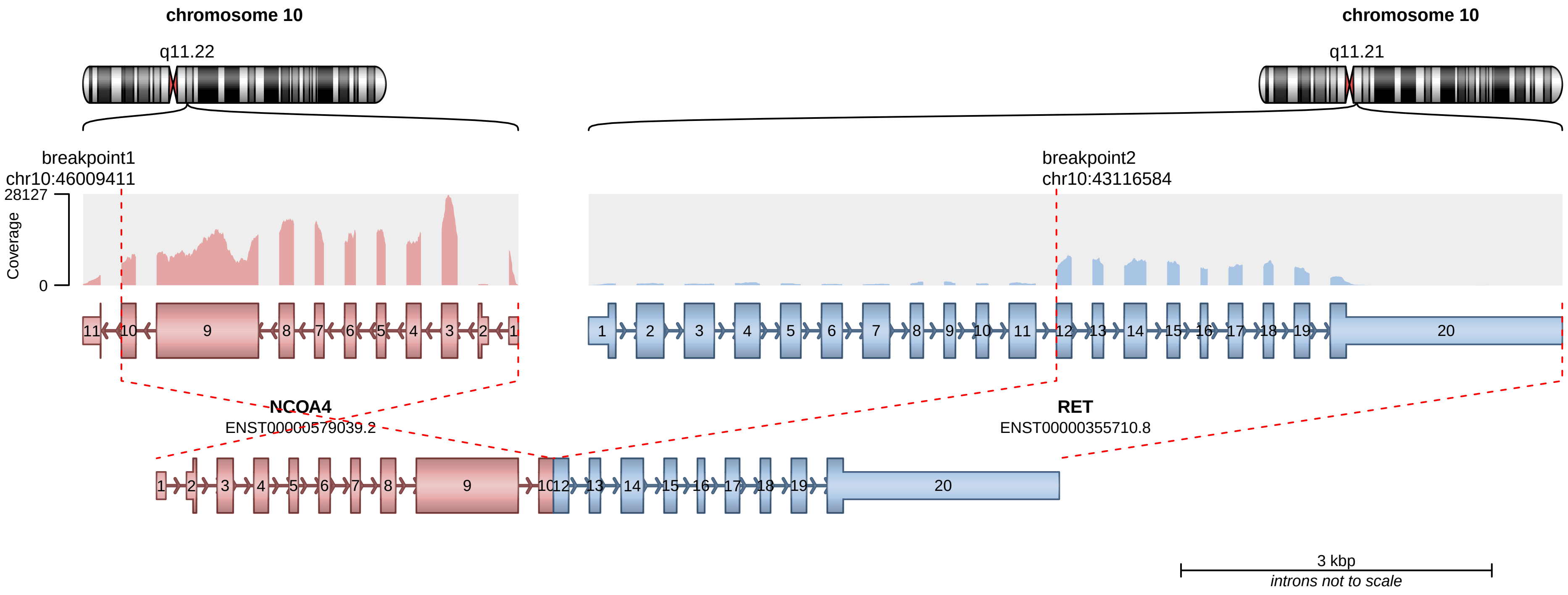
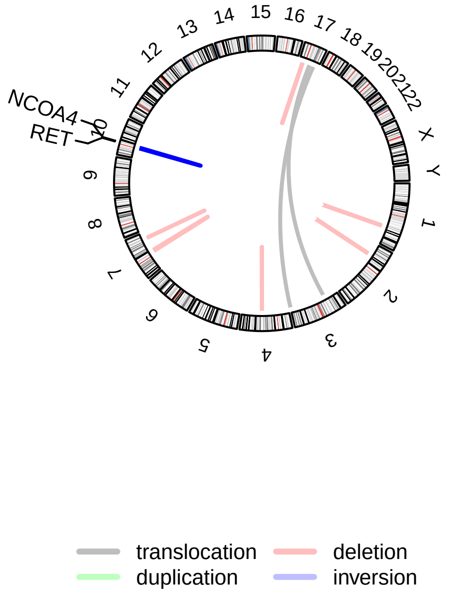
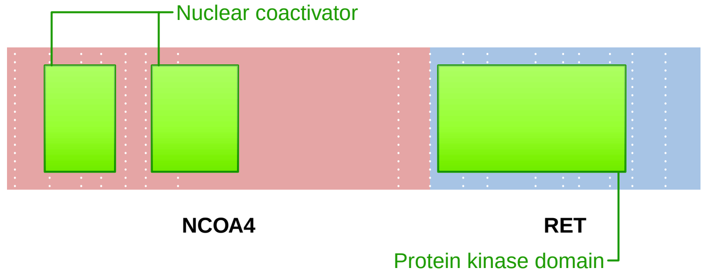


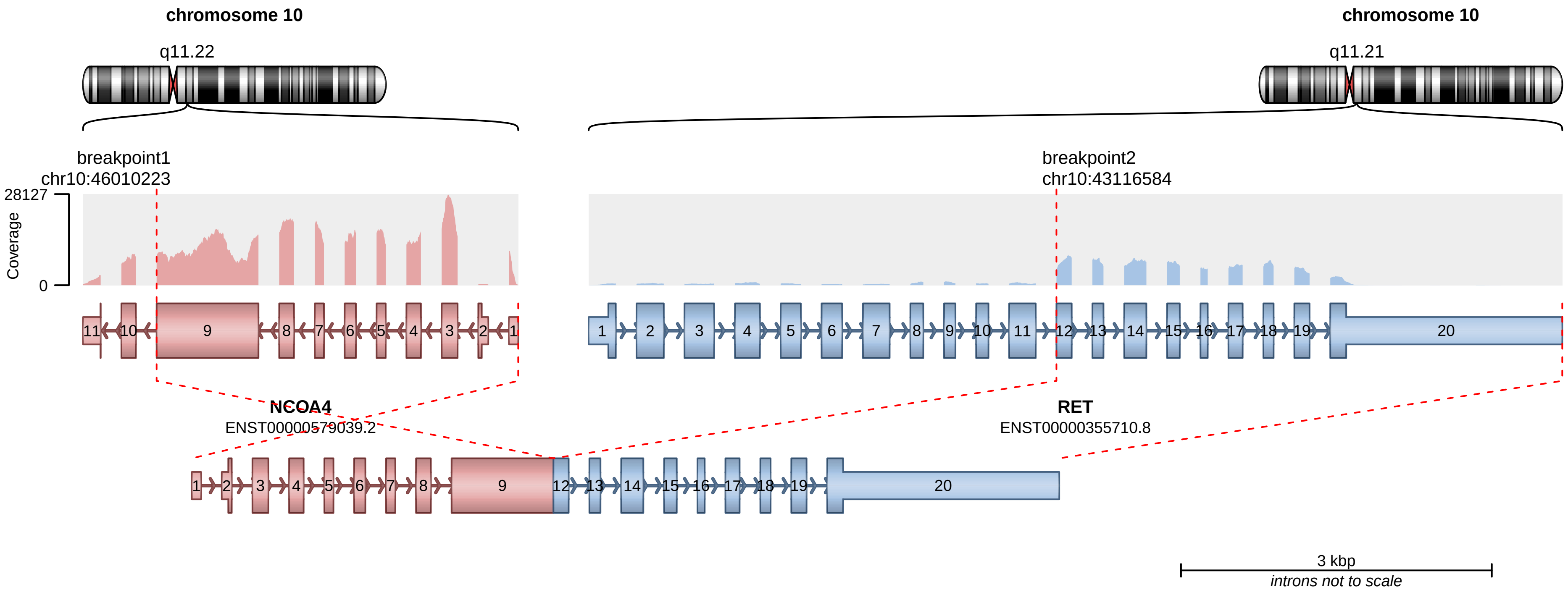


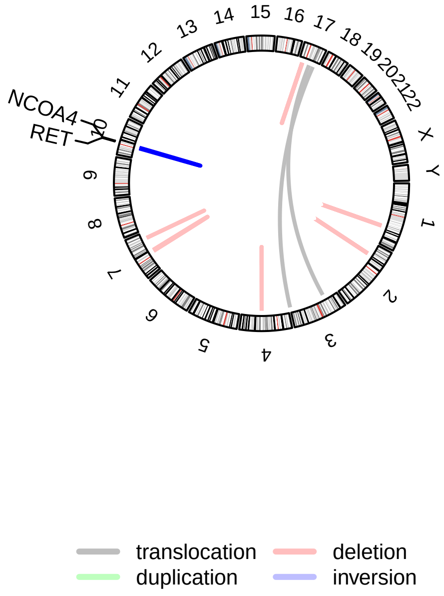
RETAINED PROTEIN DOMAINS
reading frame unclear

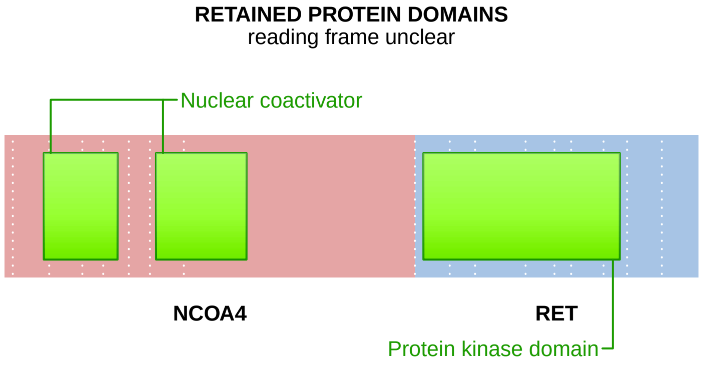


SUPPORTING READ COUNT

Split reads = 871
Discordant mates = 3

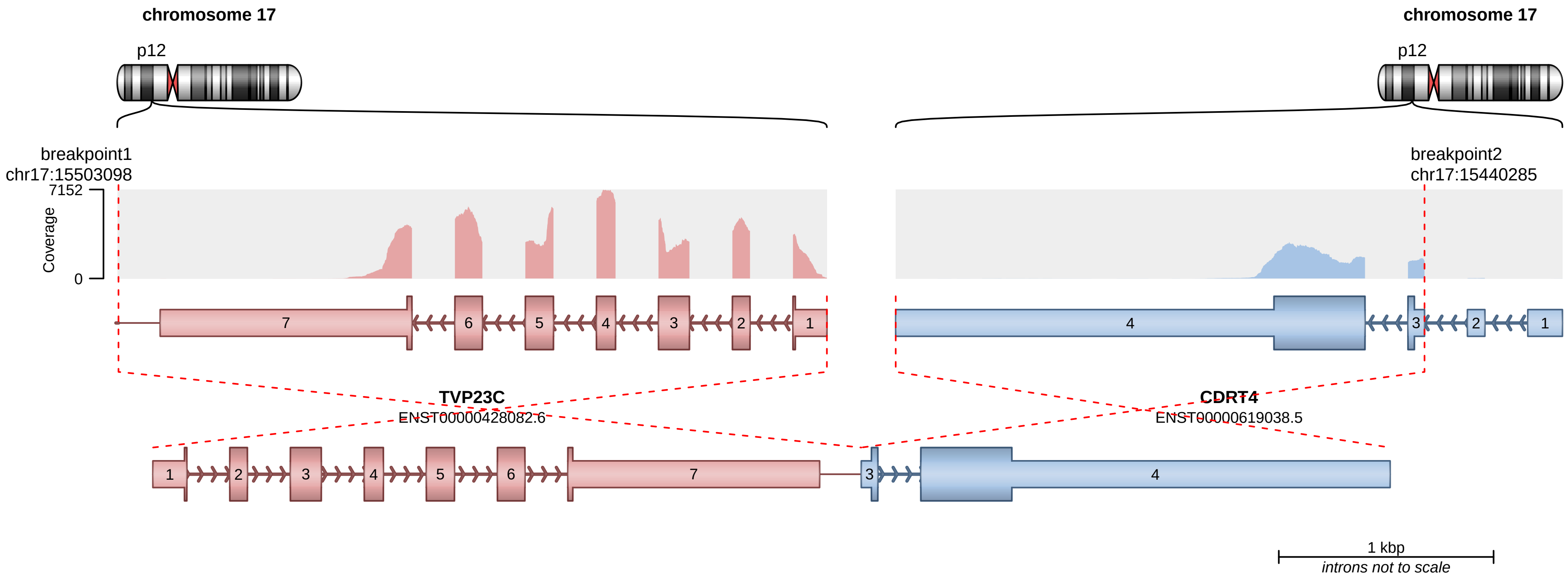


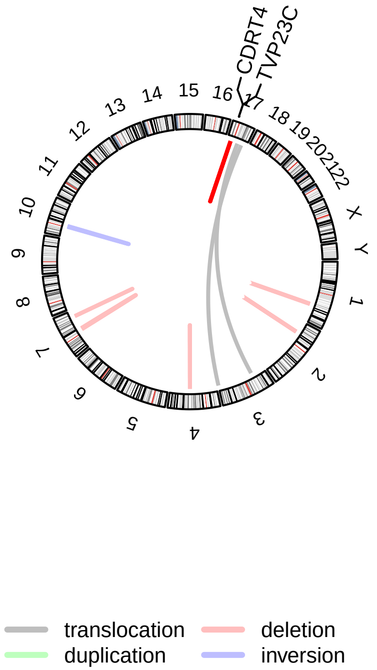




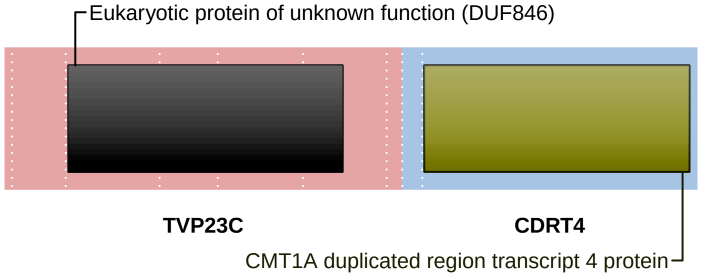
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 2



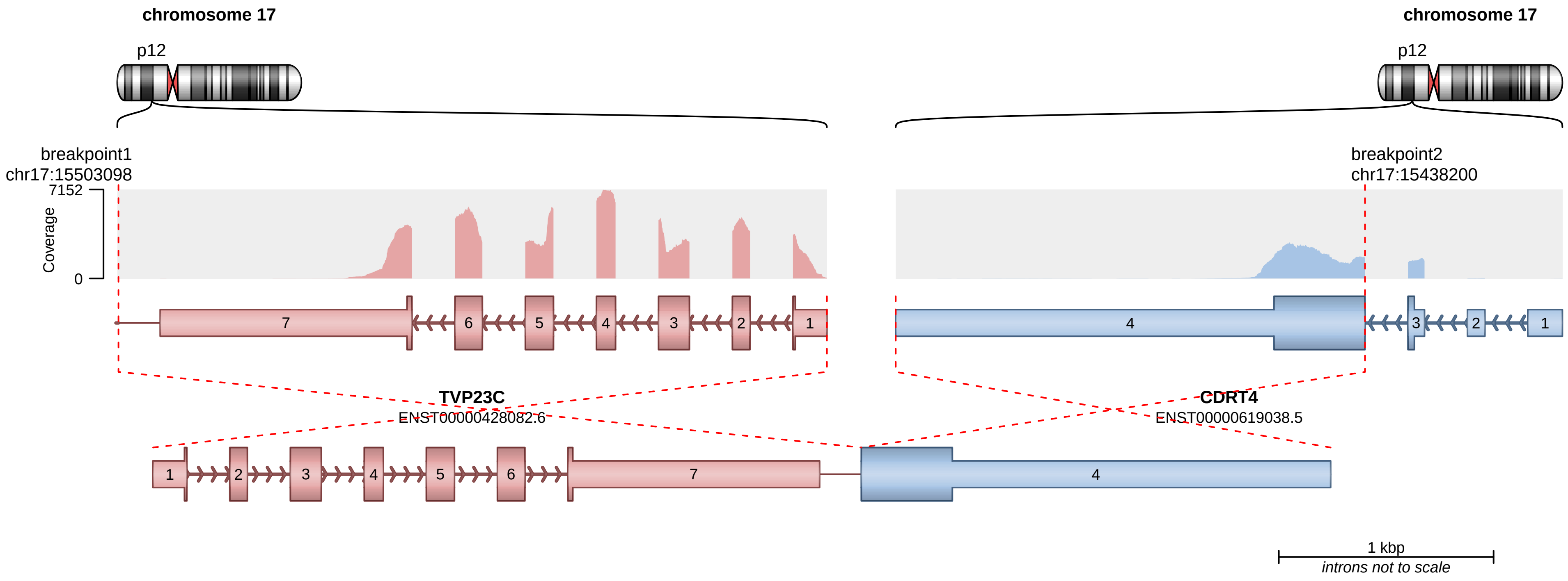


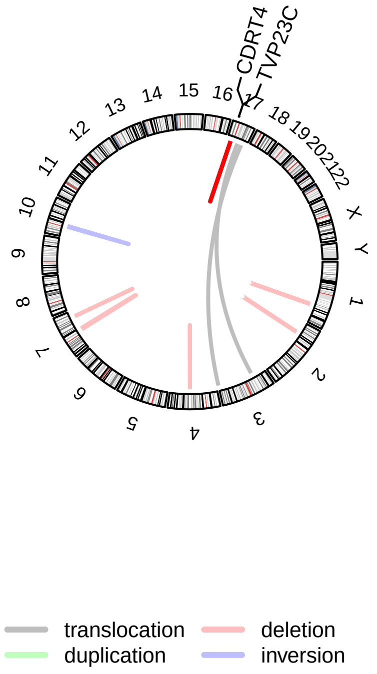
RETAINED PROTEIN DOMAINS
reading frame unclear



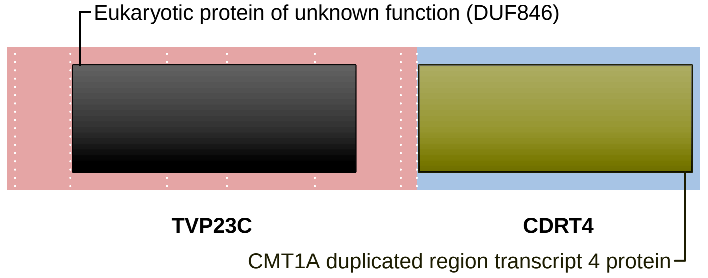
SUPPORTING READ COUNT

Split reads = 197
Discordant mates = 2



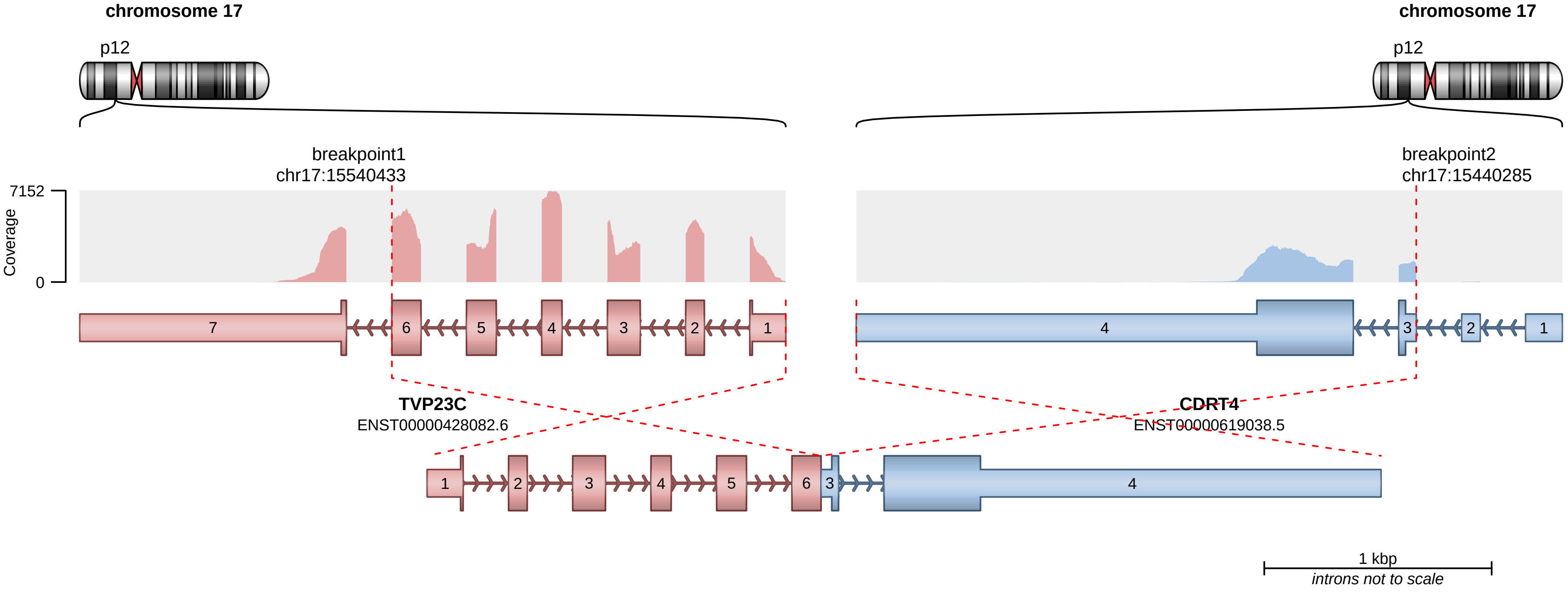


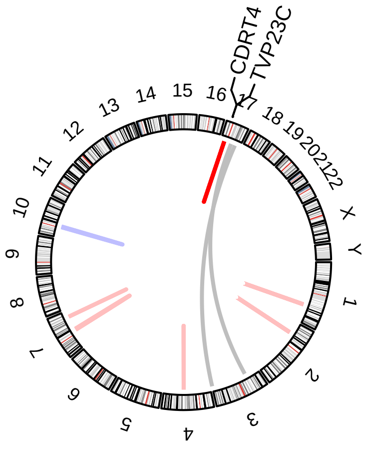
RETAINED PROTEIN DOMAINS
reading frame unclear



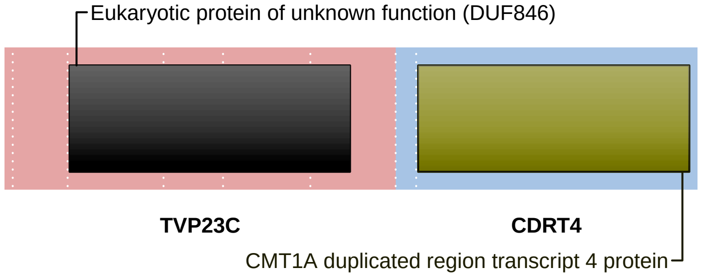
SUPPORTING READ COUNT

Split reads = 53
Discordant mates = 1





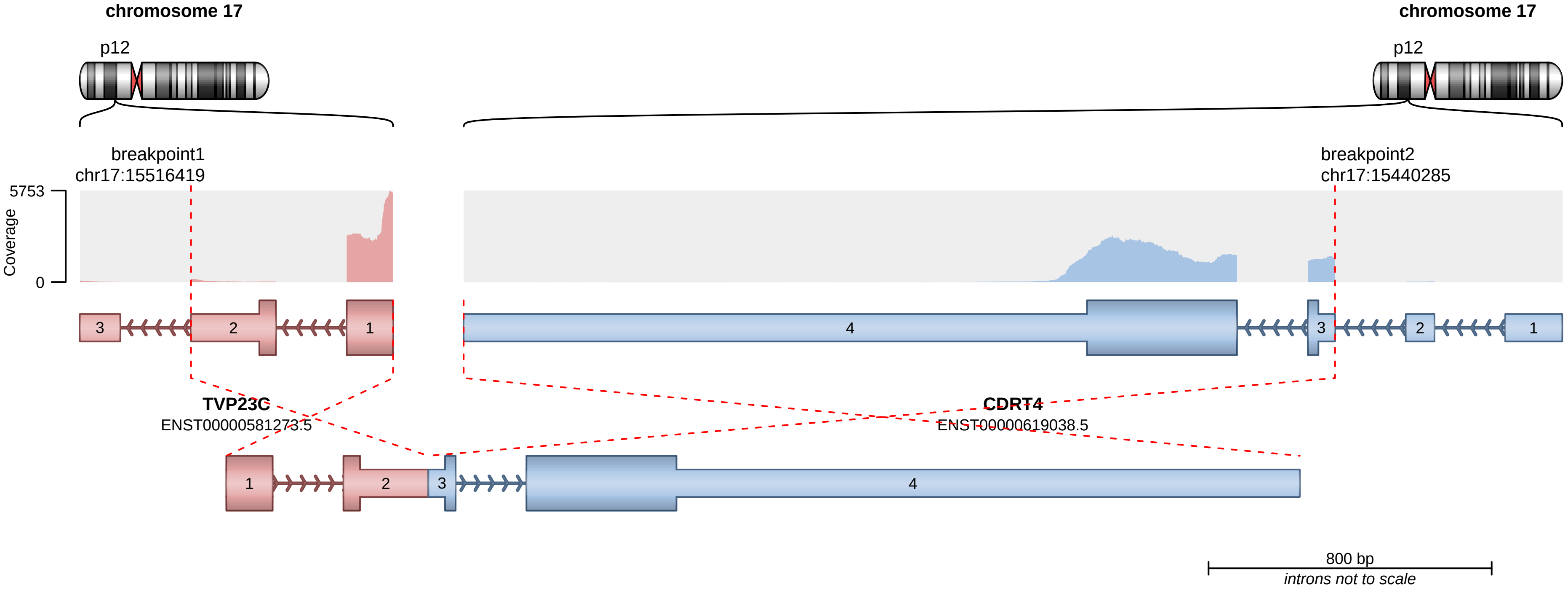
RETAINED PROTEIN DOMAINS
reading frame unclear

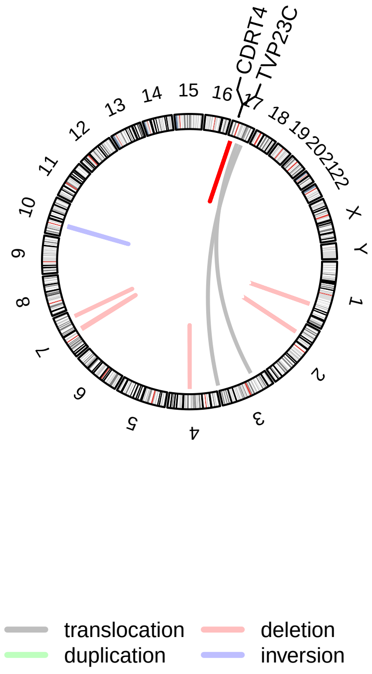


SUPPORTING READ COUNT

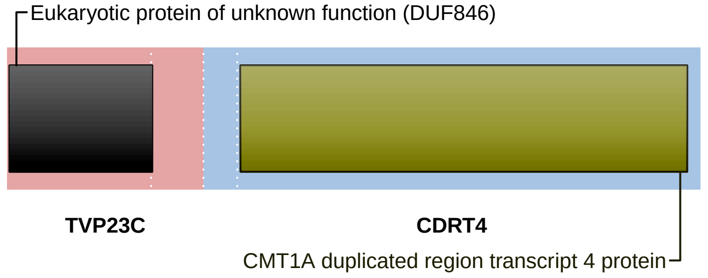
Split reads = 37
Discordant mates = 1

— translocation — deletion
— duplication — inversion



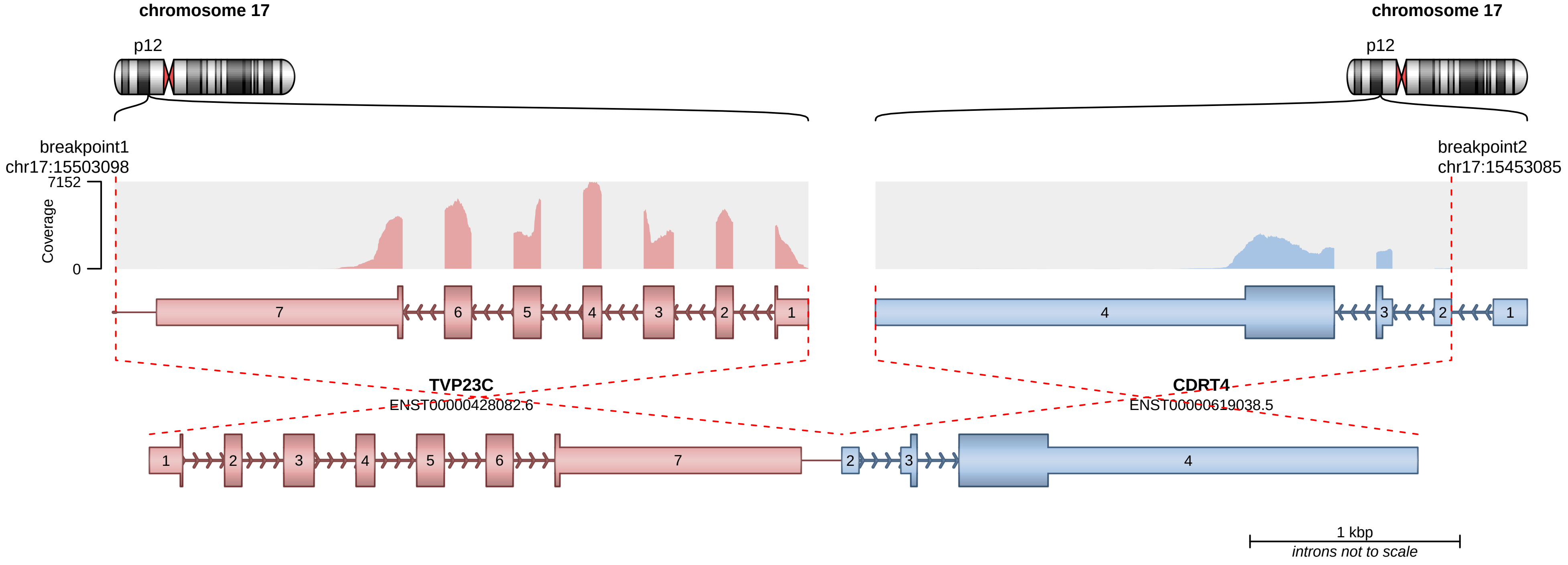


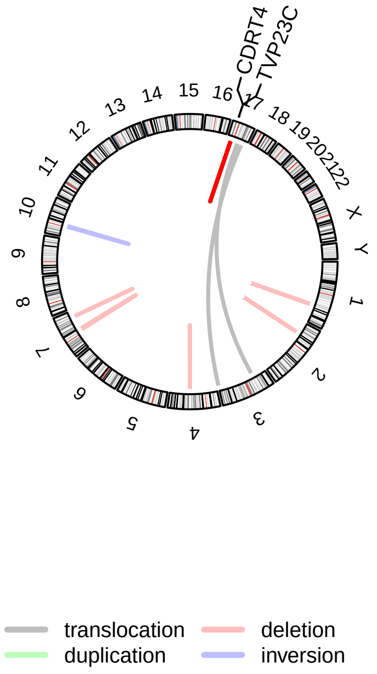
RETAINED PROTEIN DOMAINS
reading frame unclear

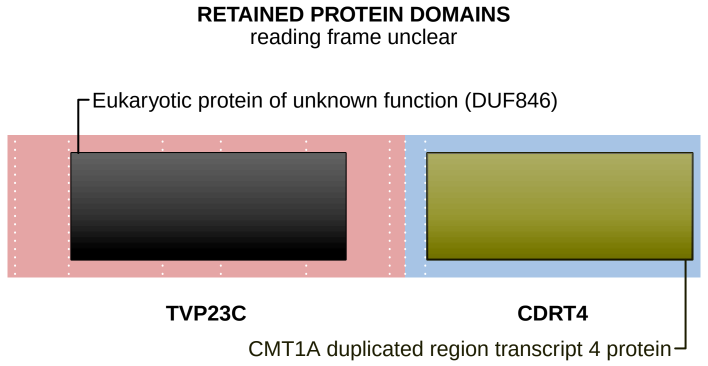


SUPPORTING READ COUNT

Split reads = 27
Discordant mates = 1

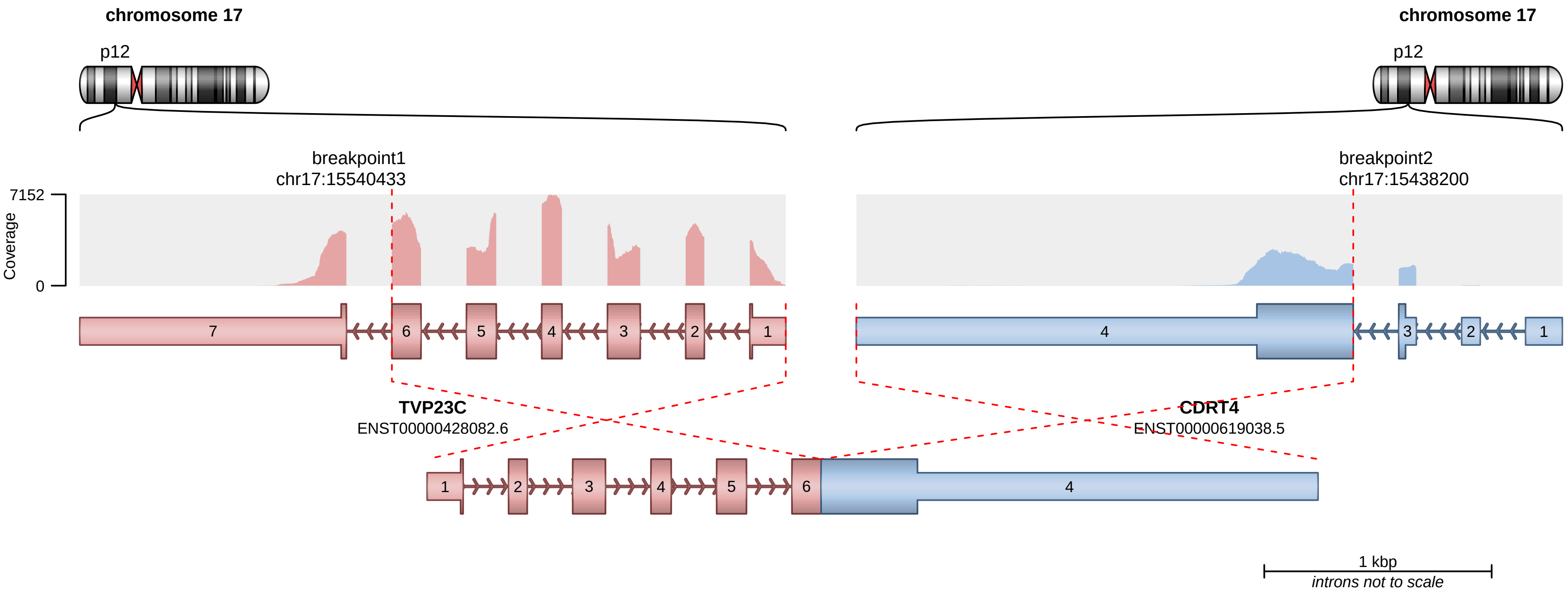


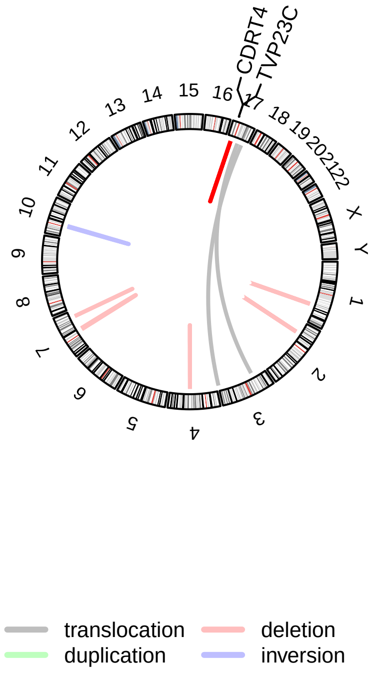


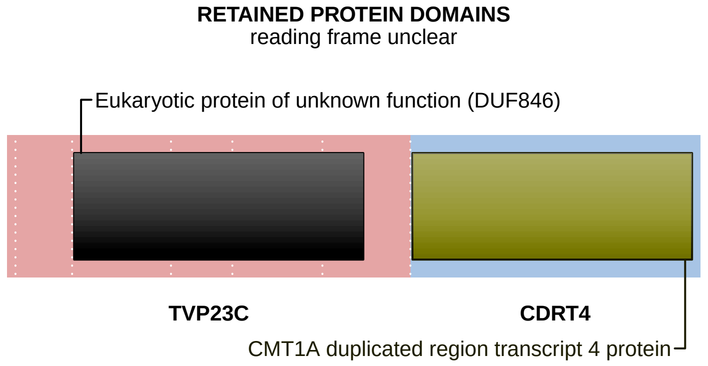


SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 2

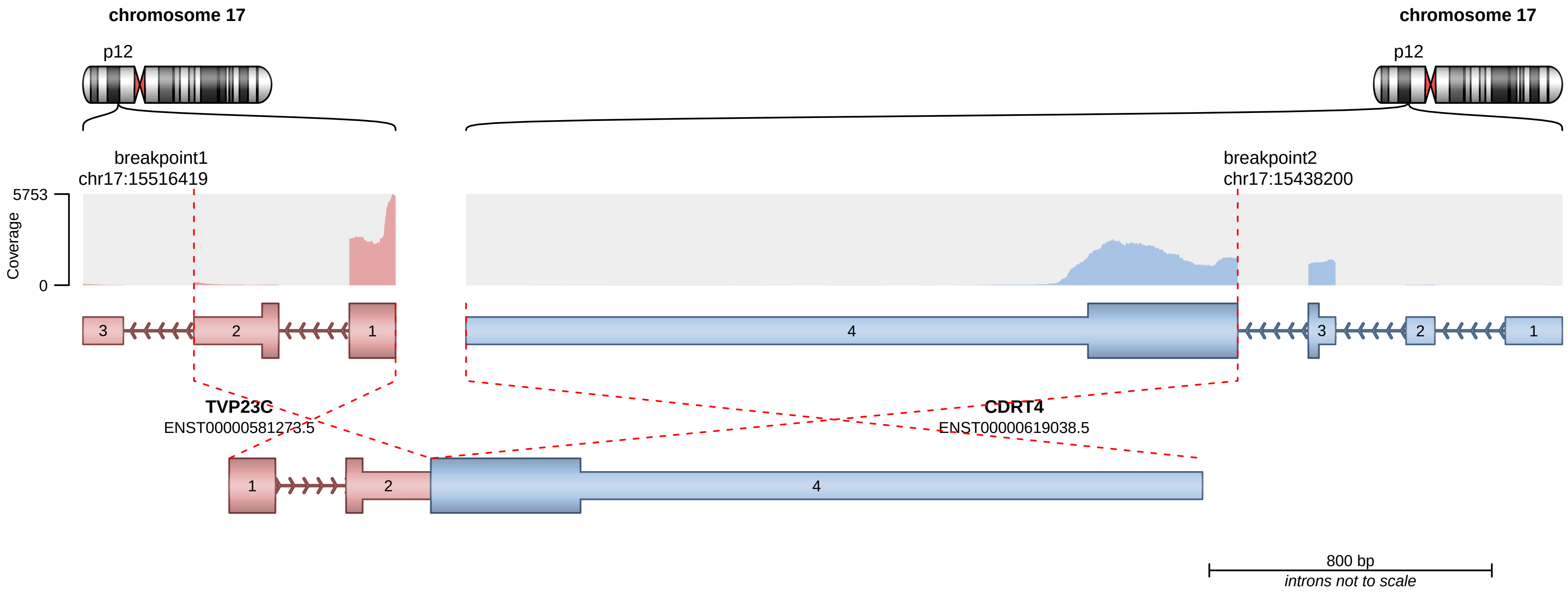


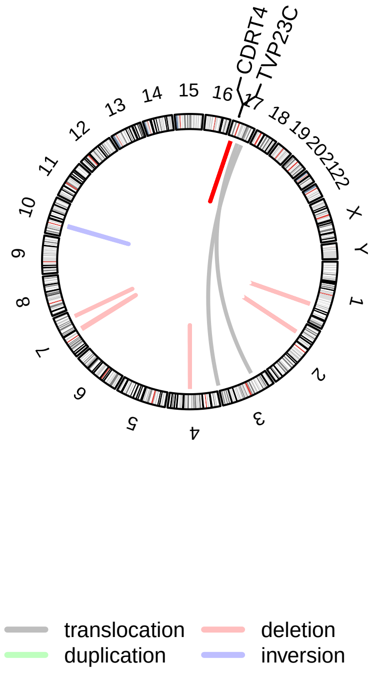


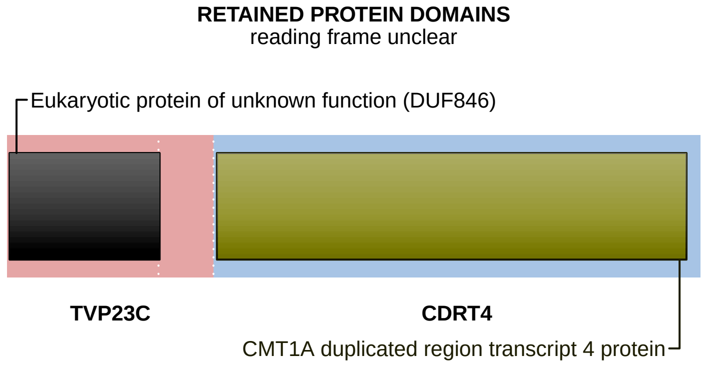


SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0

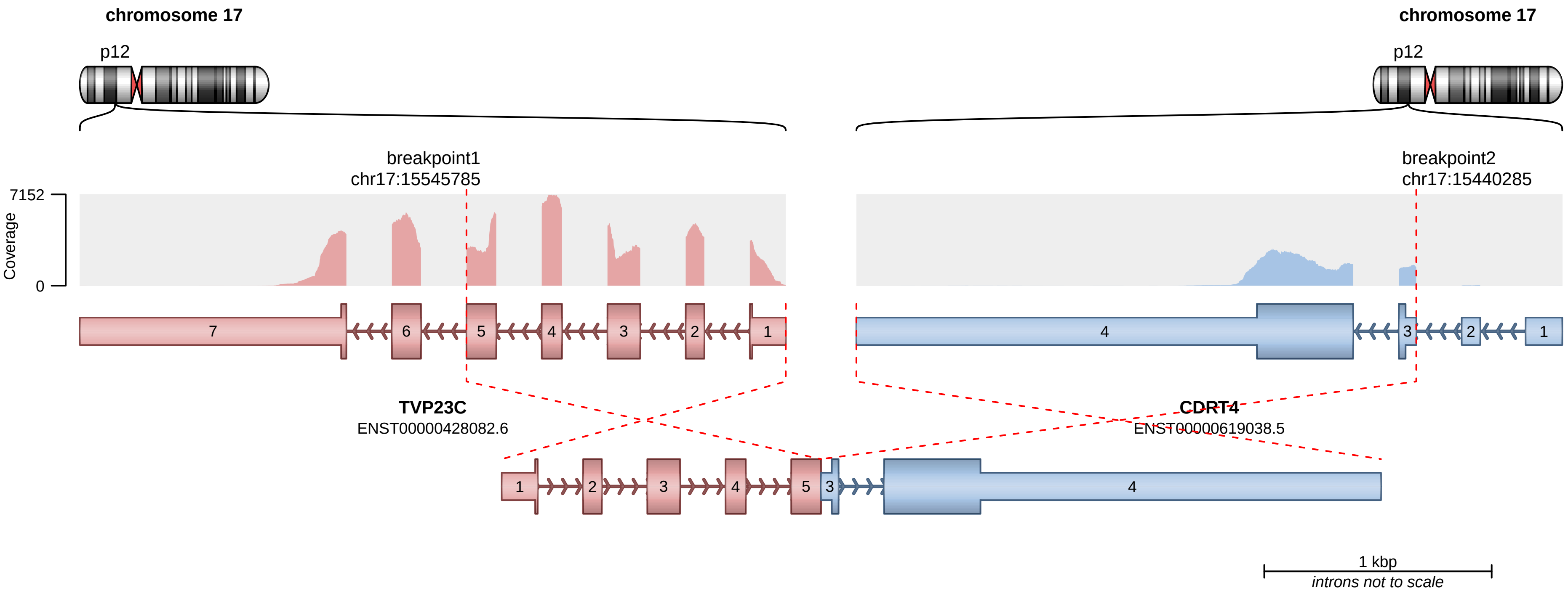


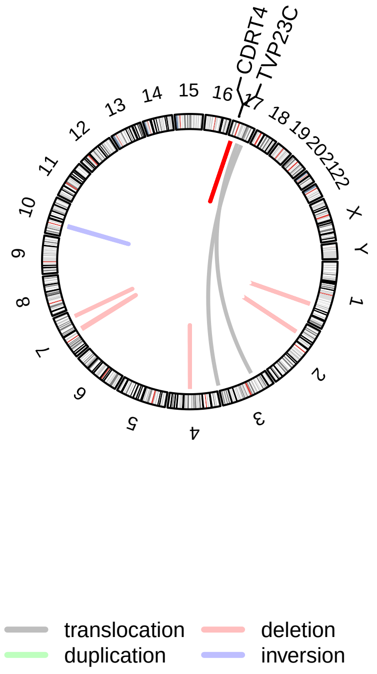


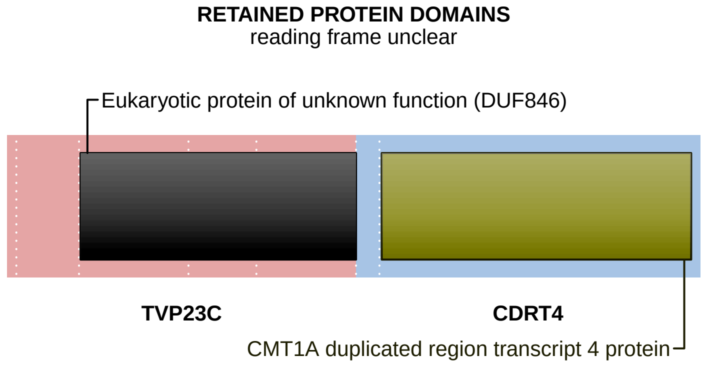


SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

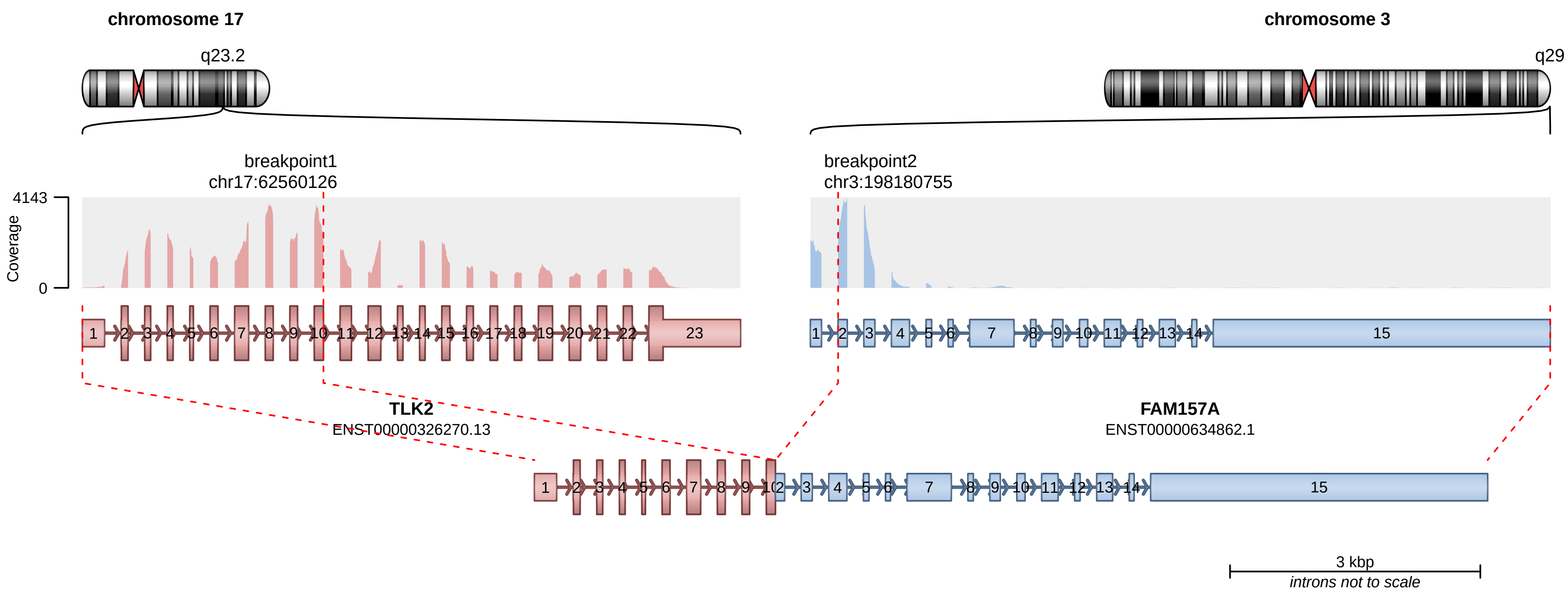


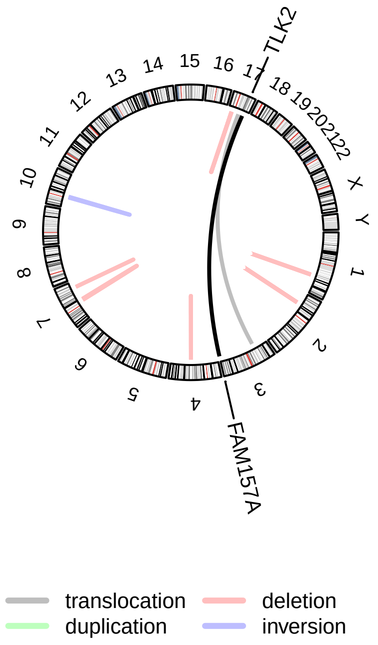




SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

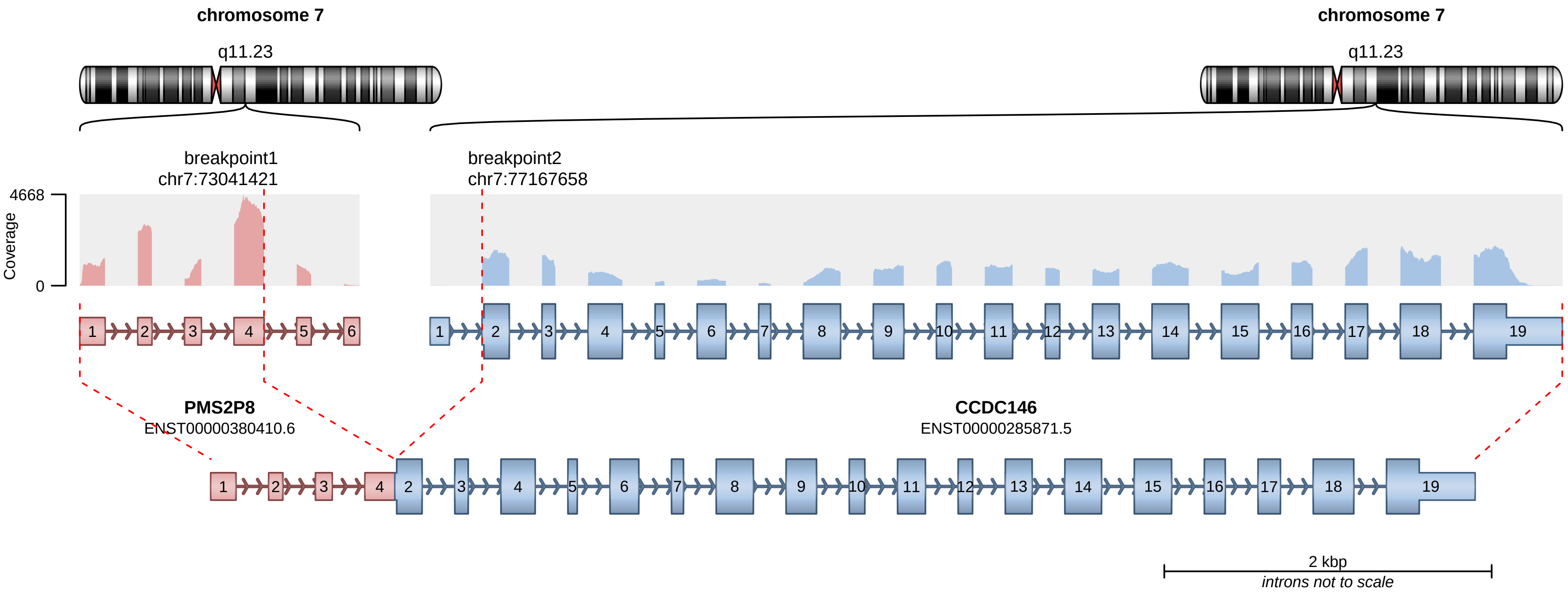


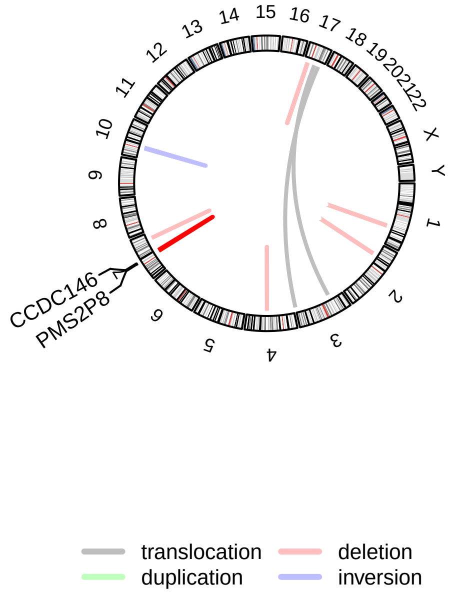


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 140
Discordant mates = 3

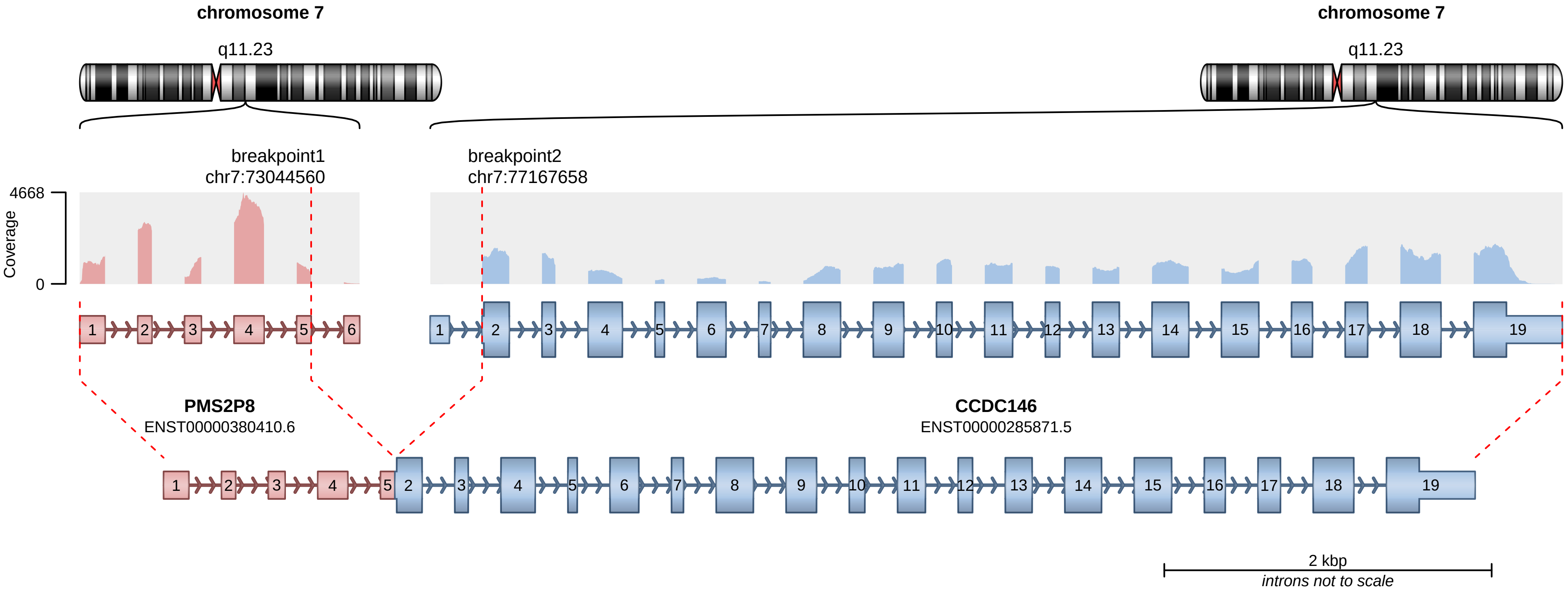


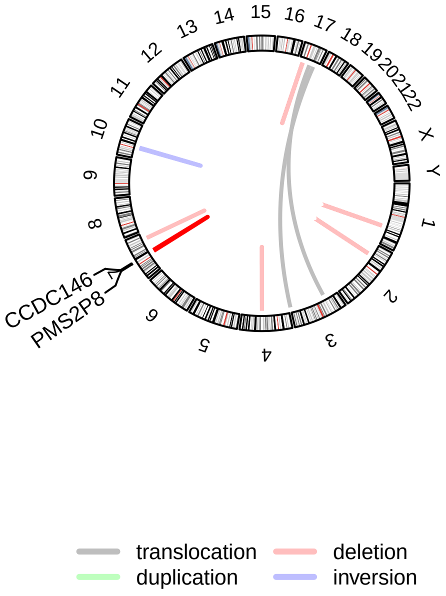


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 133
Discordant mates = 8

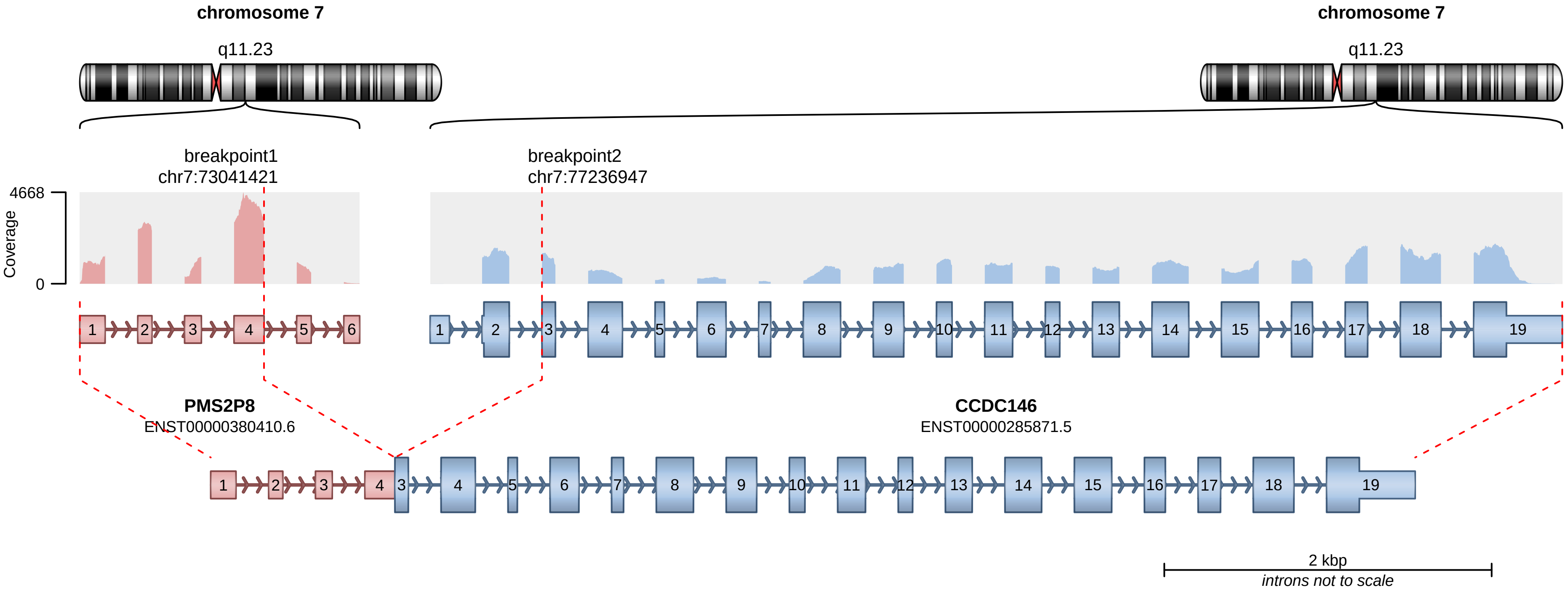


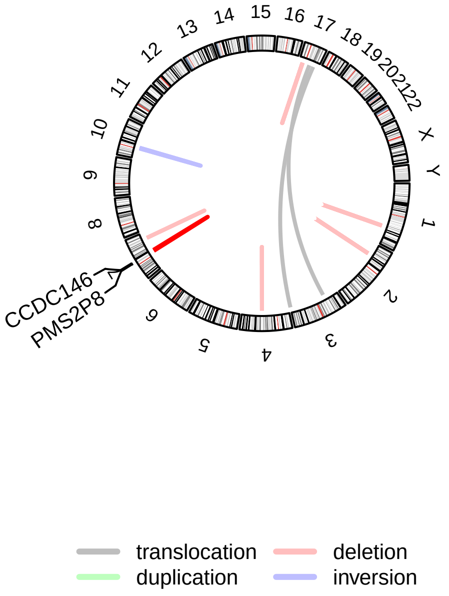


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 41
Discordant mates = 9

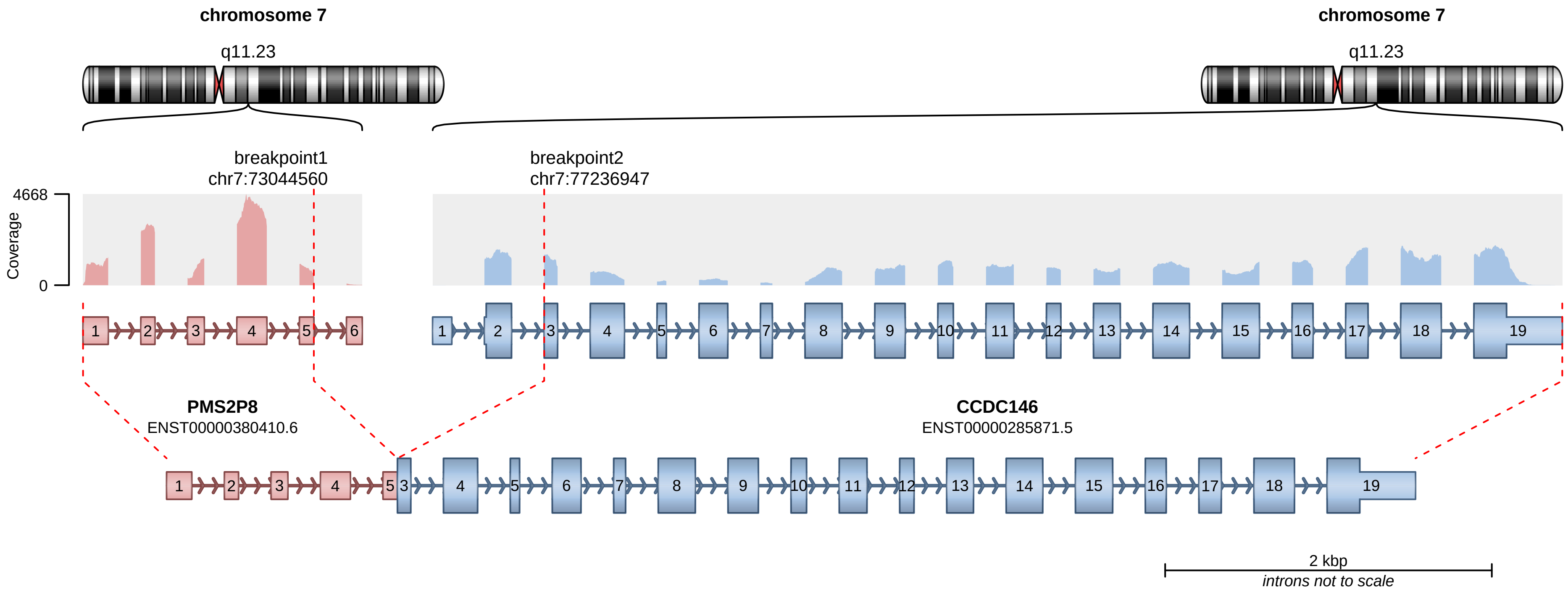


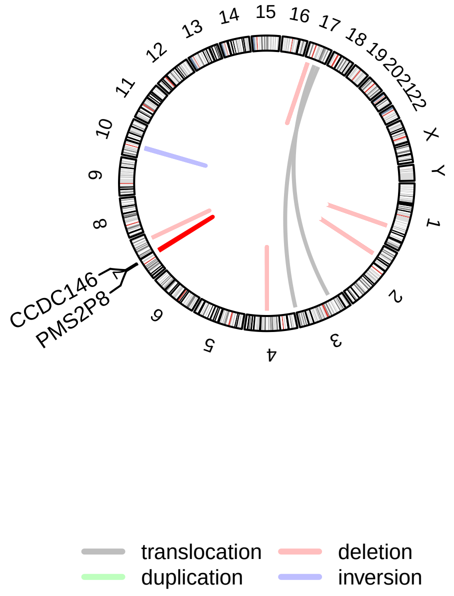


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 14
Discordant mates = 0

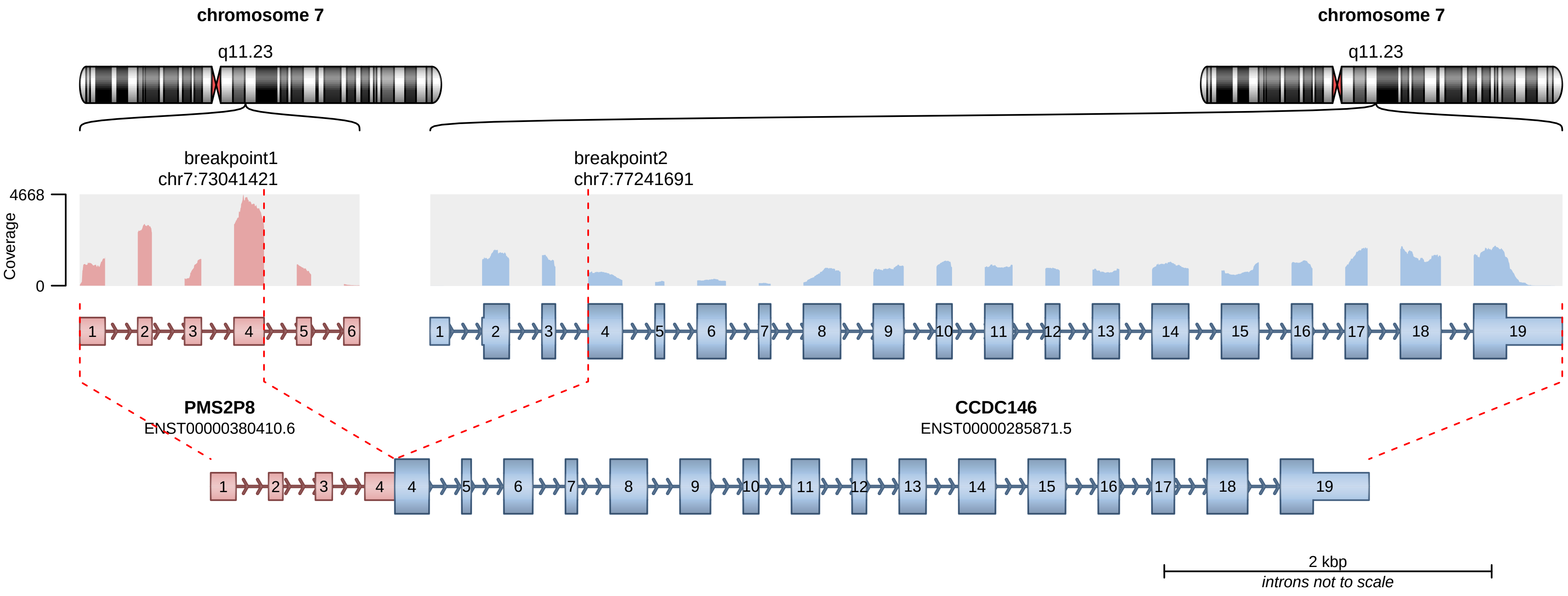


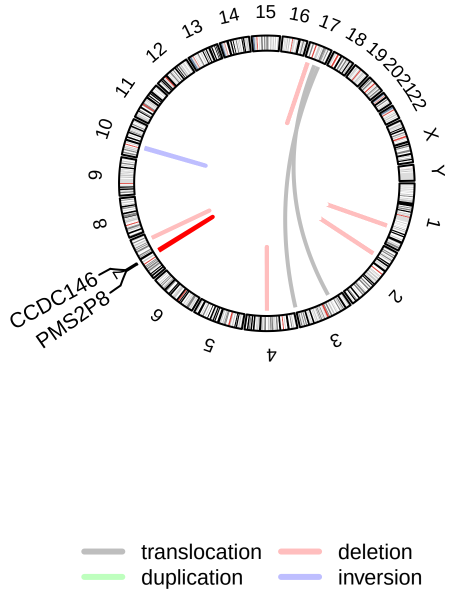


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 0

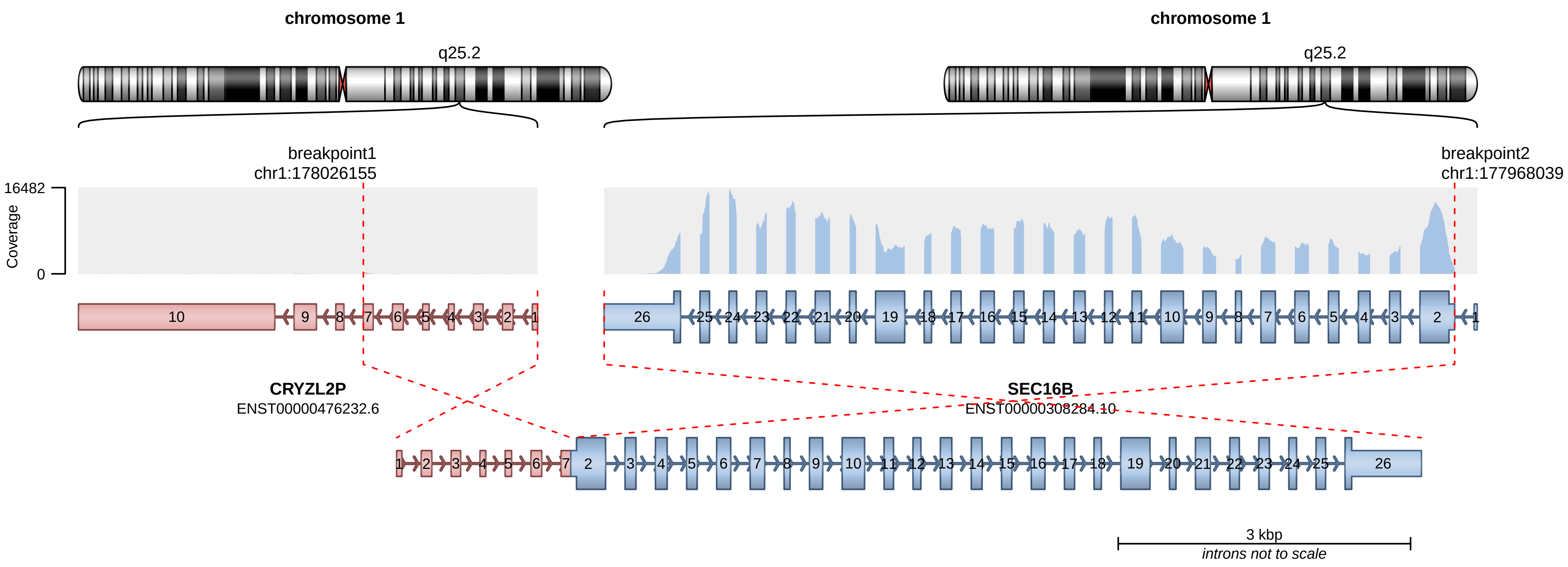


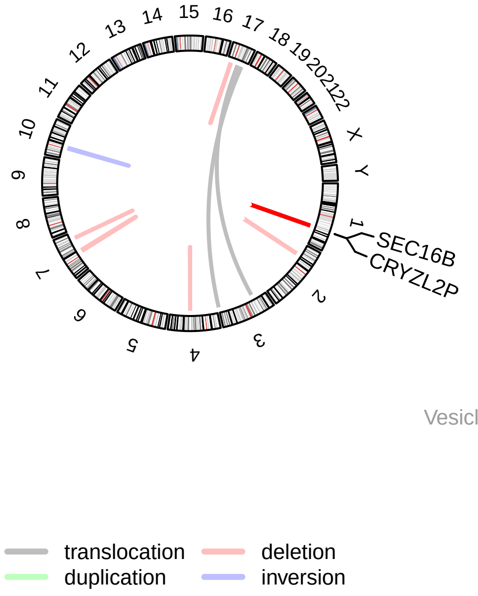


No protein domains retained in fusion.

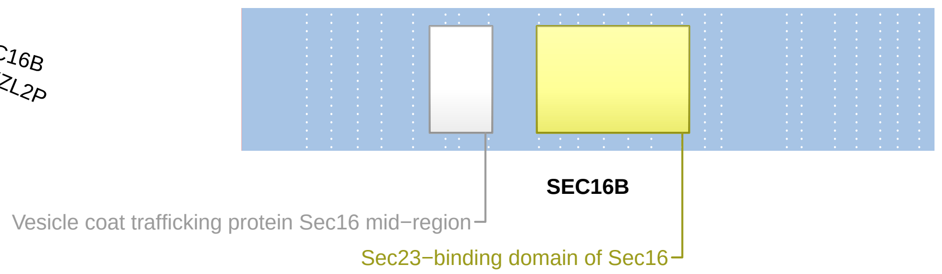
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



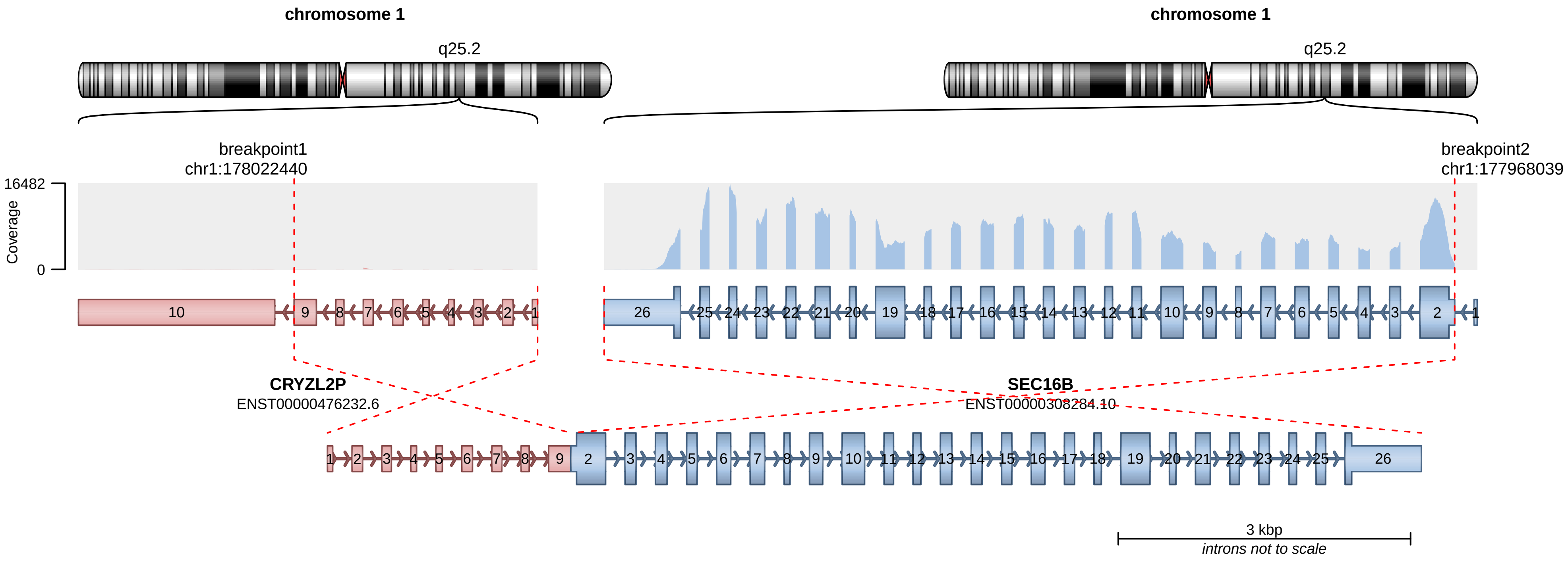


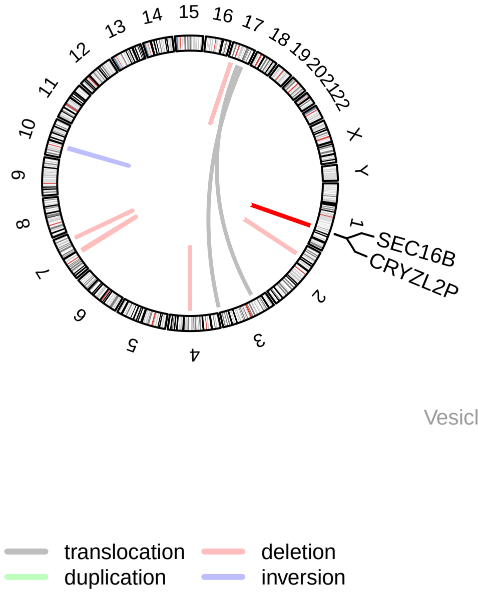
RETAINED PROTEIN DOMAINS
reading frame unclear



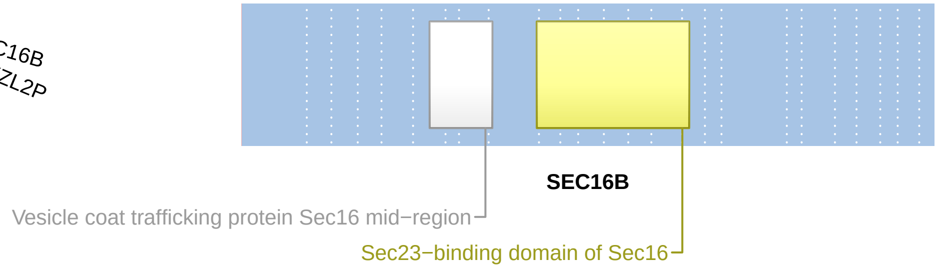
SUPPORTING READ COUNT

Split reads = 80
Discordant mates = 1



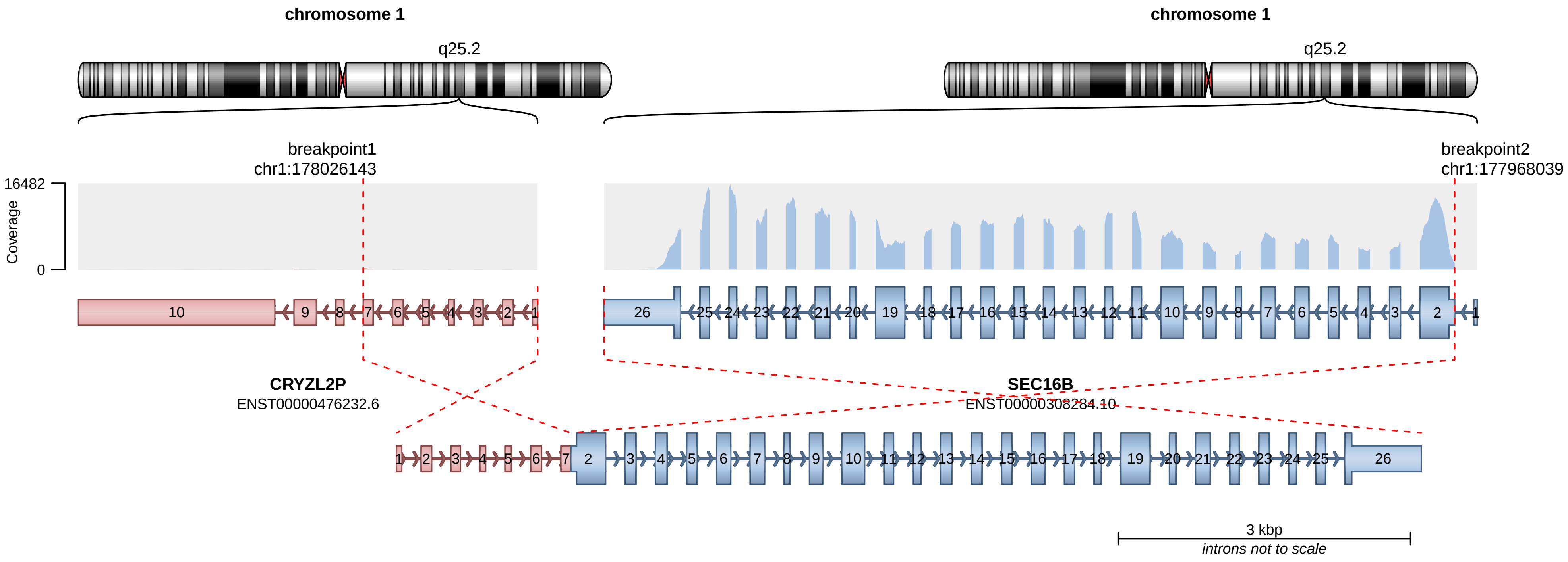


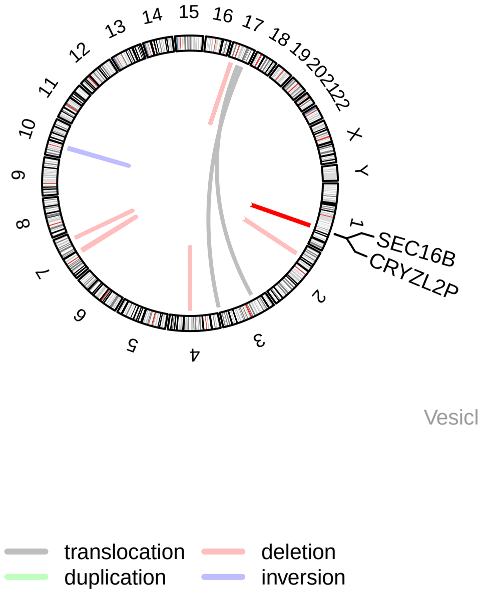
RETAINED PROTEIN DOMAINS
reading frame unclear

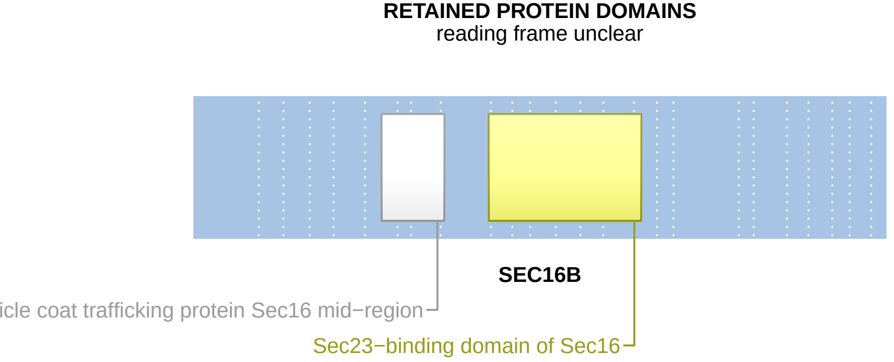


SUPPORTING READ COUNT

Split reads = 11
Discordant mates = 2

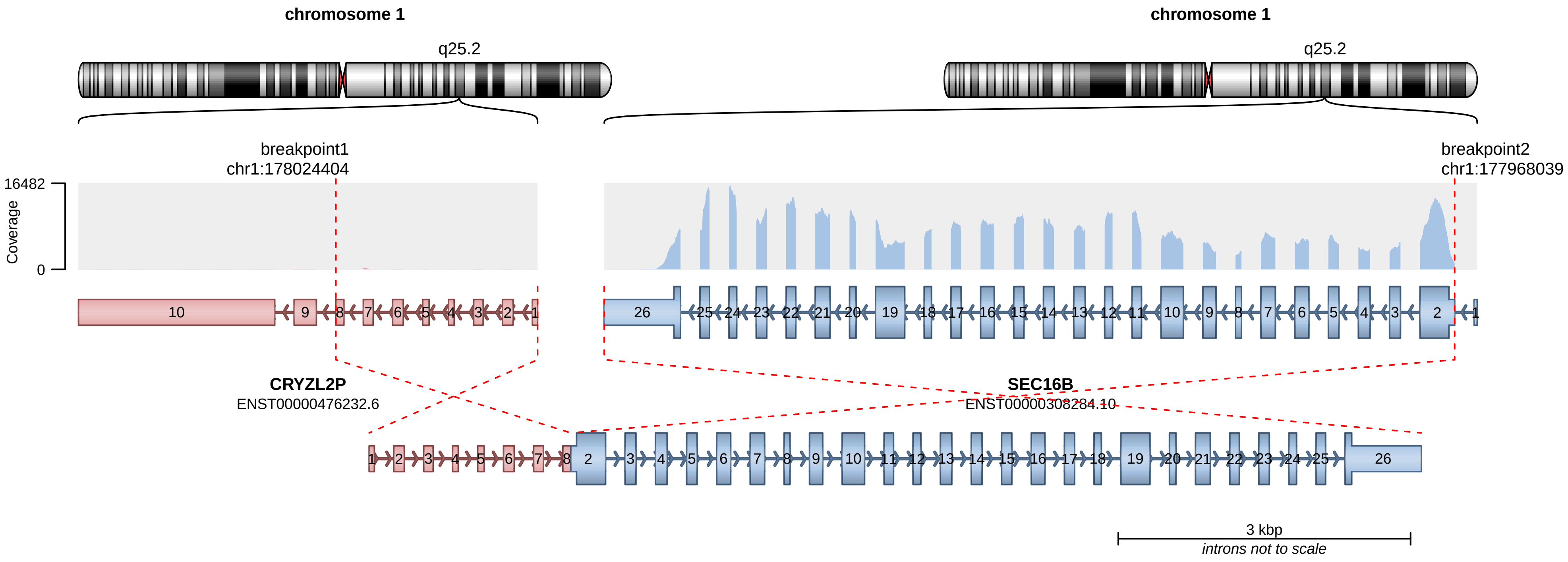


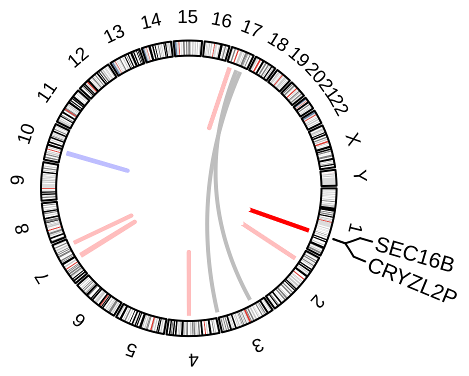




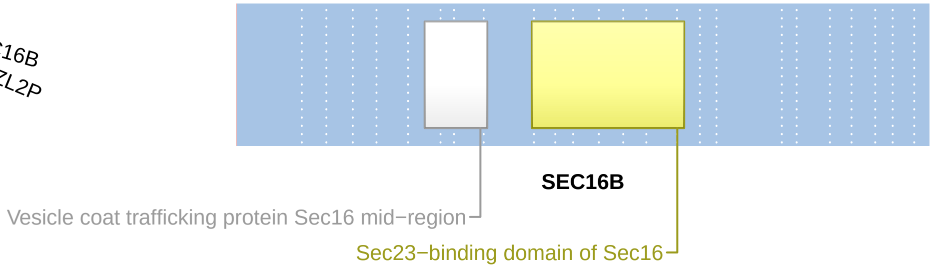
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 1





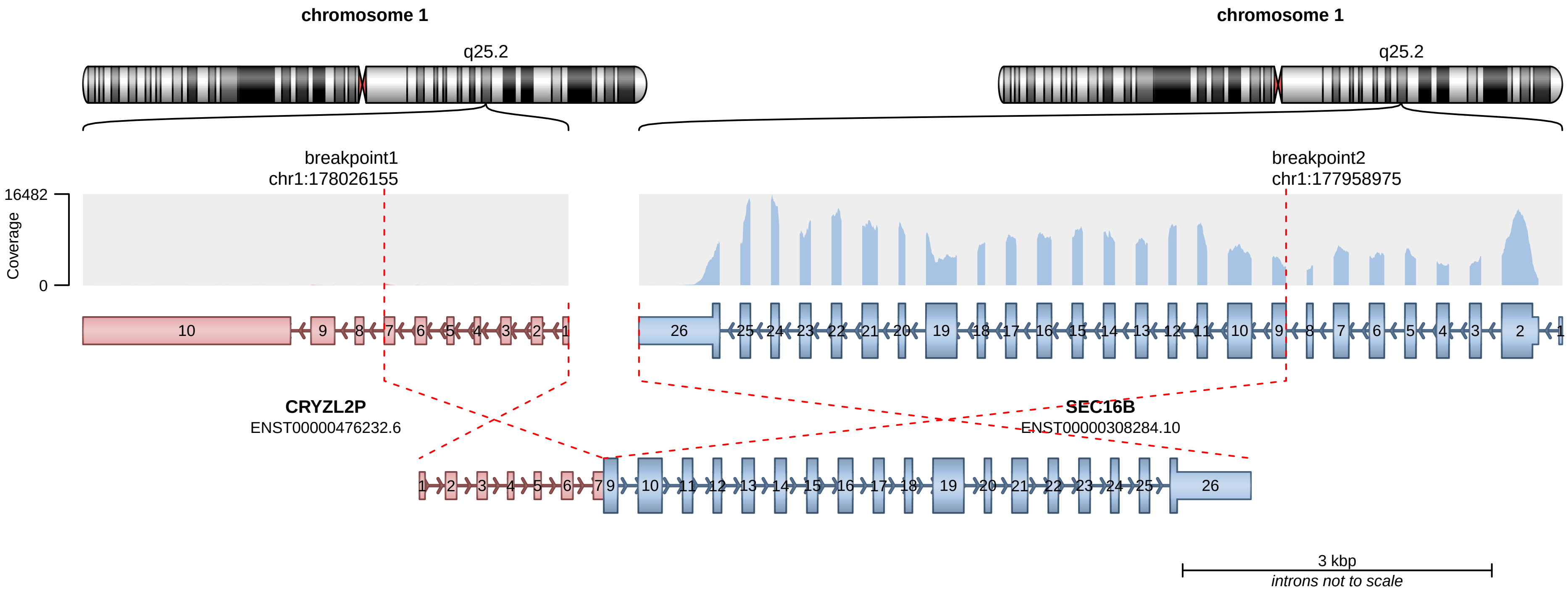
RETAINED PROTEIN DOMAINS
reading frame unclear

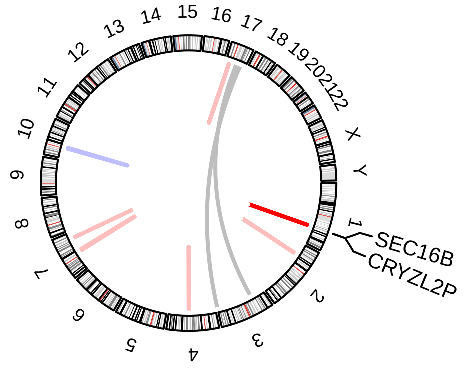


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

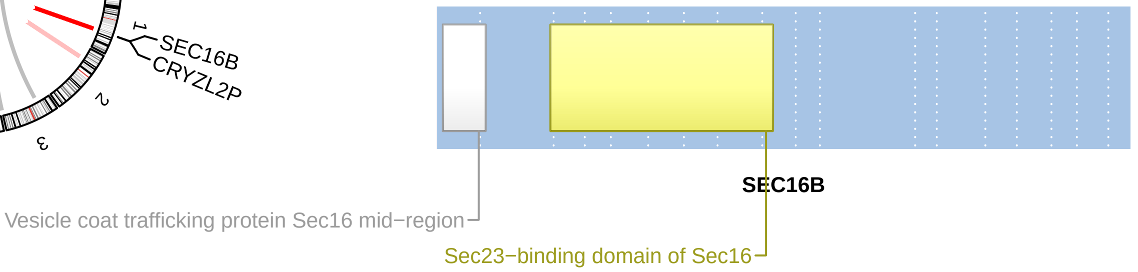
— translocation — deletion
— duplication — inversion





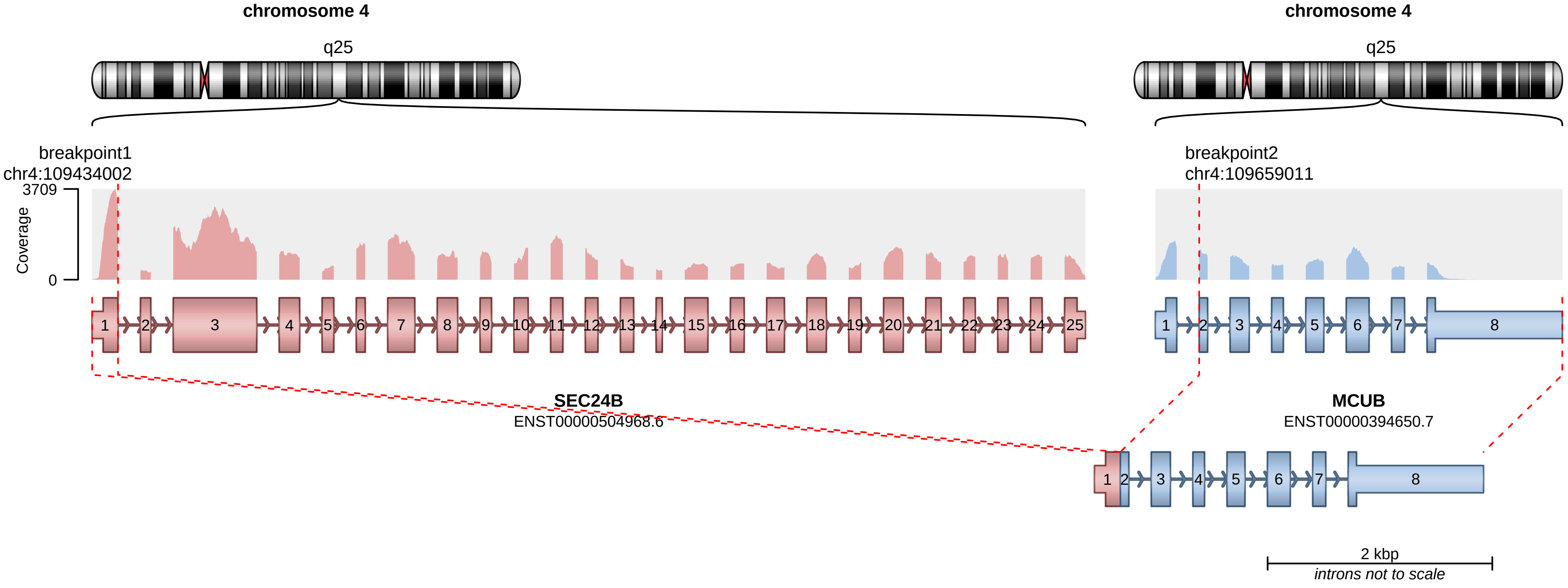
▬ translocation ▬ deletion
▬ duplication ▬ inversion

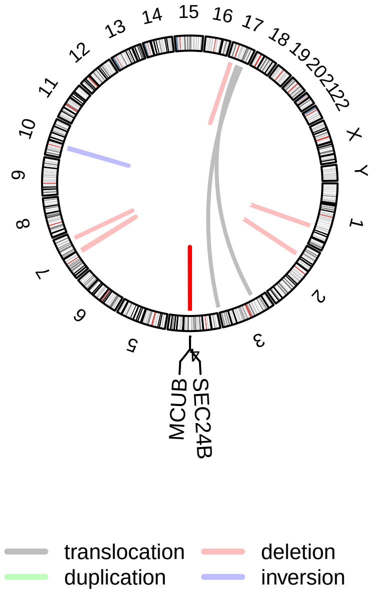
RETAINED PROTEIN DOMAINS
reading frame unclear



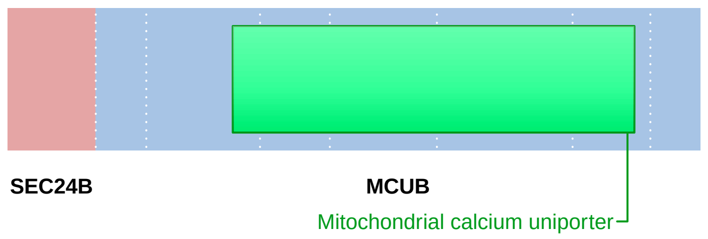
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



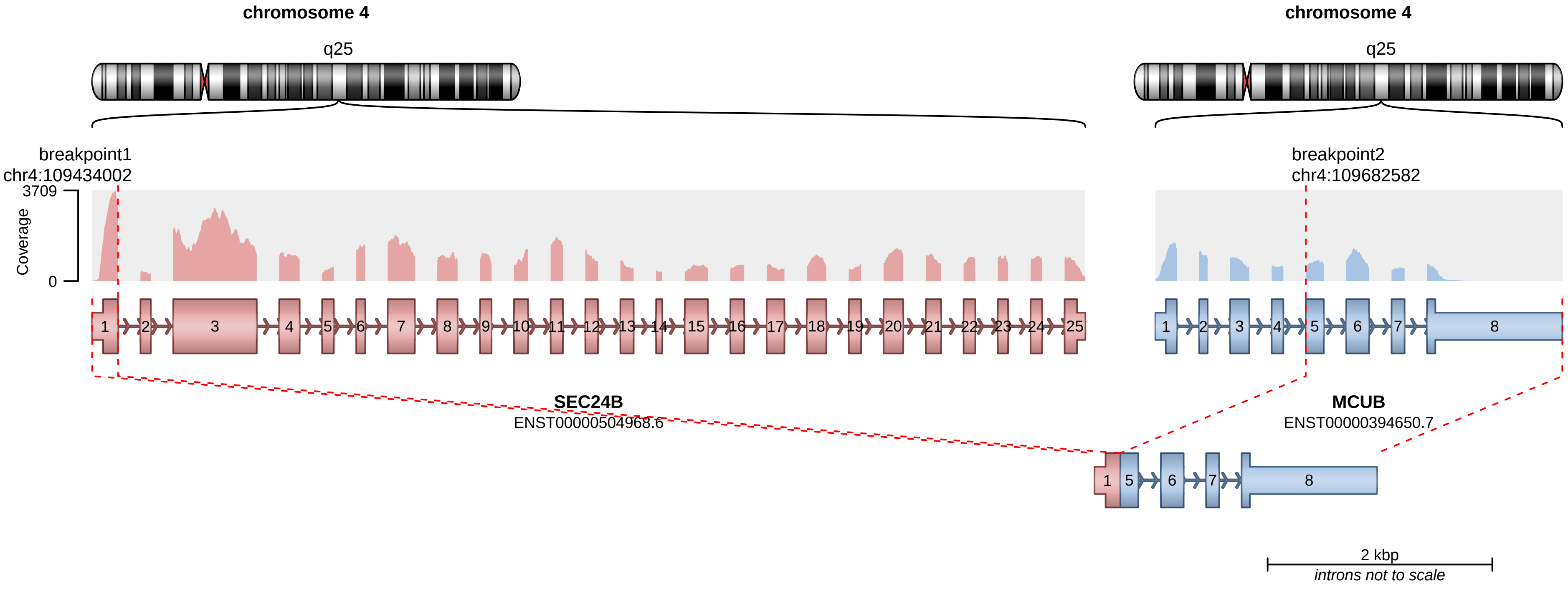


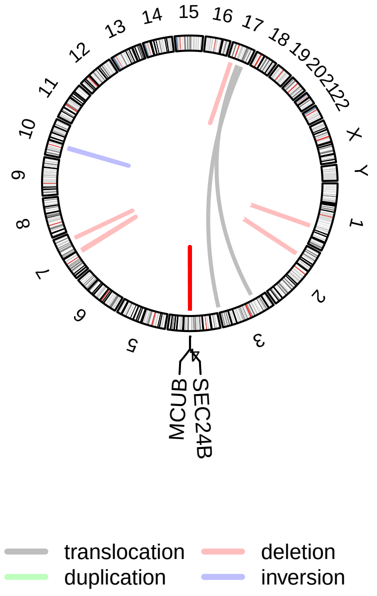
RETAINED PROTEIN DOMAINS
reading frame unclear

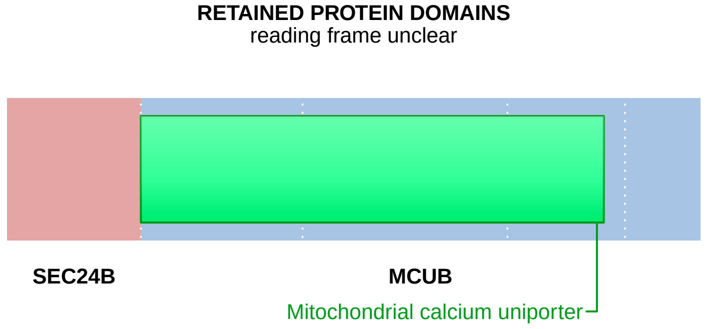


SUPPORTING READ COUNT

Split reads = 38
Discordant mates = 0

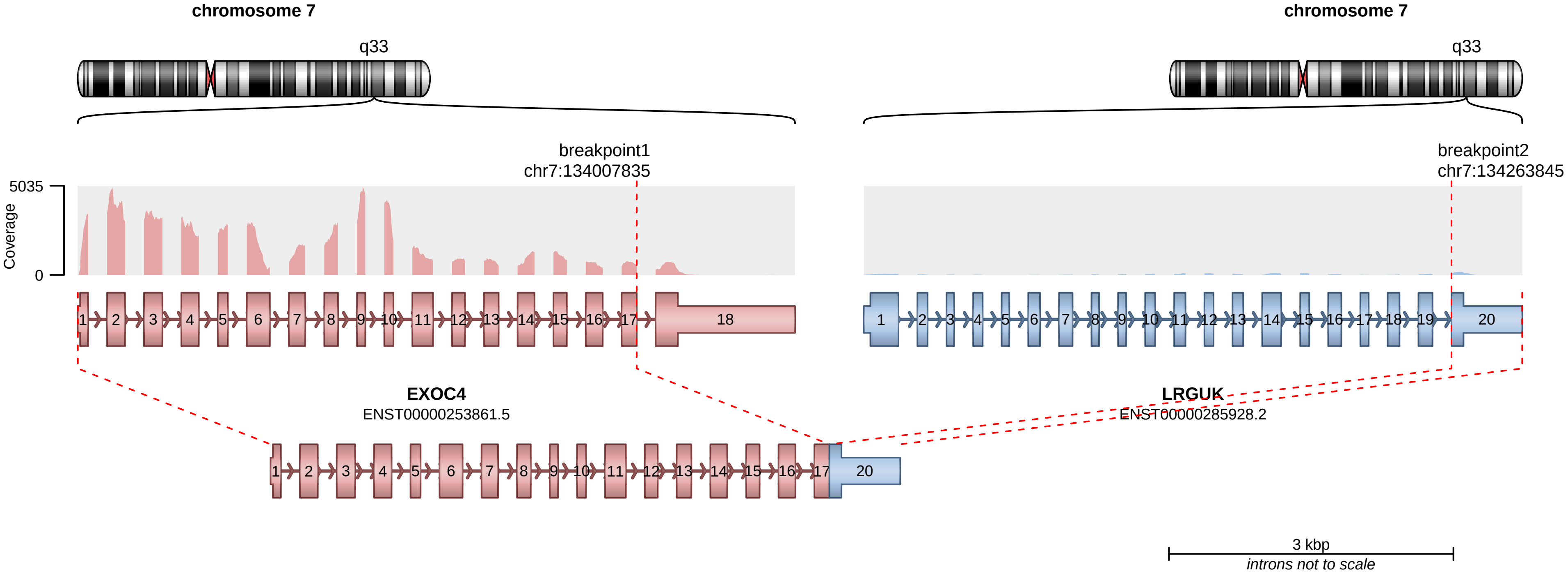


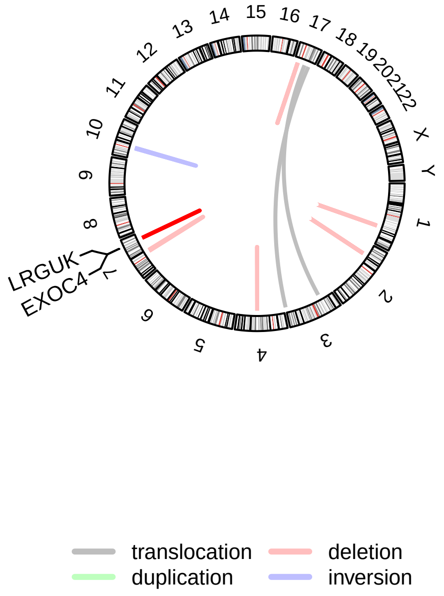




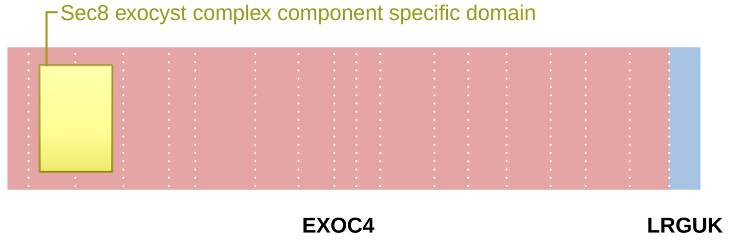
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



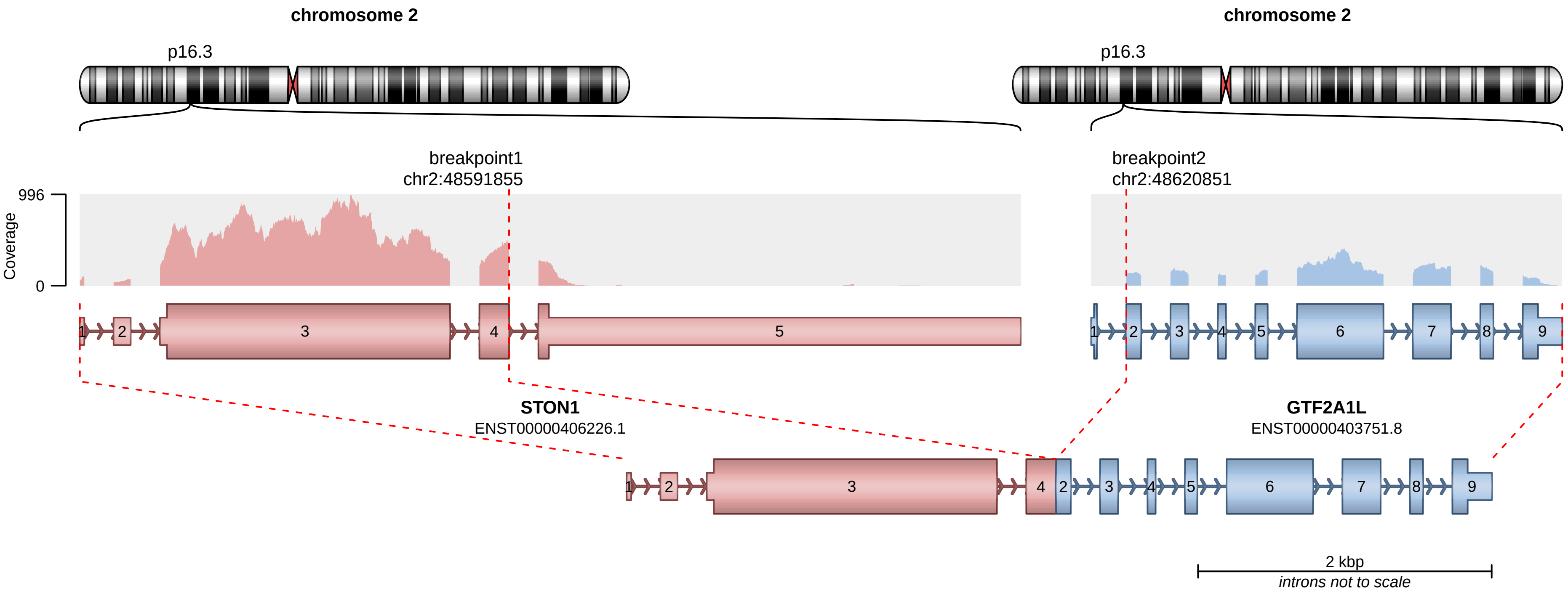


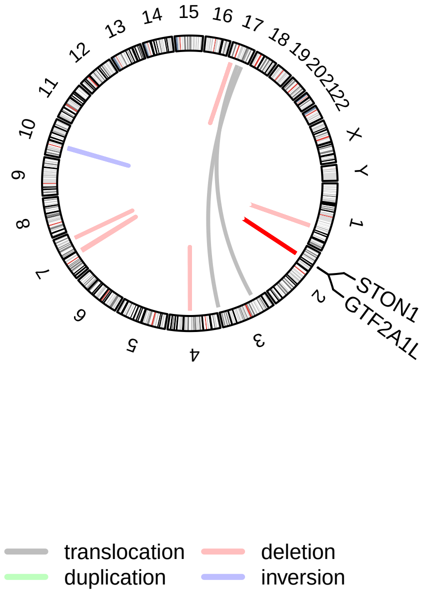
RETAINED PROTEIN DOMAINS
reading frame unclear

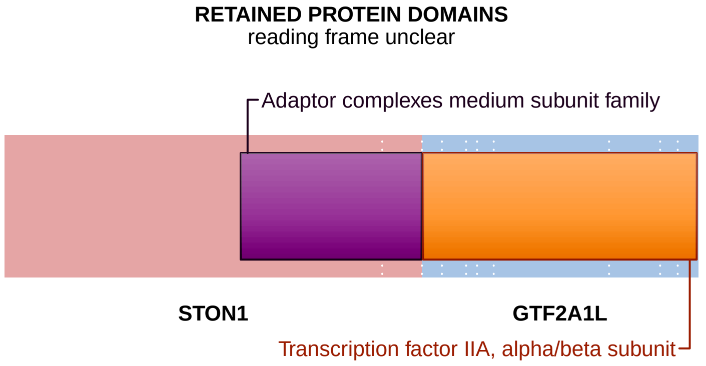


SUPPORTING READ COUNT

Split reads = 16
Discordant mates = 1

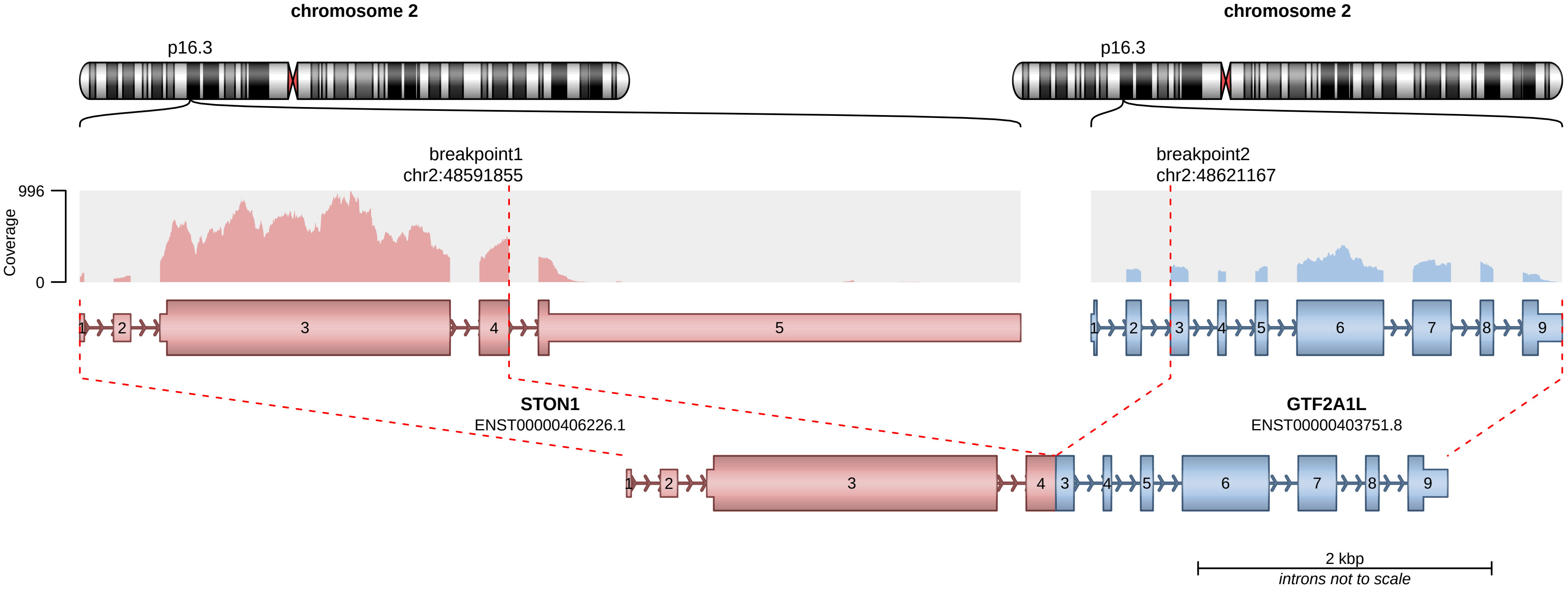


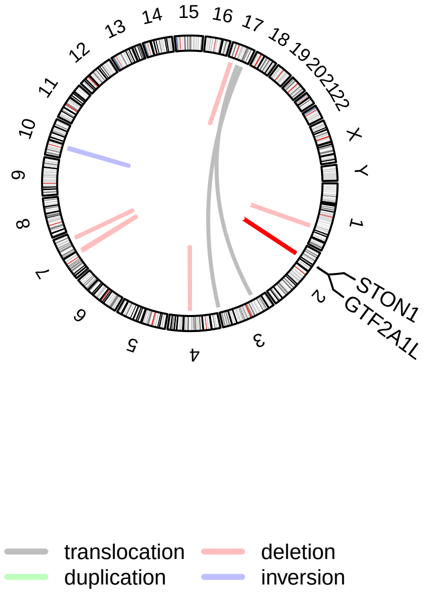


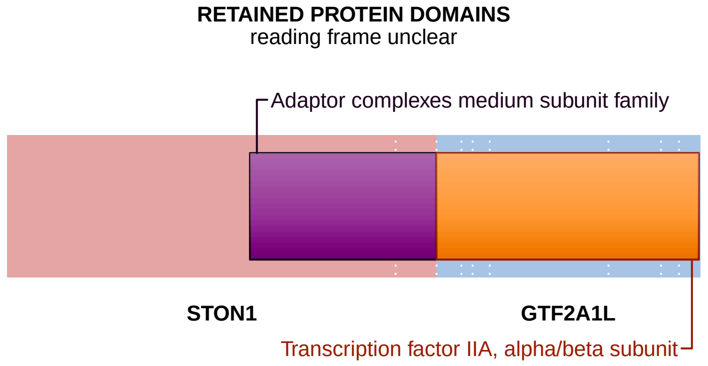


SUPPORTING READ COUNT

Split reads = 15
Discordant mates = 1

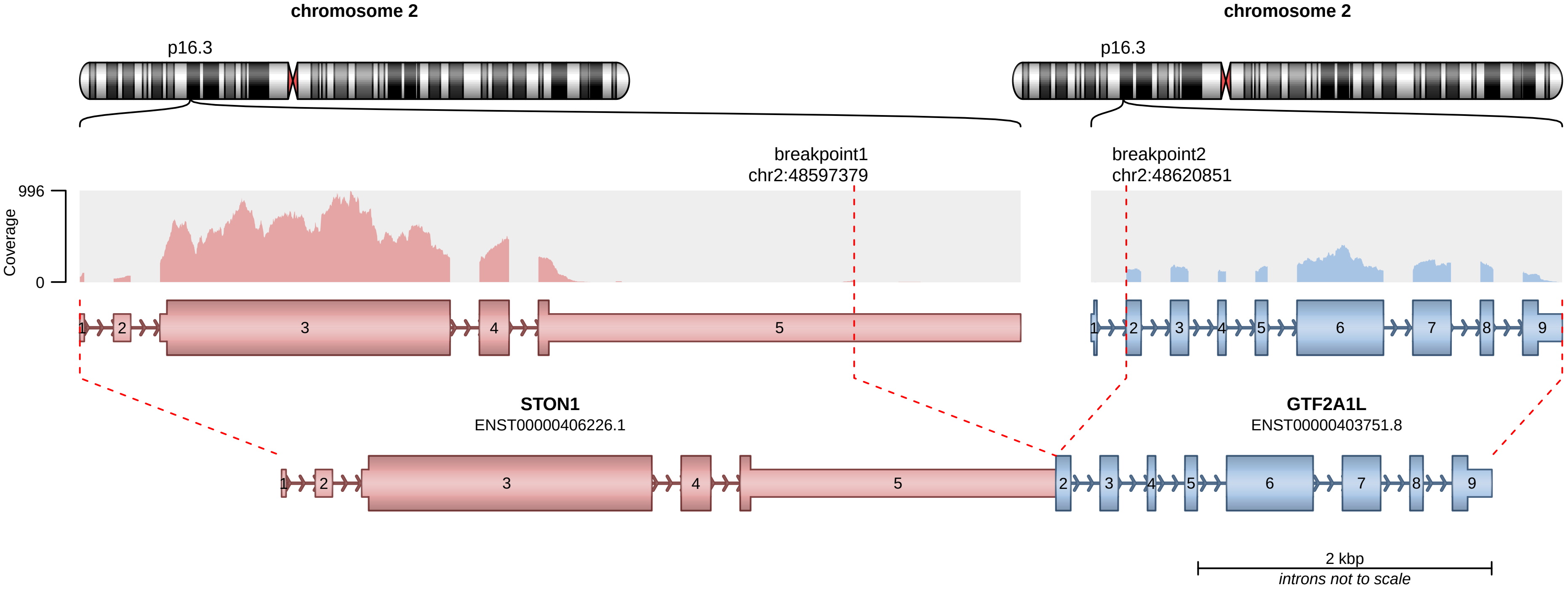


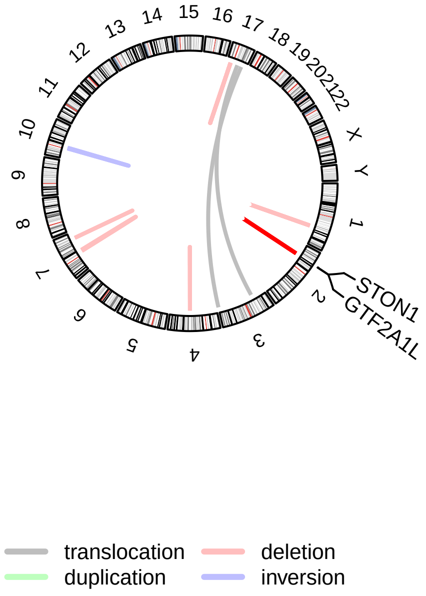


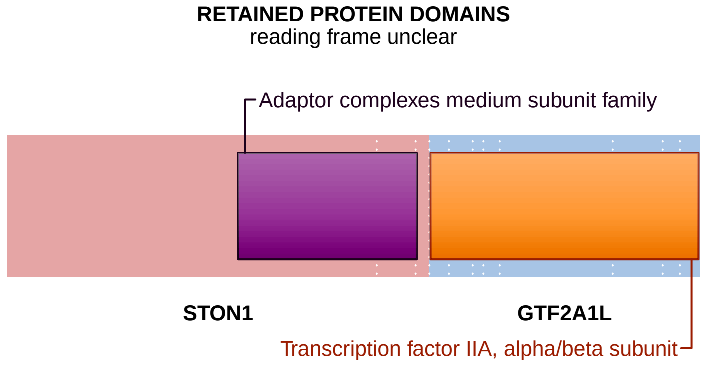


SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 1

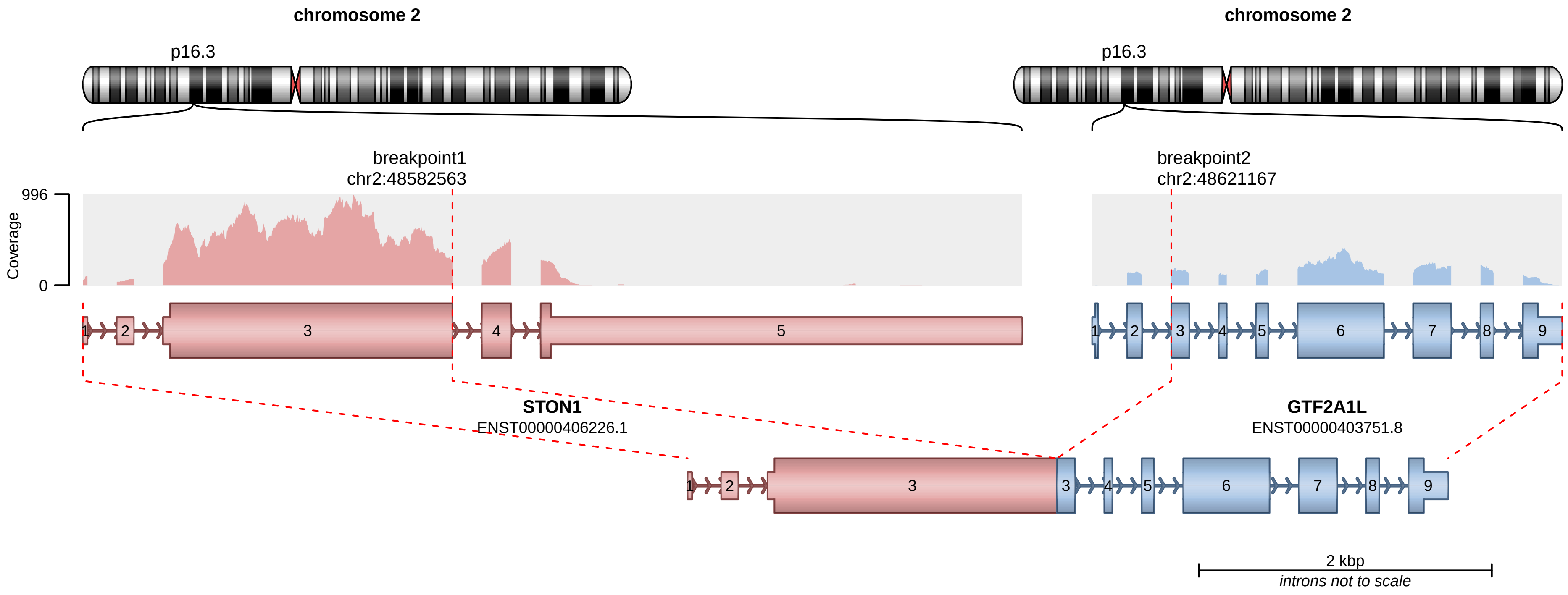


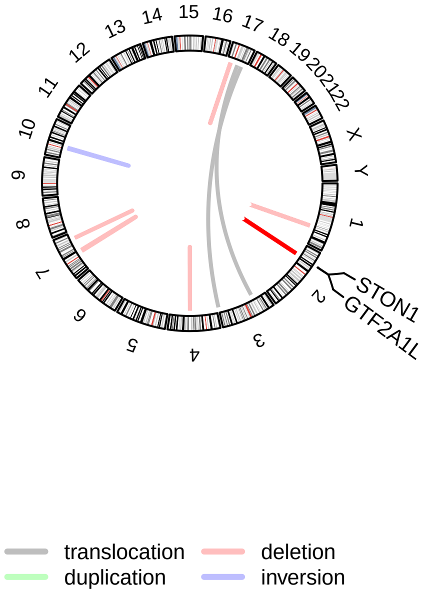


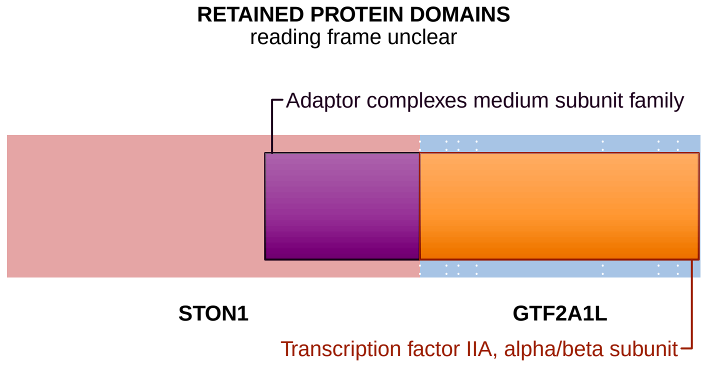


SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 2

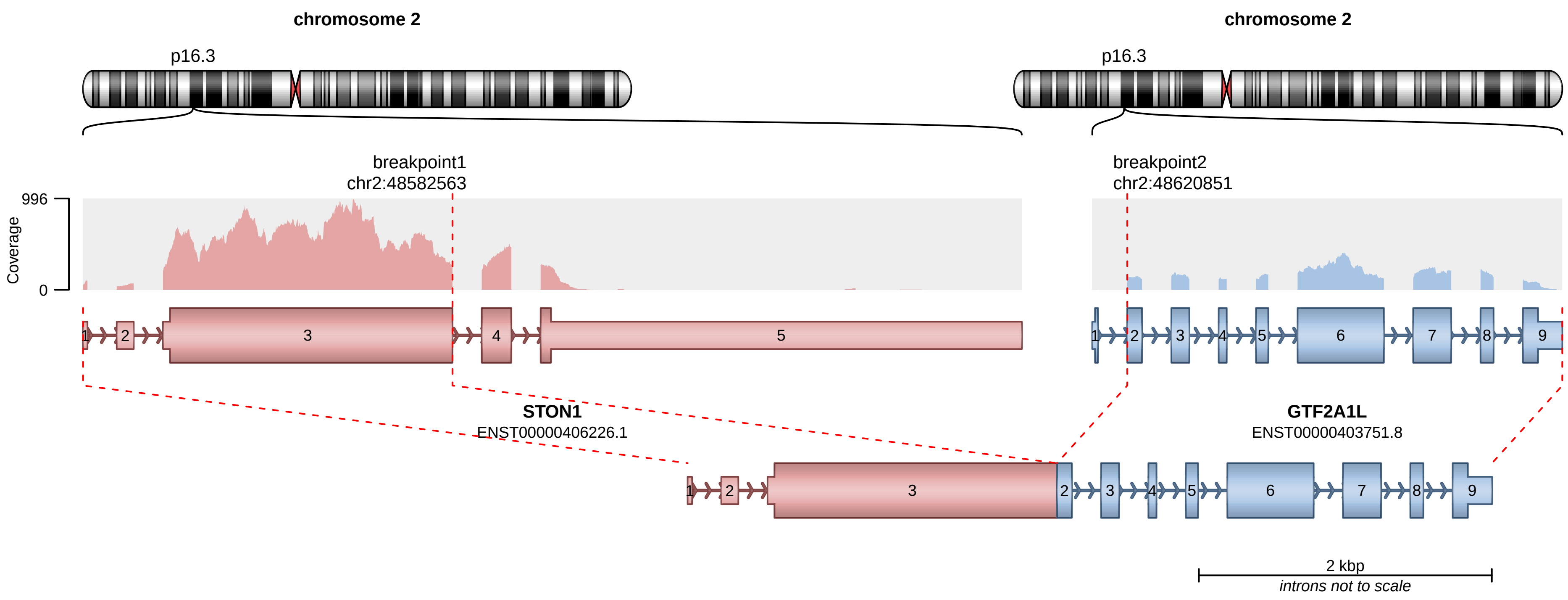


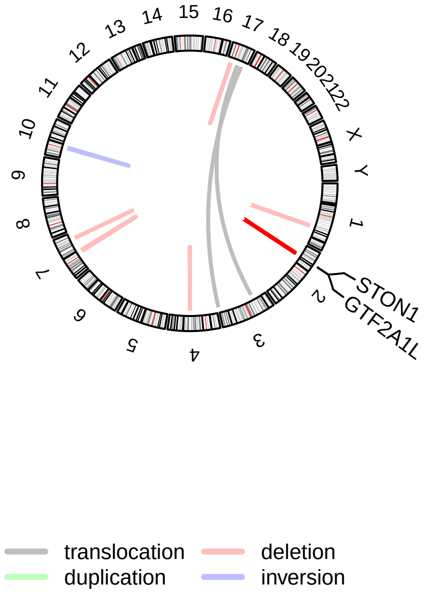




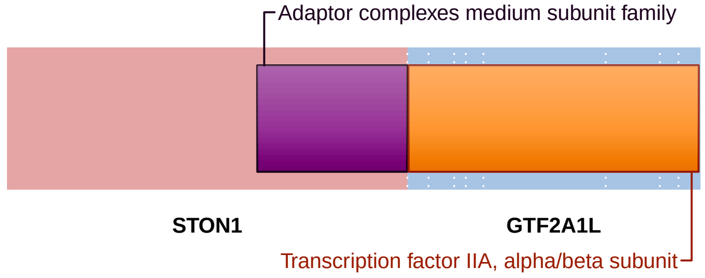
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



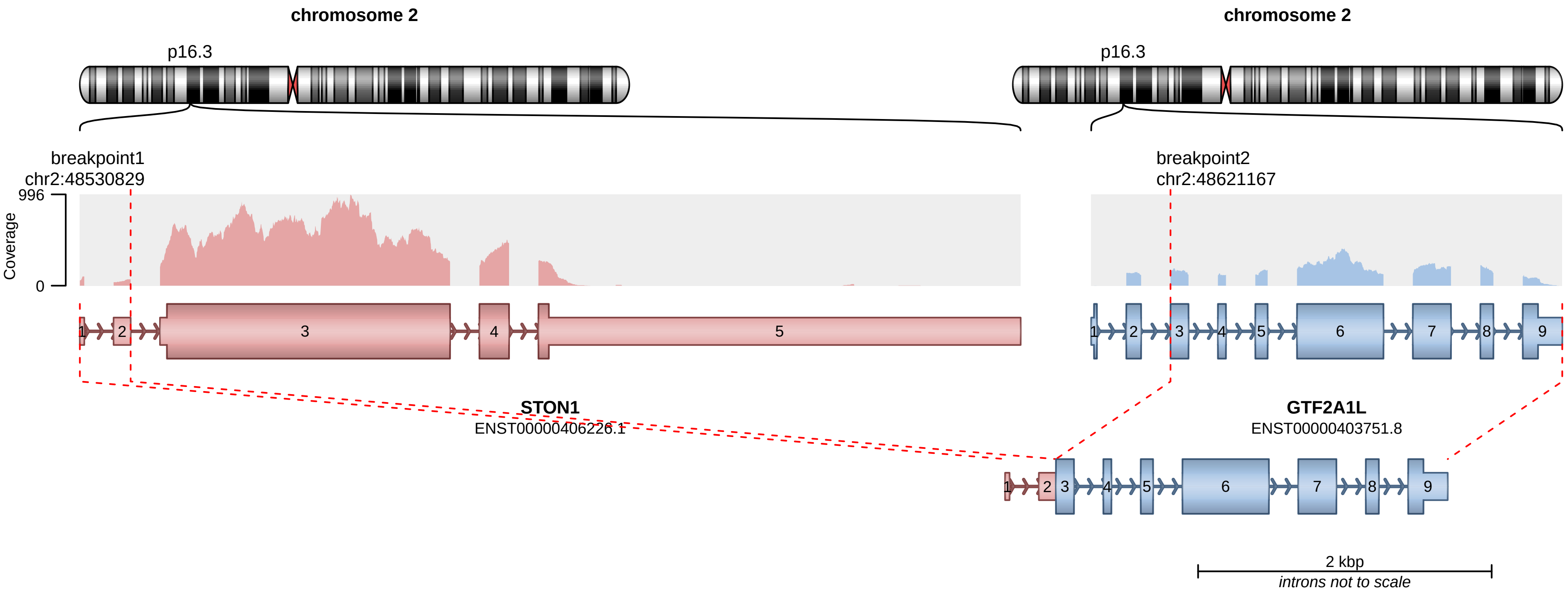


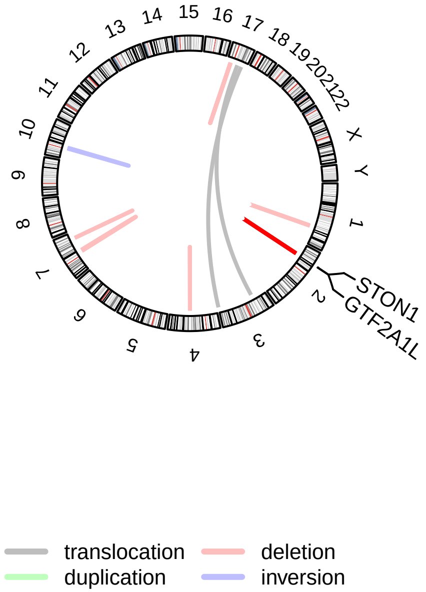
RETAINED PROTEIN DOMAINS
reading frame unclear

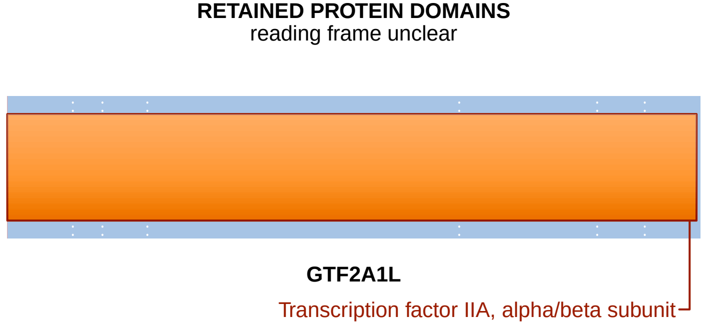


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

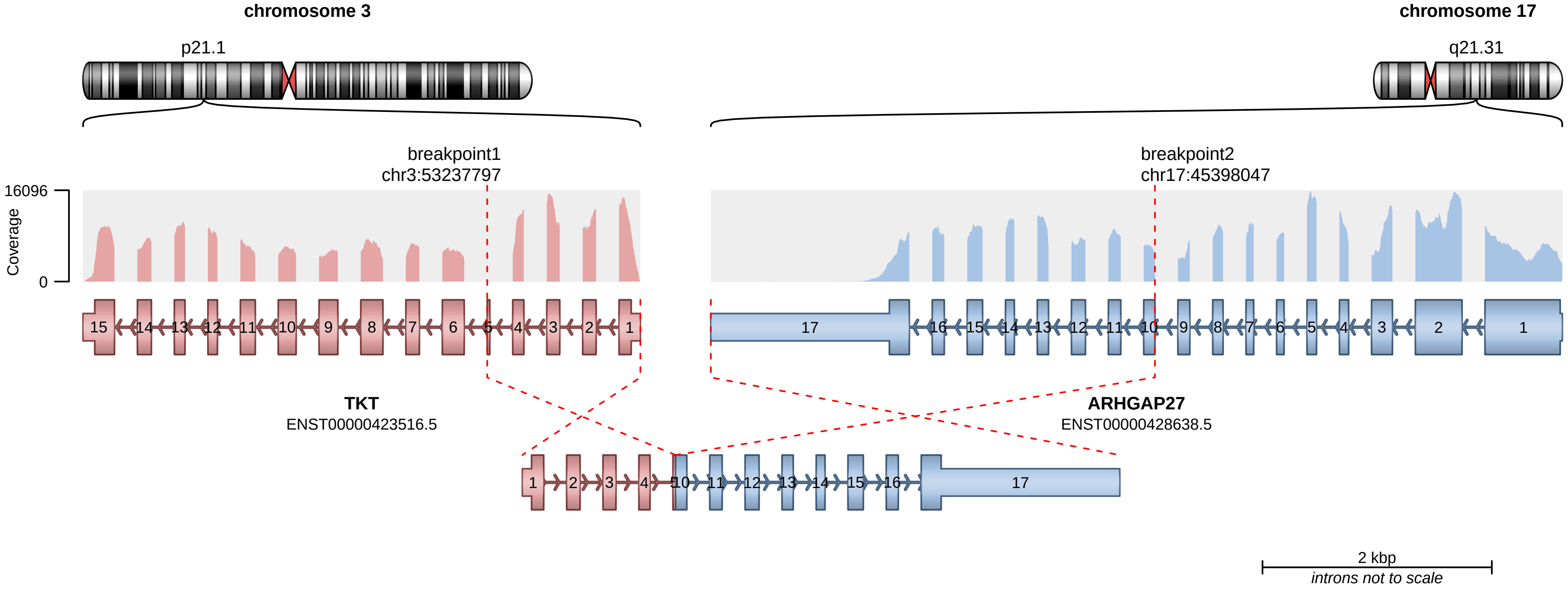


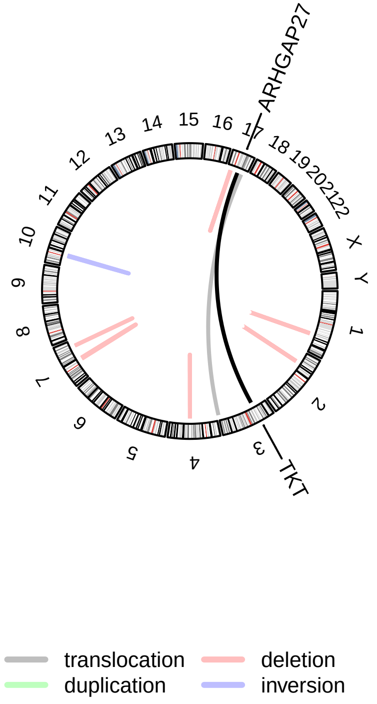




SUPPORTING READ COUNT

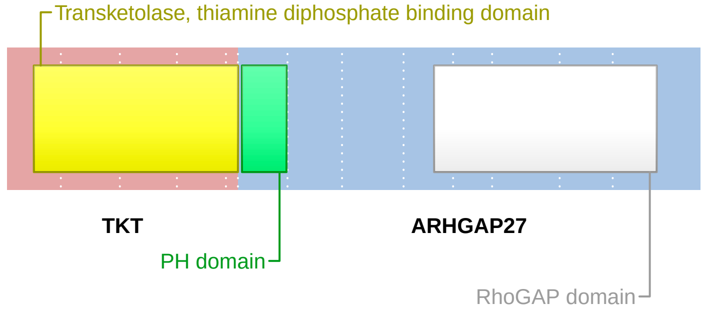
Split reads = 1
Discordant mates = 0





RETAINED PROTEIN DOMAINS

reading frame unclear



SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 0