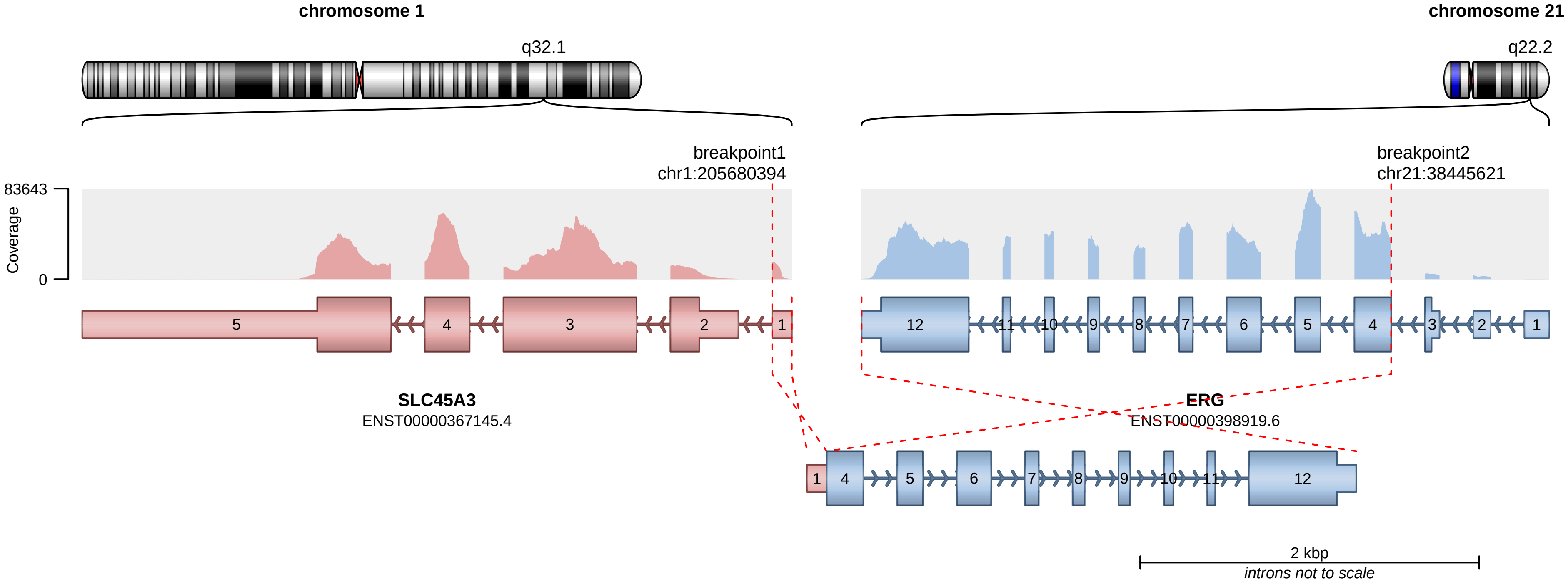
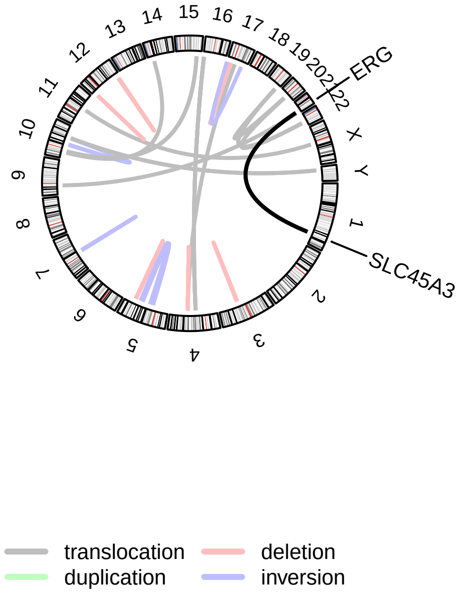
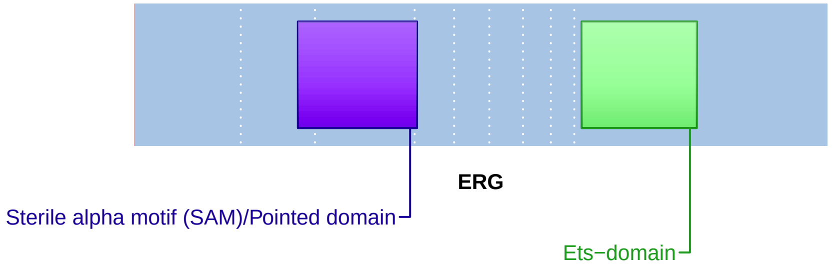


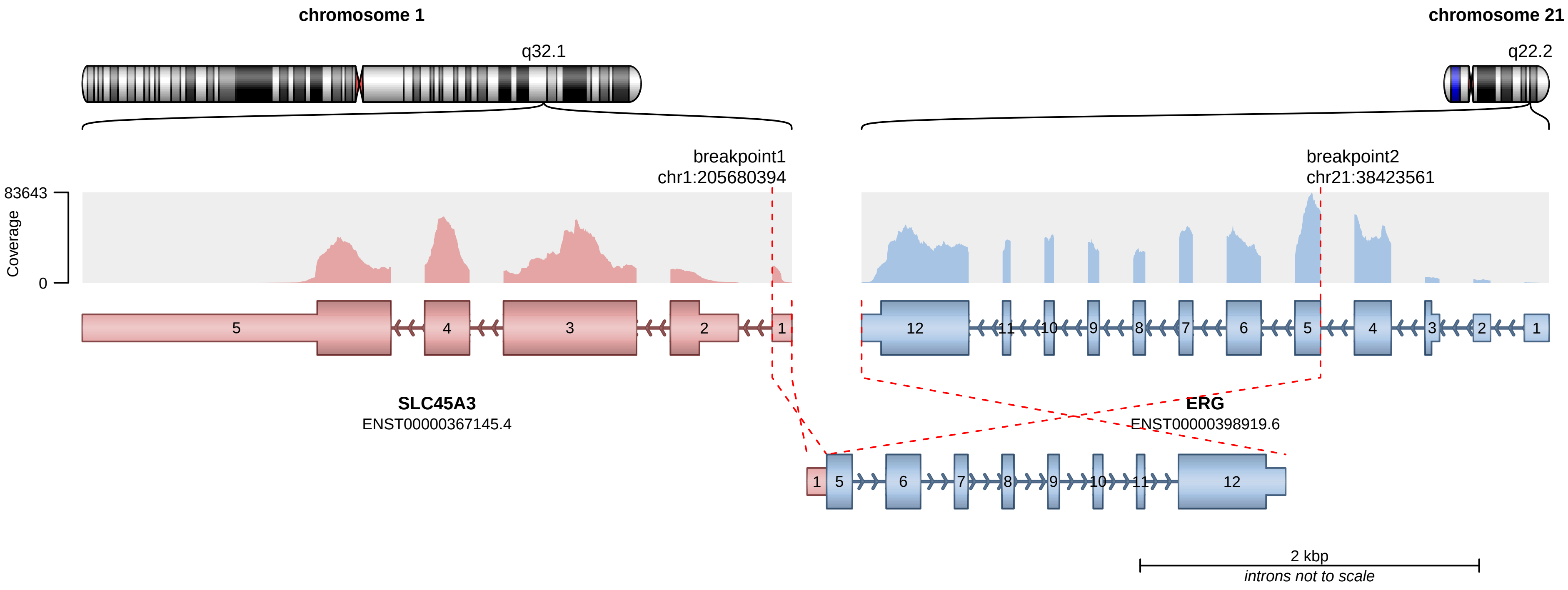


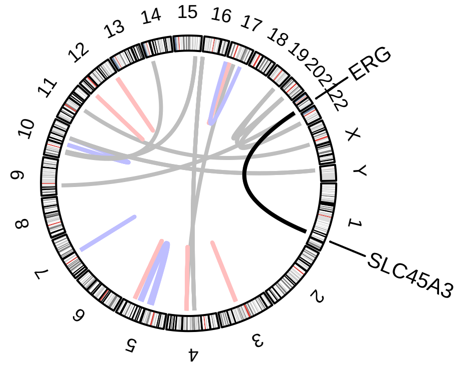
RETAINED PROTEIN DOMAINS
reading frame unclear



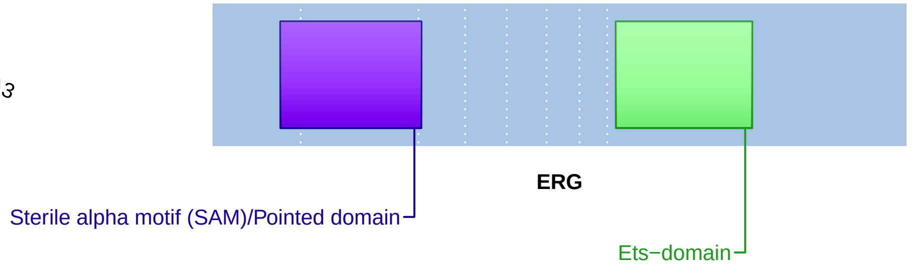
SUPPORTING READ COUNT

Split reads = 10657
Discordant mates = 3



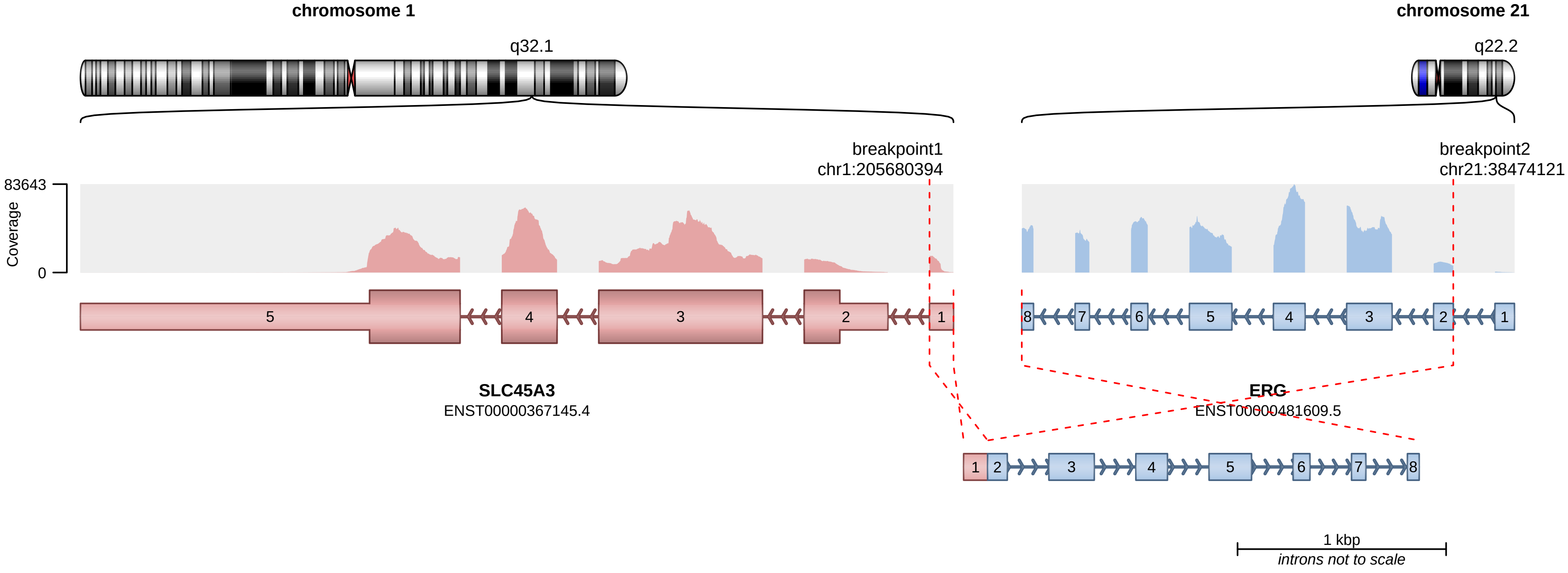


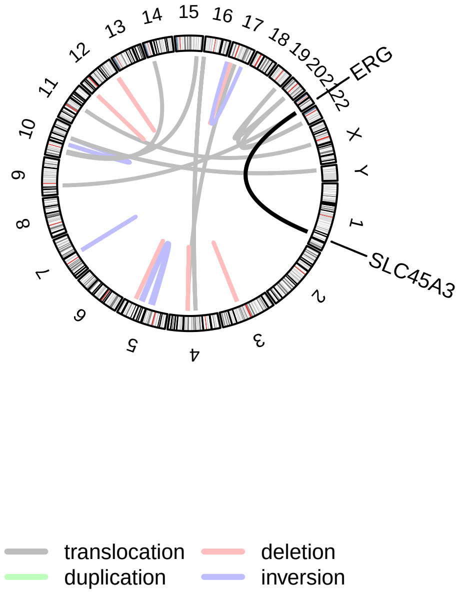
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 149
Discordant mates = 0

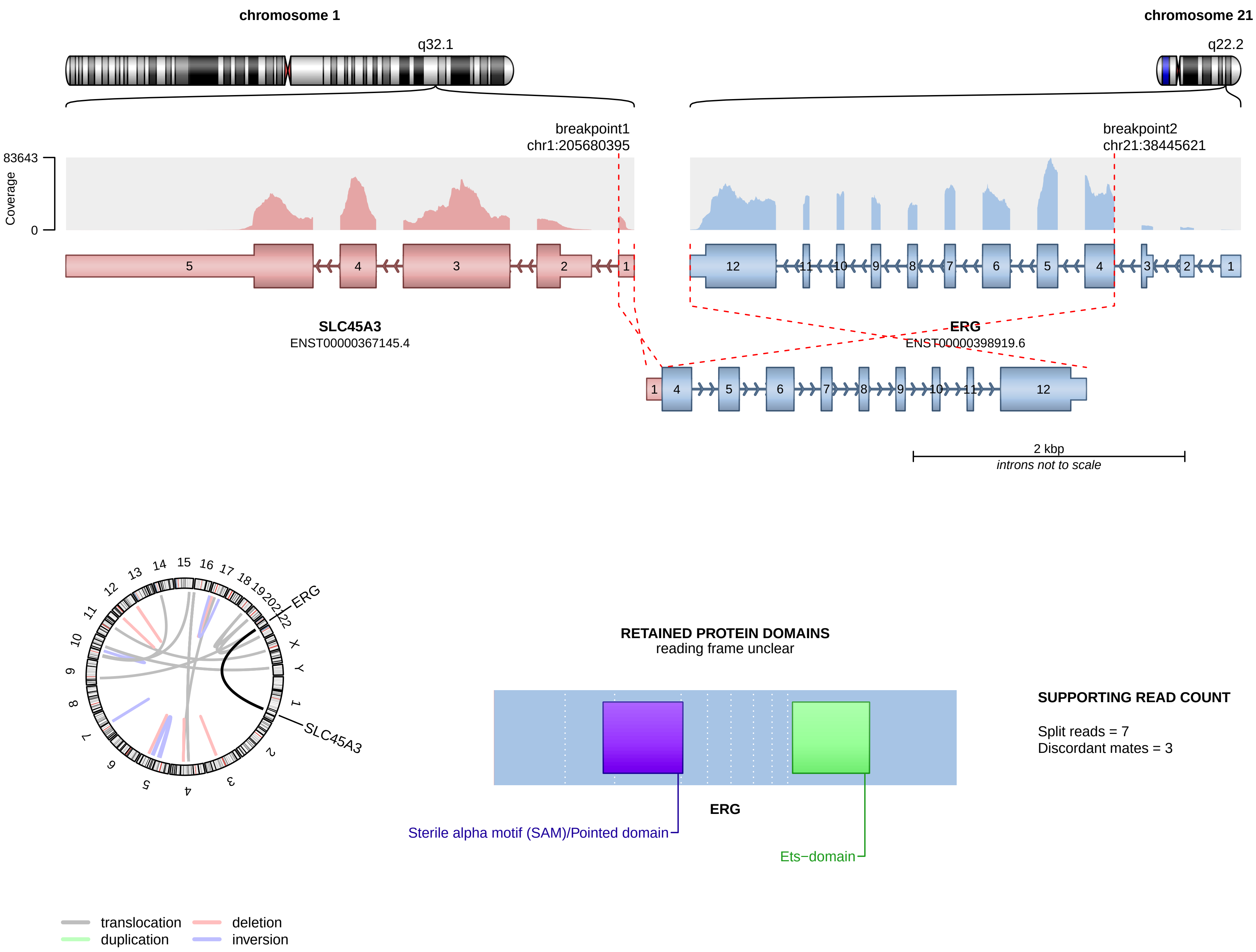




No coding regions retained in fusion transcript.

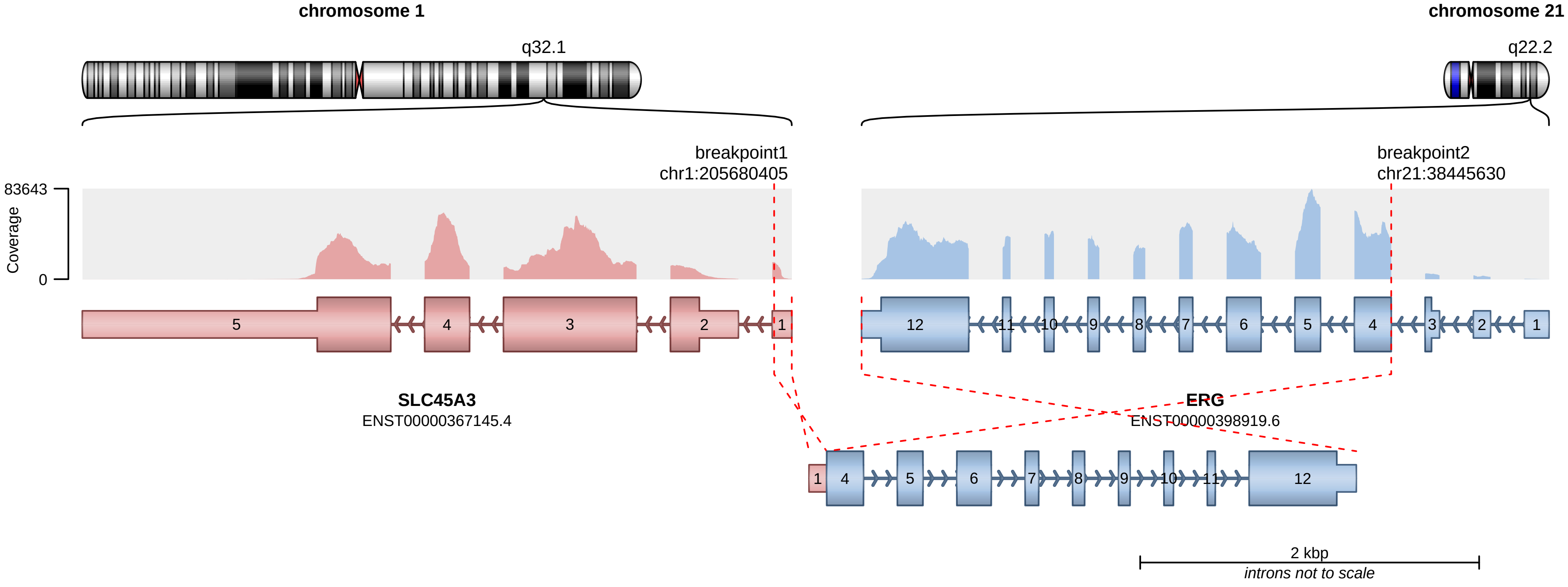
SUPPORTING READ COUNT

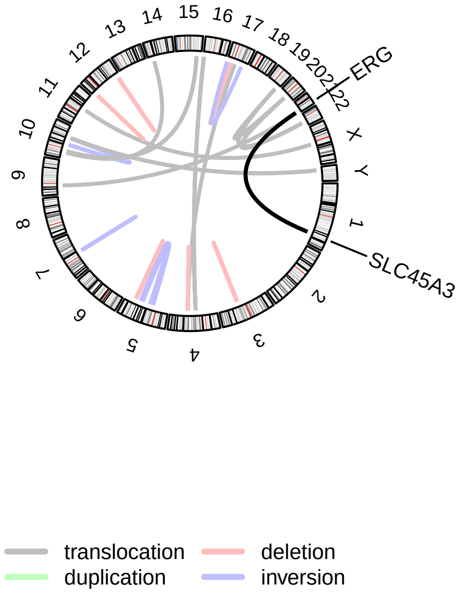
Split reads = 100
Discordant mates = 4

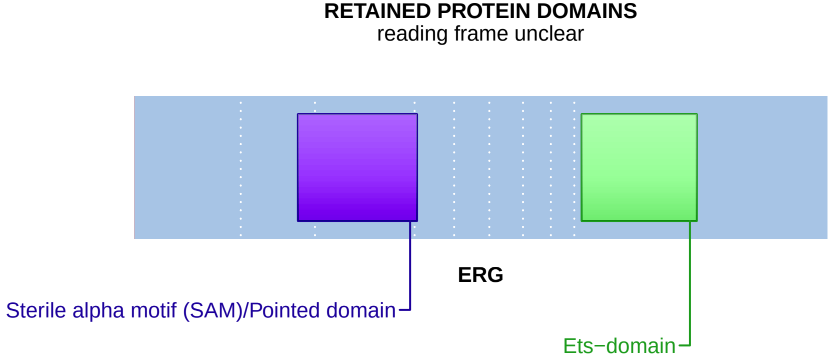


SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 3

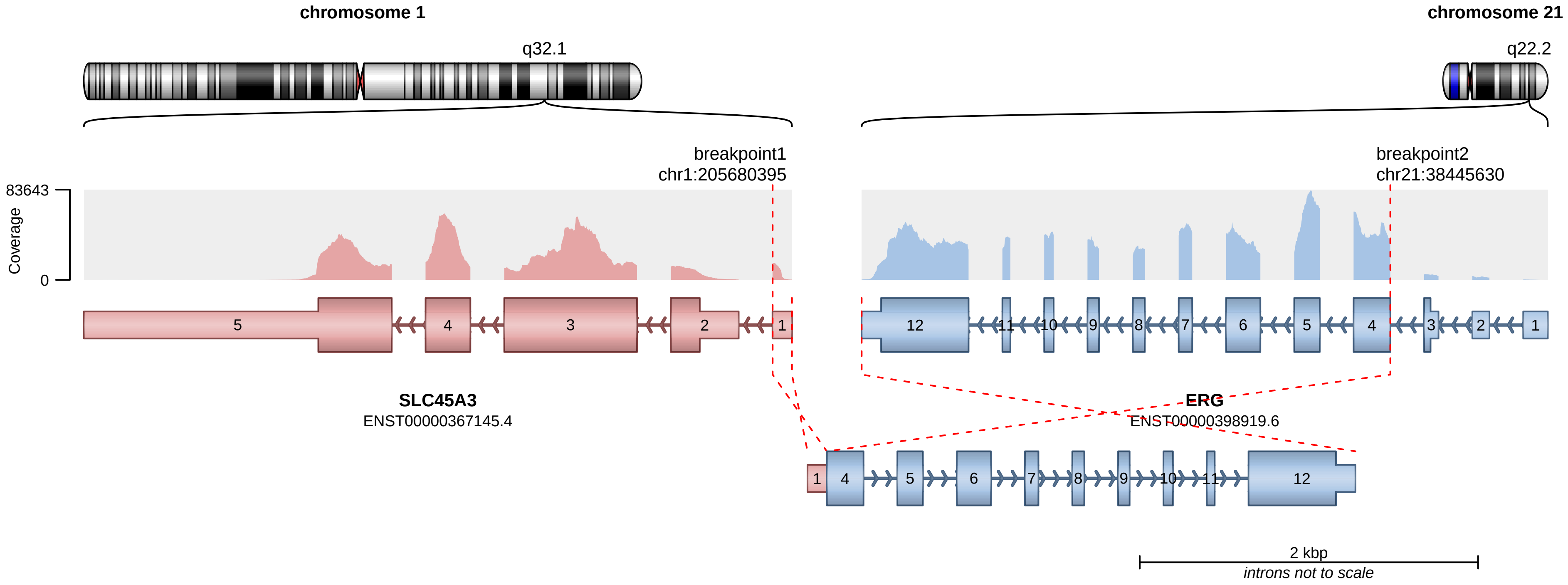


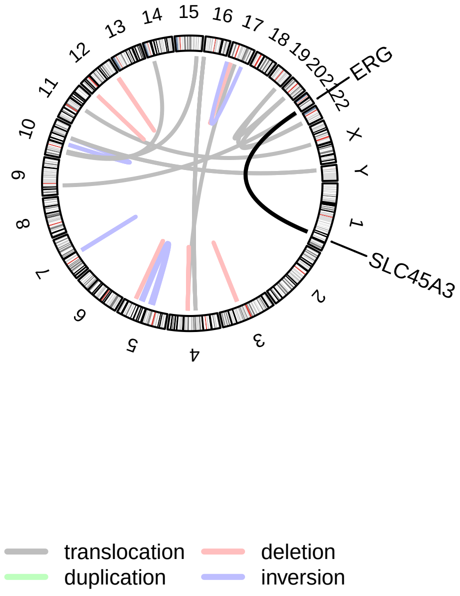


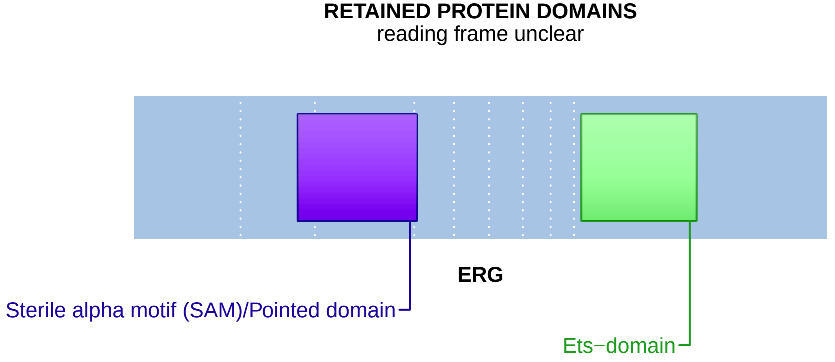


SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 2

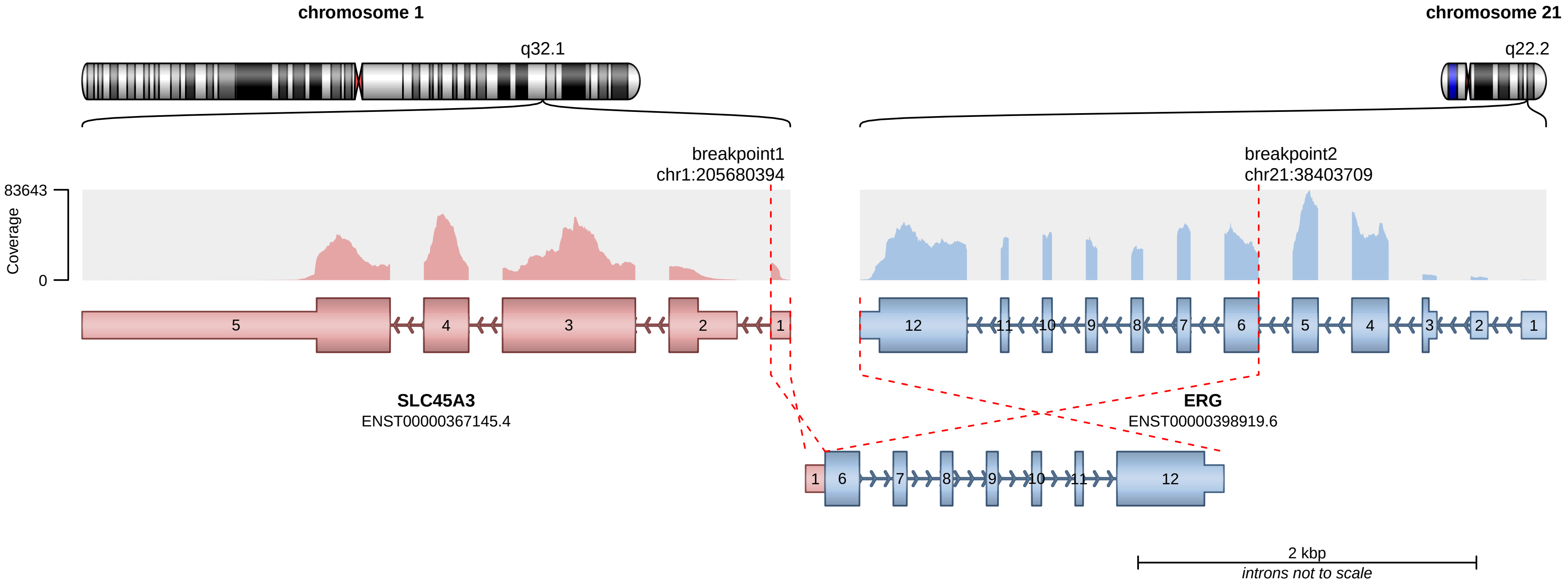


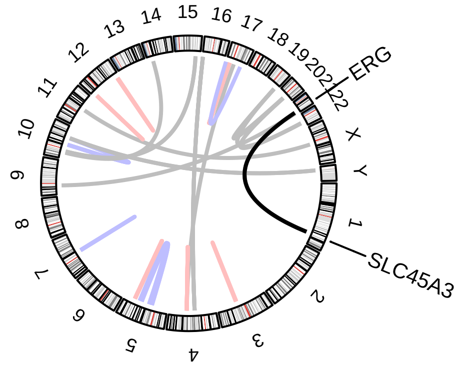


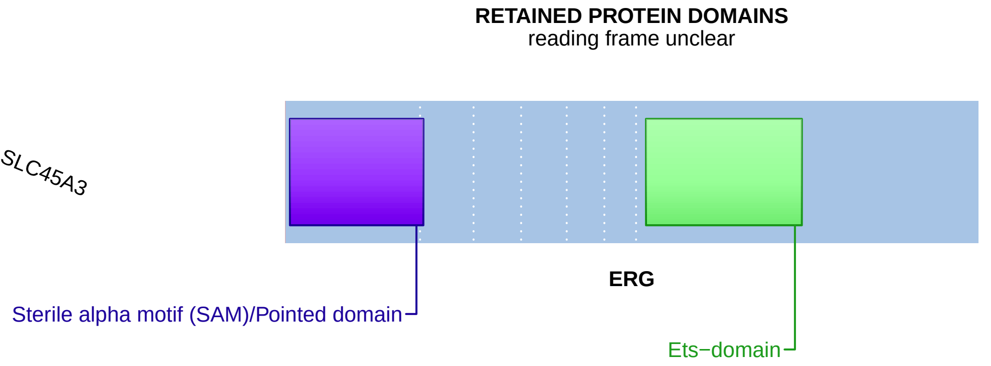


SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 3

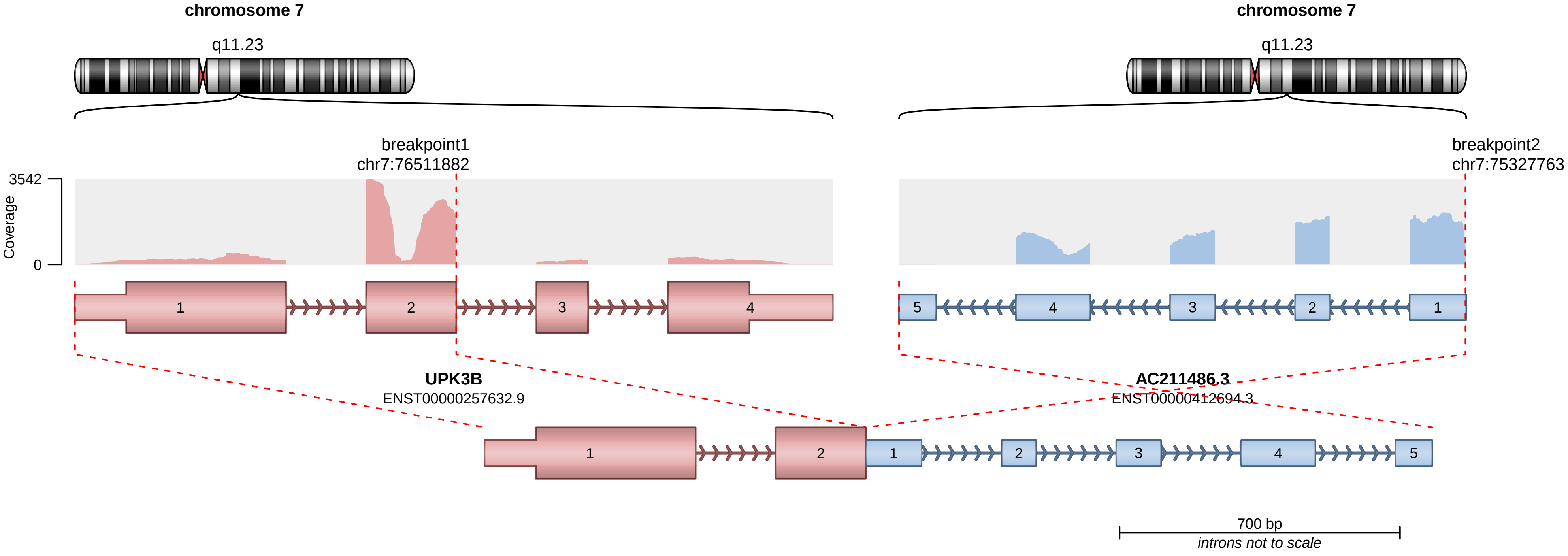


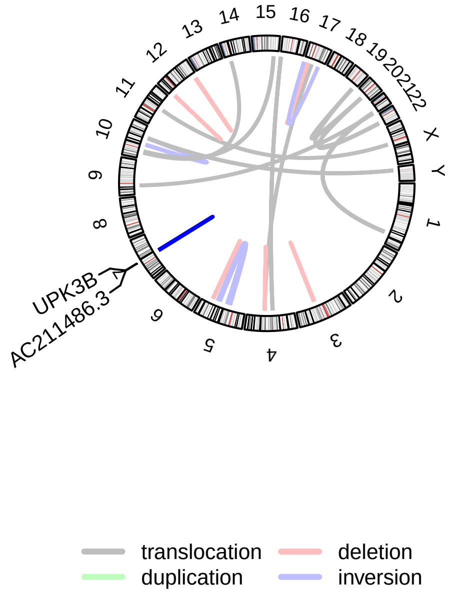




SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

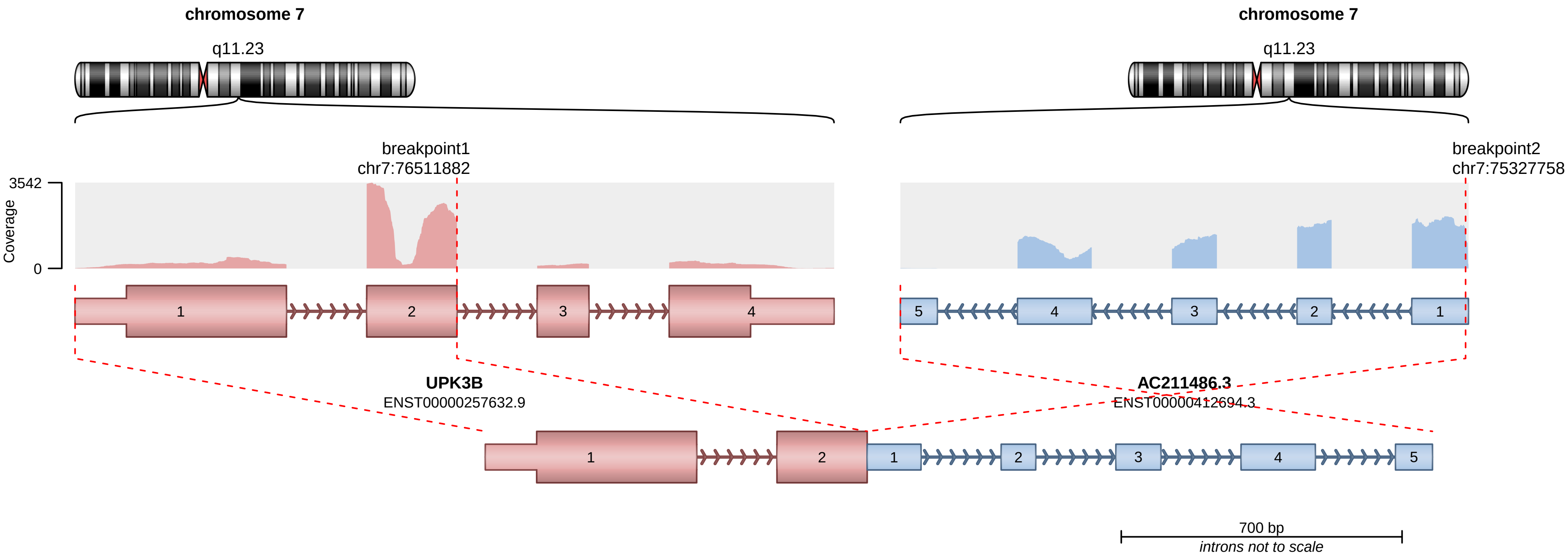


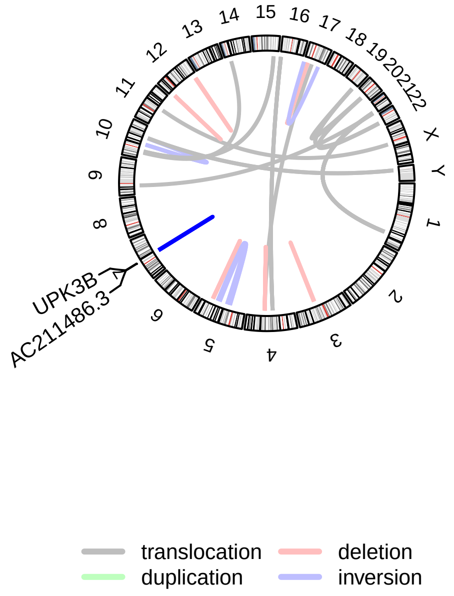


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 708
Discordant mates = 2

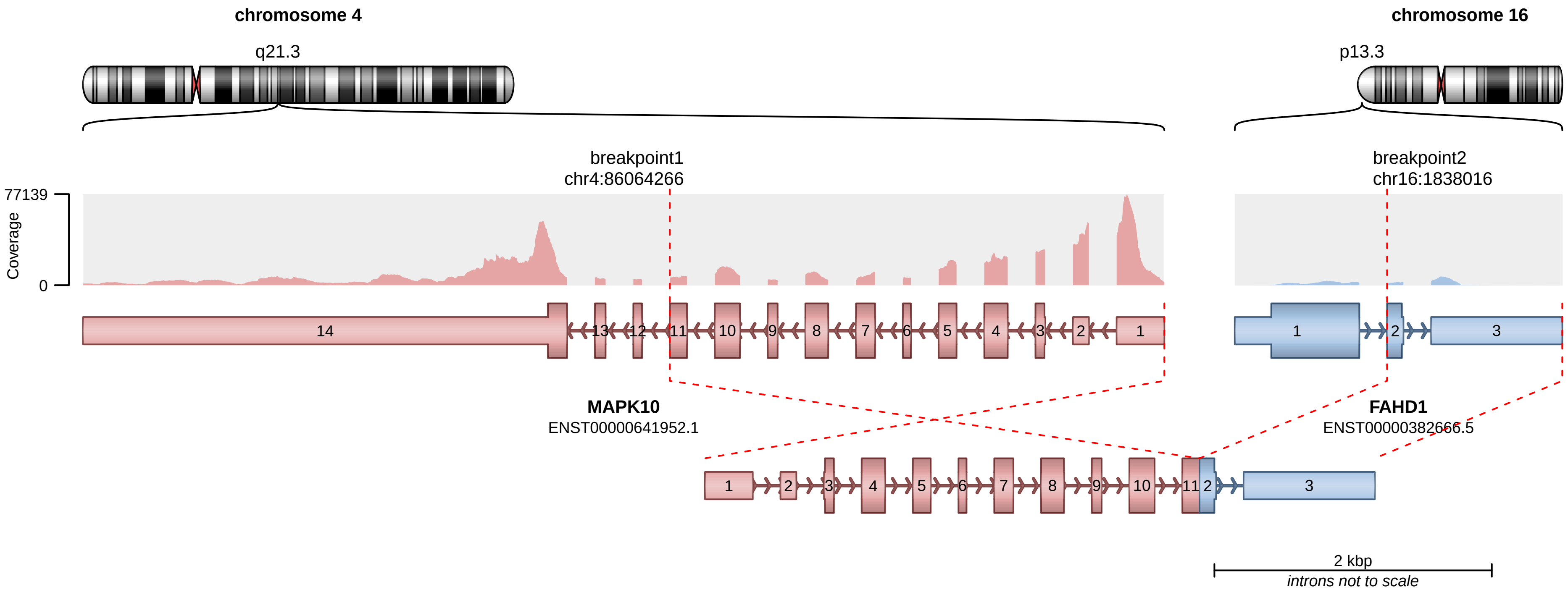


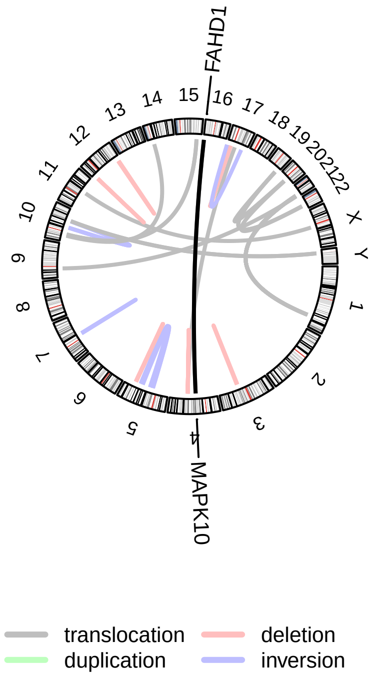


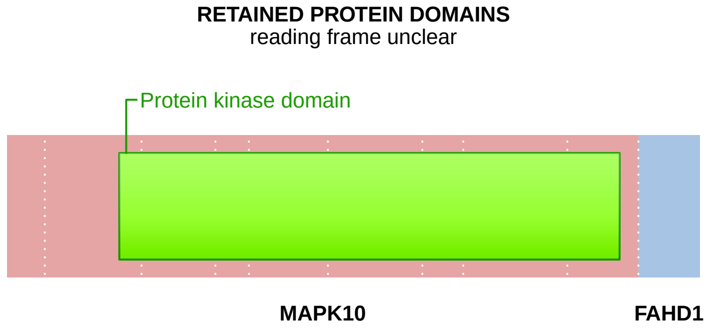
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 169
Discordant mates = 2

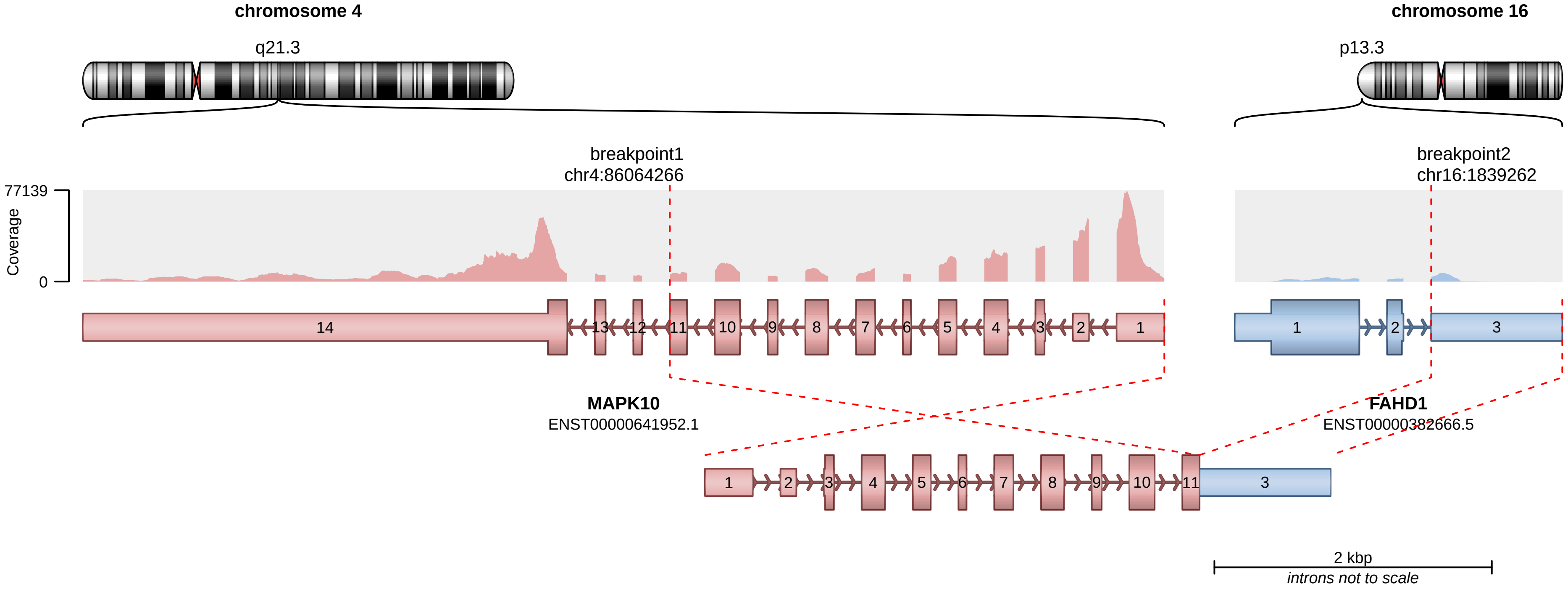


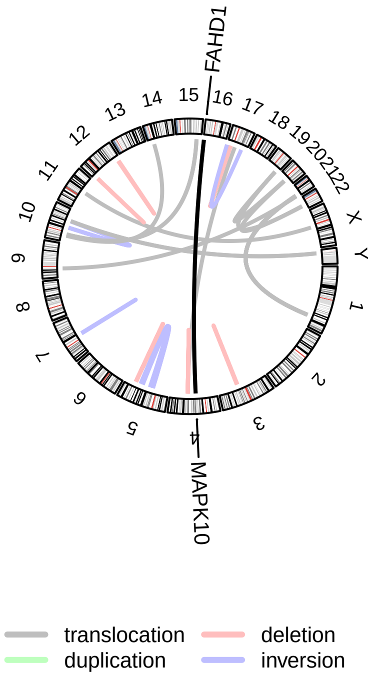


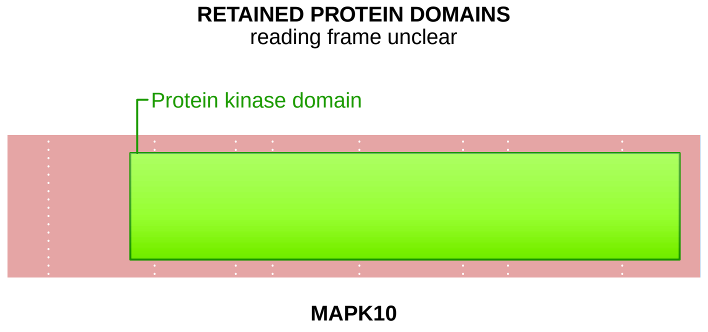


SUPPORTING READ COUNT

Split reads = 693
Discordant mates = 8

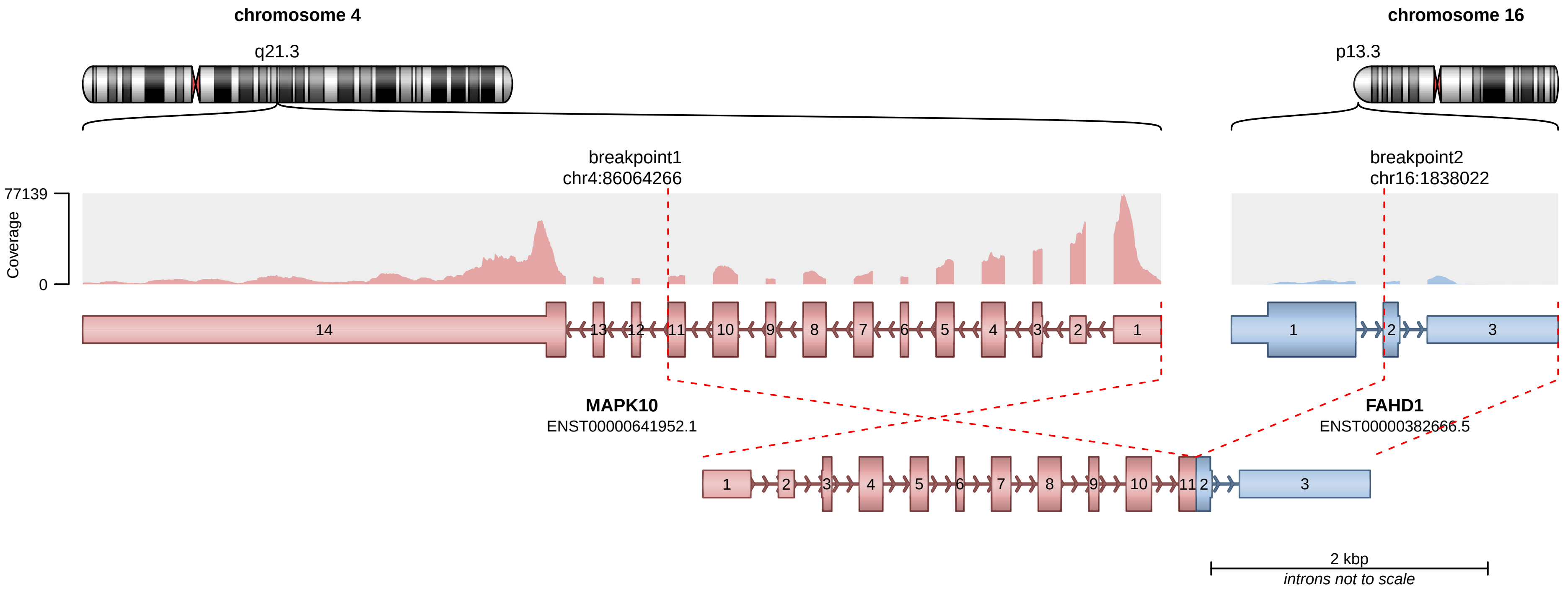


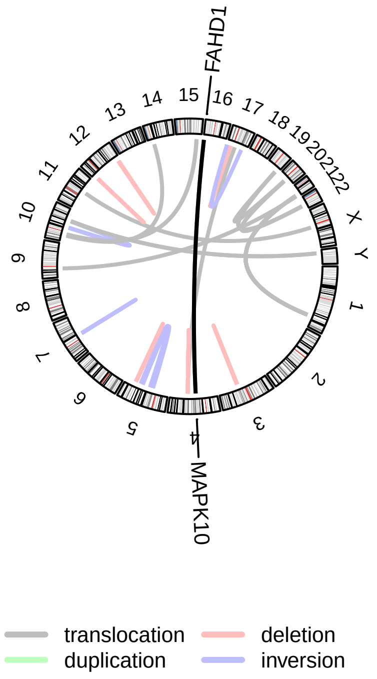


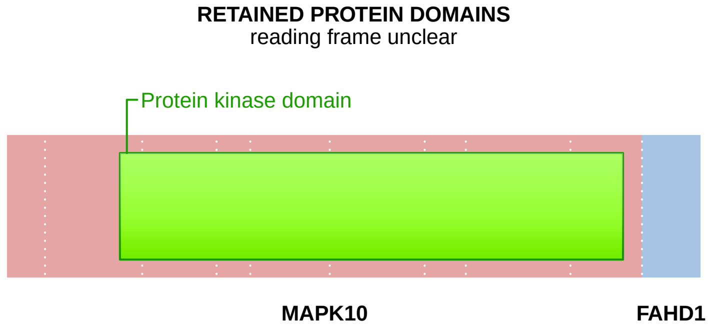


SUPPORTING READ COUNT

Split reads = 105
Discordant mates = 7

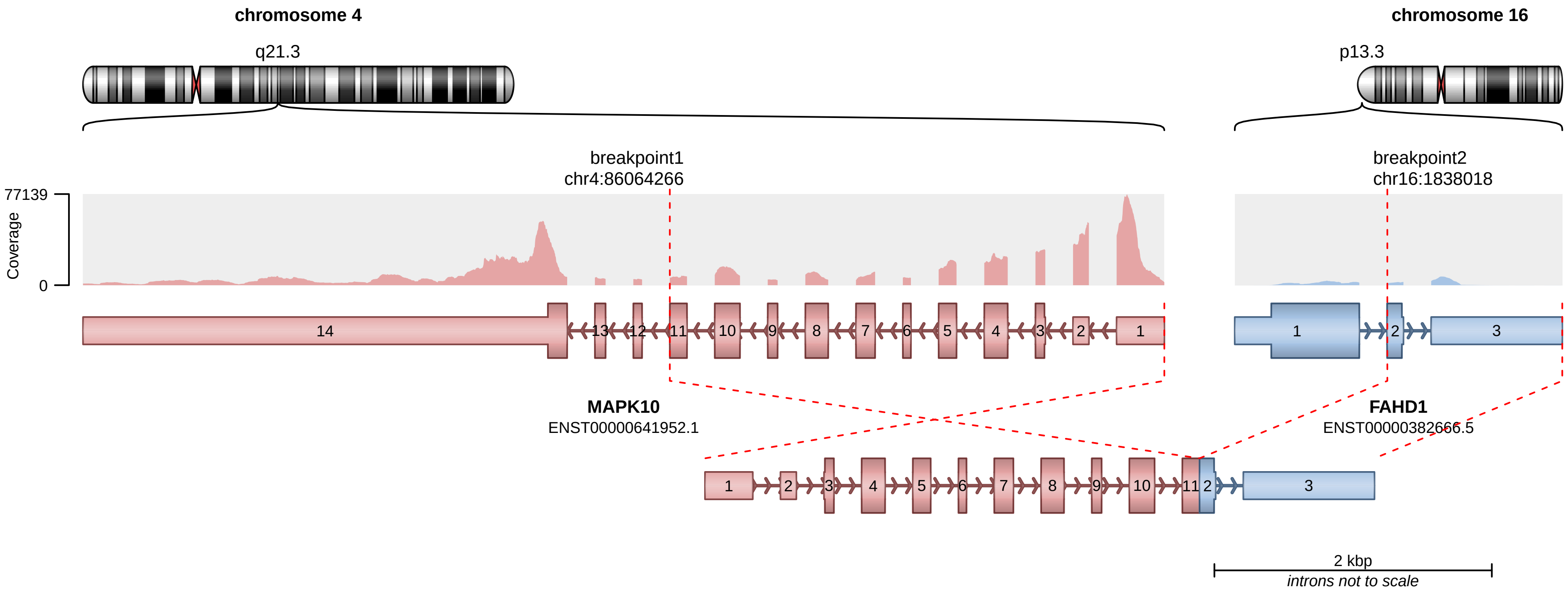


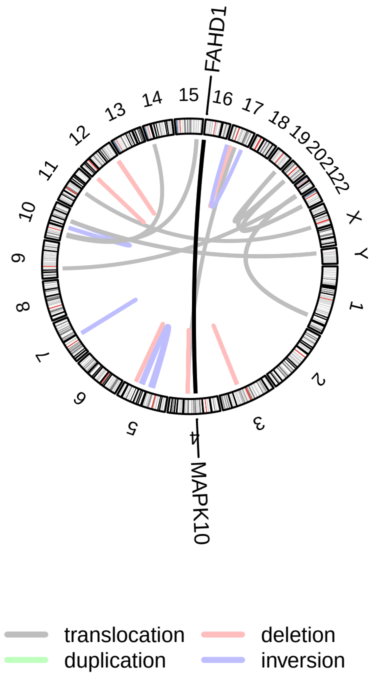




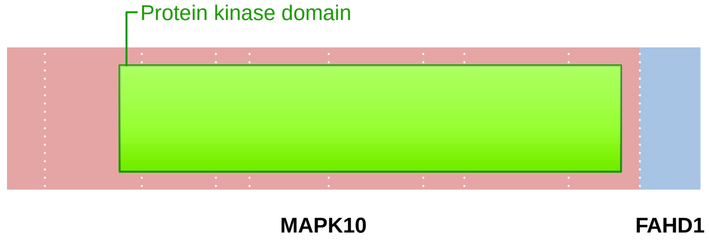
SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 8



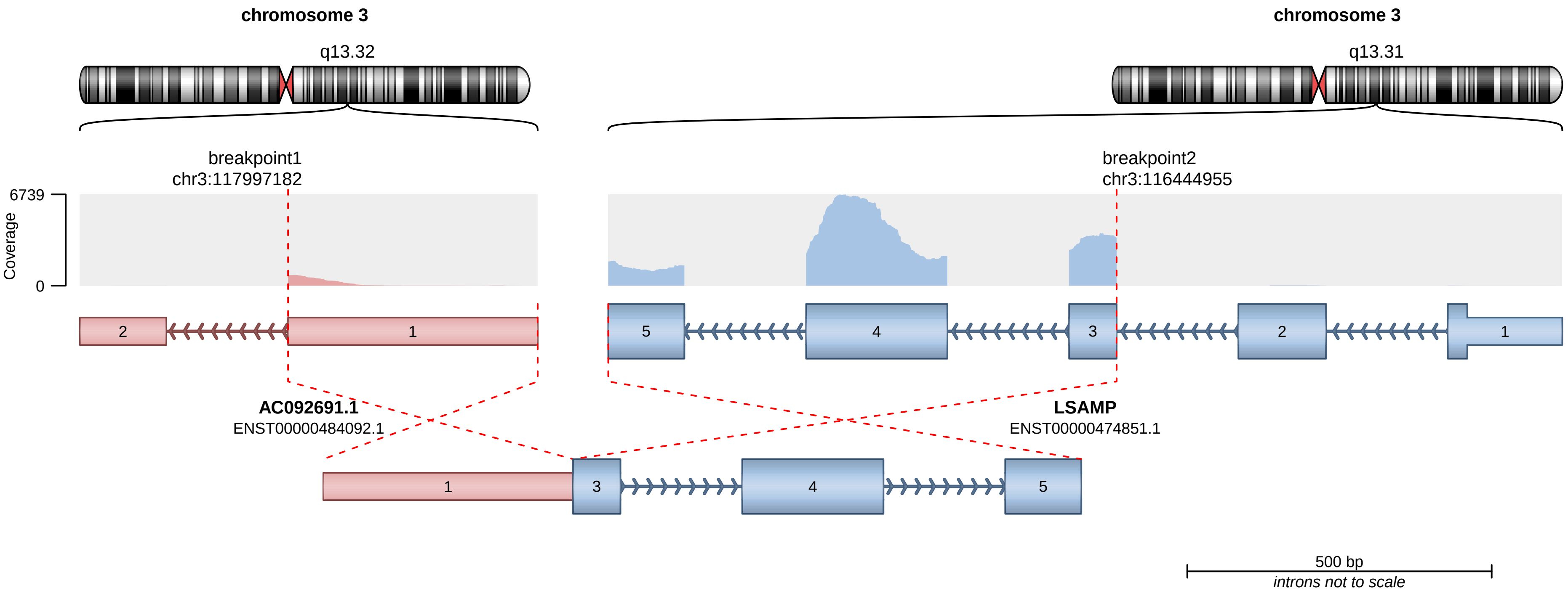


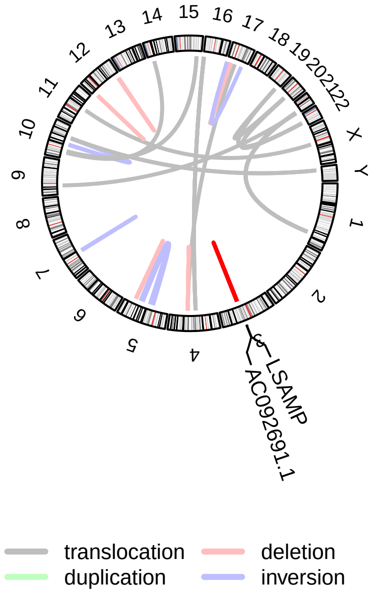
RETAINED PROTEIN DOMAINS
reading frame unclear



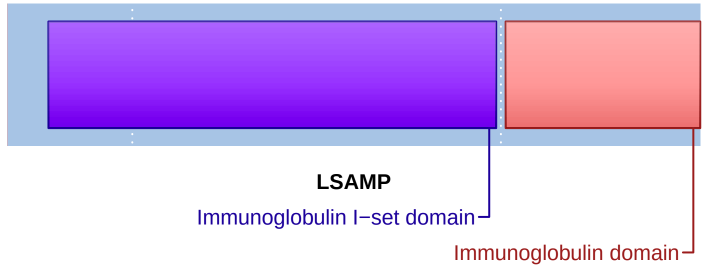
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 8



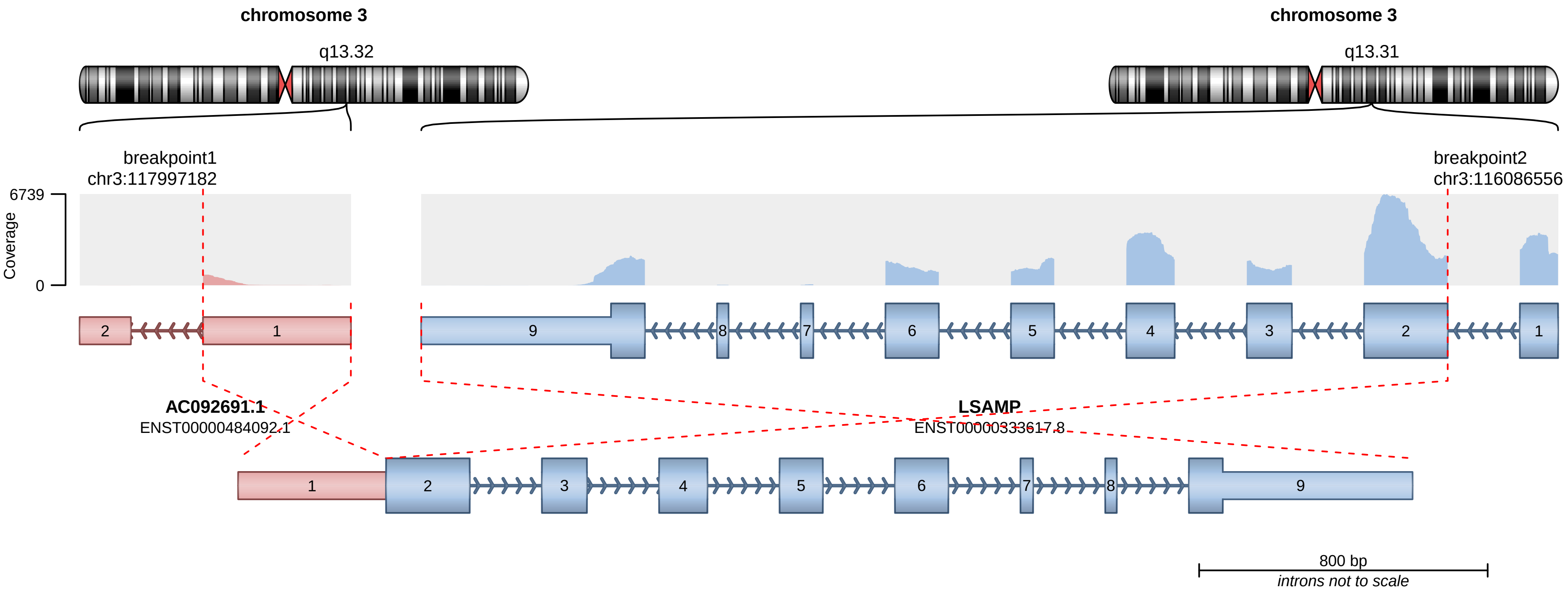


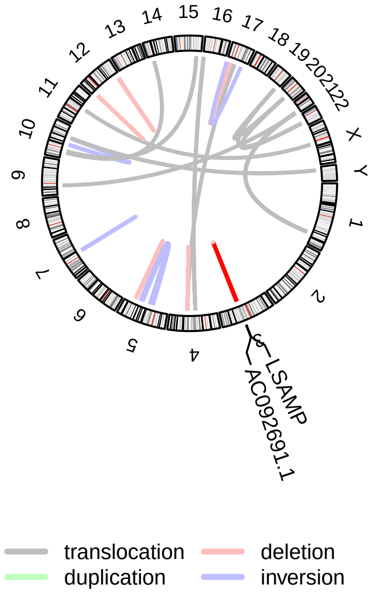
RETAINED PROTEIN DOMAINS
reading frame unclear

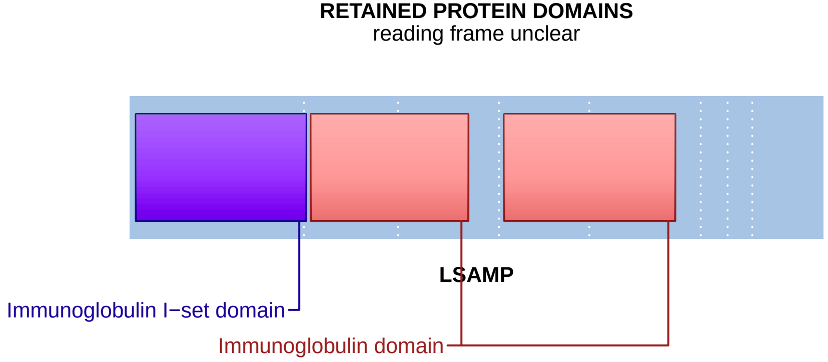


SUPPORTING READ COUNT

Split reads = 493
Discordant mates = 2

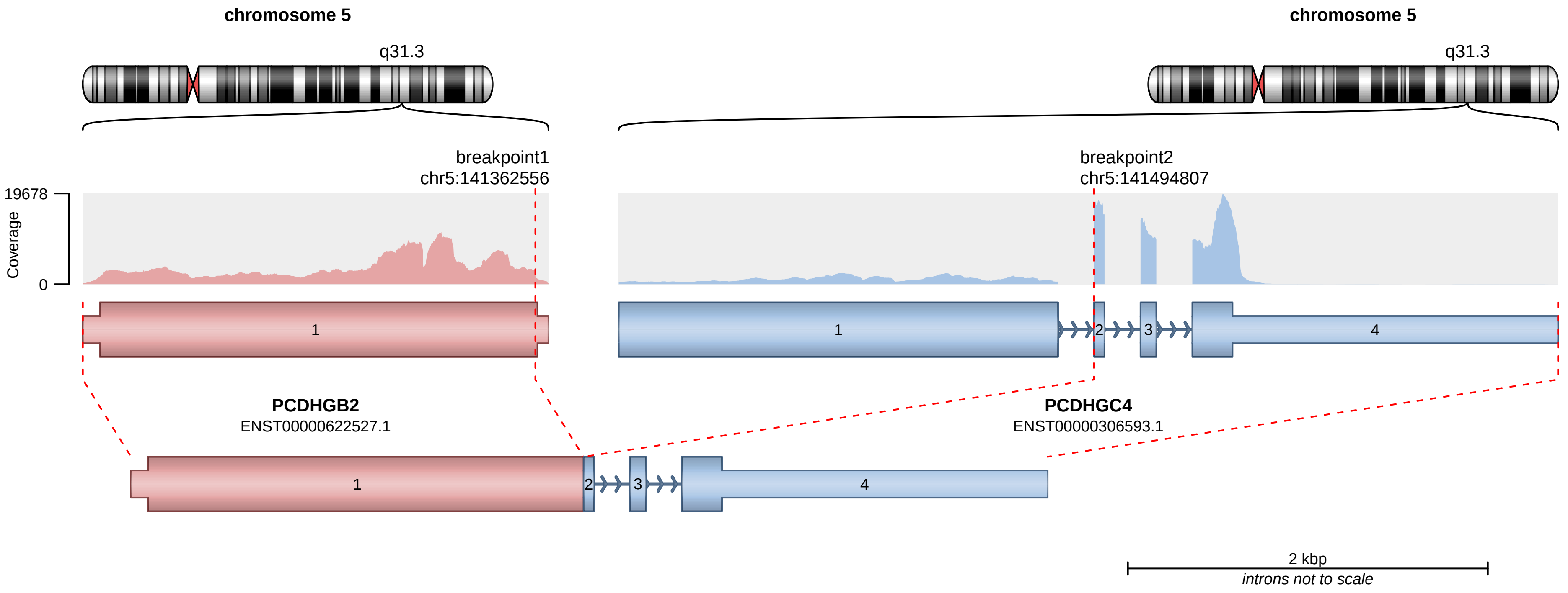


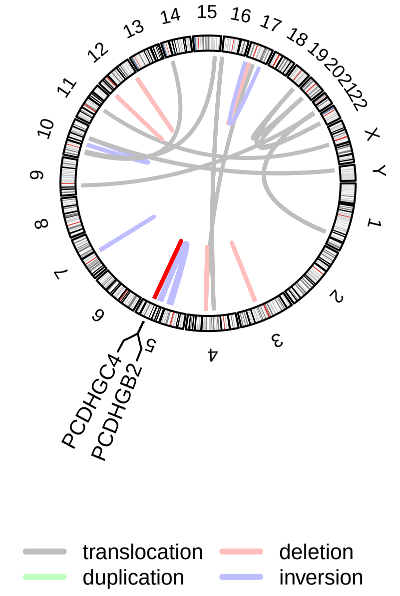


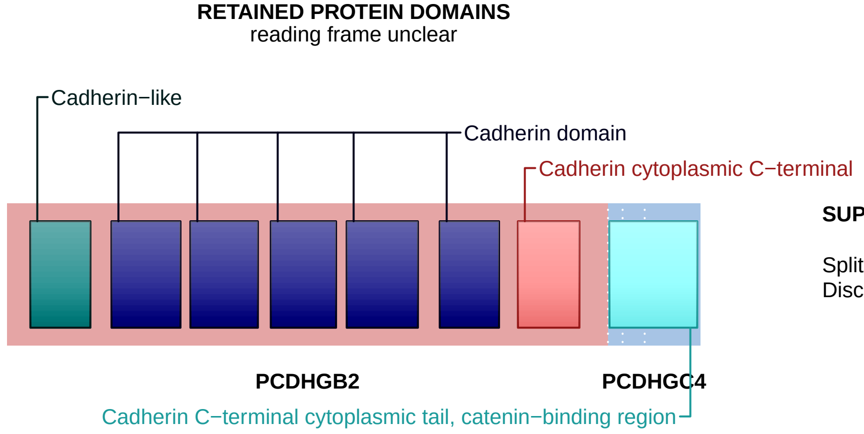


SUPPORTING READ COUNT

Split reads = 17
Discordant mates = 2

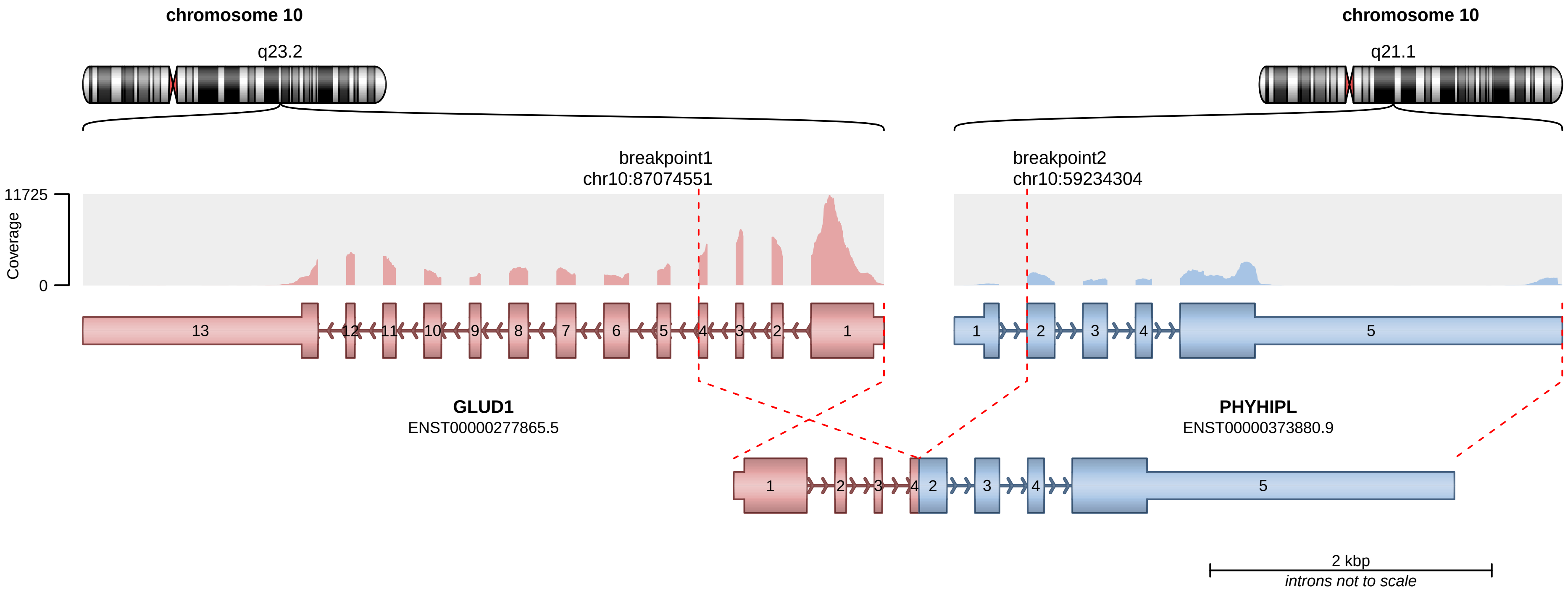


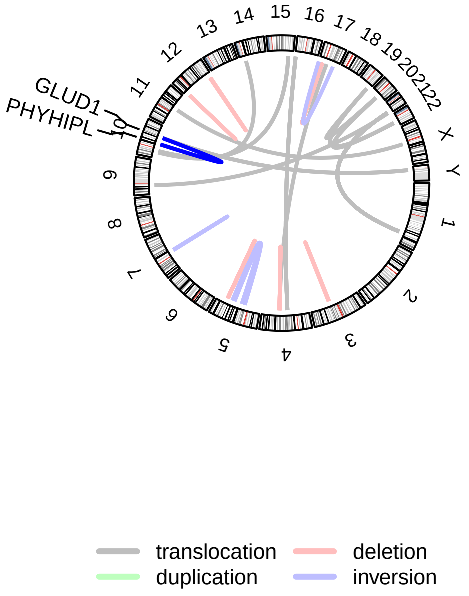


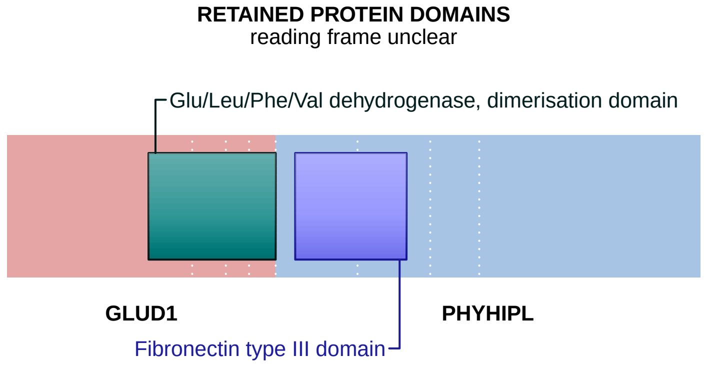


SUPPORTING READ COUNT

Split reads = 480
Discordant mates = 0

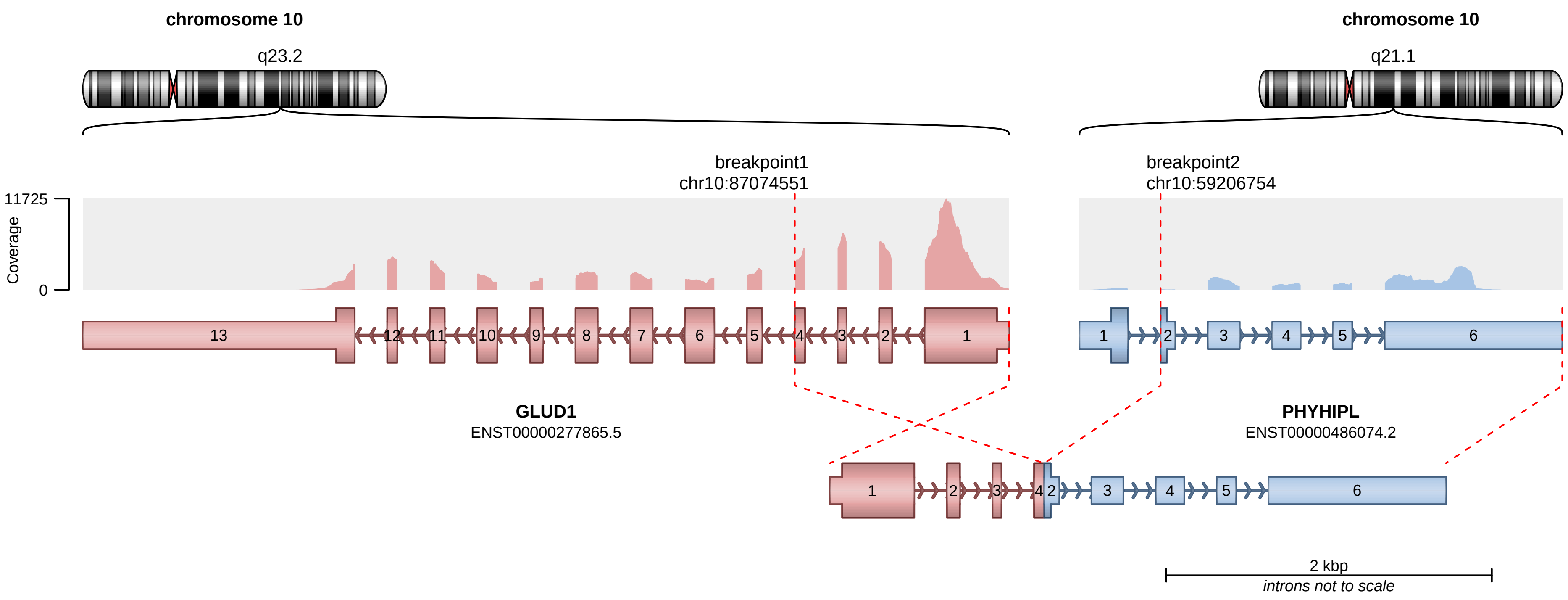


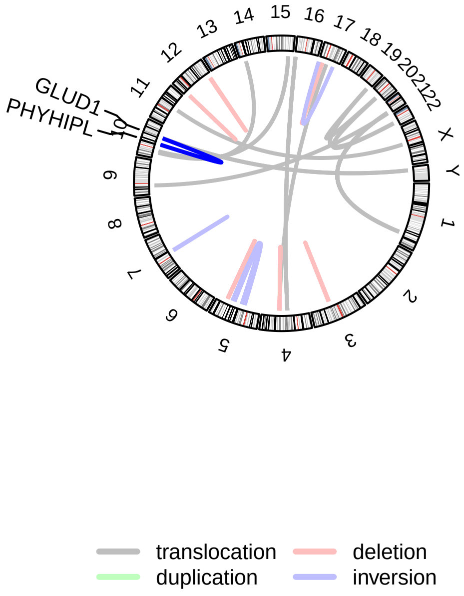




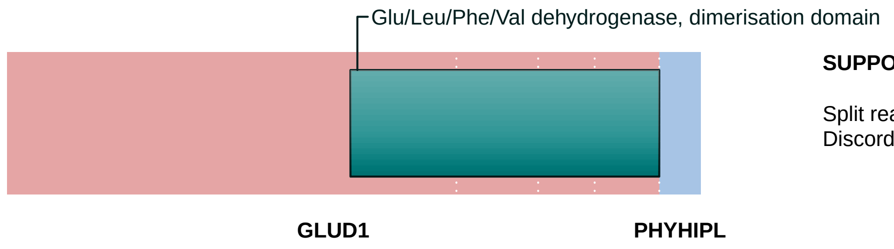
SUPPORTING READ COUNT

Split reads = 331
Discordant mates = 5



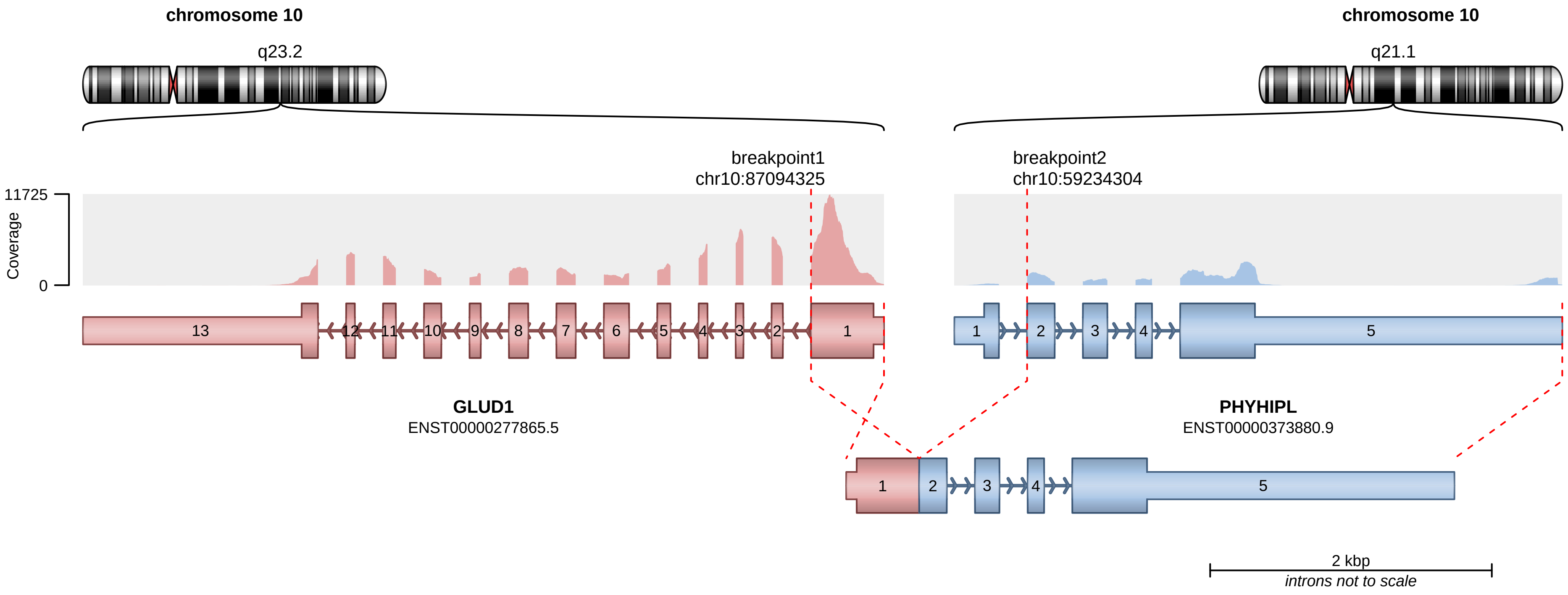


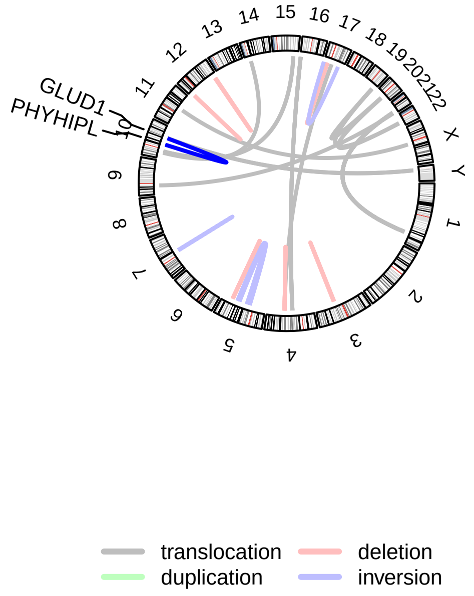
RETAINED PROTEIN DOMAINS
reading frame unclear

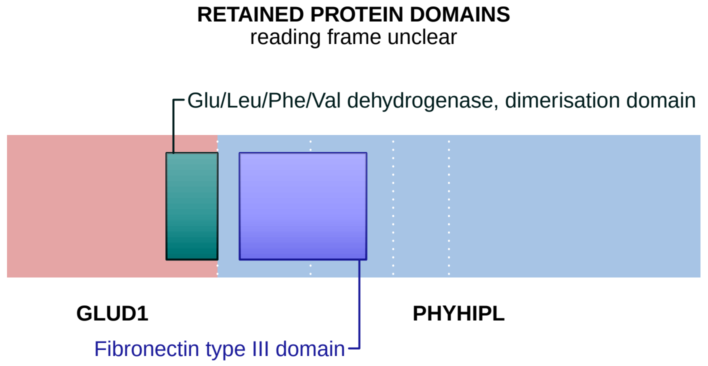


SUPPORTING READ COUNT

Split reads = 36
Discordant mates = 5

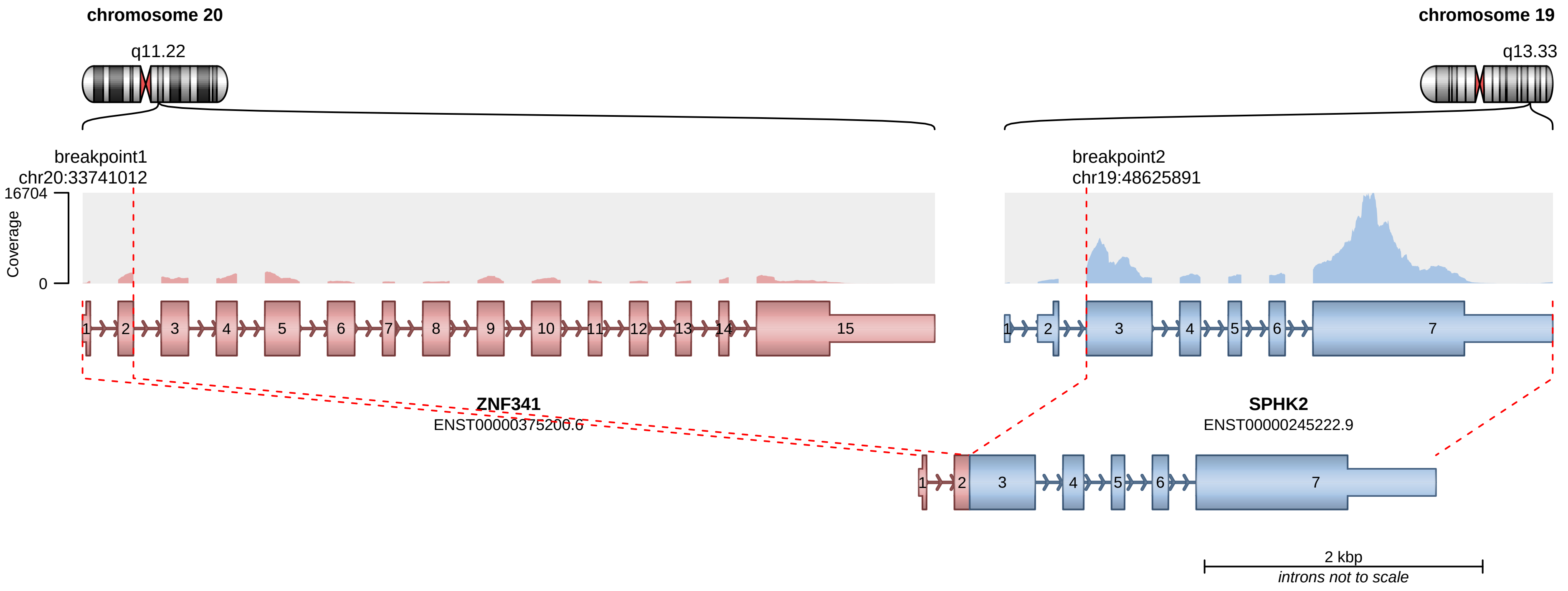


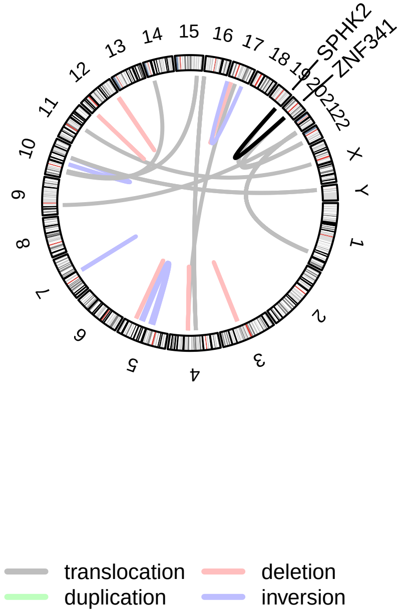




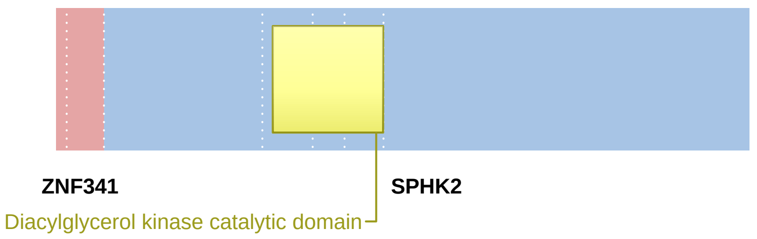
SUPPORTING READ COUNT

Split reads = 28
Discordant mates = 0



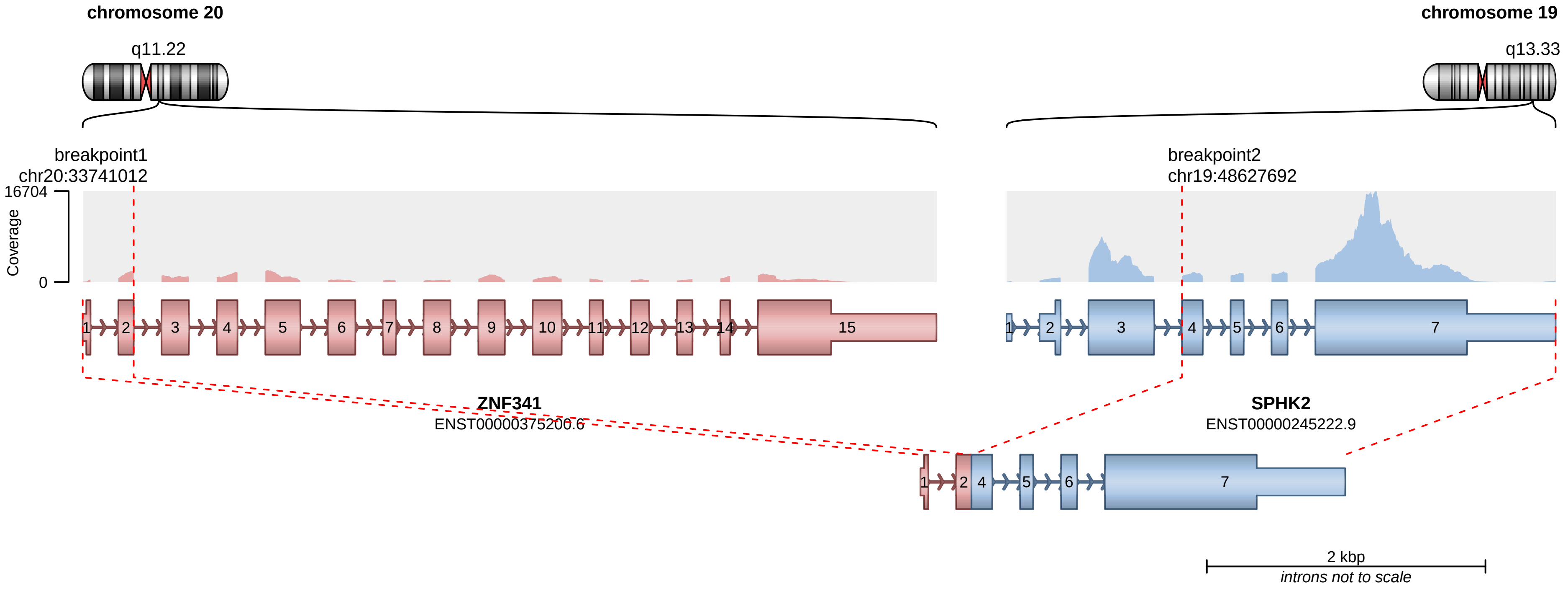


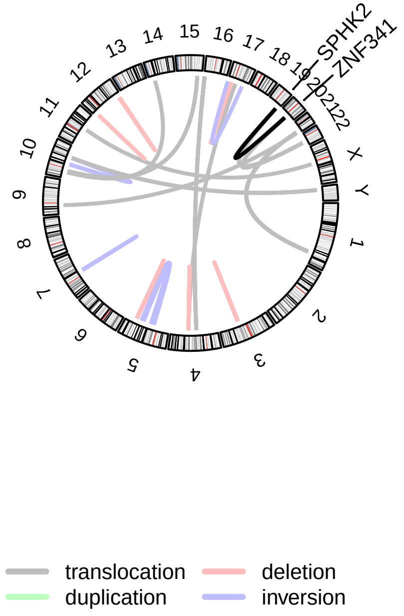
RETAINED PROTEIN DOMAINS
reading frame unclear



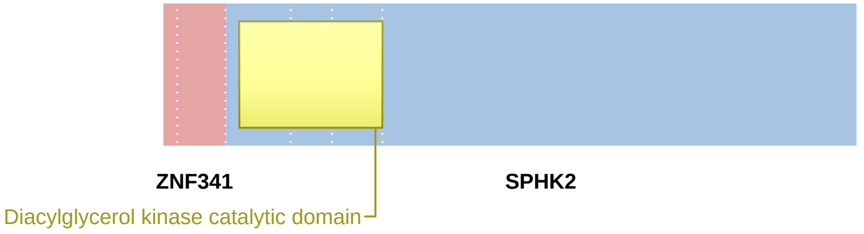
SUPPORTING READ COUNT

Split reads = 306
Discordant mates = 6



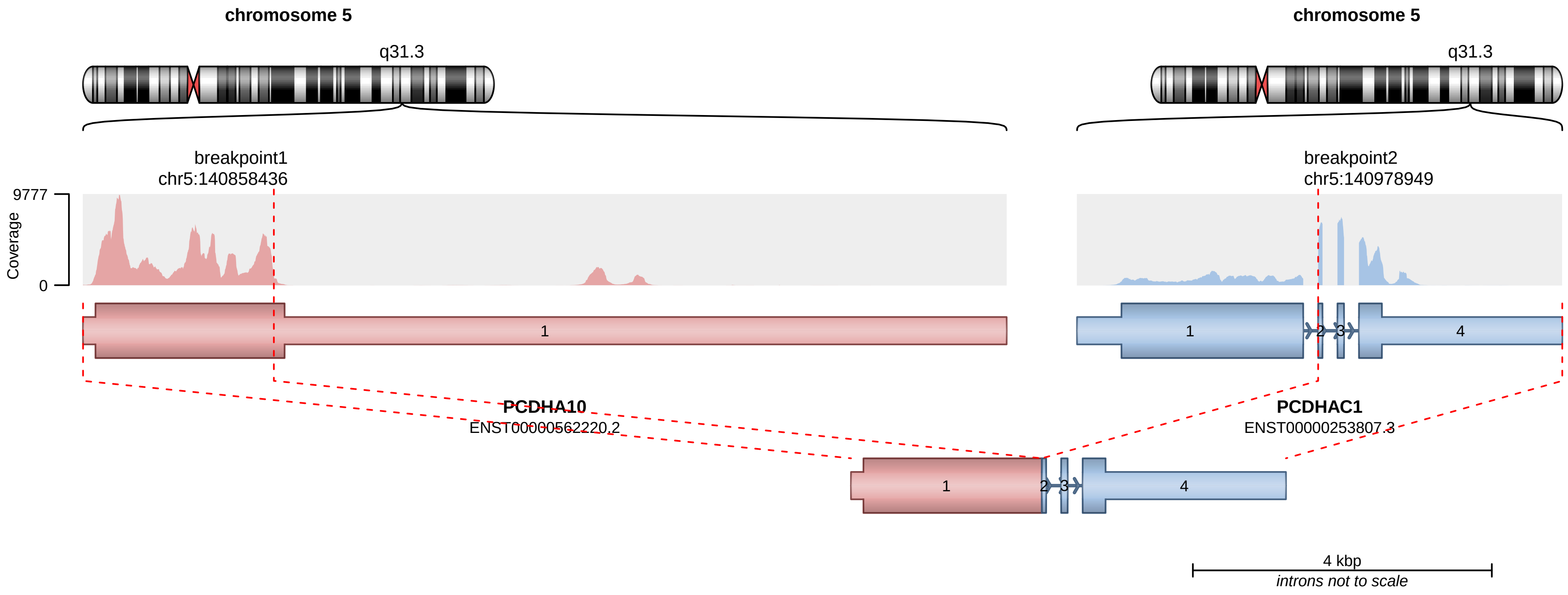


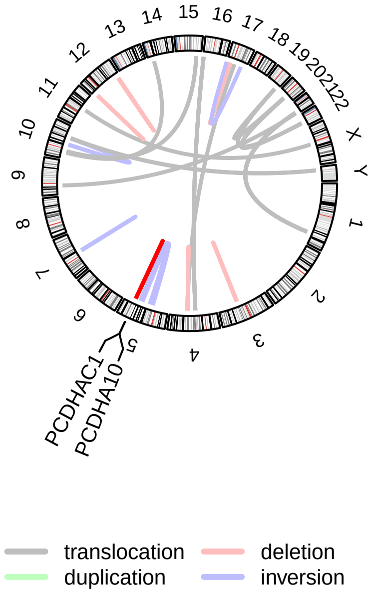
RETAINED PROTEIN DOMAINS
reading frame unclear

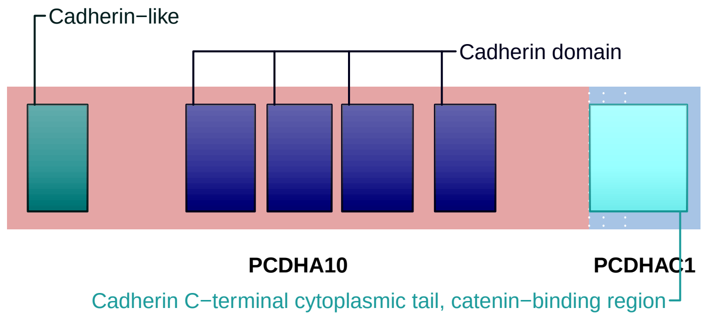


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

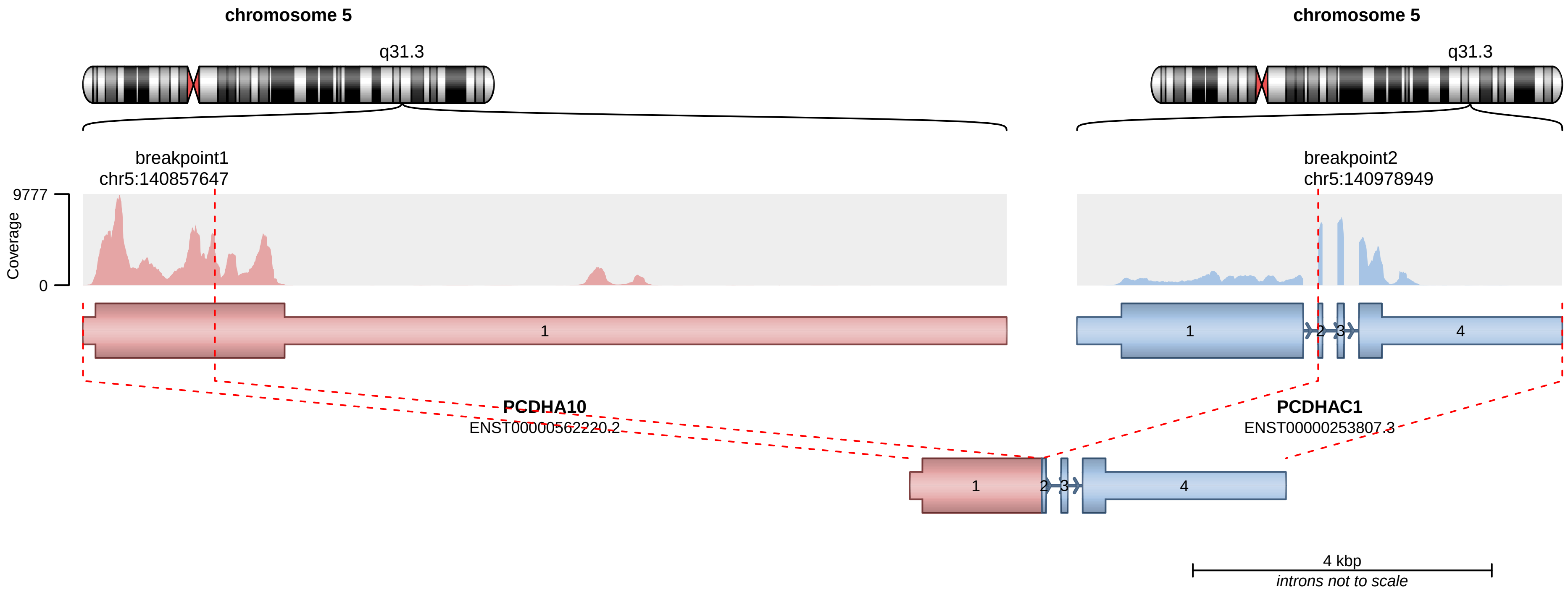


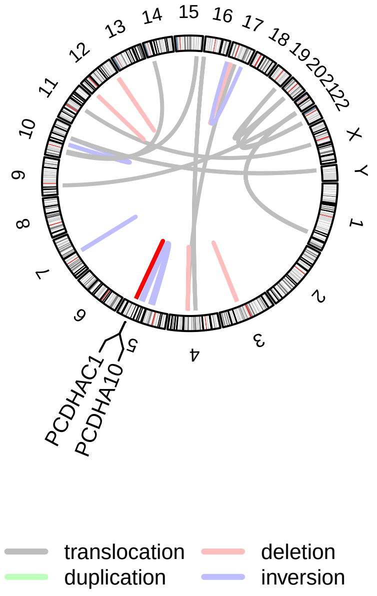


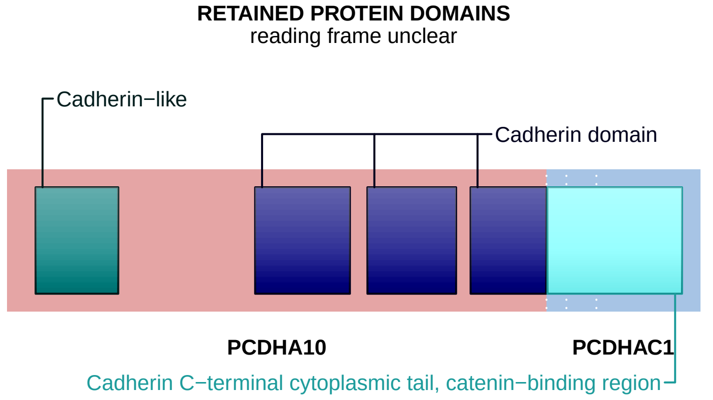

RETAINED PROTEIN DOMAINS
reading frame unclear

SUPPORTING READ COUNT

Split reads = 231
Discordant mates = 1

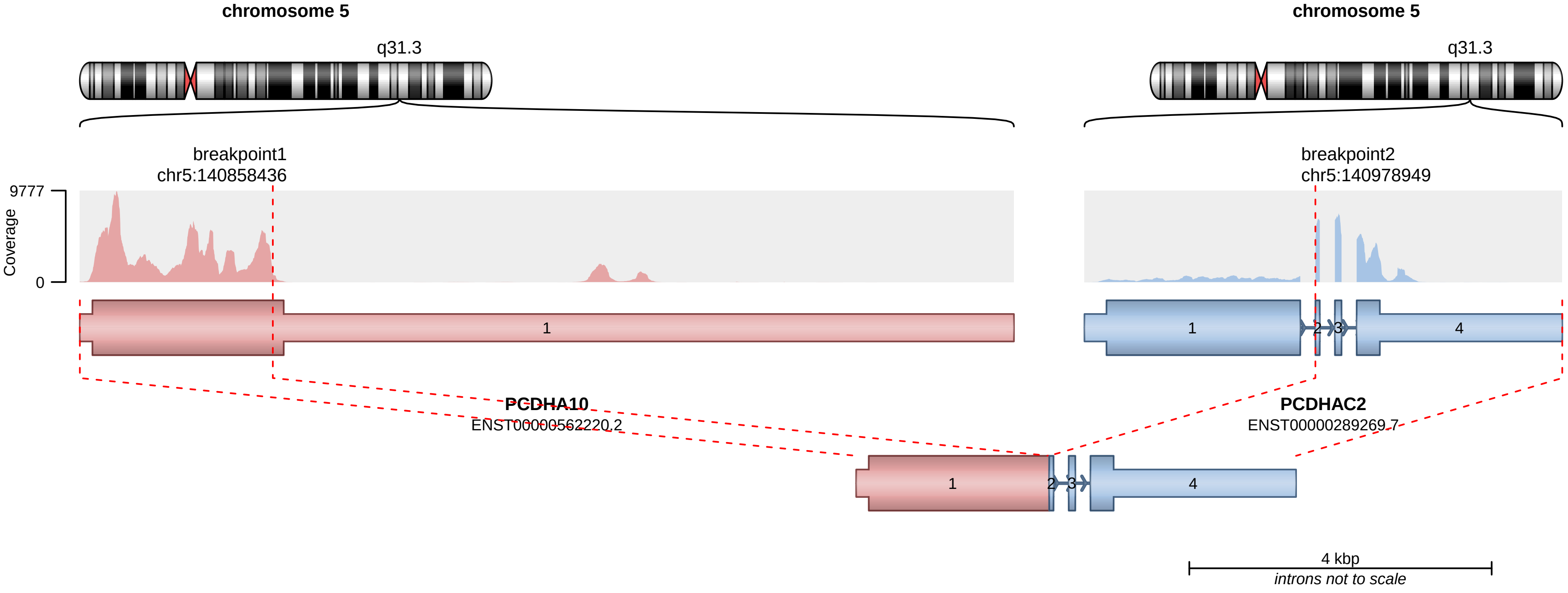


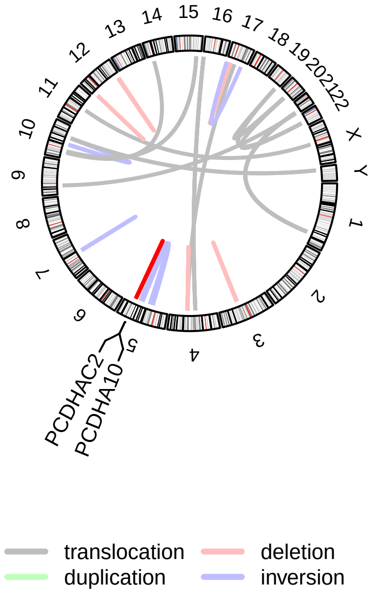


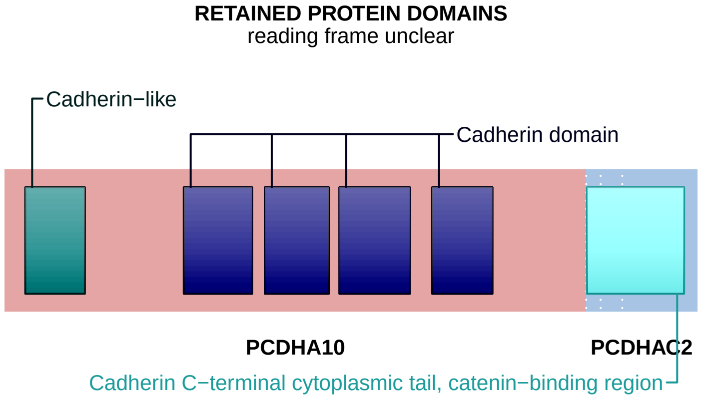


SUPPORTING READ COUNT

Split reads = 30
Discordant mates = 0

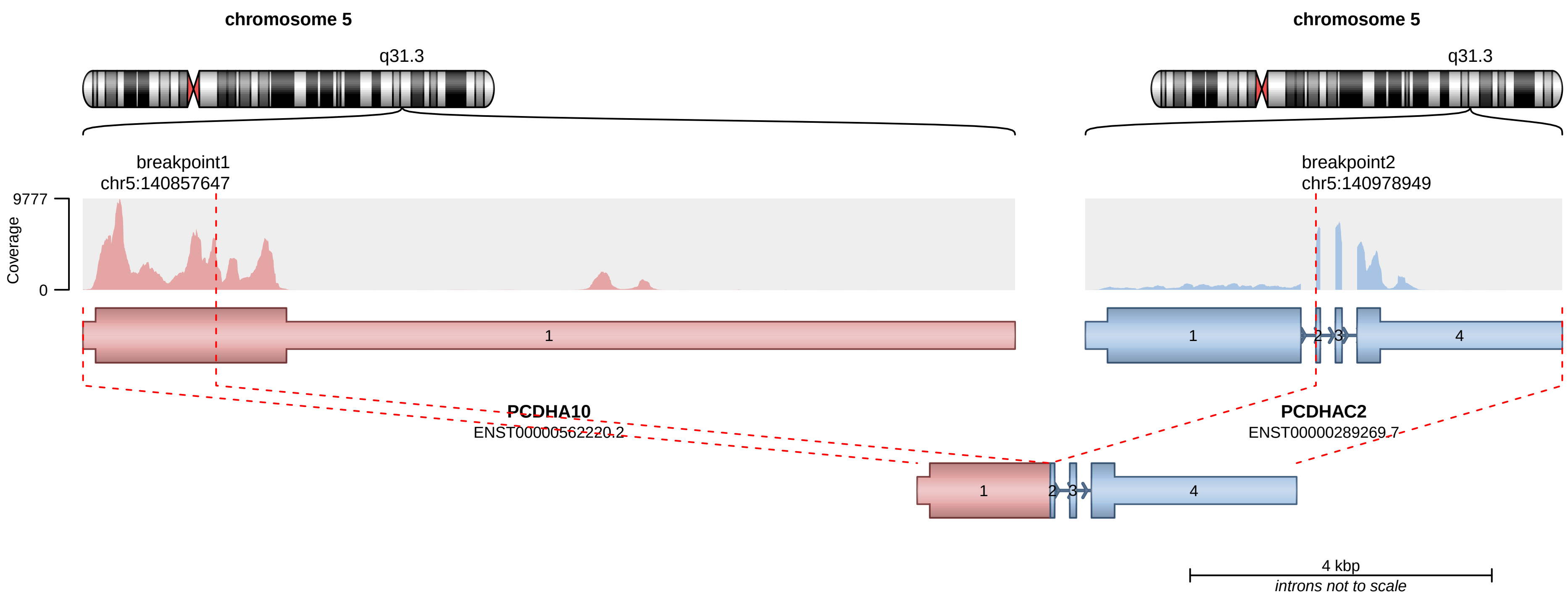


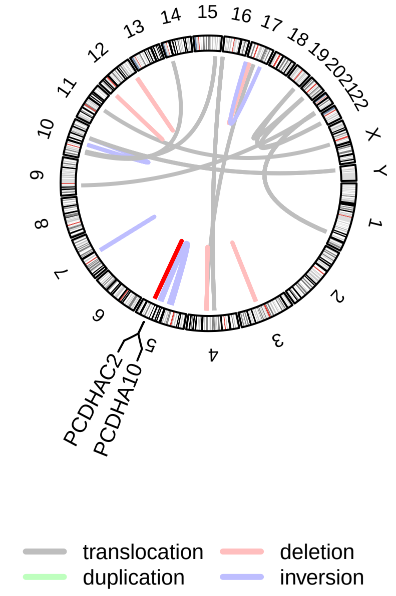


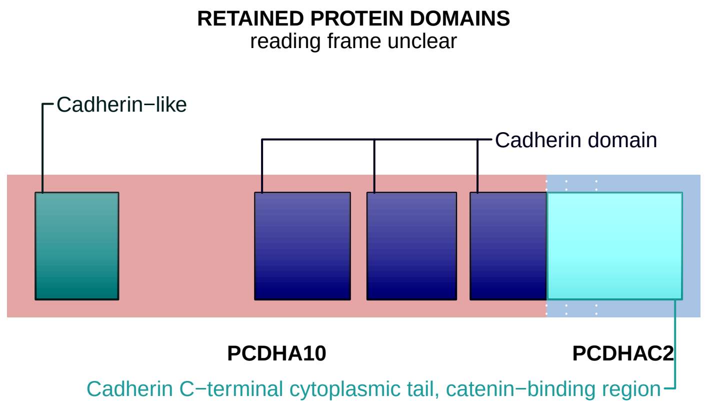


SUPPORTING READ COUNT

Split reads = 231
Discordant mates = 1

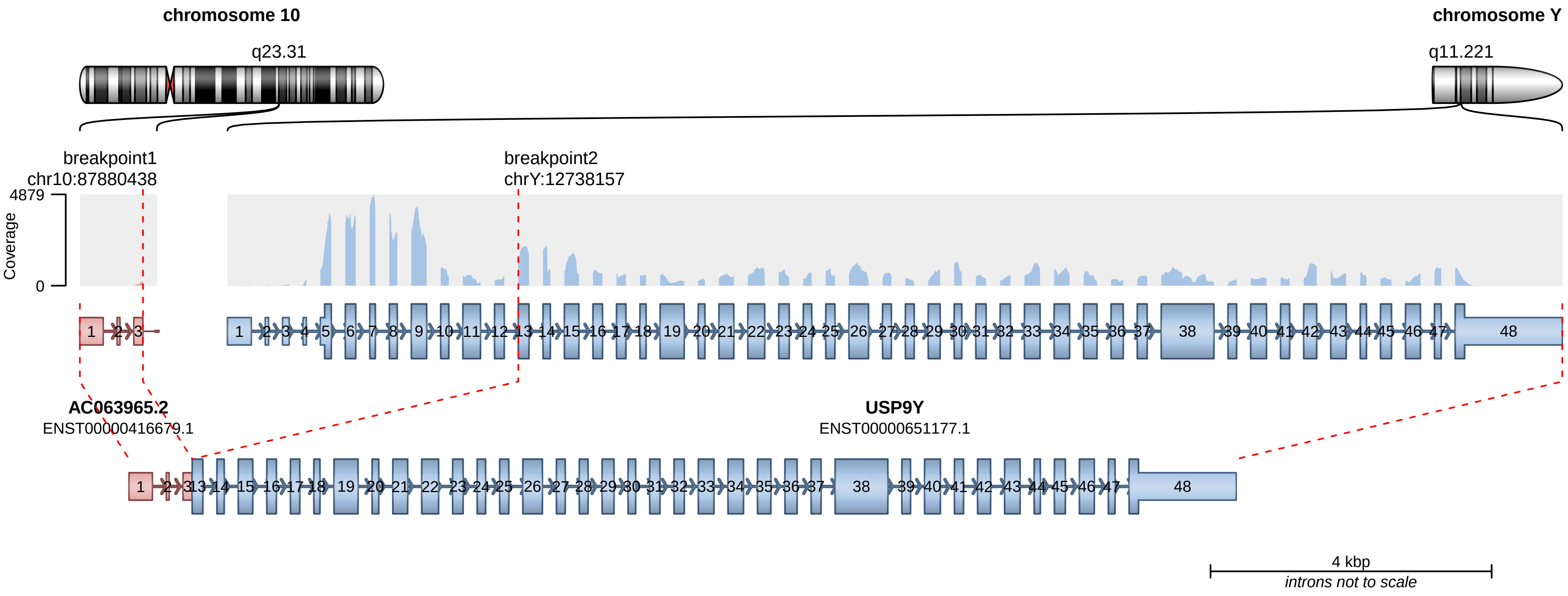


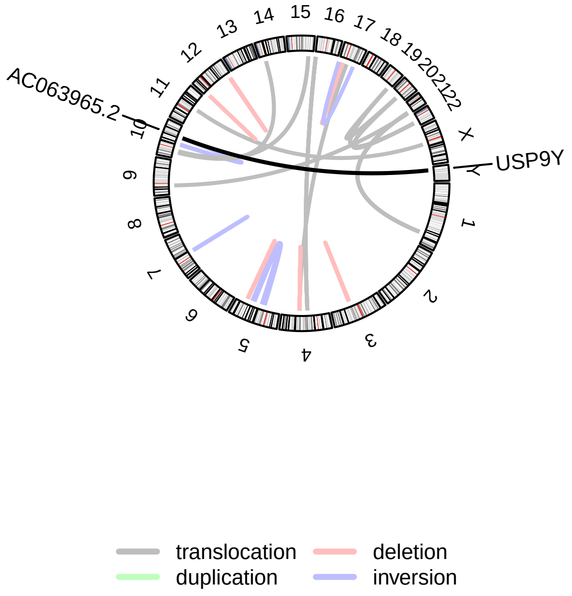




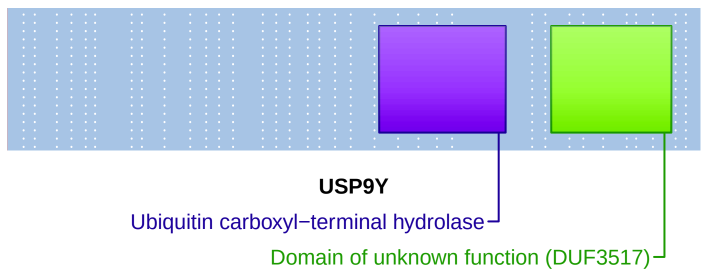
SUPPORTING READ COUNT

Split reads = 30
Discordant mates = 0



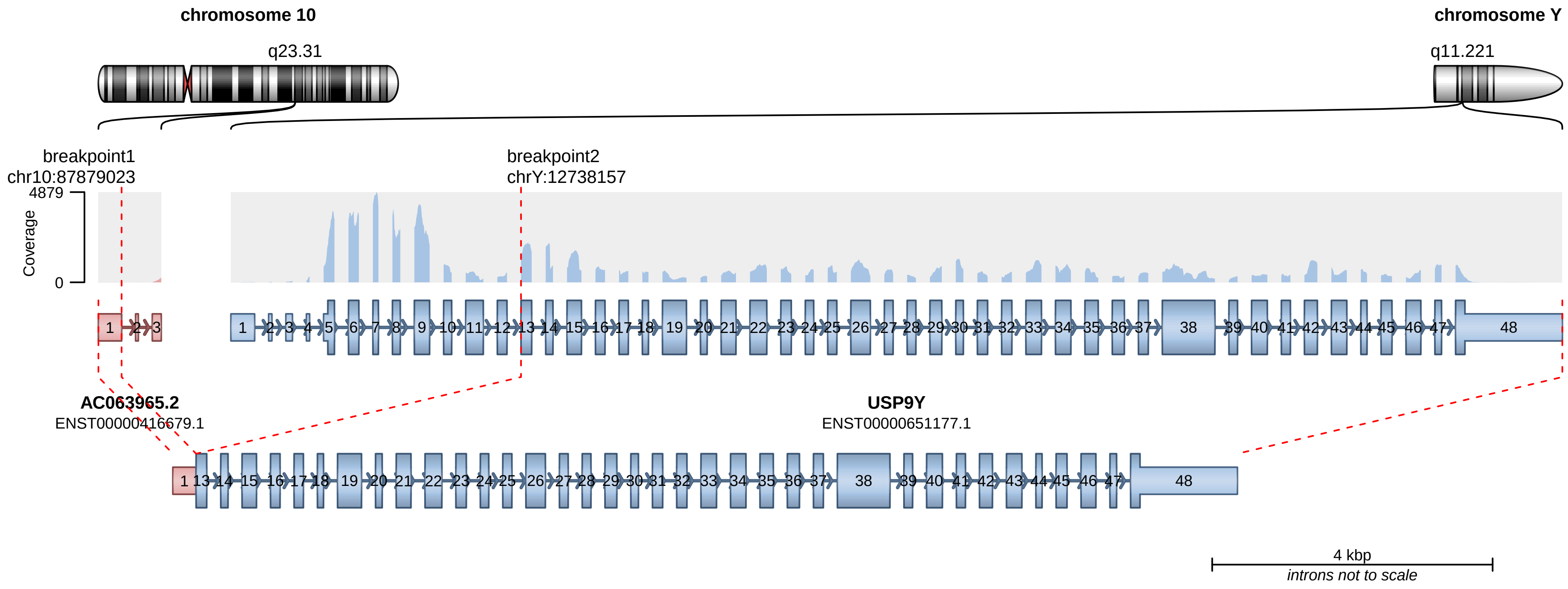


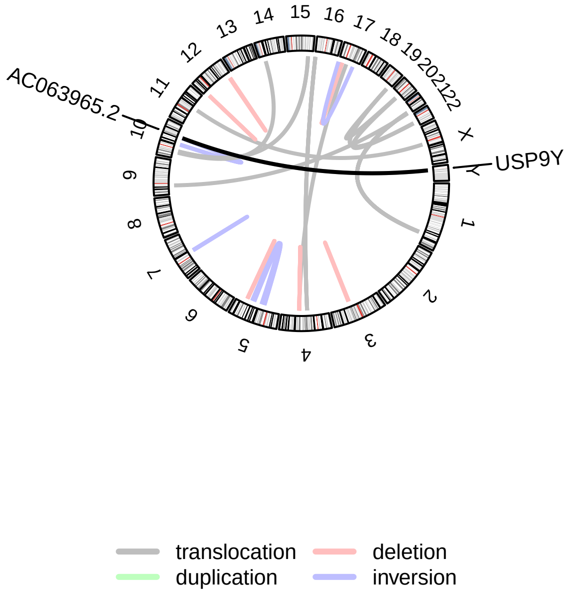
RETAINED PROTEIN DOMAINS
reading frame unclear

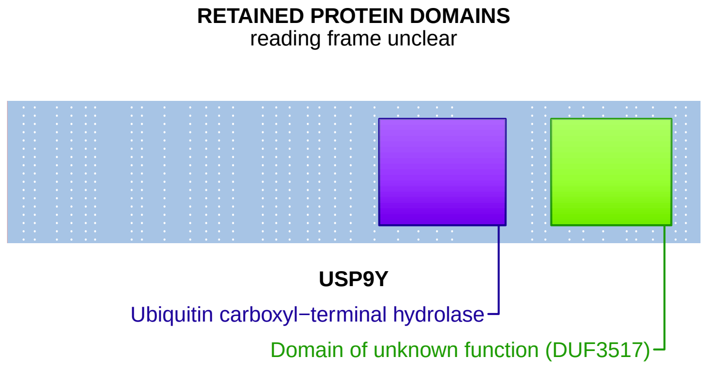


SUPPORTING READ COUNT

Split reads = 169
Discordant mates = 1

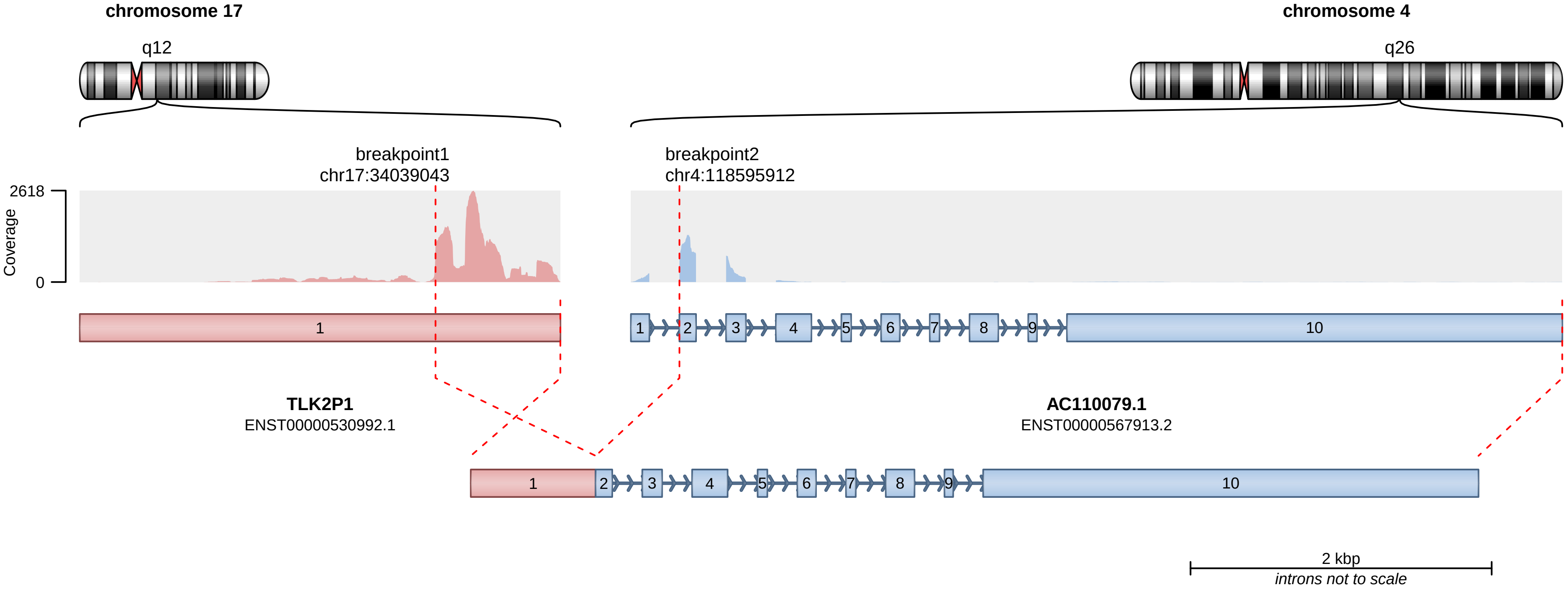


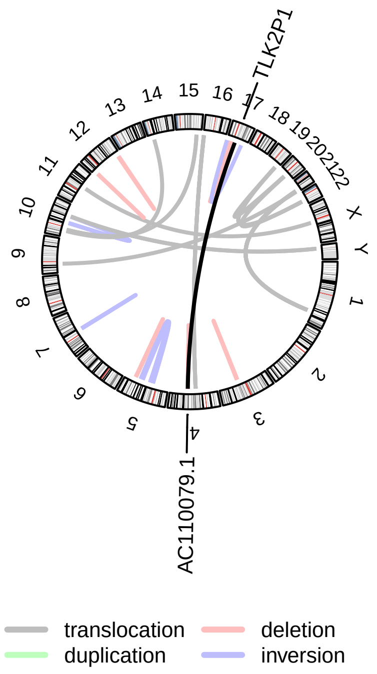




SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

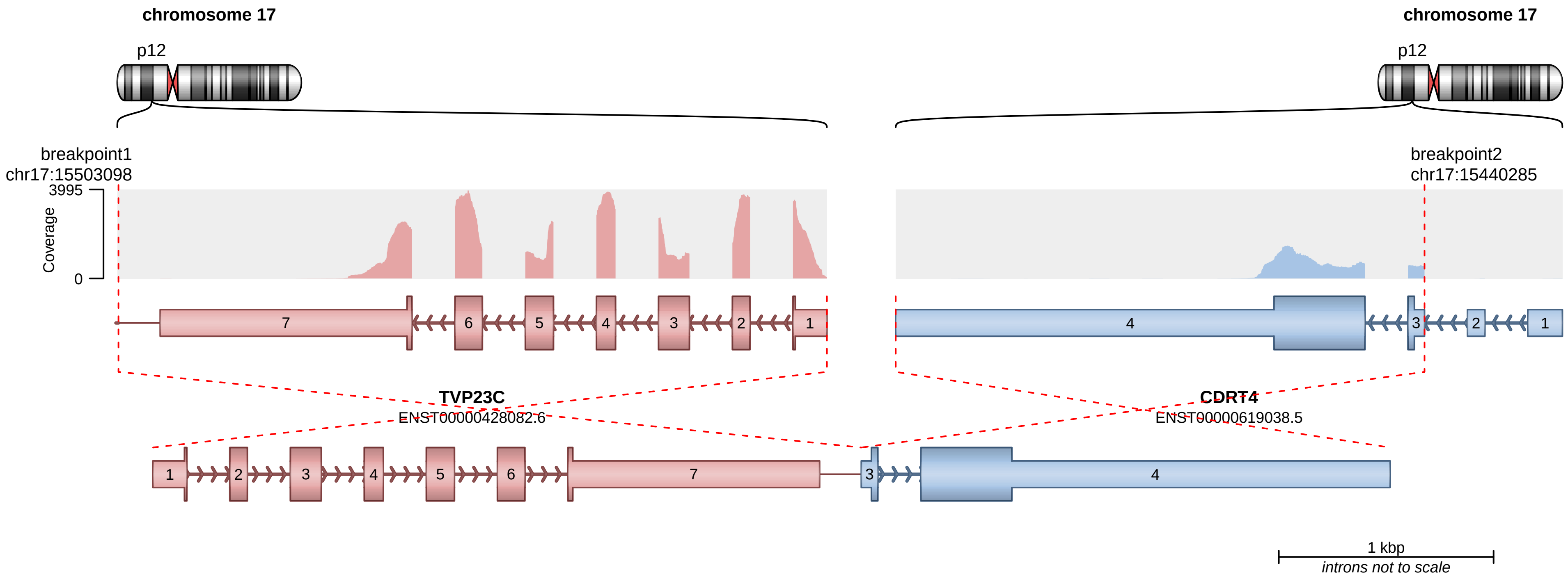


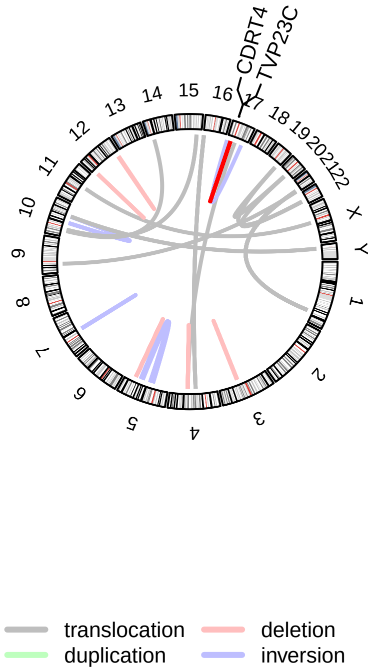


Genes are not protein−coding.

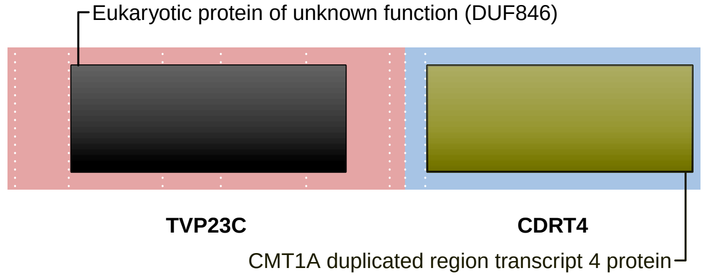
SUPPORTING READ COUNT

Split reads = 141
Discordant mates = 0



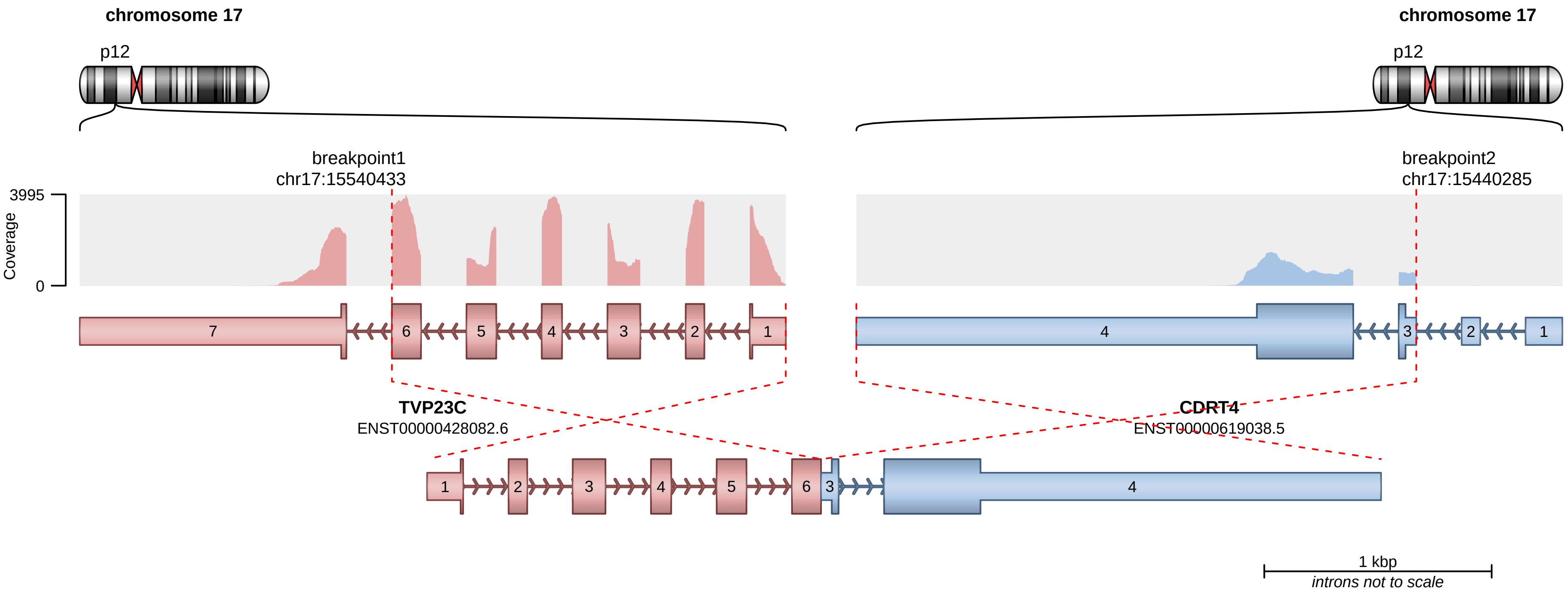


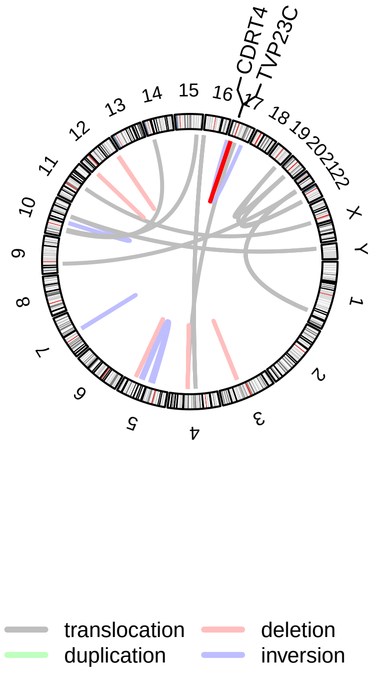
RETAINED PROTEIN DOMAINS
reading frame unclear

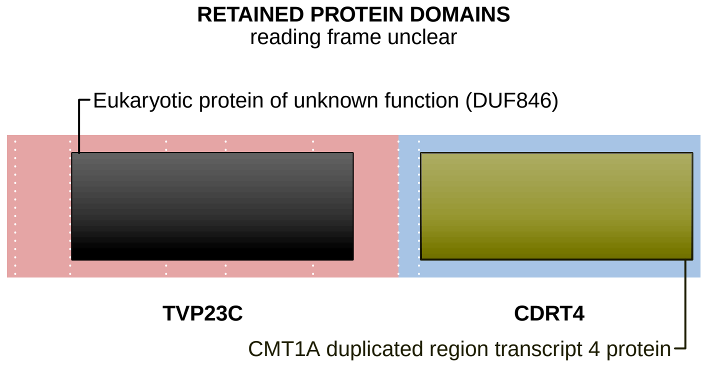


SUPPORTING READ COUNT

Split reads = 89
Discordant mates = 0

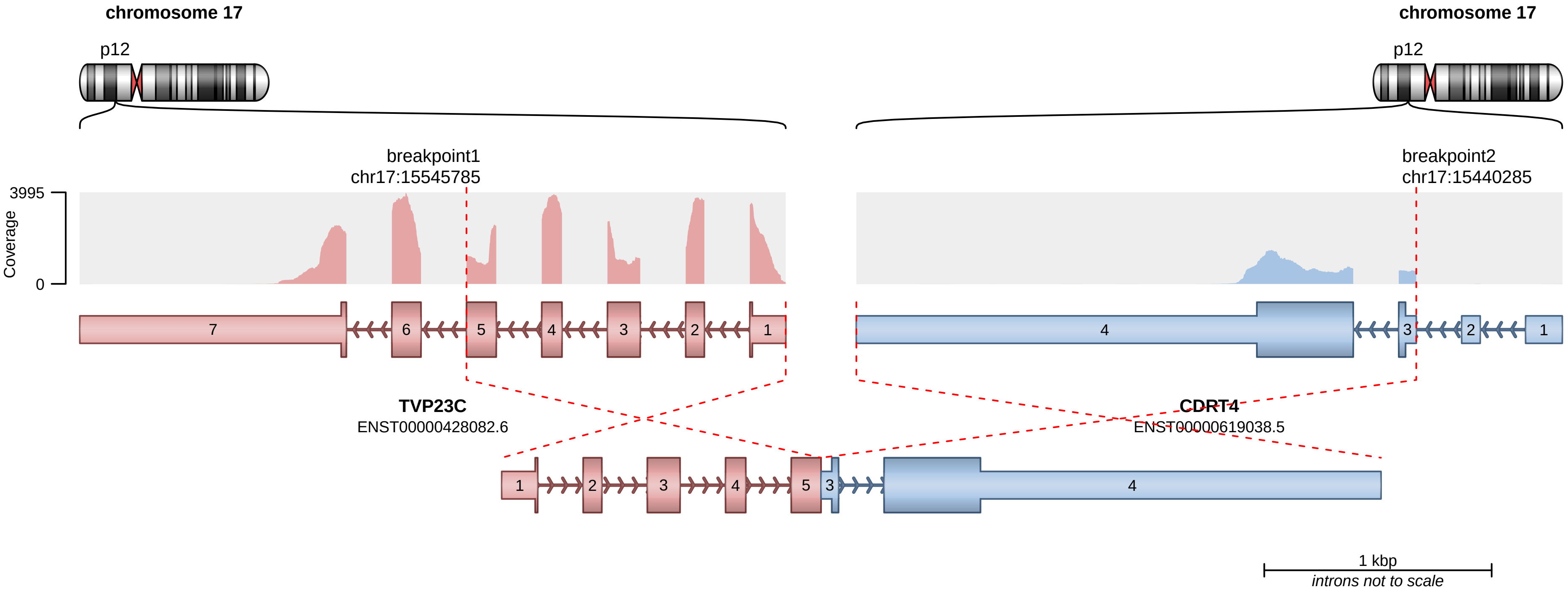


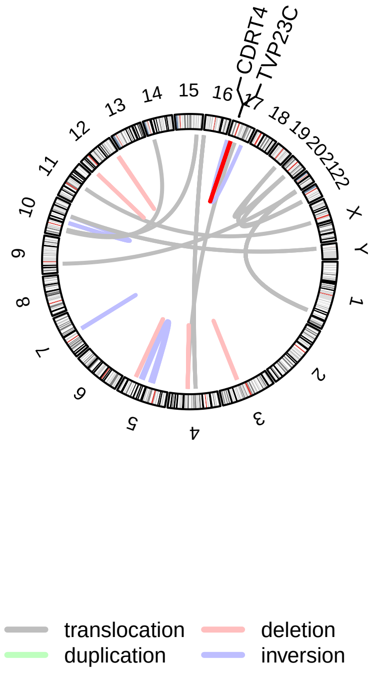


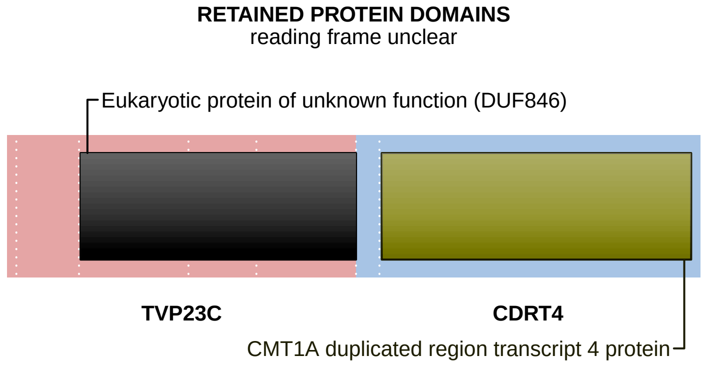

RETAINED PROTEIN DOMAINS
reading frame unclear

SUPPORTING READ COUNT

Split reads = 29
Discordant mates = 0

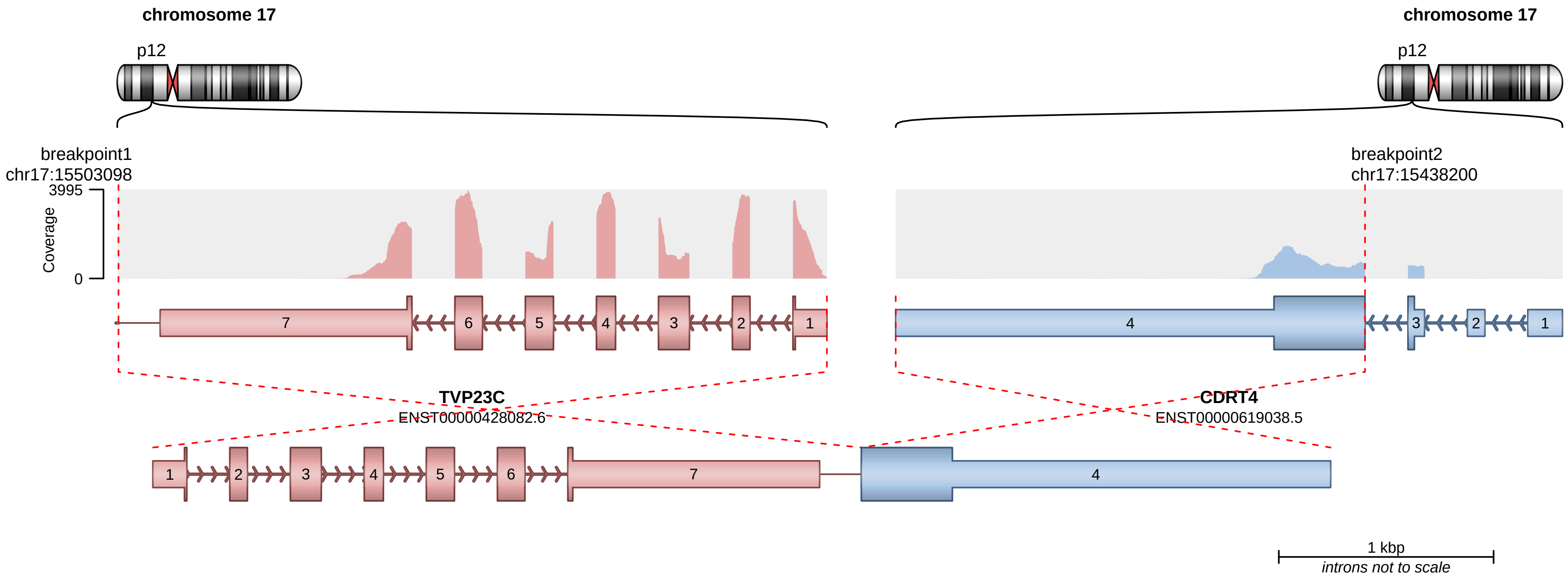


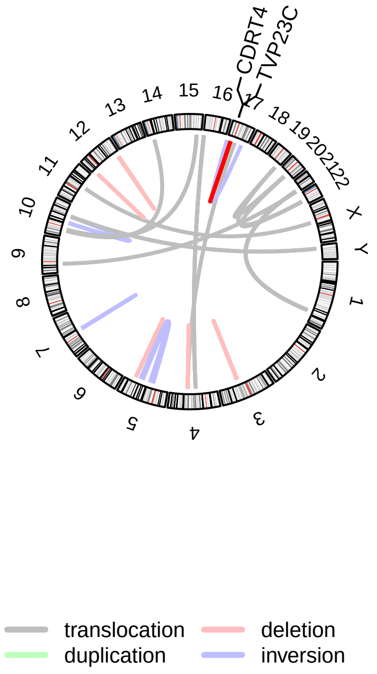


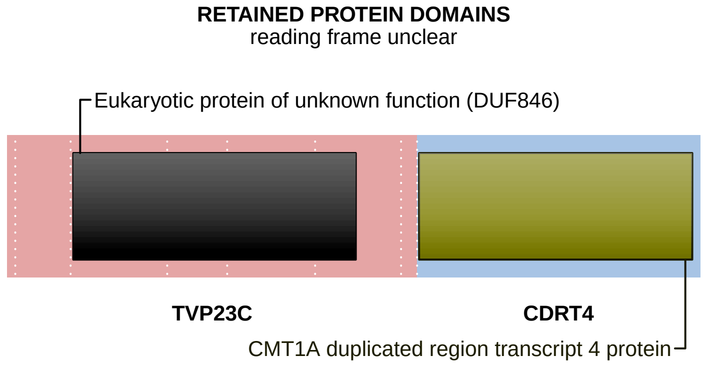


SUPPORTING READ COUNT

Split reads = 17
Discordant mates = 0

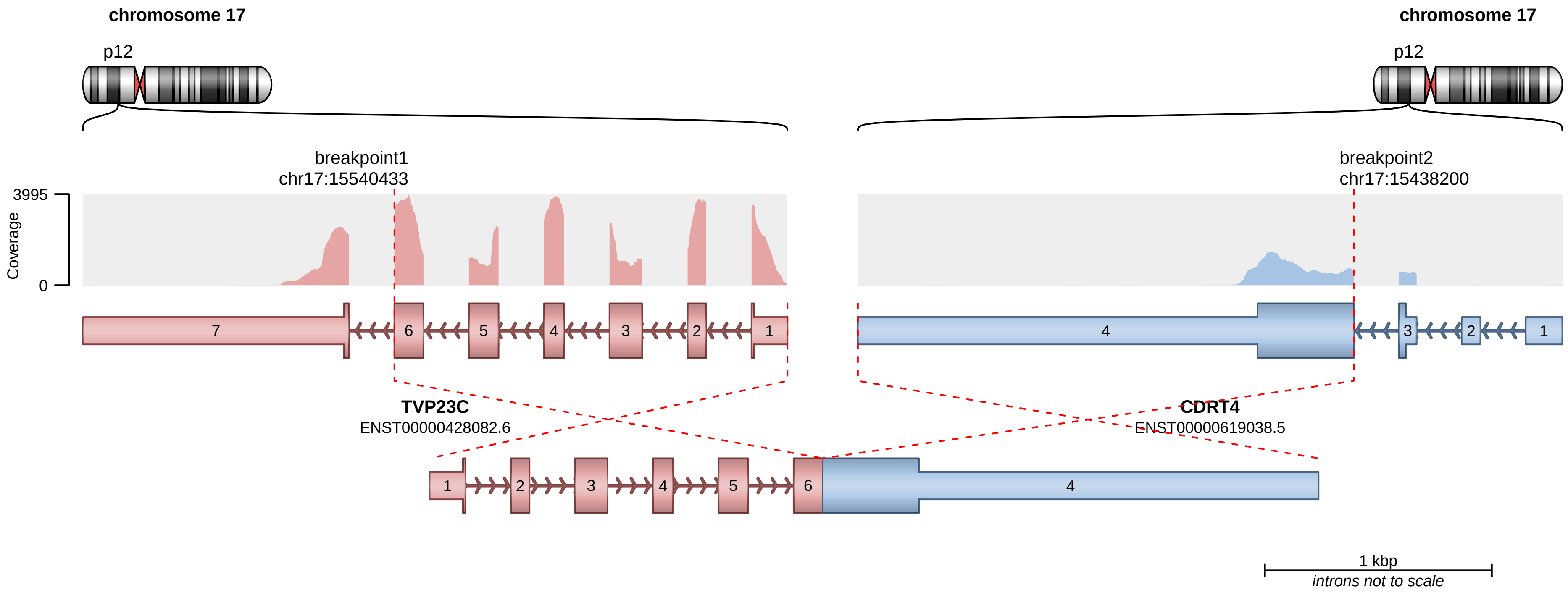


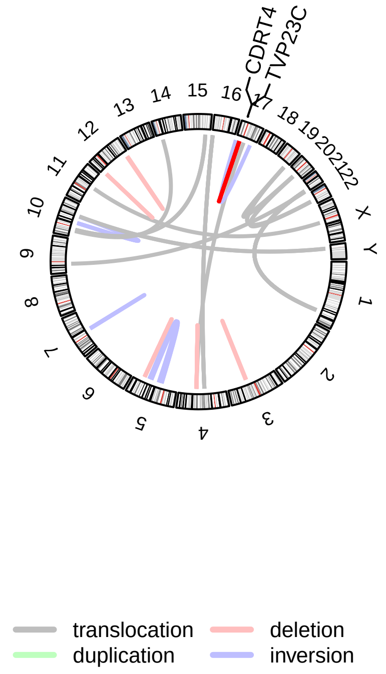




SUPPORTING READ COUNT

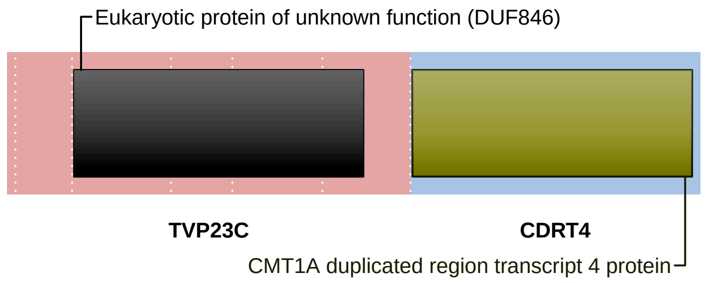
Split reads = 14
Discordant mates = 0





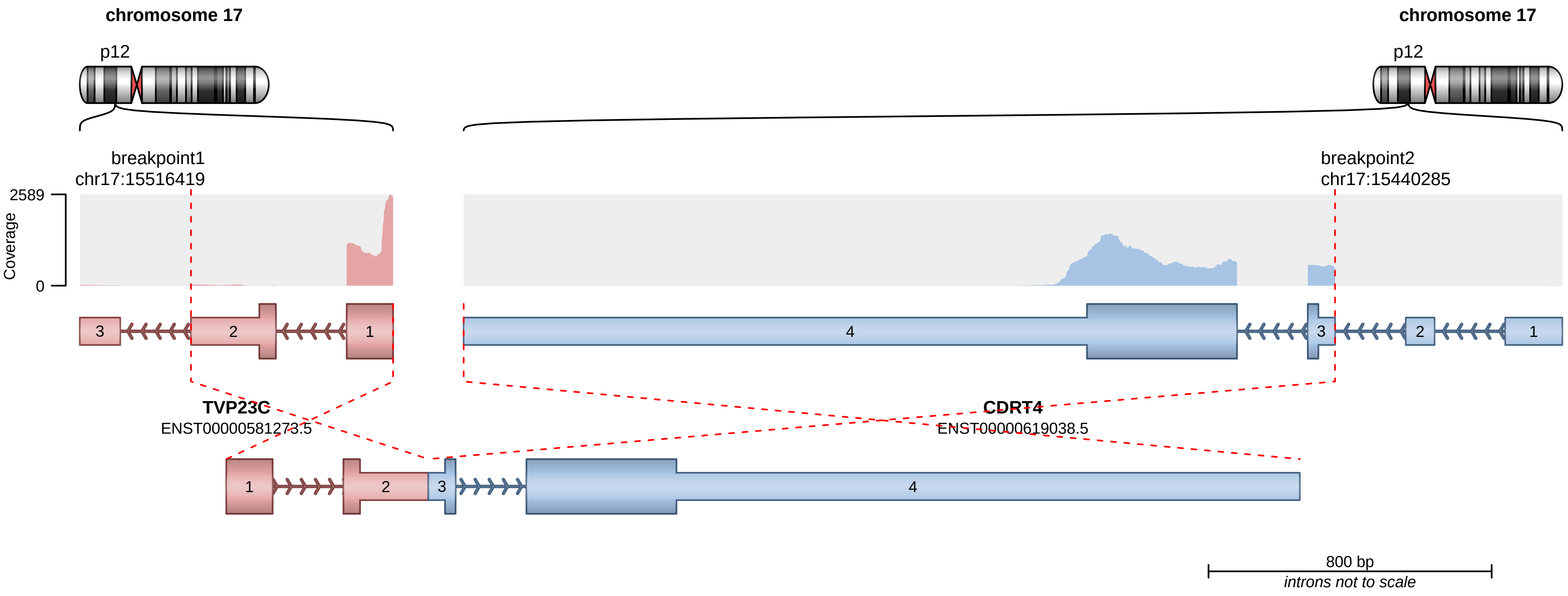
RETAINED PROTEIN DOMAINS

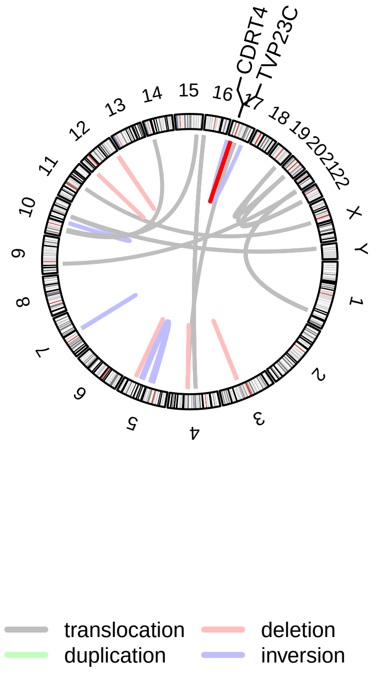
reading frame unclear

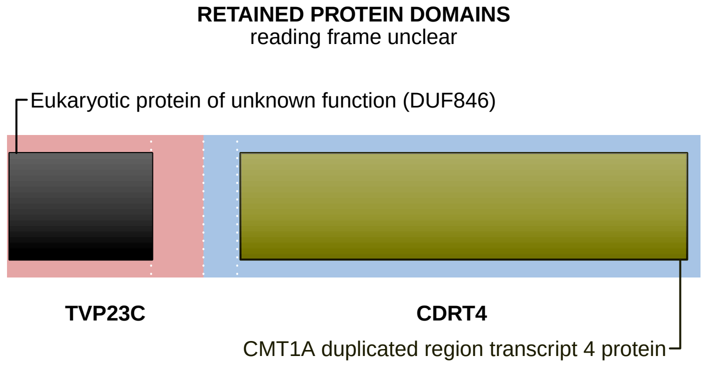


SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 0

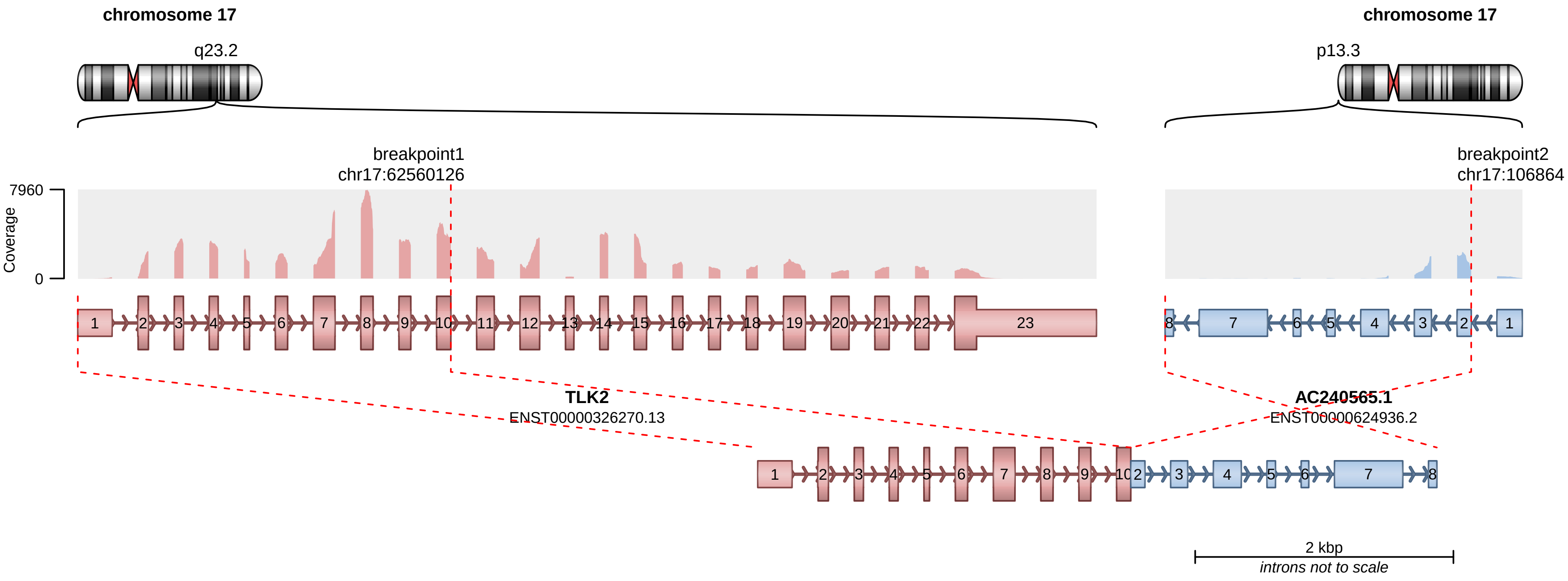


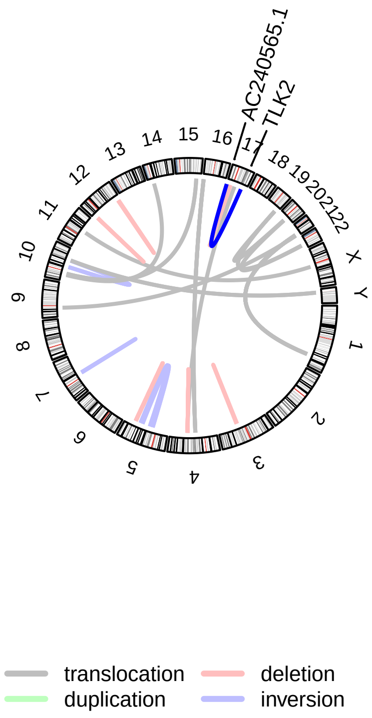




SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

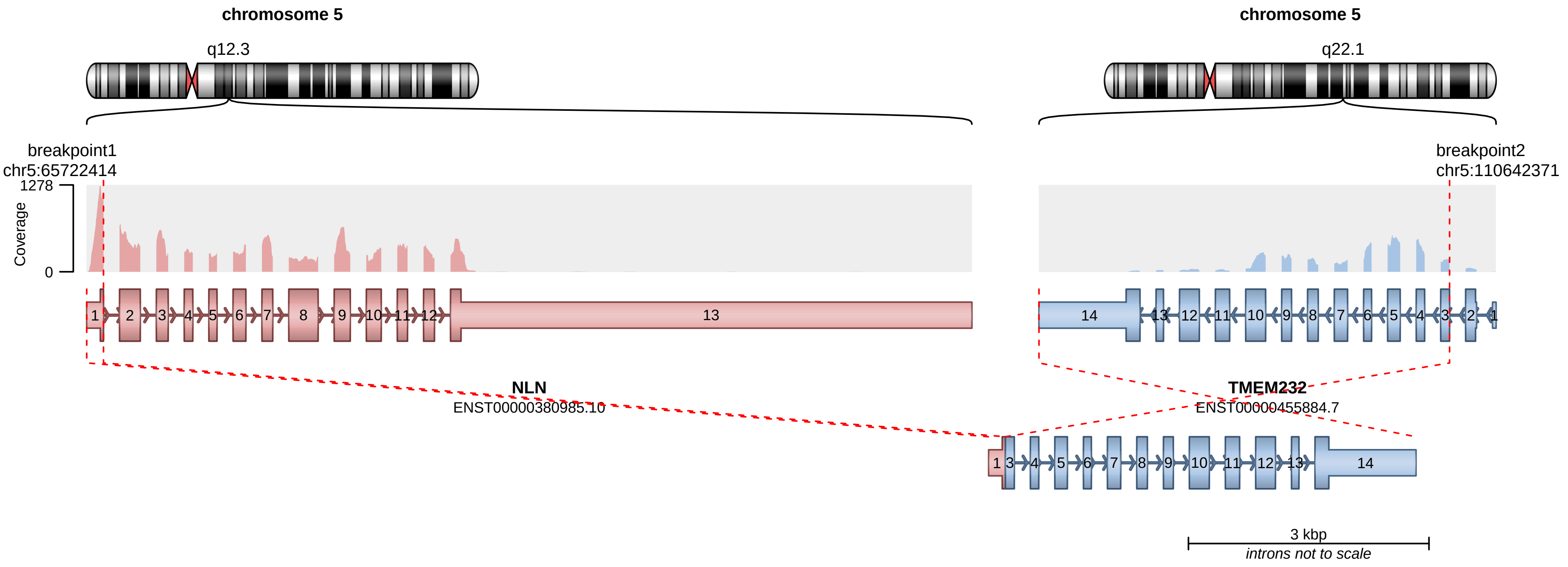


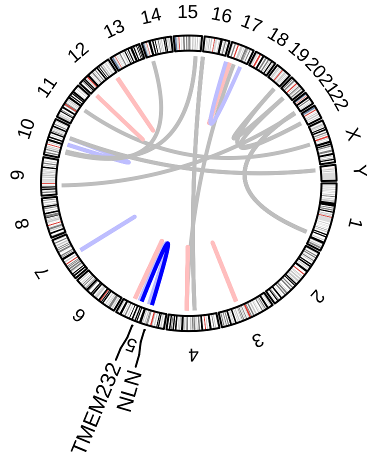


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 84
Discordant mates = 0

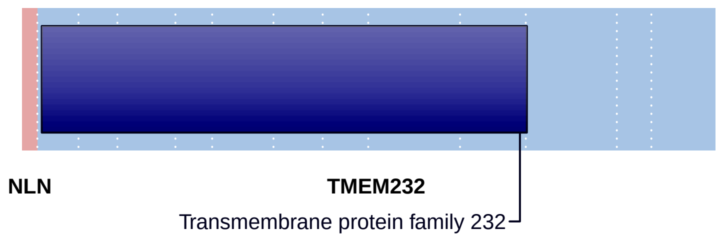




— translocation — deletion
— duplication — inversion

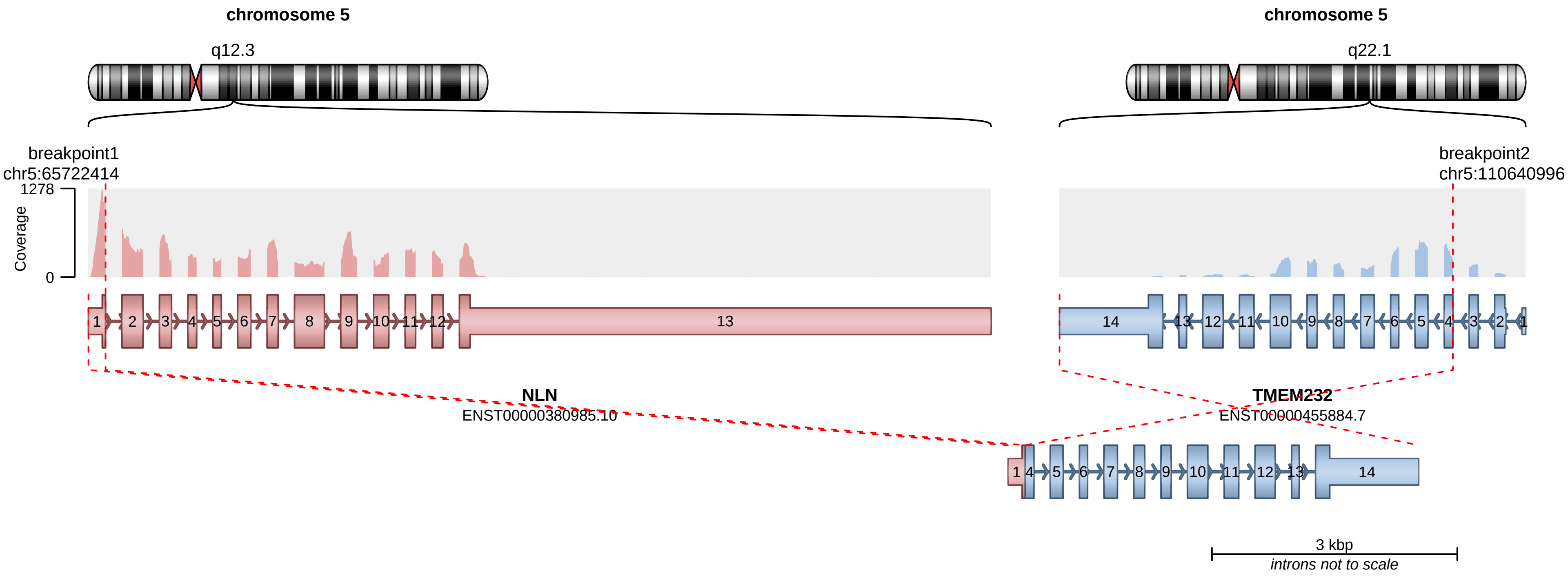
RETAINED PROTEIN DOMAINS

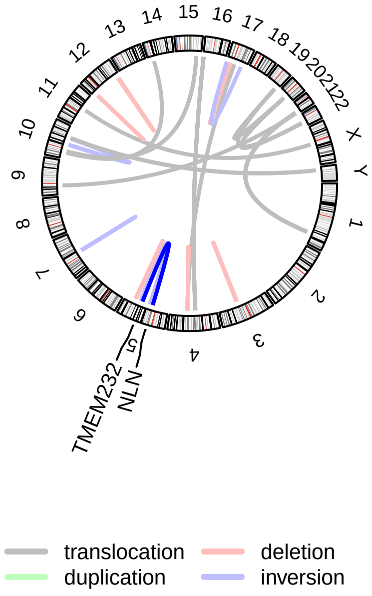
reading frame unclear



SUPPORTING READ COUNT

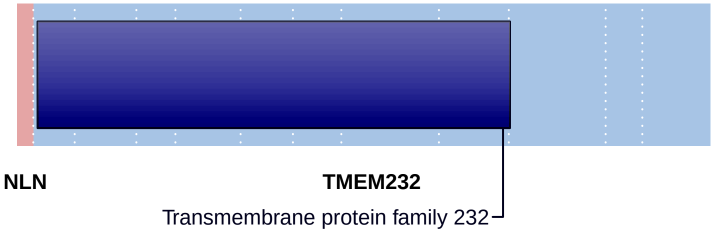
Split reads = 72
Discordant mates = 4





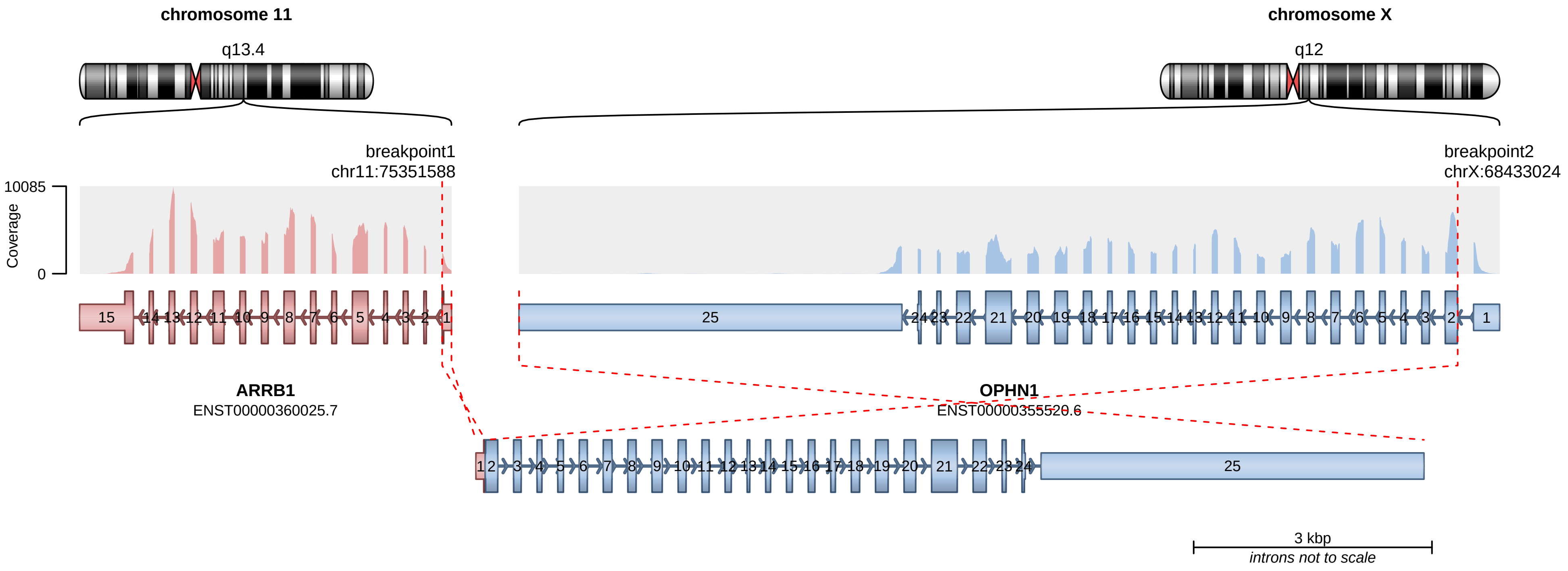
RETAINED PROTEIN DOMAINS

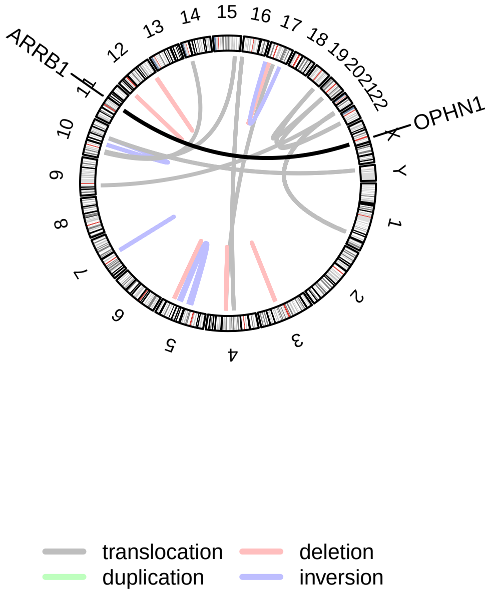
reading frame unclear

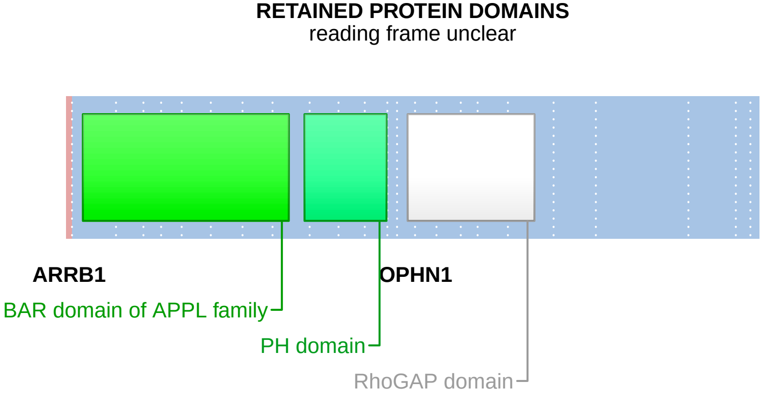


SUPPORTING READ COUNT

Split reads = 52
Discordant mates = 1

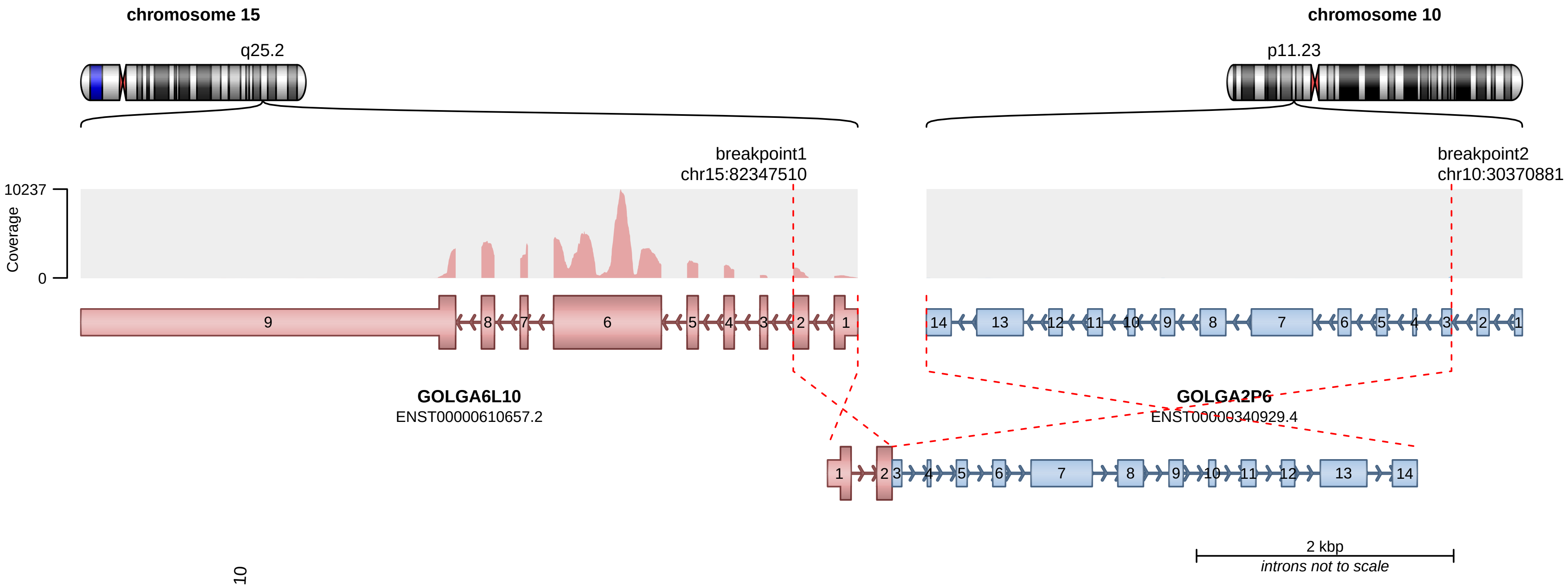


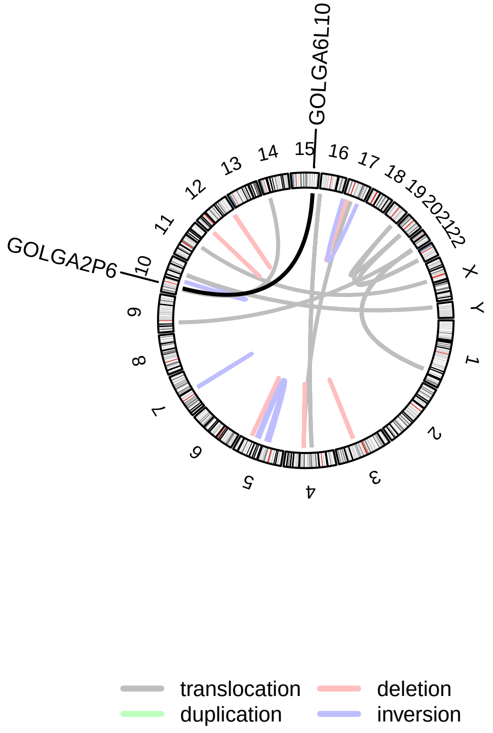




SUPPORTING READ COUNT

Split reads = 55
Discordant mates = 0

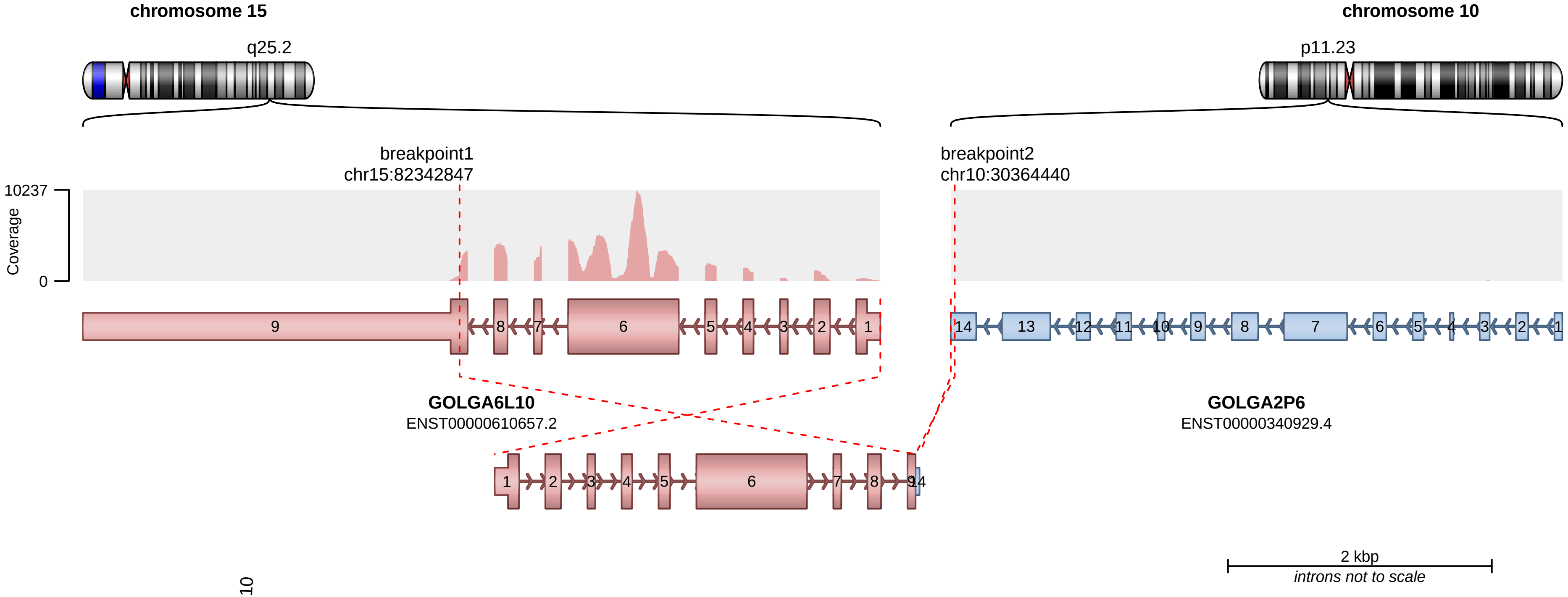


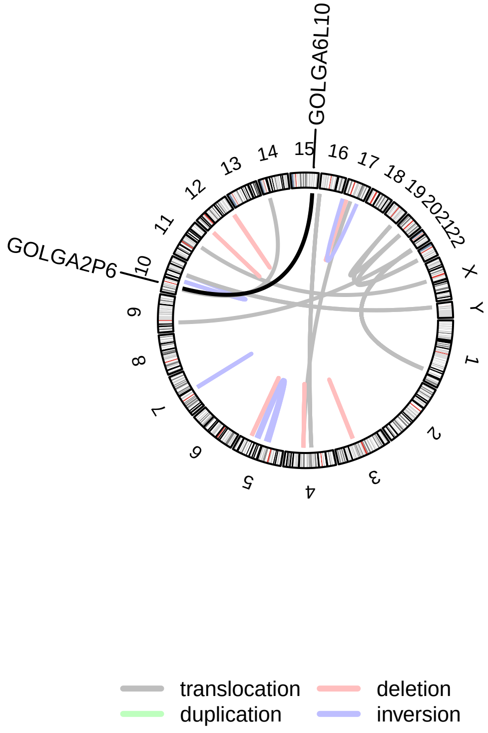


No protein domains retained in fusion.

SUPPORTING READ COUNT

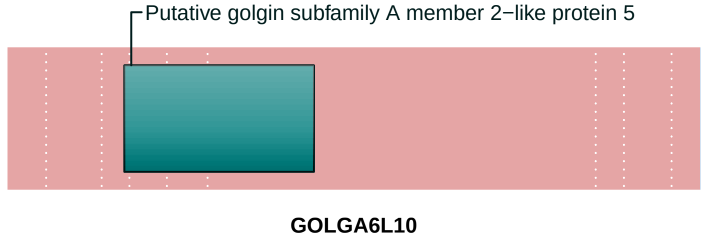
Split reads = 43
Discordant mates = 0





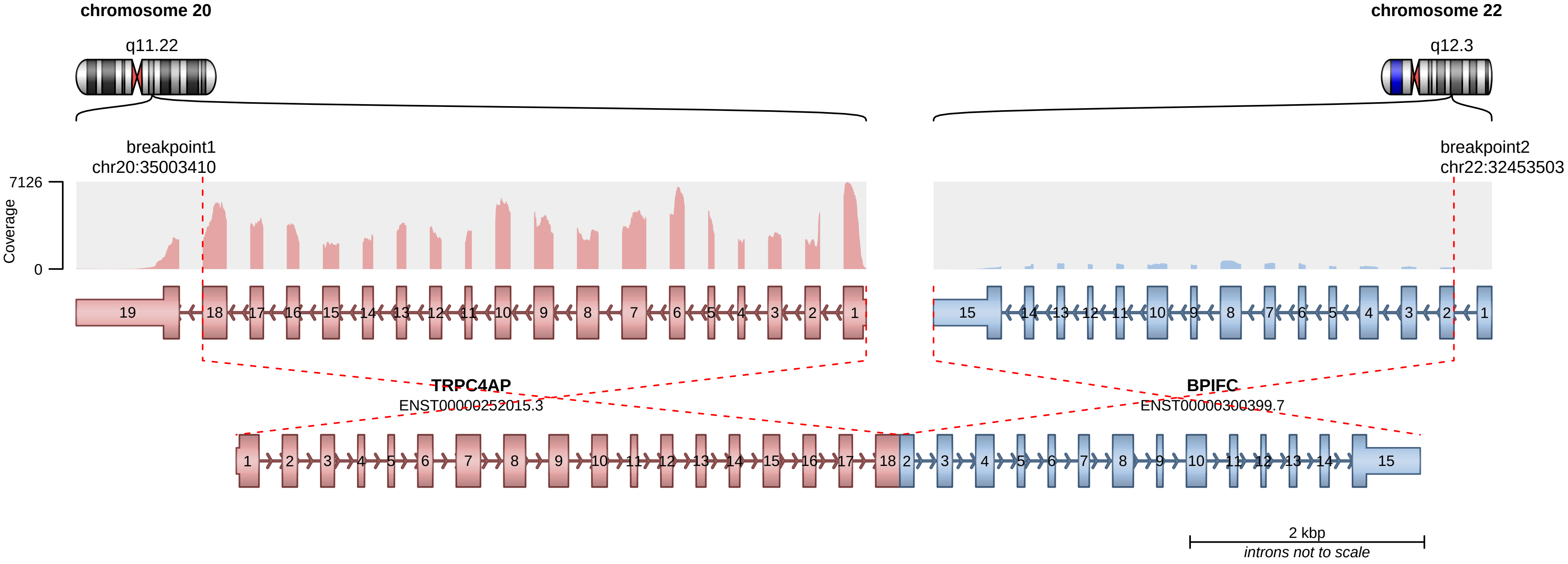
RETAINED PROTEIN DOMAINS

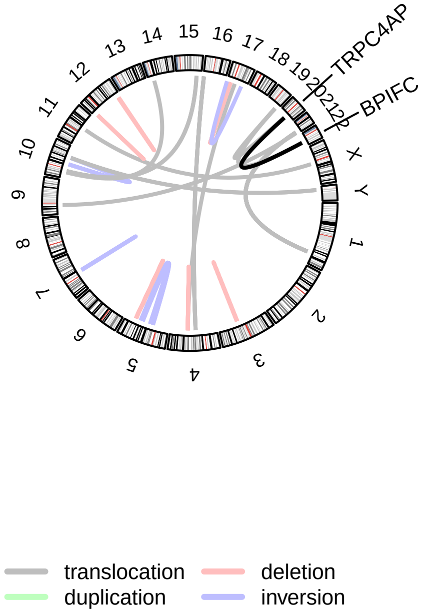
reading frame unclear



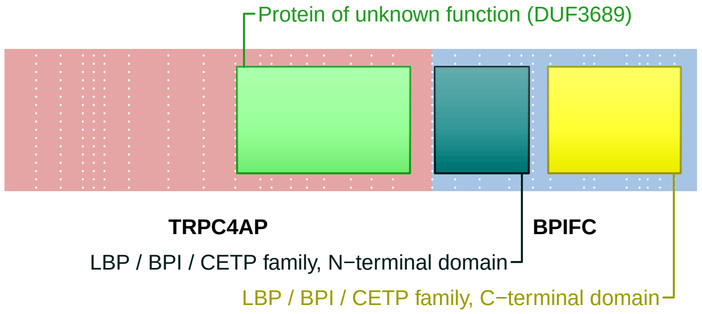
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0



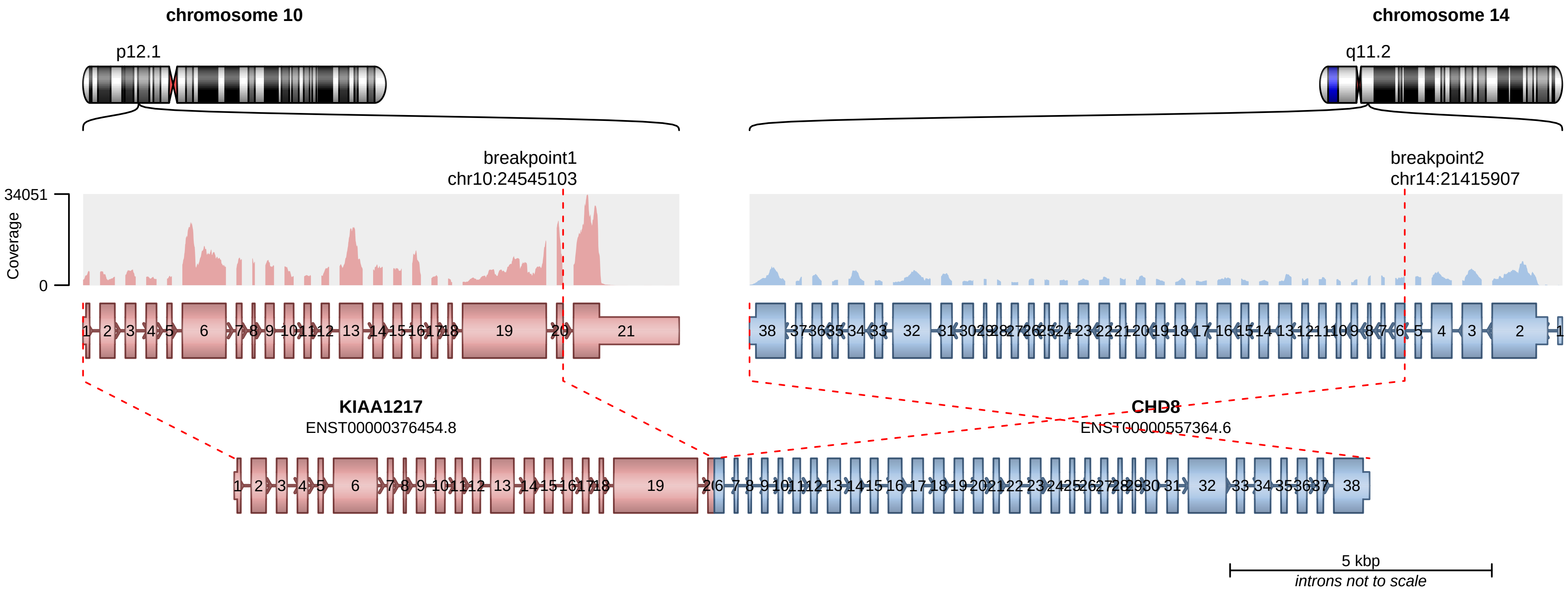


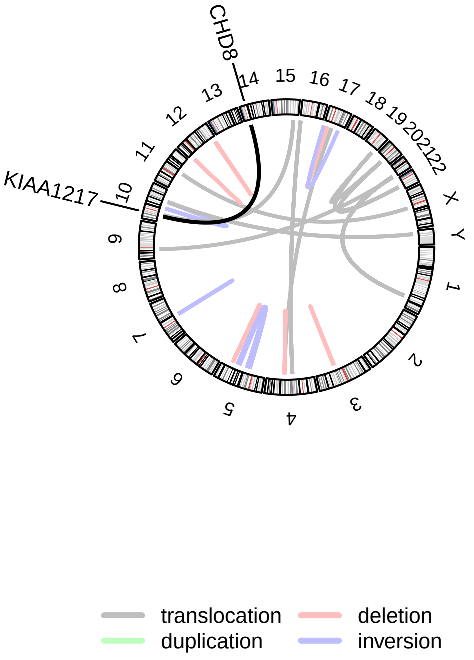
RETAINED PROTEIN DOMAINS
reading frame unclear

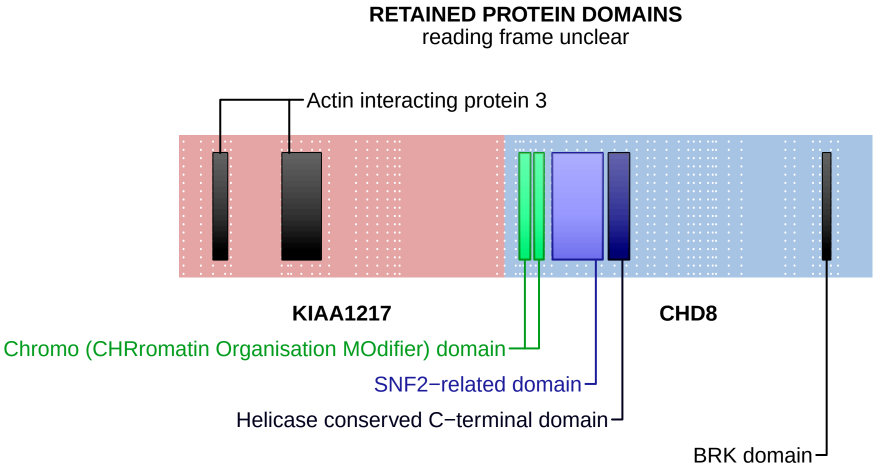


SUPPORTING READ COUNT

Split reads = 26
Discordant mates = 0

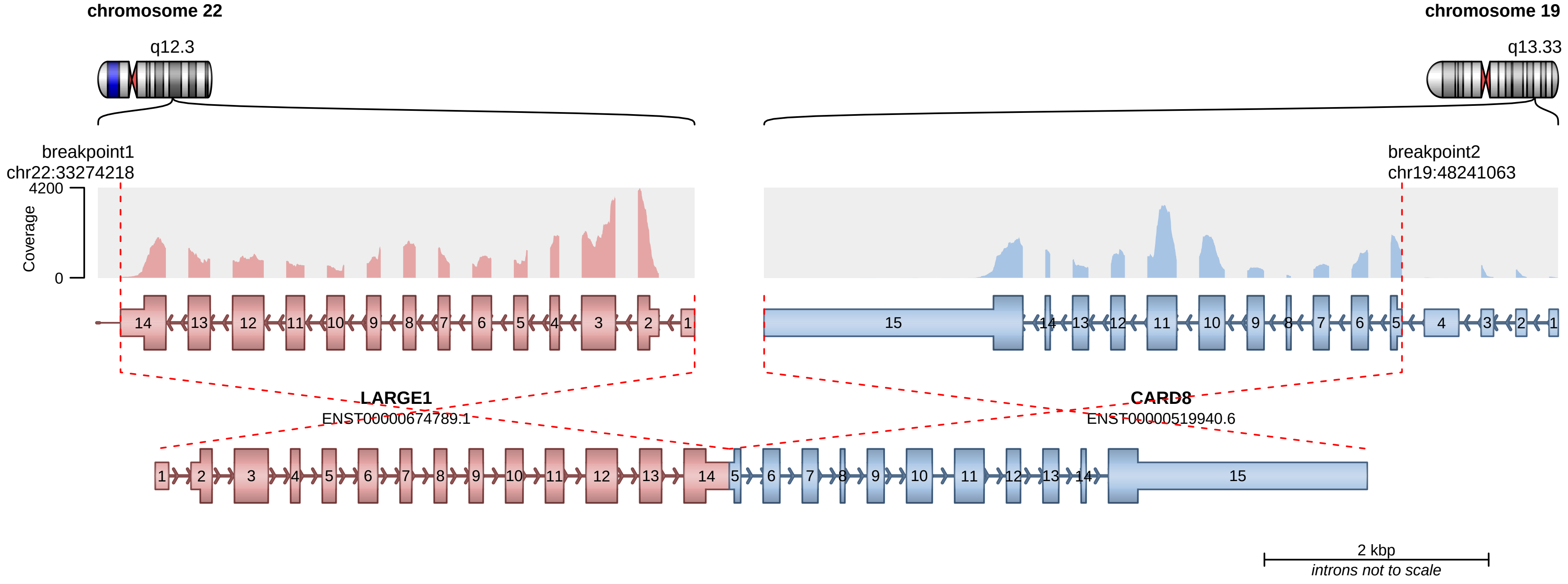


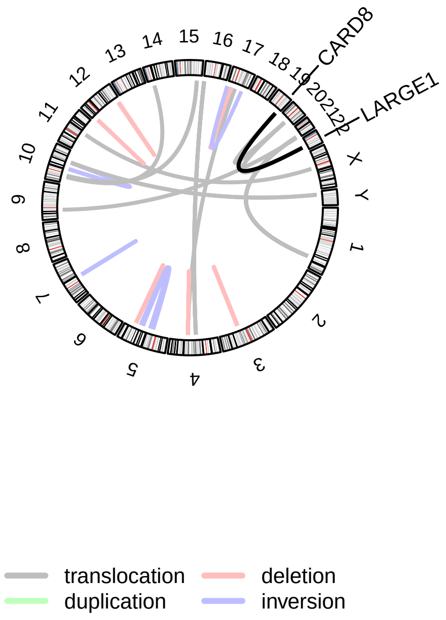




SUPPORTING READ COUNT

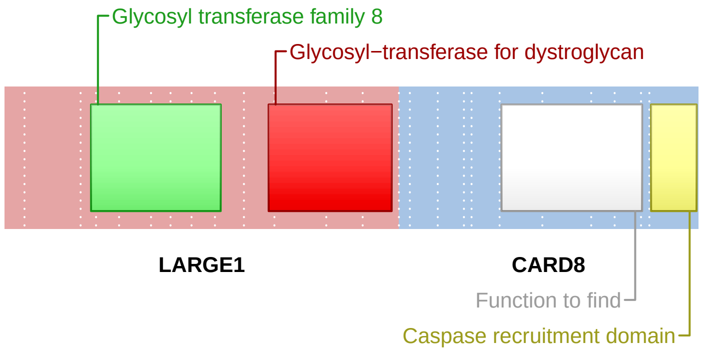
Split reads = 22
Discordant mates = 0





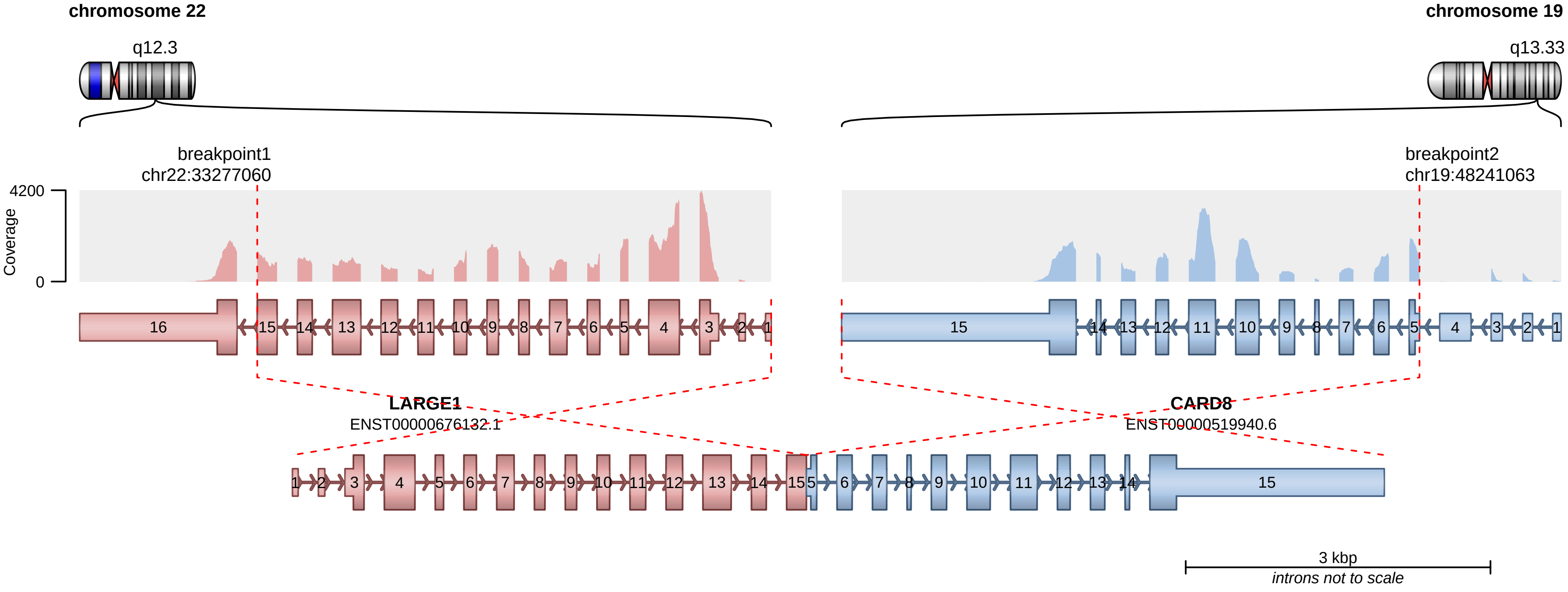
RETAINED PROTEIN DOMAINS

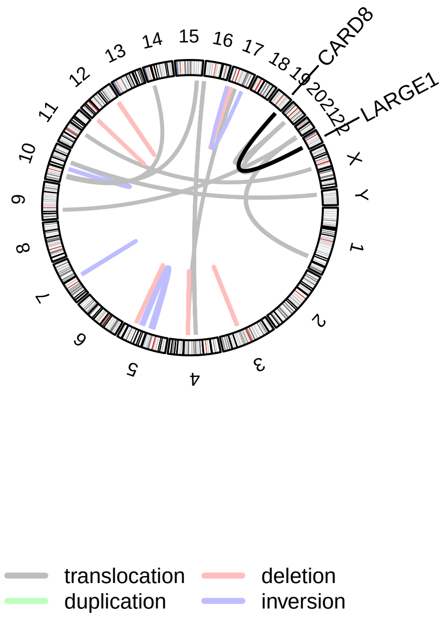
reading frame unclear



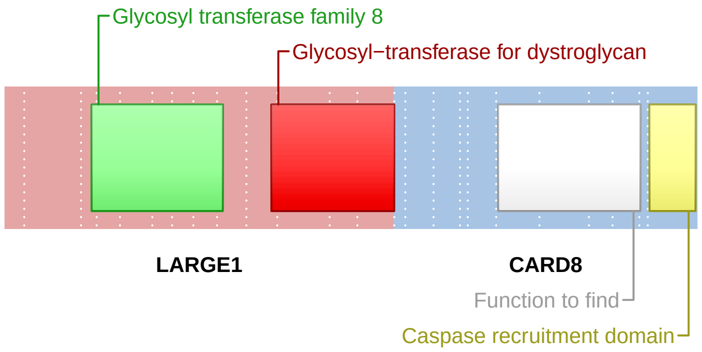
SUPPORTING READ COUNT

Split reads = 16
Discordant mates = 0



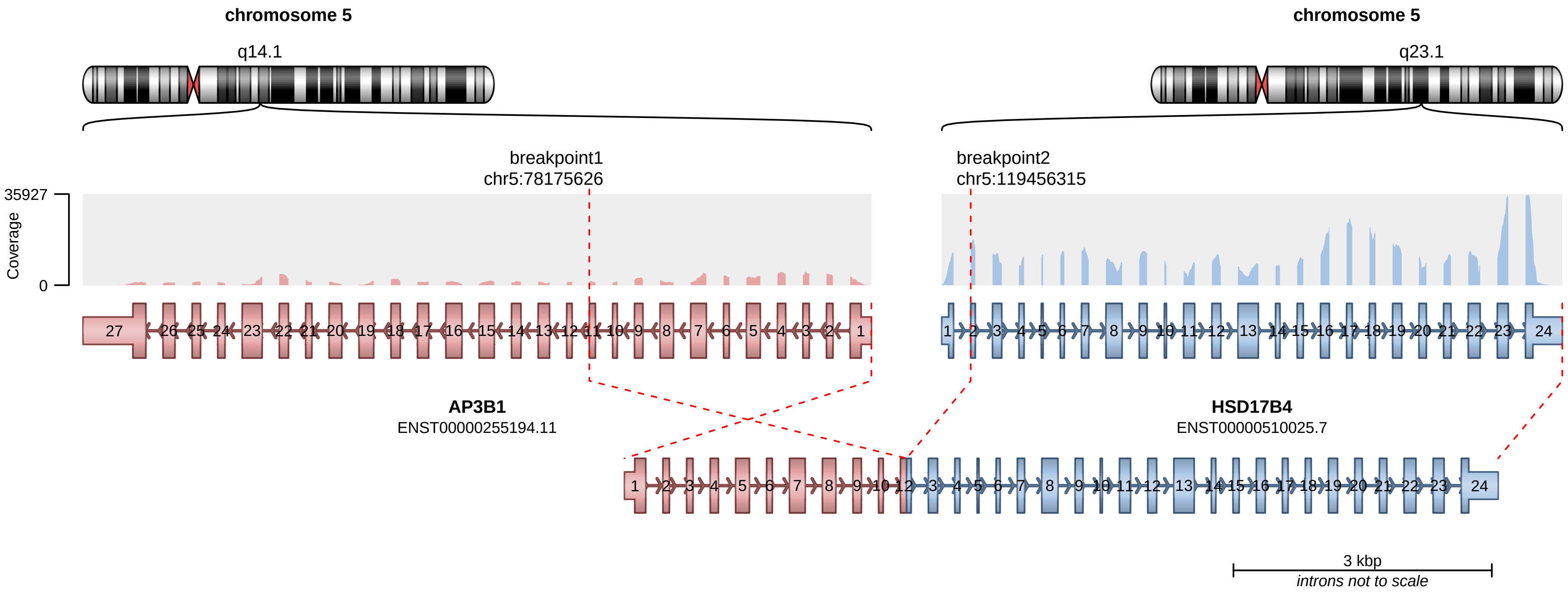


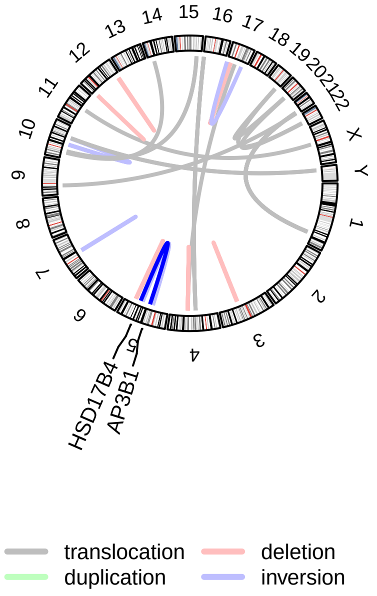
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

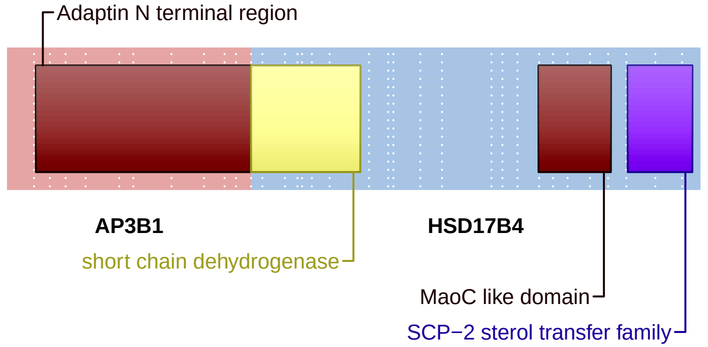
Split reads = 2
Discordant mates = 0





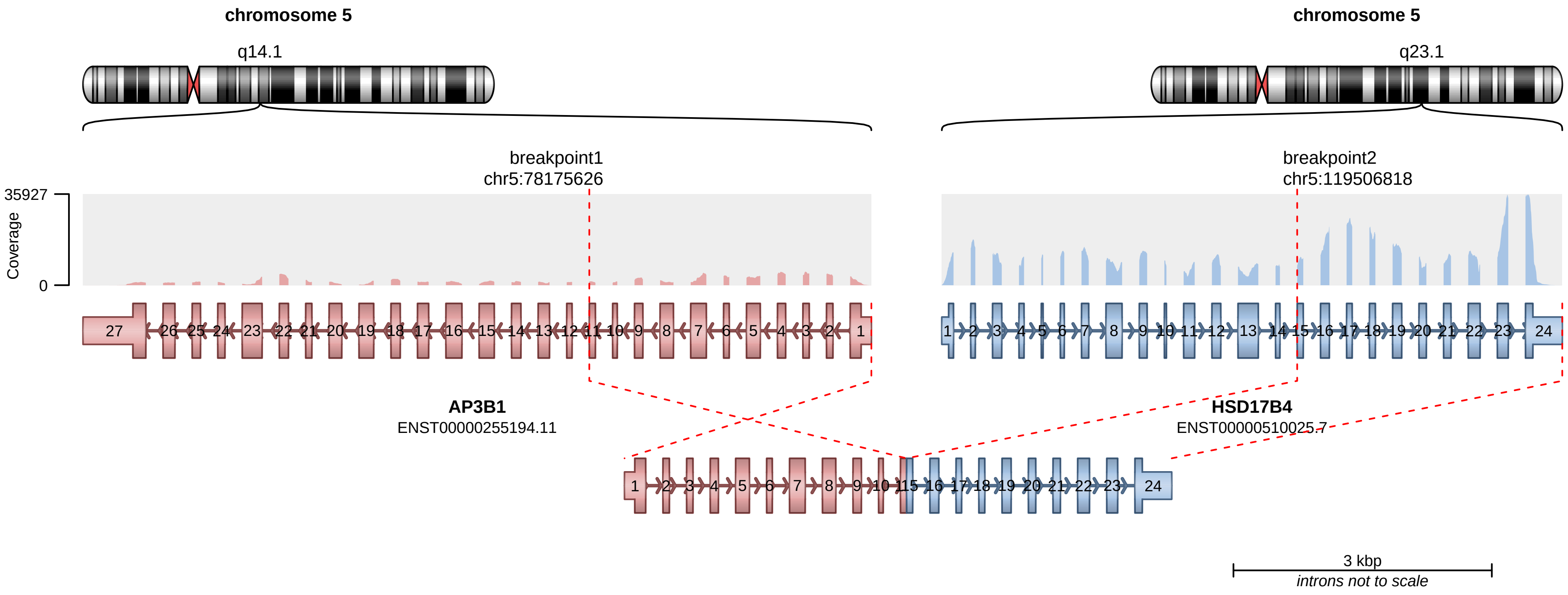
RETAINED PROTEIN DOMAINS

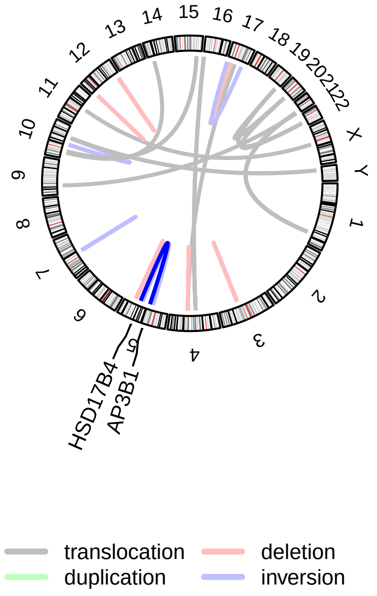
reading frame unclear

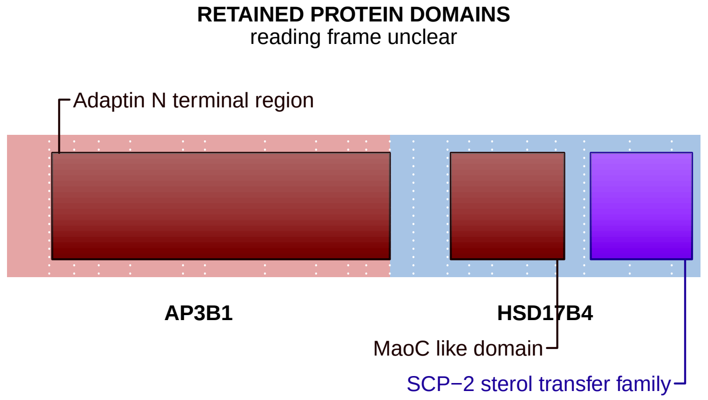


SUPPORTING READ COUNT

Split reads = 15
Discordant mates = 0

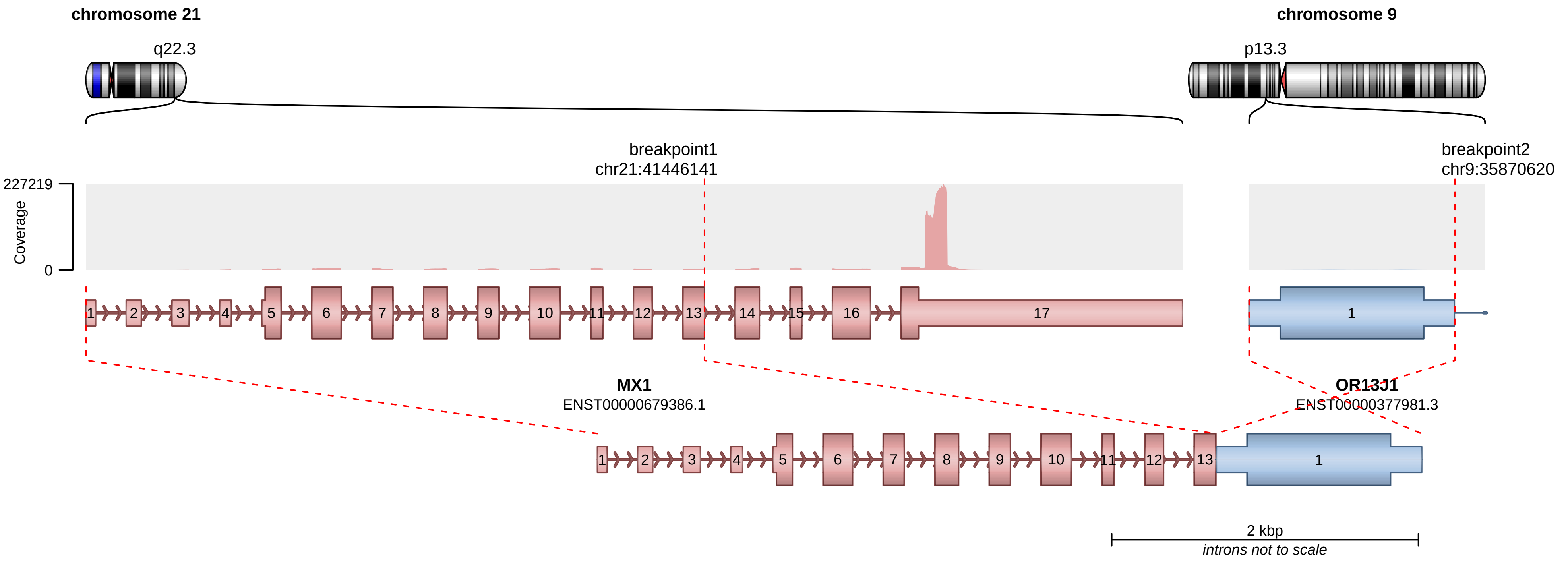


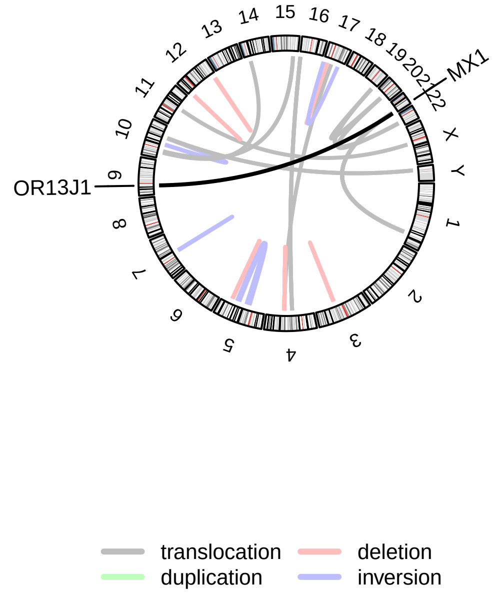




SUPPORTING READ COUNT

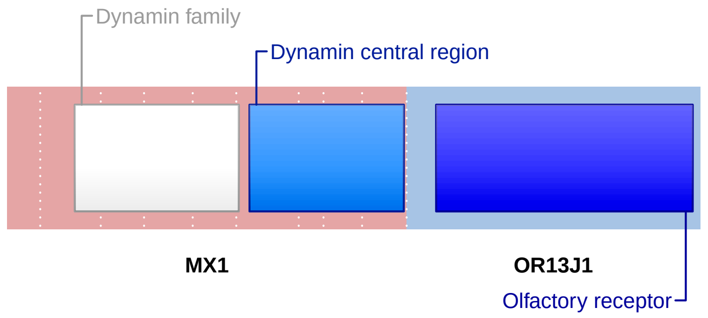
Split reads = 1
Discordant mates = 0





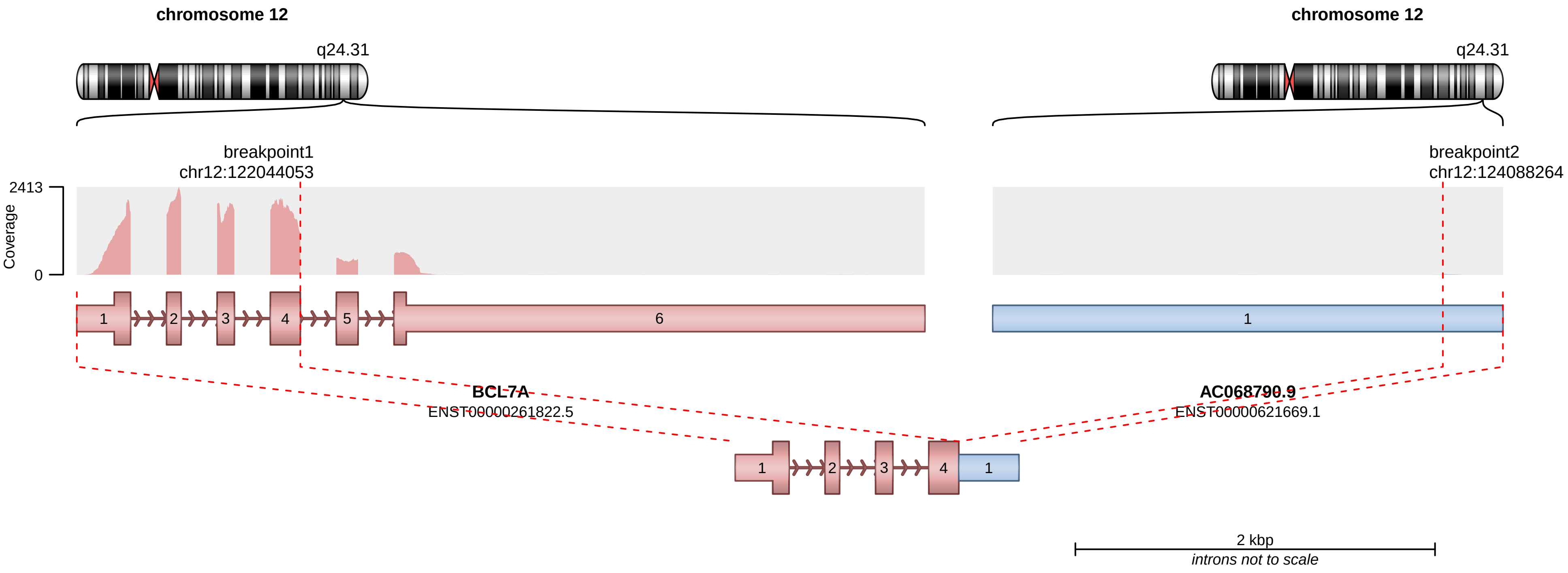
RETAINED PROTEIN DOMAINS

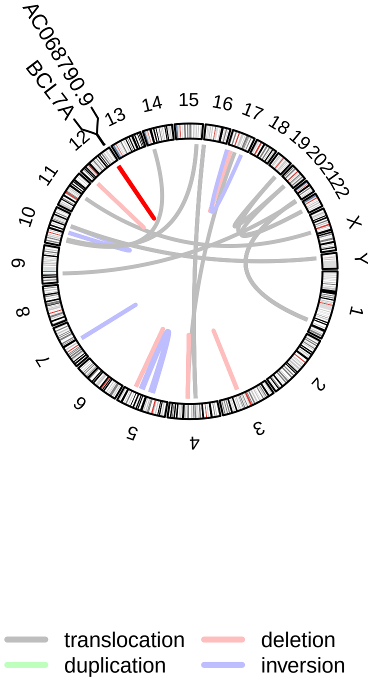
reading frame unclear



SUPPORTING READ COUNT

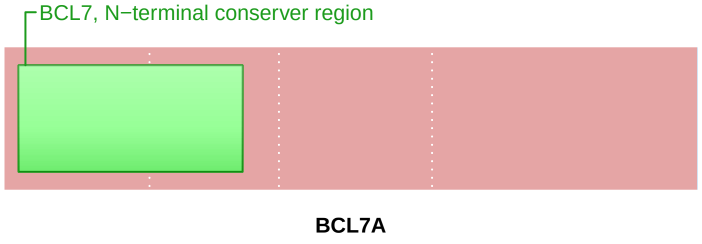
Split reads = 14
Discordant mates = 0





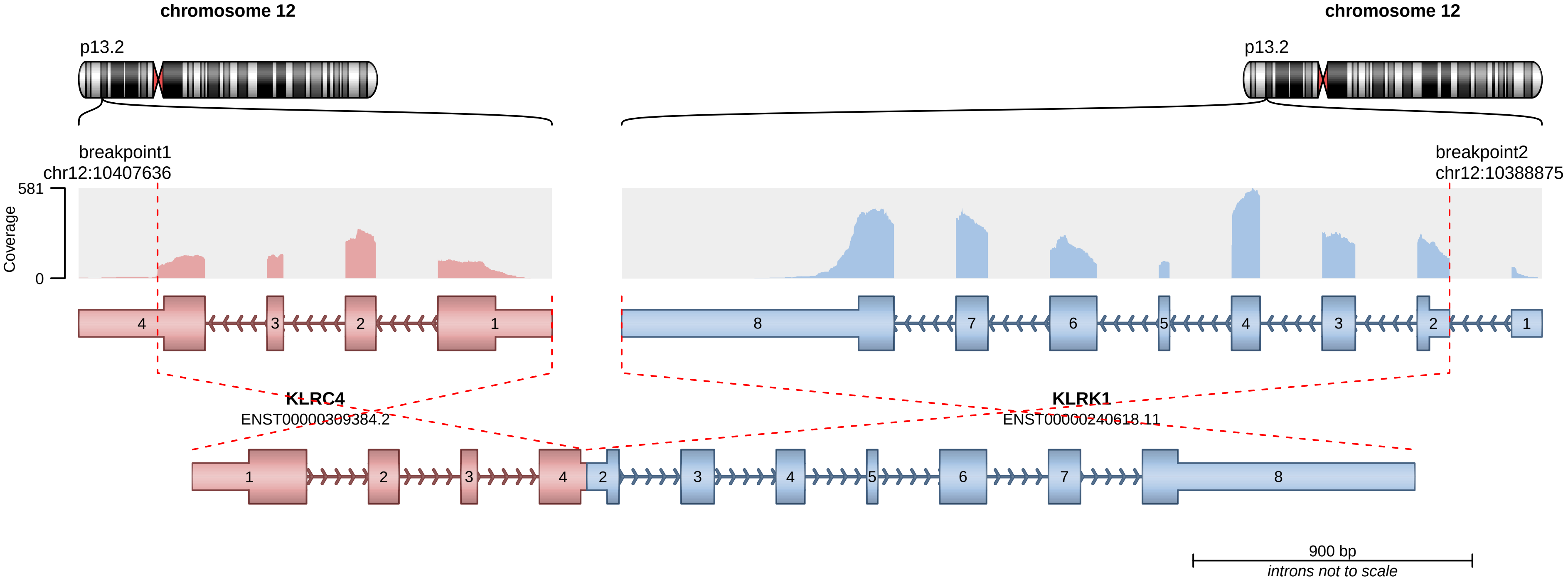
RETAINED PROTEIN DOMAINS

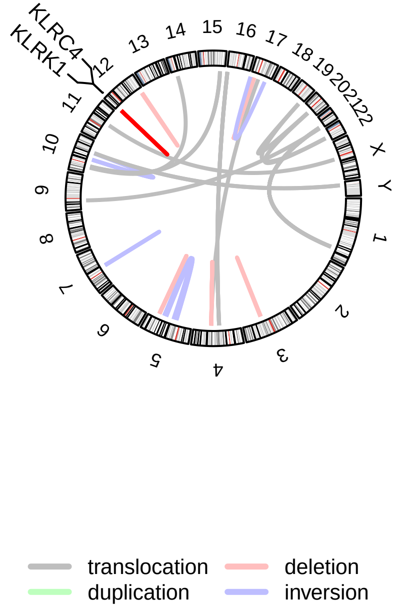
reading frame unclear



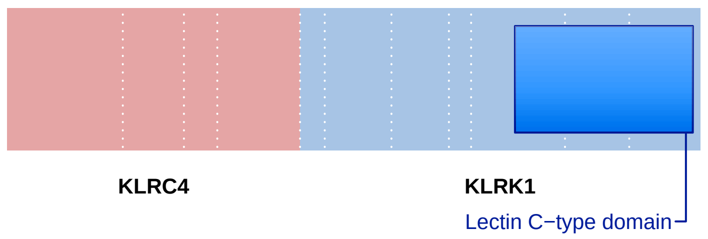
SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 0



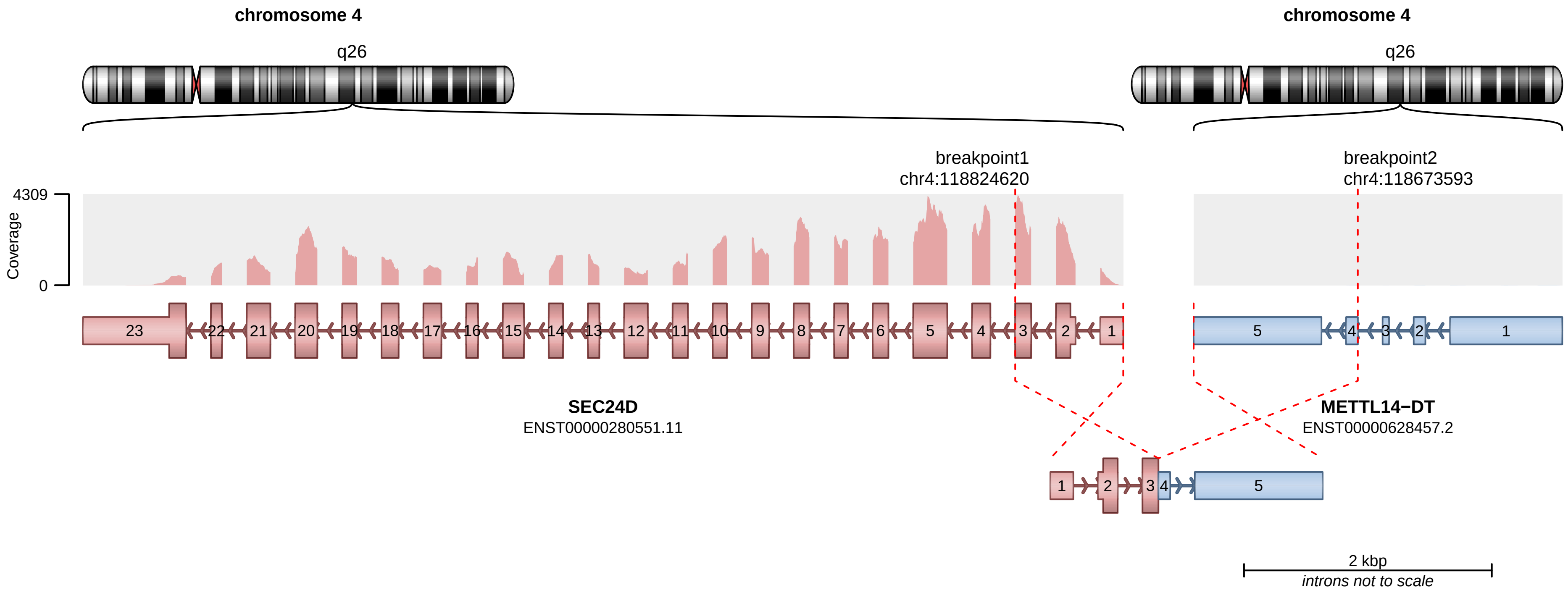


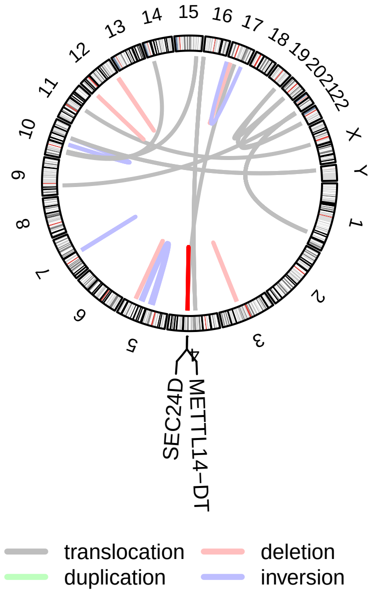
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 0

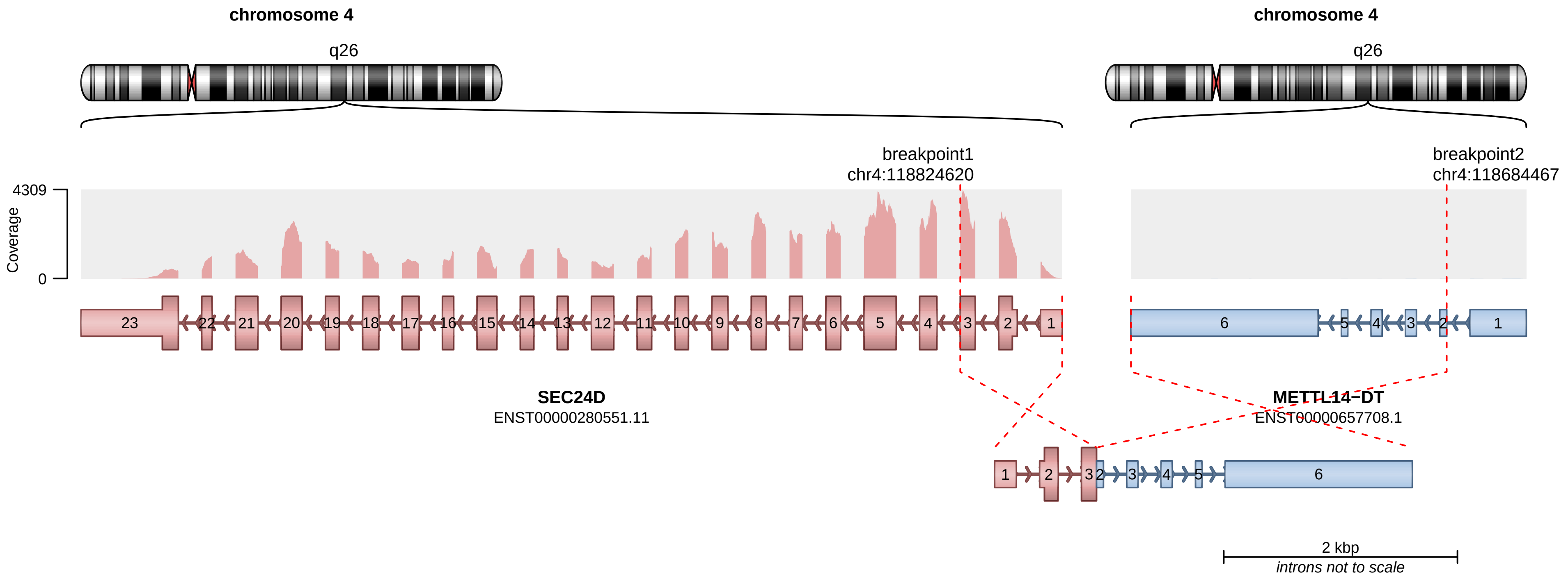


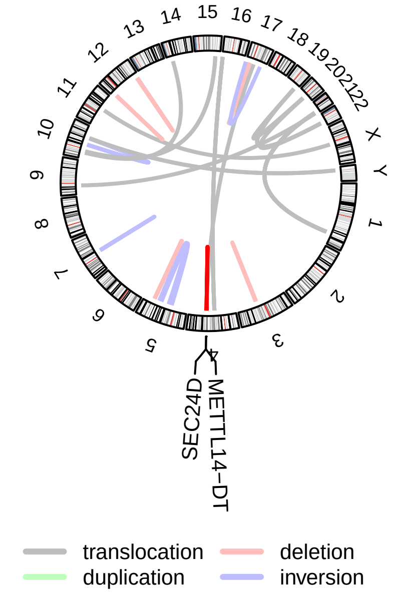


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 0

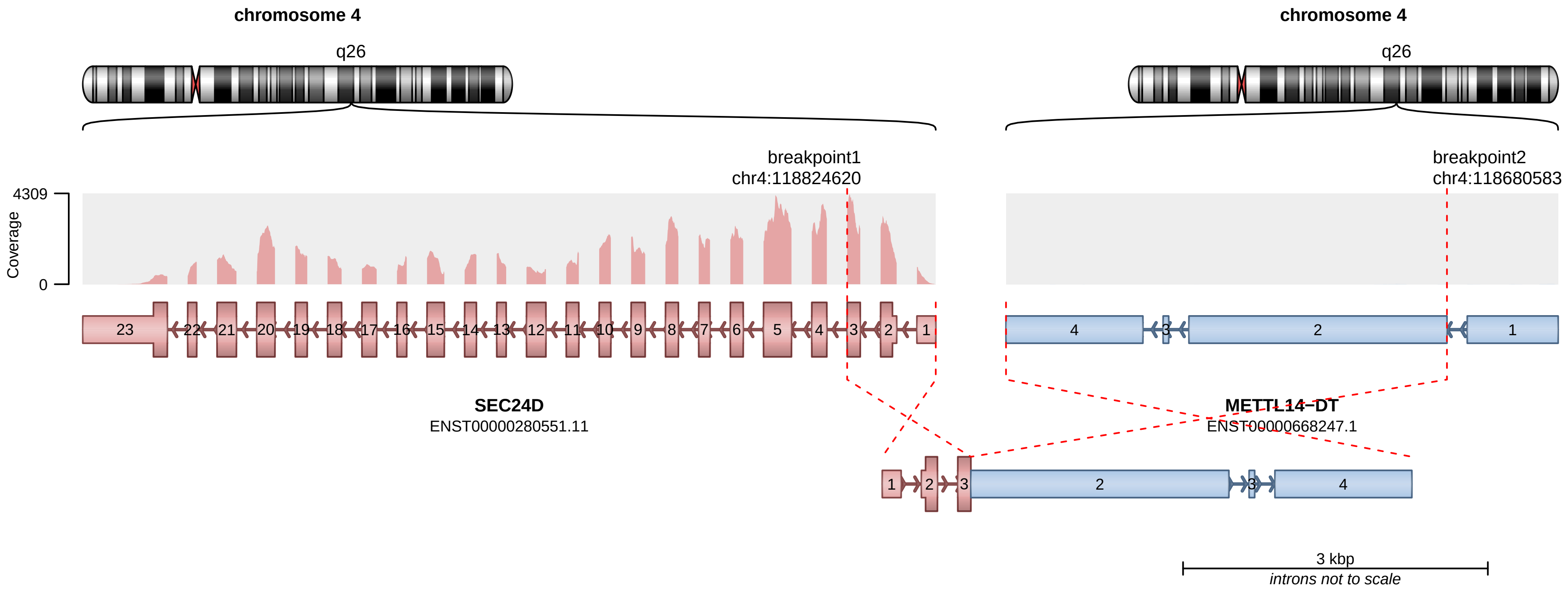


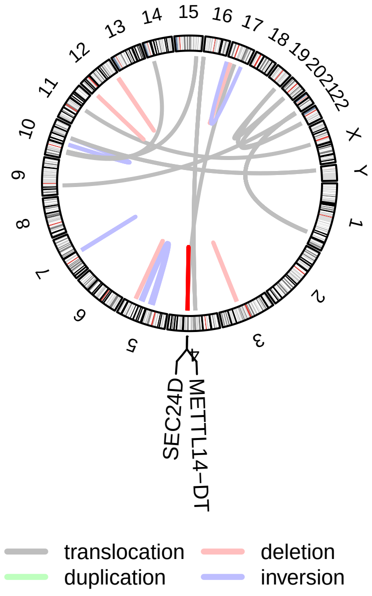


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

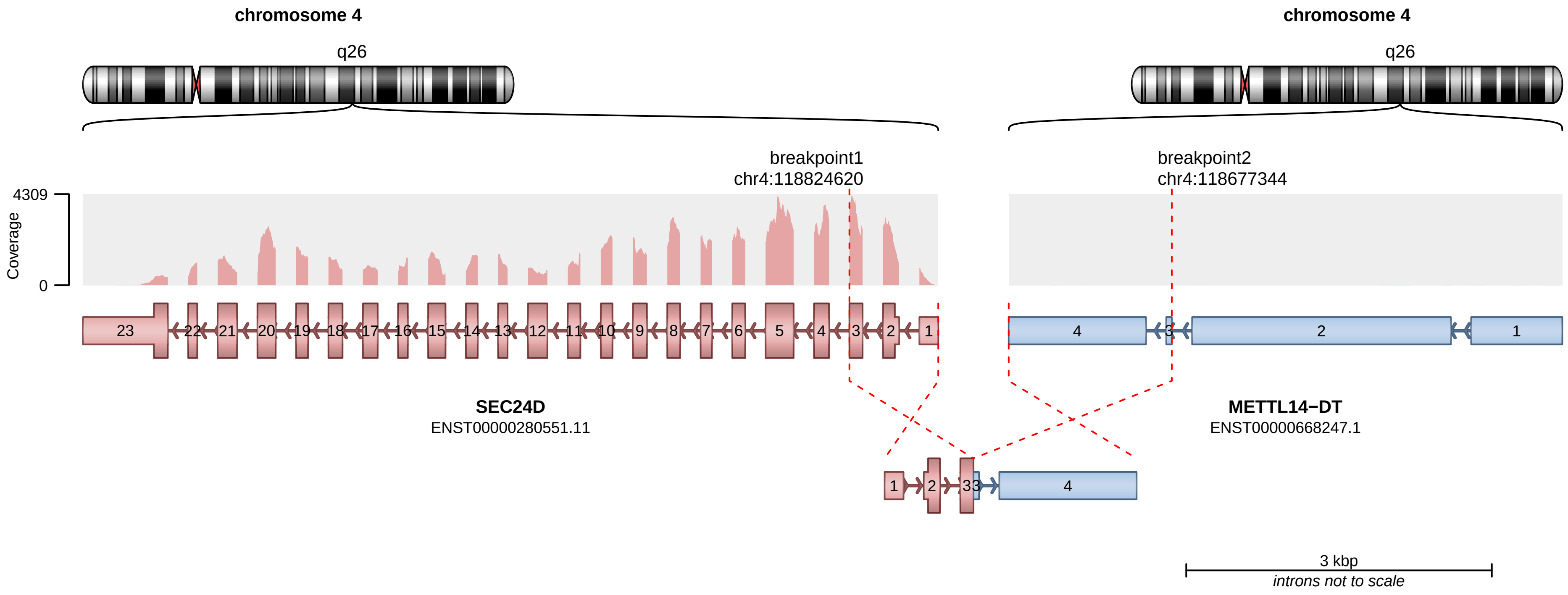


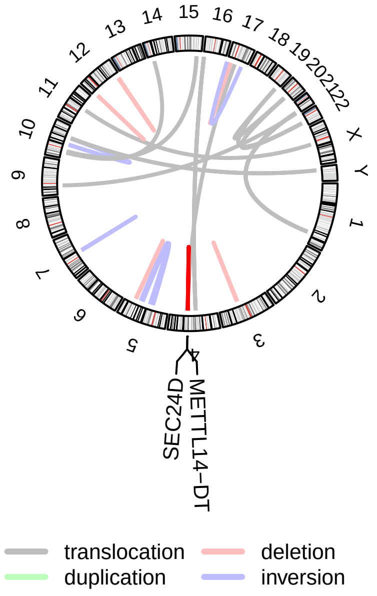


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

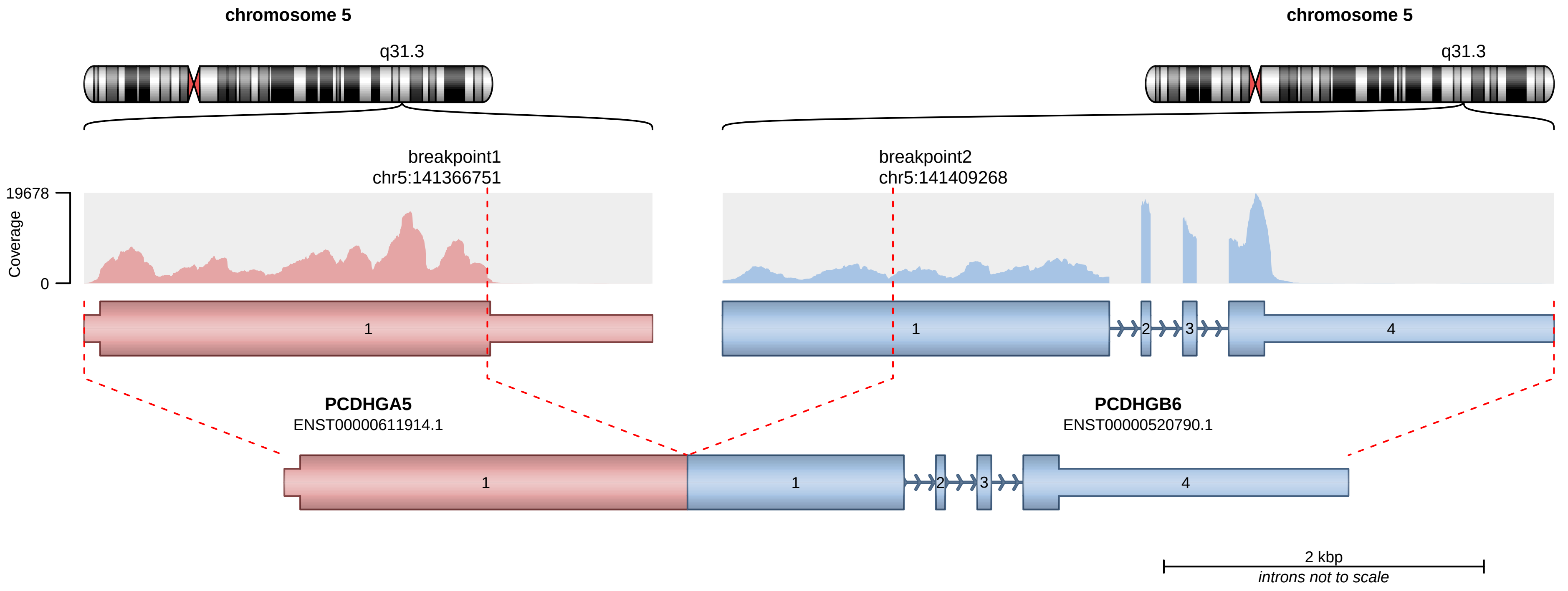


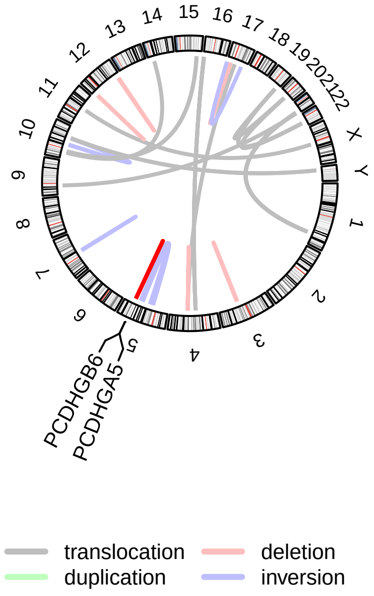


No protein domains retained in fusion.

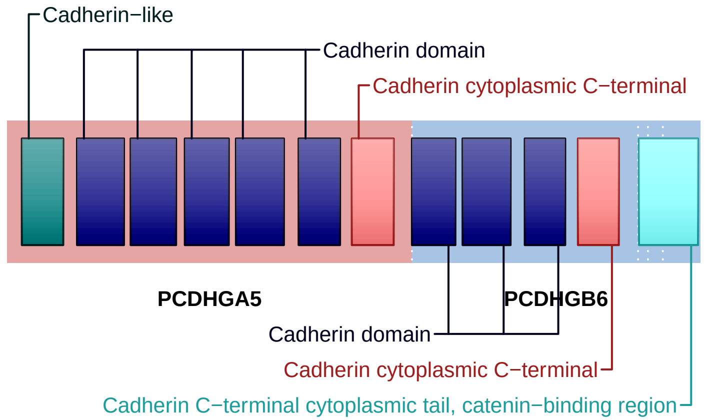
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



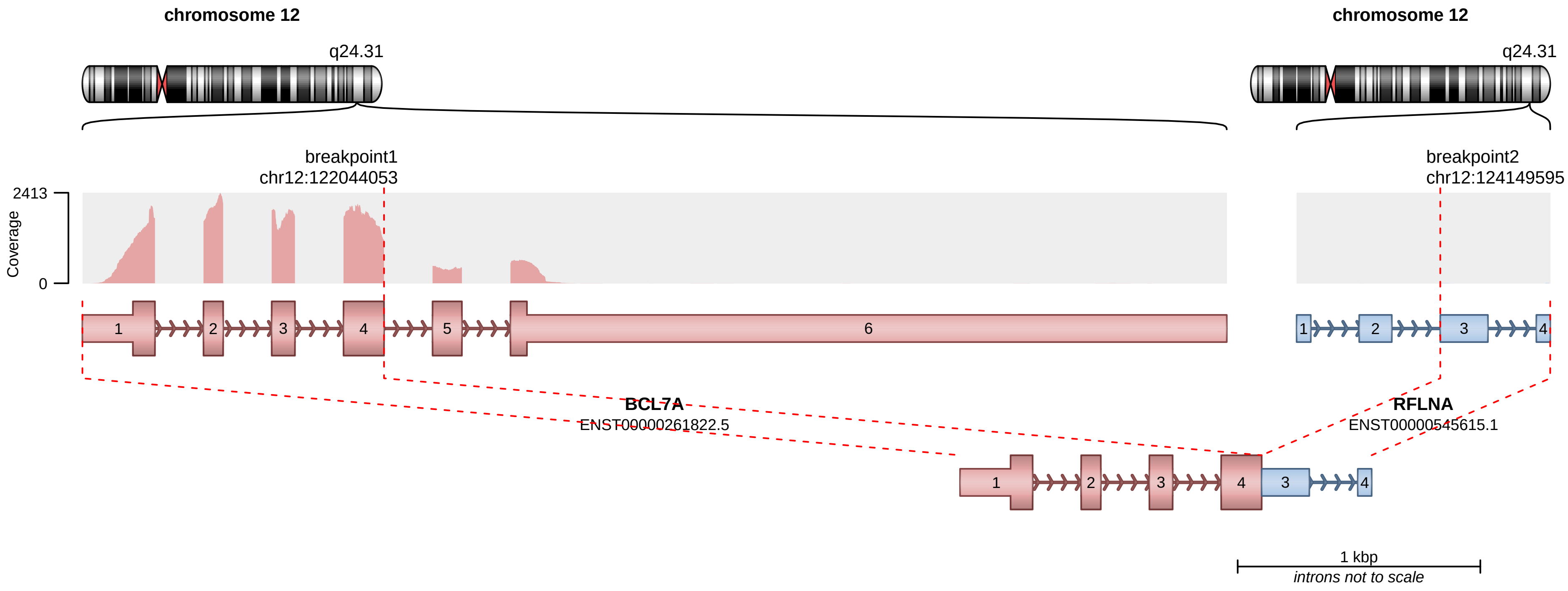


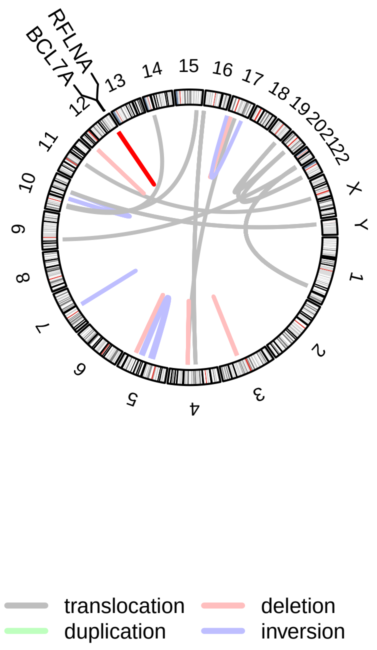
RETAINED PROTEIN DOMAINS
reading frame unclear



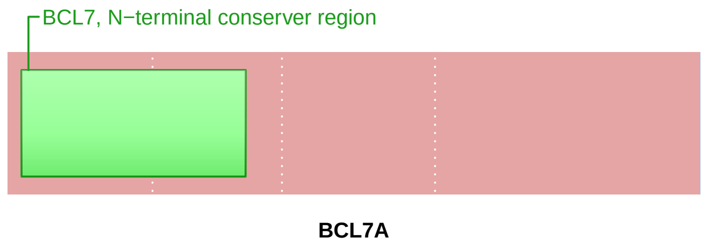
SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 0





RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0