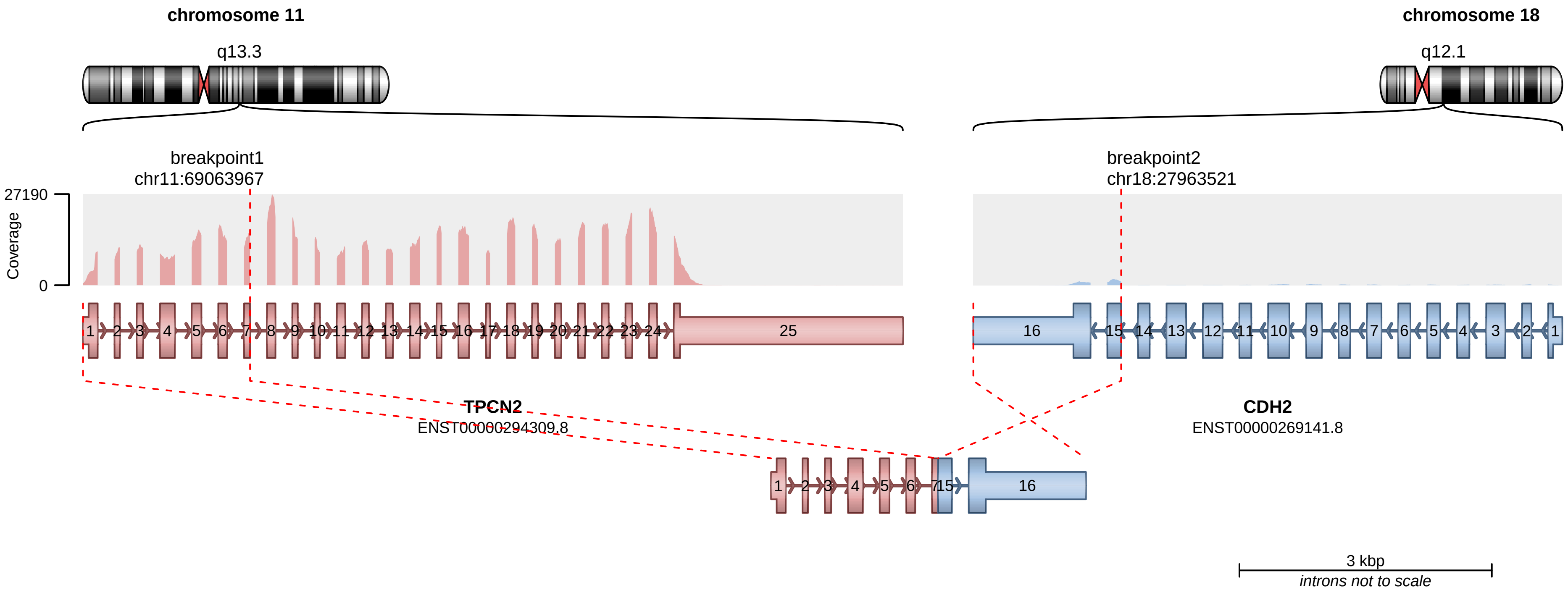
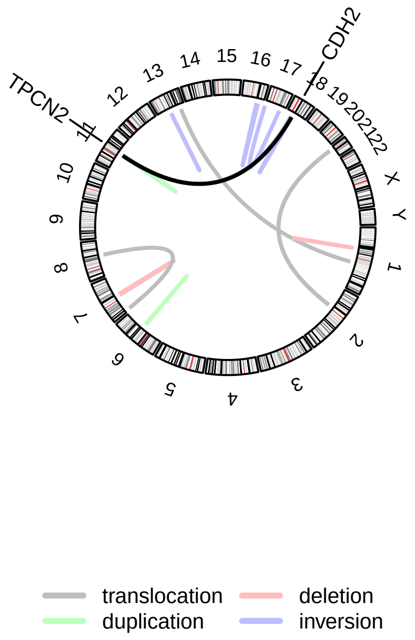
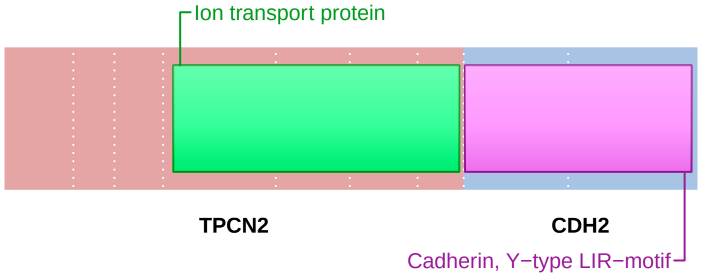


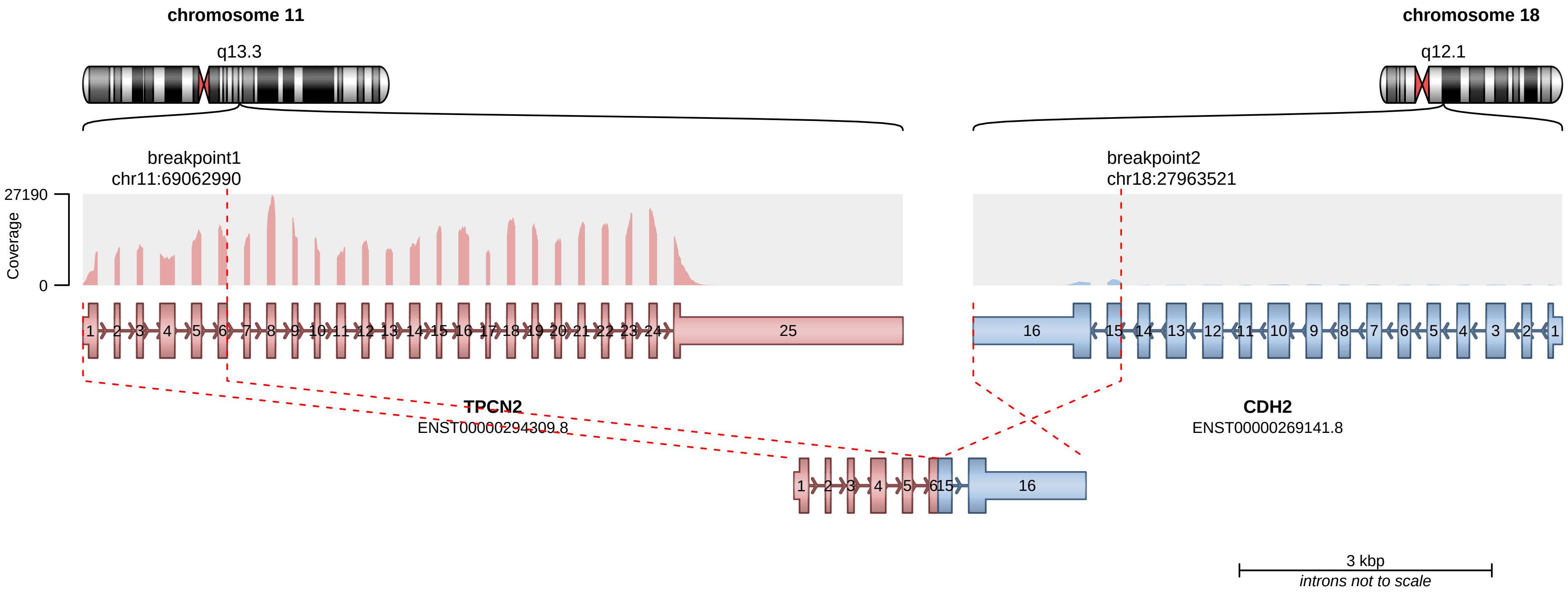


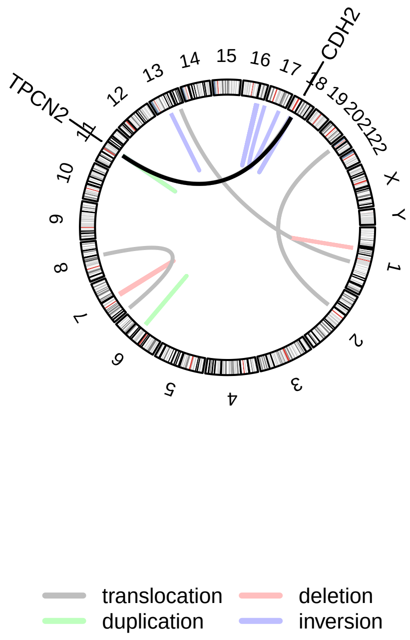
RETAINED PROTEIN DOMAINS
reading frame unclear



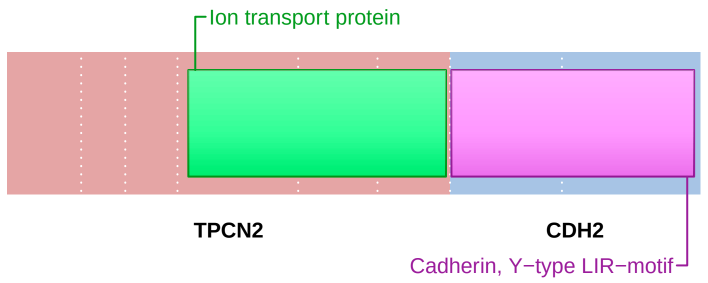
SUPPORTING READ COUNT

Split reads = 200
Discordant mates = 2



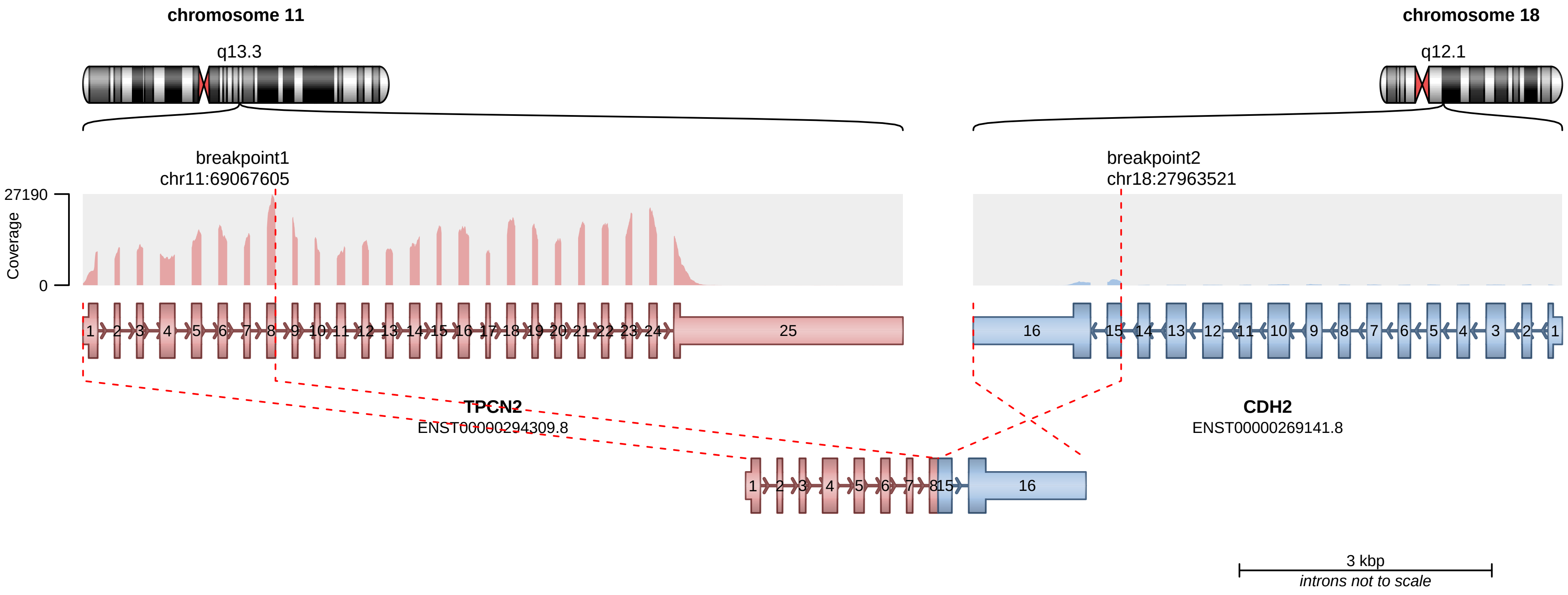


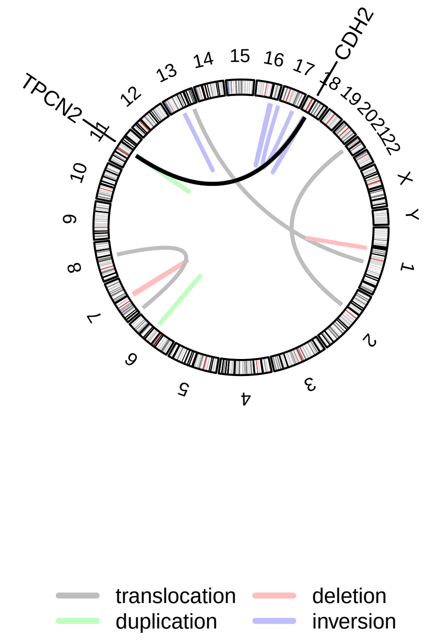
RETAINED PROTEIN DOMAINS
reading frame unclear



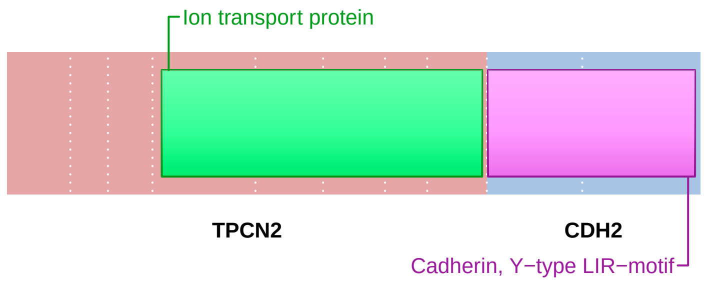
SUPPORTING READ COUNT

Split reads = 85
Discordant mates = 1



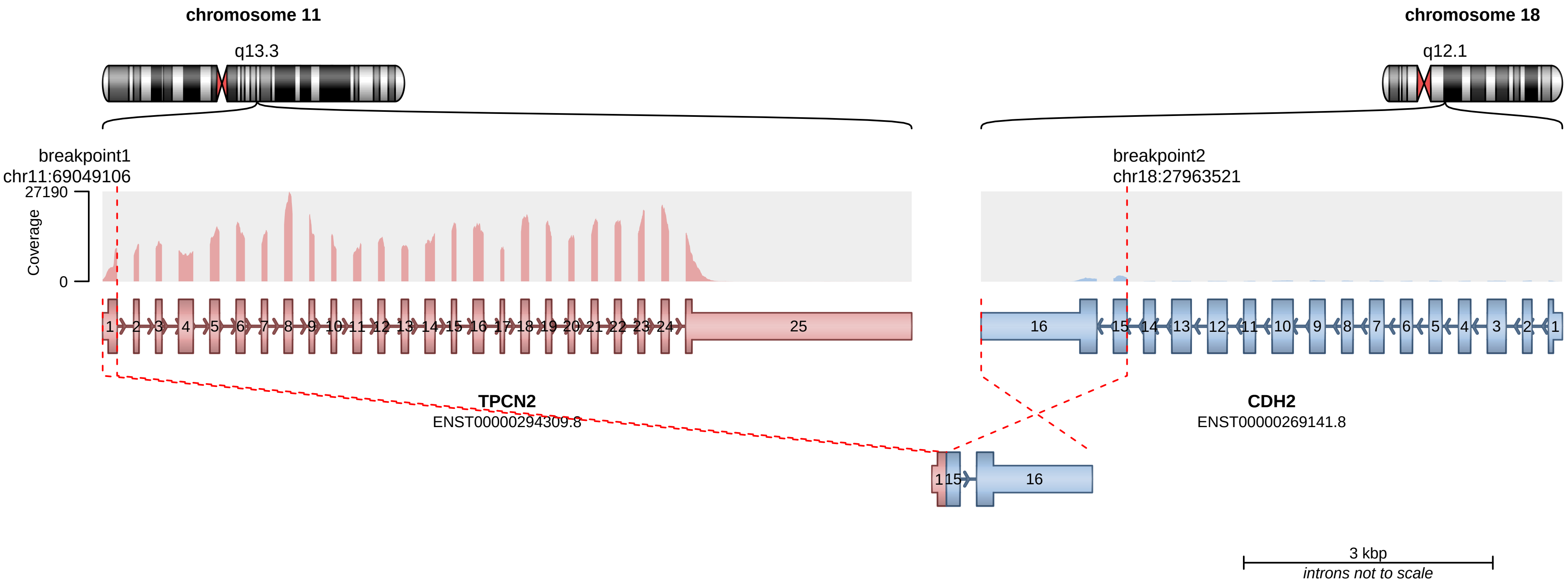


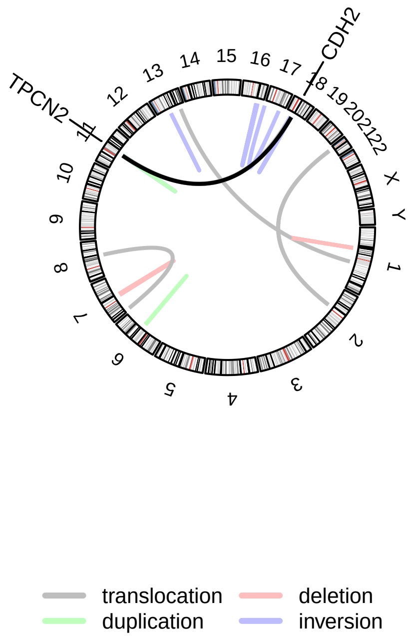
RETAINED PROTEIN DOMAINS
reading frame unclear

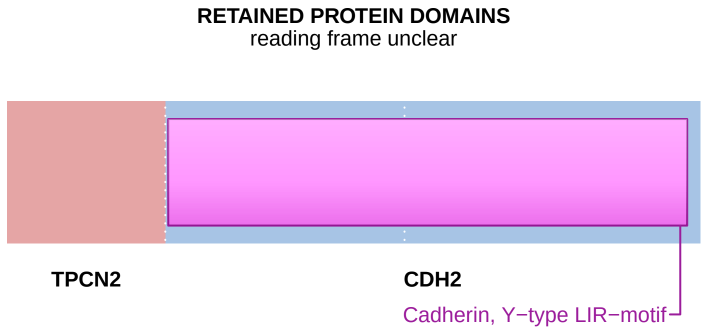


SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 2

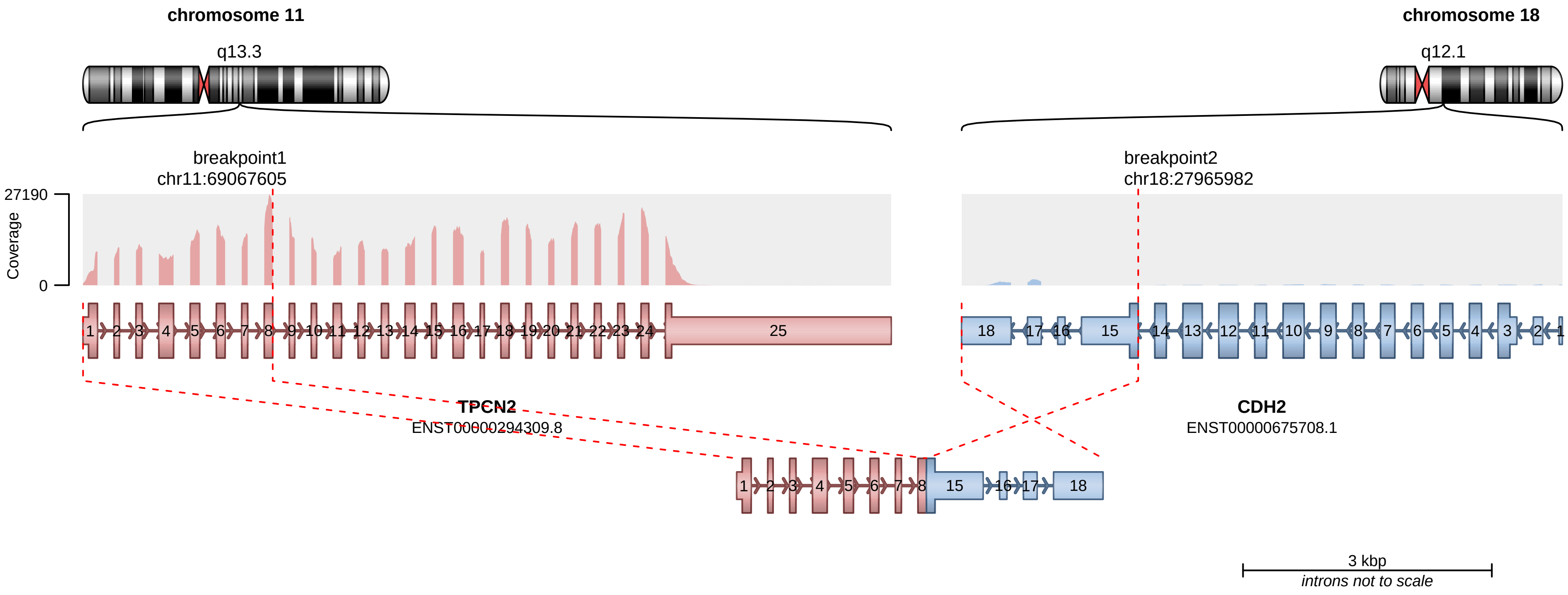


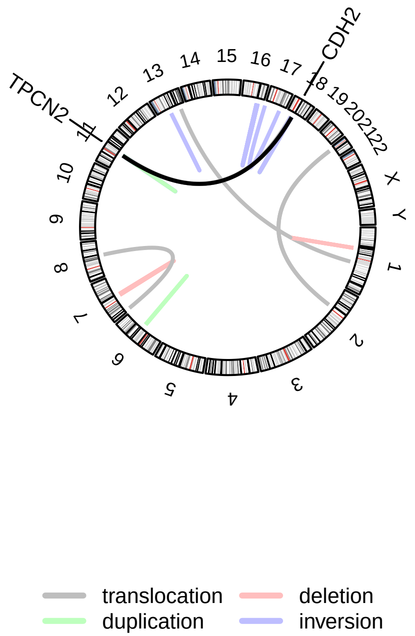




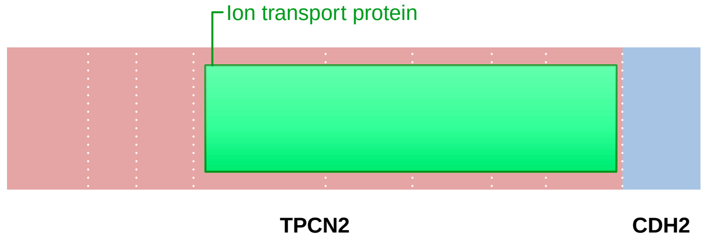
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0



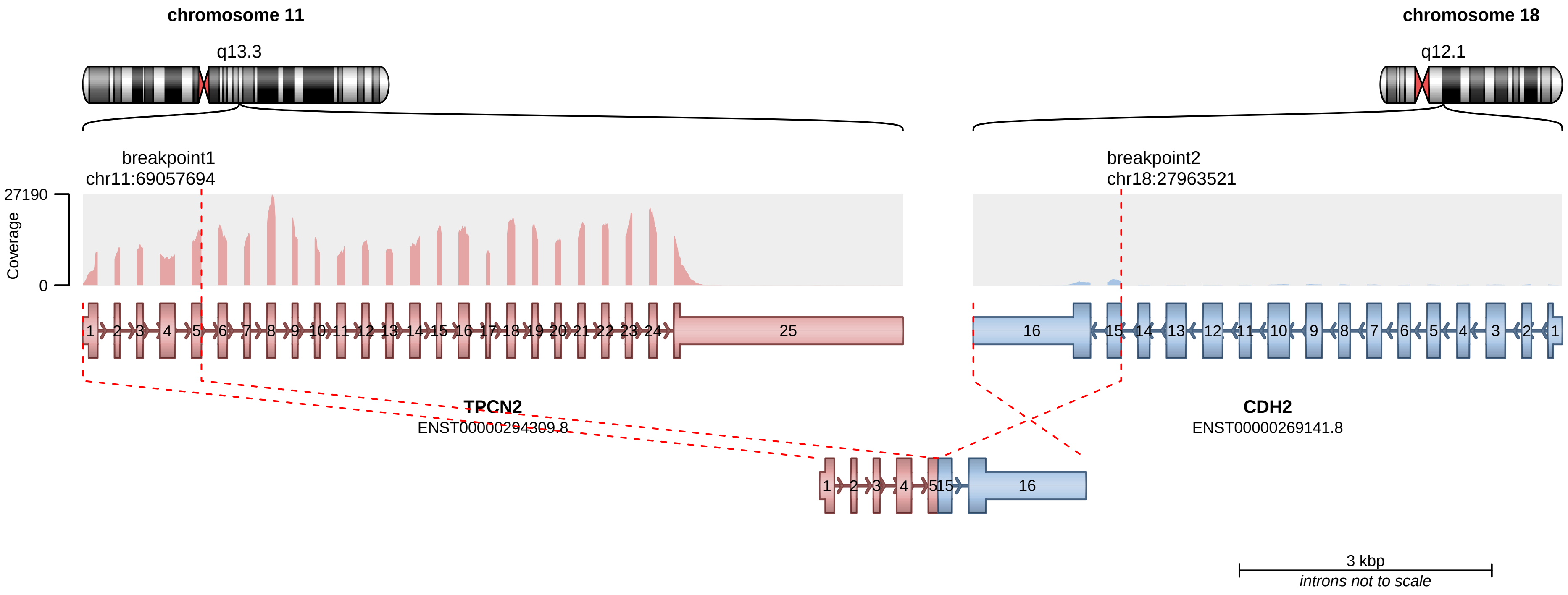


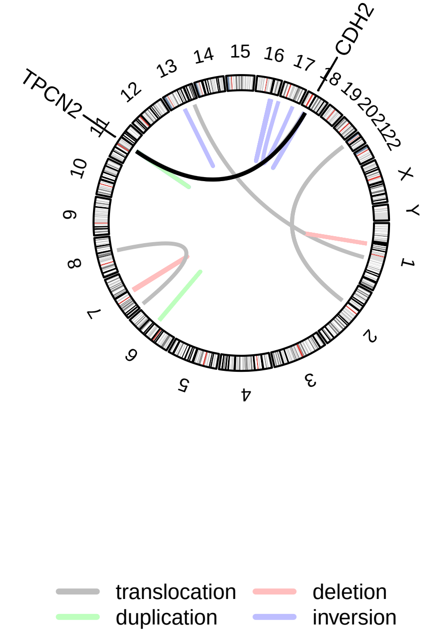
RETAINED PROTEIN DOMAINS
reading frame unclear



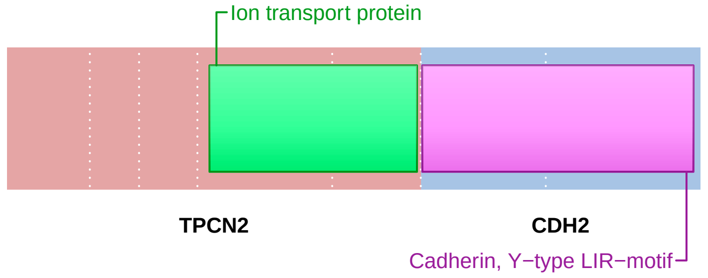
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 2



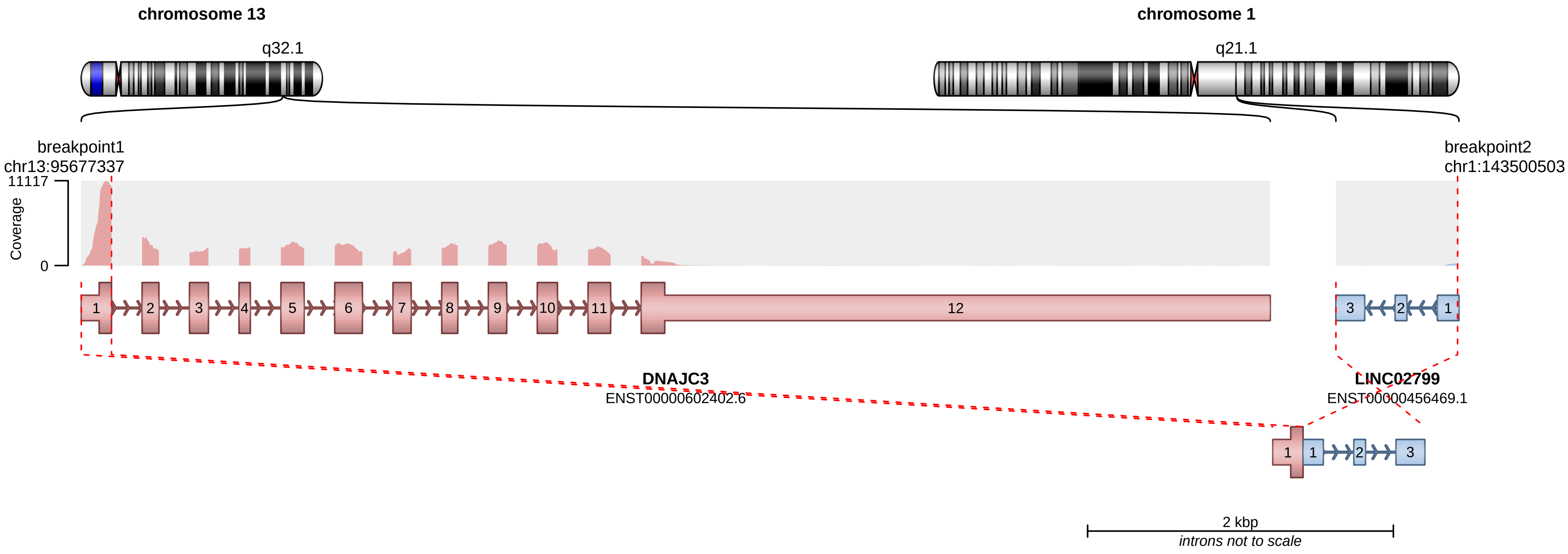


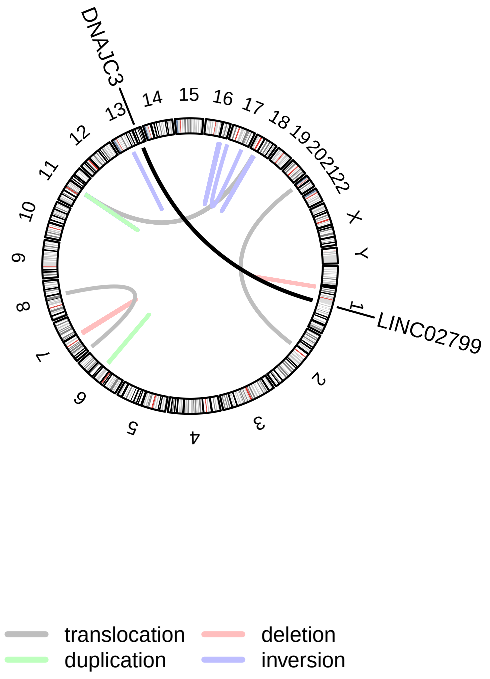
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

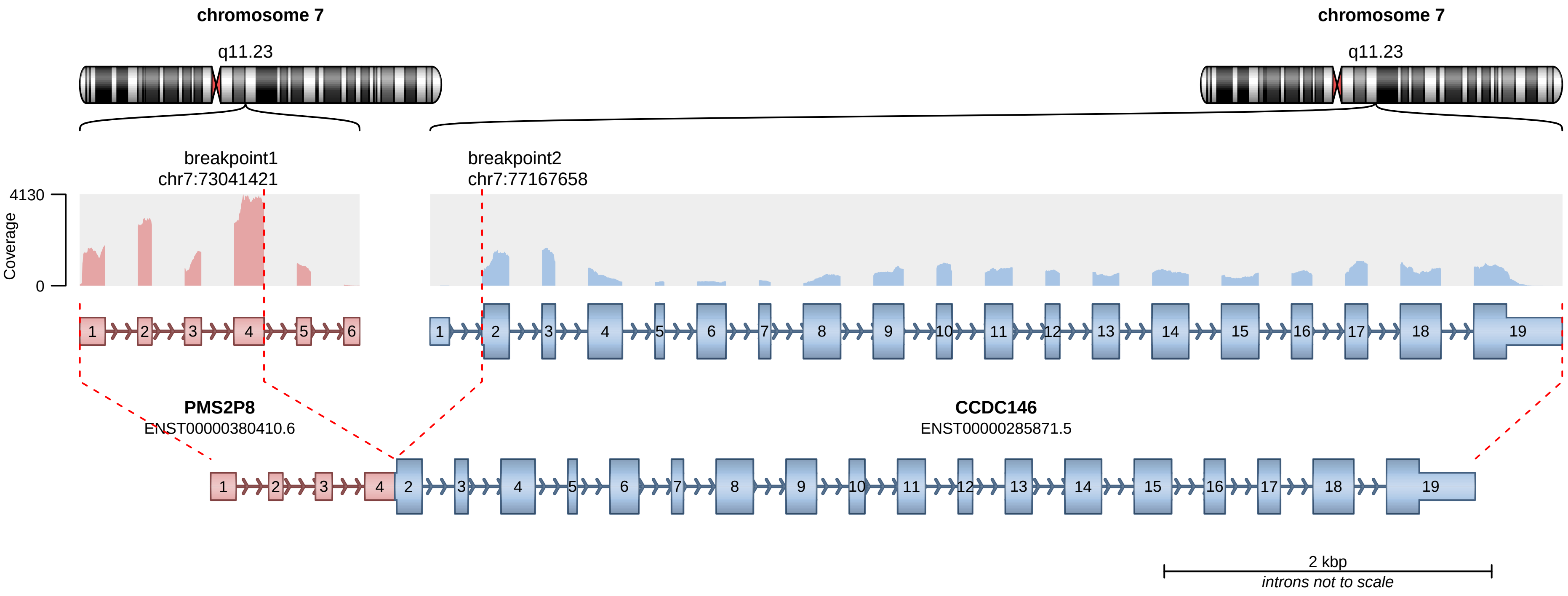


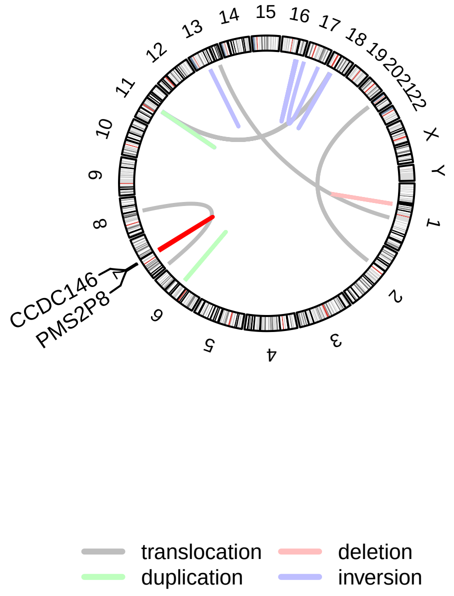


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 166
Discordant mates = 0

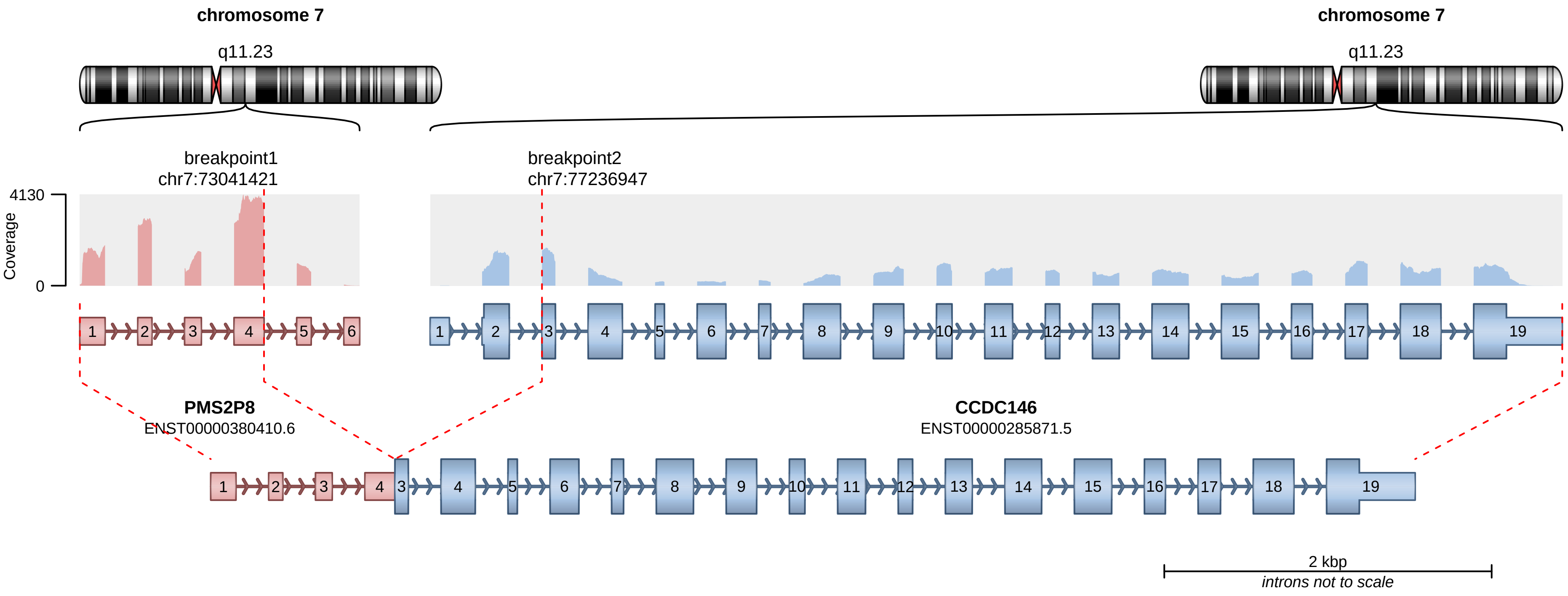


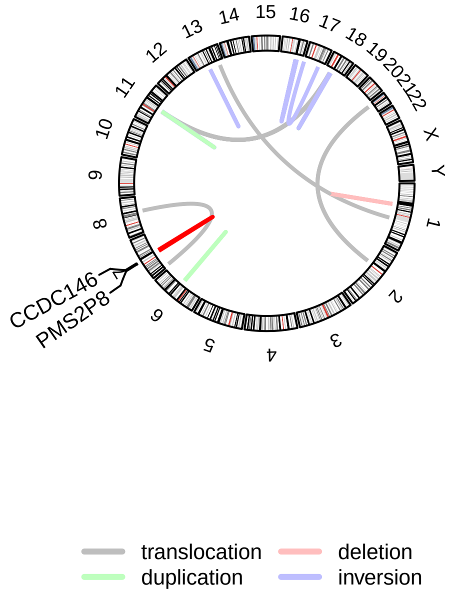


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 111
Discordant mates = 3

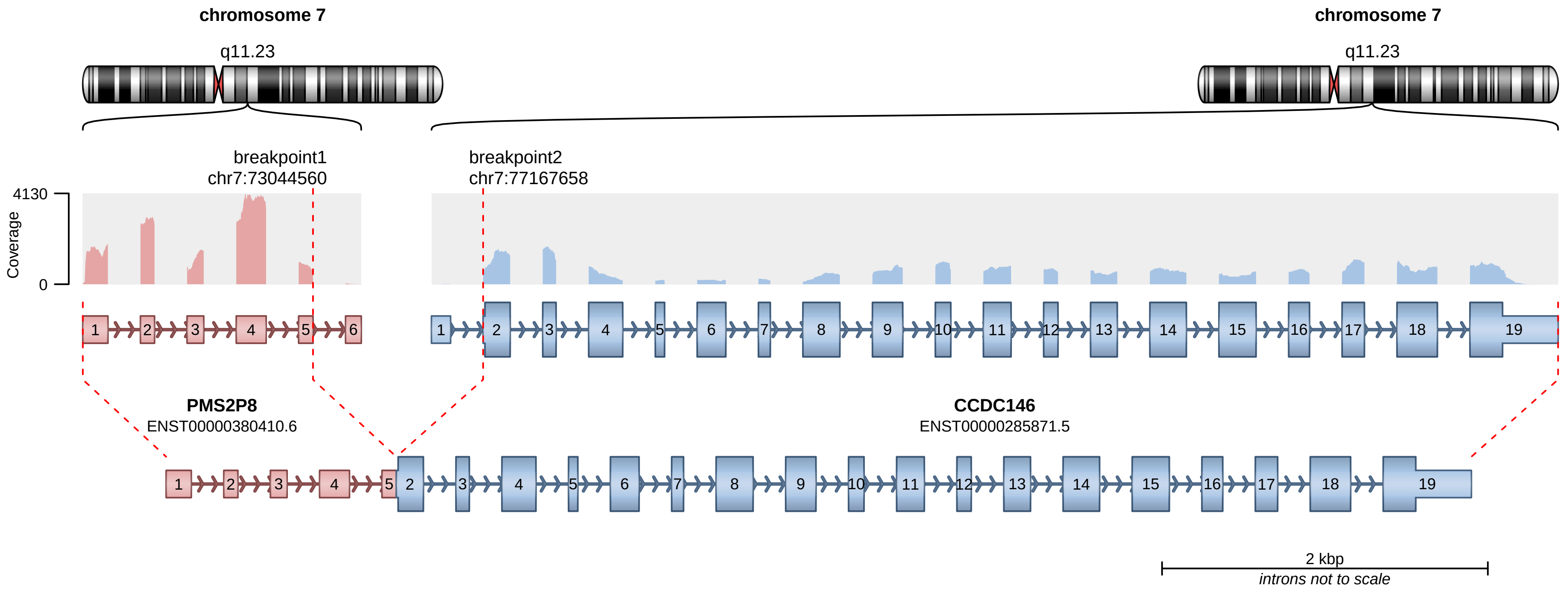


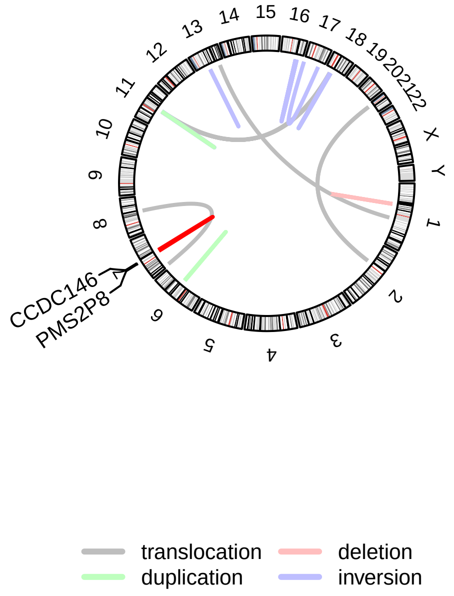


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 19
Discordant mates = 0

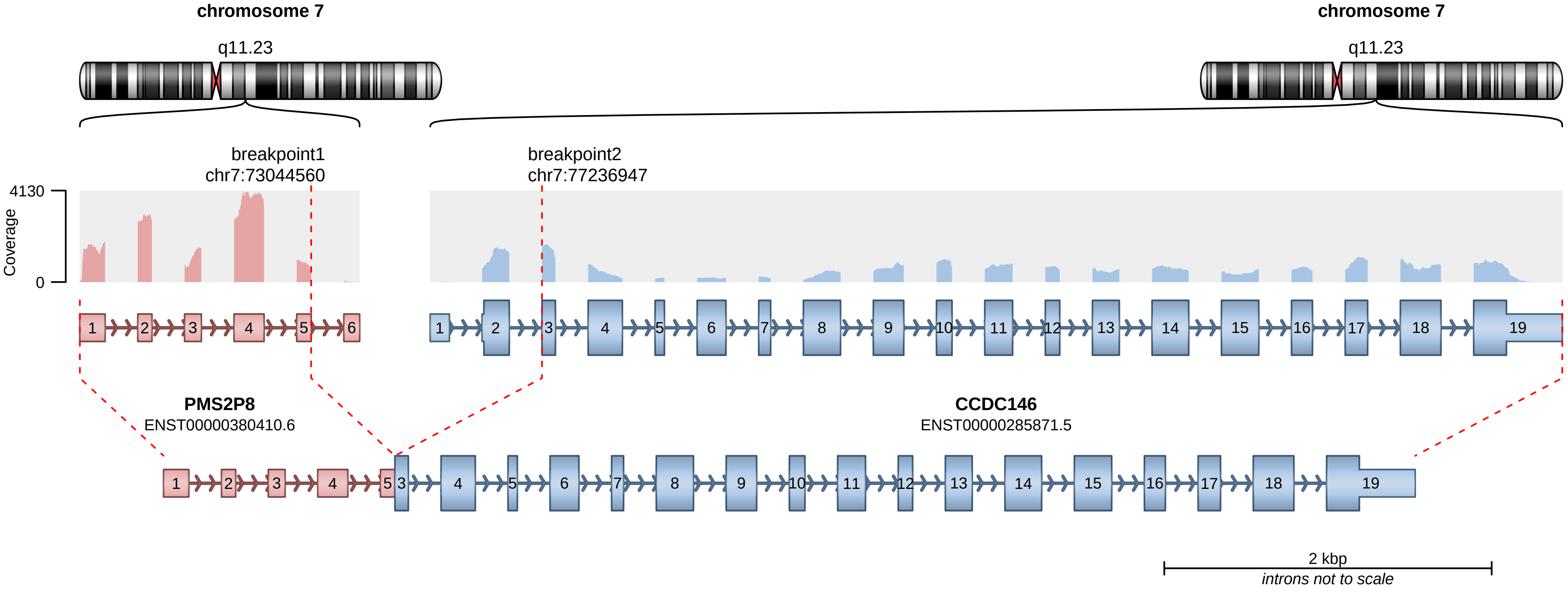


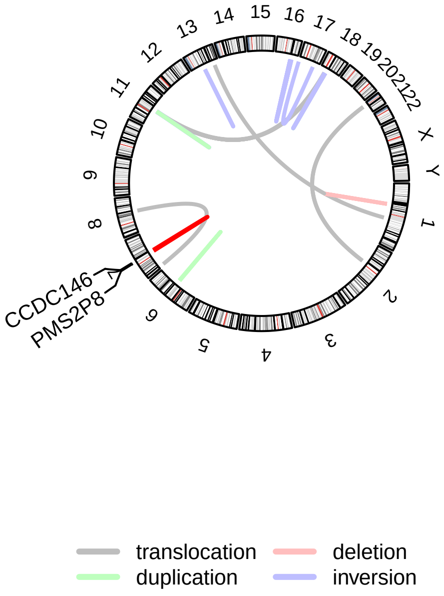


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 11
Discordant mates = 3

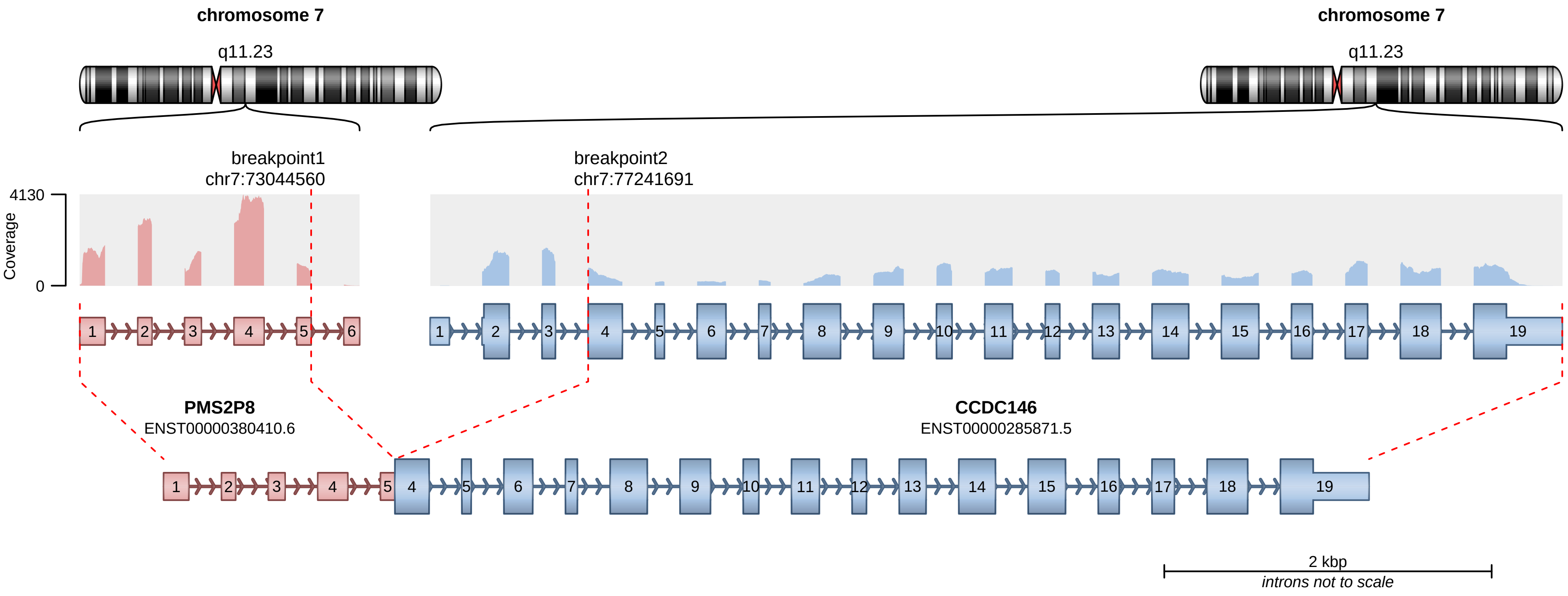


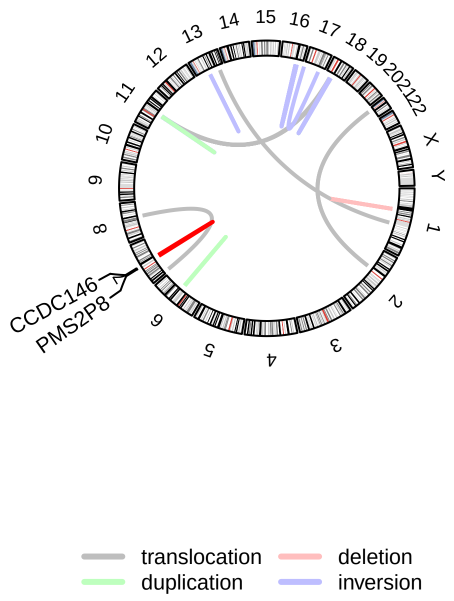


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 0

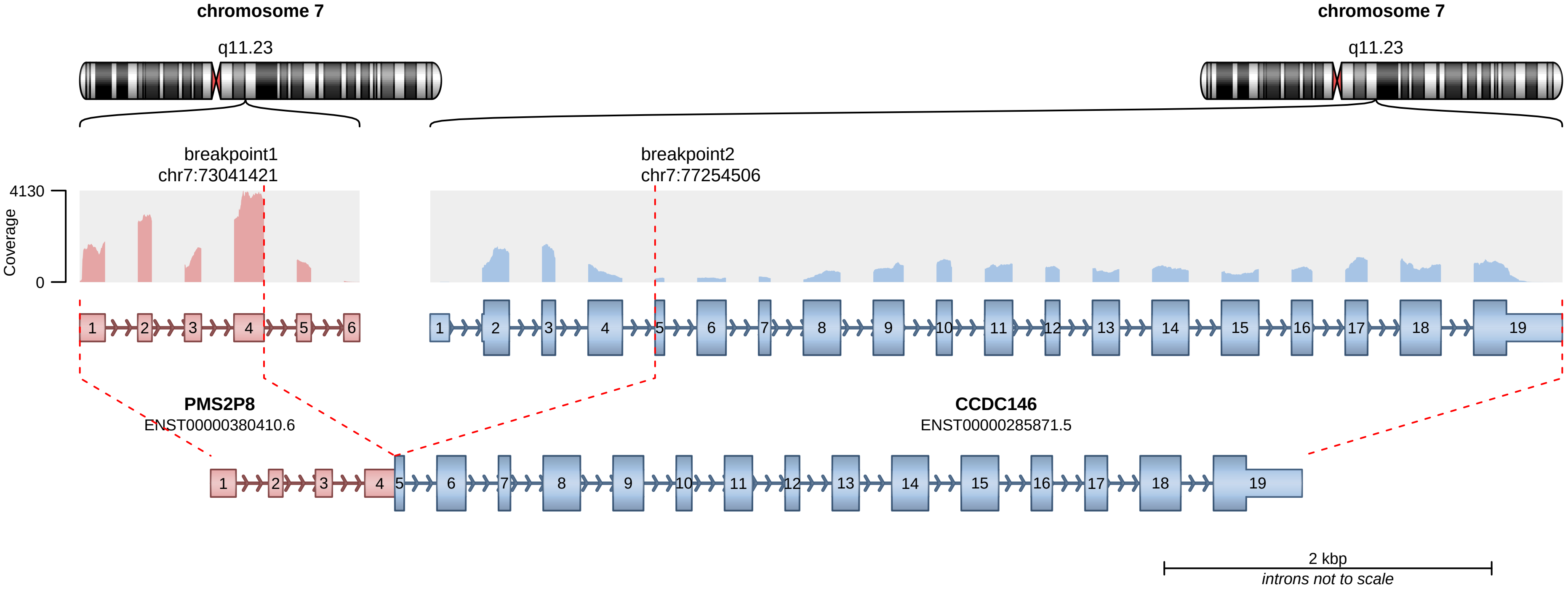


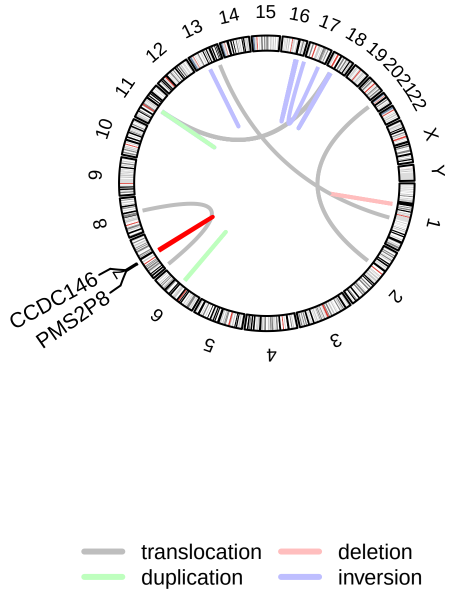


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

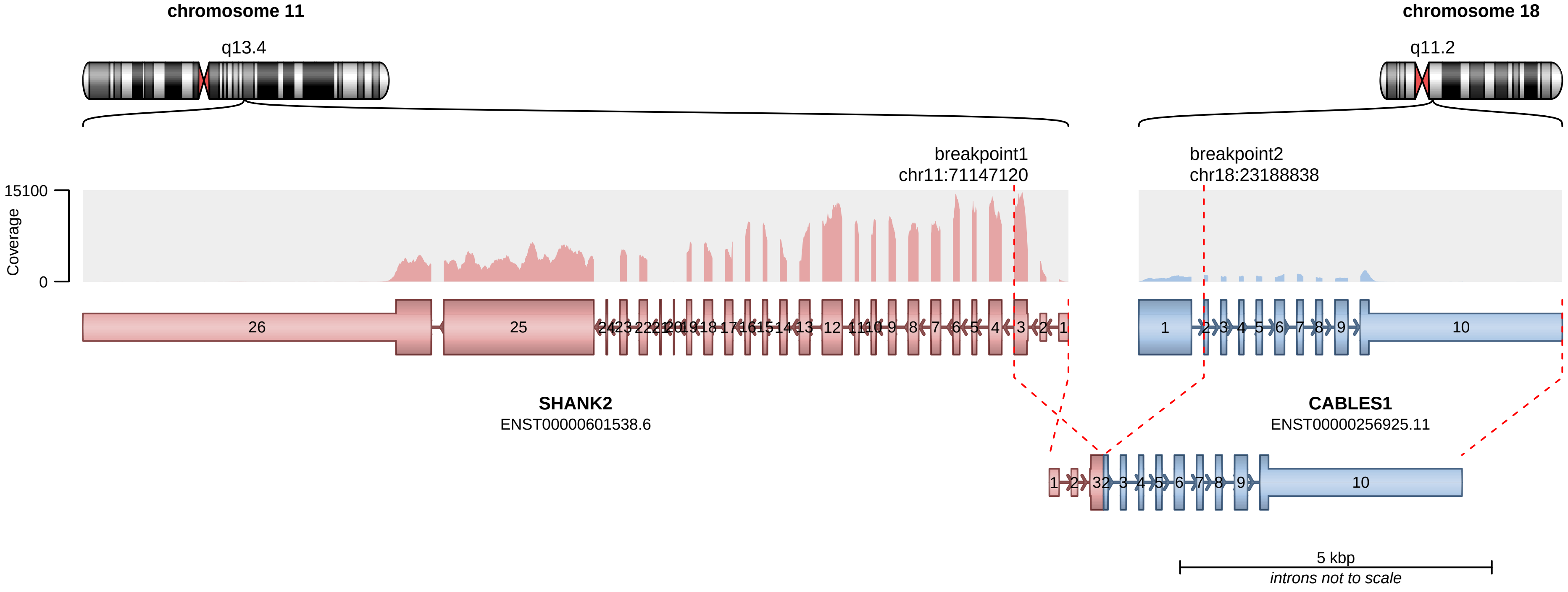


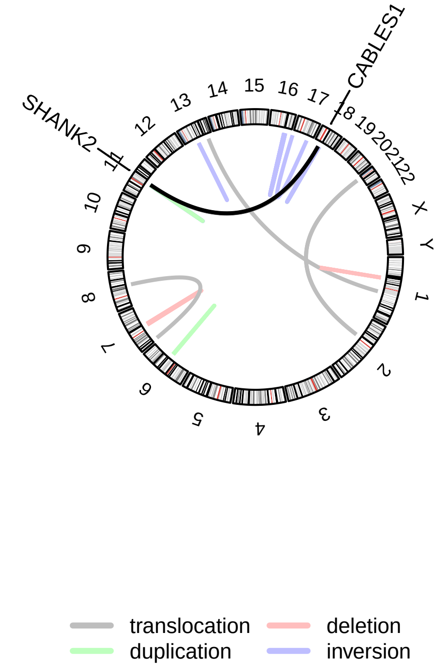


No protein domains retained in fusion.

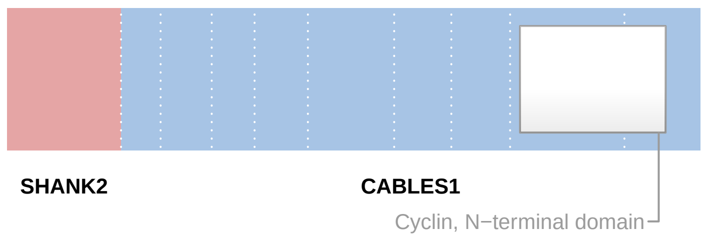
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



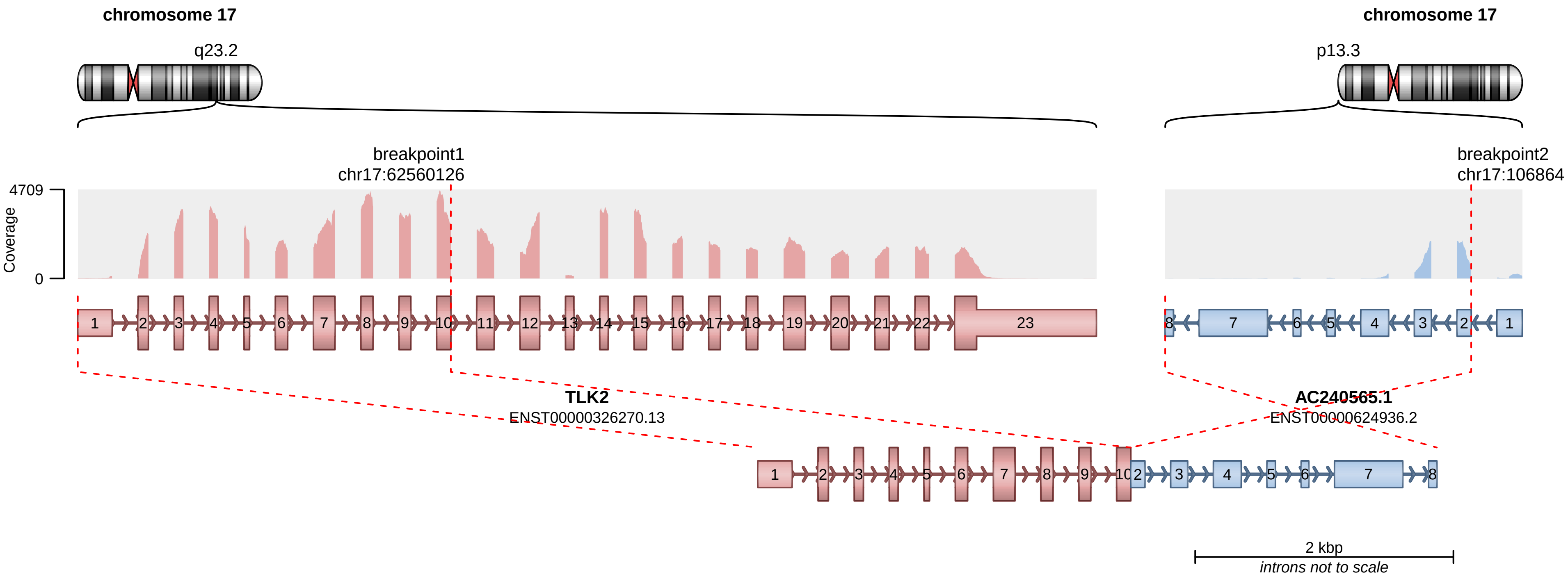


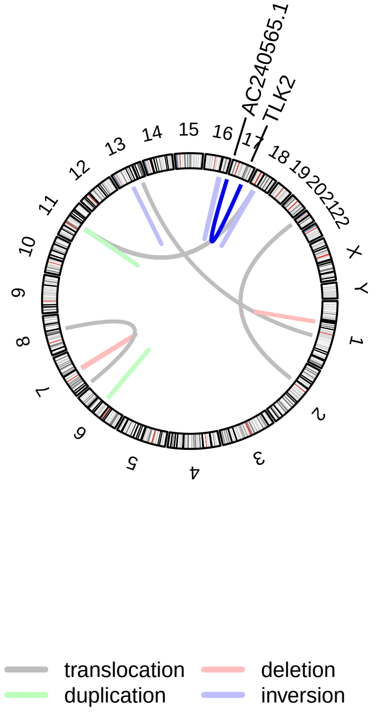
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 74
Discordant mates = 0

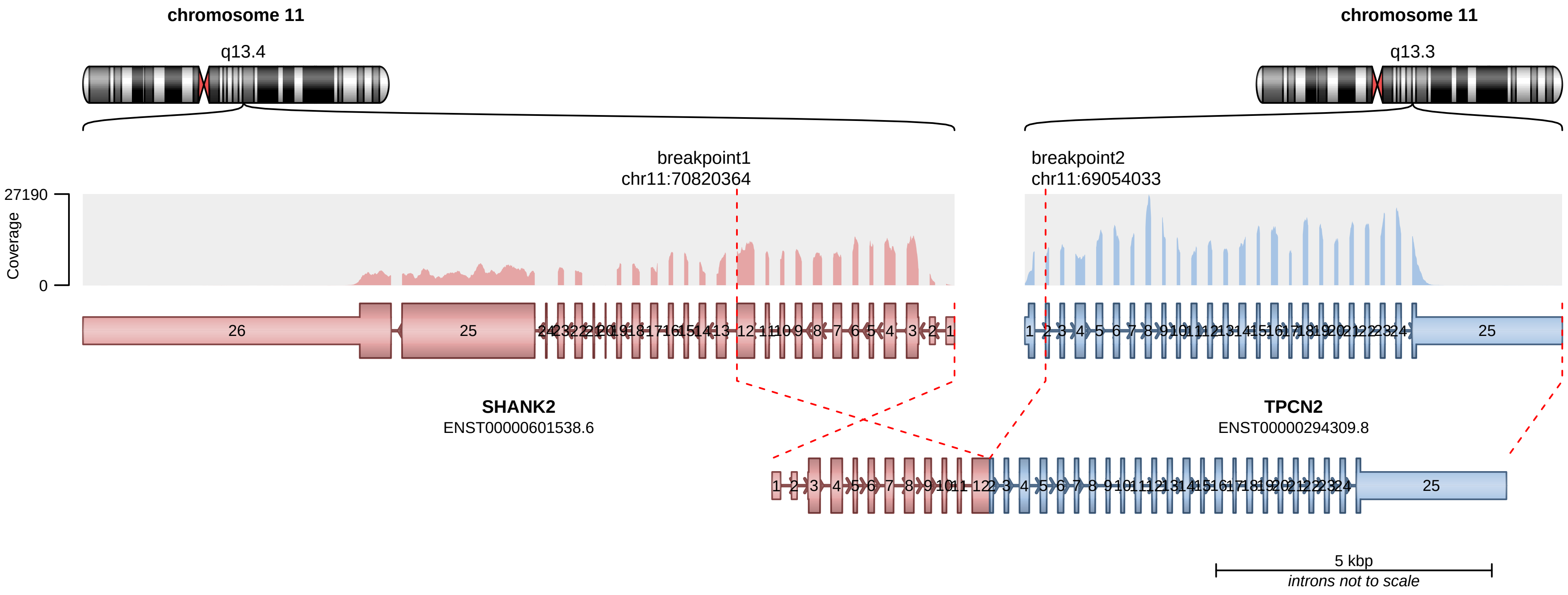


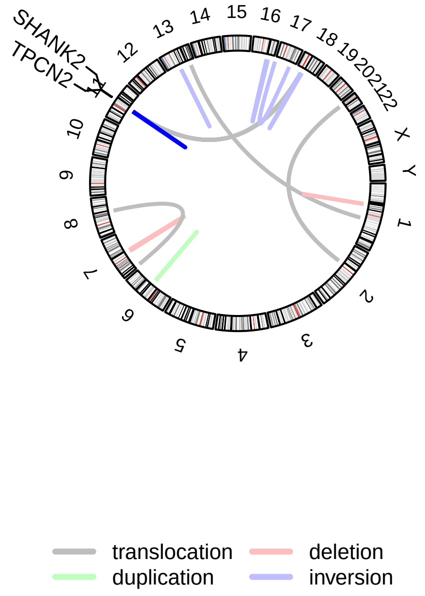


No protein domains retained in fusion.

SUPPORTING READ COUNT

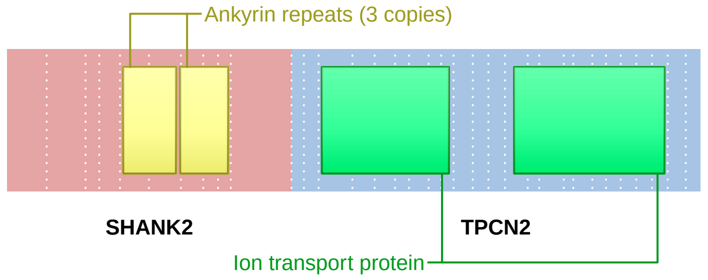
Split reads = 64
Discordant mates = 0





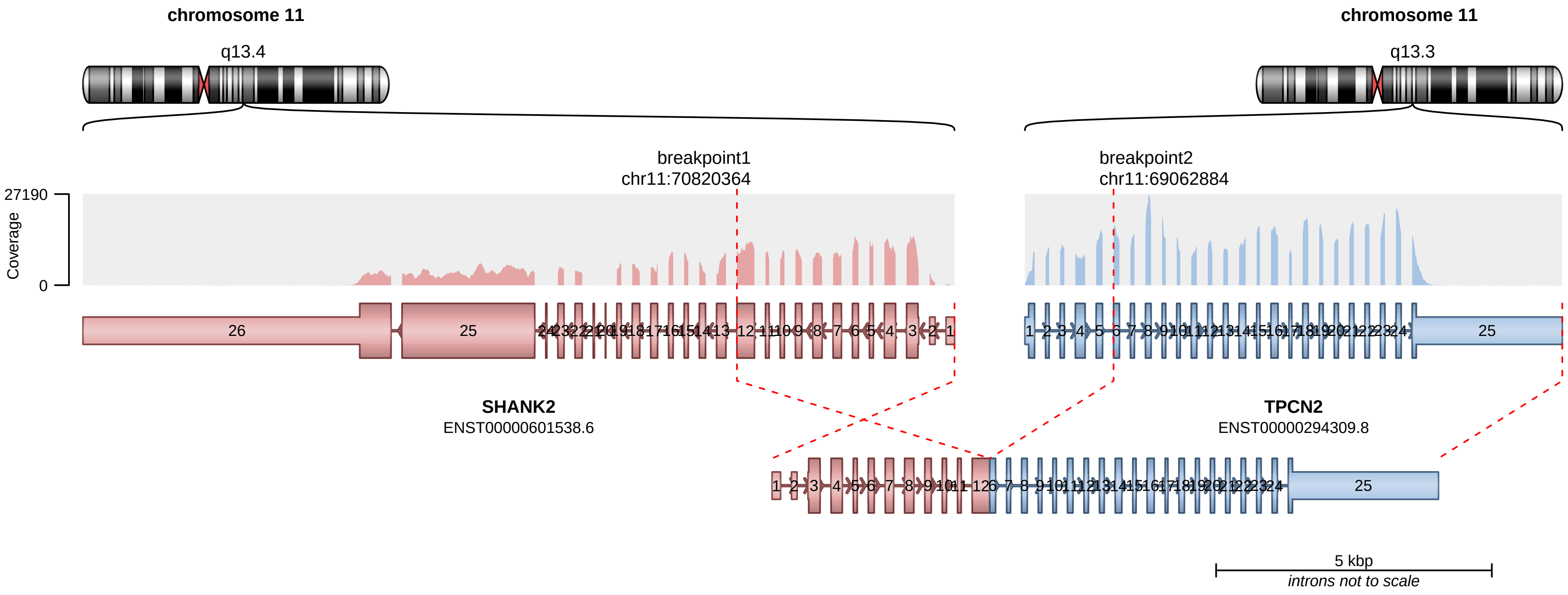
RETAINED PROTEIN DOMAINS

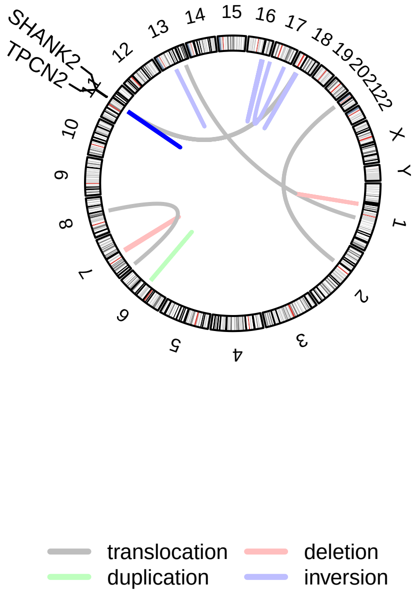
reading frame unclear



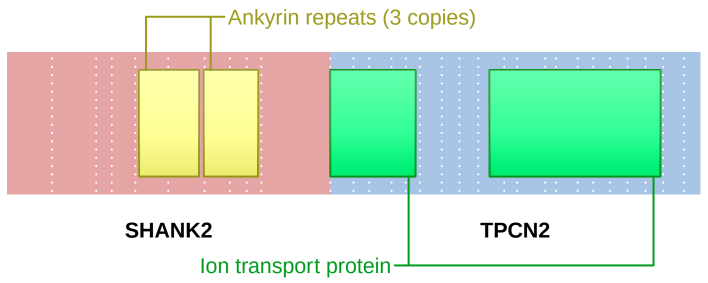
SUPPORTING READ COUNT

Split reads = 59
Discordant mates = 0



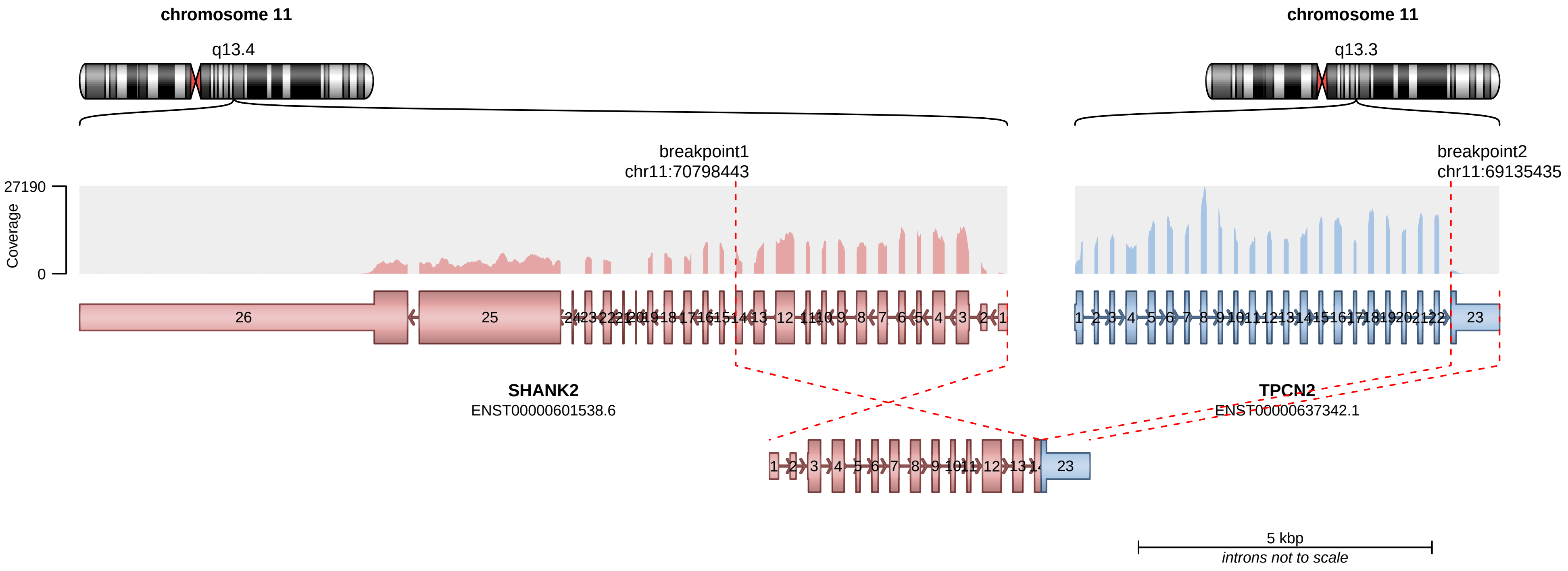


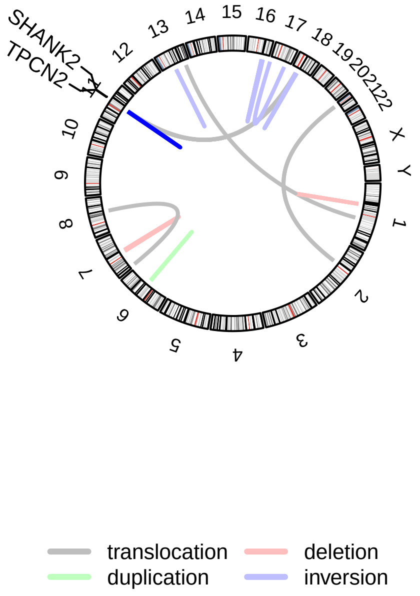
RETAINED PROTEIN DOMAINS
reading frame unclear



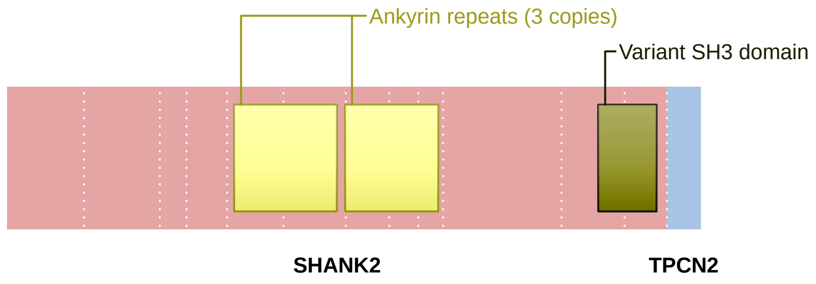
SUPPORTING READ COUNT

Split reads = 13
Discordant mates = 0



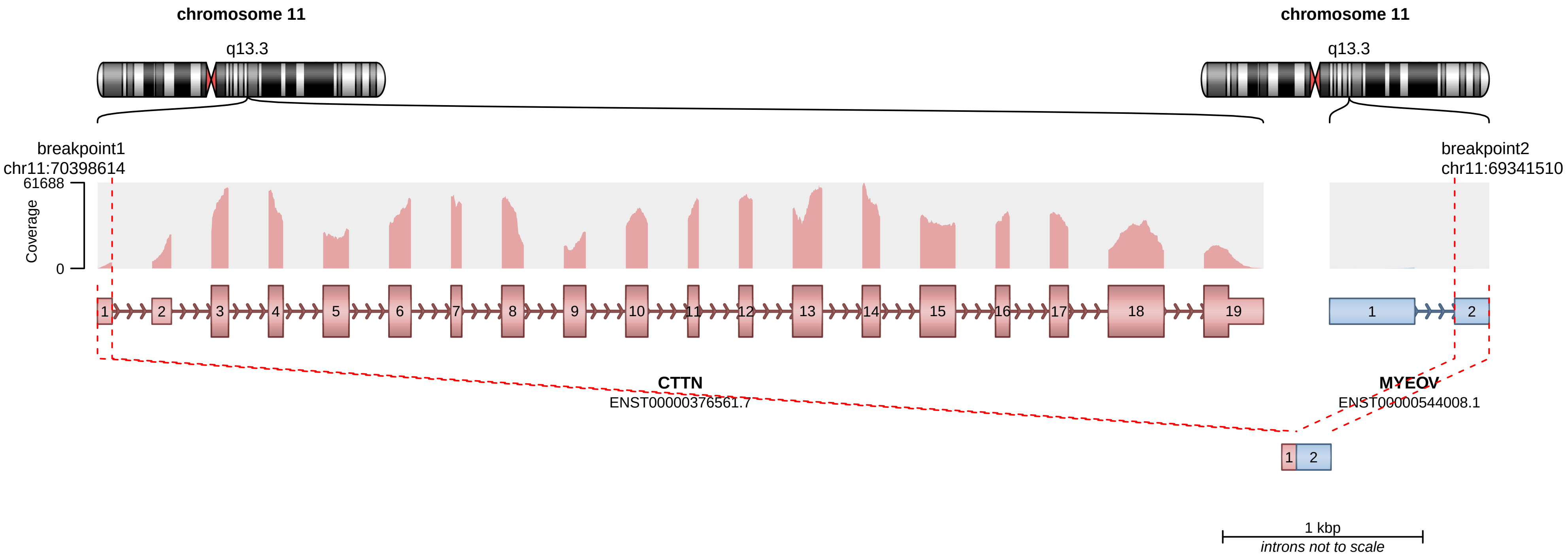


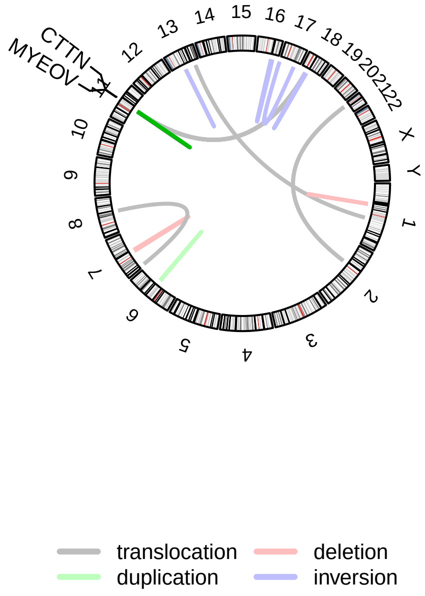
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

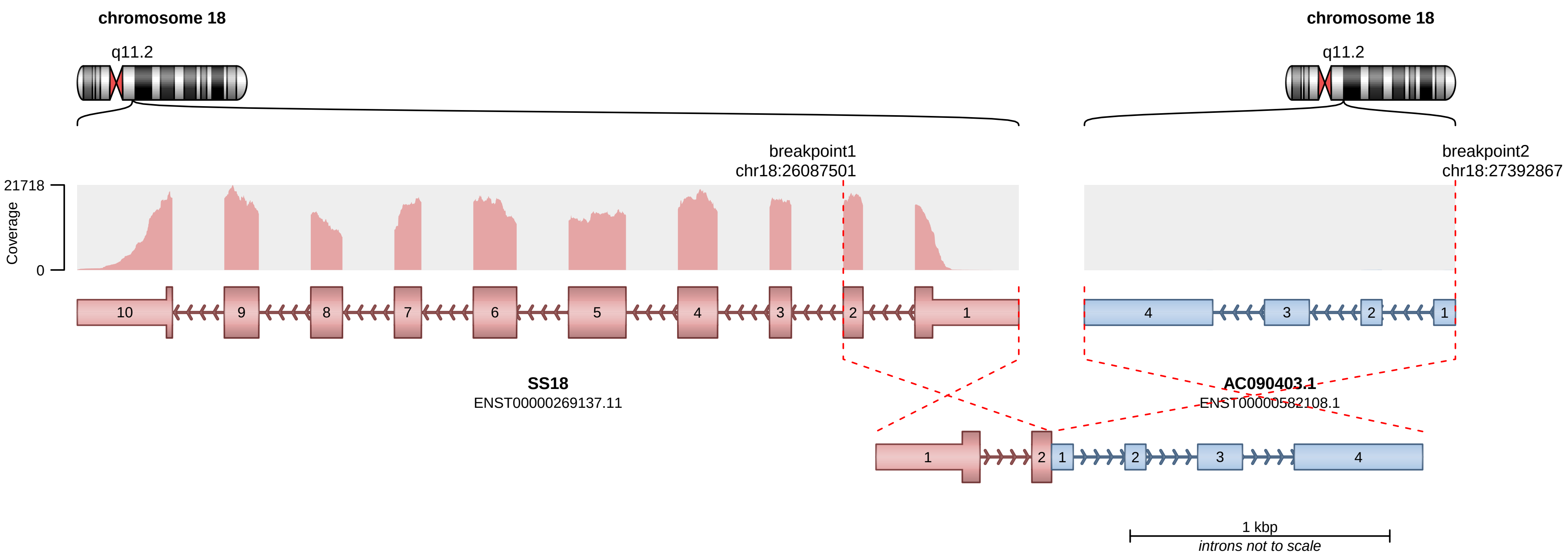


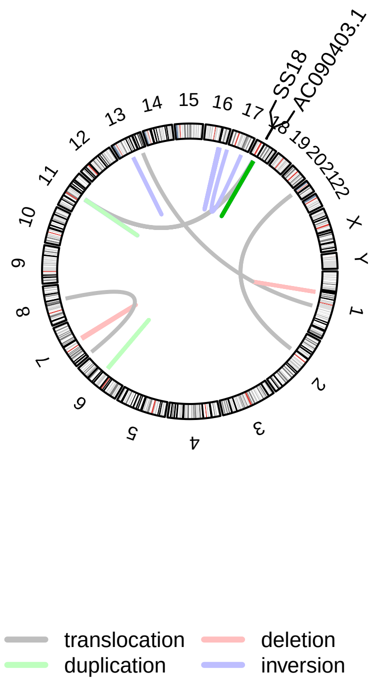


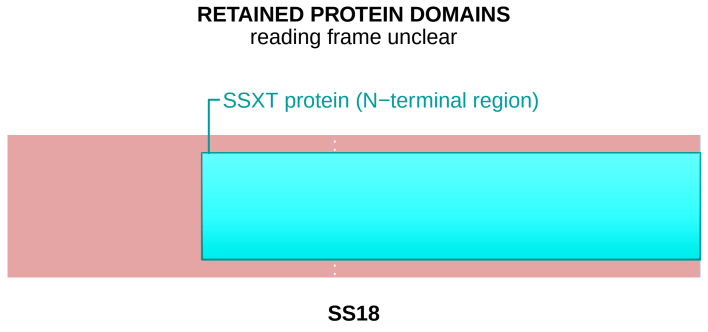
No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 24
Discordant mates = 0

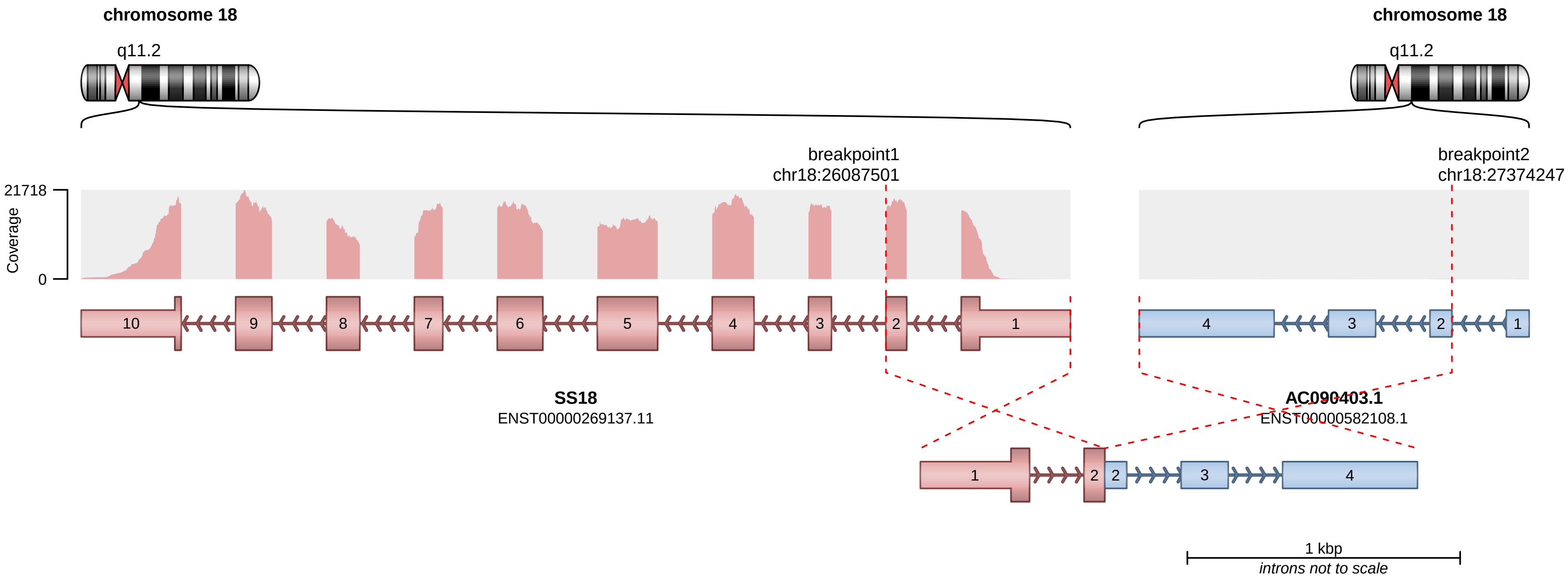


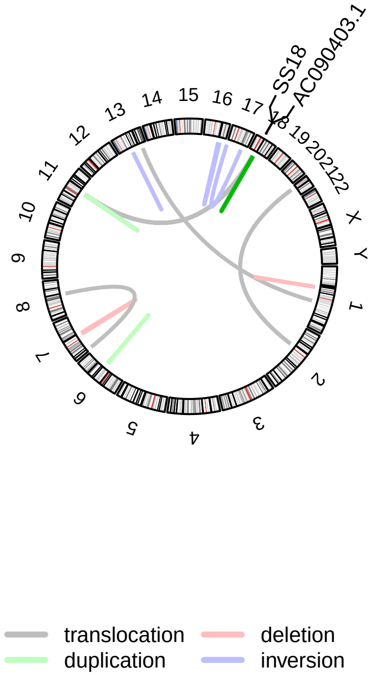




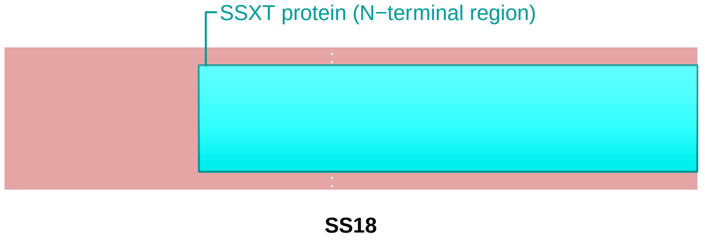
SUPPORTING READ COUNT

Split reads = 20
Discordant mates = 0



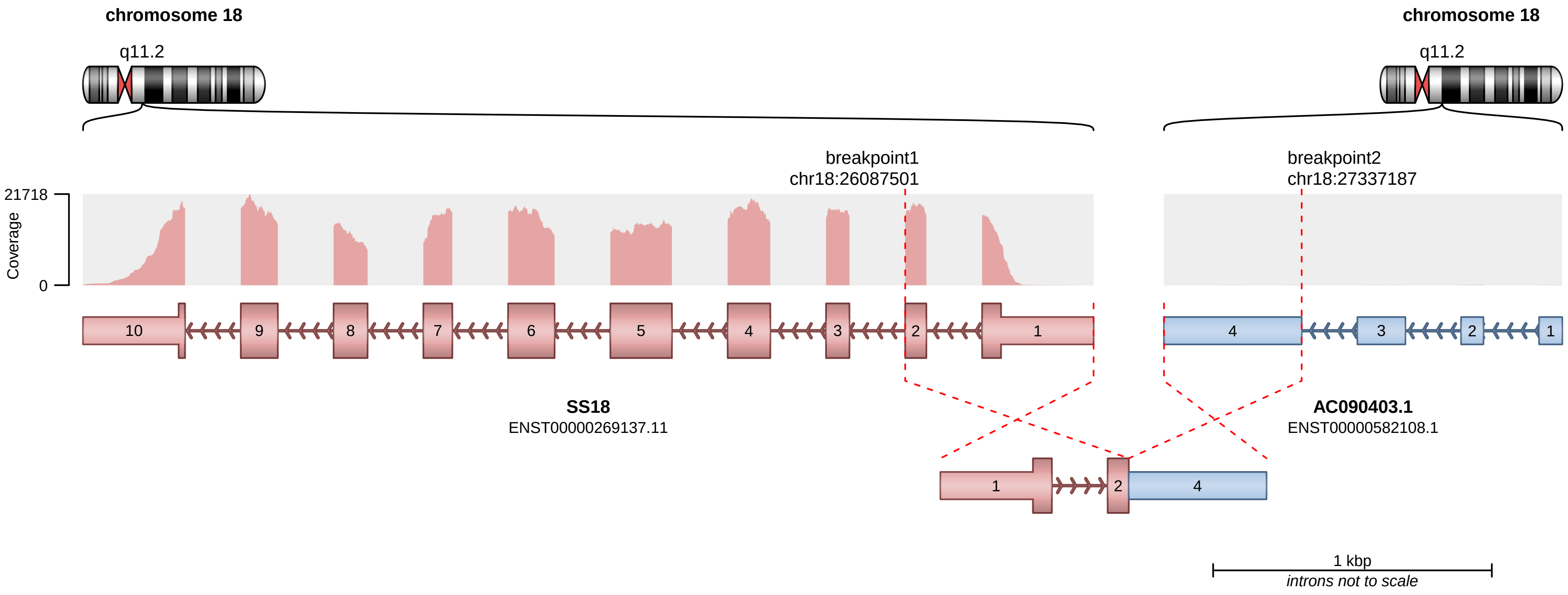


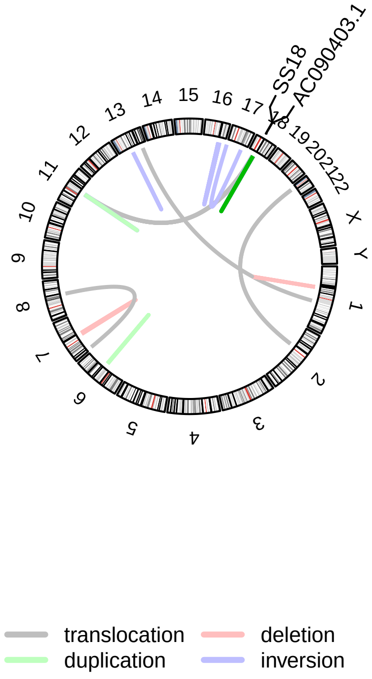
RETAINED PROTEIN DOMAINS
reading frame unclear



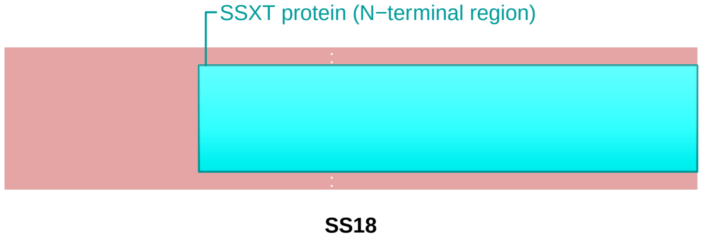
SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 0



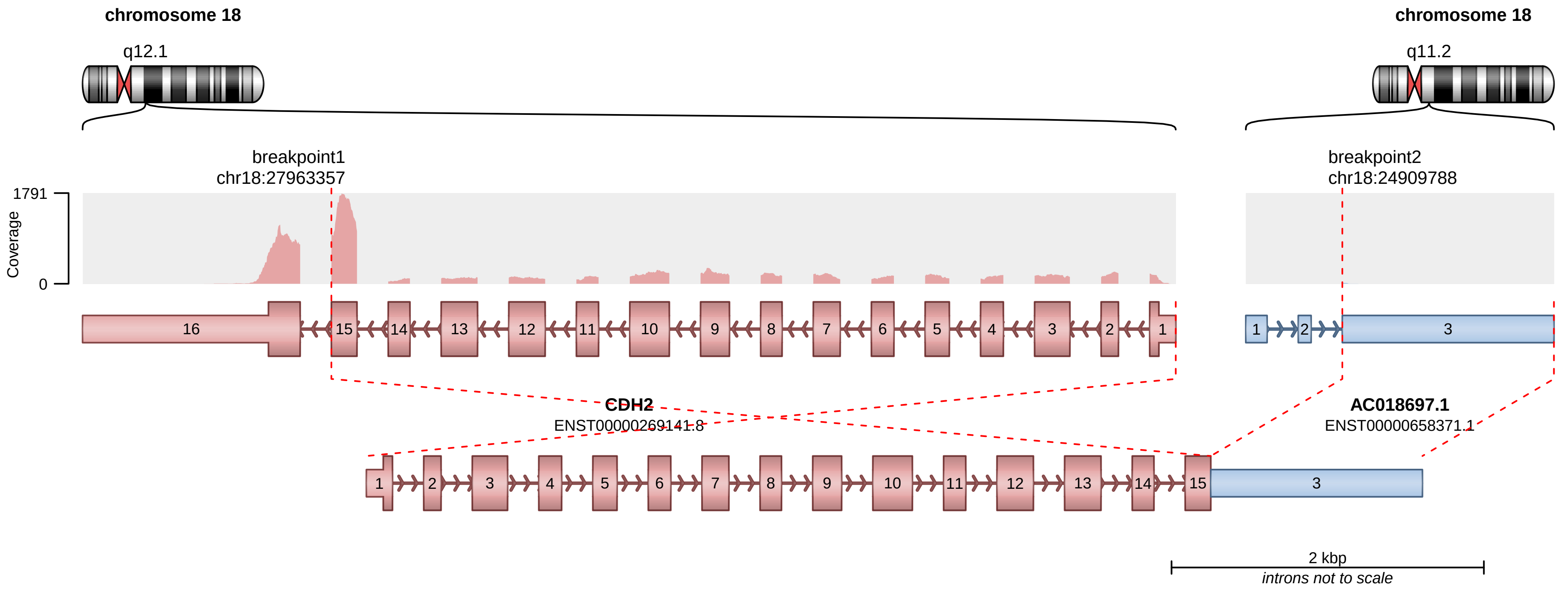


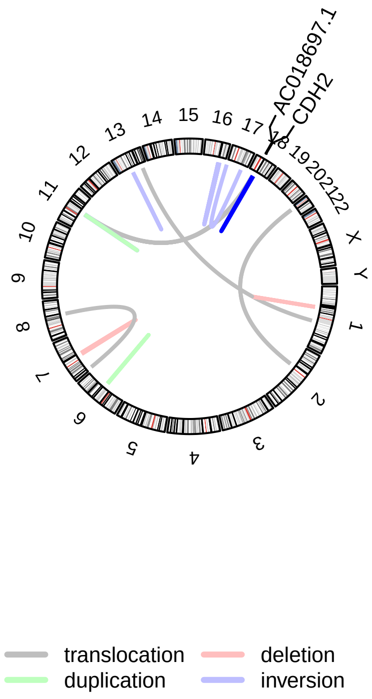
RETAINED PROTEIN DOMAINS
reading frame unclear



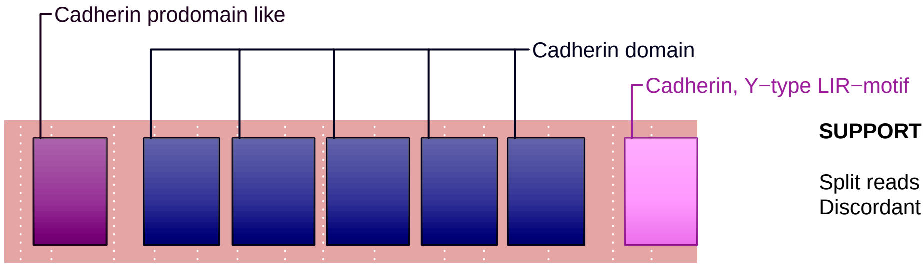
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0





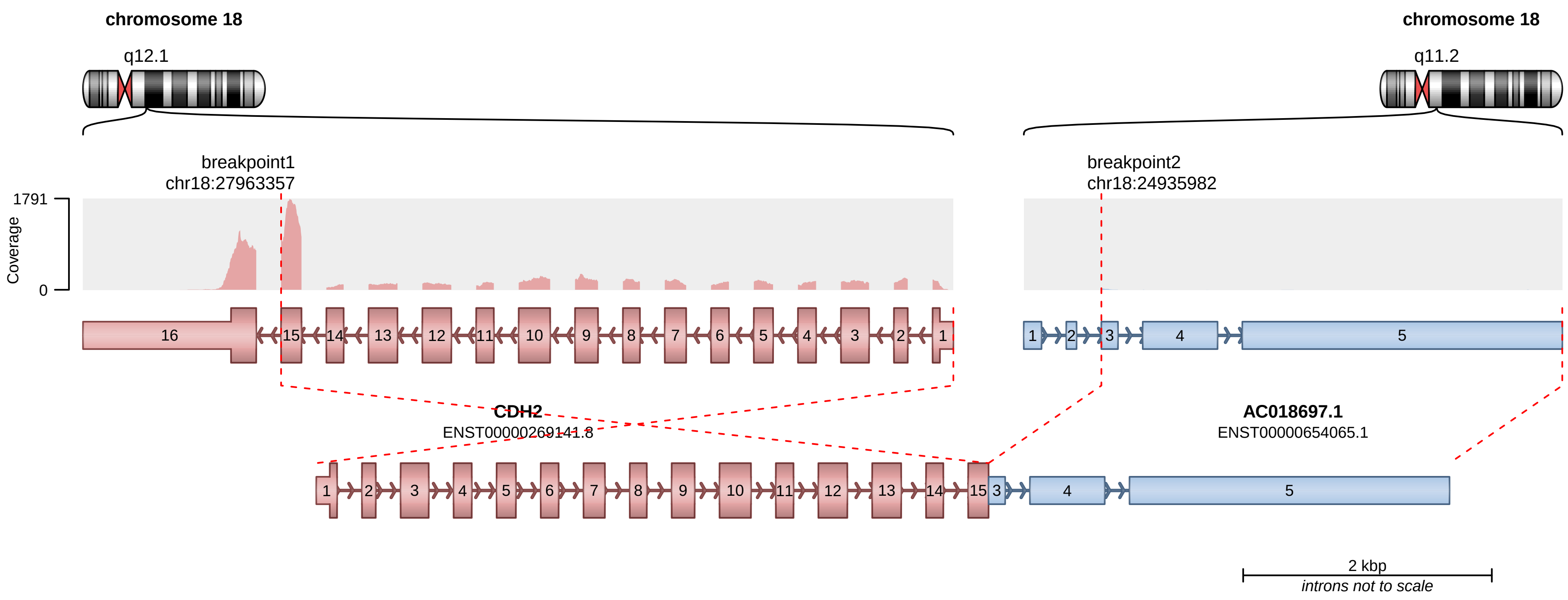
RETAINED PROTEIN DOMAINS
reading frame unclear

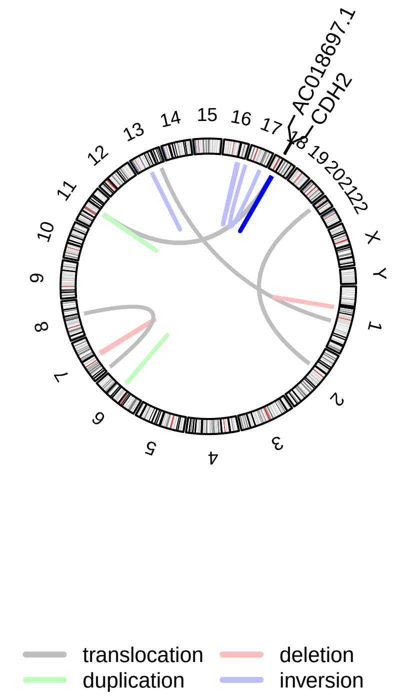


CDH2

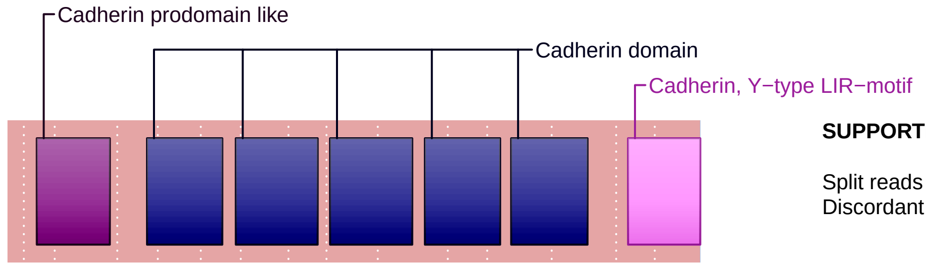
SUPPORTING READ COUNT

Split reads = 17
Discordant mates = 0





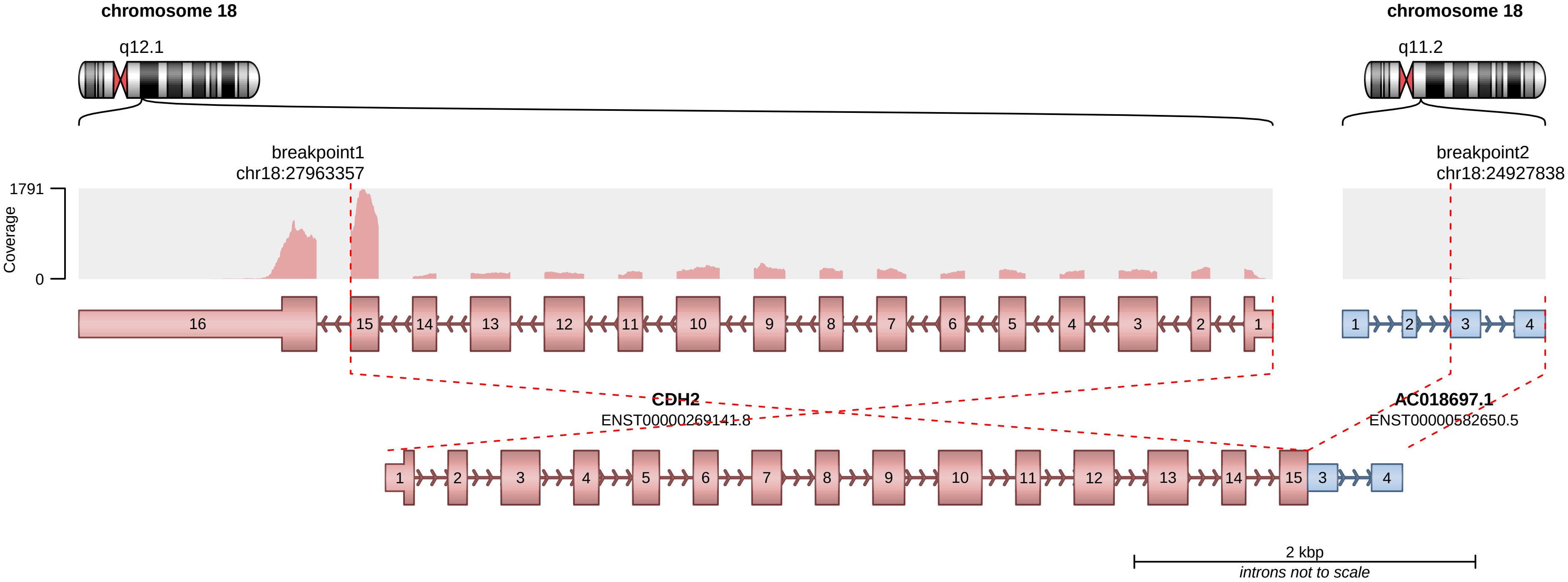
RETAINED PROTEIN DOMAINS
reading frame unclear

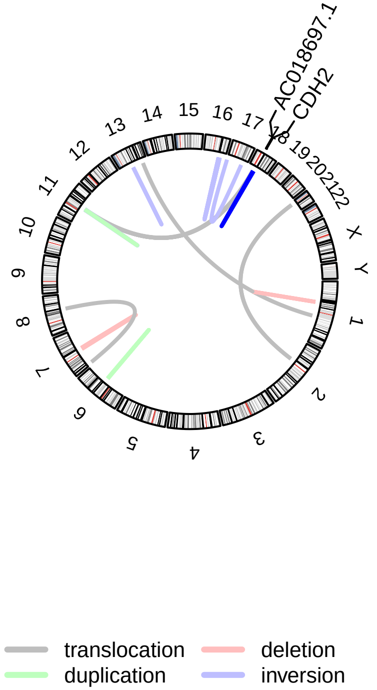


CDH2

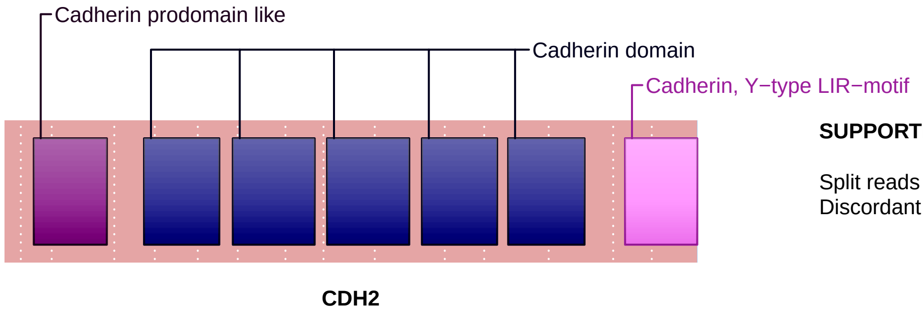
SUPPORTING READ COUNT

Split reads = 13
Discordant mates = 0



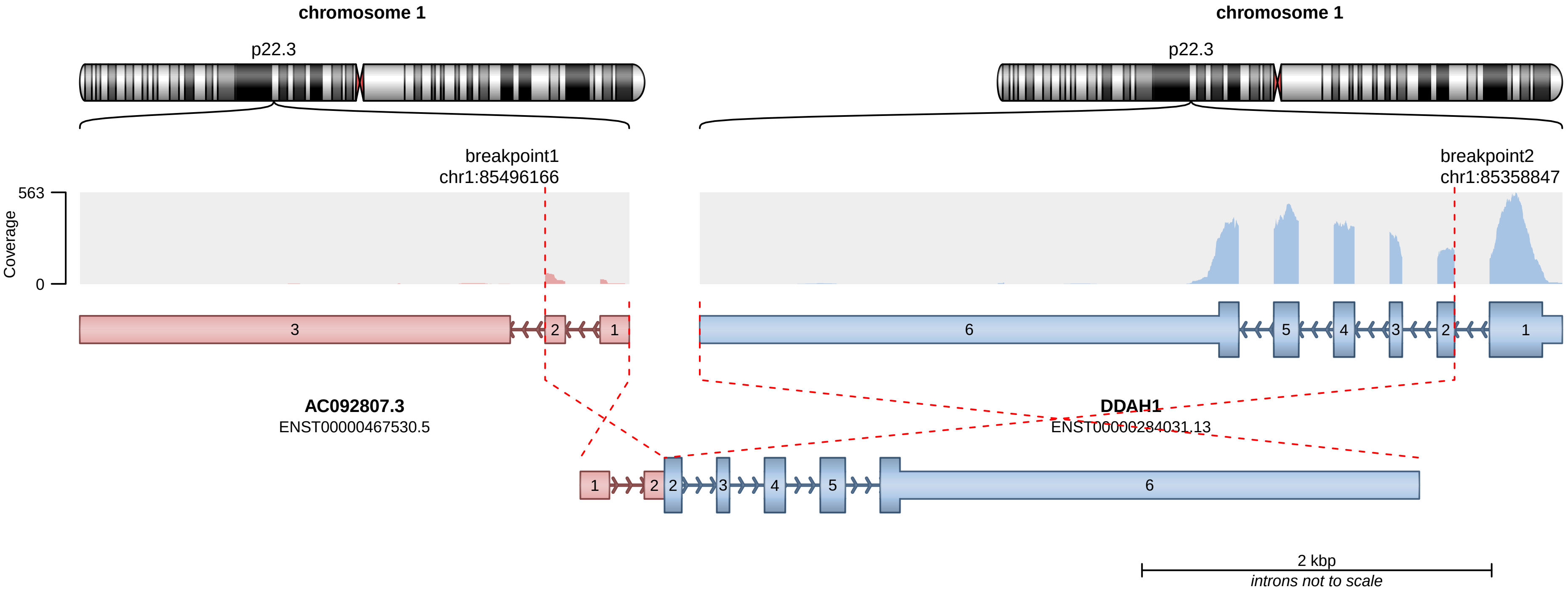


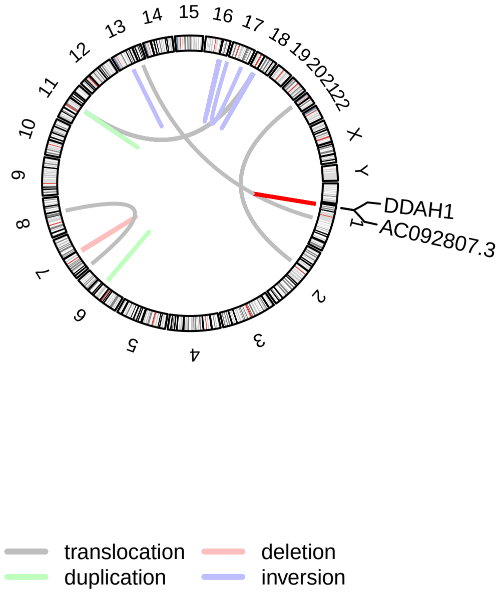
RETAINED PROTEIN DOMAINS
reading frame unclear



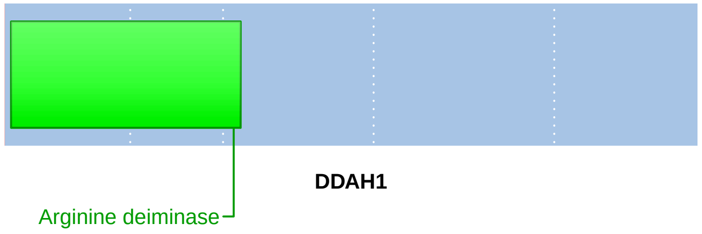
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0



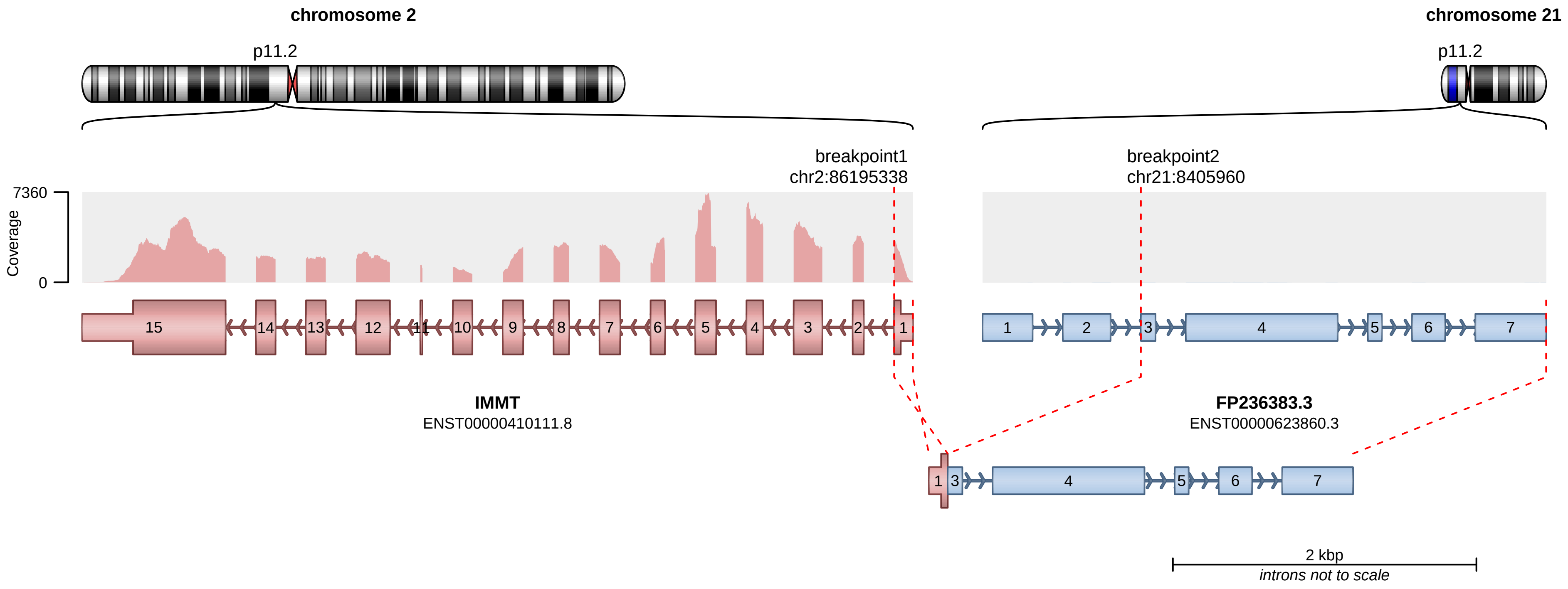


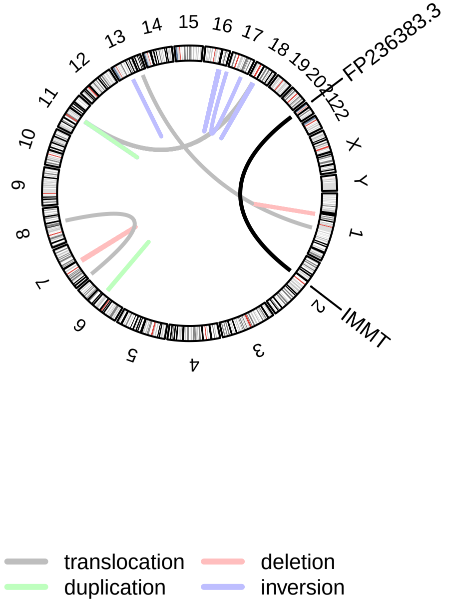
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 16
Discordant mates = 0

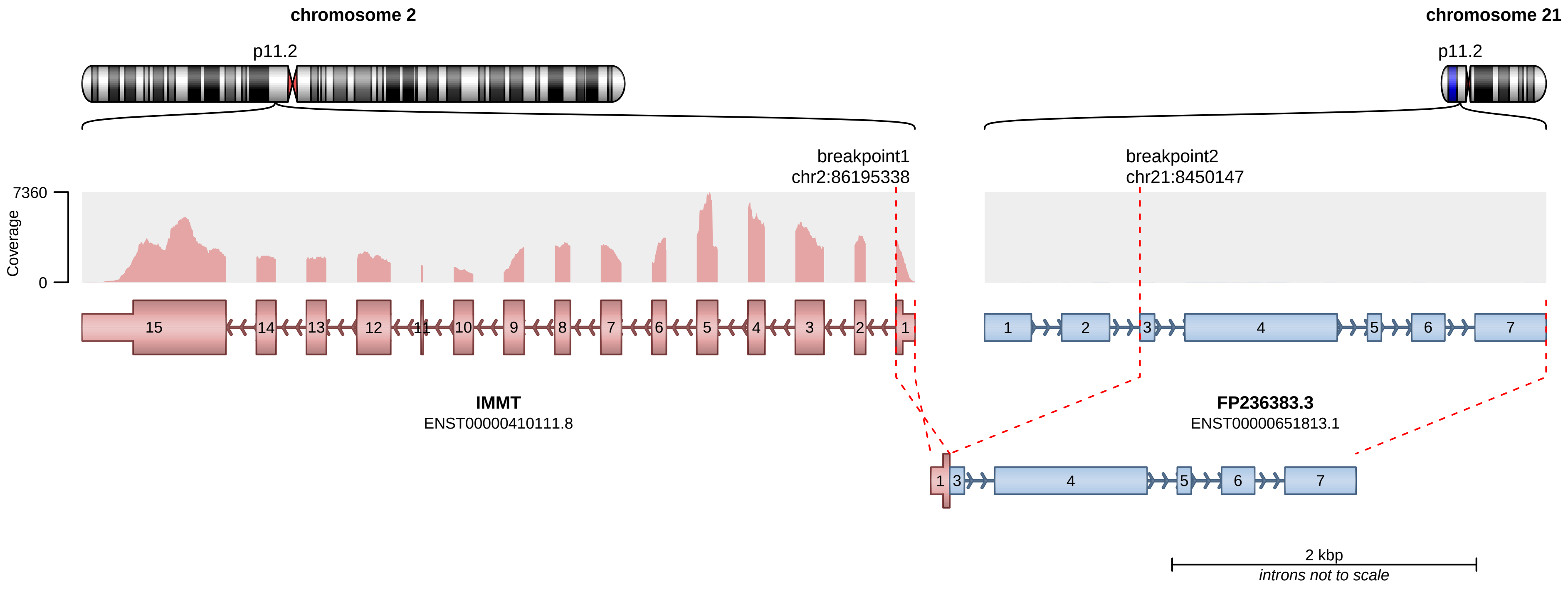


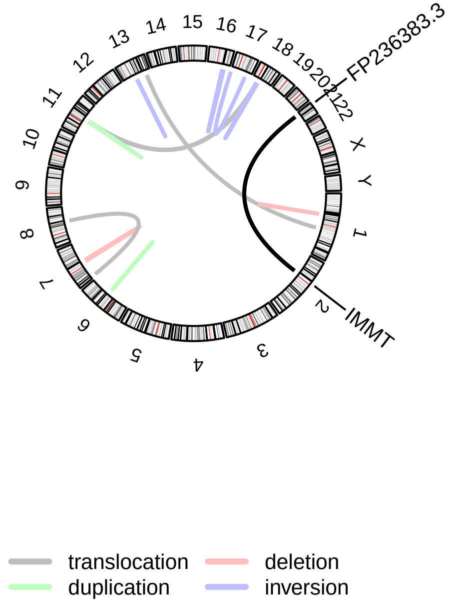


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 14
Discordant mates = 0

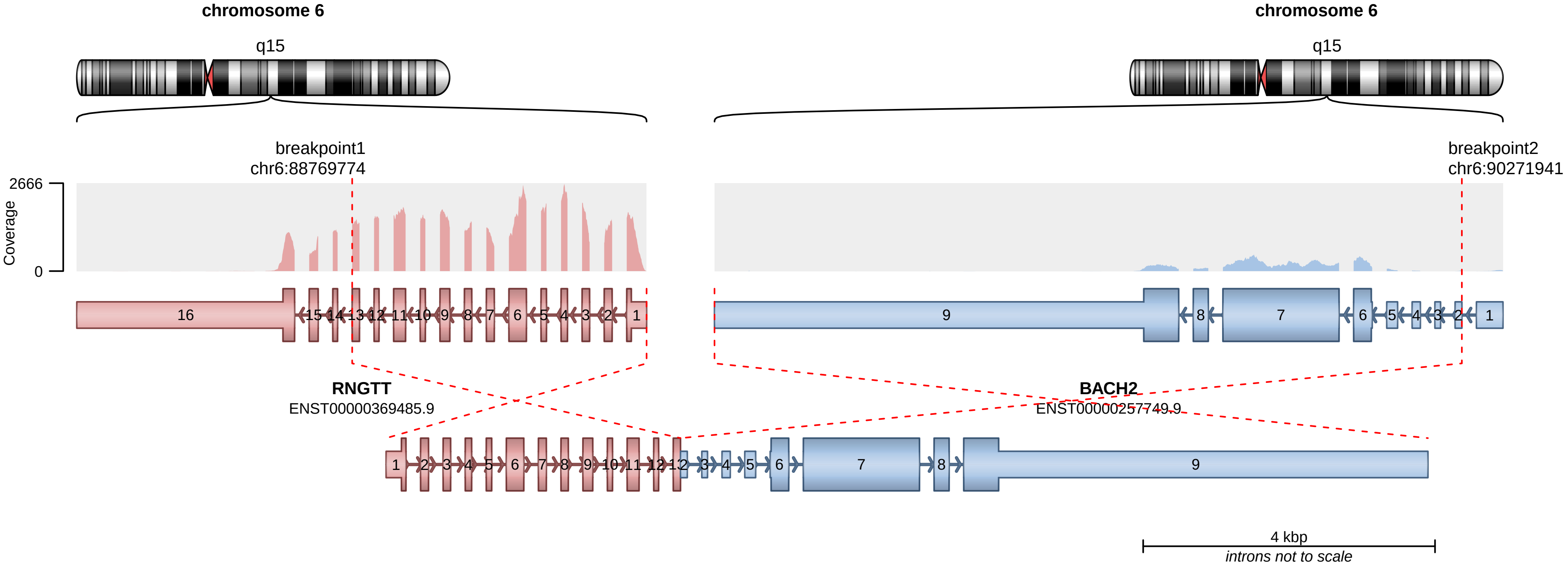


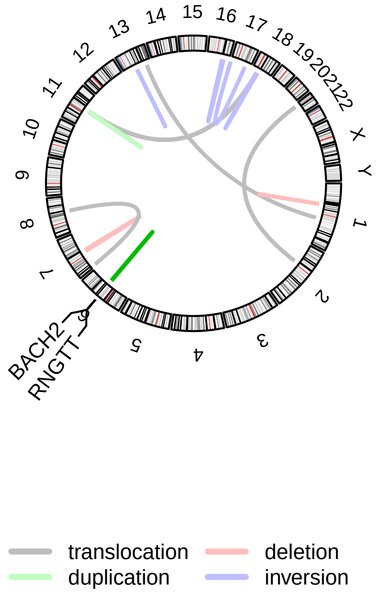


No protein domains retained in fusion.

SUPPORTING READ COUNT

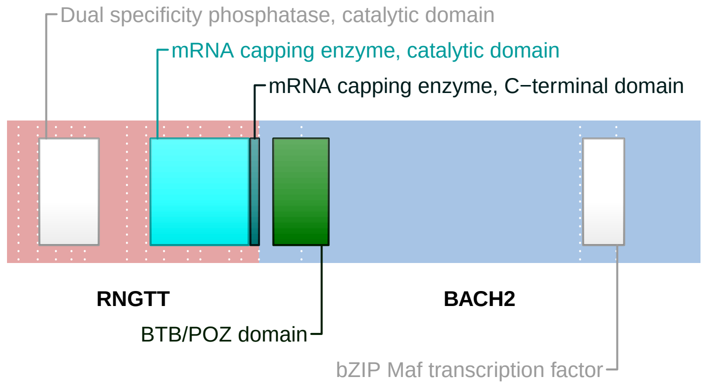
Split reads = 14
Discordant mates = 0





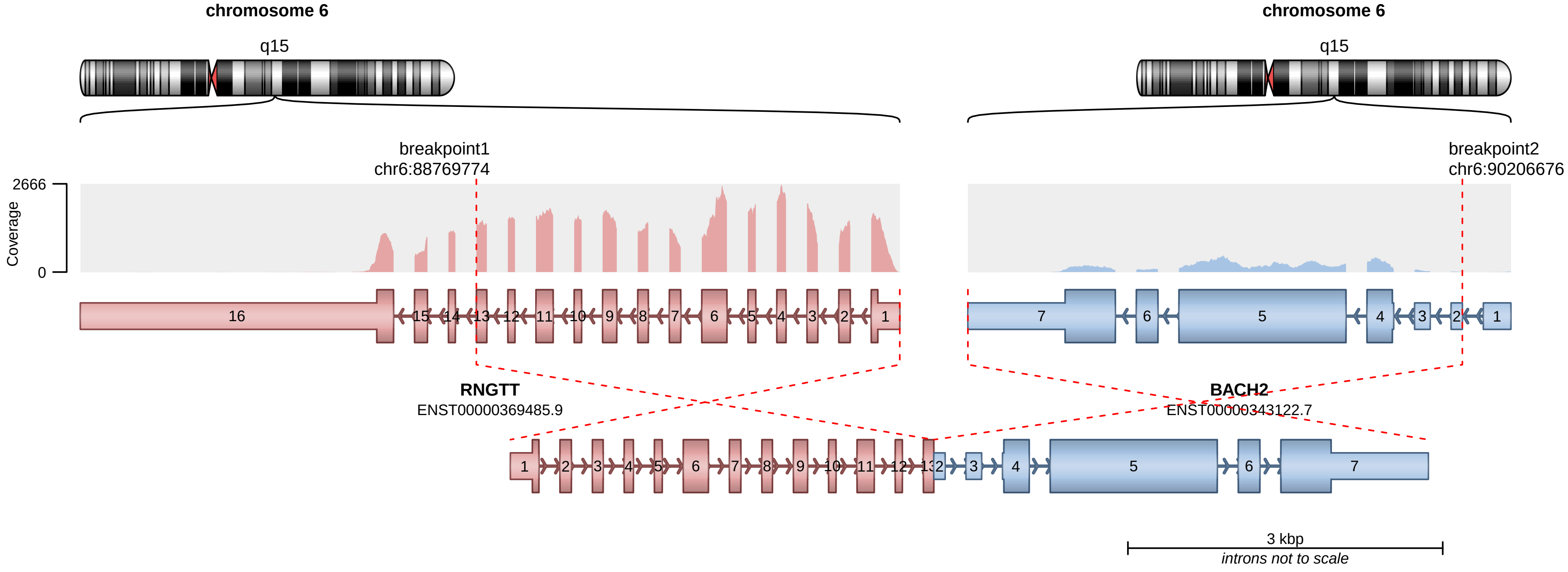
RETAINED PROTEIN DOMAINS

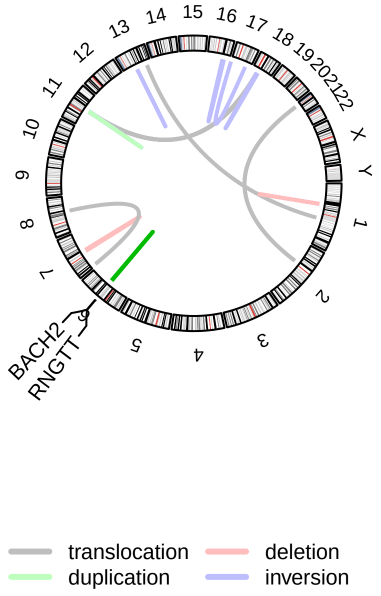
reading frame unclear



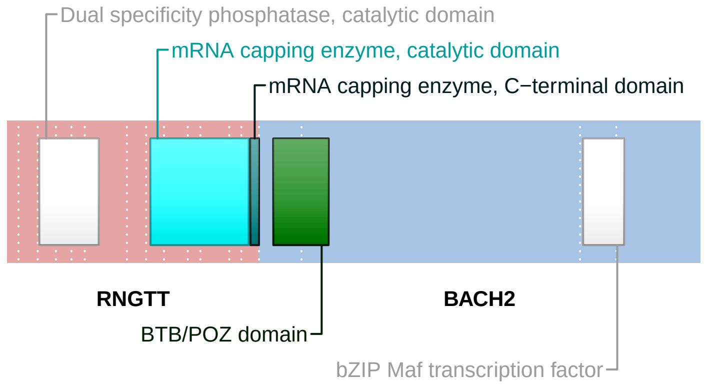
SUPPORTING READ COUNT

Split reads = 11
Discordant mates = 1



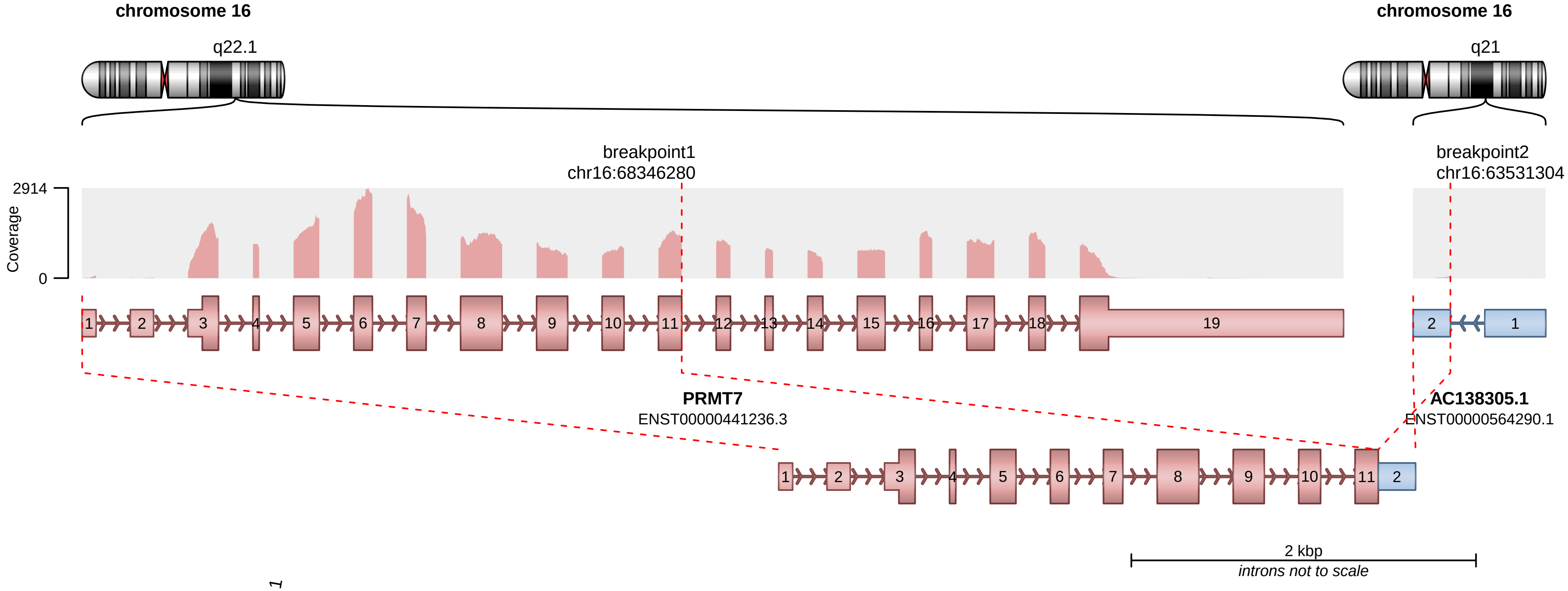


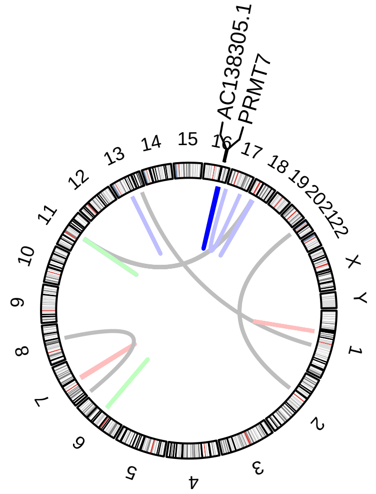
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

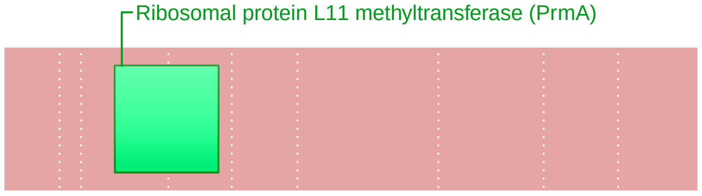
Split reads = 1
Discordant mates = 0





━ translocation ━ deletion
━ duplication ━ inversion

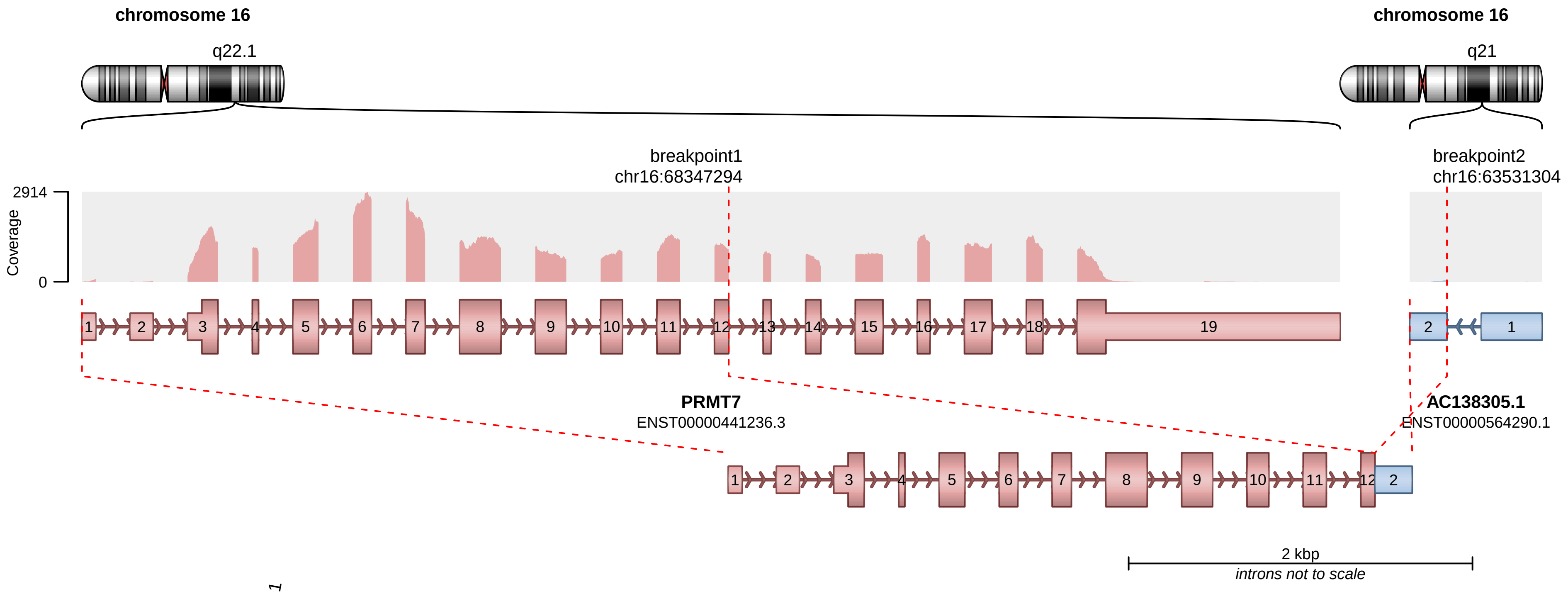
RETAINED PROTEIN DOMAINS
reading frame unclear

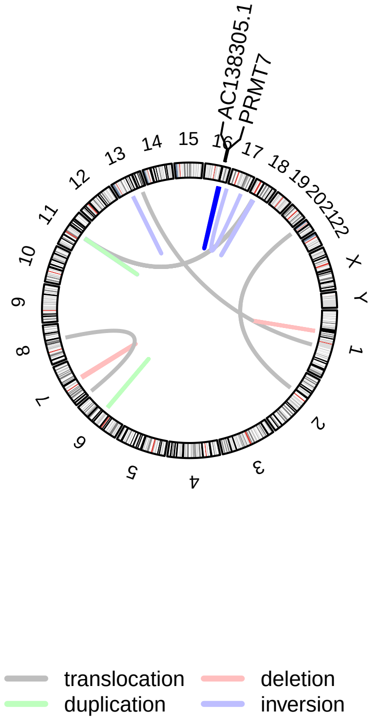


PRMT7

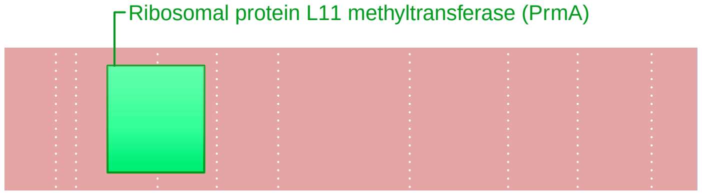
SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 0





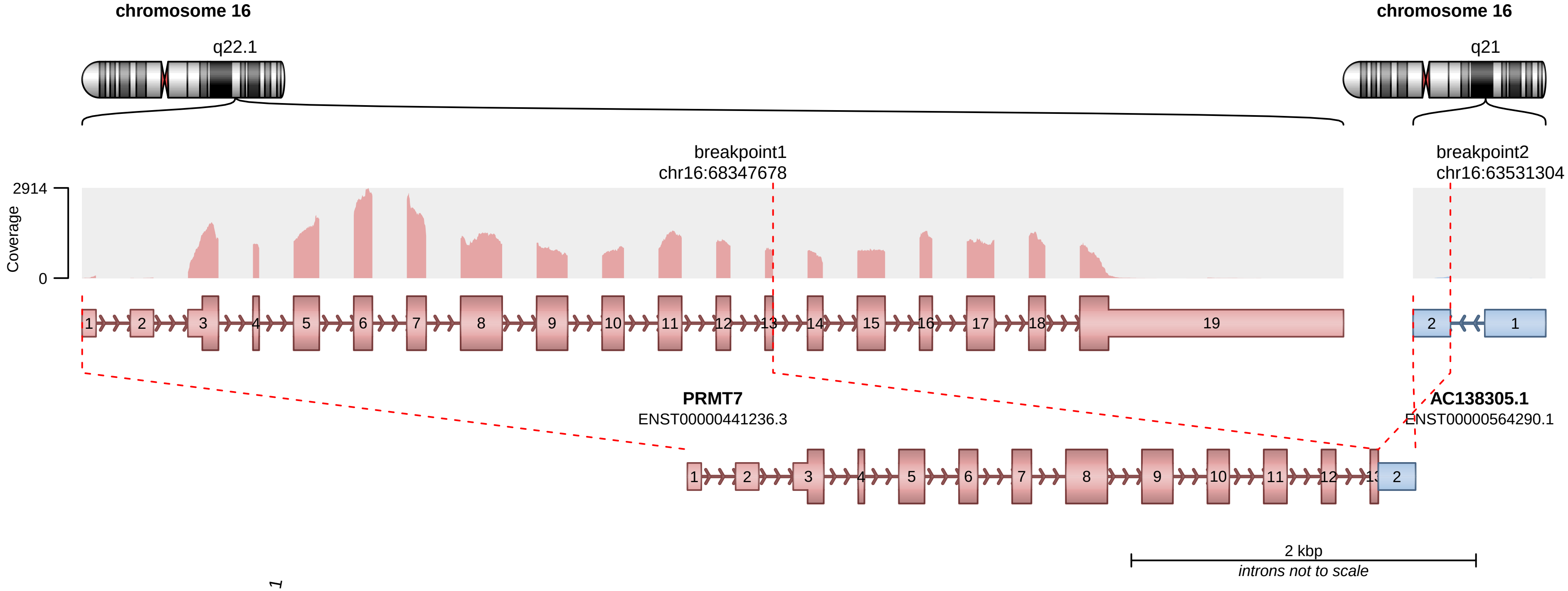
RETAINED PROTEIN DOMAINS
reading frame unclear

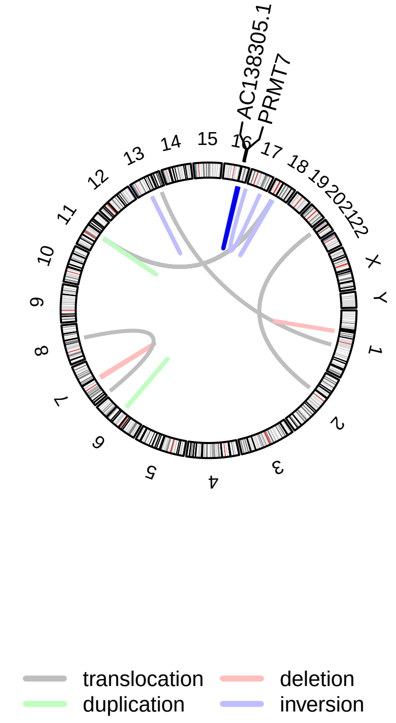


PRMT7

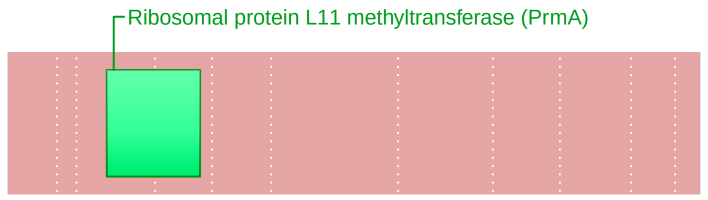
SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 0





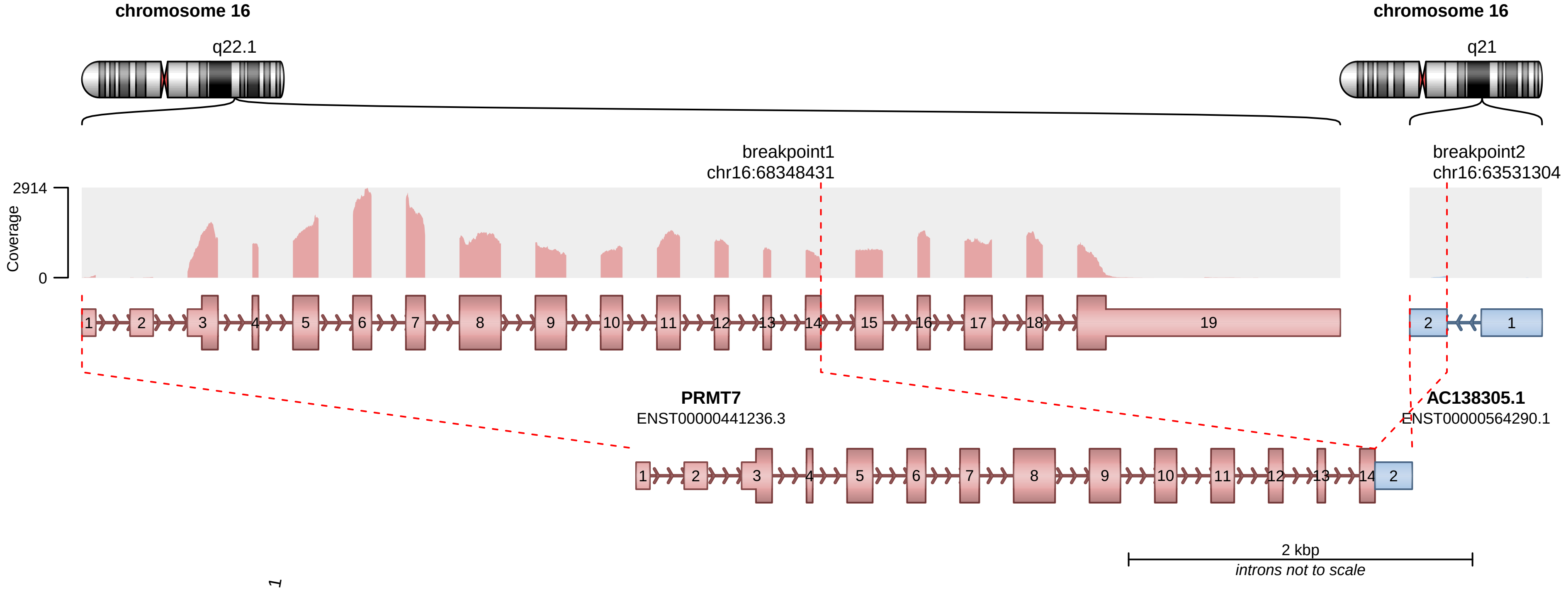
RETAINED PROTEIN DOMAINS
reading frame unclear

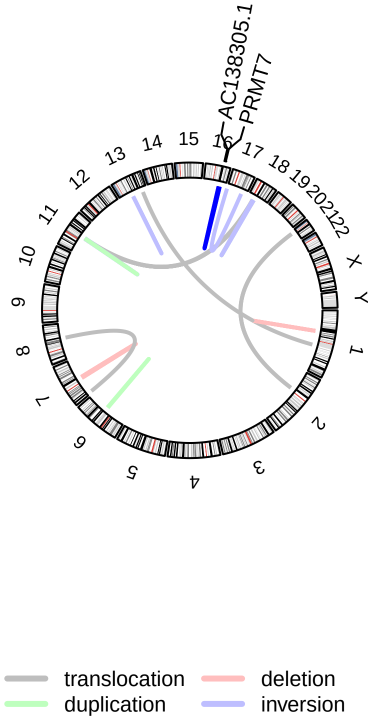


PRMT7

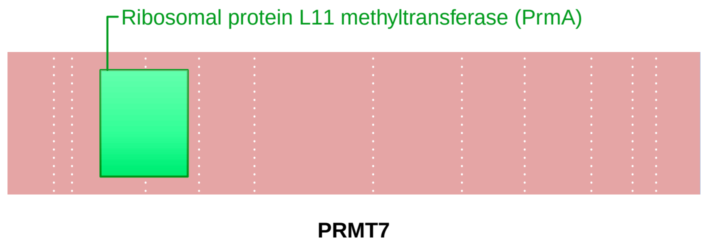
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0



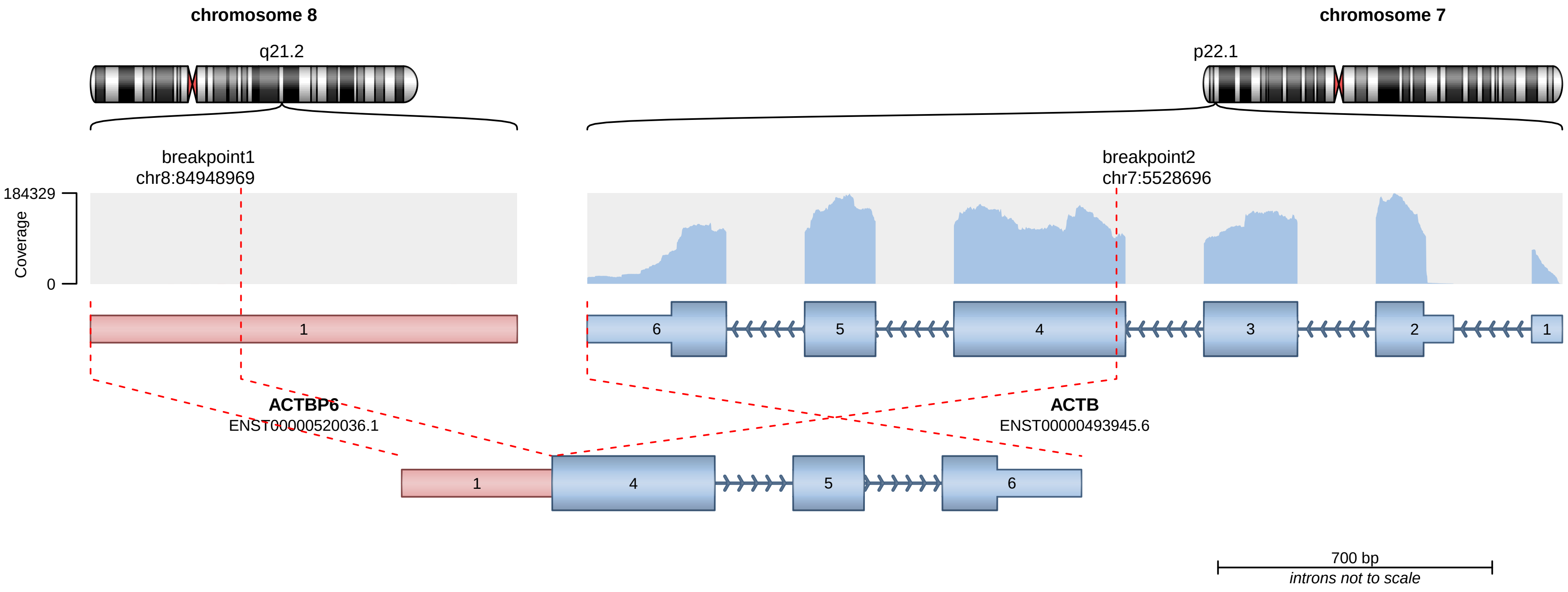


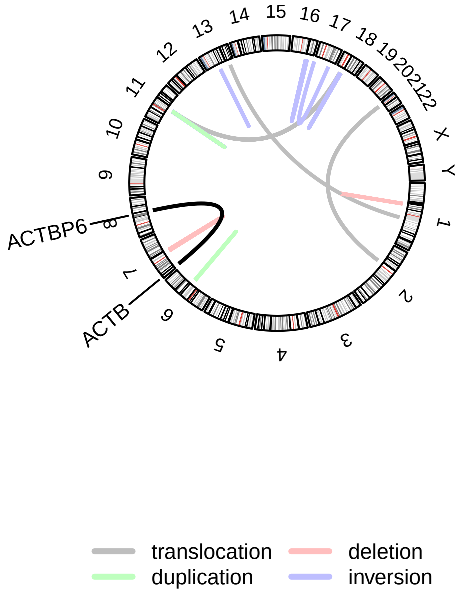
RETAINED PROTEIN DOMAINS
reading frame unclear



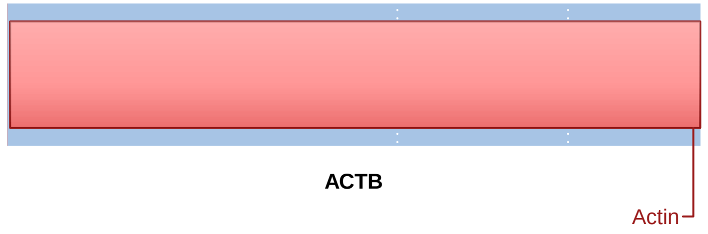
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0



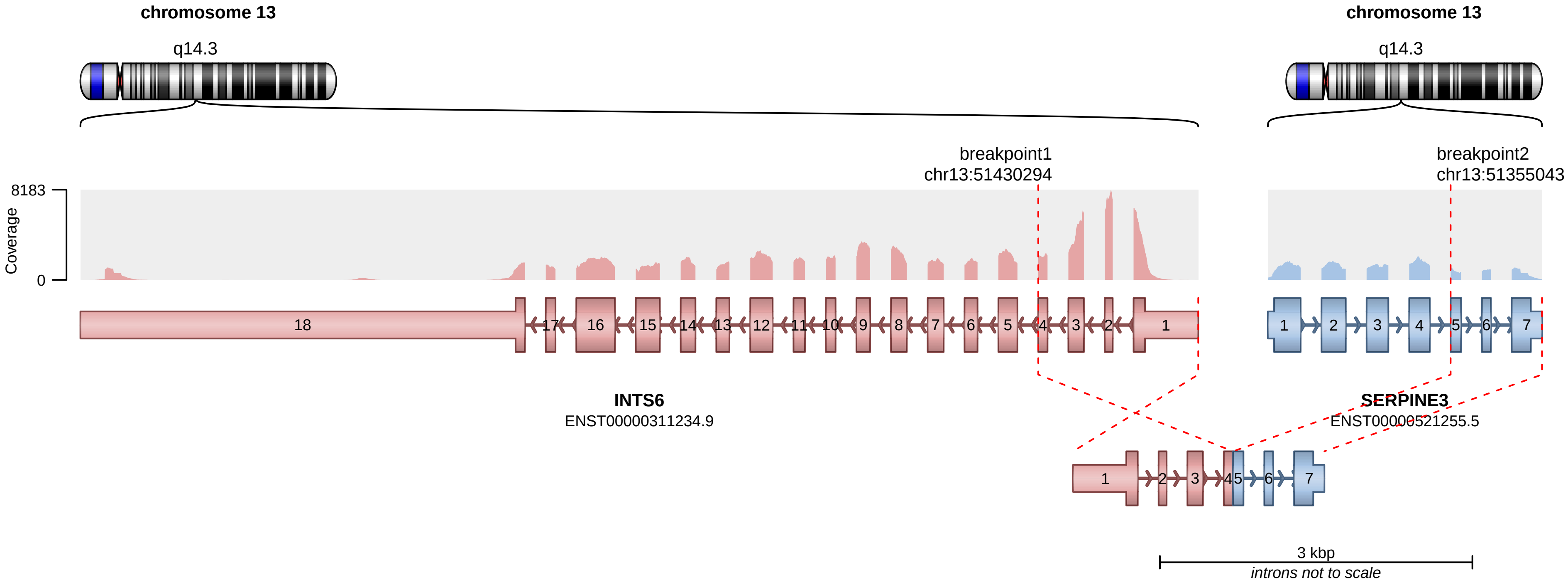


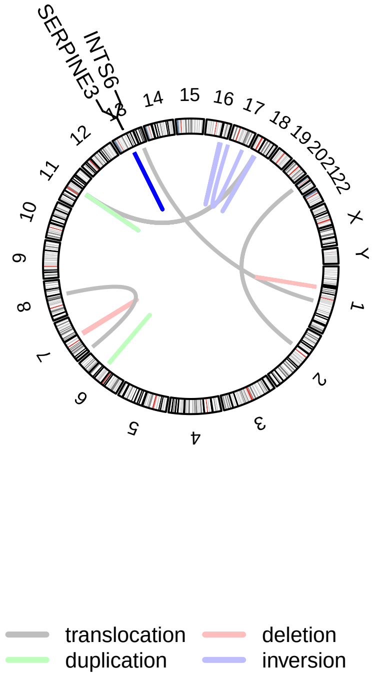
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

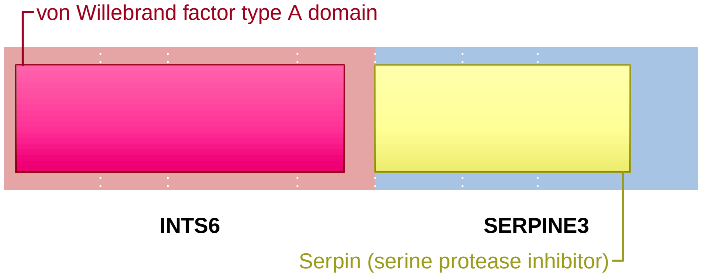
Split reads = 7
Discordant mates = 0





RETAINED PROTEIN DOMAINS

reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0