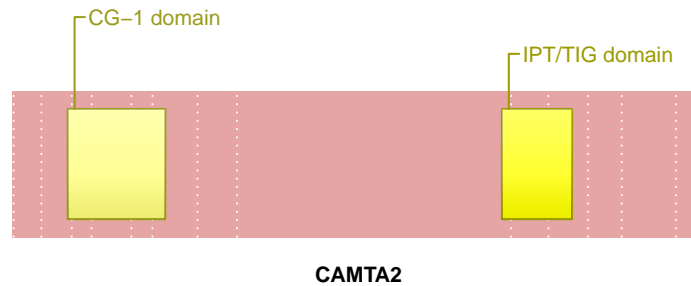


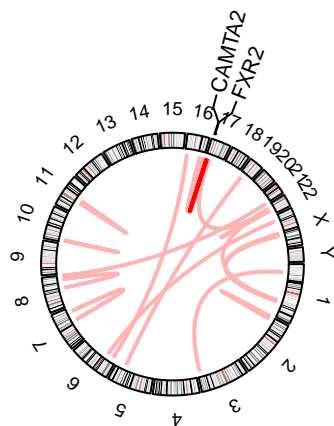
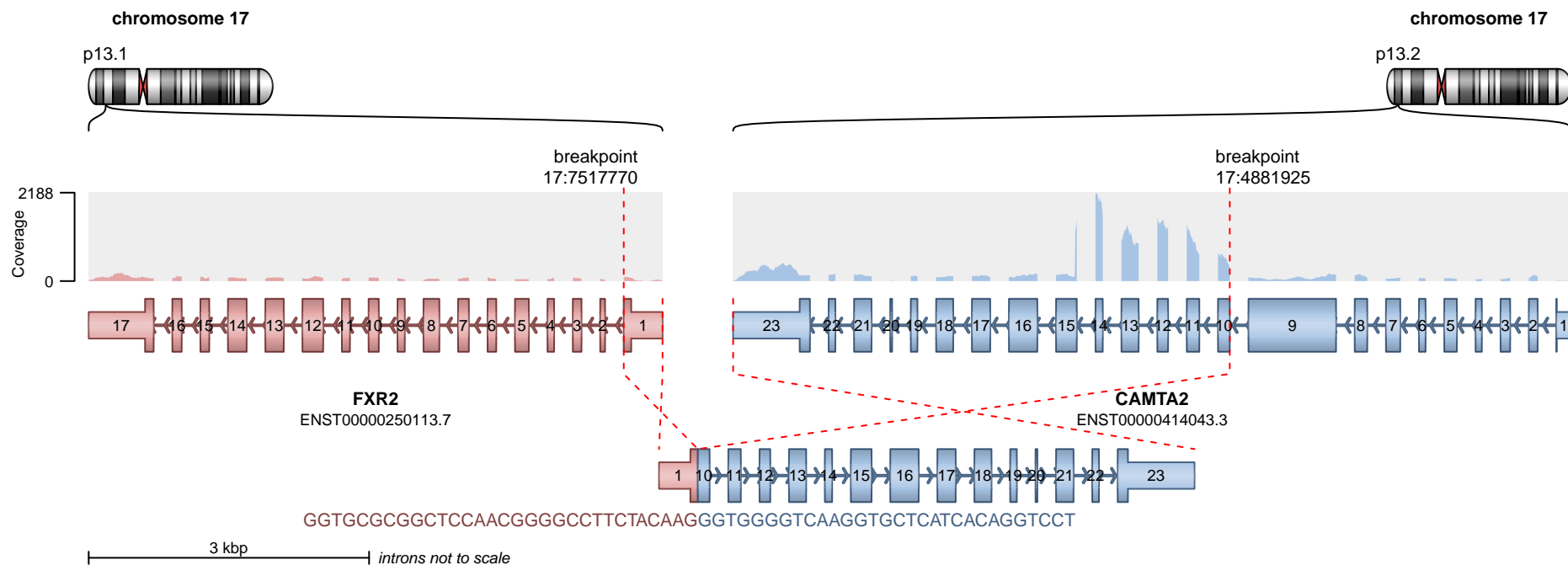
RETAINED PROTEIN DOMAINS

reading frame unclear

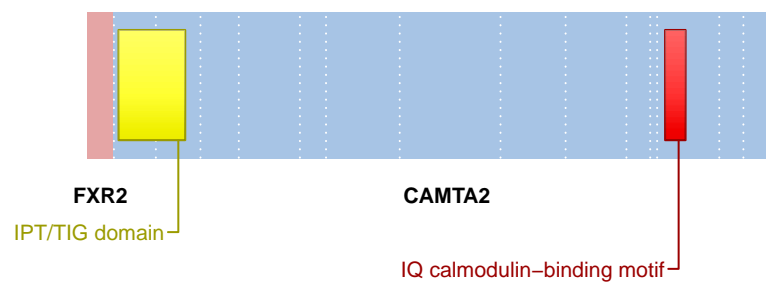


SUPPORTING READ COUNT

Split reads = 569
Discordant mates = 169

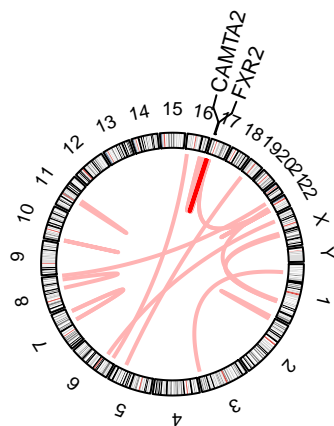
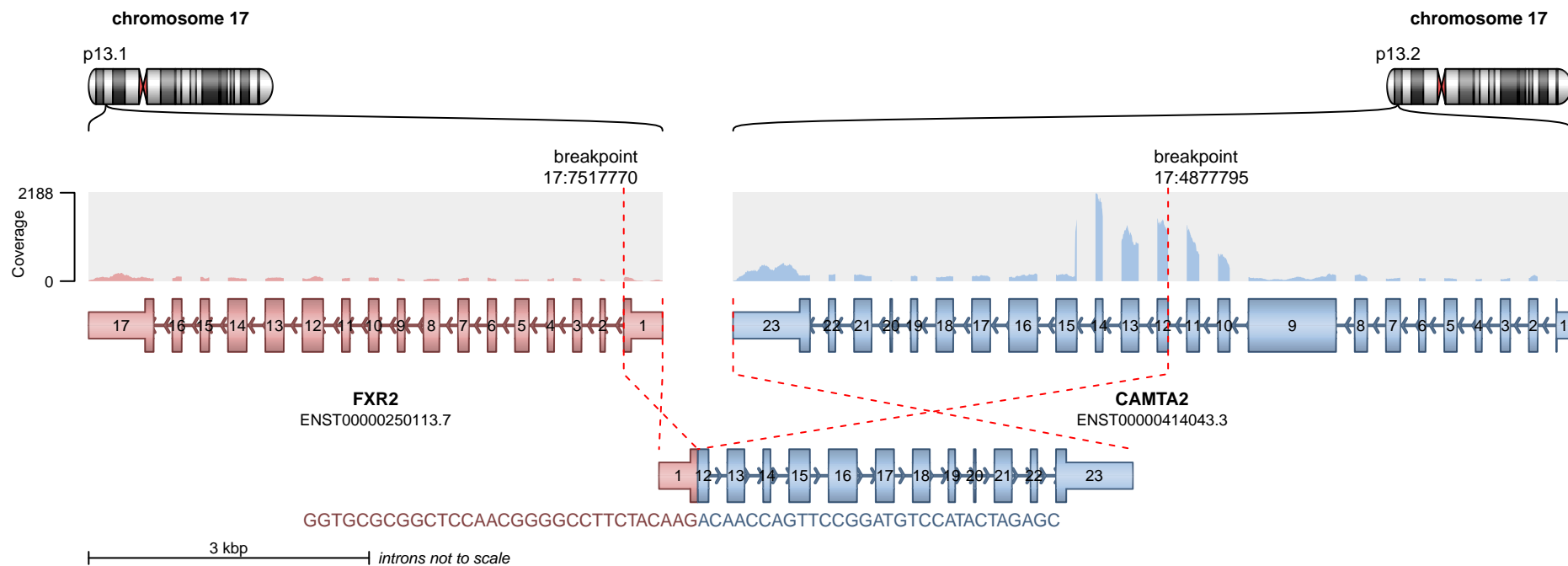


RETAINED PROTEIN DOMAINS in-frame fusion

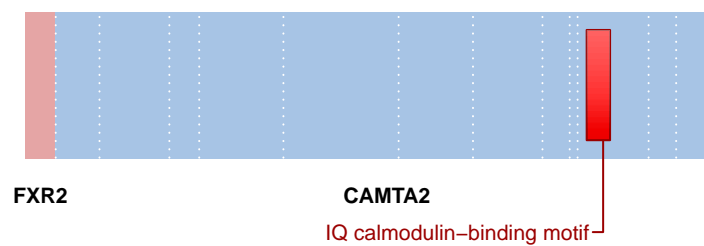


SUPPORTING READ COUNT

Split reads = 81
Discordant mates = 15



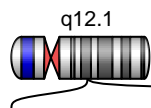
RETAINED PROTEIN DOMAINS out-of-frame fusion



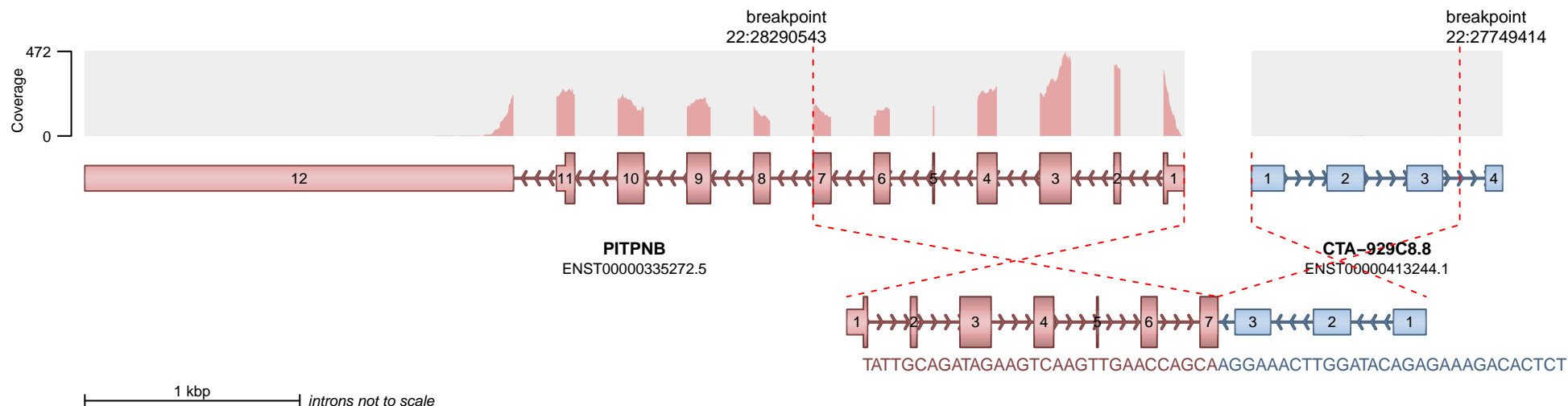
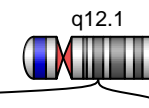
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

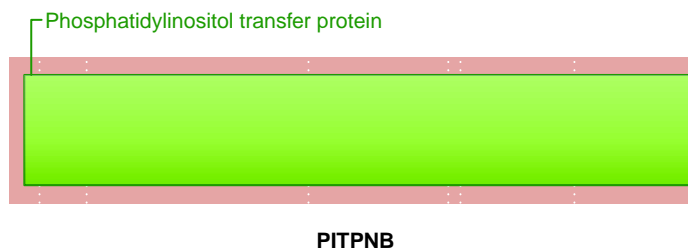
chromosome 22



chromosome 22

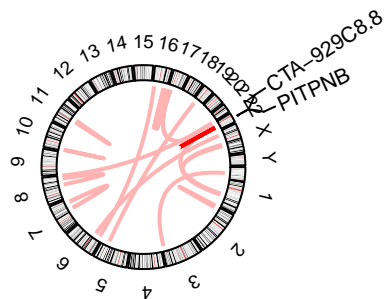


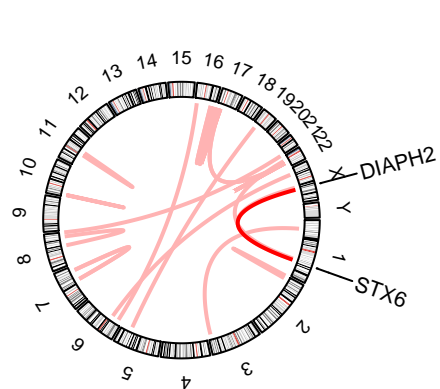
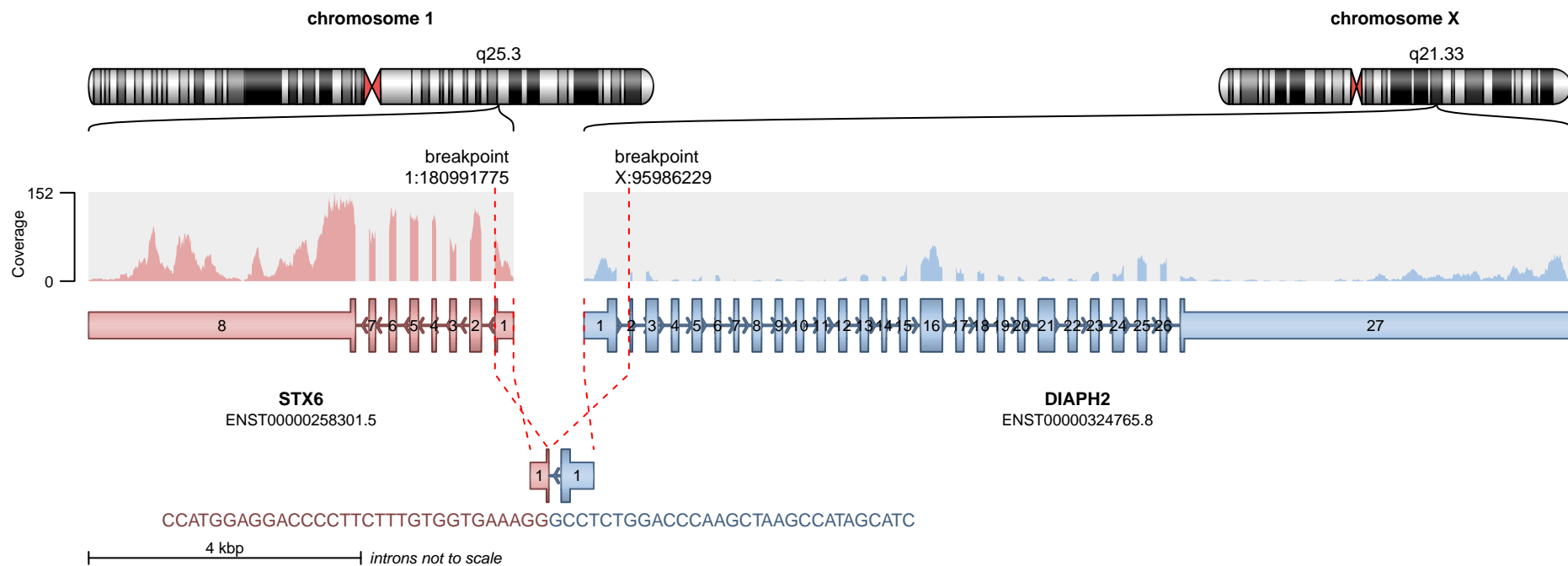
RETAINED PROTEIN DOMAINS
out-of-frame fusion

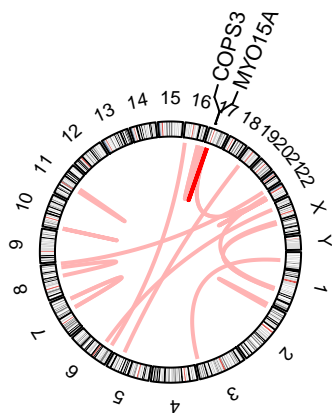
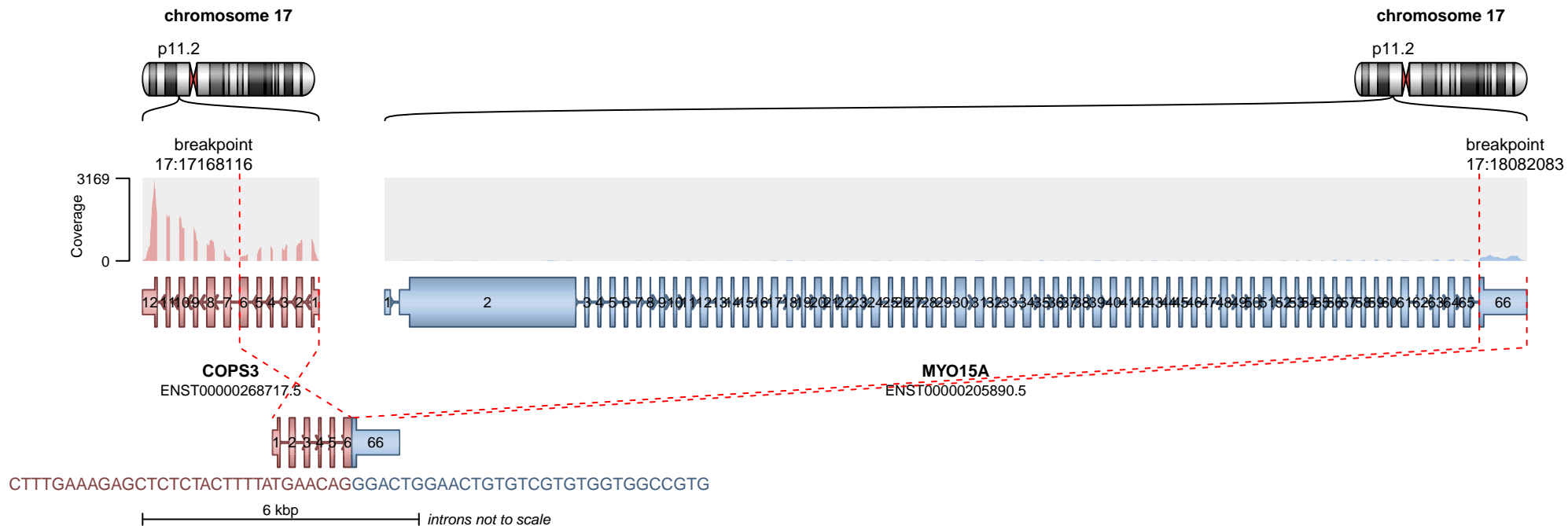


SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 3



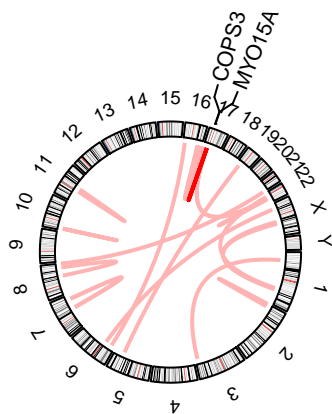
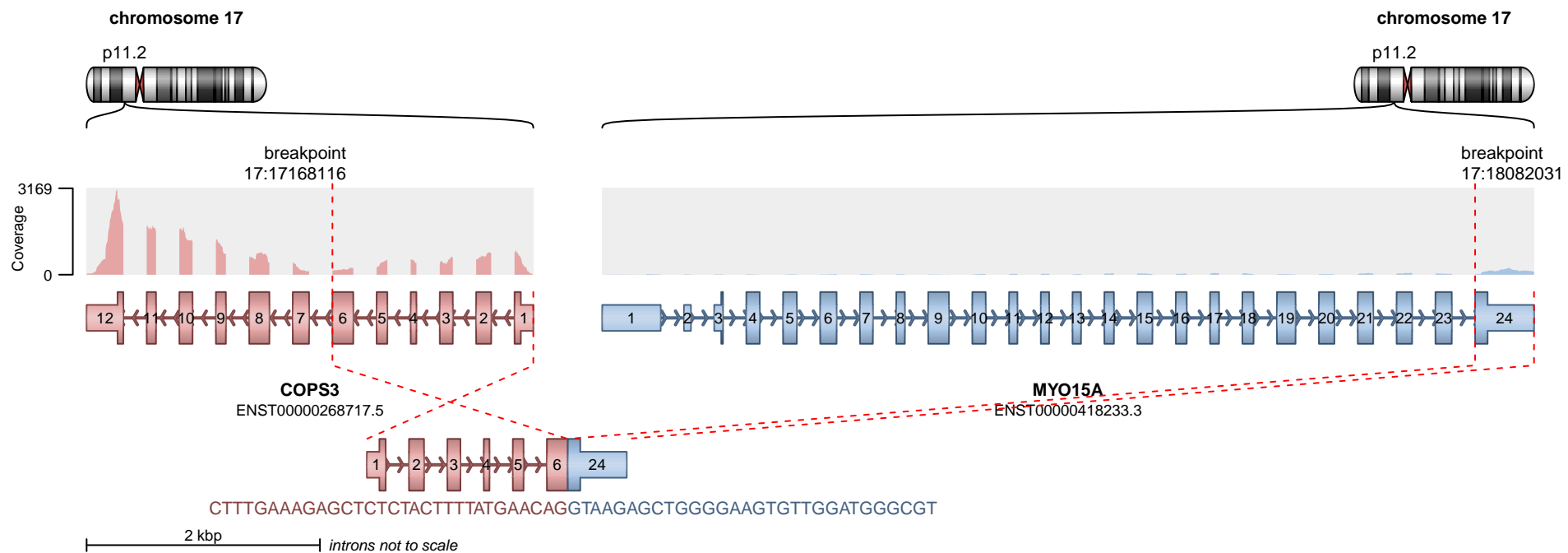




No protein domains retained in fusion.

SUPPORTING READ COUNT

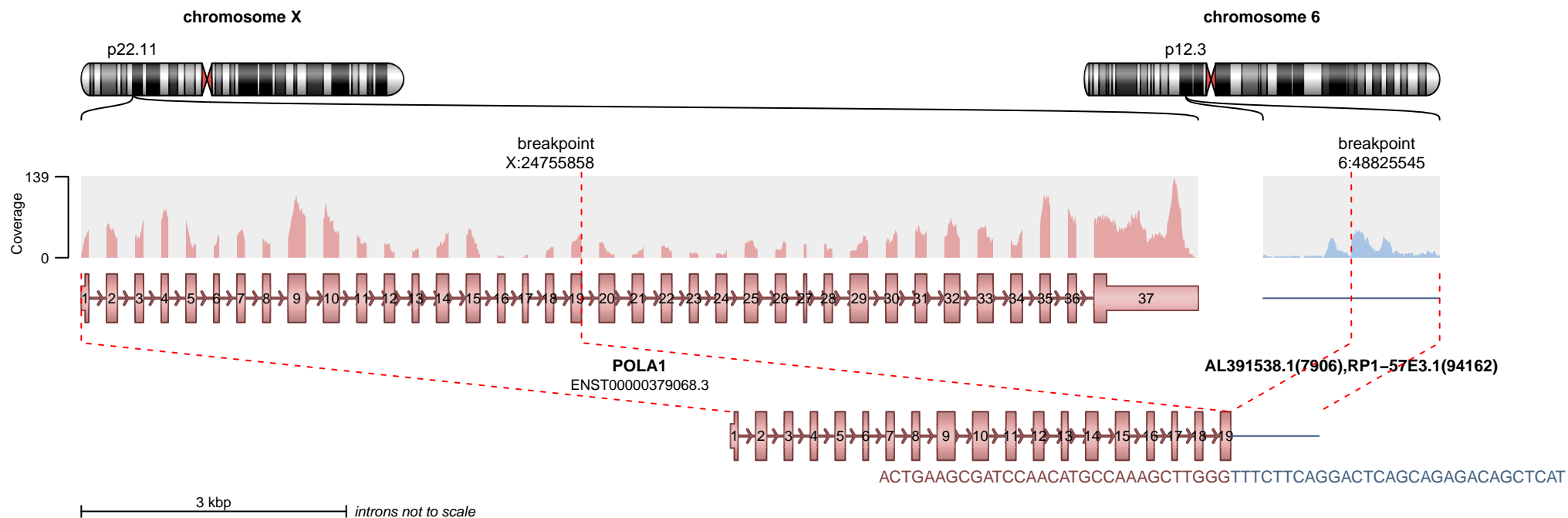
Split reads = 6
Discordant mates = 3



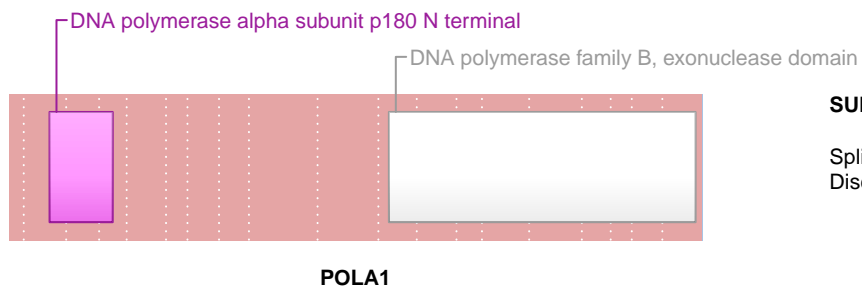
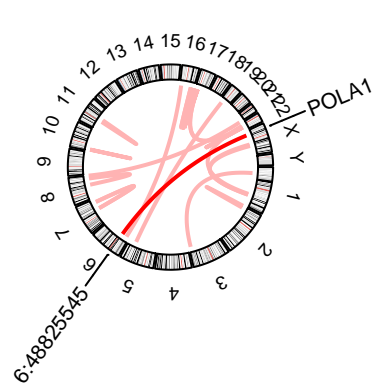
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 3

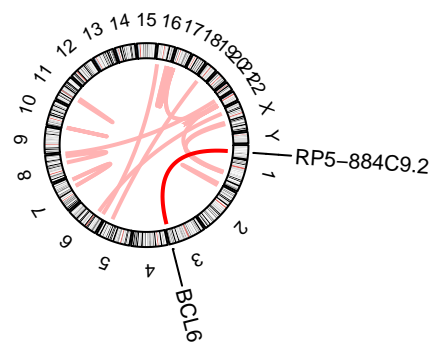
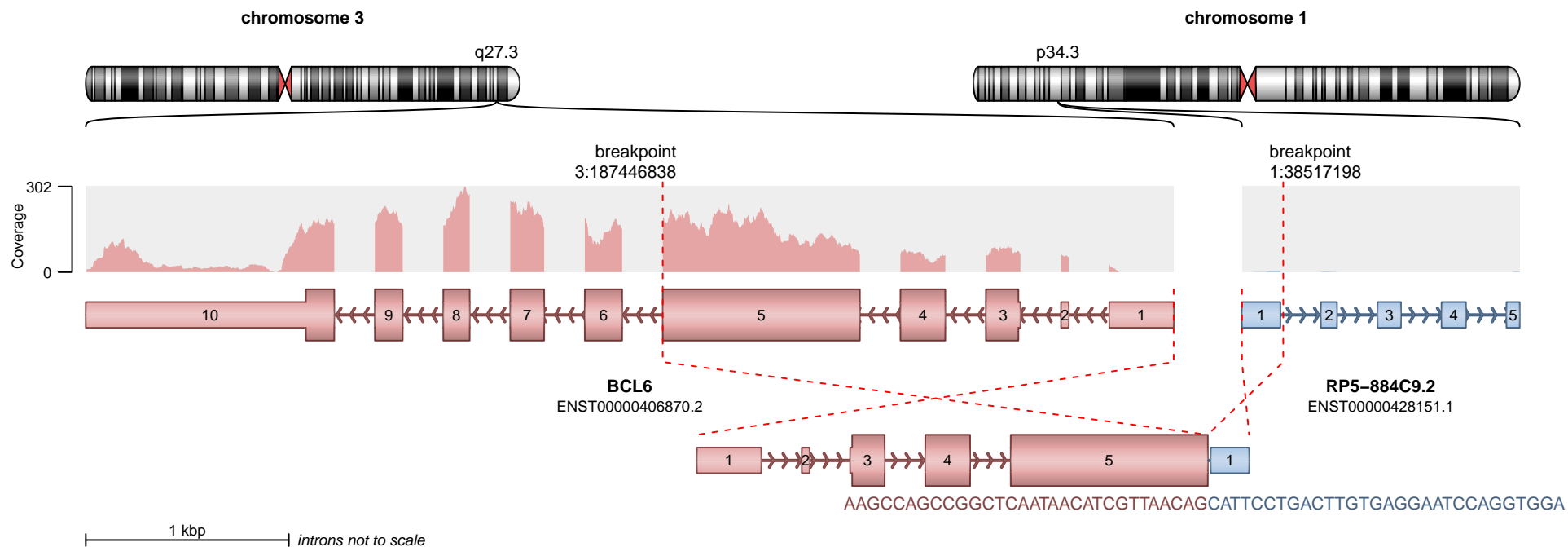


RETAINED PROTEIN DOMAINS out-of-frame fusion

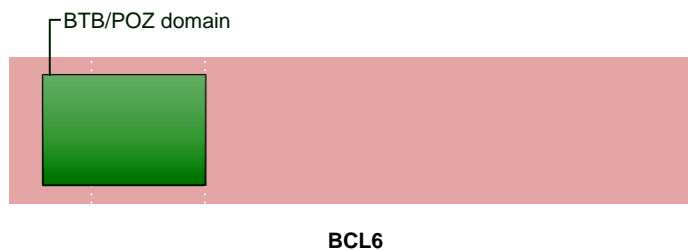


SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 1

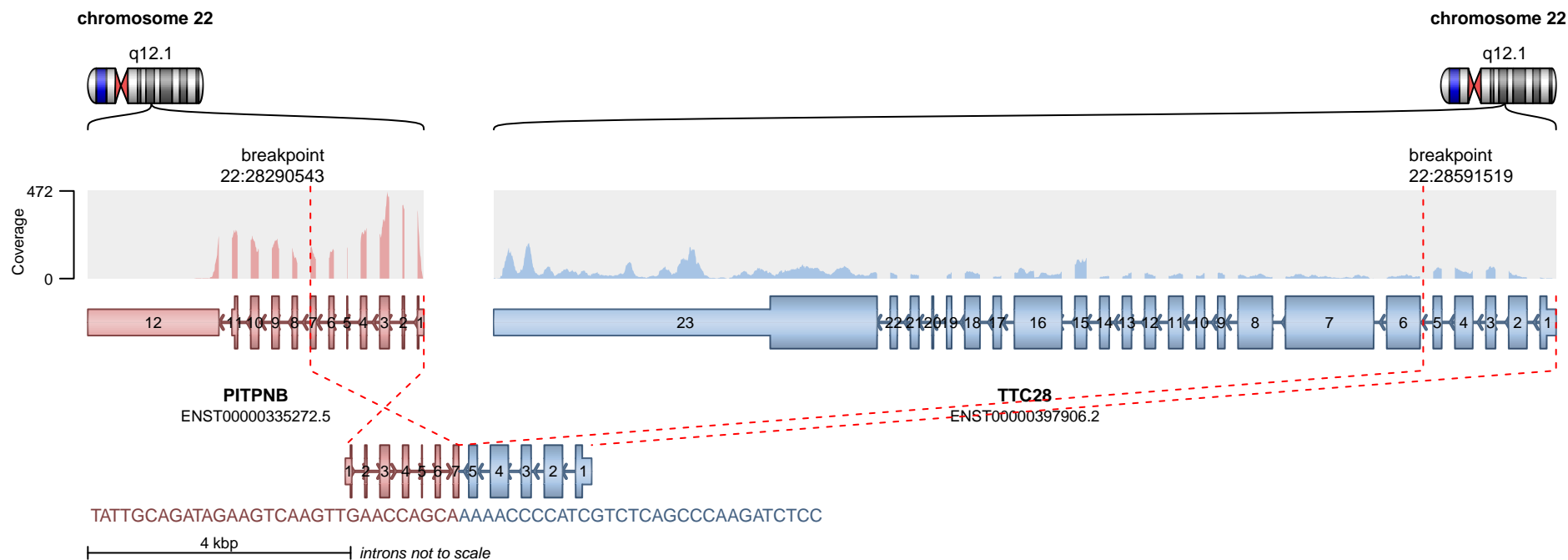


RETAINED PROTEIN DOMAINS out-of-frame fusion

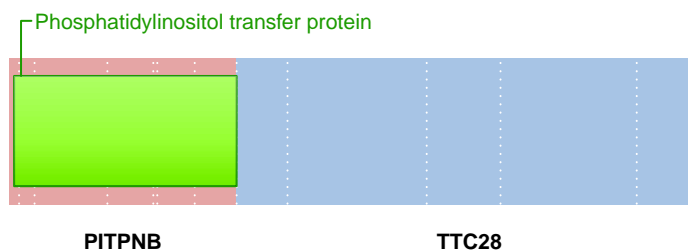


SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

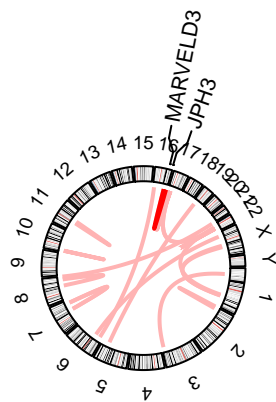
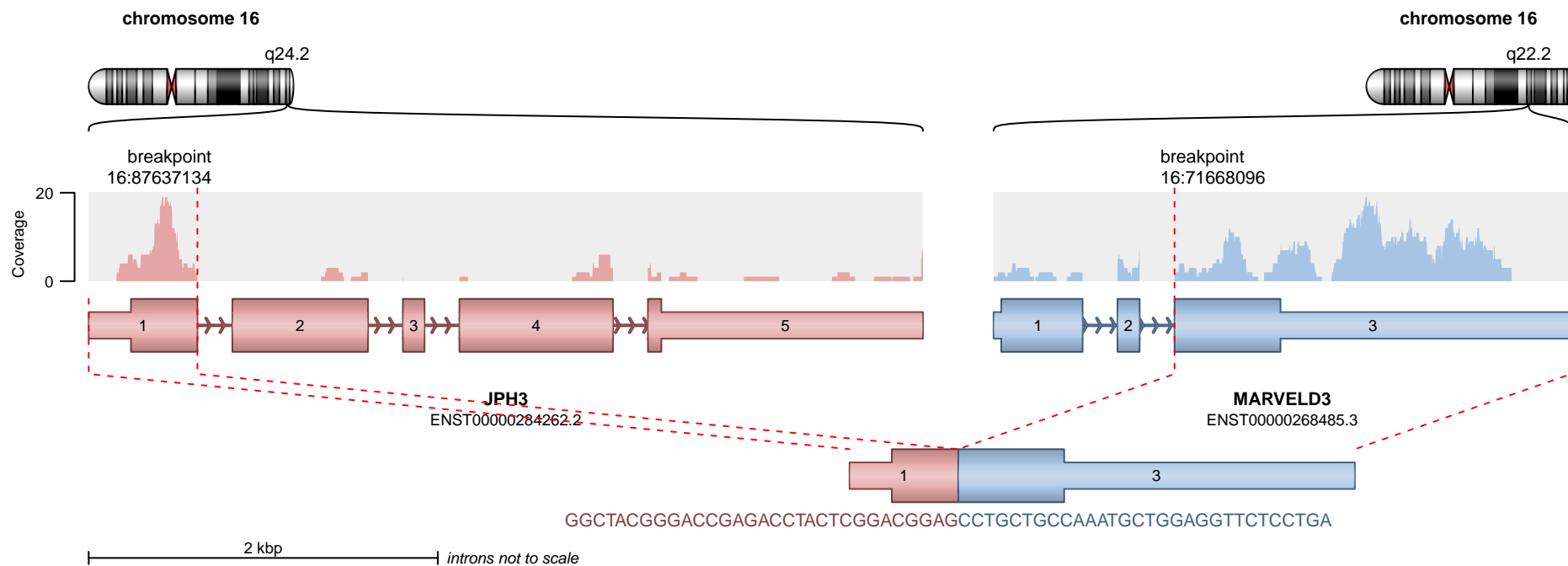


RETAINED PROTEIN DOMAINS out-of-frame fusion

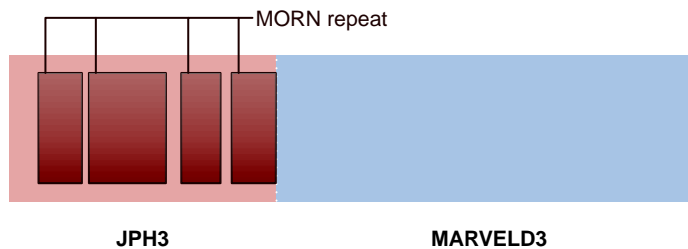


SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 1

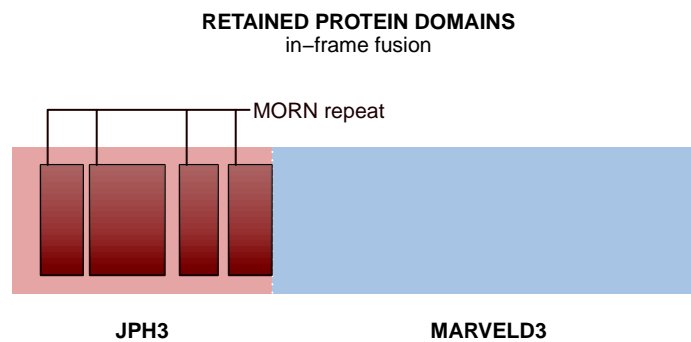
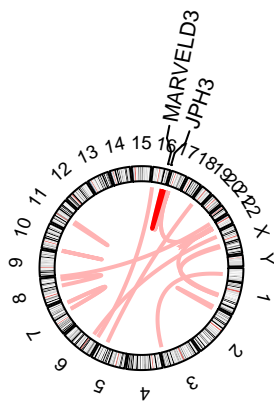
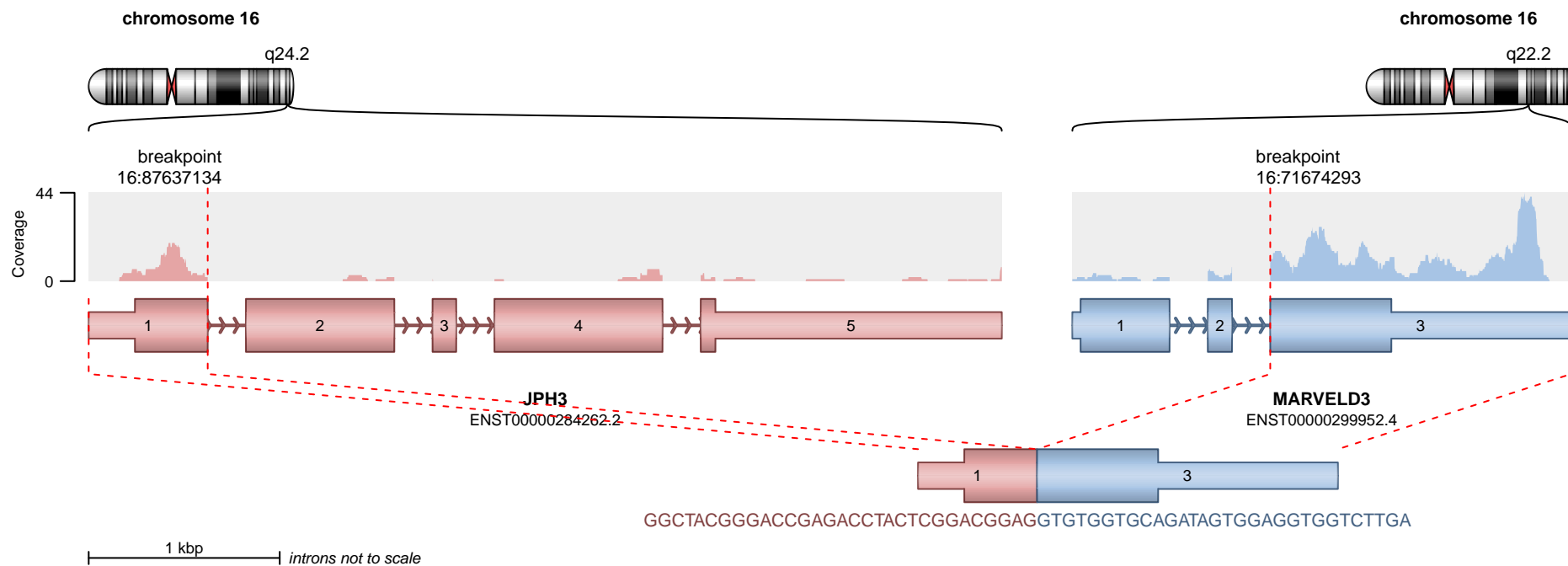


RETAINED PROTEIN DOMAINS in-frame fusion



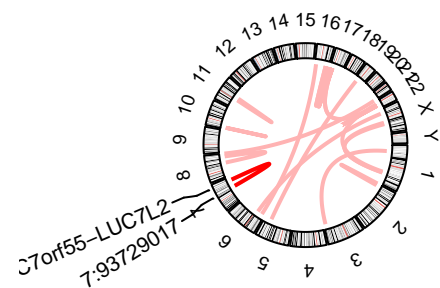
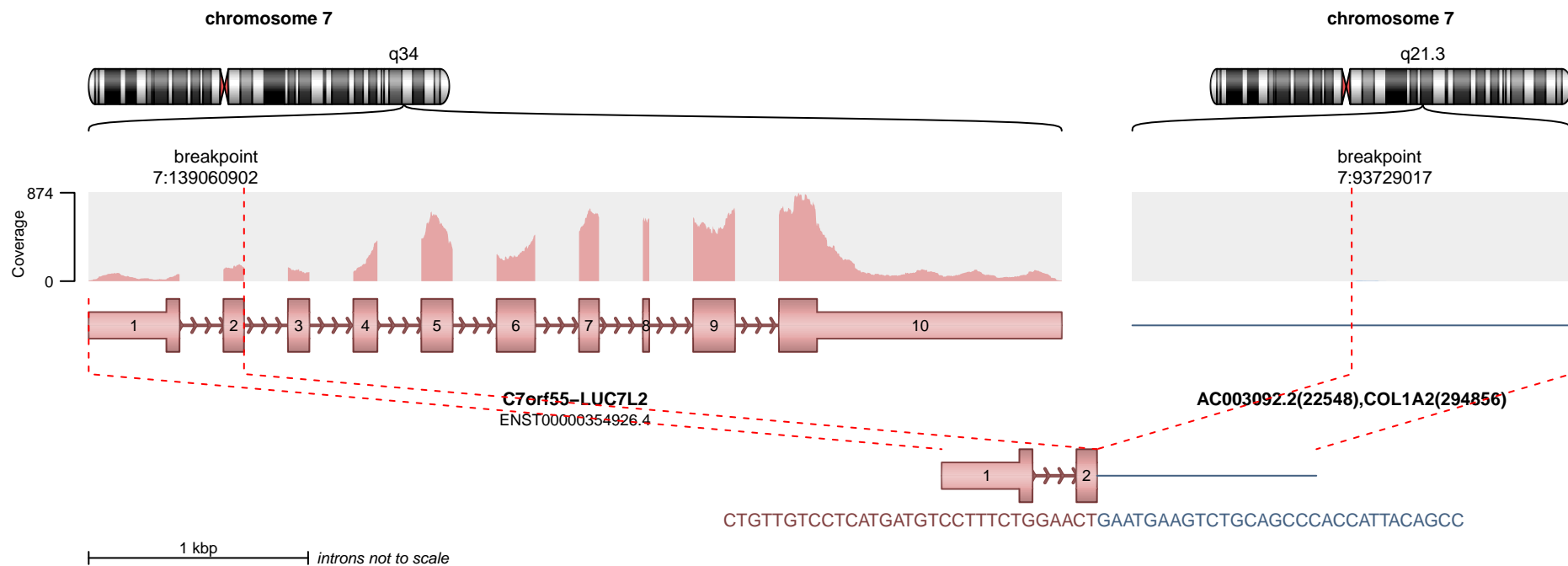
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 2



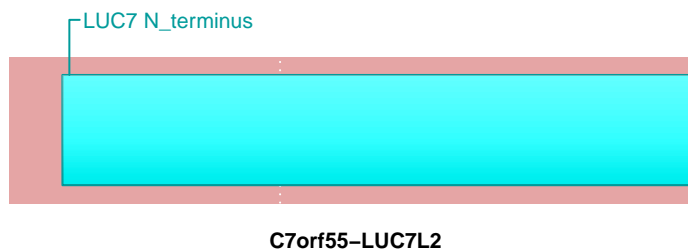
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1



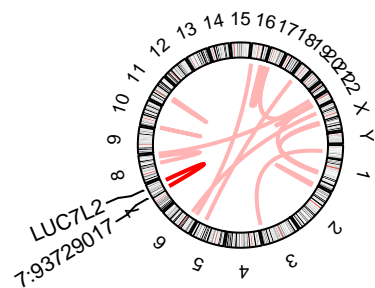
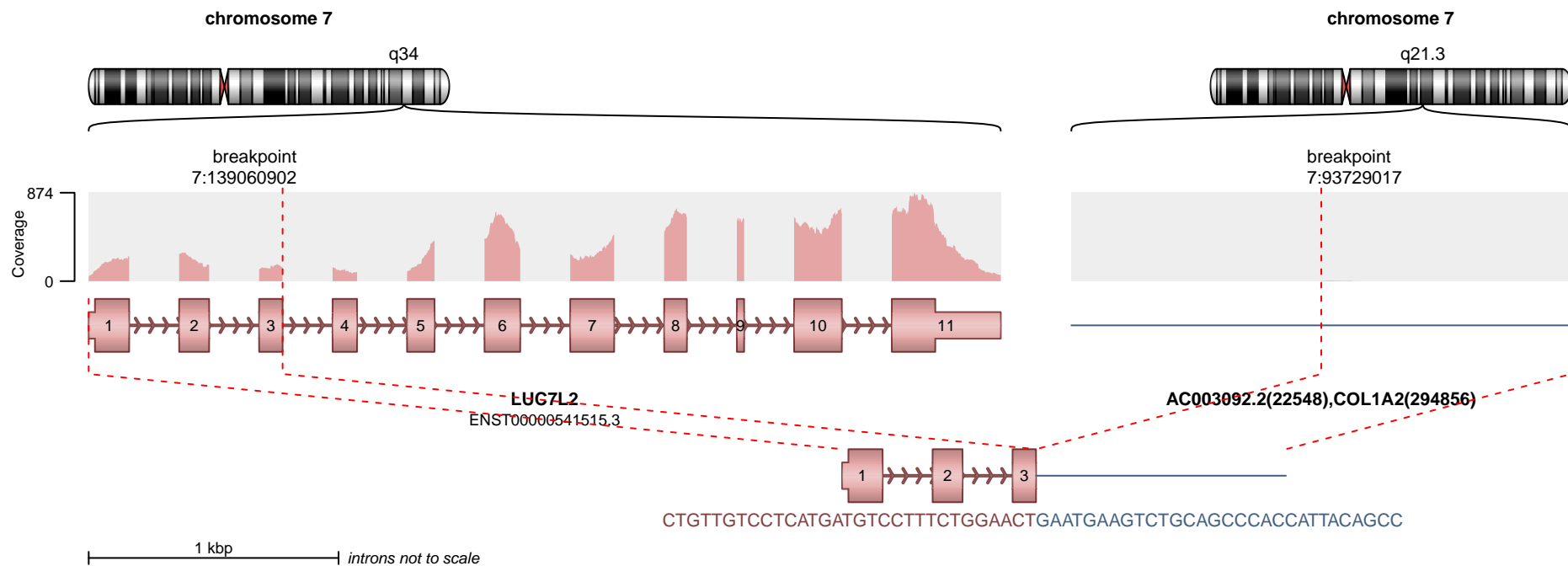
RETAINED PROTEIN DOMAINS

out-of-frame fusion



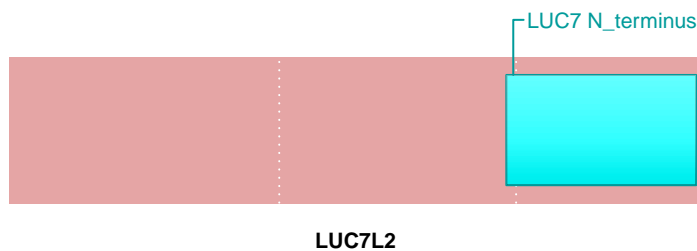
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 1



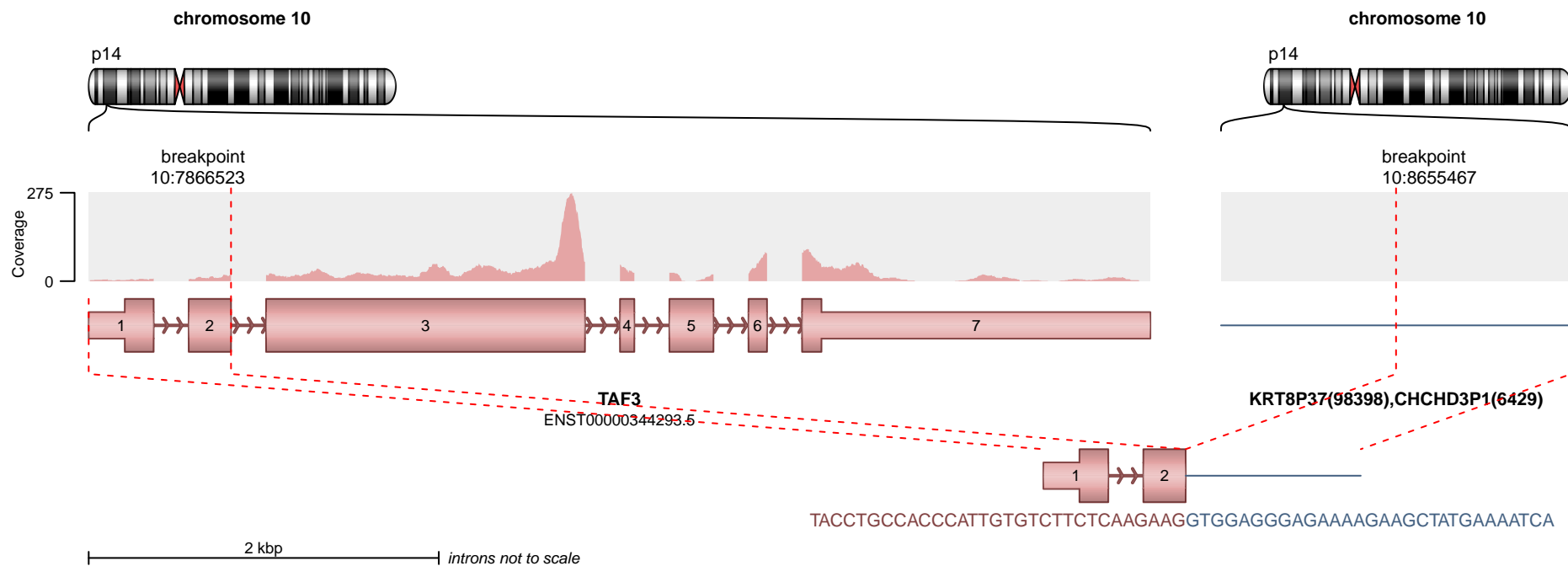
RETAINED PROTEIN DOMAINS

out-of-frame fusion

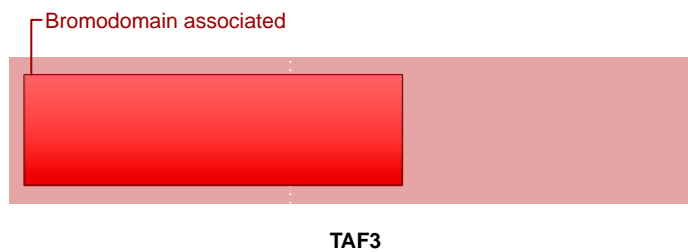


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 1

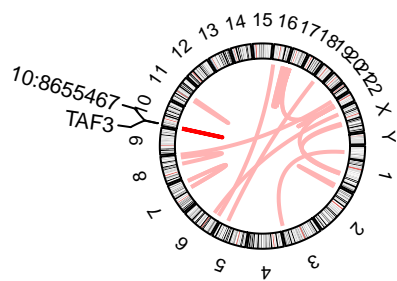


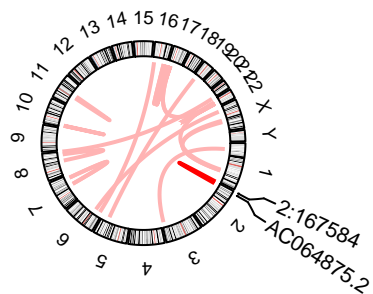
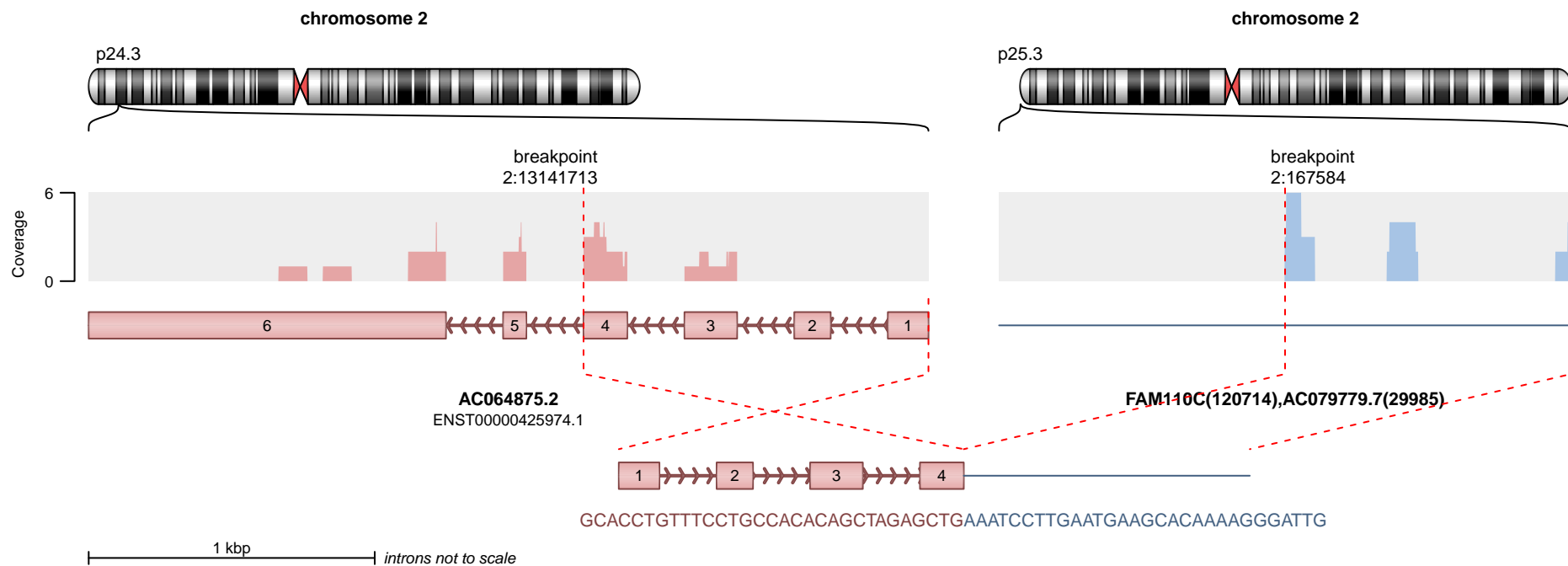
RETAINED PROTEIN DOMAINS
out-of-frame fusion



SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

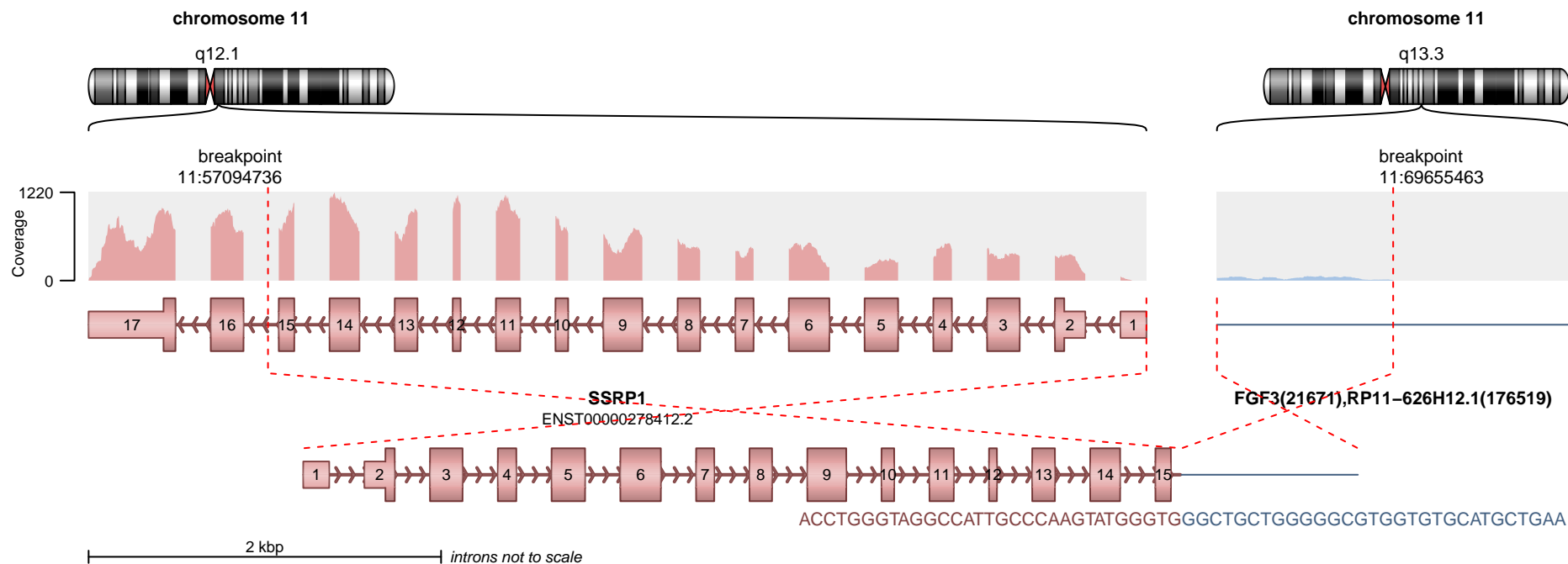




Genes are not protein-coding.

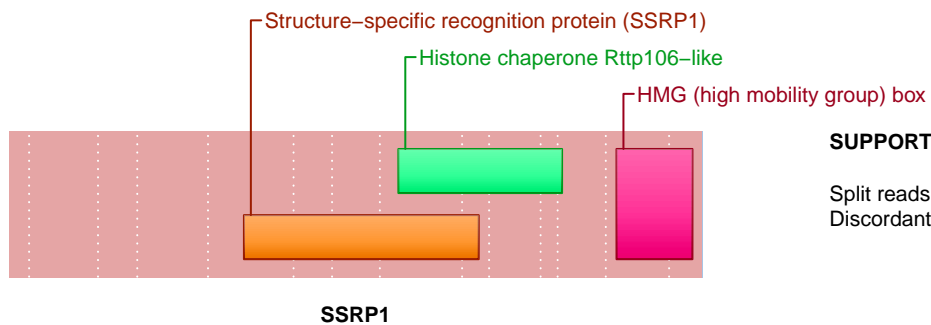
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0



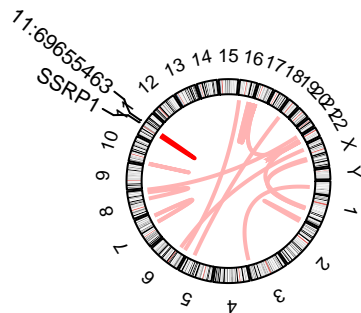
RETAINED PROTEIN DOMAINS

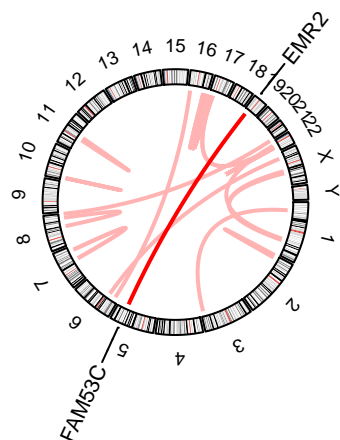
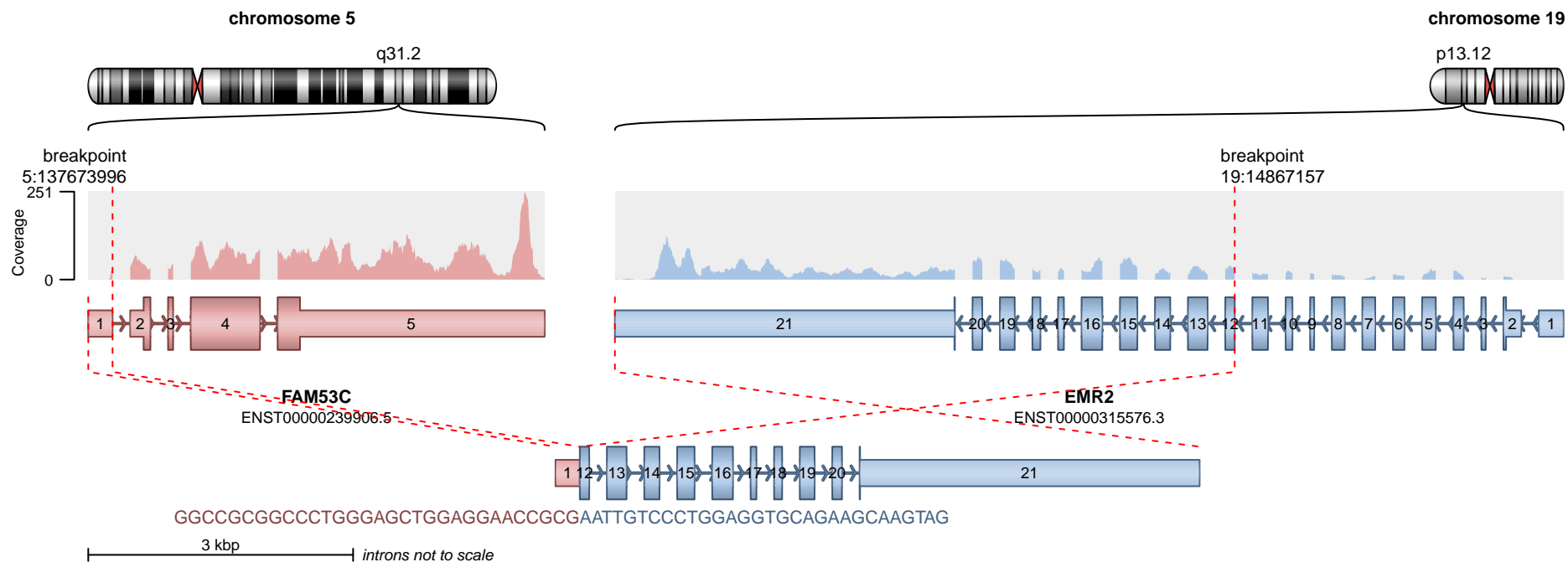
reading frame unclear



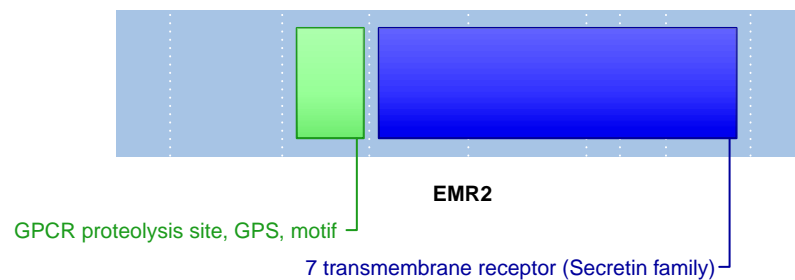
SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 2



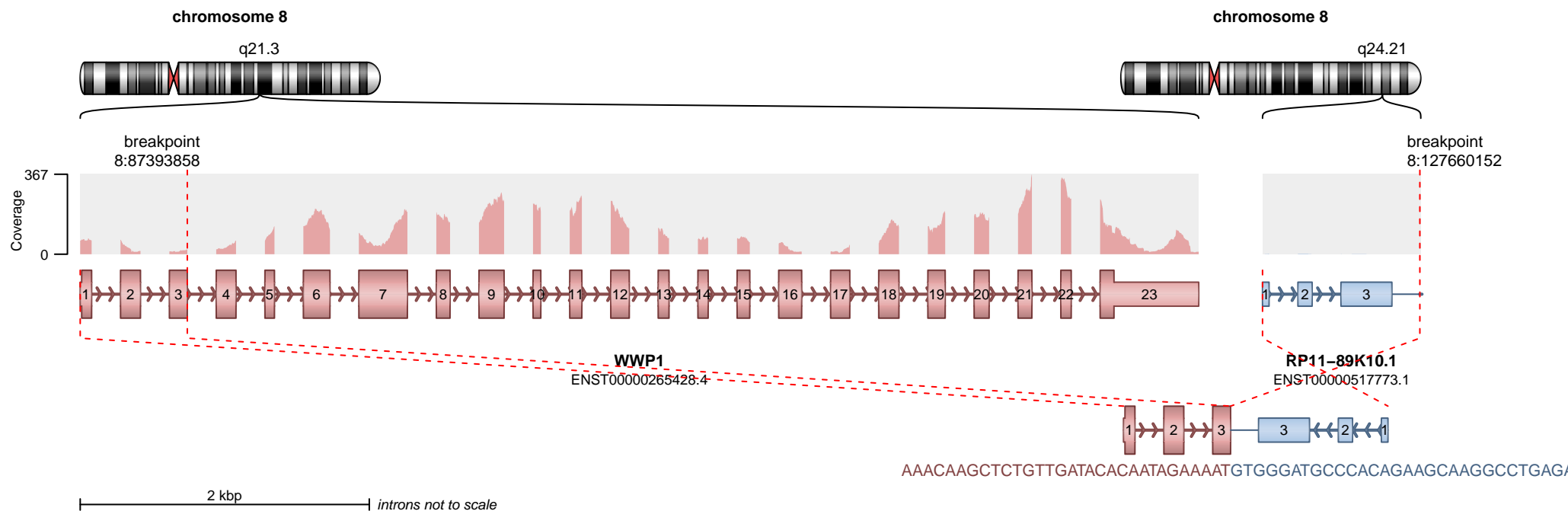


RETAINED PROTEIN DOMAINS reading frame unclear

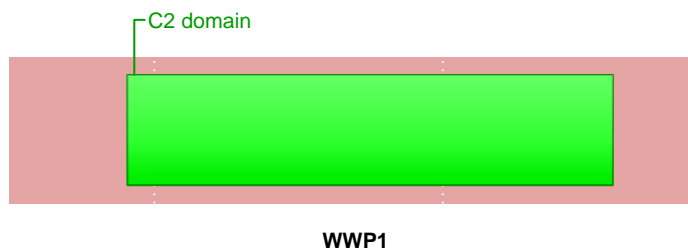


SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

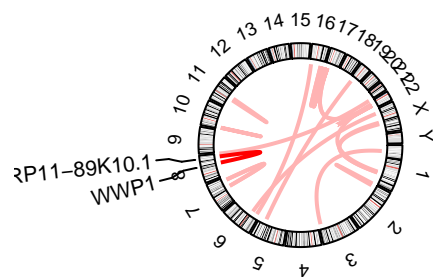


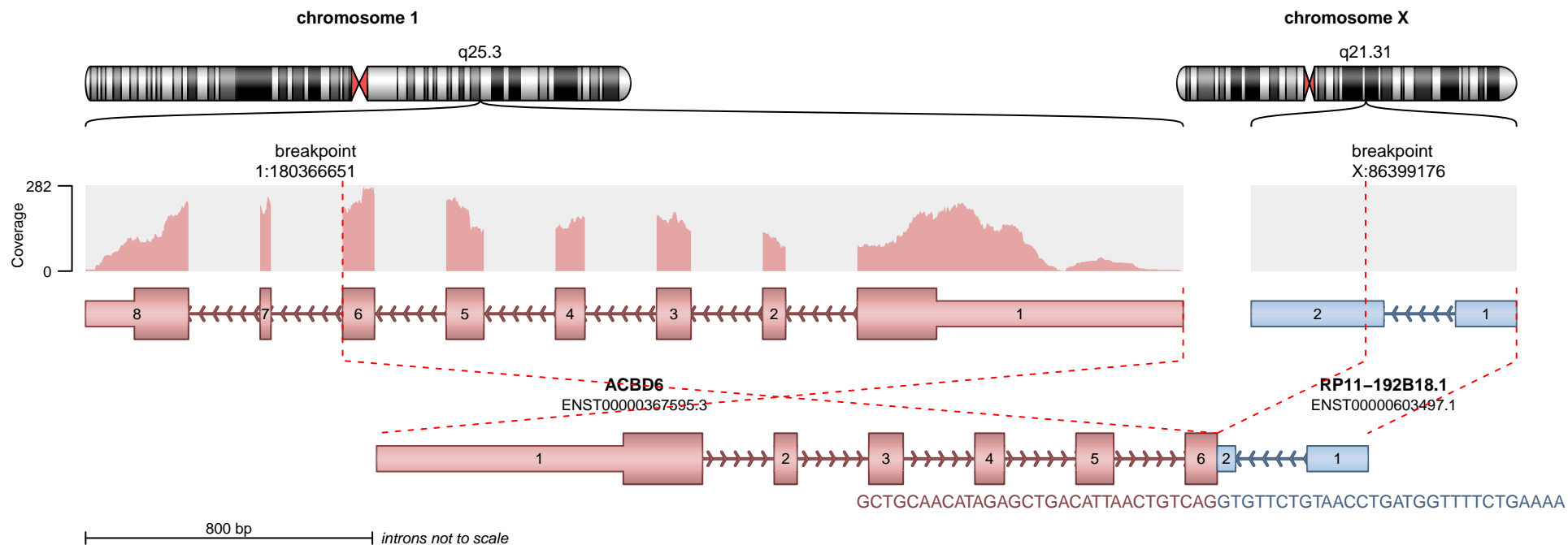
RETAINED PROTEIN DOMAINS out-of-frame fusion



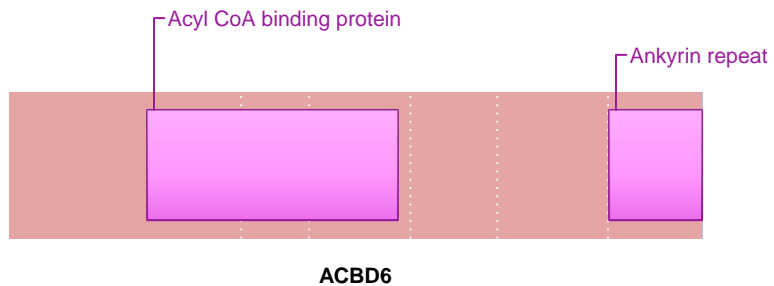
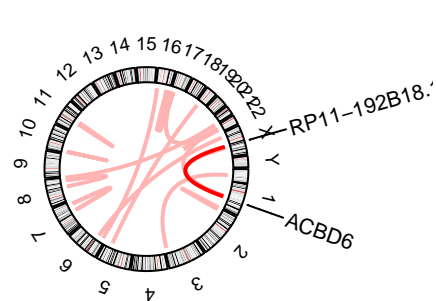
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0





RETAINED PROTEIN DOMAINS out-of-frame fusion



SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

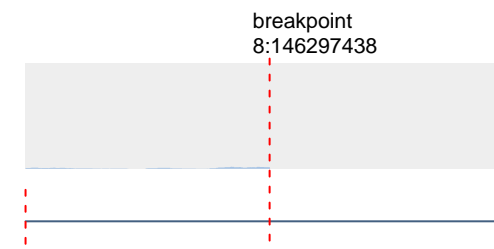
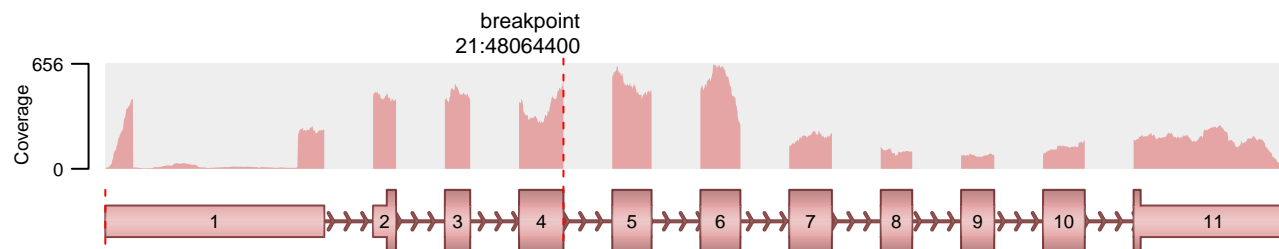
chromosome 21

q22.3



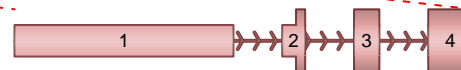
chromosome 8

q24.3



PRMT2
ENST00000397637.1

C8orf33(16022)



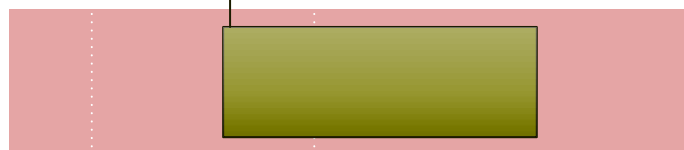
TGAAGAGTACTTCGGCAGCTATGGAAGTCTGCTCAAAGAGAACACCATGAAACCGTCTGAA

1 kbp

introns not to scale

RETAINED PROTEIN DOMAINS
out-of-frame fusion

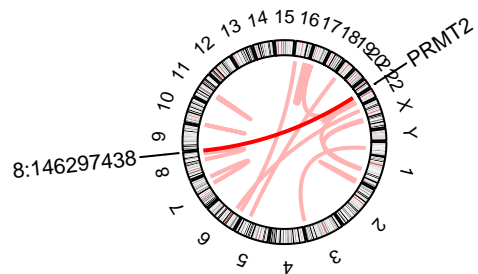
Variant SH3 domain

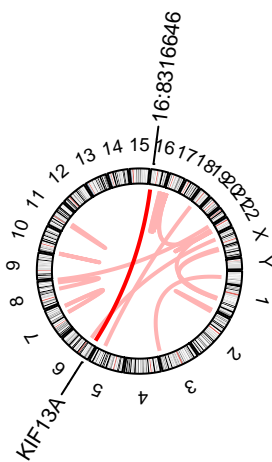
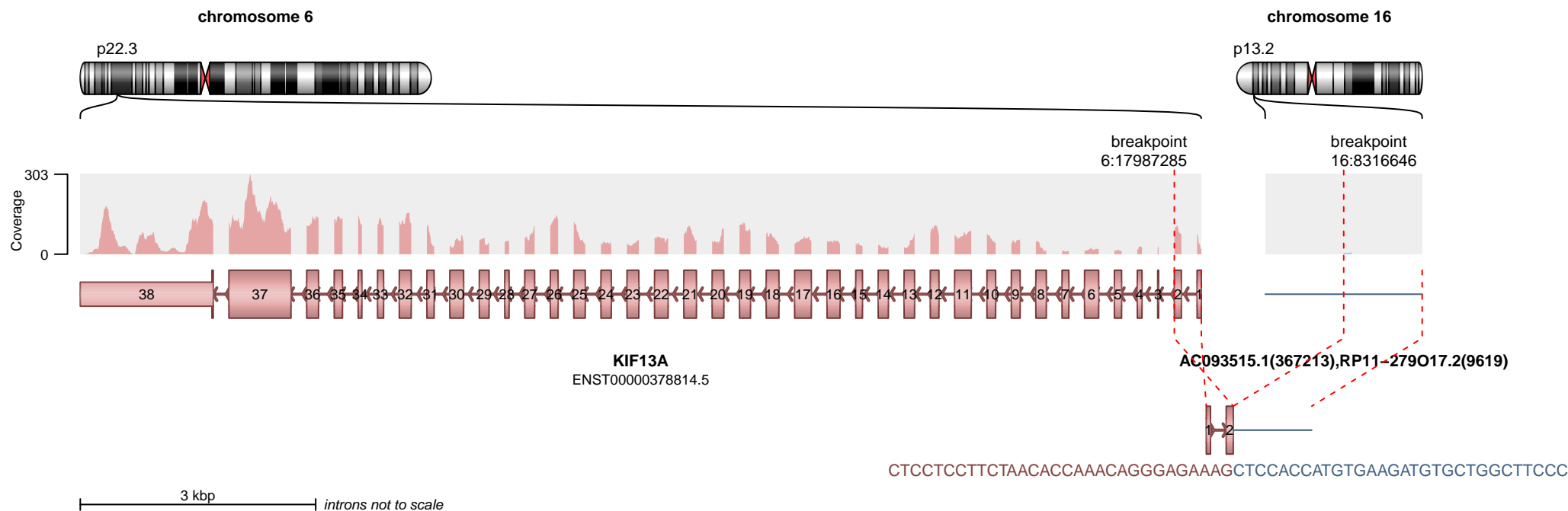


PRMT2

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0





RETAINED PROTEIN DOMAINS
out-of-frame fusion

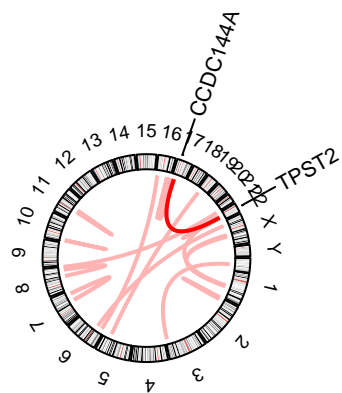
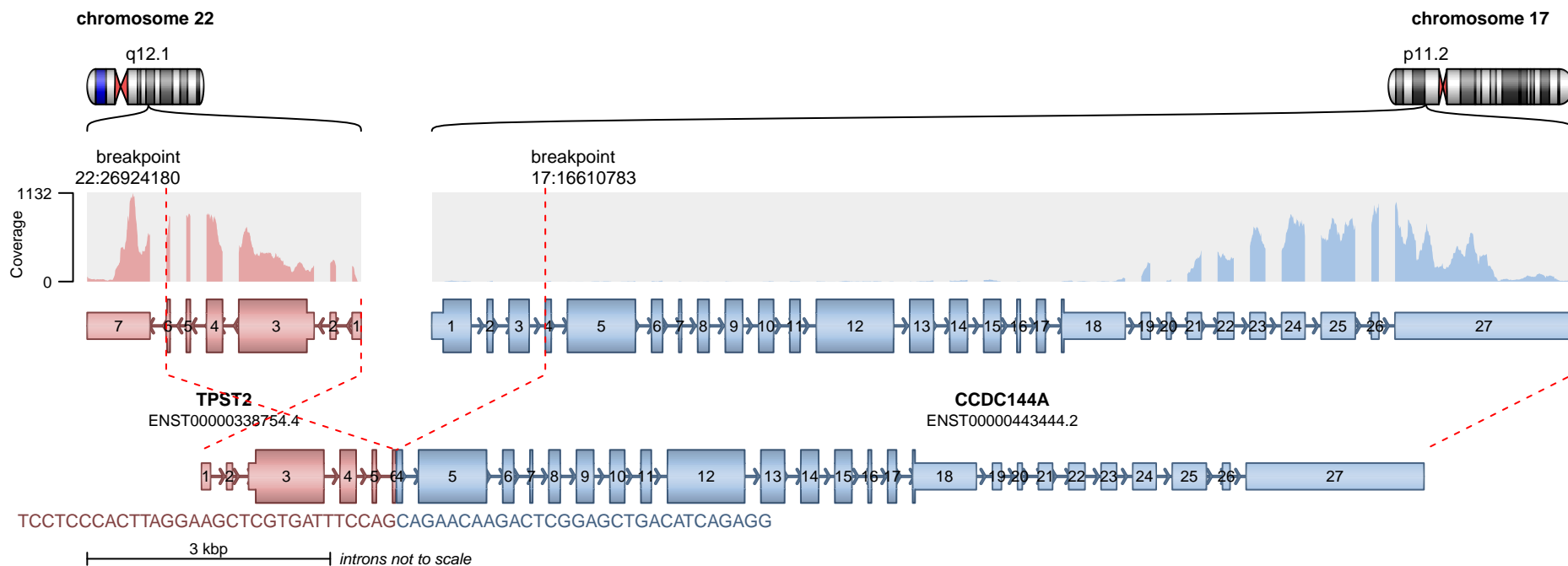
Kinesin motor domain



KIF13A

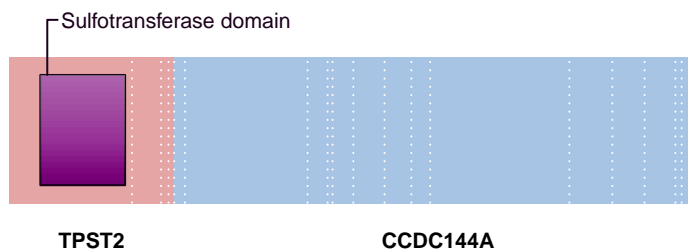
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0



RETAINED PROTEIN DOMAINS

stop codon before fusion junction



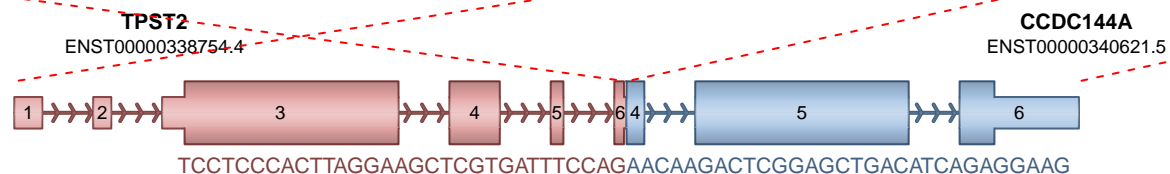
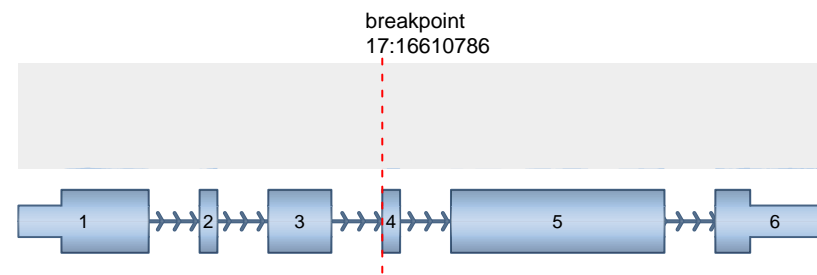
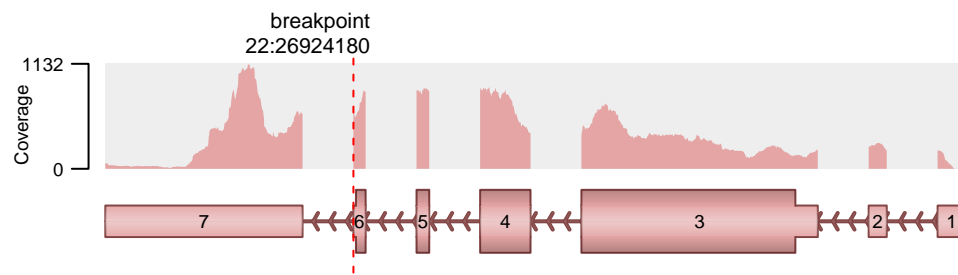
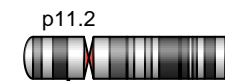
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

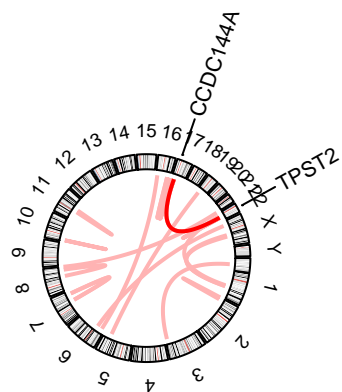
chromosome 22



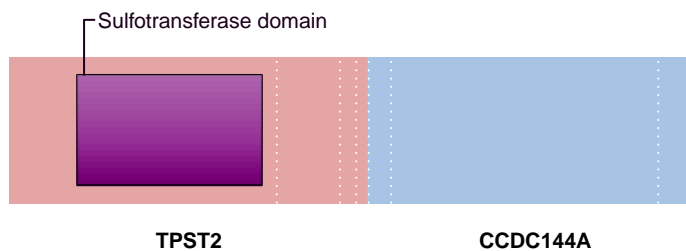
chromosome 17



1 kbp | introns not to scale

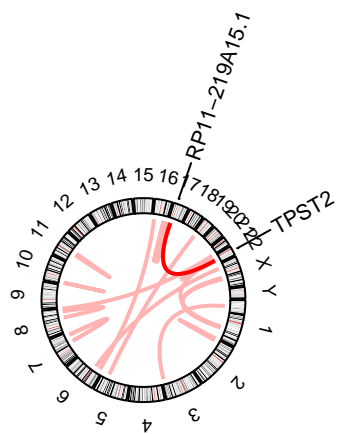
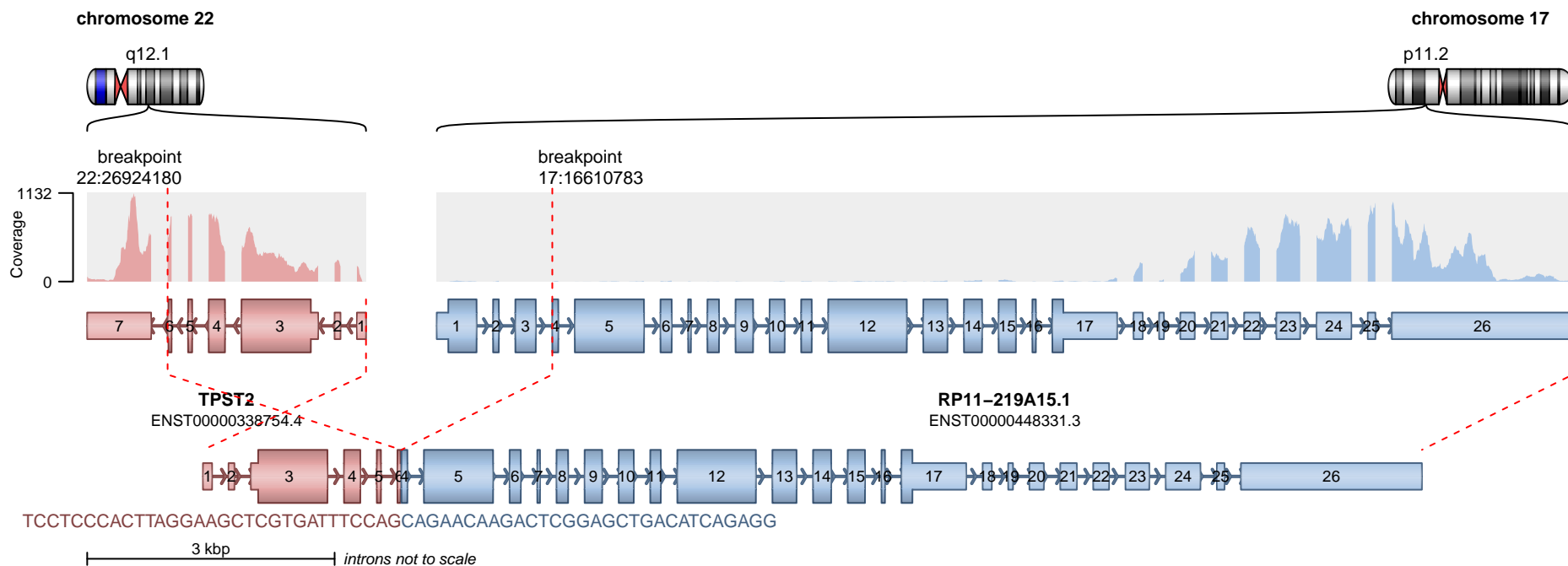


RETAINED PROTEIN DOMAINS
stop codon before fusion junction

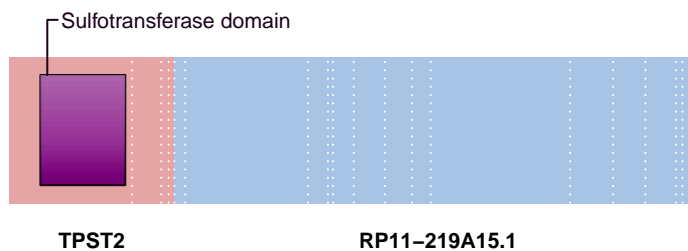


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

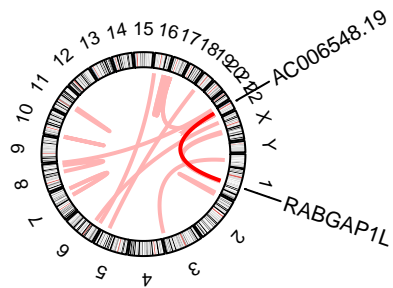
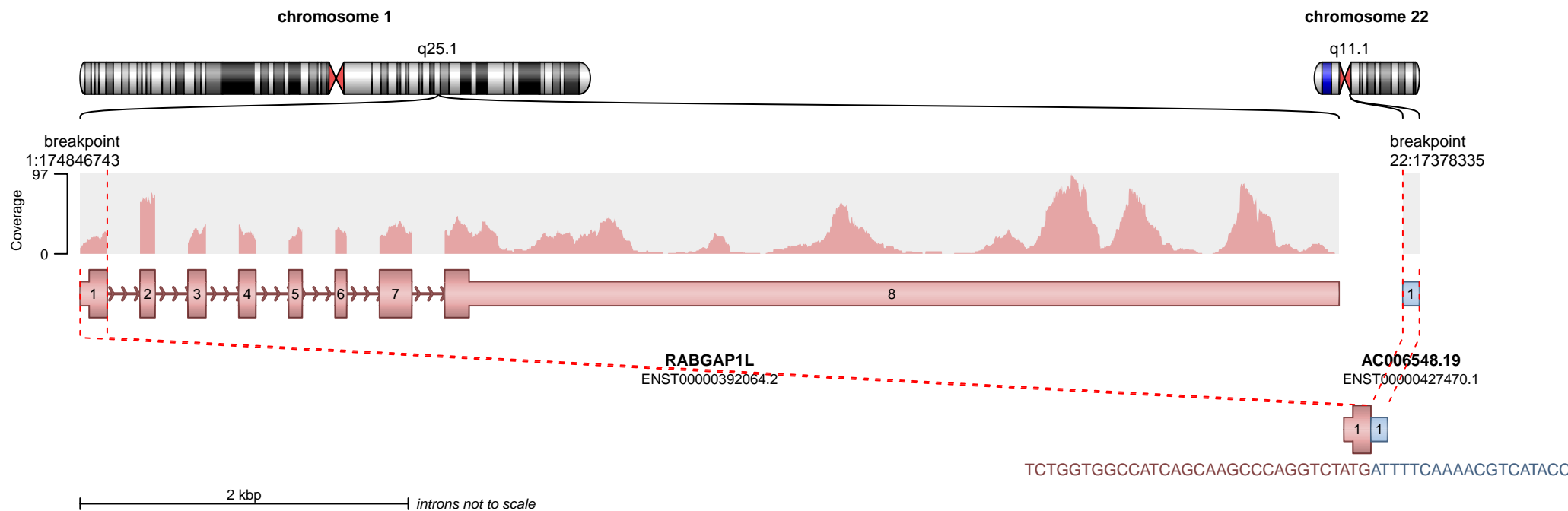


RETAINED PROTEIN DOMAINS
stop codon before fusion junction



SUPPORTING READ COUNT

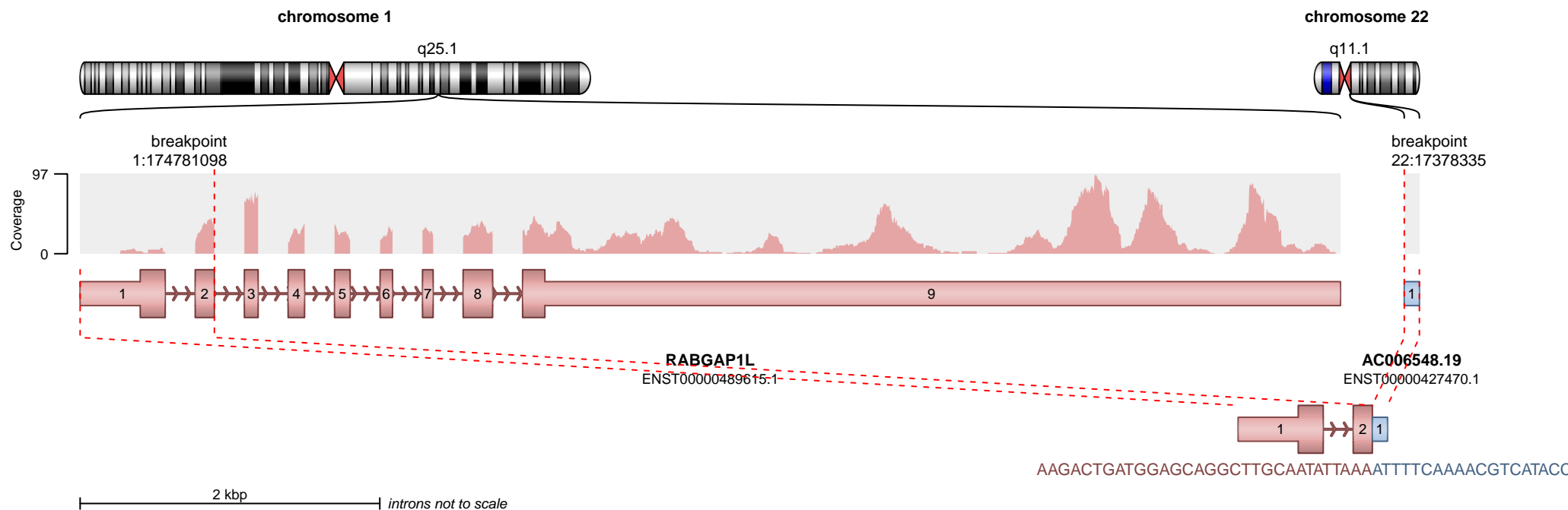
Split reads = 2
Discordant mates = 0



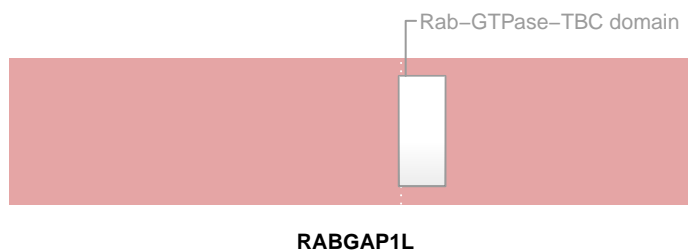
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1



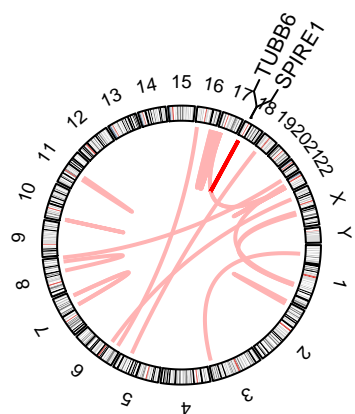
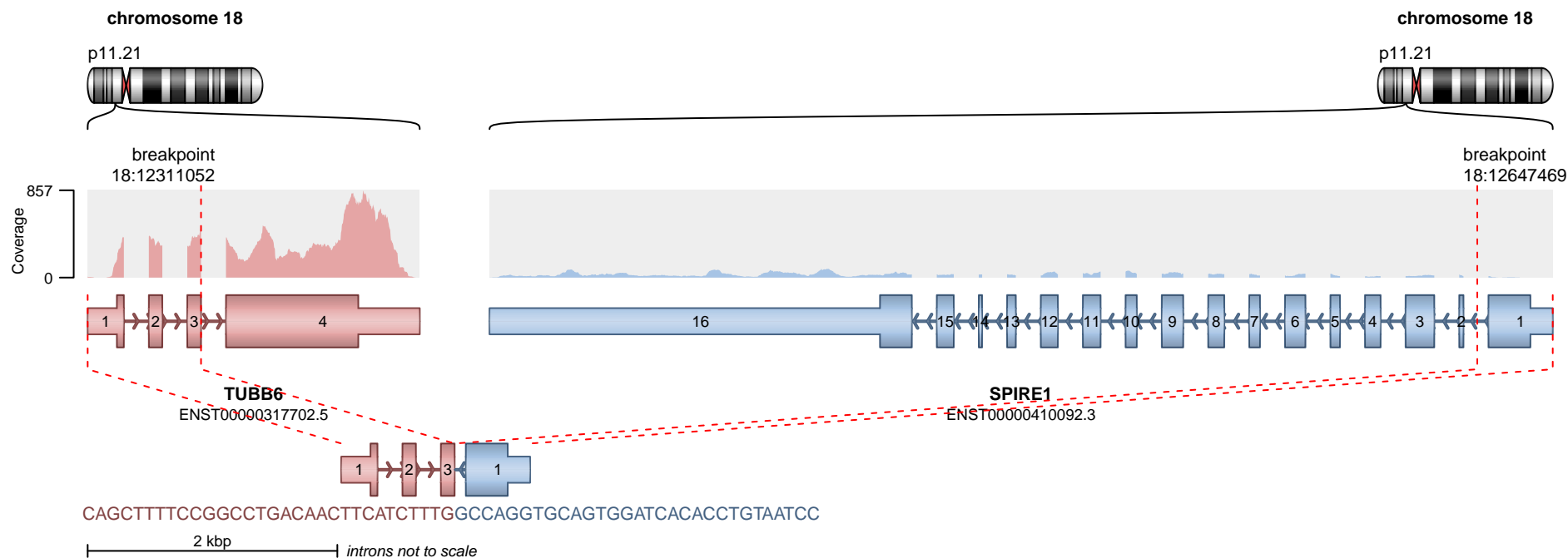
RETAINED PROTEIN DOMAINS out-of-frame fusion



SUPPORTING READ COUNT

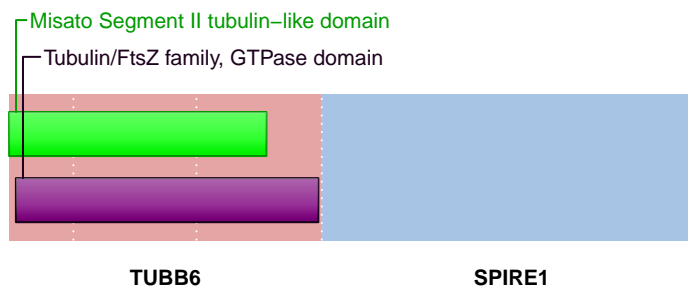
Split reads = 1

Discordant mates = 0



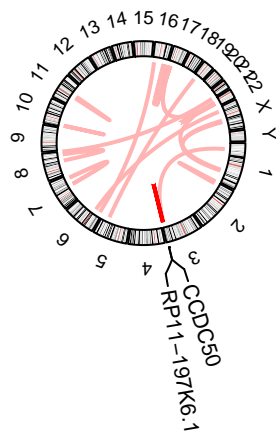
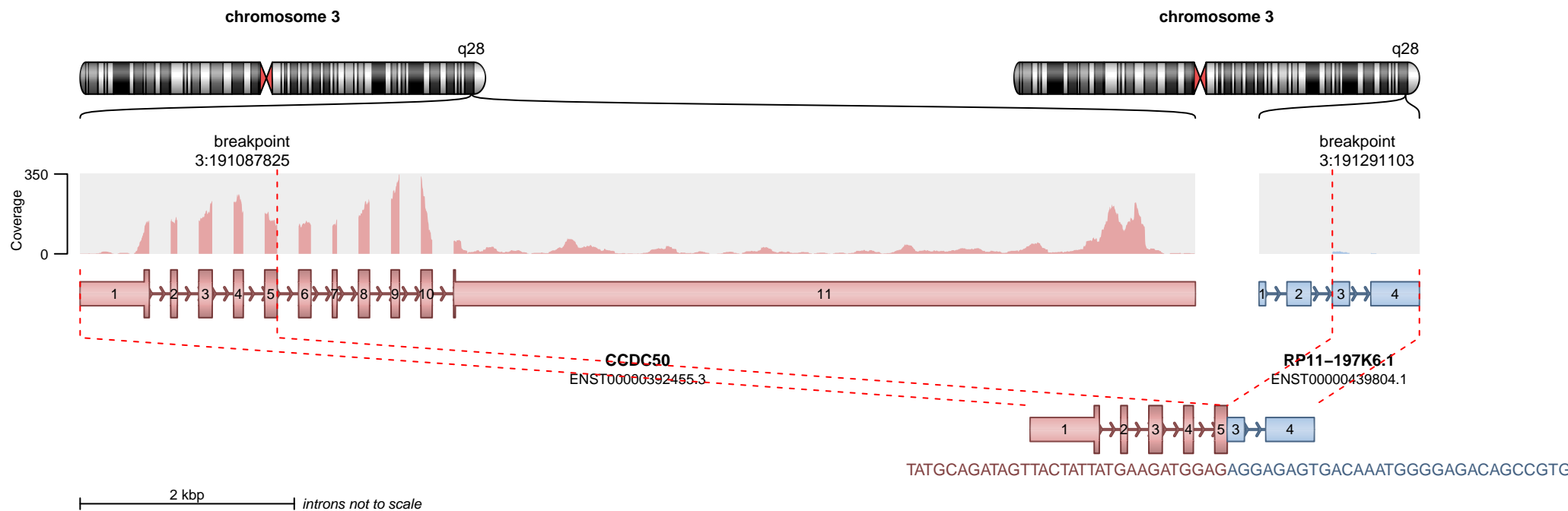
RETAINED PROTEIN DOMAINS

out-of-frame fusion



SUPPORTING READ COUNT

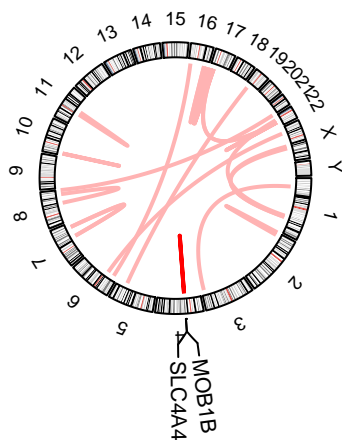
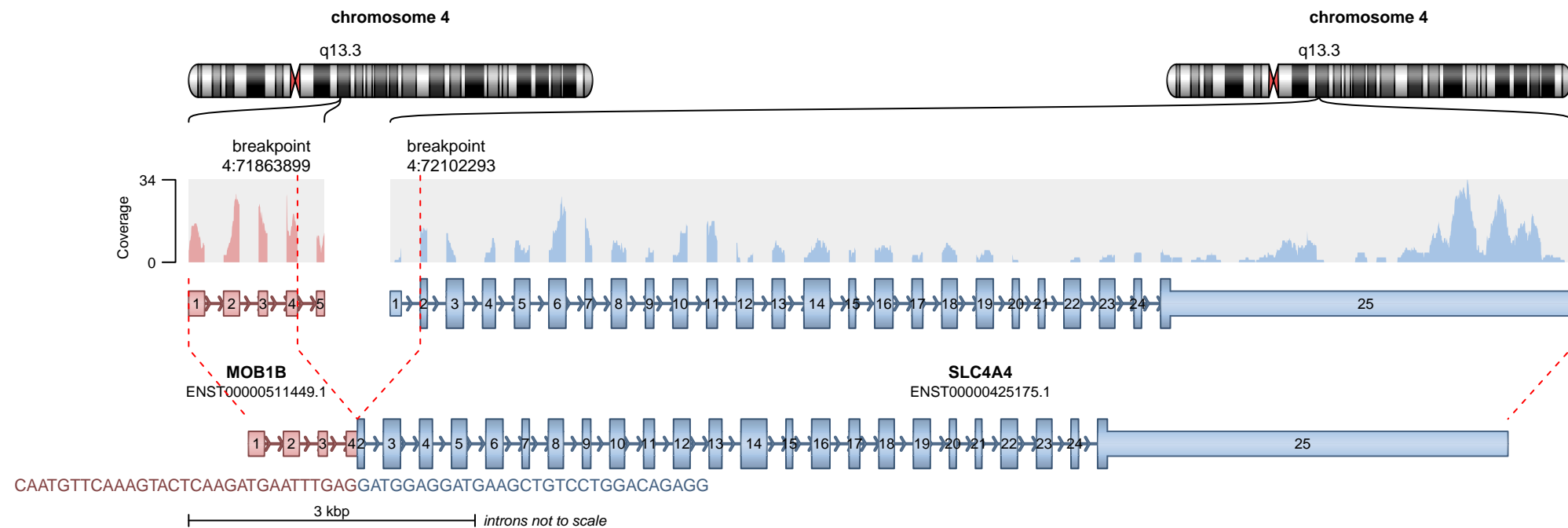
Split reads = 4
Discordant mates = 1



No protein domains retained in fusion.

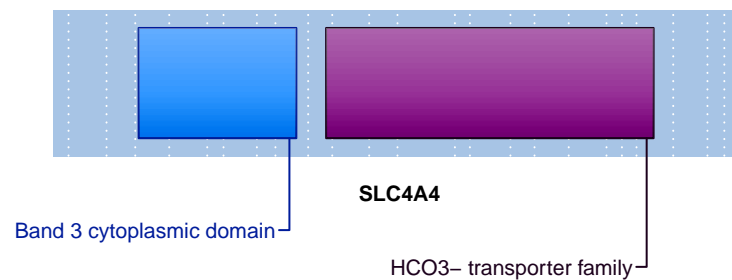
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0



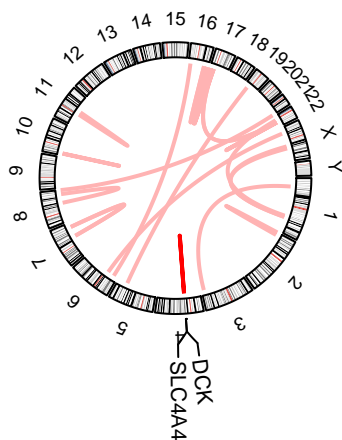
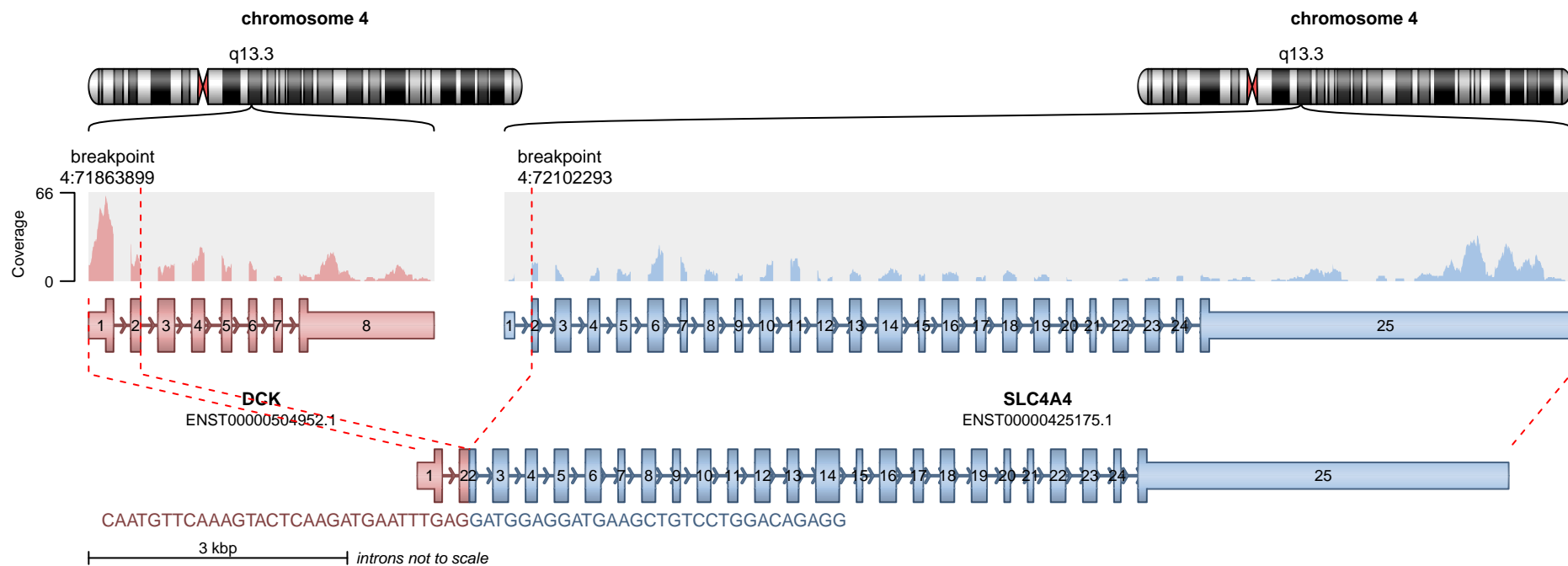
RETAINED PROTEIN DOMAINS

reading frame unclear

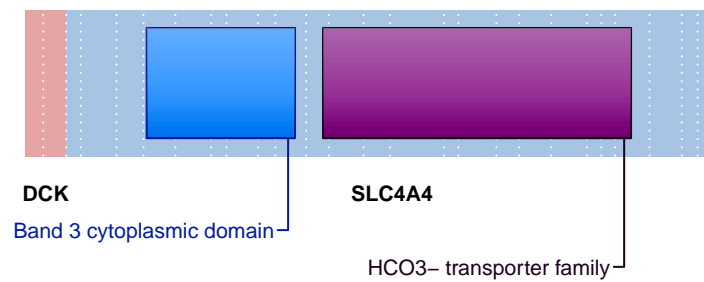


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

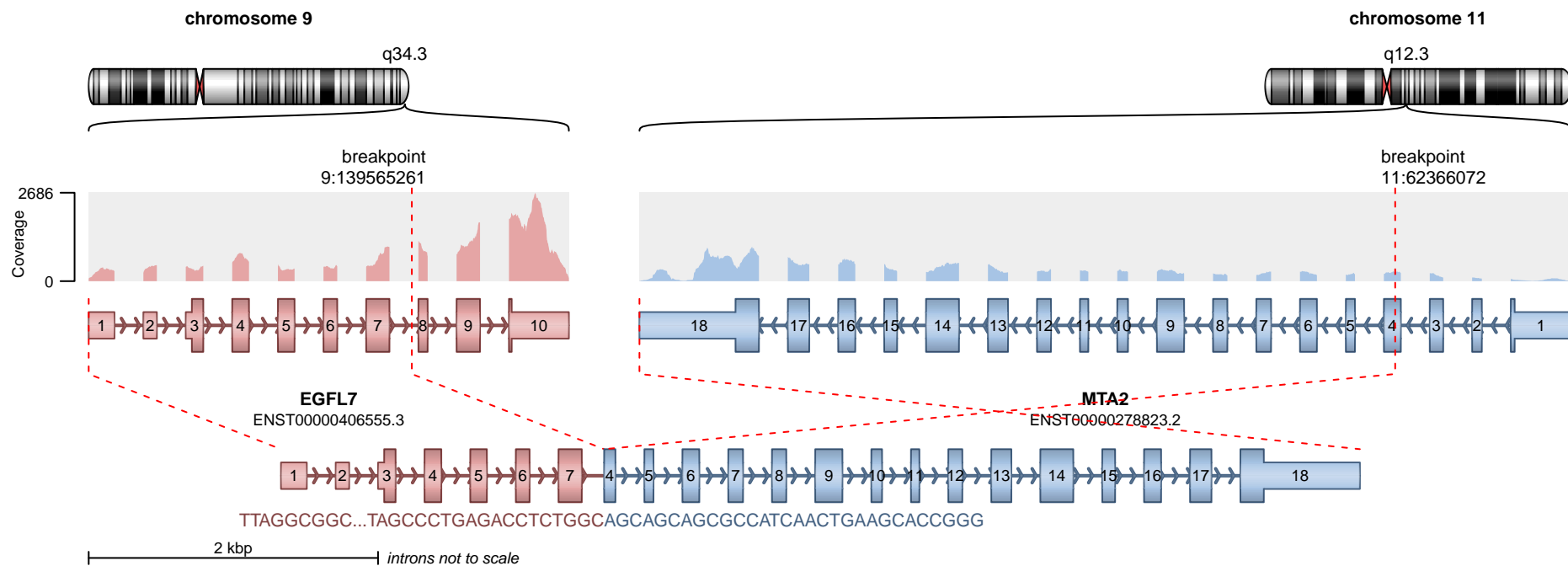


RETAINED PROTEIN DOMAINS out-of-frame fusion



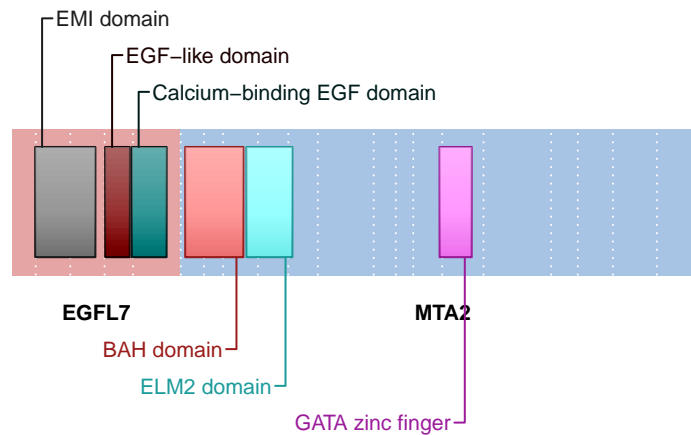
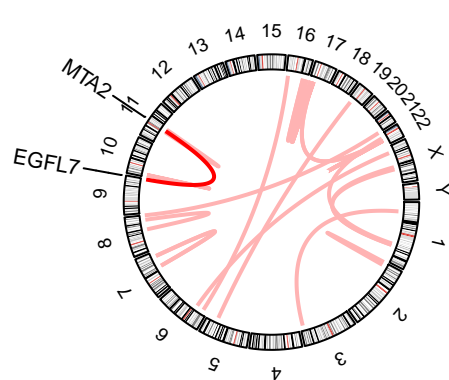
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0



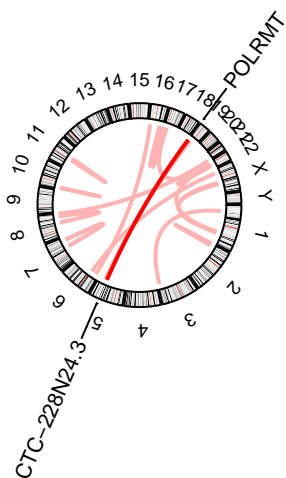
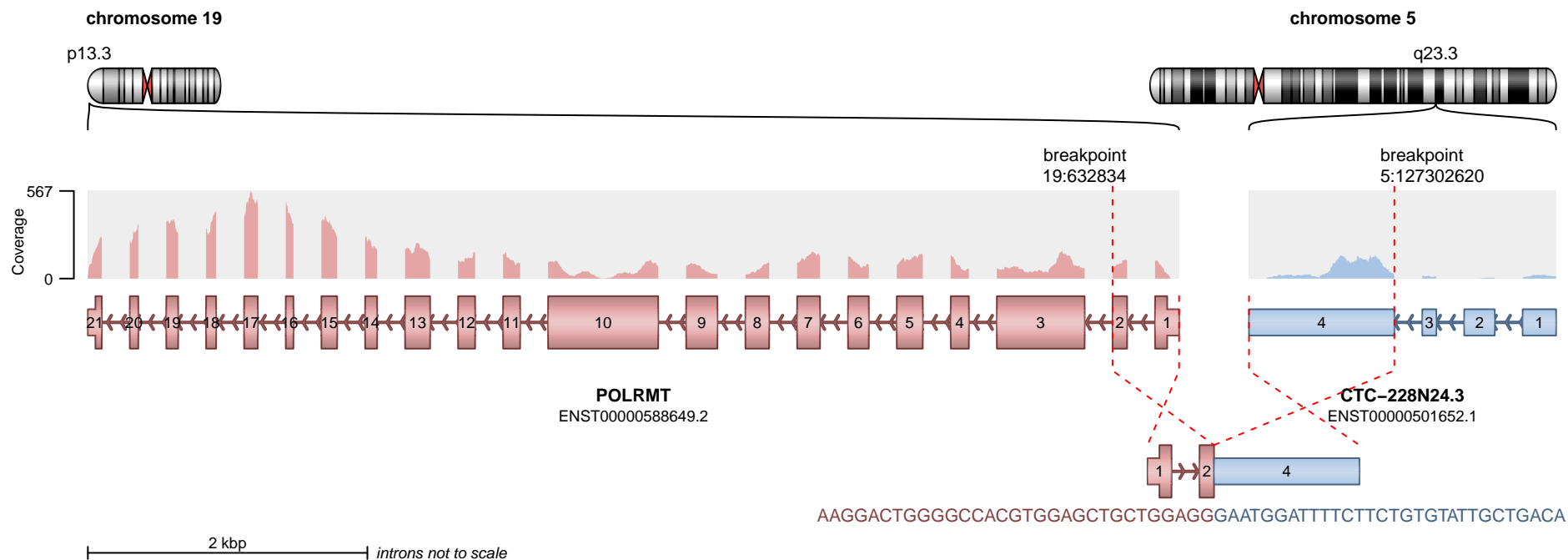
RETAINED PROTEIN DOMAINS

reading frame unclear



SUPPORTING READ COUNT

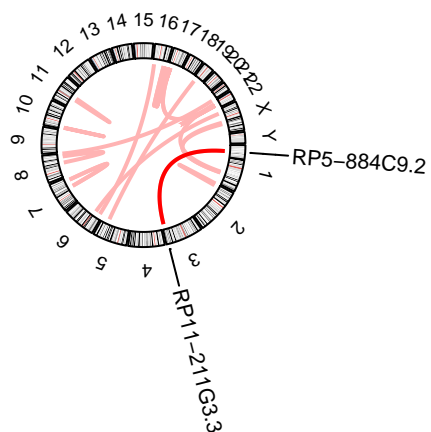
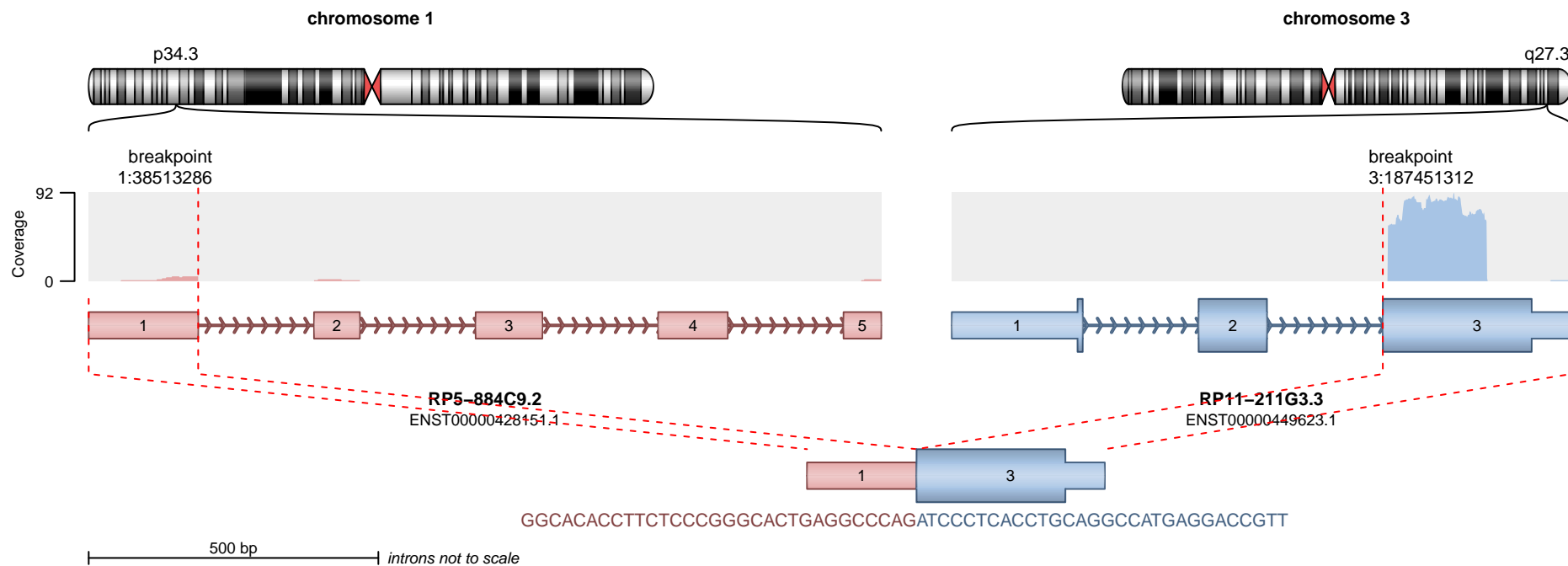
Split reads = 2
Discordant mates = 0



No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0