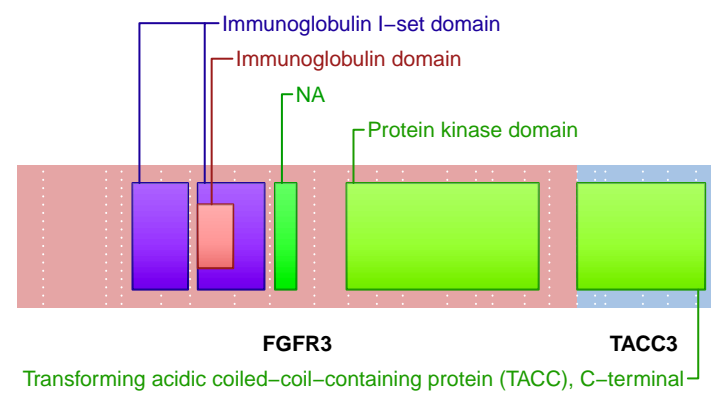


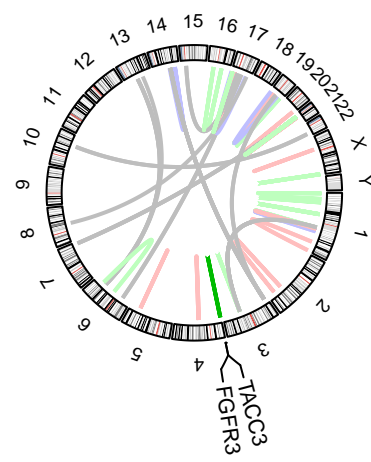
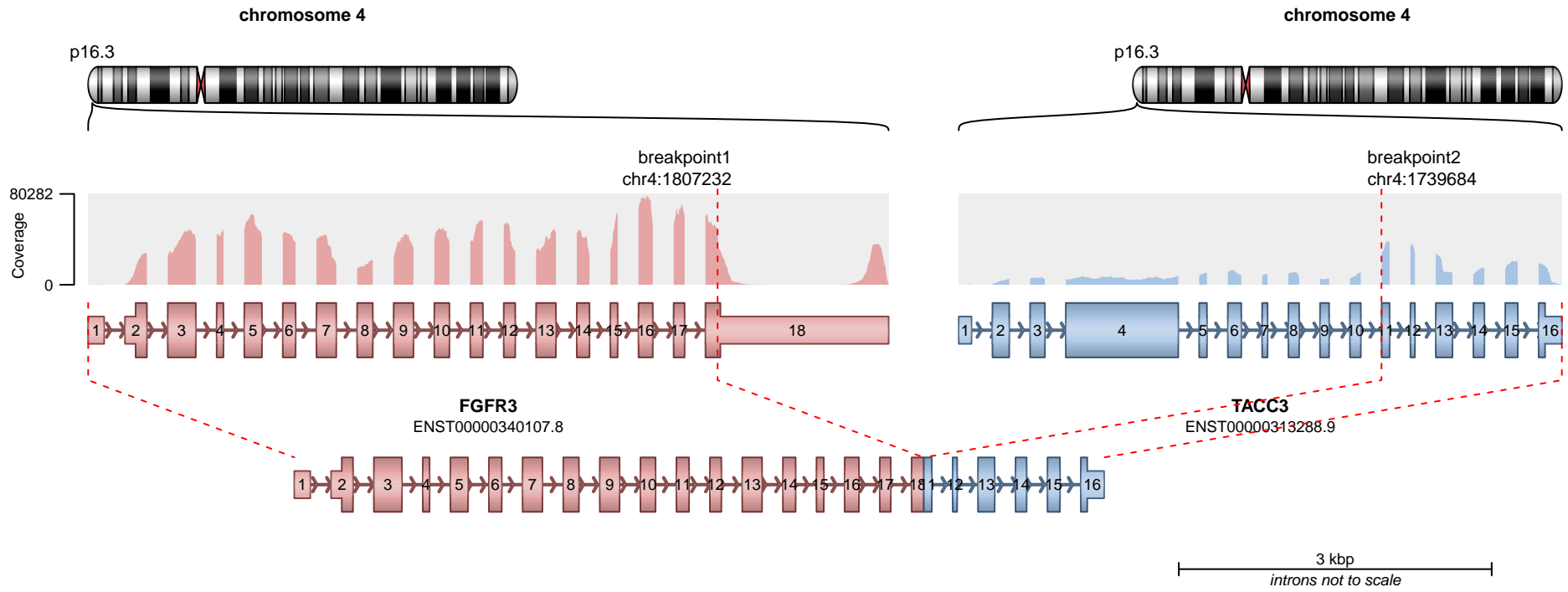
RETAINED PROTEIN DOMAINS
reading frame unclear



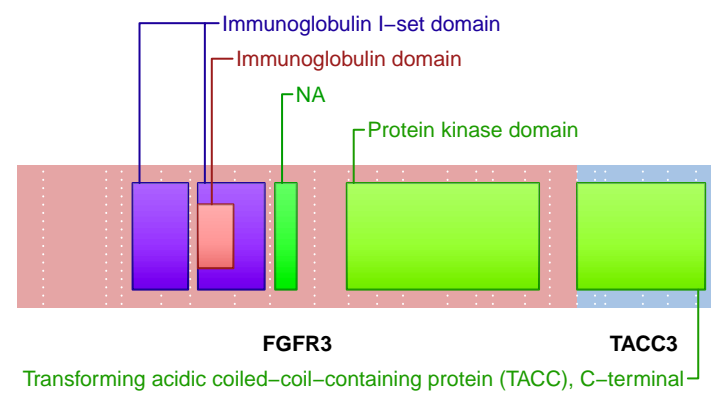
SUPPORTING READ COUNT

Split reads = 2297
Discordant mates = 66

- translocation
- duplication
- deletion
- inversion



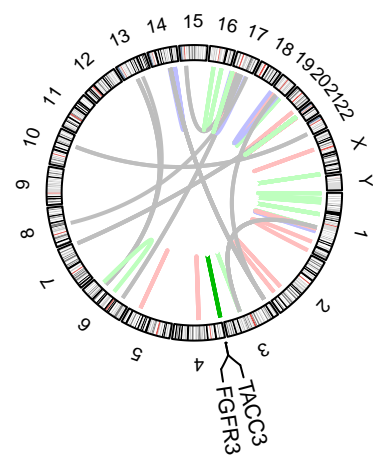
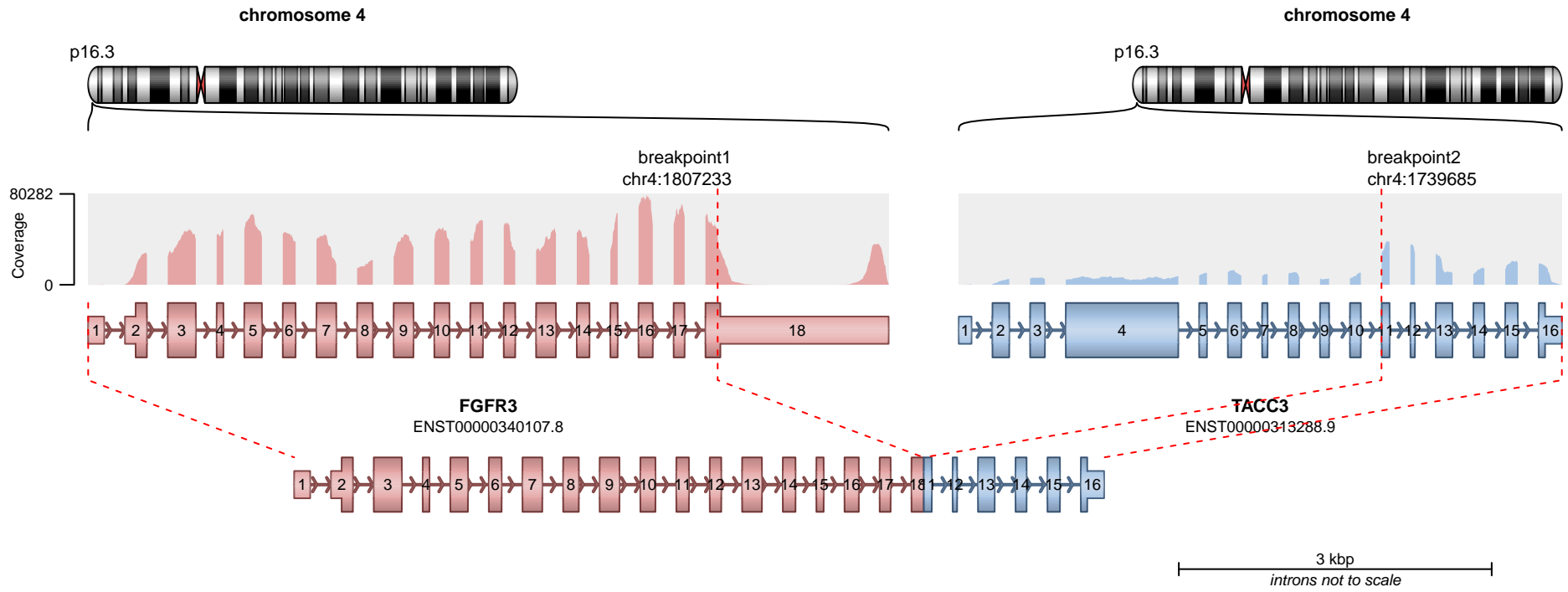
RETAINED PROTEIN DOMAINS
reading frame unclear



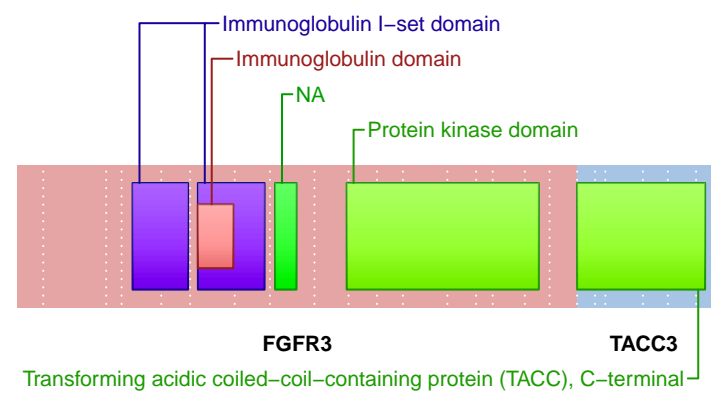
SUPPORTING READ COUNT

Split reads = 26
Discordant mates = 66

- translocation
- duplication
- deletion
- inversion



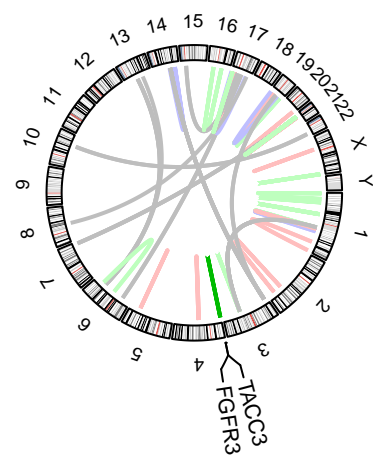
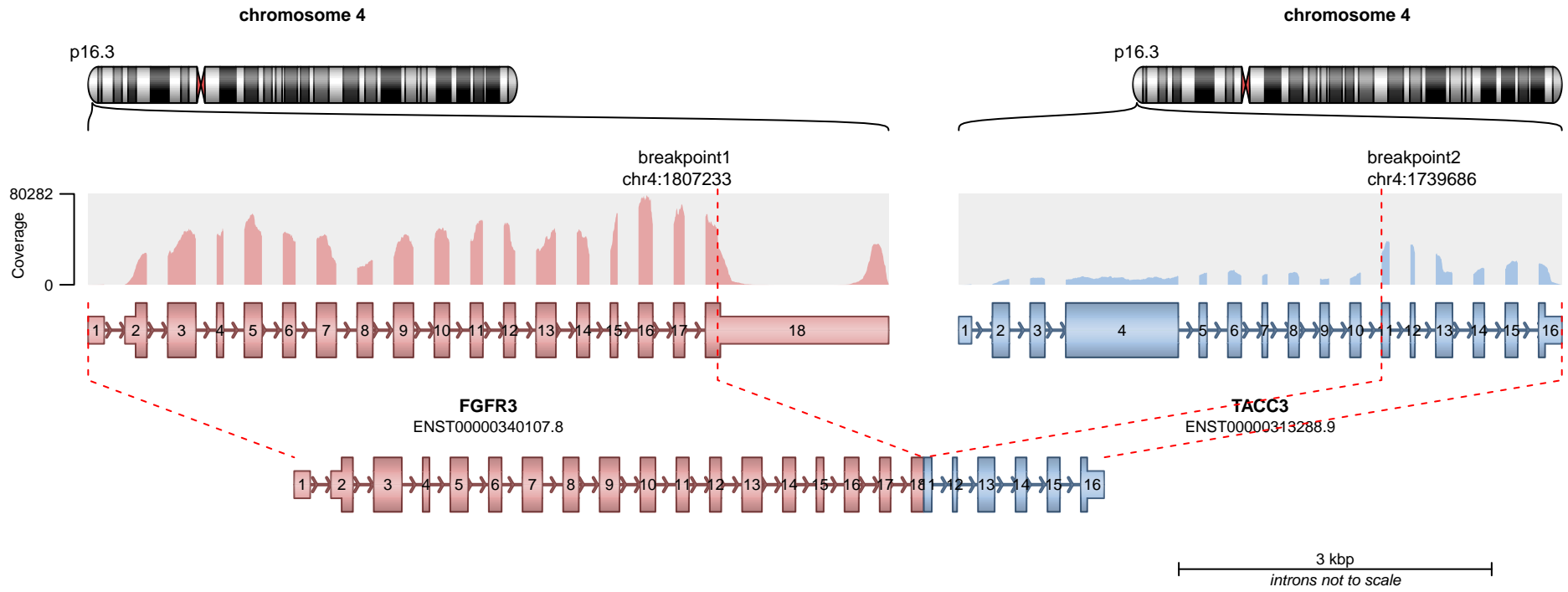
RETAINED PROTEIN DOMAINS
reading frame unclear



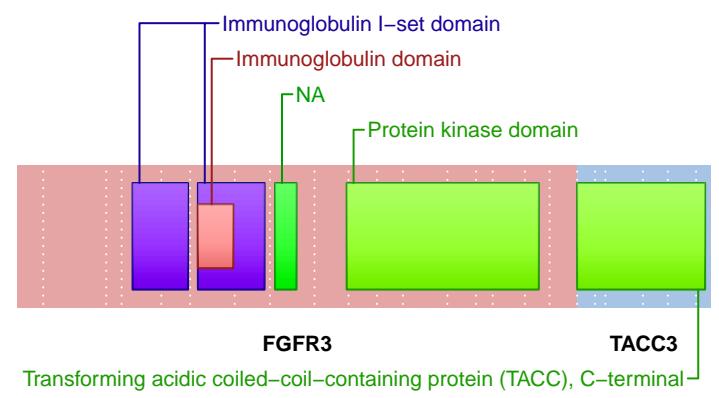
SUPPORTING READ COUNT

Split reads = 26
Discordant mates = 66

- translocation
- duplication
- deletion
- inversion



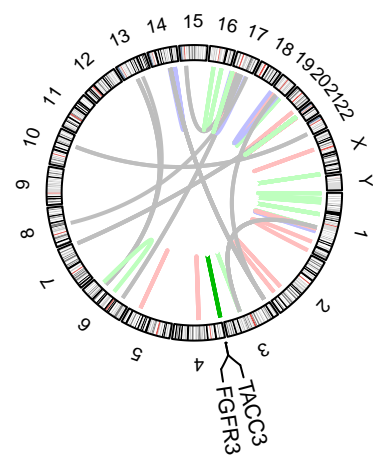
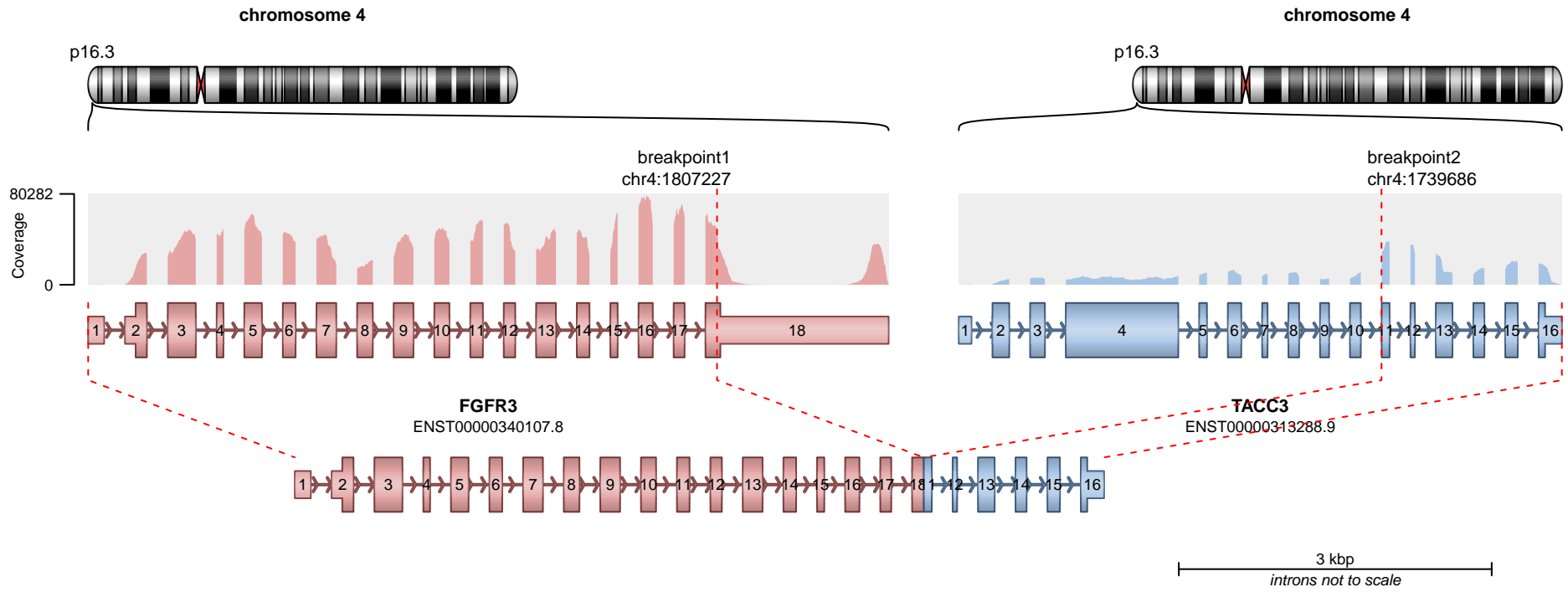
RETAINED PROTEIN DOMAINS
reading frame unclear



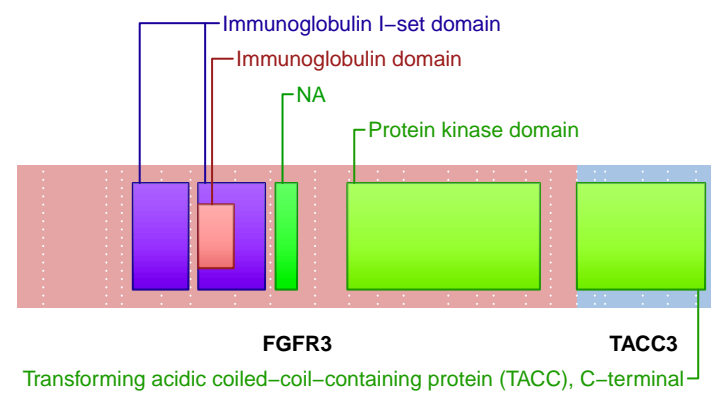
SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 66

- translocation
- duplication
- deletion
- inversion



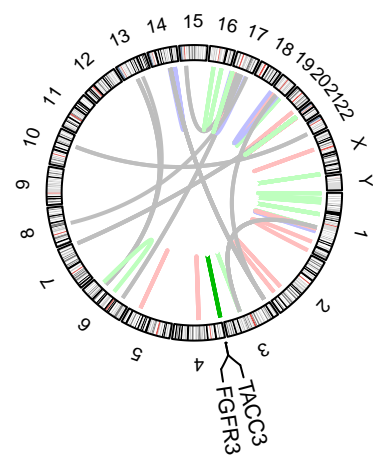
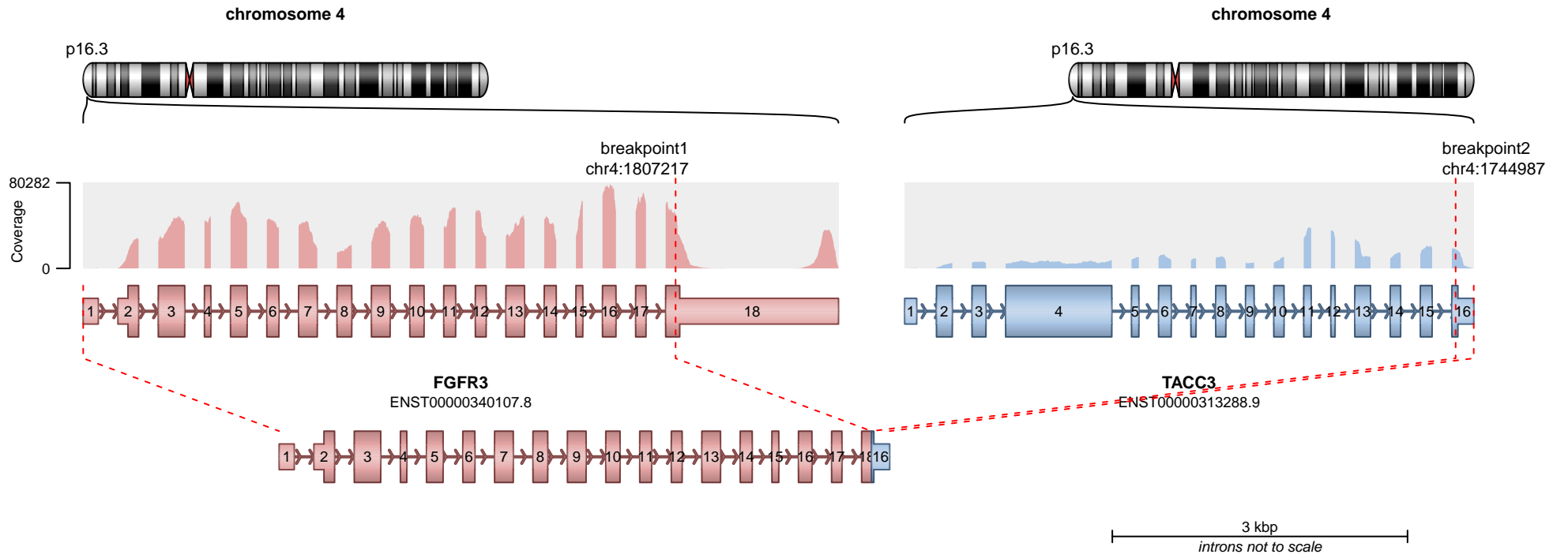
RETAINED PROTEIN DOMAINS
reading frame unclear



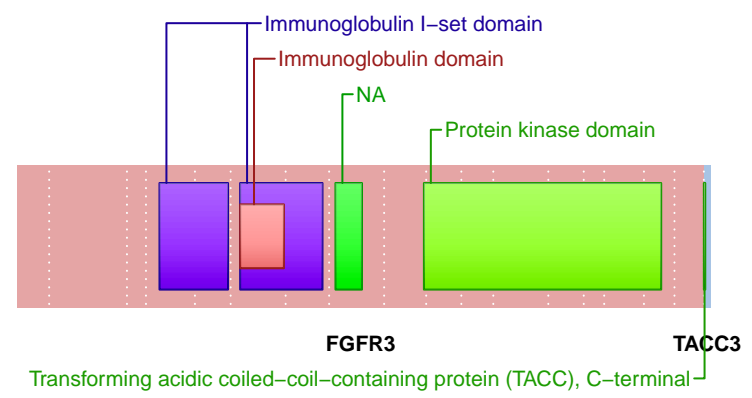
SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 59

- translocation
- duplication
- deletion
- inversion



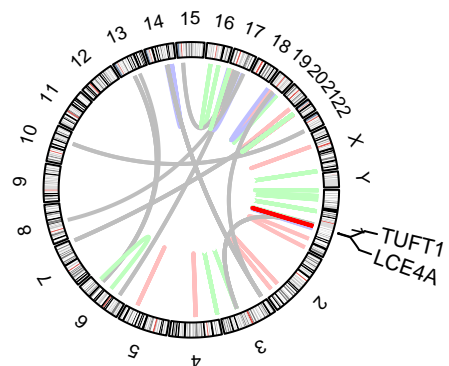
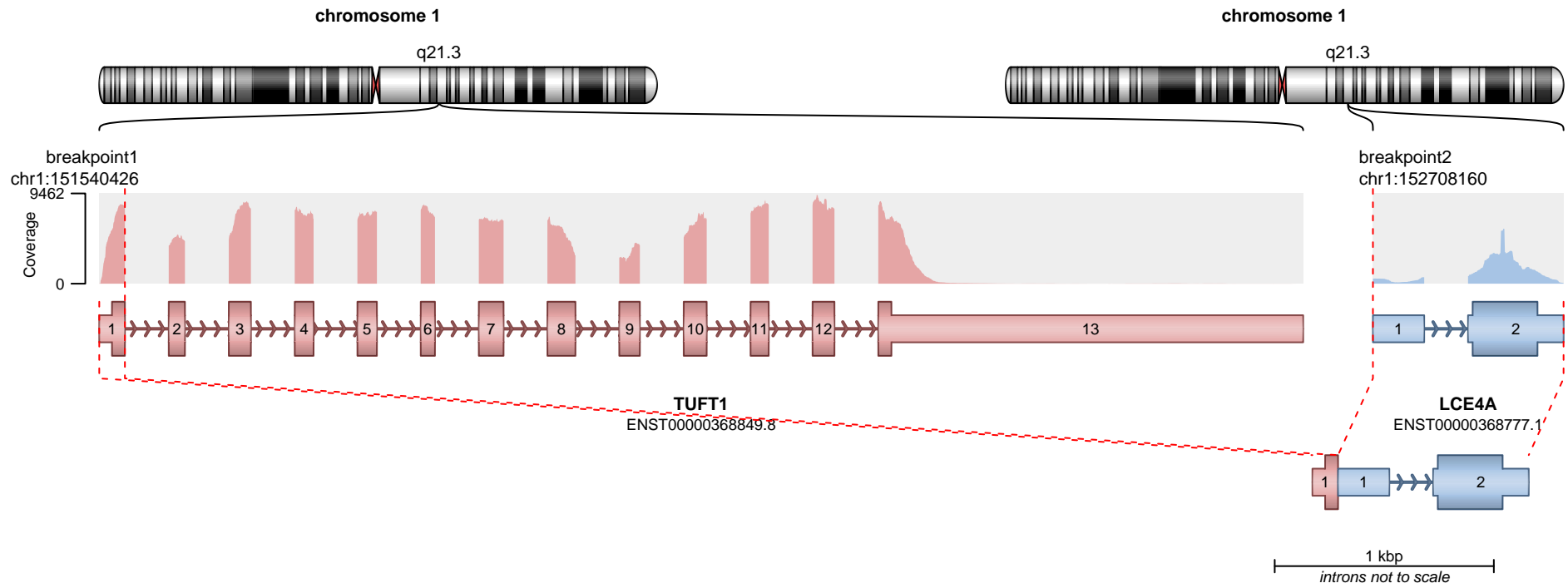
RETAINED PROTEIN DOMAINS
reading frame unclear



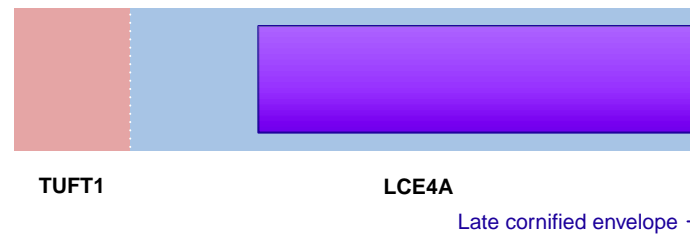
SUPPORTING READ COUNT

Split reads = 19
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



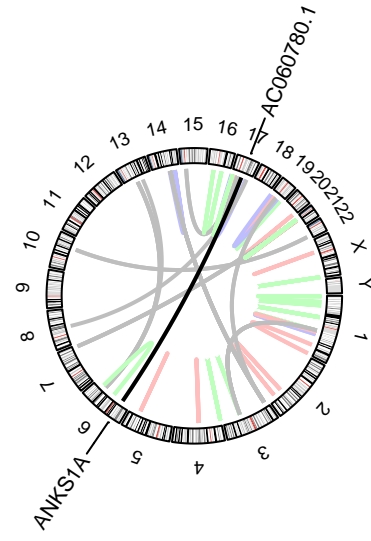
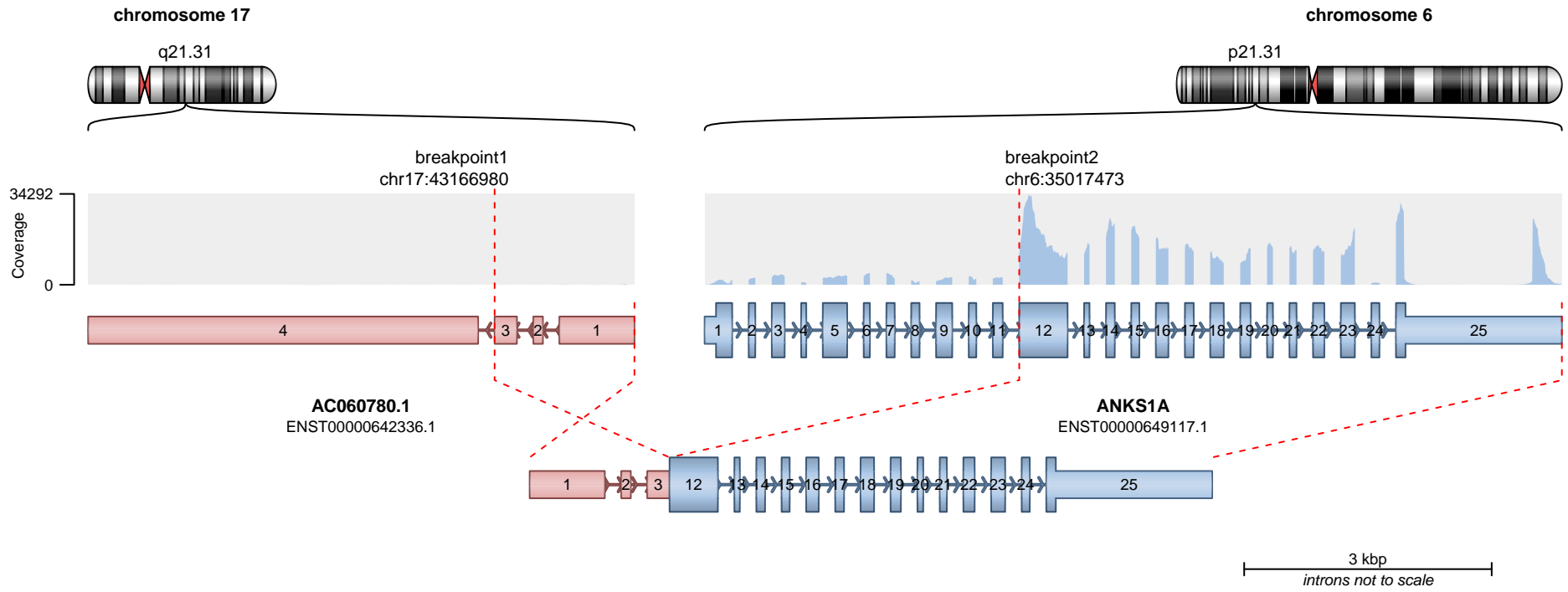
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

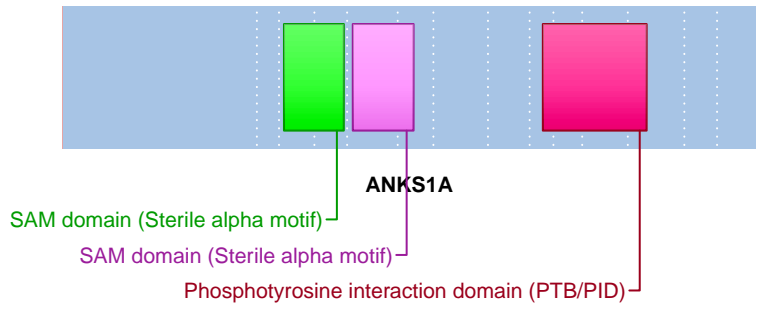
Split reads = 432
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



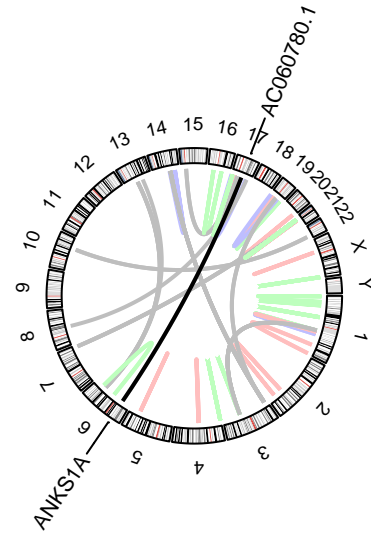
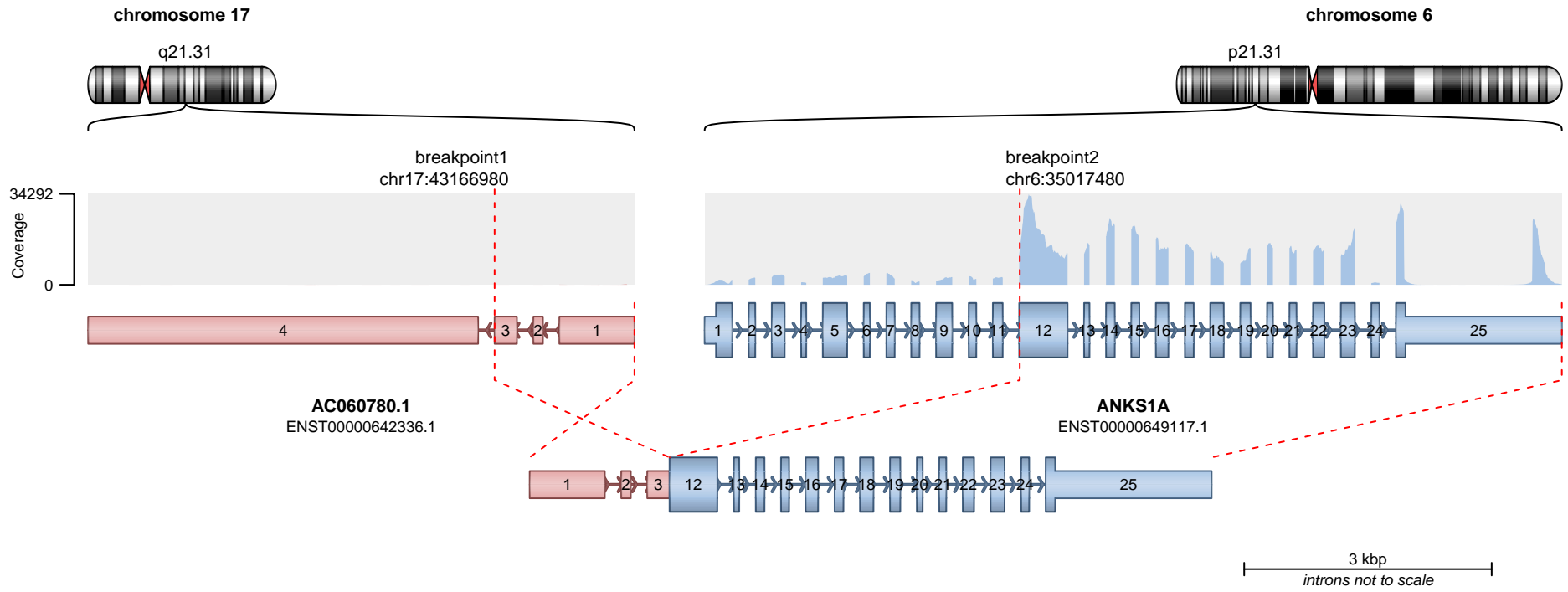
— translocation — deletion
 — duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



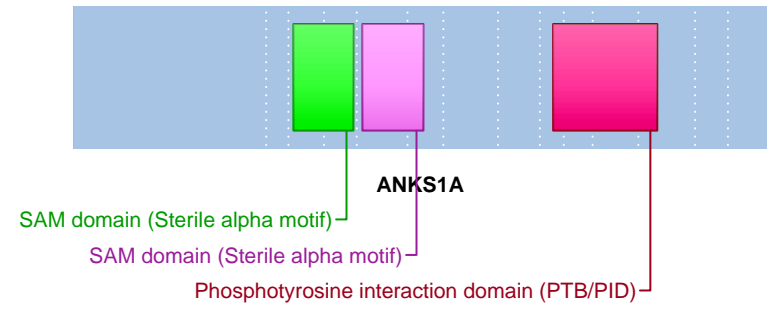
SUPPORTING READ COUNT

Split reads = 298
Discordant mates = 0



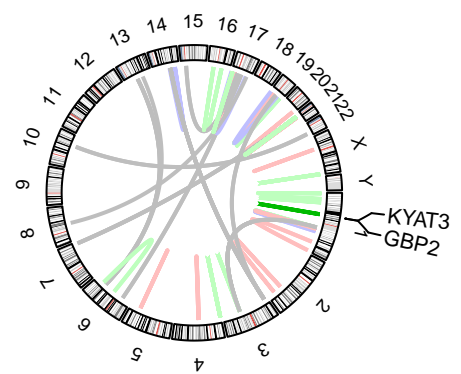
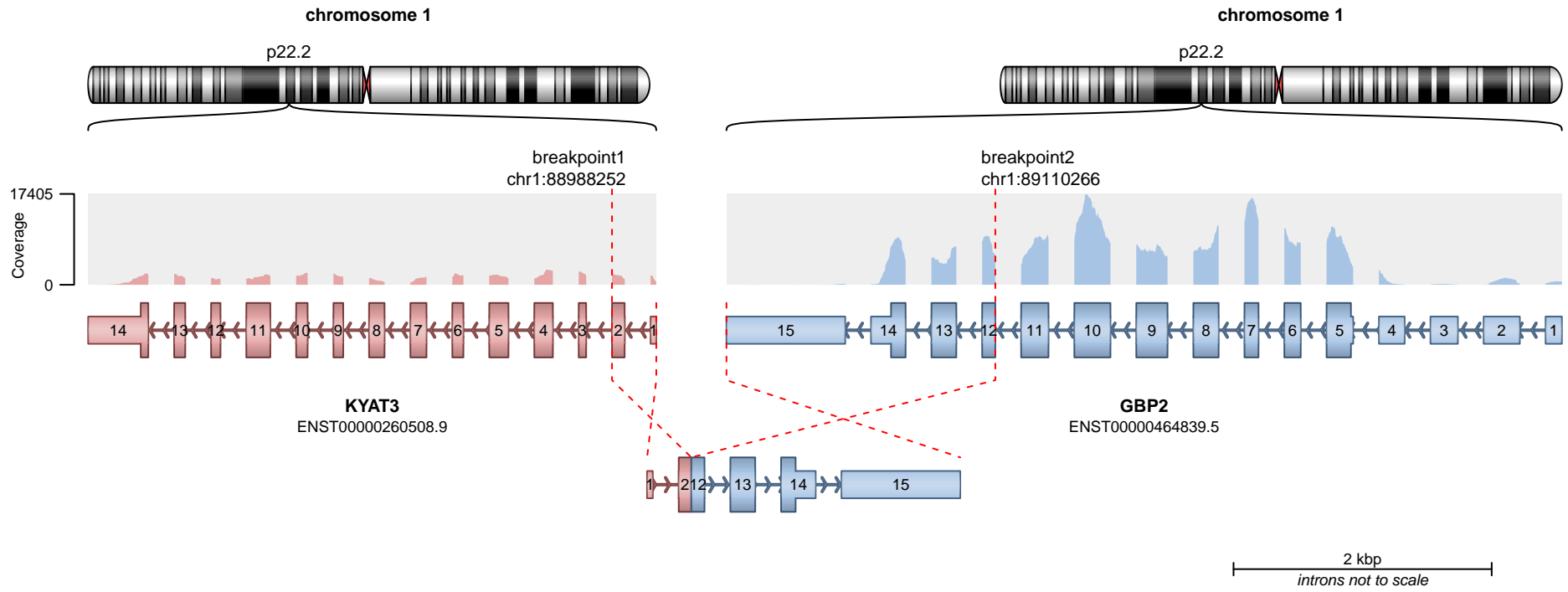
— translocation — deletion
 — duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 0



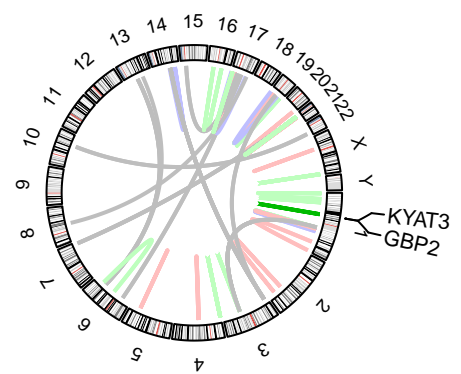
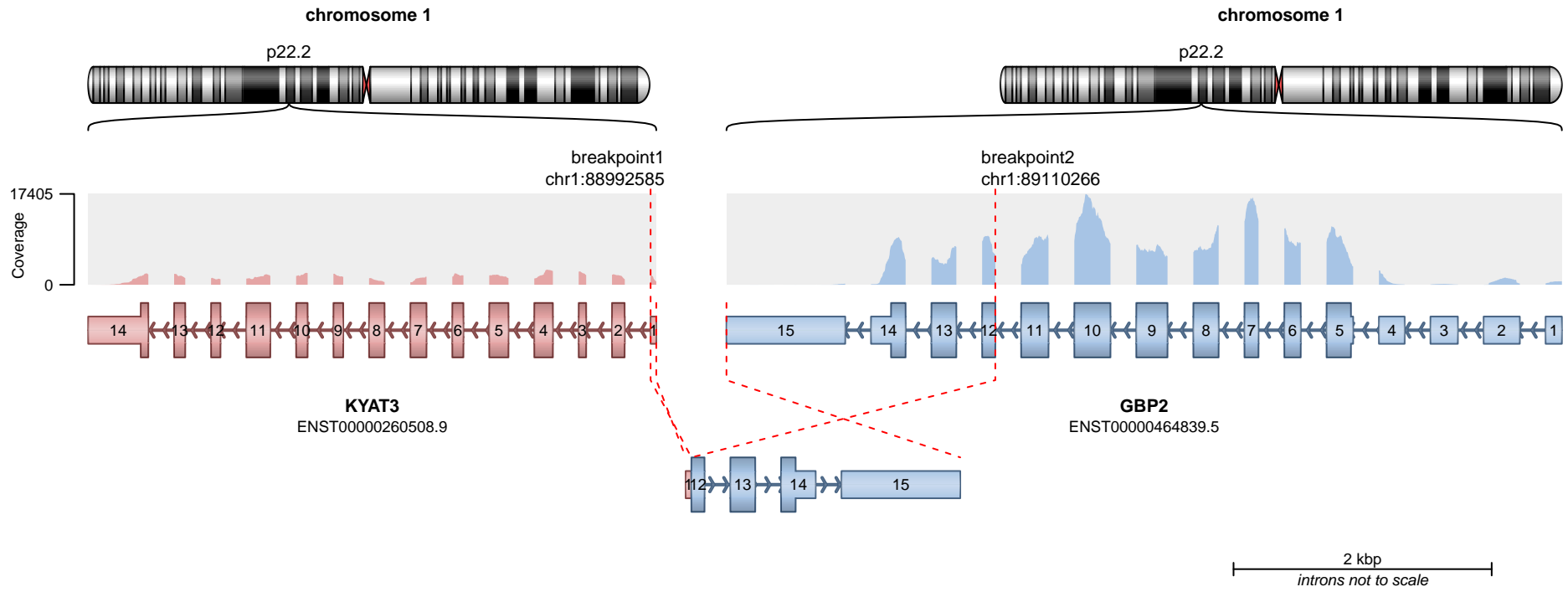
RETAINED PROTEIN DOMAINS
reading frame unclear



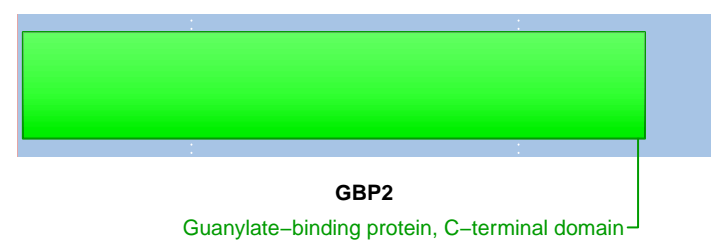
SUPPORTING READ COUNT

Split reads = 180
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



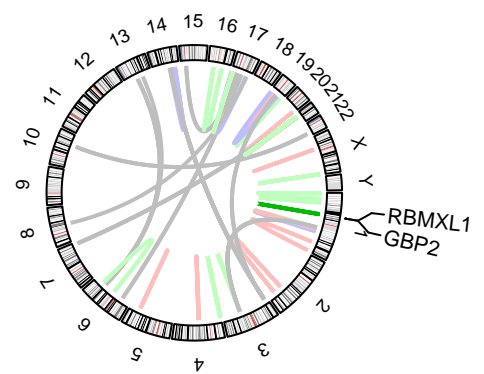
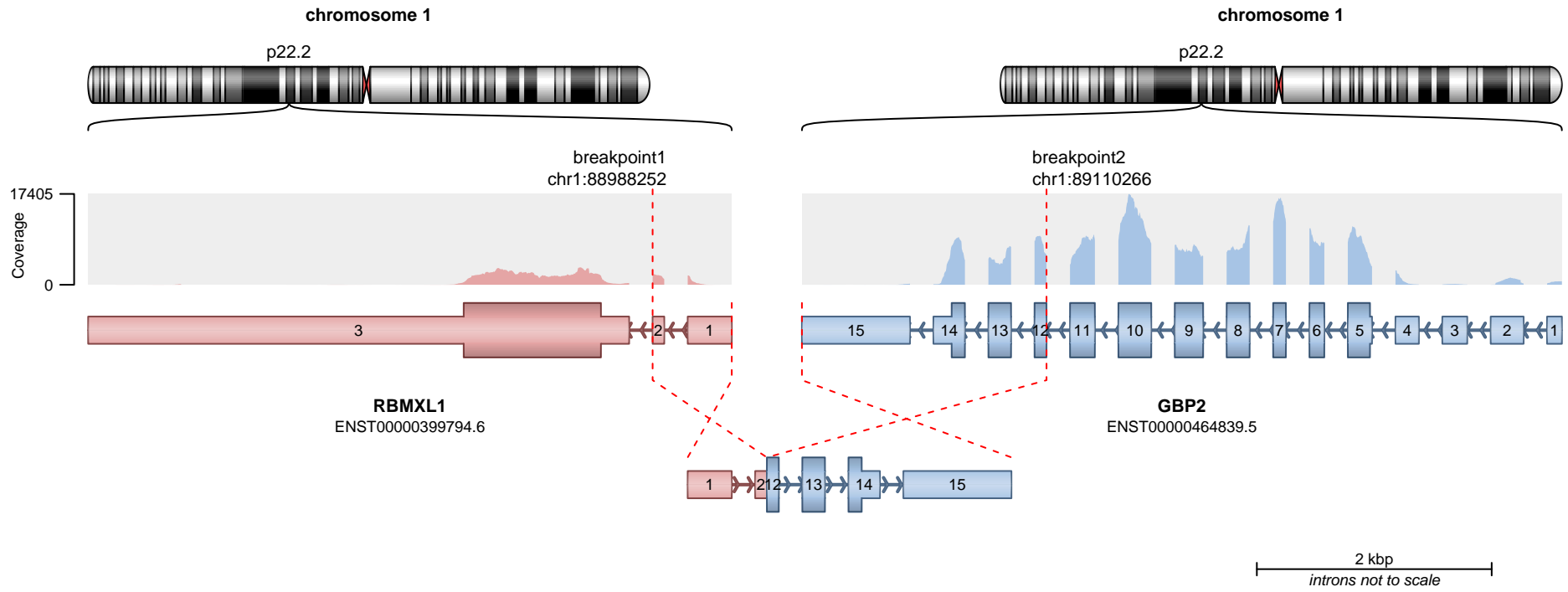
RETAINED PROTEIN DOMAINS
reading frame unclear



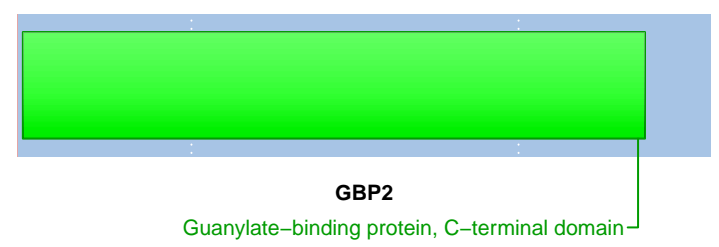
SUPPORTING READ COUNT

Split reads = 18
Discordant mates = 0

— translocation — deletion
— duplication — inversion



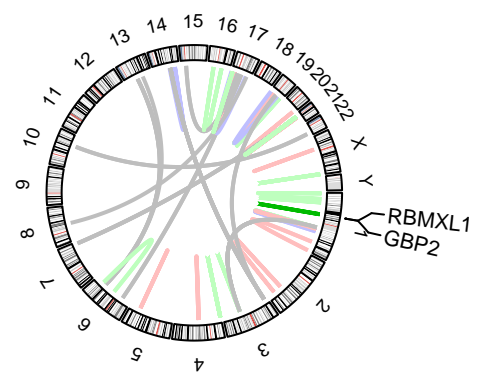
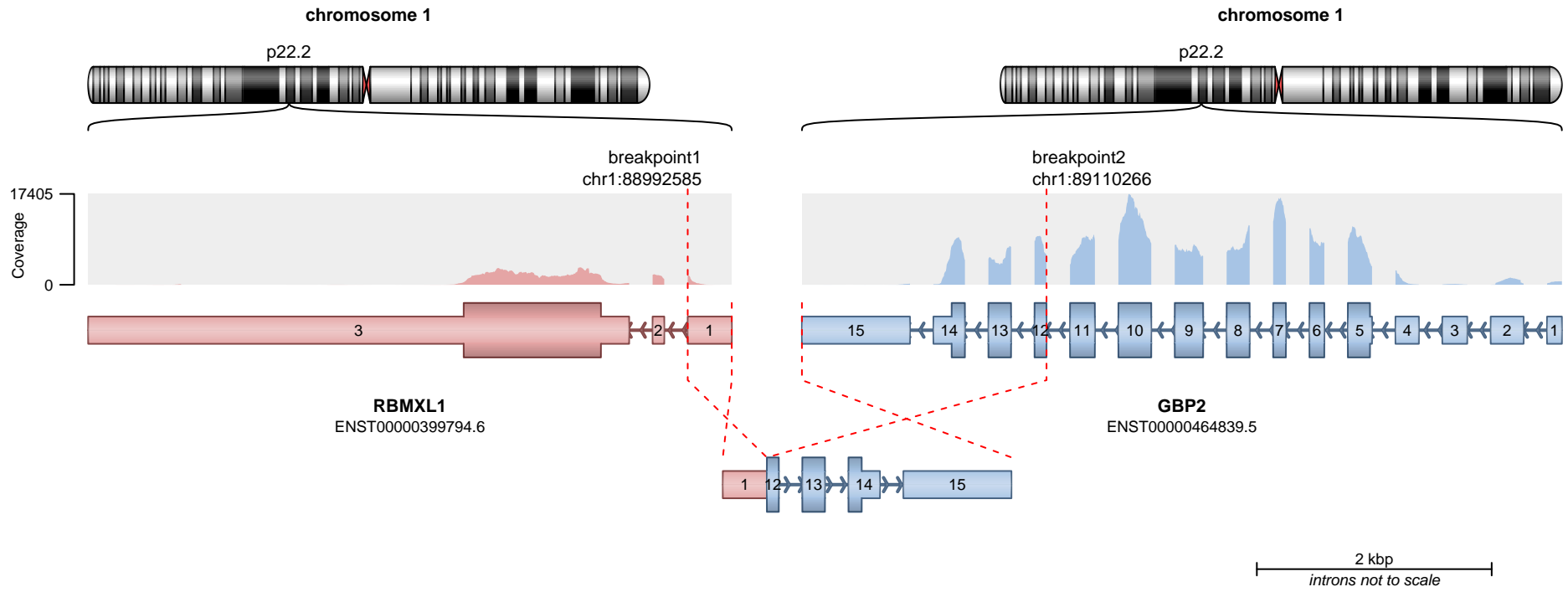
RETAINED PROTEIN DOMAINS
reading frame unclear



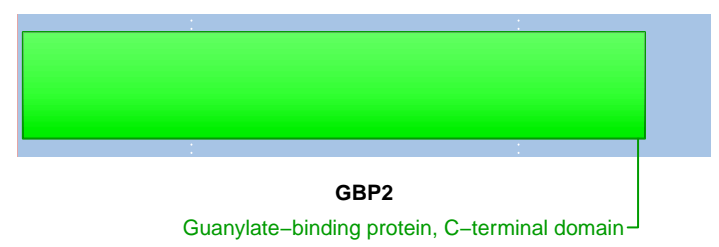
SUPPORTING READ COUNT

Split reads = 180
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



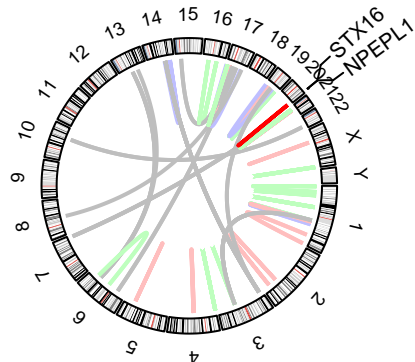
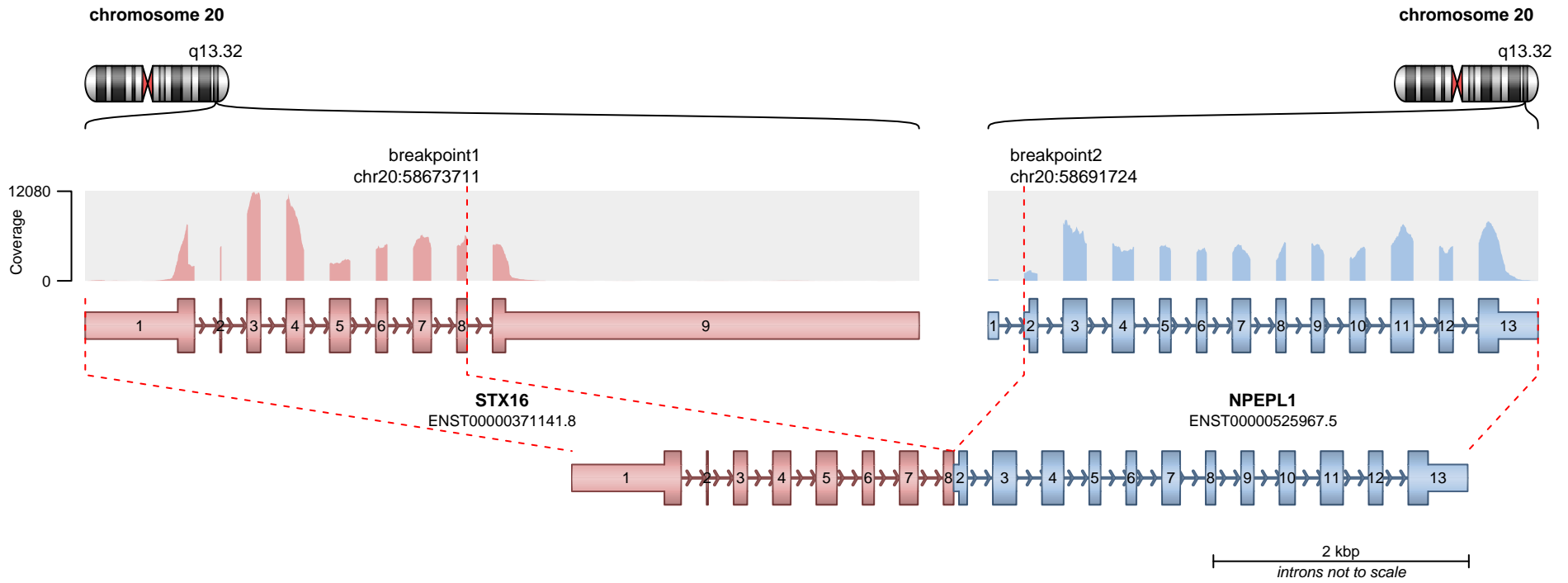
RETAINED PROTEIN DOMAINS
reading frame unclear



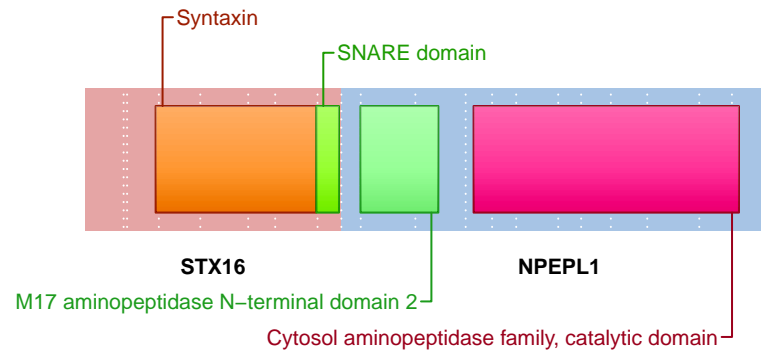
SUPPORTING READ COUNT

Split reads = 18
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



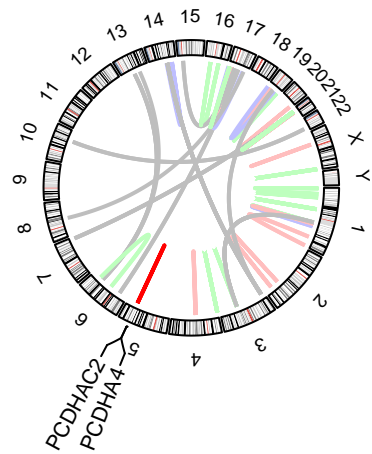
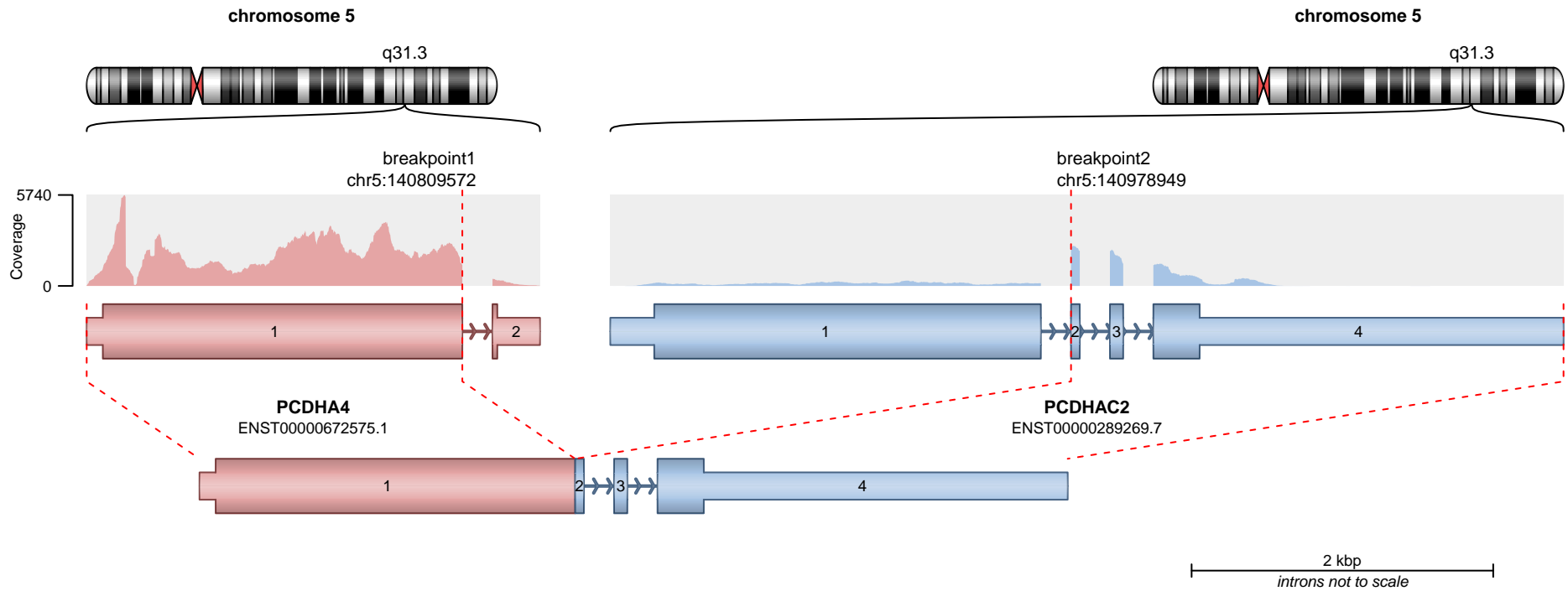
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

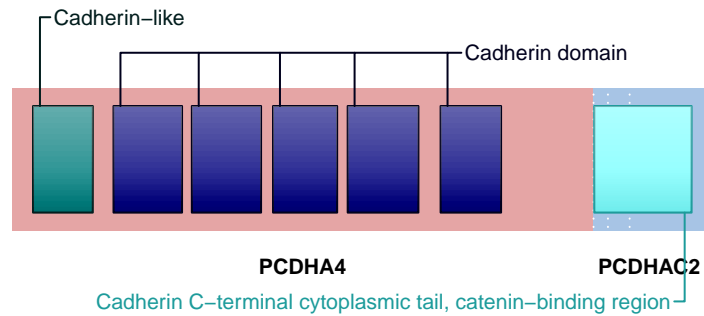
Split reads = 164
Discordant mates = 7

- translocation
- duplication
- deletion
- inversion



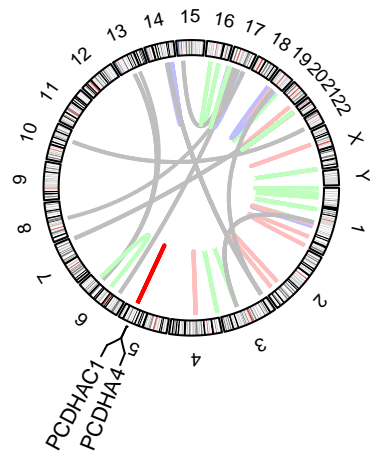
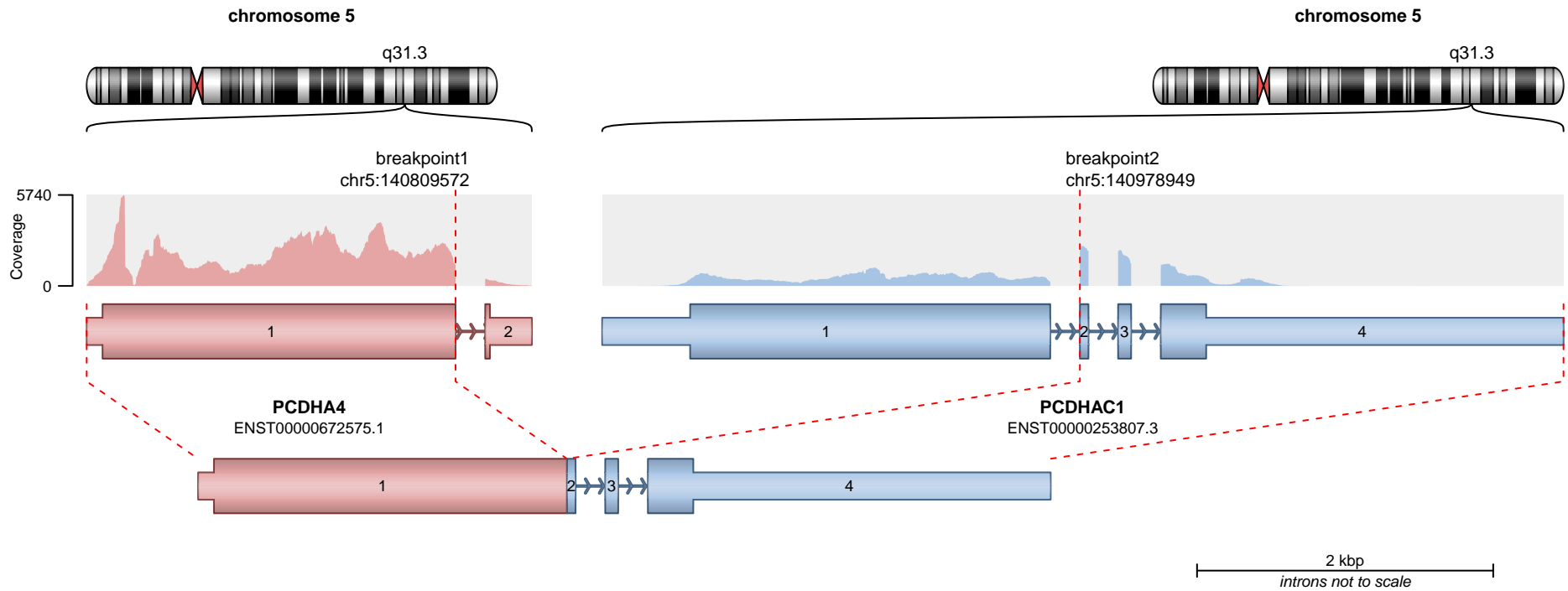
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear

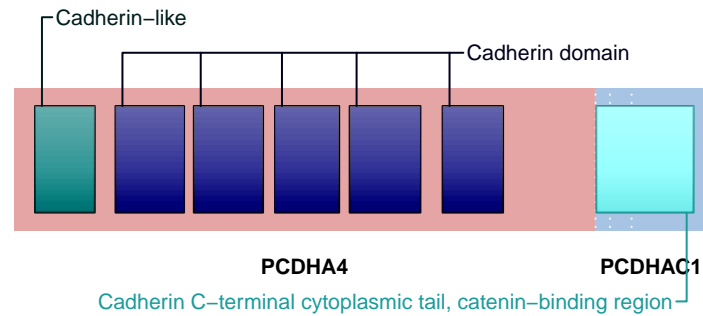


SUPPORTING READ COUNT

Split reads = 157
Discordant mates = 0



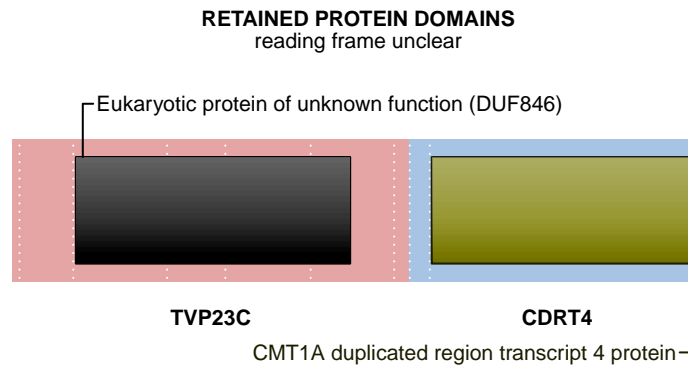
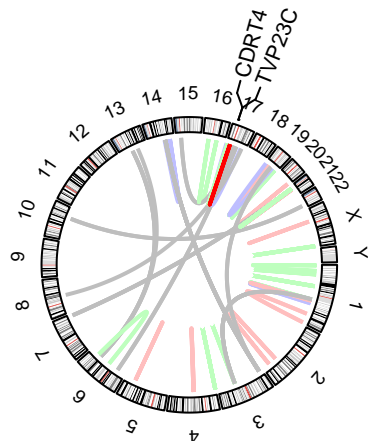
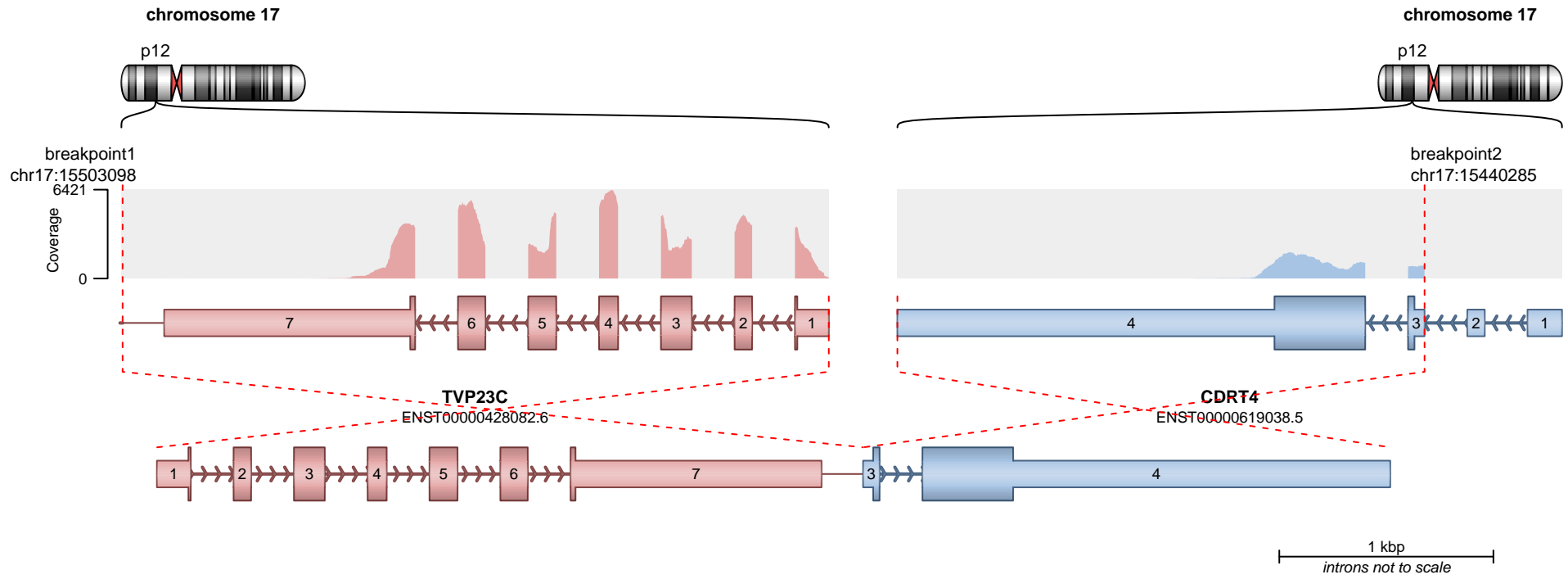
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 156
Discordant mates = 0

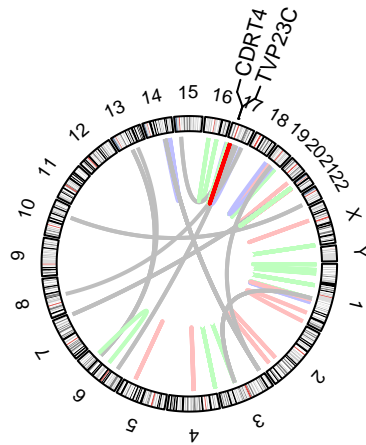
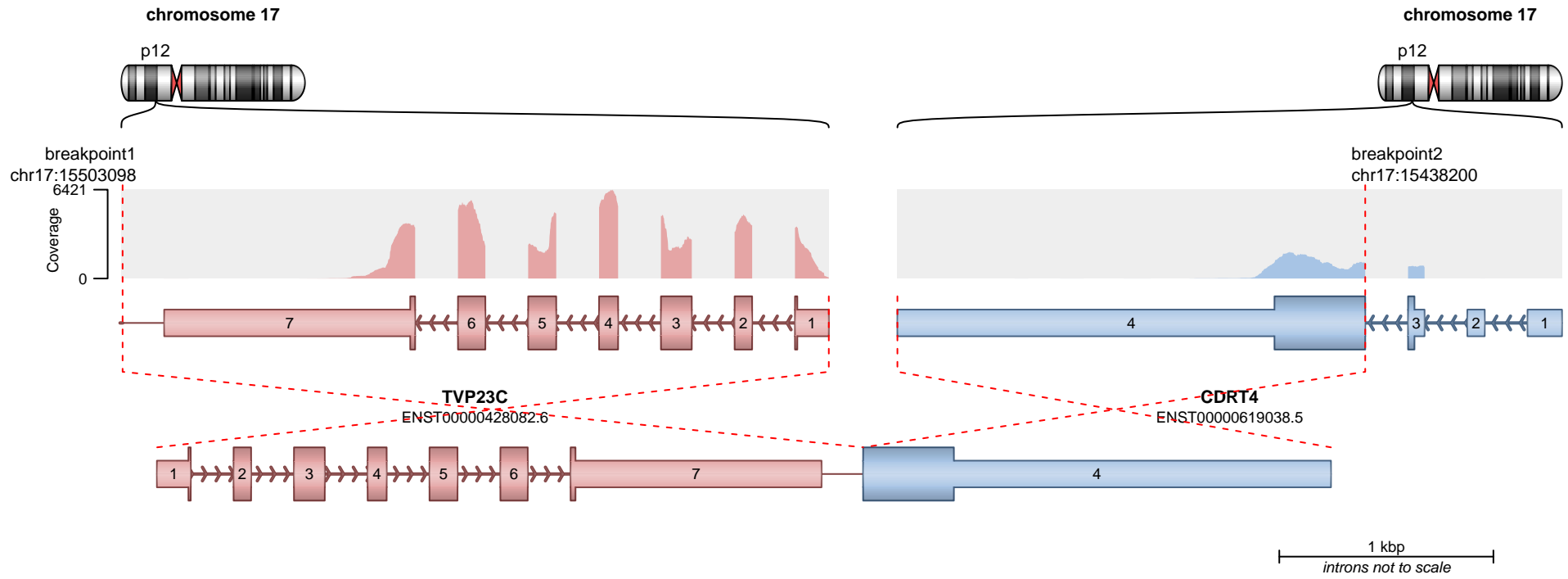
— translocation — deletion
— duplication — inversion



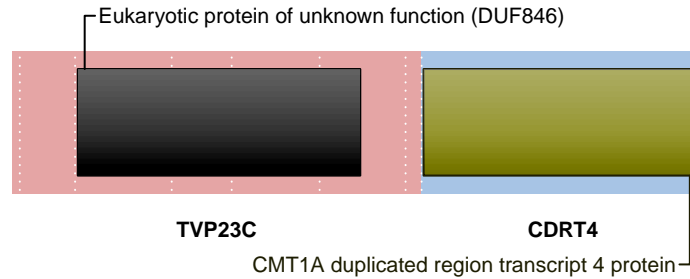
SUPPORTING READ COUNT

Split reads = 133
Discordant mates = 1

— translocation — deletion
— duplication — inversion



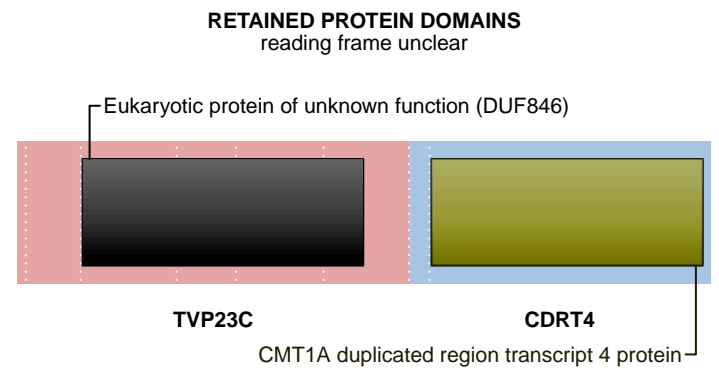
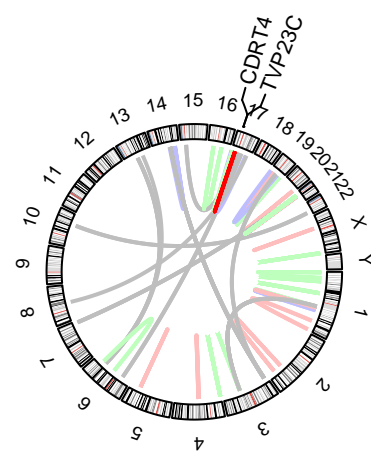
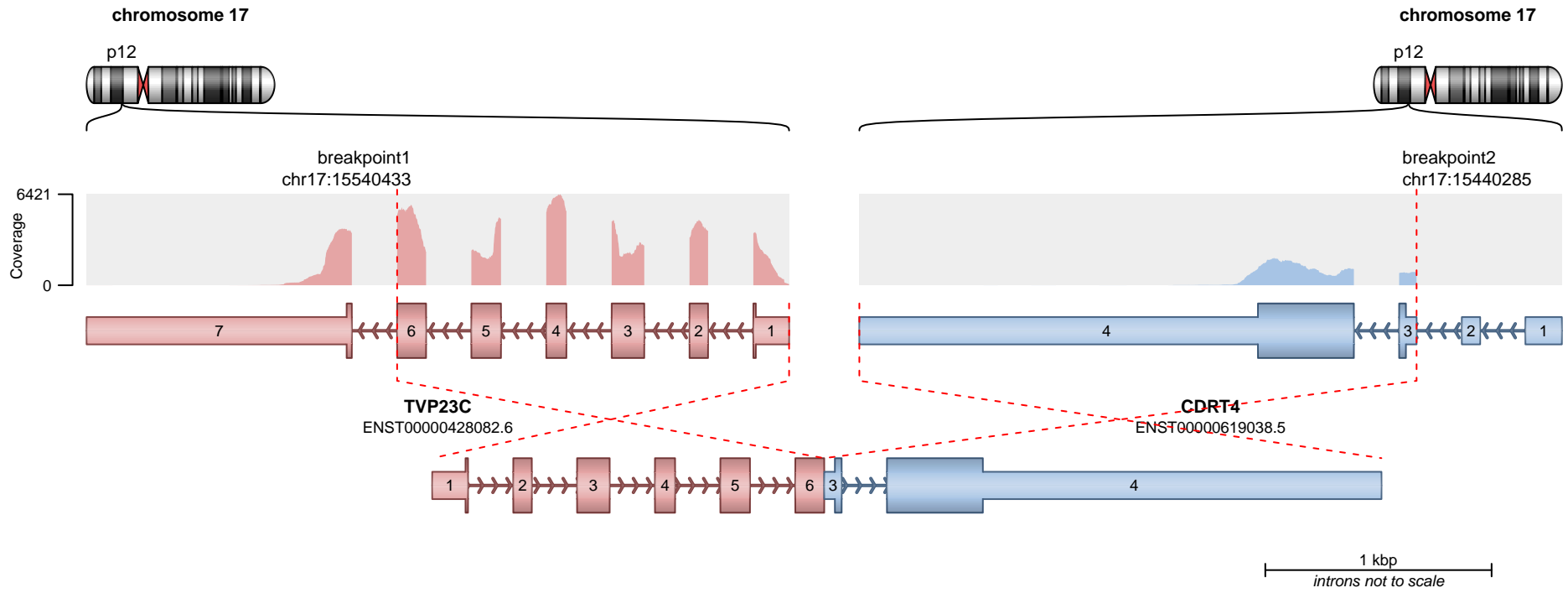
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 56
Discordant mates = 1

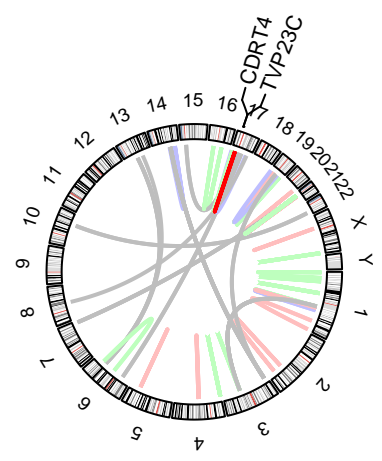
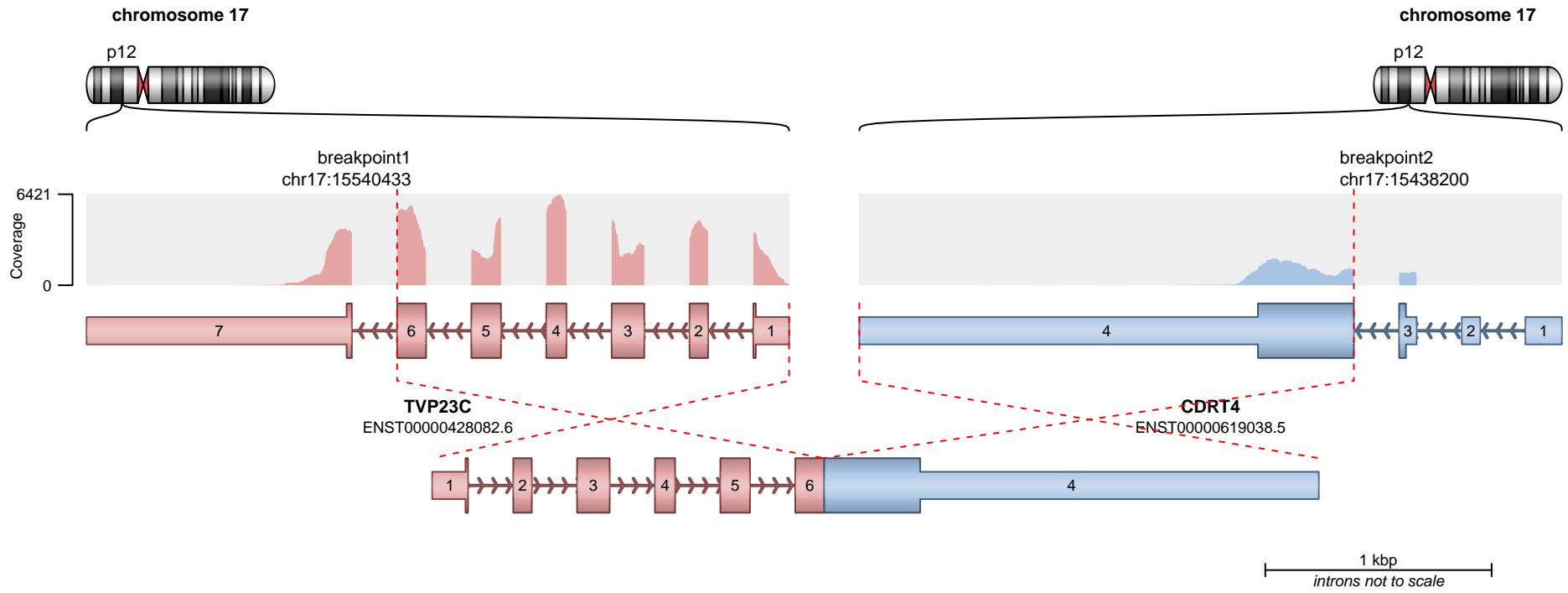
- translocation
- duplication
- deletion
- inversion



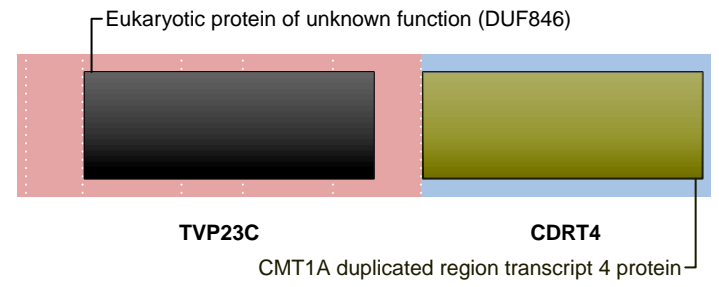
SUPPORTING READ COUNT

Split reads = 36
Discordant mates = 1

— translocation — deletion
— duplication — inversion



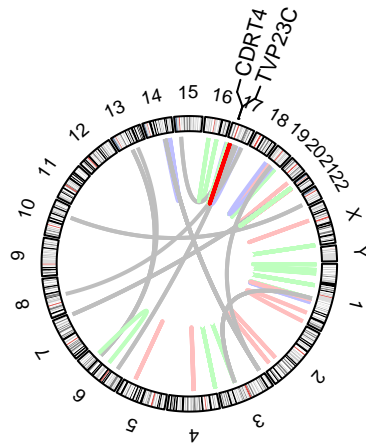
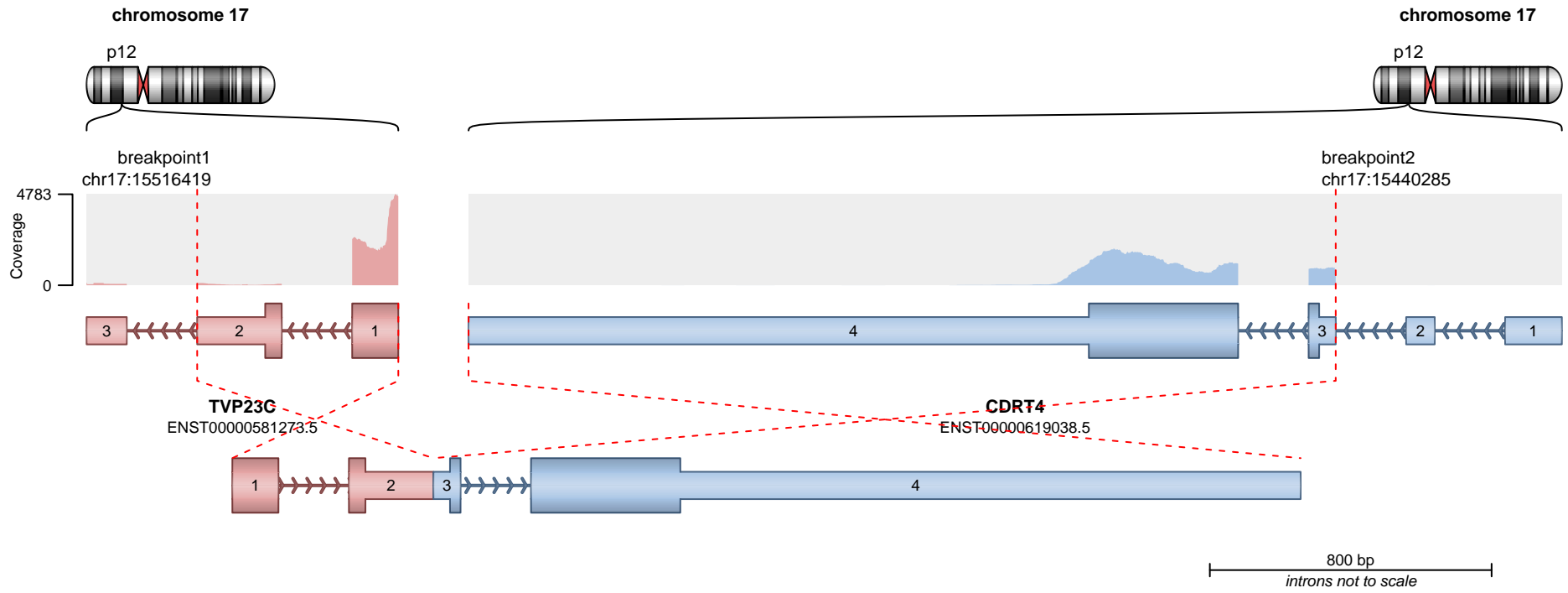
RETAINED PROTEIN DOMAINS
reading frame unclear



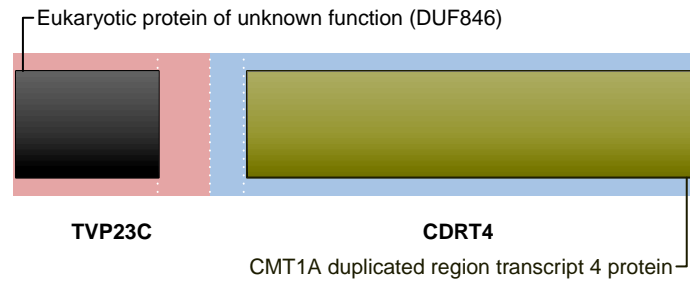
SUPPORTING READ COUNT

Split reads = 14
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



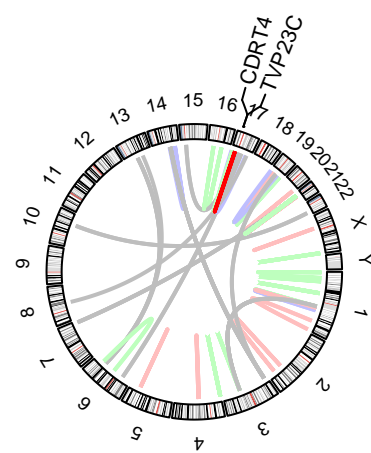
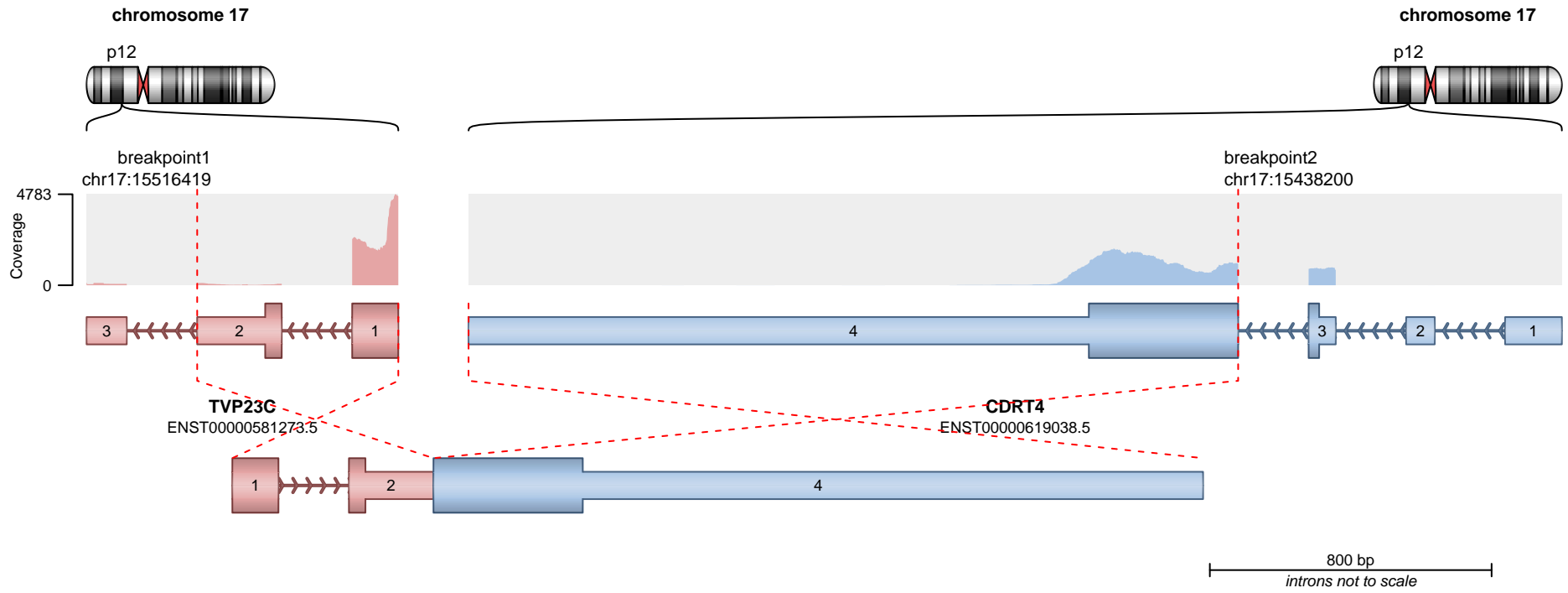
RETAINED PROTEIN DOMAINS
reading frame unclear



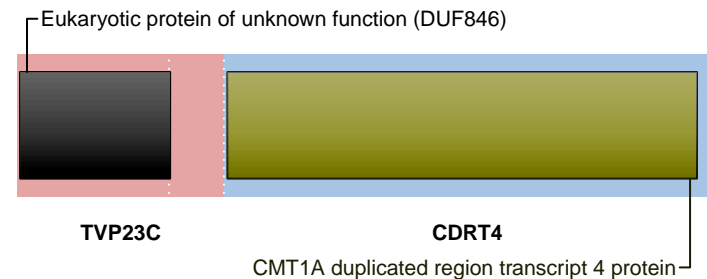
SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



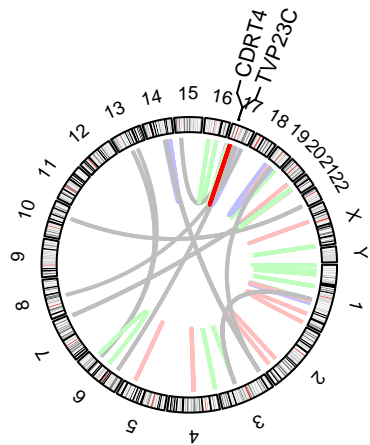
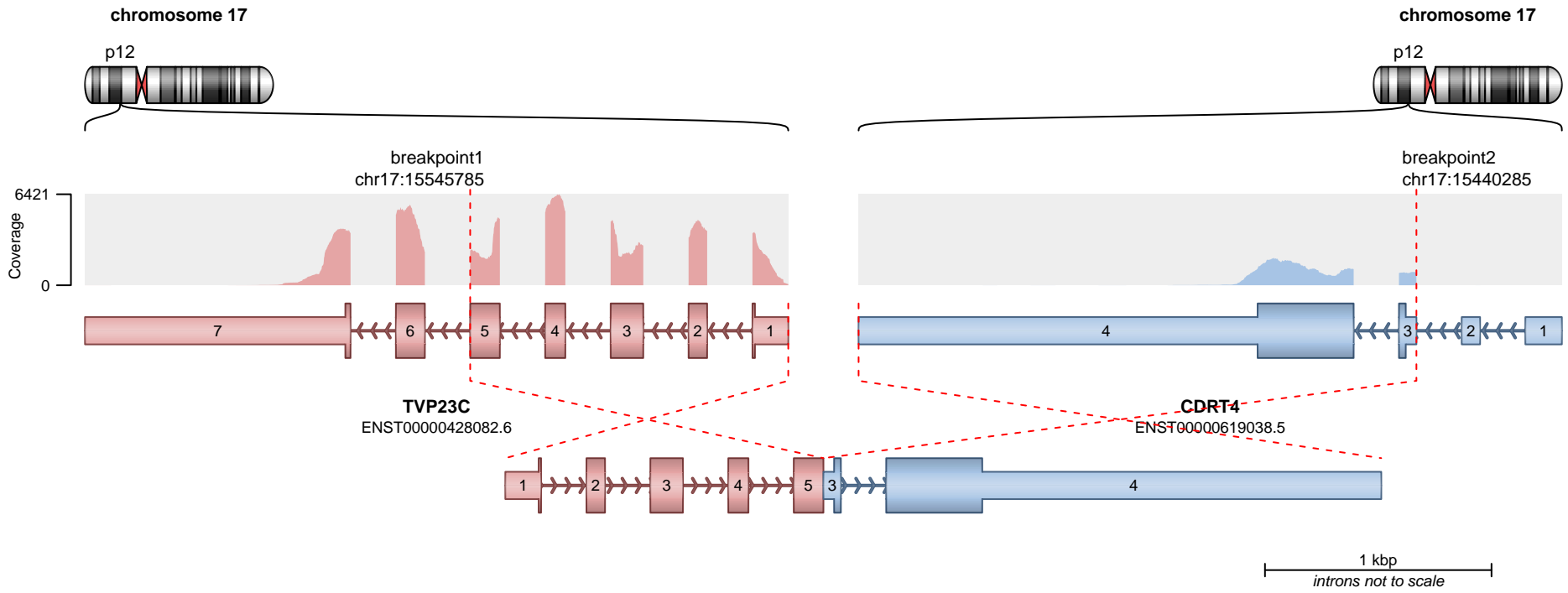
RETAINED PROTEIN DOMAINS
reading frame unclear



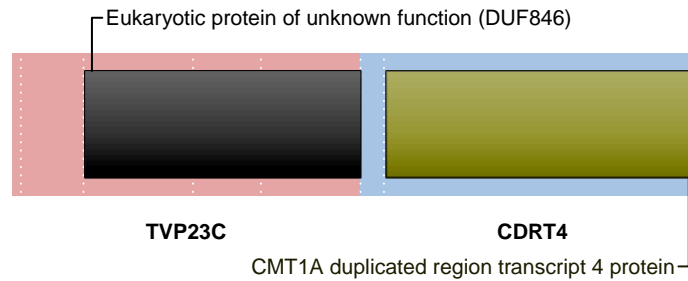
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



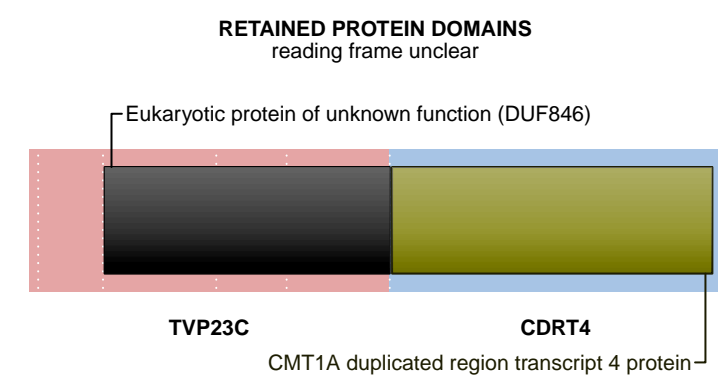
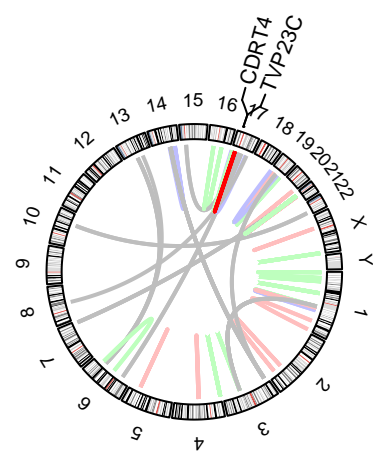
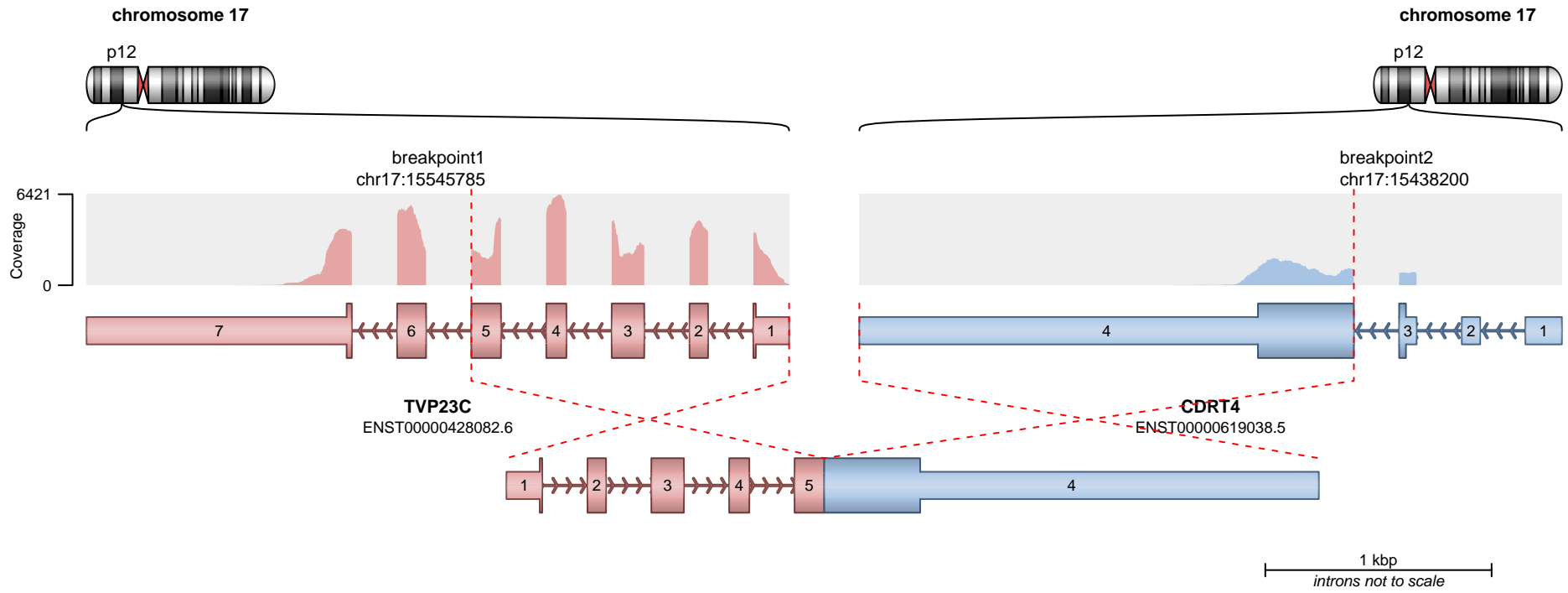
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 1

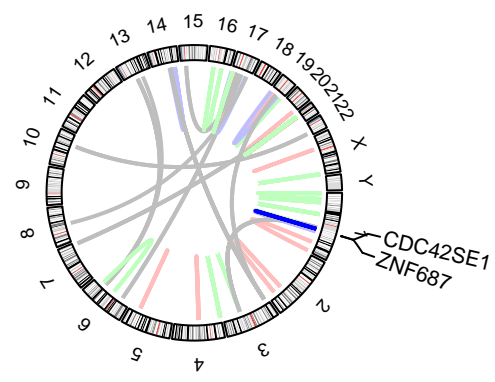
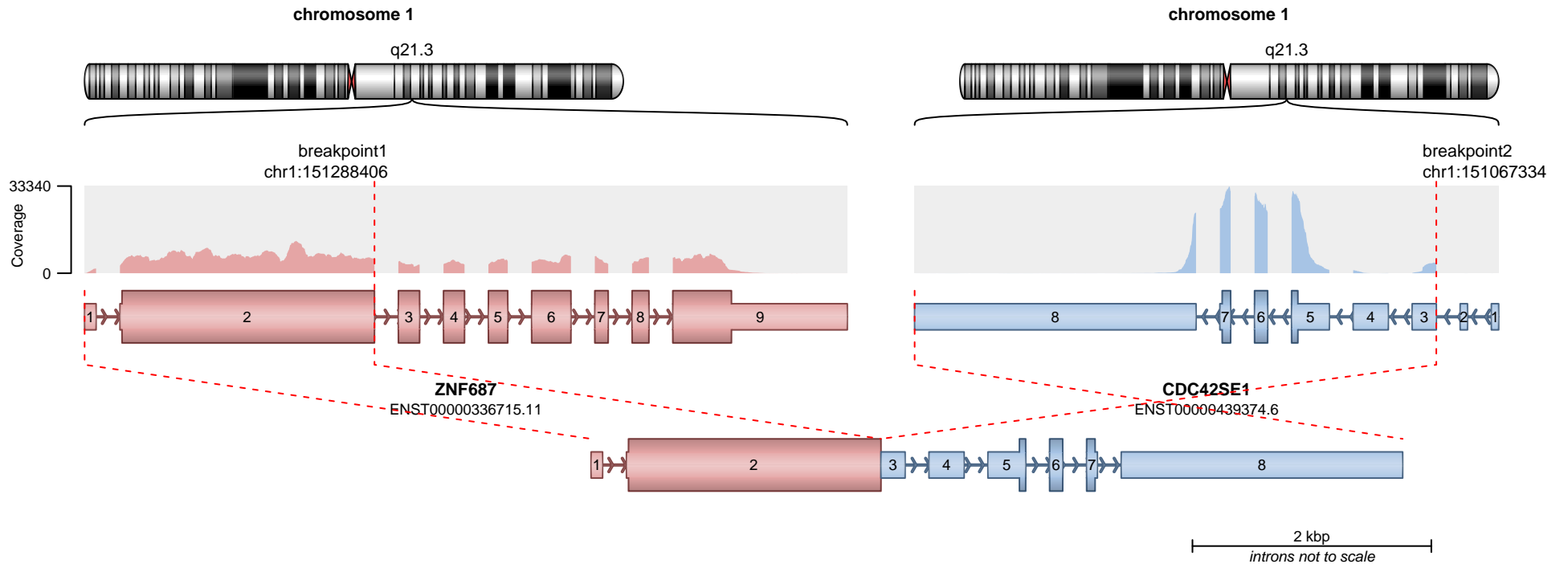
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

— translocation — deletion
— duplication — inversion

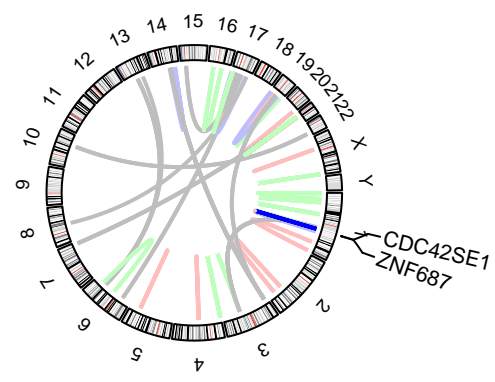
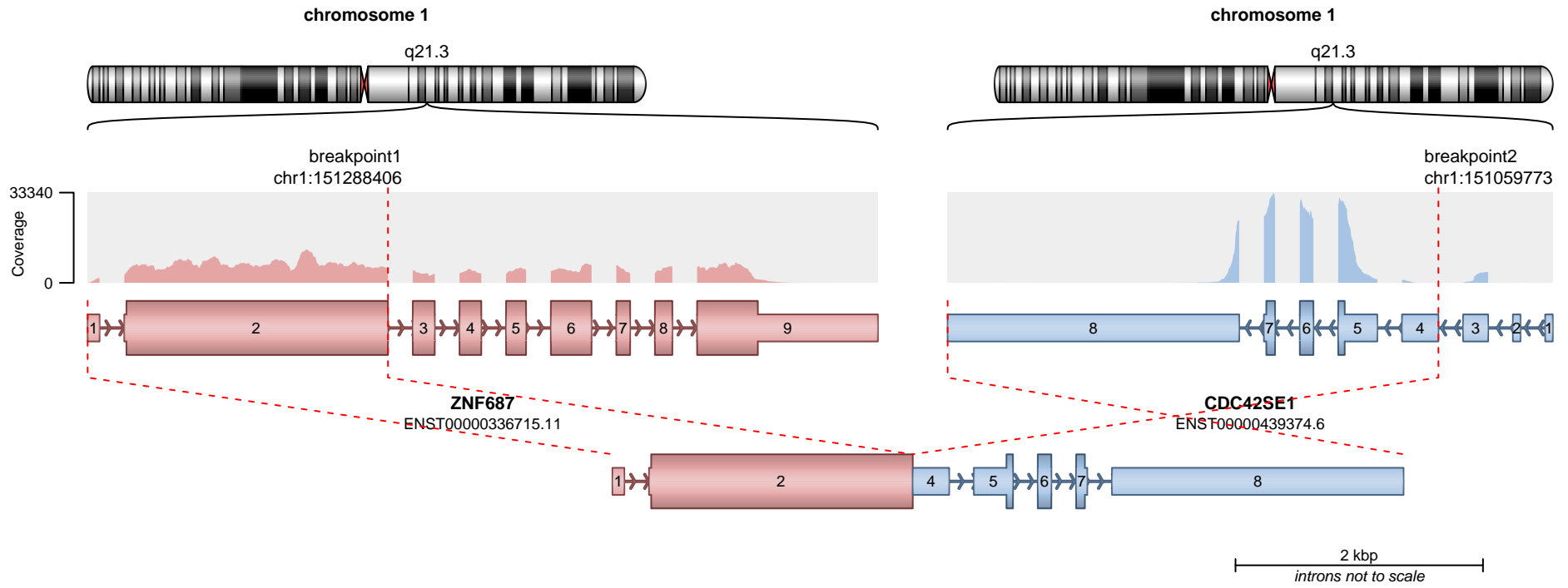


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 121
Discordant mates = 7

- translocation
- duplication
- deletion
- inversion

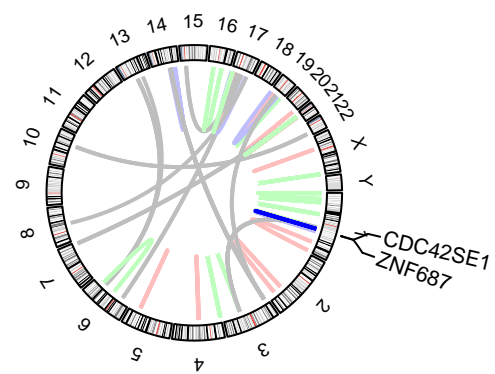
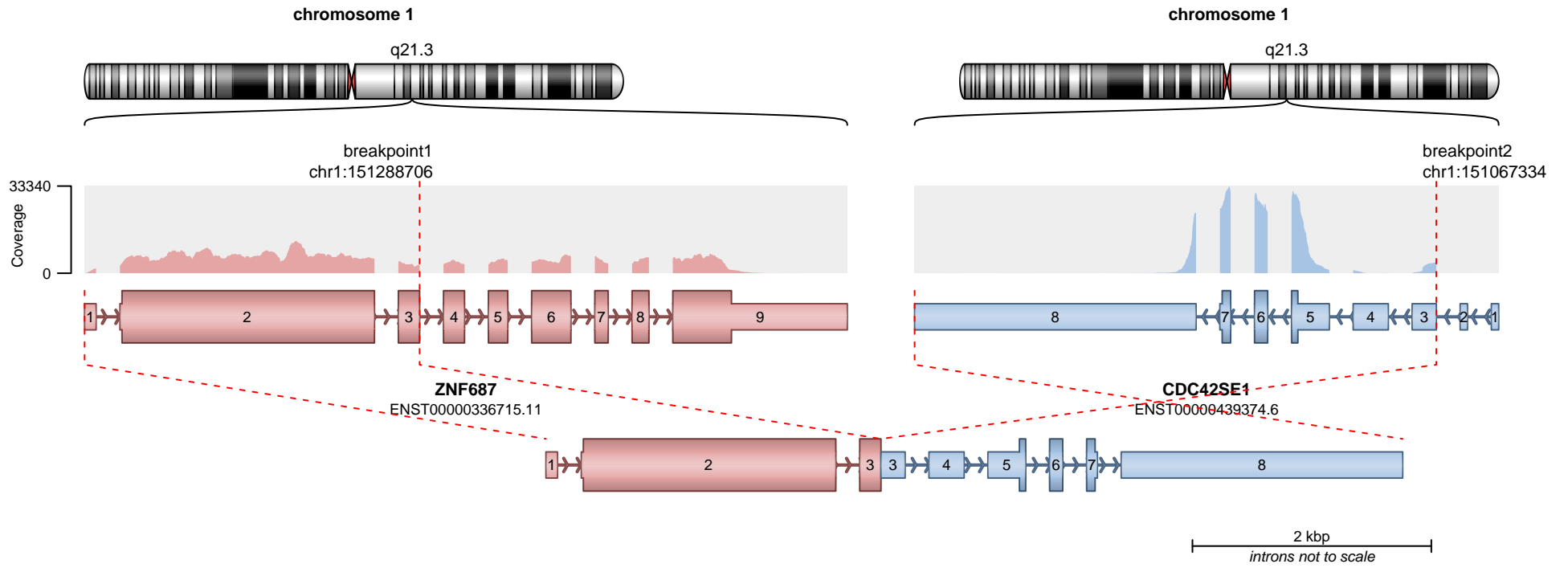


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 24
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion

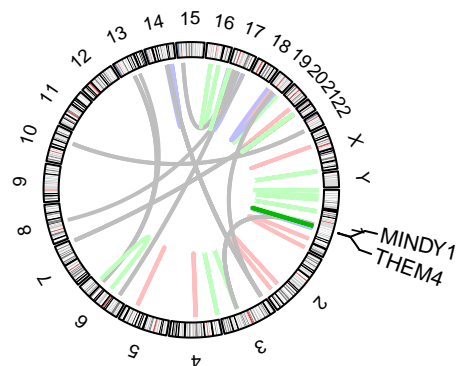
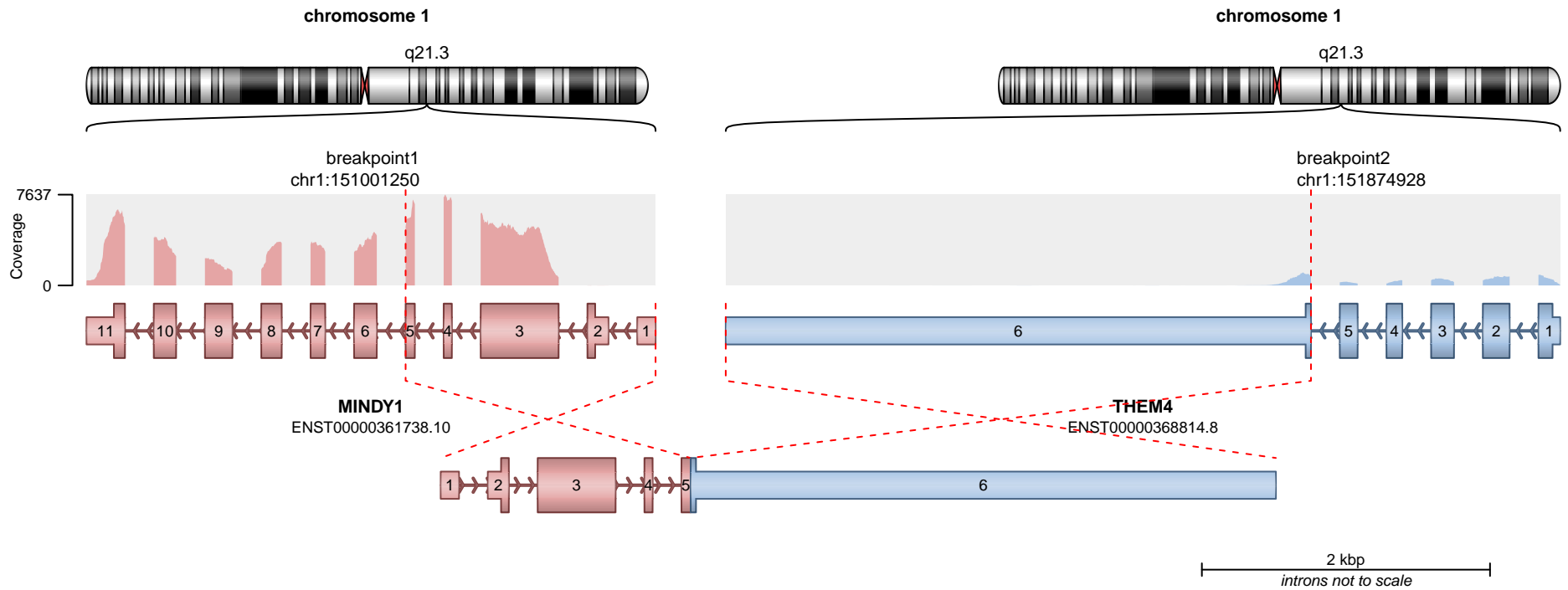


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 8

- translocation
- duplication
- deletion
- inversion



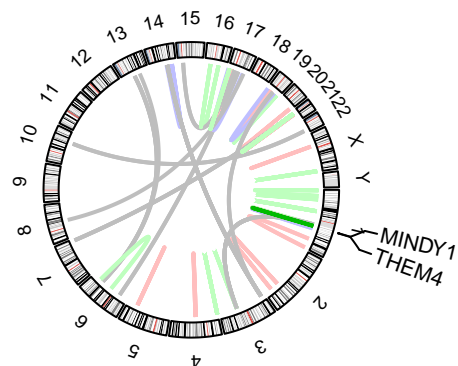
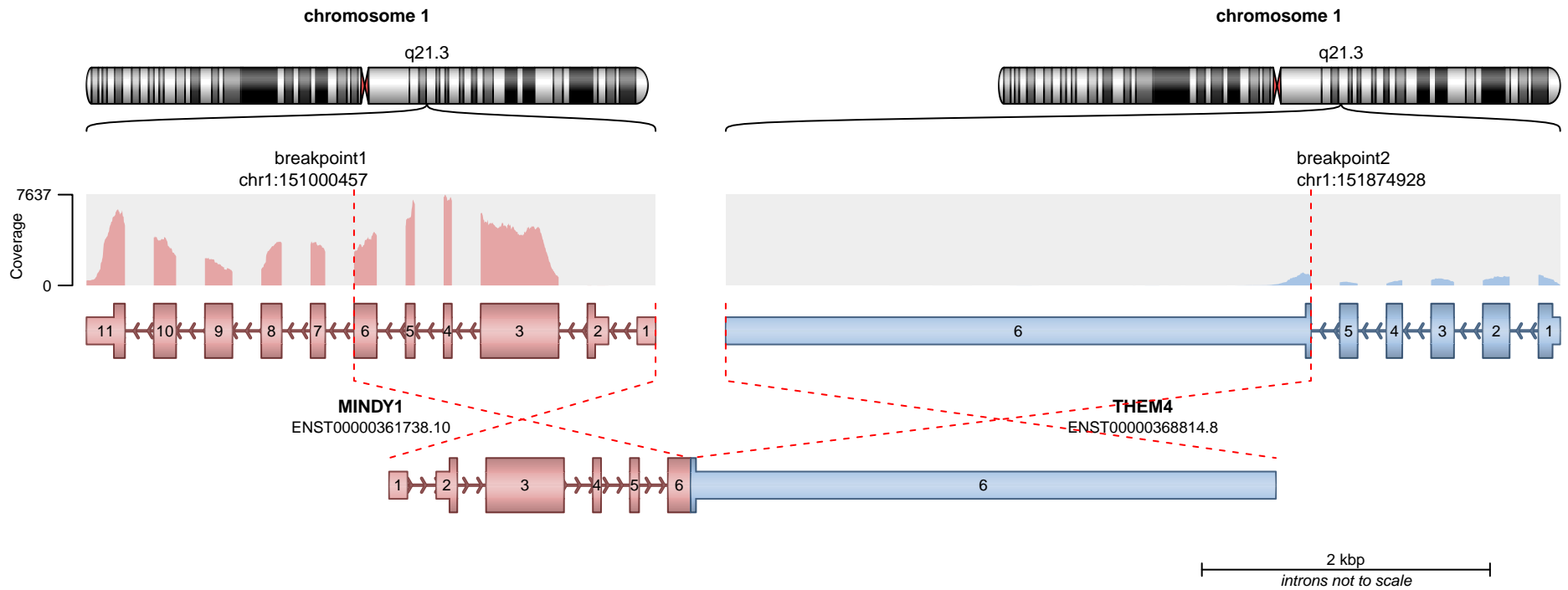
RETAINED PROTEIN DOMAINS
reading frame unclear



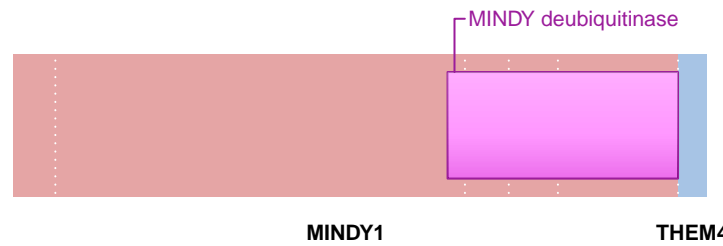
SUPPORTING READ COUNT

Split reads = 112
Discordant mates = 3

— translocation — deletion
— duplication — inversion



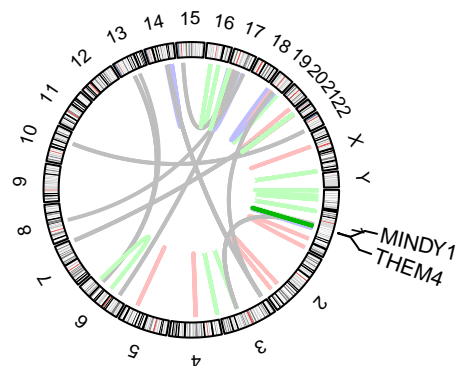
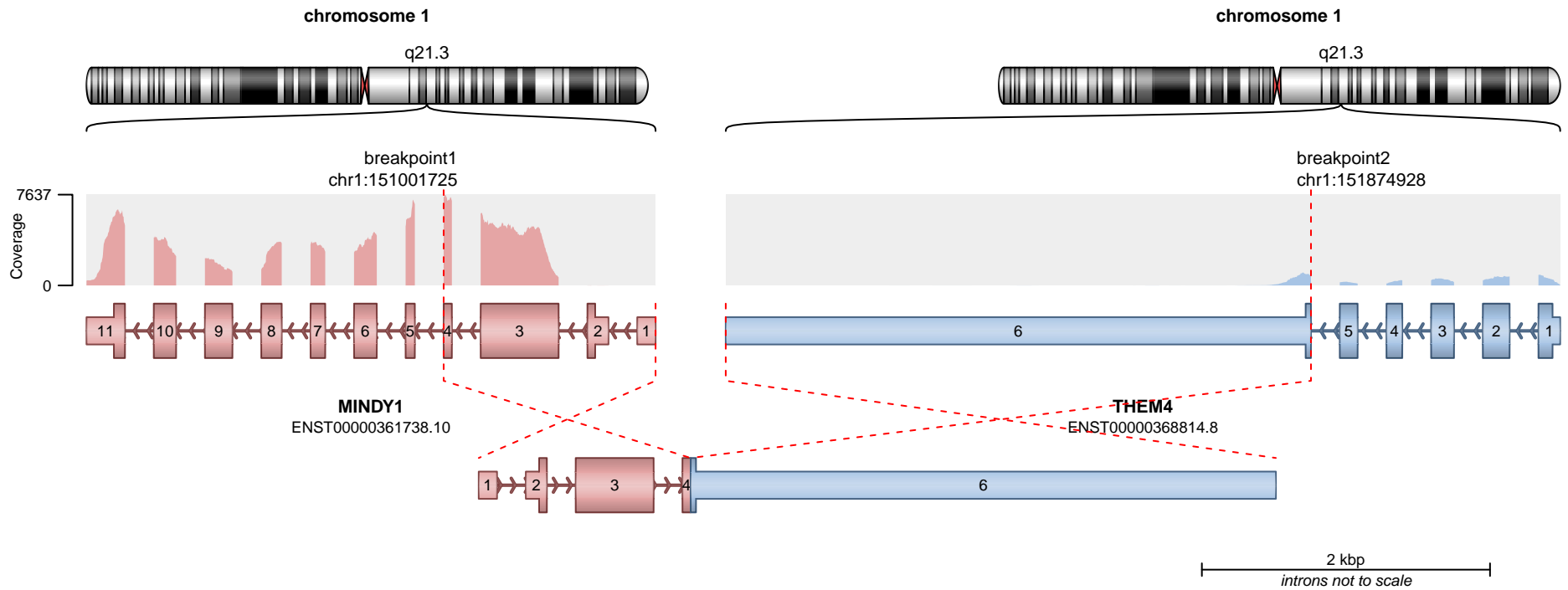
RETAINED PROTEIN DOMAINS
reading frame unclear



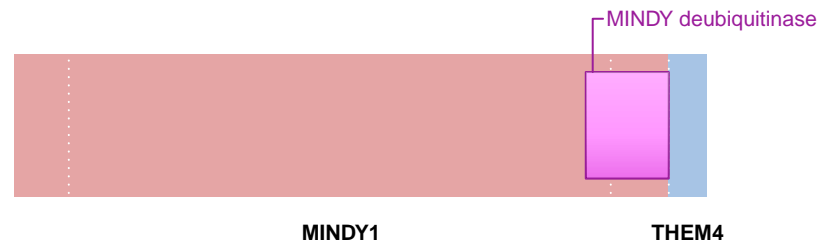
SUPPORTING READ COUNT

Split reads = 101
Discordant mates = 10

- translocation
- duplication
- deletion
- inversion



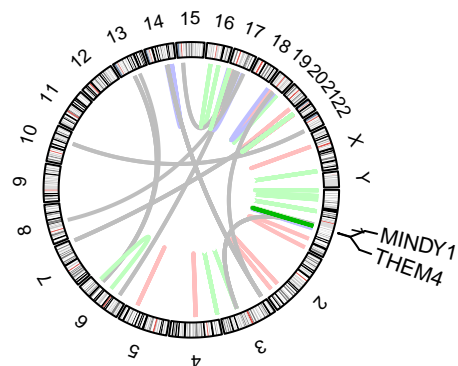
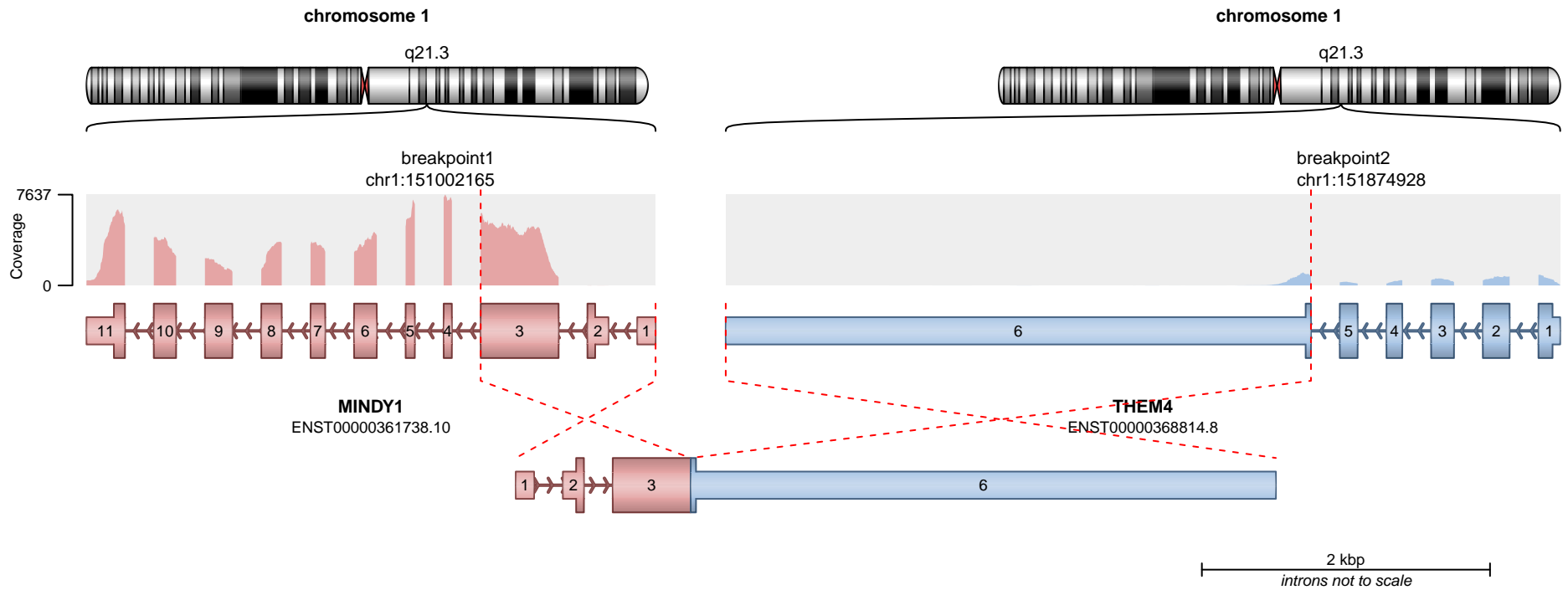
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 34
Discordant mates = 2

— translocation — deletion
— duplication — inversion



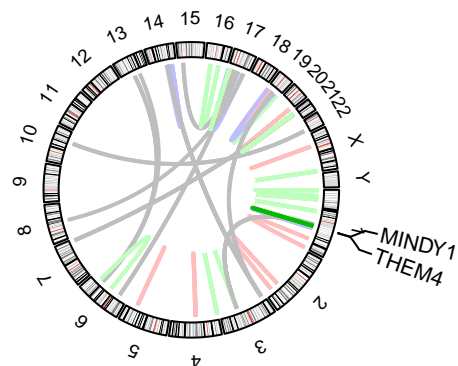
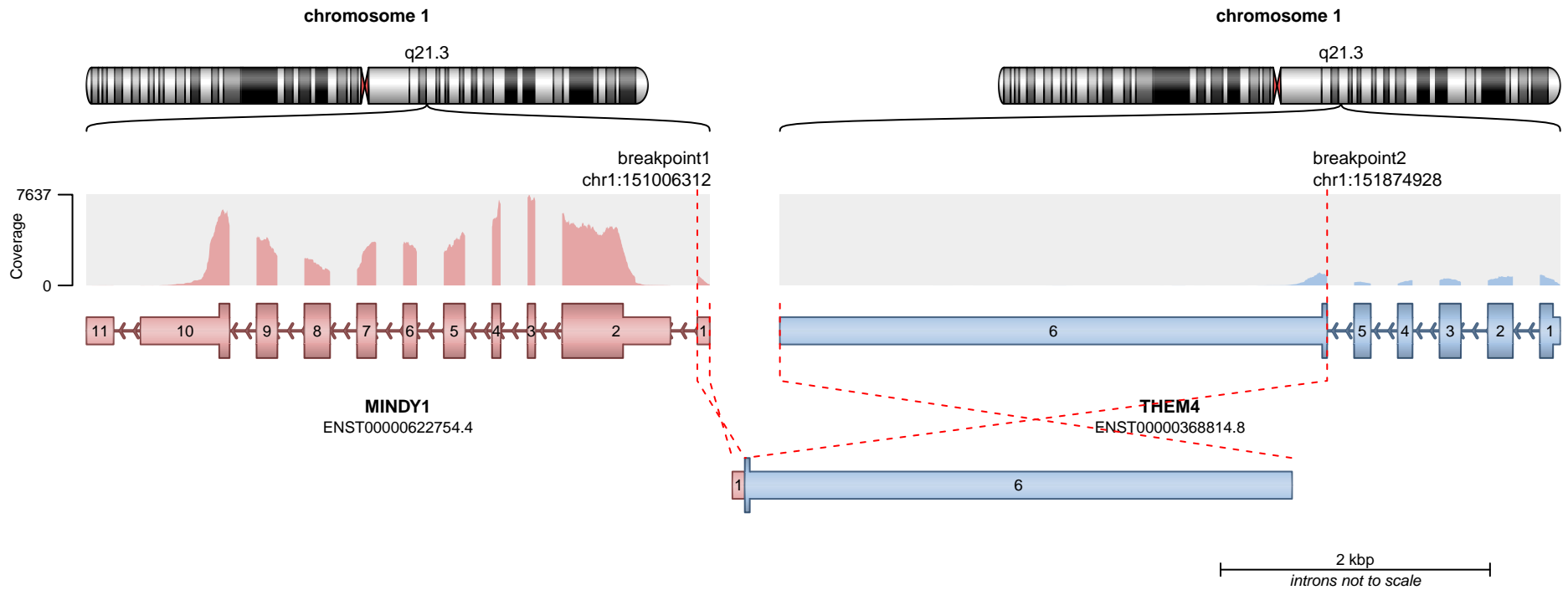
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 0

— translocation — deletion
— duplication — inversion

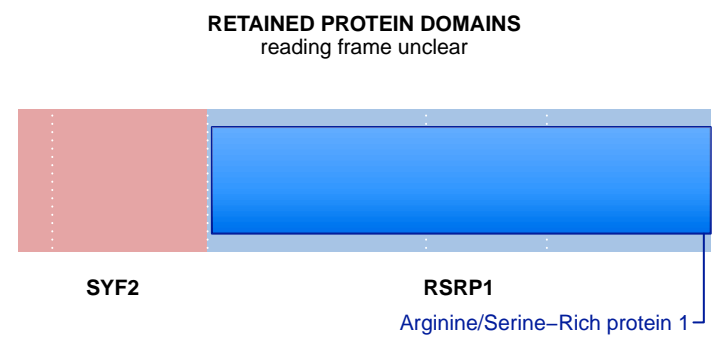
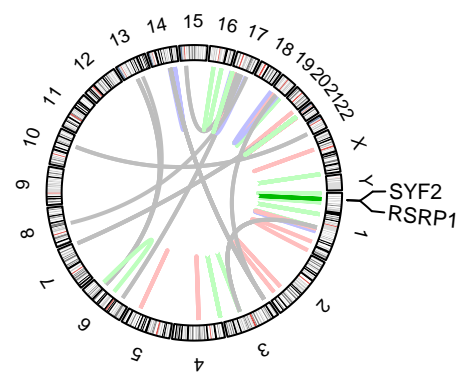
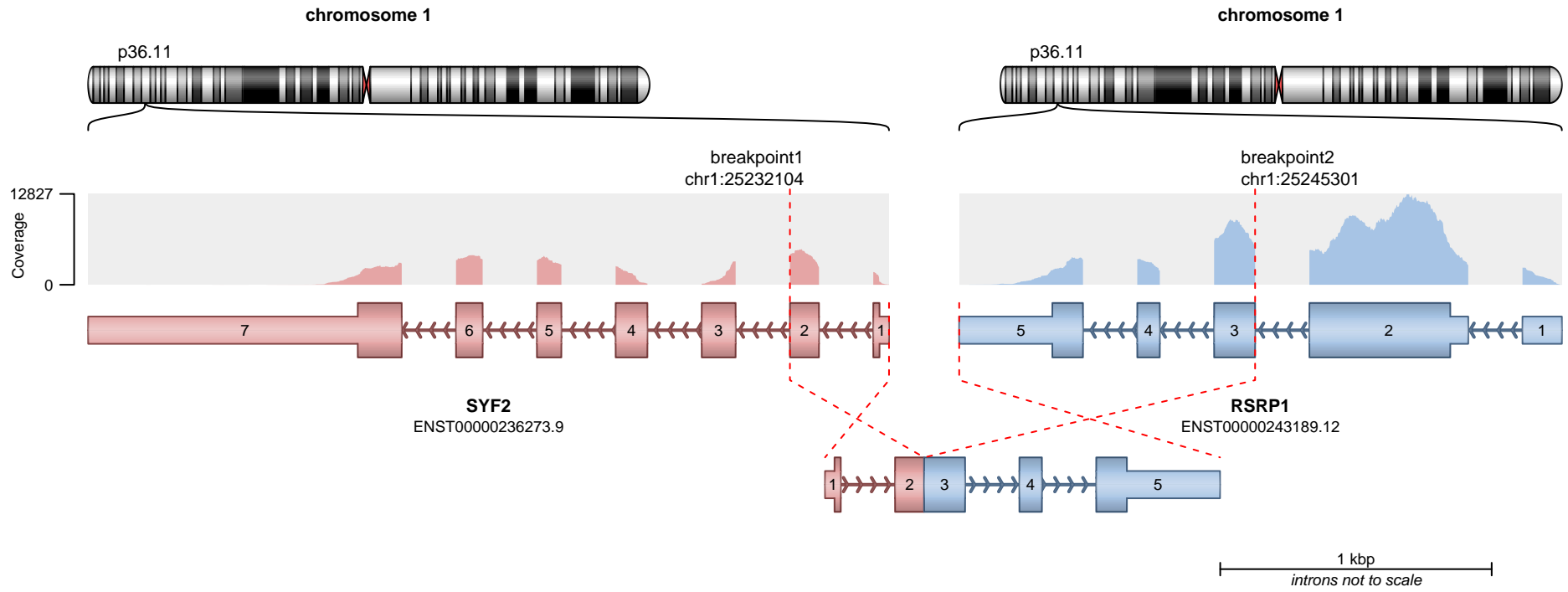


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

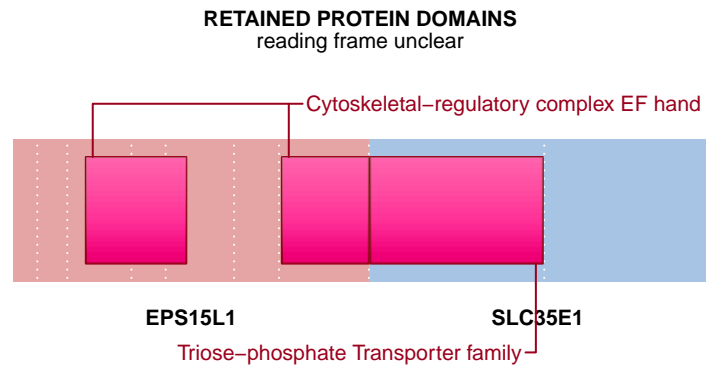
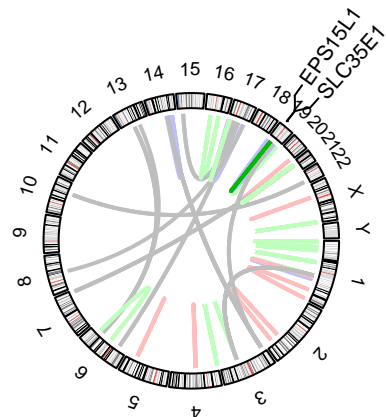
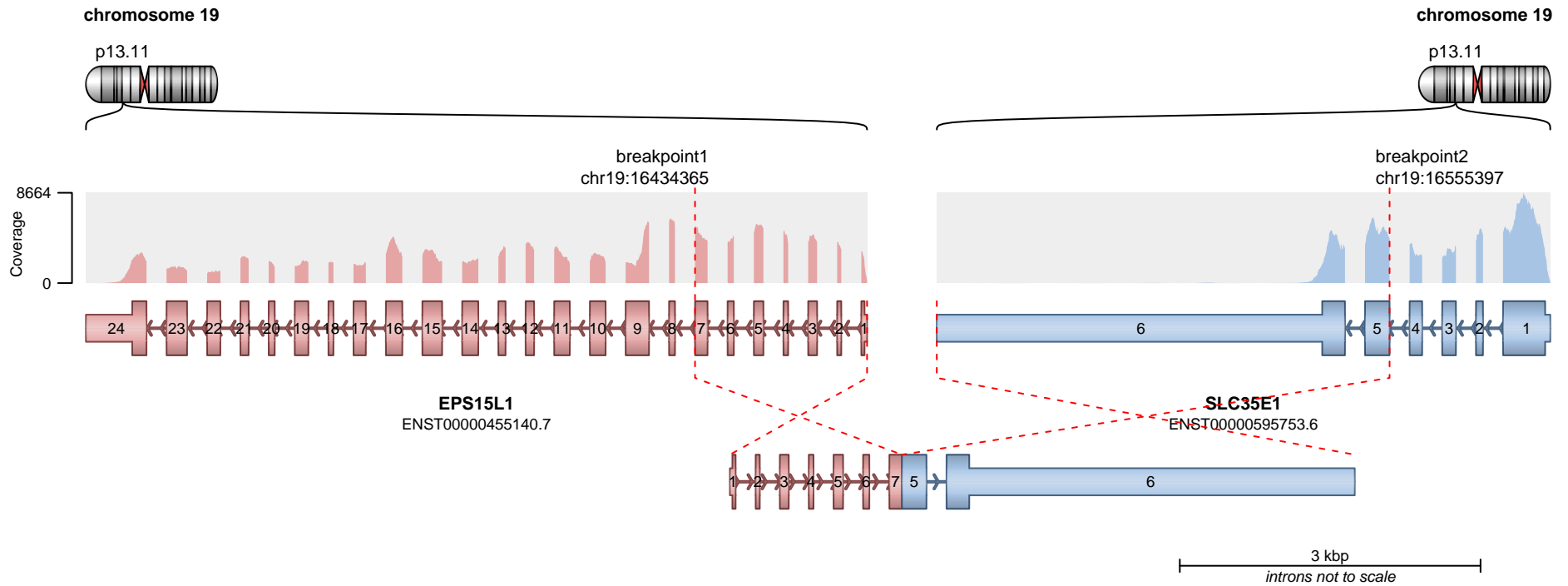
Split reads = 4
Discordant mates = 0



SUPPORTING READ COUNT

Split reads = 100
Discordant mates = 0

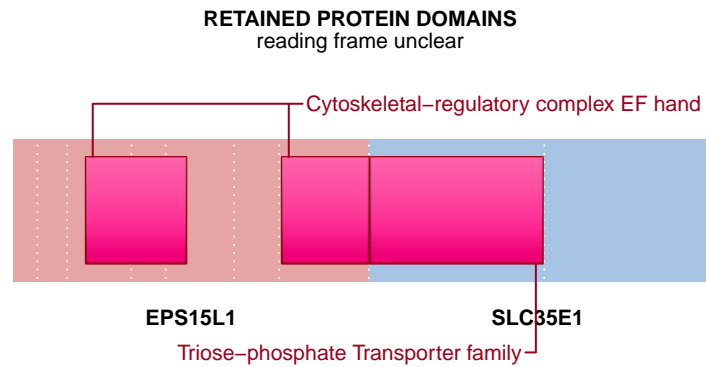
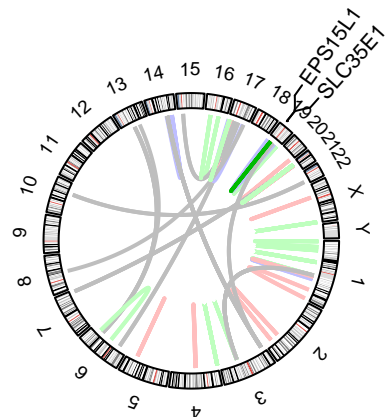
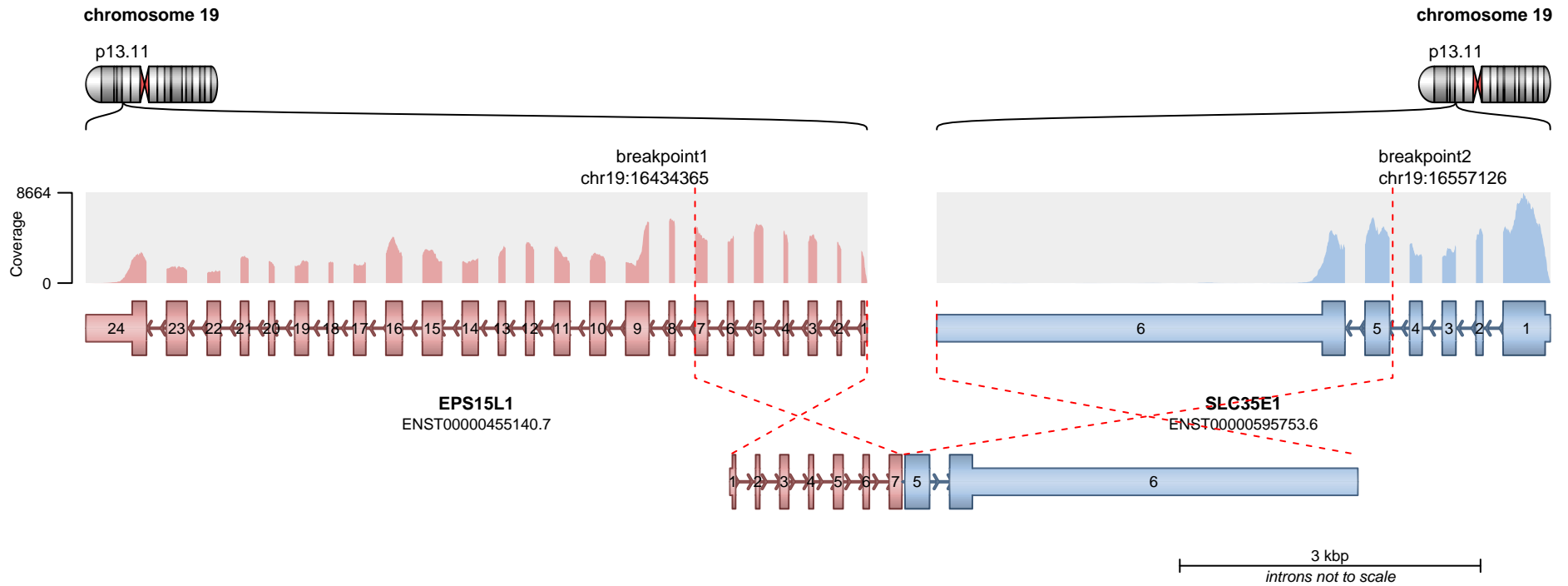
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 95
Discordant mates = 1

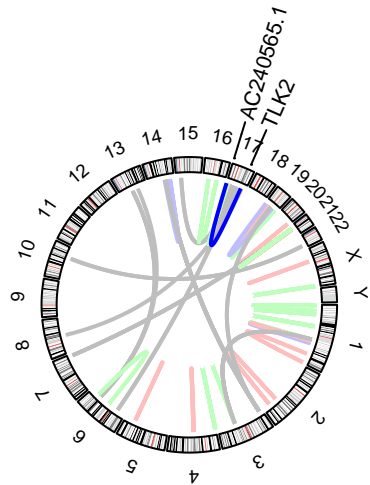
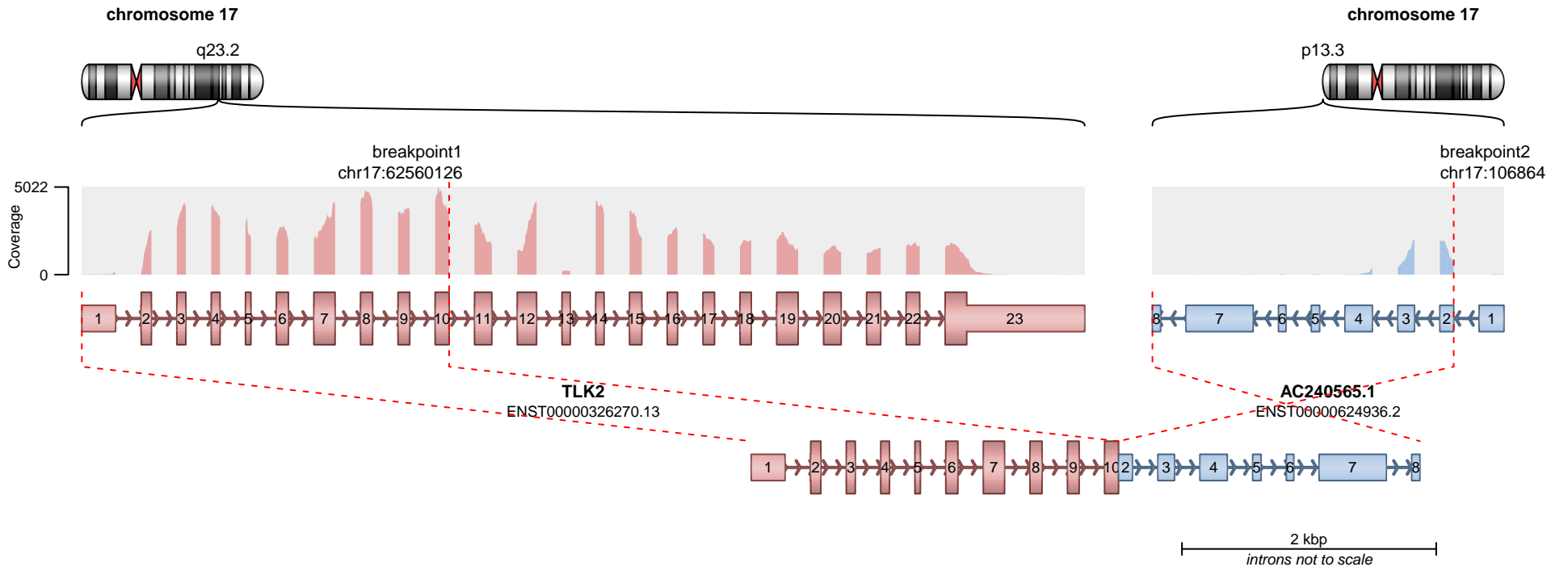
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 1

— translocation — deletion
— duplication — inversion

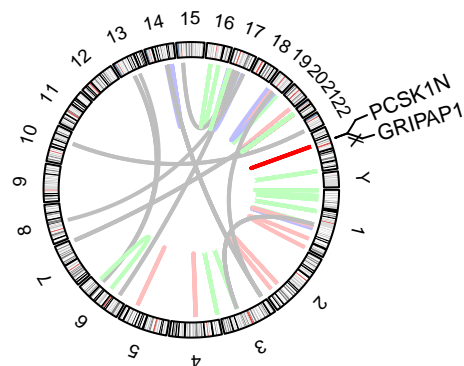
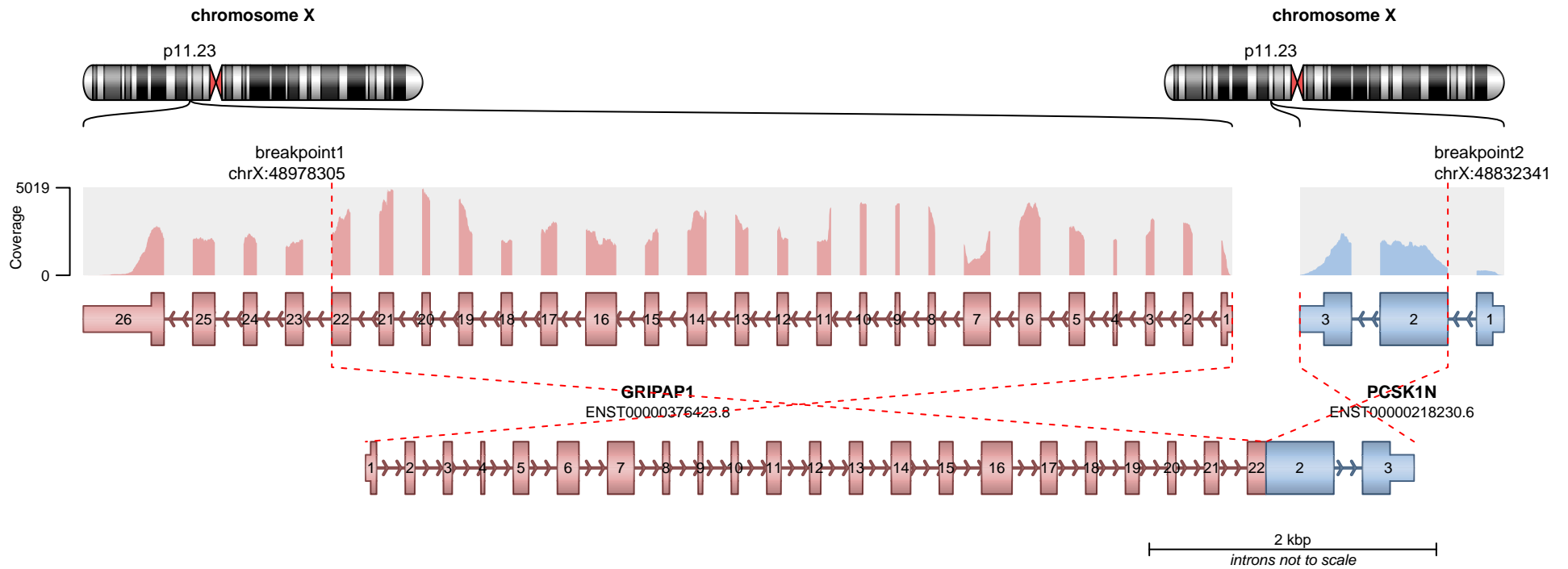


— translocation — deletion
— duplication — inversion

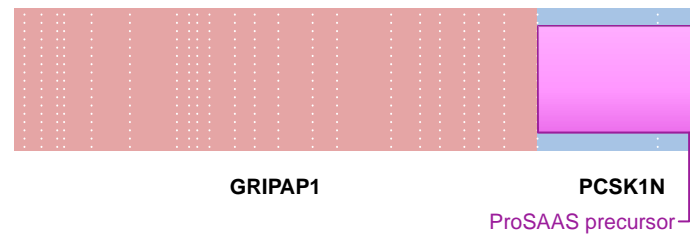
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 88
Discordant mates = 1



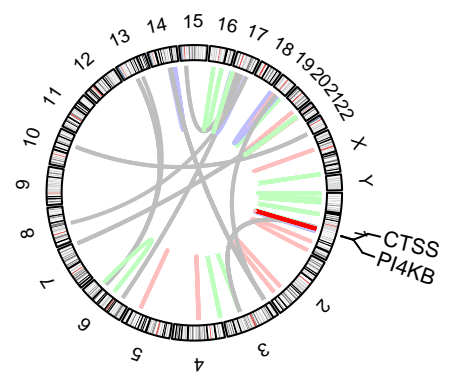
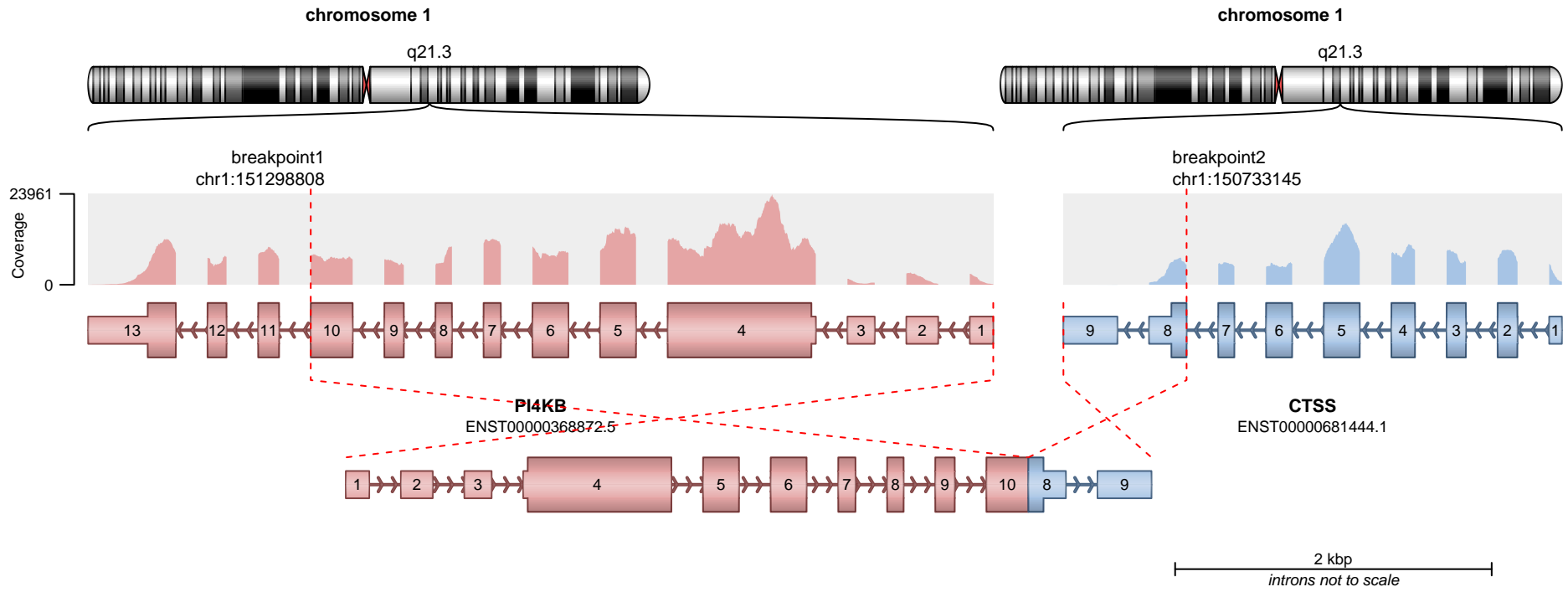
RETAINED PROTEIN DOMAINS
reading frame unclear



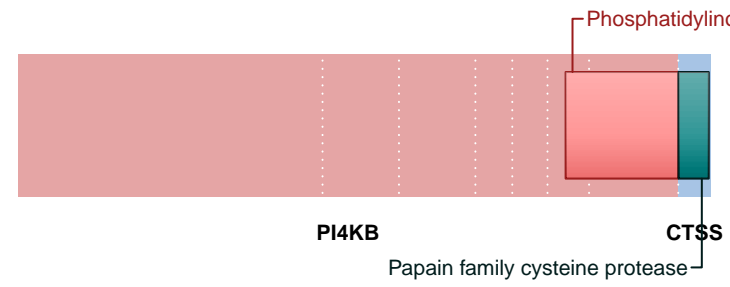
SUPPORTING READ COUNT

Split reads = 85
Discordant mates = 4

— translocation — deletion
— duplication — inversion



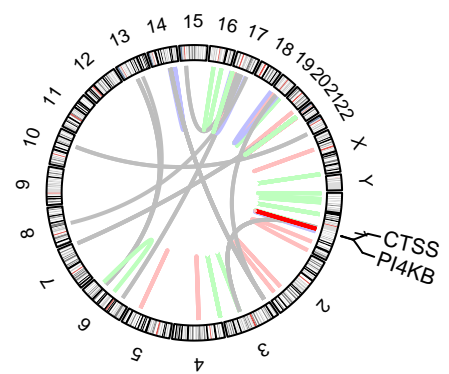
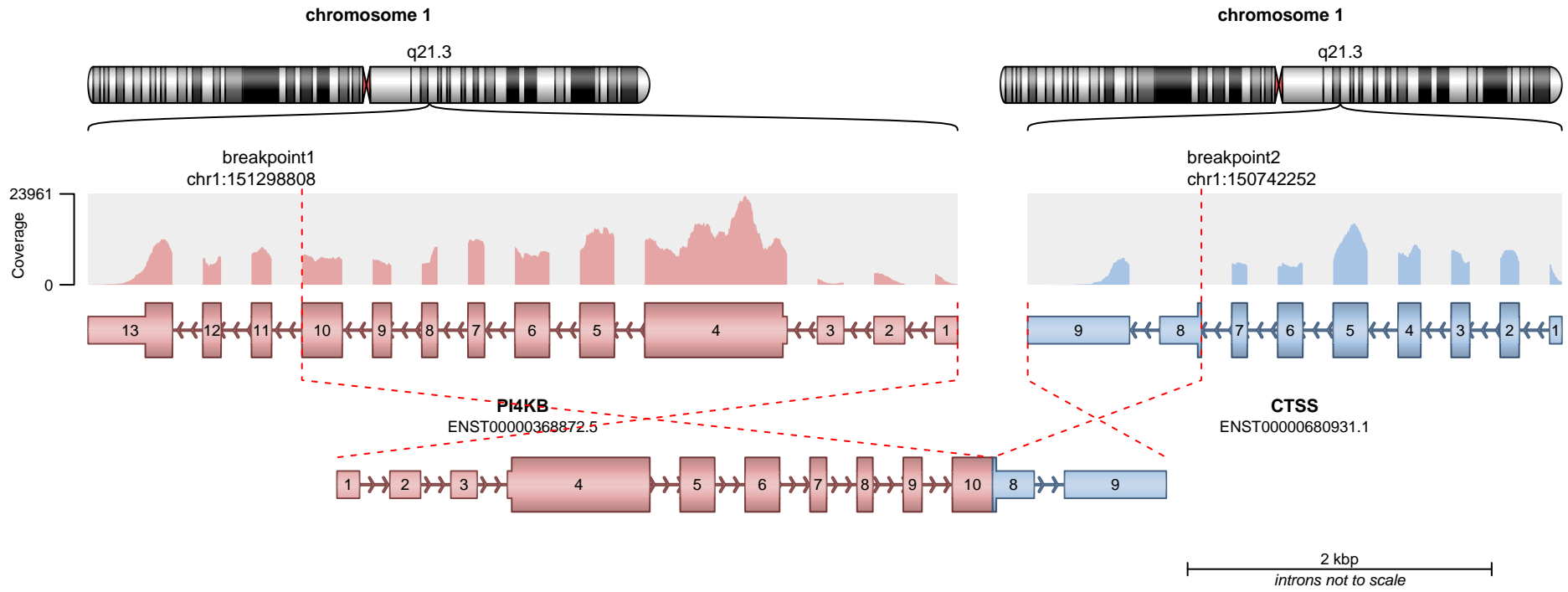
RETAINED PROTEIN DOMAINS
reading frame unclear



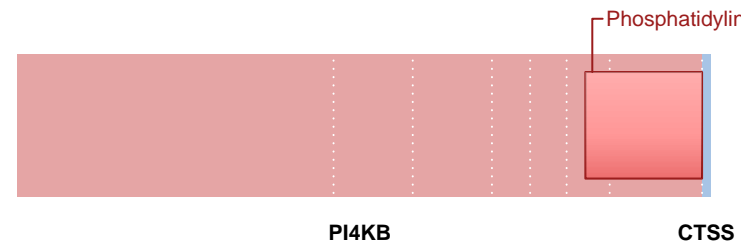
SUPPORTING READ COUNT

Split reads = 84
Discordant mates = 3

- translocation
- duplication
- deletion
- inversion



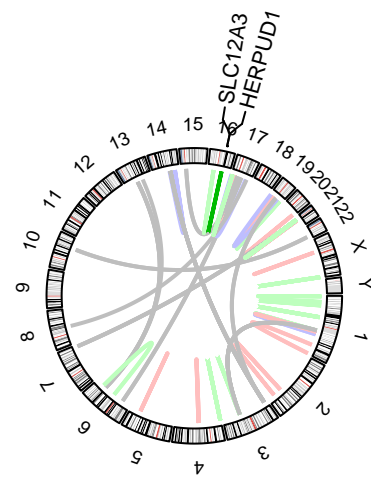
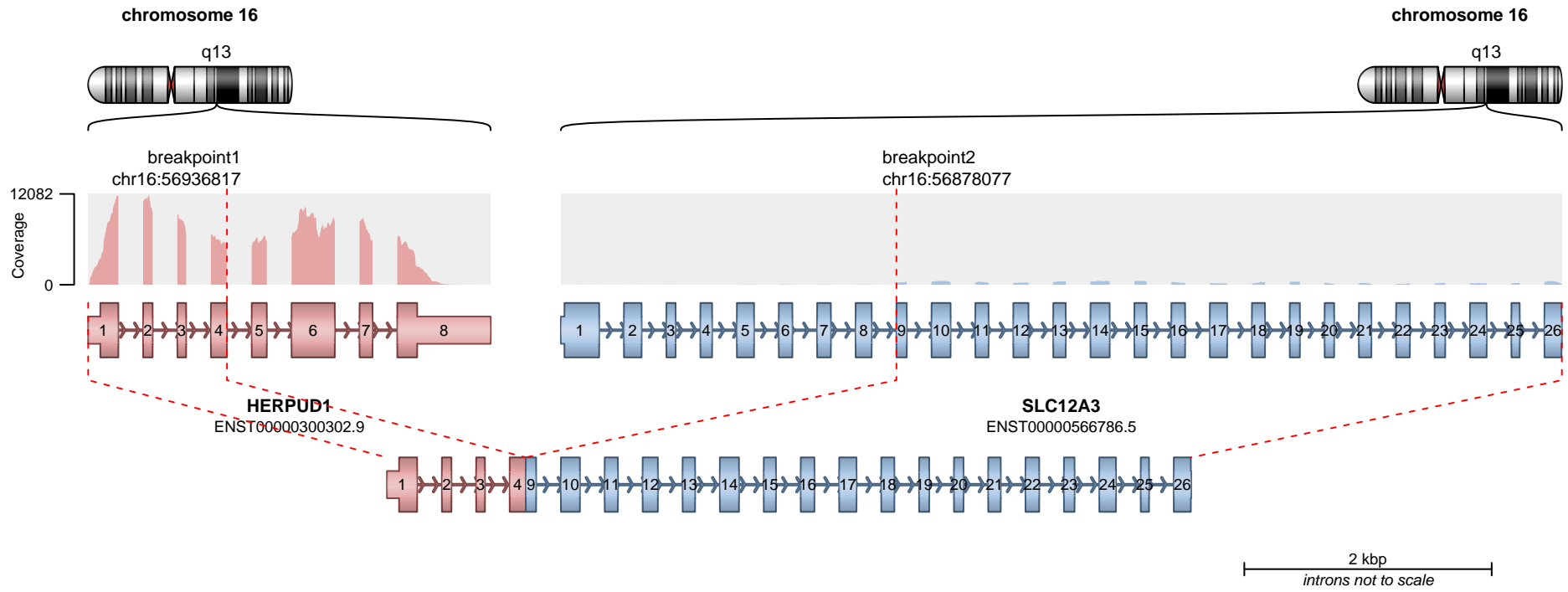
RETAINED PROTEIN DOMAINS
reading frame unclear



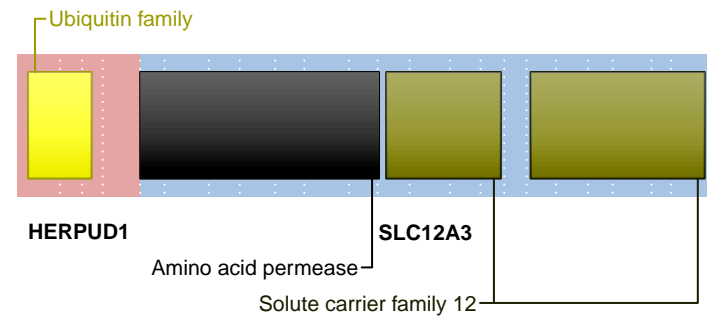
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 3

- translocation
- duplication
- deletion
- inversion



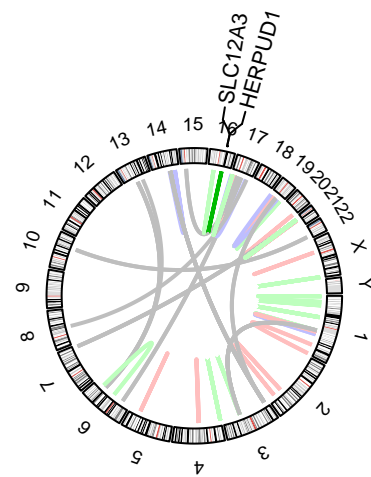
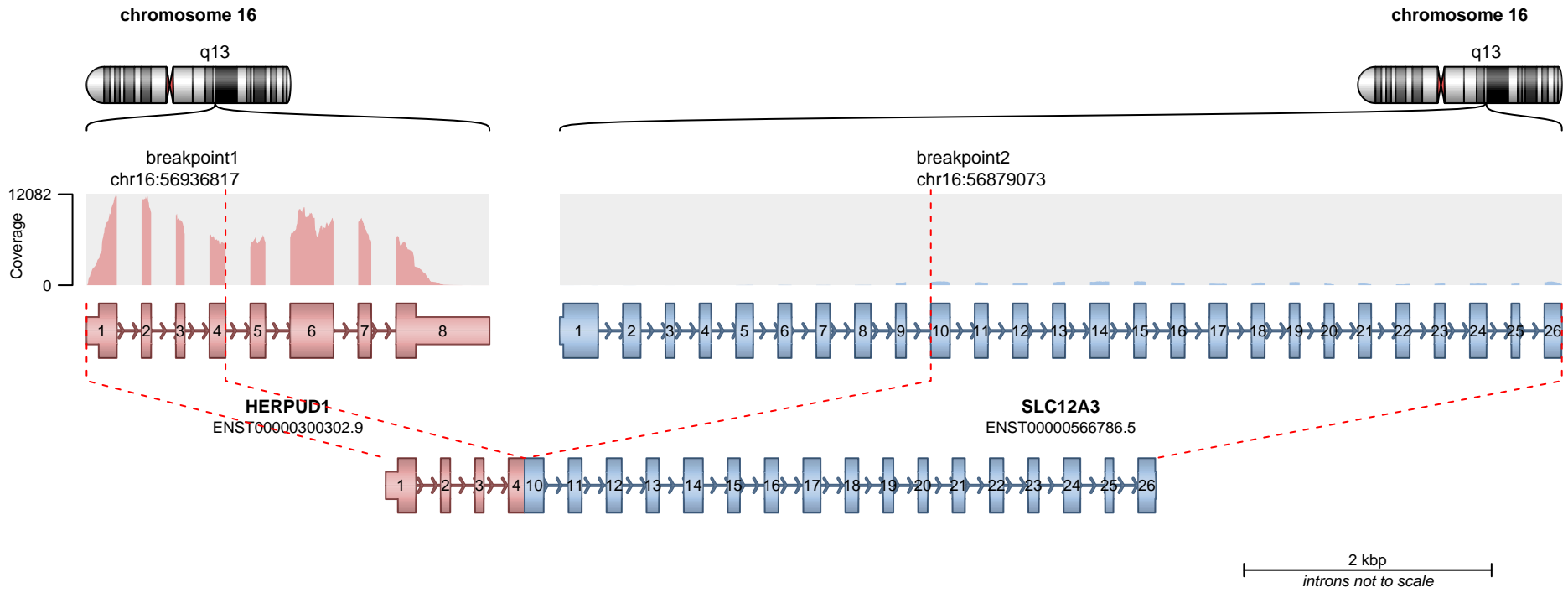
RETAINED PROTEIN DOMAINS
reading frame unclear



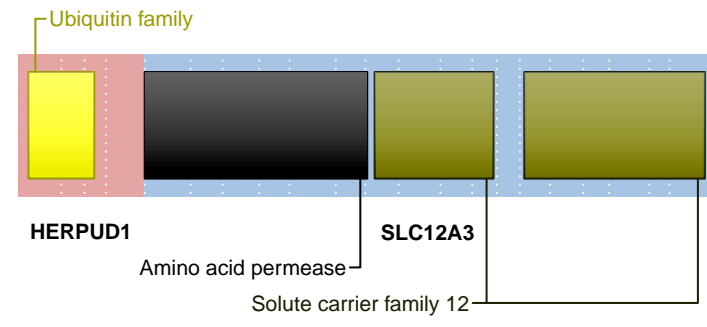
SUPPORTING READ COUNT

Split reads = 80
Discordant mates = 6

- translocation
- duplication
- deletion
- inversion



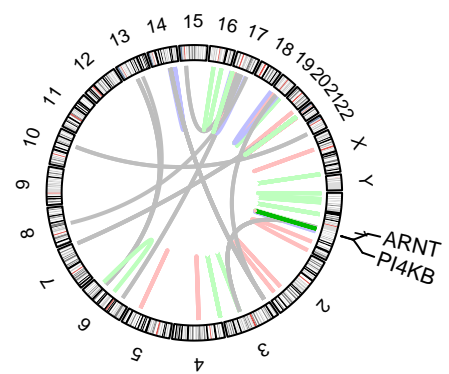
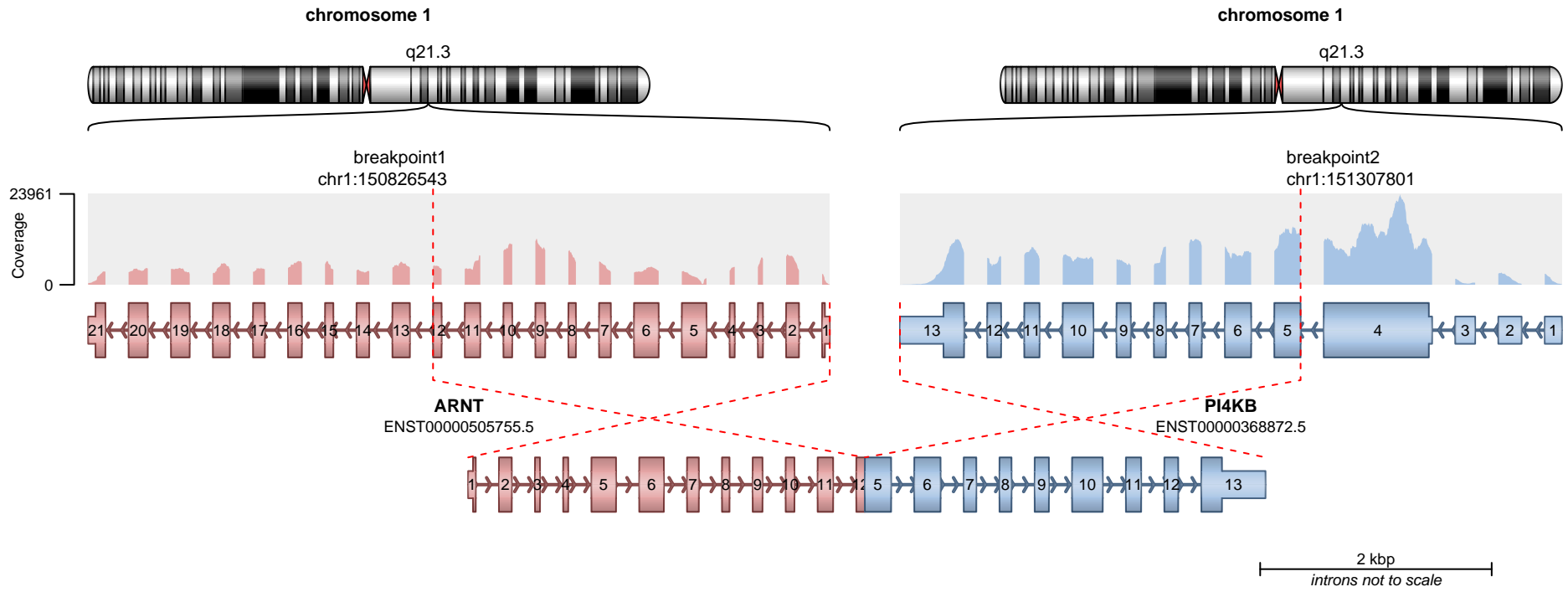
RETAINED PROTEIN DOMAINS
reading frame unclear



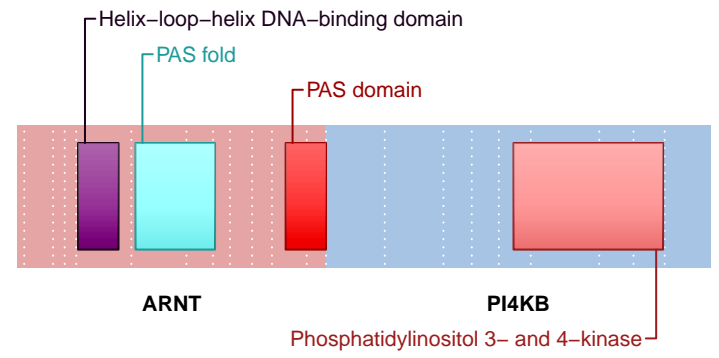
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



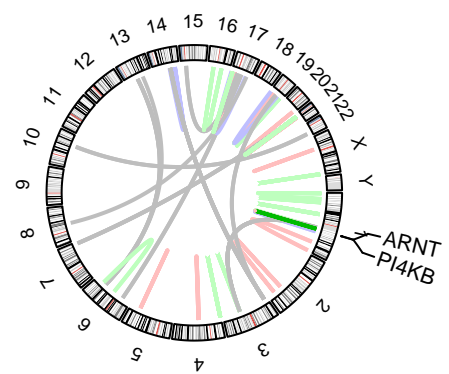
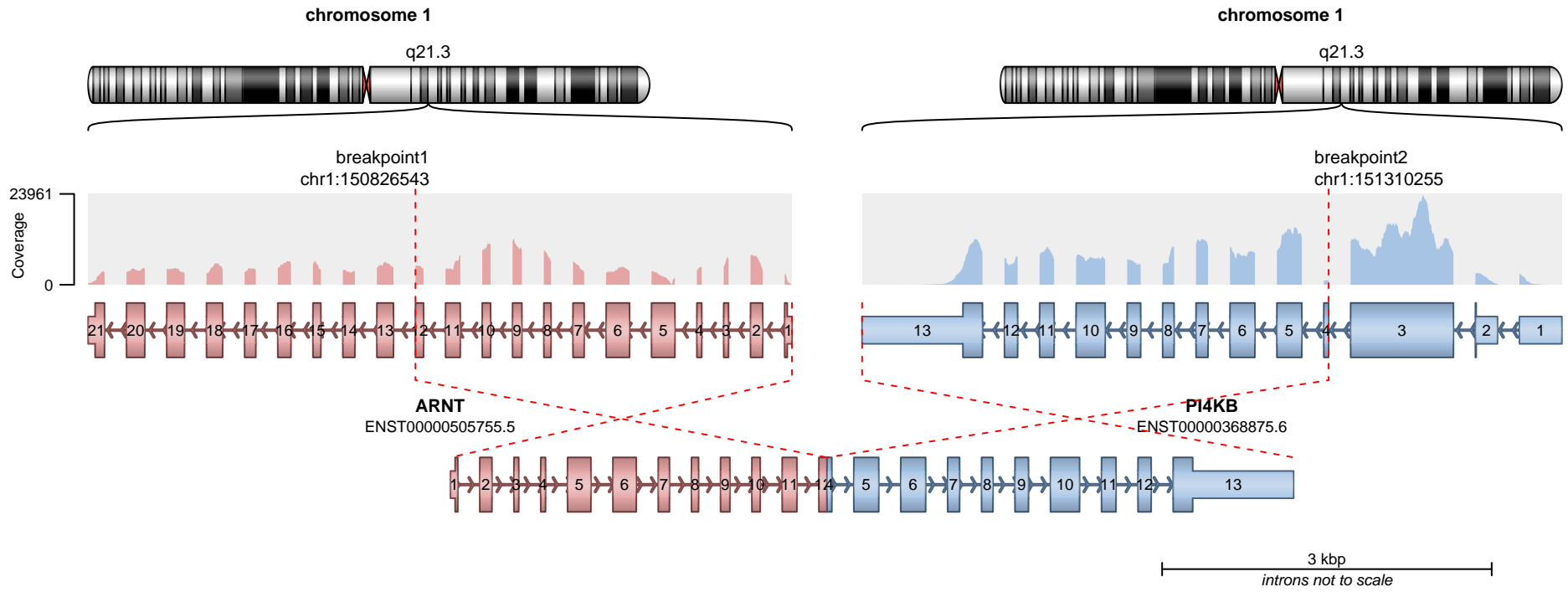
RETAINED PROTEIN DOMAINS
reading frame unclear



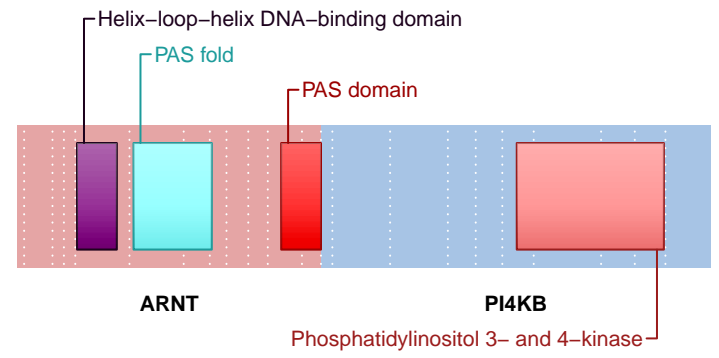
SUPPORTING READ COUNT

Split reads = 74
Discordant mates = 7

- translocation
- duplication
- deletion
- inversion



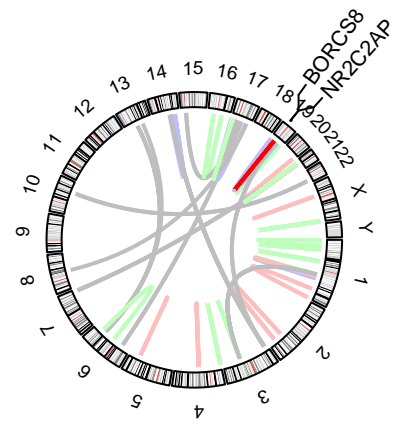
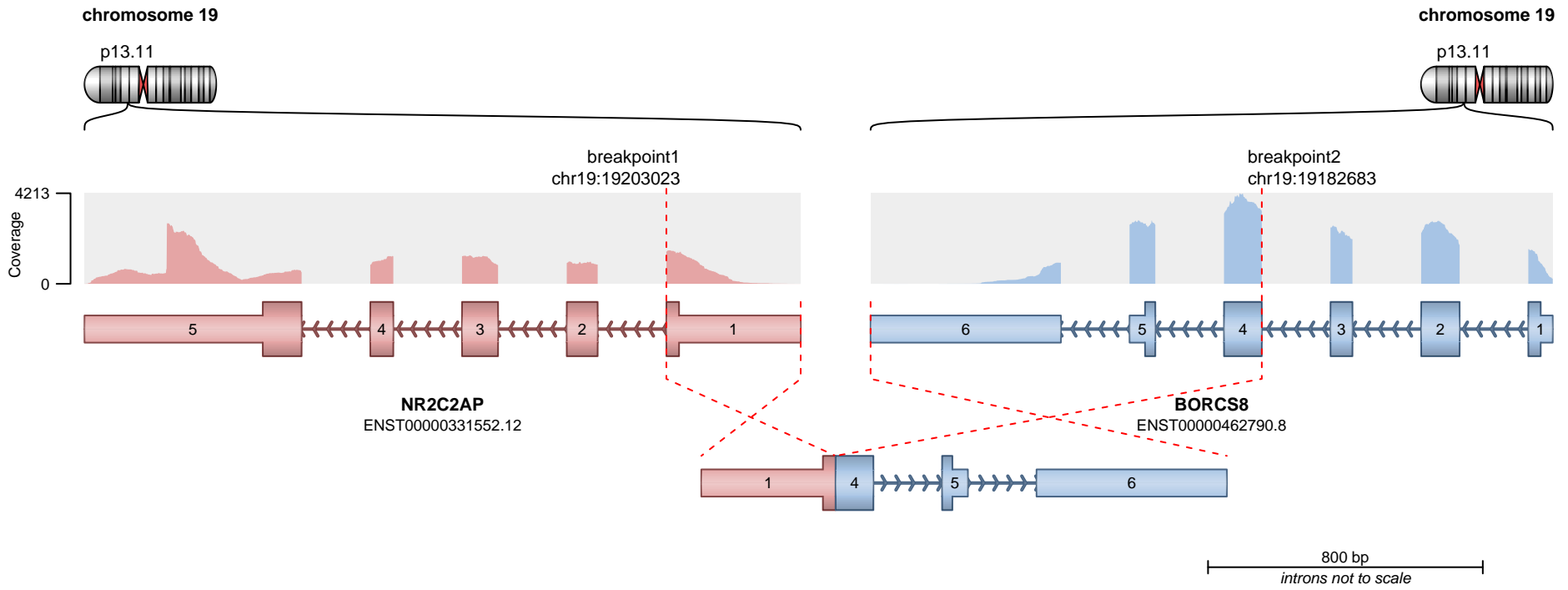
RETAINED PROTEIN DOMAINS
reading frame unclear



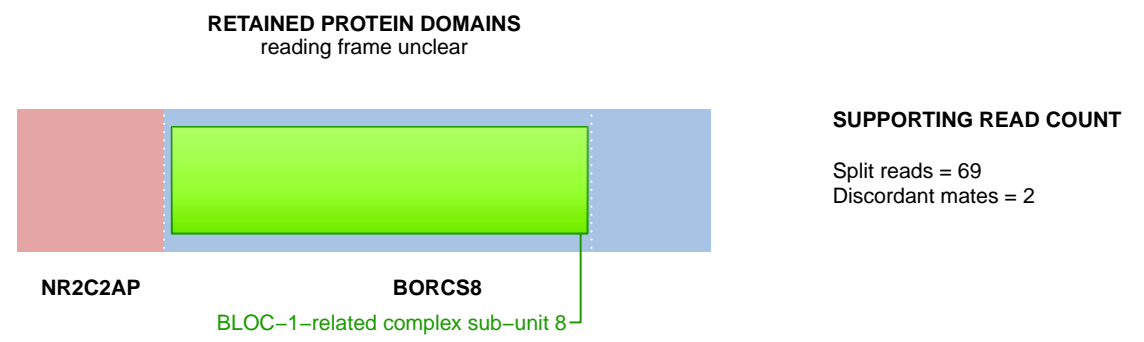
SUPPORTING READ COUNT

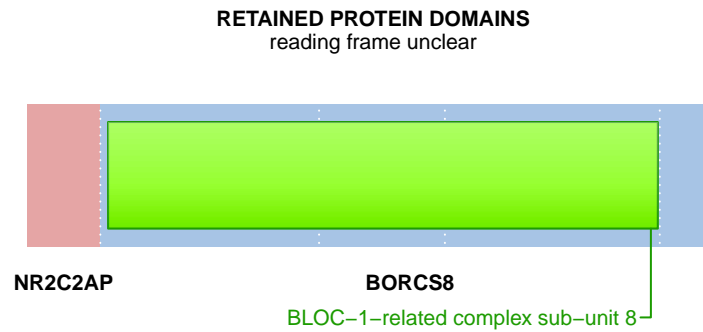
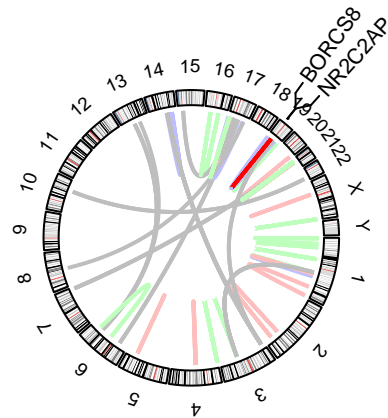
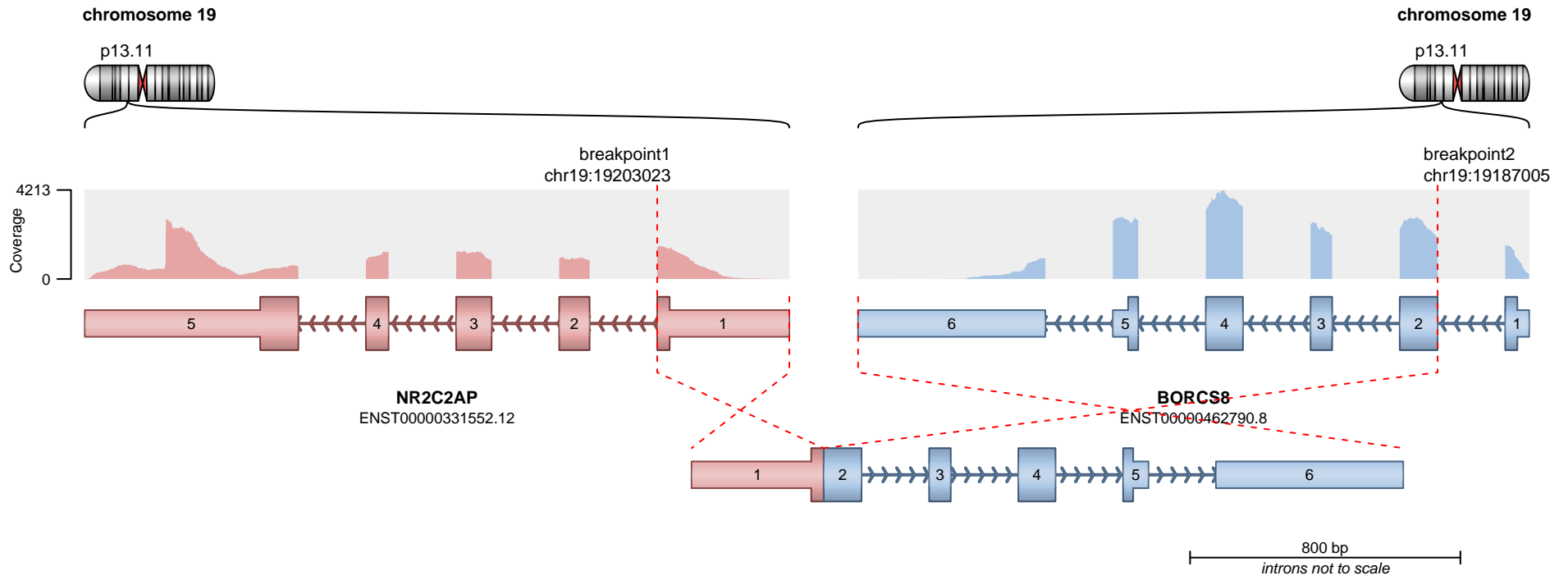
Split reads = 36
Discordant mates = 8

- translocation
- duplication
- deletion
- inversion



— translocation — deletion
— duplication — inversion

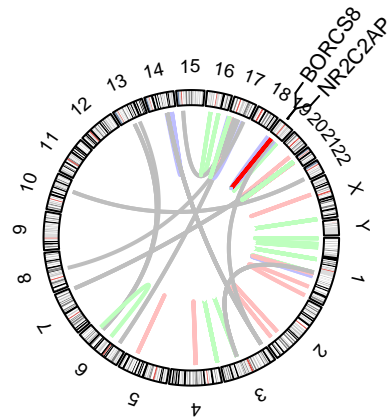
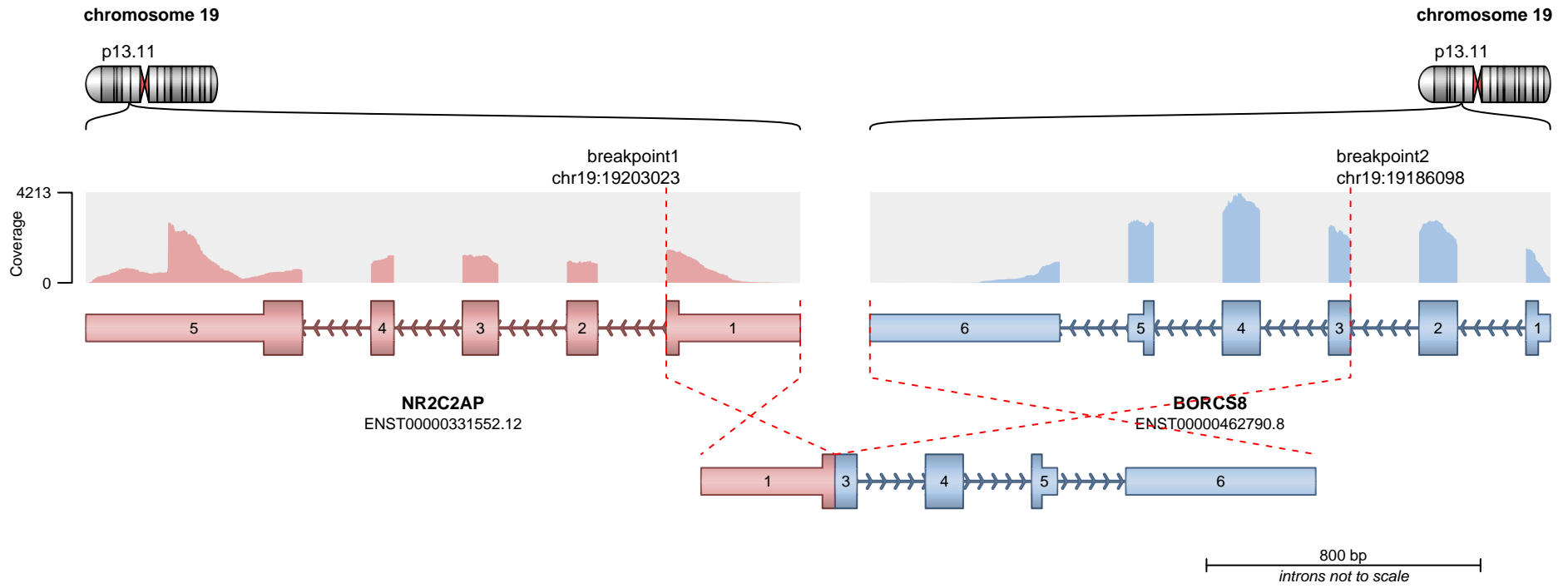




SUPPORTING READ COUNT

Split reads = 37
Discordant mates = 7

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

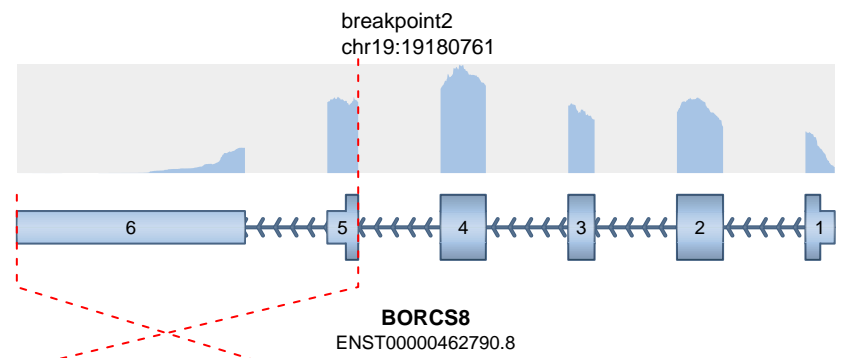
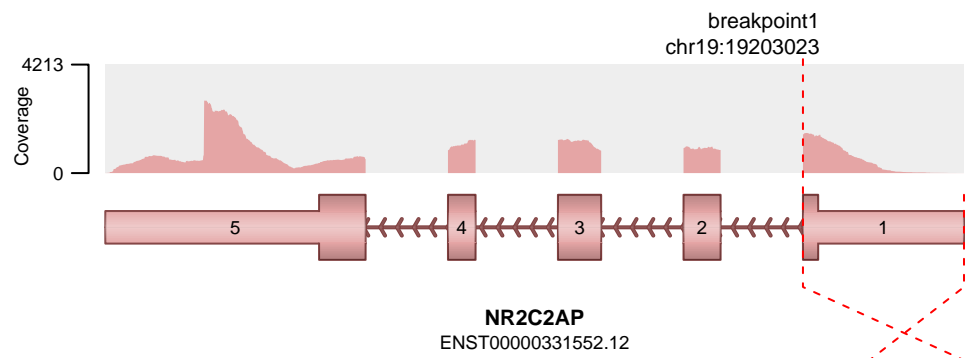
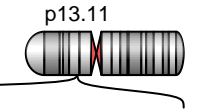
Split reads = 23
Discordant mates = 6

— translocation — deletion
— duplication — inversion

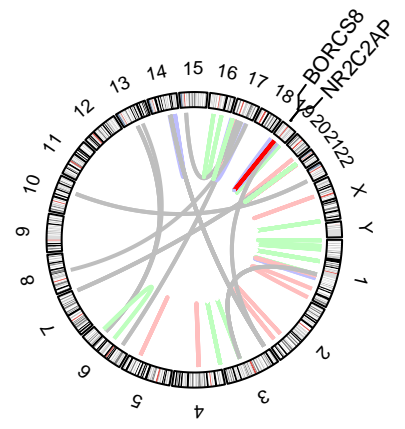
chromosome 19



chromosome 19



800 bp
introns not to scale

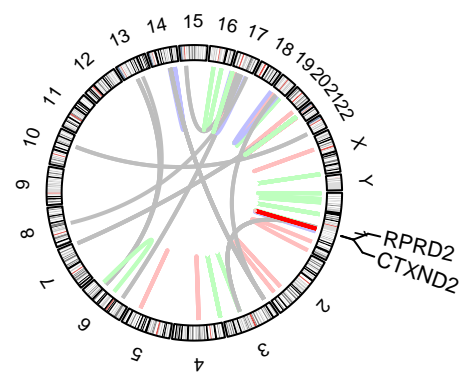
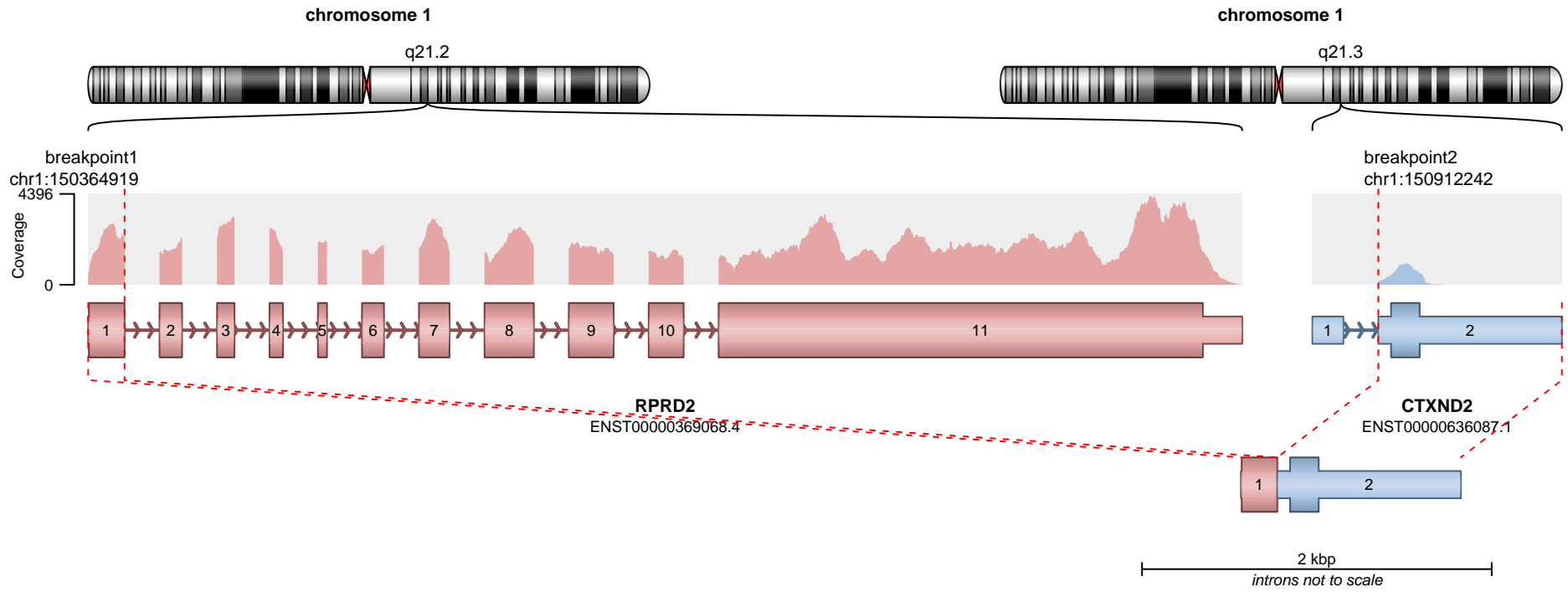


No protein domains retained in fusion.

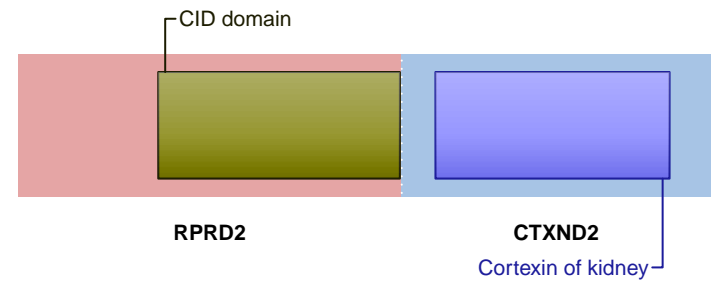
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

— translocation — deletion
— duplication — inversion



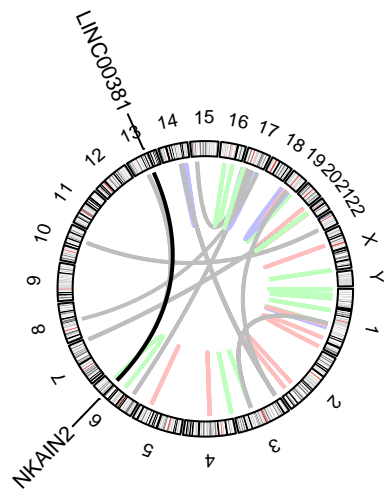
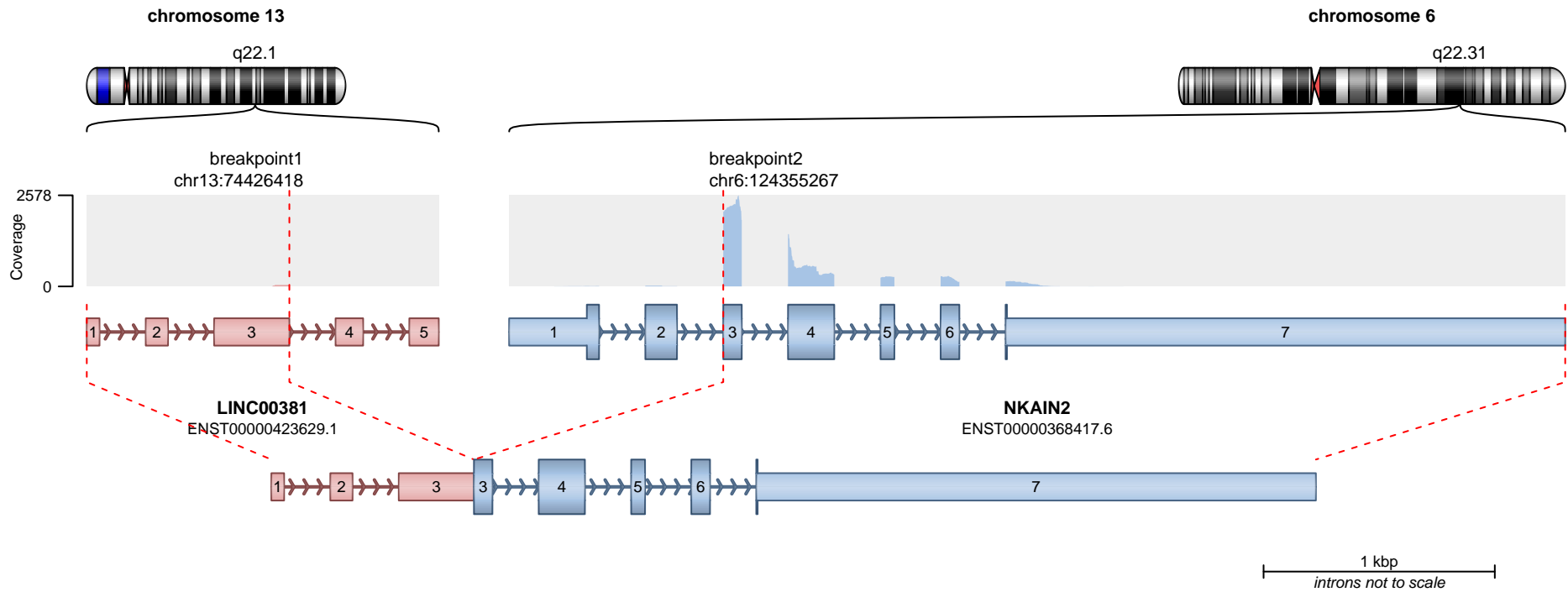
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 64
Discordant mates = 5

- translocation
- duplication
- deletion
- inversion



— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear

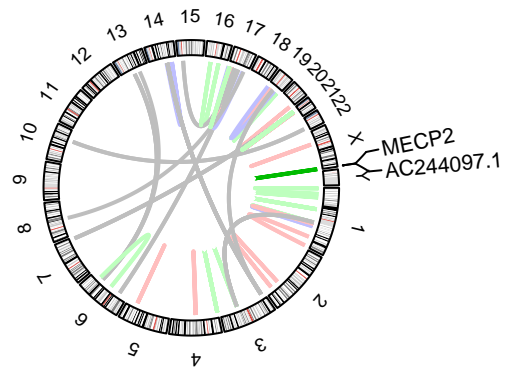
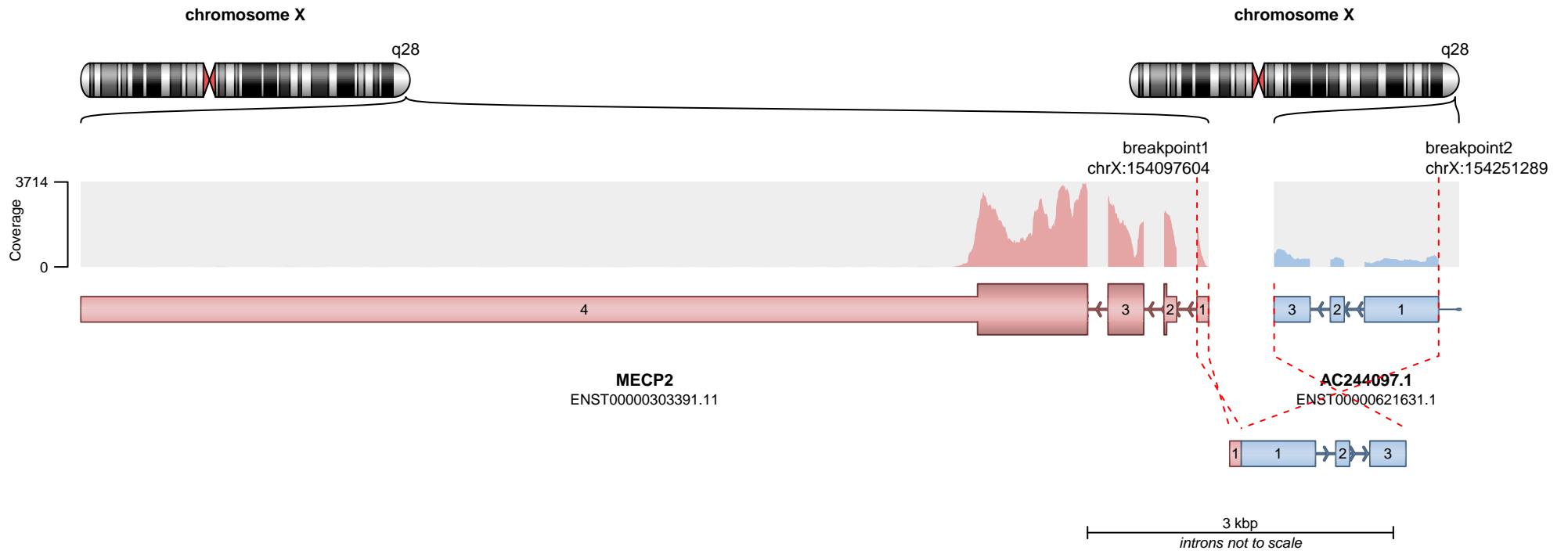


NKAIN2

Na,K-ATPase Interacting protein

SUPPORTING READ COUNT

Split reads = 65
Discordant mates = 0

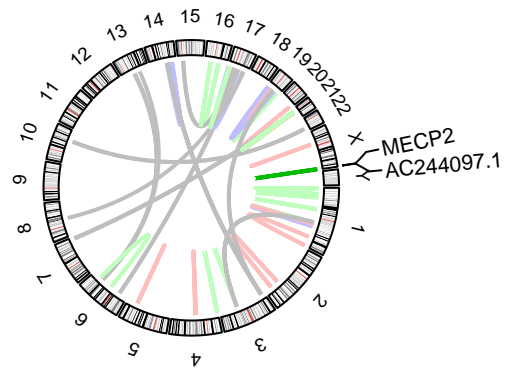
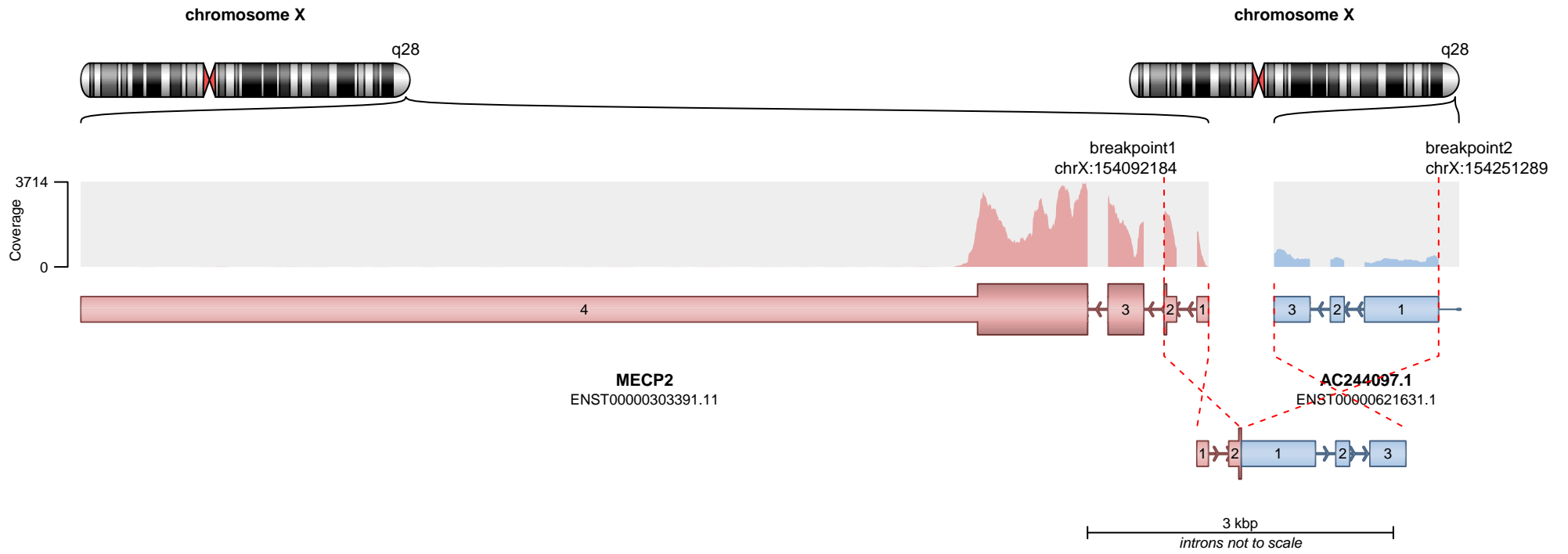


No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 52
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

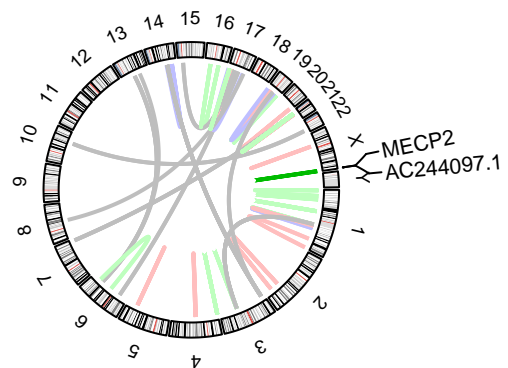
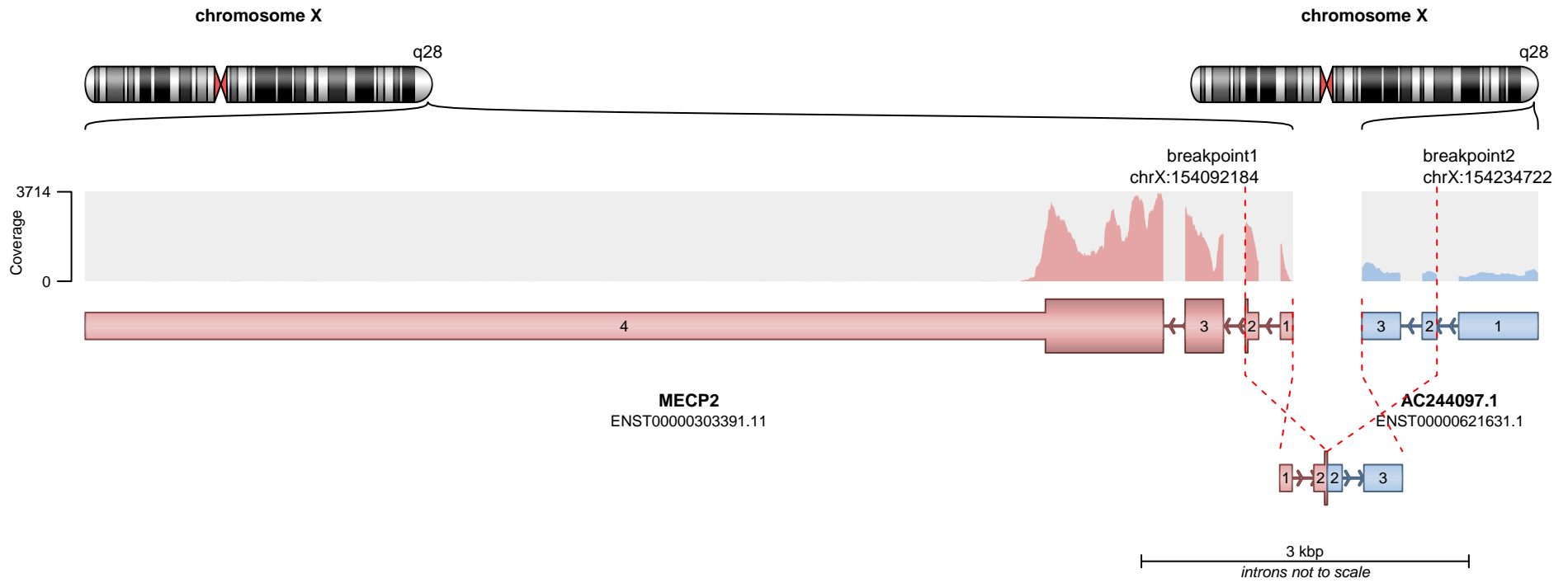


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 33
Discordant mates = 3

— translocation — deletion
— duplication — inversion

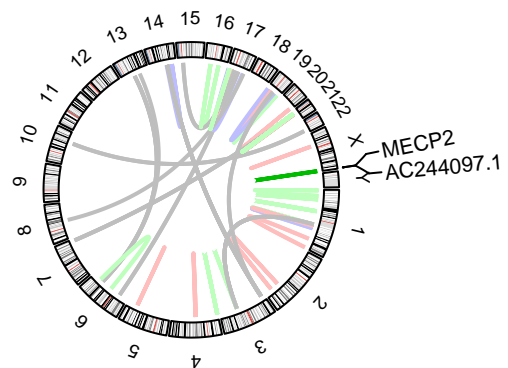
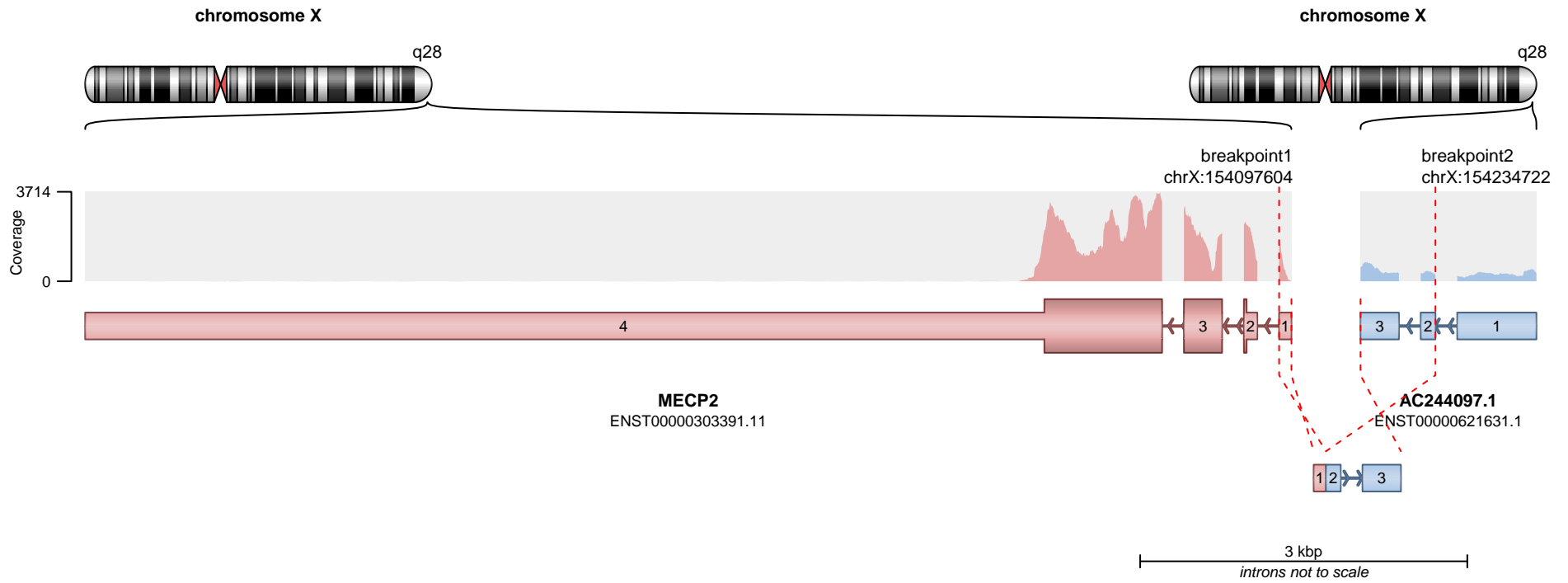


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 2

— translocation — deletion
— duplication — inversion



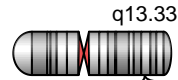
No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

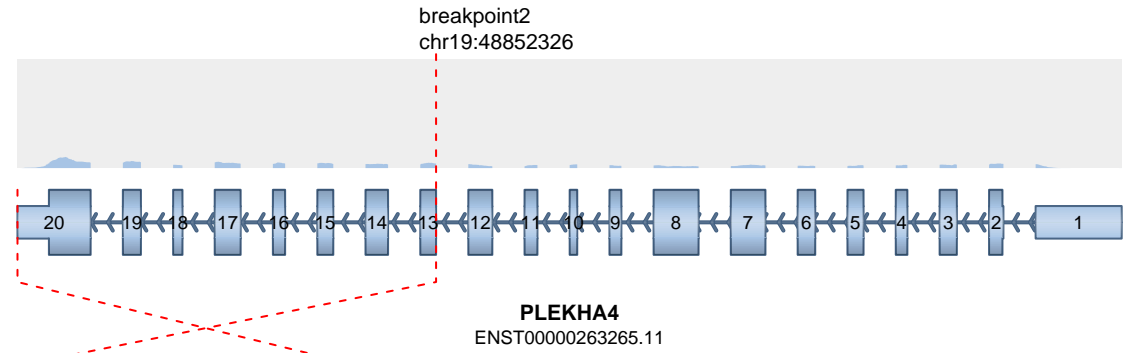
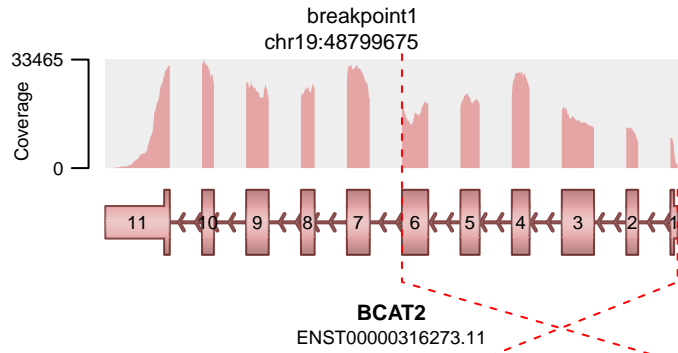
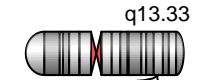
Split reads = 6
Discordant mates = 0

— translocation — deletion
— duplication — inversion

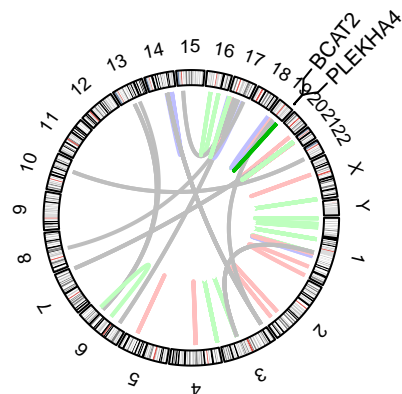
chromosome 19



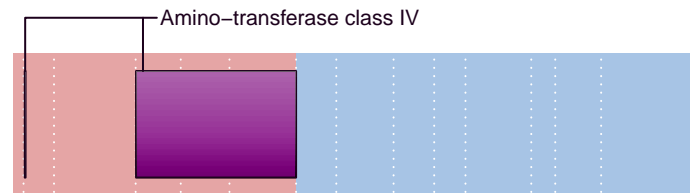
chromosome 19



2 kbp
introns not to scale



RETAINED PROTEIN DOMAINS
reading frame unclear



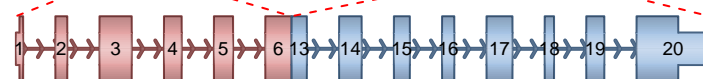
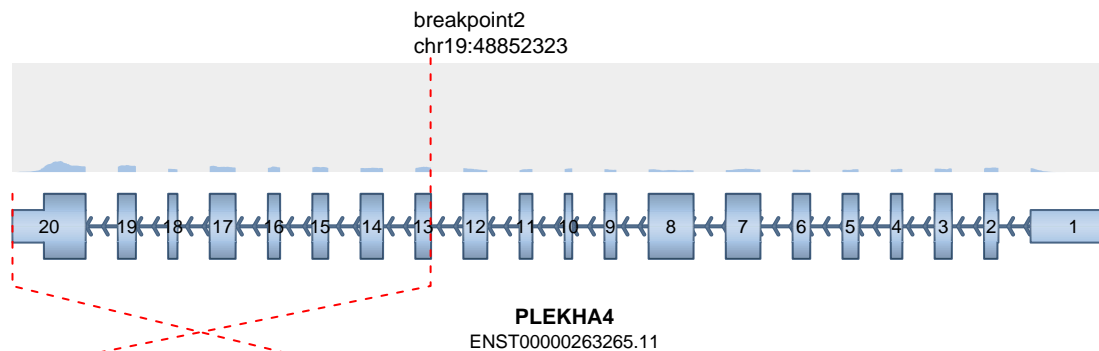
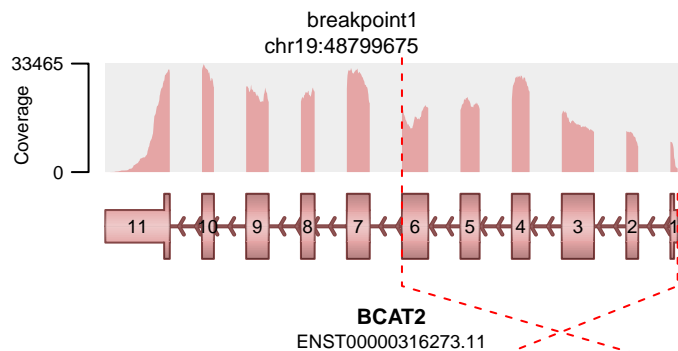
SUPPORTING READ COUNT

Split reads = 48
Discordant mates = 2

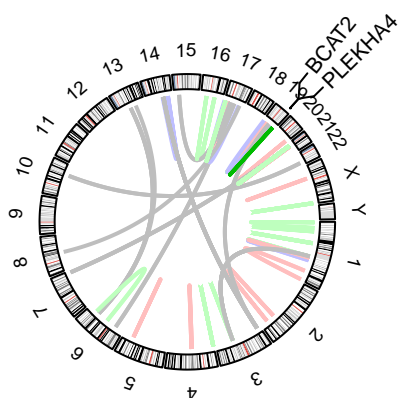
— translocation — deletion
— duplication — inversion

chromosome 19

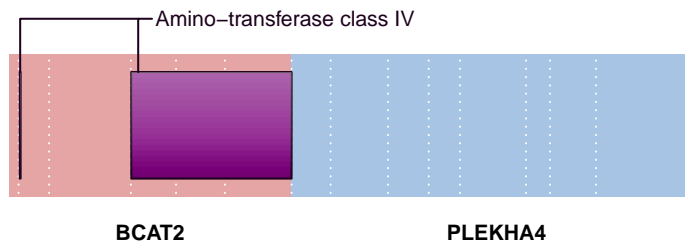
chromosome 19



2 kbp
introns not to scale



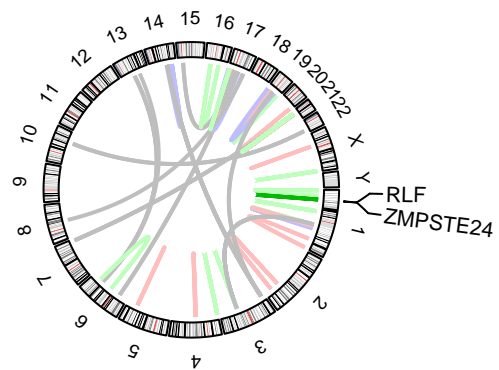
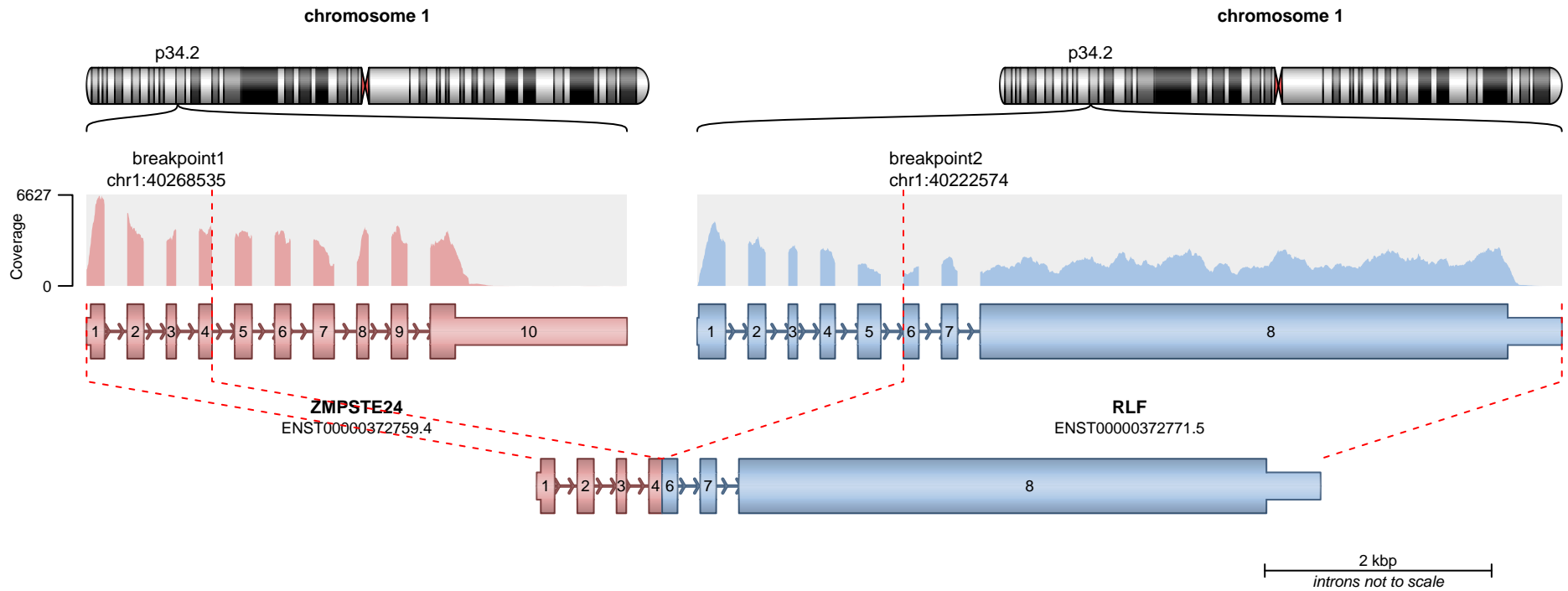
RETAINED PROTEIN DOMAINS
reading frame unclear



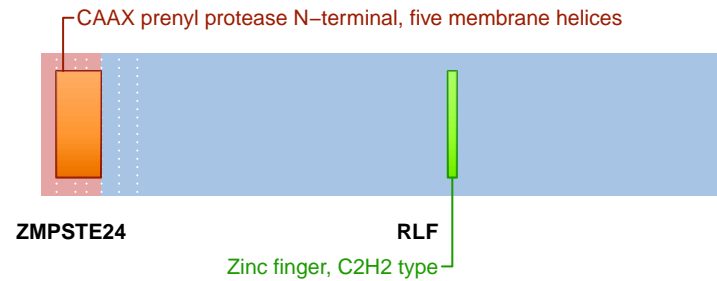
SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 2

— translocation — deletion
— duplication — inversion



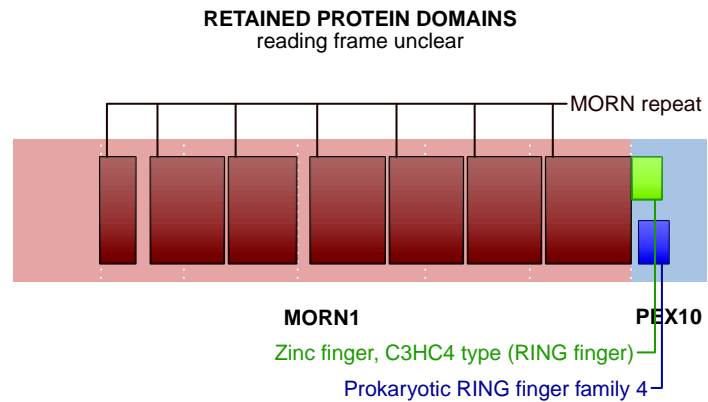
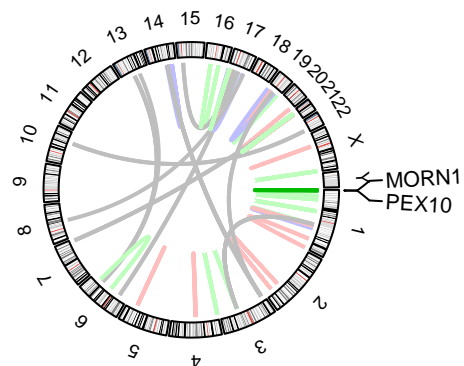
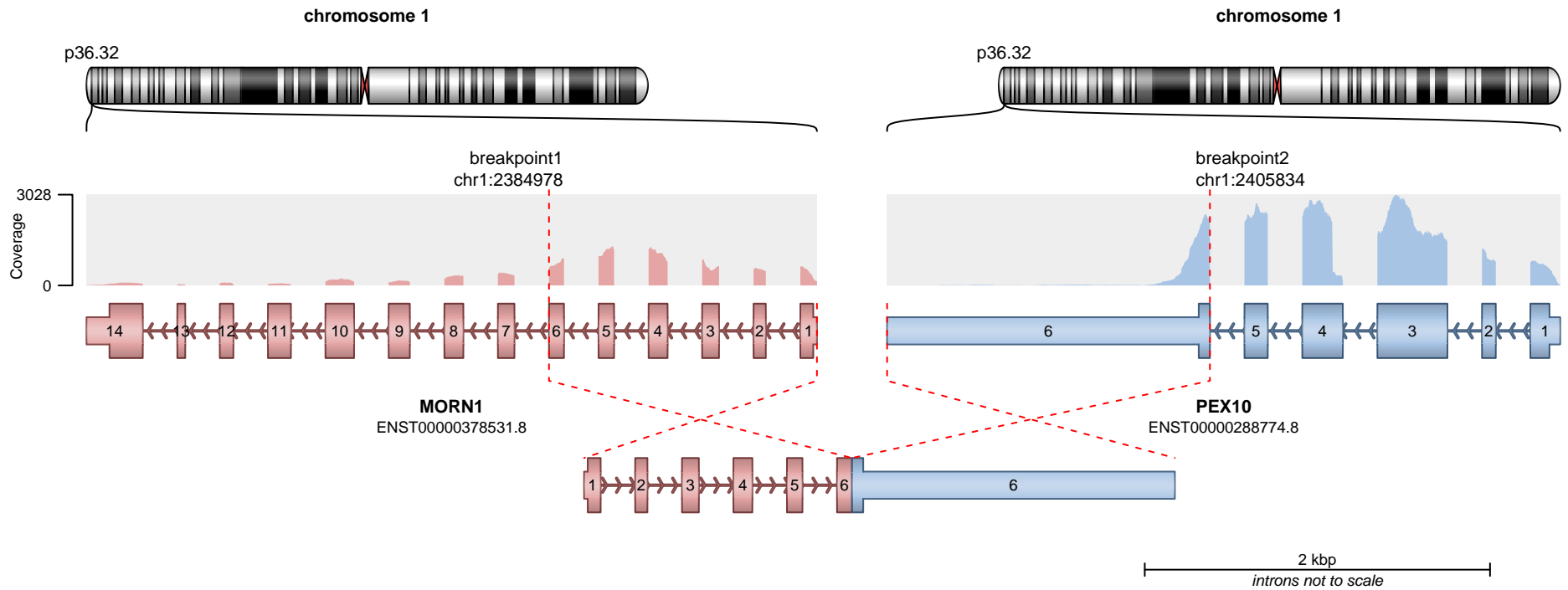
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 41
Discordant mates = 4

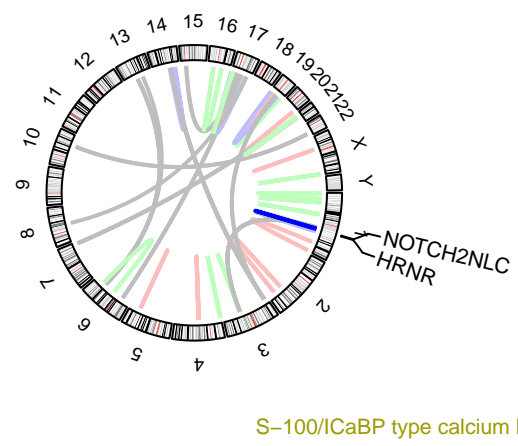
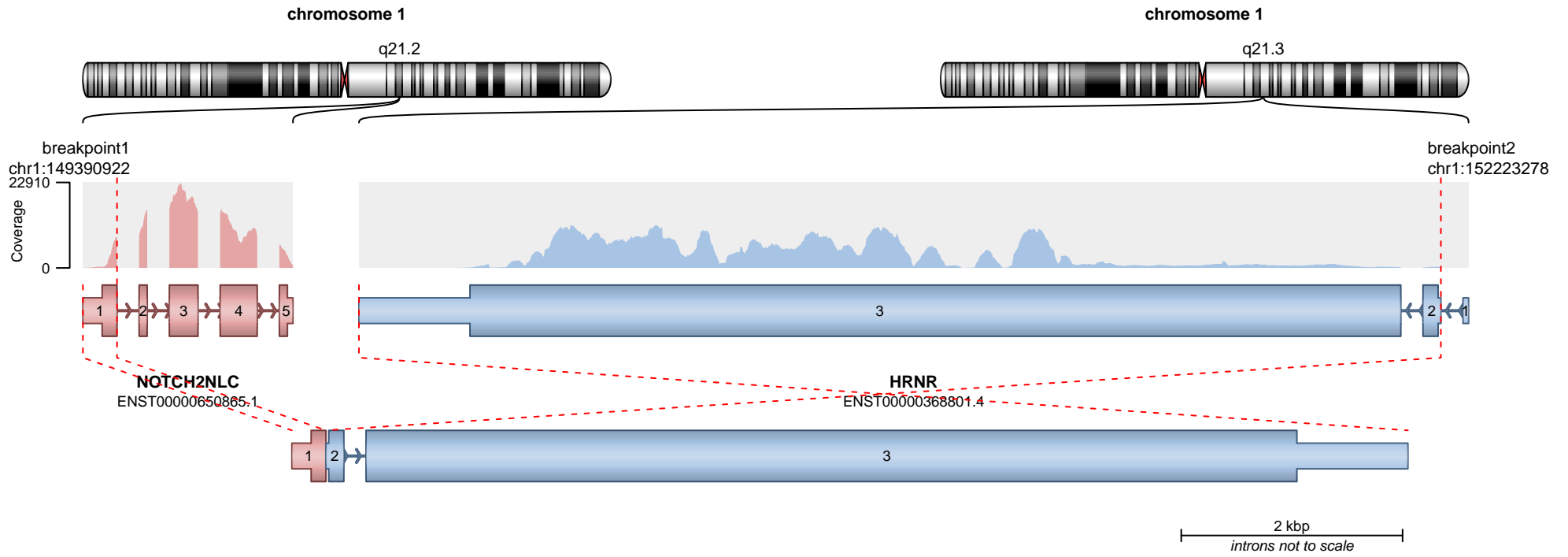
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 41
Discordant mates = 0

— translocation — deletion
— duplication — inversion



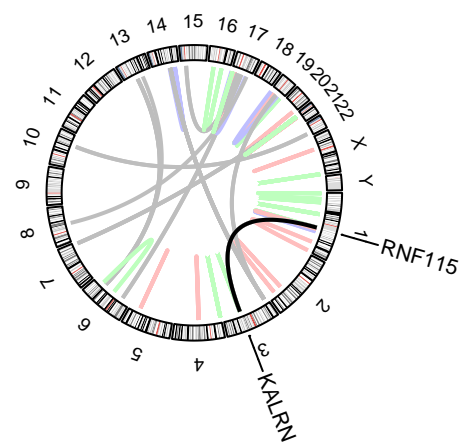
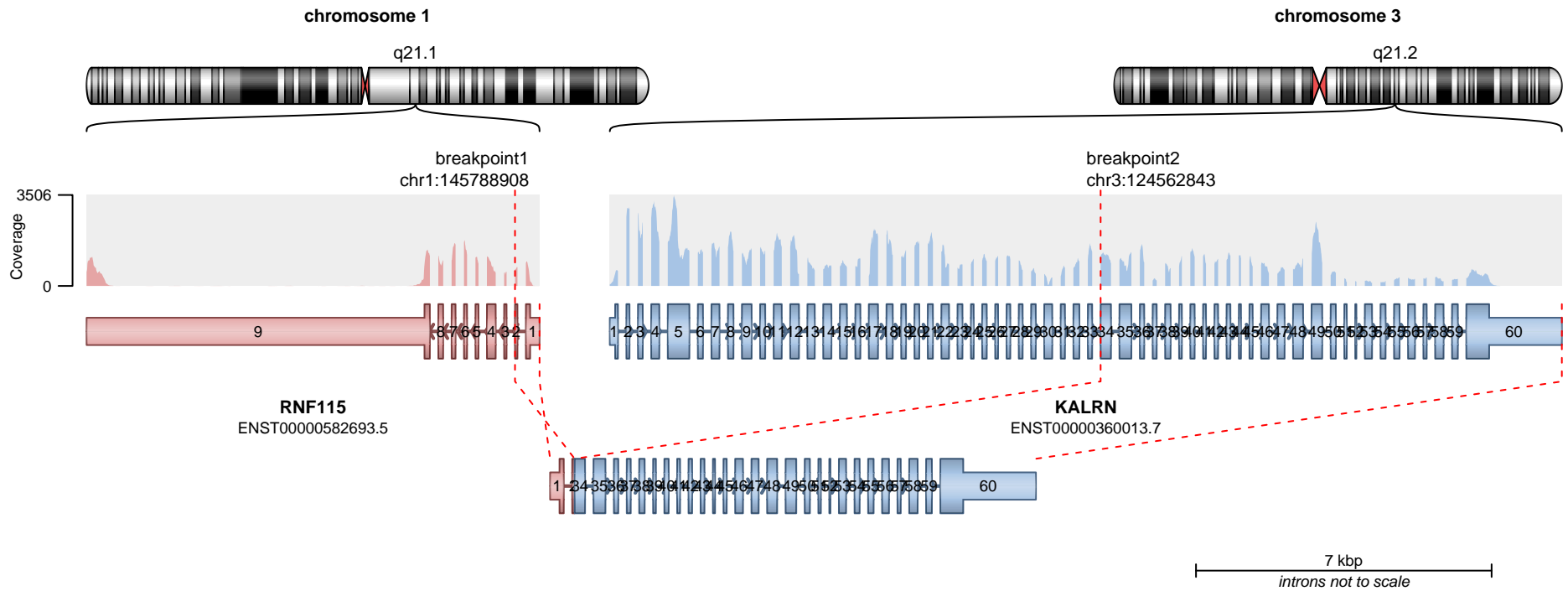
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

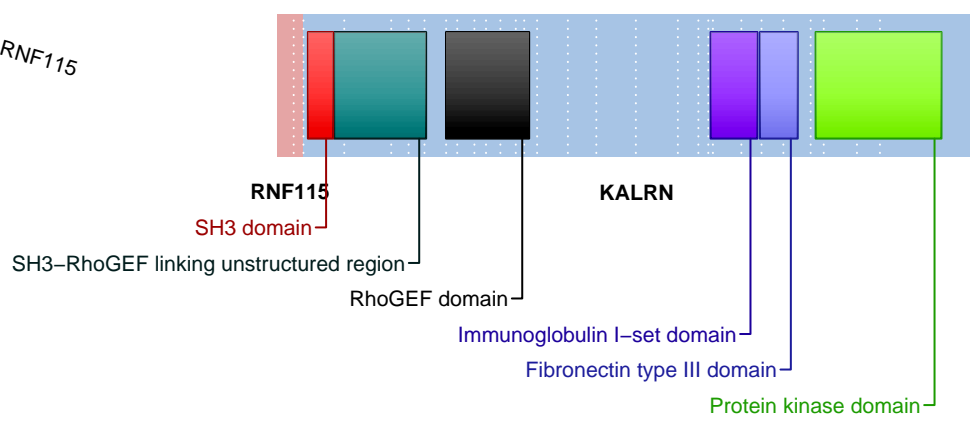
Split reads = 40
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



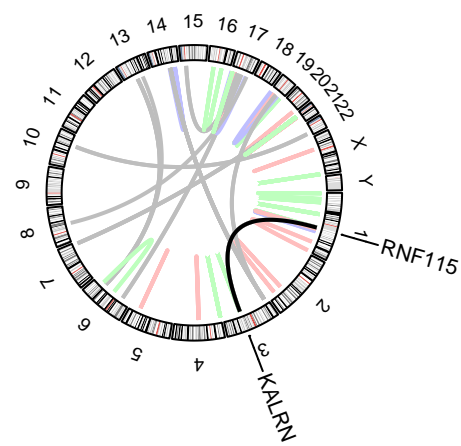
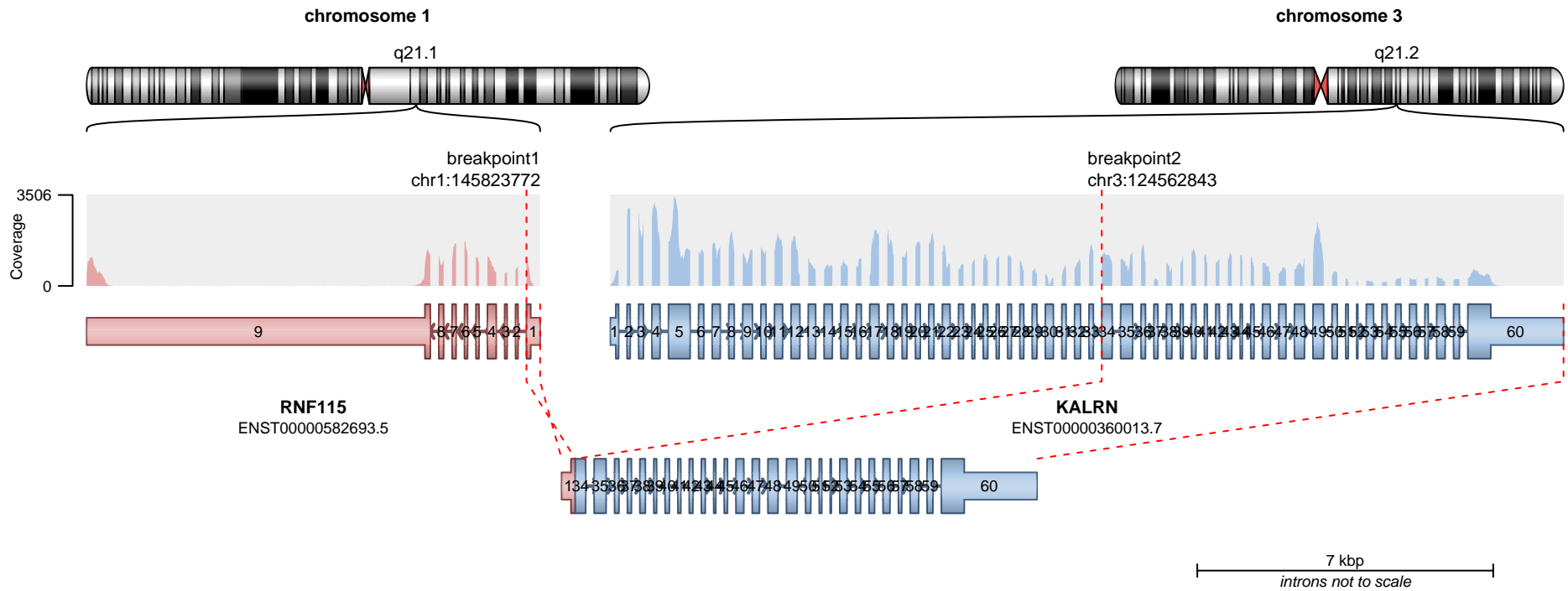
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



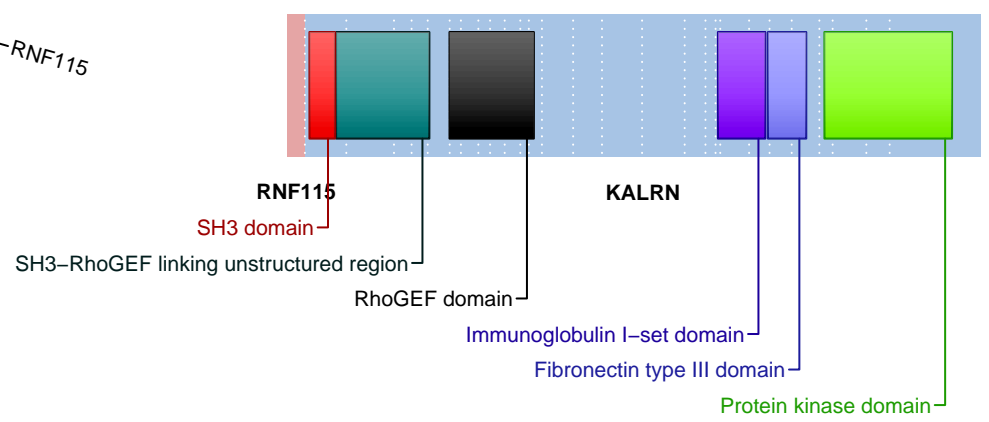
SUPPORTING READ COUNT

Split reads = 38
Discordant mates = 1



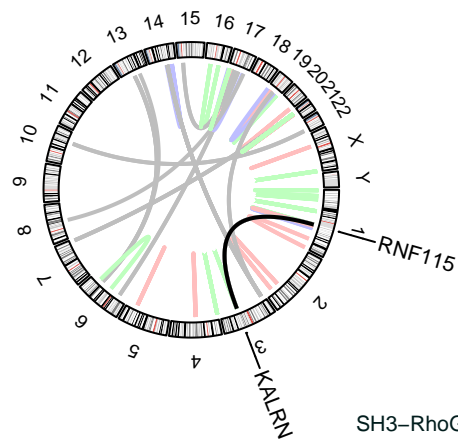
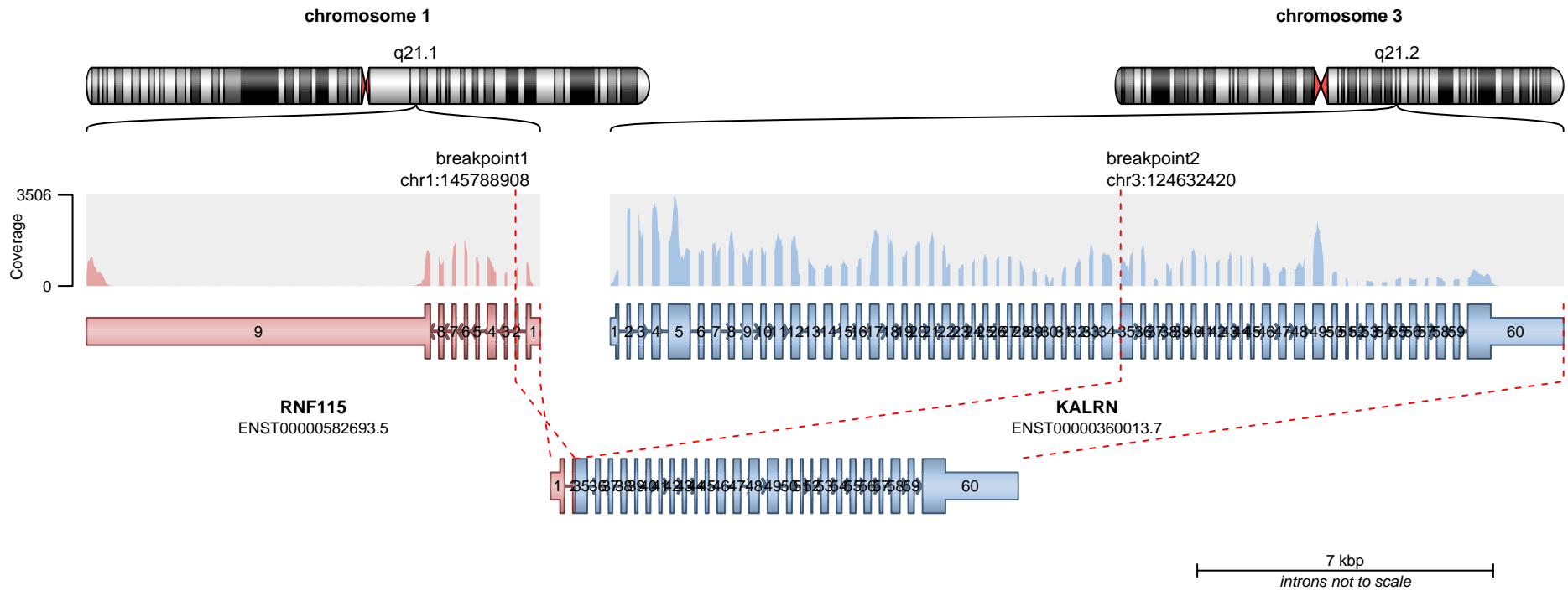
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



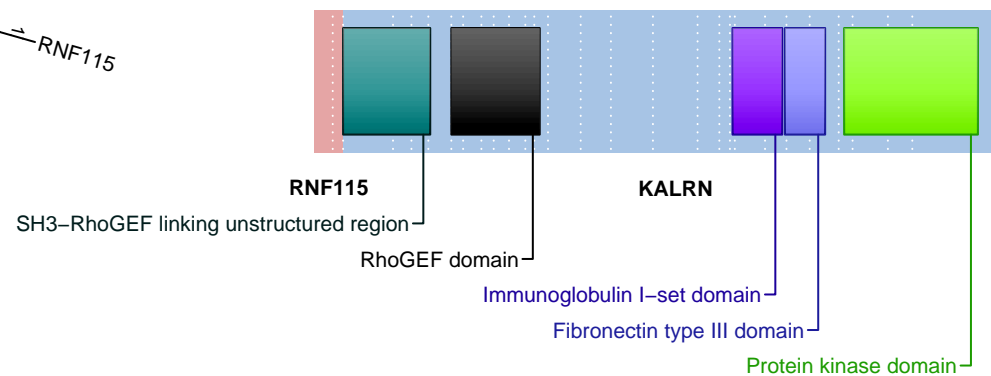
SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 1



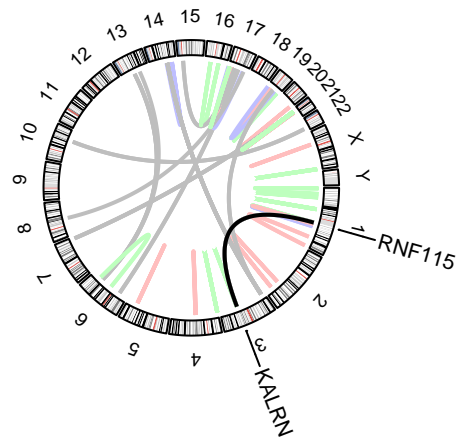
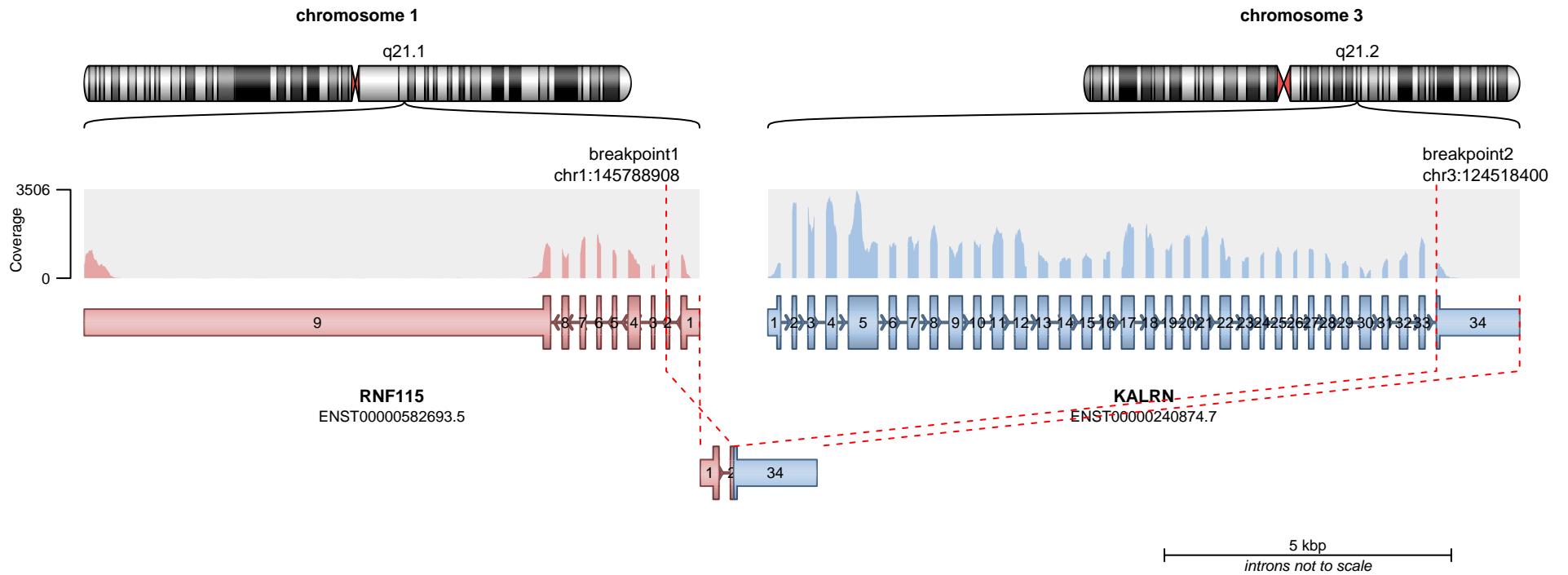
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

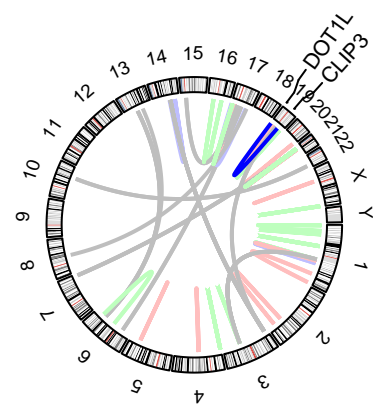
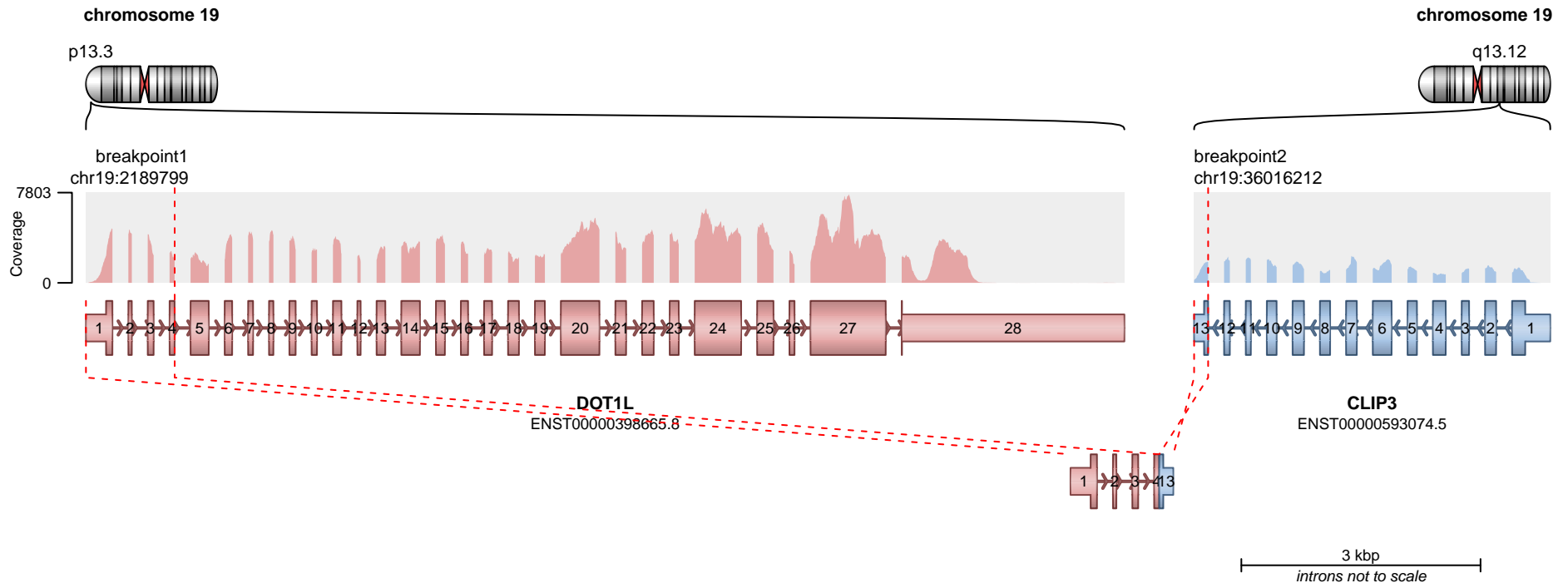


— translocation — deletion
 — duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
 Discordant mates = 1

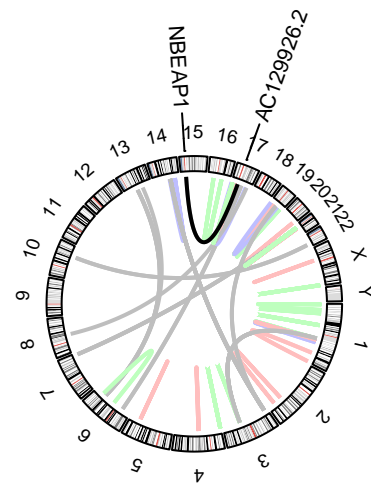
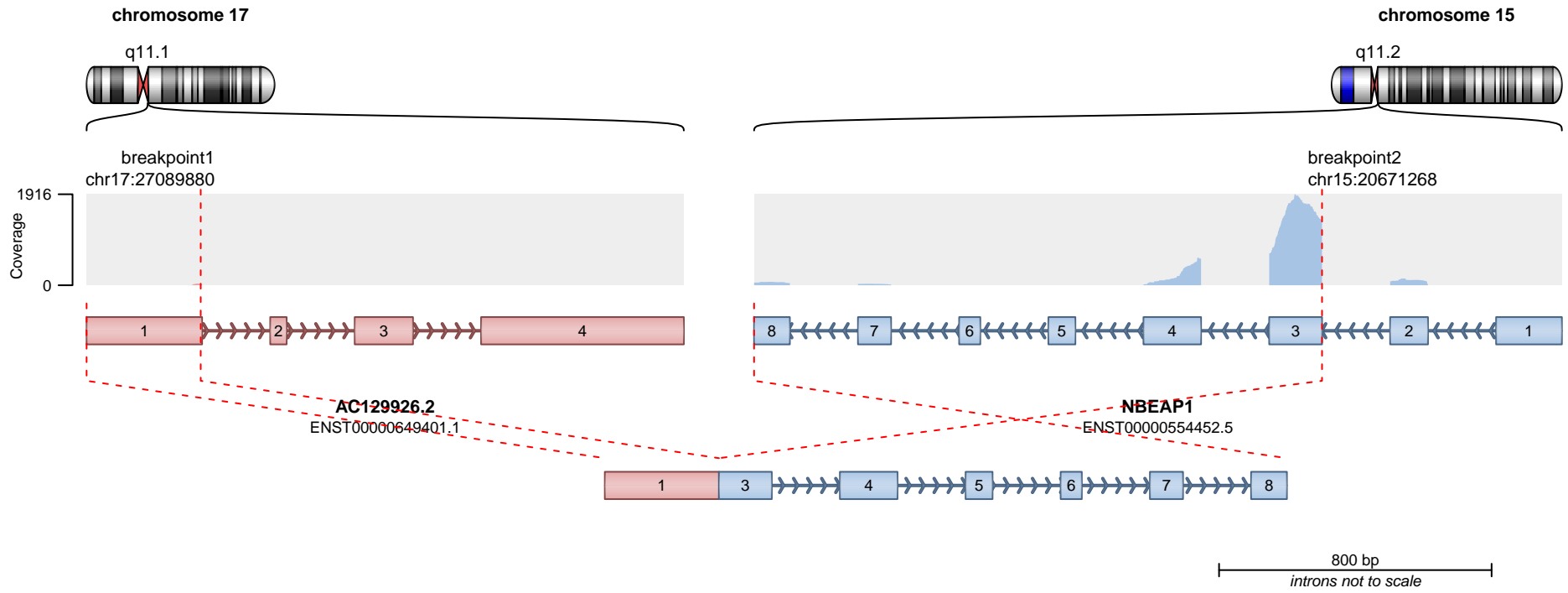


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 36
Discordant mates = 1

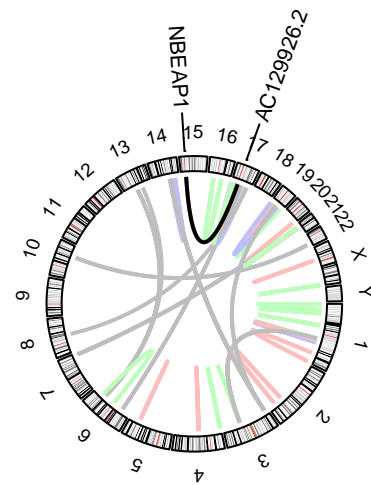
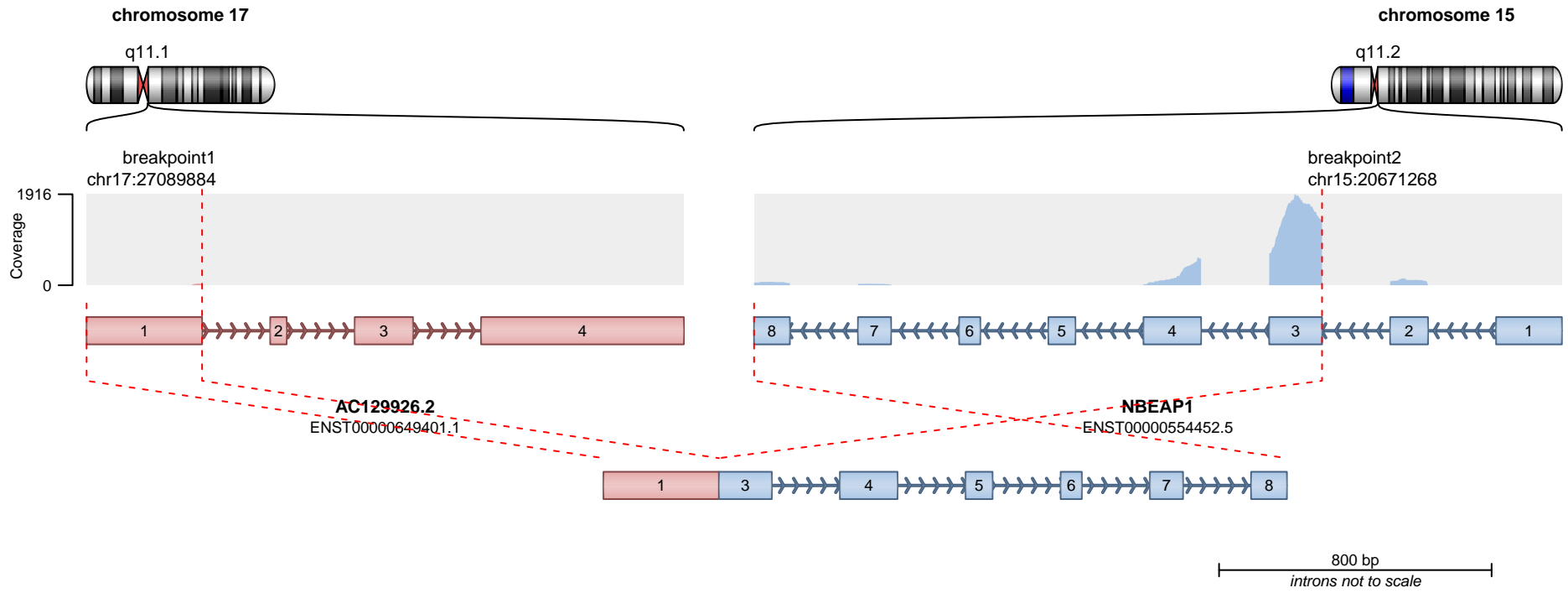


— translocation — deletion
— duplication — inversion

Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 30
Discordant mates = 0

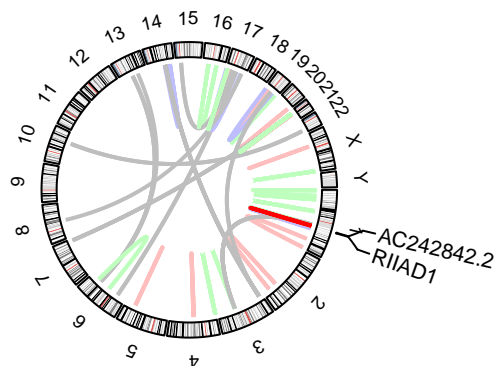
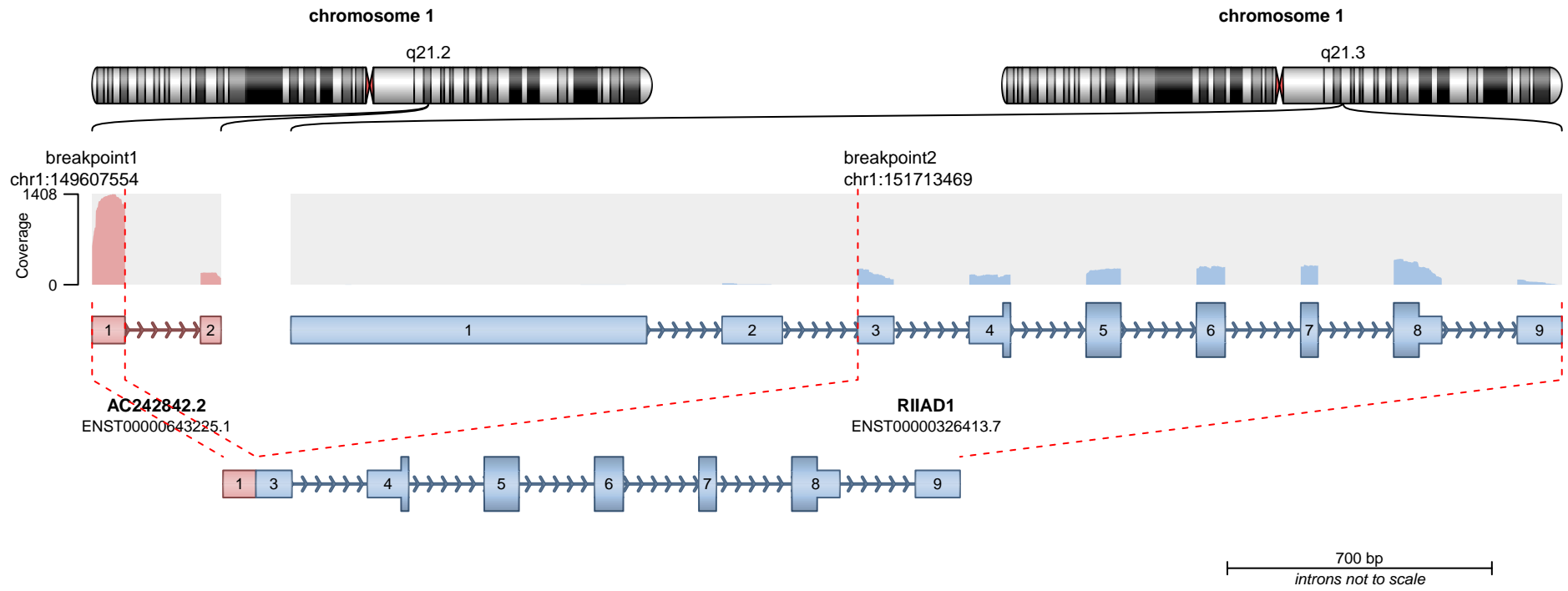


— translocation — deletion
— duplication — inversion

Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 23
Discordant mates = 0



RETAINED PROTEIN DOMAINS
reading frame unclear

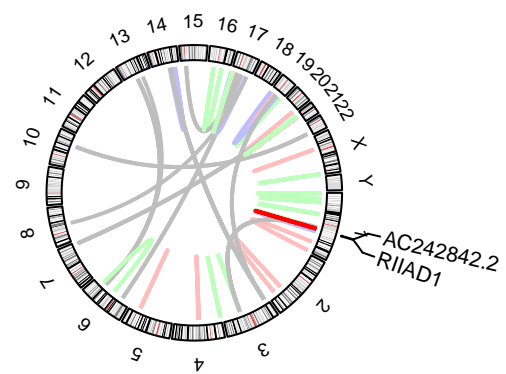
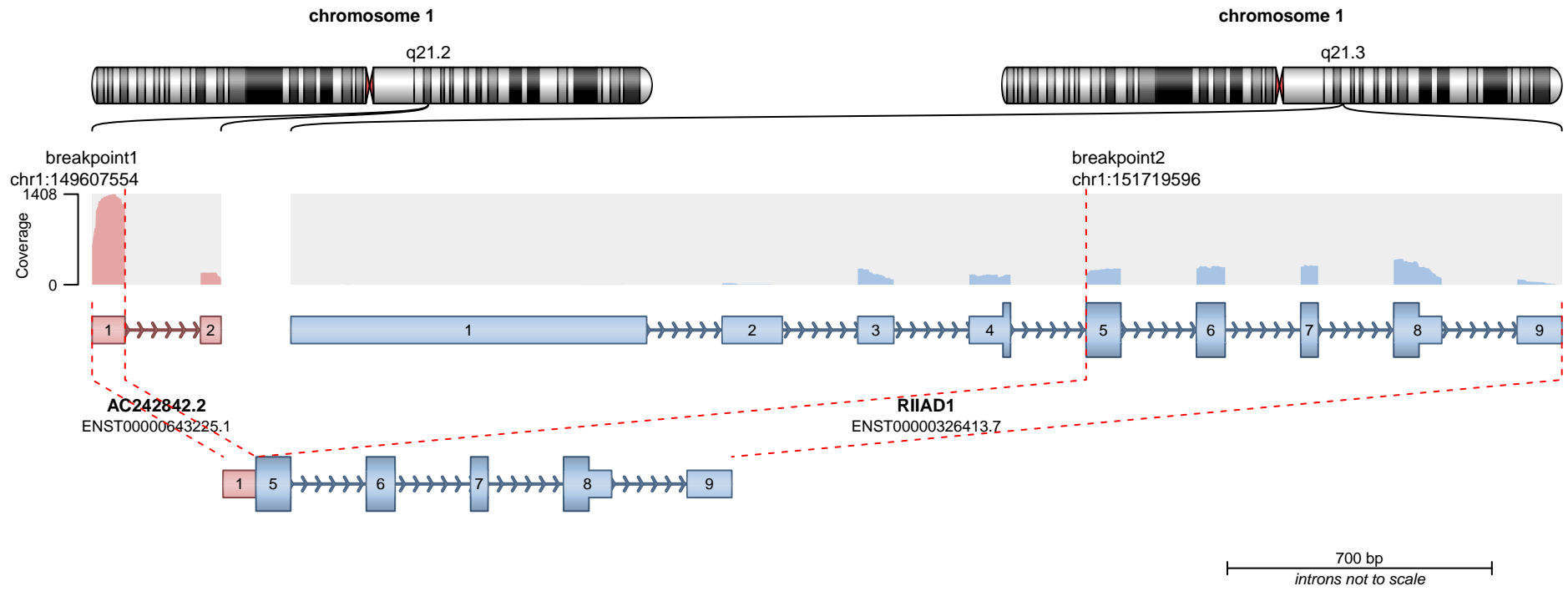


RIIAD1
Regulatory subunit of type II PKA R-subunit

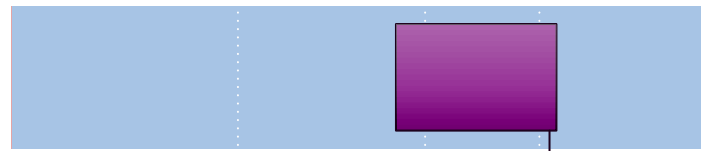
SUPPORTING READ COUNT

Split reads = 27
Discordant mates = 0

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

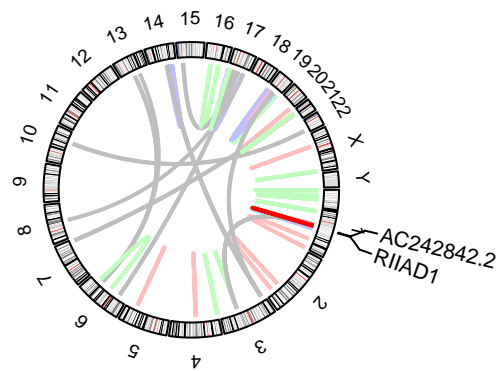
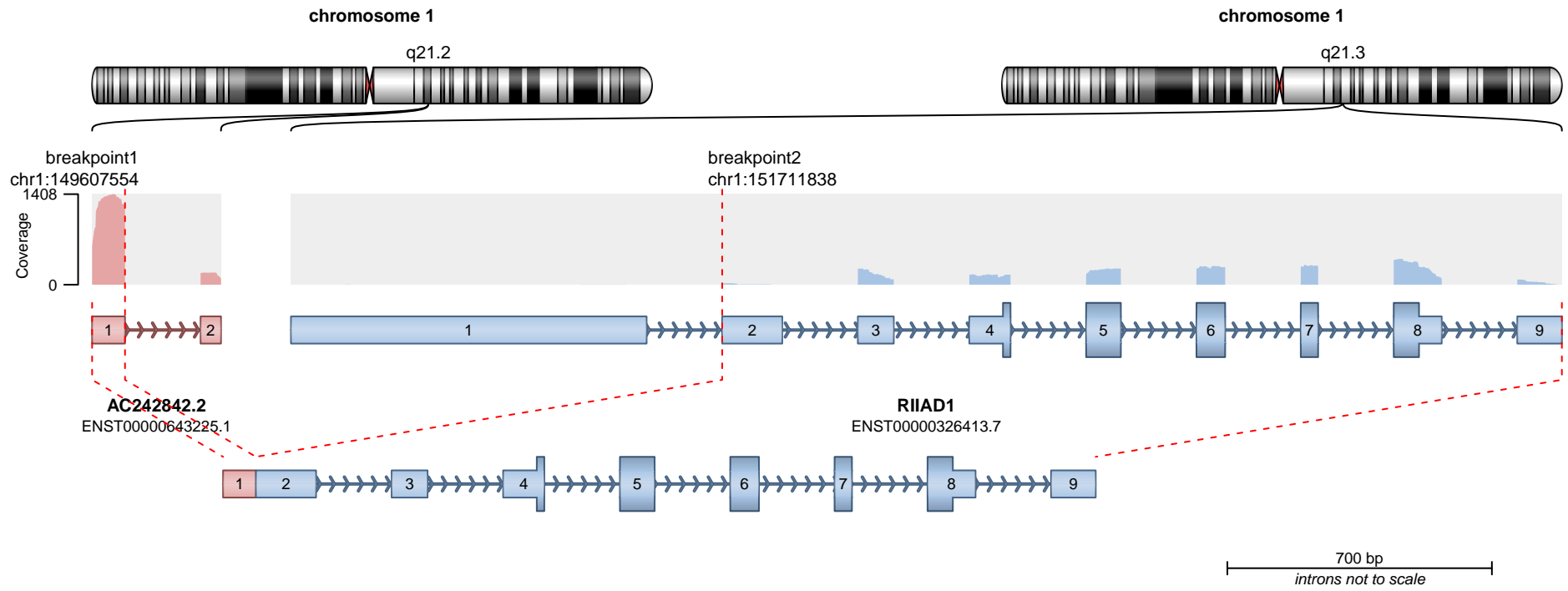


RIIAD1
Regulatory subunit of type II PKA R-subunit

SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

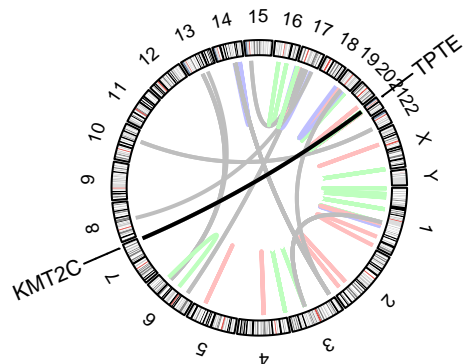
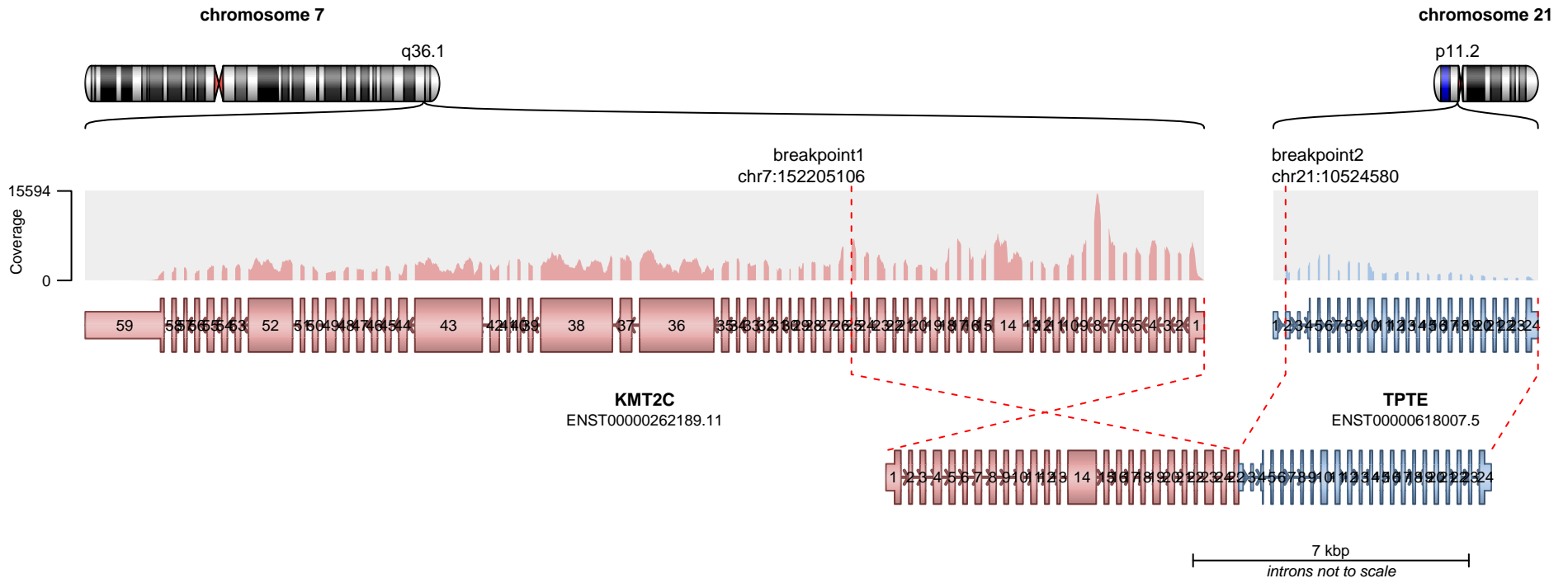


RIIAD1
Regulatory subunit of type II PKA R-subunit

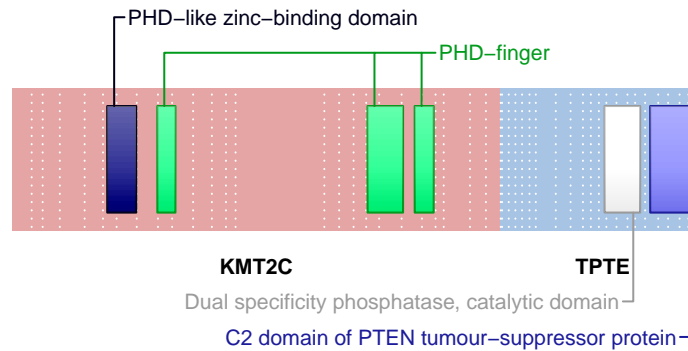
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

— translocation — deletion
— duplication — inversion



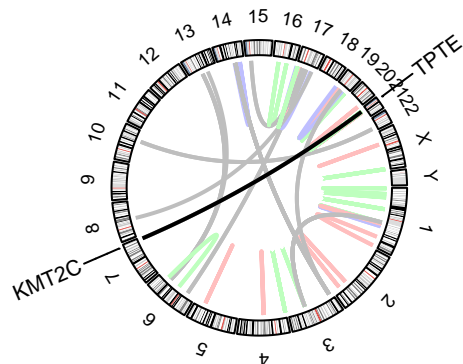
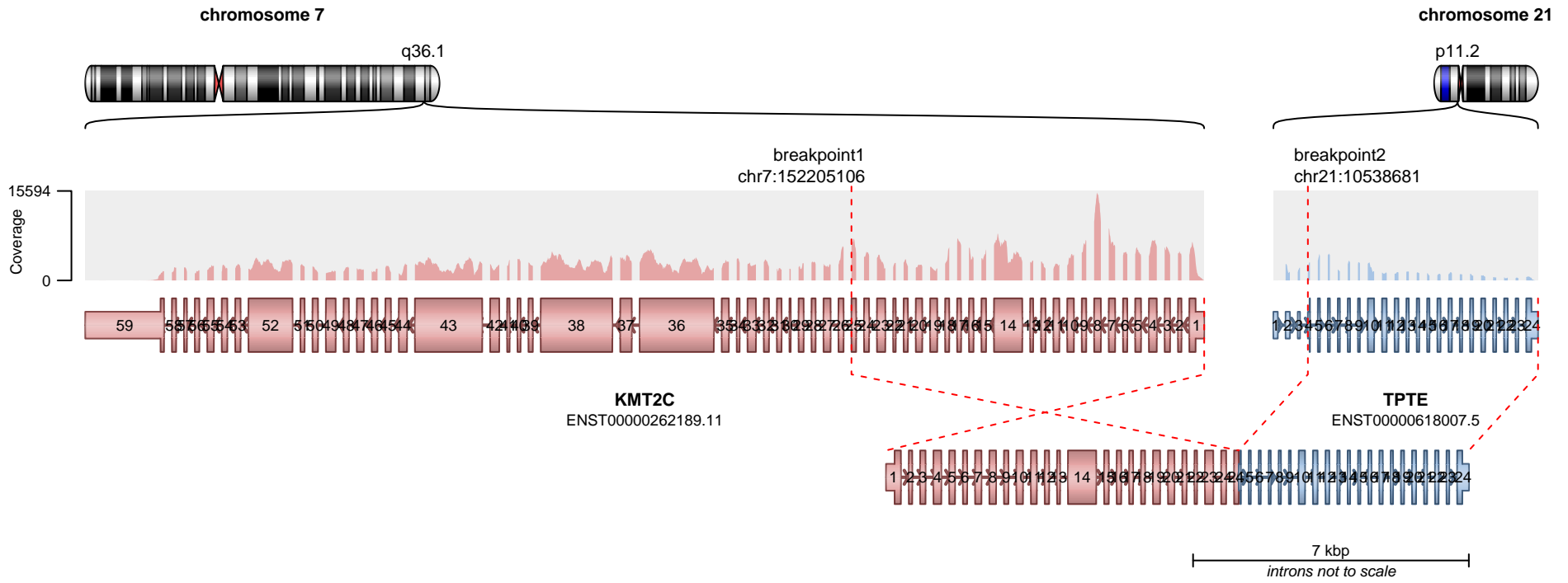
RETAINED PROTEIN DOMAINS
reading frame unclear



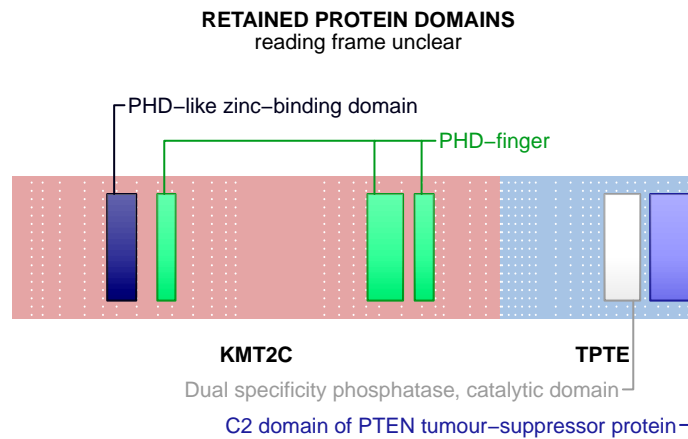
SUPPORTING READ COUNT

Split reads = 26
Discordant mates = 2

- translocation
- duplication
- deletion
- inversion

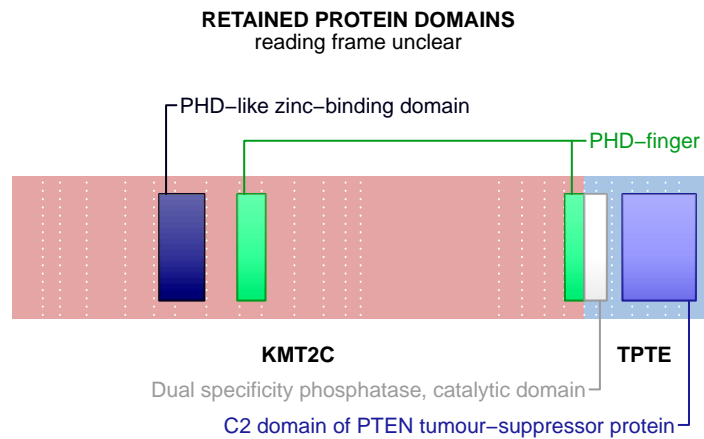
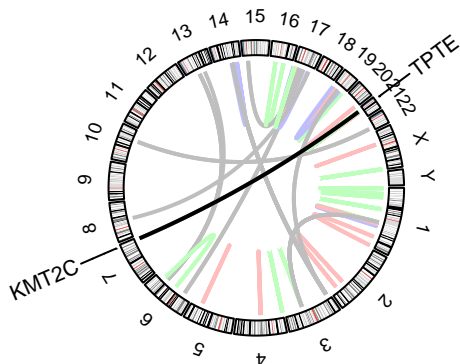
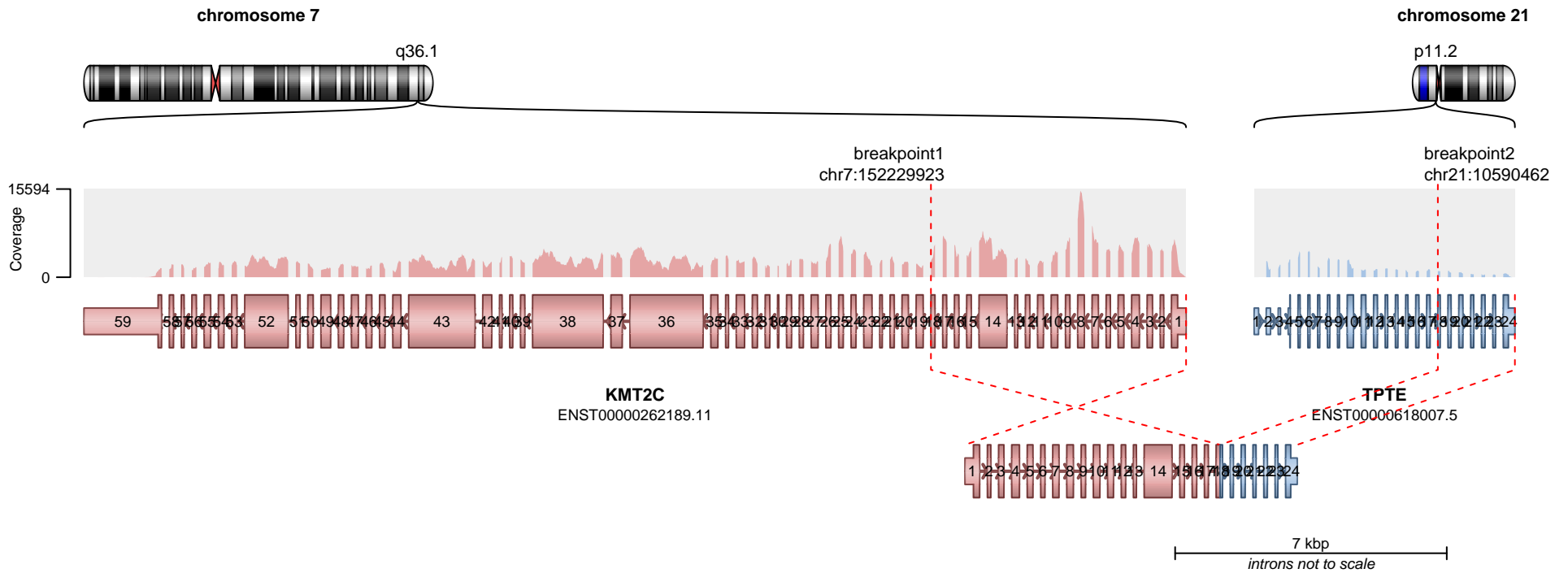


— translocation — deletion
 — duplication — inversion



SUPPORTING READ COUNT

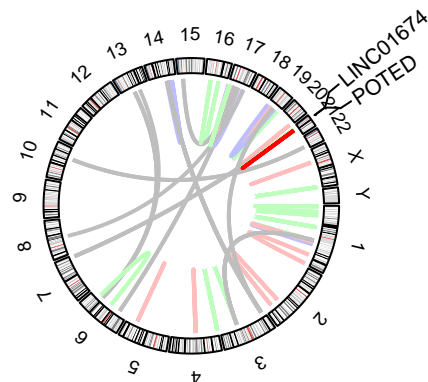
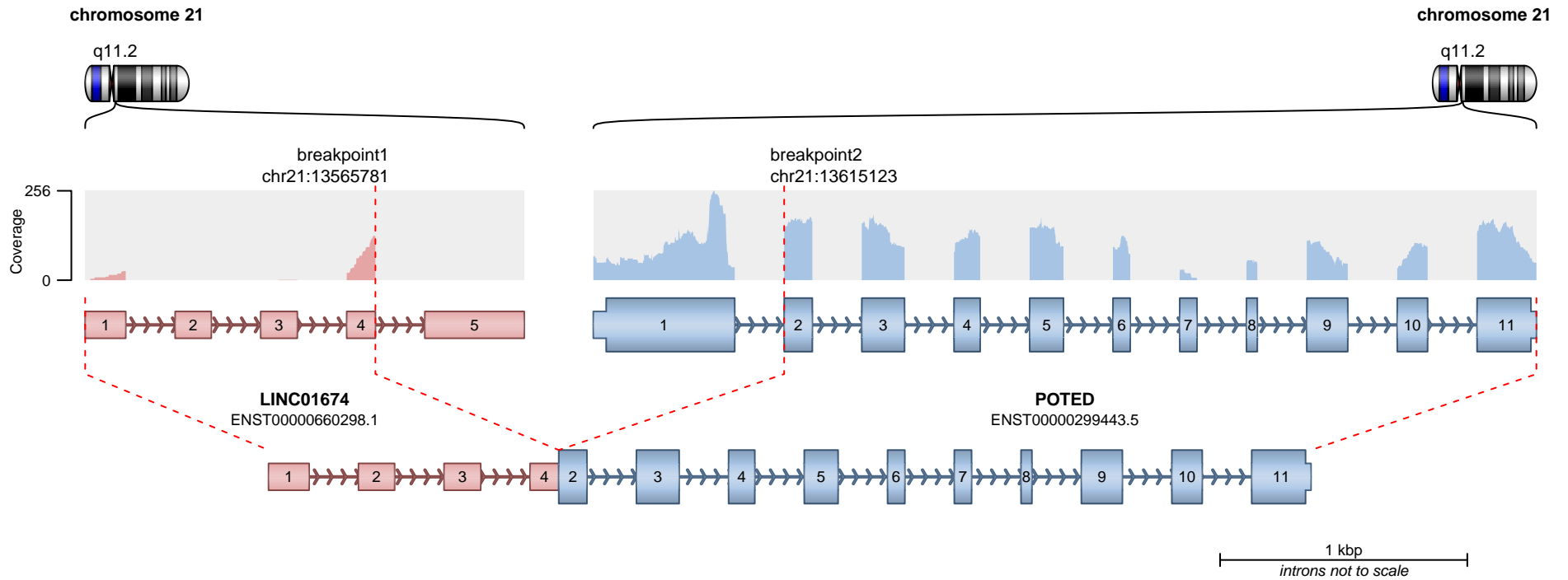
Split reads = 4
 Discordant mates = 0



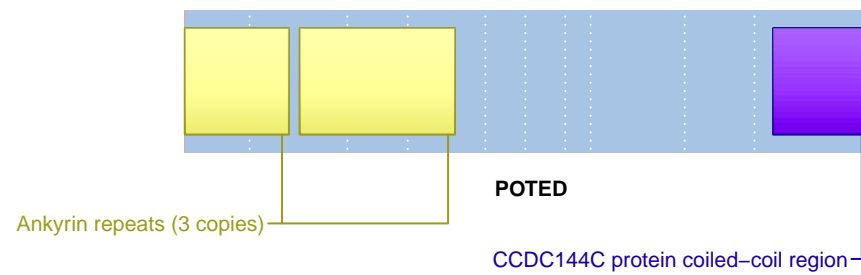
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



RETAINED PROTEIN DOMAINS
reading frame unclear



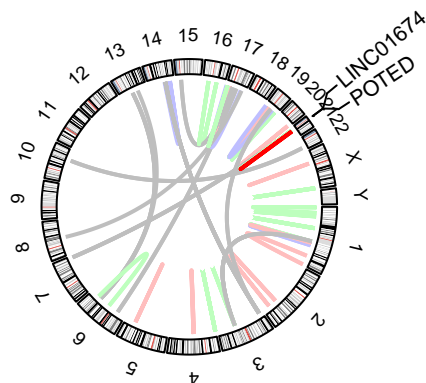
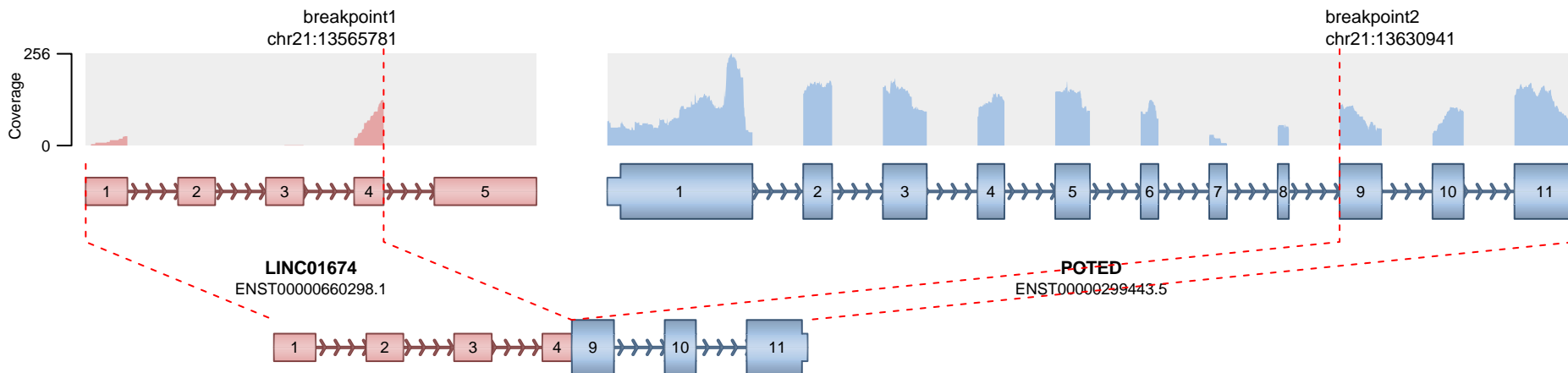
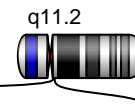
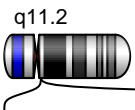
SUPPORTING READ COUNT

Split reads = 26
Discordant mates = 1

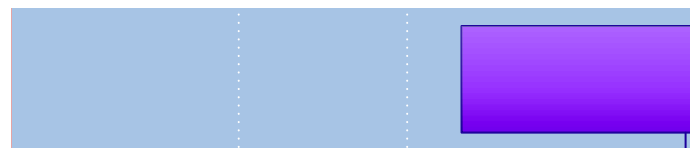
- translocation
- duplication
- deletion
- inversion

chromosome 21

chromosome 21



RETAINED PROTEIN DOMAINS
reading frame unclear

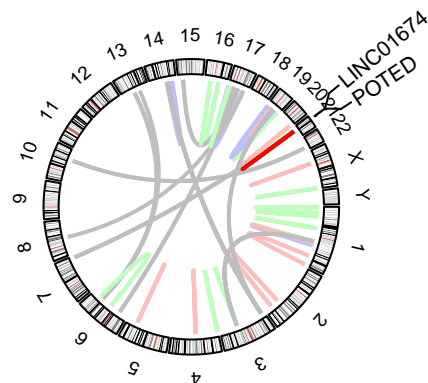
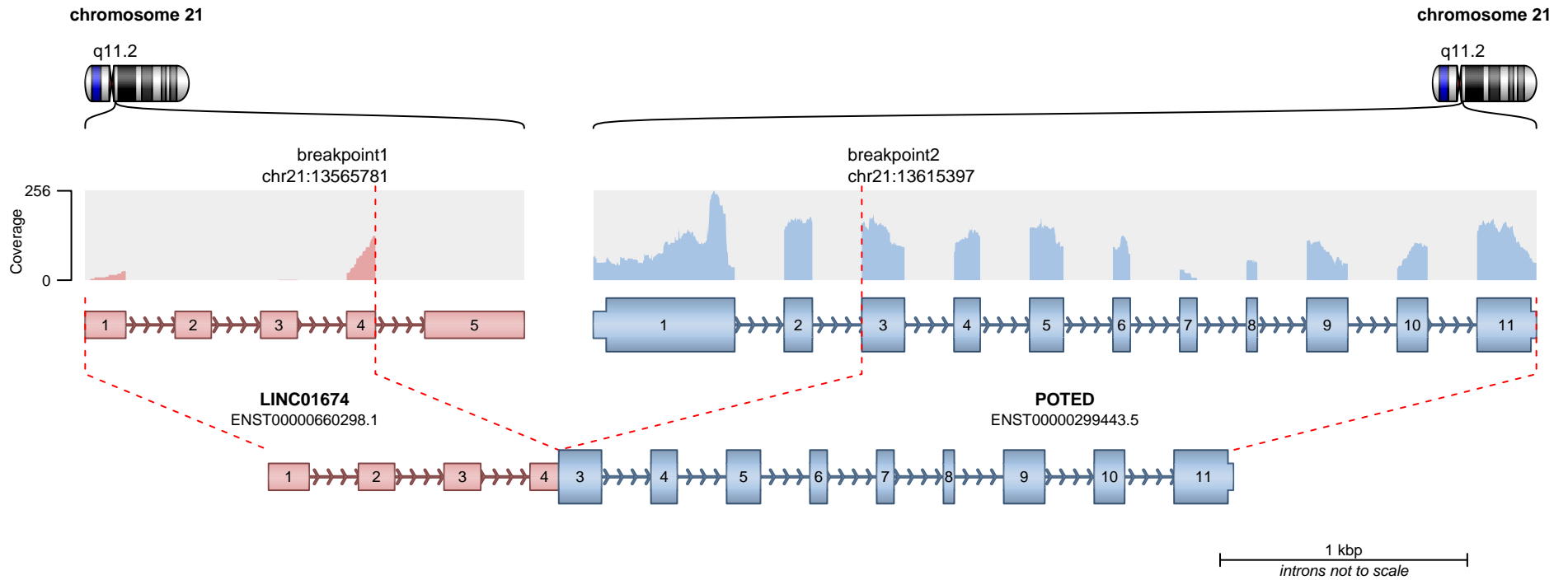


POTES
CCDC144C protein coiled-coil region

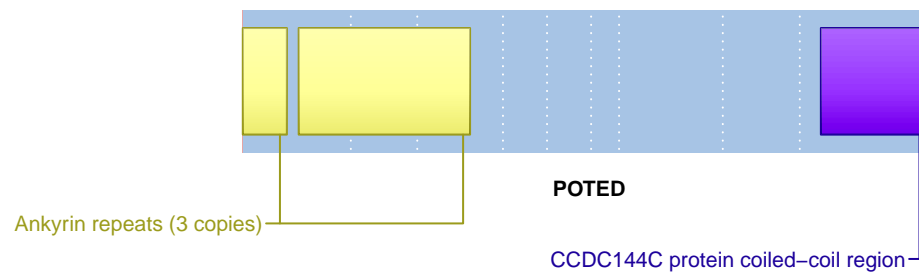
SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 0

— translocation — deletion
— duplication — inversion



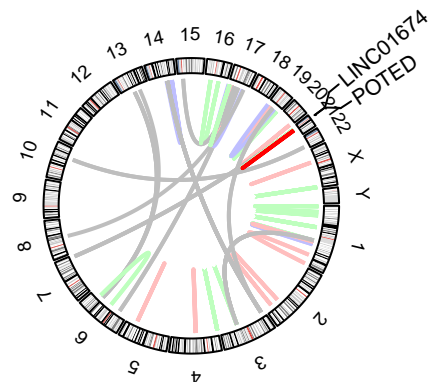
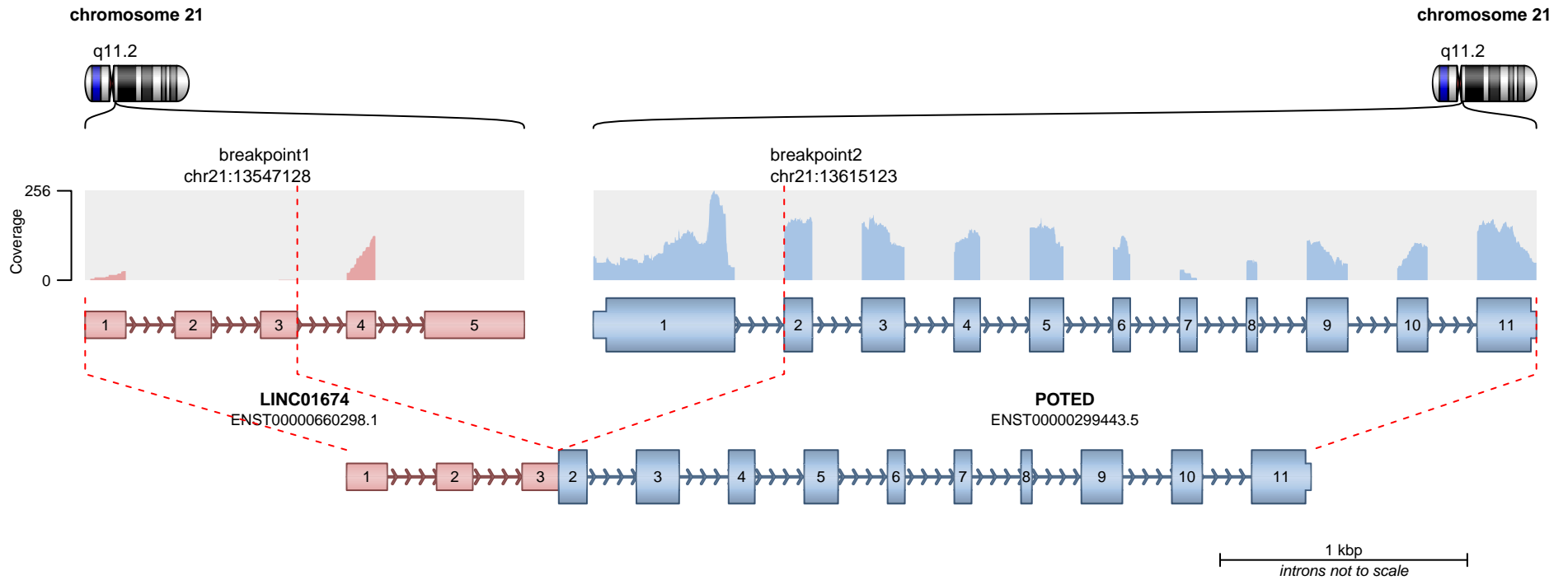
RETAINED PROTEIN DOMAINS
reading frame unclear



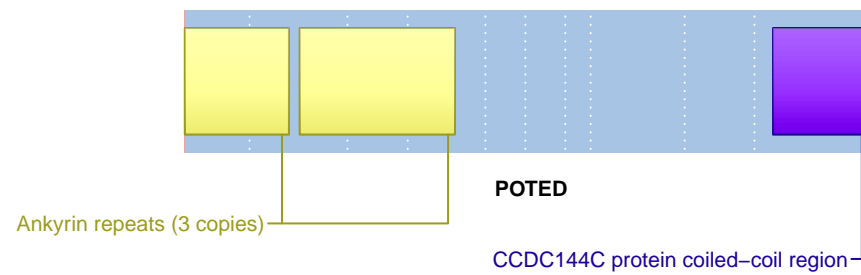
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 1

— translocation — deletion
— duplication — inversion



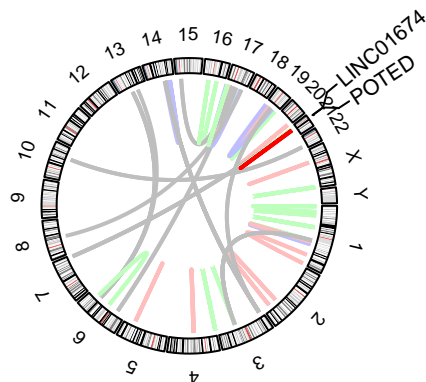
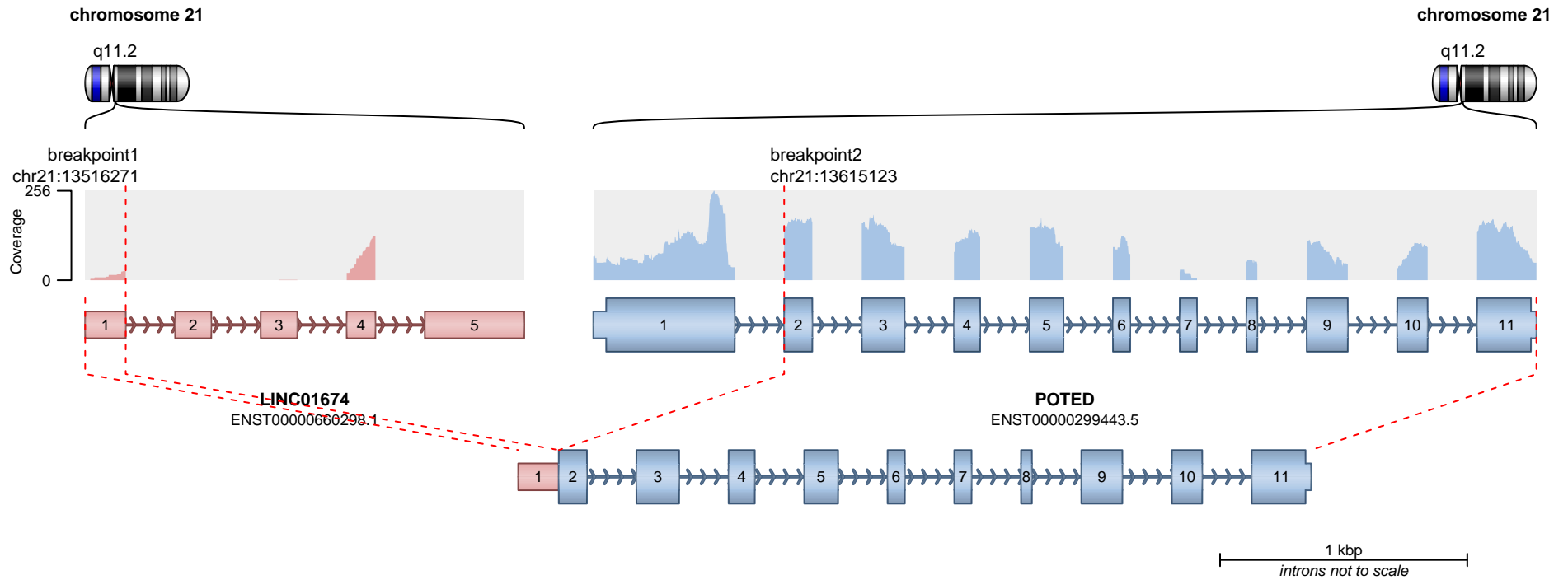
RETAINED PROTEIN DOMAINS
reading frame unclear



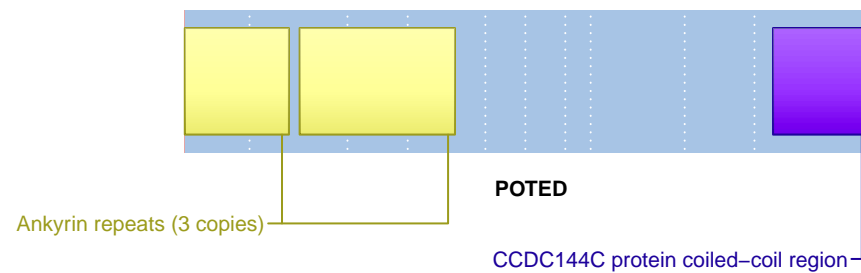
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



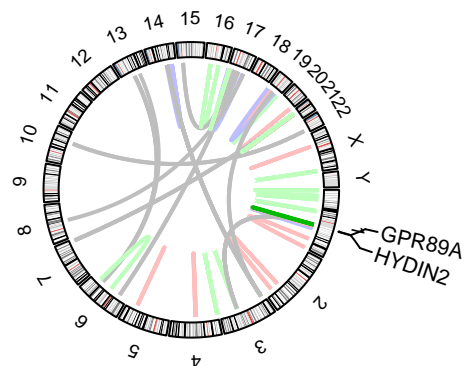
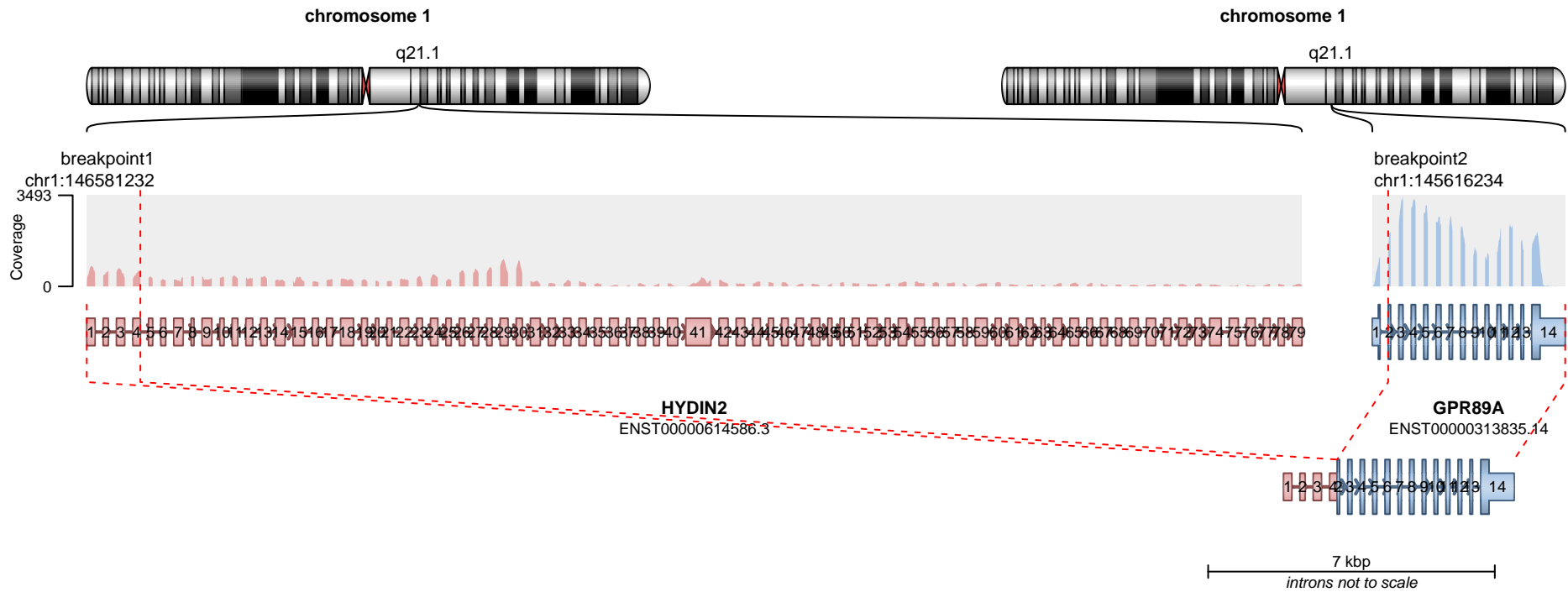
RETAINED PROTEIN DOMAINS
reading frame unclear



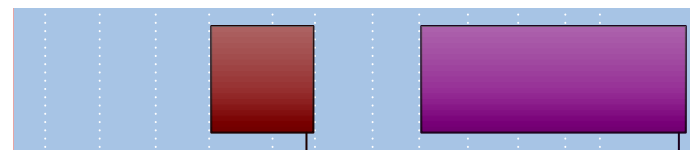
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

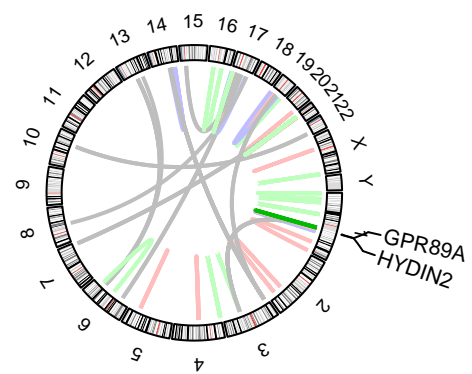
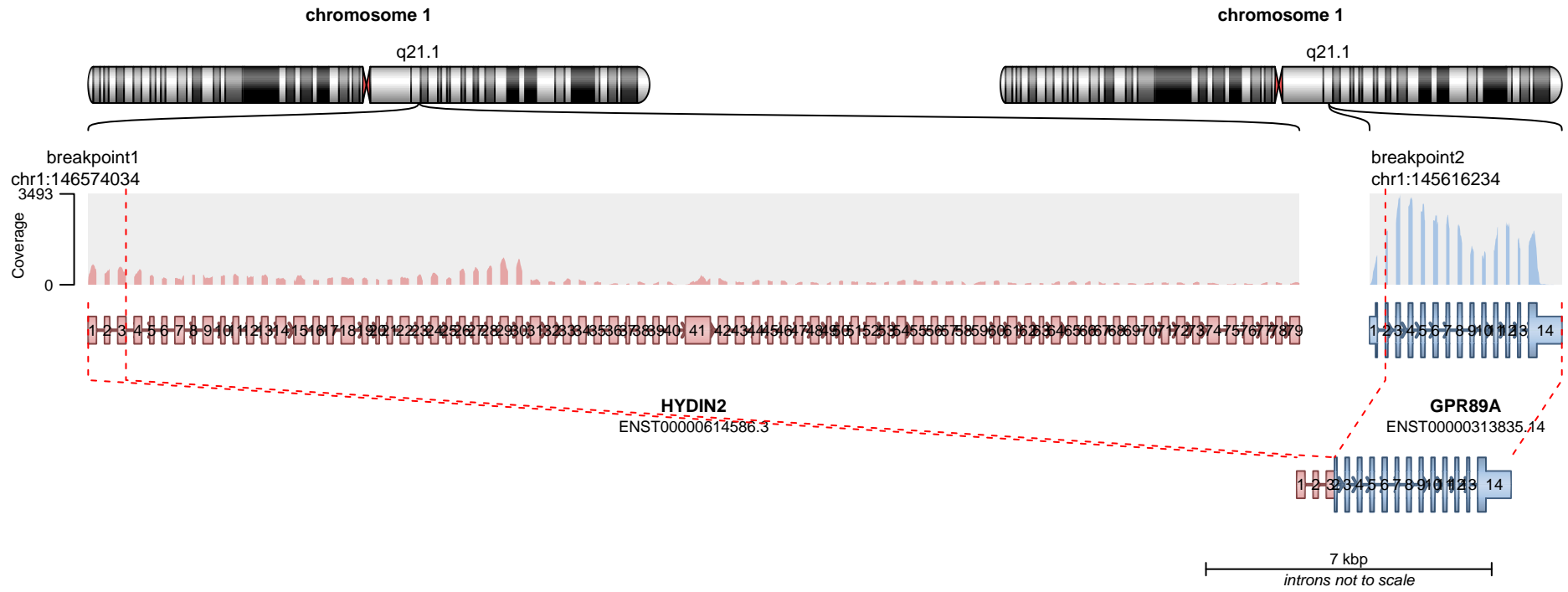


SUPPORTING READ COUNT

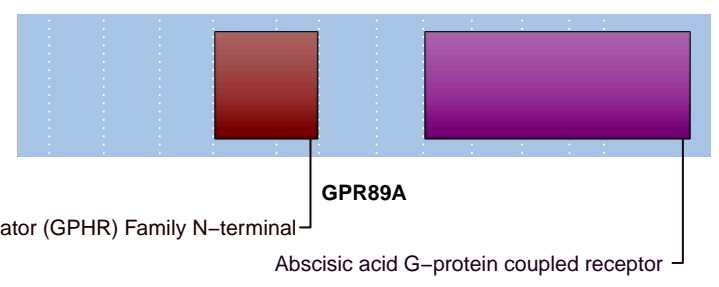
Split reads = 25
Discordant mates = 2

The Golgi pH Regulator (GPHR) Family N-terminal

- translocation
- duplication
- deletion
- inversion



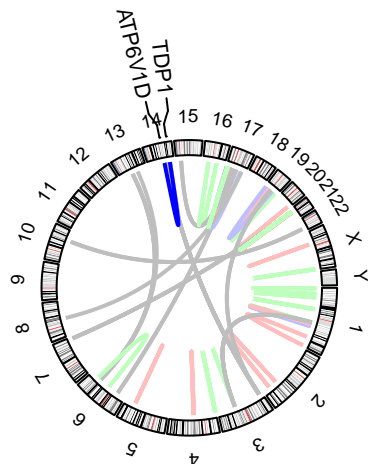
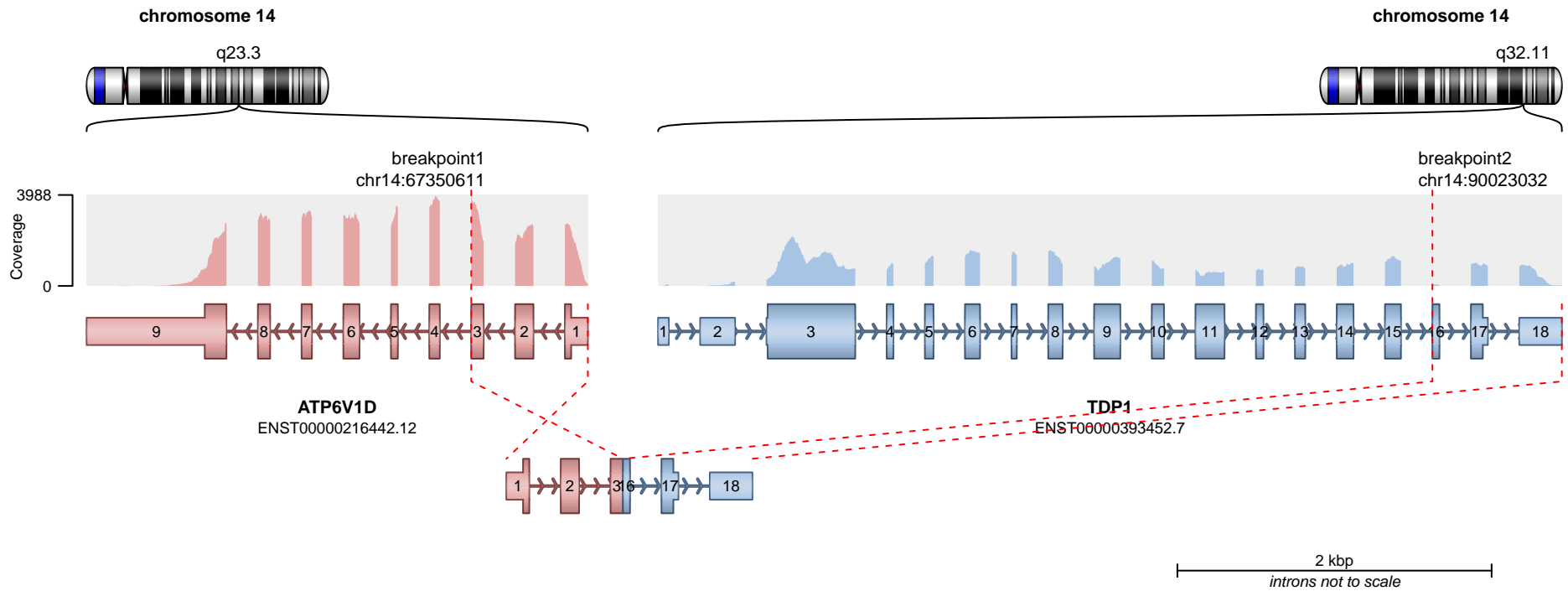
RETAINED PROTEIN DOMAINS
reading frame unclear



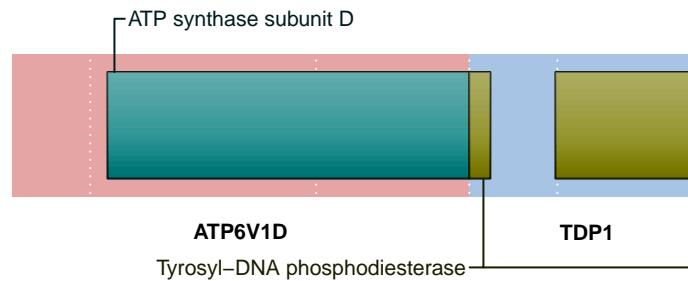
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



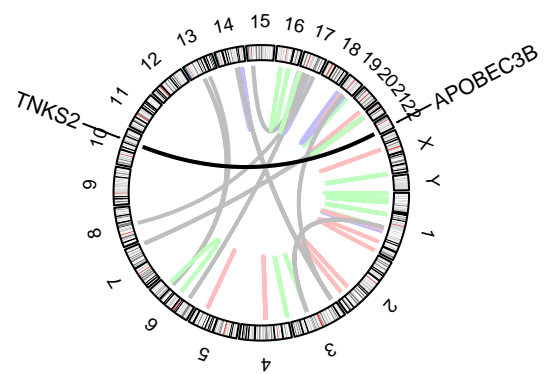
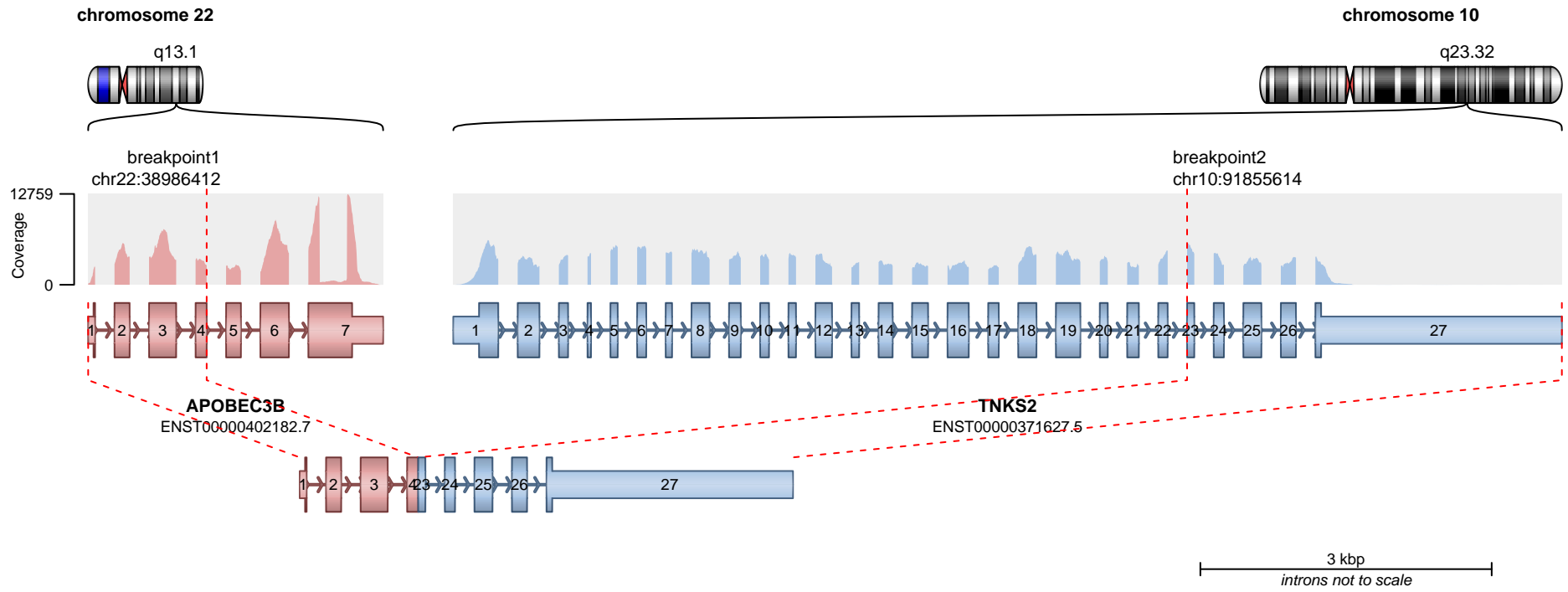
RETAINED PROTEIN DOMAINS
reading frame unclear



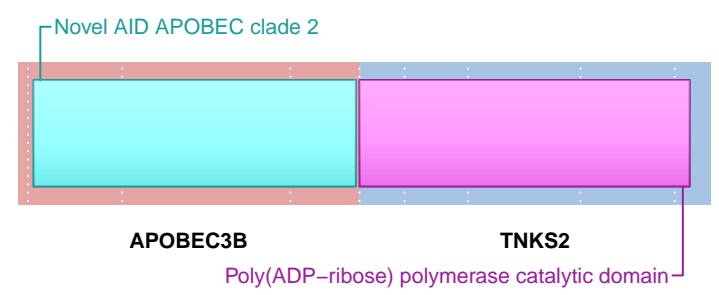
SUPPORTING READ COUNT

Split reads = 23
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



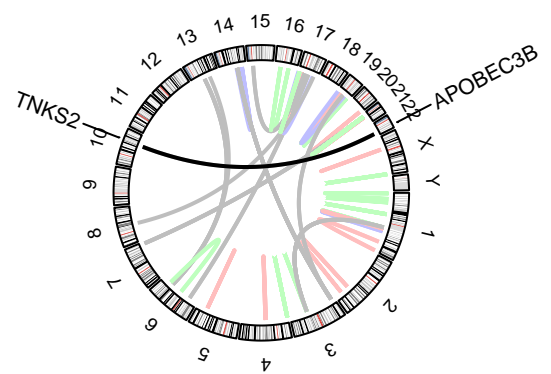
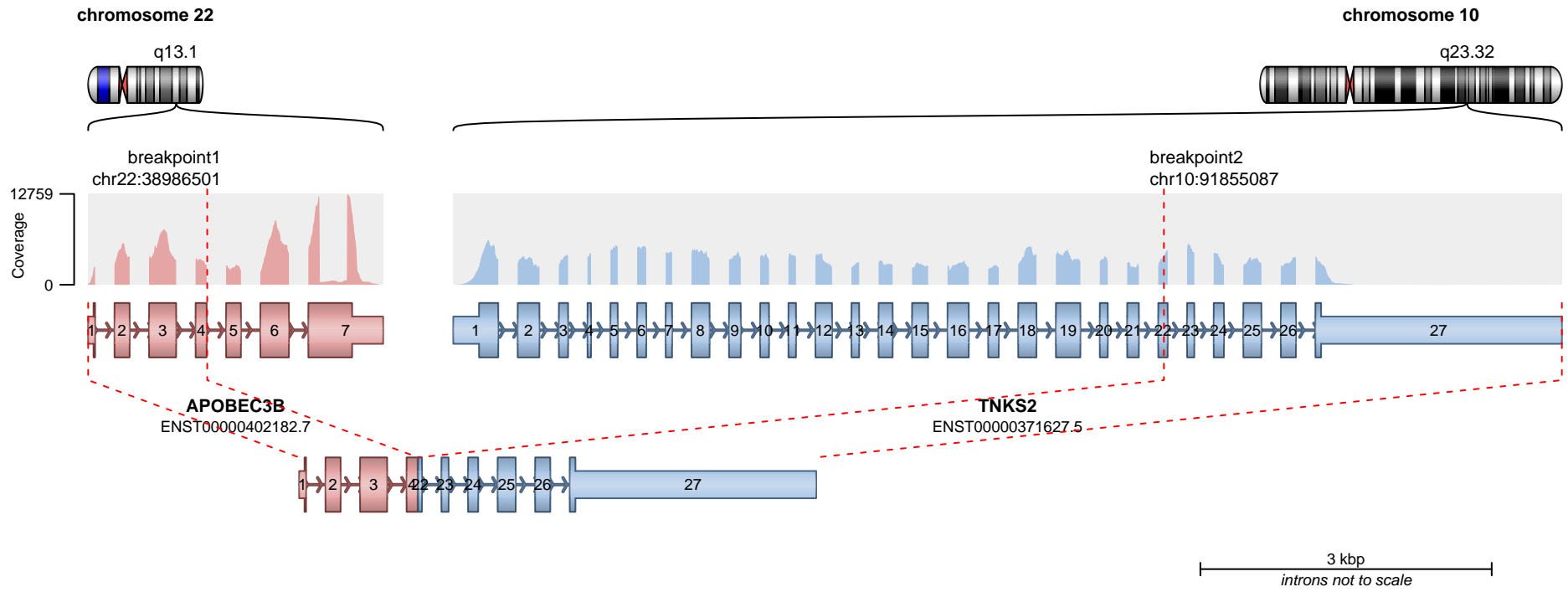
RETAINED PROTEIN DOMAINS
reading frame unclear



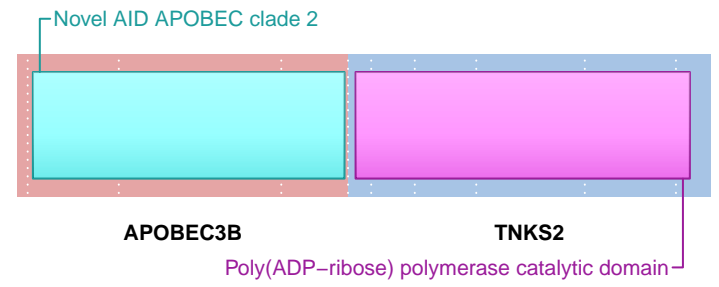
SUPPORTING READ COUNT

Split reads = 22
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



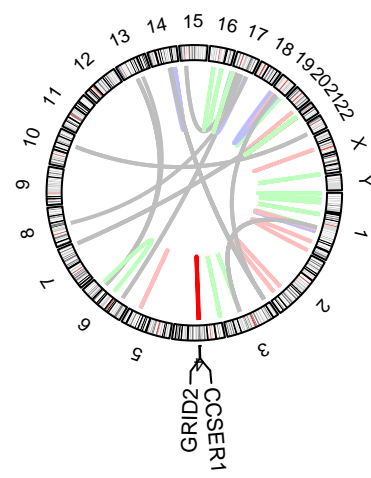
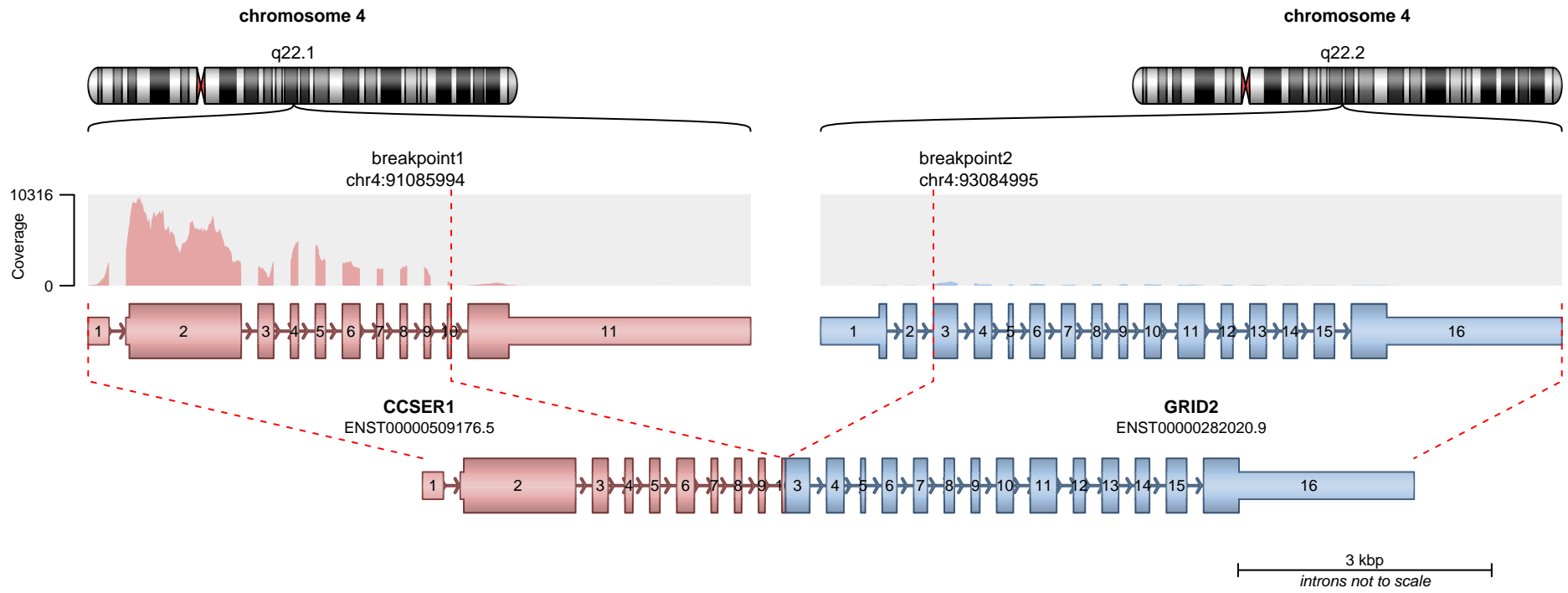
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

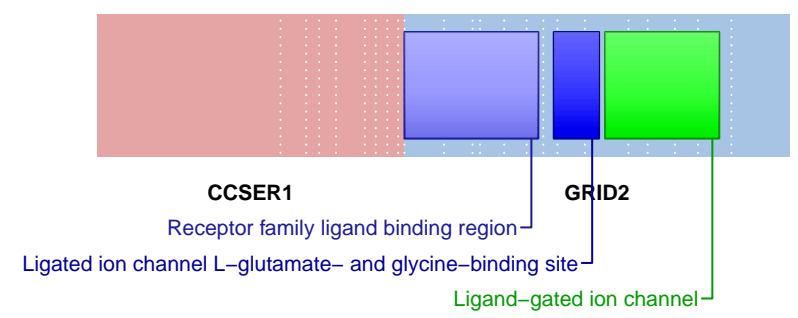
Split reads = 3
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion



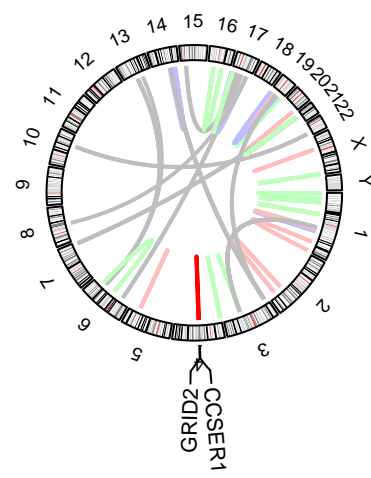
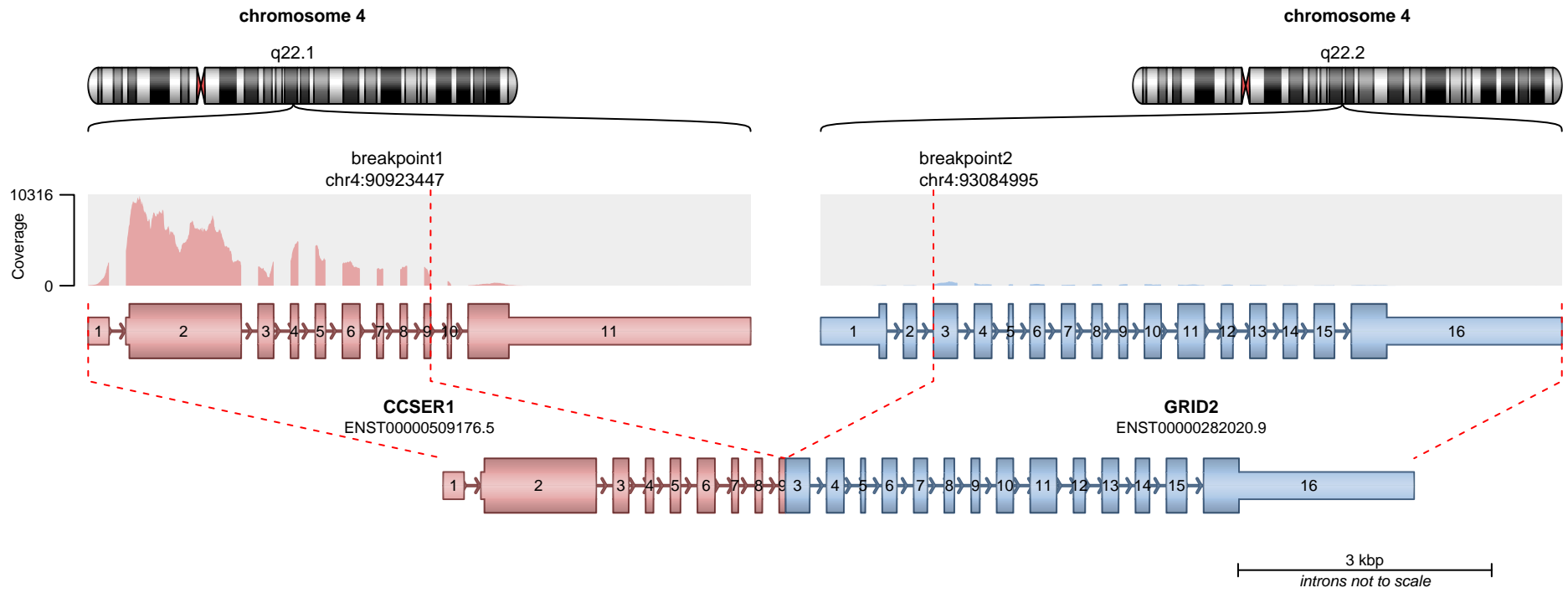
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



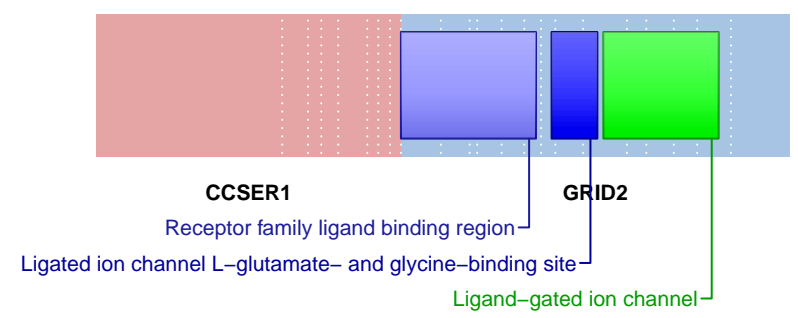
SUPPORTING READ COUNT

Split reads = 21
Discordant mates = 1



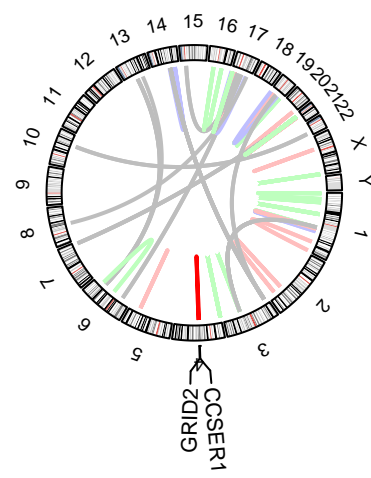
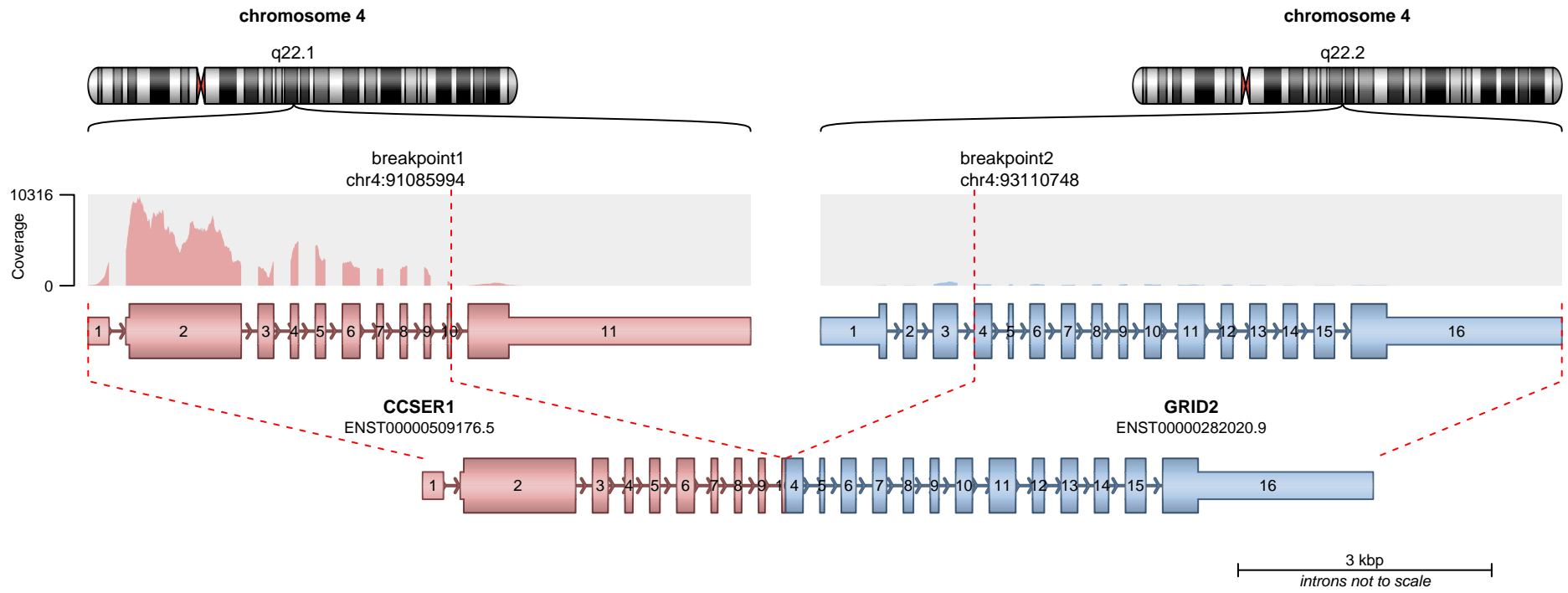
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



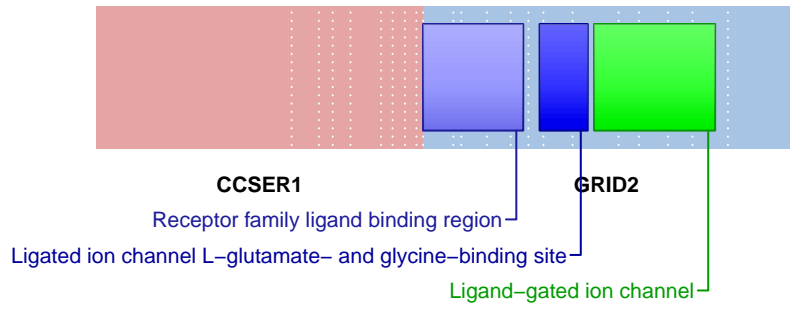
SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 1



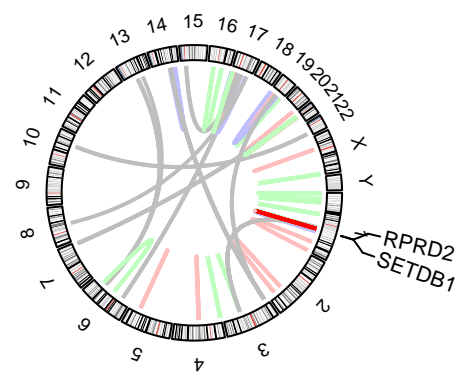
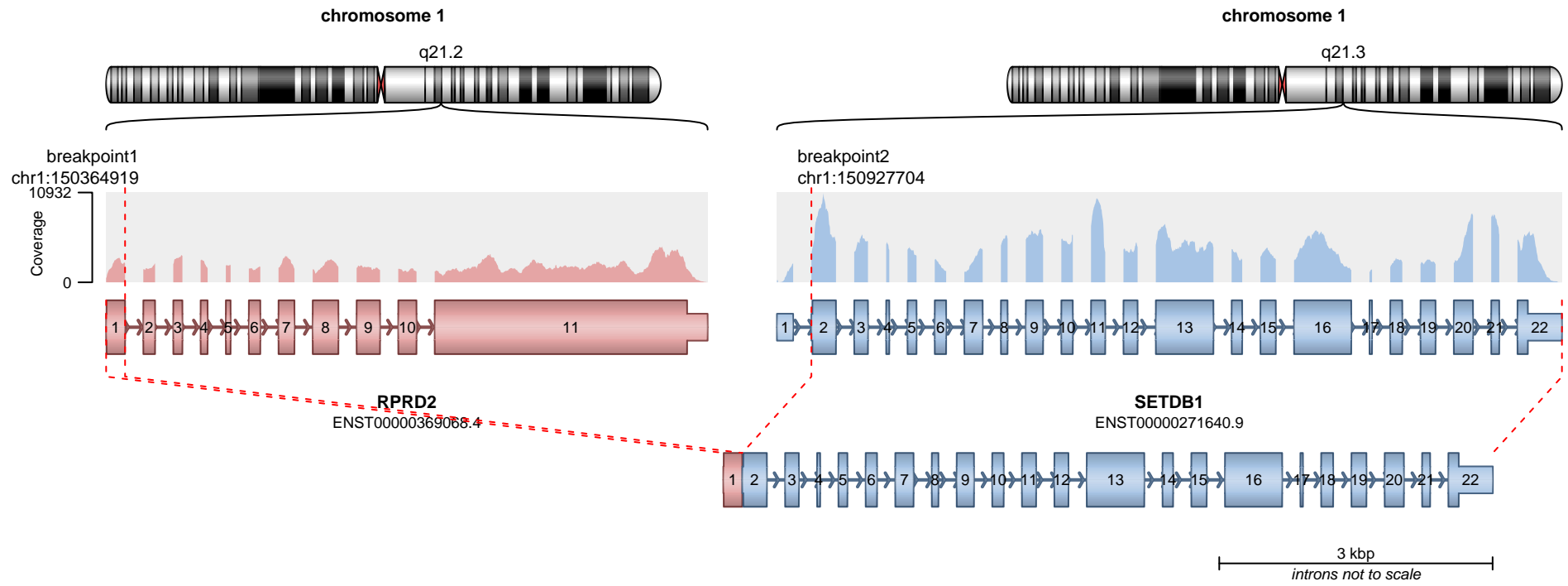
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



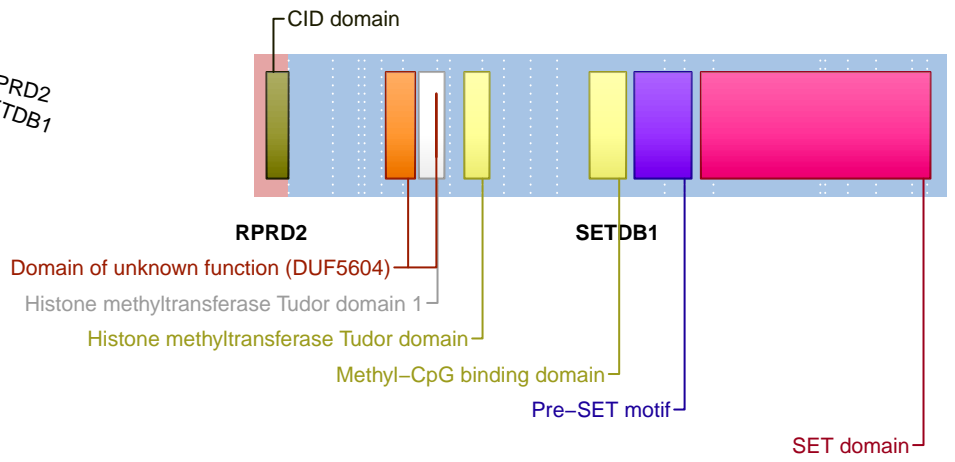
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0



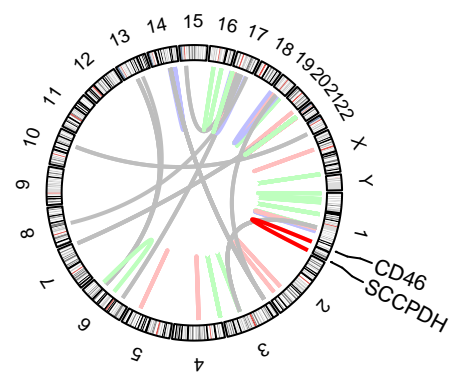
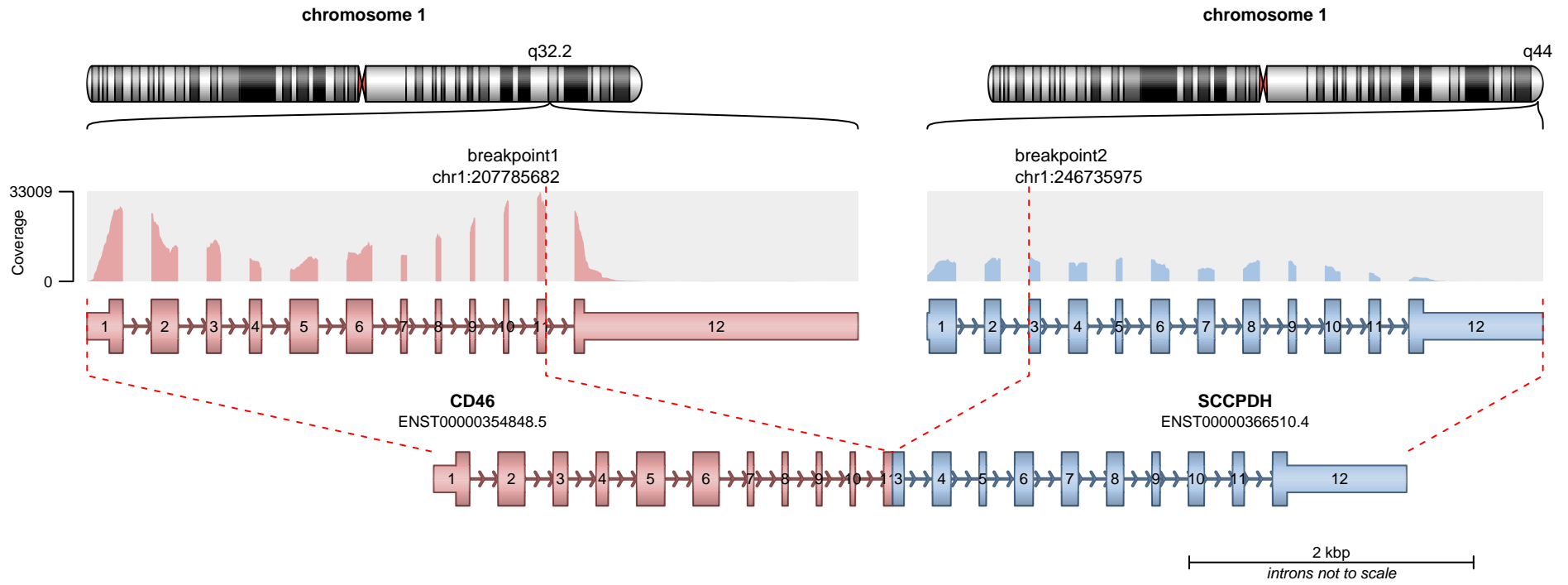
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear

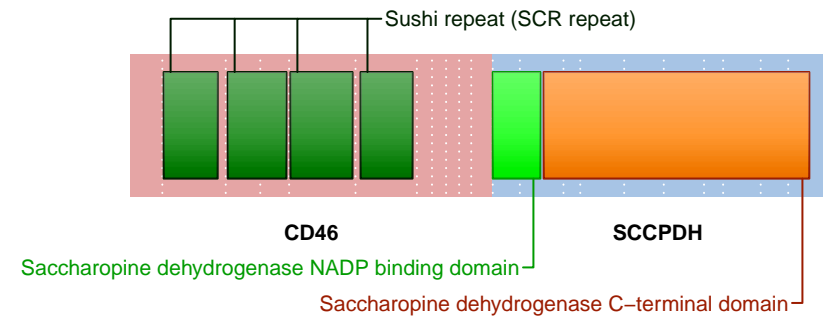


SUPPORTING READ COUNT

Split reads = 21
Discordant mates = 1



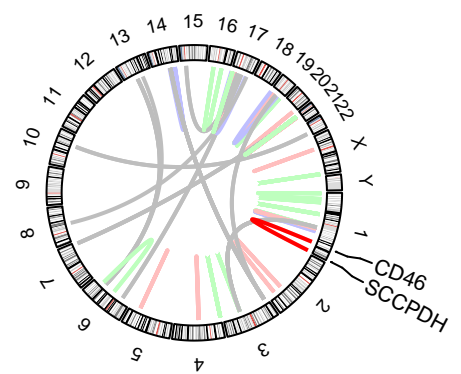
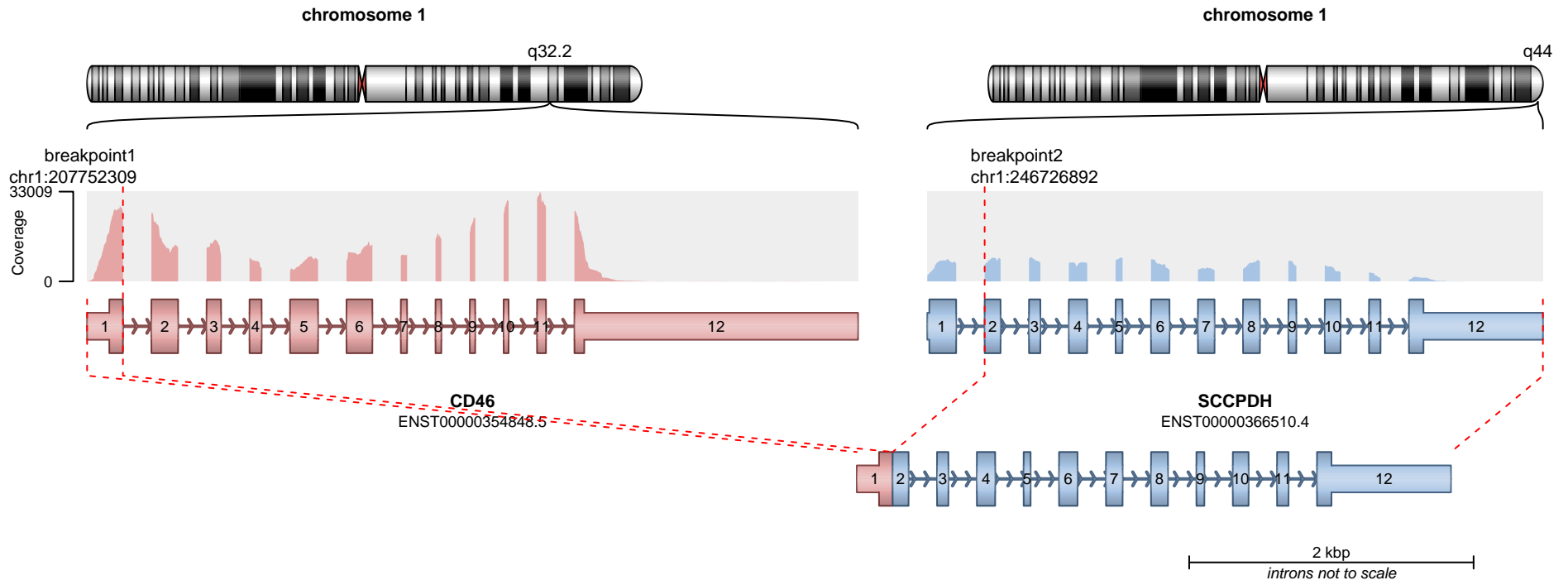
RETAINED PROTEIN DOMAINS
reading frame unclear



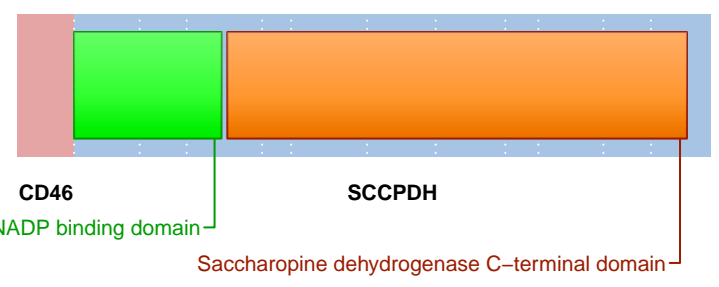
SUPPORTING READ COUNT

Split reads = 21
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



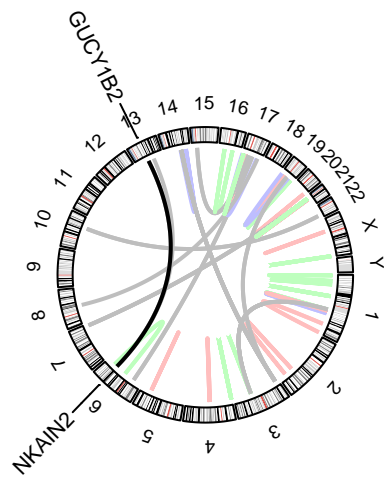
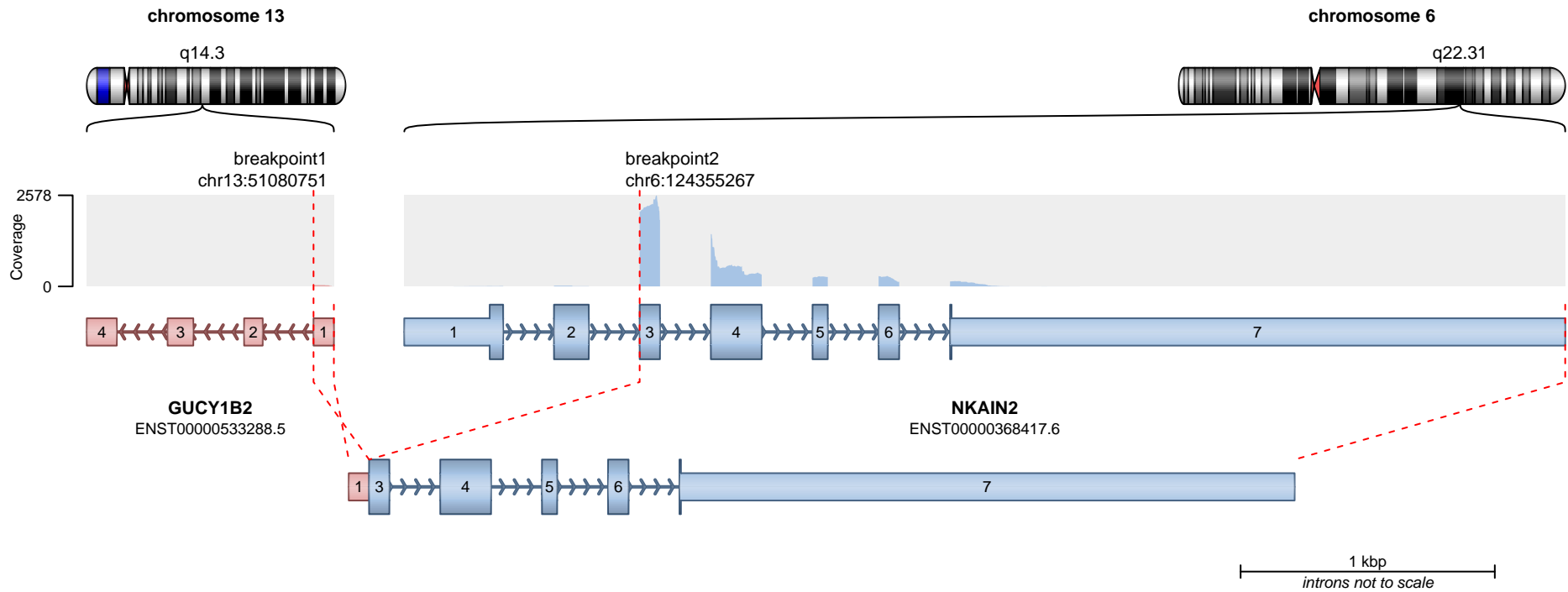
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



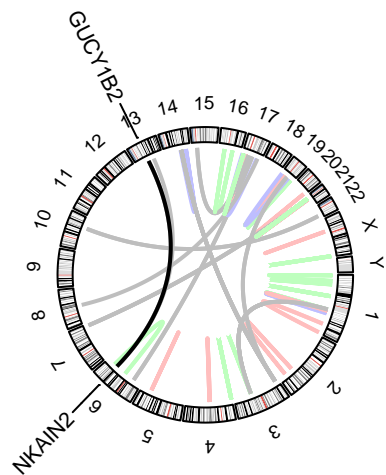
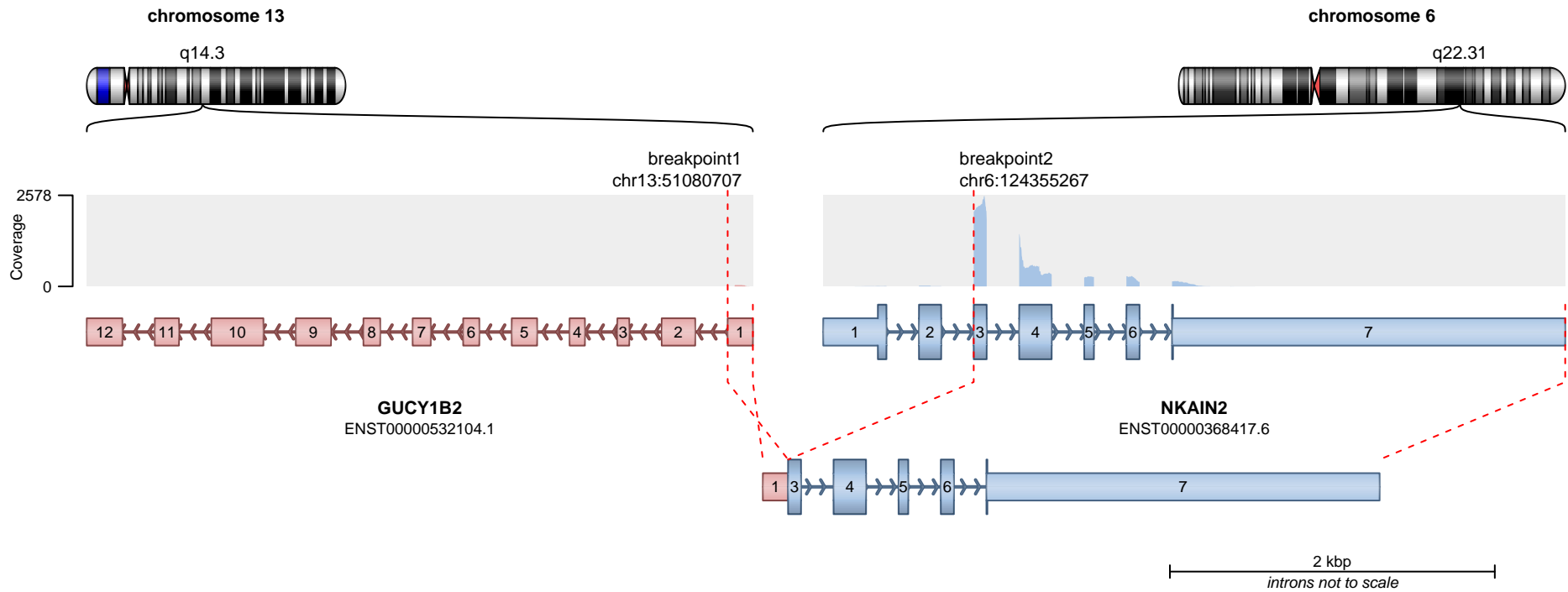
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 21
Discordant mates = 0

— translocation — deletion
— duplication — inversion



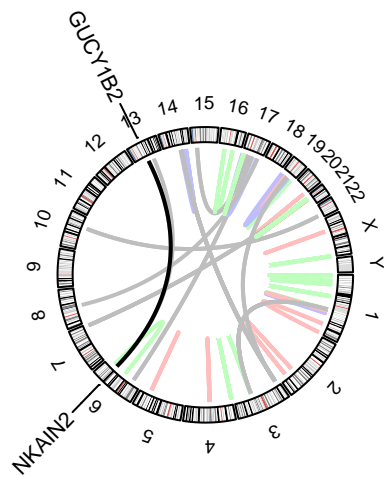
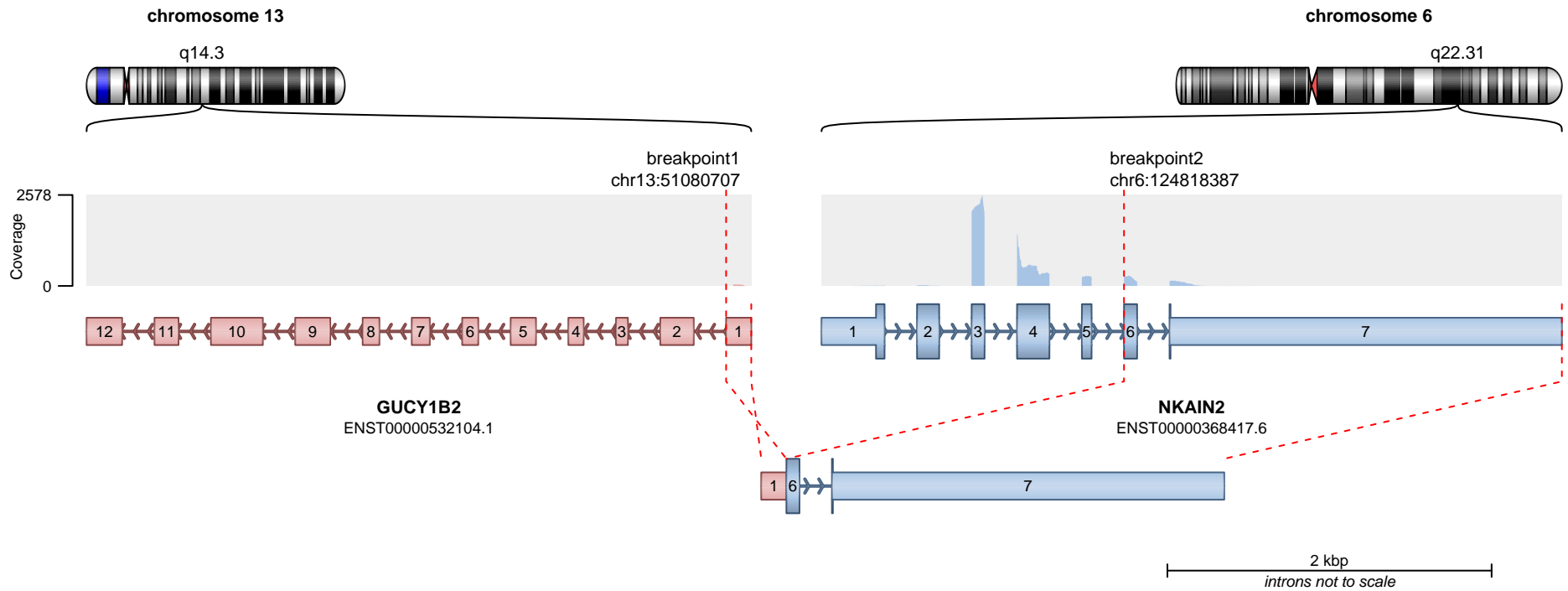
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS
reading frame unclear



NKAIN2

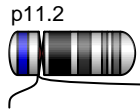
Na,K-ATpase Interacting protein

SUPPORTING READ COUNT

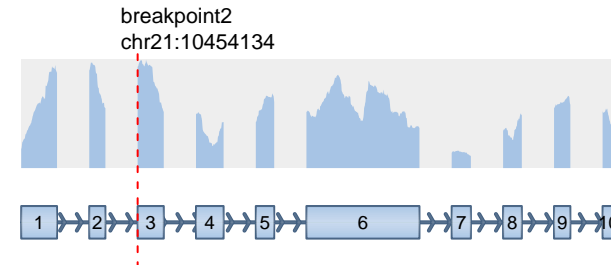
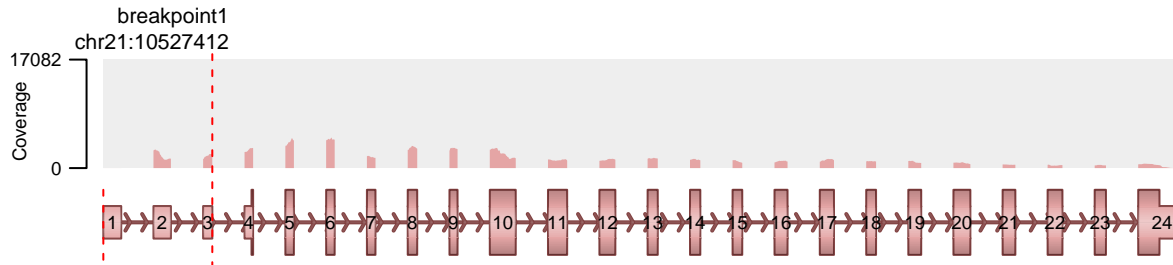
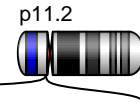
Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion

chromosome 21



chromosome 21

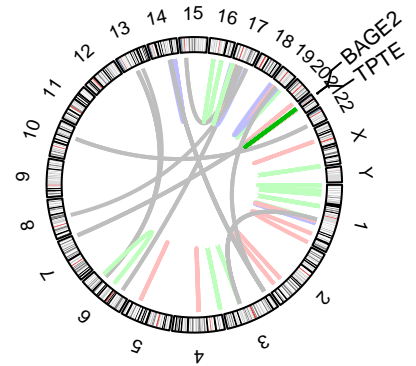


TPTE
ENST00000618007.5

BAGE2
ENST00000470054.5



2 kbp
introns not to scale



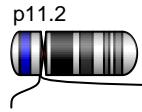
— translocation — deletion
— duplication — inversion

No coding regions retained in fusion transcript.

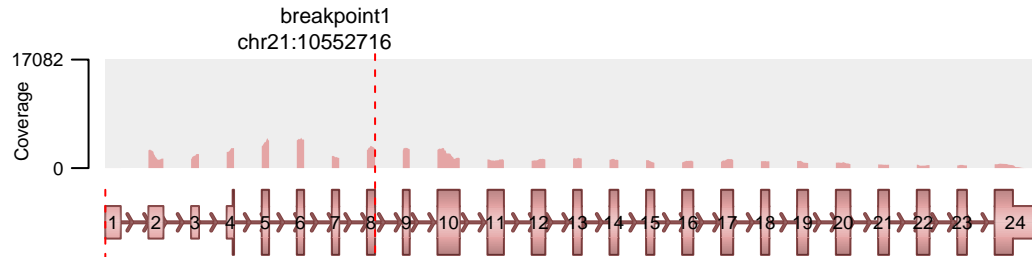
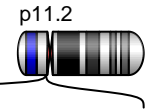
SUPPORTING READ COUNT

Split reads = 18
Discordant mates = 2

chromosome 21

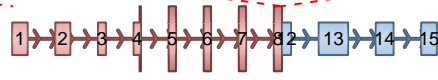


chromosome 21

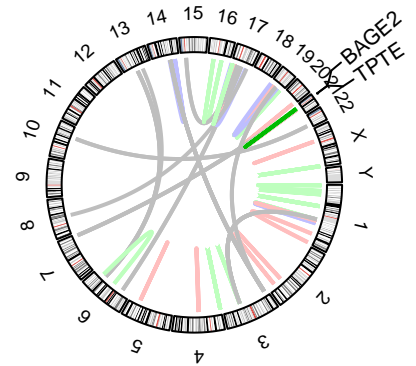


TPTE
ENST00000618007.5

BAGE2
ENST00000496773.1



2 kbp
introns not to scale



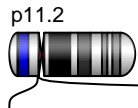
No protein domains retained in fusion.

SUPPORTING READ COUNT

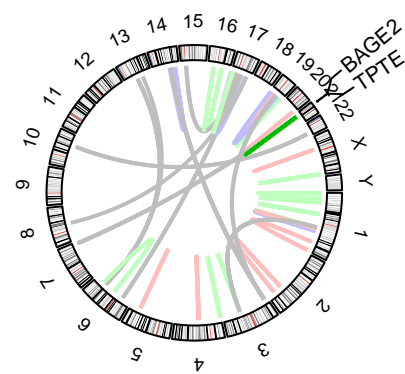
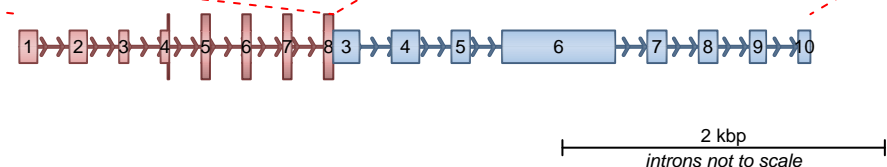
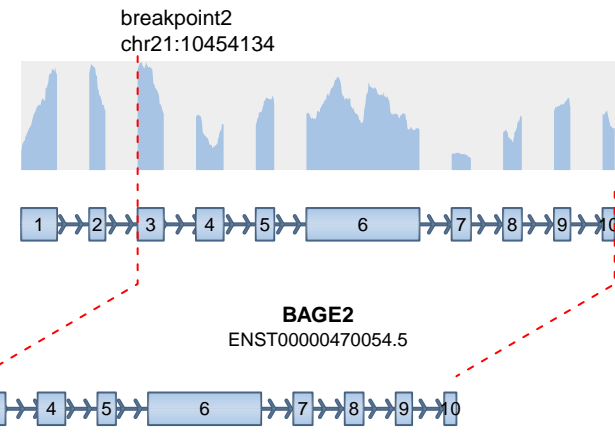
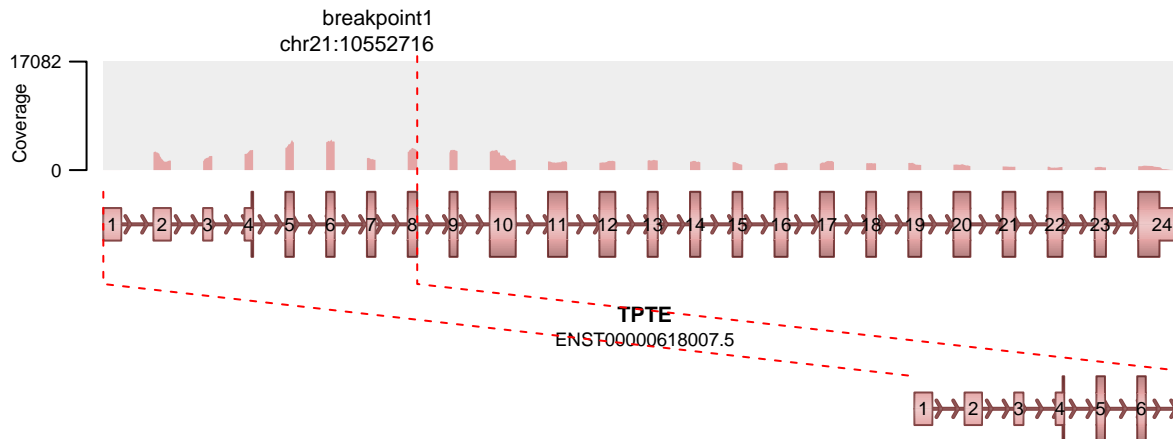
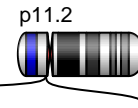
Split reads = 11
Discordant mates = 1

— translocation — deletion
— duplication — inversion

chromosome 21



chromosome 21



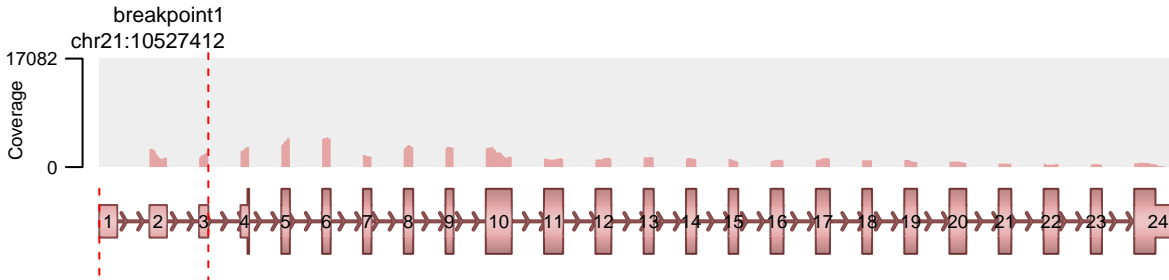
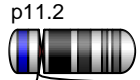
— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

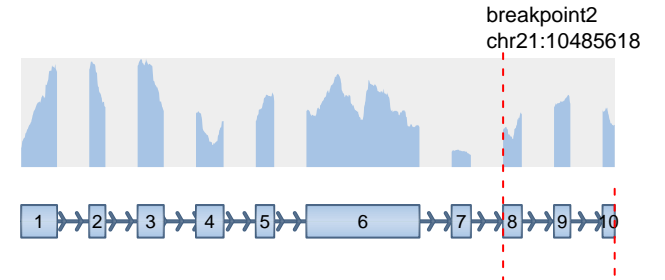
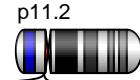
SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 3

chromosome 21

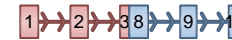


chromosome 21

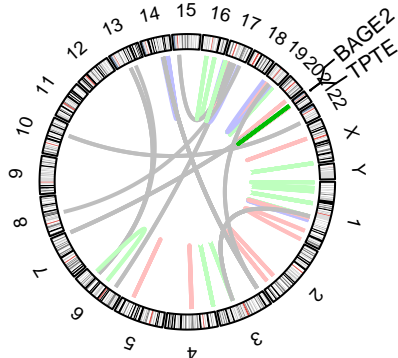


TPTE
ENST00000618007.5

BAGE2
ENST00000470054.5



2 kbp
introns not to scale



No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

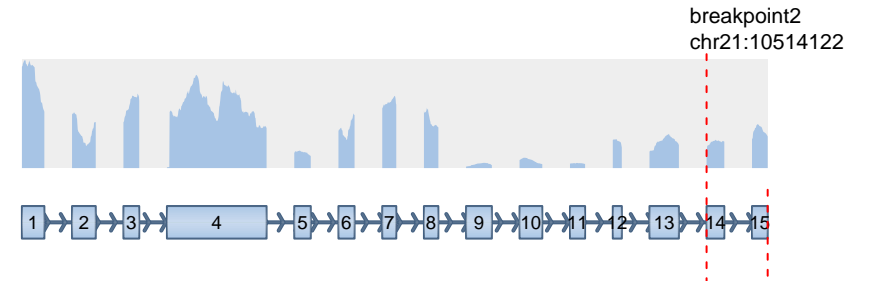
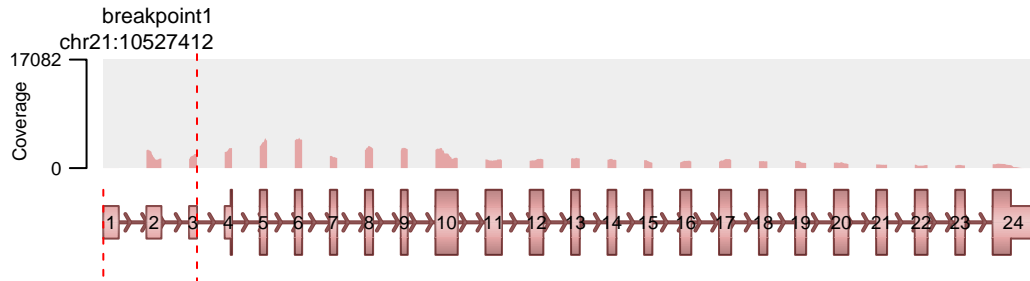
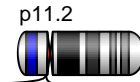
Split reads = 10
Discordant mates = 1

— translocation — deletion
— duplication — inversion

chromosome 21

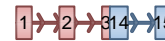


chromosome 21

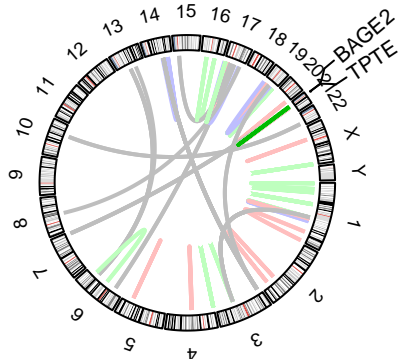


TPTE
ENST00000618007.6

BAGE2
ENST00000496773.1



2 kbp
introns not to scale



No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

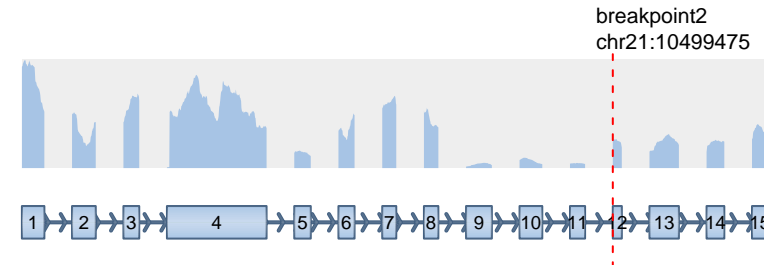
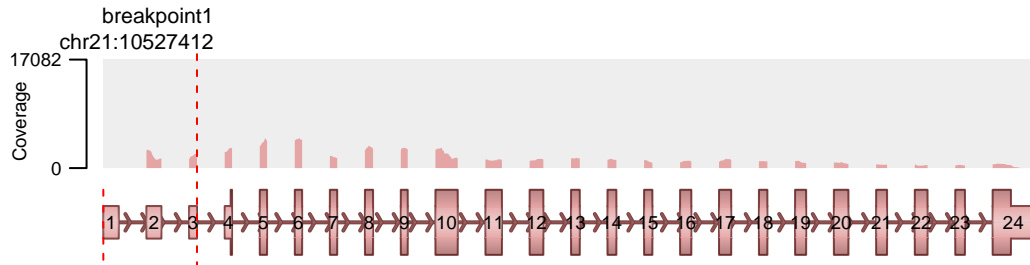
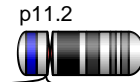
Split reads = 9
Discordant mates = 1

— translocation — deletion
— duplication — inversion

chromosome 21

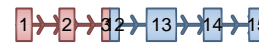


chromosome 21

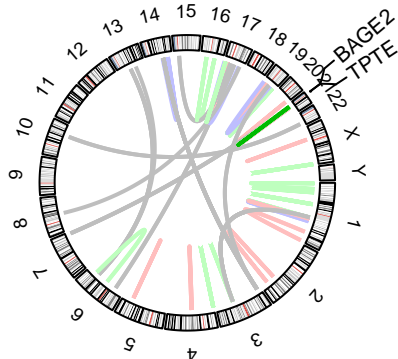


TPTE
ENST00000618007.6

BAGE2
ENST00000496773.1



2 kbp
introns not to scale



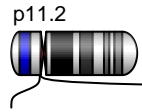
No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

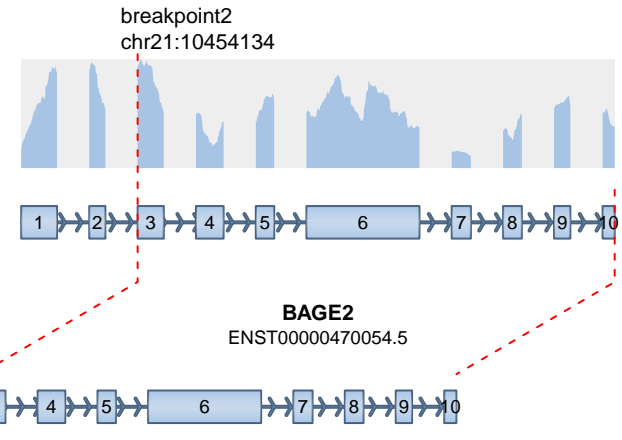
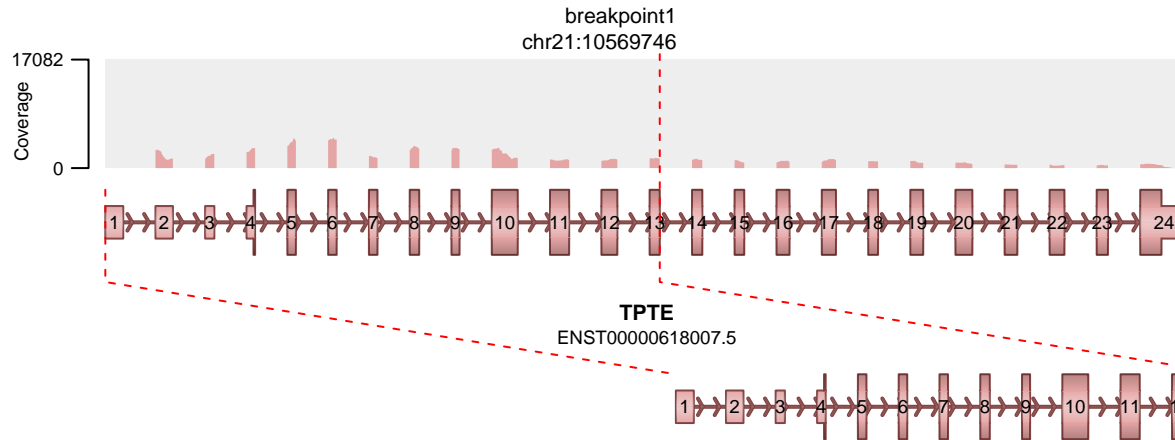
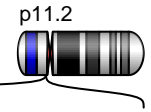
Split reads = 9
Discordant mates = 1

— translocation — deletion
— duplication — inversion

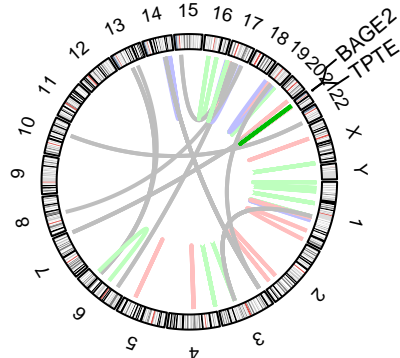
chromosome 21



chromosome 21



2 kbp
introns not to scale



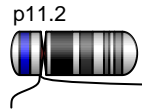
— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

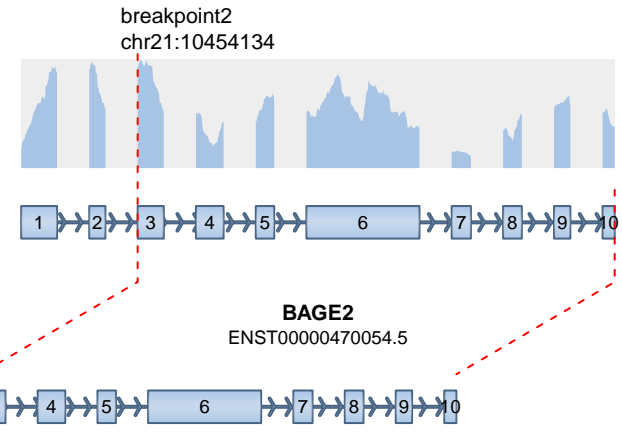
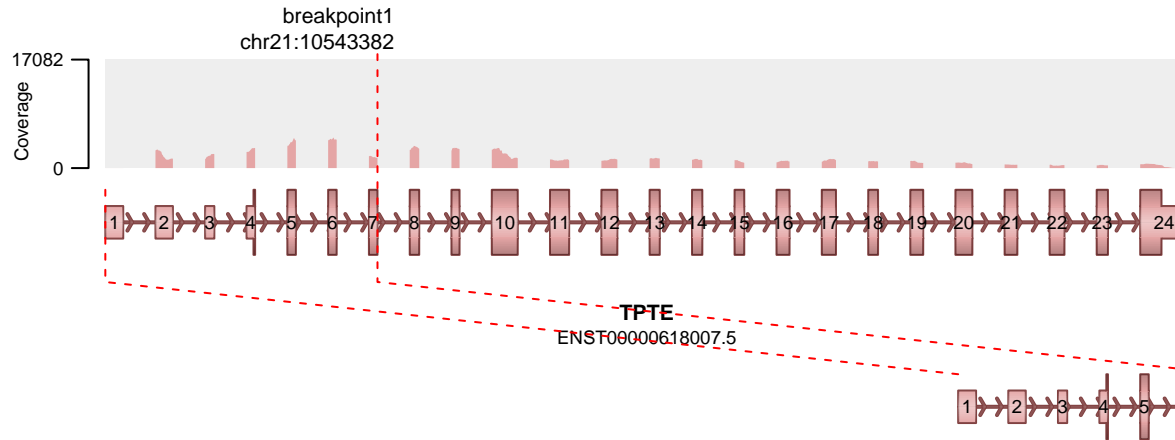
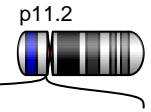
SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 3

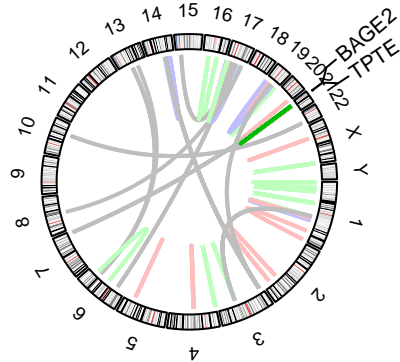
chromosome 21



chromosome 21



2 kbp
introns not to scale



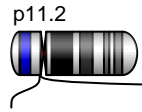
No protein domains retained in fusion.

SUPPORTING READ COUNT

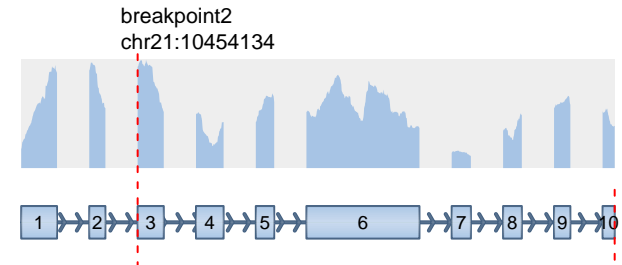
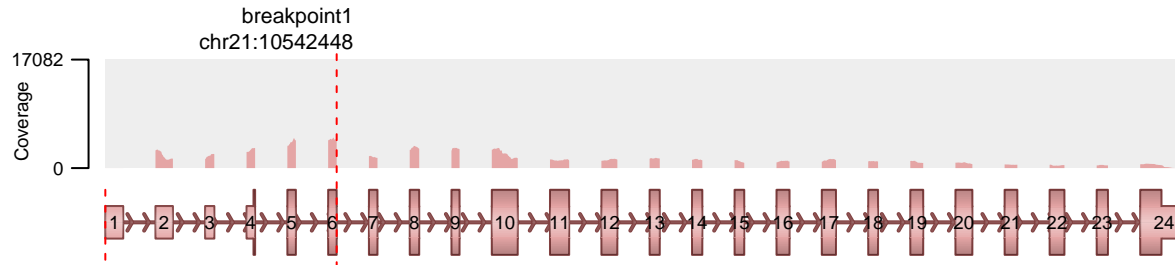
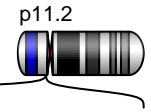
Split reads = 7
Discordant mates = 3

— translocation — deletion
— duplication — inversion

chromosome 21

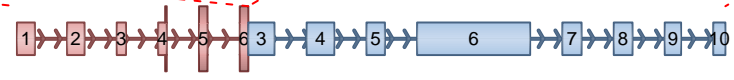


chromosome 21

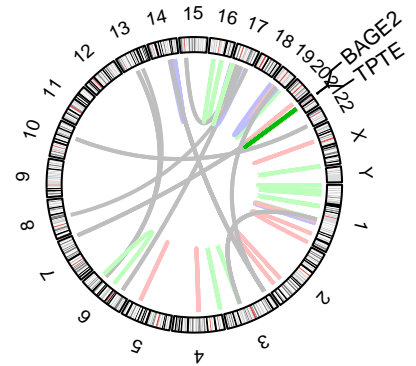


TPTE
ENST00000618007.5

BAGE2
ENST00000470054.5



2 kbp
introns not to scale



— translocation — deletion
— duplication — inversion

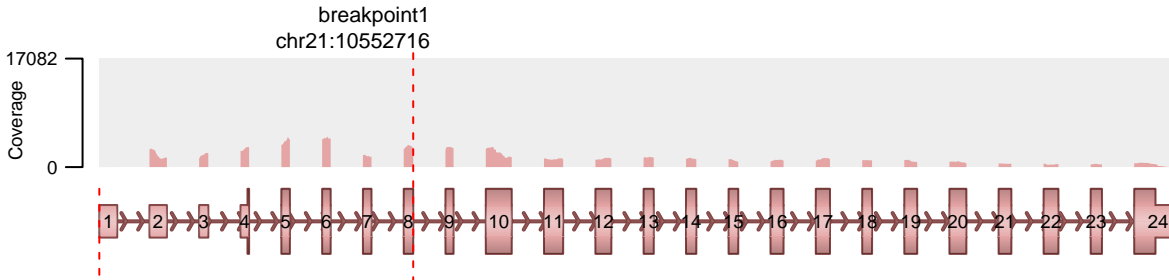
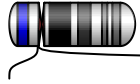
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 3

chromosome 21

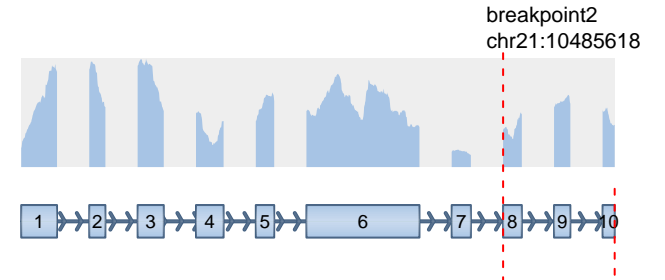
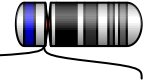
p11.2



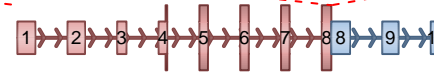
TPTE
ENST00000618007.5

chromosome 21

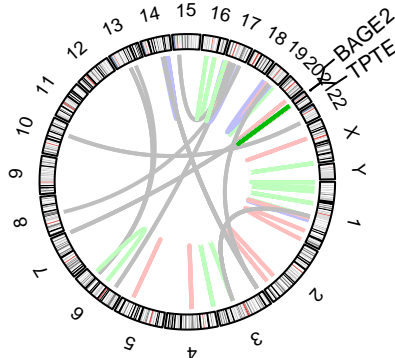
p11.2



BAGE2
ENST00000470054.5



2 kbp
introns not to scale



— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 2

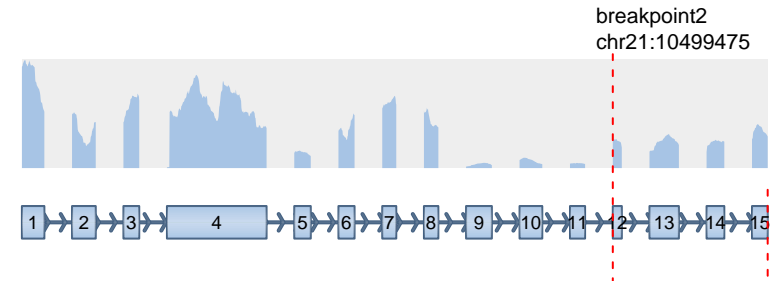
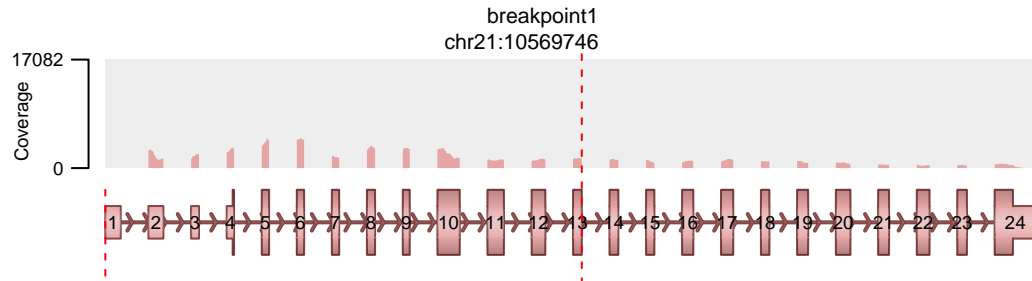
chromosome 21

p11.2



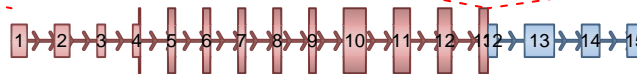
chromosome 21

p11.2

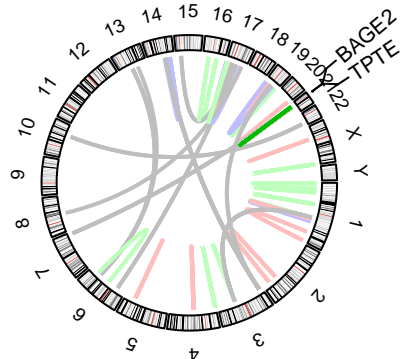


TPTE
ENST00000618007.5

BAGE2
ENST00000496773.1



2 kbp
introns not to scale



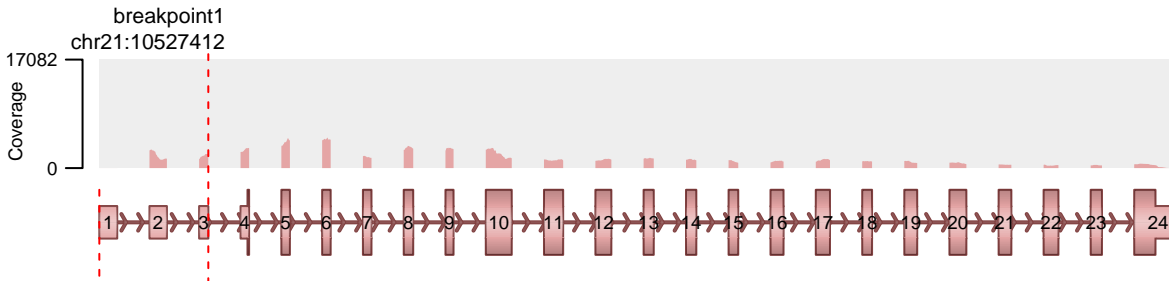
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 1

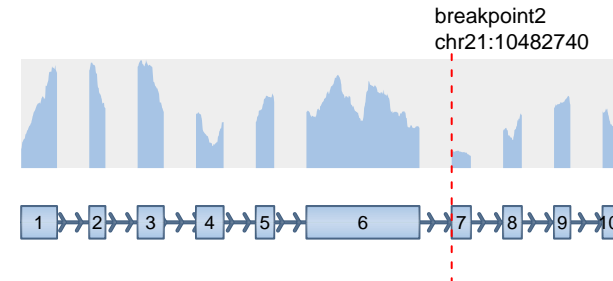
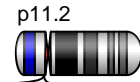
— translocation — deletion
— duplication — inversion

chromosome 21



TPTE
ENST00000618007.5

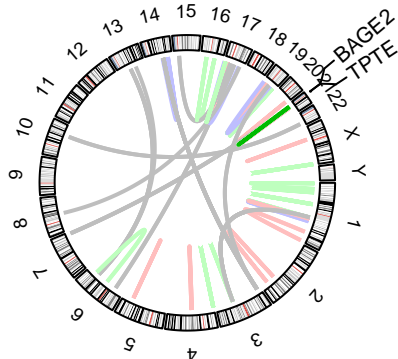
chromosome 21



BAGE2
ENST00000470054.5



2 kbp
introns not to scale



— translocation — deletion
— duplication — inversion

No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 1

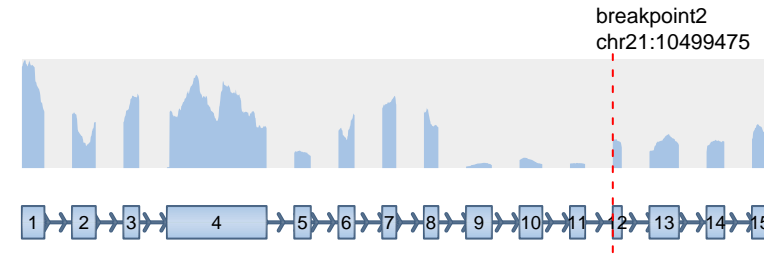
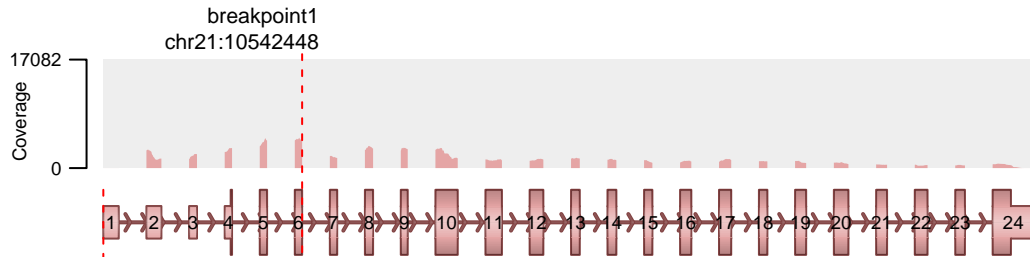
chromosome 21

p11.2



chromosome 21

p11.2

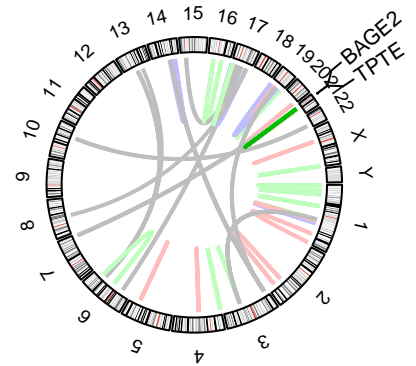


TPTE
ENST00000618007.5

BAGE2
ENST00000496773.1



2 kbp
introns not to scale



No protein domains retained in fusion.

SUPPORTING READ COUNT

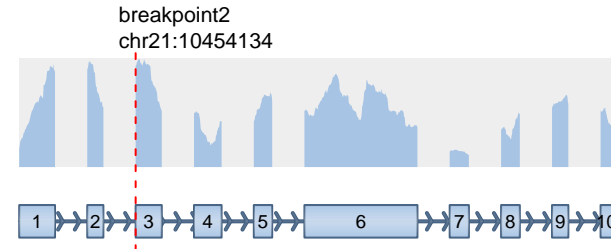
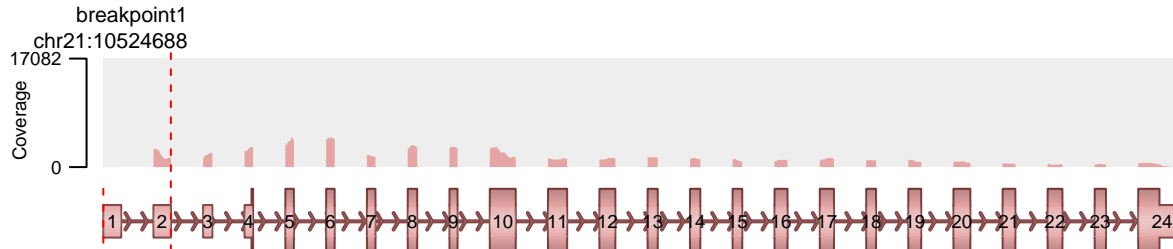
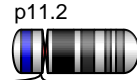
Split reads = 2
Discordant mates = 1

- translocation
- duplication
- deletion
- inversion

chromosome 21



chromosome 21

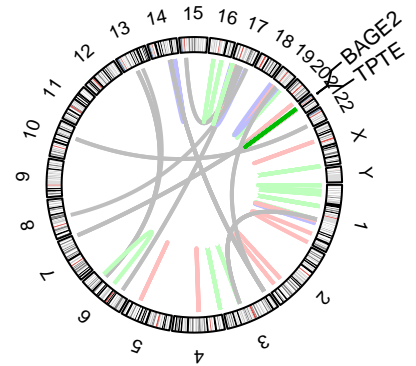


TPTE
ENST00000618007.5

BAGE2
ENST00000470054.5



2 kbp
introns not to scale



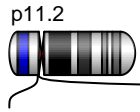
No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

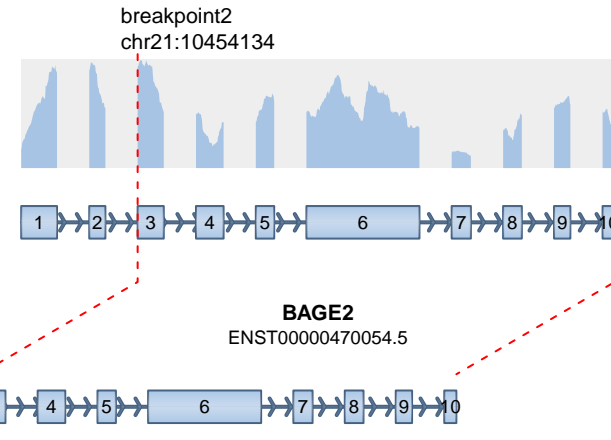
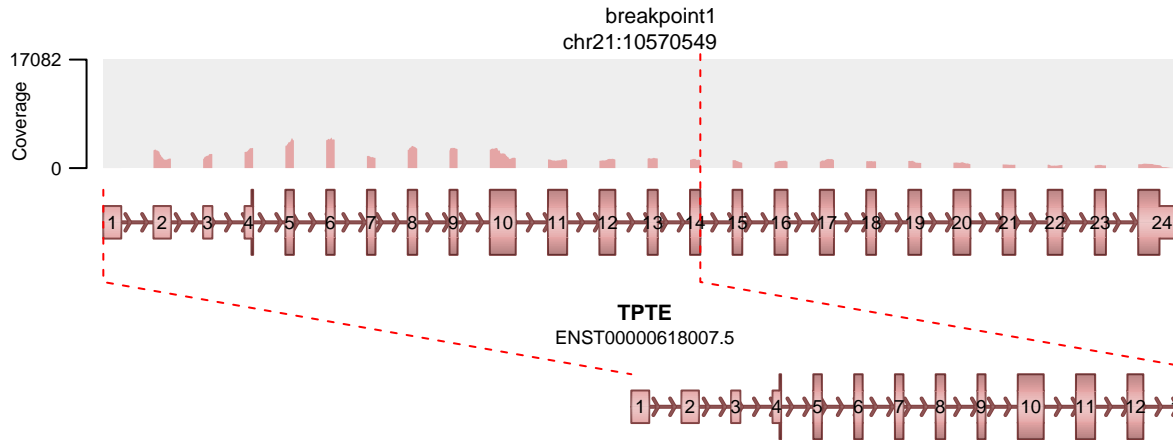
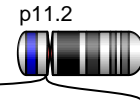
Split reads = 2
Discordant mates = 0

— translocation — deletion
— duplication — inversion

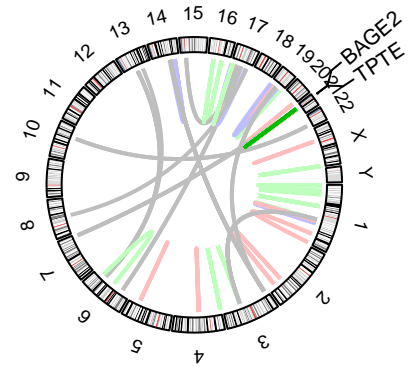
chromosome 21



chromosome 21



2 kbp
introns not to scale



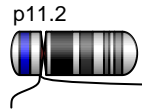
No protein domains retained in fusion.

SUPPORTING READ COUNT

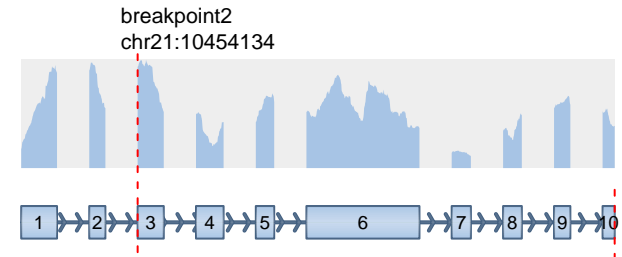
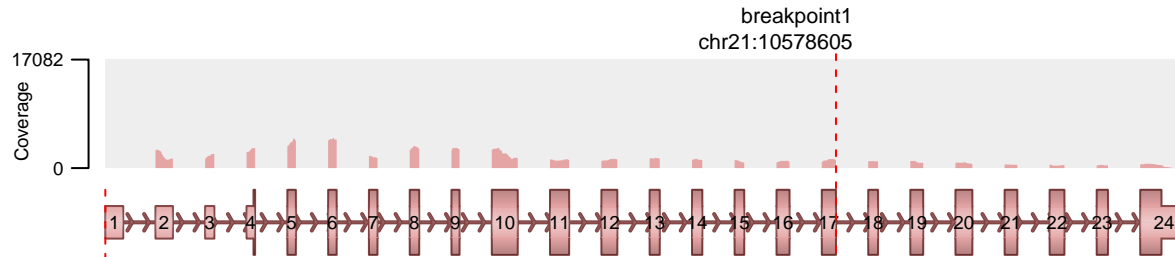
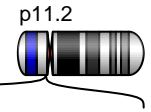
Split reads = 1
Discordant mates = 3

— translocation — deletion
— duplication — inversion

chromosome 21

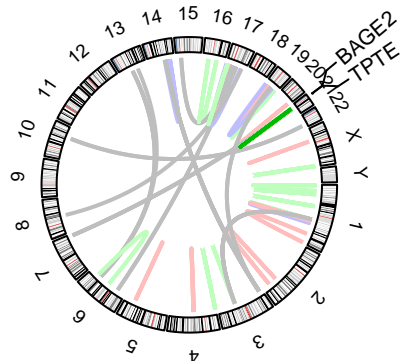


chromosome 21

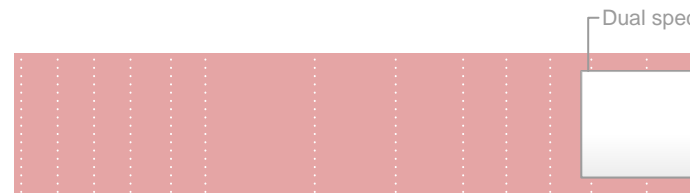


TPTE
ENST00000618007.5

BAGE2
ENST00000470054.5



RETAINED PROTEIN DOMAINS
reading frame unclear



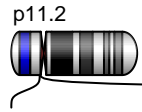
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 3

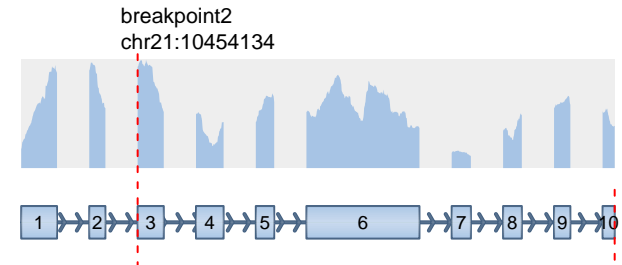
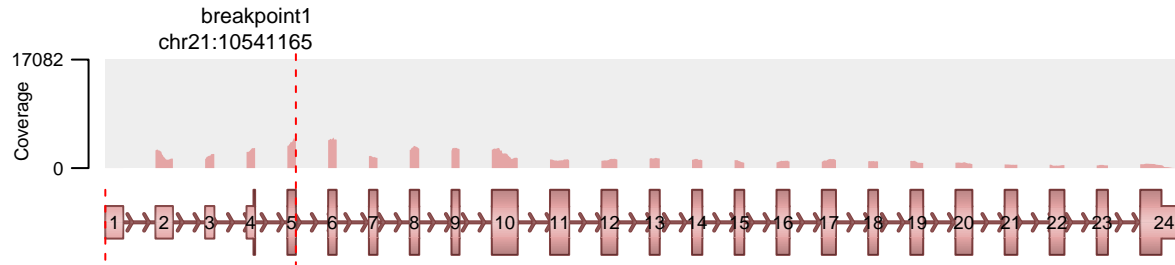
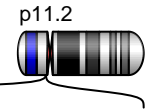
TPTE

- translocation
- duplication
- deletion
- inversion

chromosome 21

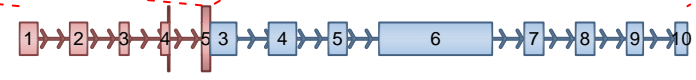


chromosome 21

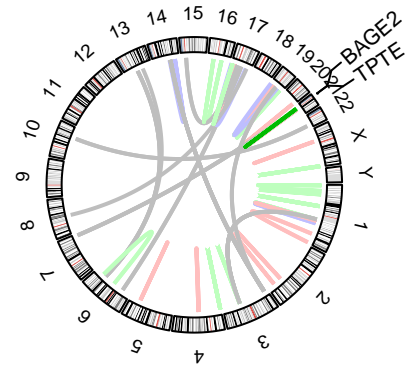


TPTE
ENST00000618007.5

BAGE2
ENST00000470054.5



2 kbp
introns not to scale



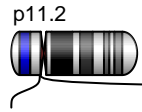
No protein domains retained in fusion.

SUPPORTING READ COUNT

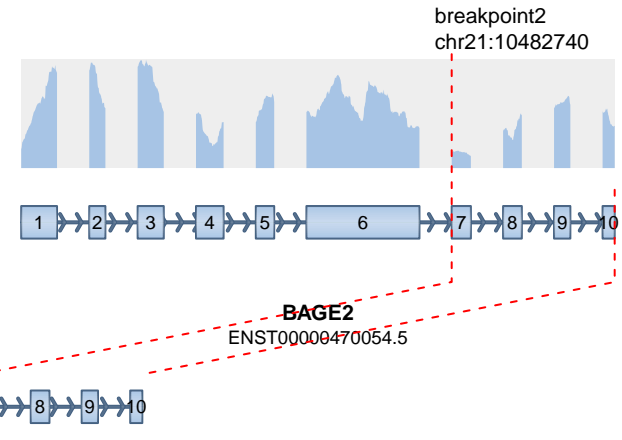
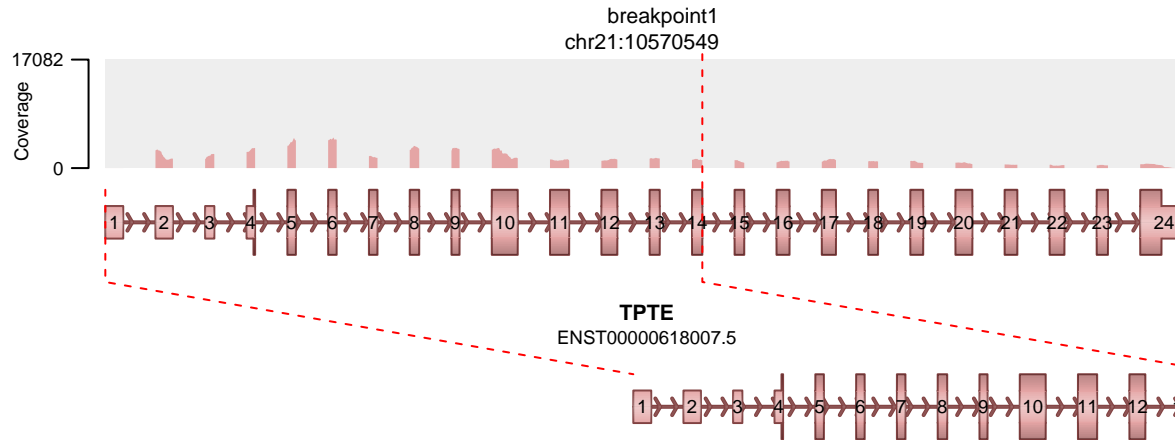
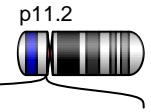
Split reads = 1
Discordant mates = 3

— translocation — deletion
— duplication — inversion

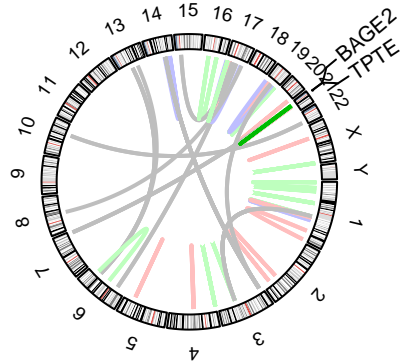
chromosome 21



chromosome 21



2 kbp
introns not to scale



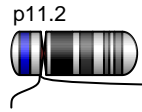
No protein domains retained in fusion.

SUPPORTING READ COUNT

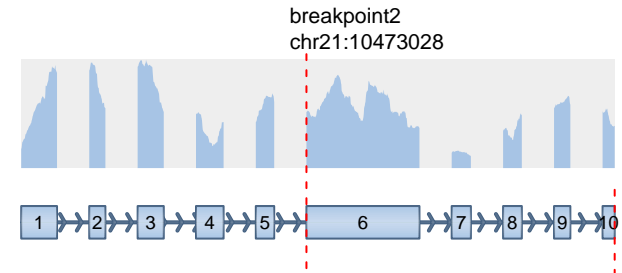
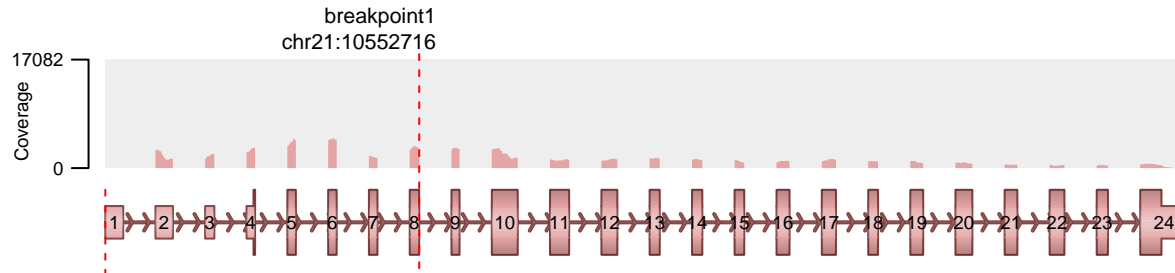
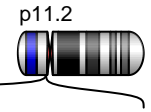
Split reads = 1
Discordant mates = 2

— translocation — deletion
— duplication — inversion

chromosome 21

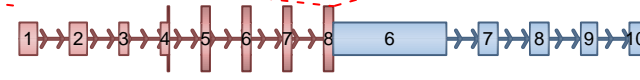


chromosome 21

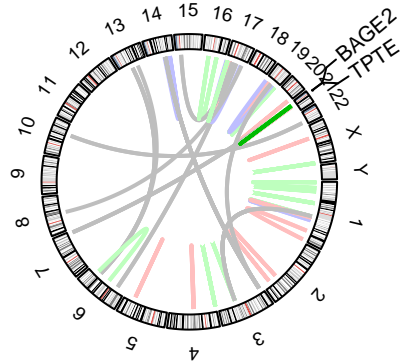


TPTE
ENST00000618007.5

BAGE2
ENST00000470054.5



2 kbp
introns not to scale



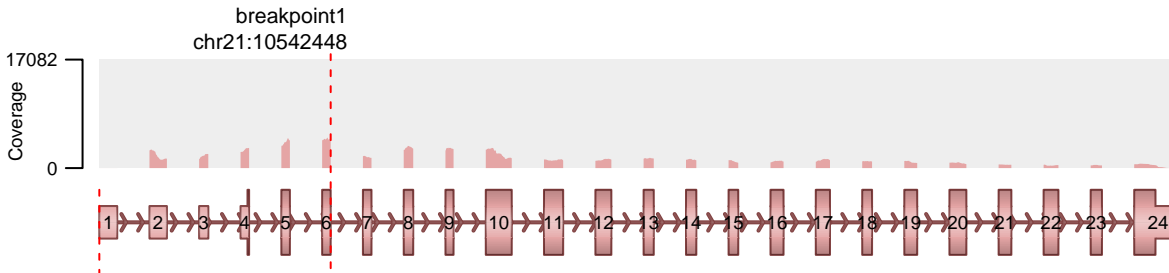
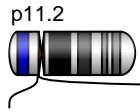
— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

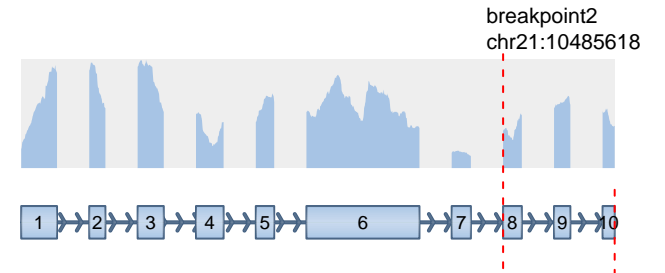
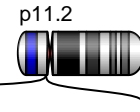
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 2

chromosome 21



chromosome 21

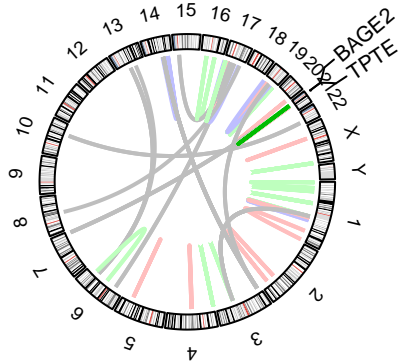


TPTE
ENST00000618007.5

BAGE2
ENST00000470054.5



2 kbp
introns not to scale



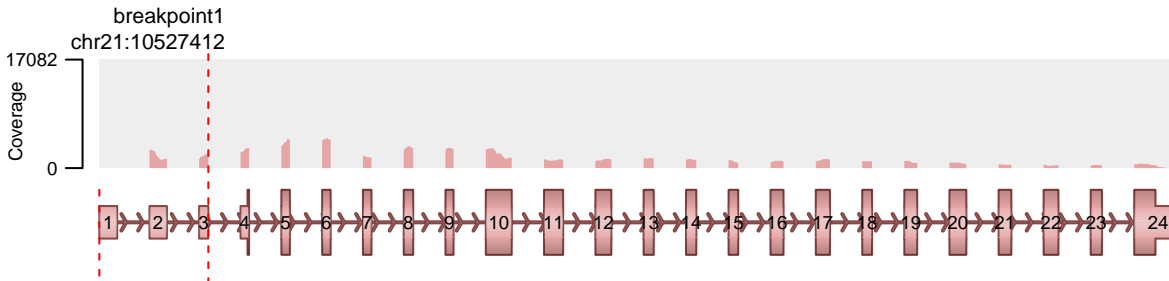
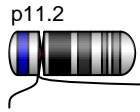
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 2

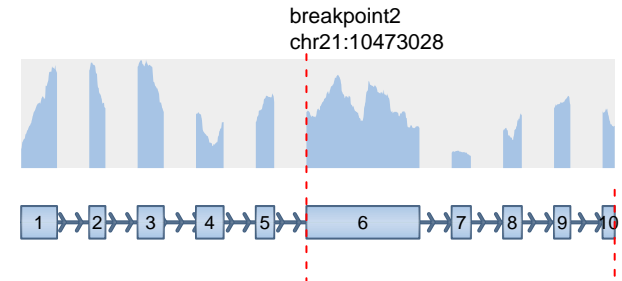
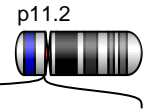
— translocation — deletion
— duplication — inversion

chromosome 21



TPTE
ENST00000618007.5

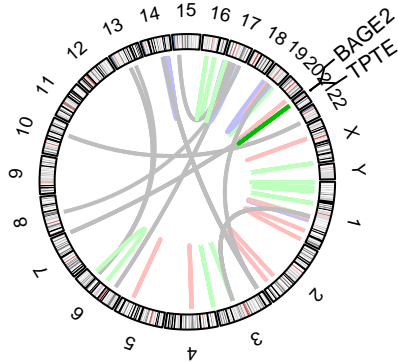
chromosome 21



BAGE2
ENST00000470054.5



2 kbp
introns not to scale



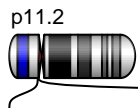
— translocation — deletion
— duplication — inversion

No coding regions retained in fusion transcript.

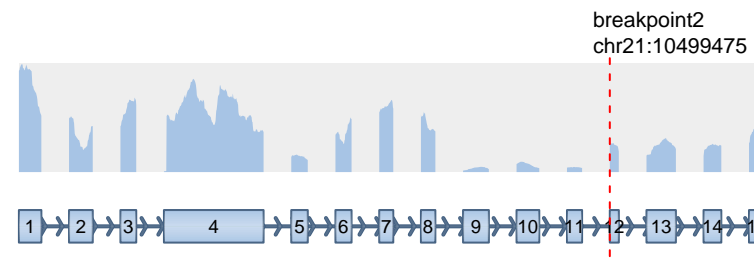
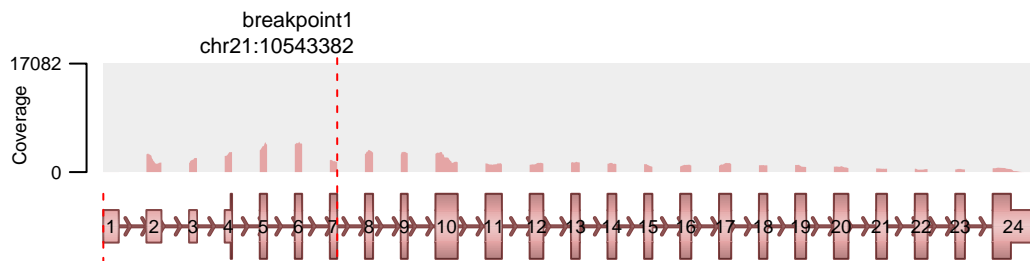
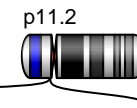
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

chromosome 21

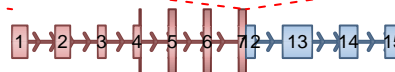


chromosome 21

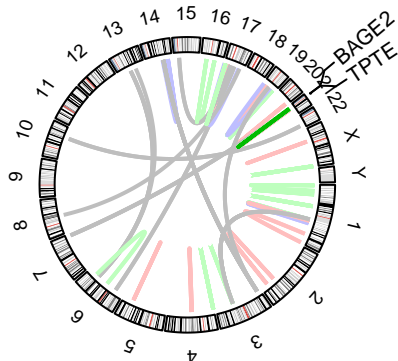


TPTE
ENST00000618007.5

BAGE2
ENST00000496773.1



2 kbp
introns not to scale



No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

— translocation — deletion
— duplication — inversion

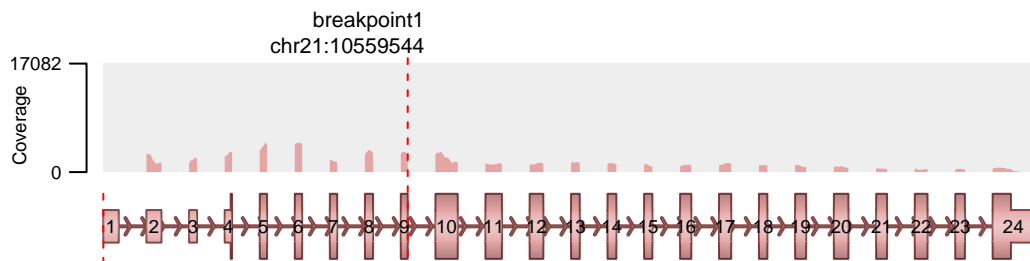
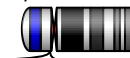
chromosome 21

p11.2



chromosome 21

p11.2

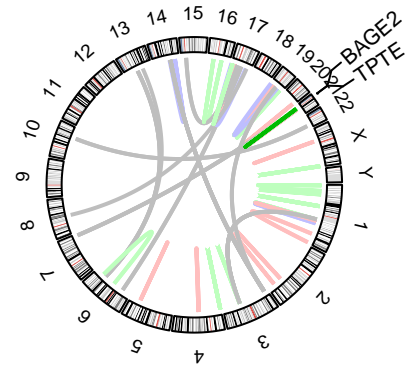


TPTE
ENST00000618007.5

BAGE2
ENST00000496773.1



2 kbp
introns not to scale



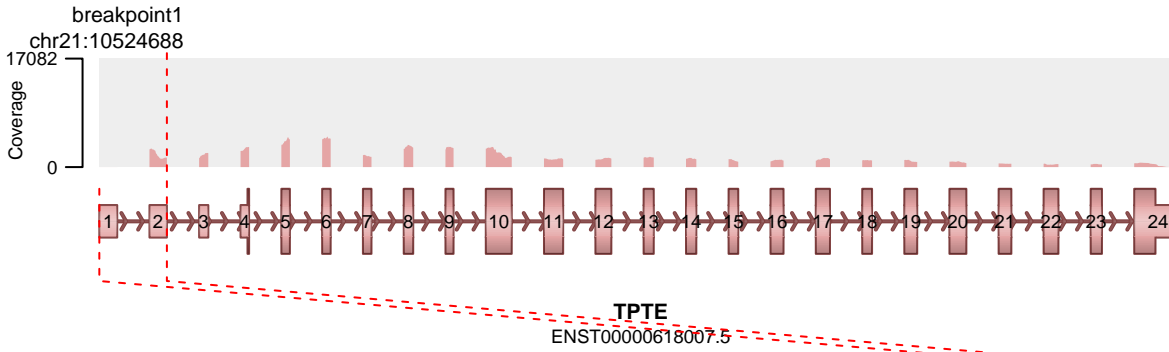
— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

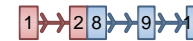
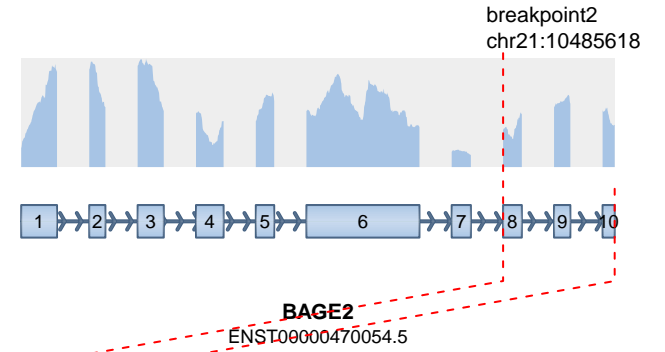
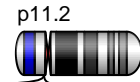
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

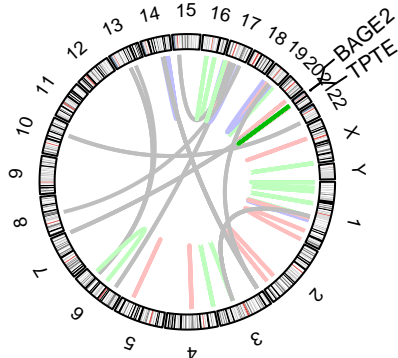
chromosome 21



chromosome 21



2 kbp
introns not to scale

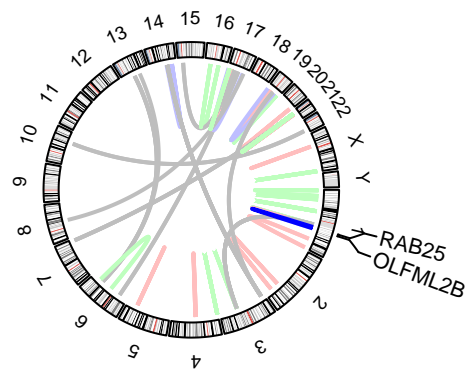
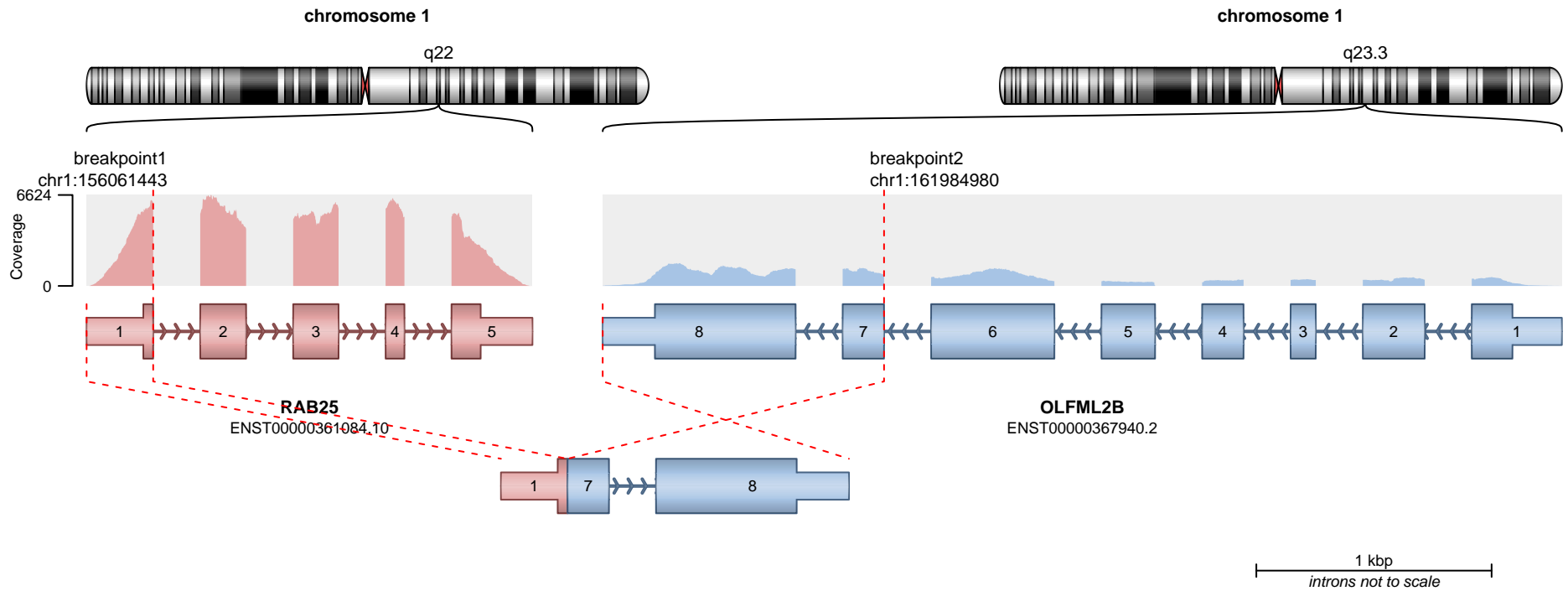


— translocation — deletion
— duplication — inversion

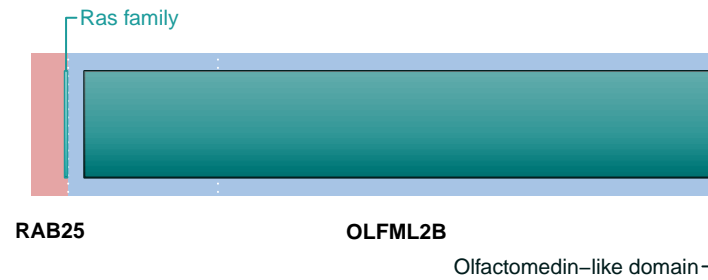
No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



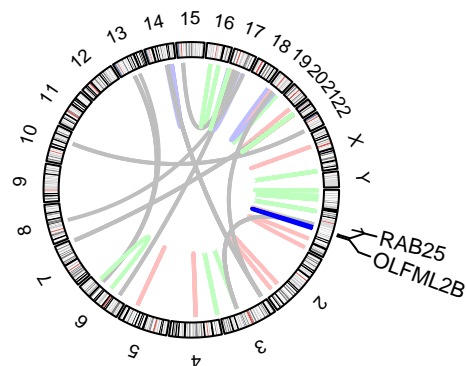
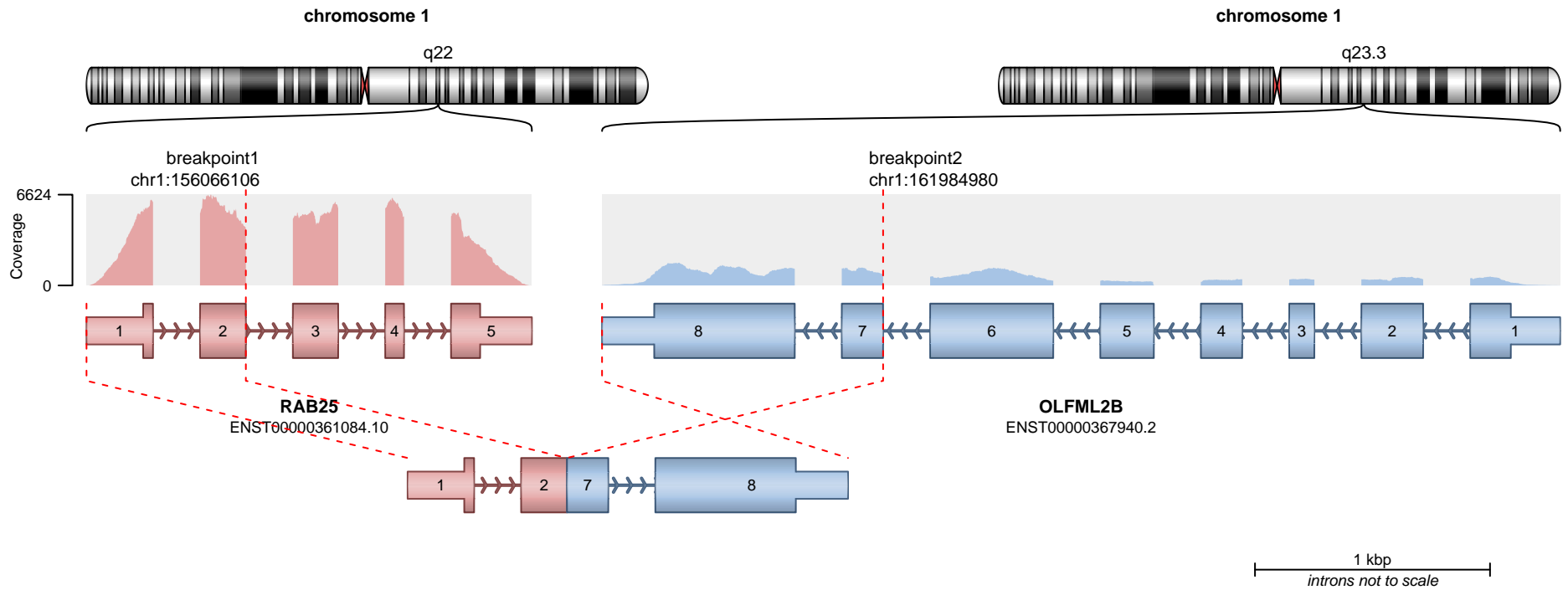
RETAINED PROTEIN DOMAINS
reading frame unclear



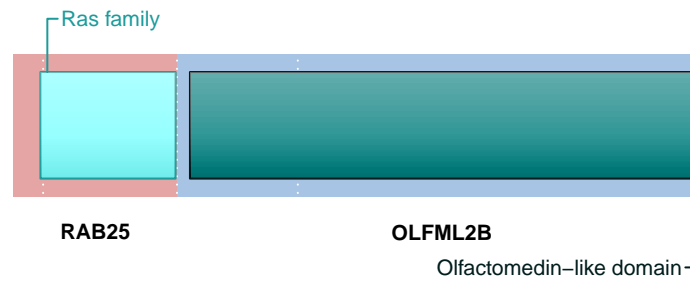
SUPPORTING READ COUNT

Split reads = 18
Discordant mates = 0

— translocation — deletion
— duplication — inversion



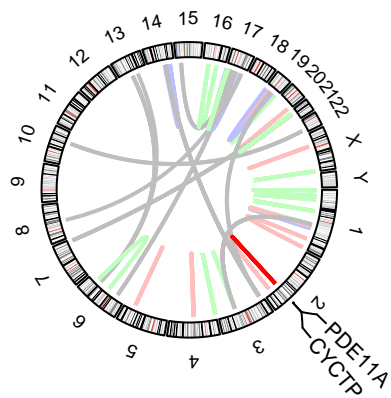
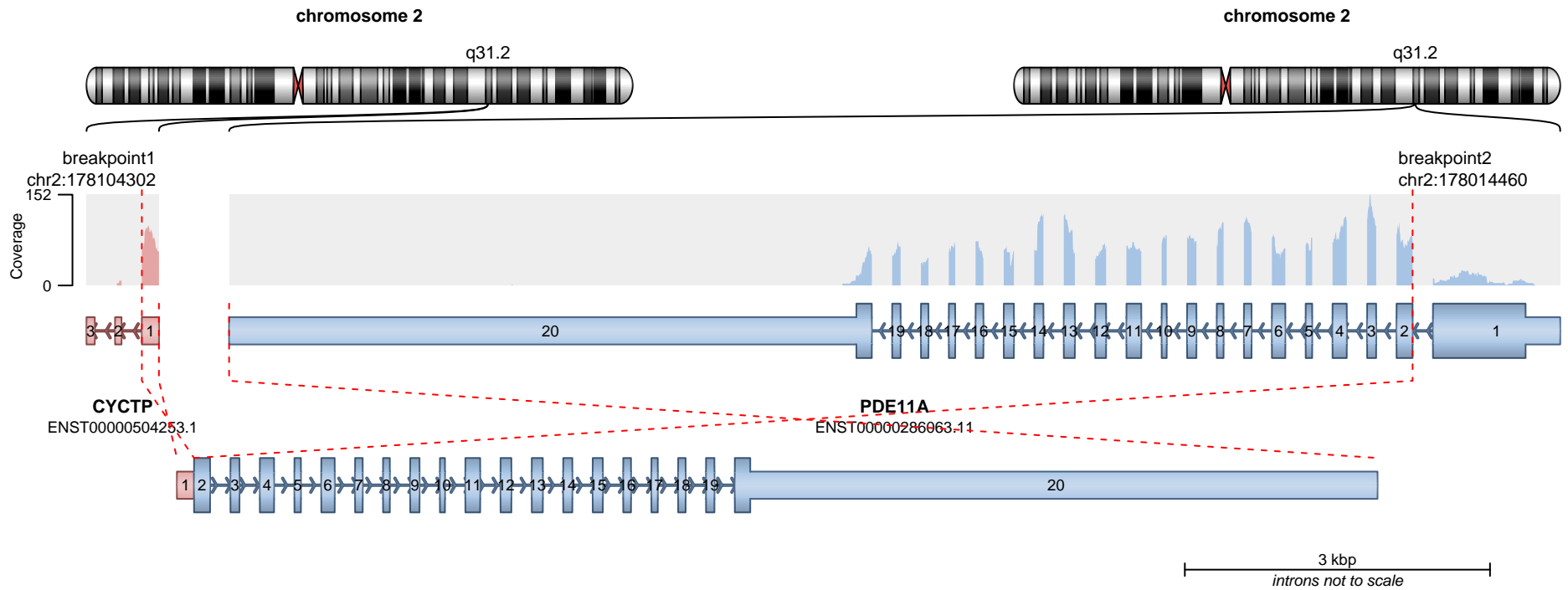
RETAINED PROTEIN DOMAINS
reading frame unclear



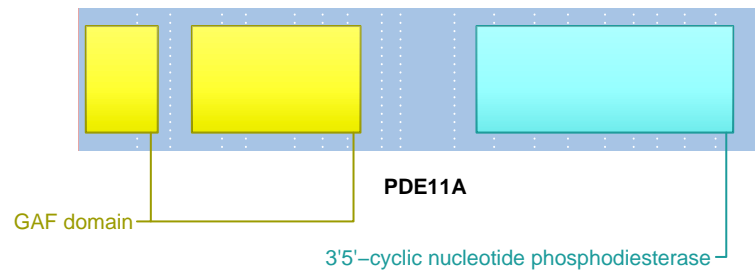
SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 0

— translocation — deletion
— duplication — inversion



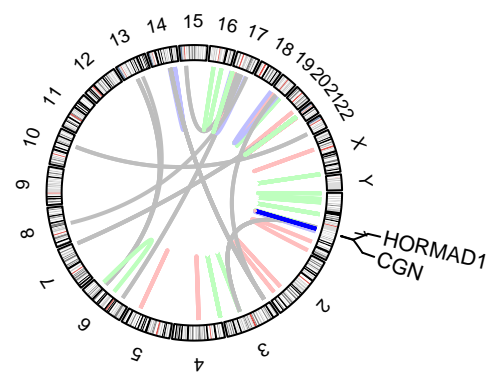
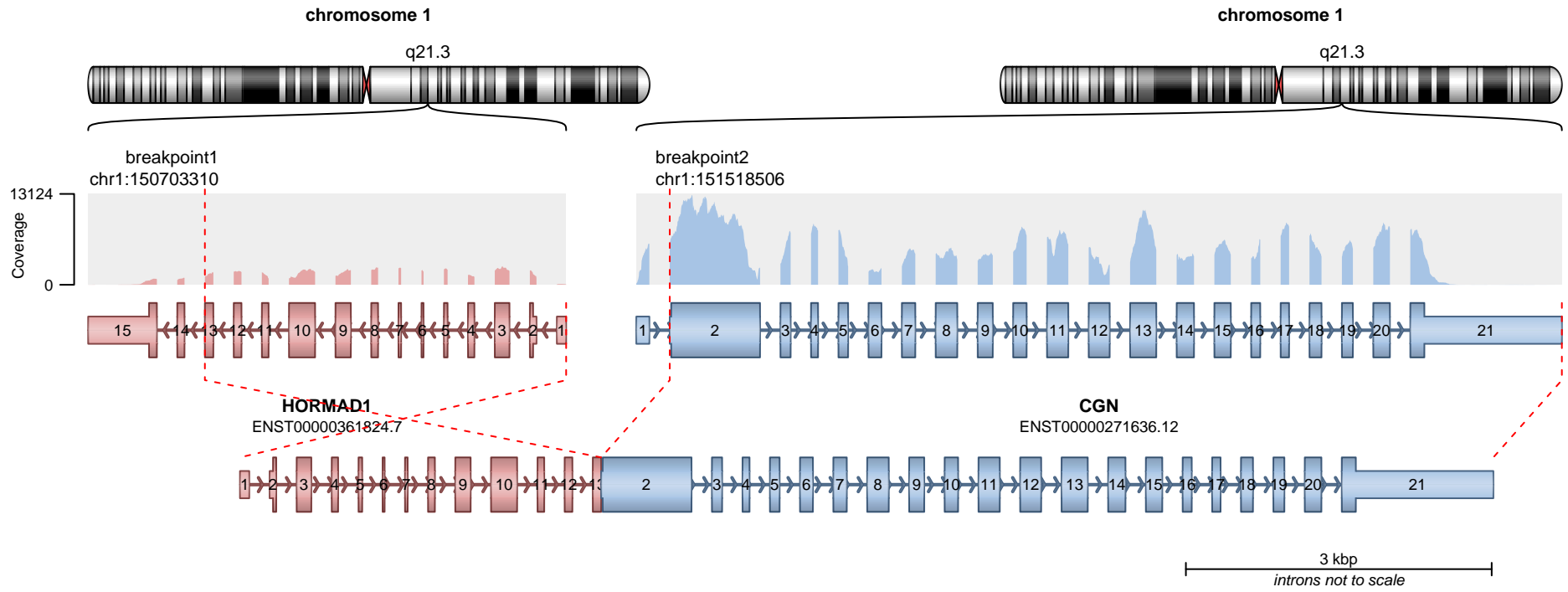
RETAINED PROTEIN DOMAINS
reading frame unclear



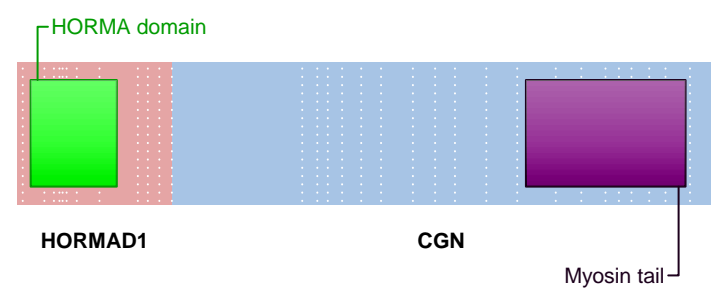
SUPPORTING READ COUNT

Split reads = 16
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



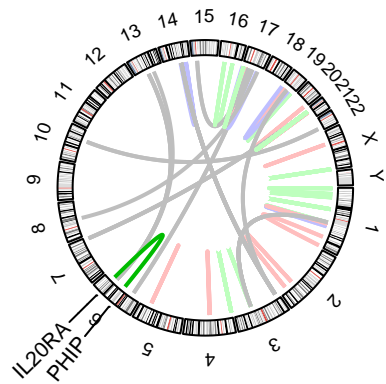
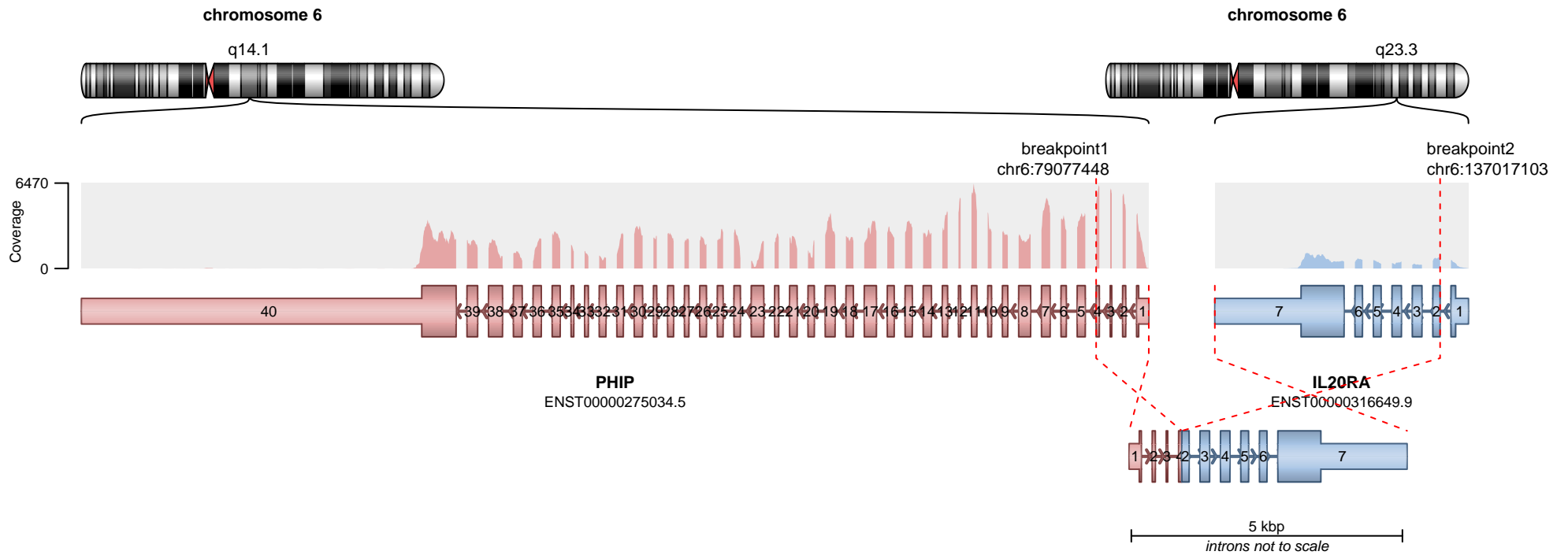
RETAINED PROTEIN DOMAINS
reading frame unclear



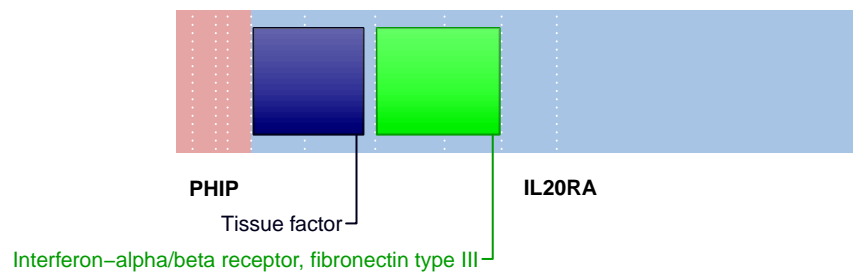
SUPPORTING READ COUNT

Split reads = 15
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



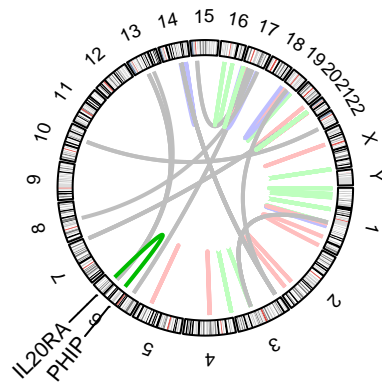
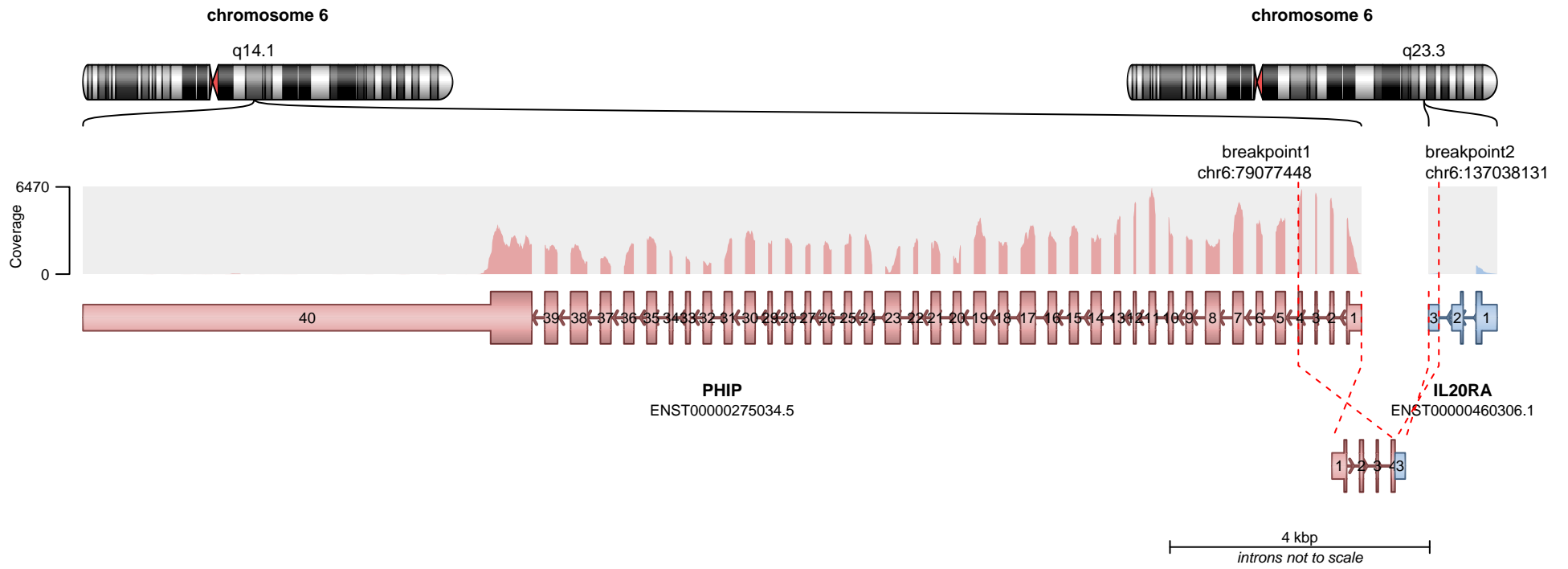
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 15
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

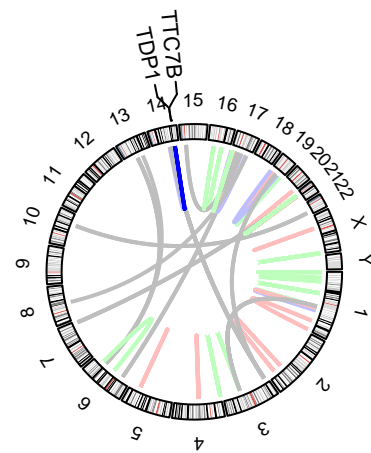
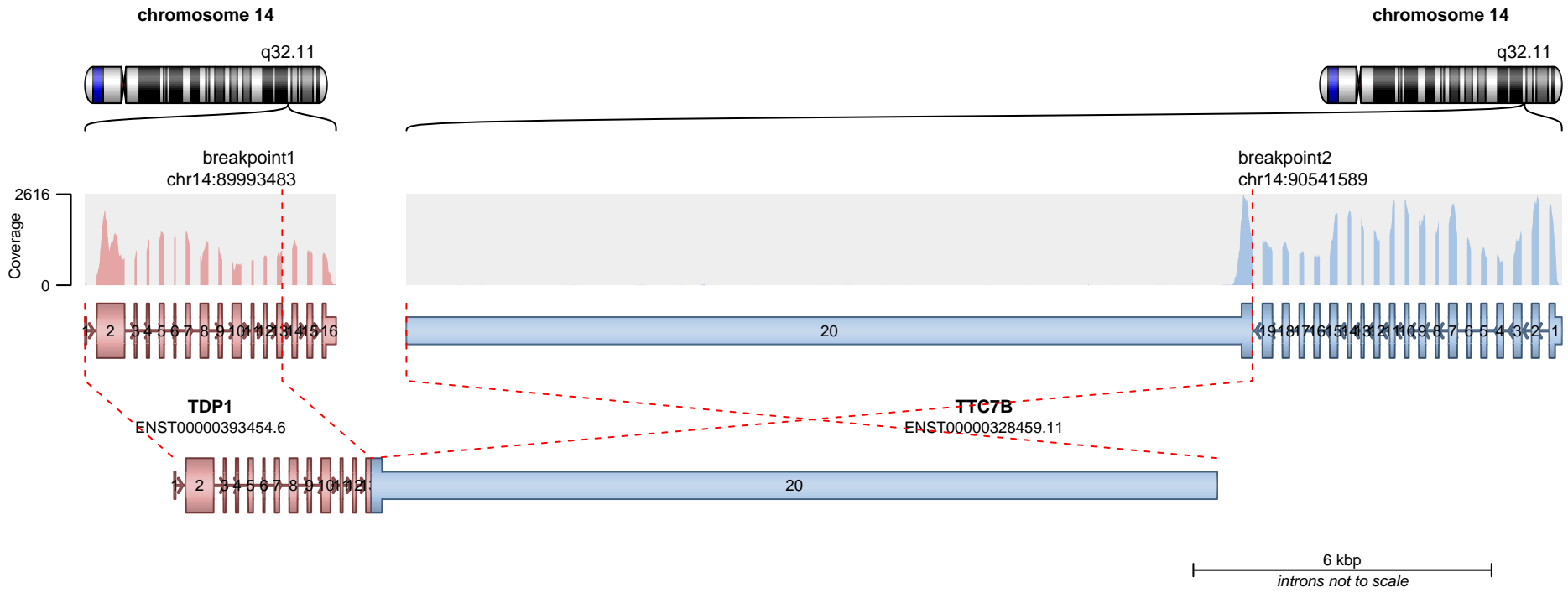


— translocation — deletion
— duplication — inversion

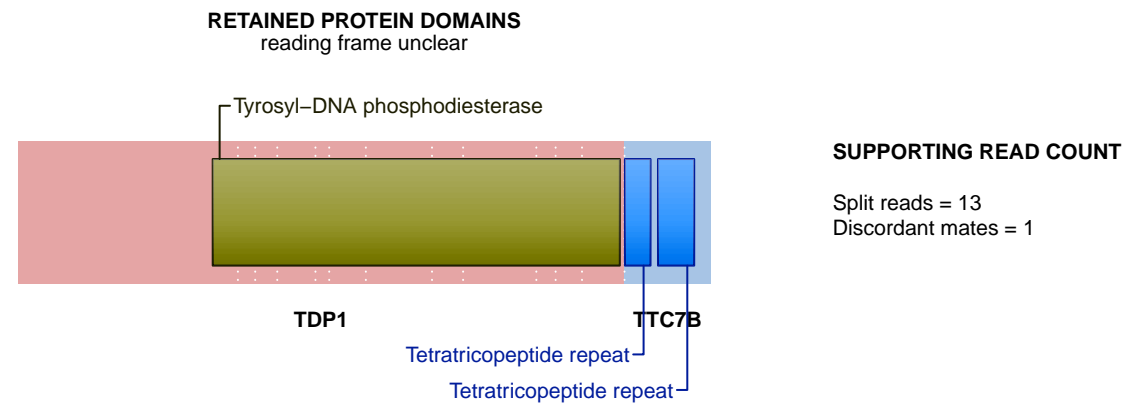
No protein domains retained in fusion.

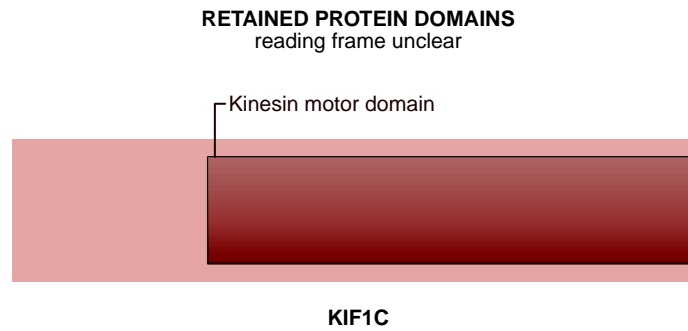
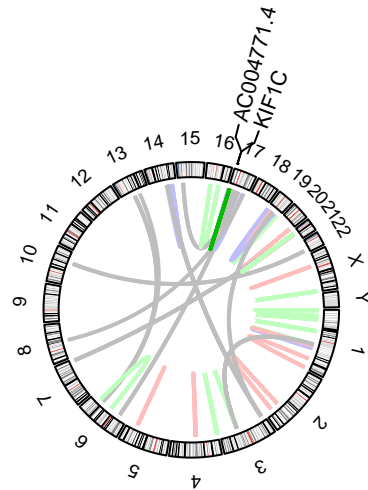
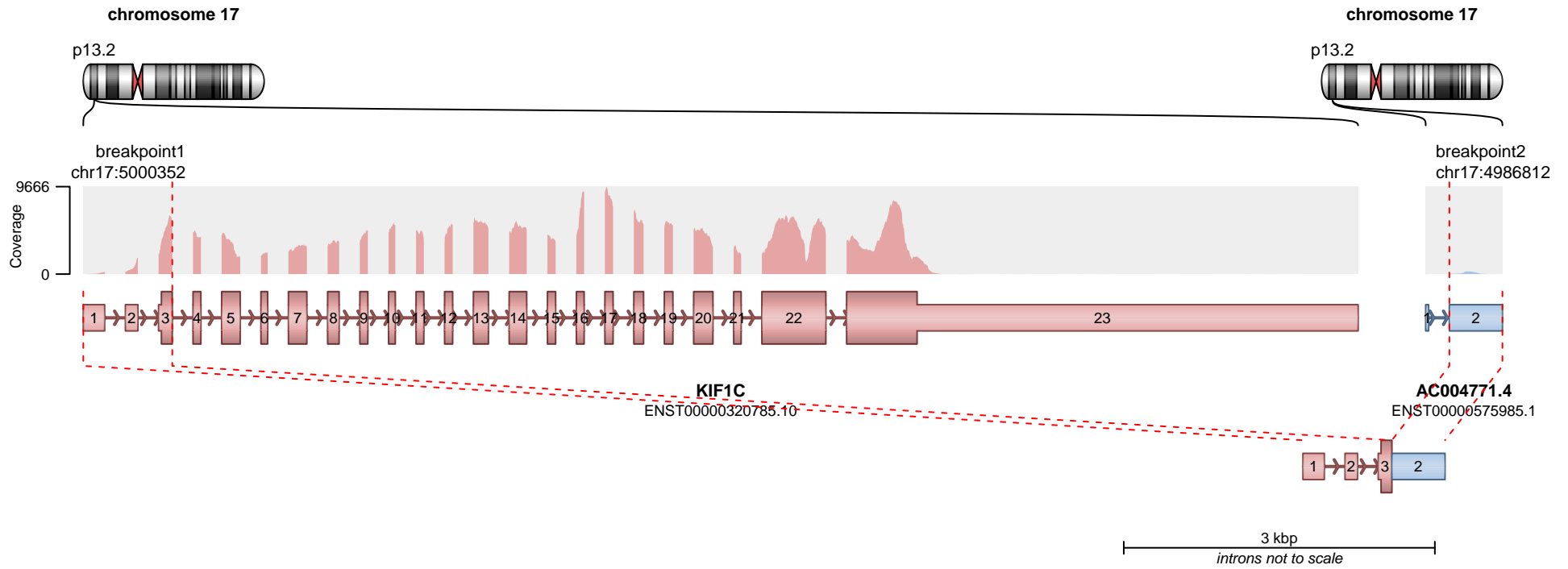
SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 1



— translocation — deletion
— duplication — inversion

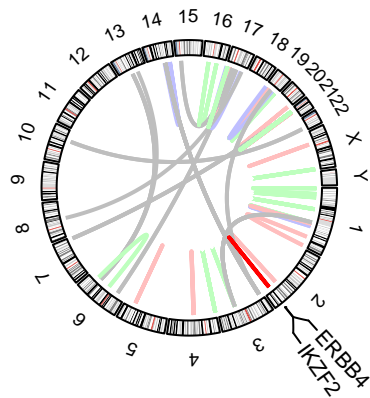
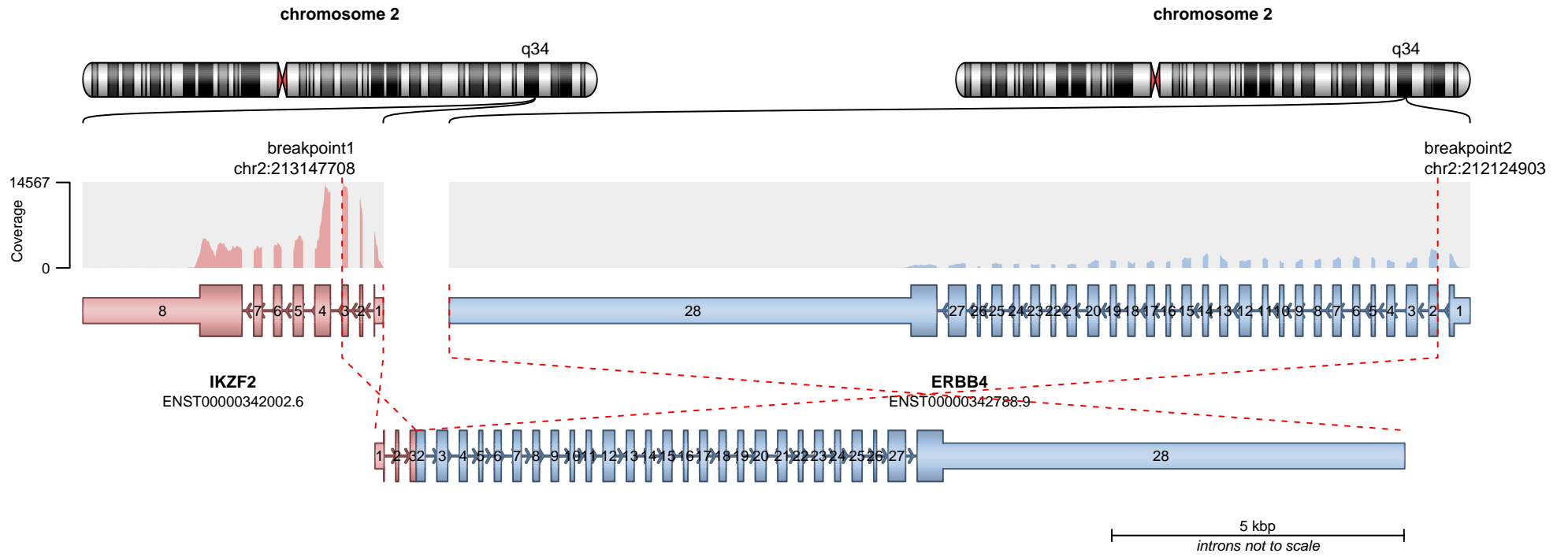




SUPPORTING READ COUNT

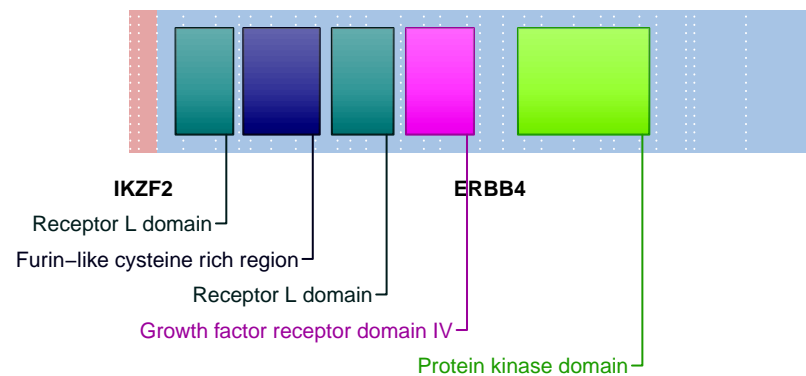
Split reads = 13
Discordant mates = 0

— translocation — deletion
— duplication — inversion



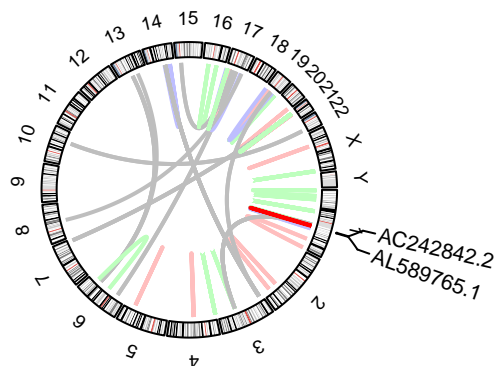
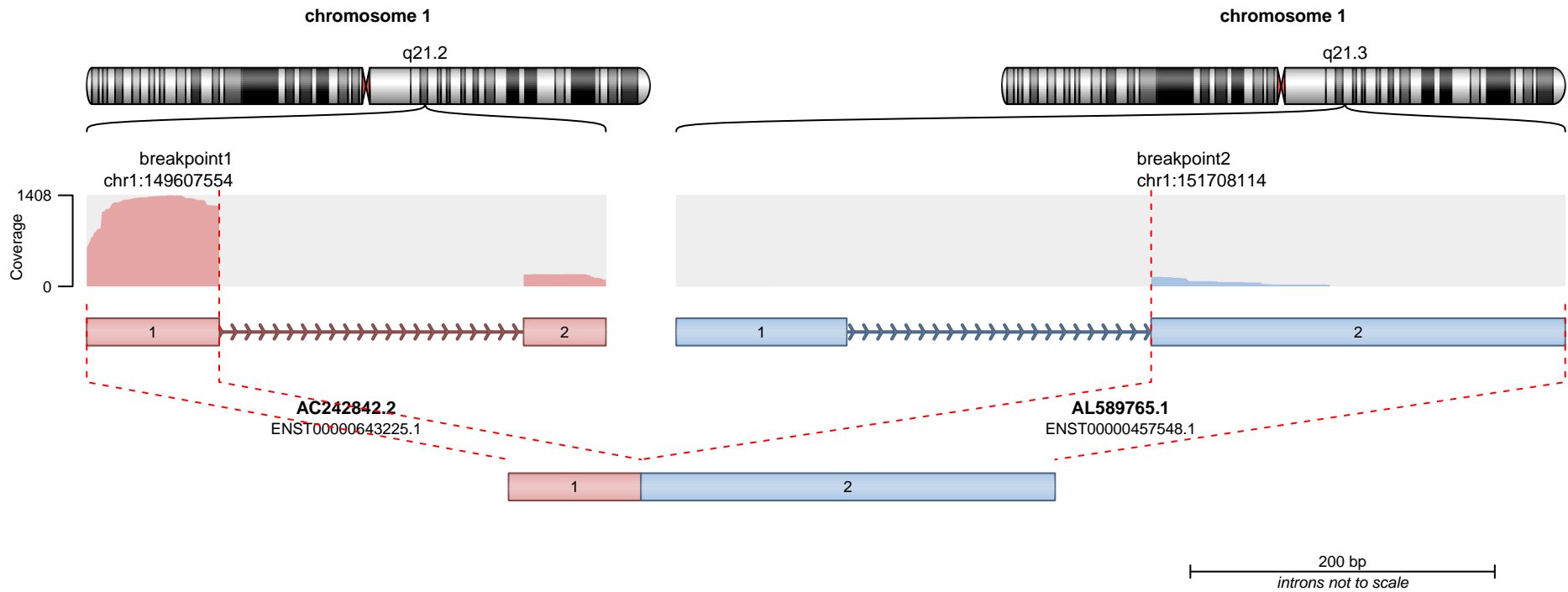
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 1

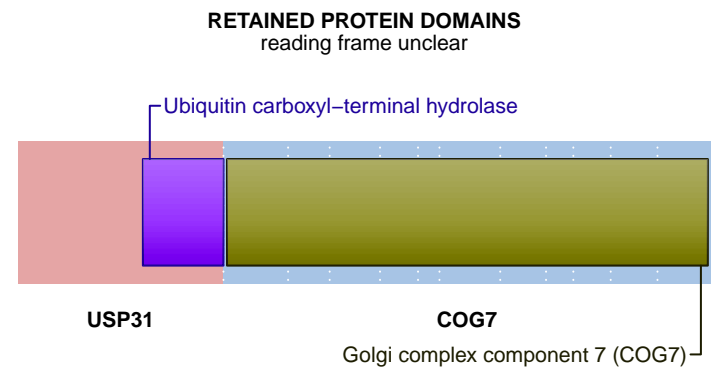
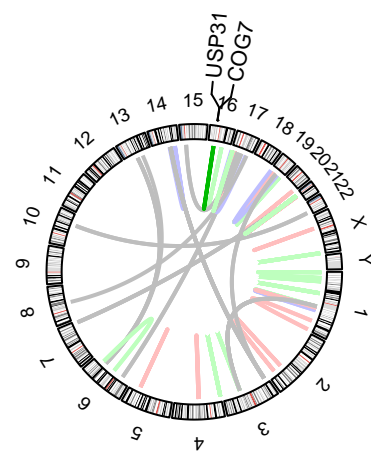
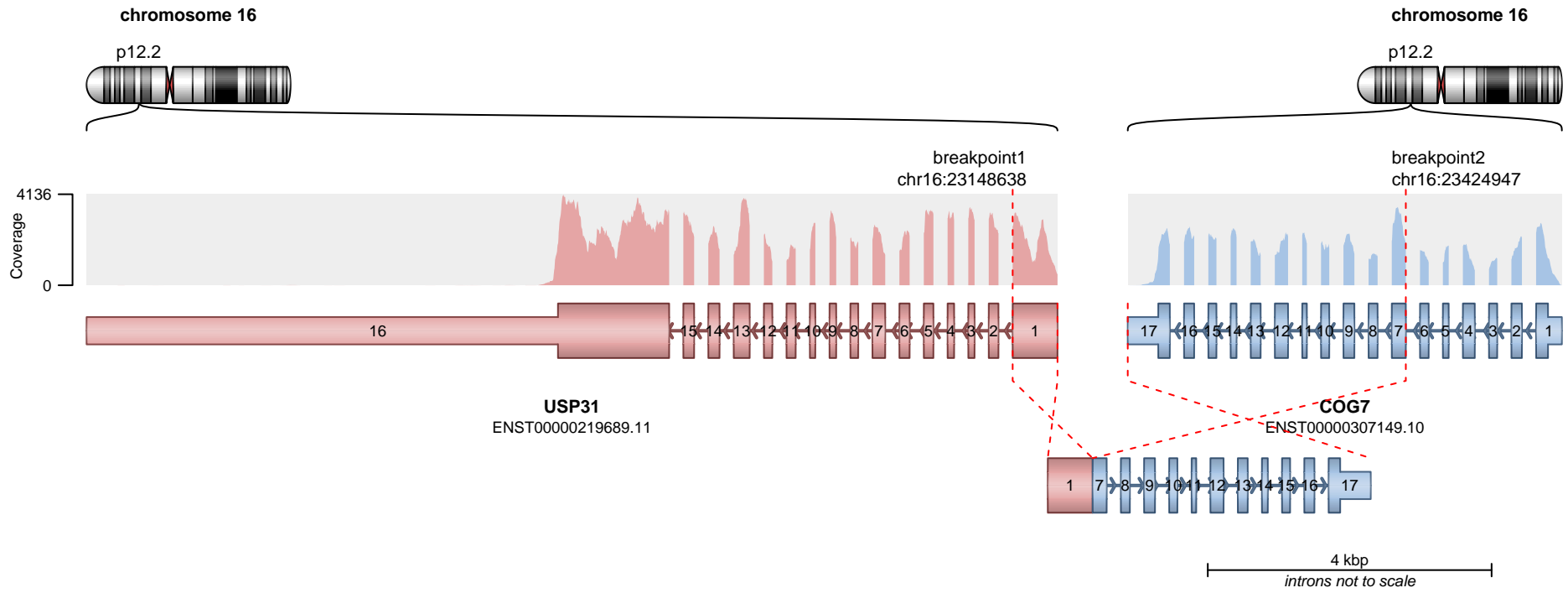


Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 0

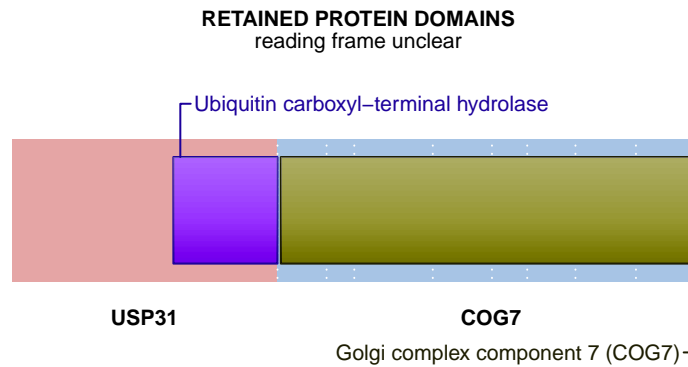
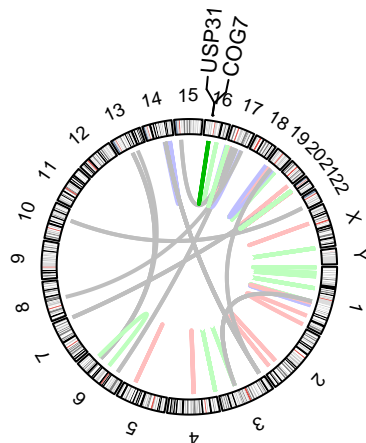
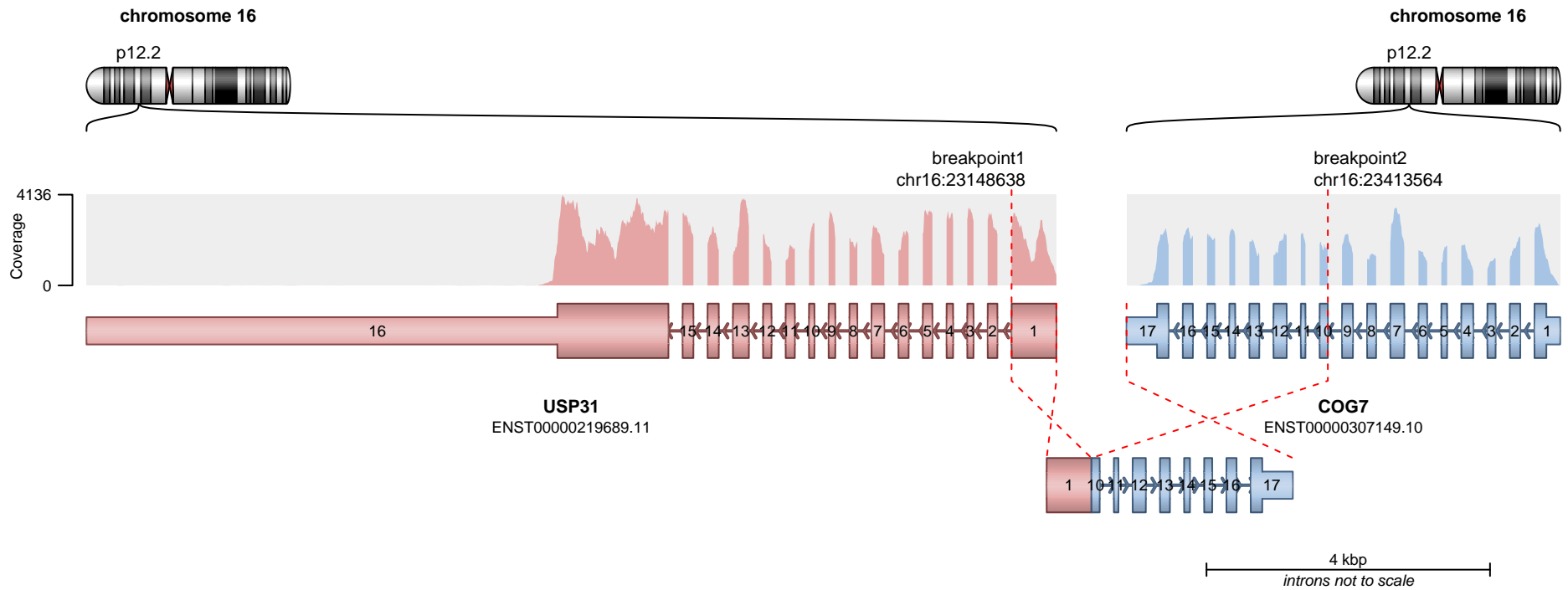
- translocation
- duplication
- deletion
- inversion



SUPPORTING READ COUNT

Split reads = 11
Discordant mates = 2

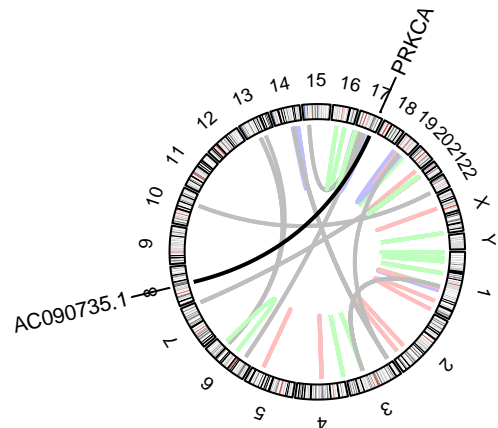
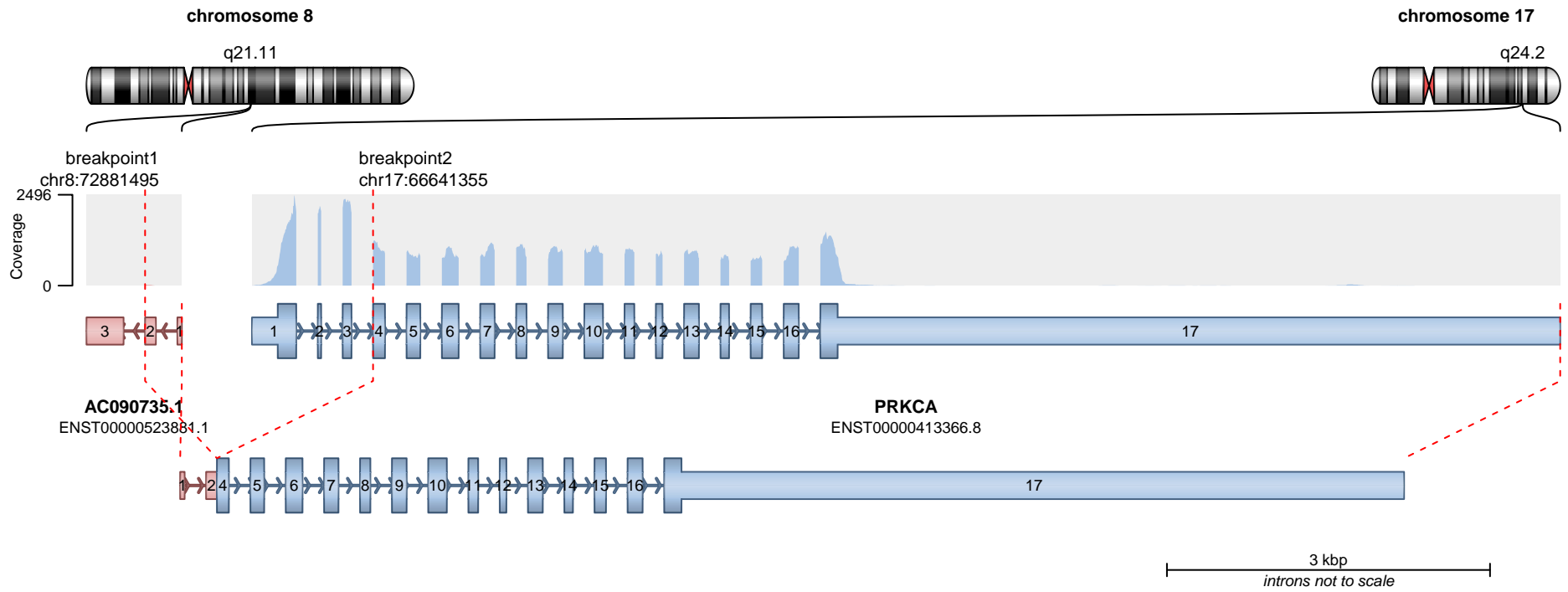
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



Phorbol esters/diacylglycerol binding domain (C1 domain)

C2 domain

PRKCA

Protein kinase domain

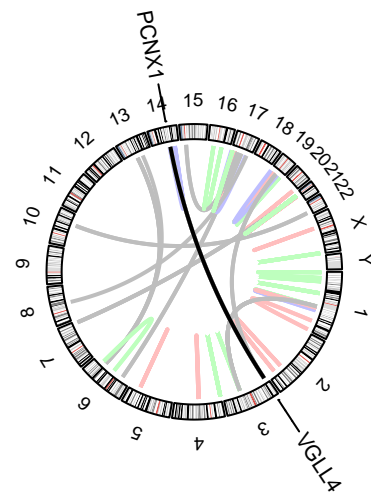
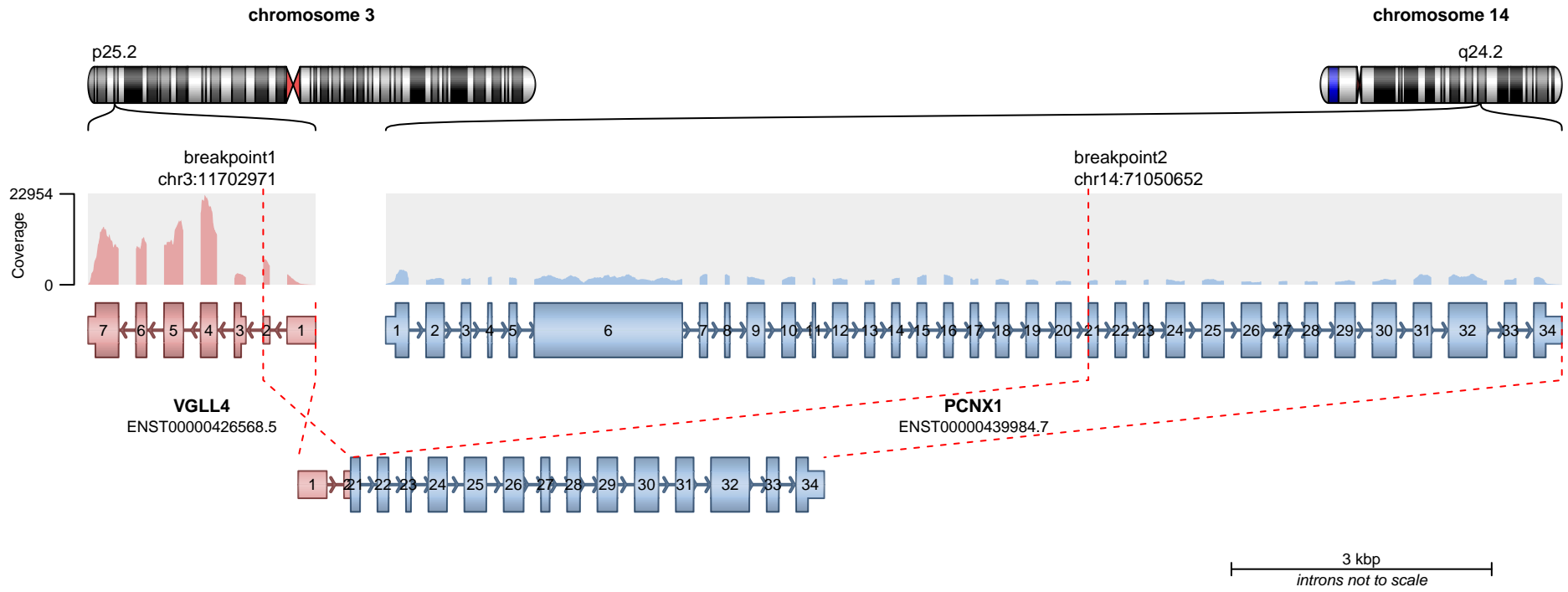
Protein kinase C terminal domain

RETAINED PROTEIN DOMAINS
reading frame unclear

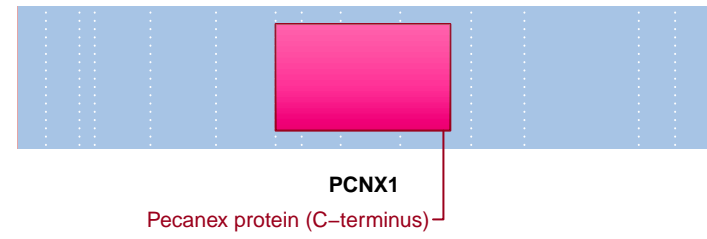
SUPPORTING READ COUNT

Split reads = 11
Discordant mates = 0

— translocation — deletion
— duplication — inversion



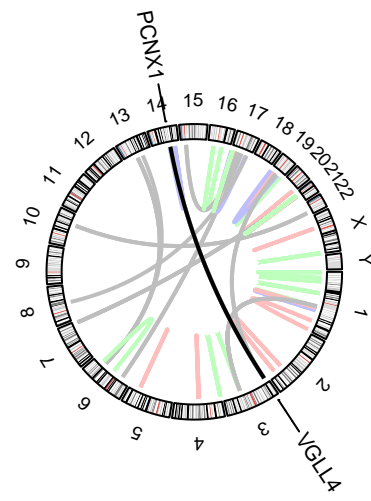
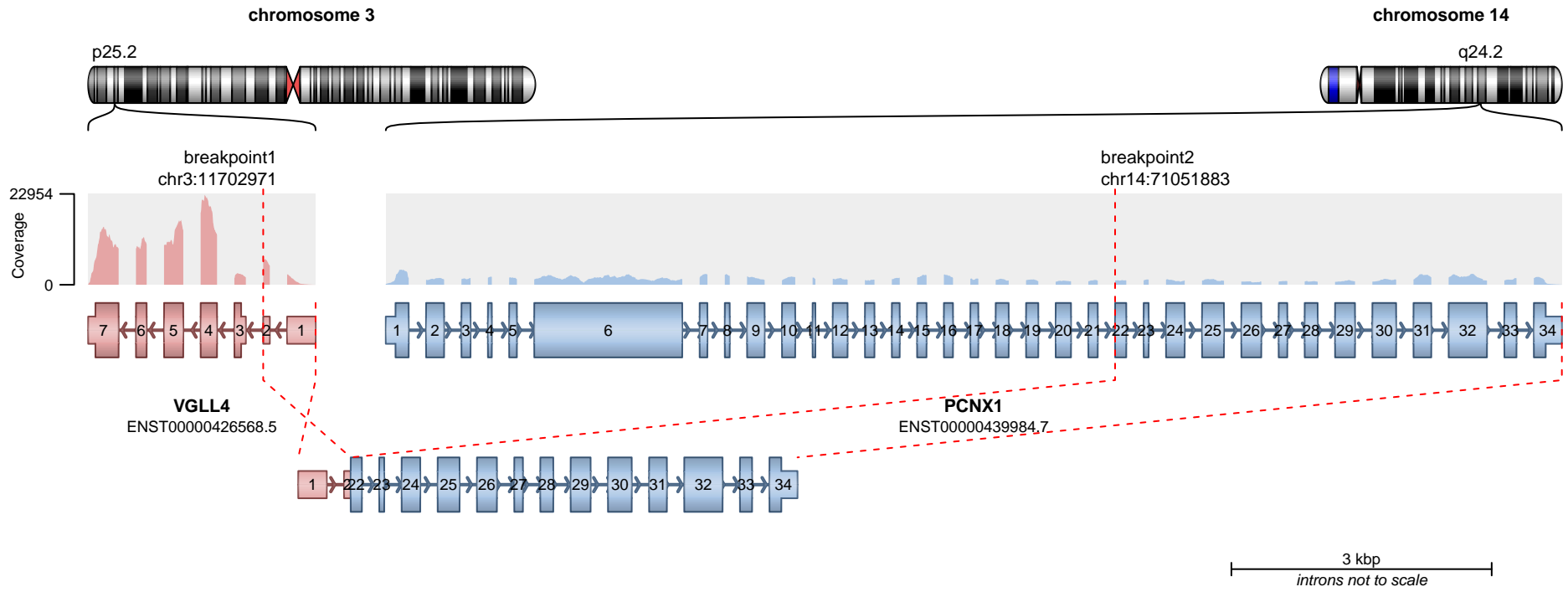
RETAINED PROTEIN DOMAINS
reading frame unclear



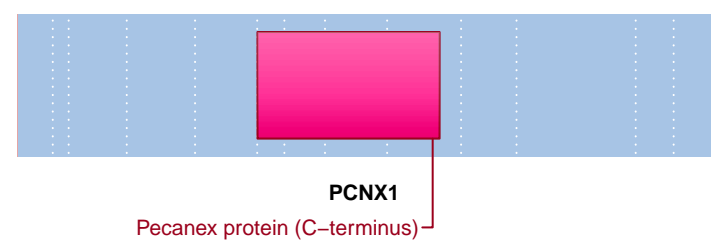
SUPPORTING READ COUNT

Split reads = 11
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



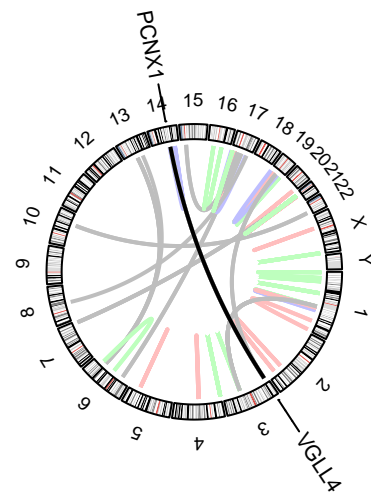
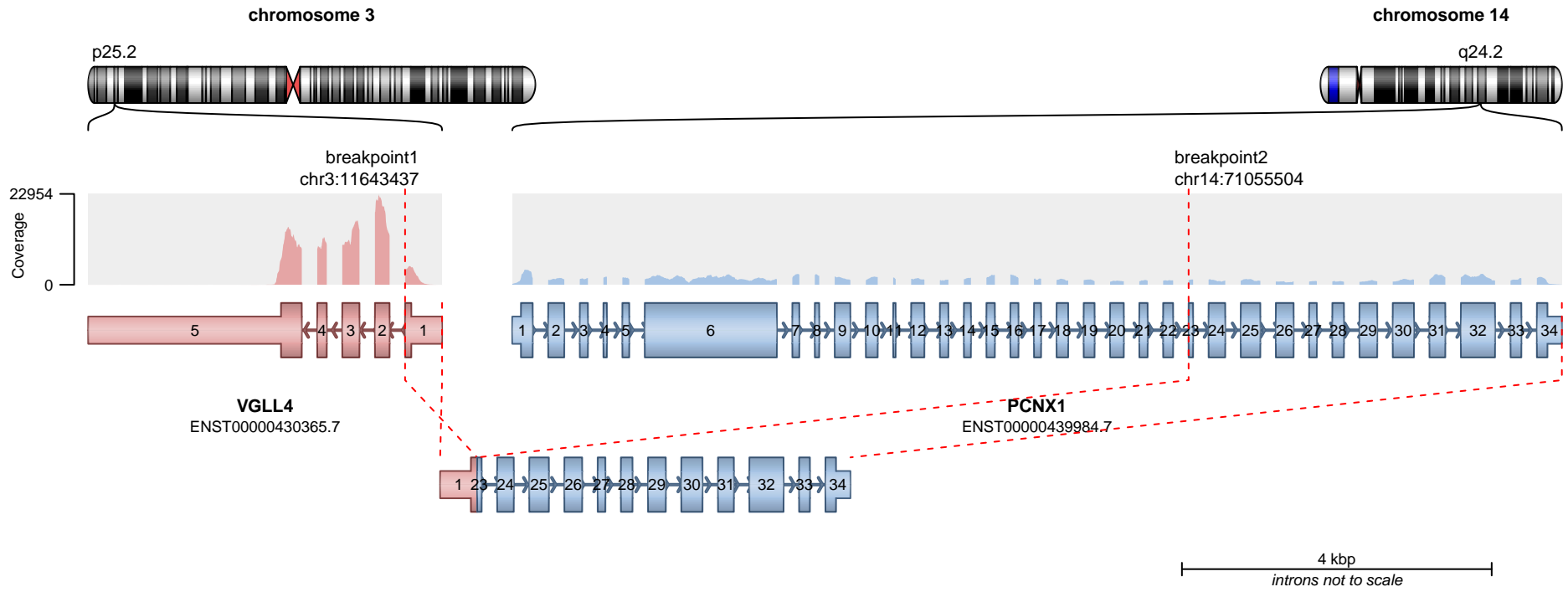
RETAINED PROTEIN DOMAINS
reading frame unclear



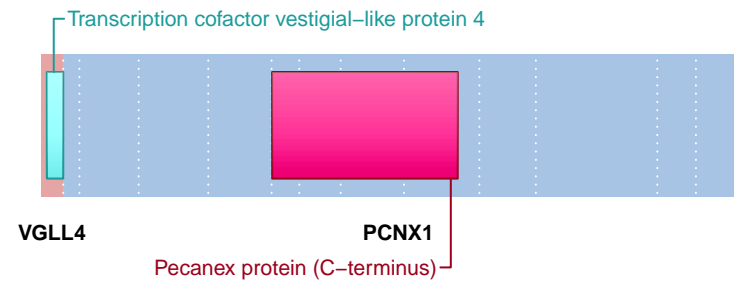
SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



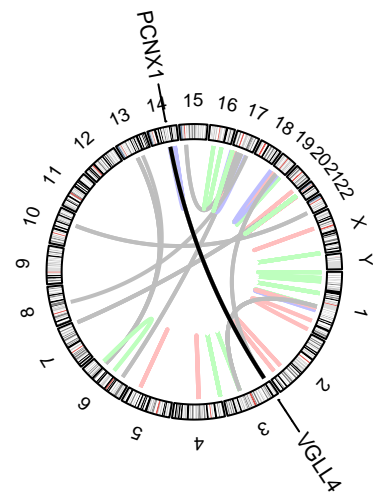
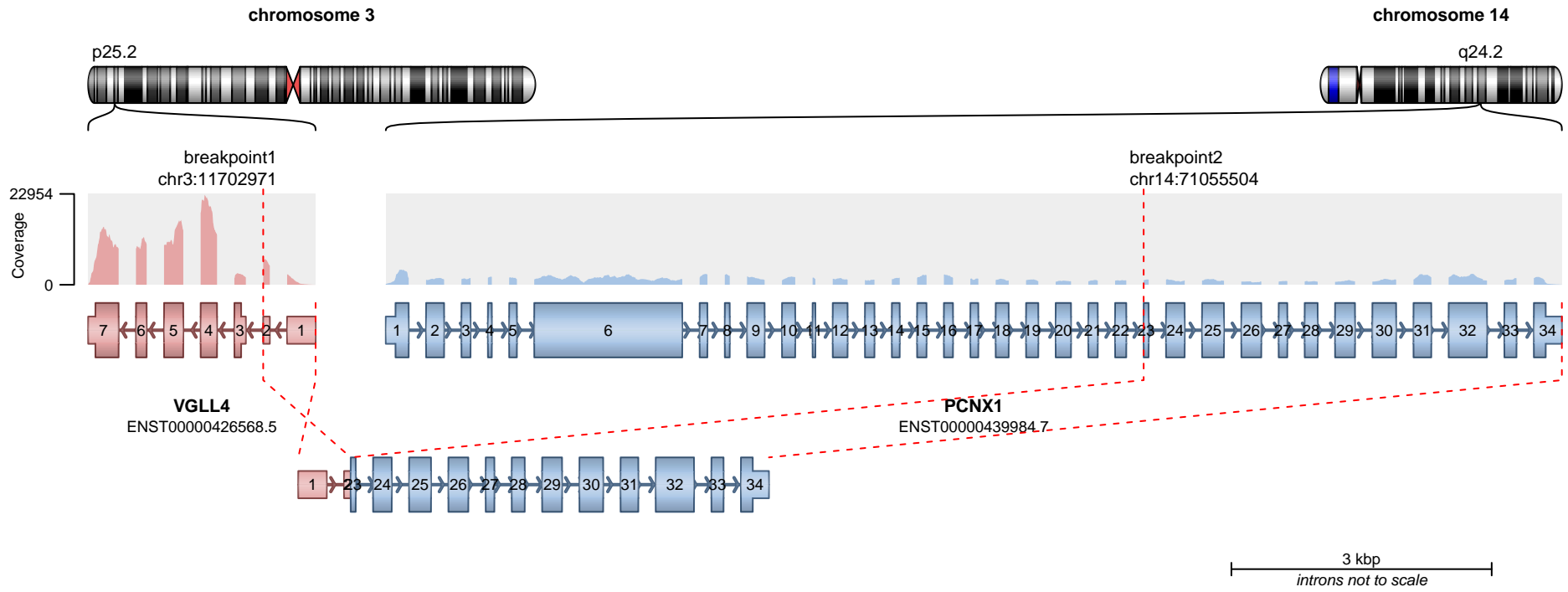
RETAINED PROTEIN DOMAINS
reading frame unclear



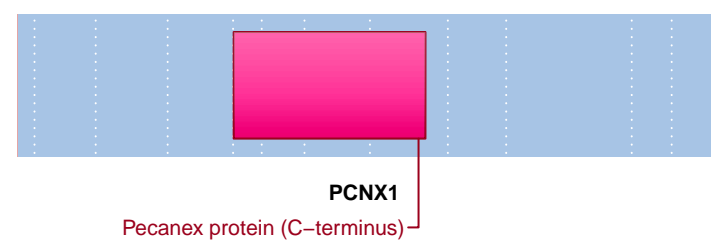
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



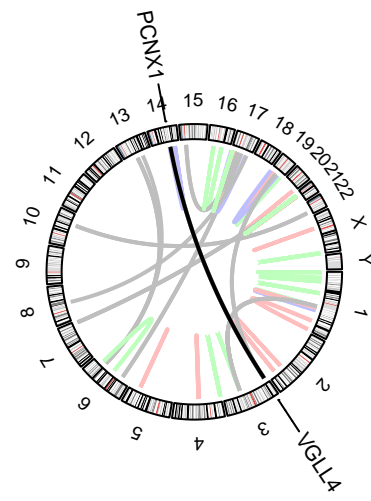
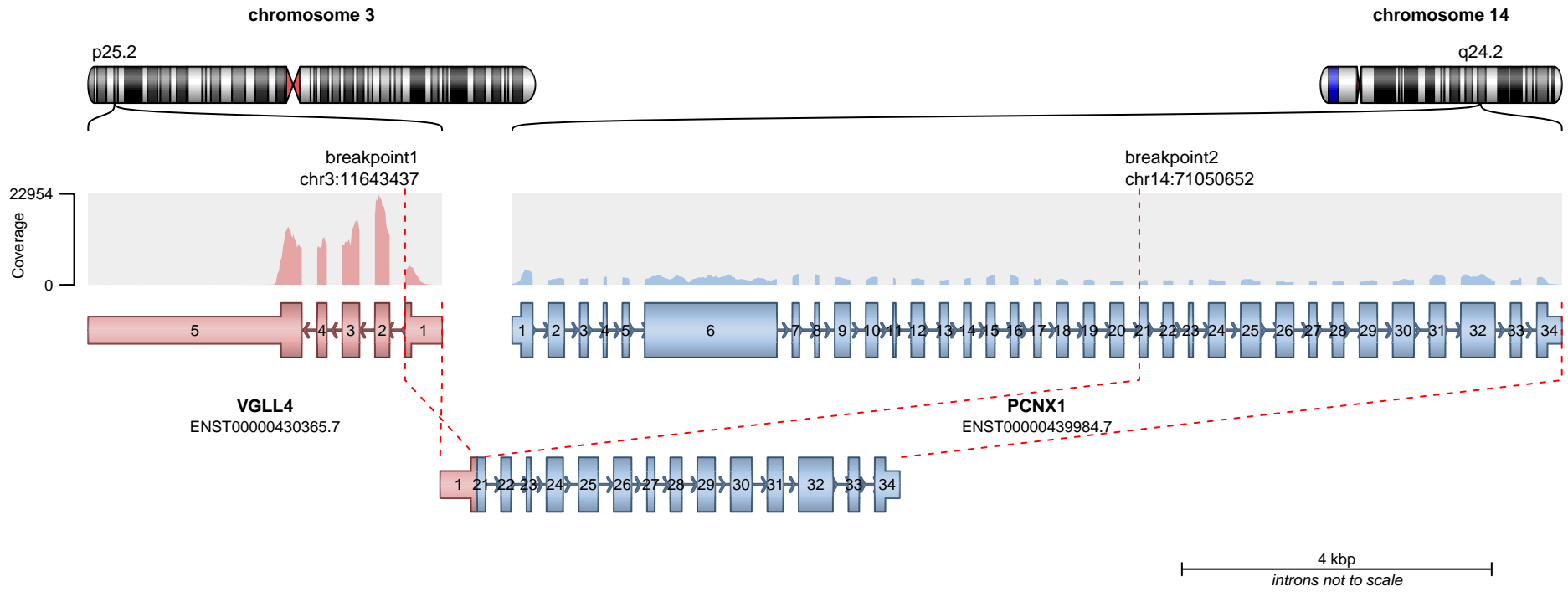
RETAINED PROTEIN DOMAINS
reading frame unclear



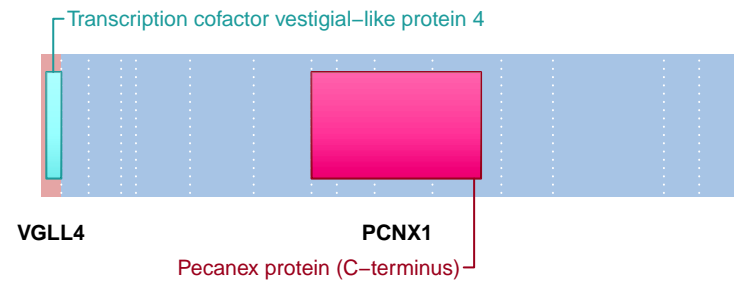
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



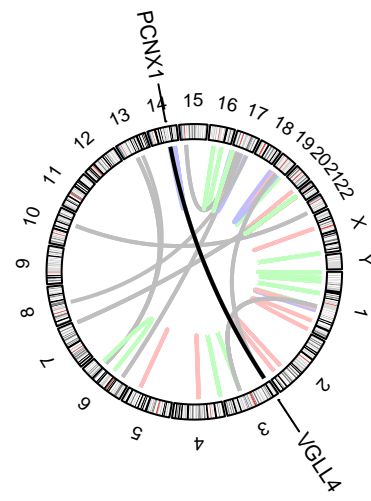
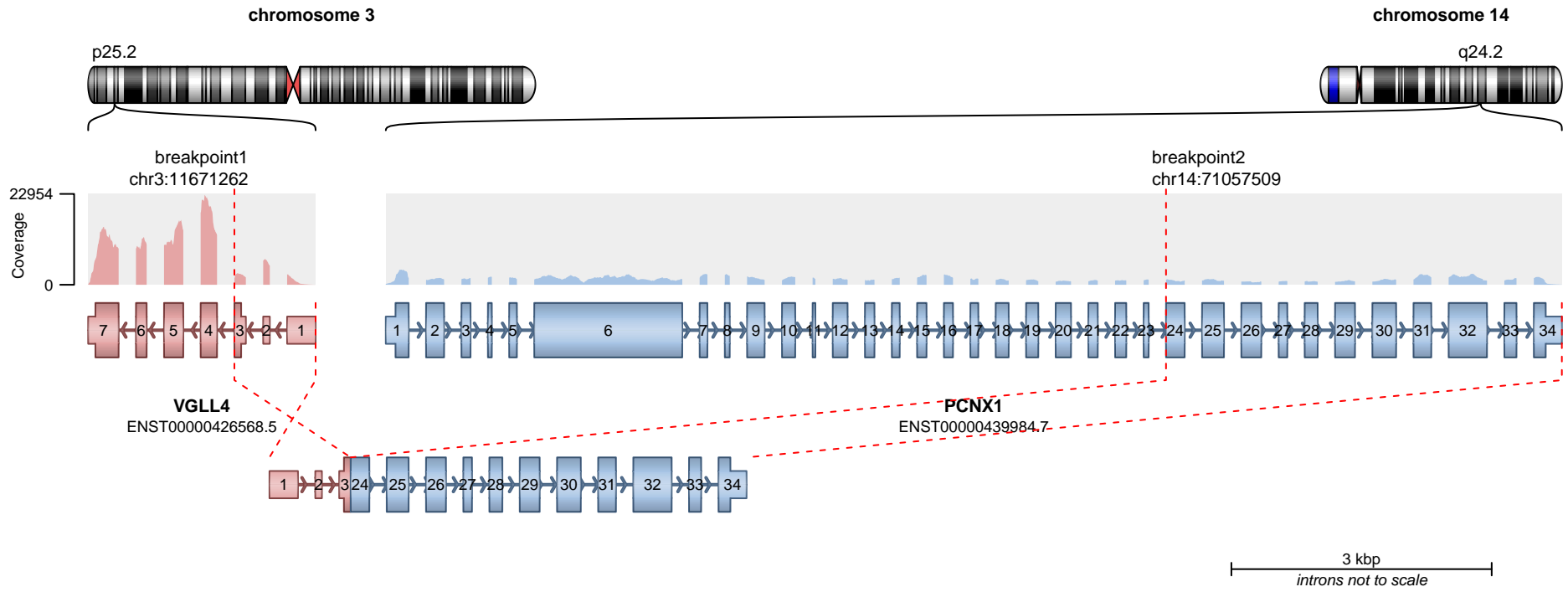
RETAINED PROTEIN DOMAINS
reading frame unclear



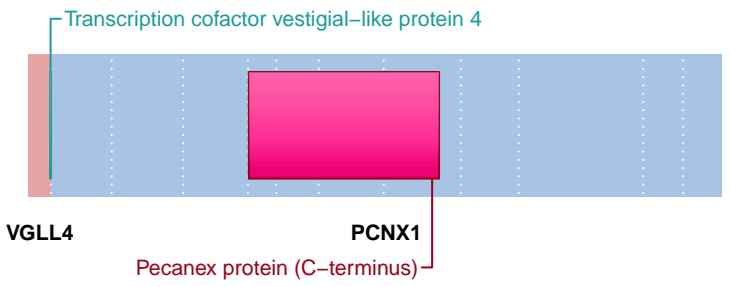
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion



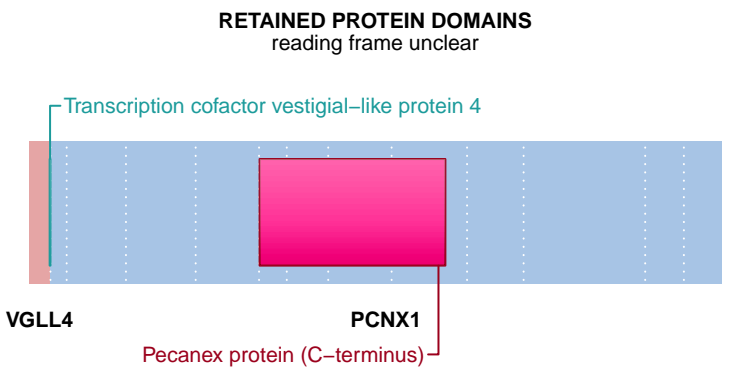
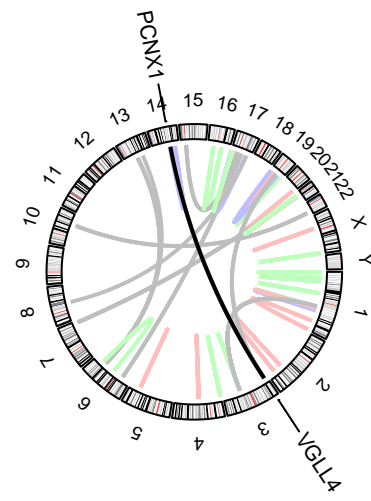
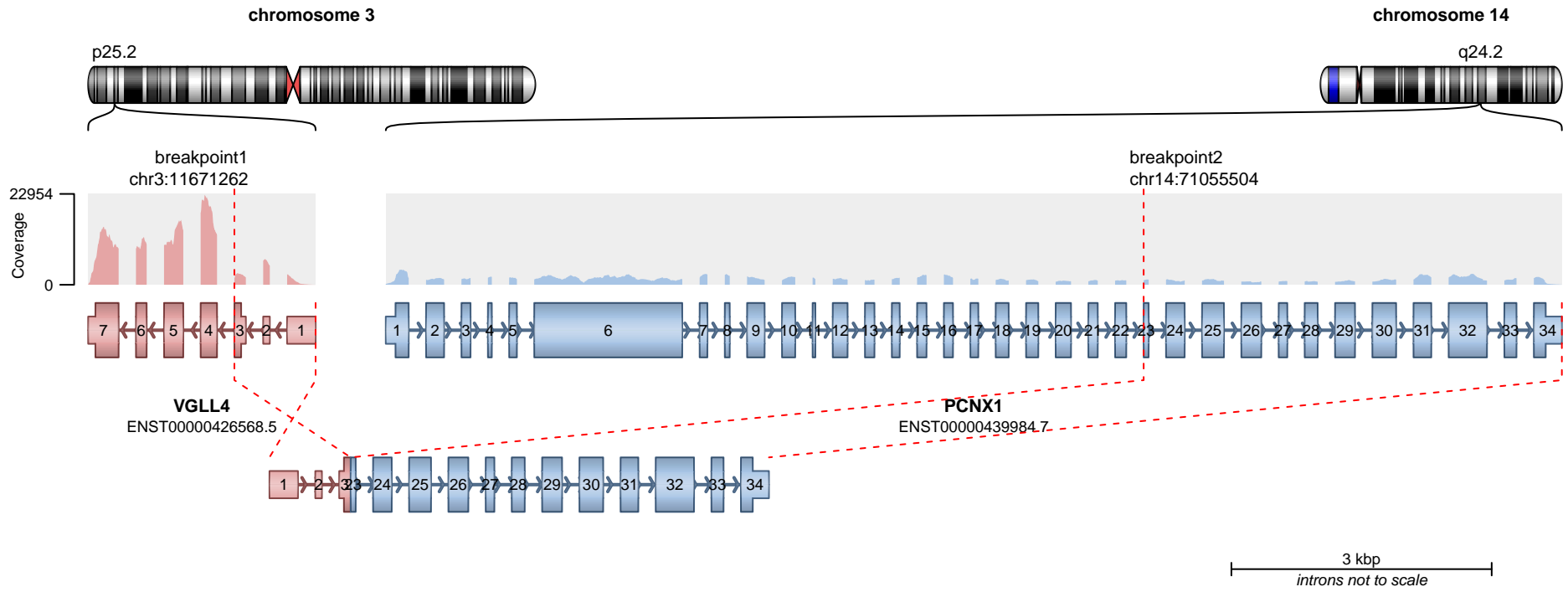
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

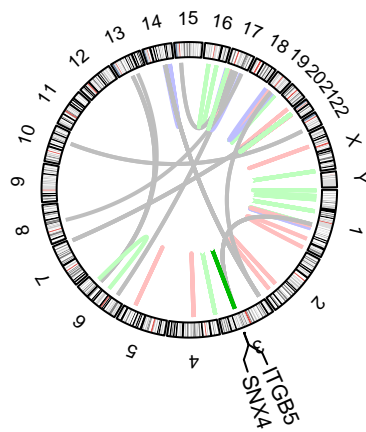
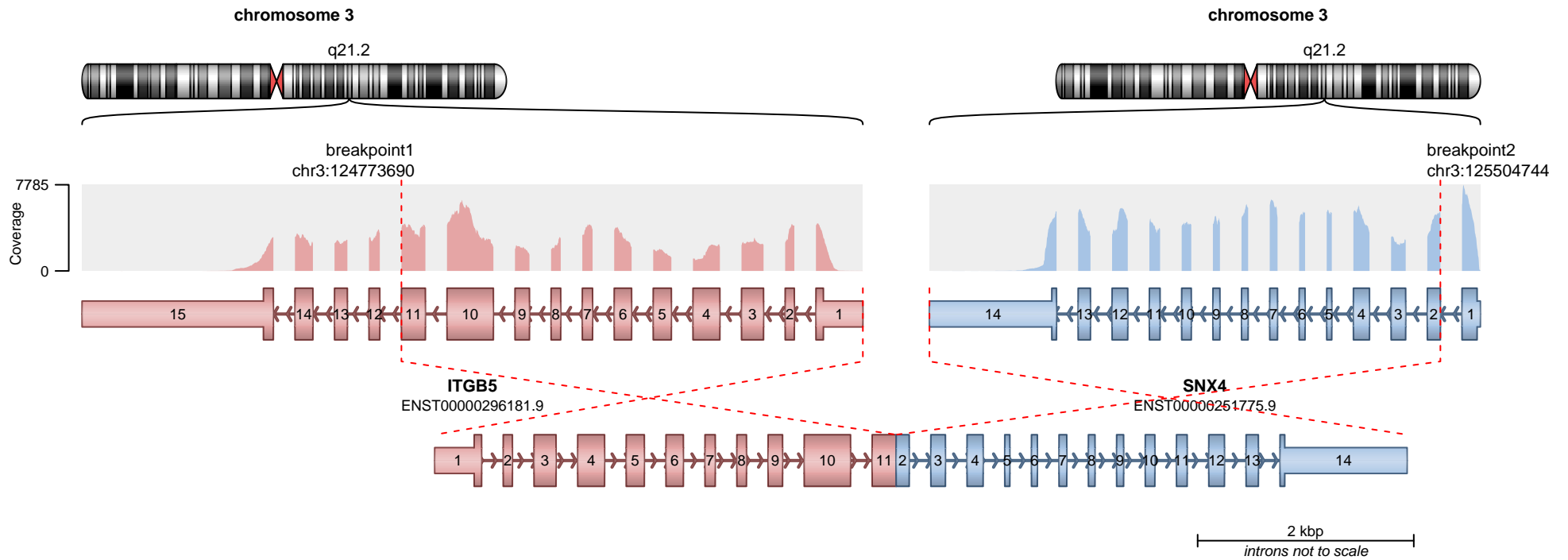
Split reads = 1
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

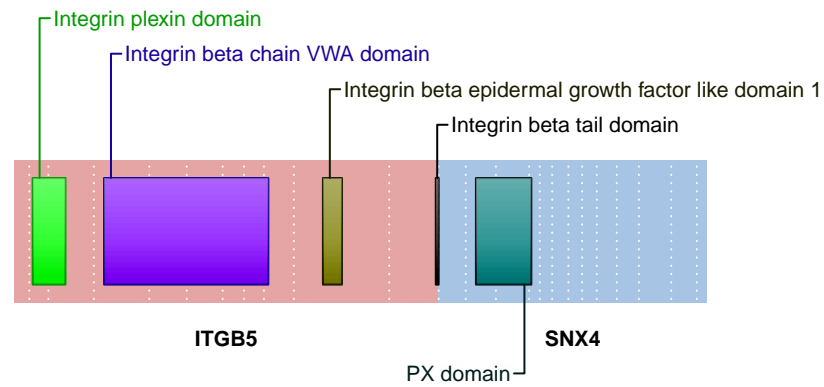


SUPPORTING READ COUNT
Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



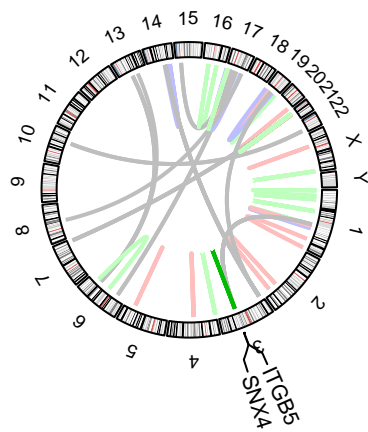
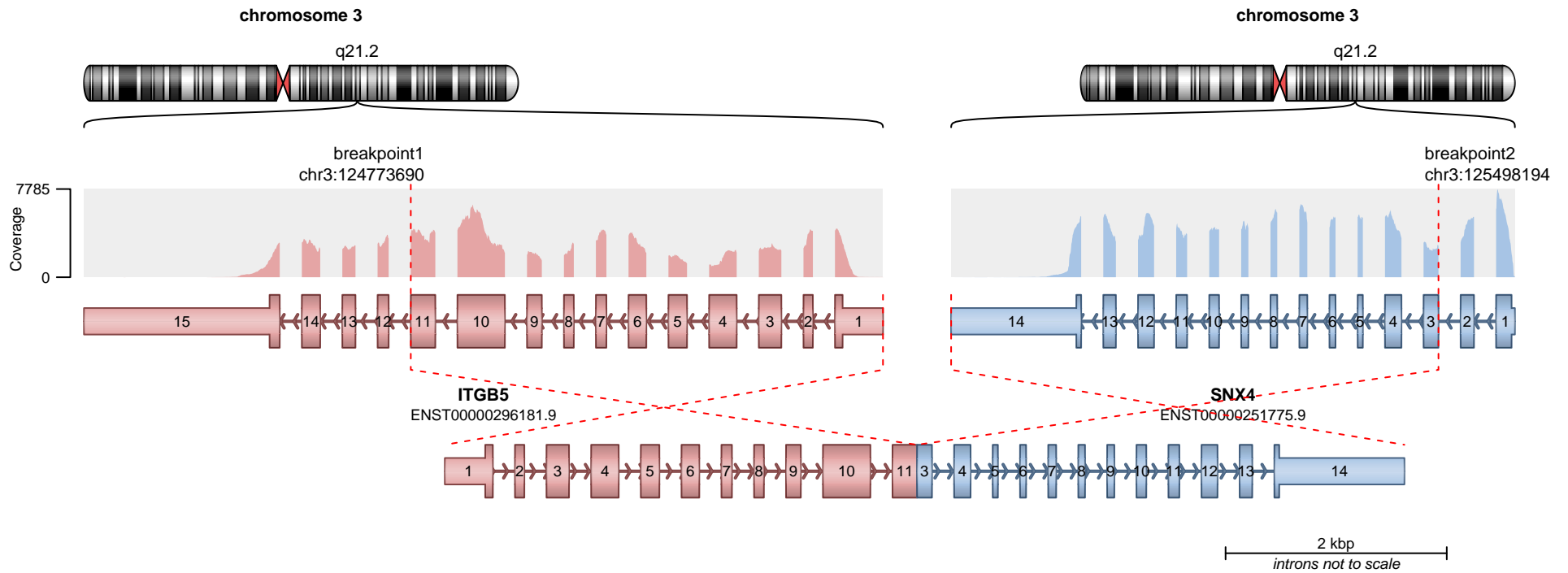
RETAINED PROTEIN DOMAINS
reading frame unclear



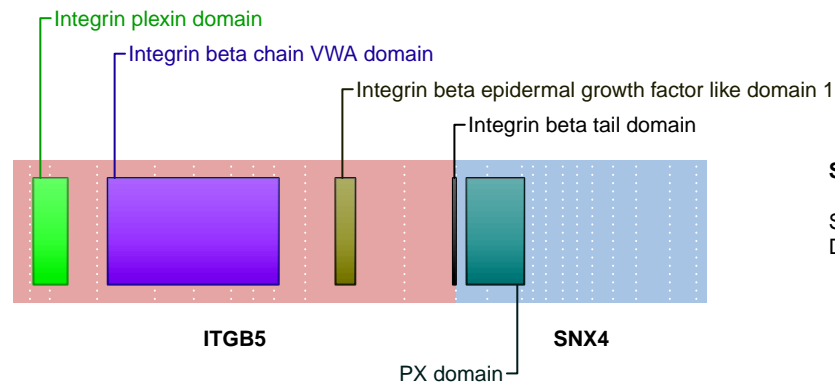
SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 0

— translocation — deletion
— duplication — inversion



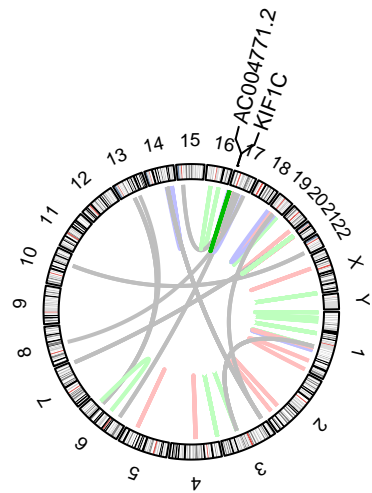
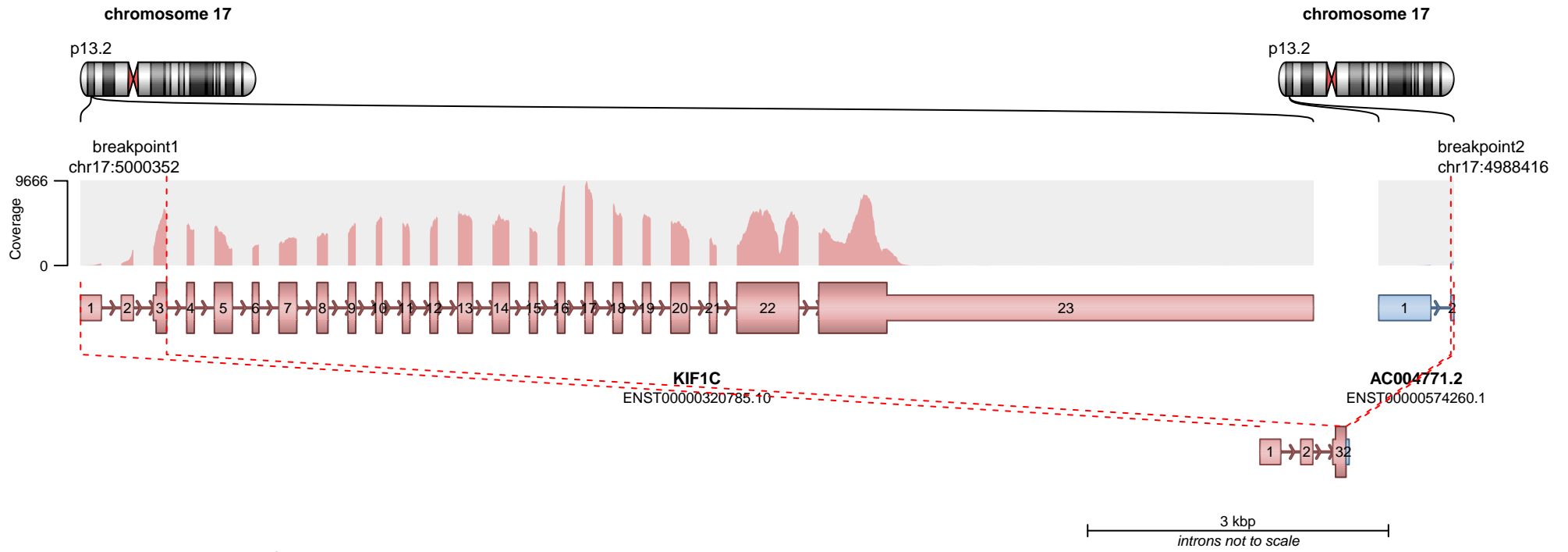
RETAINED PROTEIN DOMAINS
reading frame unclear



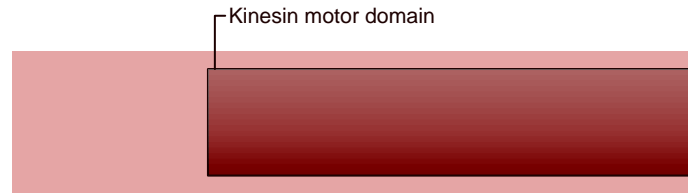
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

— translocation — deletion
— duplication — inversion



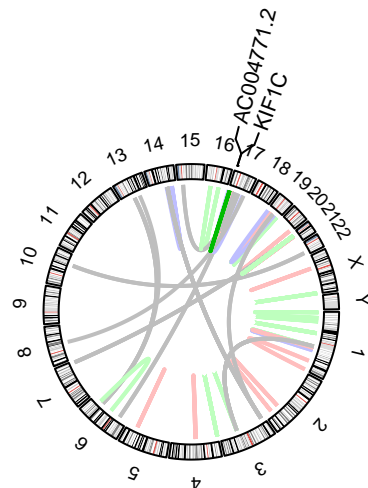
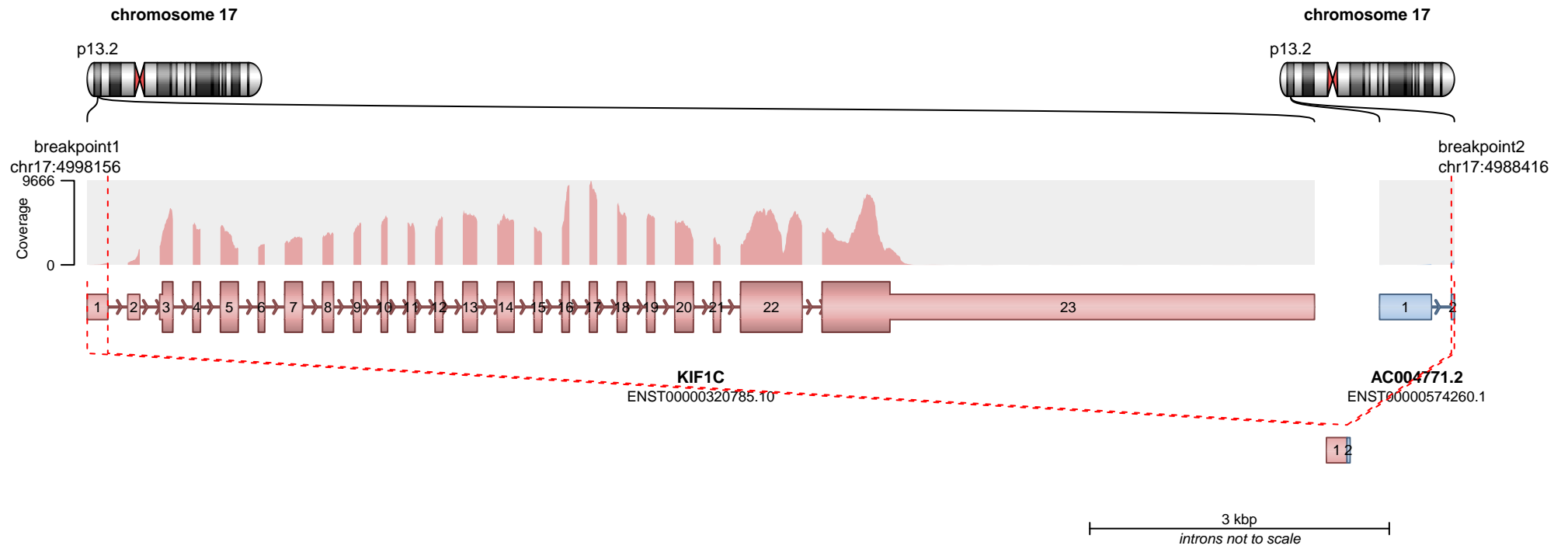
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion

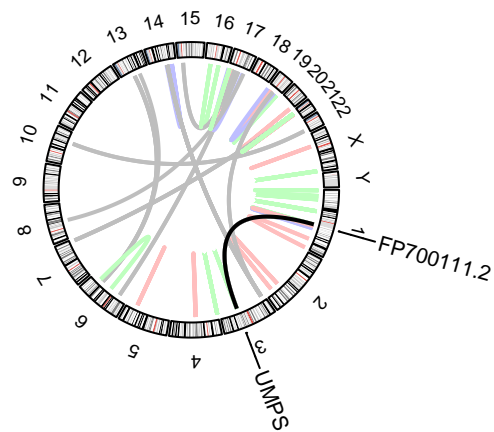
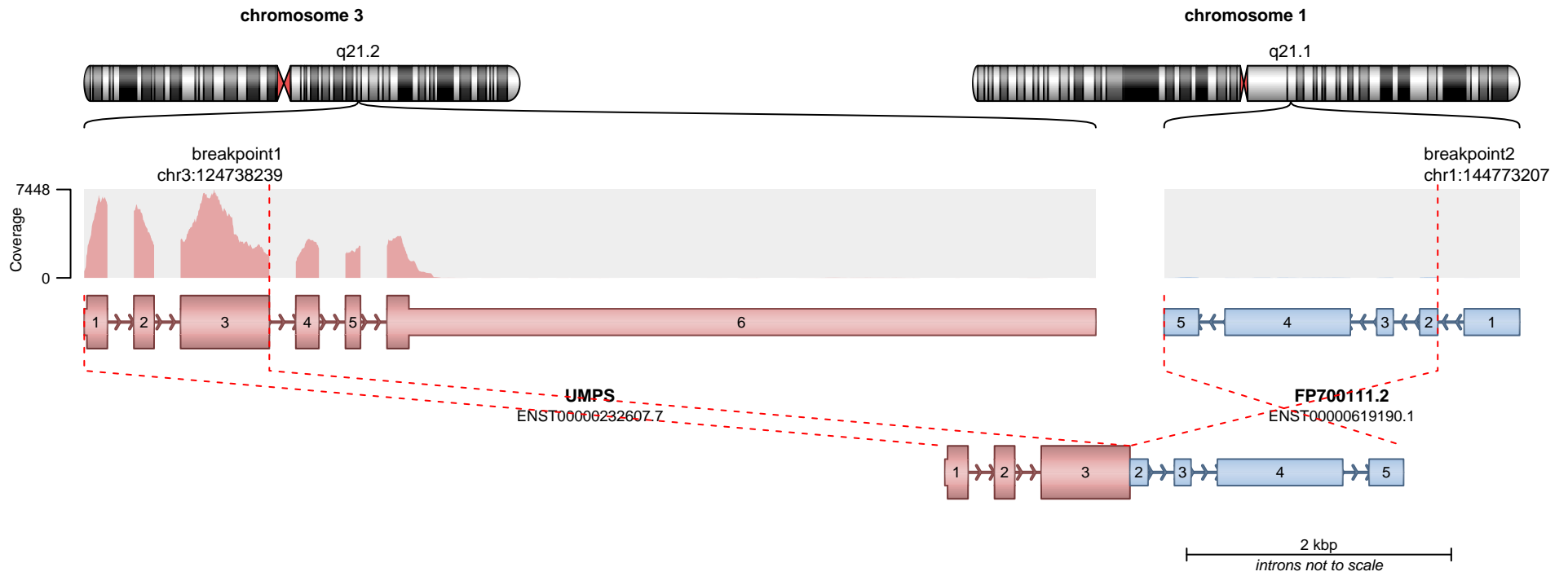


— translocation — deletion
— duplication — inversion

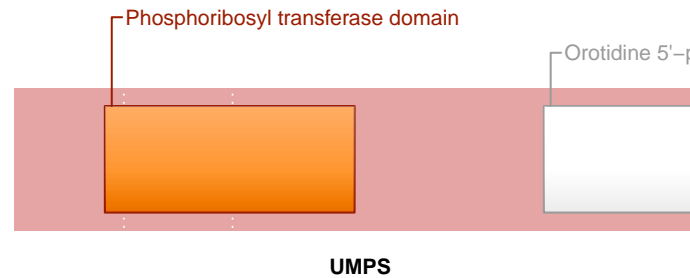
No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0



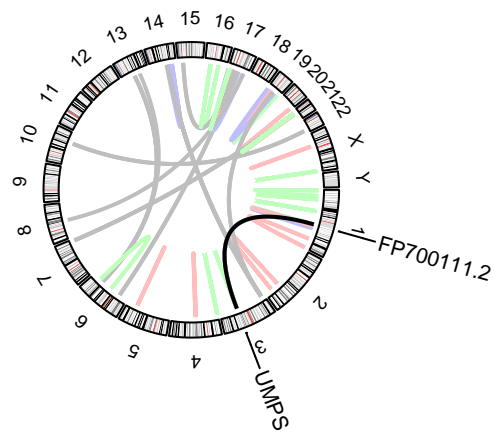
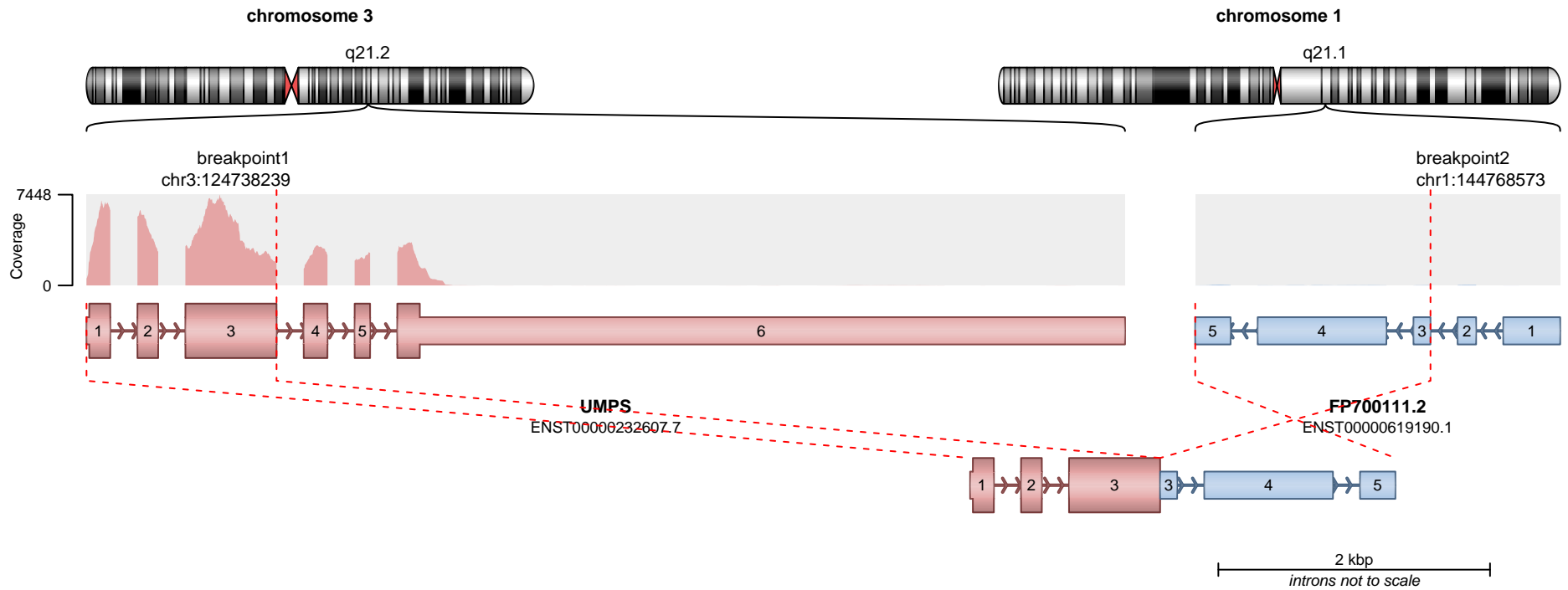
RETAINED PROTEIN DOMAINS
reading frame unclear



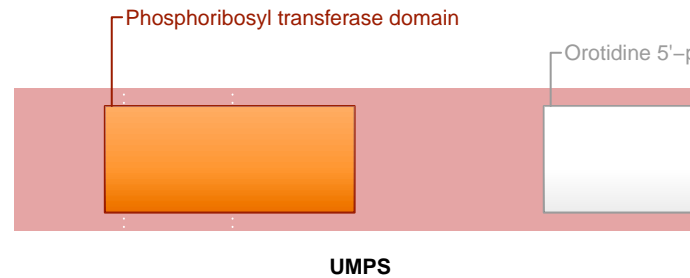
SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 0

— translocation — deletion
— duplication — inversion



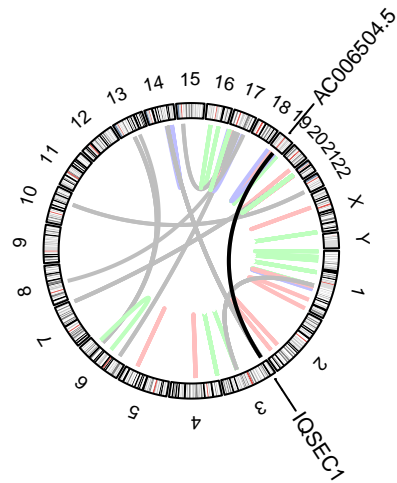
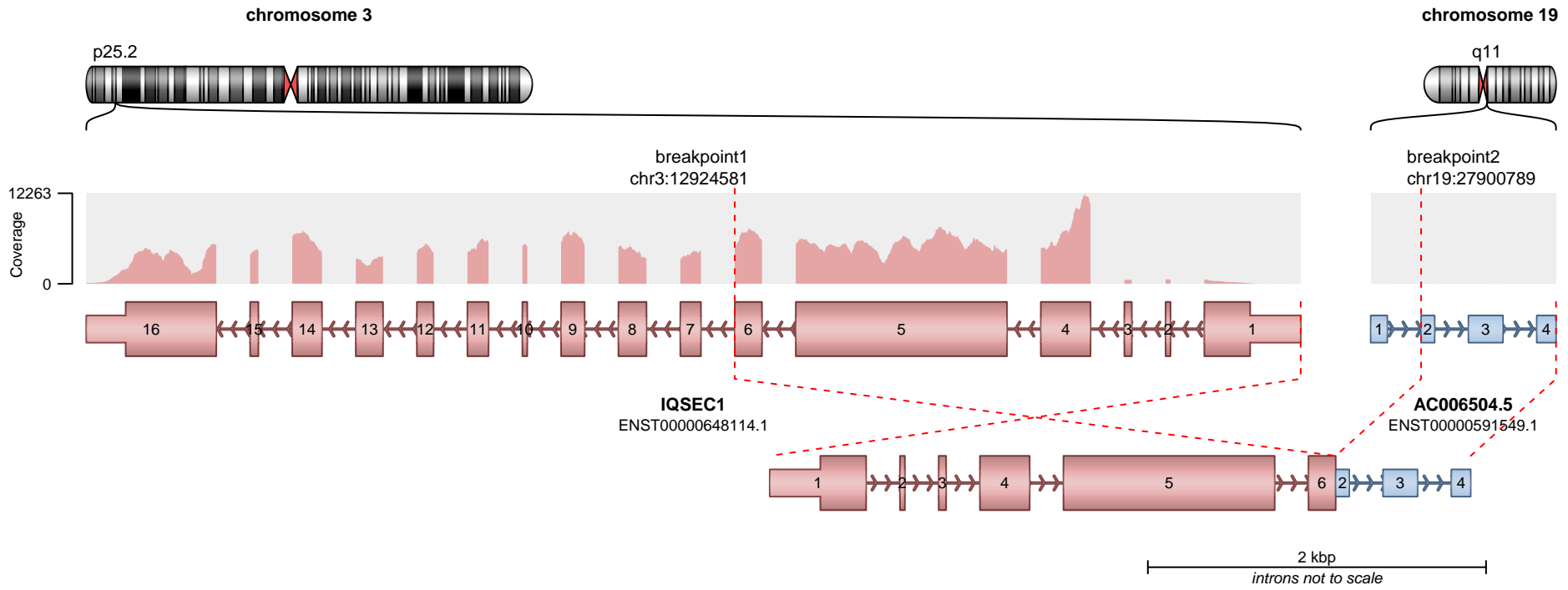
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



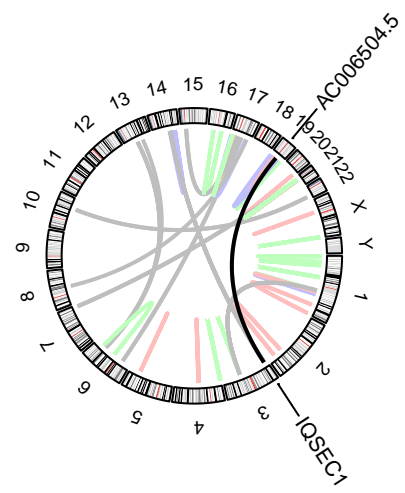
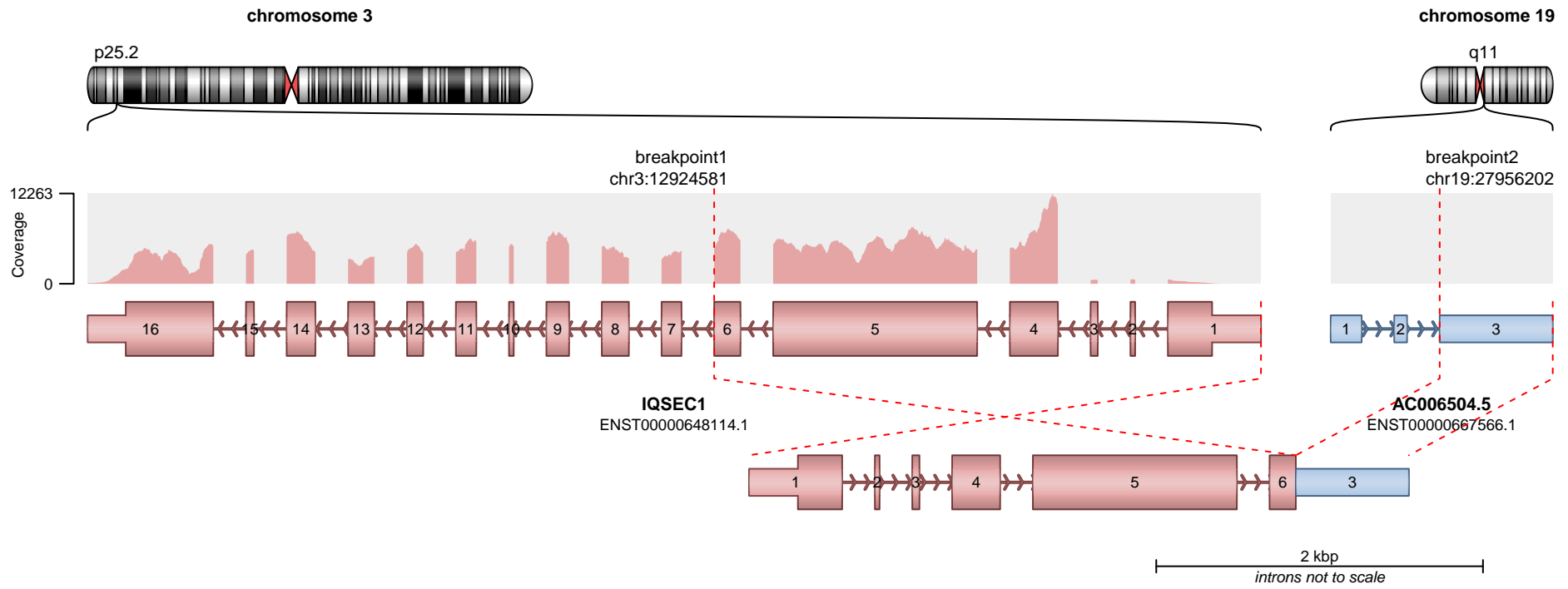
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 1

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

- translocation
- duplication
- deletion
- inversion