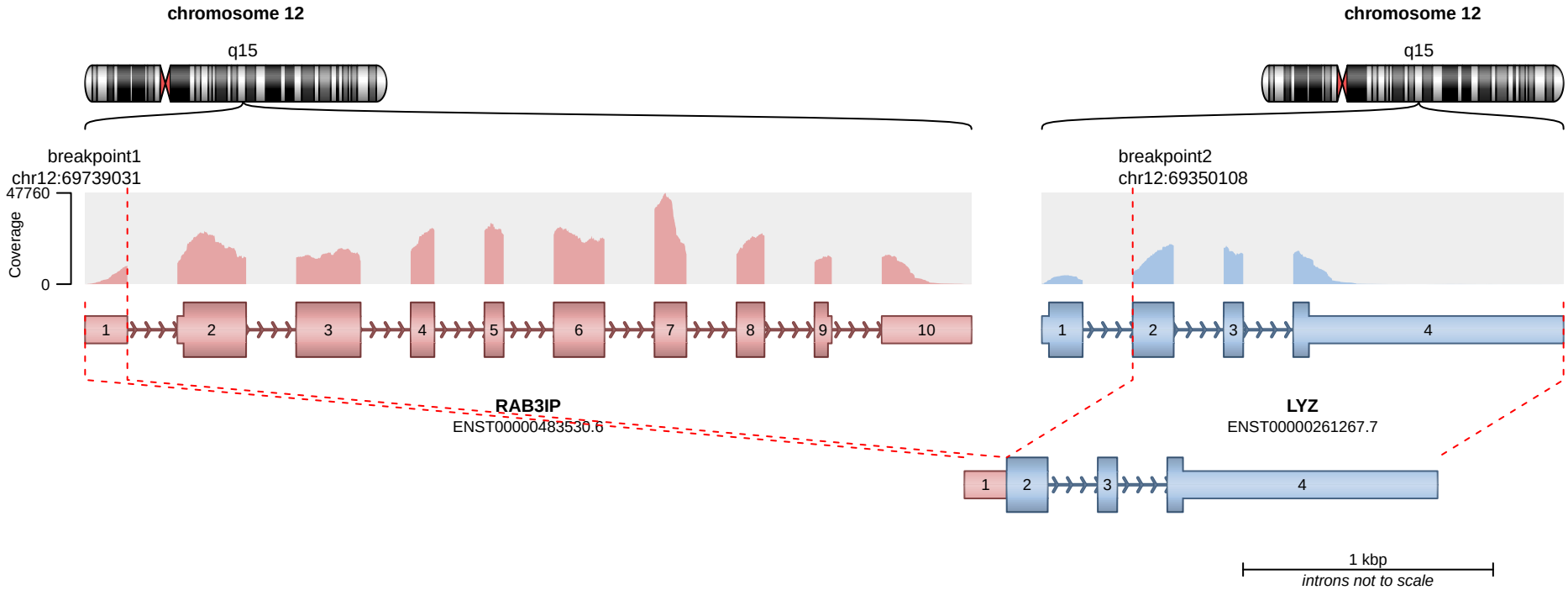
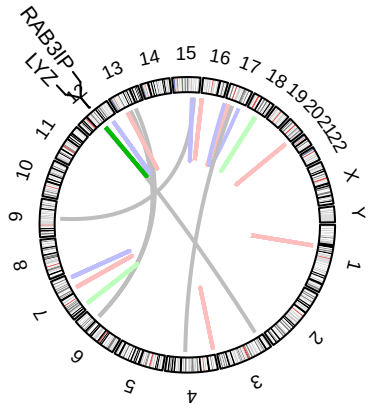


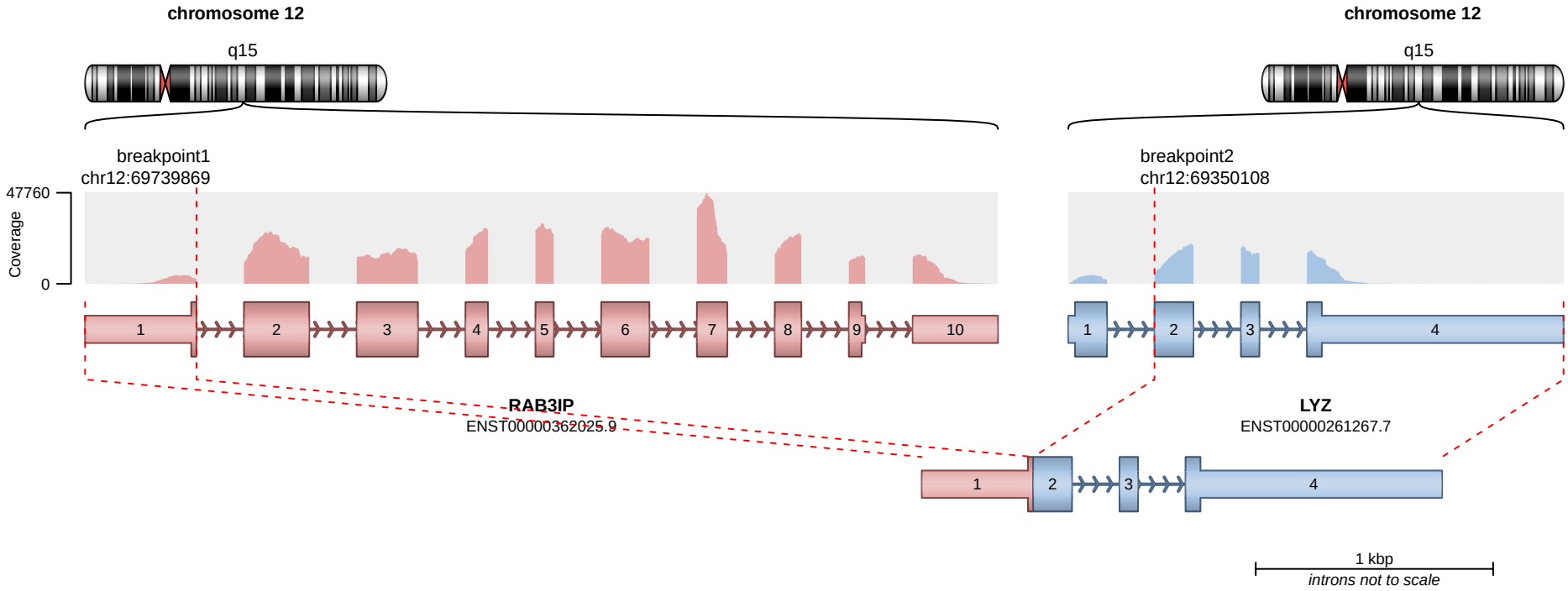


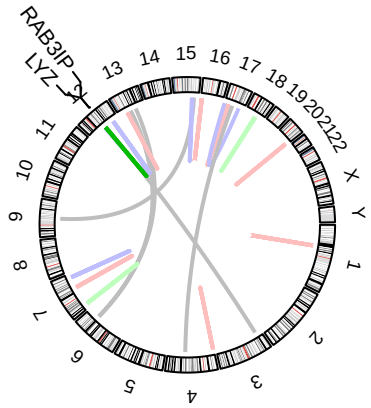
RETAINED PROTEIN DOMAINS
reading frame unclear

SUPPORTING READ COUNT

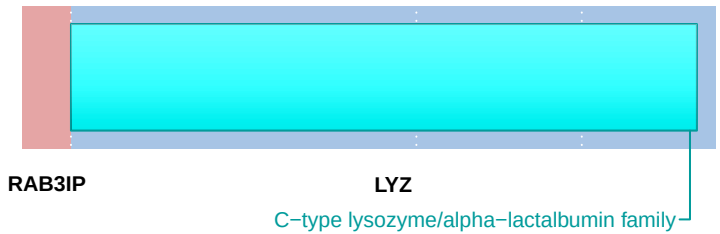
Split reads = 1418
Discordant mates = 33

translocation
deletion
duplication
inversion





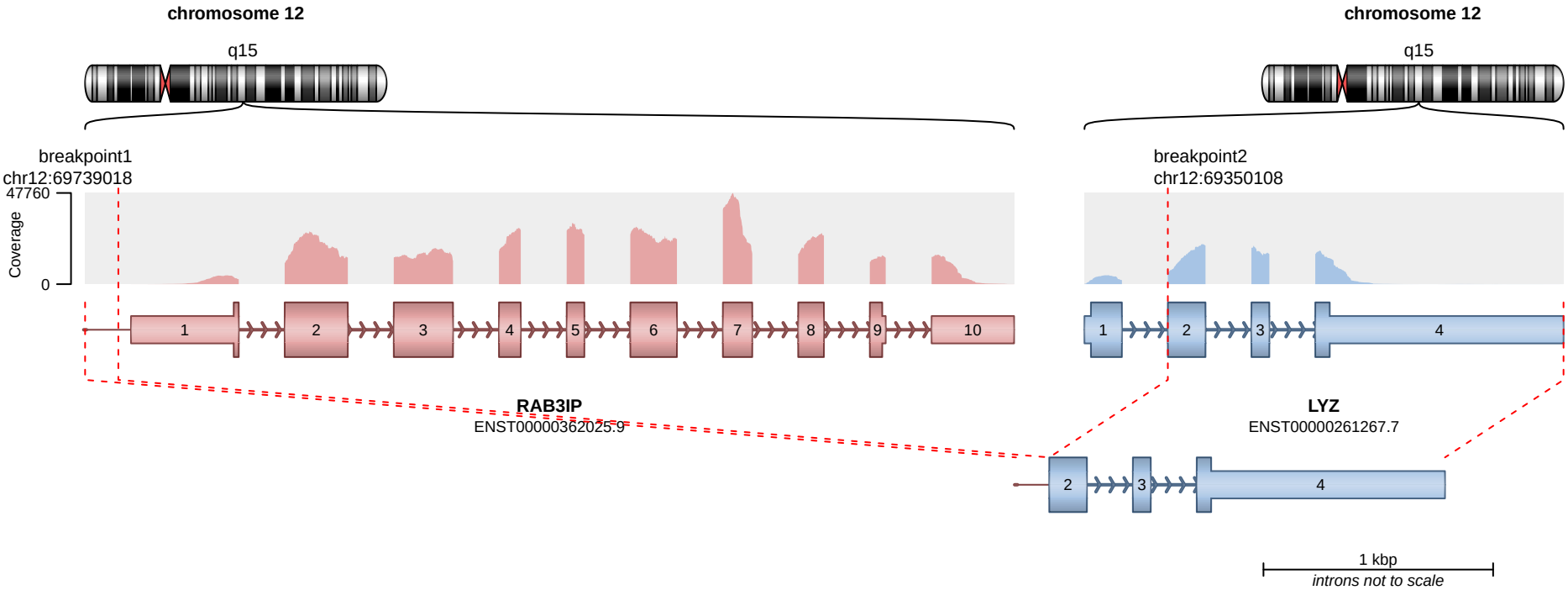
RETAINED PROTEIN DOMAINS
reading frame unclear

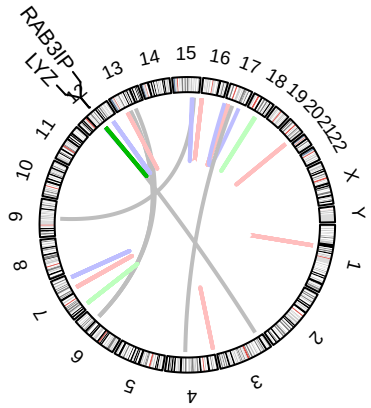


SUPPORTING READ COUNT

Split reads = 54
Discordant mates = 34

translocation
deletion
duplication
inversion





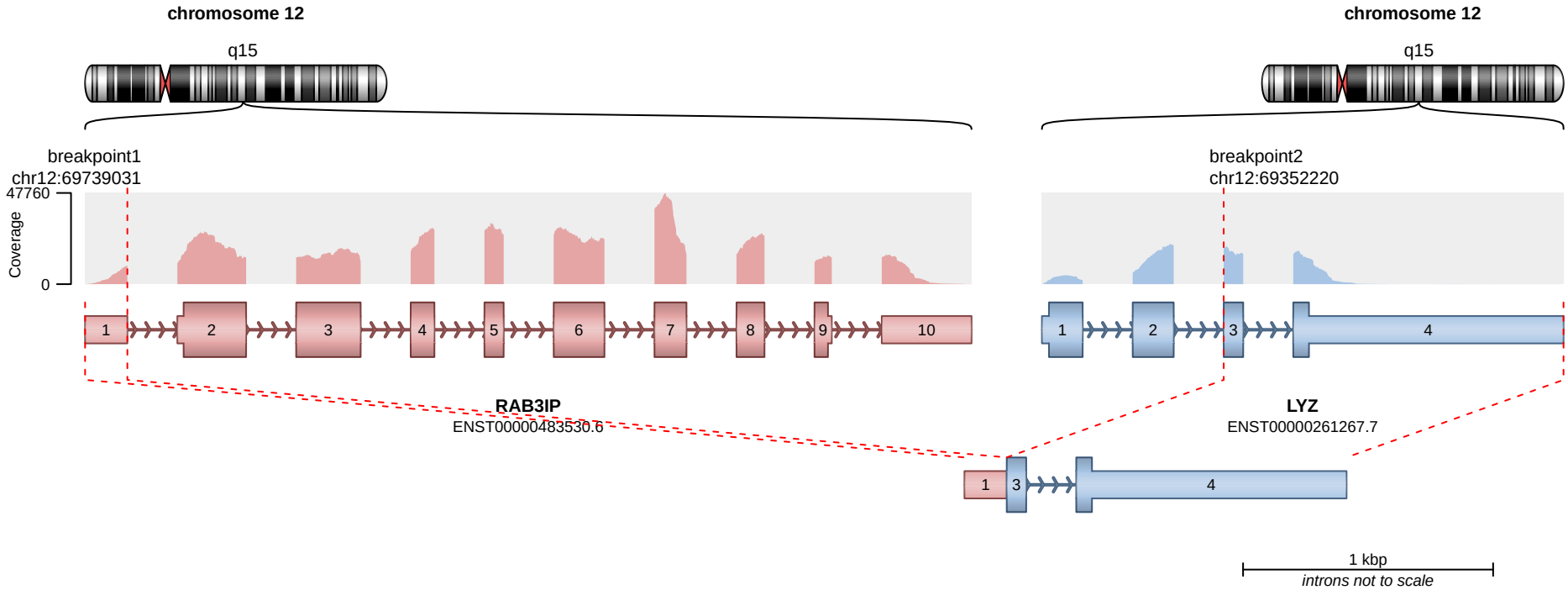
RETAINED PROTEIN DOMAINS
reading frame unclear

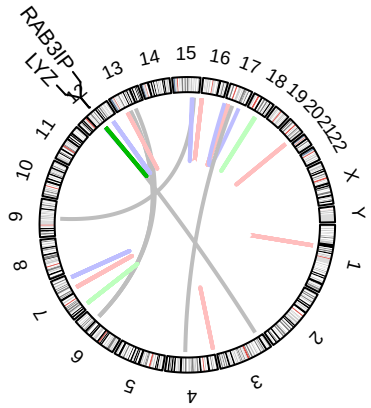
LYZ
C−type lysozyme/alpha−lactalbumin family

SUPPORTING READ COUNT

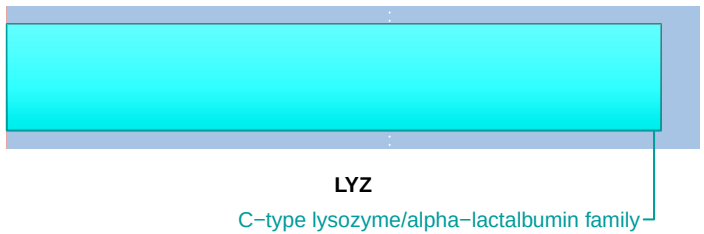
Split reads = 4
Discordant mates = 13

translocation
deletion
duplication
inversion



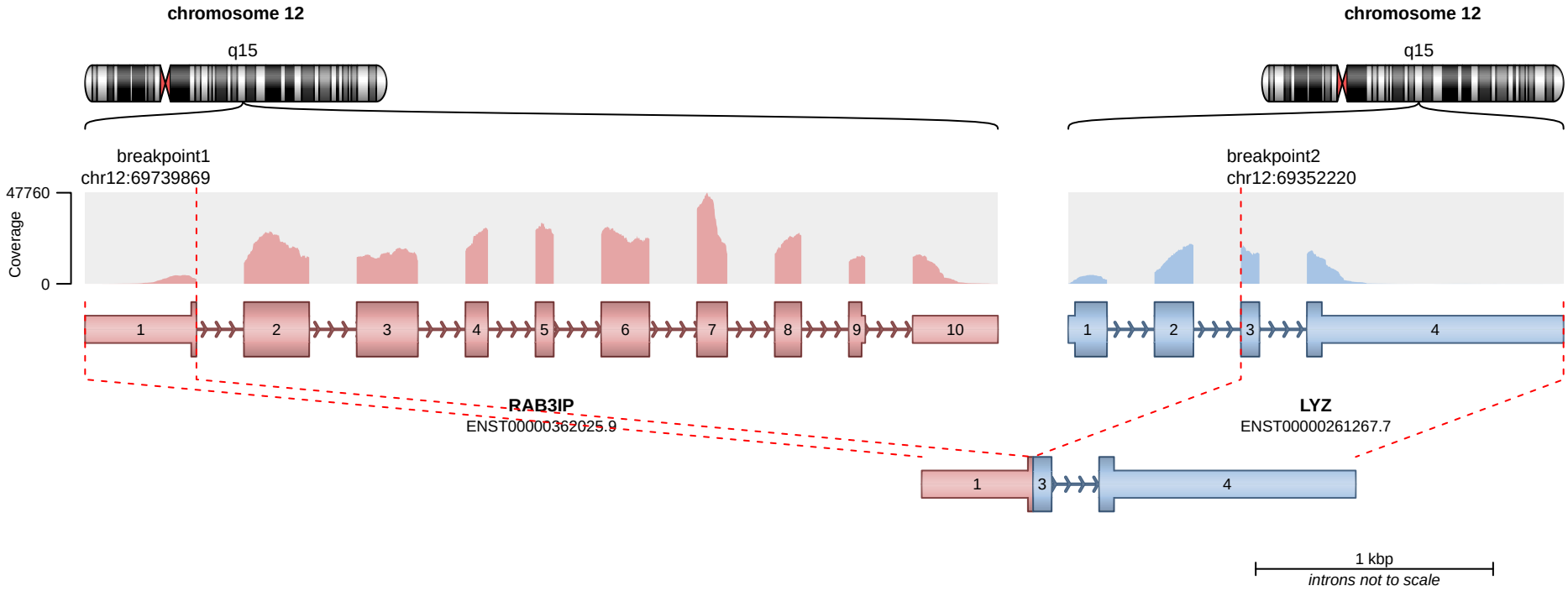


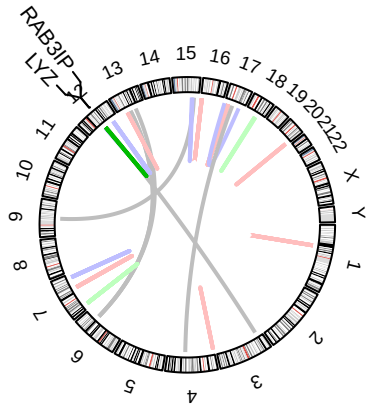
RETAINED PROTEIN DOMAINS
reading frame unclear



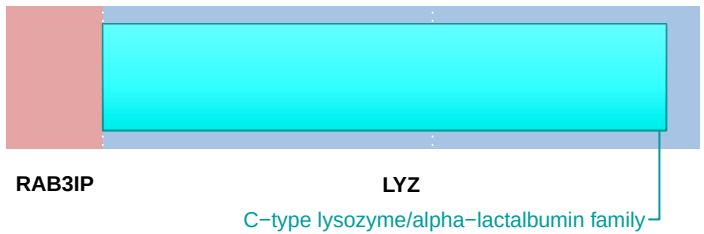
SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 4





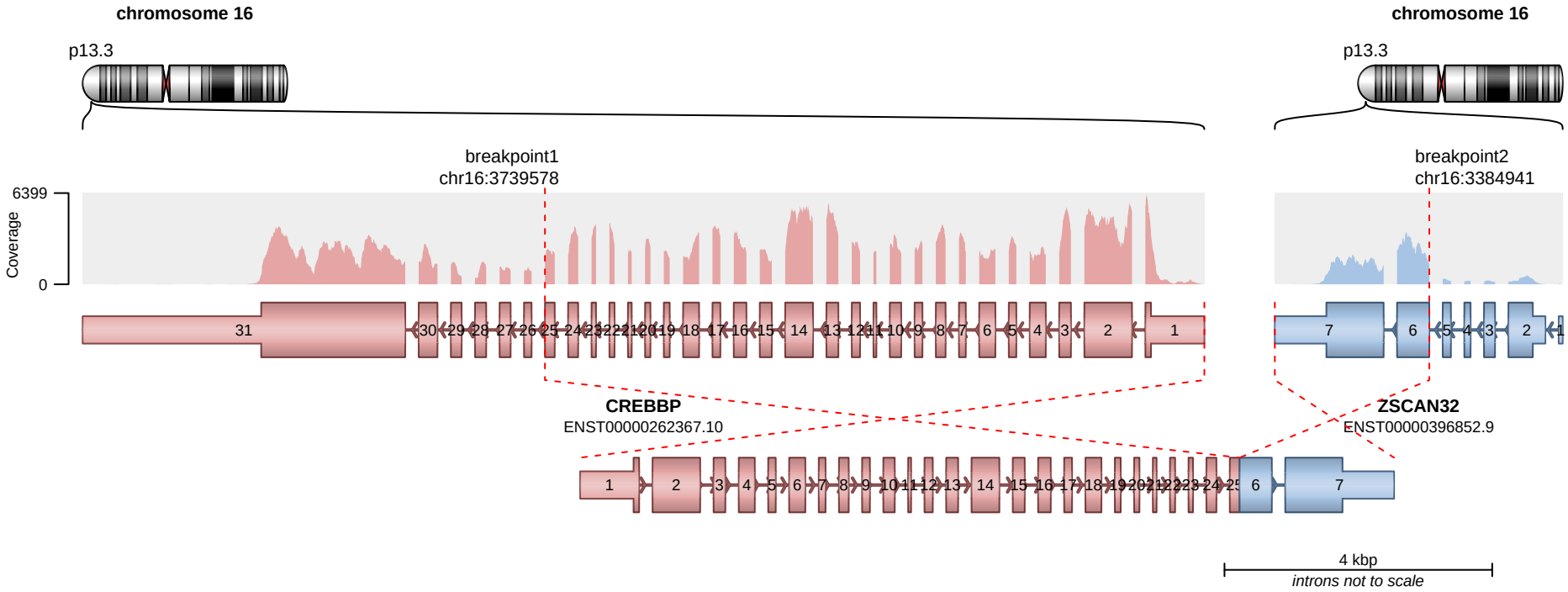
RETAINED PROTEIN DOMAINS
reading frame unclear

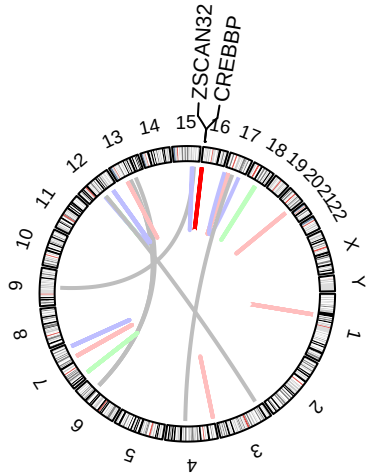


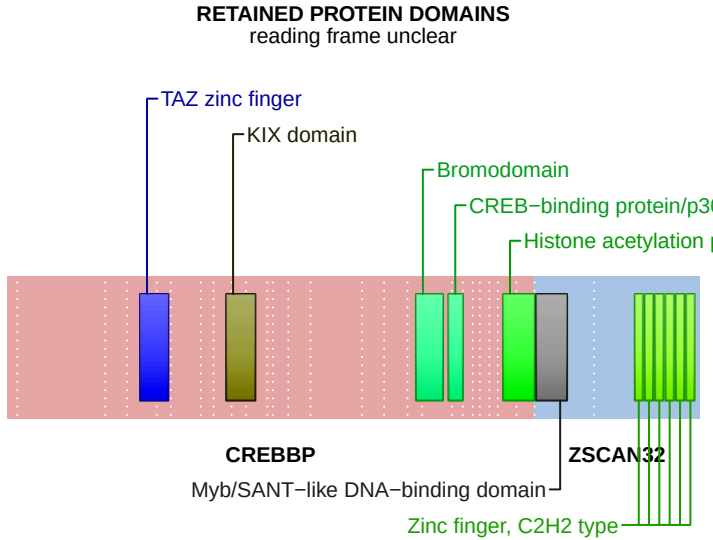
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 4

translocation
deletion
duplication
inversion



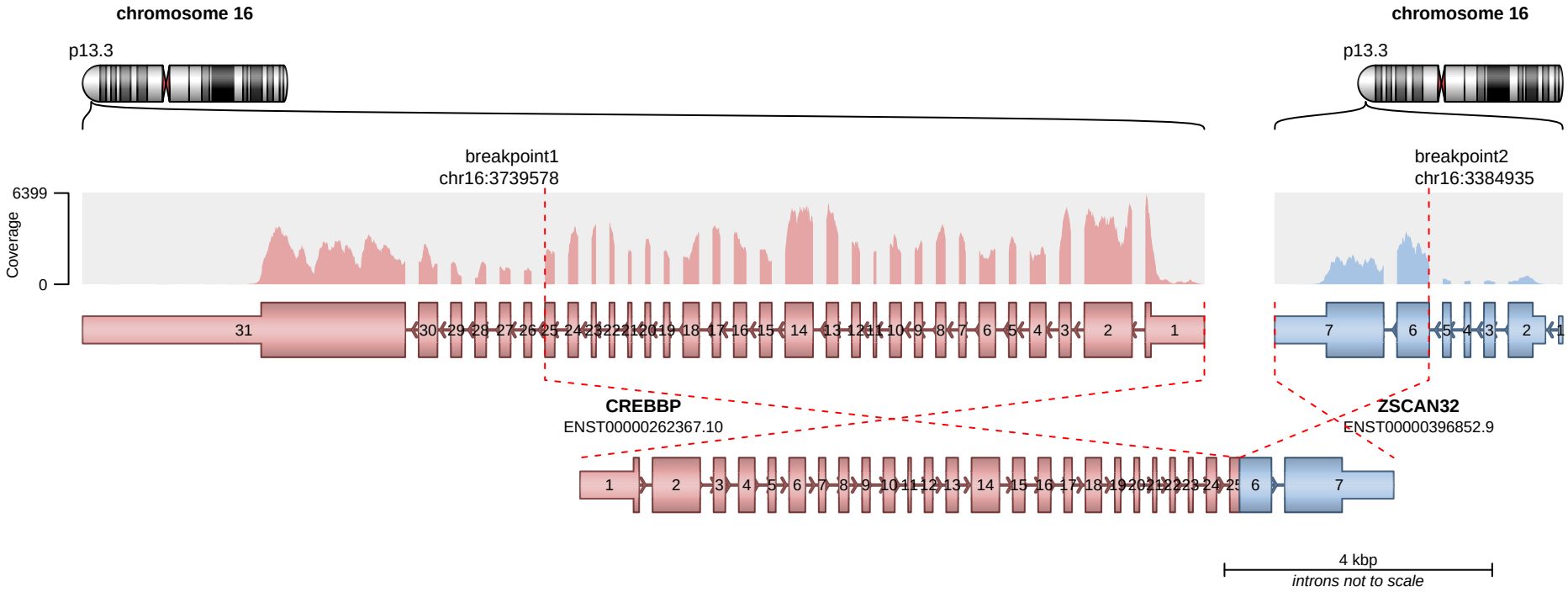


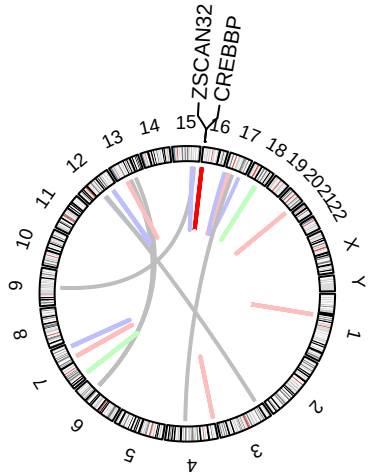


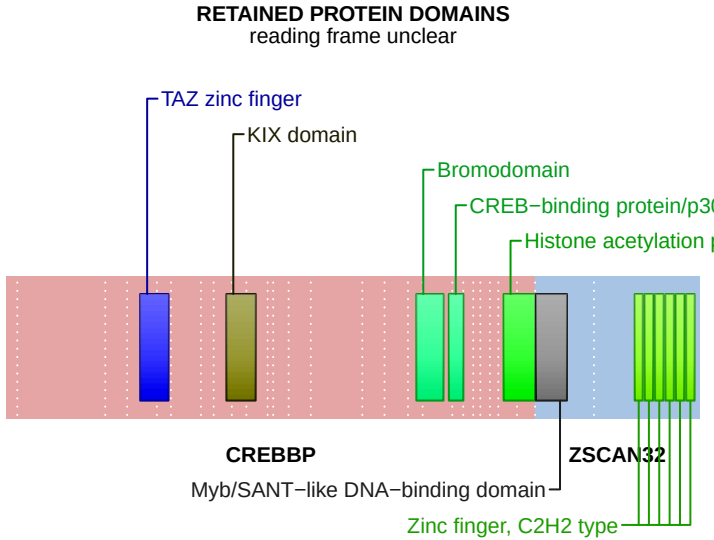
SUPPORTING READ COUNT

Split reads = 371
Discordant mates = 8

translocation
deletion
duplication
inversion



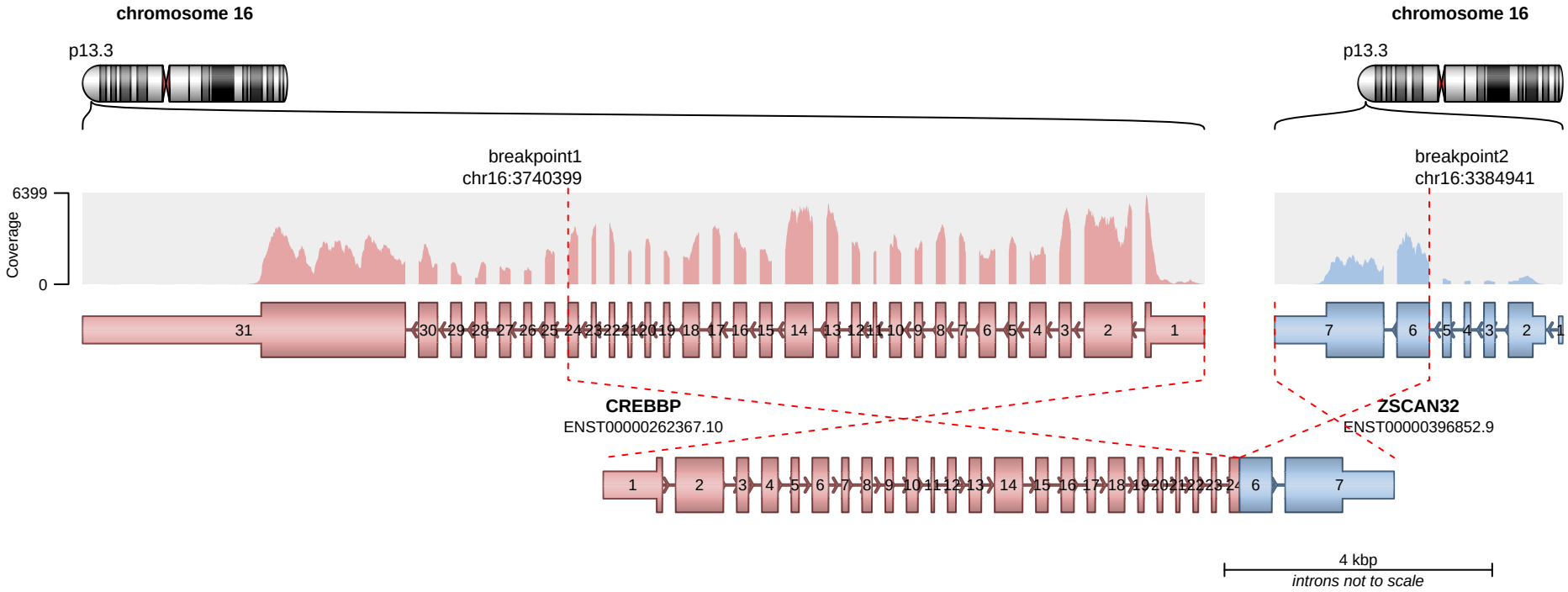


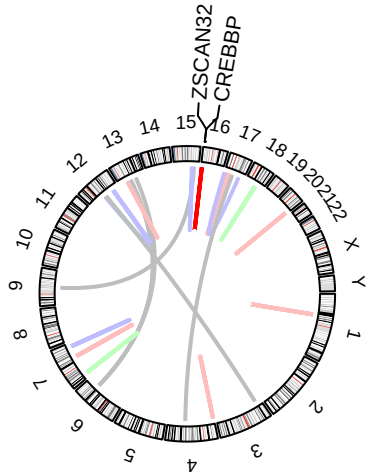


SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 8

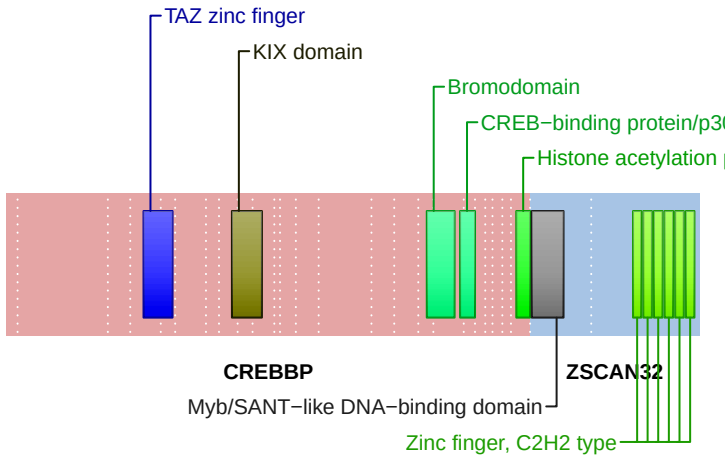
translocation
deletion
duplication
inversion





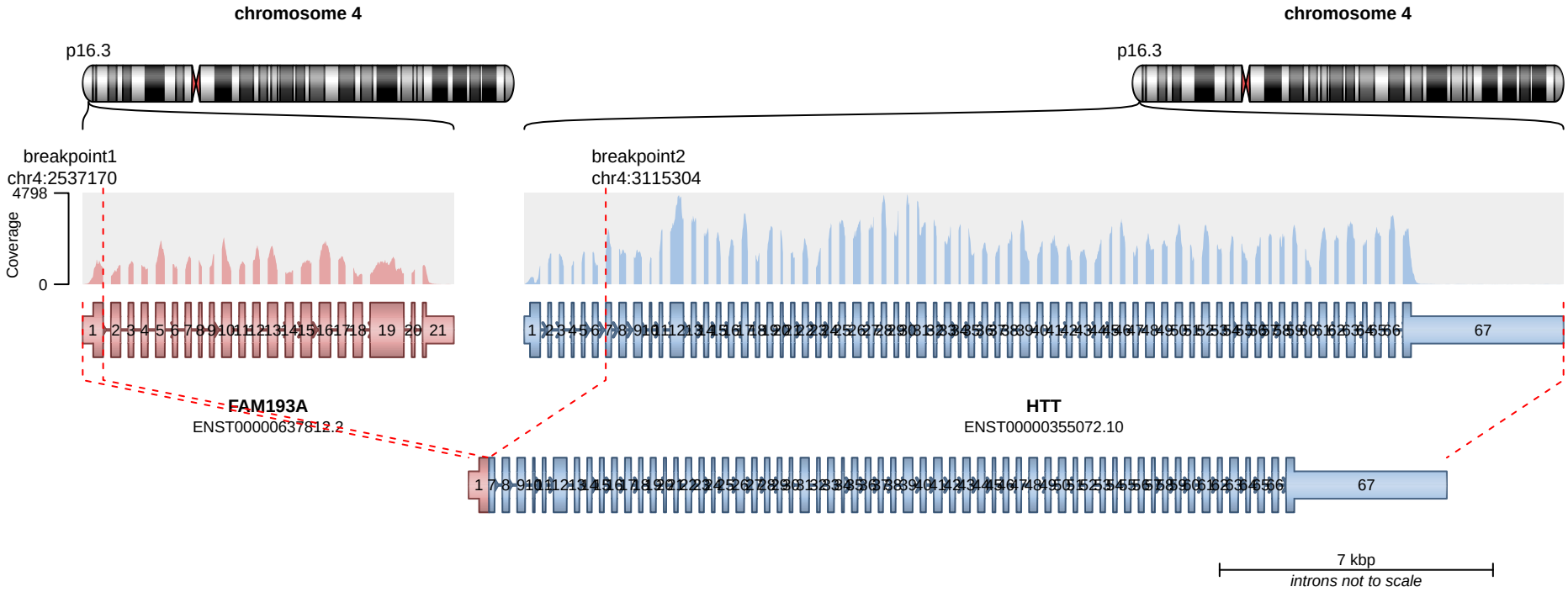
translocation
deletion
duplication
inversion

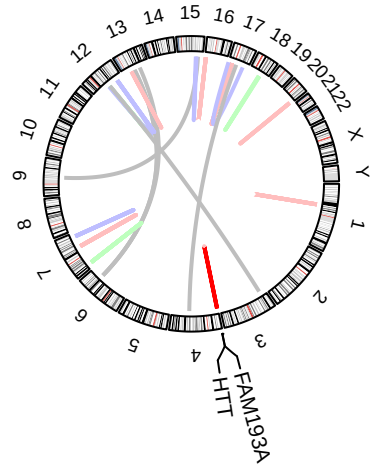
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

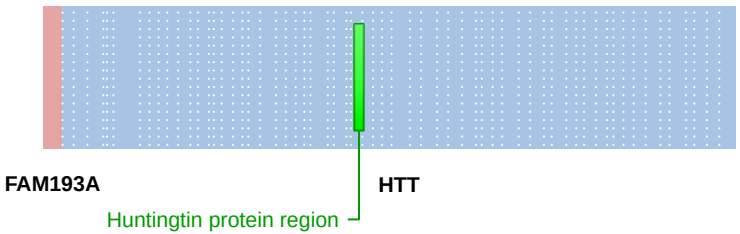
Split reads = 2
Discordant mates = 1





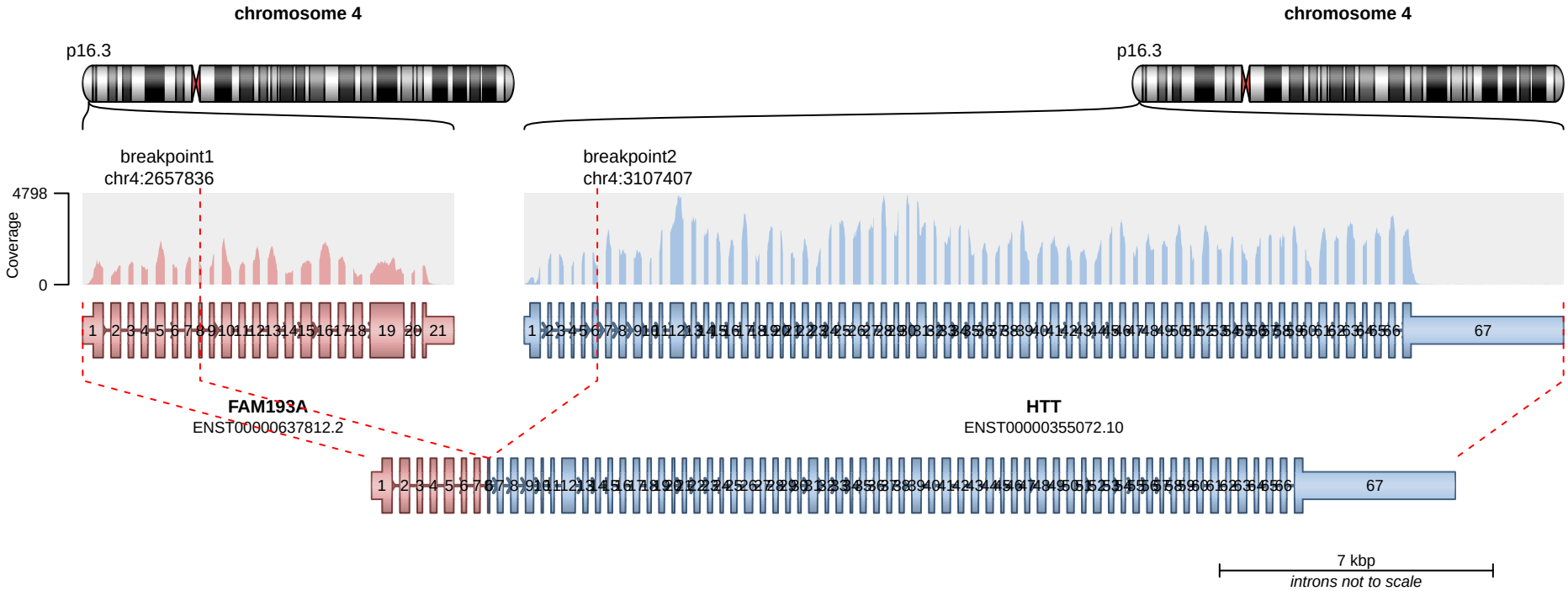
translocation
deletion
duplication
inversion

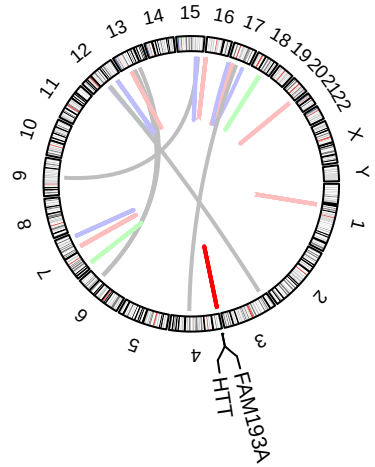
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

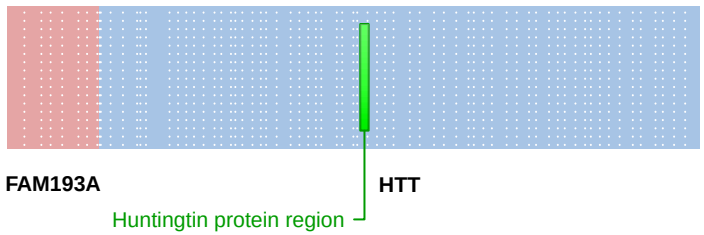
Split reads = 277
Discordant mates = 3





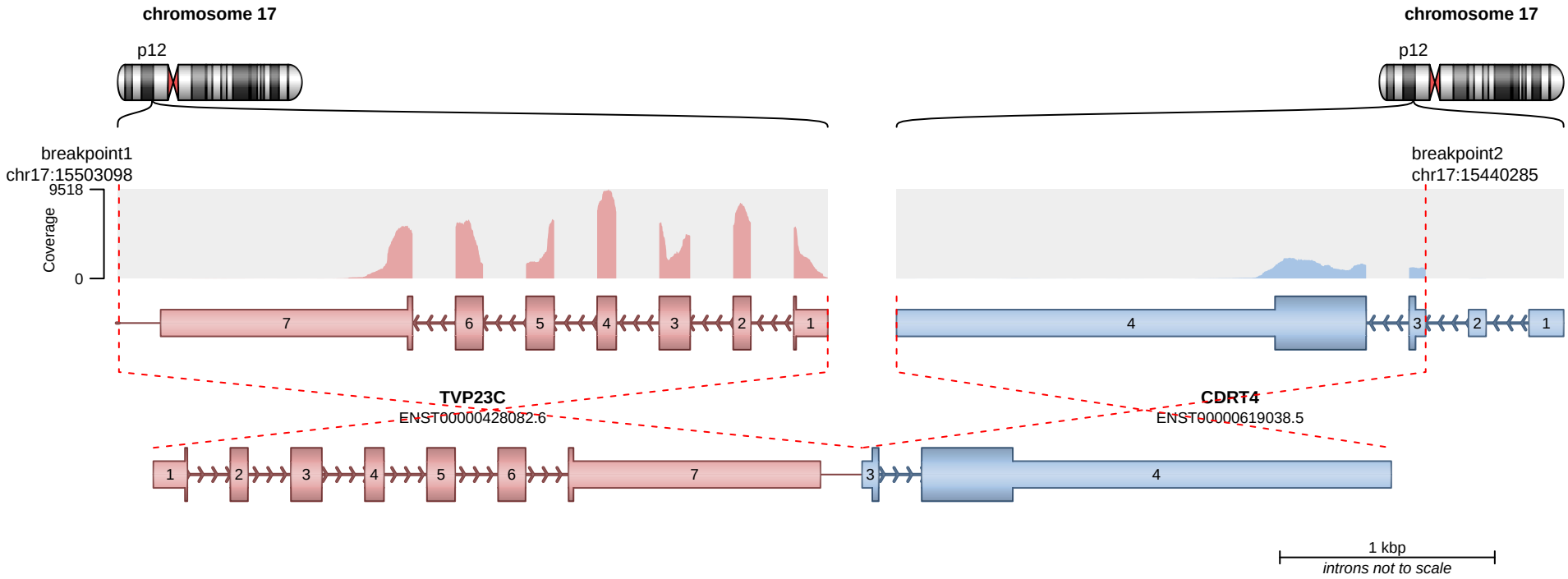
translocation
deletion
duplication
inversion

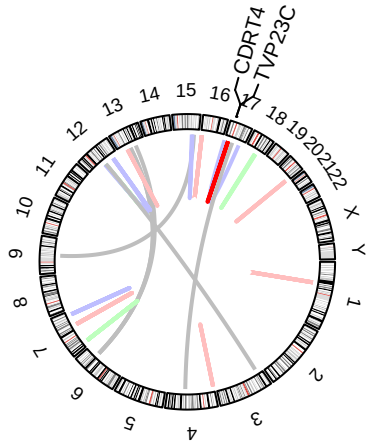
RETAINED PROTEIN DOMAINS
reading frame unclear



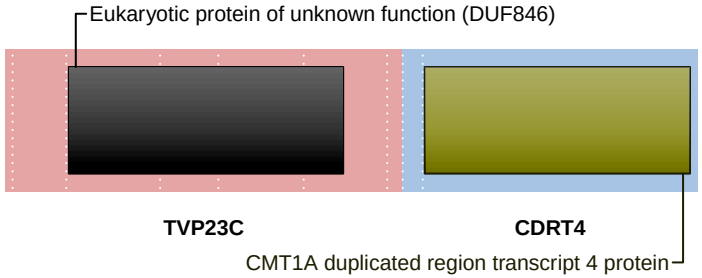
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 3





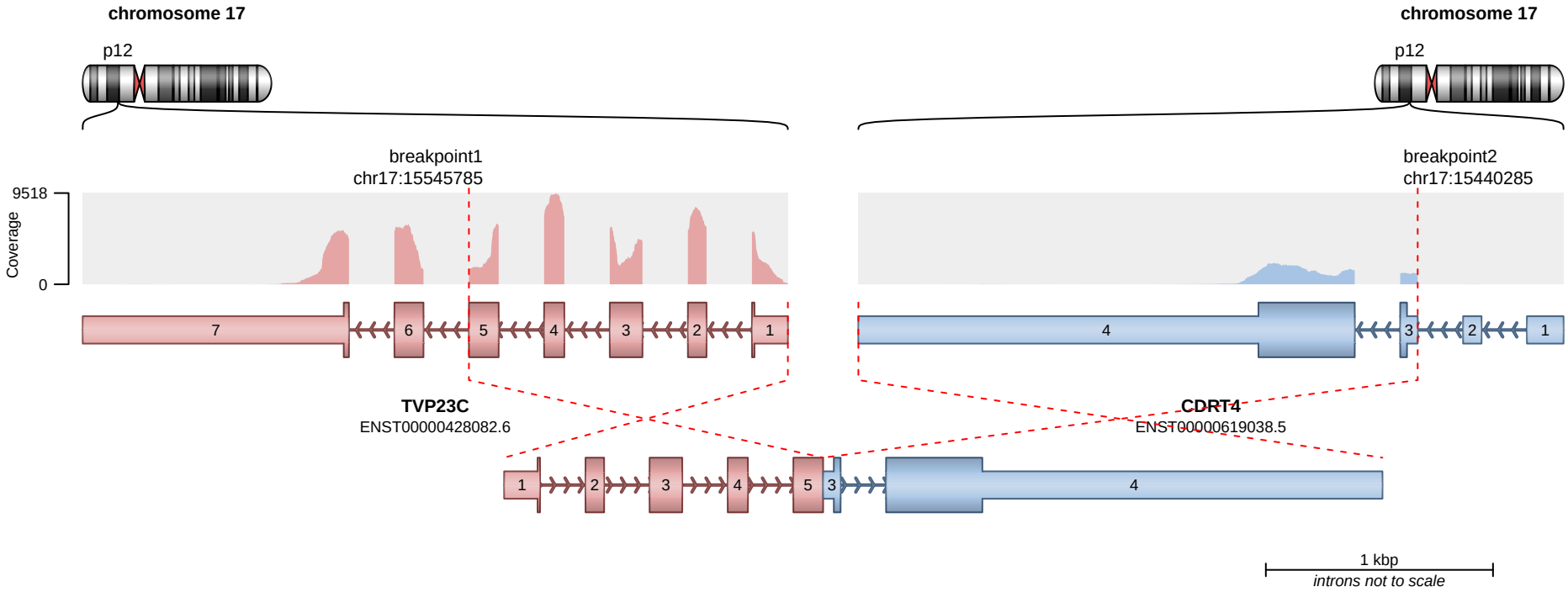
RETAINED PROTEIN DOMAINS
reading frame unclear

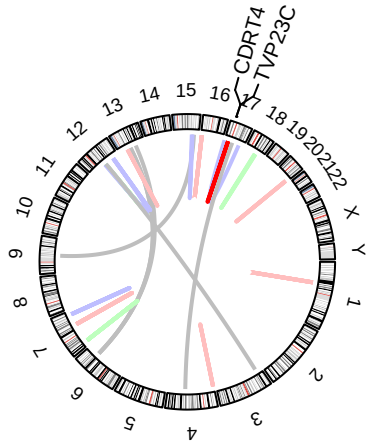


SUPPORTING READ COUNT

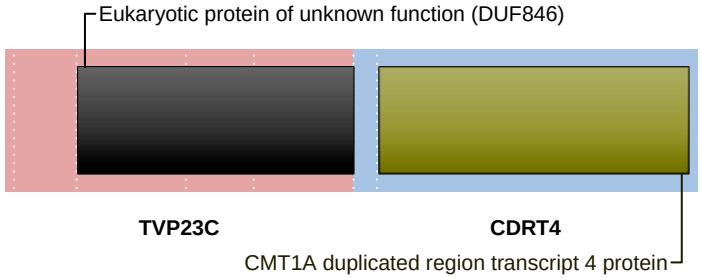
Split reads = 243
Discordant mates = 5

translocation
deletion
duplication
inversion





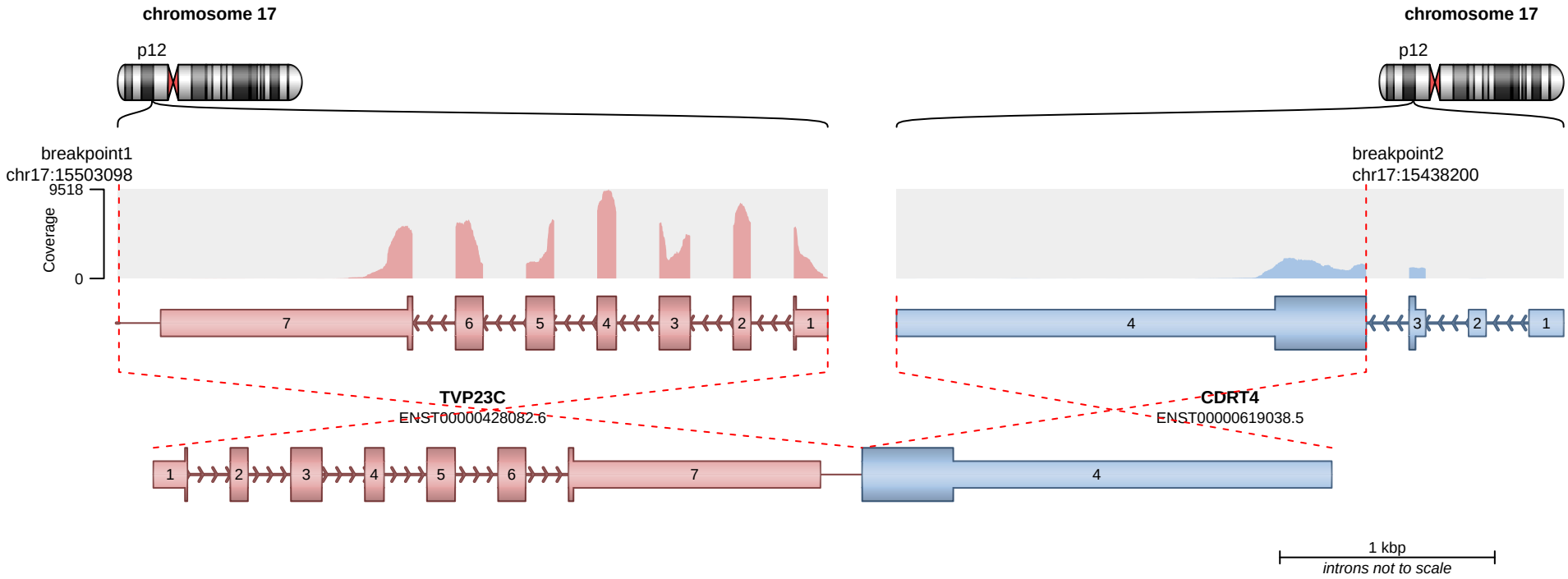
RETAINED PROTEIN DOMAINS
reading frame unclear

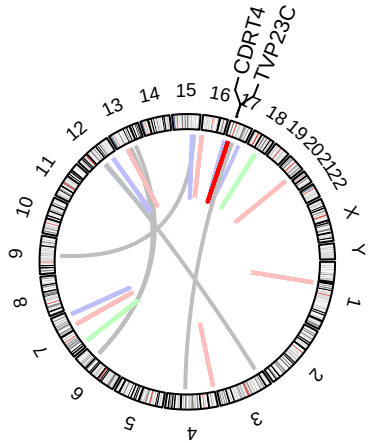


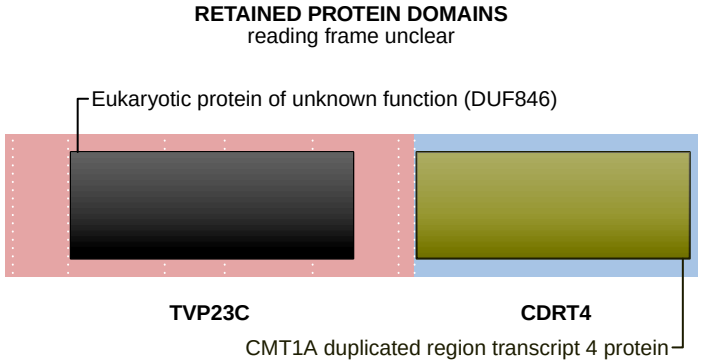
SUPPORTING READ COUNT

Split reads = 108
Discordant mates = 1

translocation
deletion
duplication
inversion



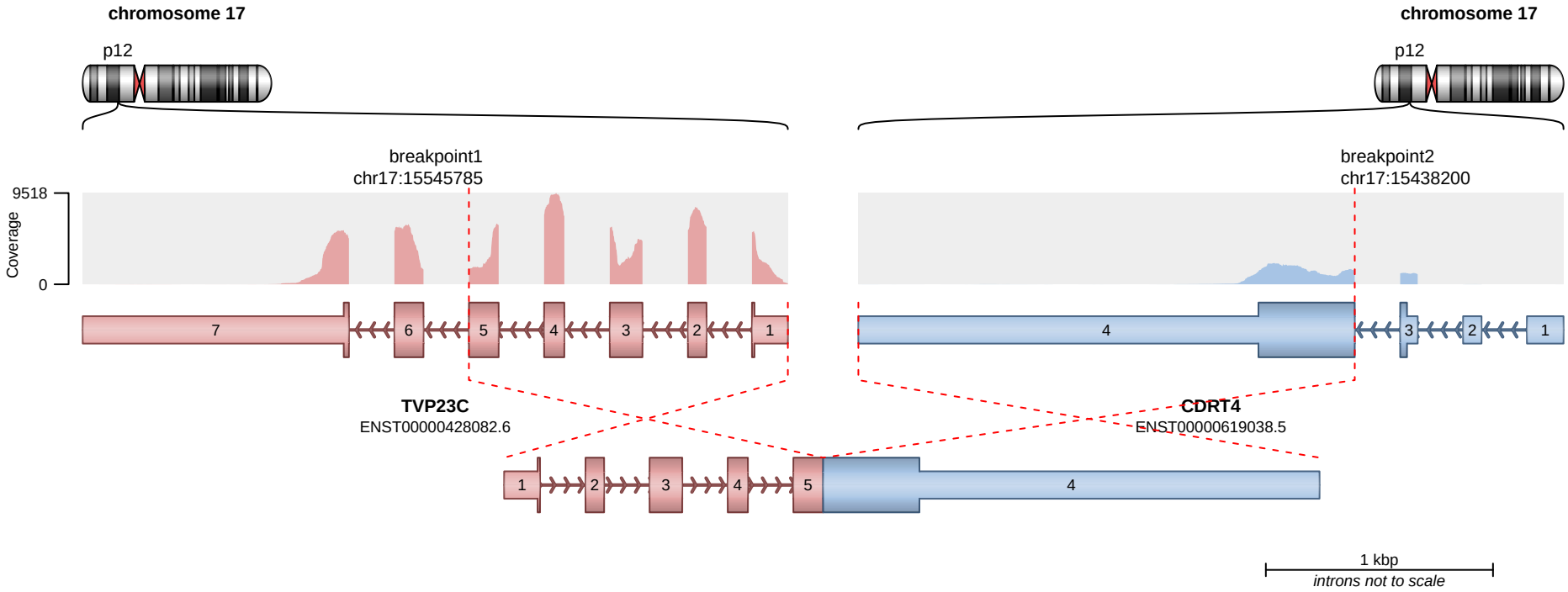


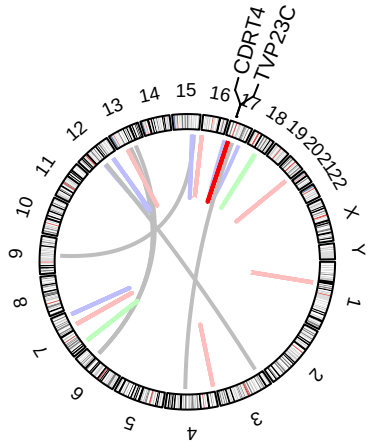


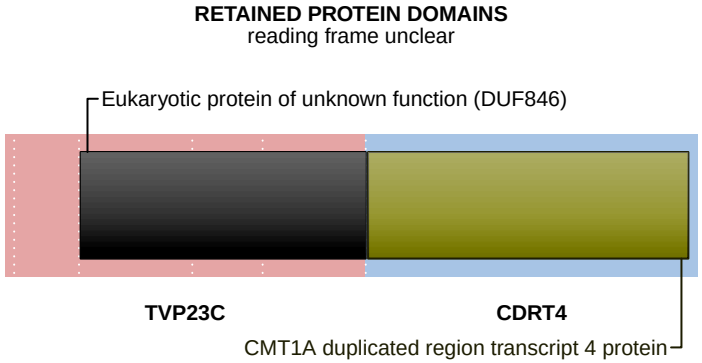
SUPPORTING READ COUNT

Split reads = 50
Discordant mates = 1

translocation
deletion
duplication
inversion



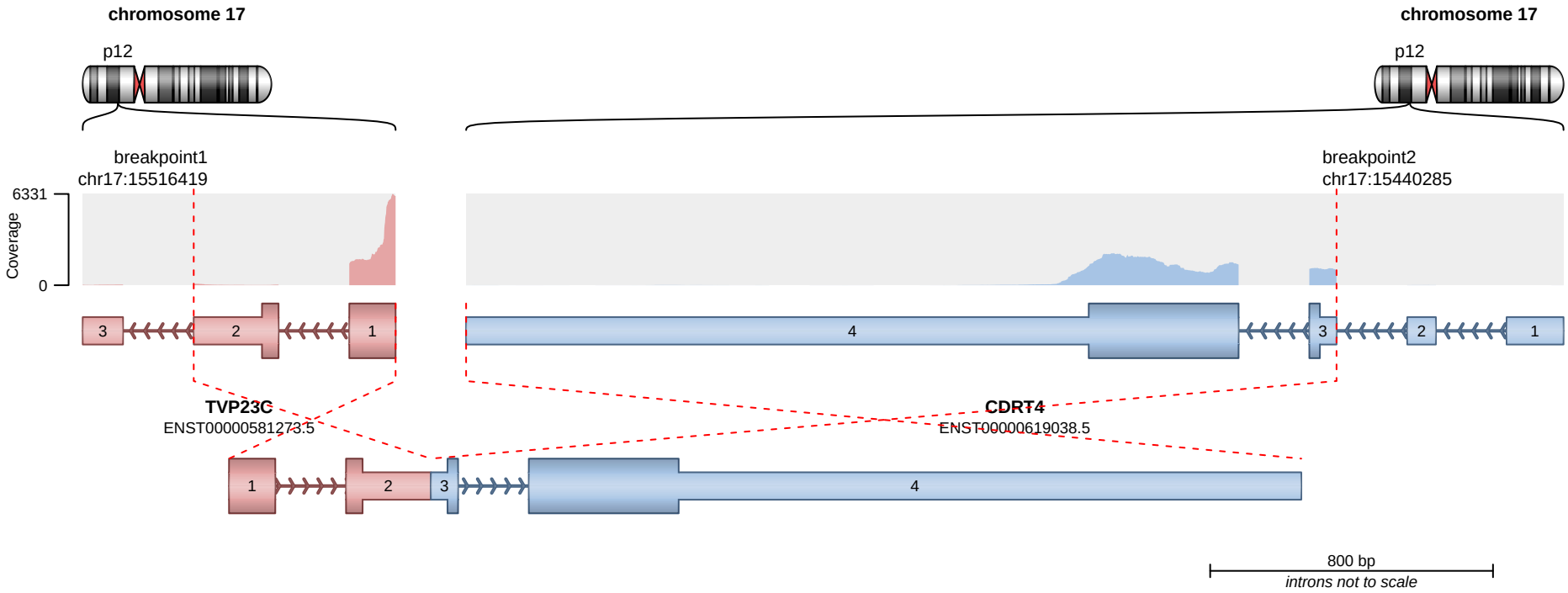


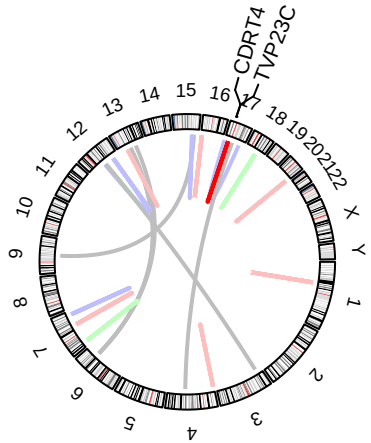


SUPPORTING READ COUNT

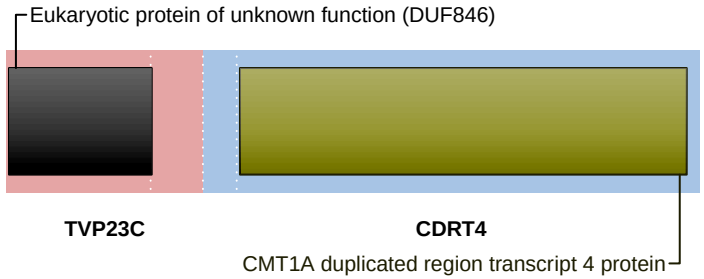
Split reads = 22
Discordant mates = 0

translocation
deletion
duplication
inversion





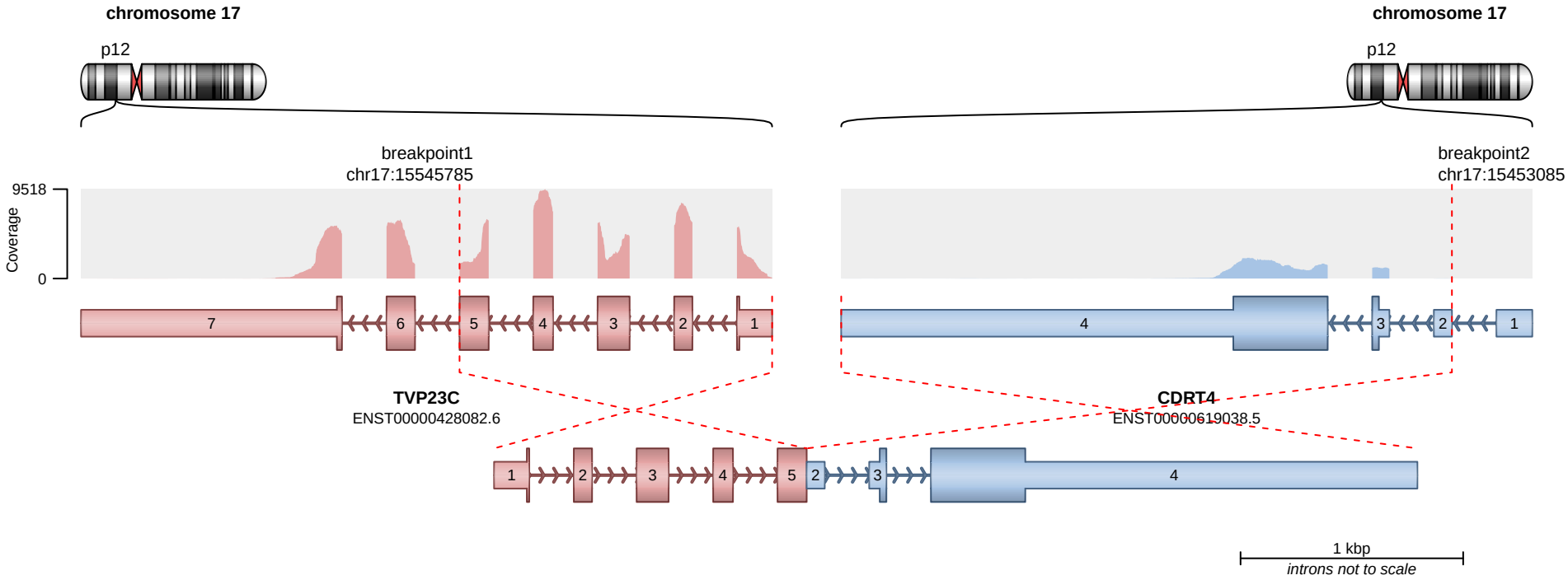
RETAINED PROTEIN DOMAINS
reading frame unclear

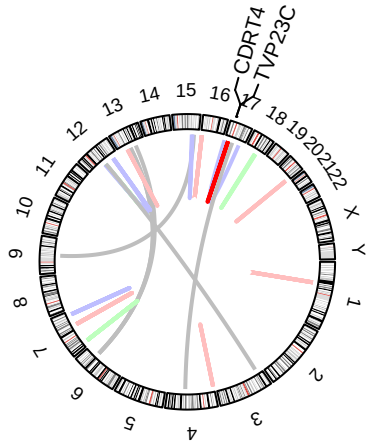


SUPPORTING READ COUNT

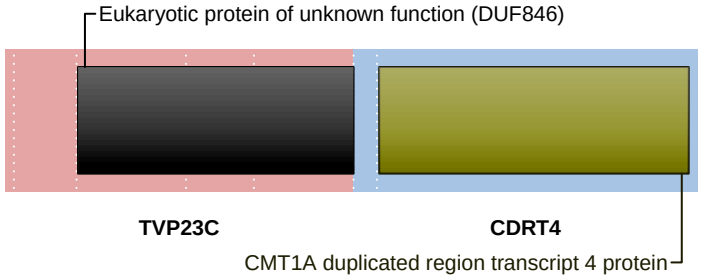
Split reads = 17
Discordant mates = 1

translocation
deletion
duplication
inversion





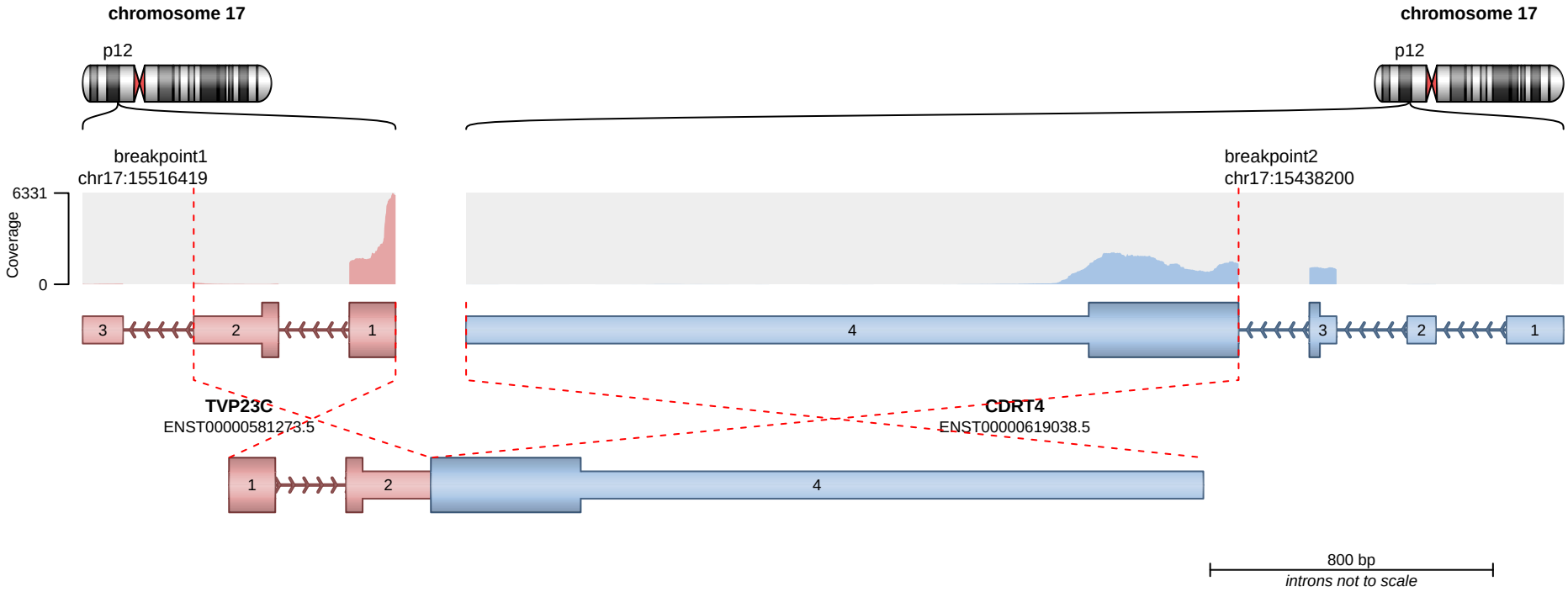
RETAINED PROTEIN DOMAINS
reading frame unclear

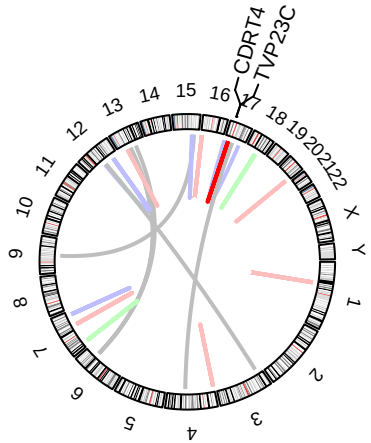


SUPPORTING READ COUNT

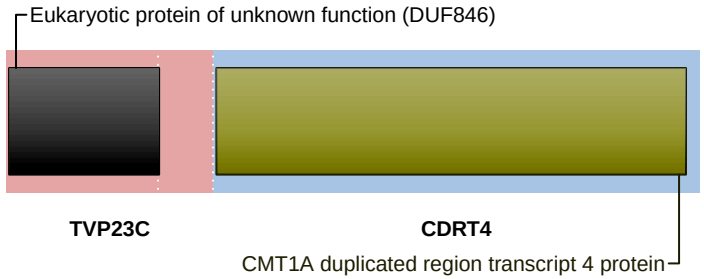
Split reads = 4
Discordant mates = 1

translocation
deletion
duplication
inversion





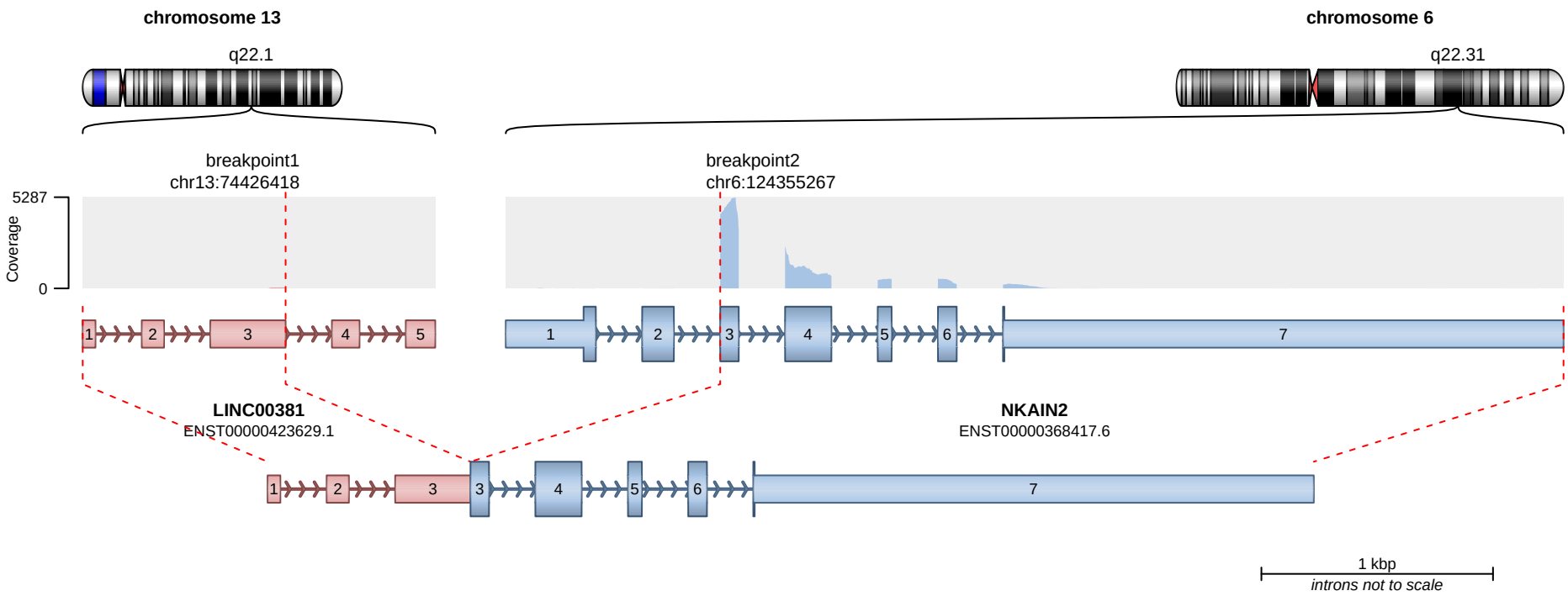
RETAINED PROTEIN DOMAINS
reading frame unclear

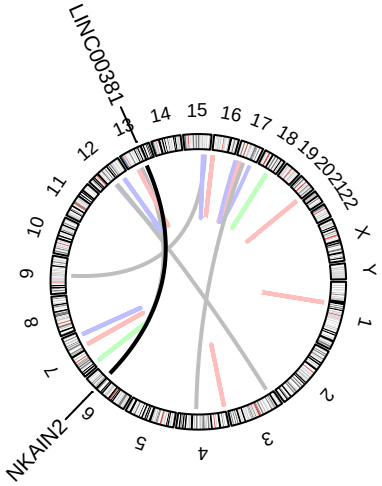


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

translocation
deletion
duplication
inversion



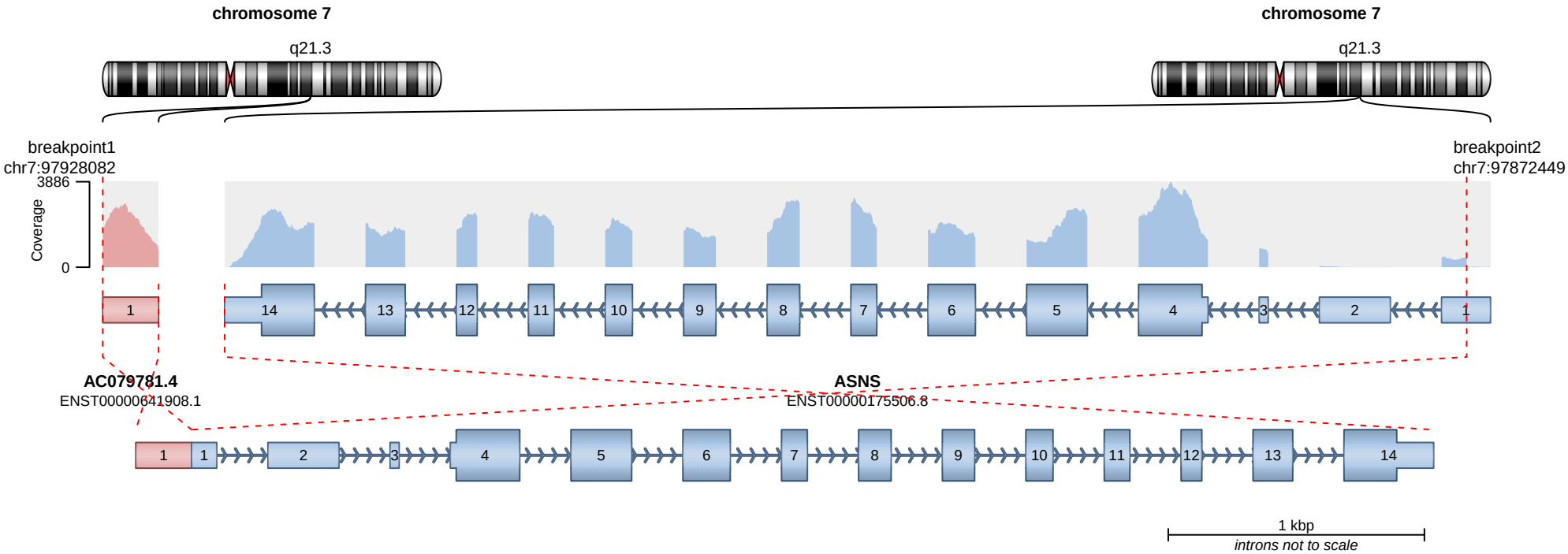


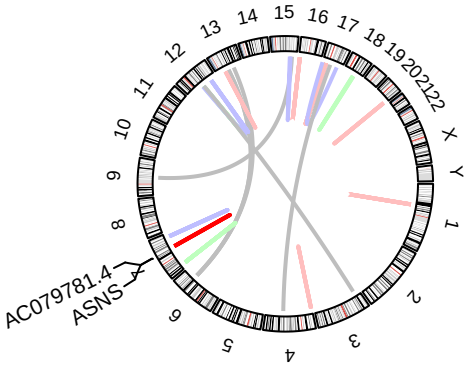
RETAINED PROTEIN DOMAINS
reading frame unclear

SUPPORTING READ COUNT

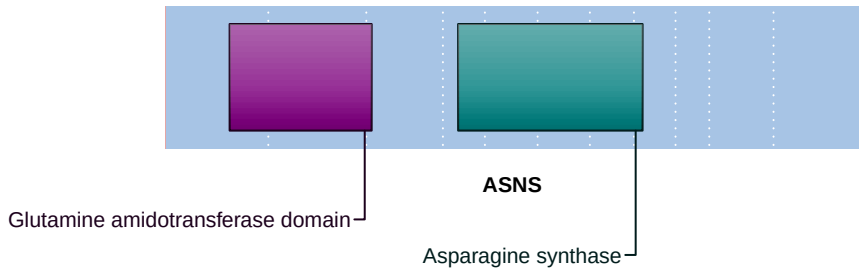
Split reads = 229
Discordant mates = 0

translocation
deletion
duplication
inversion





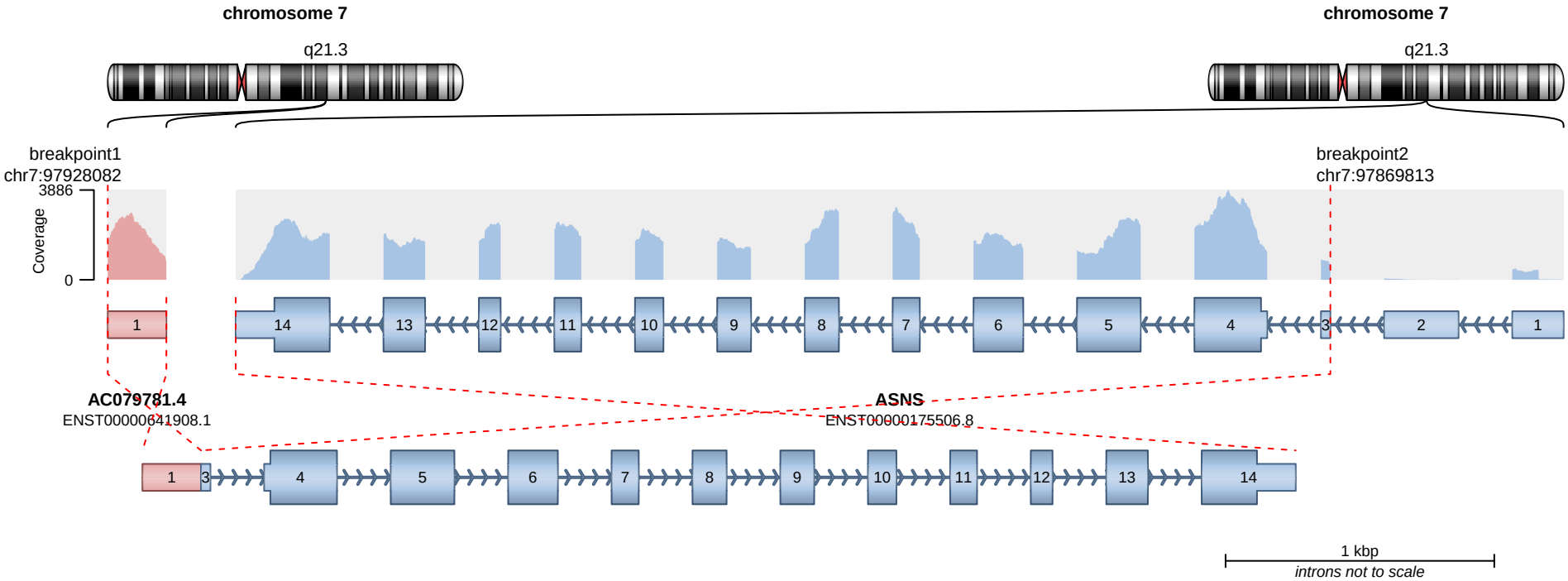
RETAINED PROTEIN DOMAINS
reading frame unclear

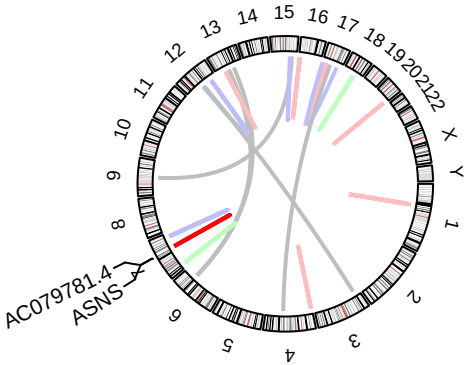


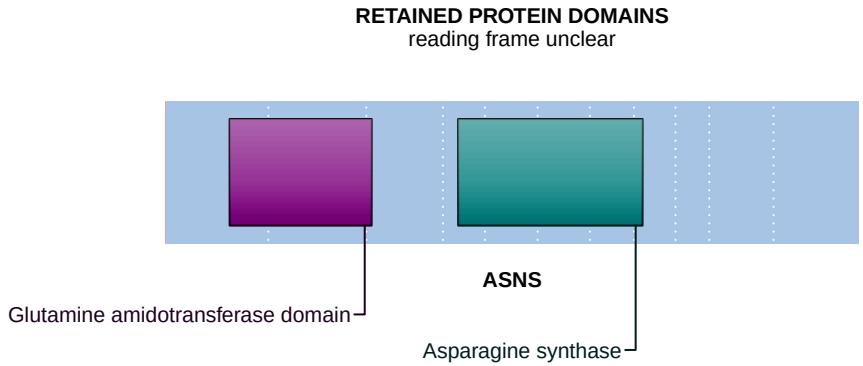
SUPPORTING READ COUNT

Split reads = 172
Discordant mates = 2

translocation
deletion
duplication
inversion



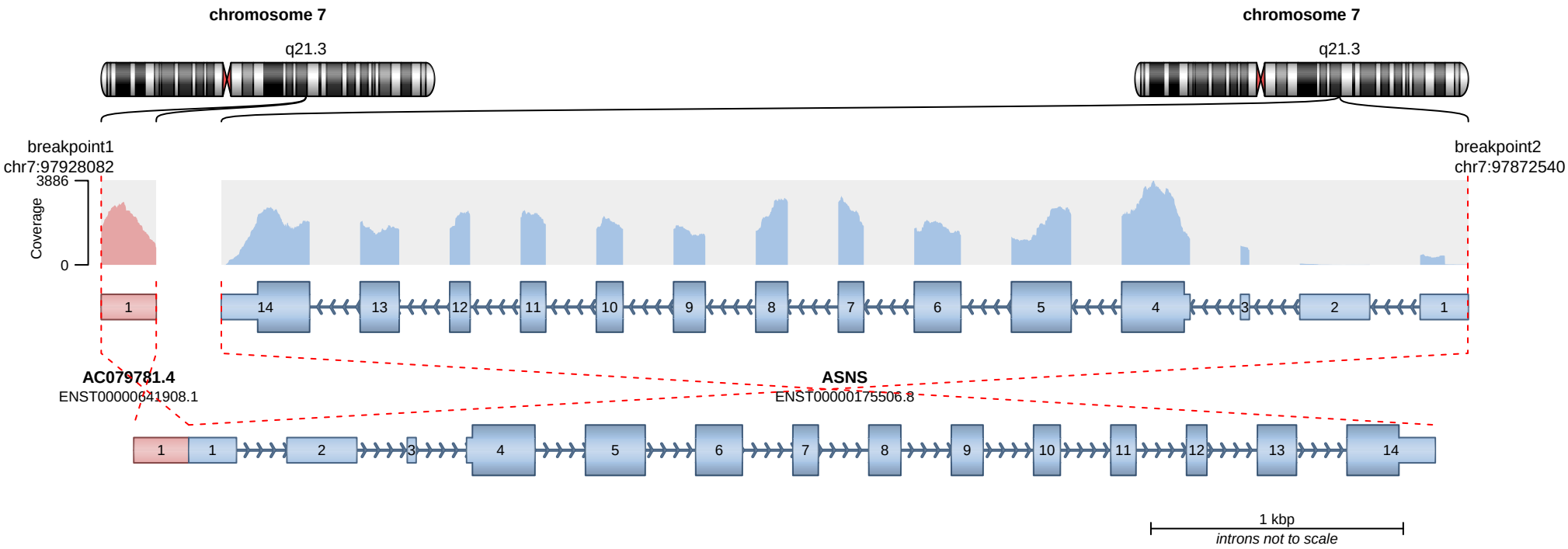


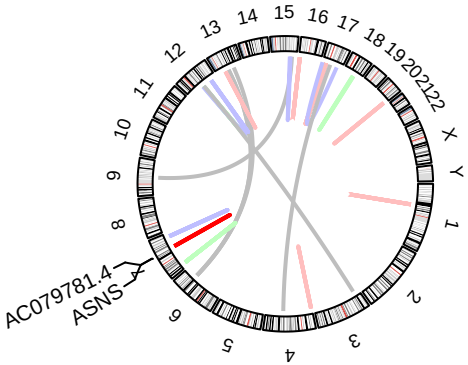


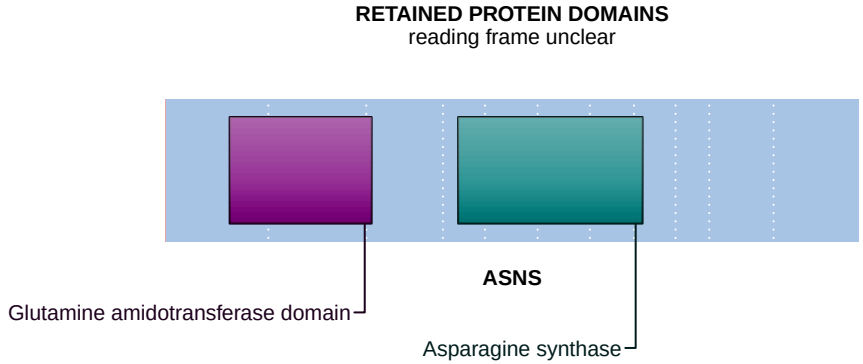
SUPPORTING READ COUNT

Split reads = 63
Discordant mates = 1

translocation
deletion
duplication
inversion



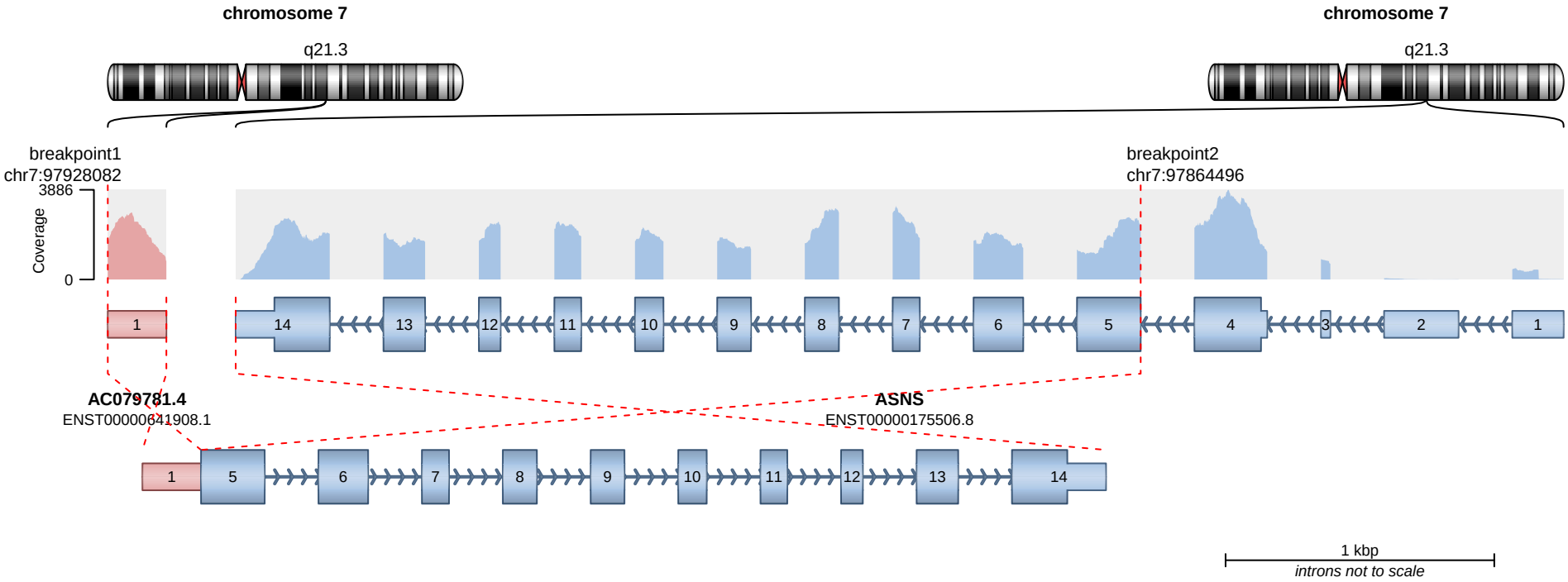


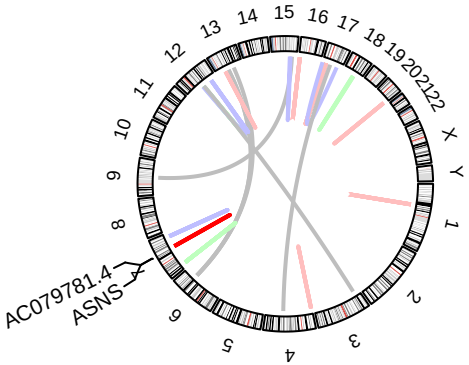


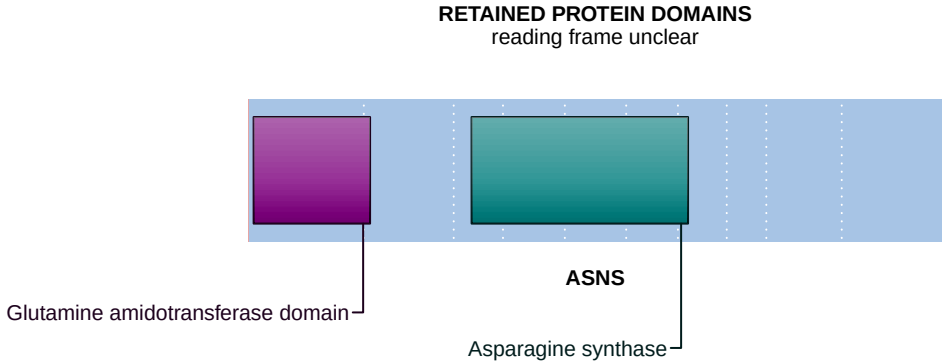
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 2

translocation
deletion
duplication
inversion



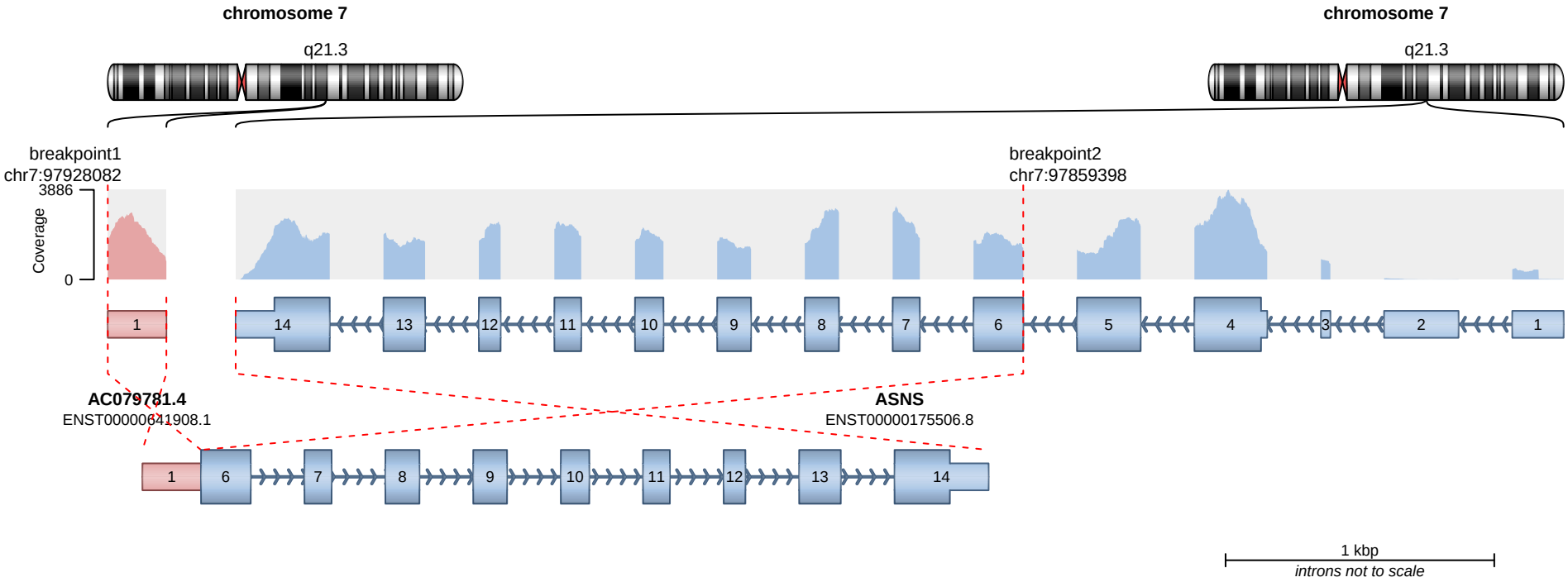


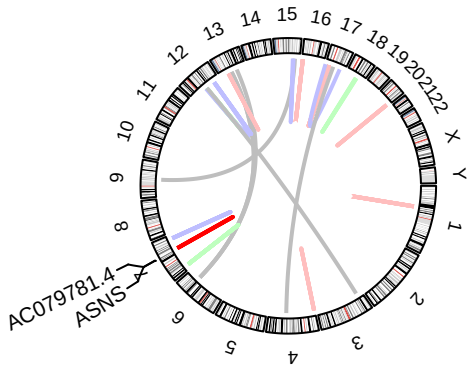


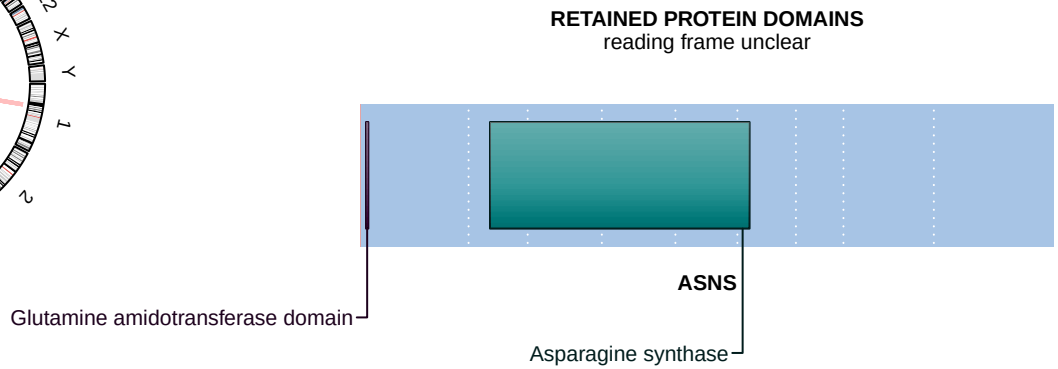
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

translocation
deletion
duplication
inversion



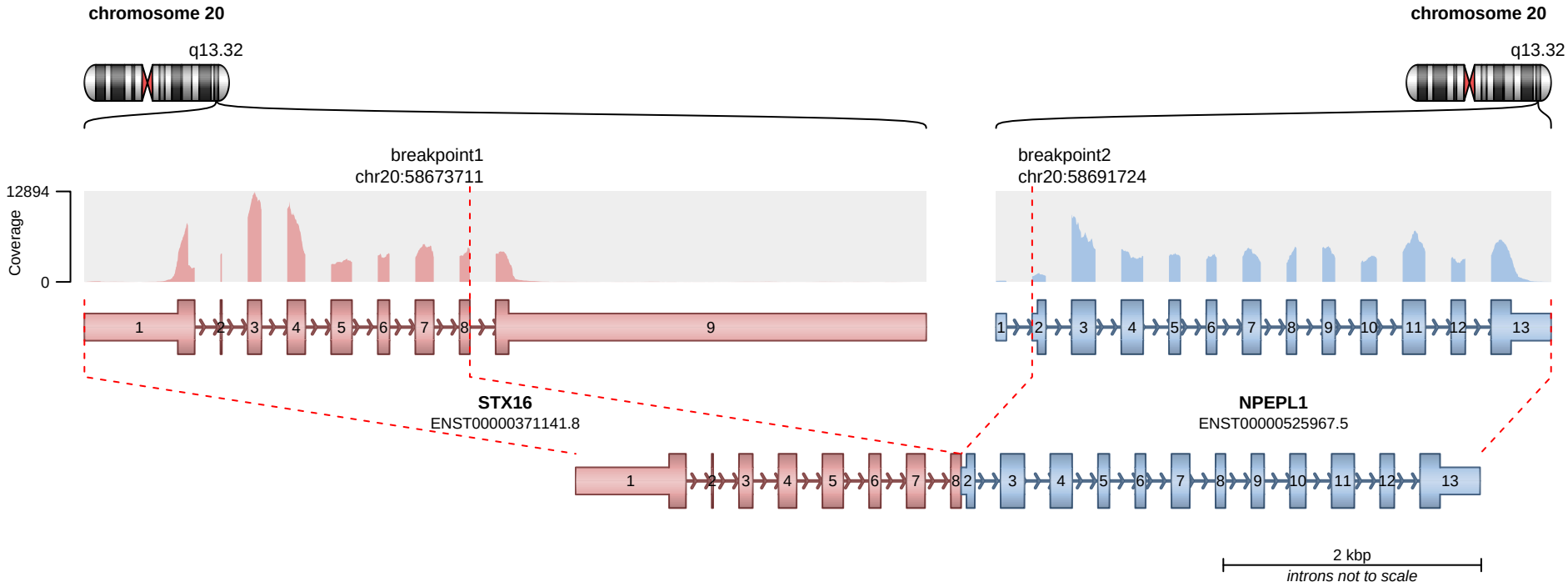


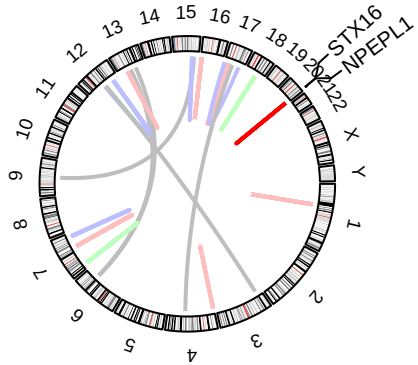


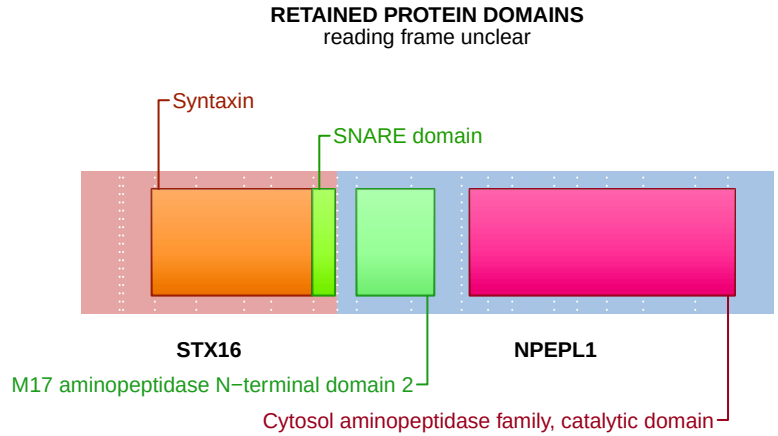
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

translocation
deletion
duplication
inversion



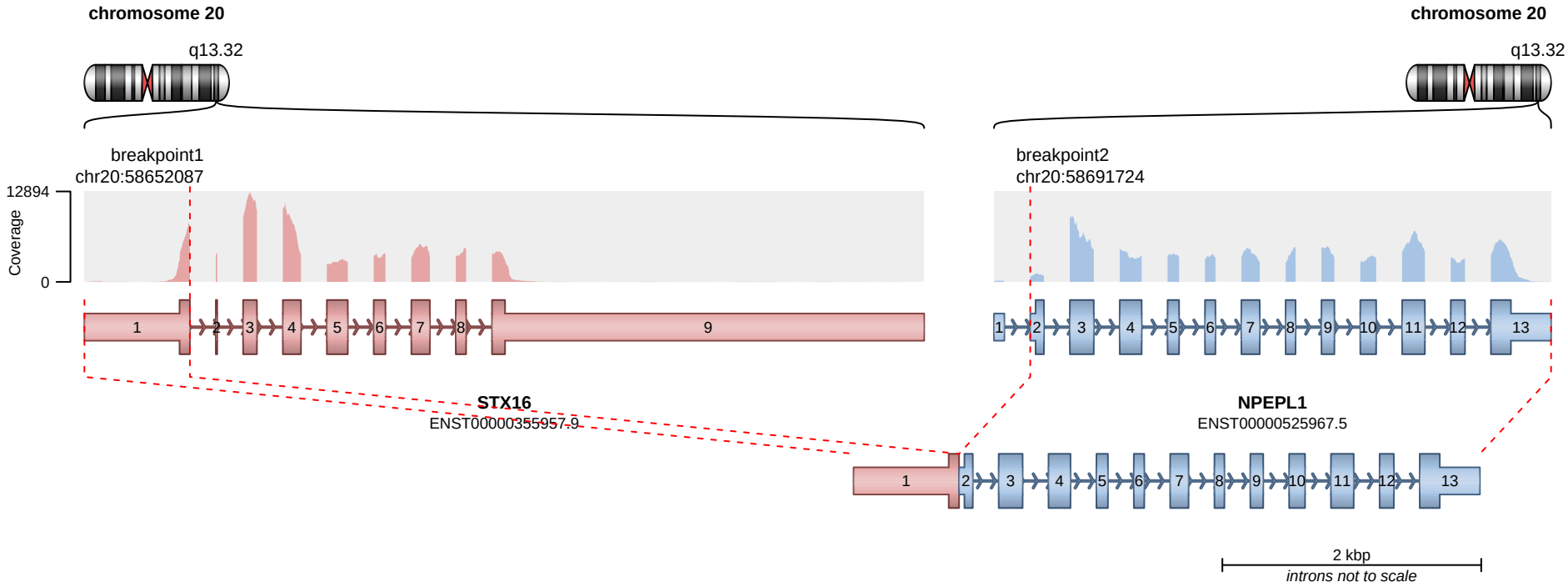


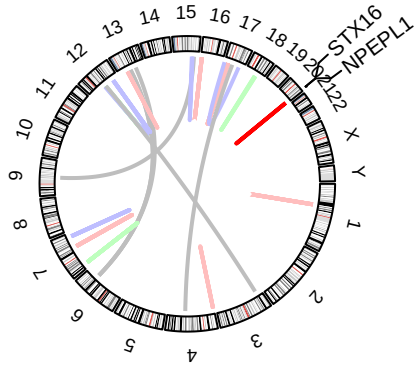


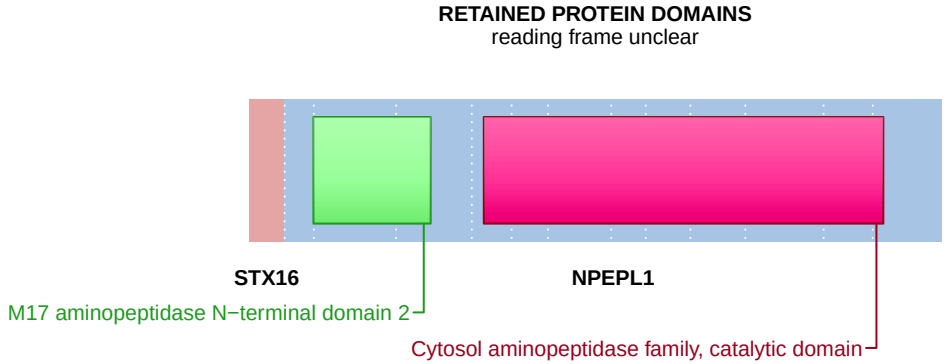
SUPPORTING READ COUNT

Split reads = 149
Discordant mates = 2

translocation
deletion
duplication
inversion



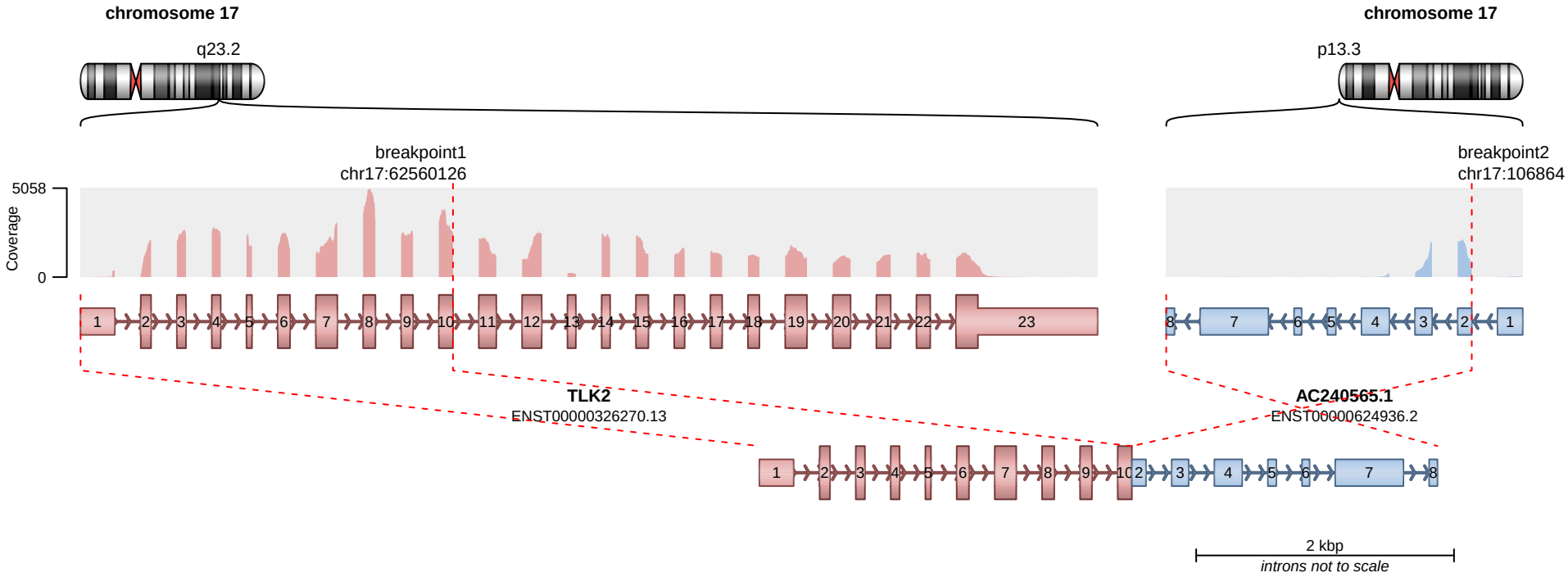


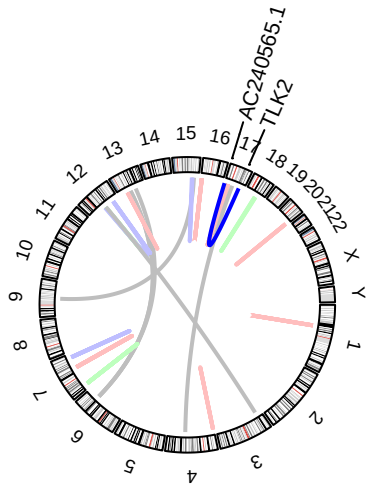


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

translocation
deletion
duplication
inversion



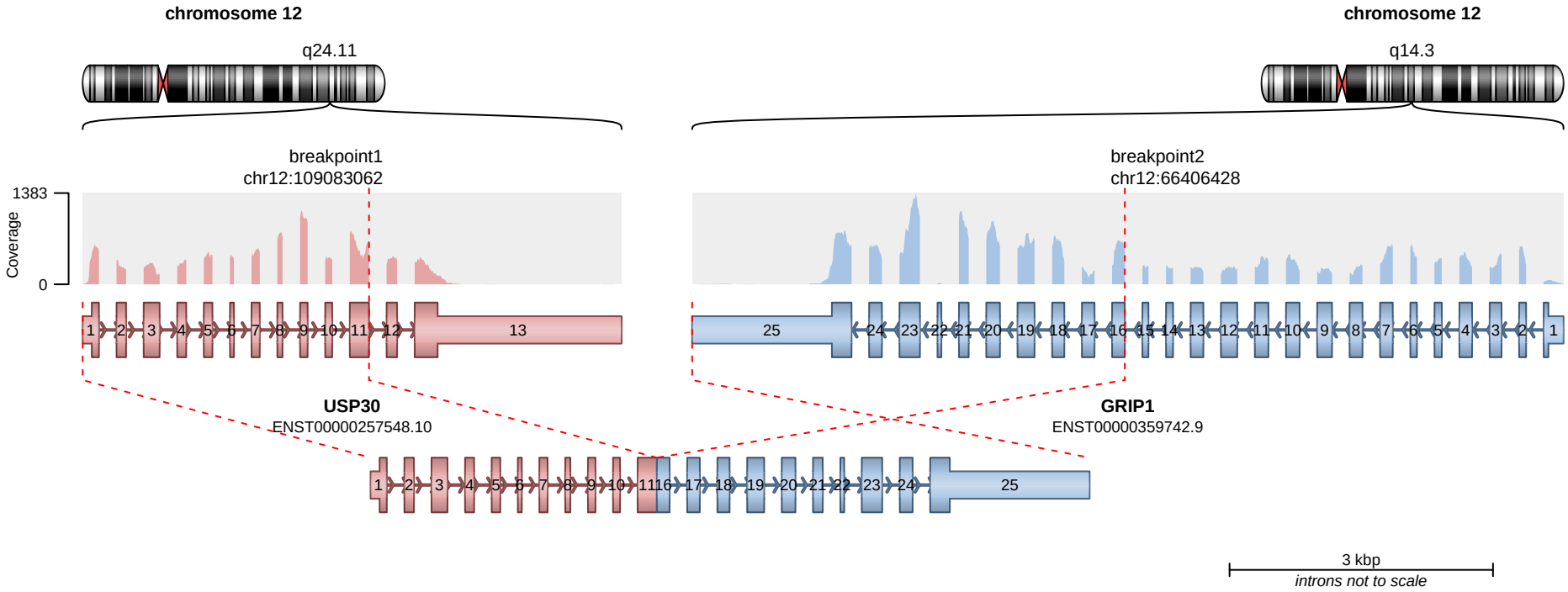


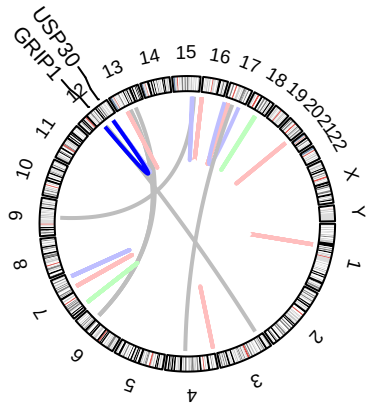
No protein domains retained in fusion.

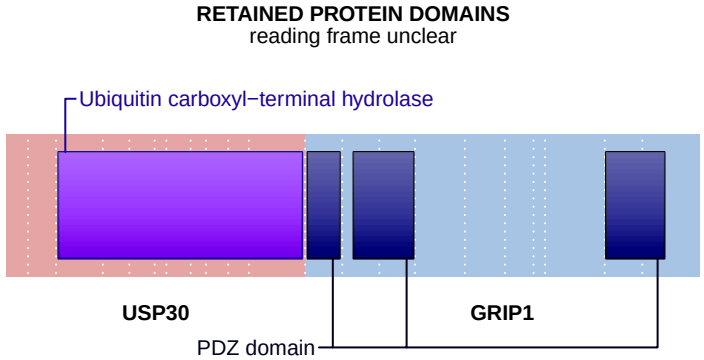
SUPPORTING READ COUNT

Split reads = 132
Discordant mates = 1

translocation
deletion
duplication
inversion



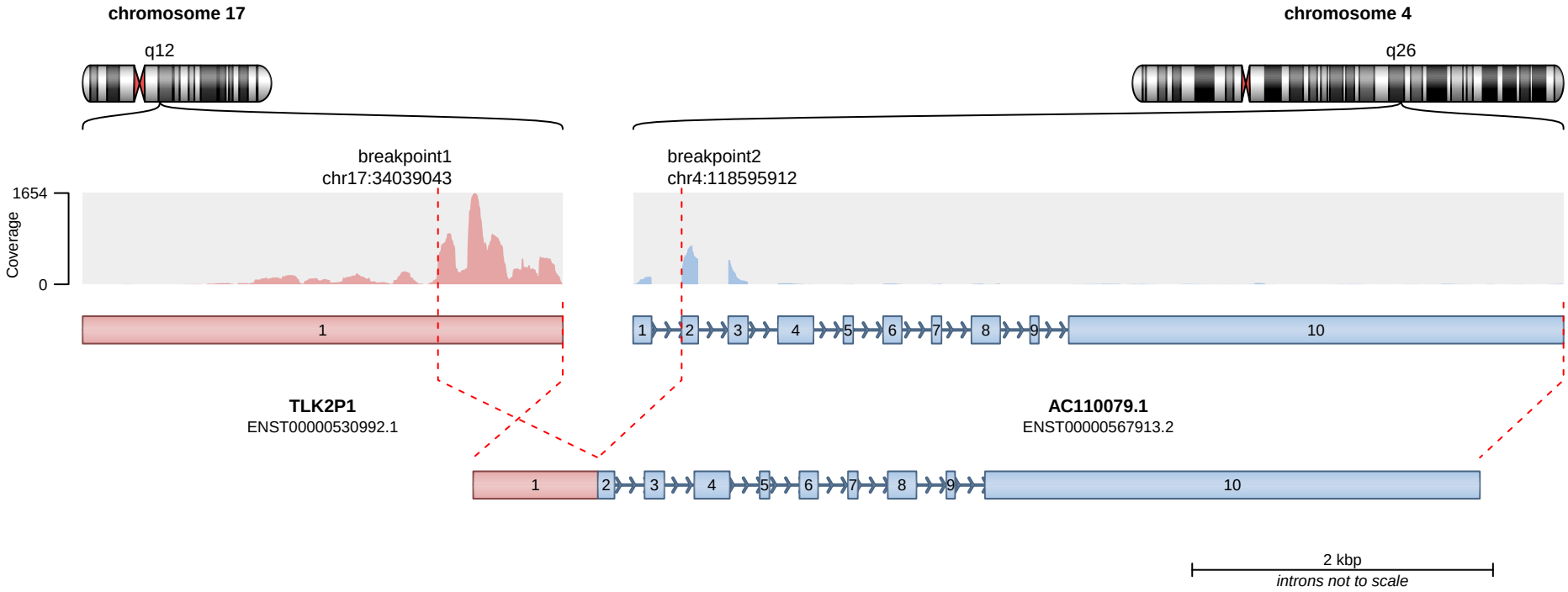


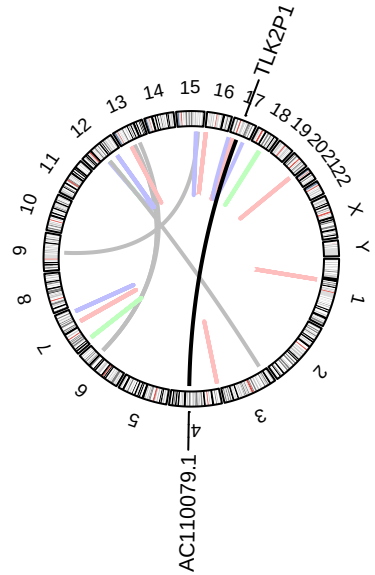


SUPPORTING READ COUNT

Split reads = 116
Discordant mates = 1

translocation
deletion
duplication
inversion



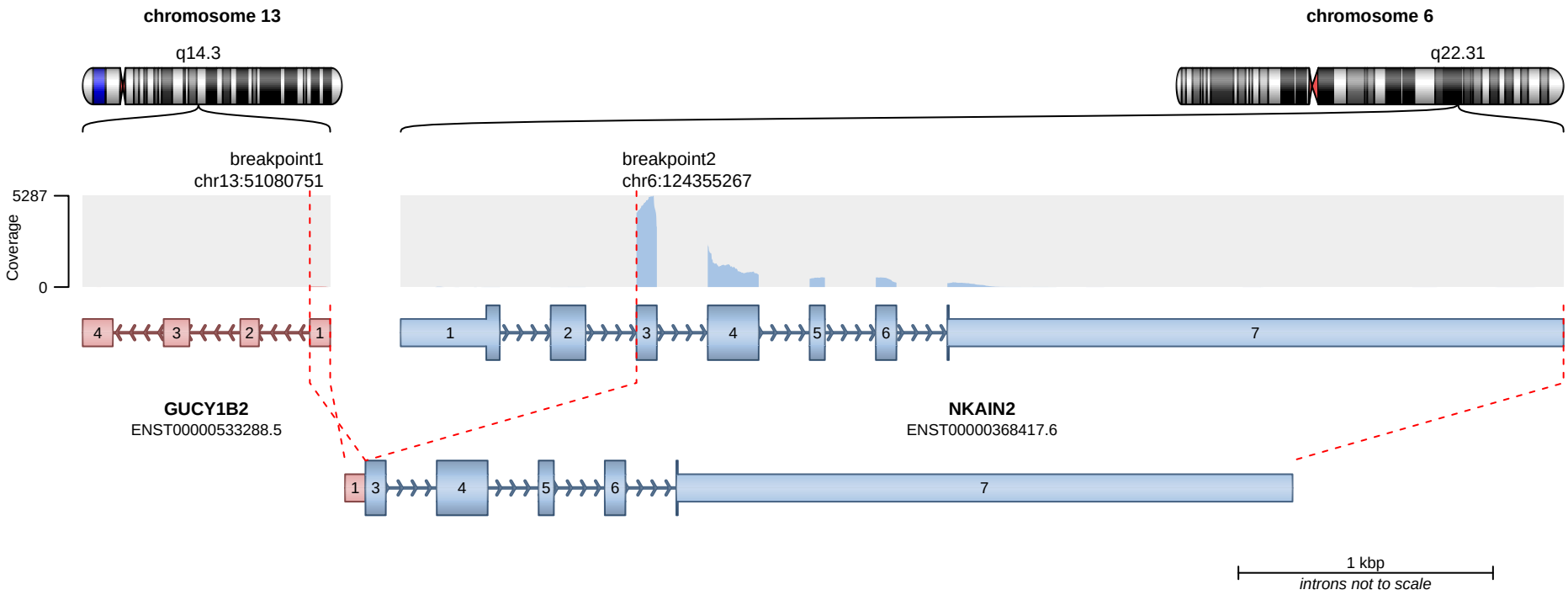


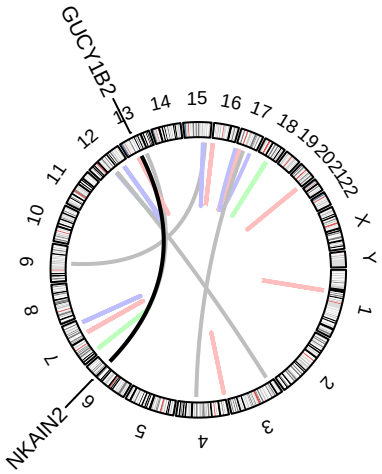
translocation
deletion
duplication
inversion

Genes are not protein−coding.

SUPPORTING READ COUNT

Split reads = 111
Discordant mates = 0





RETAINED PROTEIN DOMAINS
reading frame unclear

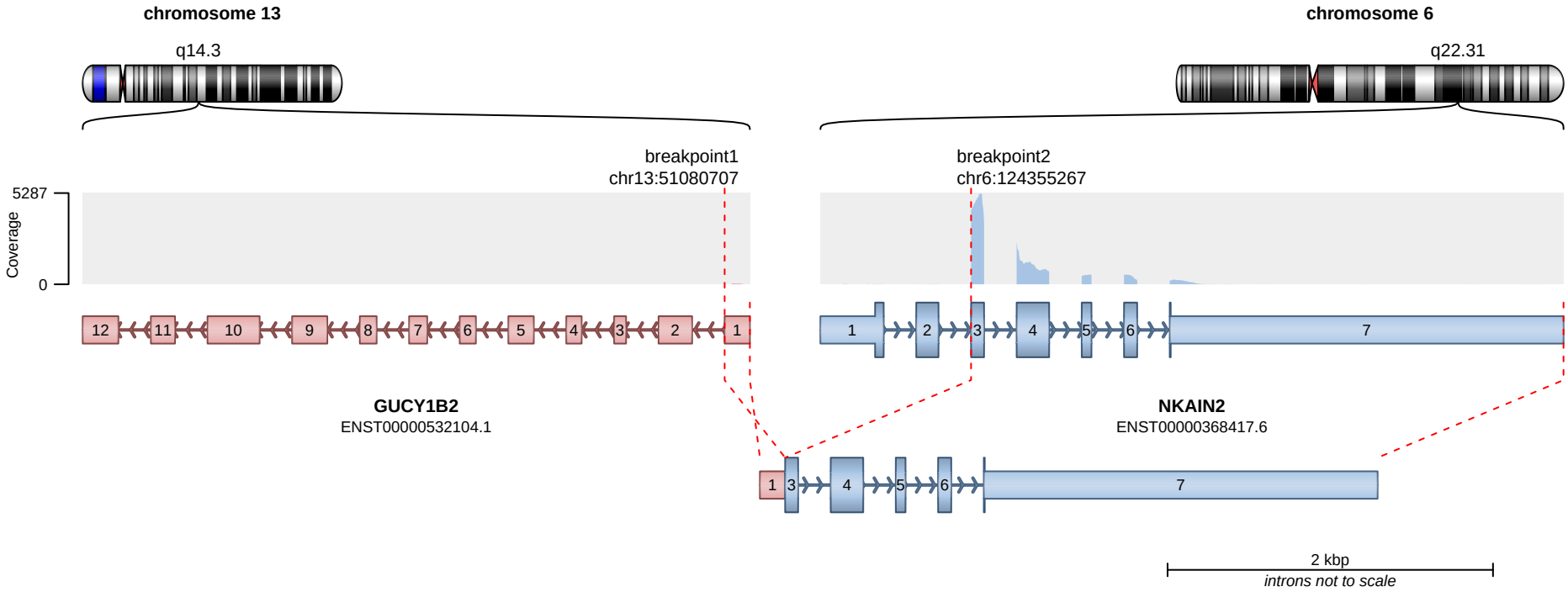
NKAIN2

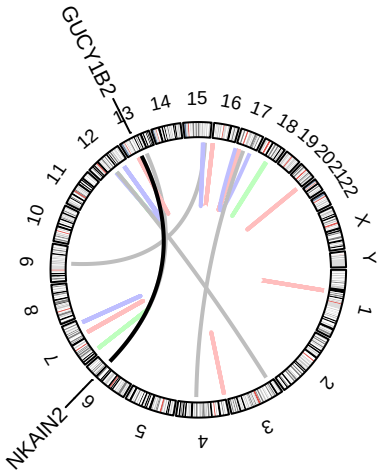
Na,K−Atpase Interacting protein

SUPPORTING READ COUNT

Split reads = 74
Discordant mates = 0

translocation
deletion
duplication
inversion



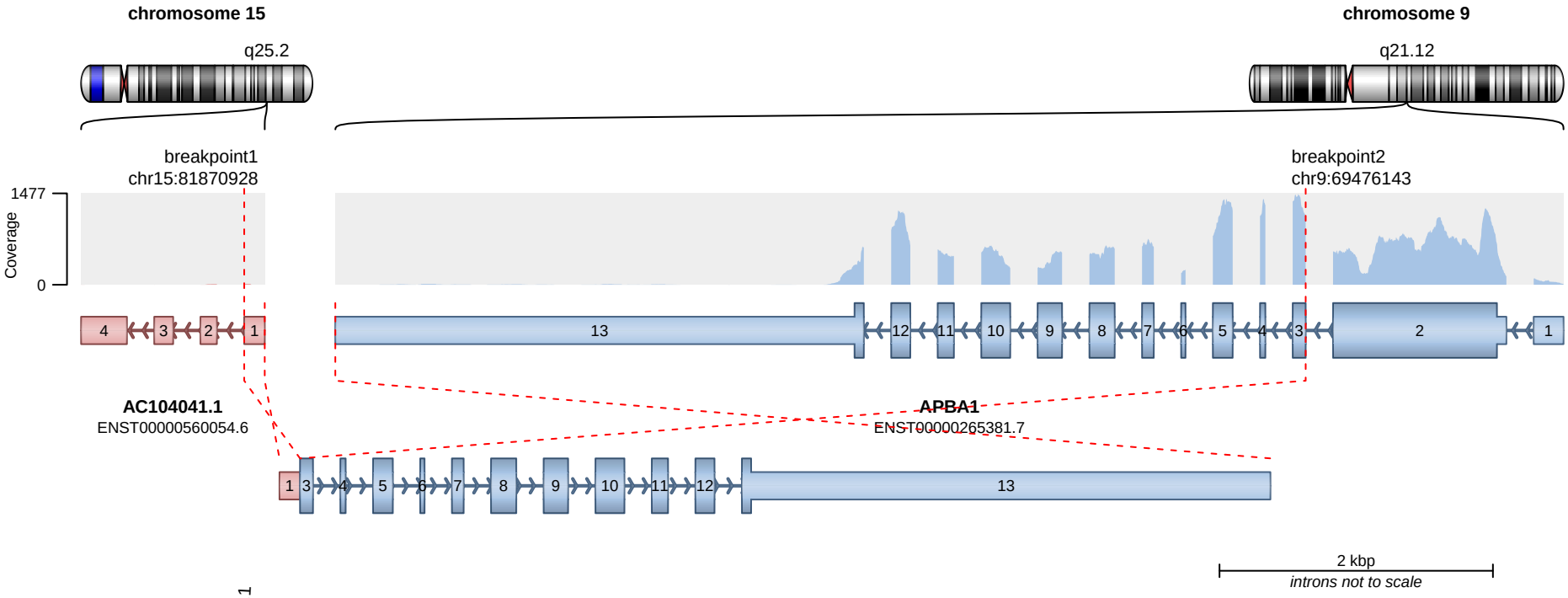


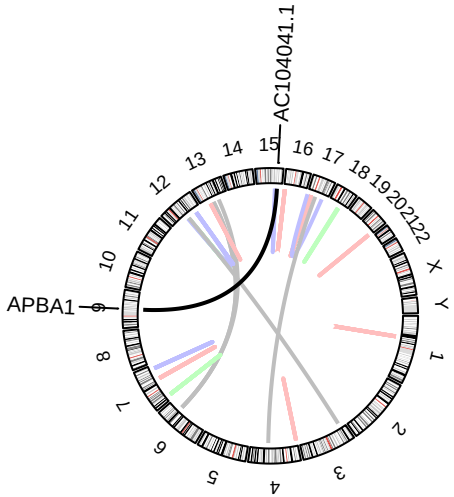
RETAINED PROTEIN DOMAINS
reading frame unclear

SUPPORTING READ COUNT

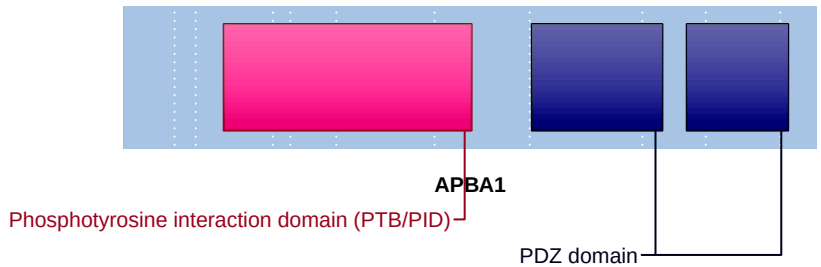
Split reads = 2
Discordant mates = 0

translocation
deletion
duplication
inversion





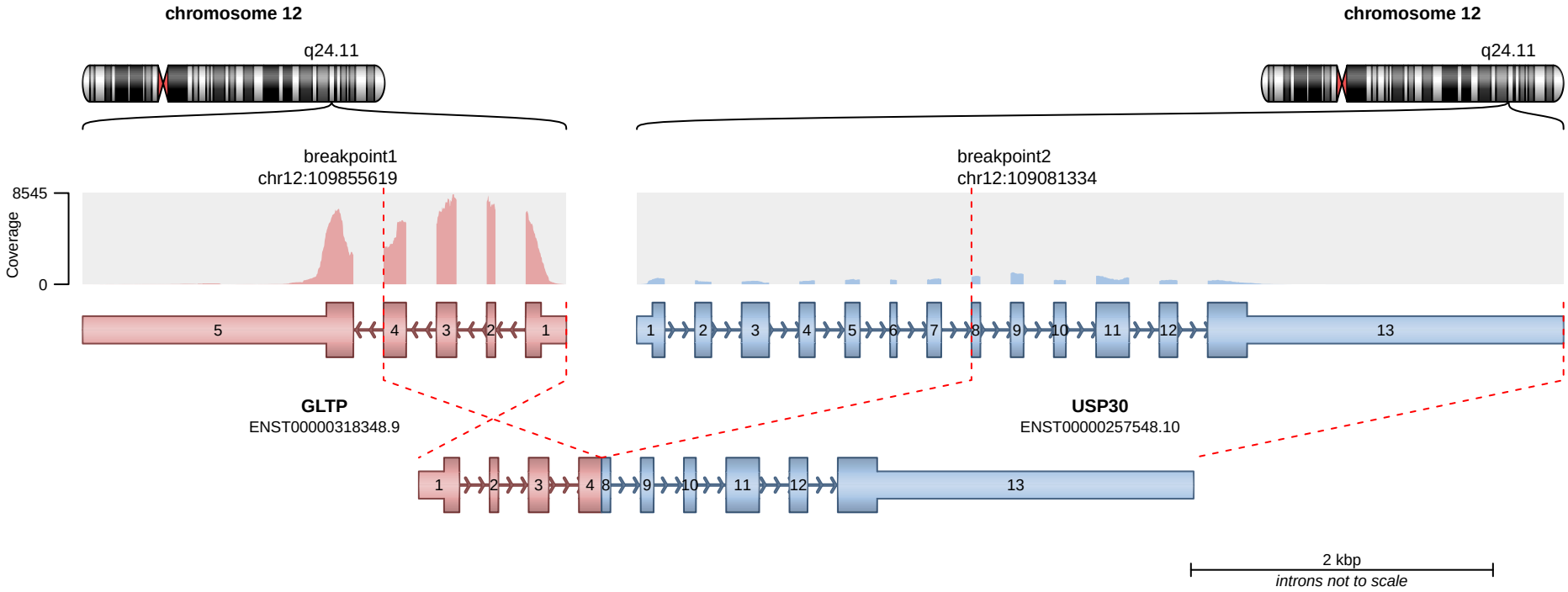
RETAINED PROTEIN DOMAINS
reading frame unclear

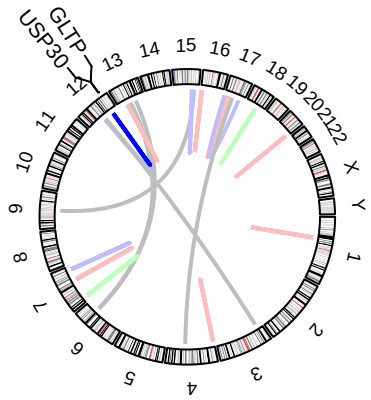


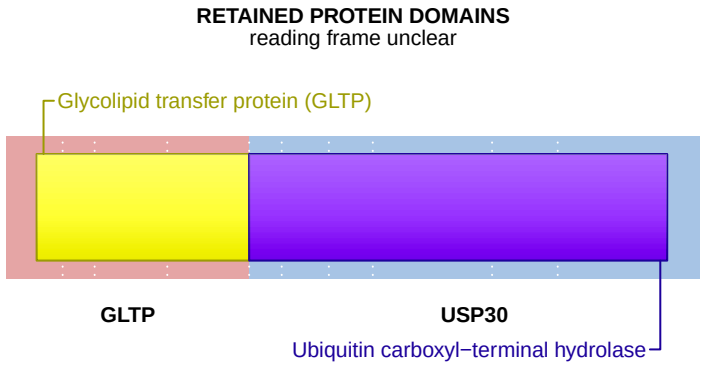
SUPPORTING READ COUNT

Split reads = 69
Discordant mates = 0

translocation
deletion
duplication
inversion



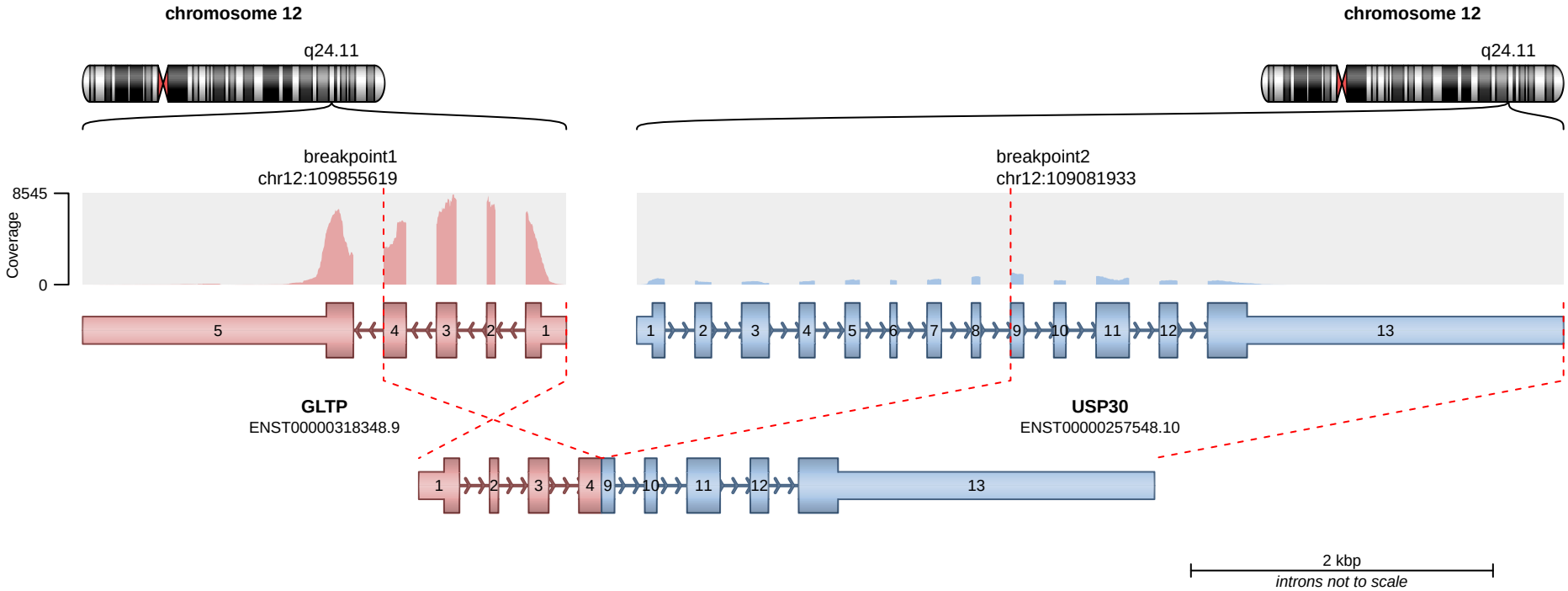


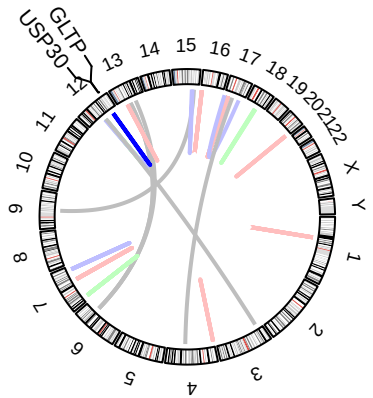


SUPPORTING READ COUNT

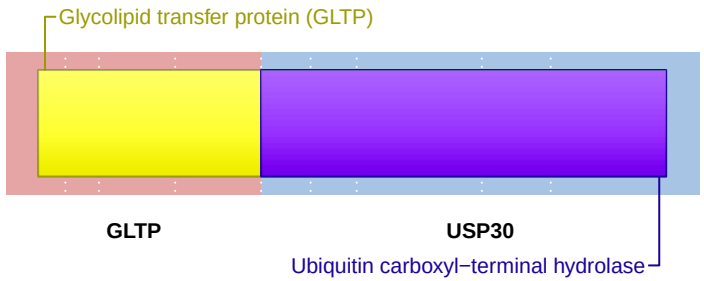
Split reads = 50
Discordant mates = 0

translocation
deletion
duplication
inversion



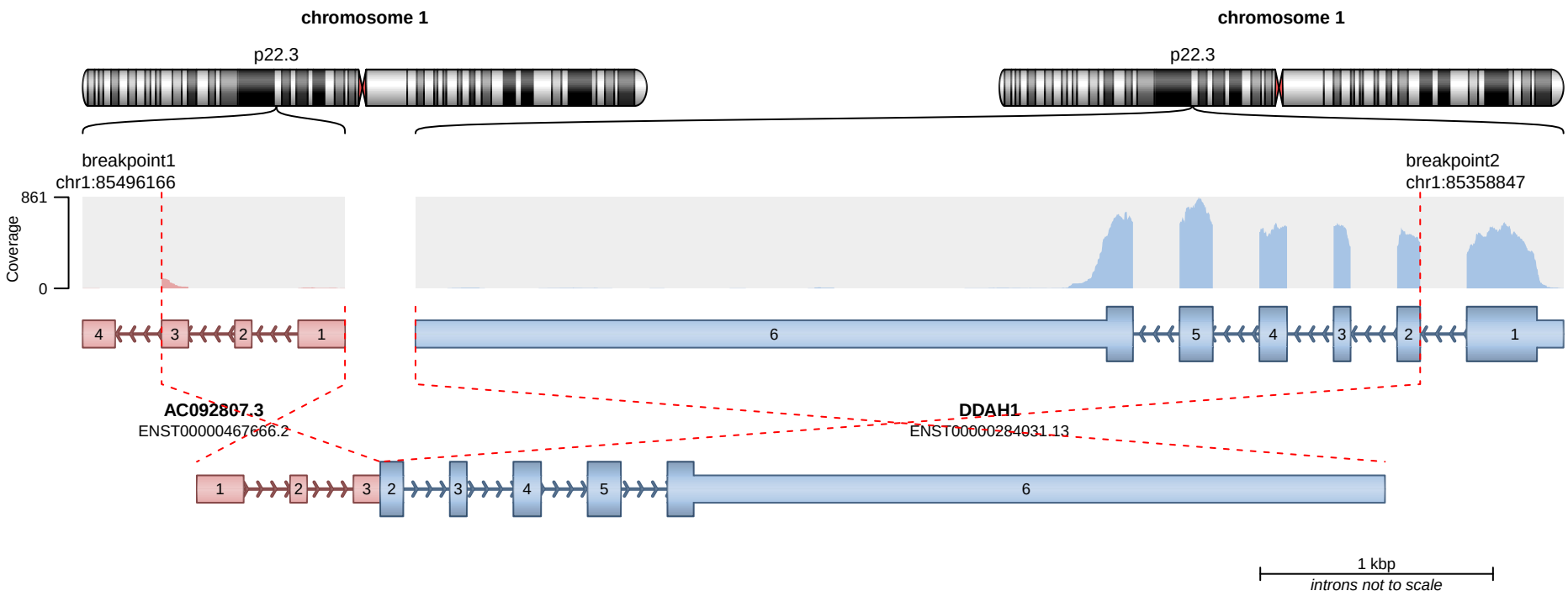


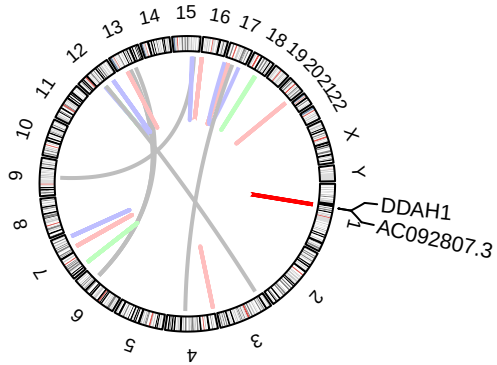
RETAINED PROTEIN DOMAINS
reading frame unclear



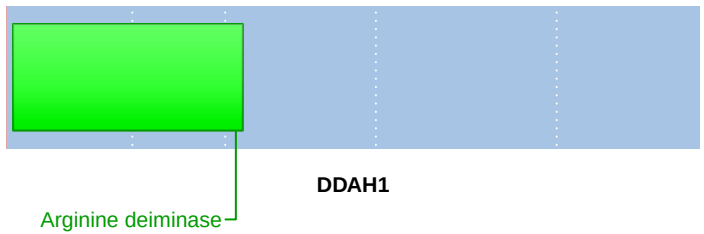
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0





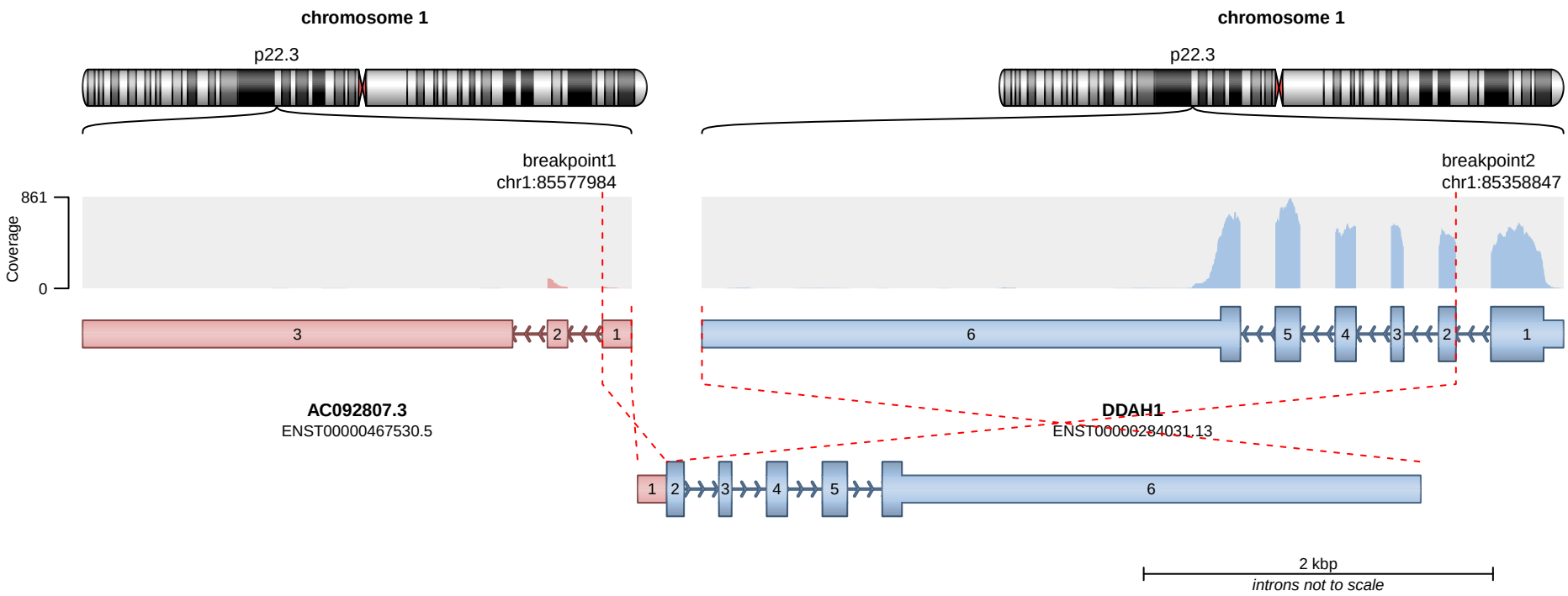
RETAINED PROTEIN DOMAINS
reading frame unclear

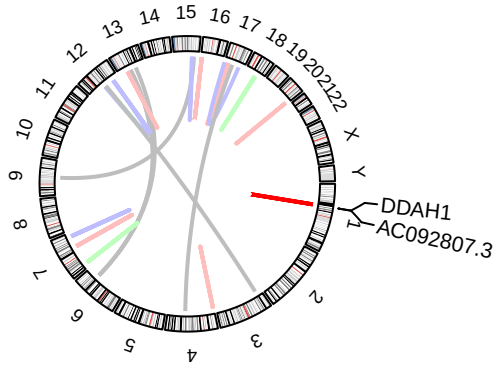


SUPPORTING READ COUNT

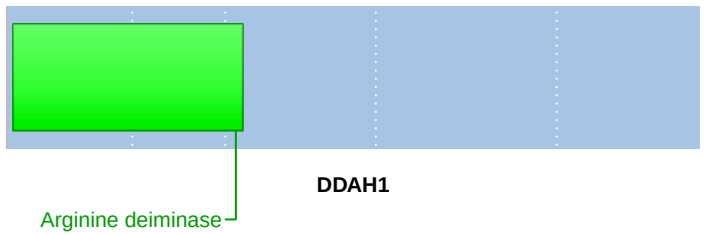
Split reads = 43
Discordant mates = 1

translocation
deletion
duplication
inversion





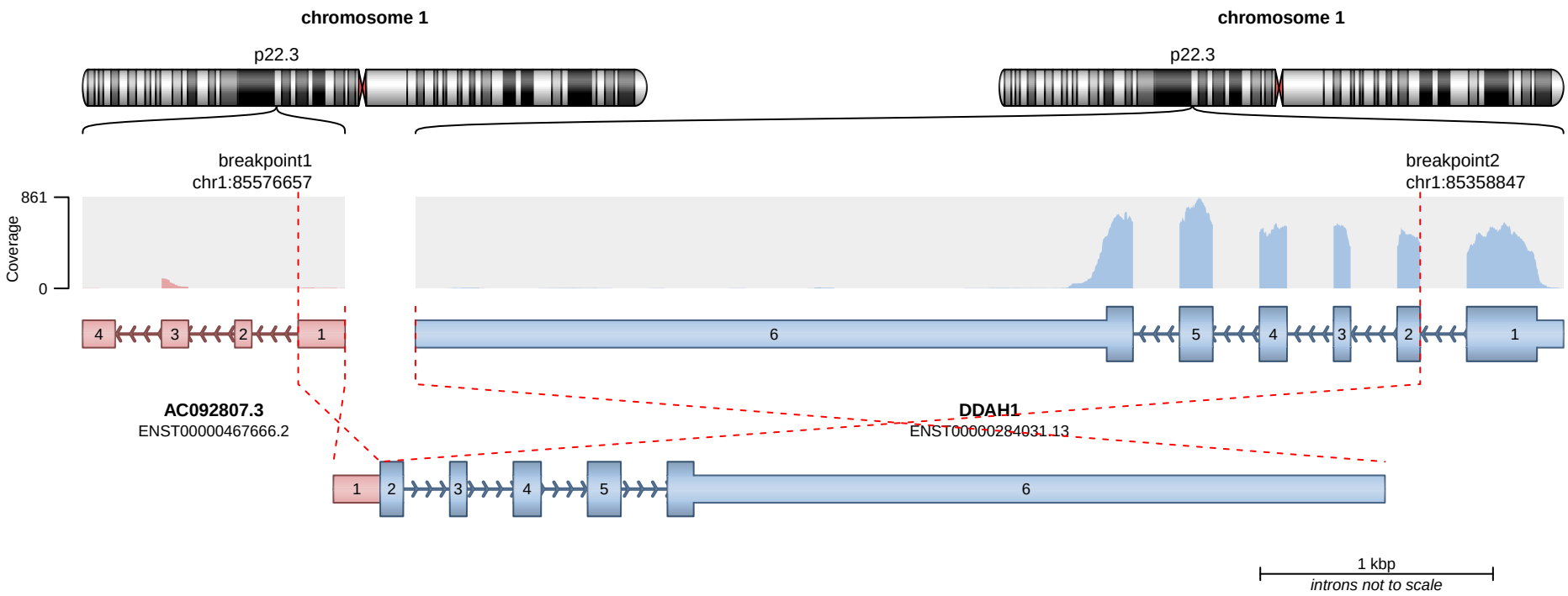
RETAINED PROTEIN DOMAINS
reading frame unclear

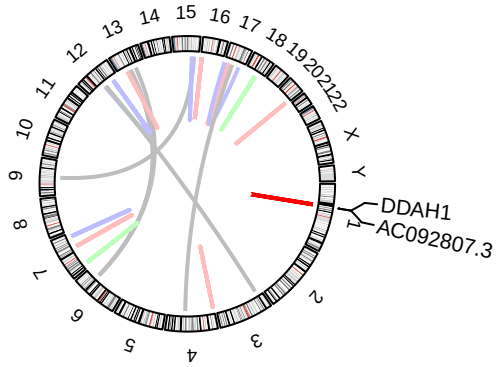


SUPPORTING READ COUNT

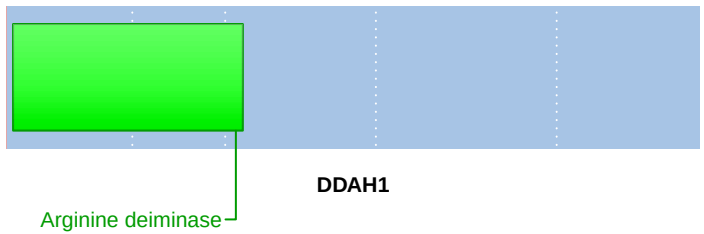
Split reads = 4
Discordant mates = 0

translocation
deletion
duplication
inversion





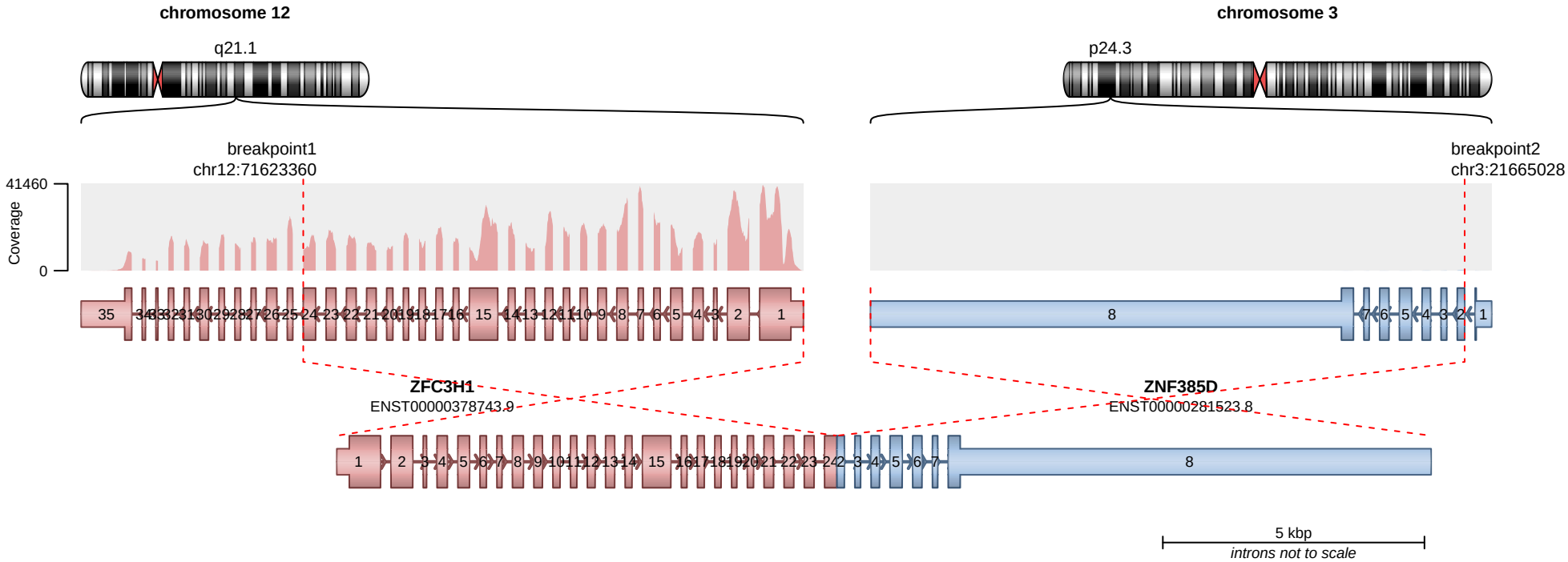
RETAINED PROTEIN DOMAINS
reading frame unclear

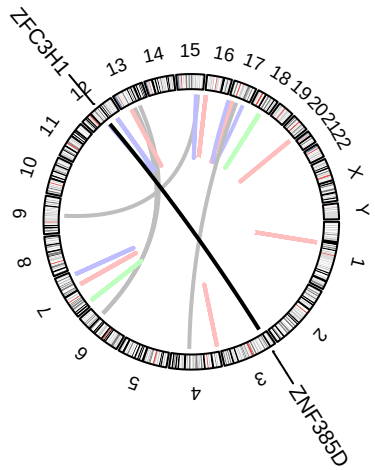


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

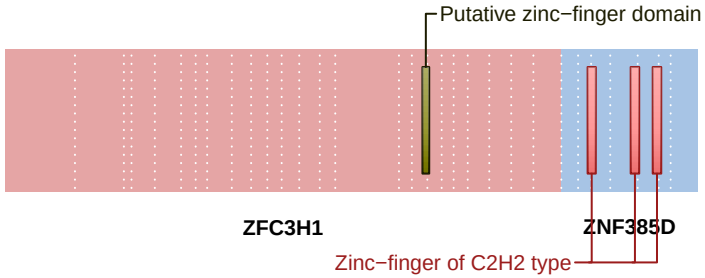
translocation
deletion
duplication
inversion





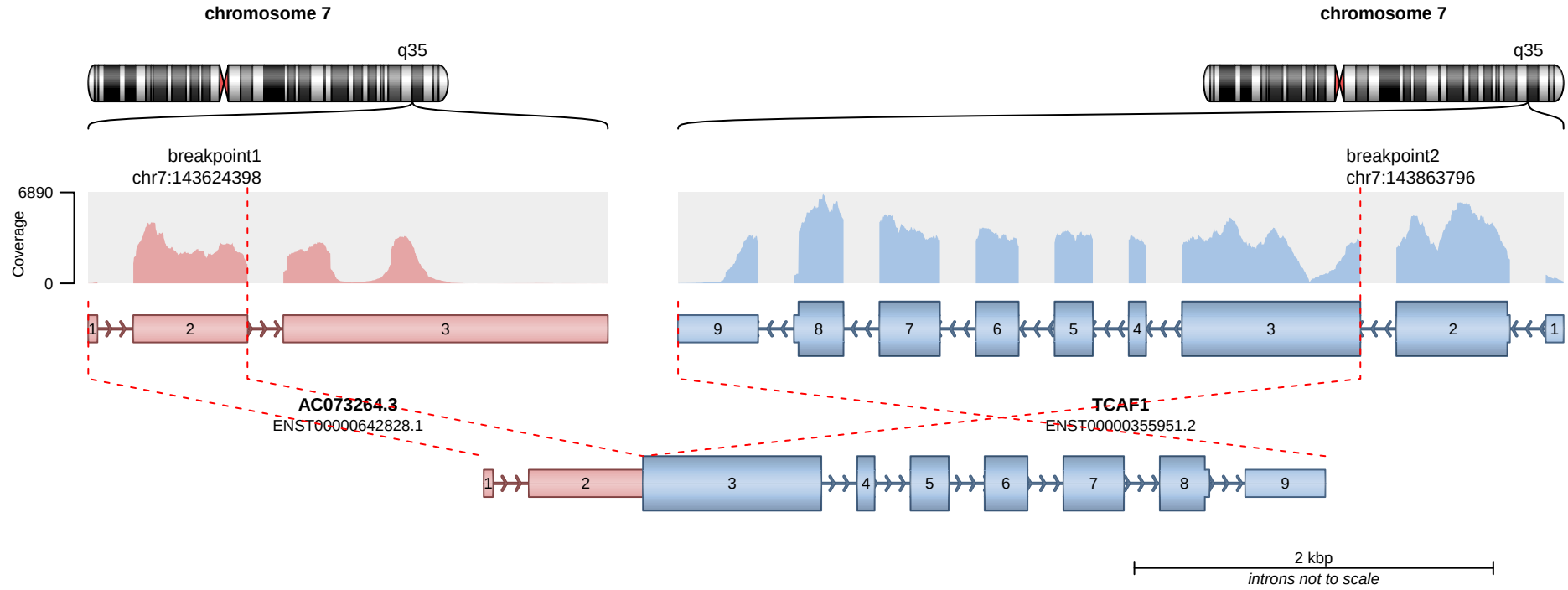
translocation
deletion
duplication
inversion

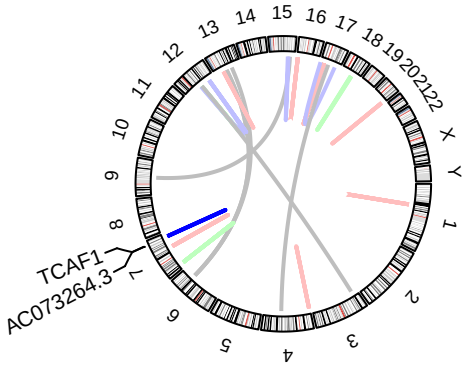
RETAINED PROTEIN DOMAINS
reading frame unclear

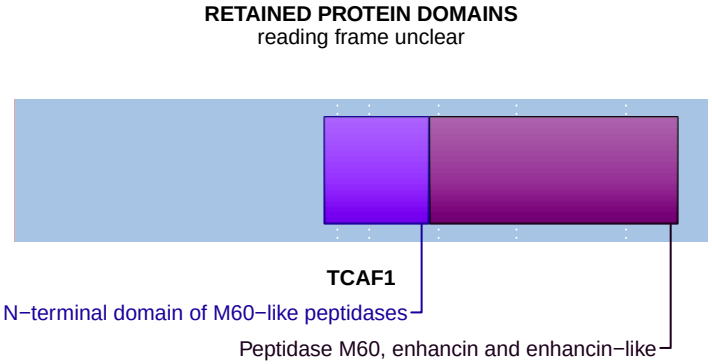


SUPPORTING READ COUNT

Split reads = 41
Discordant mates = 0



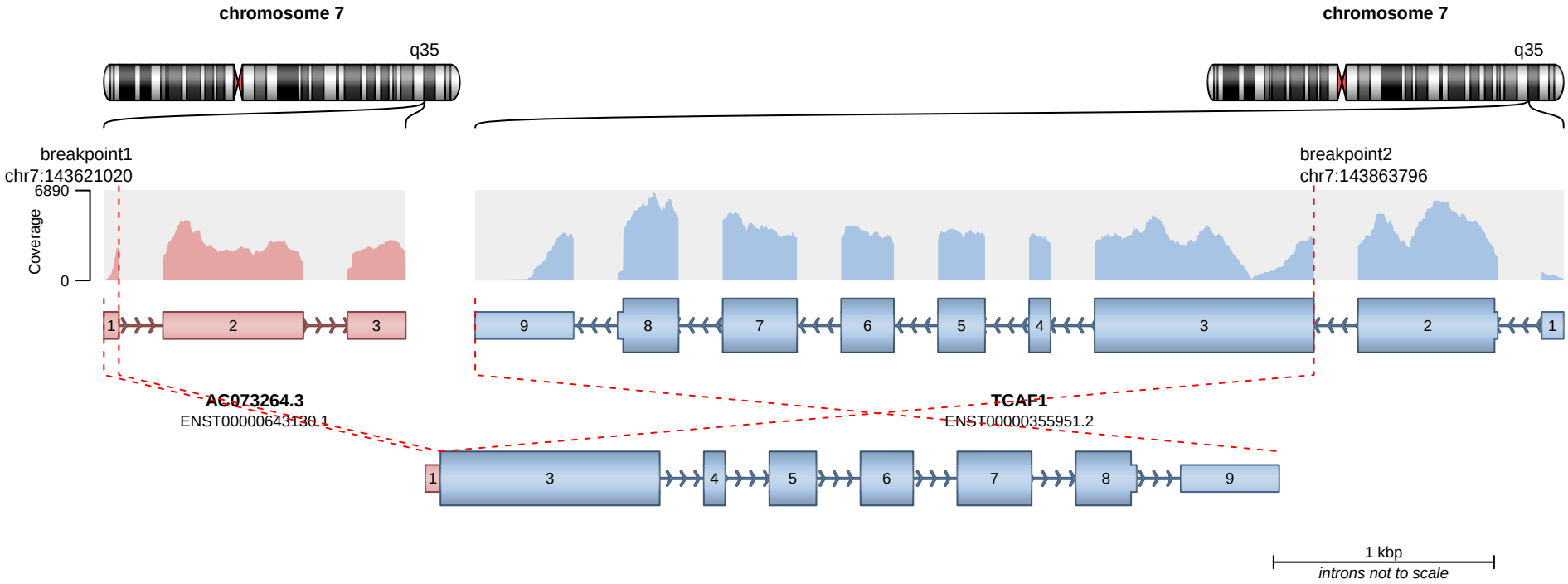


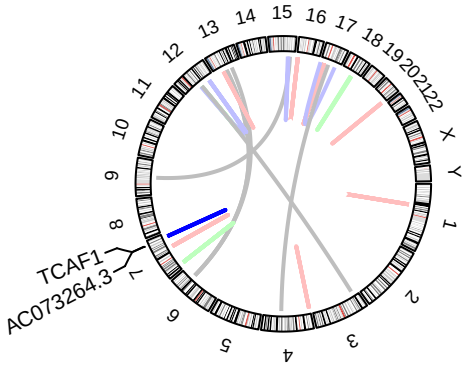


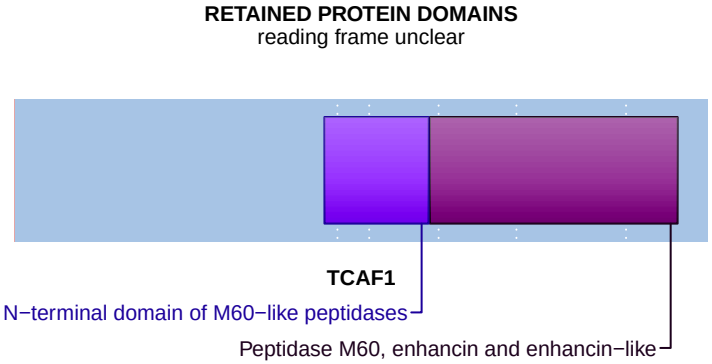
SUPPORTING READ COUNT

Split reads = 40
Discordant mates = 0

translocation
deletion
duplication
inversion



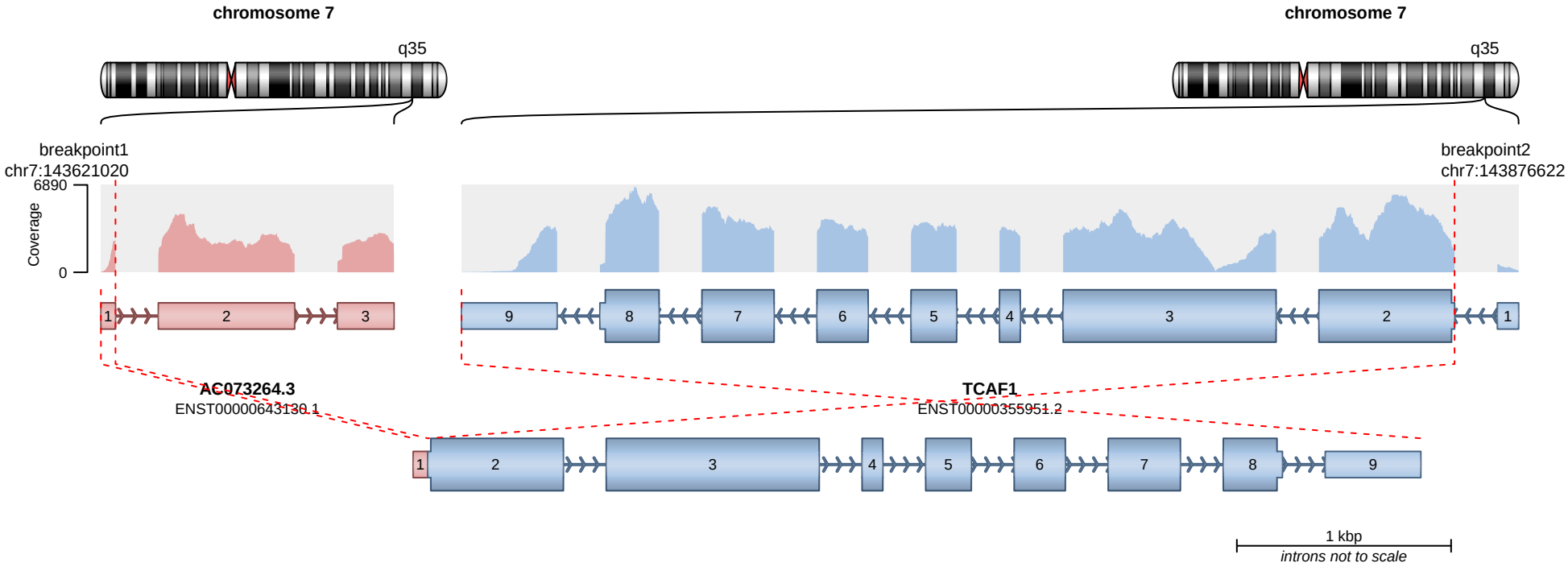


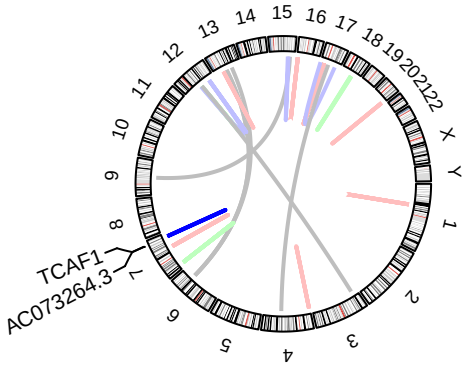


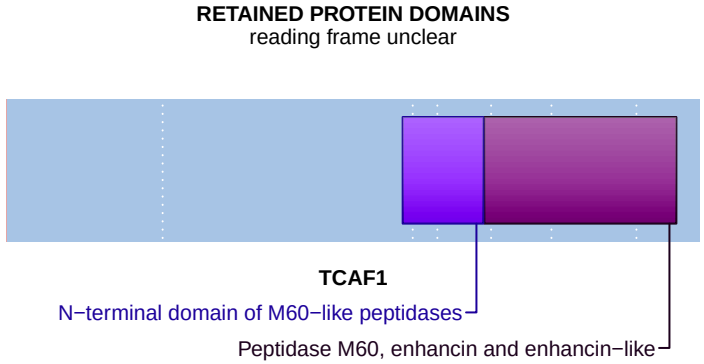
SUPPORTING READ COUNT

Split reads = 36
Discordant mates = 0

translocation
deletion
duplication
inversion



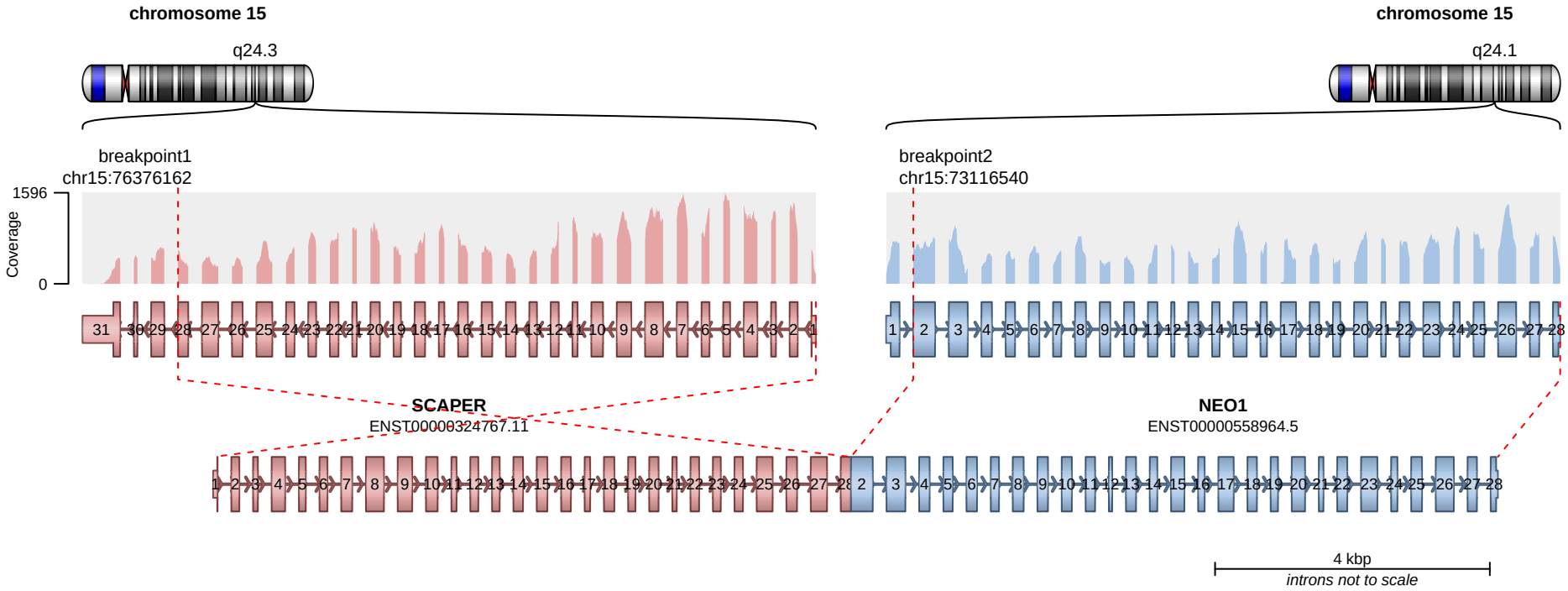


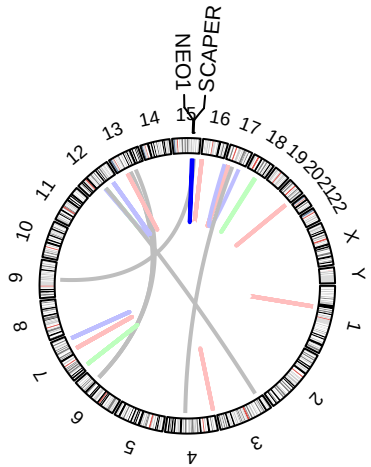


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

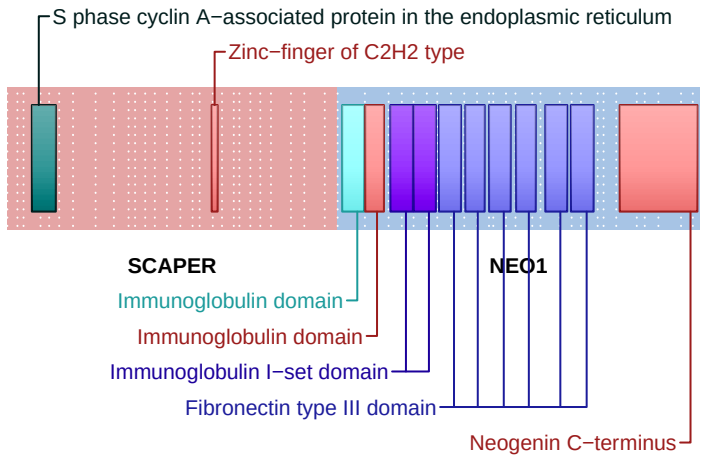
translocation
deletion
duplication
inversion





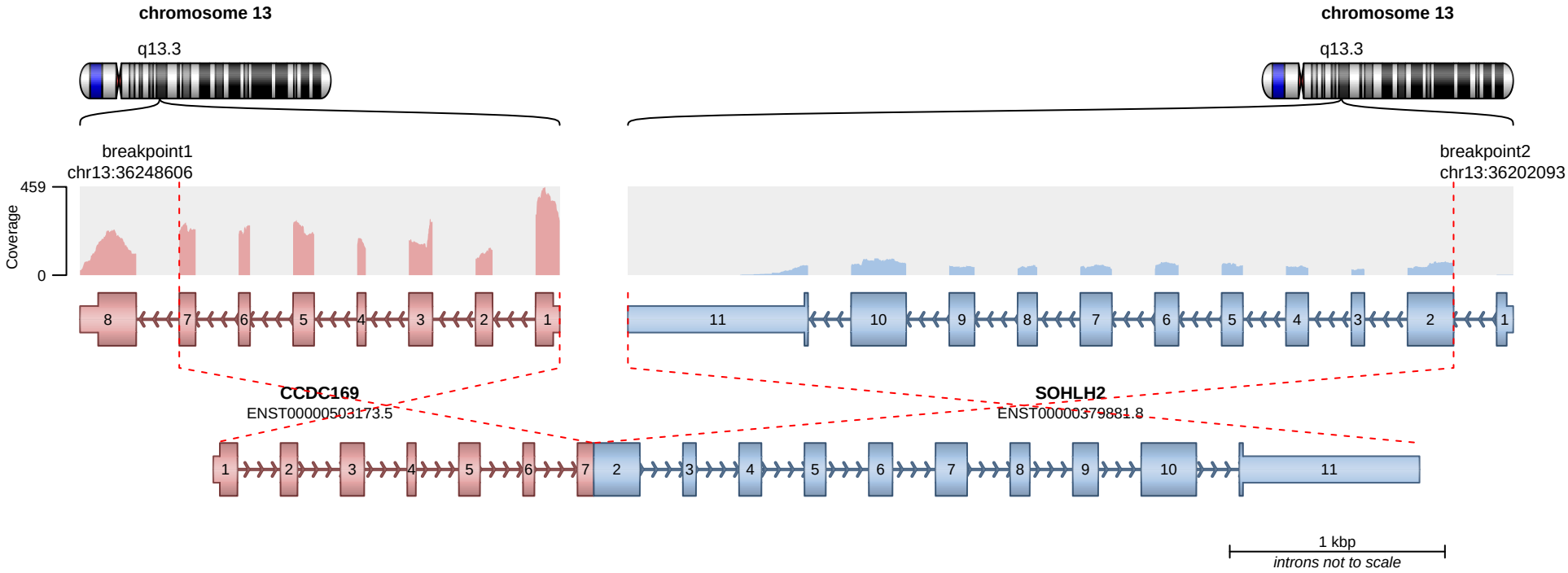
translocation
deletion
duplication
inversion

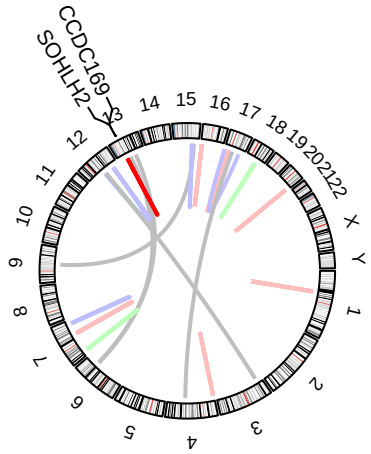
RETAINED PROTEIN DOMAINS
reading frame unclear



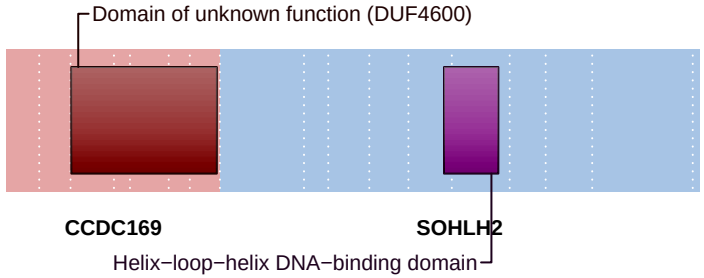
SUPPORTING READ COUNT

Split reads = 24
Discordant mates = 0





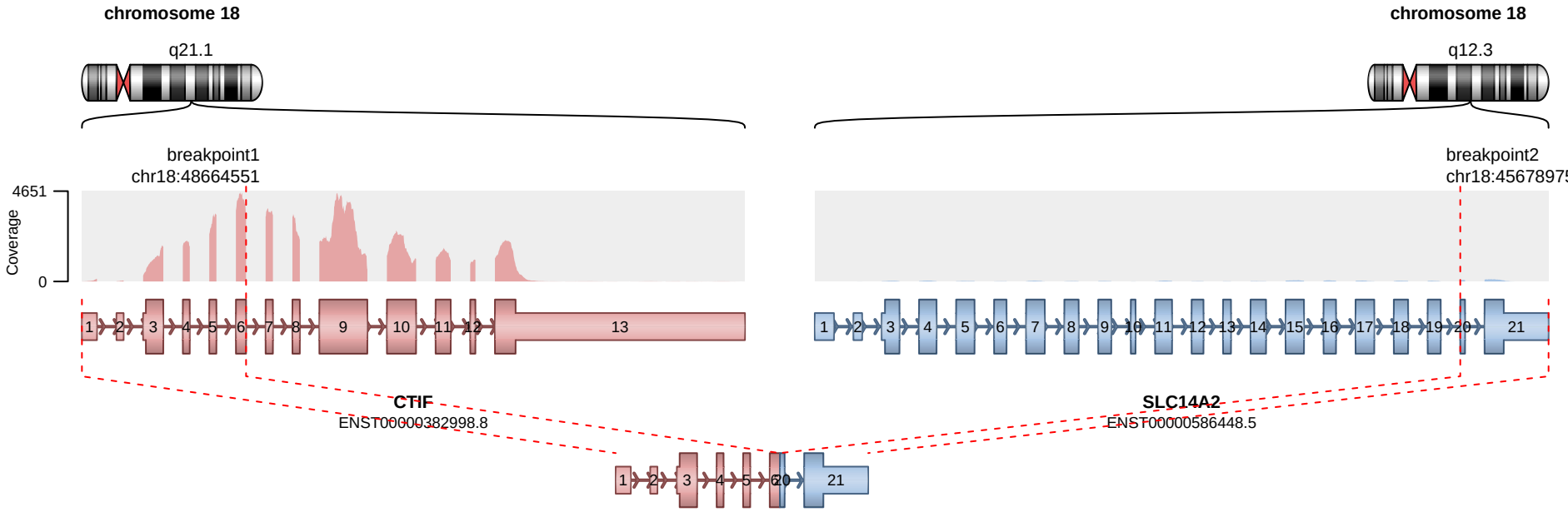
RETAINED PROTEIN DOMAINS
reading frame unclear

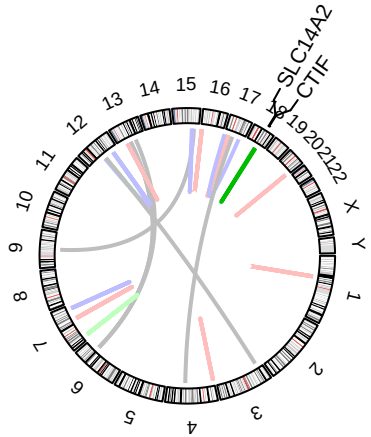


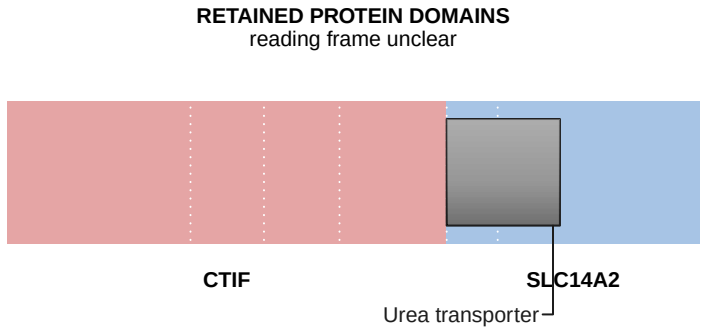
SUPPORTING READ COUNT

Split reads = 23
Discordant mates = 0

translocation
deletion
duplication
inversion



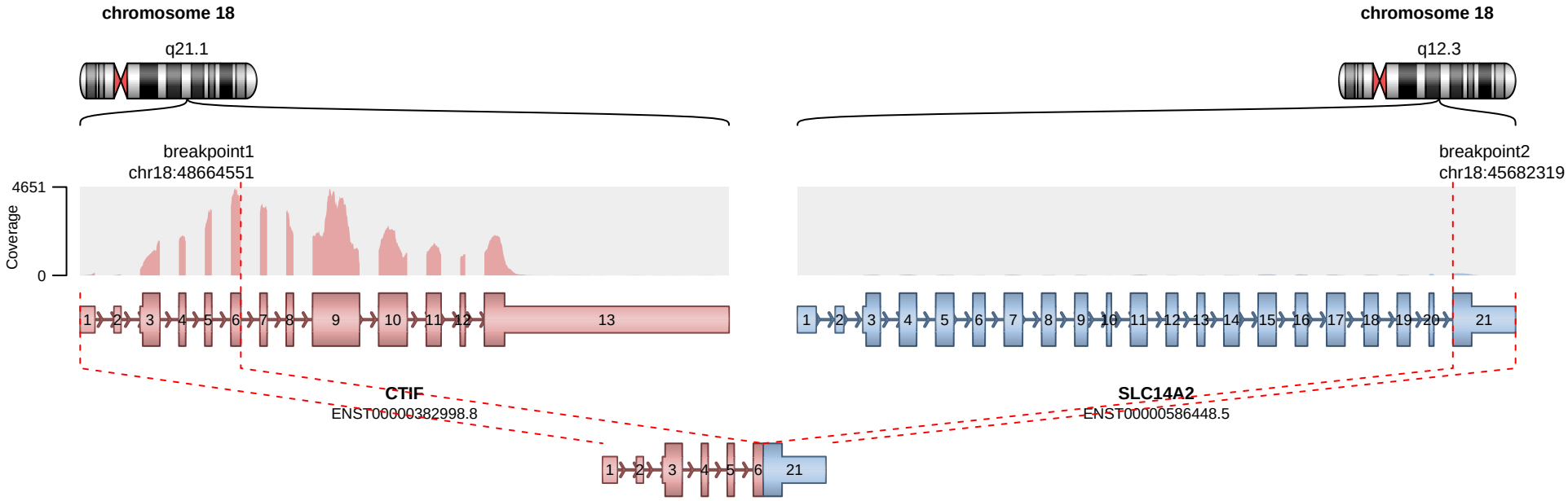


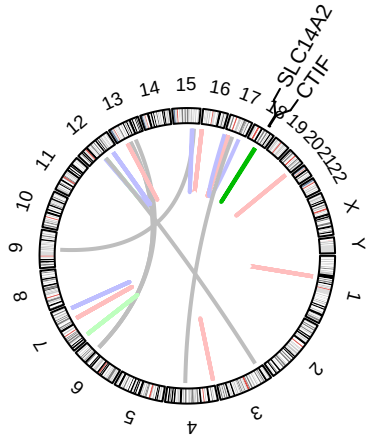


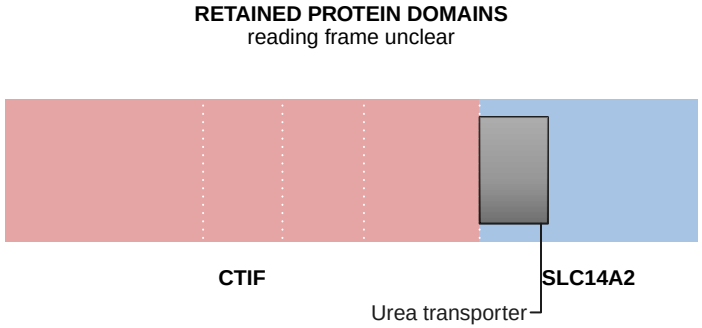
SUPPORTING READ COUNT

Split reads = 14
Discordant mates = 0

translocation
deletion
duplication
inversion



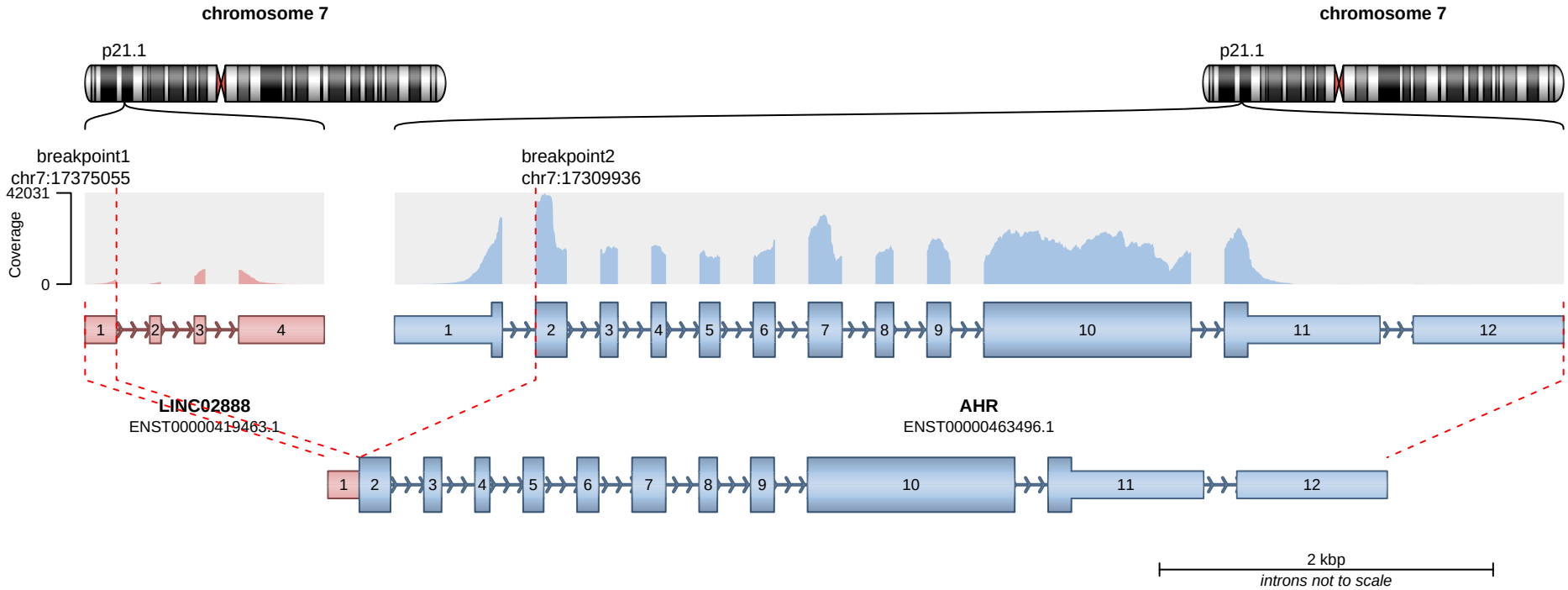


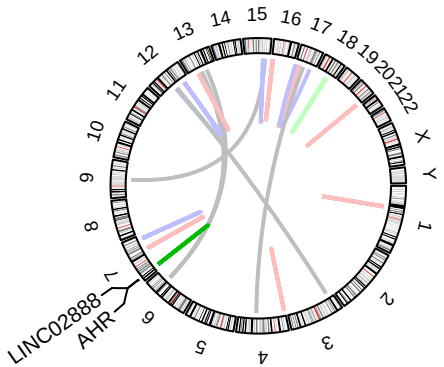


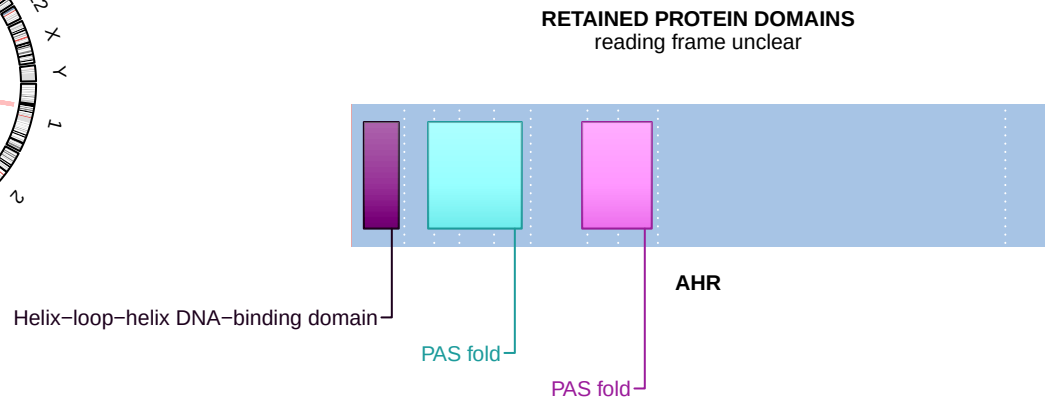
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

translocation
deletion
duplication
inversion



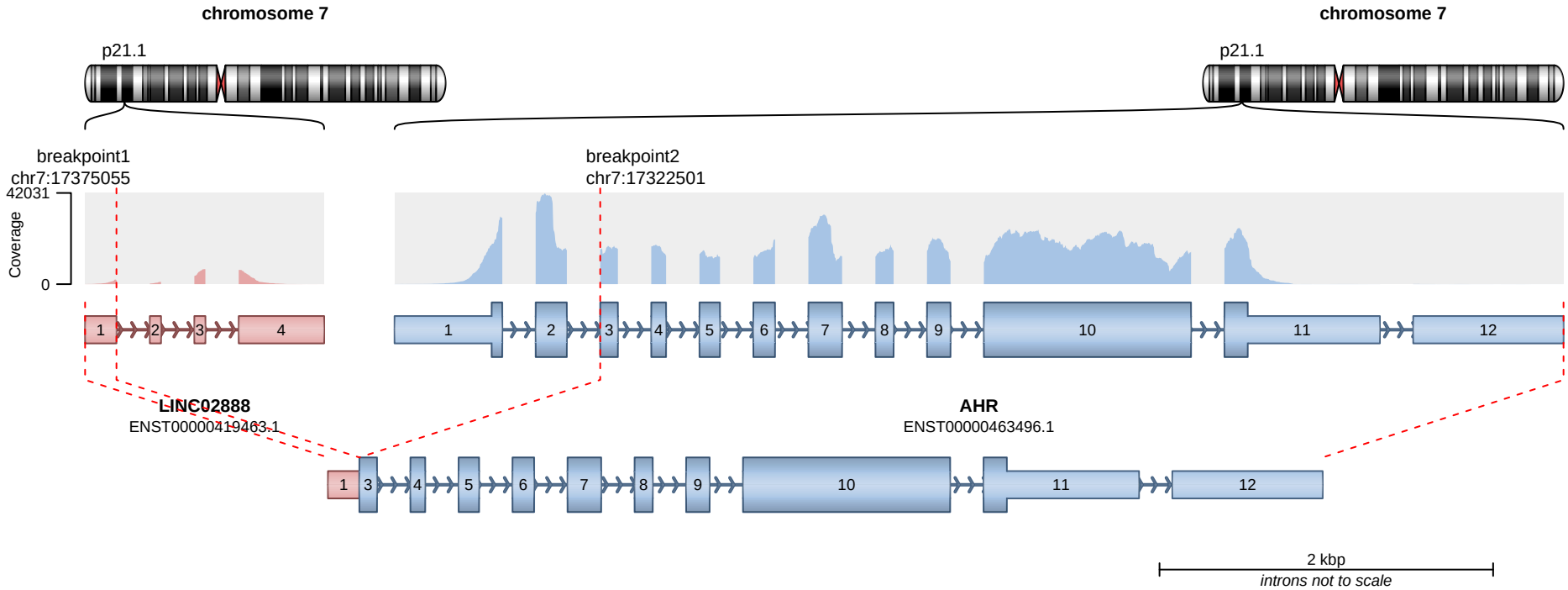


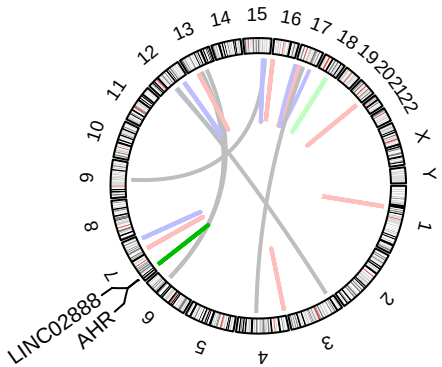


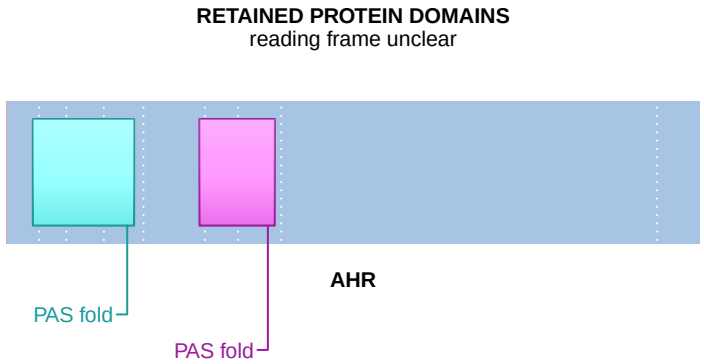
SUPPORTING READ COUNT

Split reads = 9
Discordant mates = 0

translocation
deletion
duplication
inversion



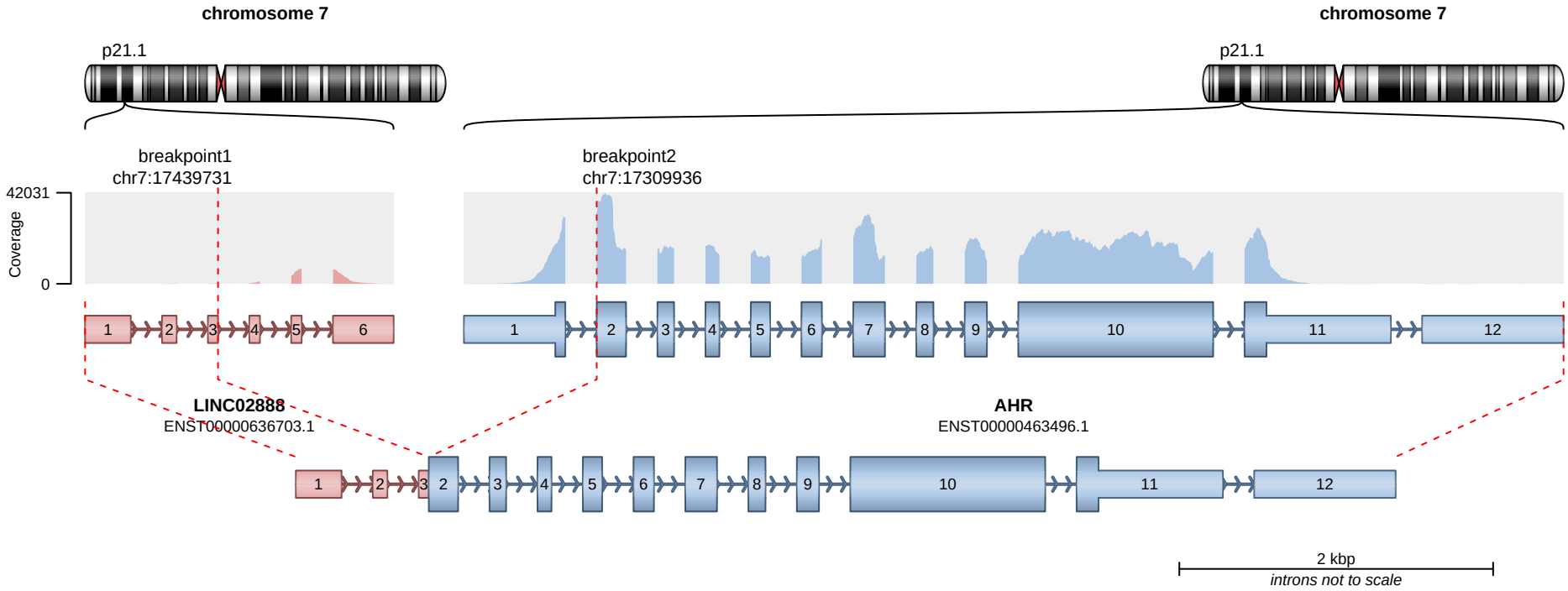


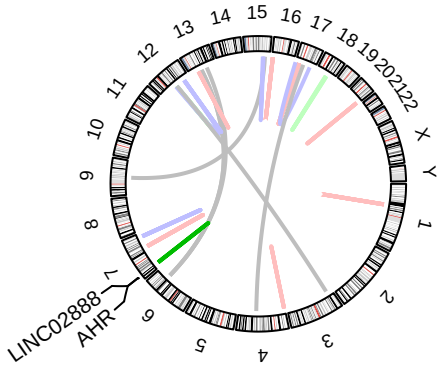


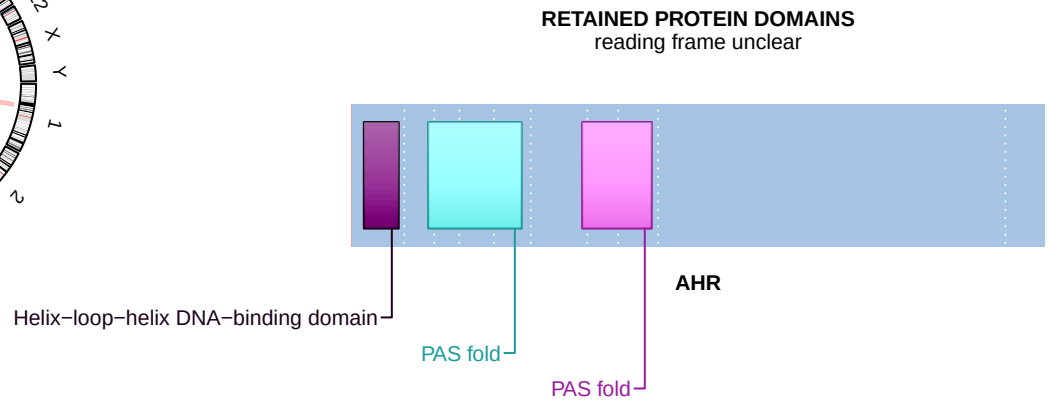
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

translocation
deletion
duplication
inversion



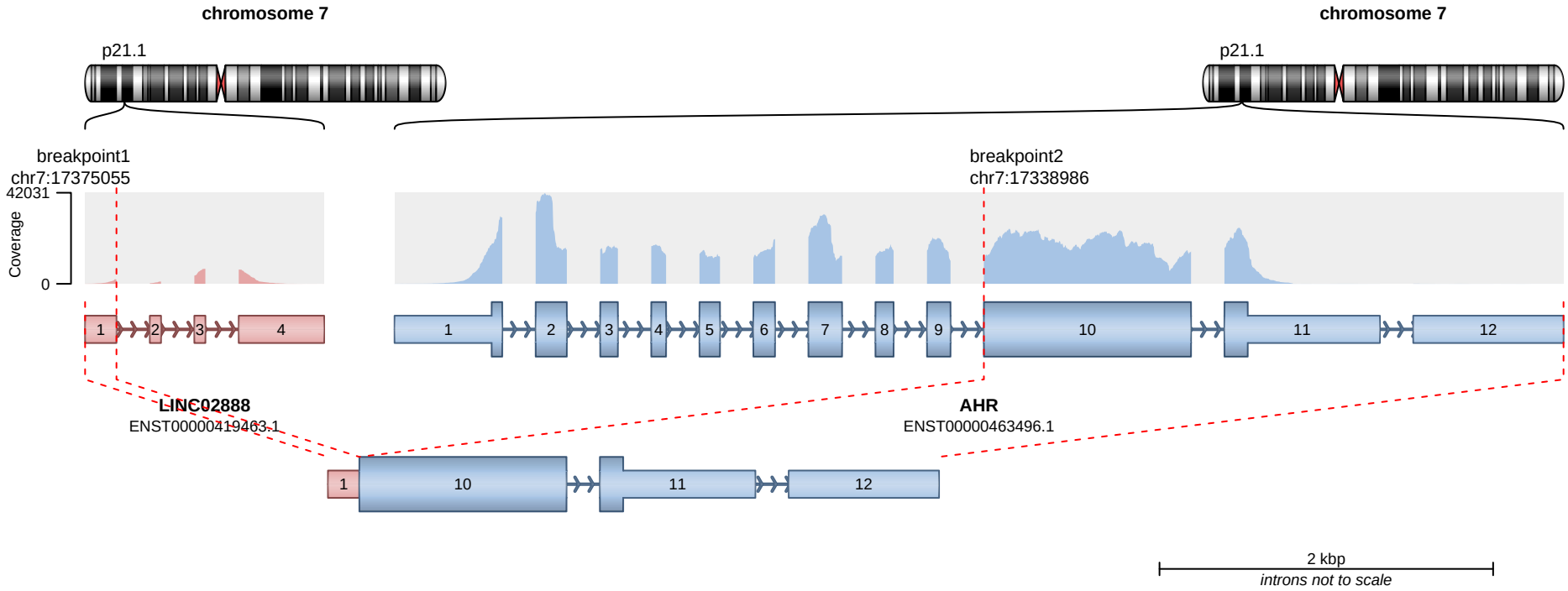


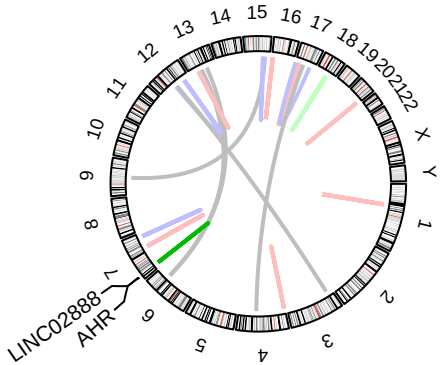


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

translocation
deletion
duplication
inversion



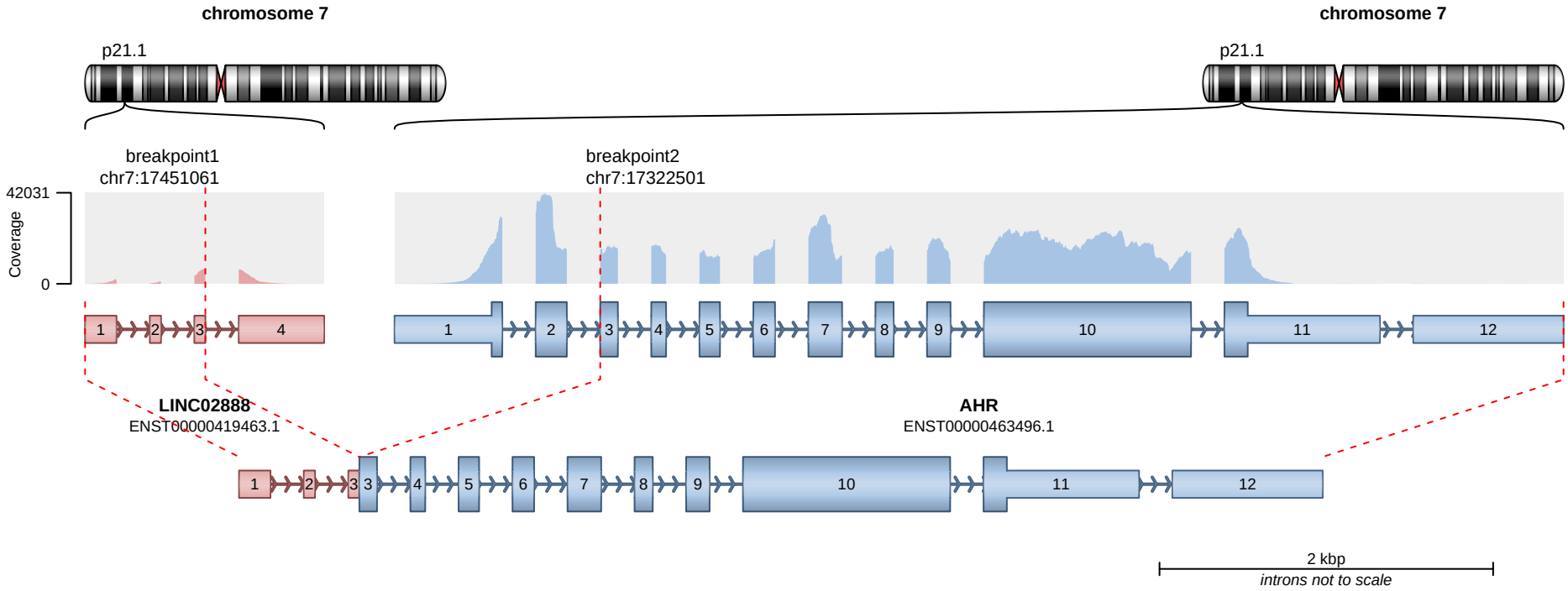


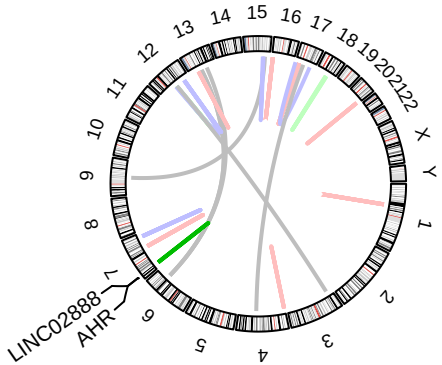
No protein domains retained in fusion.

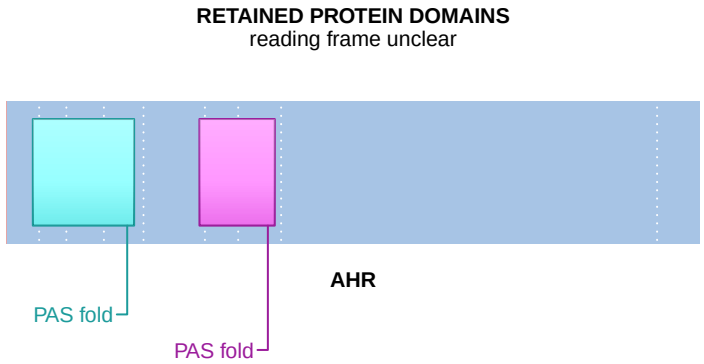
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

translocation
deletion
duplication
inversion







SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

translocation
deletion
duplication
inversion