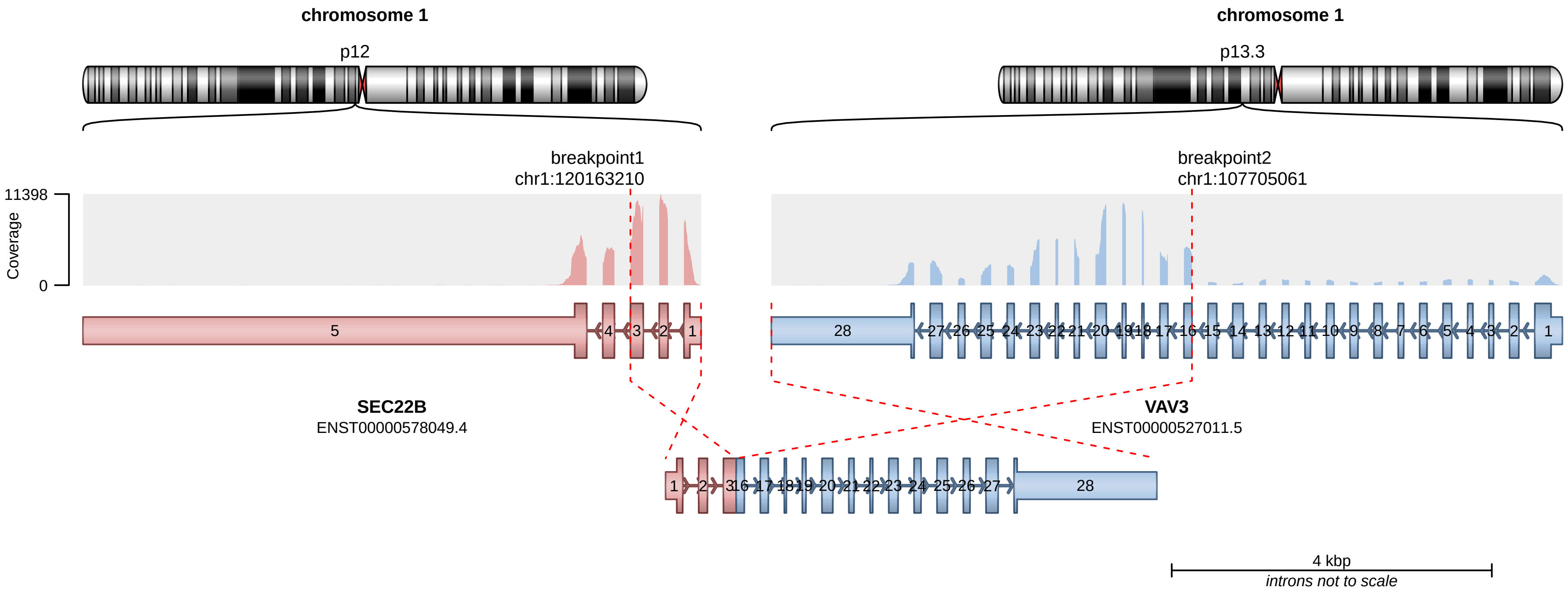
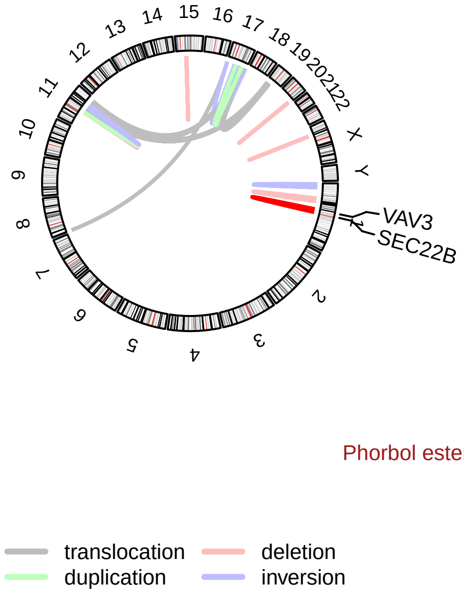
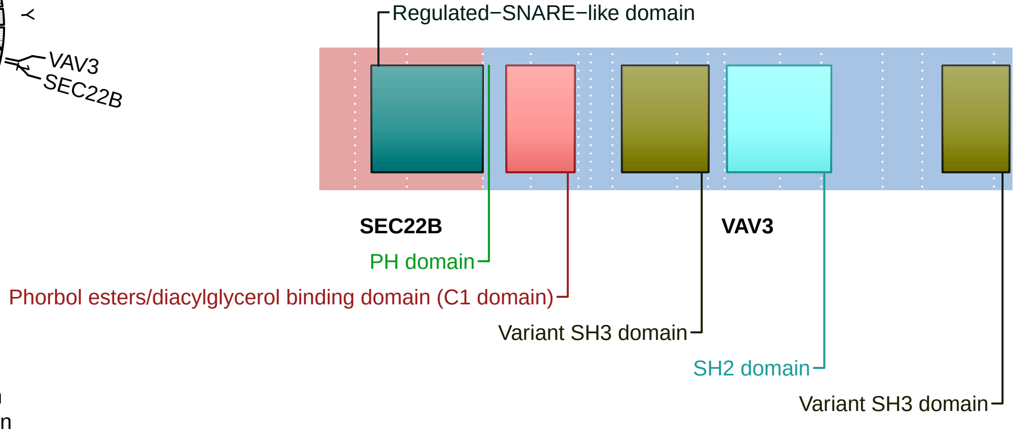


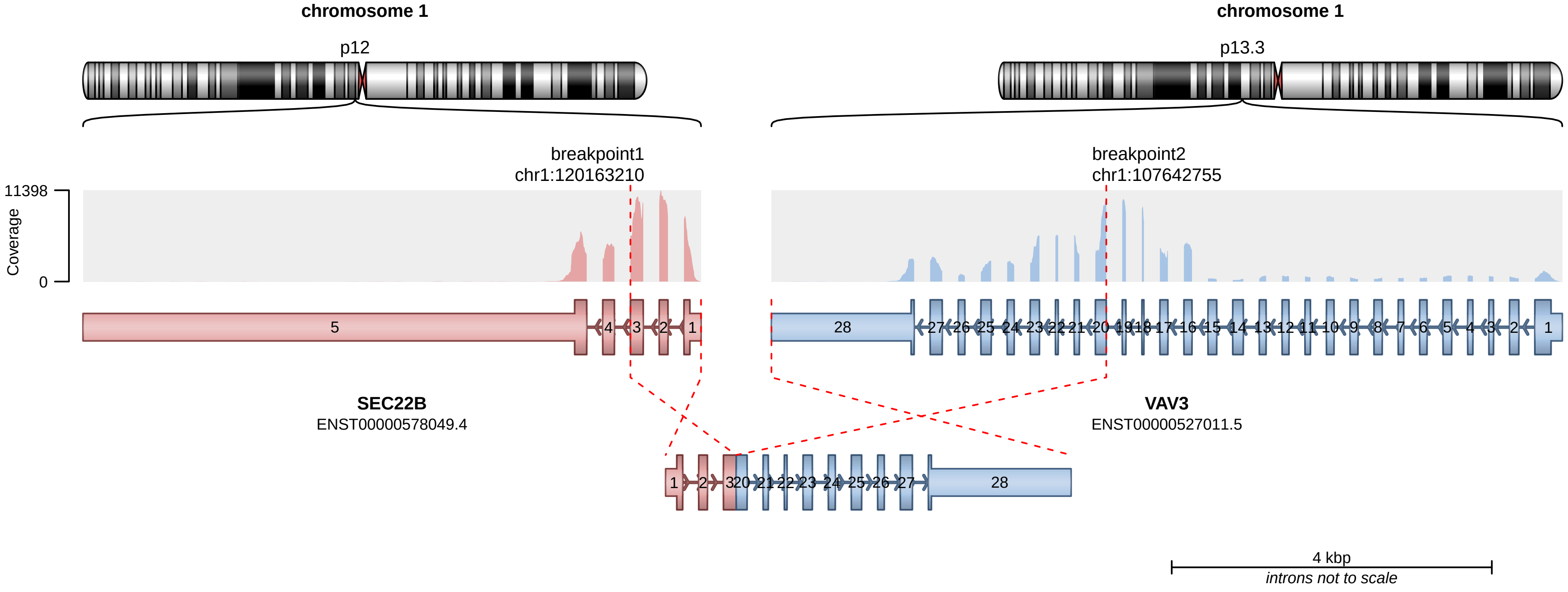


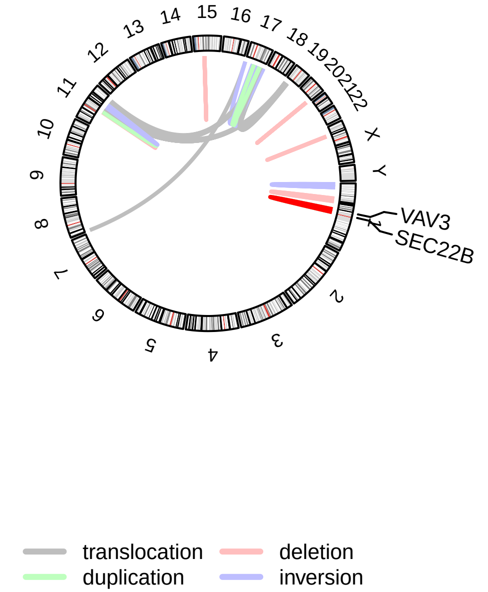
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

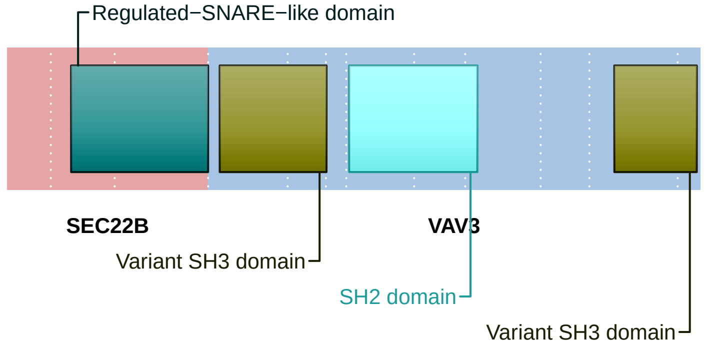
Split reads = 703
Discordant mates = 15





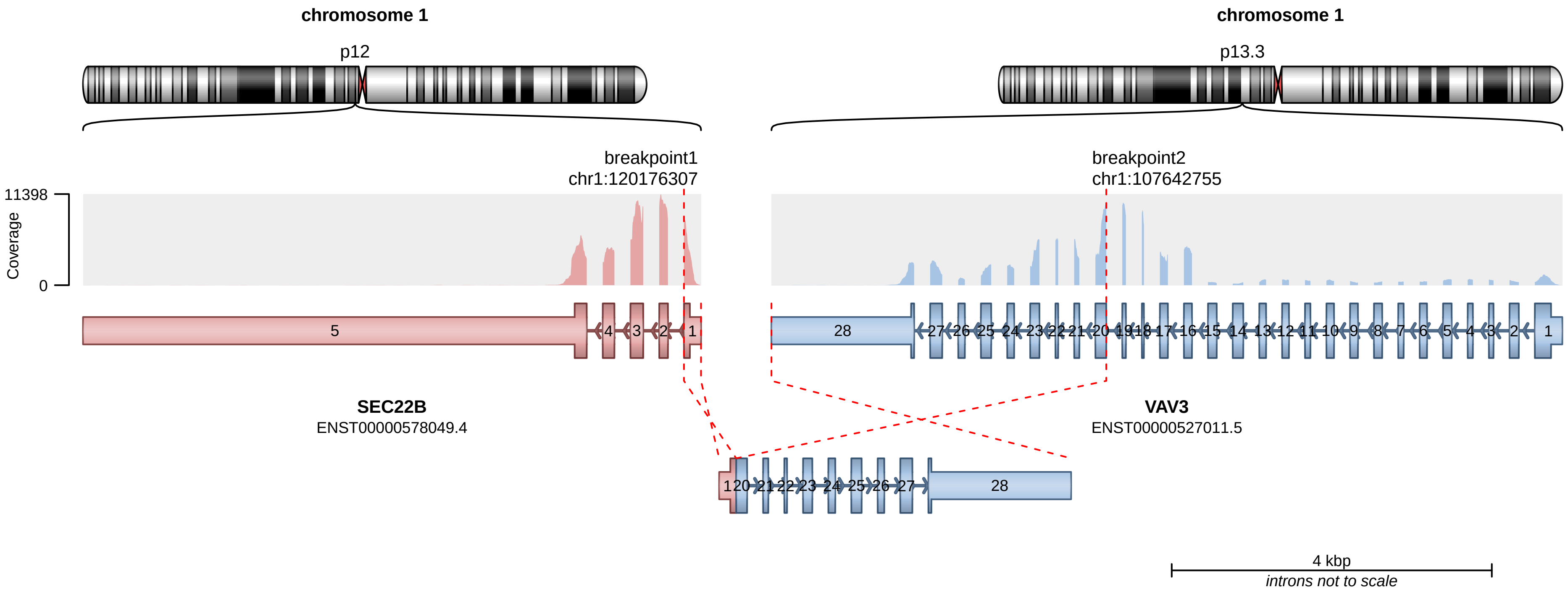
RETAINED PROTEIN DOMAINS

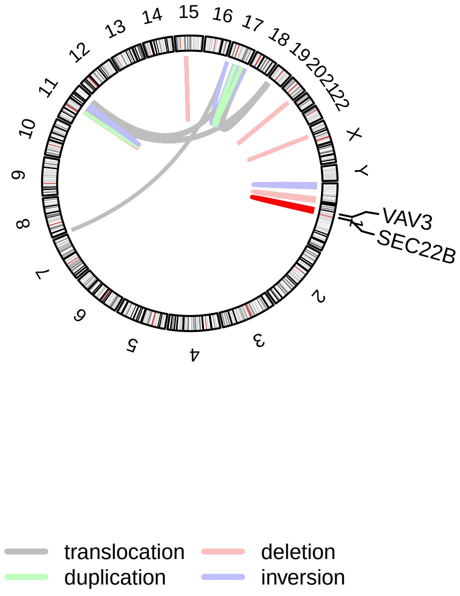
reading frame unclear



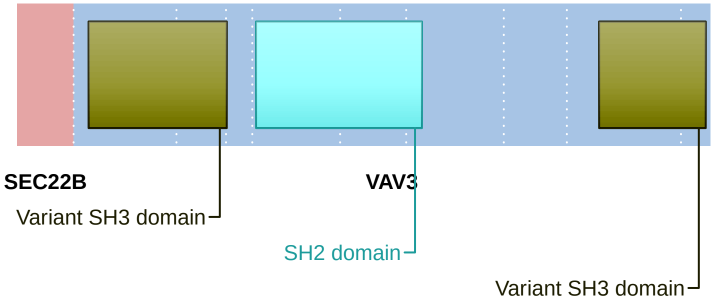
SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0



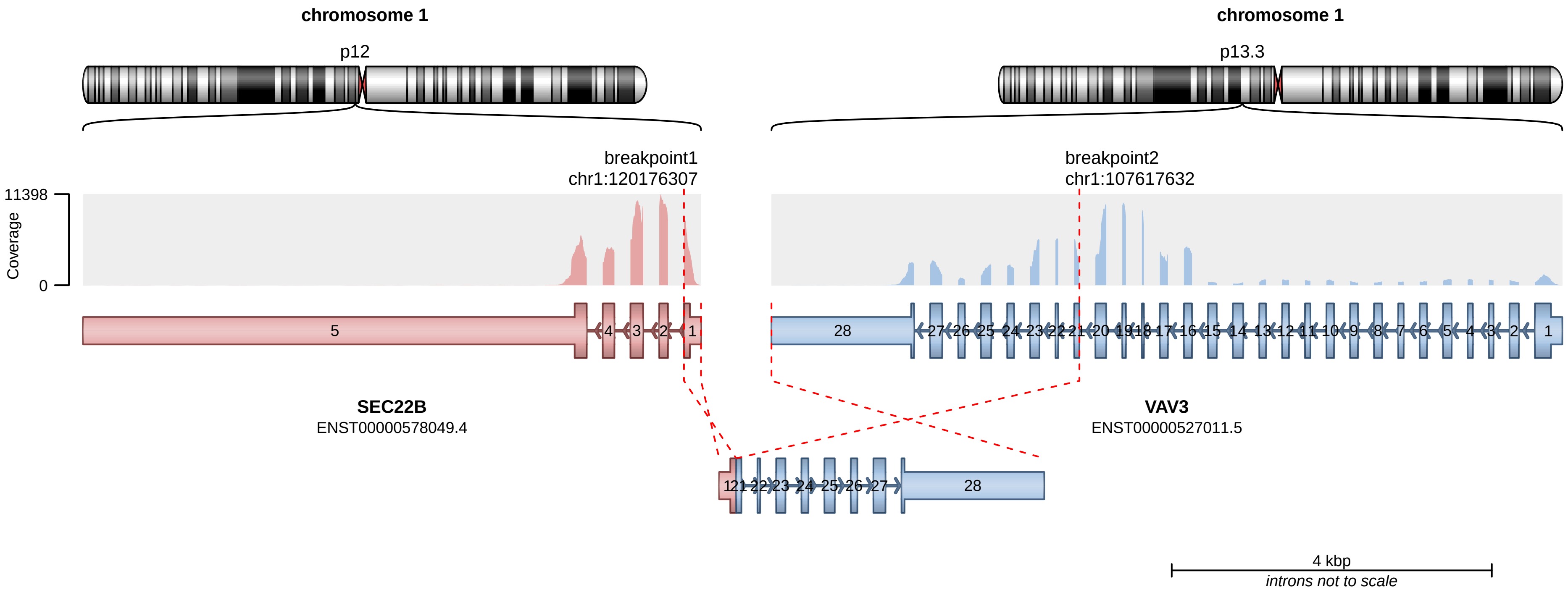


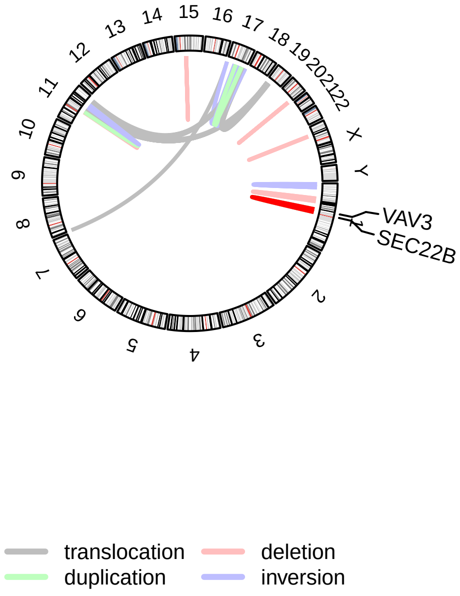
RETAINED PROTEIN DOMAINS
reading frame unclear

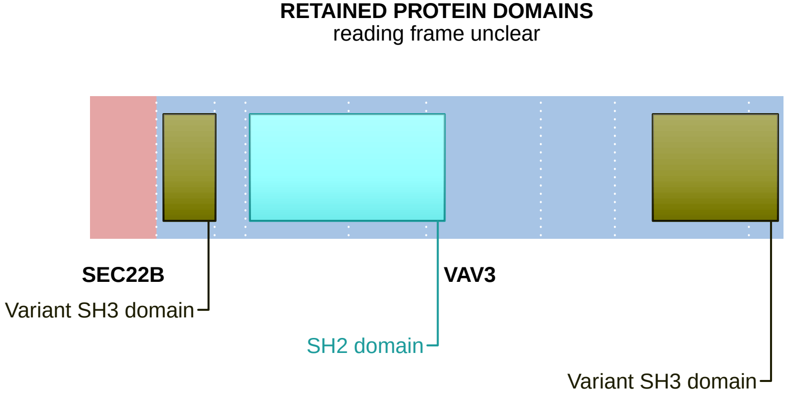


SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

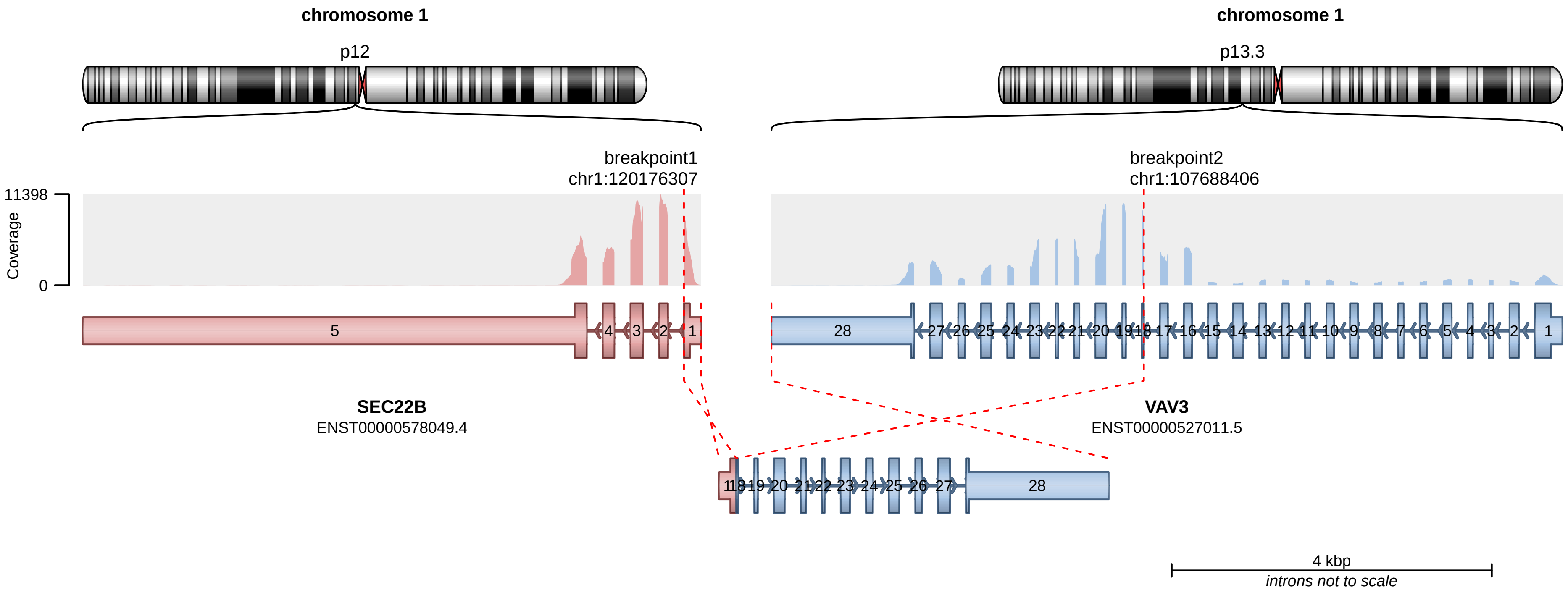


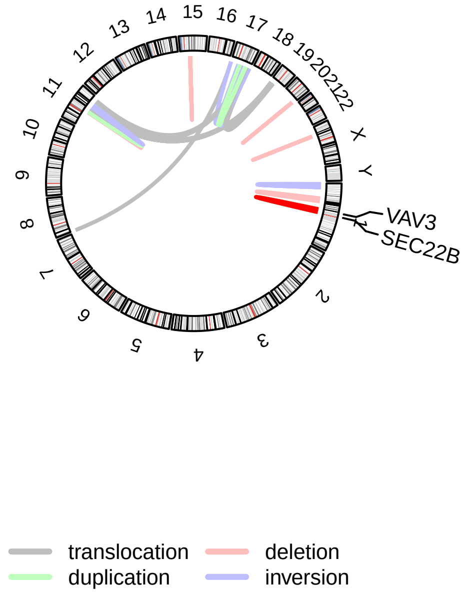




SUPPORTING READ COUNT

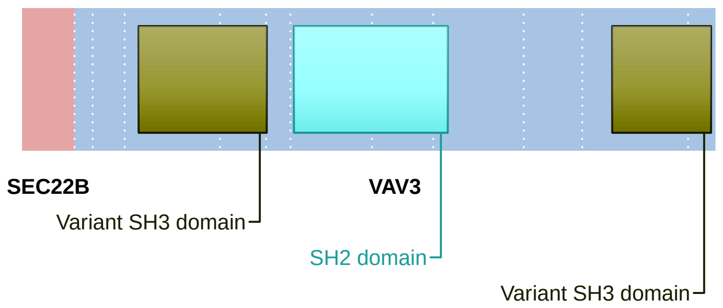
Split reads = 1
Discordant mates = 0





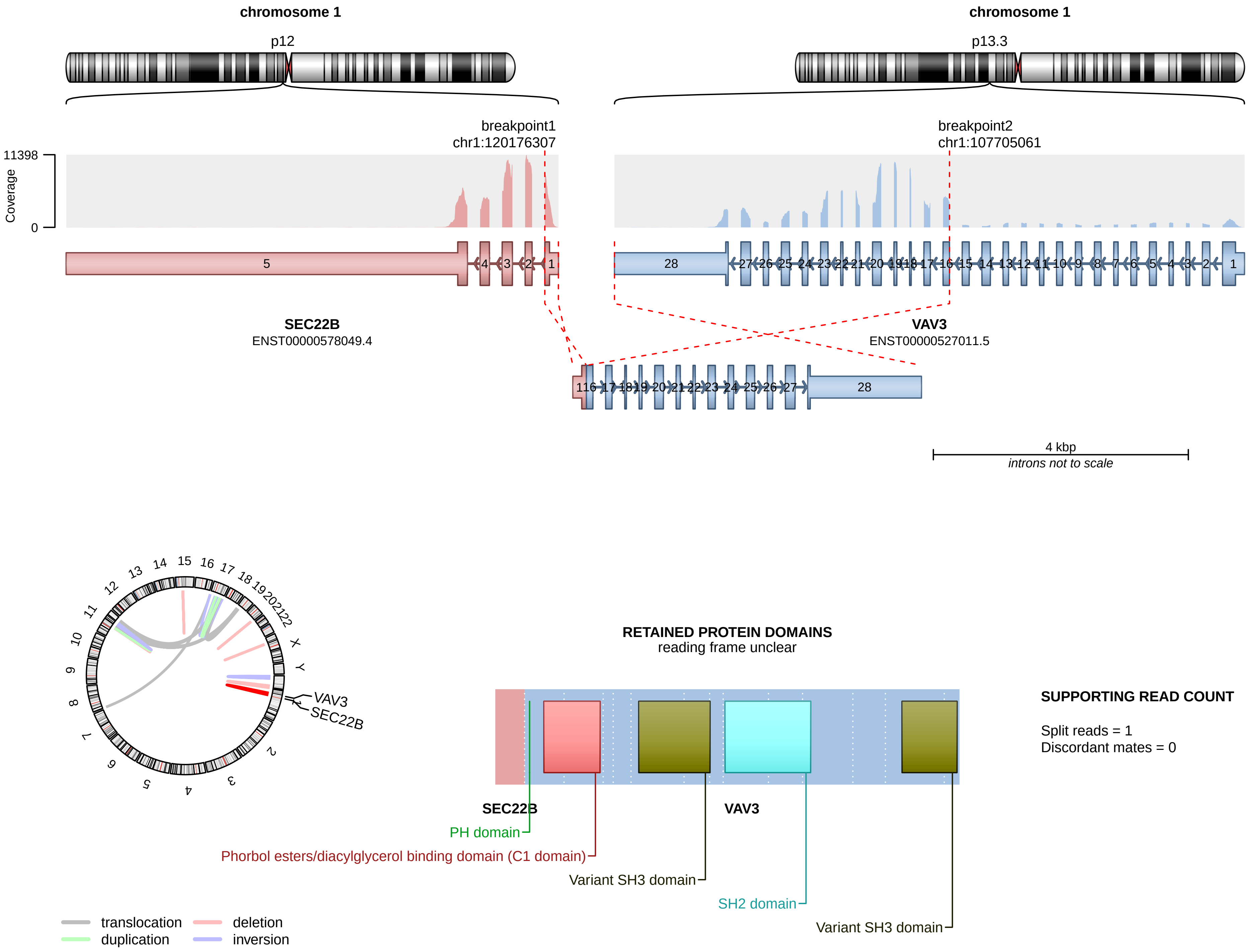
RETAINED PROTEIN DOMAINS

reading frame unclear



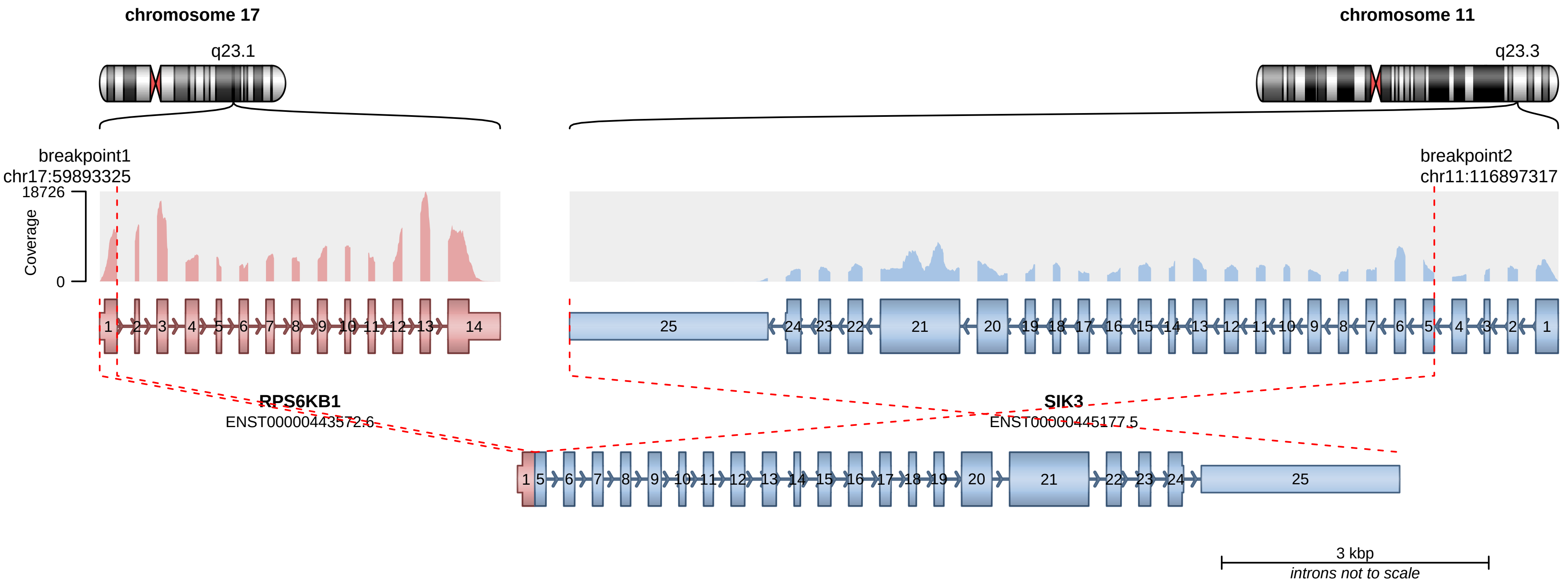
SUPPORTING READ COUNT

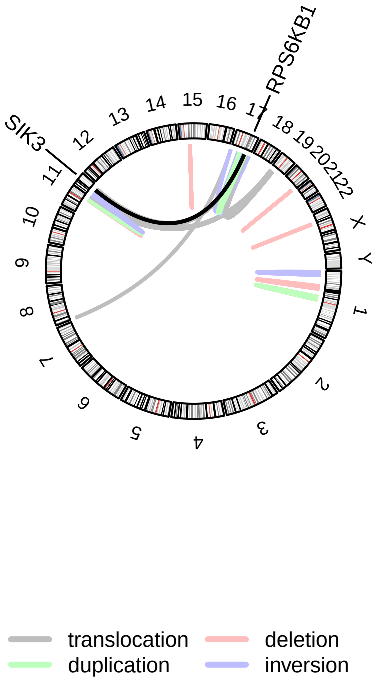
Split reads = 1
Discordant mates = 0

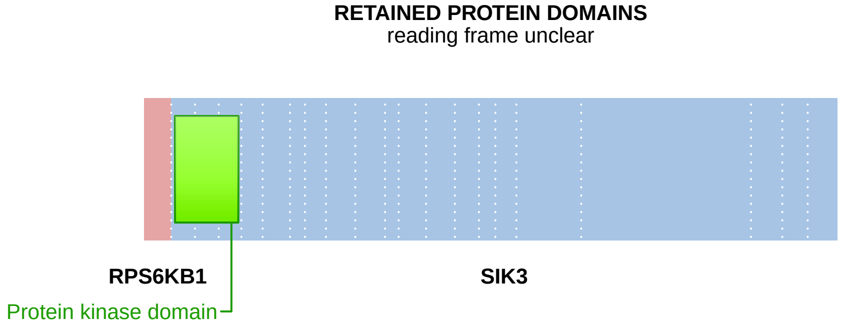


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

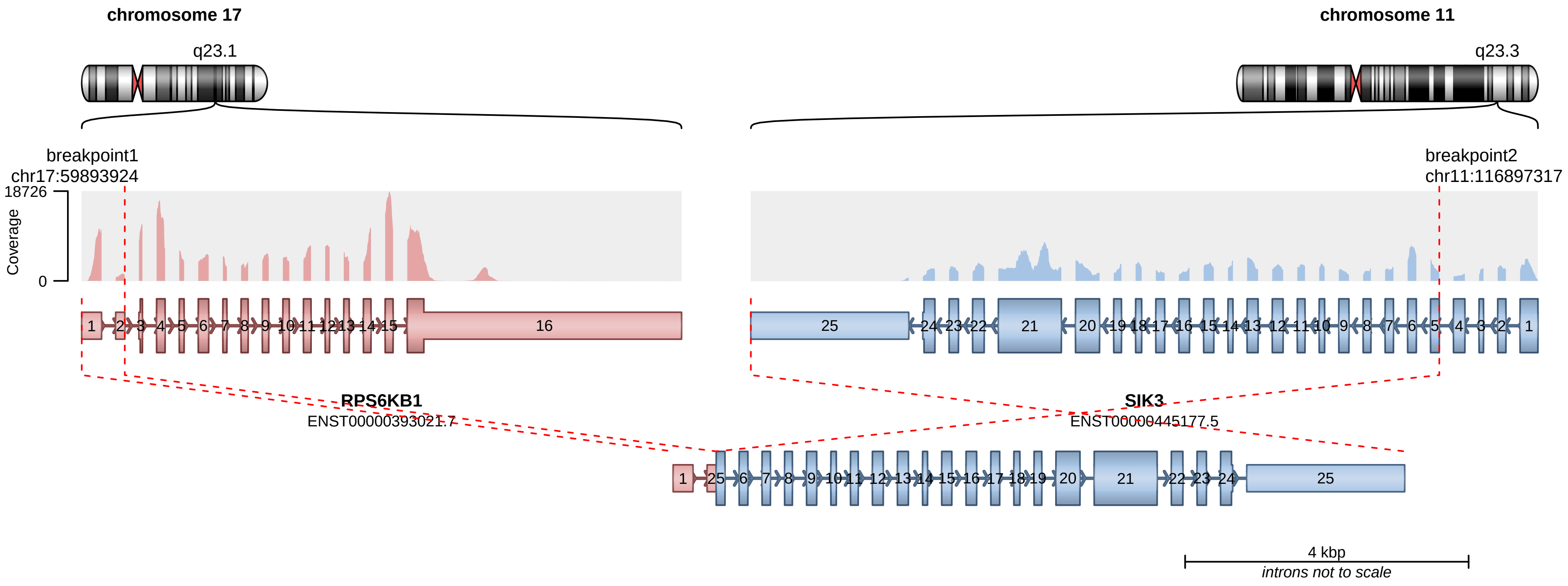


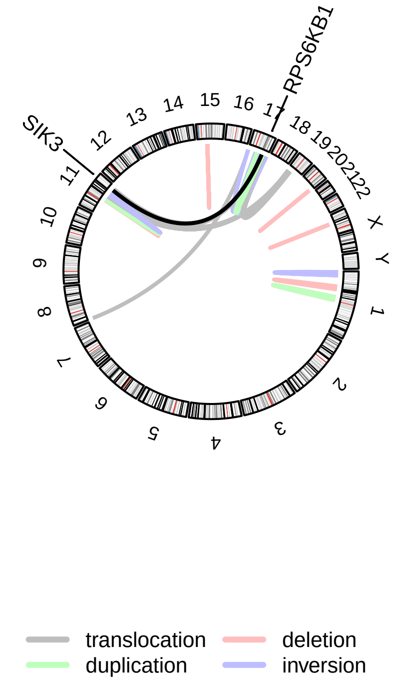


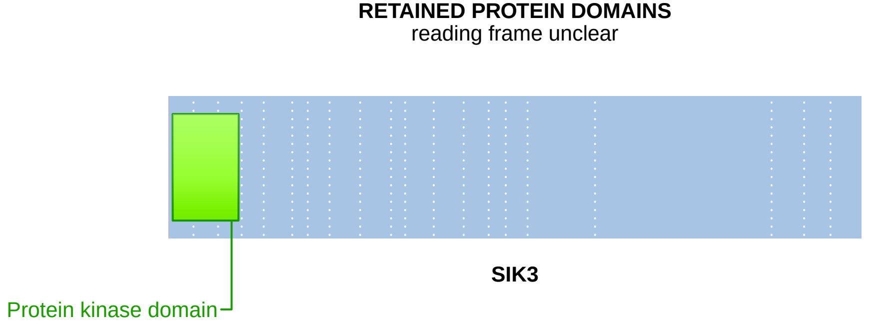


SUPPORTING READ COUNT

Split reads = 372
Discordant mates = 3

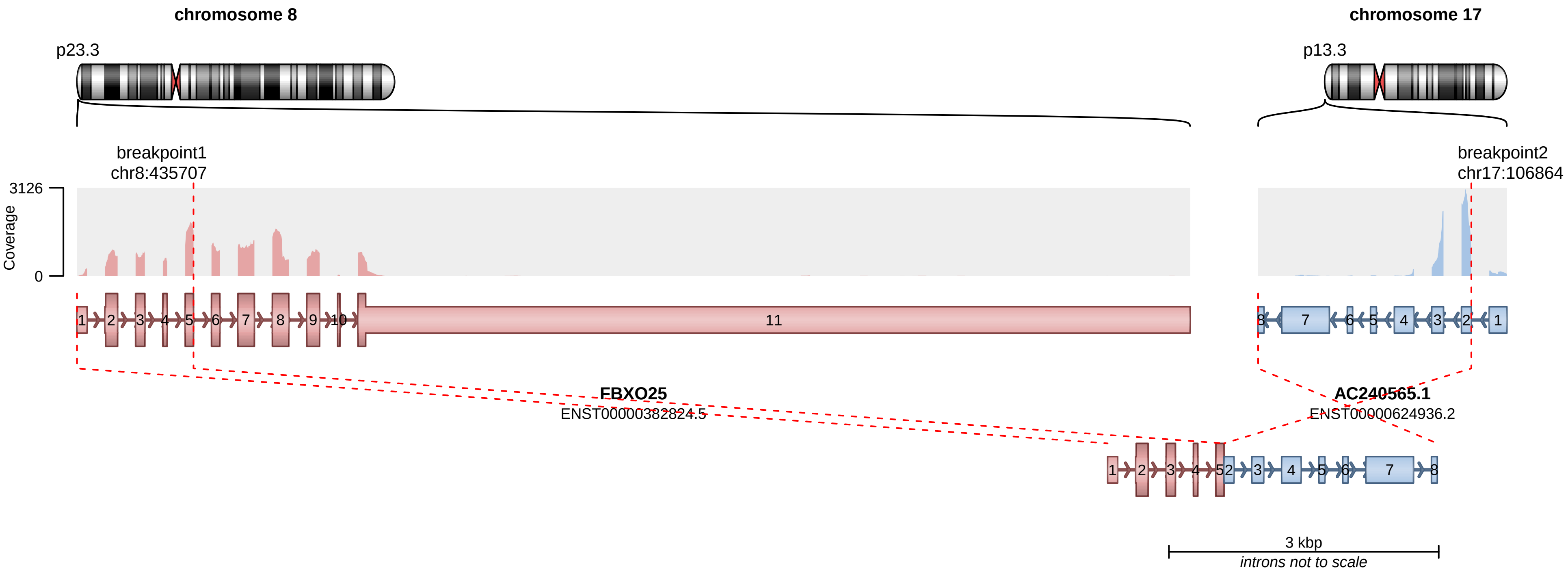


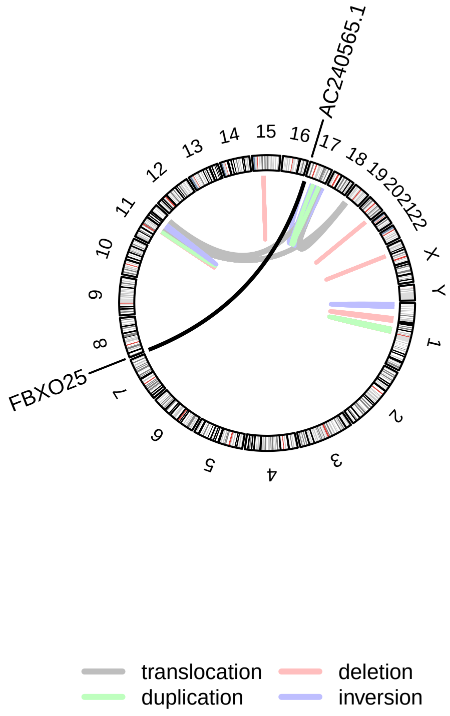




SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 4

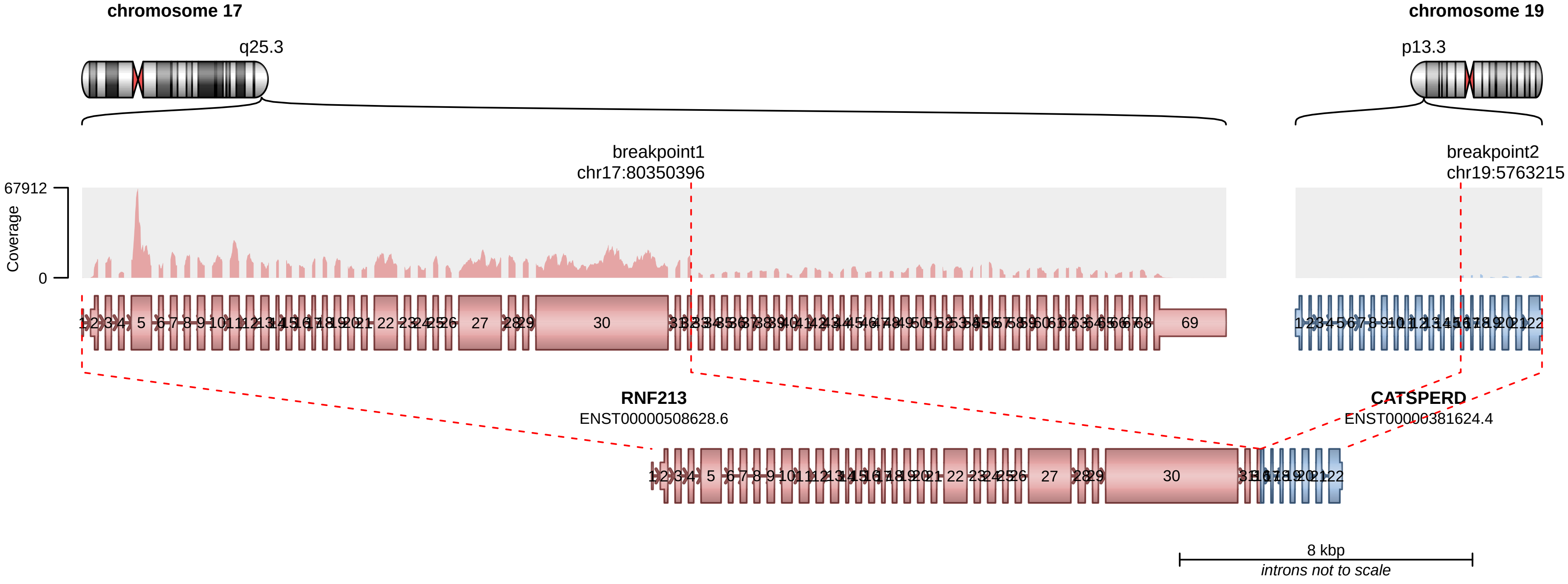


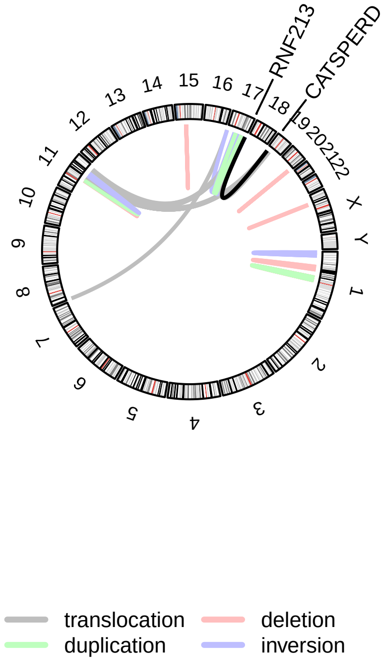


No protein domains retained in fusion.

SUPPORTING READ COUNT

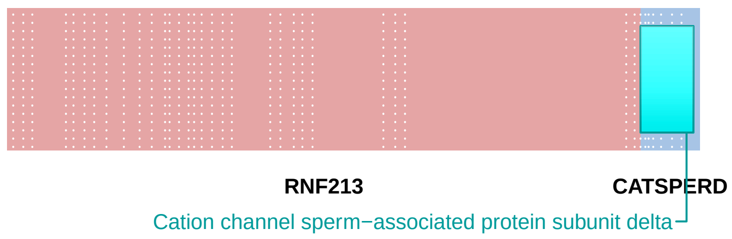
Split reads = 275
Discordant mates = 0





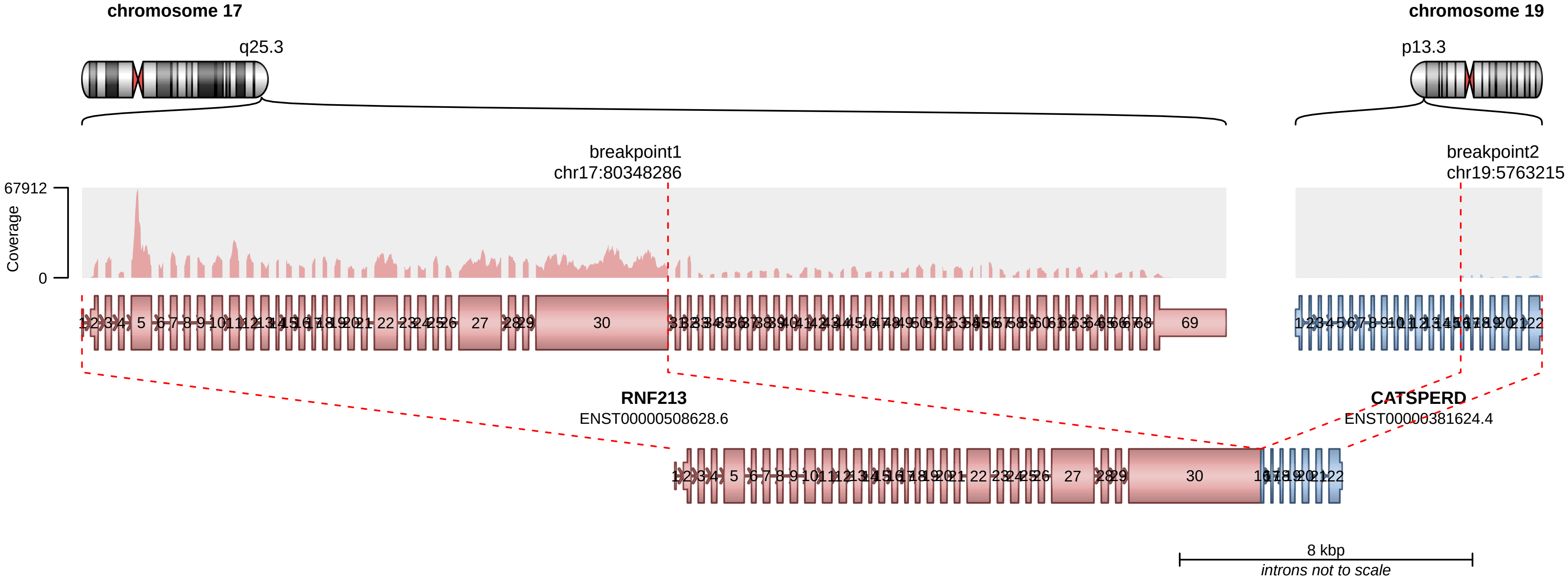
RETAINED PROTEIN DOMAINS

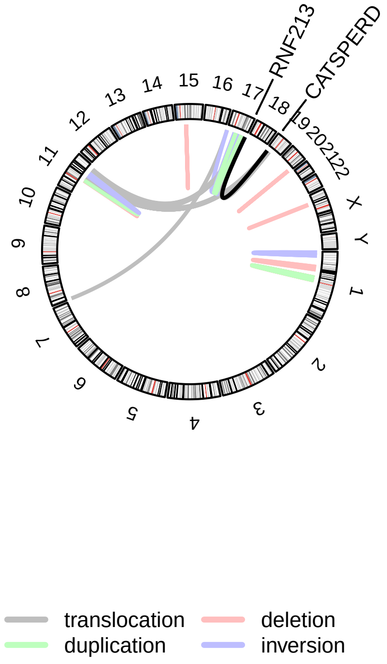
reading frame unclear

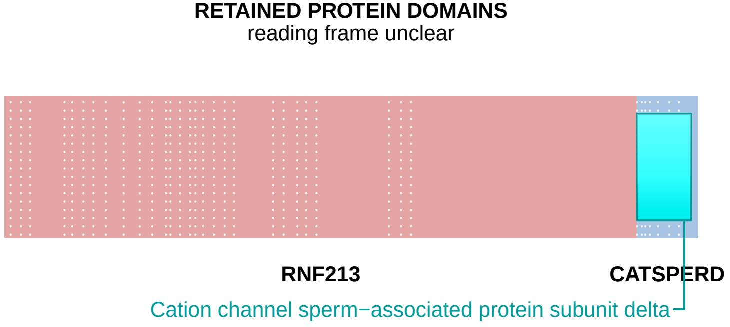


SUPPORTING READ COUNT

Split reads = 240
Discordant mates = 9

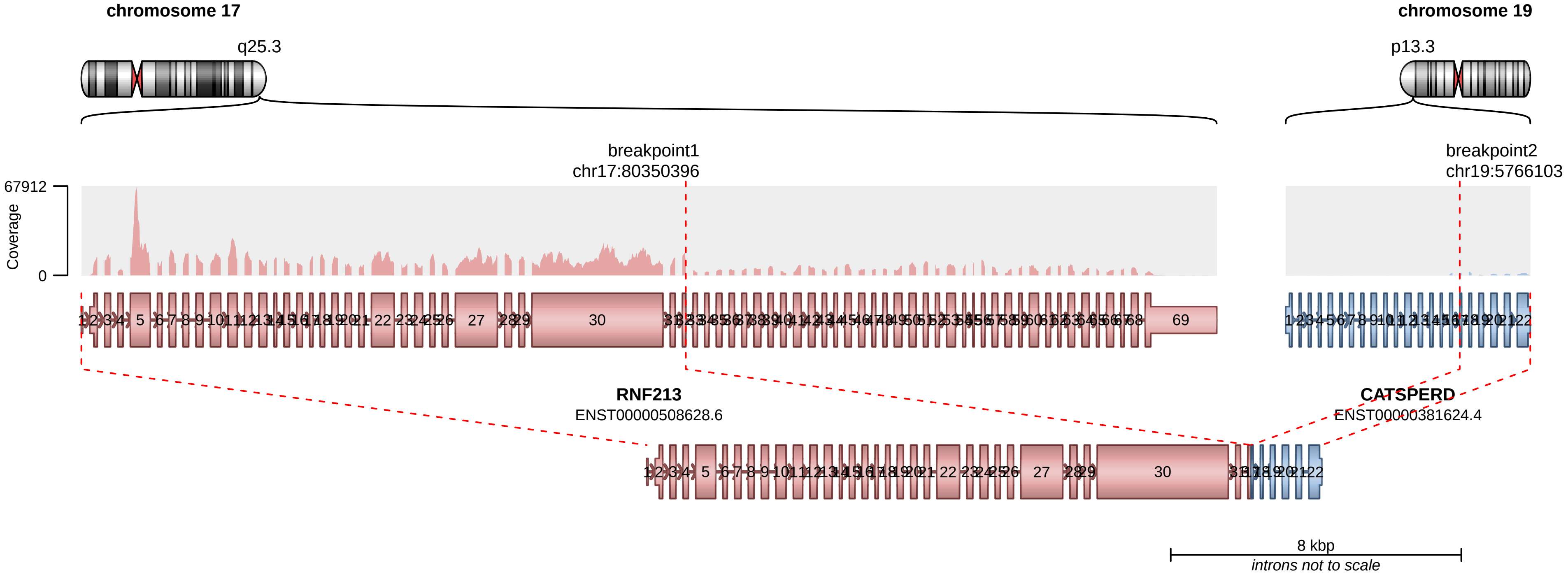


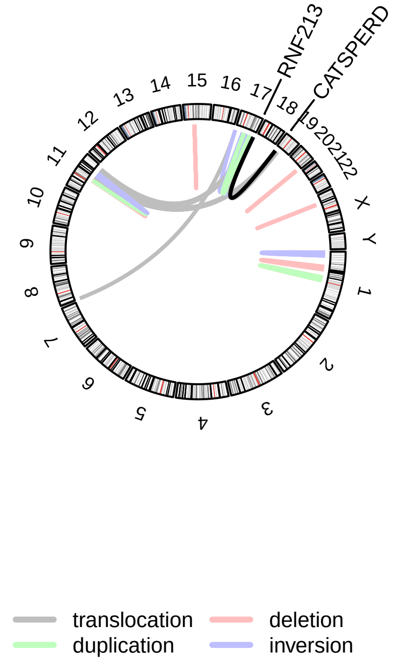


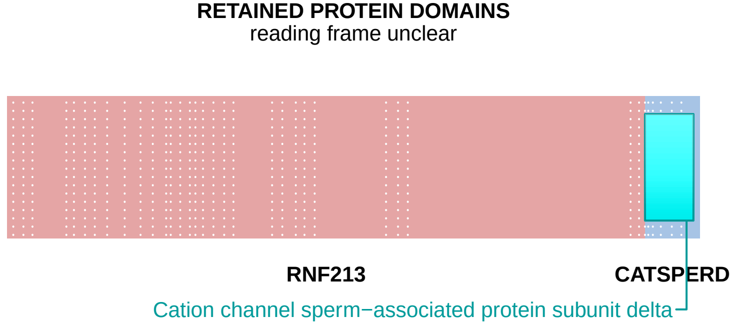


SUPPORTING READ COUNT

Split reads = 41
Discordant mates = 2

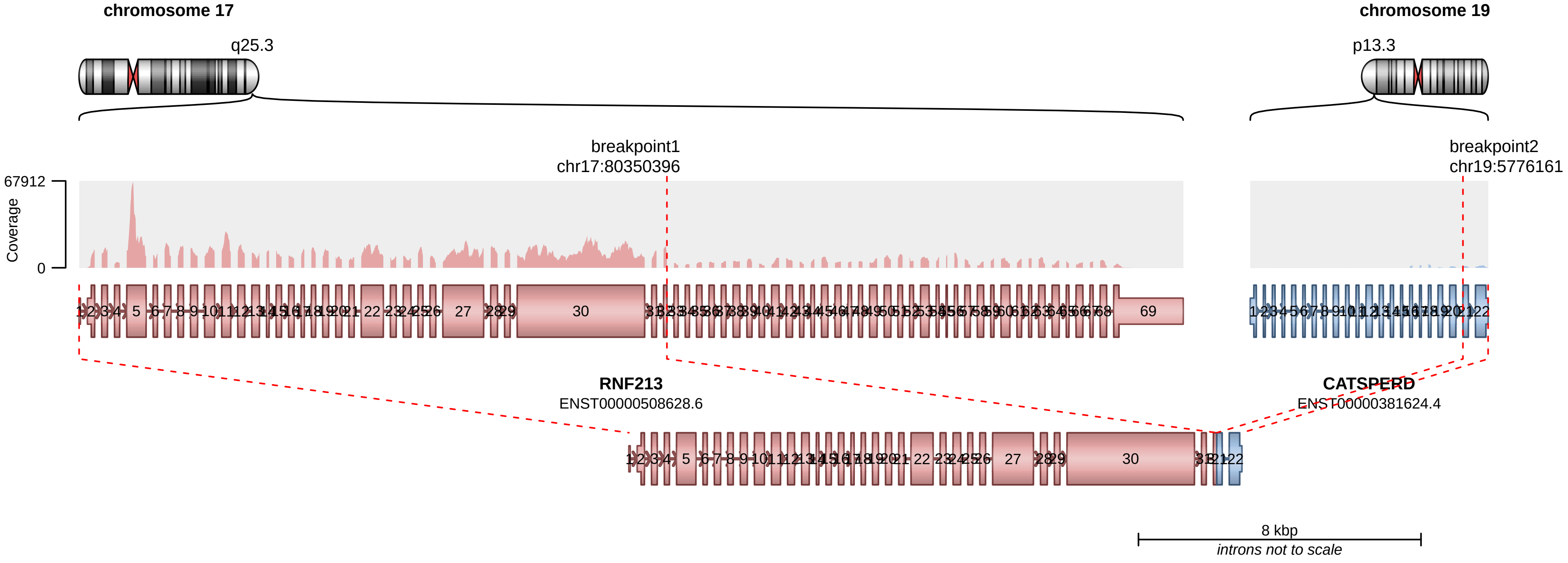


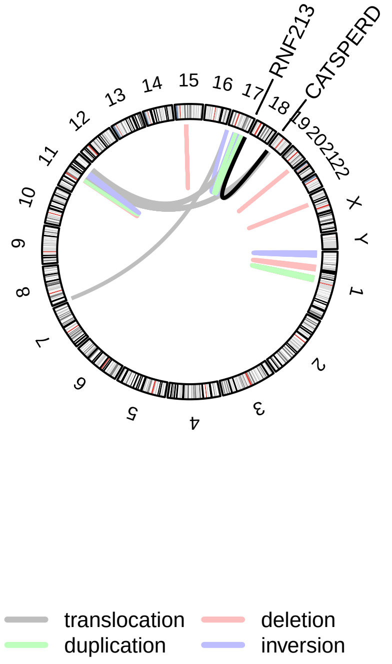




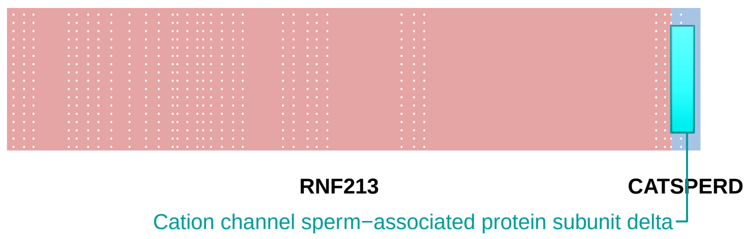
SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 4



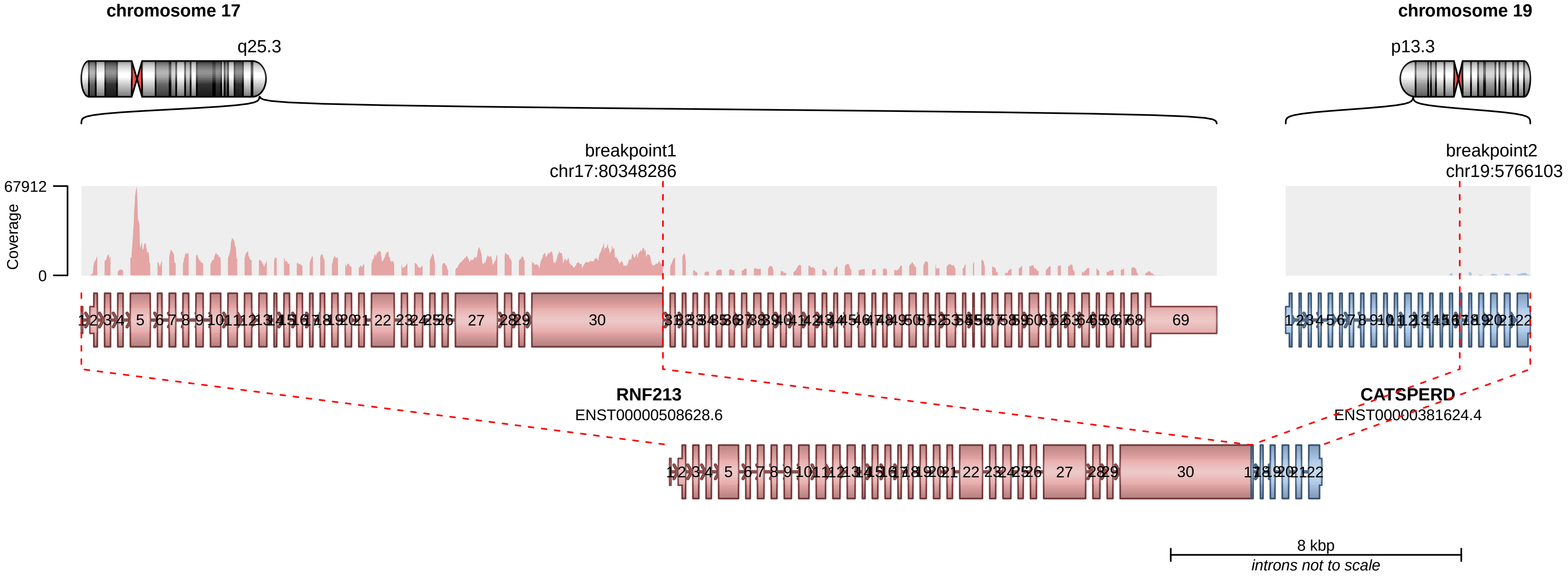


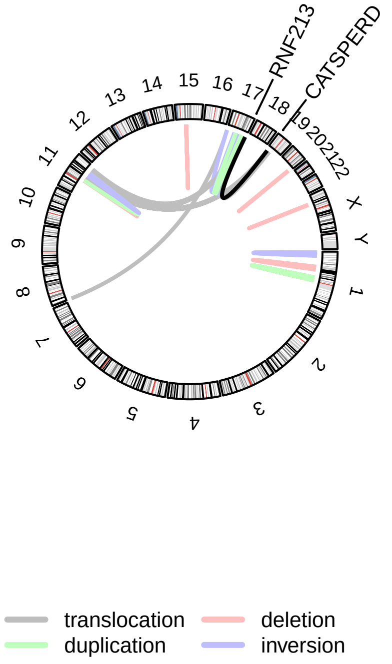
RETAINED PROTEIN DOMAINS
reading frame unclear

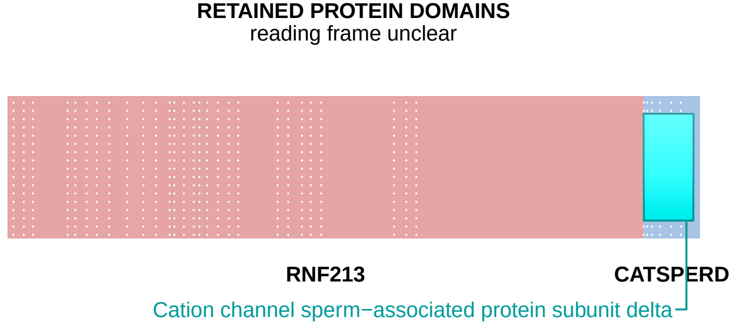


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

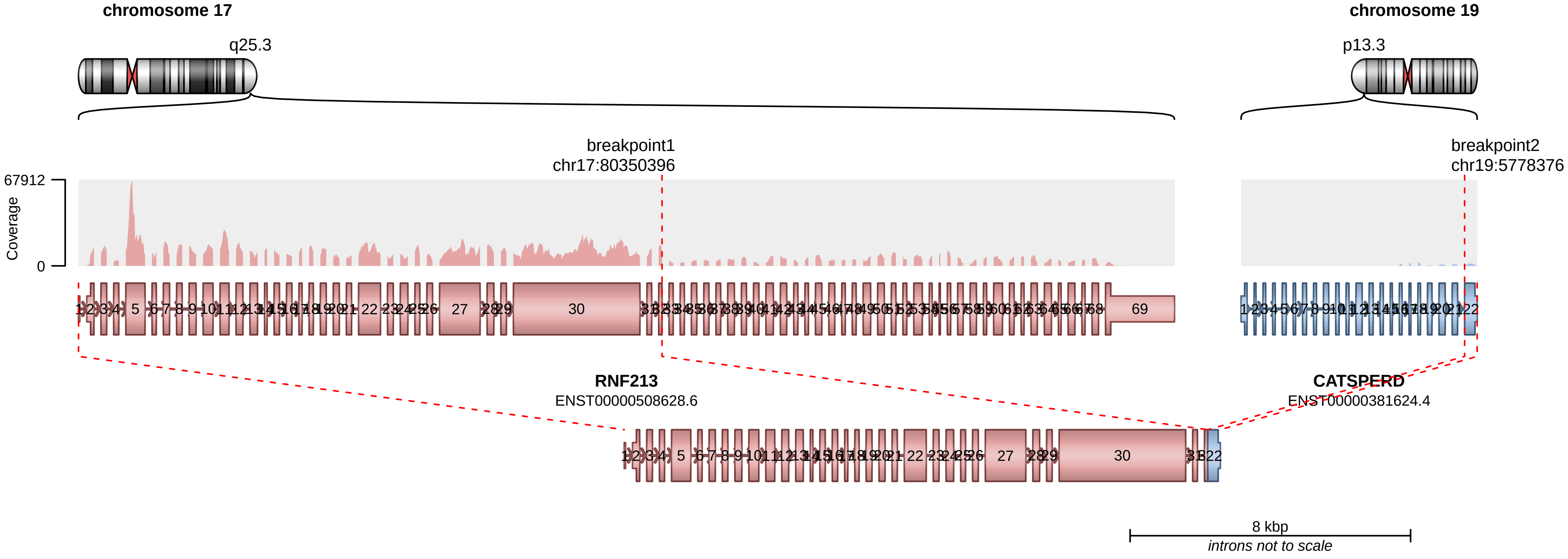


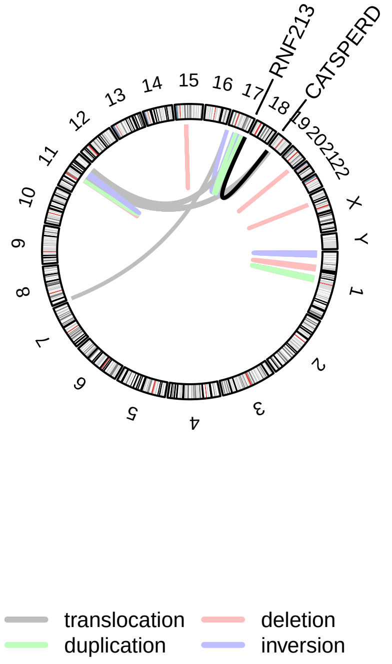


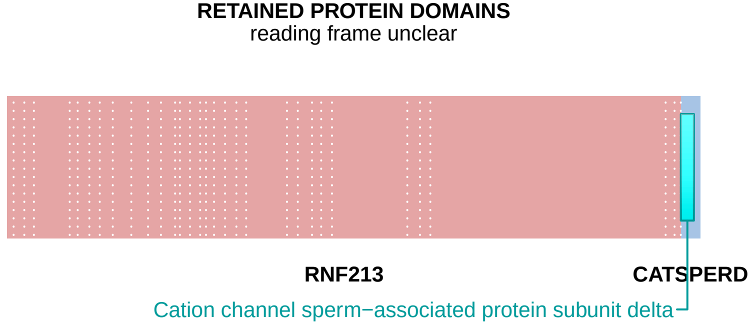


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 2

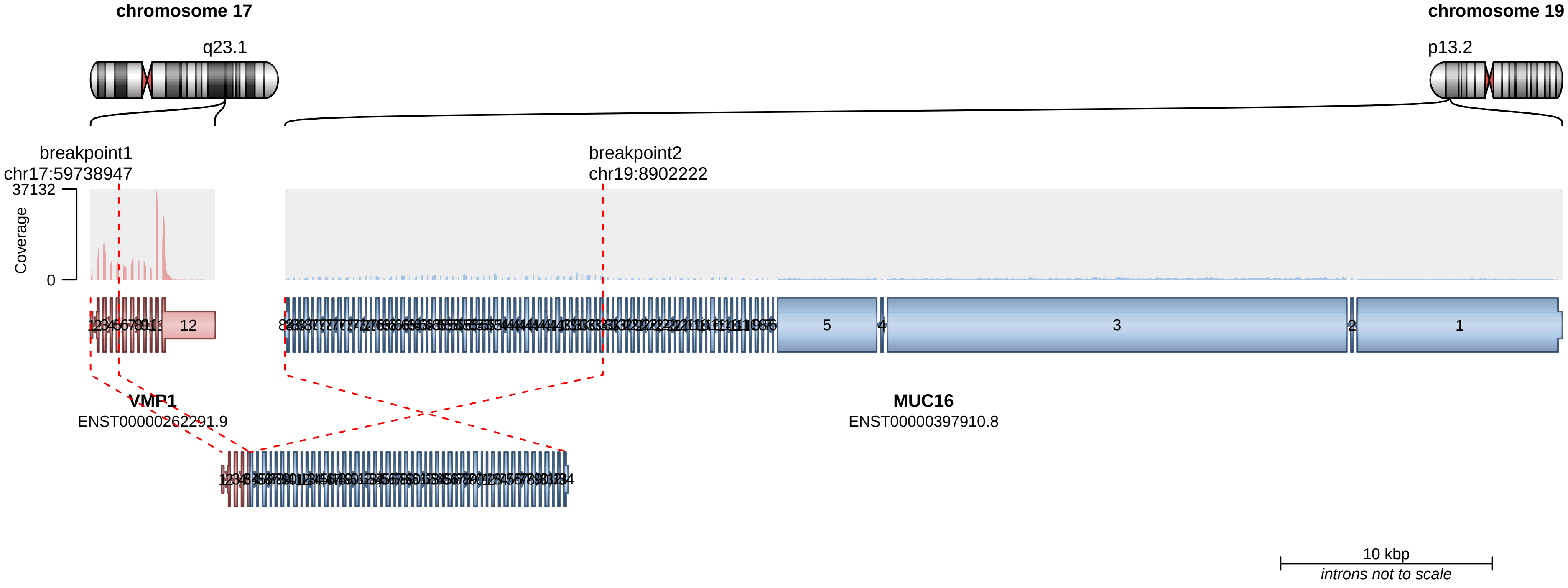


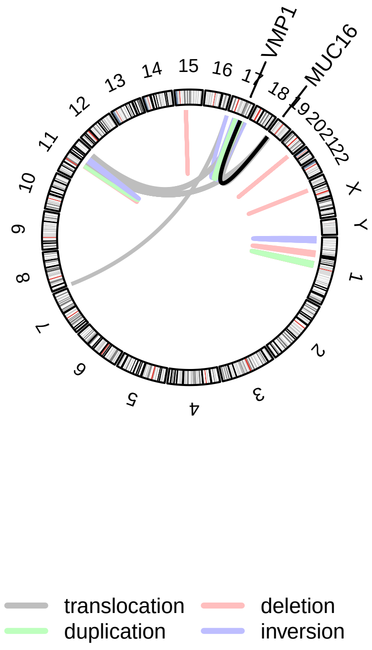




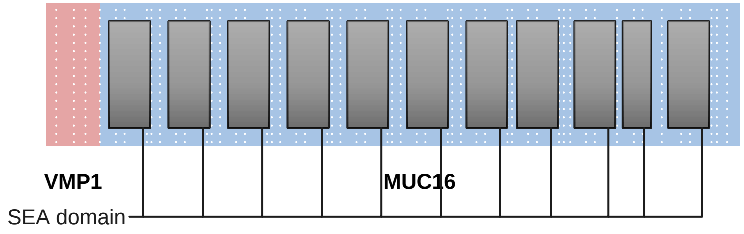
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



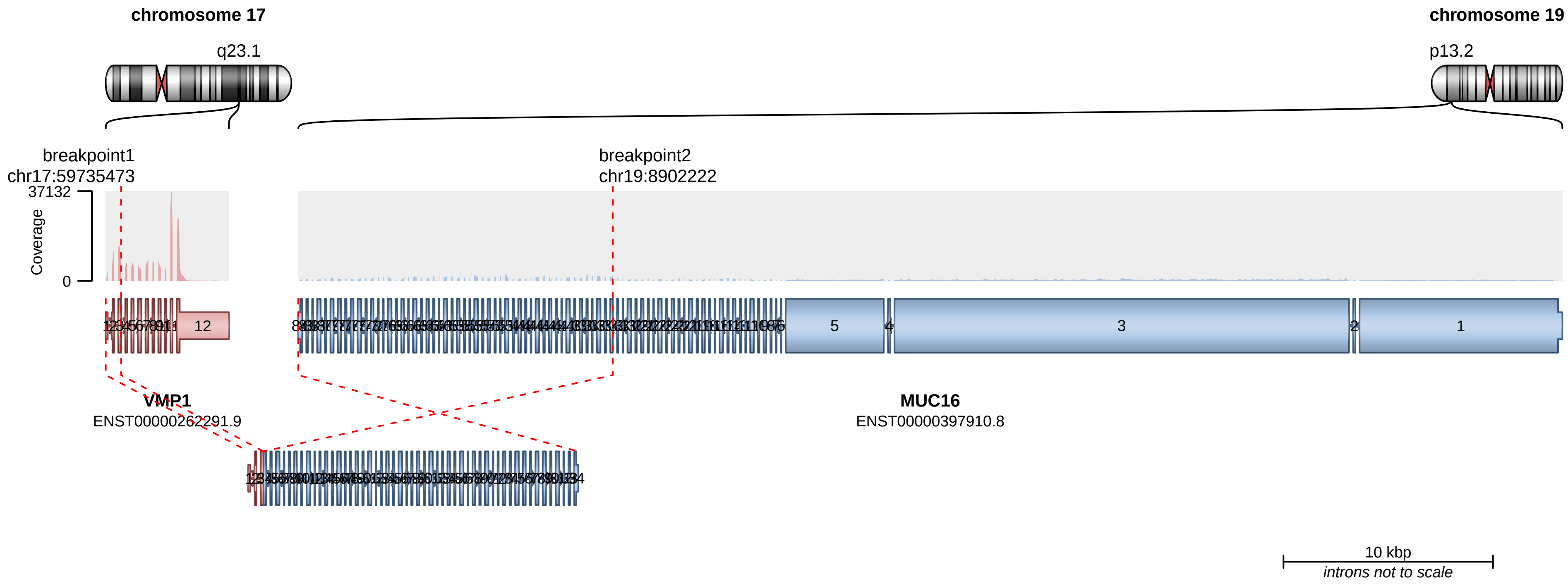


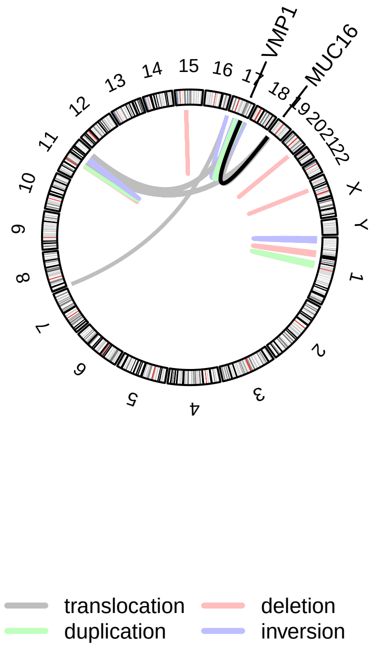
RETAINED PROTEIN DOMAINS
reading frame unclear



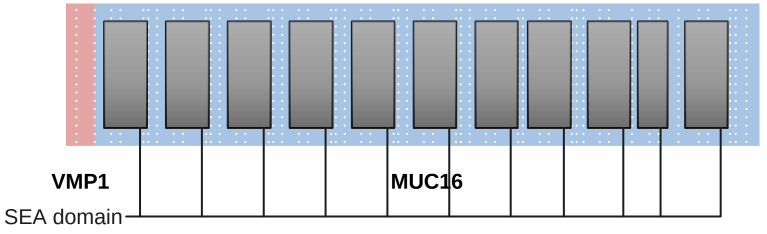
SUPPORTING READ COUNT

Split reads = 235
Discordant mates = 8



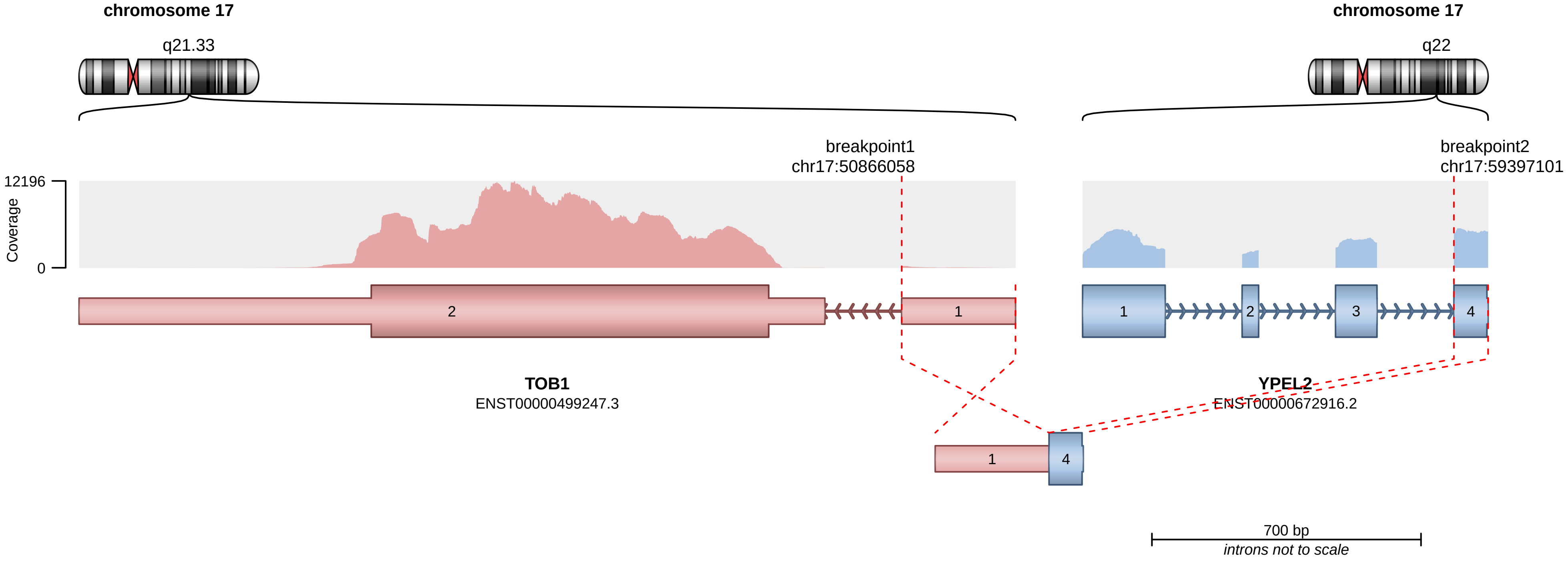


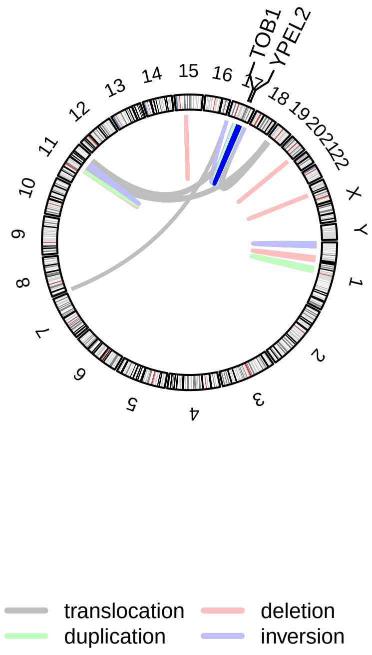
RETAINED PROTEIN DOMAINS
reading frame unclear



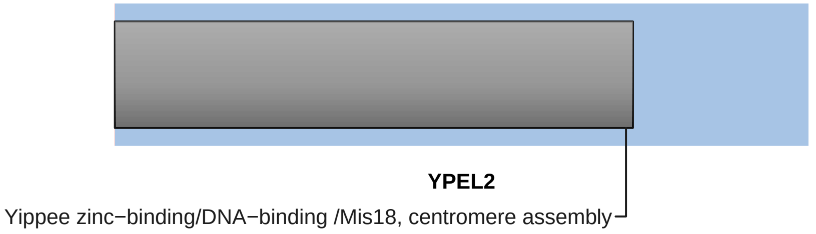
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 1



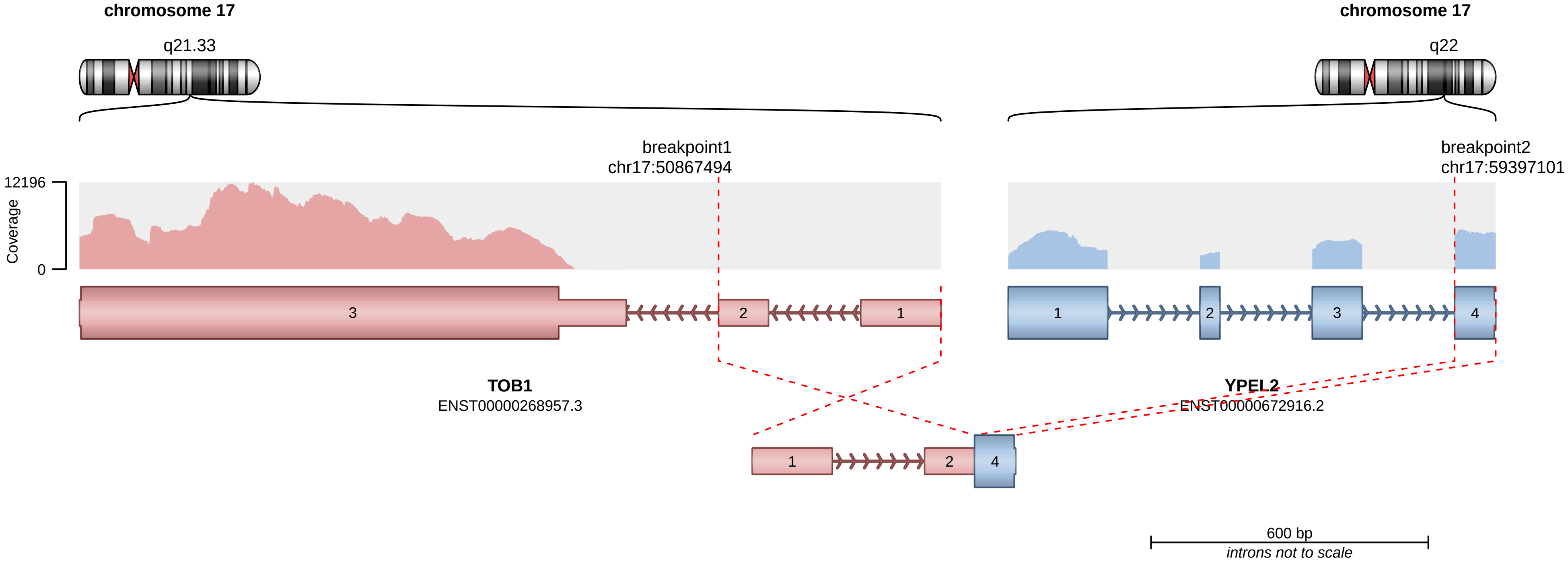


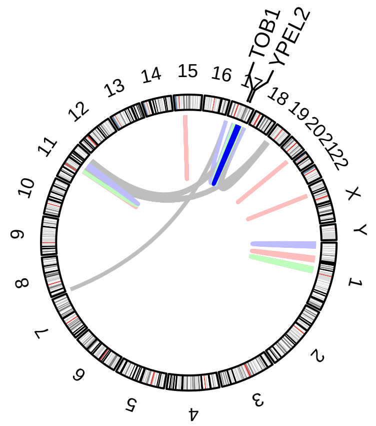
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

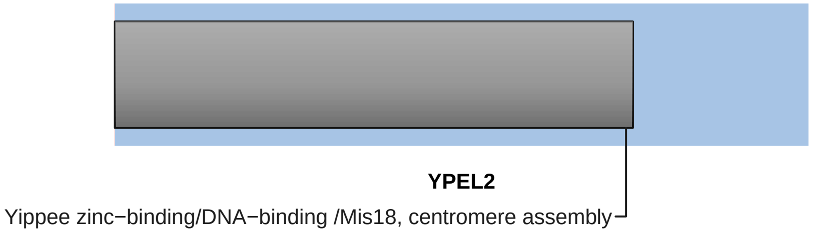
Split reads = 214
Discordant mates = 2





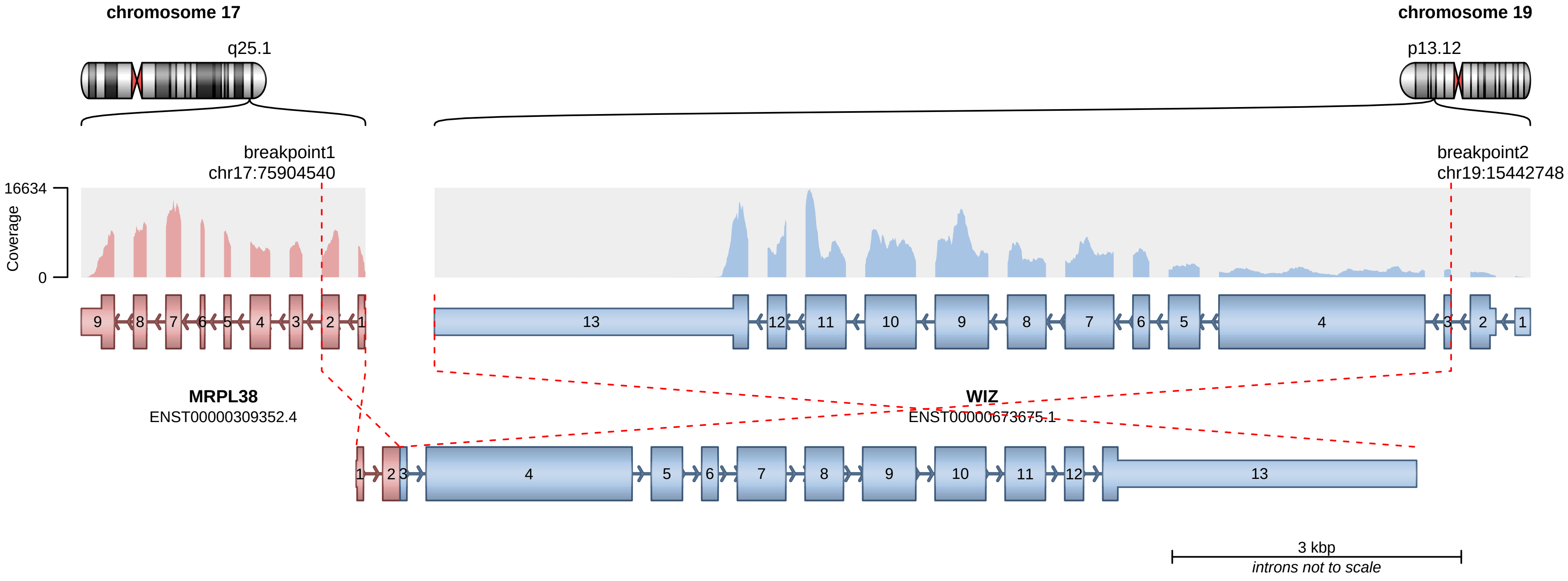
▬ translocation ▬ deletion
▬ duplication ▬ inversion

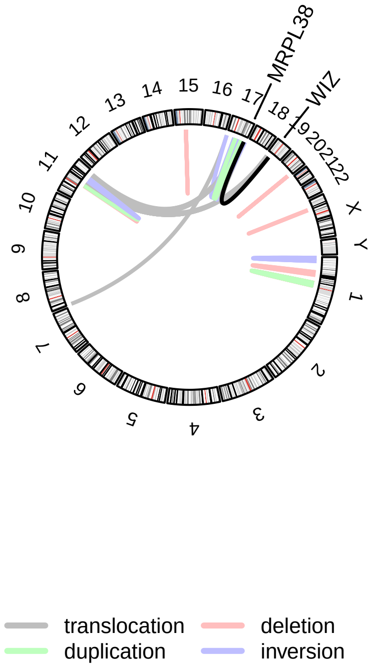
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

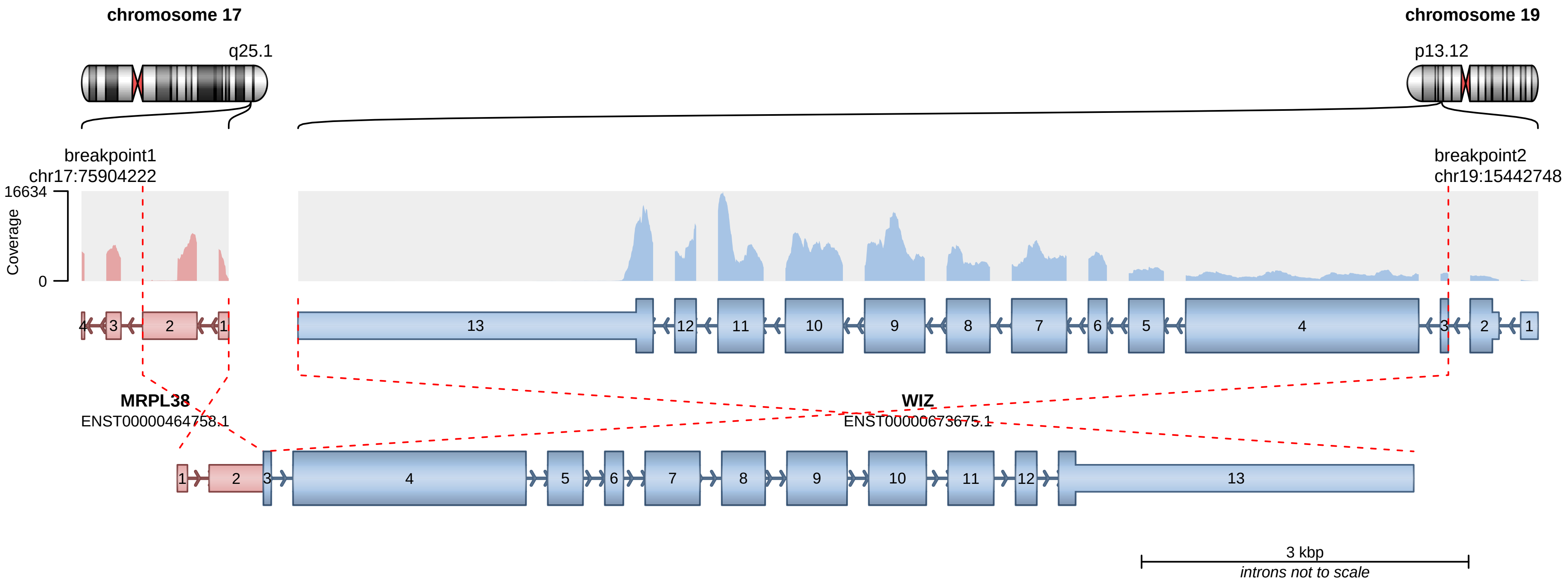


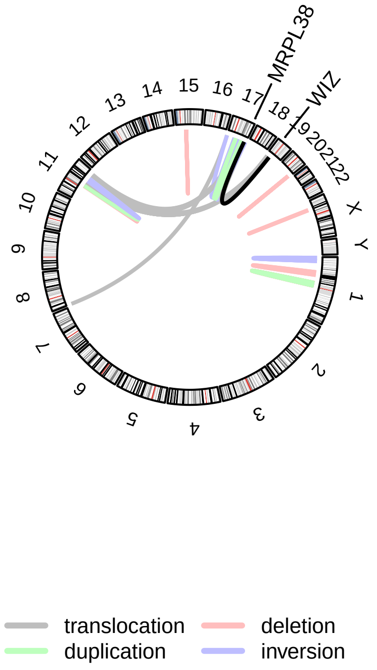


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 174
Discordant mates = 1

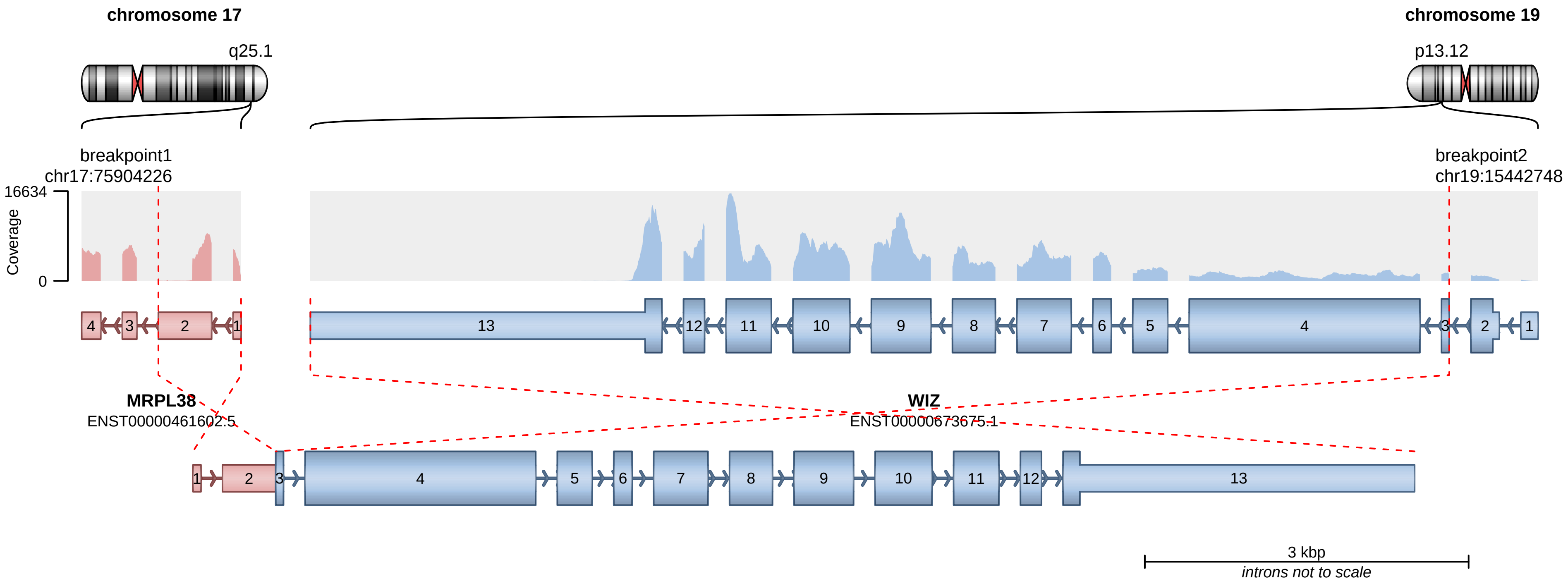


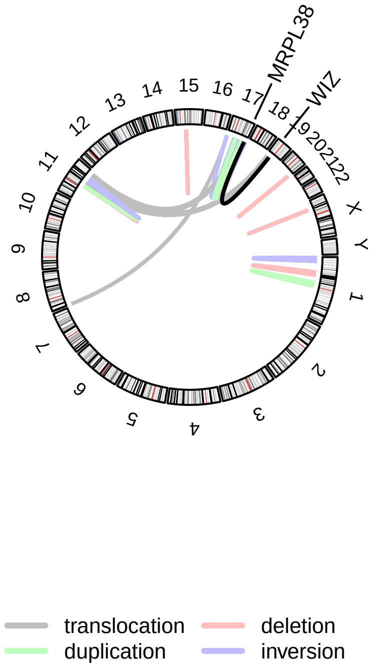


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 1

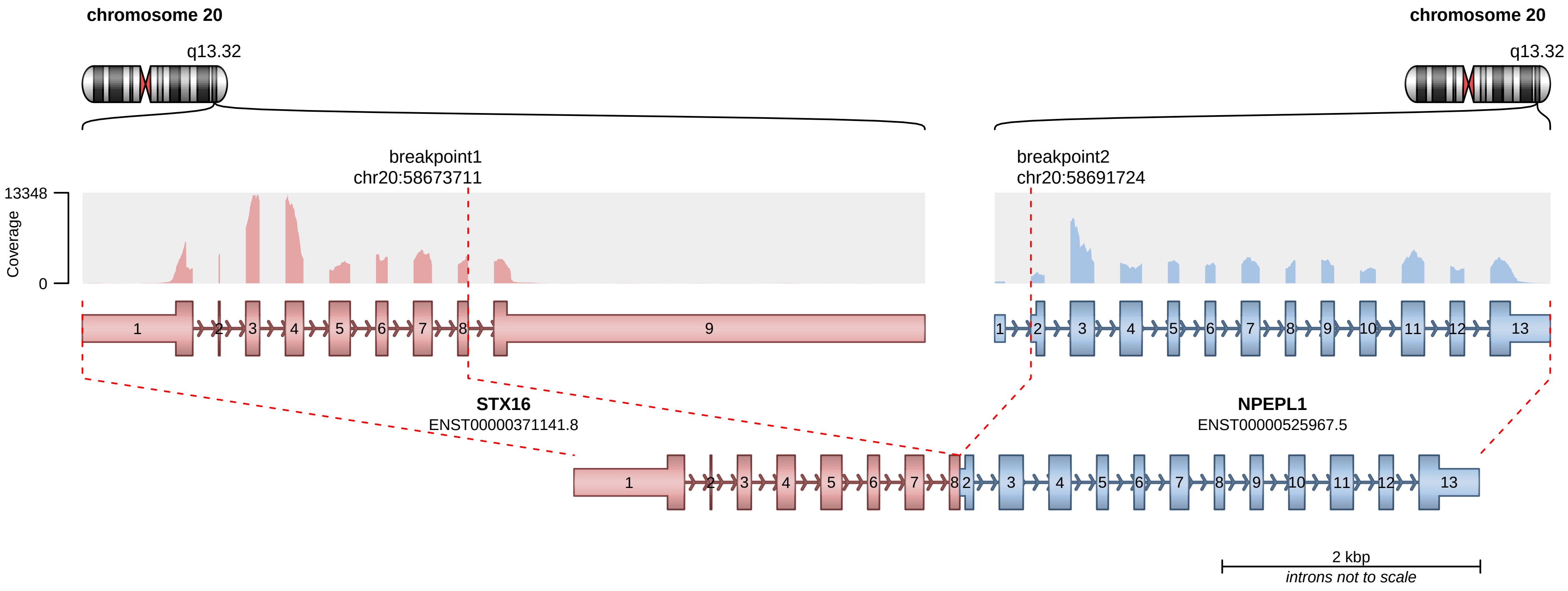


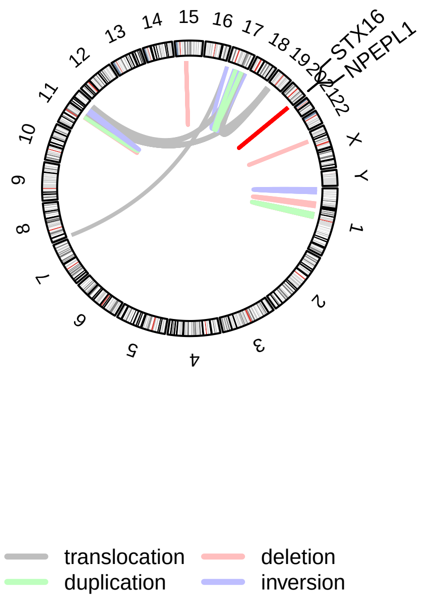


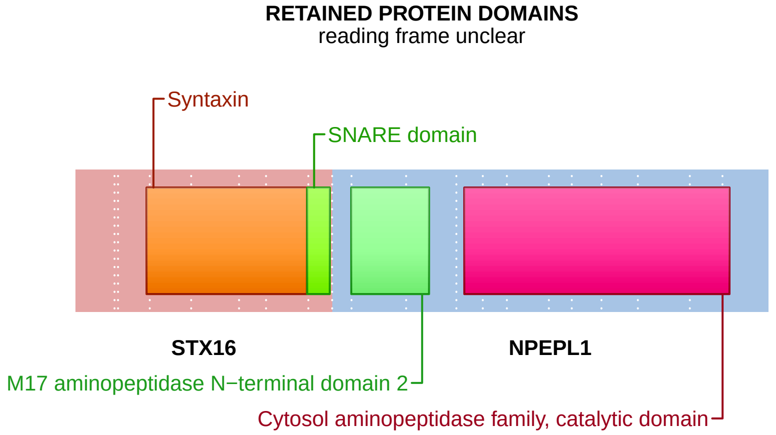
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

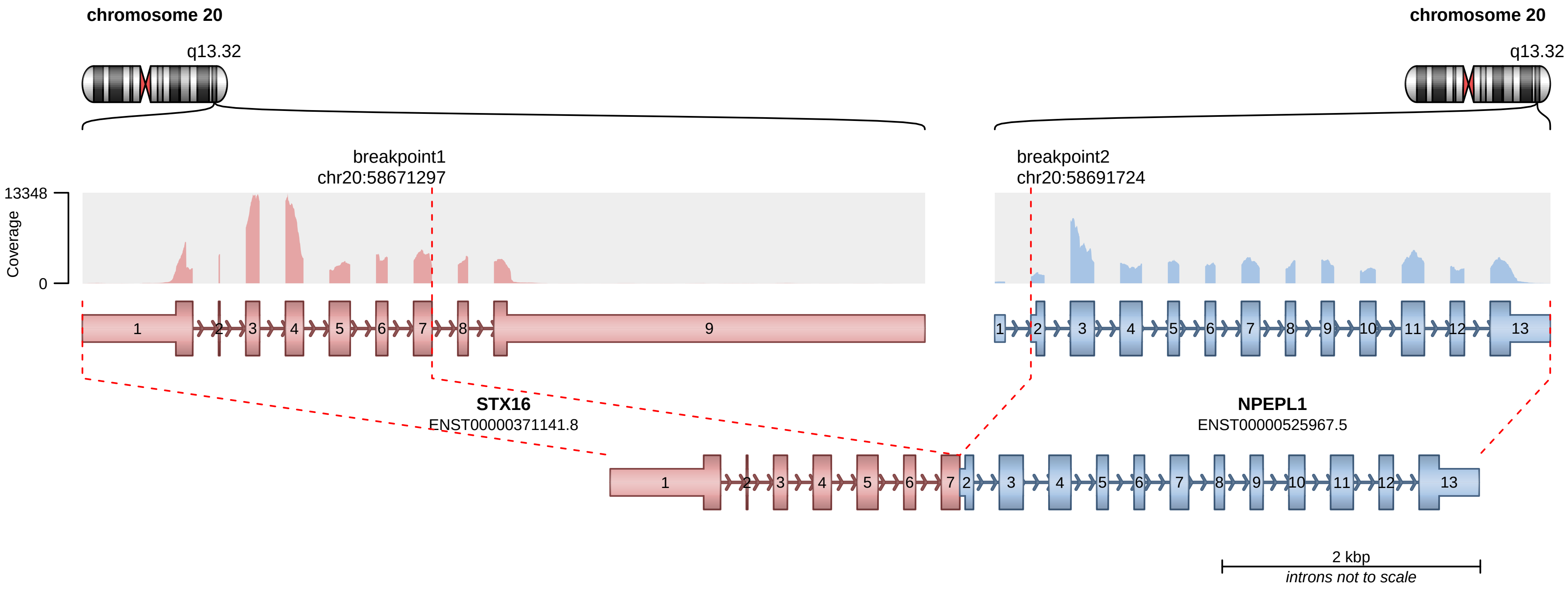


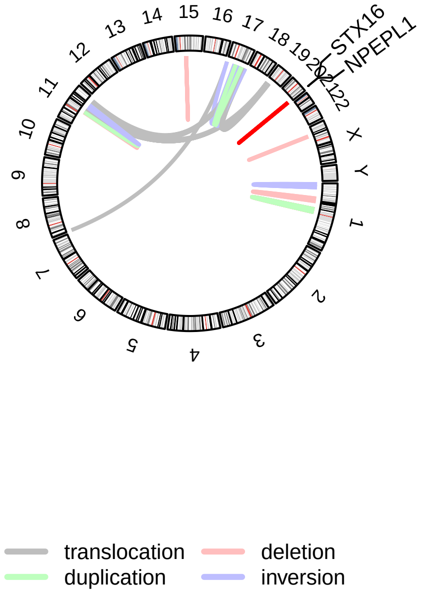




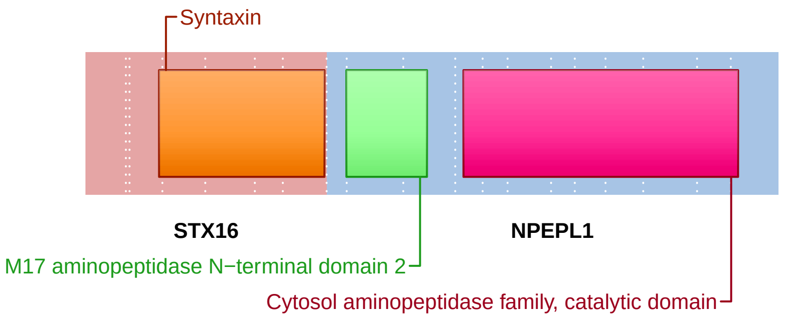
SUPPORTING READ COUNT

Split reads = 162
Discordant mates = 2



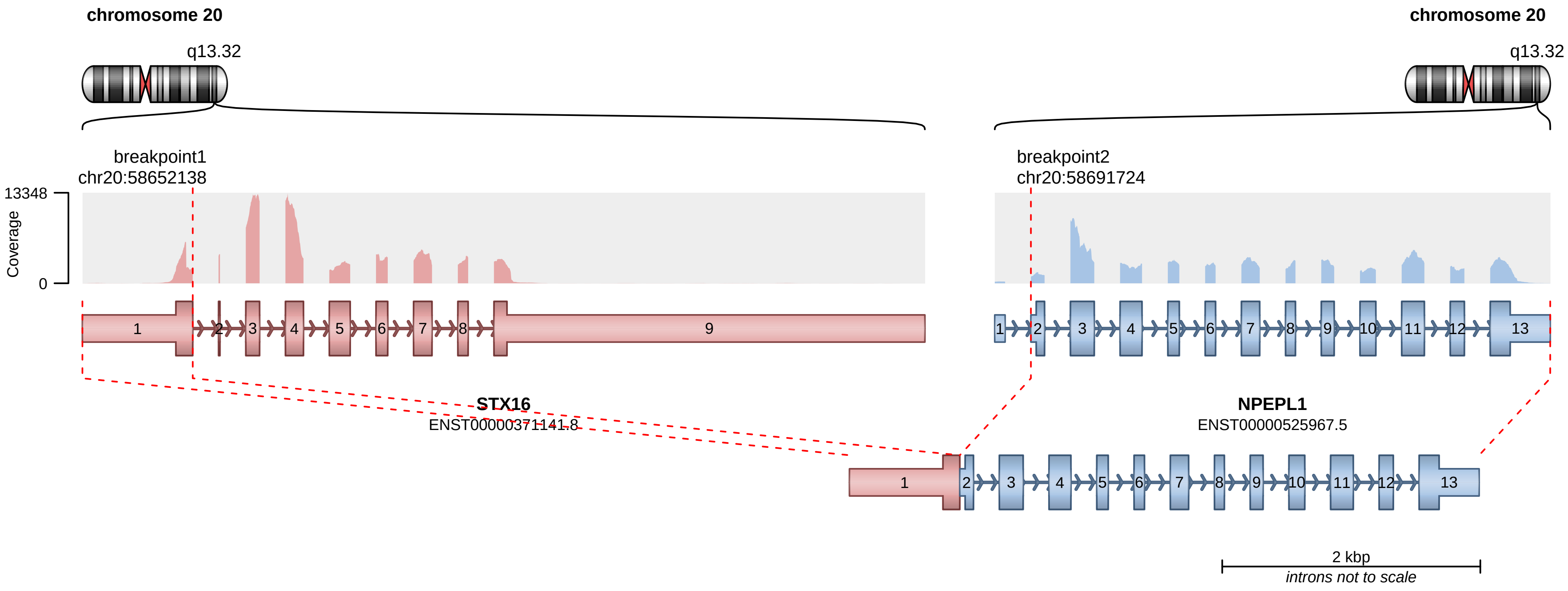


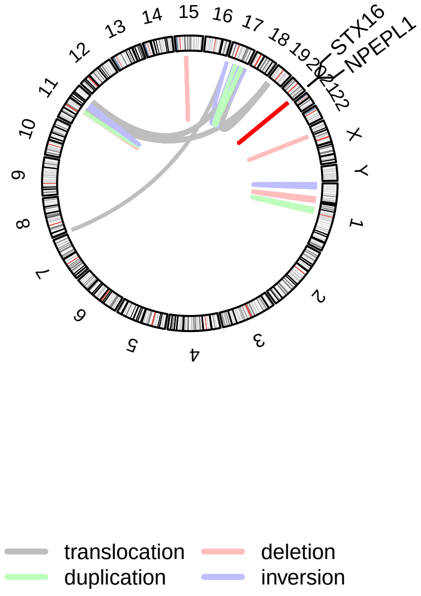
RETAINED PROTEIN DOMAINS
reading frame unclear

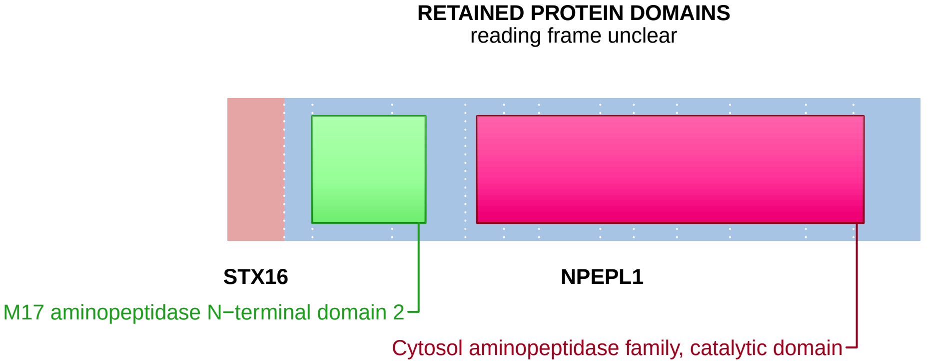


SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

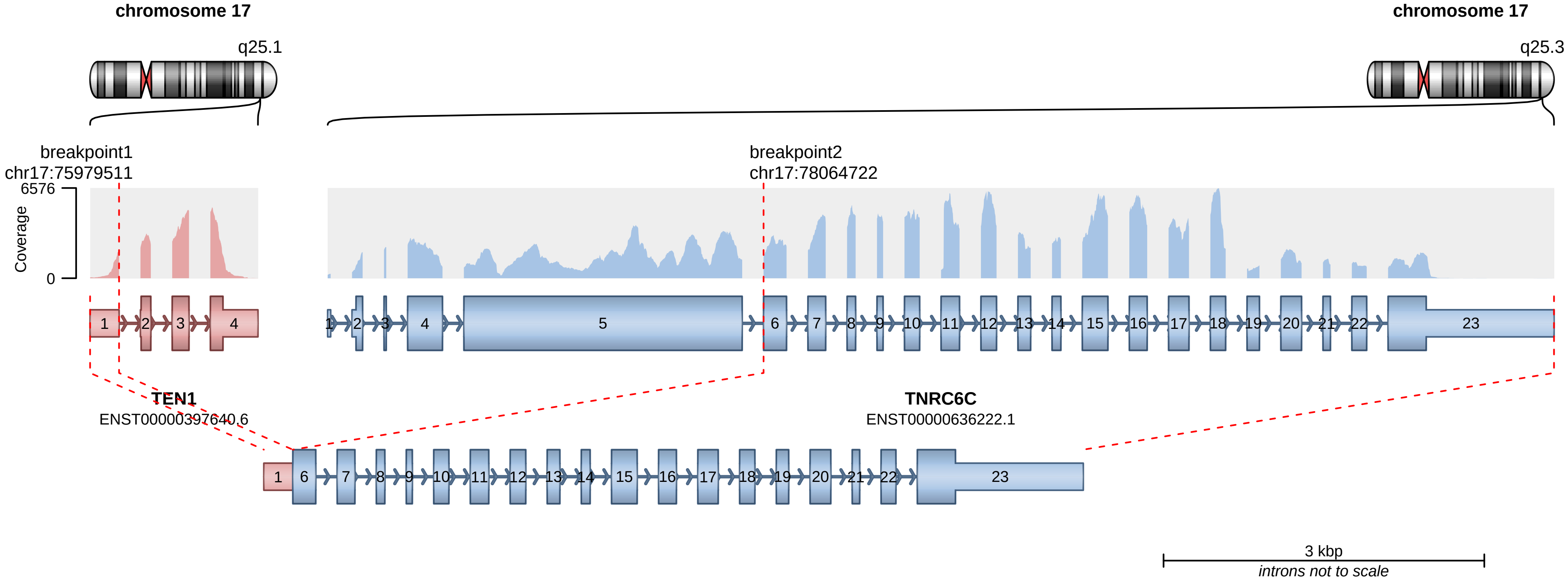


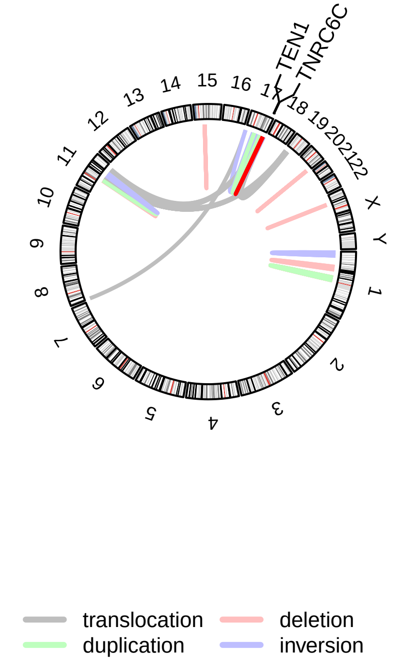


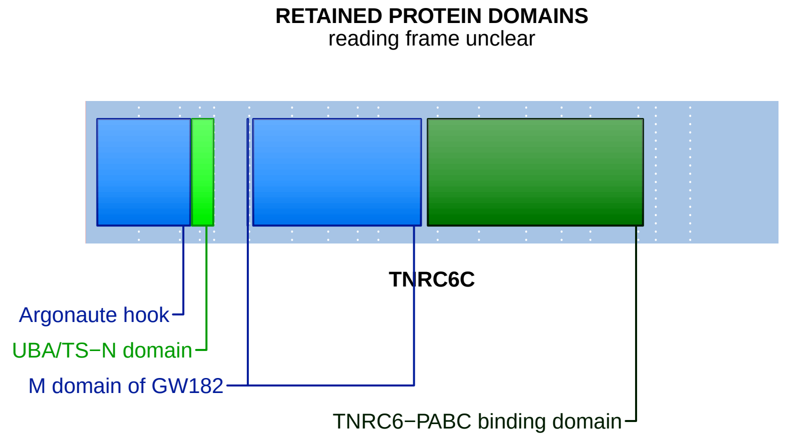


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

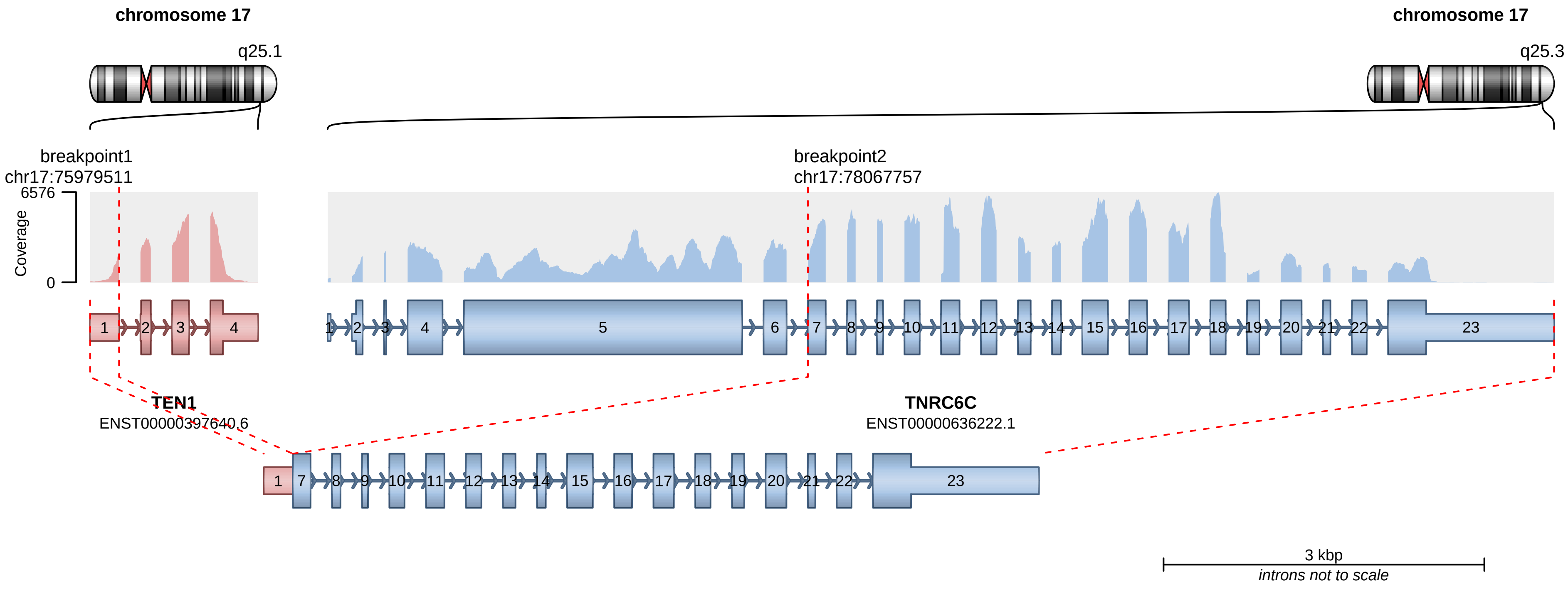


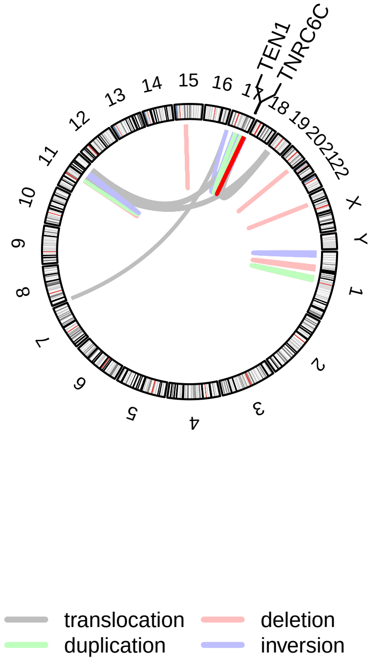


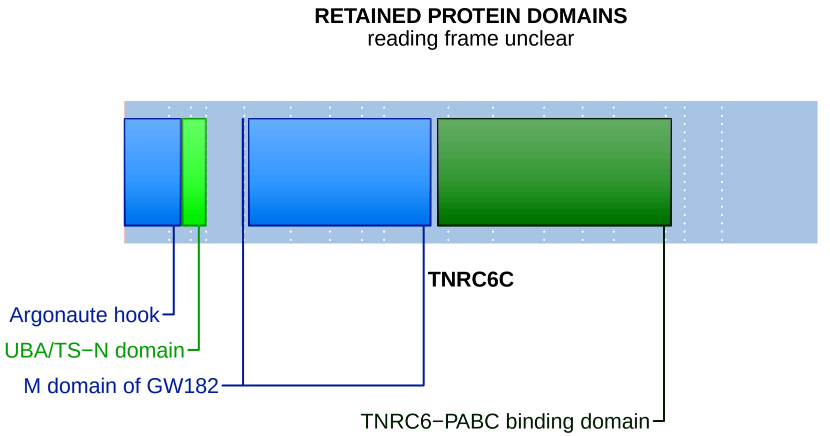


SUPPORTING READ COUNT

Split reads = 152
Discordant mates = 8

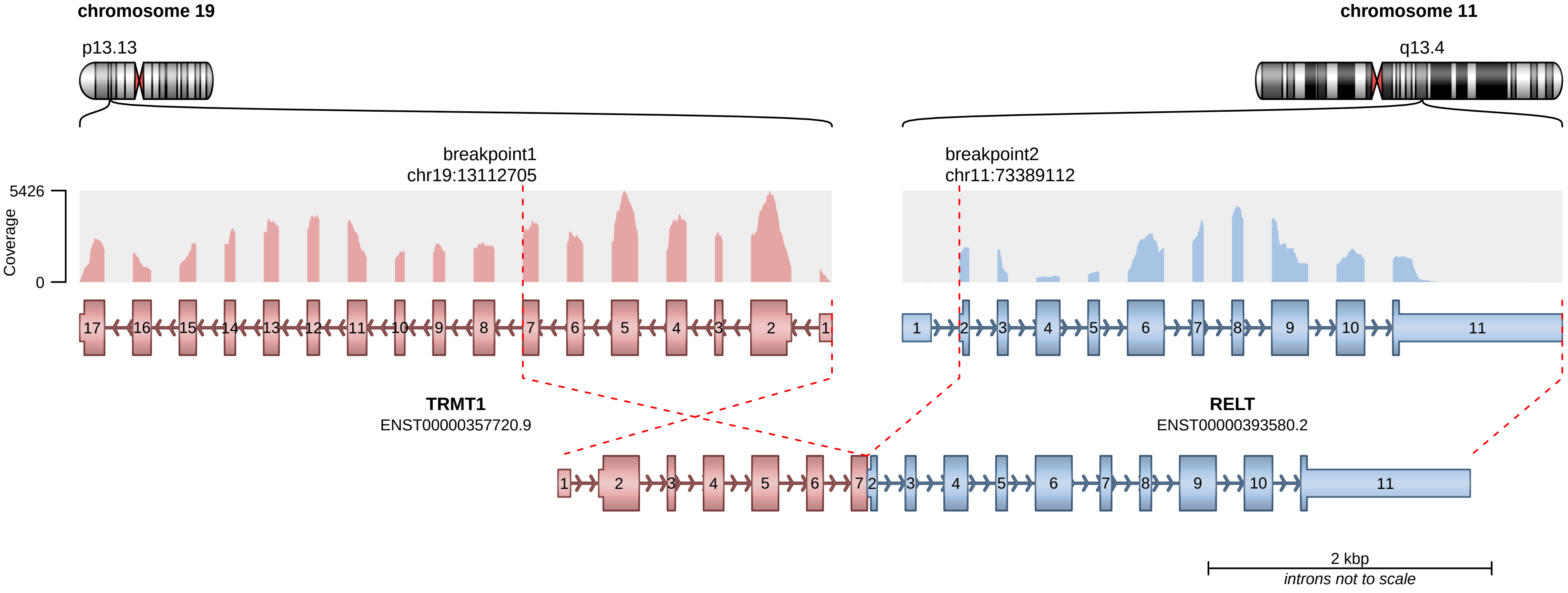


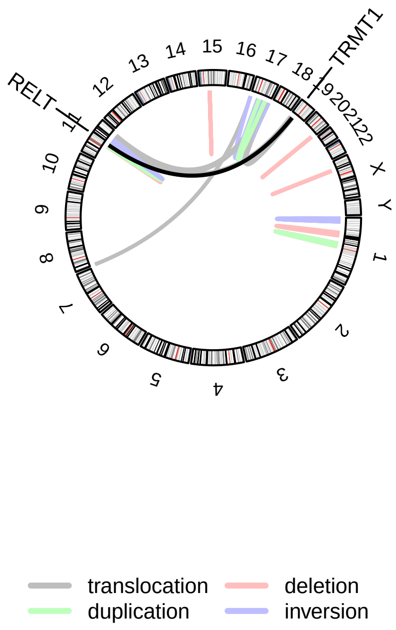




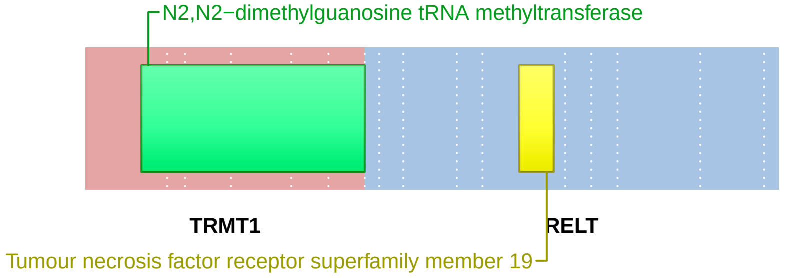
SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 1



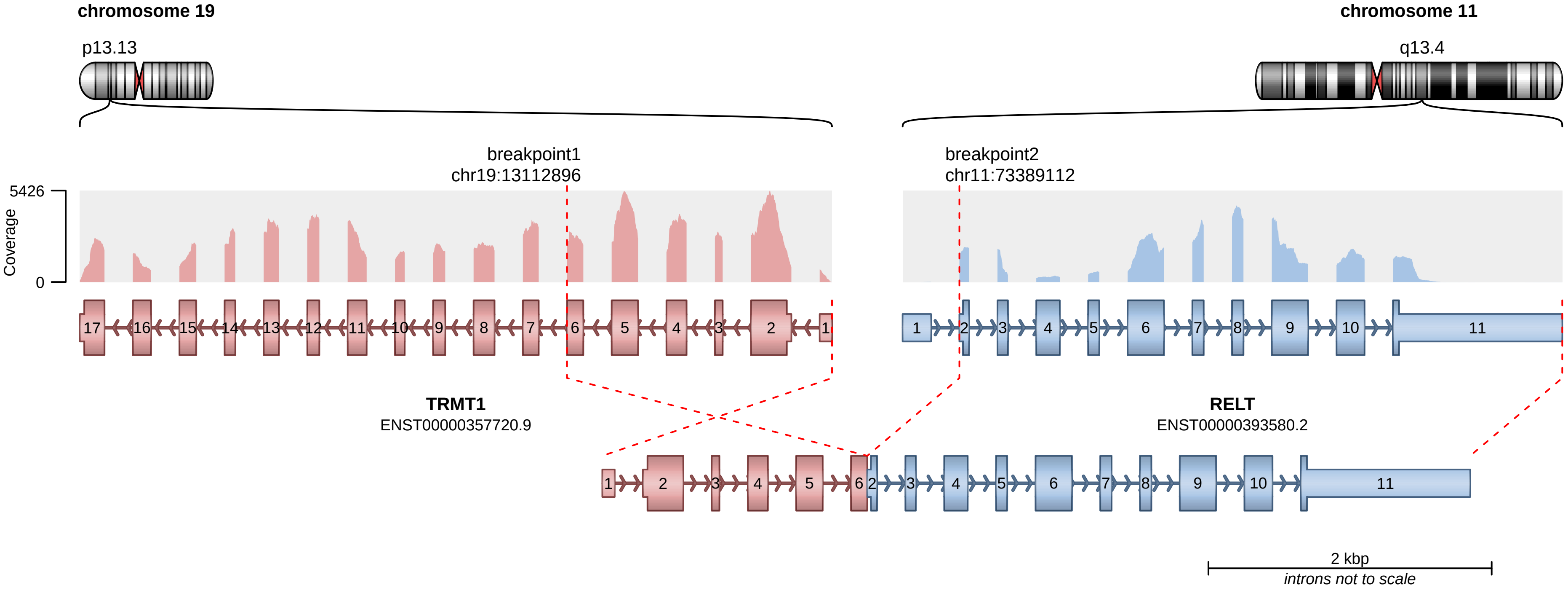


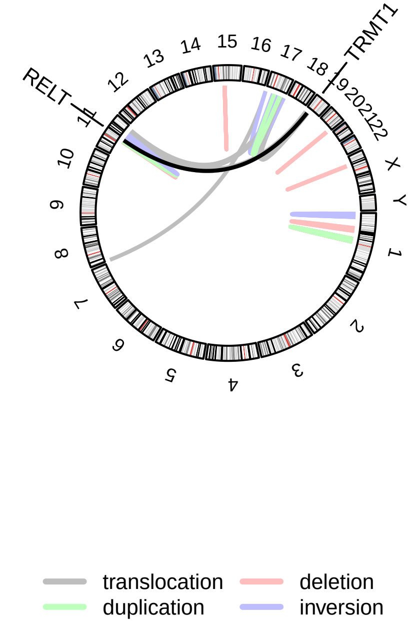
RETAINED PROTEIN DOMAINS
reading frame unclear



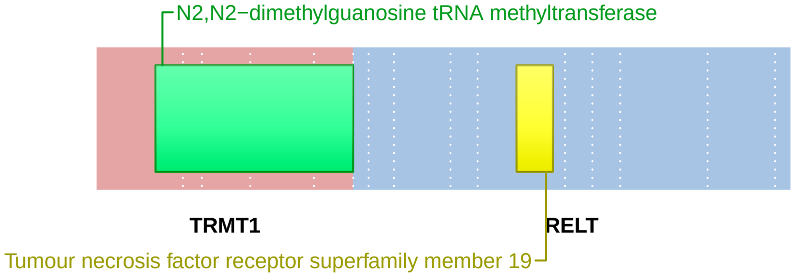
SUPPORTING READ COUNT

Split reads = 139
Discordant mates = 2



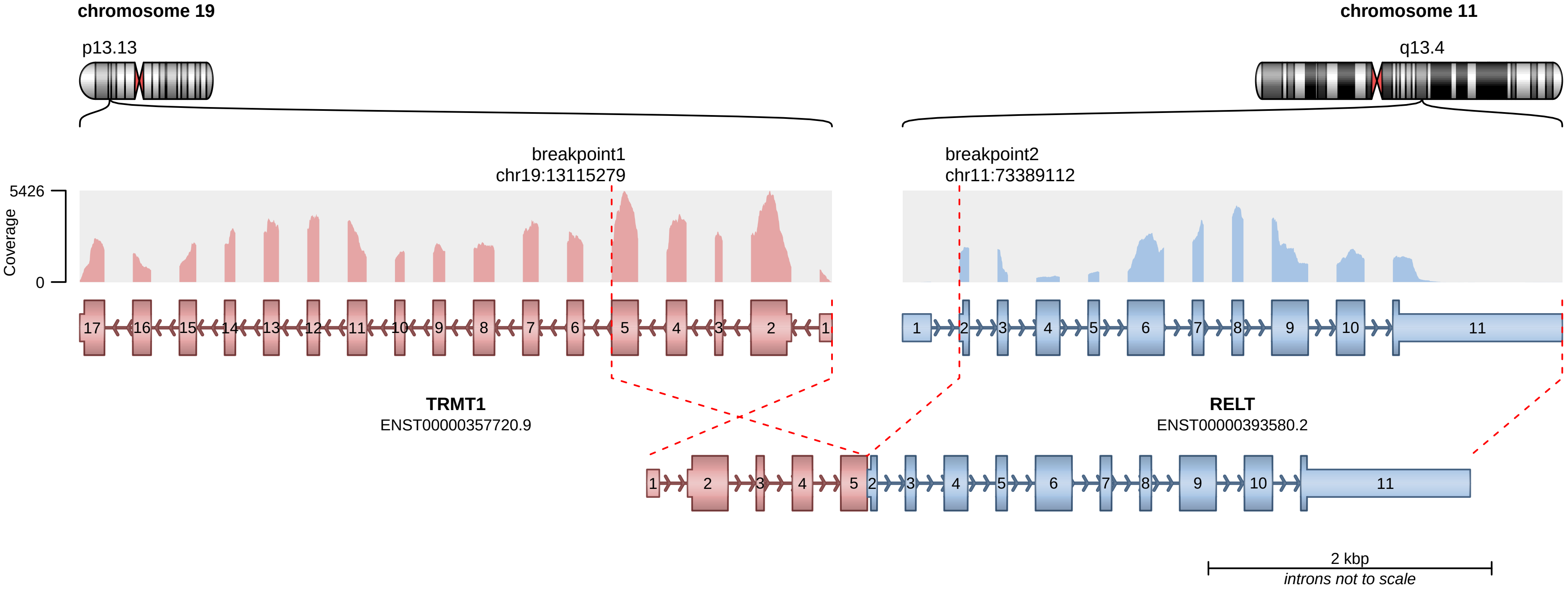


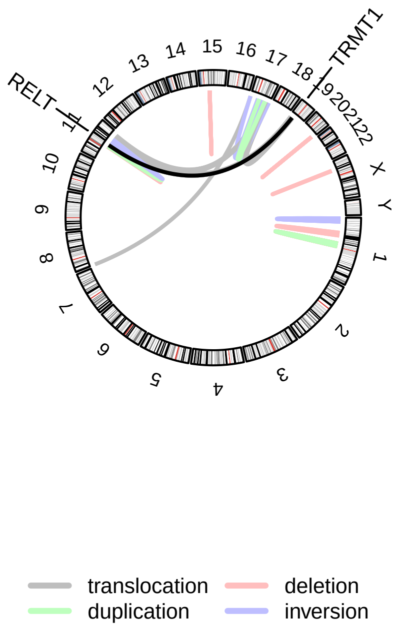
RETAINED PROTEIN DOMAINS
reading frame unclear



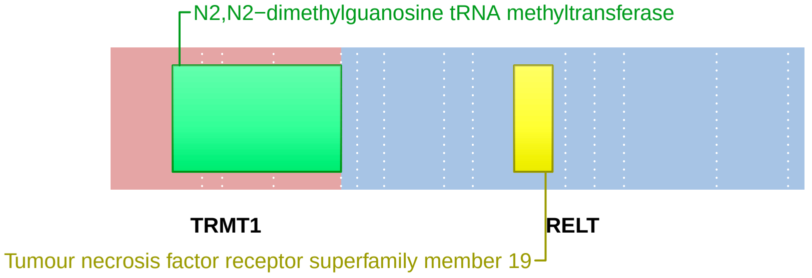
SUPPORTING READ COUNT

Split reads = 64
Discordant mates = 1



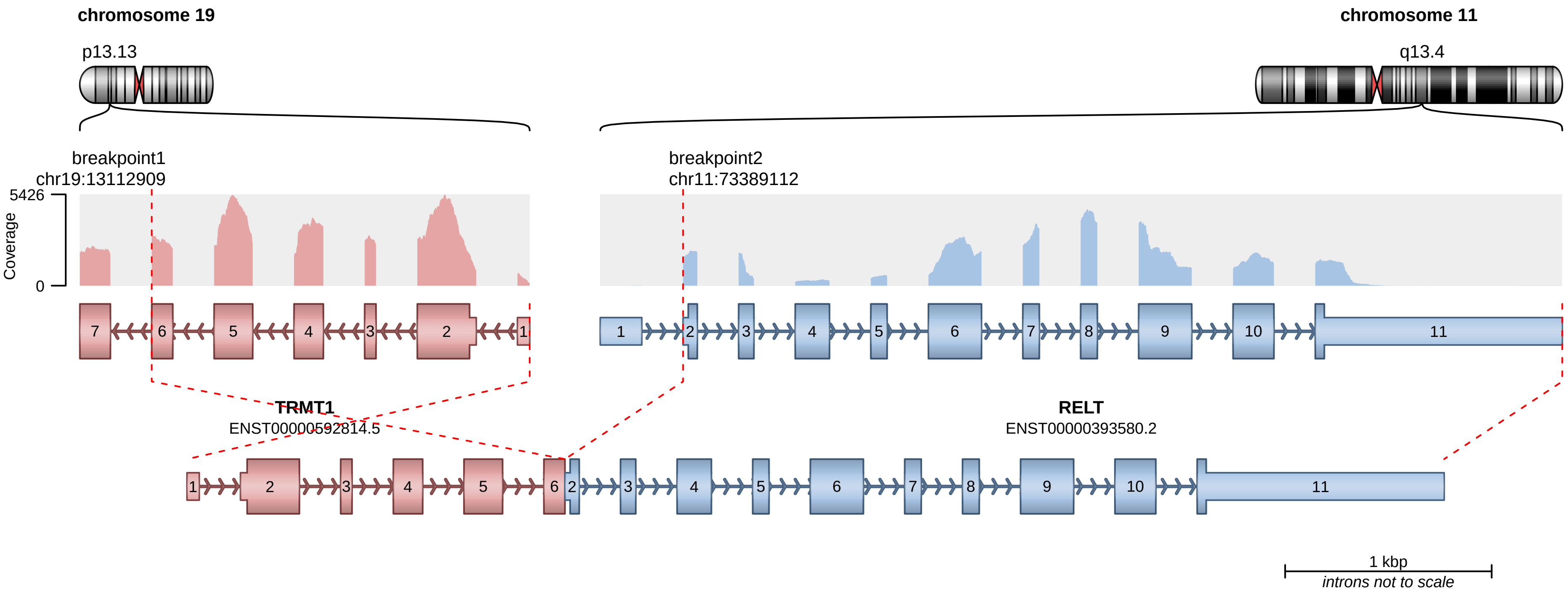


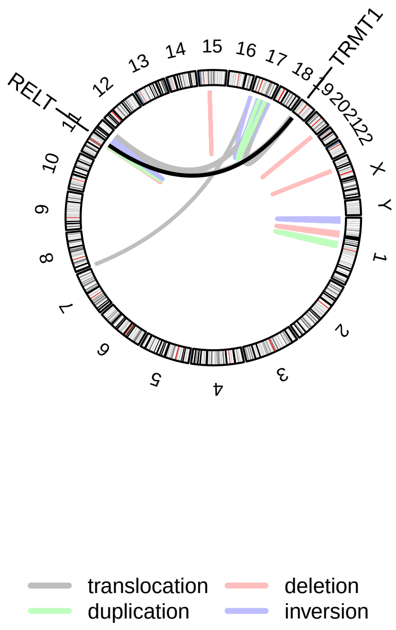
RETAINED PROTEIN DOMAINS
reading frame unclear

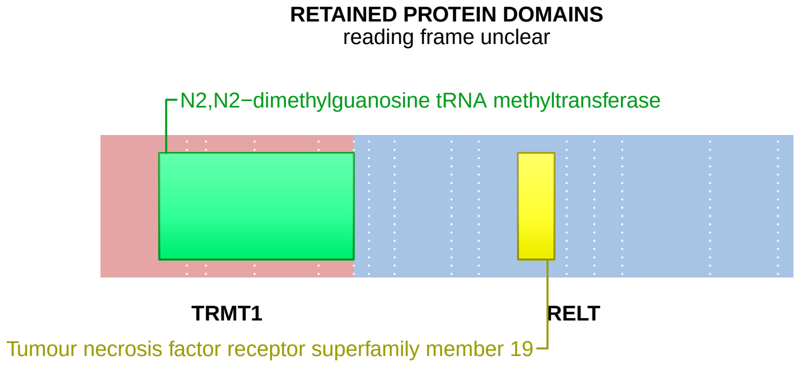


SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 0

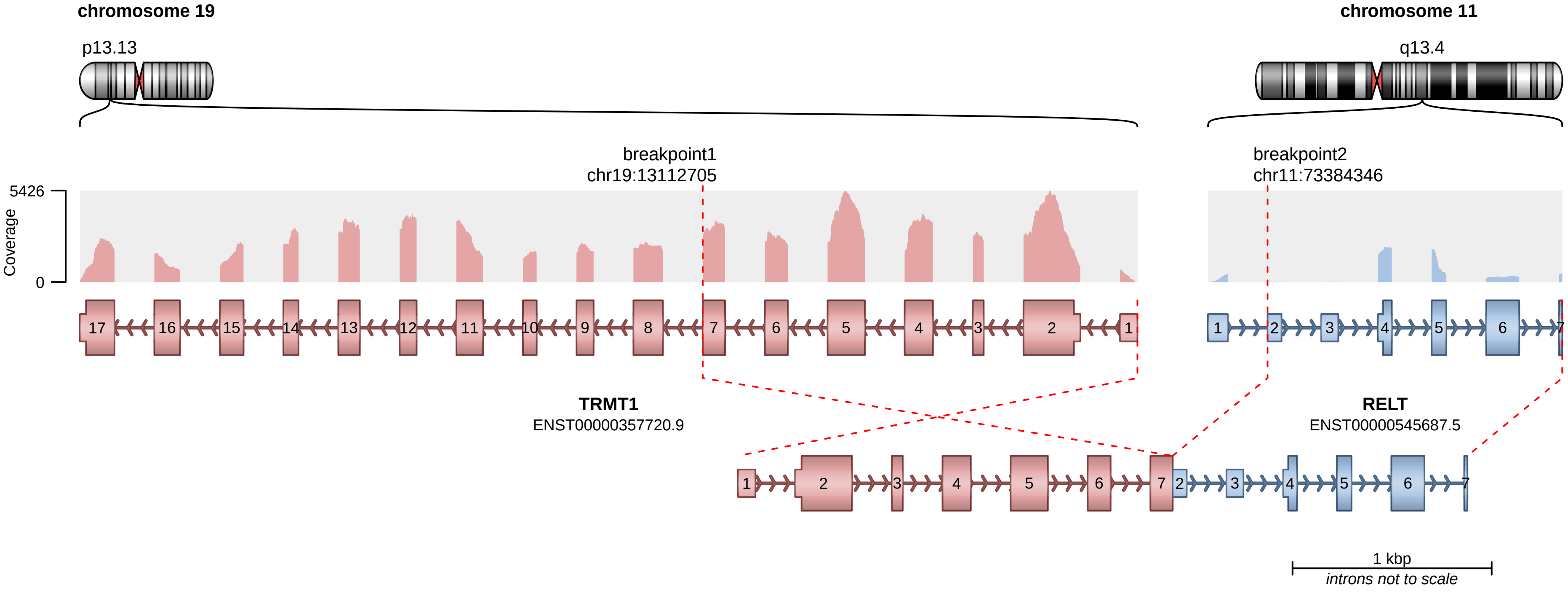


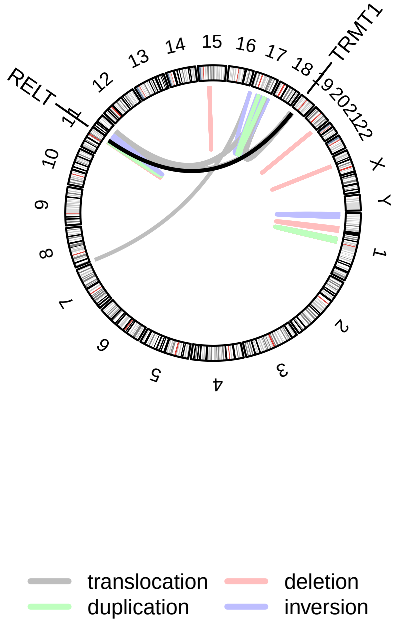


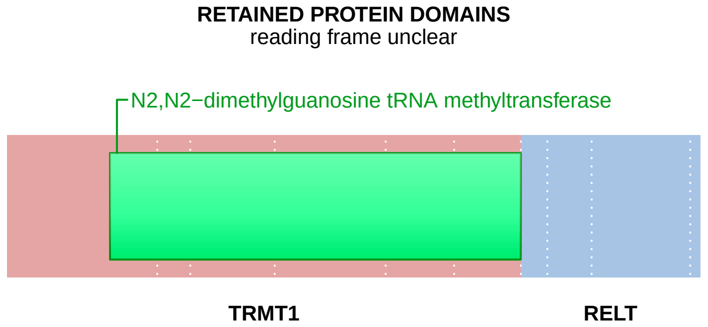


SUPPORTING READ COUNT

Split reads = 11
Discordant mates = 1

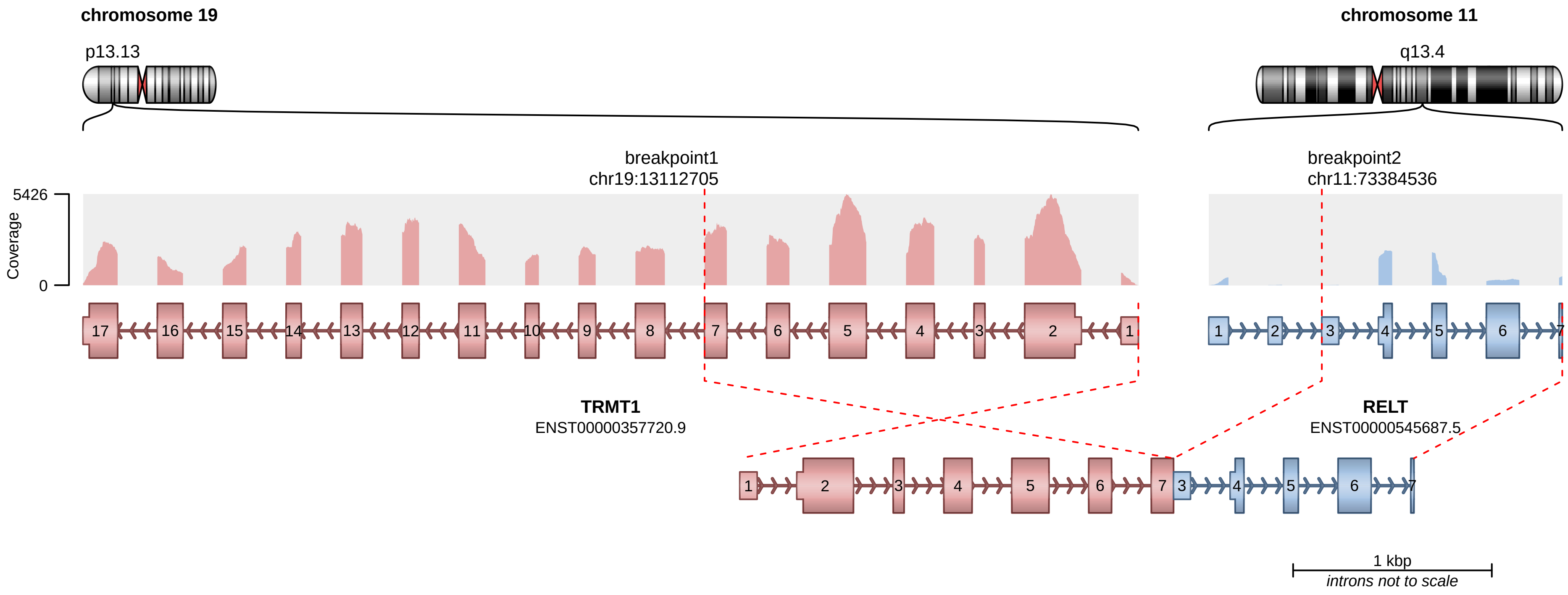


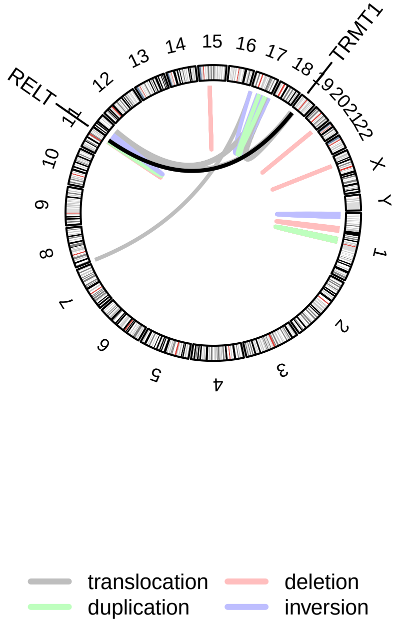




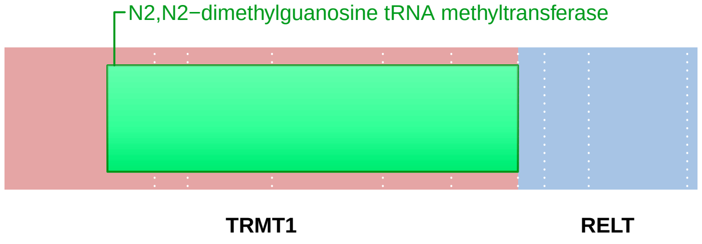
SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 2



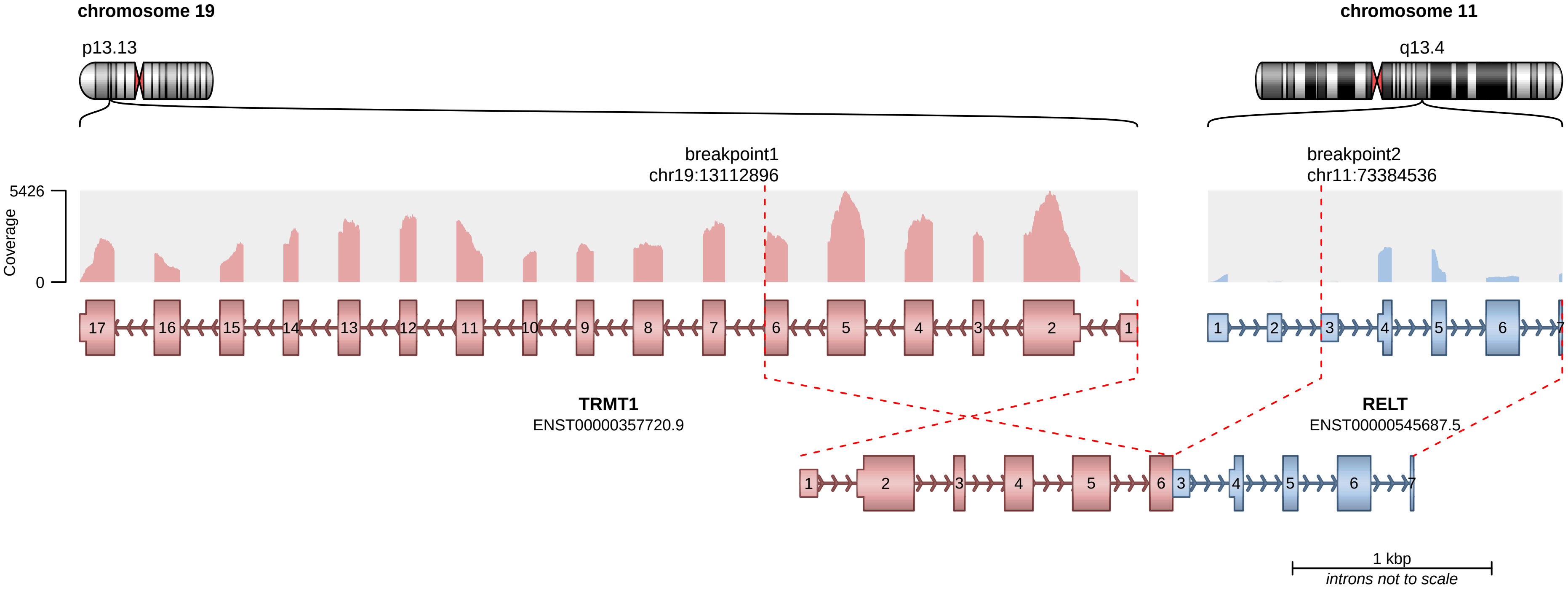


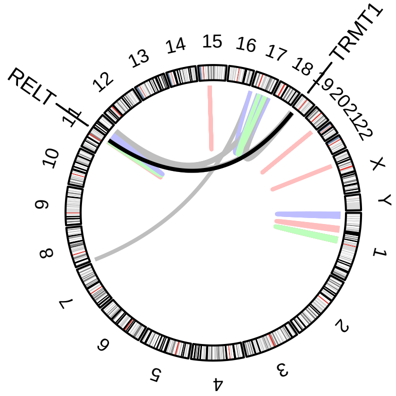
RETAINED PROTEIN DOMAINS
reading frame unclear

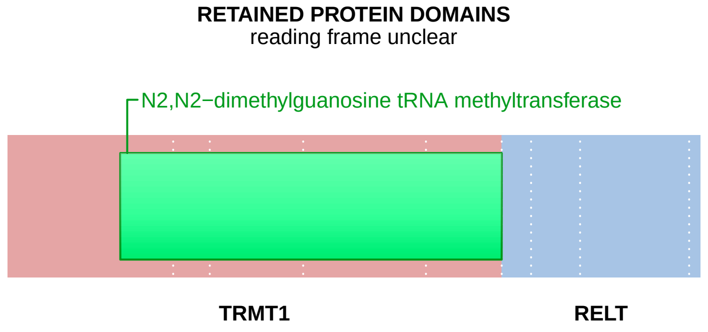


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 2



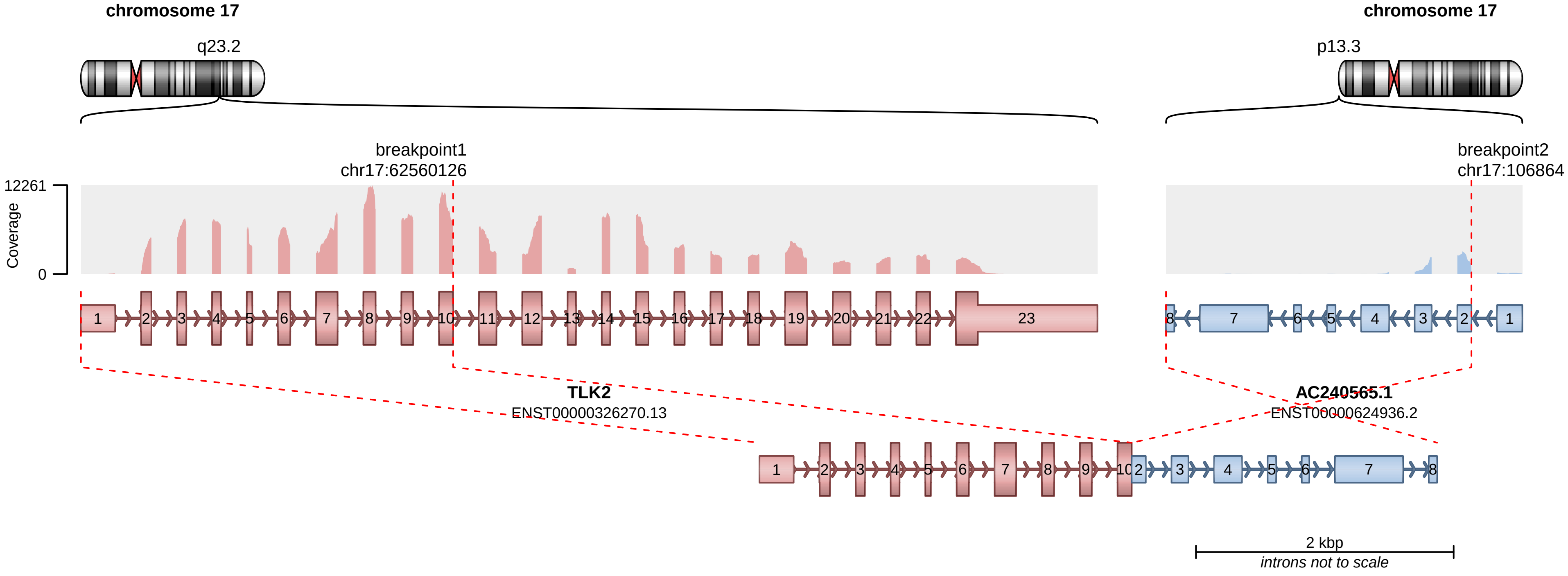


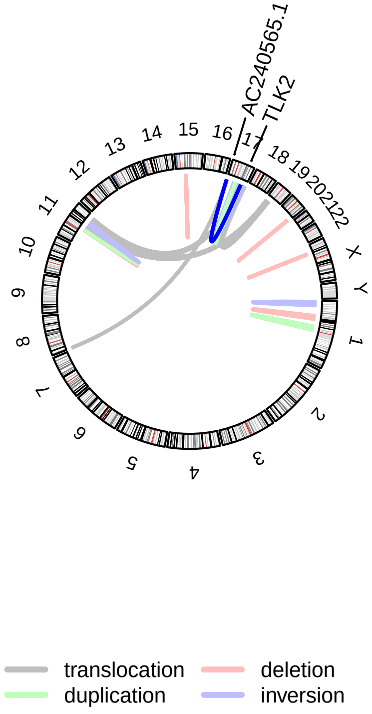


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

— translocation	— deletion
— duplication	— inversion

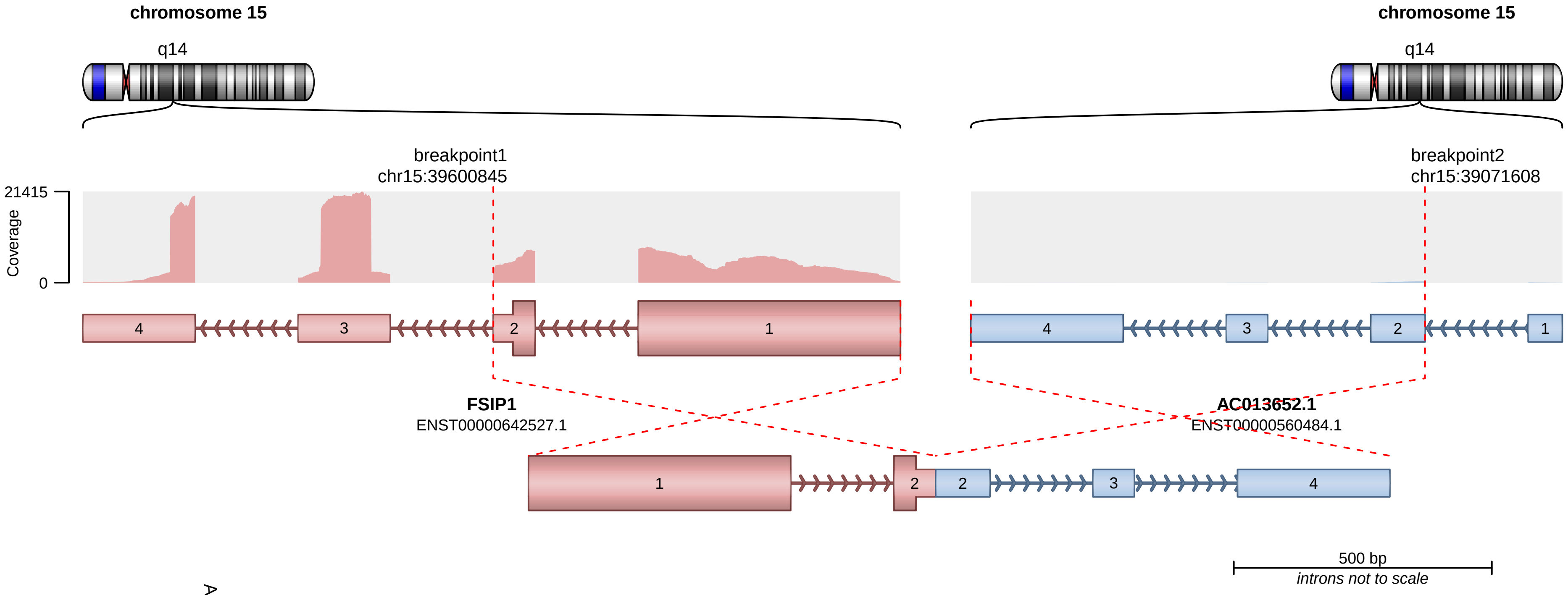


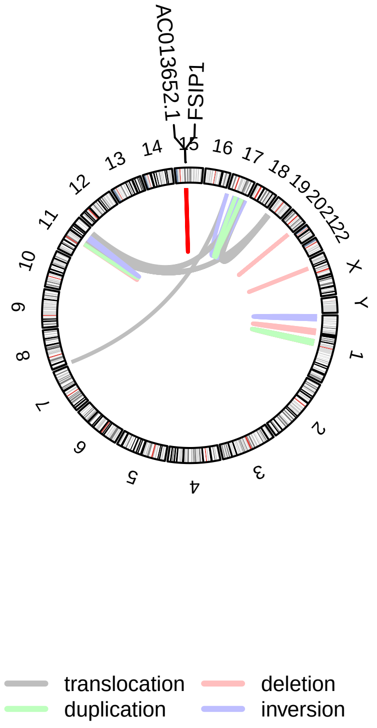


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 117
Discordant mates = 0

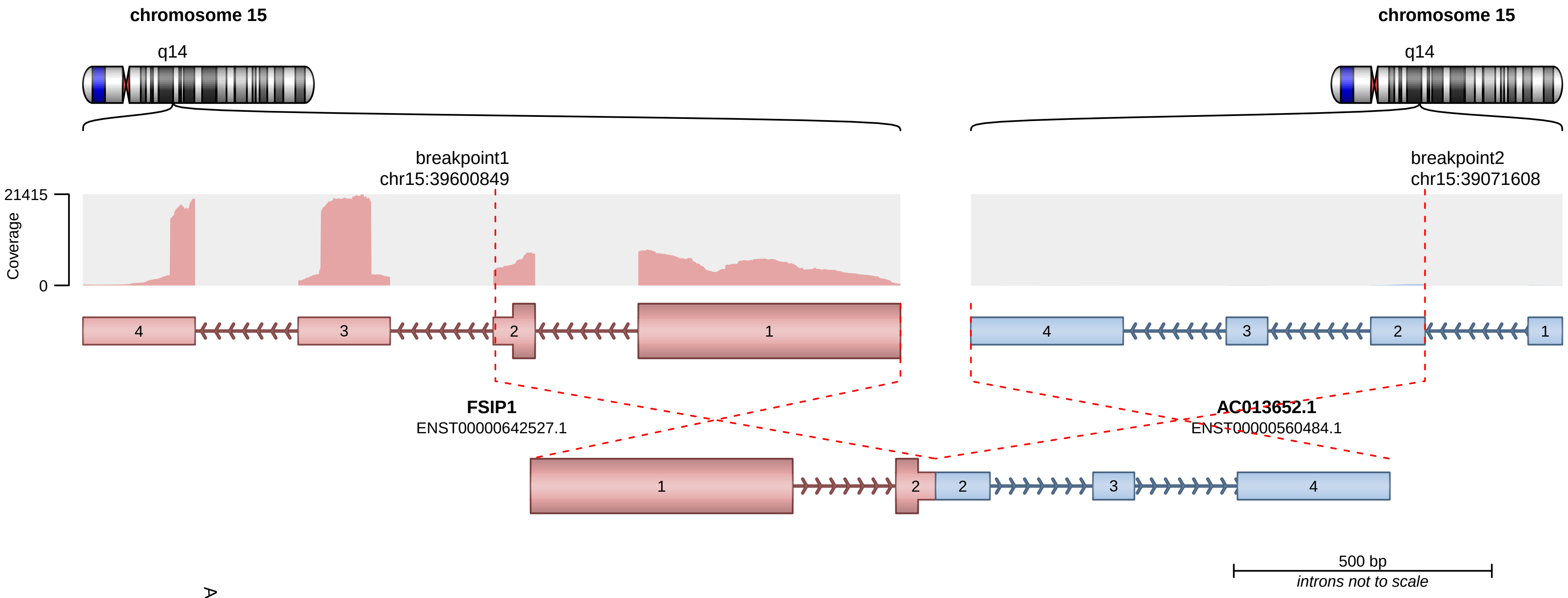


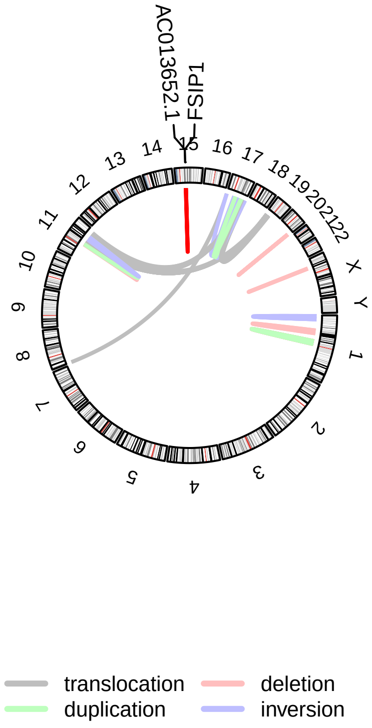


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 113
Discordant mates = 3

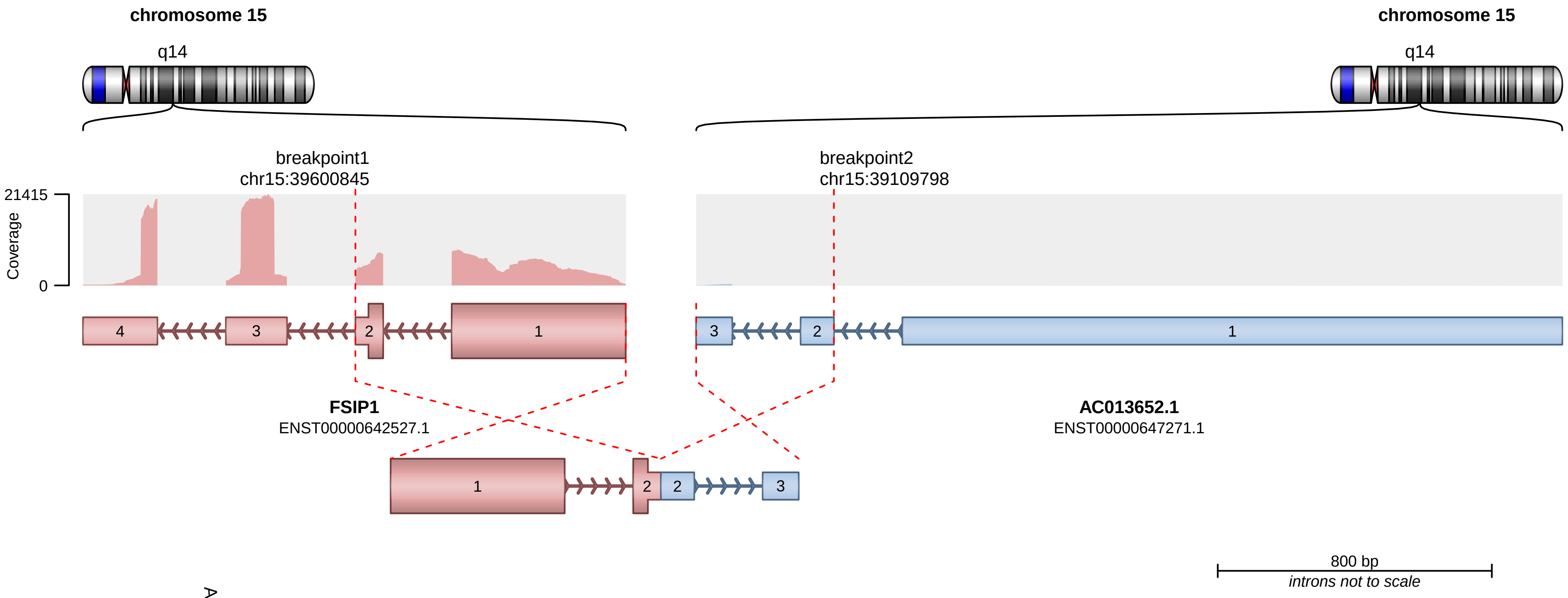


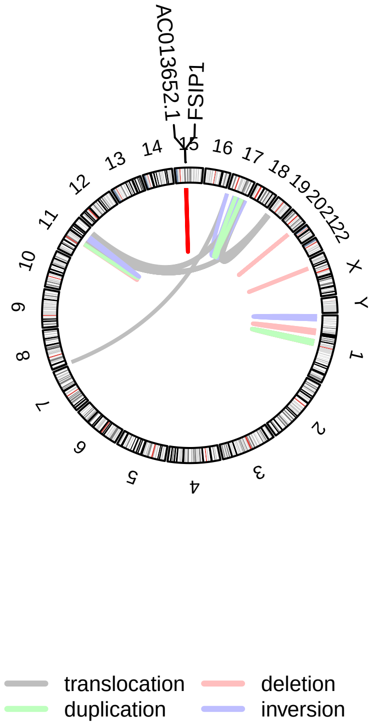


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 37
Discordant mates = 3

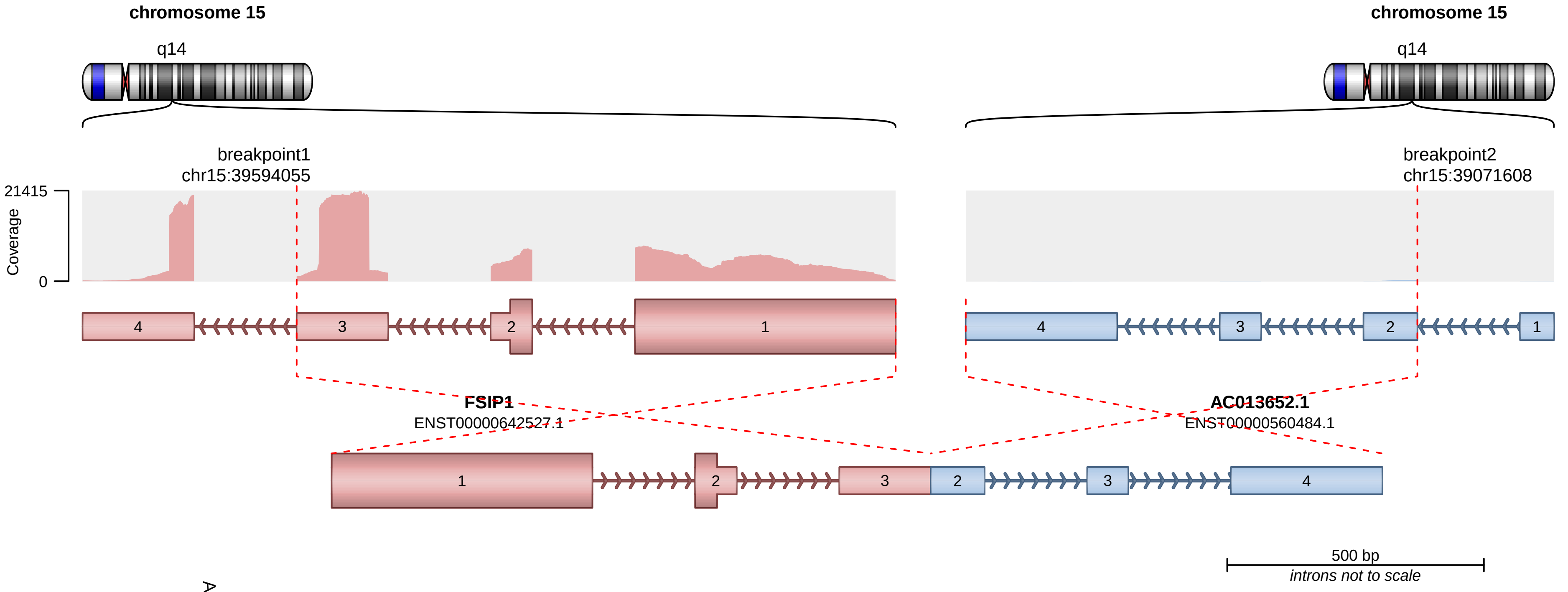


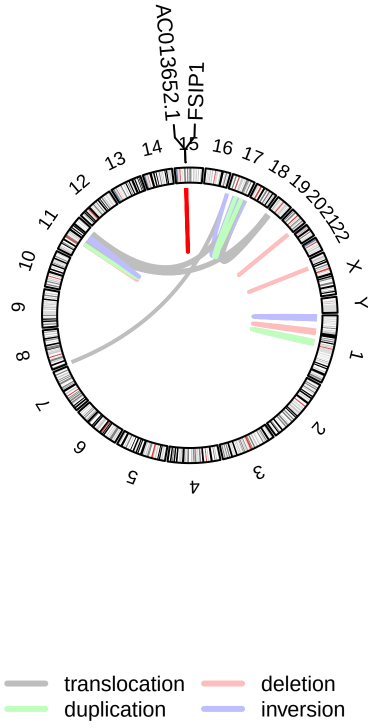


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 3

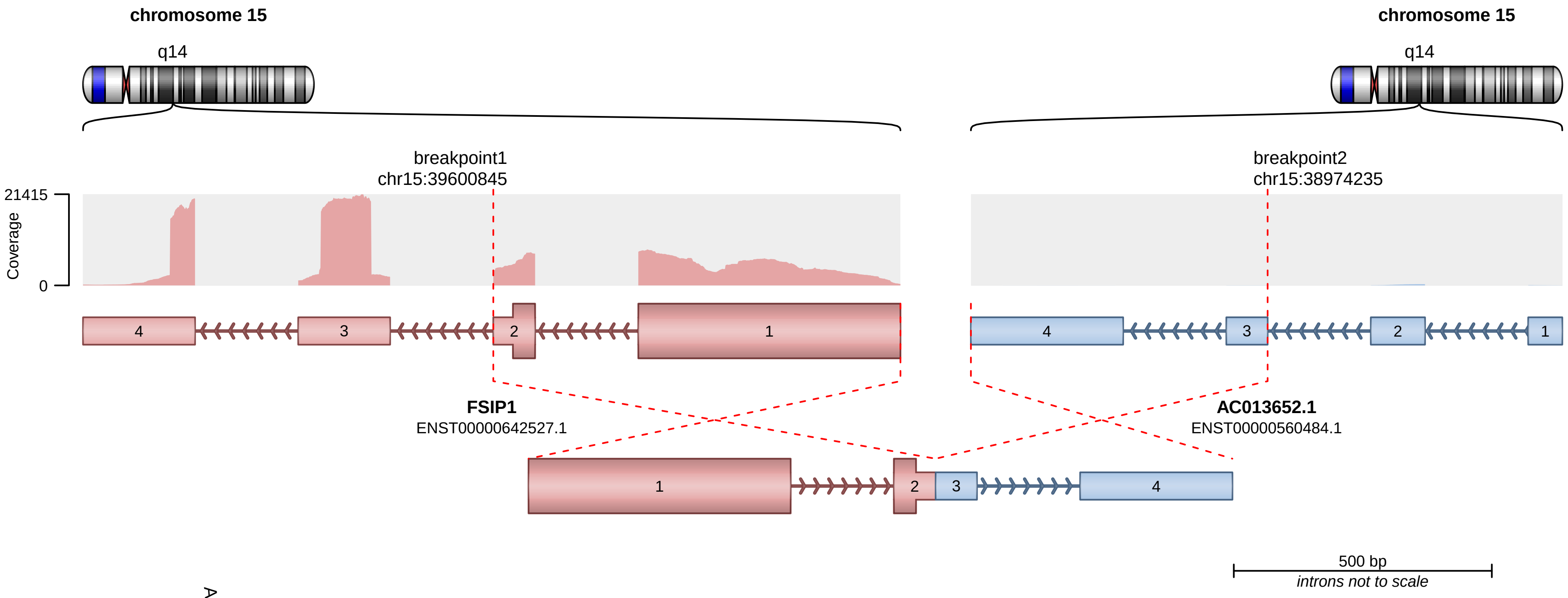


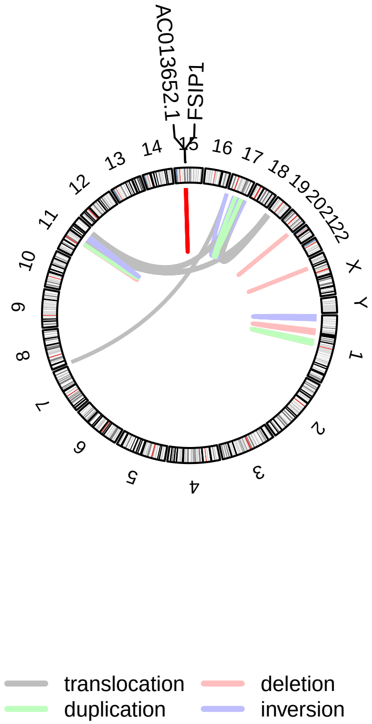


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 3

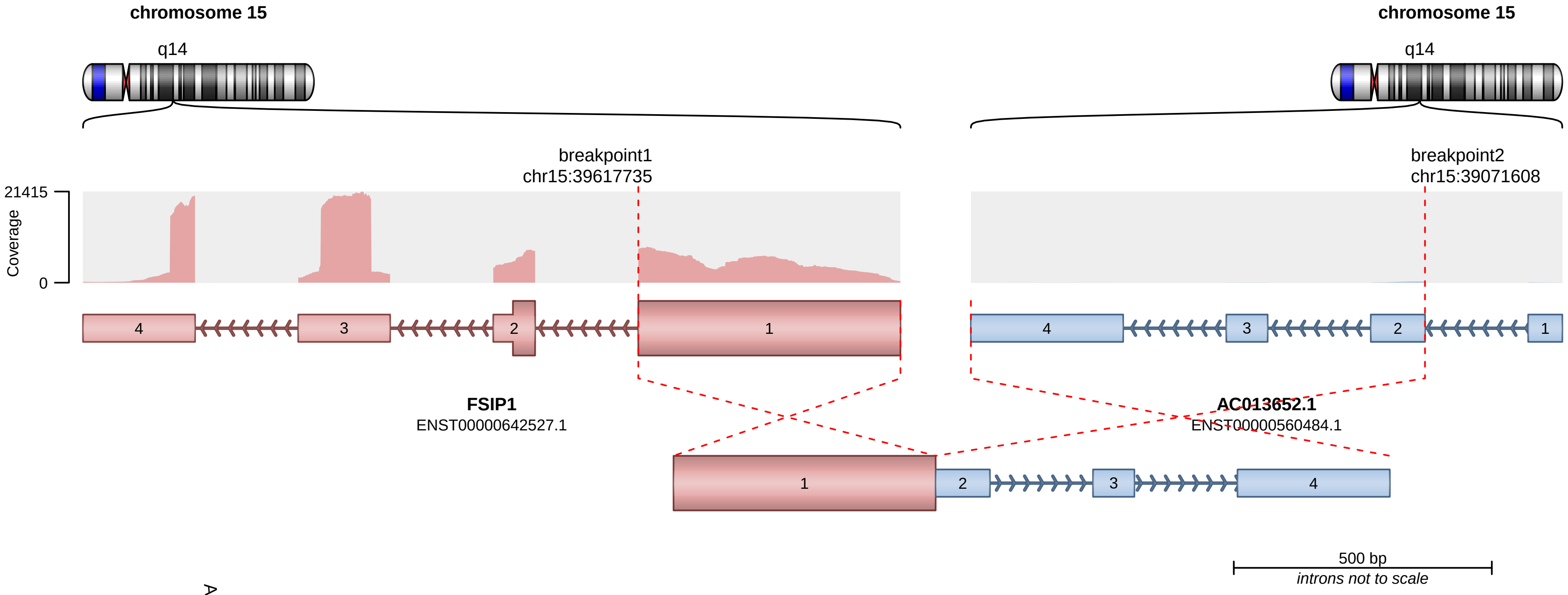


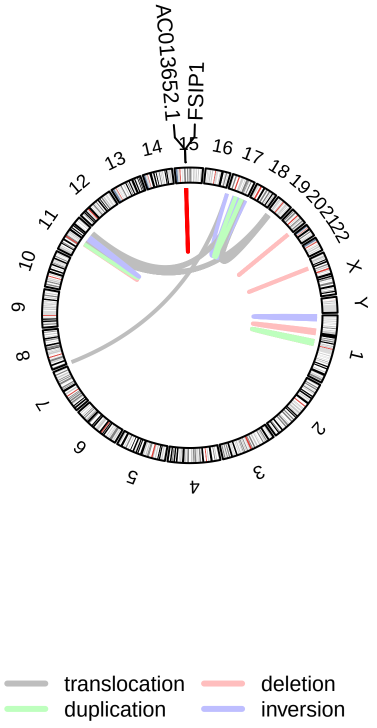


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

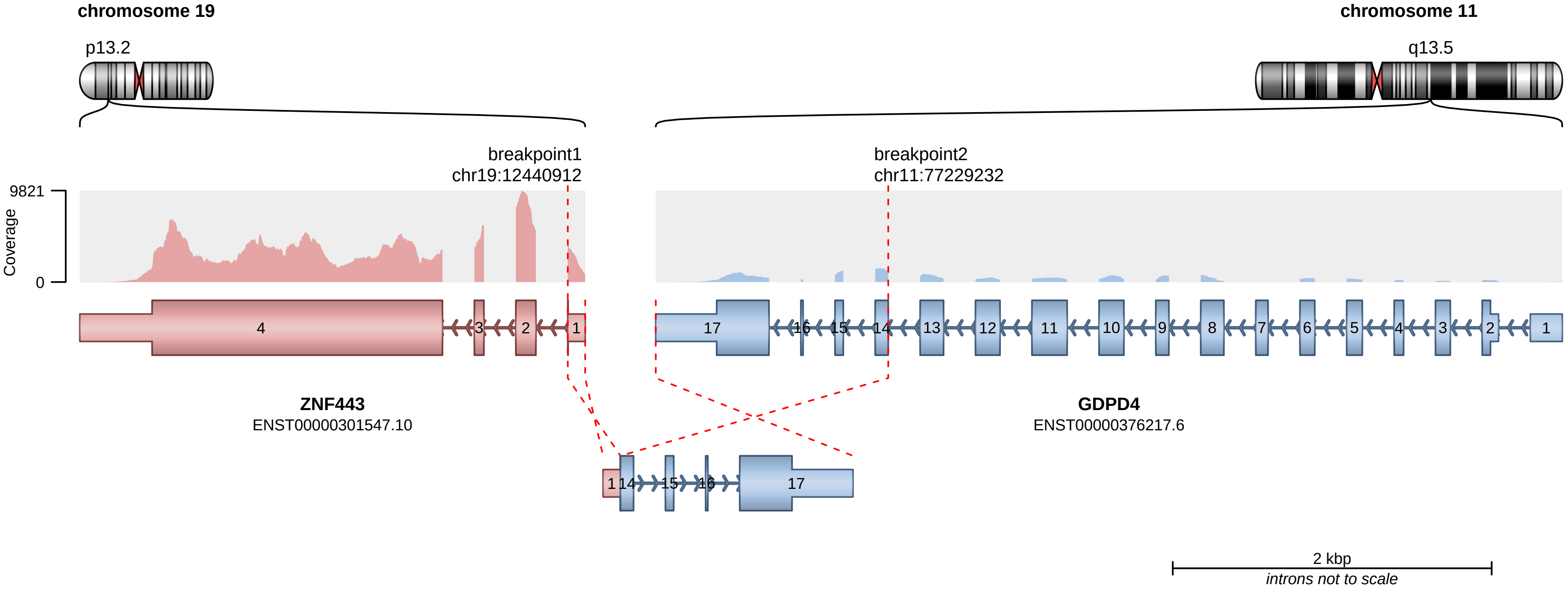


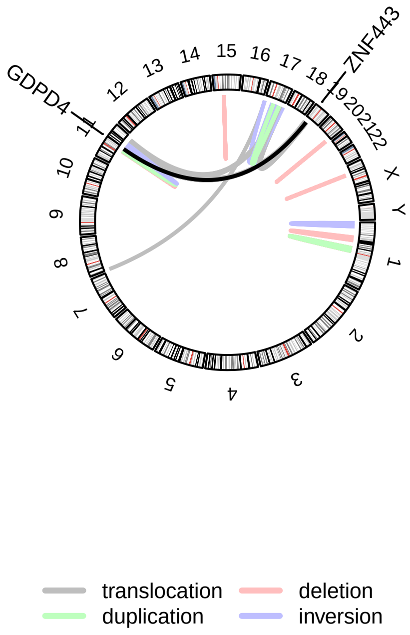


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

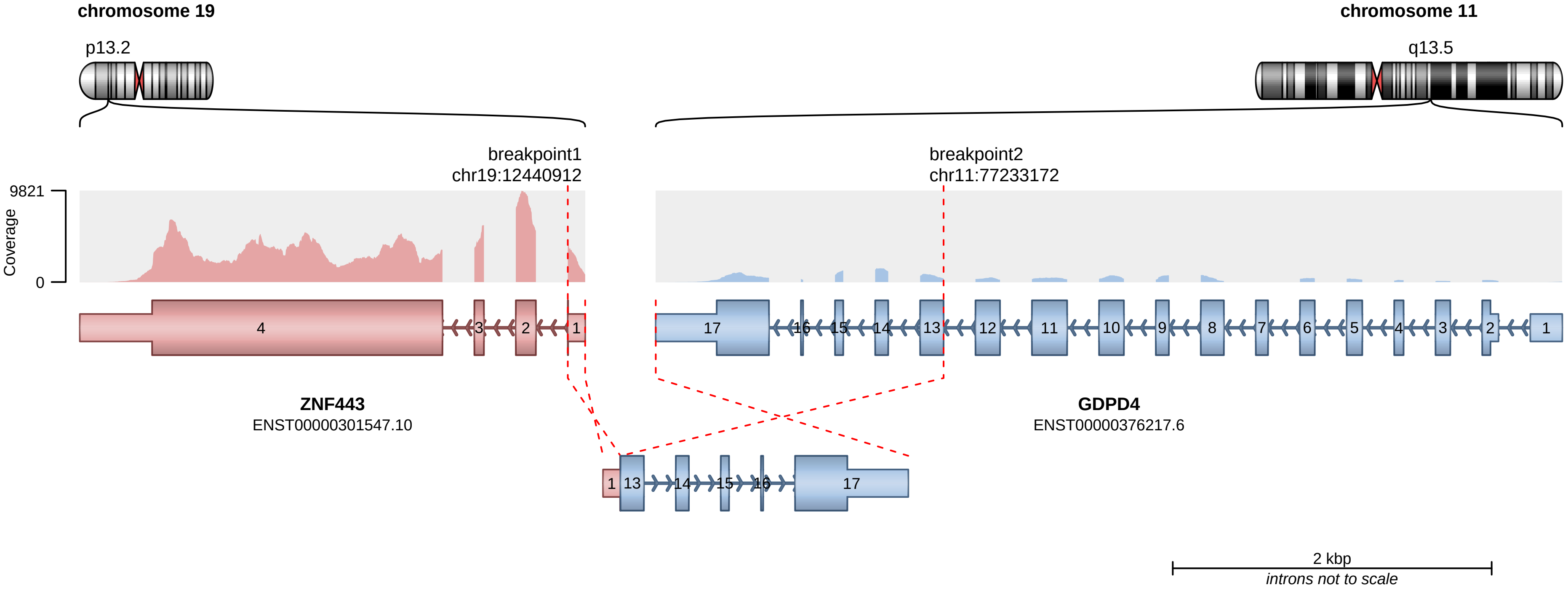


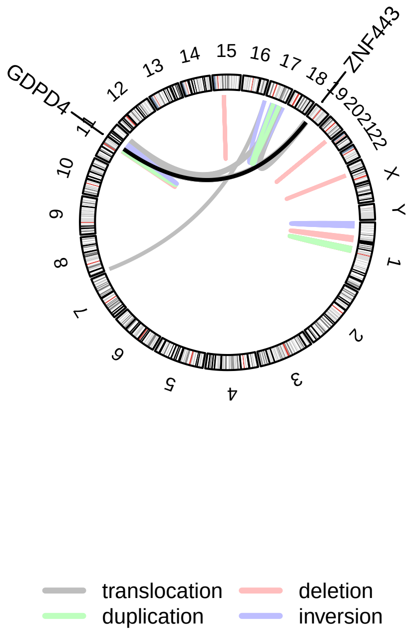


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 104
Discordant mates = 0

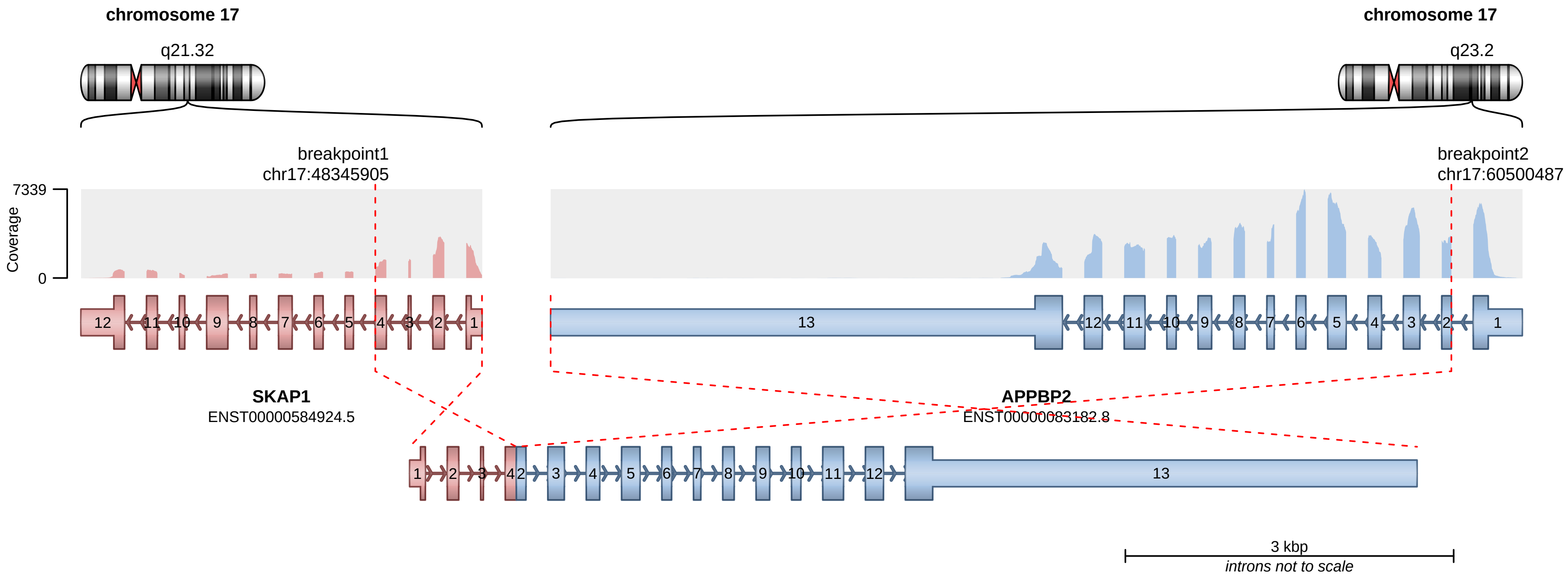


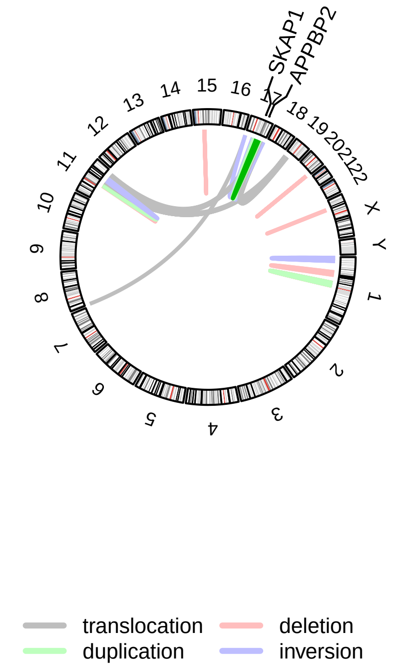


No protein domains retained in fusion.

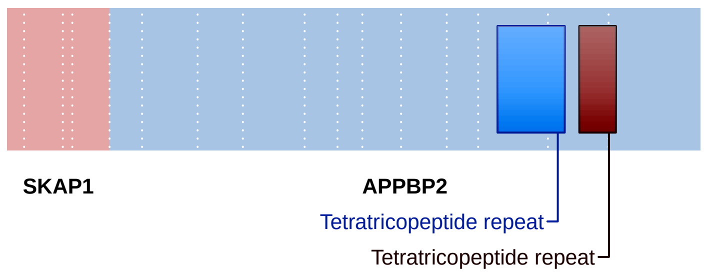
SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 0



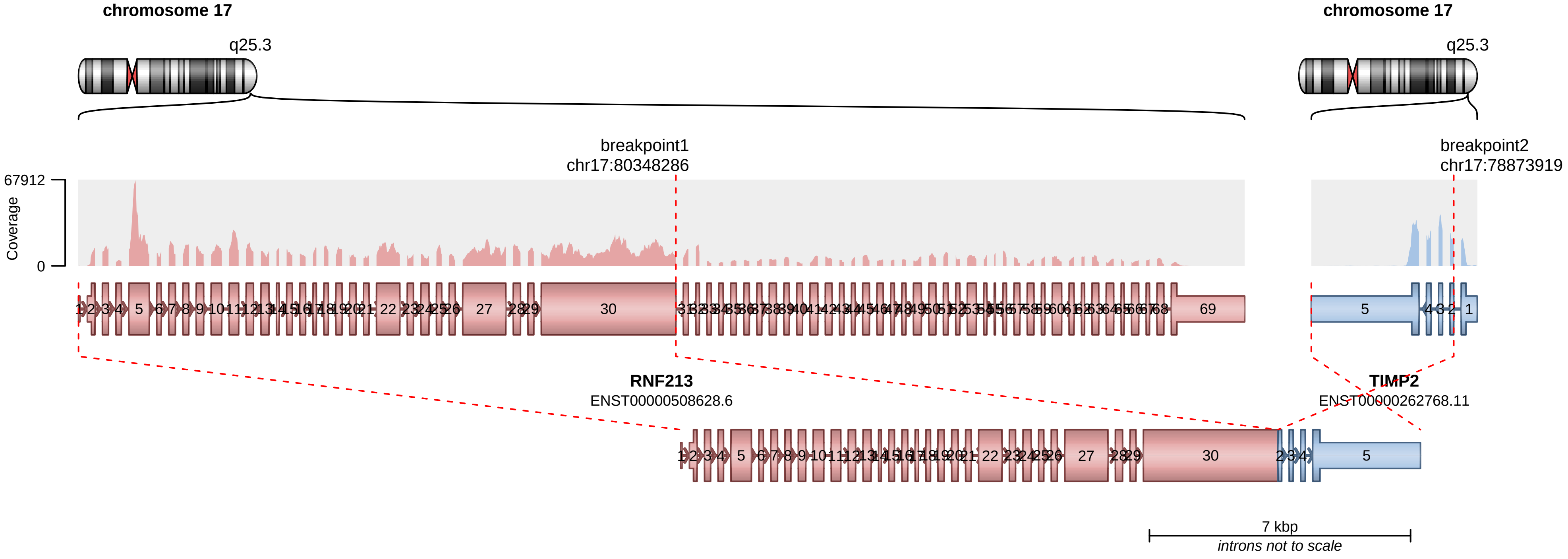


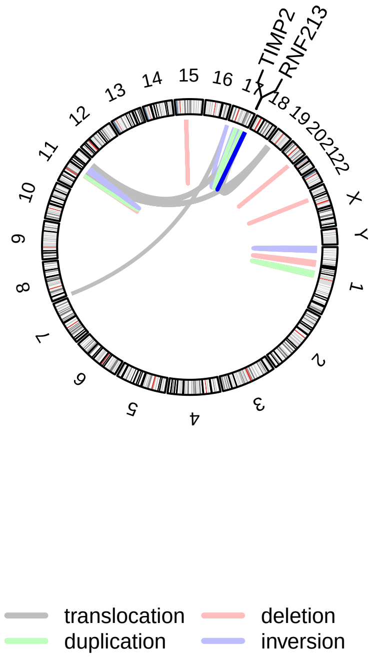
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 78
Discordant mates = 2



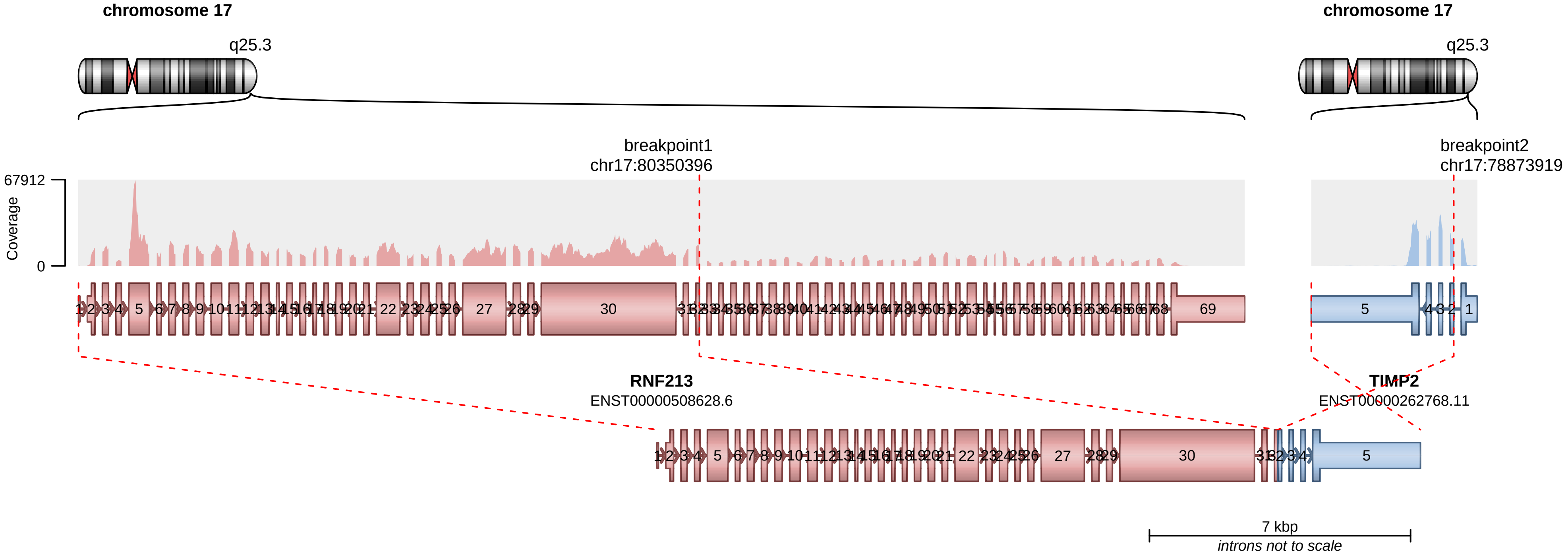


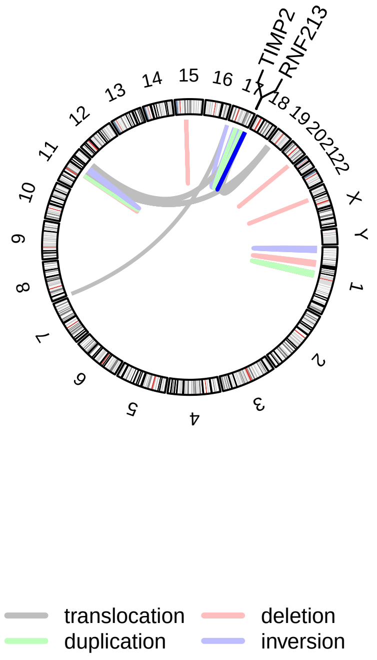
RETAINED PROTEIN DOMAINS

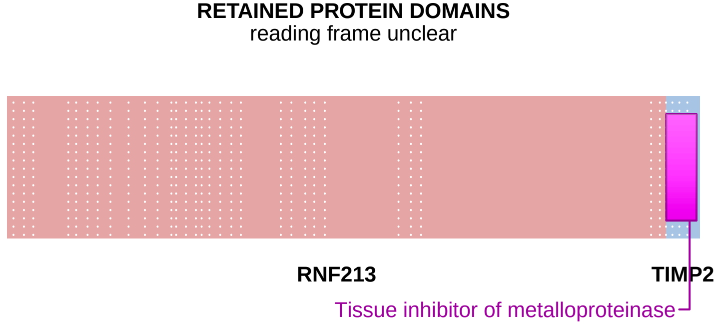
reading frame unclear

SUPPORTING READ COUNT

Split reads = 76
Discordant mates = 1

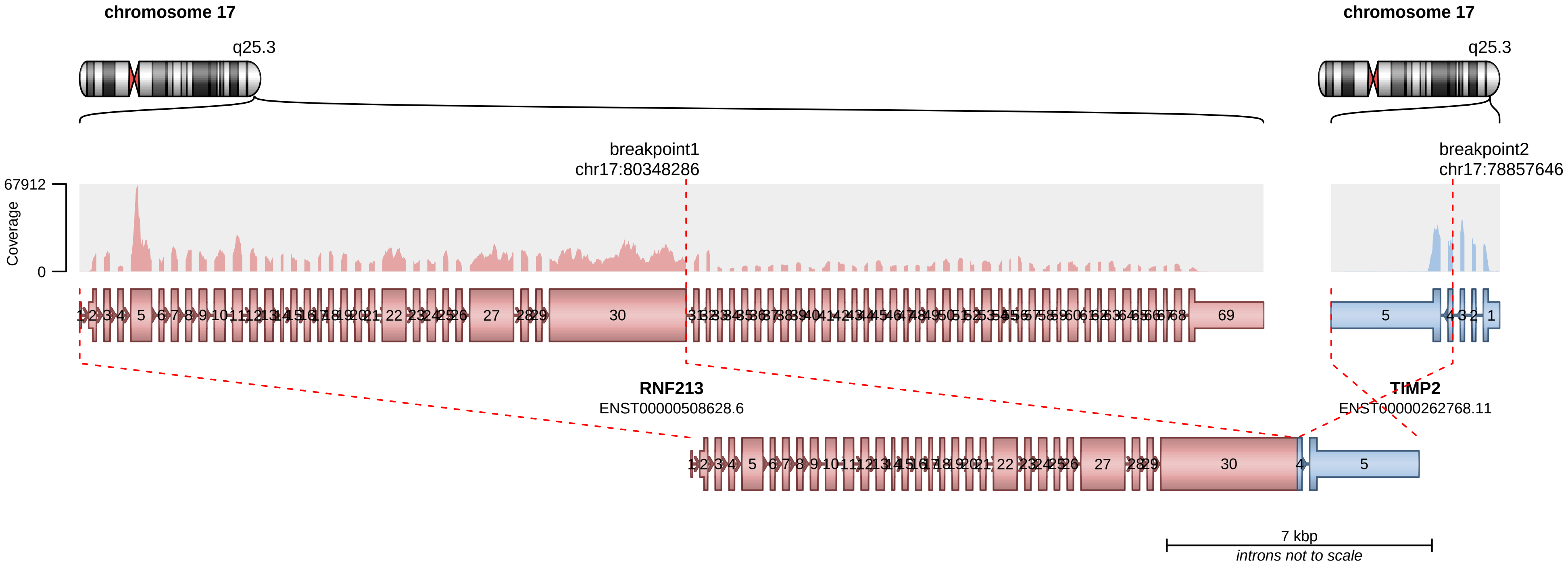


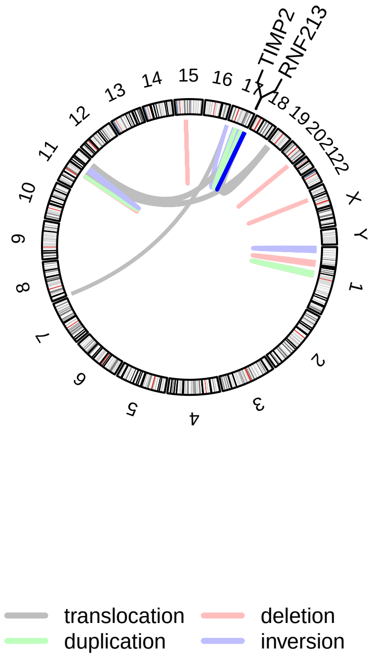


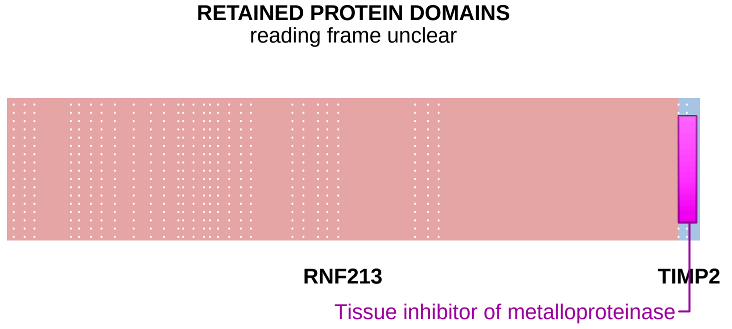


SUPPORTING READ COUNT

Split reads = 38
Discordant mates = 1

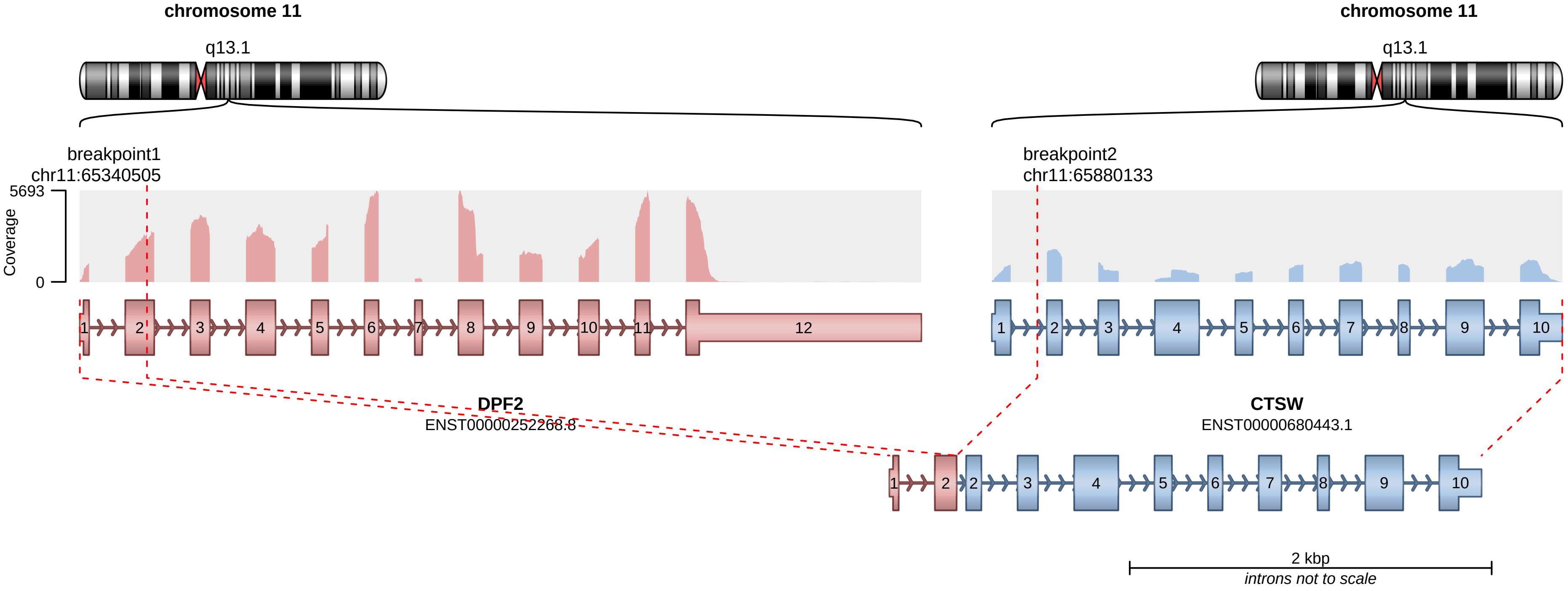


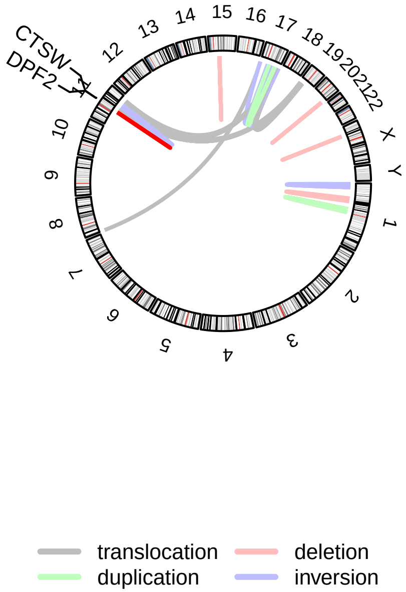




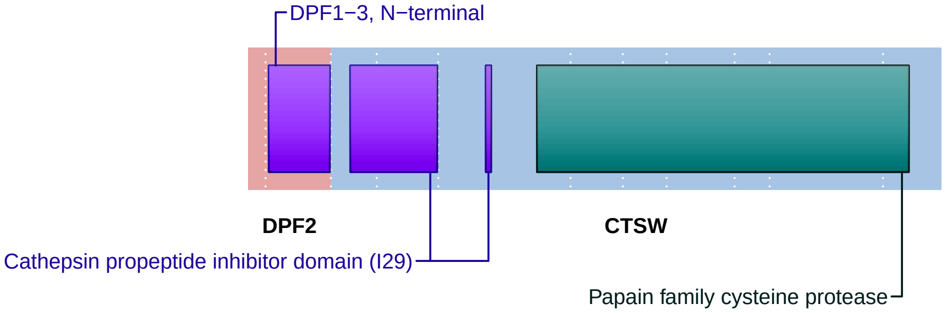
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



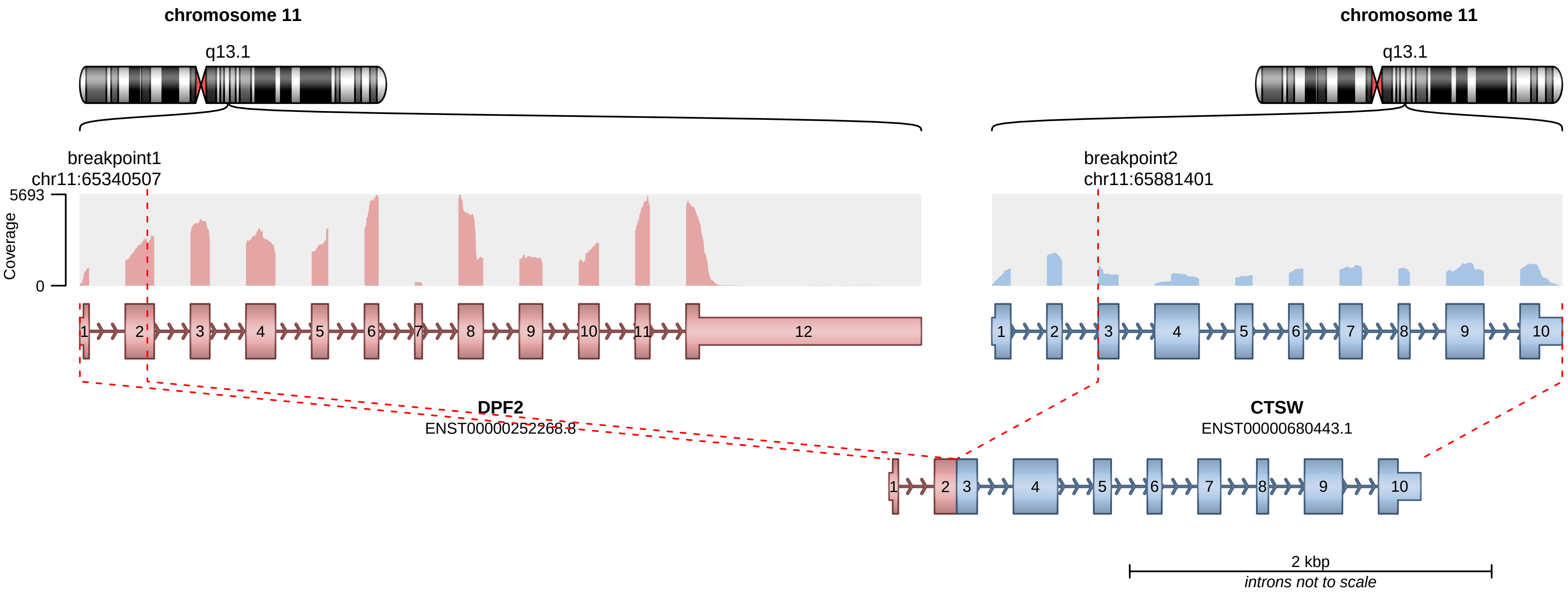


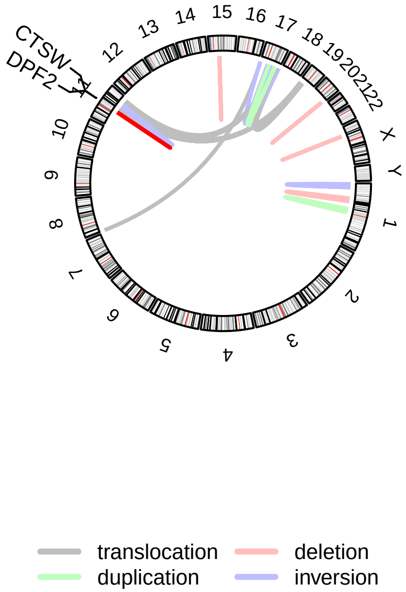
RETAINED PROTEIN DOMAINS
reading frame unclear



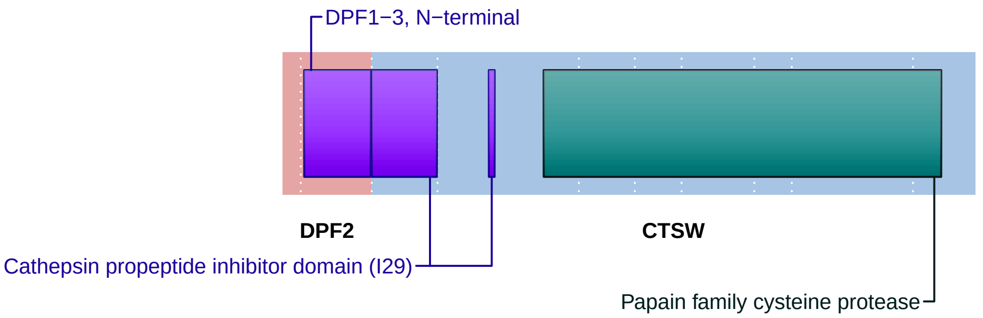
SUPPORTING READ COUNT

Split reads = 60
Discordant mates = 4



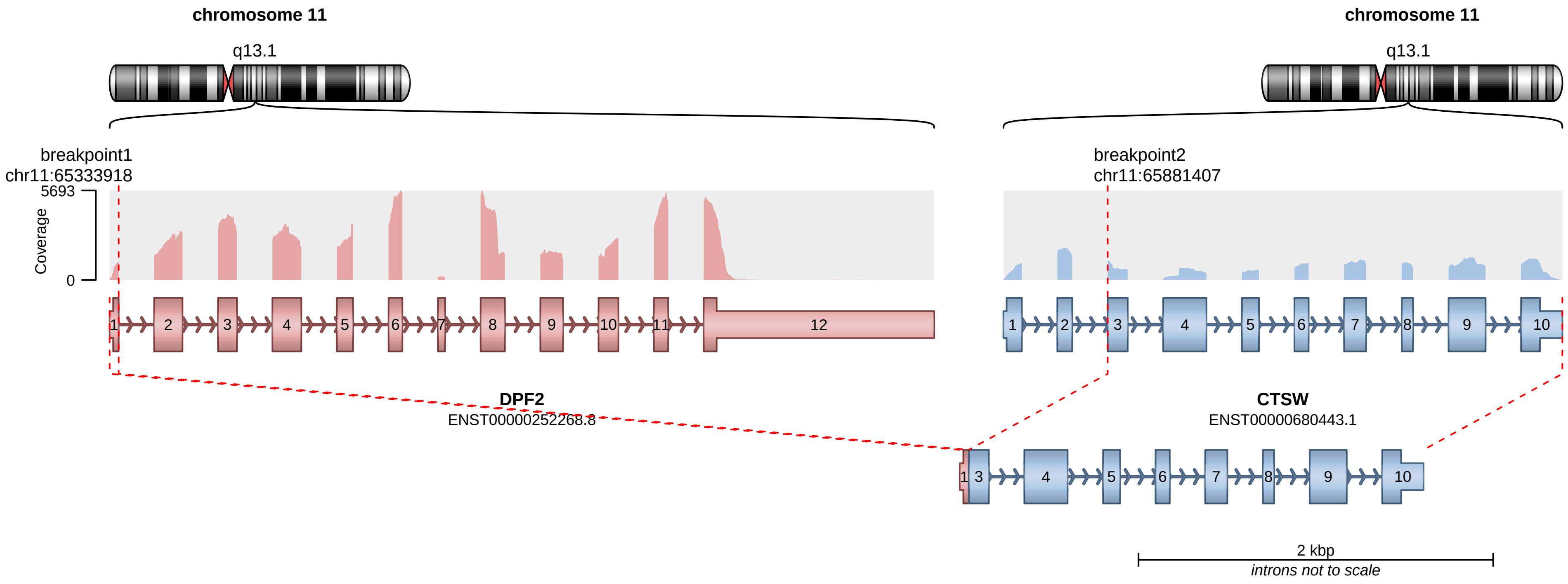


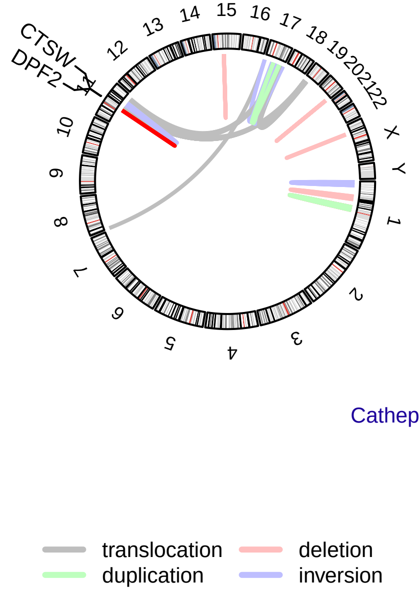
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

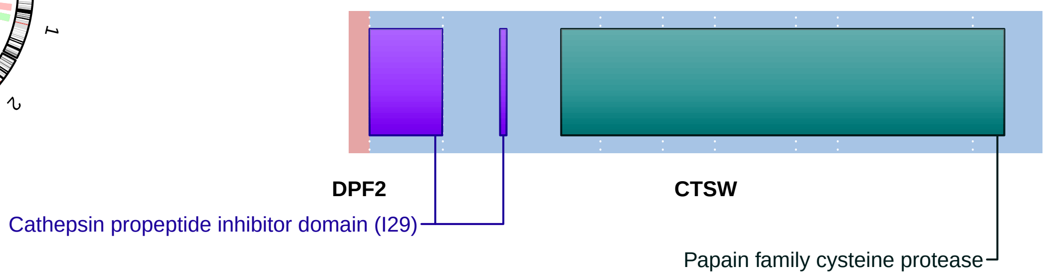
Split reads = 13
Discordant mates = 0





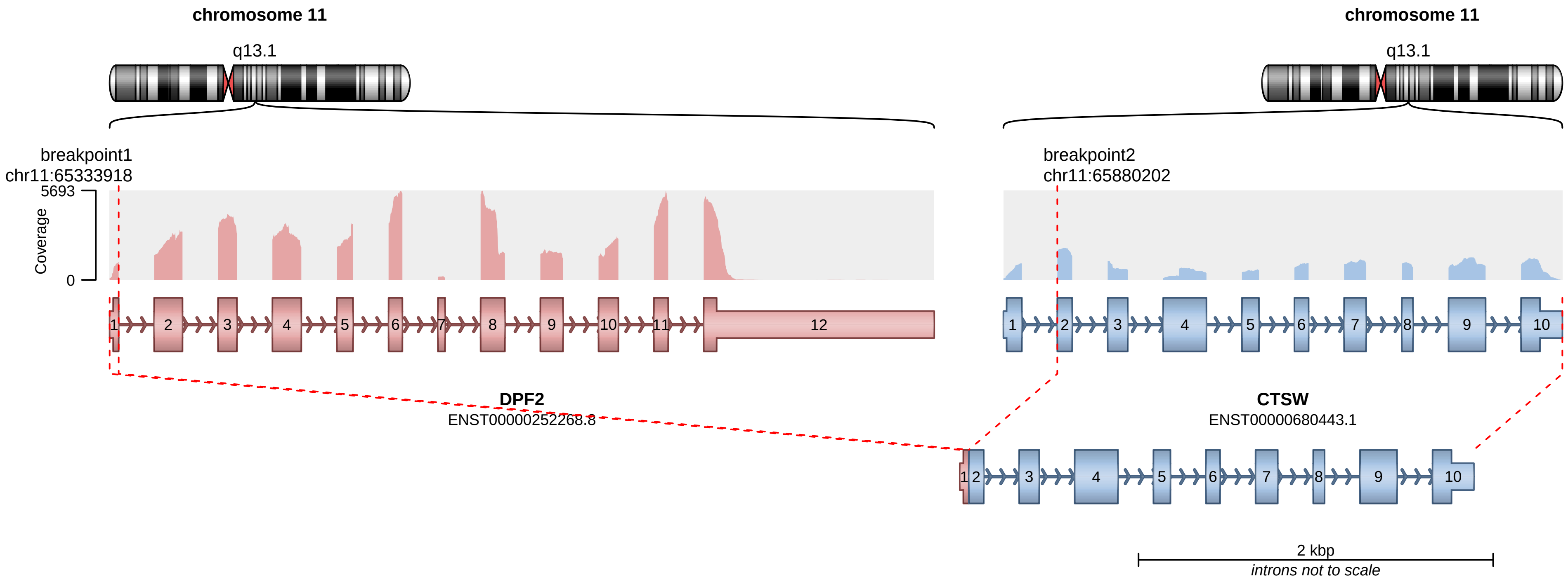
RETAINED PROTEIN DOMAINS

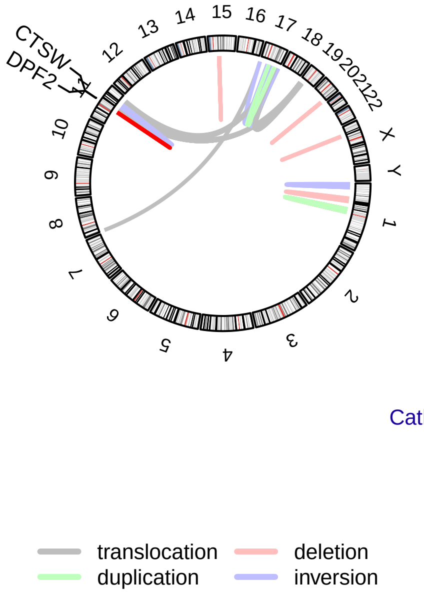
reading frame unclear



SUPPORTING READ COUNT

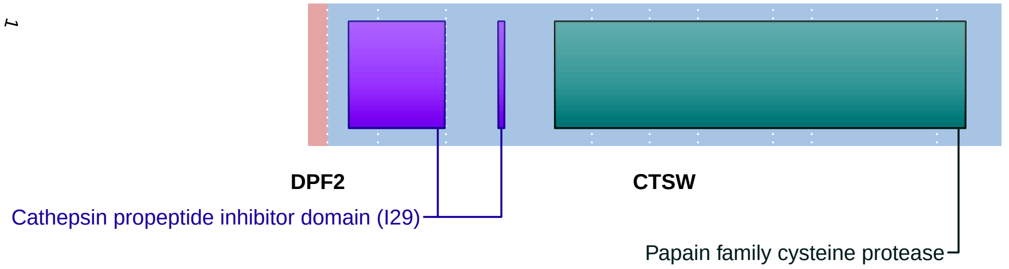
Split reads = 2
Discordant mates = 0





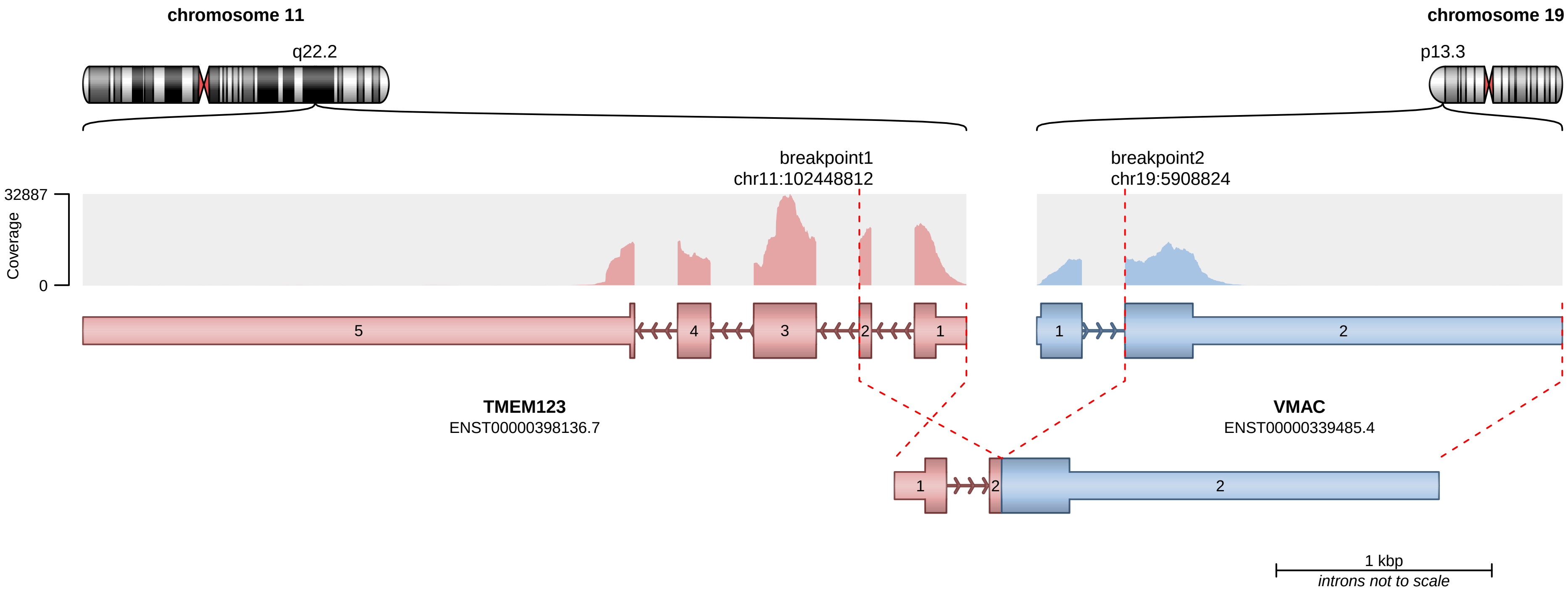
RETAINED PROTEIN DOMAINS

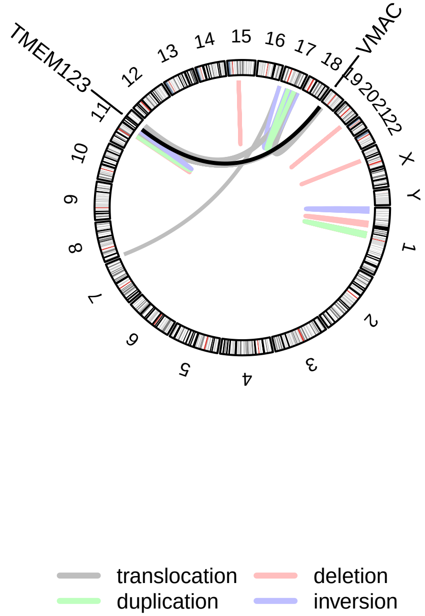
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

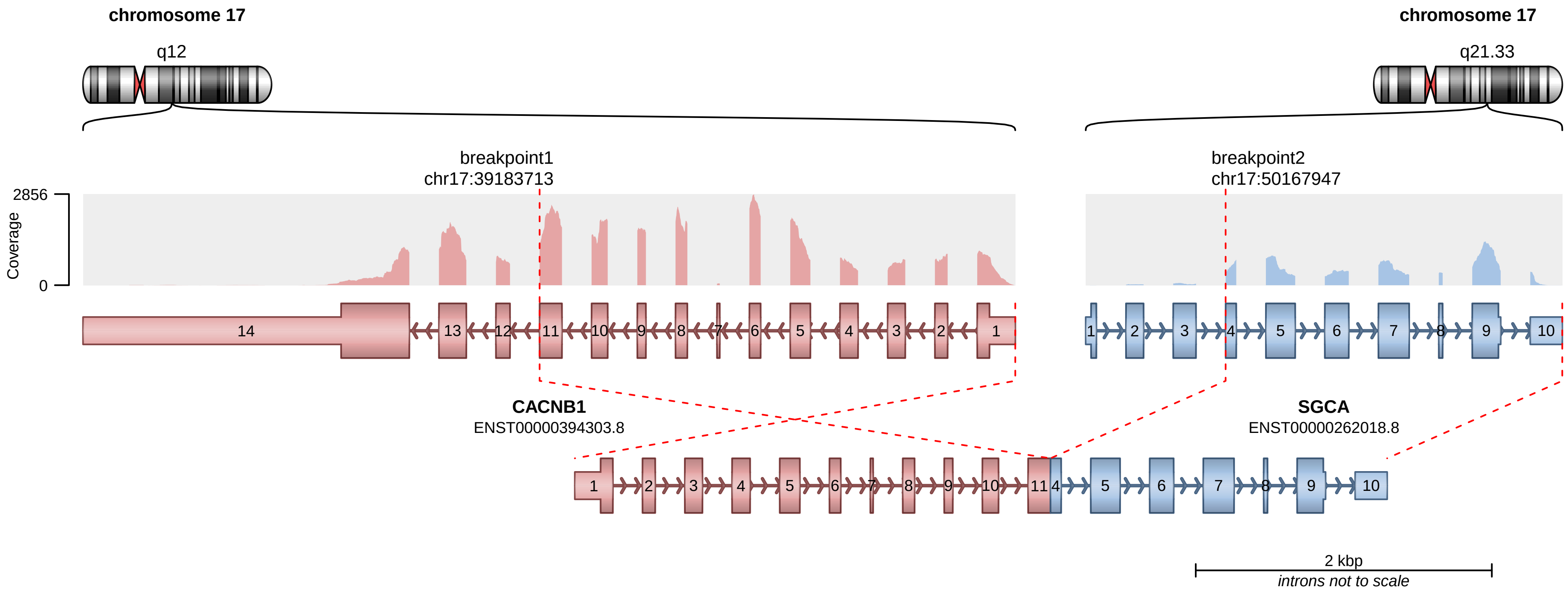


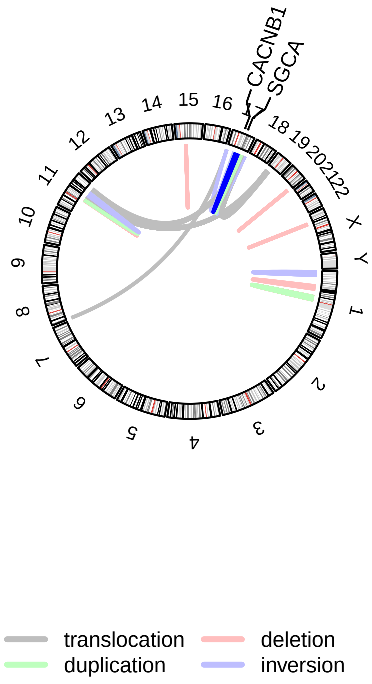


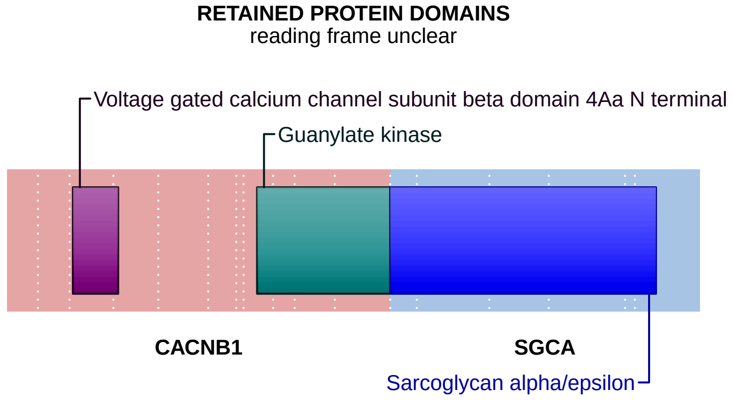
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 60
Discordant mates = 0

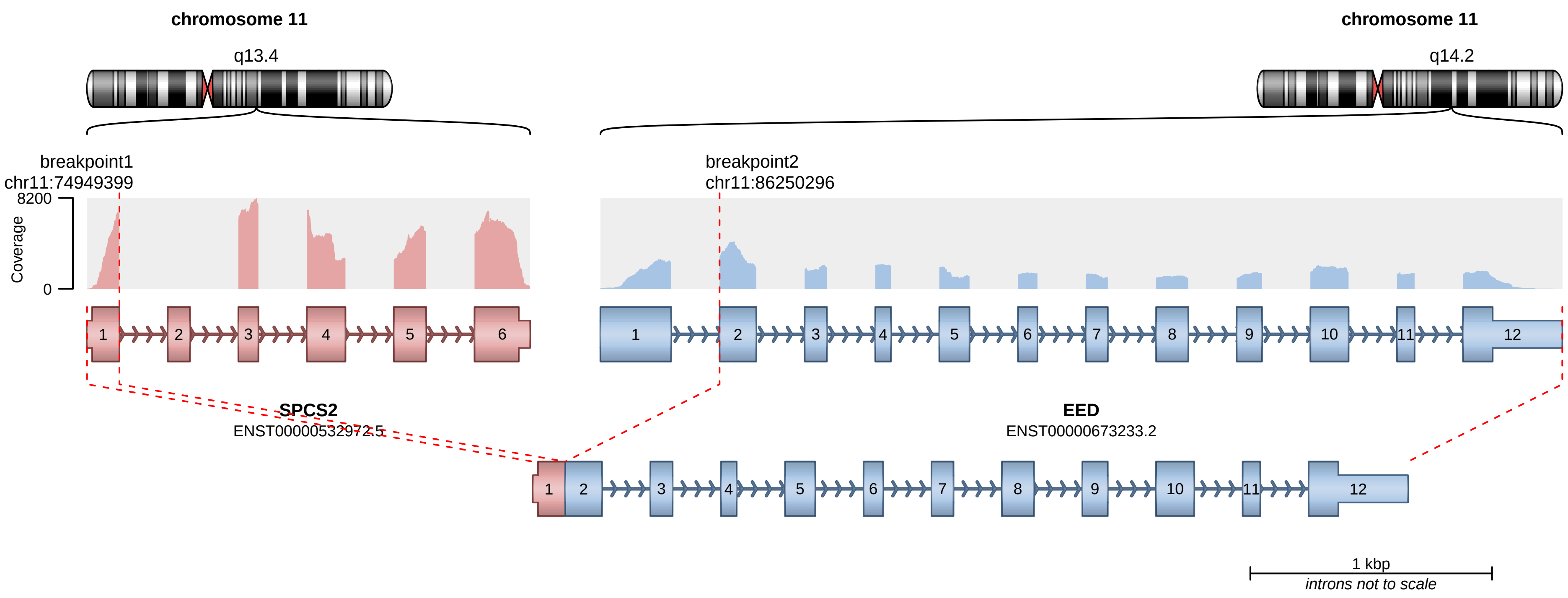


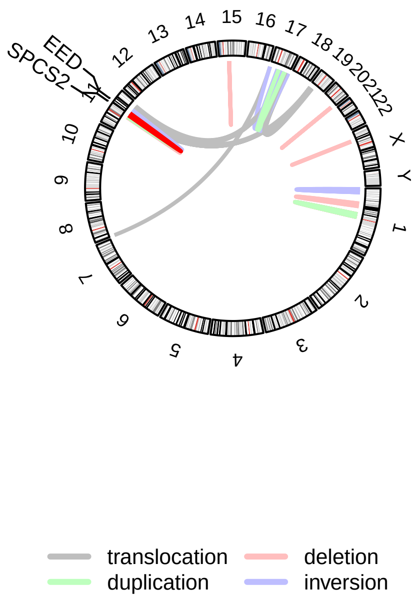


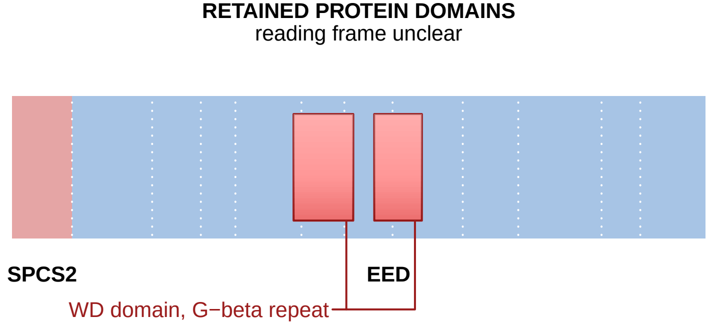


SUPPORTING READ COUNT

Split reads = 53
Discordant mates = 0

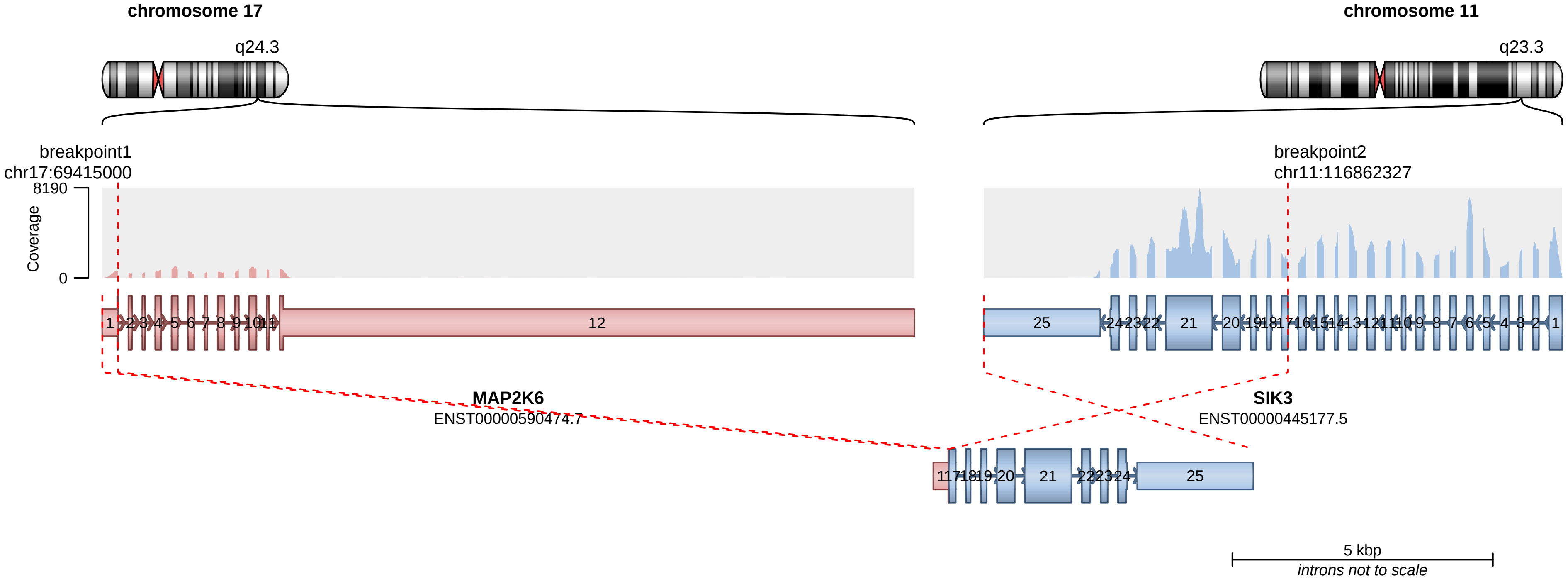


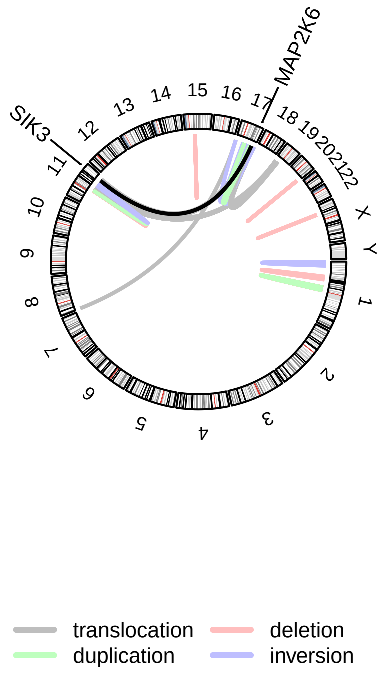




SUPPORTING READ COUNT

Split reads = 44
Discordant mates = 0

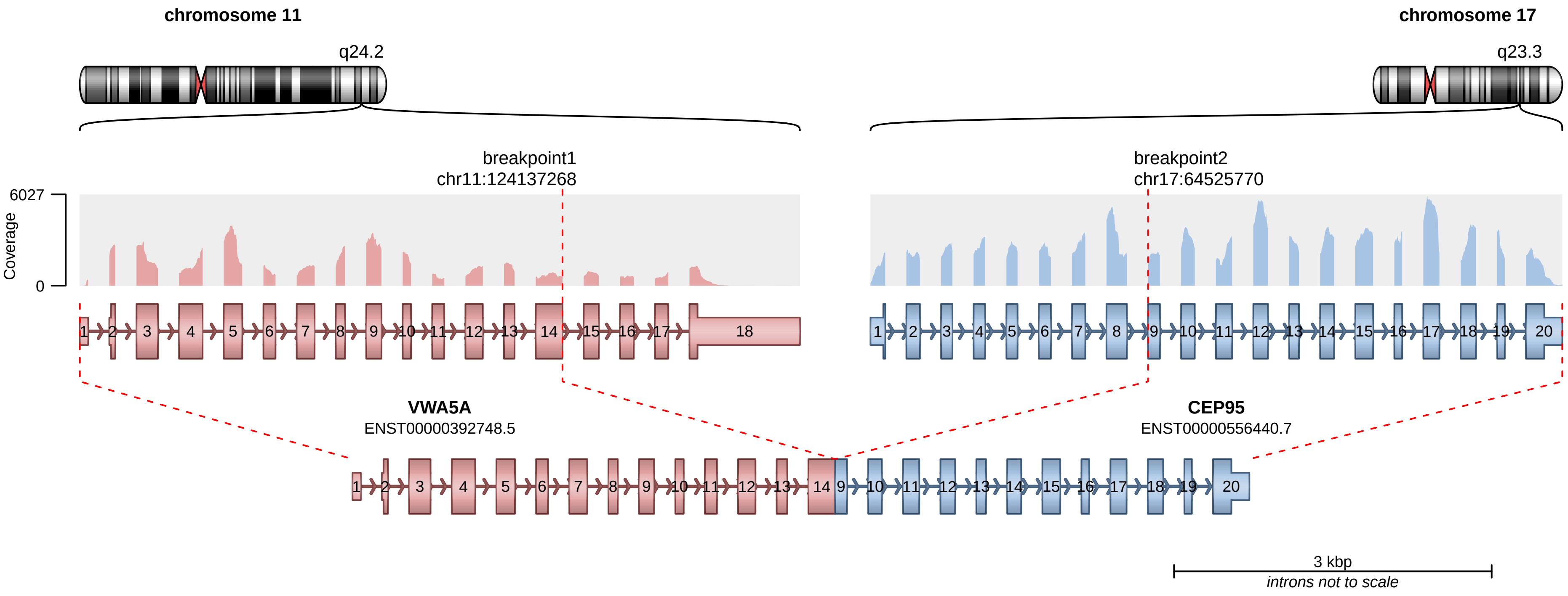


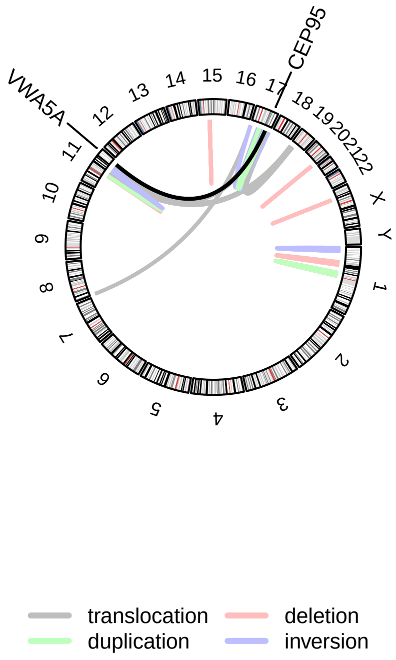


No protein domains retained in fusion.

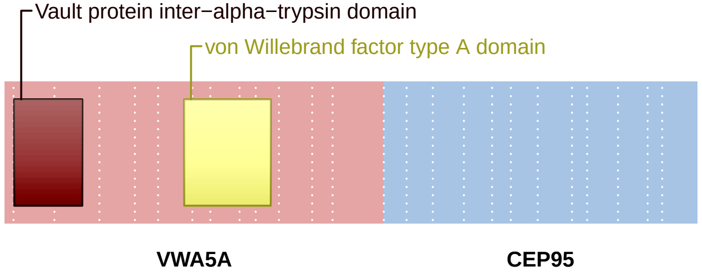
SUPPORTING READ COUNT

Split reads = 42
Discordant mates = 0



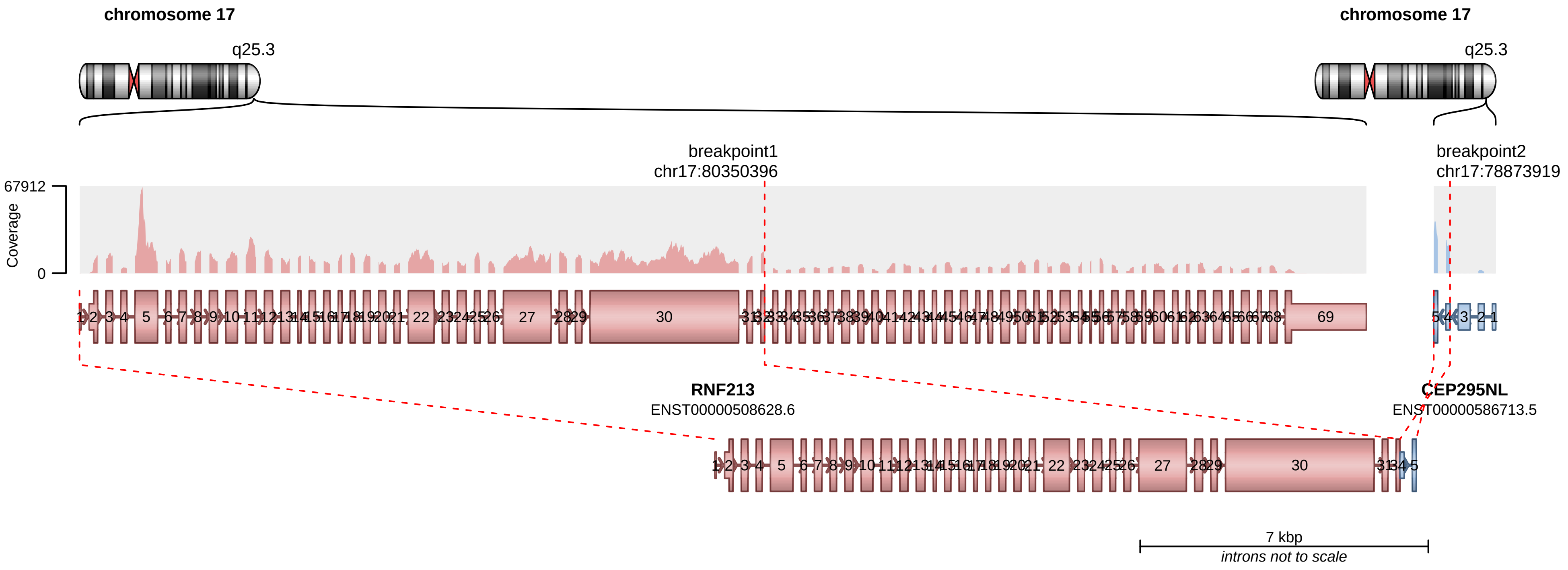


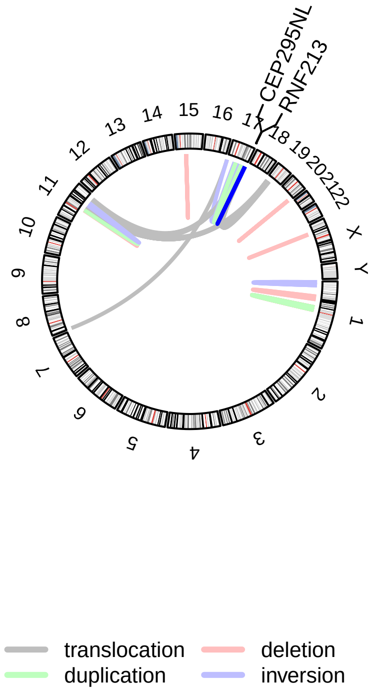
RETAINED PROTEIN DOMAINS
reading frame unclear

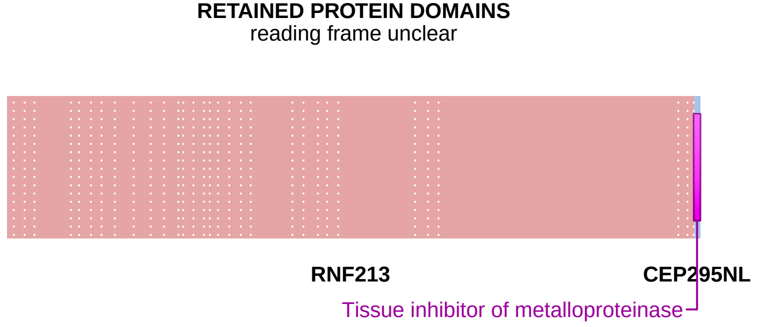


SUPPORTING READ COUNT

Split reads = 41
Discordant mates = 3

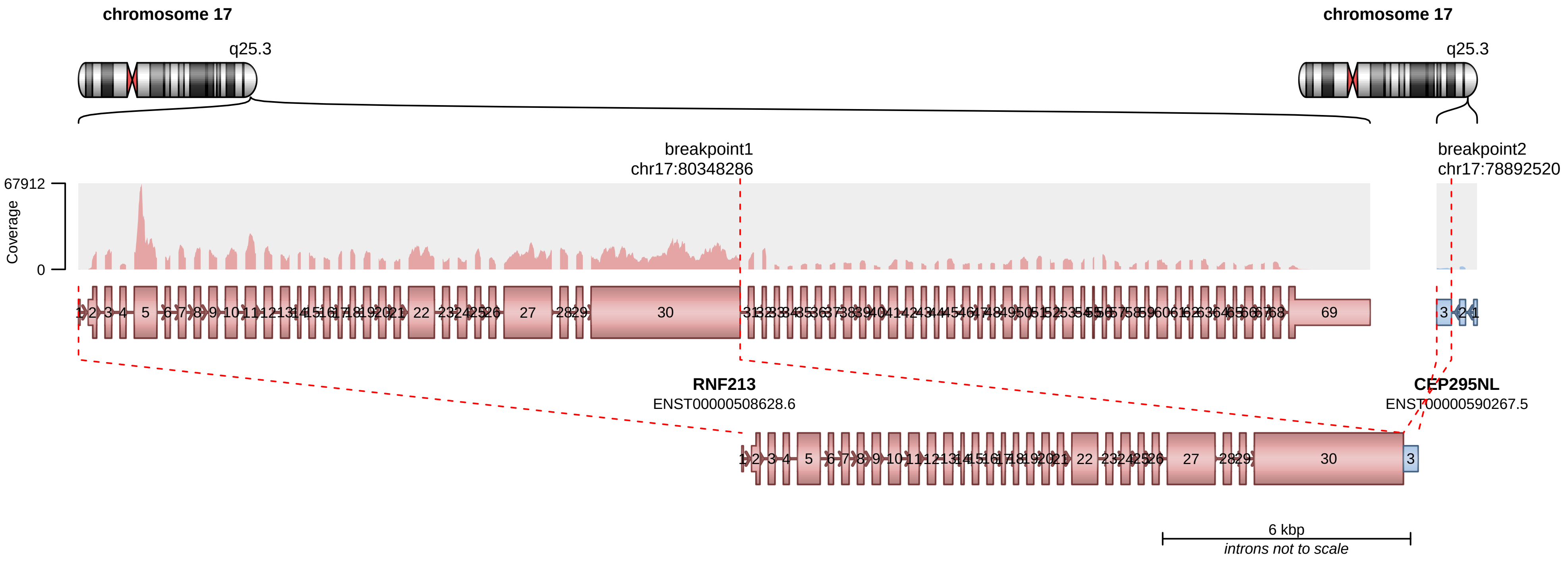


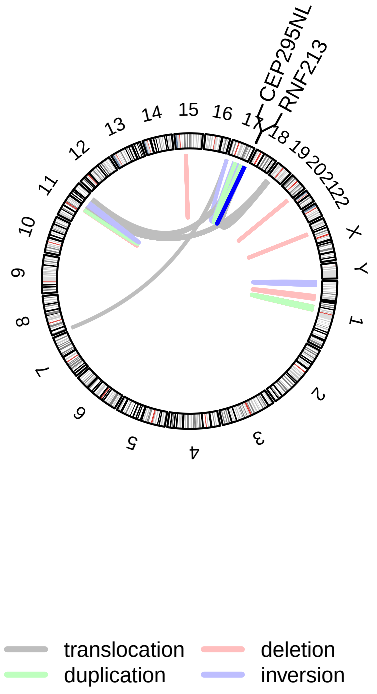




SUPPORTING READ COUNT

Split reads = 38
Discordant mates = 1

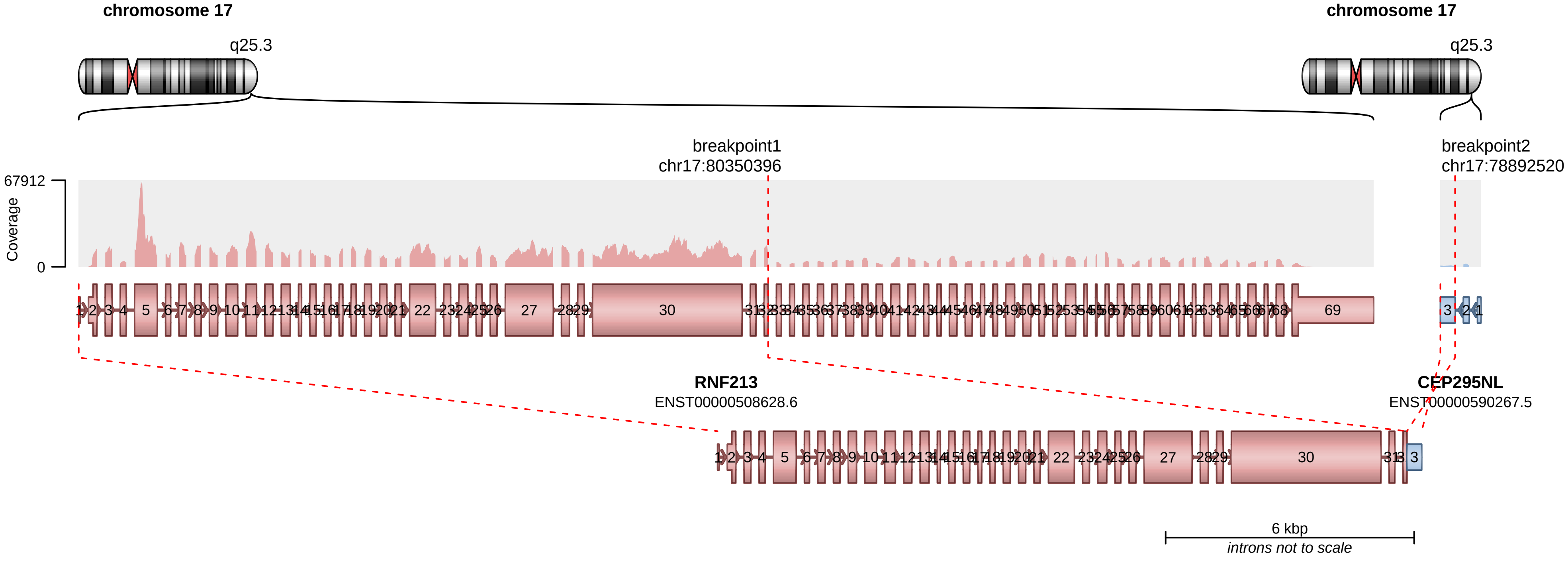


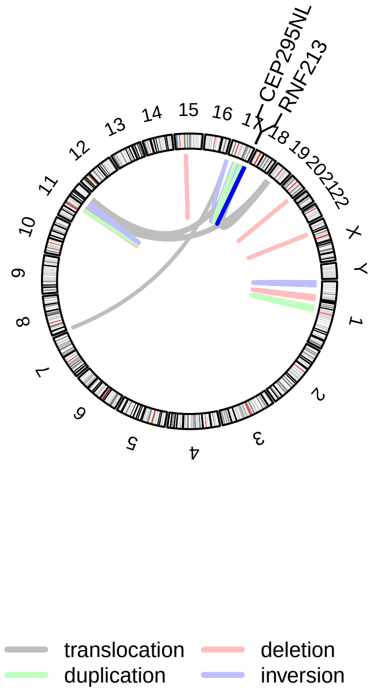


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 1

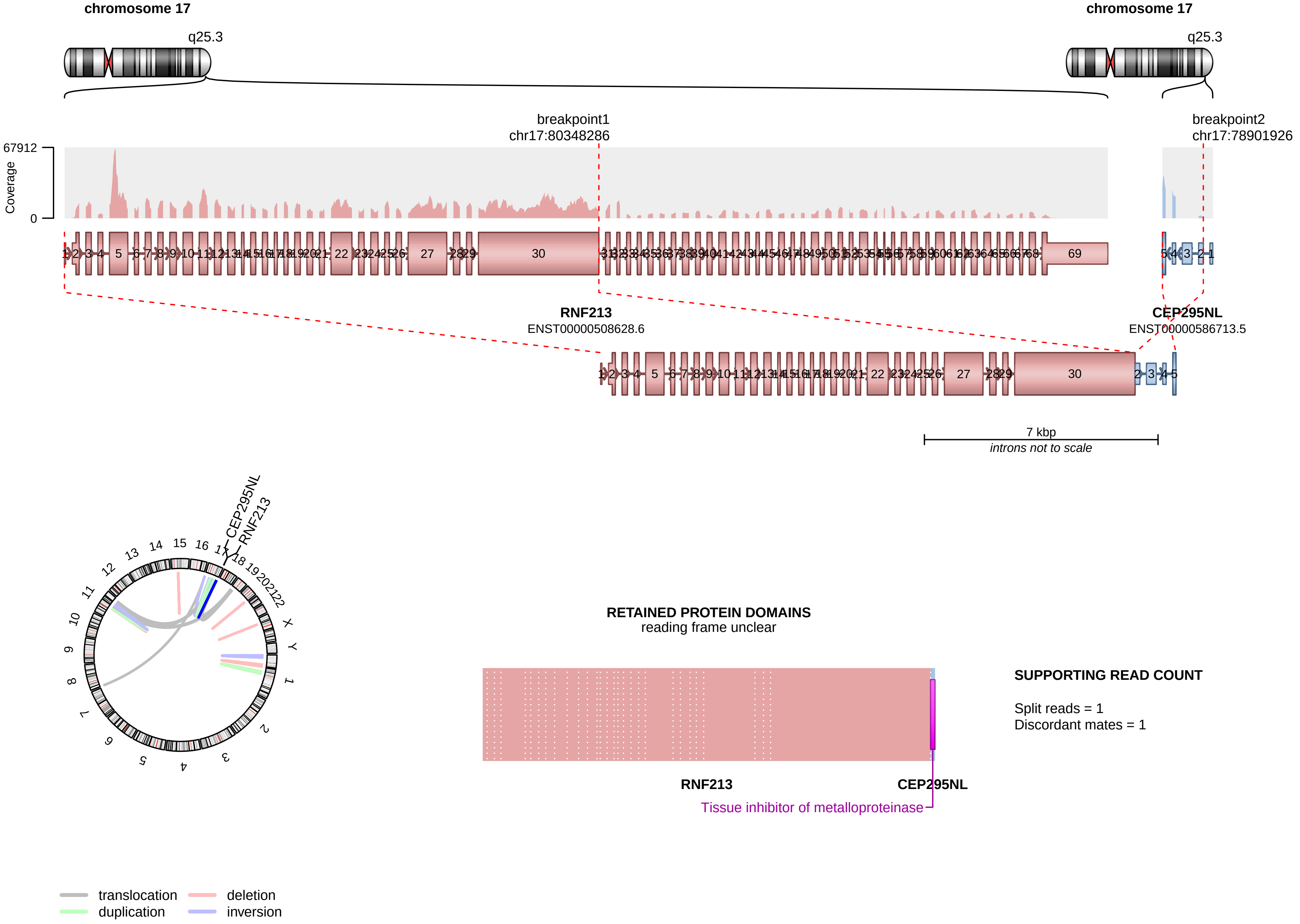


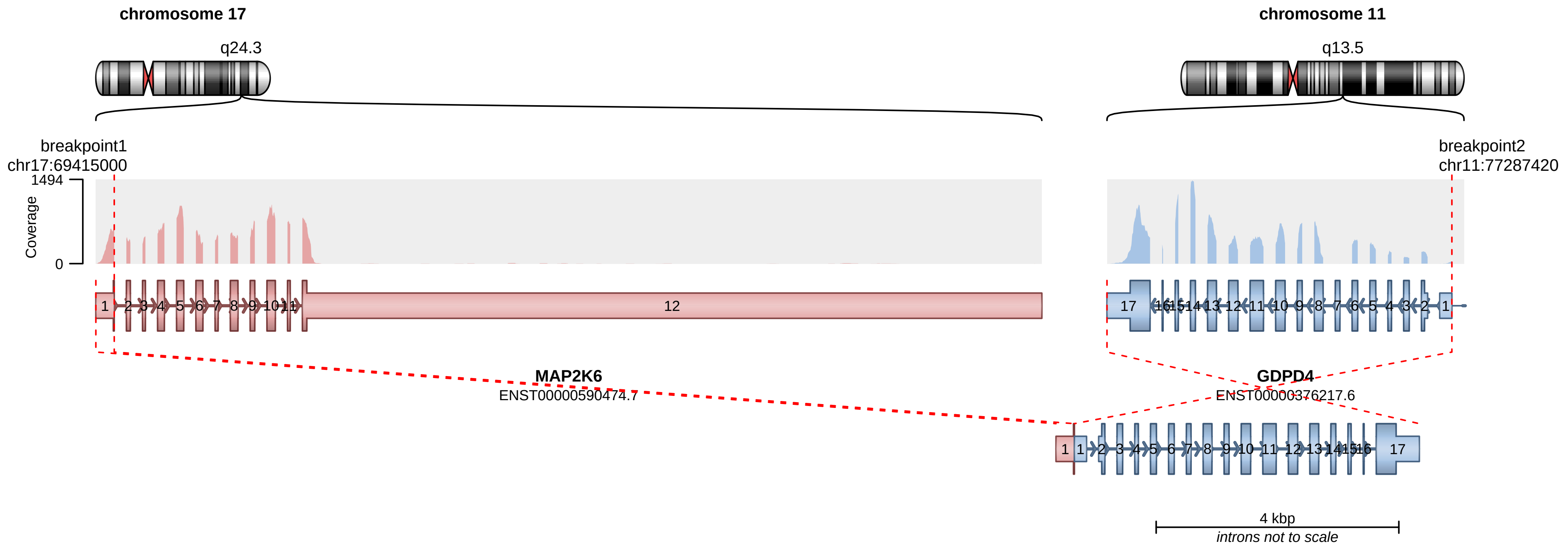


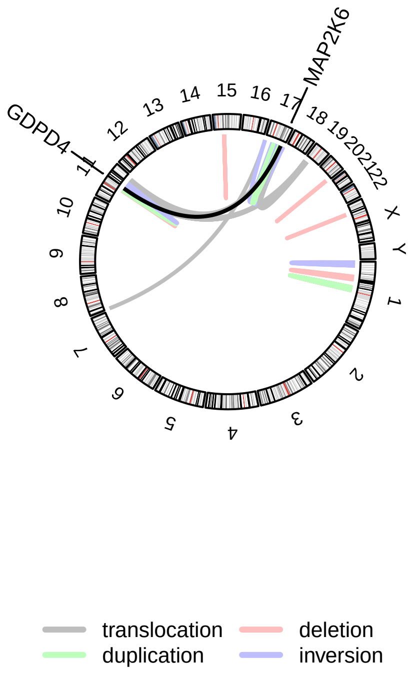
No protein domains retained in fusion.

SUPPORTING READ COUNT

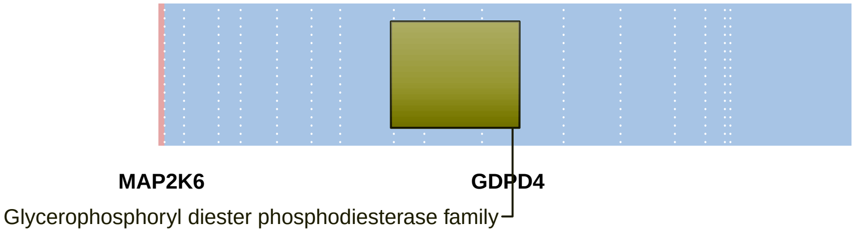
Split reads = 3
Discordant mates = 1


chromosome 17
q25.3
chromosome 17
q25.3
breakpoint1
chr17:80348286
breakpoint2
chr17:78901926
67912
Coverage
0
RNF213
ENST00000508628.6
CEP295NL
ENST00000586713.5
7 kbp
introns not to scale
CEP295NL
RNF213
RETAINED PROTEIN DOMAINS
reading frame unclear
SUPPORTING READ COUNT
Split reads = 1
Discordant mates = 1
RNF213
CEP295NL
Tissue inhibitor of metalloproteinase
translocation
duplication
deletion
inversion



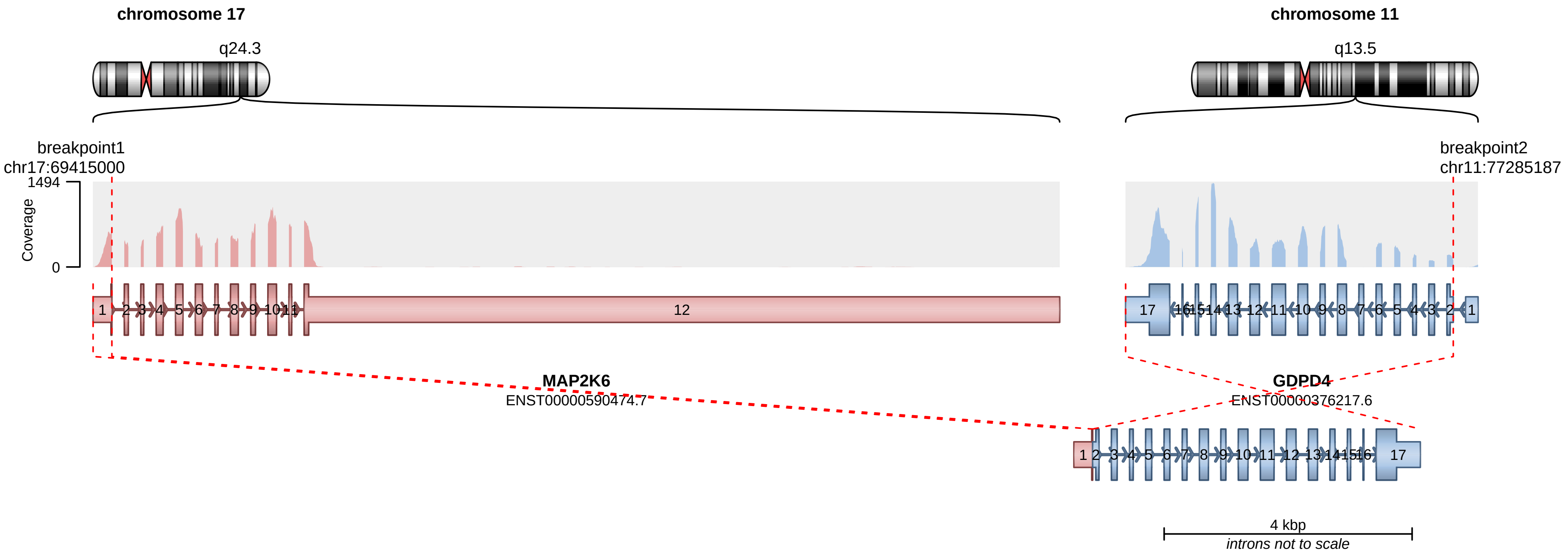


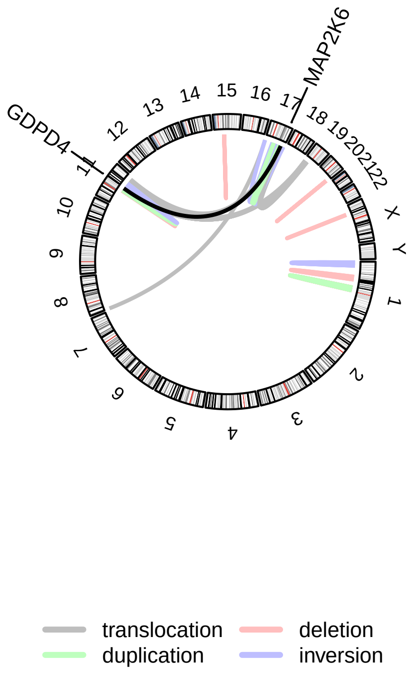
RETAINED PROTEIN DOMAINS
reading frame unclear

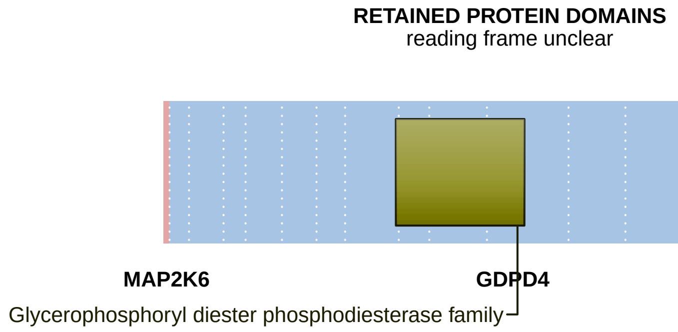


SUPPORTING READ COUNT

Split reads = 36
Discordant mates = 1

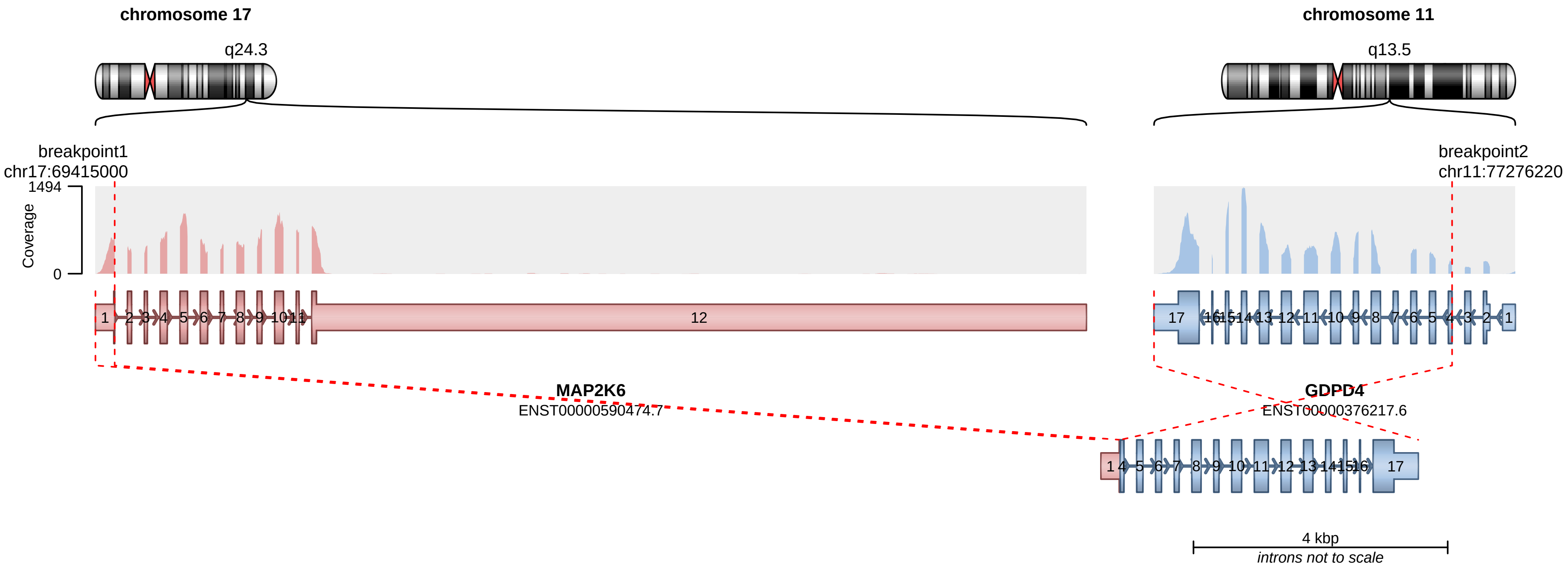


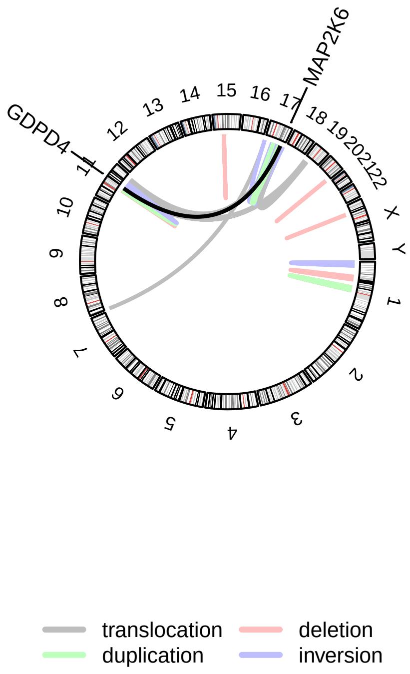


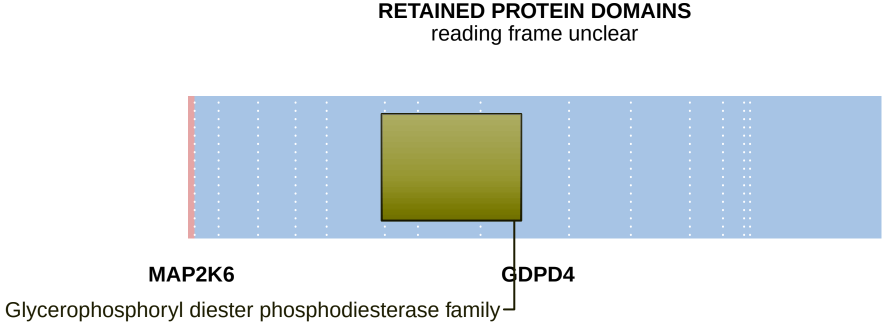


SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 1

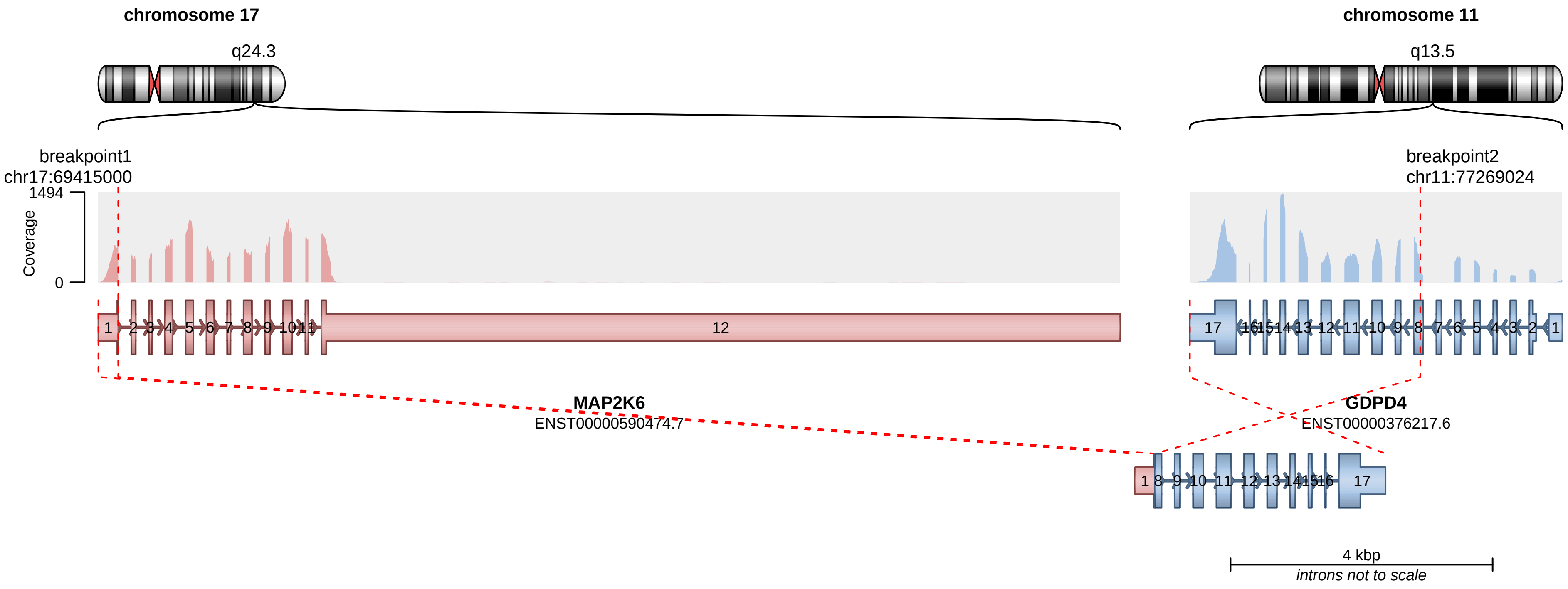


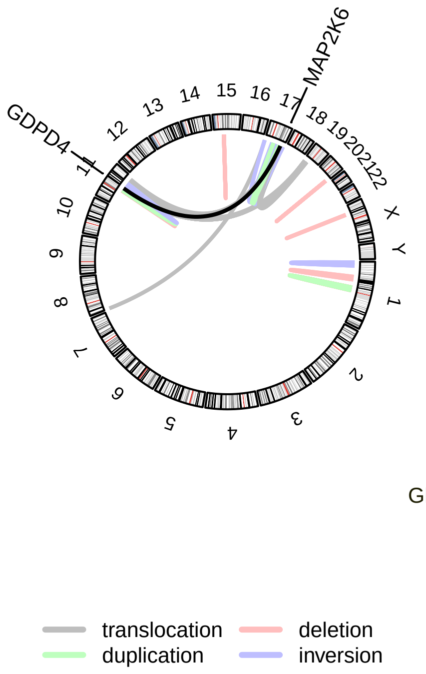




SUPPORTING READ COUNT

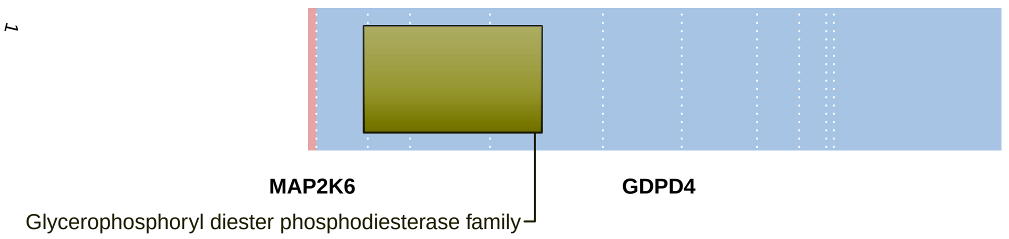
Split reads = 7
Discordant mates = 0





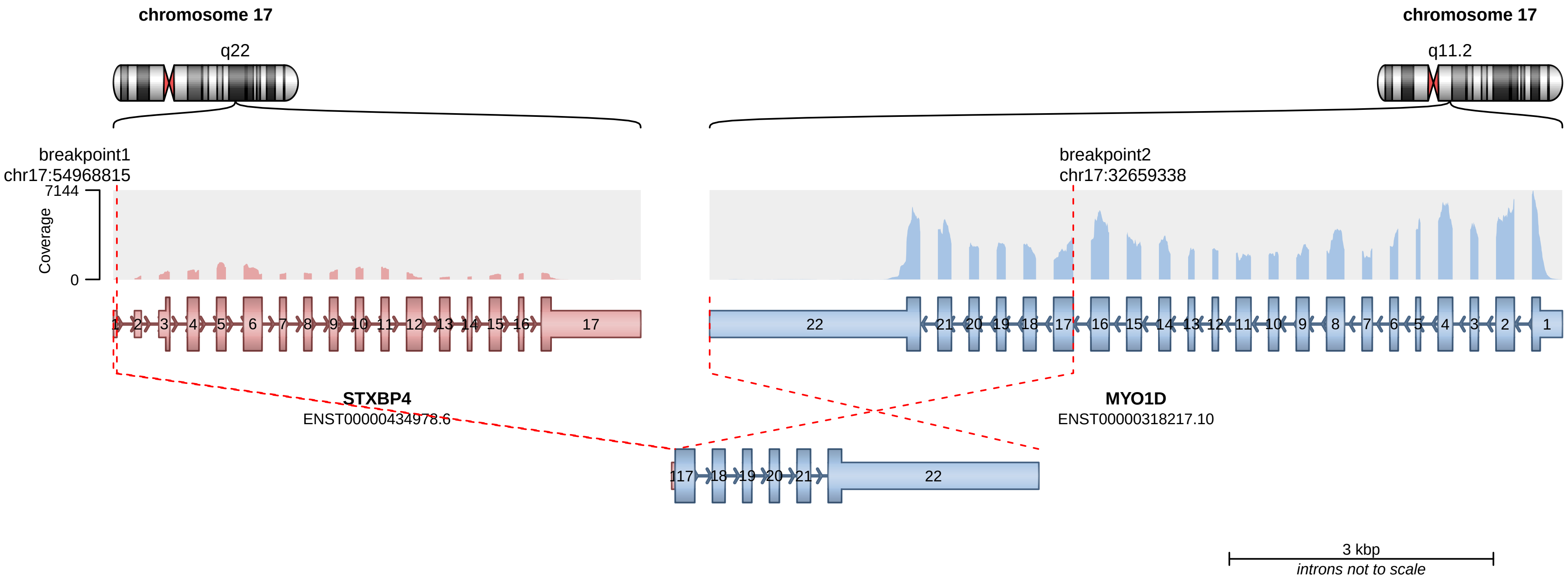
RETAINED PROTEIN DOMAINS

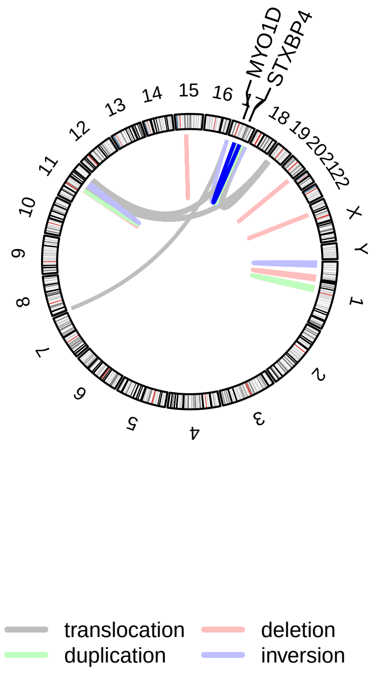
reading frame unclear

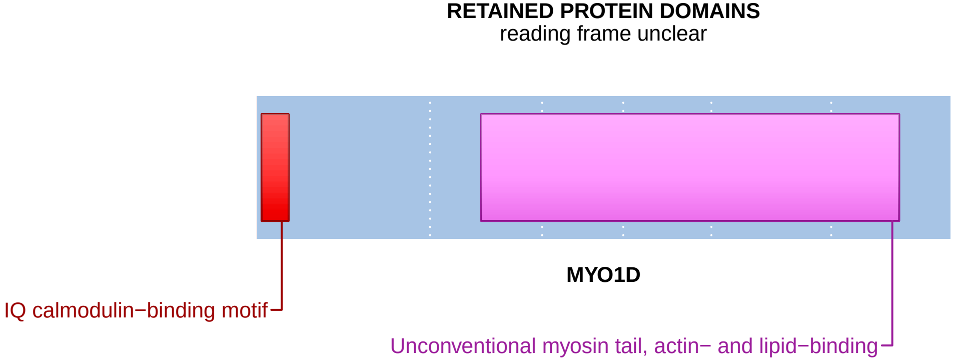


SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

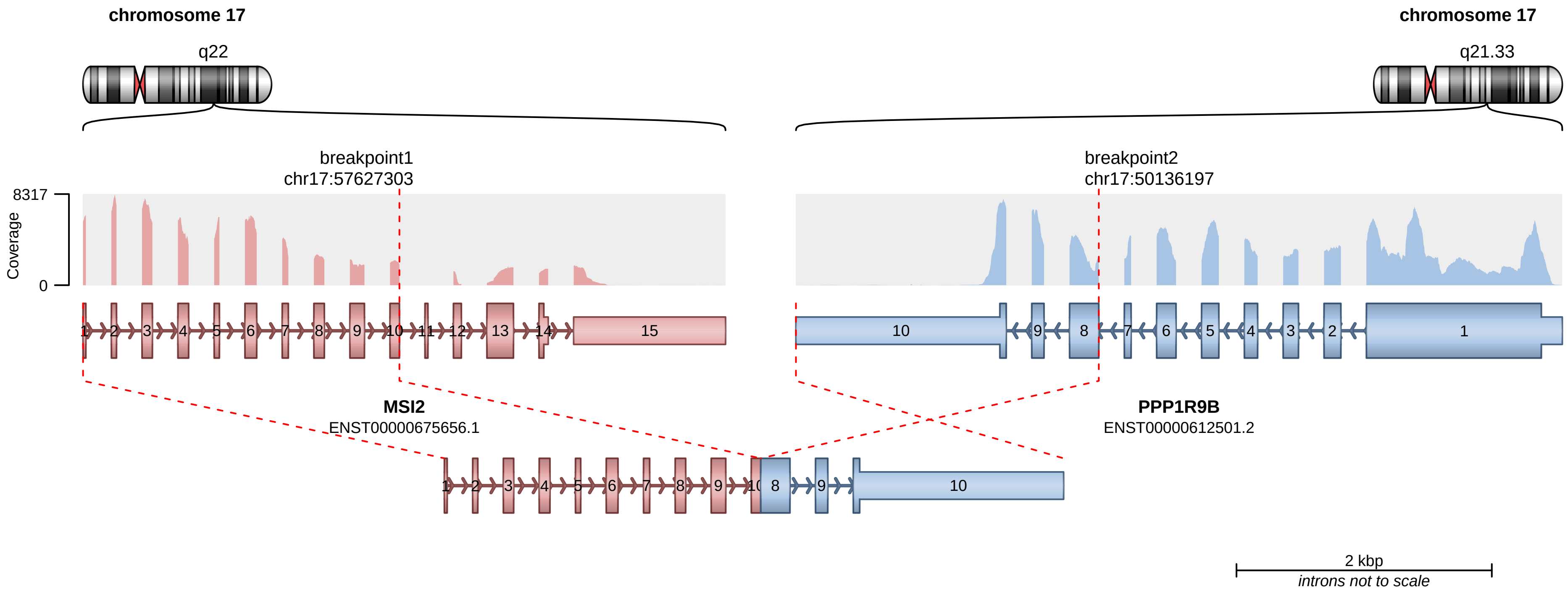


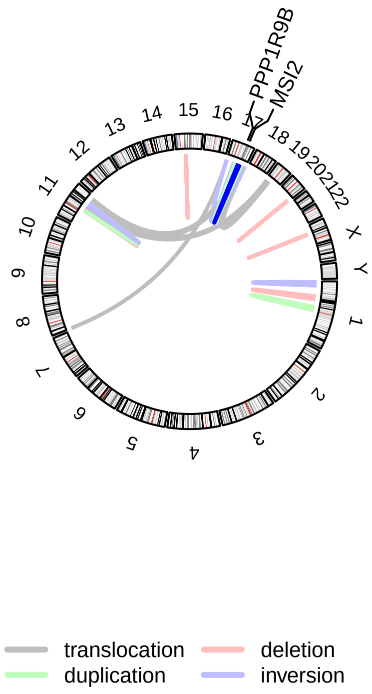




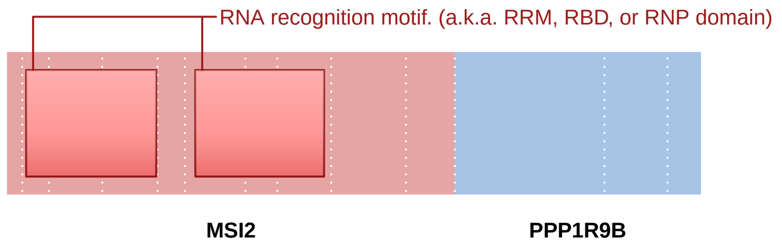
SUPPORTING READ COUNT

Split reads = 35
Discordant mates = 0



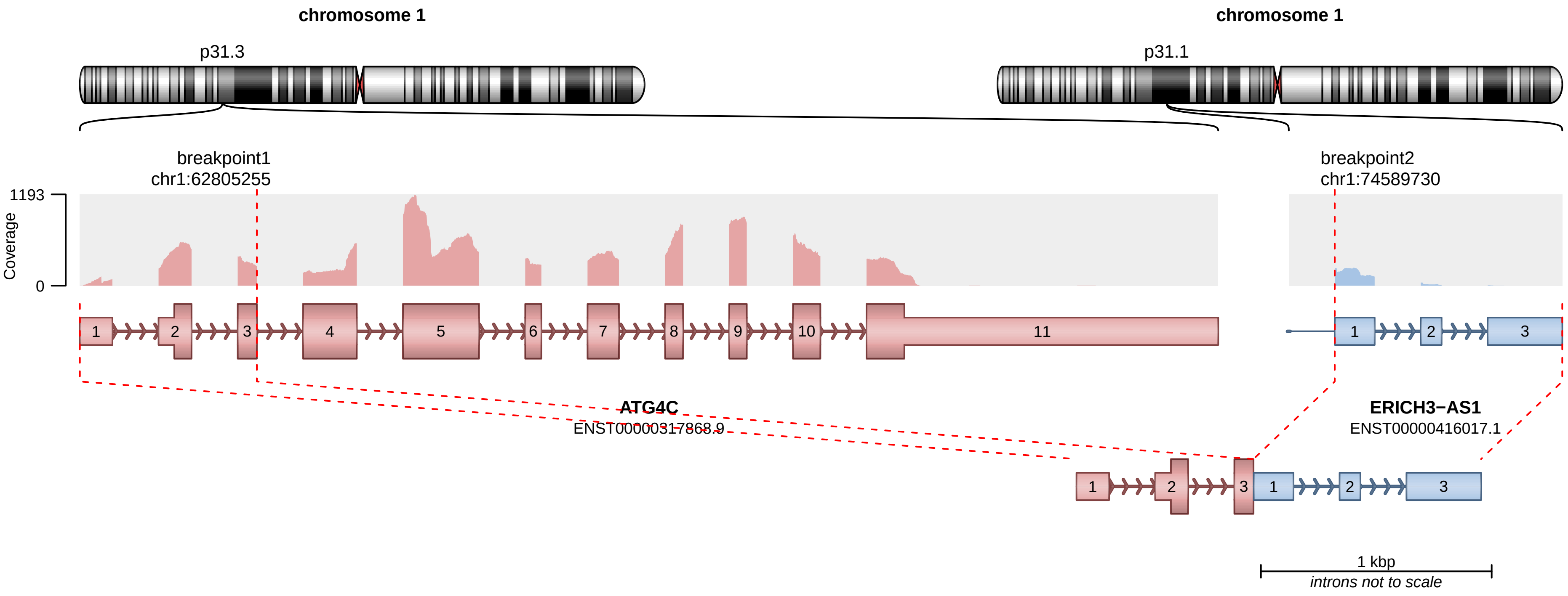


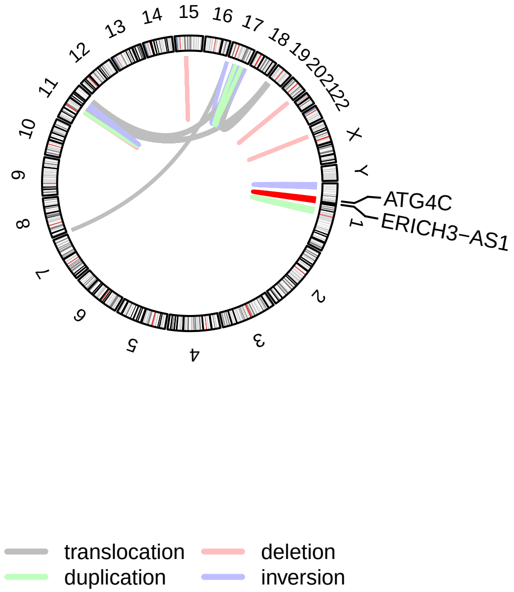
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 33
Discordant mates = 0

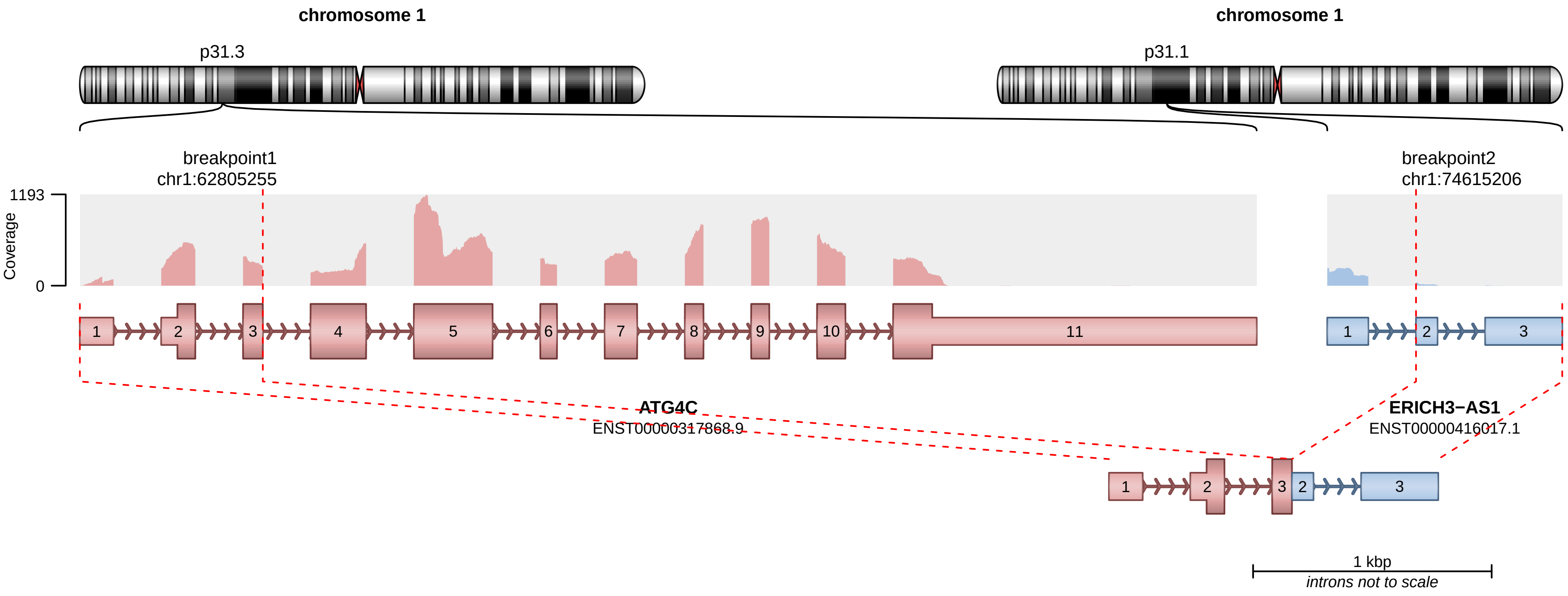


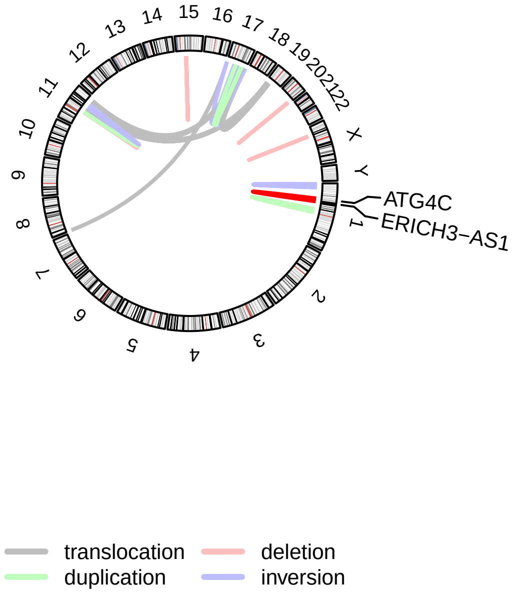


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 31
Discordant mates = 3

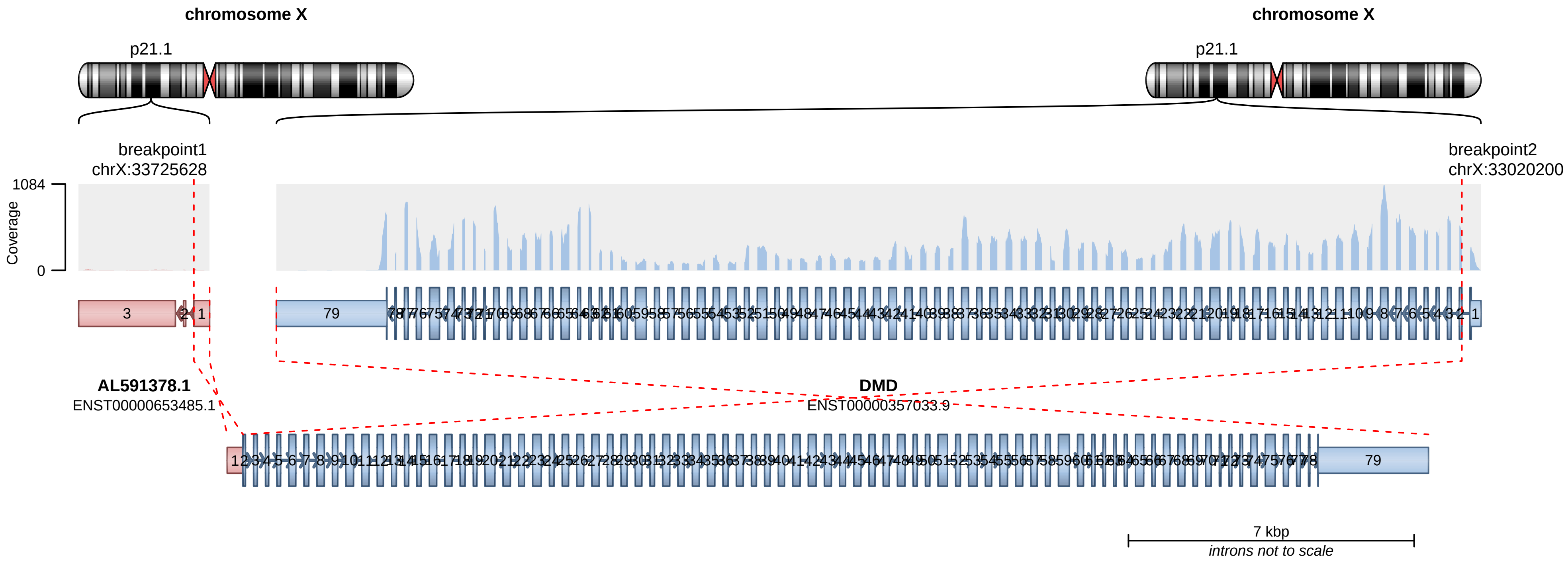


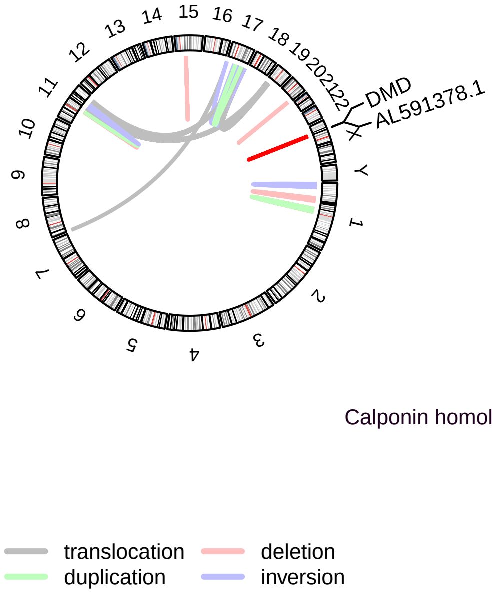


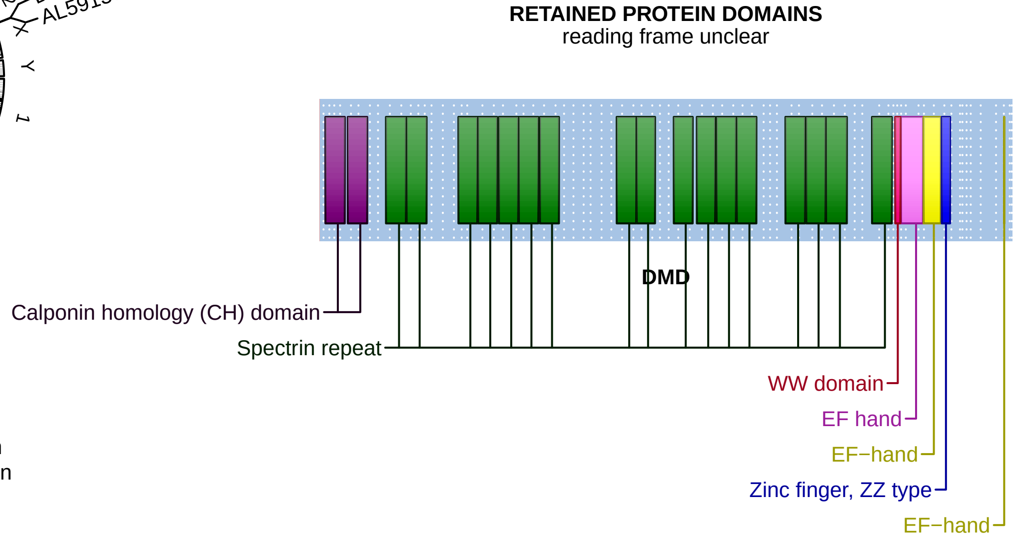
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 16
Discordant mates = 1

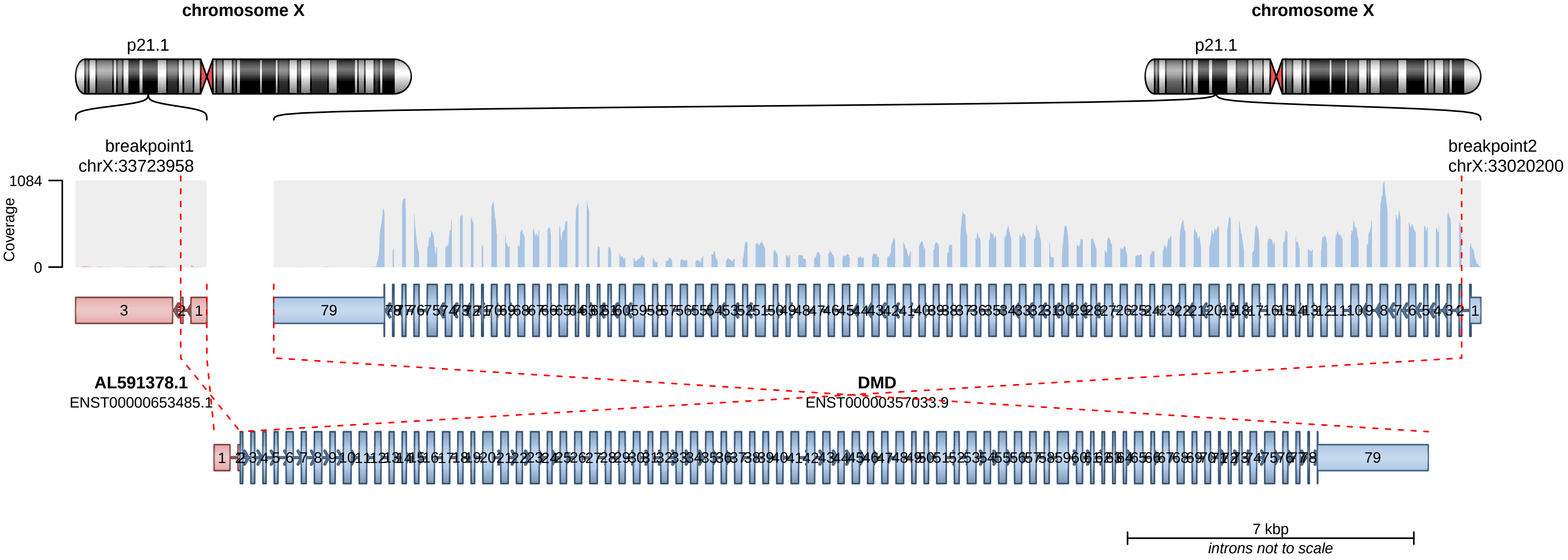


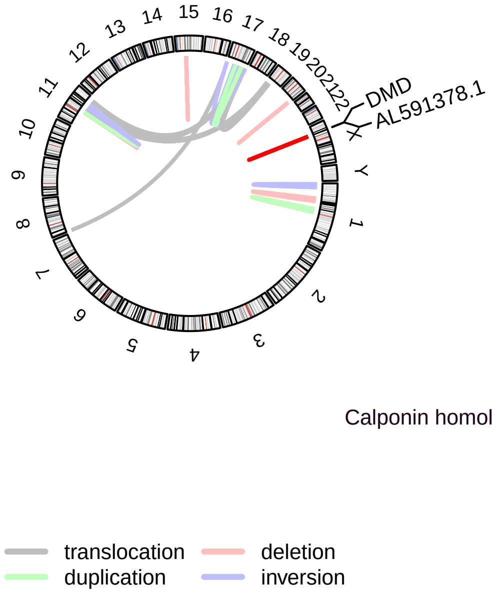


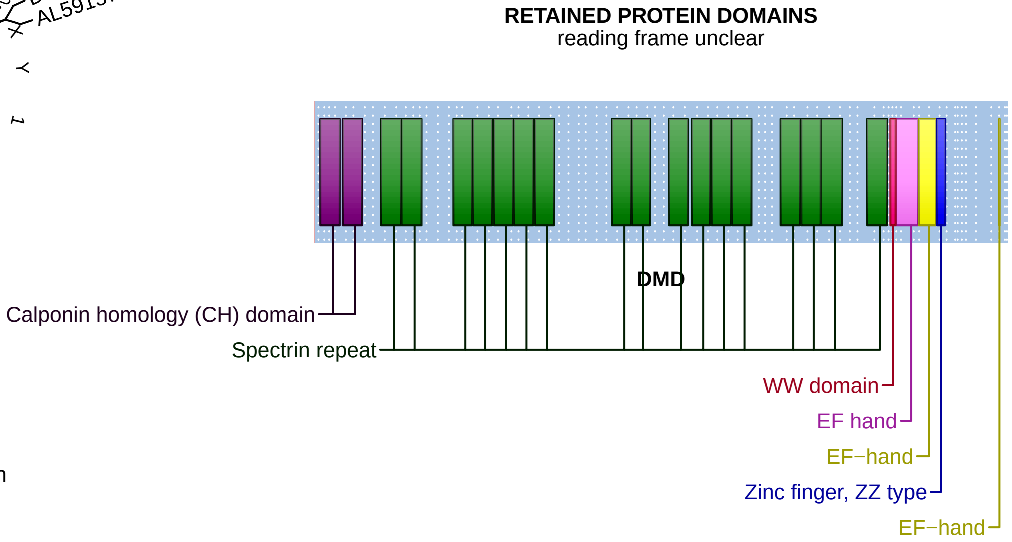


SUPPORTING READ COUNT

Split reads = 16
Discordant mates = 1

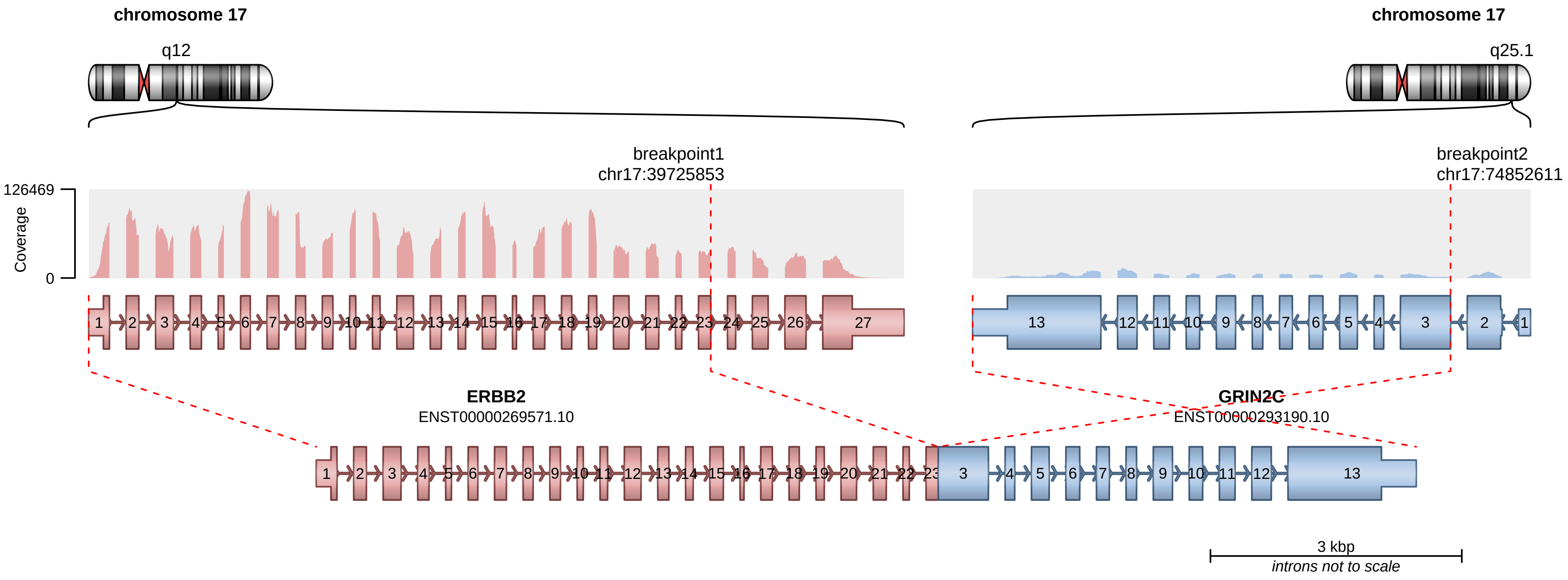


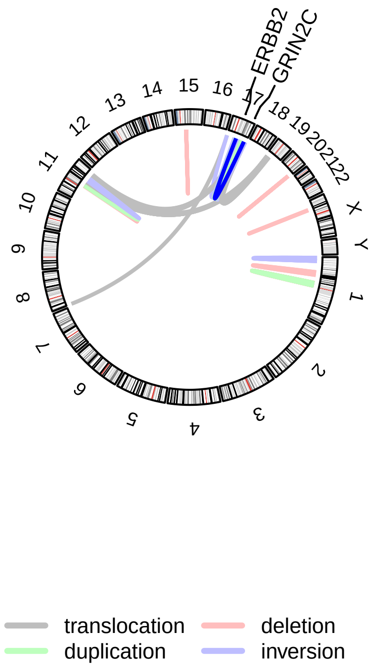


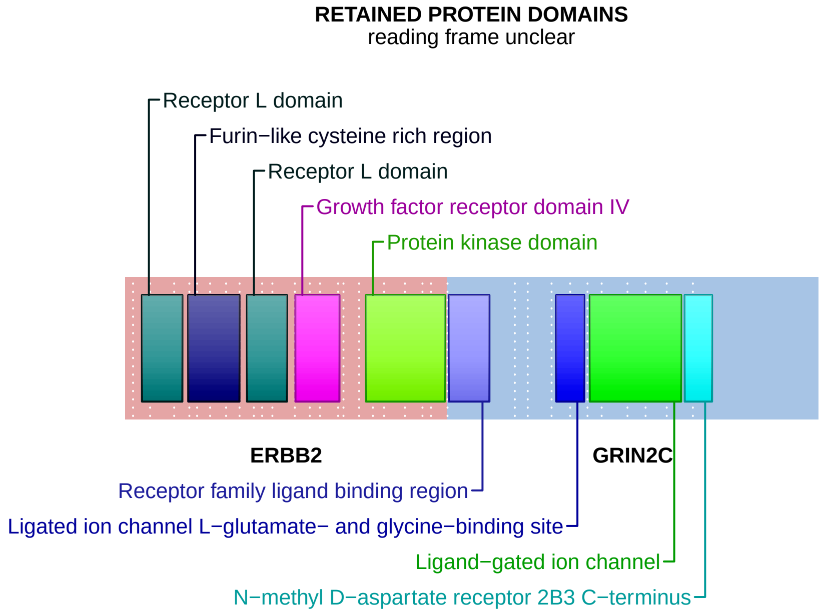


SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 1

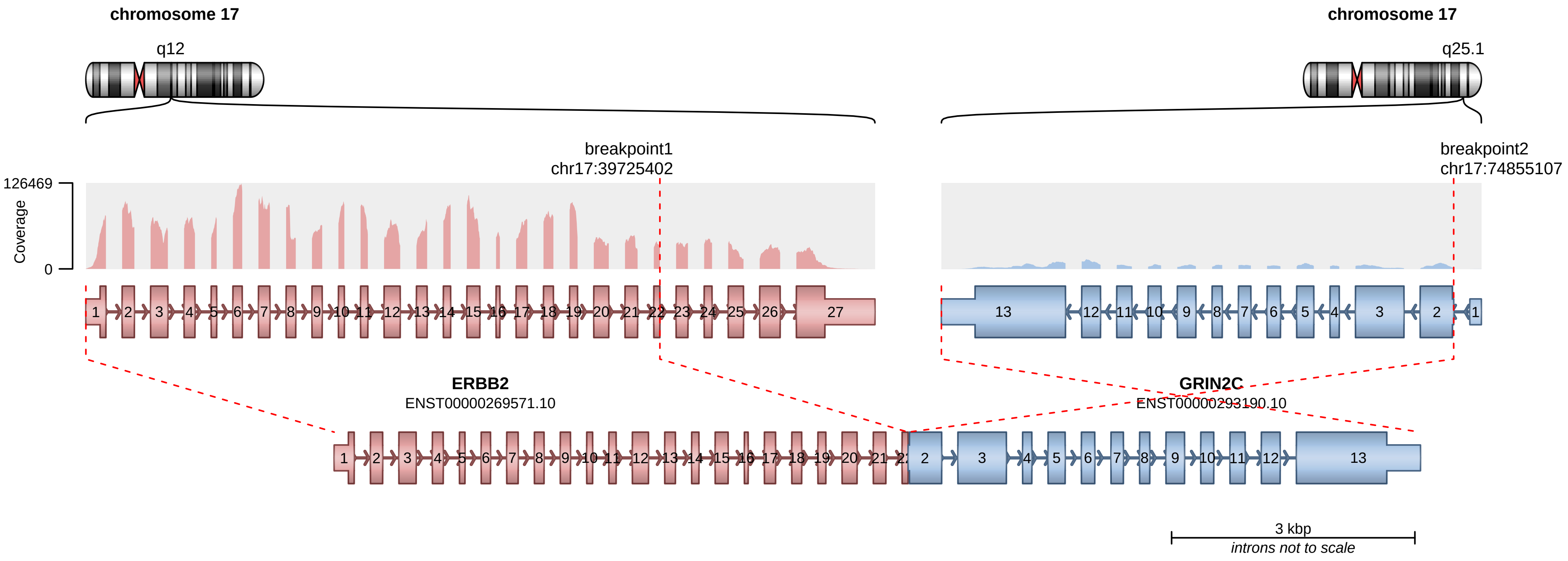


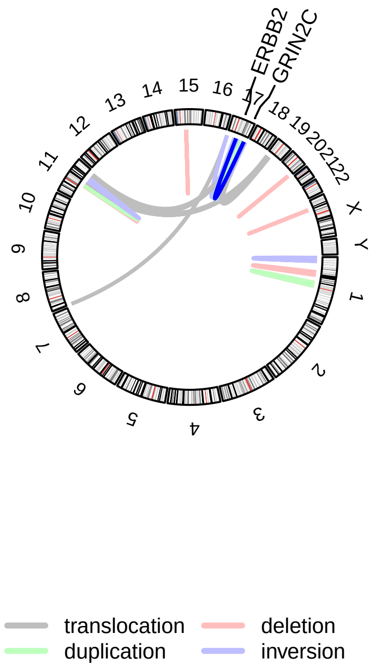




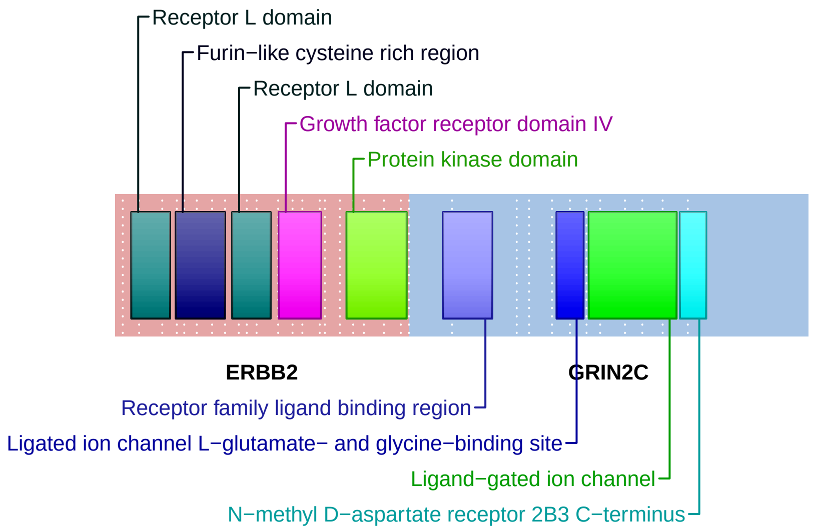
SUPPORTING READ COUNT

Split reads = 16
Discordant mates = 0



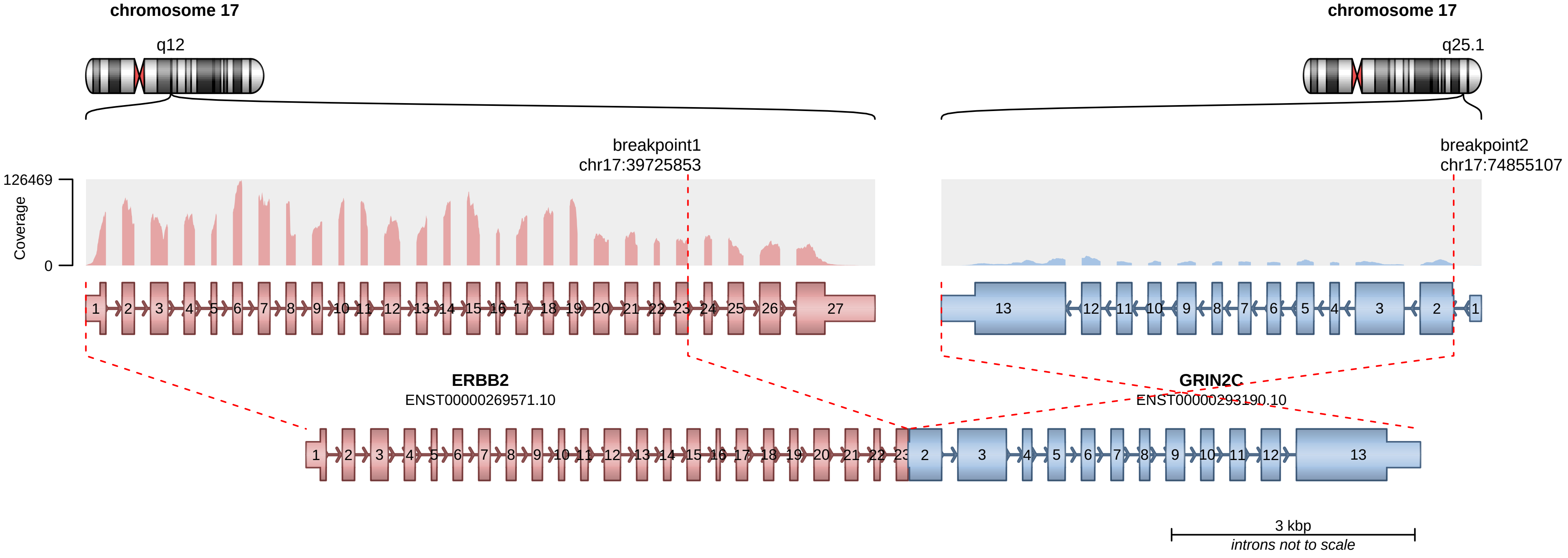


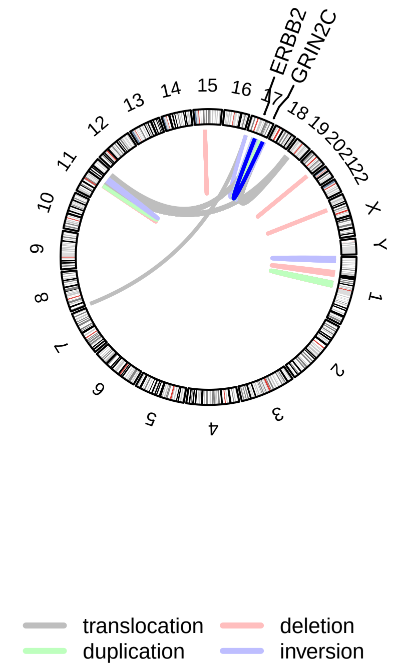
RETAINED PROTEIN DOMAINS
reading frame unclear

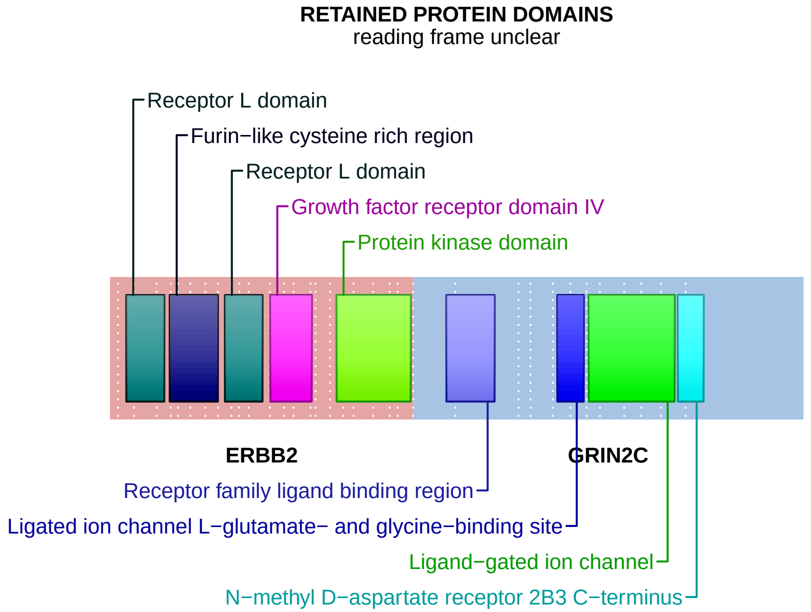


SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 1

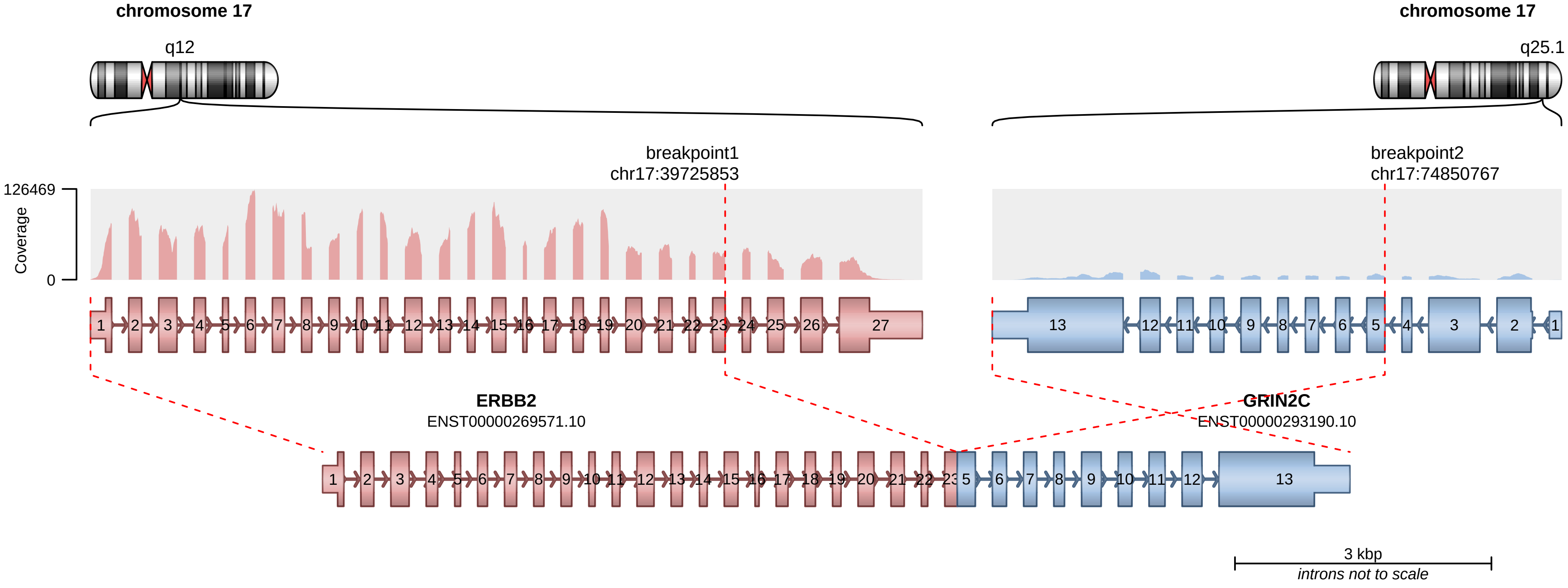


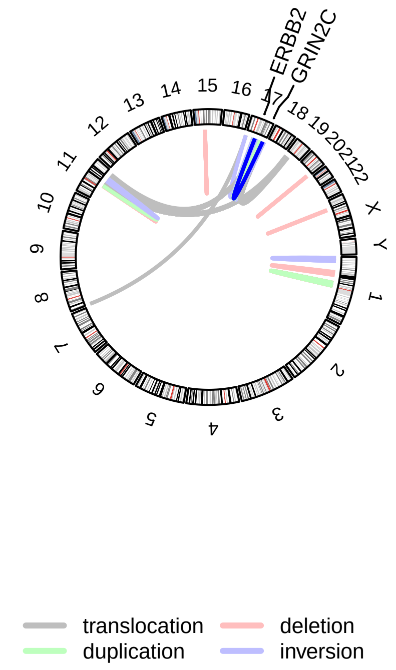


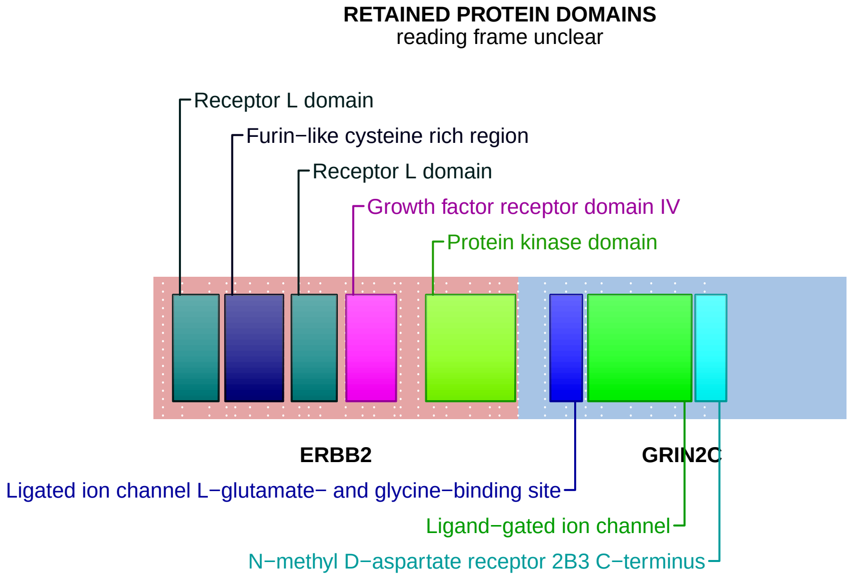


SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 1

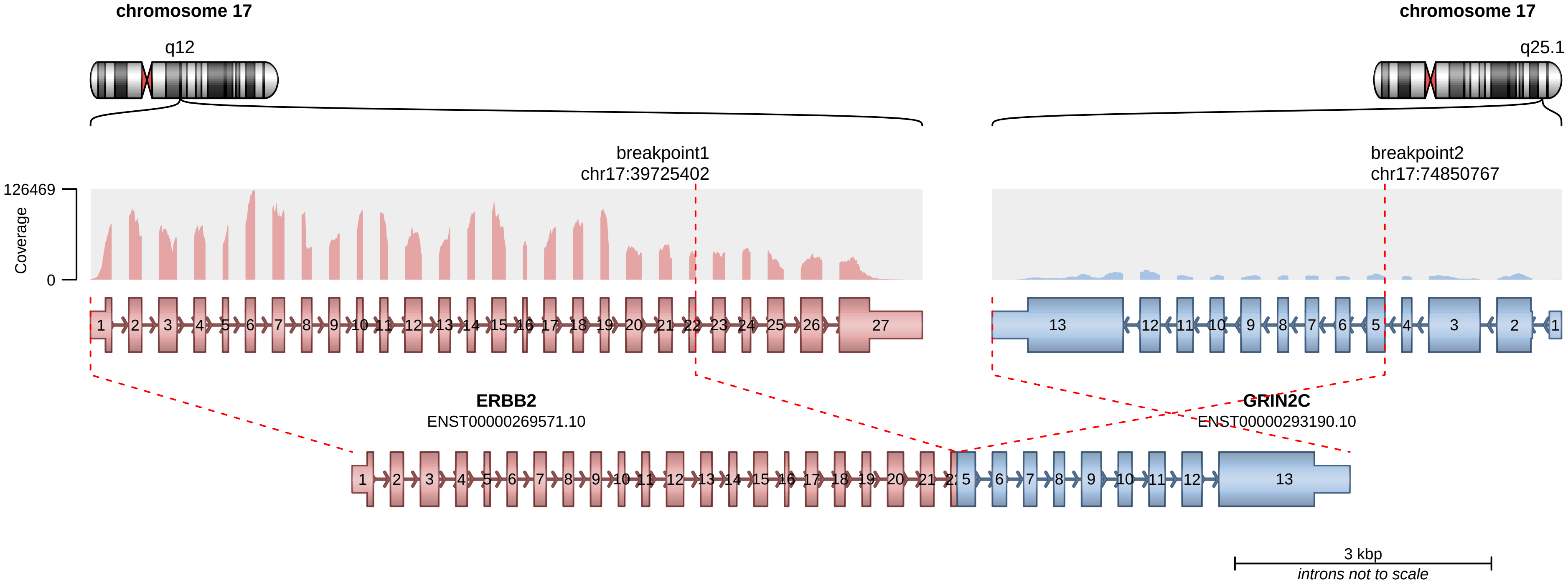


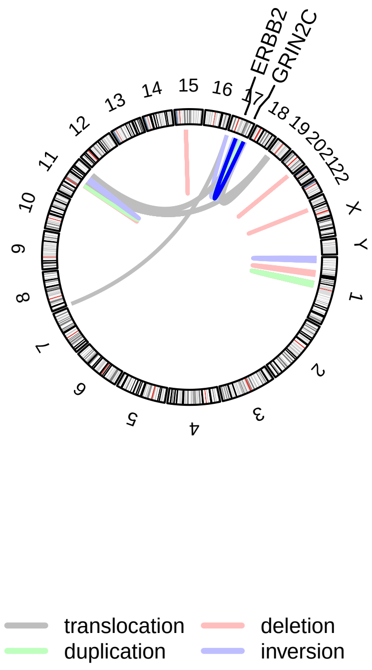


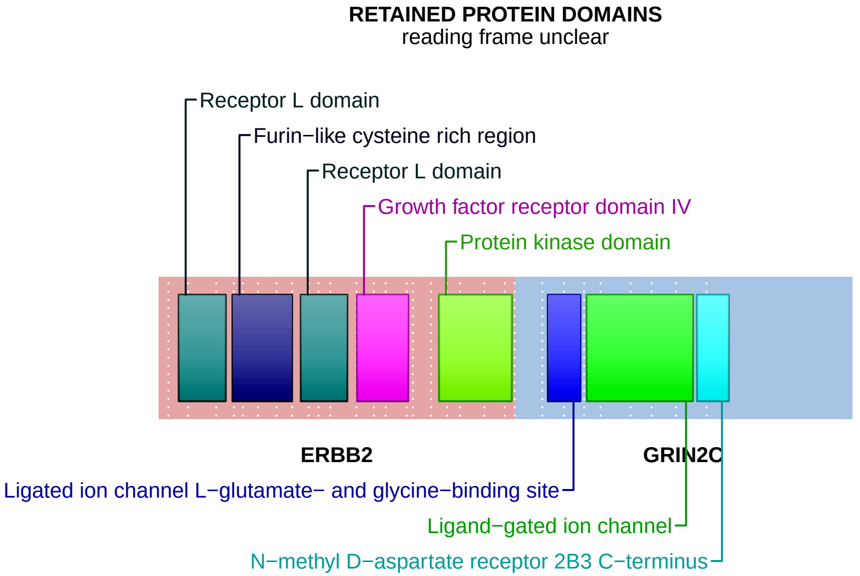


SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

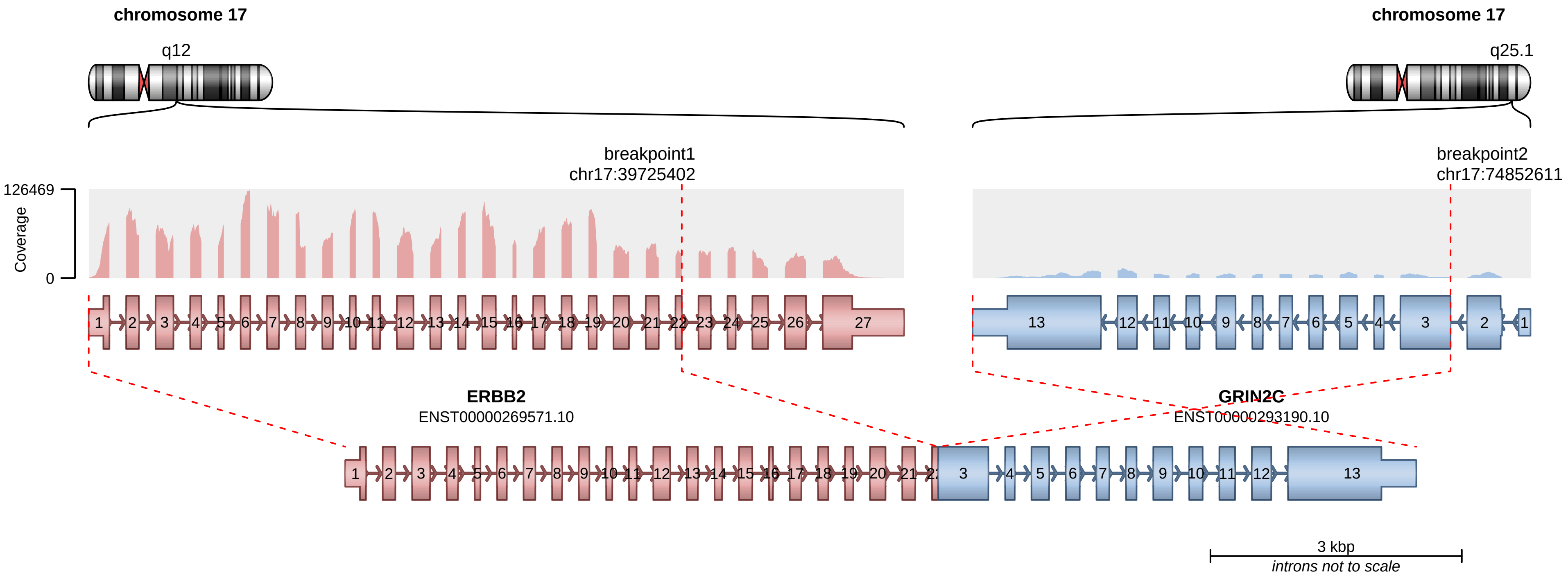


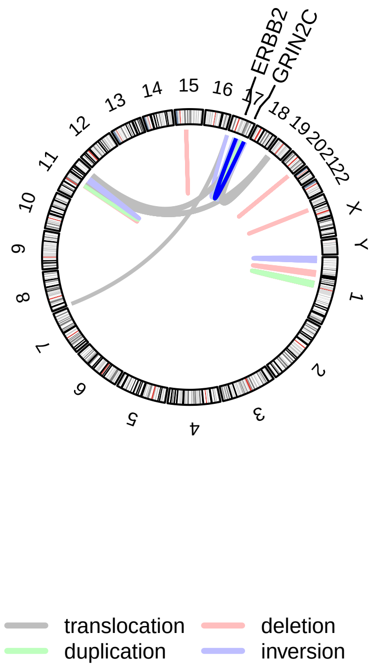




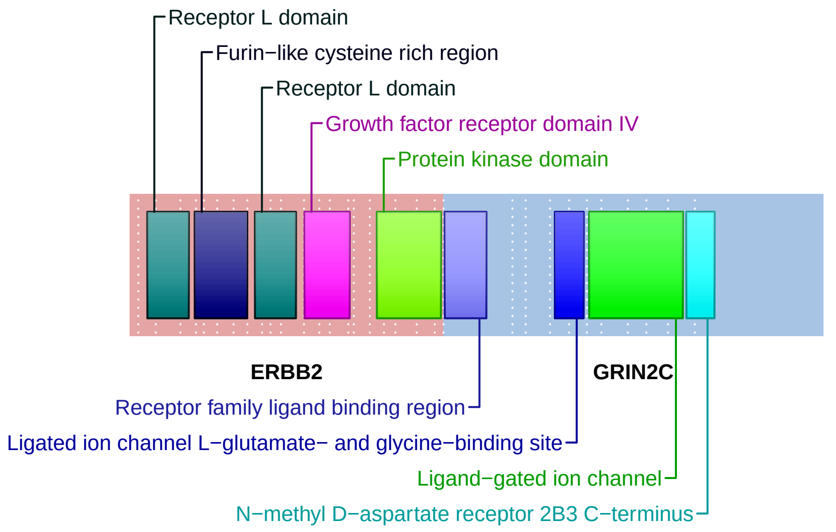
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0



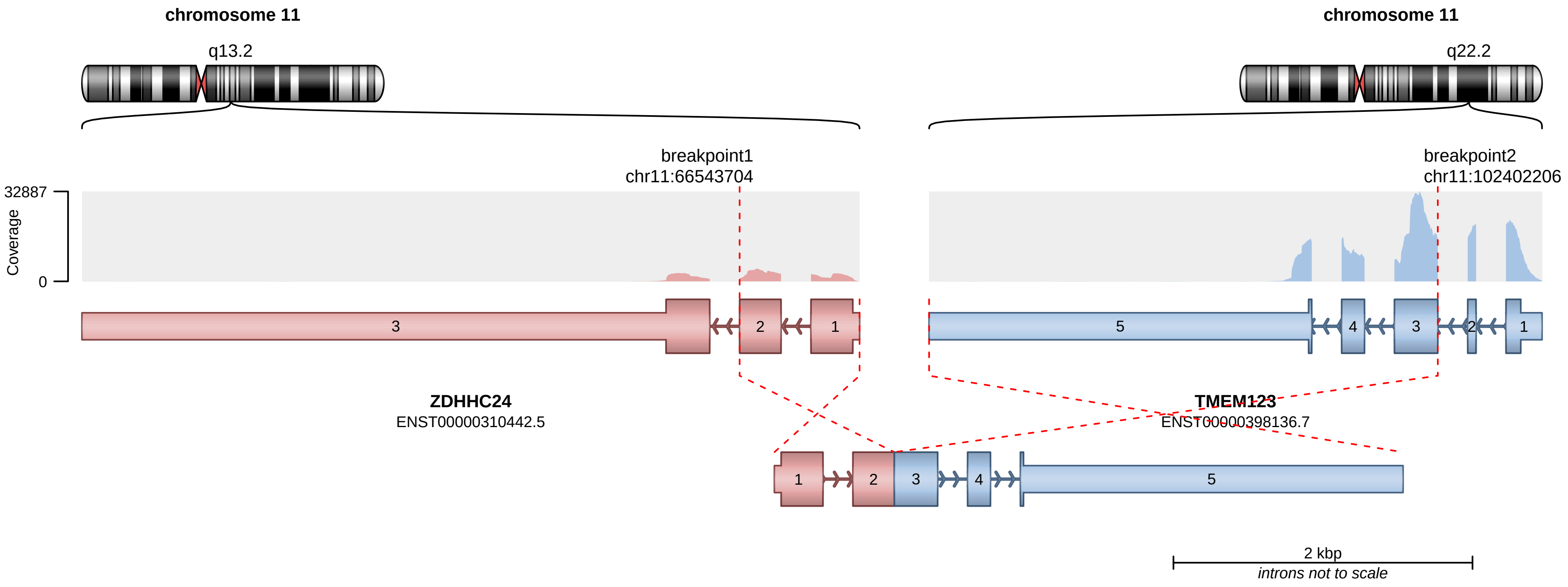


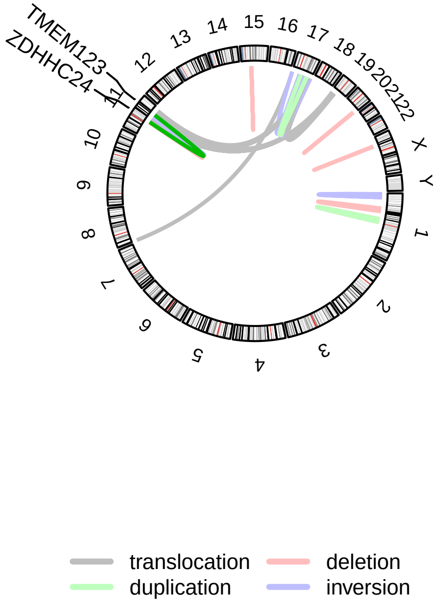
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

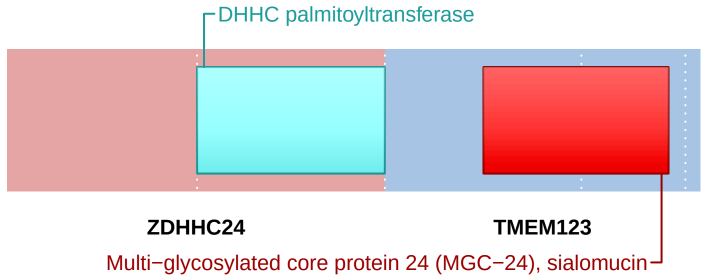
Split reads = 1
Discordant mates = 0





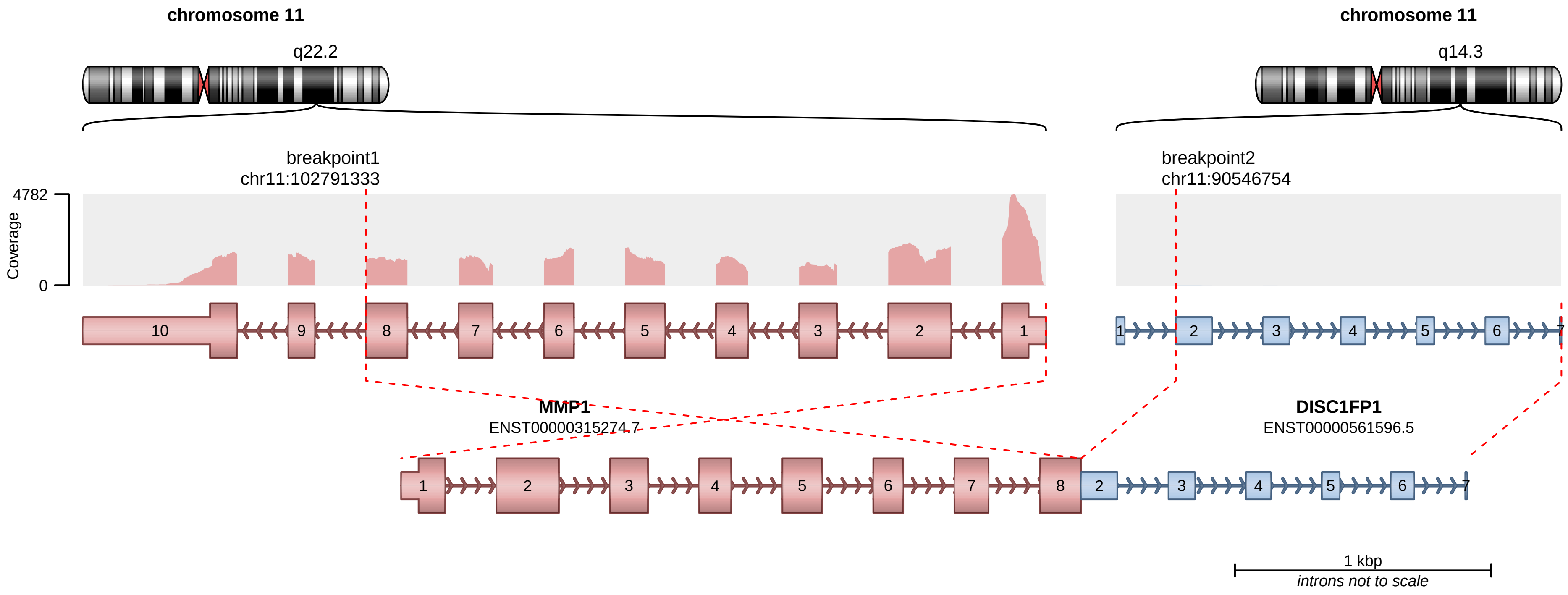
RETAINED PROTEIN DOMAINS

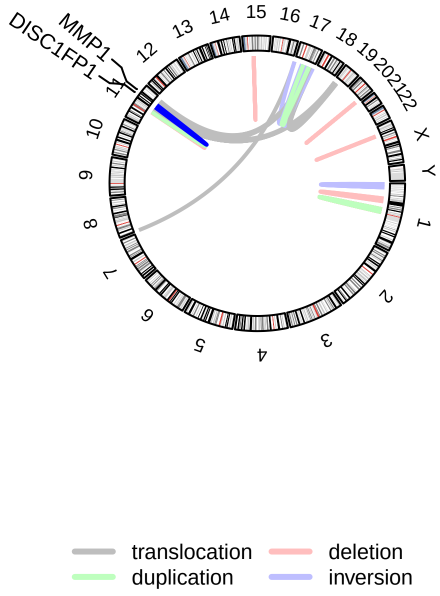
reading frame unclear



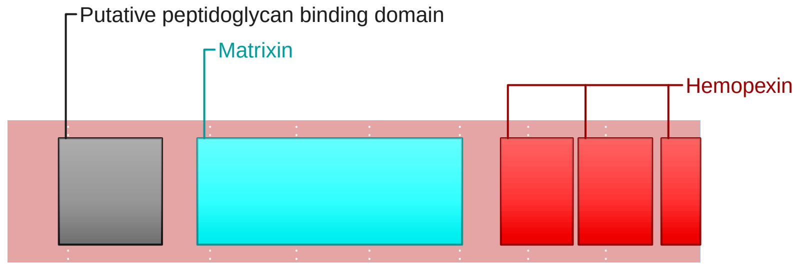
SUPPORTING READ COUNT

Split reads = 14
Discordant mates = 0





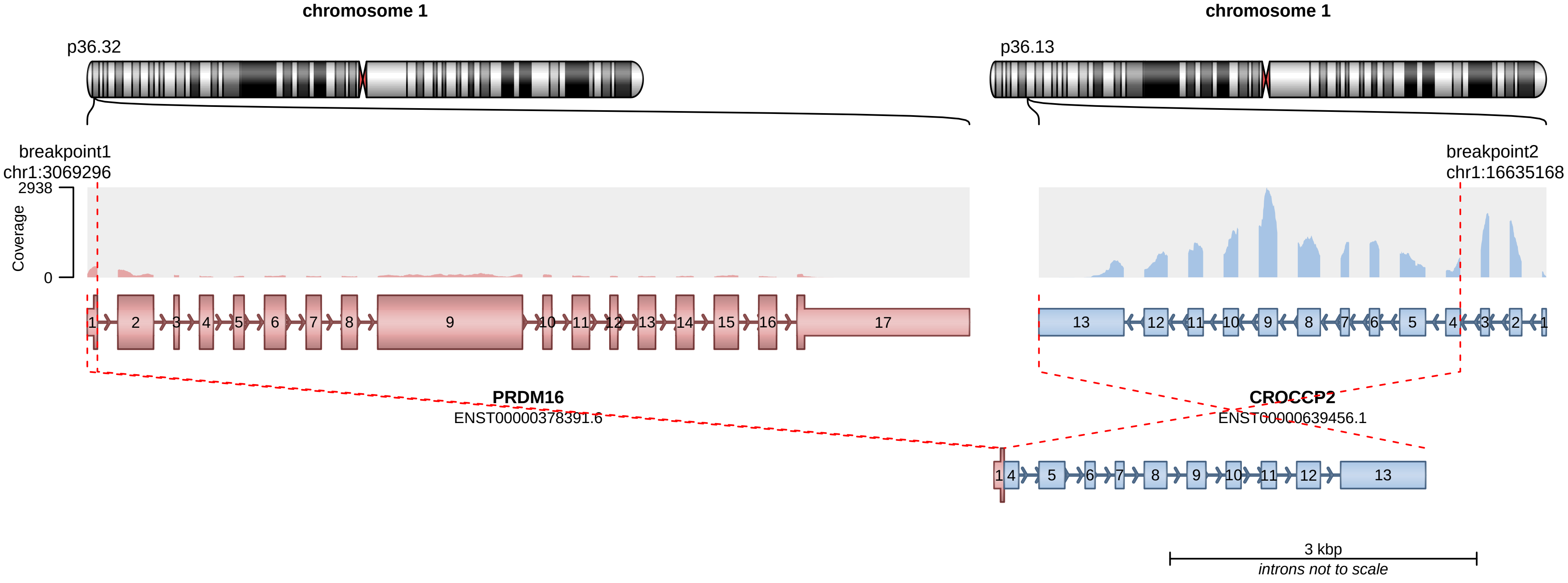
RETAINED PROTEIN DOMAINS
reading frame unclear

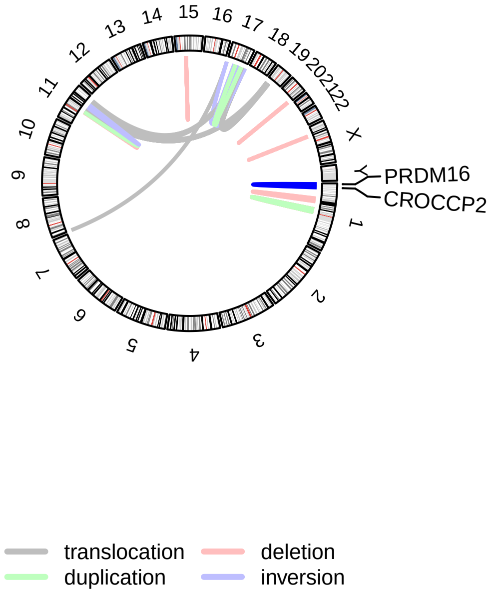


MMP1

SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 1

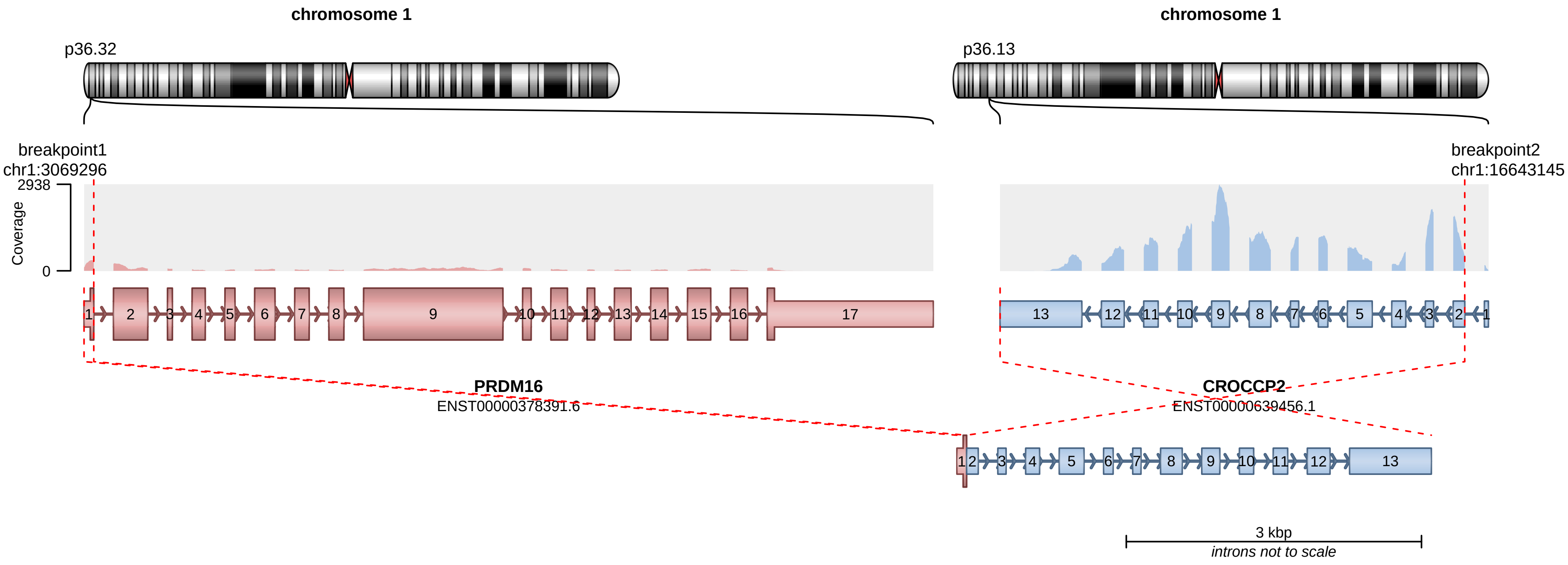


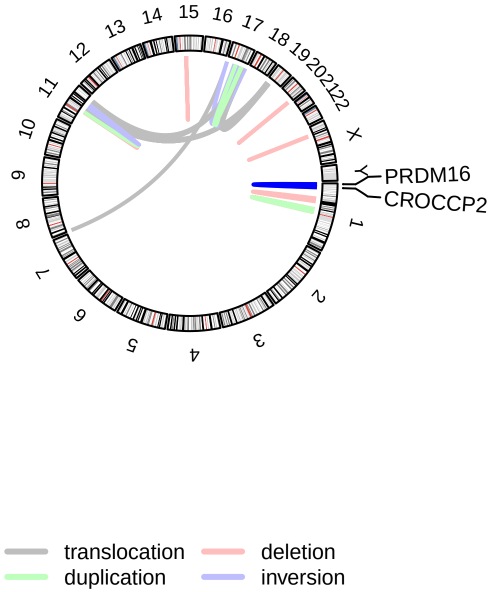


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 0

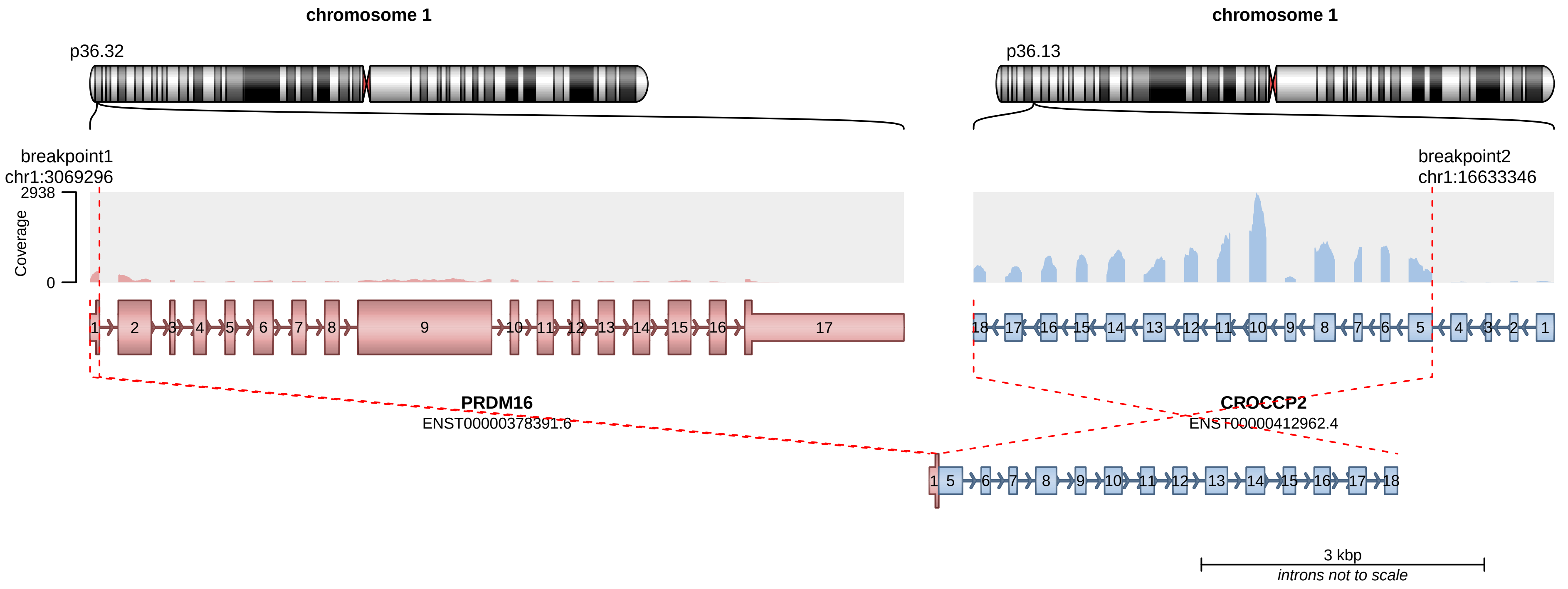


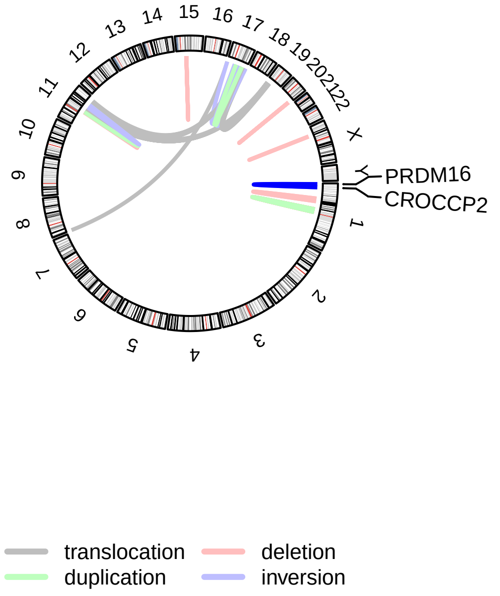


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

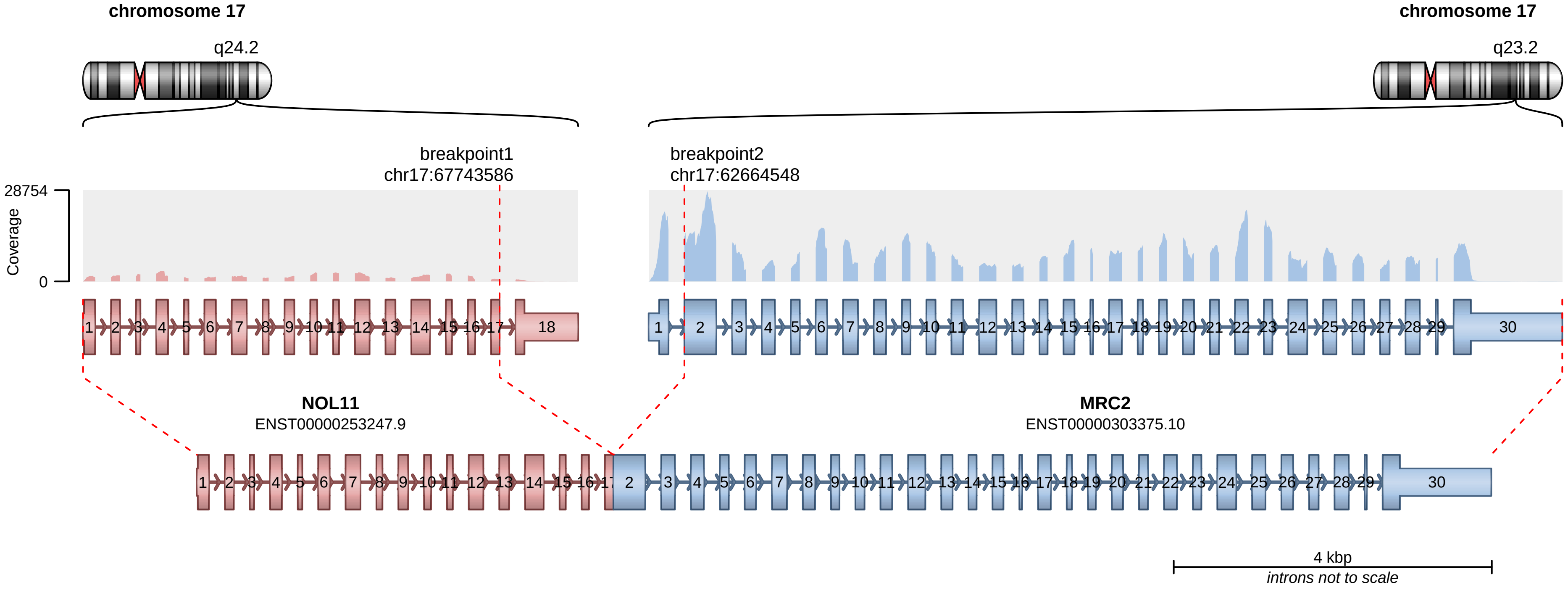


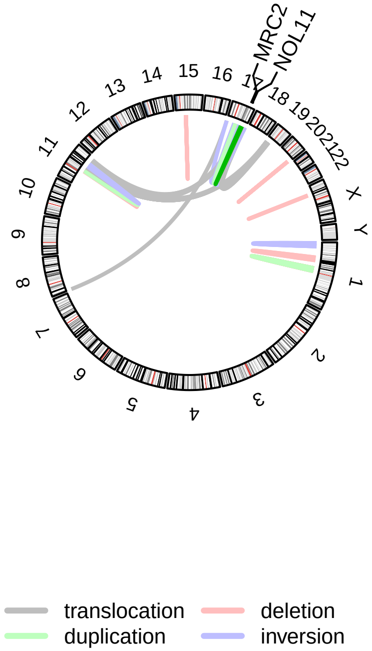


No protein domains retained in fusion.

SUPPORTING READ COUNT

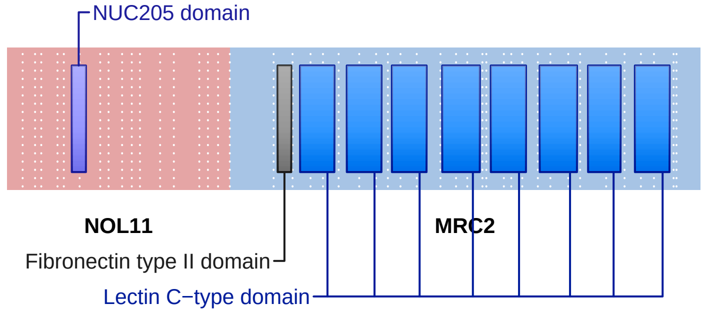
Split reads = 1
Discordant mates = 0





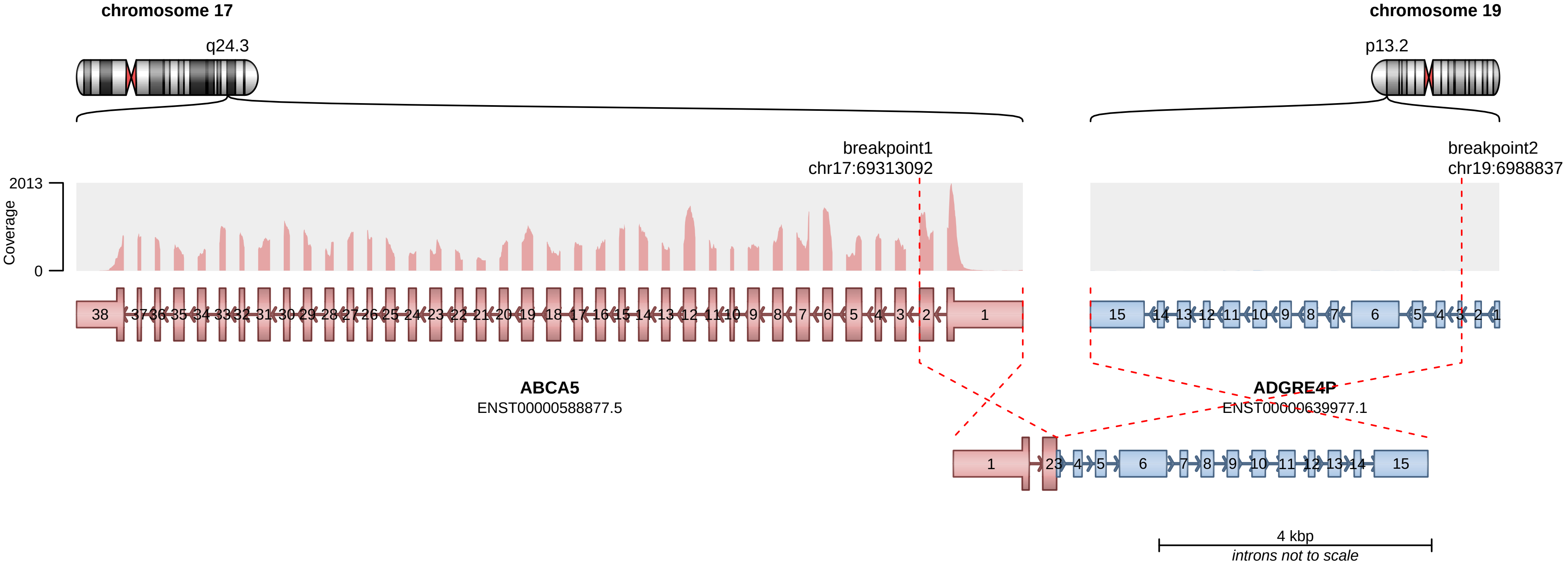
RETAINED PROTEIN DOMAINS

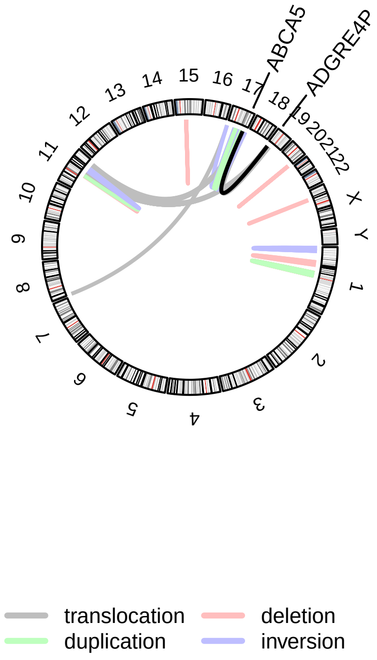
reading frame unclear

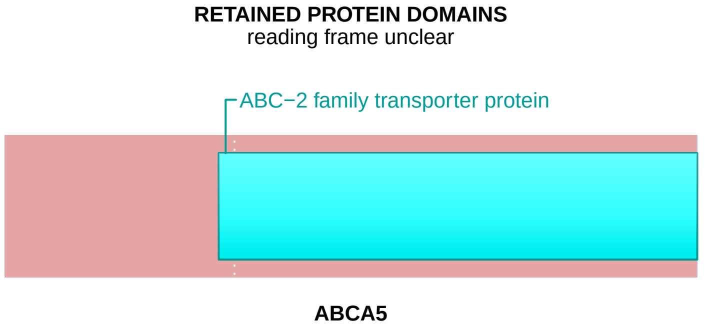


SUPPORTING READ COUNT

Split reads = 9
Discordant mates = 0

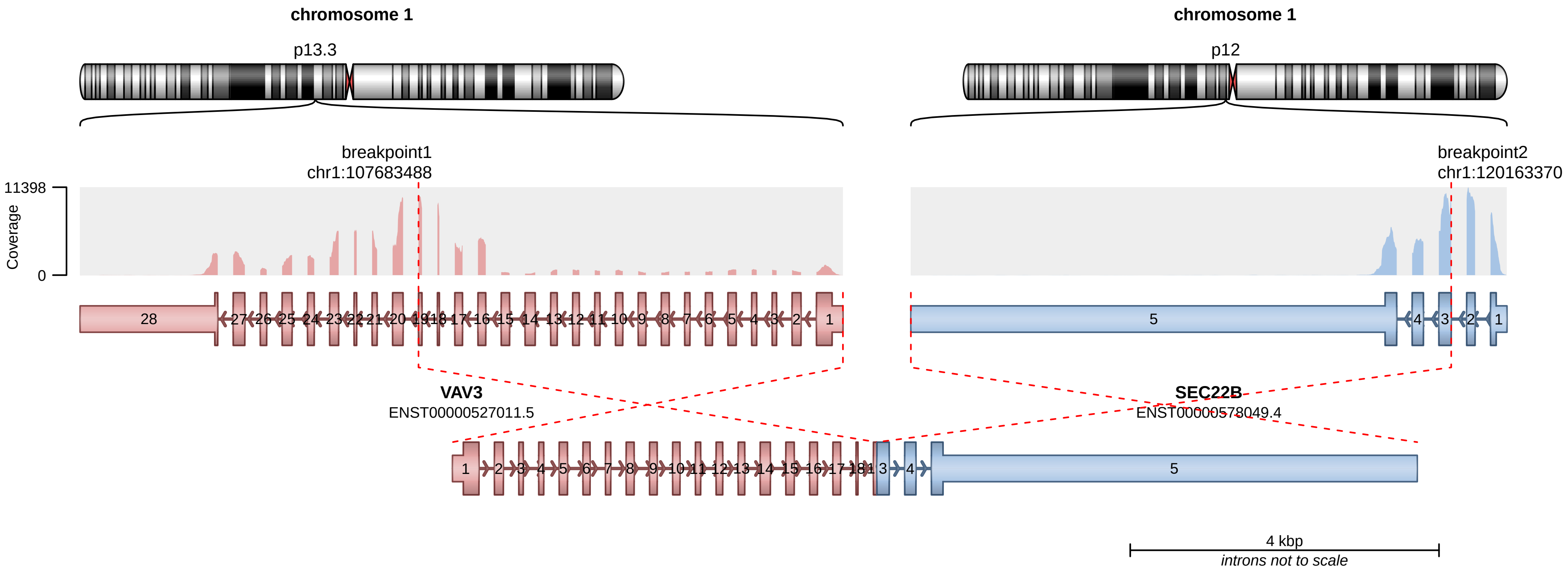


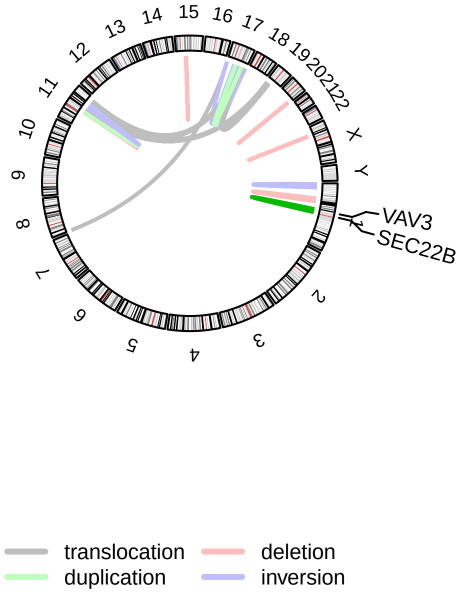


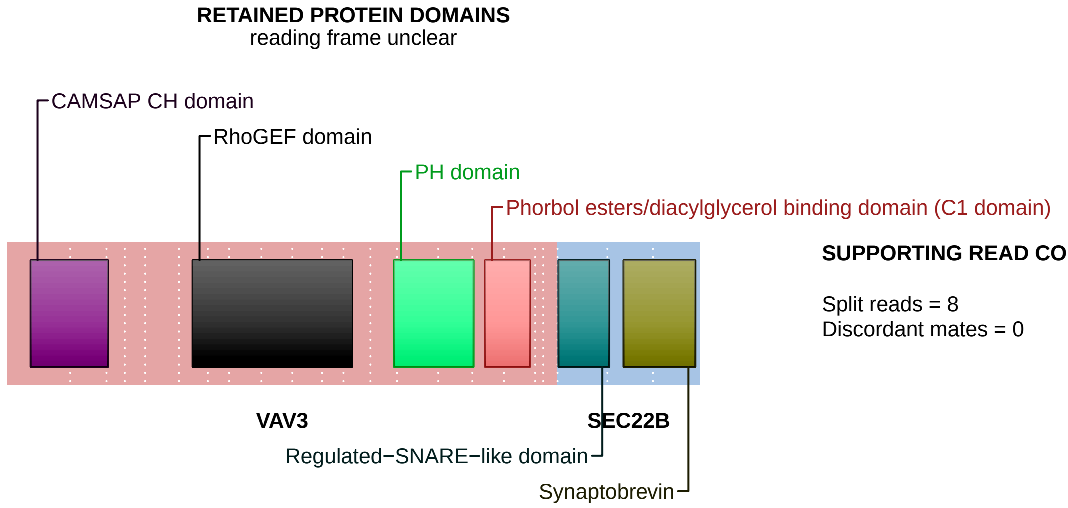


SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 0

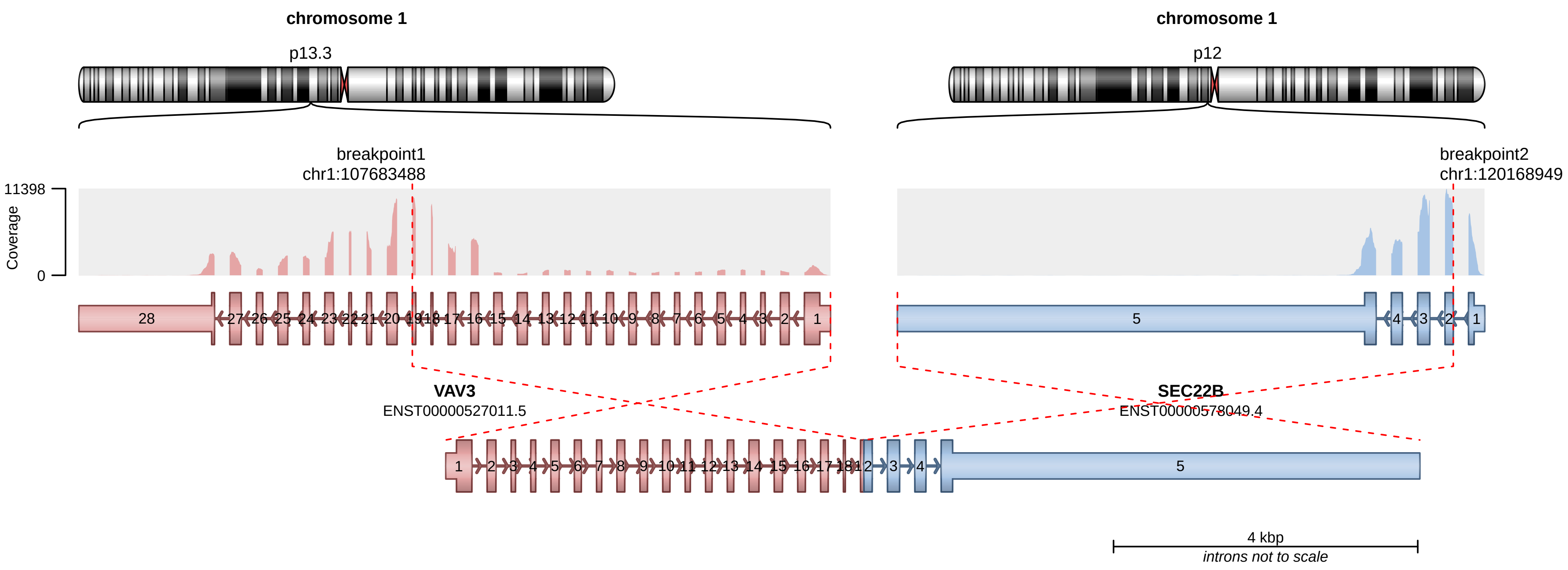


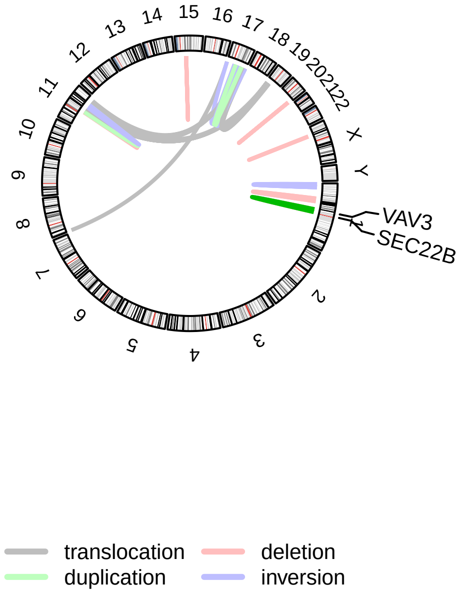


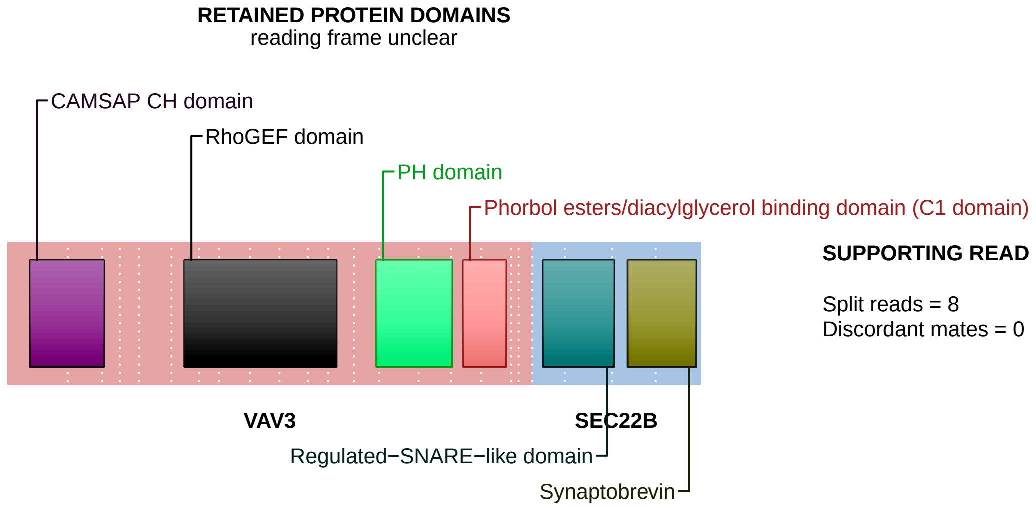


SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 0

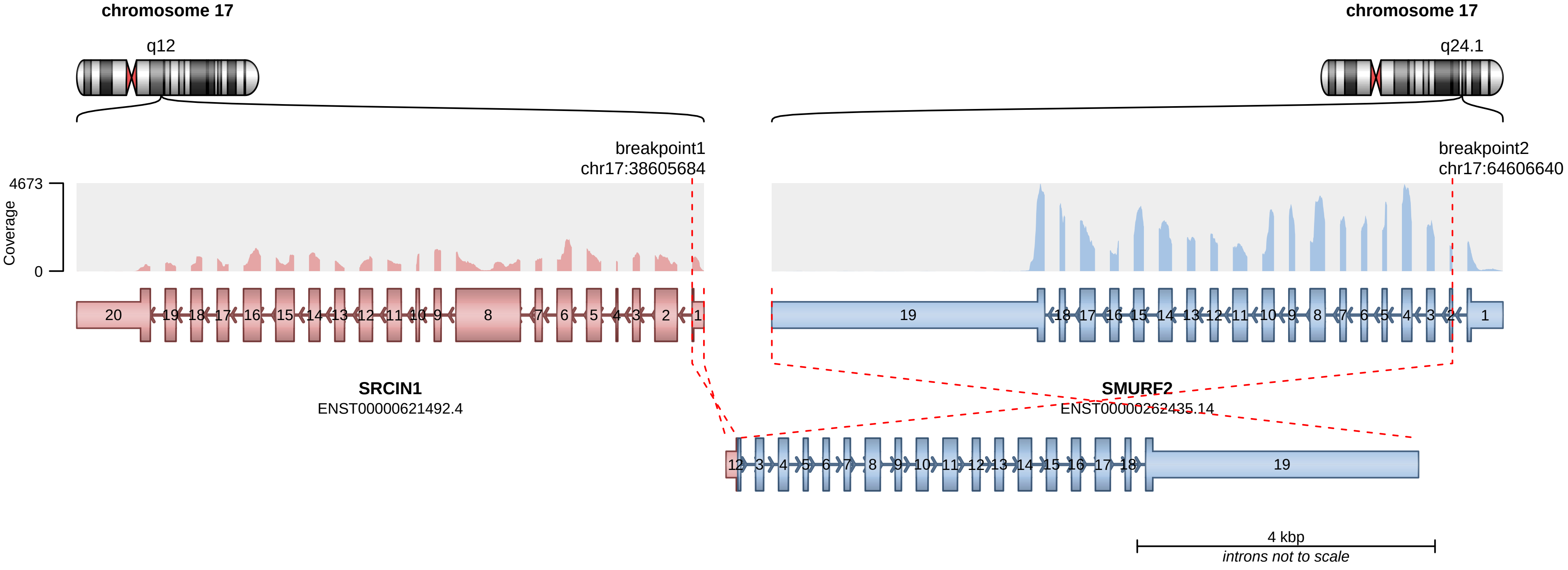


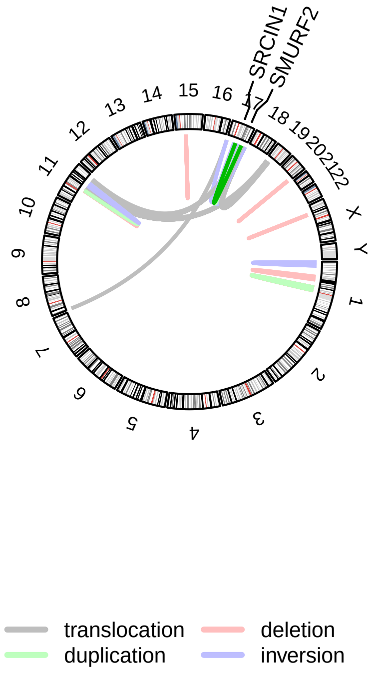




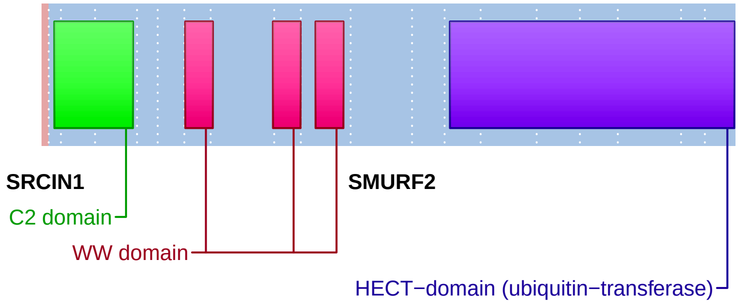
SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 0



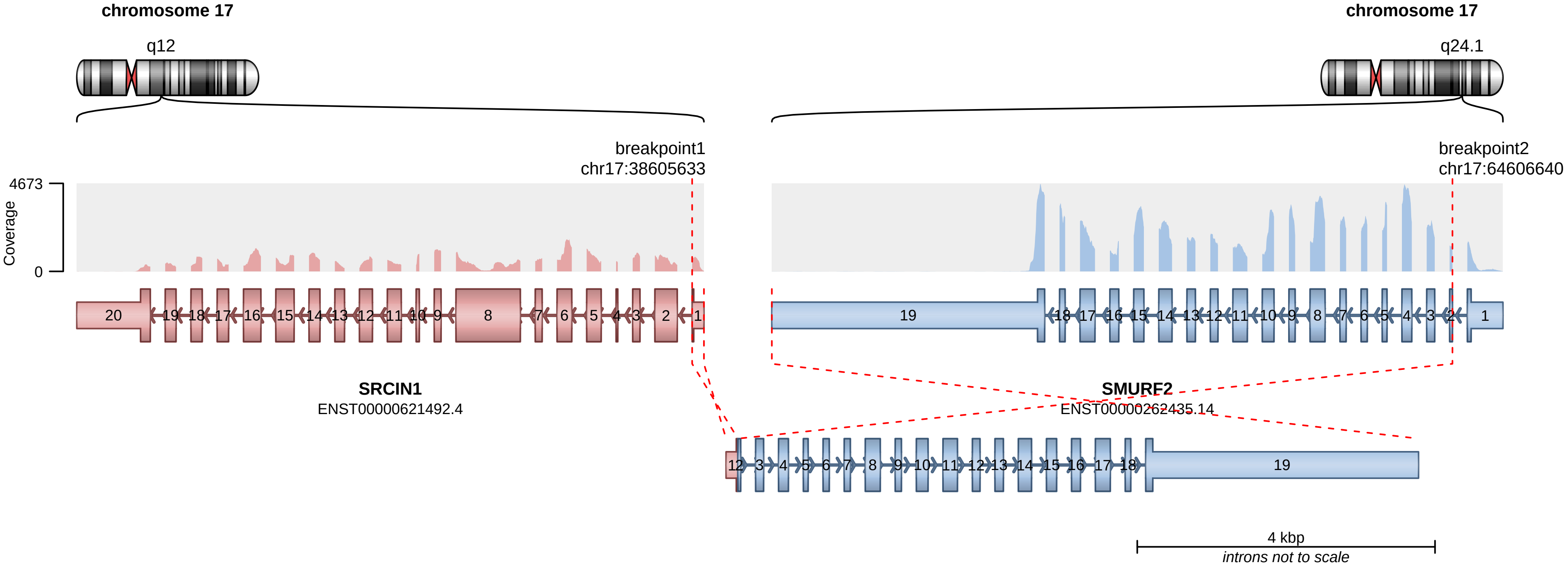


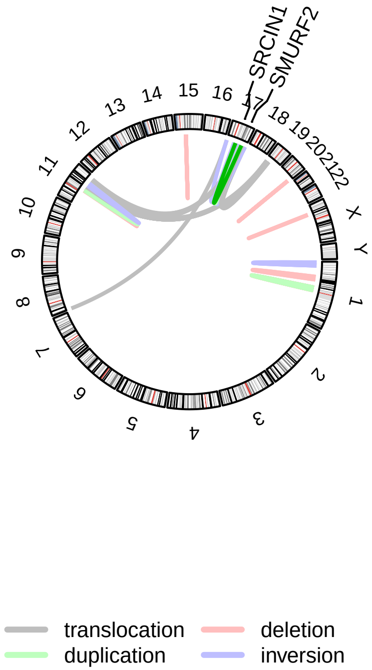
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

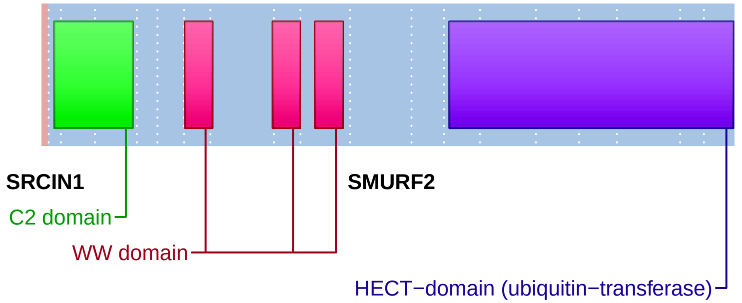
Split reads = 7
Discordant mates = 0





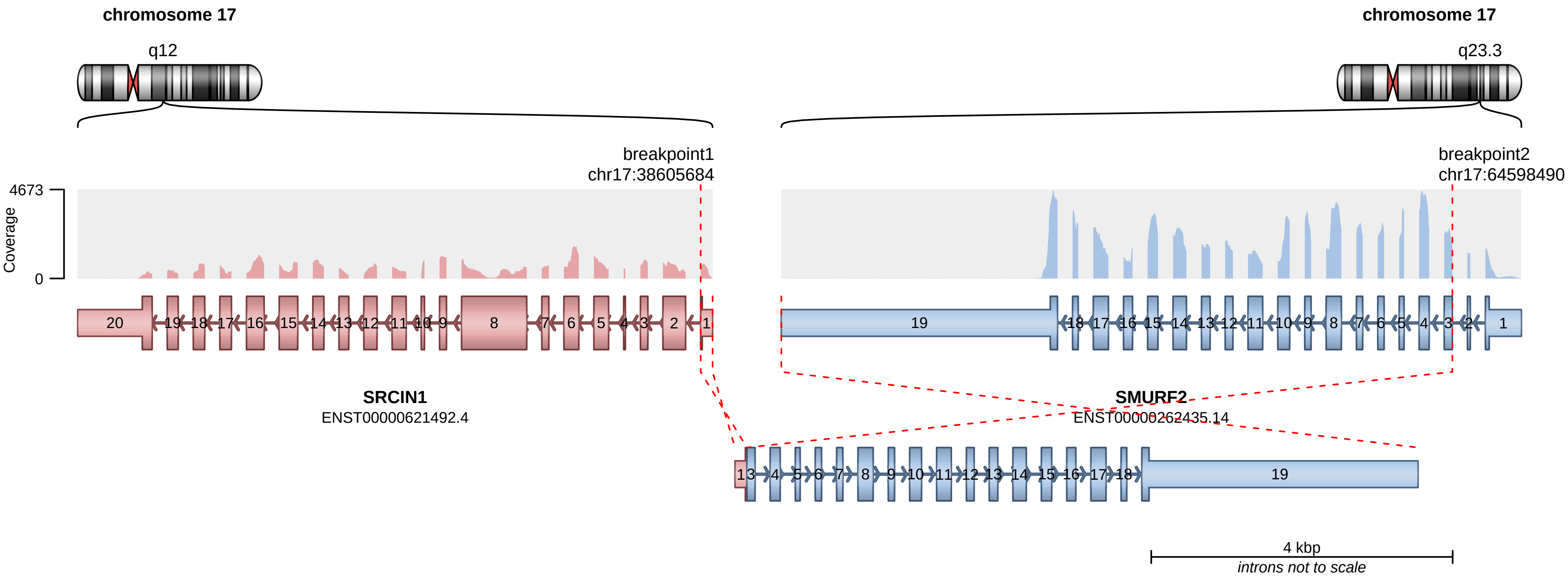
RETAINED PROTEIN DOMAINS

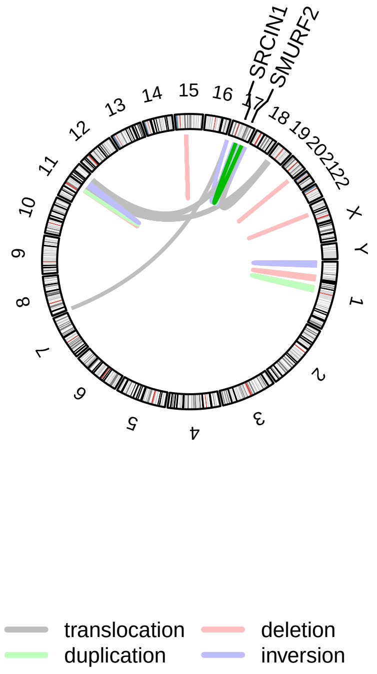
reading frame unclear



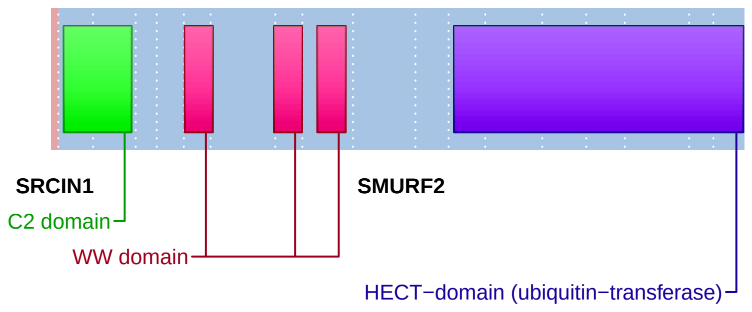
SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 0





RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0