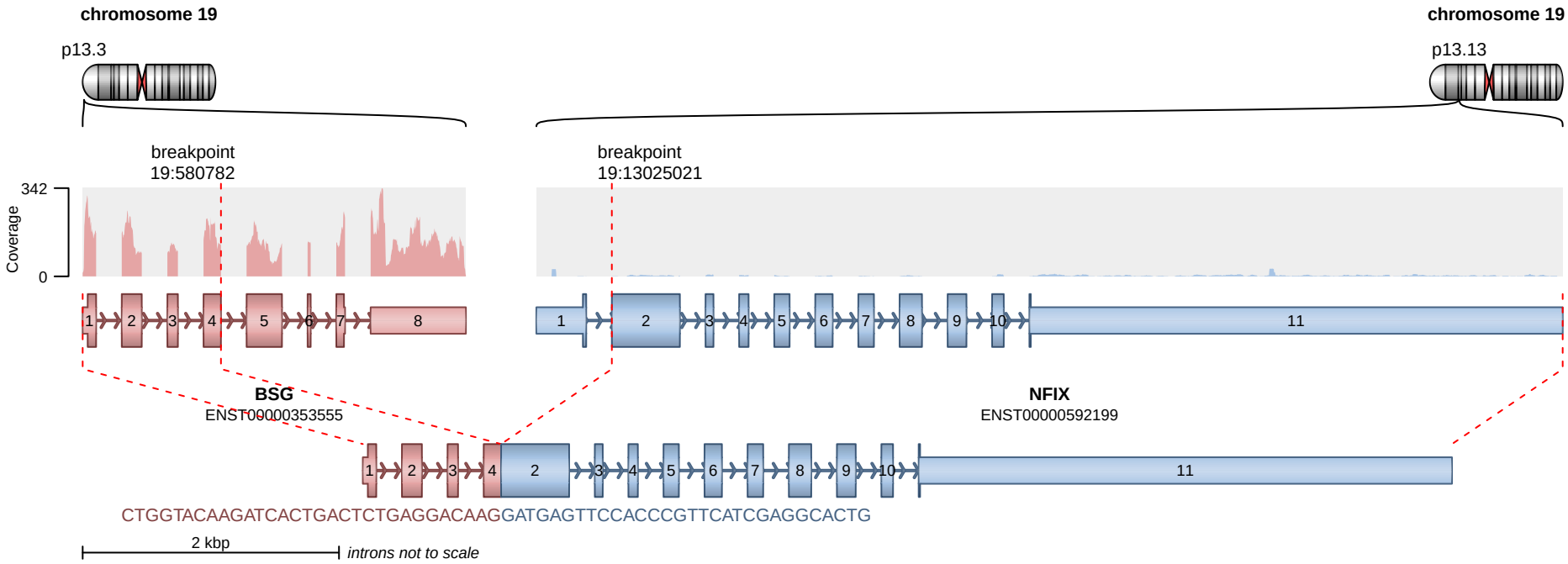
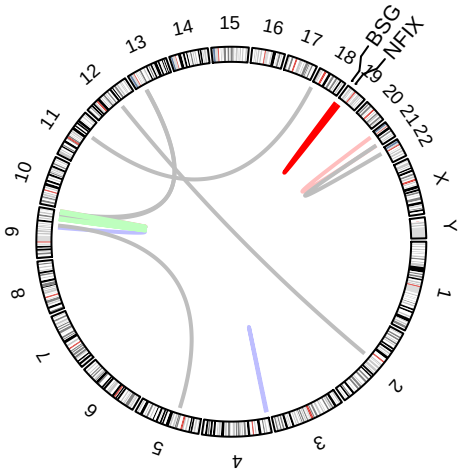
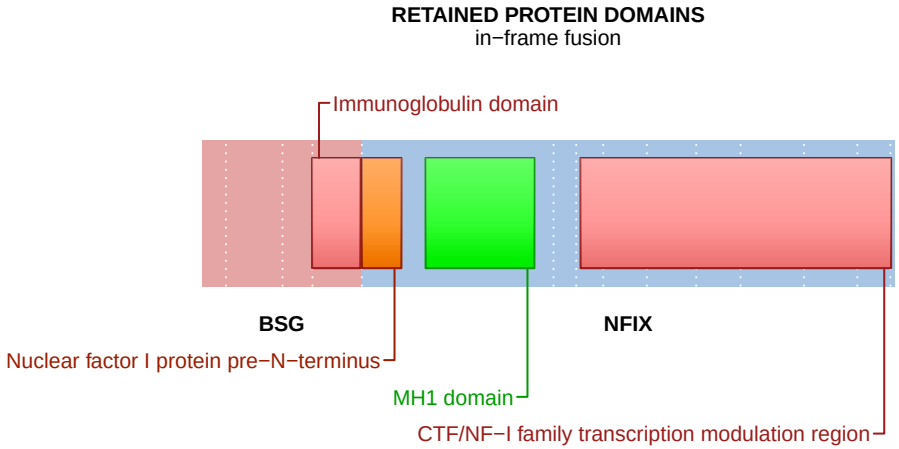
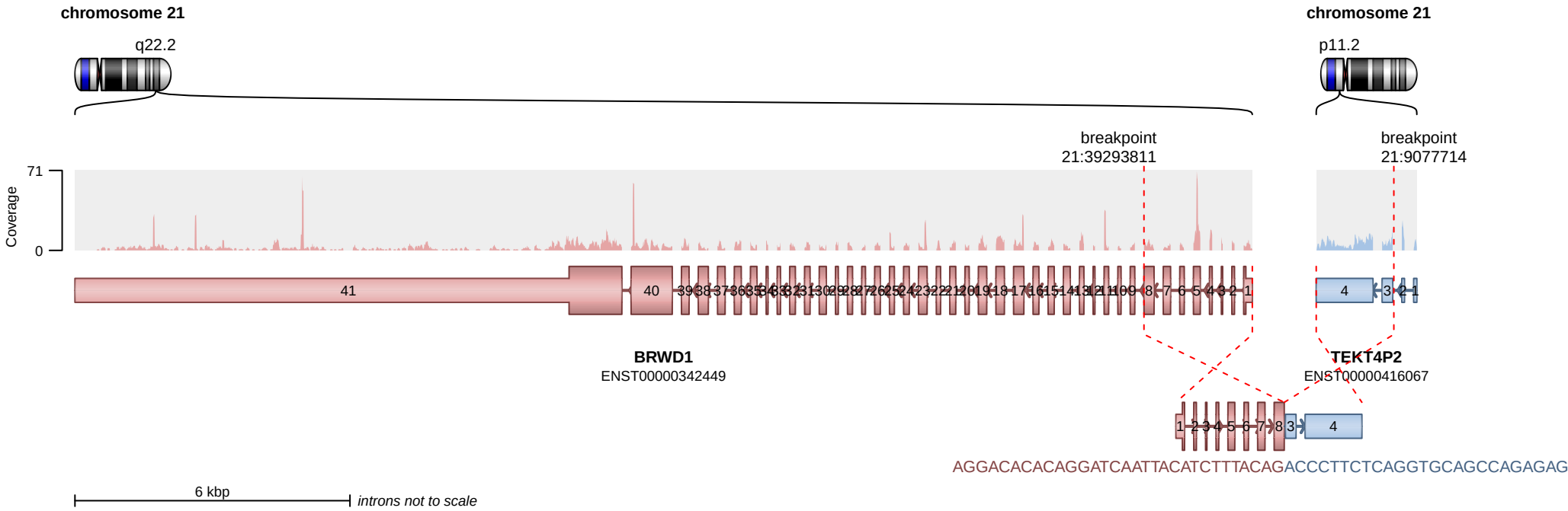


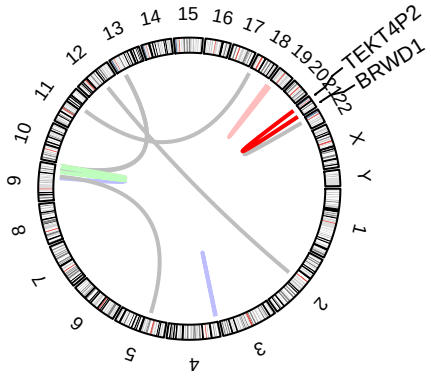




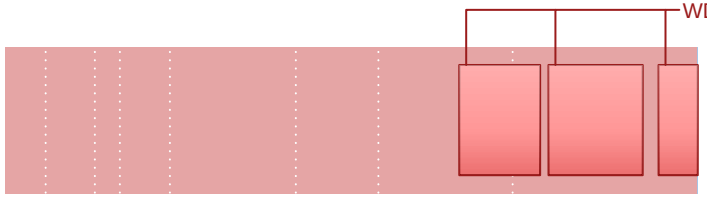
SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 23





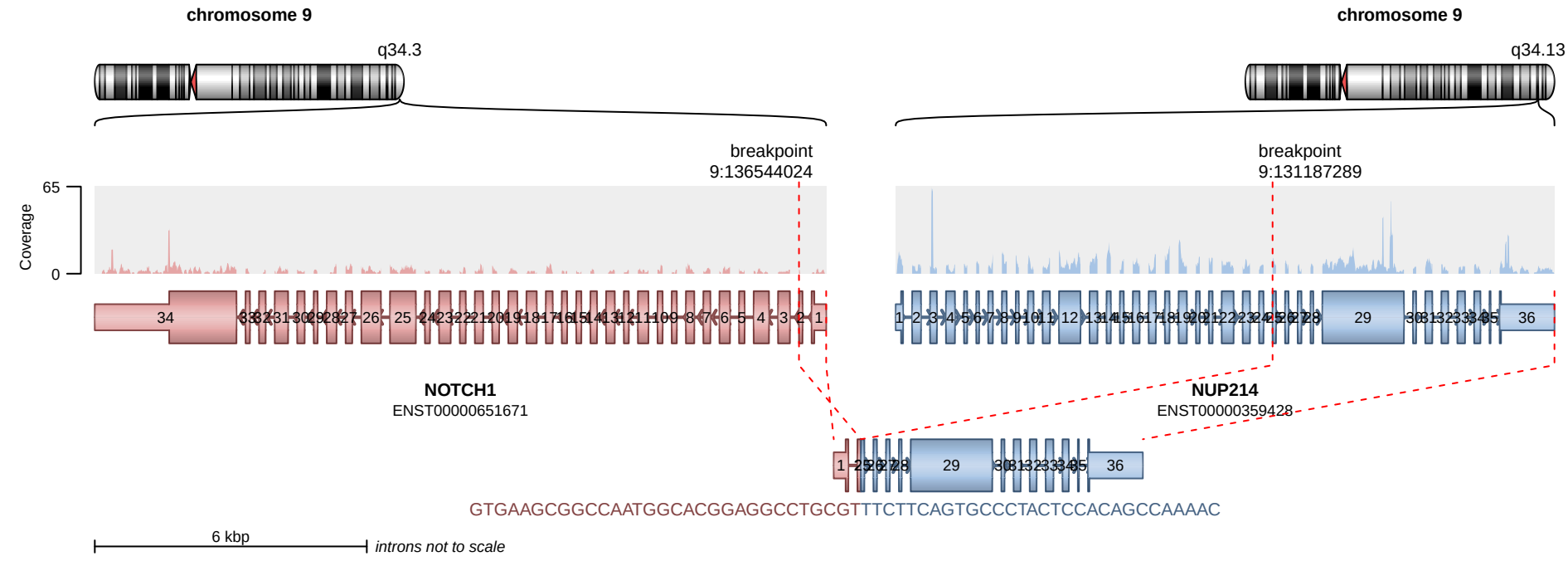
RETAINED PROTEIN DOMAINS
out−of−frame fusion

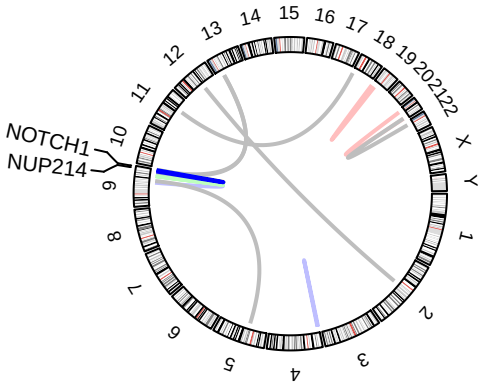


SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 6

translocation
deletion
duplication
inversion

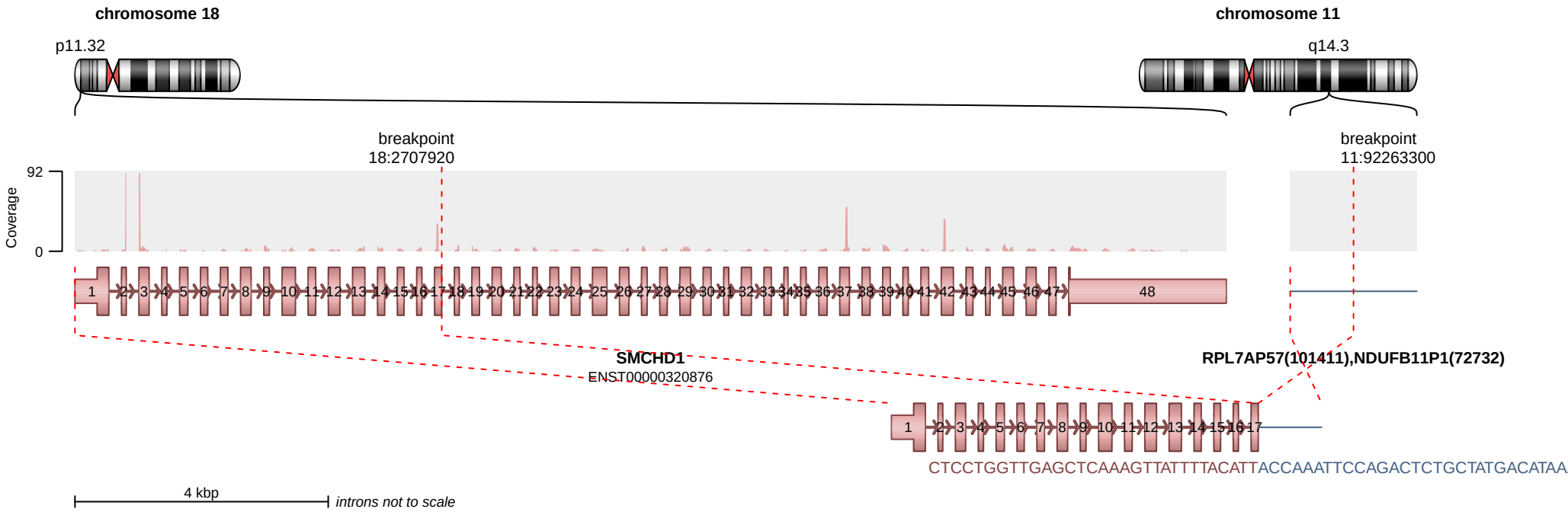


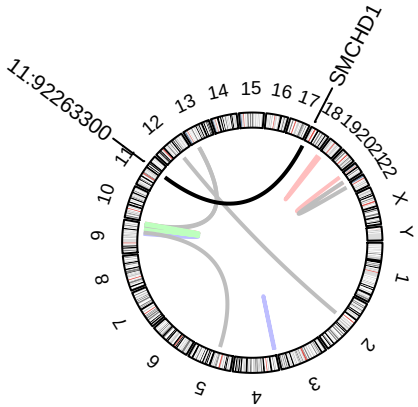


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 7

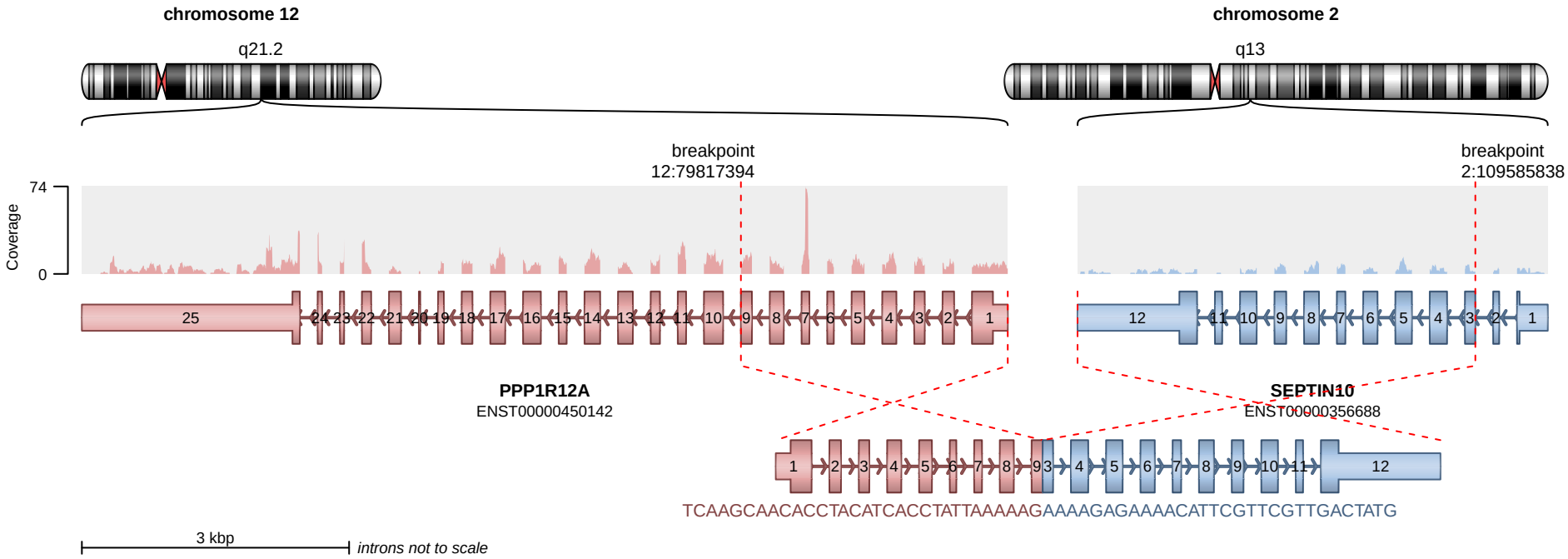


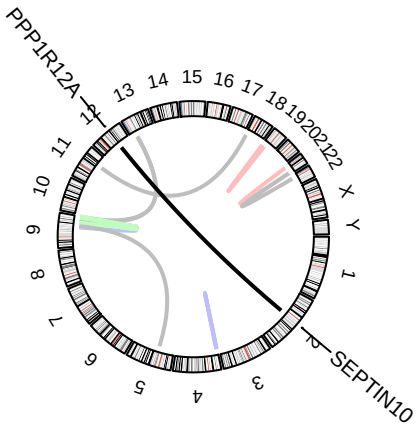


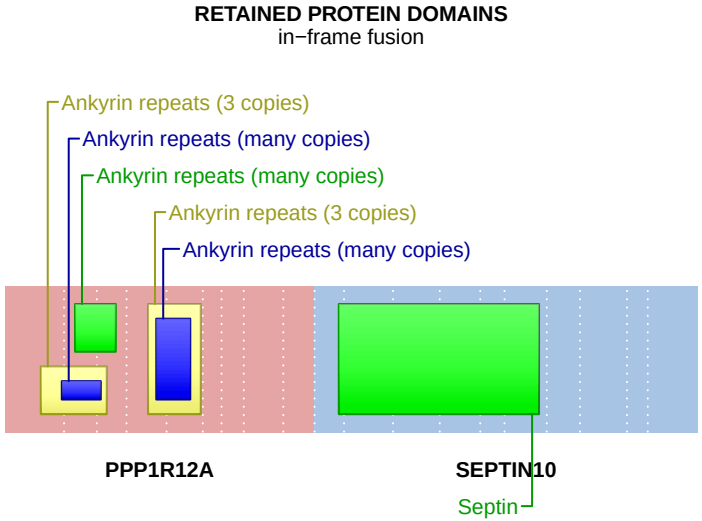
RETAINED PROTEIN DOMAINS
out−of−frame fusion

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 4



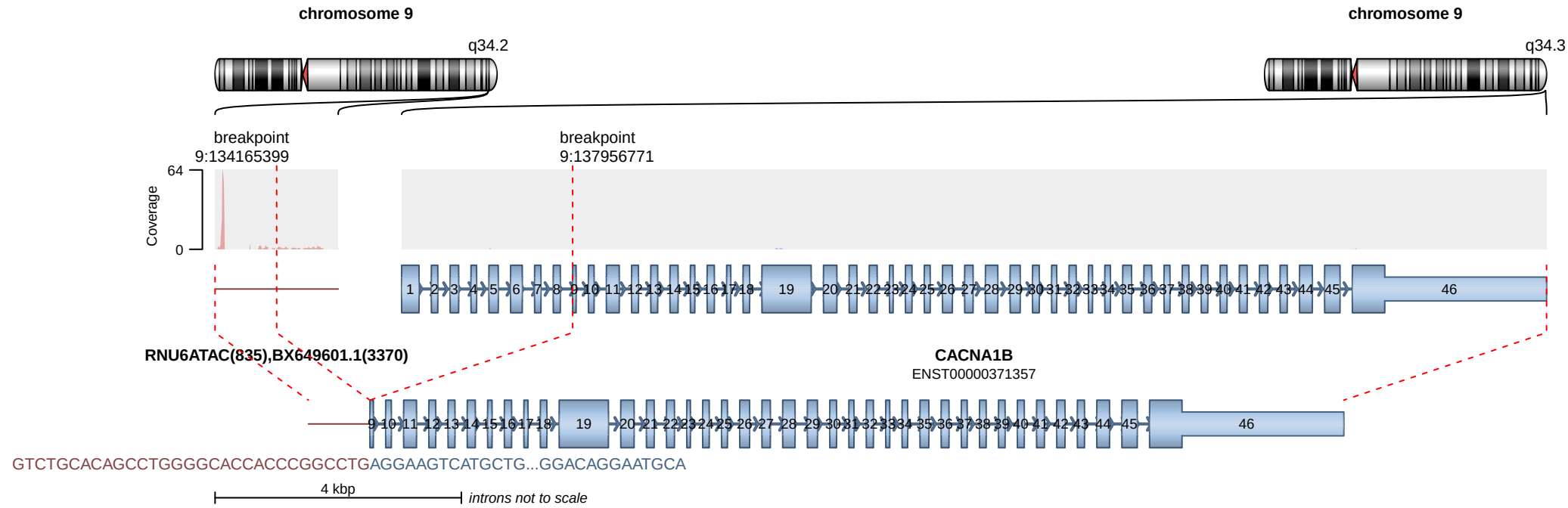


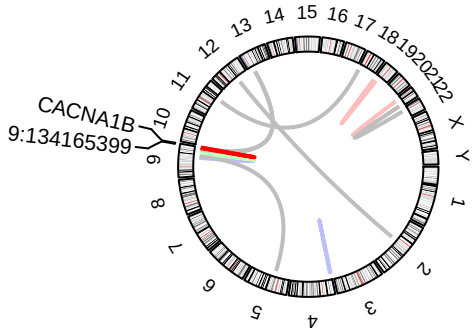


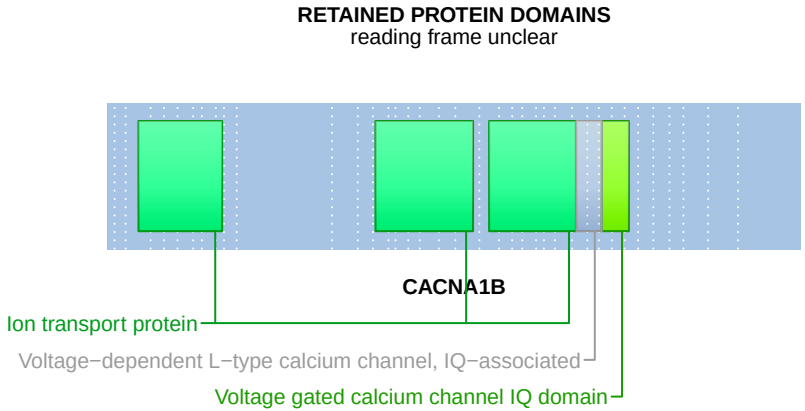
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 2

translocation
deletion
duplication
inversion

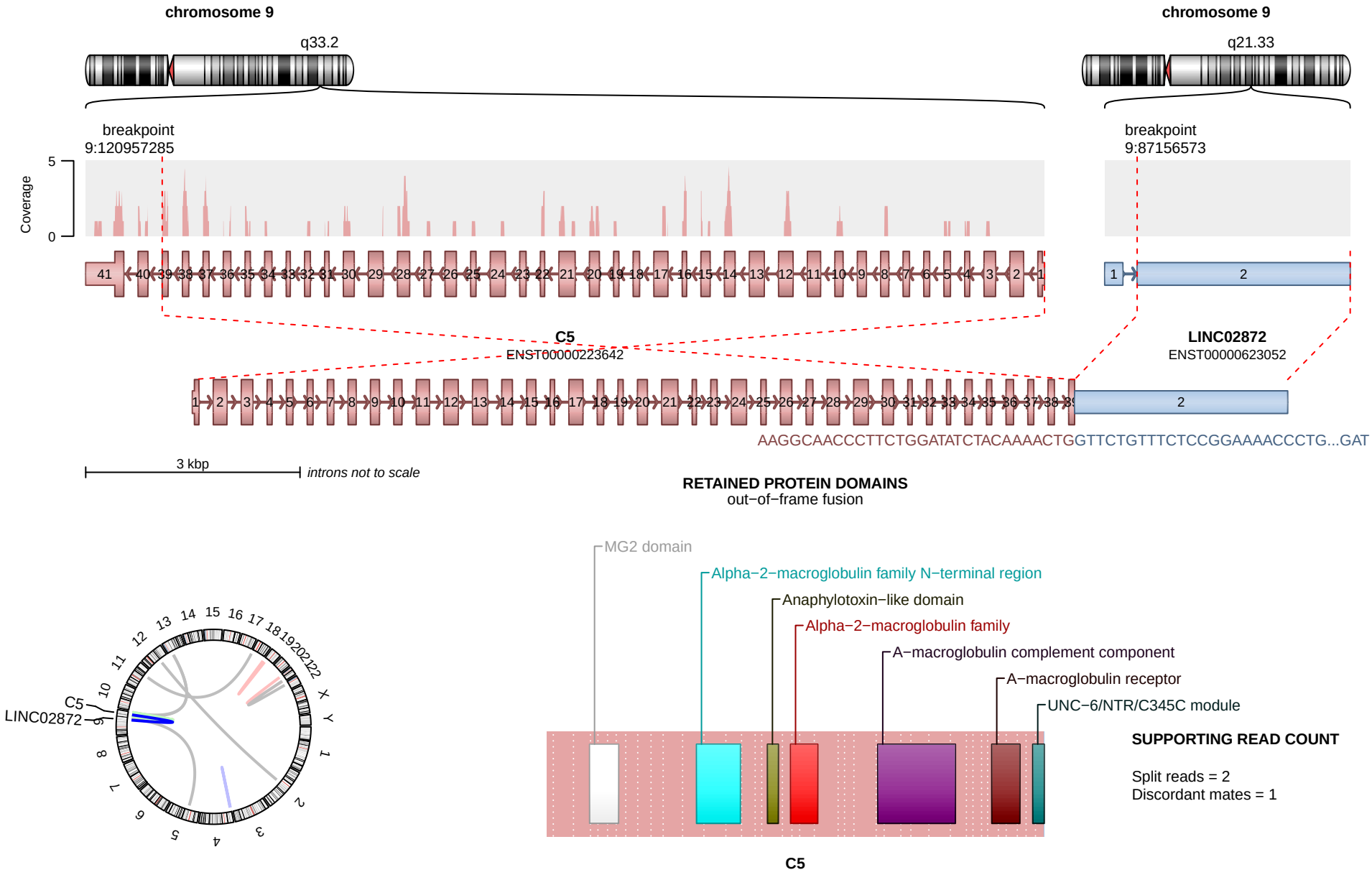


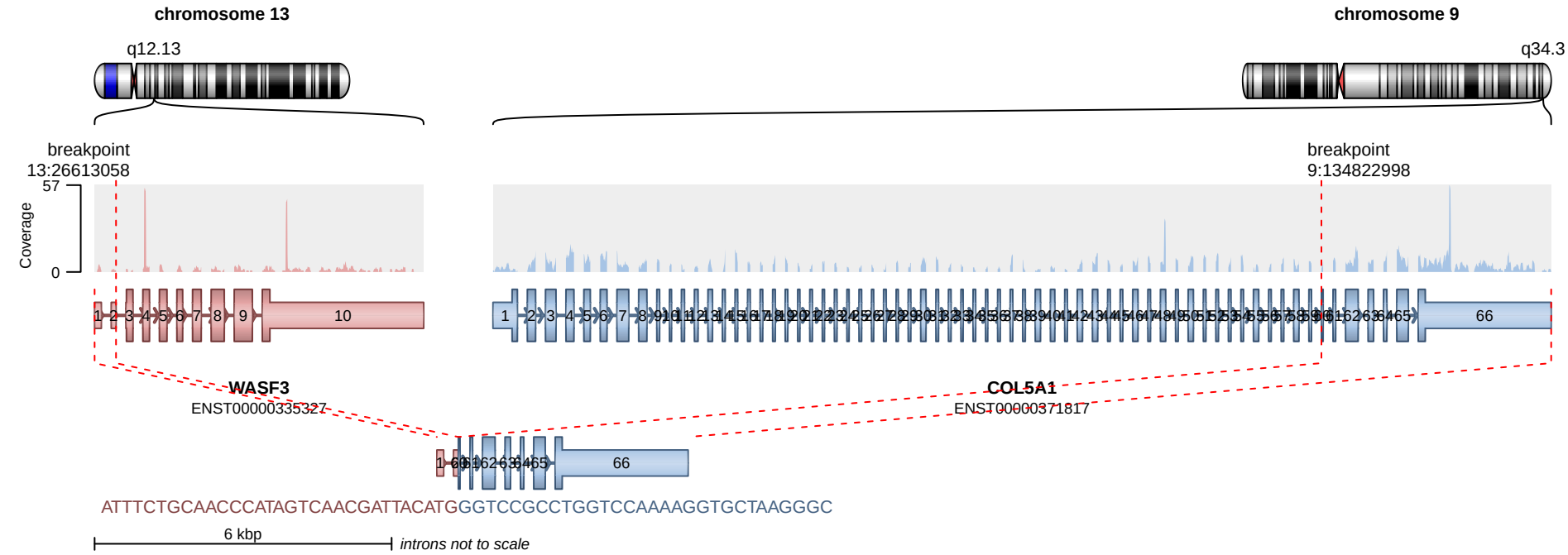


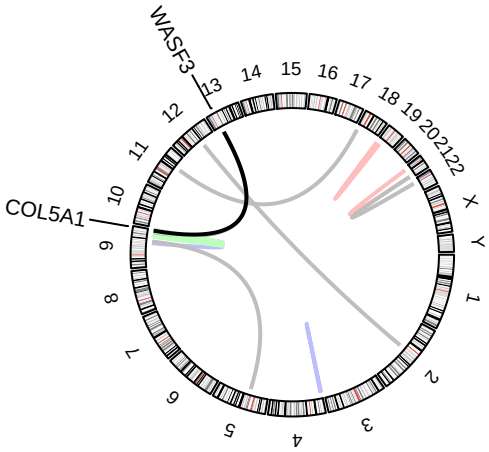


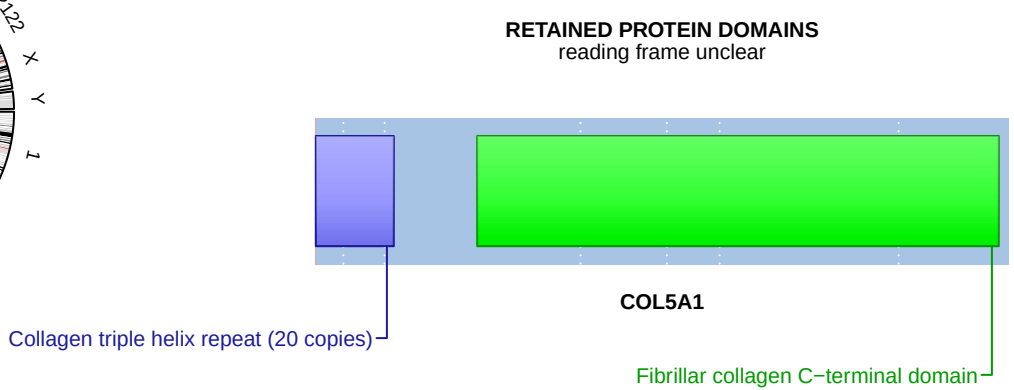
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 4


chromosome 9
q33.2
chromosome 9
q21.33
breakpoint
9:120957285
breakpoint
9:87156573
Coverage
5
0
C5
ENST00000223642
LINC02872
ENST00000623052
AAGGCAACCCTTCTGGATATCTACAAAACTGGTTCTGTTTCTCCGGAAAACCCTG...GAT
3 kbp
introns not to scale
RETAINED PROTEIN DOMAINS
out−of−frame fusion
MG2 domain
Alpha−2−macroglobulin family N−terminal region
Anaphylotoxin−like domain
Alpha−2−macroglobulin family
A−macroglobulin complement component
A−macroglobulin receptor
UNC−6/NTR/C345C module
SUPPORTING READ COUNT
Split reads = 2
Discordant mates = 1
C5
LINC02872
translocation
deletion
duplication
inversion



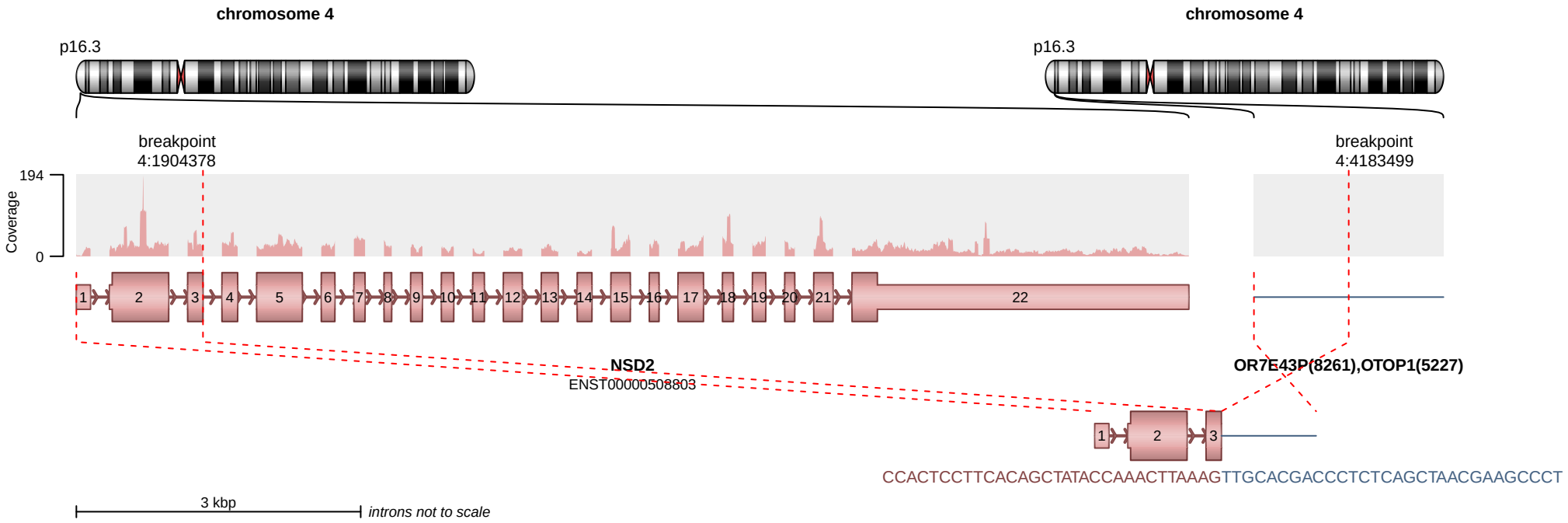


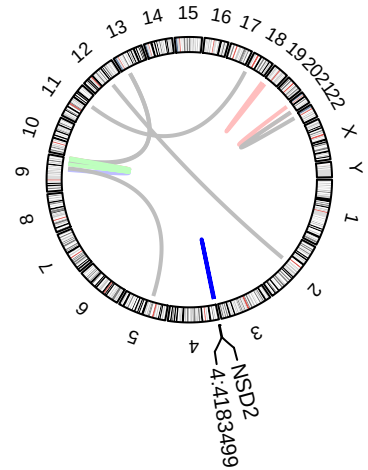


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

translocation
deletion
duplication
inversion

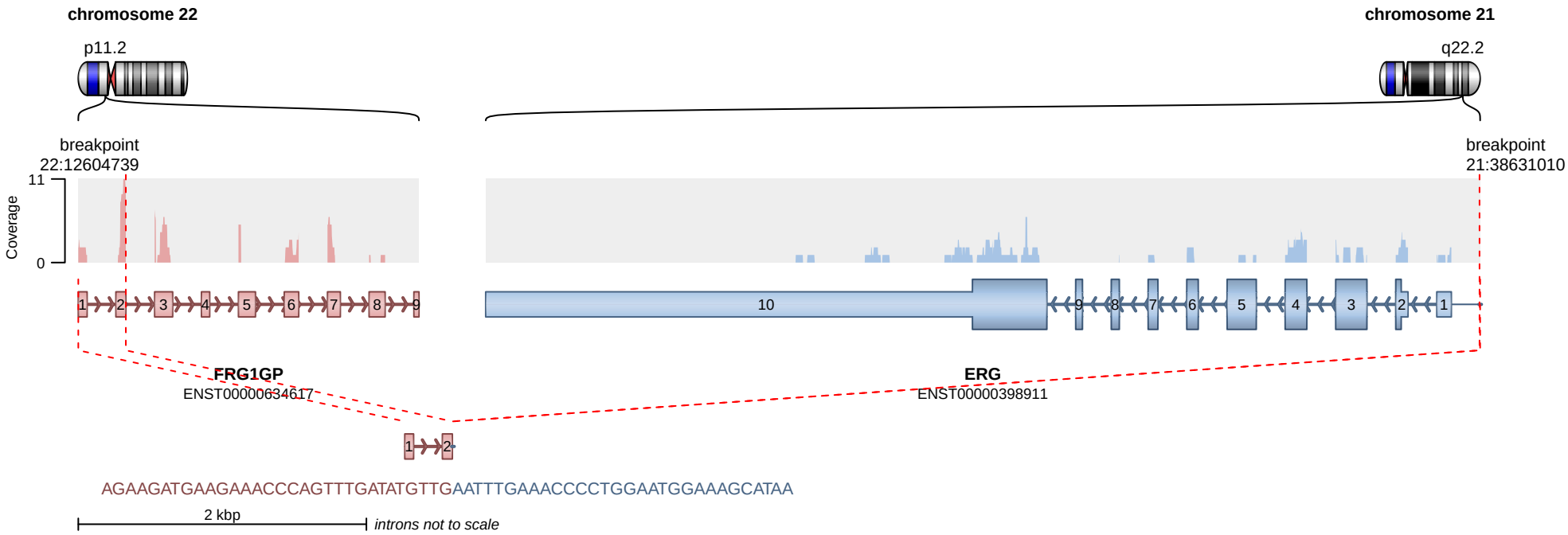


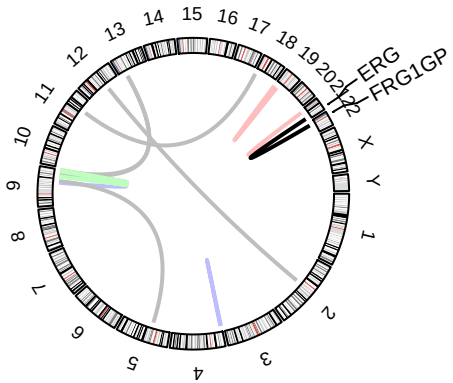


RETAINED PROTEIN DOMAINS
out−of−frame fusion

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

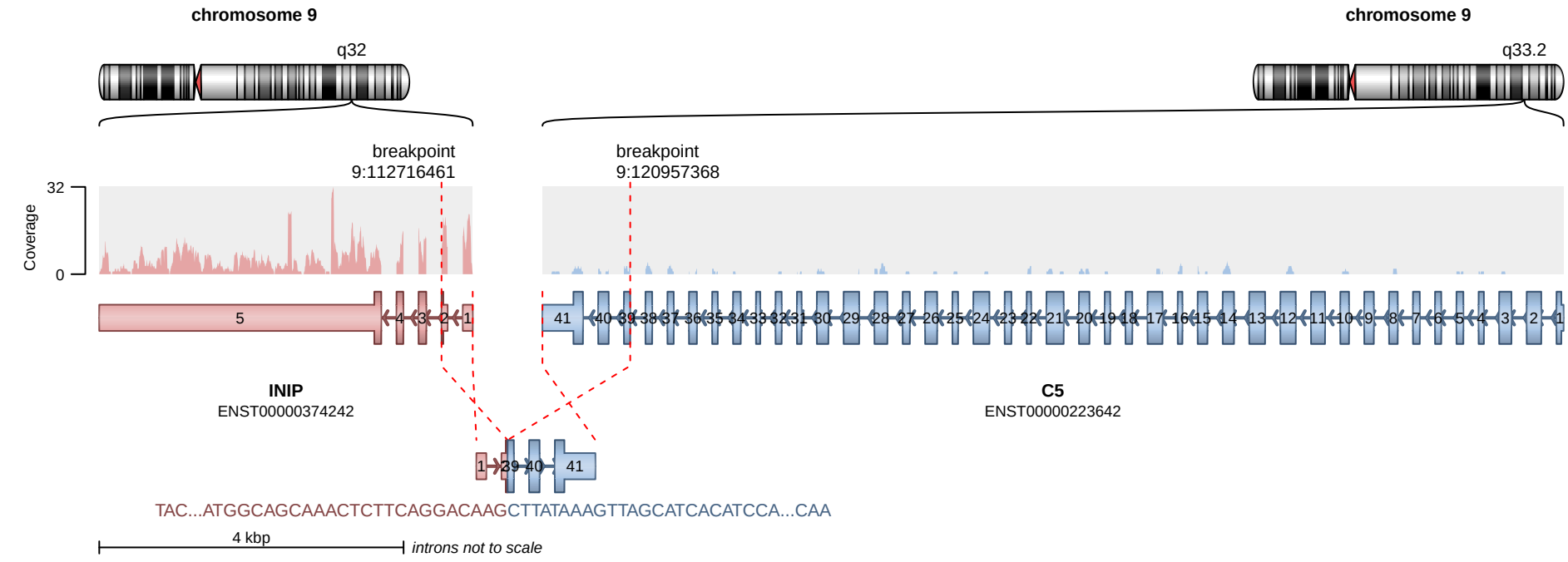


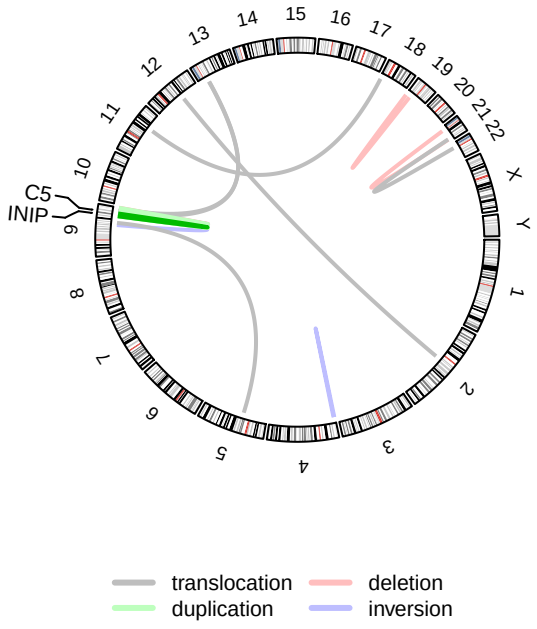


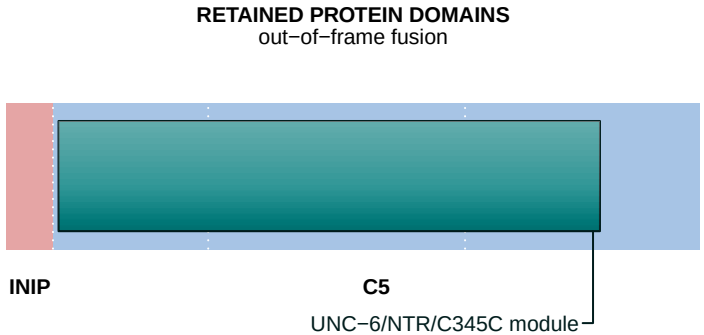
No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

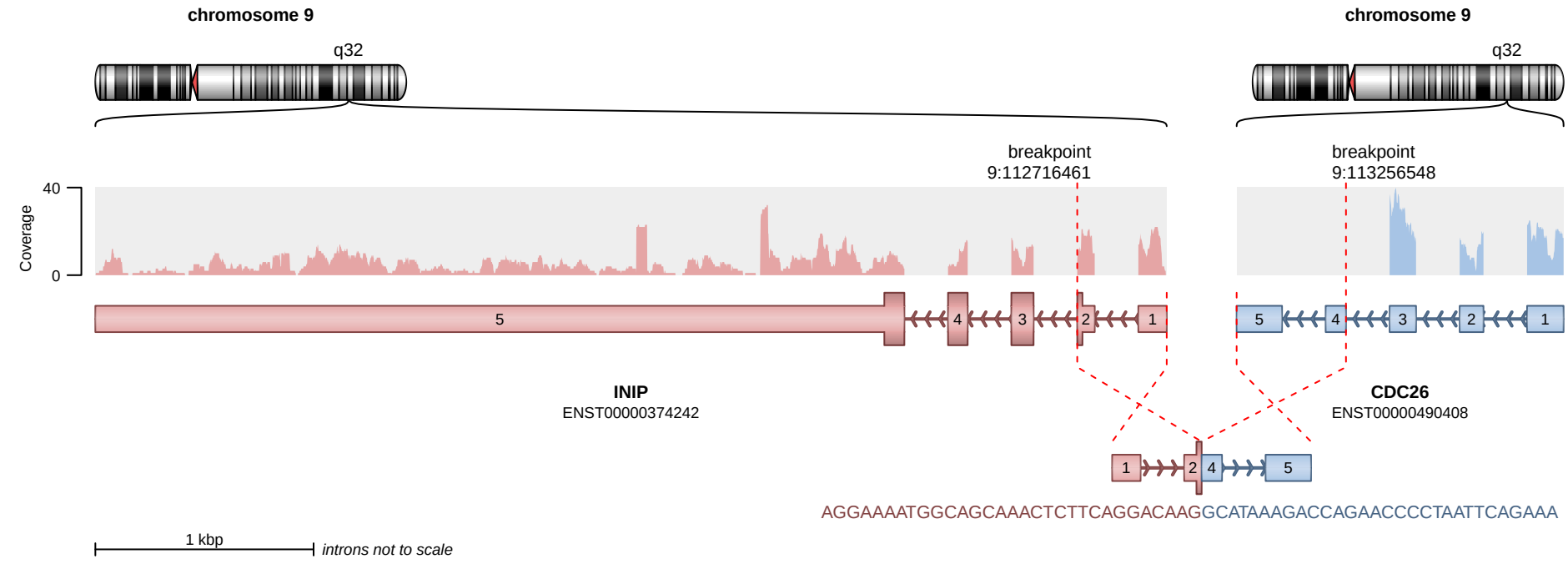


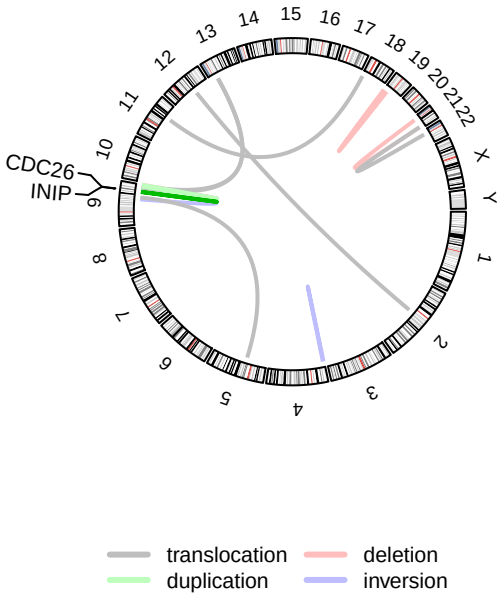




SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

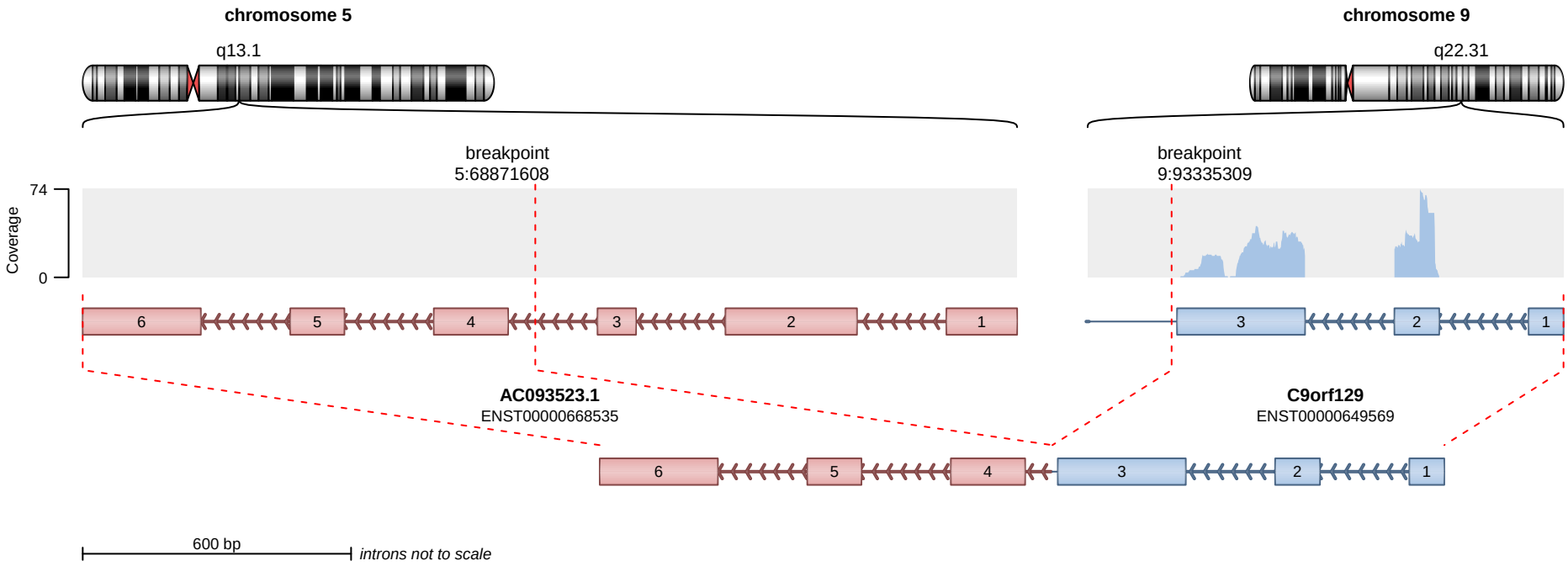


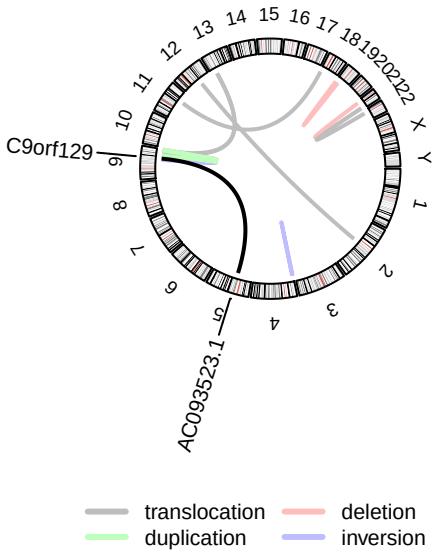


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

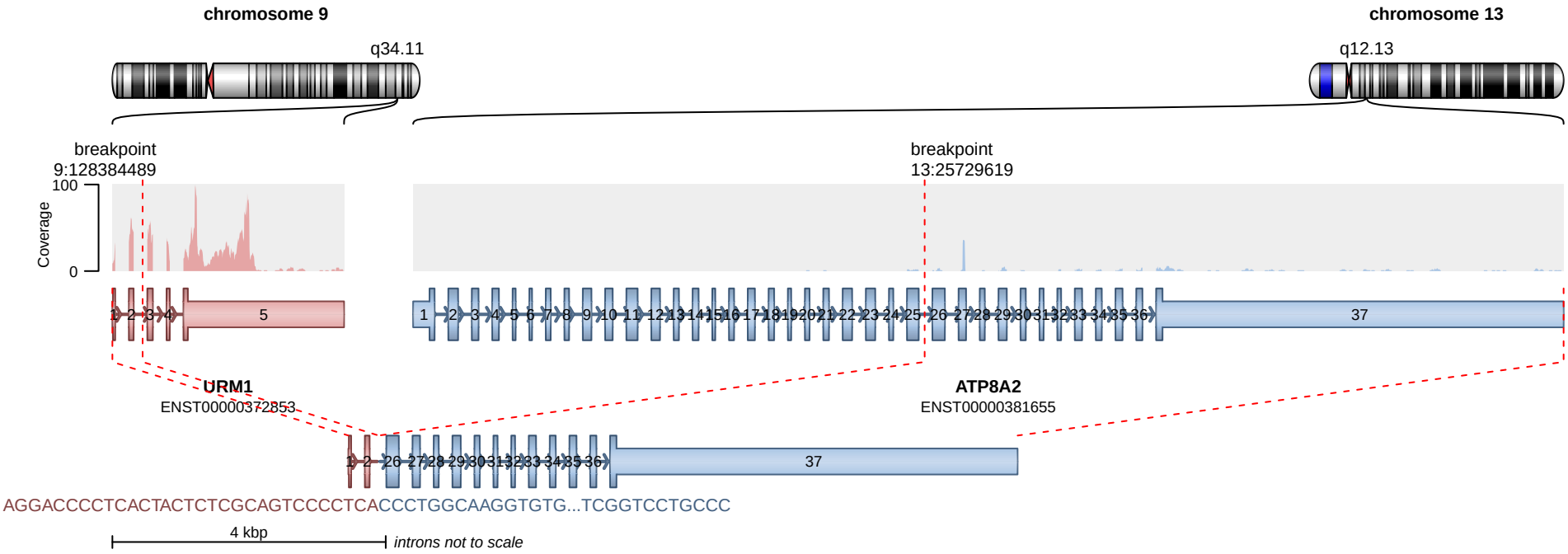


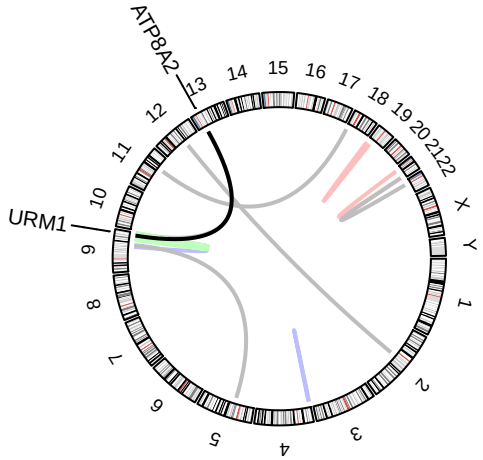


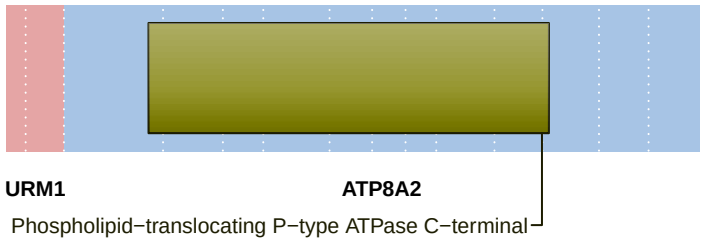
Genes are not protein−coding.

SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 27



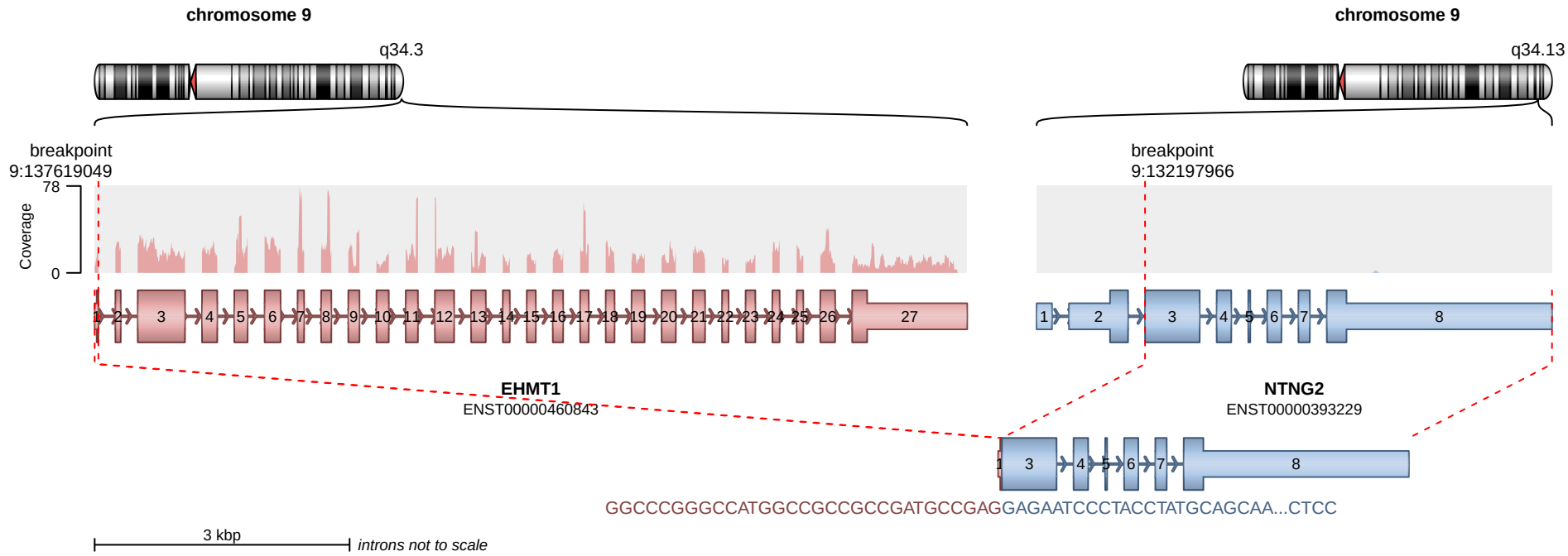


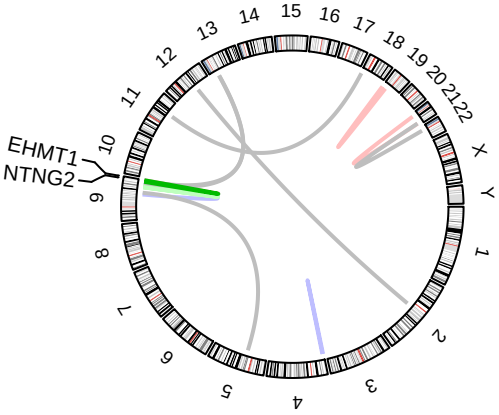


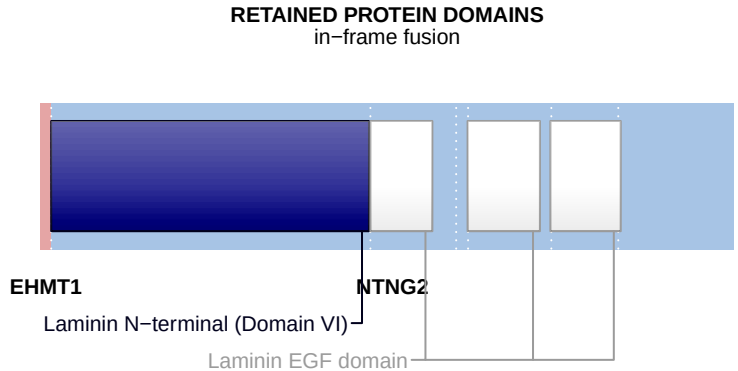
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 3

translocation
deletion
duplication
inversion

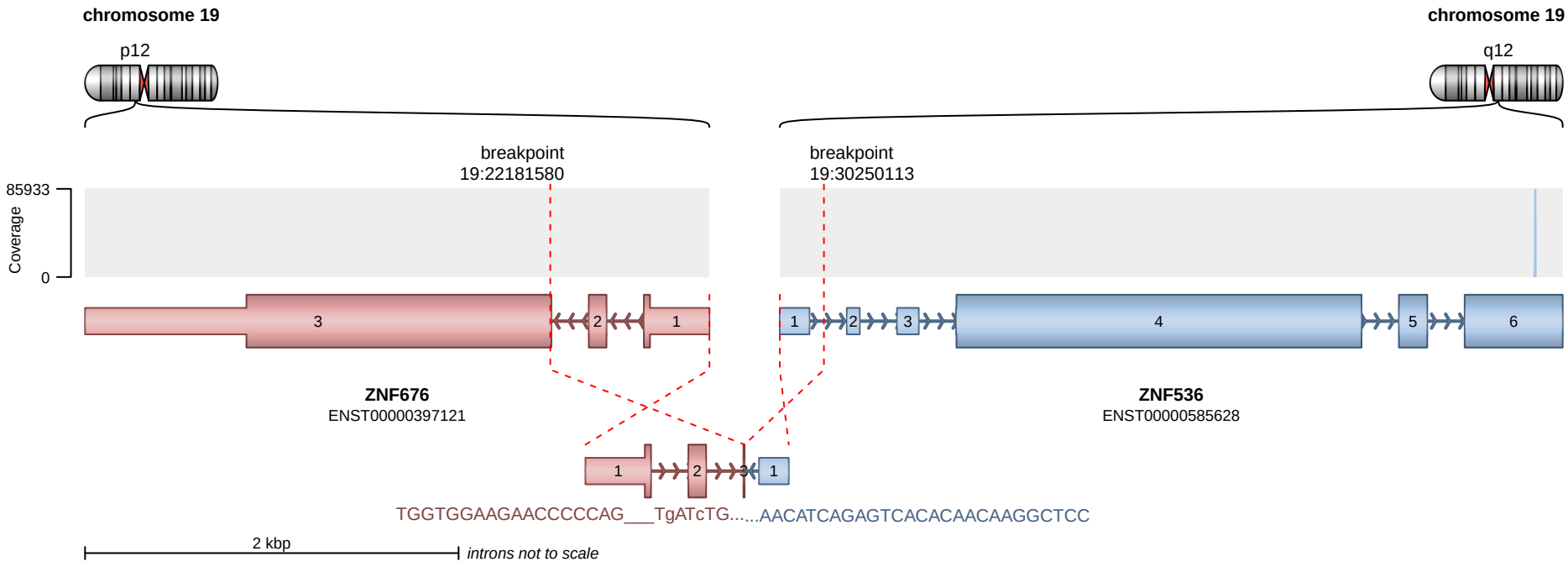


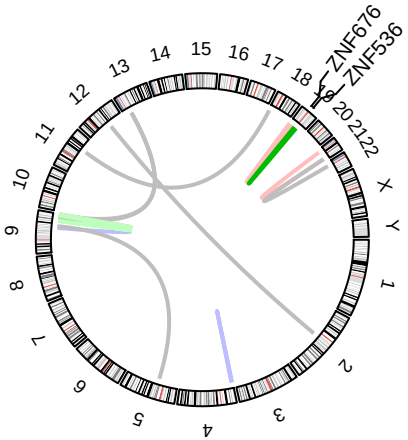




SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

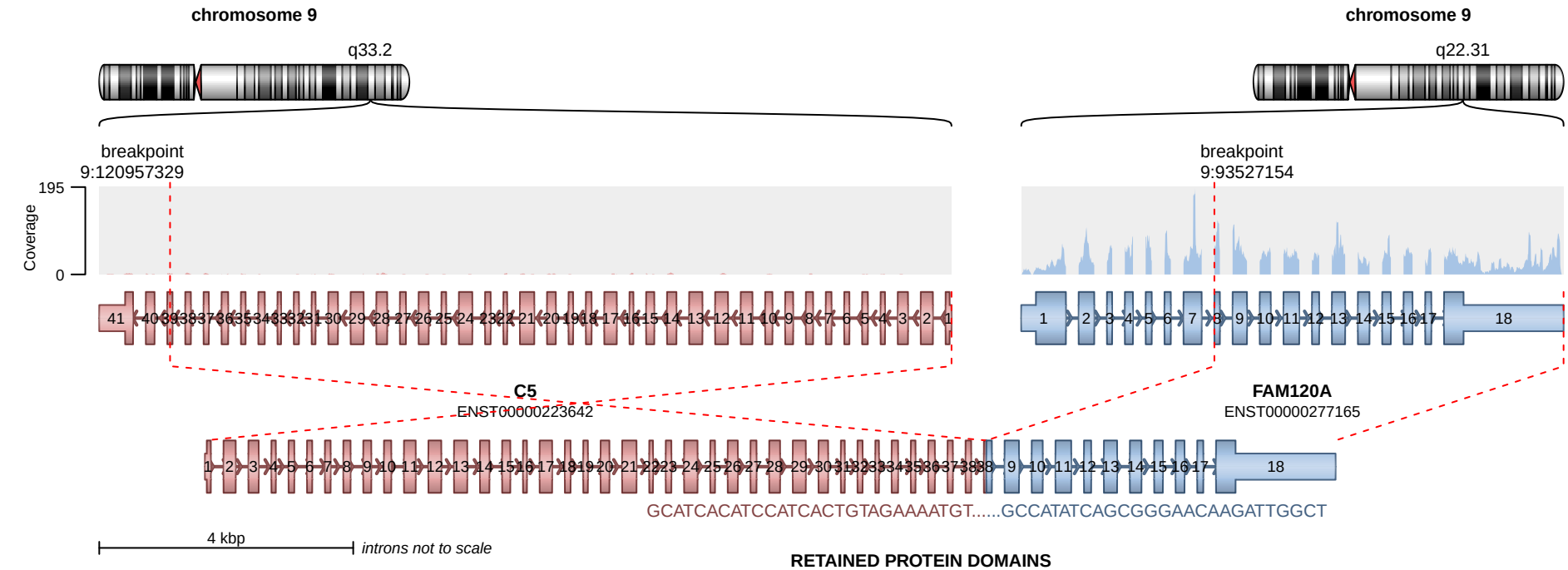




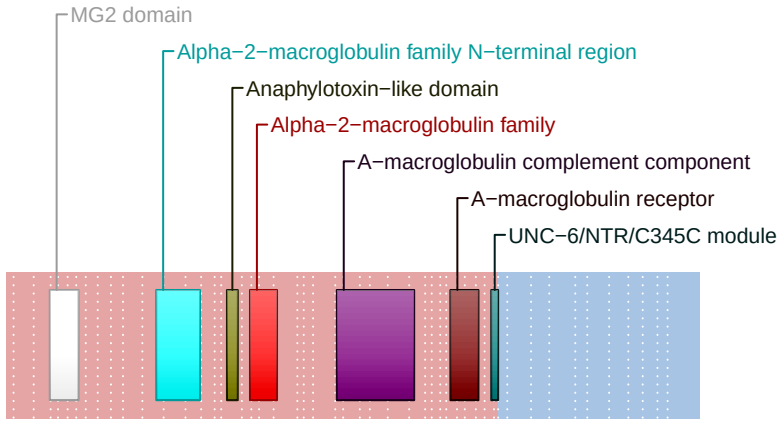
No protein domains retained in fusion.

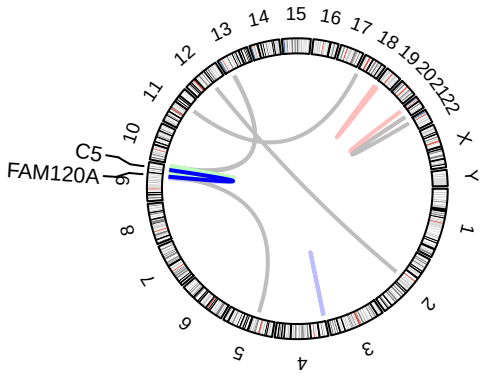
SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 3



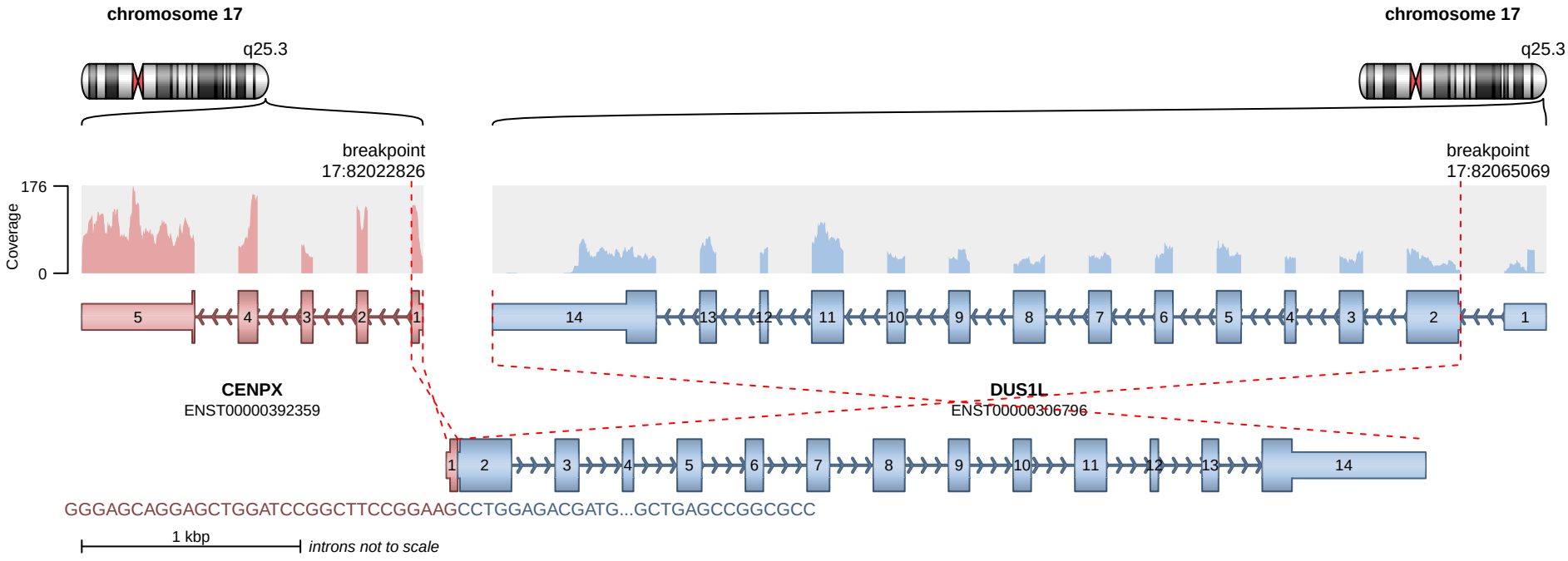
RETAINED PROTEIN DOMAINS
reading frame unclear

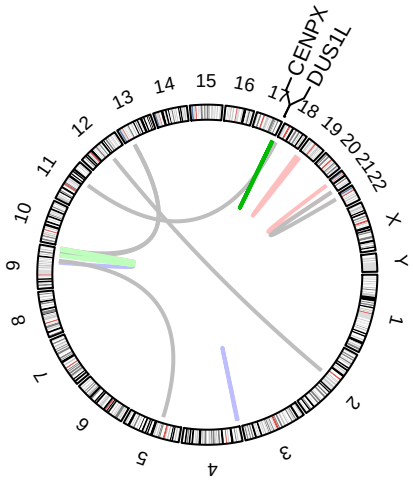


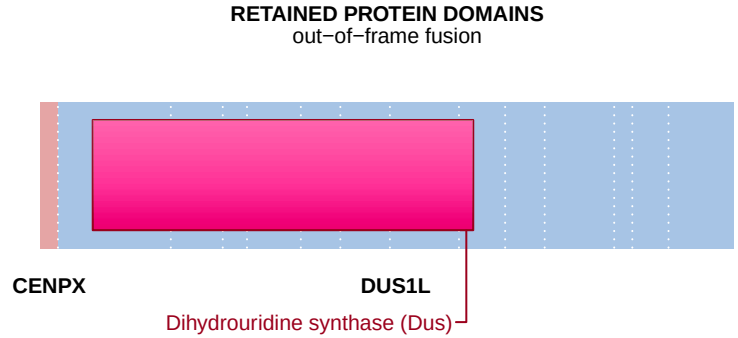


SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 3







SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

translocation
deletion
duplication
inversion