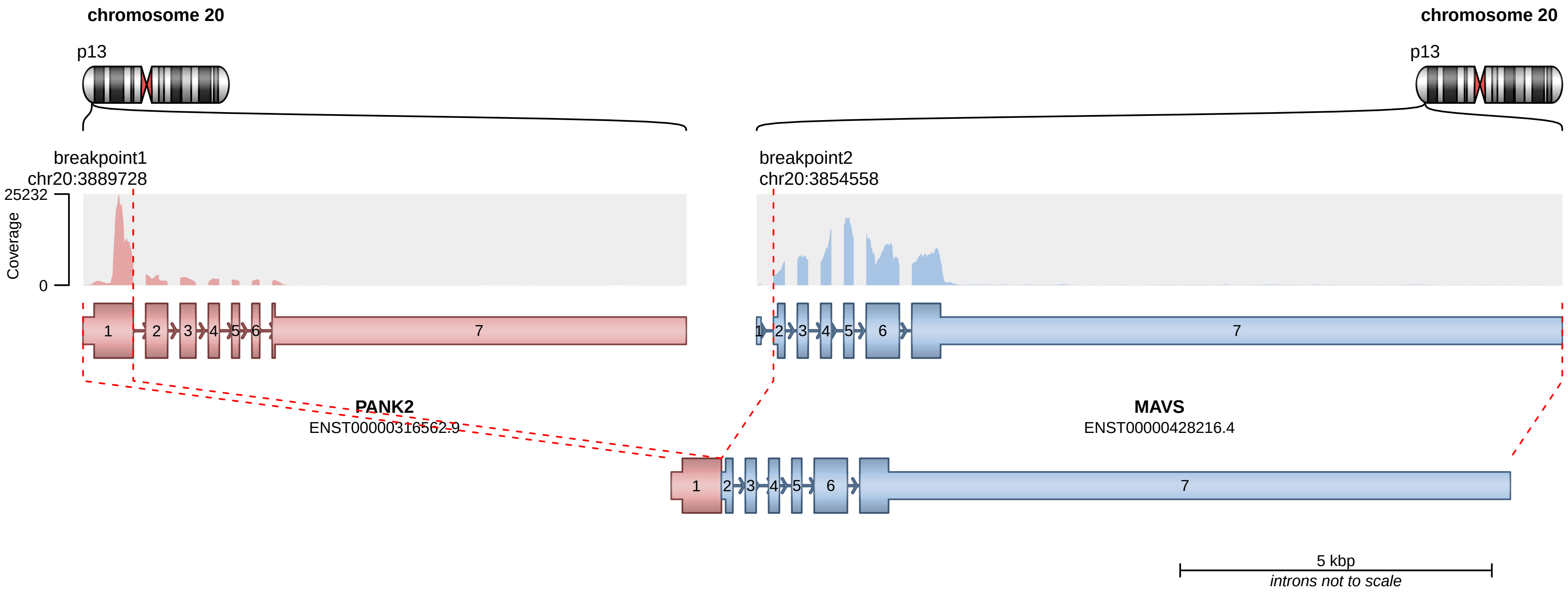
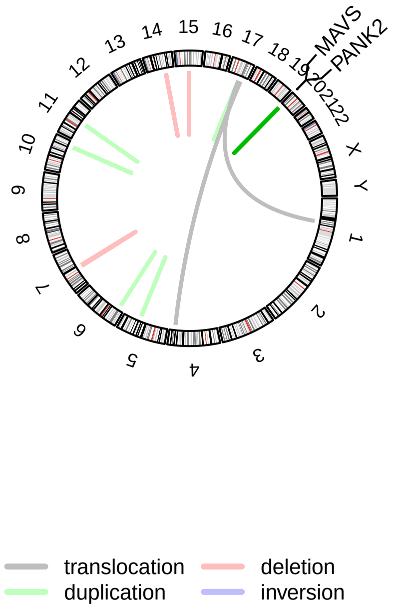
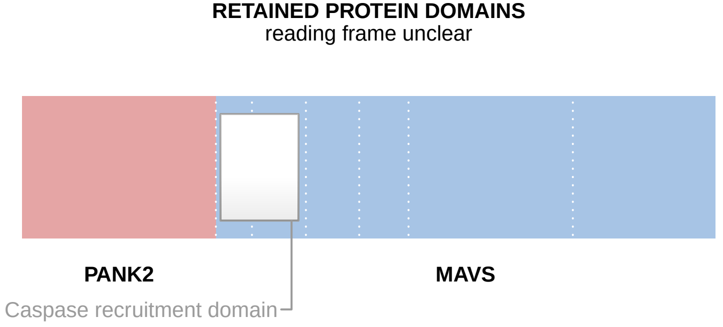
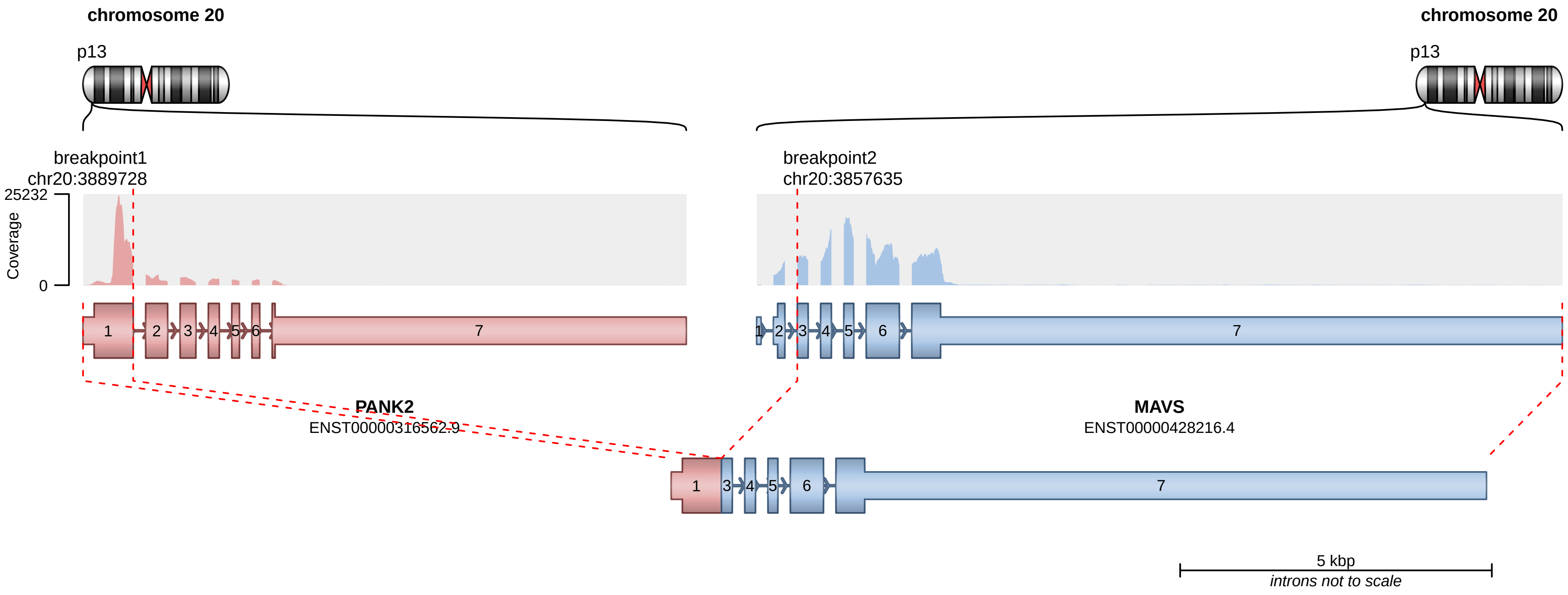


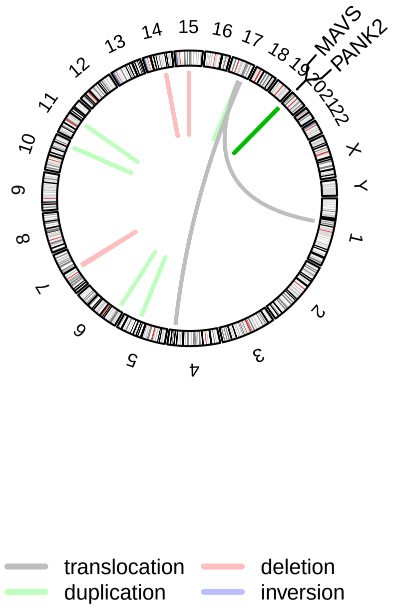




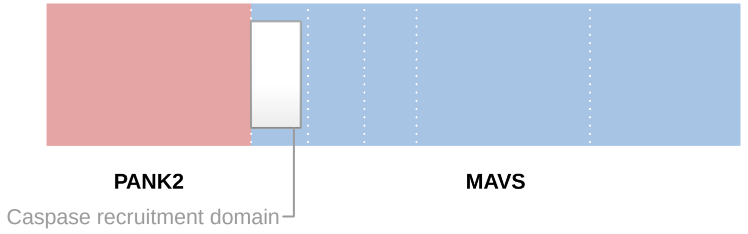
SUPPORTING READ COUNT

Split reads = 1605
Discordant mates = 23



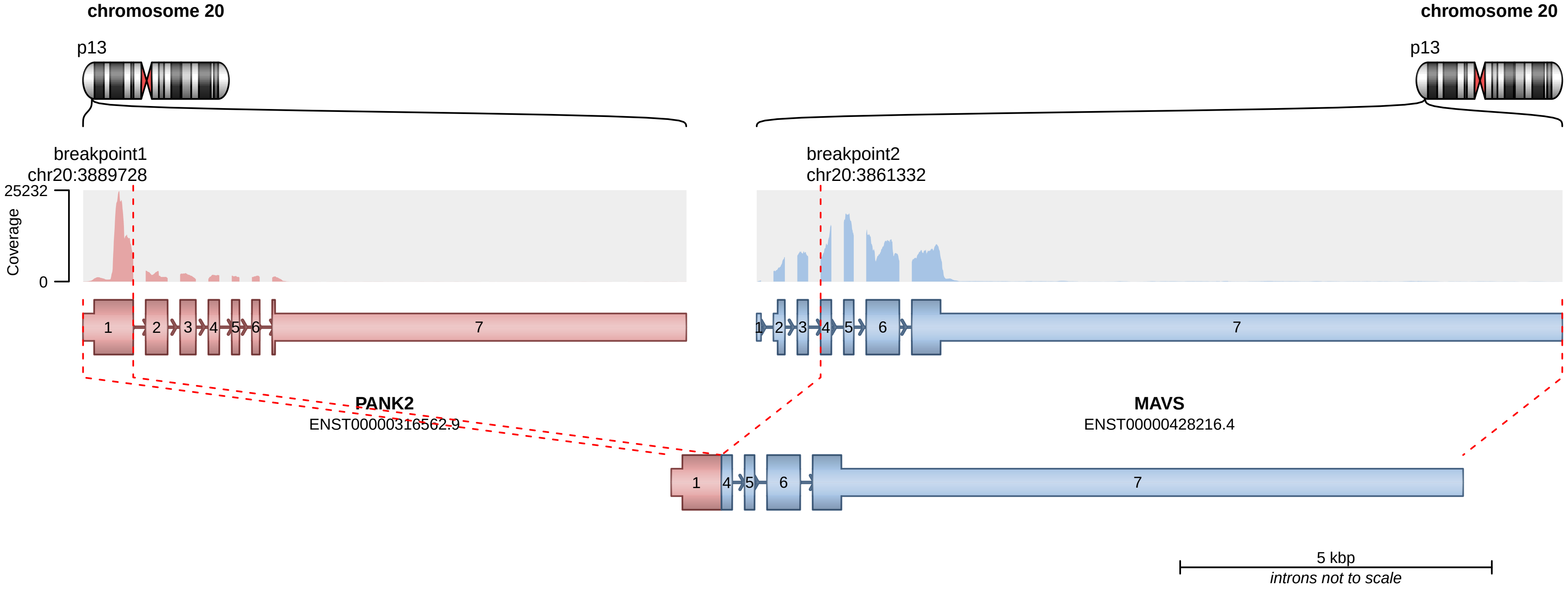


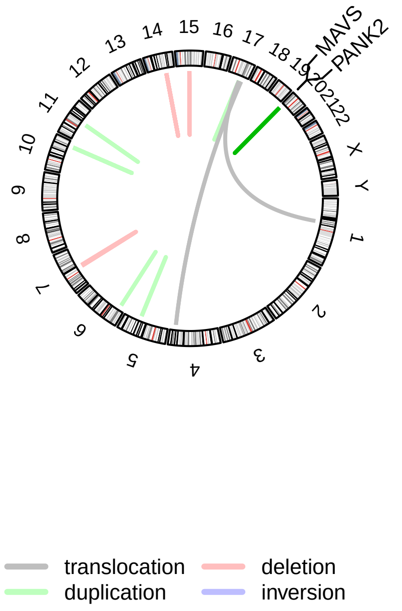
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 115
Discordant mates = 3

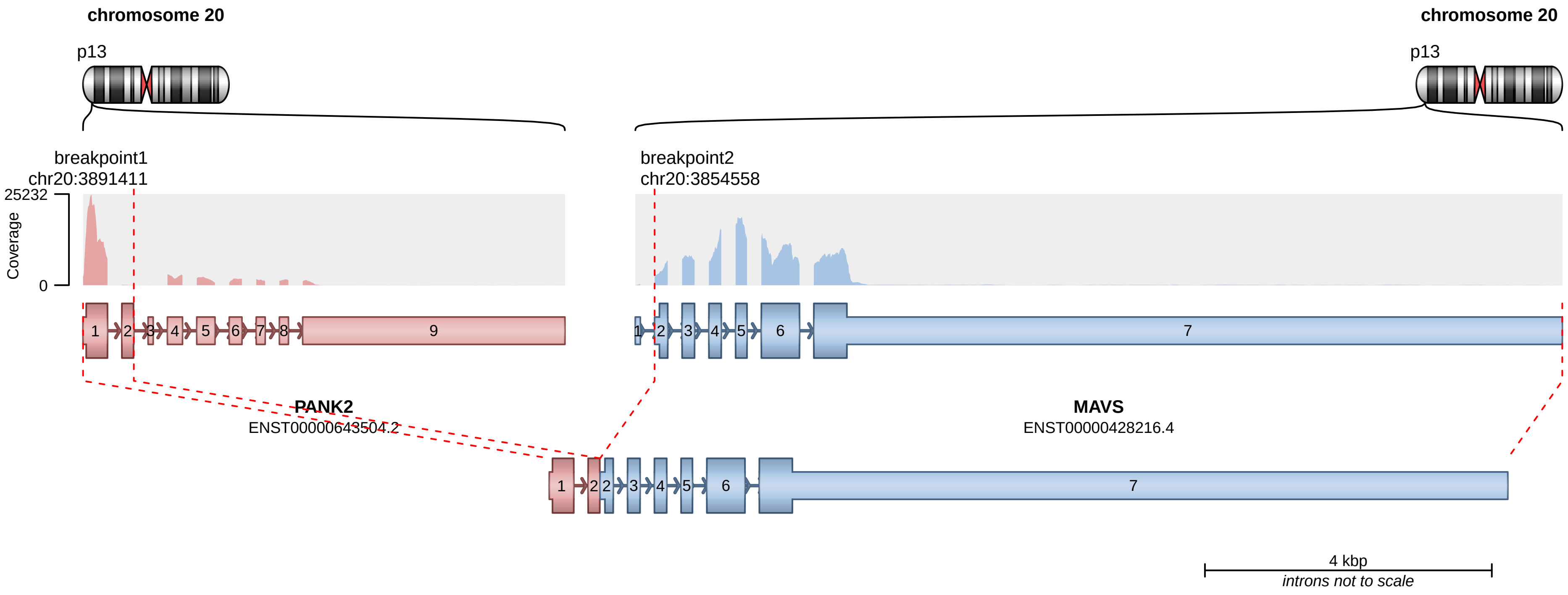


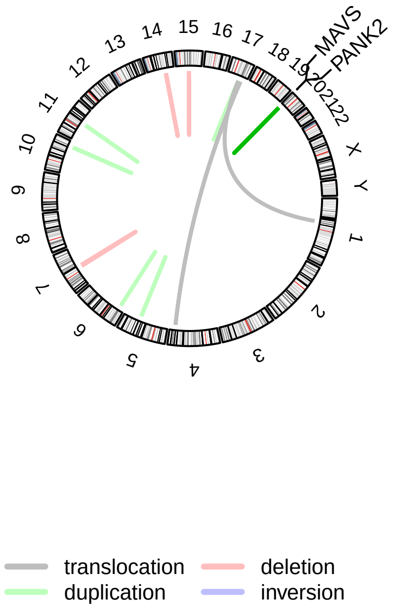


No protein domains retained in fusion.

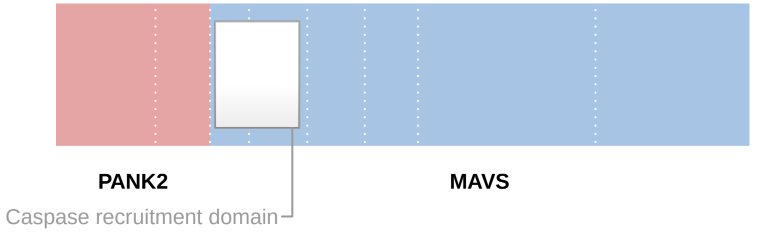
SUPPORTING READ COUNT

Split reads = 27
Discordant mates = 0



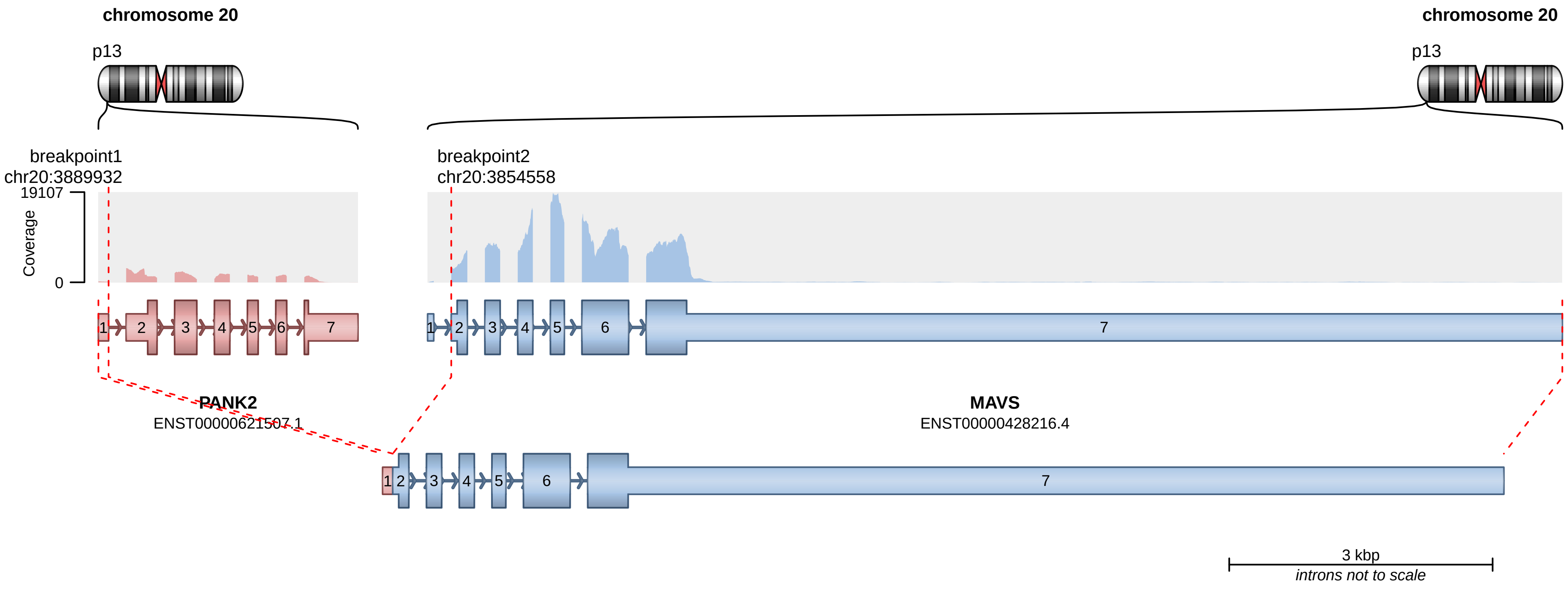


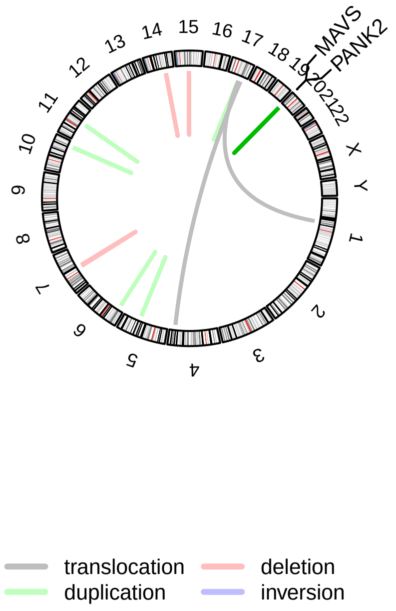
RETAINED PROTEIN DOMAINS
reading frame unclear



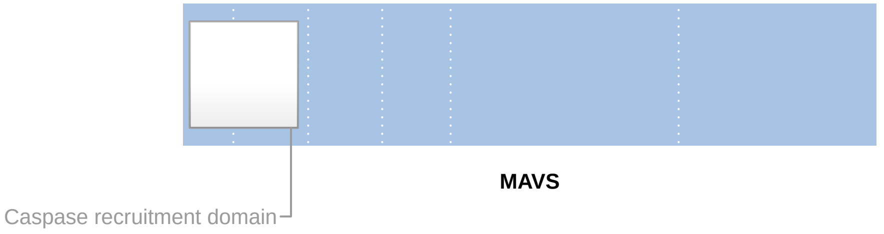
SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 23



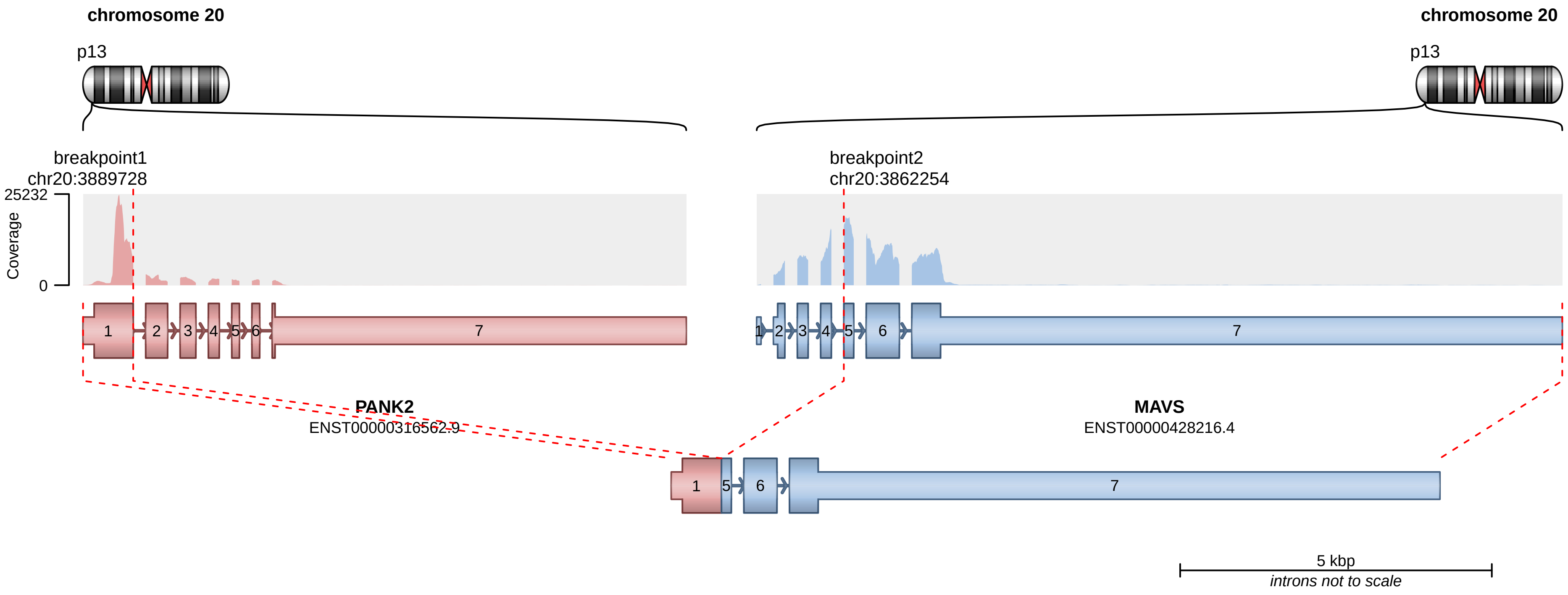


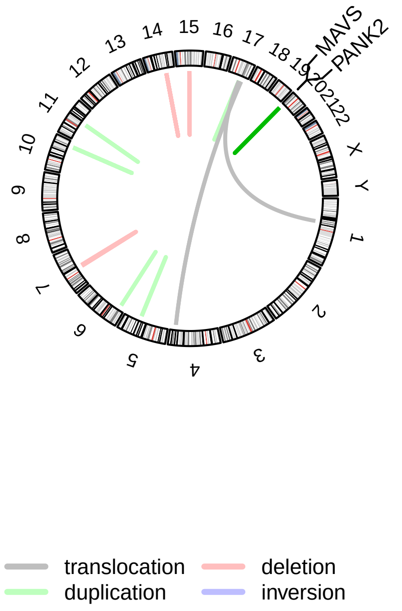
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 23

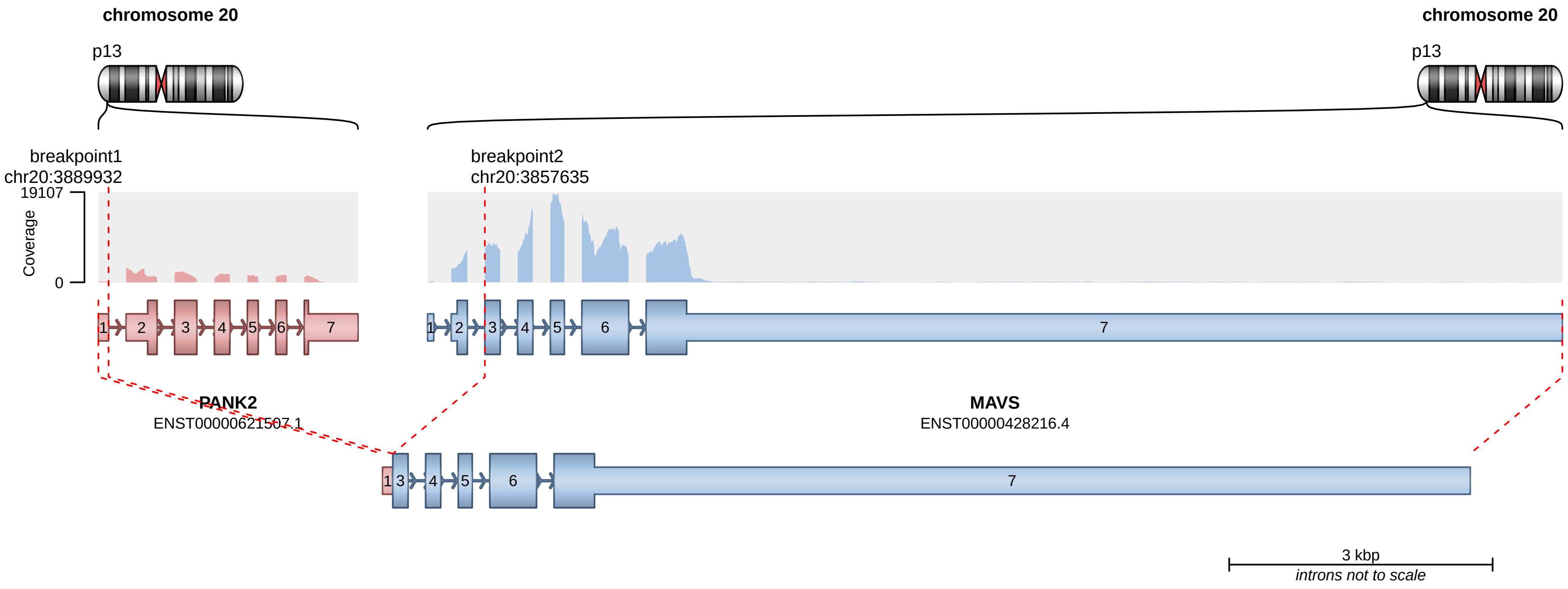


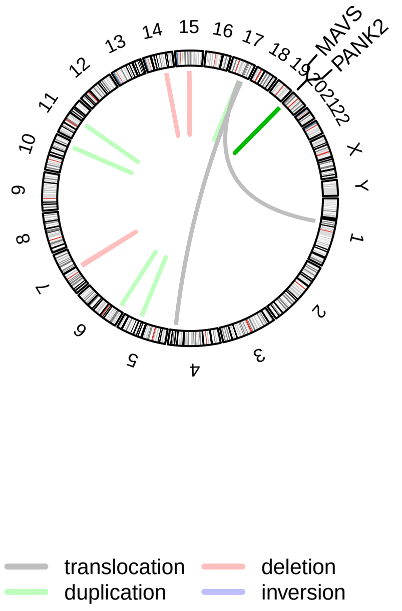


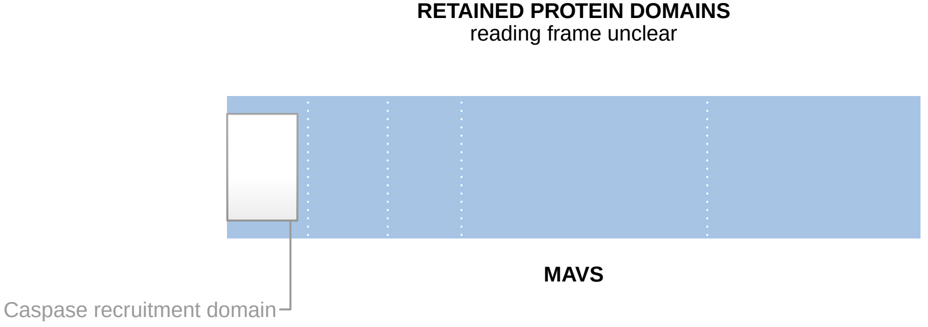
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0

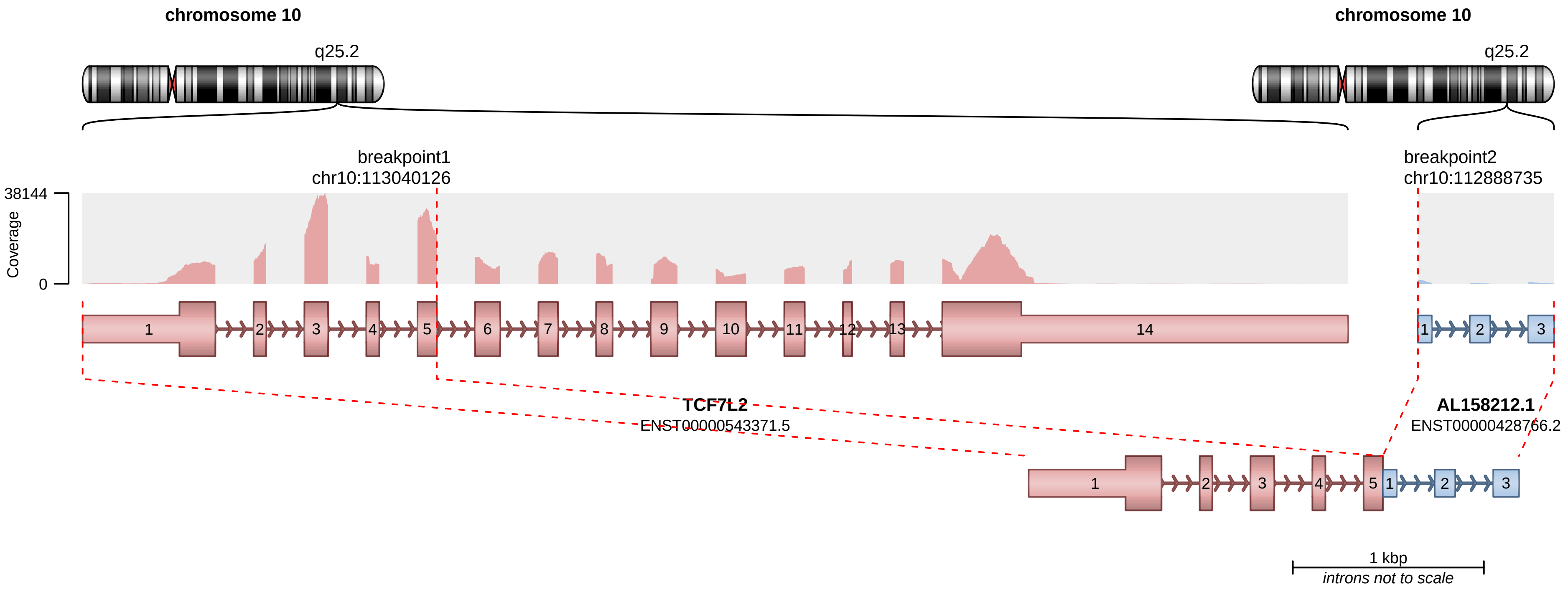


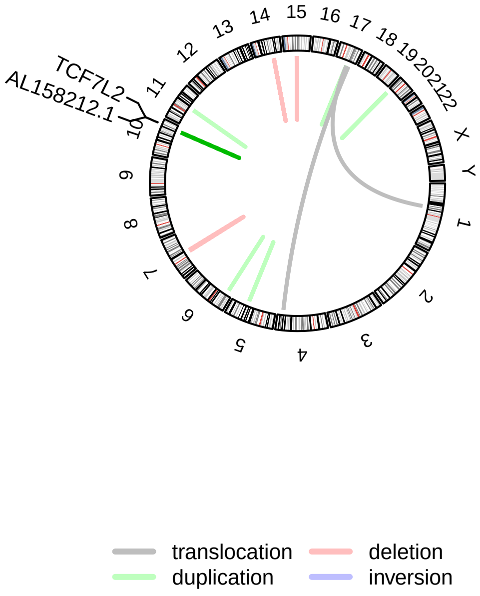




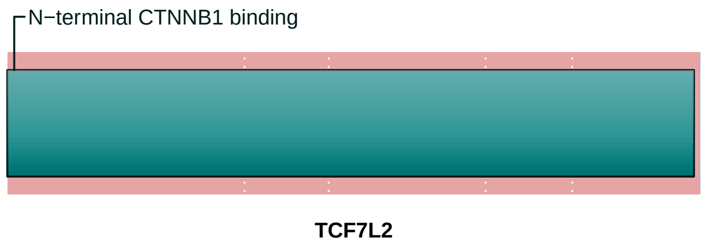
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 3



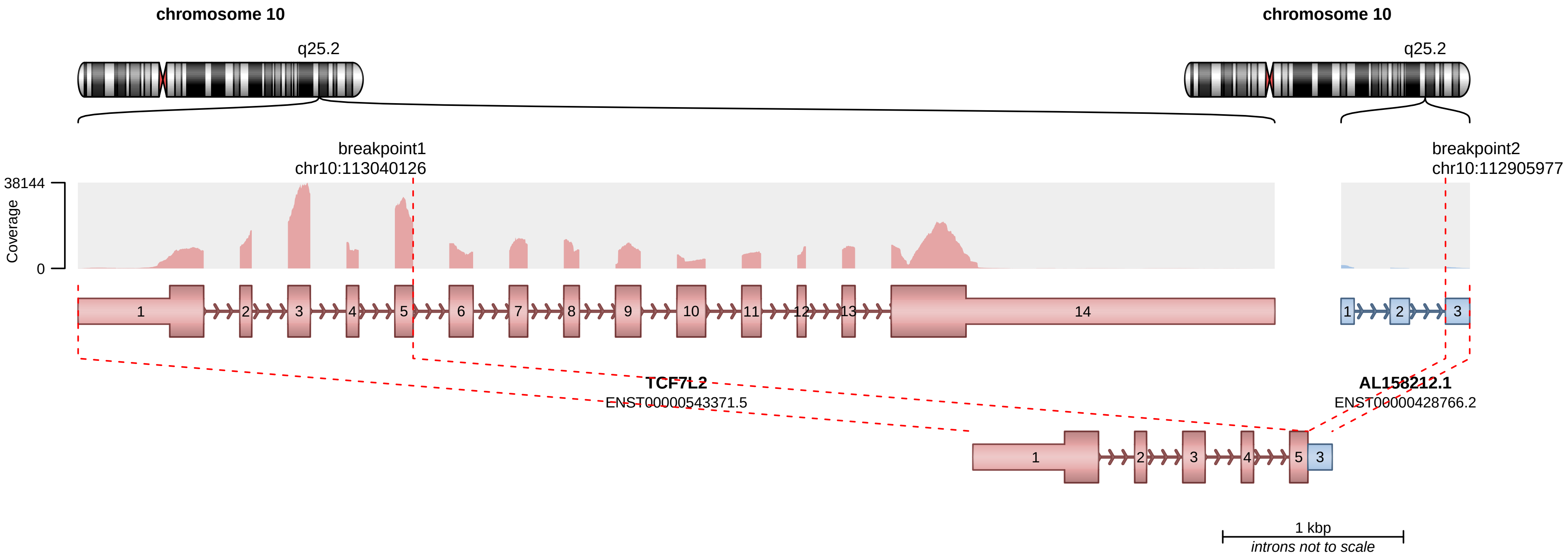


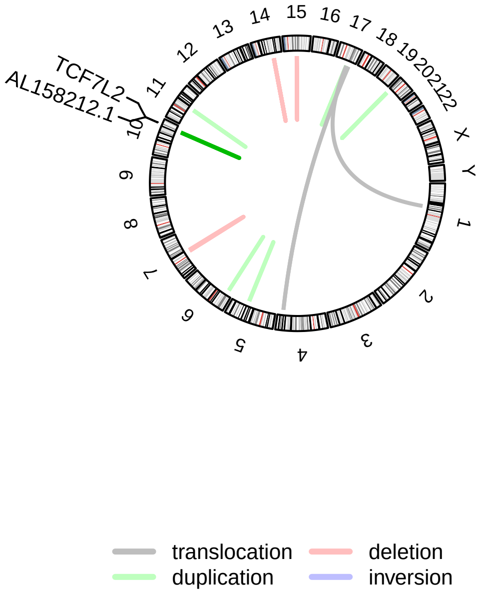
RETAINED PROTEIN DOMAINS
reading frame unclear

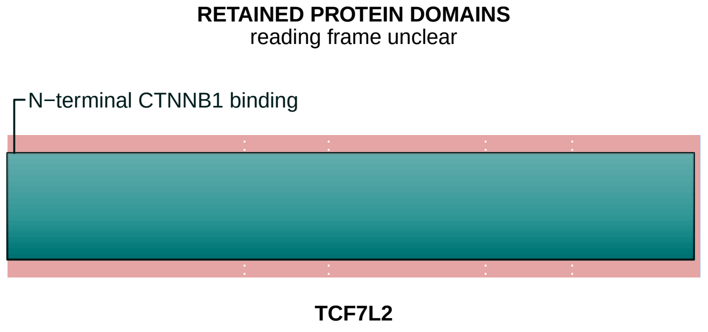


SUPPORTING READ COUNT

Split reads = 786
Discordant mates = 27

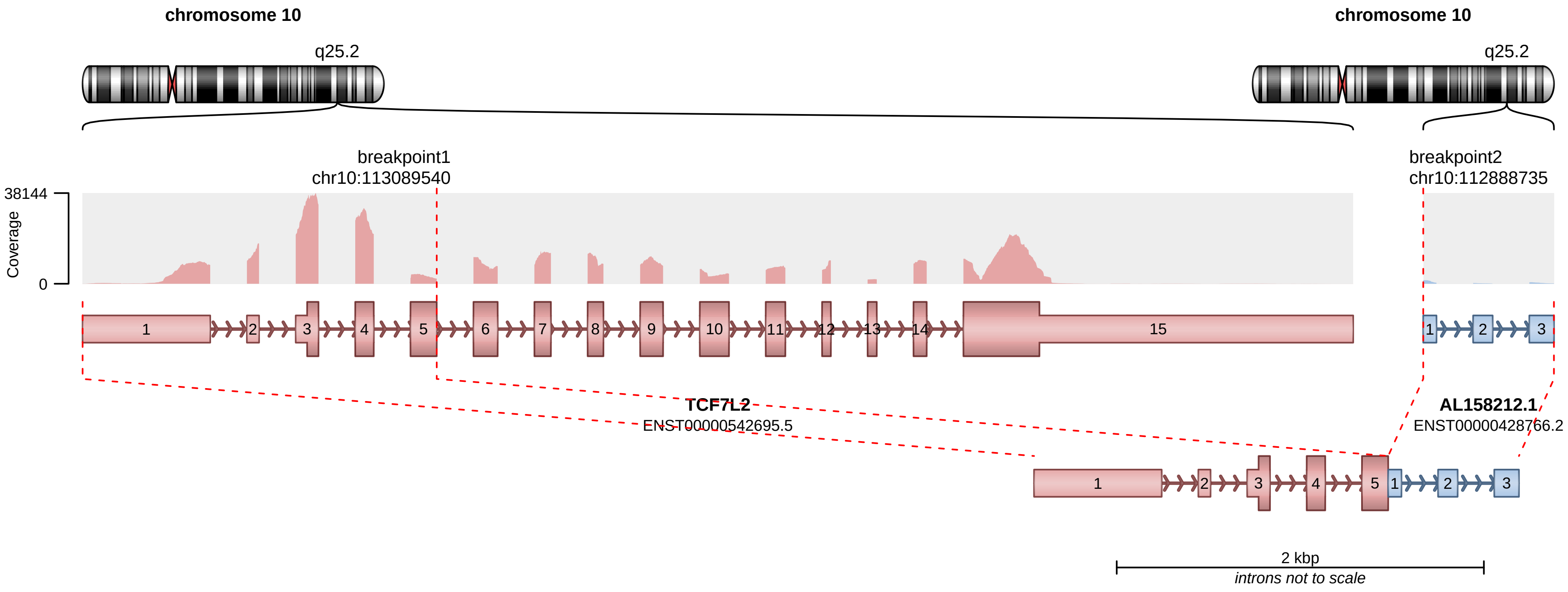


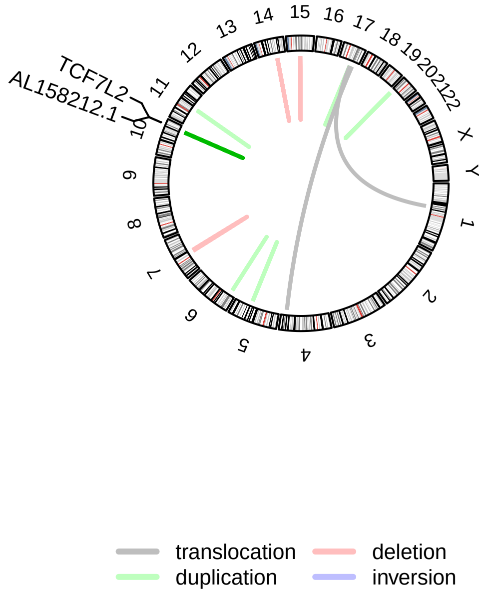




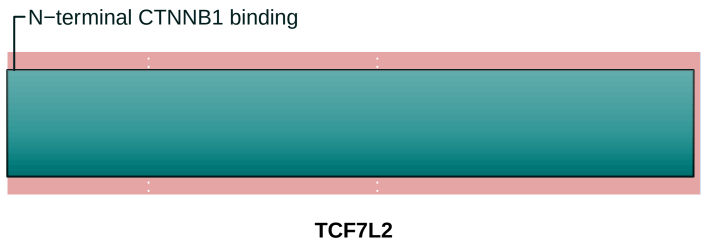
SUPPORTING READ COUNT

Split reads = 216
Discordant mates = 14



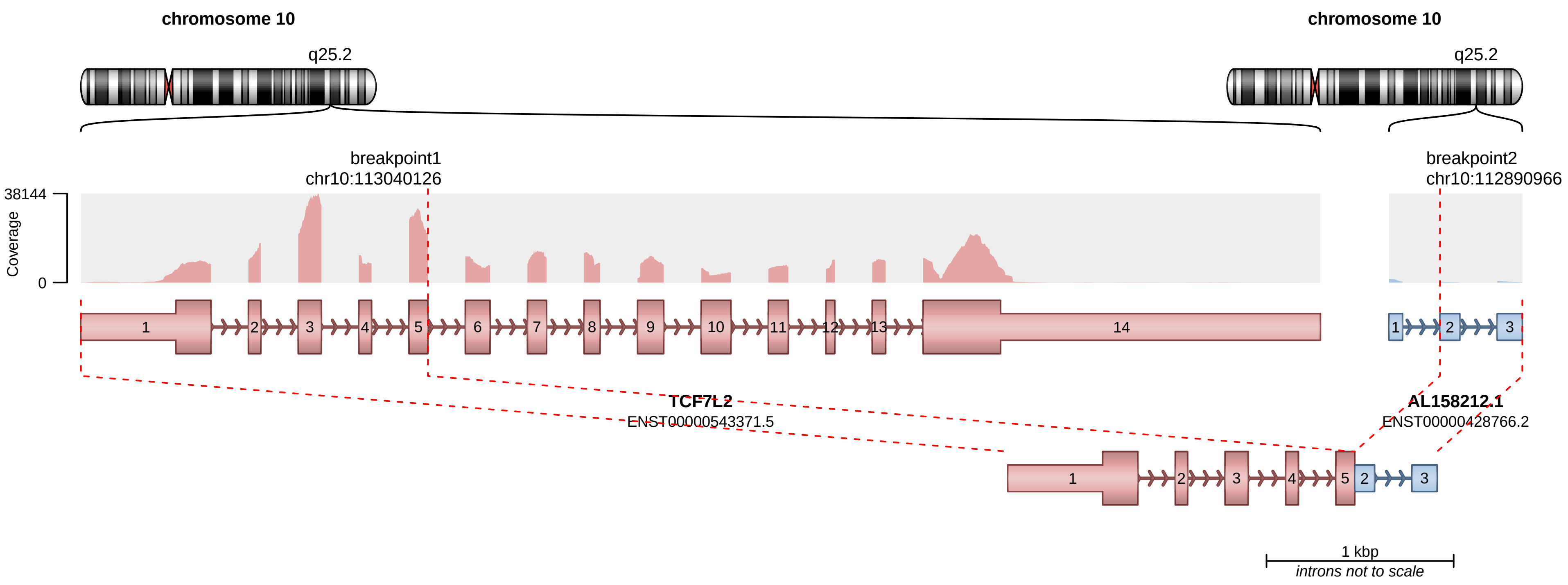


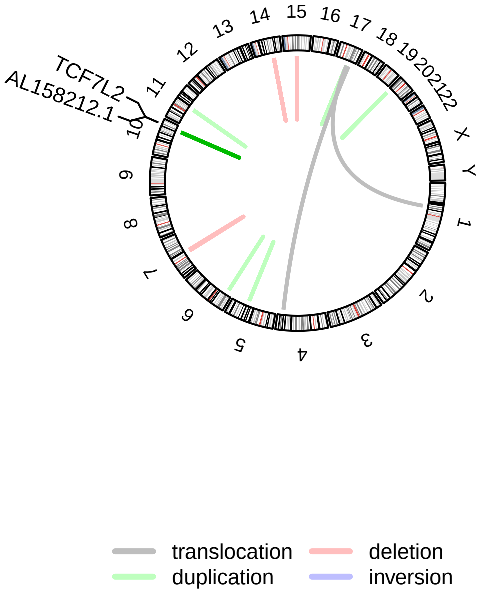
RETAINED PROTEIN DOMAINS
reading frame unclear



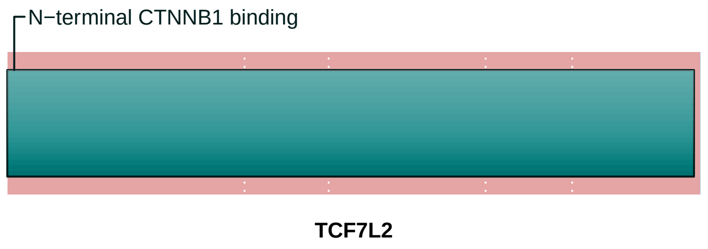
SUPPORTING READ COUNT

Split reads = 121
Discordant mates = 31



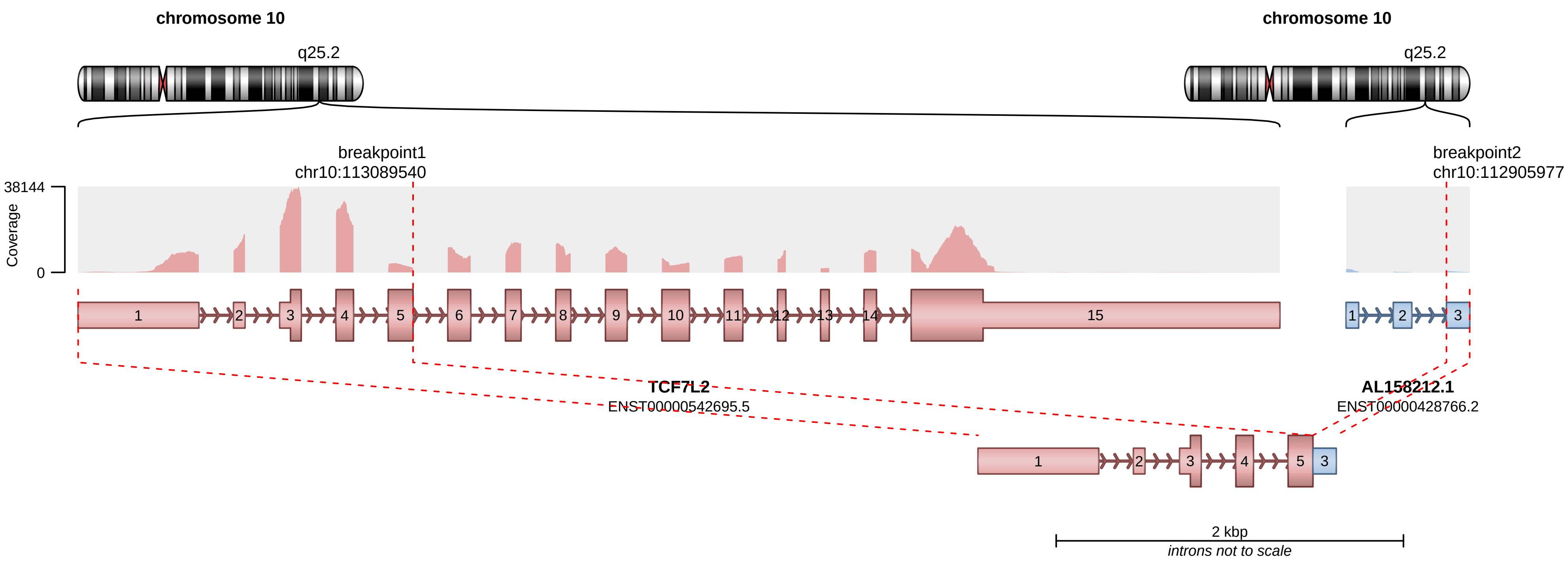


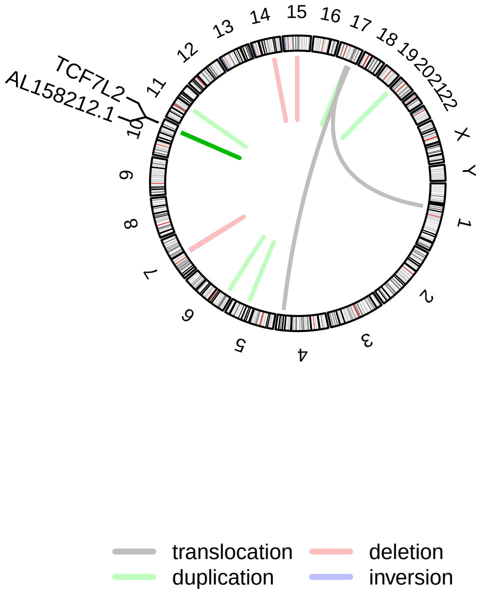
RETAINED PROTEIN DOMAINS
reading frame unclear

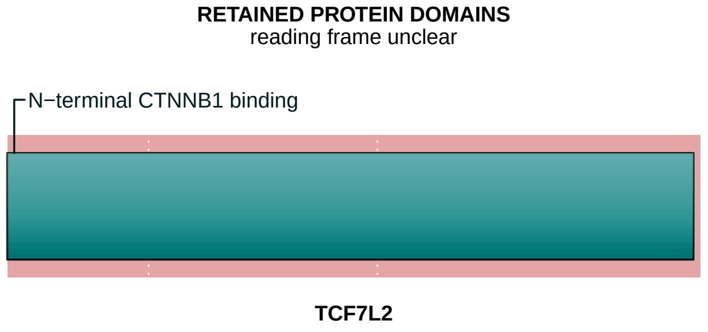


SUPPORTING READ COUNT

Split reads = 54
Discordant mates = 15

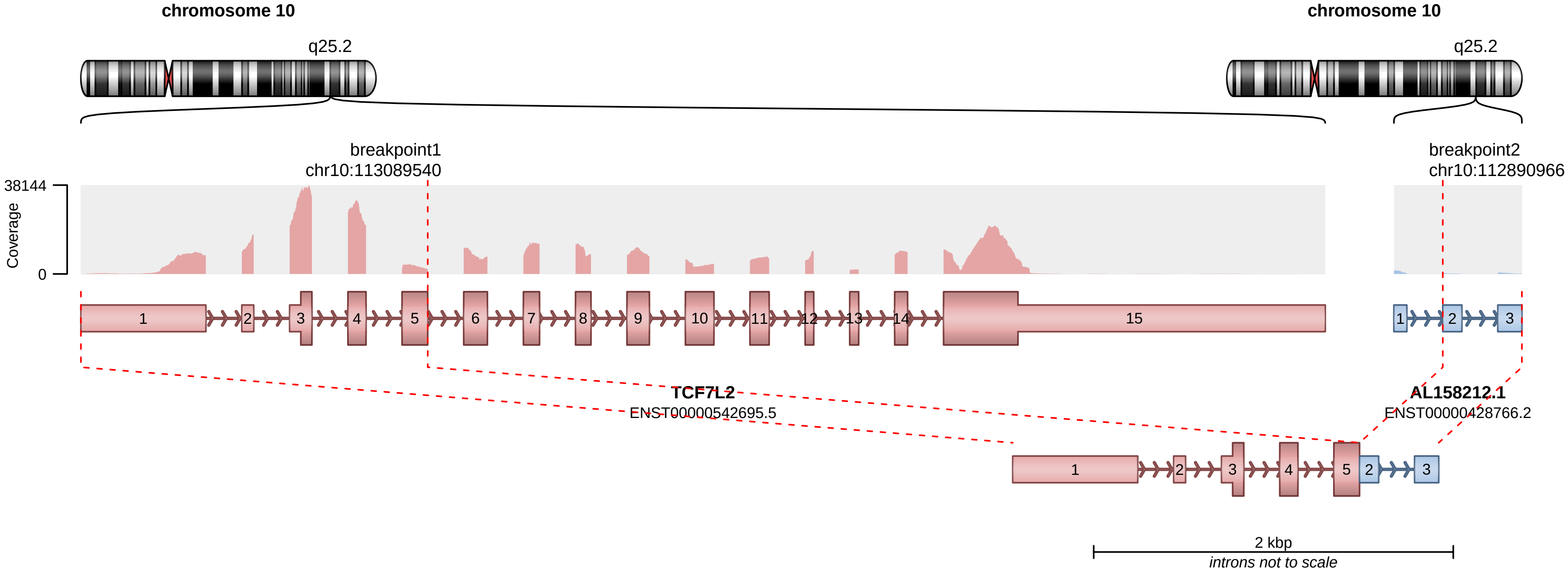


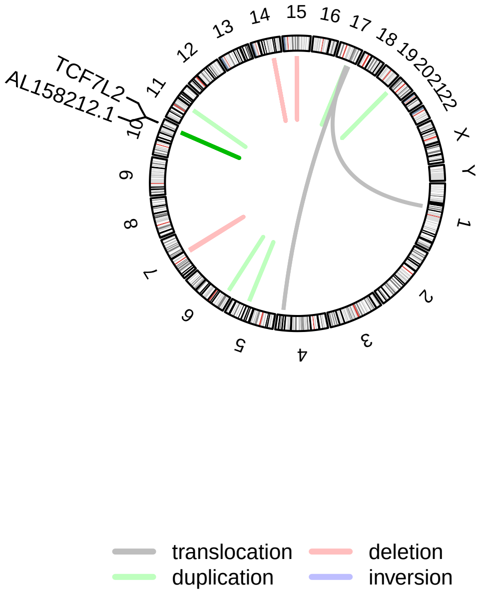




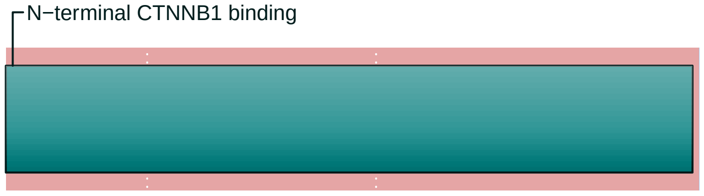
SUPPORTING READ COUNT

Split reads = 19
Discordant mates = 15





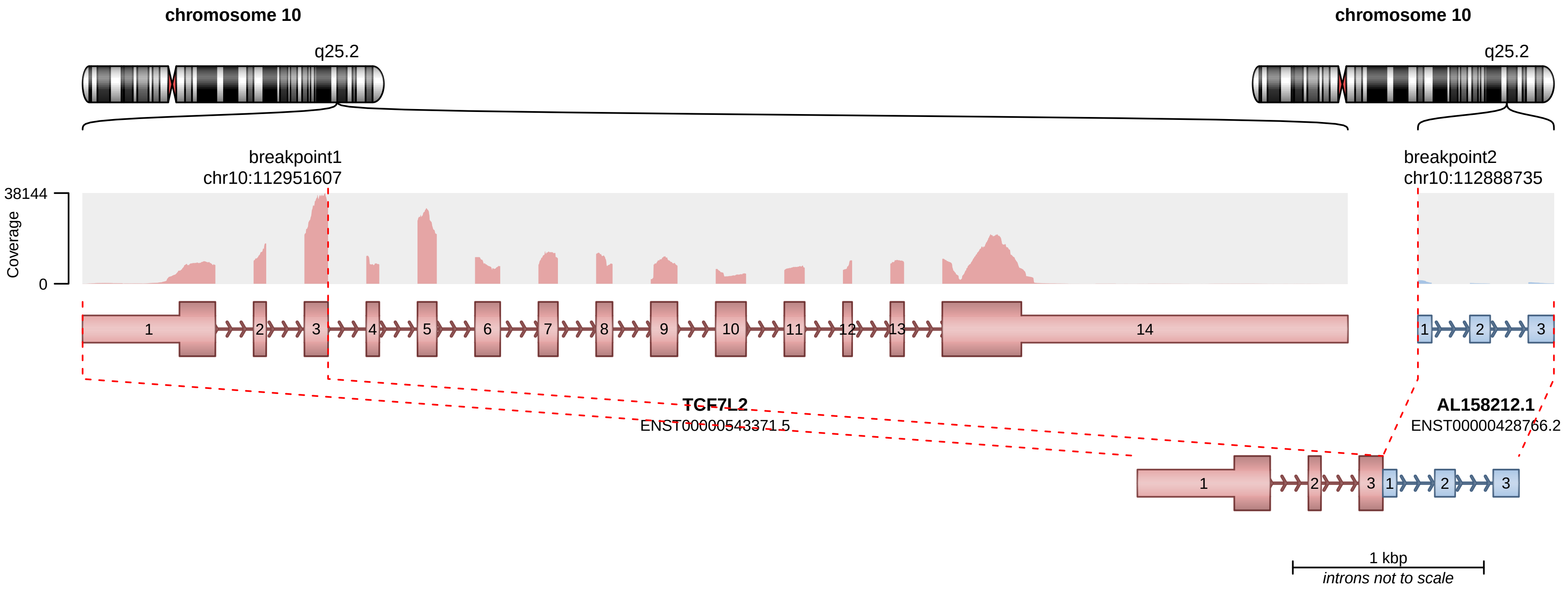
RETAINED PROTEIN DOMAINS
reading frame unclear

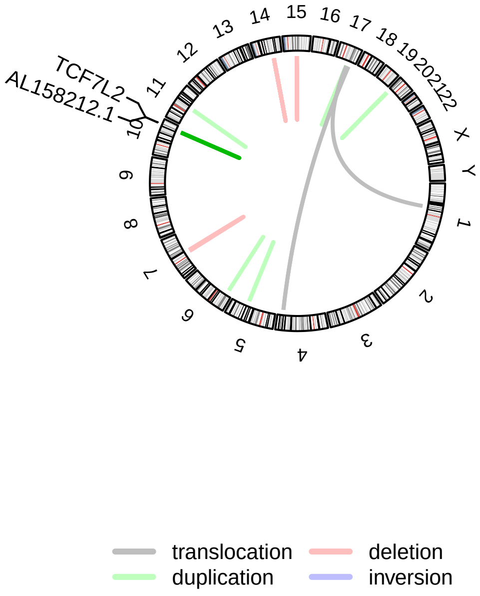


TCF7L2

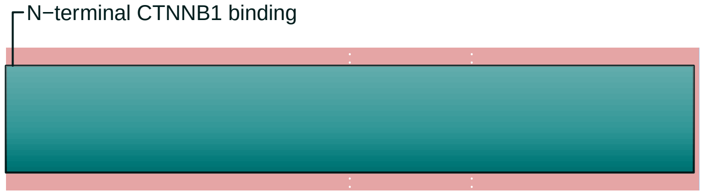
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 17





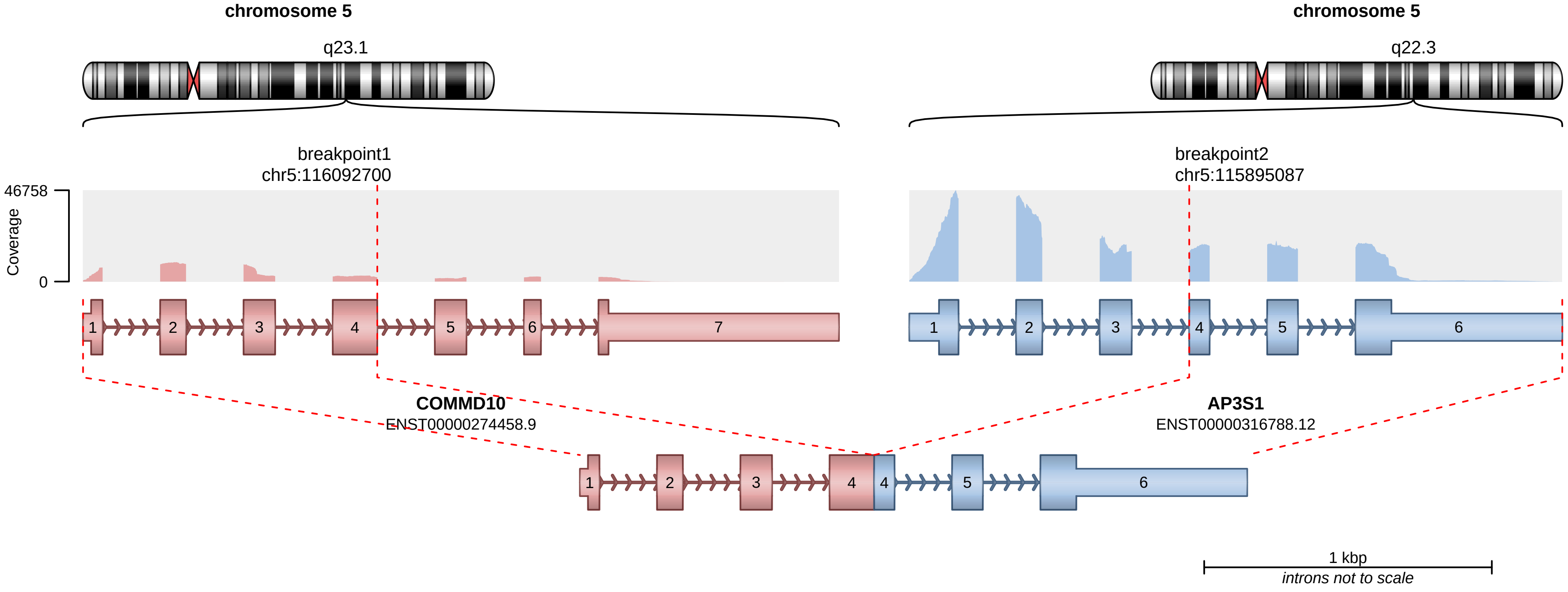
RETAINED PROTEIN DOMAINS
reading frame unclear

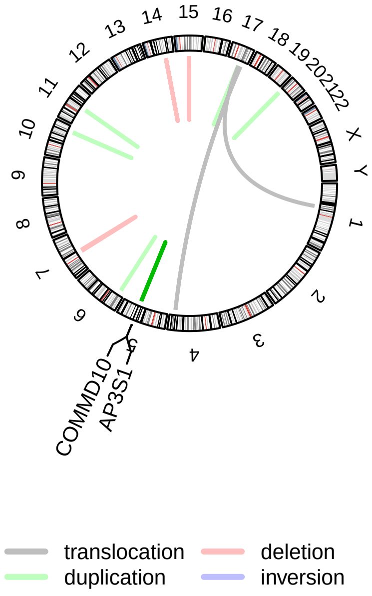


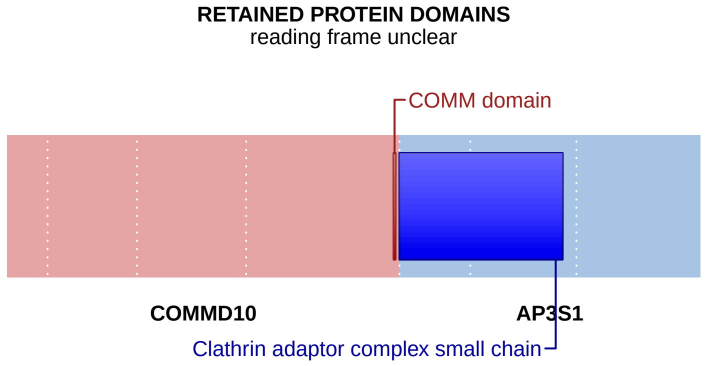
TCF7L2

SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 2

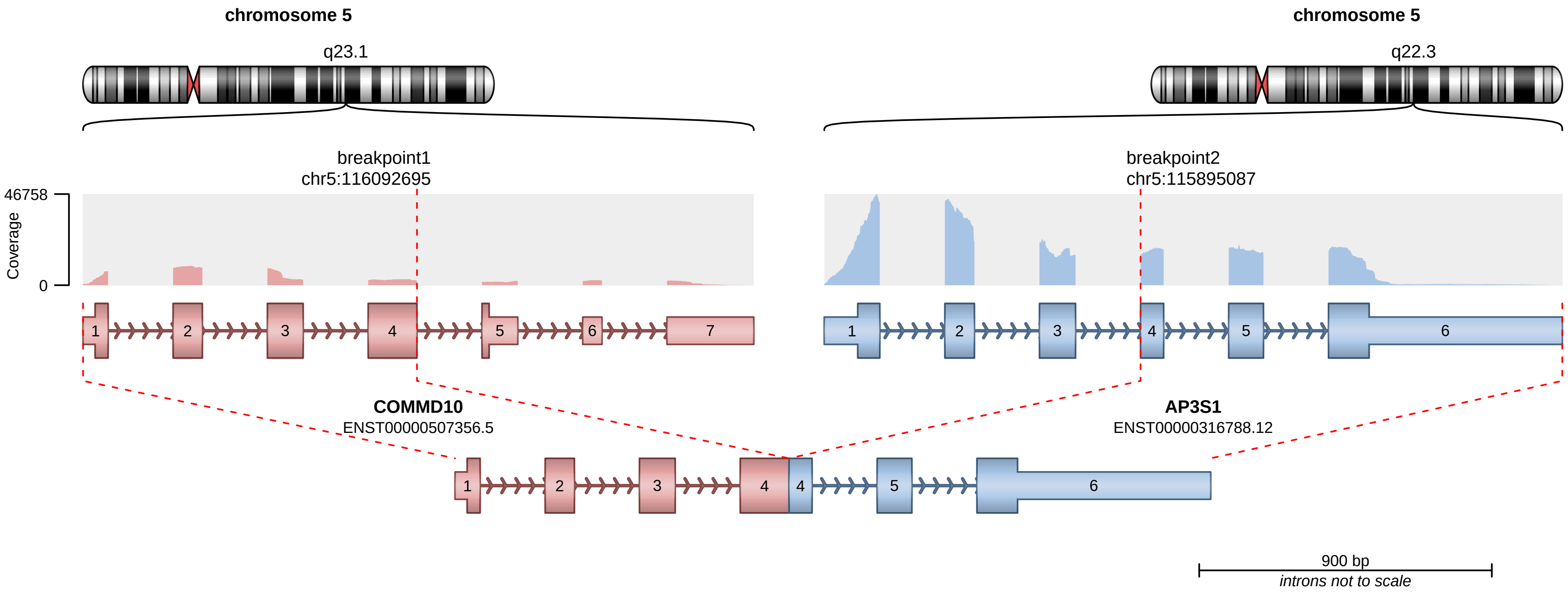


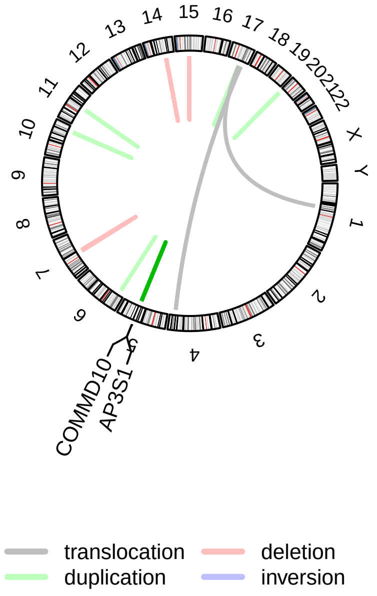




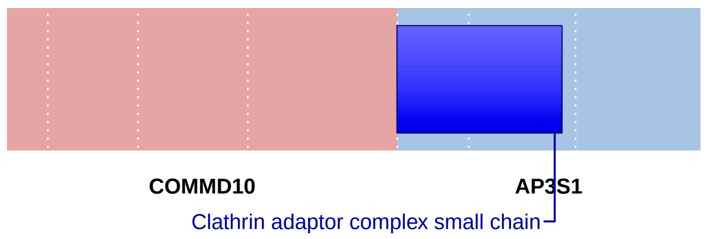
SUPPORTING READ COUNT

Split reads = 301
Discordant mates = 17



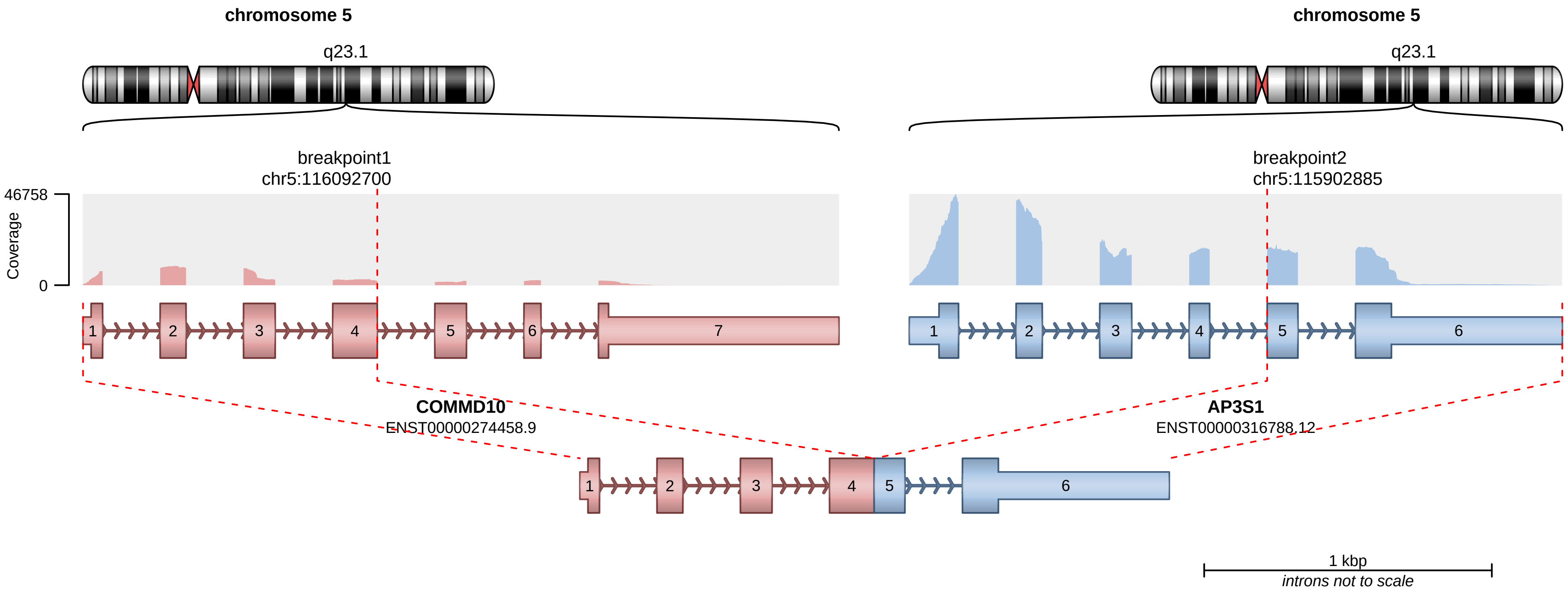


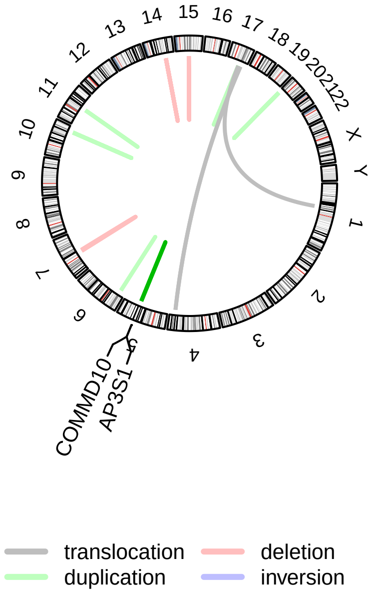
RETAINED PROTEIN DOMAINS
reading frame unclear

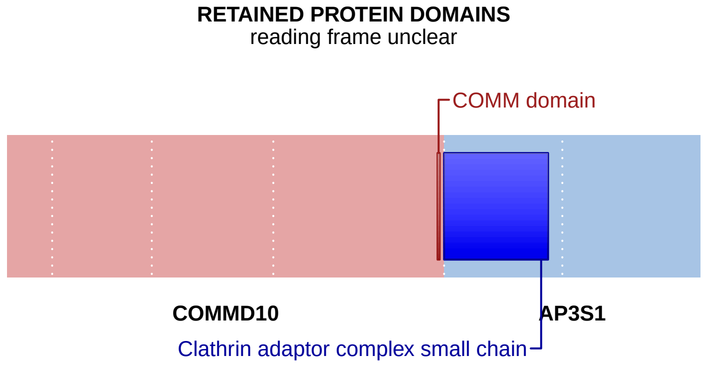


SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 15

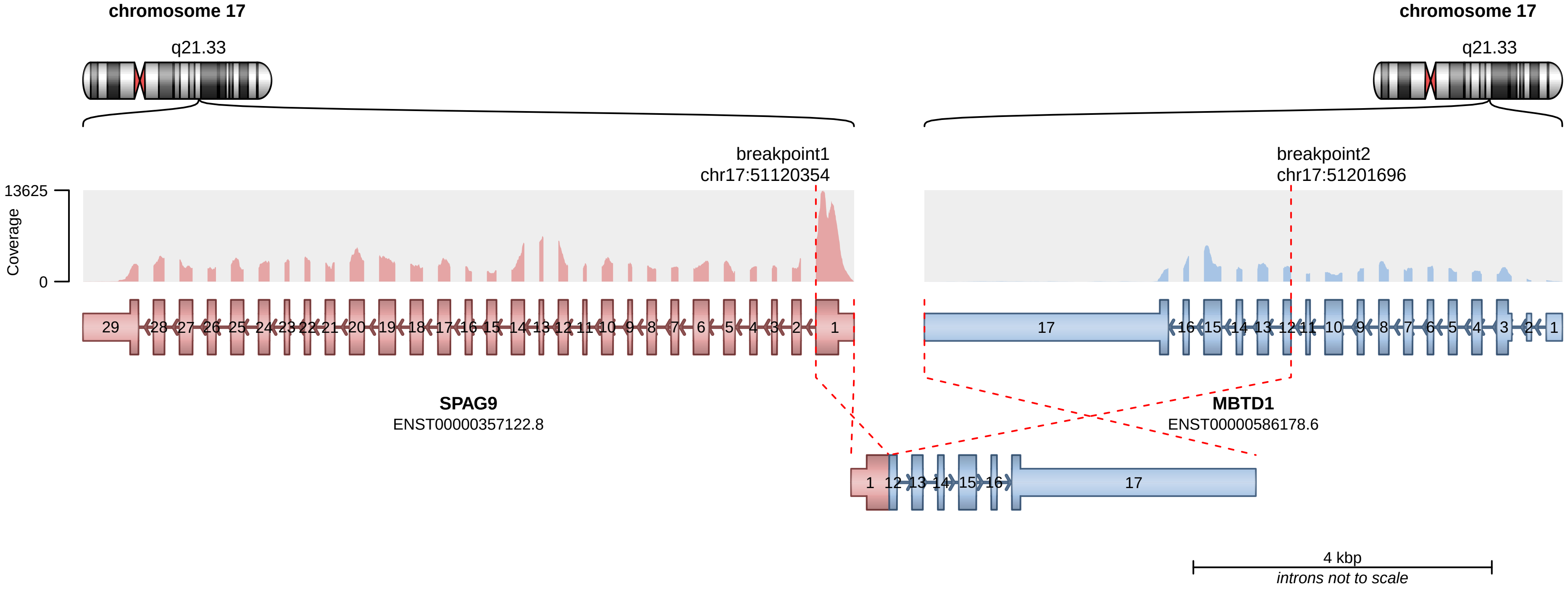


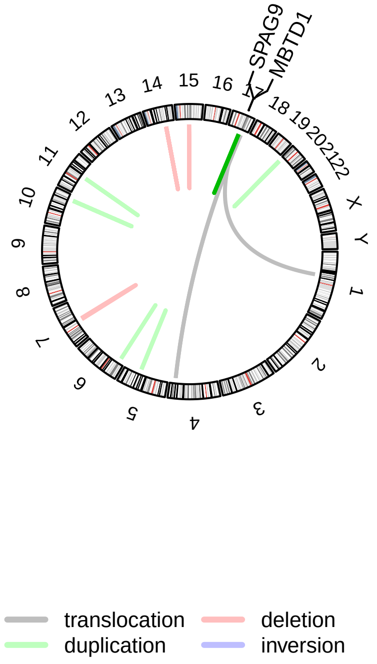


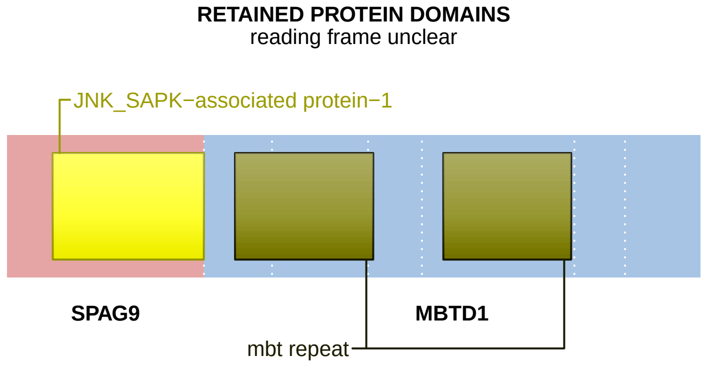


SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 2

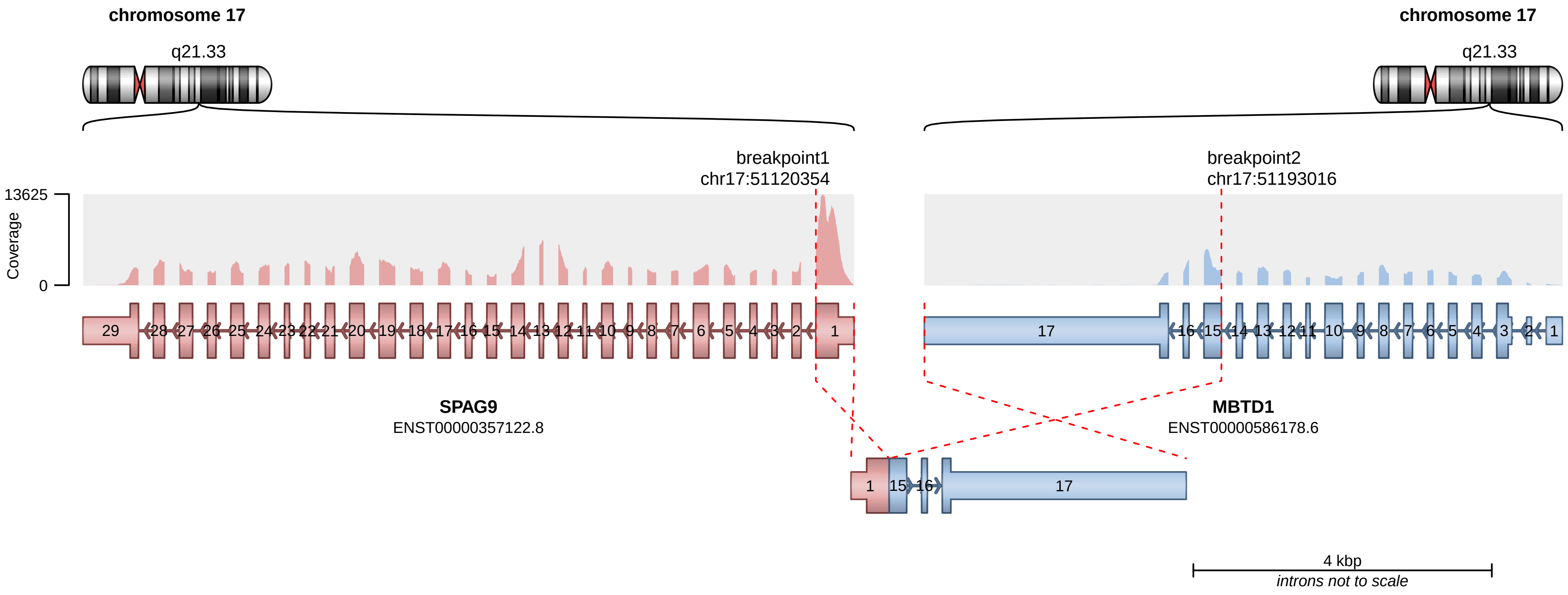


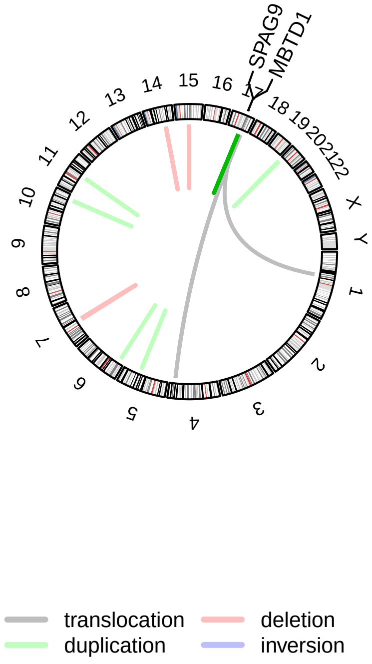




SUPPORTING READ COUNT

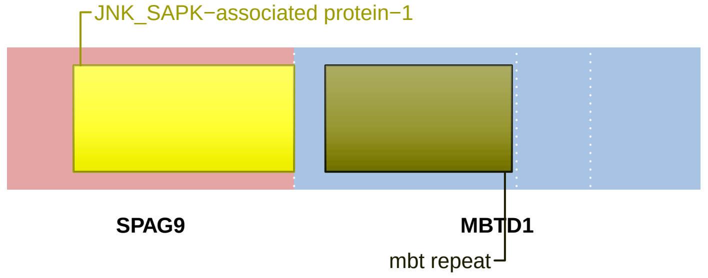
Split reads = 257
Discordant mates = 5





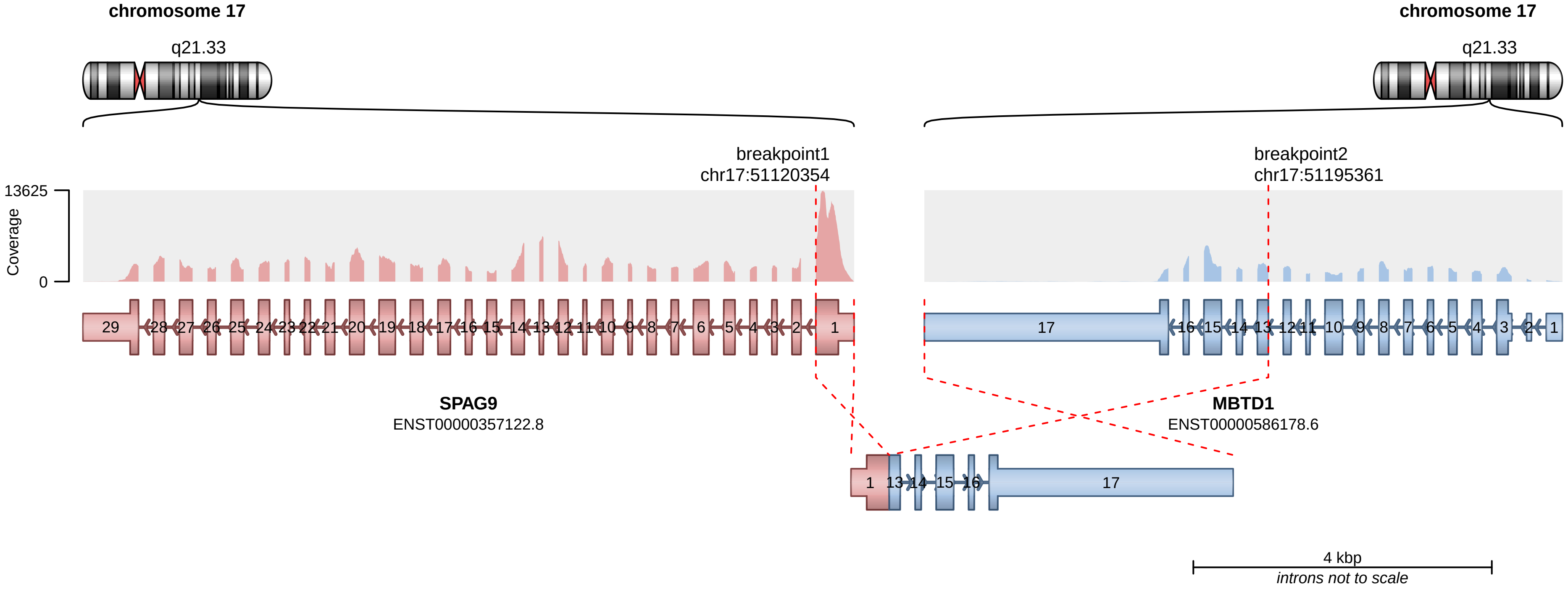
RETAINED PROTEIN DOMAINS

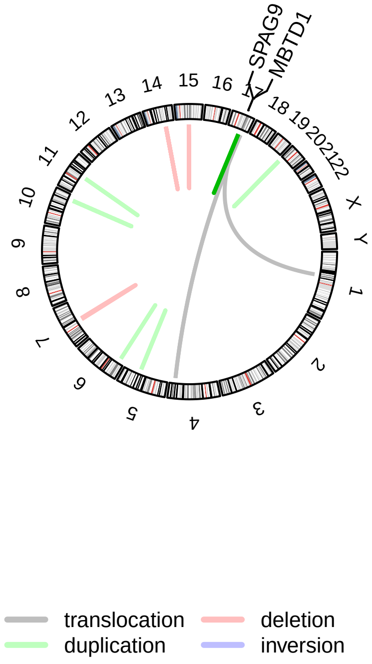
reading frame unclear



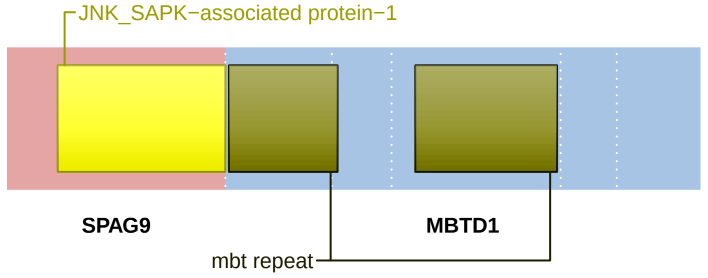
SUPPORTING READ COUNT

Split reads = 26
Discordant mates = 0



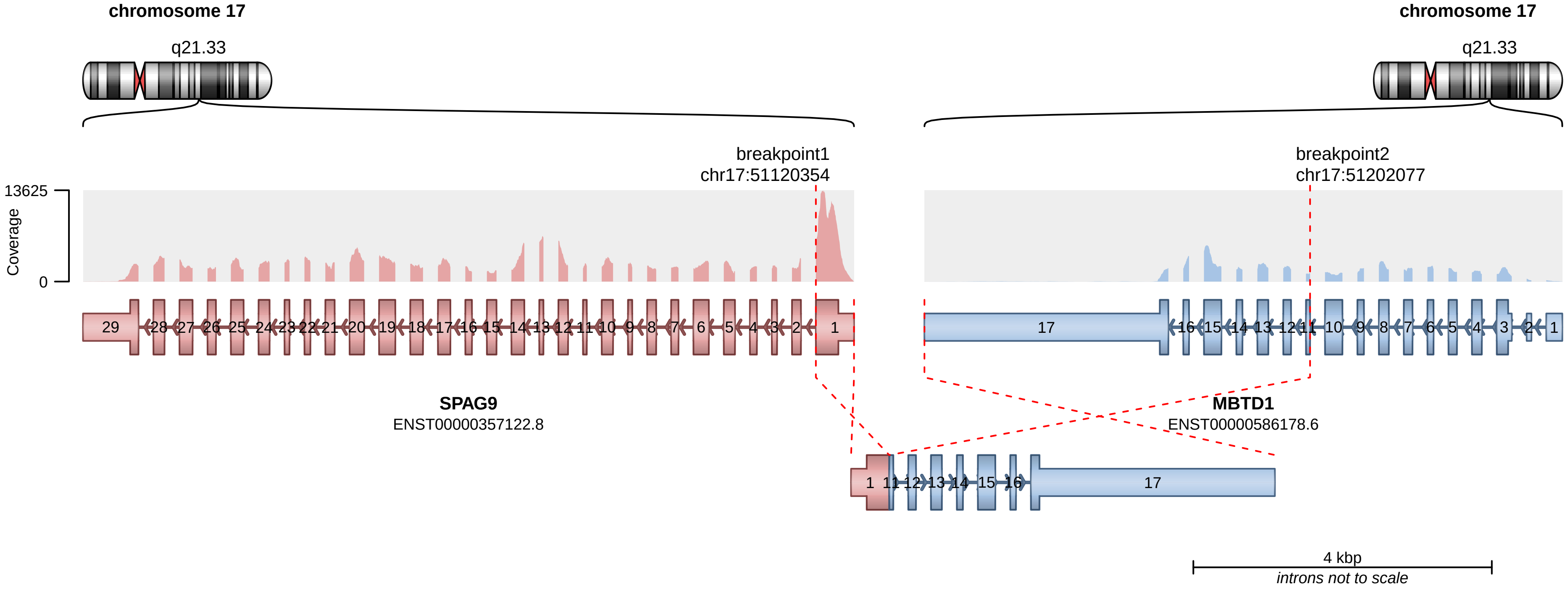


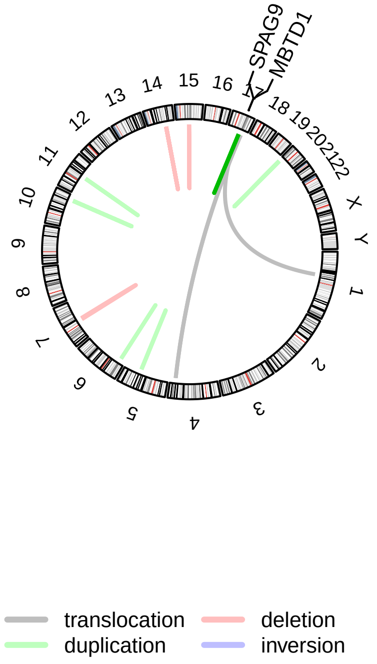
RETAINED PROTEIN DOMAINS
reading frame unclear



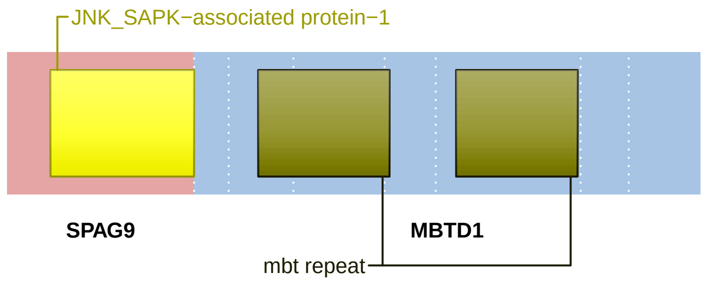
SUPPORTING READ COUNT

Split reads = 19
Discordant mates = 1



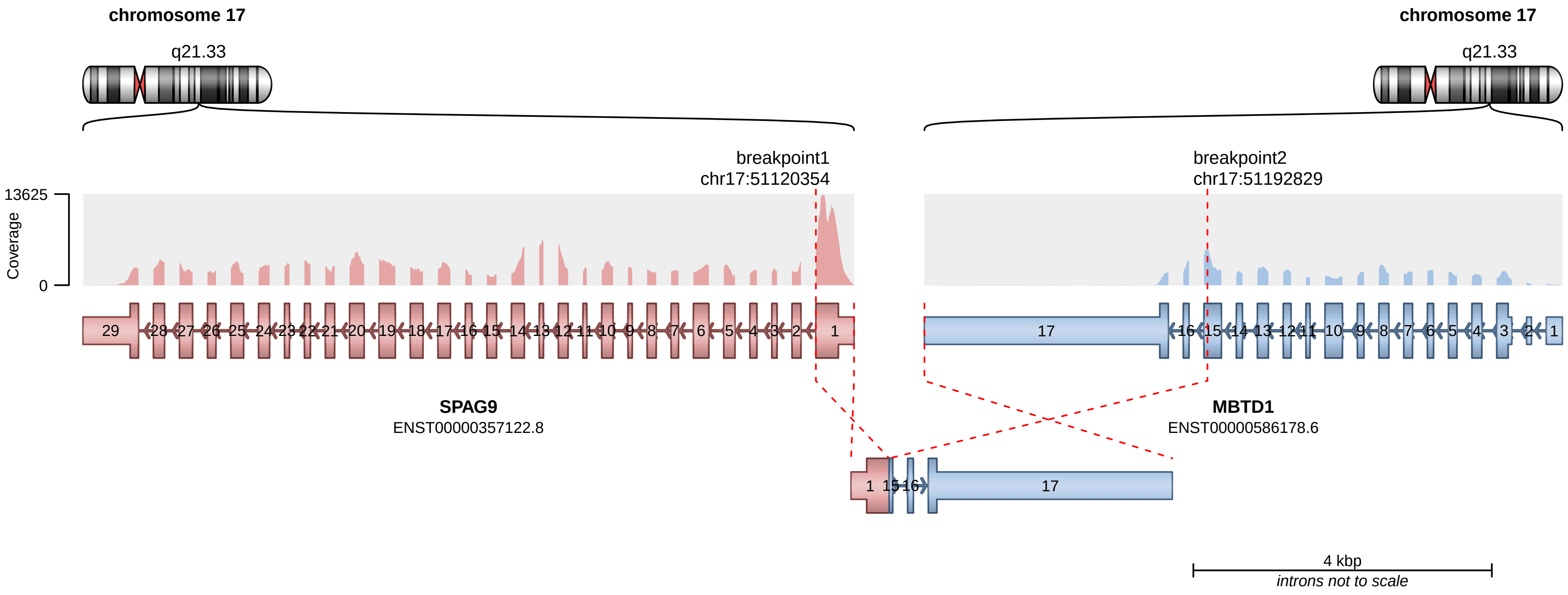


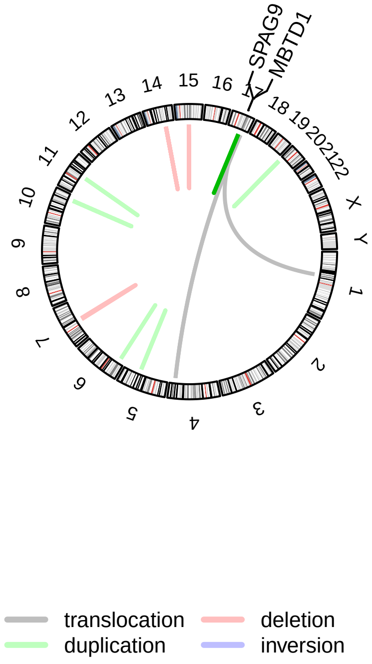
RETAINED PROTEIN DOMAINS
reading frame unclear

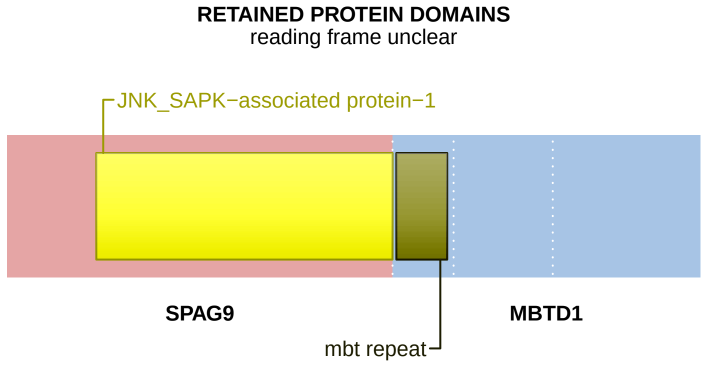


SUPPORTING READ COUNT

Split reads = 14
Discordant mates = 5

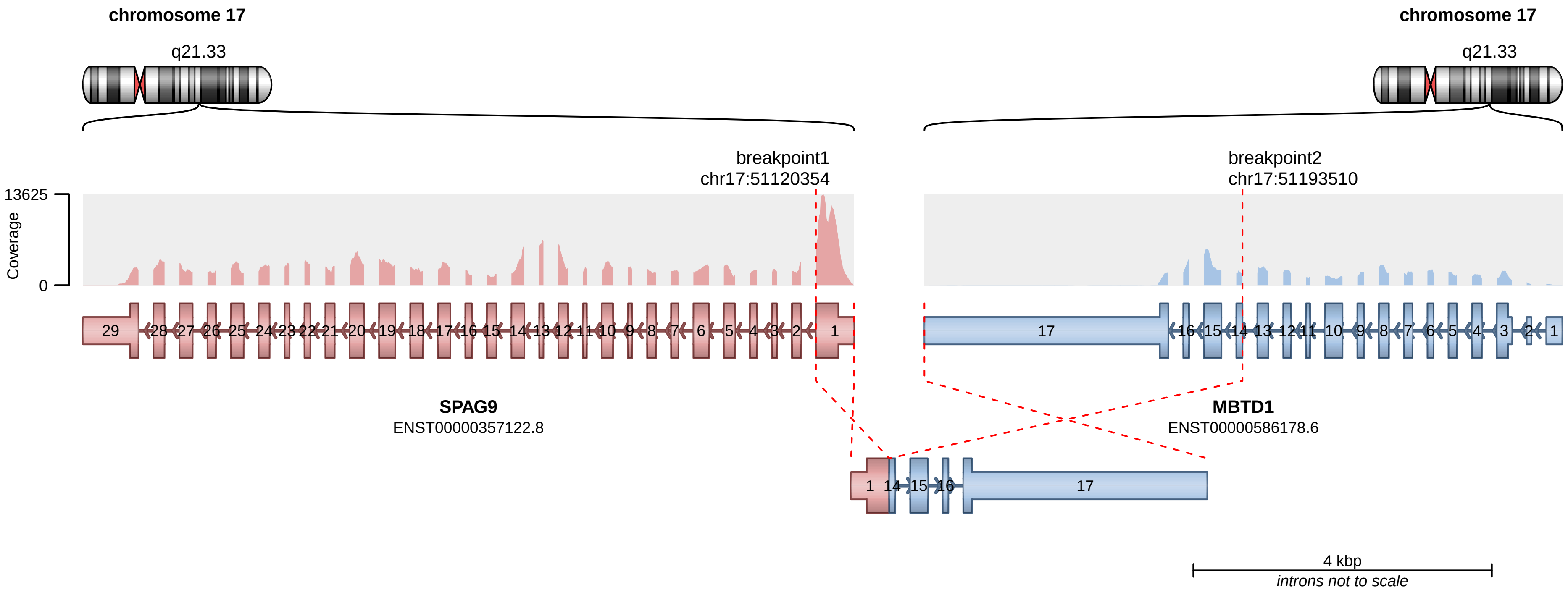


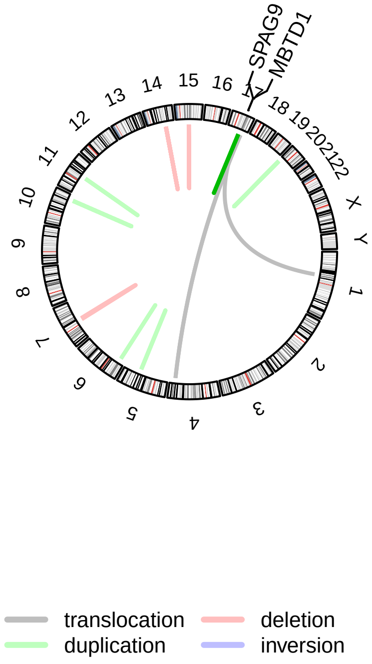




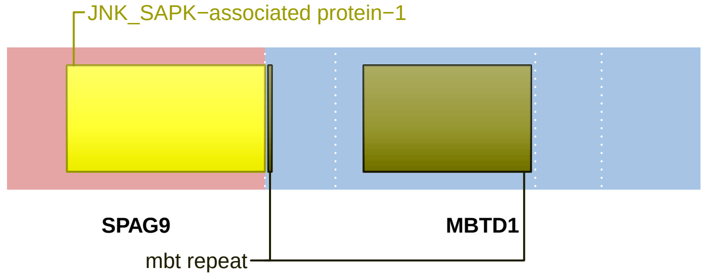
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0



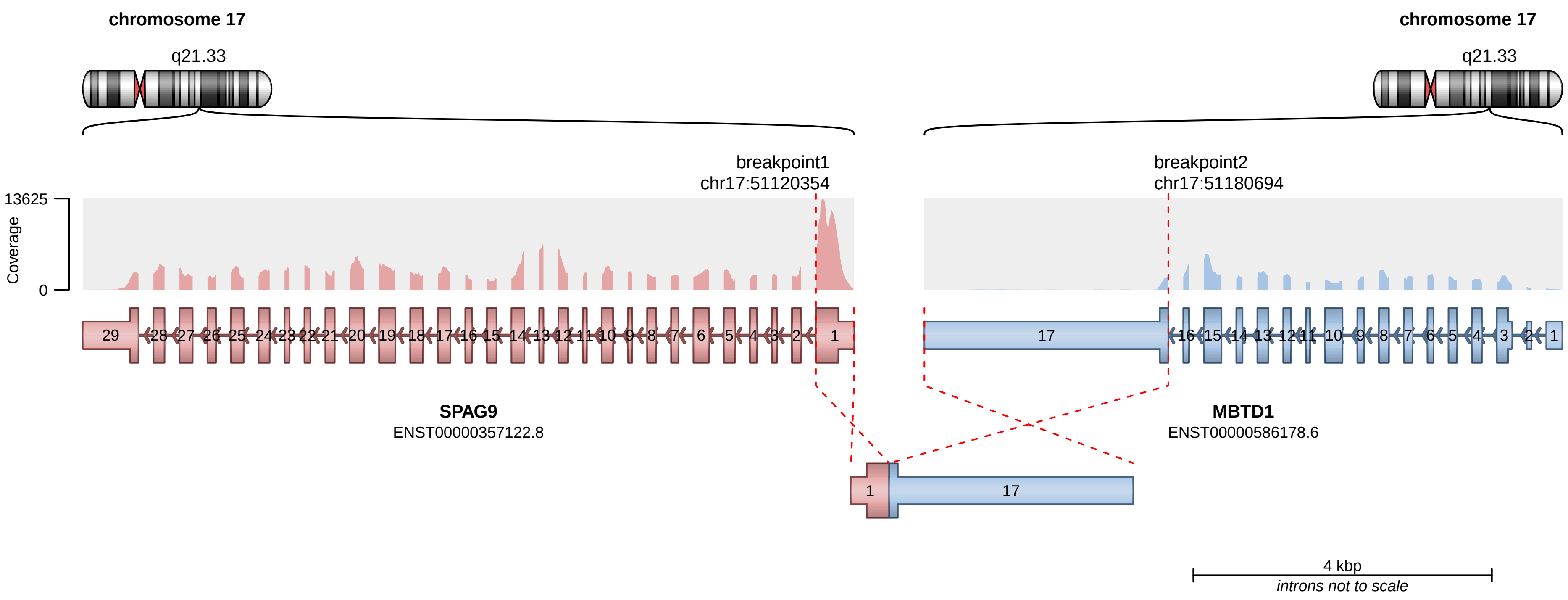


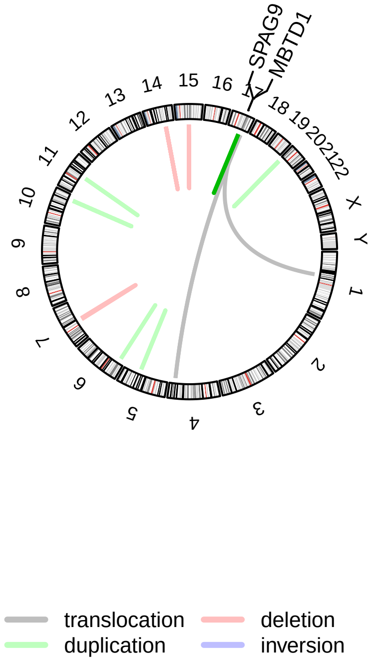
RETAINED PROTEIN DOMAINS
reading frame unclear

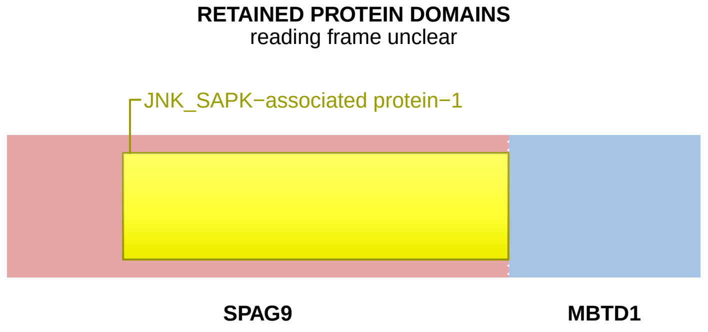


SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

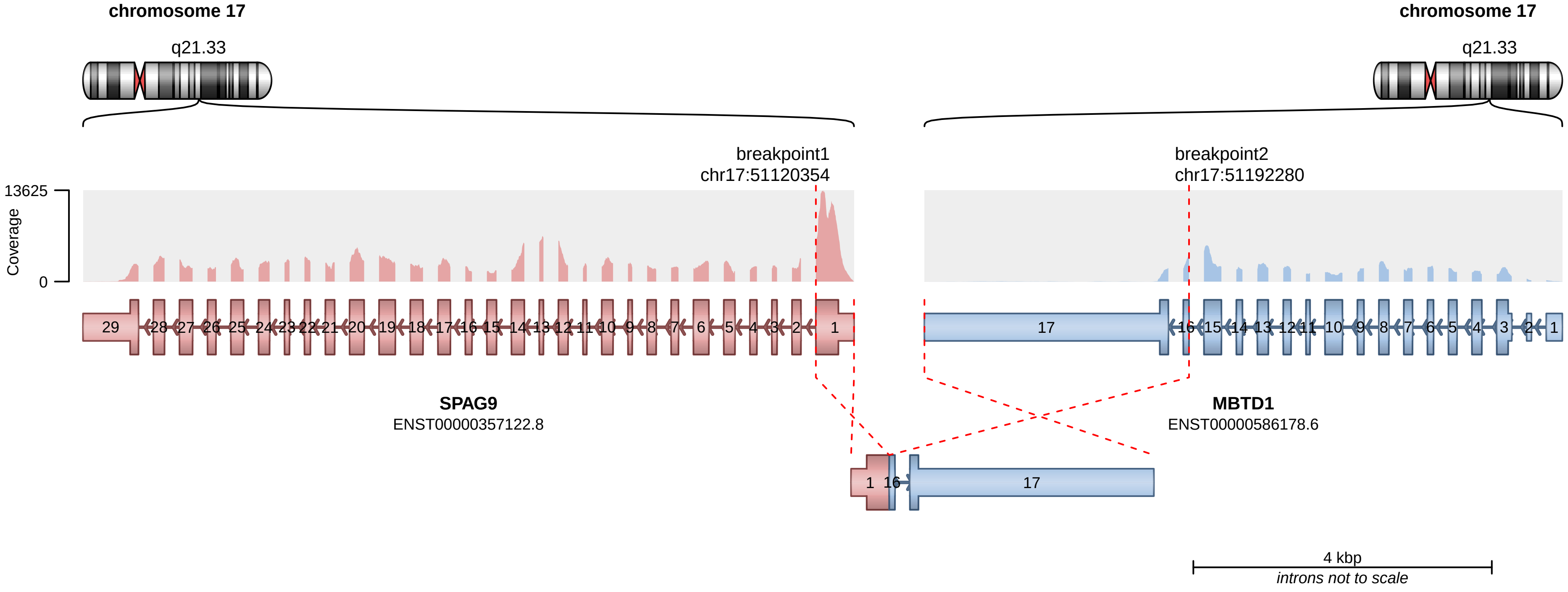


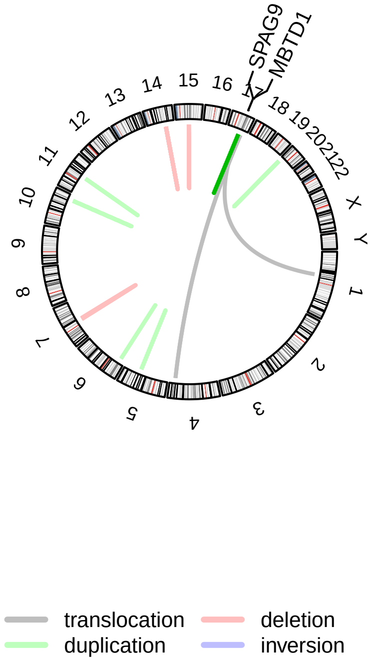




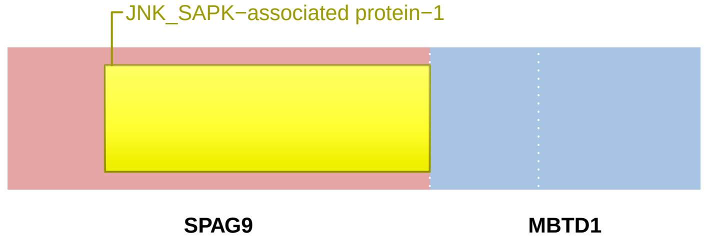
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0



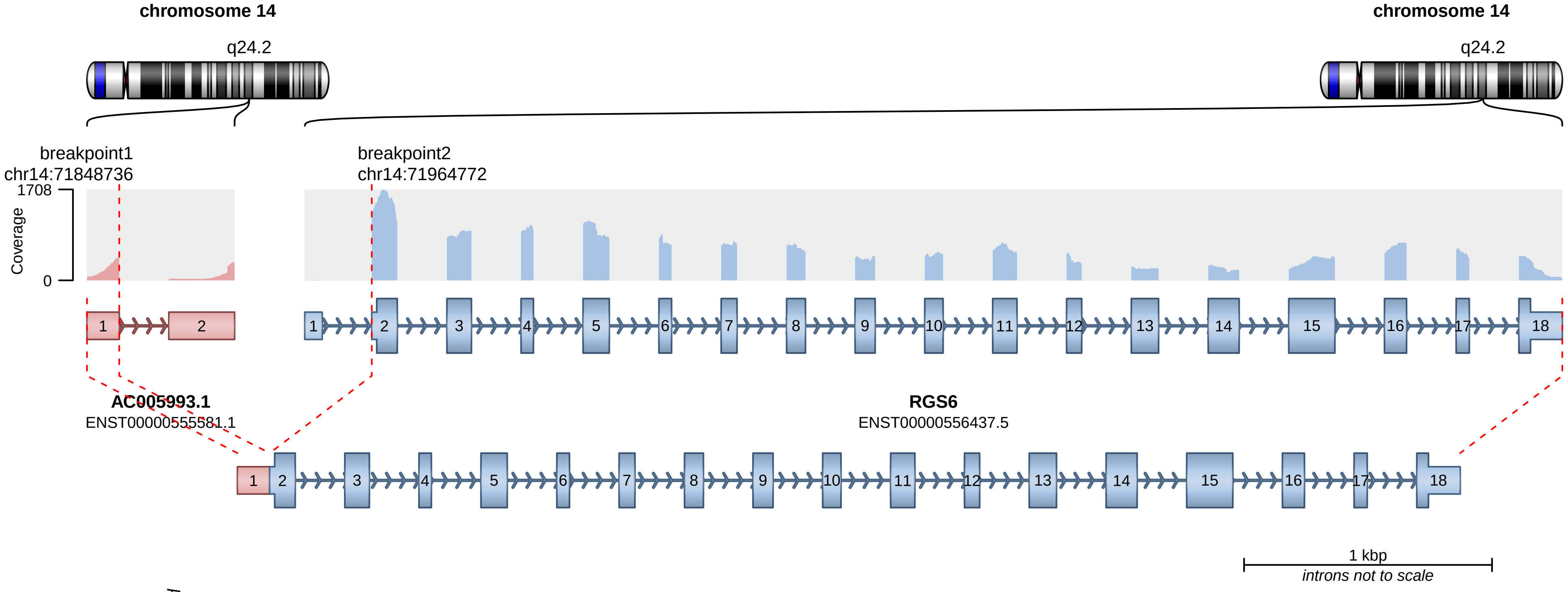


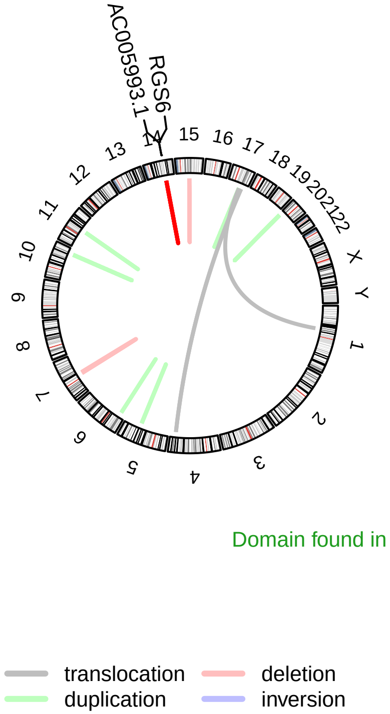
RETAINED PROTEIN DOMAINS
reading frame unclear

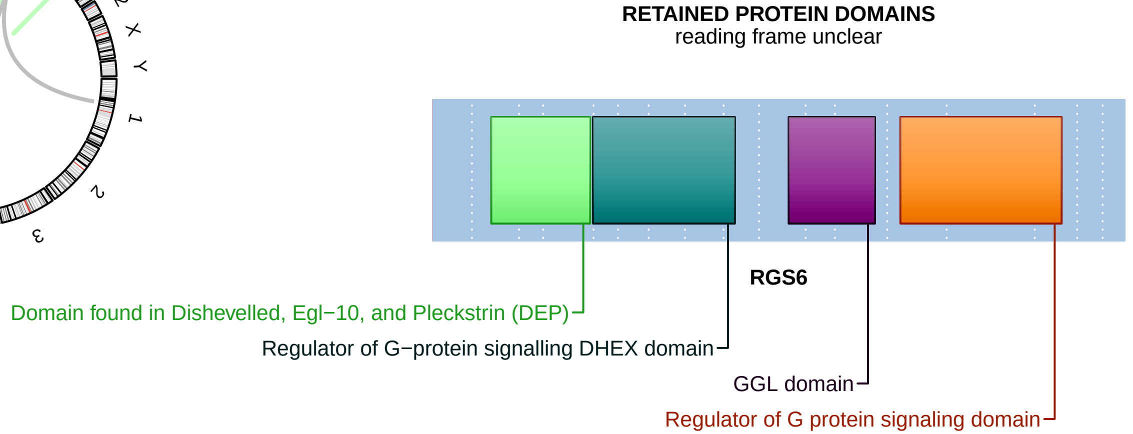


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

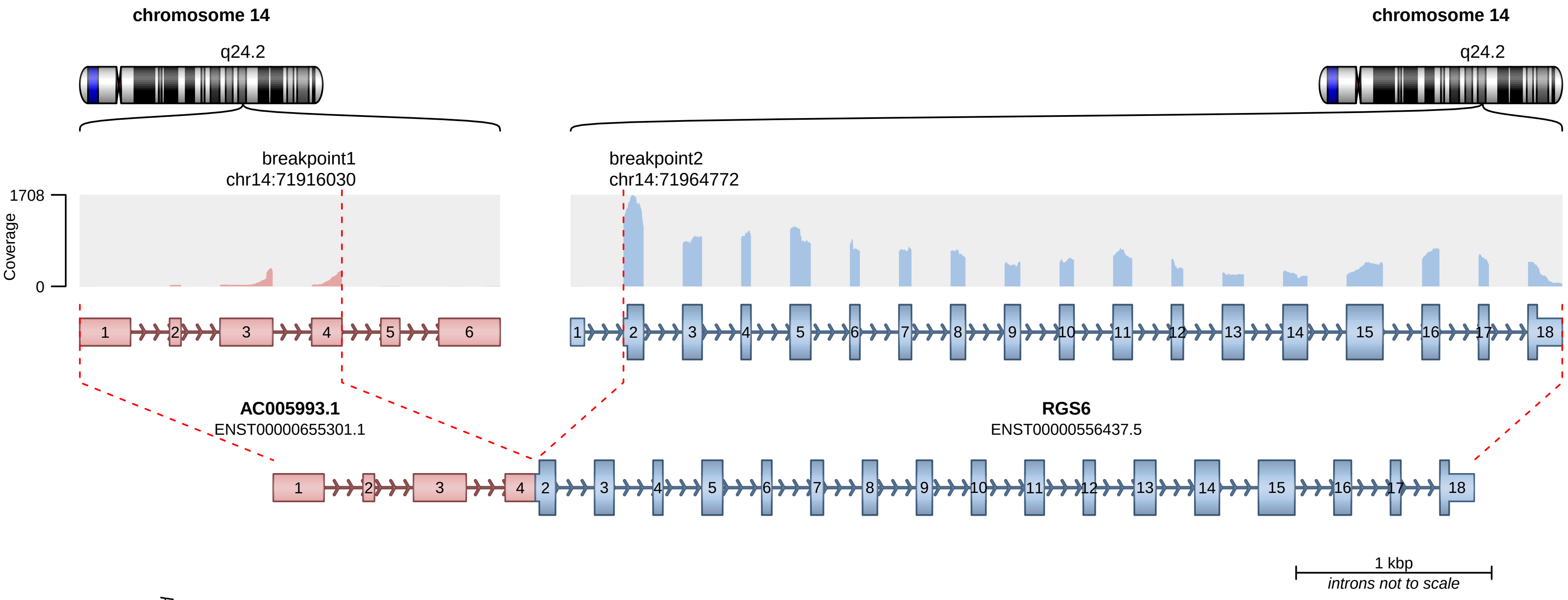


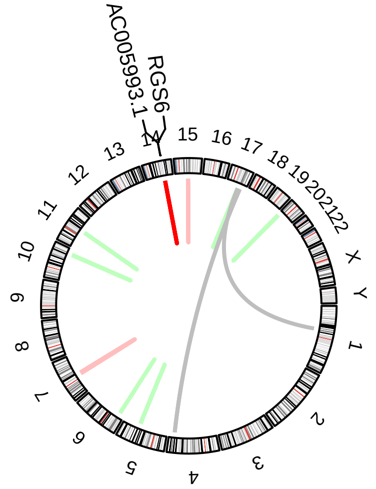




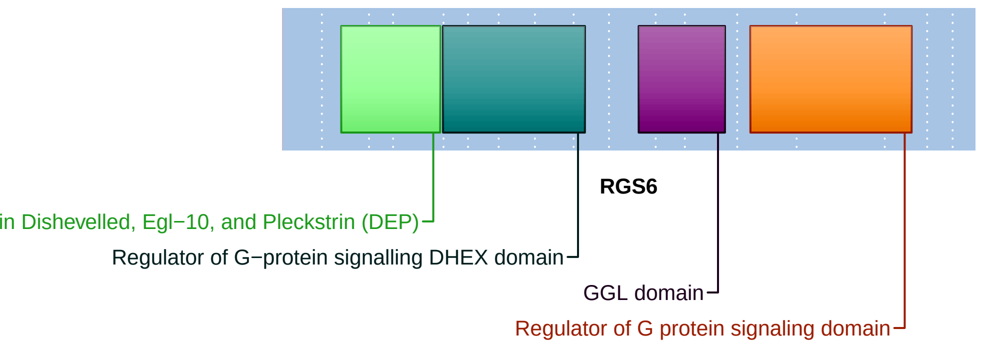
SUPPORTING READ COUNT

Split reads = 175
Discordant mates = 0





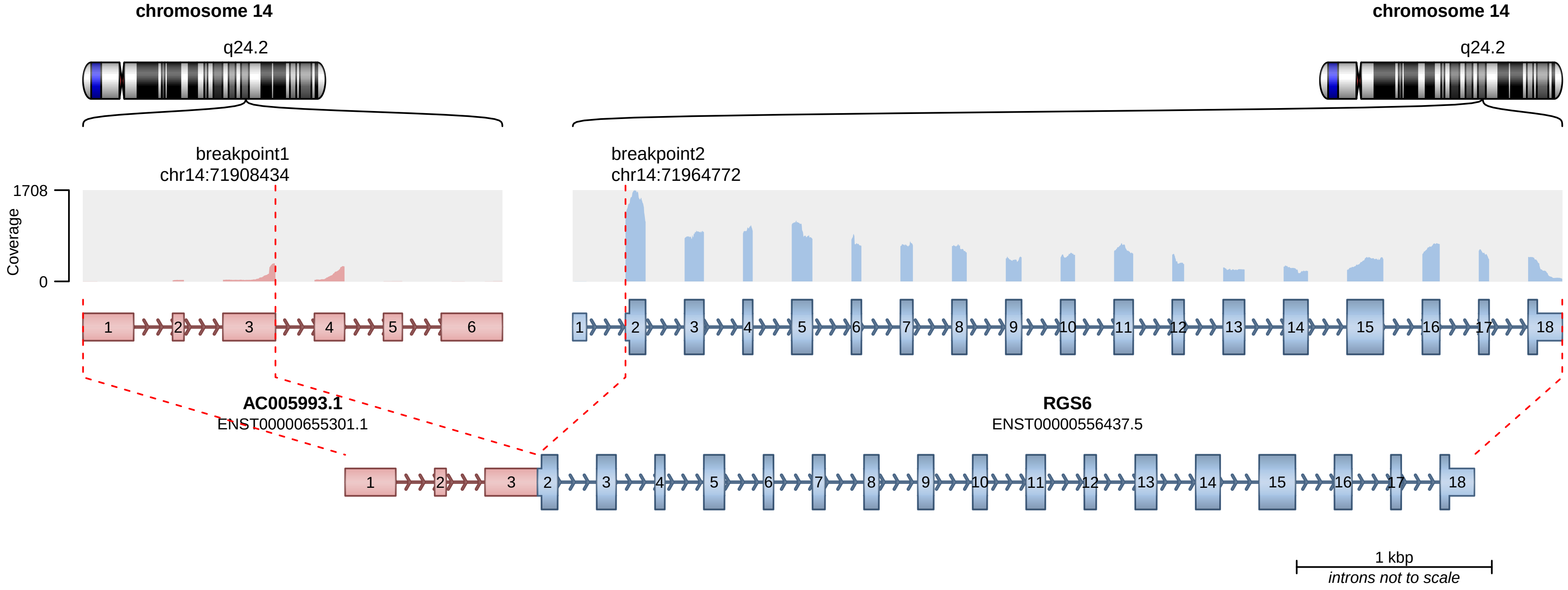
RETAINED PROTEIN DOMAINS
reading frame unclear

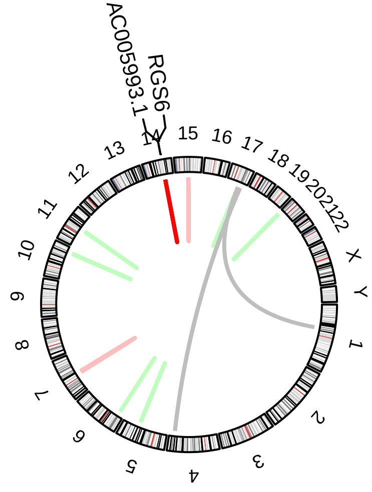


SUPPORTING READ COUNT

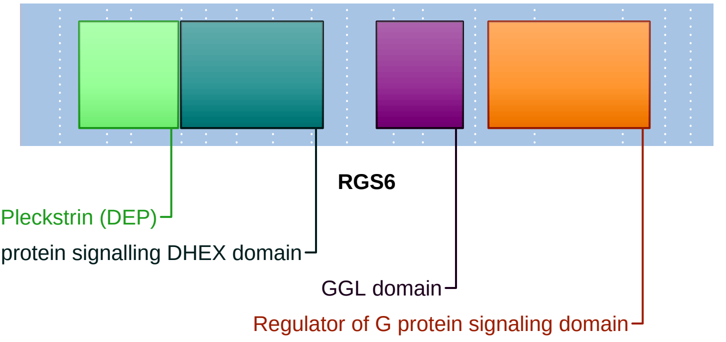
Split reads = 121
Discordant mates = 8

— translocation	— deletion
— duplication	— inversion



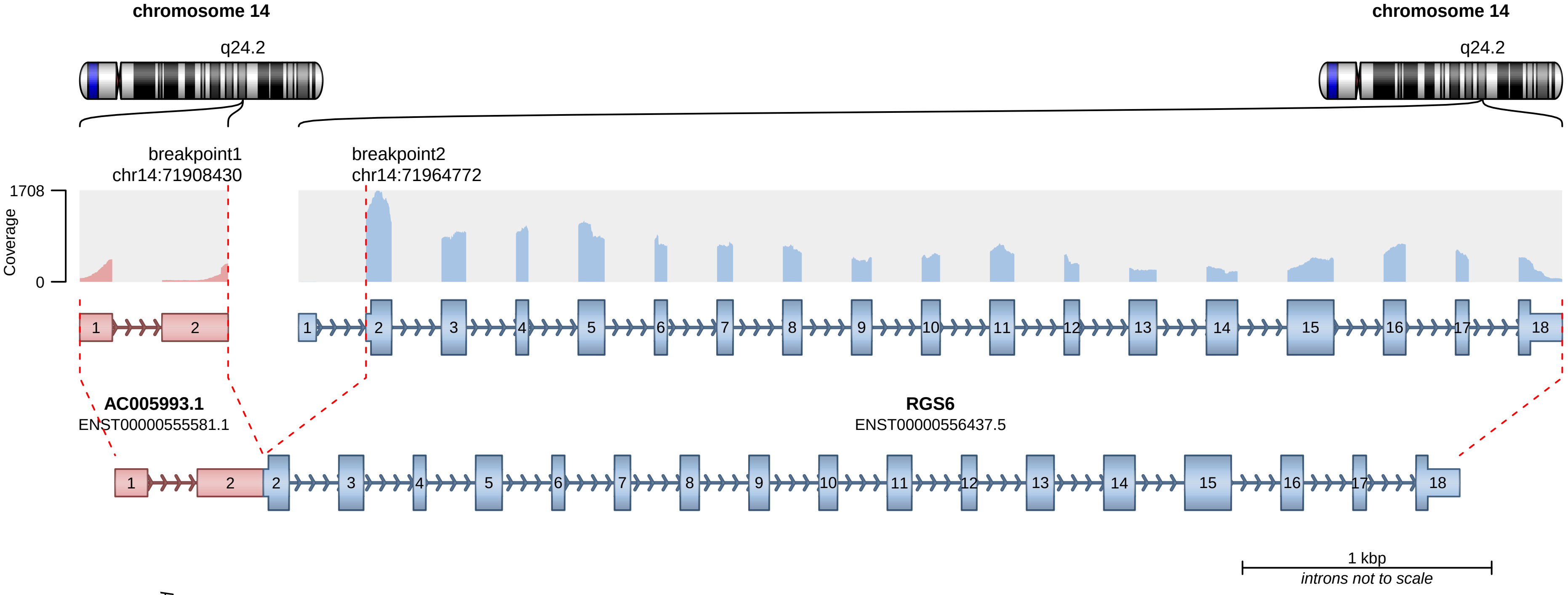


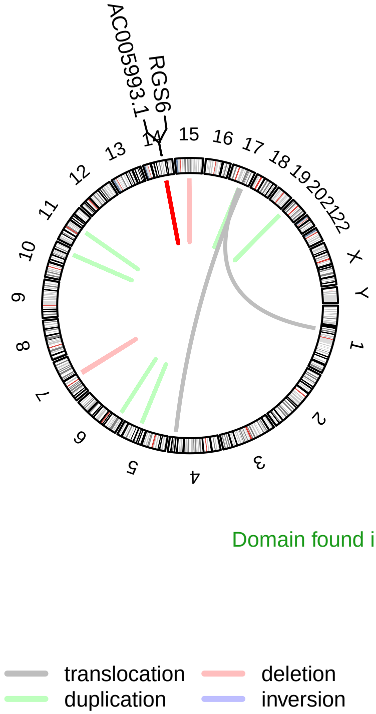
RETAINED PROTEIN DOMAINS
reading frame unclear

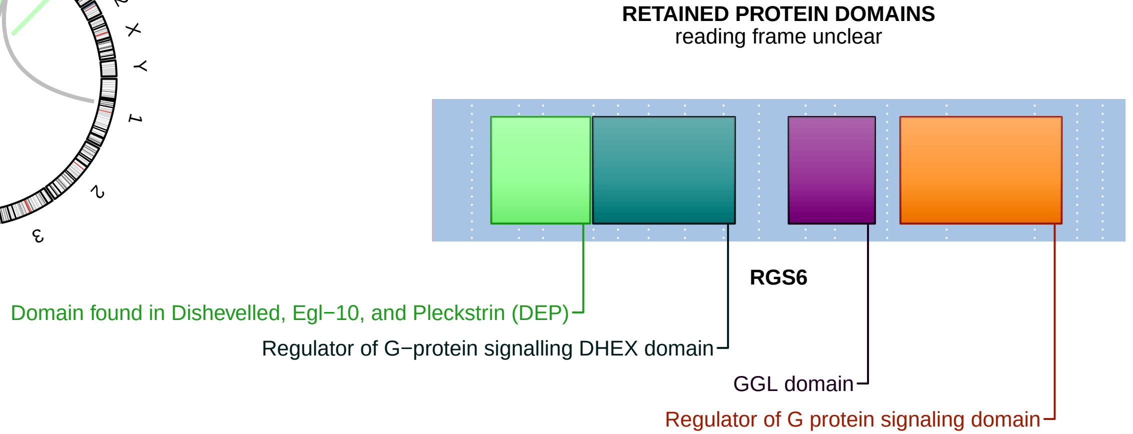


SUPPORTING READ COUNT

Split reads = 79
Discordant mates = 4

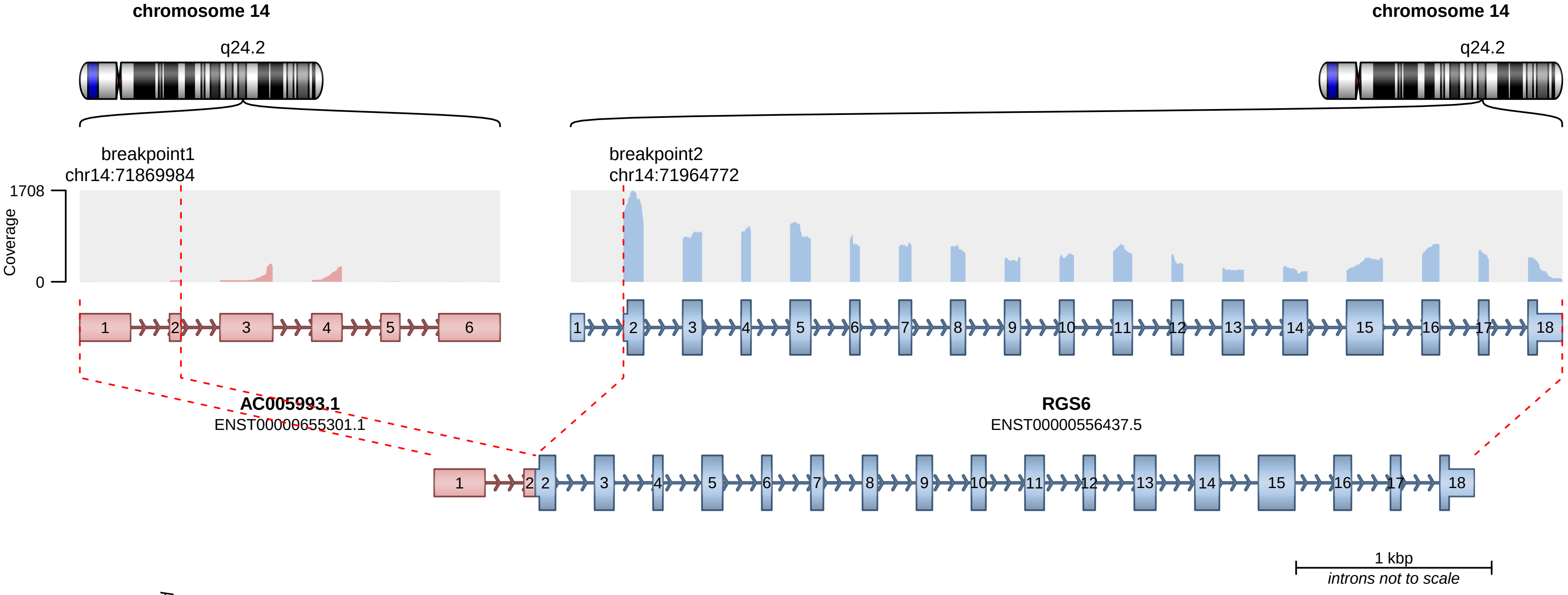


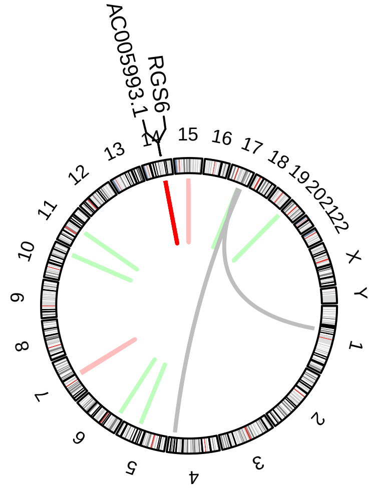


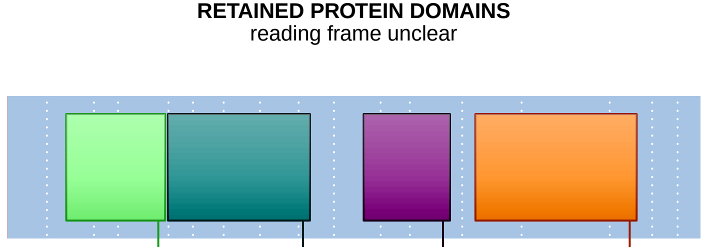


SUPPORTING READ COUNT

Split reads = 25
Discordant mates = 4

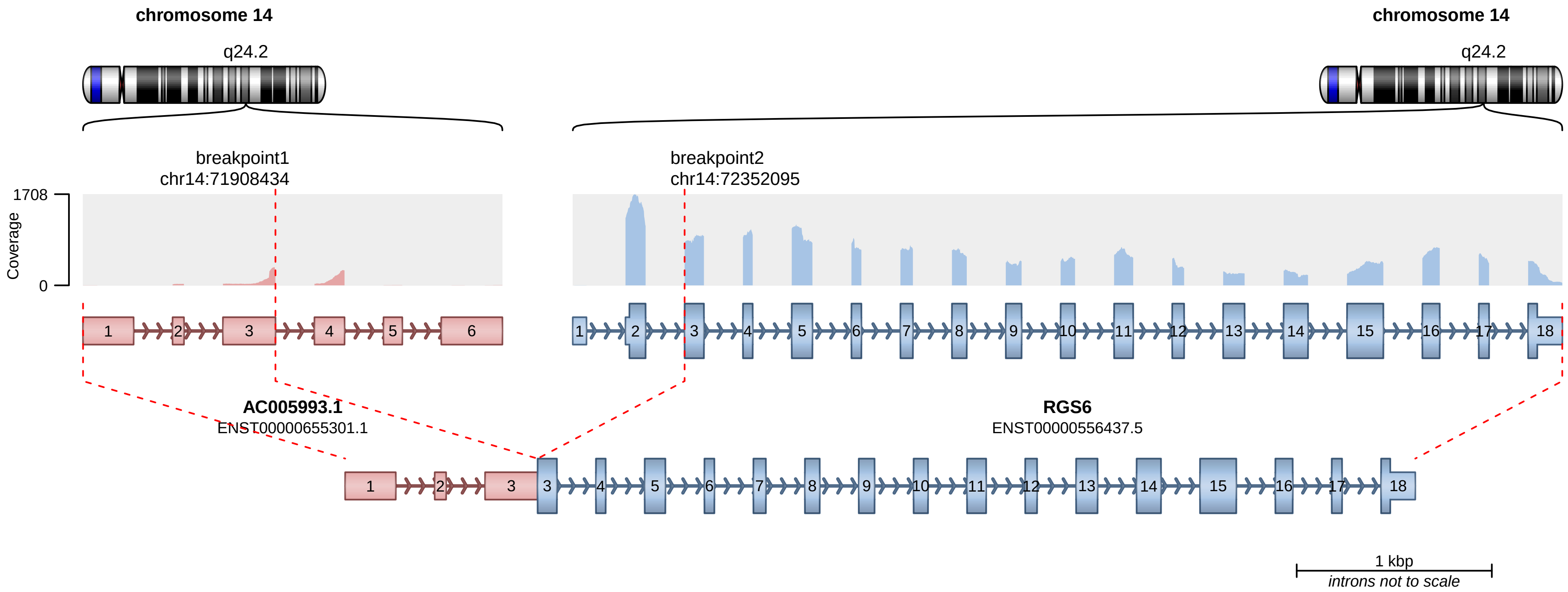


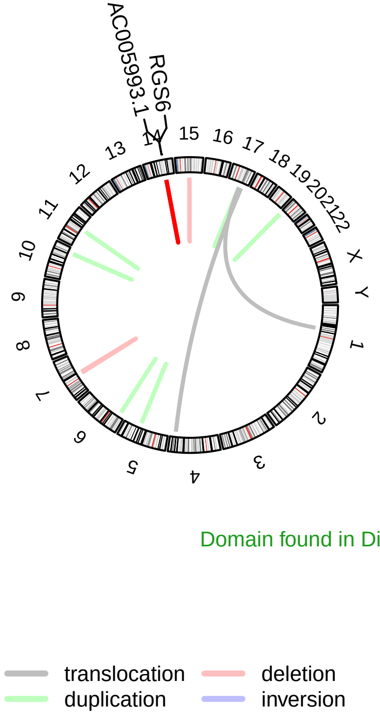




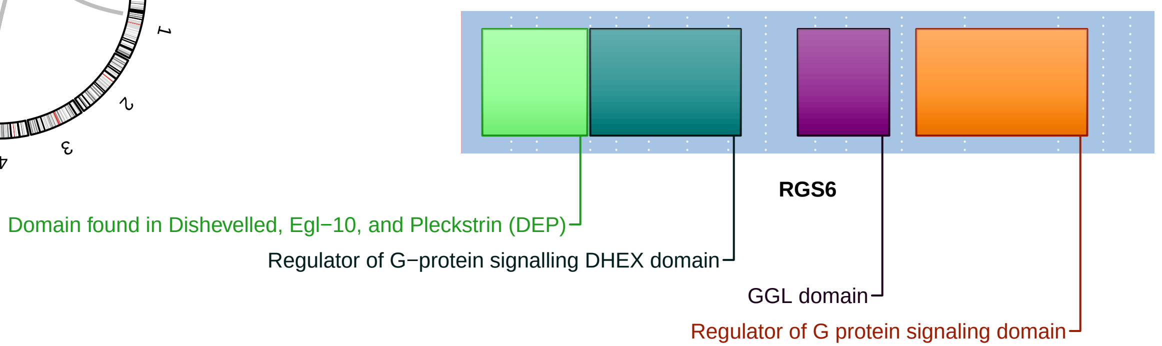
SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 2



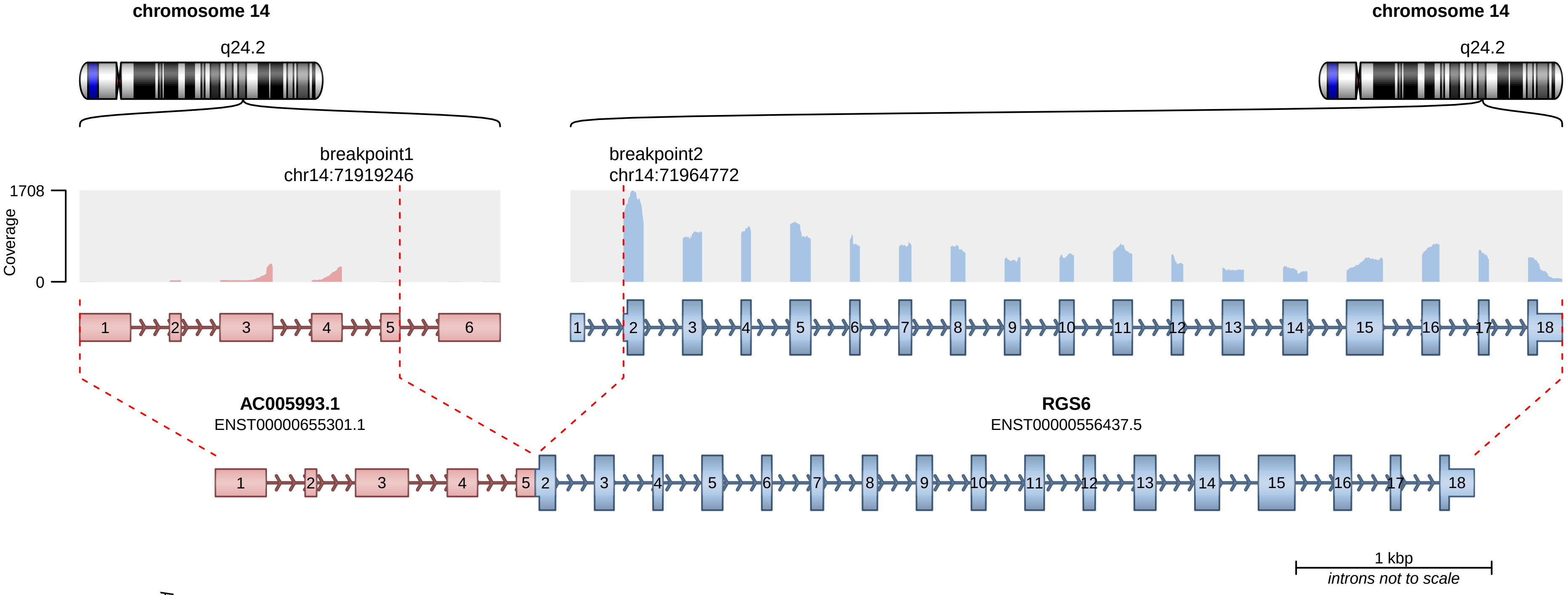


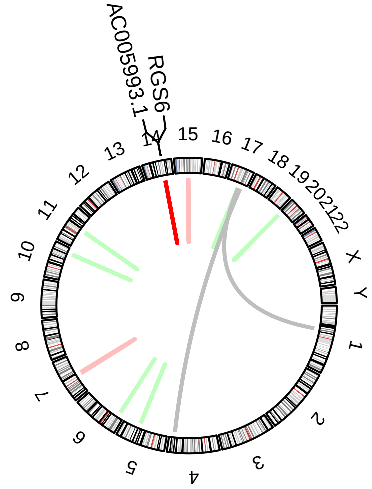
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

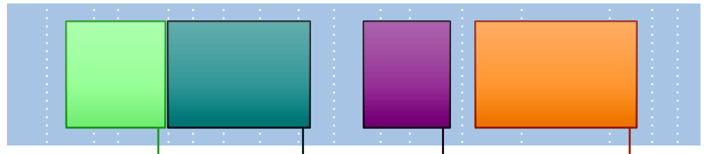
Split reads = 3
Discordant mates = 1





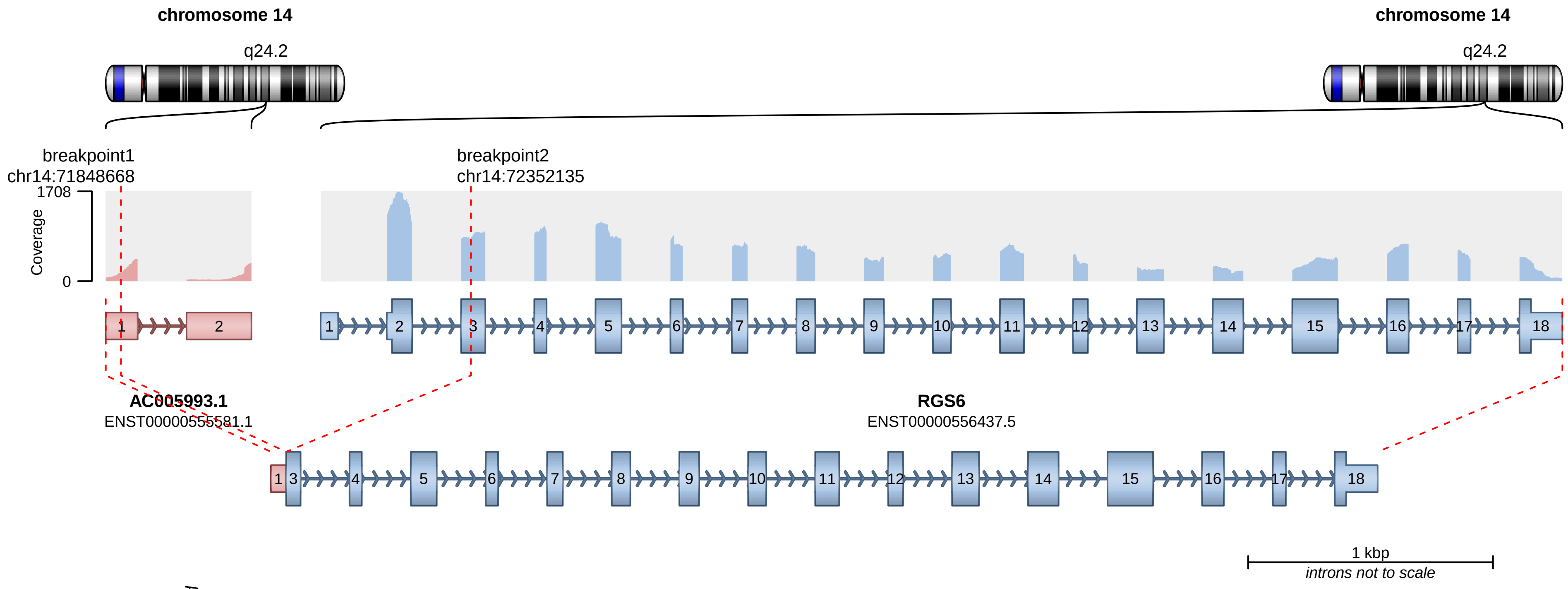
translocation
duplication
deletion
inversion

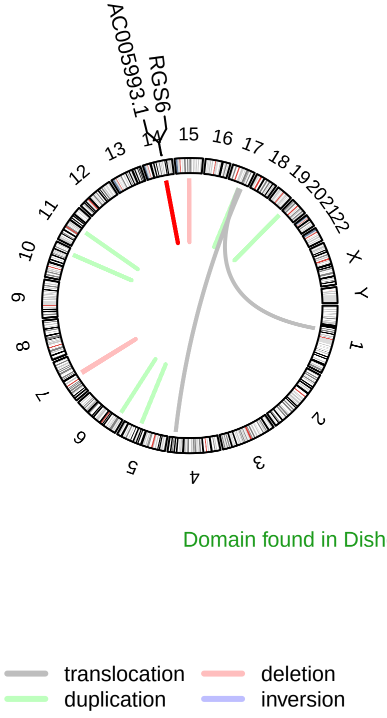
RETAINED PROTEIN DOMAINS
reading frame unclear



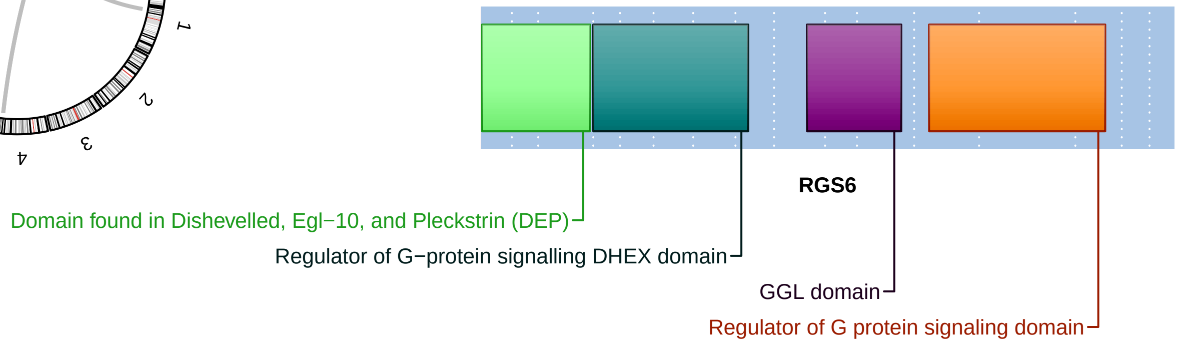
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 8



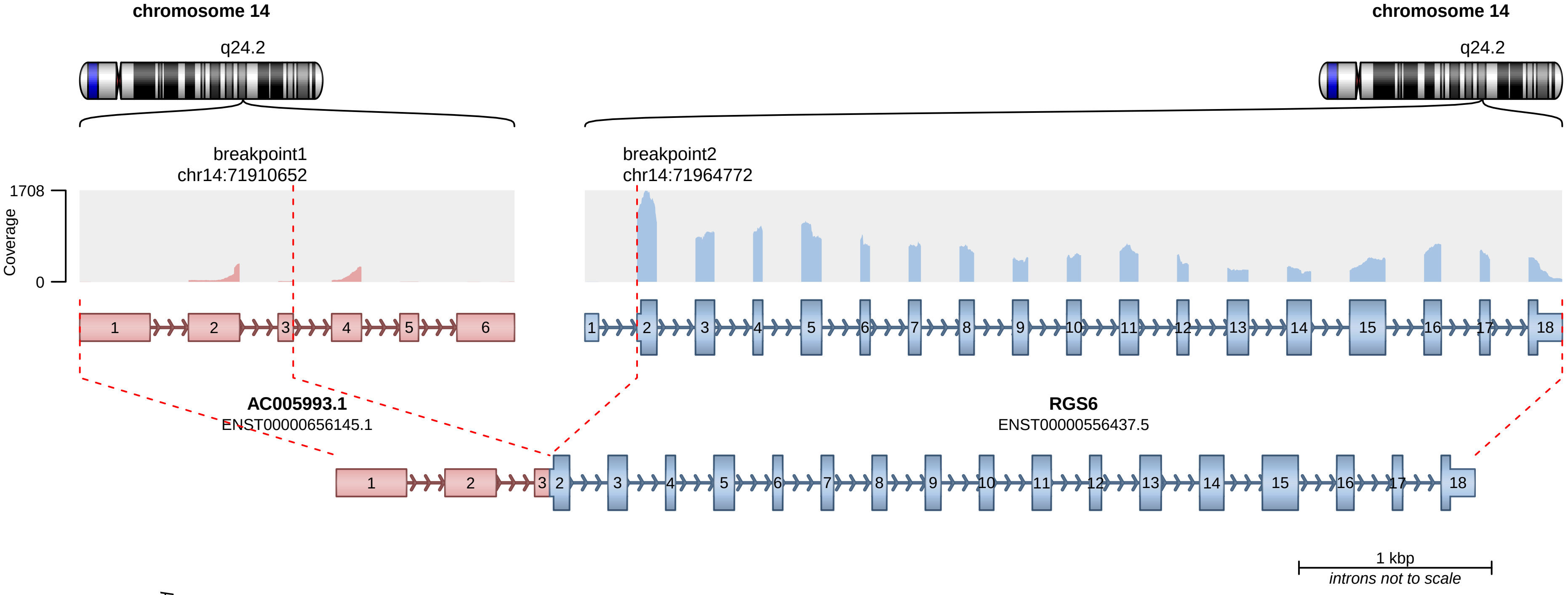


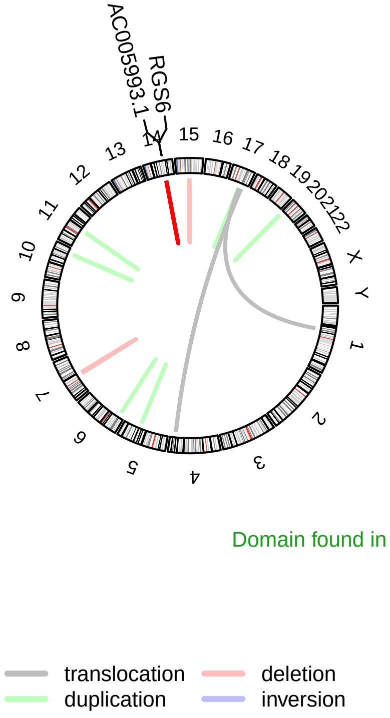
RETAINED PROTEIN DOMAINS
reading frame unclear



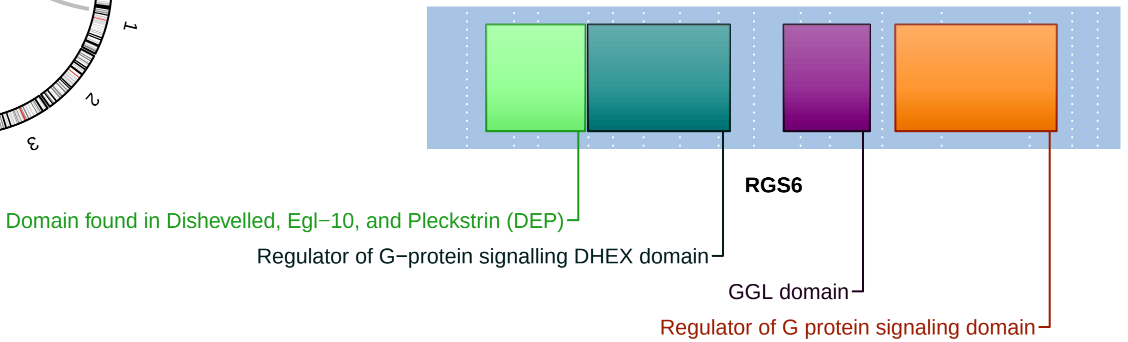
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0



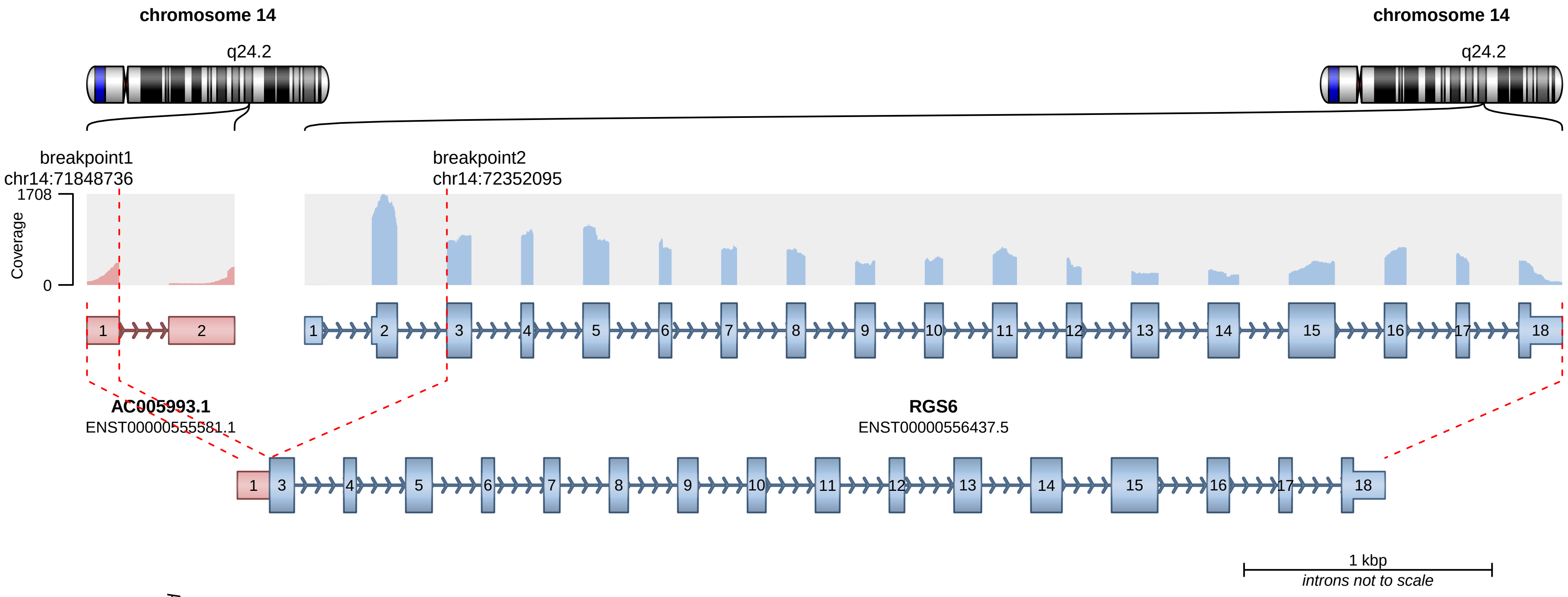


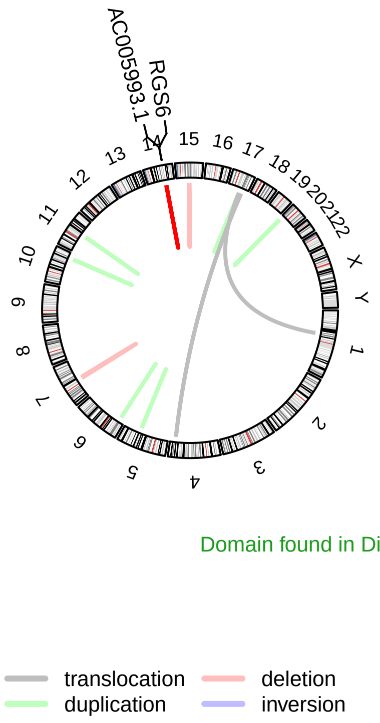
RETAINED PROTEIN DOMAINS
reading frame unclear

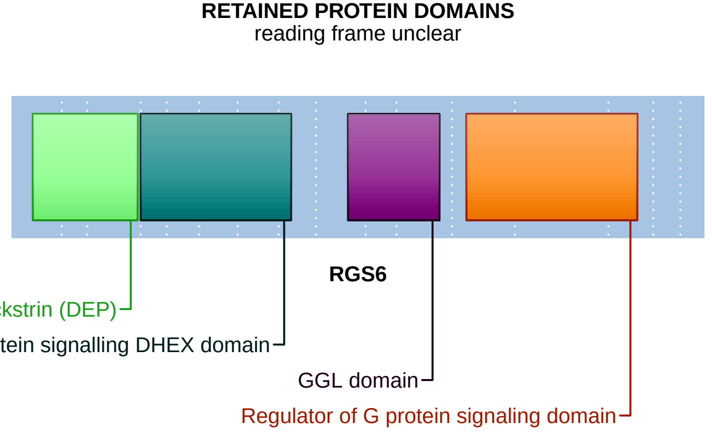


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 4

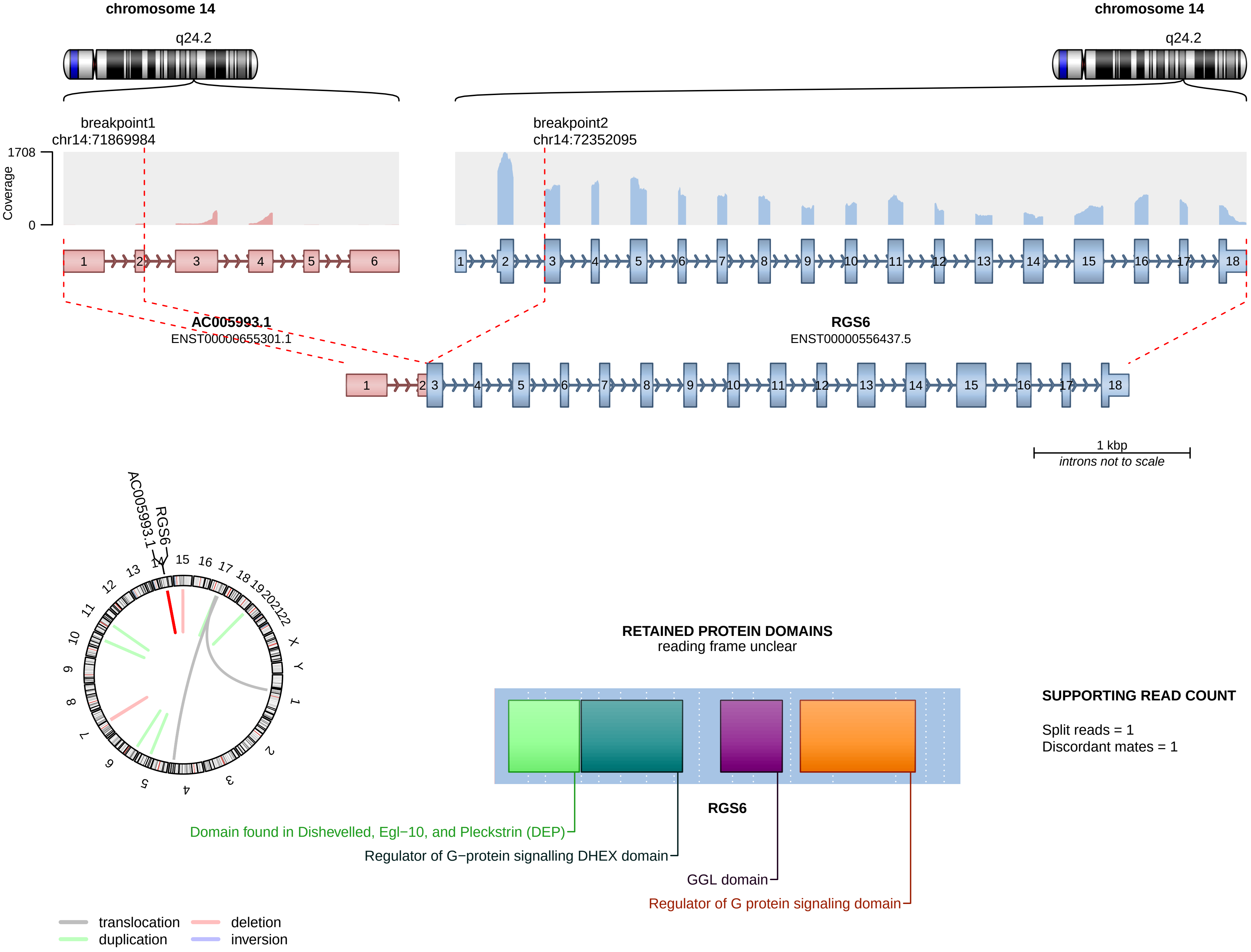






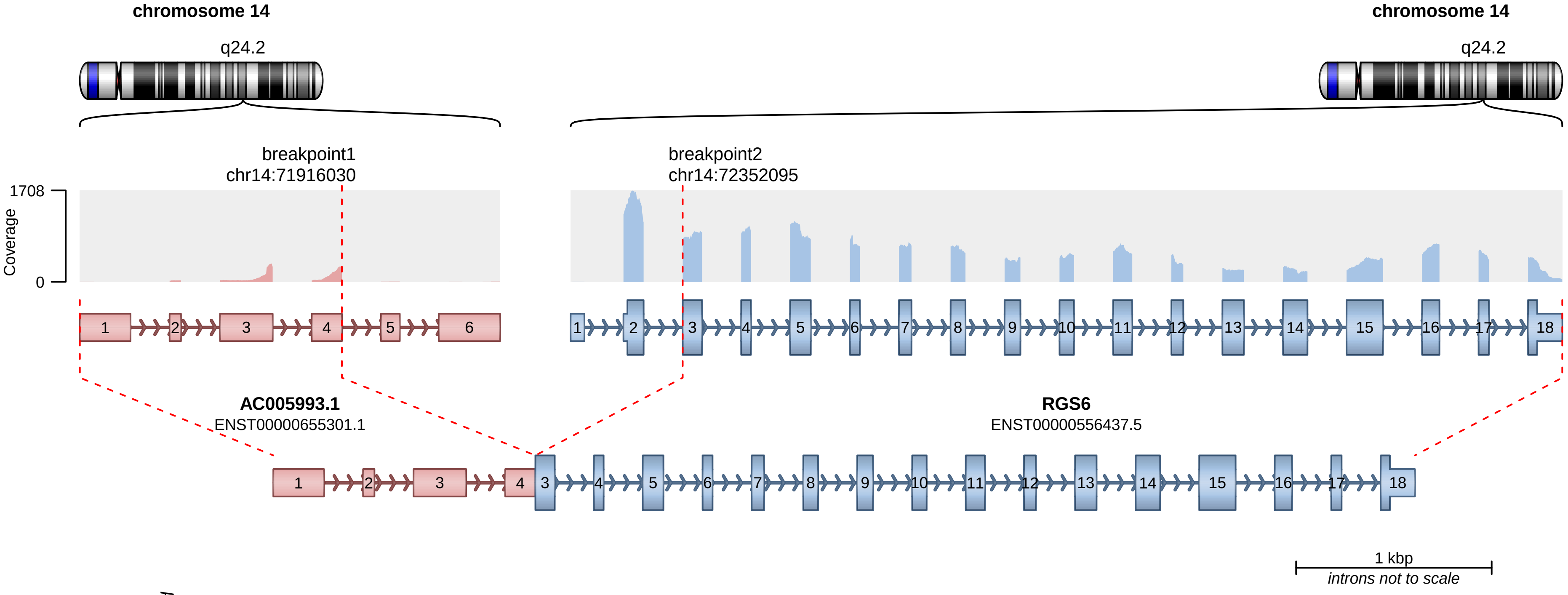
SUPPORTING READ COUNT

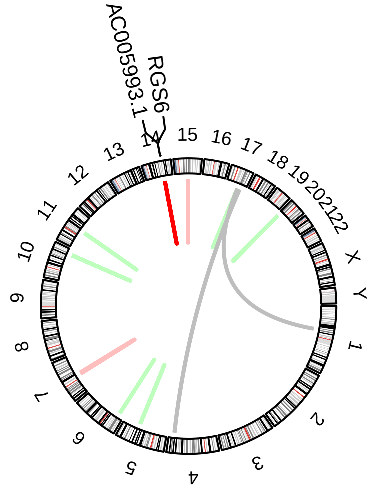
Split reads = 2
Discordant mates = 0



SUPPORTING READ COUNT

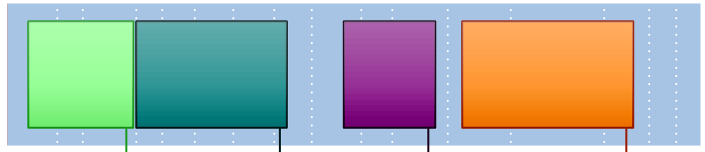
Split reads = 1
Discordant mates = 1





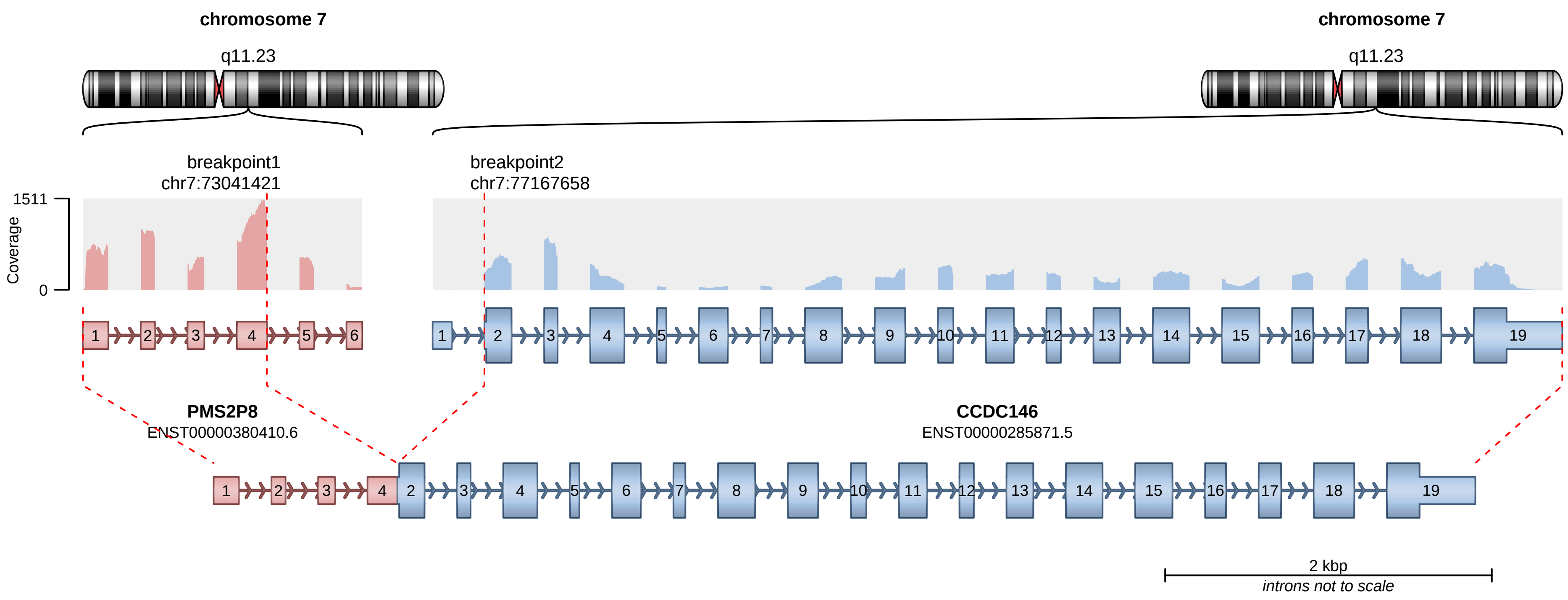
translocation
deletion
duplication
inversion

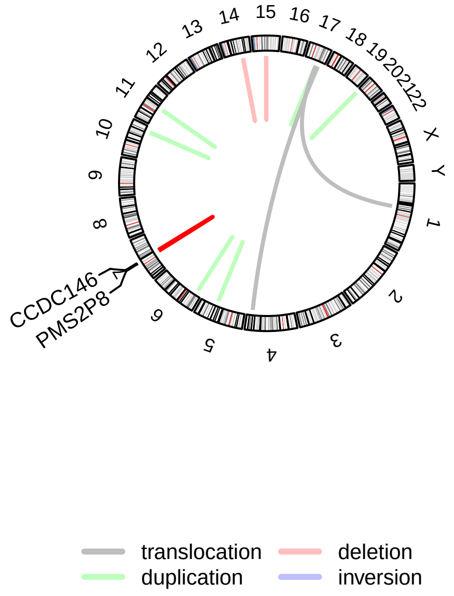
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

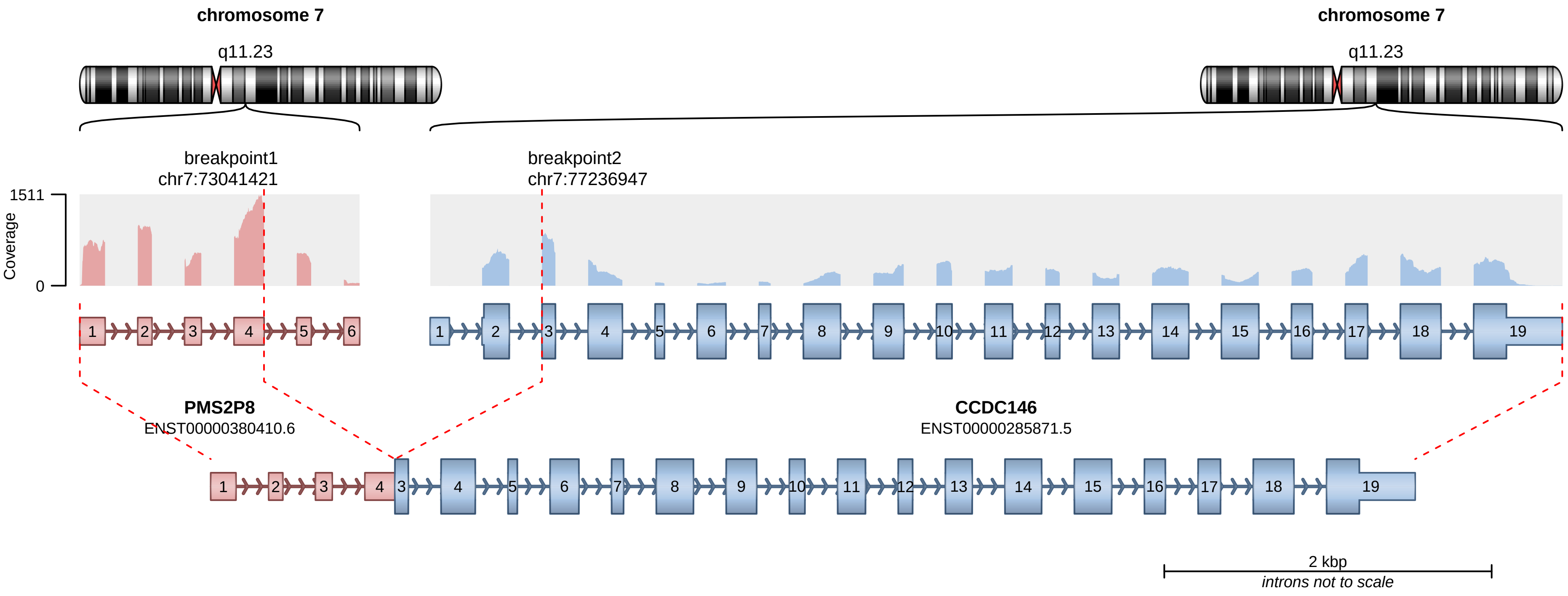


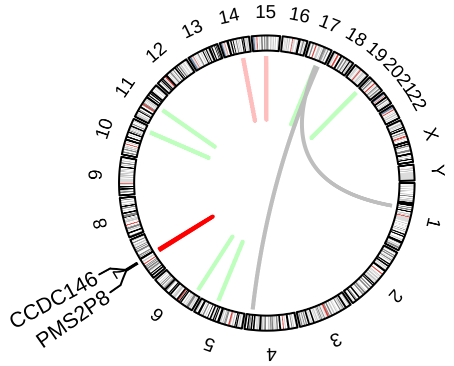


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 106
Discordant mates = 4



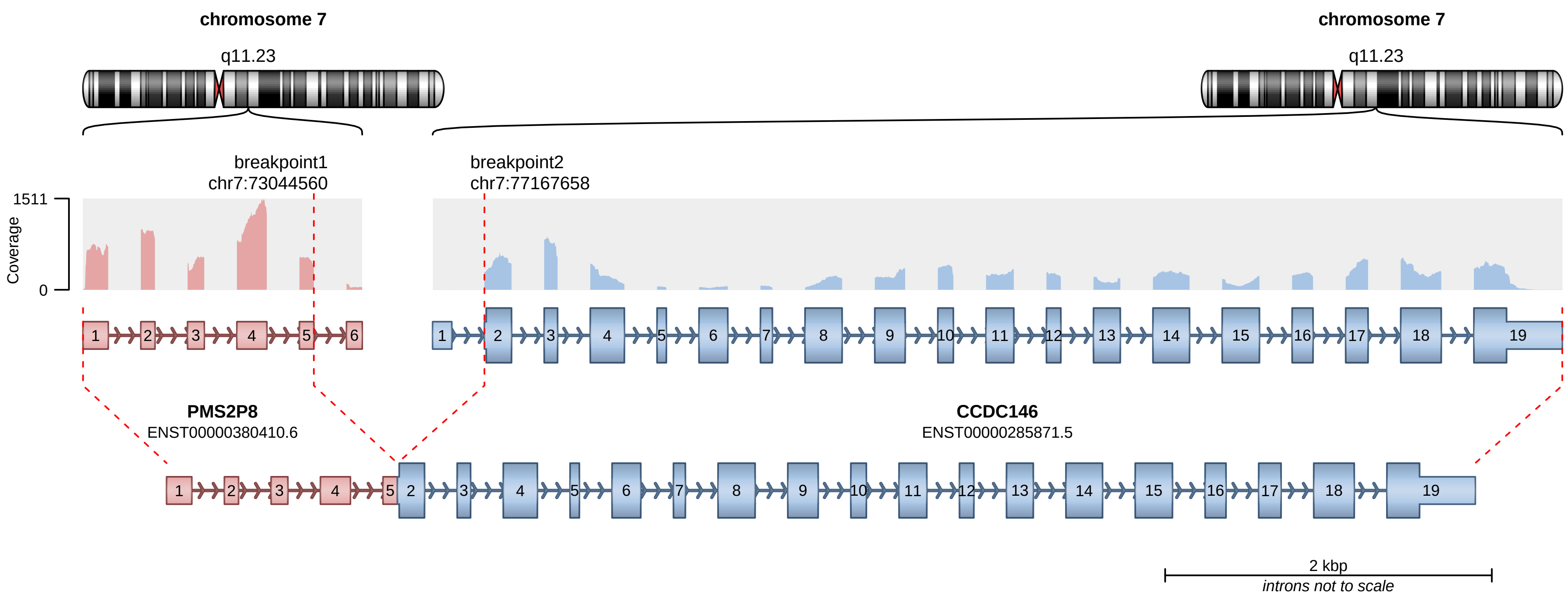


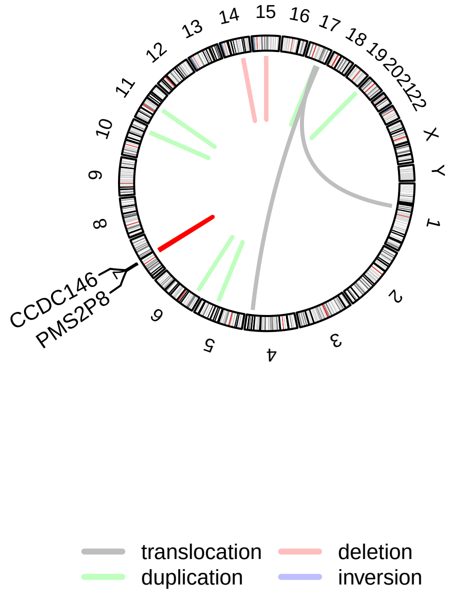
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 24
Discordant mates = 1

translocation
duplication
deletion
inversion

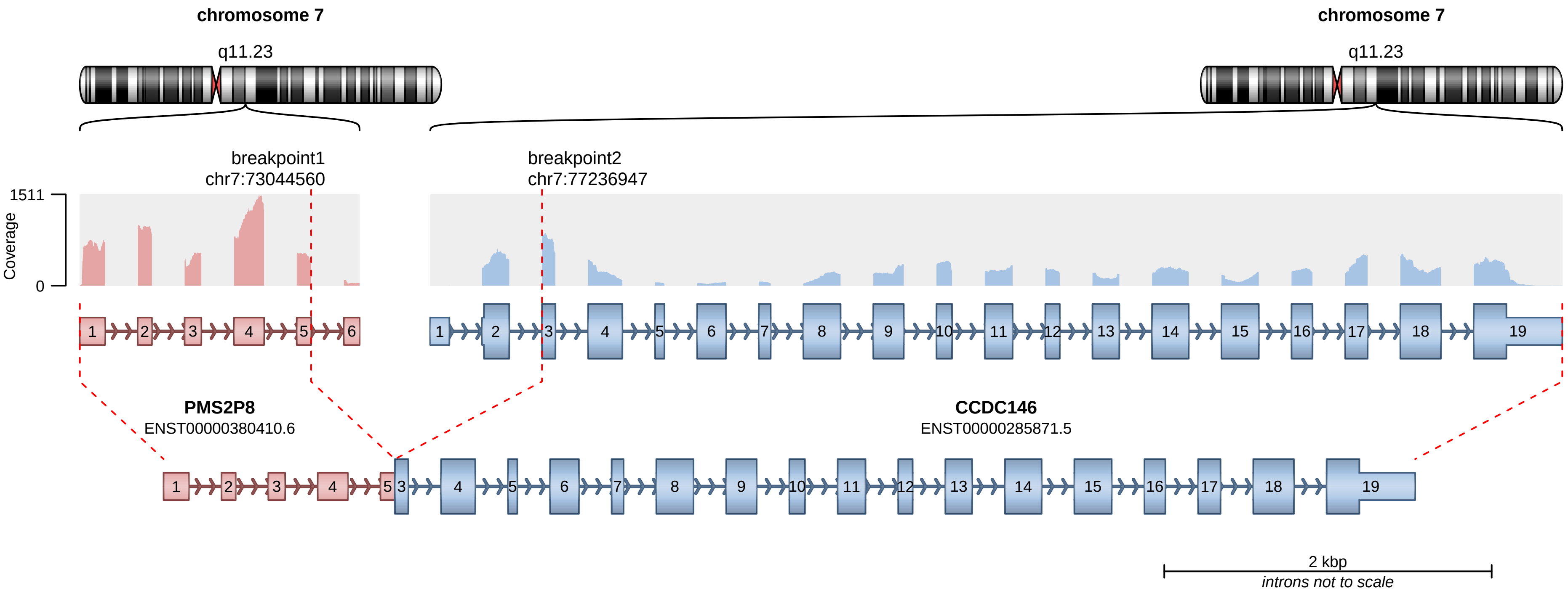


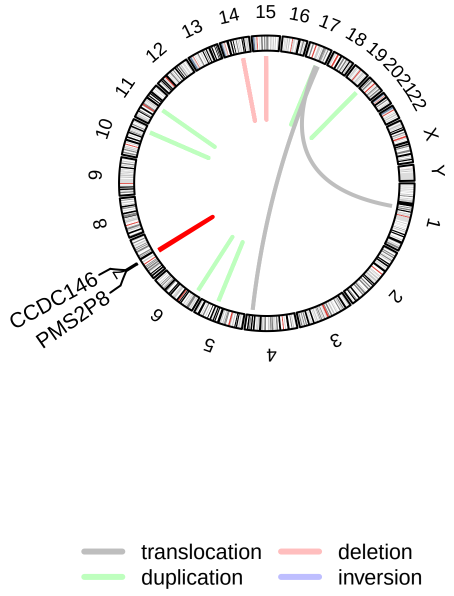


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 4

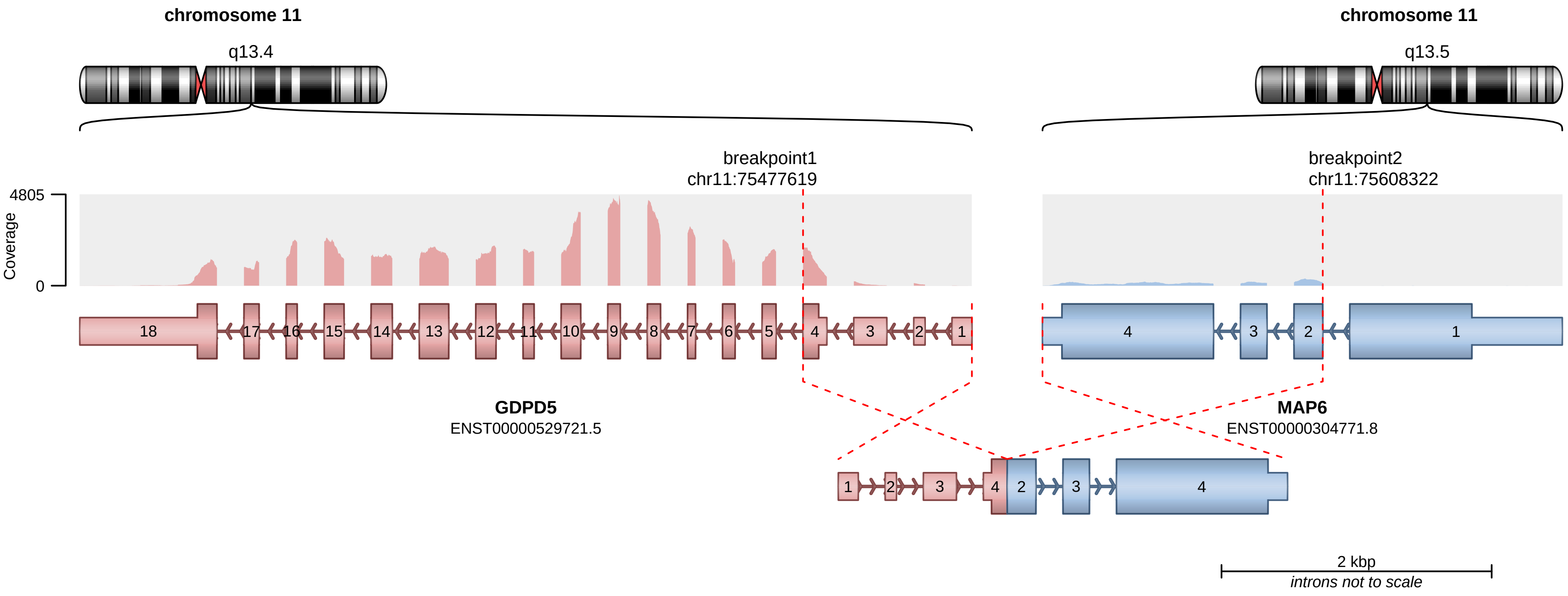


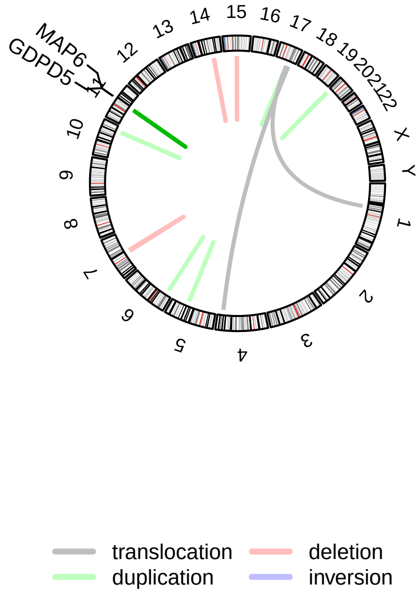


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 1

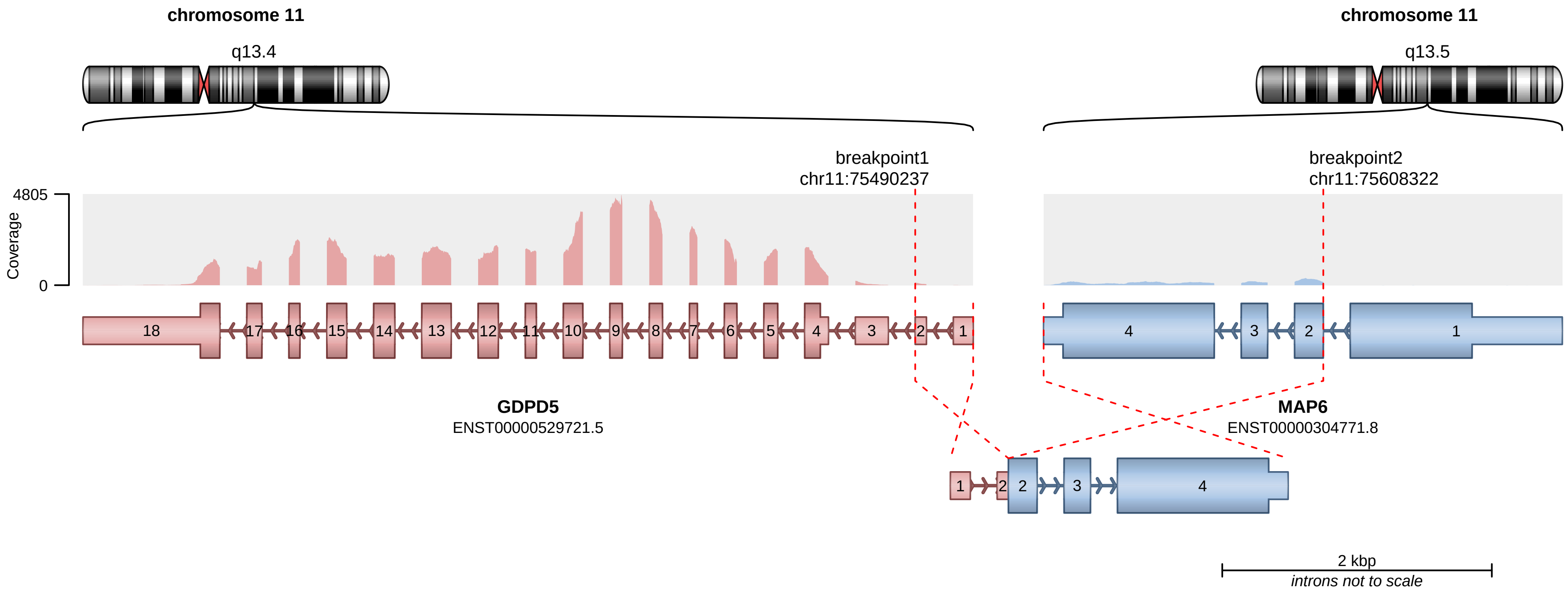


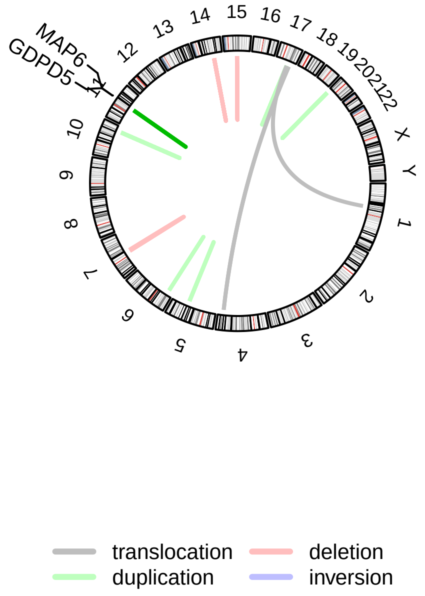


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 97
Discordant mates = 4

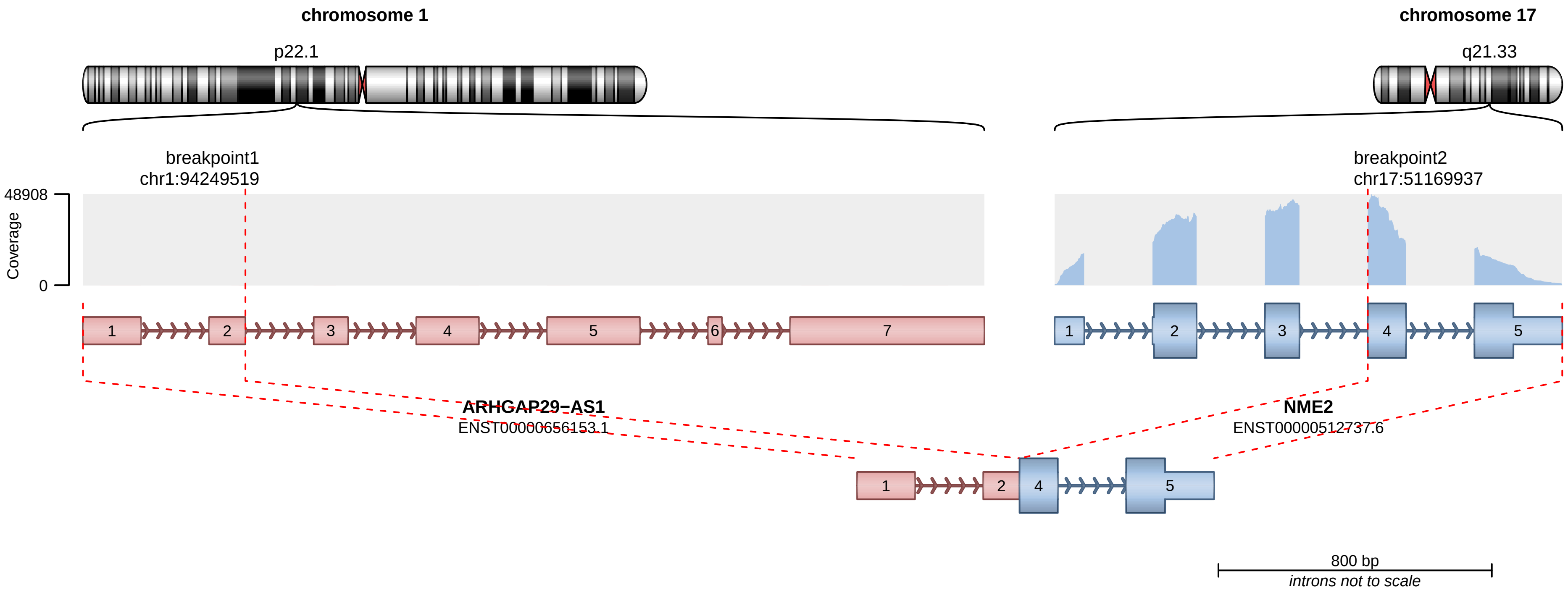


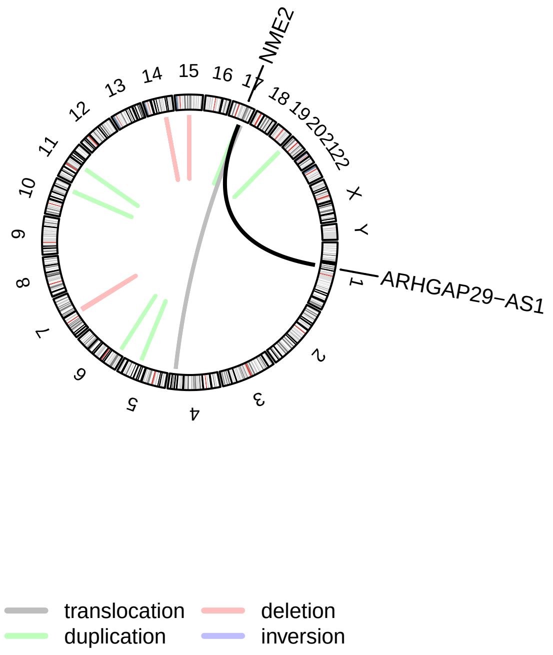


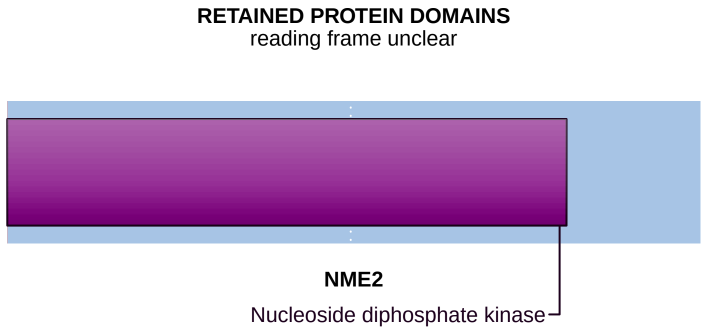
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

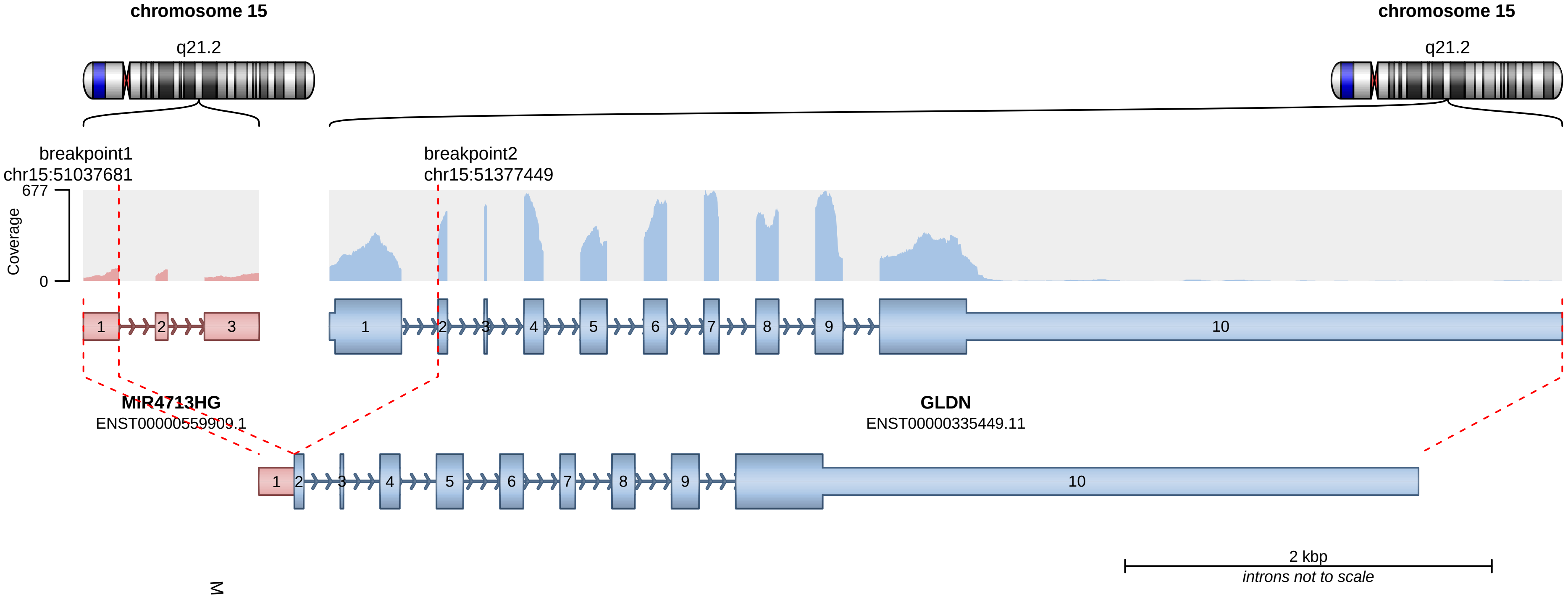


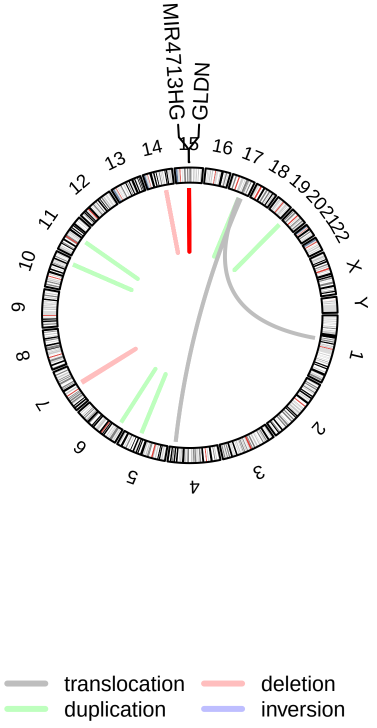


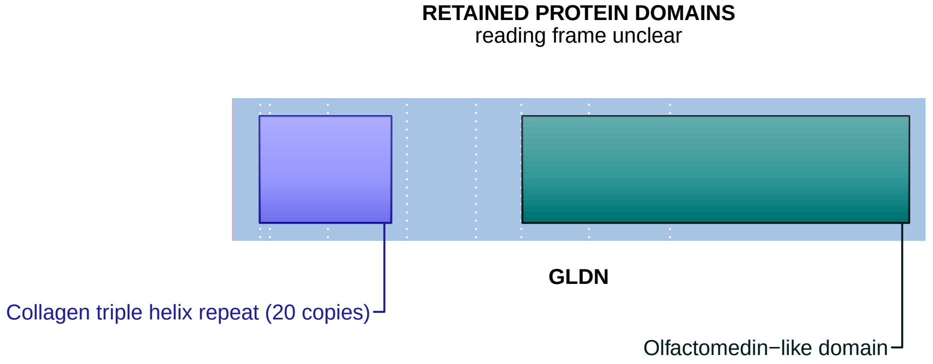


SUPPORTING READ COUNT

Split reads = 61
Discordant mates = 0

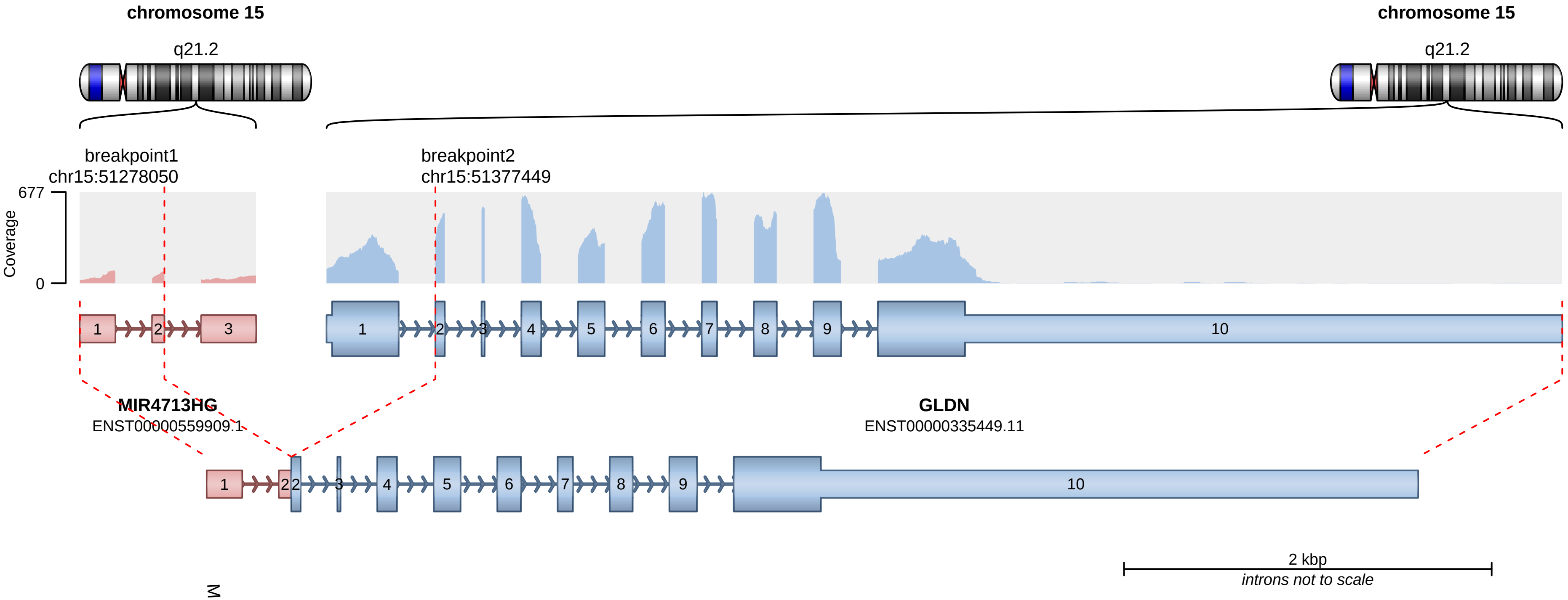


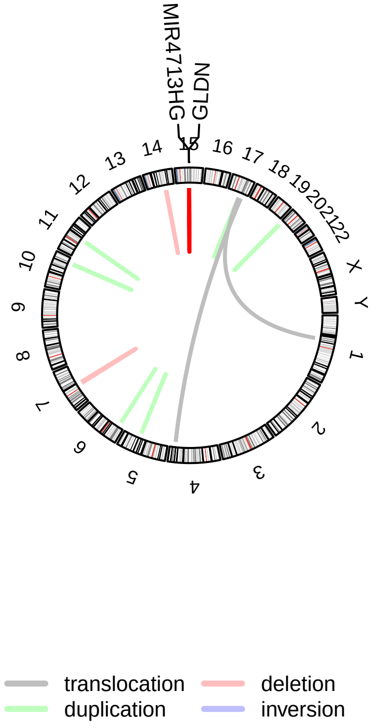


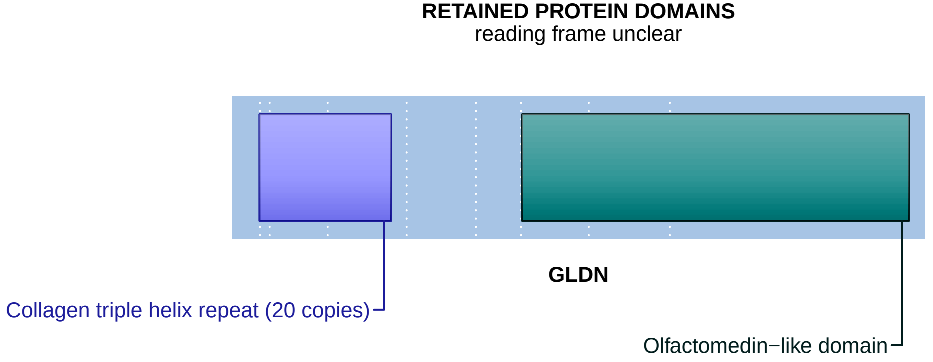


SUPPORTING READ COUNT

Split reads = 23
Discordant mates = 0

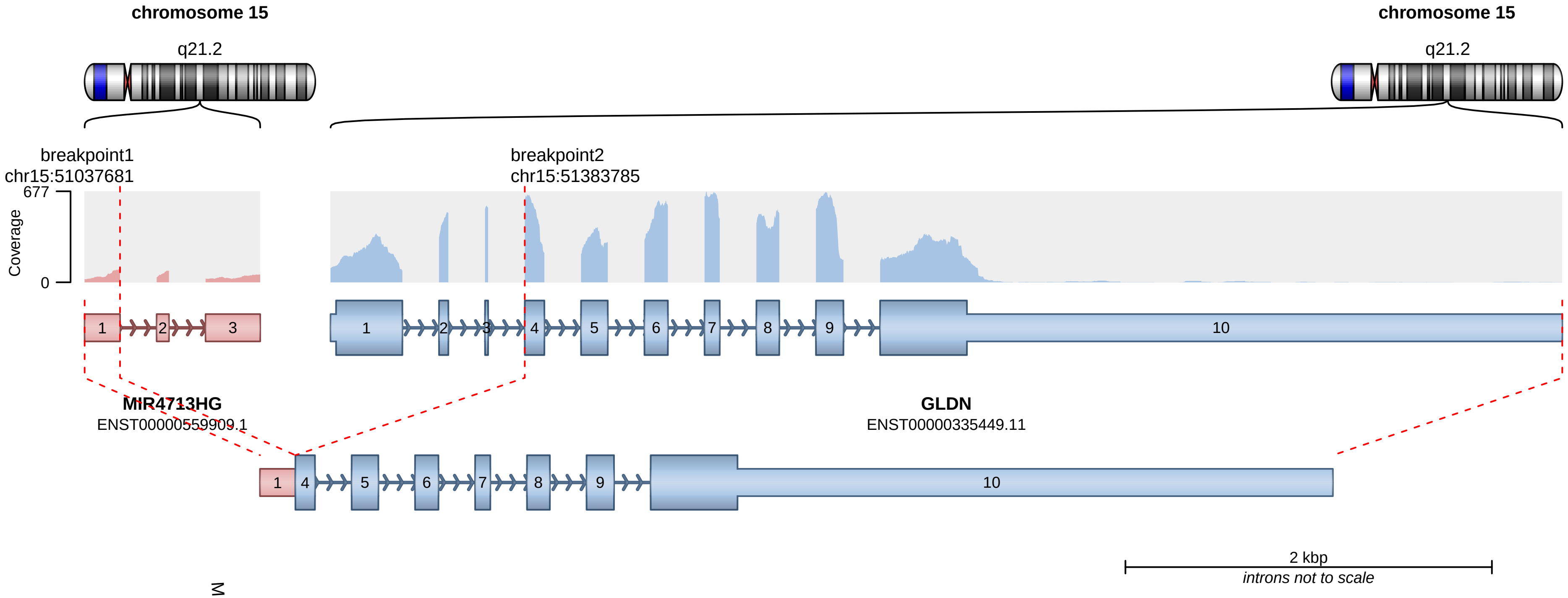


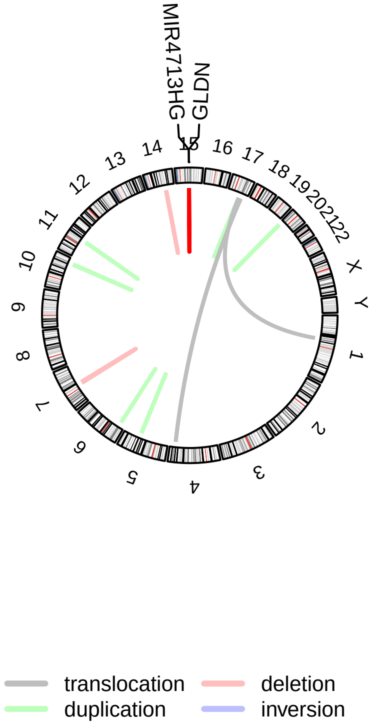


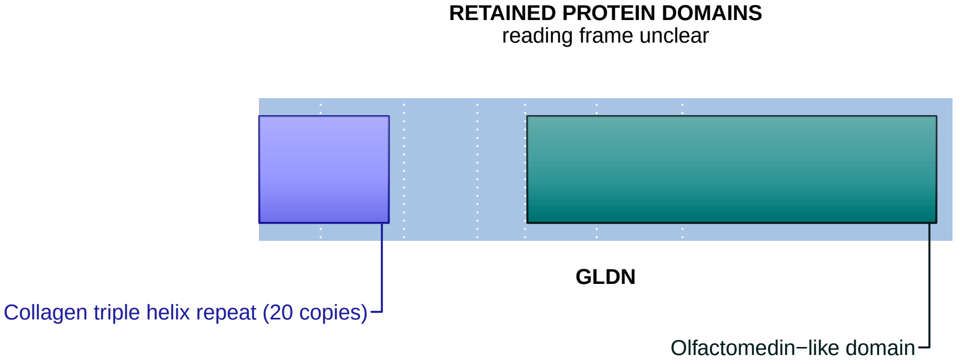


SUPPORTING READ COUNT

Split reads = 21
Discordant mates = 1

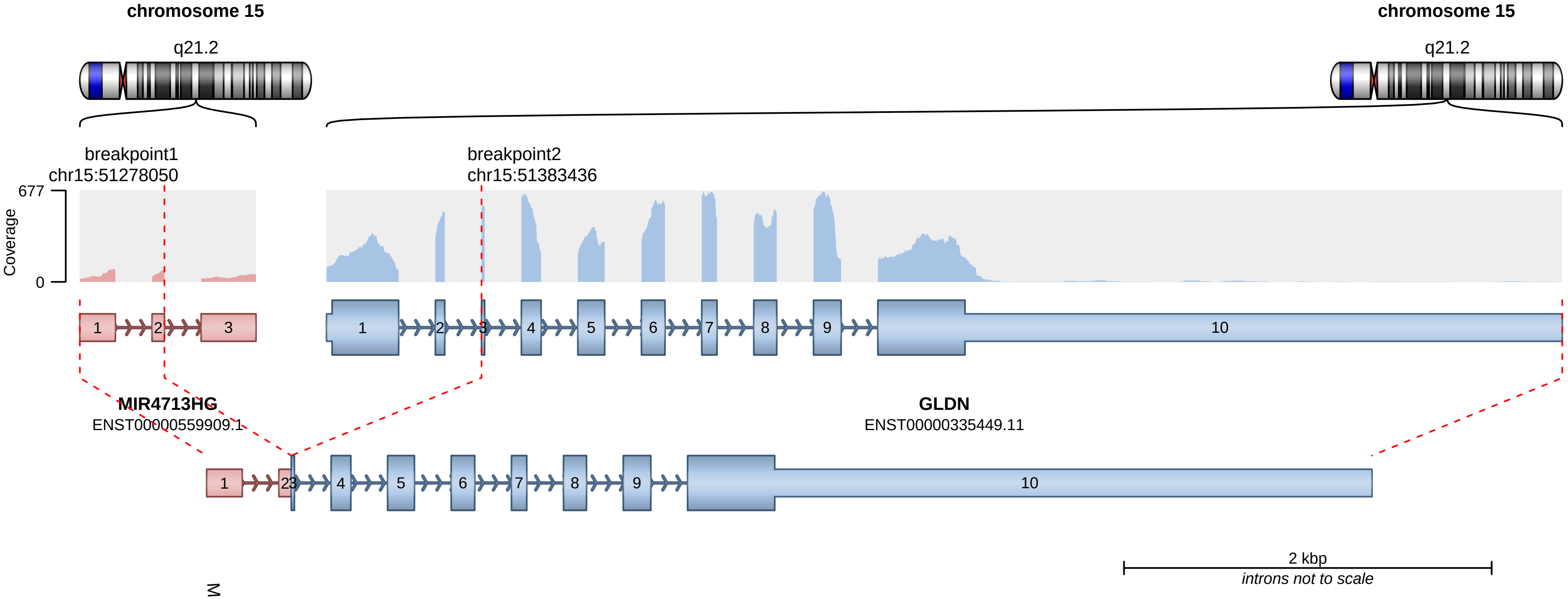


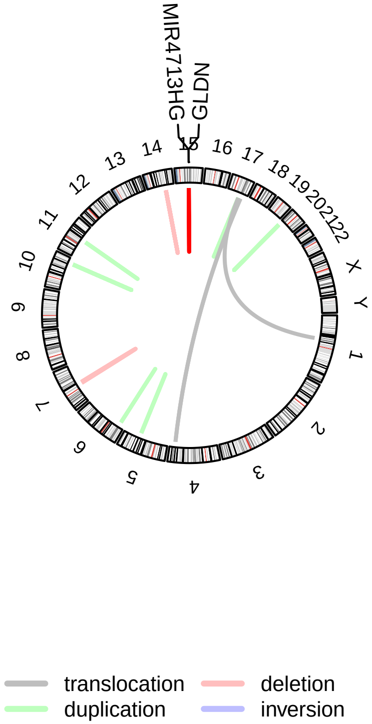


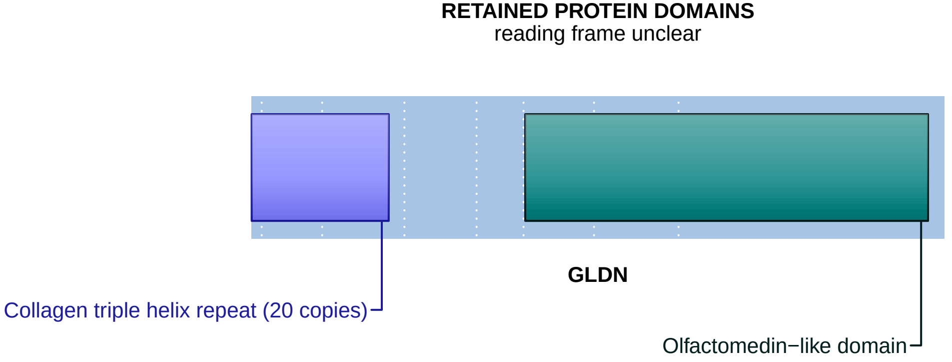


SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0

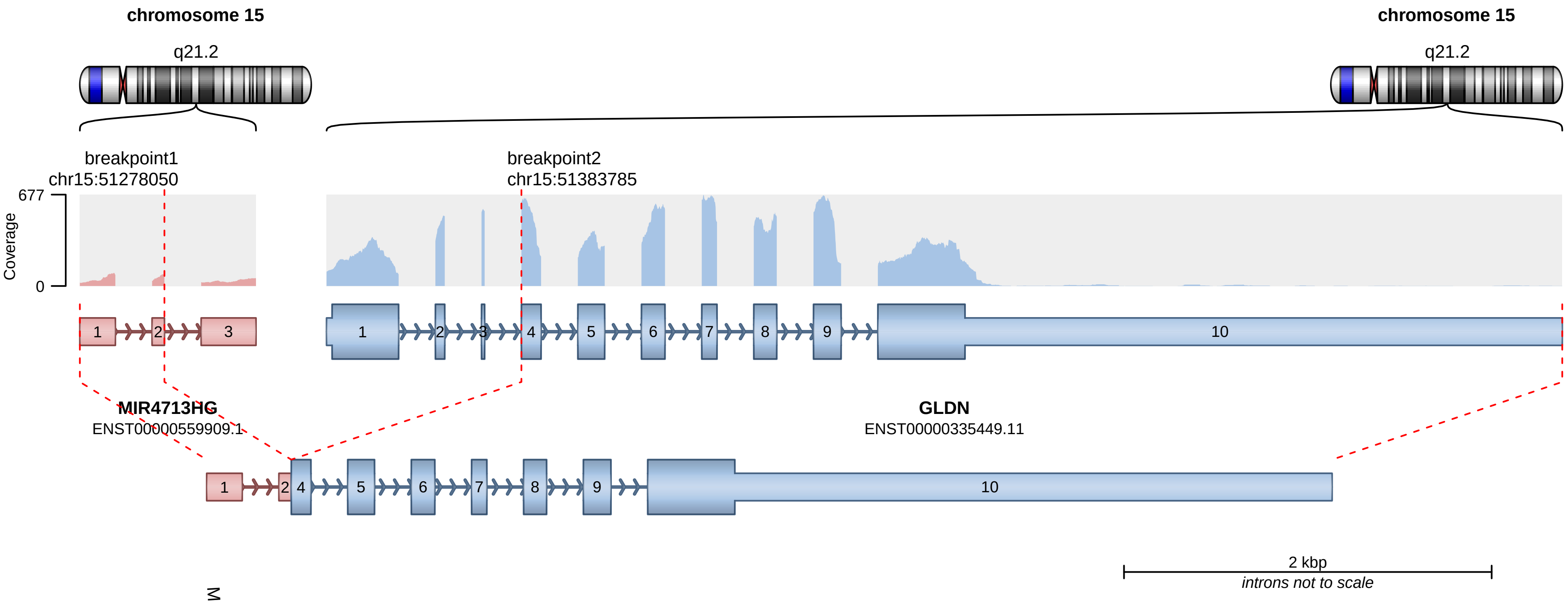


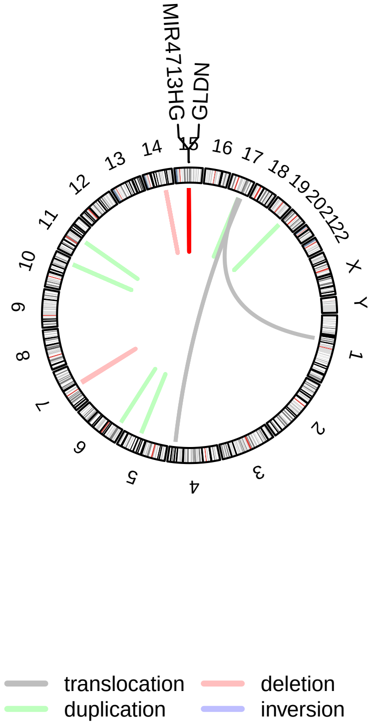




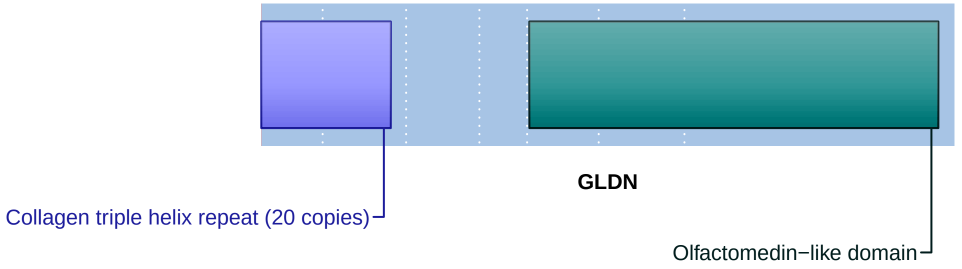
SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0



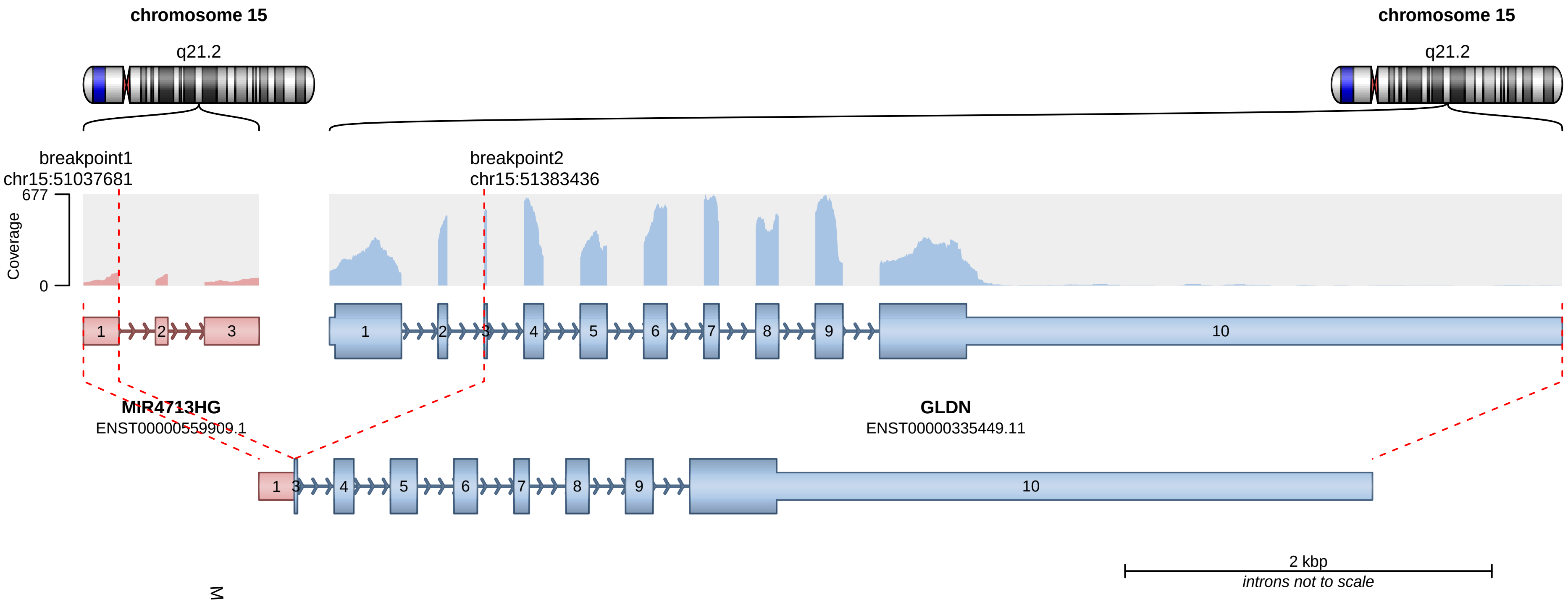


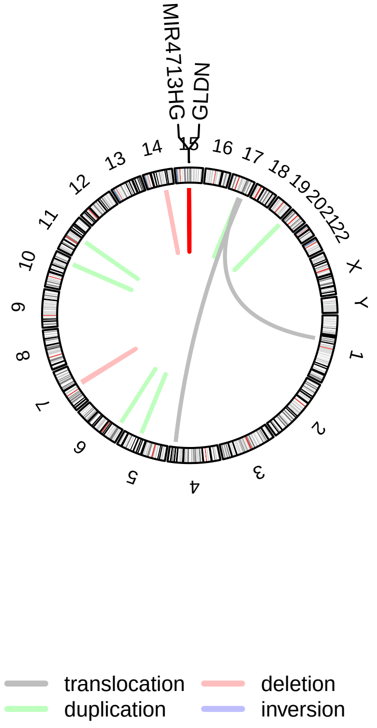
RETAINED PROTEIN DOMAINS
reading frame unclear

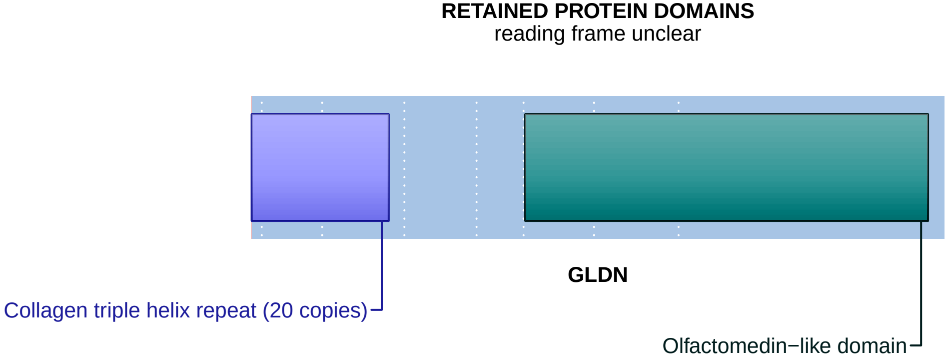


SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

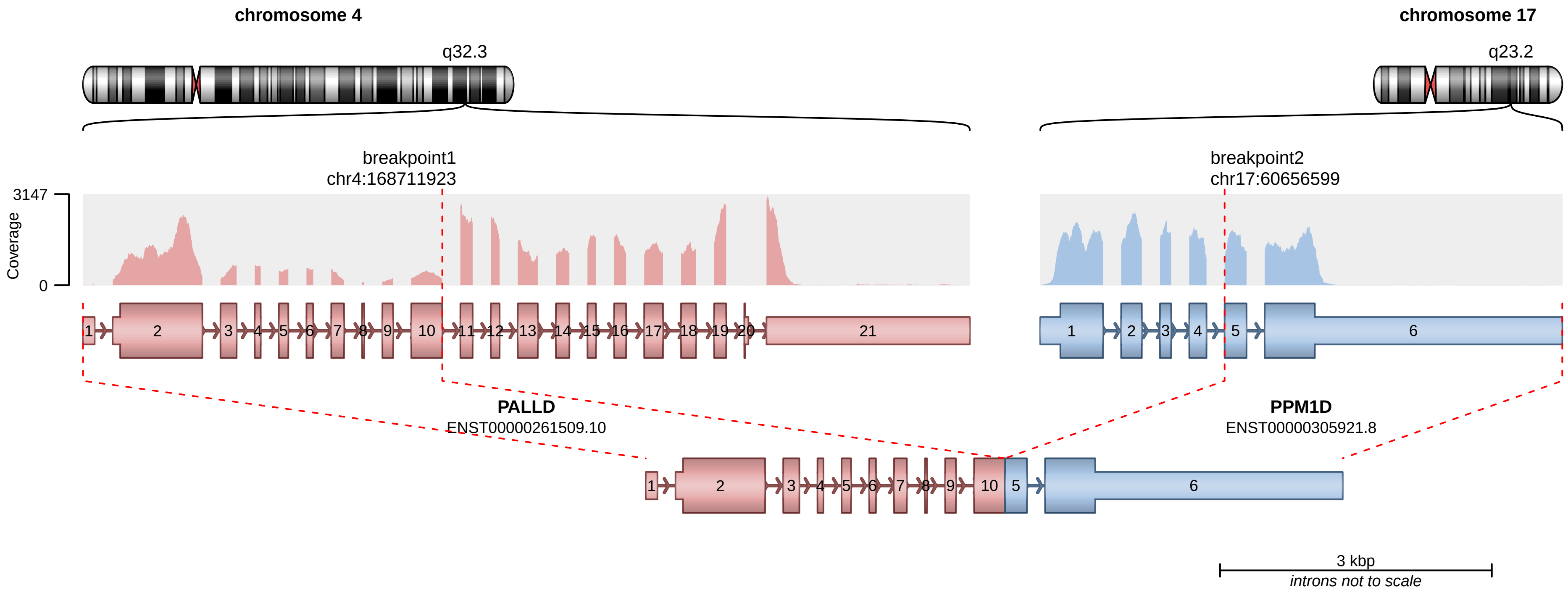


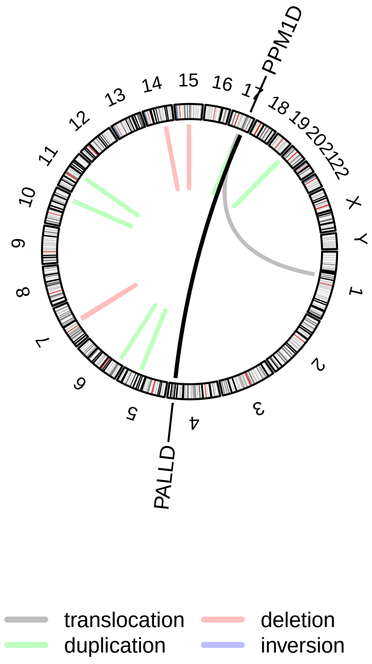


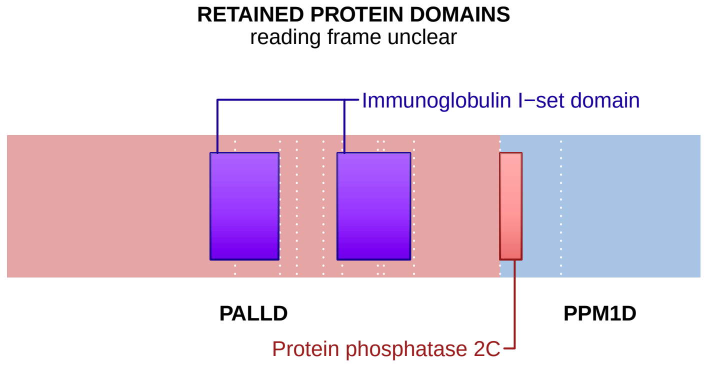


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

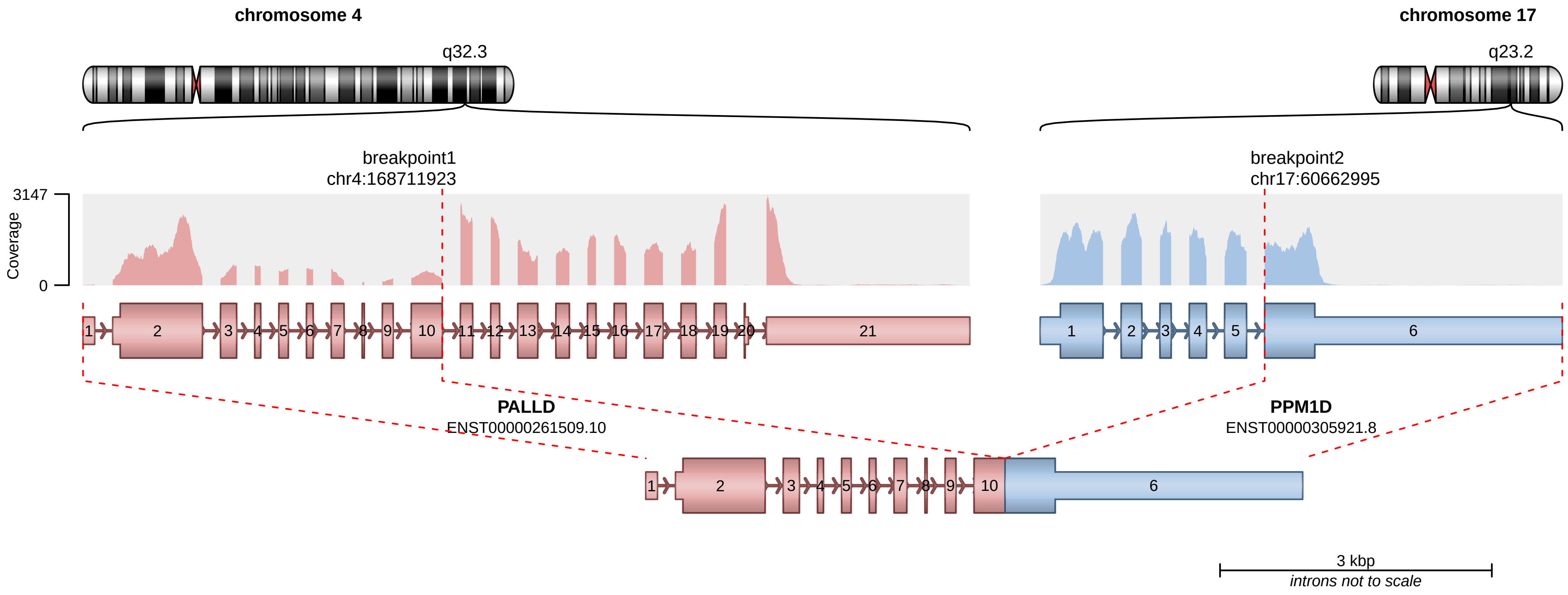


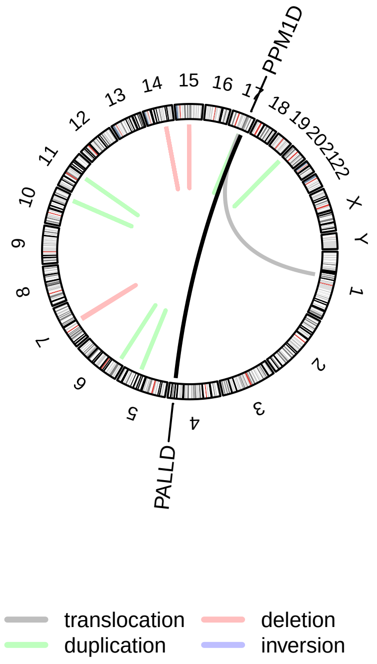


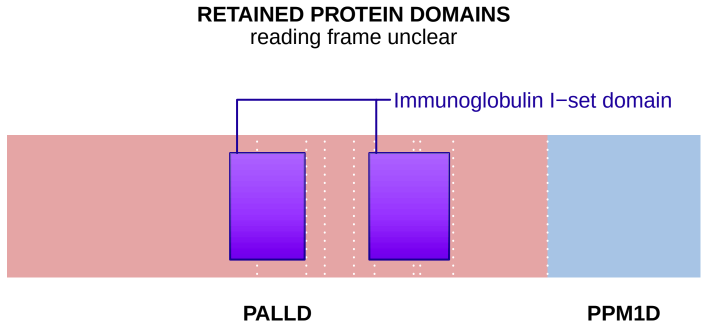


SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 0

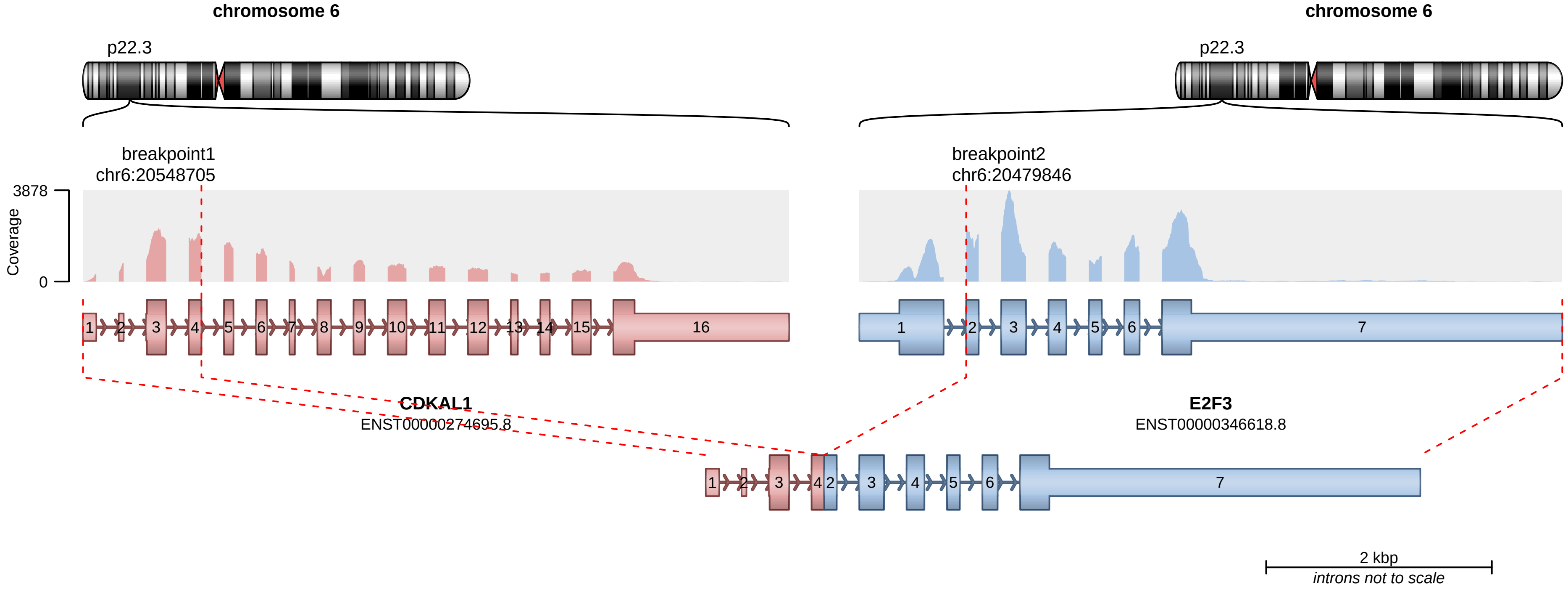


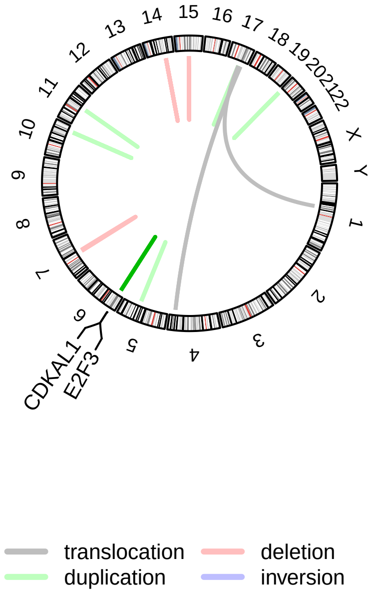


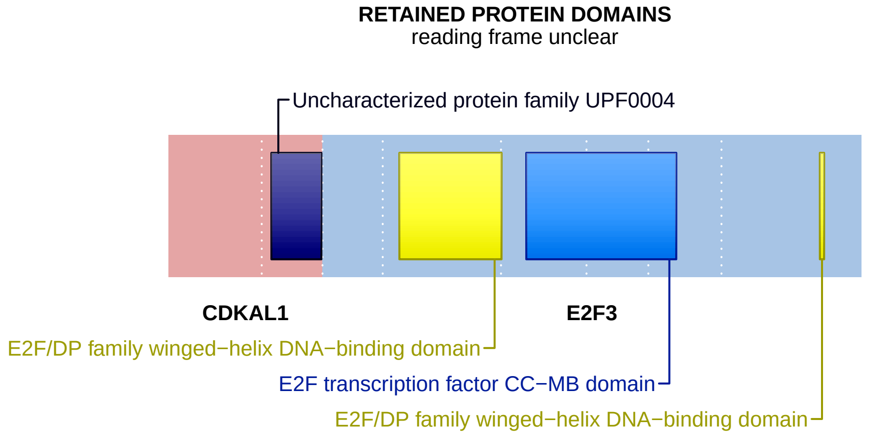


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0







SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0