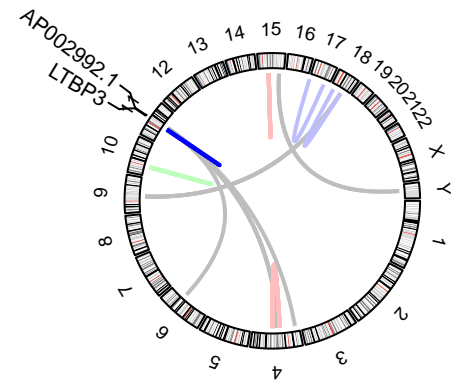
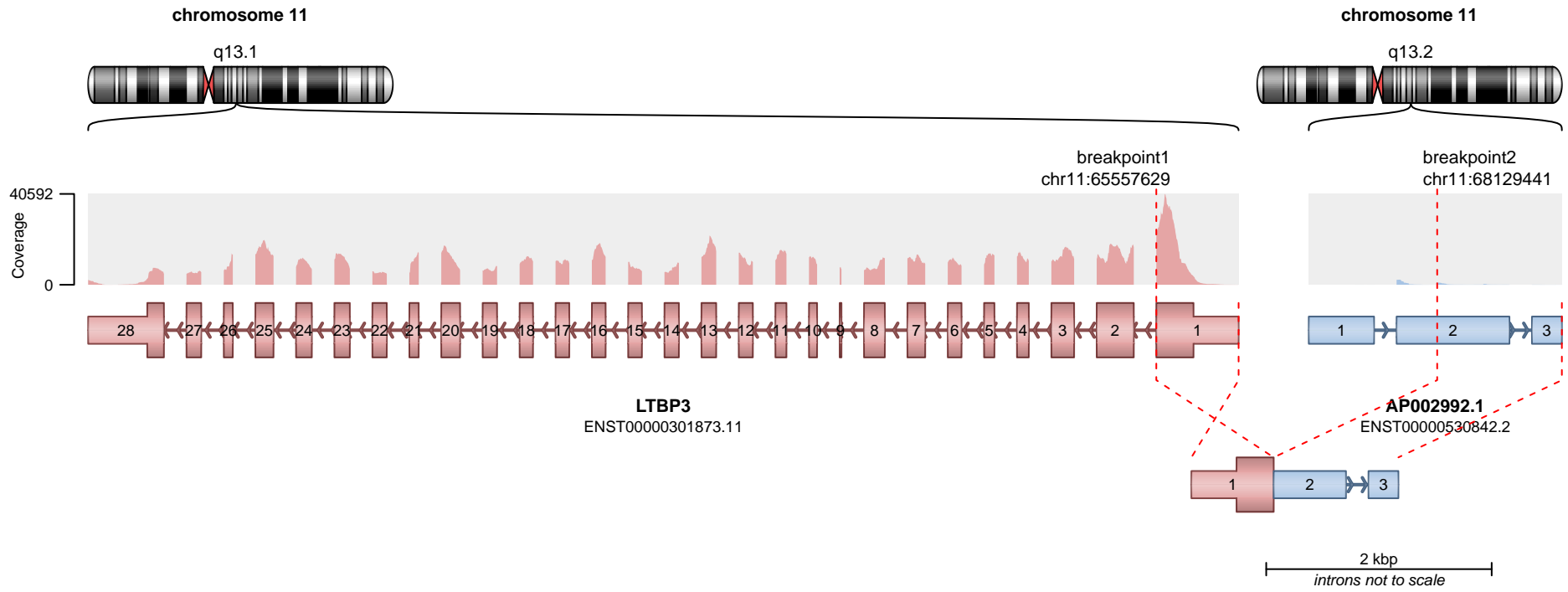


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1095
Discordant mates = 12

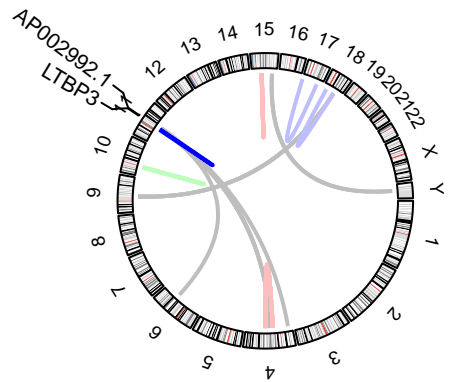
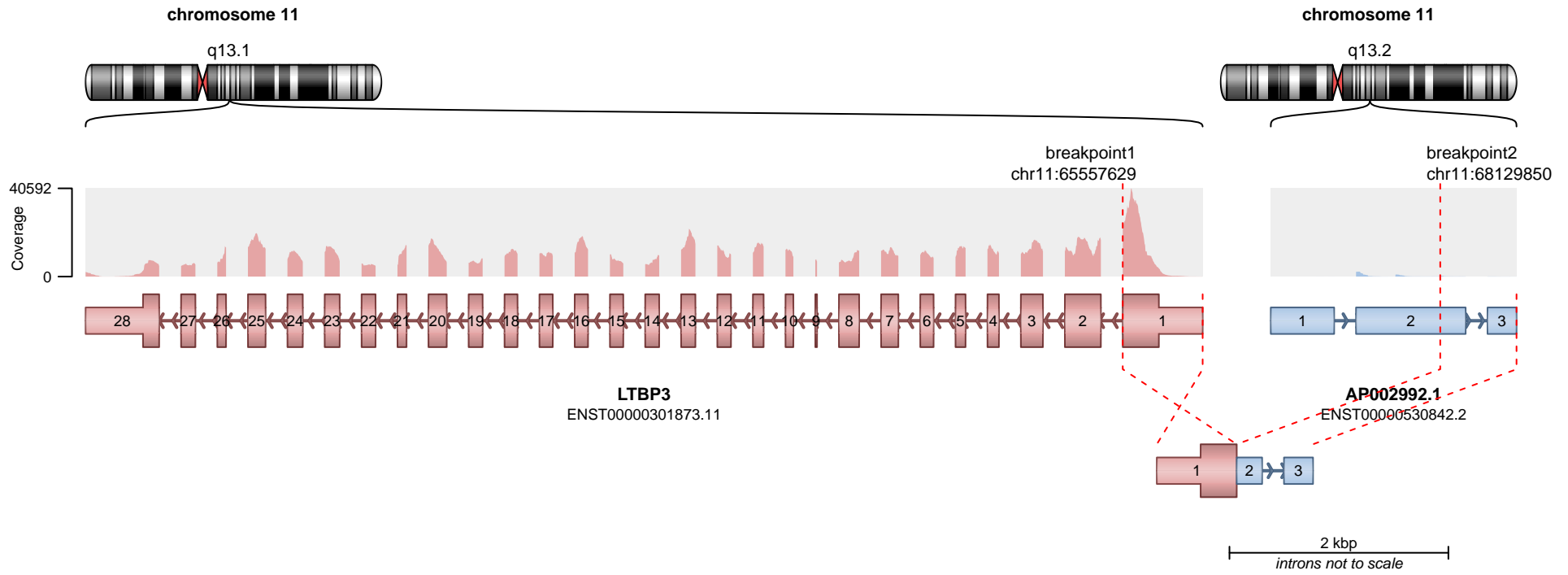


— translocation — deletion
 — duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 384
 Discordant mates = 2

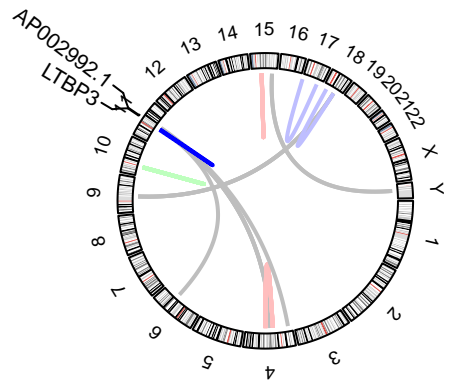
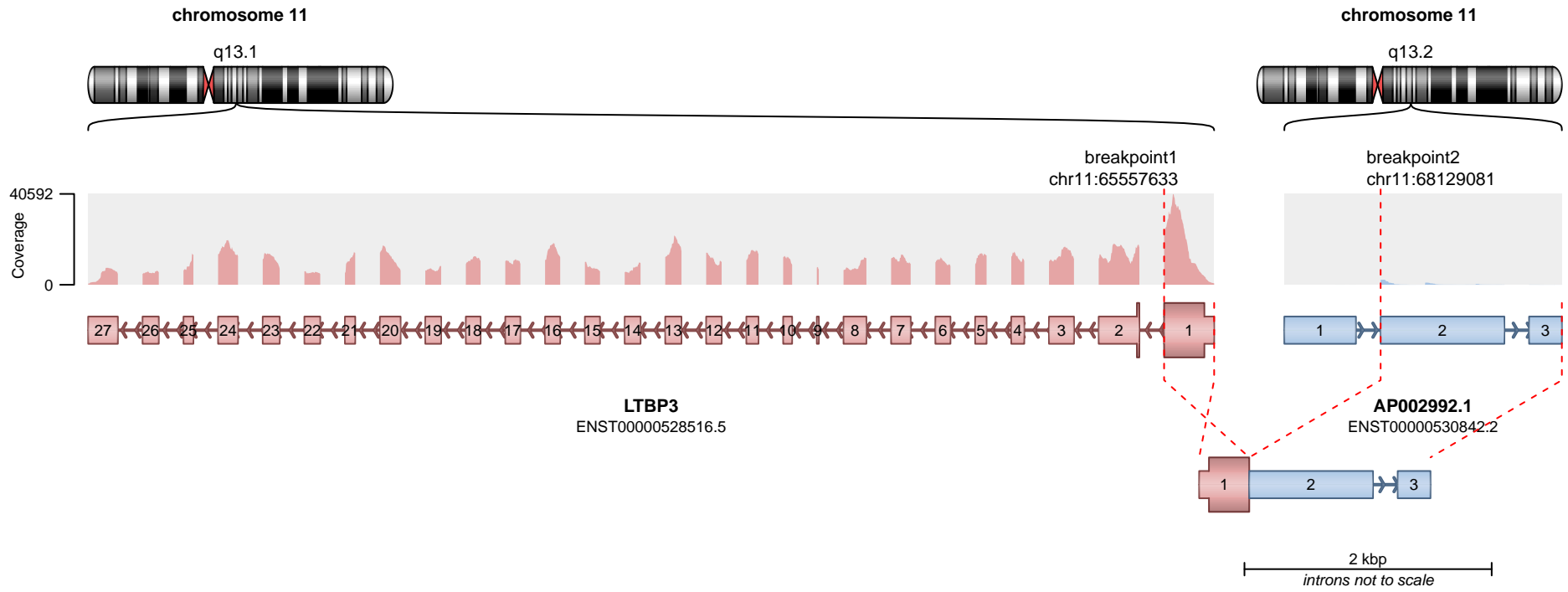


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 193
Discordant mates = 2

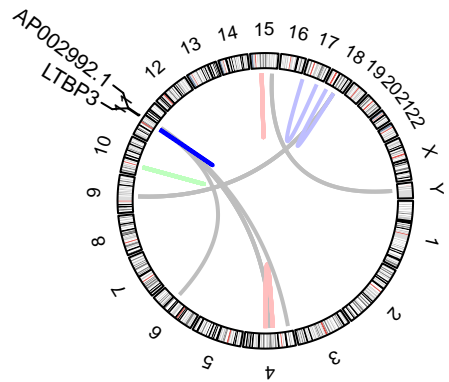
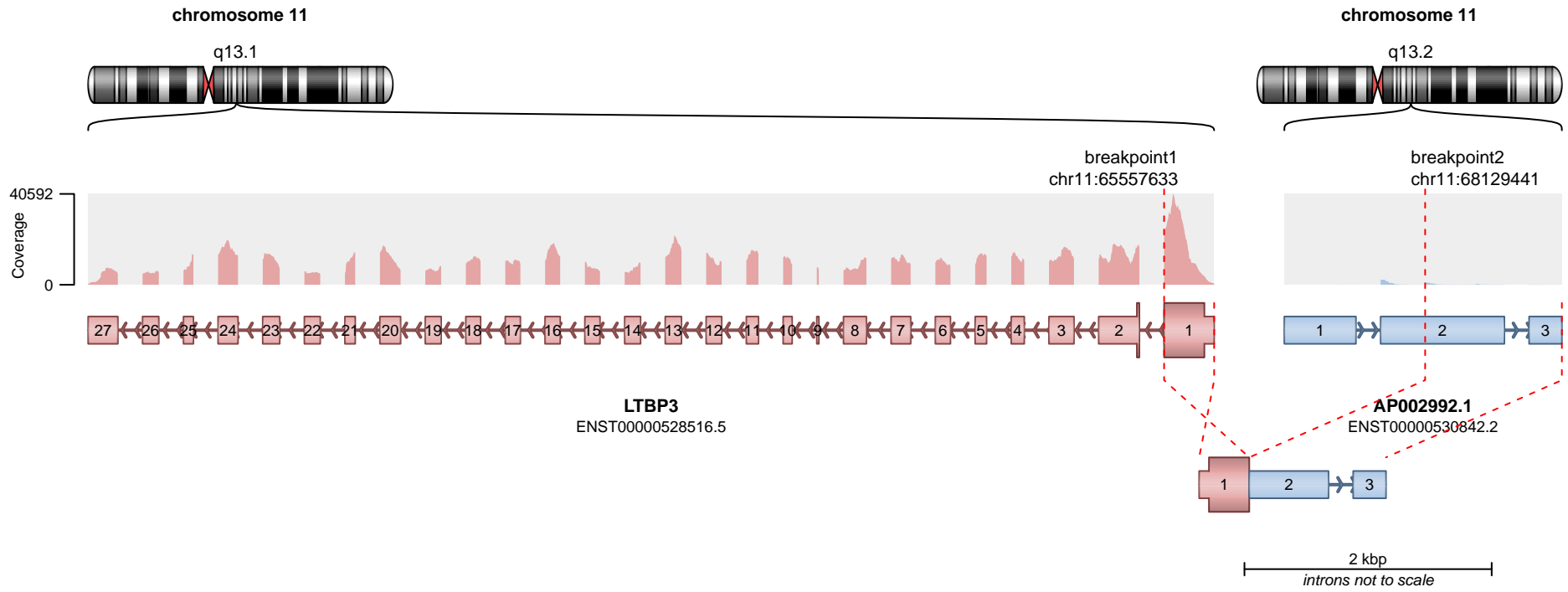


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 179
Discordant mates = 12

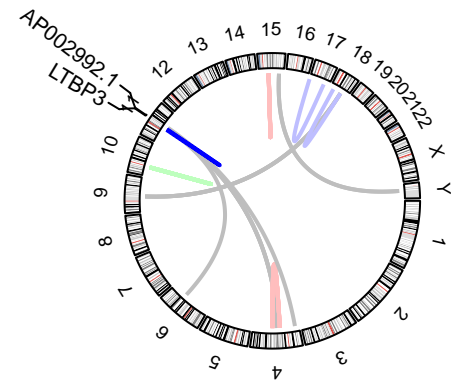
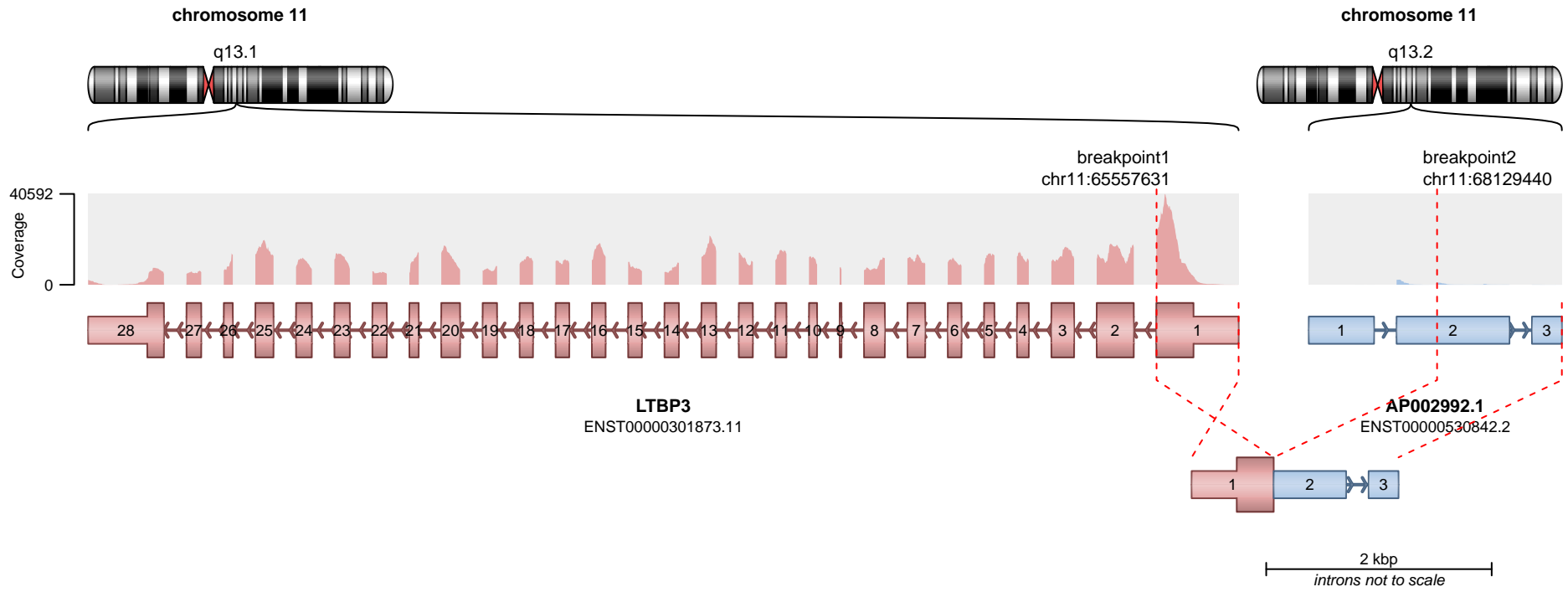


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 77
Discordant mates = 2

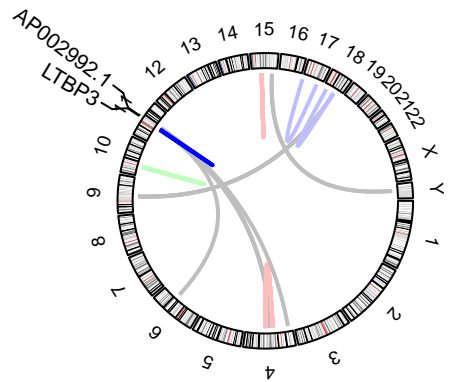
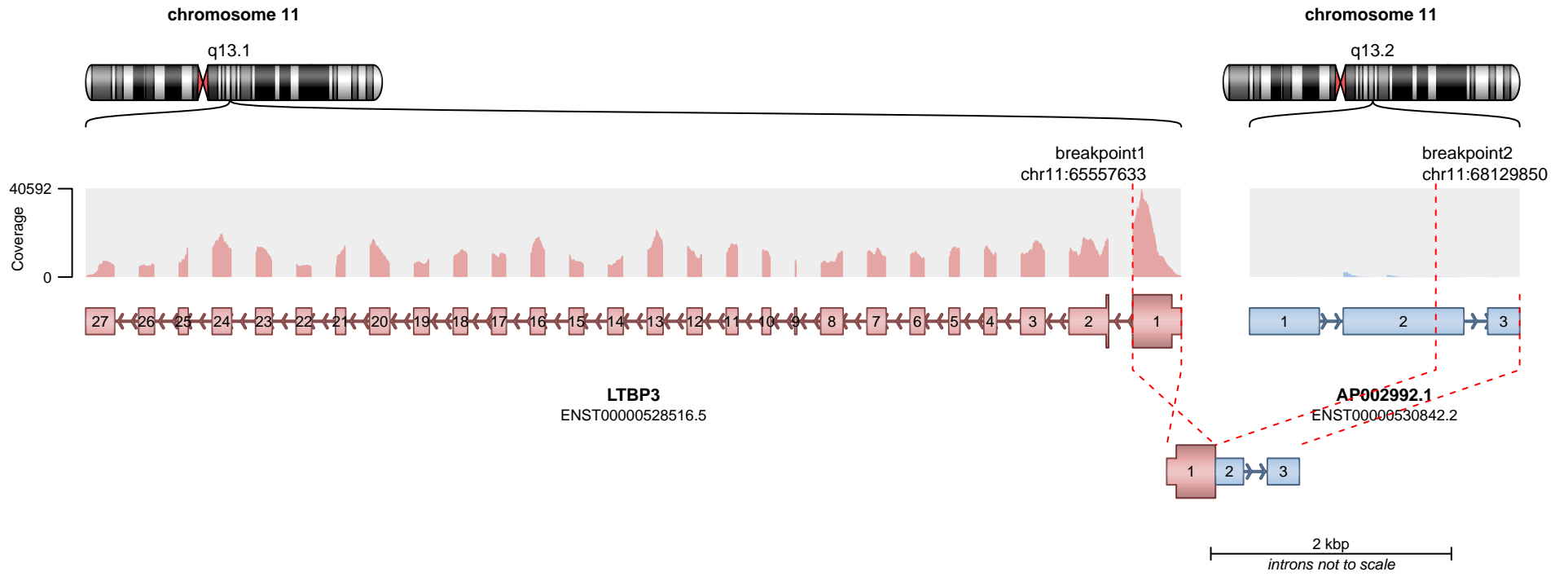


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 2

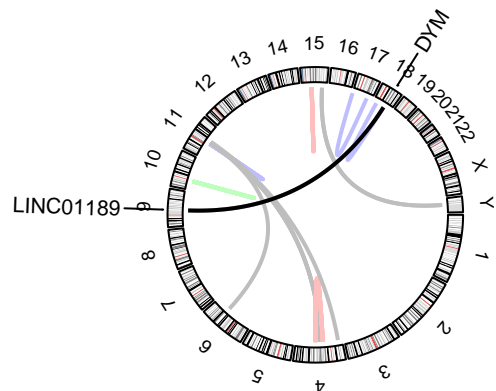
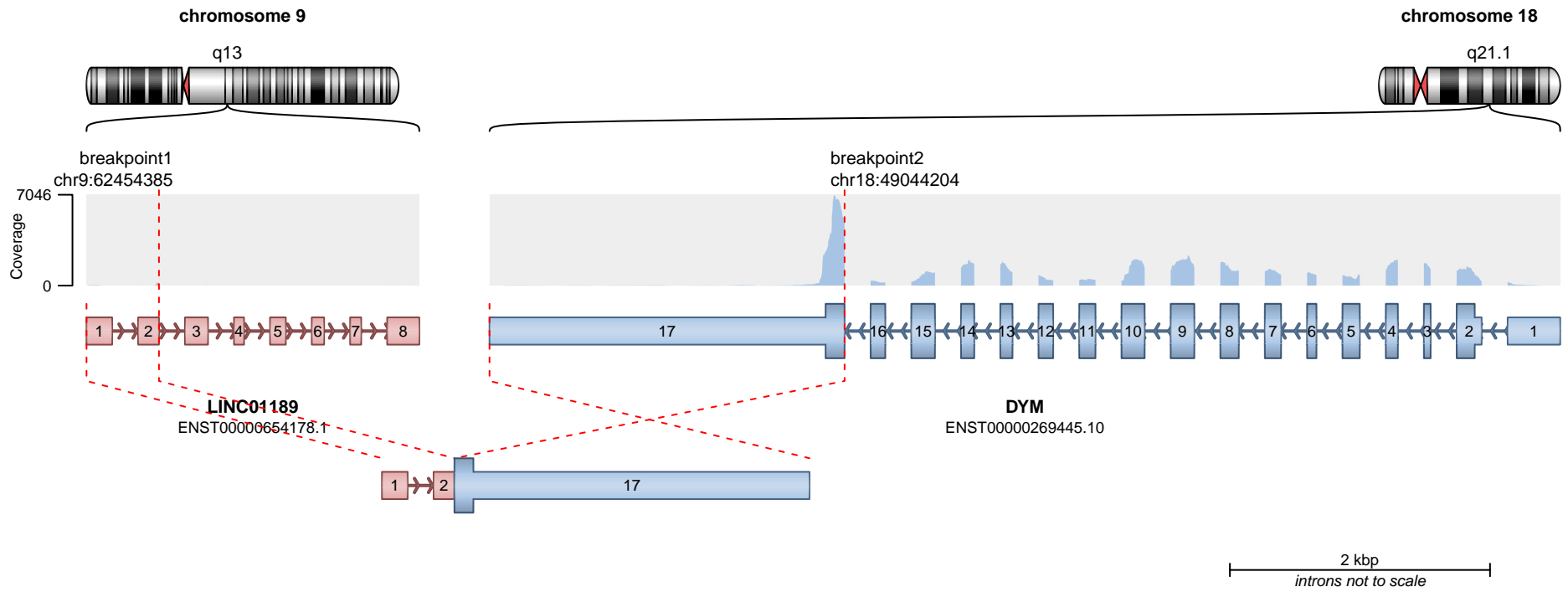


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

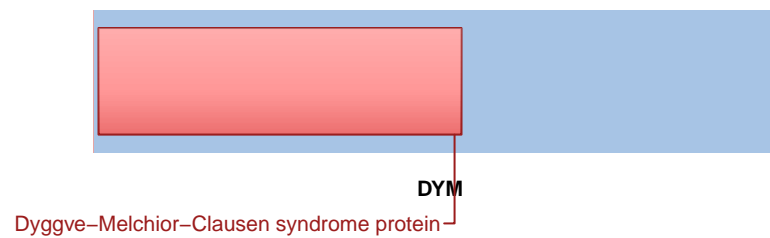
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 2



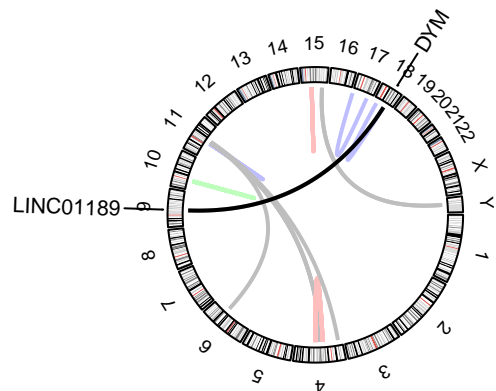
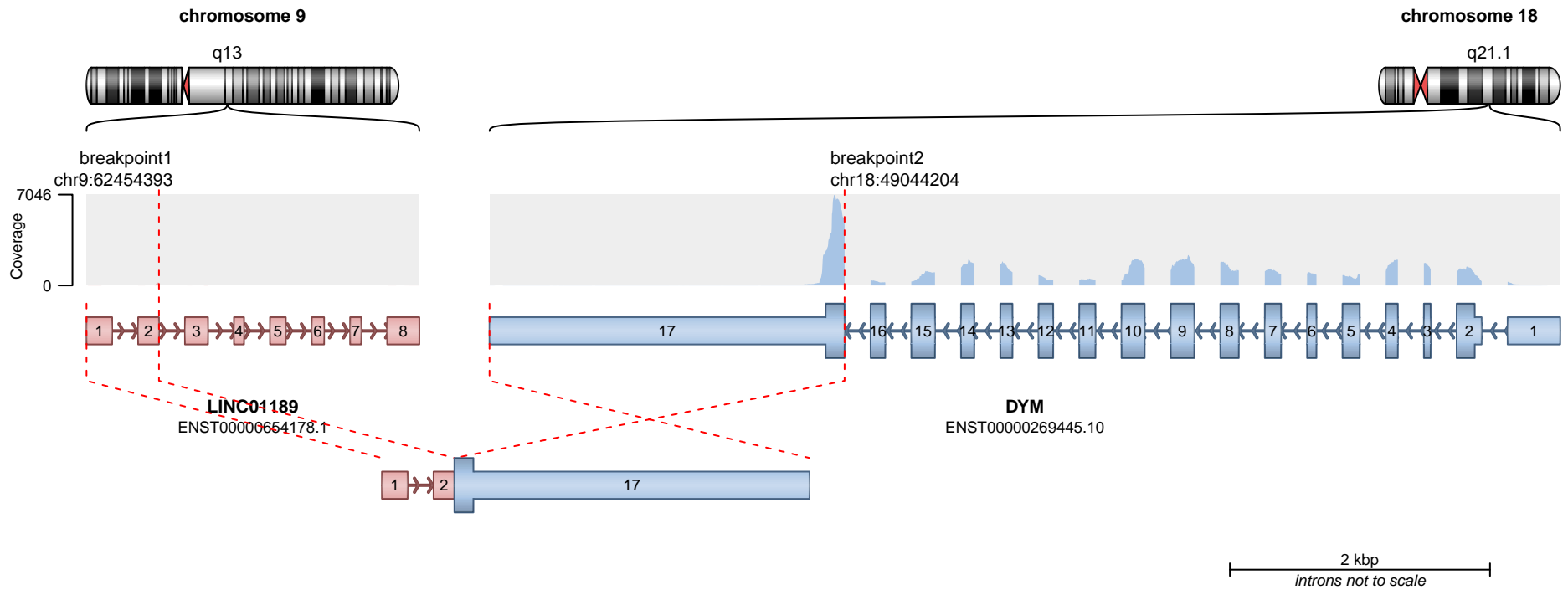
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 260
Discordant mates = 0



— translocation — deletion
— duplication — inversion

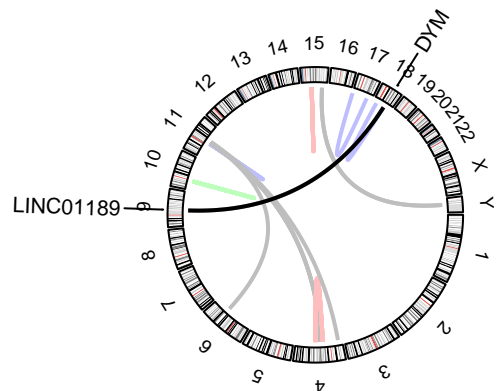
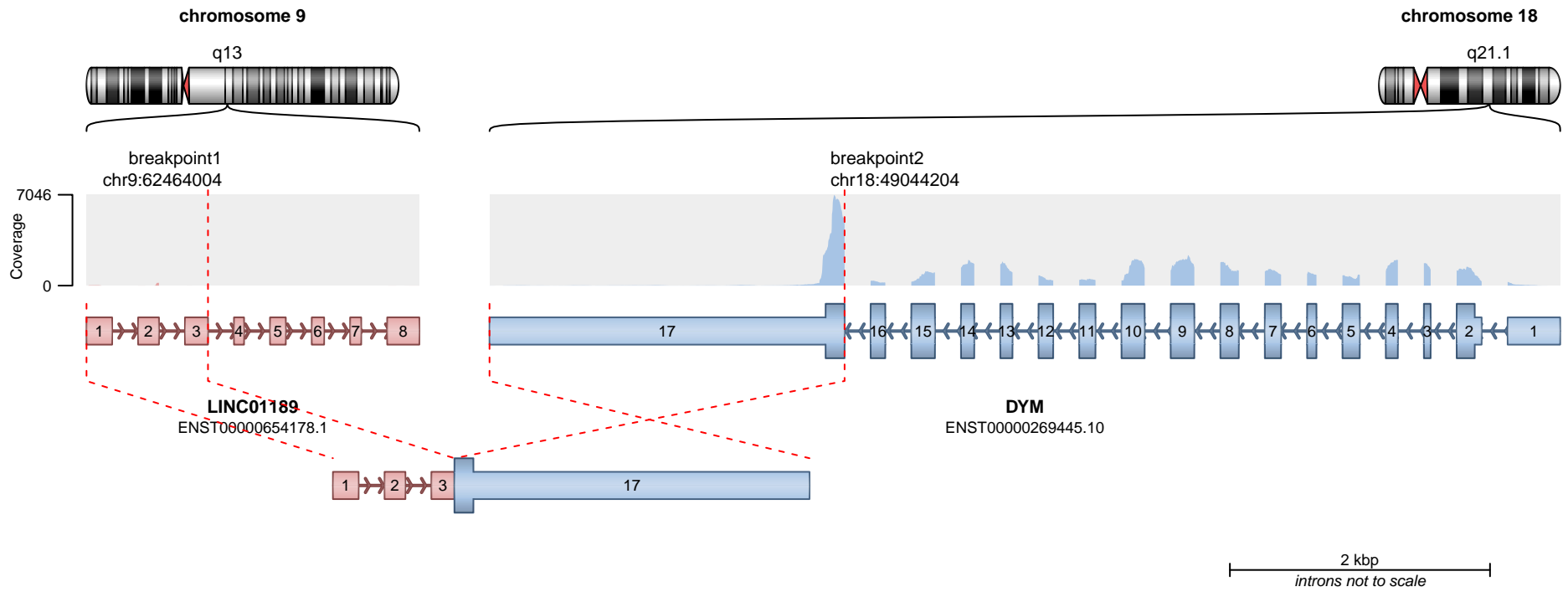
RETAINED PROTEIN DOMAINS
reading frame unclear



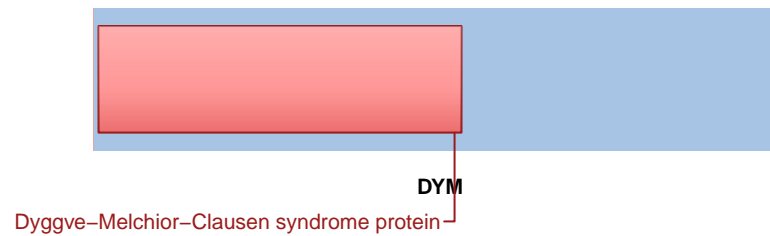
DYM
Dyggve–Melchior–Clausen syndrome protein

SUPPORTING READ COUNT

Split reads = 9
Discordant mates = 0



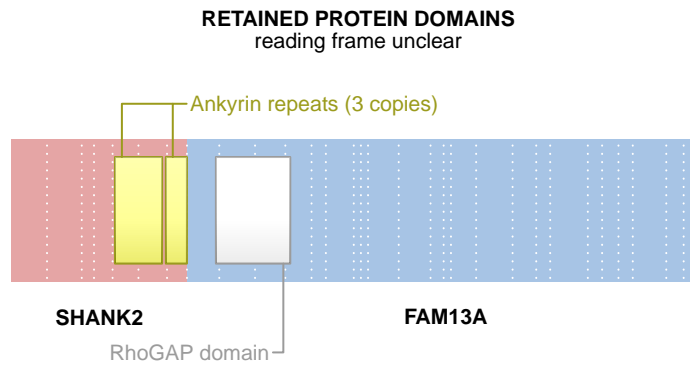
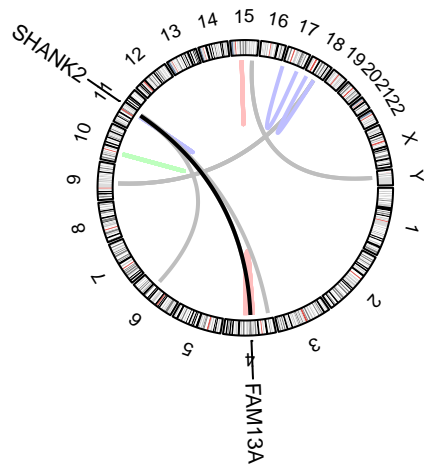
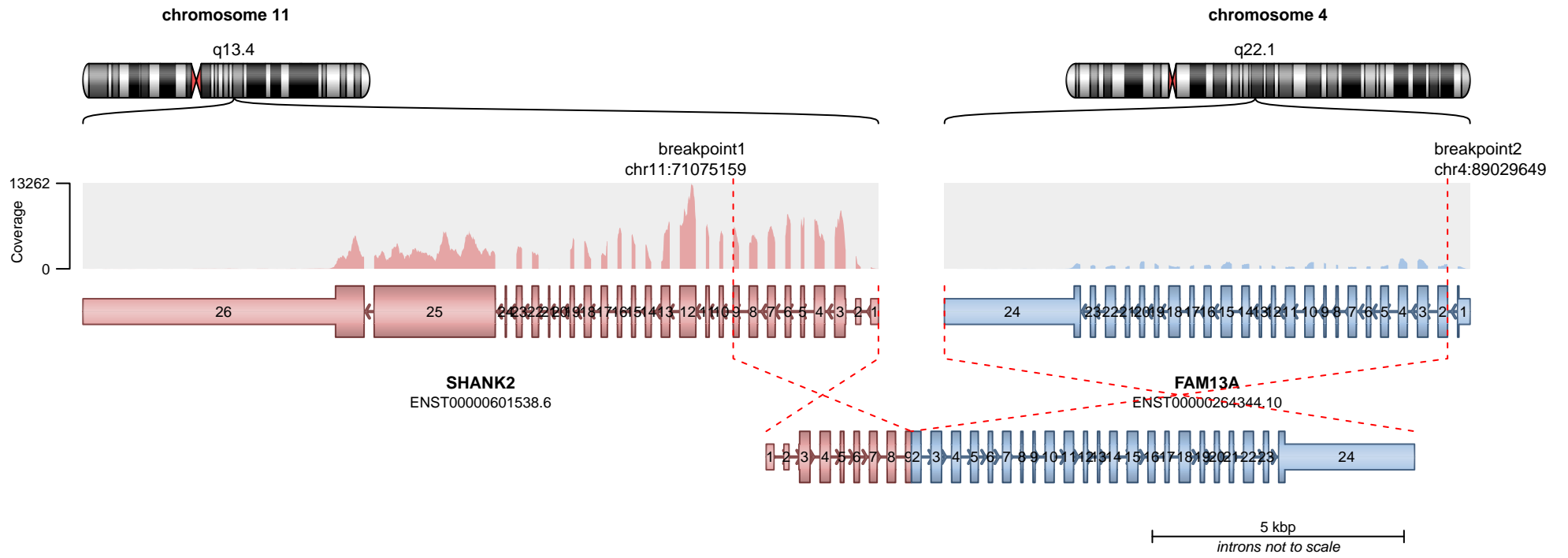
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

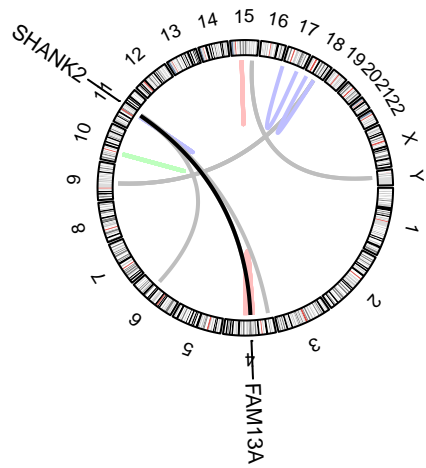
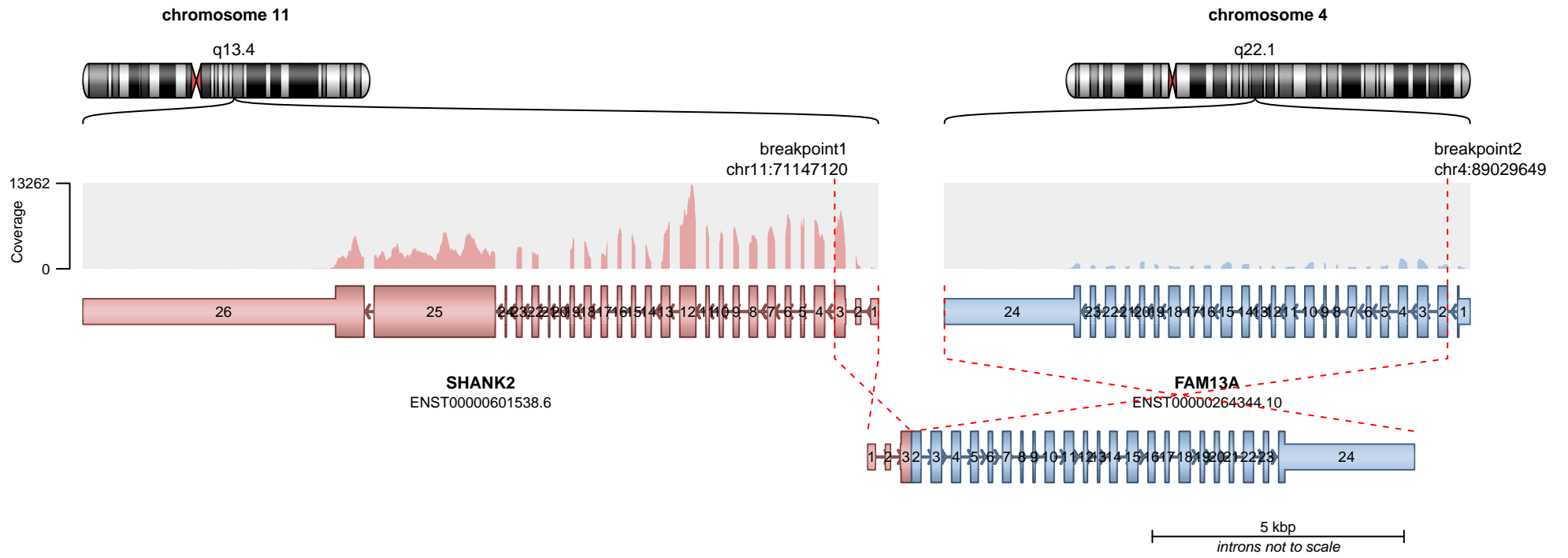
- translocation
- duplication
- deletion
- inversion



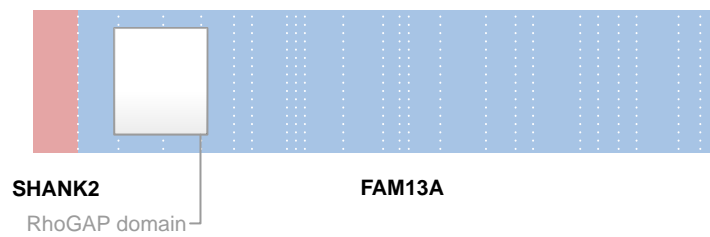
SUPPORTING READ COUNT

Split reads = 181
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



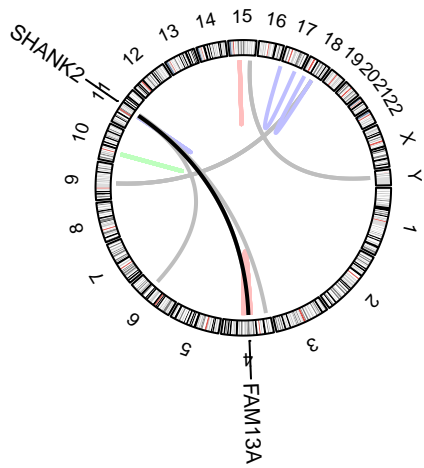
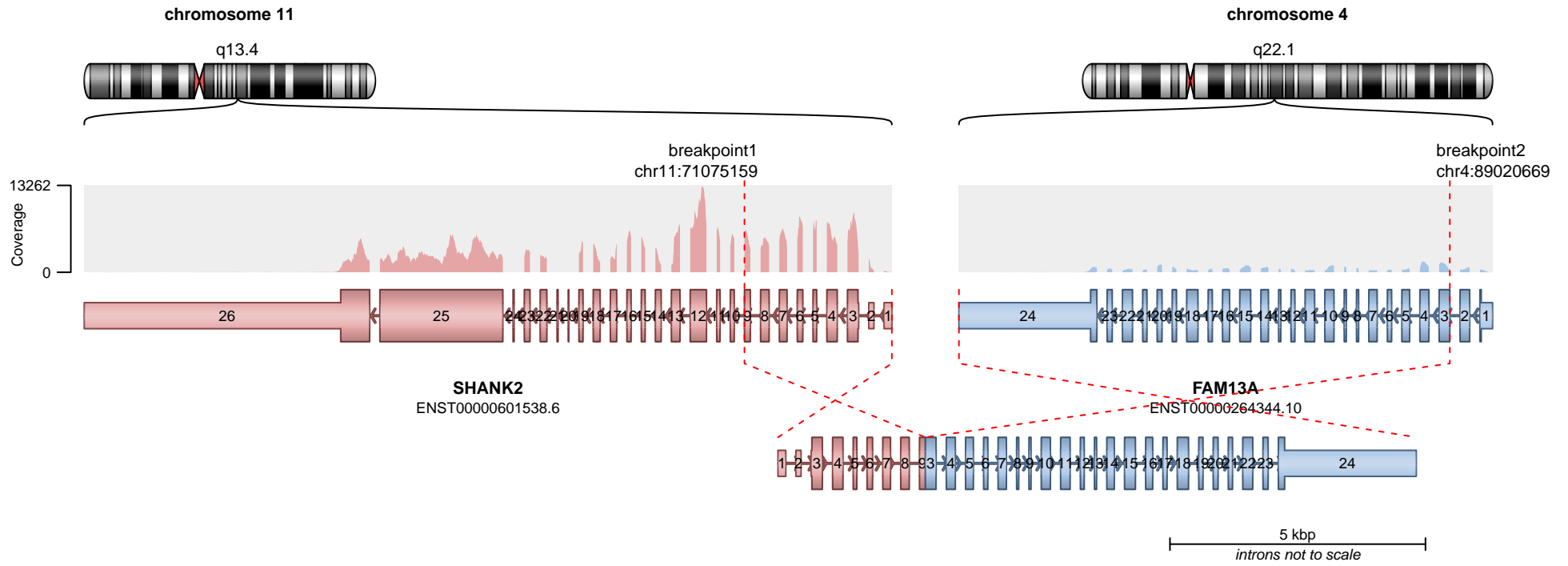
RETAINED PROTEIN DOMAINS
reading frame unclear



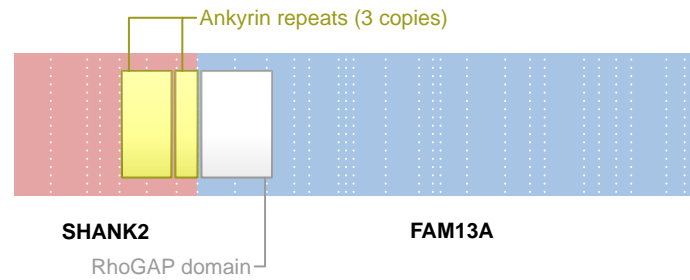
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



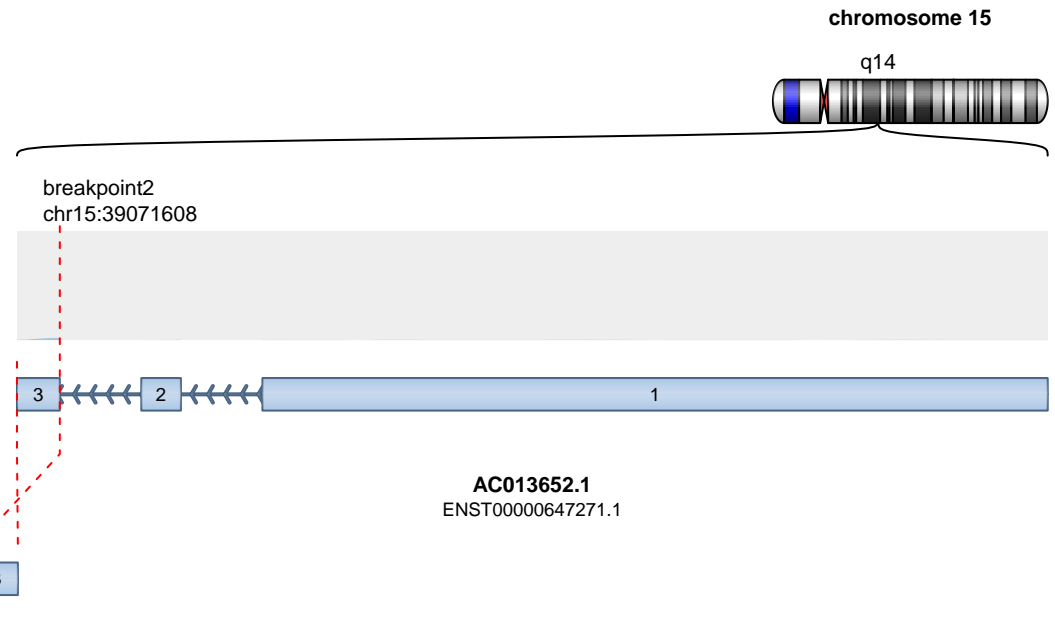
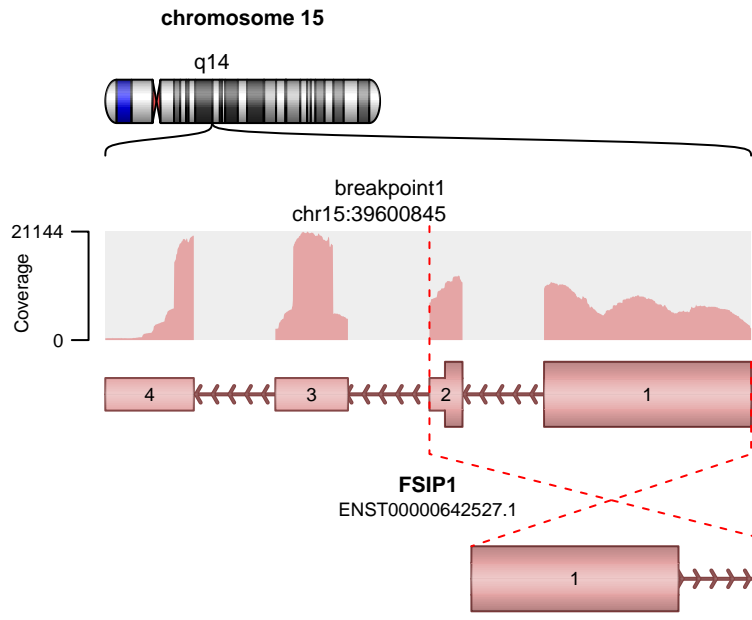
RETAINED PROTEIN DOMAINS
reading frame unclear



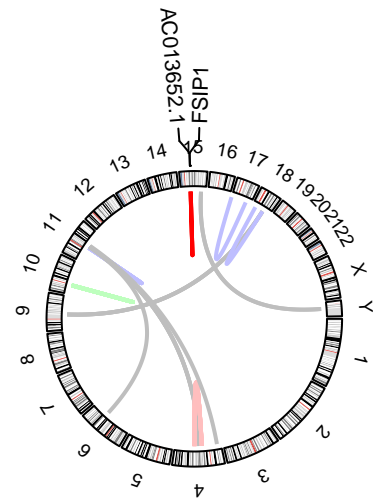
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



800 bp
introns not to scale

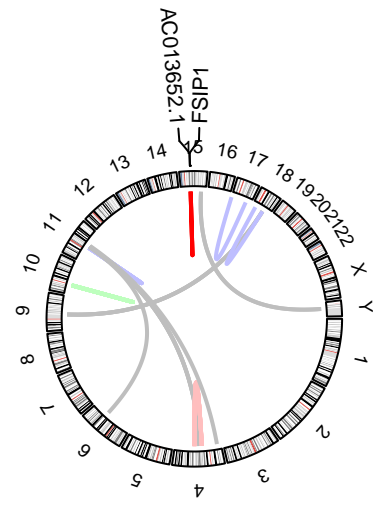
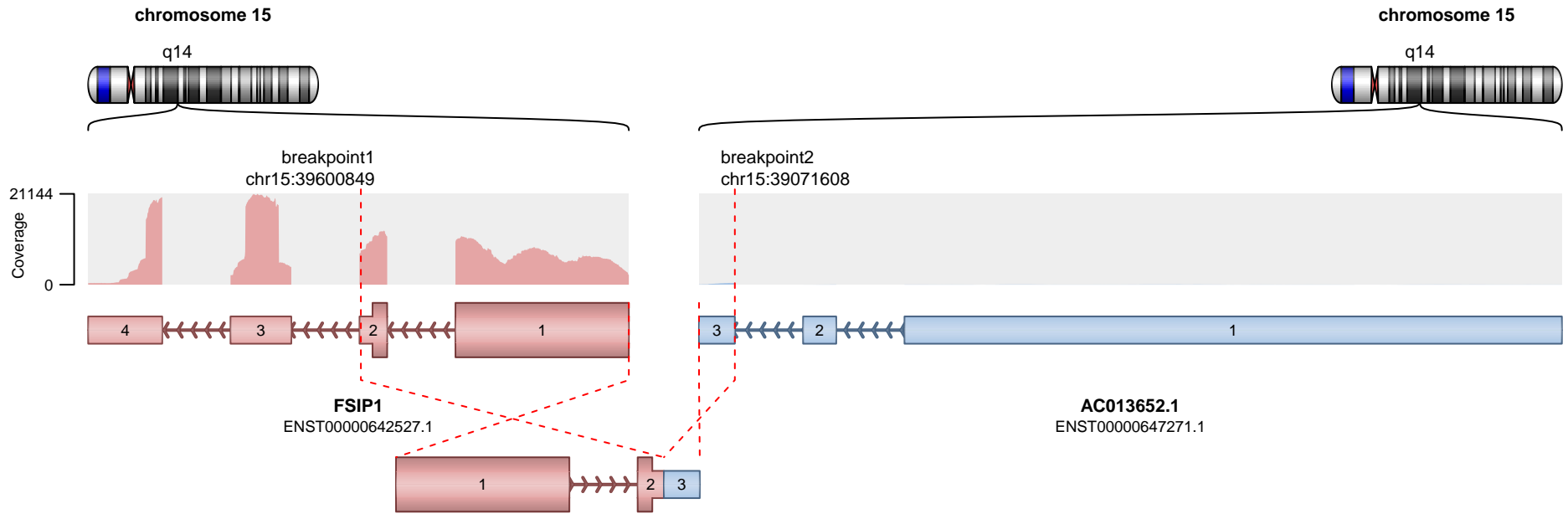


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 170
Discordant mates = 0

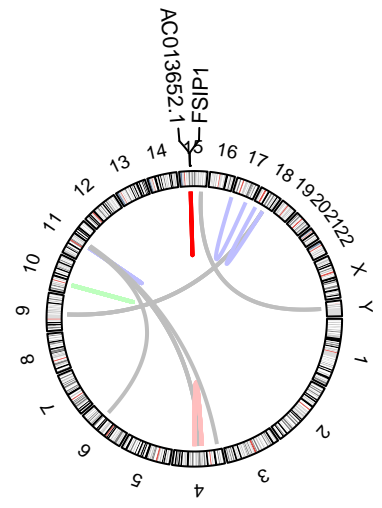
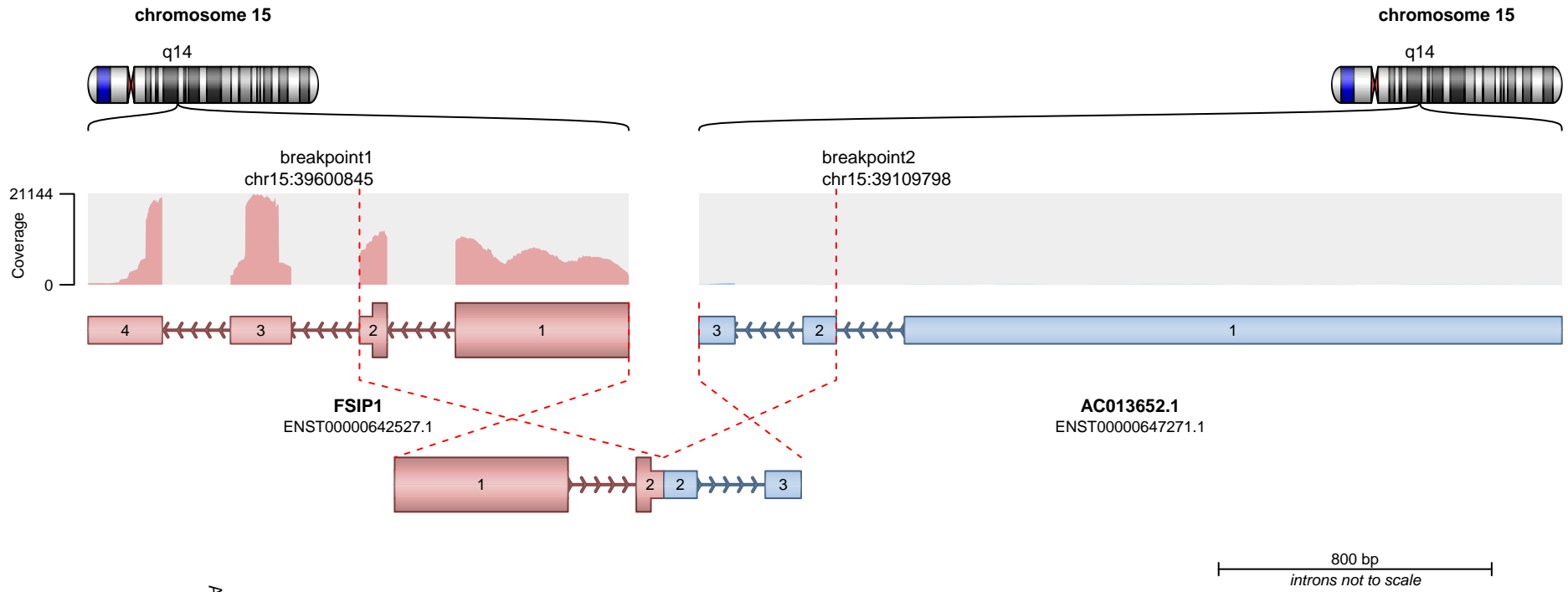


— translocation — deletion
 — duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 39
 Discordant mates = 0

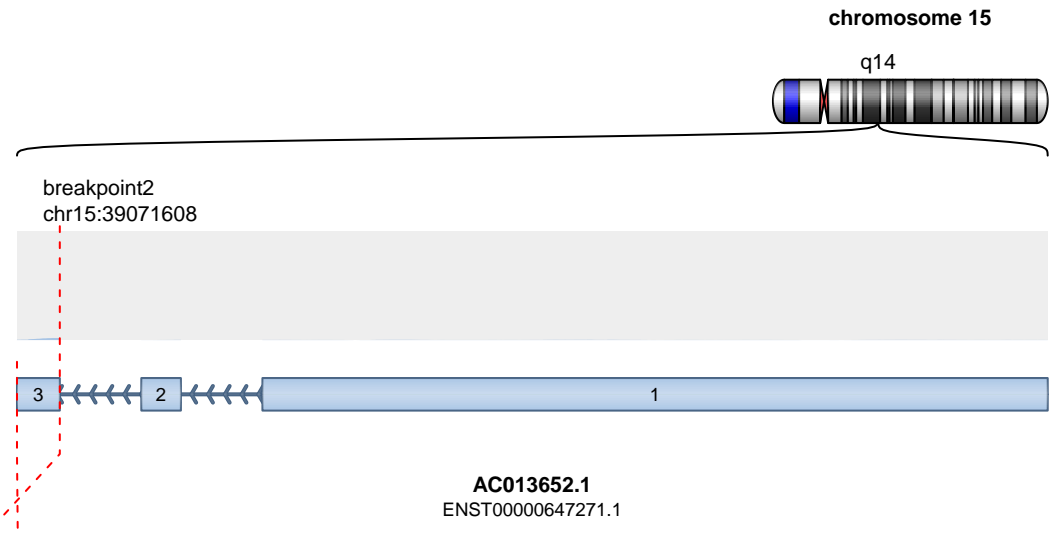
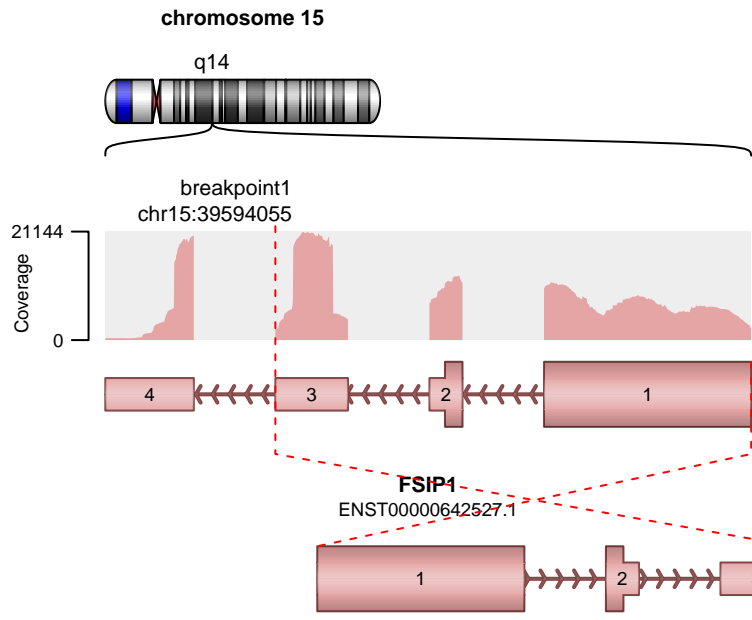


— translocation — deletion
— duplication — inversion

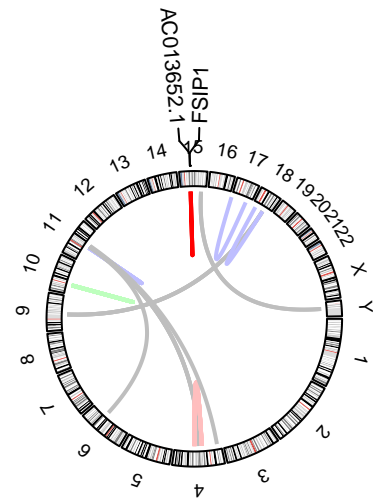
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 31
Discordant mates = 0



800 bp
introns not to scale

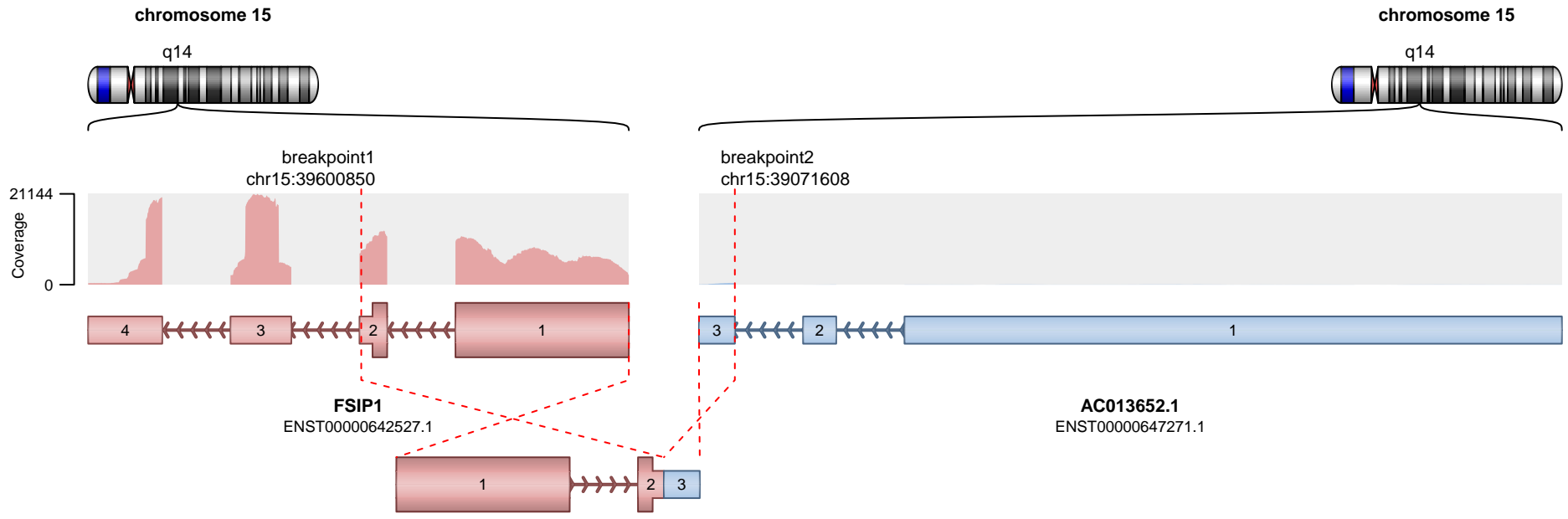


— translocation — deletion
— duplication — inversion

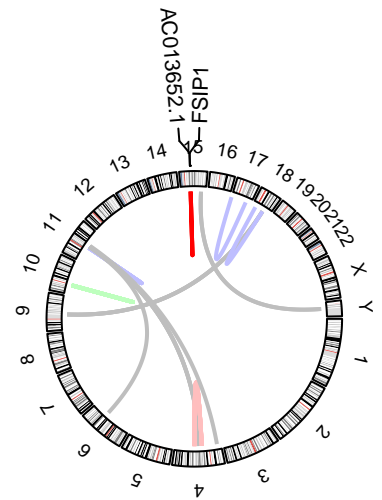
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0



800 bp
introns not to scale

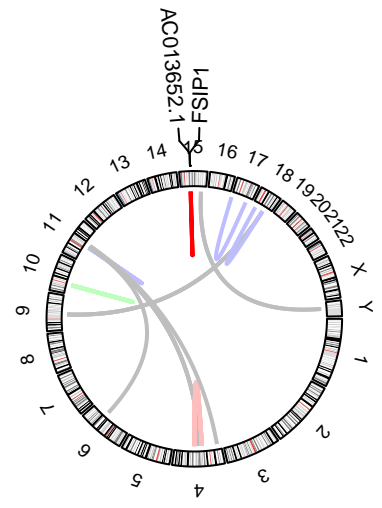
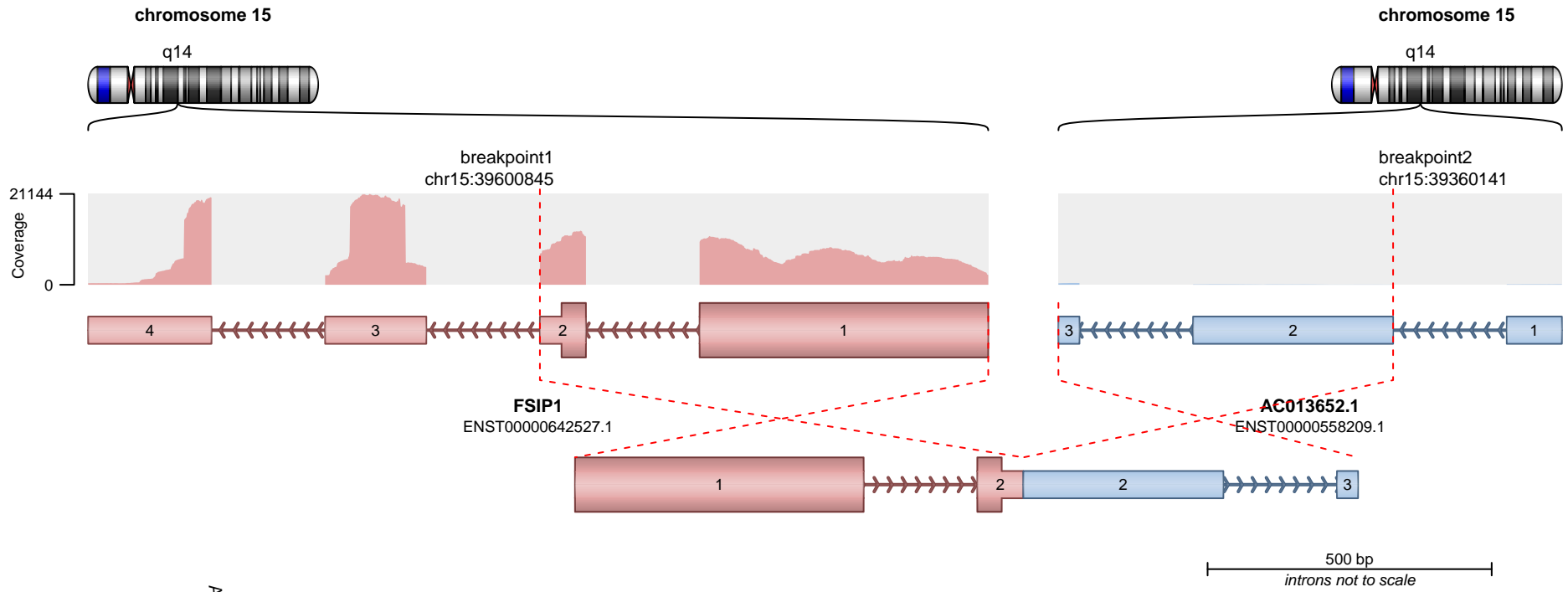


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

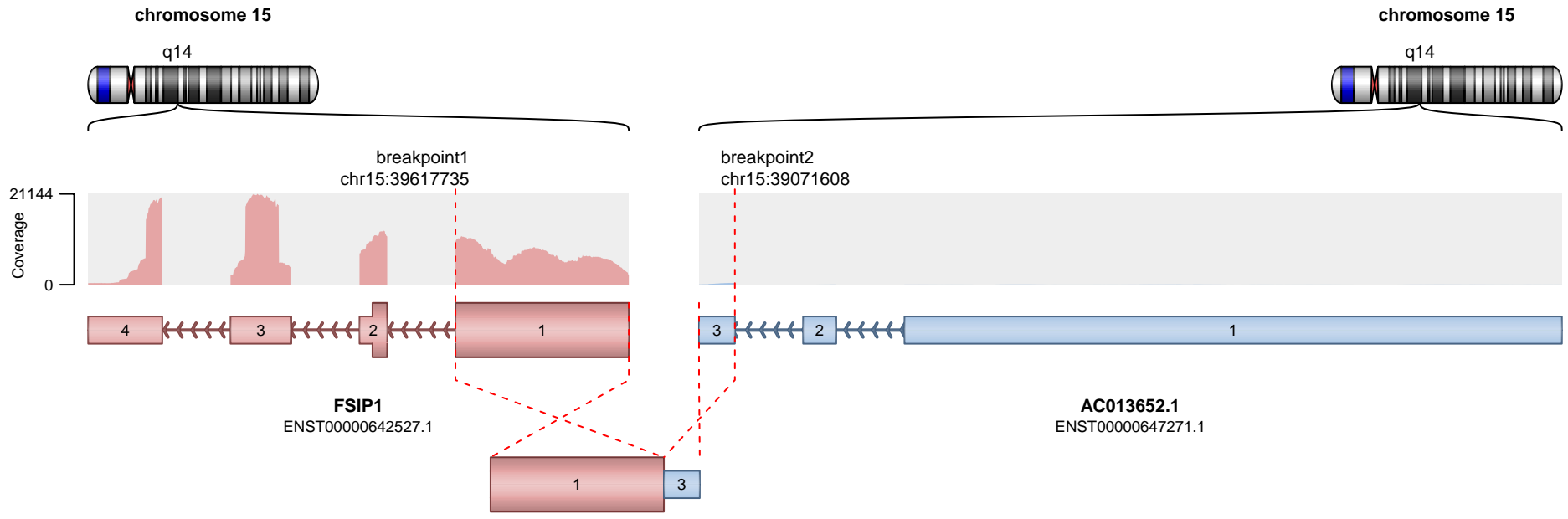


— translocation — deletion
— duplication — inversion

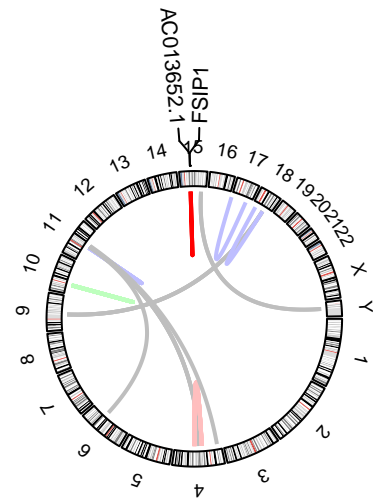
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



800 bp
introns not to scale

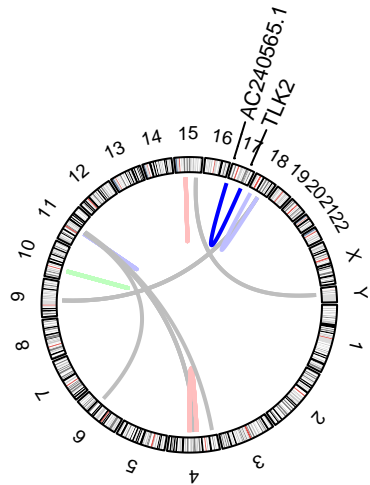
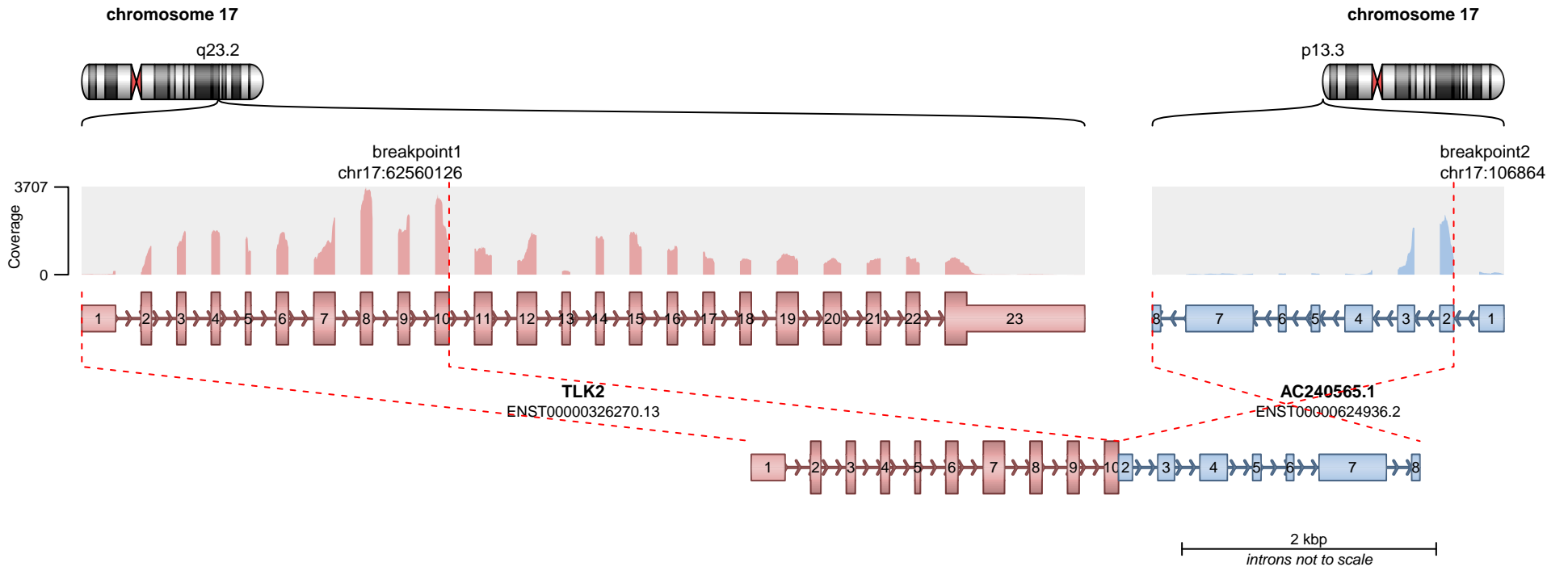


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

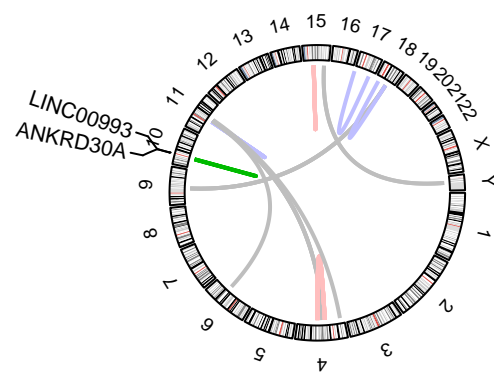
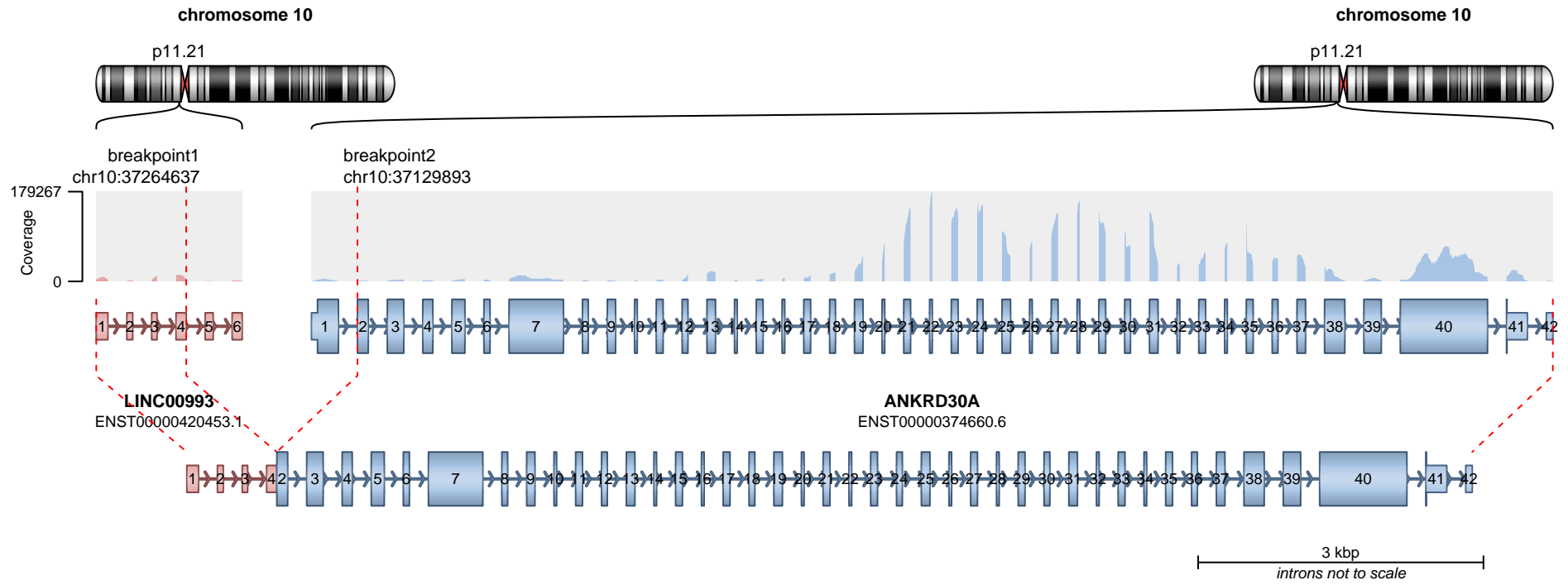


No protein domains retained in fusion.

SUPPORTING READ COUNT

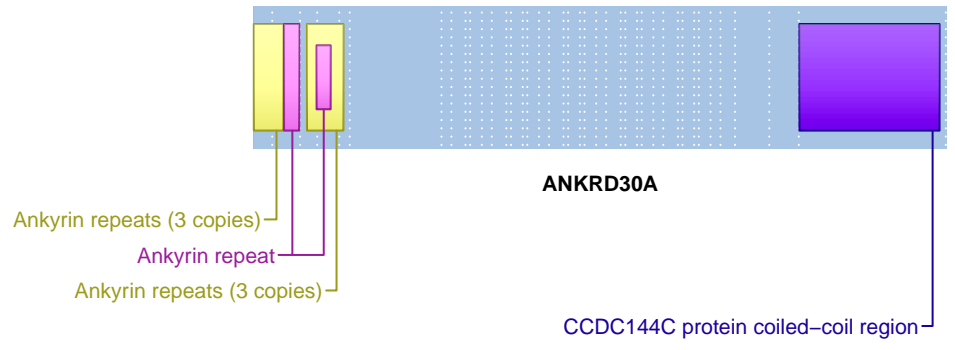
Split reads = 51
Discordant mates = 0

— translocation — deletion
— duplication — inversion



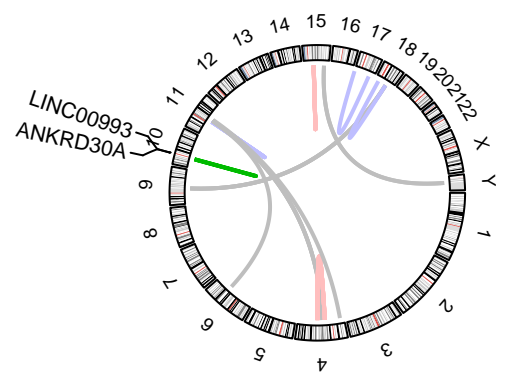
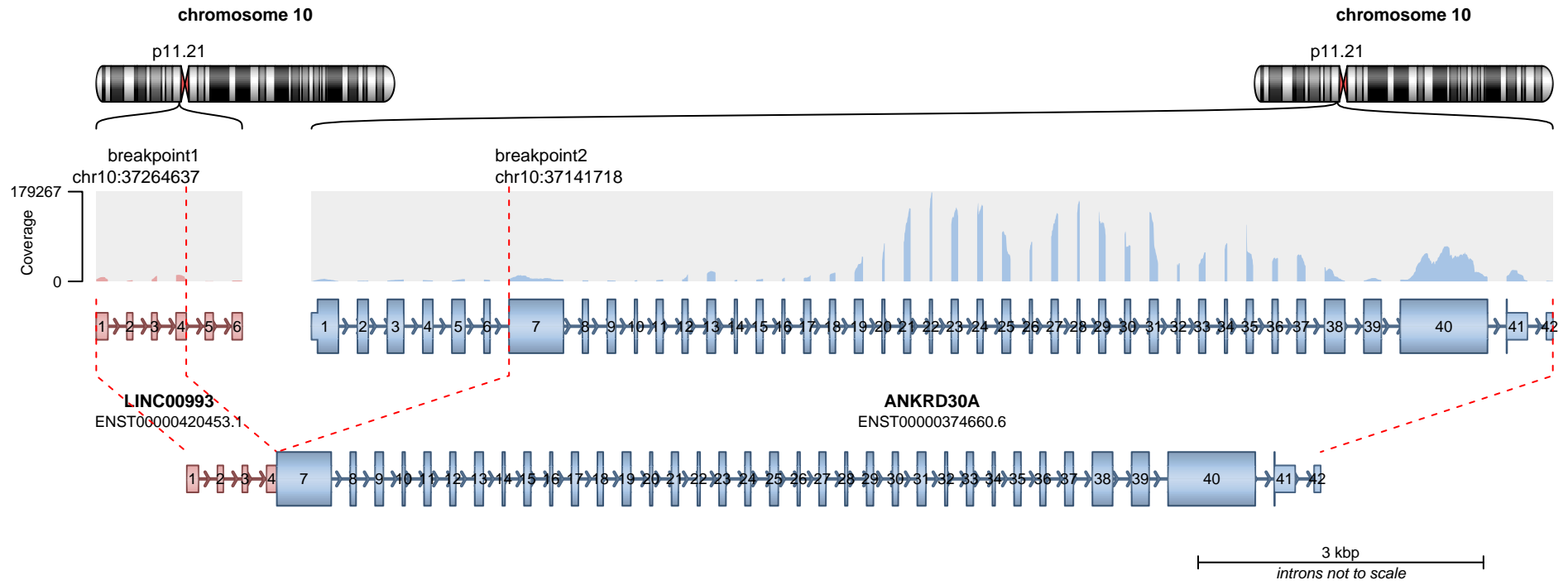
— translocation — deletion
 — duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear

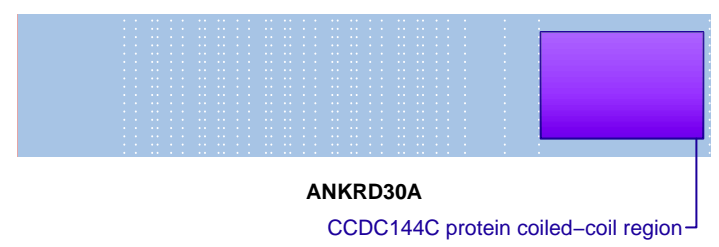


SUPPORTING READ COUNT

Split reads = 48
Discordant mates = 2



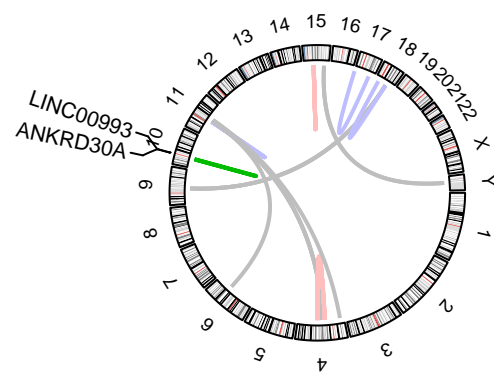
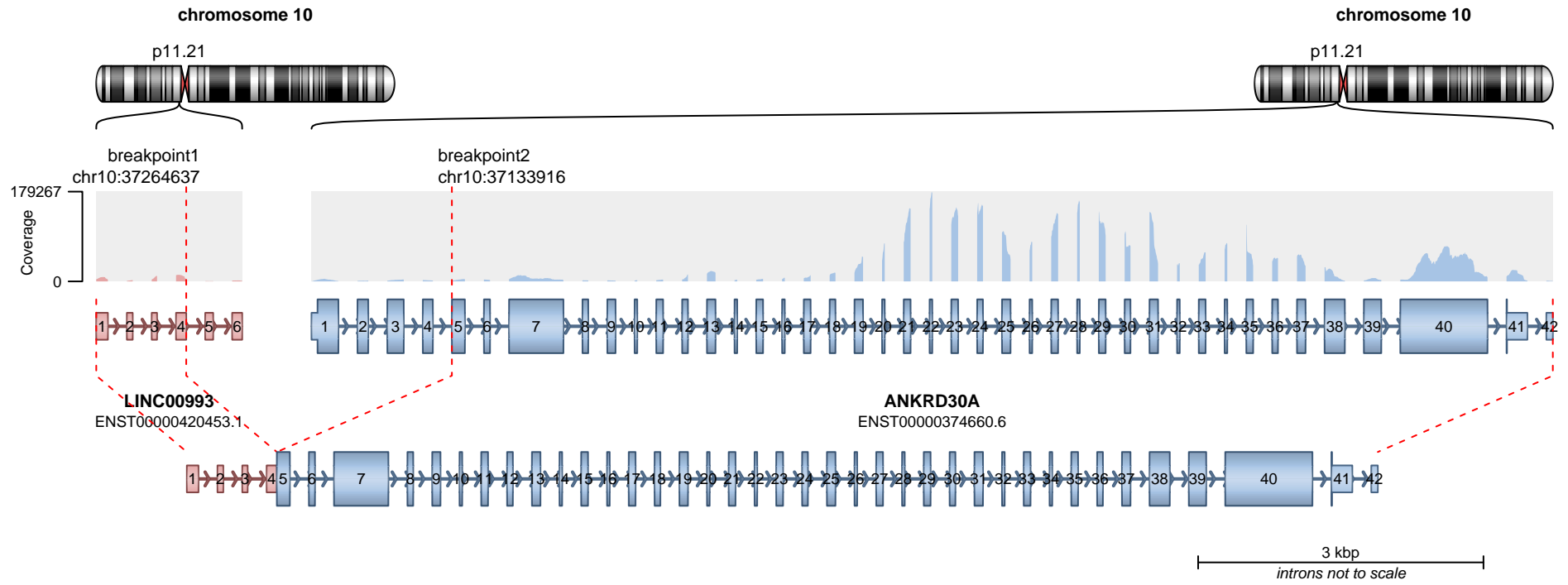
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

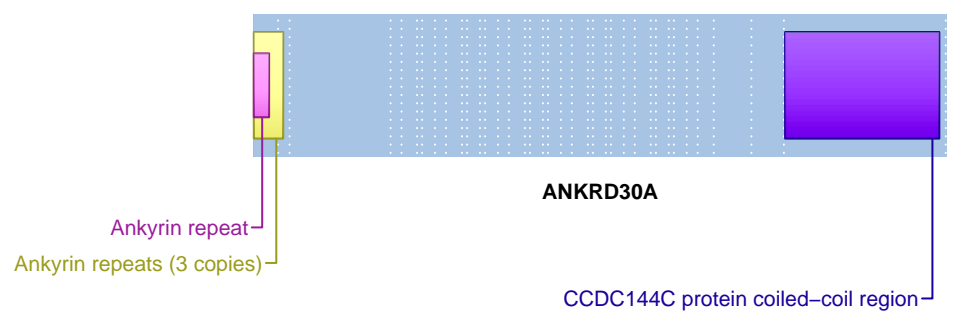
Split reads = 31
Discordant mates = 0

— translocation — deletion
— duplication — inversion



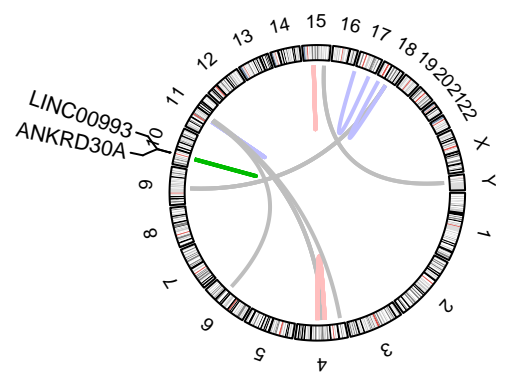
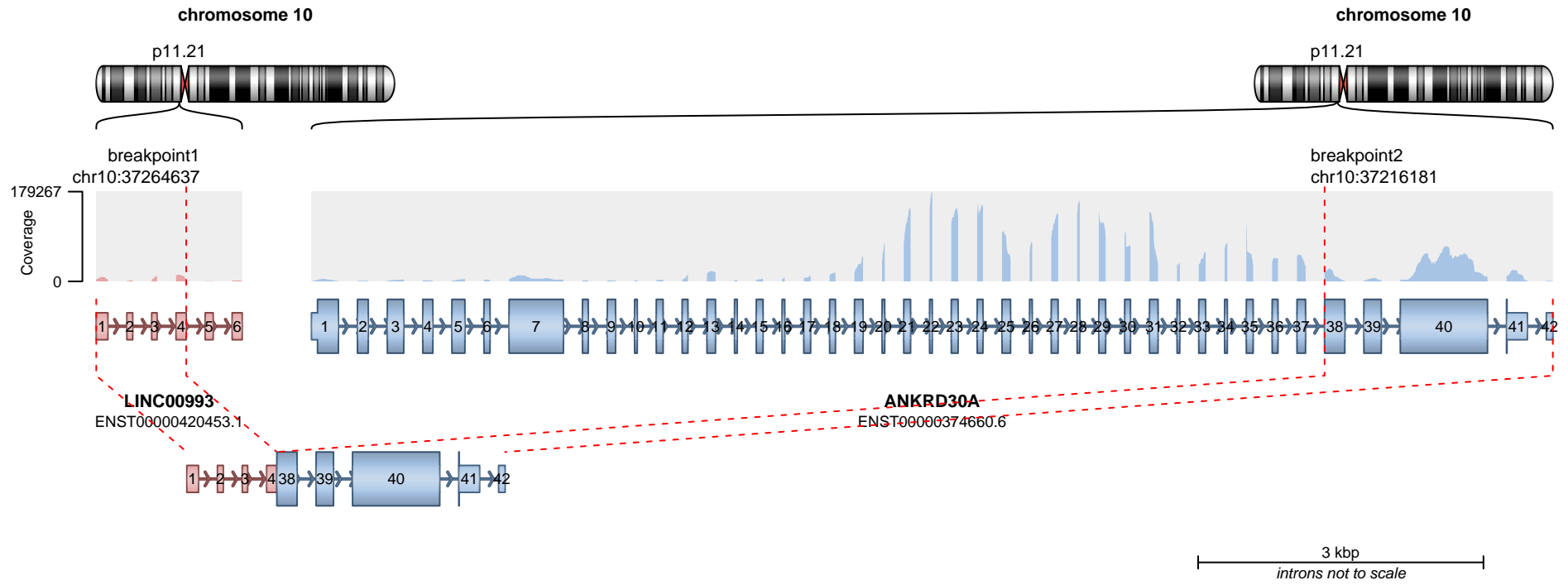
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear

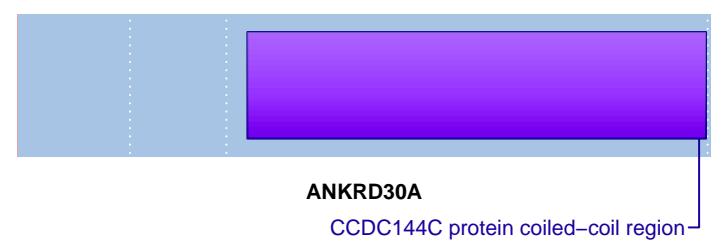


SUPPORTING READ COUNT

Split reads = 29
Discordant mates = 1



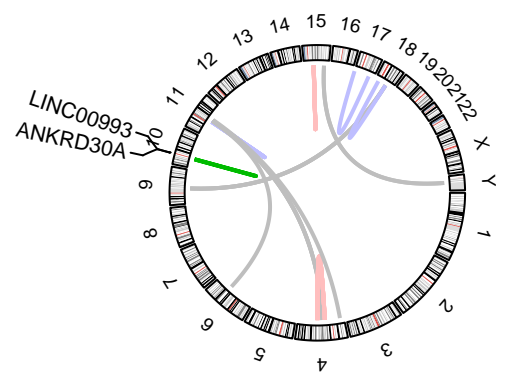
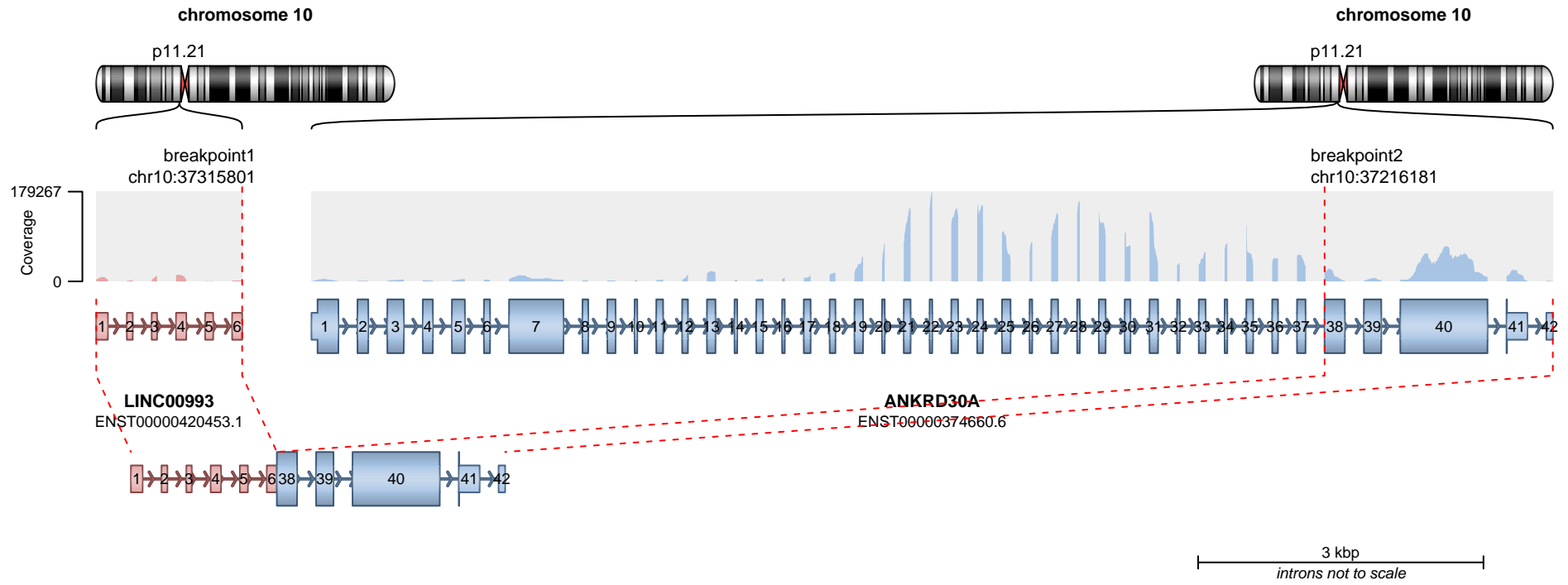
RETAINED PROTEIN DOMAINS
reading frame unclear



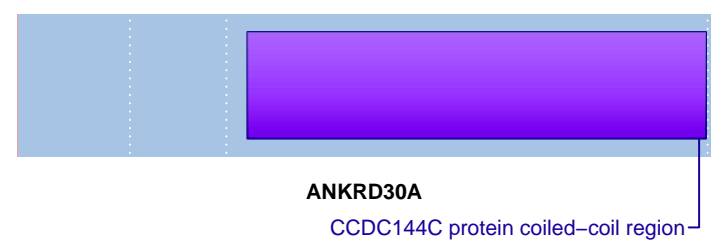
SUPPORTING READ COUNT

Split reads = 18
Discordant mates = 0

— translocation — deletion
— duplication — inversion



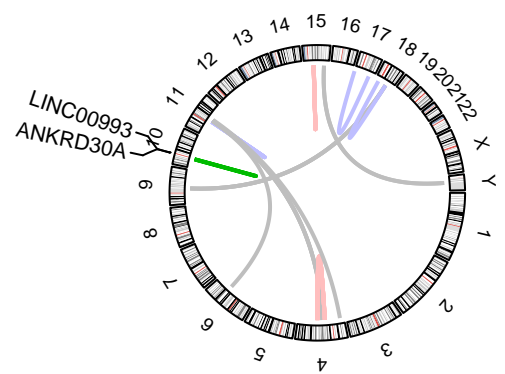
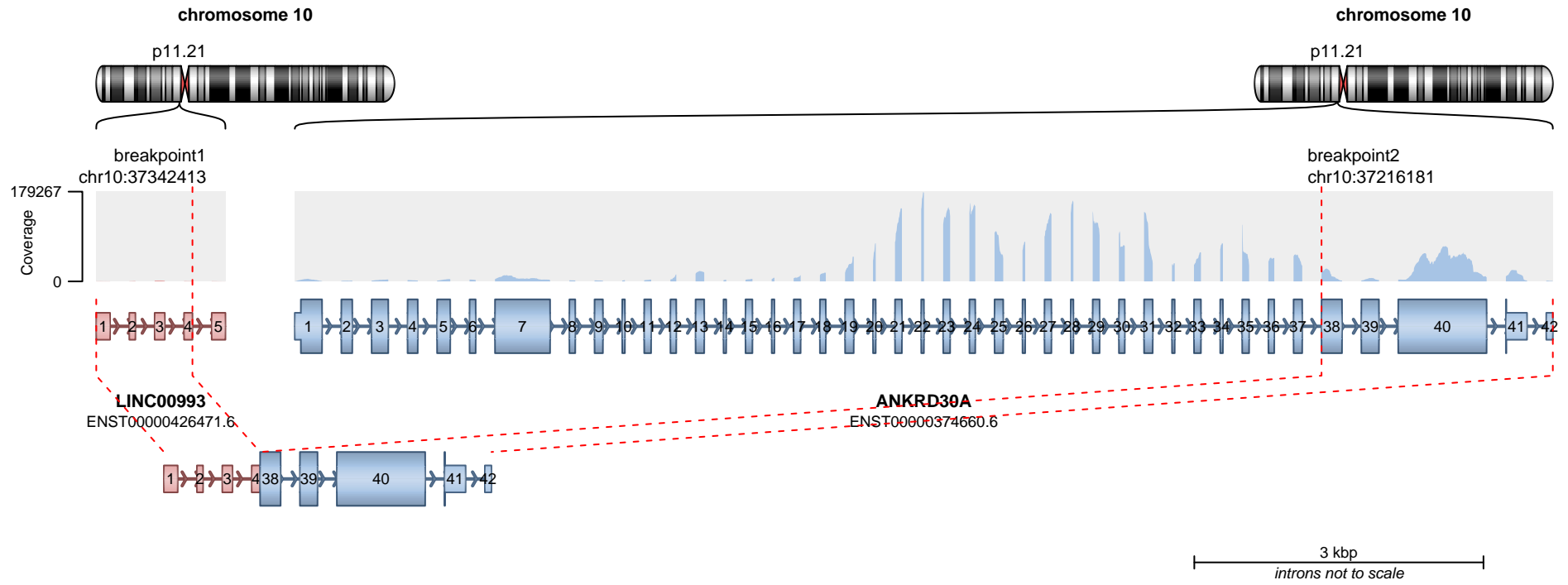
RETAINED PROTEIN DOMAINS
reading frame unclear



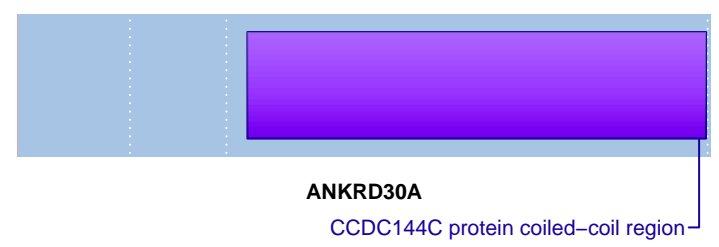
SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 0

— translocation — deletion
— duplication — inversion



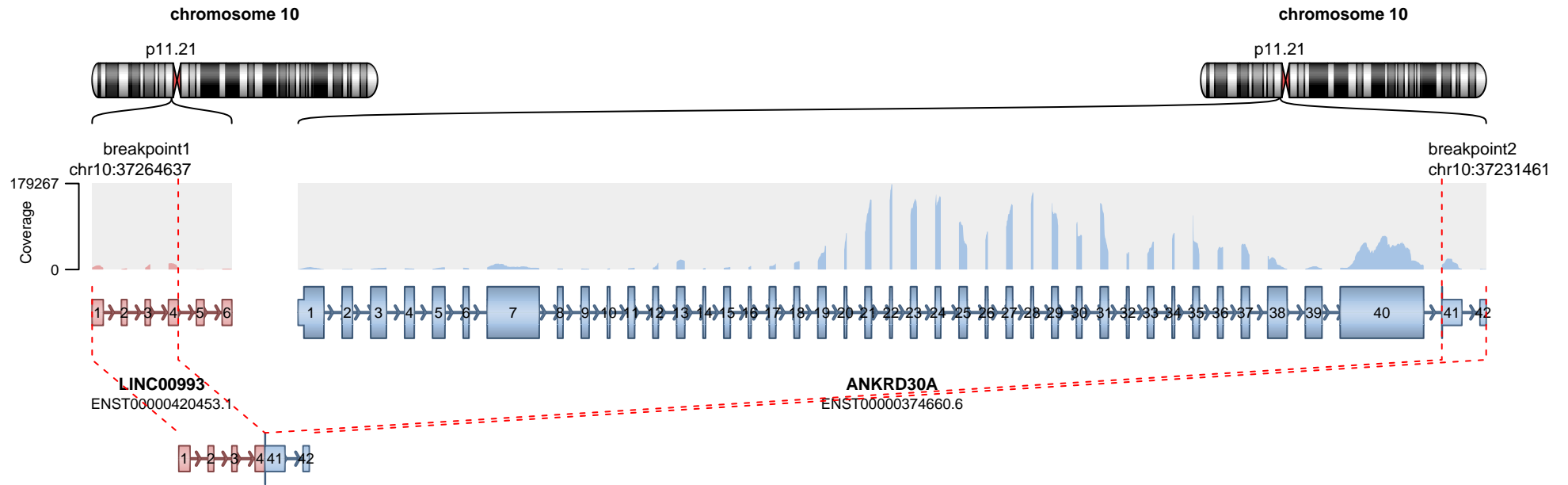
RETAINED PROTEIN DOMAINS
reading frame unclear



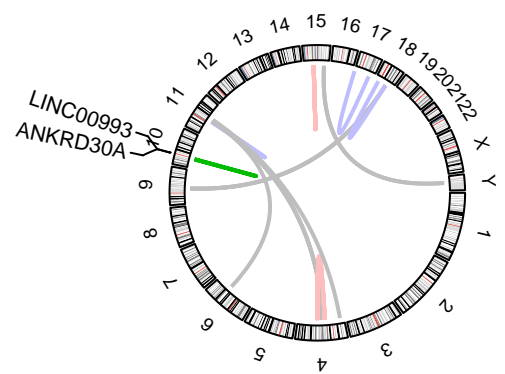
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

— translocation — deletion
— duplication — inversion



3 kbp
introns not to scale

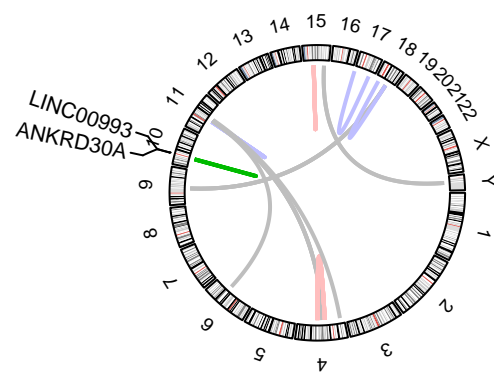
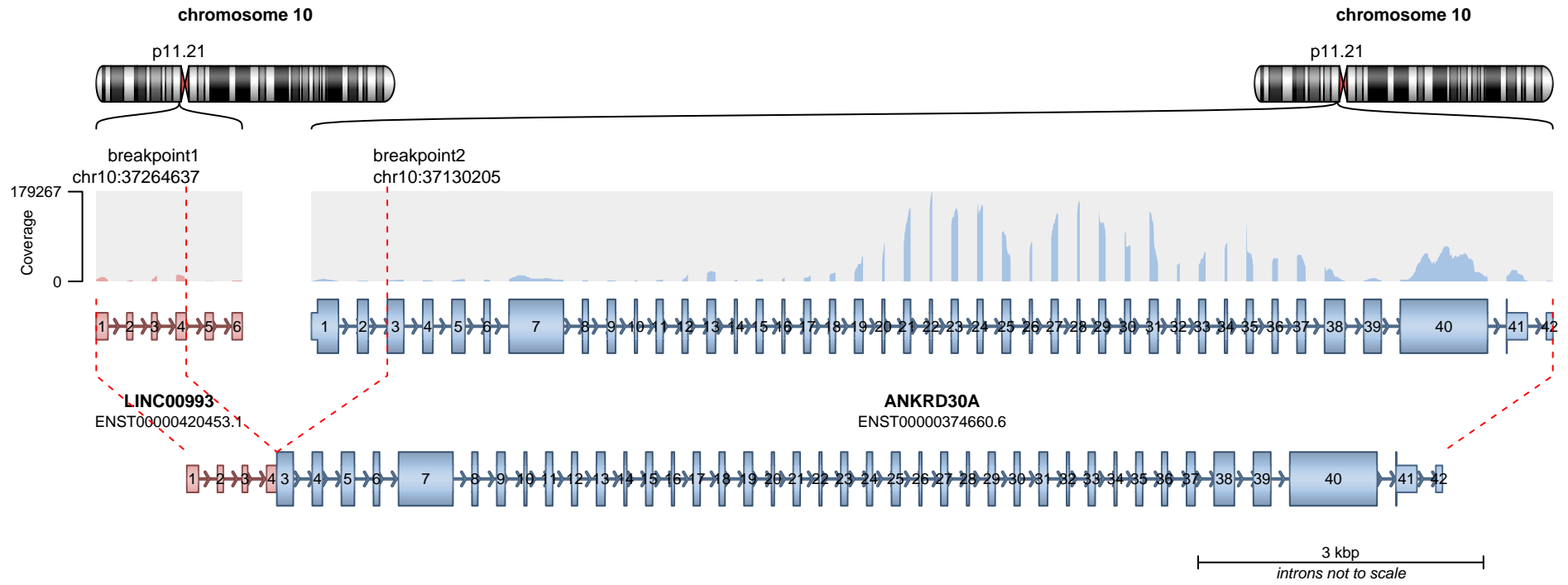


No protein domains retained in fusion.

SUPPORTING READ COUNT

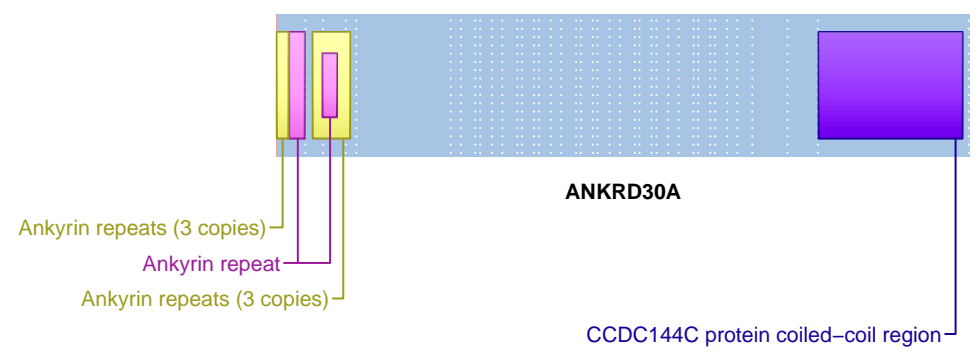
Split reads = 3
Discordant mates = 0

— translocation — deletion
— duplication — inversion



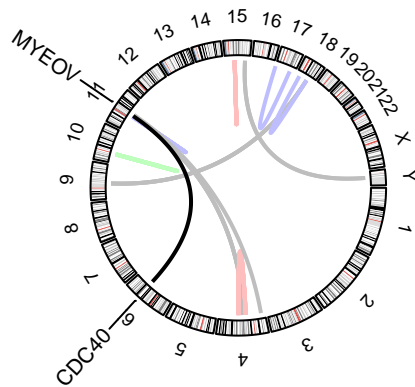
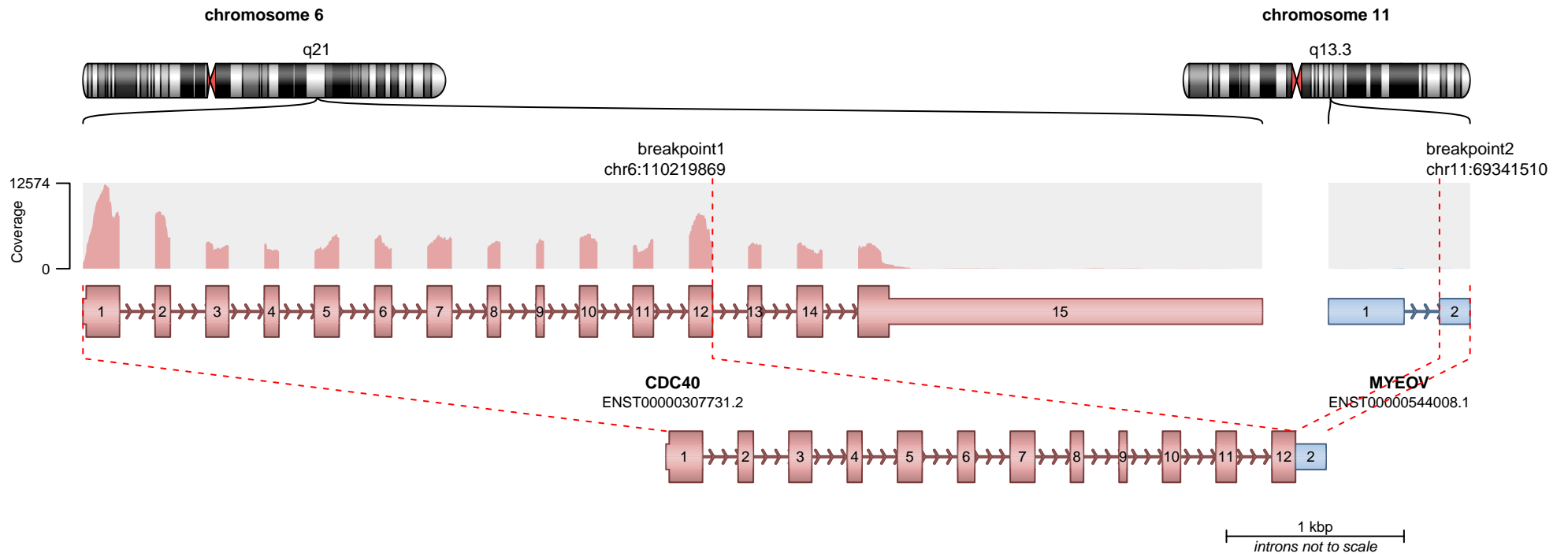
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear

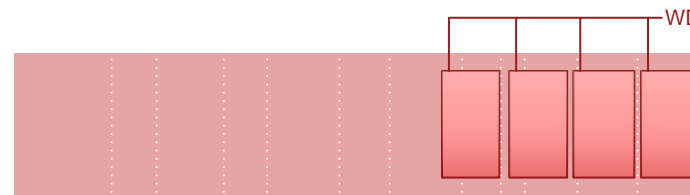


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 1



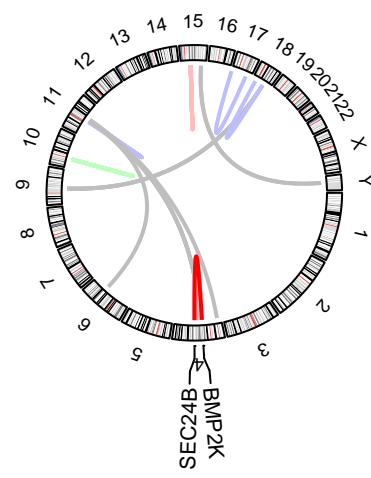
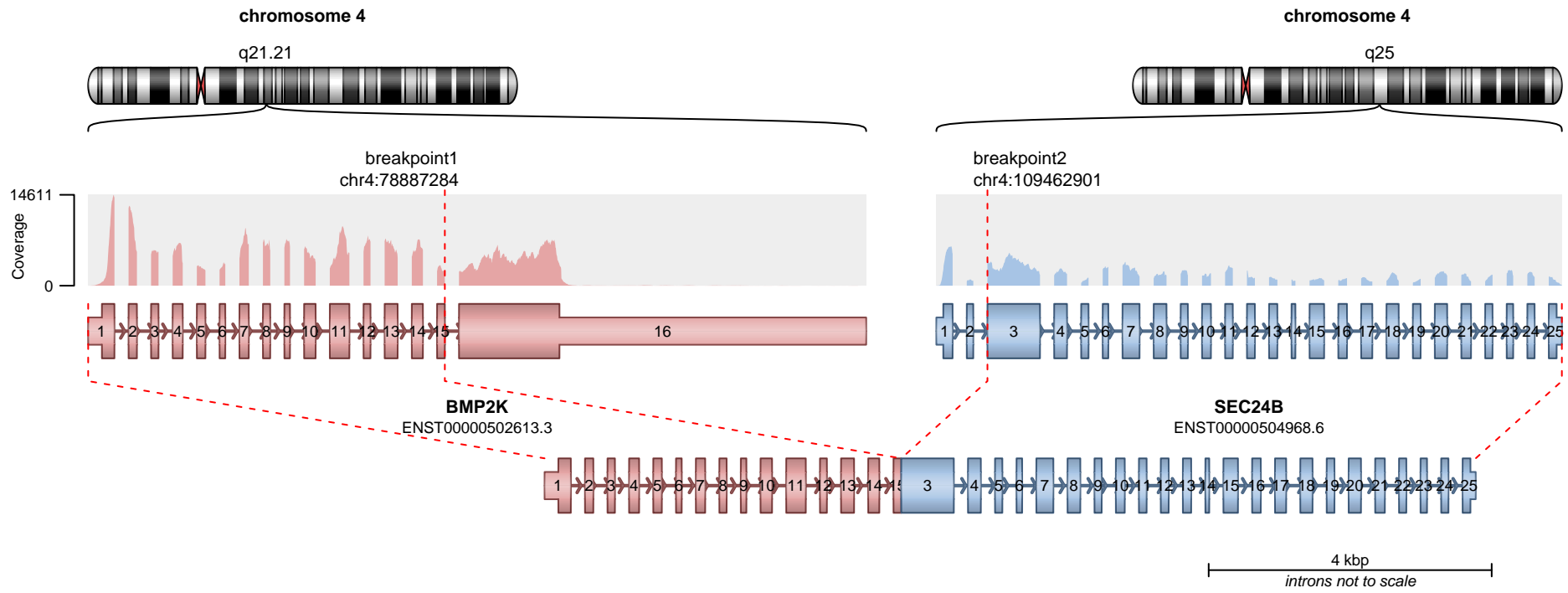
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

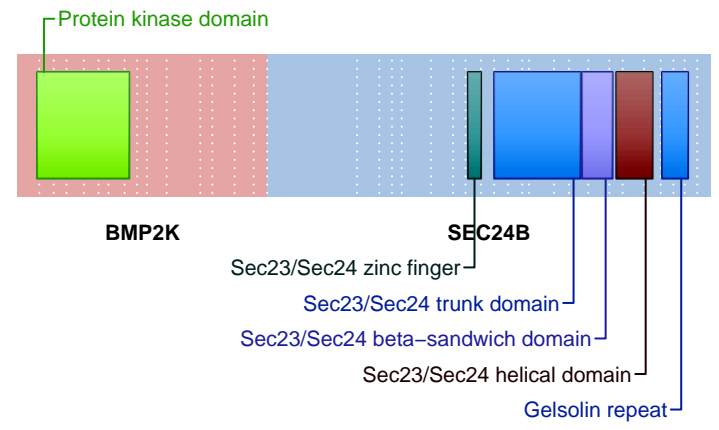
Split reads = 29
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



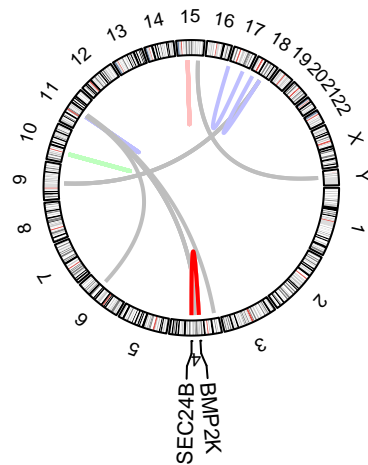
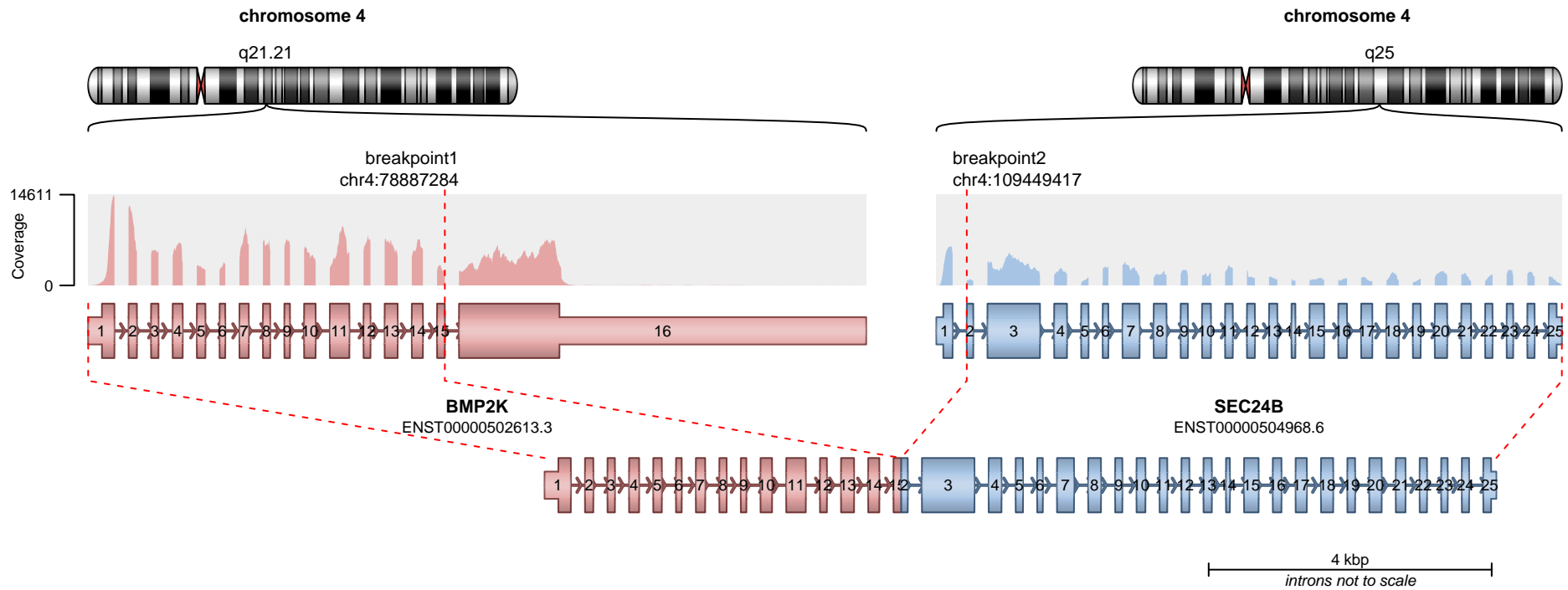
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



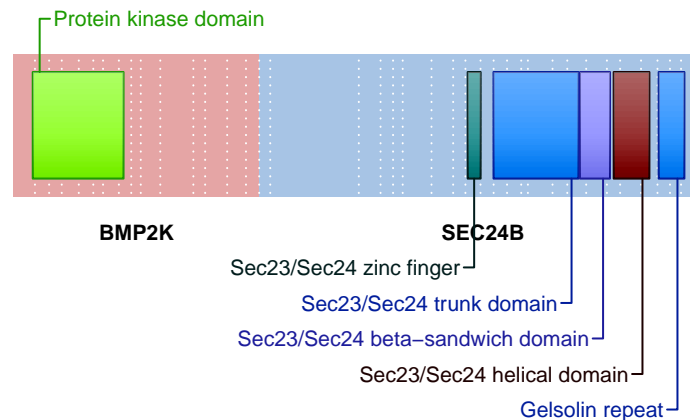
SUPPORTING READ COUNT

Split reads = 23
Discordant mates = 0



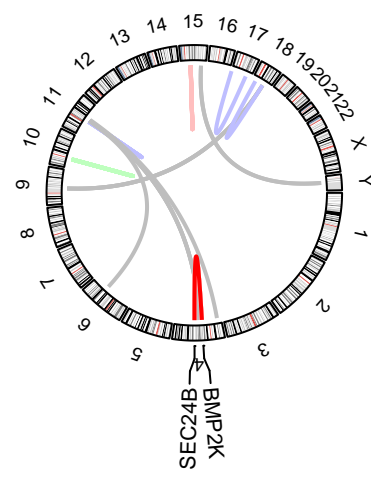
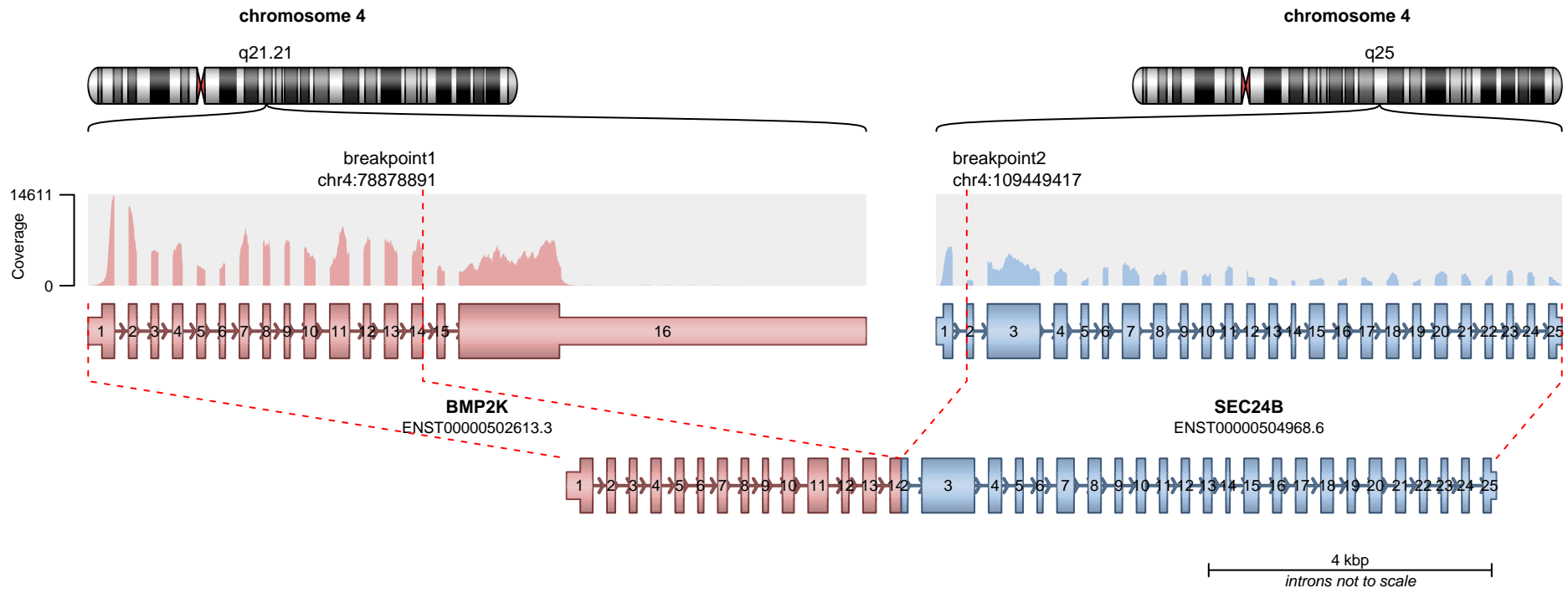
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



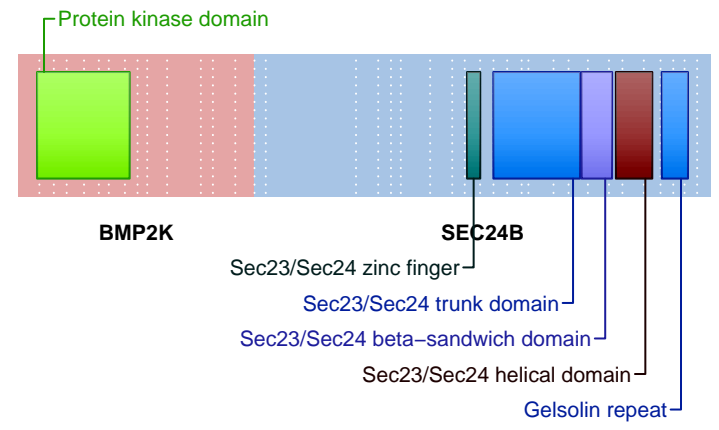
SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 0



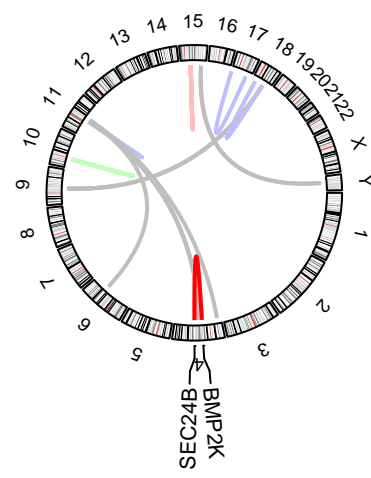
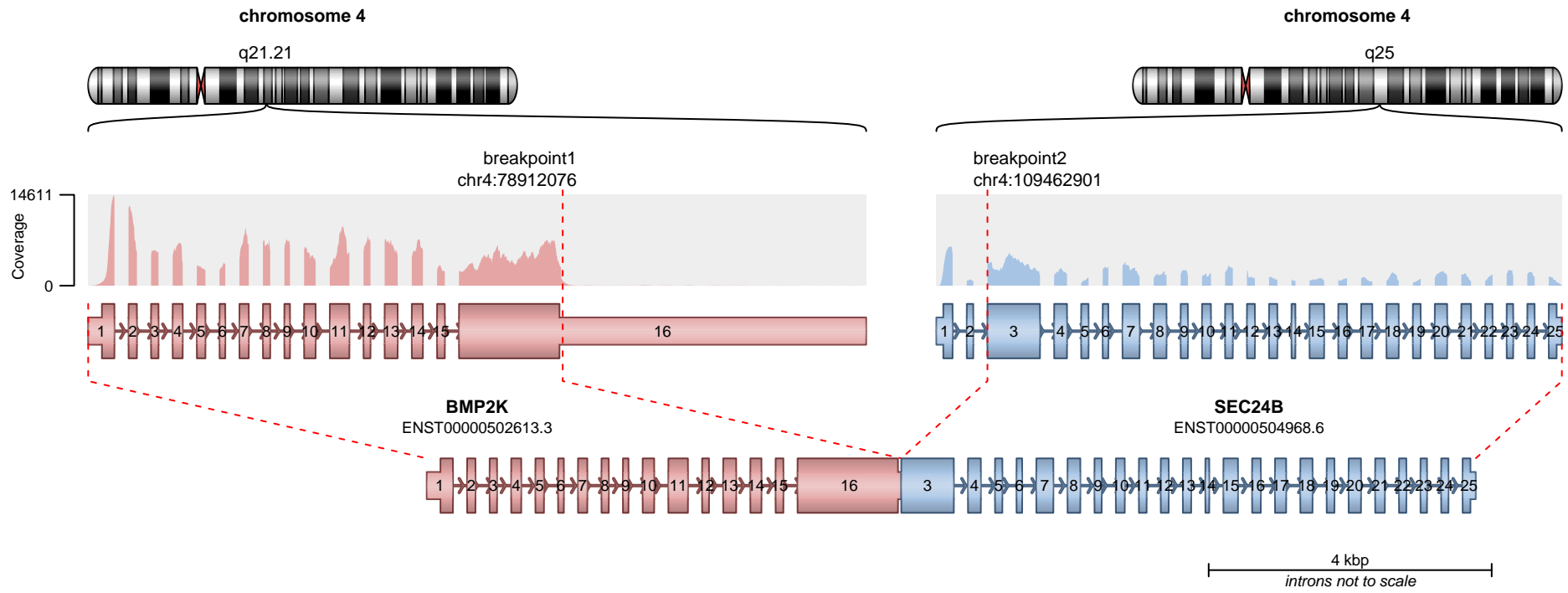
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



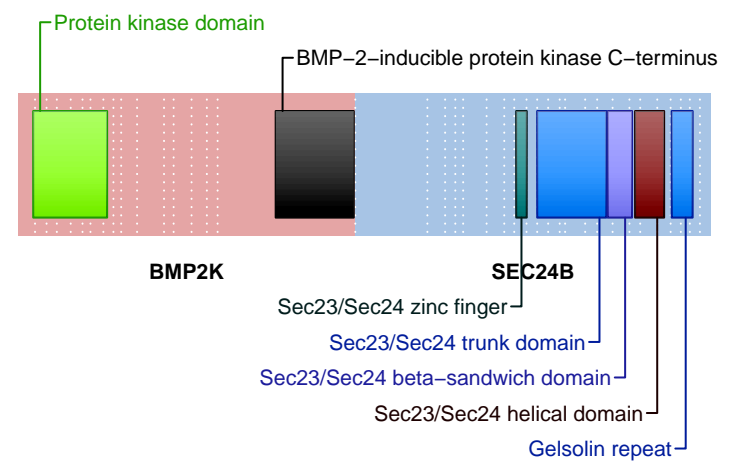
SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 0



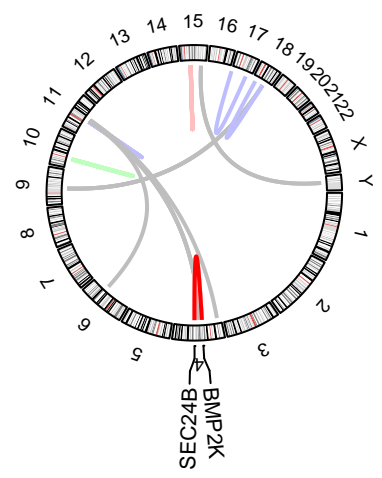
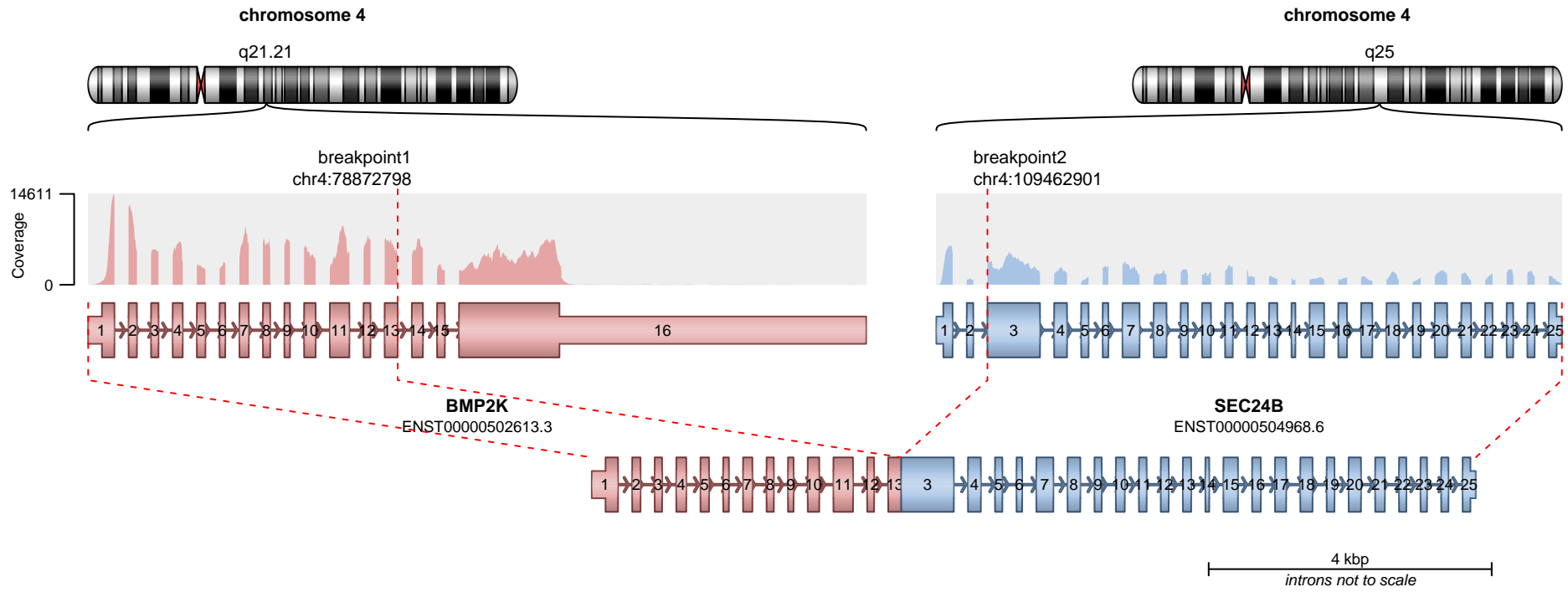
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



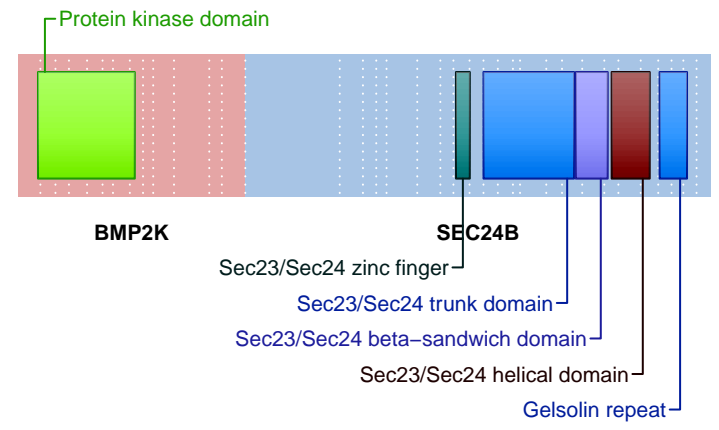
SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0



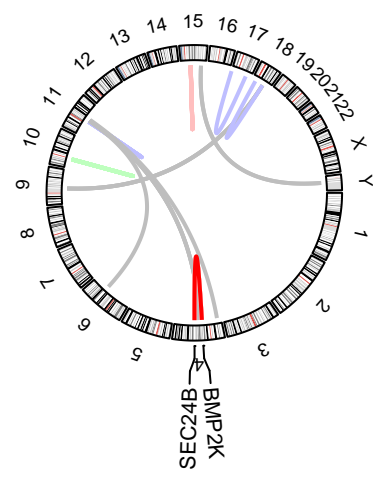
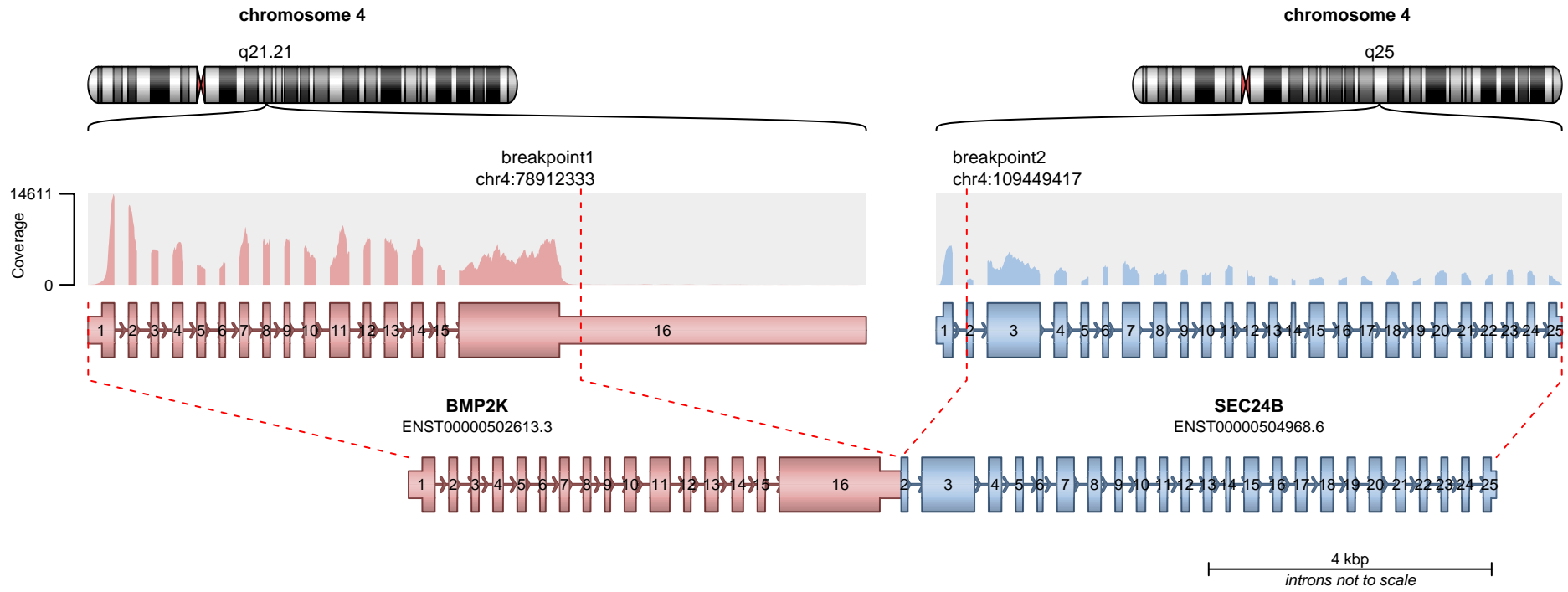
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



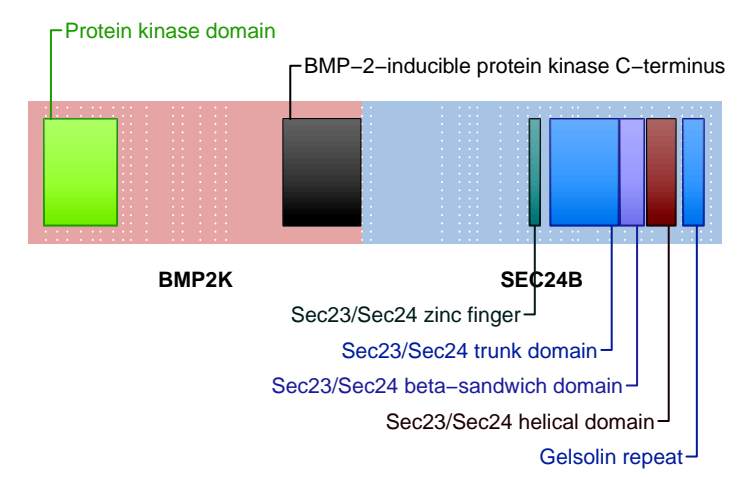
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0



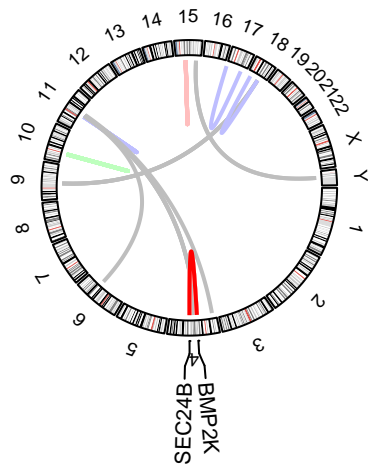
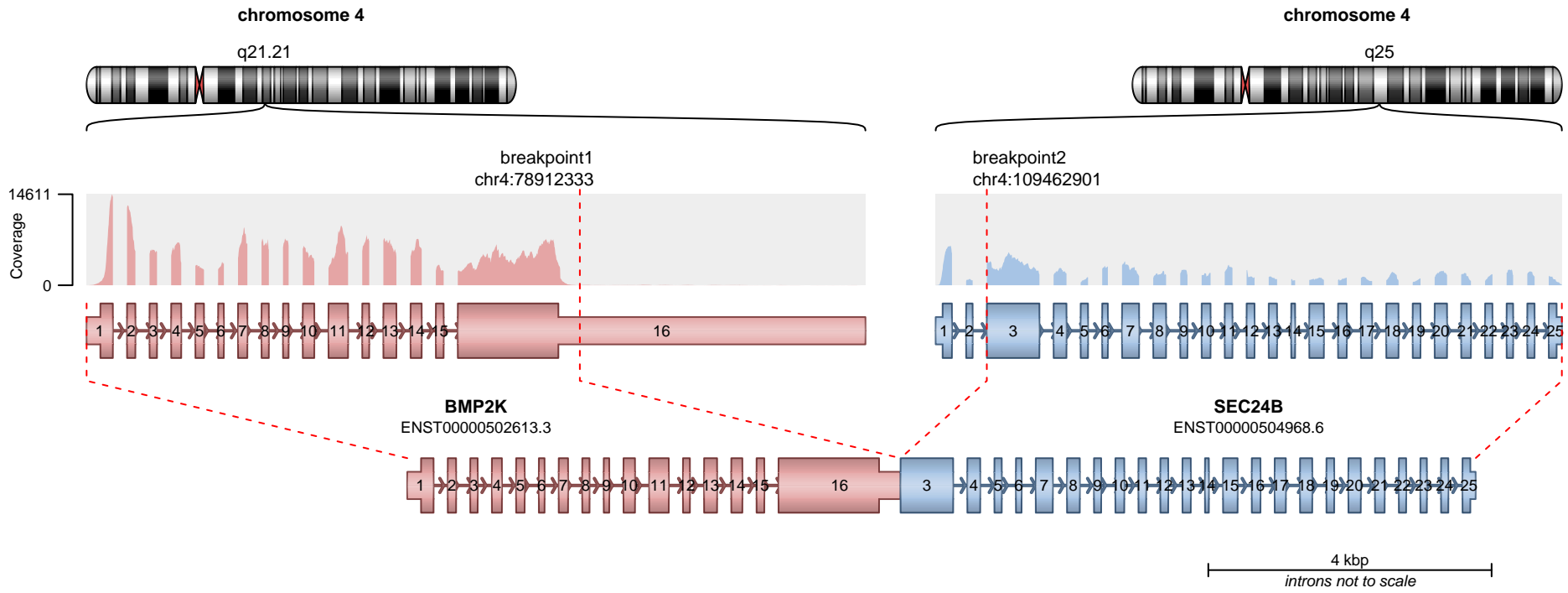
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



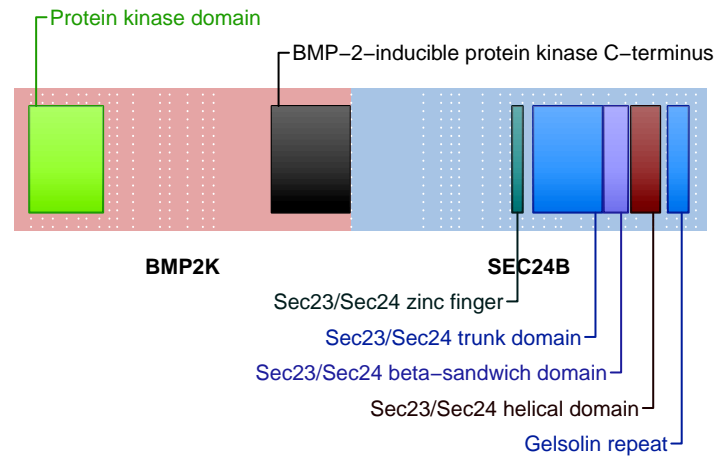
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0



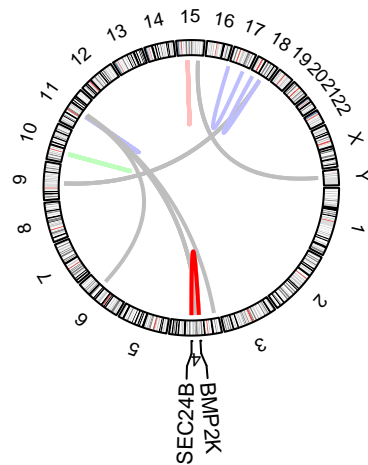
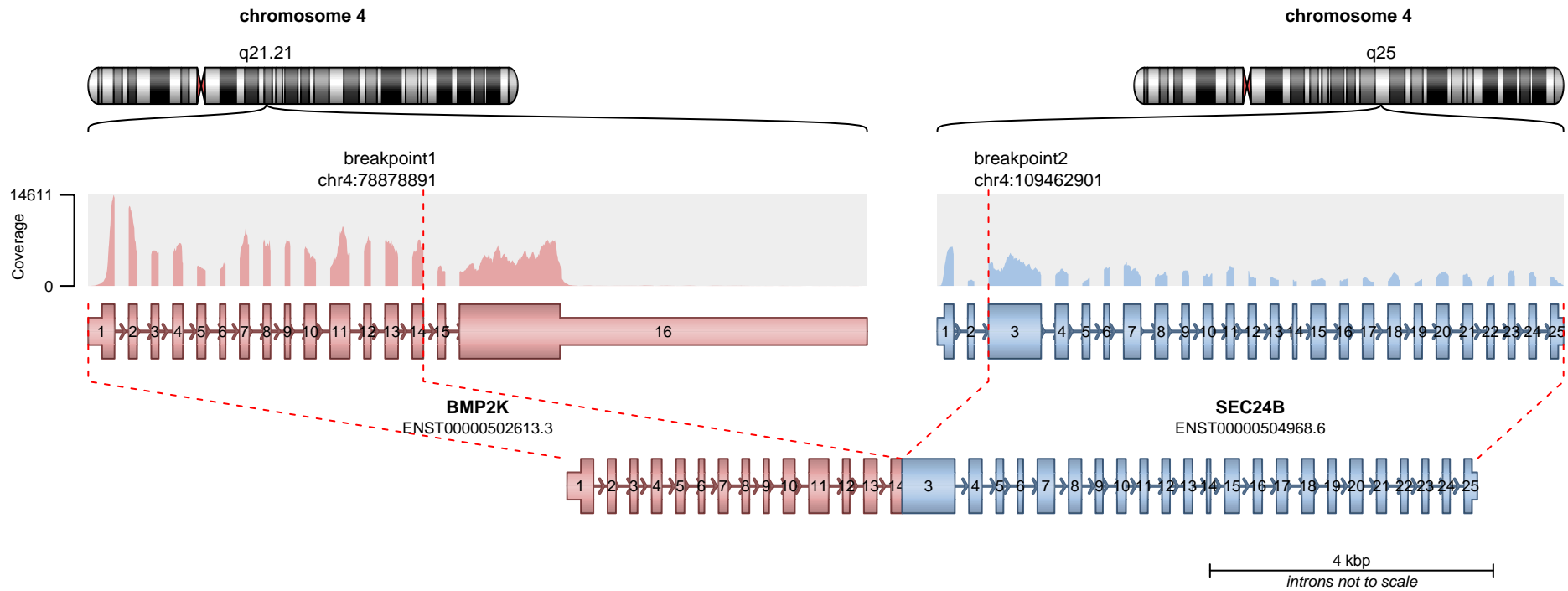
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



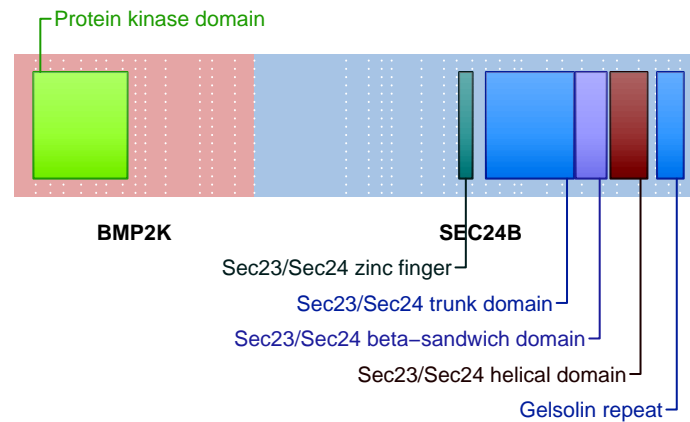
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0



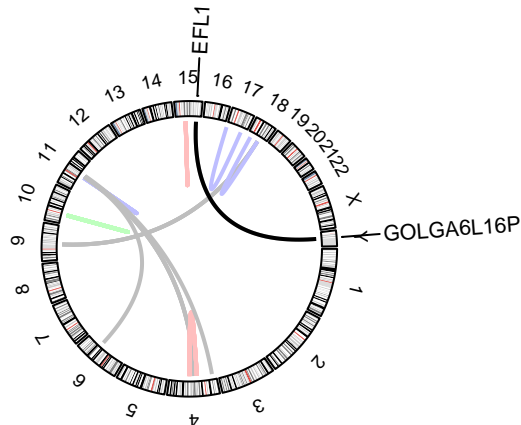
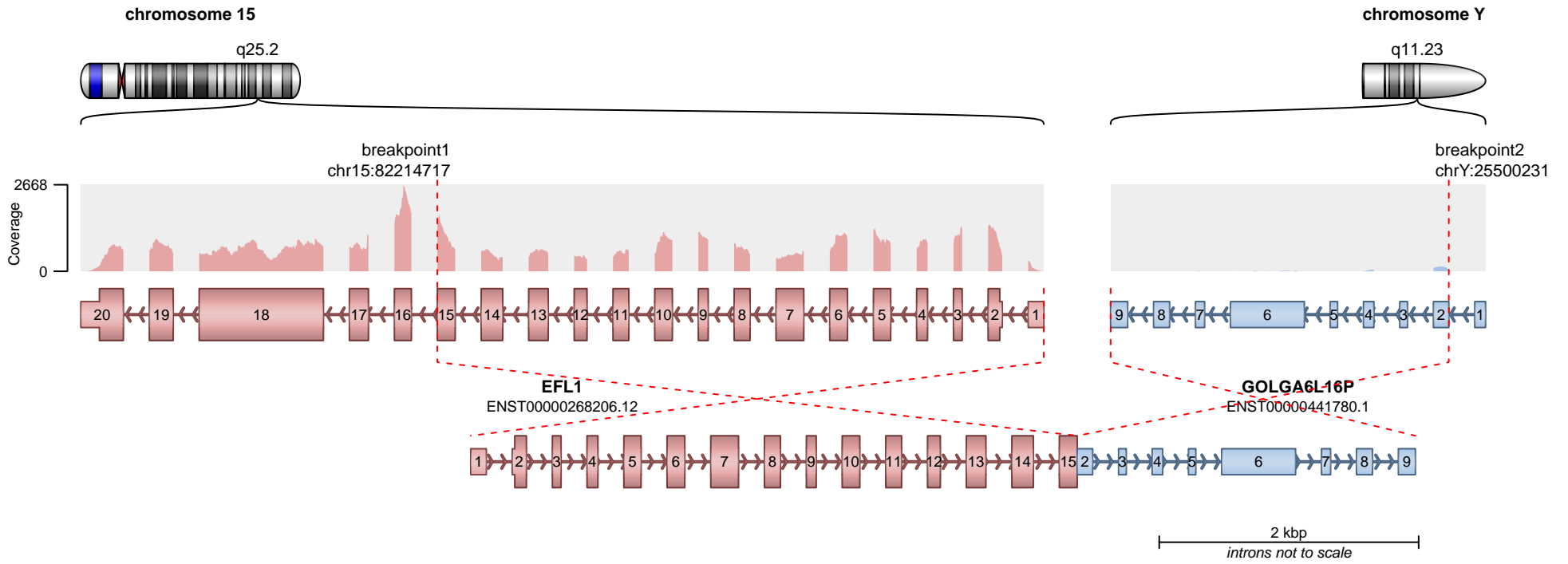
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear

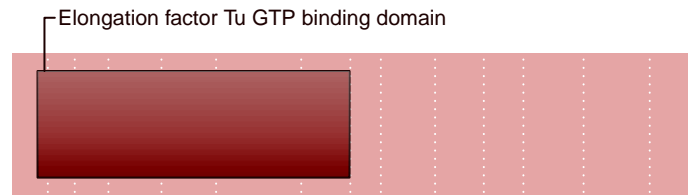


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



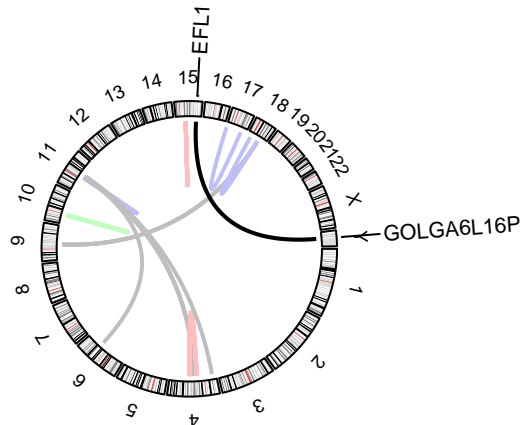
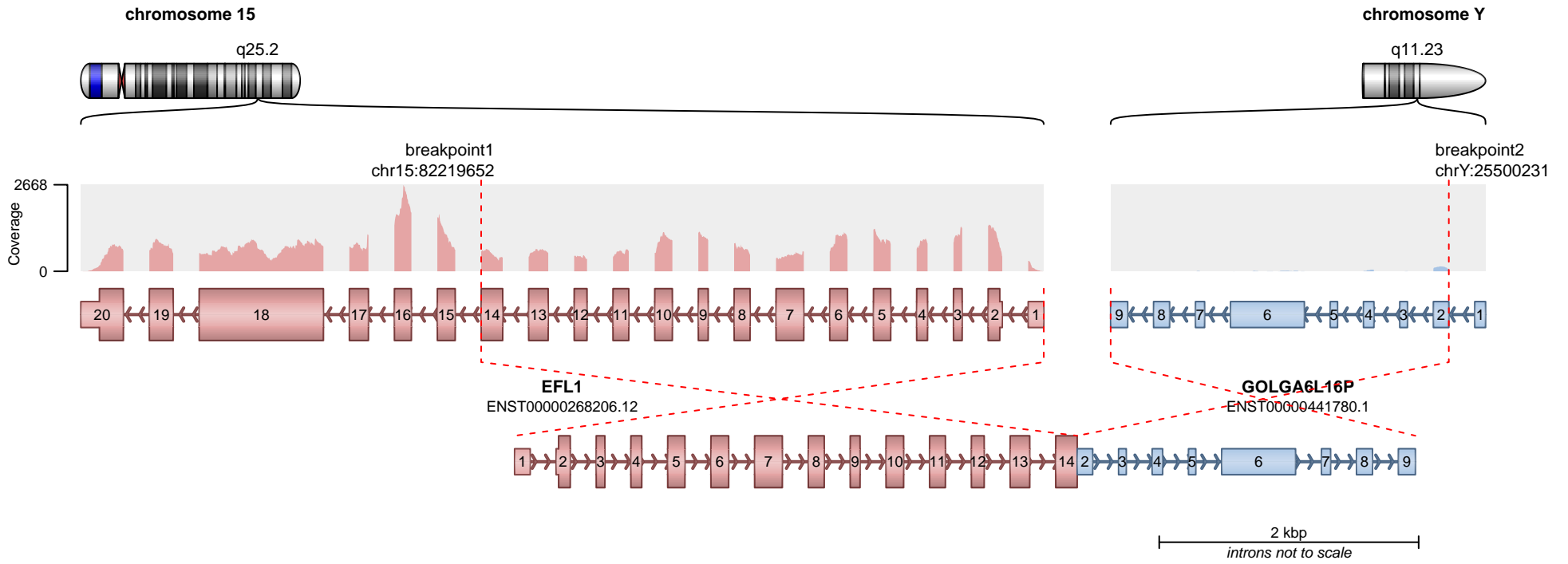
RETAINED PROTEIN DOMAINS
reading frame unclear



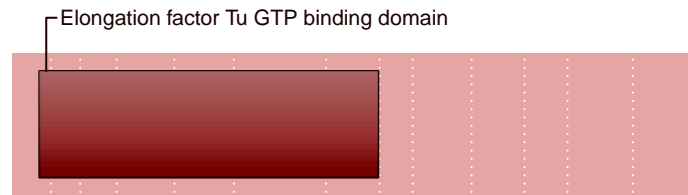
SUPPORTING READ COUNT

Split reads = 21
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



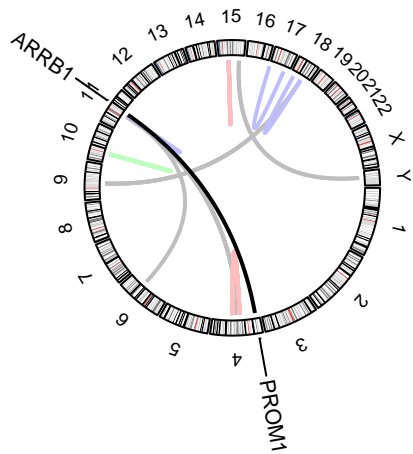
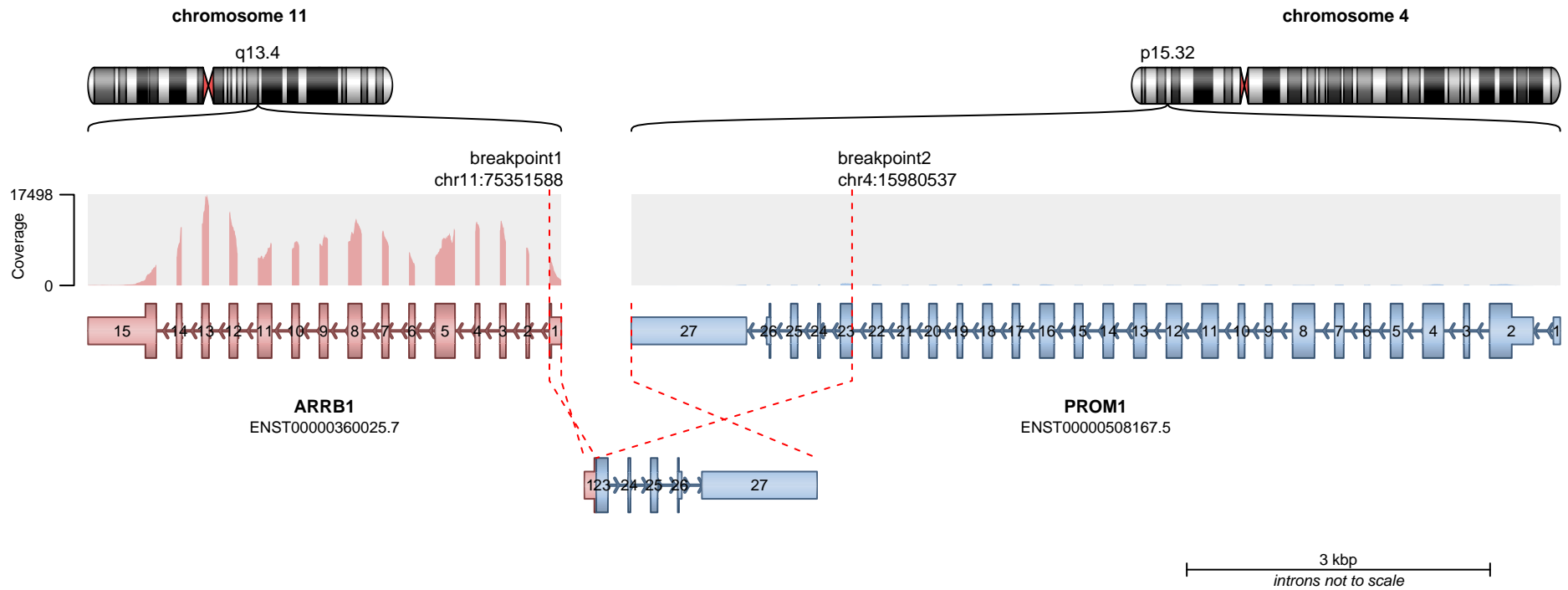
RETAINED PROTEIN DOMAINS
reading frame unclear



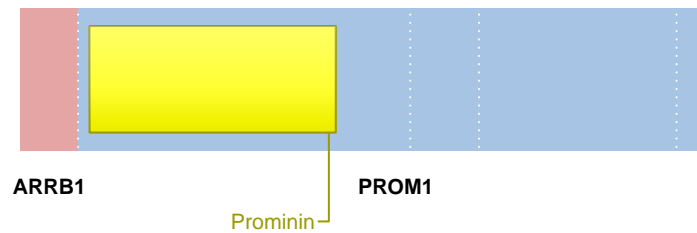
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



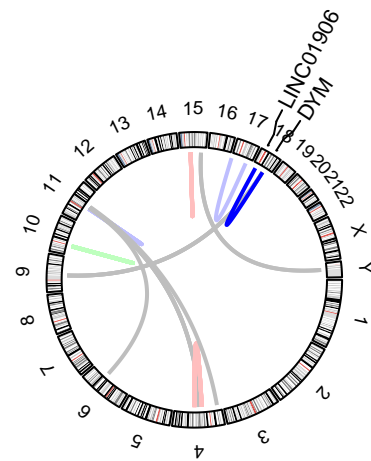
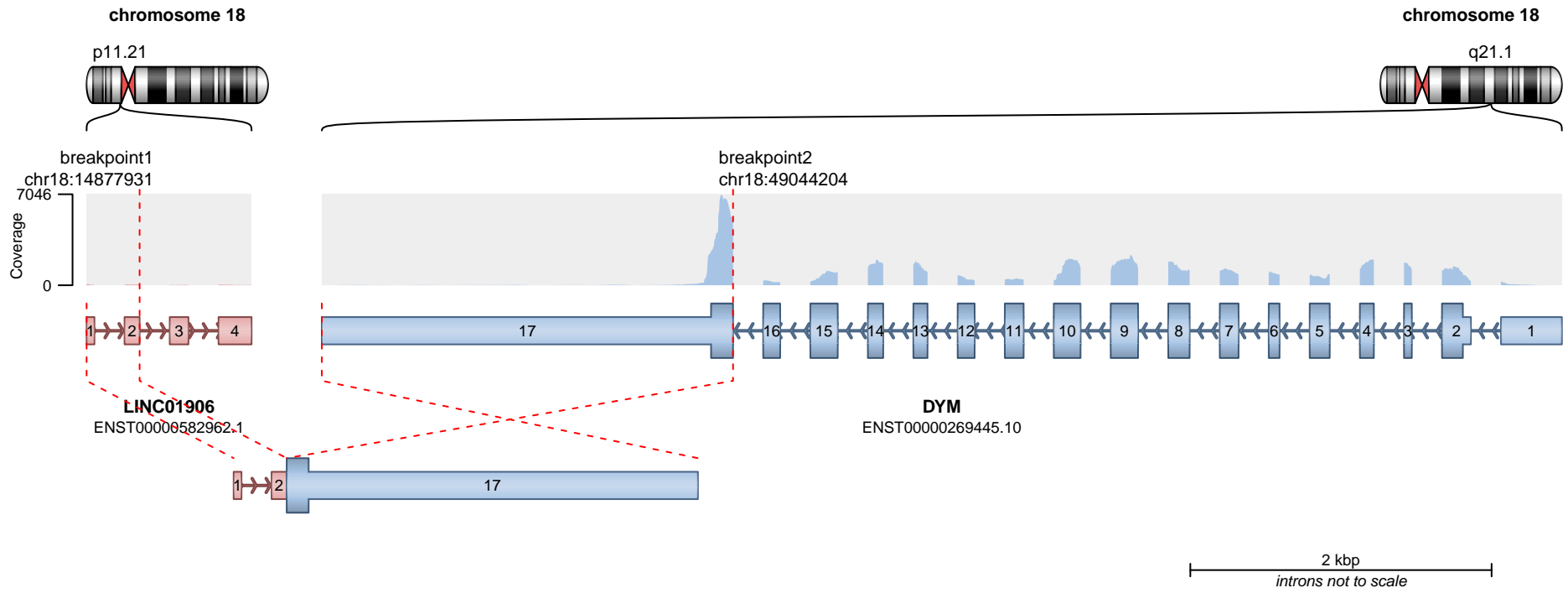
RETAINED PROTEIN DOMAINS
reading frame unclear



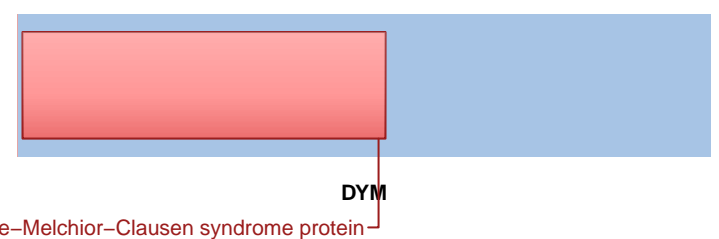
SUPPORTING READ COUNT

Split reads = 20
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0

— translocation — deletion
— duplication — inversion