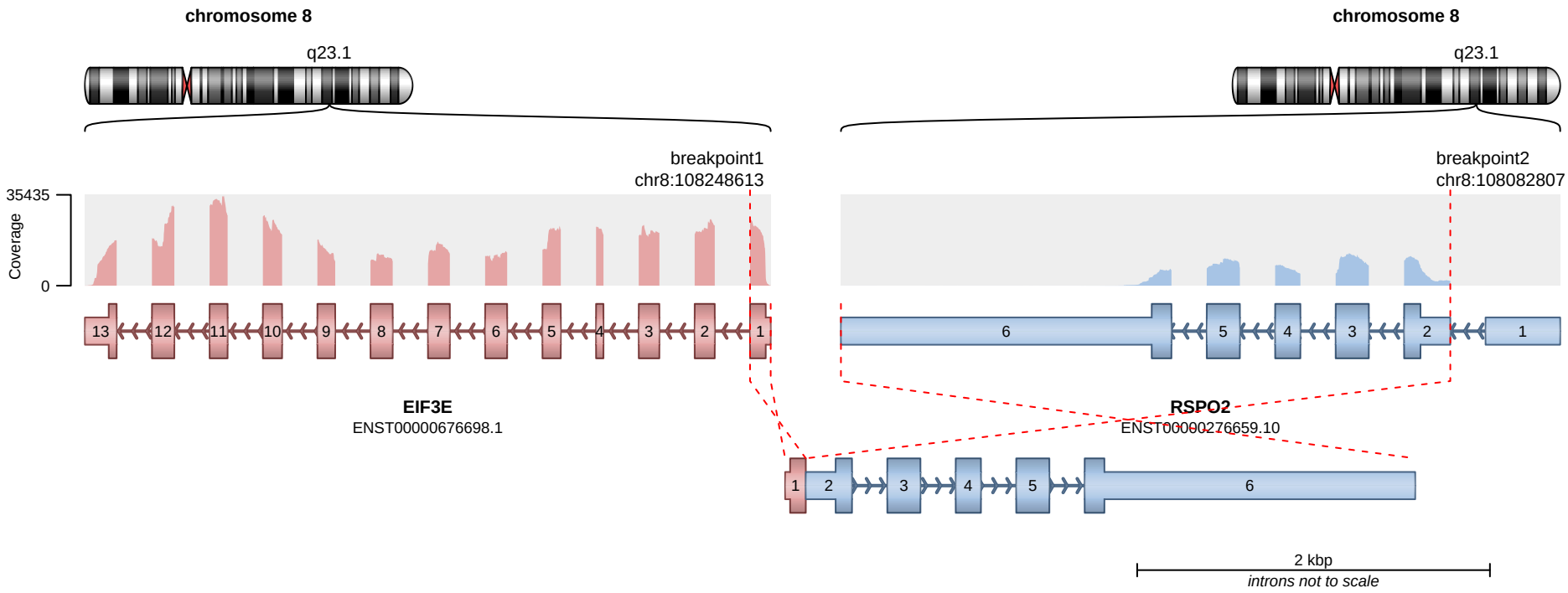
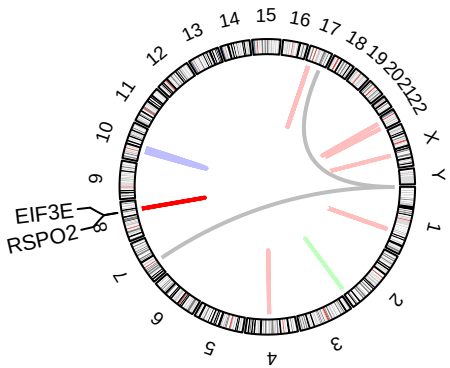
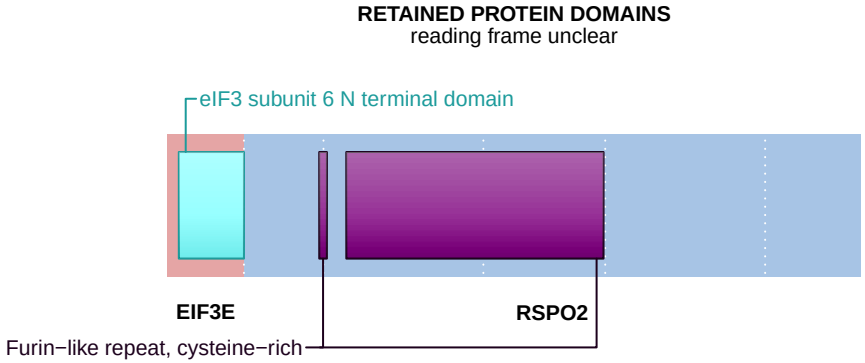


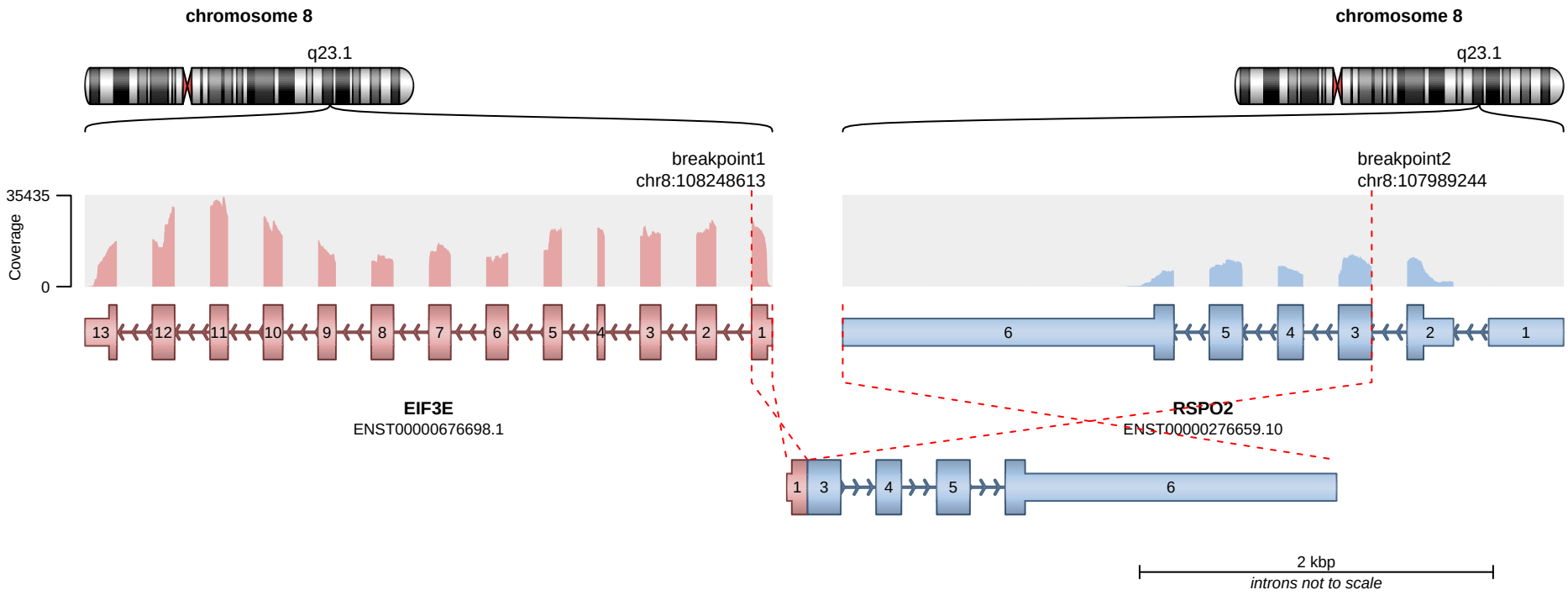


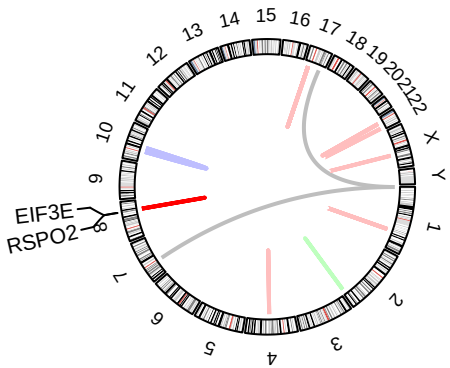


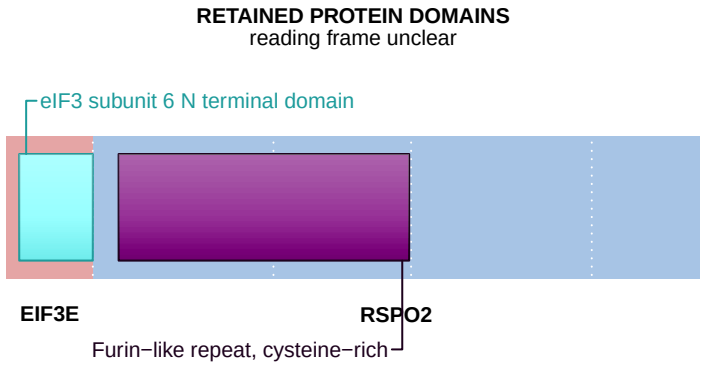
SUPPORTING READ COUNT

Split reads = 1089
Discordant mates = 0

translocation
deletion
duplication
inversion



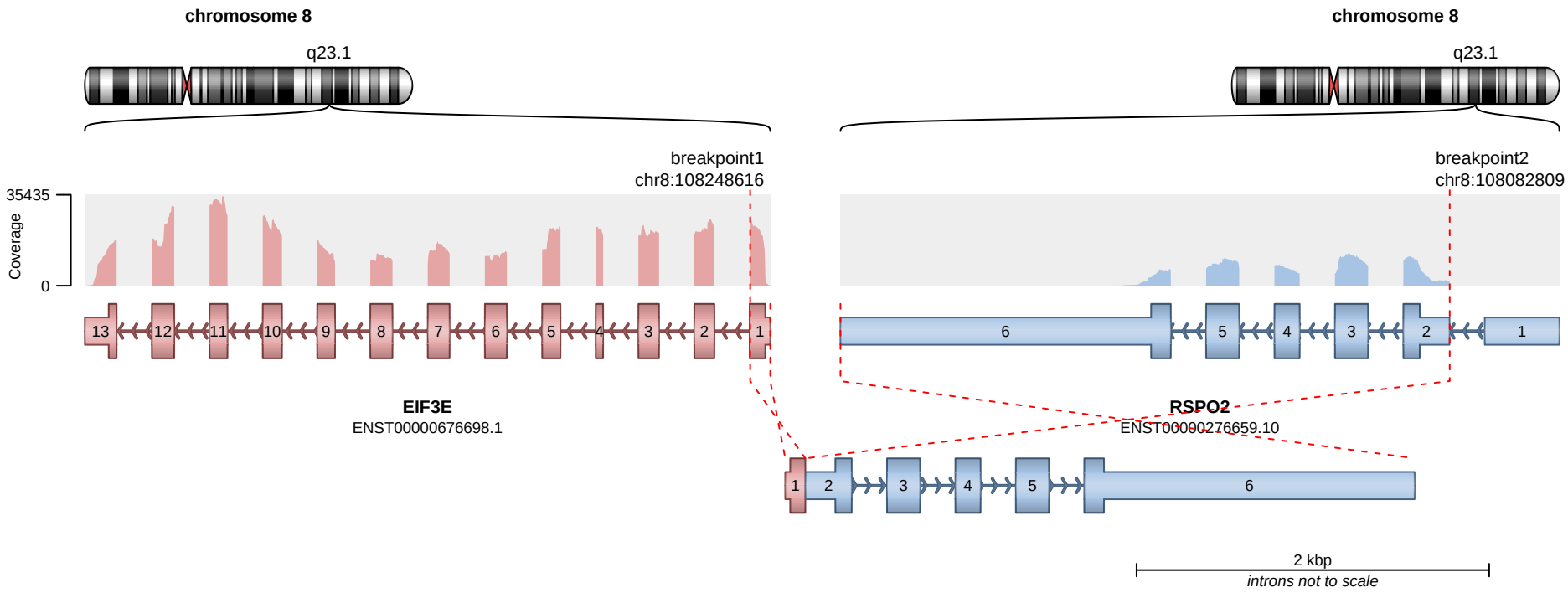


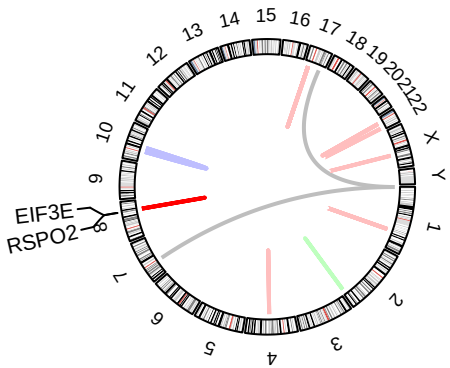


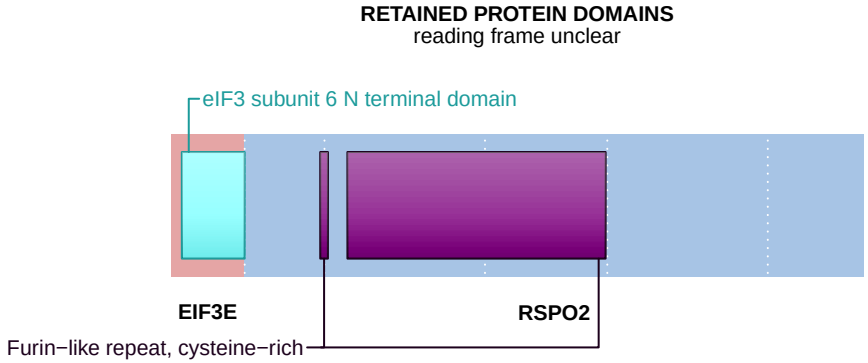
SUPPORTING READ COUNT

Split reads = 22
Discordant mates = 0

translocation
deletion
duplication
inversion

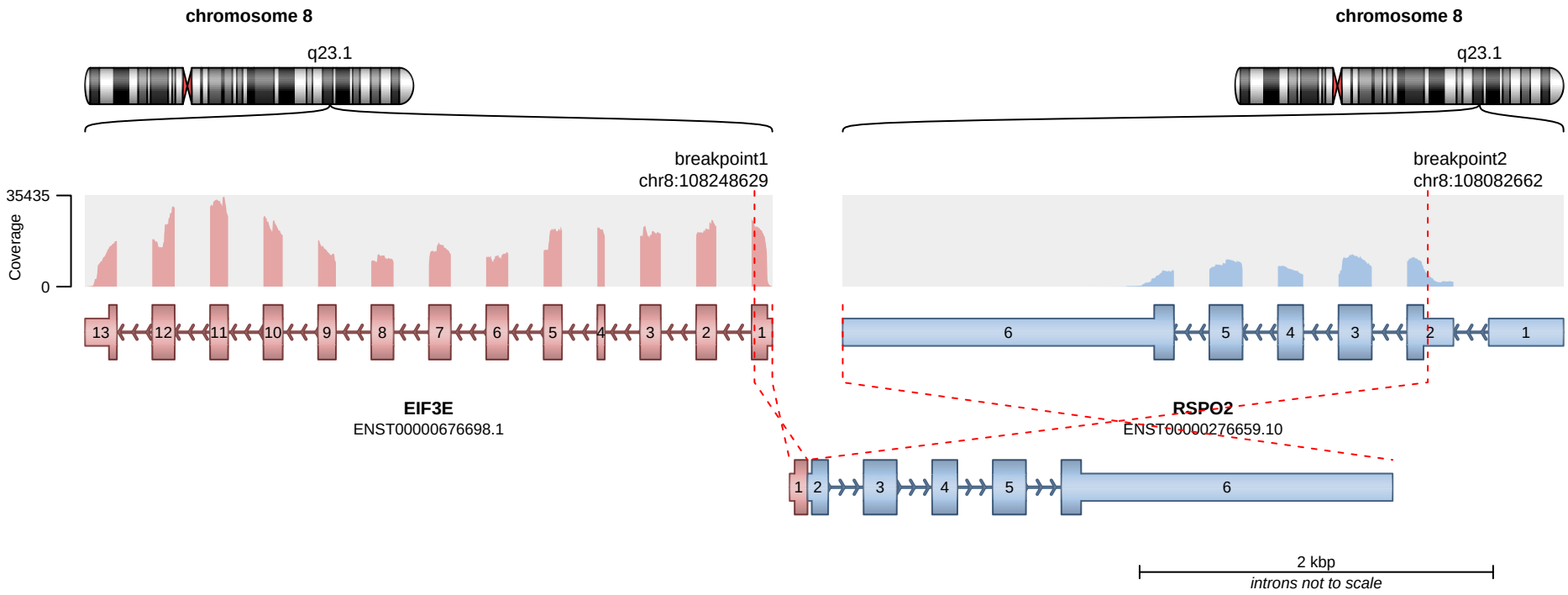


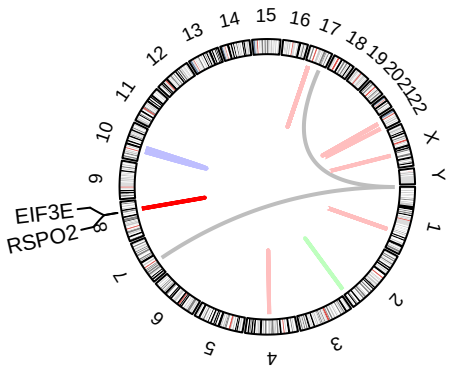


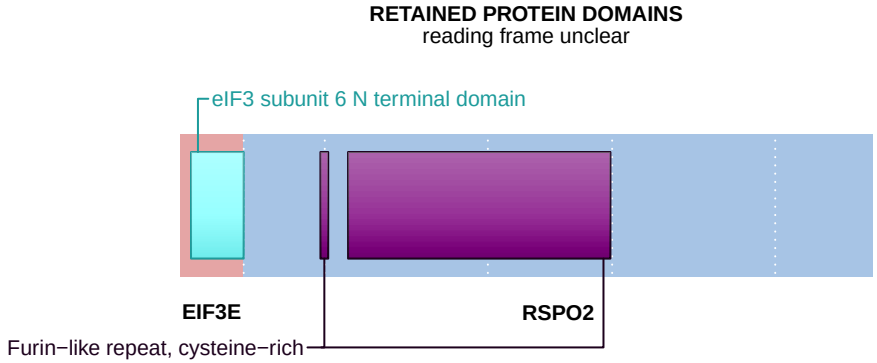


SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

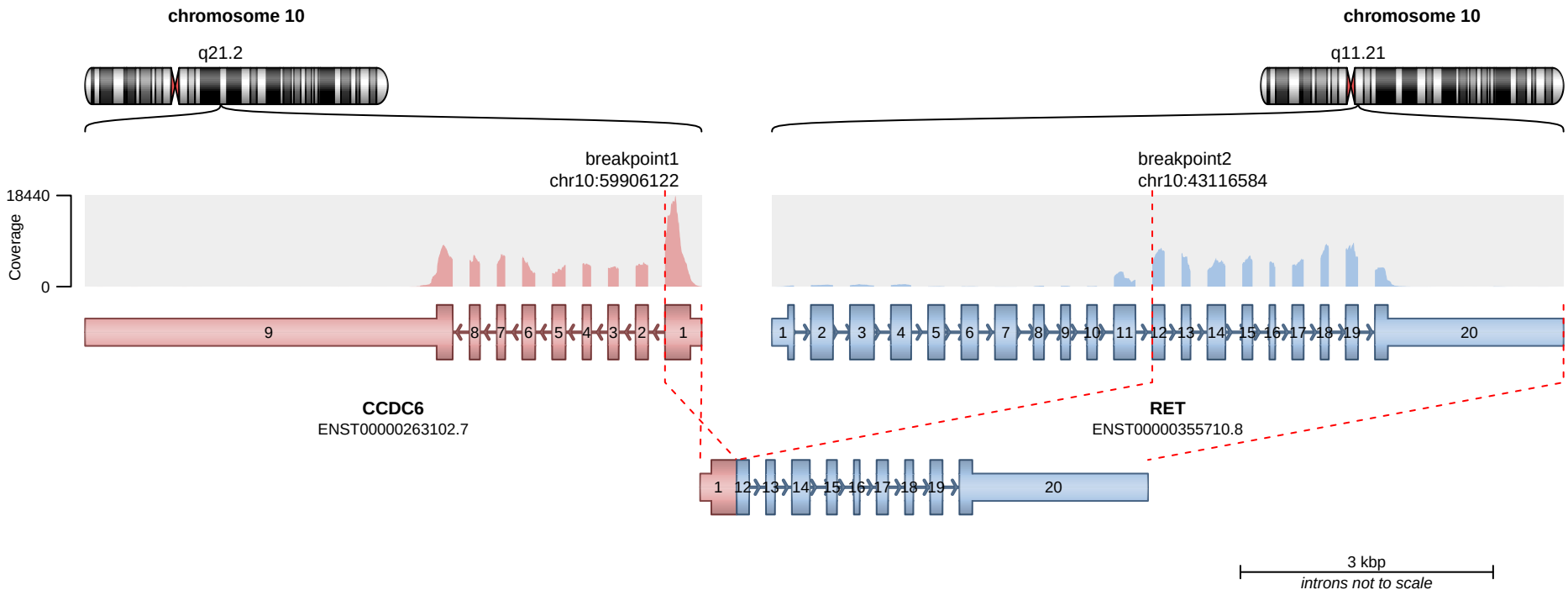


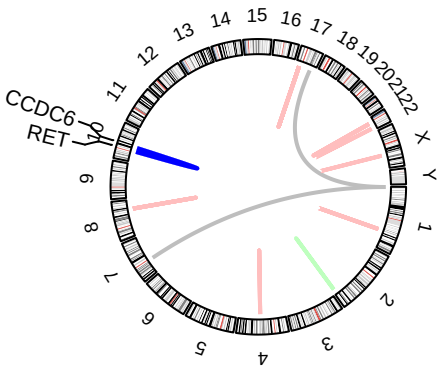


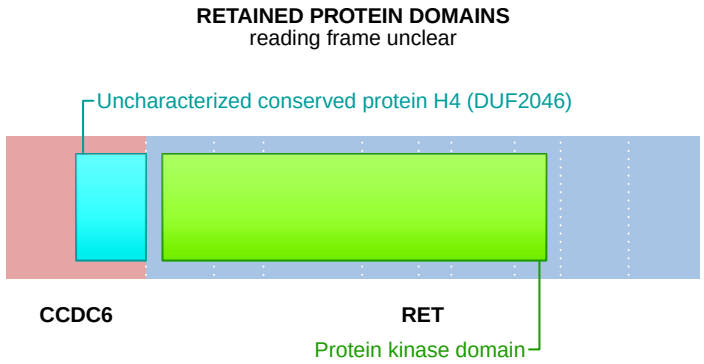


SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0



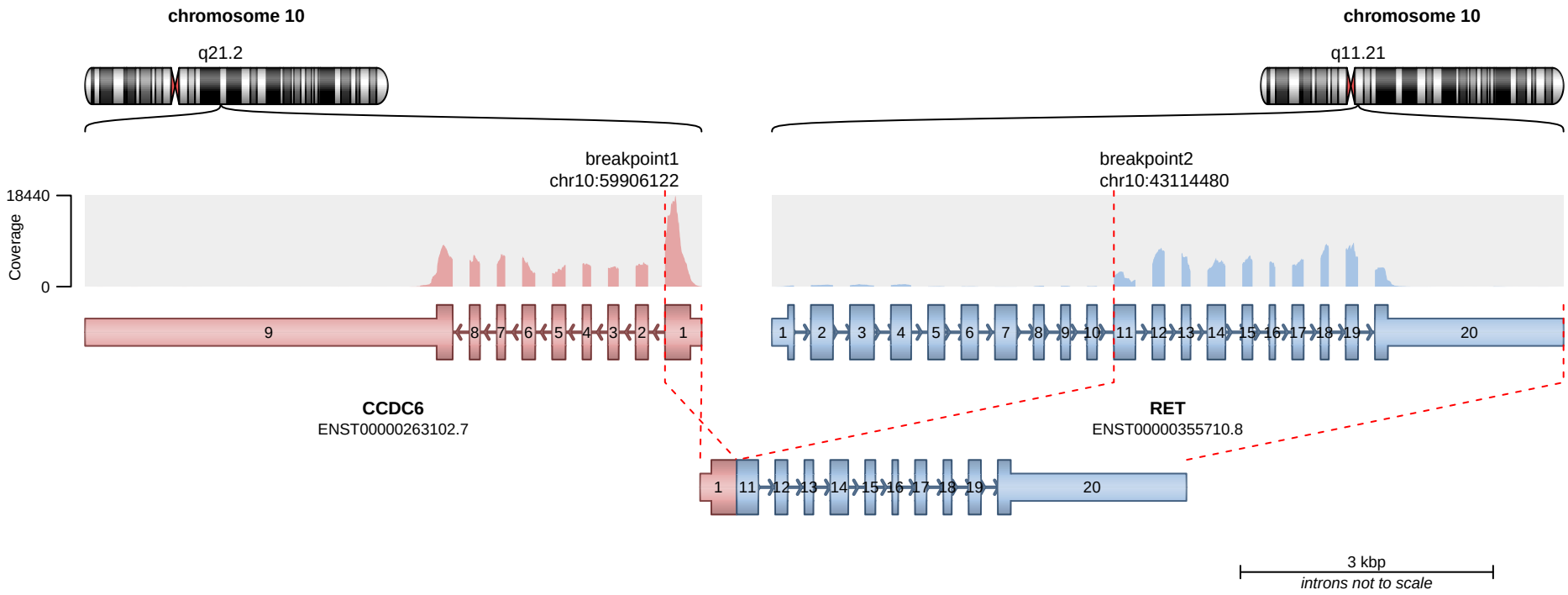


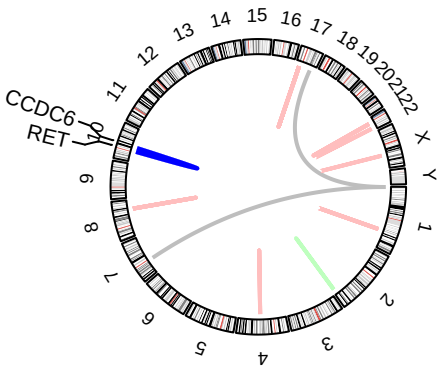


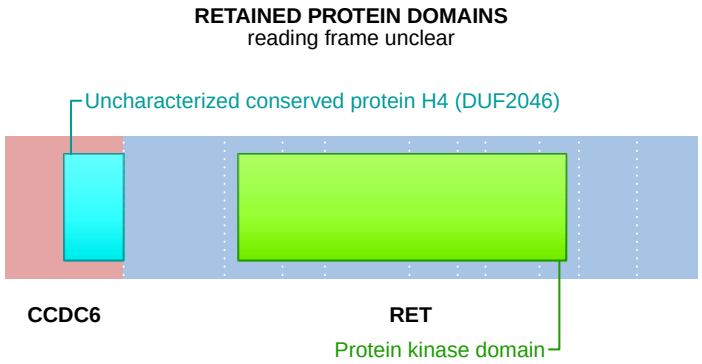
SUPPORTING READ COUNT

Split reads = 989
Discordant mates = 17

translocation
deletion
duplication
inversion



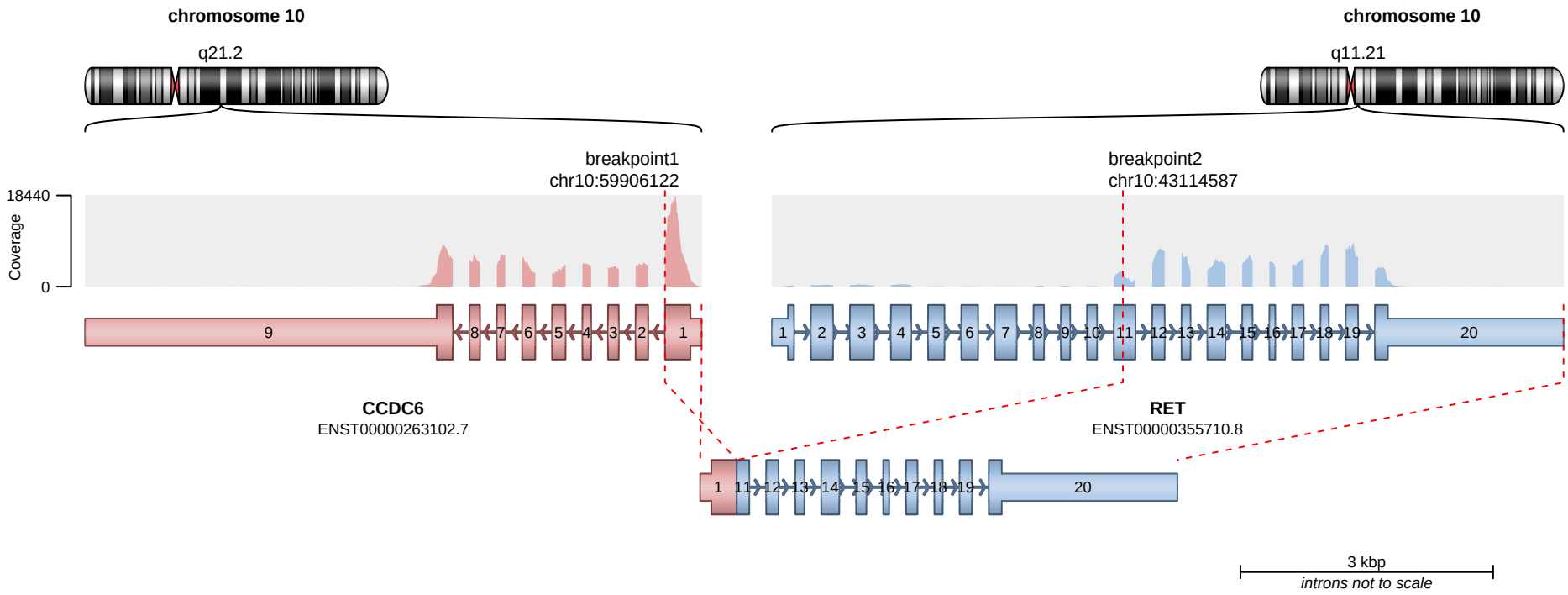


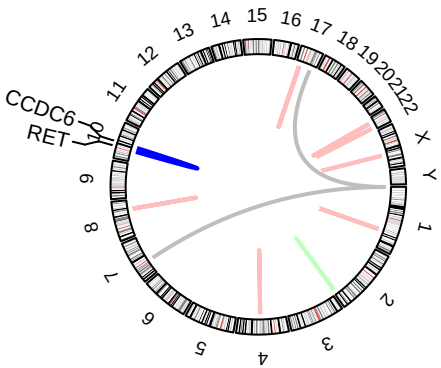


SUPPORTING READ COUNT

Split reads = 355
Discordant mates = 20

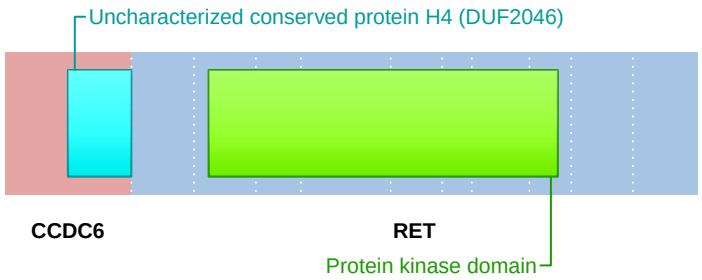
translocation
deletion
duplication
inversion





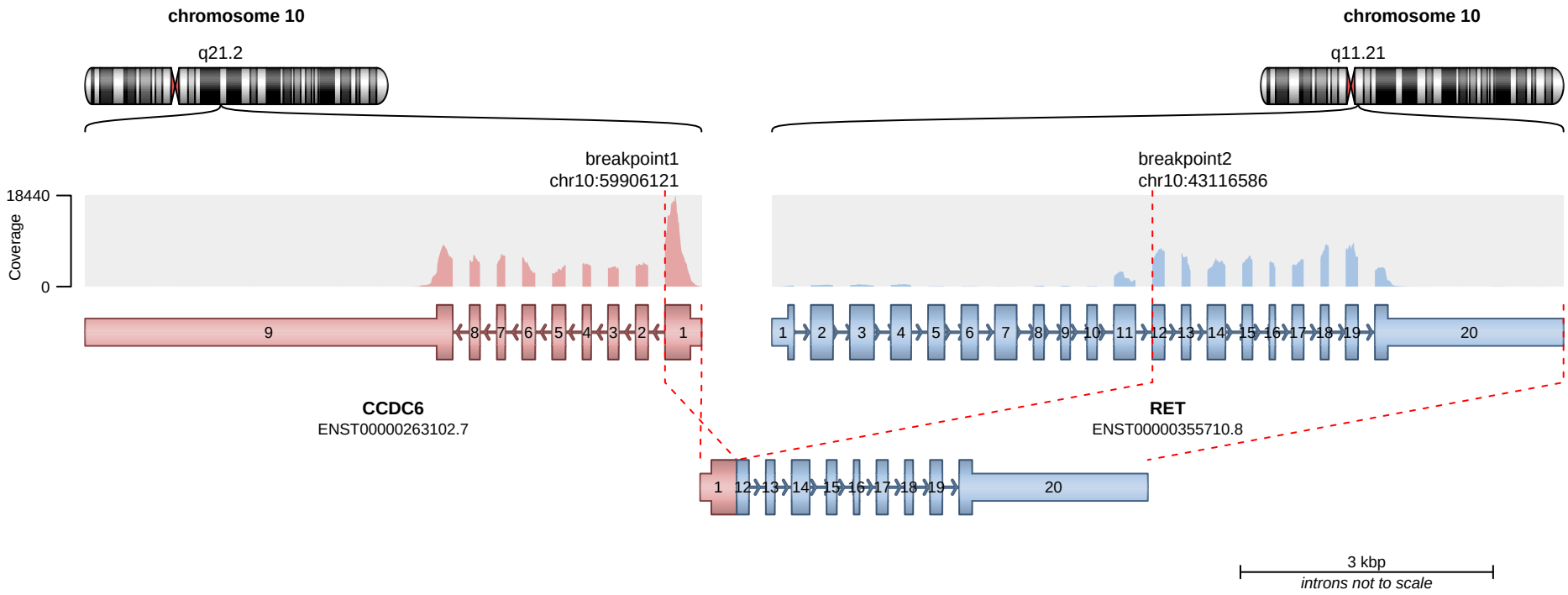
translocation
deletion
duplication
inversion

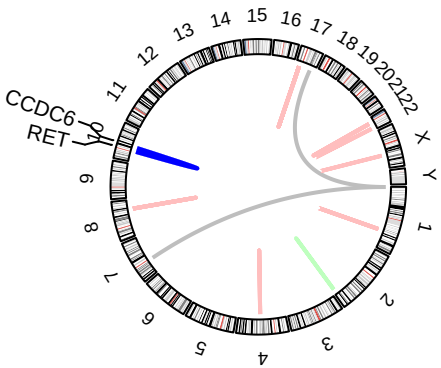
RETAINED PROTEIN DOMAINS
reading frame unclear

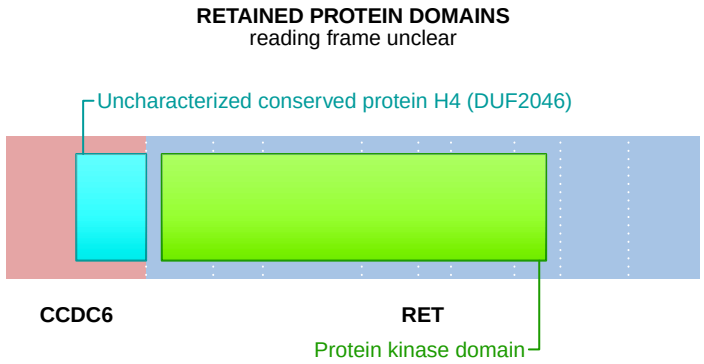


SUPPORTING READ COUNT

Split reads = 29
Discordant mates = 18



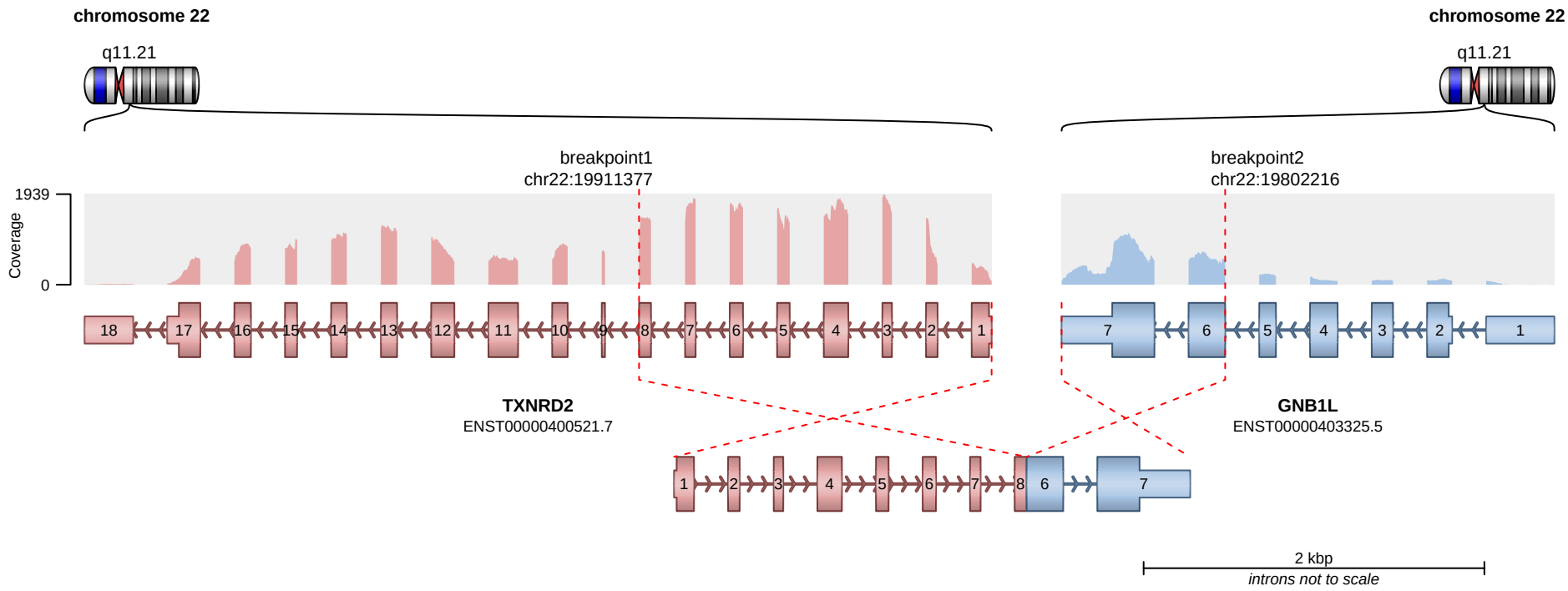


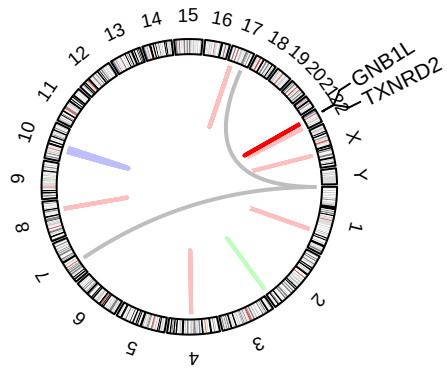


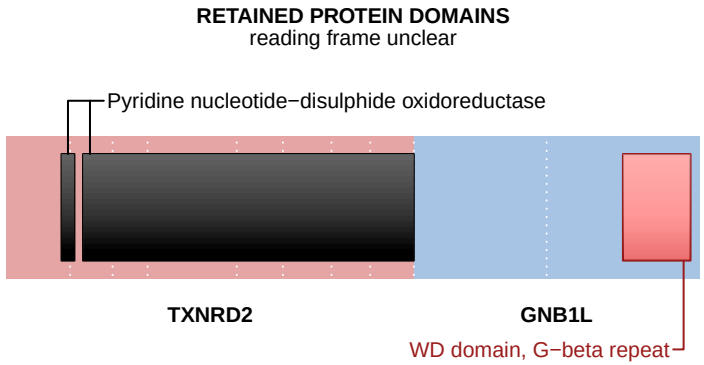
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 17

translocation
deletion
duplication
inversion



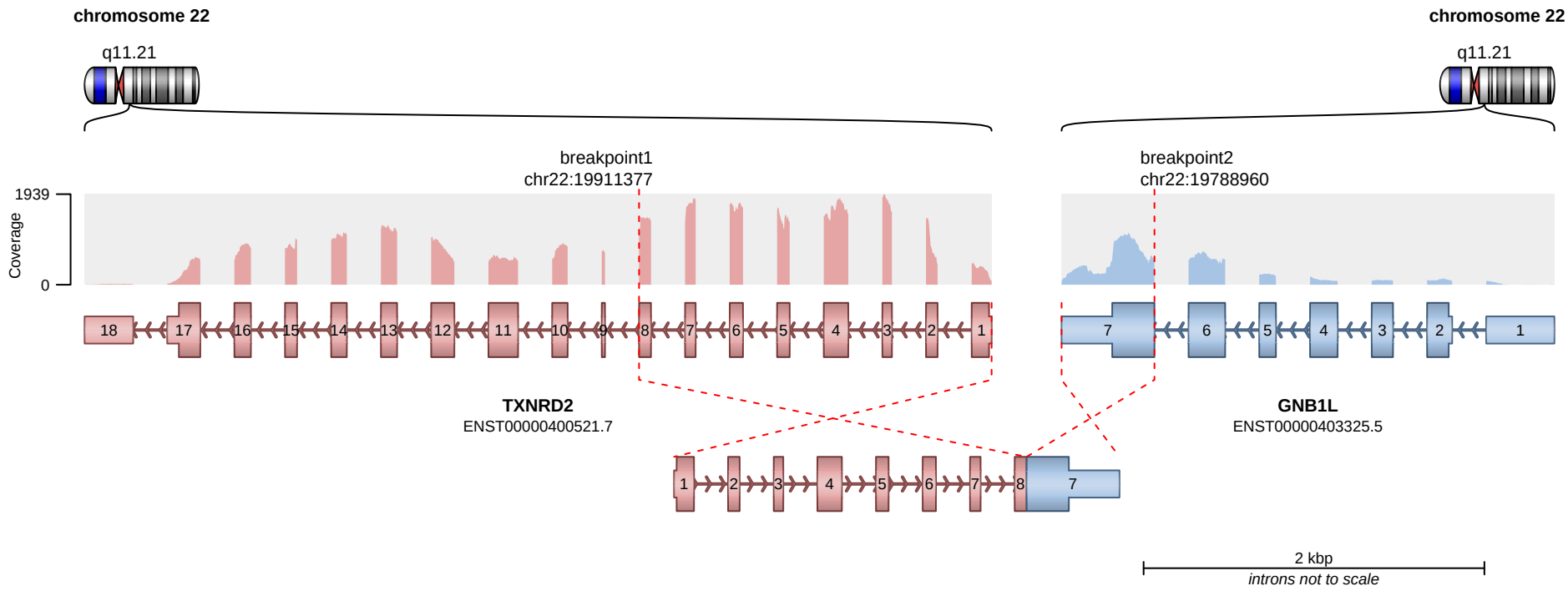


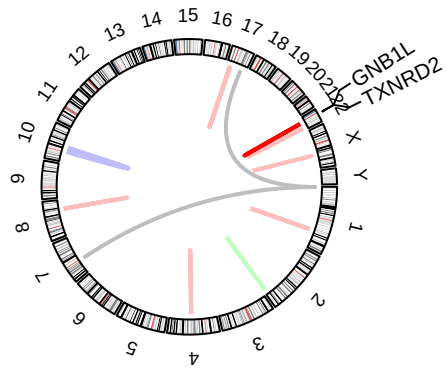


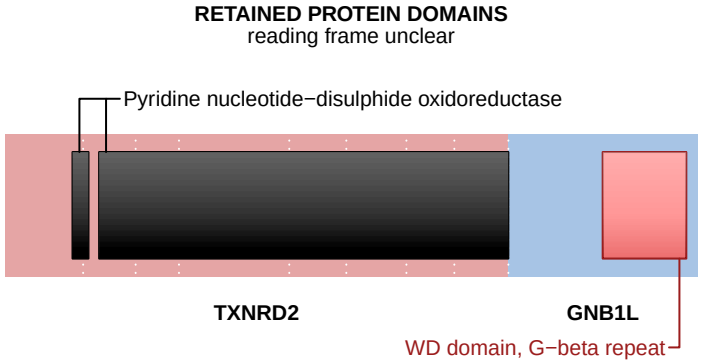
SUPPORTING READ COUNT

Split reads = 143
Discordant mates = 4

translocation
deletion
duplication
inversion



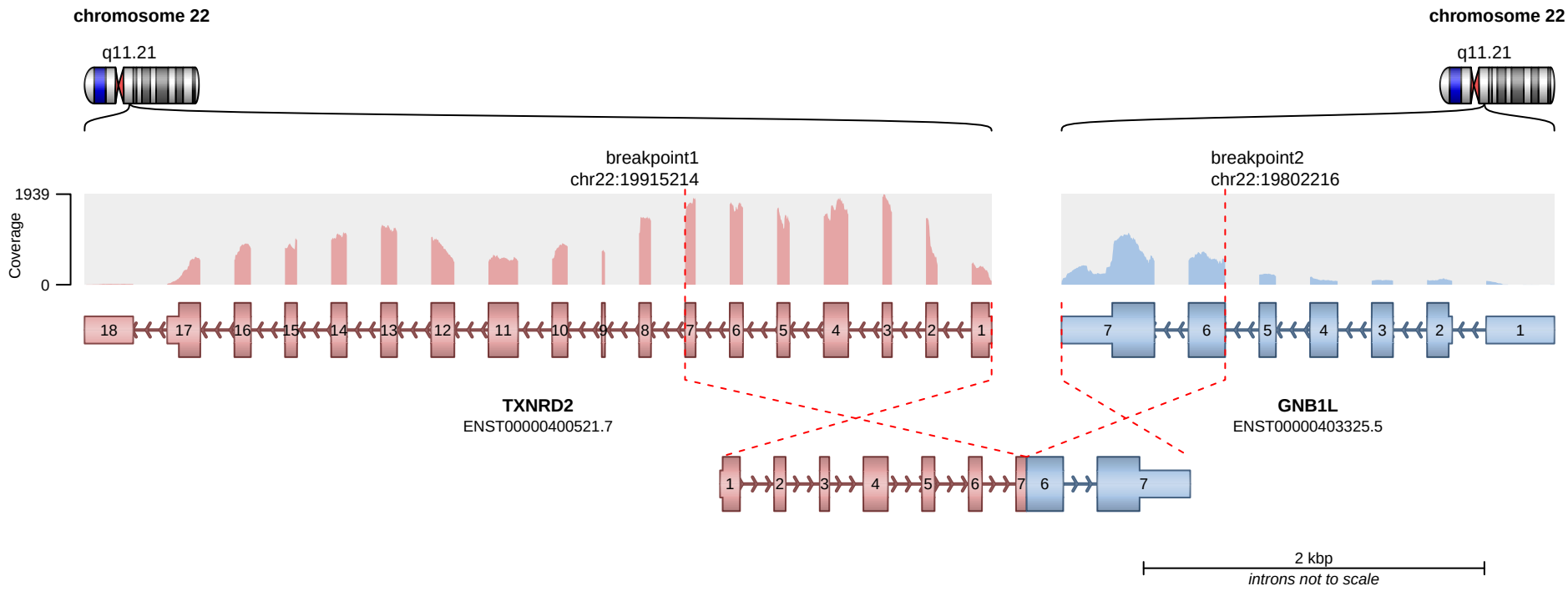


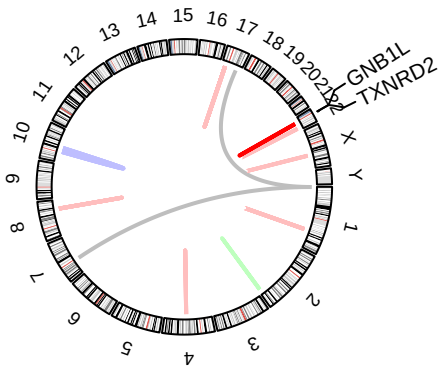


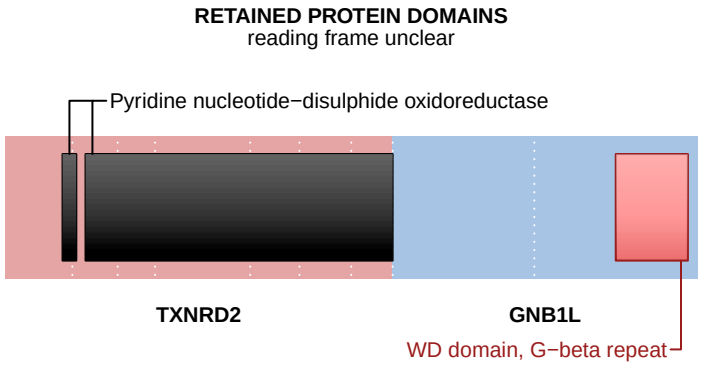
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

translocation
deletion
duplication
inversion



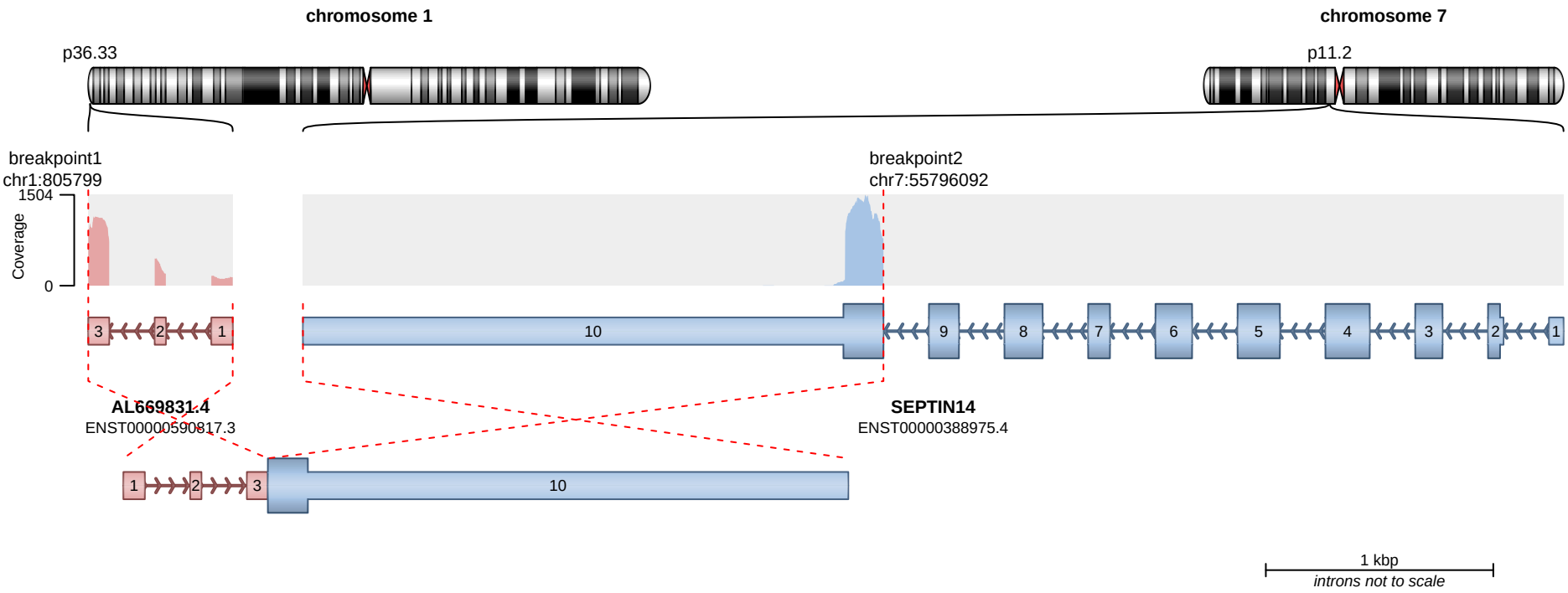


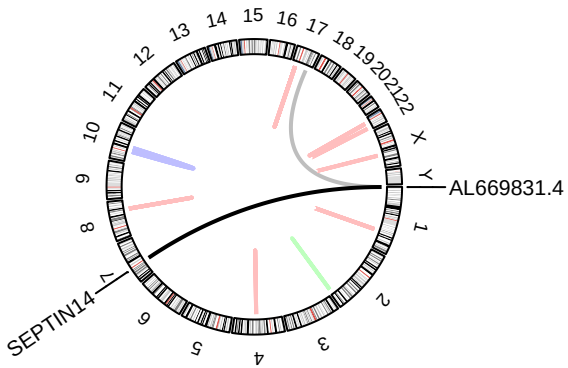


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 3

translocation
deletion
duplication
inversion



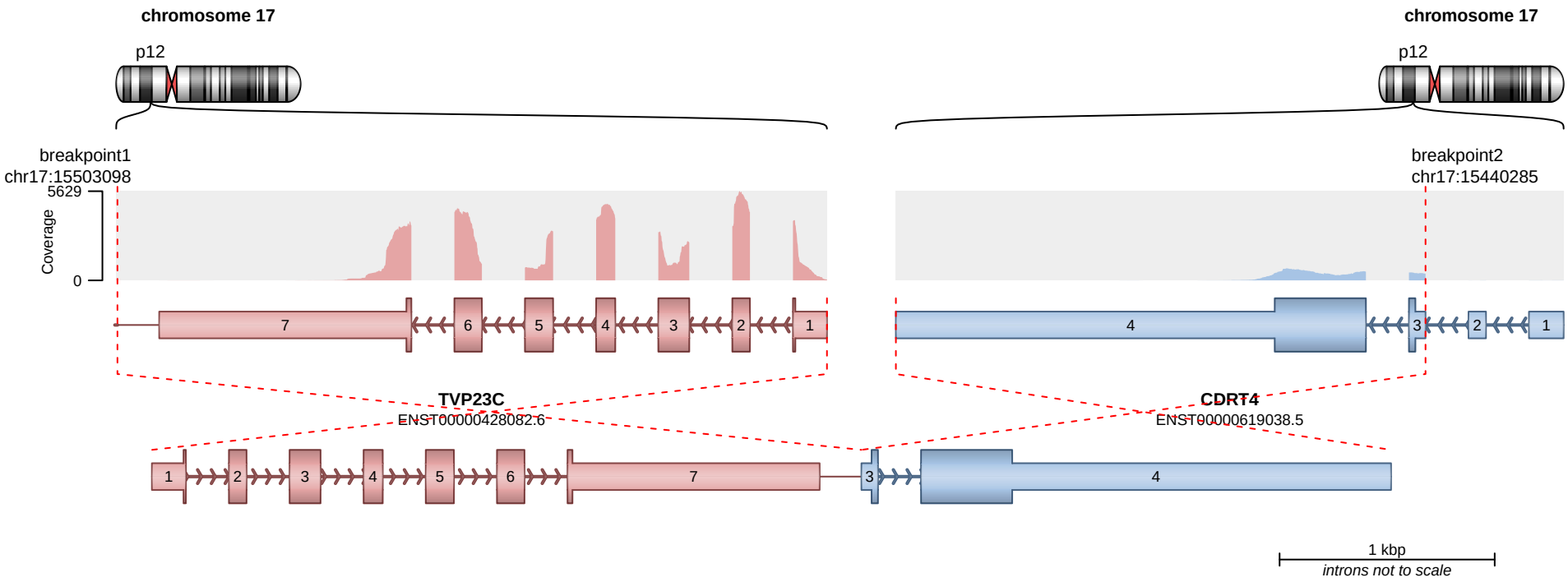


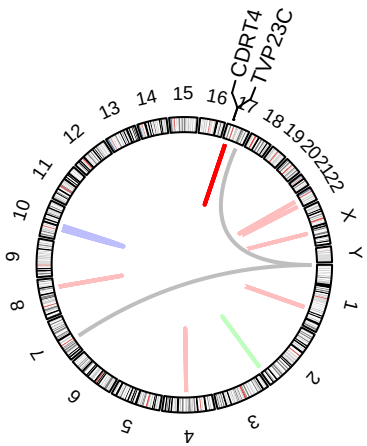
No protein domains retained in fusion.

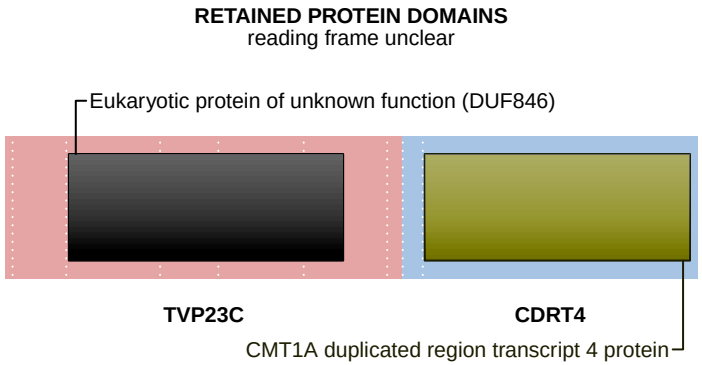
SUPPORTING READ COUNT

Split reads = 97
Discordant mates = 0

translocation
deletion
duplication
inversion



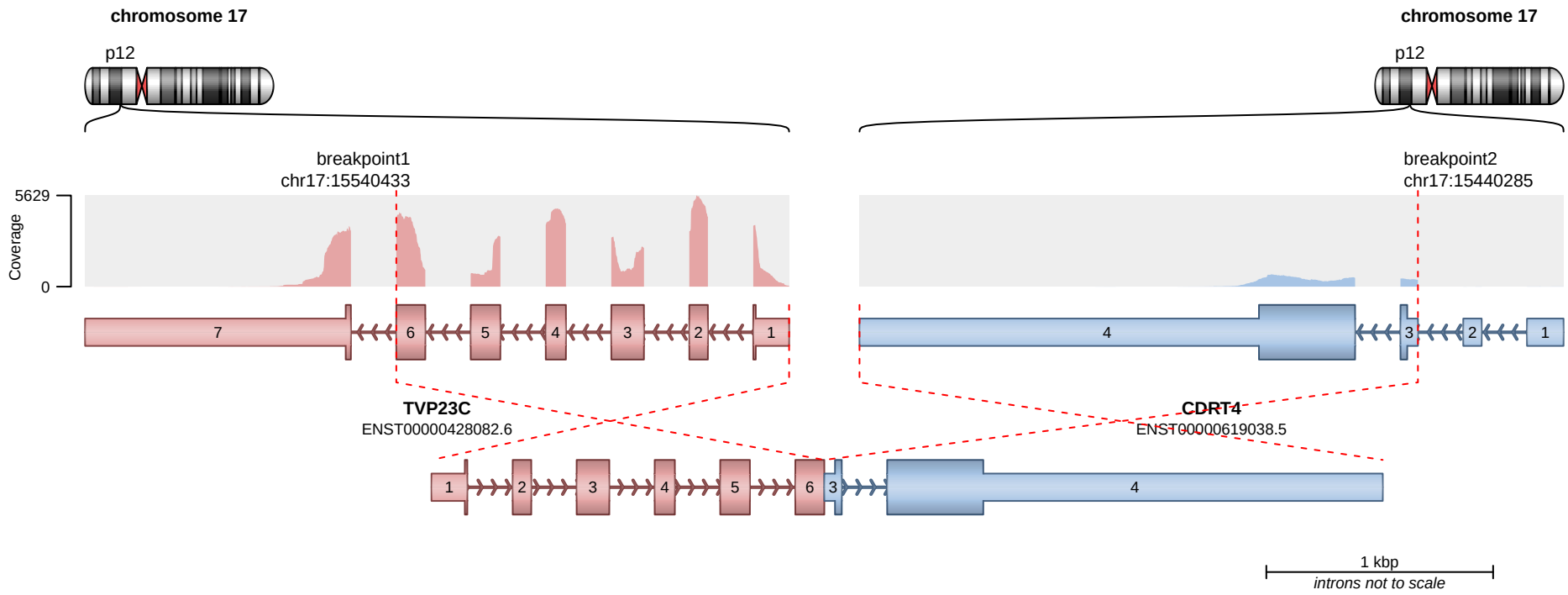


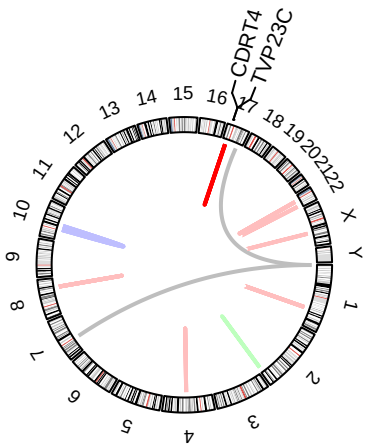


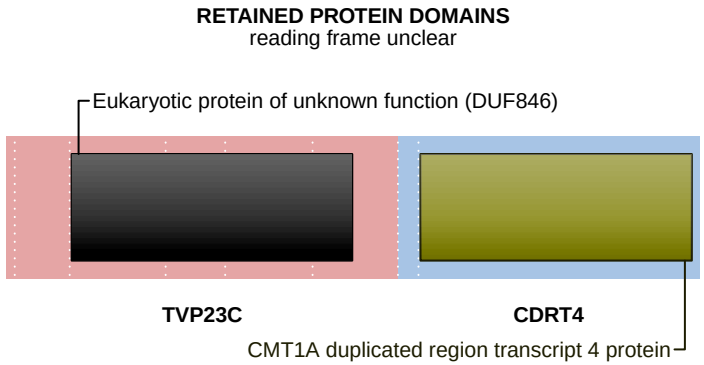
SUPPORTING READ COUNT

Split reads = 81
Discordant mates = 3

translocation
deletion
duplication
inversion



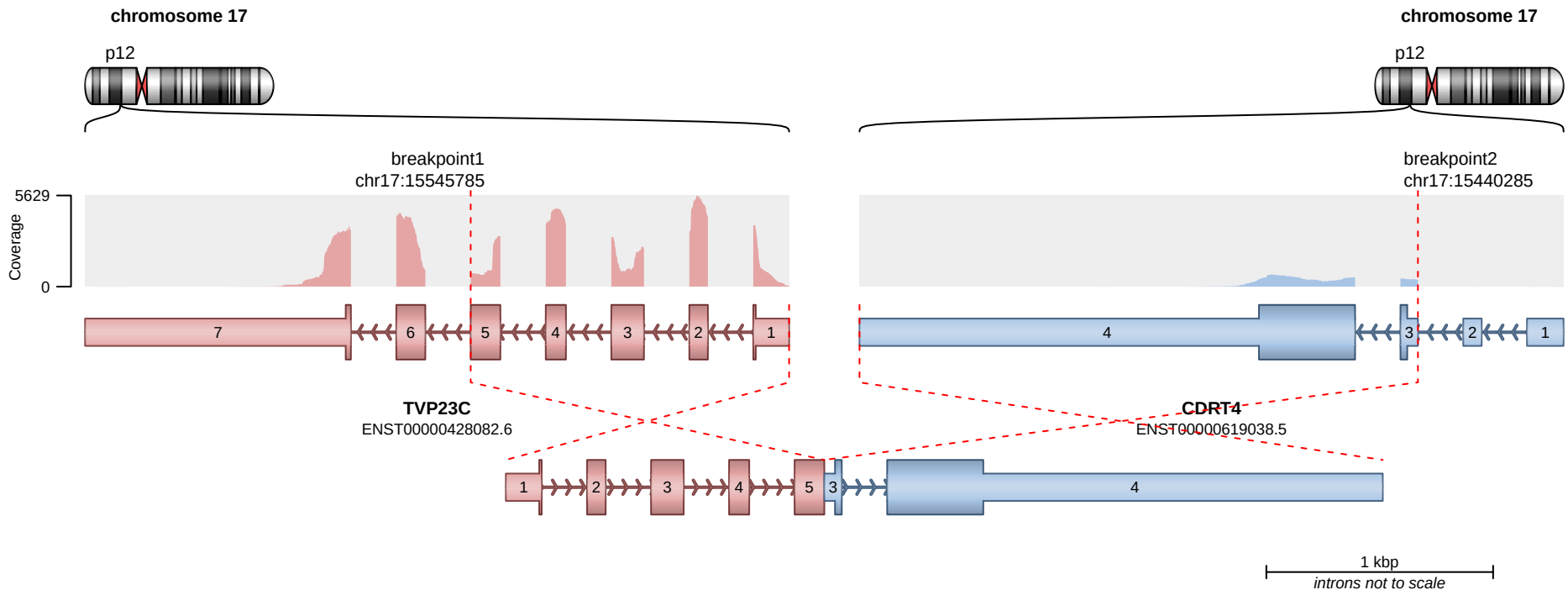


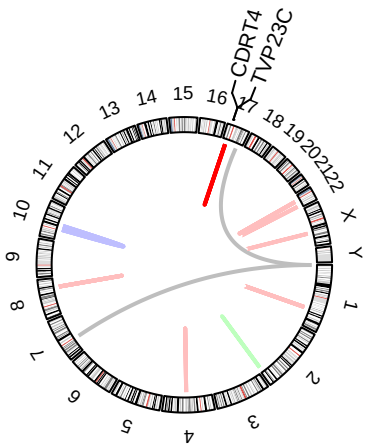


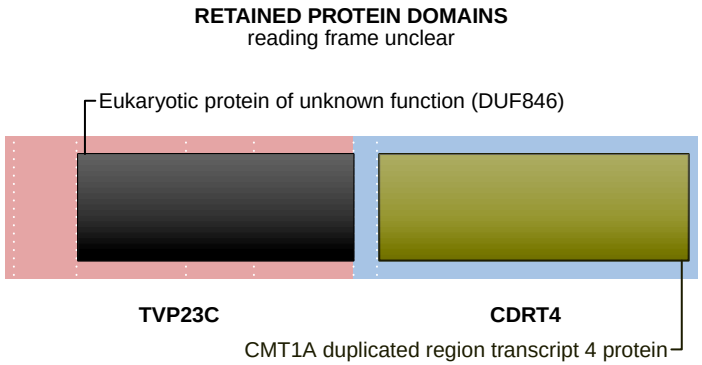
SUPPORTING READ COUNT

Split reads = 46
Discordant mates = 0

translocation
deletion
duplication
inversion



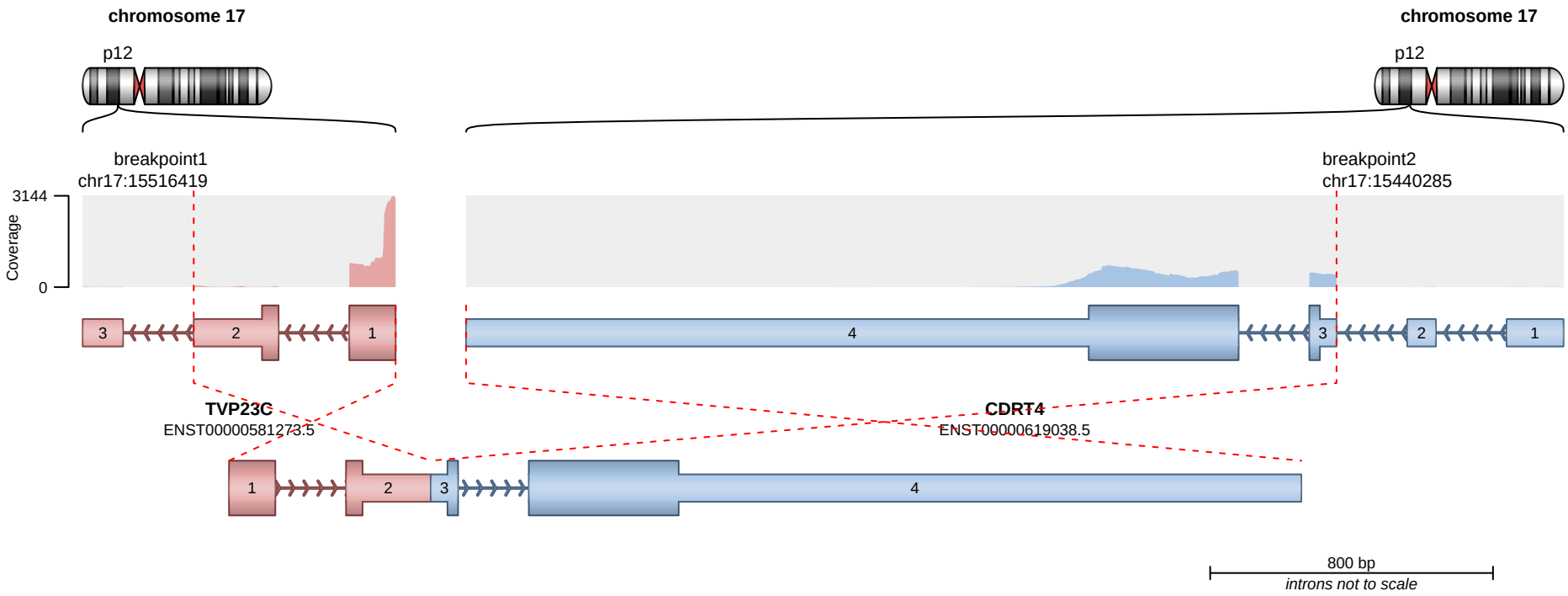


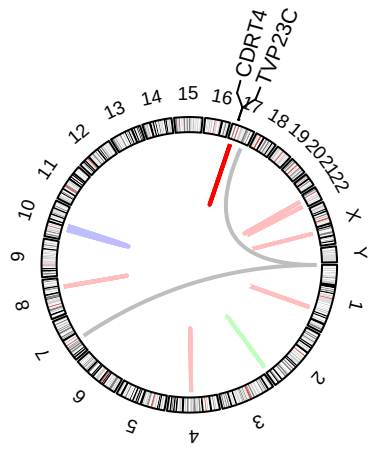


SUPPORTING READ COUNT

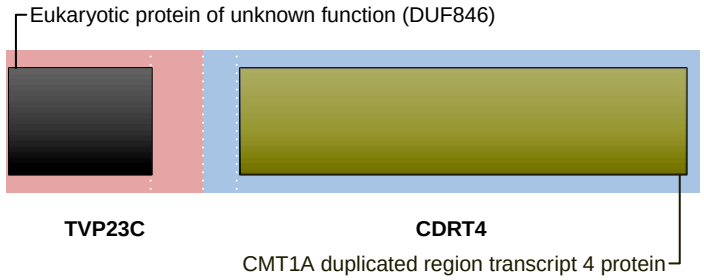
Split reads = 32
Discordant mates = 0

translocation
deletion
duplication
inversion





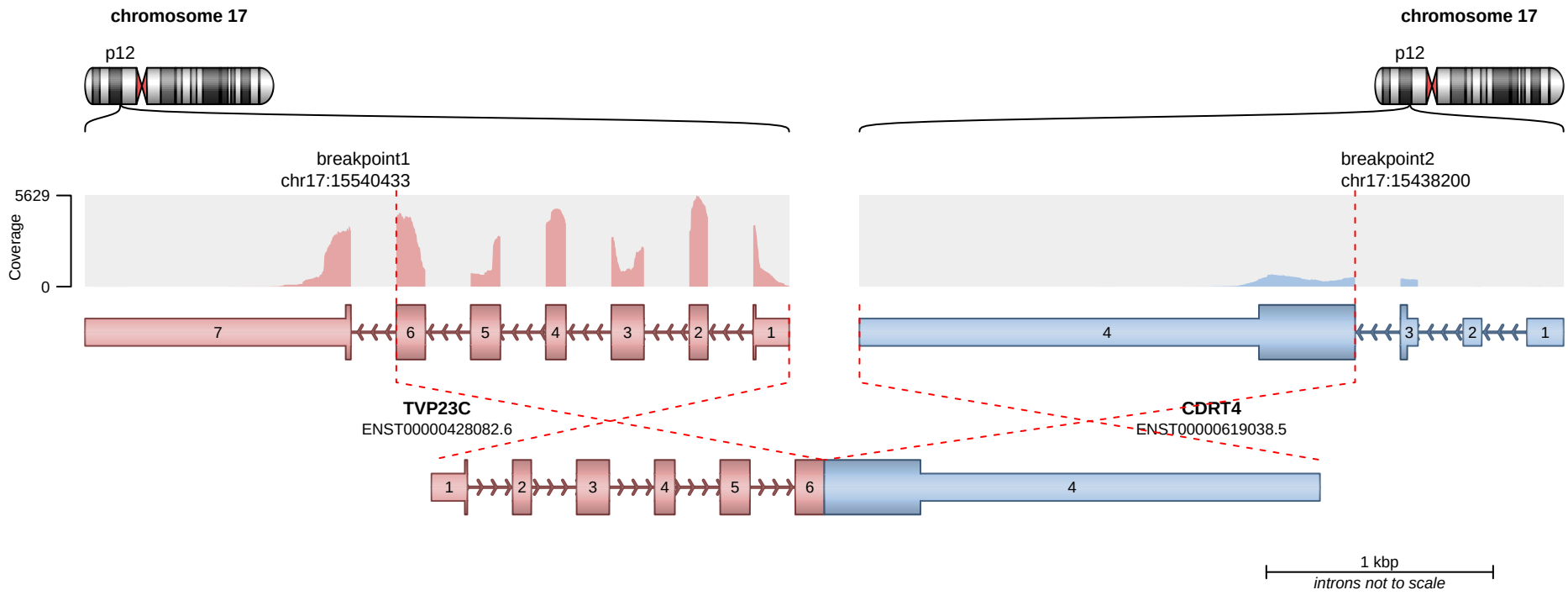
RETAINED PROTEIN DOMAINS
reading frame unclear

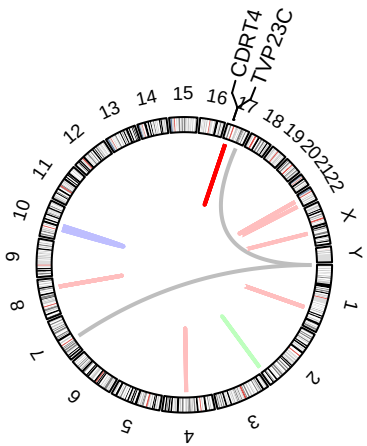


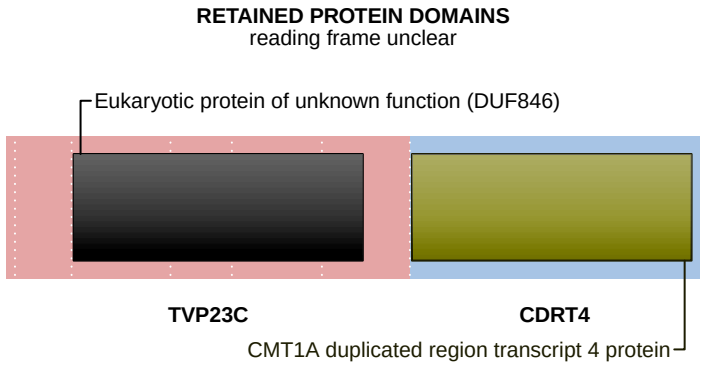
SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 0

translocation
deletion
duplication
inversion



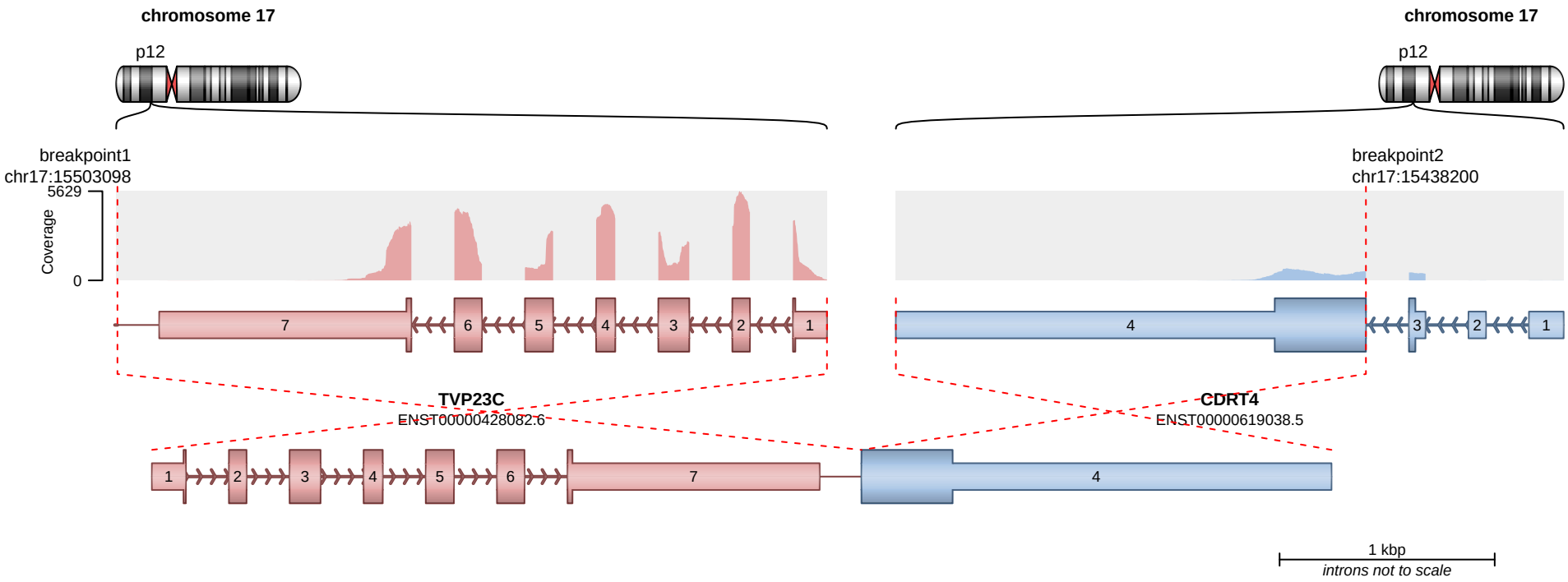


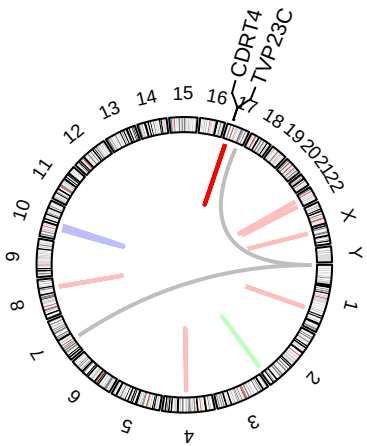


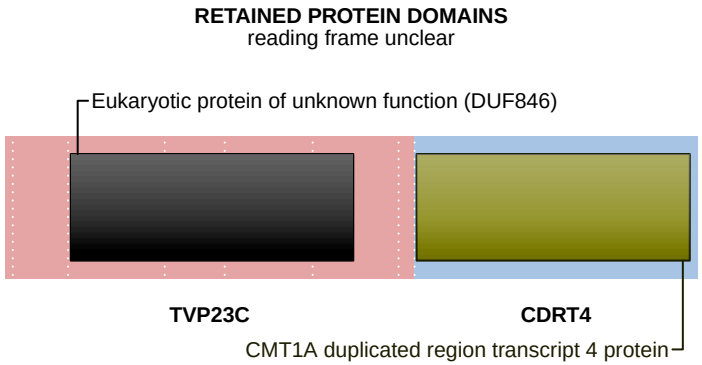
SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 0

translocation
deletion
duplication
inversion



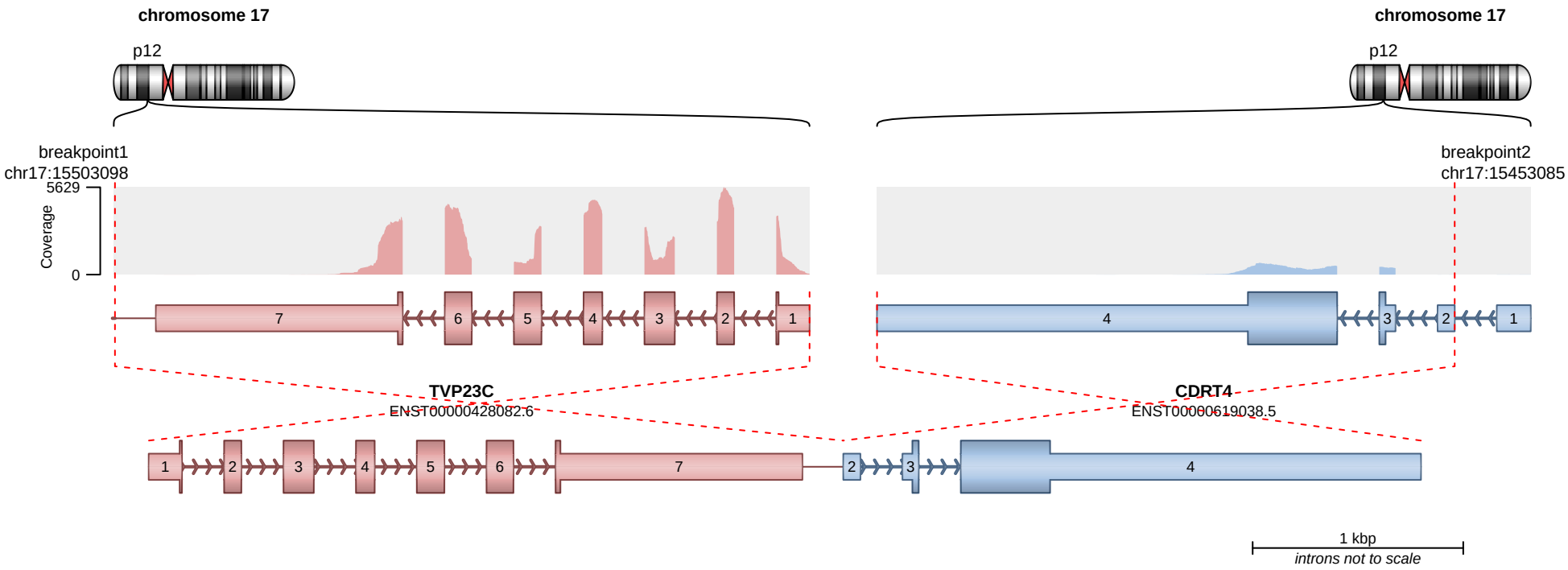


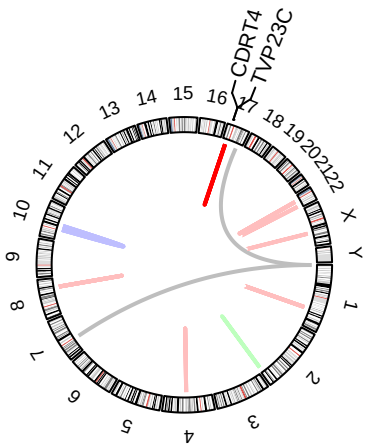


SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 0

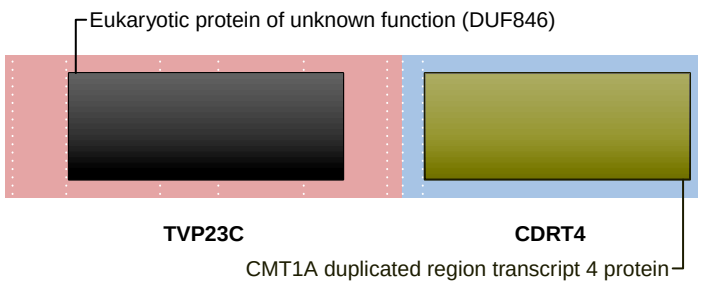
translocation
deletion
duplication
inversion





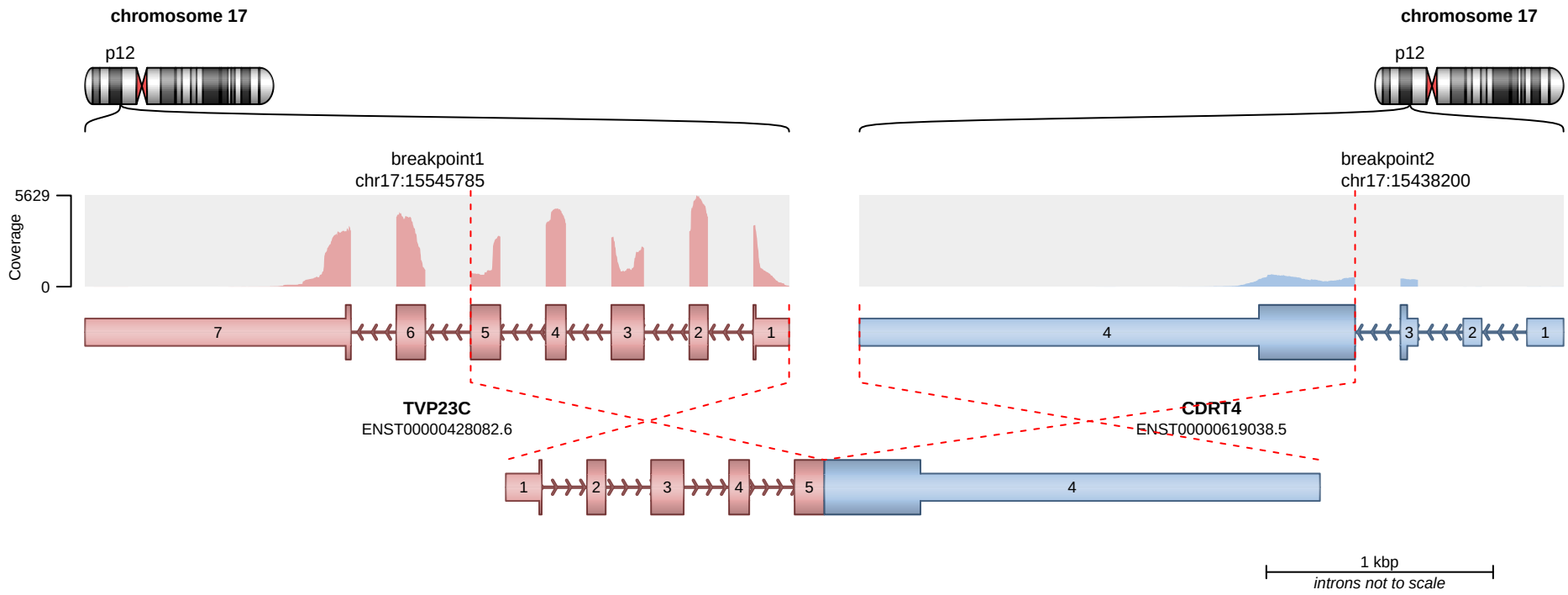
translocation
deletion
duplication
inversion

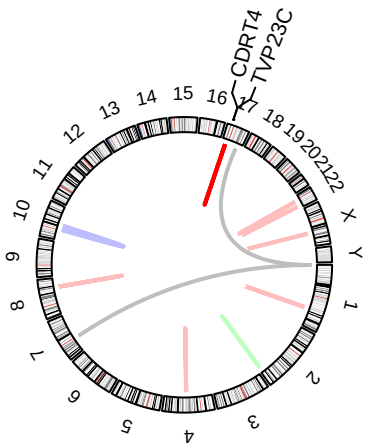
RETAINED PROTEIN DOMAINS
reading frame unclear

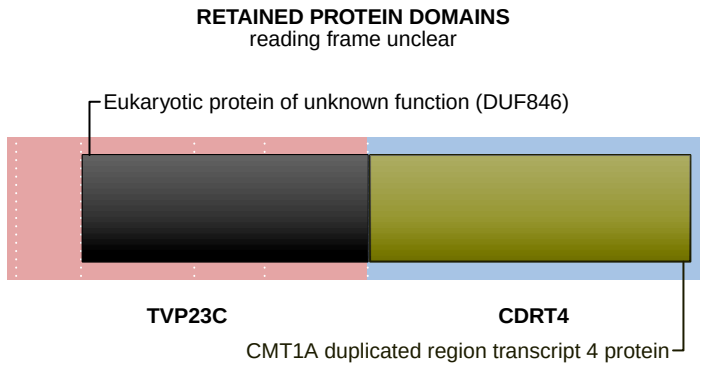


SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 3



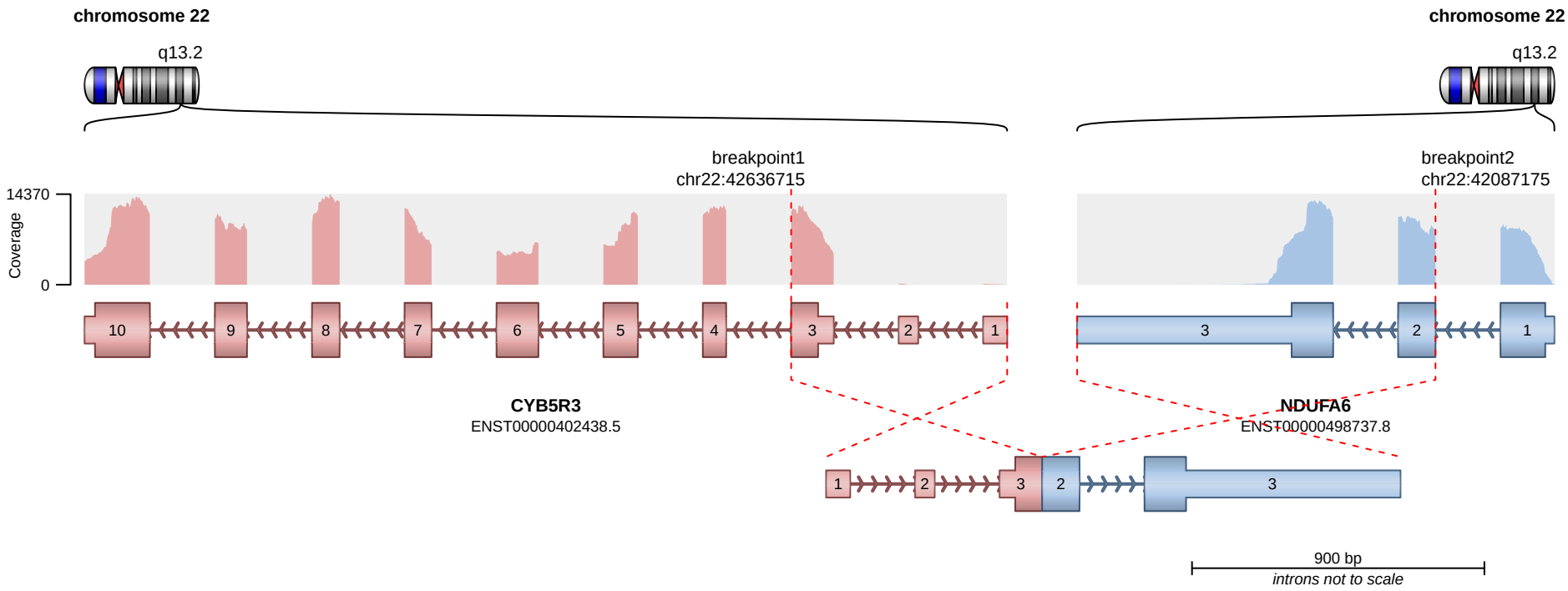


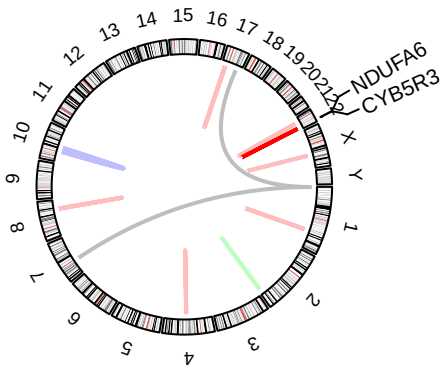


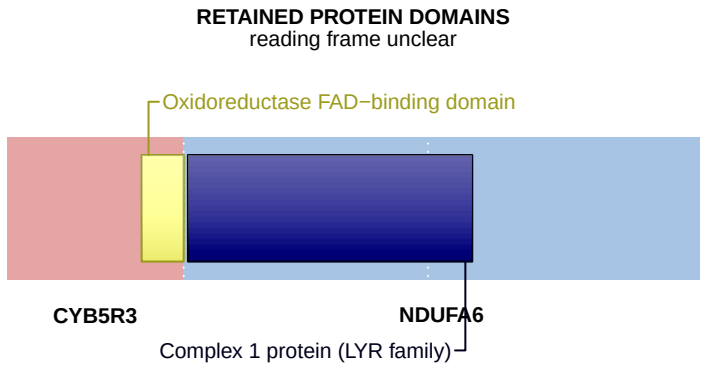
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

translocation
deletion
duplication
inversion

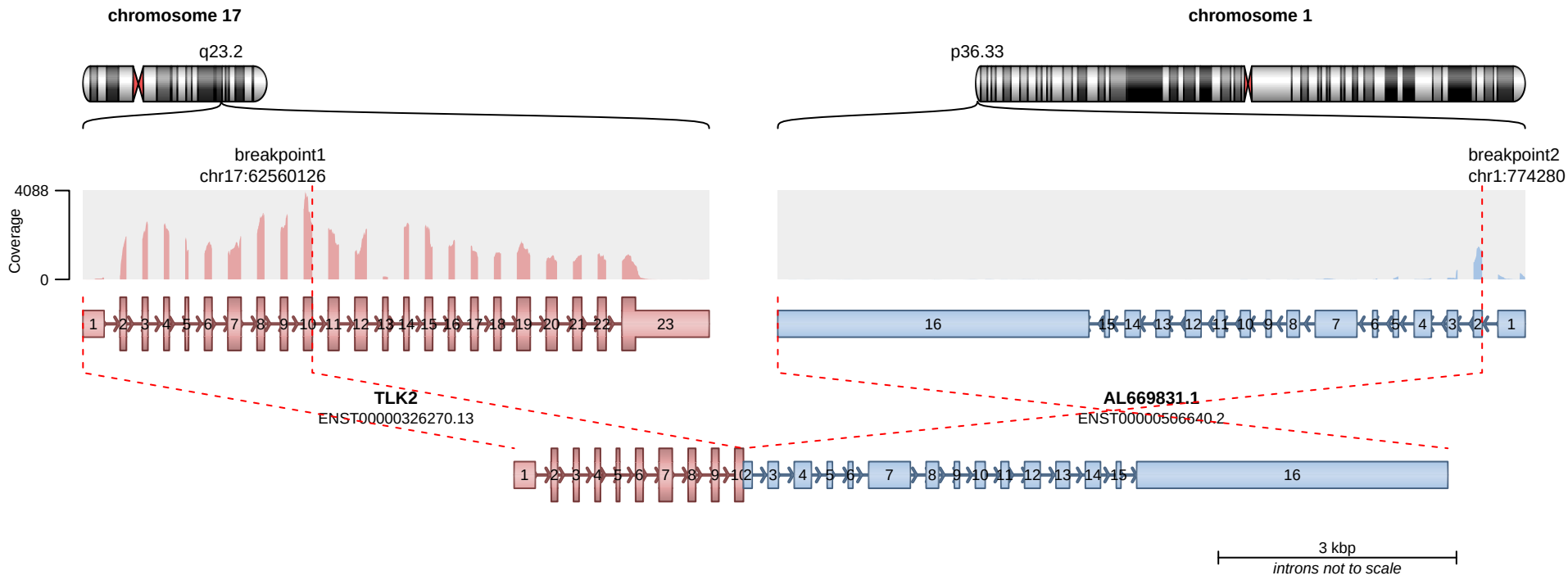


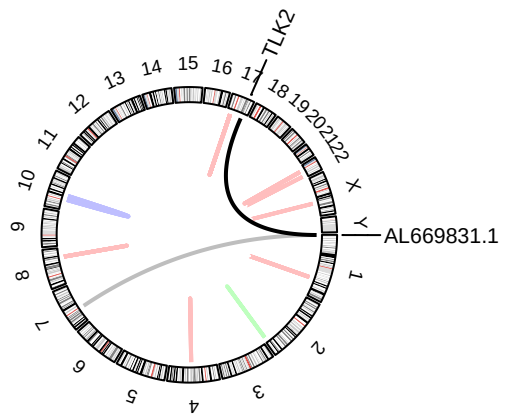




SUPPORTING READ COUNT

Split reads = 58
Discordant mates = 4



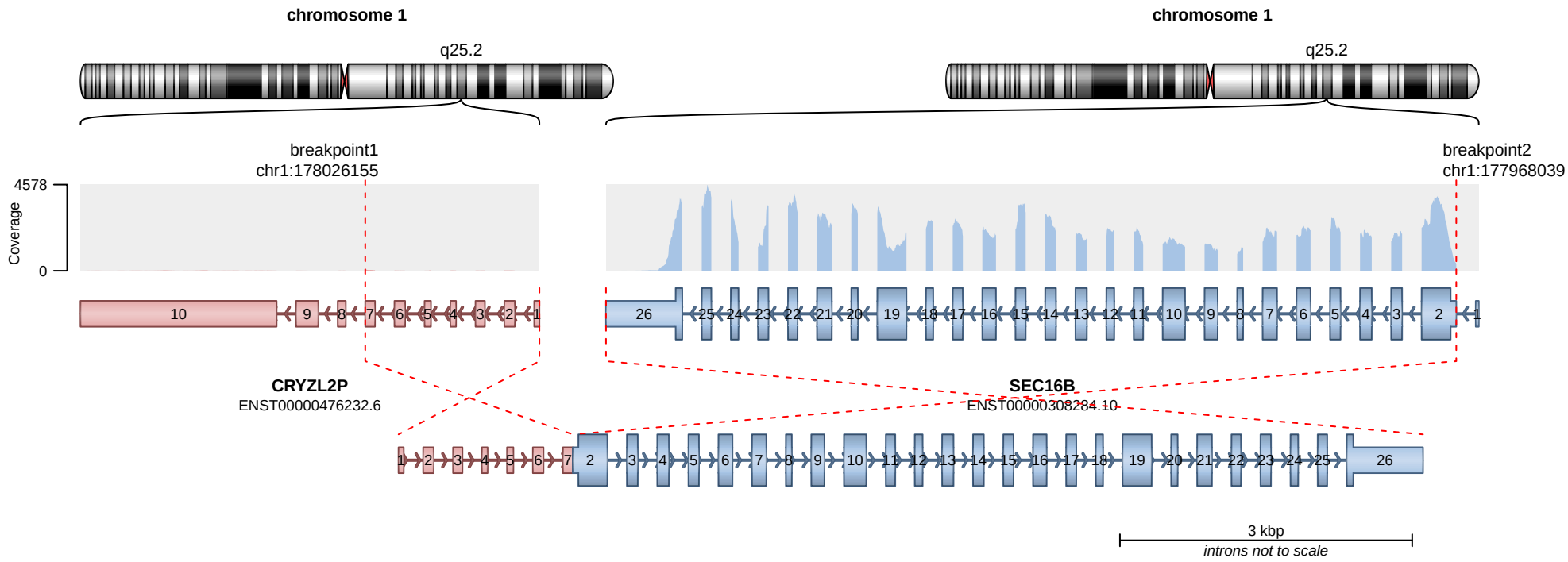


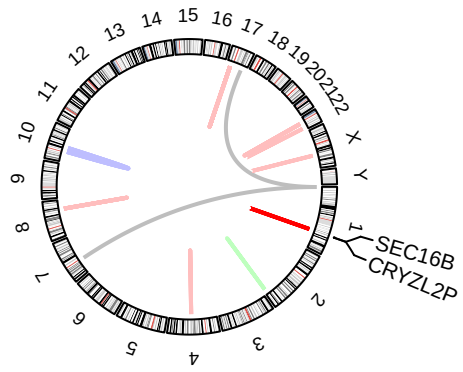
No protein domains retained in fusion.

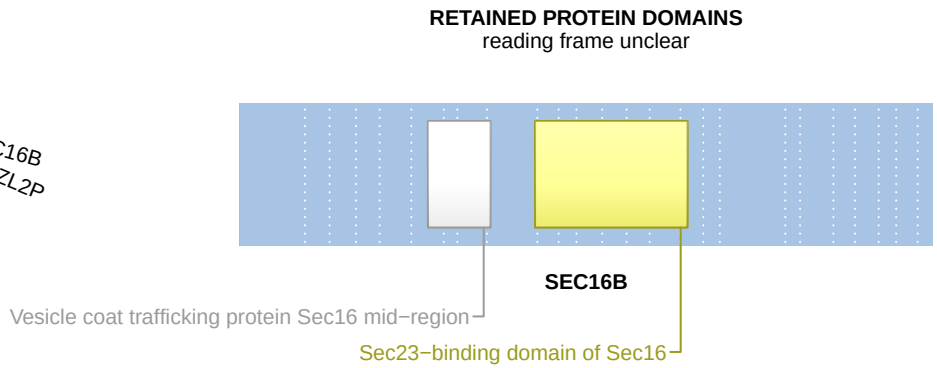
SUPPORTING READ COUNT

Split reads = 49
Discordant mates = 0

translocation
deletion
duplication
inversion



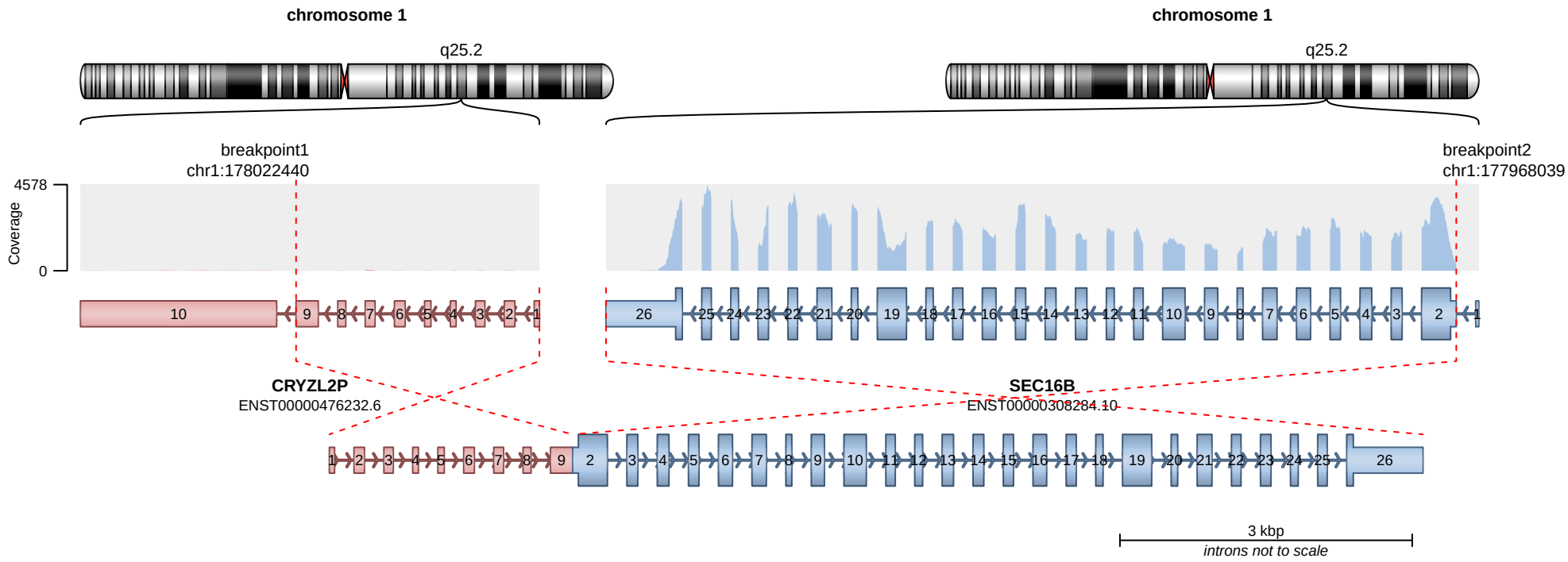


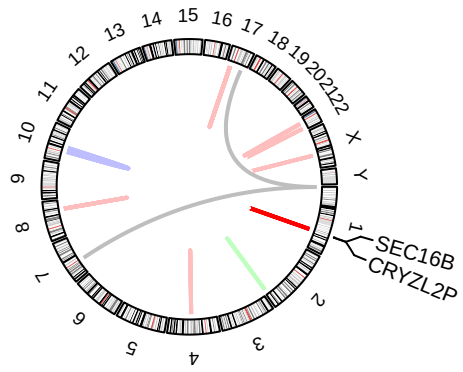


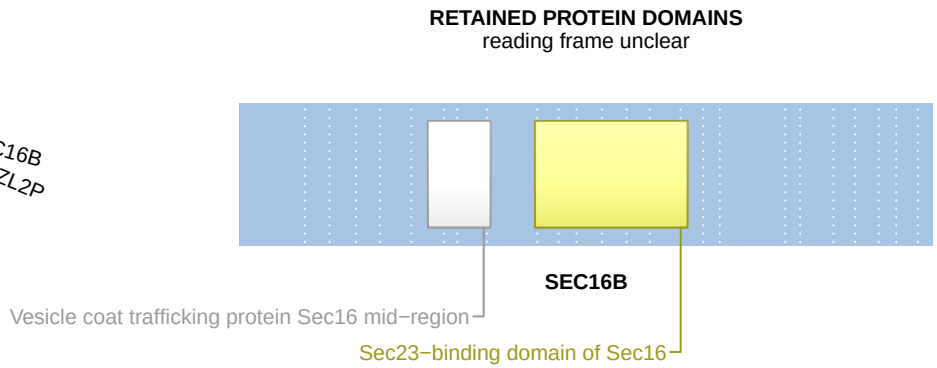
SUPPORTING READ COUNT

Split reads = 32
Discordant mates = 3

translocation
deletion
duplication
inversion



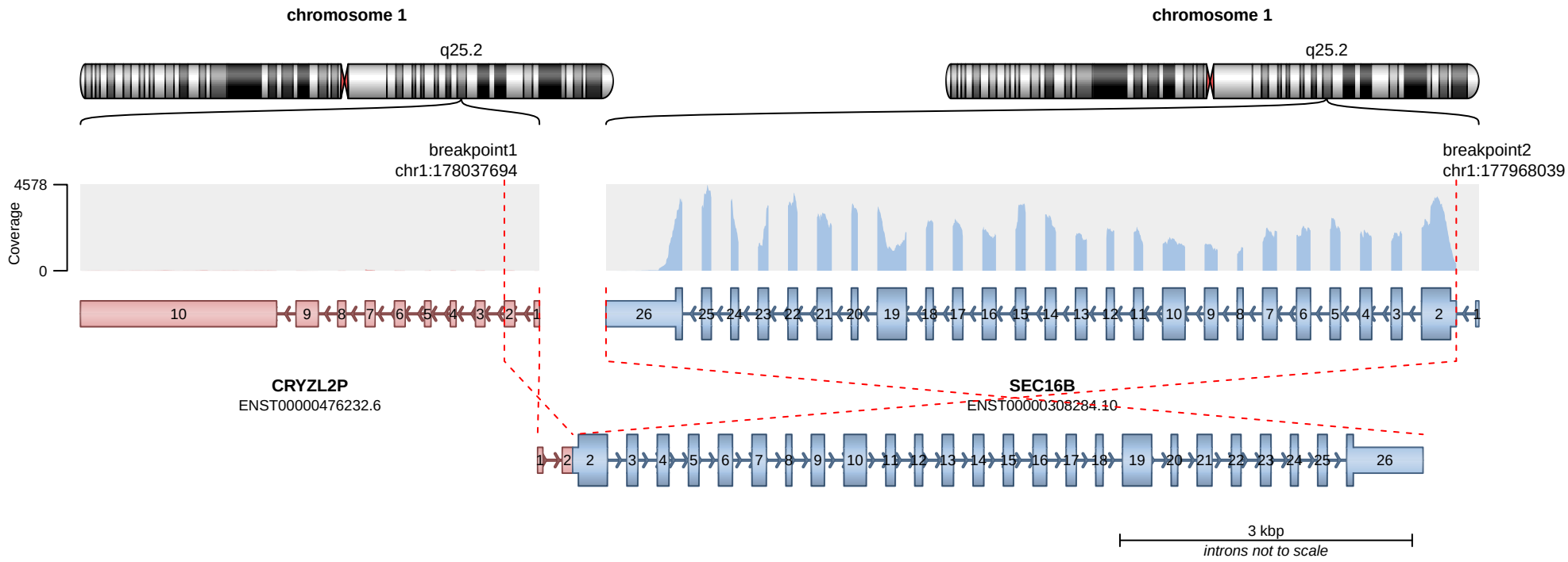


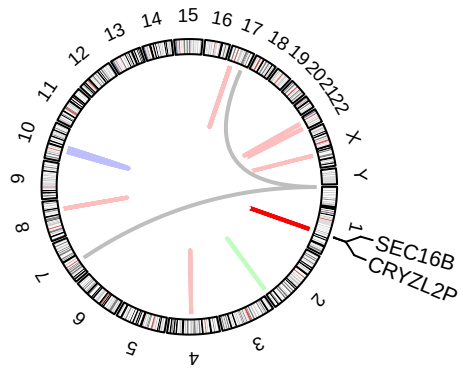


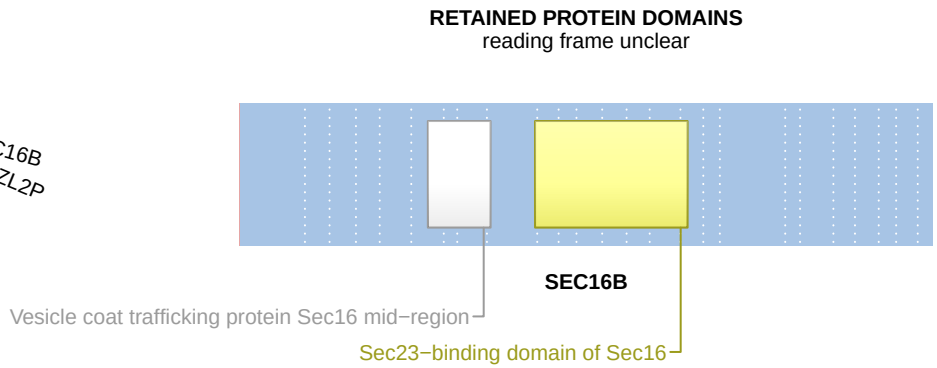
SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 3

translocation
deletion
duplication
inversion



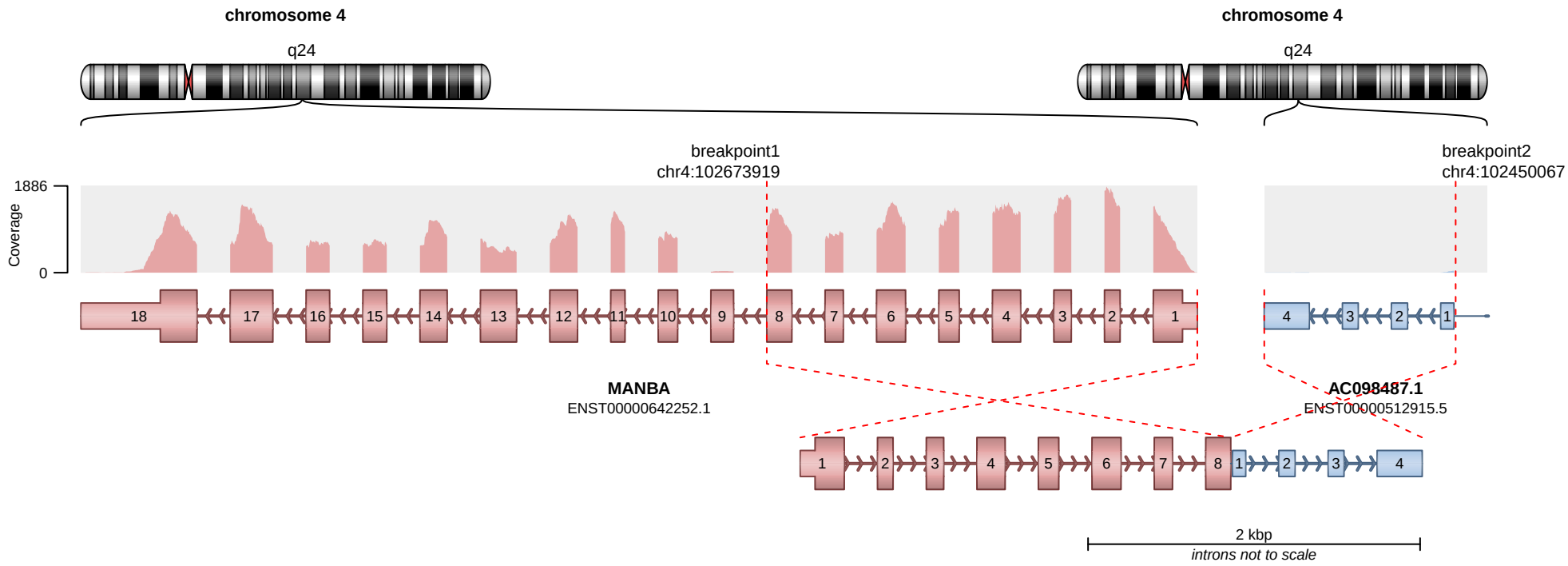


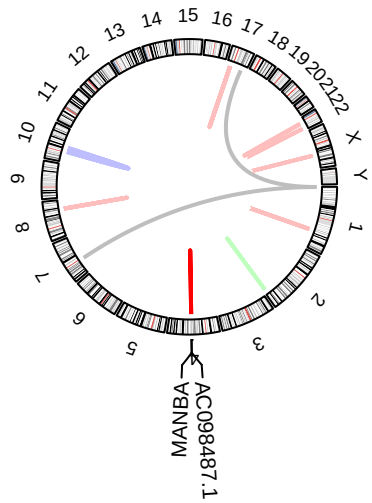


SUPPORTING READ COUNT

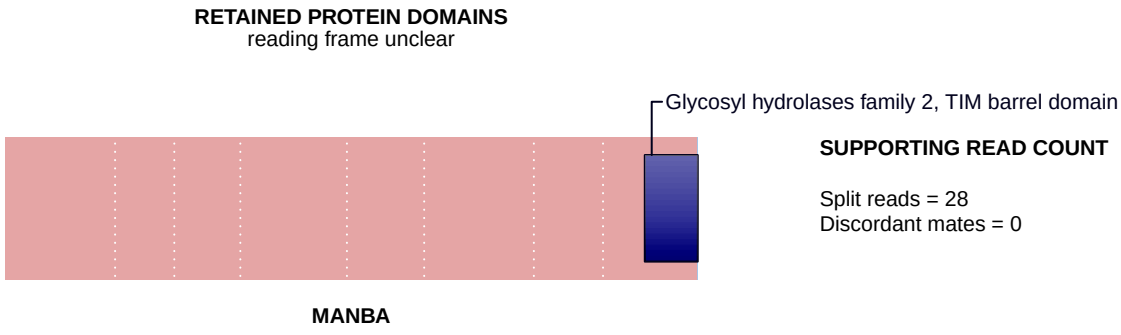
Split reads = 1
Discordant mates = 0

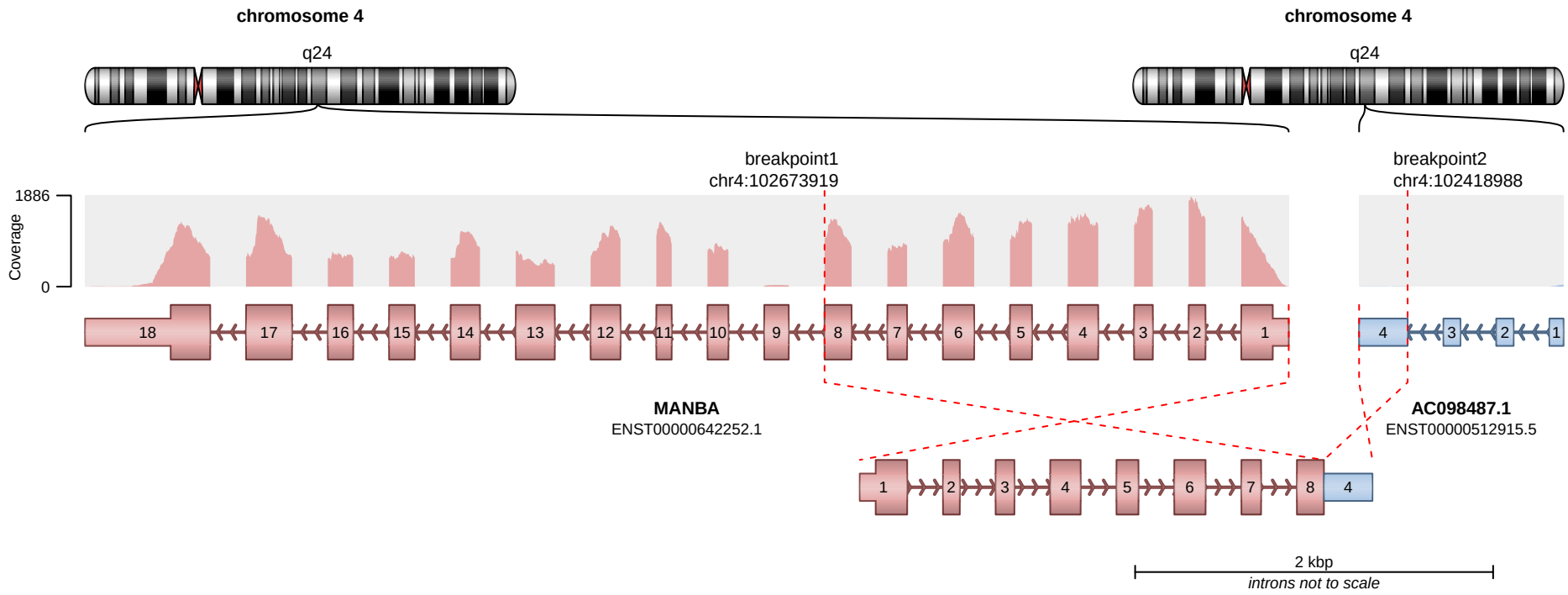
translocation
deletion
duplication
inversion

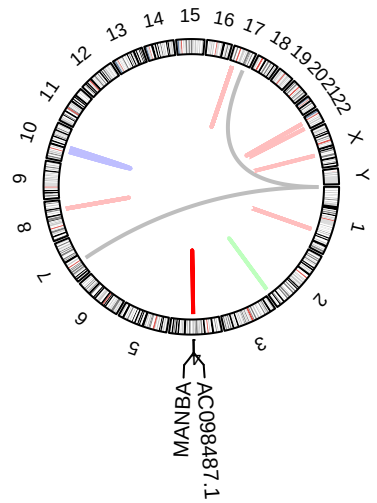




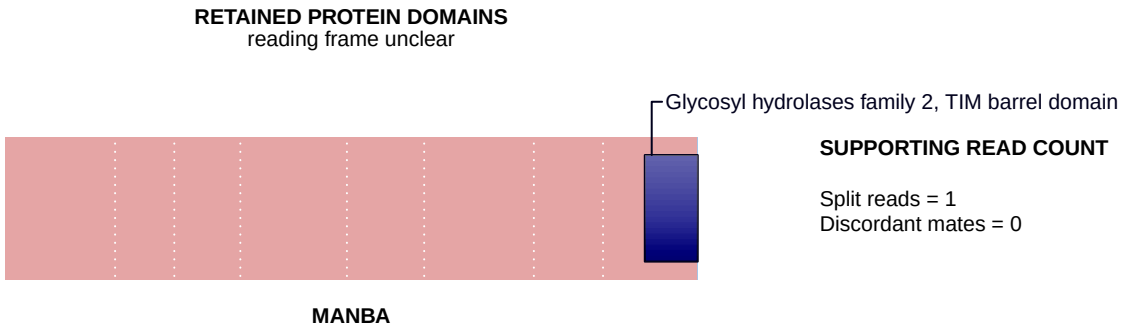
translocation
deletion
duplication
inversion

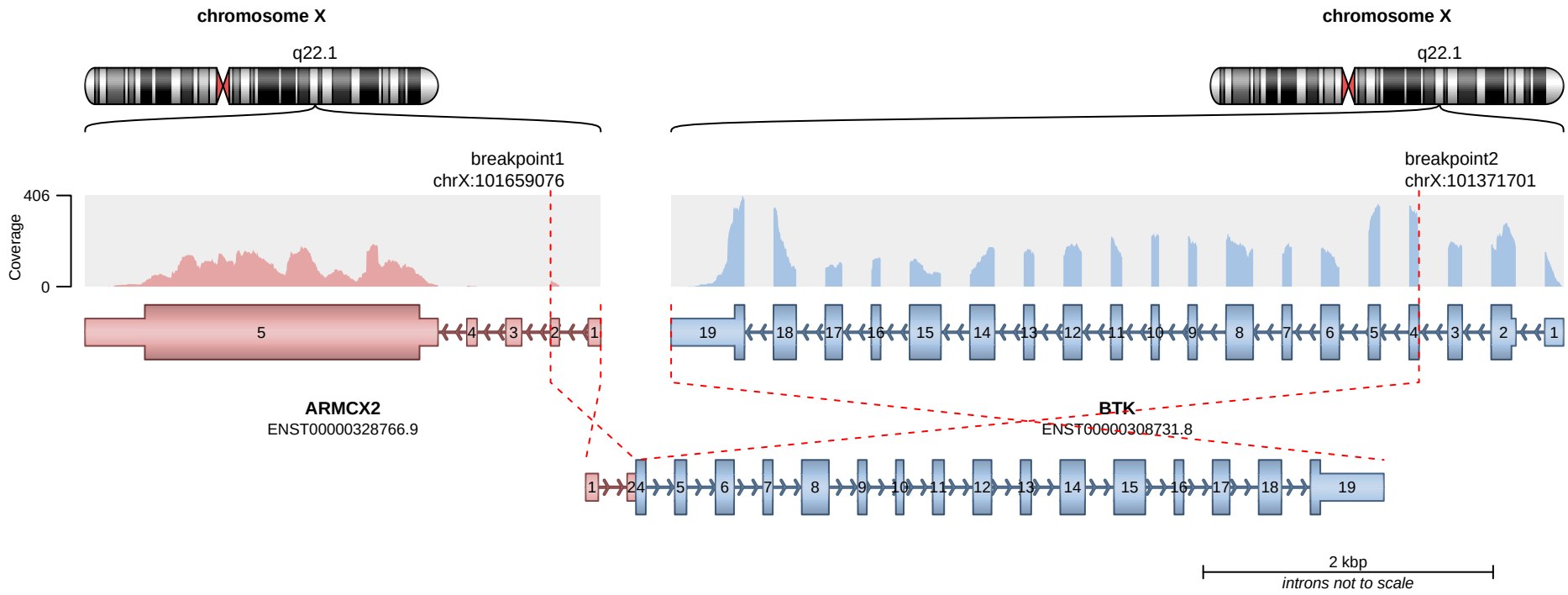


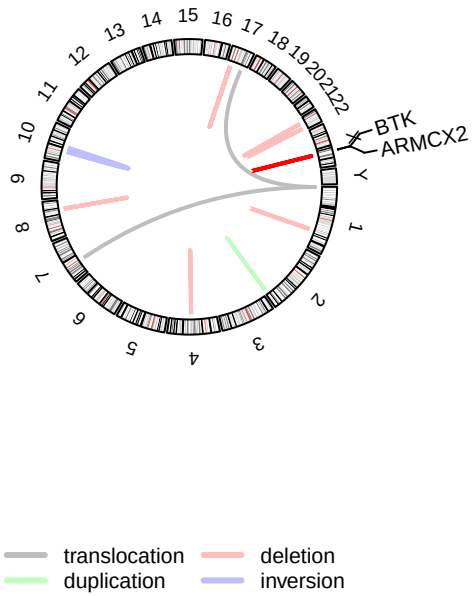


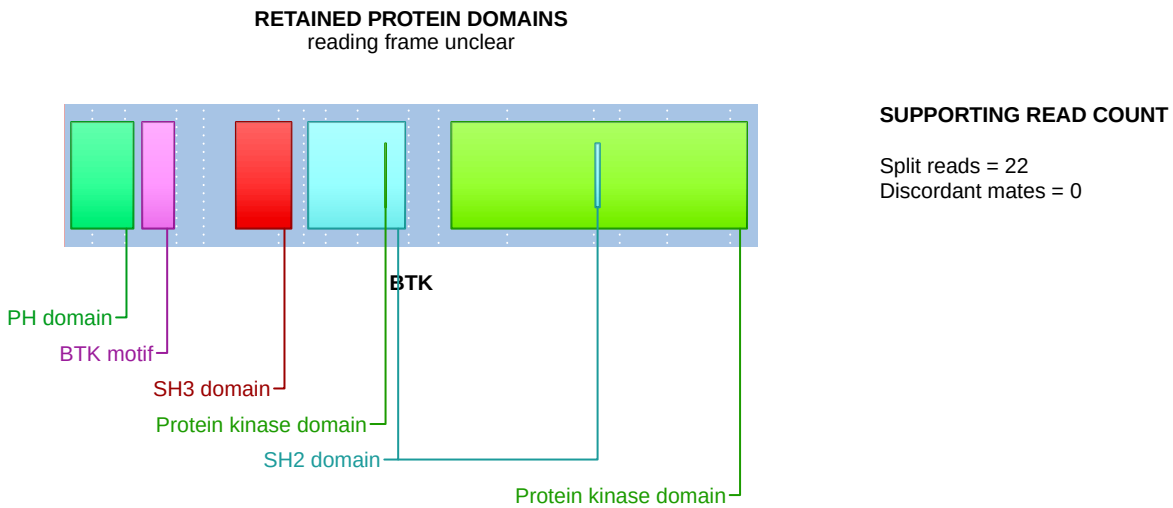


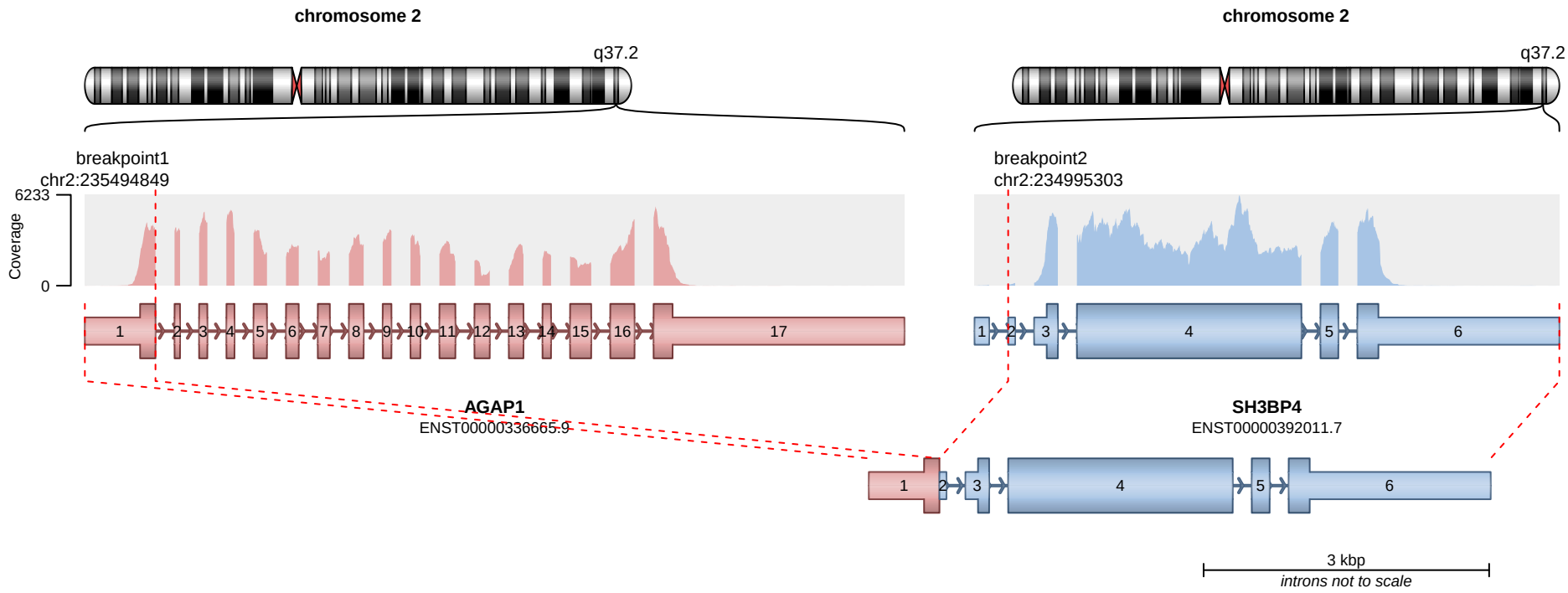
translocation
deletion
duplication
inversion

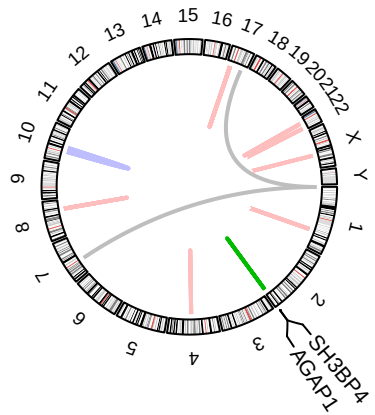
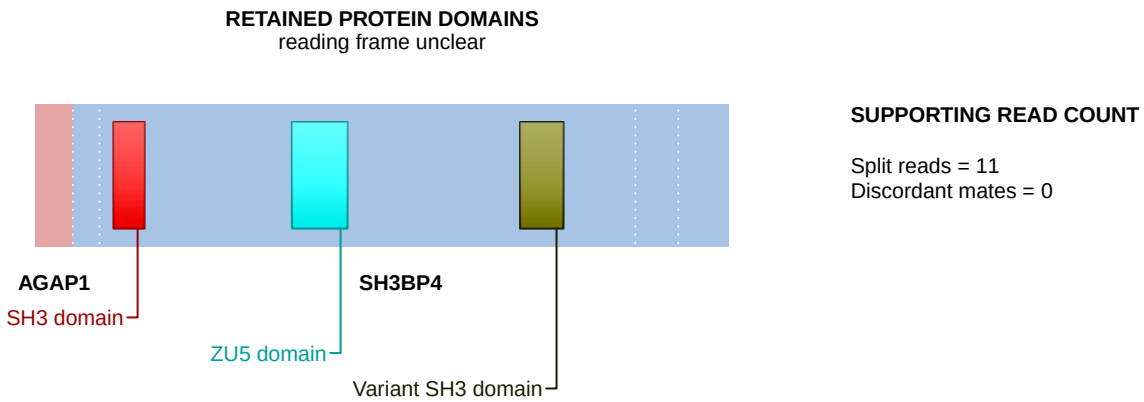



chromosome X
q22.1
chromosome X
q22.1
breakpoint1
chrX:101659076
breakpoint2
chrX:101371701
406
Coverage
0
ARMCX2
ENST00000328766.9
BTK
ENST00000308731.8
2 kbp
introns not to scale


BTK
ARMCX2
translocation
deletion
duplication
inversion


RETAINED PROTEIN DOMAINS
reading frame unclear
BTK
PH domain
BTK motif
SH3 domain
Protein kinase domain
SH2 domain
Protein kinase domain
SUPPORTING READ COUNT
Split reads = 22
Discordant mates = 0





translocation
deletion
duplication
inversion