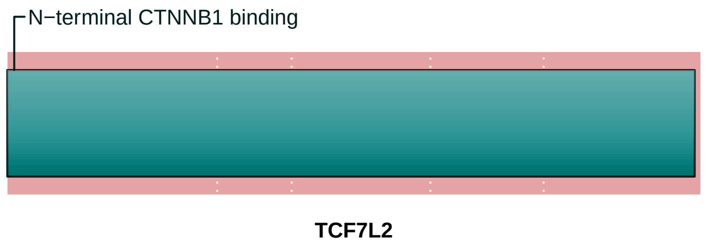
SUPPORTING READ COUNT

Split reads = 46
Discordant mates = 11



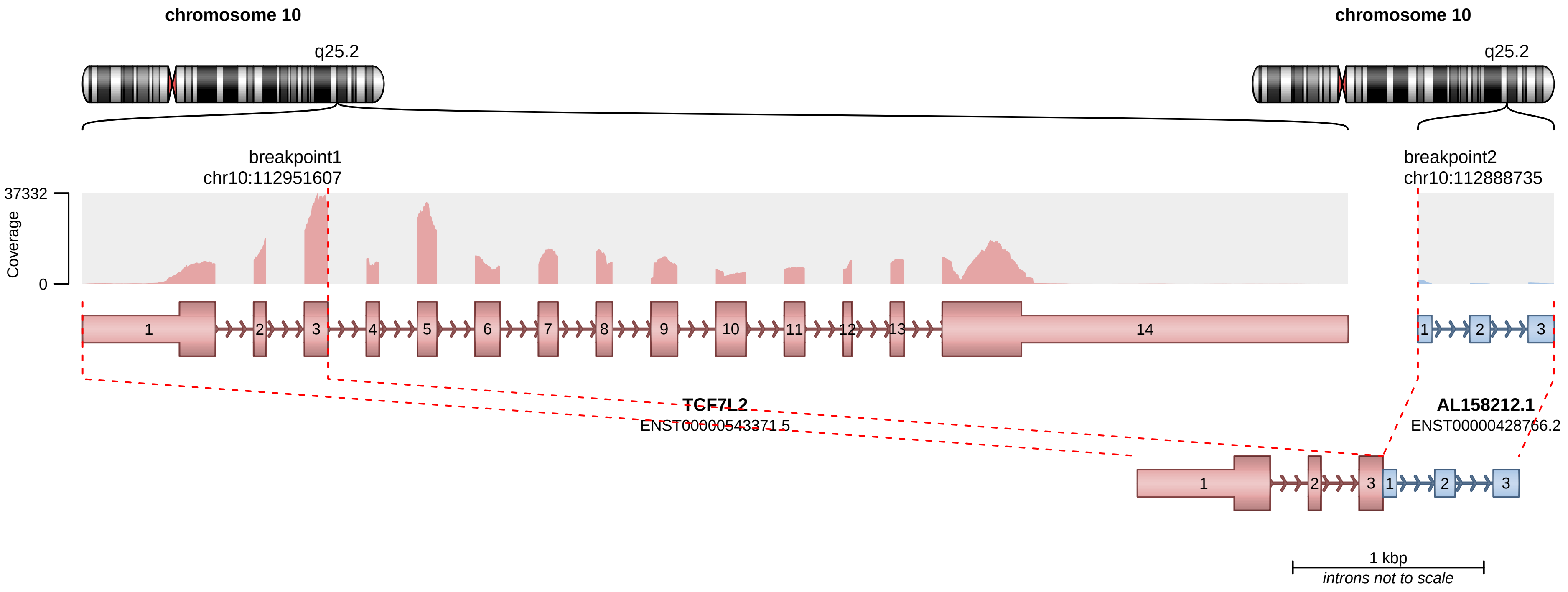


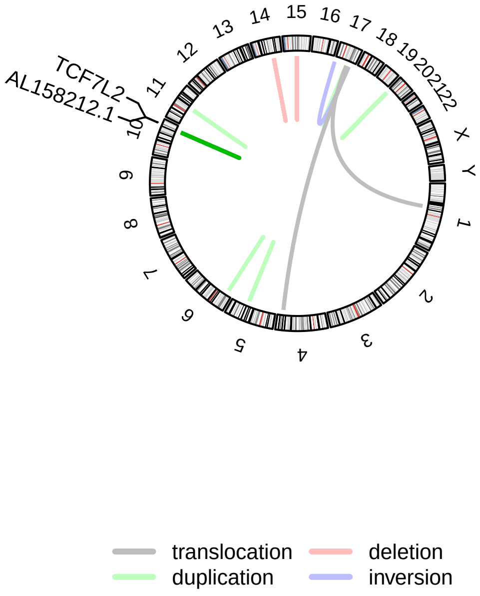
RETAINED PROTEIN DOMAINS
reading frame unclear



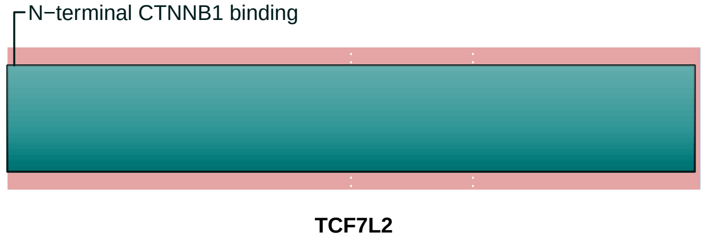
SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 11



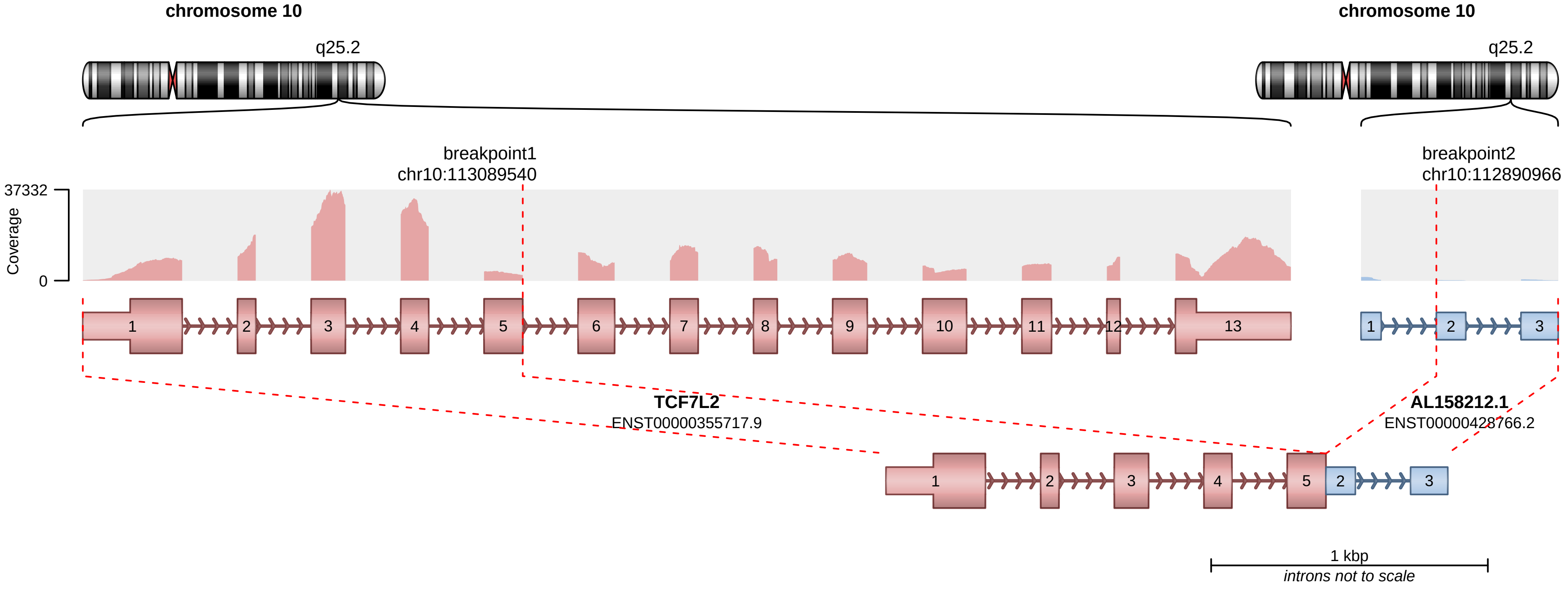


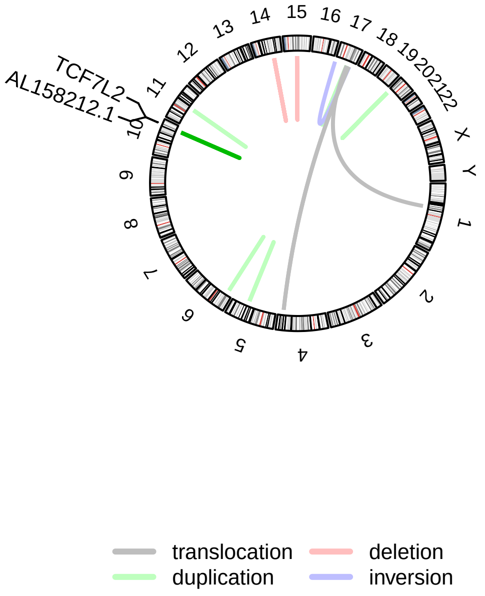
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

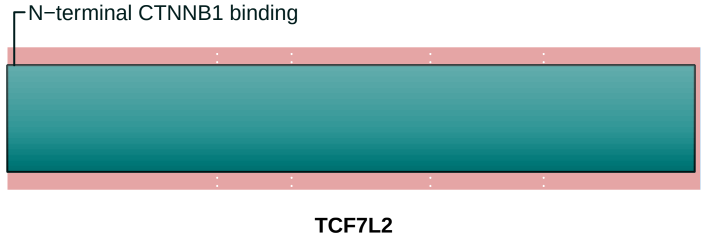
Split reads = 4
Discordant mates = 1





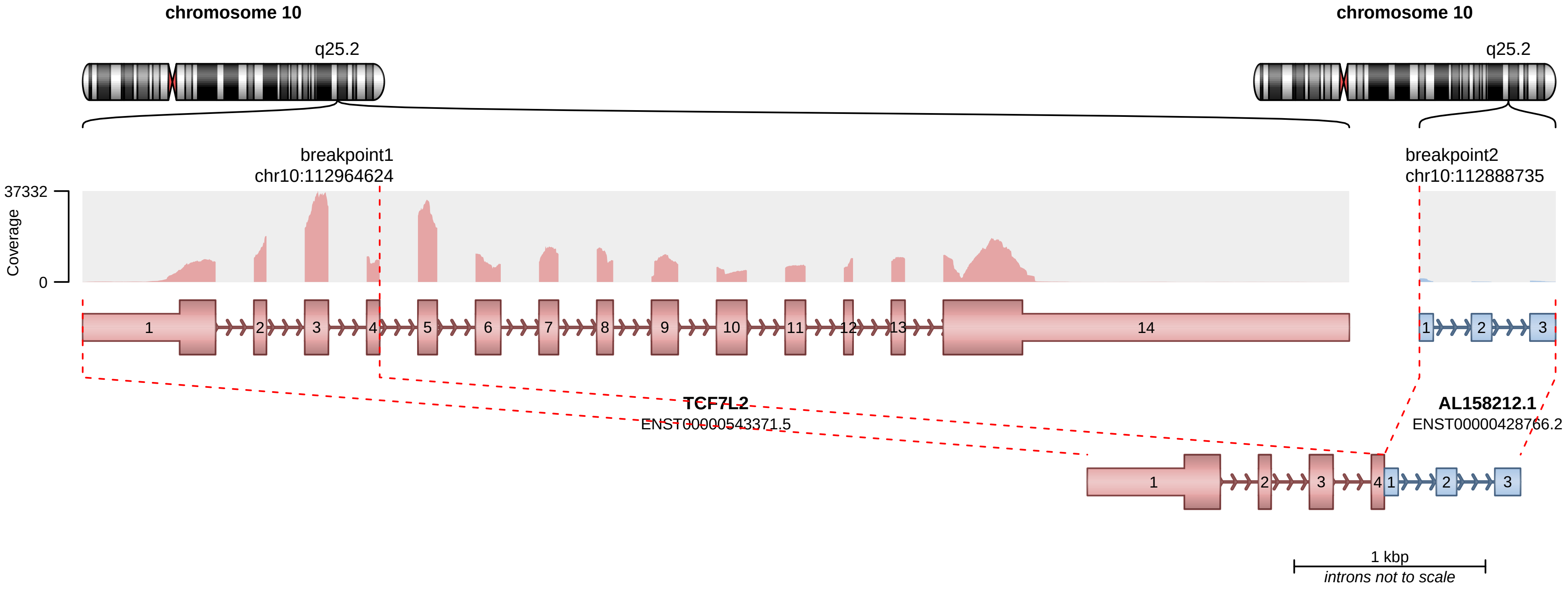
RETAINED PROTEIN DOMAINS

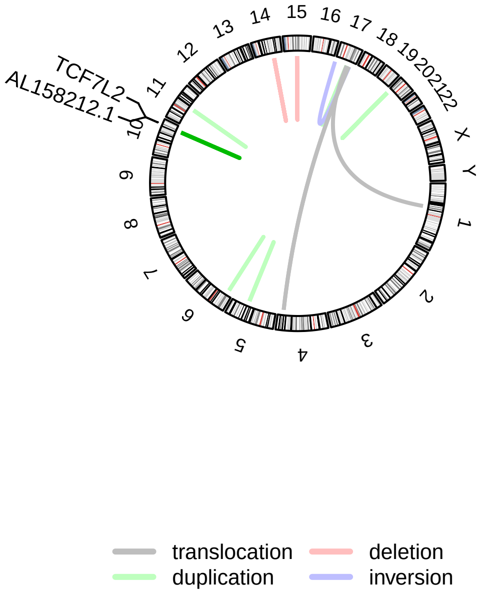
reading frame unclear



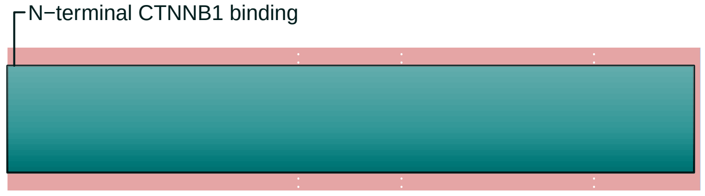
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 11





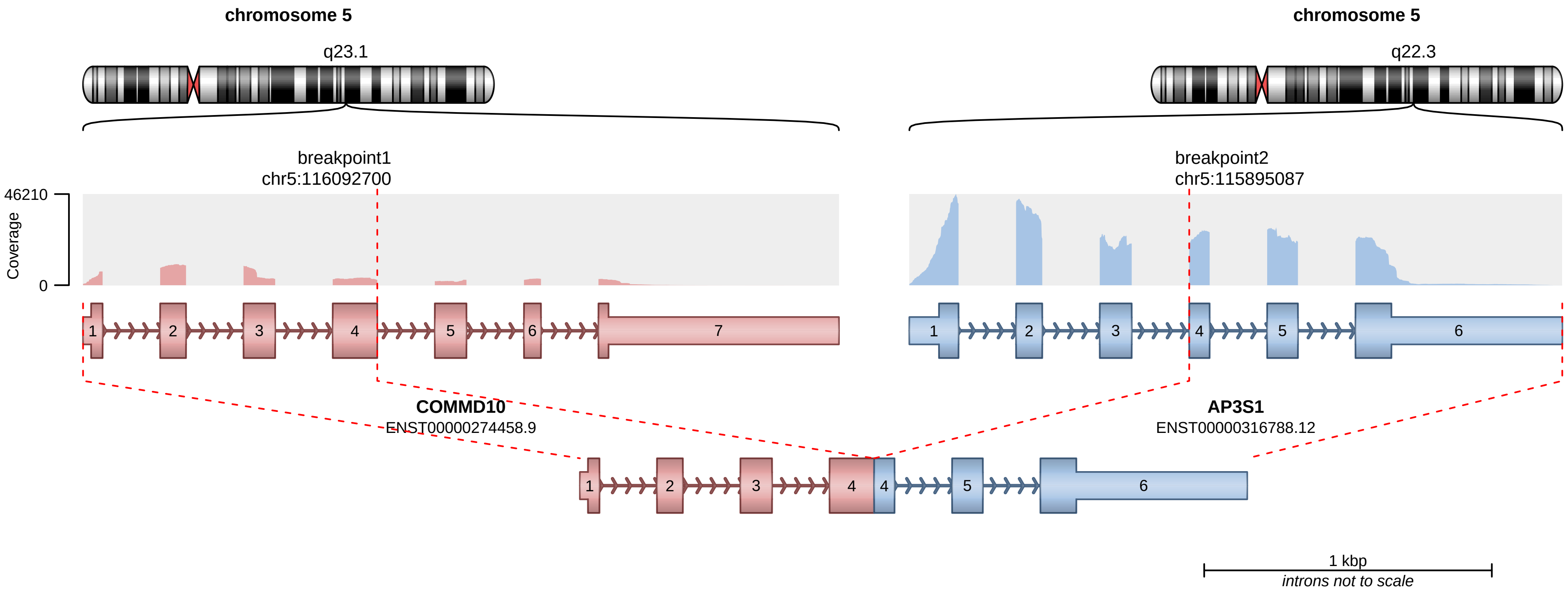
RETAINED PROTEIN DOMAINS
reading frame unclear

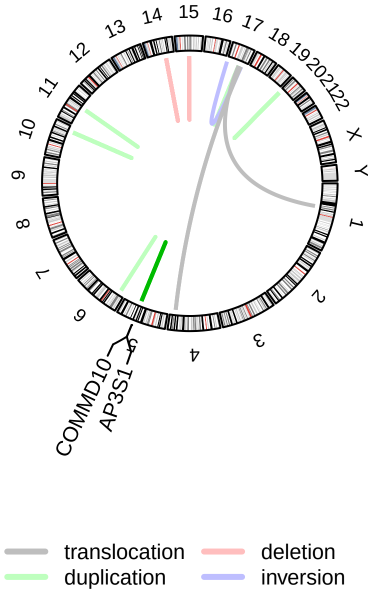


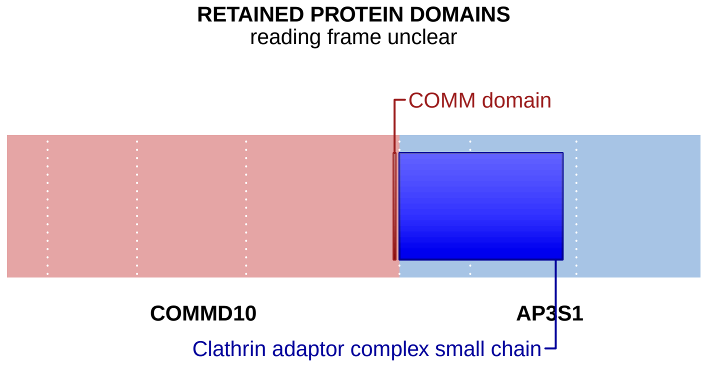
TCF7L2

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

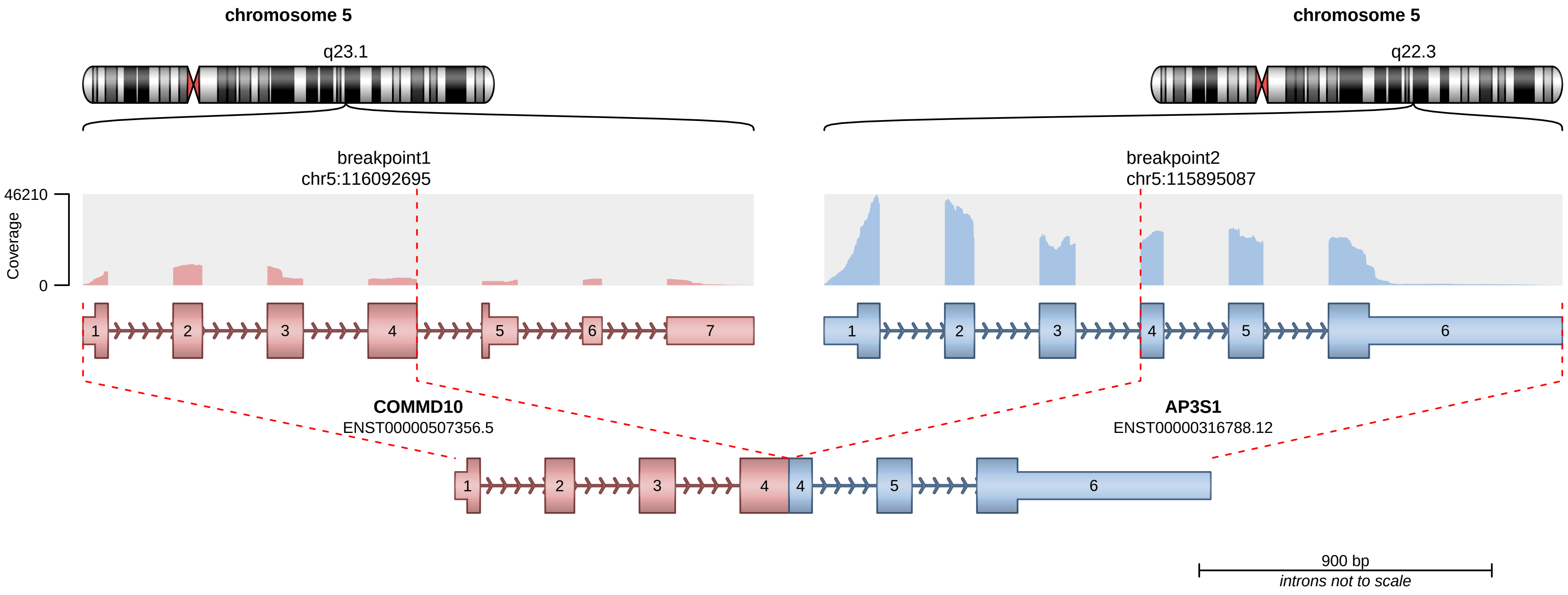


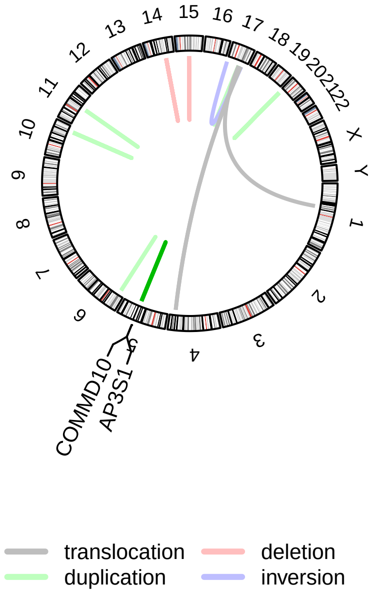




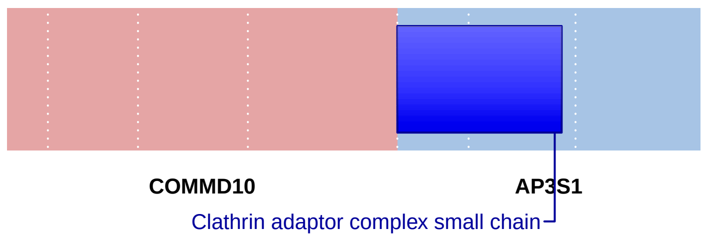
SUPPORTING READ COUNT

Split reads = 369
Discordant mates = 21



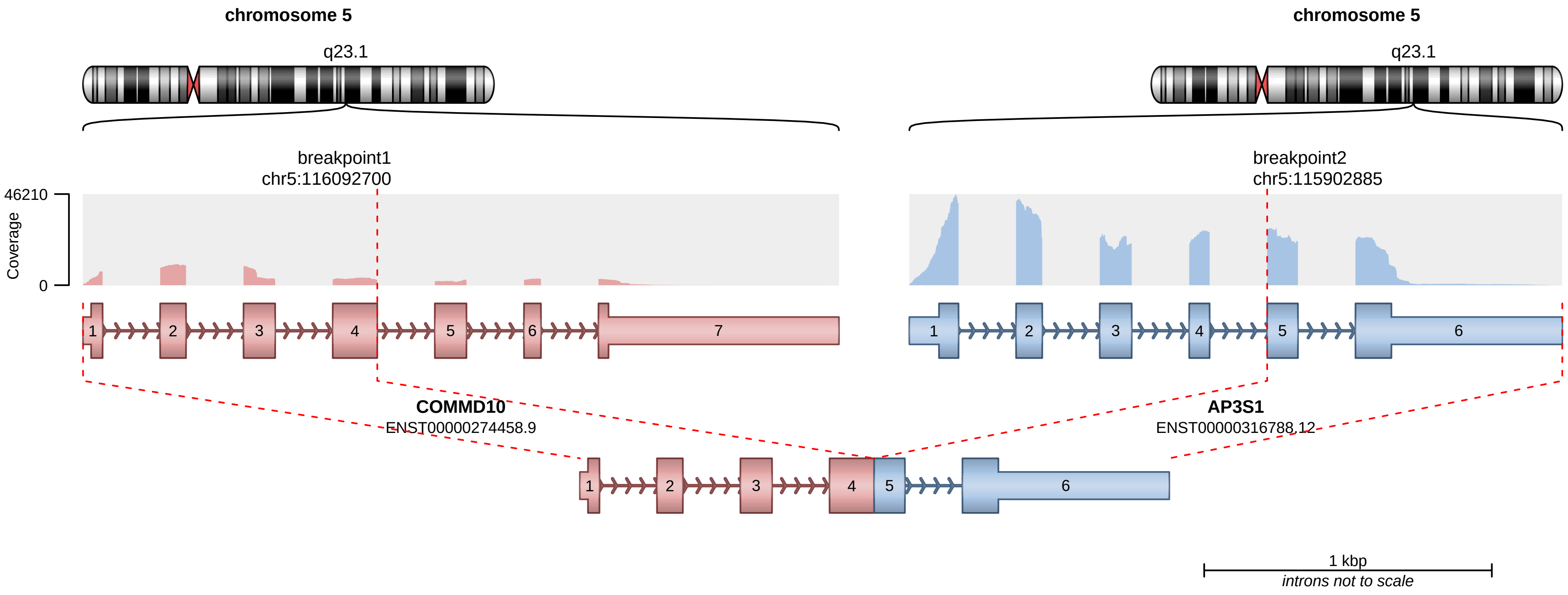


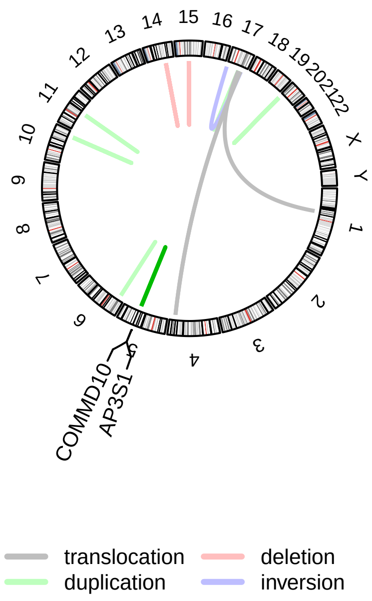
RETAINED PROTEIN DOMAINS
reading frame unclear

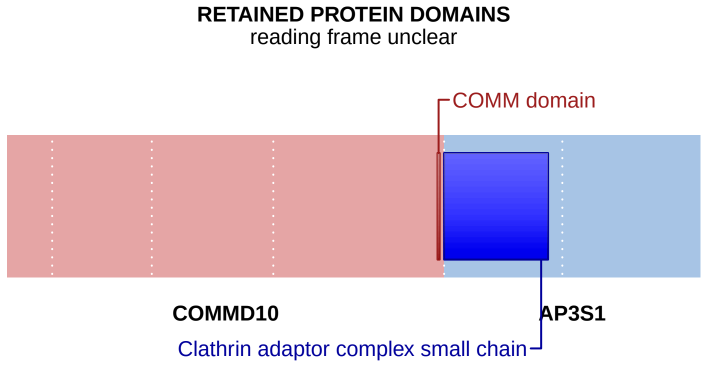


SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 16

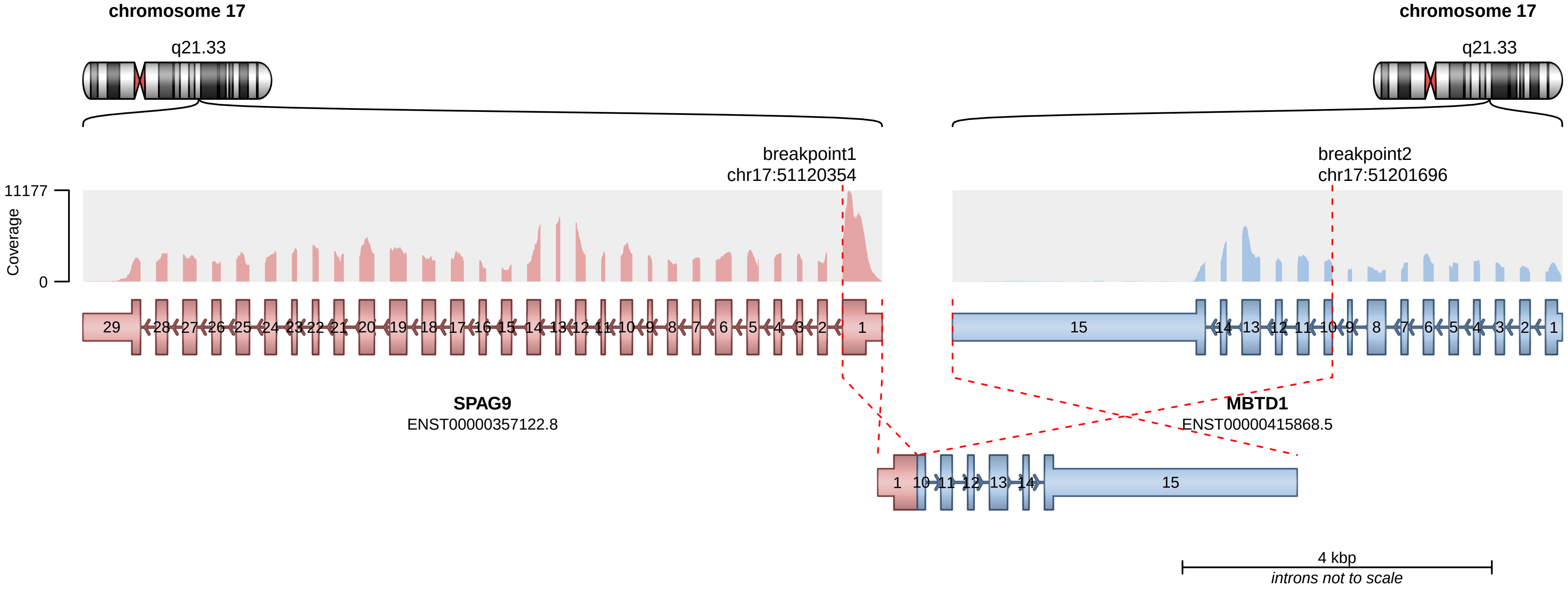


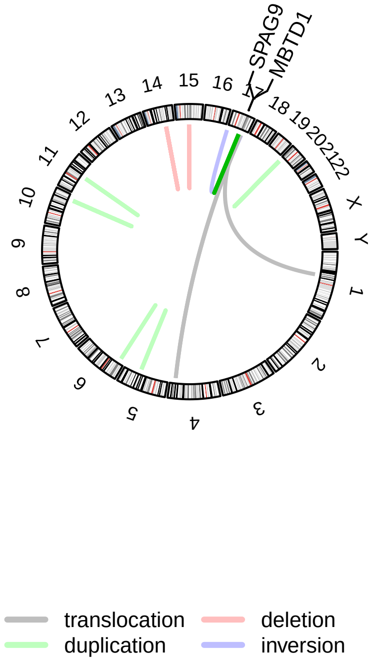


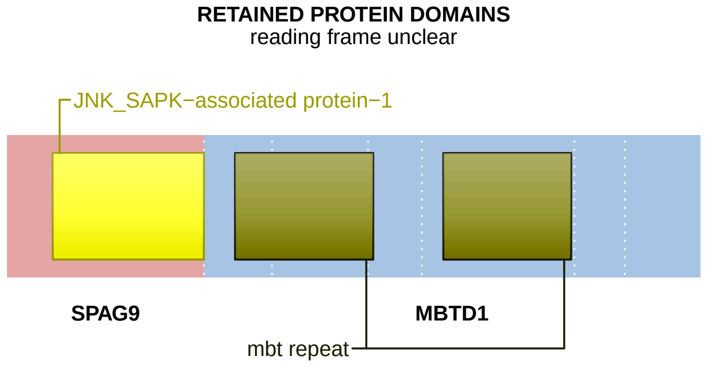


SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 3

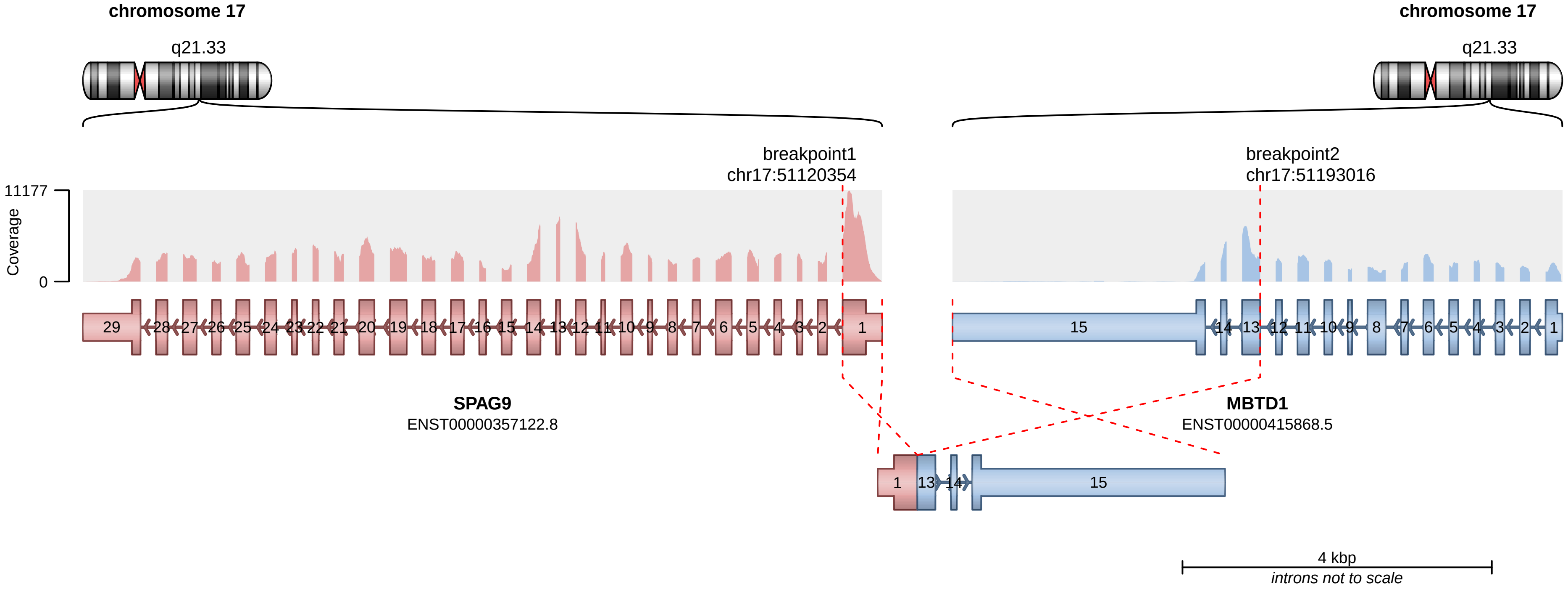


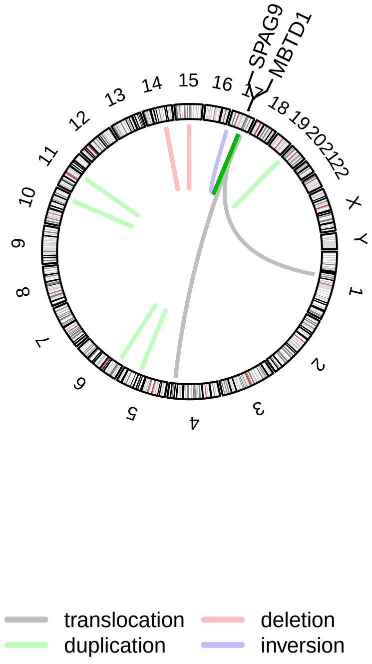




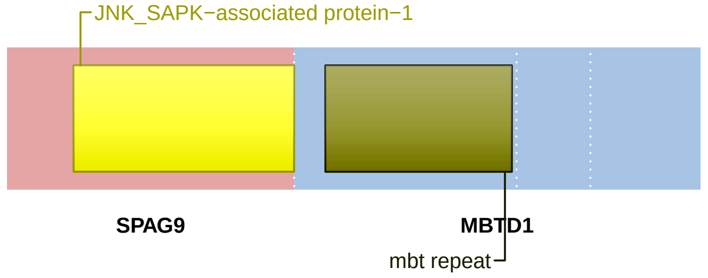
SUPPORTING READ COUNT

Split reads = 209
Discordant mates = 3



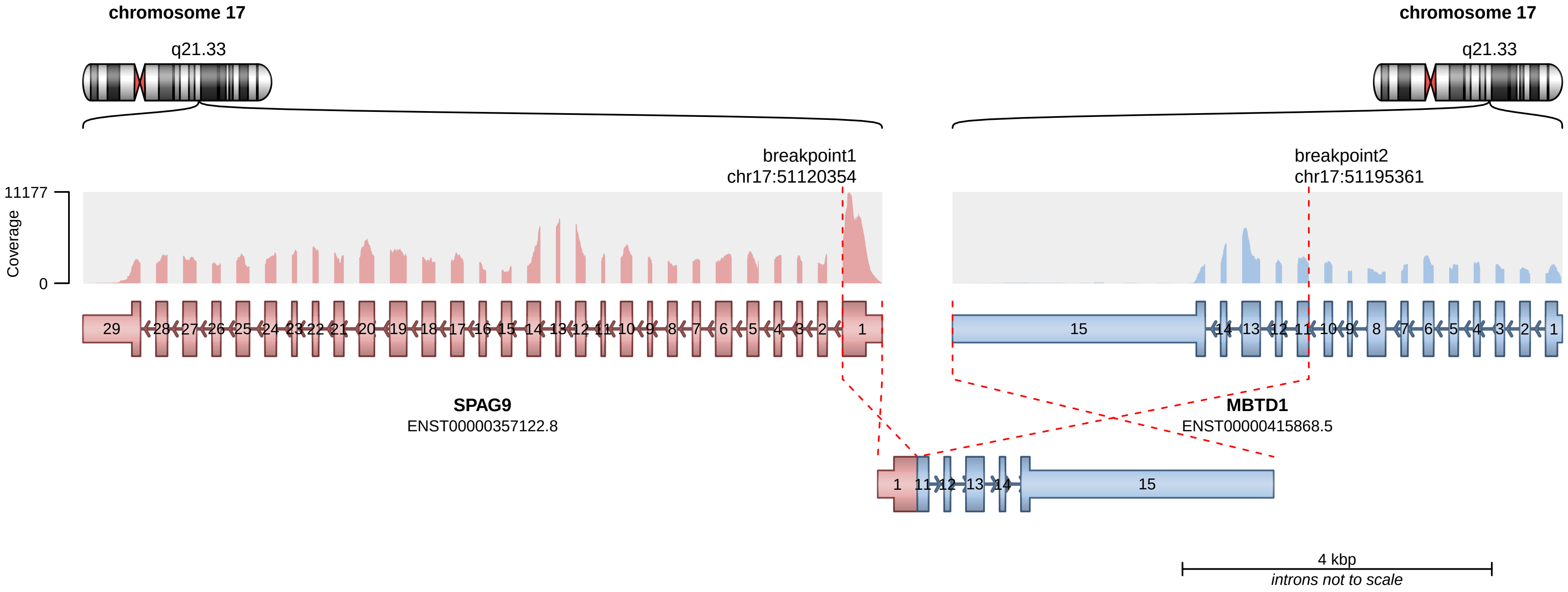


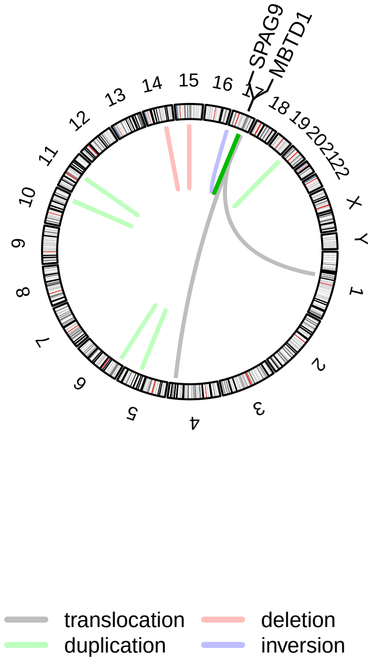
RETAINED PROTEIN DOMAINS
reading frame unclear

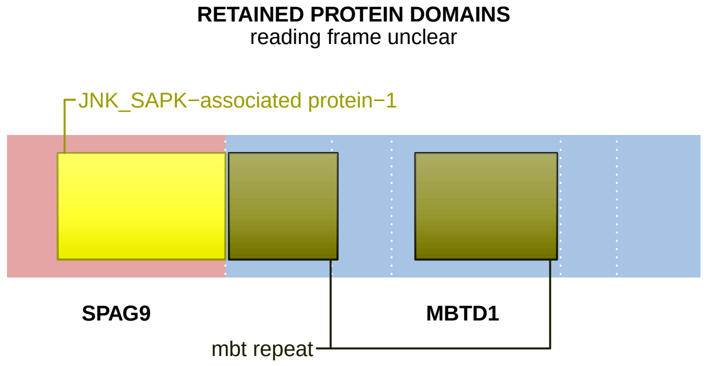


SUPPORTING READ COUNT

Split reads = 24
Discordant mates = 0

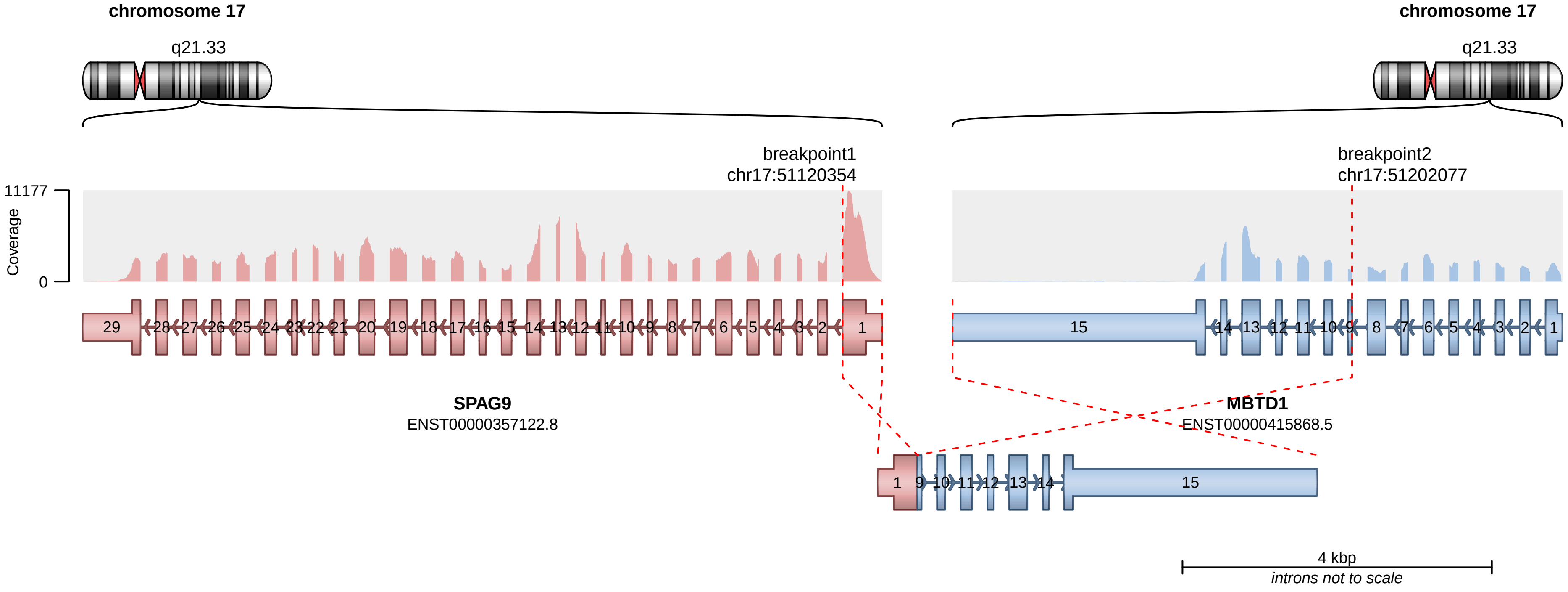


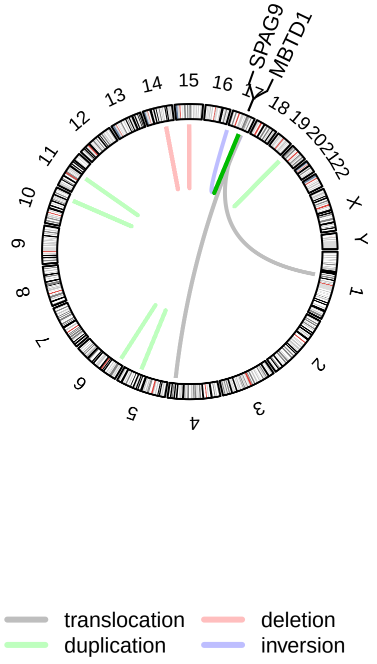


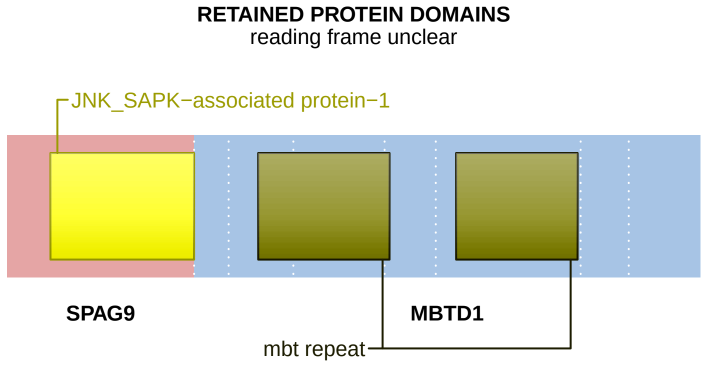


SUPPORTING READ COUNT

Split reads = 20
Discordant mates = 0

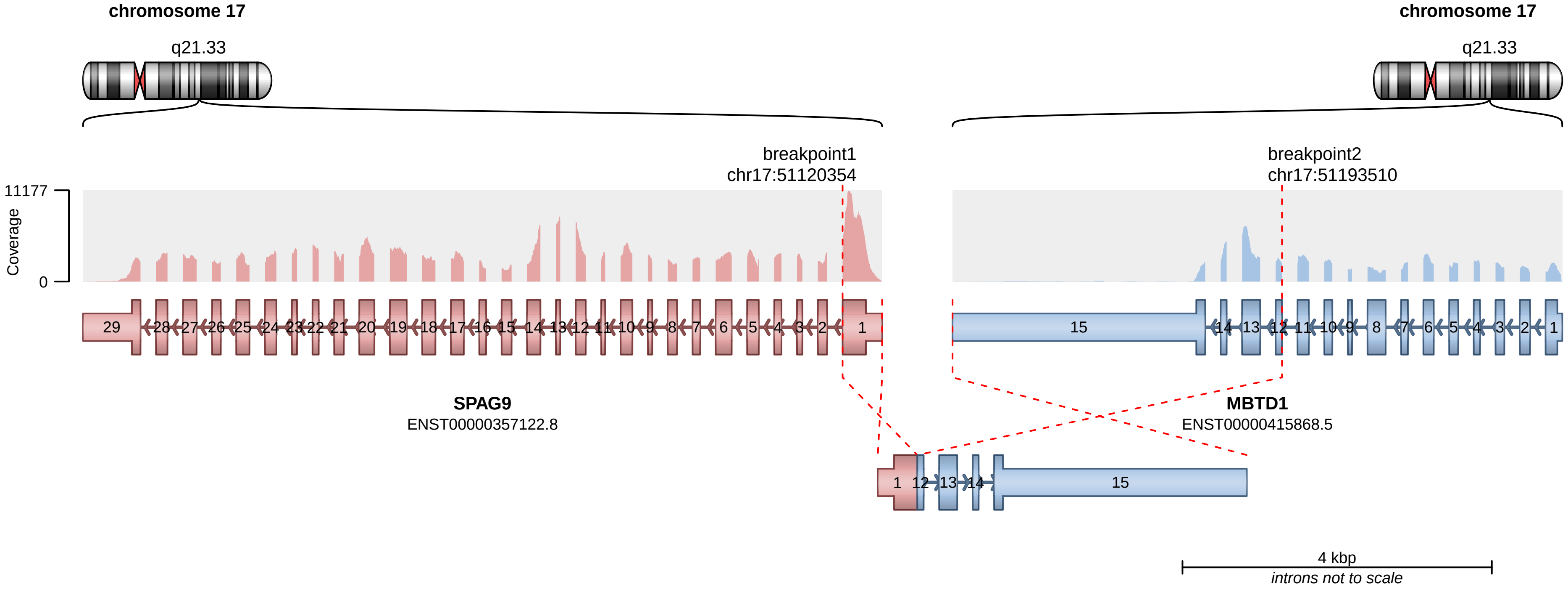


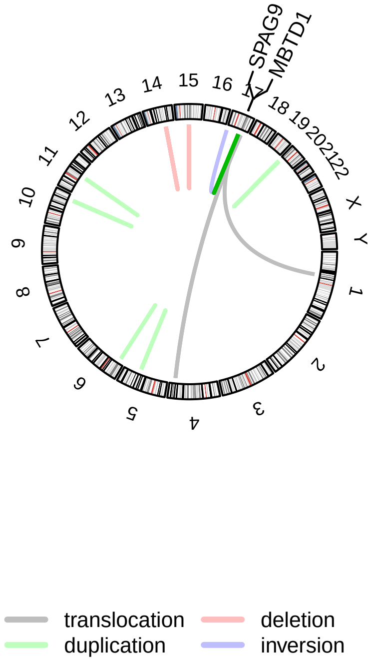


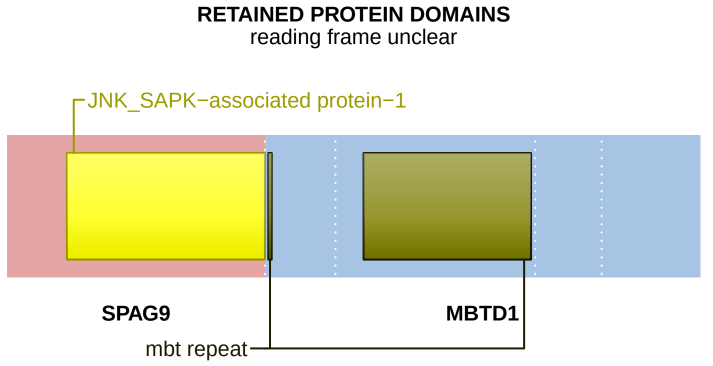


SUPPORTING READ COUNT

Split reads = 15
Discordant mates = 3

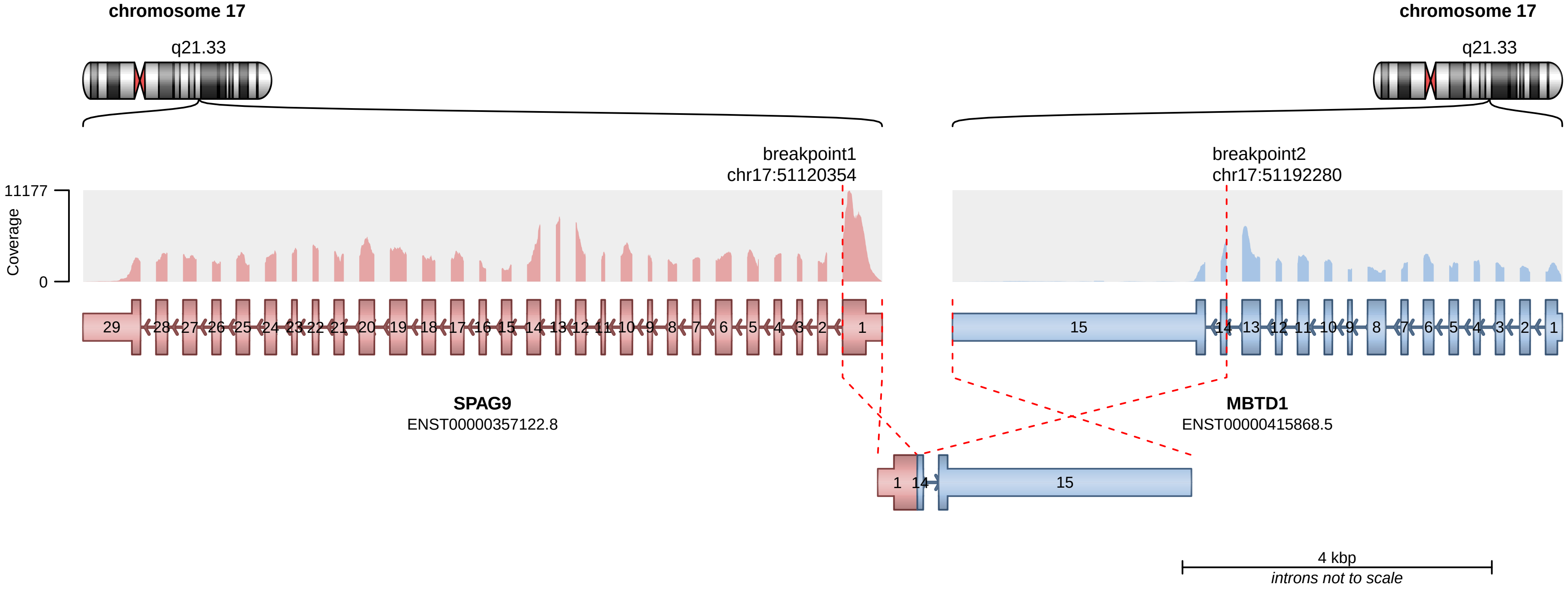


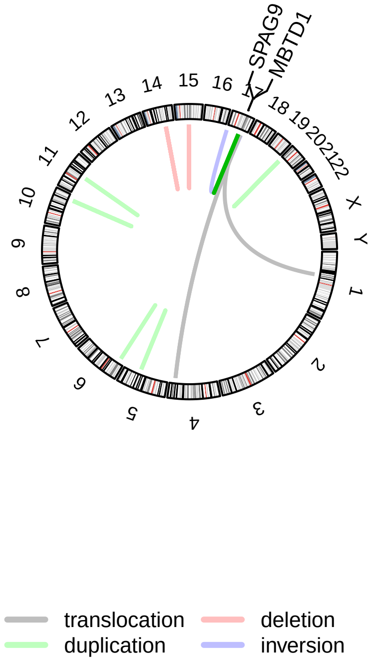




SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 0

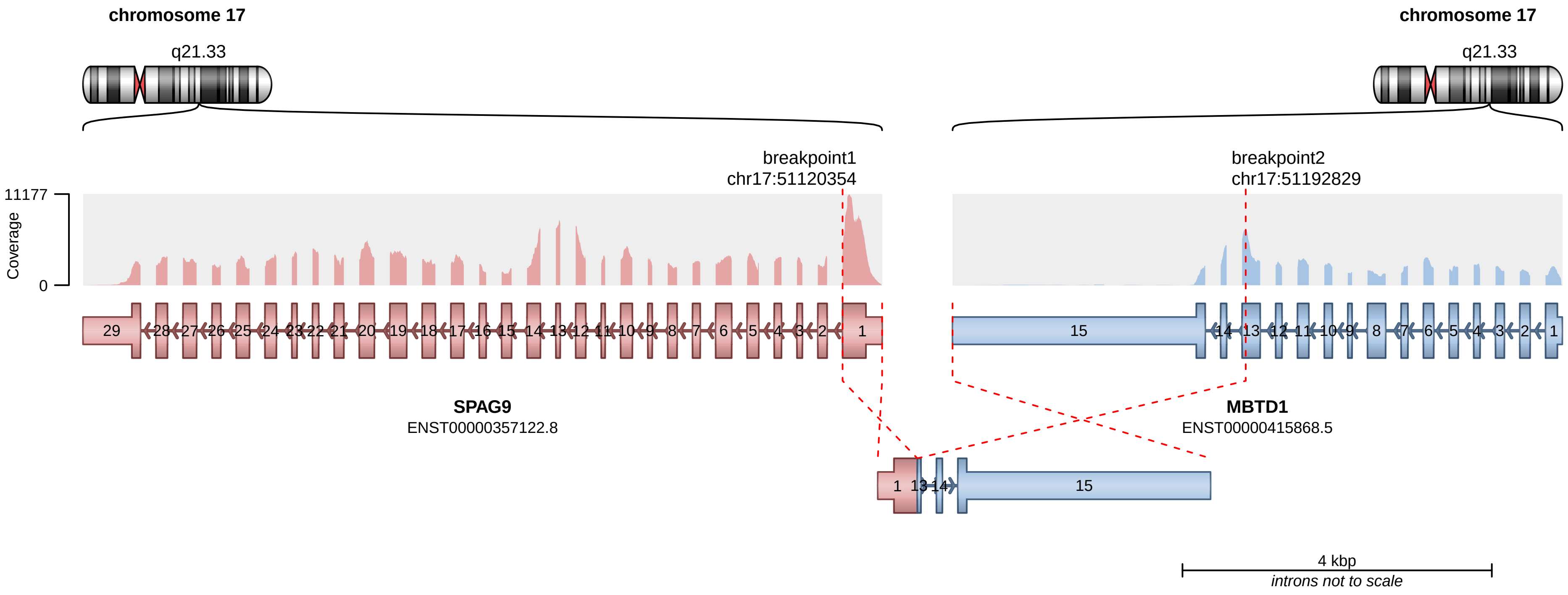


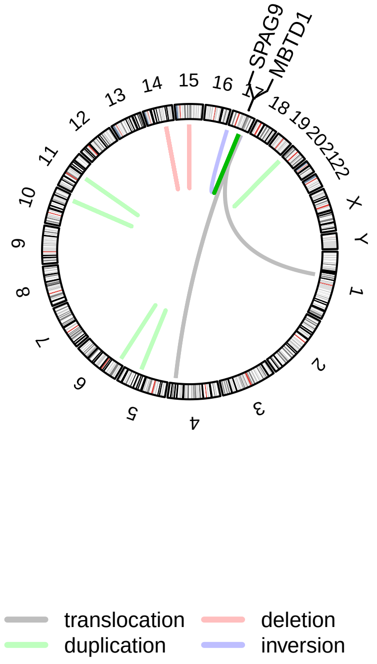


RETAINED PROTEIN DOMAINS
reading frame unclear

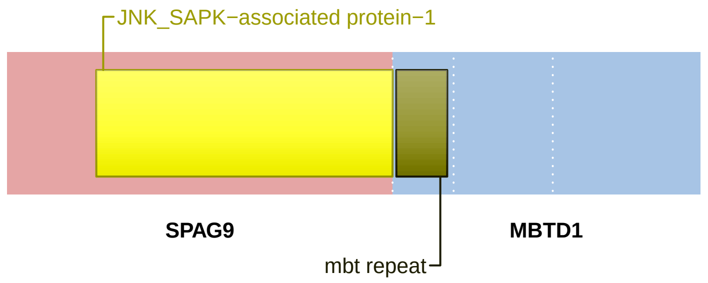
SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0



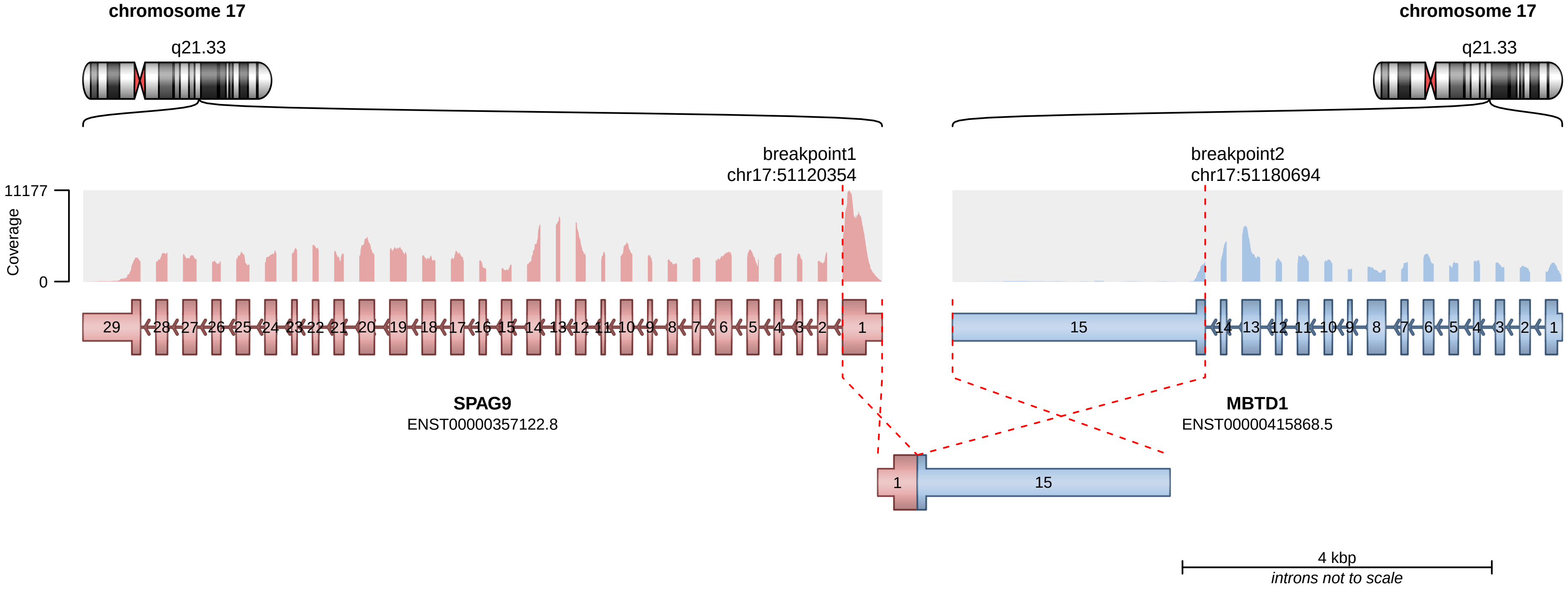


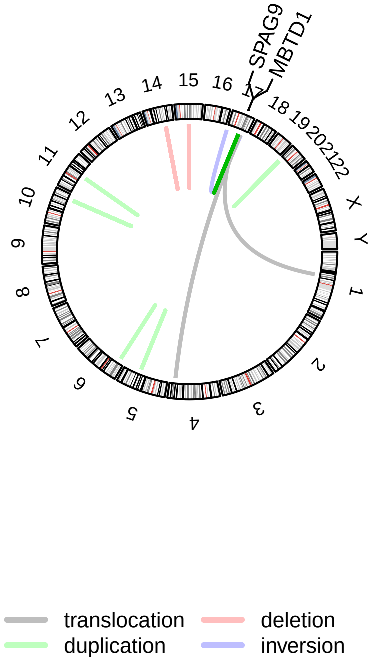
RETAINED PROTEIN DOMAINS
reading frame unclear

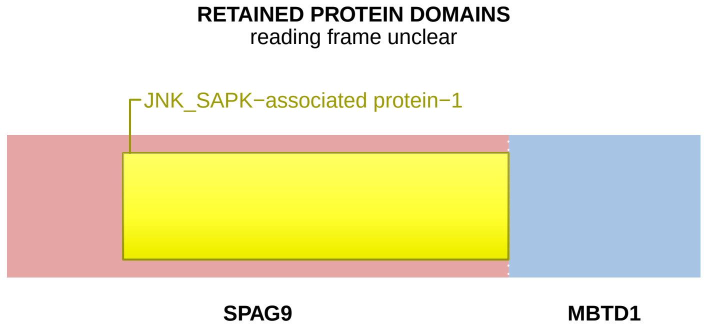


SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0

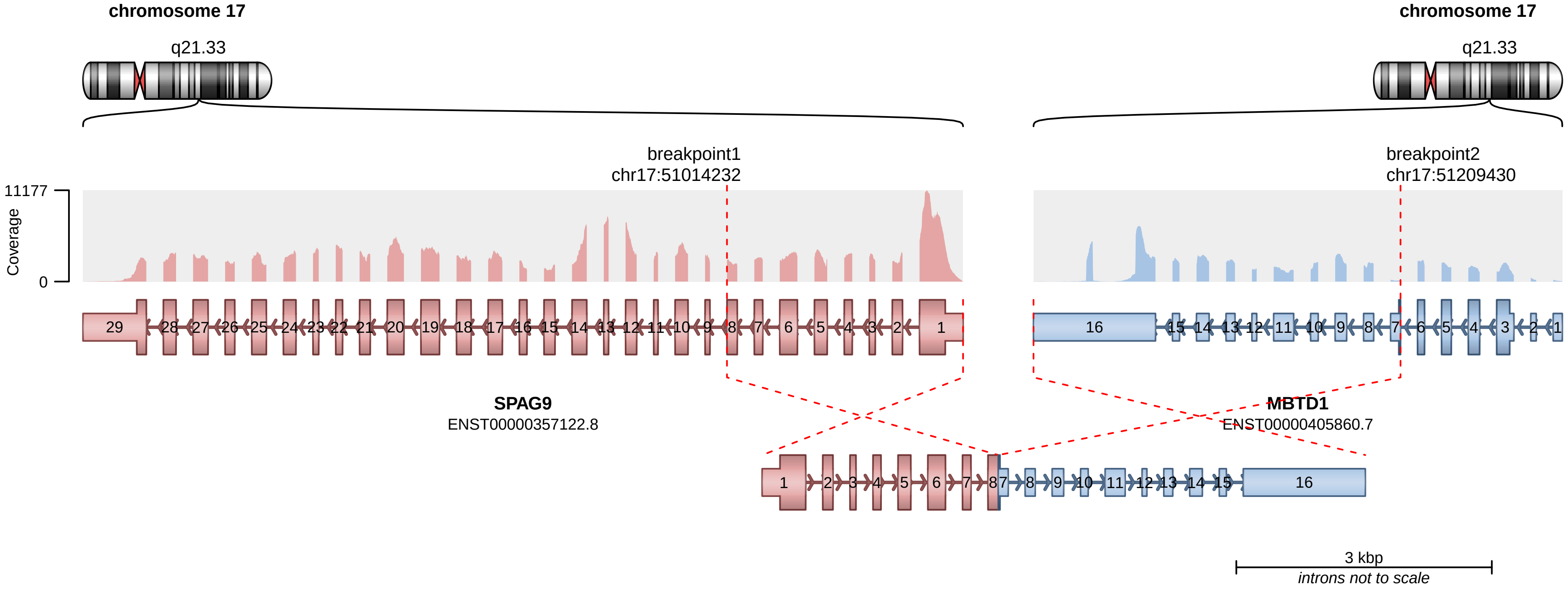


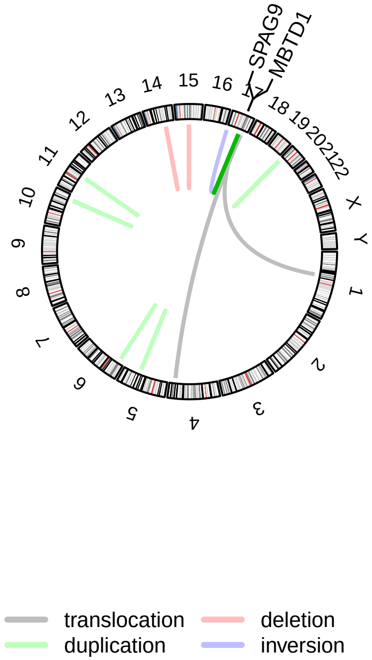


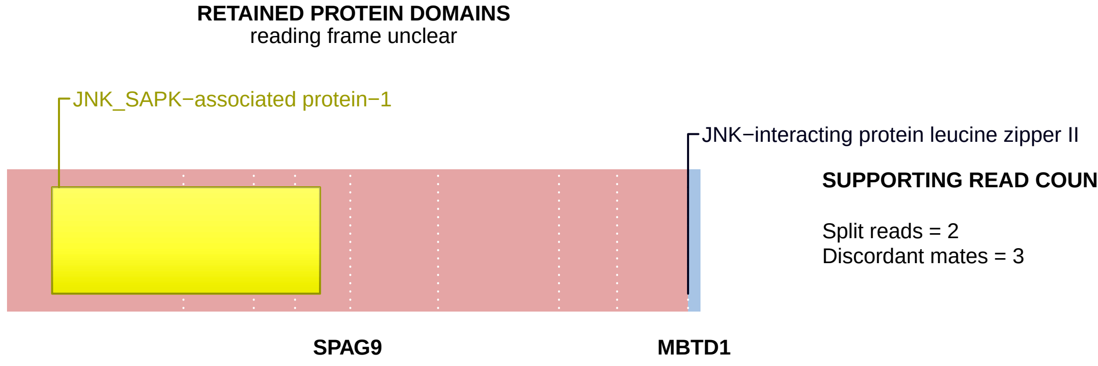


SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

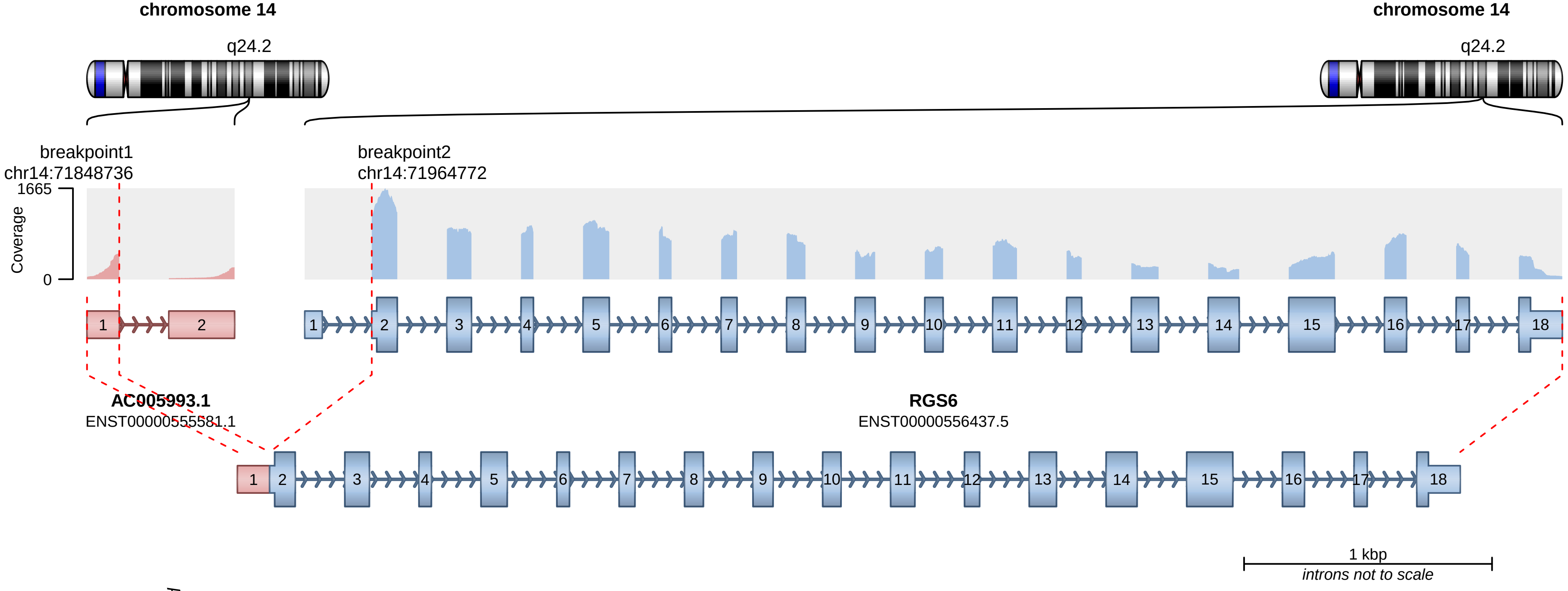


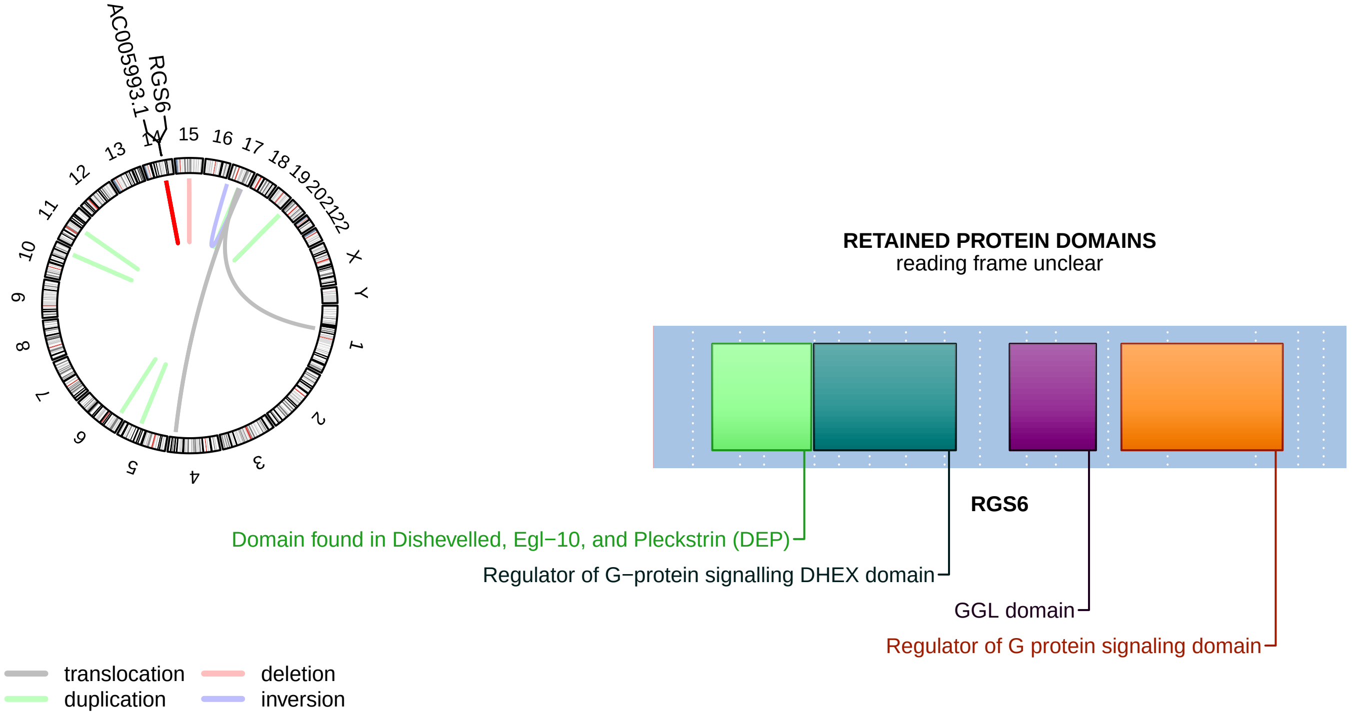




SUPPORTING READ COUNT

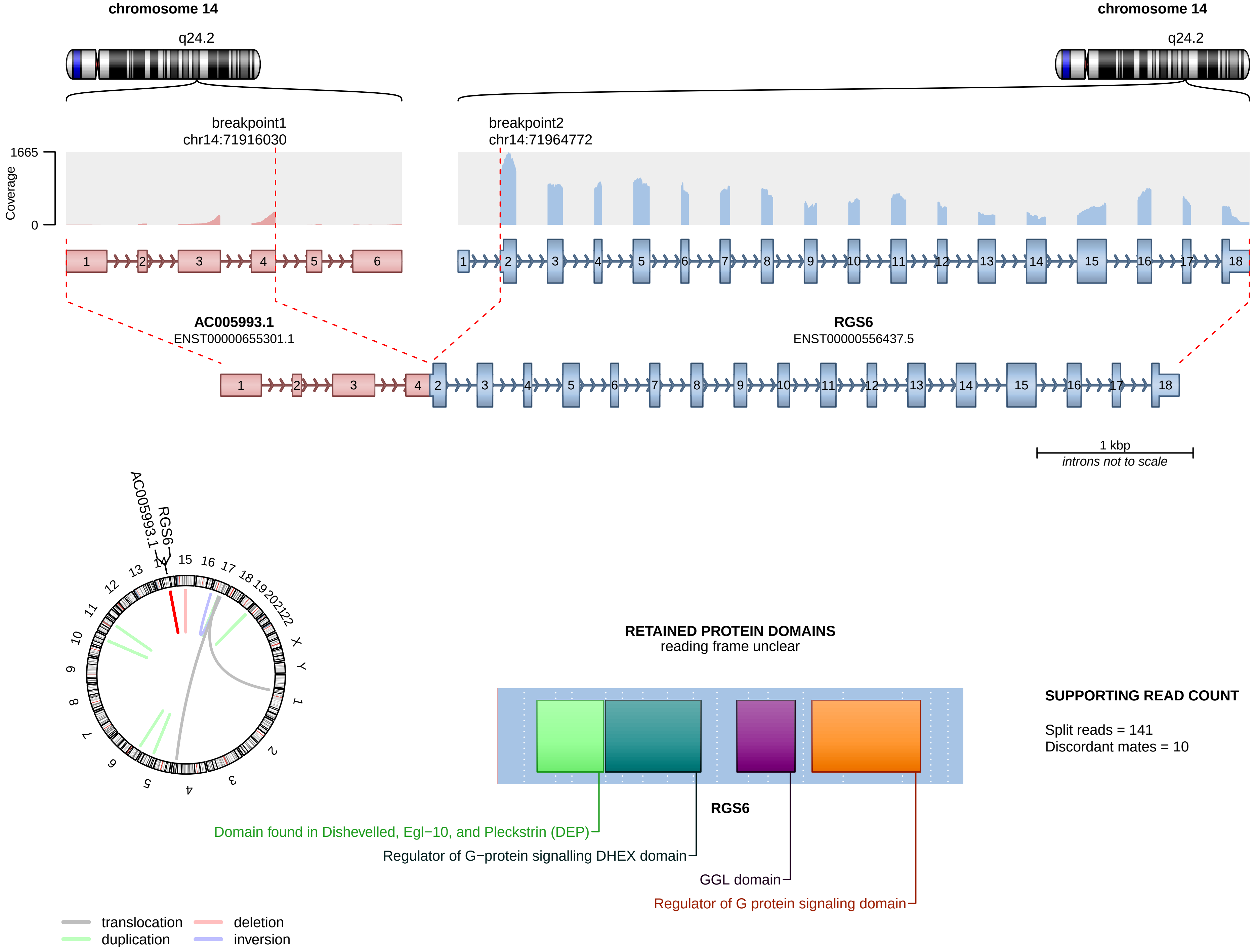
Split reads = 2
Discordant mates = 3





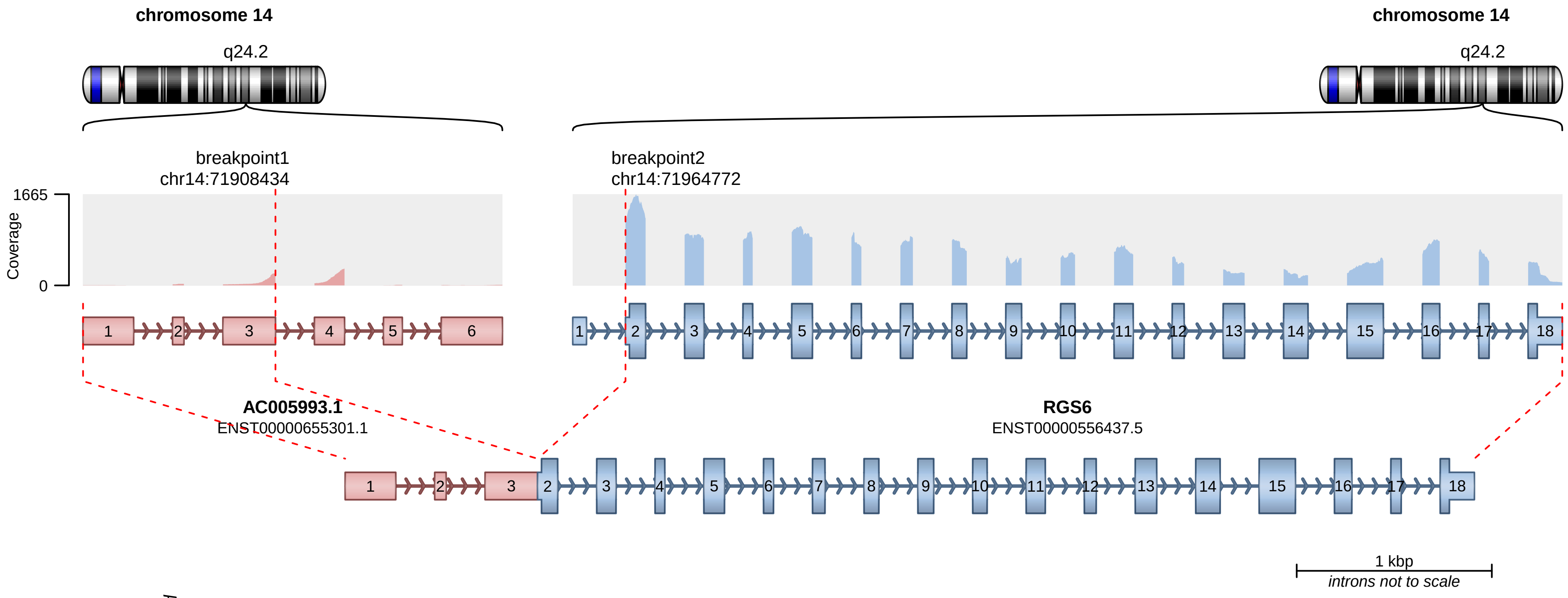
SUPPORTING READ COUNT

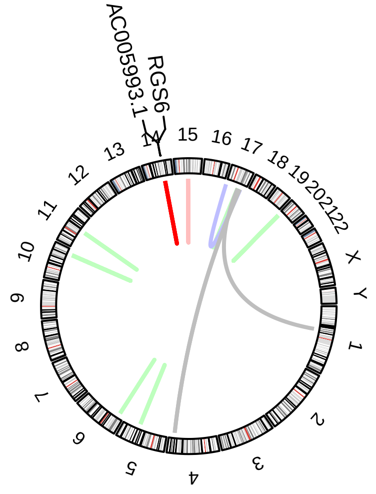
Split reads = 181
Discordant mates = 4

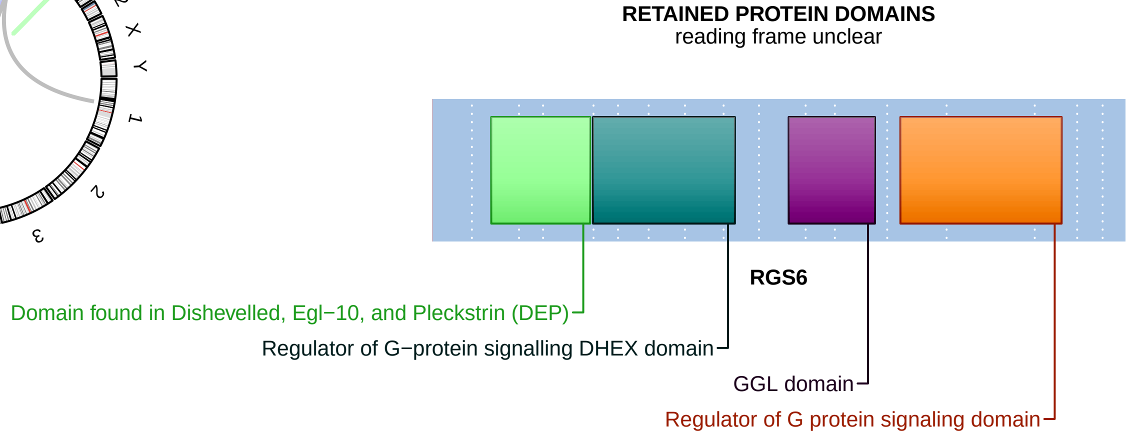


SUPPORTING READ COUNT

Split reads = 141
Discordant mates = 10

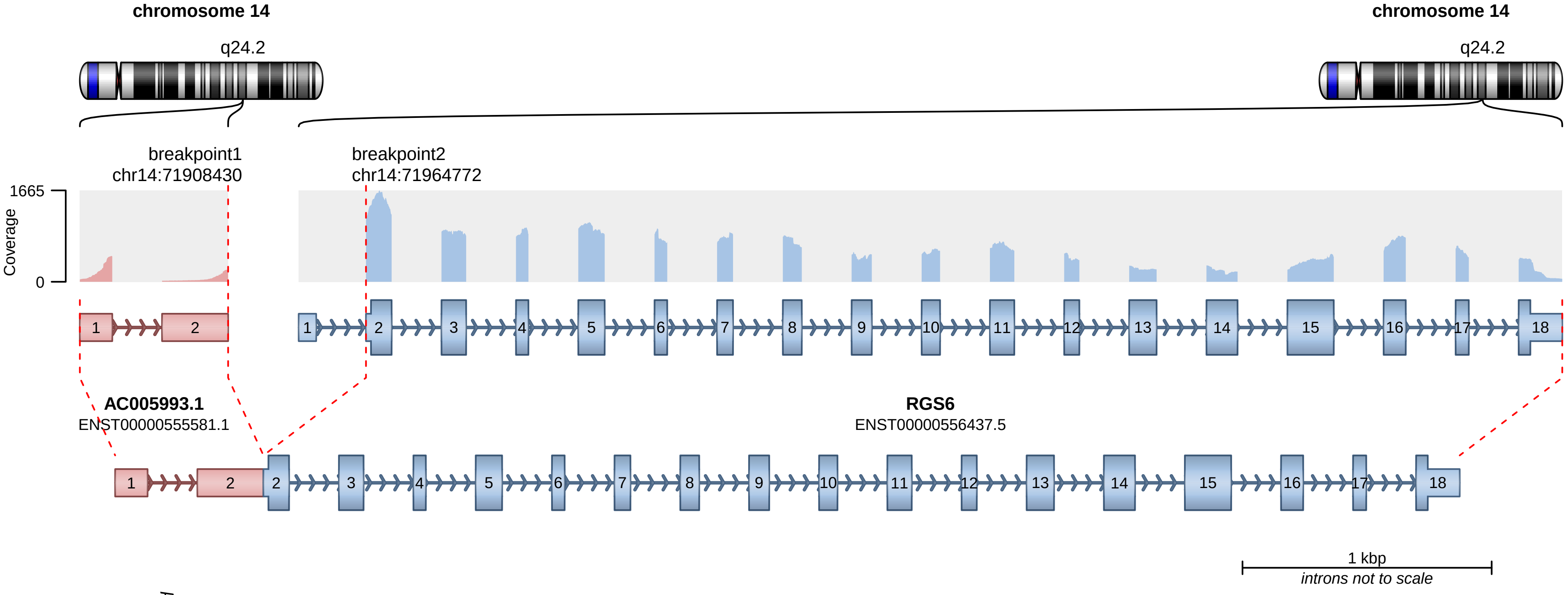


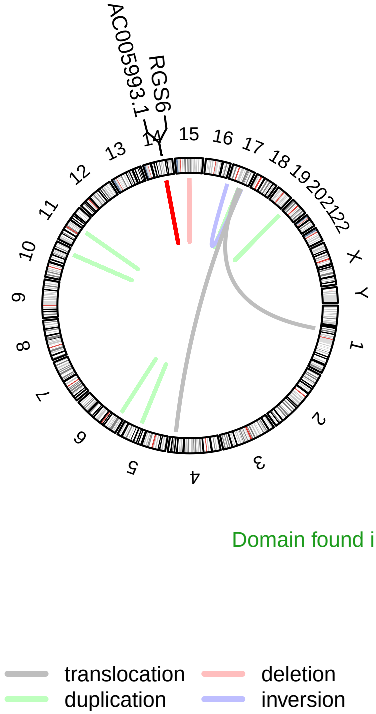




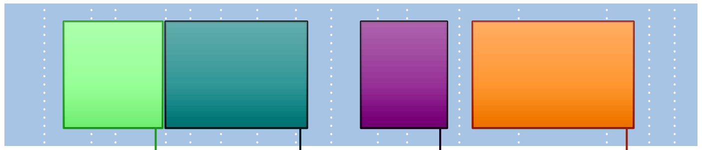
SUPPORTING READ COUNT

Split reads = 94
Discordant mates = 9



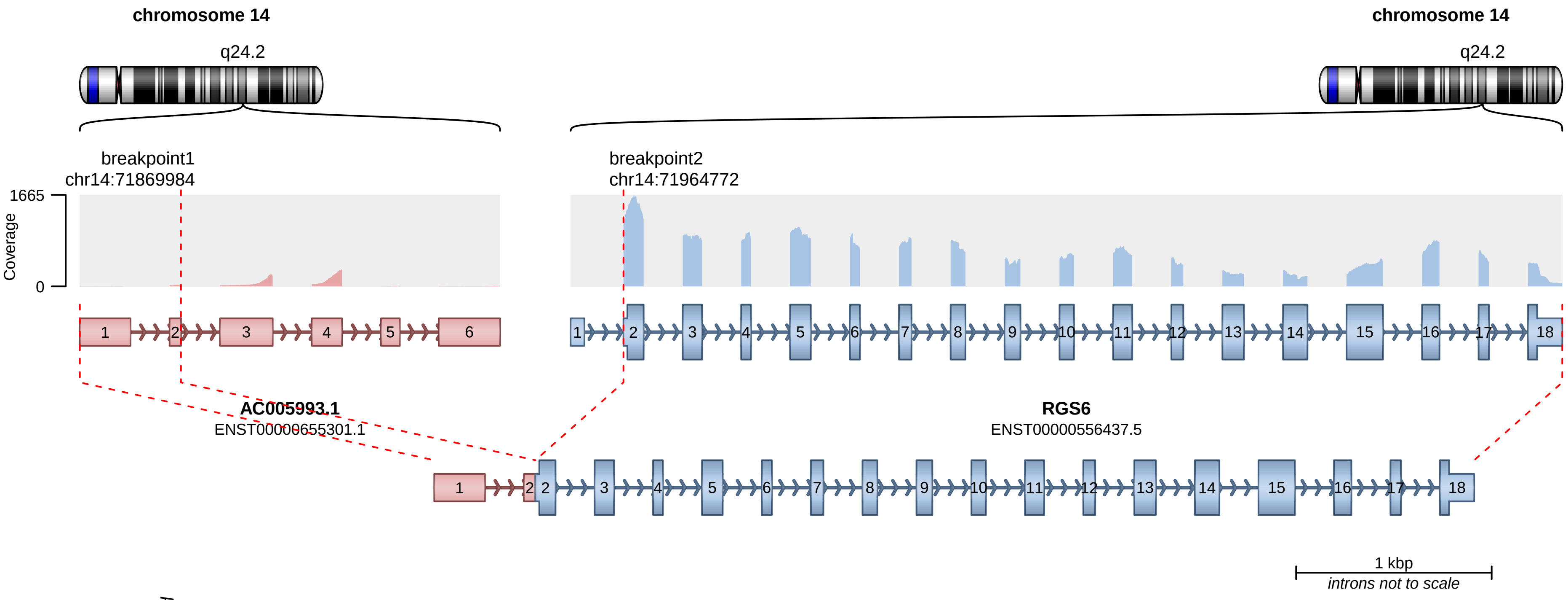


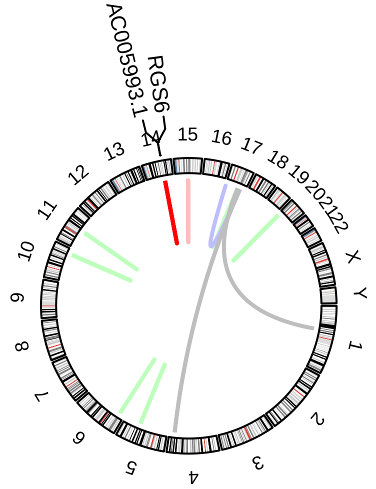
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

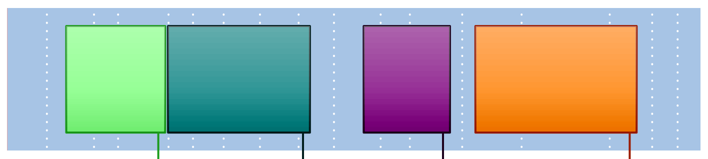
Split reads = 12
Discordant mates = 9





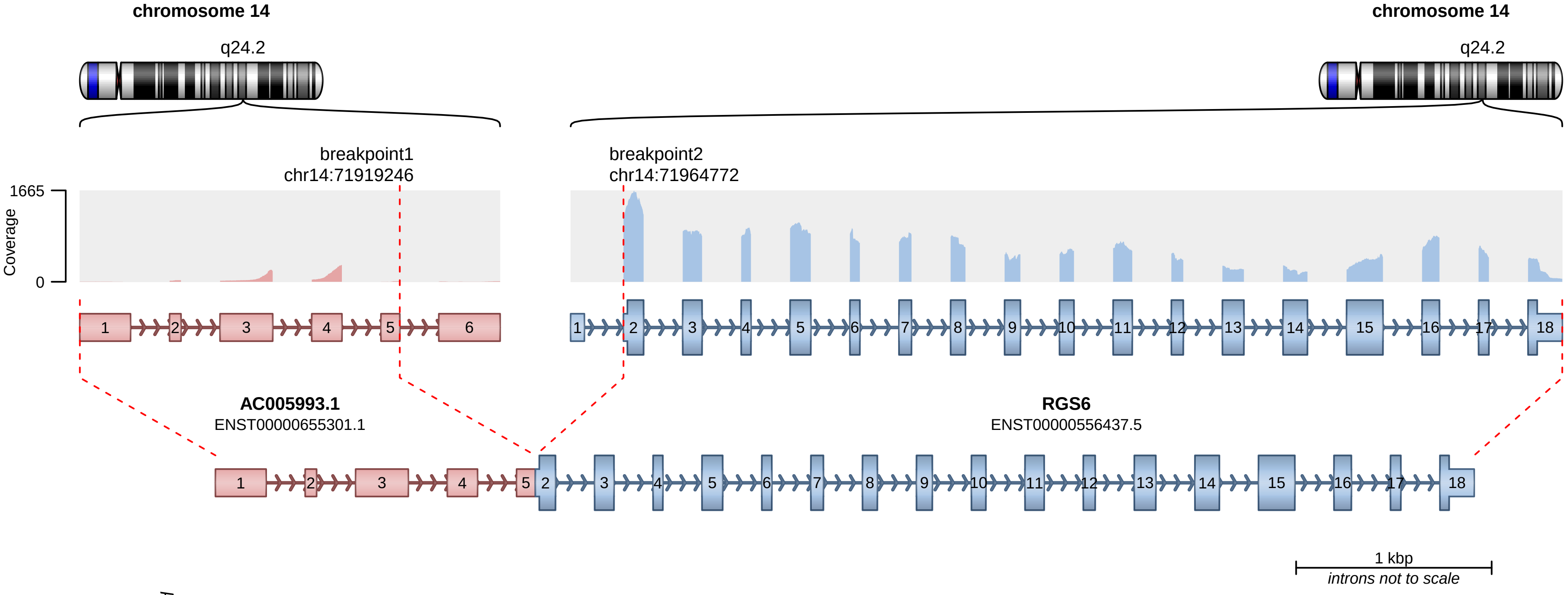
RETAINED PROTEIN DOMAINS

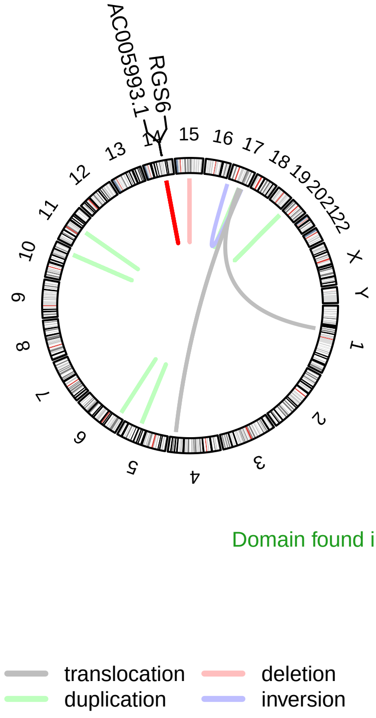
reading frame unclear

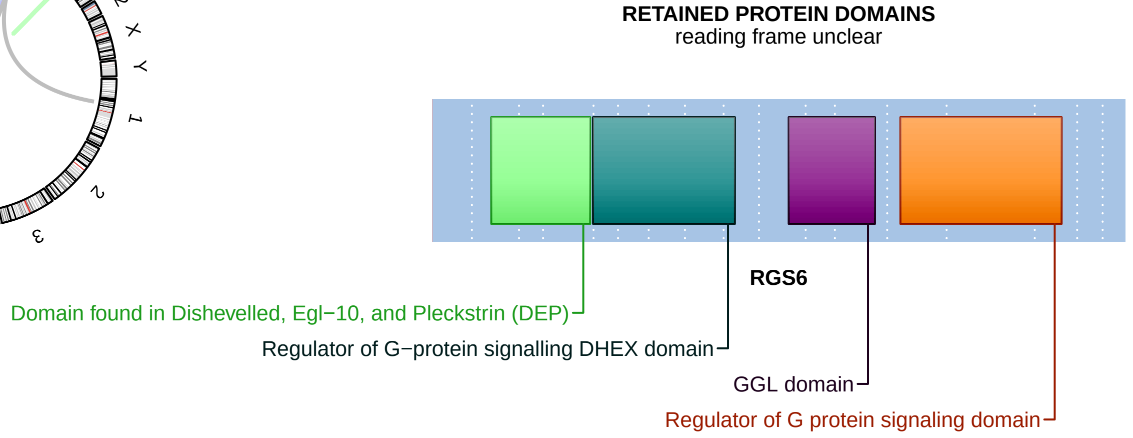


SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 6

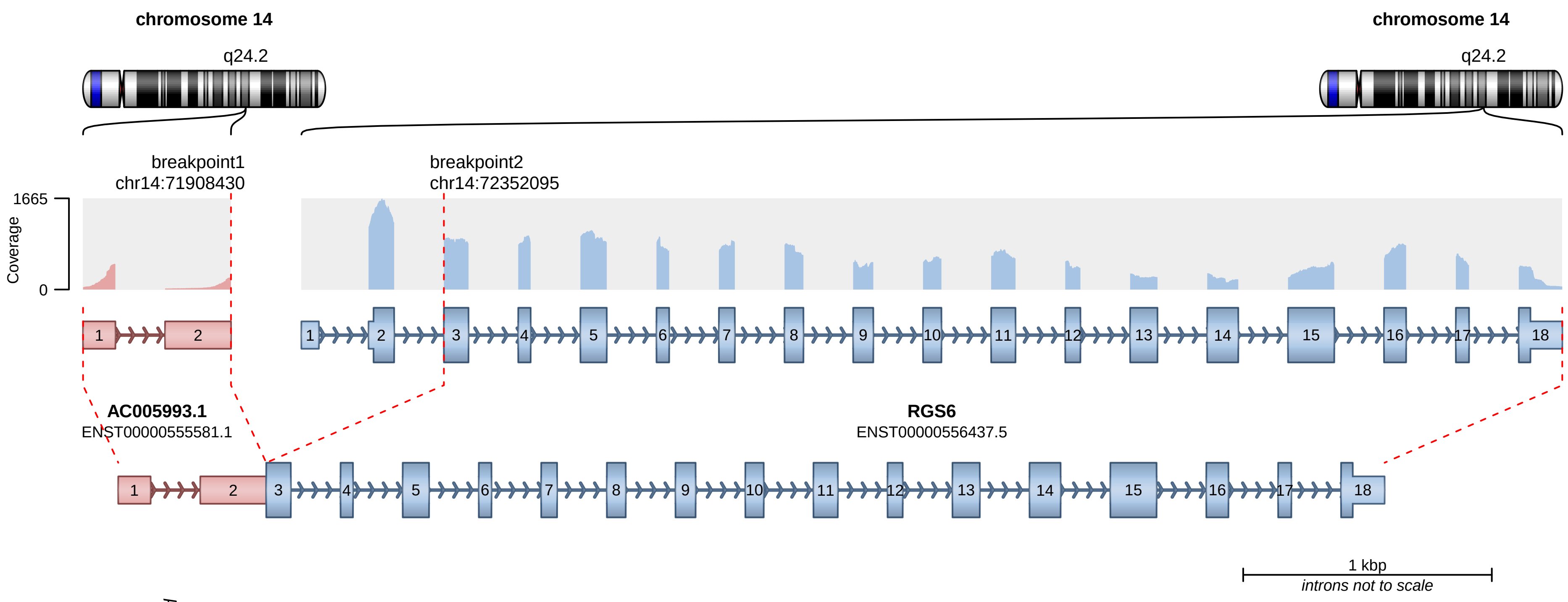


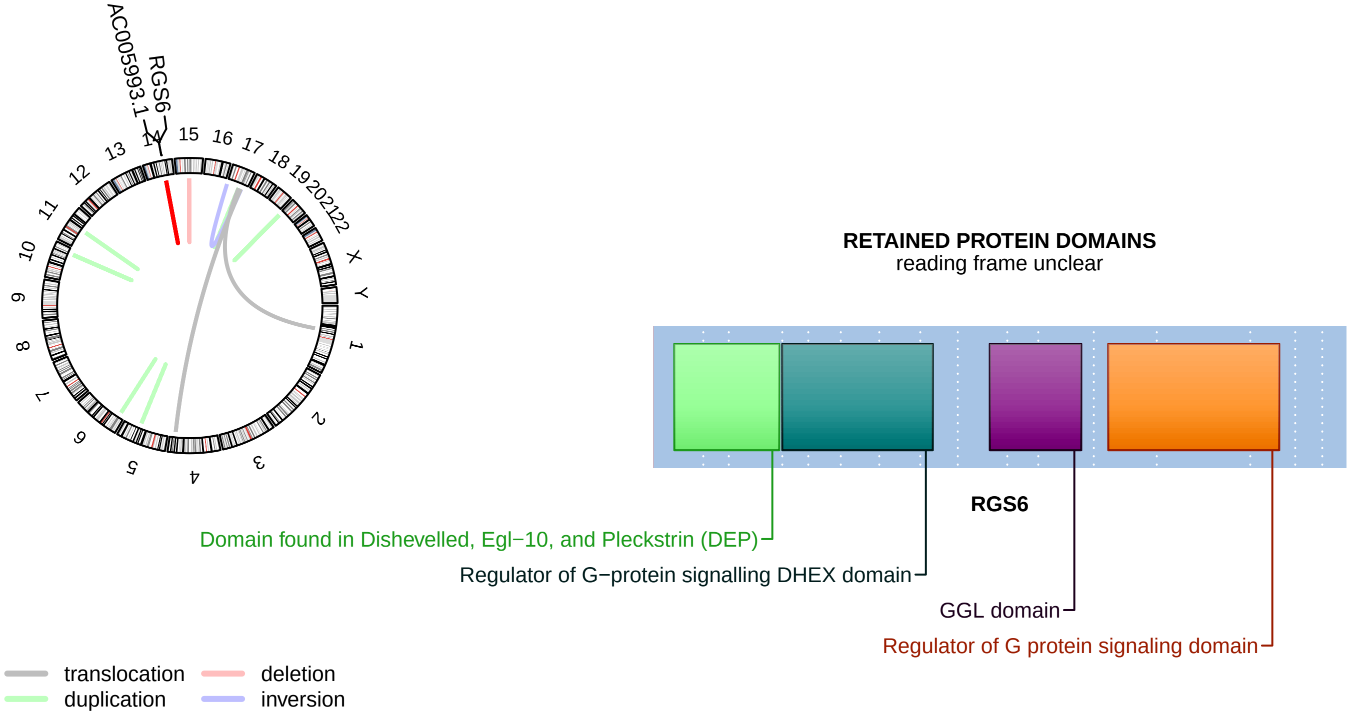




SUPPORTING READ COUNT

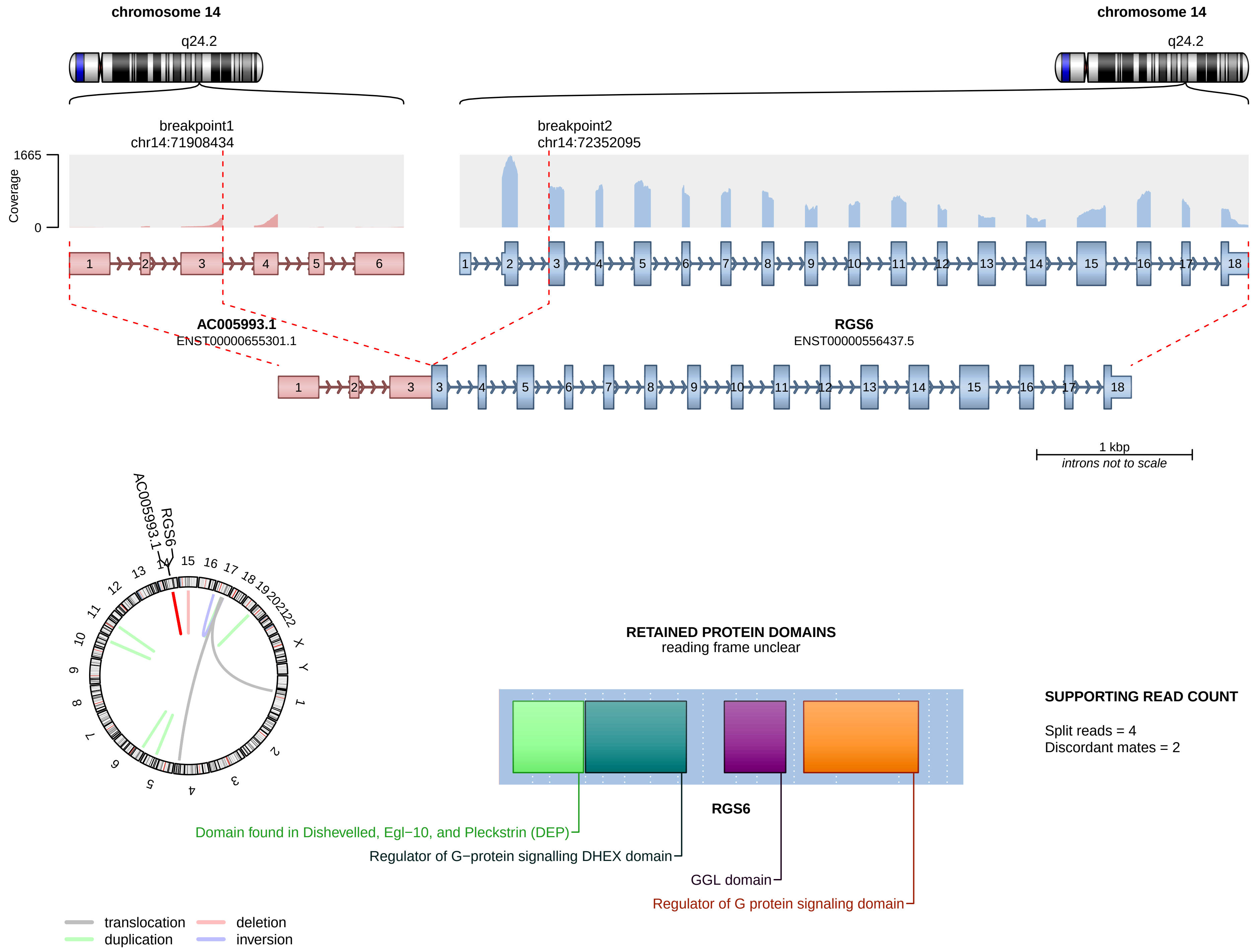
Split reads = 3
Discordant mates = 10





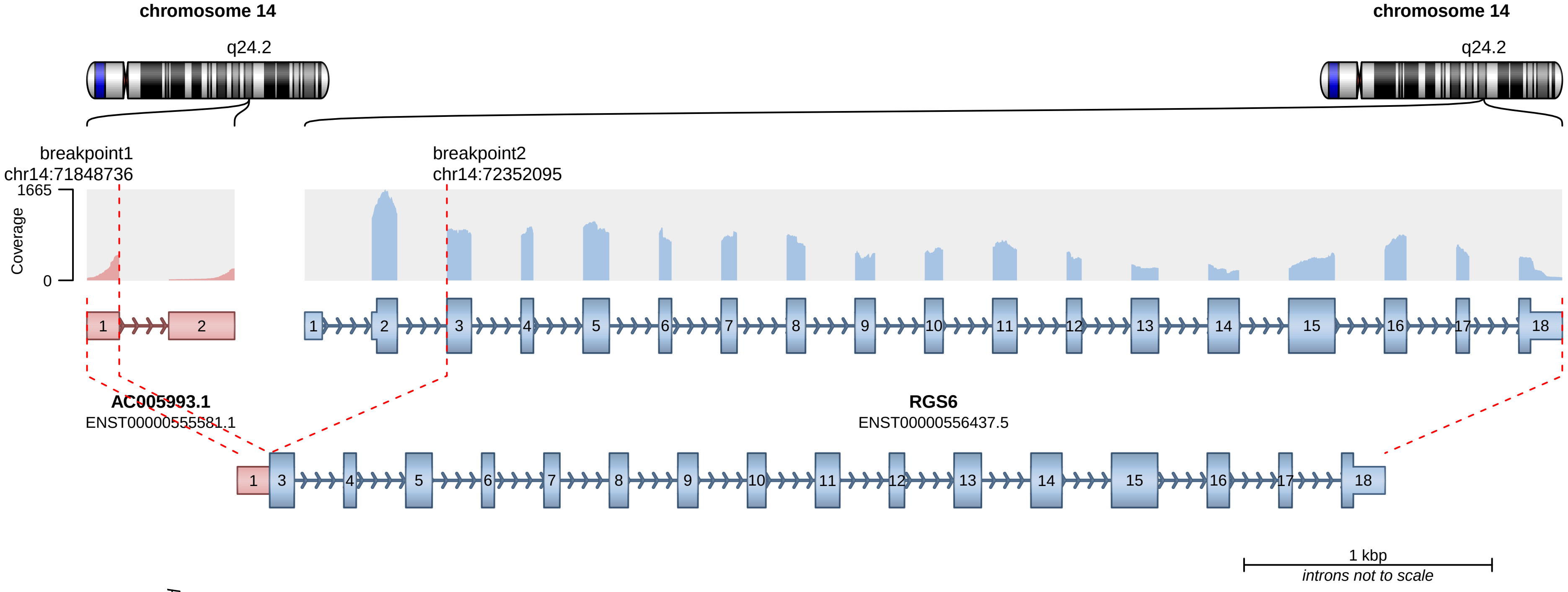
SUPPORTING READ COUNT

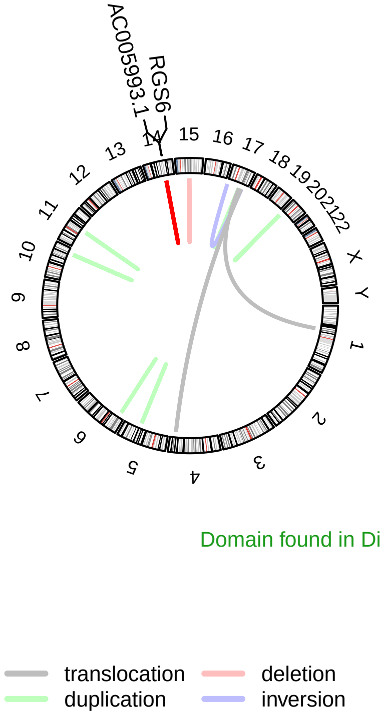
Split reads = 5
Discordant mates = 2

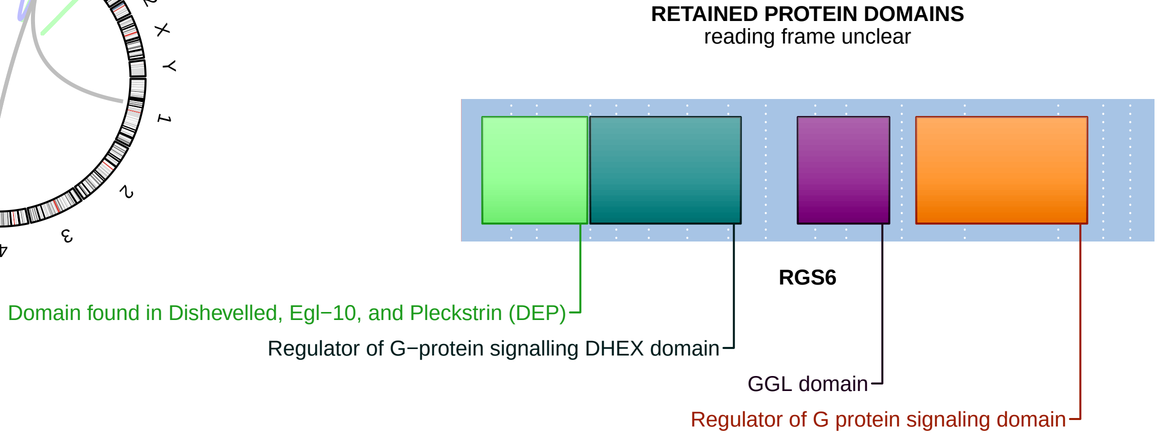


SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 2

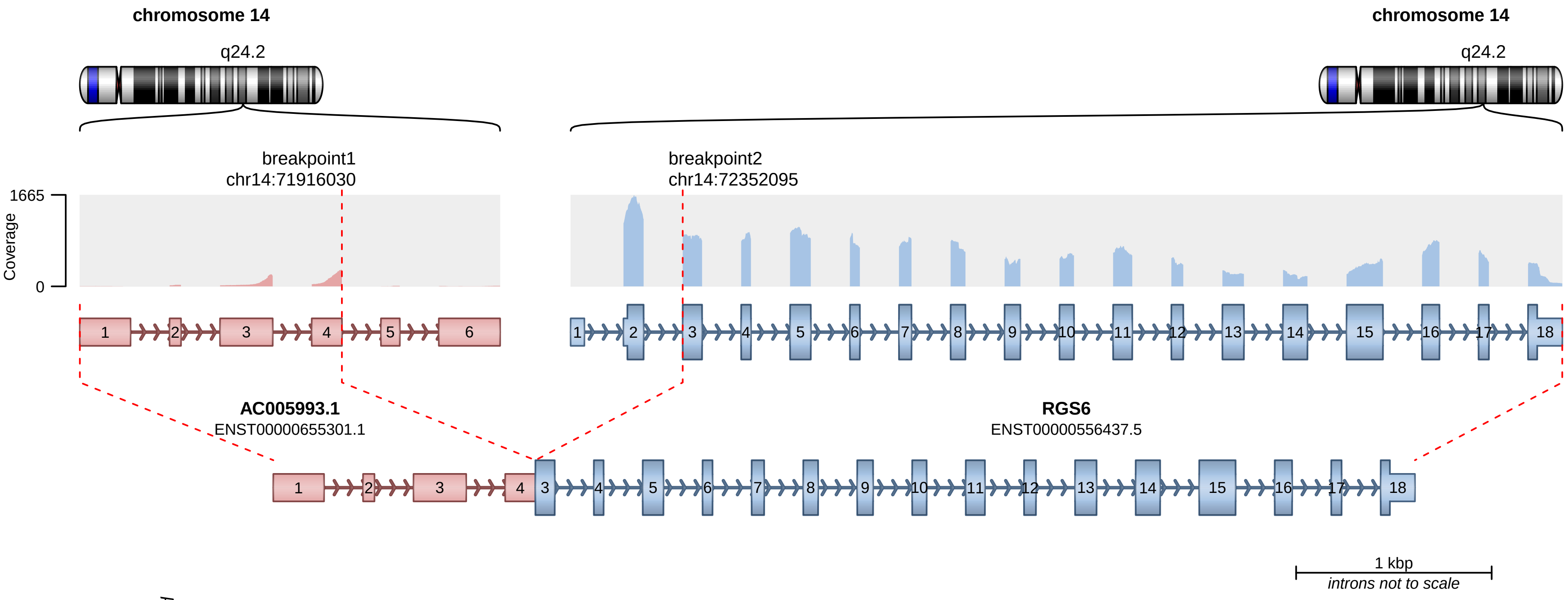


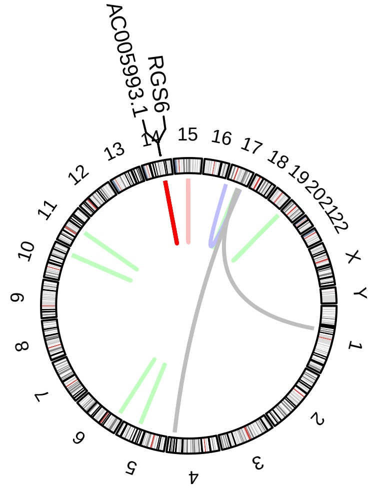


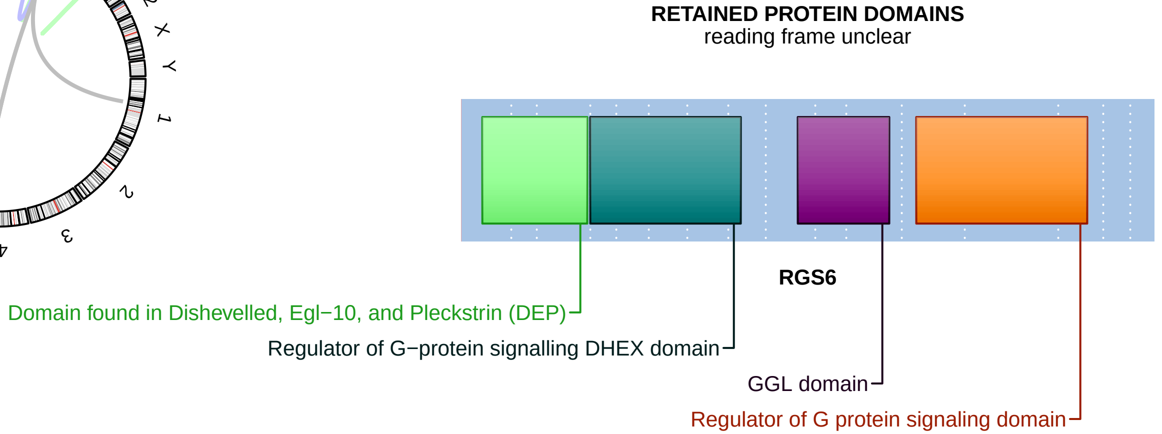


SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 1



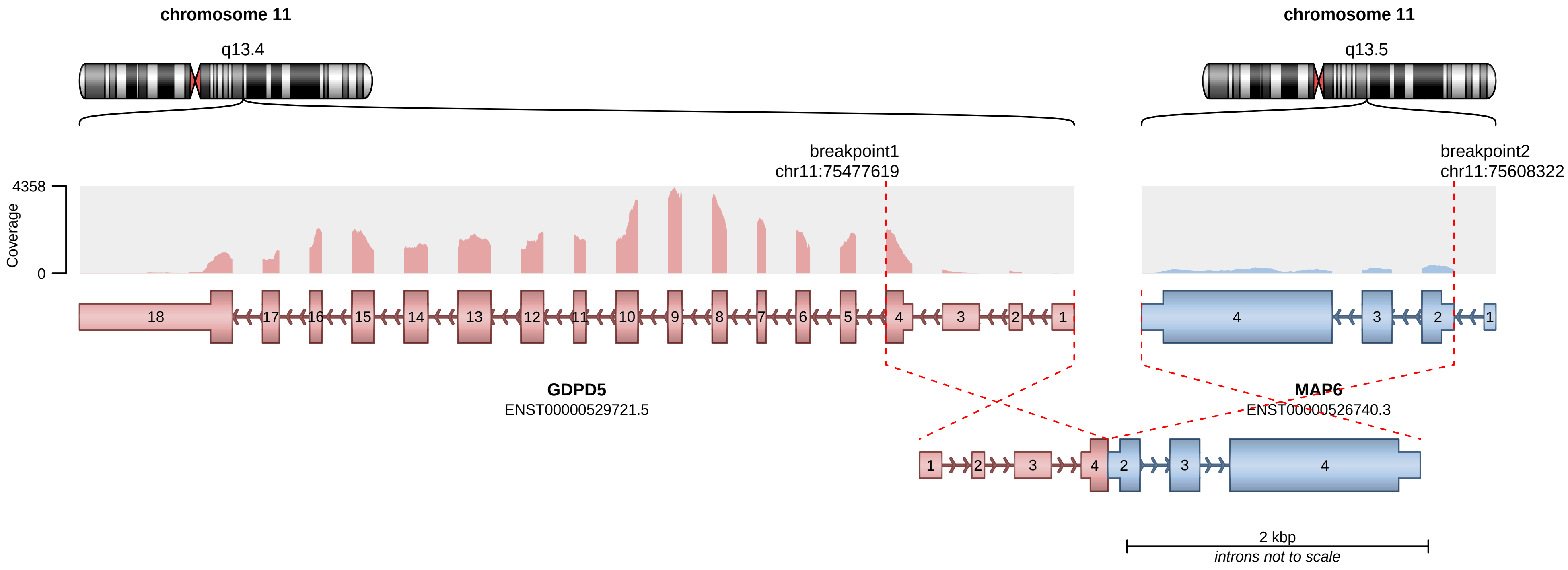


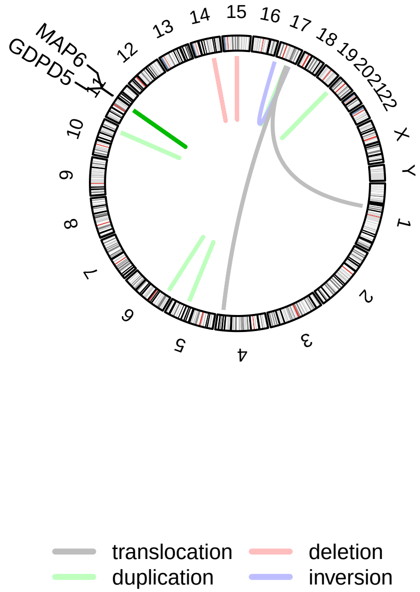


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 2

⬜ translocation
🟥 deletion
🟩 duplication
🟦 inversion

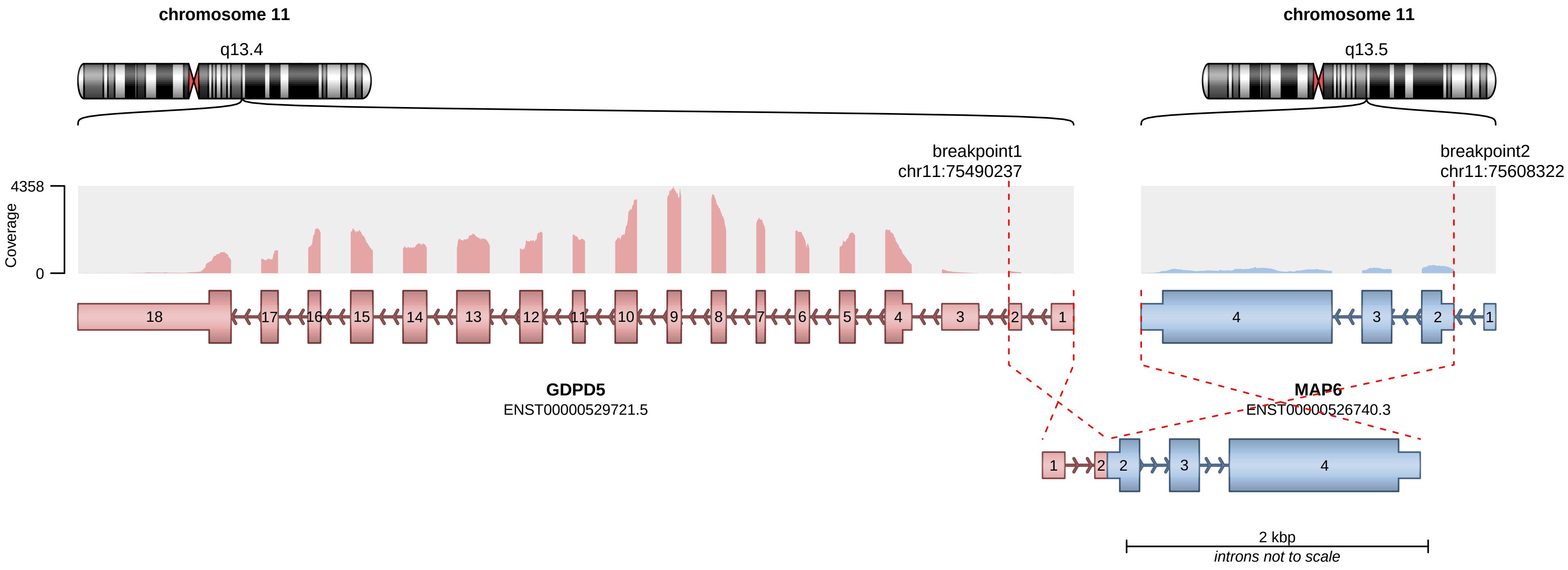


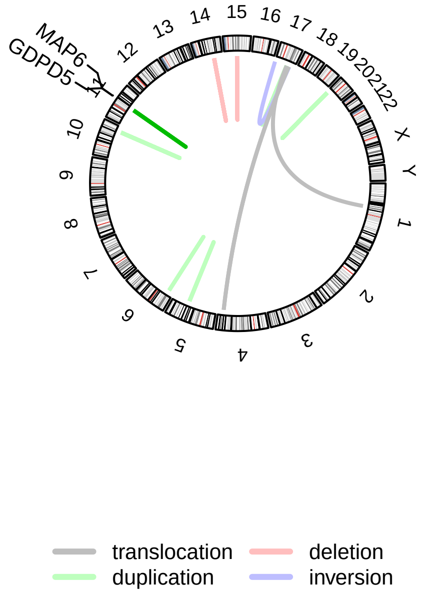


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 98
Discordant mates = 6

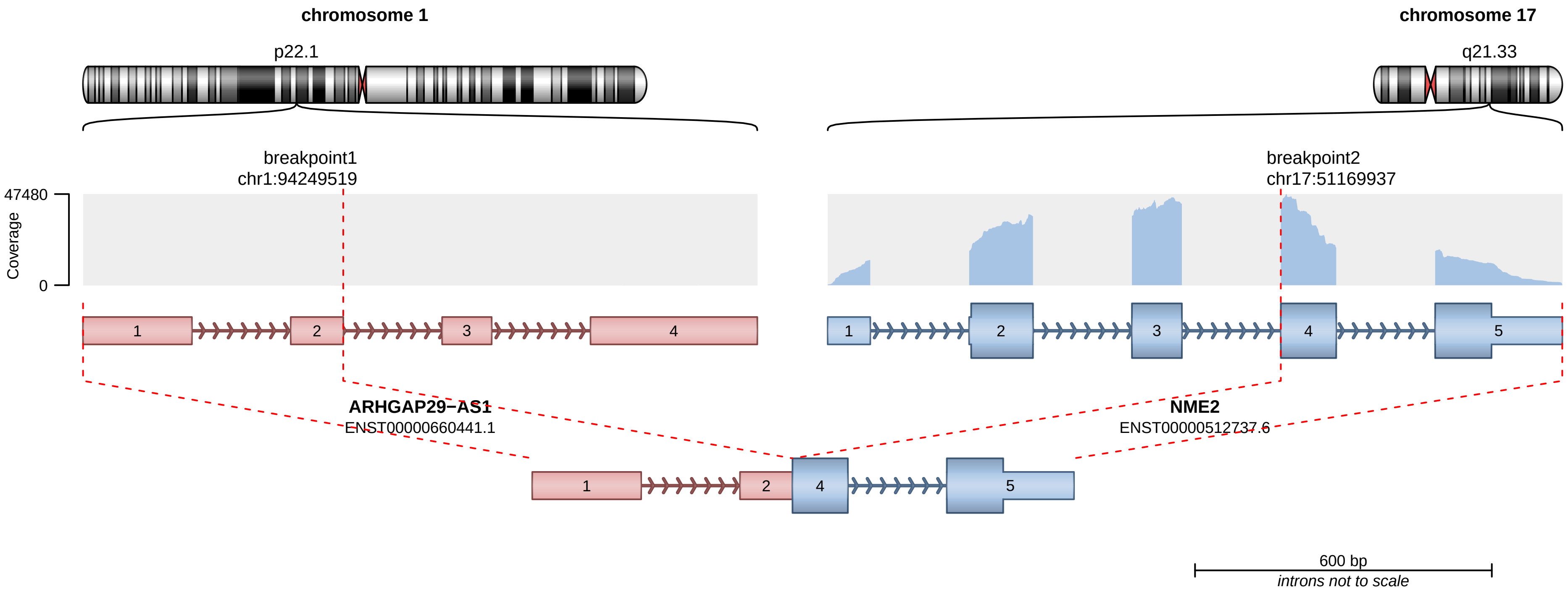


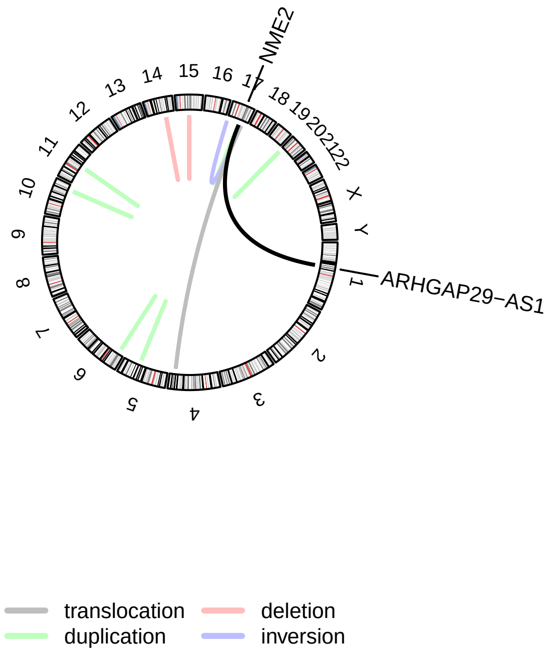


No protein domains retained in fusion.

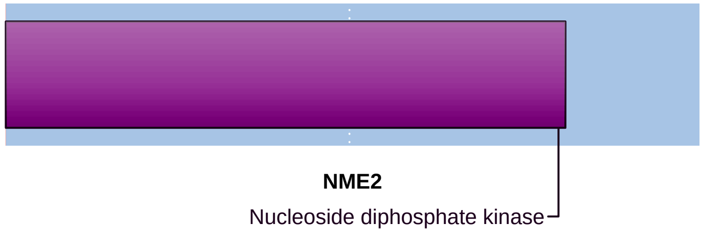
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0



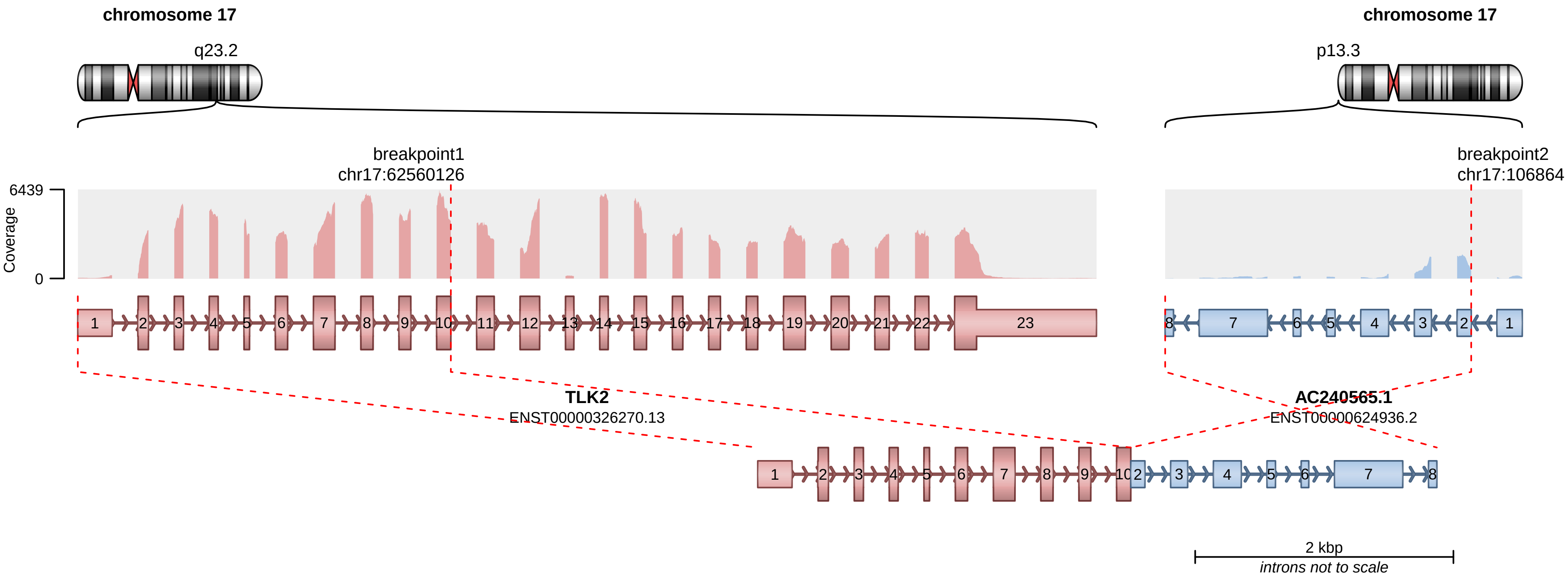


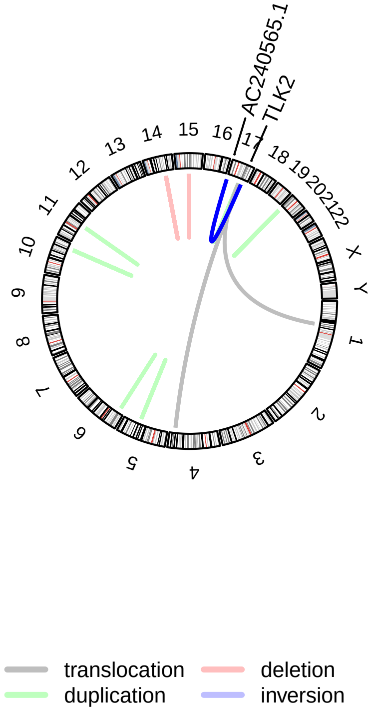
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 58
Discordant mates = 0

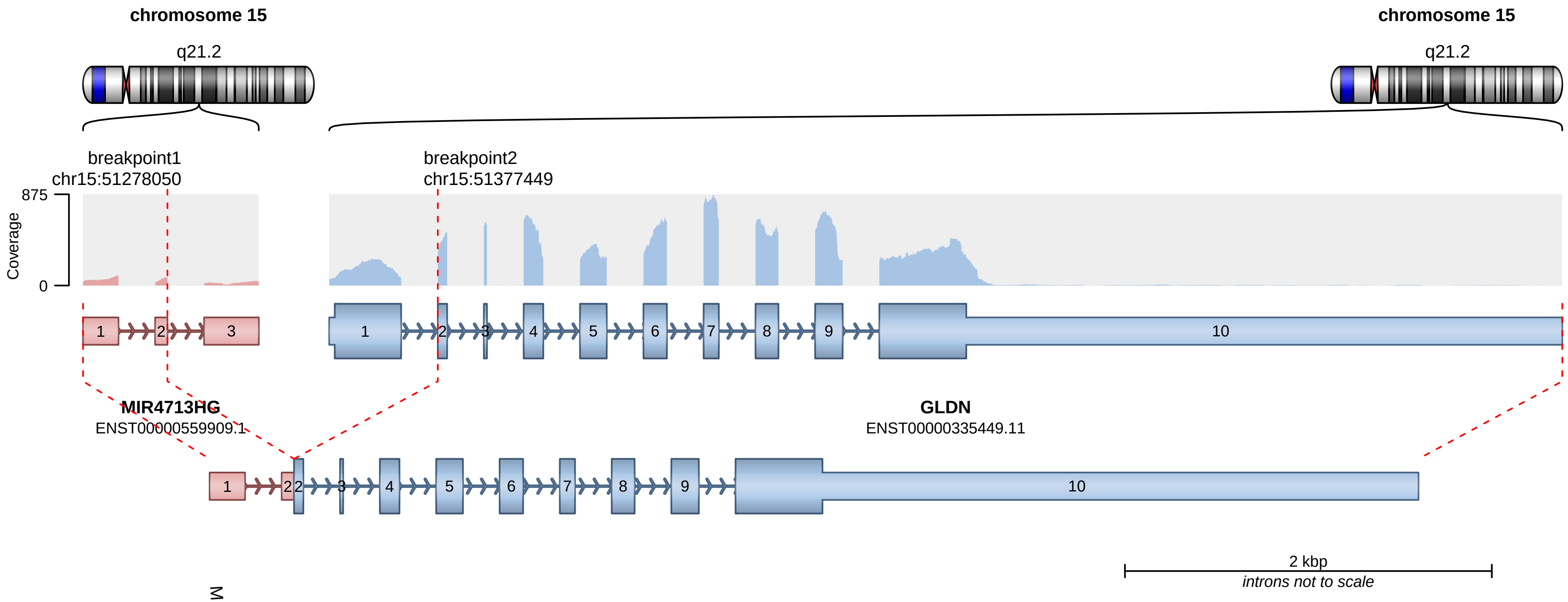


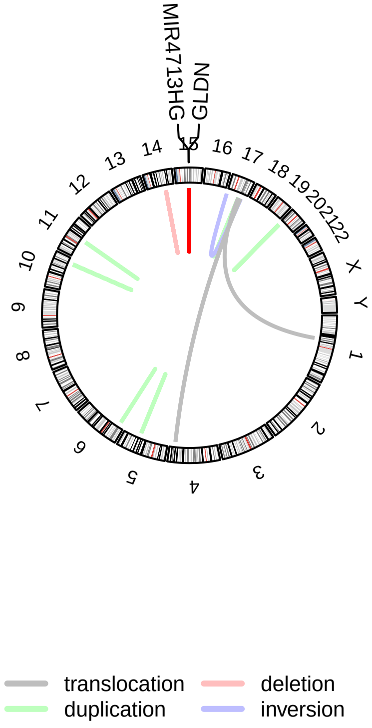


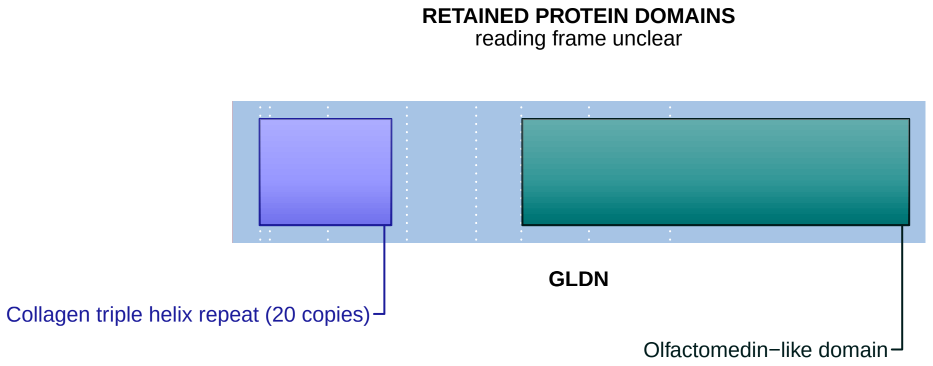
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 46
Discordant mates = 0

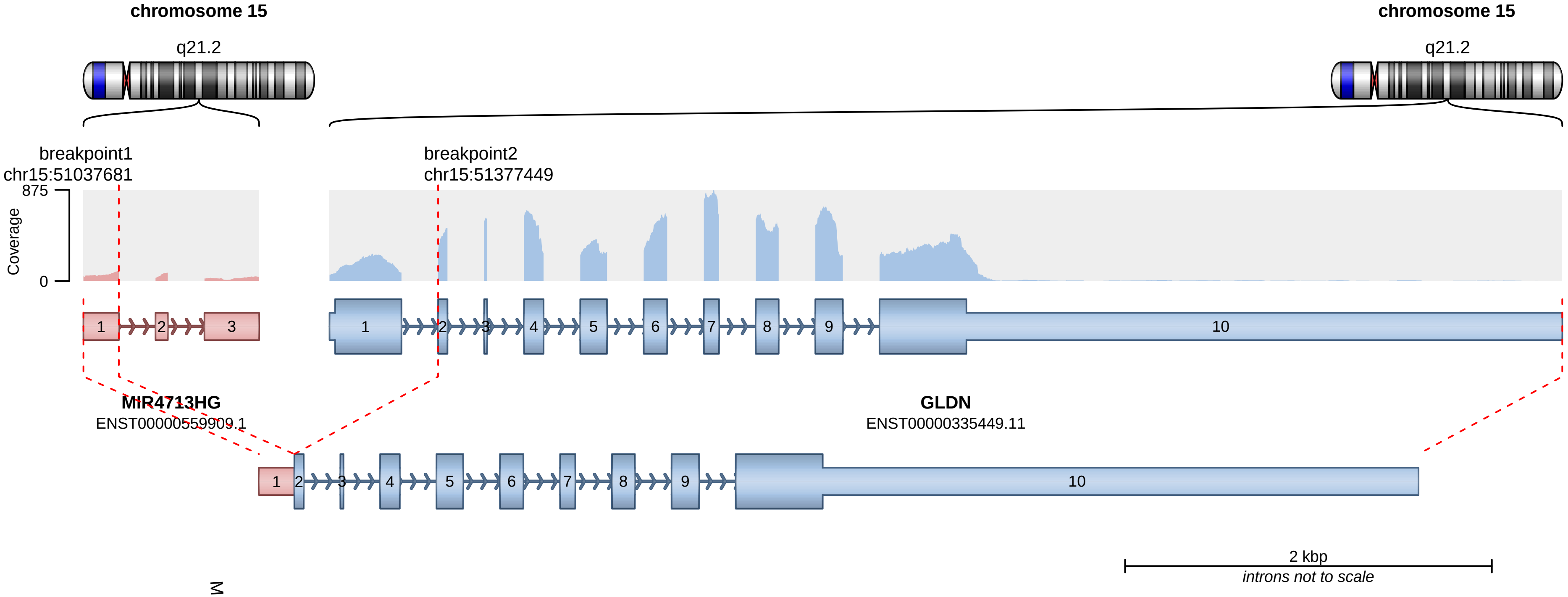


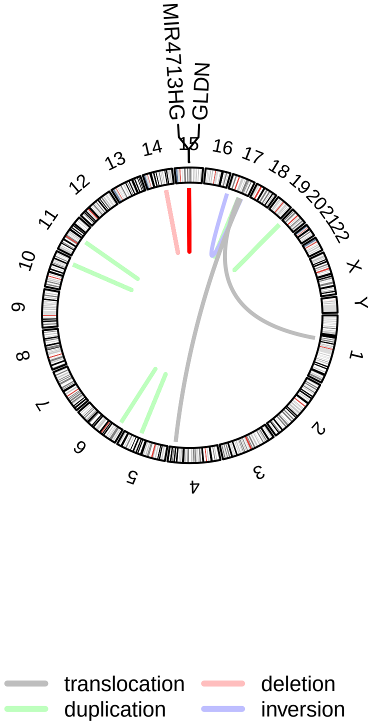


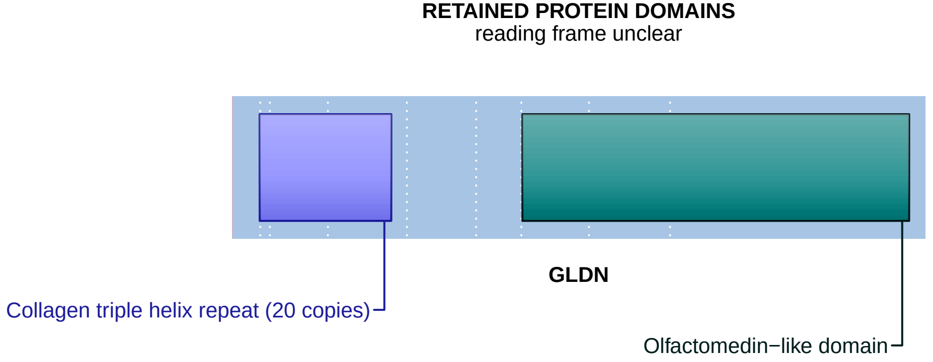


SUPPORTING READ COUNT

Split reads = 25
Discordant mates = 3

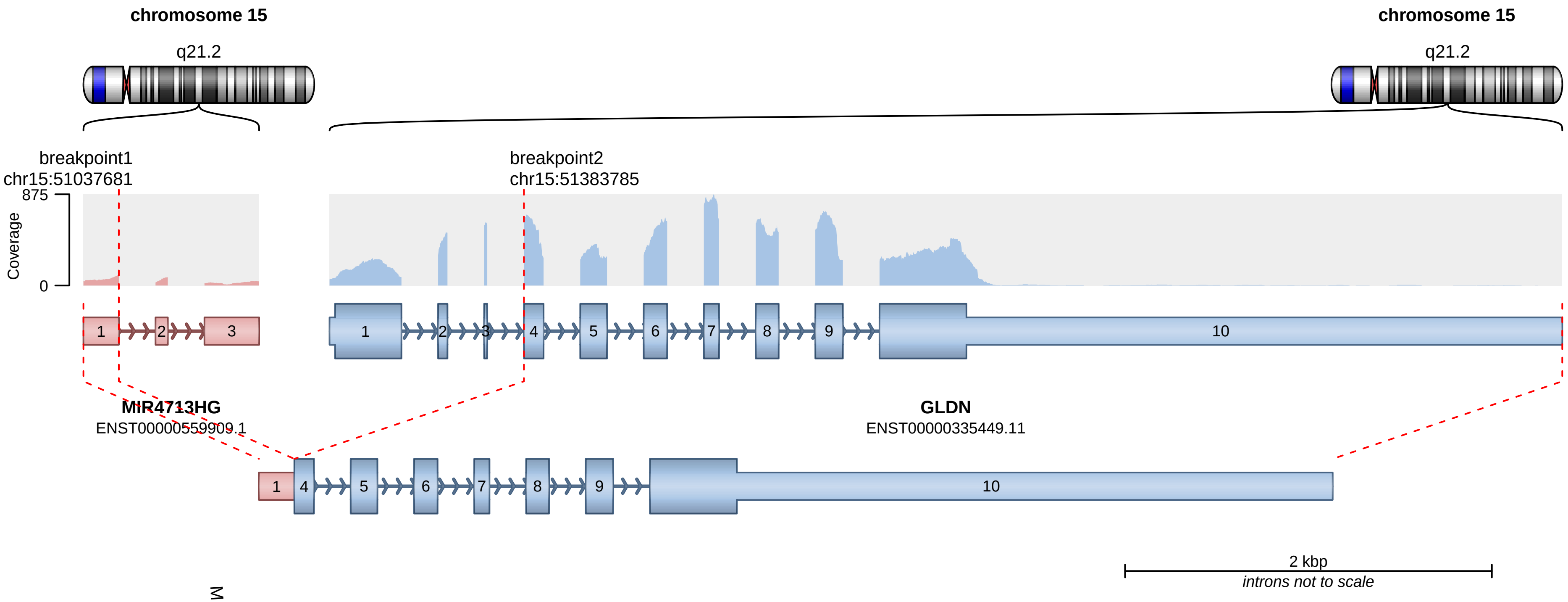


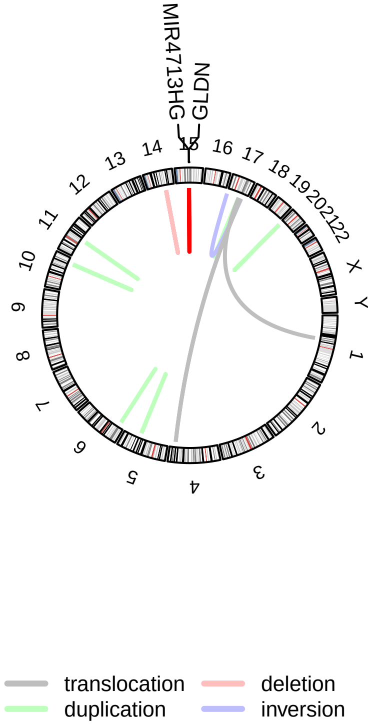


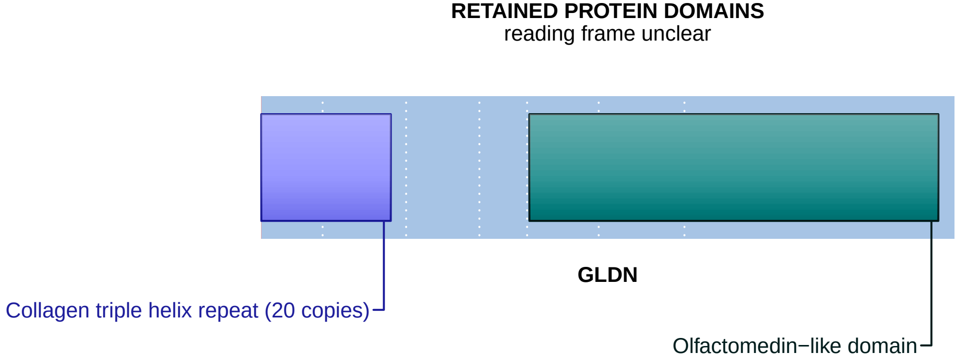


SUPPORTING READ COUNT

Split reads = 24
Discordant mates = 2

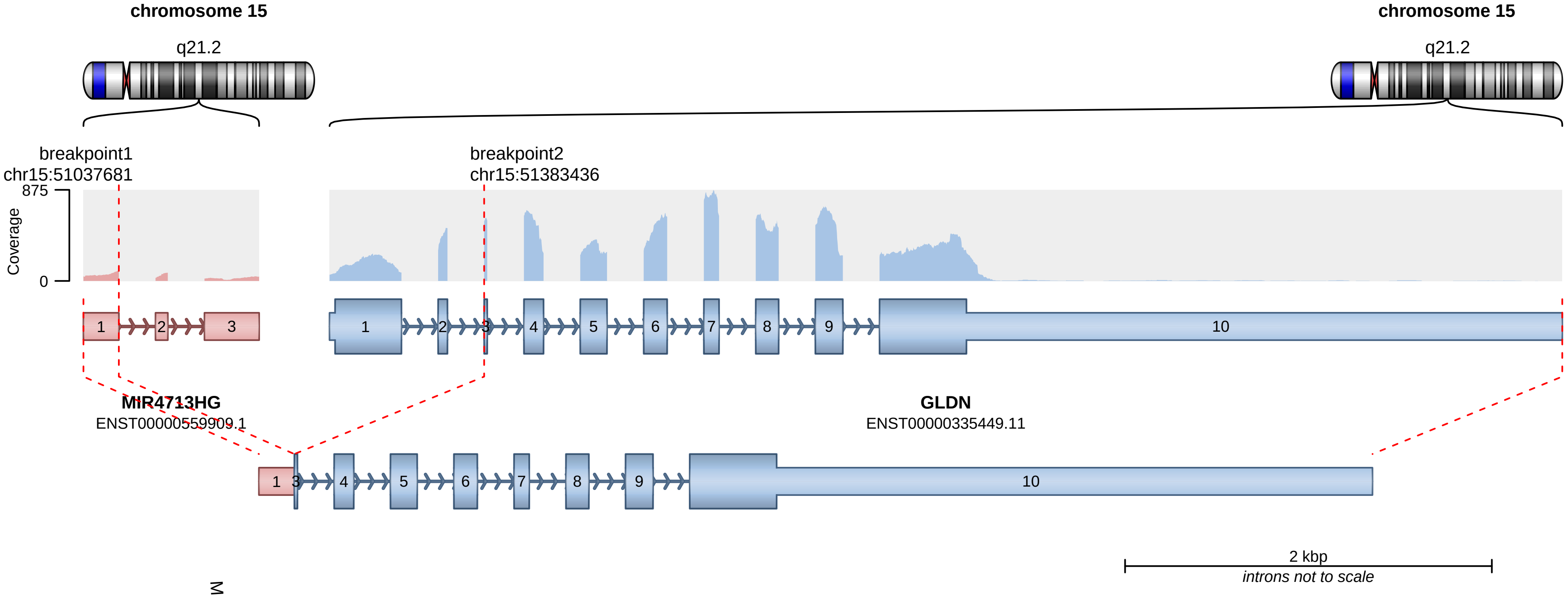


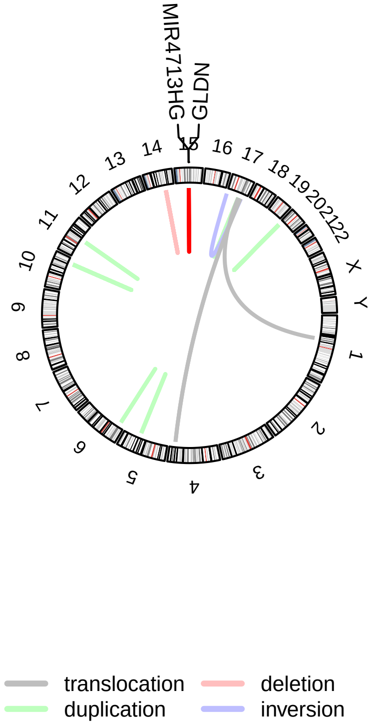


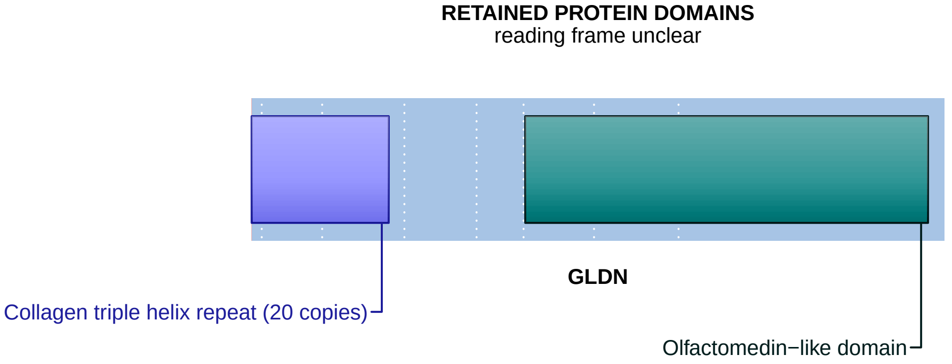


SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 1

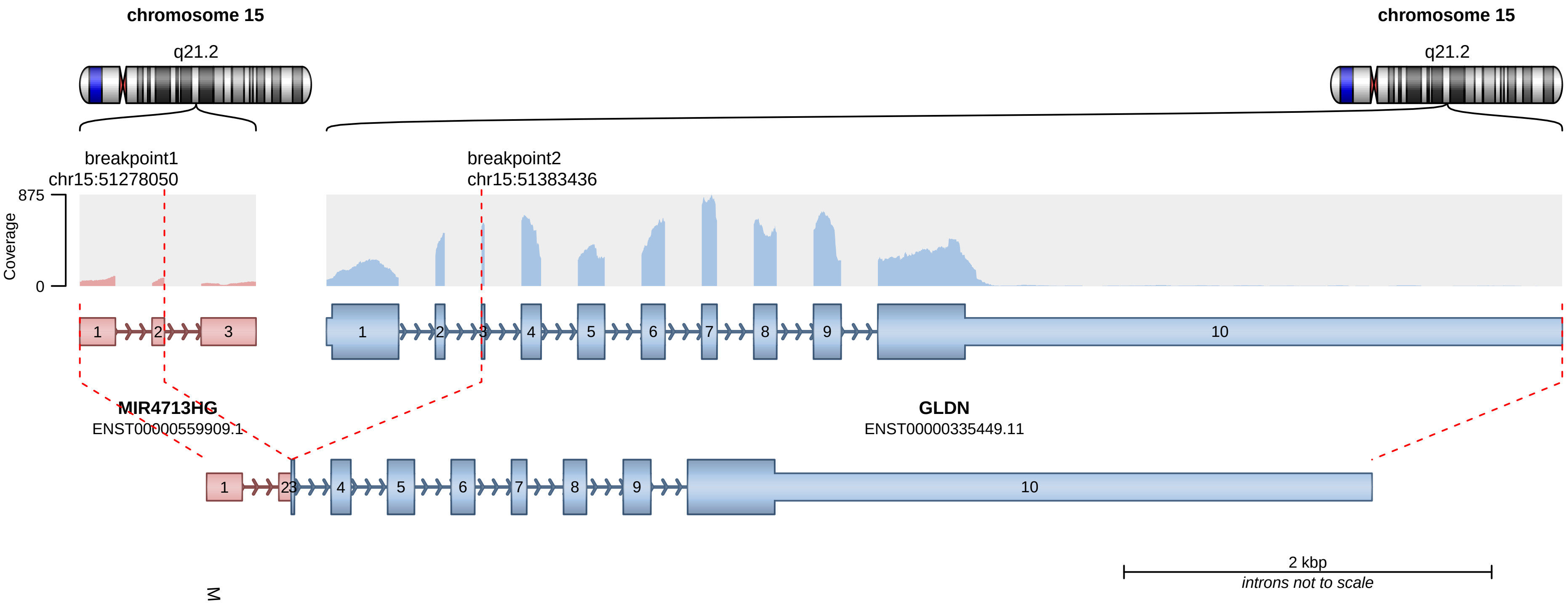


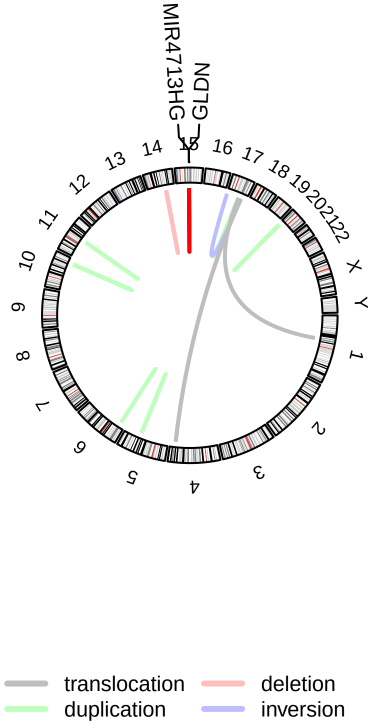


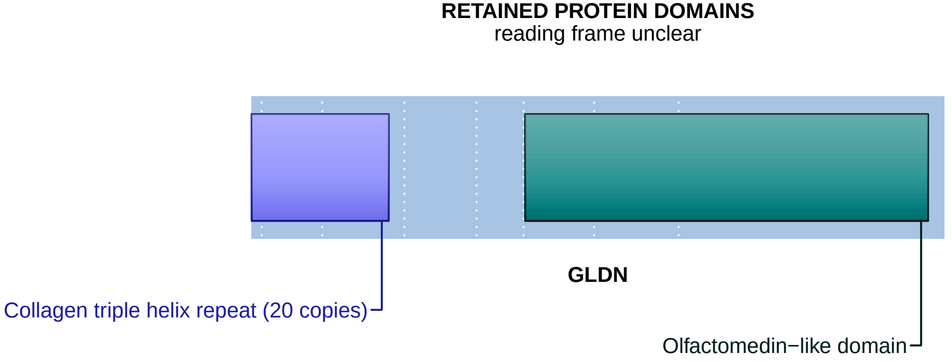


SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 1

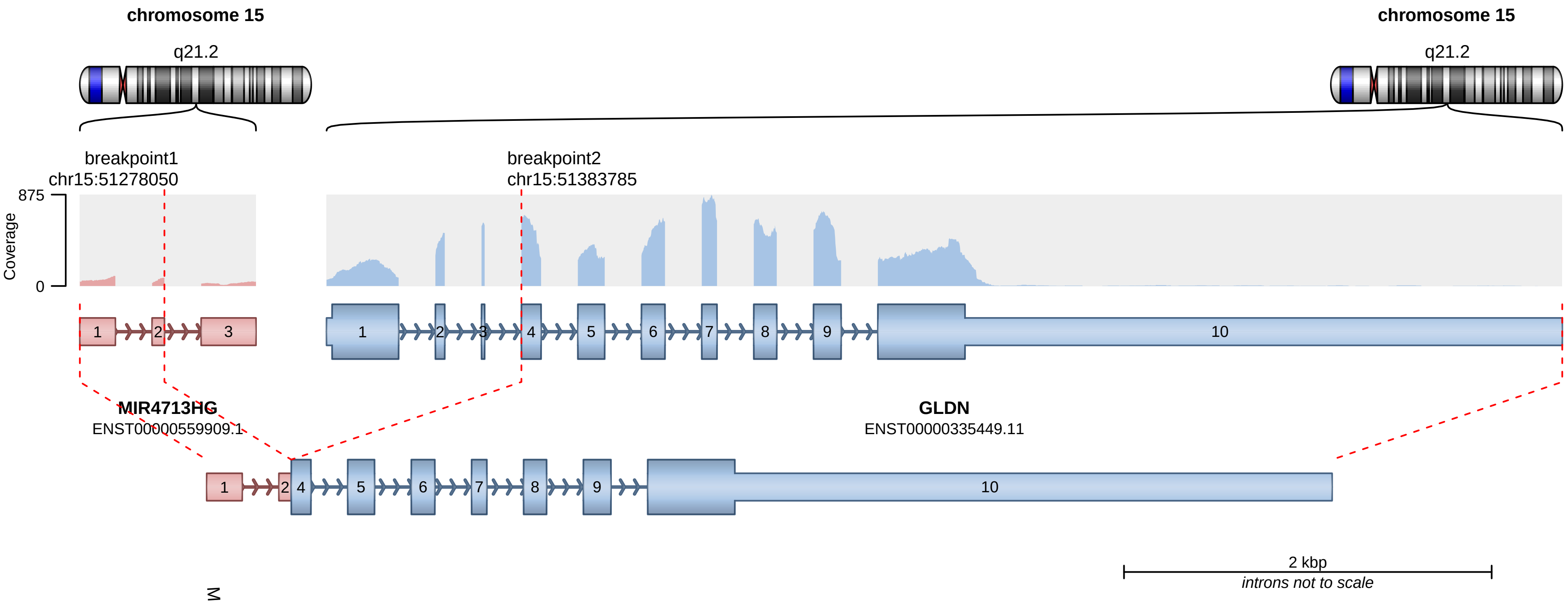


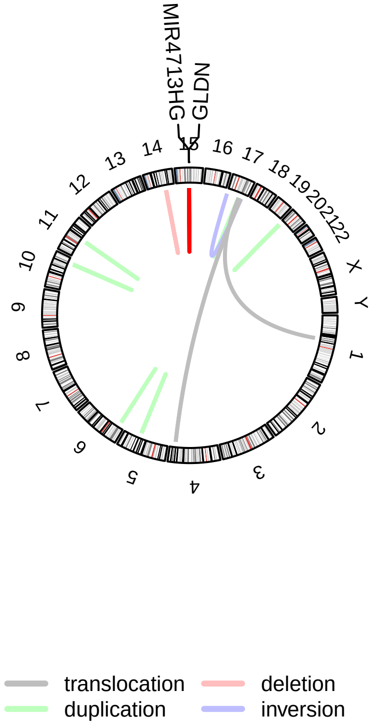




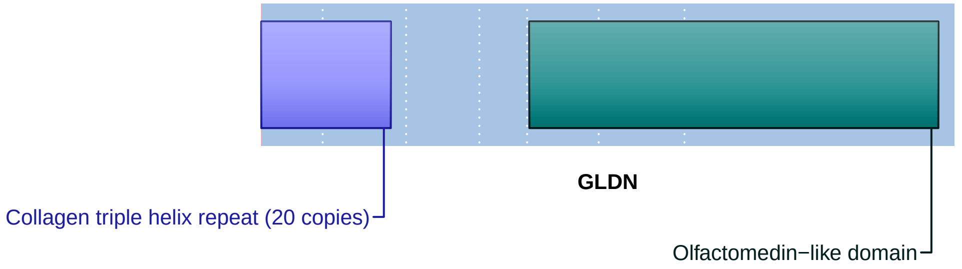
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 2



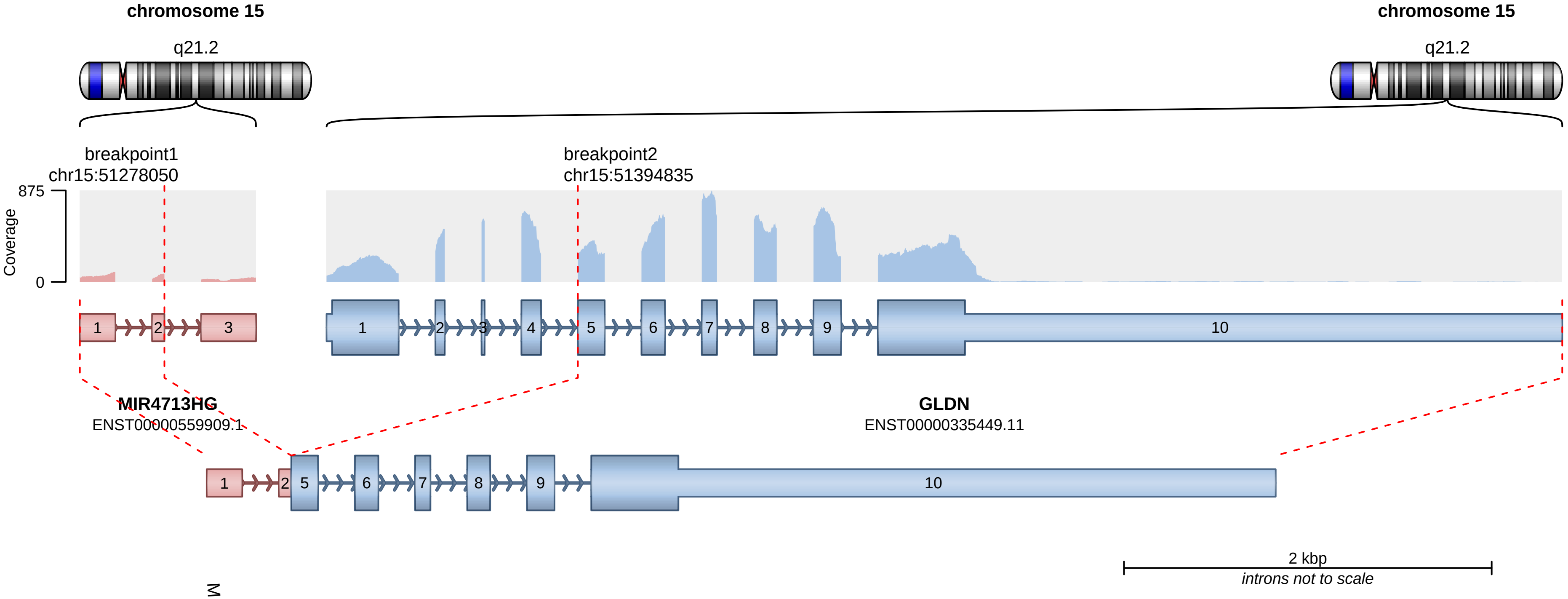


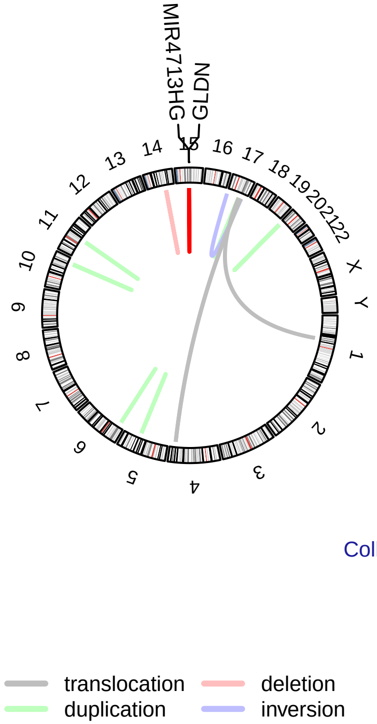
RETAINED PROTEIN DOMAINS
reading frame unclear



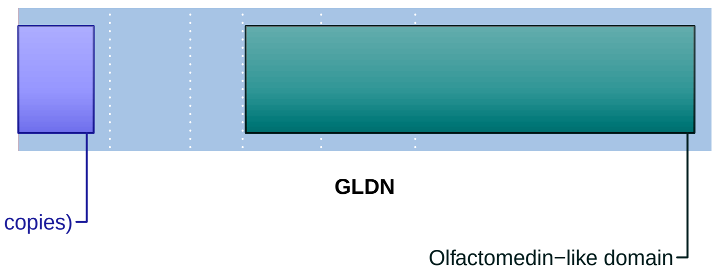
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 2



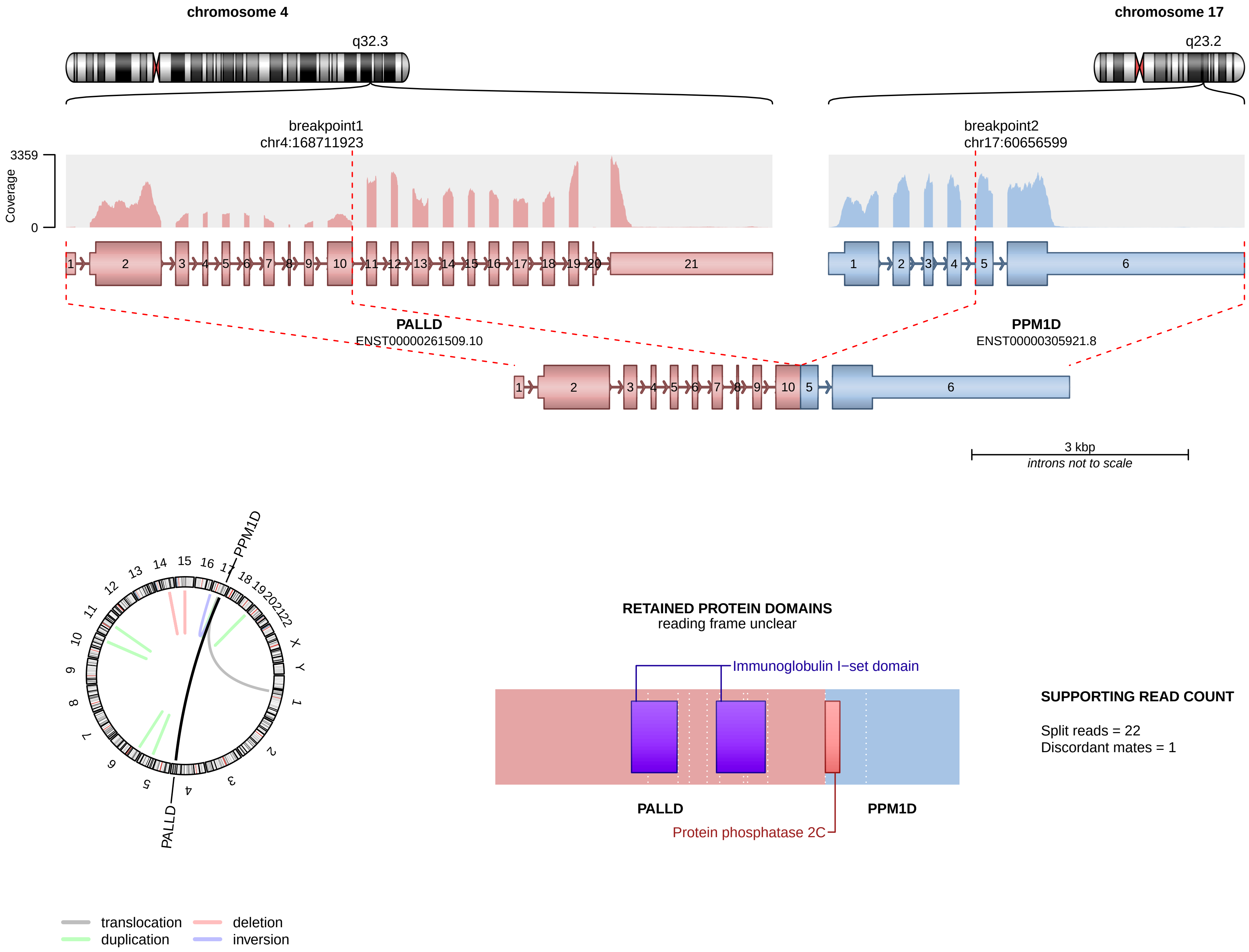


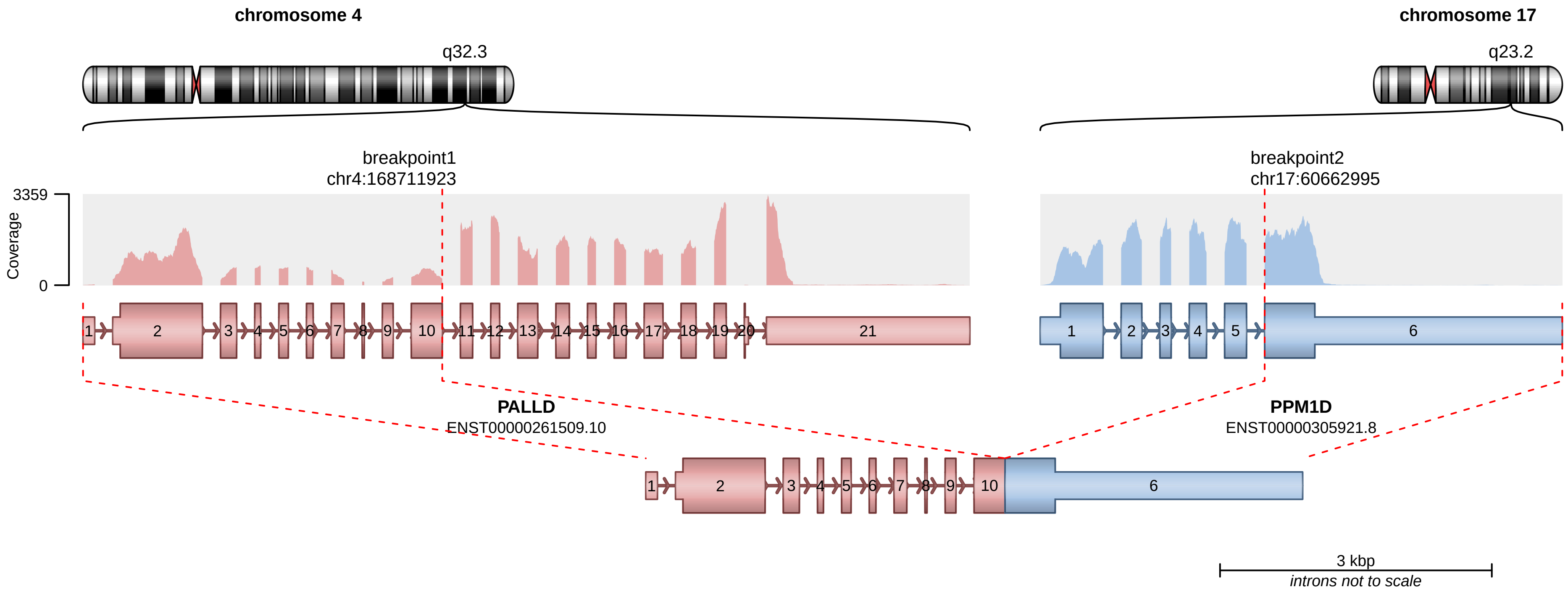
RETAINED PROTEIN DOMAINS
reading frame unclear

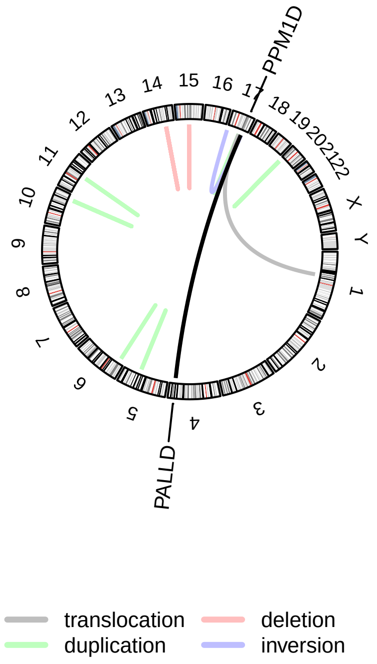


SUPPORTING READ COUNT

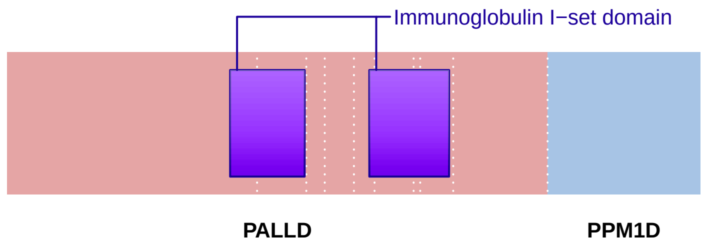
Split reads = 1
Discordant mates = 0


chromosome 4
q32.3
chromosome 17
q23.2
breakpoint1
chr4:168711923
breakpoint2
chr17:60656599
Coverage
3359
0
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21
1 2 3 4 5 6
PALLD
ENST00000261509.10
PPM1D
ENST00000305921.8
1 2 3 4 5 6 7 8 9 10 5 6
3 kbp
introns not to scale
PPM1D
PALLD
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
Immunoglobulin I−set domain
PALLD
PPM1D
Protein phosphatase 2C
SUPPORTING READ COUNT
Split reads = 22
Discordant mates = 1
translocation
deletion
duplication
inversion



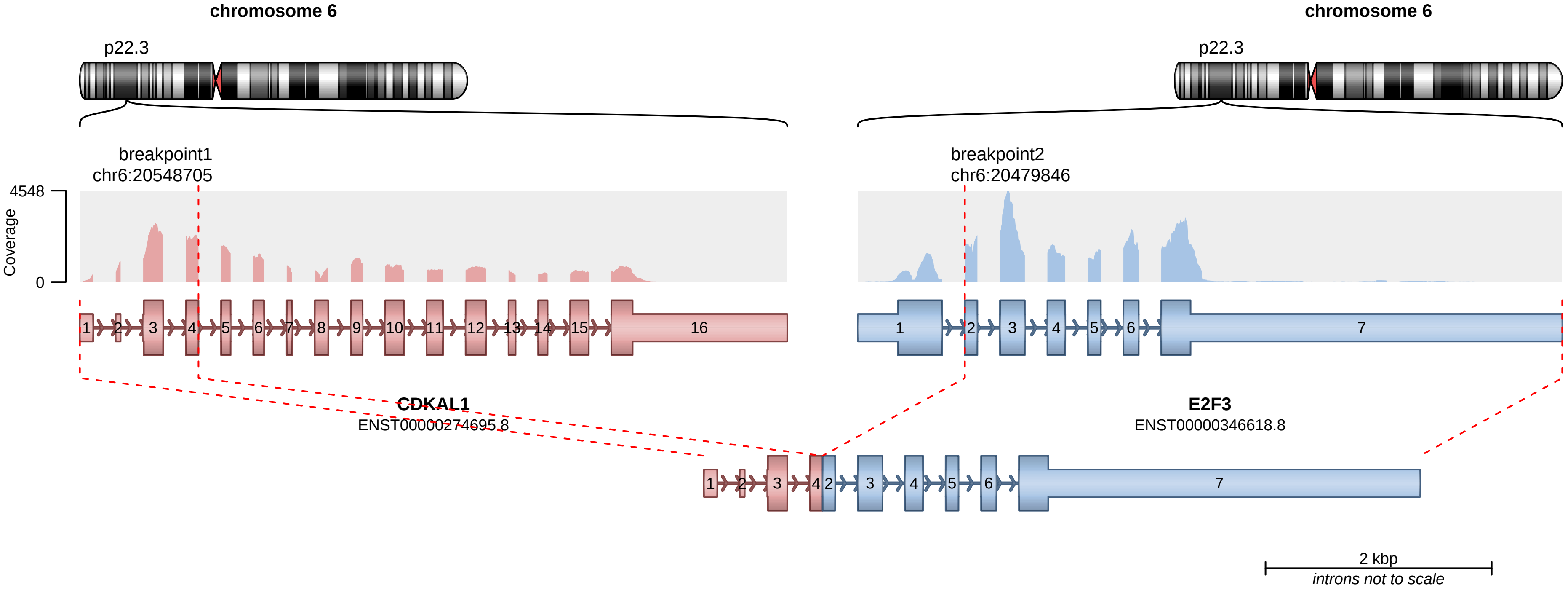


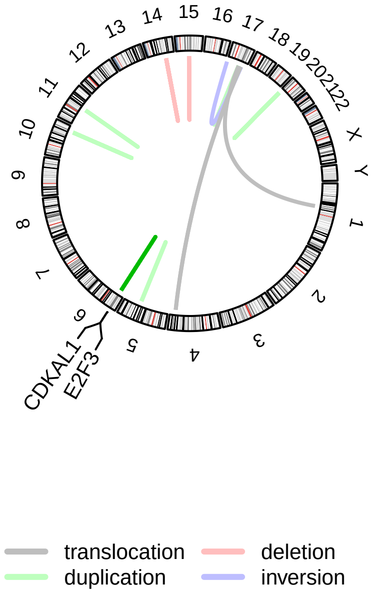
RETAINED PROTEIN DOMAINS
reading frame unclear

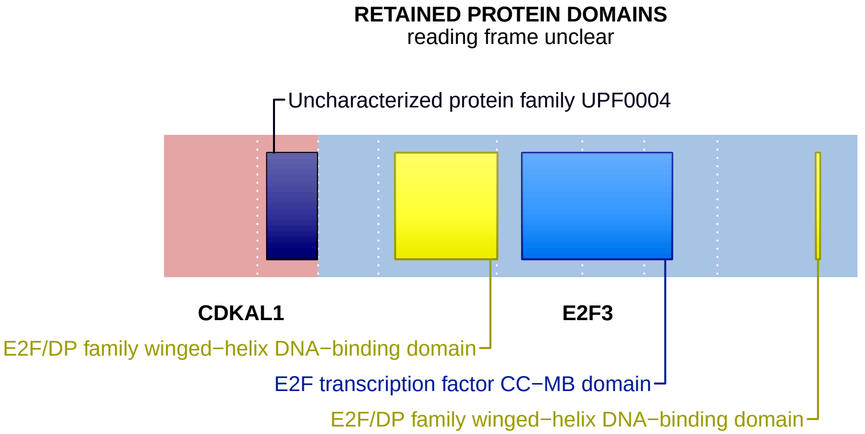


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0







SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0