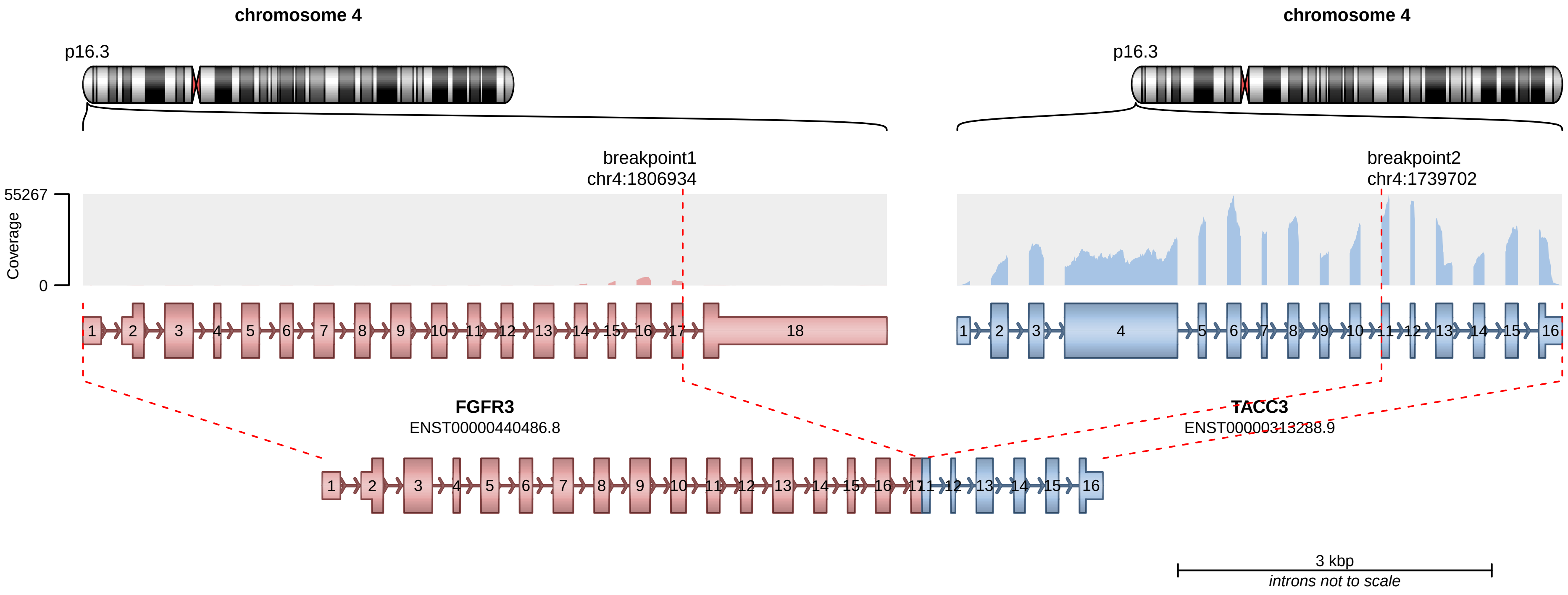
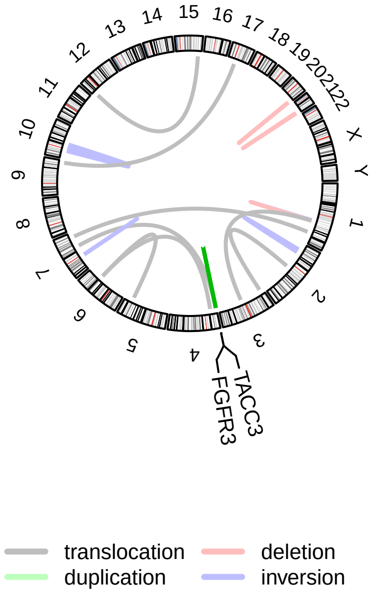
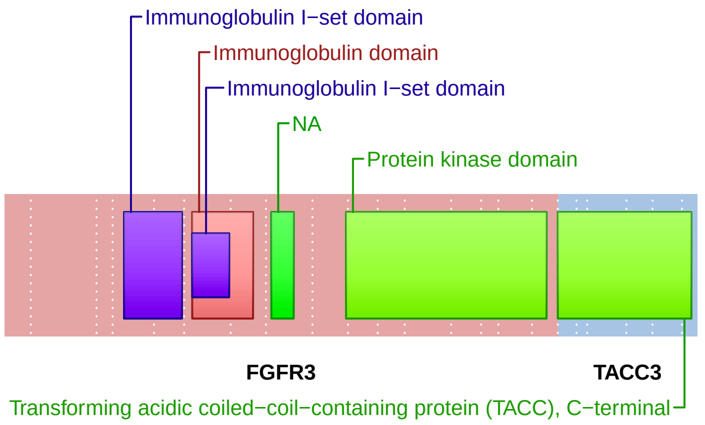


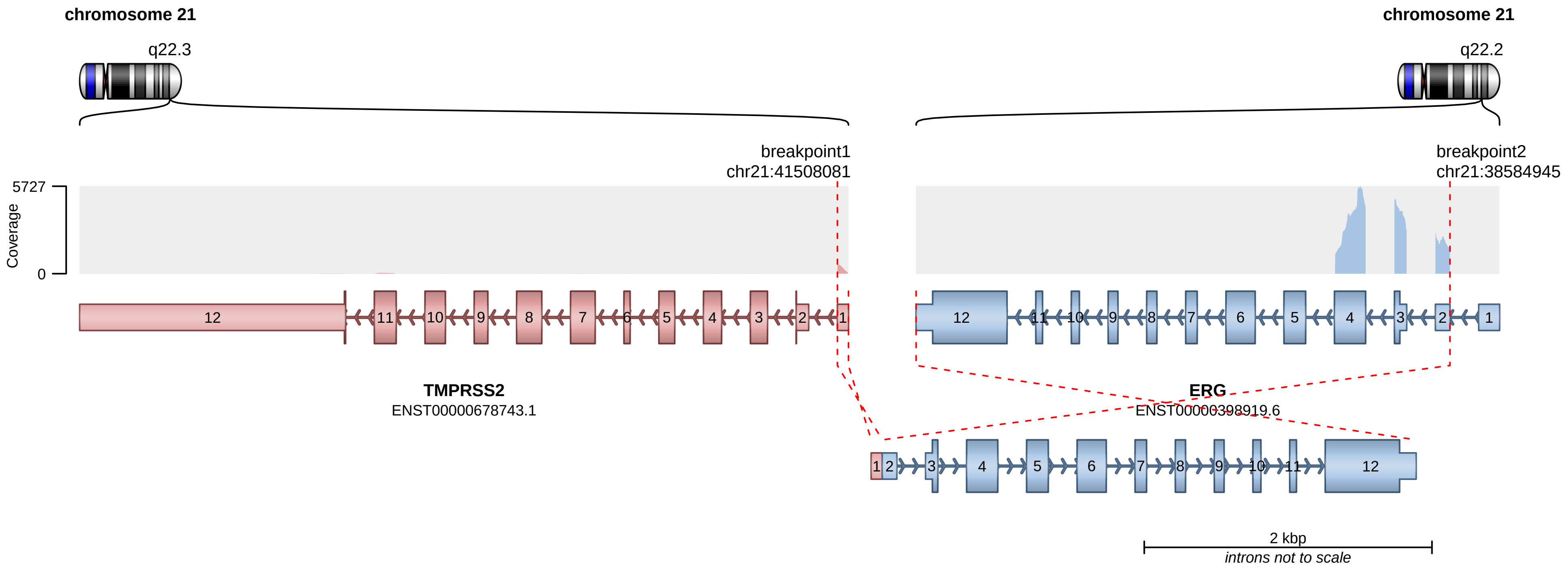


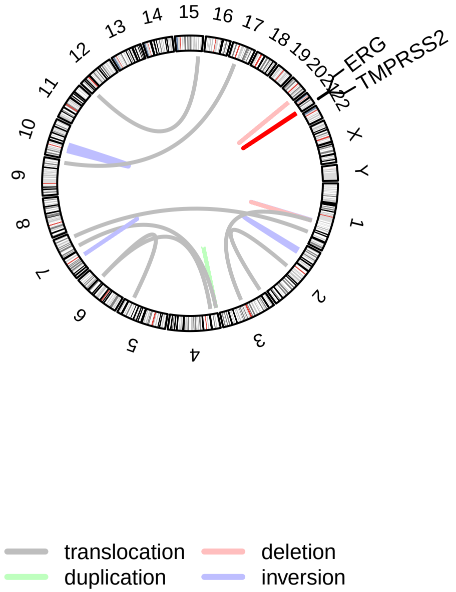
RETAINED PROTEIN DOMAINS
reading frame unclear

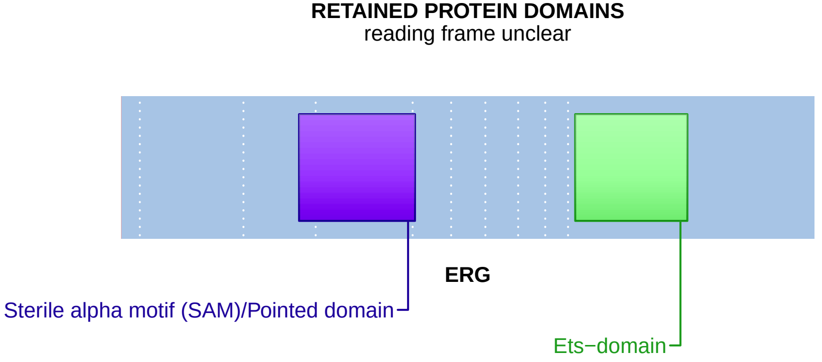


SUPPORTING READ COUNT

Split reads = 649
Discordant mates = 0

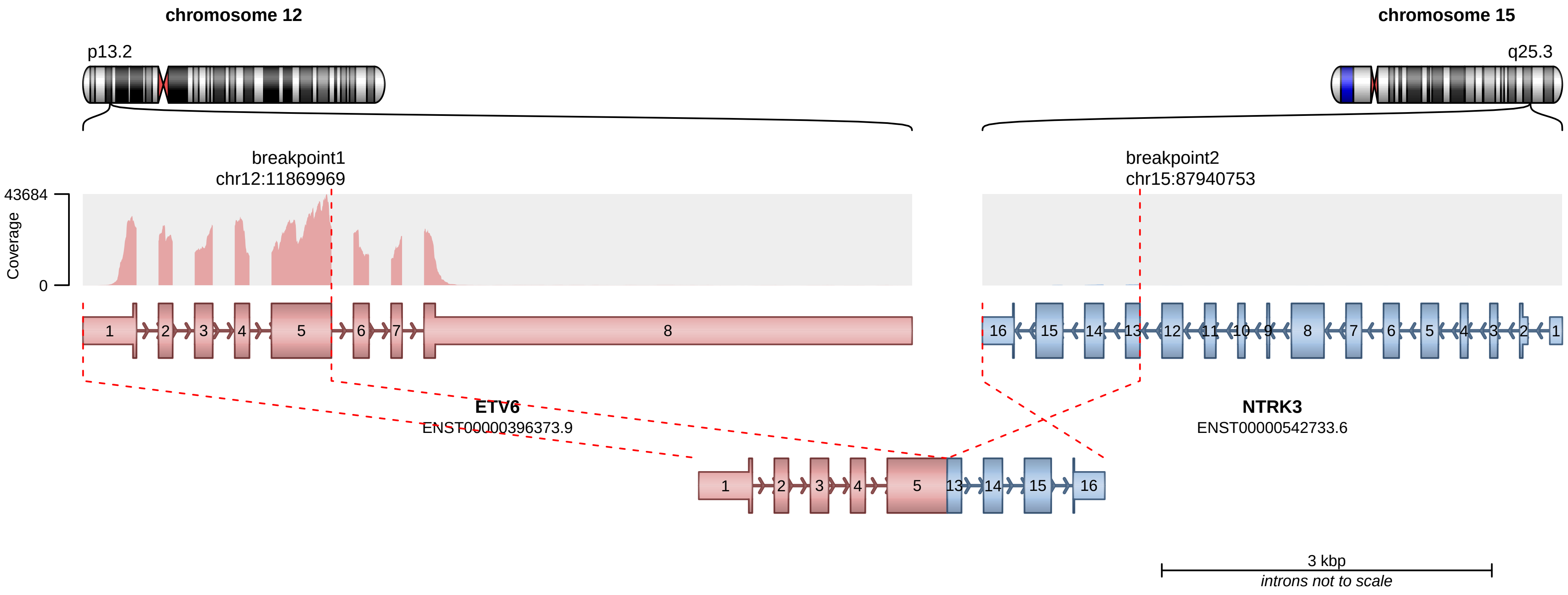


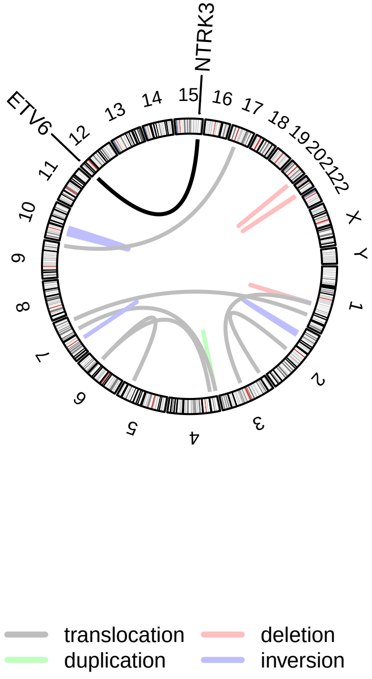




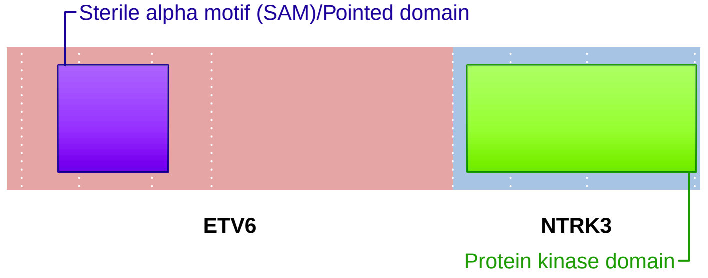
SUPPORTING READ COUNT

Split reads = 593
Discordant mates = 0



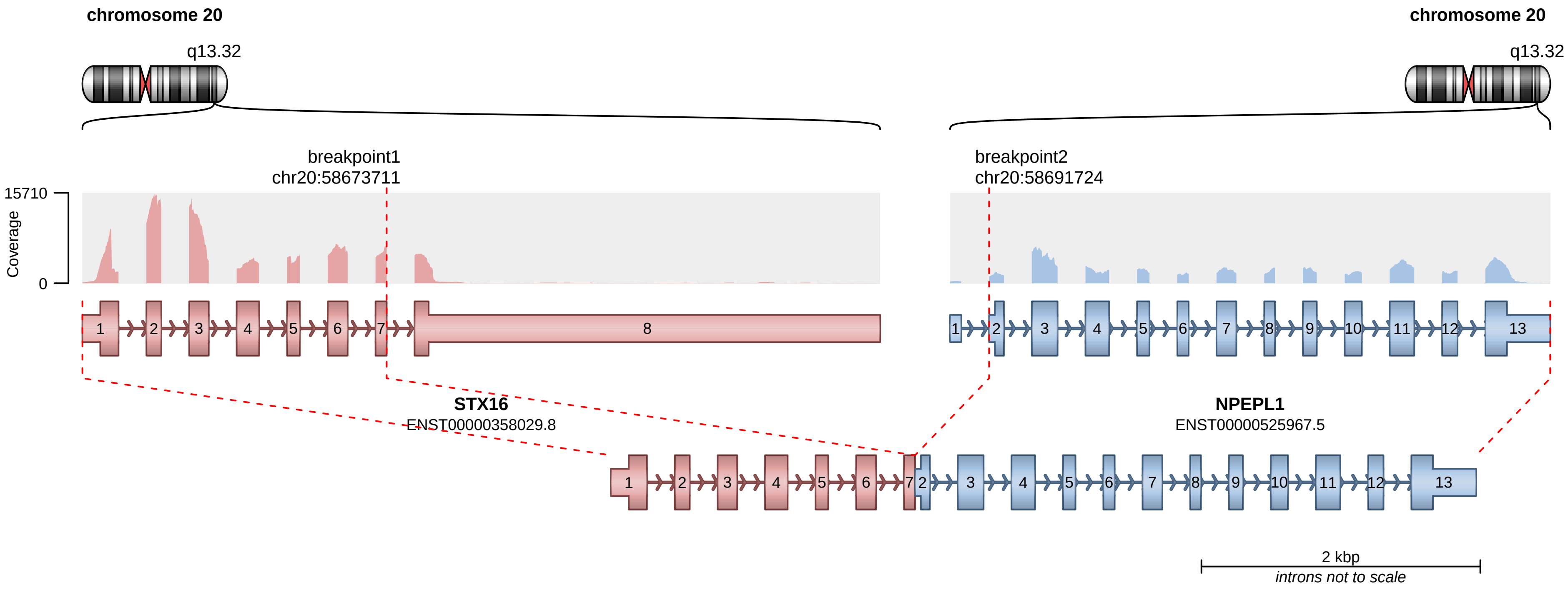


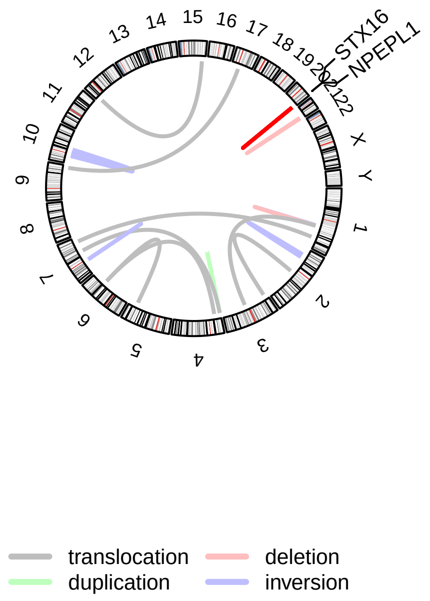
RETAINED PROTEIN DOMAINS
reading frame unclear

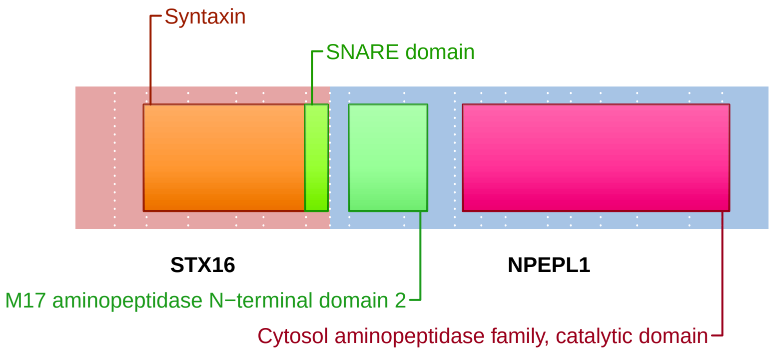


SUPPORTING READ COUNT

Split reads = 191
Discordant mates = 0



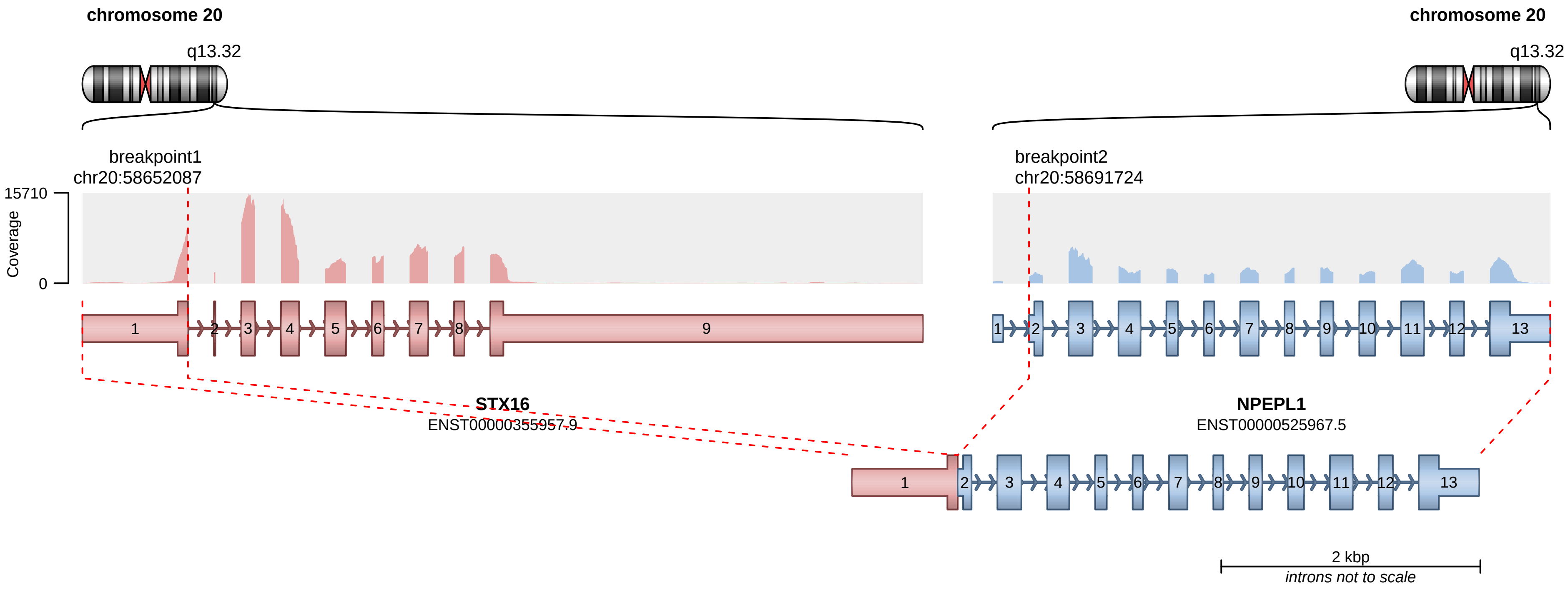


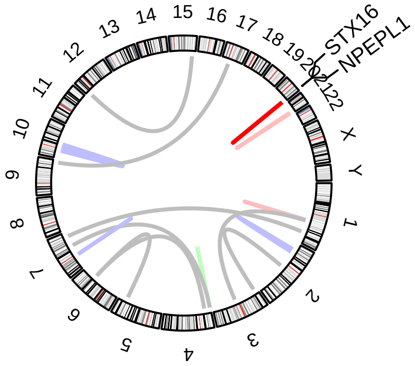


RETAINED PROTEIN DOMAINS
reading frame unclear

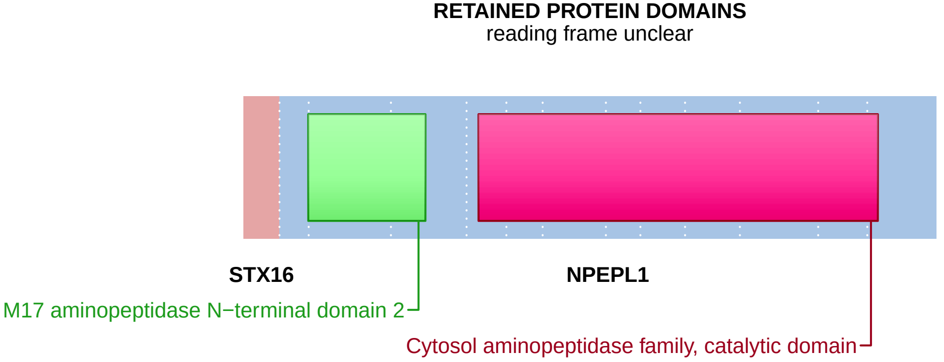
SUPPORTING READ COUNT

Split reads = 168
Discordant mates = 2



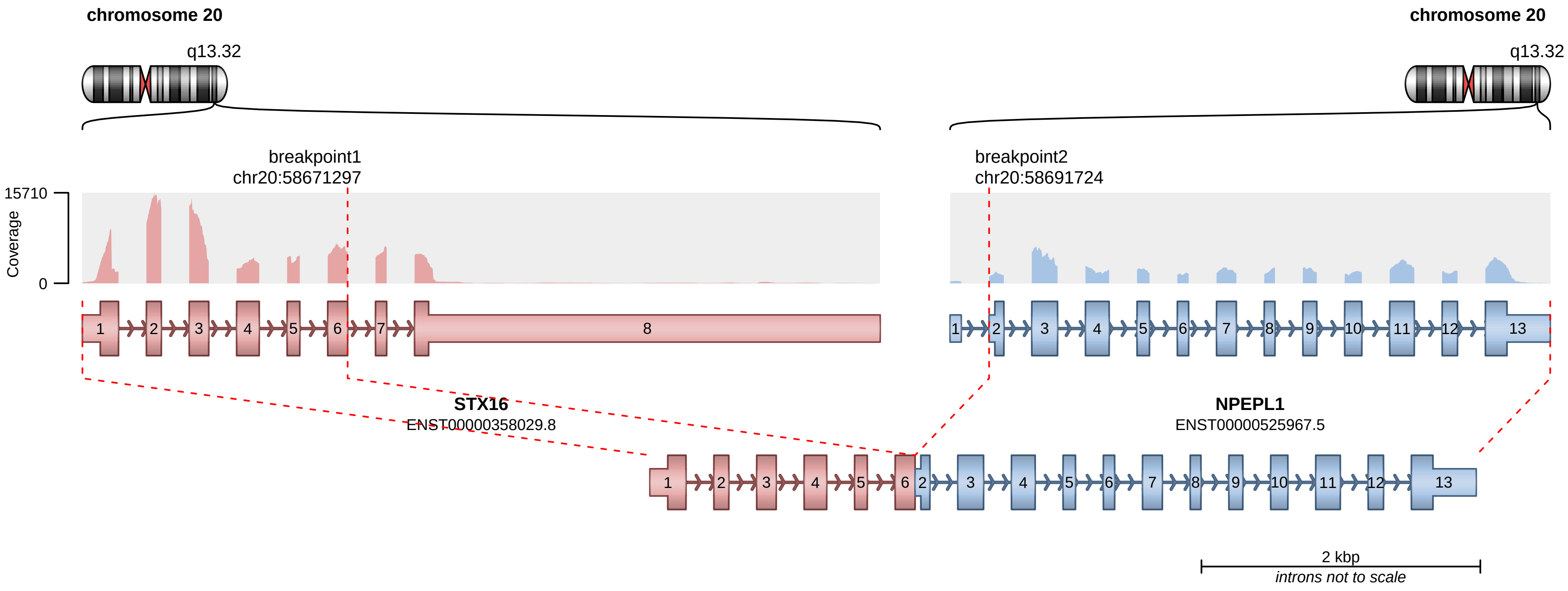


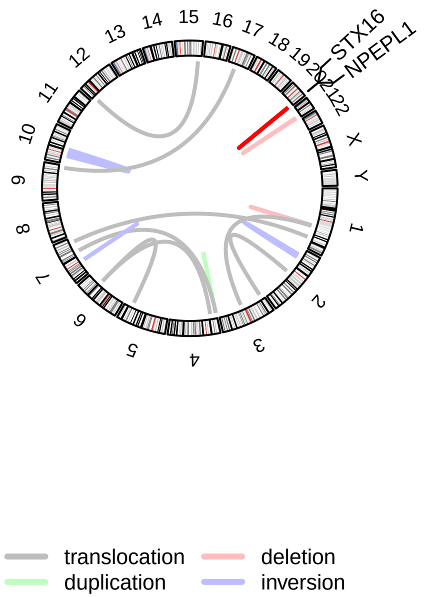
translocation
duplication
deletion
inversion

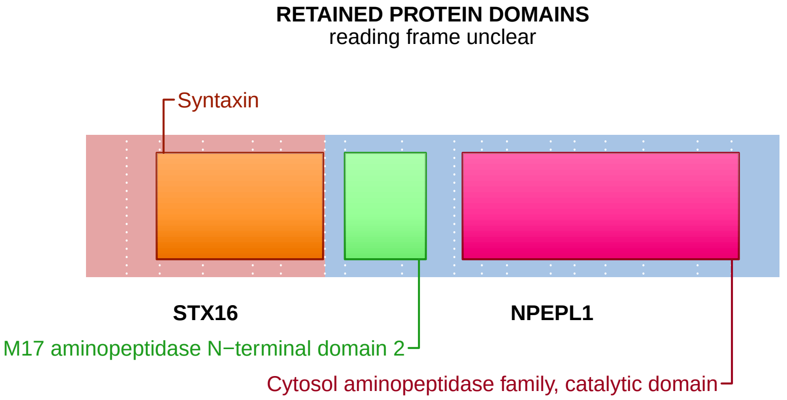


SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 0

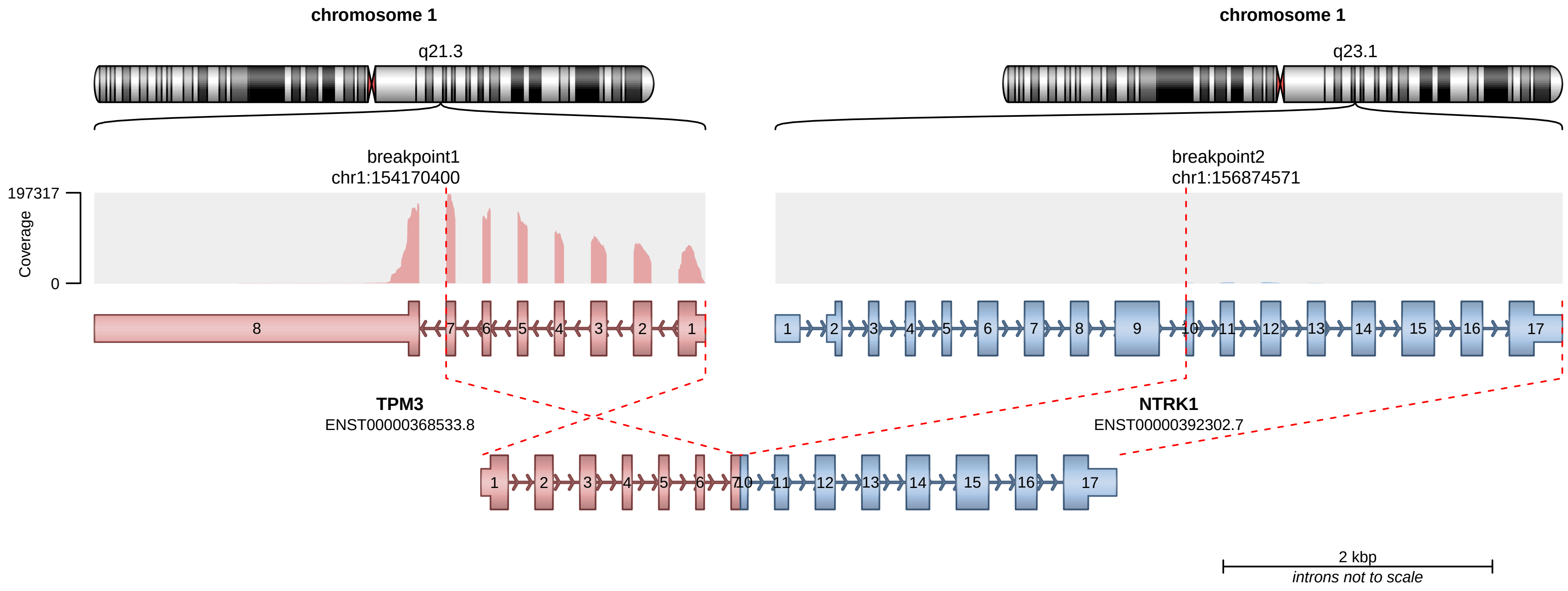


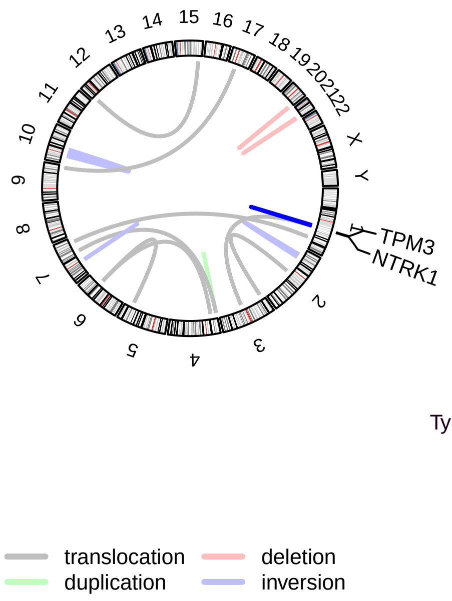




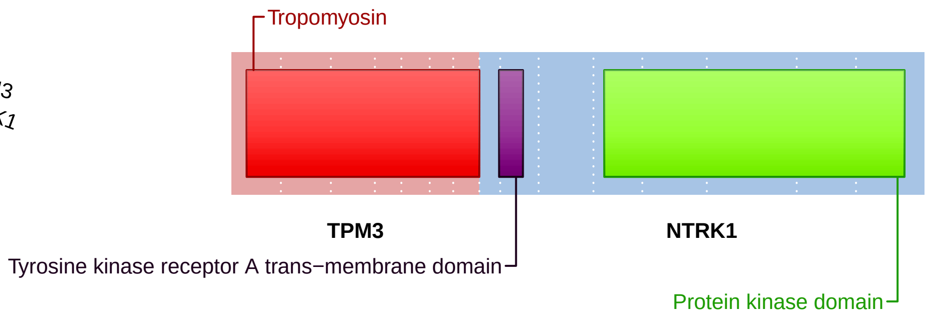
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 1



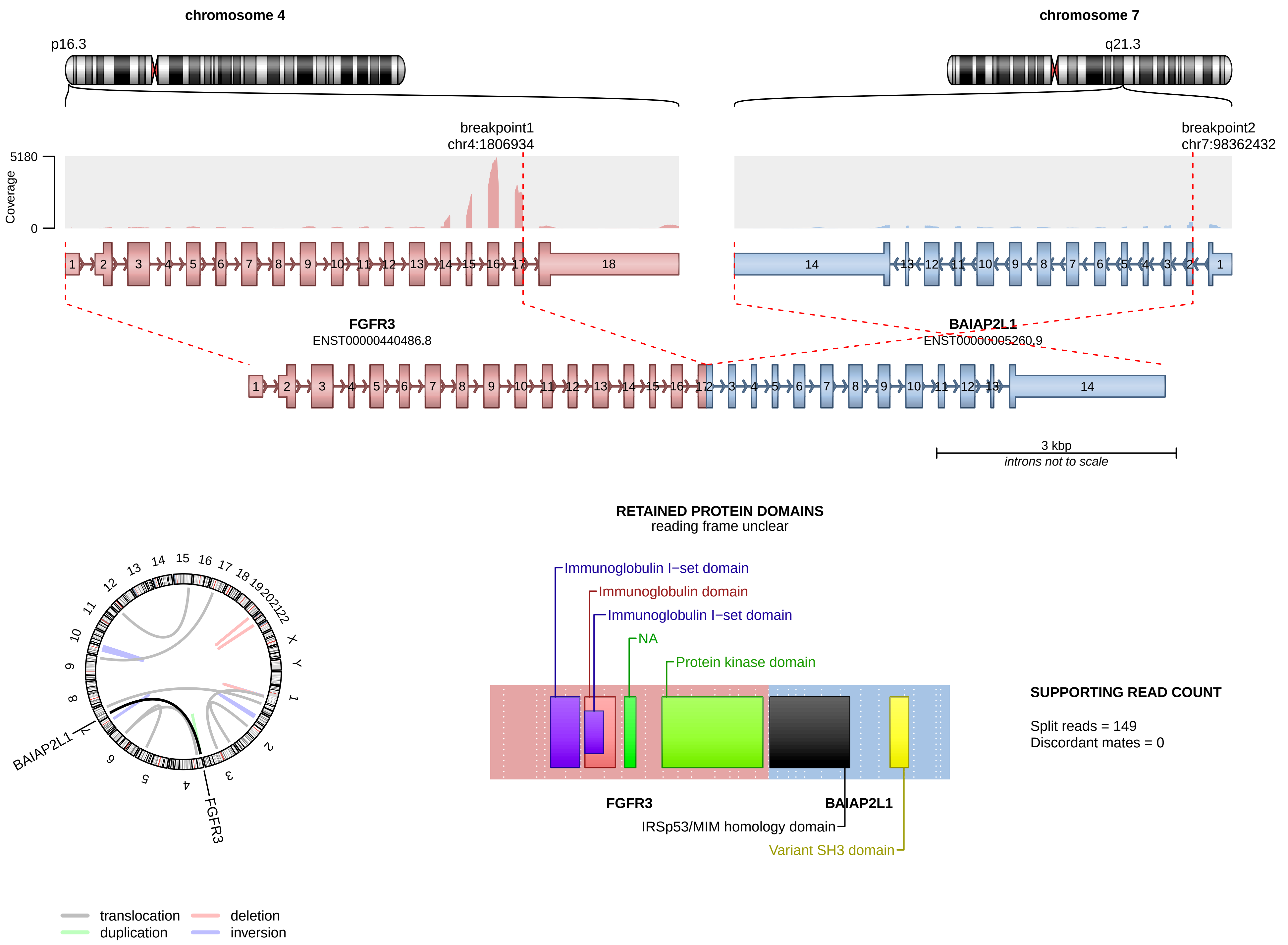


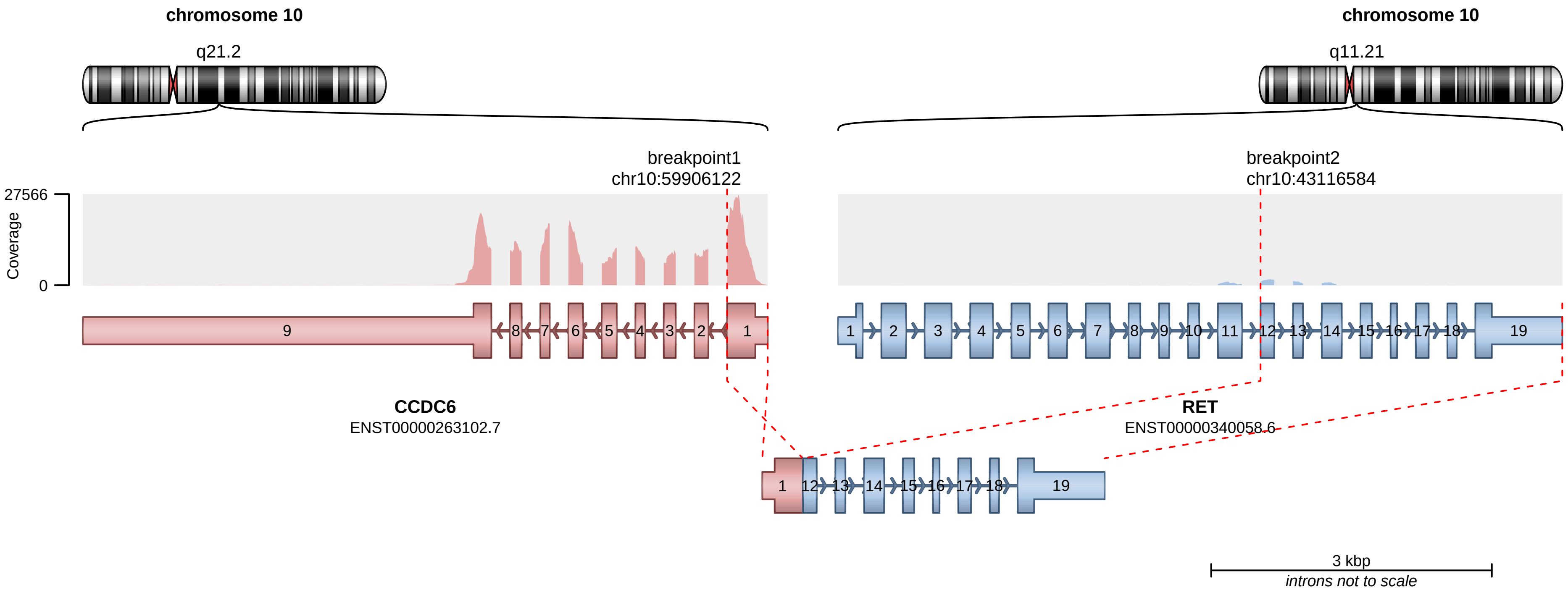
RETAINED PROTEIN DOMAINS
reading frame unclear

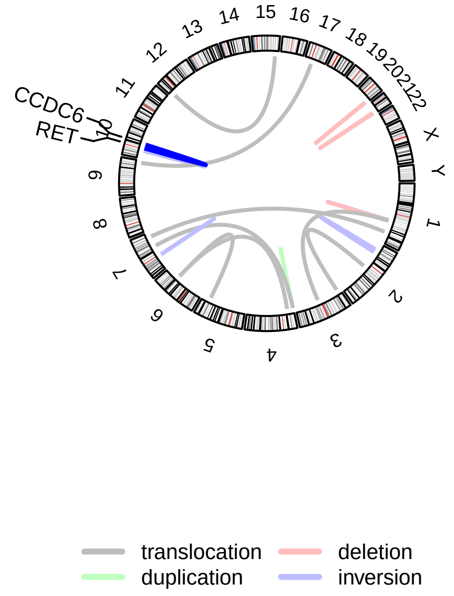


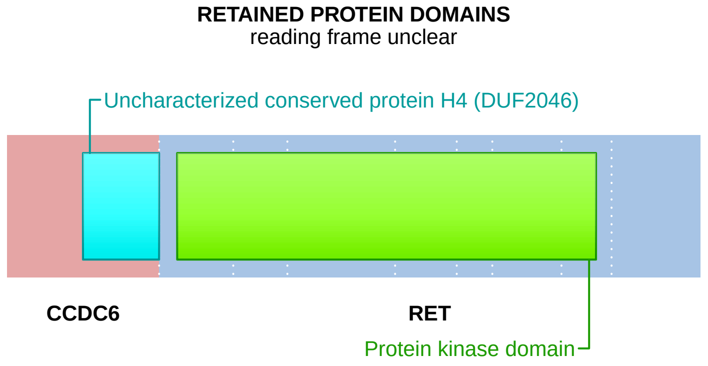
SUPPORTING READ COUNT

Split reads = 151
Discordant mates = 0


chromosome 4
p16.3
chromosome 7
q21.3
breakpoint1
chr4:1806934
breakpoint2
chr7:98362432
Coverage
5180
0
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18
14 13 12 11 10 9 8 7 6 5 4 3 2 1
FGFR3
ENST00000440486.8
BAIAP2L1
ENST00000005260.9
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 2 3 4 5 6 7 8 9 10 11 12 13 14
3 kbp
introns not to scale
RETAINED PROTEIN DOMAINS
reading frame unclear
Immunoglobulin I−set domain
Immunoglobulin domain
Immunoglobulin I−set domain
NA
Protein kinase domain
FGFR3
BAIAP2L1
IRSp53/MIM homology domain
Variant SH3 domain
SUPPORTING READ COUNT
Split reads = 149
Discordant mates = 0
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y
BAIAP2L1
FGFR3
translocation
deletion
duplication
inversion

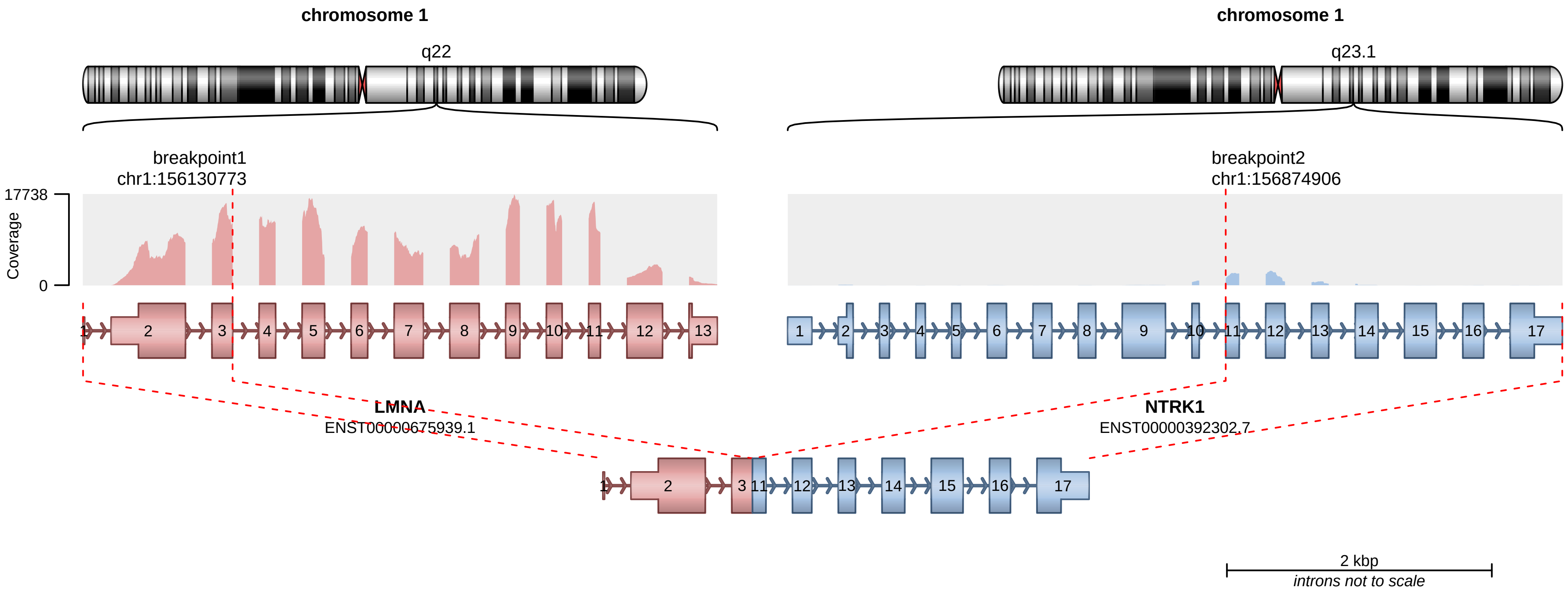


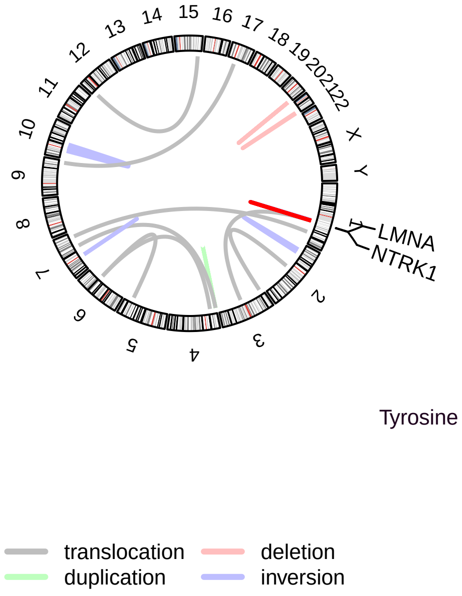


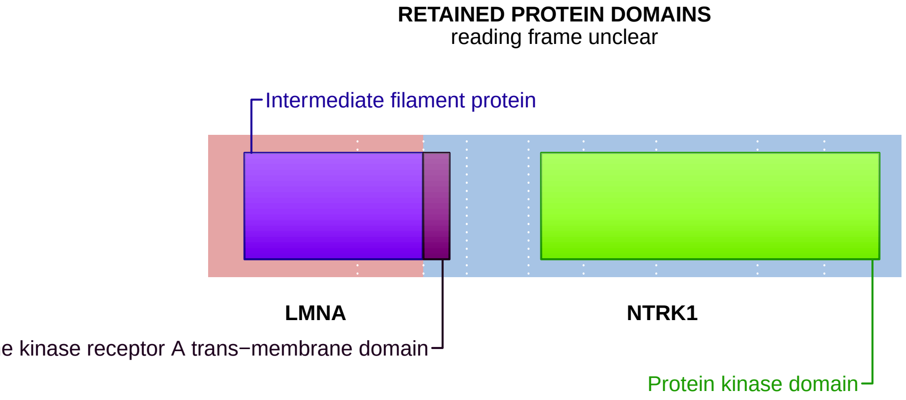


SUPPORTING READ COUNT

Split reads = 140
Discordant mates = 0

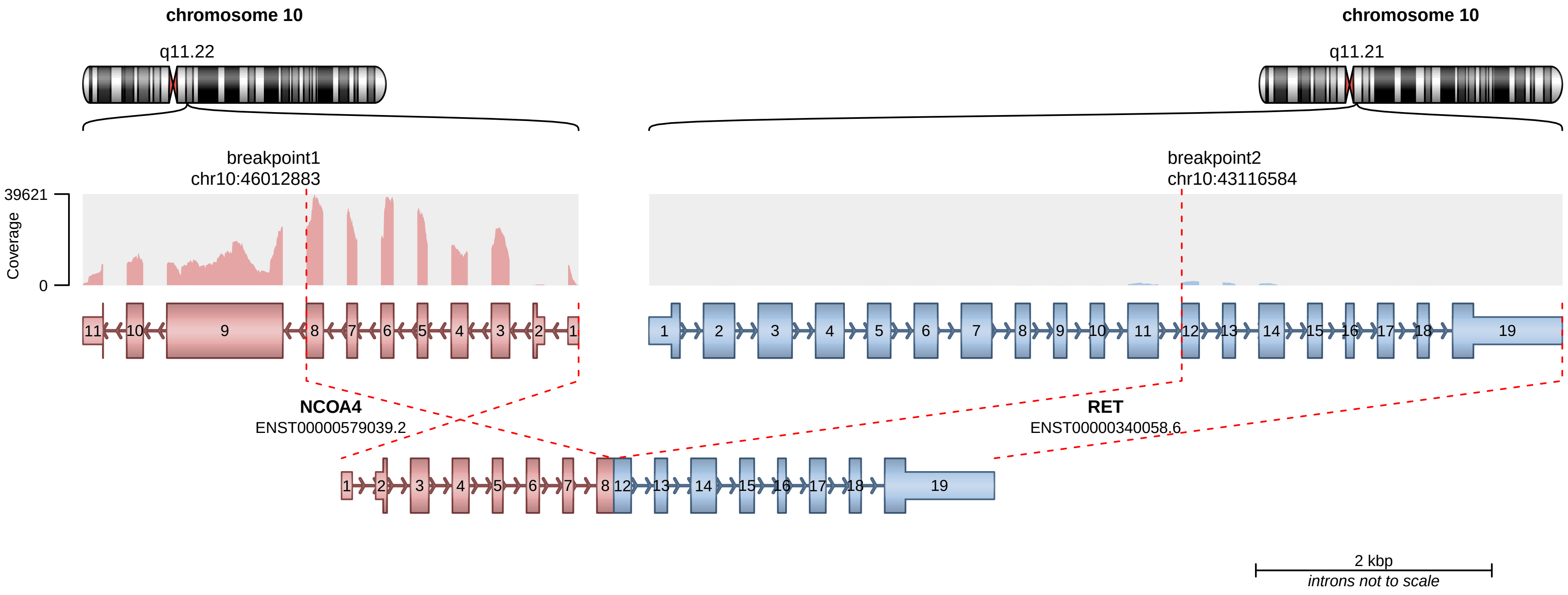


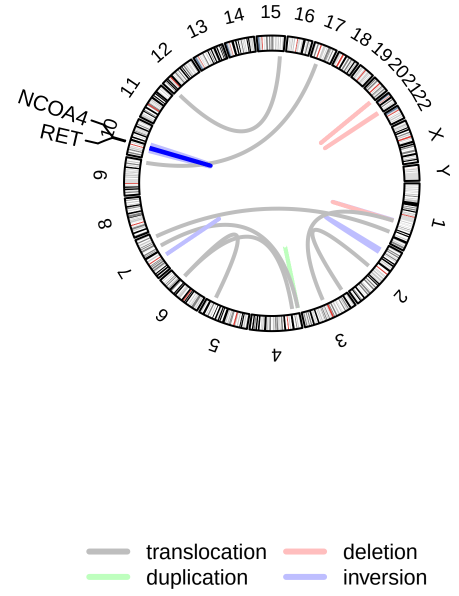




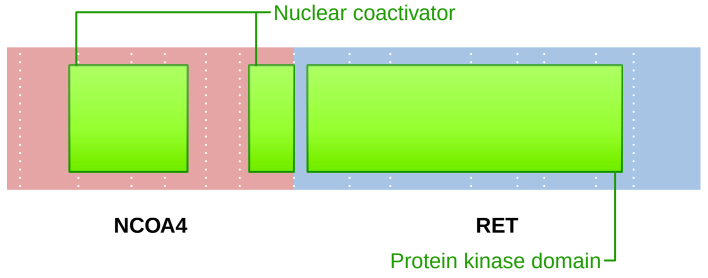
SUPPORTING READ COUNT

Split reads = 138
Discordant mates = 0



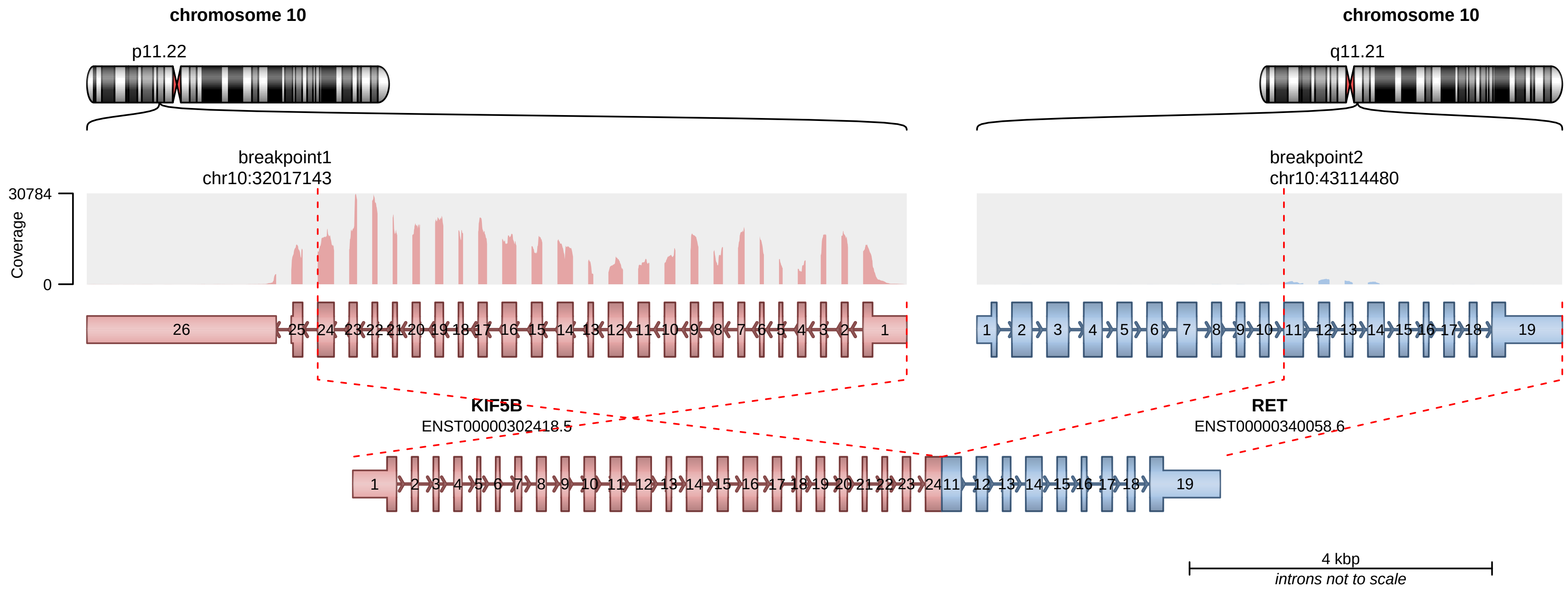


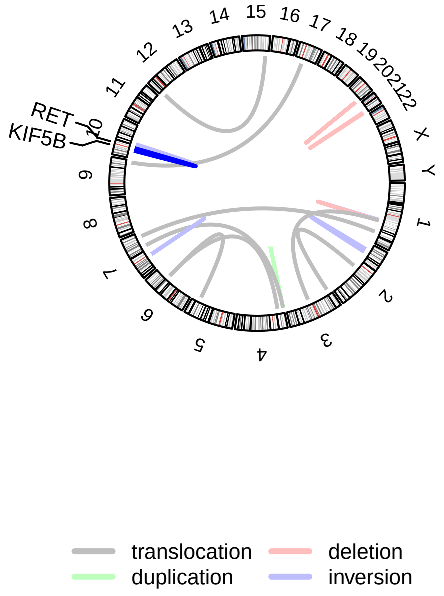
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

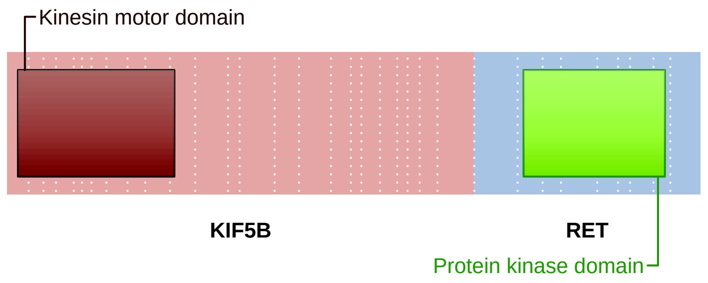
Split reads = 93
Discordant mates = 0





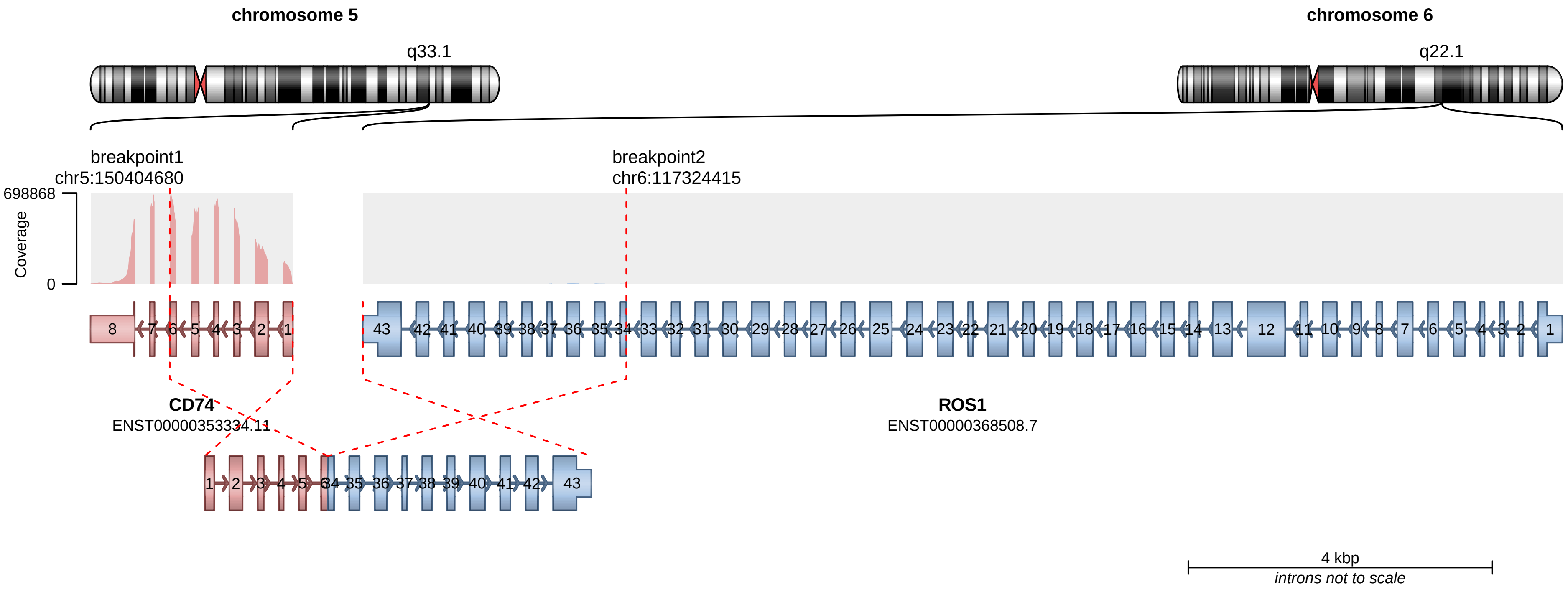
RETAINED PROTEIN DOMAINS

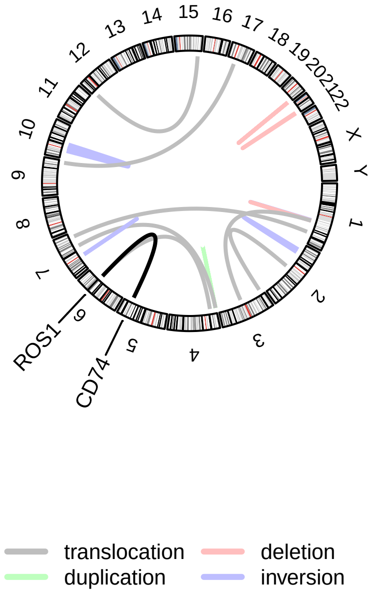
reading frame unclear

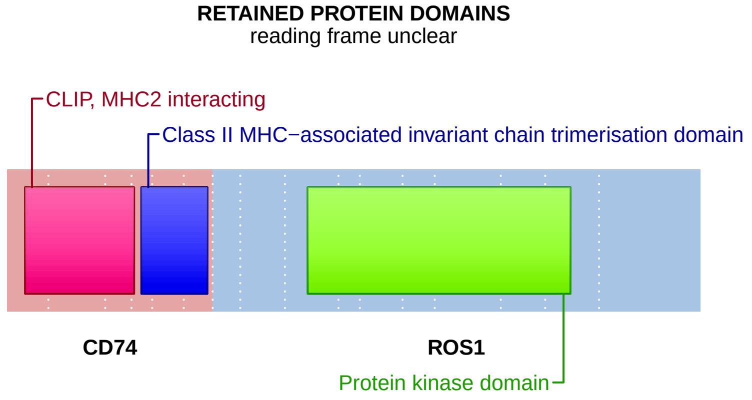


SUPPORTING READ COUNT

Split reads = 88
Discordant mates = 1

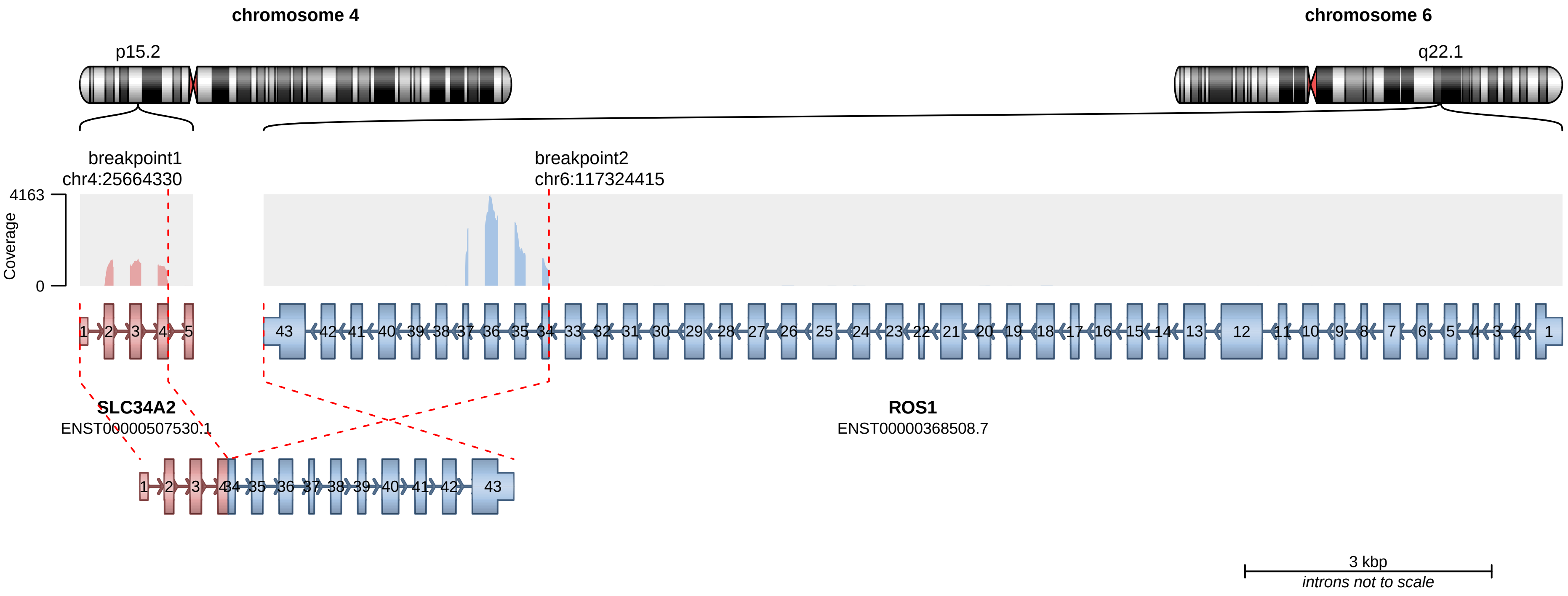


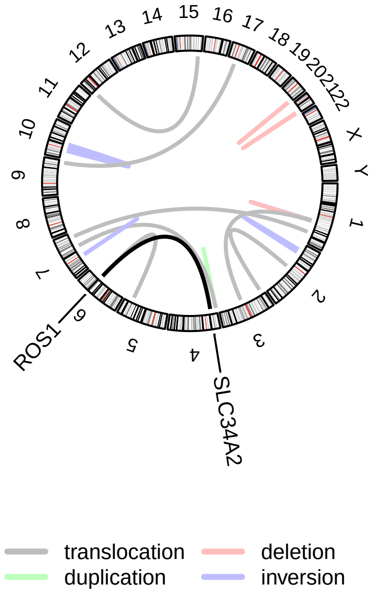




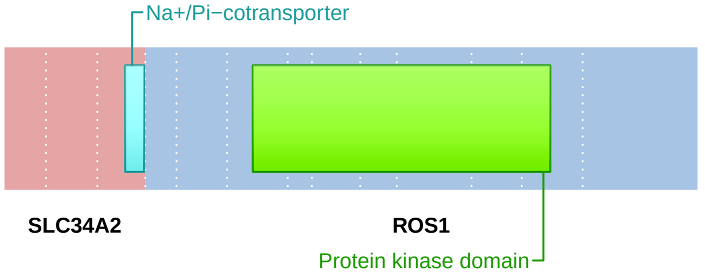
SUPPORTING READ COUNT

Split reads = 82
Discordant mates = 0



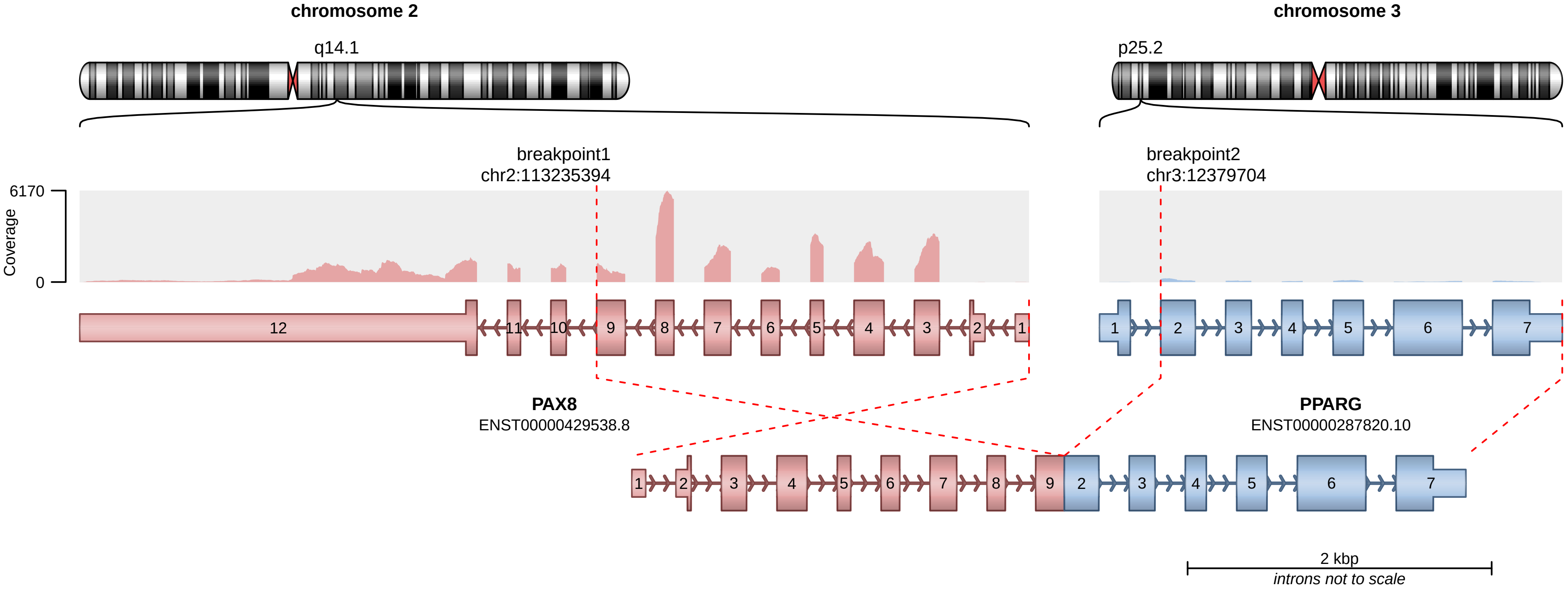


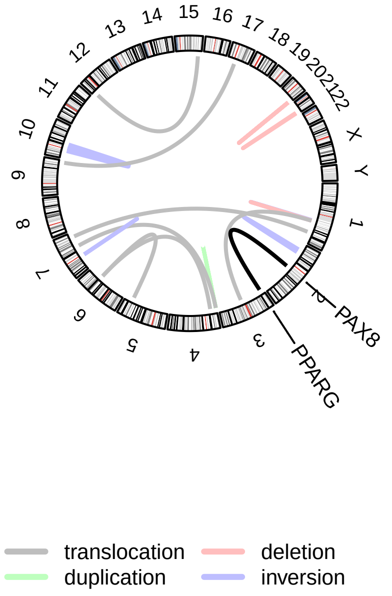
RETAINED PROTEIN DOMAINS
reading frame unclear

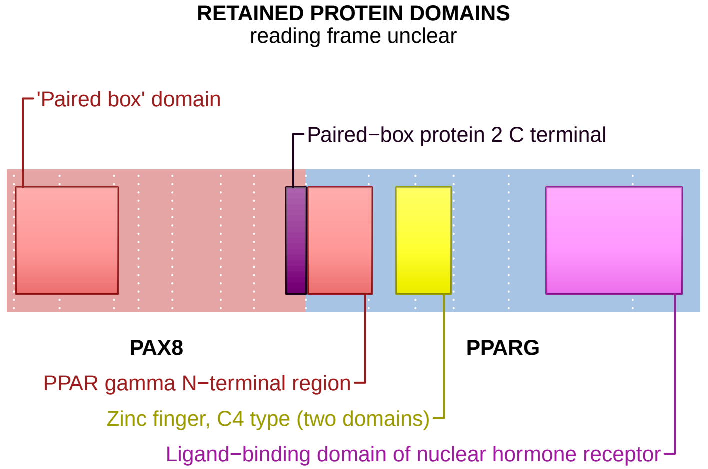


SUPPORTING READ COUNT

Split reads = 76
Discordant mates = 3

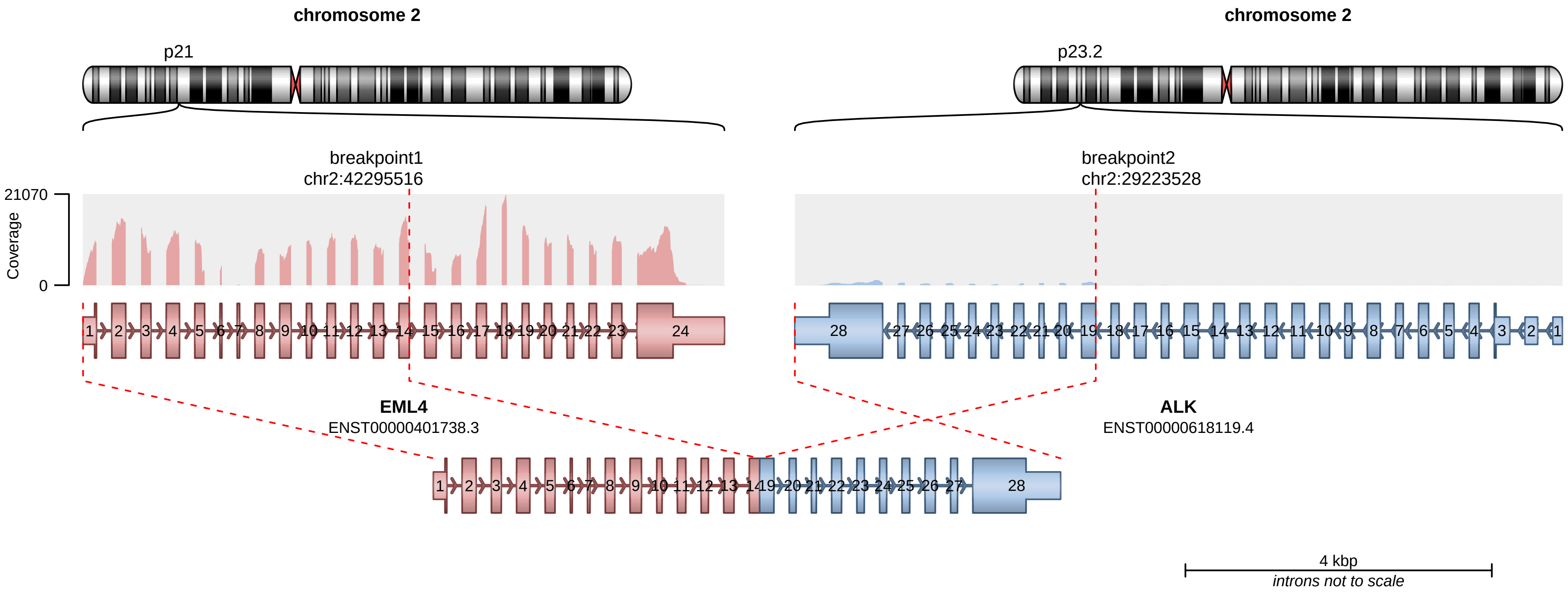


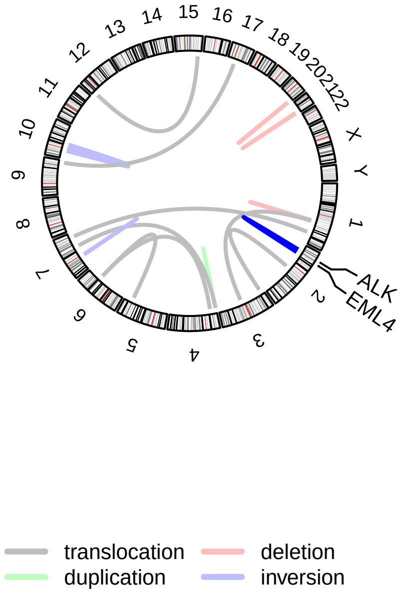


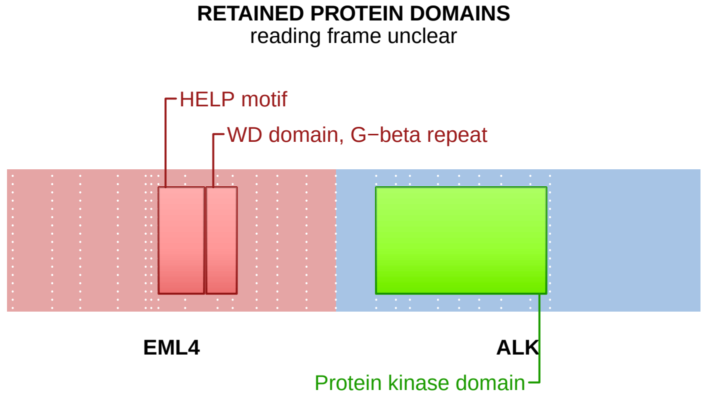


SUPPORTING READ COUNT

Split reads = 75
Discordant mates = 0

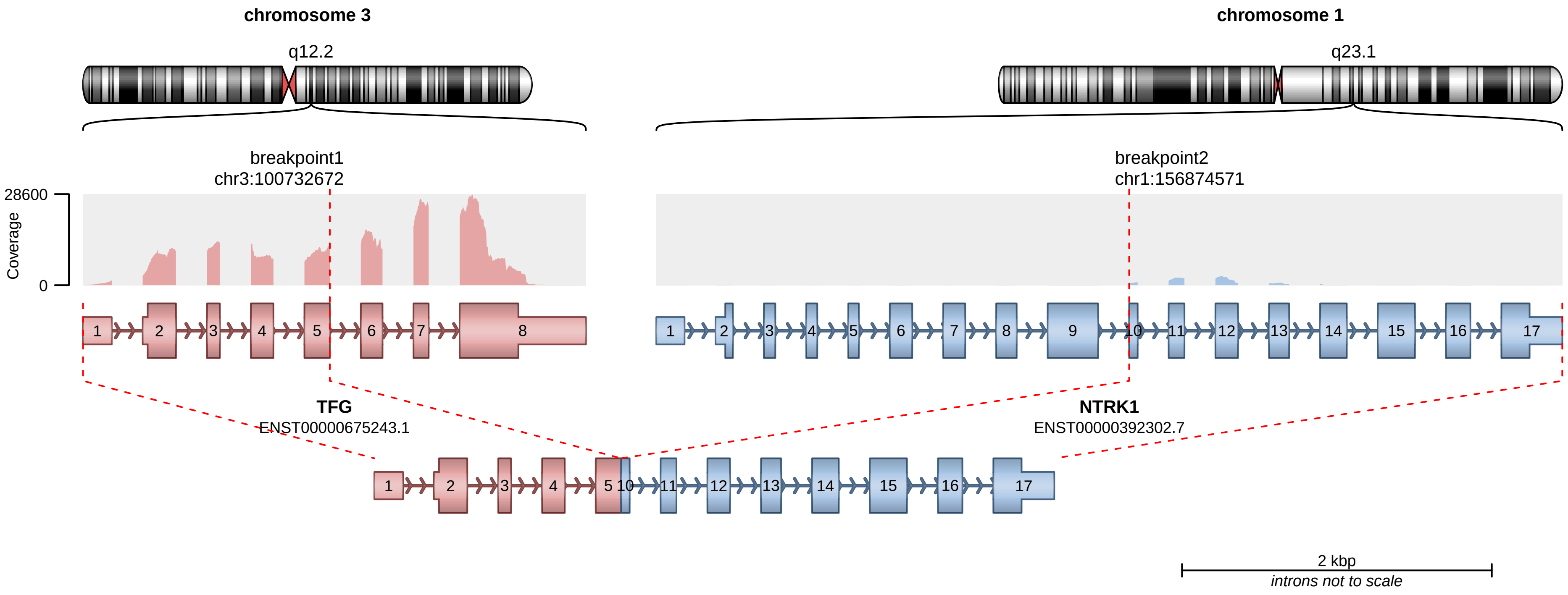


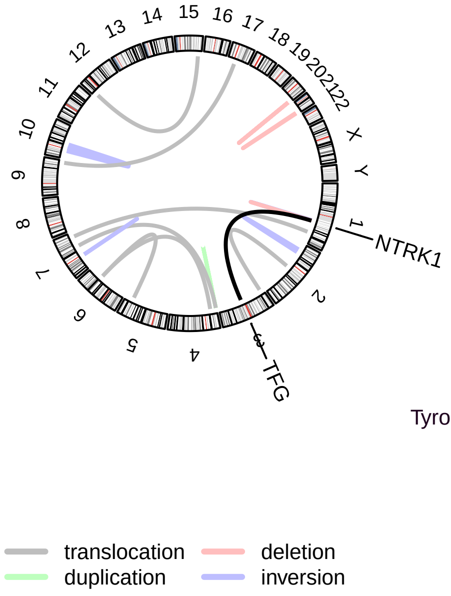


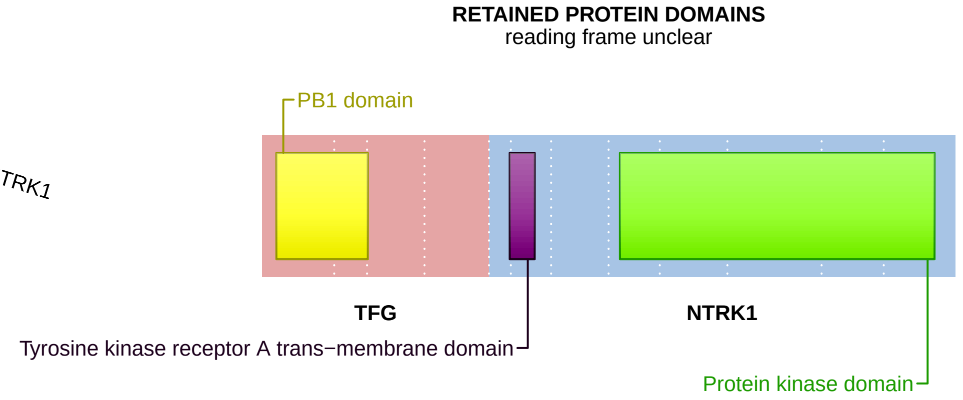


SUPPORTING READ COUNT

Split reads = 74
Discordant mates = 0

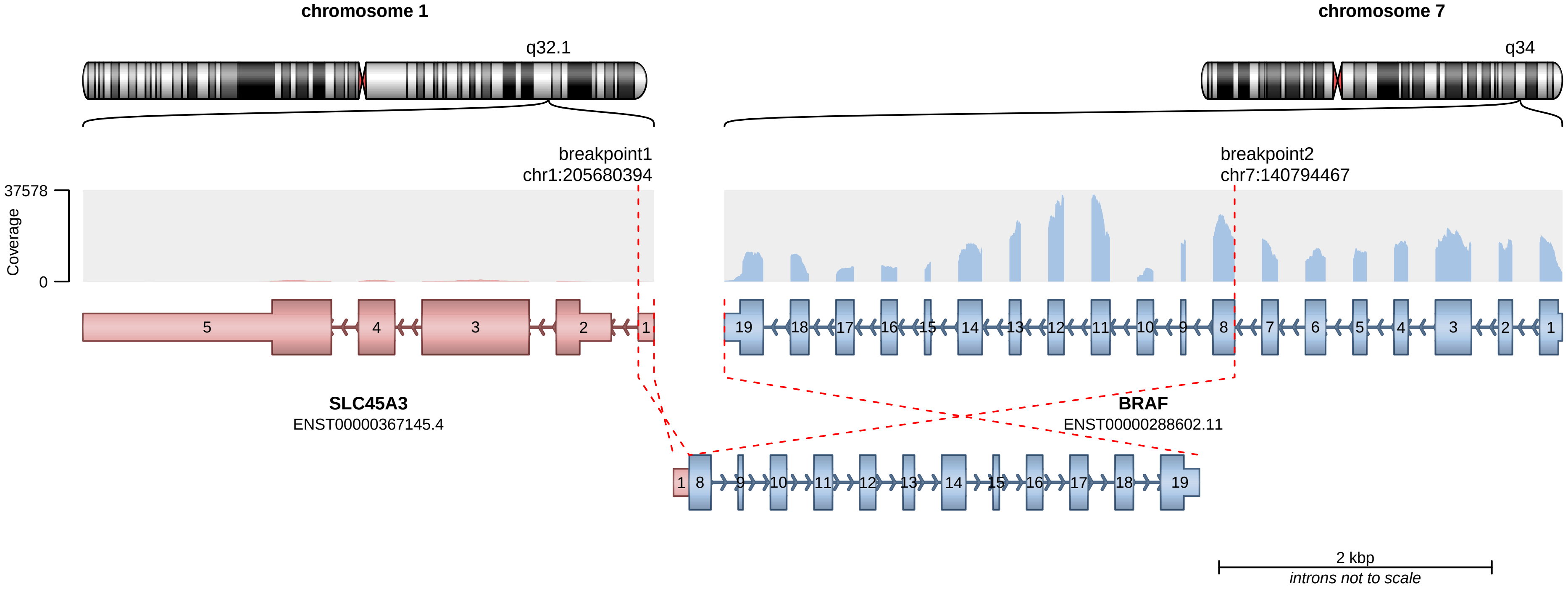


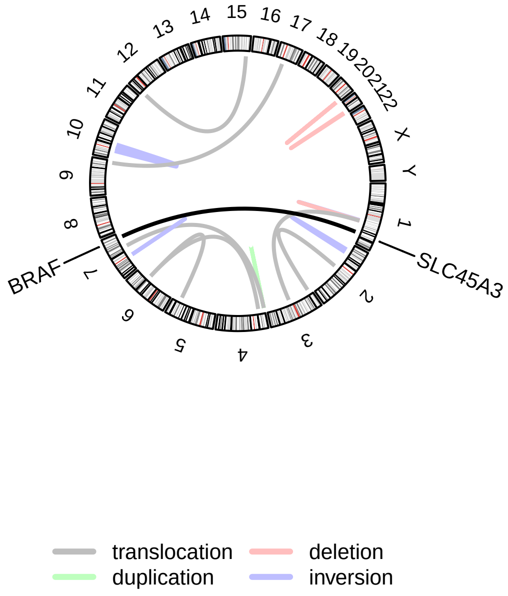




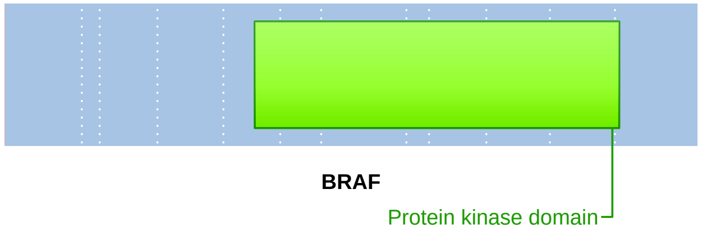
SUPPORTING READ COUNT

Split reads = 64
Discordant mates = 0



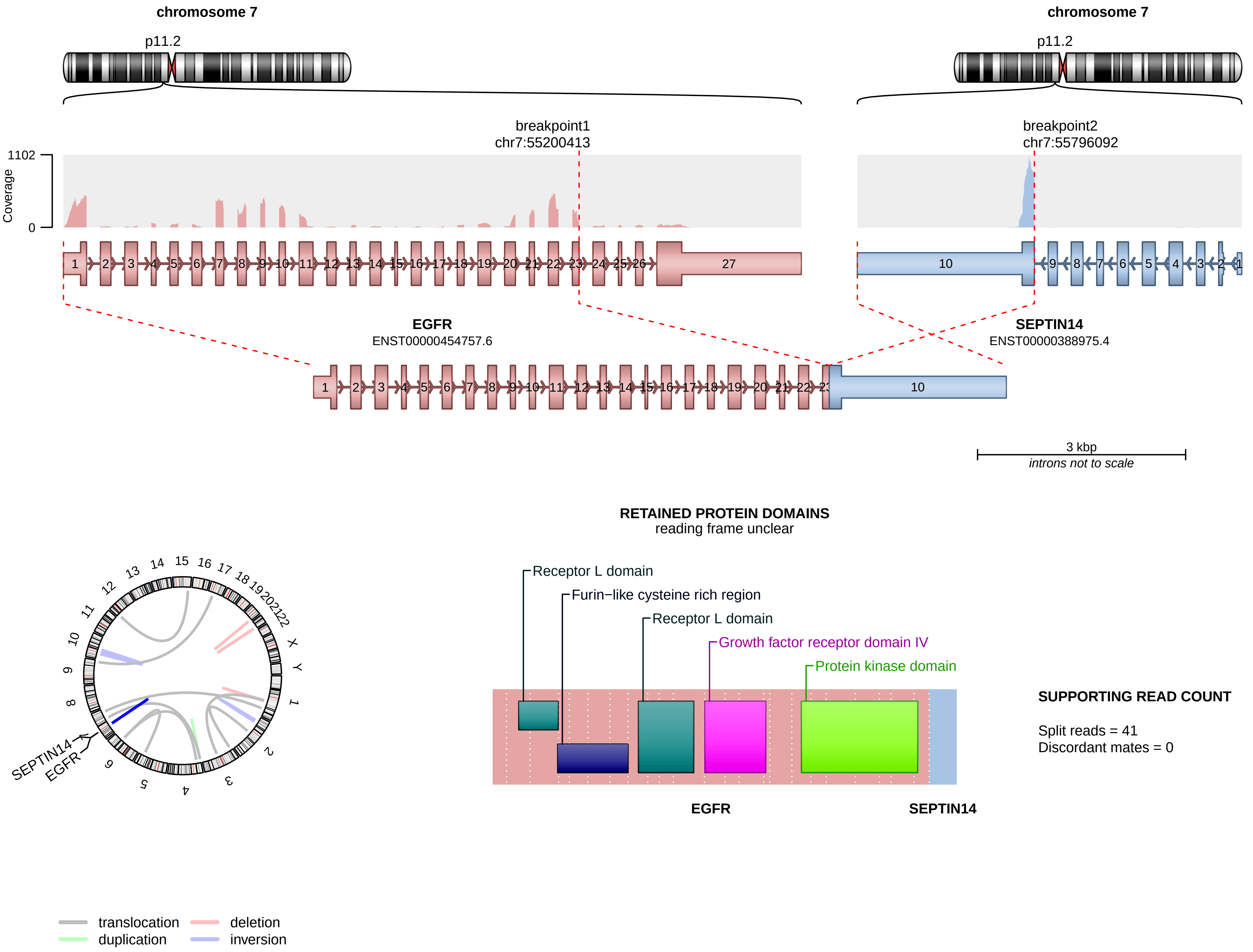


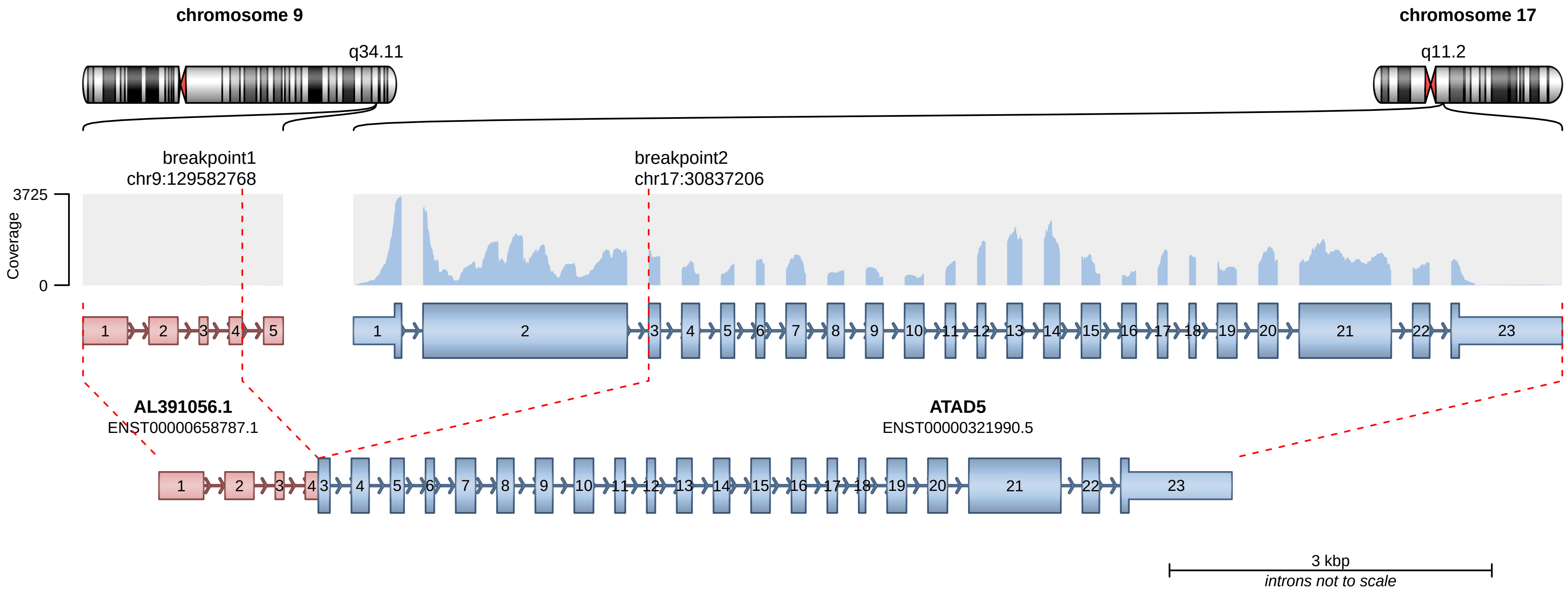
RETAINED PROTEIN DOMAINS
reading frame unclear

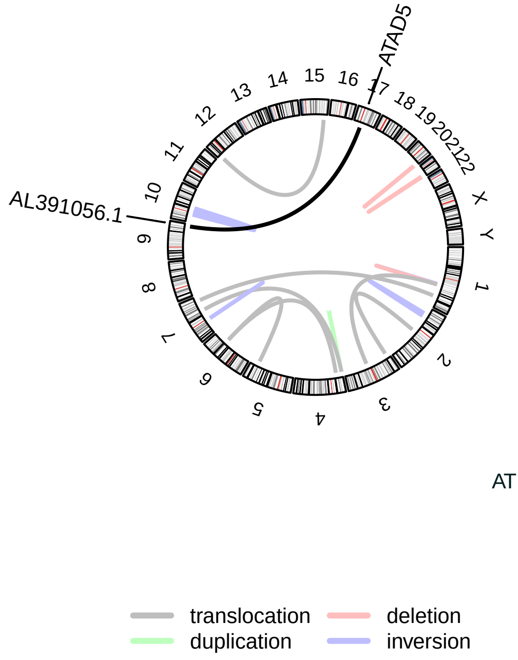


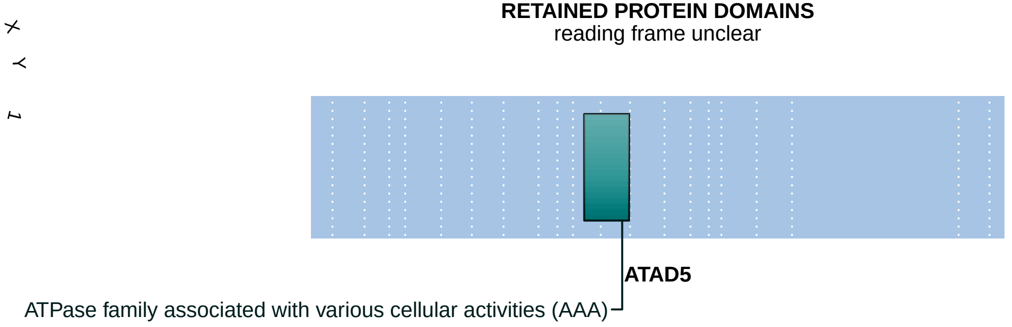
SUPPORTING READ COUNT

Split reads = 60
Discordant mates = 0


chromosome 7
p11.2
chromosome 7
p11.2
breakpoint1
chr7:55200413
breakpoint2
chr7:55796092
Coverage
1102
0
EGFR
ENST00000454757.6
SEPTIN14
ENST00000388975.4
3 kbp
introns not to scale
RETAINED PROTEIN DOMAINS
reading frame unclear
Receptor L domain
Furin−like cysteine rich region
Receptor L domain
Growth factor receptor domain IV
Protein kinase domain
EGFR
SEPTIN14
SUPPORTING READ COUNT
Split reads = 41
Discordant mates = 0
SEPTIN14
EGFR
translocation
duplication
deletion
inversion







SUPPORTING READ COUNT

Split reads = 27
Discordant mates = 0