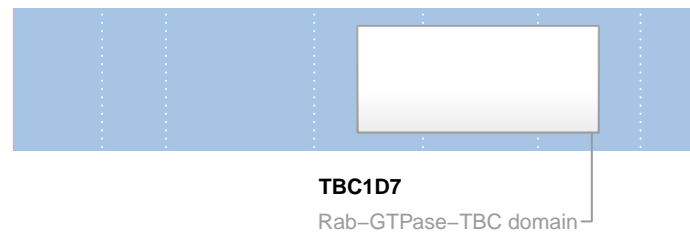


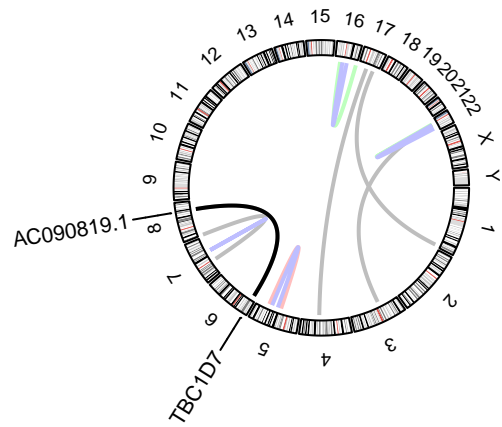
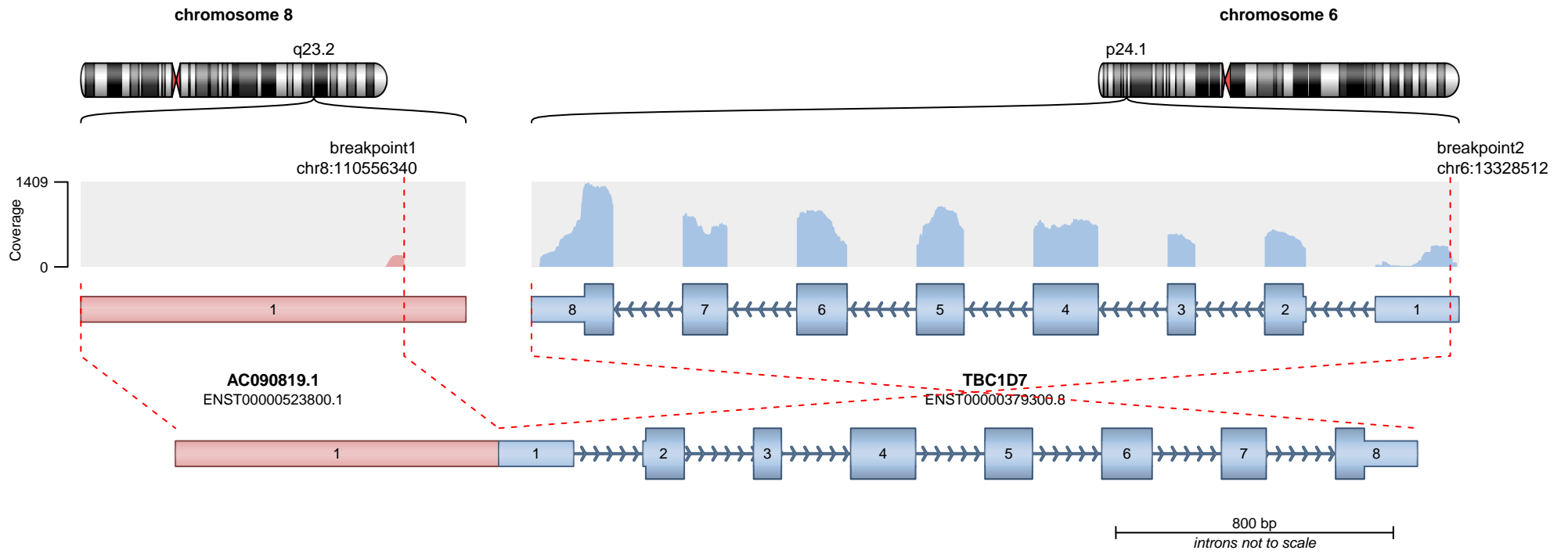
RETAINED PROTEIN DOMAINS
reading frame unclear



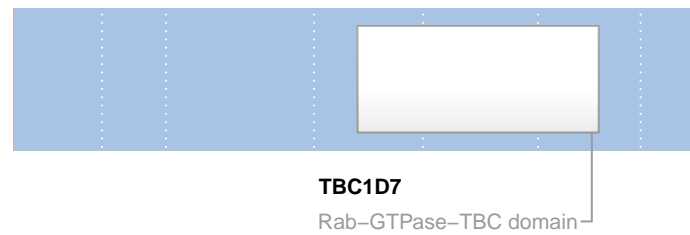
SUPPORTING READ COUNT

Split reads = 77
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



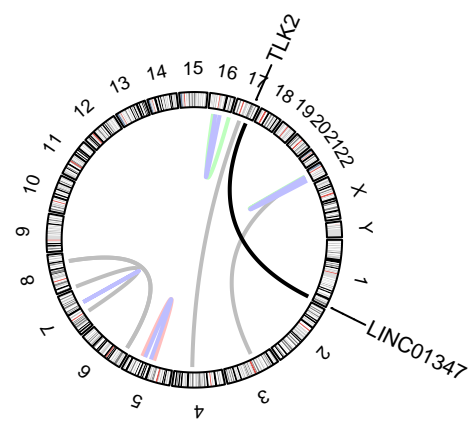
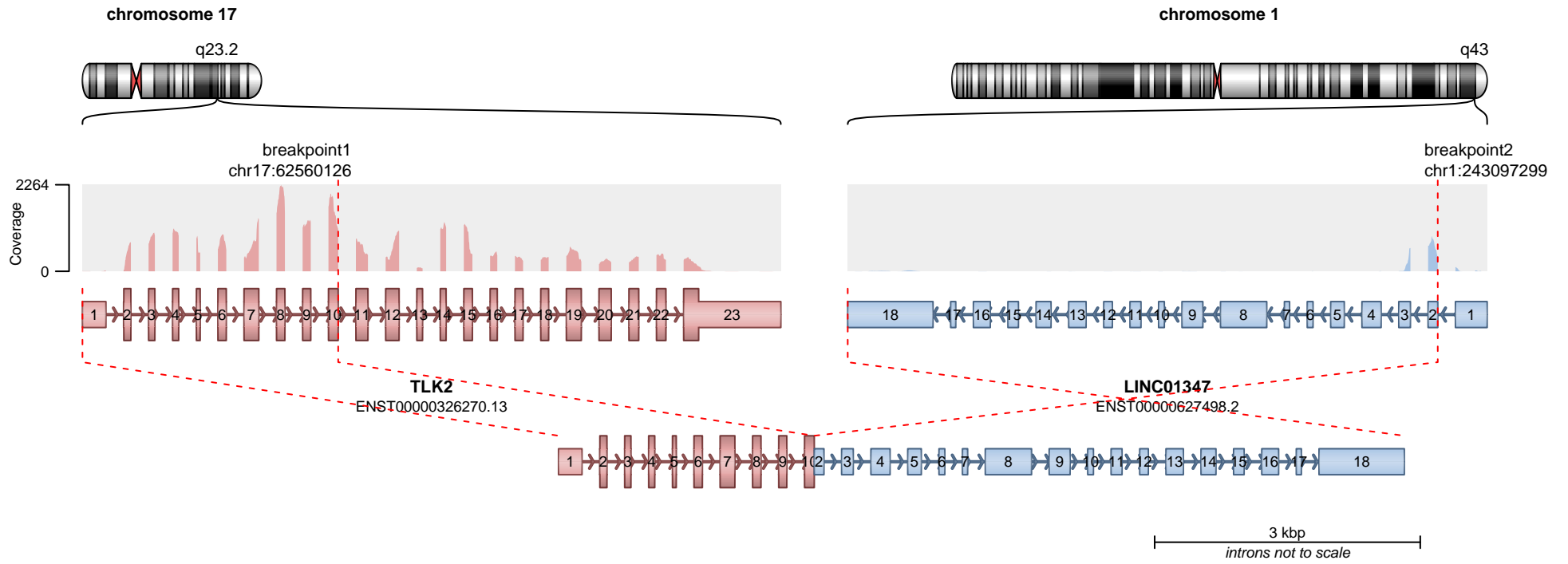
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 69
Discordant mates = 0

— translocation — deletion
— duplication — inversion

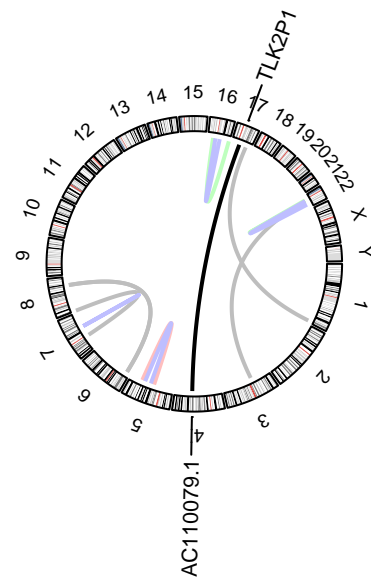
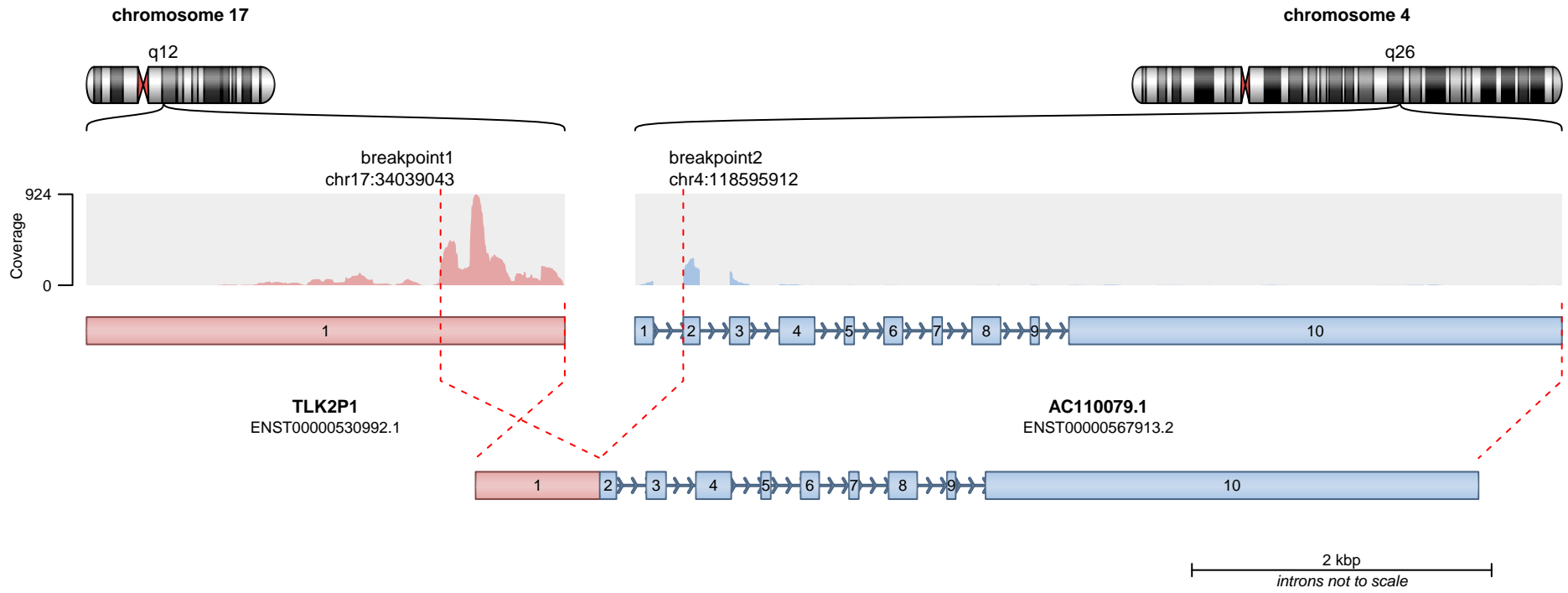


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 43
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

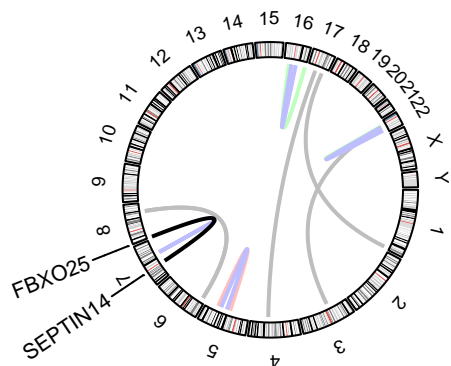
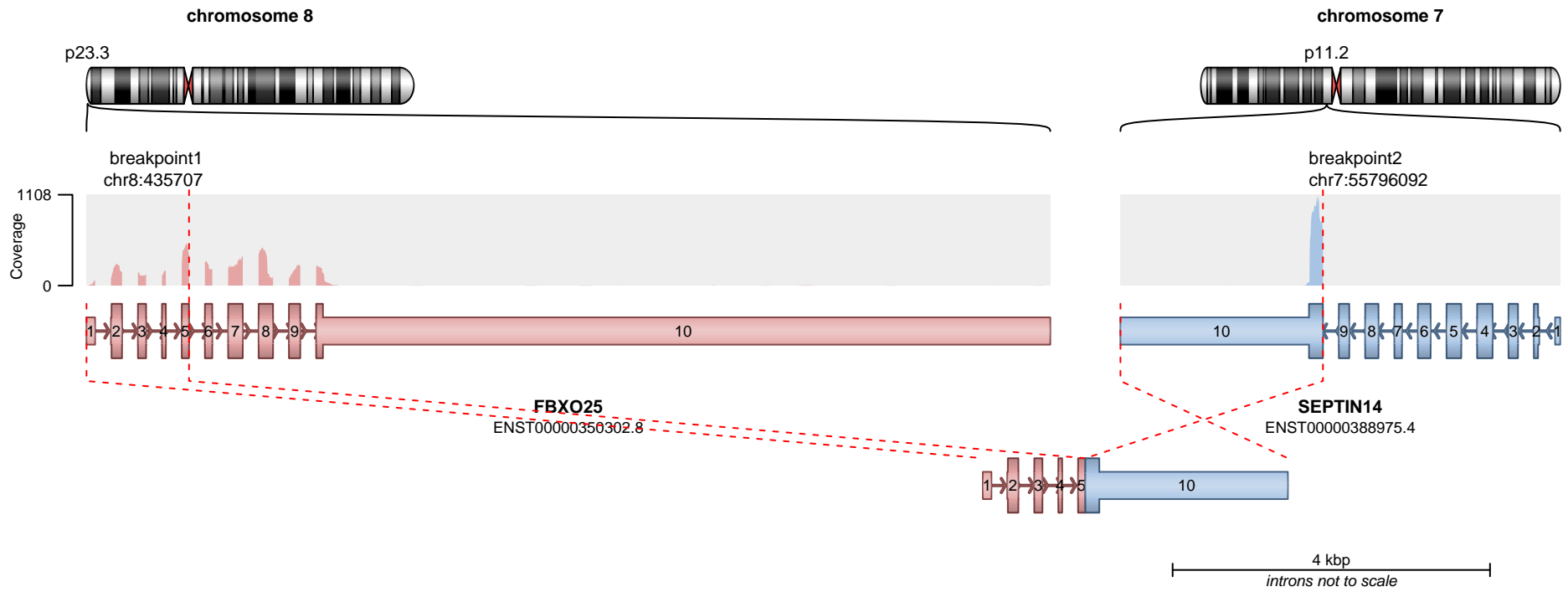


— translocation — deletion
 — duplication — inversion

Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 42
Discordant mates = 0

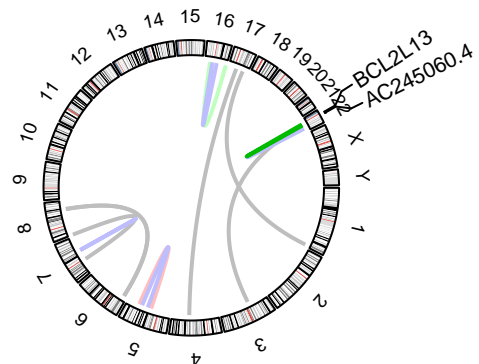
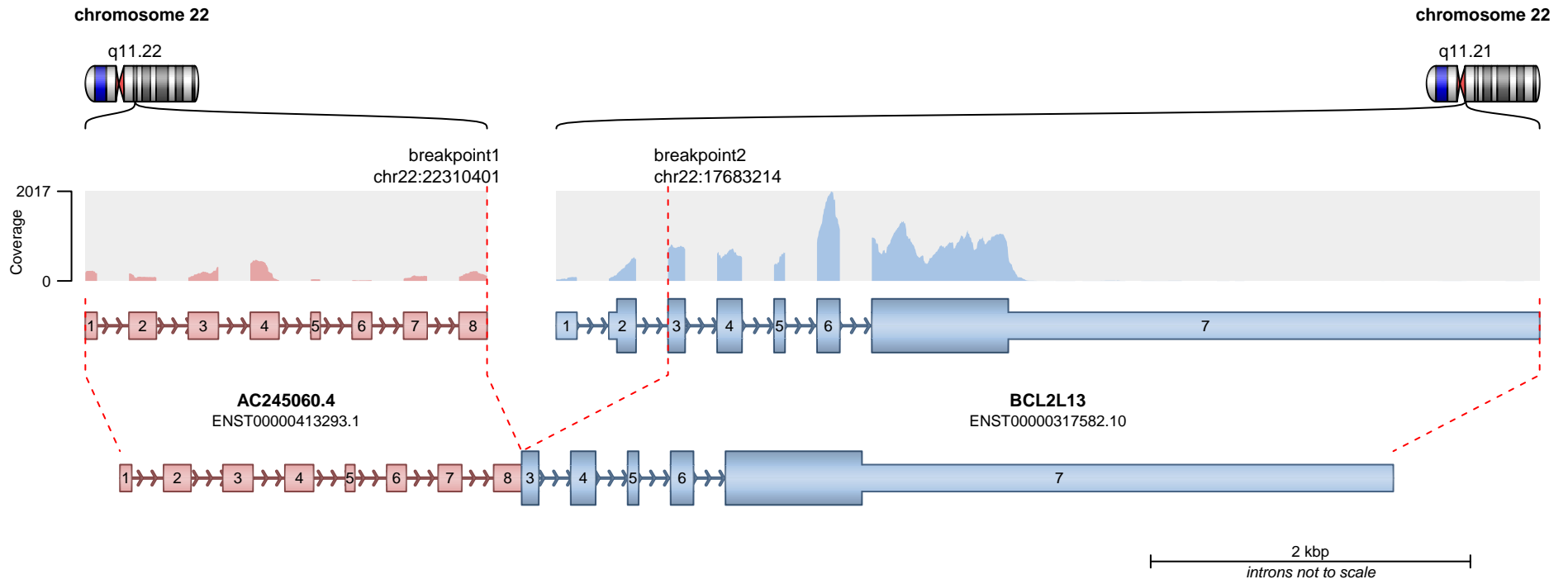


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 15
Discordant mates = 0

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

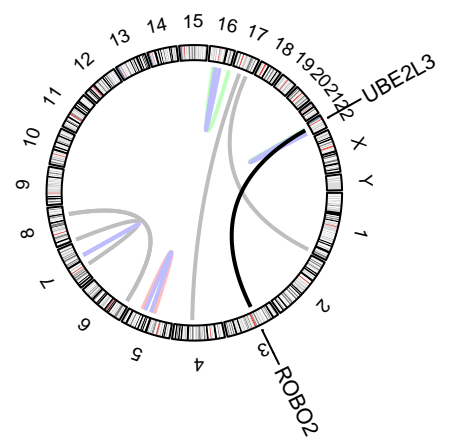
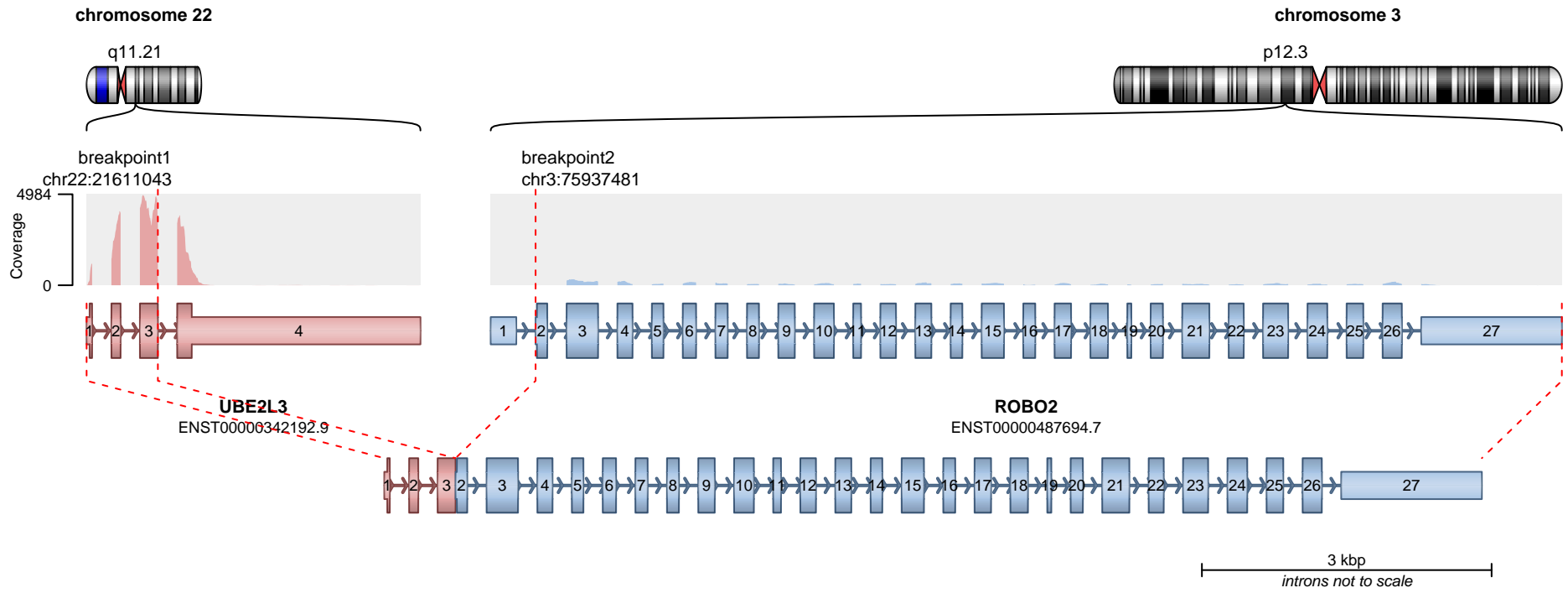


Apoptosis regulator proteins, Bcl-2 family

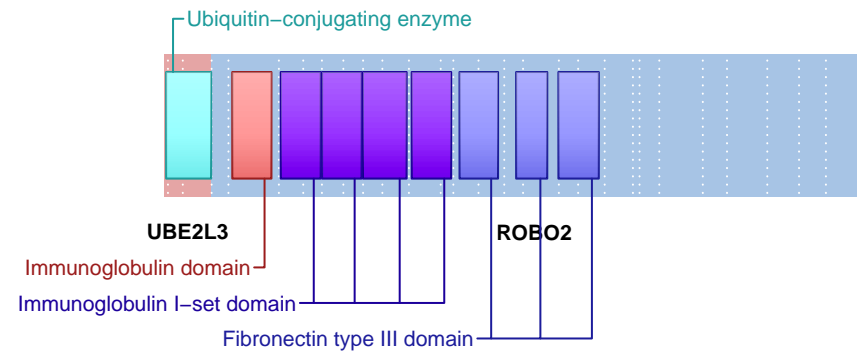
SUPPORTING READ COUNT

Split reads = 14
Discordant mates = 0

— translocation — deletion
— duplication — inversion



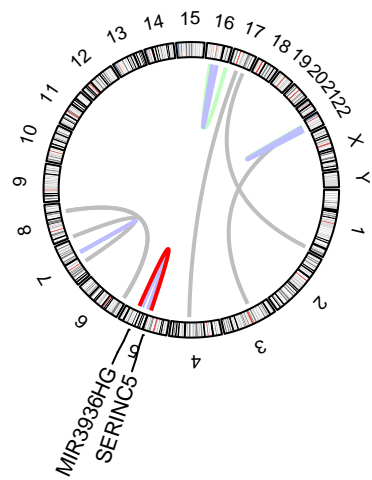
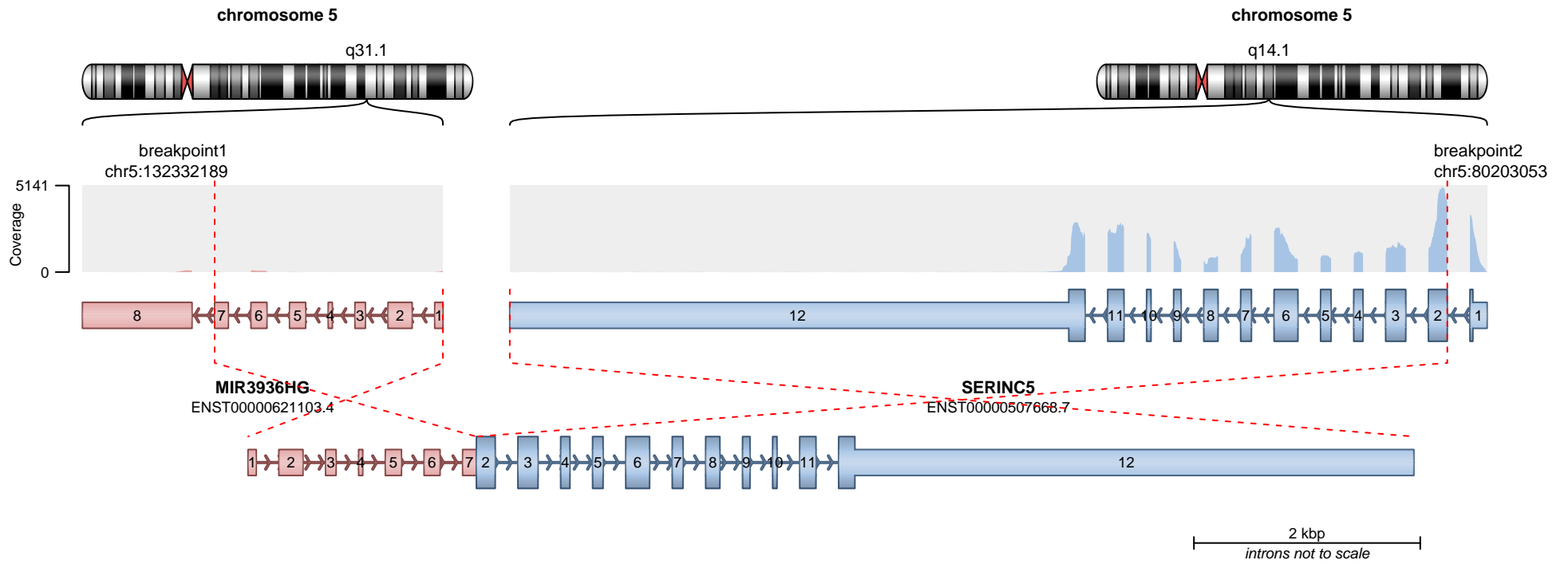
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

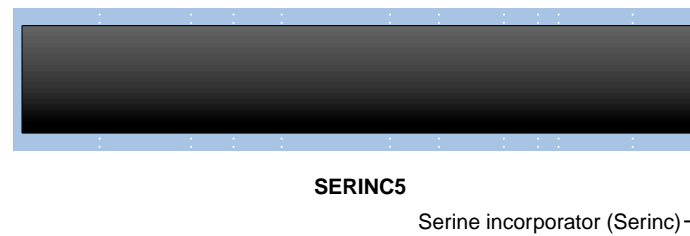
Split reads = 12
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



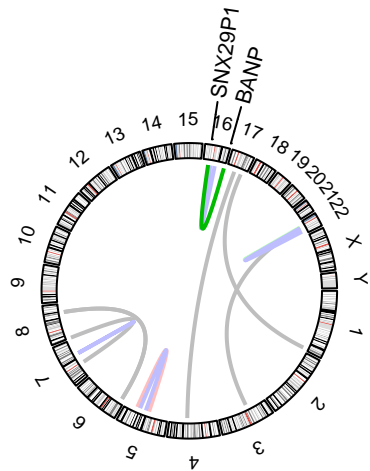
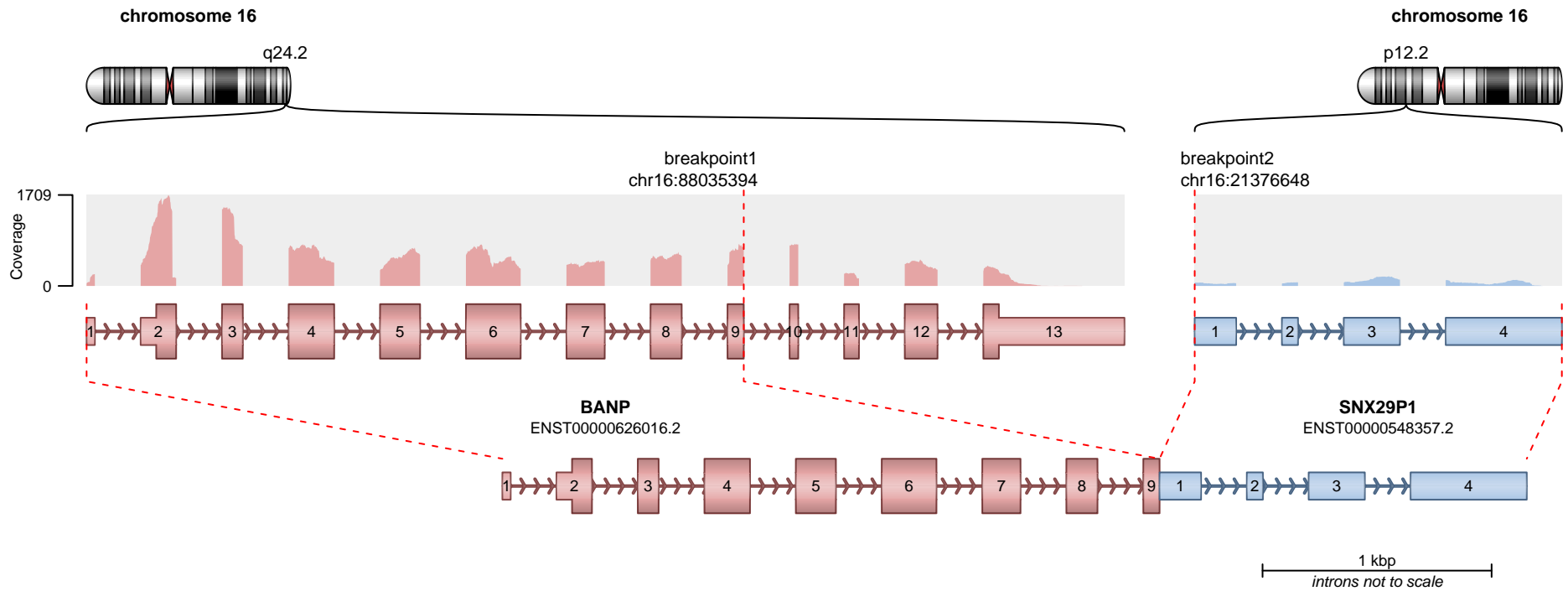
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear

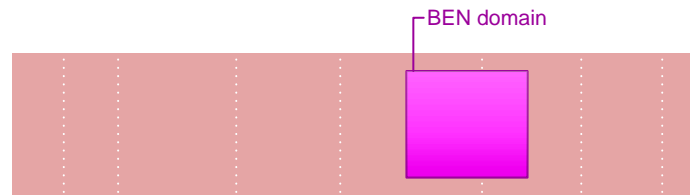


SUPPORTING READ COUNT

Split reads = 9
Discordant mates = 0



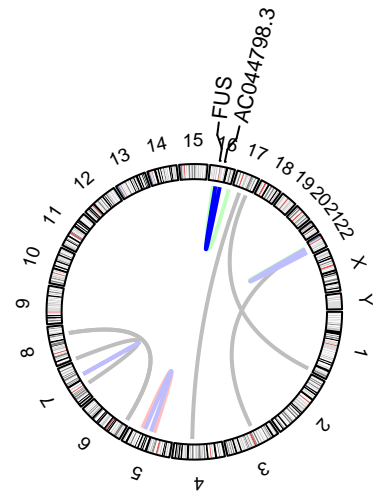
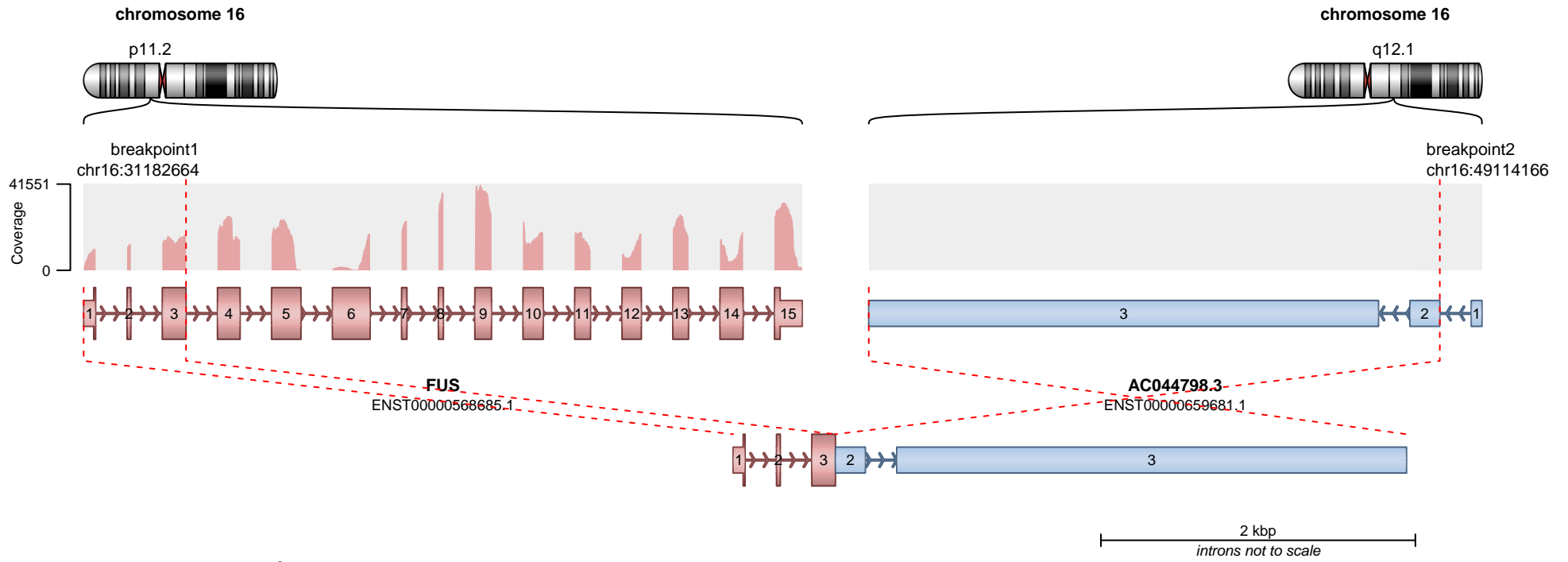
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 0

— translocation — deletion
— duplication — inversion

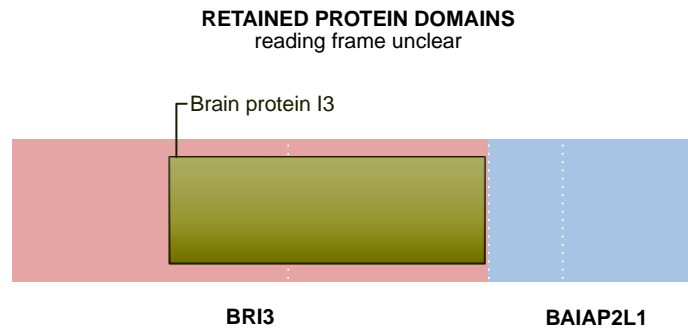
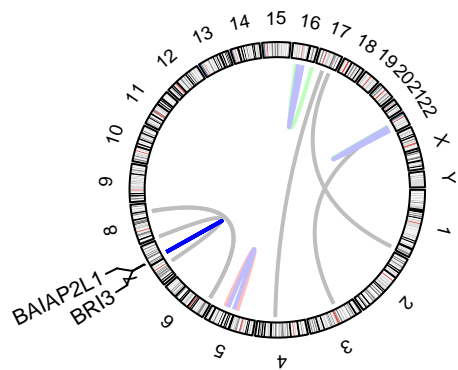
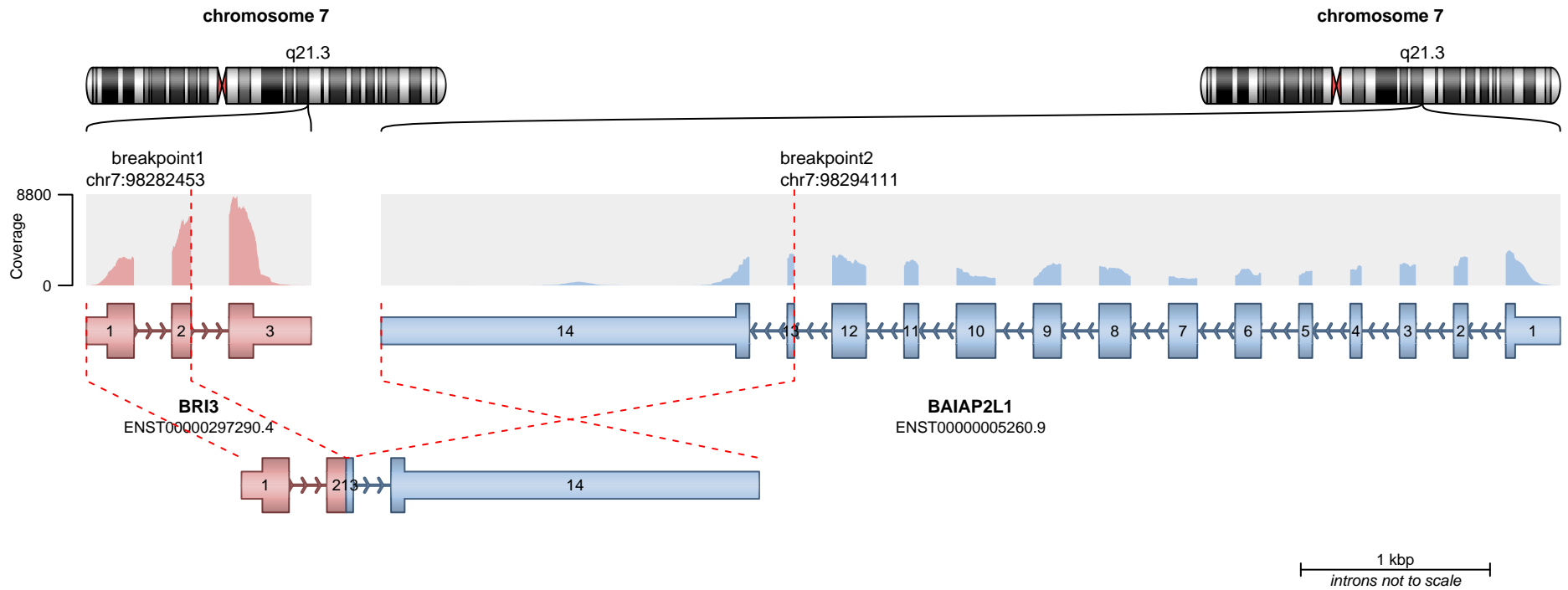


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0

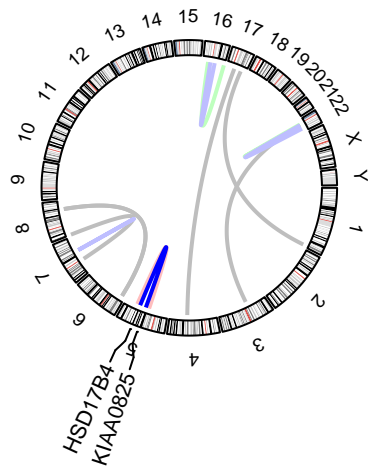
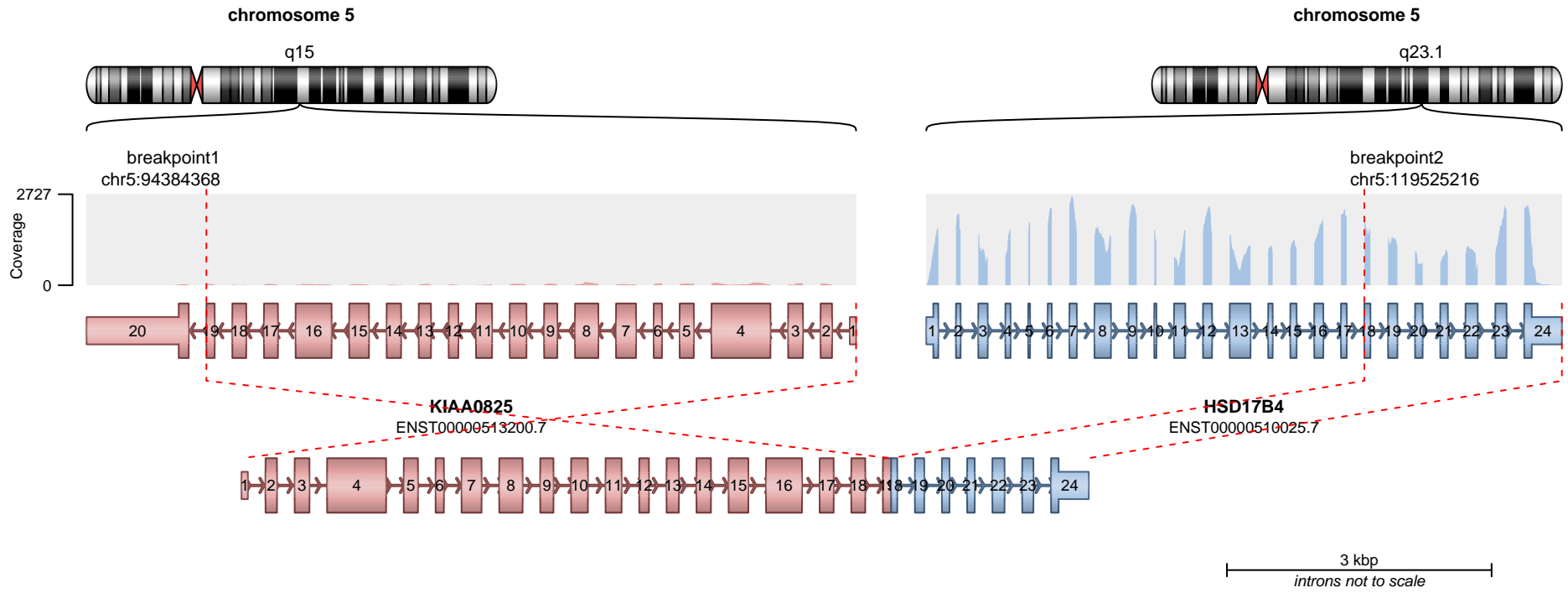
- translocation
- duplication
- deletion
- inversion



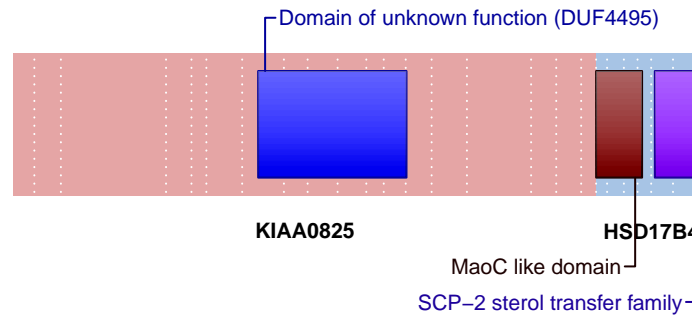
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

— translocation — deletion
— duplication — inversion



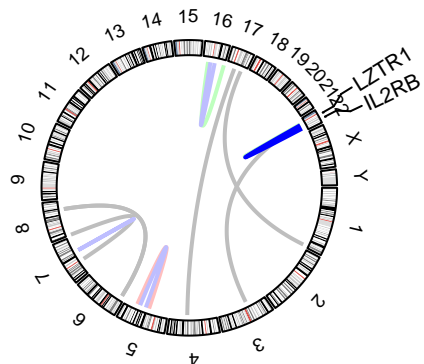
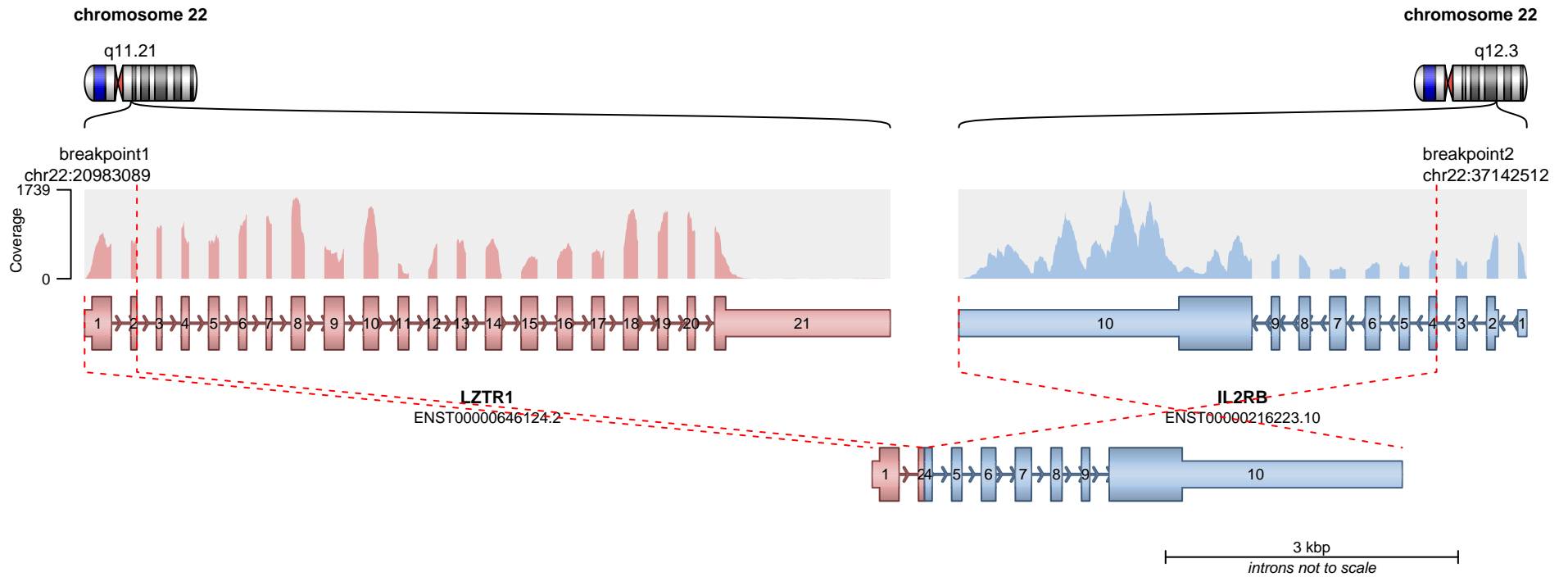
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

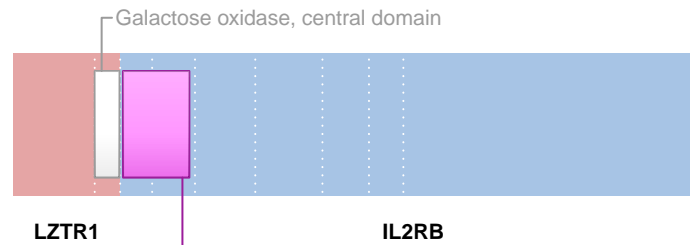
Split reads = 2
Discordant mates = 0

— translocation — deletion
— duplication — inversion



Interleukin-2 receptor subunit beta N-terminal domain 1

RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion