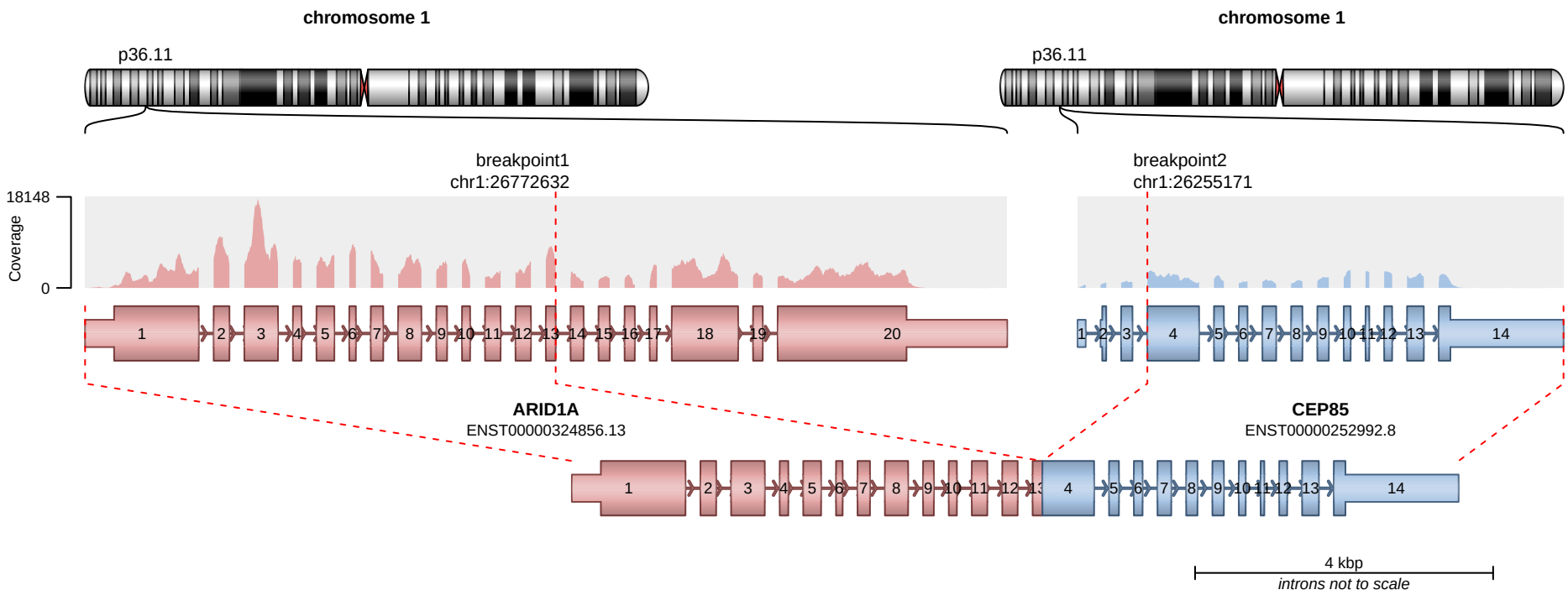
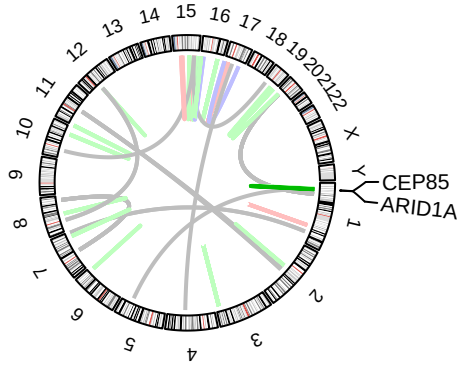
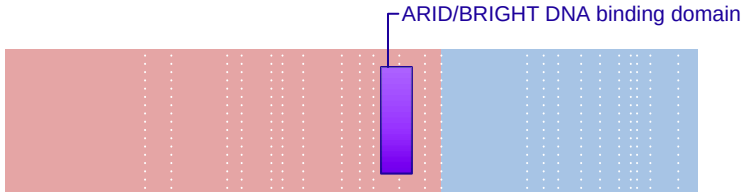




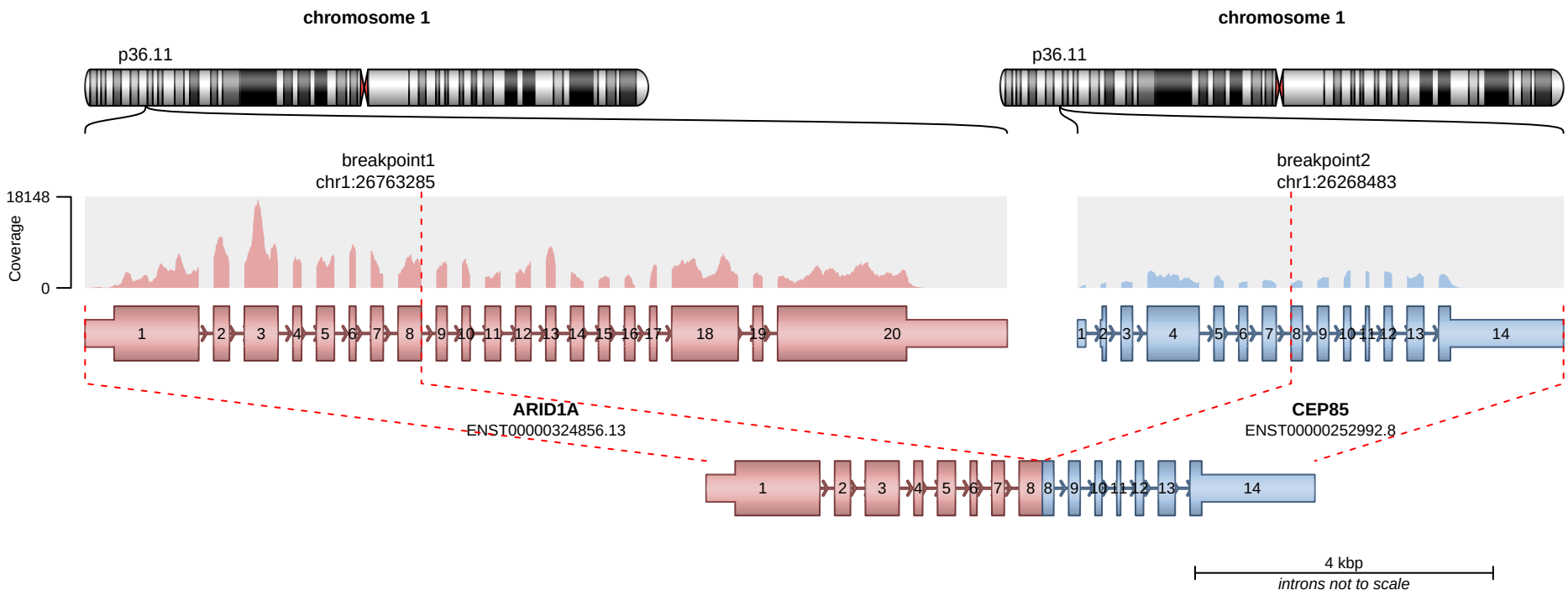
RETAINED PROTEIN DOMAINS
reading frame unclear

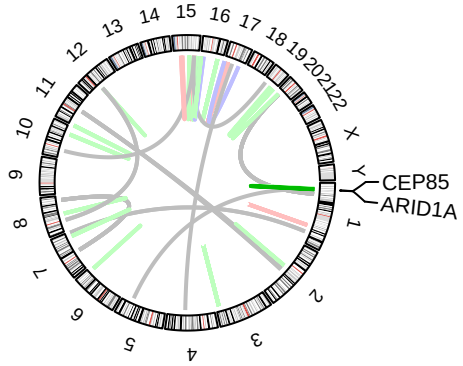


SUPPORTING READ COUNT

Split reads = 709
Discordant mates = 5

translocation
deletion
duplication
inversion



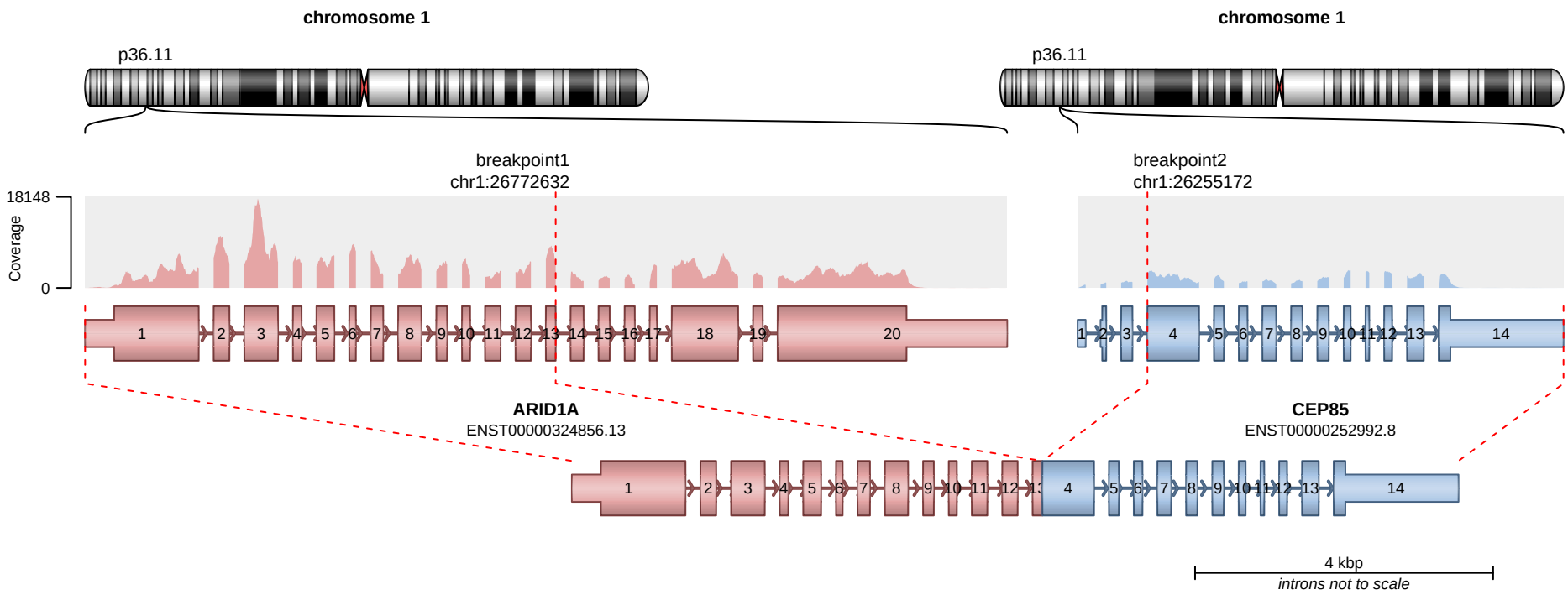


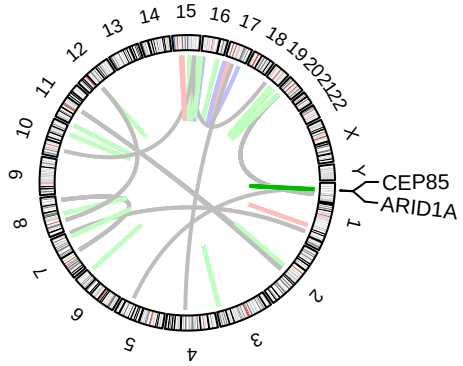
No protein domains retained in fusion.

SUPPORTING READ COUNT

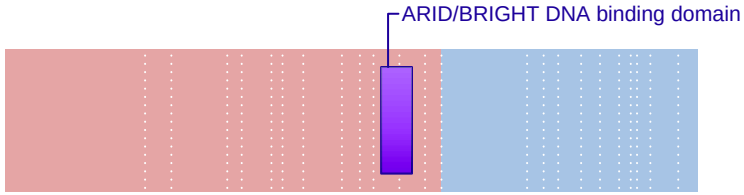
Split reads = 130
Discordant mates = 1

translocation
deletion
duplication
inversion





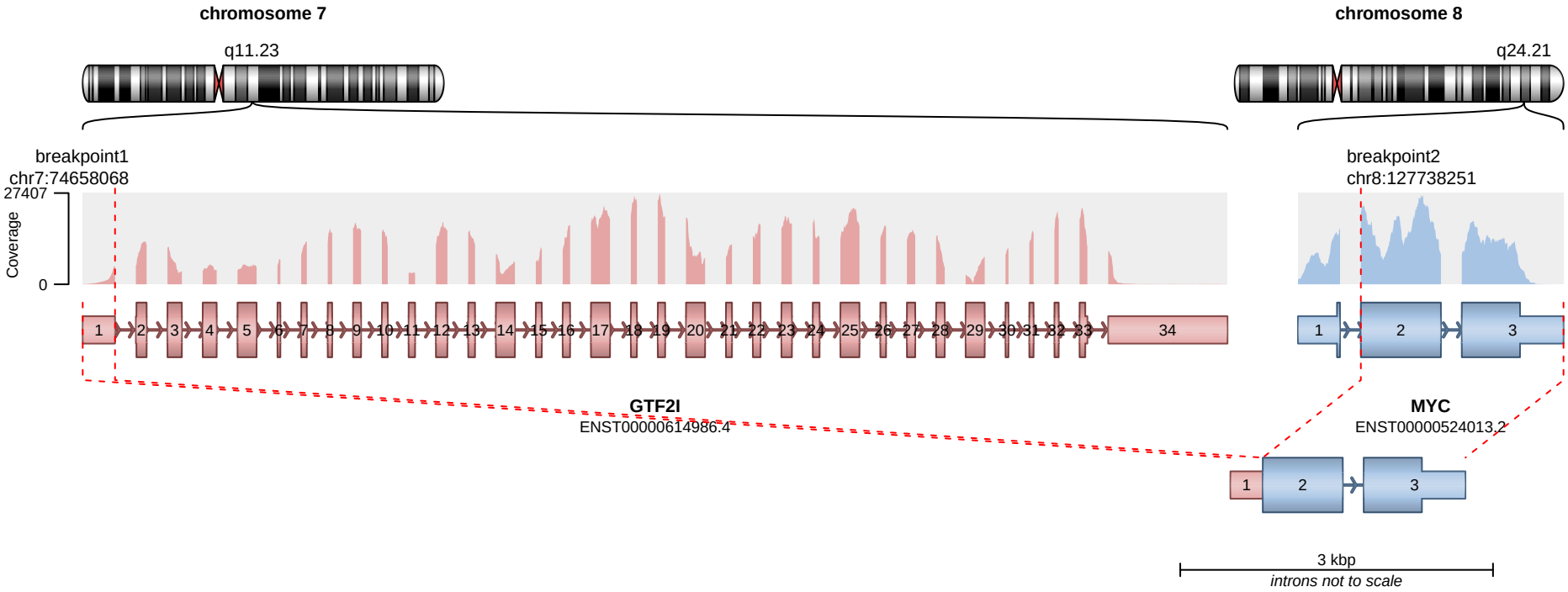
RETAINED PROTEIN DOMAINS
reading frame unclear

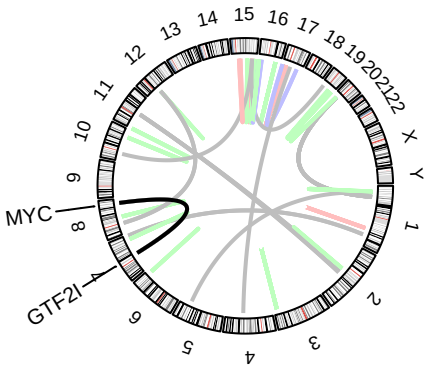


SUPPORTING READ COUNT

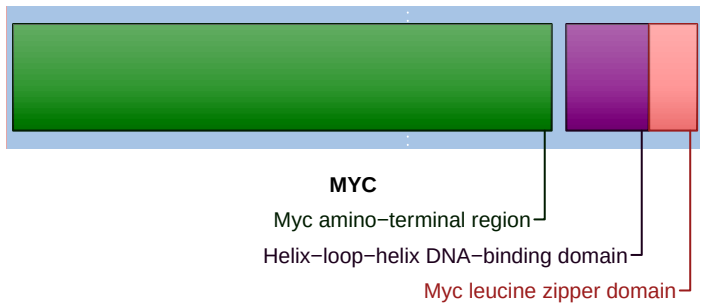
Split reads = 3
Discordant mates = 5

translocation
deletion
duplication
inversion



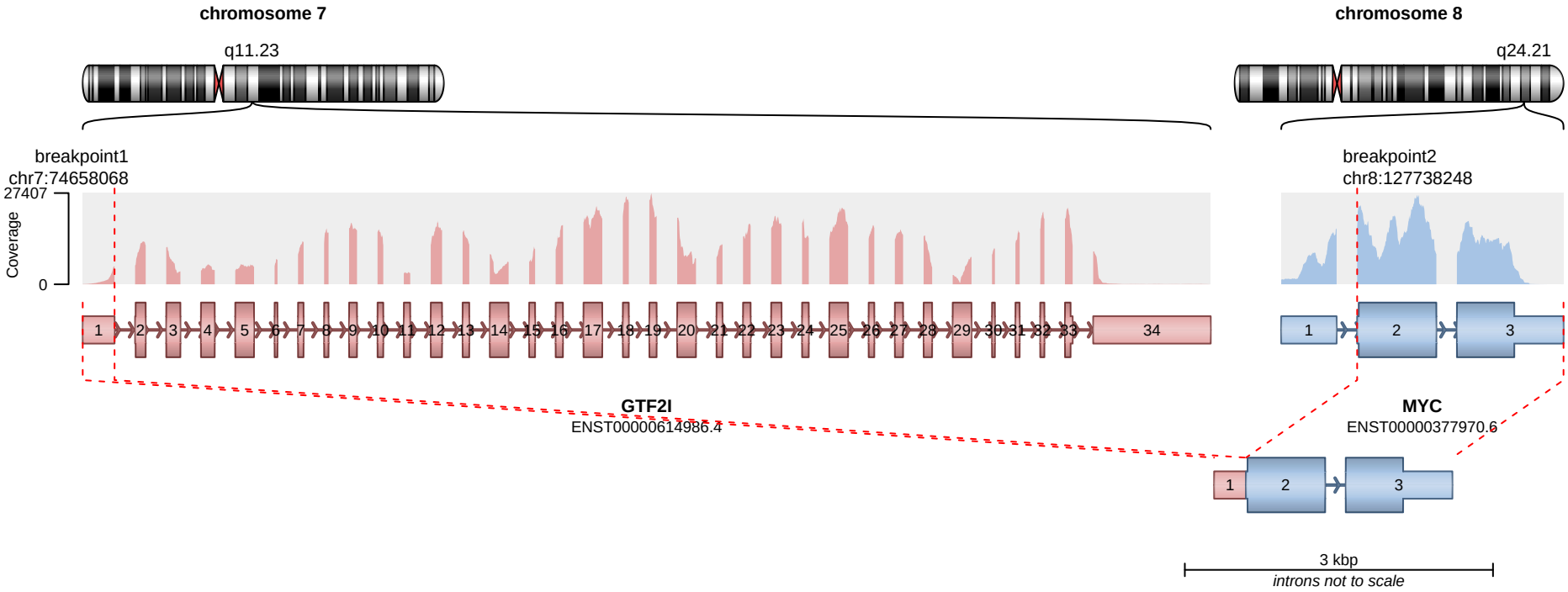


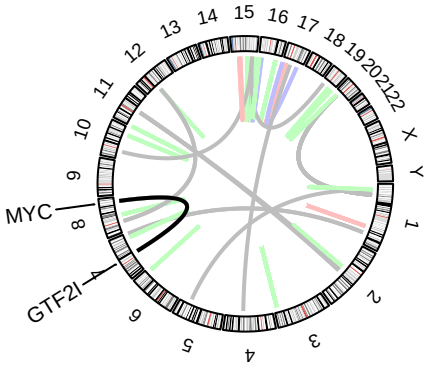
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

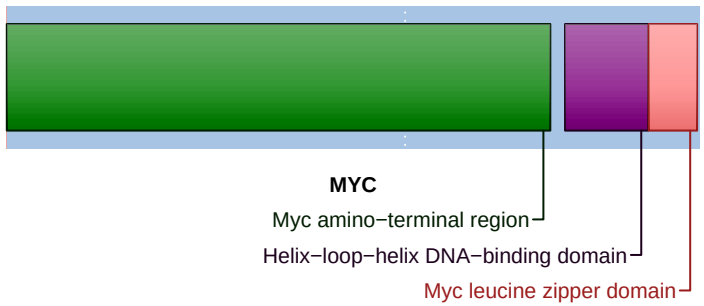
Split reads = 537
Discordant mates = 0





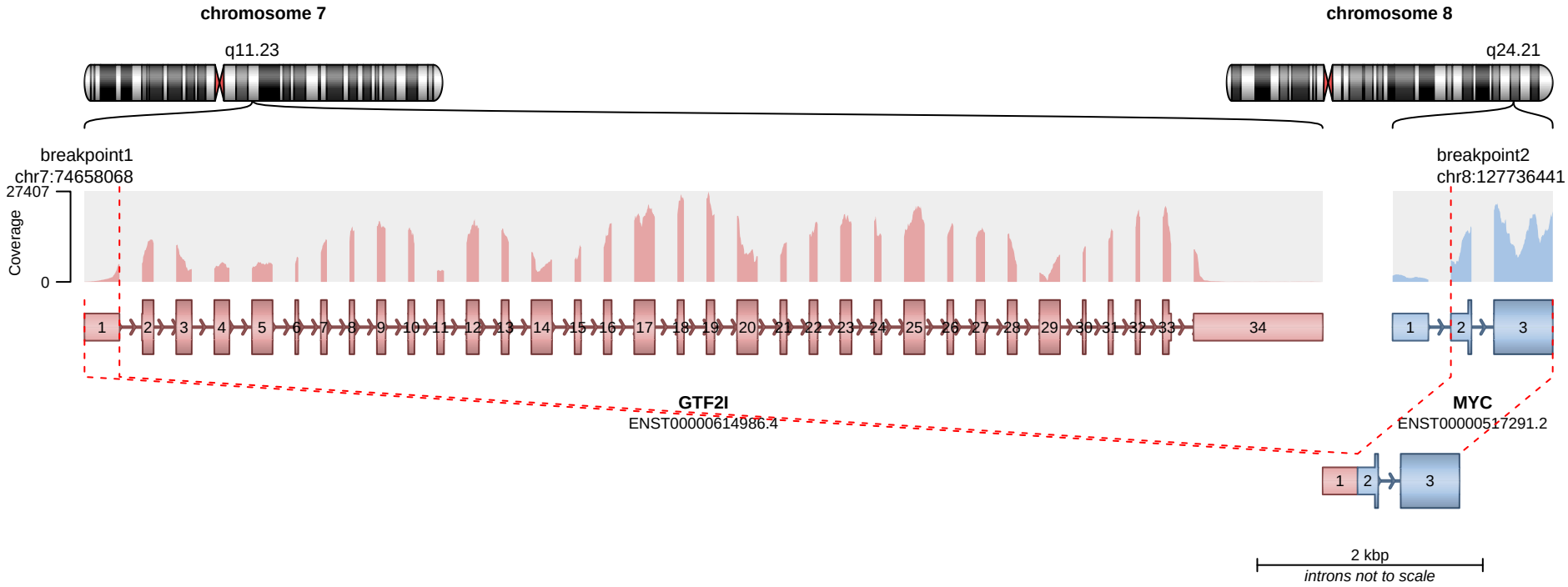
translocation
deletion
duplication
inversion

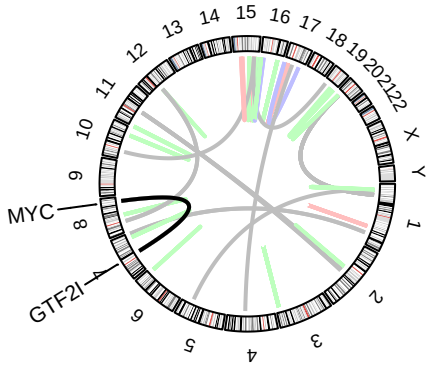
RETAINED PROTEIN DOMAINS
reading frame unclear

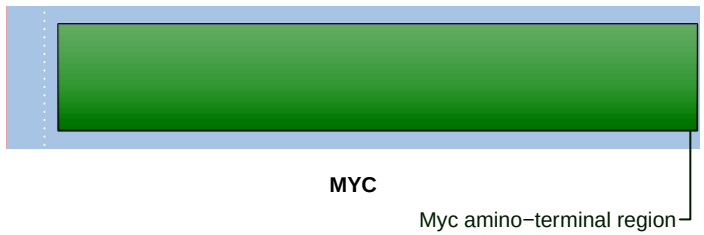


SUPPORTING READ COUNT

Split reads = 245
Discordant mates = 0



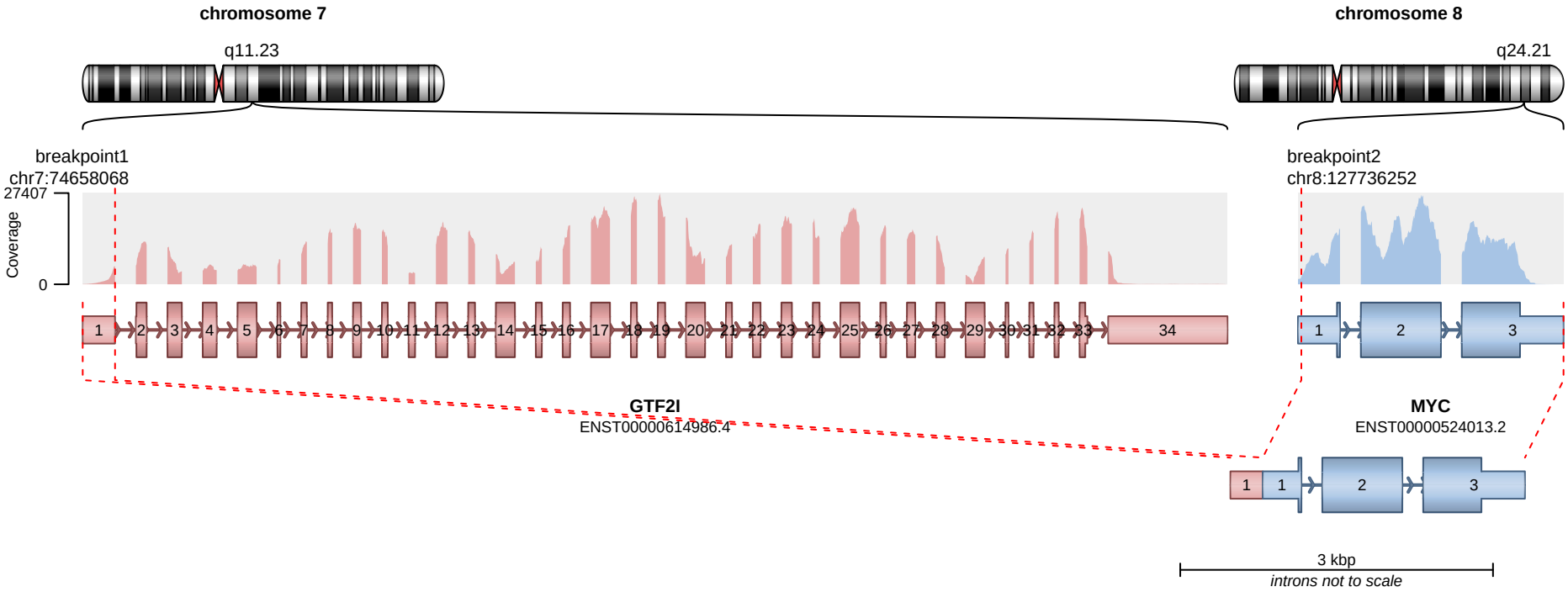


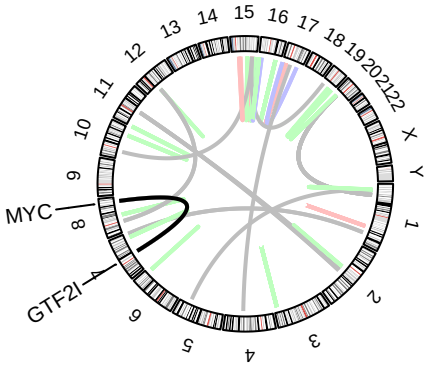


SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 0

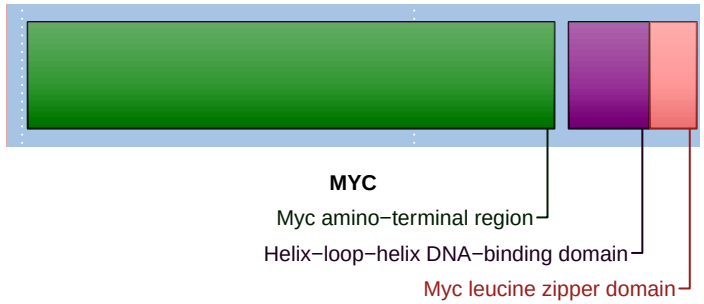
translocation
deletion
duplication
inversion





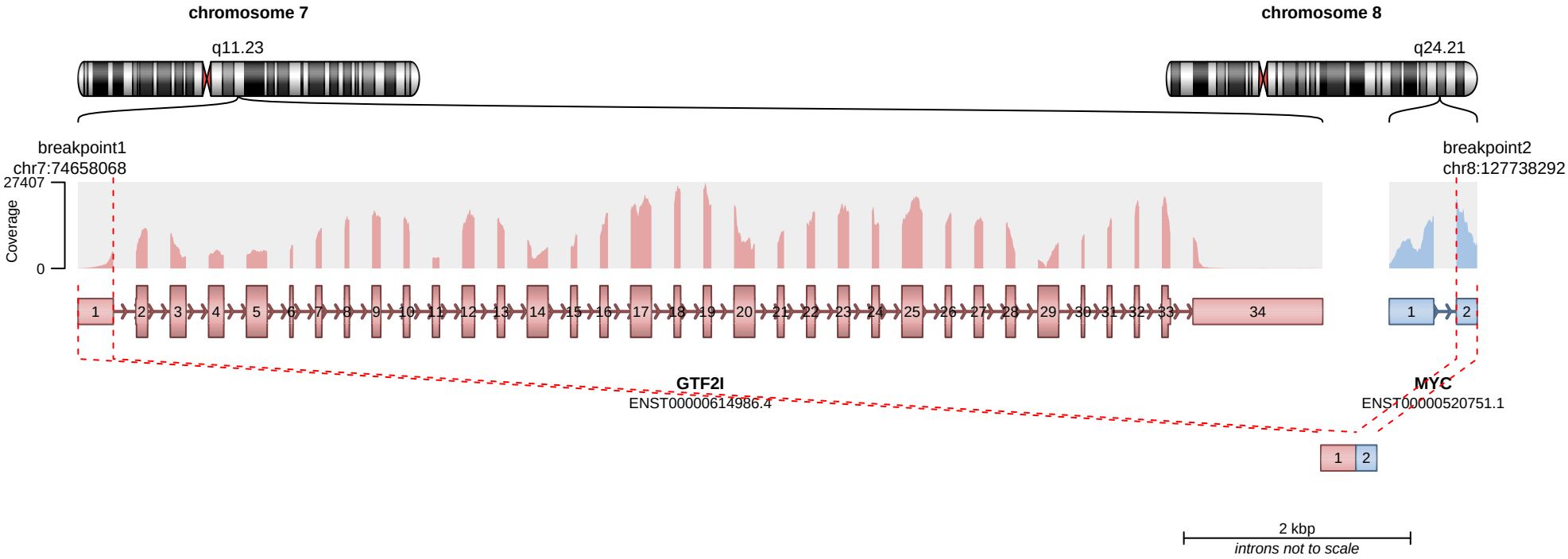
translocation
deletion
duplication
inversion

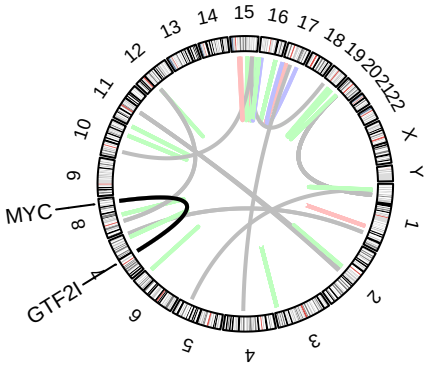
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0



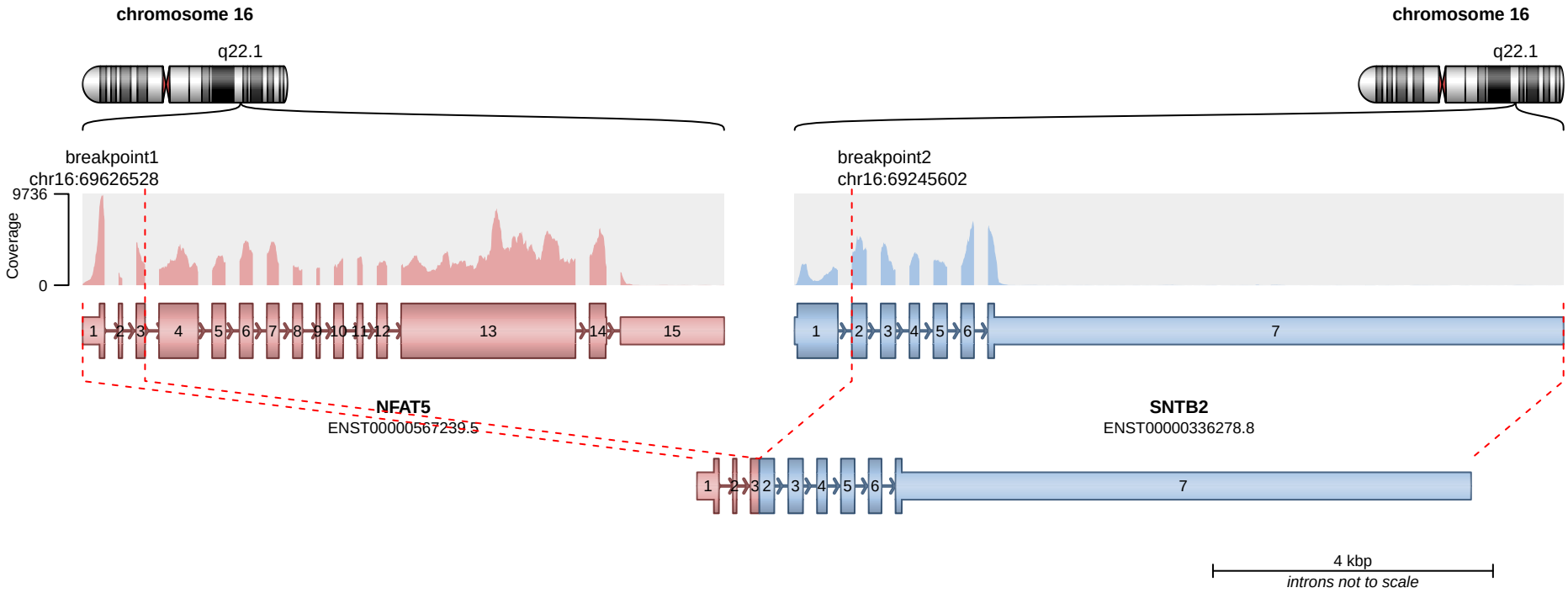


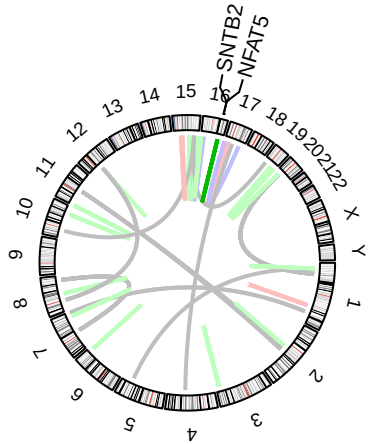
translocation
deletion
duplication
inversion

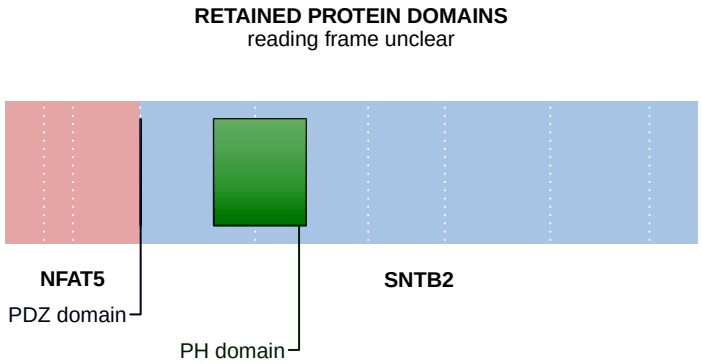
No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



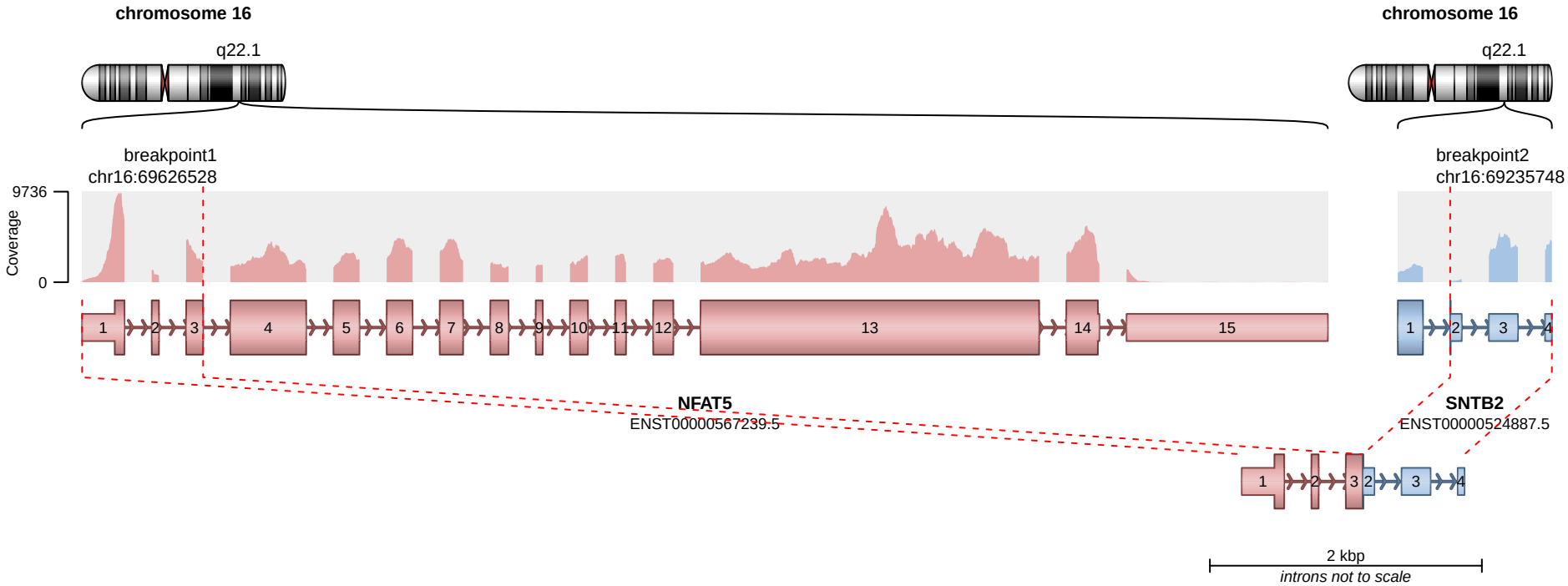


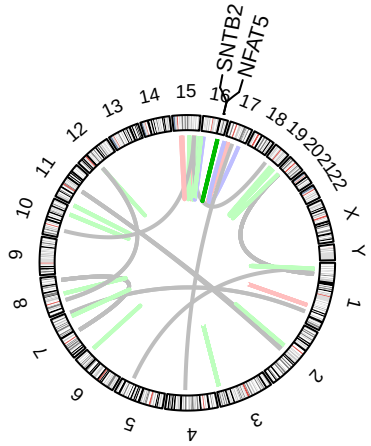


SUPPORTING READ COUNT

Split reads = 406
Discordant mates = 4

translocation
deletion
duplication
inversion



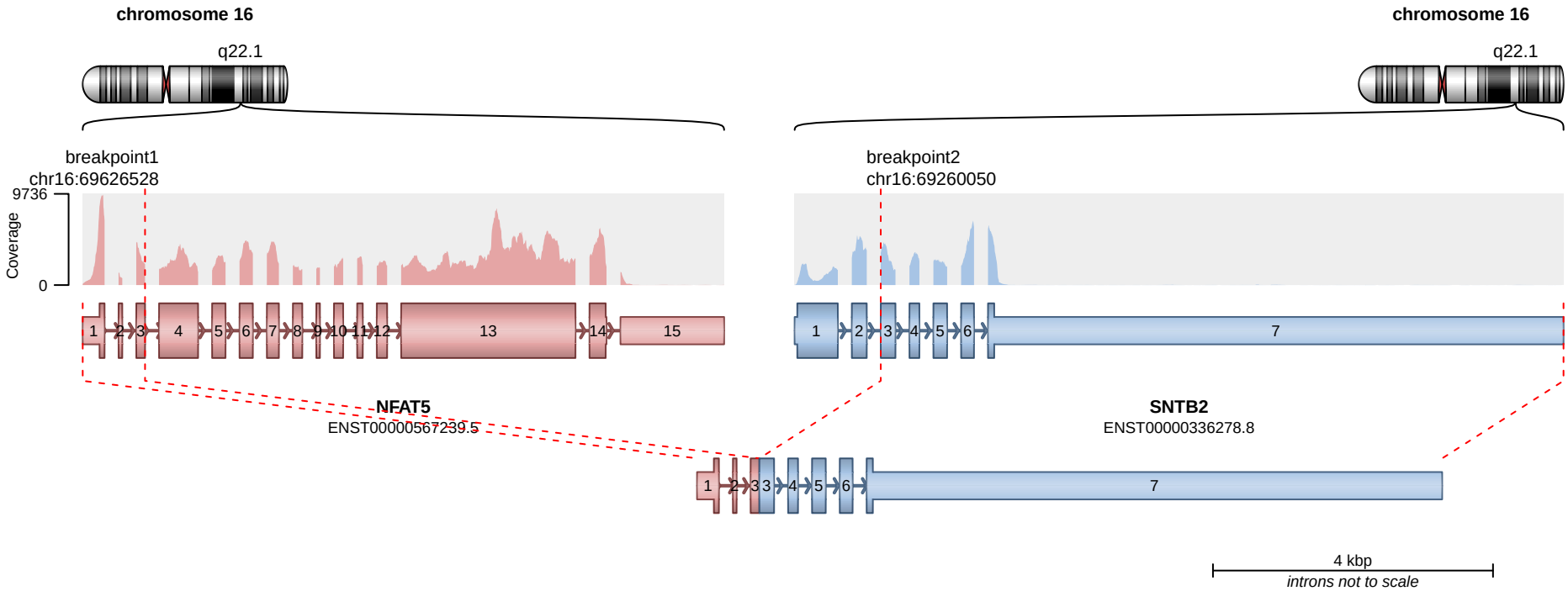


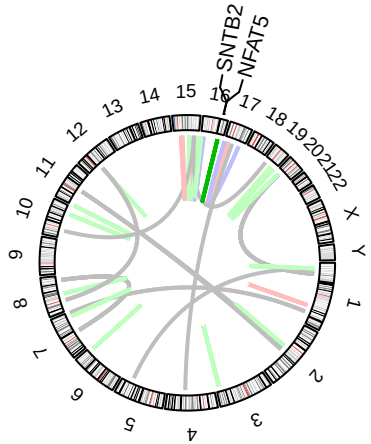
translocation
deletion
duplication
inversion

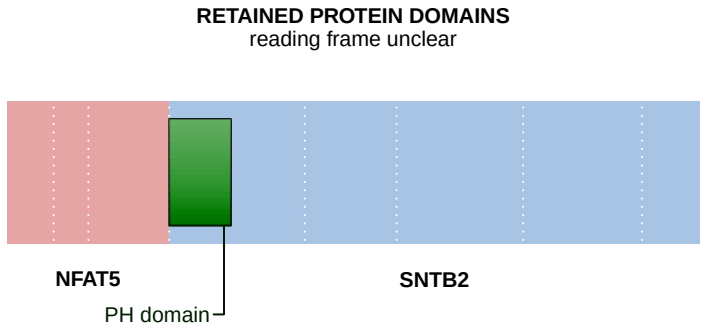
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 53
Discordant mates = 5



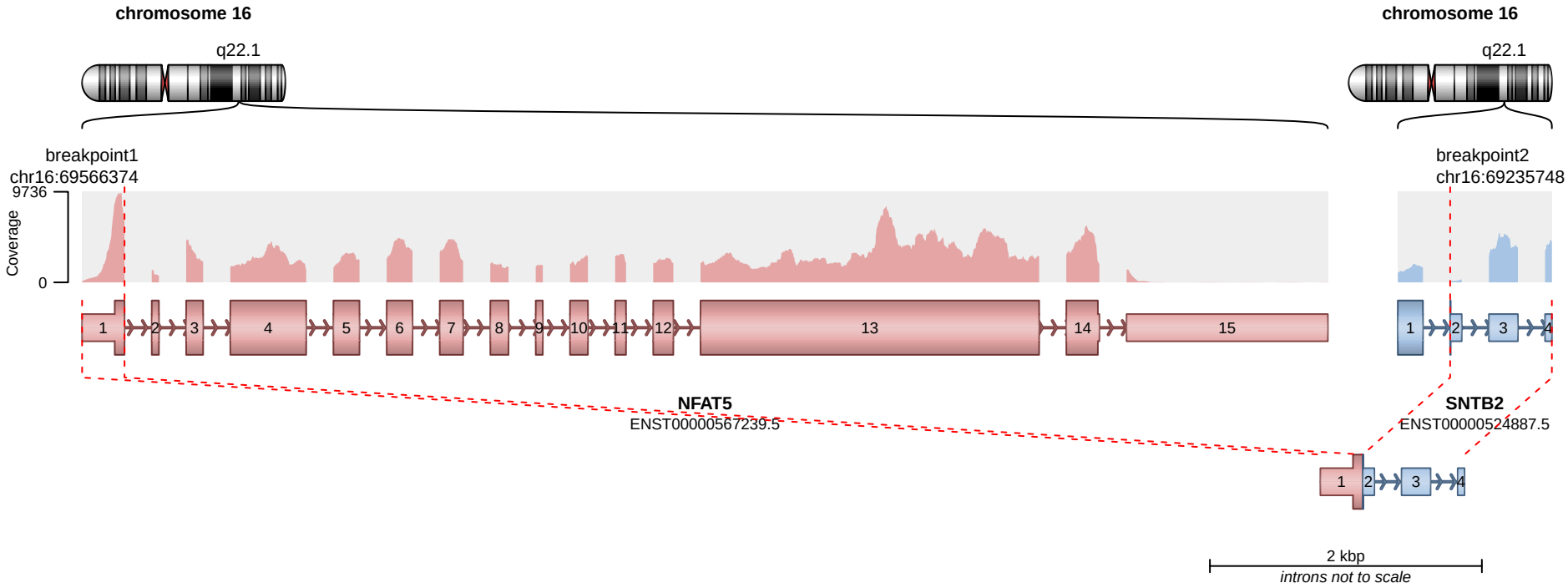


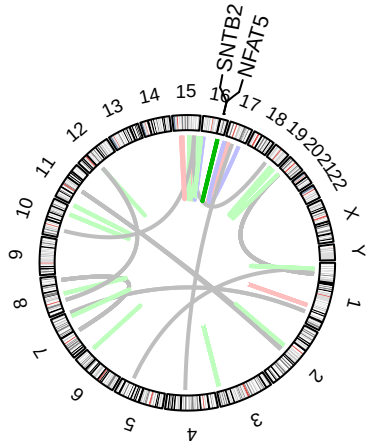


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

translocation
deletion
duplication
inversion



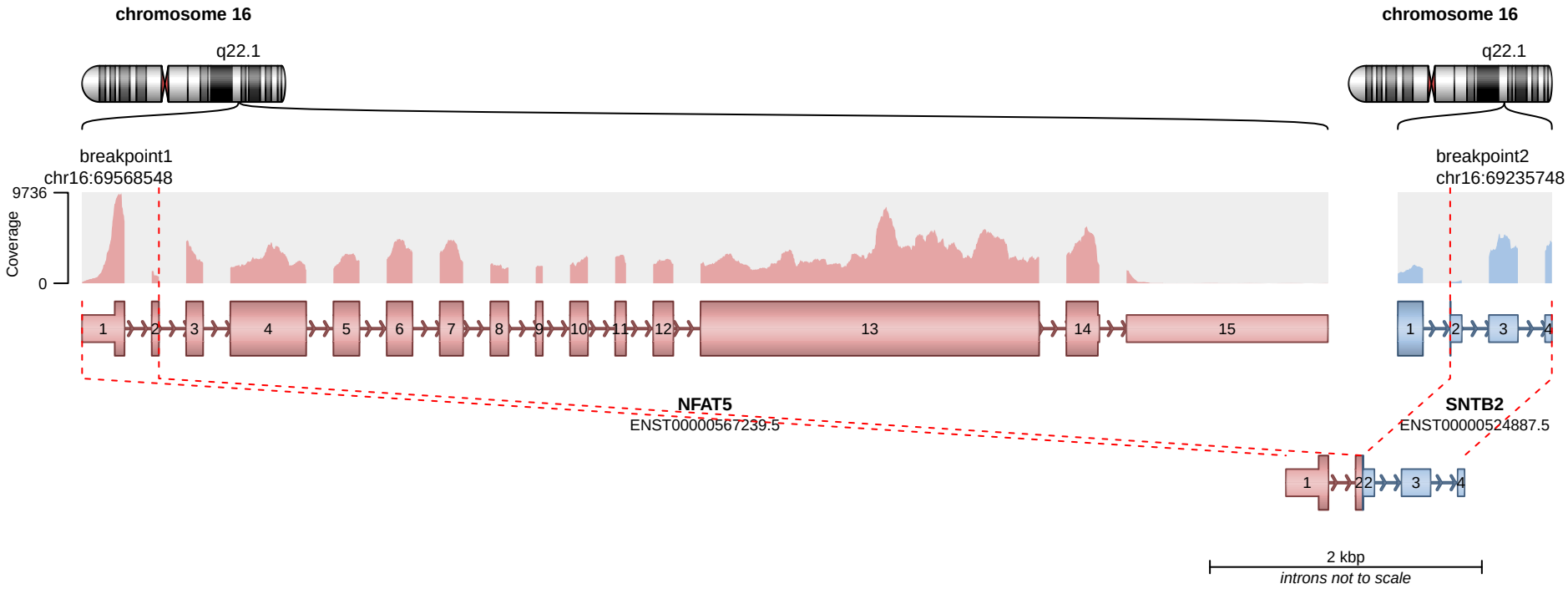


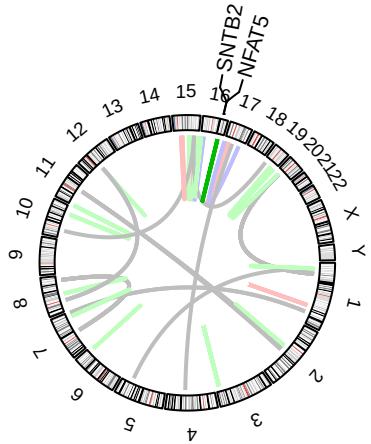
translocation
deletion
duplication
inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1



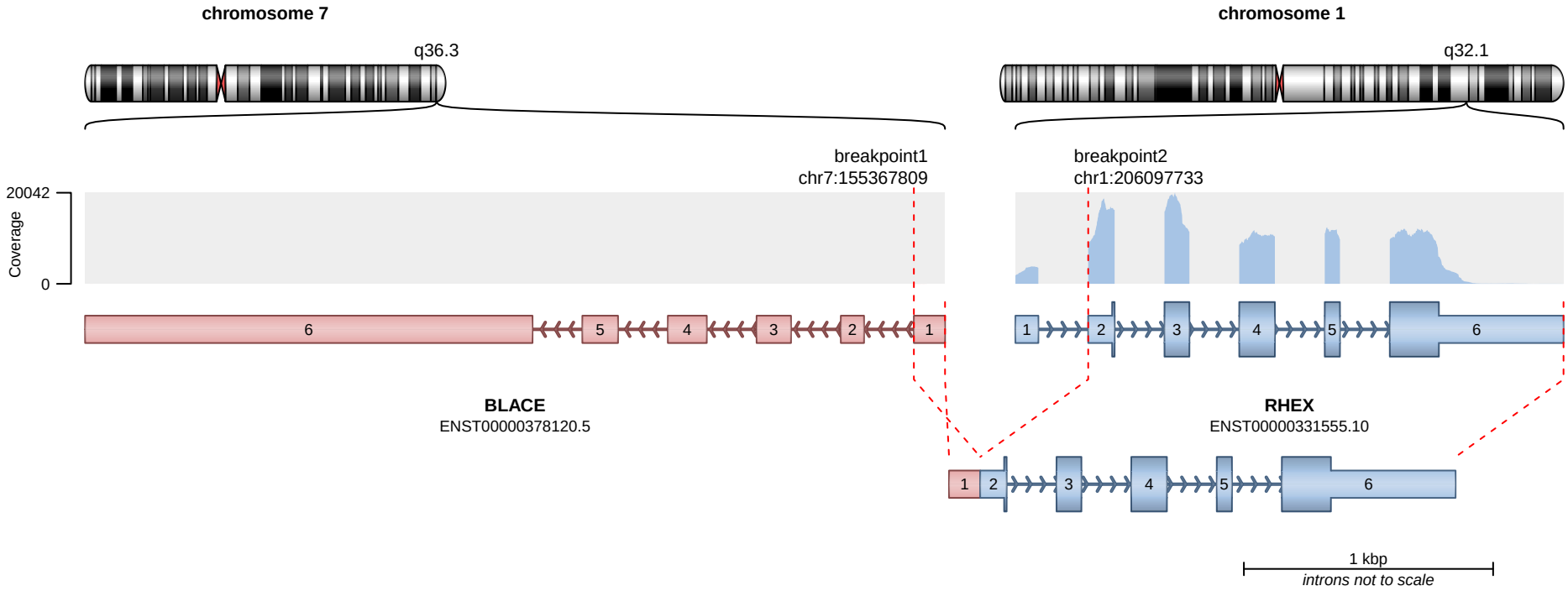


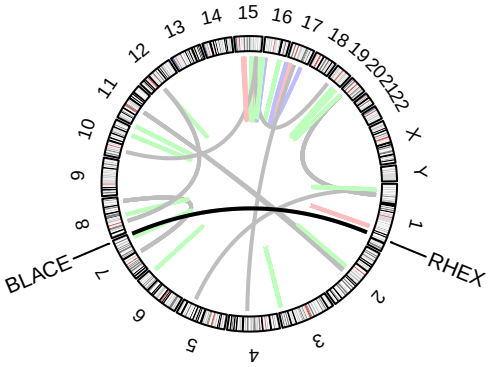
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

translocation
deletion
duplication
inversion





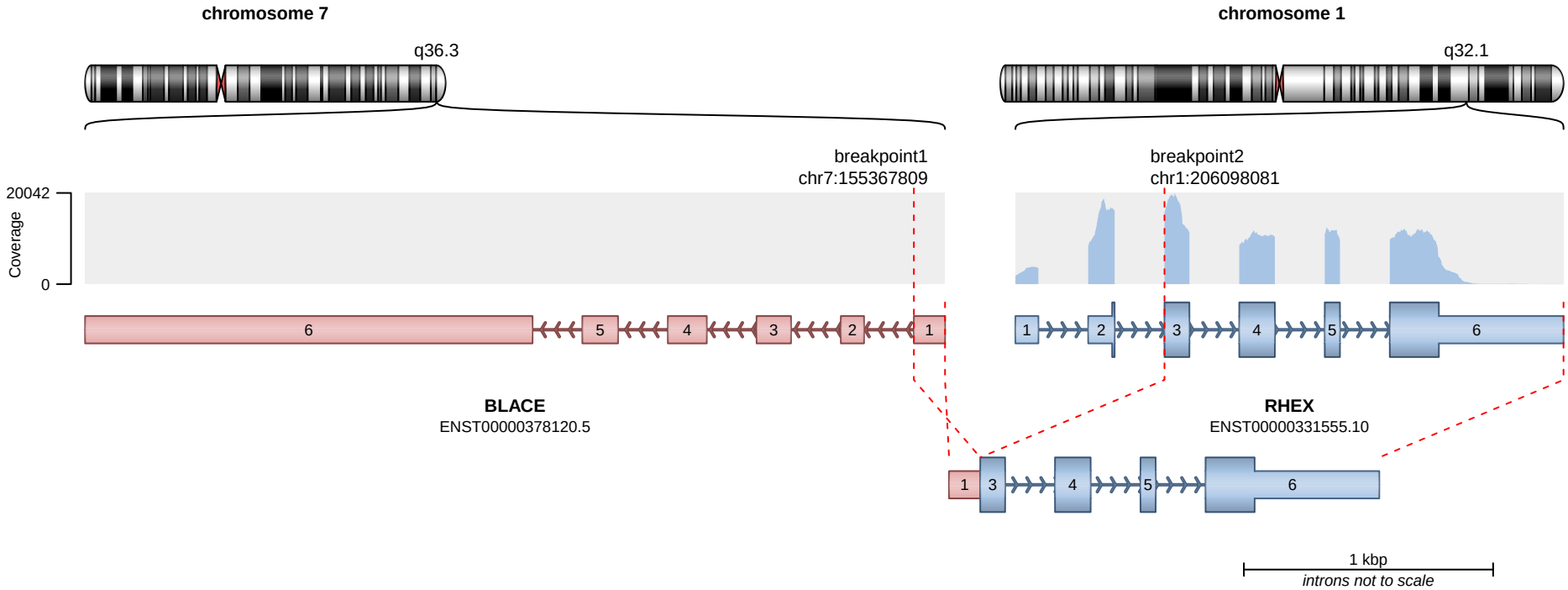
RETAINED PROTEIN DOMAINS
reading frame unclear

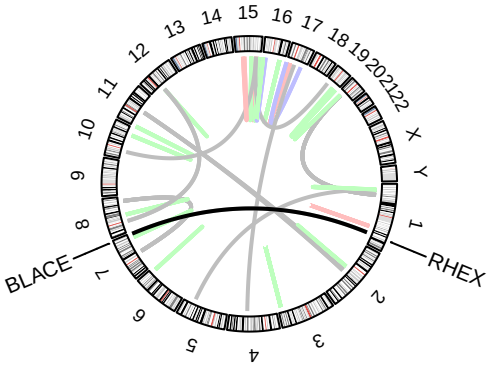
RHEX
Regulator of human erythroid cell expansion (RHEX)

SUPPORTING READ COUNT

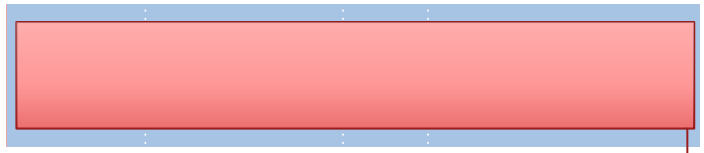
Split reads = 316
Discordant mates = 0

translocation
deletion
duplication
inversion





RETAINED PROTEIN DOMAINS
reading frame unclear

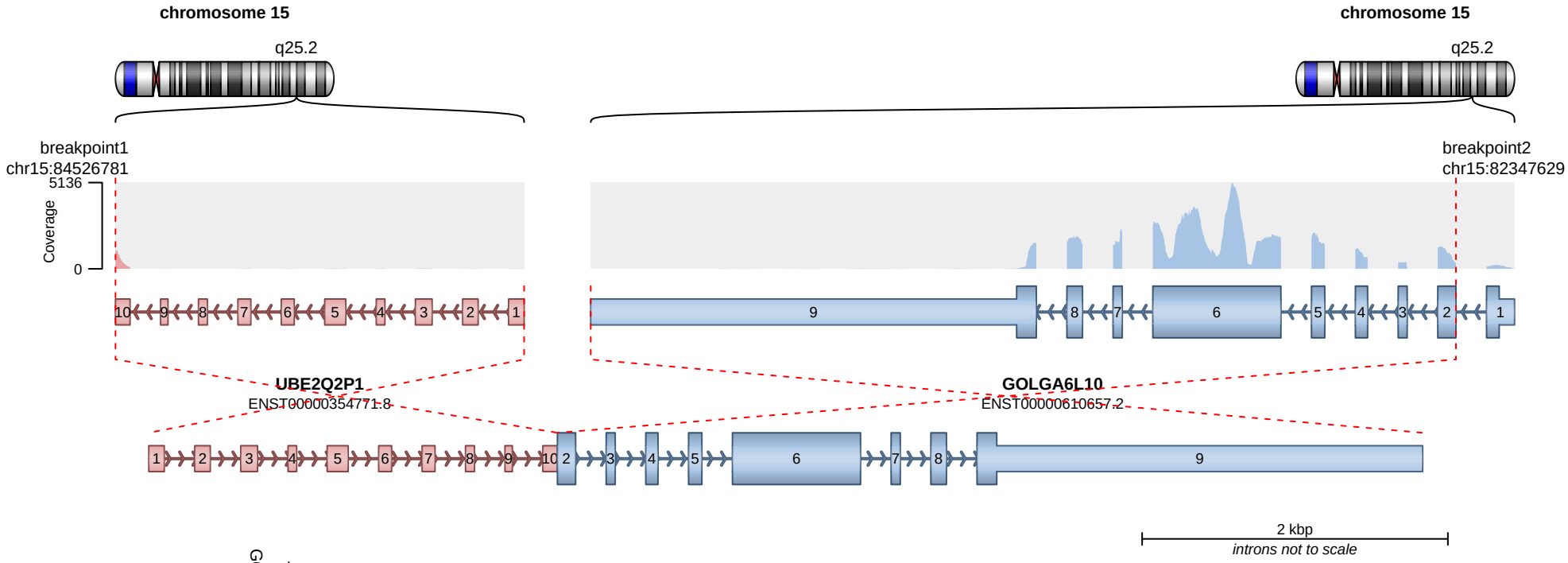


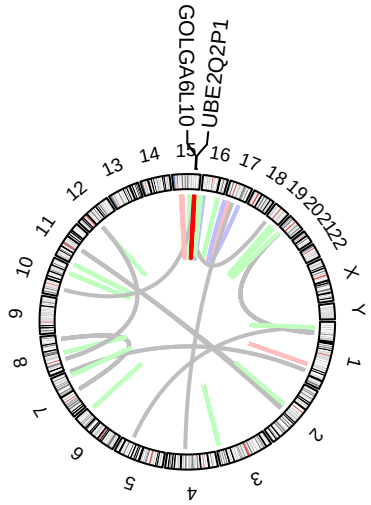
RHEX
Regulator of human erythroid cell expansion (RHEX)

SUPPORTING READ COUNT

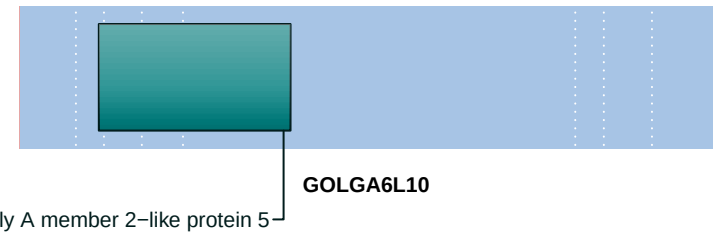
Split reads = 10
Discordant mates = 0

translocation
deletion
duplication
inversion





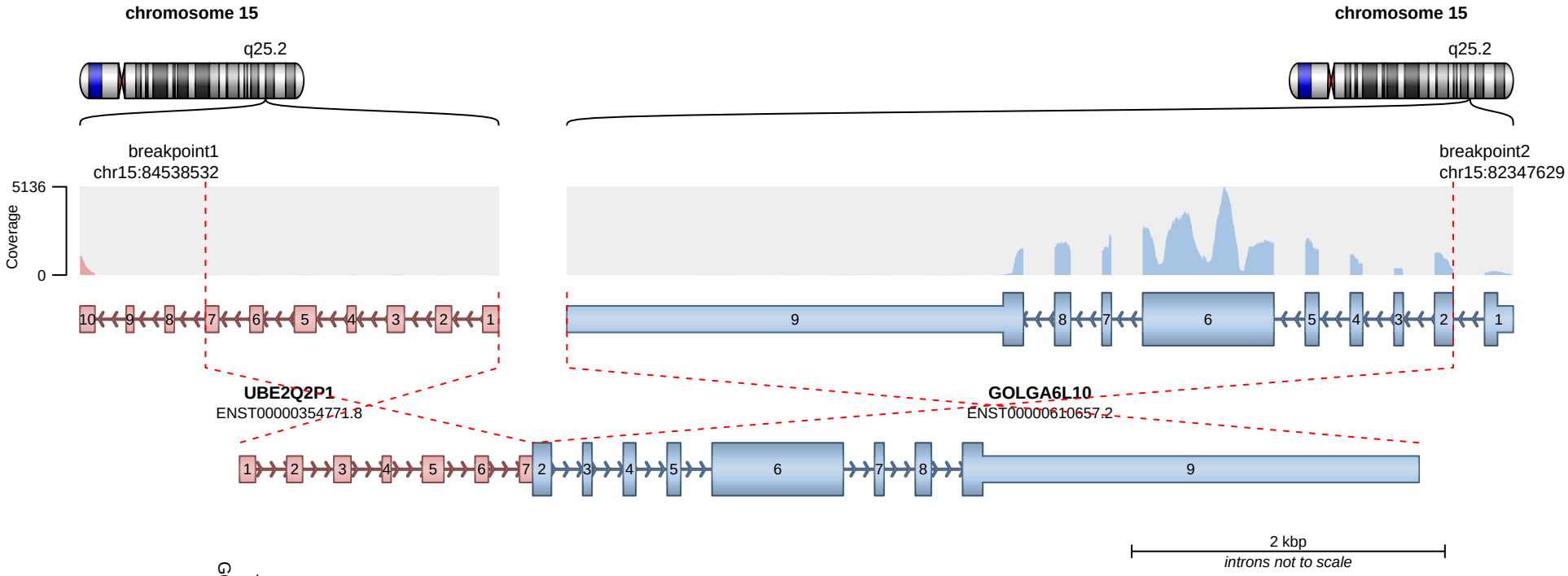
RETAINED PROTEIN DOMAINS
reading frame unclear

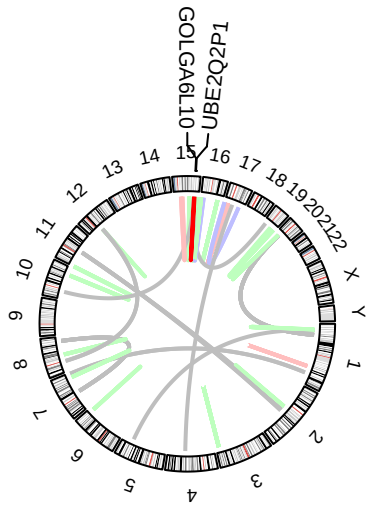


SUPPORTING READ COUNT

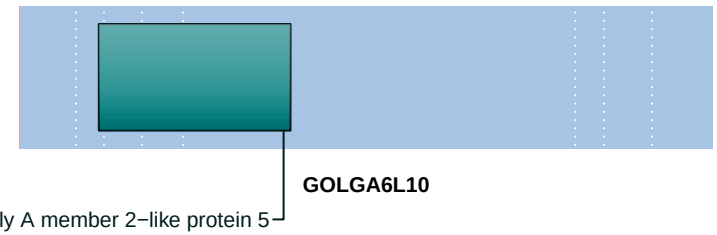
Split reads = 191
Discordant mates = 0

translocation
deletion
duplication
inversion





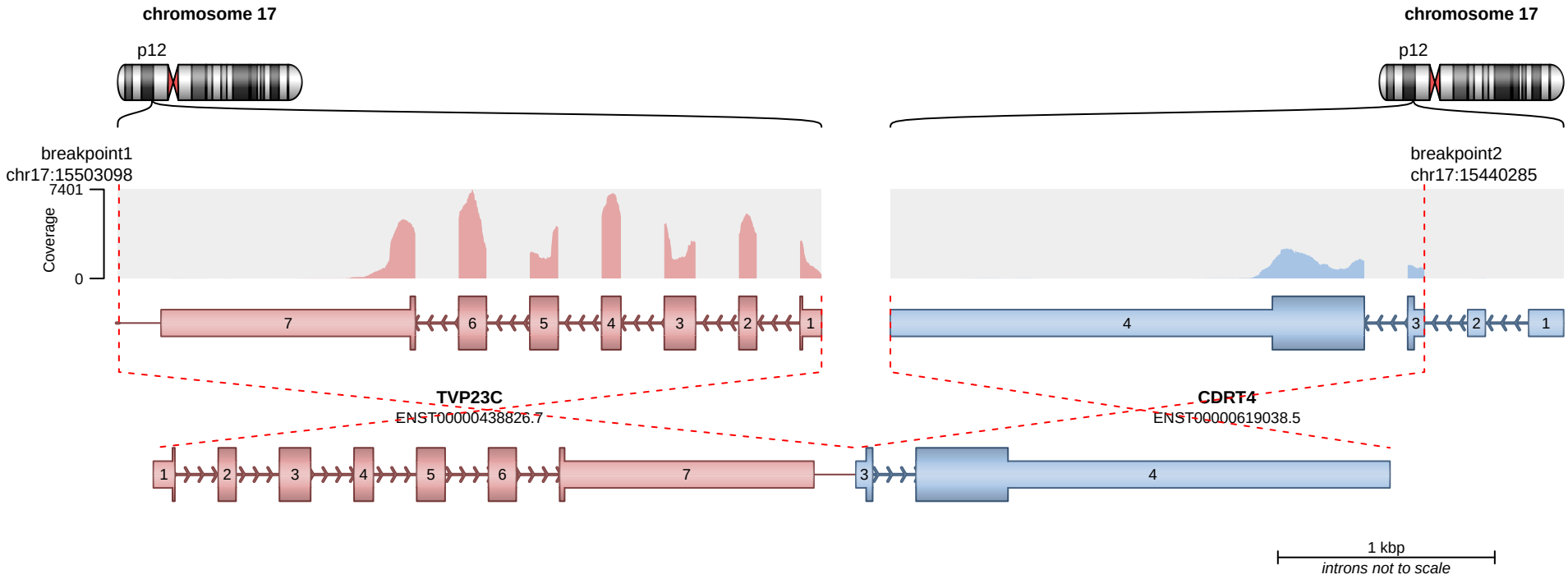
RETAINED PROTEIN DOMAINS
reading frame unclear

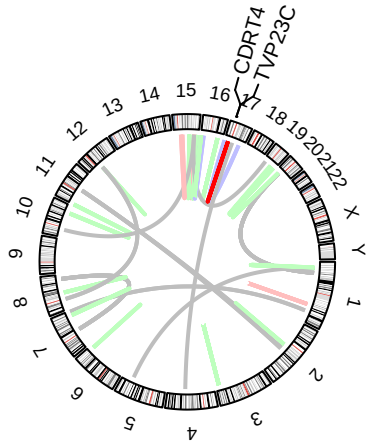


SUPPORTING READ COUNT

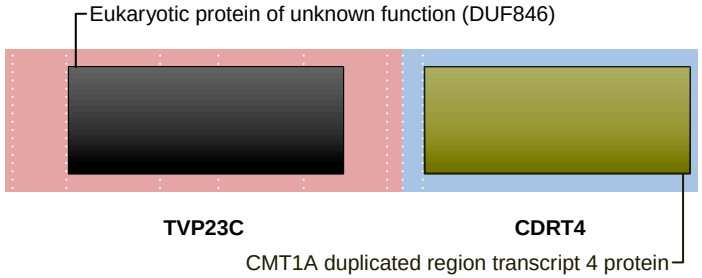
Split reads = 2
Discordant mates = 0

translocation
deletion
duplication
inversion





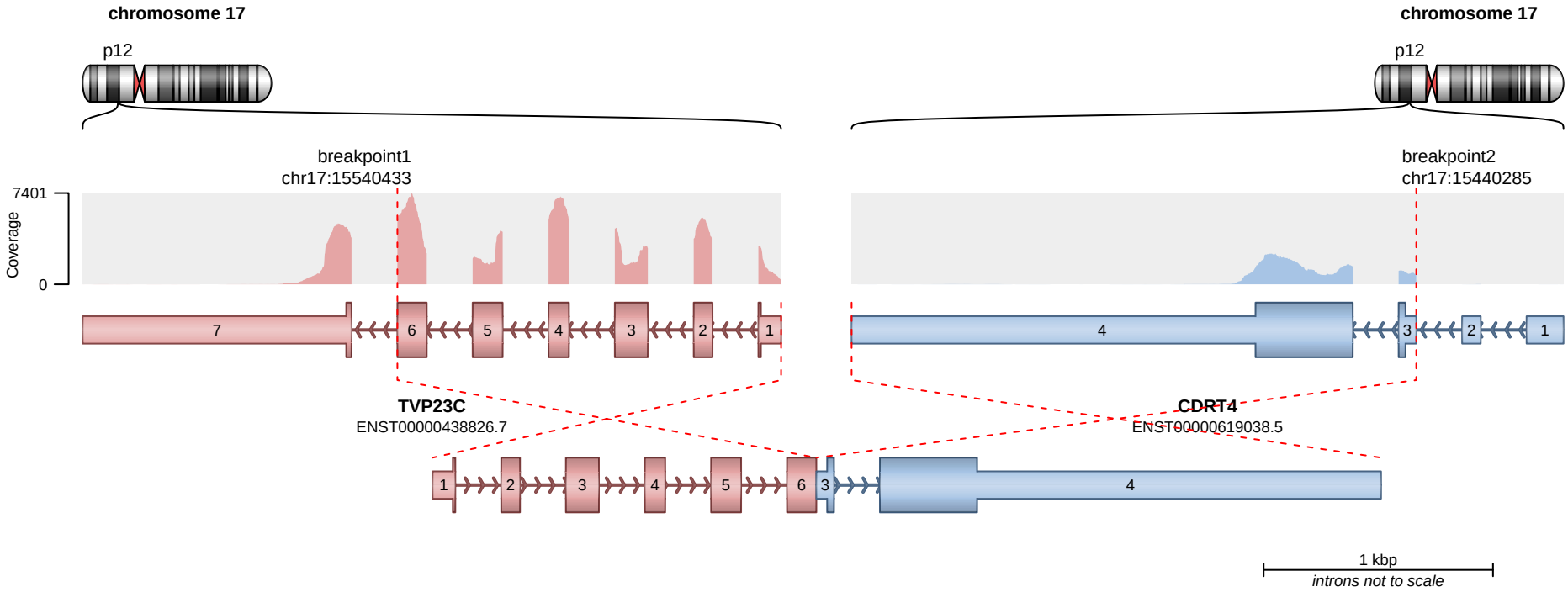
RETAINED PROTEIN DOMAINS
reading frame unclear

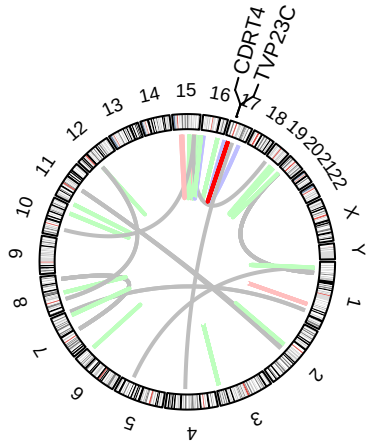


SUPPORTING READ COUNT

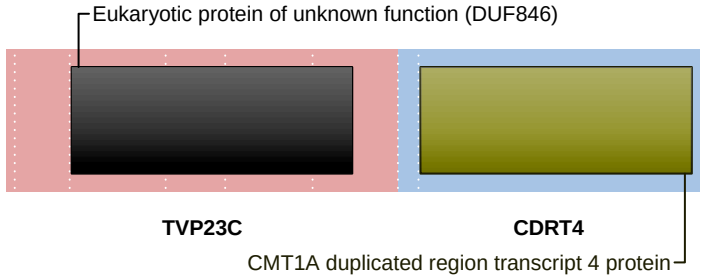
Split reads = 155
Discordant mates = 1

translocation
deletion
duplication
inversion





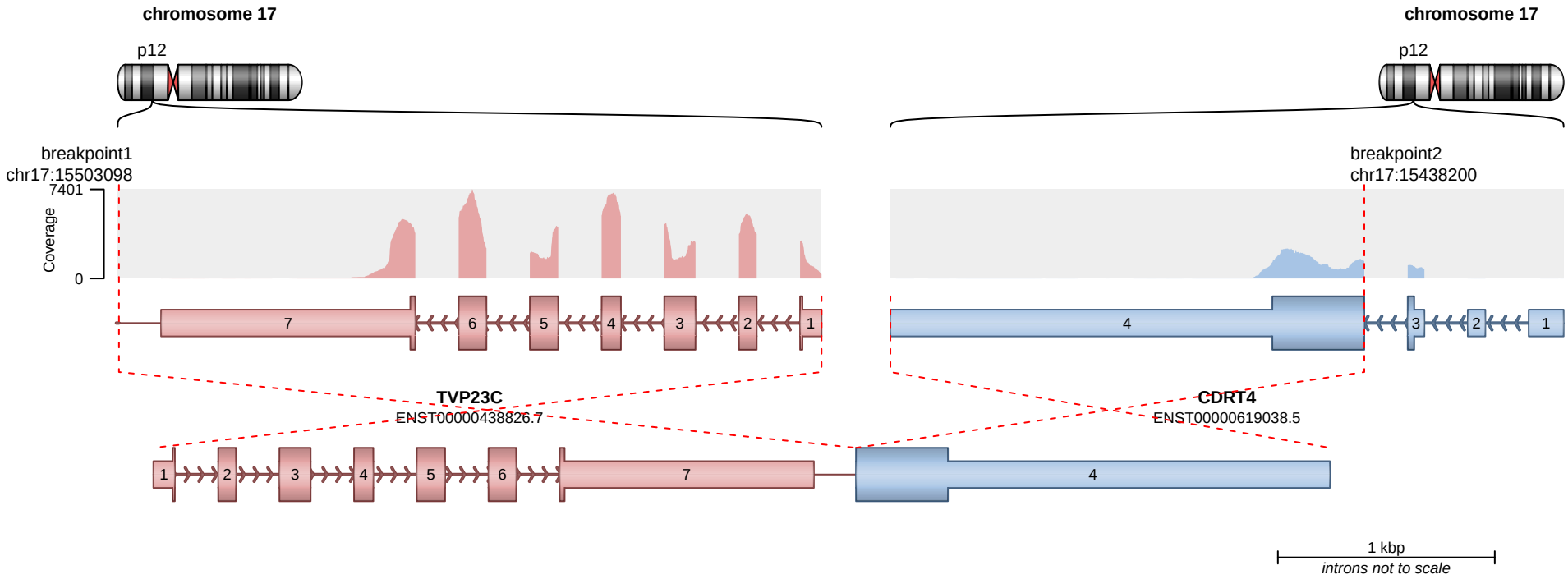
RETAINED PROTEIN DOMAINS
reading frame unclear

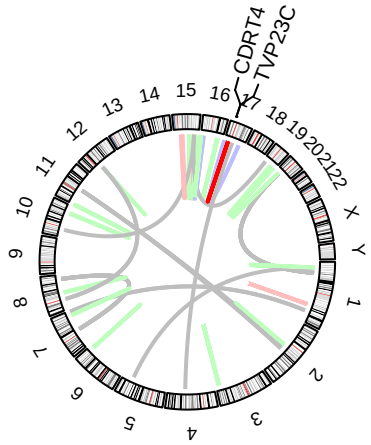


SUPPORTING READ COUNT

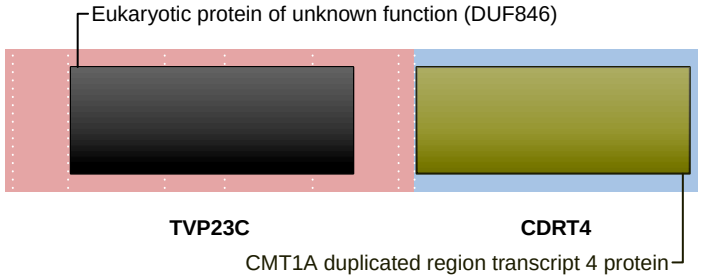
Split reads = 84
Discordant mates = 1

translocation
duplication
deletion
inversion





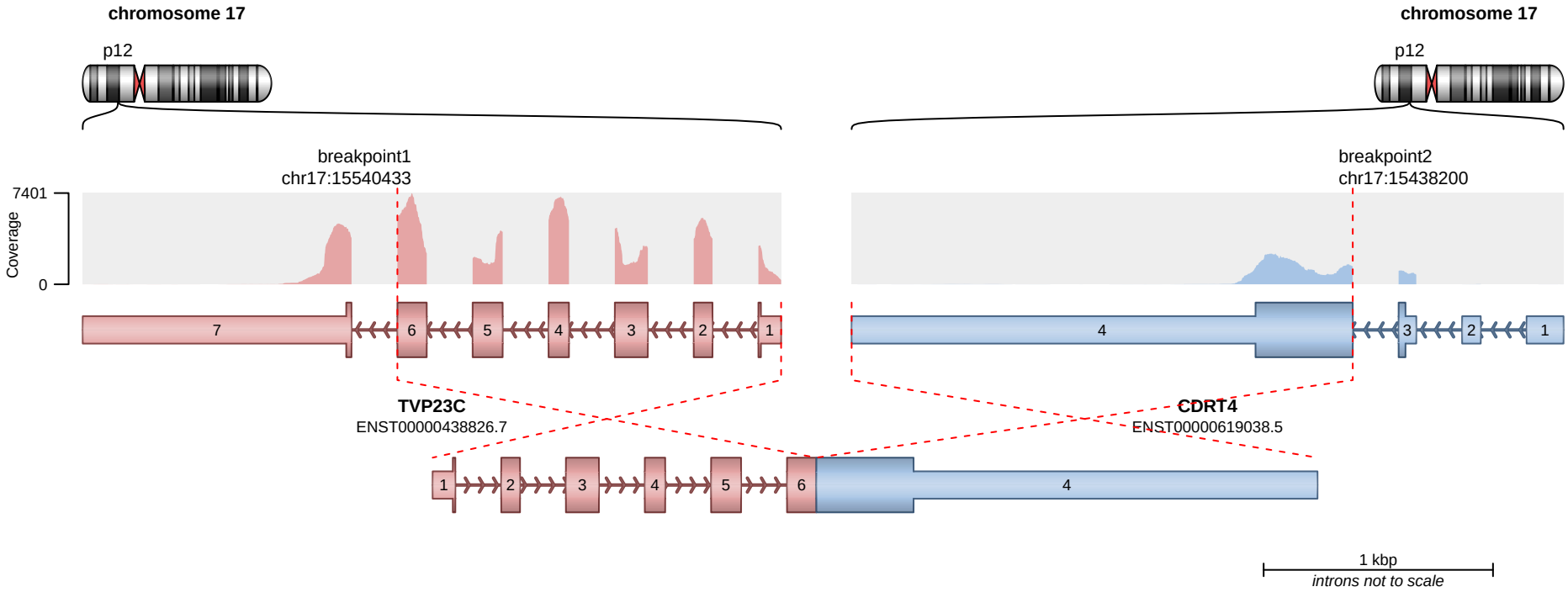
RETAINED PROTEIN DOMAINS
reading frame unclear

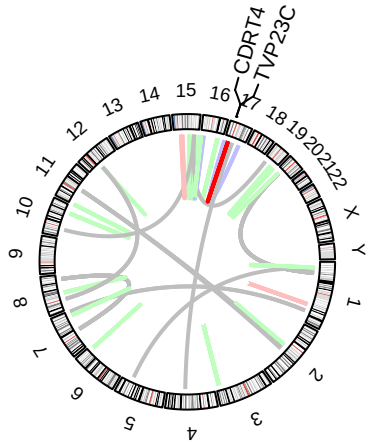


SUPPORTING READ COUNT

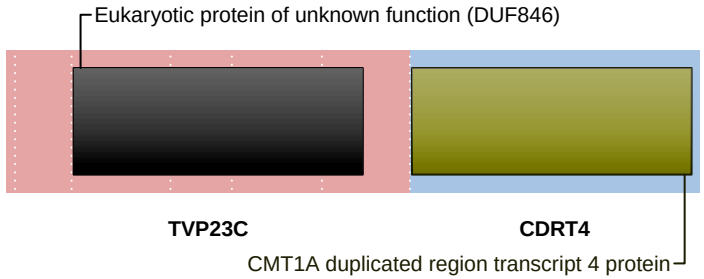
Split reads = 57
Discordant mates = 0

translocation
deletion
duplication
inversion



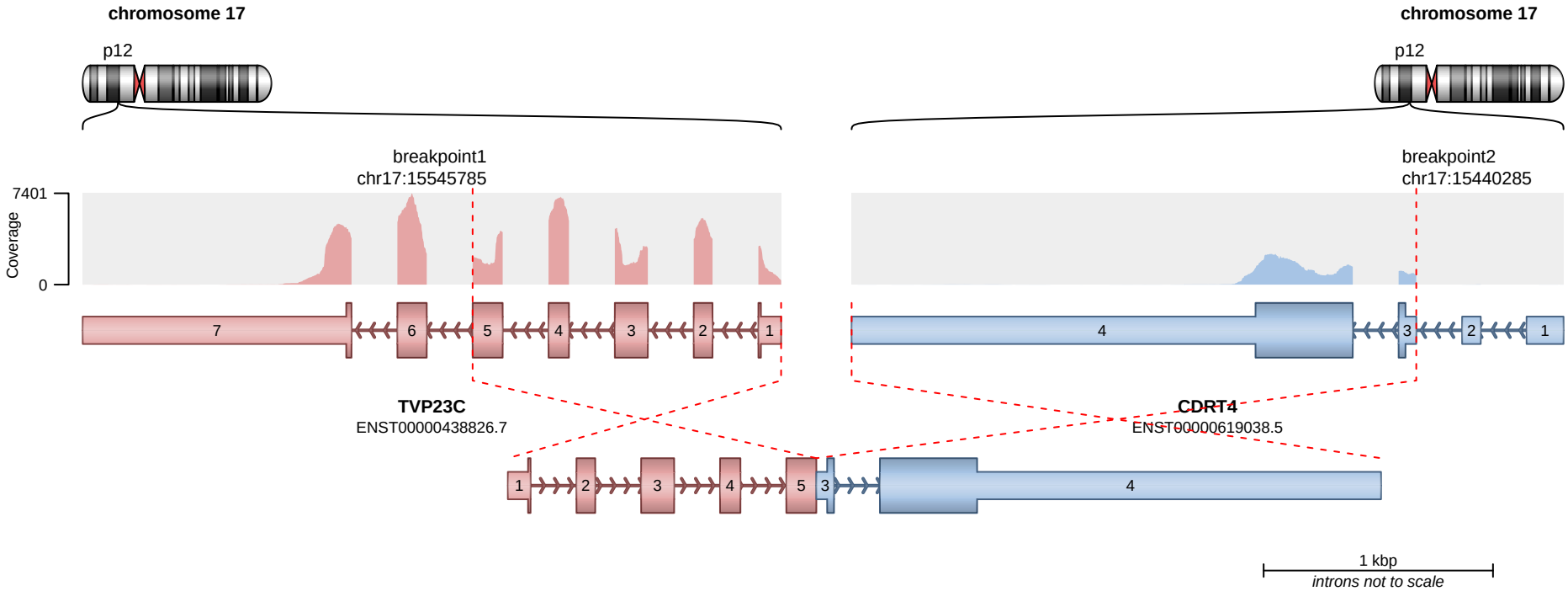


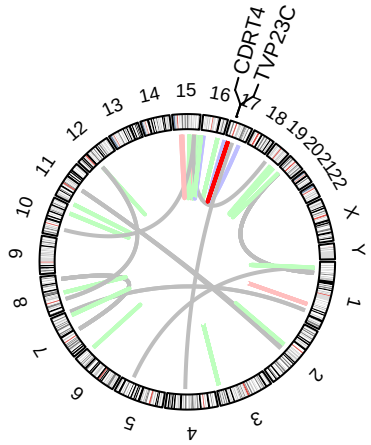
RETAINED PROTEIN DOMAINS
reading frame unclear



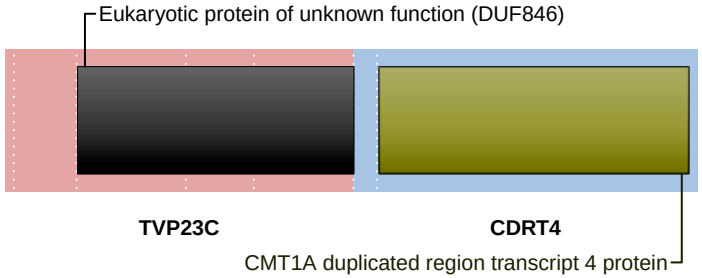
SUPPORTING READ COUNT

Split reads = 31
Discordant mates = 0





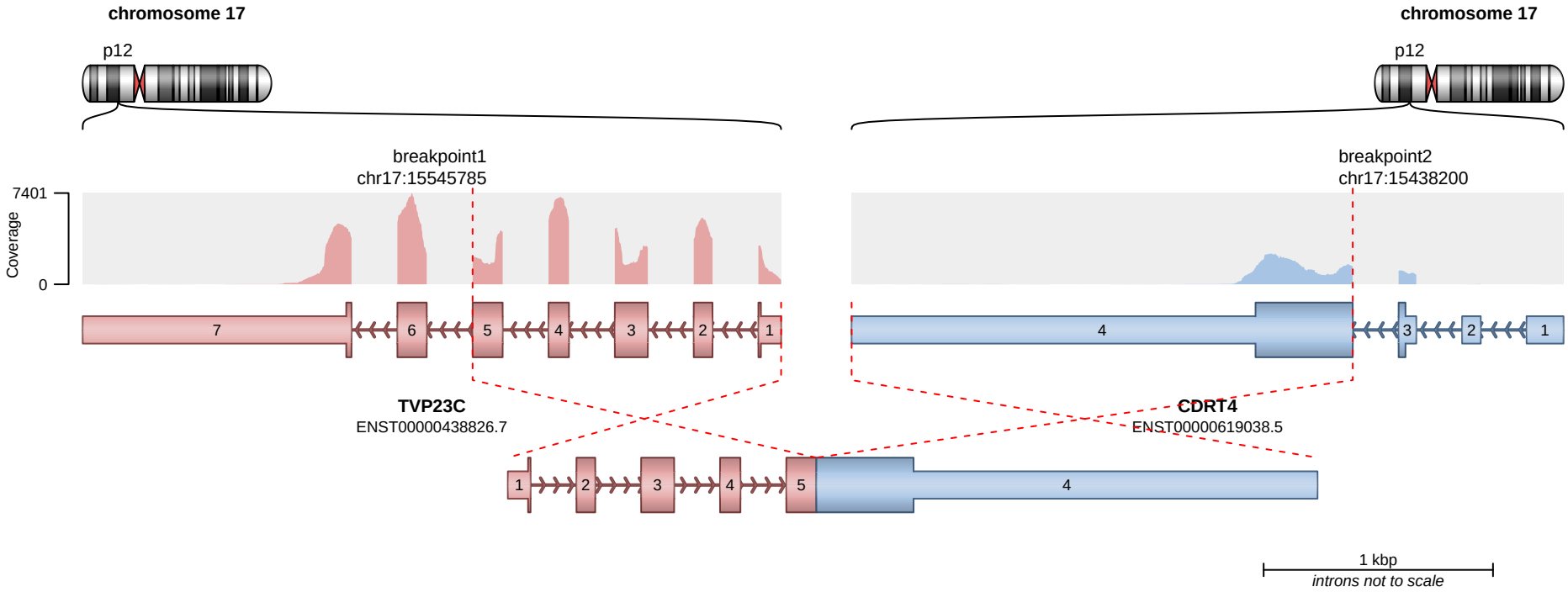
RETAINED PROTEIN DOMAINS
reading frame unclear

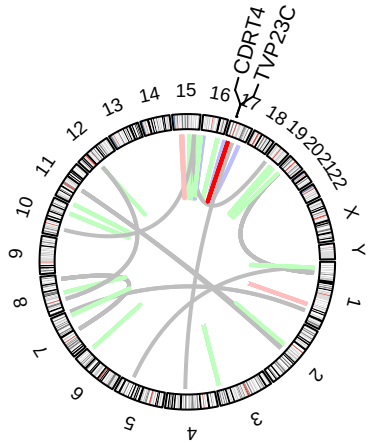


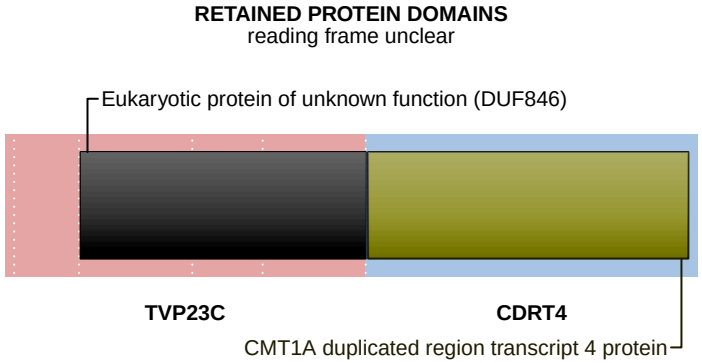
SUPPORTING READ COUNT

Split reads = 16
Discordant mates = 0

translocation
deletion
duplication
inversion



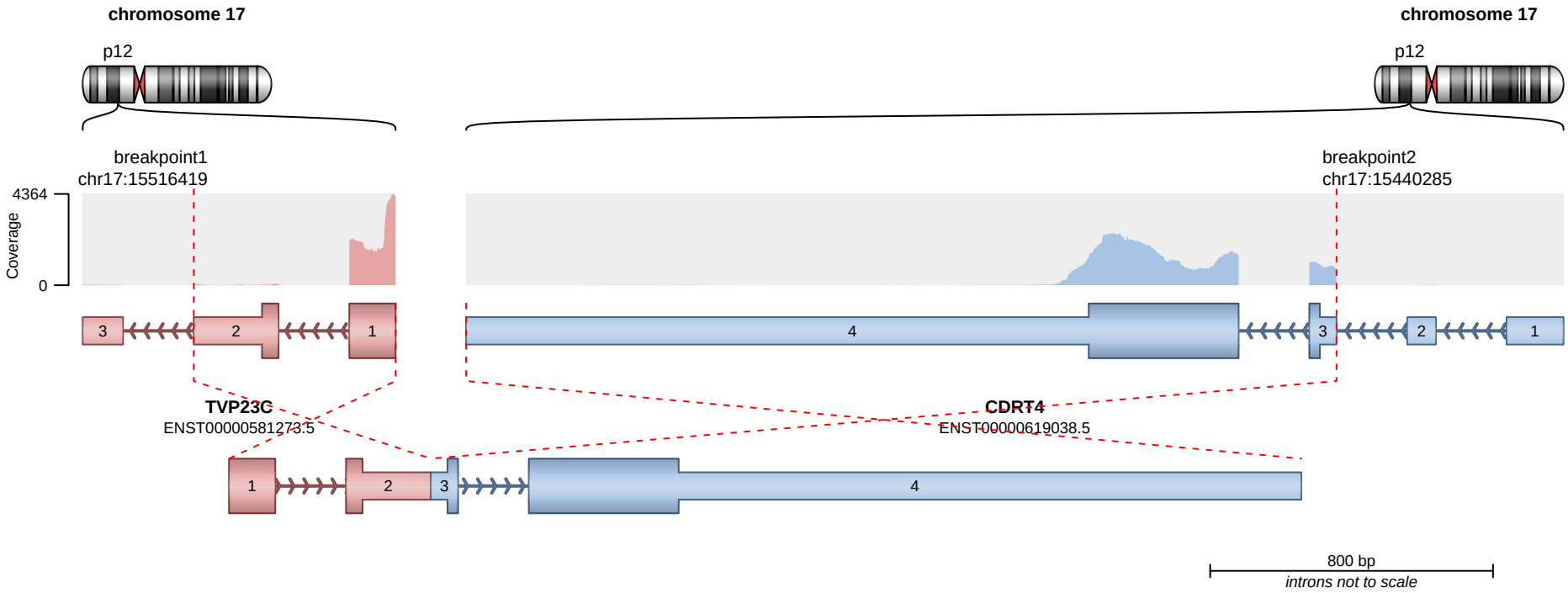


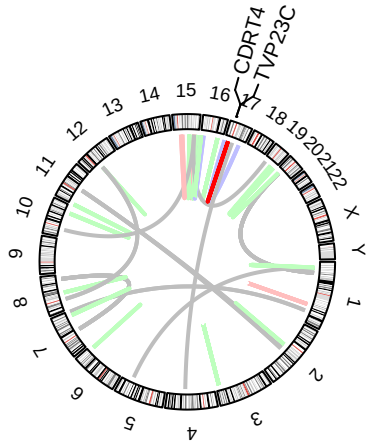


SUPPORTING READ COUNT

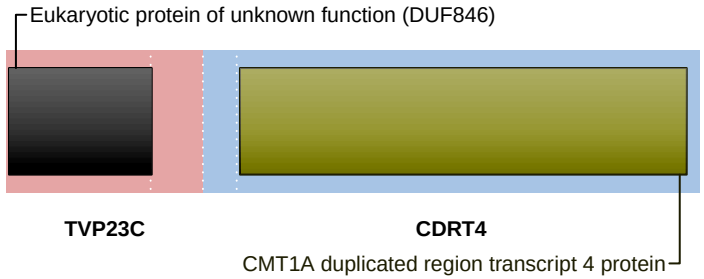
Split reads = 8
Discordant mates = 0

translocation
deletion
duplication
inversion





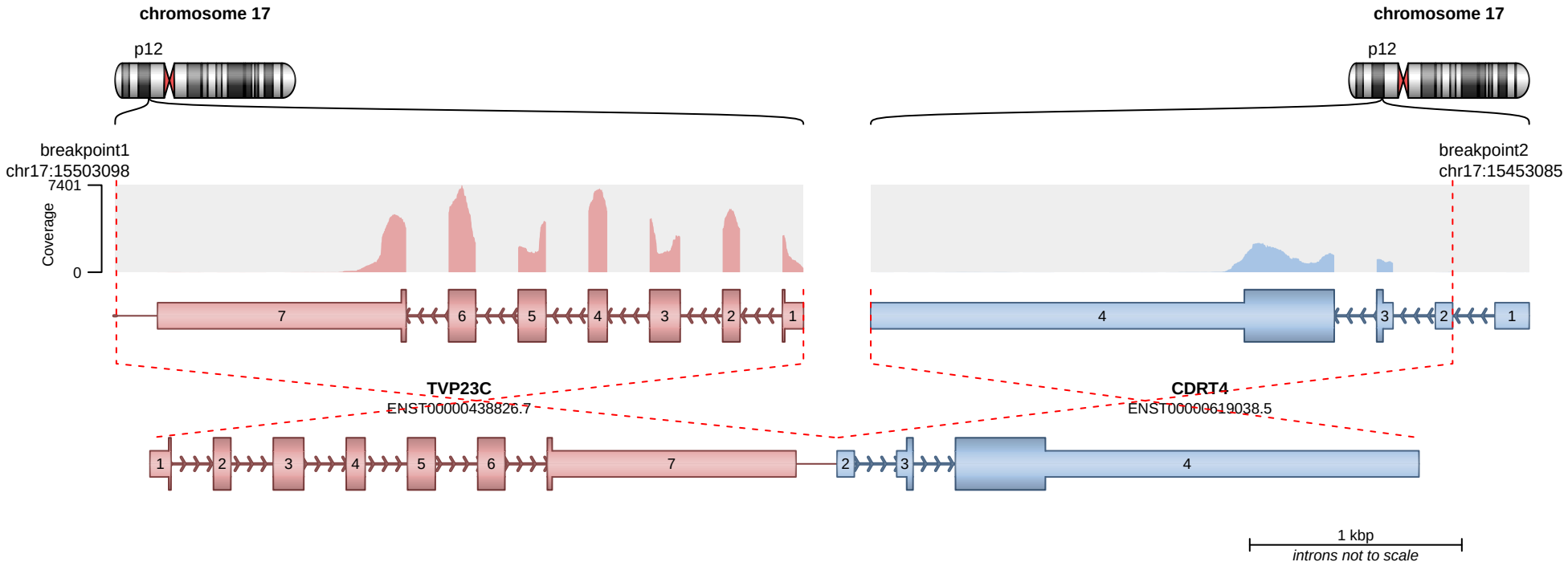
RETAINED PROTEIN DOMAINS
reading frame unclear

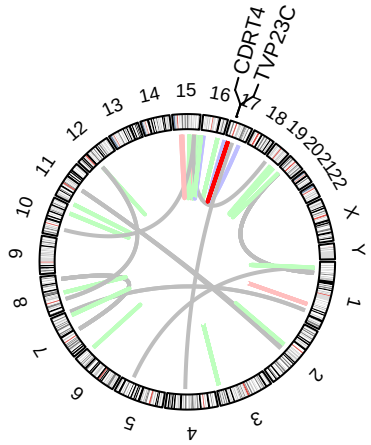


SUPPORTING READ COUNT

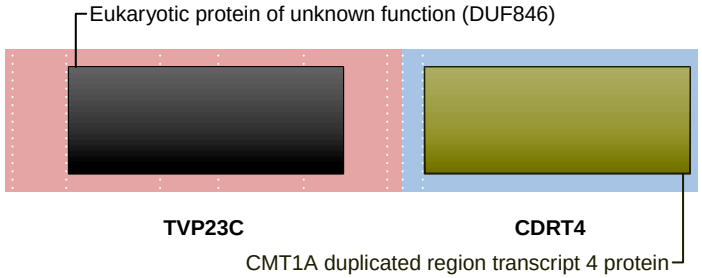
Split reads = 7
Discordant mates = 1

translocation
deletion
duplication
inversion





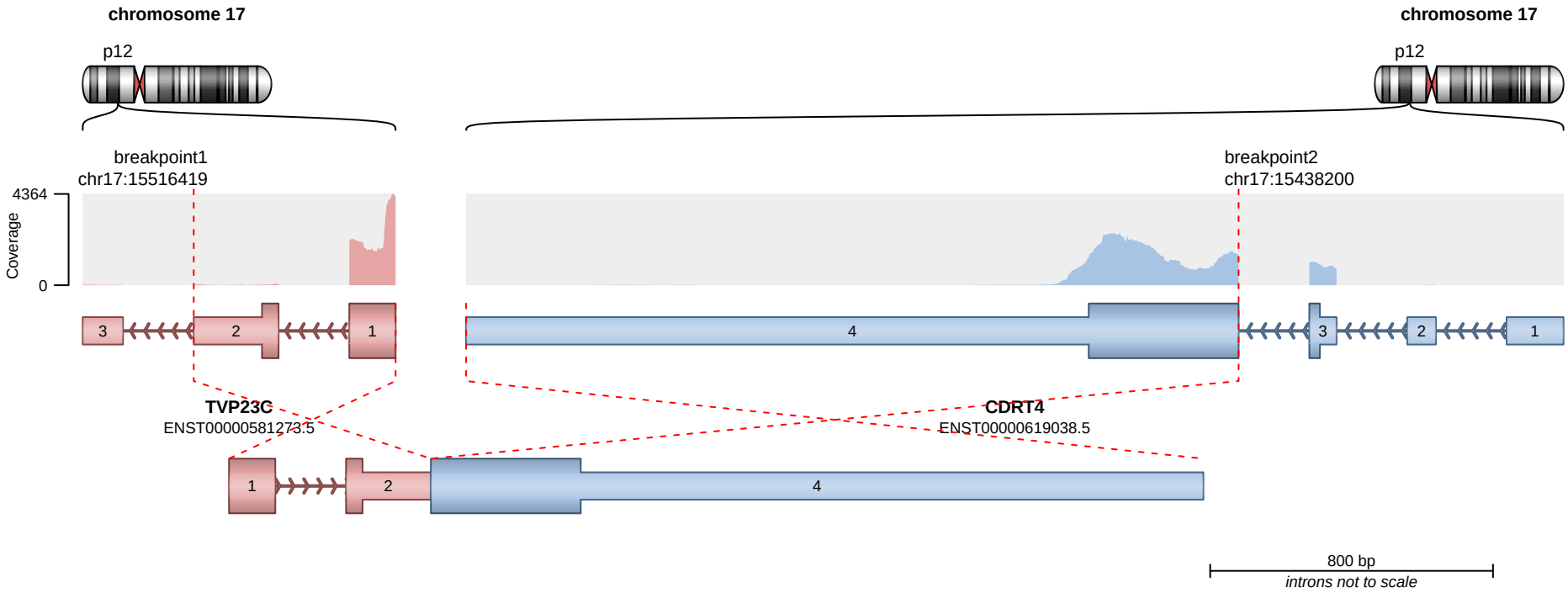
RETAINED PROTEIN DOMAINS
reading frame unclear

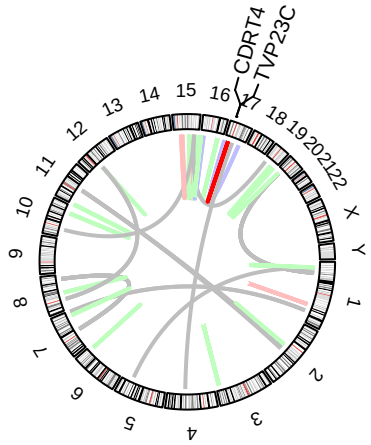


SUPPORTING READ COUNT

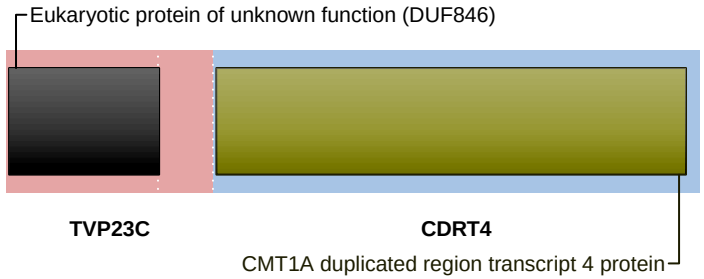
Split reads = 6
Discordant mates = 1

translocation
duplication
deletion
inversion





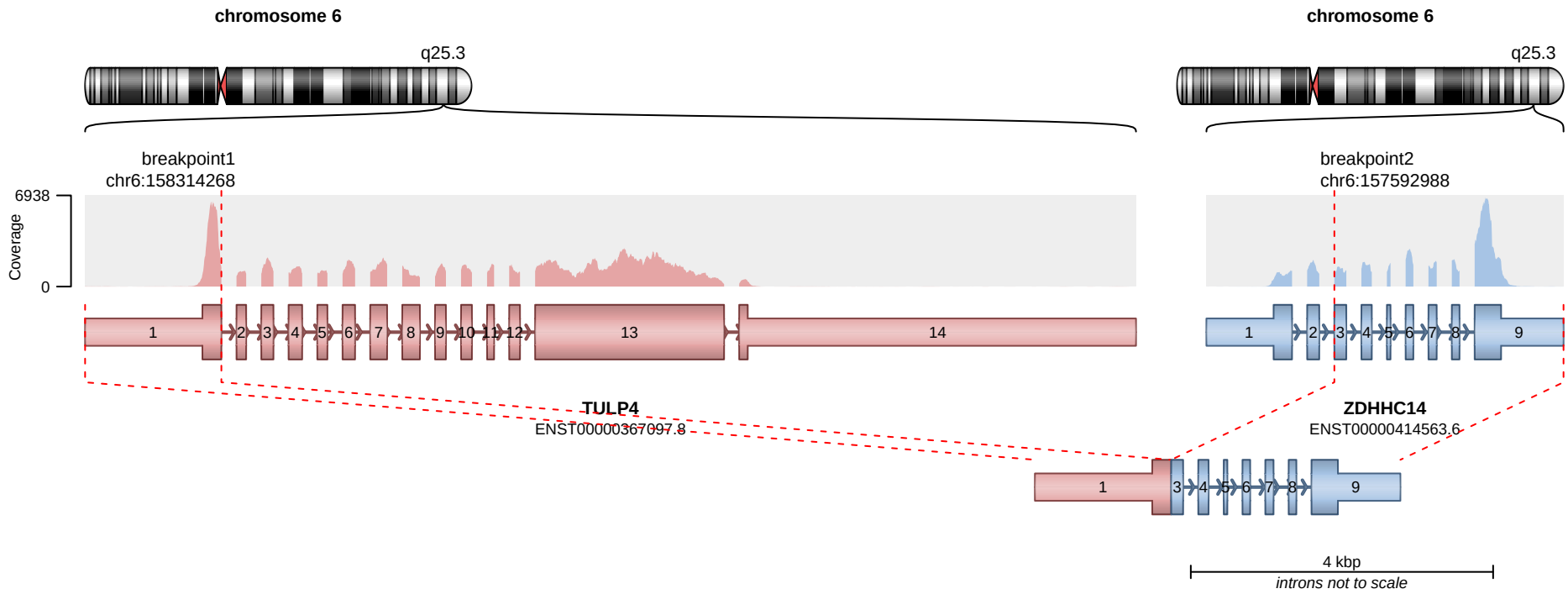
RETAINED PROTEIN DOMAINS
reading frame unclear

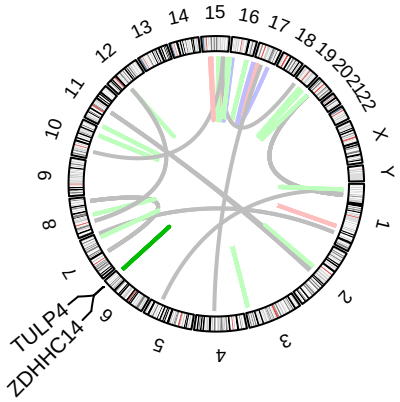


SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

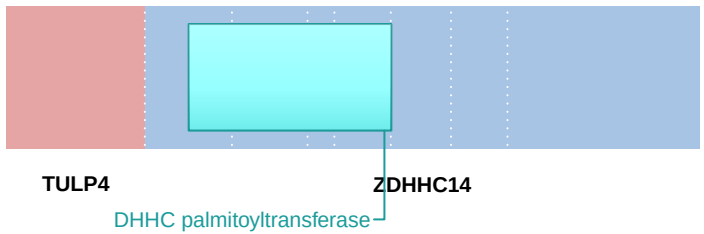
translocation
duplication
deletion
inversion





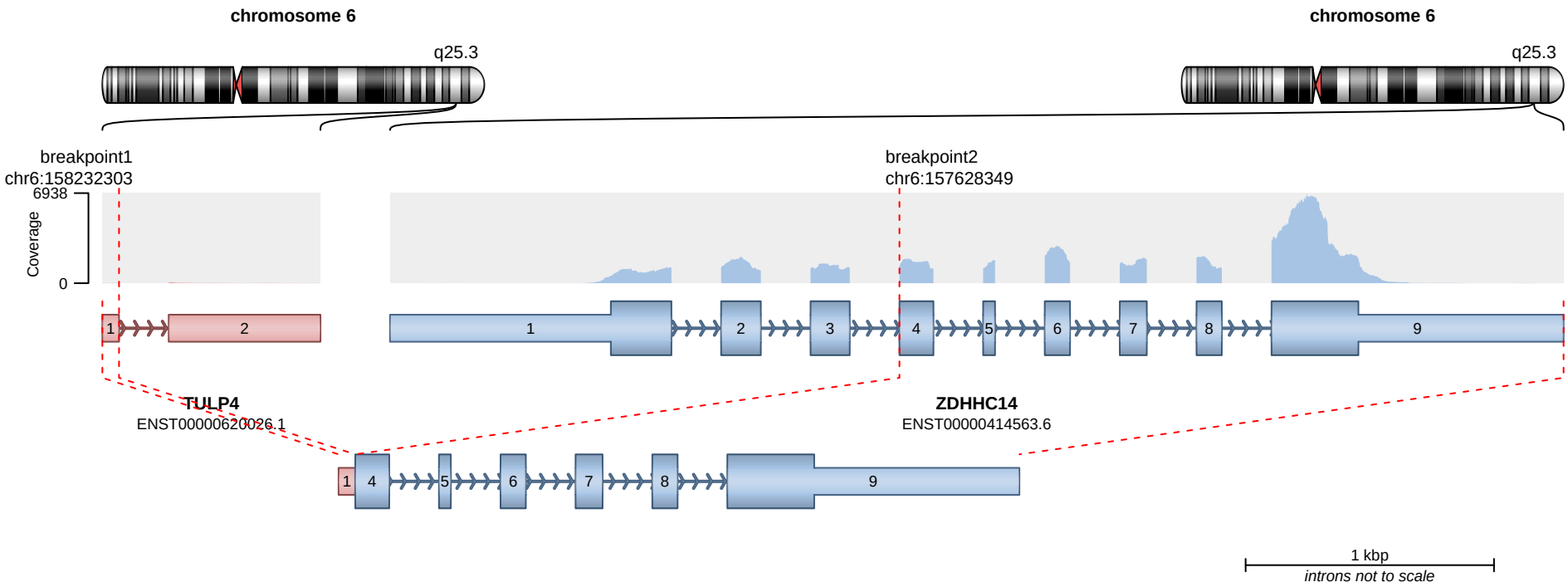
translocation
deletion
duplication
inversion

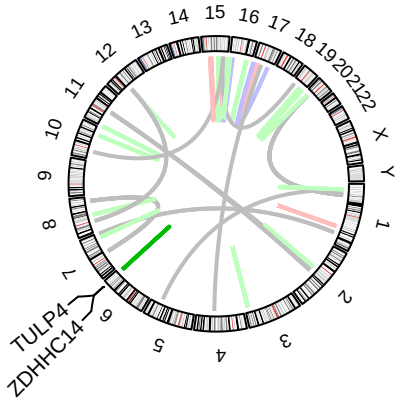
RETAINED PROTEIN DOMAINS
reading frame unclear

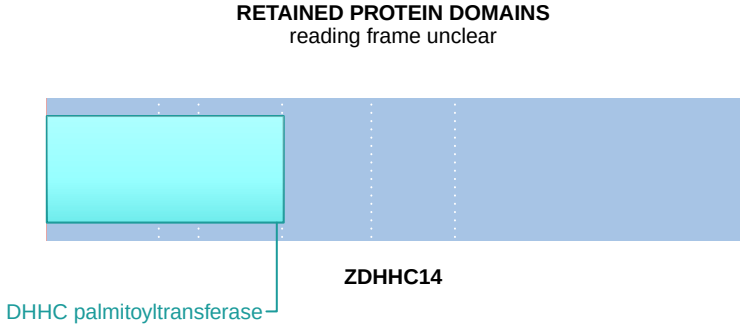


SUPPORTING READ COUNT

Split reads = 145
Discordant mates = 1



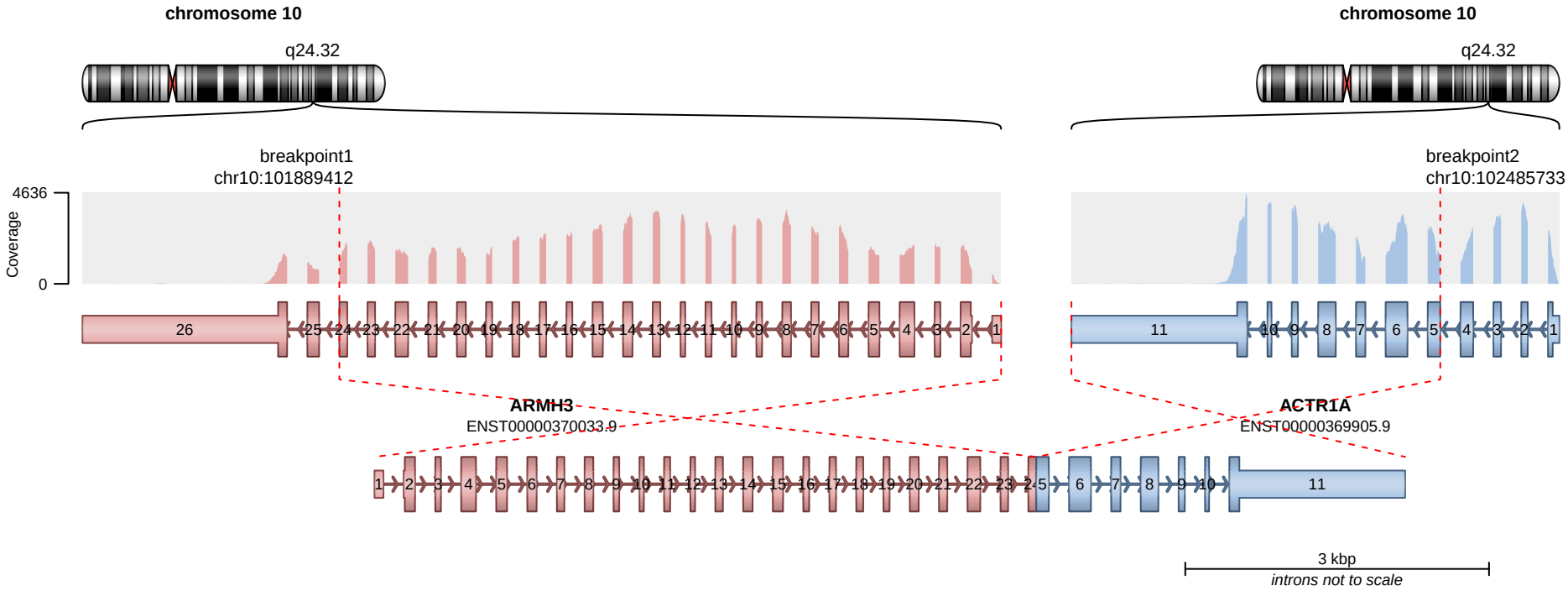


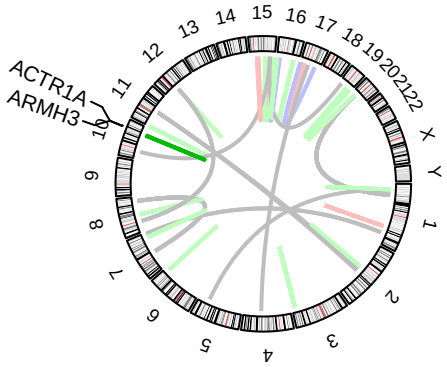


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

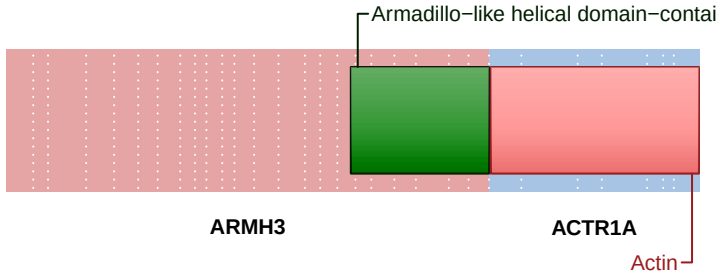
translocation
deletion
duplication
inversion





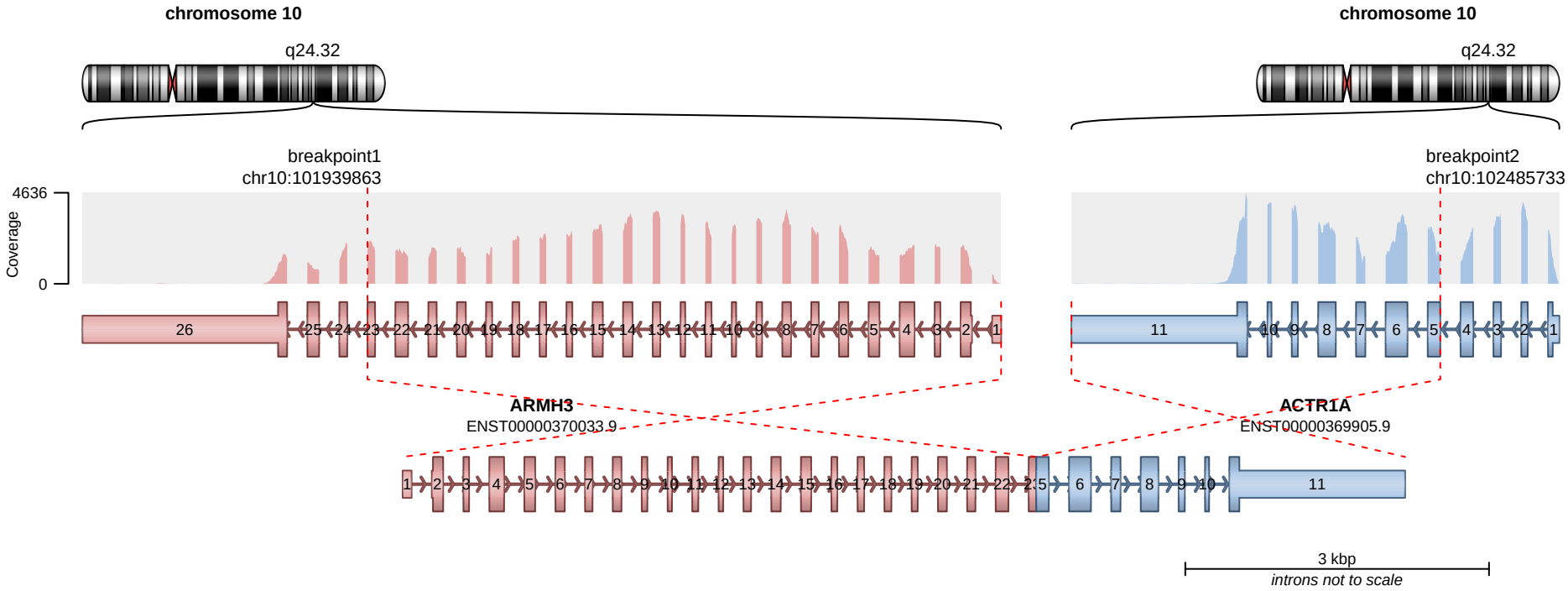
translocation
deletion
duplication
inversion

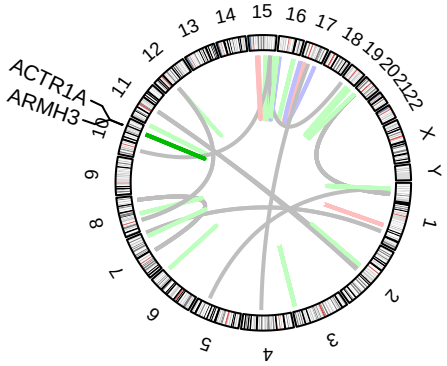
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

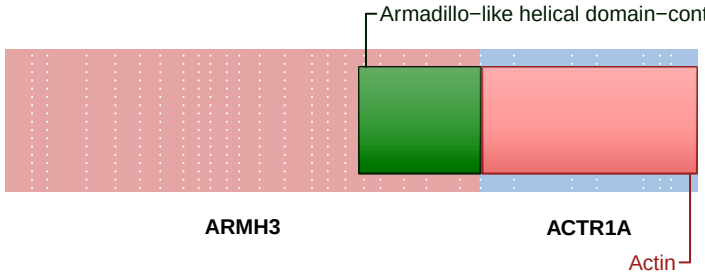
Split reads = 143
Discordant mates = 0





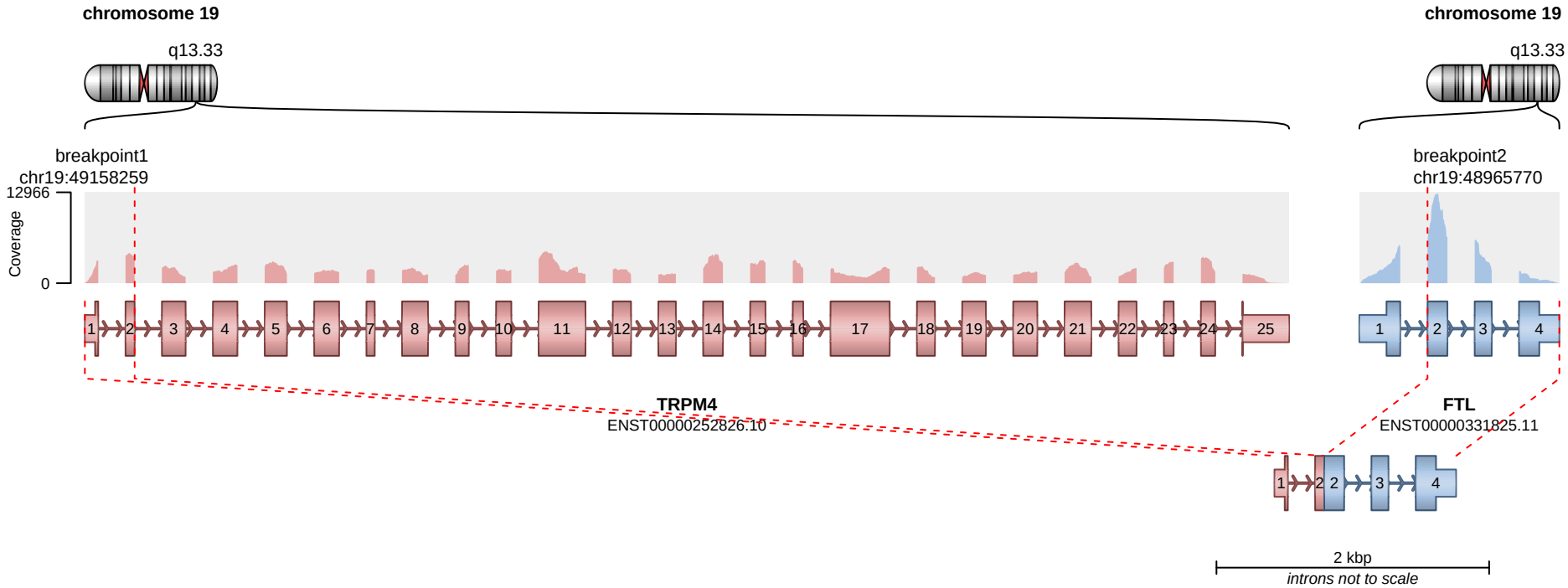
translocation
deletion
duplication
inversion

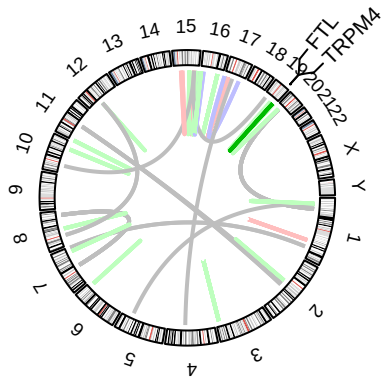
RETAINED PROTEIN DOMAINS
reading frame unclear

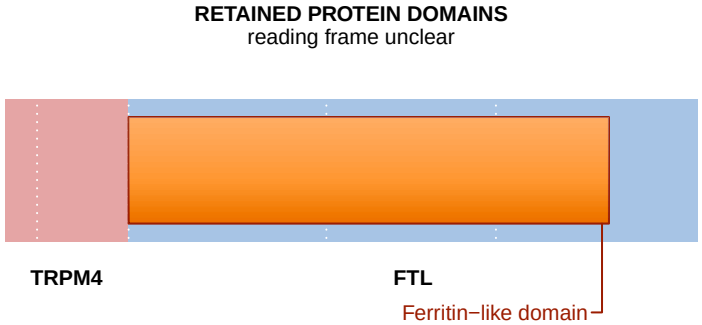


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0



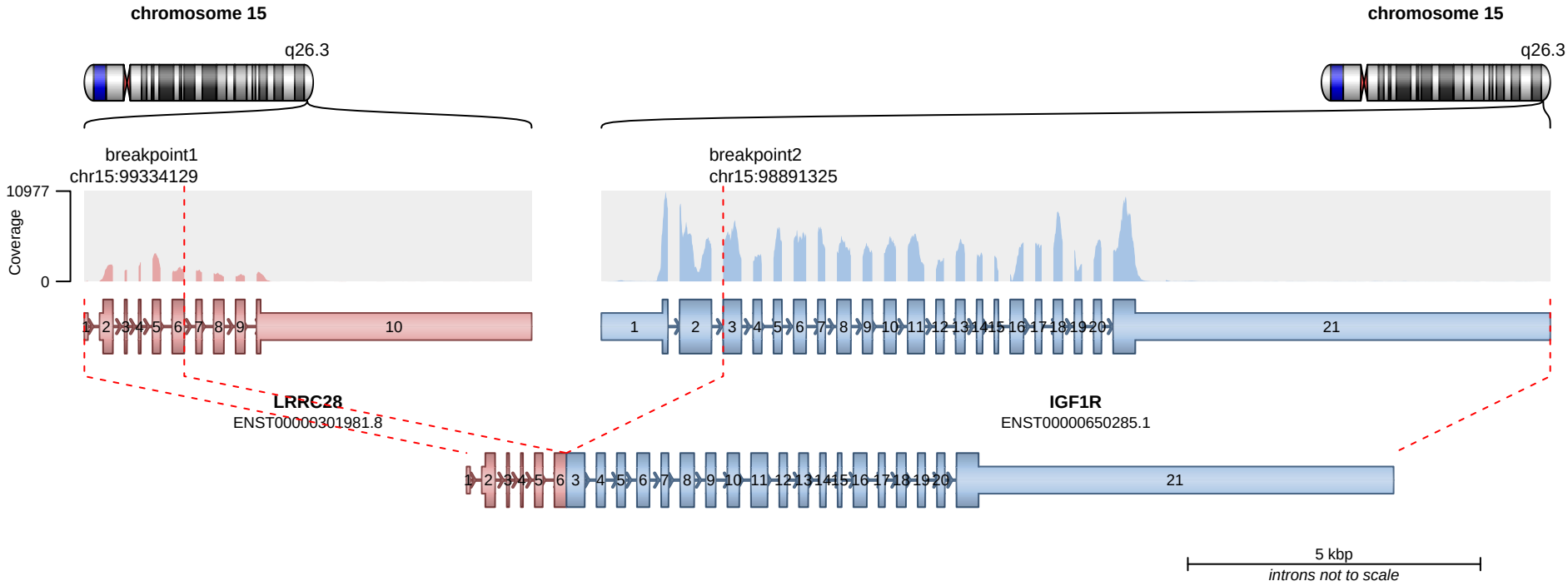


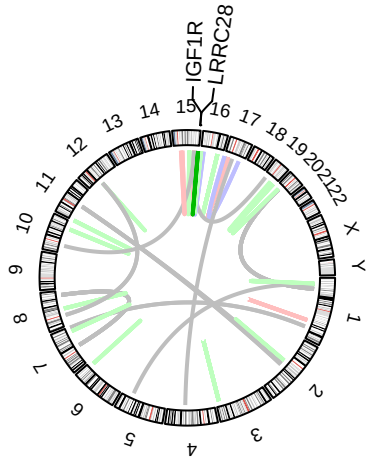


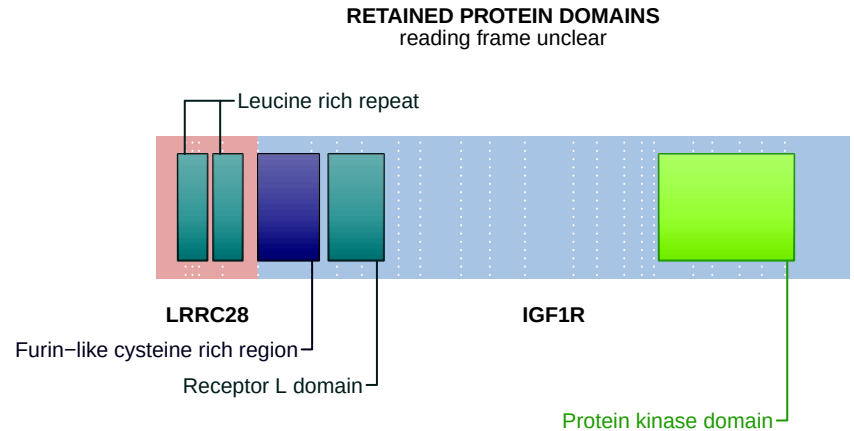
SUPPORTING READ COUNT

Split reads = 117
Discordant mates = 0

translocation
deletion
duplication
inversion



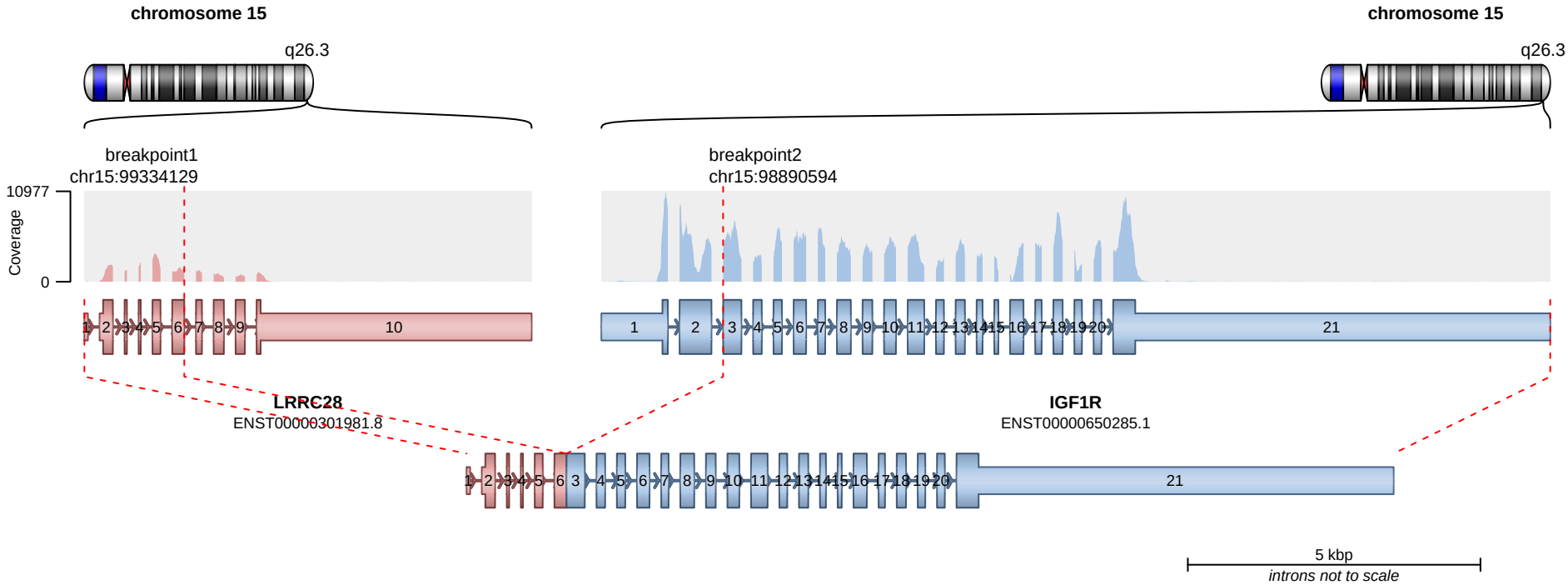


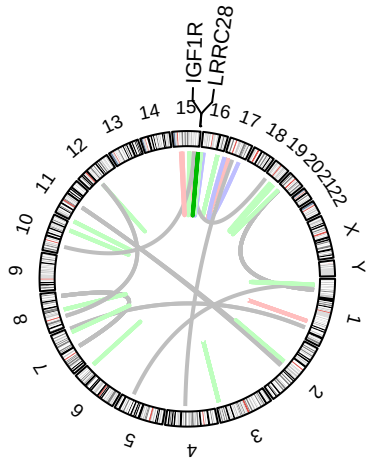


SUPPORTING READ COUNT

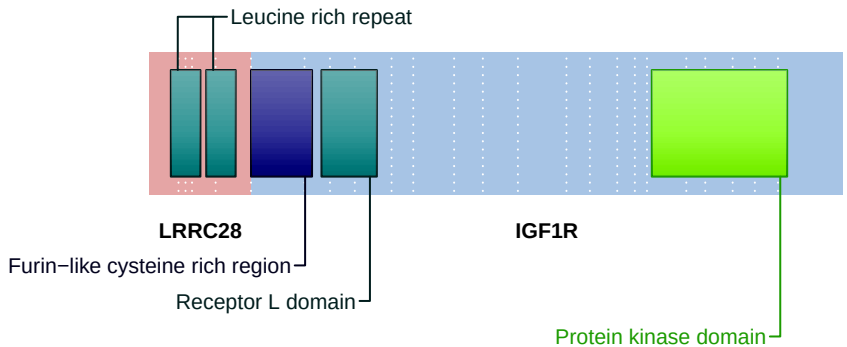
Split reads = 103
Discordant mates = 0

translocation
deletion
duplication
inversion





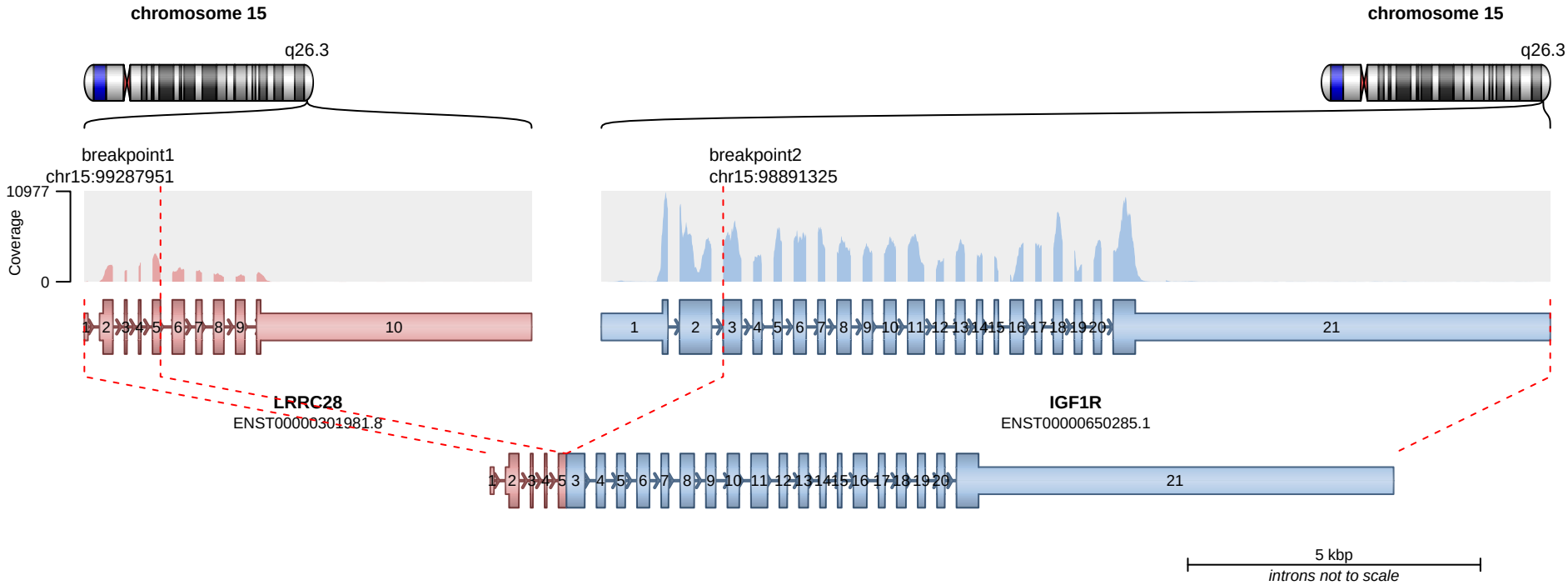
RETAINED PROTEIN DOMAINS
reading frame unclear

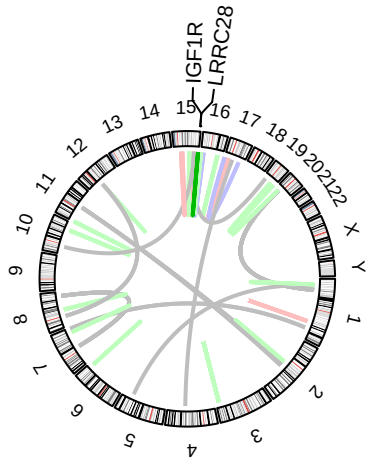


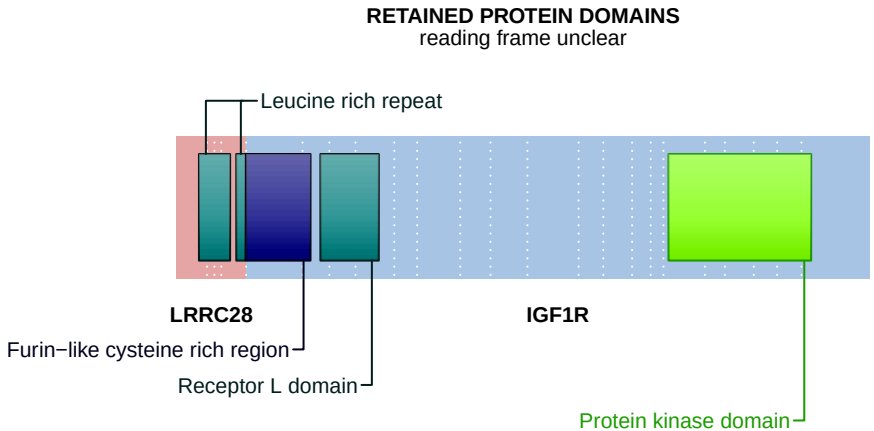
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

translocation
deletion
duplication
inversion



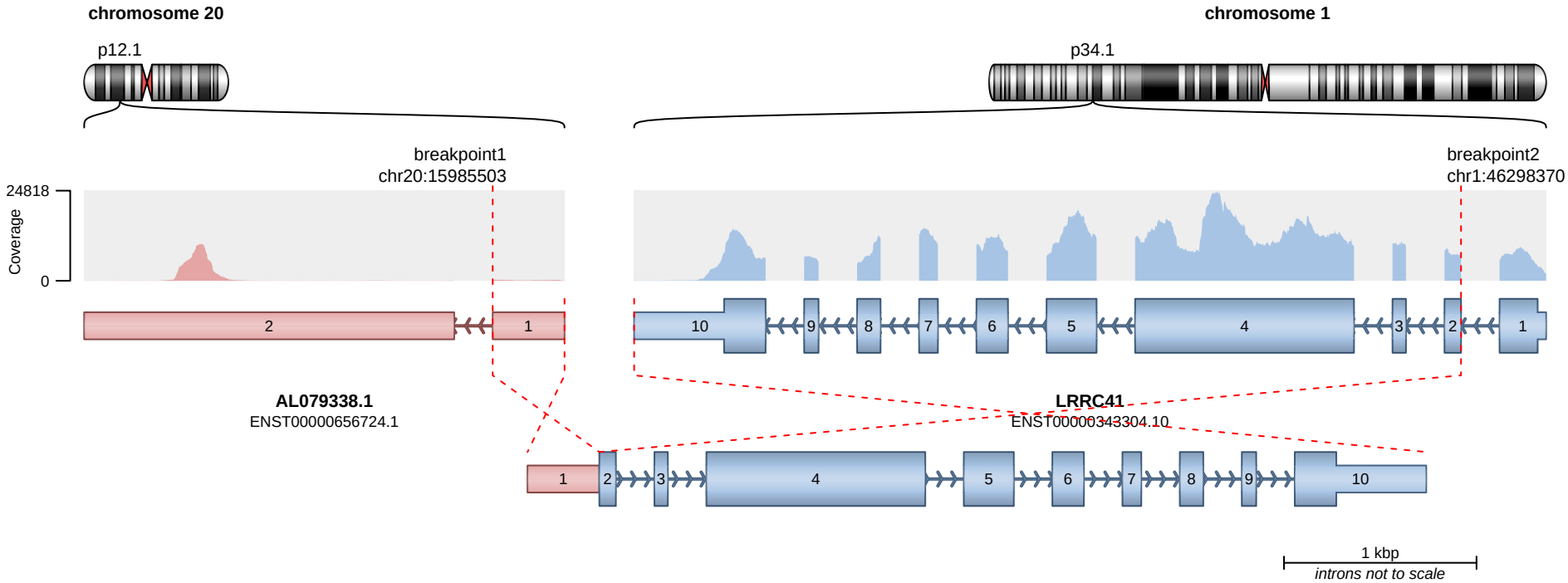


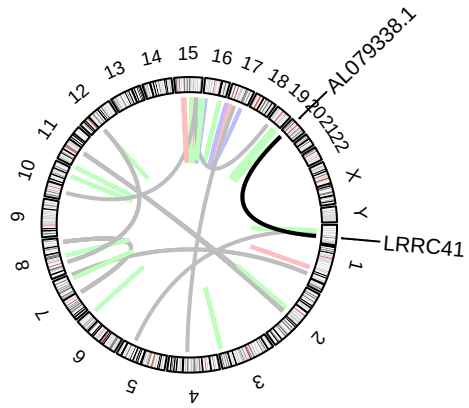


SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

translocation
deletion
duplication
inversion



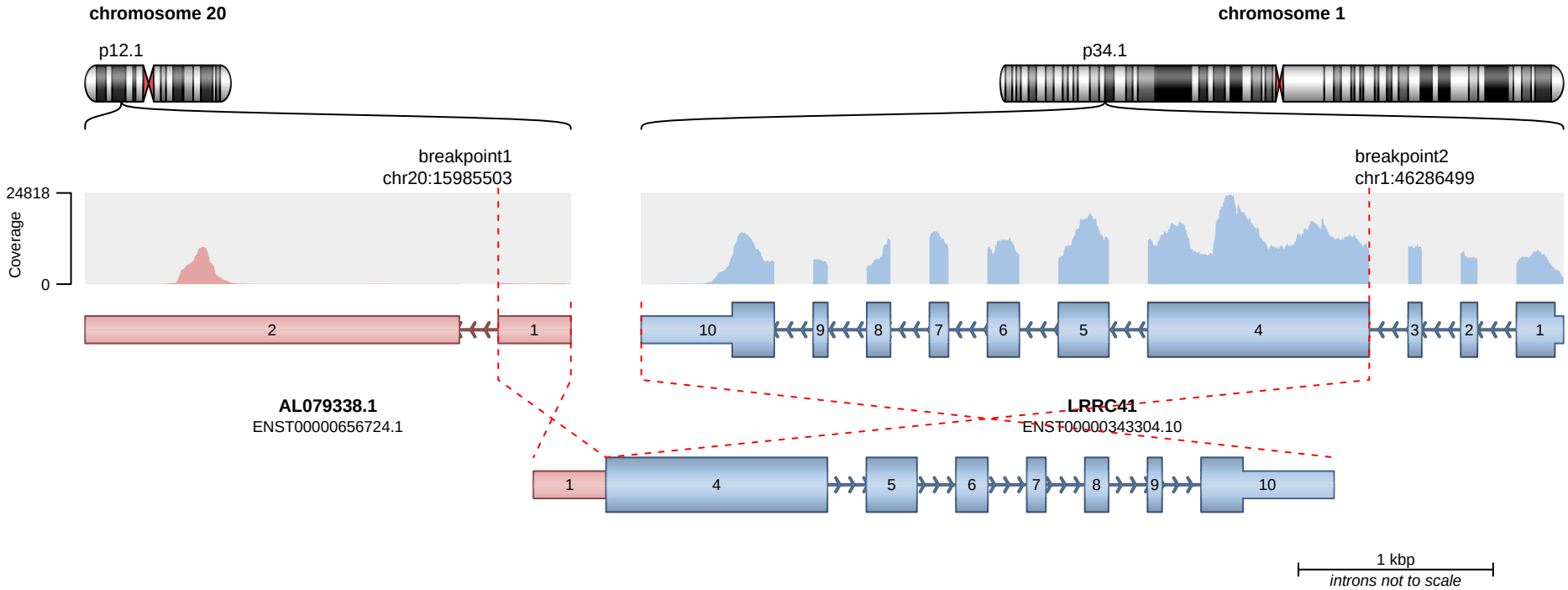


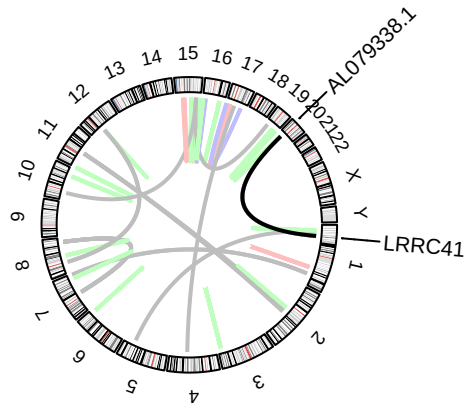
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 94
Discordant mates = 0

translocation
deletion
duplication
inversion



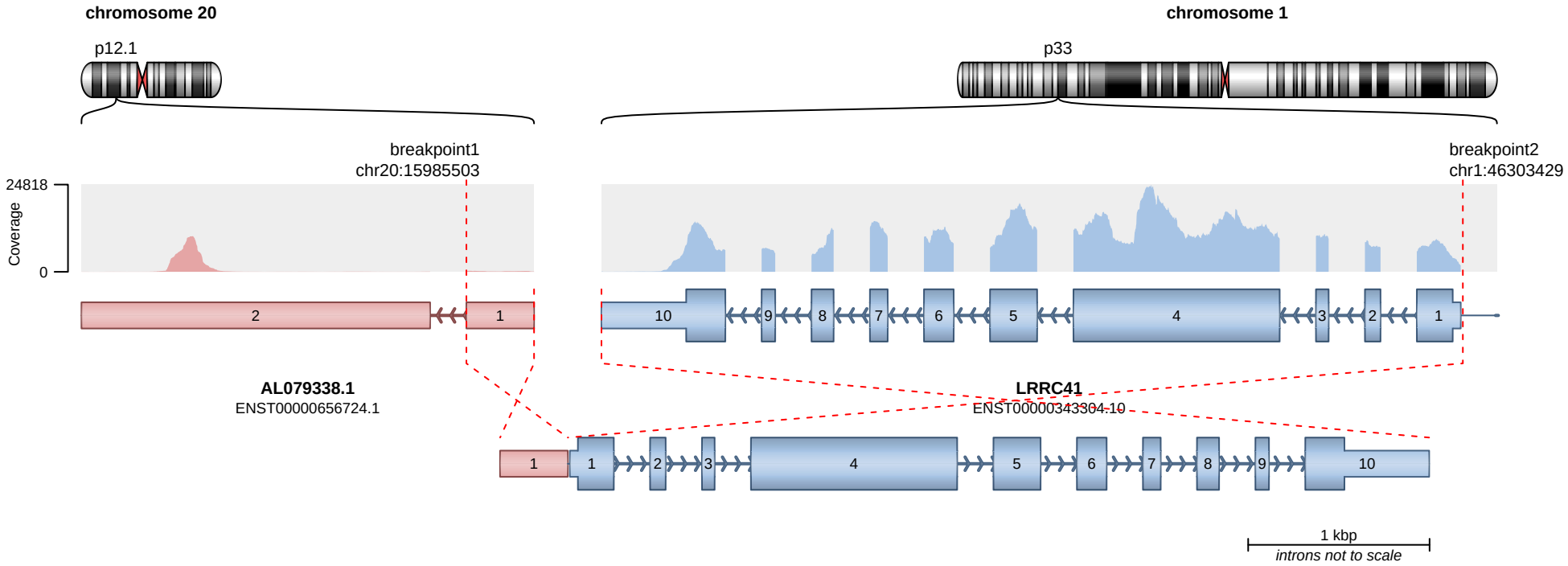


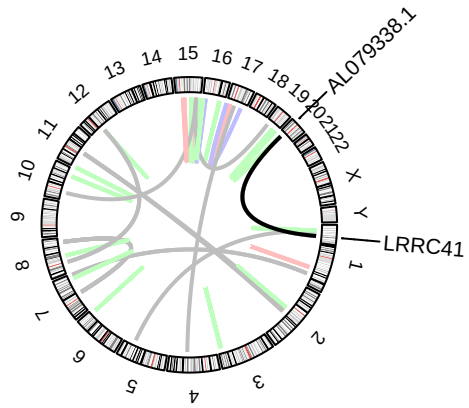
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 0

translocation
deletion
duplication
inversion



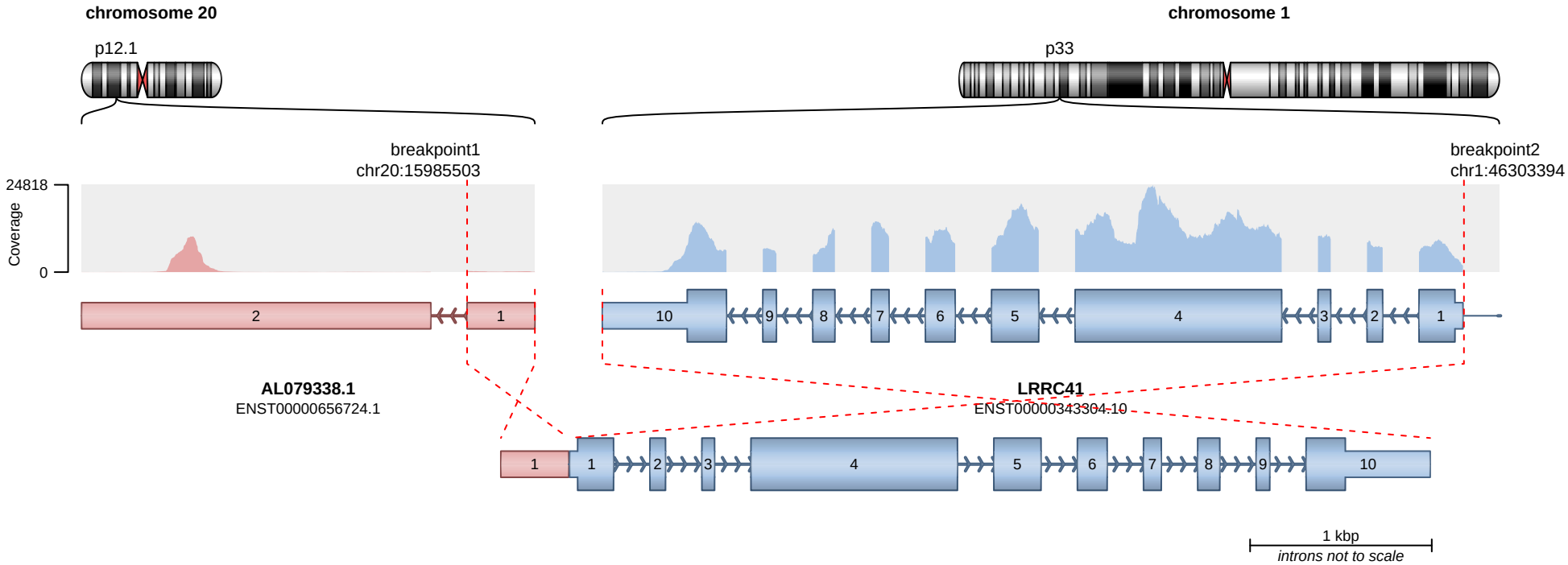


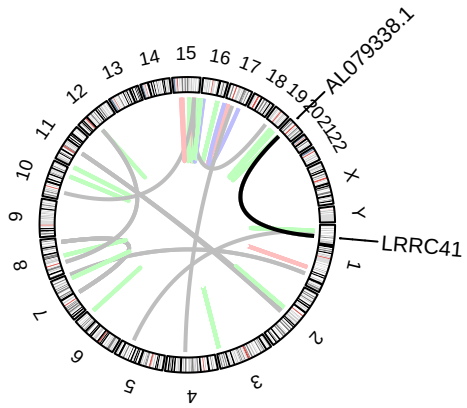
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 0

translocation
deletion
duplication
inversion



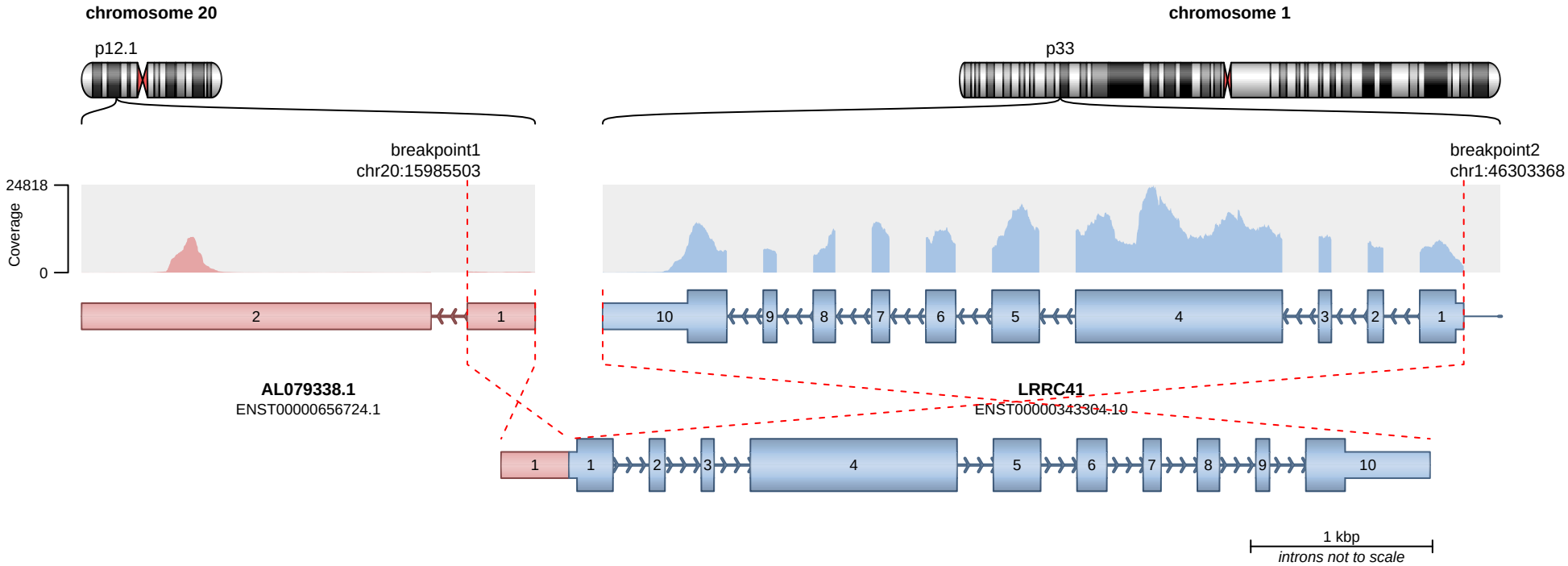


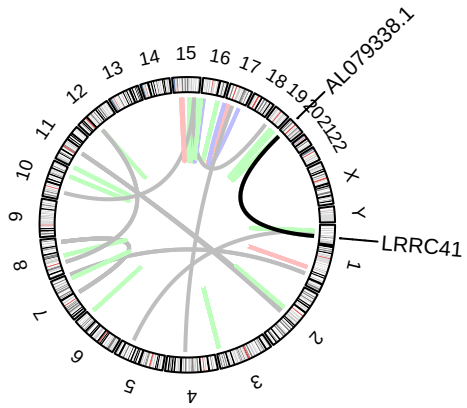
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0

translocation
deletion
duplication
inversion



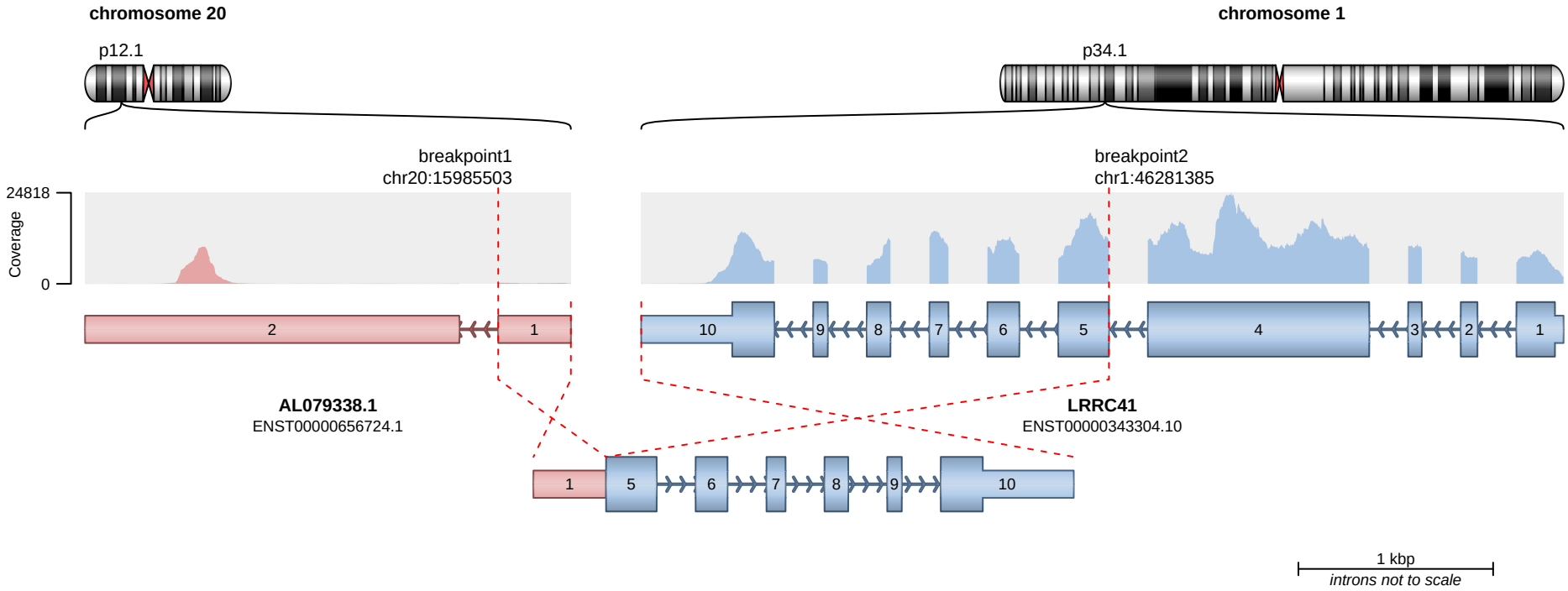


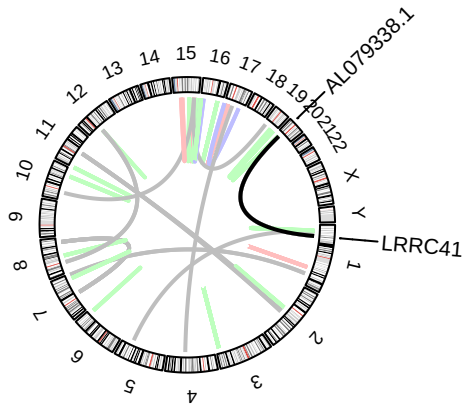
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

translocation
deletion
duplication
inversion



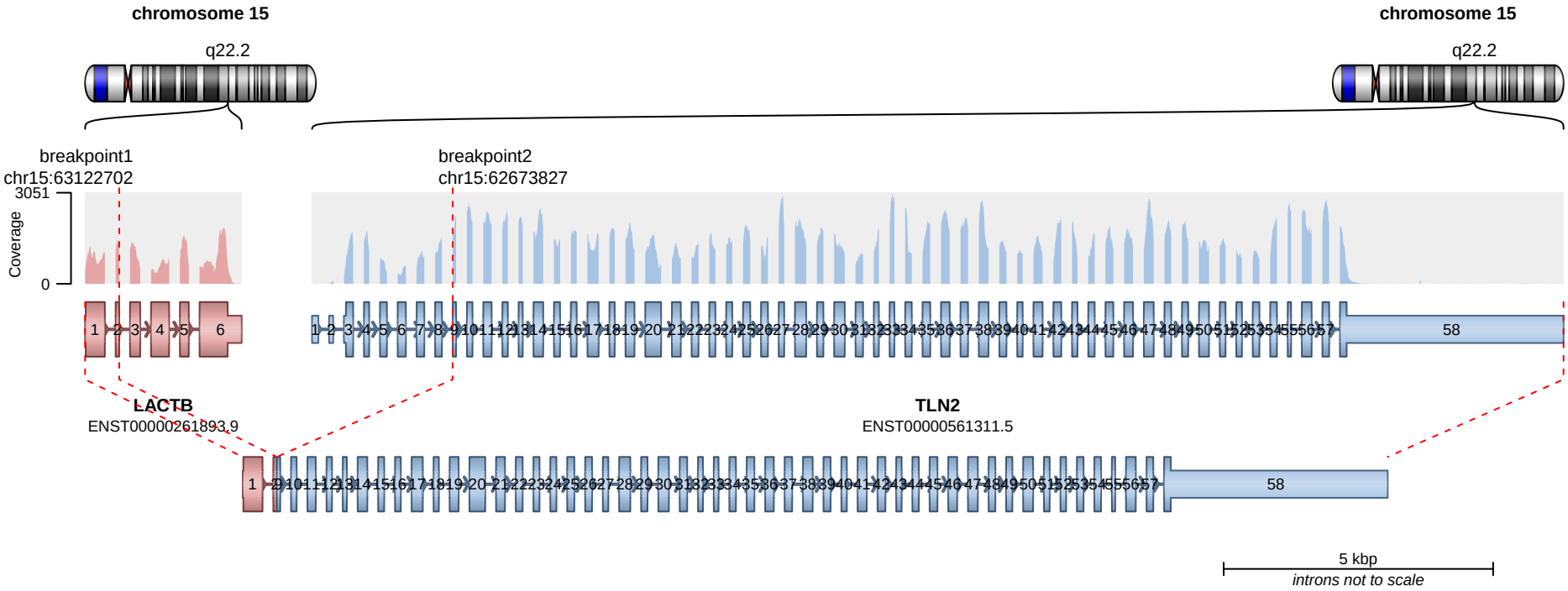


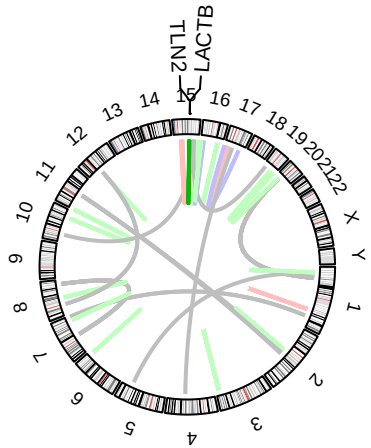
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

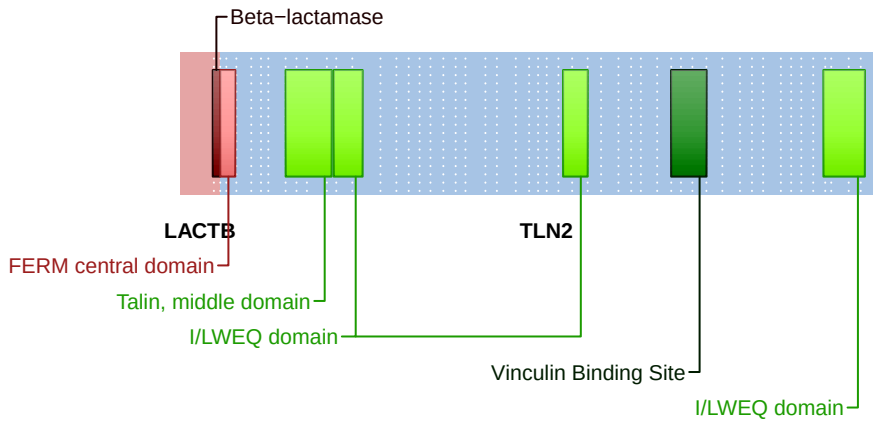
translocation
deletion
duplication
inversion





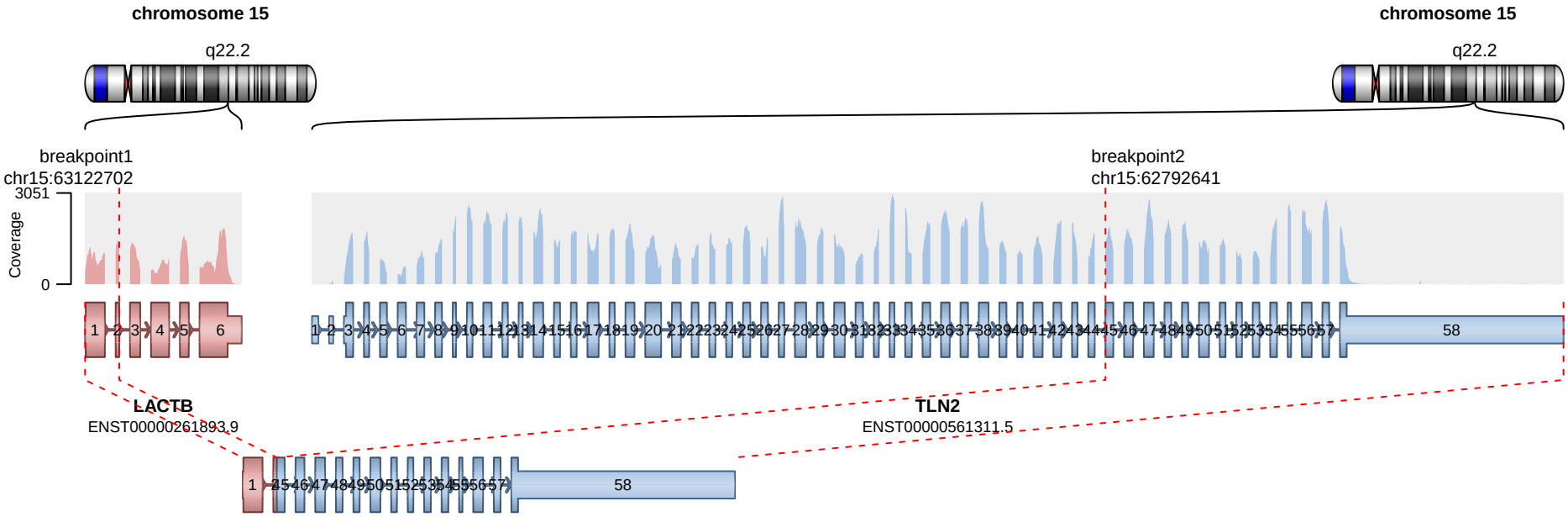
translocation
deletion
duplication
inversion

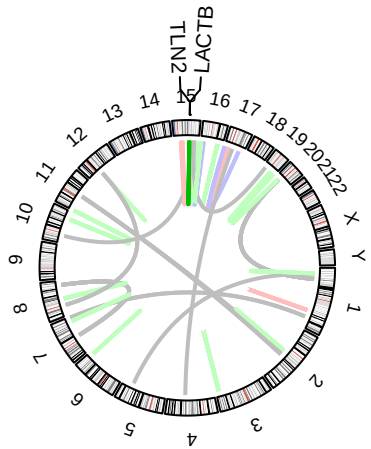
RETAINED PROTEIN DOMAINS
reading frame unclear

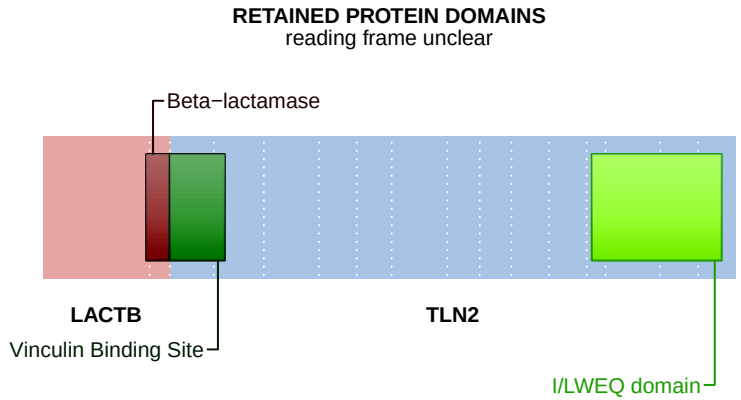


SUPPORTING READ COUNT

Split reads = 94
Discordant mates = 0



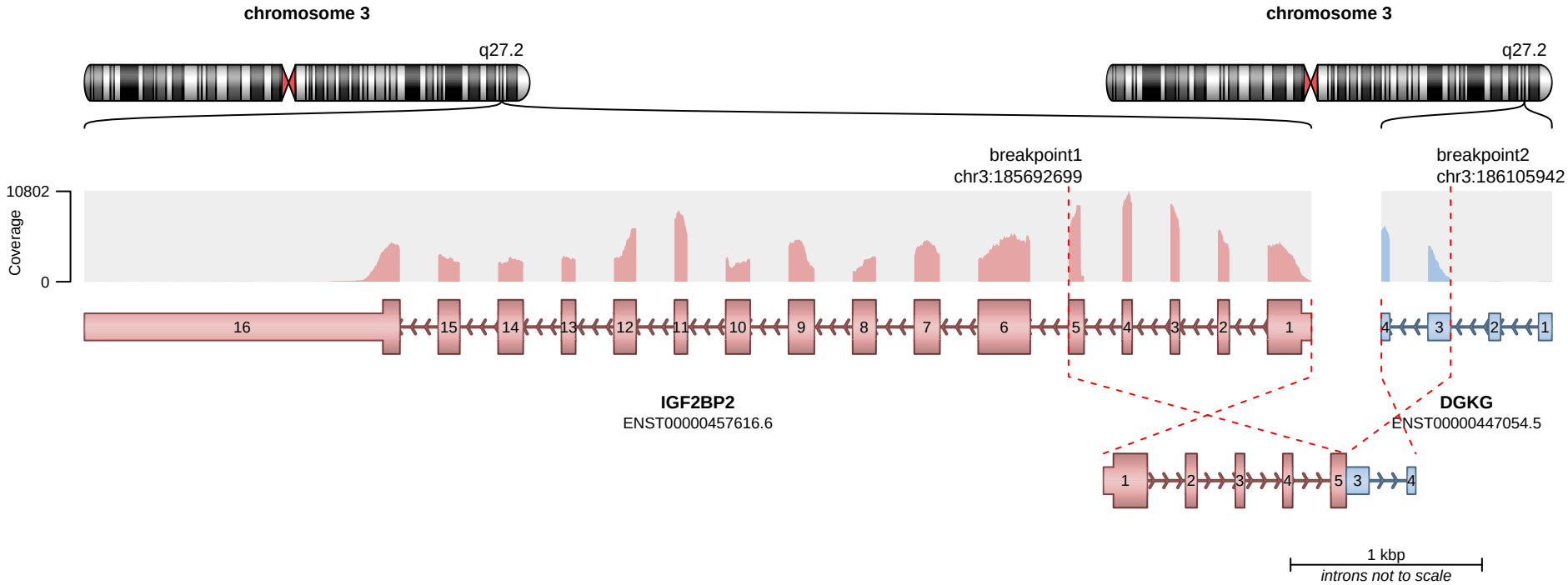


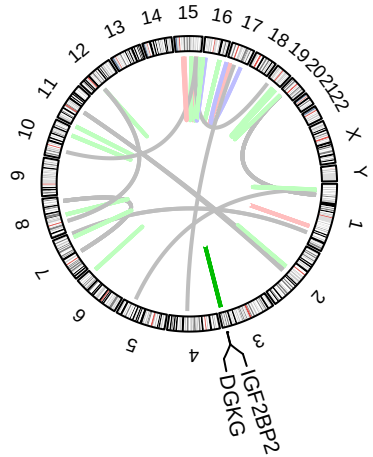


SUPPORTING READ COUNT

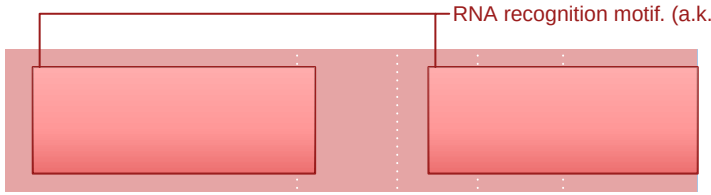
Split reads = 22
Discordant mates = 0

translocation
deletion
duplication
inversion





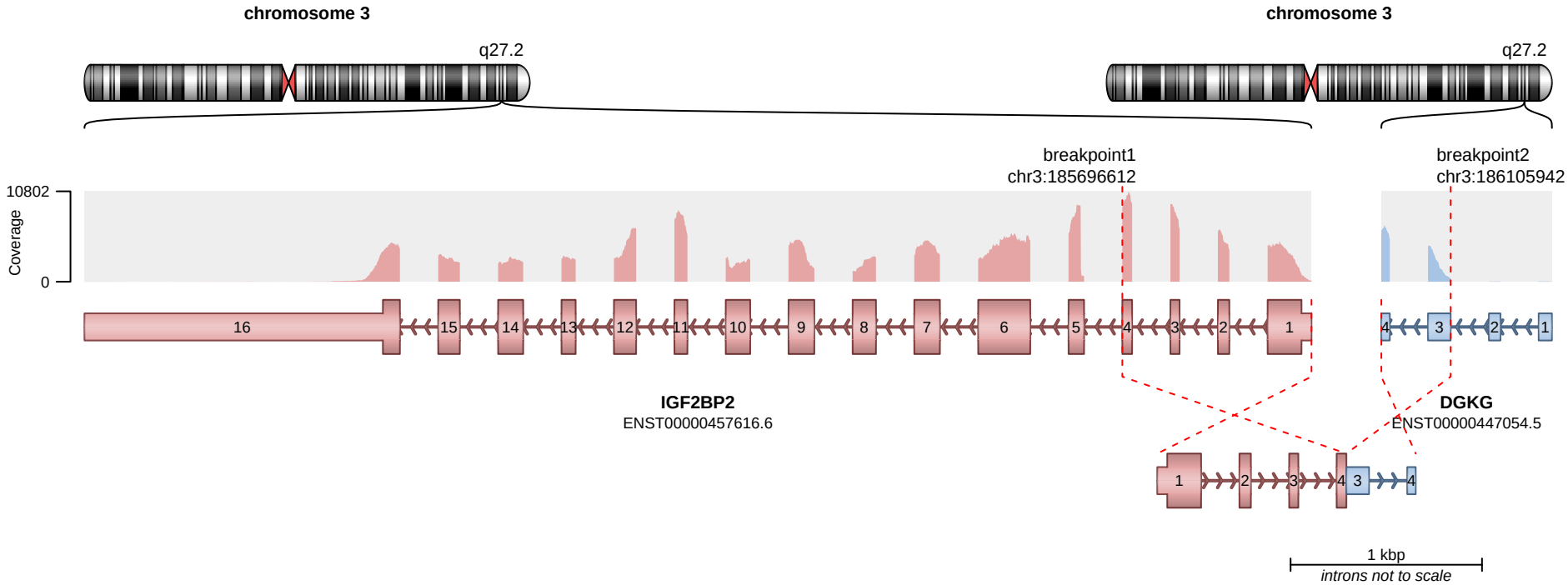
RETAINED PROTEIN DOMAINS
reading frame unclear

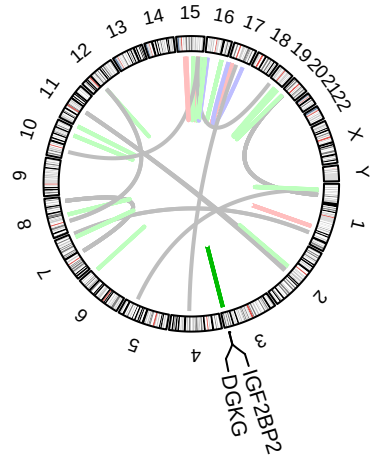


IGF2BP2

SUPPORTING READ COUNT

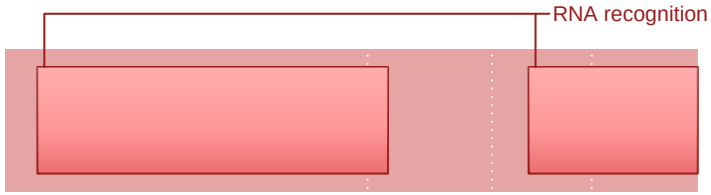
Split reads = 90
Discordant mates = 0





translocation
deletion
duplication
inversion

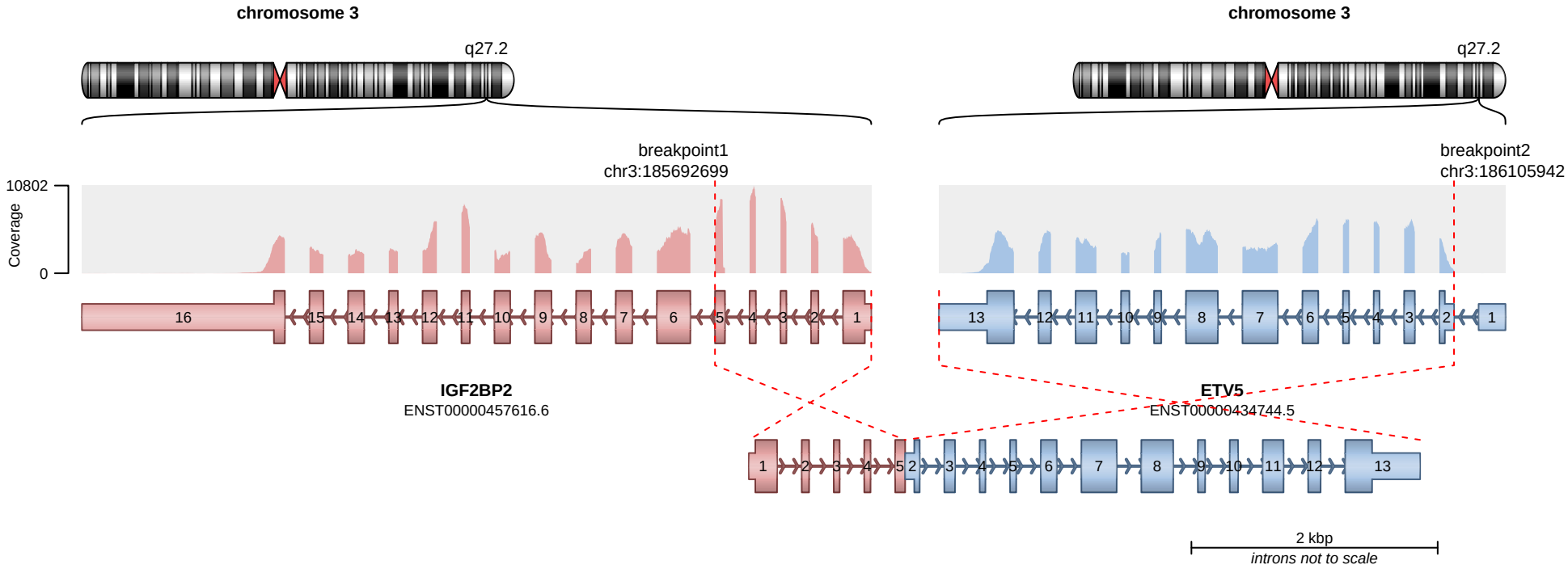
RETAINED PROTEIN DOMAINS
reading frame unclear

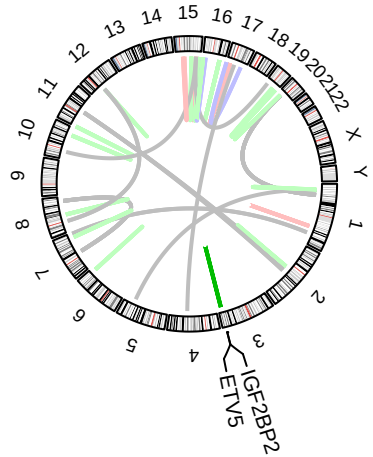


IGF2BP2

SUPPORTING READ COUNT

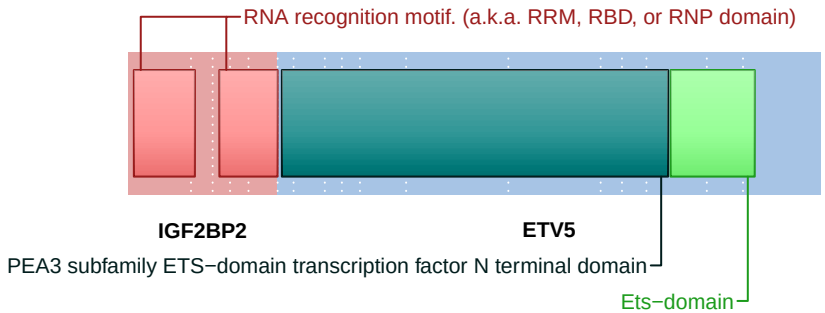
Split reads = 2
Discordant mates = 0





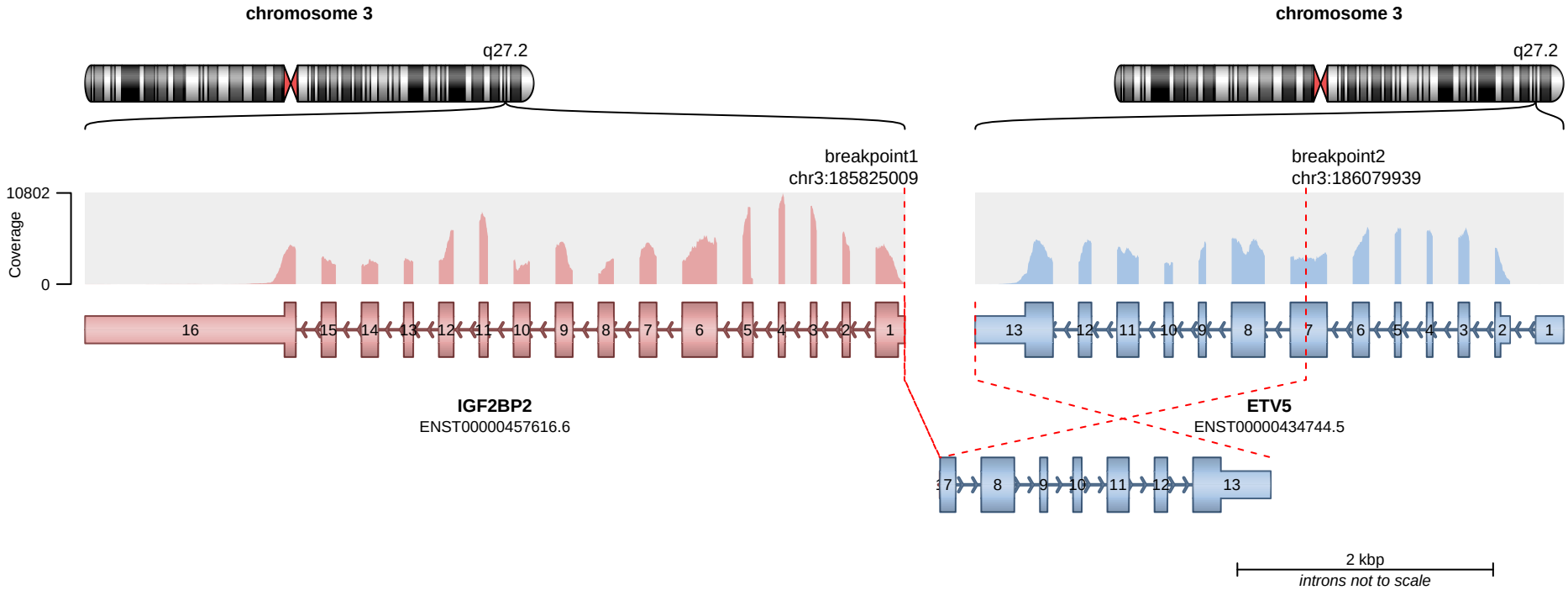
translocation
deletion
duplication
inversion

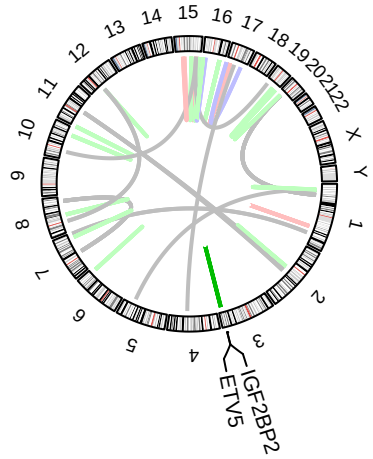
RETAINED PROTEIN DOMAINS
reading frame unclear

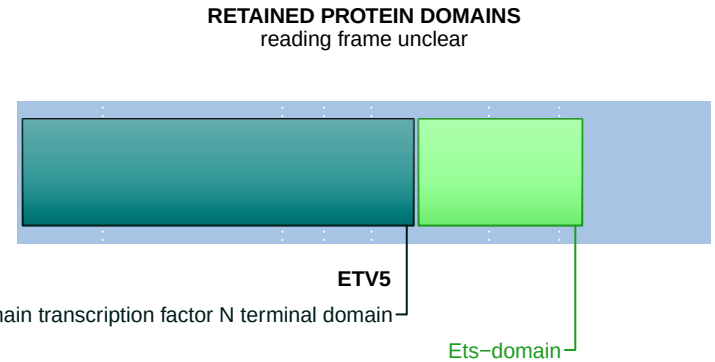


SUPPORTING READ COUNT

Split reads = 90
Discordant mates = 0



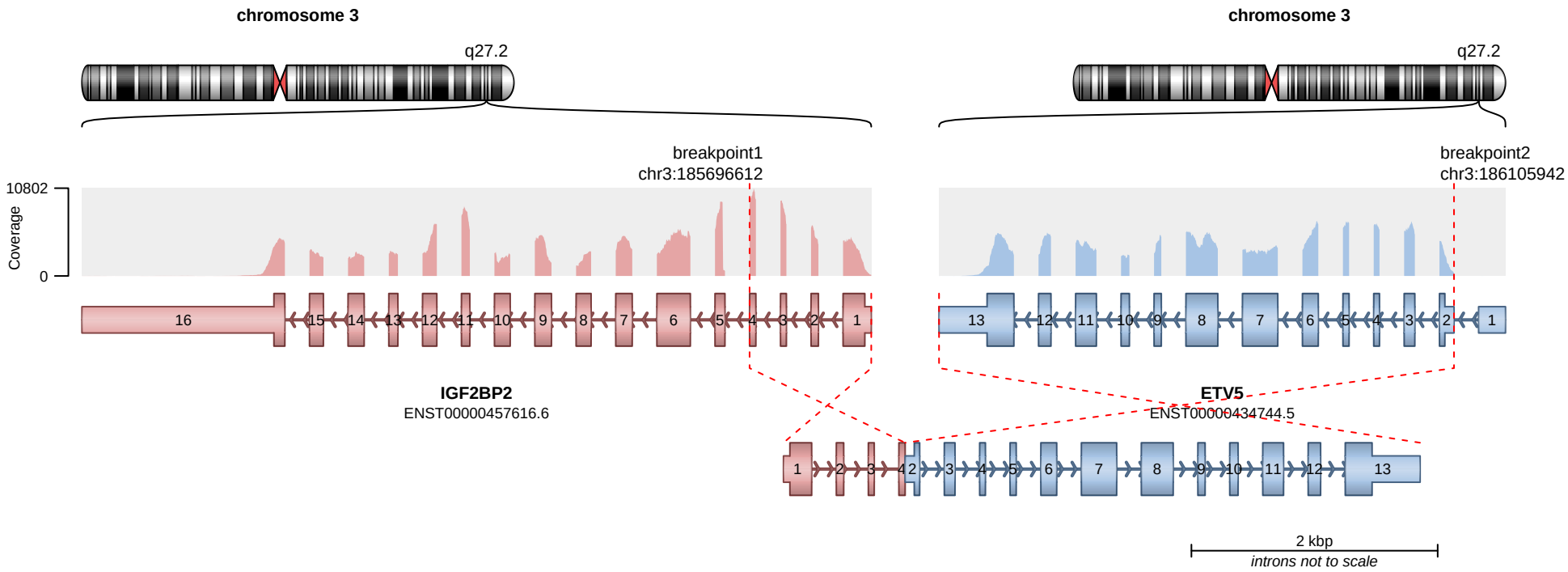


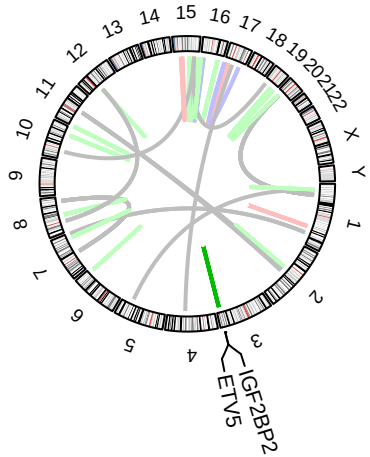


SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0

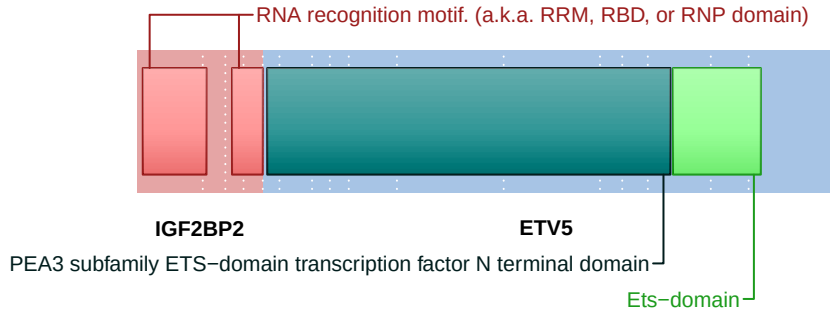
translocation
deletion
duplication
inversion





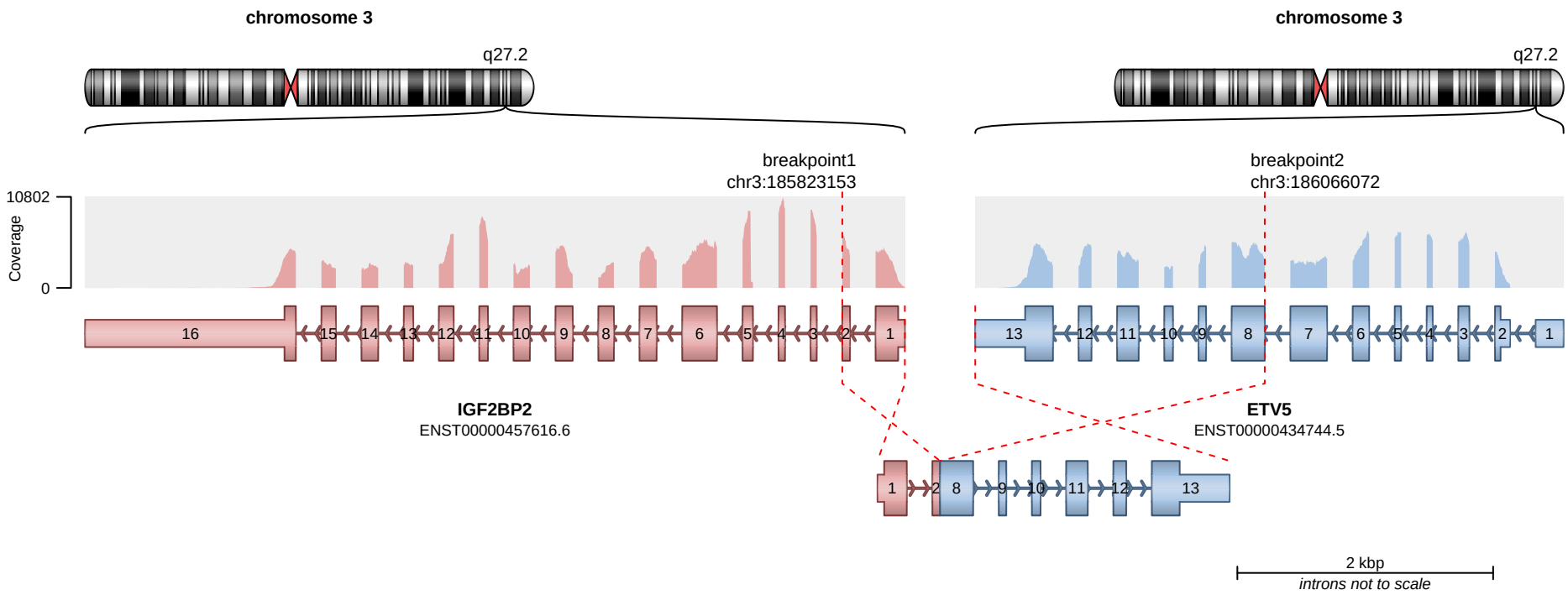
translocation
deletion
duplication
inversion

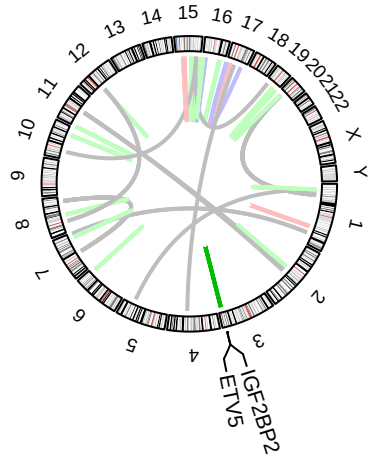
RETAINED PROTEIN DOMAINS
reading frame unclear

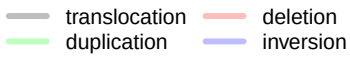


SUPPORTING READ COUNT

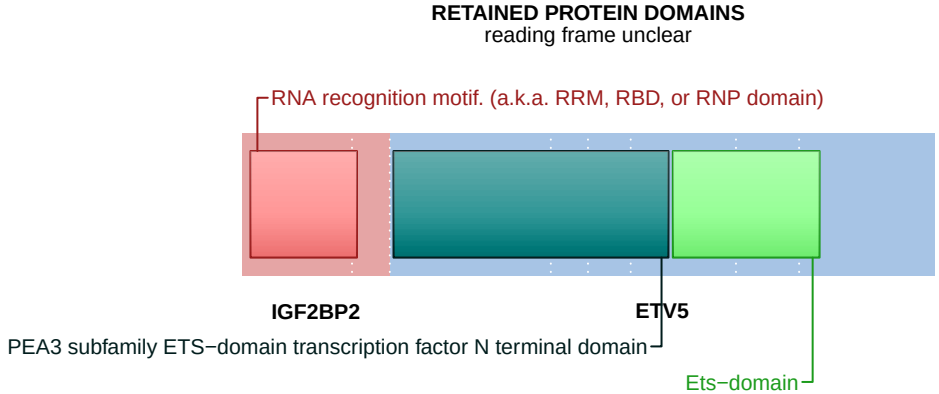
Split reads = 2
Discordant mates = 0





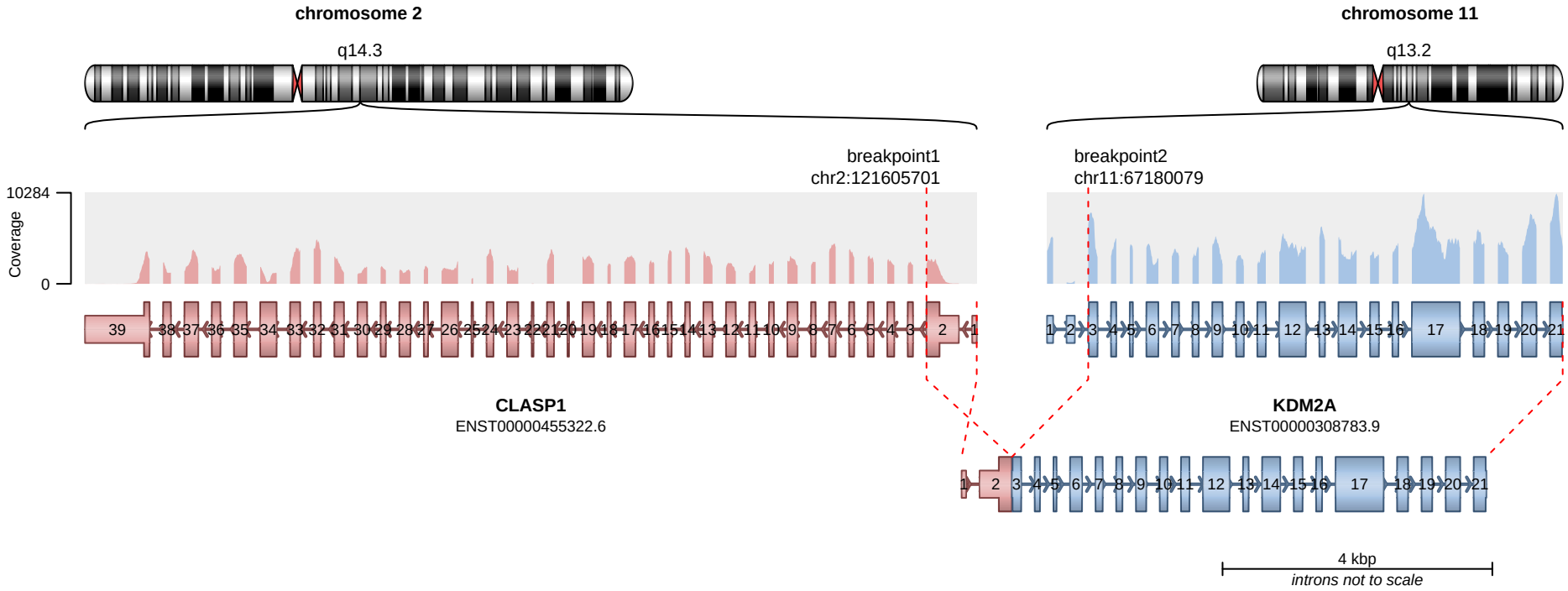


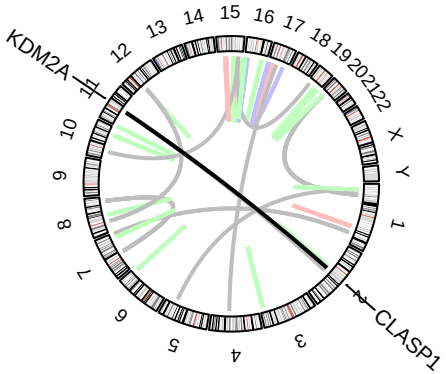
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

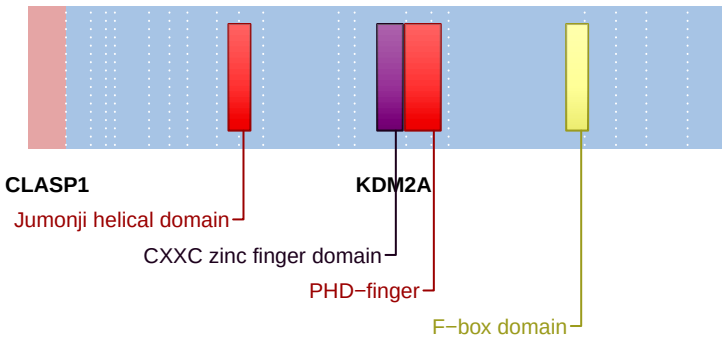
Split reads = 1
Discordant mates = 0





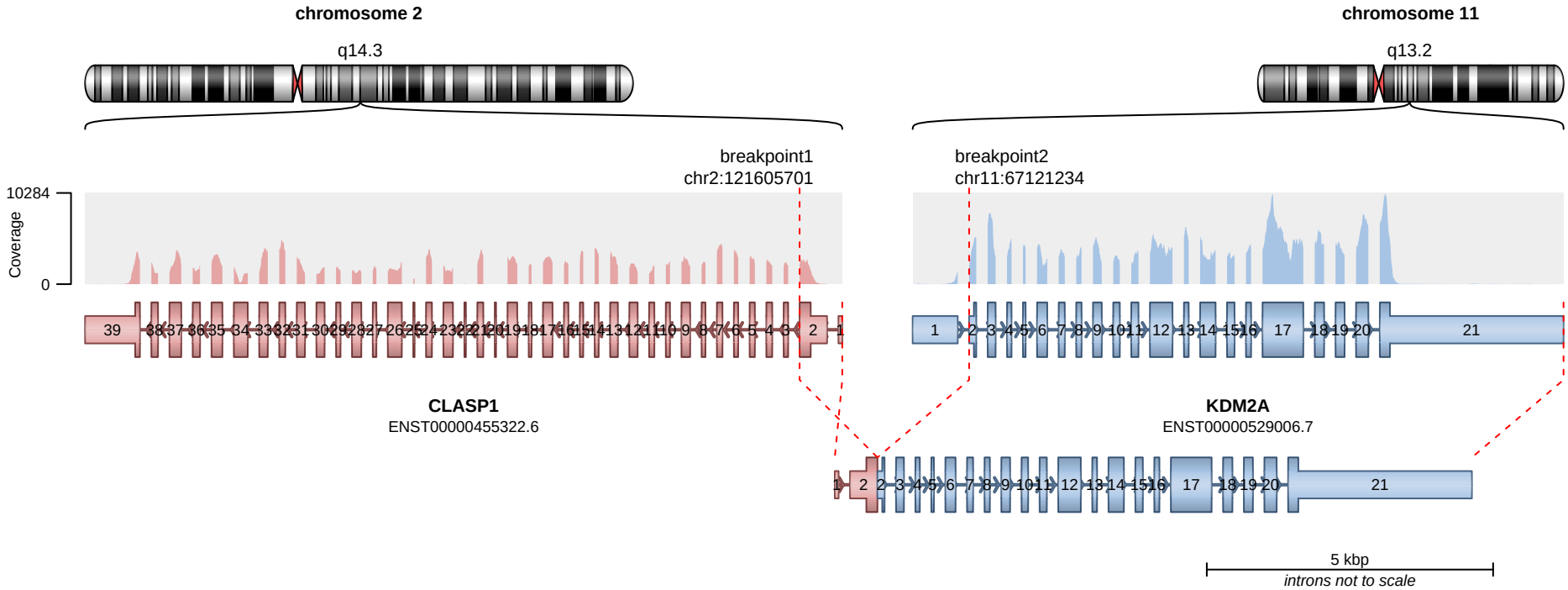
translocation
deletion
duplication
inversion

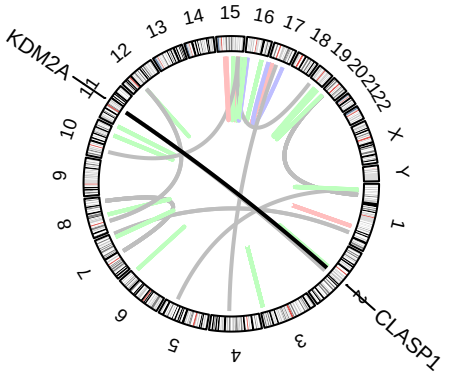
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

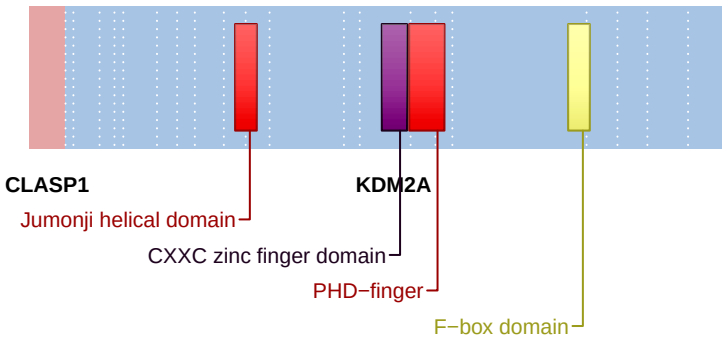
Split reads = 88
Discordant mates = 1





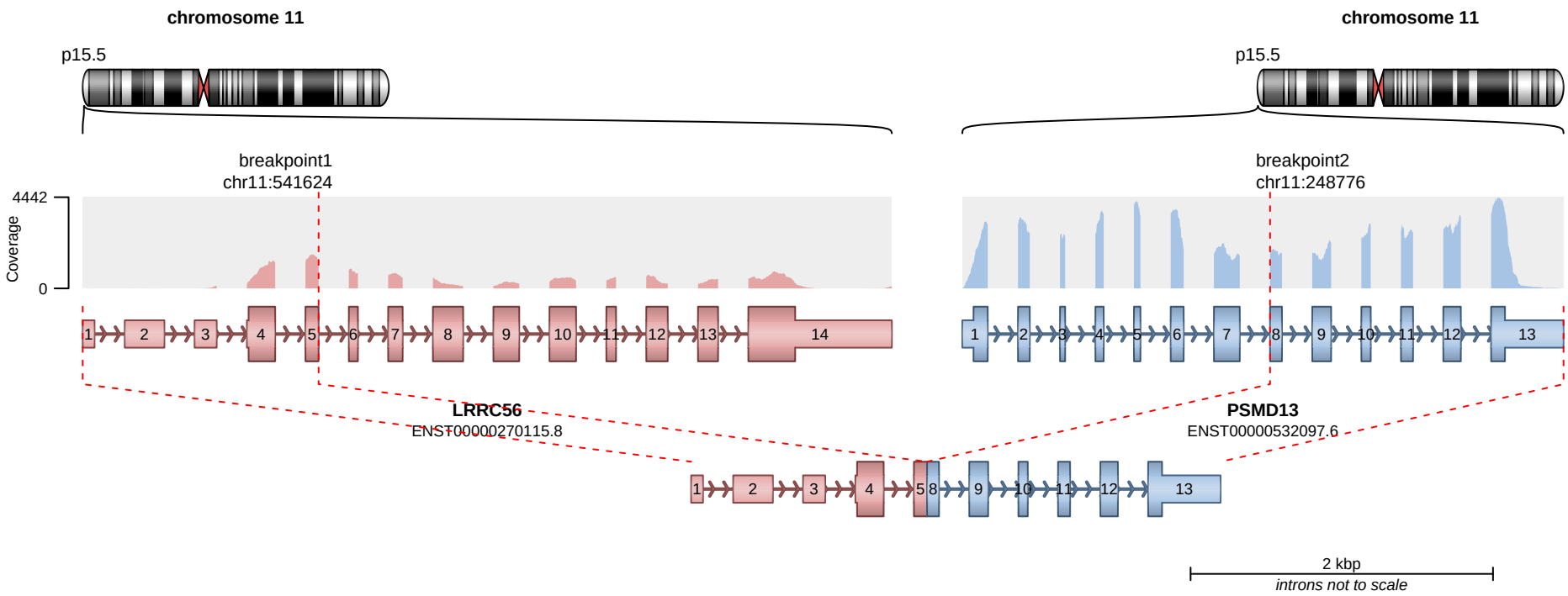
translocation
deletion
duplication
inversion

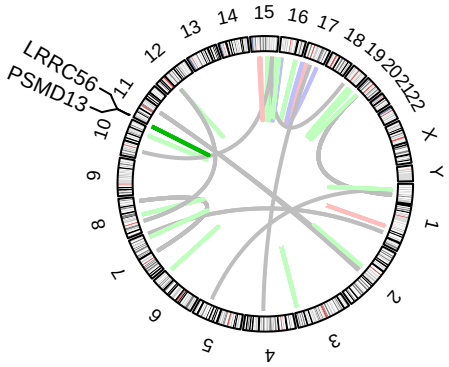
RETAINED PROTEIN DOMAINS
reading frame unclear

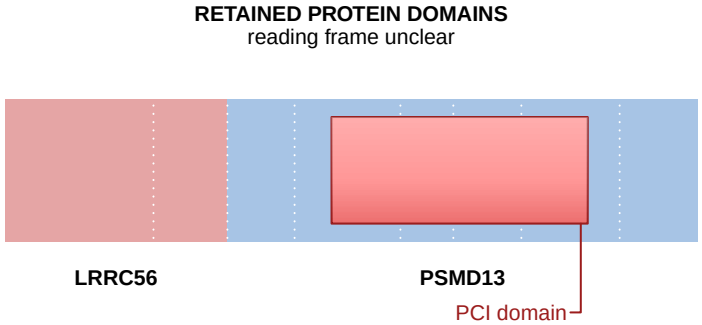


SUPPORTING READ COUNT

Split reads = 35
Discordant mates = 1



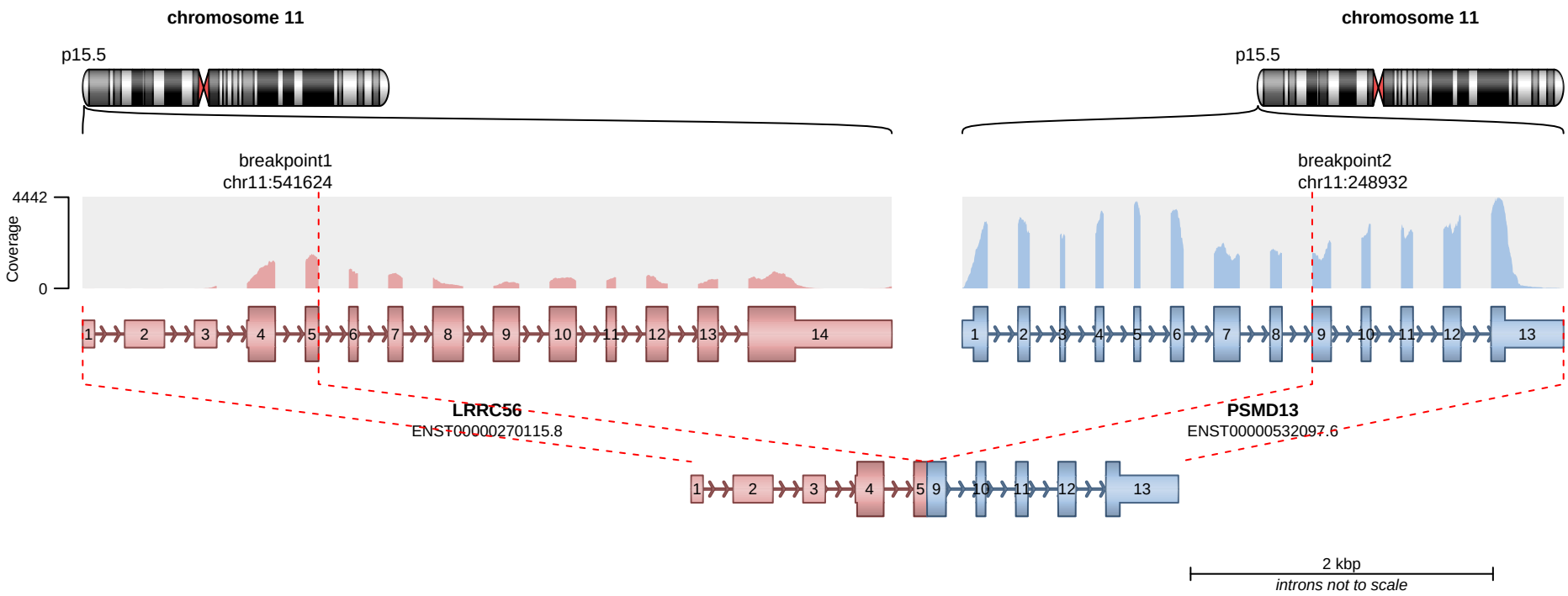


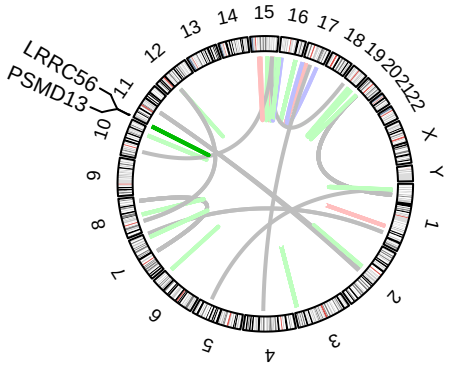


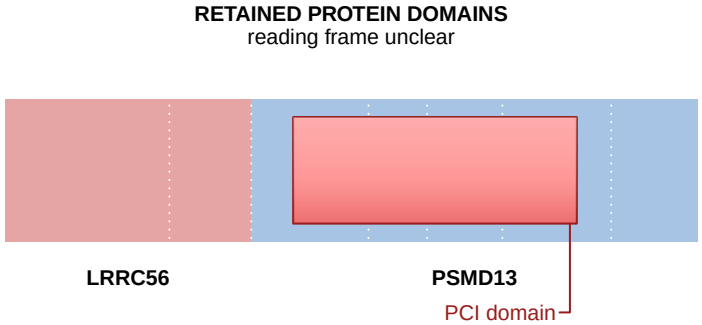
SUPPORTING READ COUNT

Split reads = 87
Discordant mates = 0

translocation
deletion
duplication
inversion



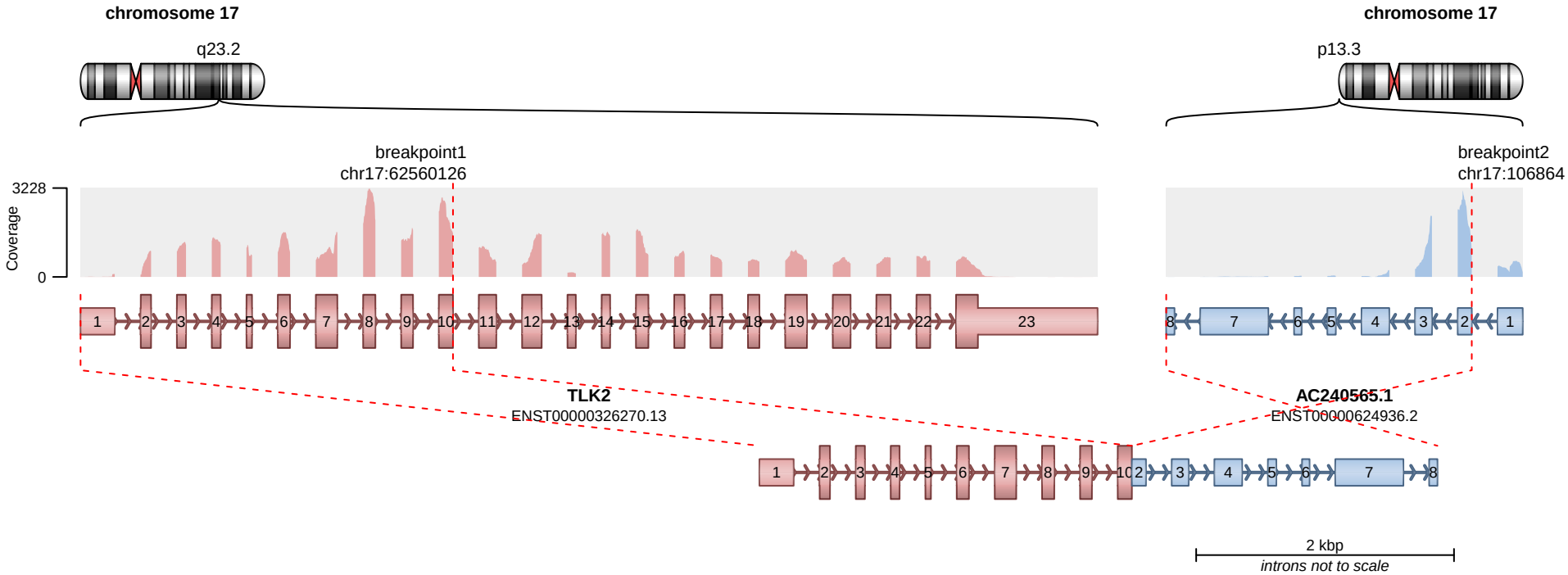


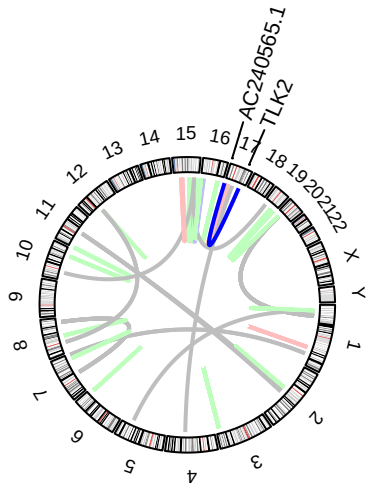


SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 0

translocation
deletion
duplication
inversion



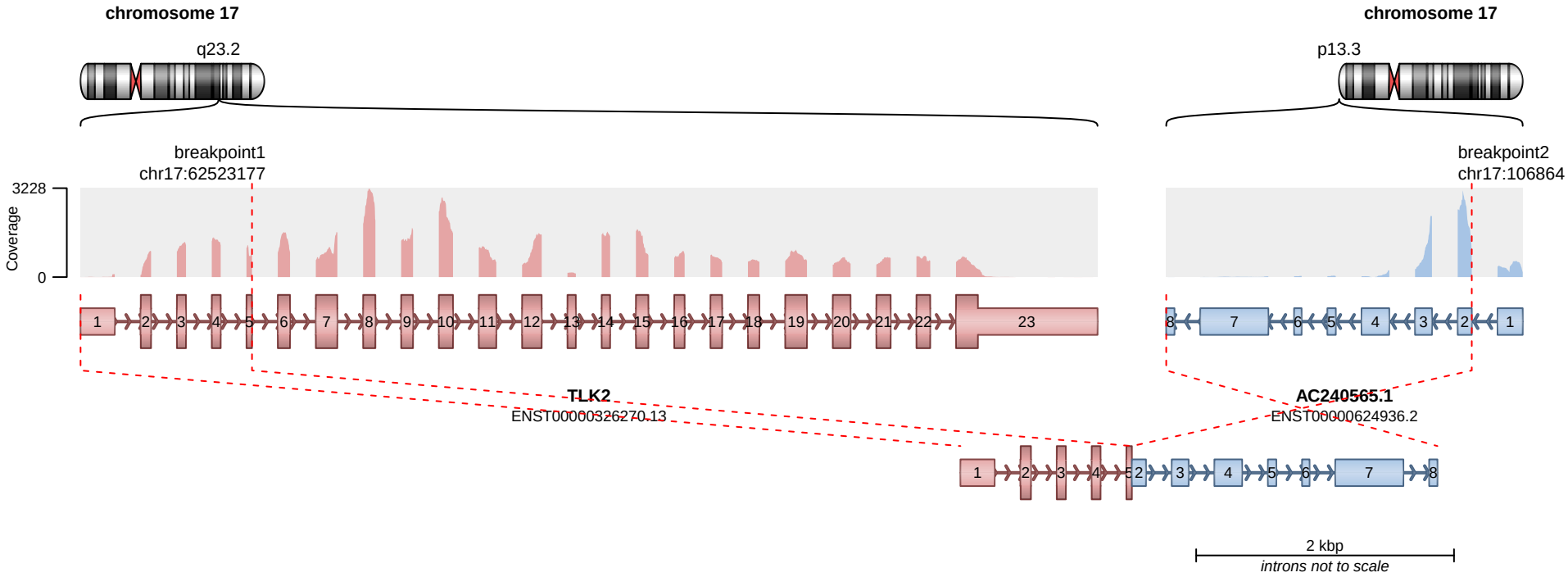


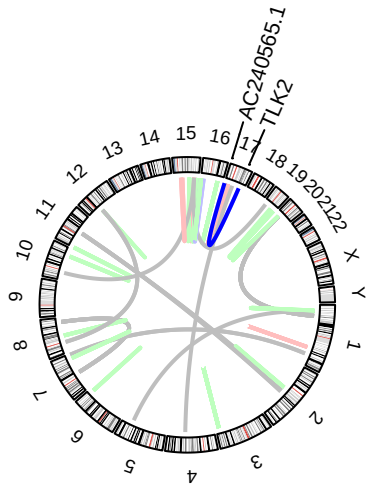
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 83
Discordant mates = 0

translocation
deletion
duplication
inversion



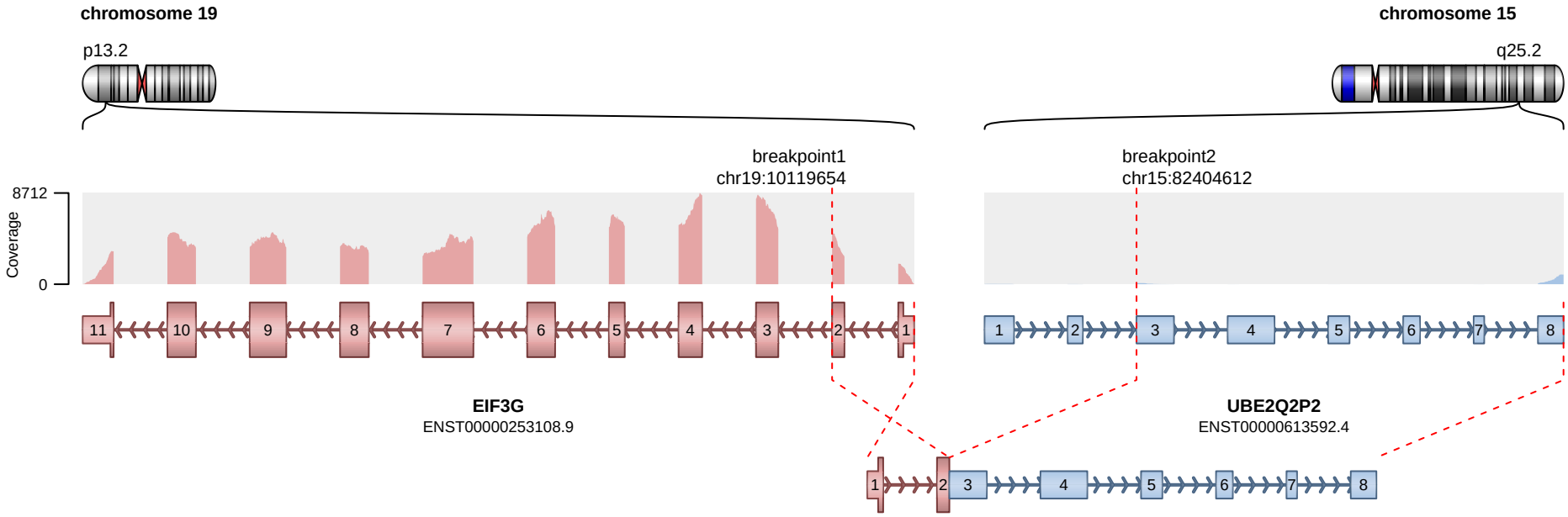


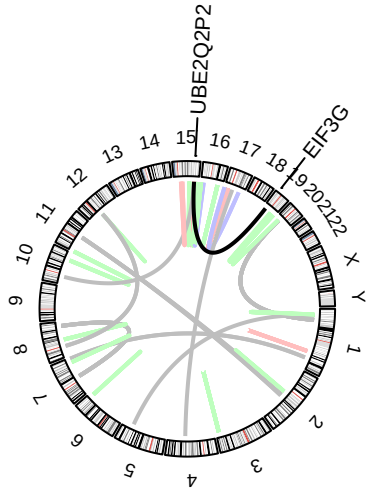
translocation
deletion
duplication
inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



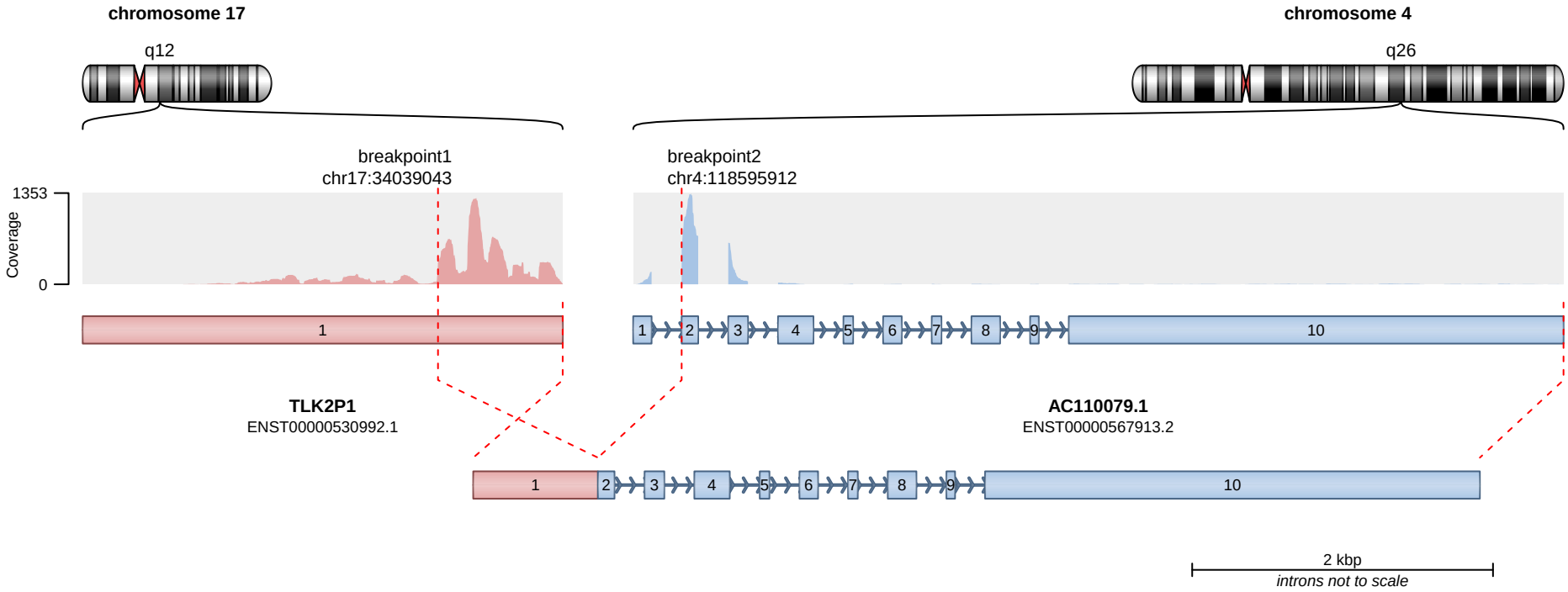


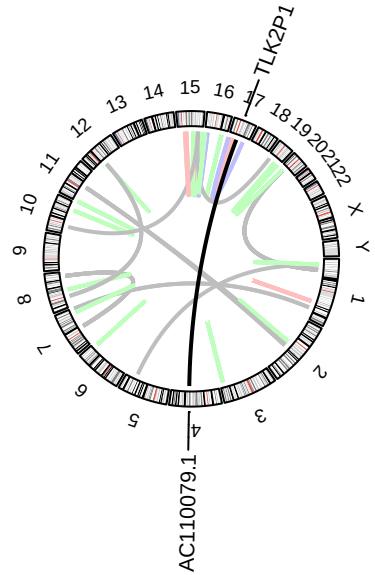
translocation
deletion
duplication
inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 71
Discordant mates = 0



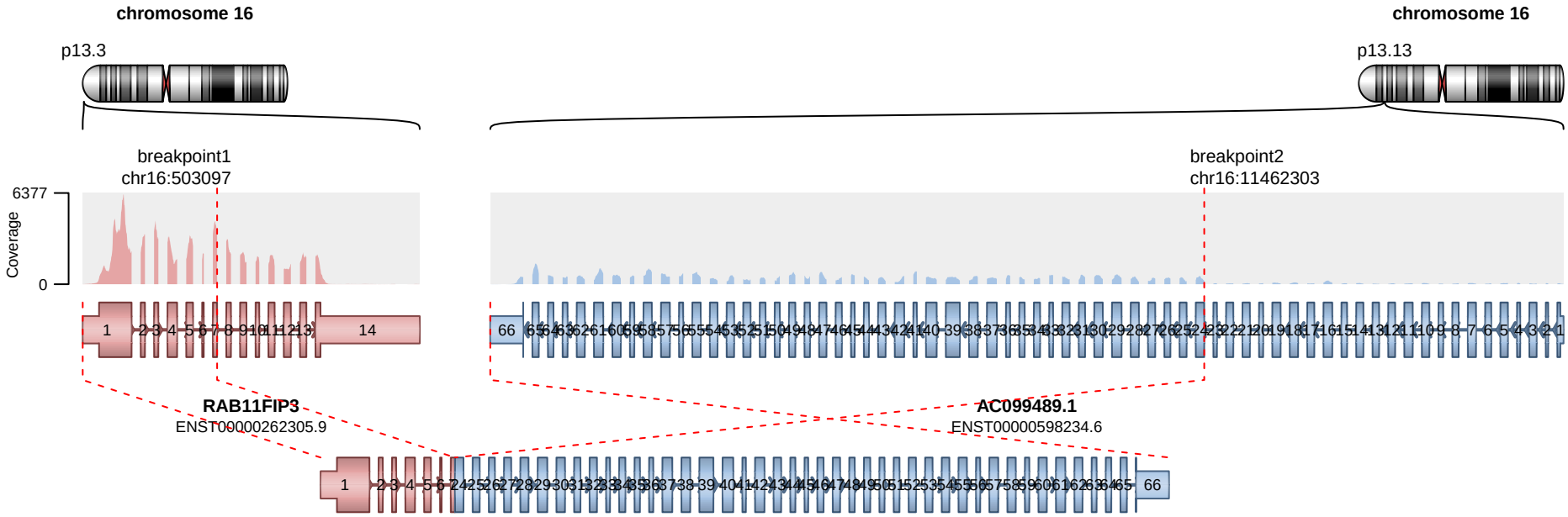


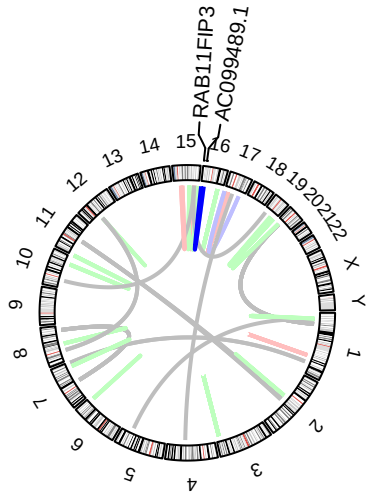
translocation
deletion
duplication
inversion

Genes are not protein−coding.

SUPPORTING READ COUNT

Split reads = 71
Discordant mates = 0



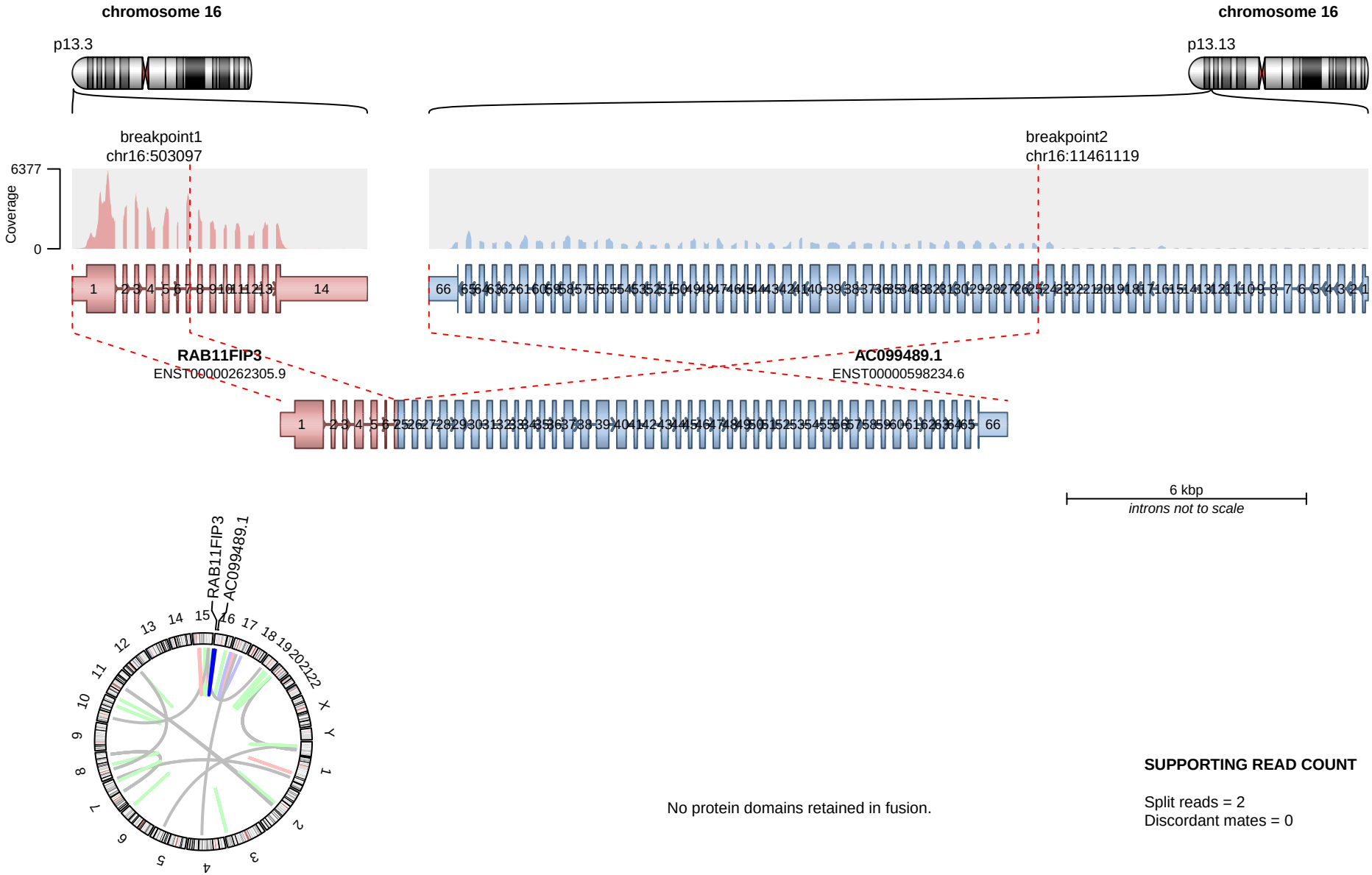


translocation
deletion
duplication
inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

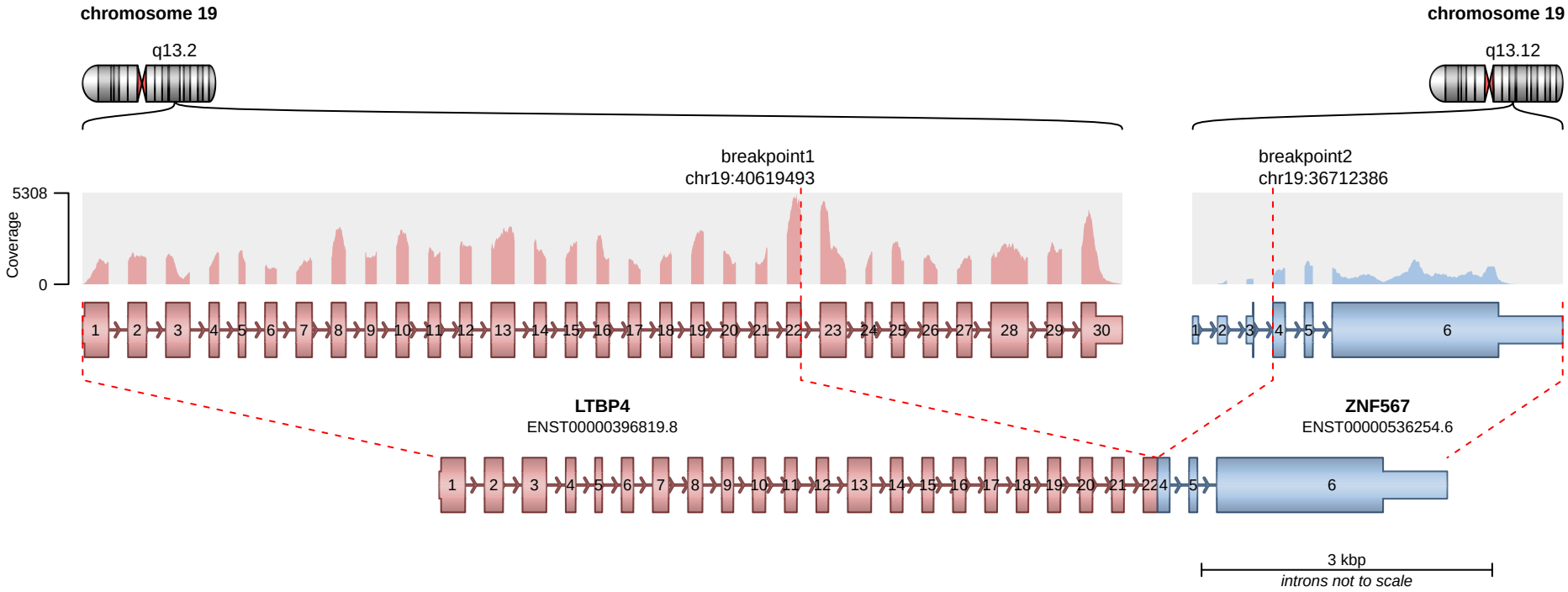
Split reads = 67
Discordant mates = 1

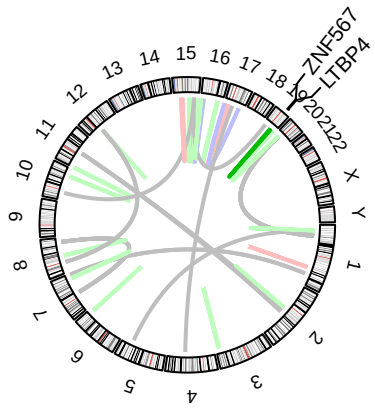


No protein domains retained in fusion.

SUPPORTING READ COUNT

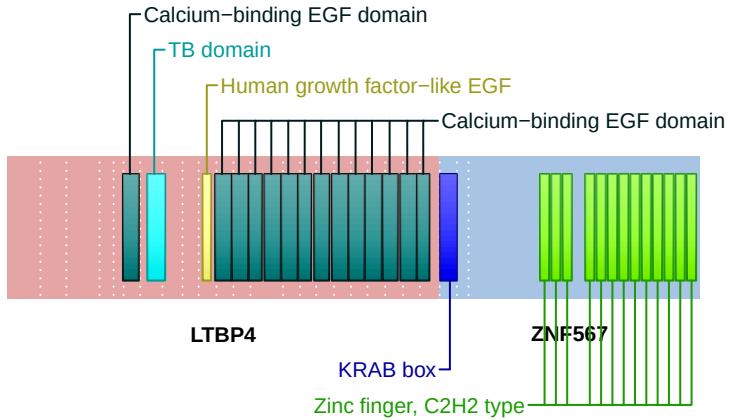
Split reads = 2
Discordant mates = 0





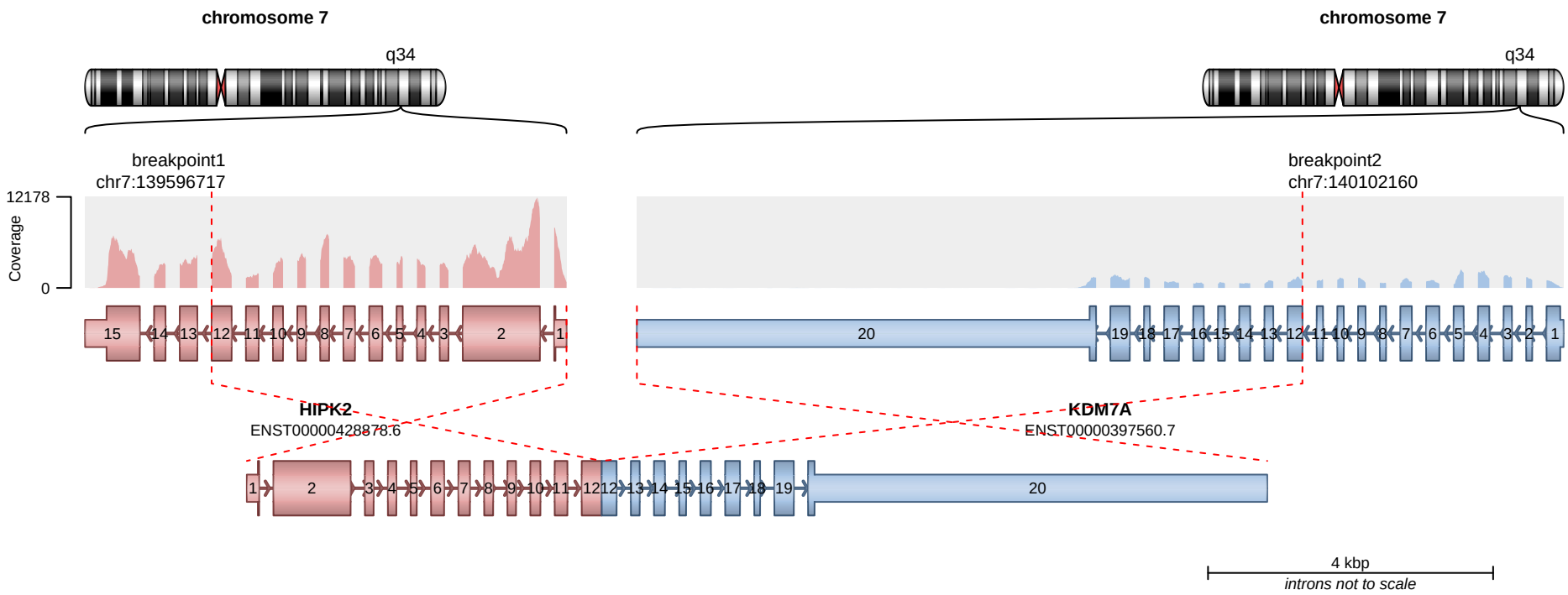
translocation
deletion
duplication
inversion

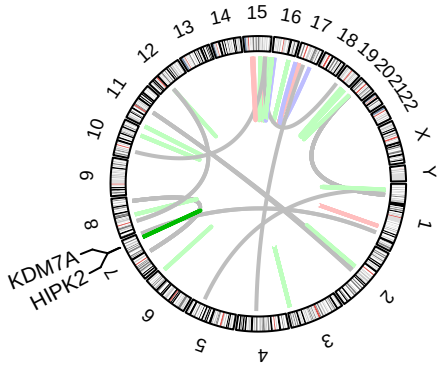
RETAINED PROTEIN DOMAINS
reading frame unclear



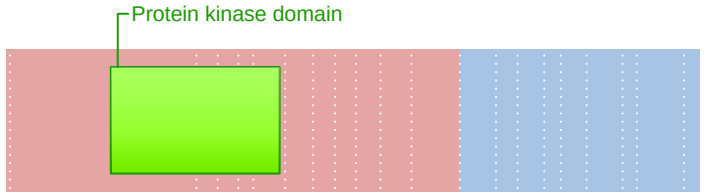
SUPPORTING READ COUNT

Split reads = 59
Discordant mates = 0





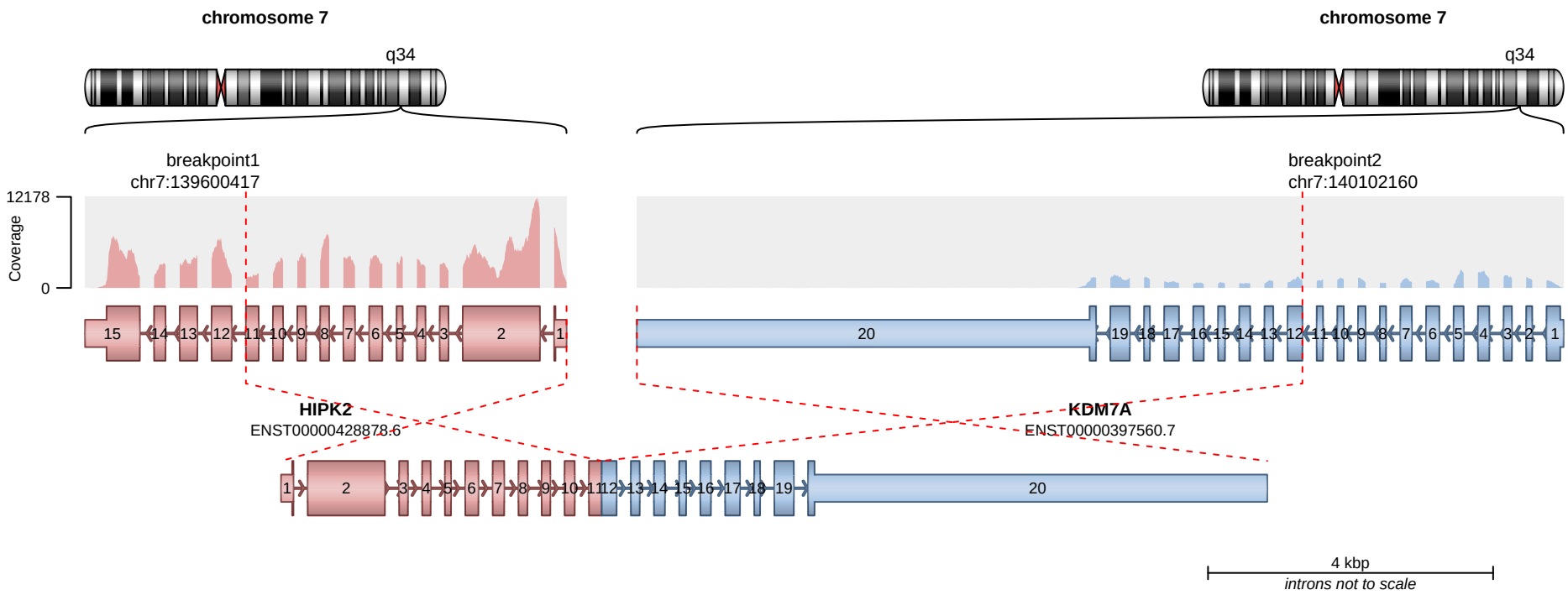
RETAINED PROTEIN DOMAINS
reading frame unclear

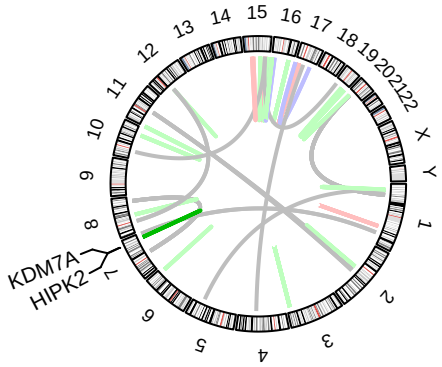


SUPPORTING READ COUNT

Split reads = 53
Discordant mates = 0

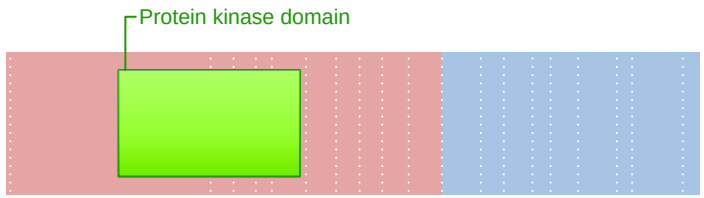
translocation
deletion
duplication
inversion





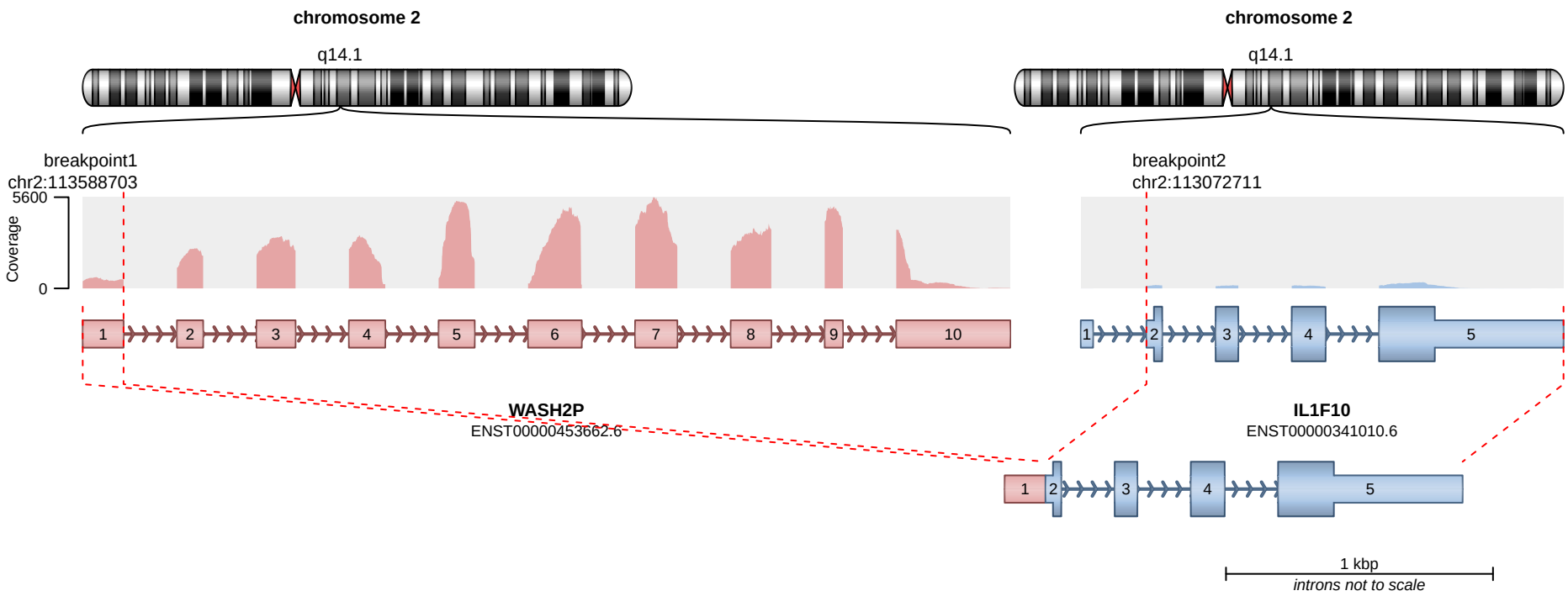
translocation
deletion
duplication
inversion

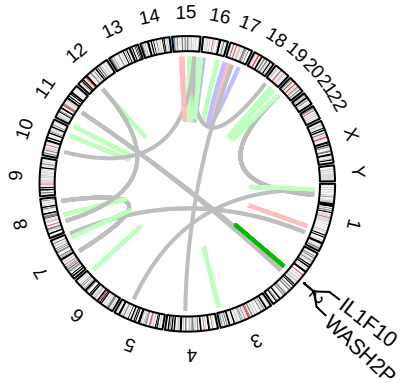
RETAINED PROTEIN DOMAINS
reading frame unclear



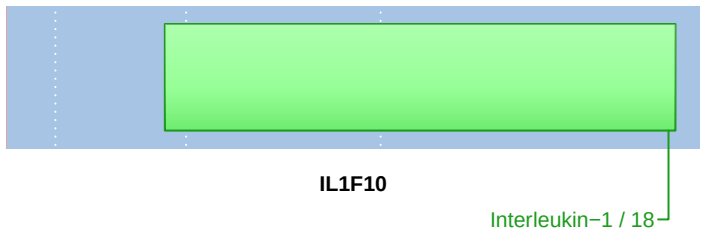
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0





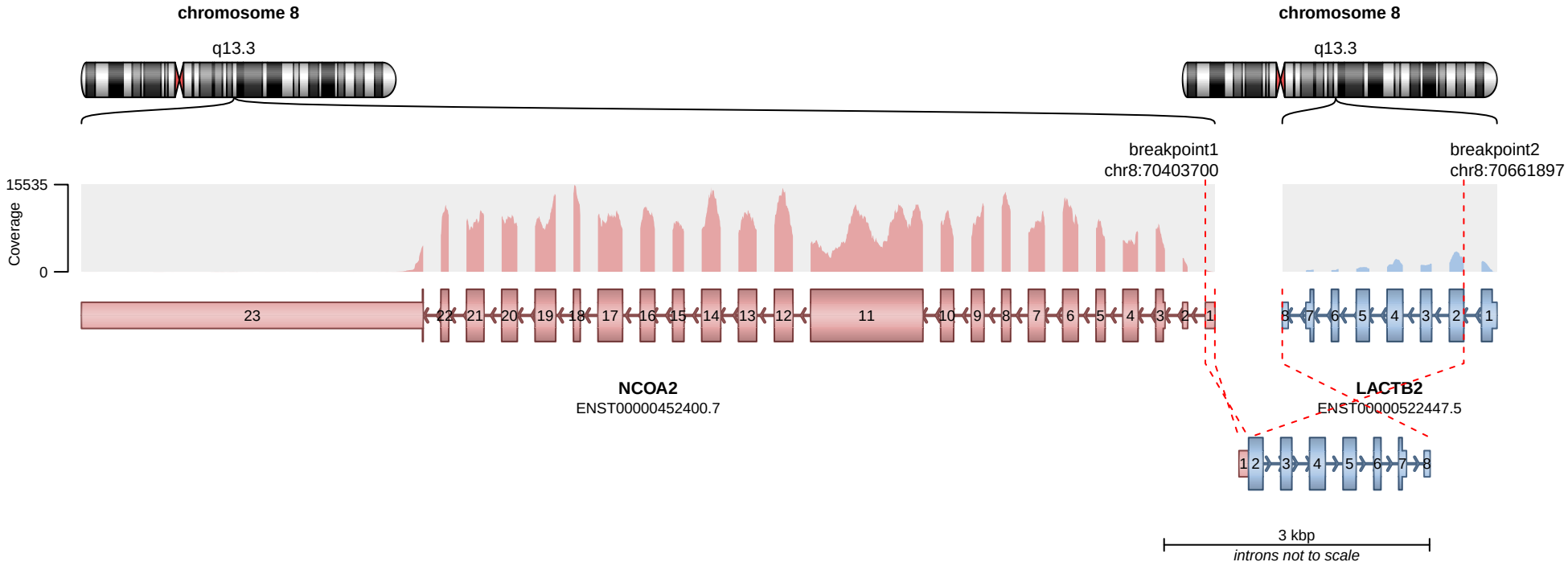
RETAINED PROTEIN DOMAINS
reading frame unclear

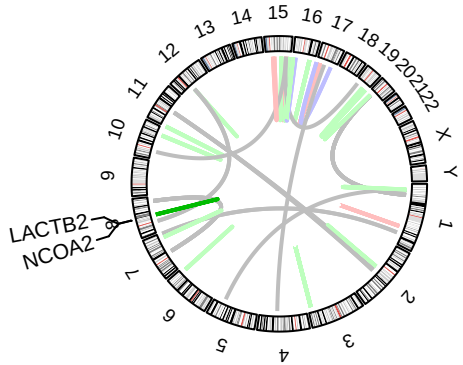


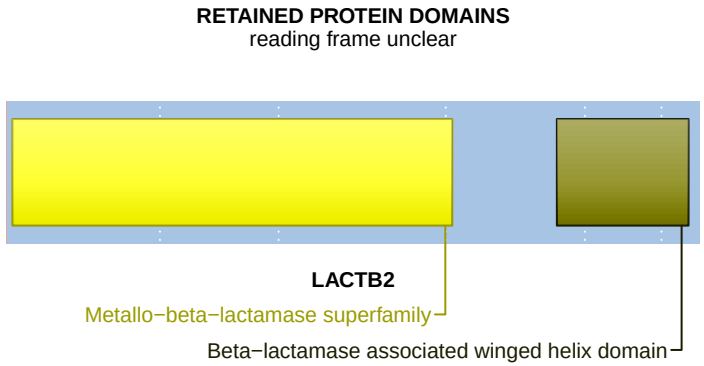
SUPPORTING READ COUNT

Split reads = 53
Discordant mates = 0

translocation
deletion
duplication
inversion



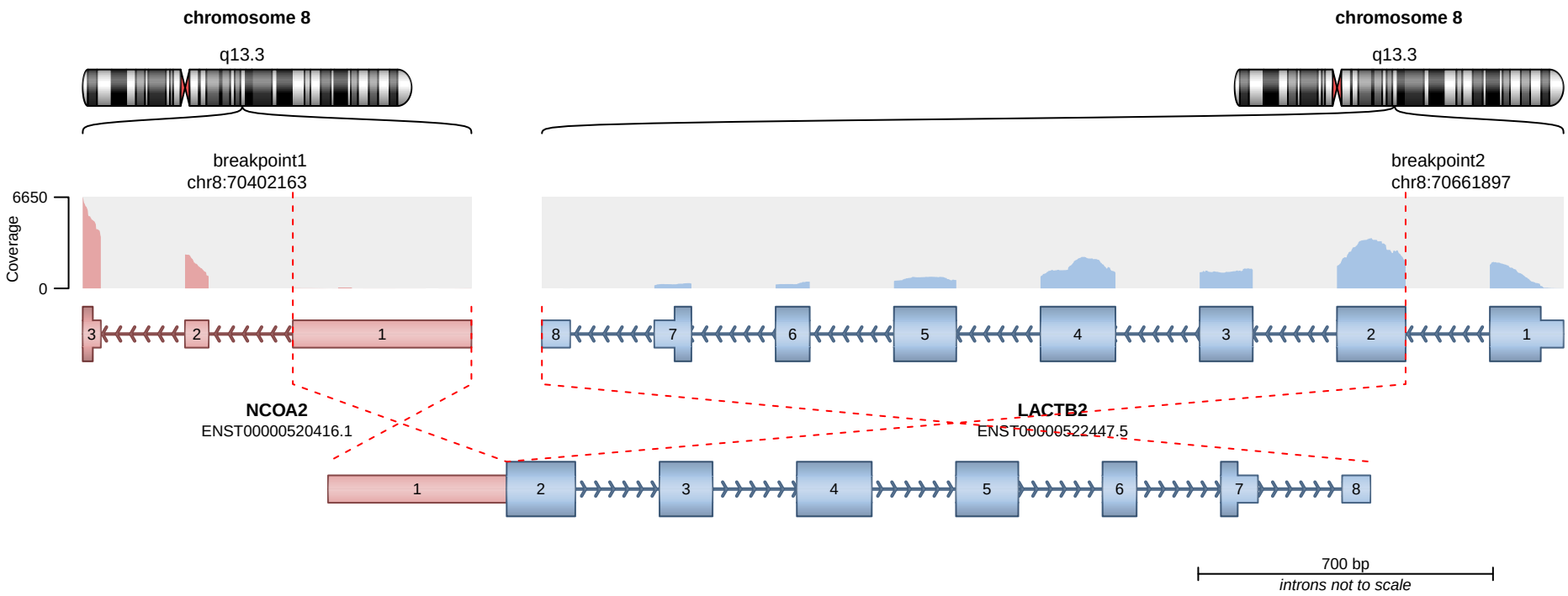


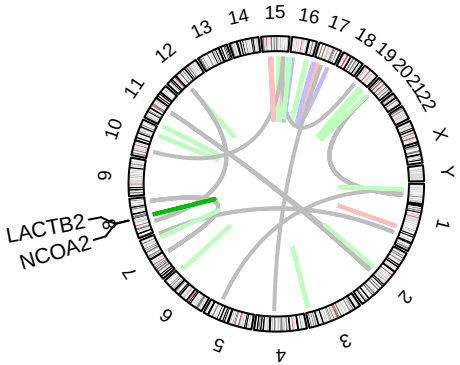


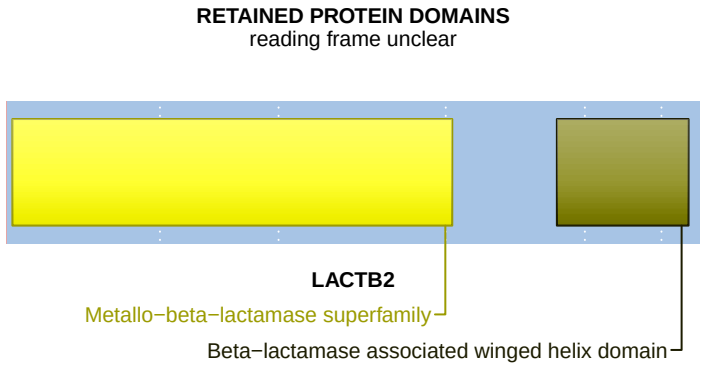
SUPPORTING READ COUNT

Split reads = 41
Discordant mates = 0

translocation
deletion
duplication
inversion

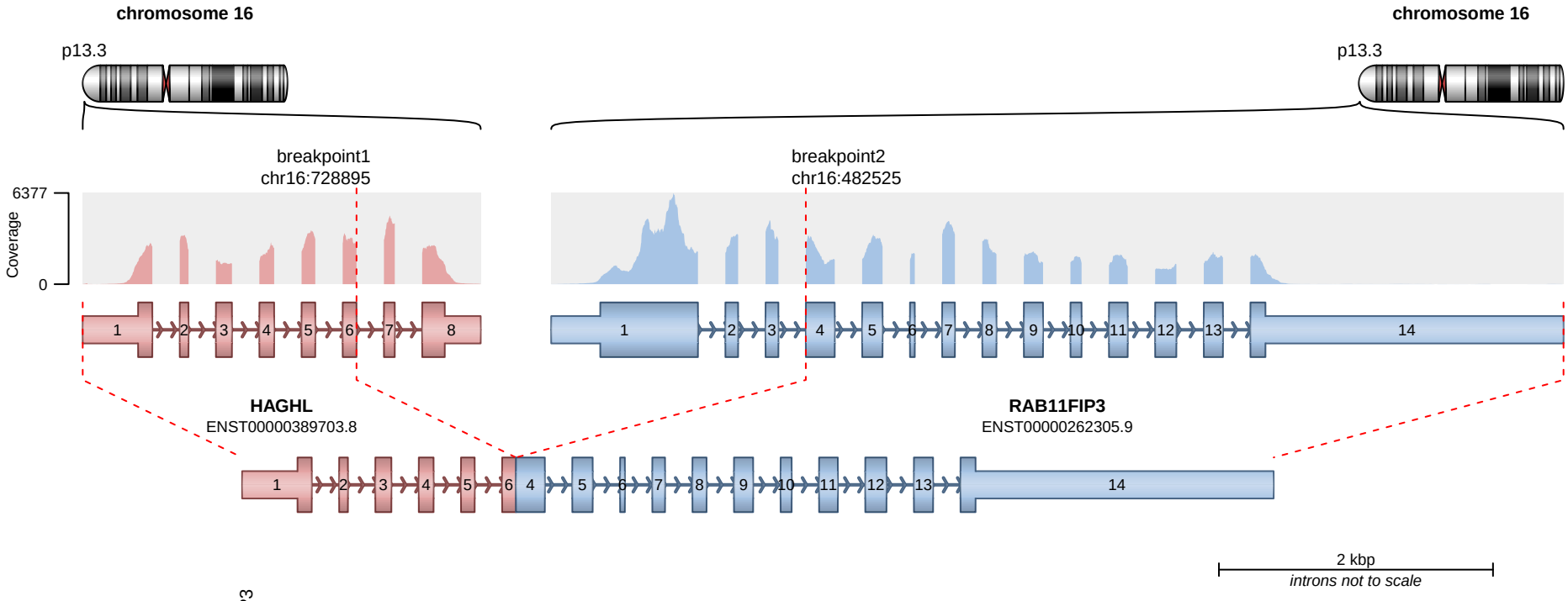


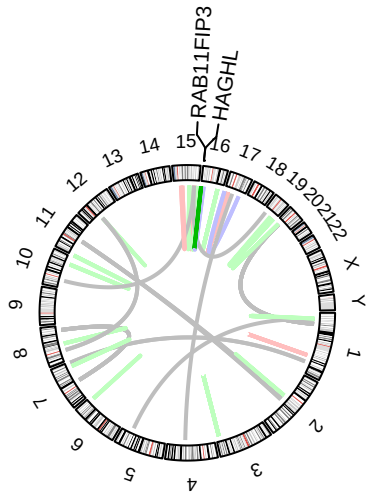


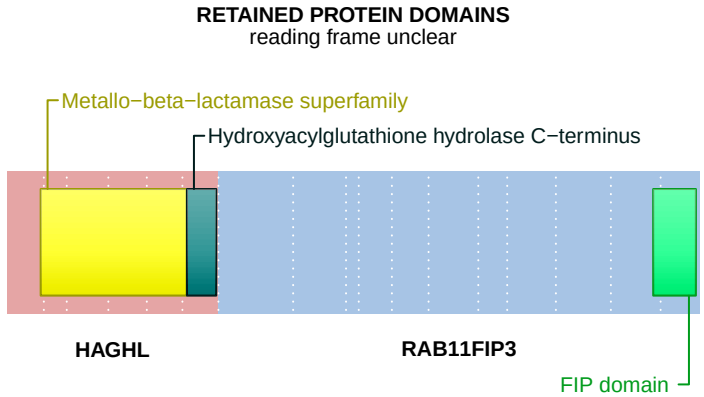


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



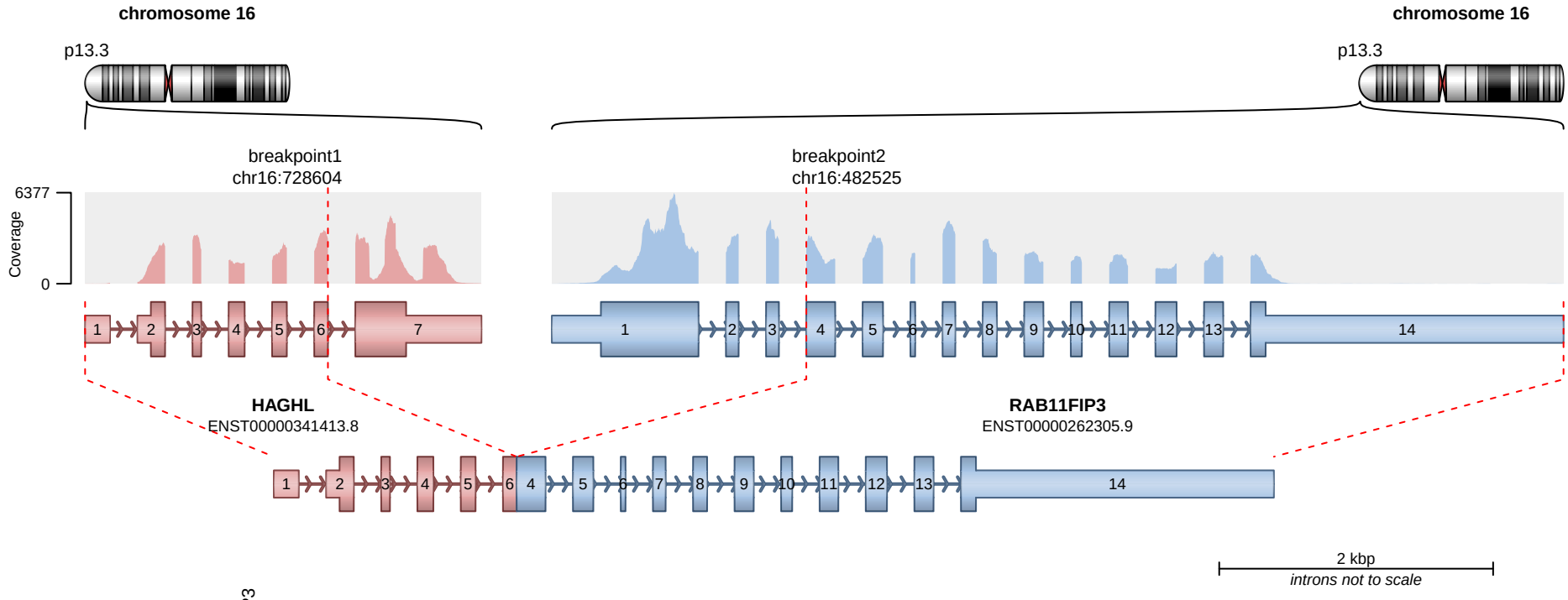


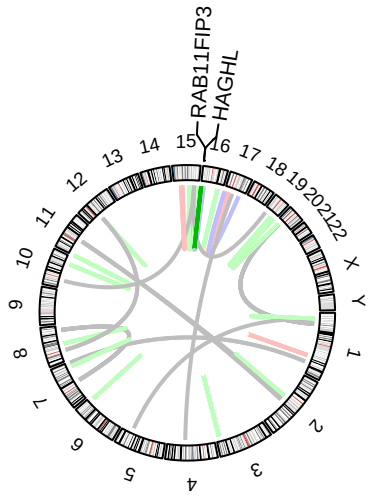


SUPPORTING READ COUNT

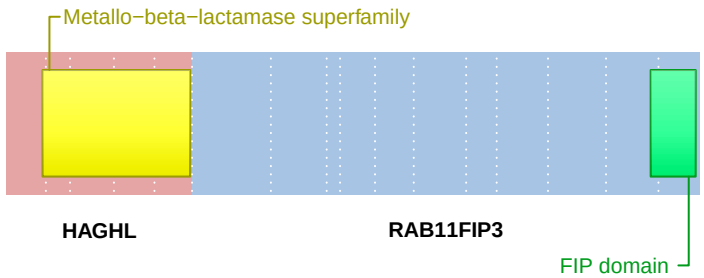
Split reads = 35
Discordant mates = 0

translocation
deletion
duplication
inversion





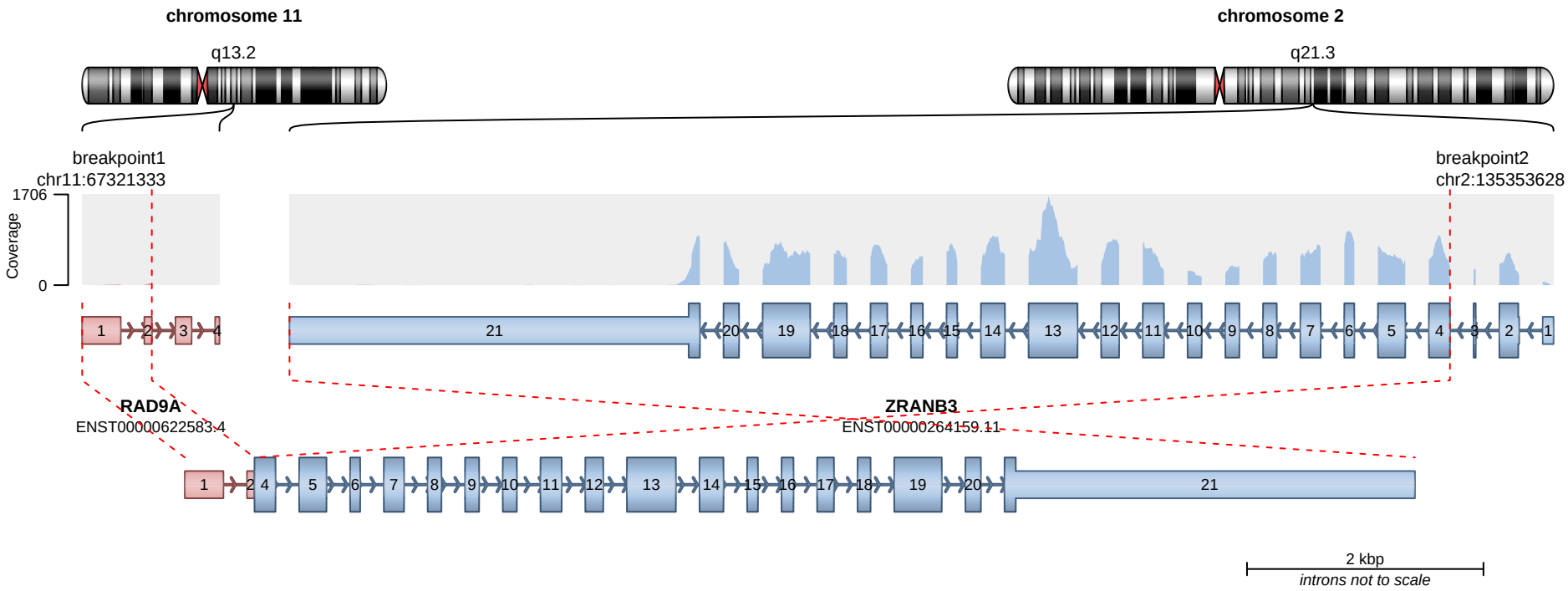
RETAINED PROTEIN DOMAINS
reading frame unclear

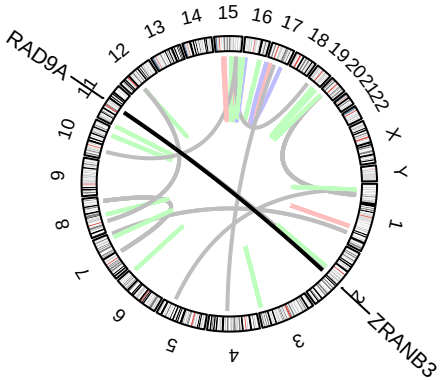


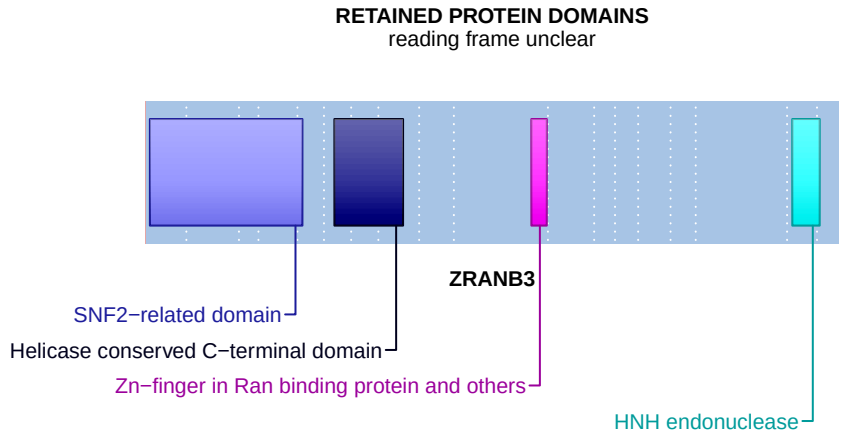
SUPPORTING READ COUNT

Split reads = 15
Discordant mates = 0

translocation
deletion
duplication
inversion

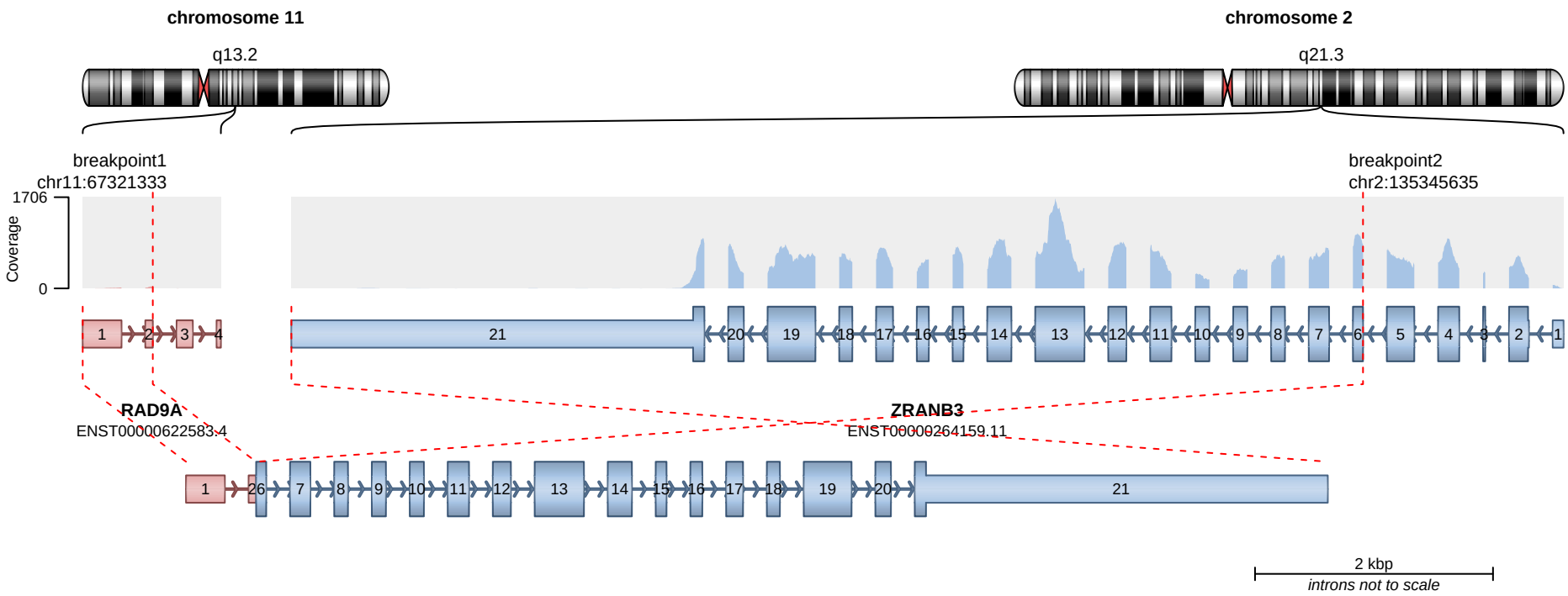


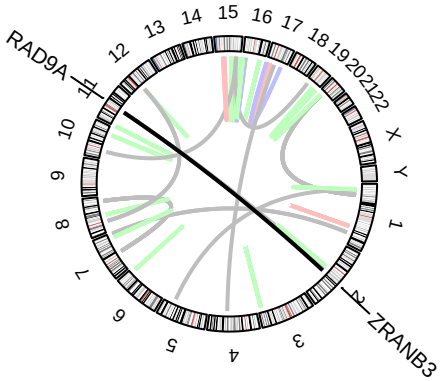


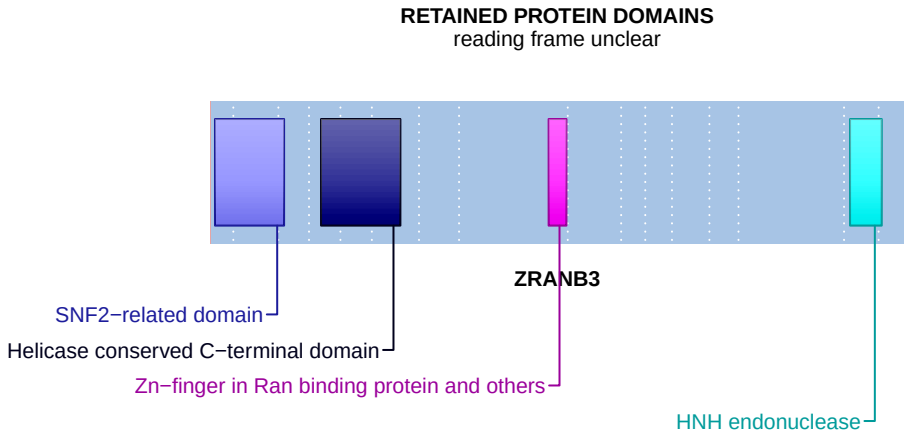


SUPPORTING READ COUNT

Split reads = 31
Discordant mates = 1

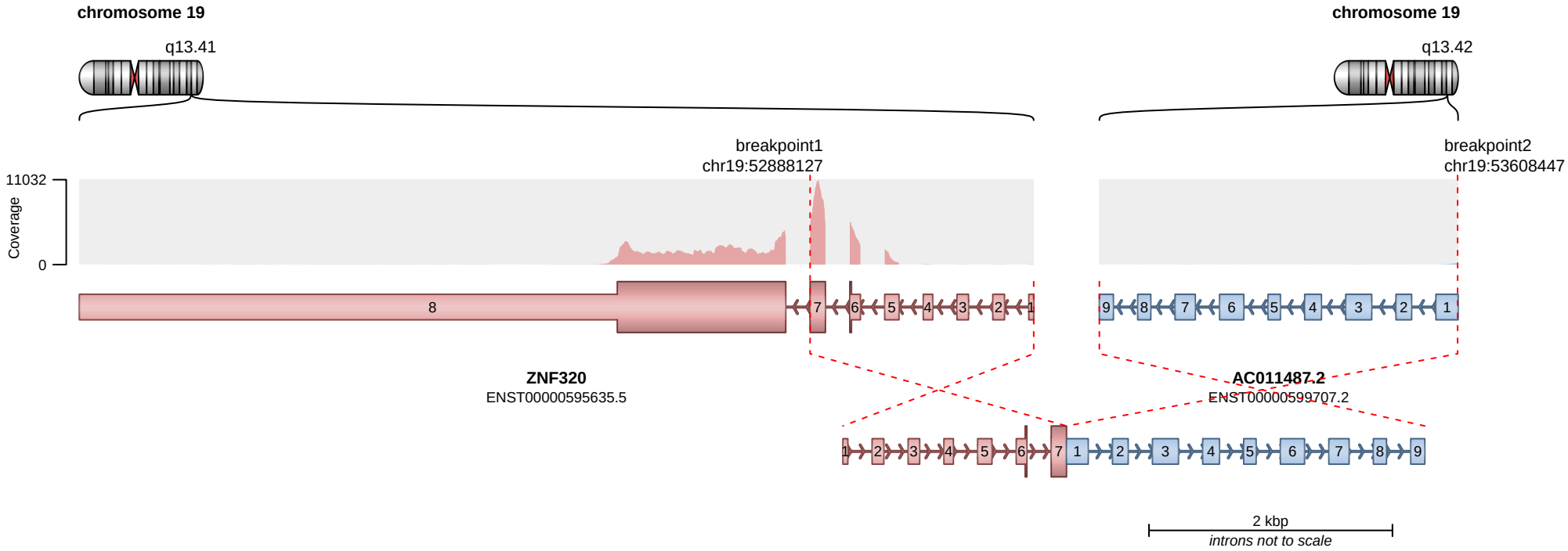


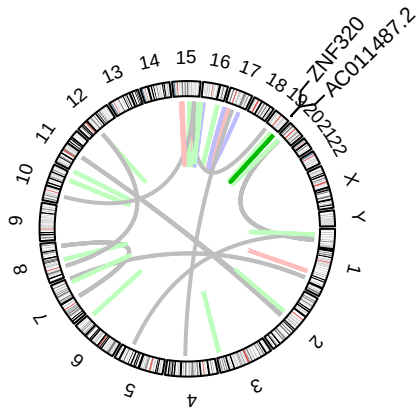




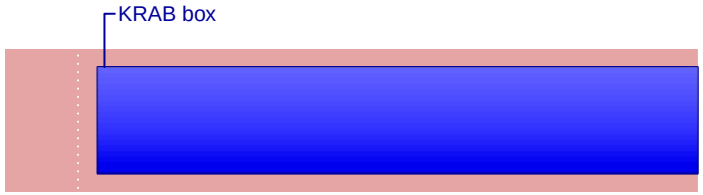
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0





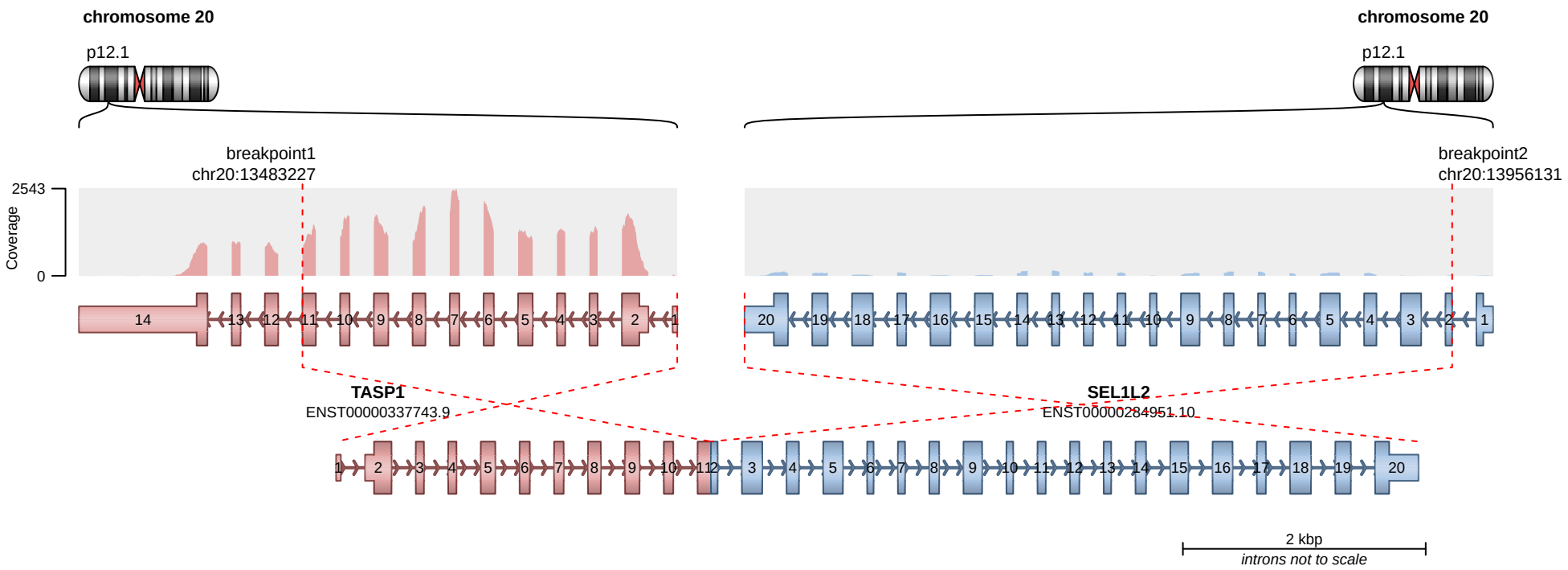
RETAINED PROTEIN DOMAINS
reading frame unclear

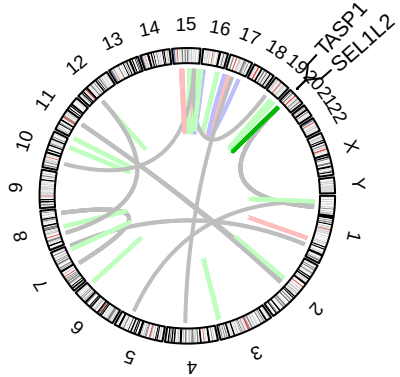


SUPPORTING READ COUNT

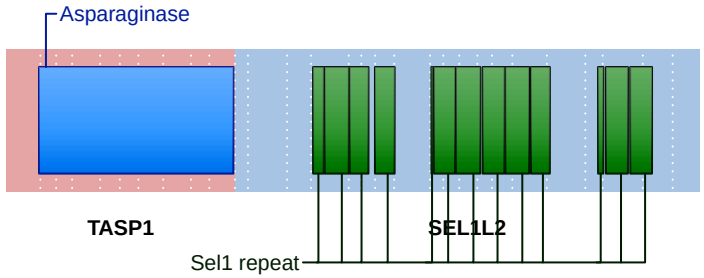
Split reads = 31
Discordant mates = 0

translocation
deletion
duplication
inversion





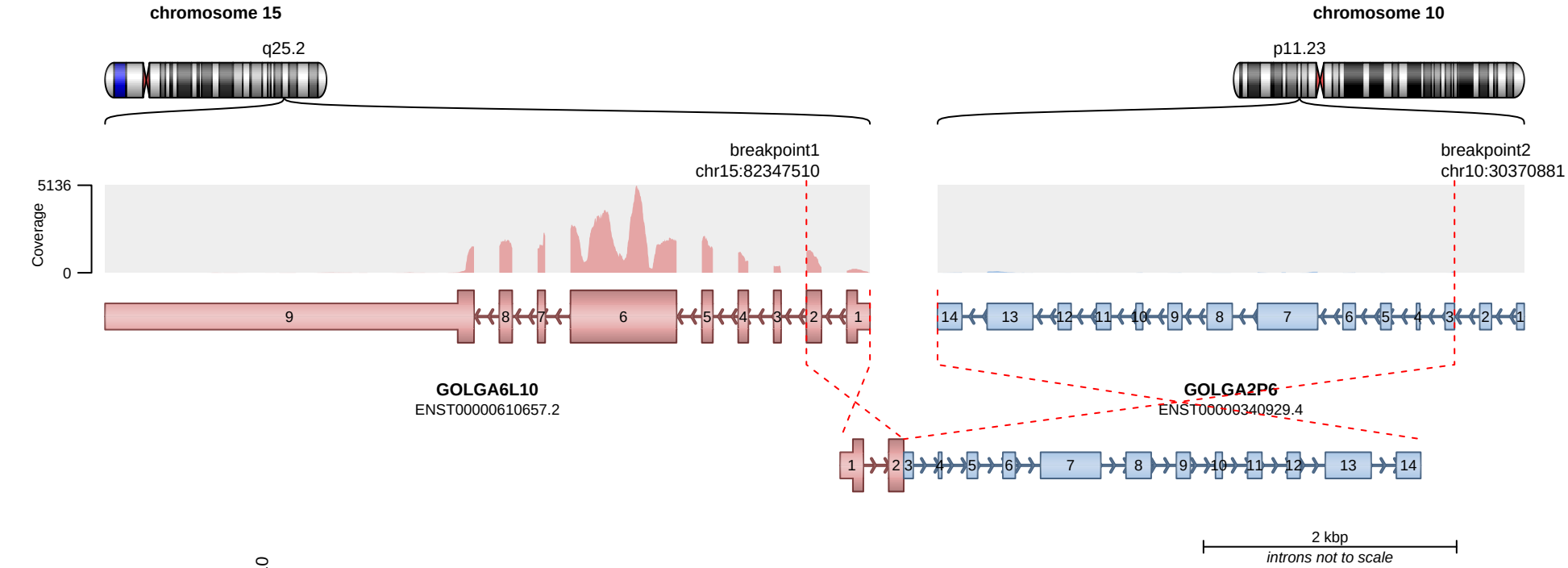
RETAINED PROTEIN DOMAINS
reading frame unclear

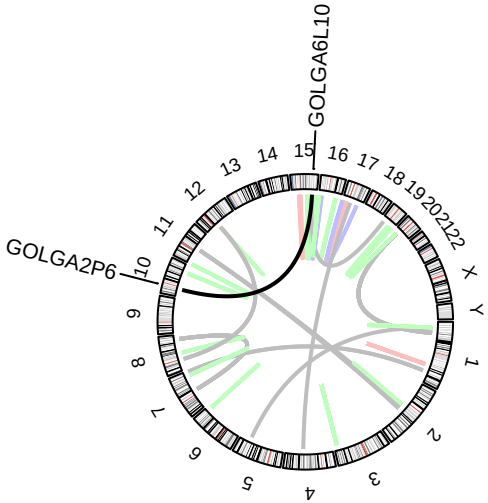


SUPPORTING READ COUNT

Split reads = 22
Discordant mates = 0

translocation
deletion
duplication
inversion



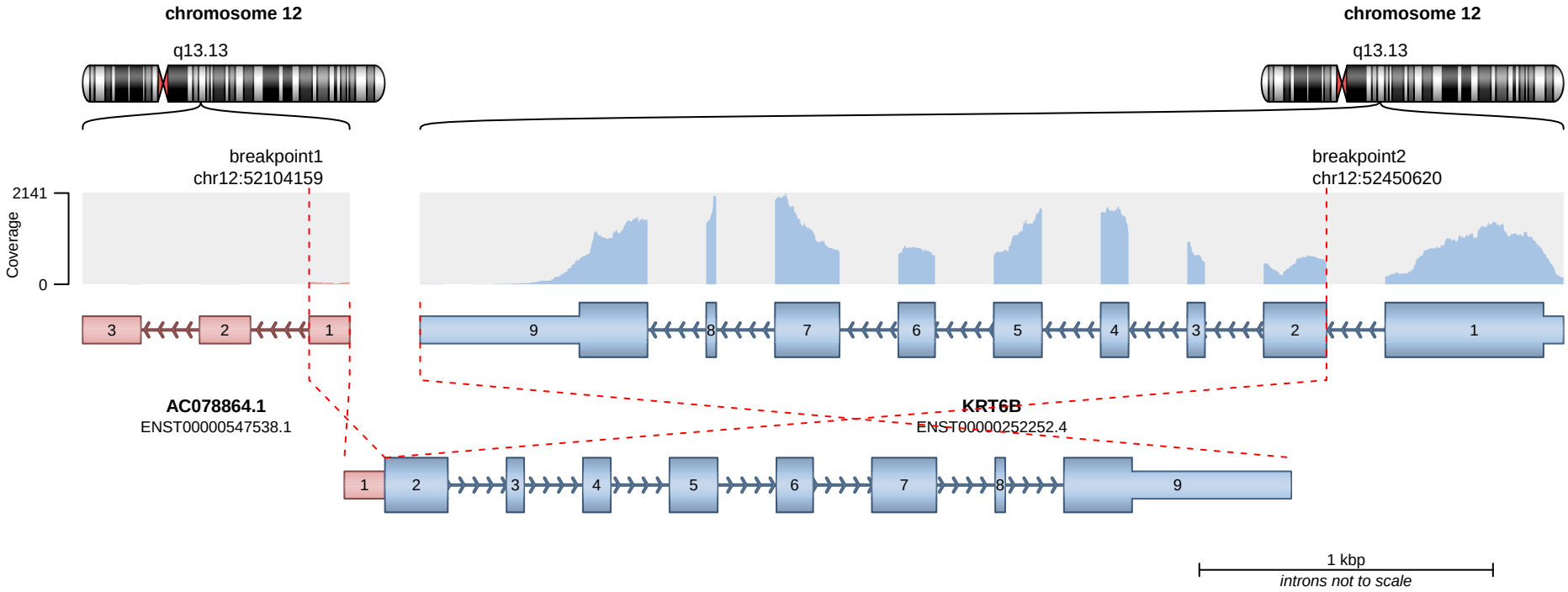


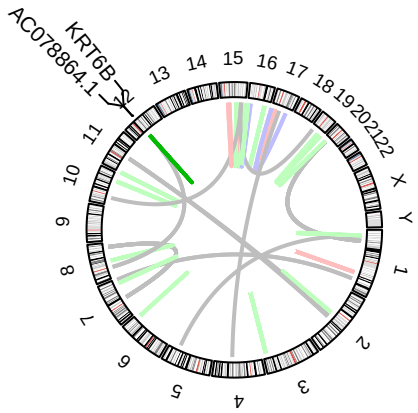
translocation
deletion
duplication
inversion

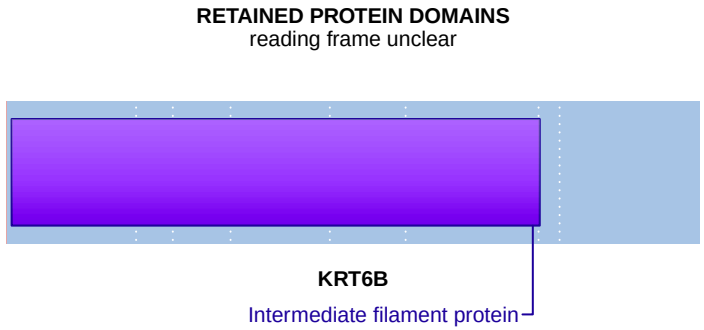
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 19
Discordant mates = 0



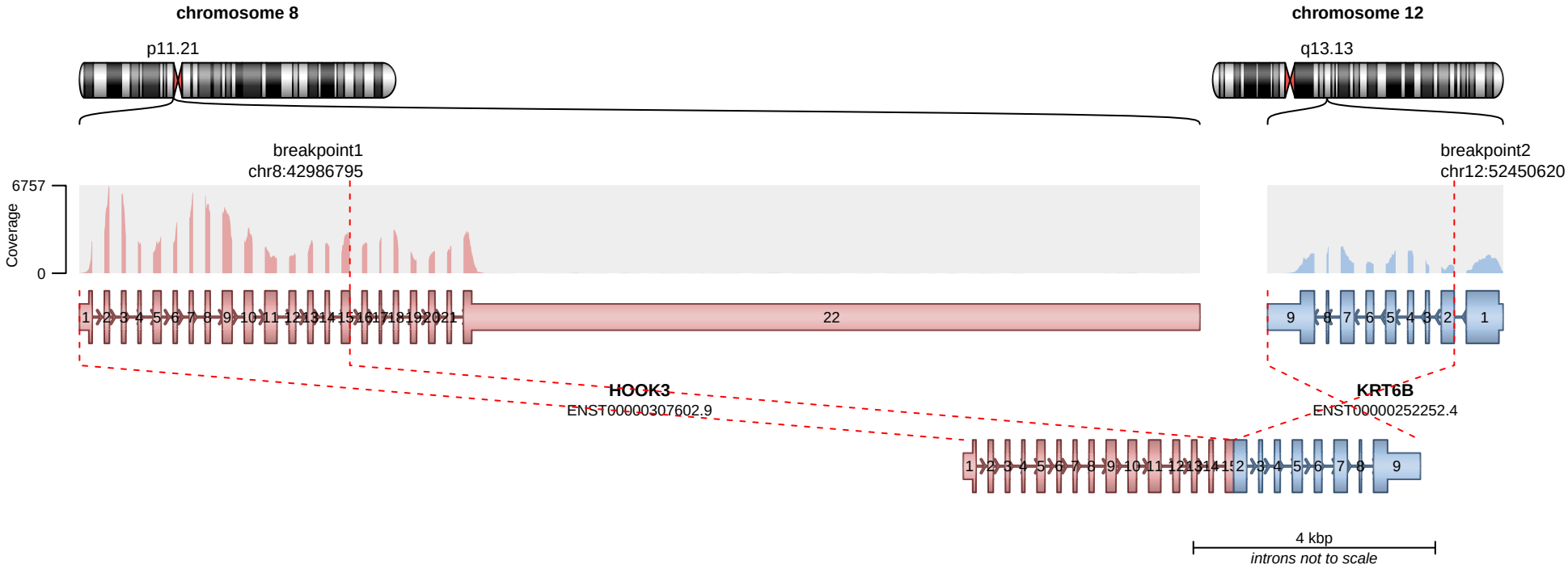


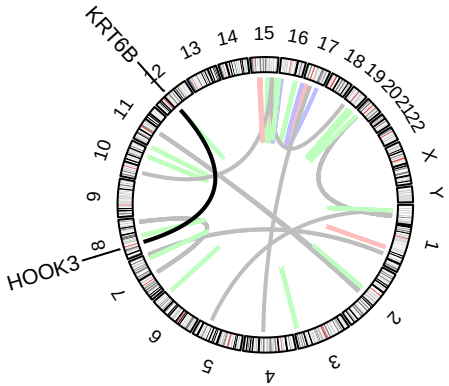


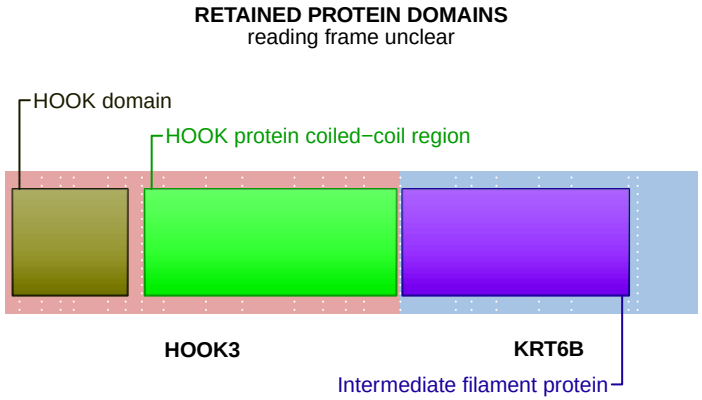
SUPPORTING READ COUNT

Split reads = 18
Discordant mates = 0

translocation
deletion
duplication
inversion



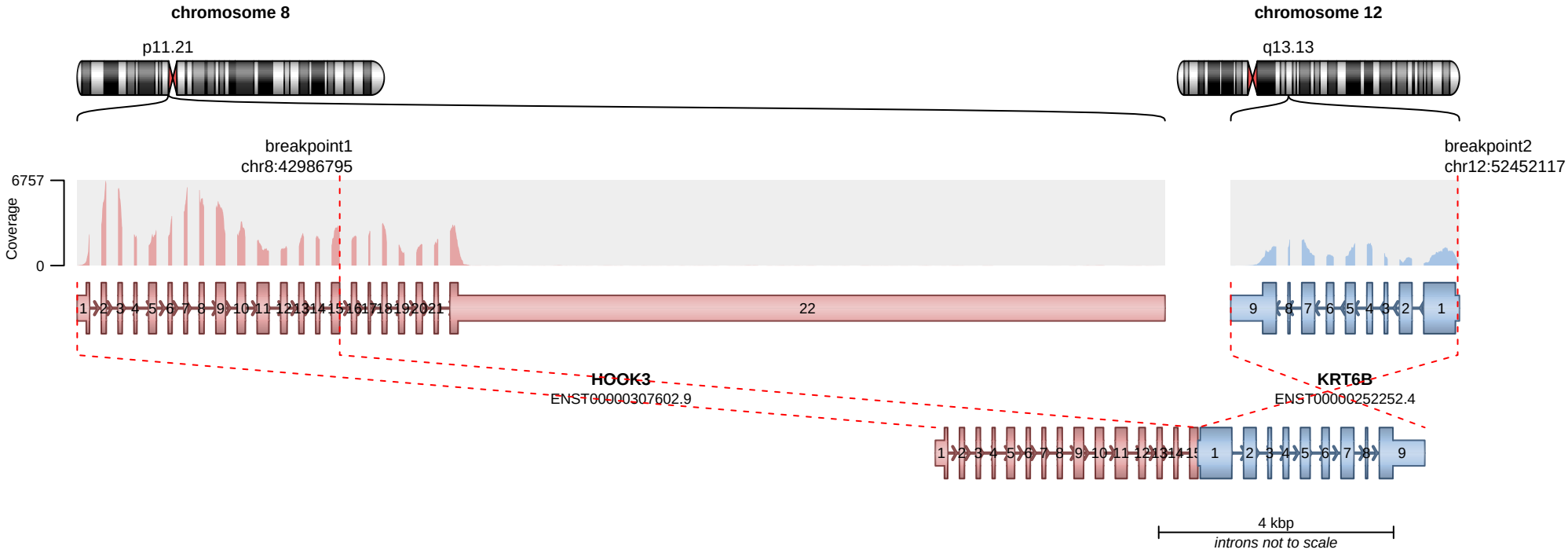


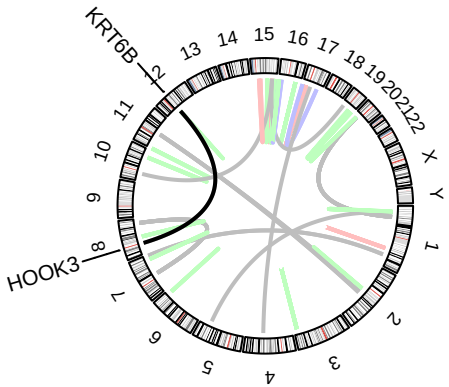


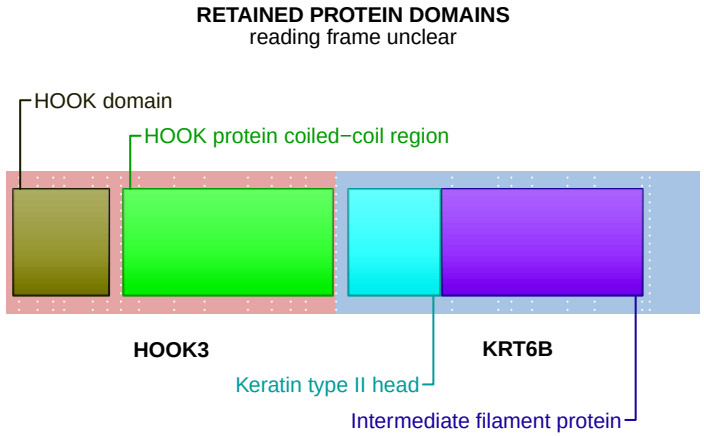
SUPPORTING READ COUNT

Split reads = 18
Discordant mates = 0

translocation
deletion
duplication
inversion



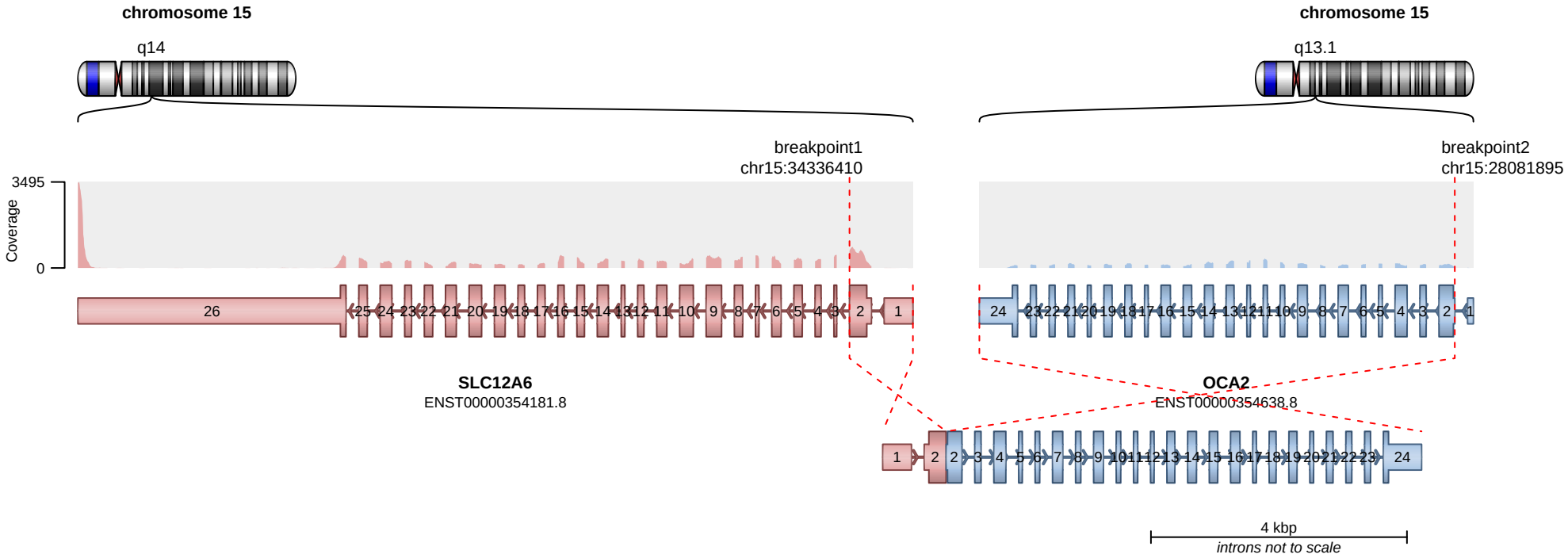


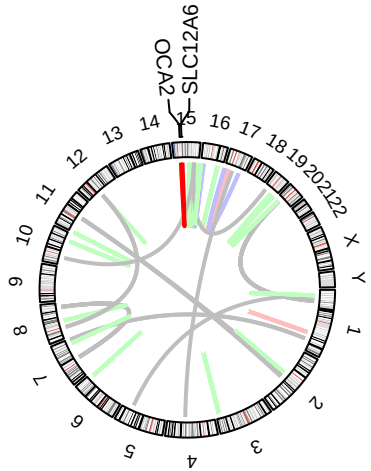


SUPPORTING READ COUNT

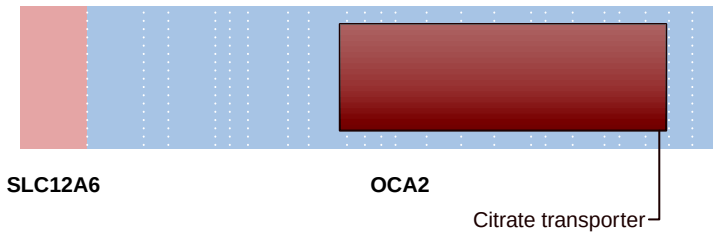
Split reads = 8
Discordant mates = 0

translocation
deletion
duplication
inversion





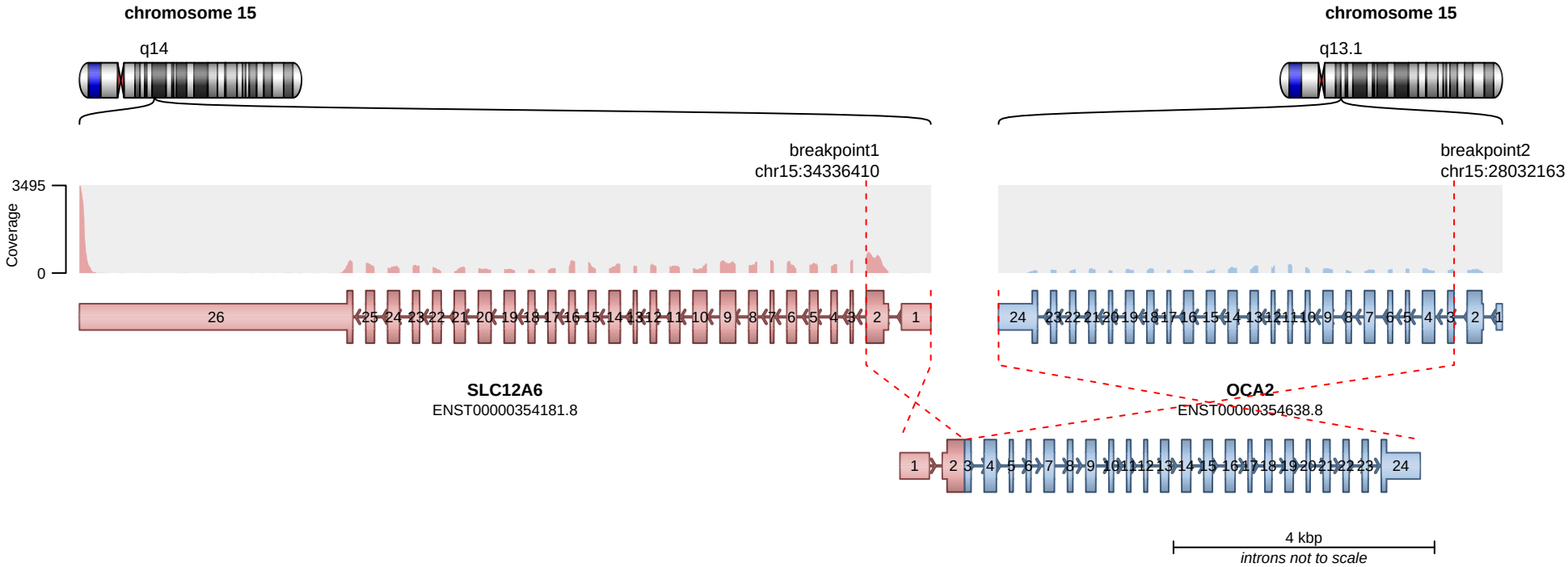
RETAINED PROTEIN DOMAINS
reading frame unclear

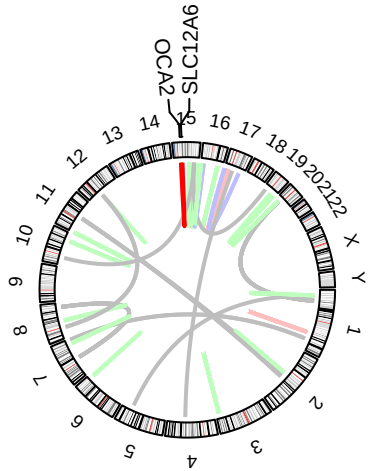


SUPPORTING READ COUNT

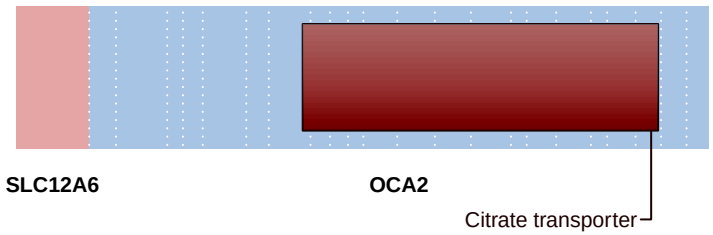
Split reads = 18
Discordant mates = 0

translocation
deletion
duplication
inversion





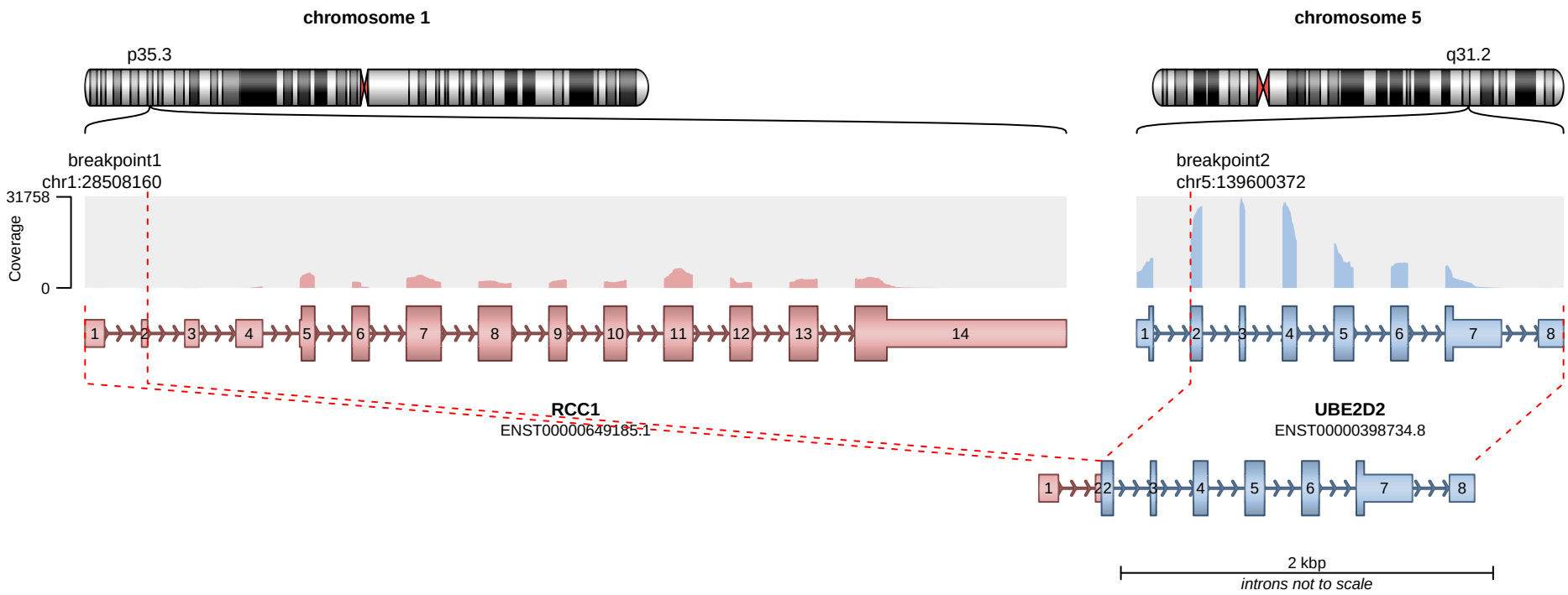
RETAINED PROTEIN DOMAINS
reading frame unclear

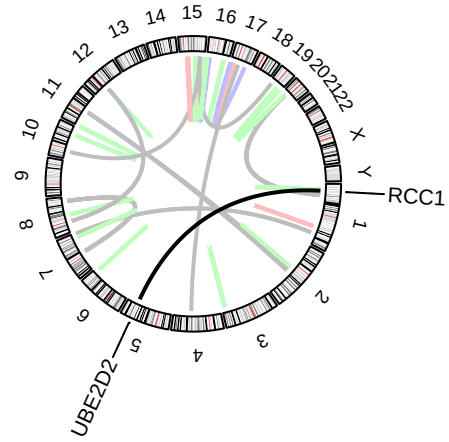


SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 0

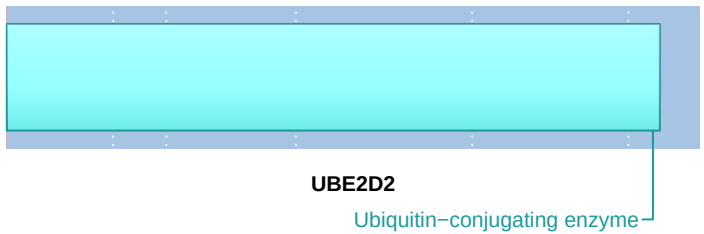
translocation
deletion
duplication
inversion





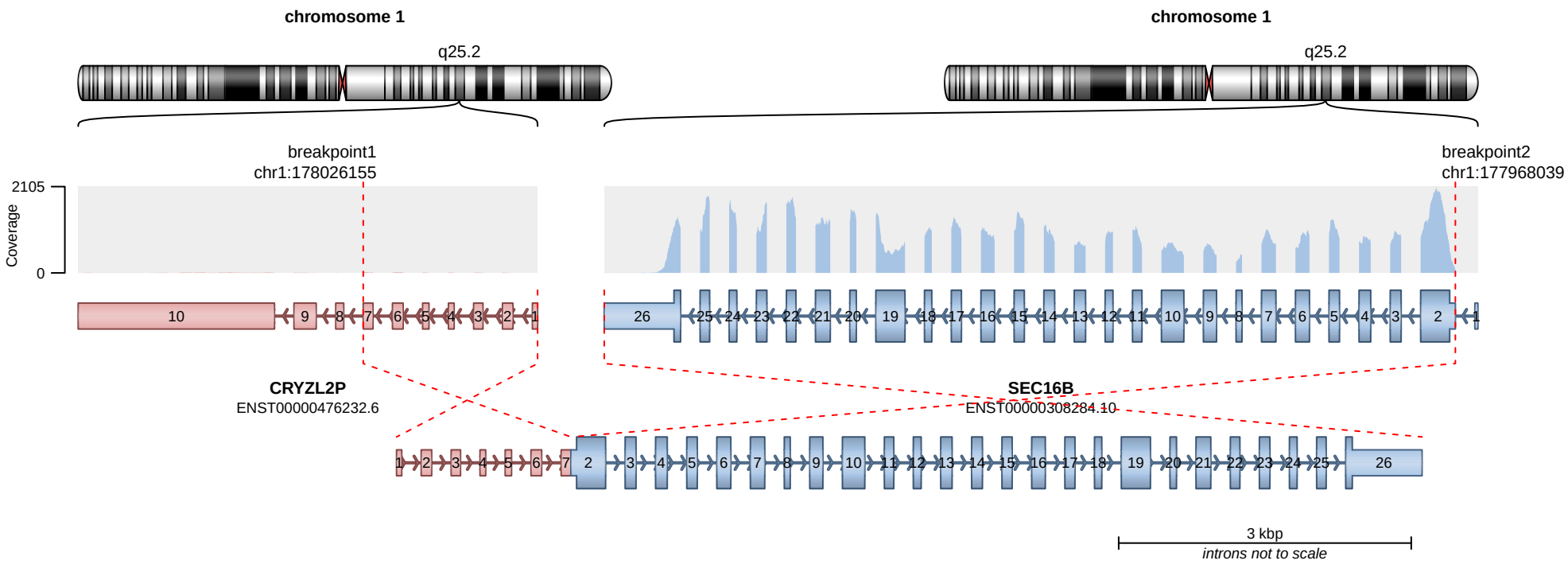
translocation
deletion
duplication
inversion

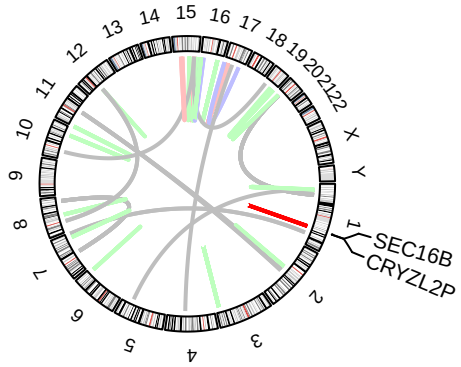
RETAINED PROTEIN DOMAINS
reading frame unclear

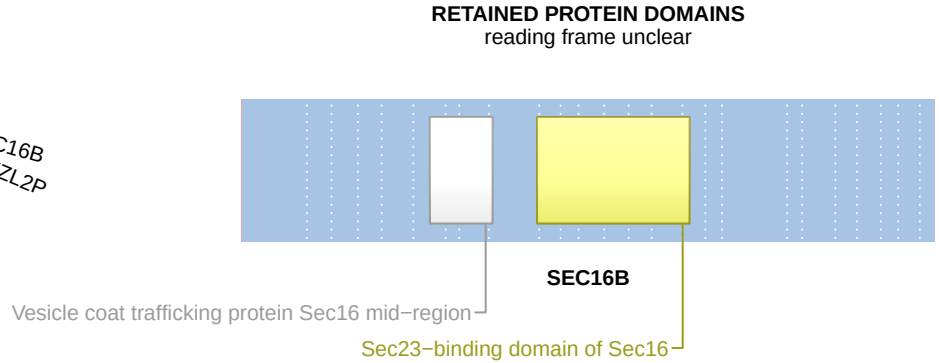


SUPPORTING READ COUNT

Split reads = 14
Discordant mates = 0



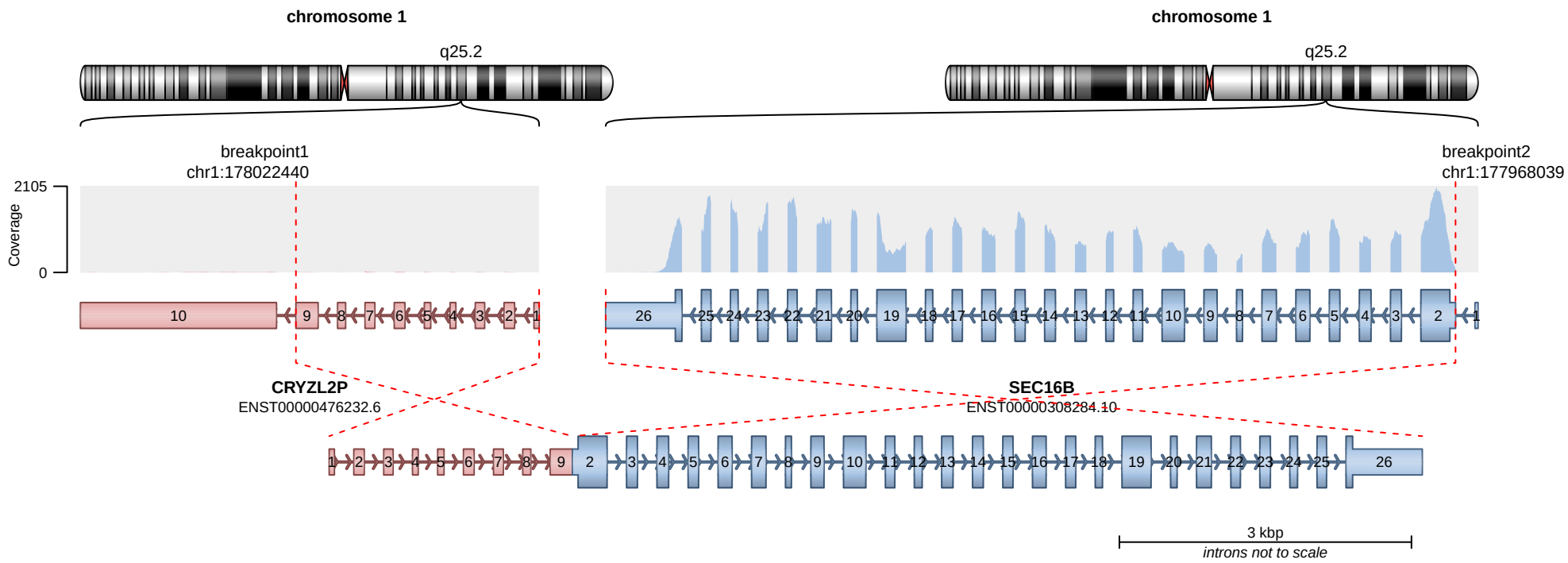


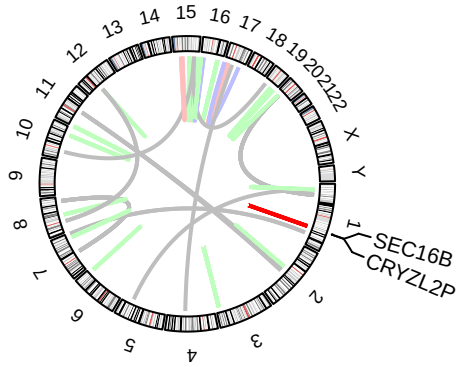


SUPPORTING READ COUNT

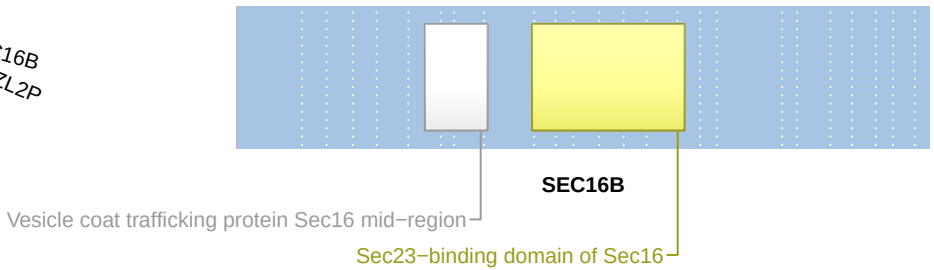
Split reads = 13
Discordant mates = 0

translocation
deletion
duplication
inversion





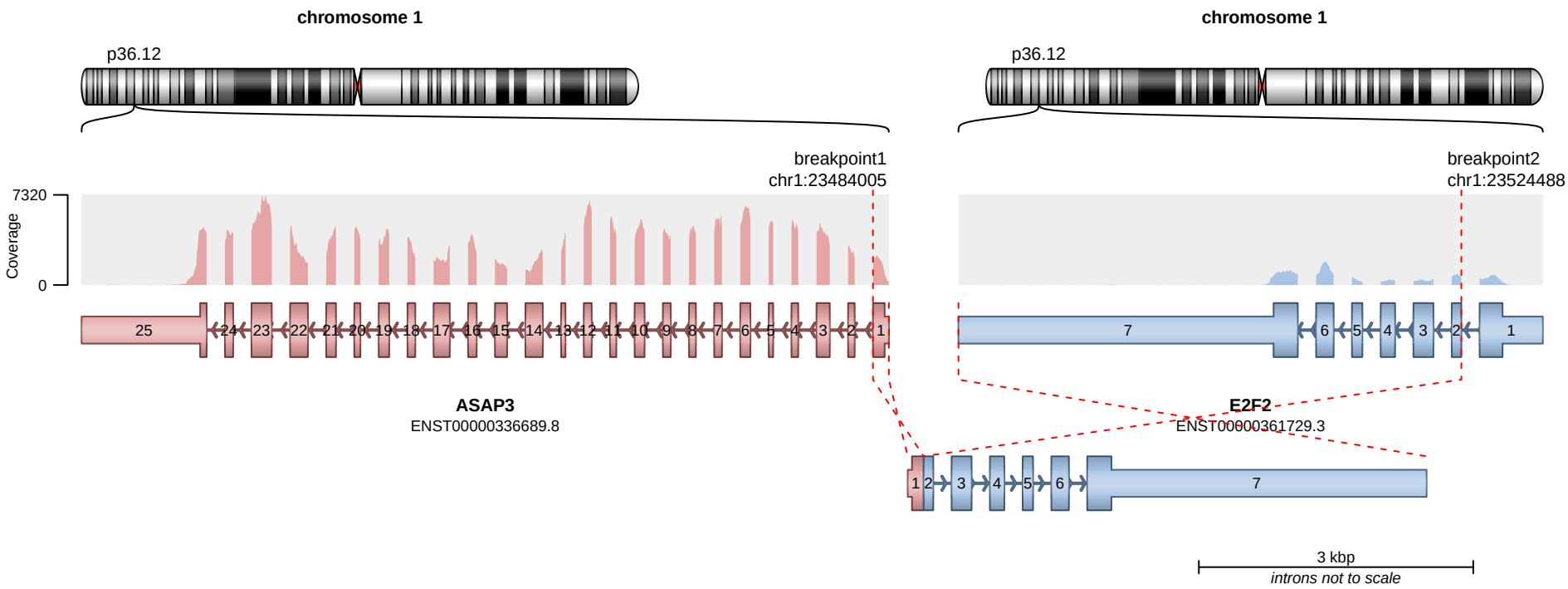
RETAINED PROTEIN DOMAINS
reading frame unclear

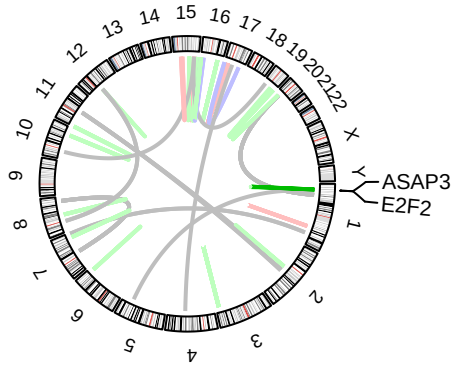


SUPPORTING READ COUNT

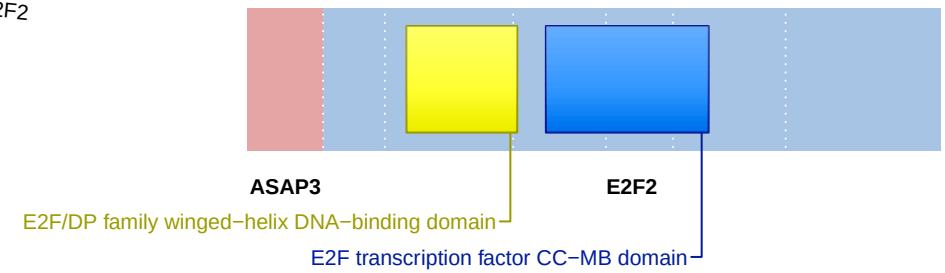
Split reads = 2
Discordant mates = 0

translocation
deletion
duplication
inversion





RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 11
Discordant mates = 0

translocation
deletion
duplication
inversion