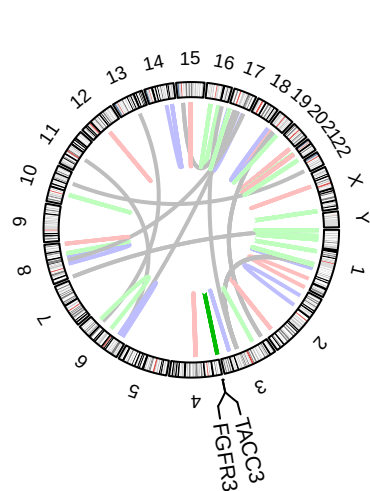
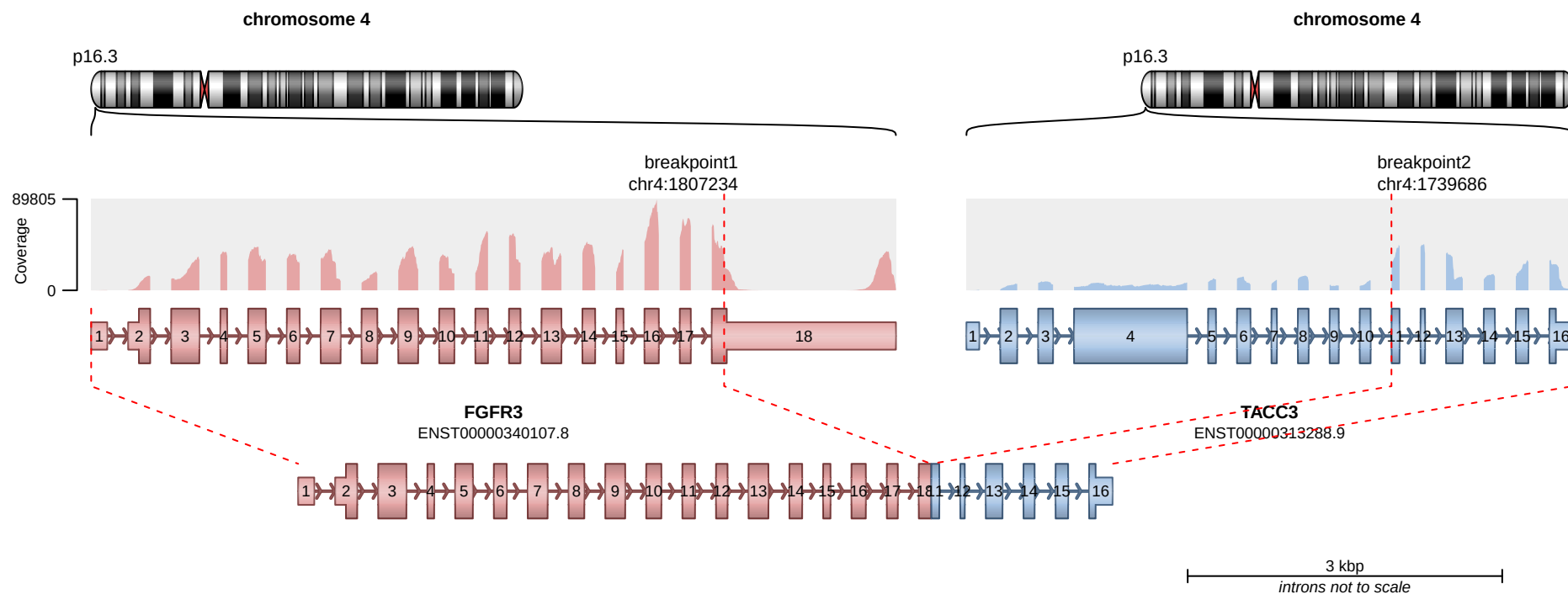
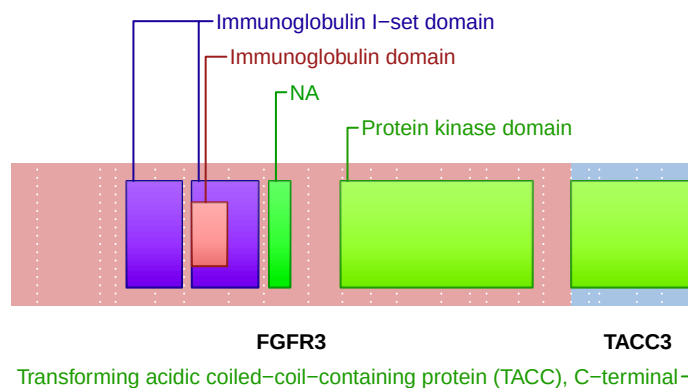




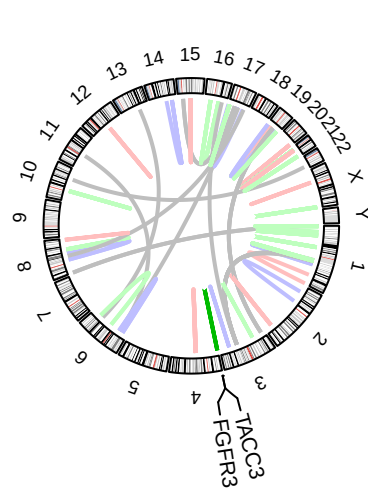
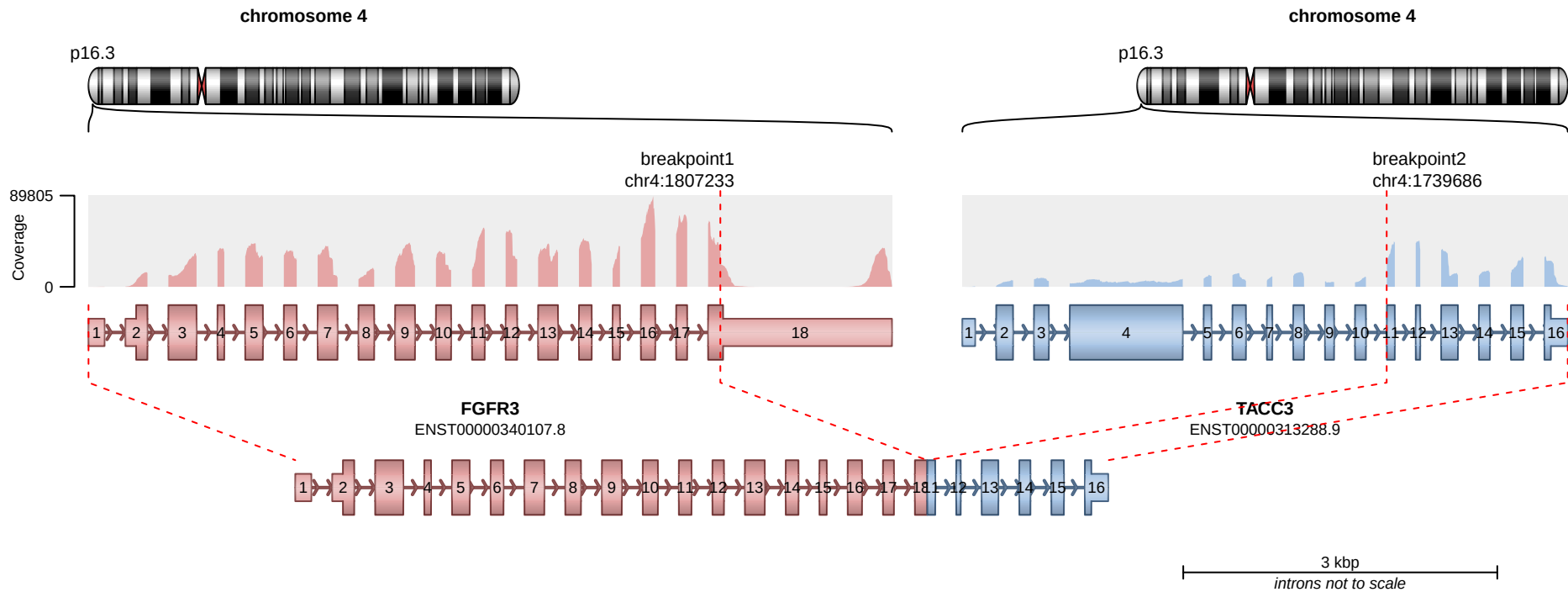
RETAINED PROTEIN DOMAINS reading frame unclear



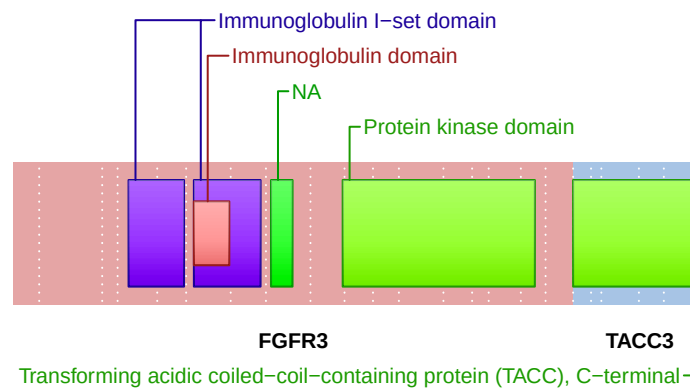
SUPPORTING READ COUNT

Split reads = 2325
Discordant mates = 117

— translocation — deletion
— duplication — inversion



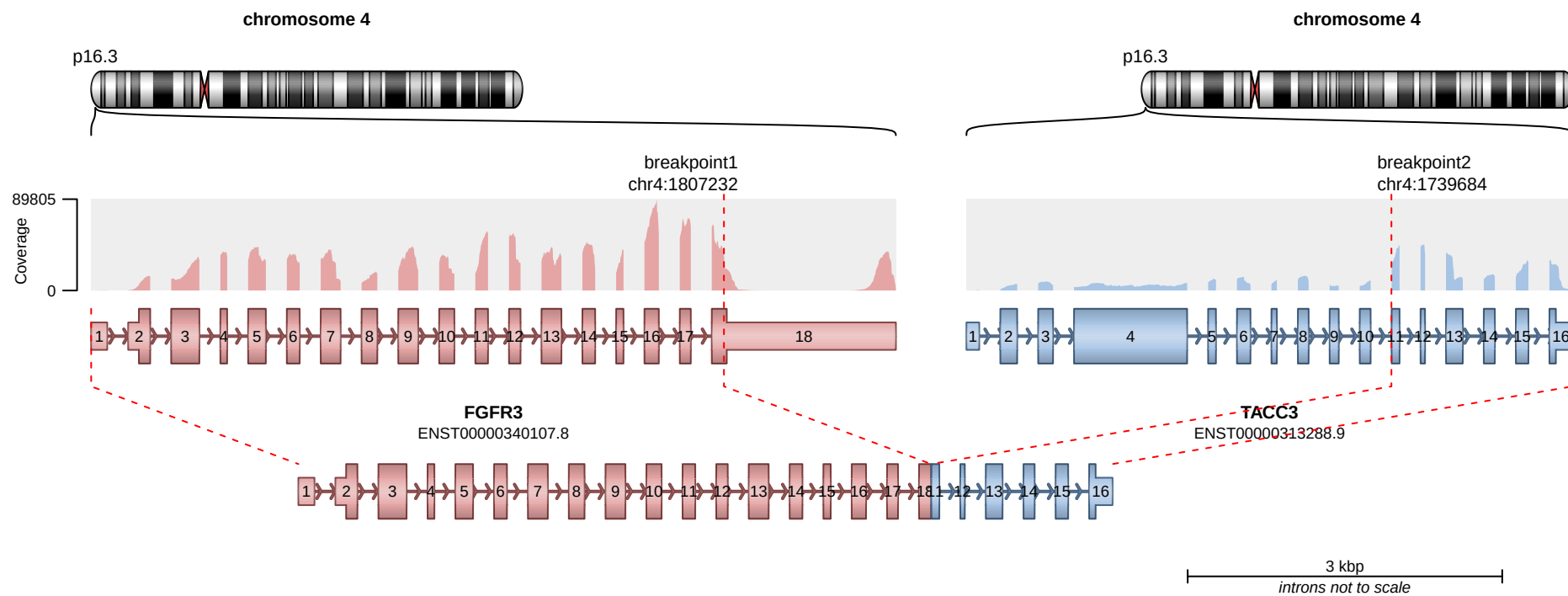
RETAINED PROTEIN DOMAINS reading frame unclear

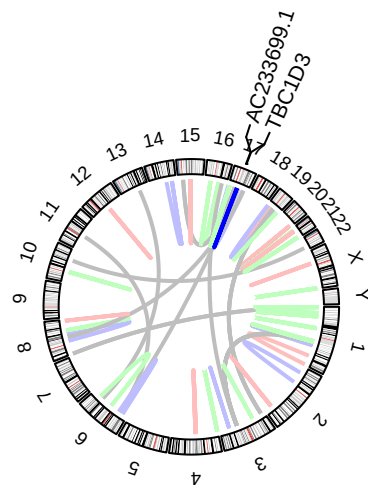
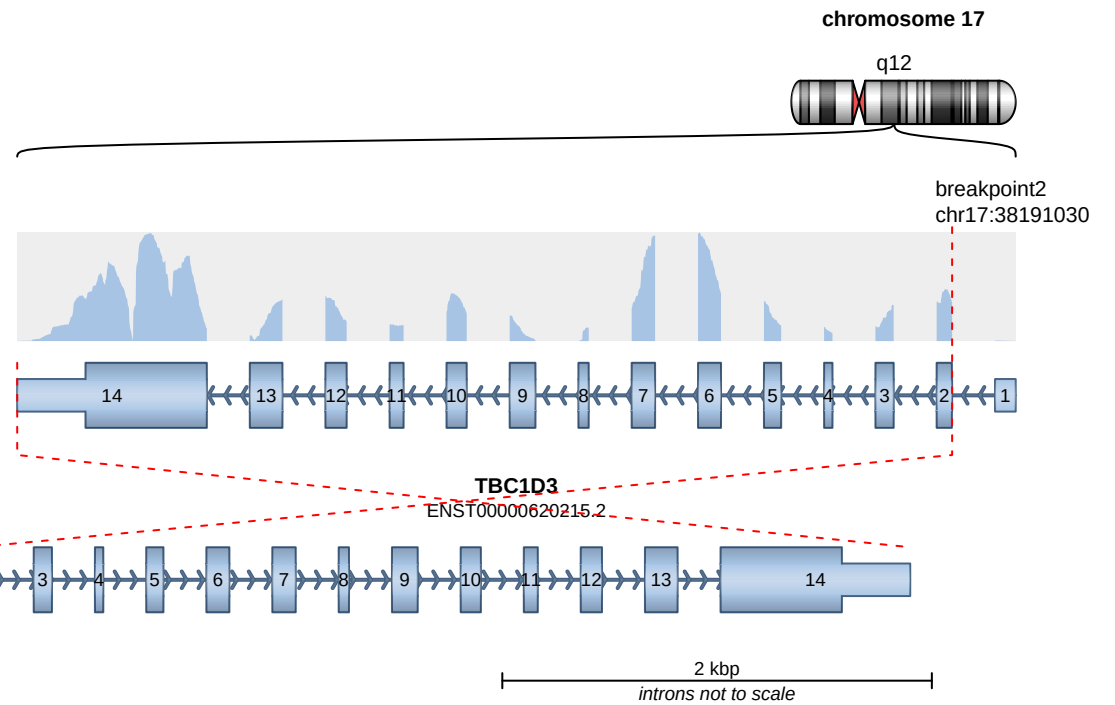
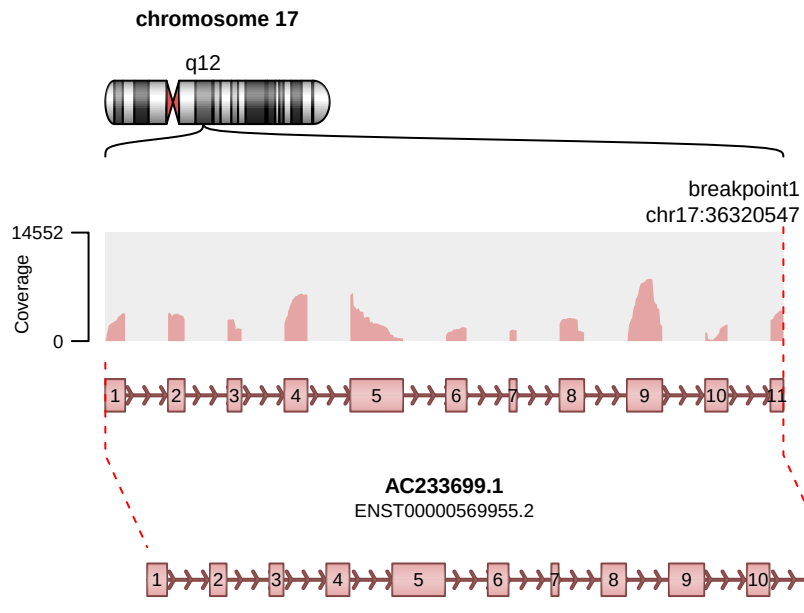


SUPPORTING READ COUNT

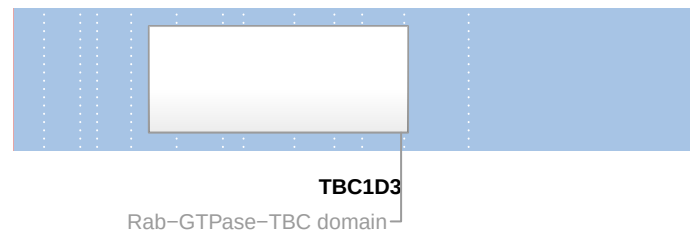
Split reads = 10
Discordant mates = 117

— translocation — deletion
— duplication — inversion





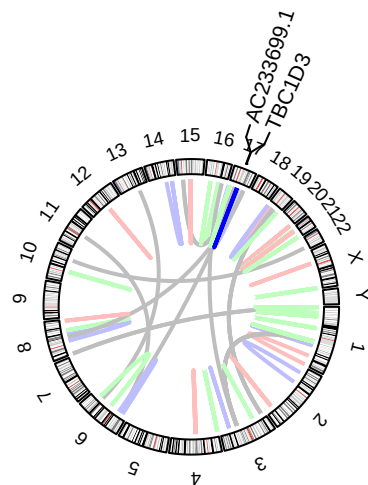
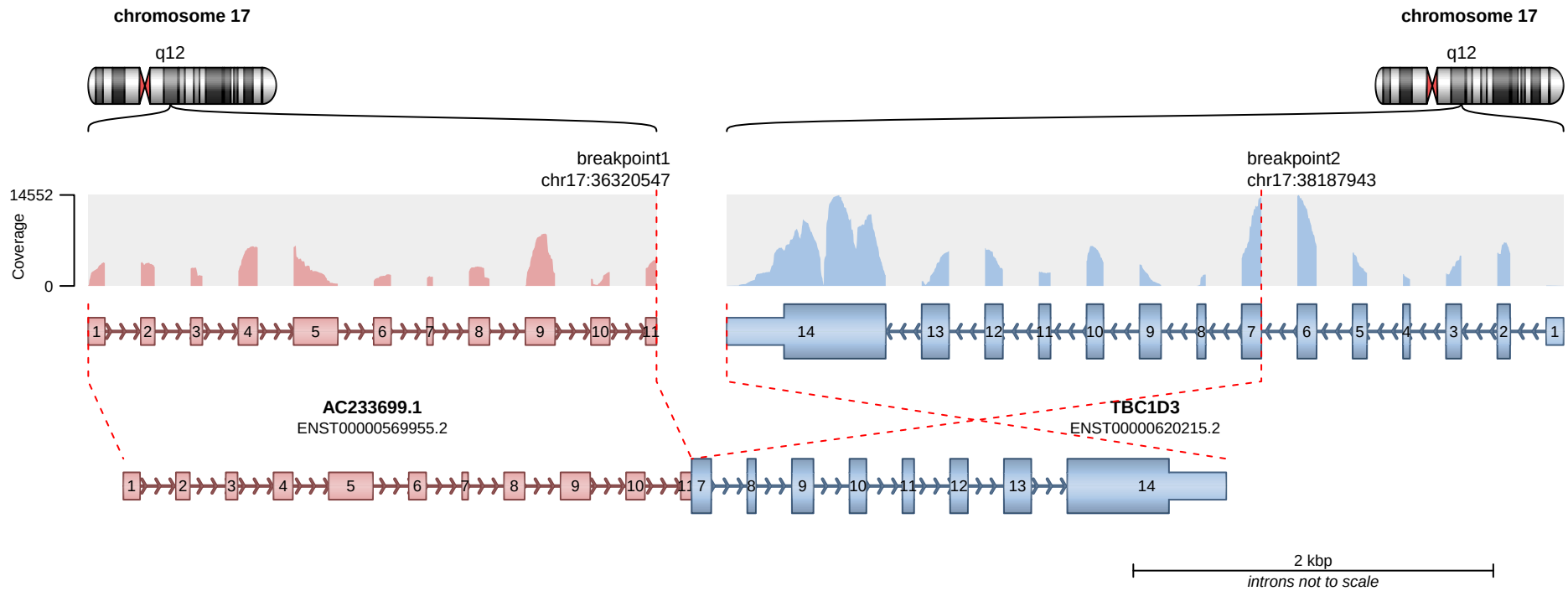
RETAINED PROTEIN DOMAINS
reading frame unclear



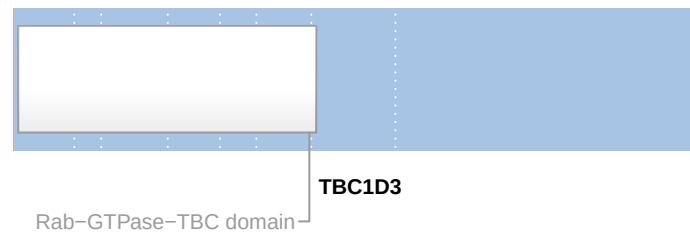
SUPPORTING READ COUNT

Split reads = 1238
Discordant mates = 0

— translocation — deletion
— duplication — inversion



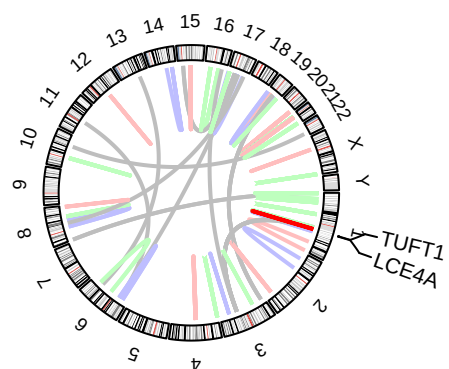
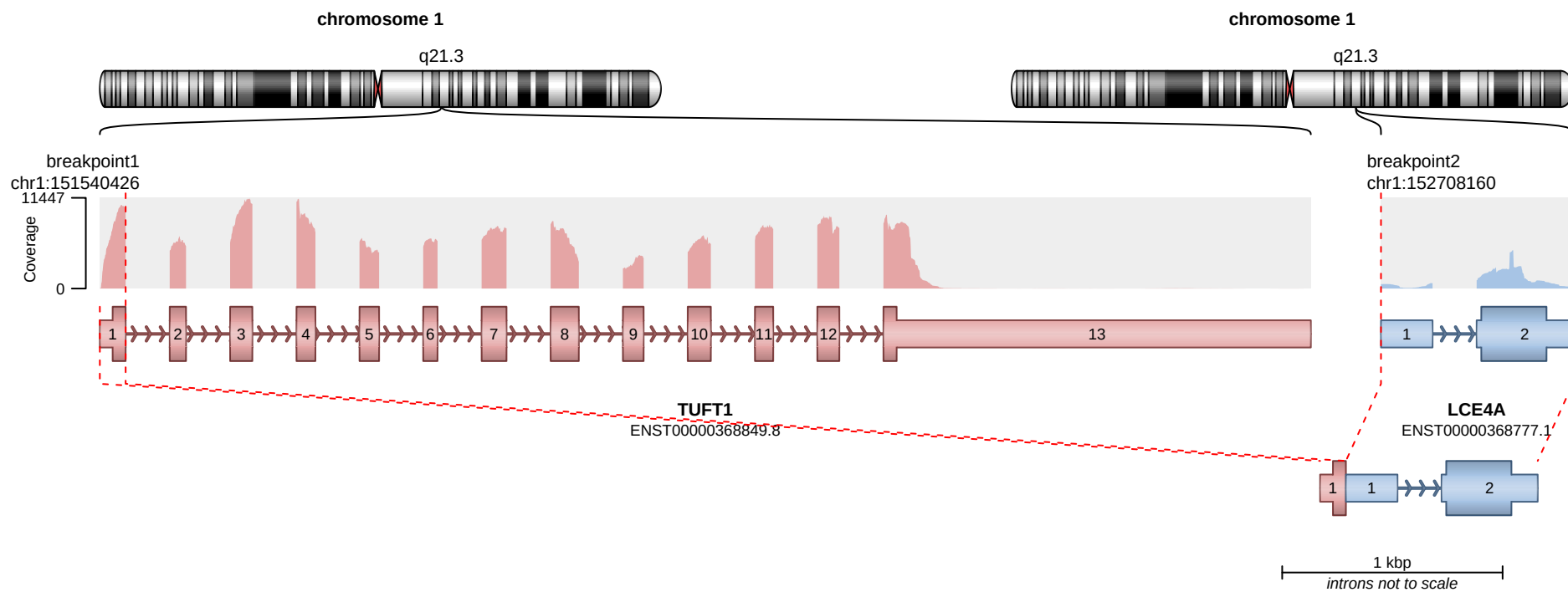
RETAINED PROTEIN DOMAINS reading frame unclear



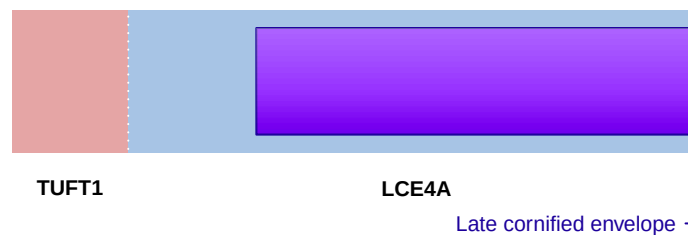
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

— translocation — deletion
— duplication — inversion



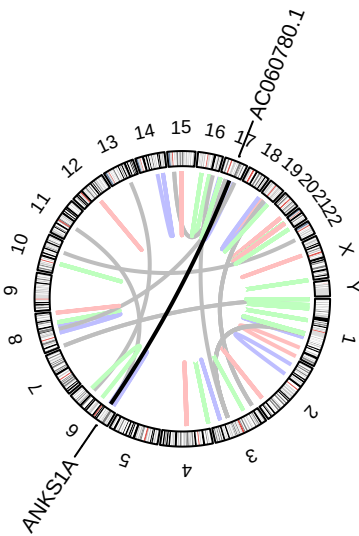
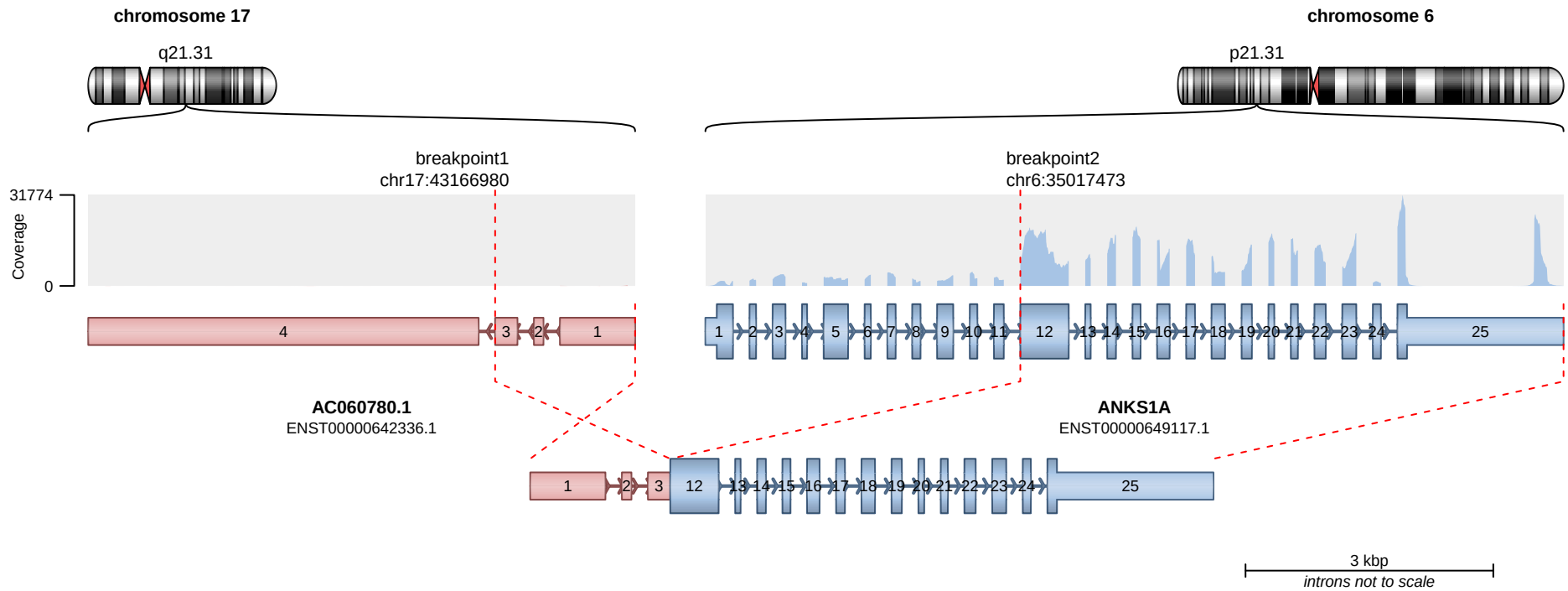
RETAINED PROTEIN DOMAINS
reading frame unclear



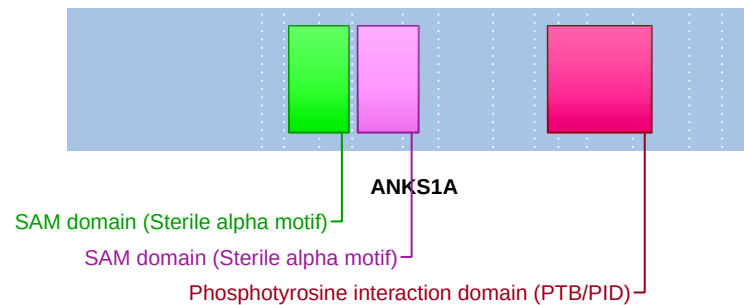
SUPPORTING READ COUNT

Split reads = 530
Discordant mates = 0

— translocation — deletion
— duplication — inversion



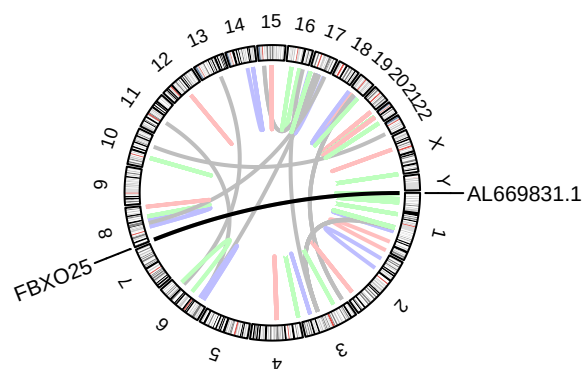
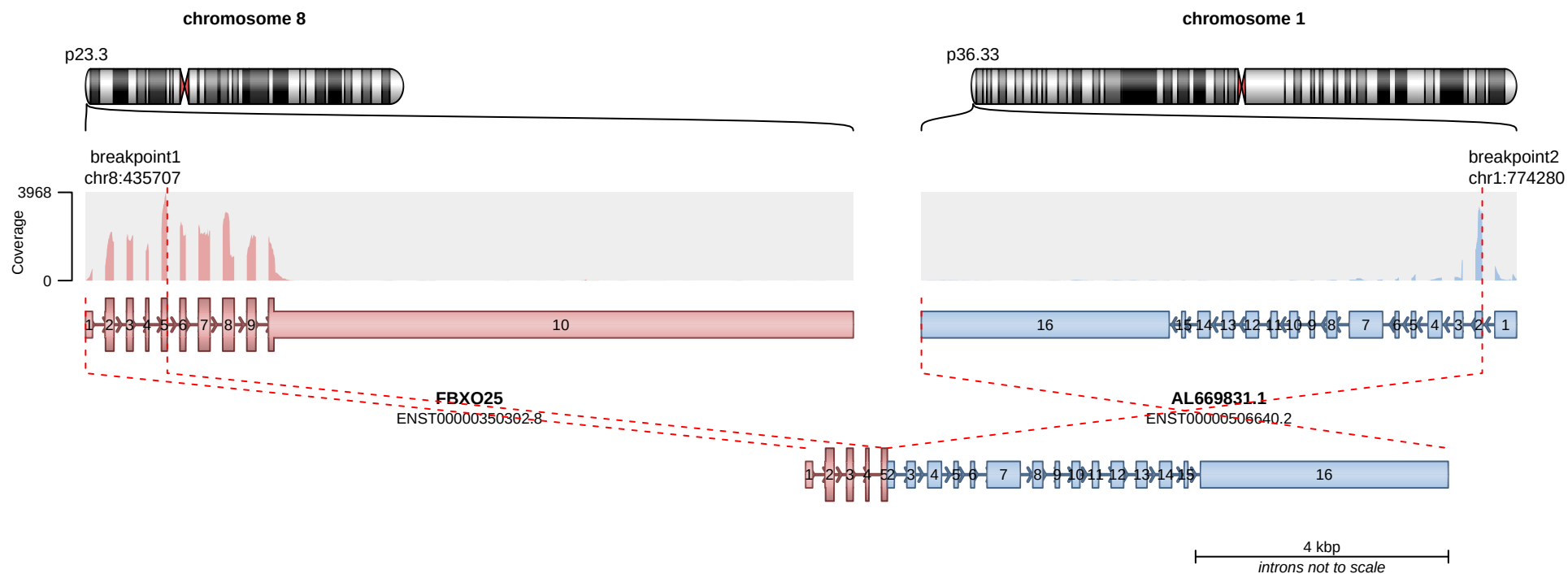
RETAINED PROTEIN DOMAINS reading frame unclear



SUPPORTING READ COUNT

Split reads = 457
Discordant mates = 0

— translocation — deletion
— duplication — inversion

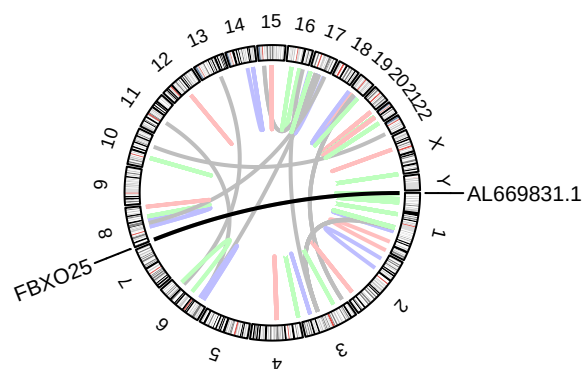
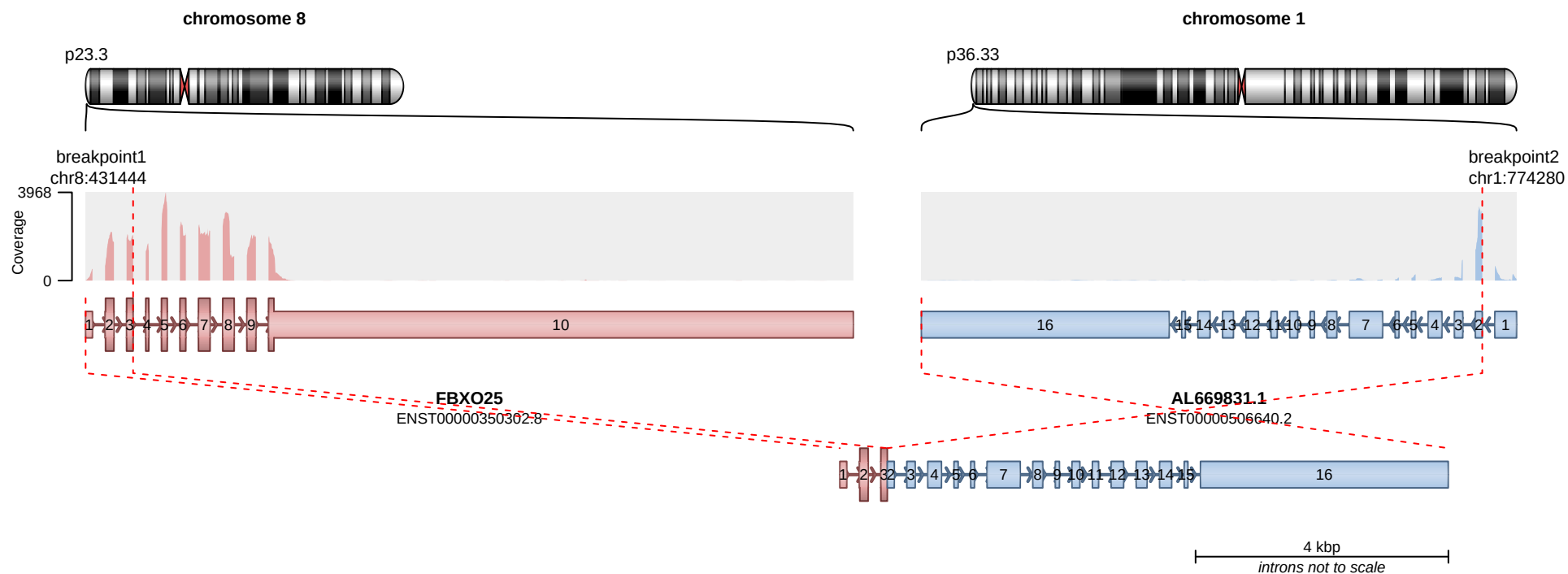


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 350
Discordant mates = 0

— translocation — deletion
— duplication — inversion

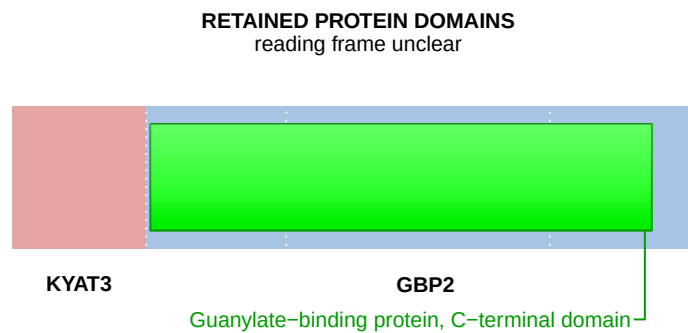
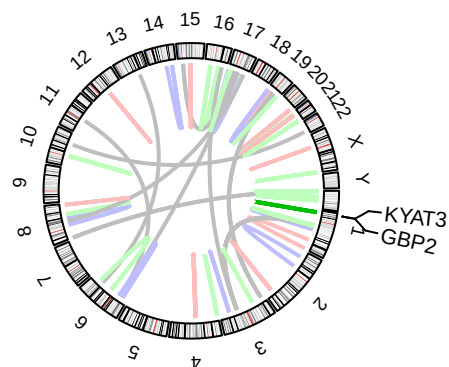
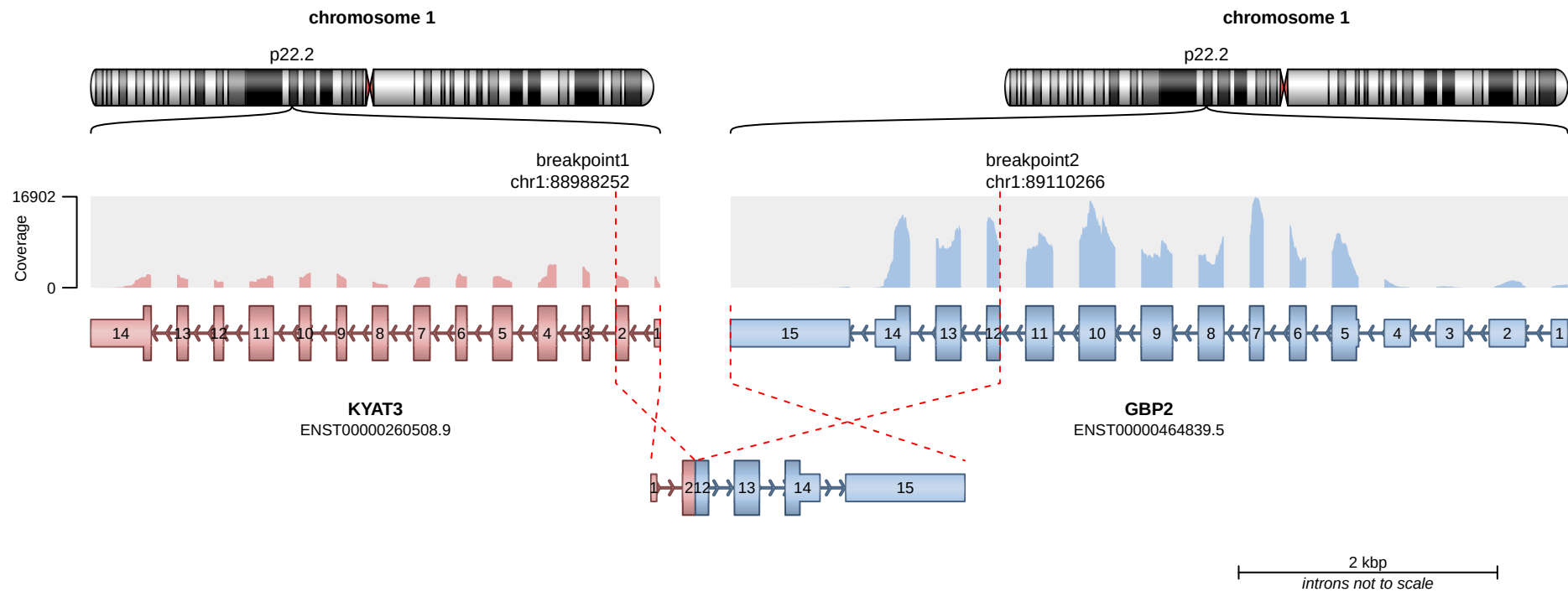


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

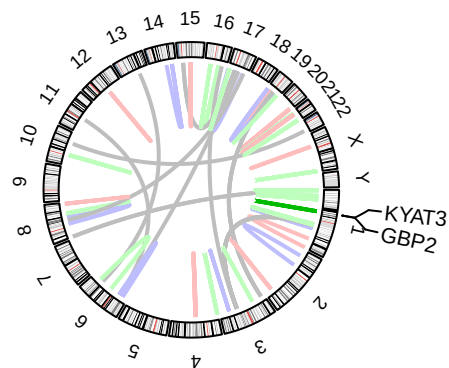
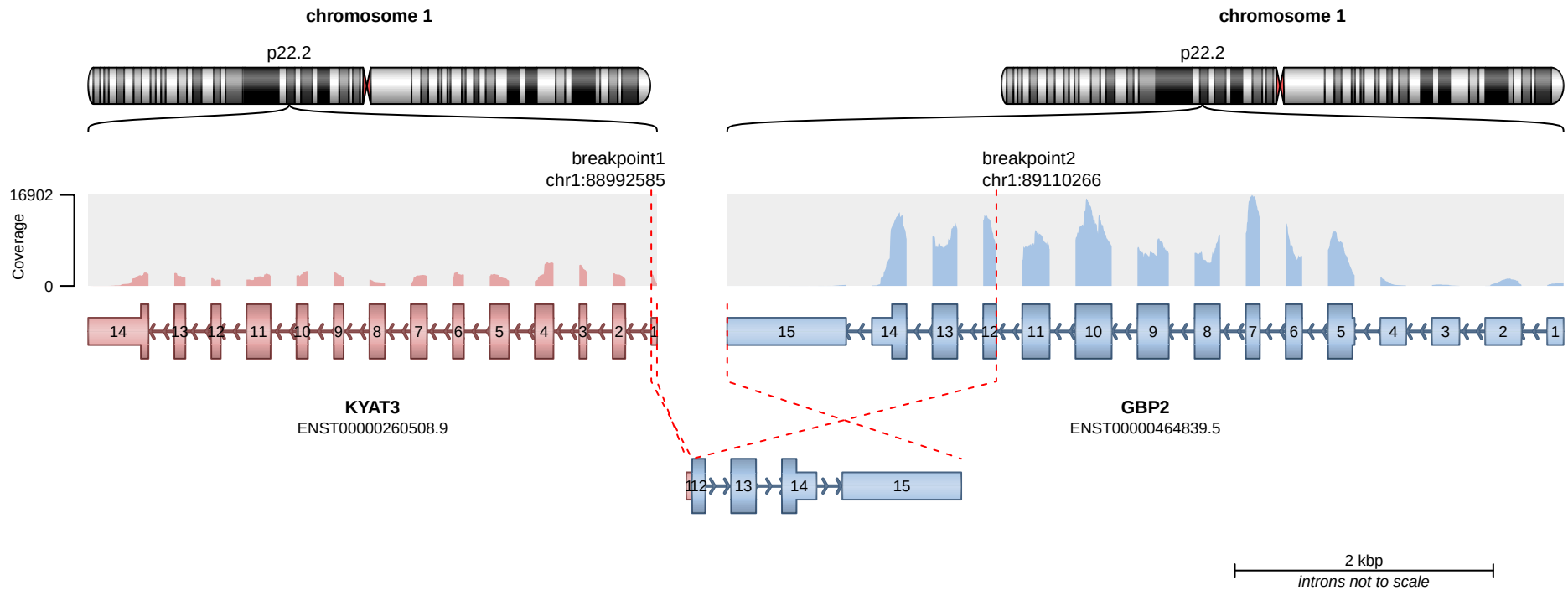
— translocation — deletion
— duplication — inversion



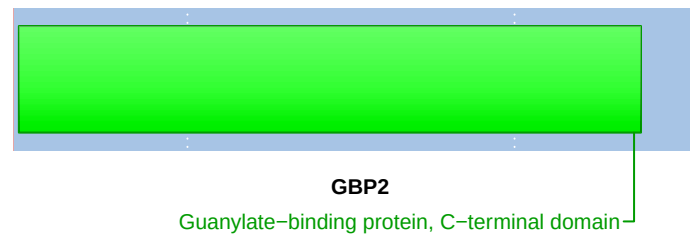
SUPPORTING READ COUNT

Split reads = 269
Discordant mates = 1

— translocation — deletion
— duplication — inversion



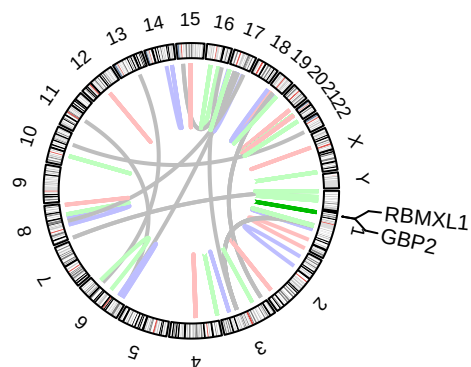
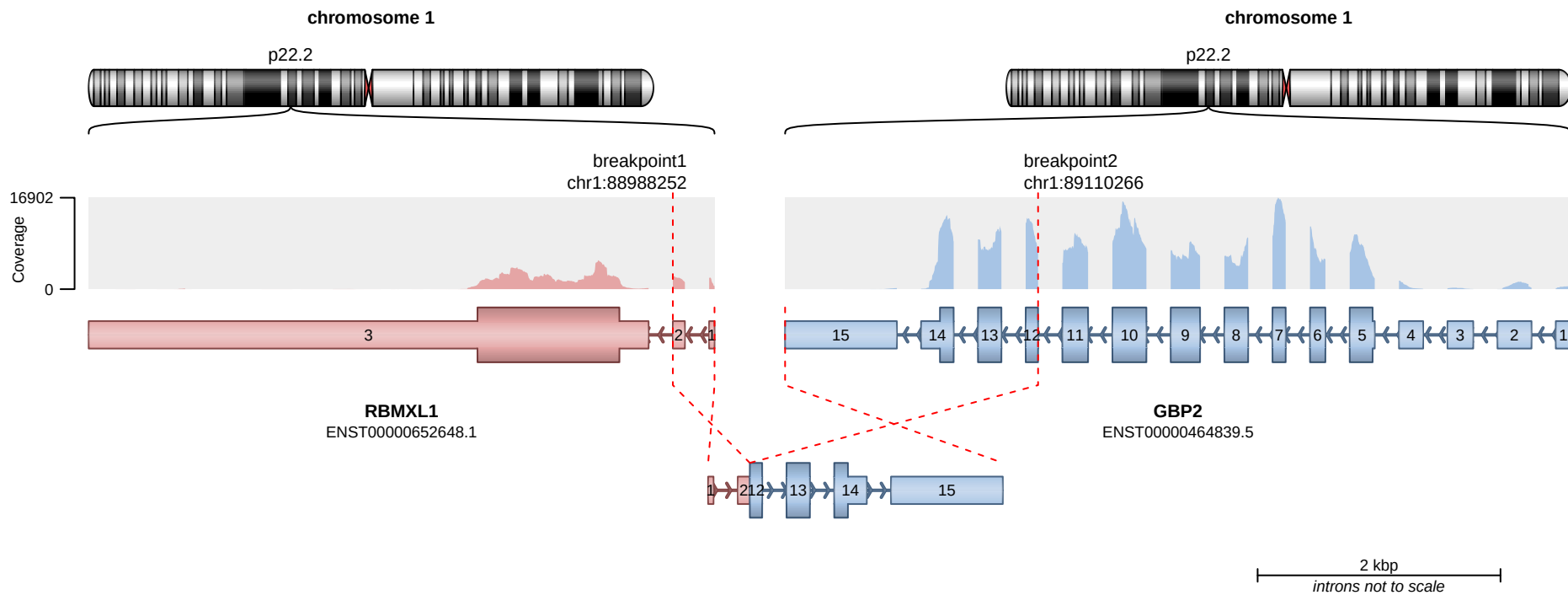
RETAINED PROTEIN DOMAINS
reading frame unclear



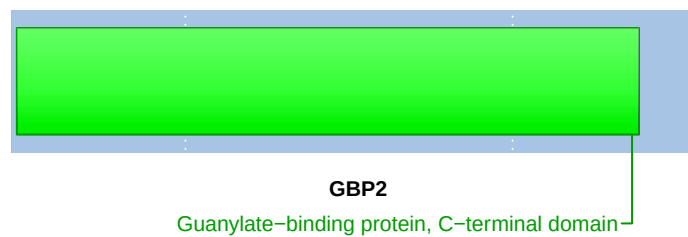
SUPPORTING READ COUNT

Split reads = 53
Discordant mates = 0

— translocation — deletion
— duplication — inversion



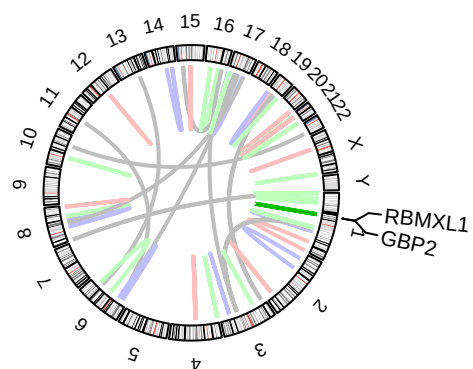
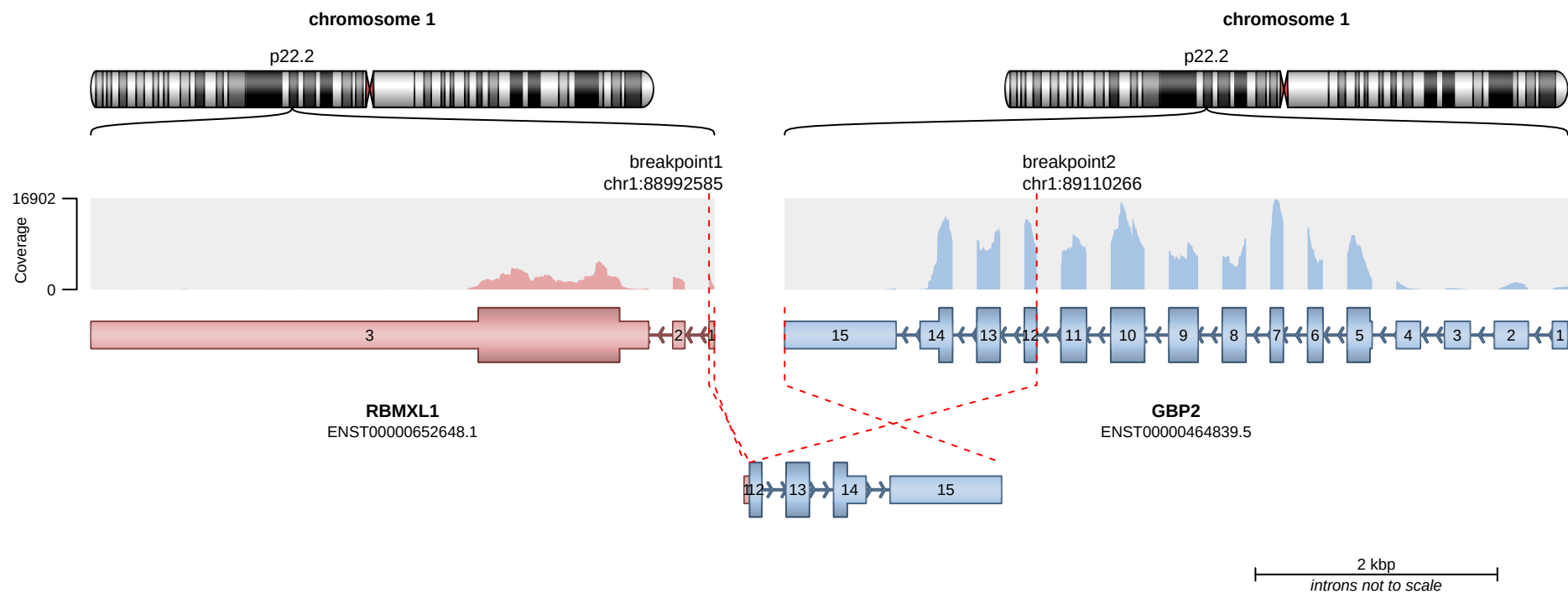
RETAINED PROTEIN DOMAINS reading frame unclear



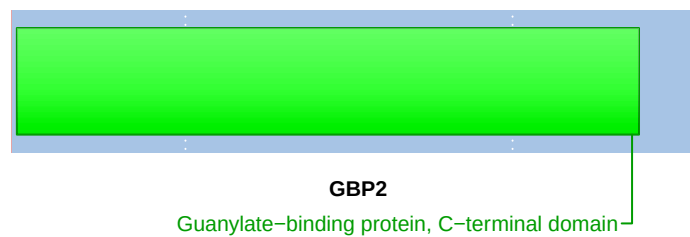
SUPPORTING READ COUNT

Split reads = 269
Discordant mates = 1

— translocation — deletion
— duplication — inversion



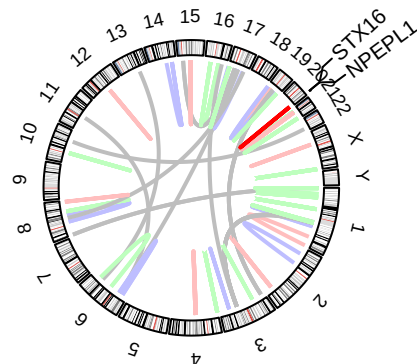
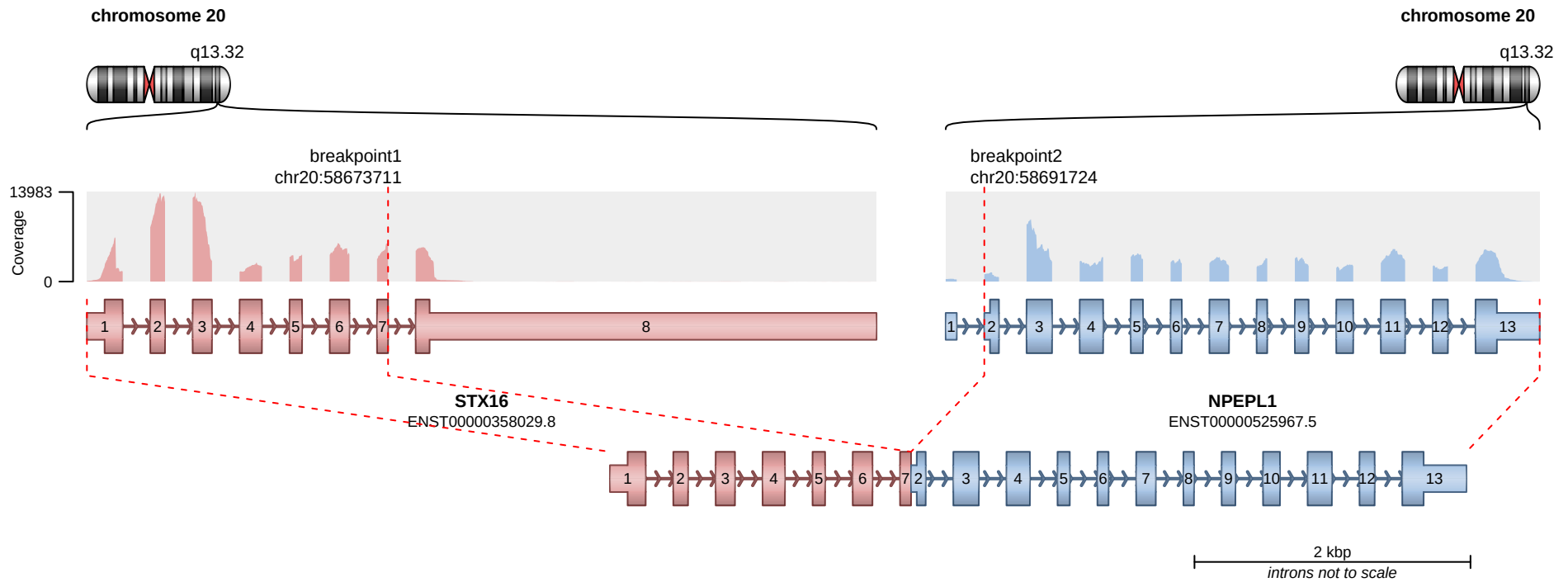
RETAINED PROTEIN DOMAINS
reading frame unclear



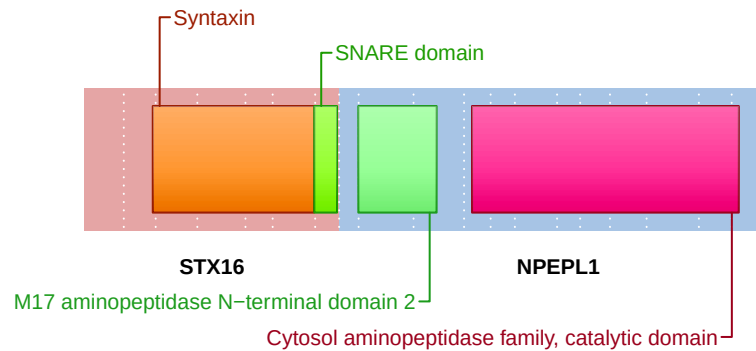
SUPPORTING READ COUNT

Split reads = 53
Discordant mates = 0

— translocation — deletion
— duplication — inversion



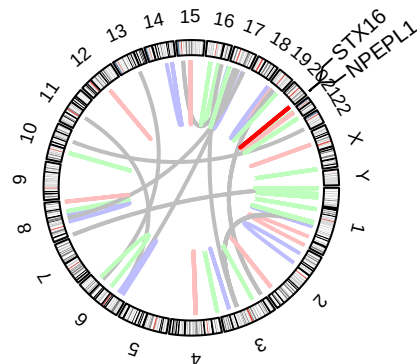
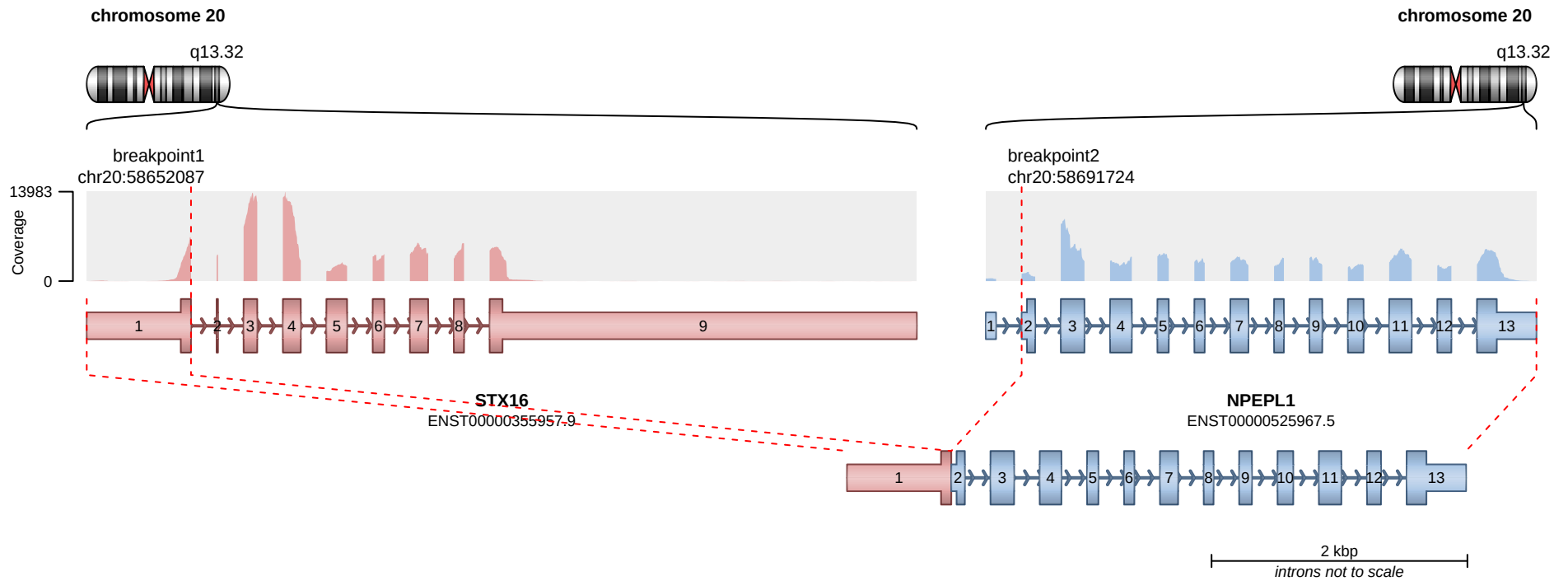
RETAINED PROTEIN DOMAINS reading frame unclear



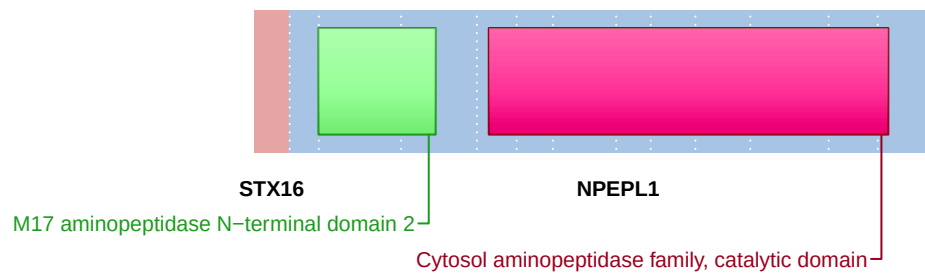
SUPPORTING READ COUNT

Split reads = 265
Discordant mates = 9

— translocation — deletion
— duplication — inversion



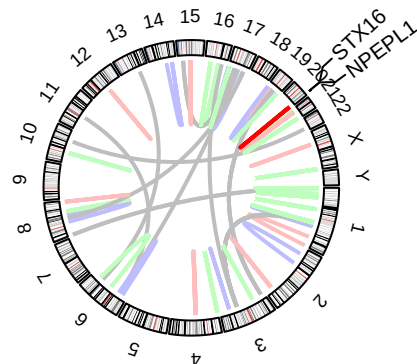
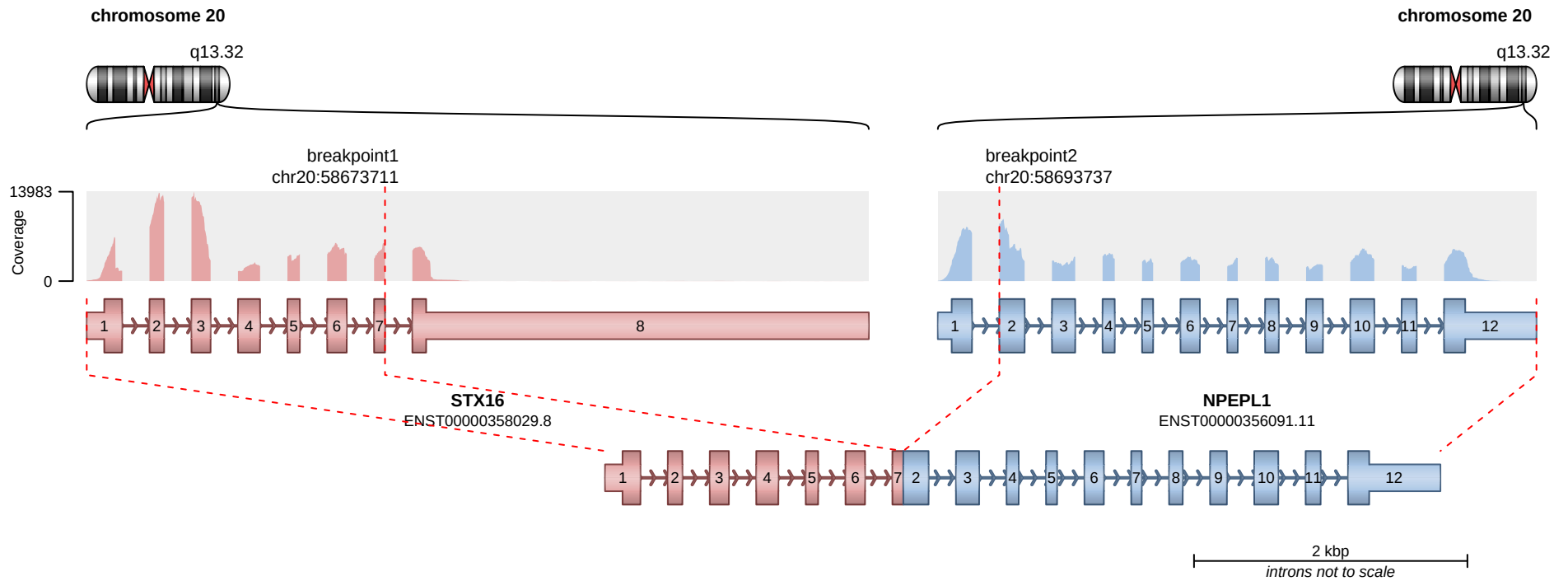
RETAINED PROTEIN DOMAINS reading frame unclear



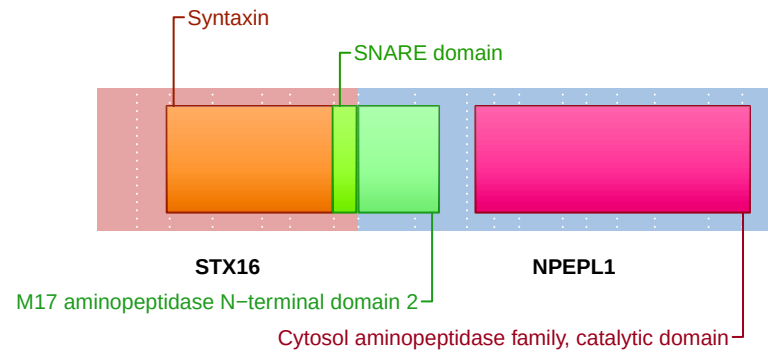
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



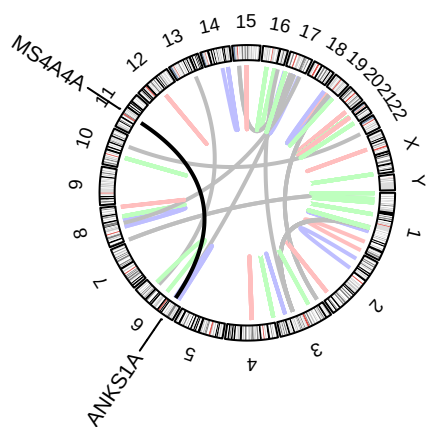
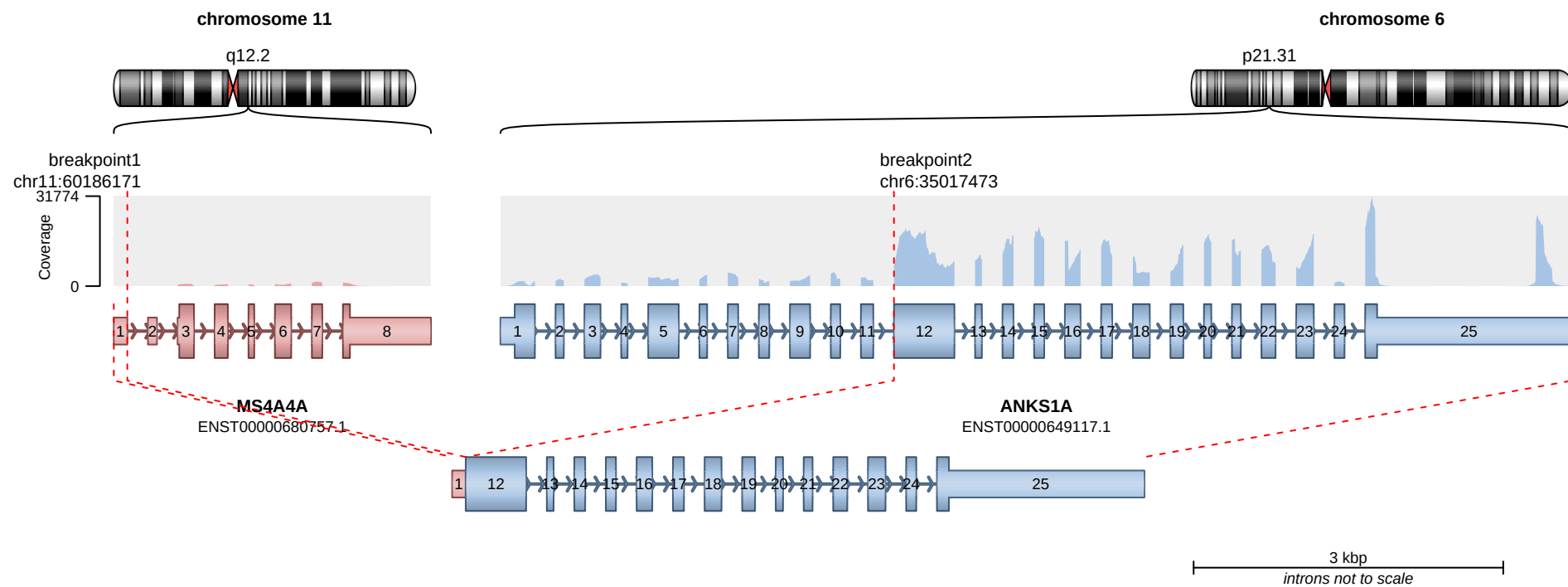
RETAINED PROTEIN DOMAINS reading frame unclear



SUPPORTING READ COUNT

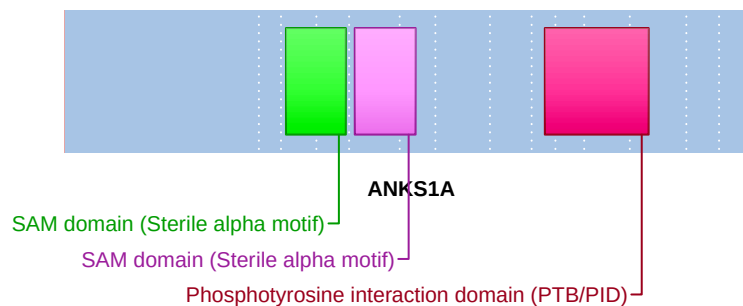
Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



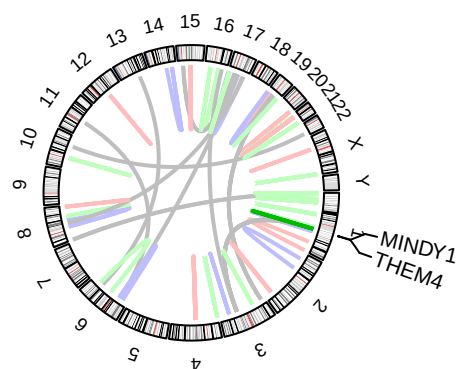
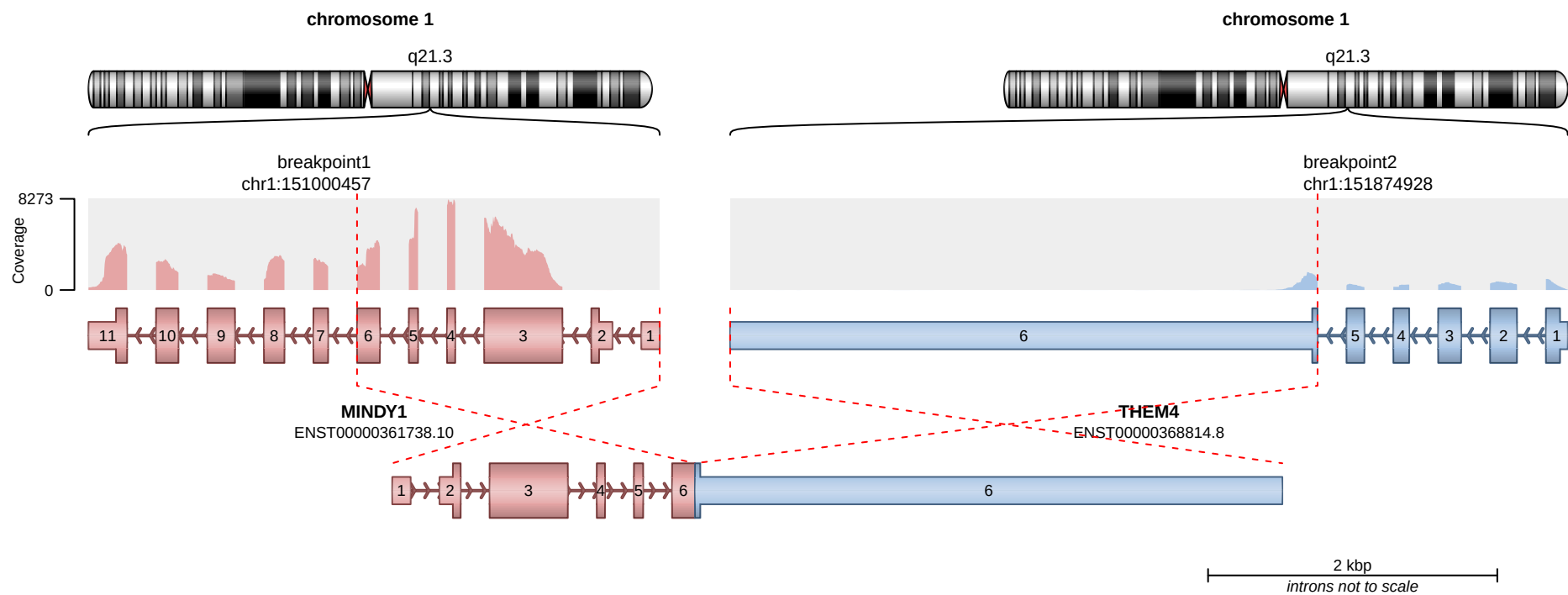
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS reading frame unclear

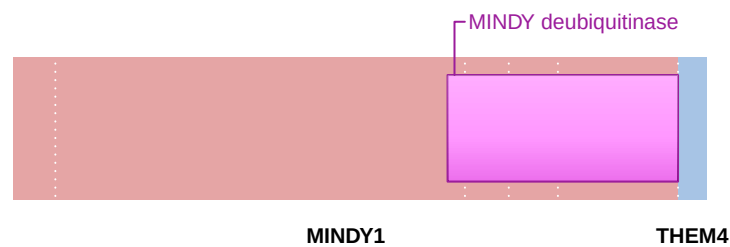


SUPPORTING READ COUNT

Split reads = 168
Discordant mates = 0



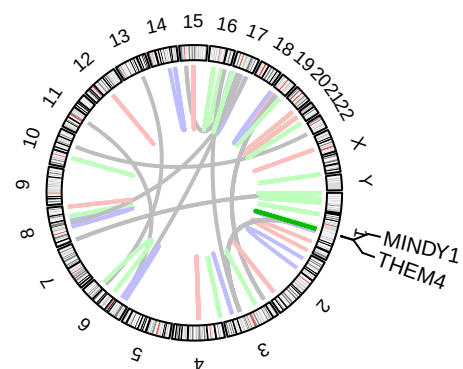
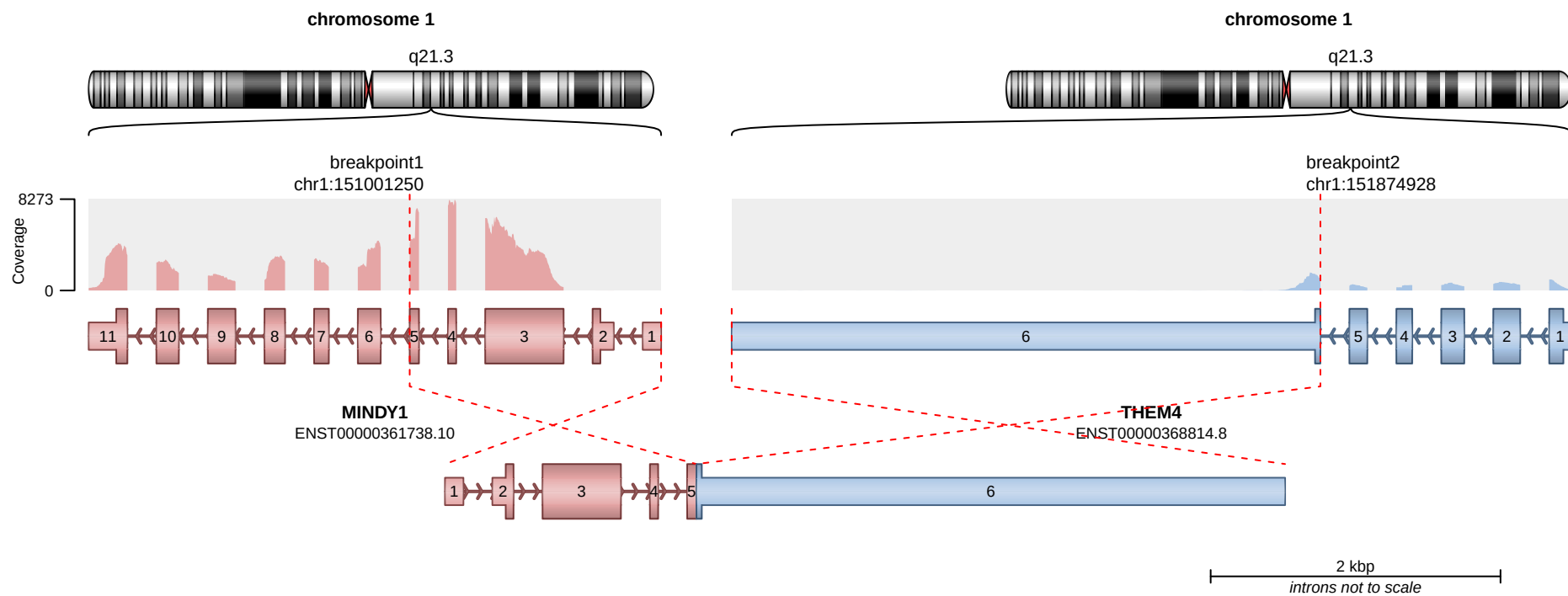
RETAINED PROTEIN DOMAINS
reading frame unclear



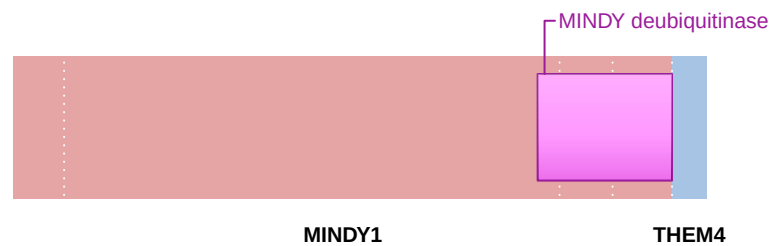
SUPPORTING READ COUNT

Split reads = 137
Discordant mates = 5

— translocation — deletion
— duplication — inversion



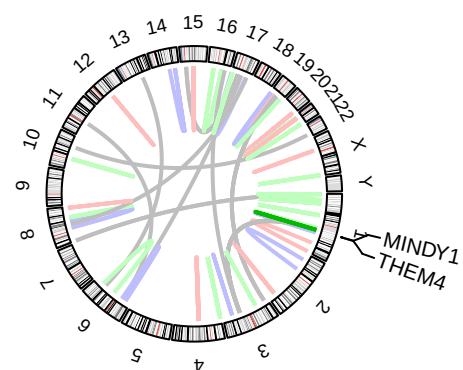
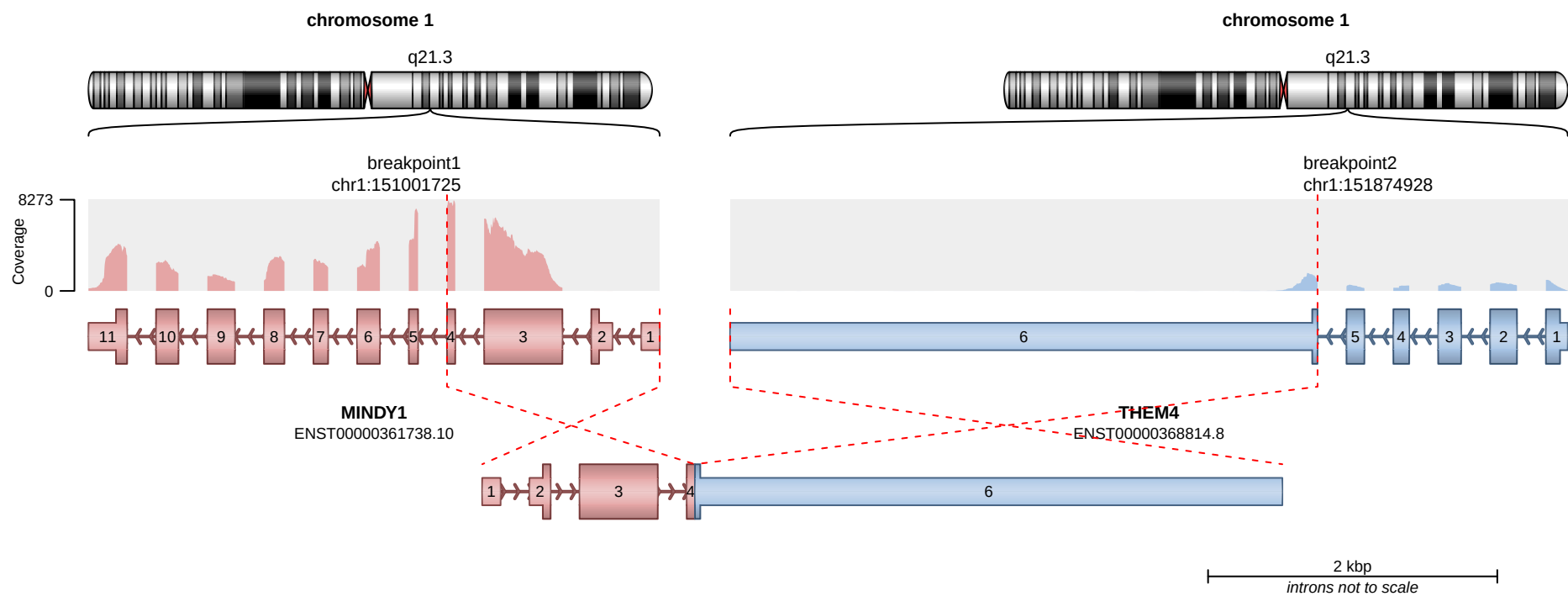
RETAINED PROTEIN DOMAINS
reading frame unclear



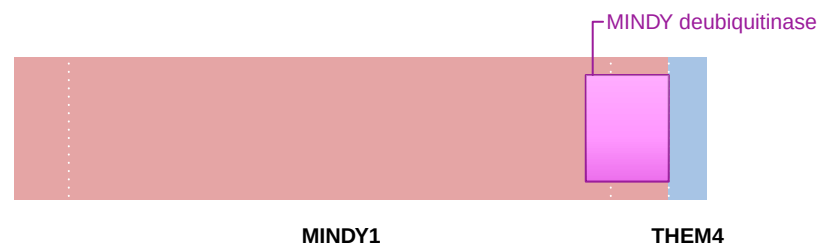
SUPPORTING READ COUNT

Split reads = 126
Discordant mates = 4

— translocation — deletion
— duplication — inversion



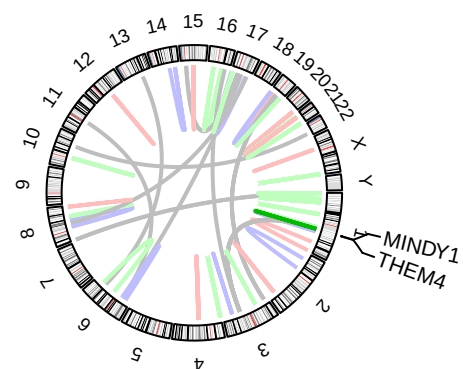
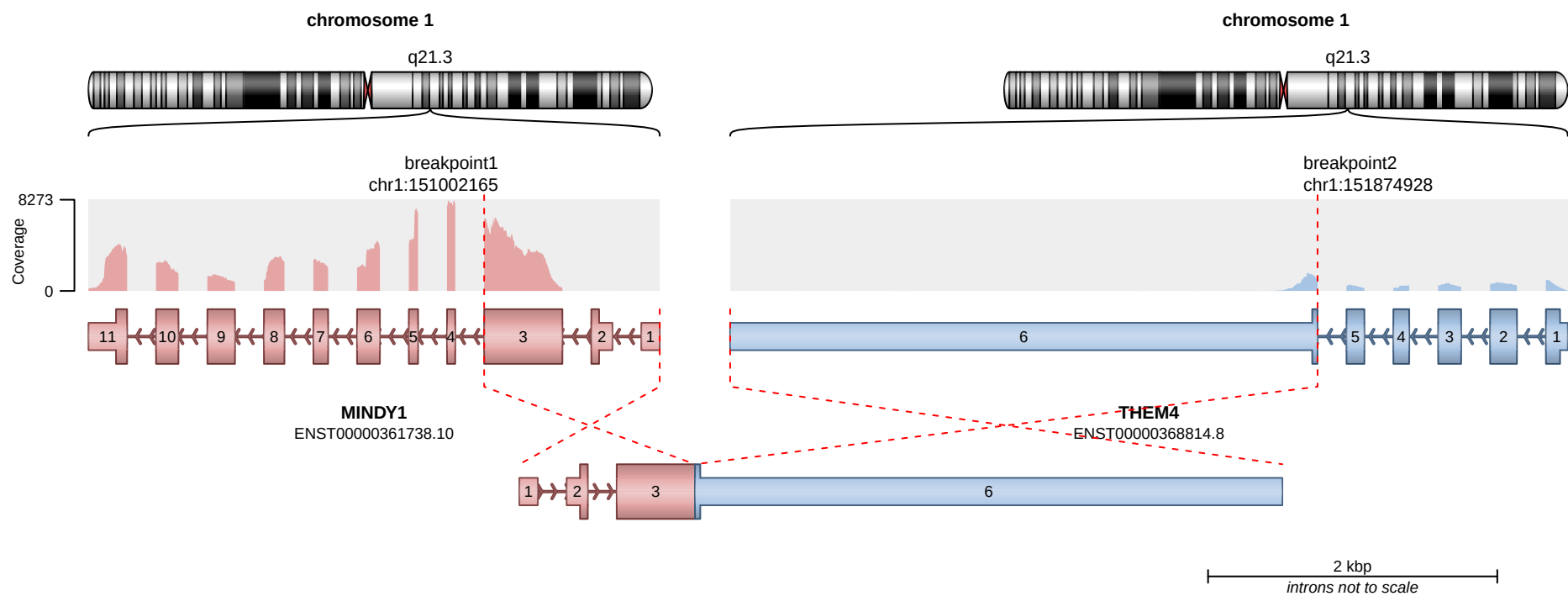
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 84
Discordant mates = 1

— translocation — deletion
— duplication — inversion



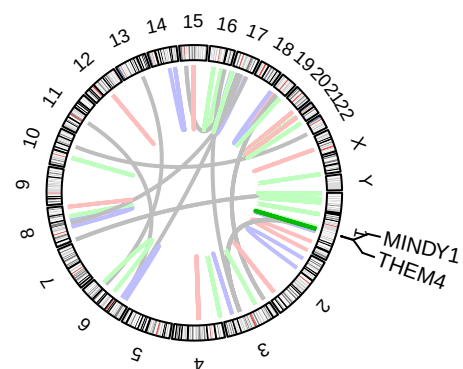
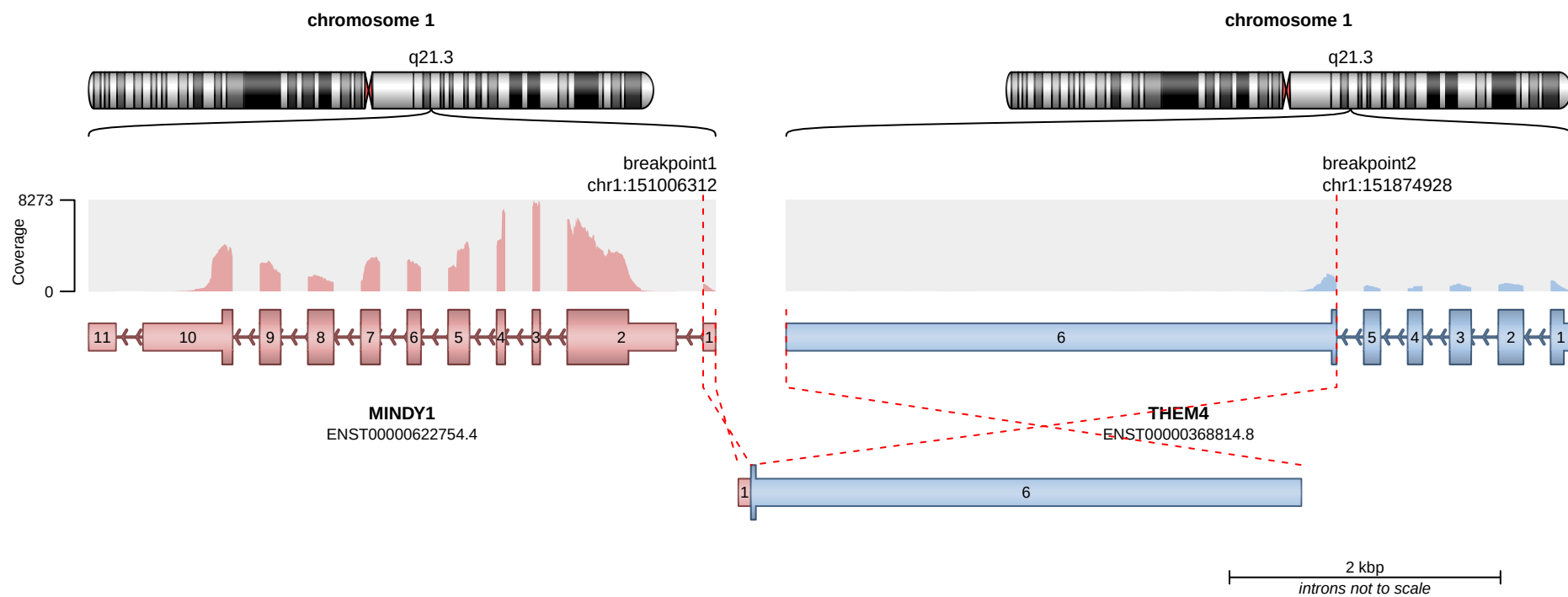
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 19
Discordant mates = 0

— translocation — deletion
— duplication — inversion

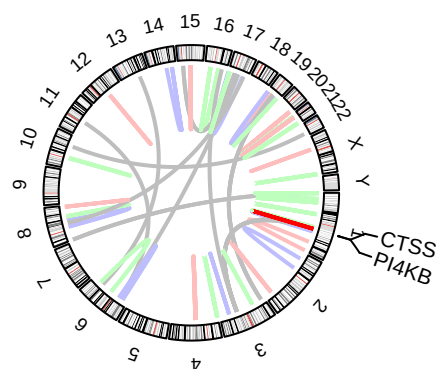
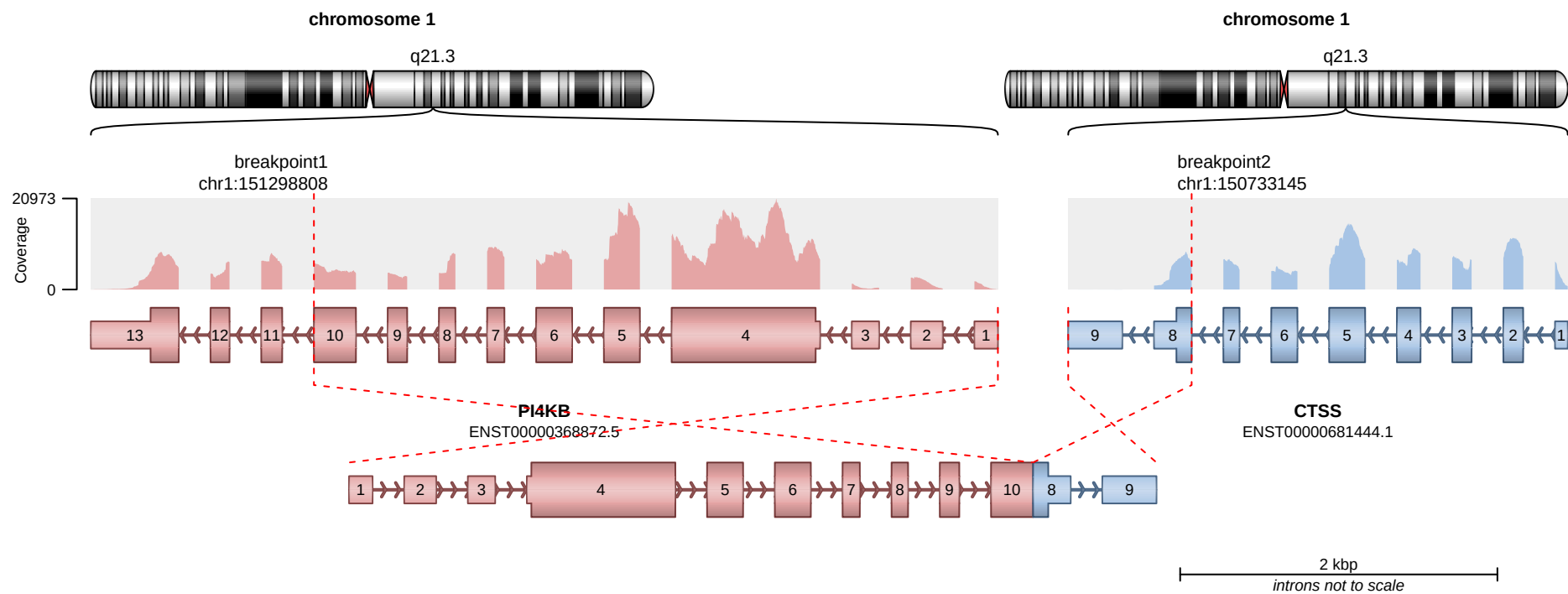


— translocation — deletion
— duplication — inversion

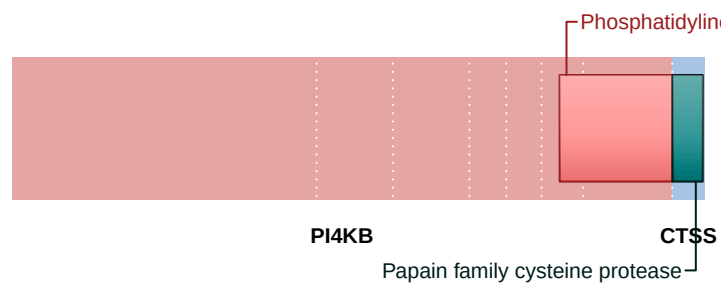
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0



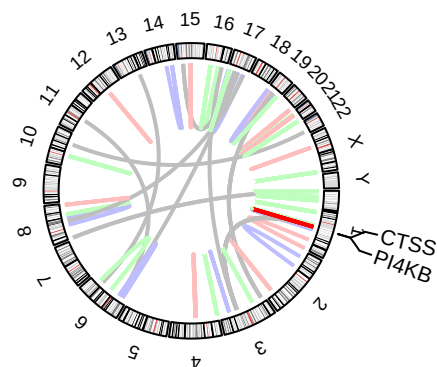
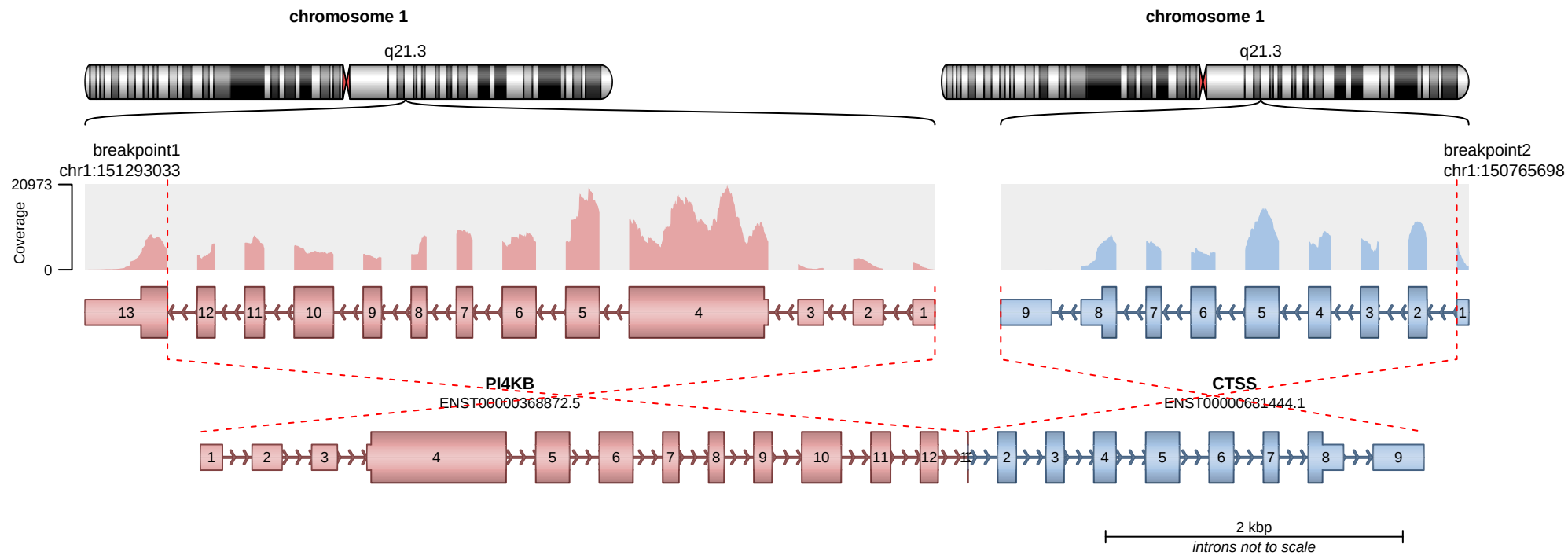
RETAINED PROTEIN DOMAINS reading frame unclear



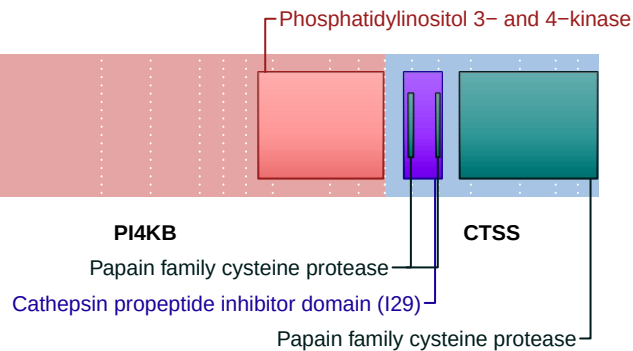
SUPPORTING READ COUNT

Split reads = 117
Discordant mates = 3

— translocation — deletion
— duplication — inversion



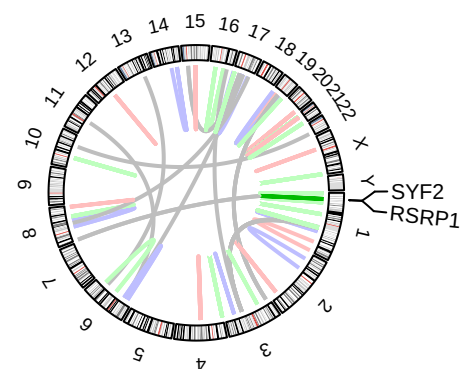
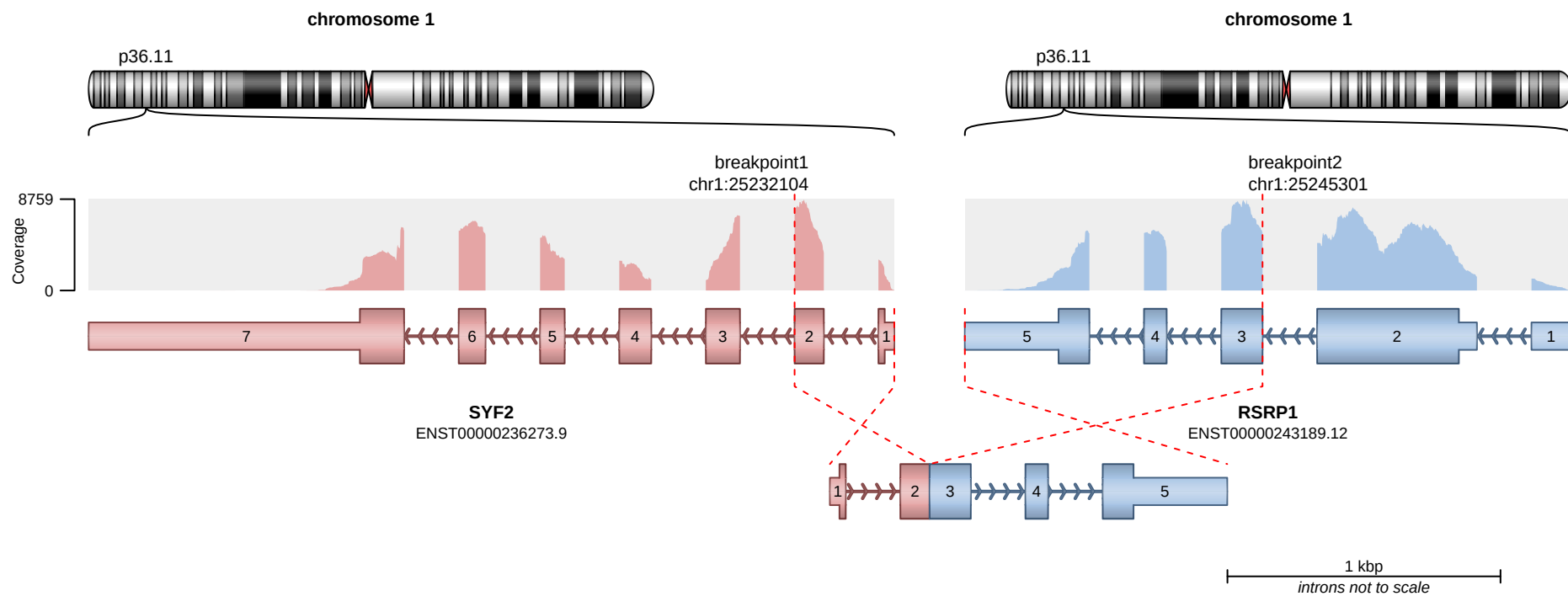
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 5

— translocation — deletion
— duplication — inversion



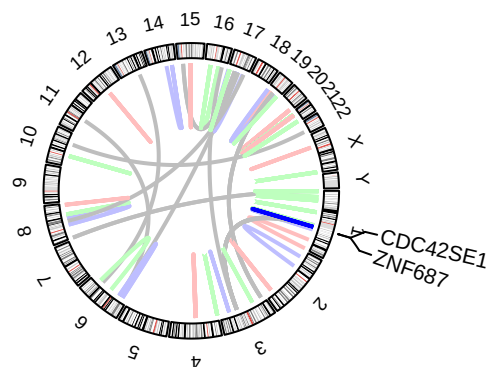
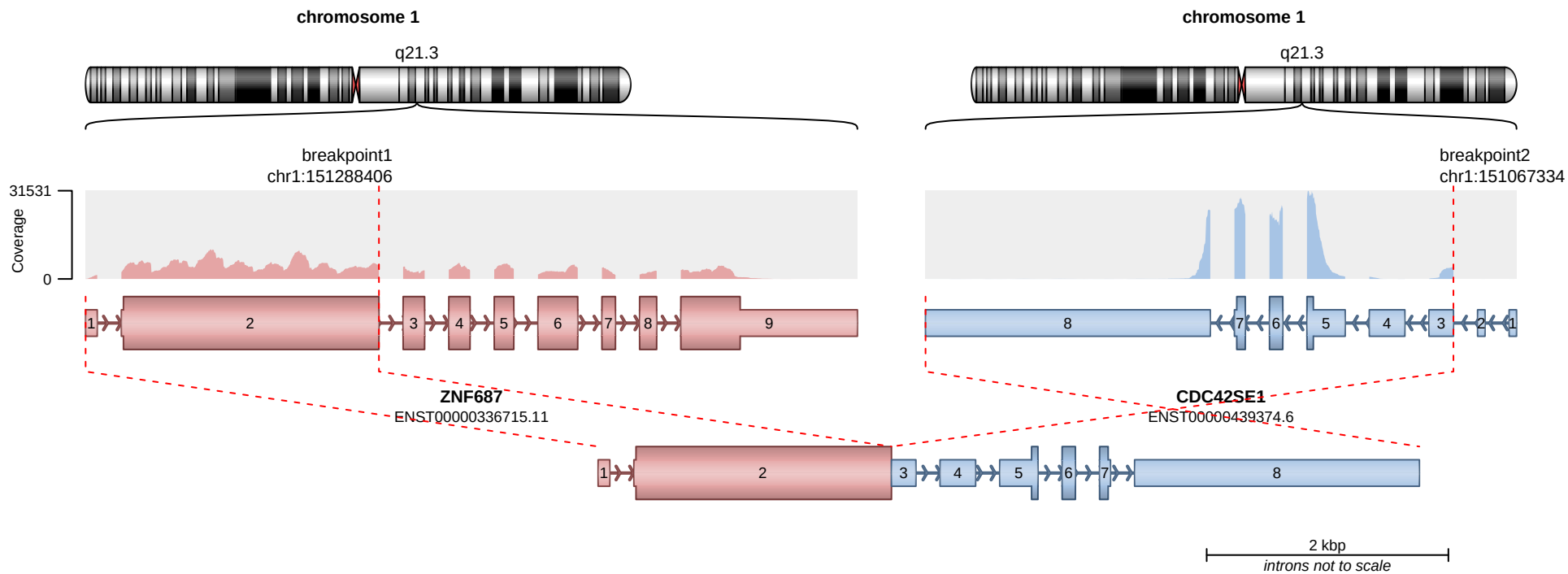
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 117
Discordant mates = 2

— translocation — deletion
— duplication — inversion

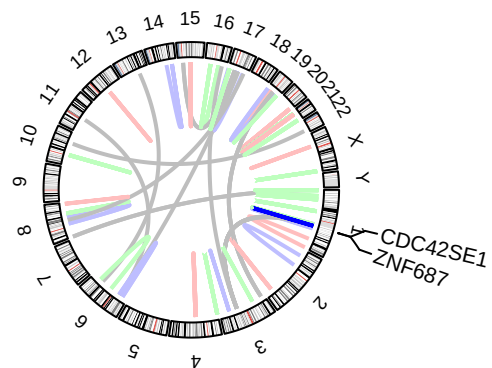
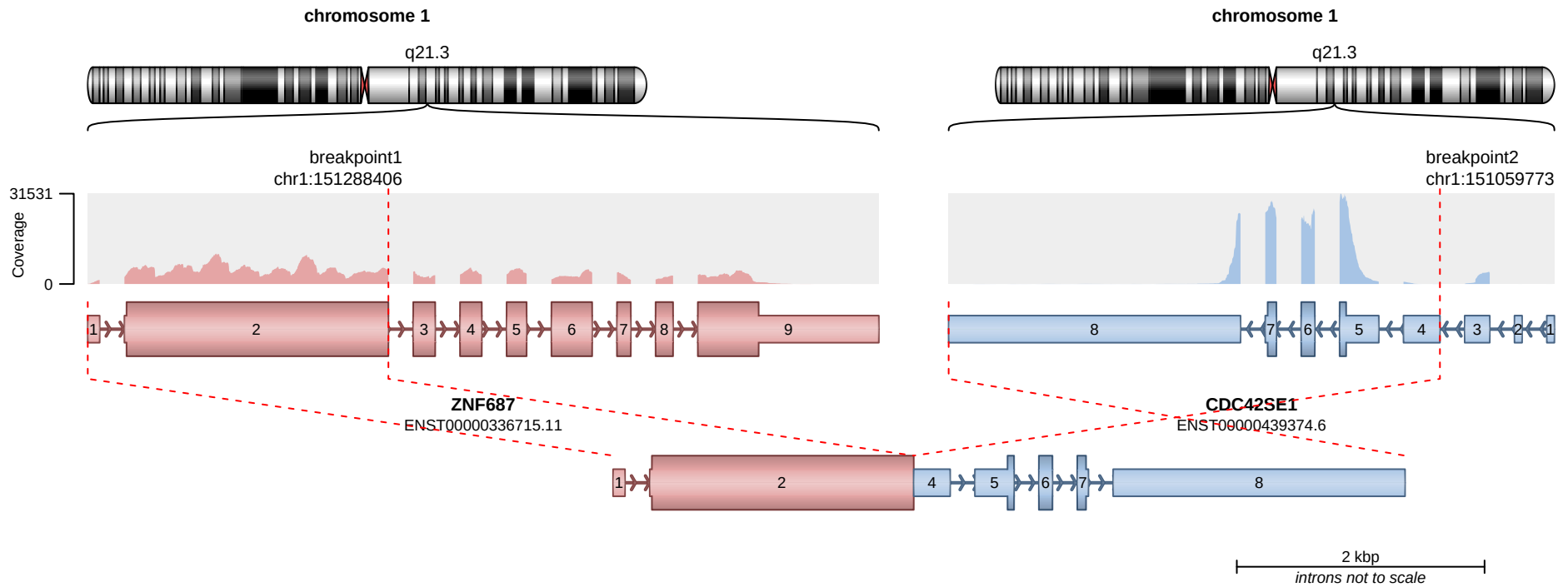


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 103
Discordant mates = 4

— translocation — deletion
— duplication — inversion

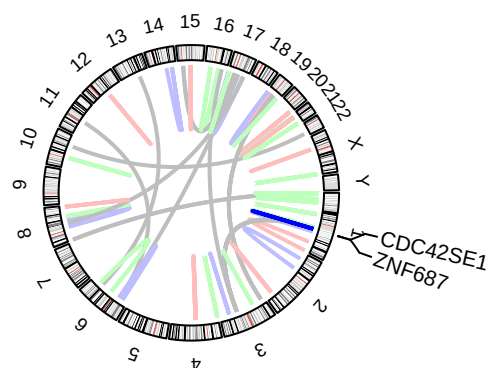
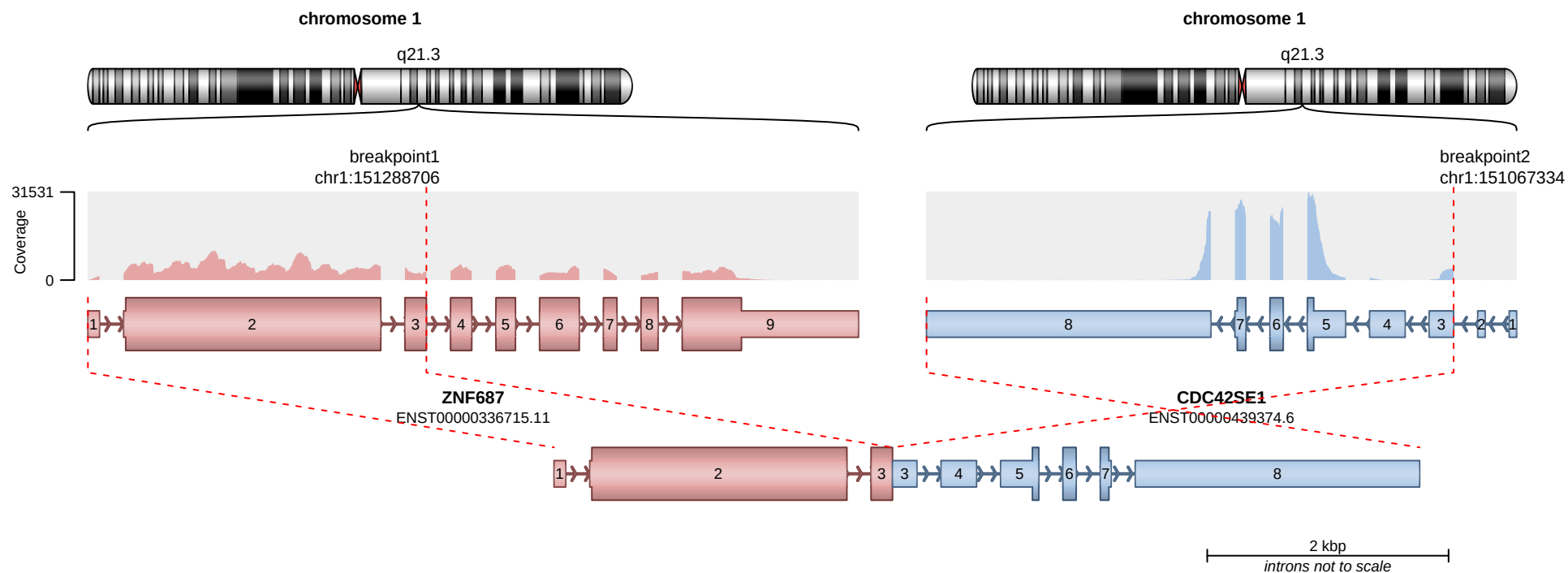


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 19
Discordant mates = 1

— translocation — deletion
— duplication — inversion

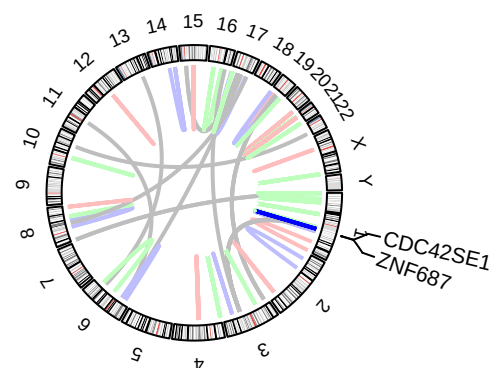
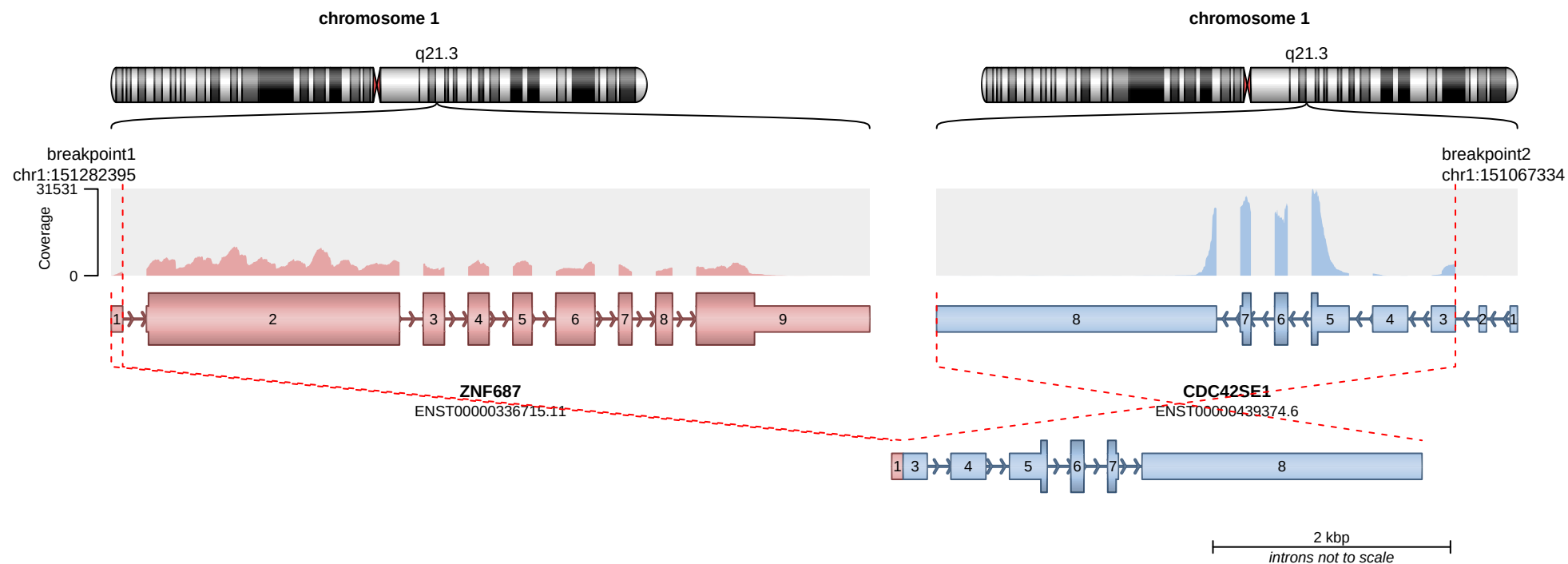


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 4

— translocation — deletion
— duplication — inversion

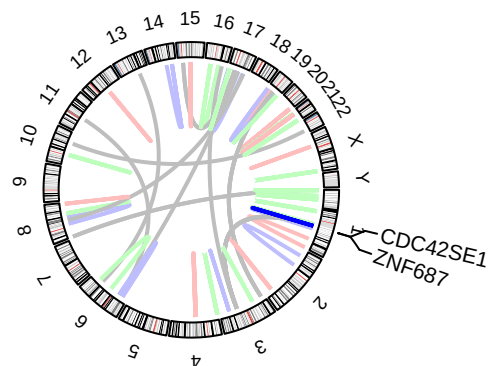
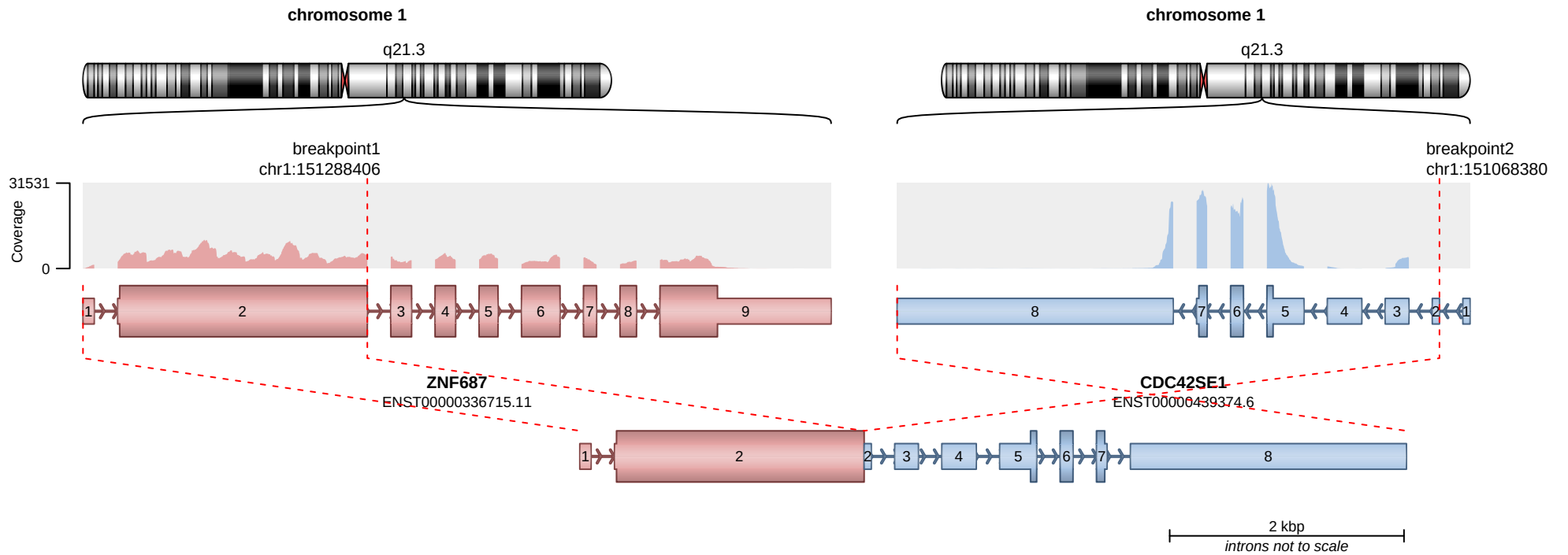


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

— translocation — deletion
— duplication — inversion

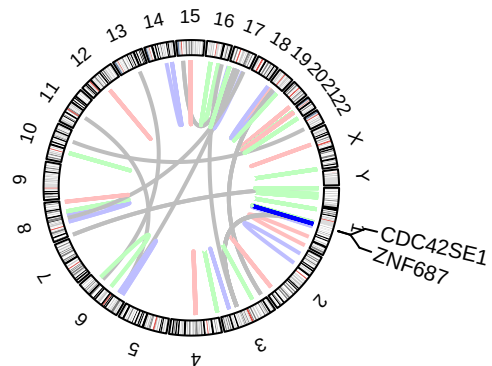
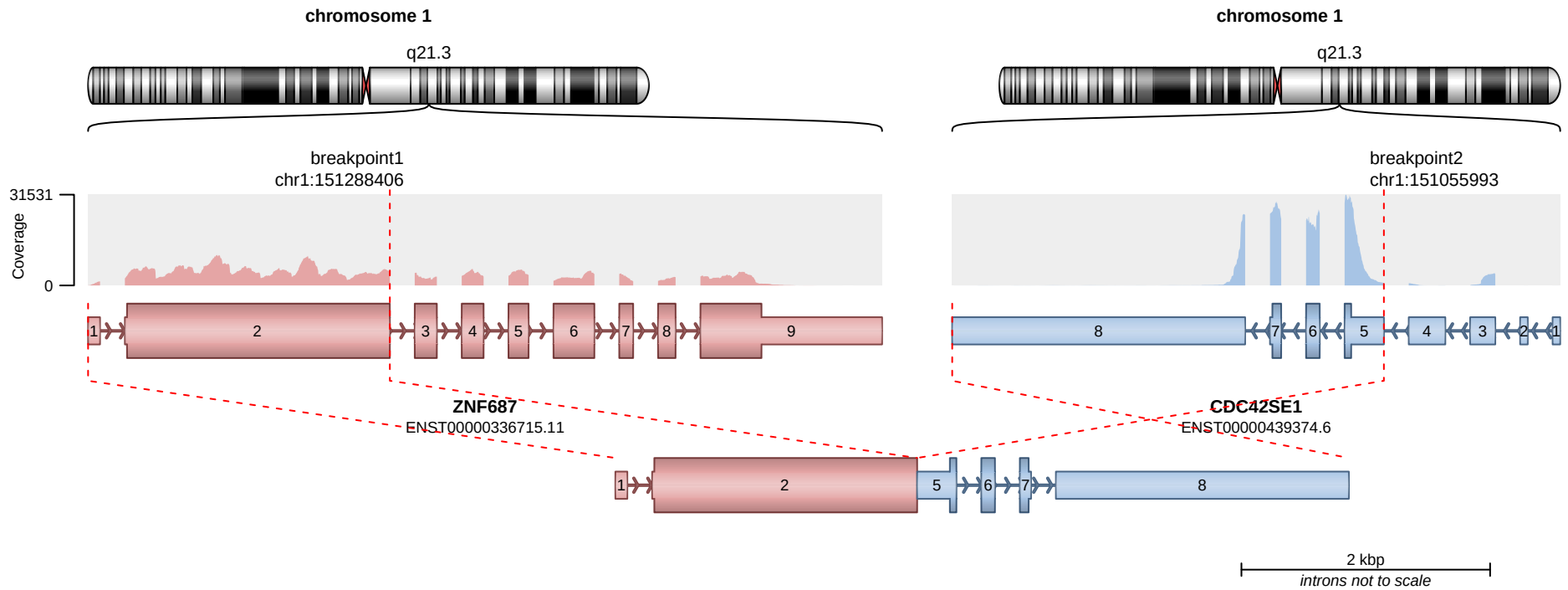


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 4

— translocation — deletion
— duplication — inversion

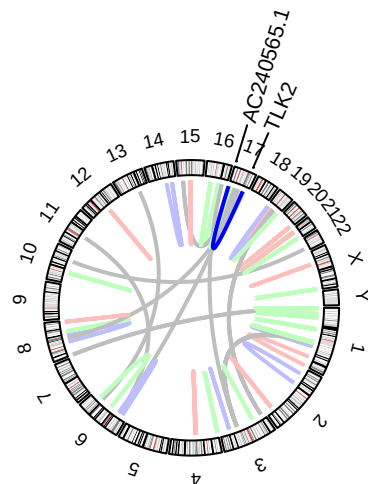
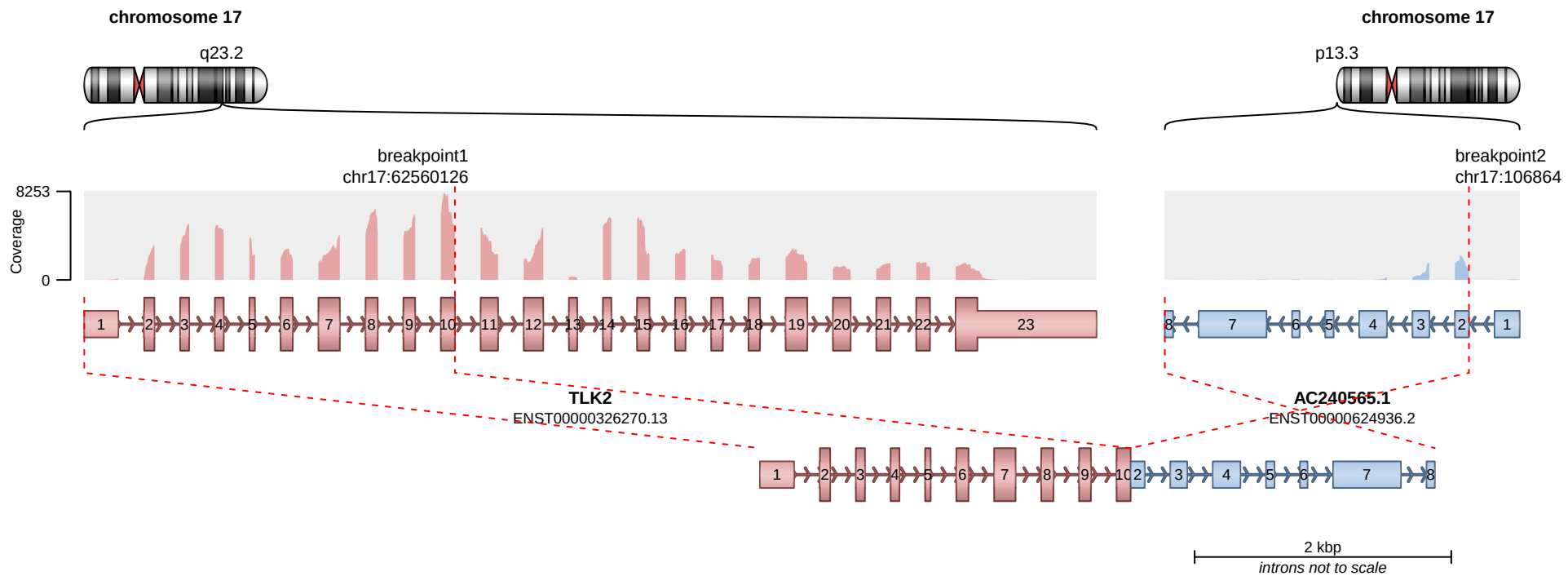


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

— translocation — deletion
— duplication — inversion

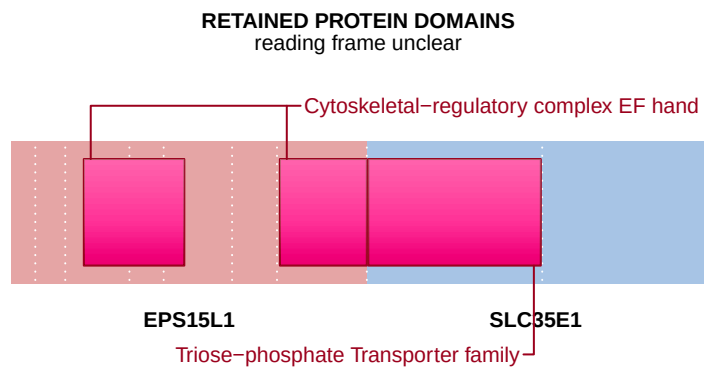
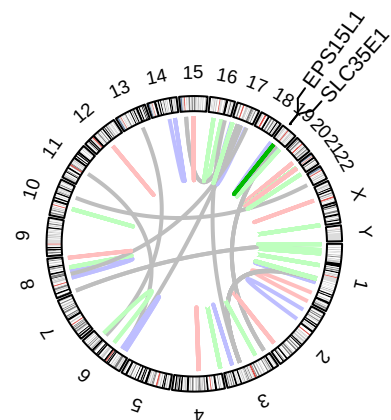
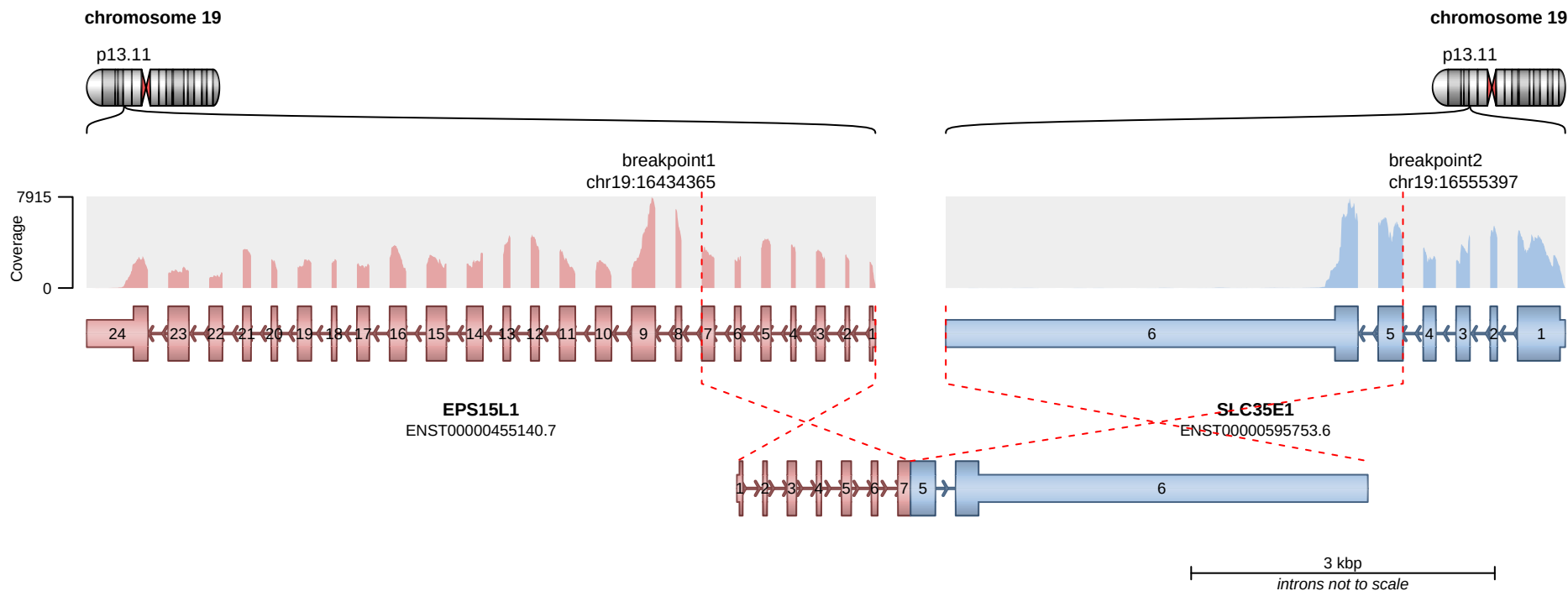


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 90
Discordant mates = 0



SUPPORTING READ COUNT

Split reads = 82
Discordant mates = 0

— translocation — deletion
— duplication — inversion

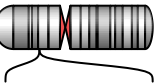
chromosome 19

p13.11

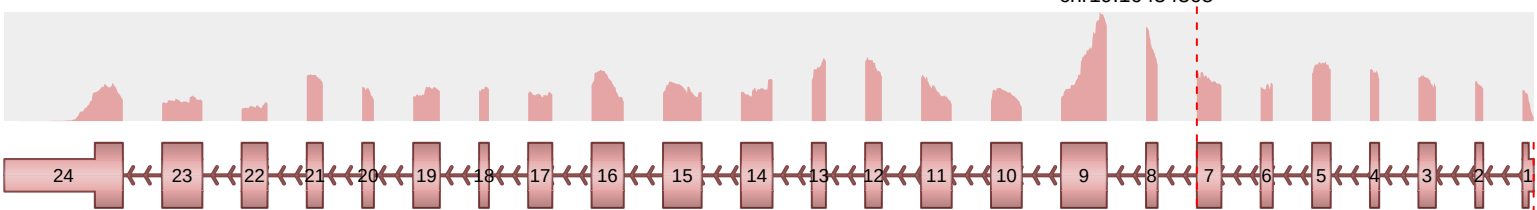


chromosome 19

p13.11

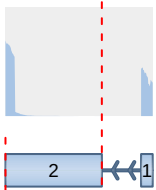


Coverage
7915
0

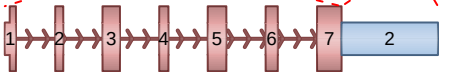


EPS15L1
ENST00000455140.7

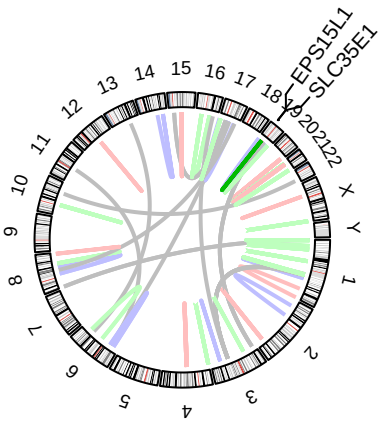
breakpoint2
chr19:16555840



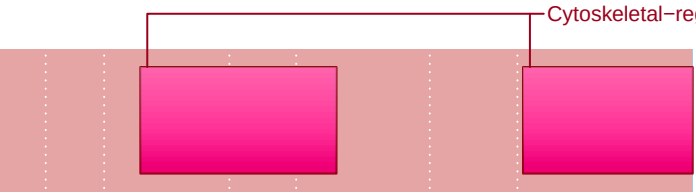
SLC35E1
ENST00000470077.1



2 kbp
introns not to scale



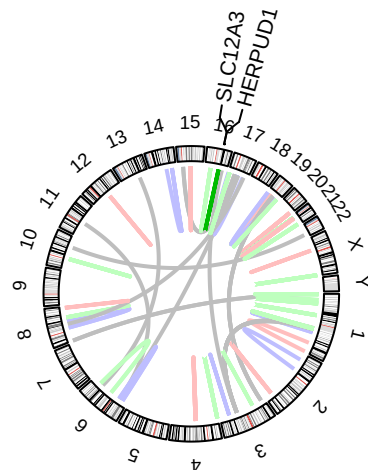
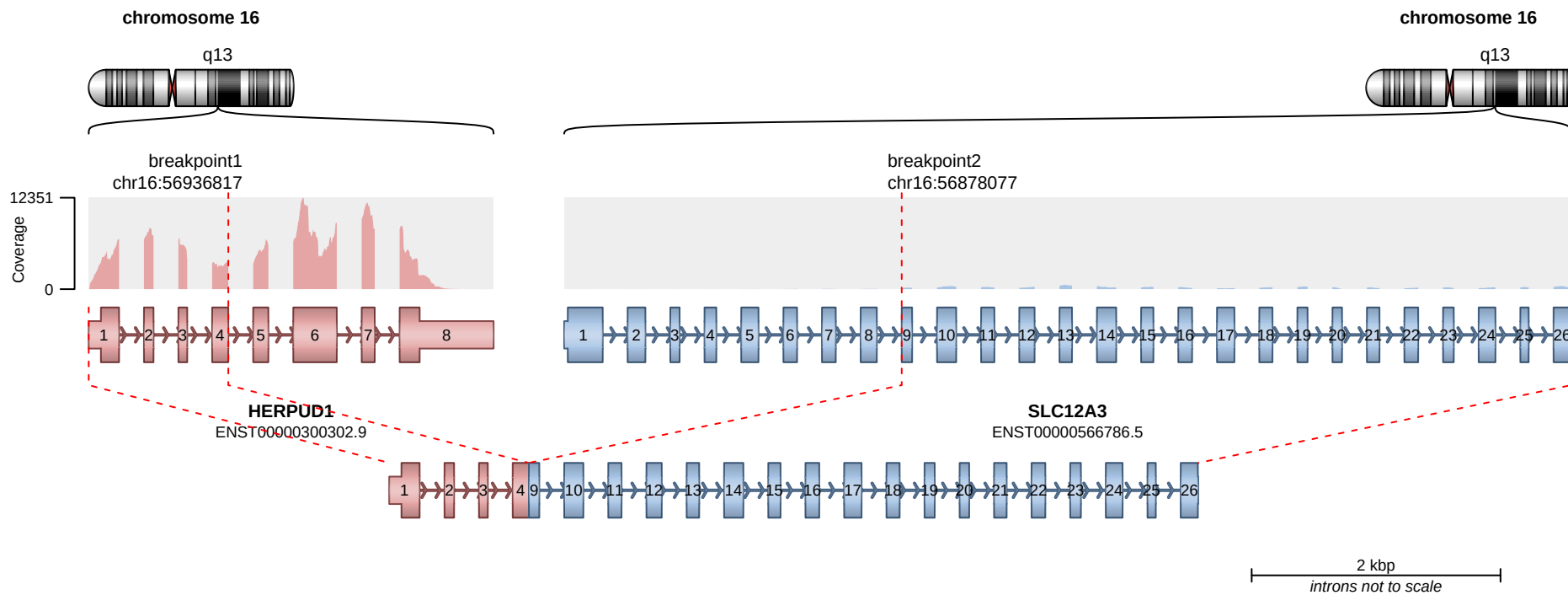
RETAINED PROTEIN DOMAINS
reading frame unclear



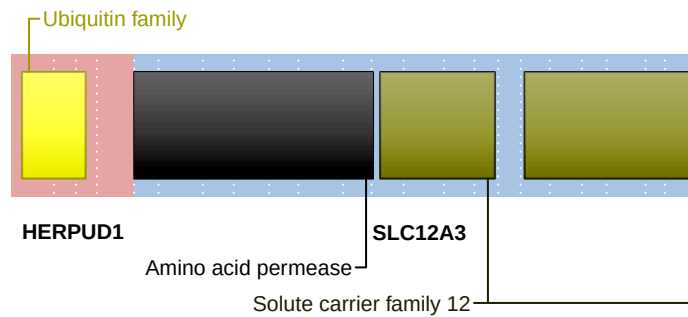
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



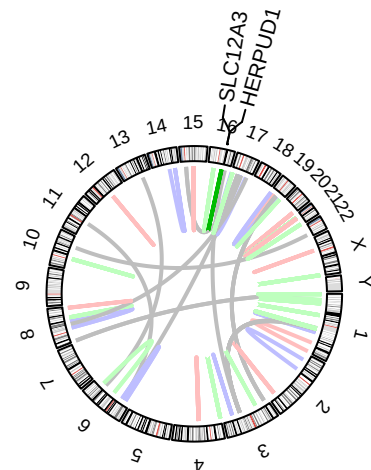
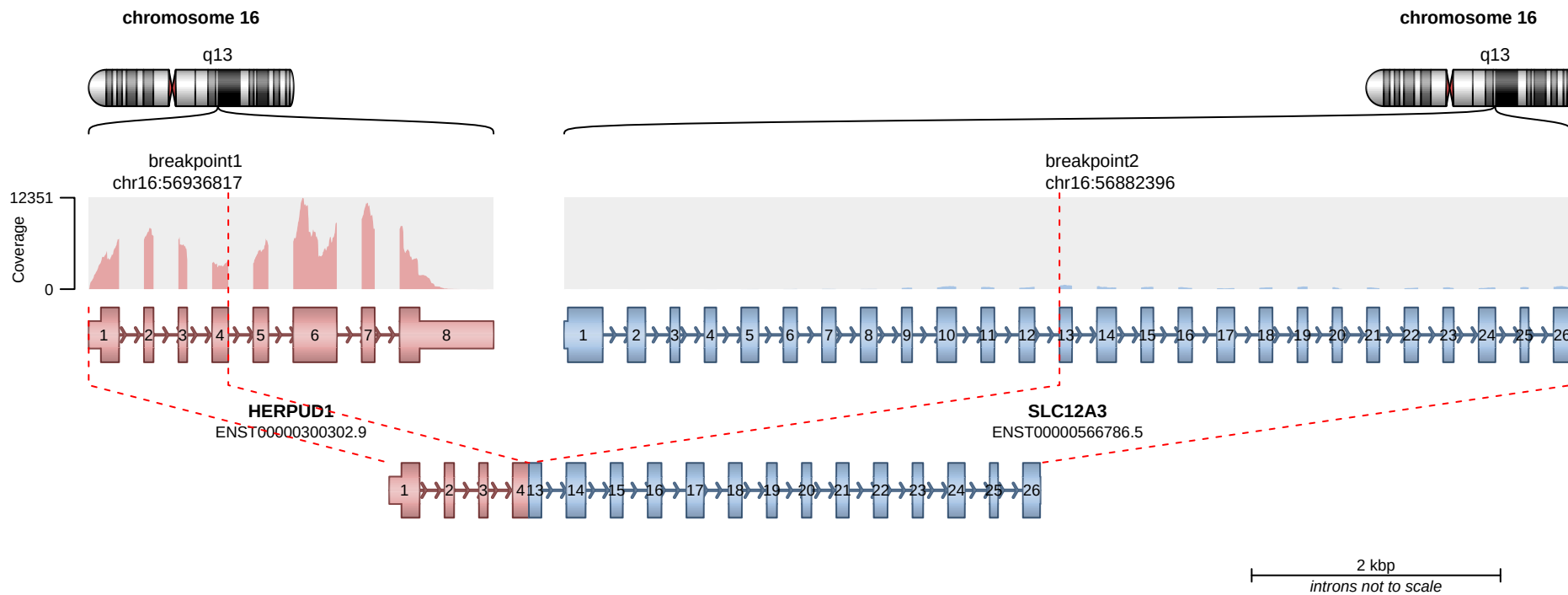
RETAINED PROTEIN DOMAINS reading frame unclear



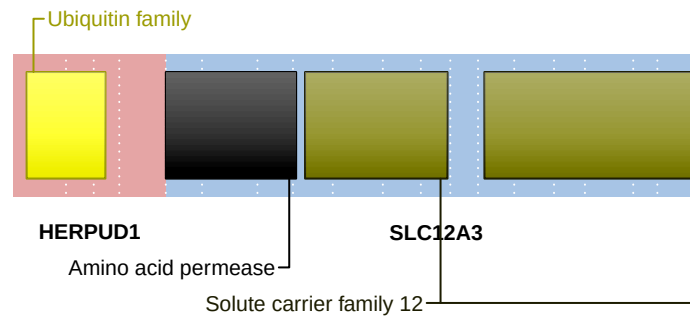
SUPPORTING READ COUNT

Split reads = 81
Discordant mates = 4

— translocation — deletion
— duplication — inversion



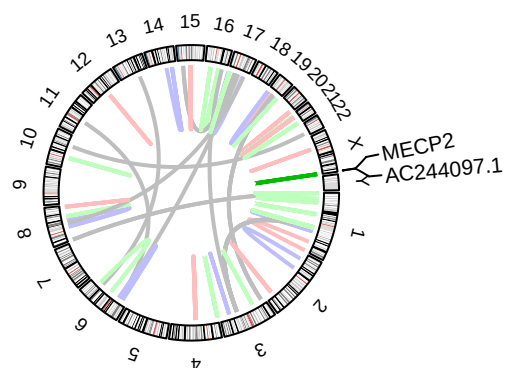
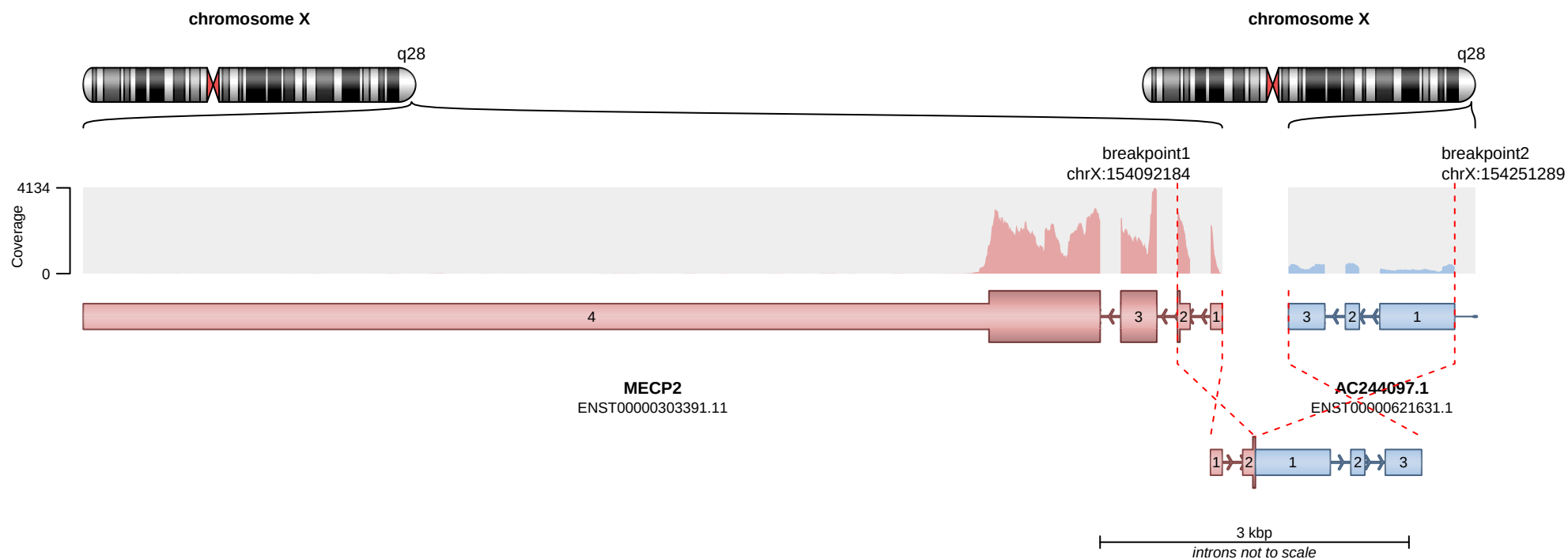
RETAINED PROTEIN DOMAINS reading frame unclear



SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

— translocation — deletion
— duplication — inversion

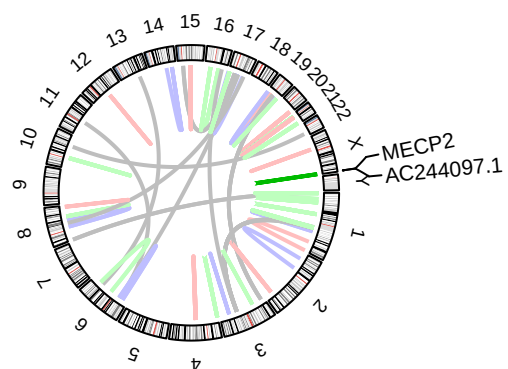
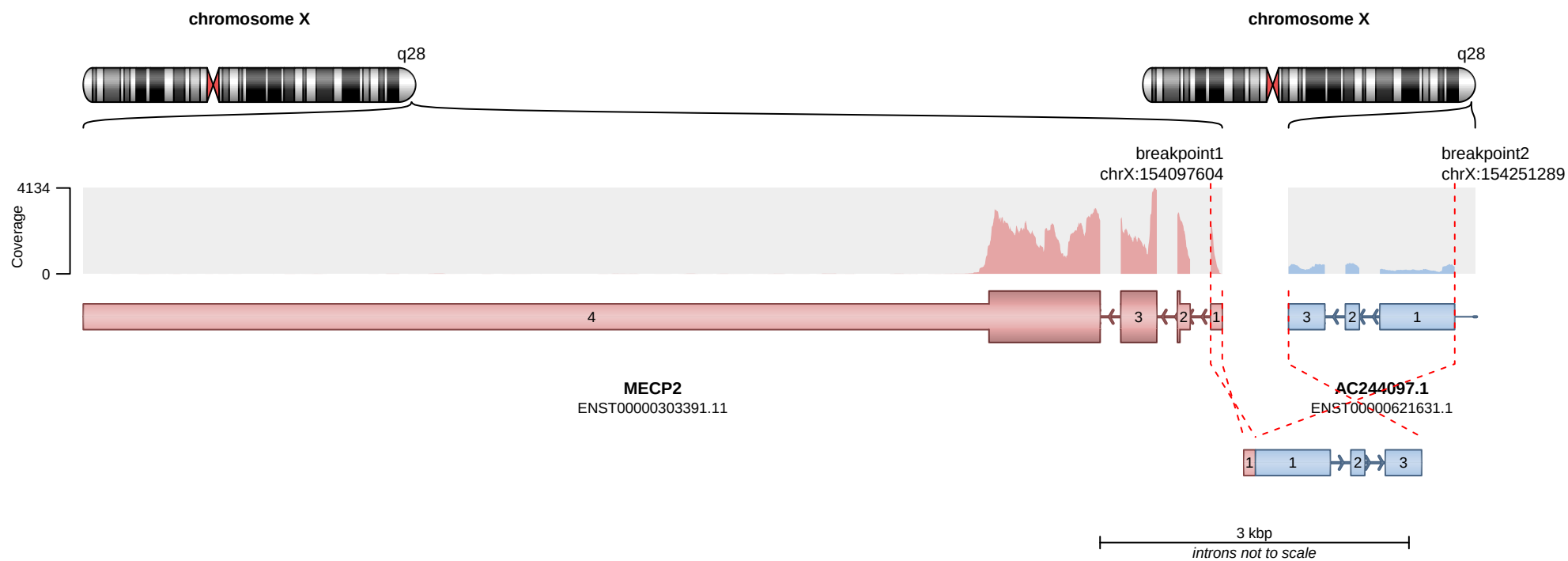


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 82
Discordant mates = 0

translocation deletion
duplication inversion

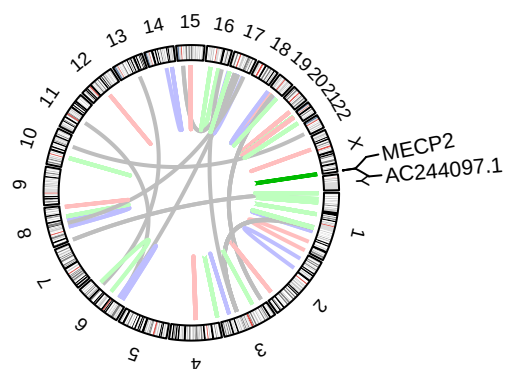
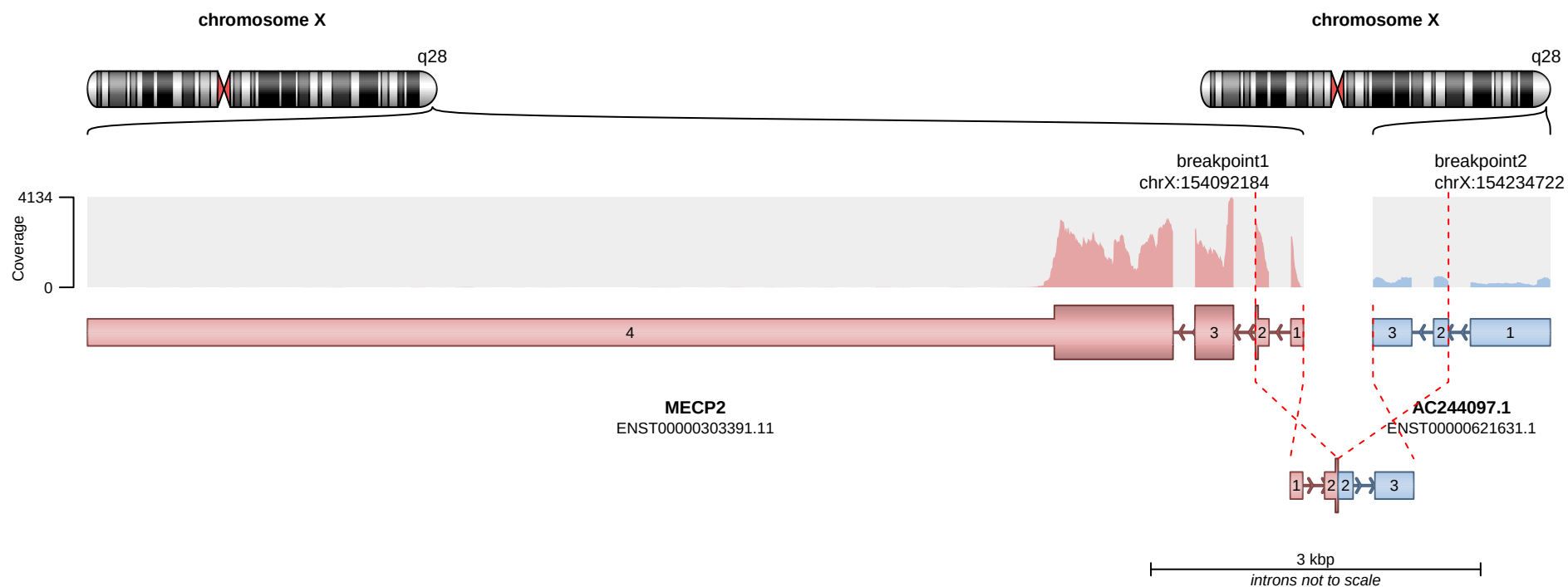


No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 44
Discordant mates = 0

— translocation — deletion
— duplication — inversion

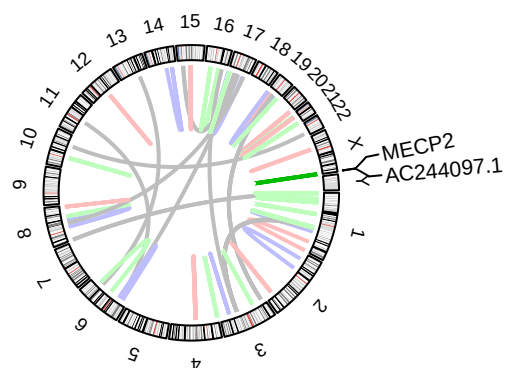
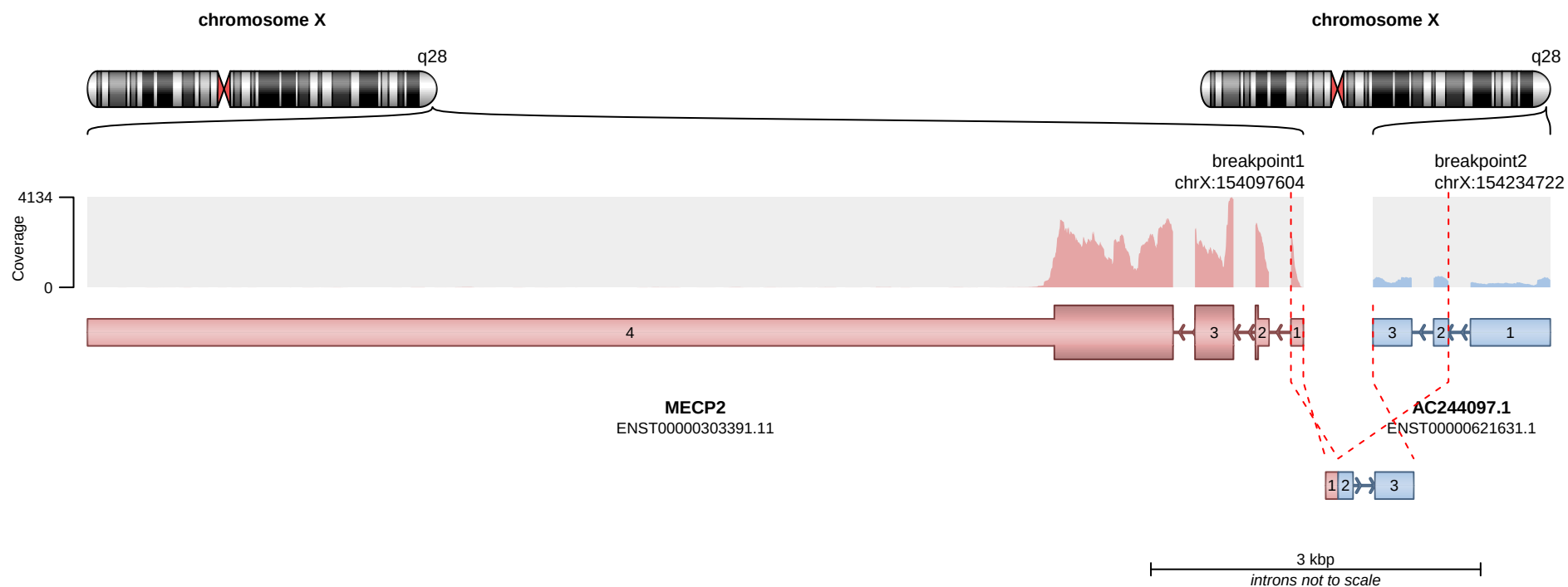


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 20
Discordant mates = 0

— translocation — deletion
— duplication — inversion

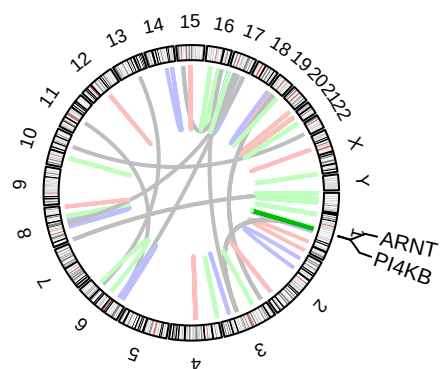
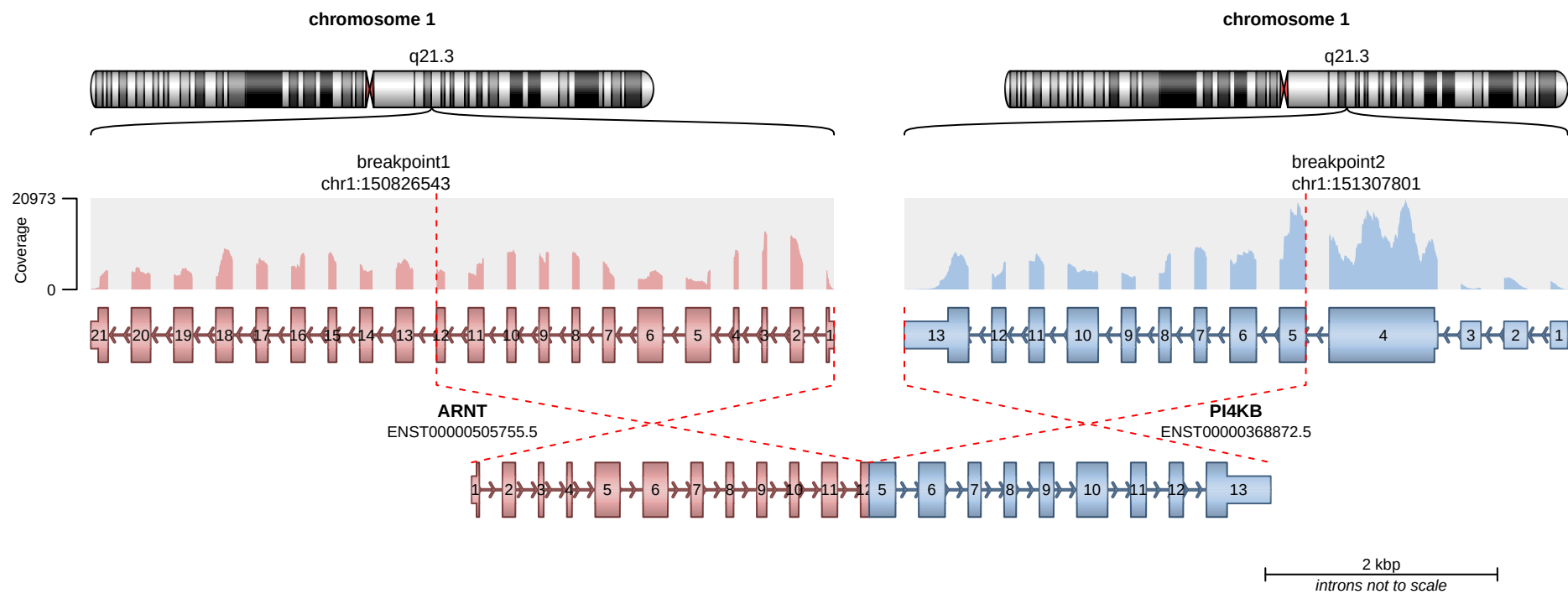


No coding regions retained in fusion transcript.

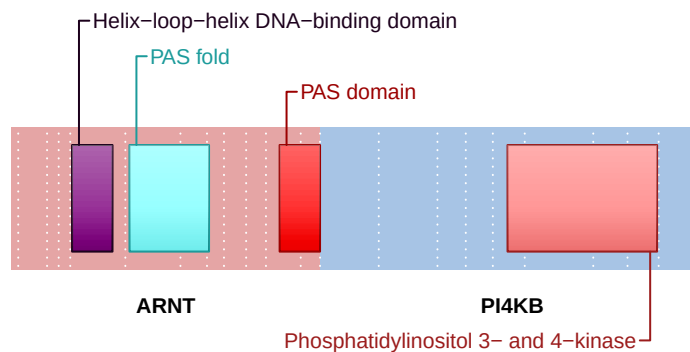
SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 0

translocation deletion
duplication inversion



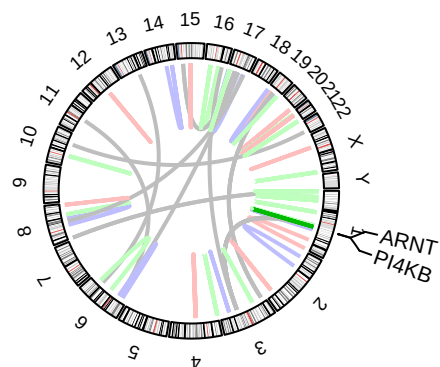
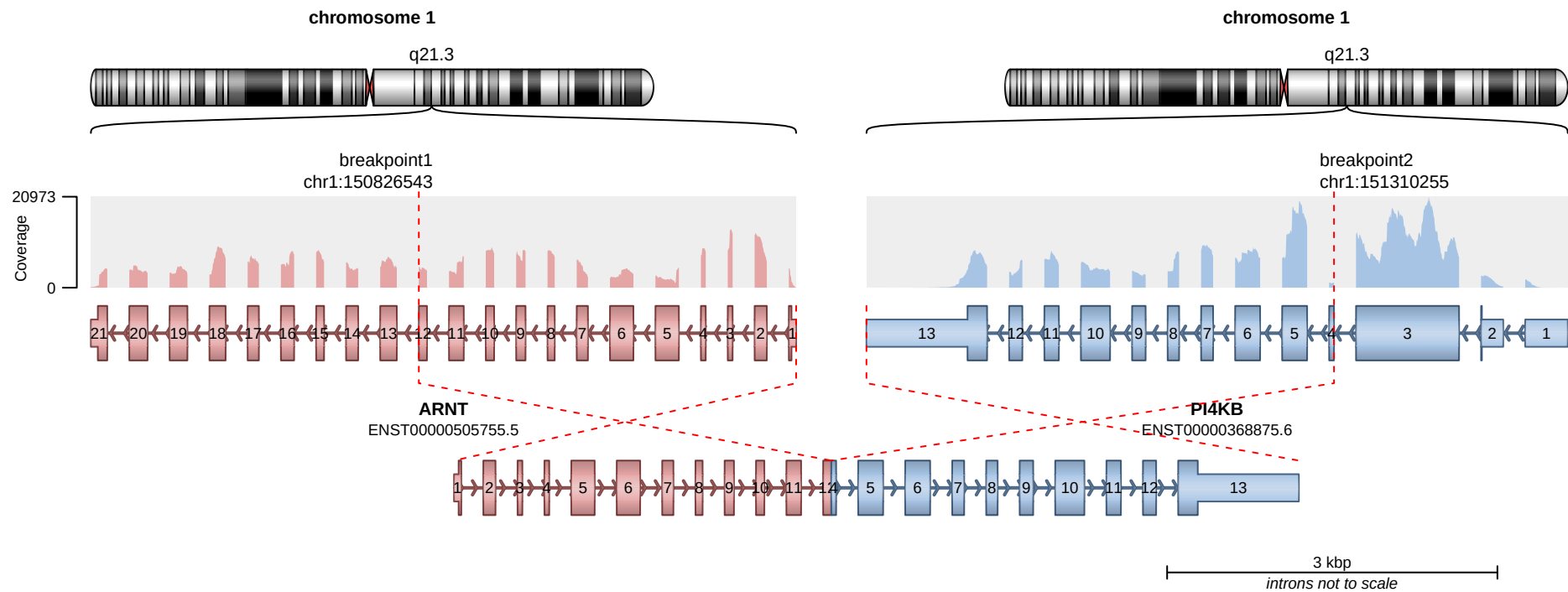
RETAINED PROTEIN DOMAINS reading frame unclear



SUPPORTING READ COUNT

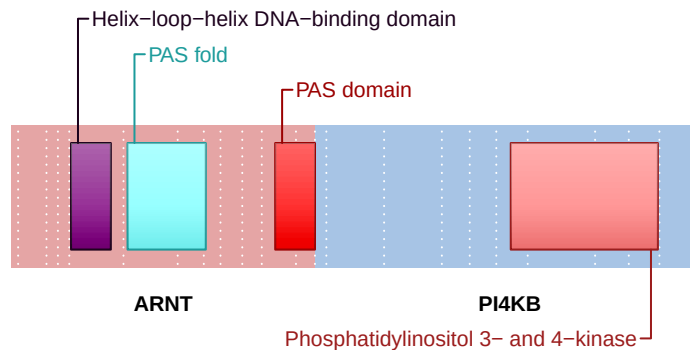
Split reads = 81
Discordant mates = 1

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS

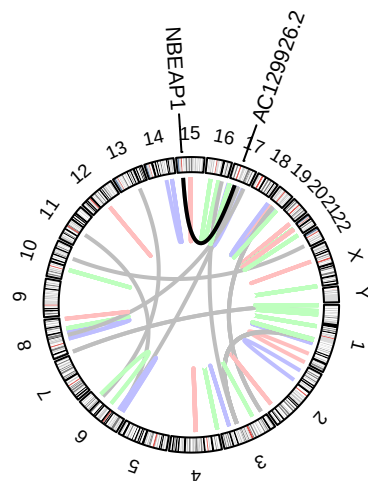
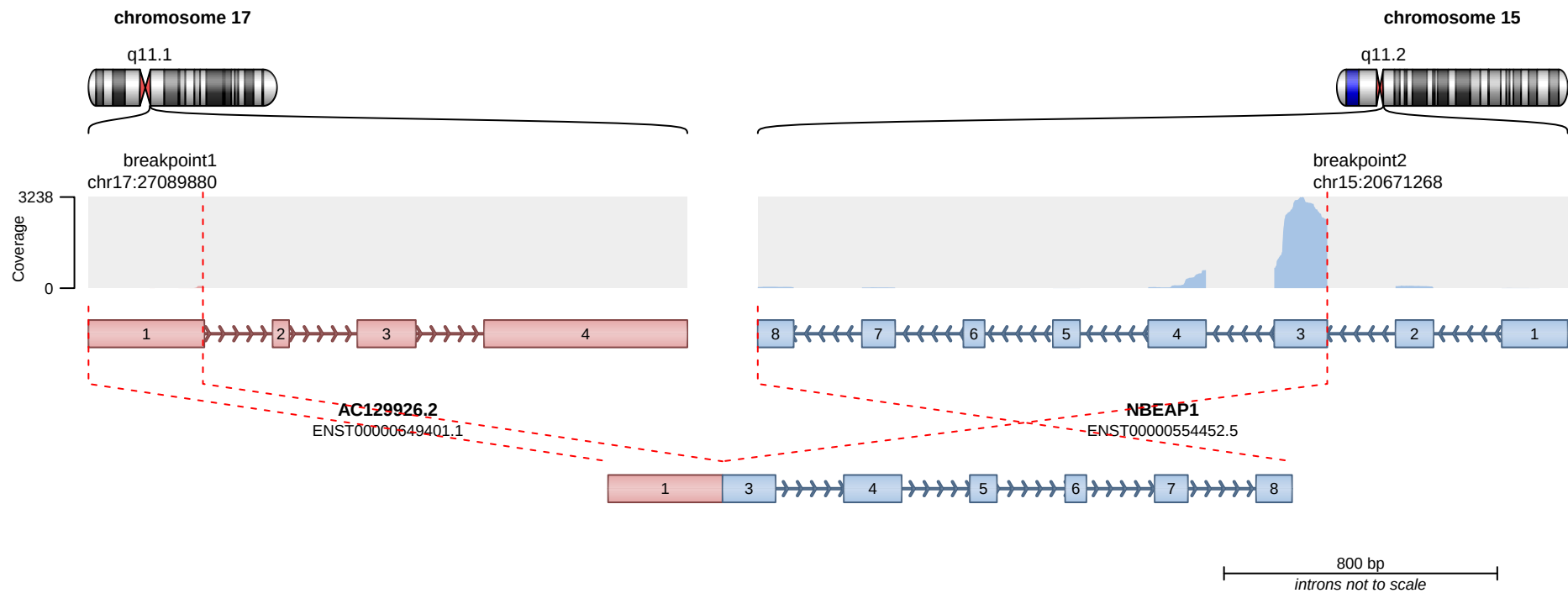
reading frame unclear



SUPPORTING READ COUNT

Split reads = 59
Discordant mates = 3

— translocation — deletion
— duplication — inversion

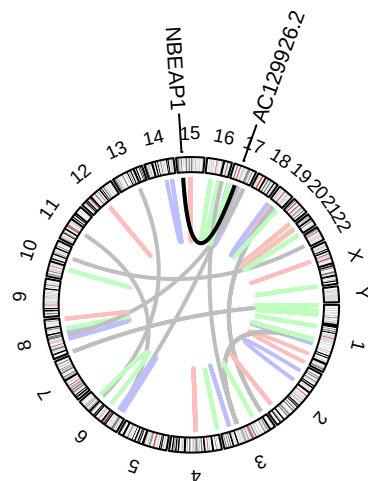
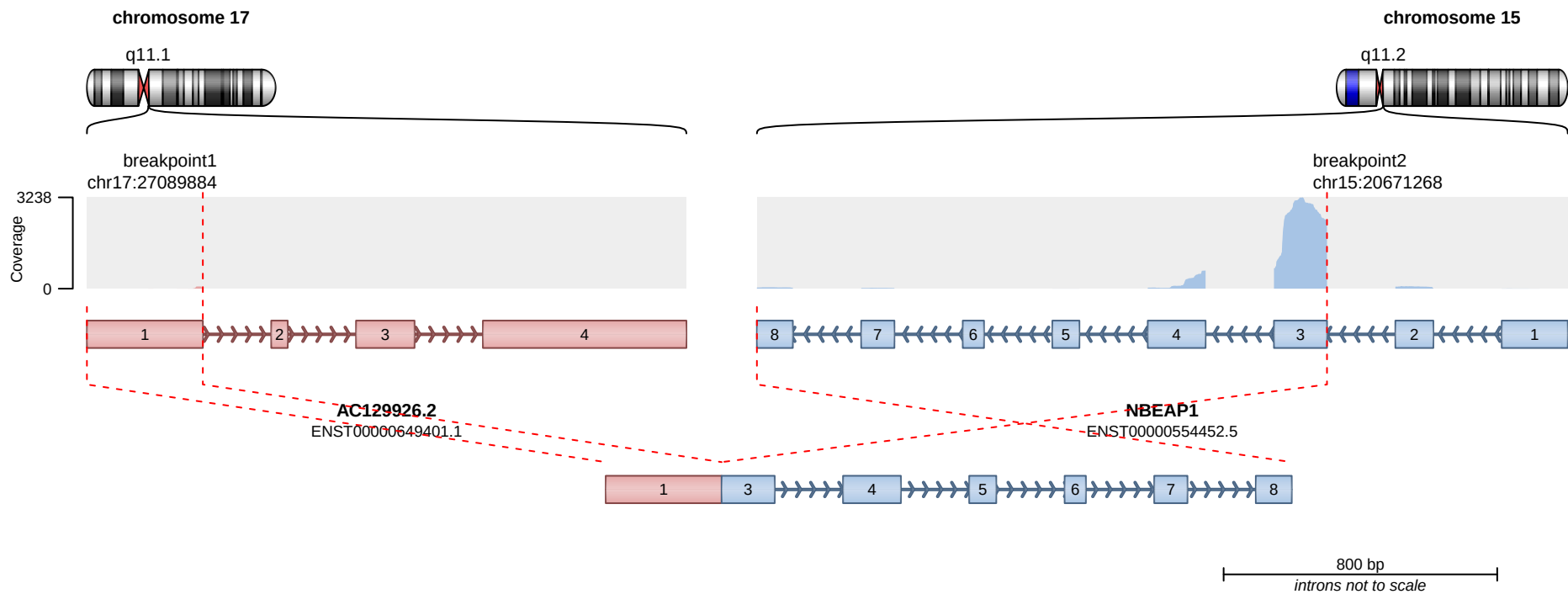


Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 67
Discordant mates = 0

— translocation — deletion
— duplication — inversion

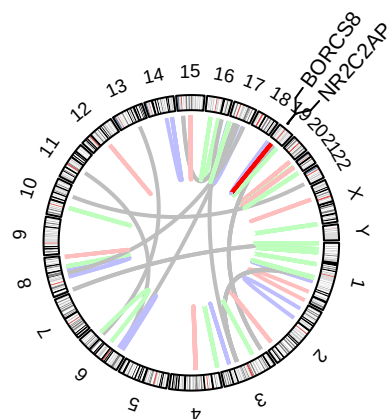
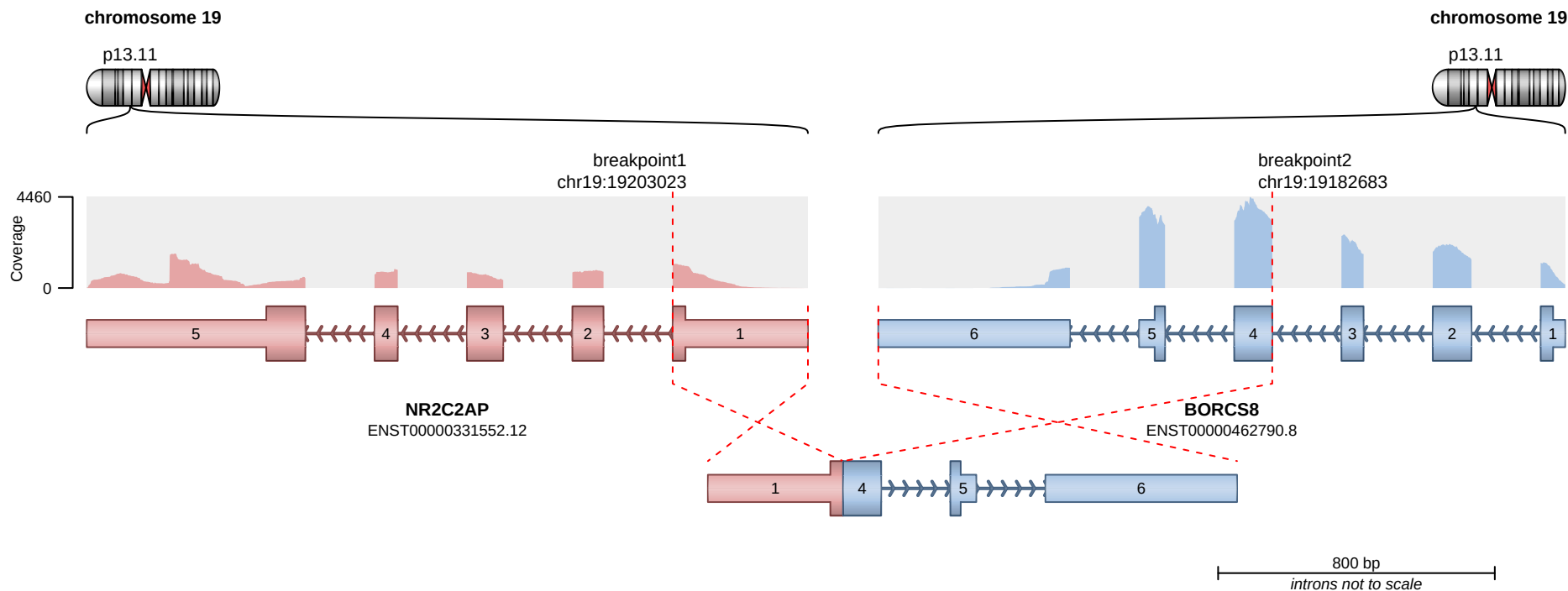


Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 45
Discordant mates = 0

— translocation — deletion
— duplication — inversion



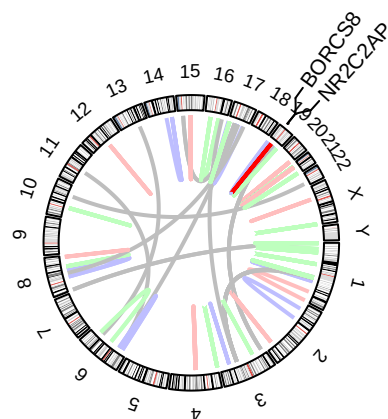
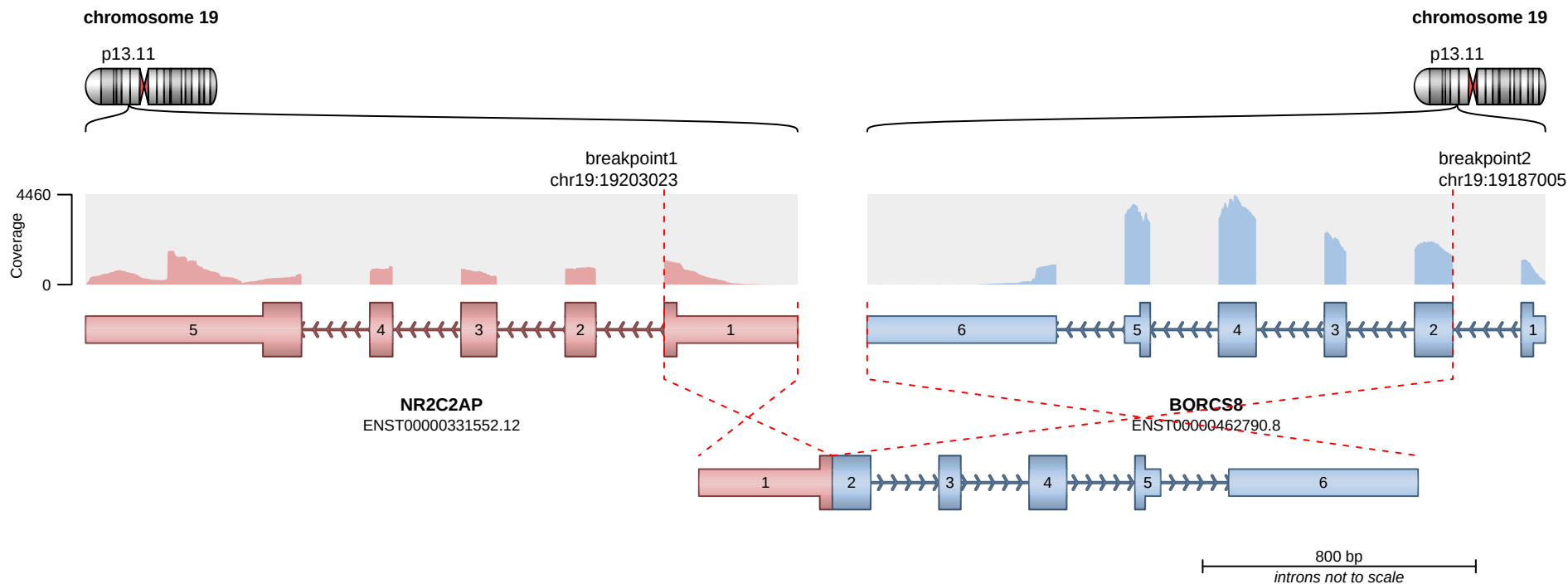
RETAINED PROTEIN DOMAINS
reading frame unclear



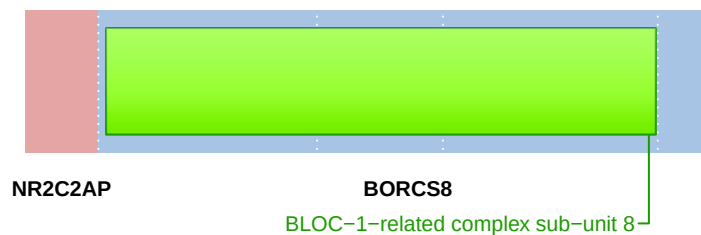
SUPPORTING READ COUNT

Split reads = 67
Discordant mates = 0

— translocation — deletion
— duplication — inversion



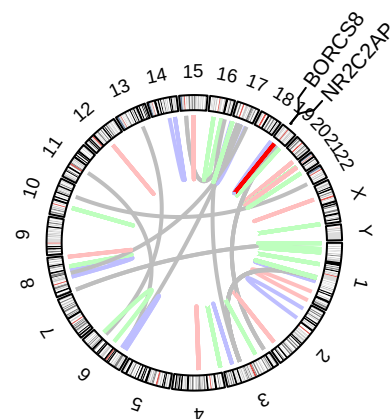
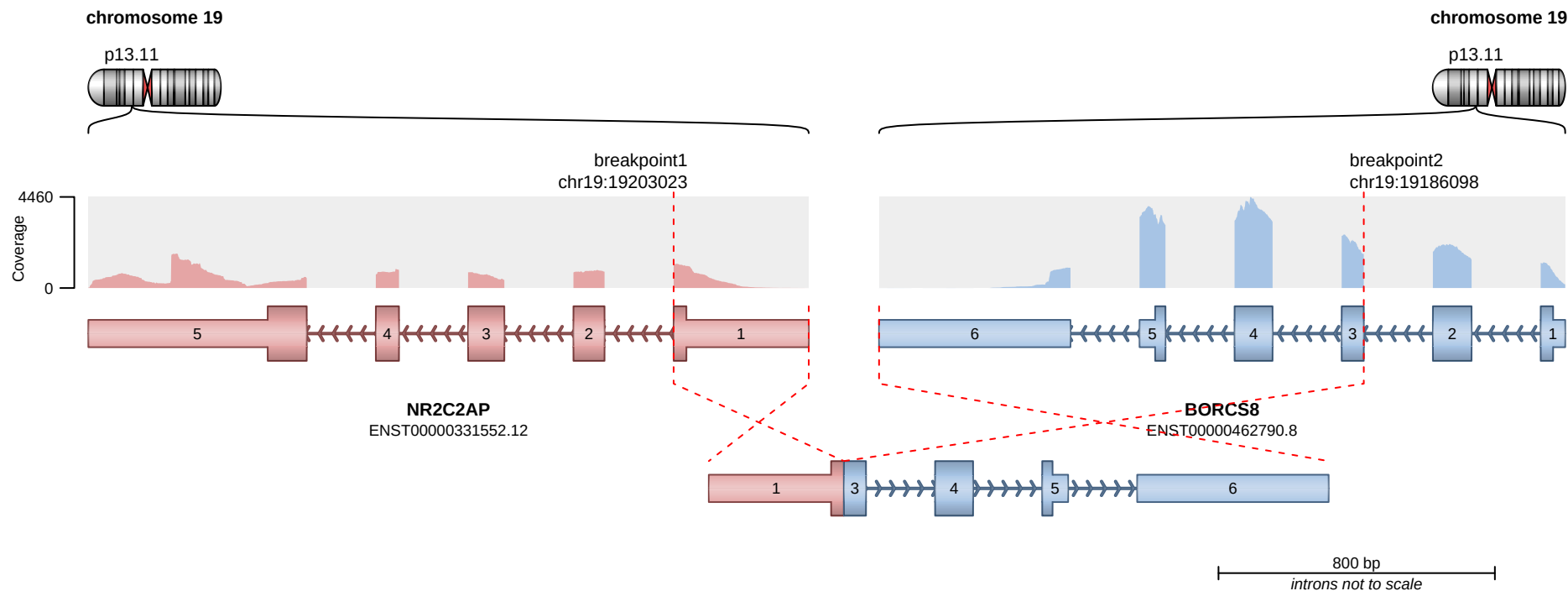
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 45
Discordant mates = 2

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

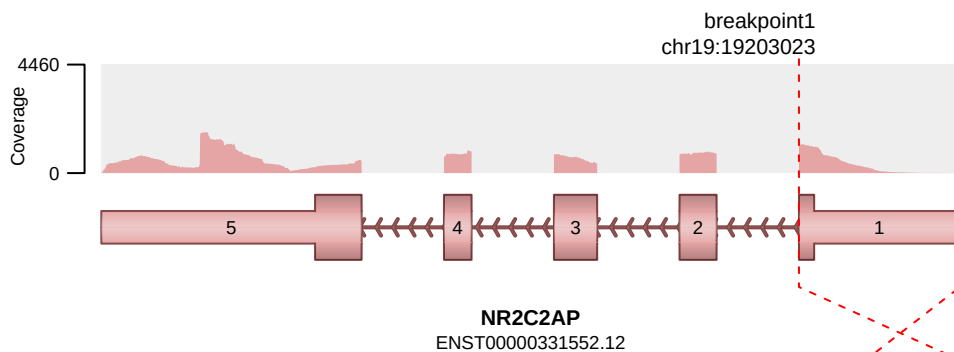
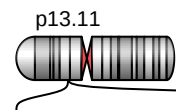


SUPPORTING READ COUNT

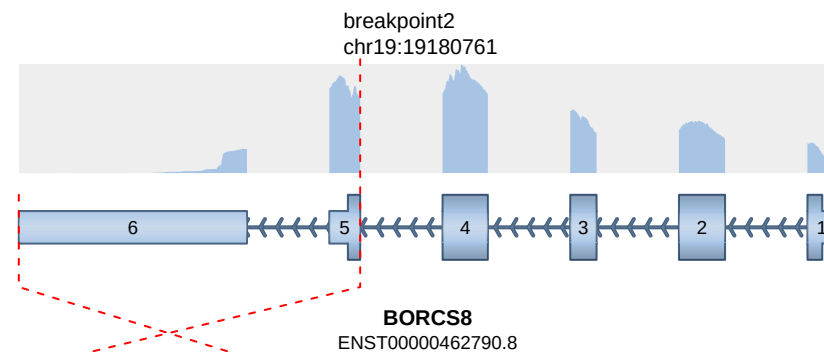
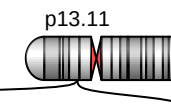
Split reads = 29
Discordant mates = 1

— translocation — deletion
— duplication — inversion

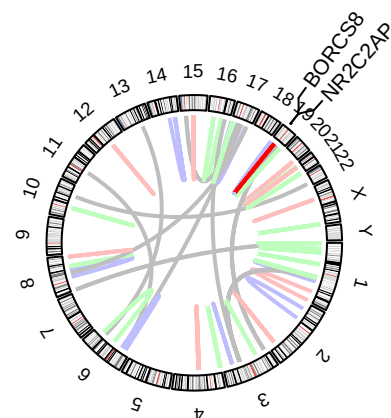
chromosome 19



chromosome 19



800 bp
introns not to scale

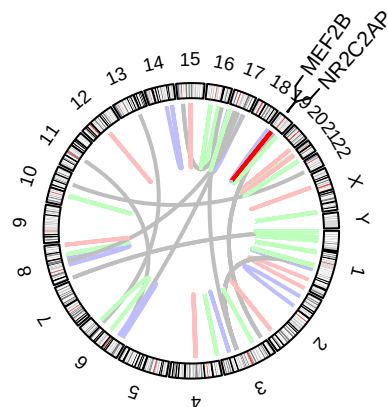
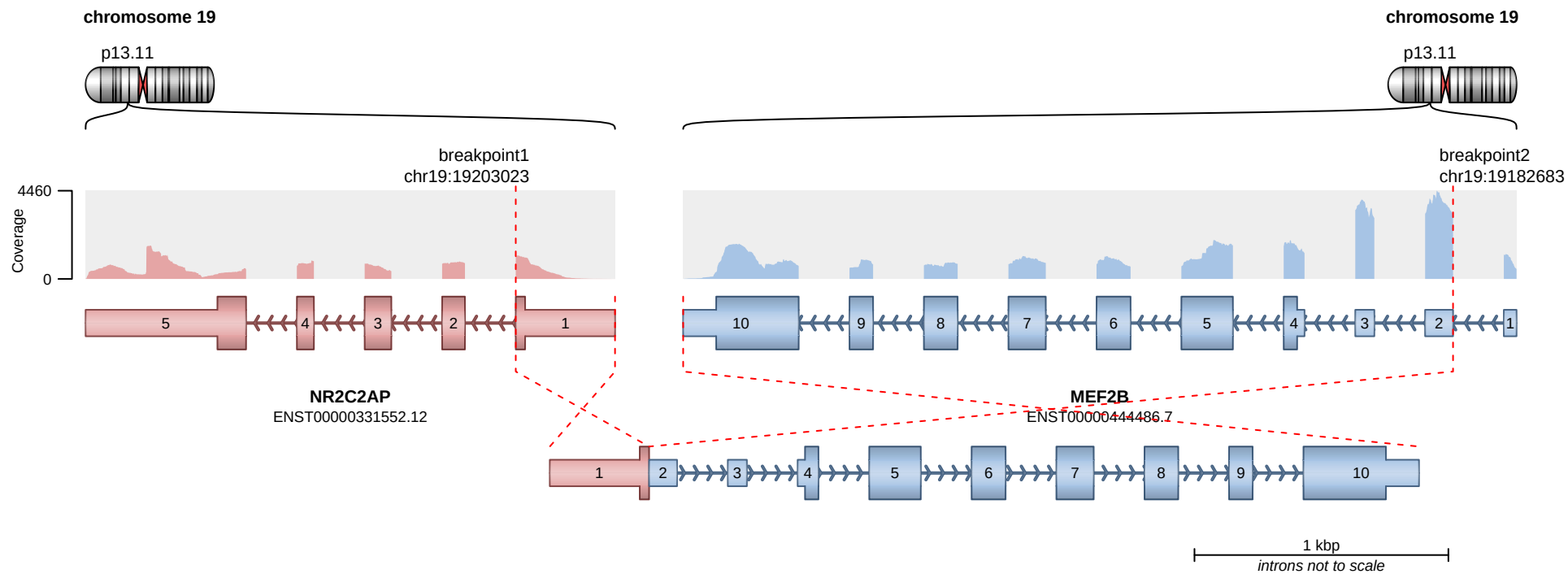


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

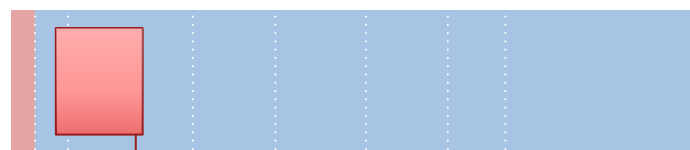
SUPPORTING READ COUNT

Split reads = 9
Discordant mates = 0



SRF-type transcription factor (DNA-binding and dimerisation domain)

RETAINED PROTEIN DOMAINS
reading frame unclear



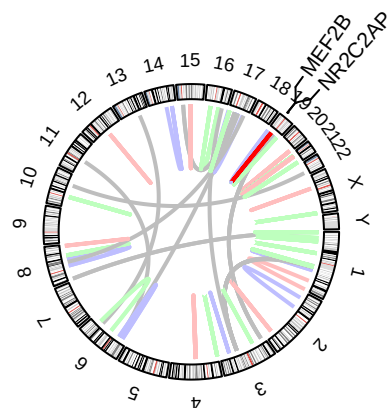
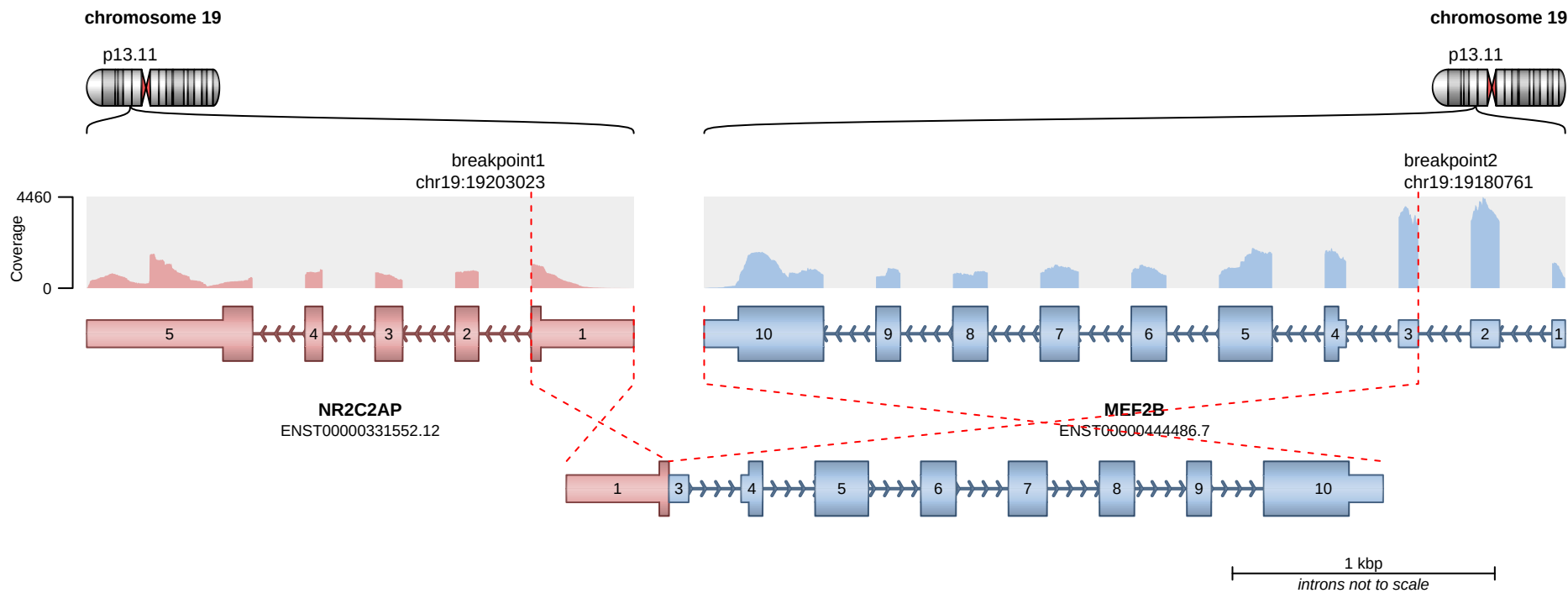
NR2C2AP

MEF2B

SUPPORTING READ COUNT

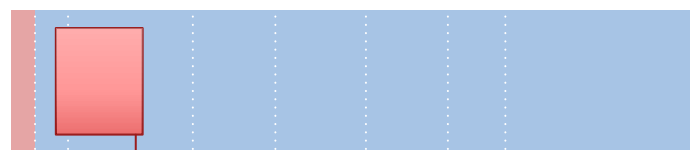
Split reads = 67
Discordant mates = 0

— translocation — deletion
— duplication — inversion



SRF-type transcription factor (DNA-binding and dimerisation domain)

RETAINED PROTEIN DOMAINS
reading frame unclear



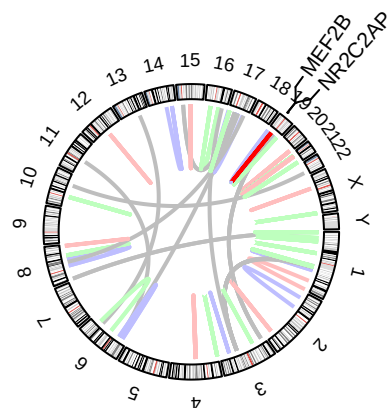
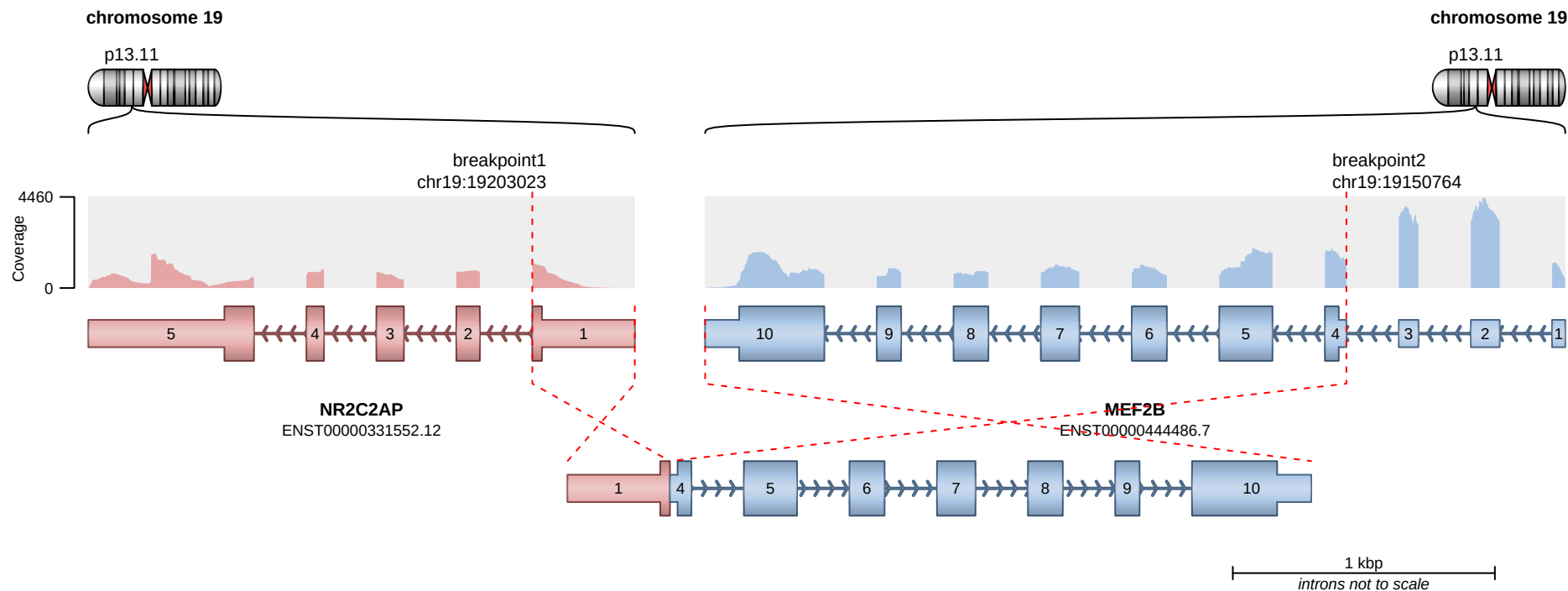
NR2C2AP

MEF2B

SUPPORTING READ COUNT

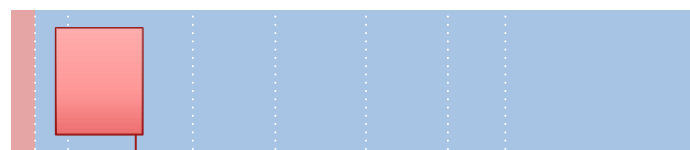
Split reads = 9
Discordant mates = 0

— translocation — deletion
— duplication — inversion



SRF-type transcription factor (DNA-binding and dimerisation domain)

RETAINED PROTEIN DOMAINS
reading frame unclear



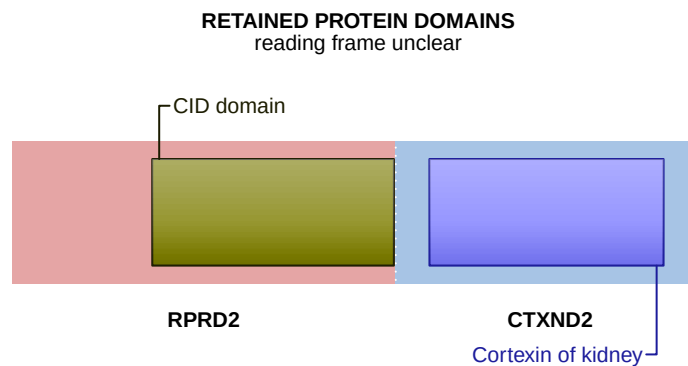
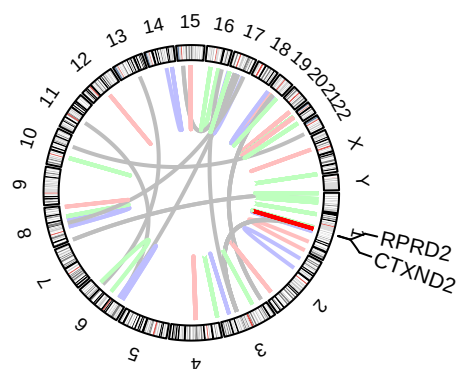
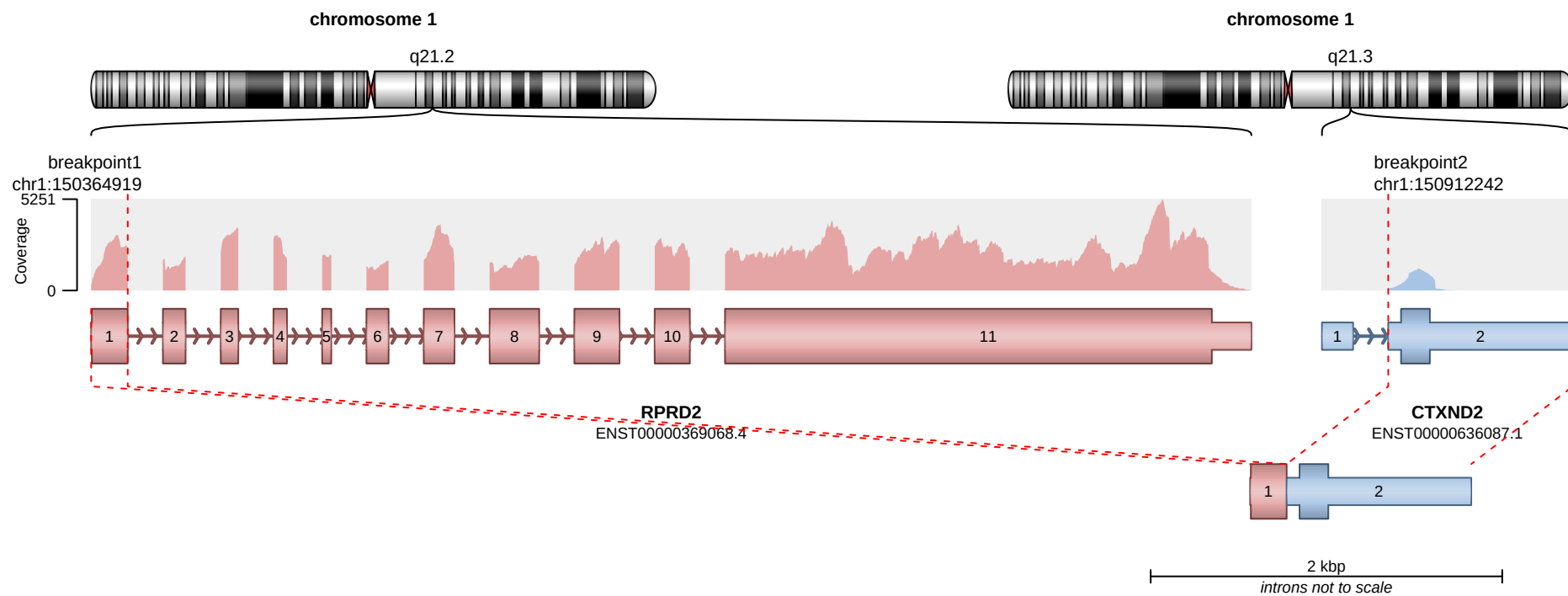
NR2C2AP

MEF2B

SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 0

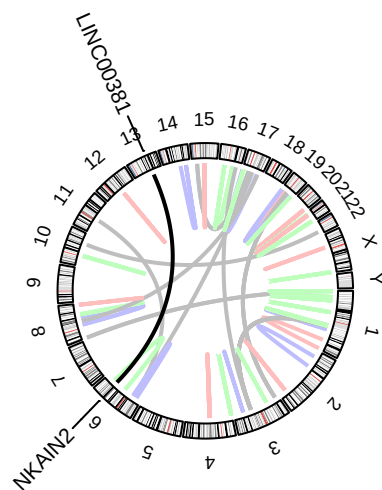
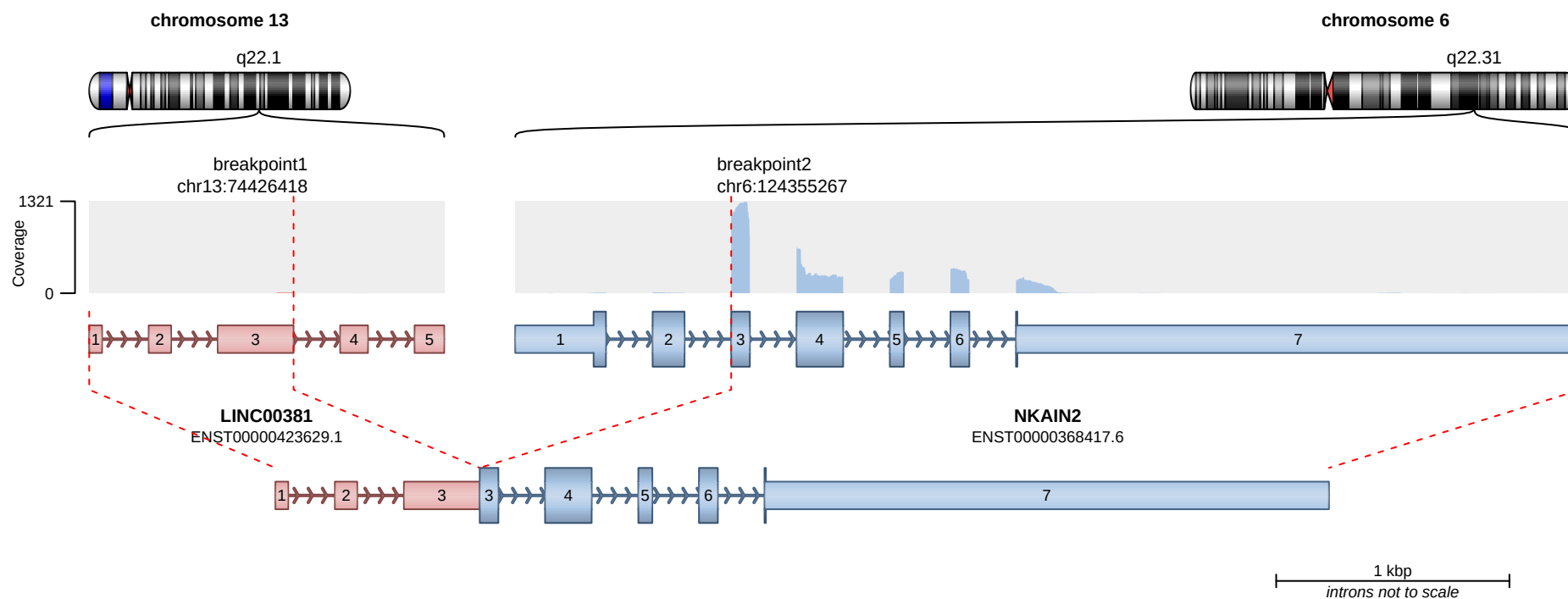
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 64
Discordant mates = 7

— translocation — deletion
— duplication — inversion



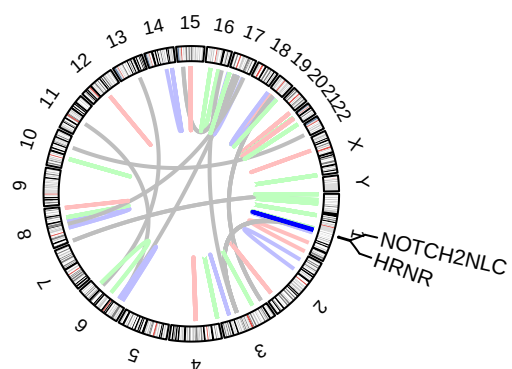
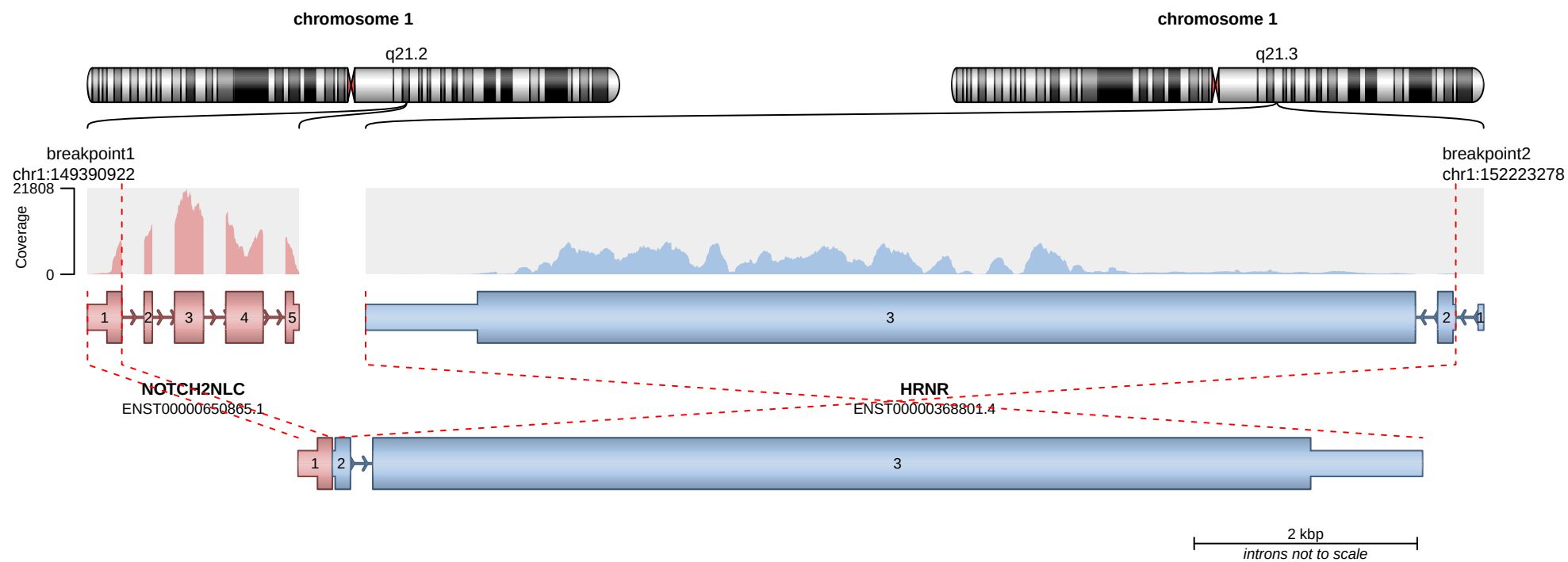
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 63
Discordant mates = 0

— translocation — deletion
— duplication — inversion



S-100/ICaBP type calcium binding domain

NOTCH2NLC

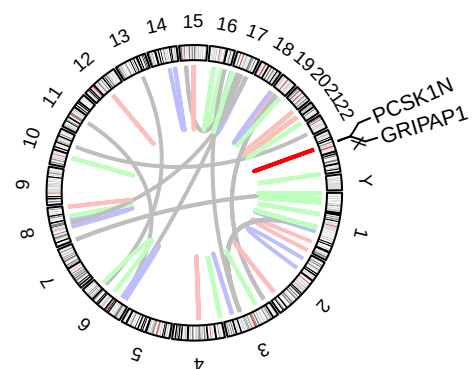
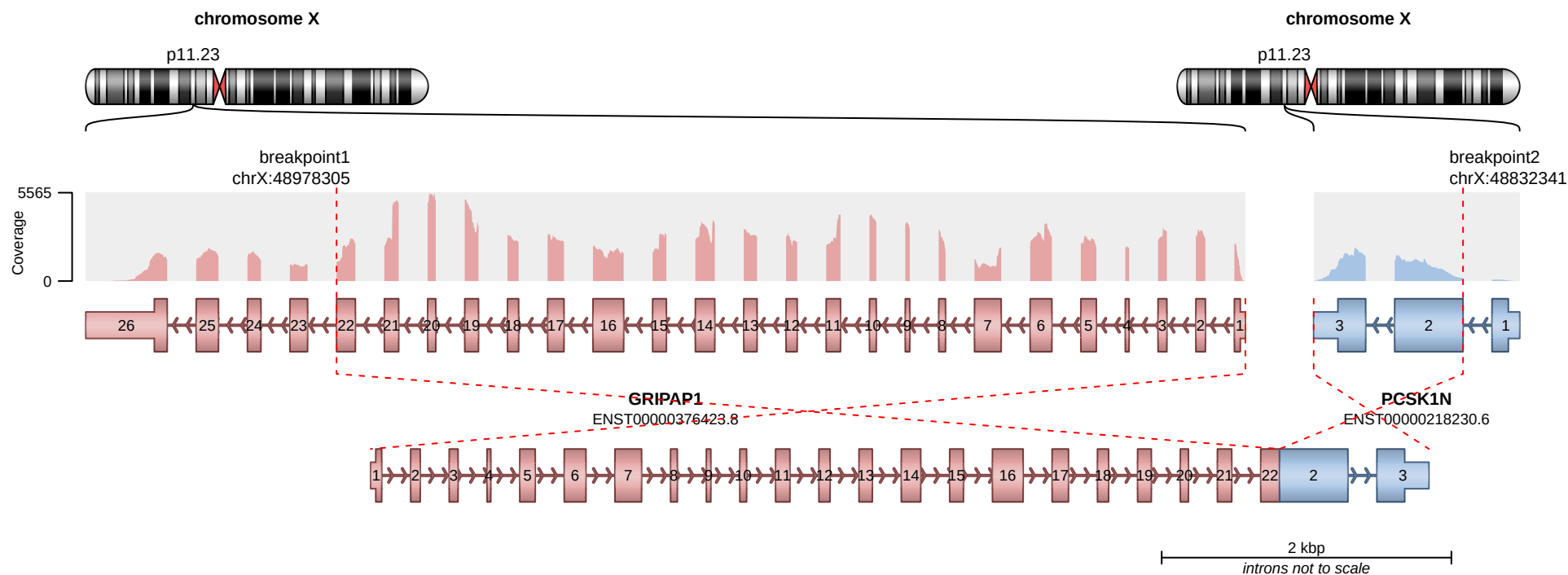
HRNR

RETAINED PROTEIN DOMAINS
reading frame unclear

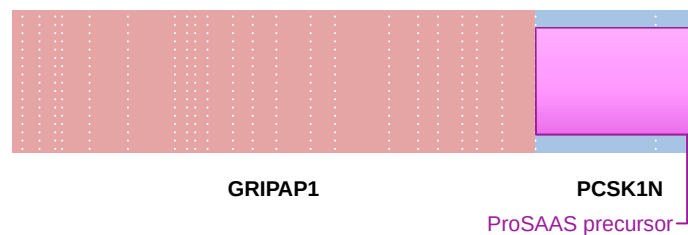
SUPPORTING READ COUNT

Split reads = 61
Discordant mates = 0

— translocation — deletion
— duplication — inversion



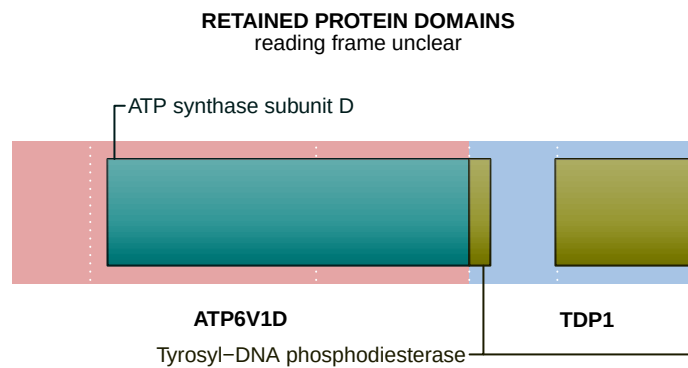
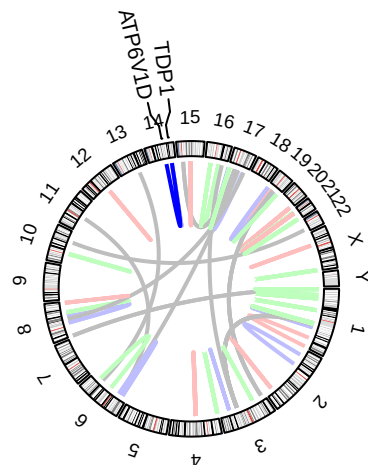
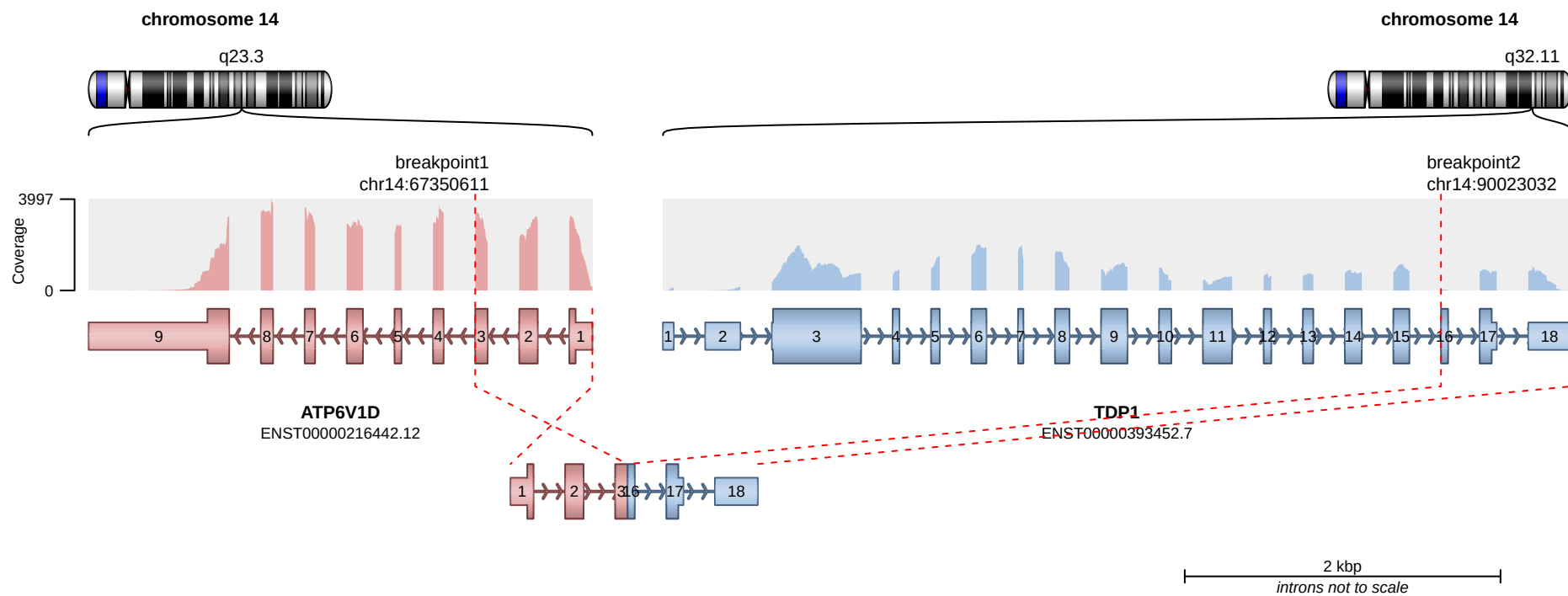
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 52
Discordant mates = 1

— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 39
Discordant mates = 0

— translocation — deletion
— duplication — inversion

chromosome 21

p11.2



breakpoint1

chr21:10527412



TPTE

ENST00000618007.5

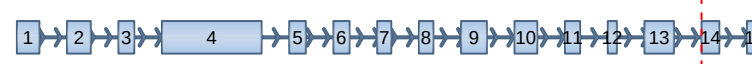
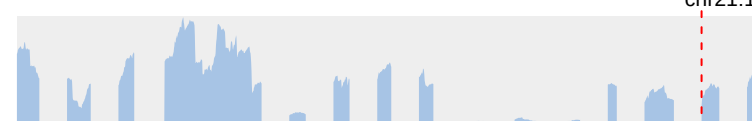
chromosome 21

p11.2



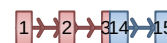
breakpoint2

chr21:10514122

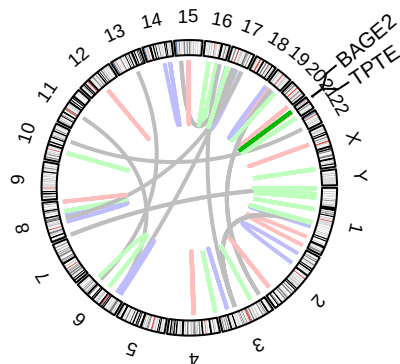


BAGE2

ENST00000496773.1



2 kbp
introns not to scale



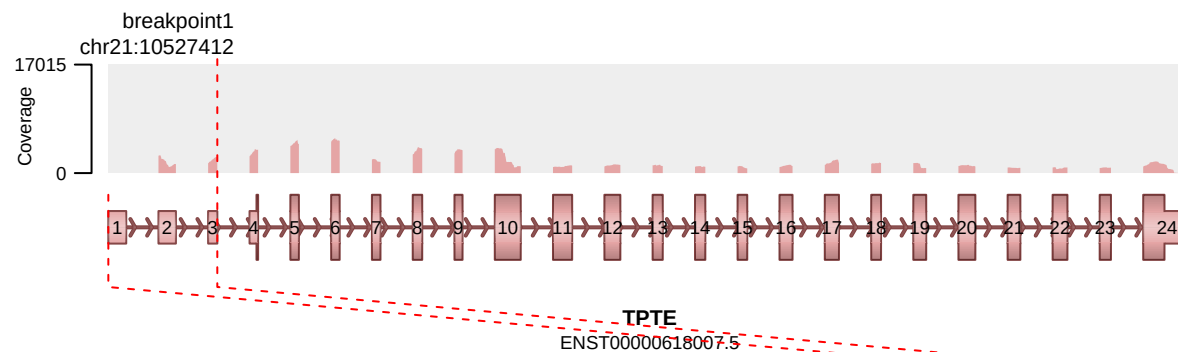
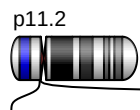
No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

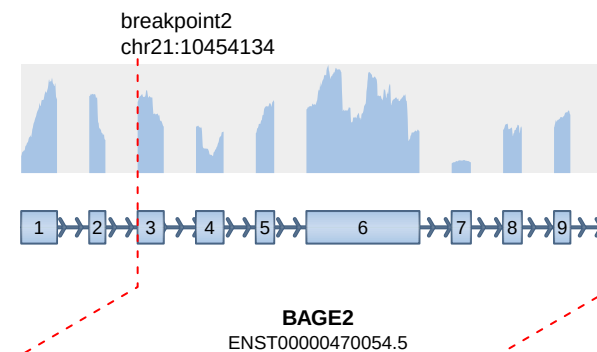
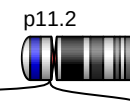
Split reads = 37
Discordant mates = 1

— translocation — deletion
— duplication — inversion

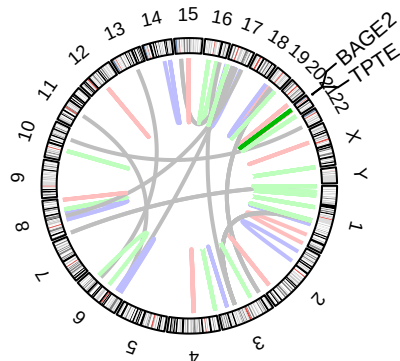
chromosome 21



chromosome 21



2 kbp
introns not to scale



translocation deletion
duplication inversion

No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 22
Discordant mates = 2

chromosome 21

p11.2



breakpoint1

chr21:10527412



TPTE

ENST00000618007.5

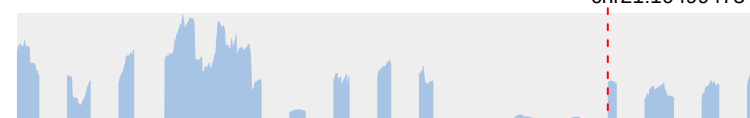
chromosome 21

p11.2



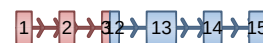
breakpoint2

chr21:10499475

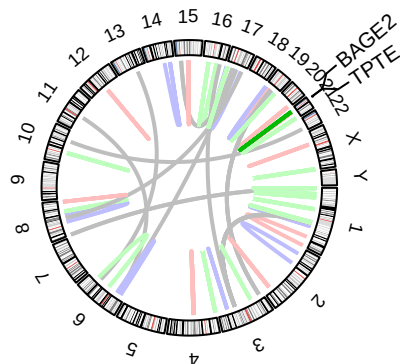


BAGE2

ENST00000496773.1



2 kbp
introns not to scale



No coding regions retained in fusion transcript.

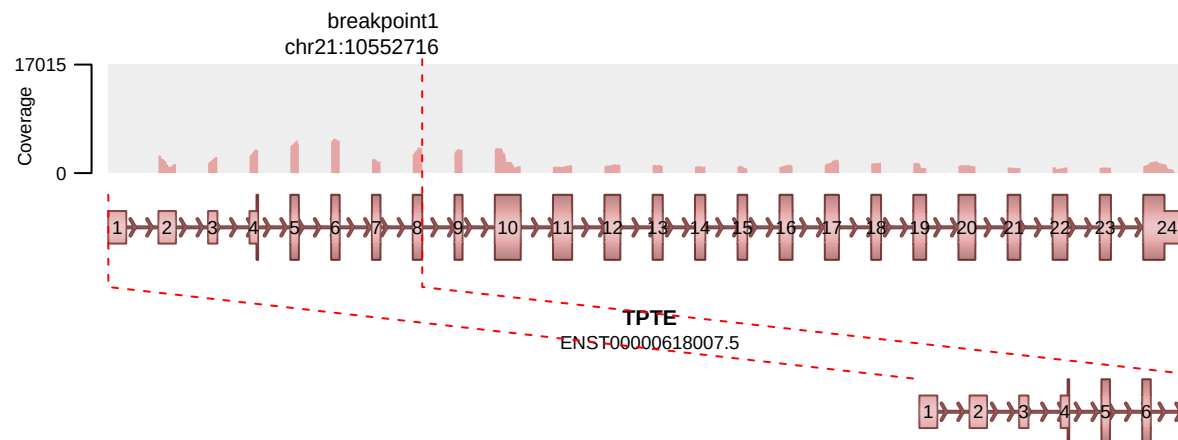
SUPPORTING READ COUNT

Split reads = 20
Discordant mates = 1

— translocation — deletion
— duplication — inversion

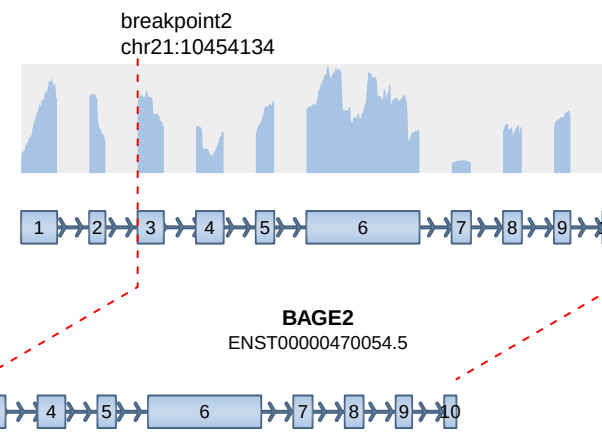
chromosome 21

p11.2

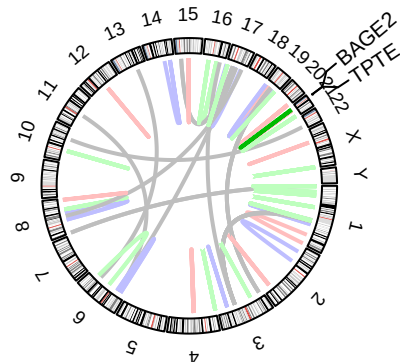


chromosome 21

p11.2



2 kbp
introns not to scale



No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 18
Discordant mates = 3

— translocation — deletion
— duplication — inversion

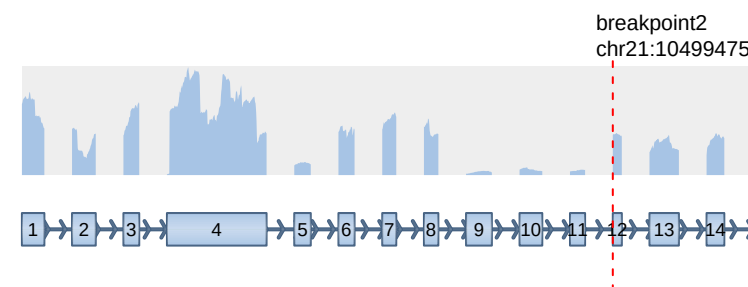
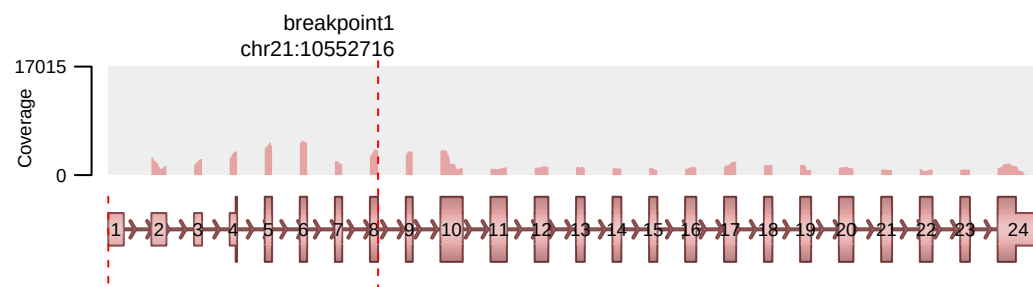
chromosome 21

p11.2



chromosome 21

p11.2

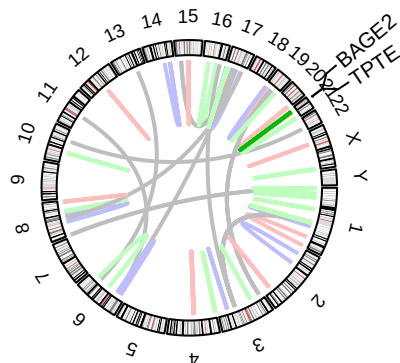


TPTE
ENST00000618007.5

BAGE2
ENST00000496773.1



2 kbp
introns not to scale



No protein domains retained in fusion.

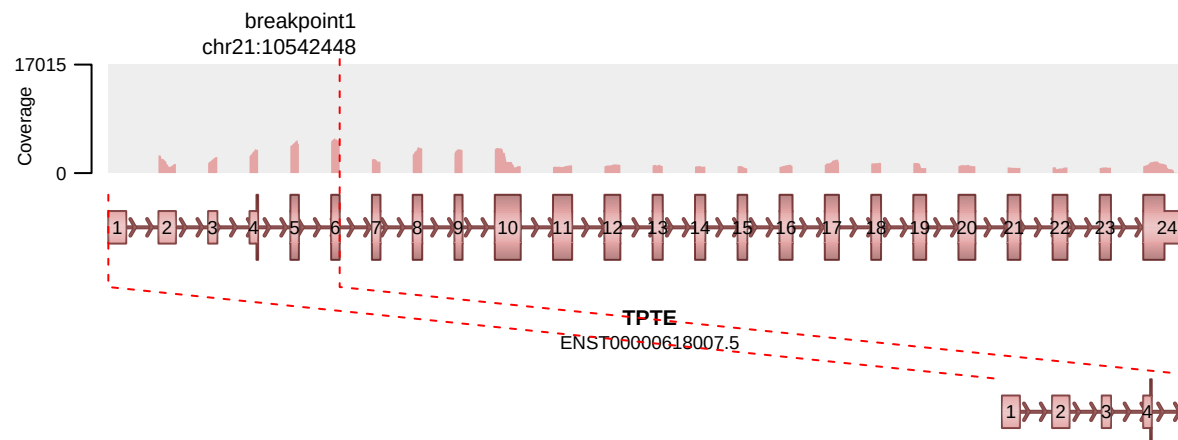
SUPPORTING READ COUNT

Split reads = 16
Discordant mates = 1

— translocation — deletion
— duplication — inversion

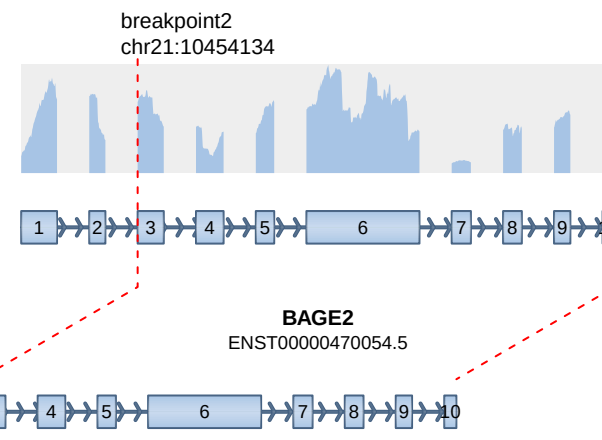
chromosome 21

p11.2

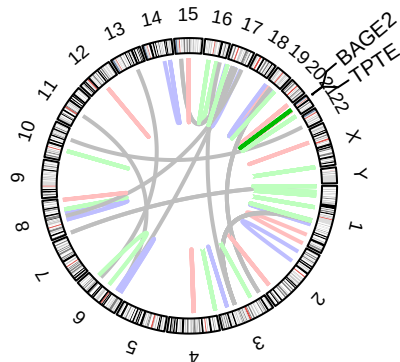


chromosome 21

p11.2



2 kbp
introns not to scale



translocation deletion
duplication inversion

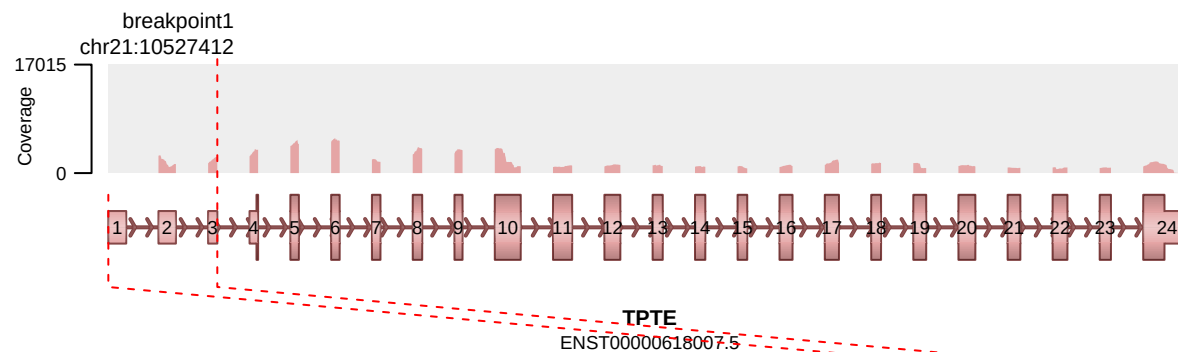
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 9
Discordant mates = 3

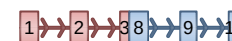
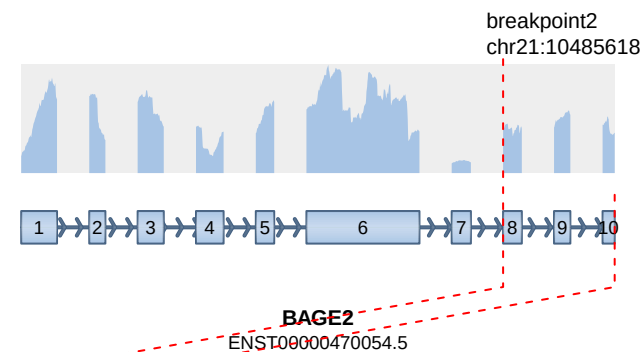
chromosome 21

p11.2

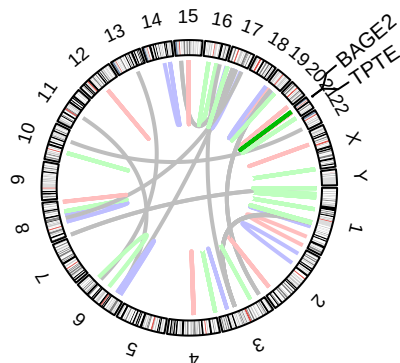


chromosome 21

p11.2



2 kbp
introns not to scale



No coding regions retained in fusion transcript.

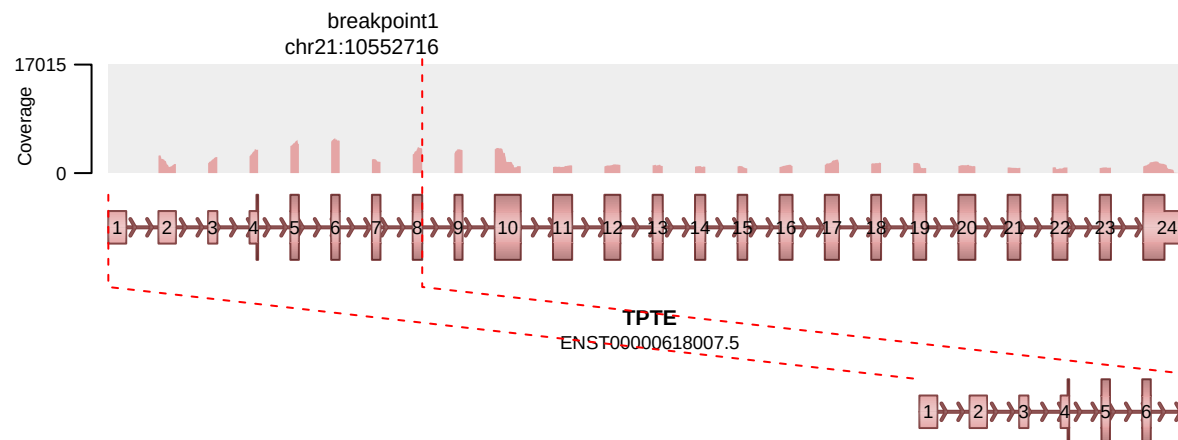
SUPPORTING READ COUNT

Split reads = 9
Discordant mates = 1

translocation deletion
duplication inversion

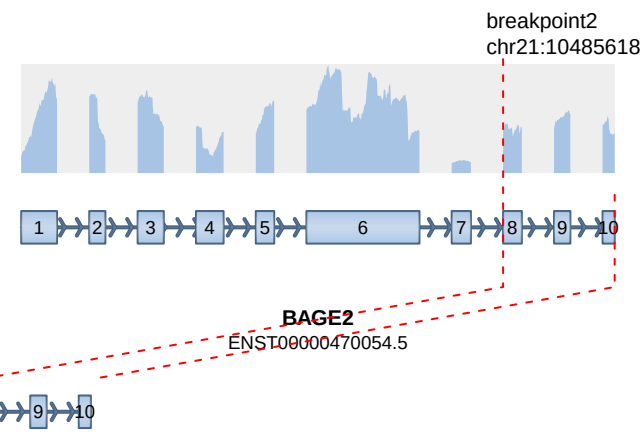
chromosome 21

p11.2

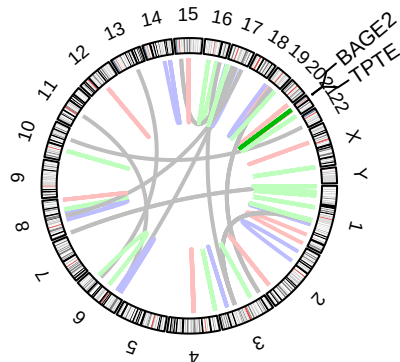


chromosome 21

p11.2



2 kbp
introns not to scale



translocation deletion
duplication inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 2

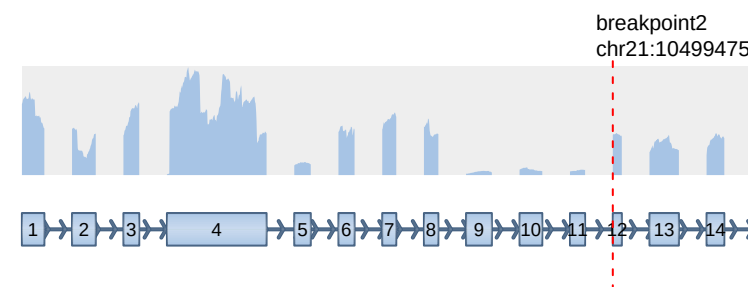
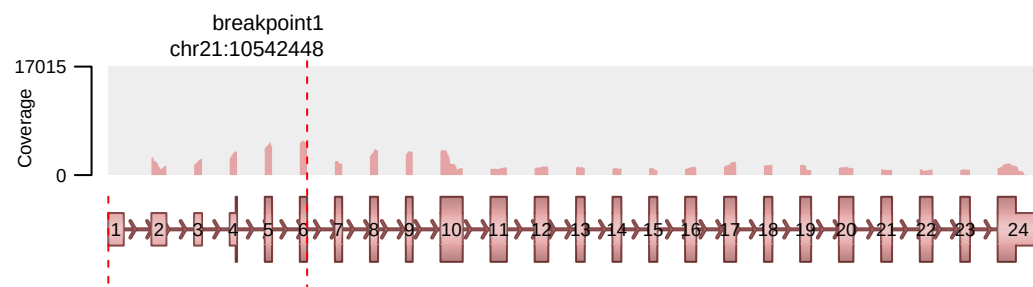
chromosome 21

p11.2



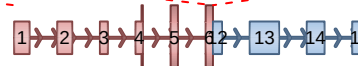
chromosome 21

p11.2

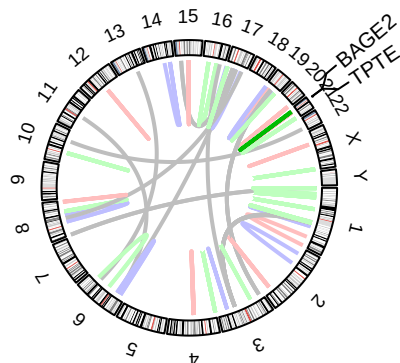


TPTE
ENST00000618007.5

BAGE2
ENST00000496773.1



2 kbp
introns not to scale



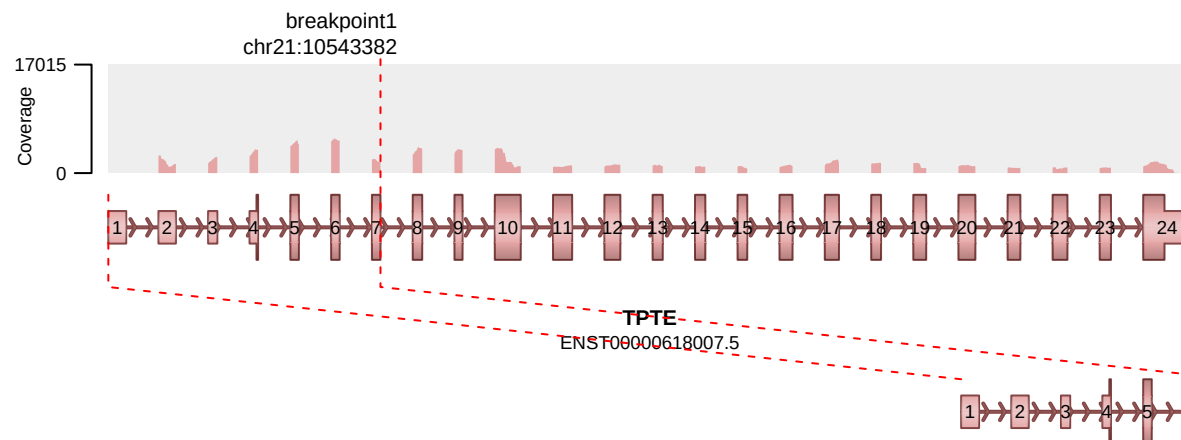
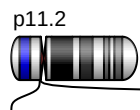
No protein domains retained in fusion.

SUPPORTING READ COUNT

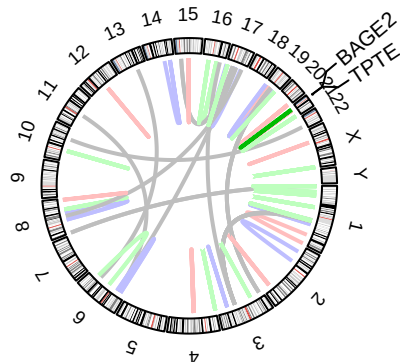
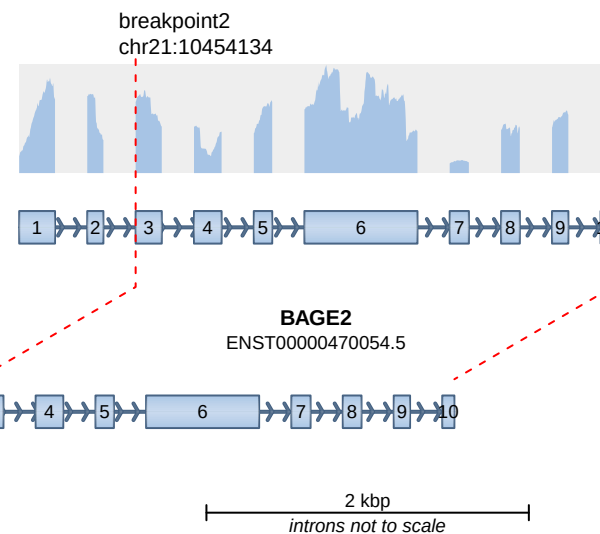
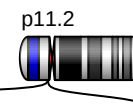
Split reads = 6
Discordant mates = 1

translocation deletion
duplication inversion

chromosome 21



chromosome 21



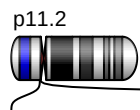
No protein domains retained in fusion.

SUPPORTING READ COUNT

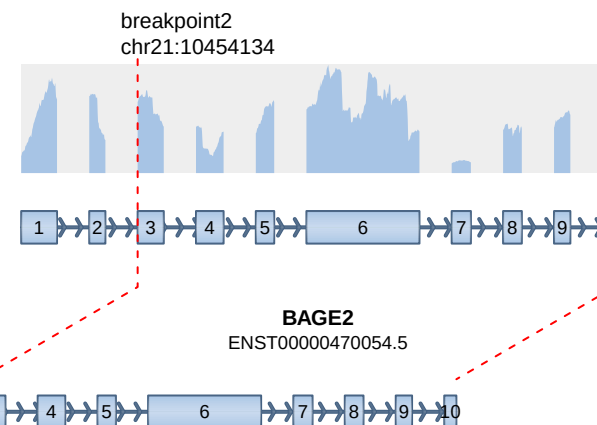
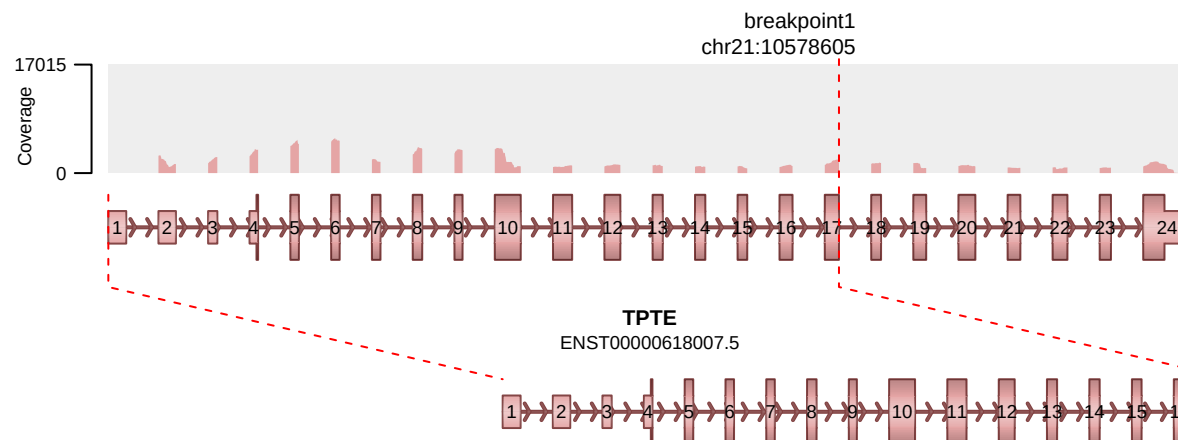
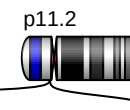
Split reads = 5
Discordant mates = 3

— translocation — deletion
— duplication — inversion

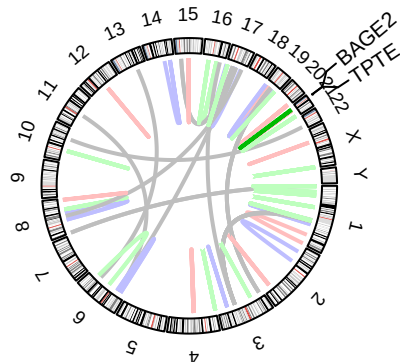
chromosome 21



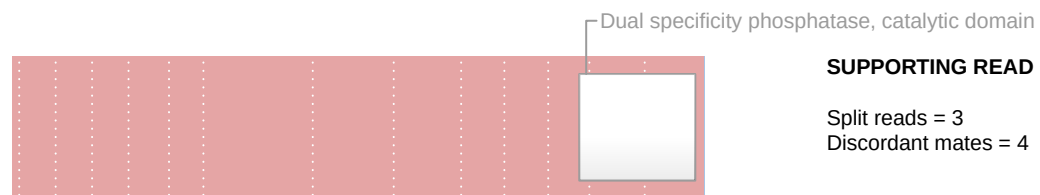
chromosome 21



2 kbp
introns not to scale



RETAINED PROTEIN DOMAINS
reading frame unclear



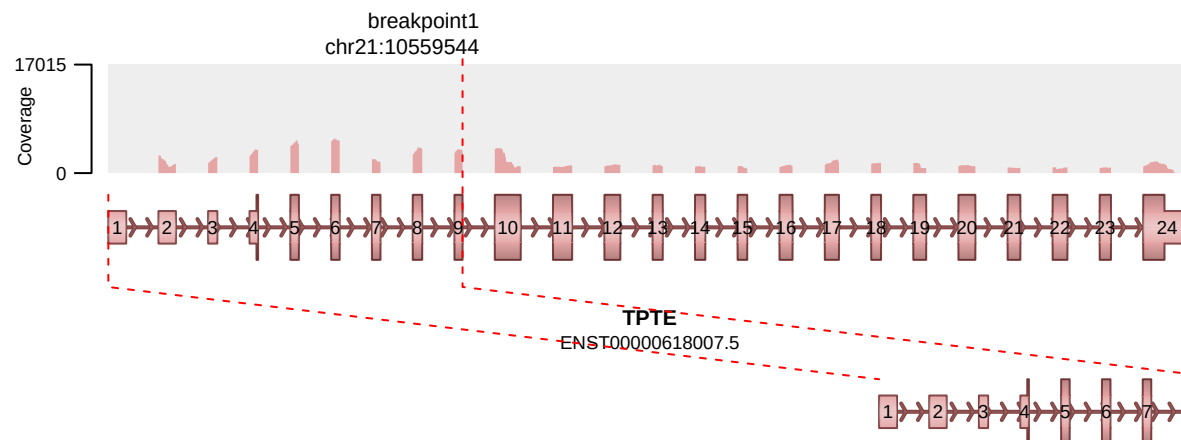
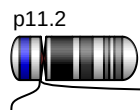
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 4

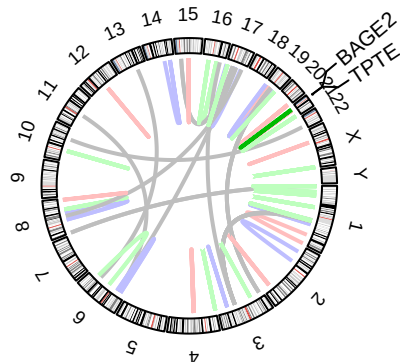
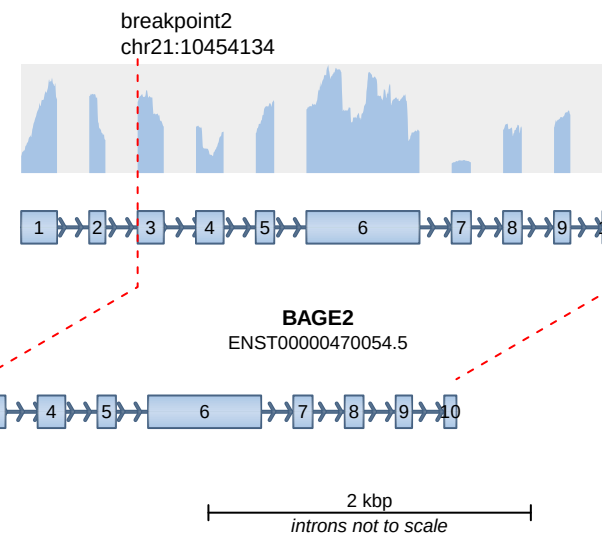
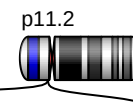
TPTE

— translocation — deletion
— duplication — inversion

chromosome 21



chromosome 21



No protein domains retained in fusion.

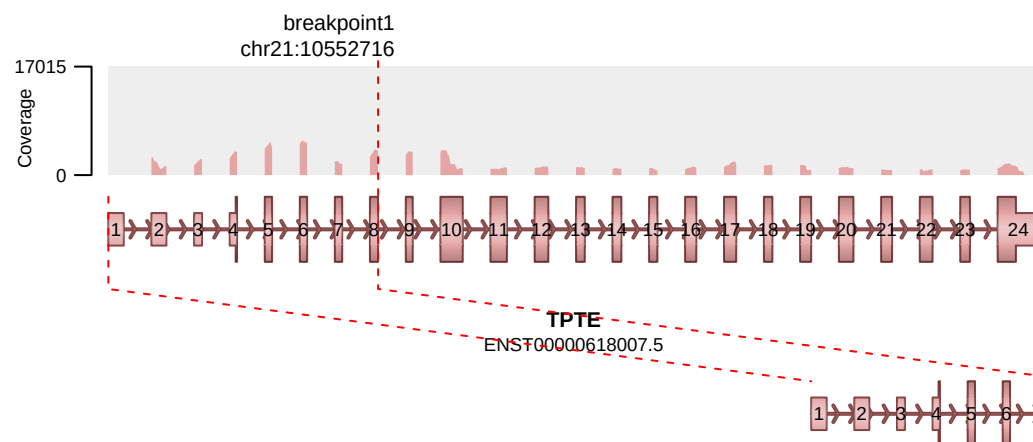
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 3

translocation
duplication
deletion
inversion

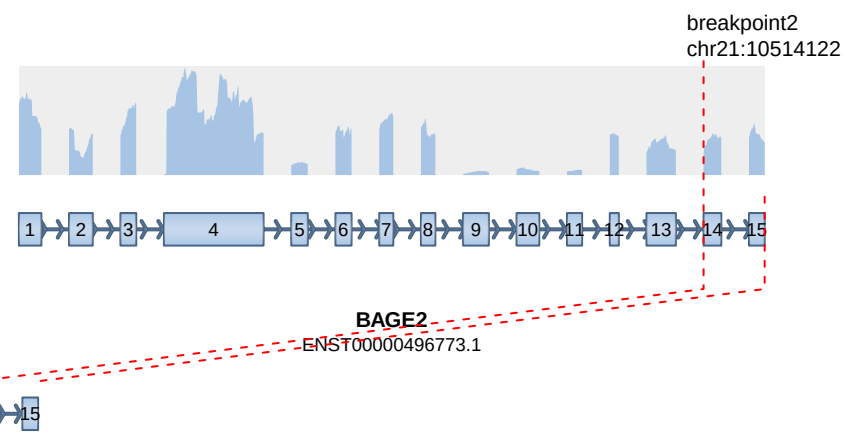
chromosome 21

p11.2

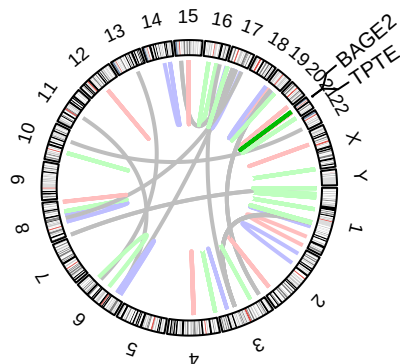


chromosome 21

p11.2



2 kbp
introns not to scale



No protein domains retained in fusion.

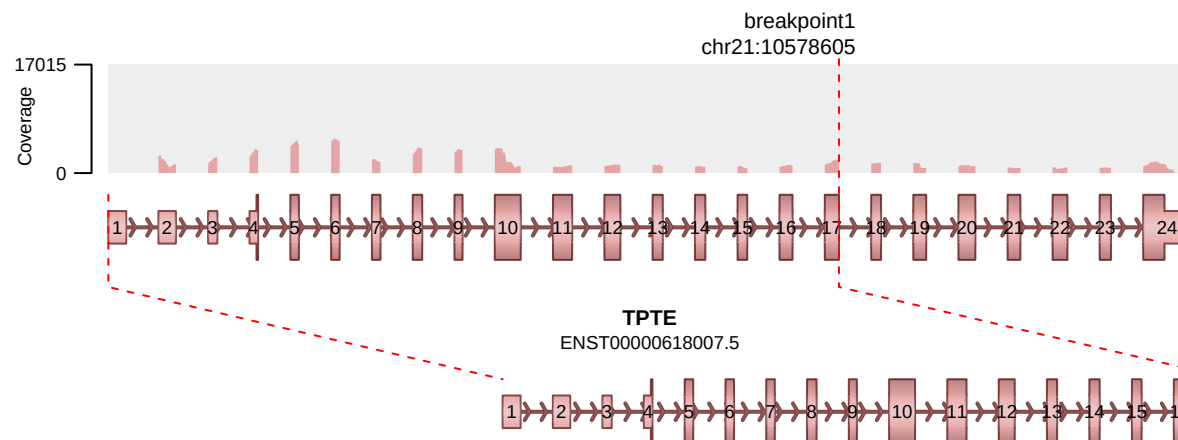
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 1

translocation deletion
duplication inversion

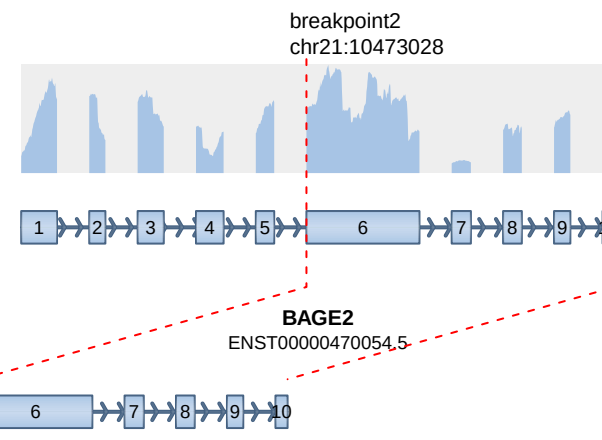
chromosome 21

p11.2

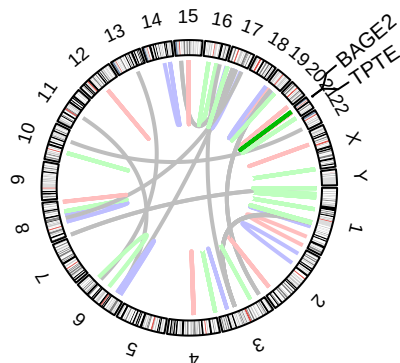


chromosome 21

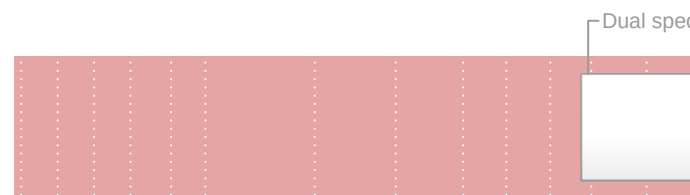
p11.2



2 kbp
introns not to scale



RETAINED PROTEIN DOMAINS
reading frame unclear



TPTE

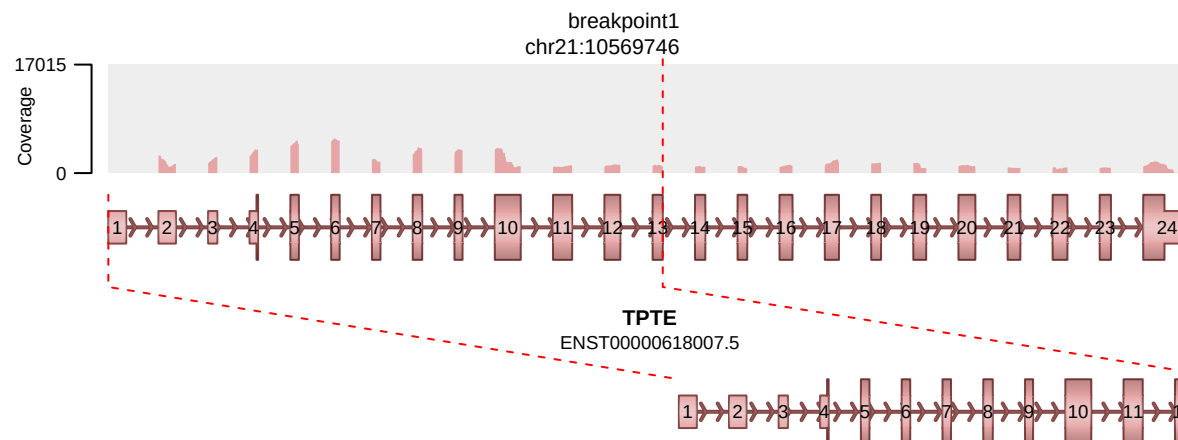
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 3

— translocation — deletion
— duplication — inversion

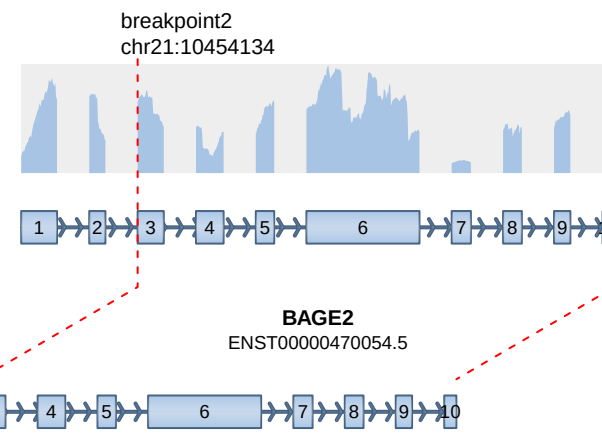
chromosome 21

p11.2

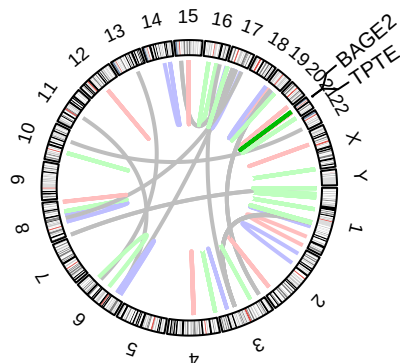


chromosome 21

p11.2



2 kbp
introns not to scale



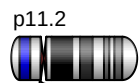
translocation
deletion
duplication
inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

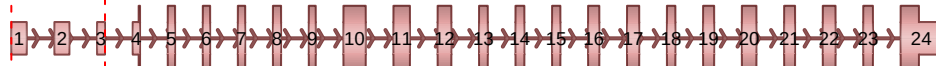
Split reads = 2
Discordant mates = 3

chromosome 21



breakpoint1

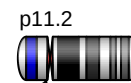
chr21:10527412



TPTE

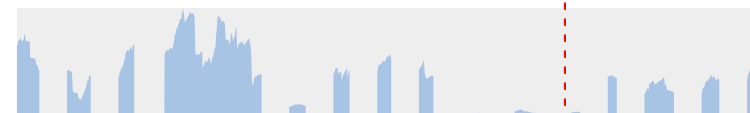
ENST00000618007.5

chromosome 21



breakpoint2

chr21:10498857

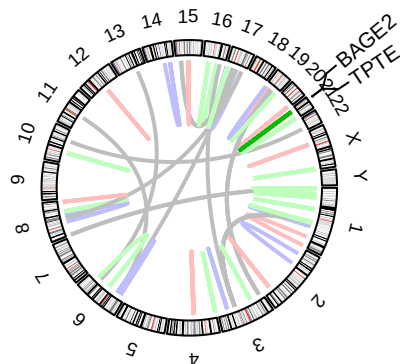


BAGE2

ENST00000496773.1



2 kbp
introns not to scale



No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 1

— translocation — deletion
— duplication — inversion

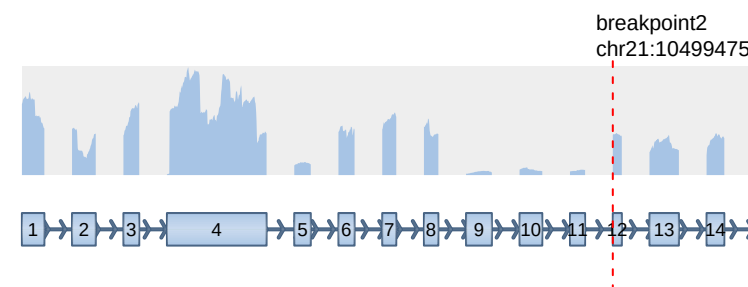
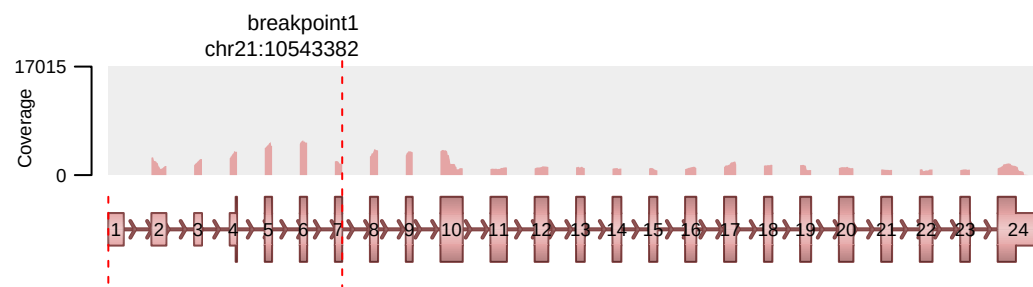
chromosome 21

p11.2



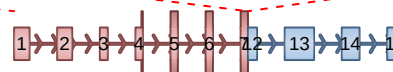
chromosome 21

p11.2

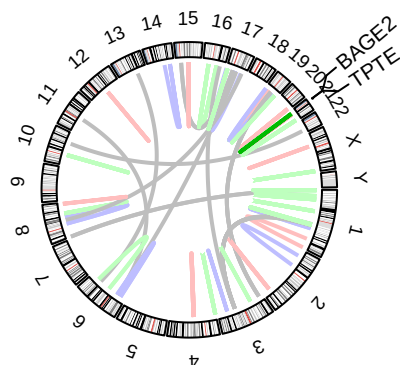


TPTE
ENST00000618007.5

BAGE2
ENST00000496773.1



2 kbp
introns not to scale



No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 1

translocation
deletion
duplication
inversion

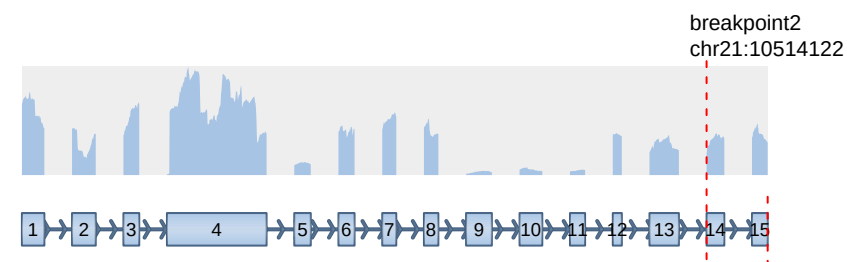
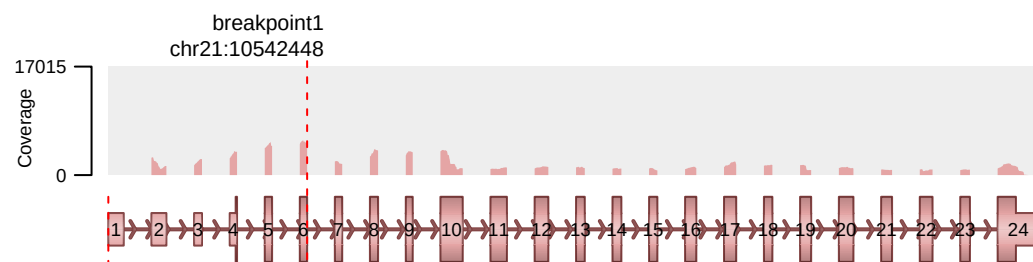
chromosome 21

p11.2



chromosome 21

p11.2

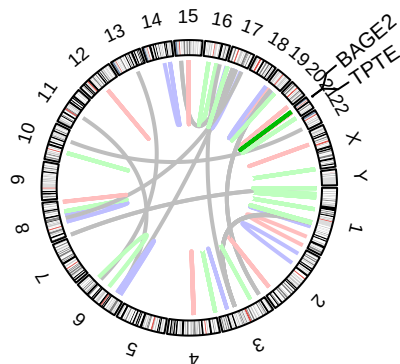


TPTE
ENST00000618007.5

BAGE2
ENST00000496773.1



2 kbp
introns not to scale



No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 1

— translocation — deletion
— duplication — inversion

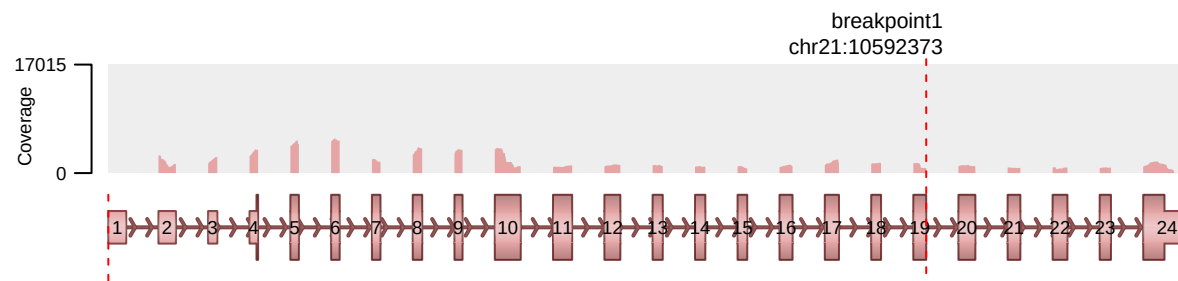
chromosome 21

p11.2

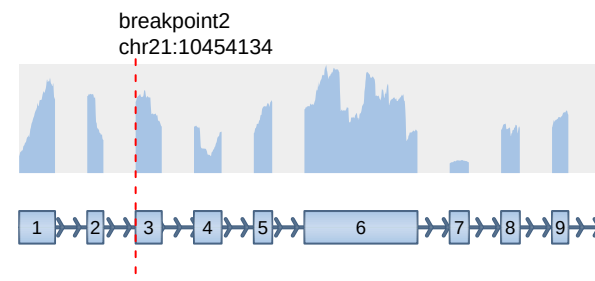
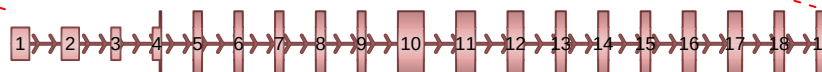


chromosome 21

p11.2



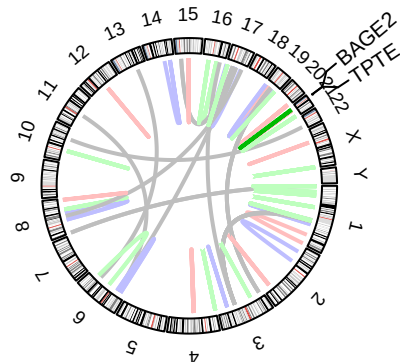
TPTE
ENST00000618007.5



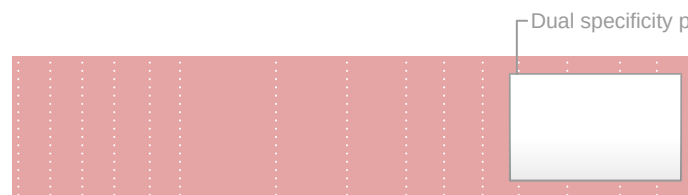
BAGE2
ENST00000470054.5



2 kbp
introns not to scale



RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 4

TPTE

— translocation — deletion
— duplication — inversion

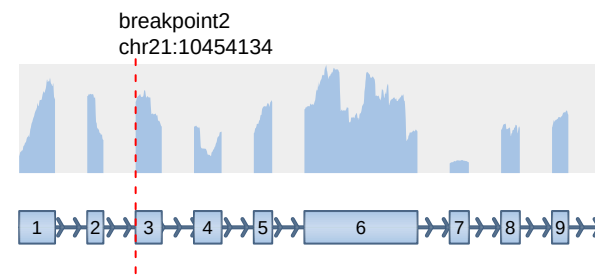
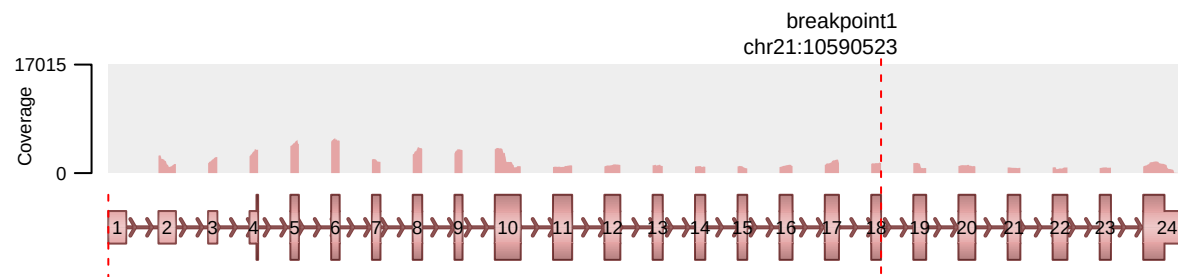
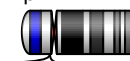
chromosome 21

p11.2



chromosome 21

p11.2

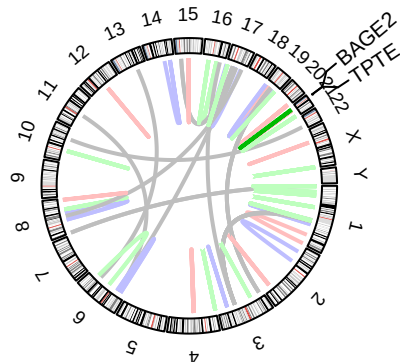


TPTE
ENST00000618007.5

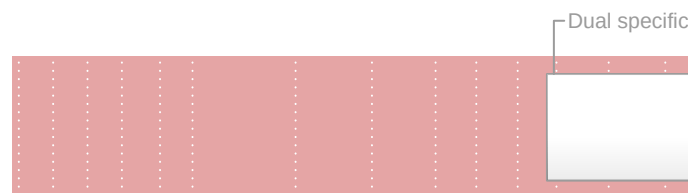
BAGE2
ENST00000470054.5



2 kbp
introns not to scale



RETAINED PROTEIN DOMAINS
reading frame unclear



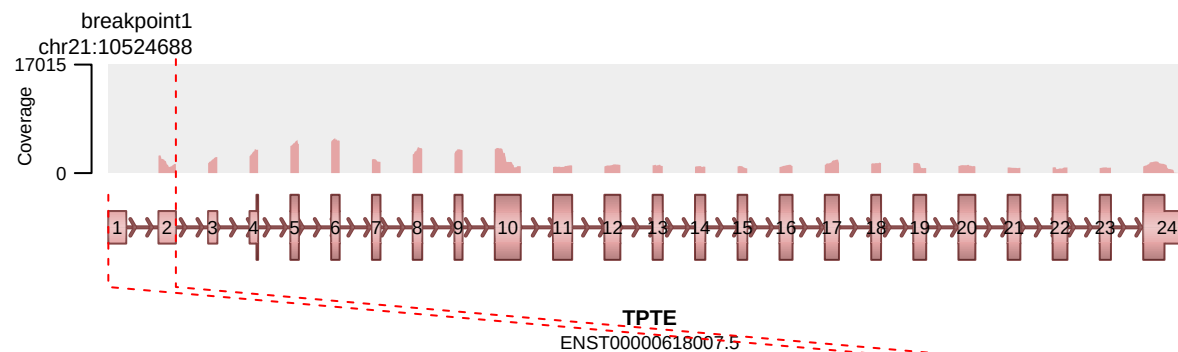
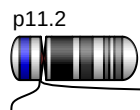
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 4

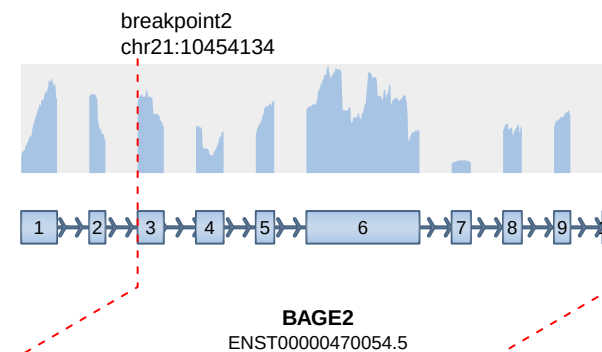
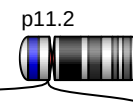
TPTE

— translocation — deletion
— duplication — inversion

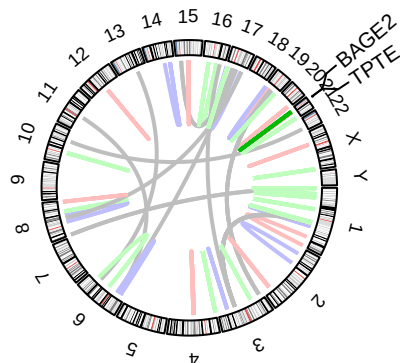
chromosome 21



chromosome 21



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

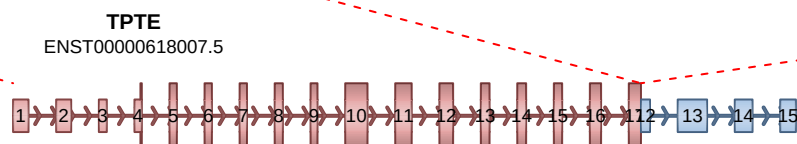
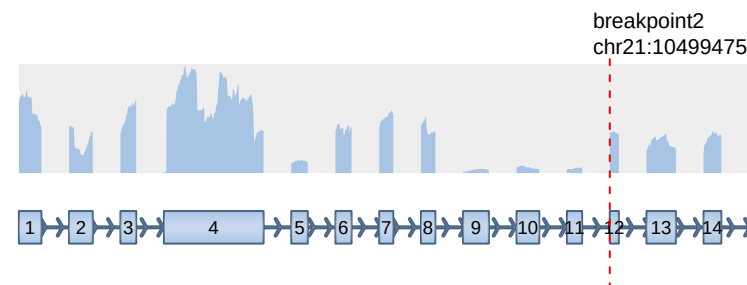
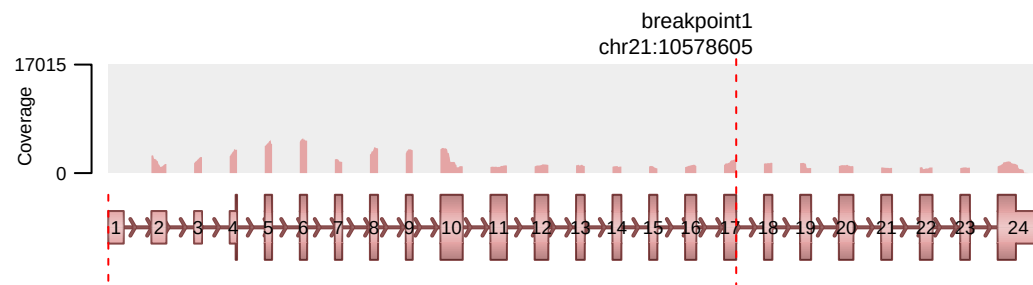
chromosome 21

p11.2



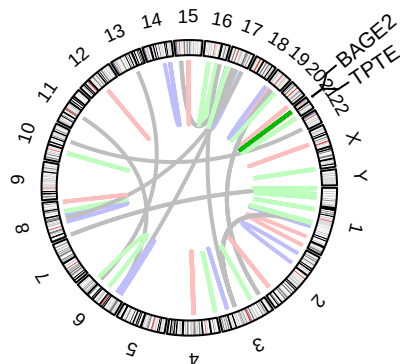
chromosome 21

p11.2

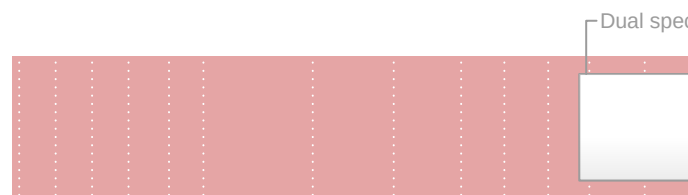


BAGE2
ENST00000496773.1

2 kbp
introns not to scale



RETAINED PROTEIN DOMAINS
reading frame unclear



TPTE

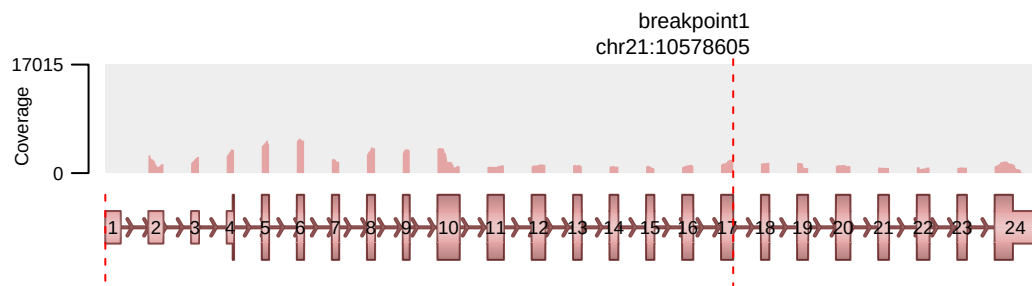
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 2

— translocation — deletion
— duplication — inversion

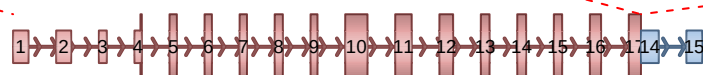
chromosome 21

p11.2



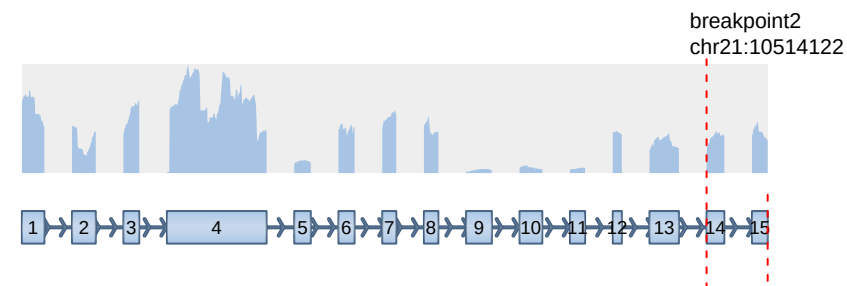
TPTE

ENST00000618007.5



chromosome 21

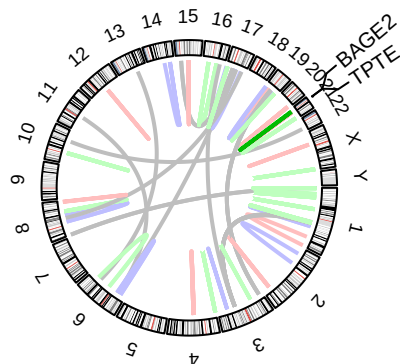
p11.2



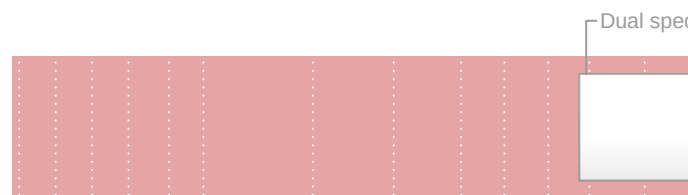
BAGE2

ENST00000496773.1

2 kbp
introns not to scale



RETAINED PROTEIN DOMAINS
reading frame unclear



Dual specificity phosphatase, catalytic domain

SUPPORTING READ COUNT

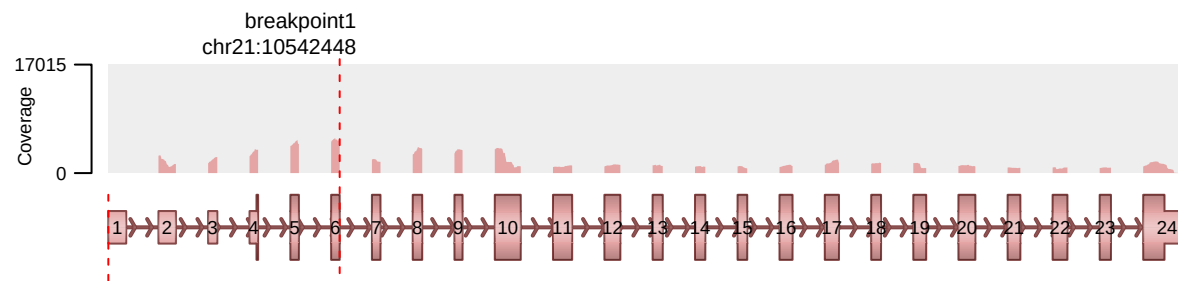
Split reads = 1
Discordant mates = 2

TPTE

— translocation — deletion
— duplication — inversion

chromosome 21

p11.2

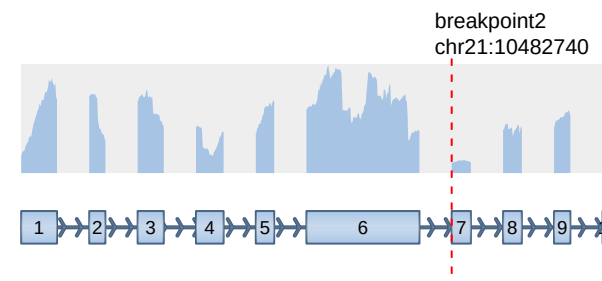


TPTE

ENST00000618007.5

chromosome 21

p11.2

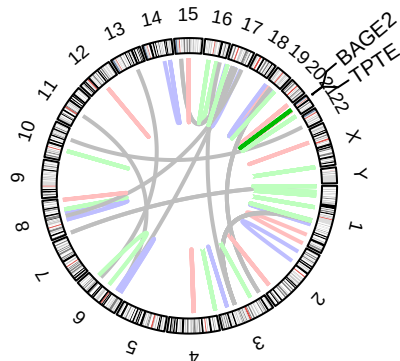


BAGE2

ENST00000470054.5



2 kbp
introns not to scale



No protein domains retained in fusion.

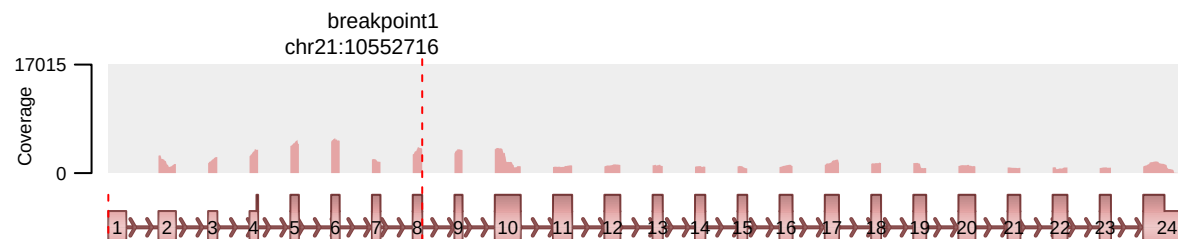
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 2

— translocation — deletion
— duplication — inversion

chromosome 21

p11.2

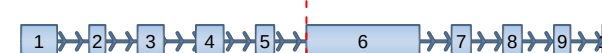
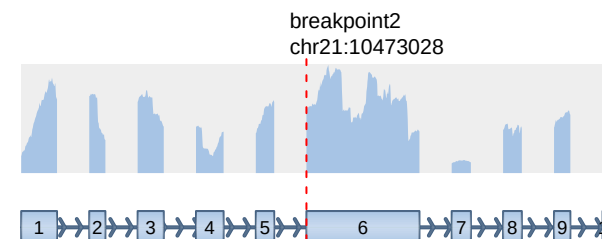


TPTE

ENST00000618007.5

chromosome 21

p11.2

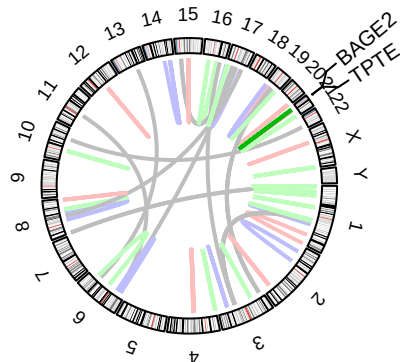


BAGE2

ENST00000470054.5



2 kbp
introns not to scale



— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 2

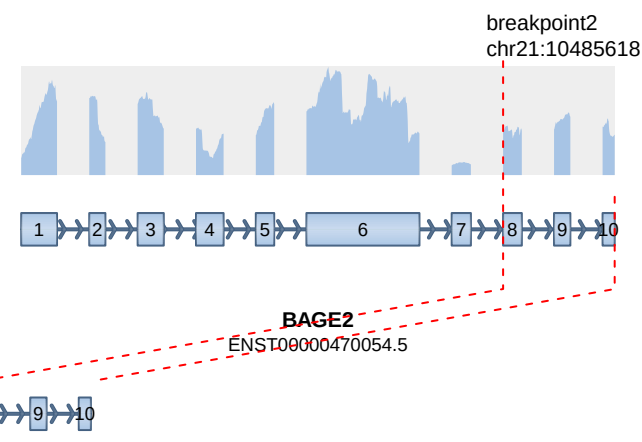
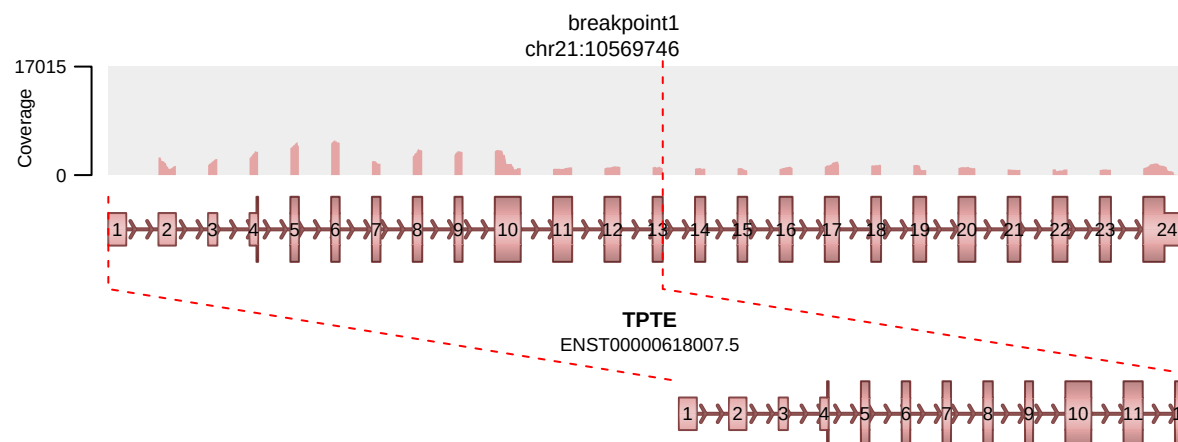
chromosome 21

p11.2

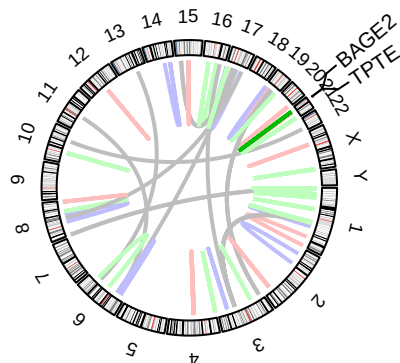


chromosome 21

p11.2



2 kbp
introns not to scale



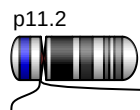
No protein domains retained in fusion.

SUPPORTING READ COUNT

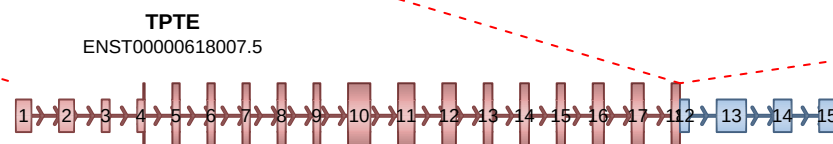
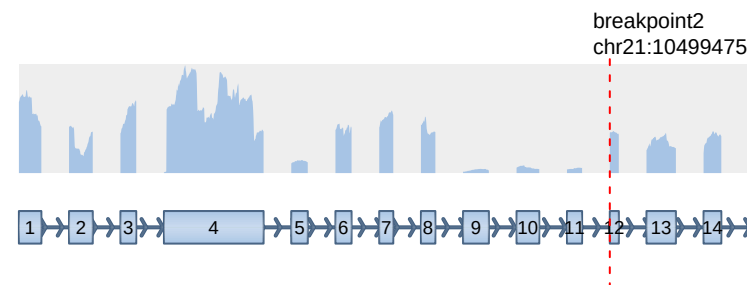
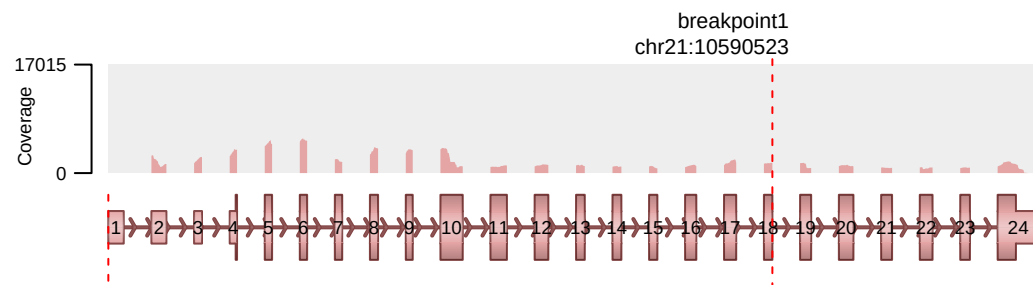
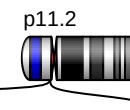
Split reads = 1
Discordant mates = 2

translocation deletion
duplication inversion

chromosome 21

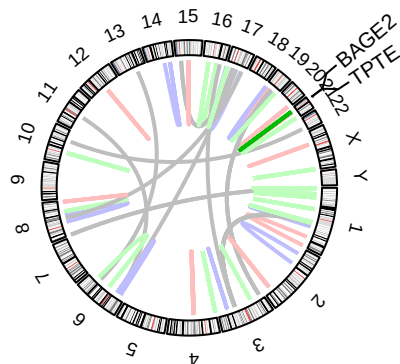


chromosome 21

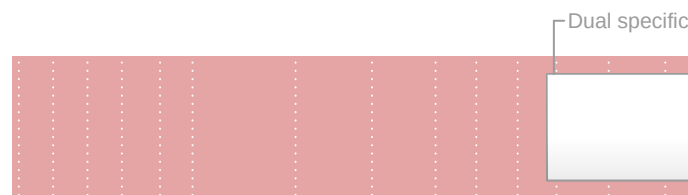


BAGE2
ENST00000496773.1

2 kbp
introns not to scale



RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

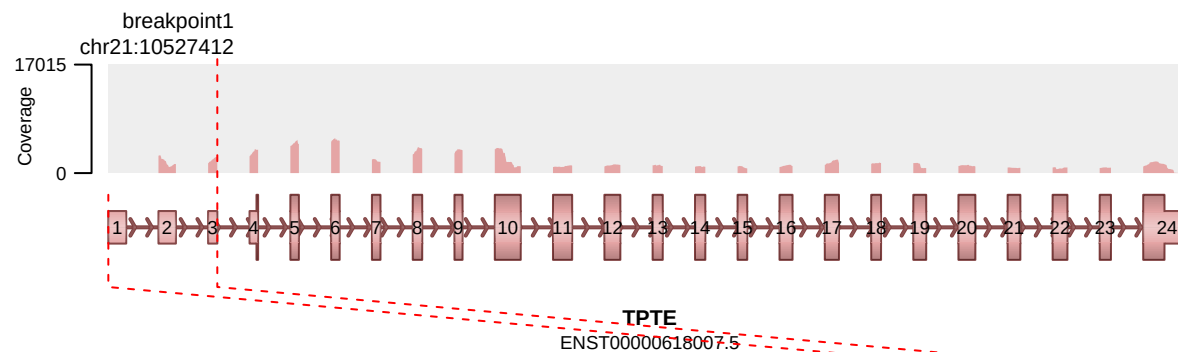
Split reads = 1
Discordant mates = 2

TPTE

— translocation — deletion
— duplication — inversion

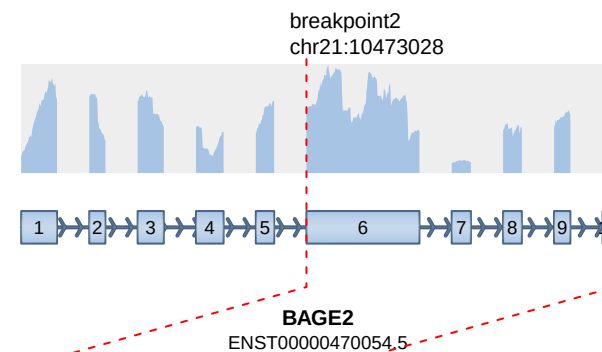
chromosome 21

p11.2

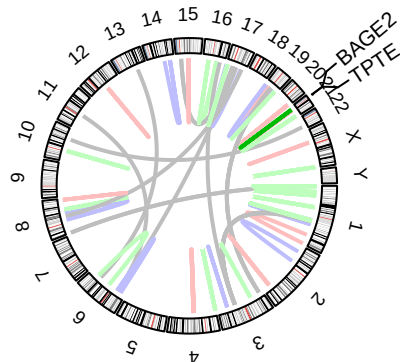


chromosome 21

p11.2



2 kbp
introns not to scale



No coding regions retained in fusion transcript.

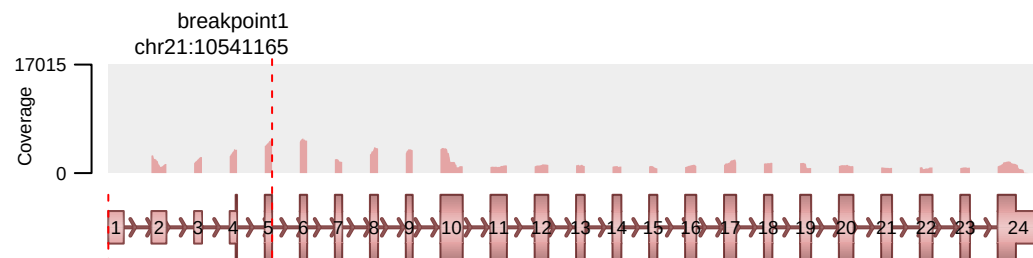
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

translocation deletion
duplication inversion

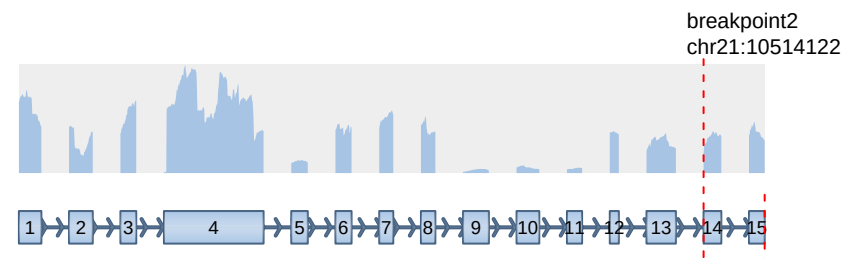
chromosome 21

p11.2



chromosome 21

p11.2

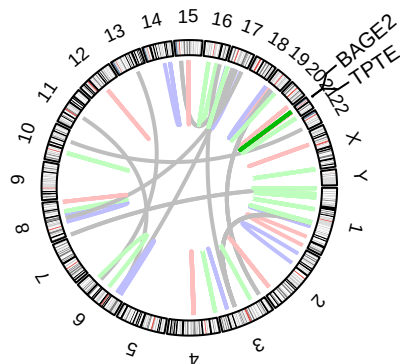


TPTE
ENST00000618007.5

BAGE2
ENST00000496773.1



2 kbp
introns not to scale



No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

— translocation — deletion
— duplication — inversion

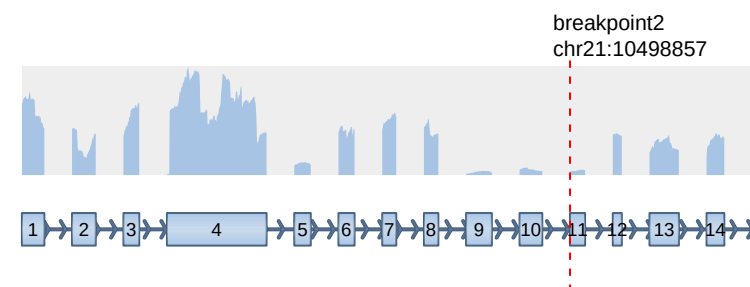
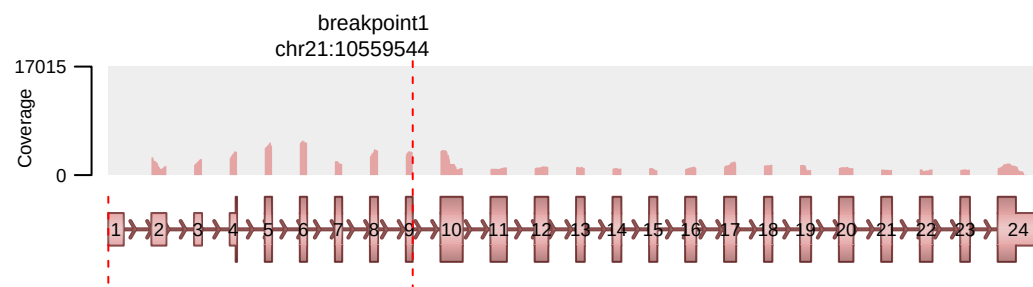
chromosome 21

p11.2



chromosome 21

p11.2

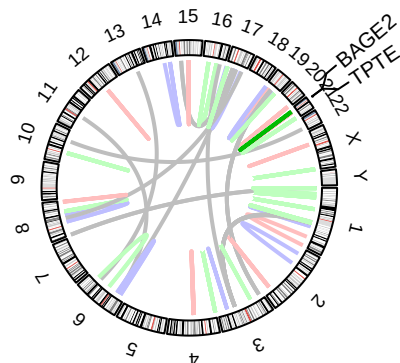


TPTE
ENST00000618007.5

BAGE2
ENST00000496773.1



2 kbp
introns not to scale



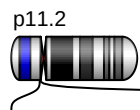
No protein domains retained in fusion.

SUPPORTING READ COUNT

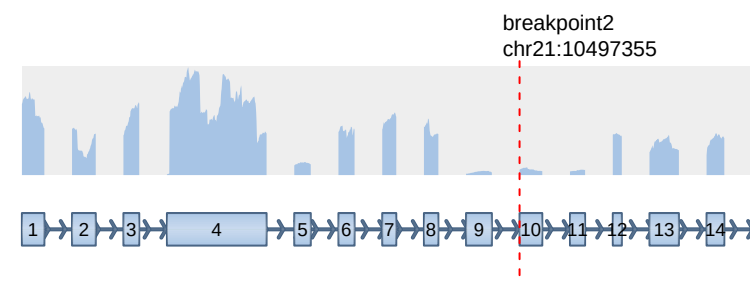
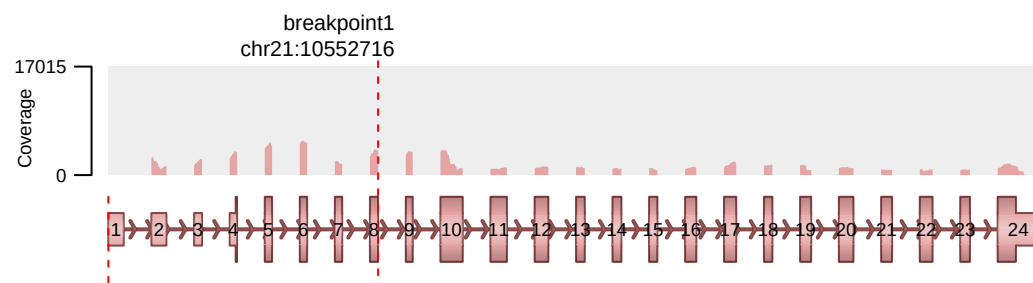
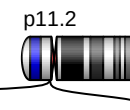
Split reads = 1
Discordant mates = 1

— translocation — deletion
— duplication — inversion

chromosome 21

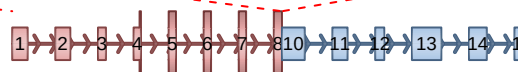


chromosome 21

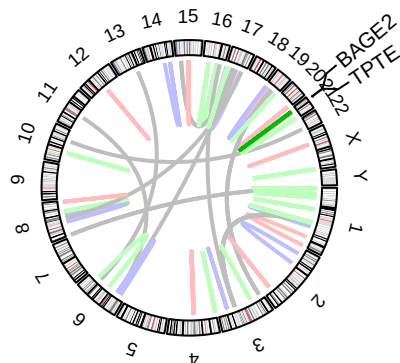


TPTE
ENST00000618007.5

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

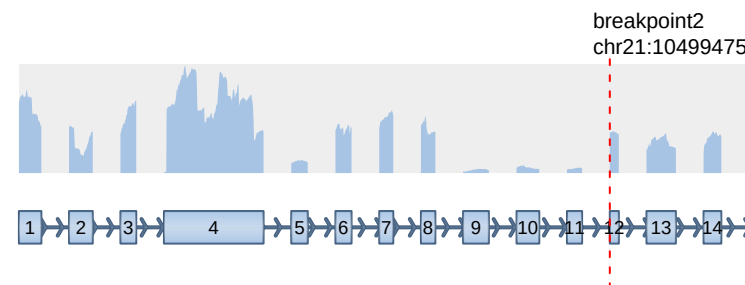
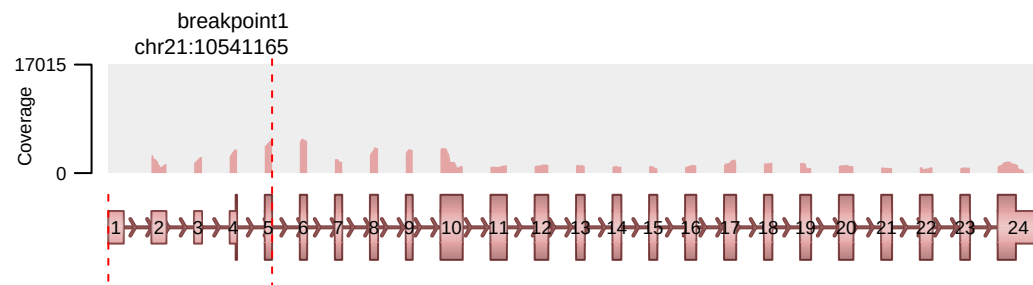
chromosome 21

p11.2



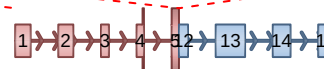
chromosome 21

p11.2

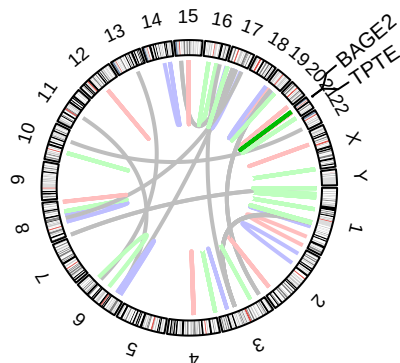


TPTE
ENST00000618007.5

BAGE2
ENST00000496773.1



2 kbp
introns not to scale



No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

— translocation — deletion
— duplication — inversion

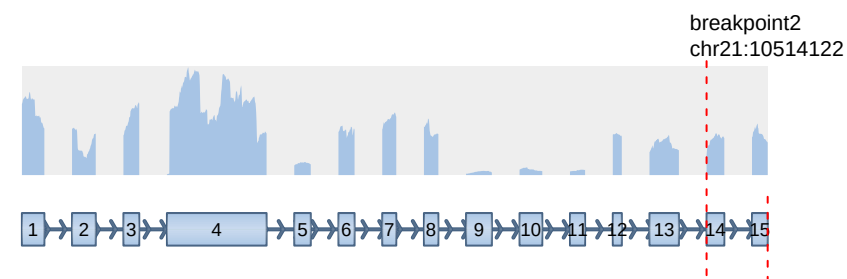
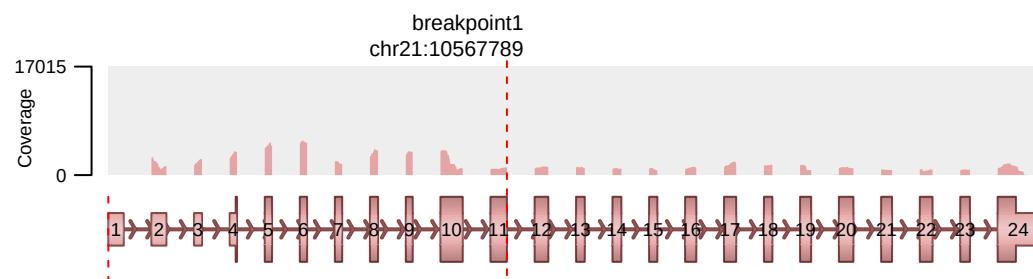
chromosome 21

p11.2



chromosome 21

p11.2



TPTE

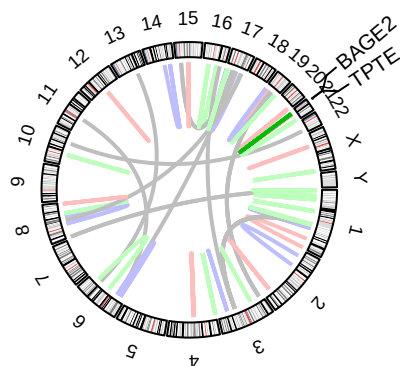
ENST00000618007.5

BAGE2

ENST00000496773.1



2 kbp
introns not to scale



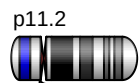
No protein domains retained in fusion.

SUPPORTING READ COUNT

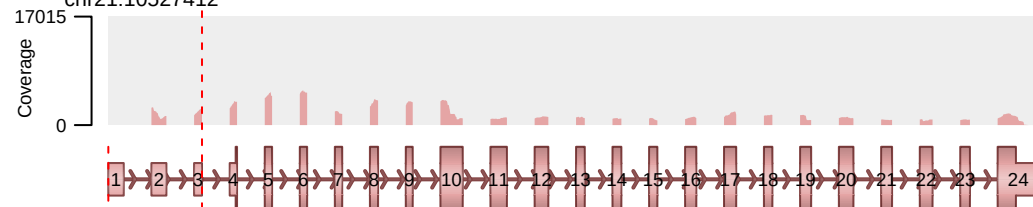
Split reads = 1
Discordant mates = 1

translocation deletion
duplication inversion

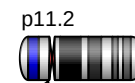
chromosome 21



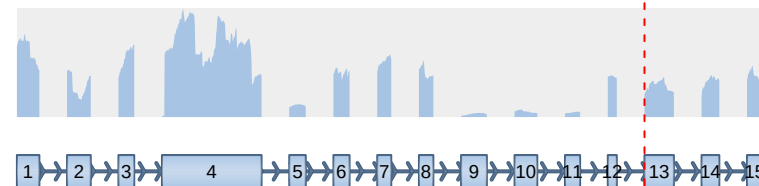
breakpoint1
chr21:10527412



chromosome 21



breakpoint2
chr21:10500807

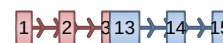


TPTE

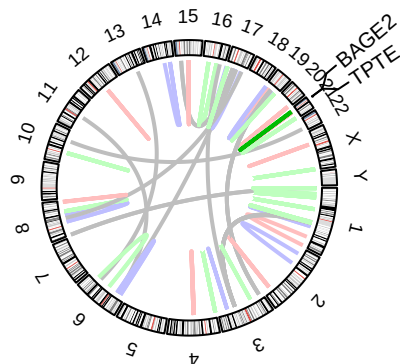
ENST00000618007.5

BAGE2

ENST00000496773.1



2 kbp
introns not to scale



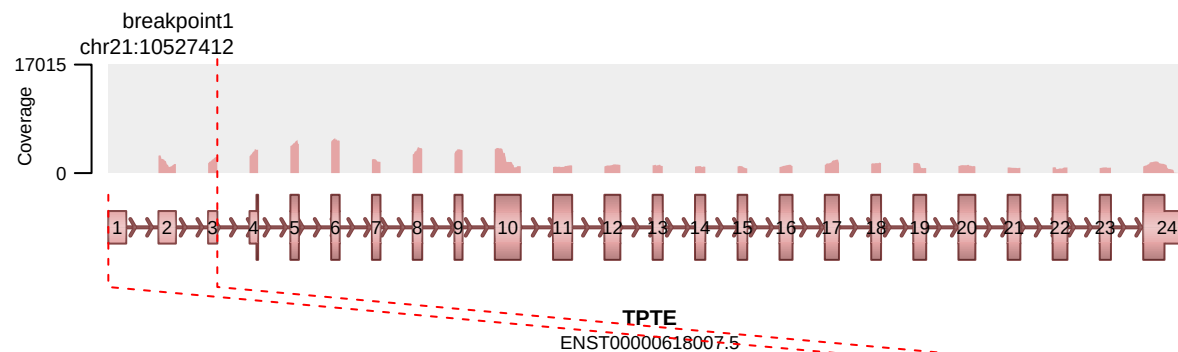
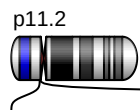
No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

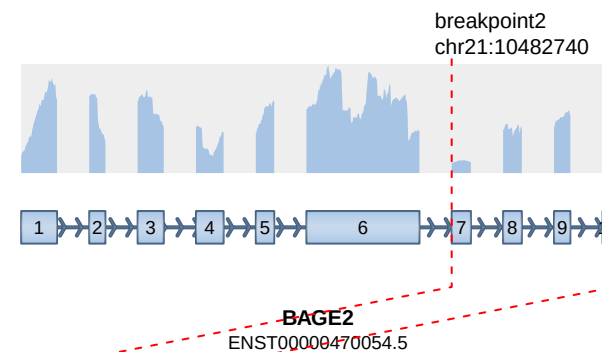
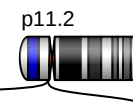
Split reads = 1
Discordant mates = 1

translocation deletion
duplication inversion

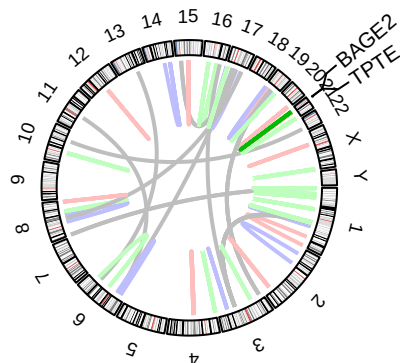
chromosome 21



chromosome 21



2 kbp
introns not to scale



No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

— translocation — deletion
— duplication — inversion

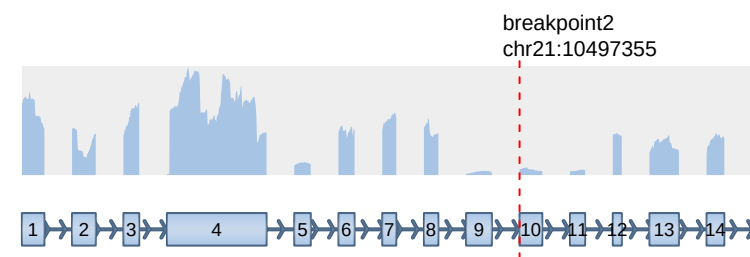
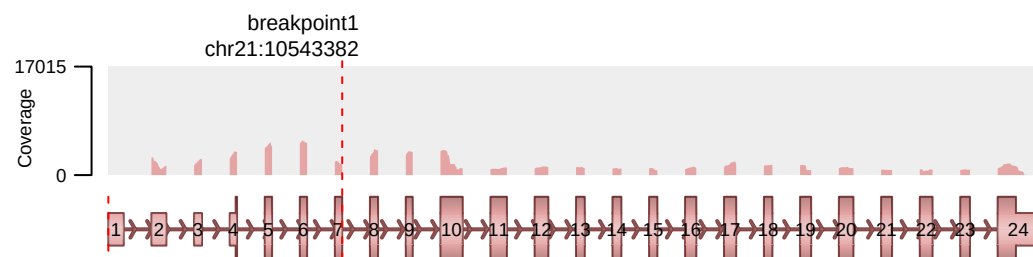
chromosome 21

p11.2



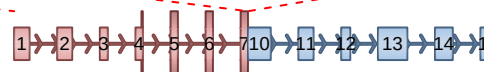
chromosome 21

p11.2

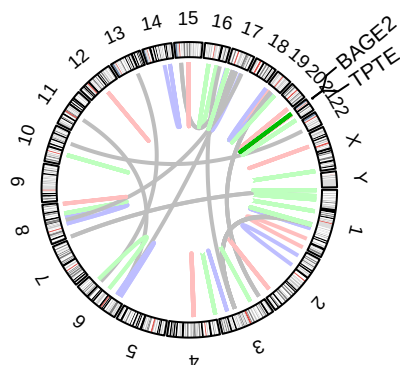


TPTE
ENST00000618007.5

BAGE2
ENST00000496773.1



2 kbp
introns not to scale



No protein domains retained in fusion.

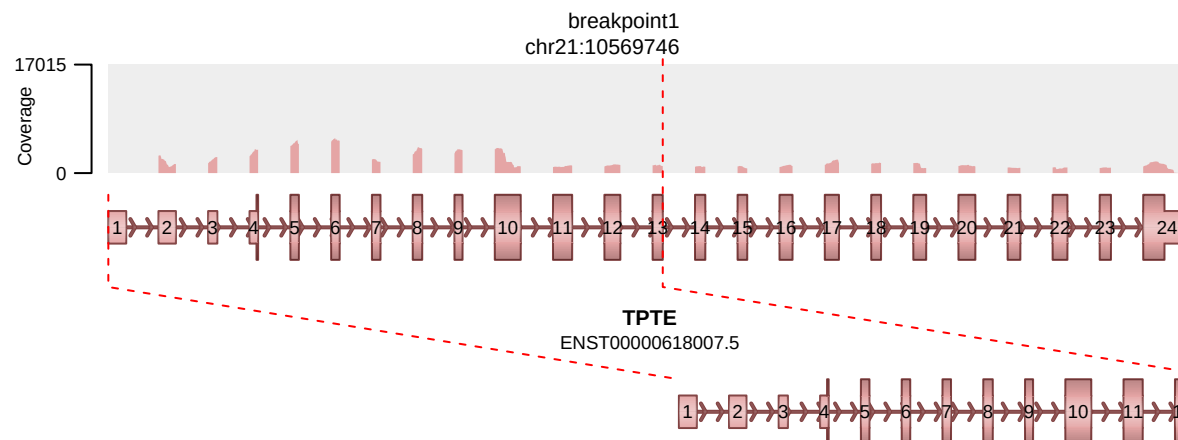
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

— translocation — deletion
— duplication — inversion

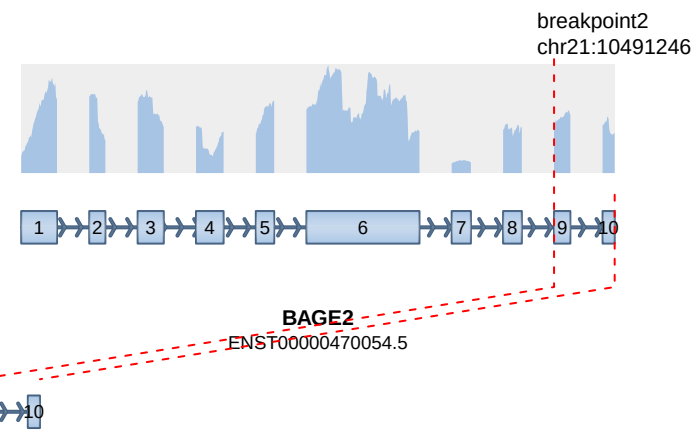
chromosome 21

p11.2

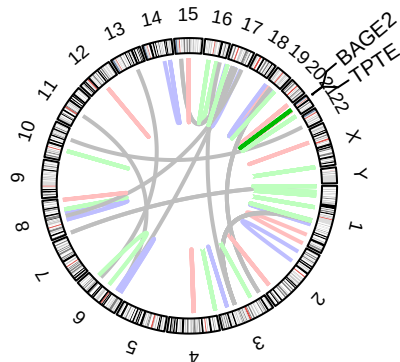


chromosome 21

p11.2



2 kbp
introns not to scale



— translocation — deletion
— duplication — inversion

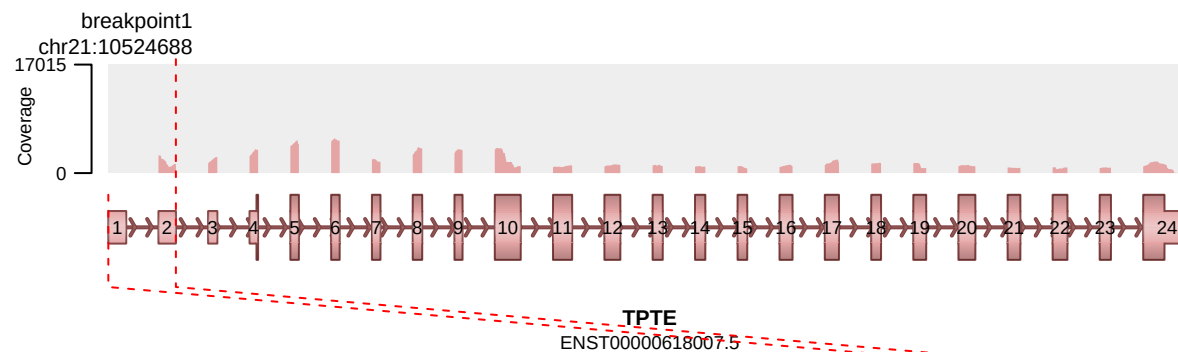
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

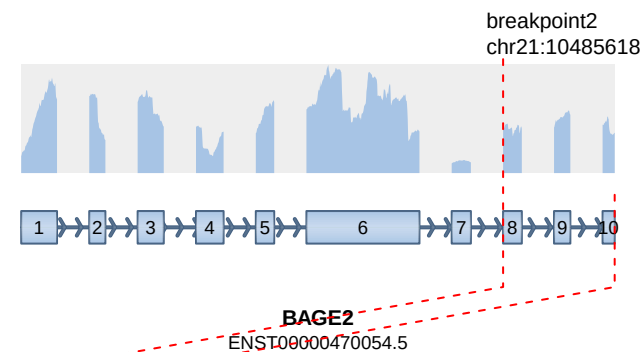
chromosome 21

p11.2

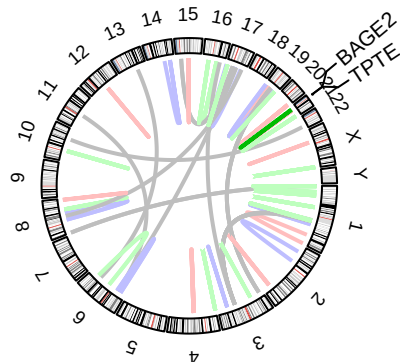


chromosome 21

p11.2



2 kbp
introns not to scale



translocation deletion
duplication inversion

No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

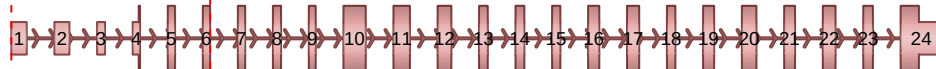
Split reads = 1
Discordant mates = 0

chromosome 21

p11.2



breakpoint1
chr21:10542448



TPTE

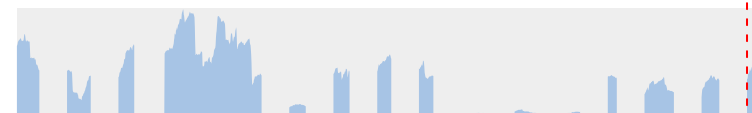
ENST00000618007.5

chromosome 21

p11.2



breakpoint2
chr21:10516318

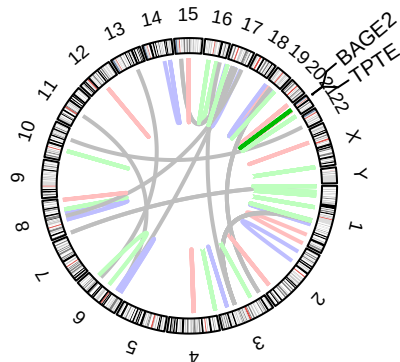


BAGE2

ENST00000496773.1



2 kbp
introns not to scale

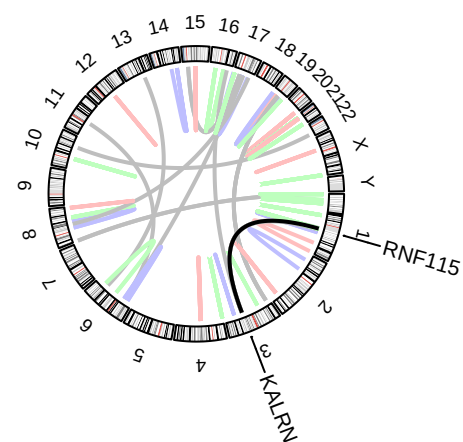
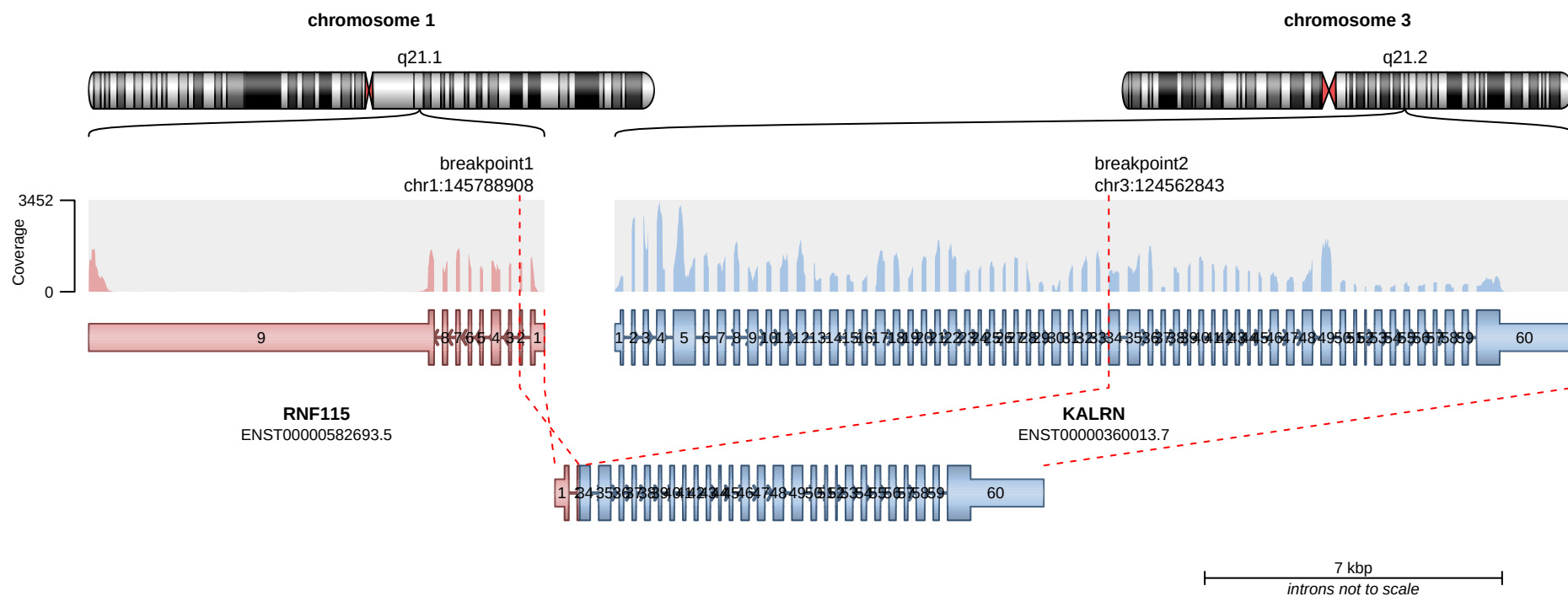


No protein domains retained in fusion.

SUPPORTING READ COUNT

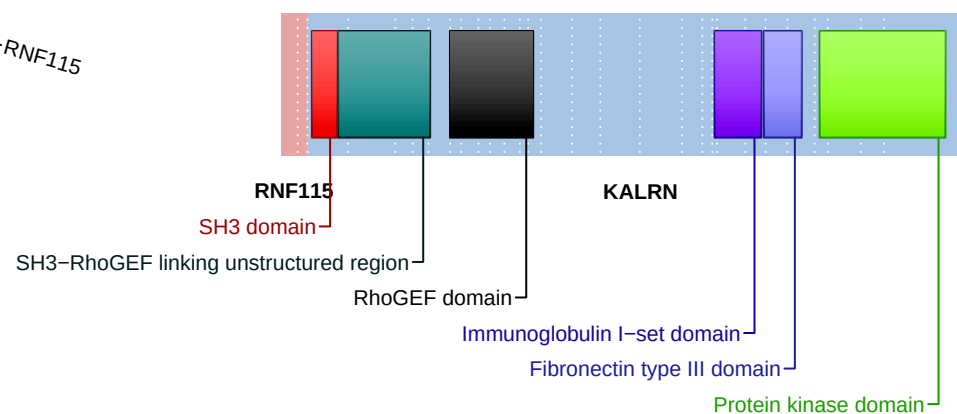
Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



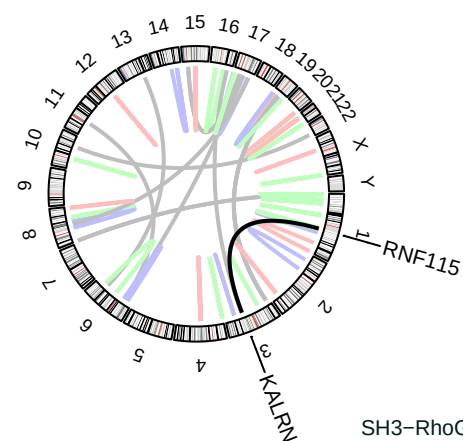
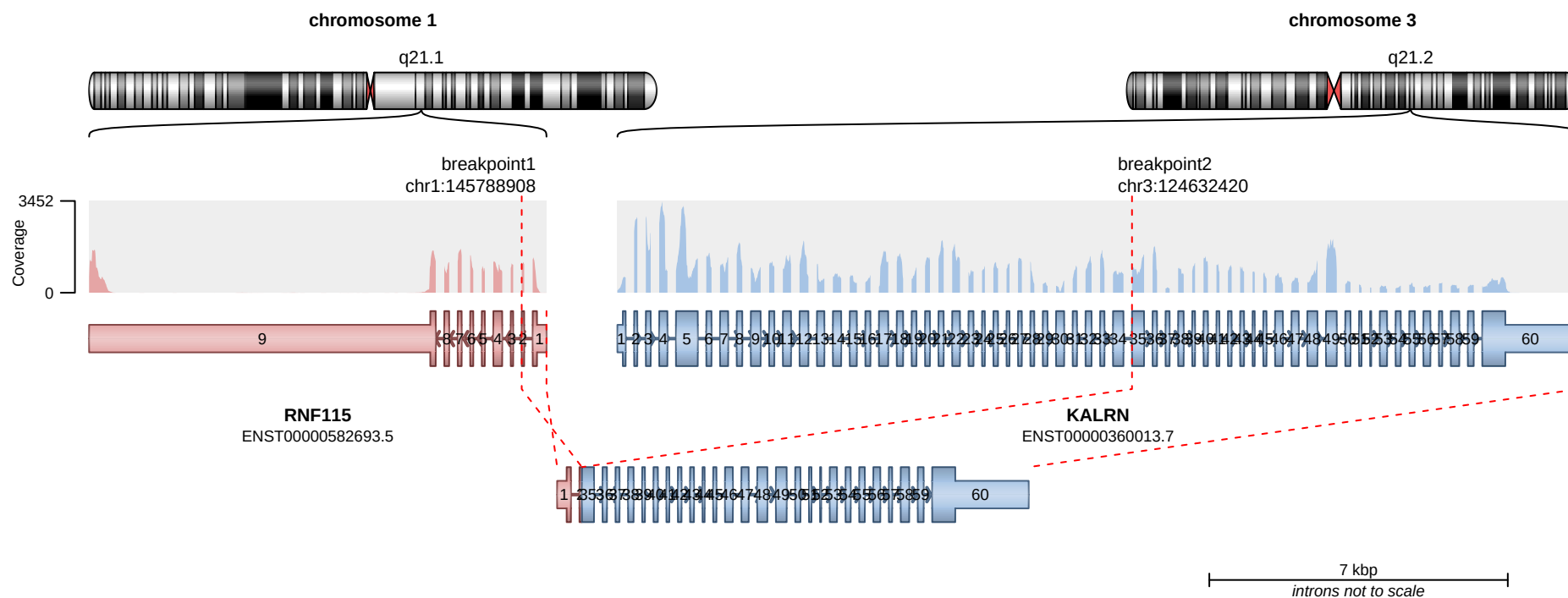
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS reading frame unclear



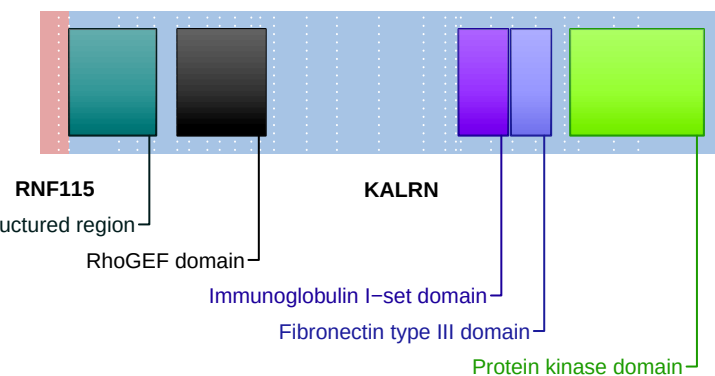
SUPPORTING READ COUNT

Split reads = 36
Discordant mates = 2



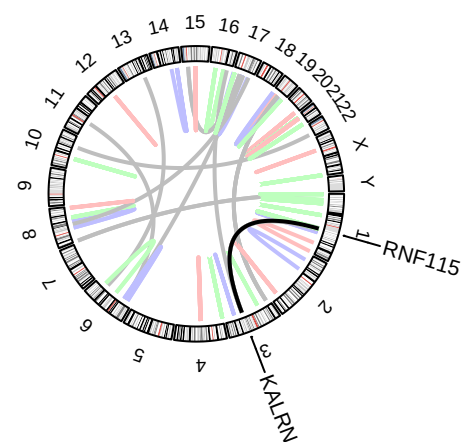
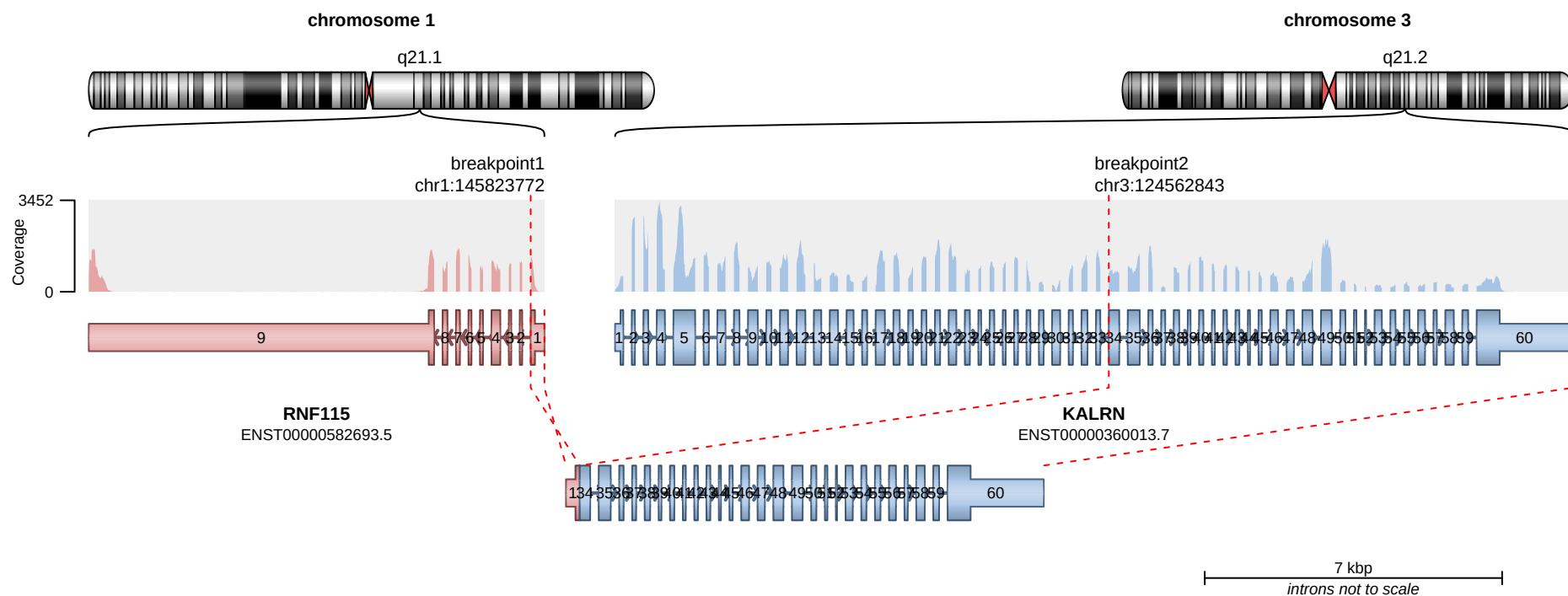
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS reading frame unclear



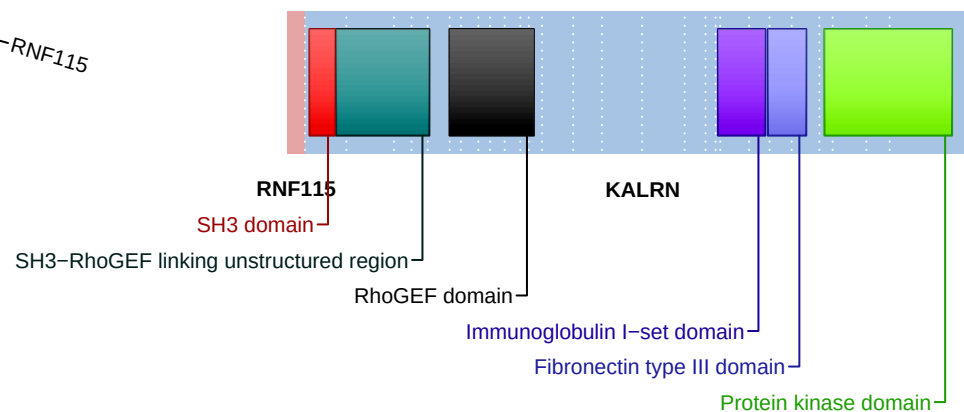
SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 0



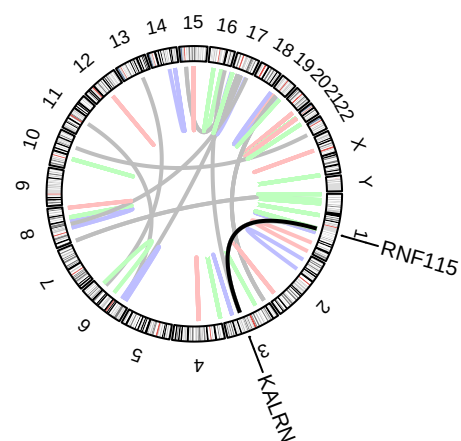
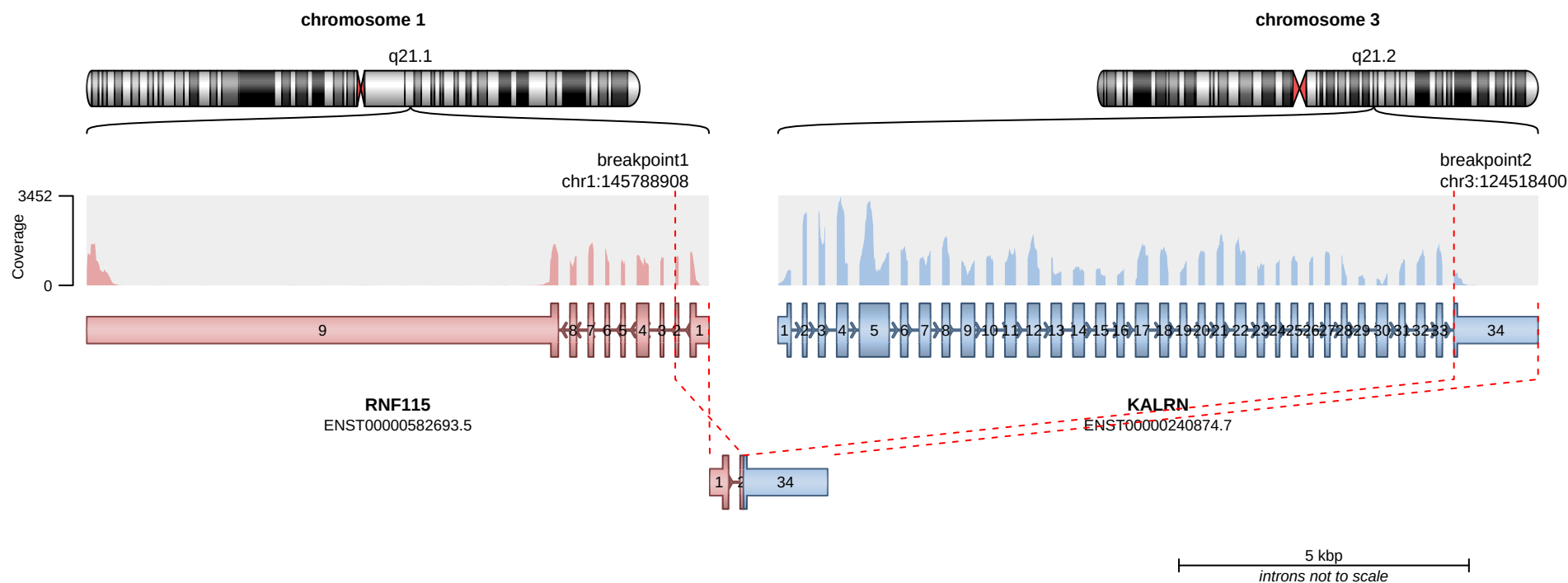
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS reading frame unclear



SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0

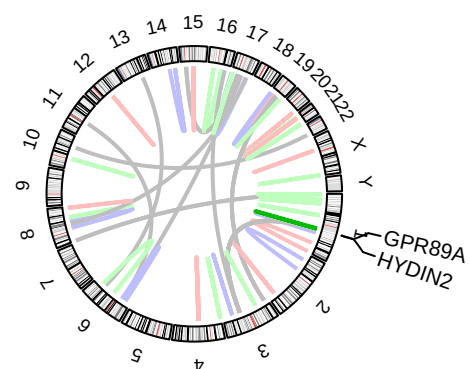
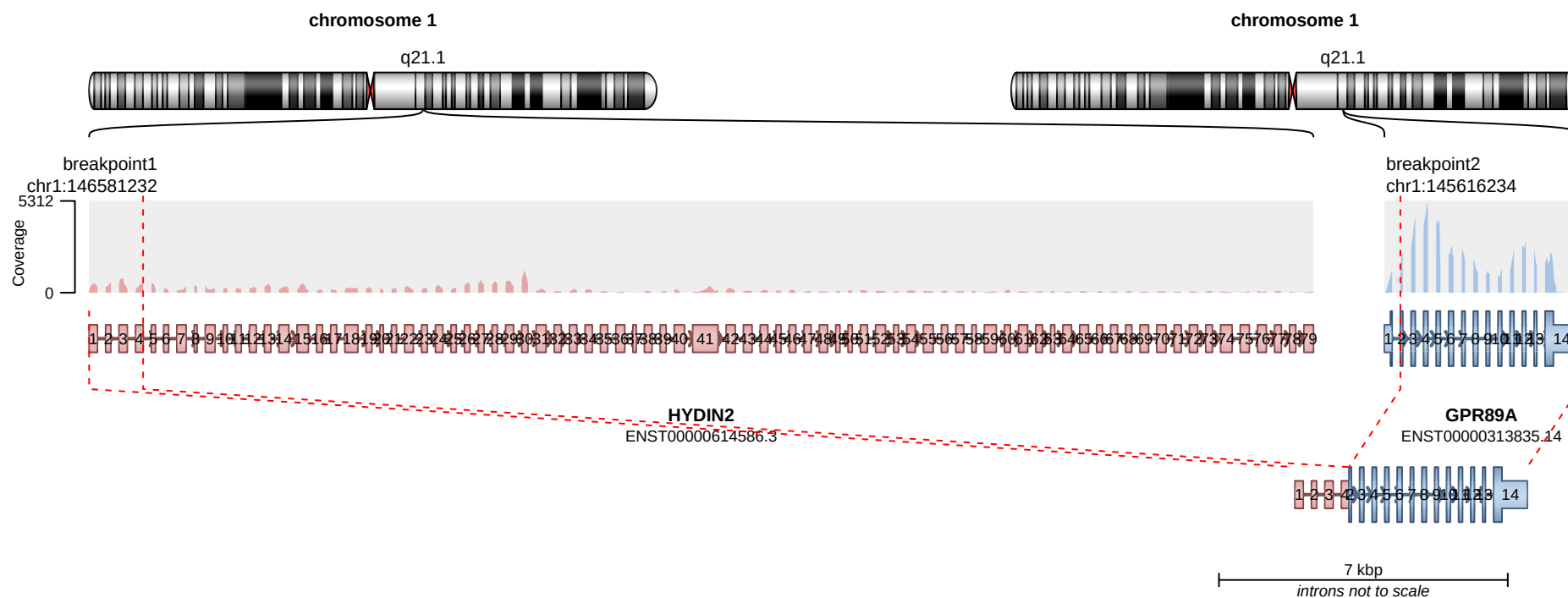


— translocation — deletion
— duplication — inversion

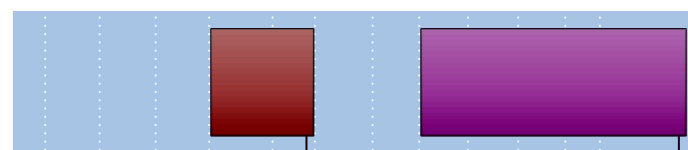
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 2



RETAINED PROTEIN DOMAINS reading frame unclear



GPR89A

The Golgi pH Regulator (GPHR) Family N-terminal

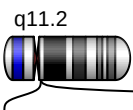
Abcissic acid G-protein coupled receptor

SUPPORTING READ COUNT

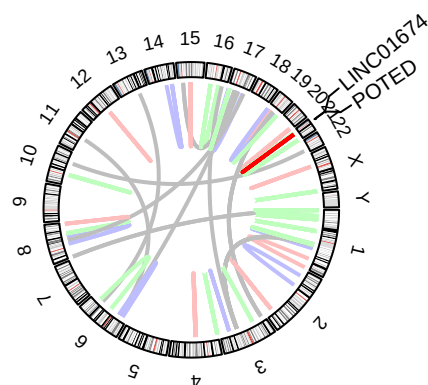
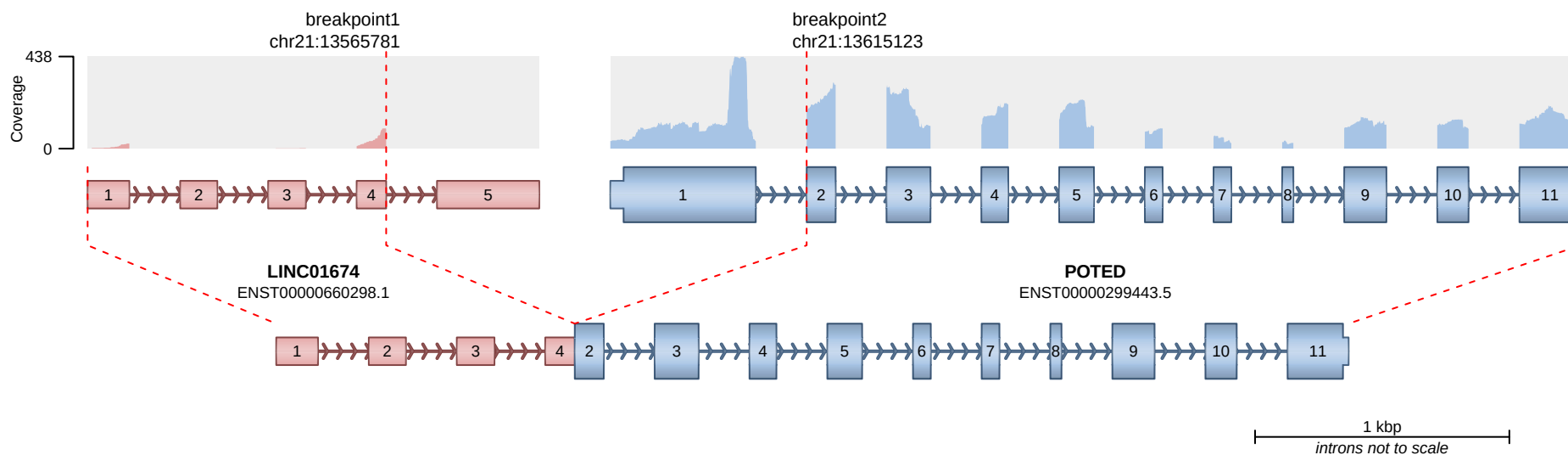
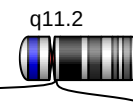
Split reads = 34
Discordant mates = 7

— translocation — deletion
— duplication — inversion

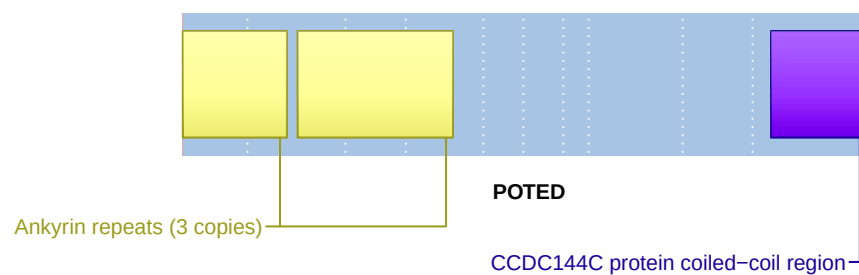
chromosome 21



chromosome 21



RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 34
Discordant mates = 3

— translocation — deletion
— duplication — inversion

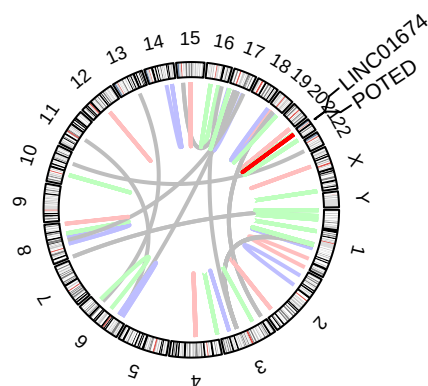
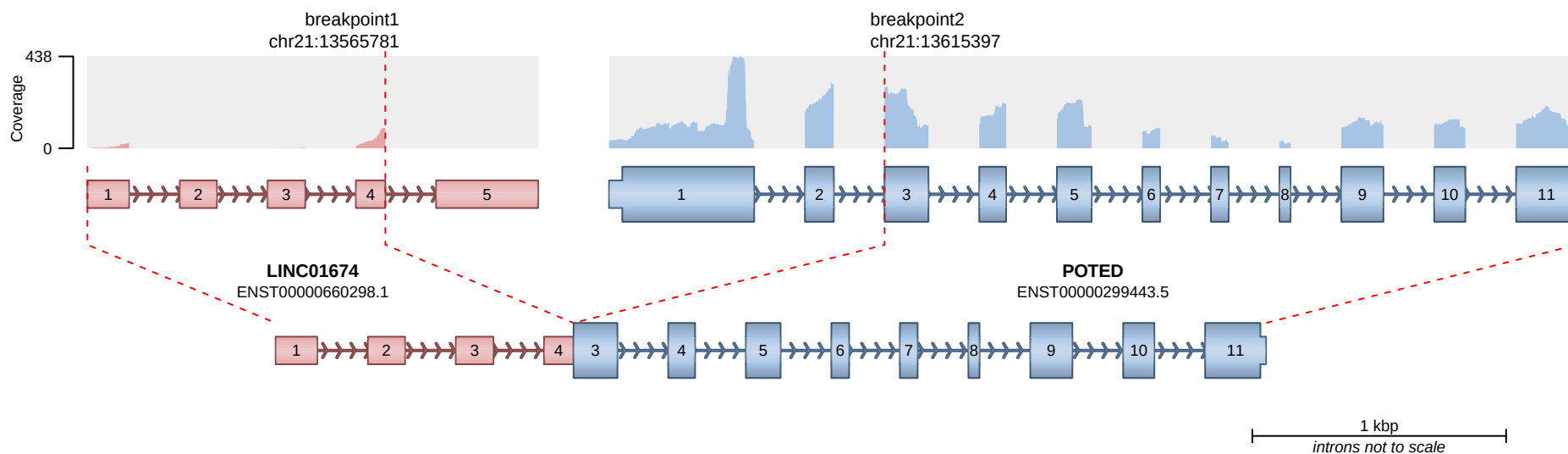
chromosome 21

q11.2

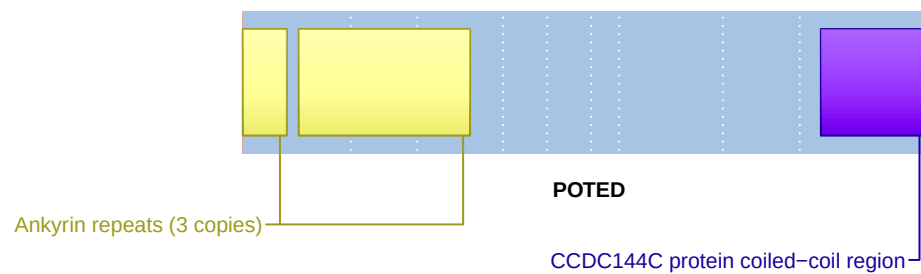


chromosome 21

q11.2



RETAINED PROTEIN DOMAINS
reading frame unclear

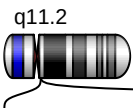


SUPPORTING READ COUNT

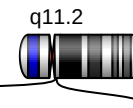
Split reads = 10
Discordant mates = 1

— translocation — deletion
— duplication — inversion

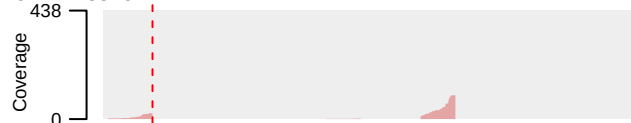
chromosome 21



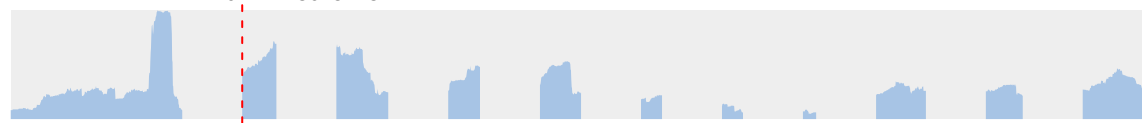
chromosome 21



breakpoint1
chr21:13516271



breakpoint2
chr21:13615123

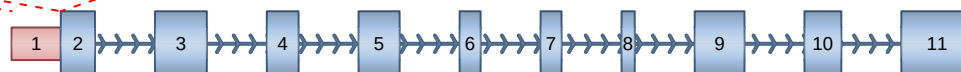


LINC01674

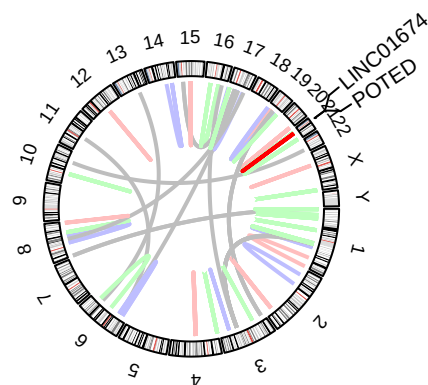
ENST00000660298.1

POTED

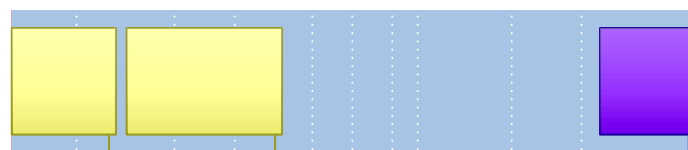
ENST00000299443.5



1 kbp
introns not to scale



RETAINED PROTEIN DOMAINS
reading frame unclear



Ankyrin repeats (3 copies)

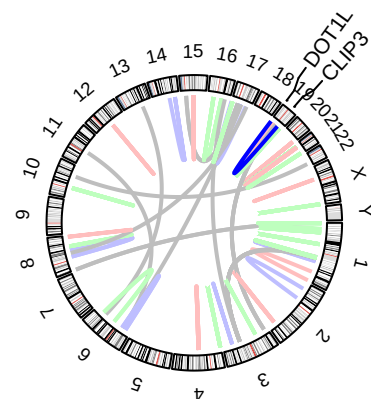
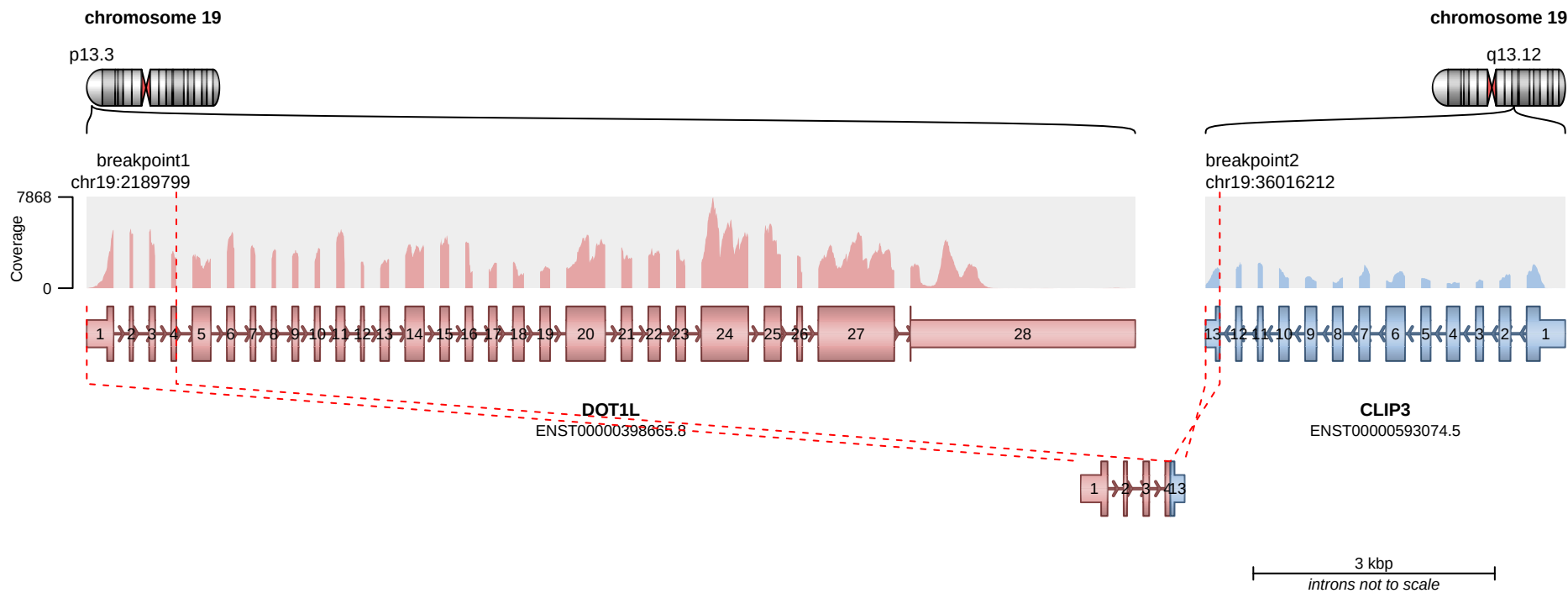
POTED

CCDC144C protein coiled-coil region

SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0

— translocation — deletion
— duplication — inversion

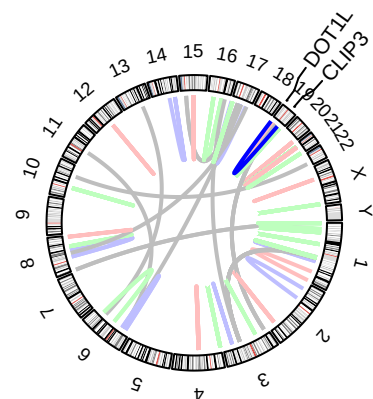
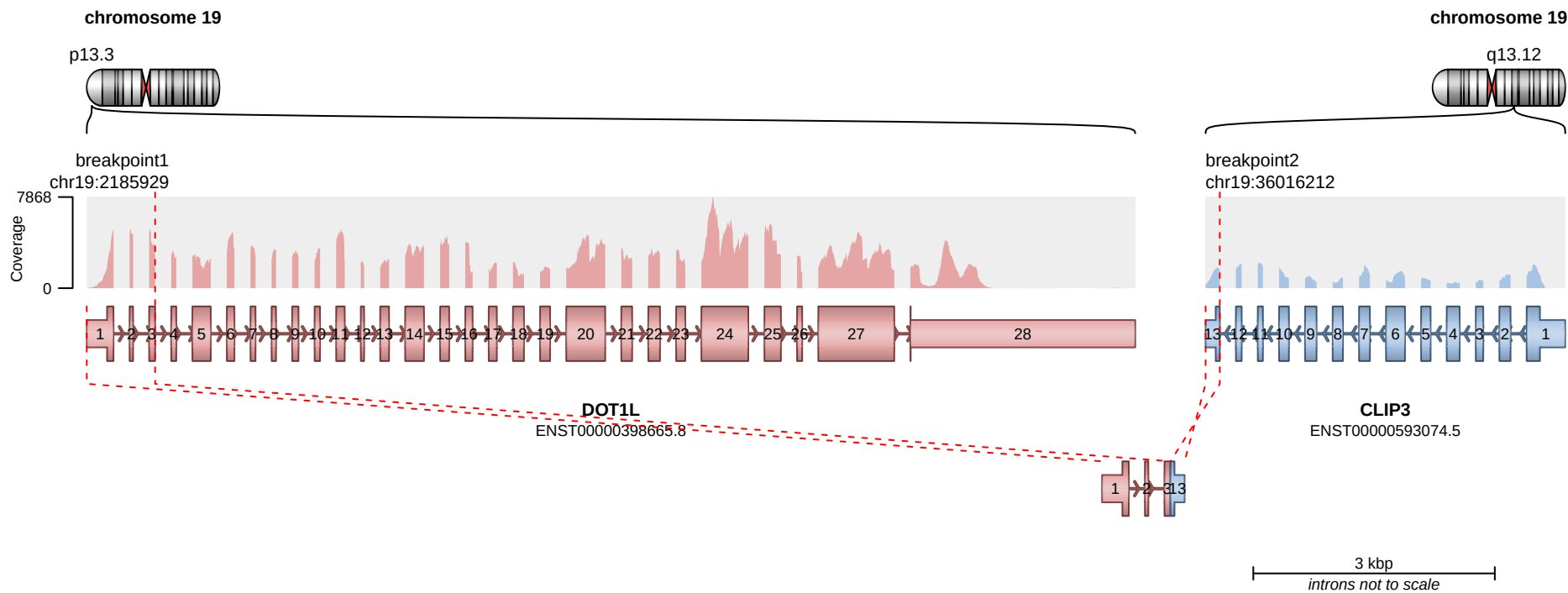


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 33
Discordant mates = 4

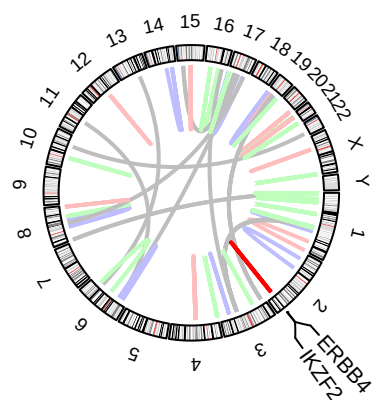
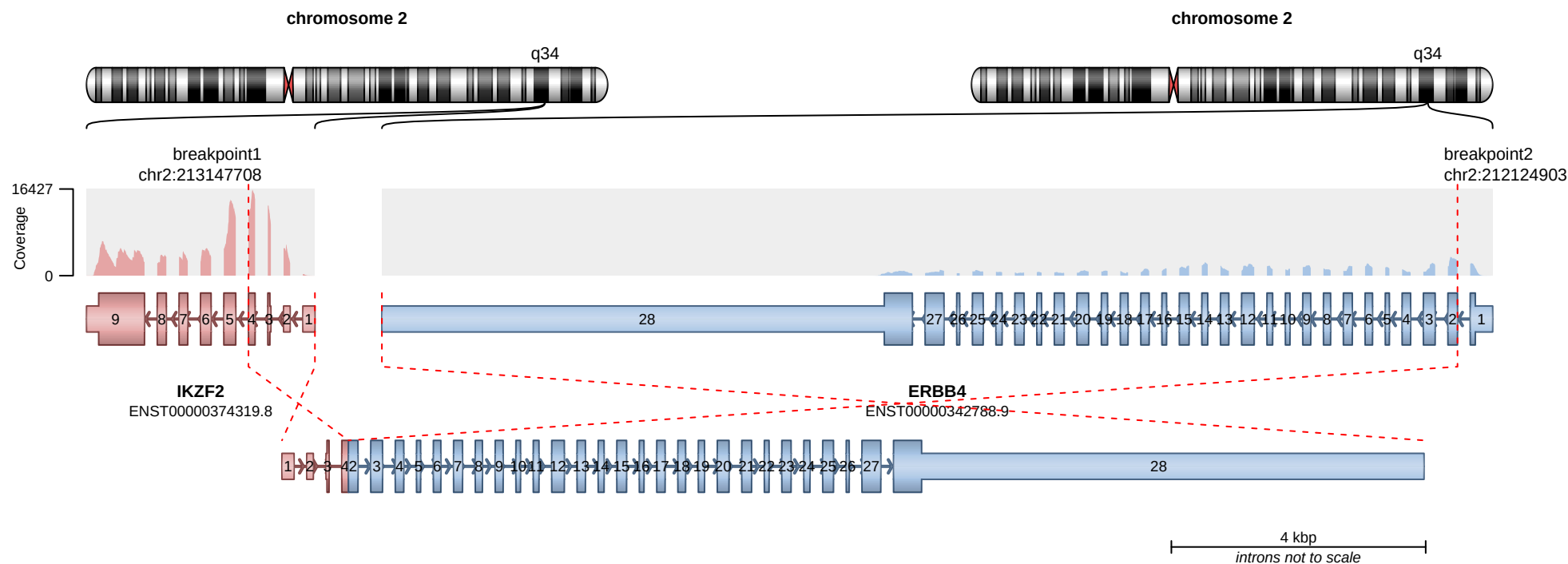


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

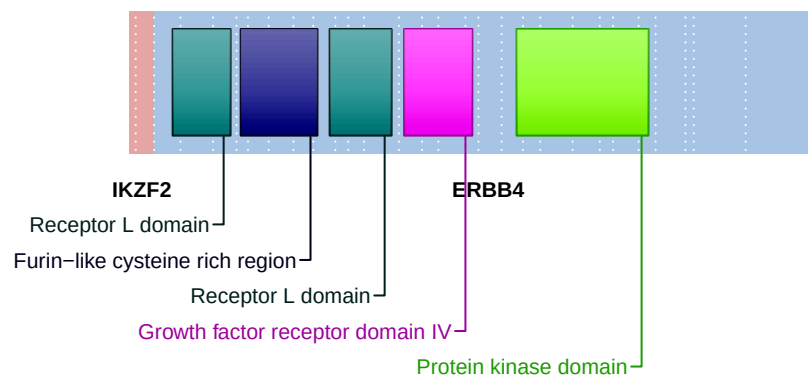
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1



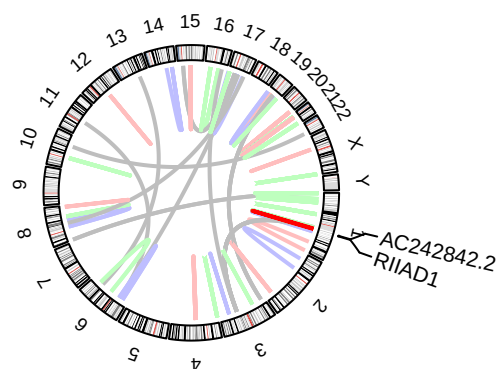
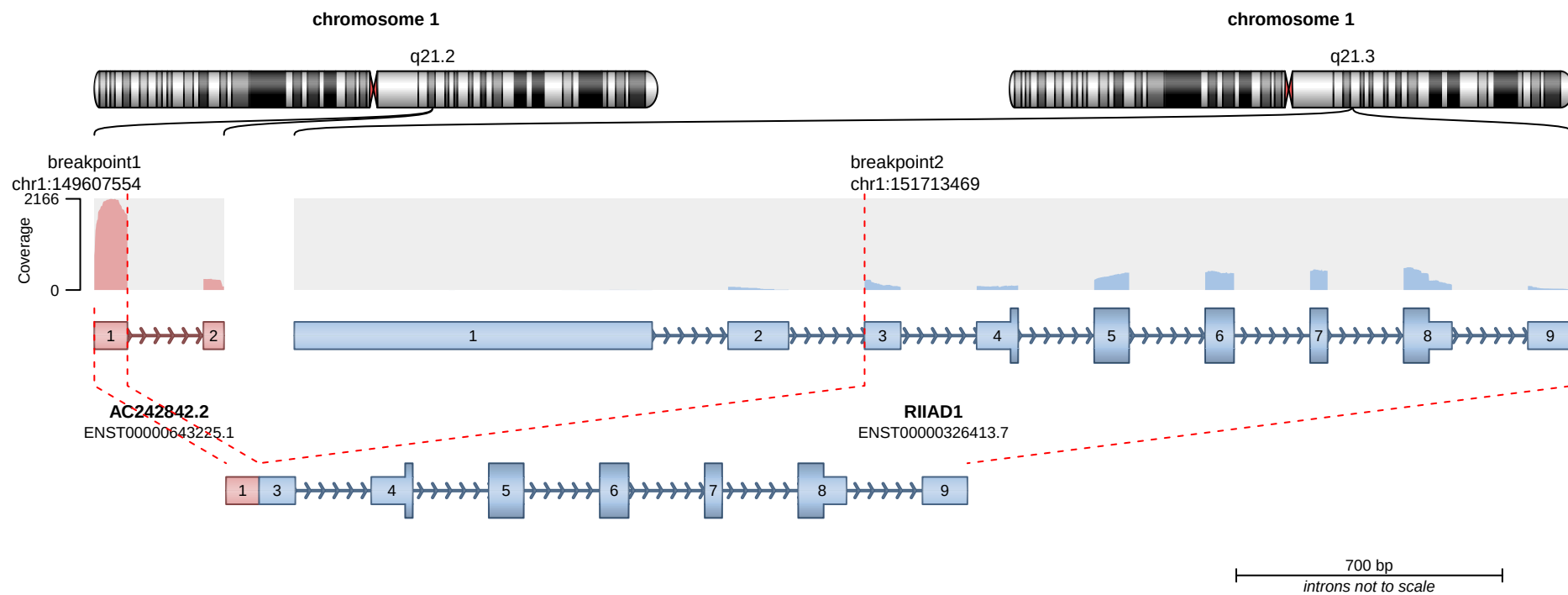
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS reading frame unclear

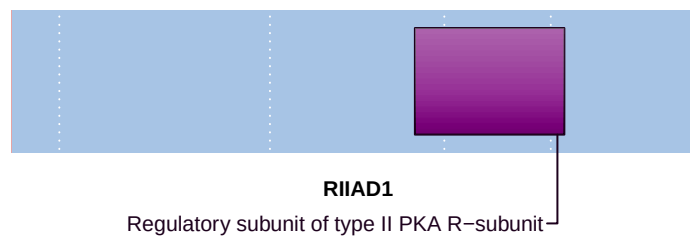


SUPPORTING READ COUNT

Split reads = 33
Discordant mates = 0



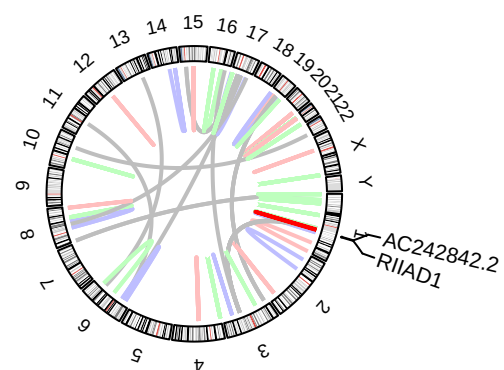
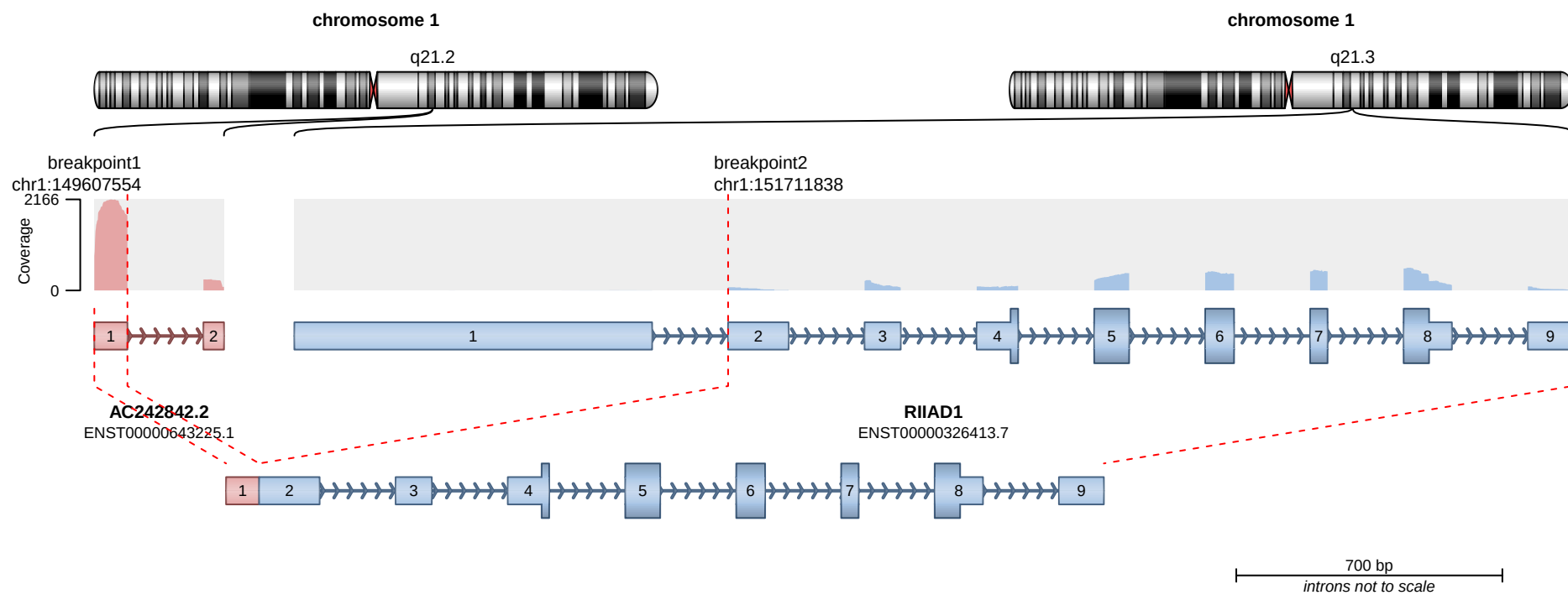
RETAINED PROTEIN DOMAINS reading frame unclear



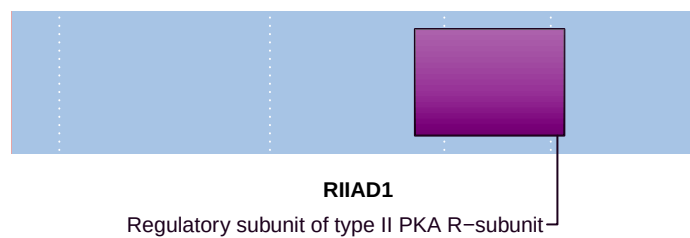
SUPPORTING READ COUNT

Split reads = 32
Discordant mates = 0

— translocation — deletion
— duplication — inversion



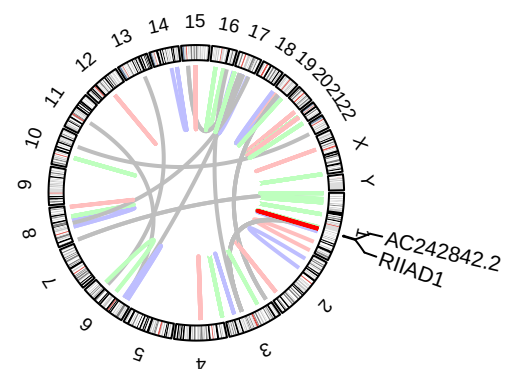
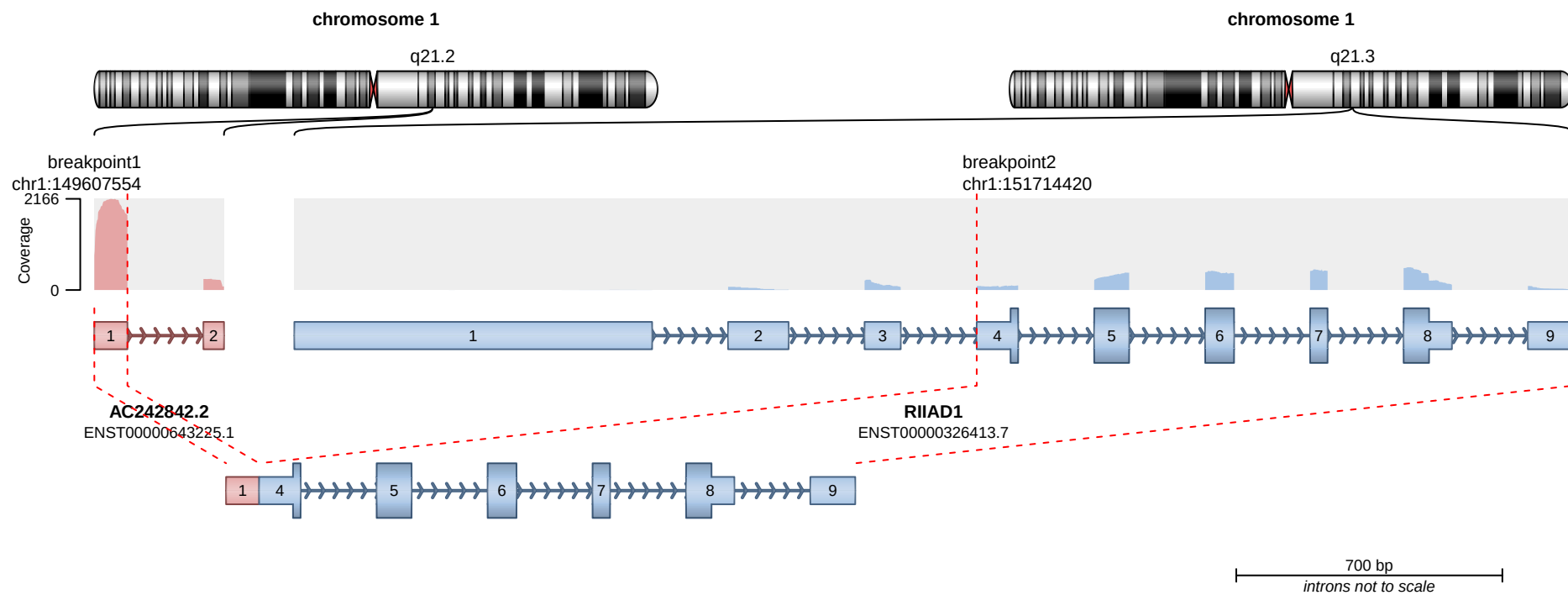
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

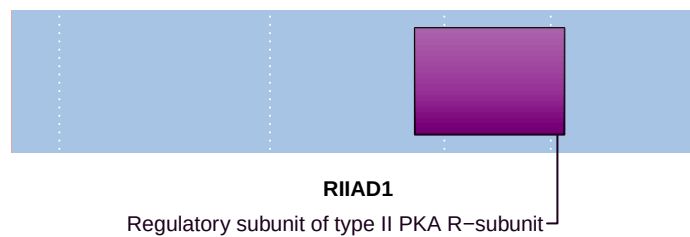
Split reads = 9
Discordant mates = 0

— translocation — deletion
— duplication — inversion



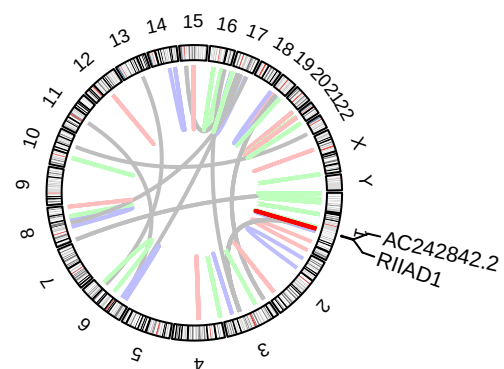
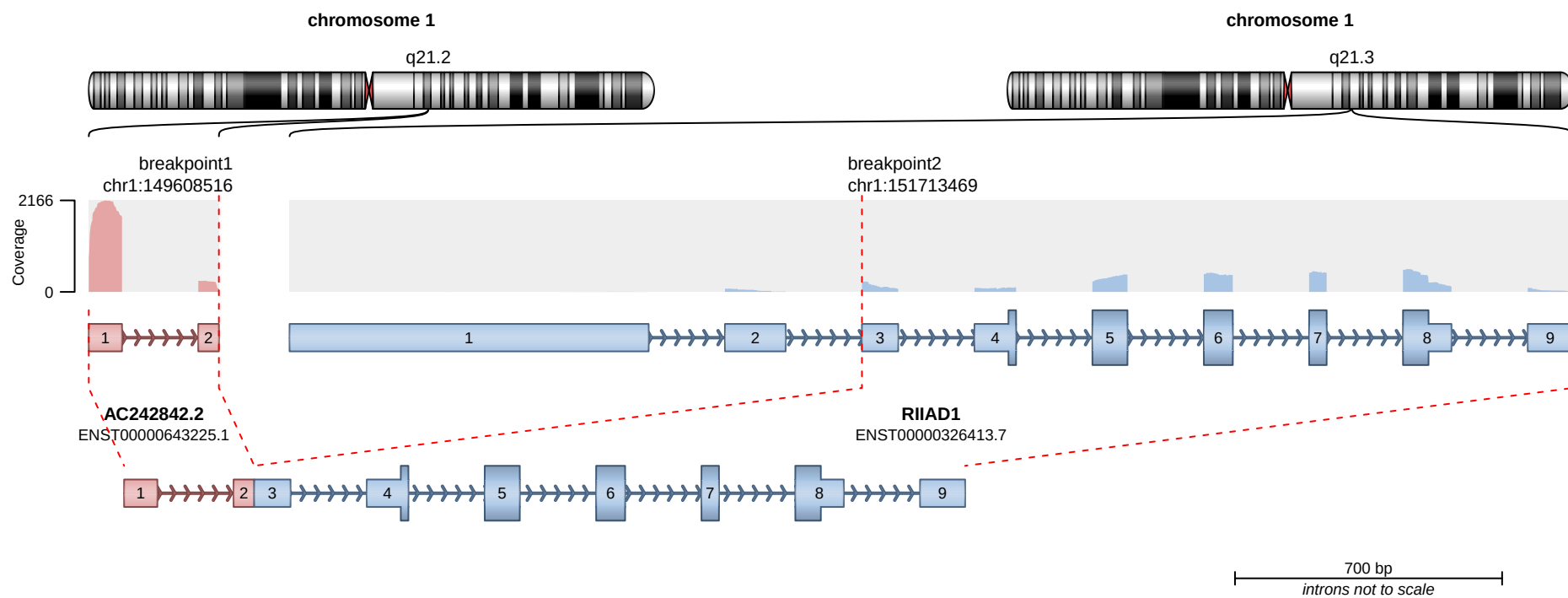
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS
reading frame unclear

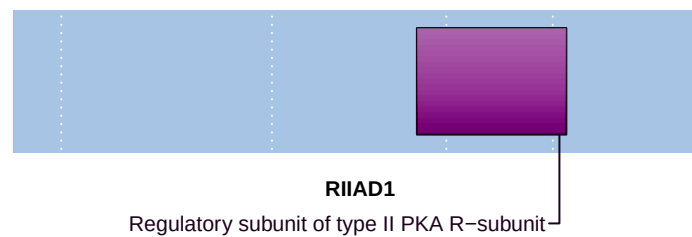


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0



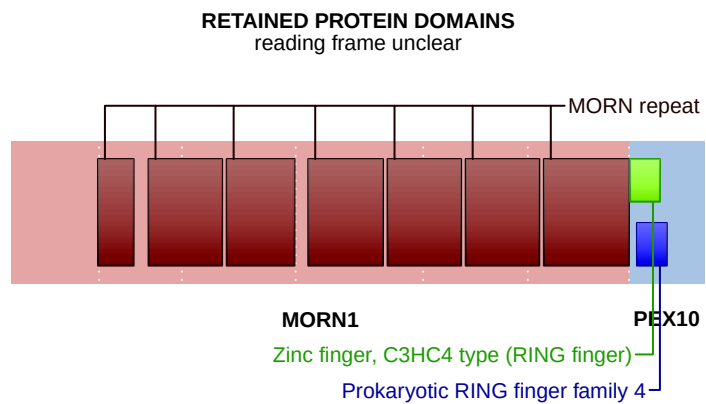
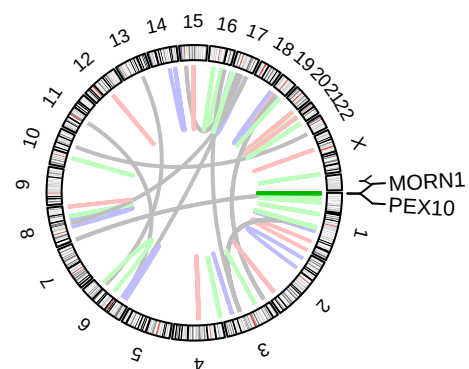
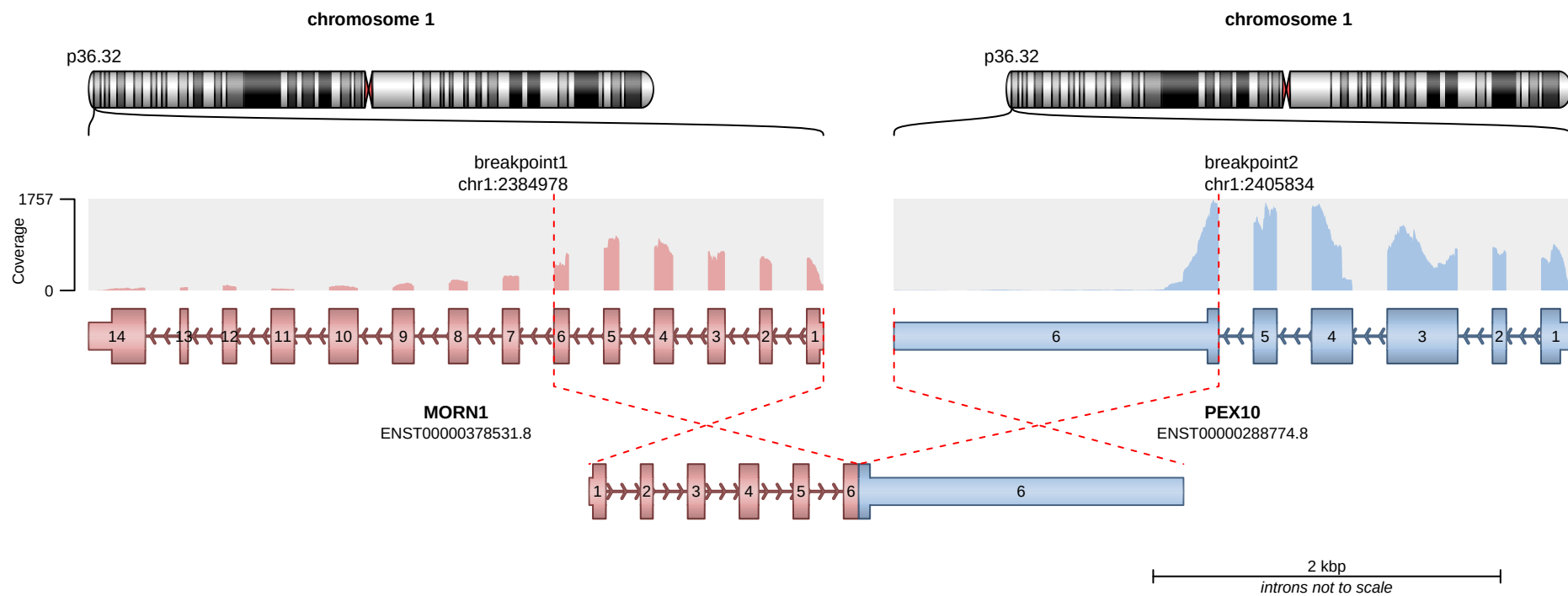
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

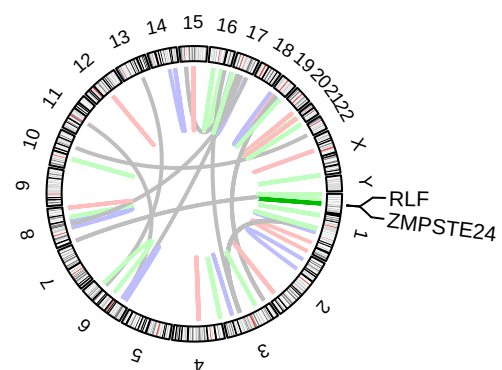
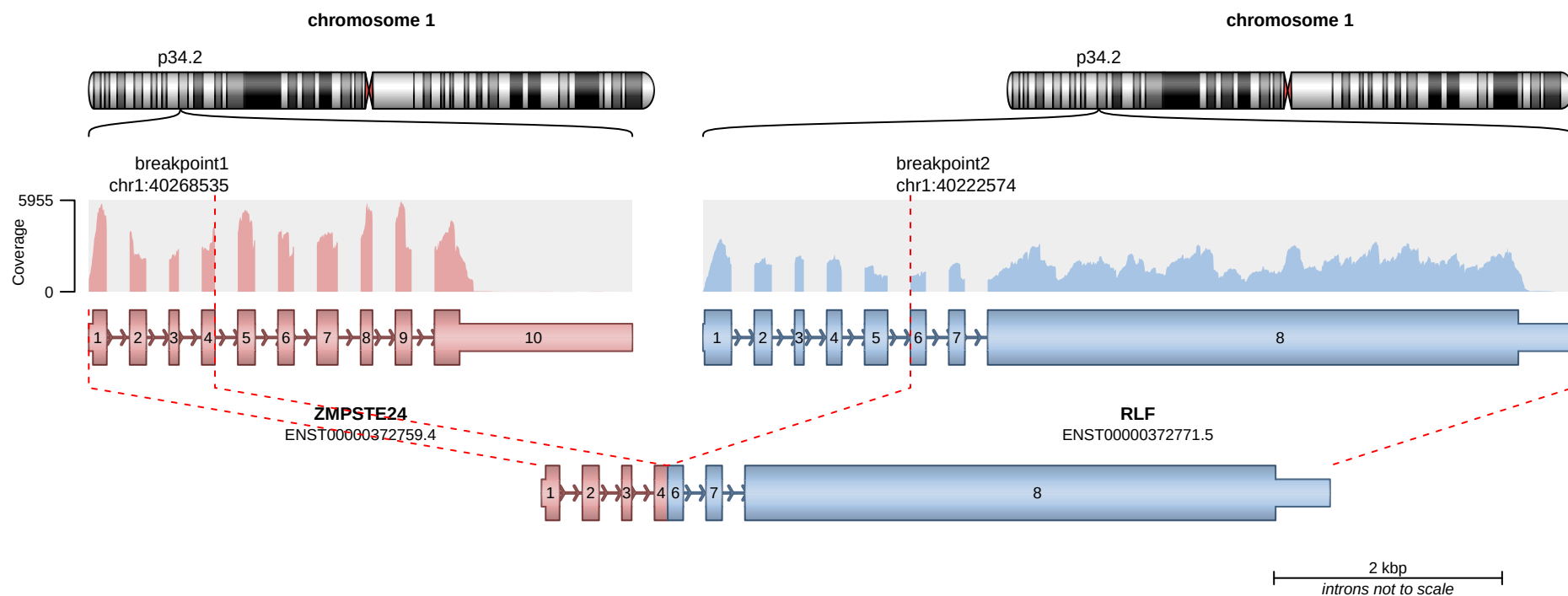
— translocation — deletion
— duplication — inversion



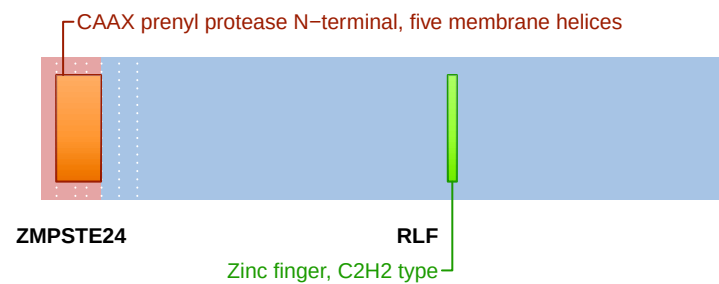
SUPPORTING READ COUNT

Split reads = 31
Discordant mates = 0

— translocation — deletion
— duplication — inversion



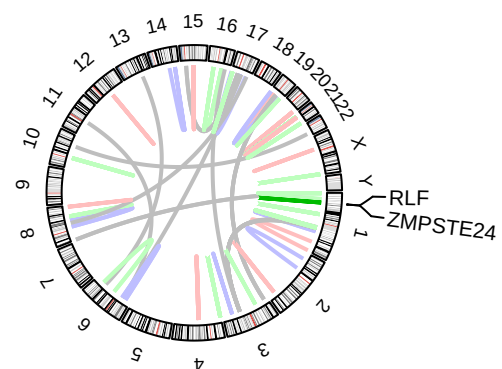
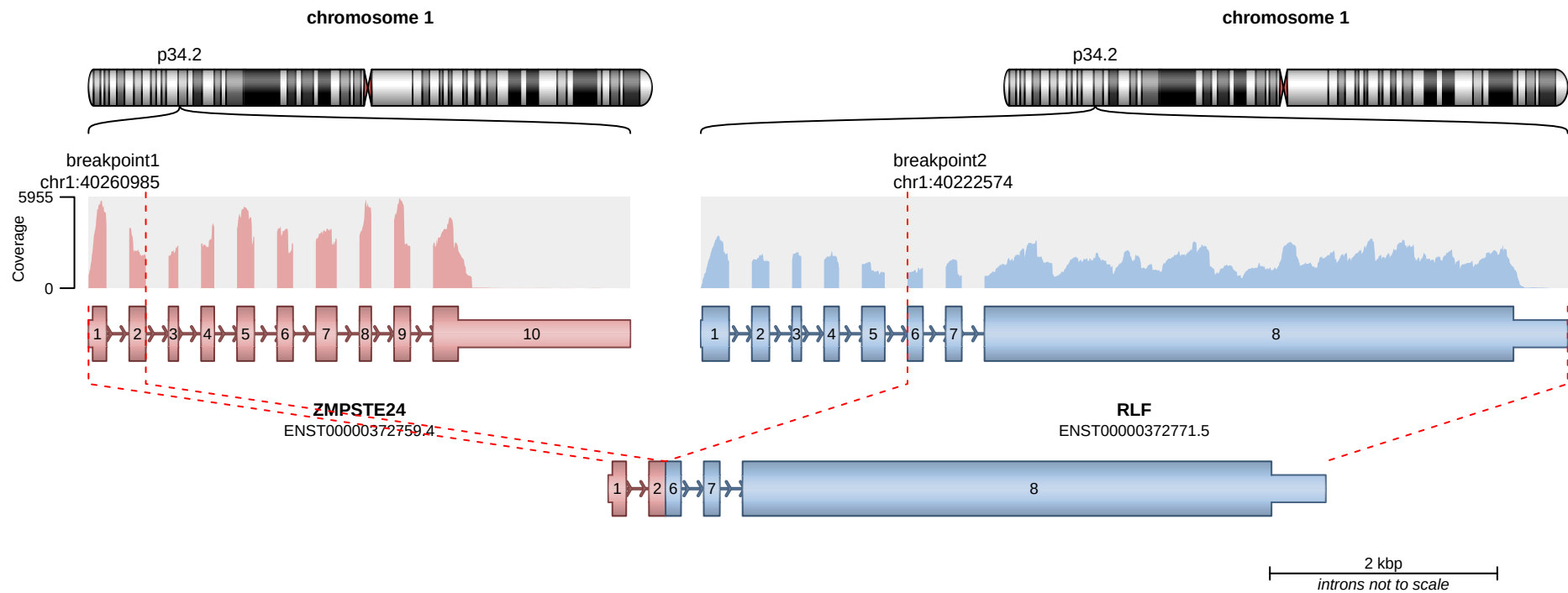
RETAINED PROTEIN DOMAINS reading frame unclear



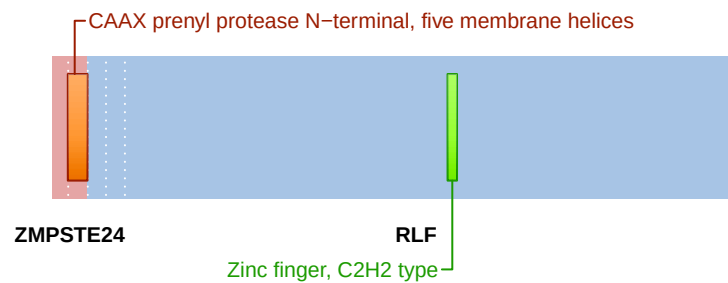
SUPPORTING READ COUNT

Split reads = 28
Discordant mates = 1

— translocation — deletion
— duplication — inversion



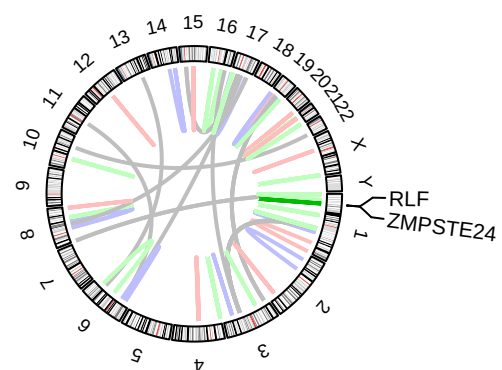
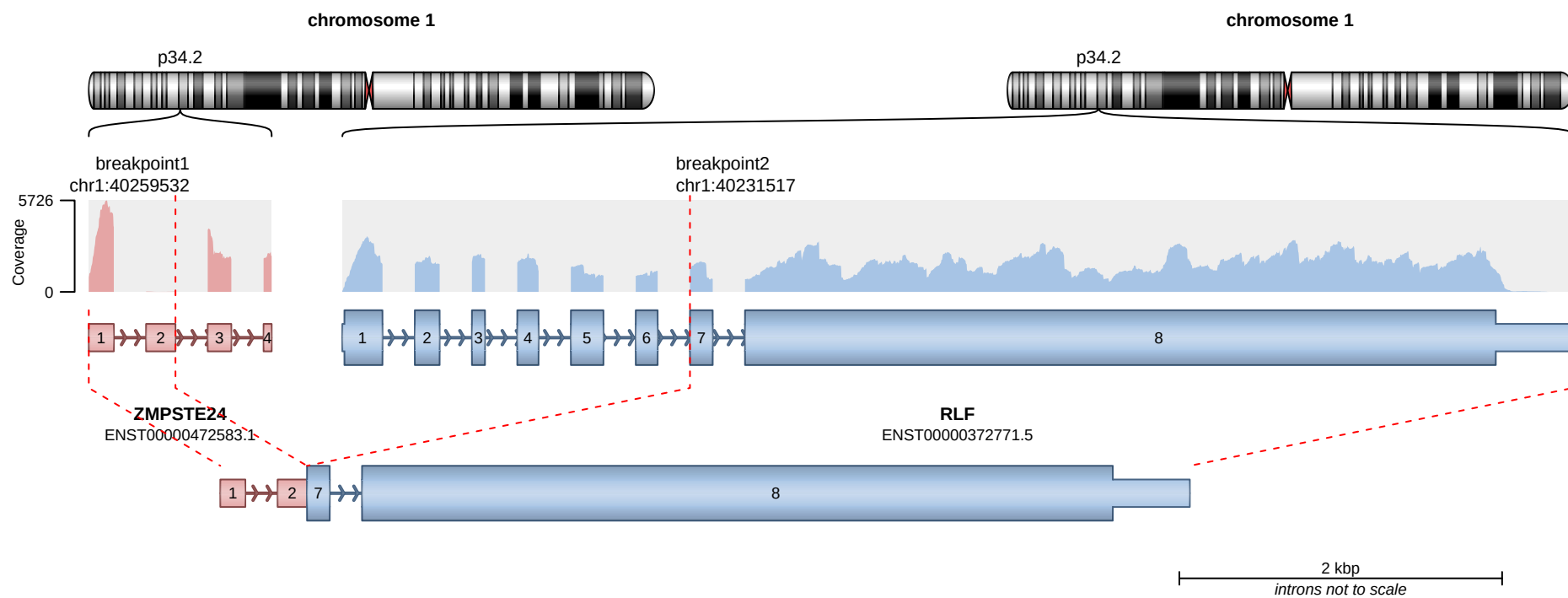
RETAINED PROTEIN DOMAINS reading frame unclear



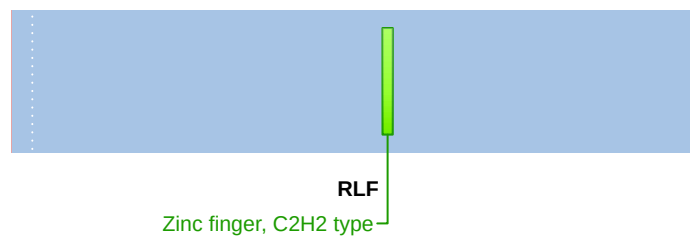
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



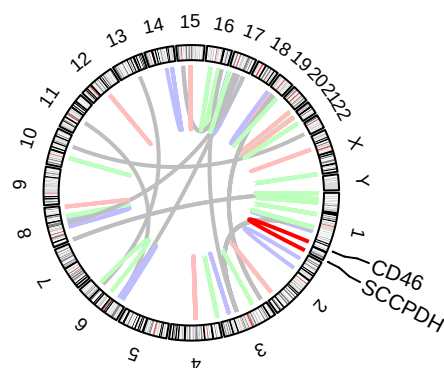
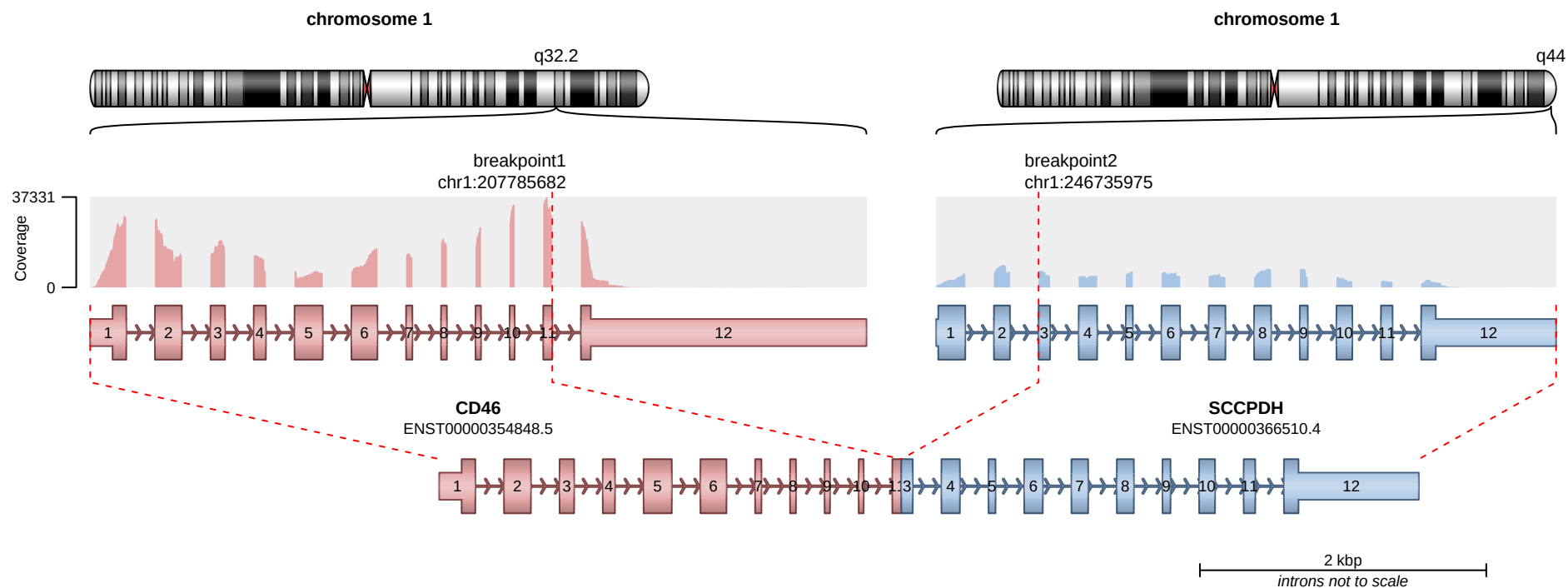
RETAINED PROTEIN DOMAINS
reading frame unclear



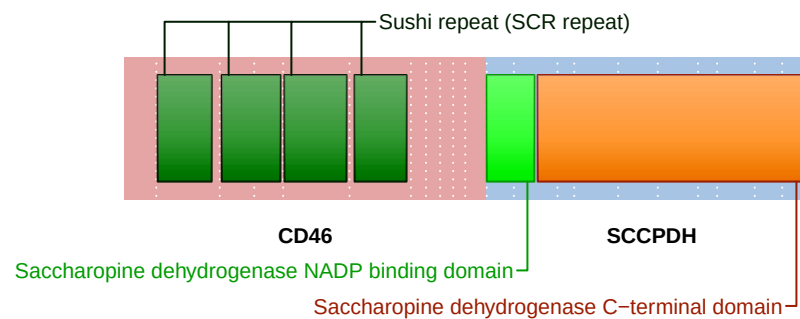
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



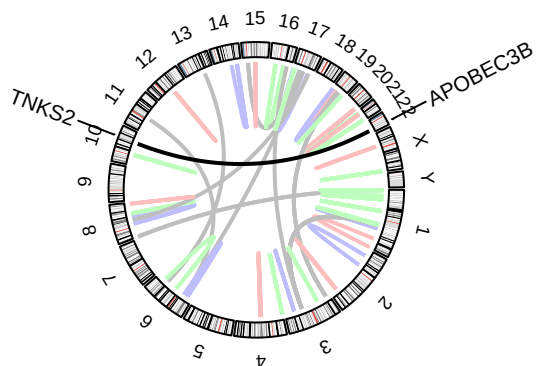
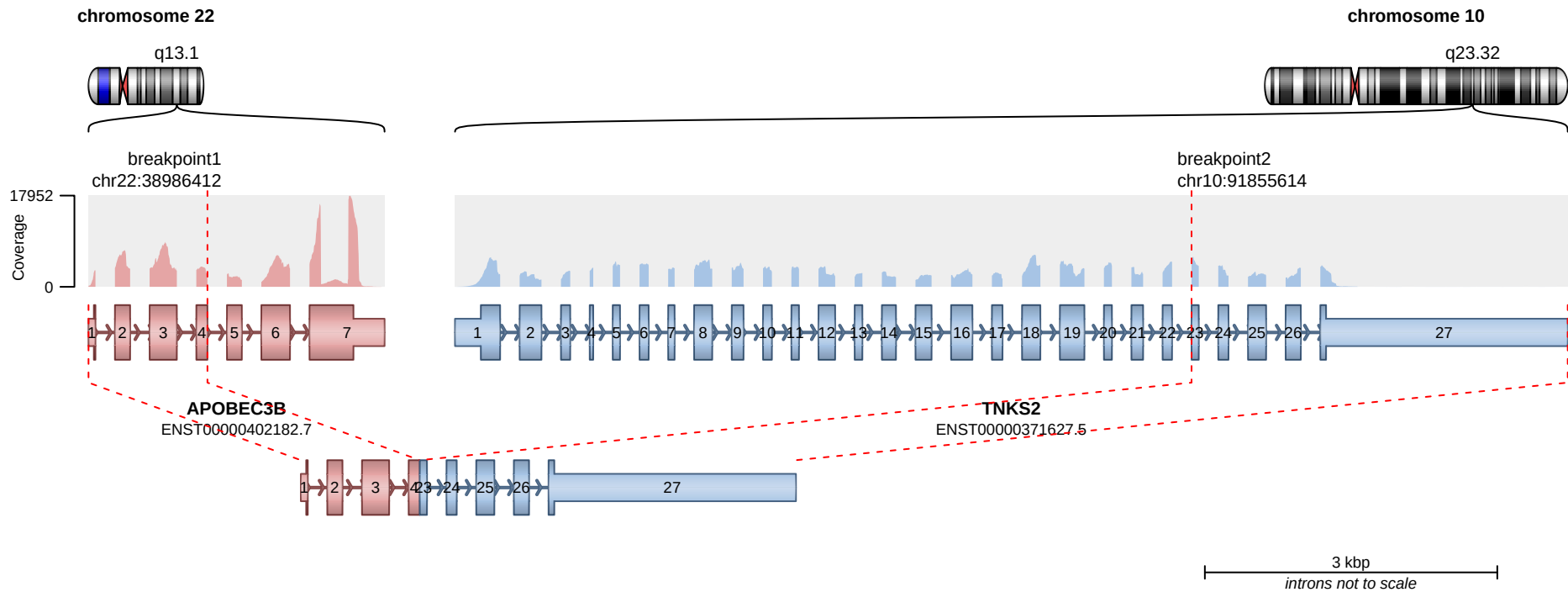
RETAINED PROTEIN DOMAINS reading frame unclear



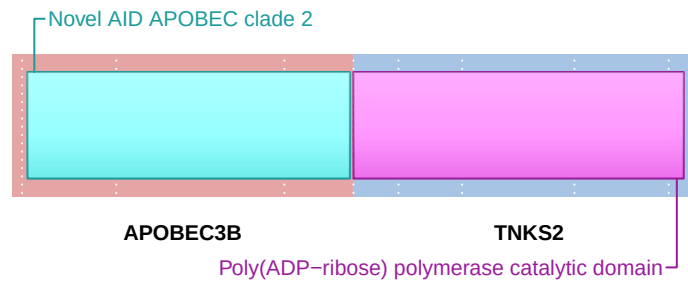
SUPPORTING READ COUNT

Split reads = 28
Discordant mates = 0

— translocation — deletion
— duplication — inversion



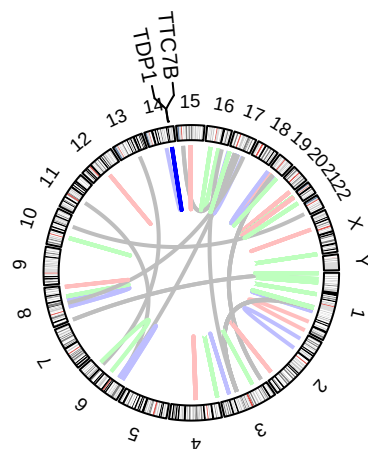
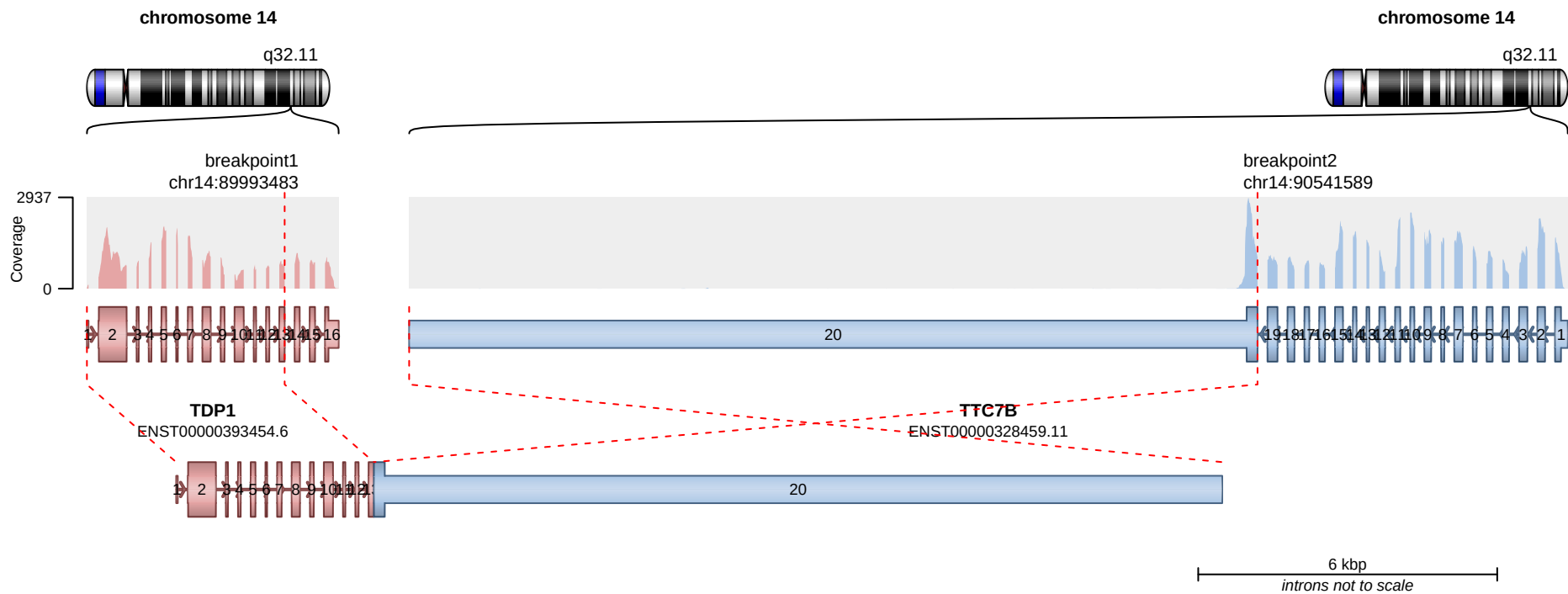
RETAINED PROTEIN DOMAINS
reading frame unclear



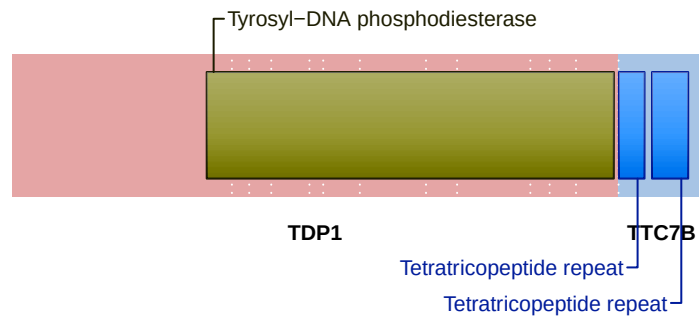
SUPPORTING READ COUNT

Split reads = 27
Discordant mates = 0

— translocation — deletion
— duplication — inversion



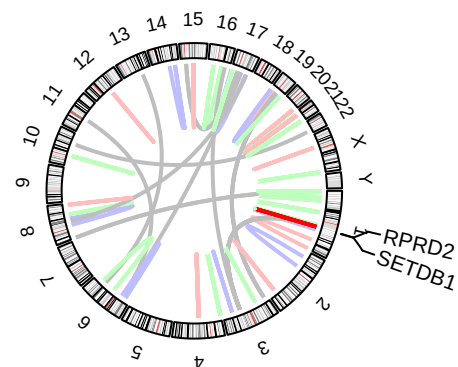
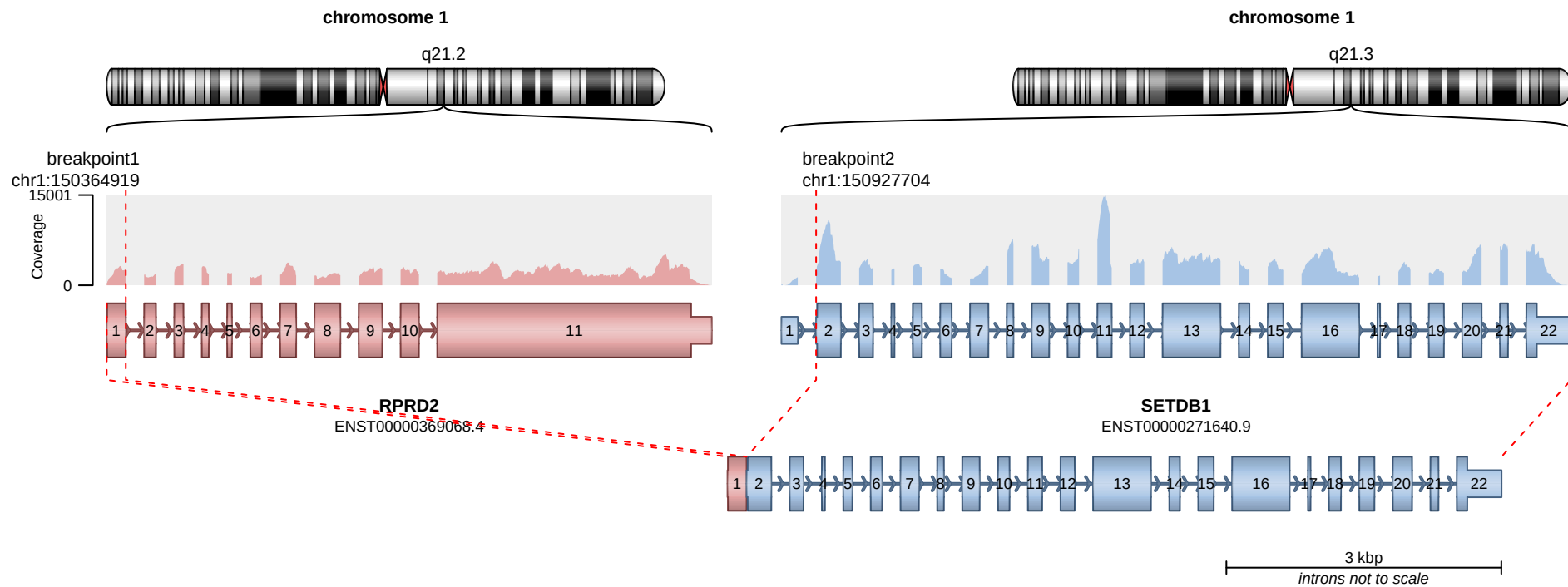
RETAINED PROTEIN DOMAINS reading frame unclear



SUPPORTING READ COUNT

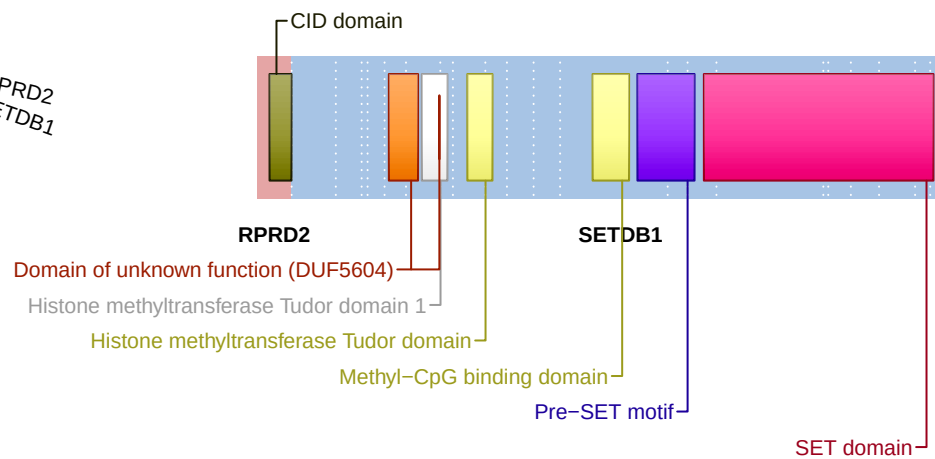
Split reads = 26
Discordant mates = 0

— translocation — deletion
— duplication — inversion



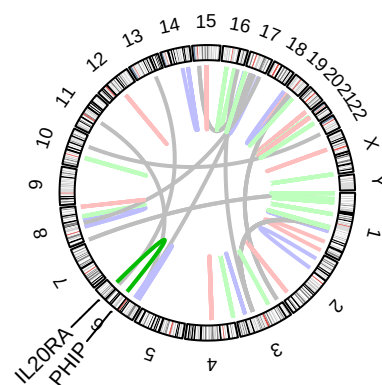
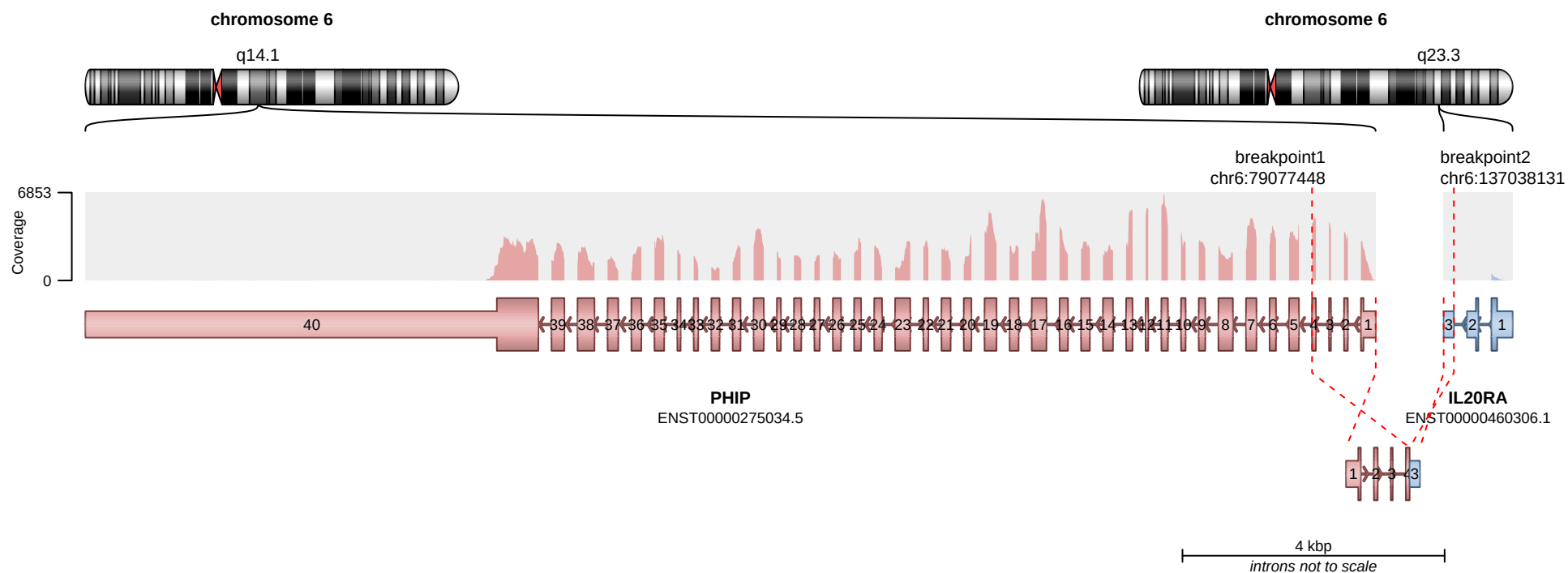
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS reading frame unclear



SUPPORTING READ COUNT

Split reads = 25
Discordant mates = 2

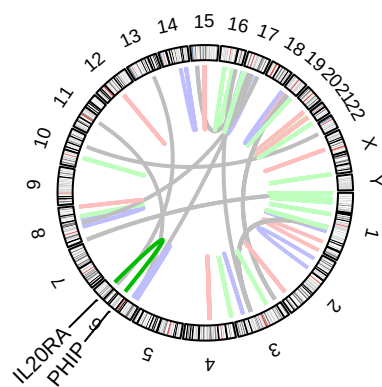
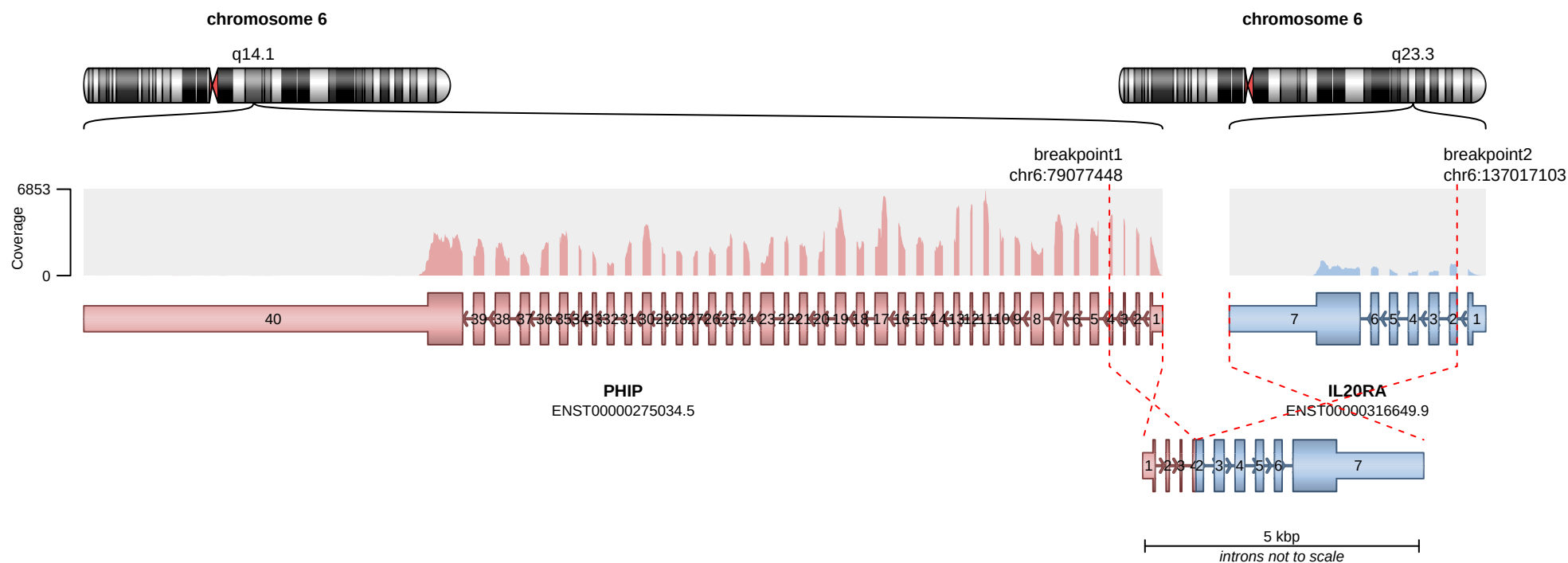


— translocation — deletion
— duplication — inversion

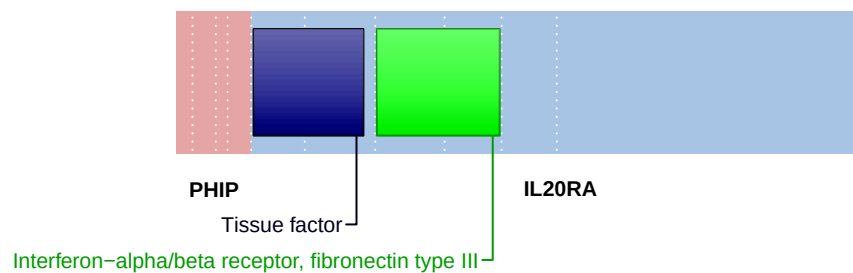
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 25
Discordant mates = 0



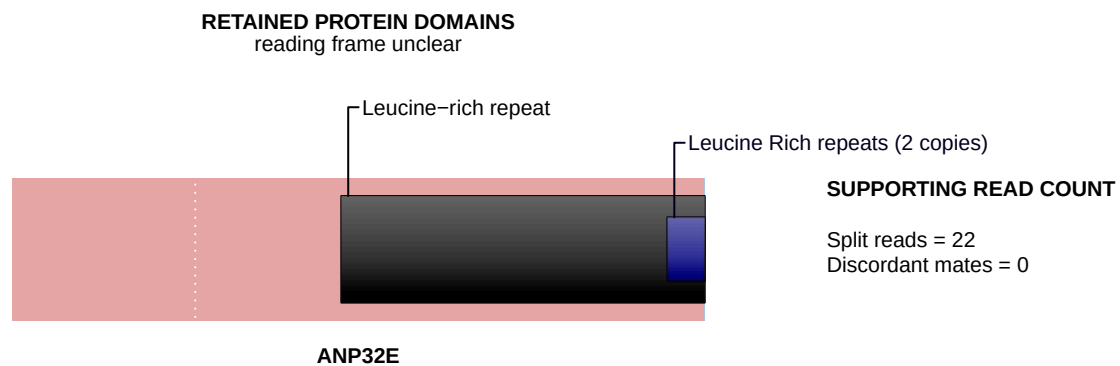
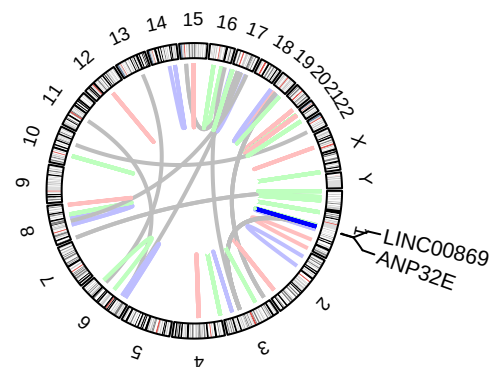
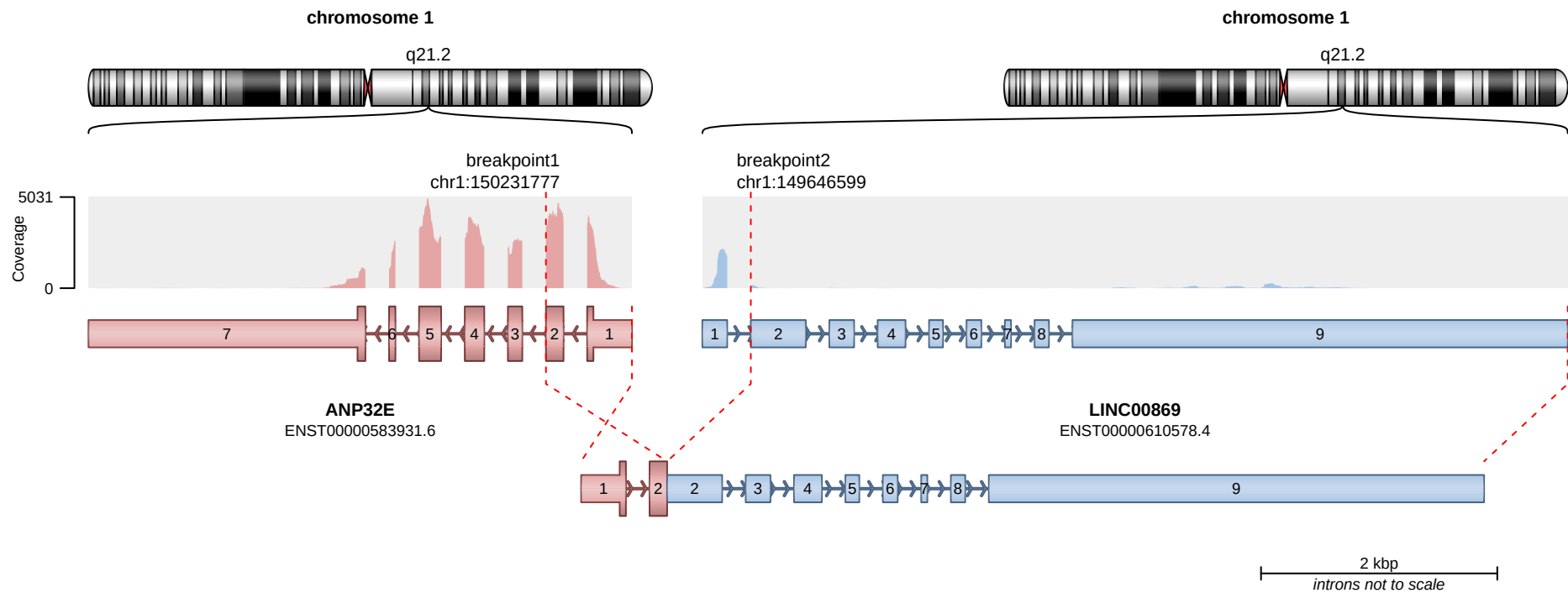
RETAINED PROTEIN DOMAINS reading frame unclear



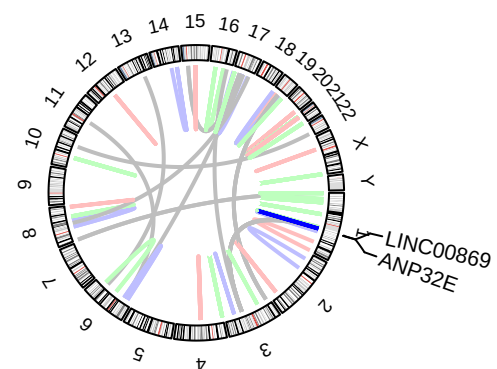
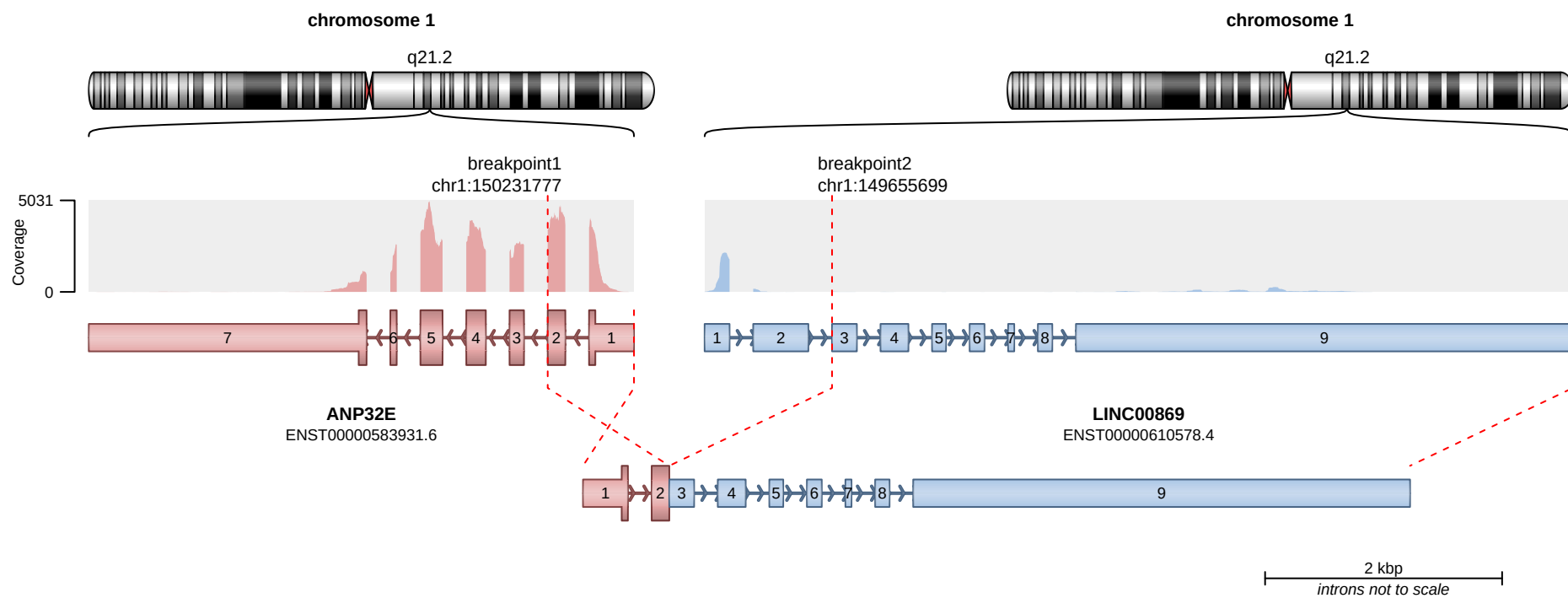
SUPPORTING READ COUNT

Split reads = 22
Discordant mates = 0

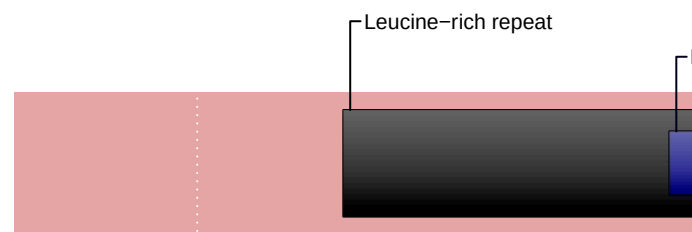
— translocation — deletion
— duplication — inversion



— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

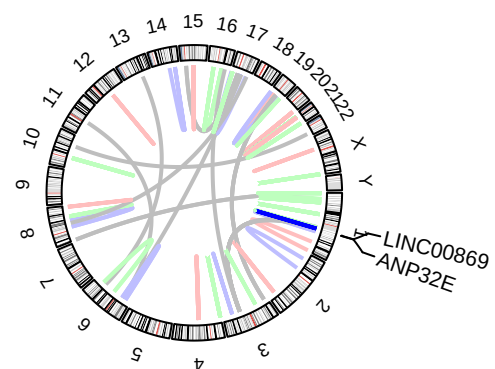
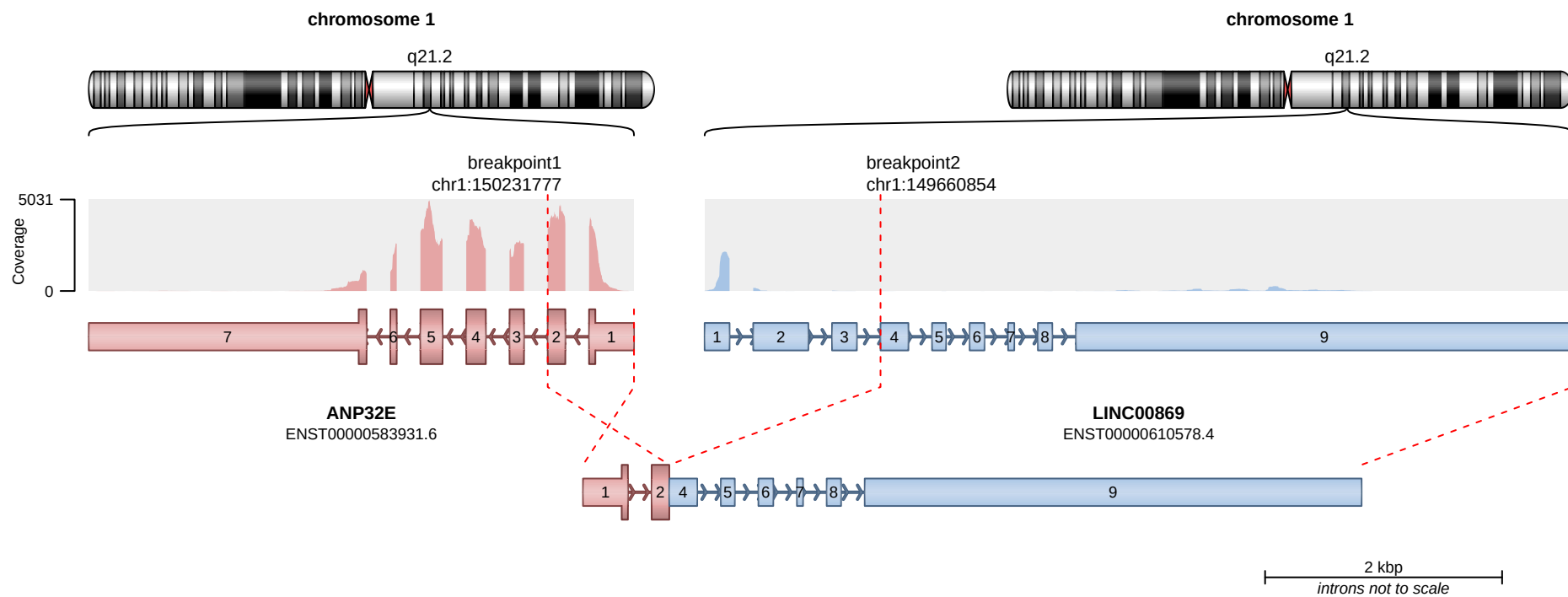


ANP32E

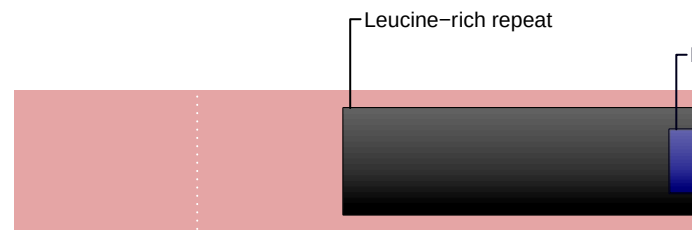
SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 0

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

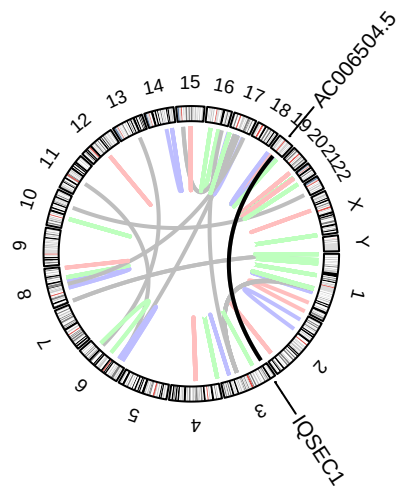
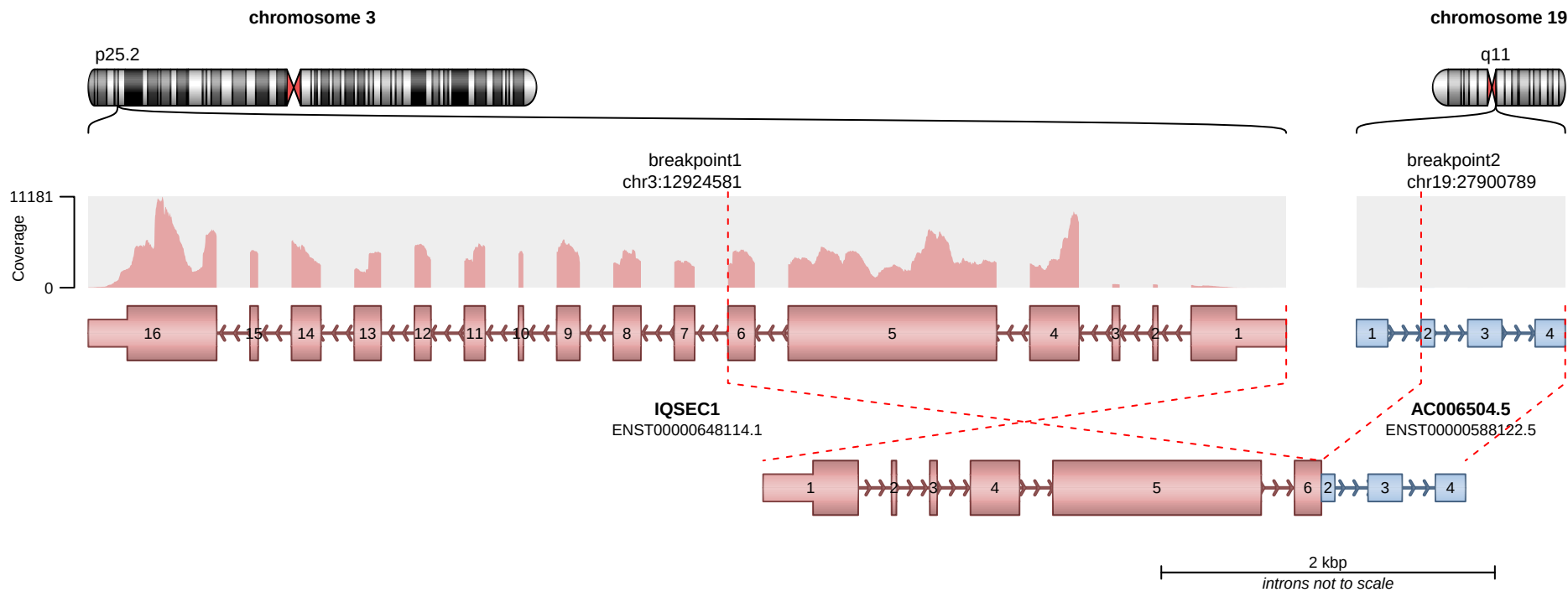


ANP32E

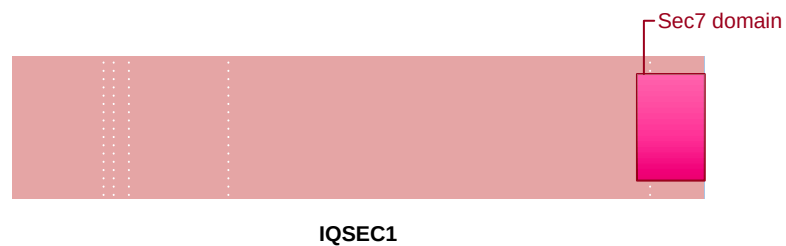
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

— translocation — deletion
— duplication — inversion



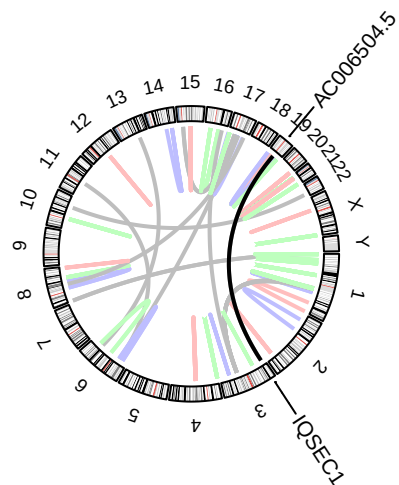
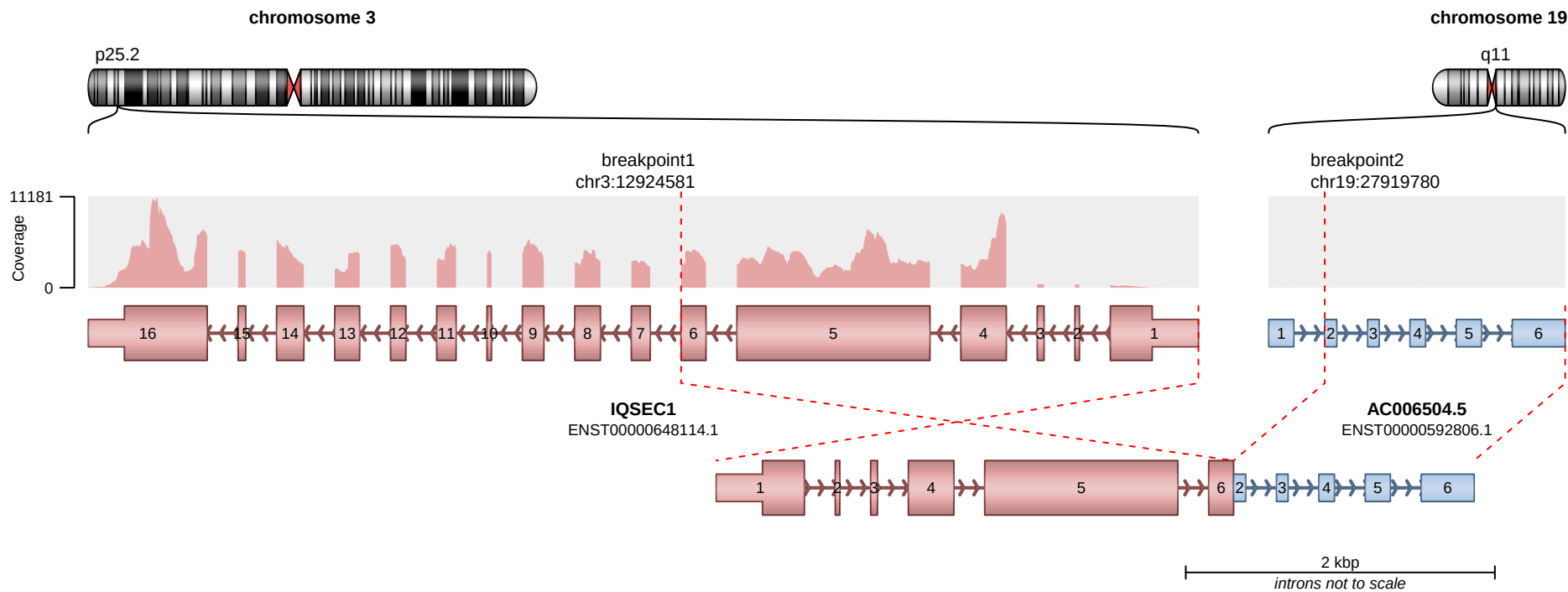
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 20
Discordant mates = 1

— translocation — deletion
— duplication — inversion



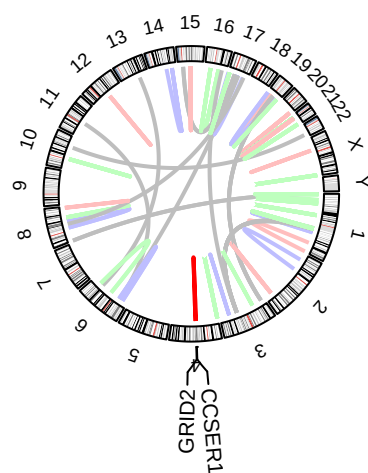
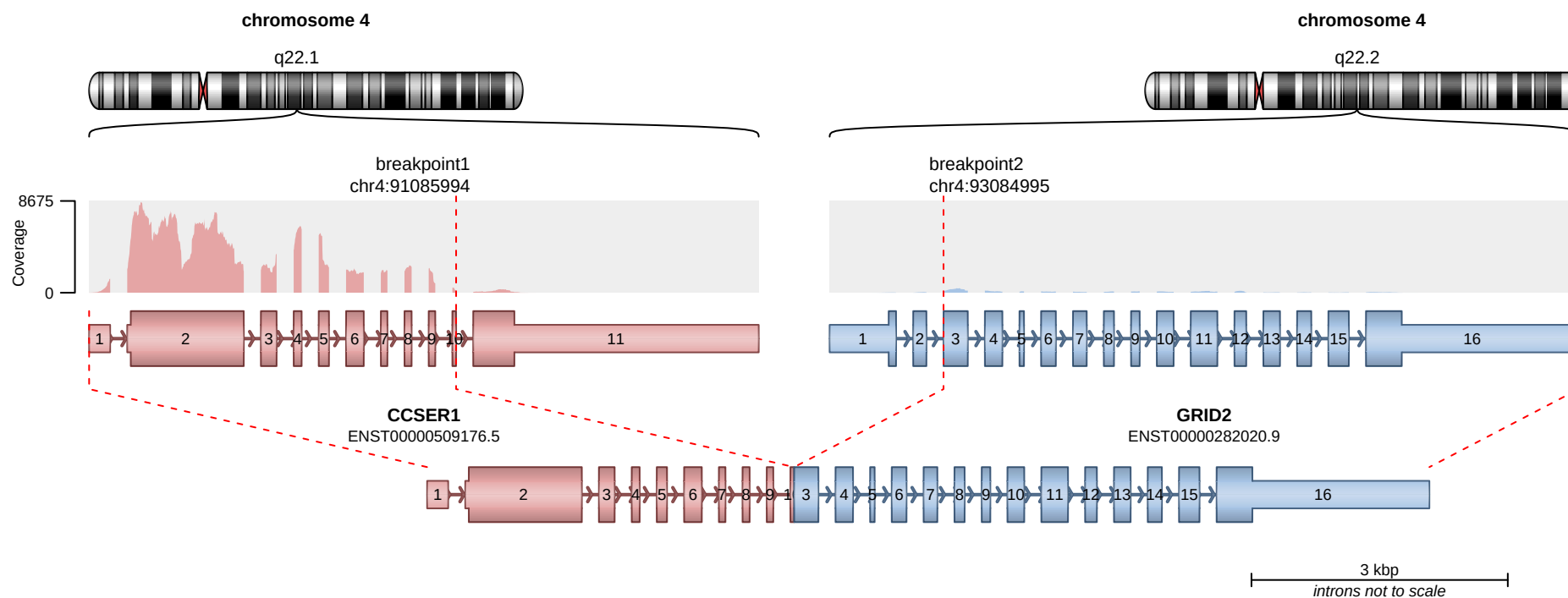
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

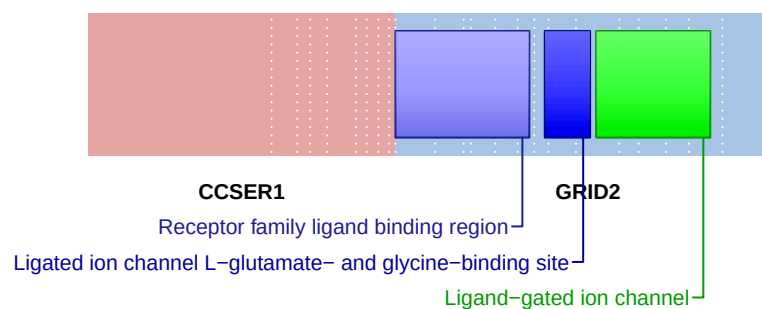
Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



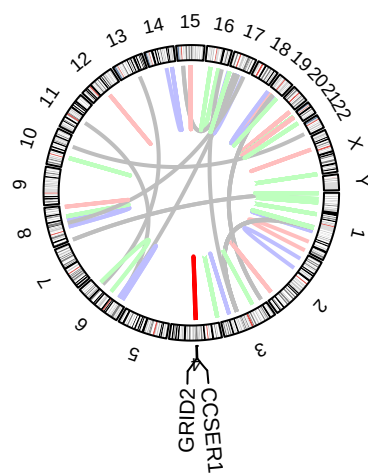
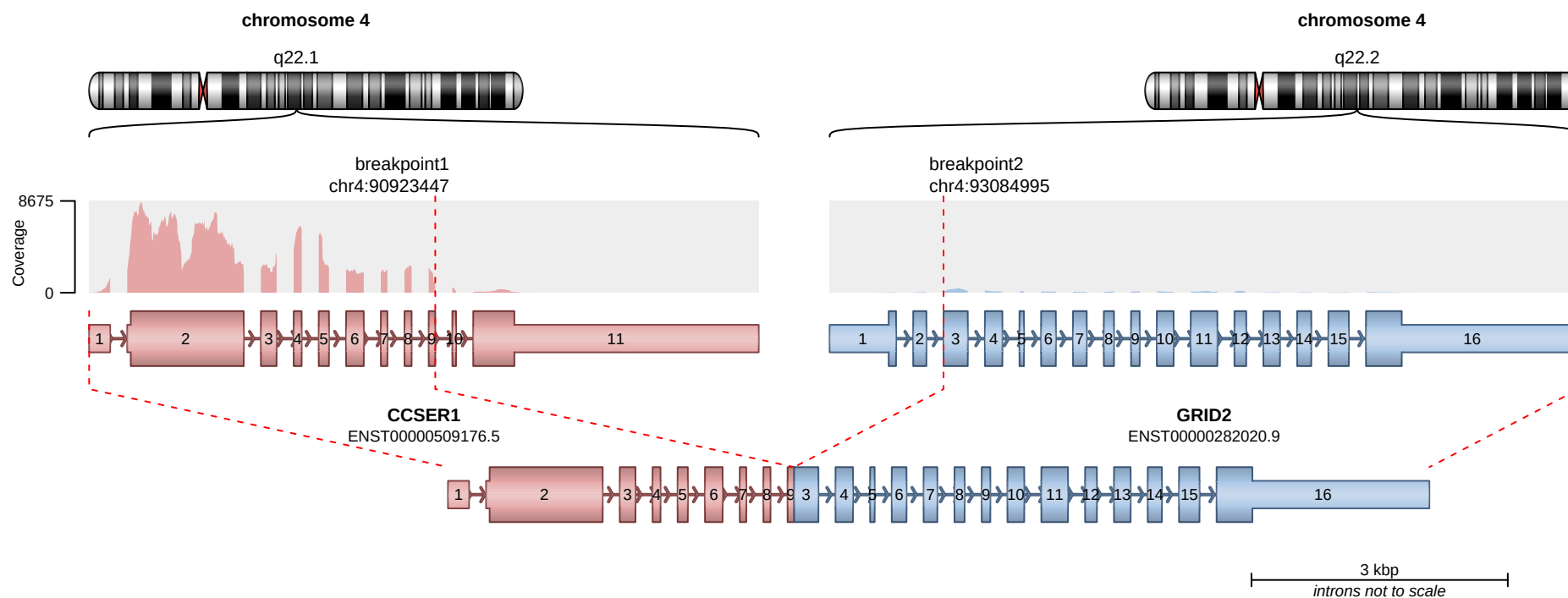
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS reading frame unclear



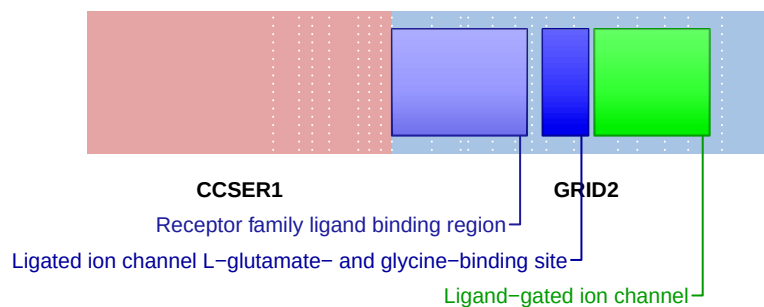
SUPPORTING READ COUNT

Split reads = 20
Discordant mates = 0



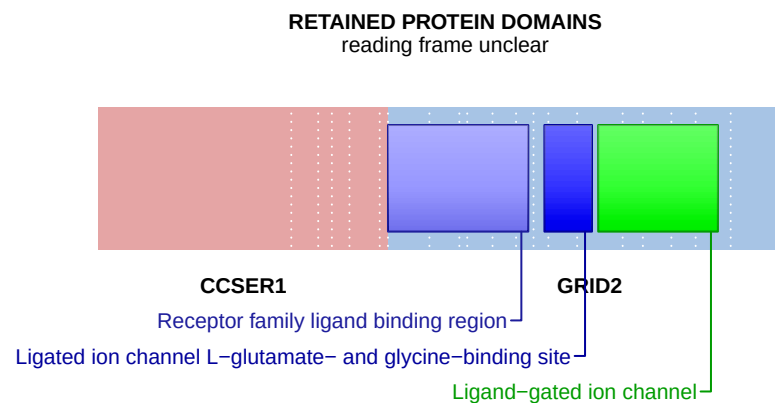
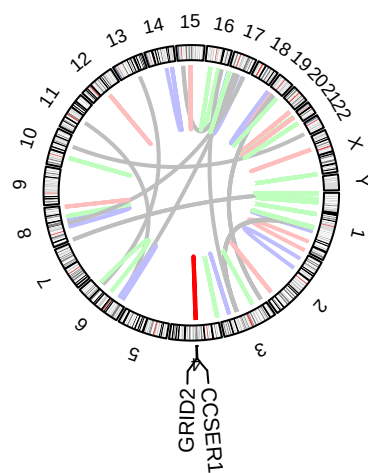
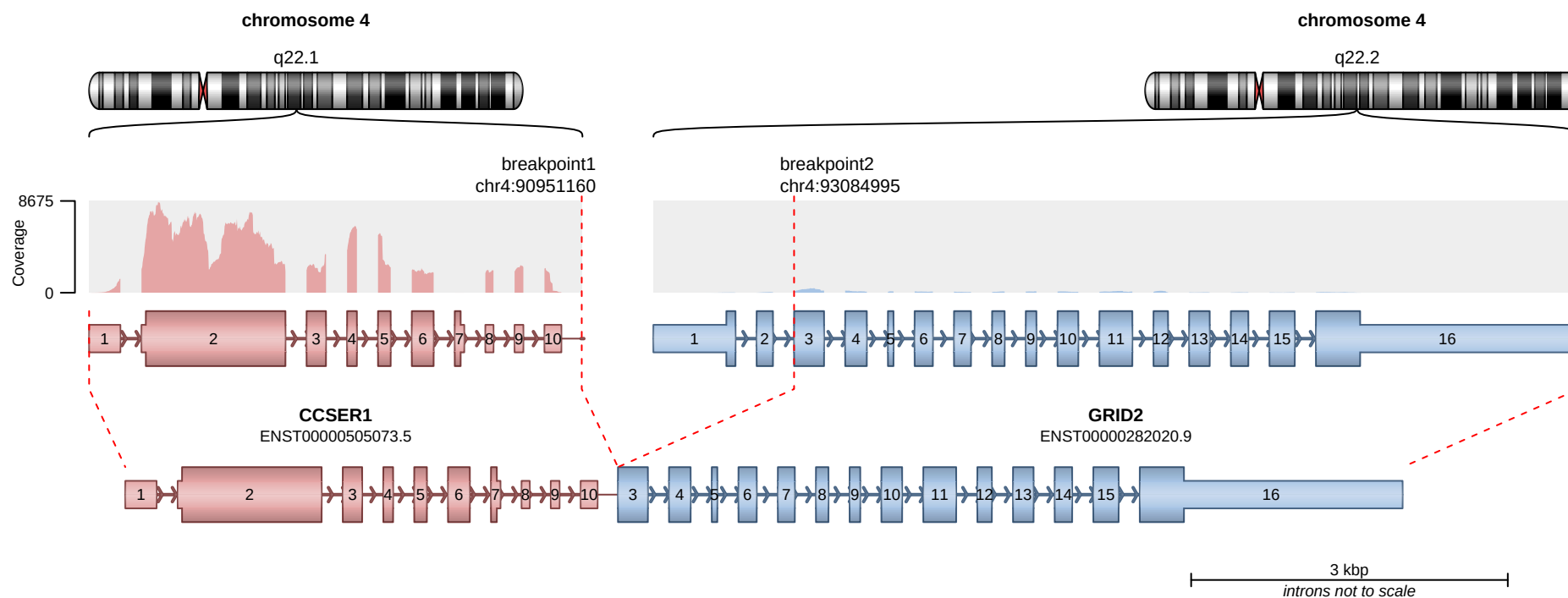
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS reading frame unclear



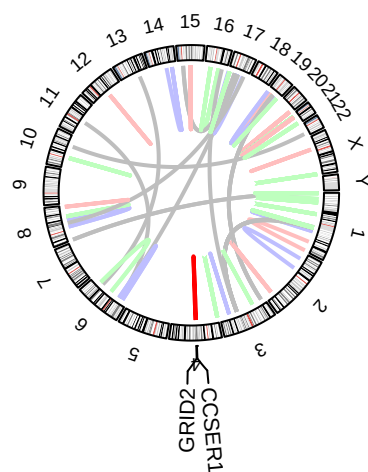
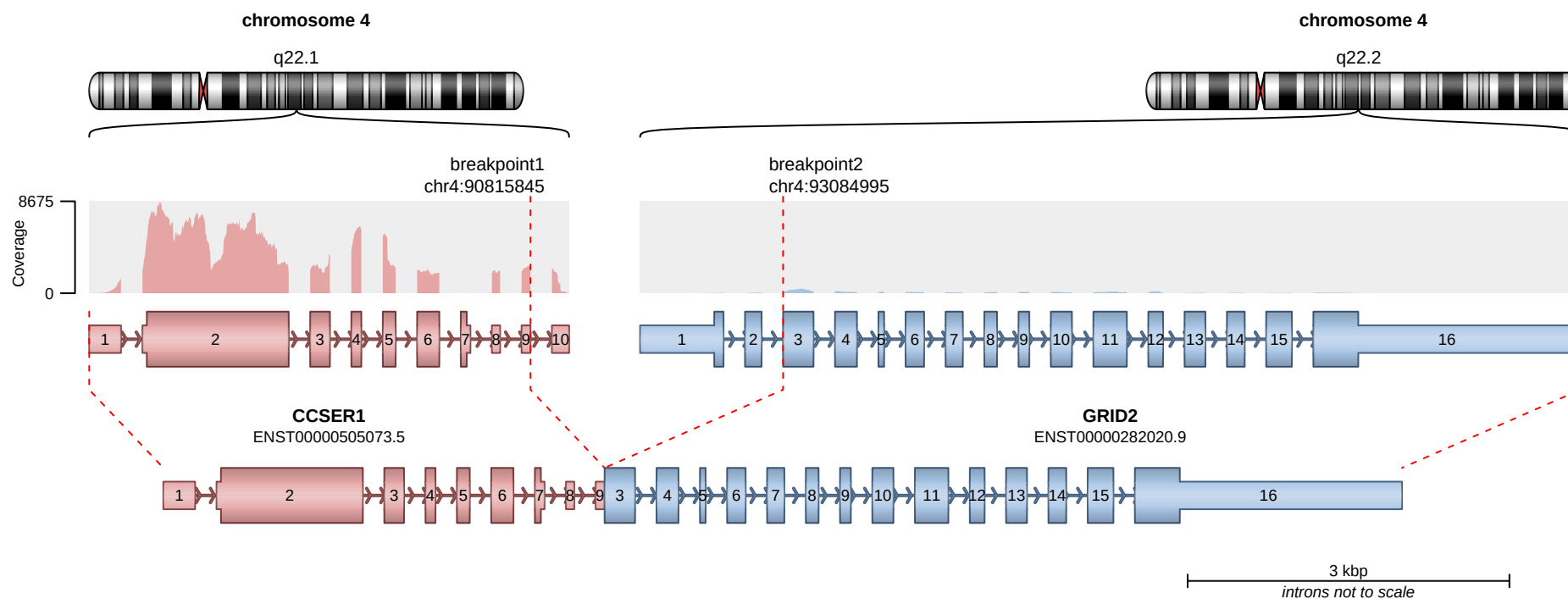
SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 0



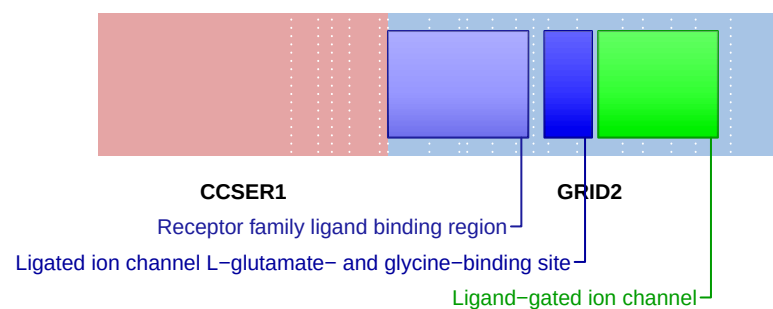
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0



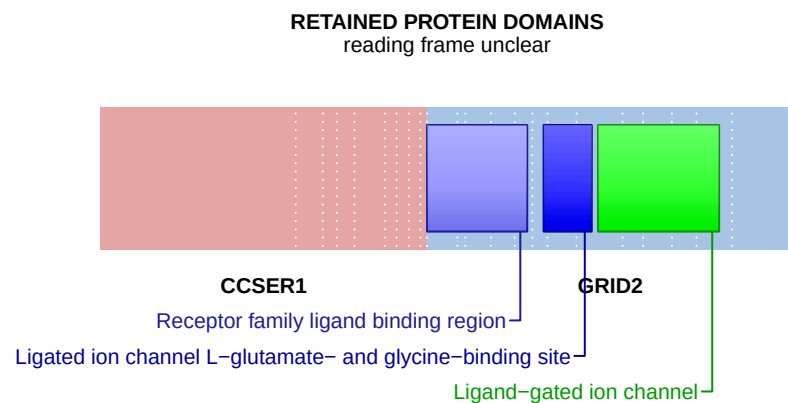
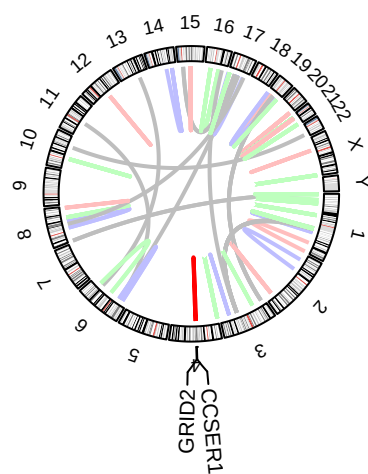
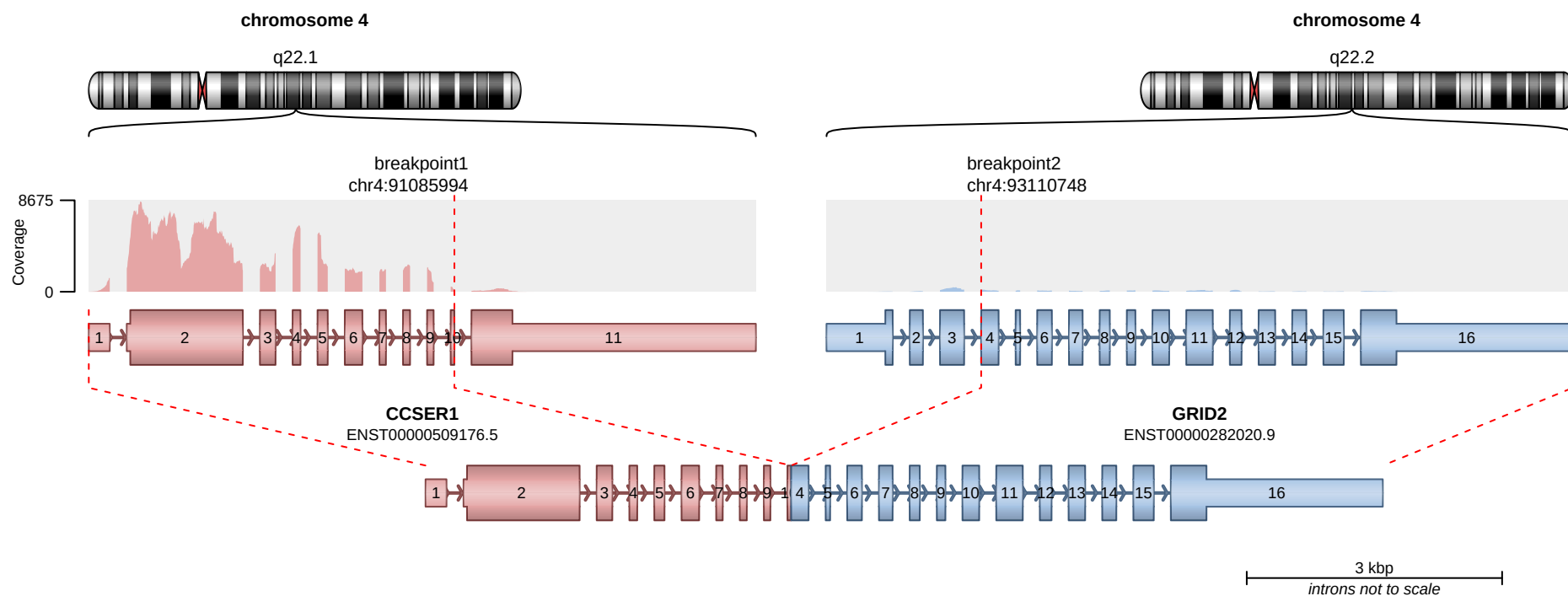
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS reading frame unclear



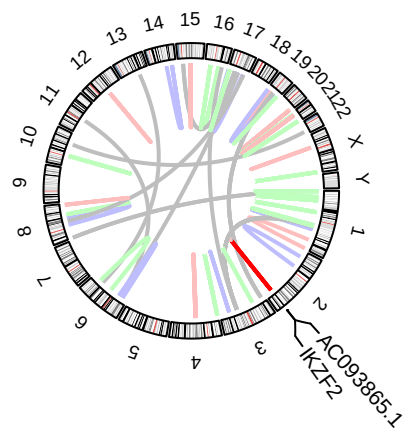
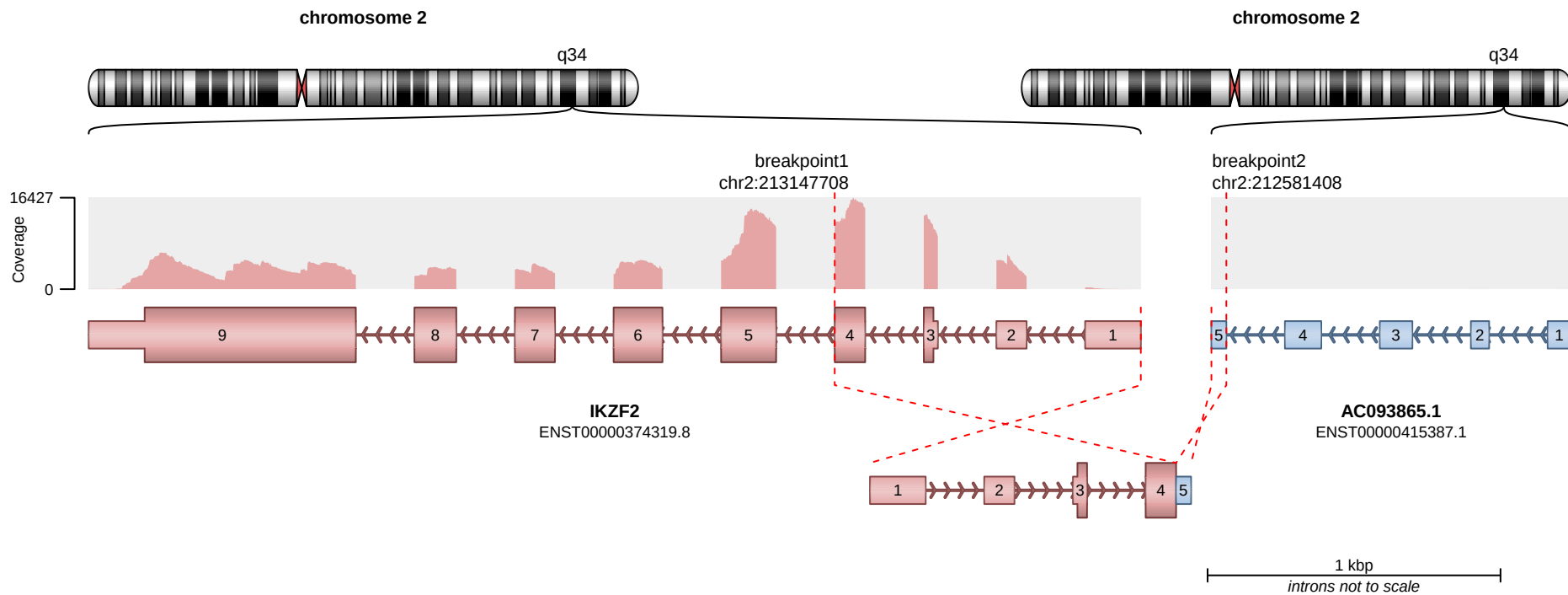
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

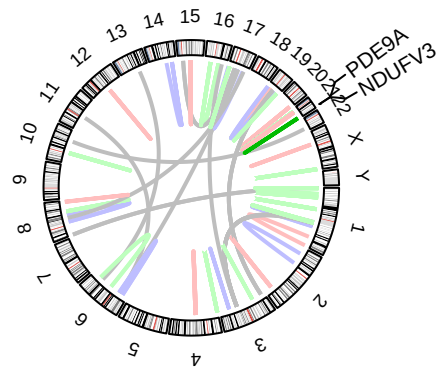
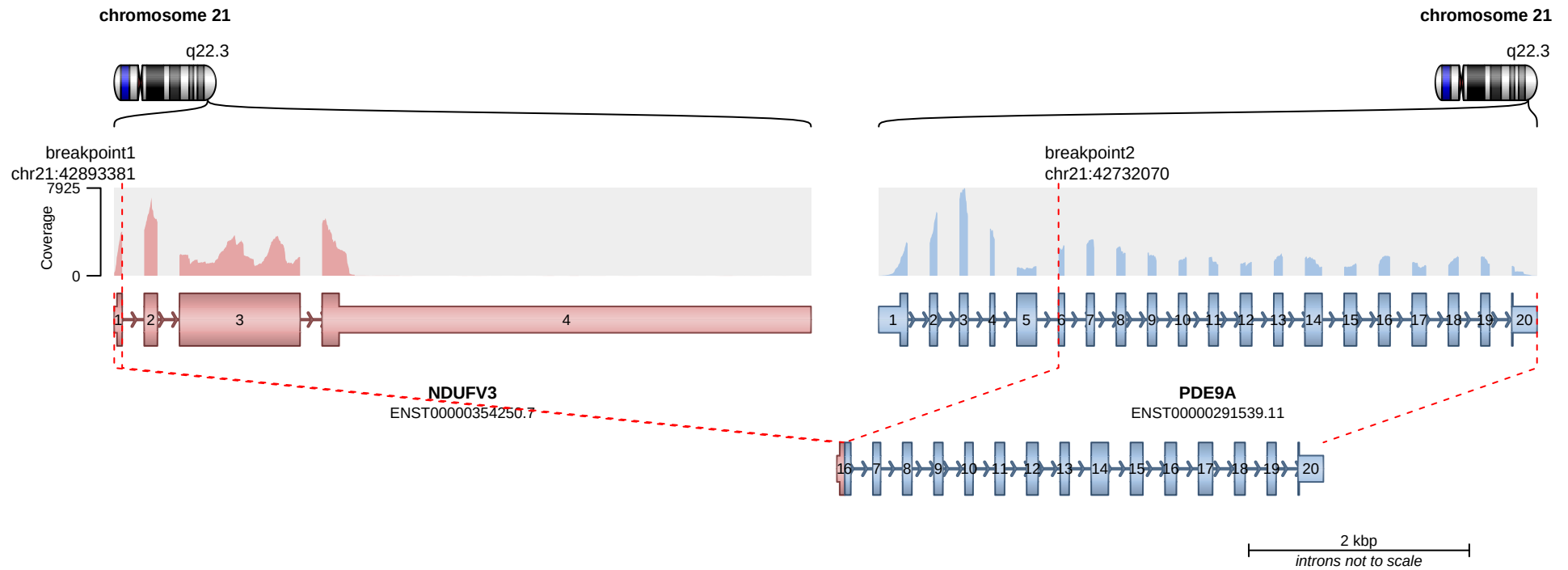


— translocation — deletion
— duplication — inversion

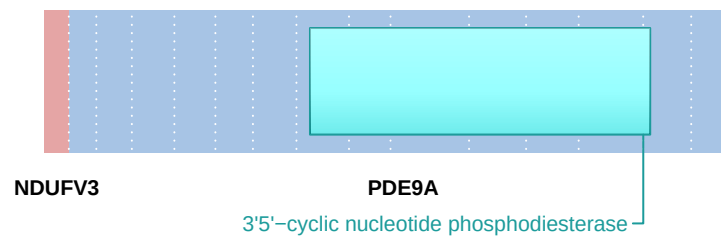
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 19
Discordant mates = 0



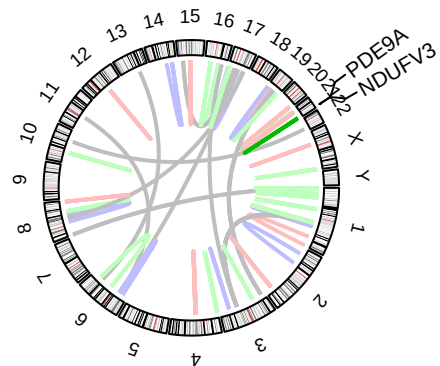
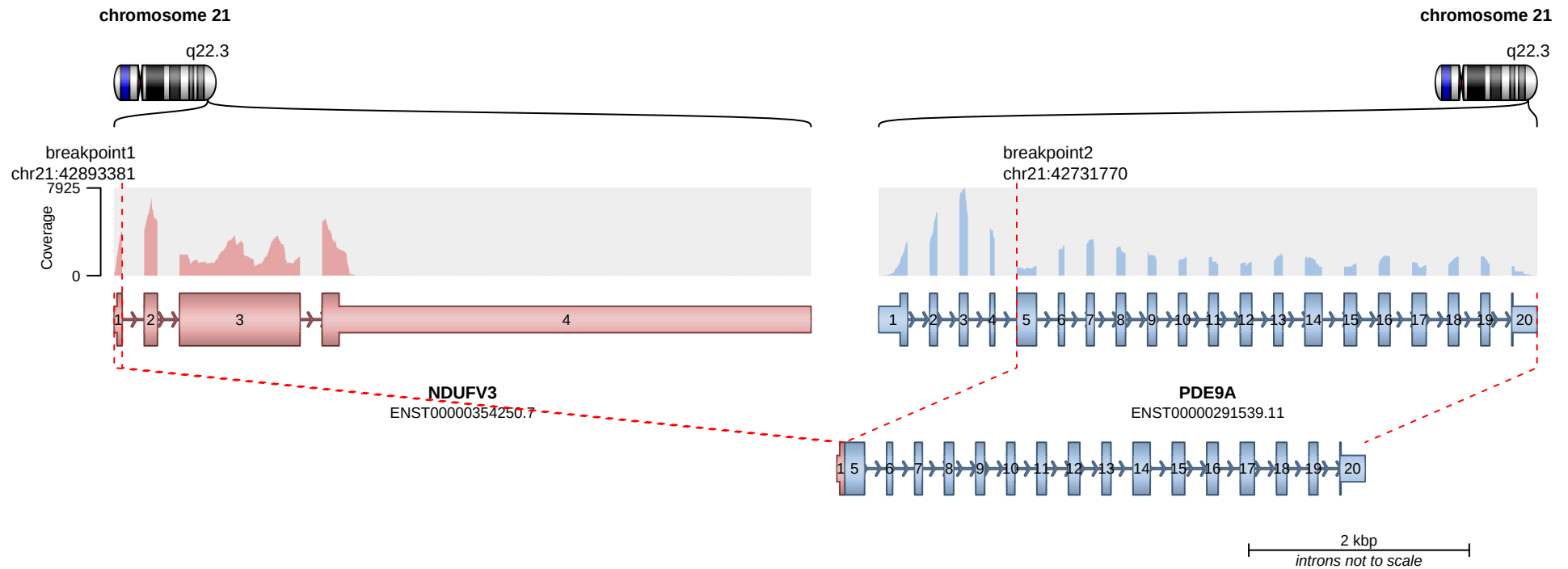
RETAINED PROTEIN DOMAINS reading frame unclear



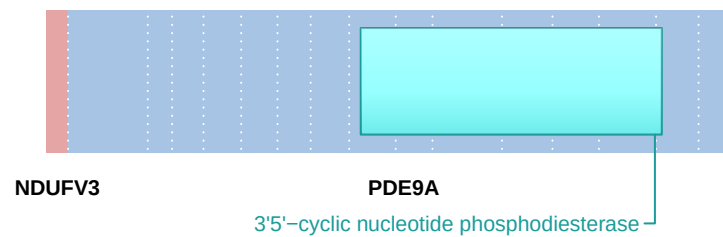
SUPPORTING READ COUNT

Split reads = 19
Discordant mates = 0

— translocation — deletion
— duplication — inversion



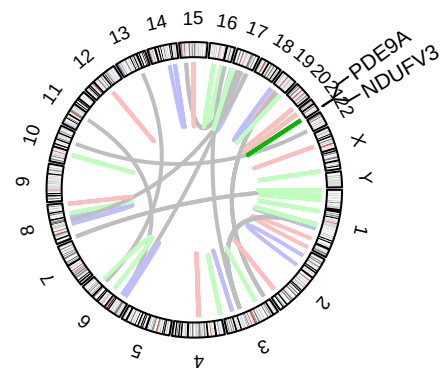
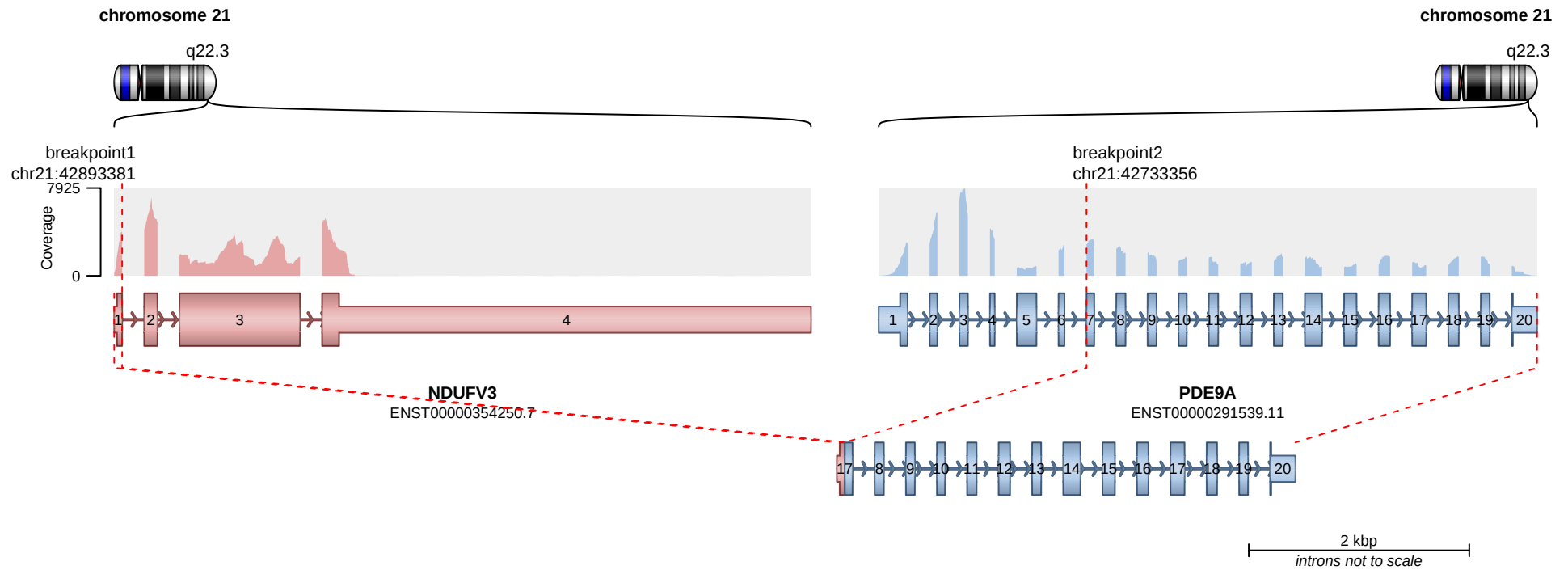
RETAINED PROTEIN DOMAINS
reading frame unclear



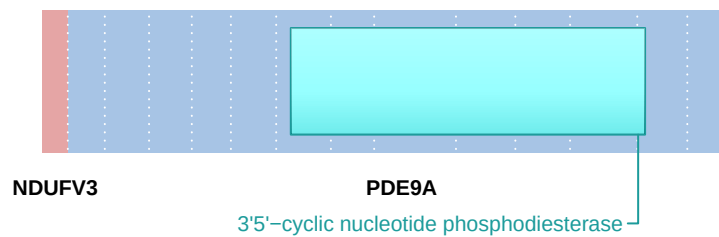
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

— translocation — deletion
— duplication — inversion



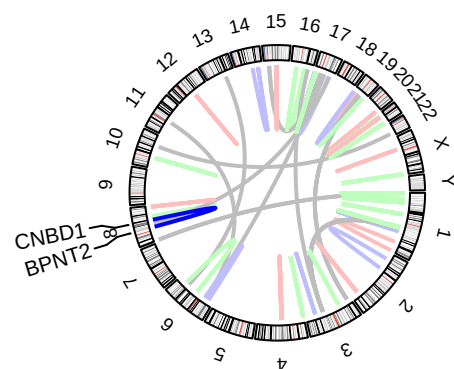
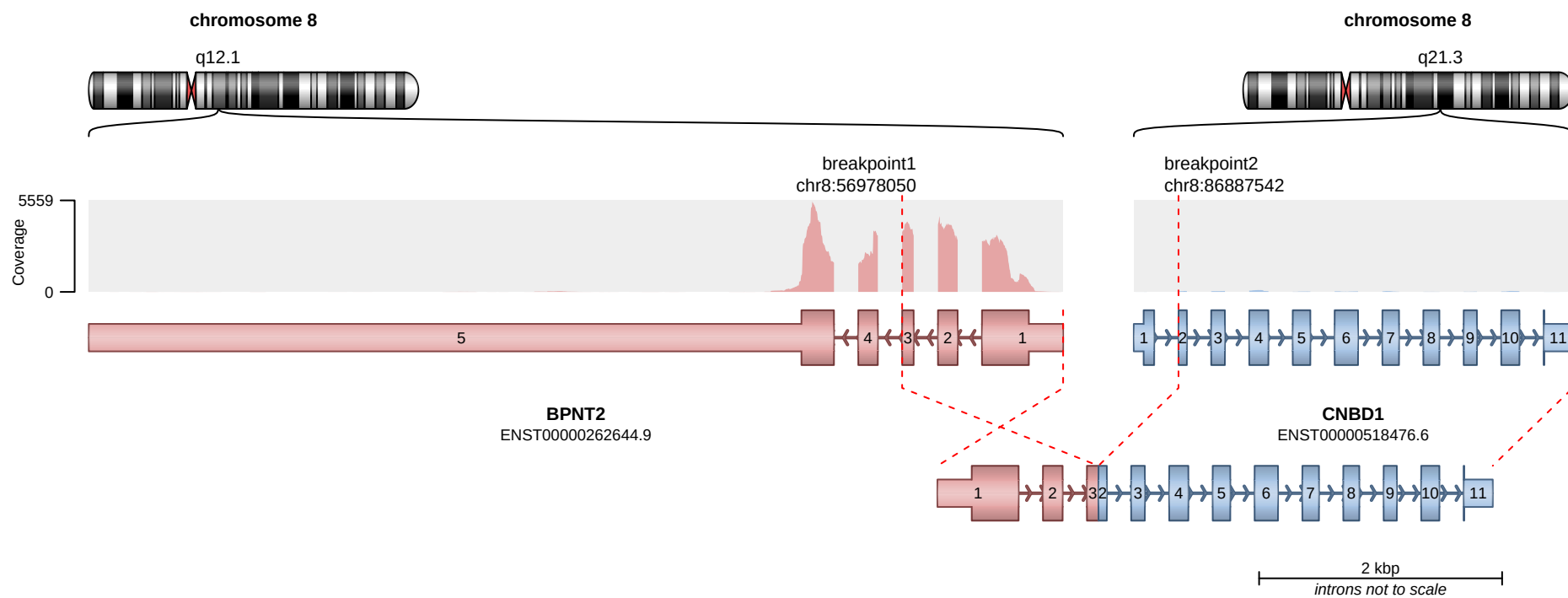
RETAINED PROTEIN DOMAINS
reading frame unclear



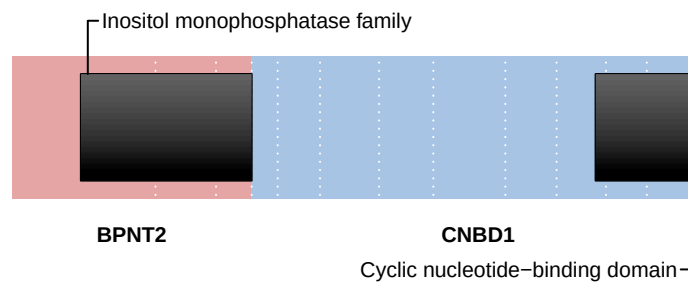
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

translocation deletion
duplication inversion



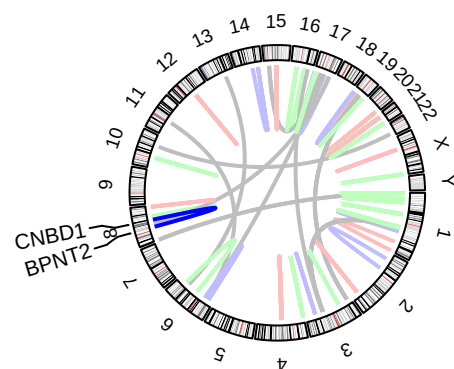
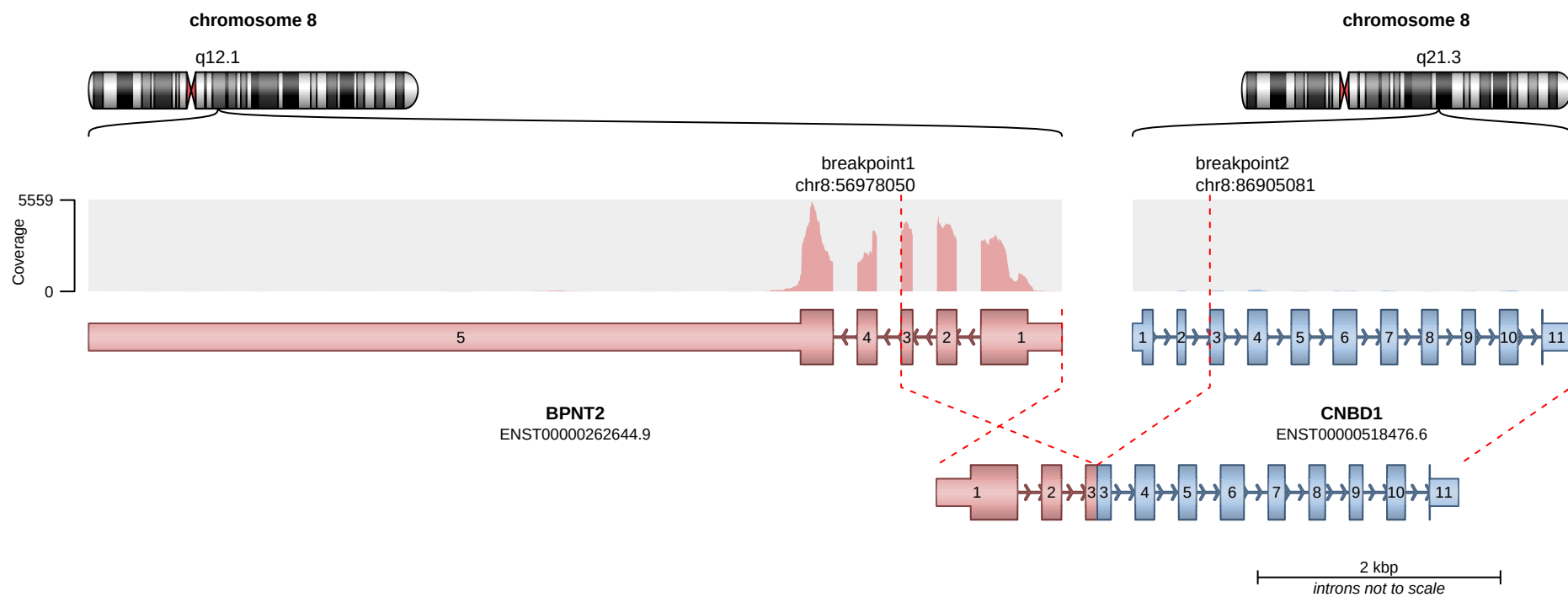
RETAINED PROTEIN DOMAINS reading frame unclear



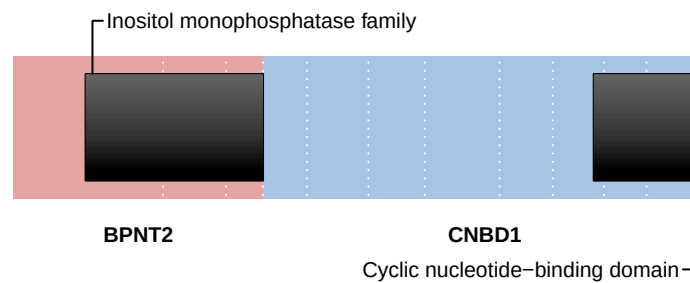
SUPPORTING READ COUNT

Split reads = 18
Discordant mates = 1

— translocation — deletion
— duplication — inversion



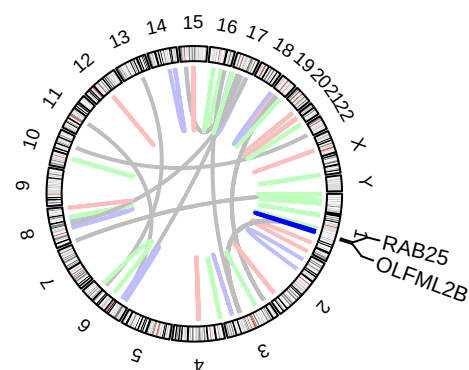
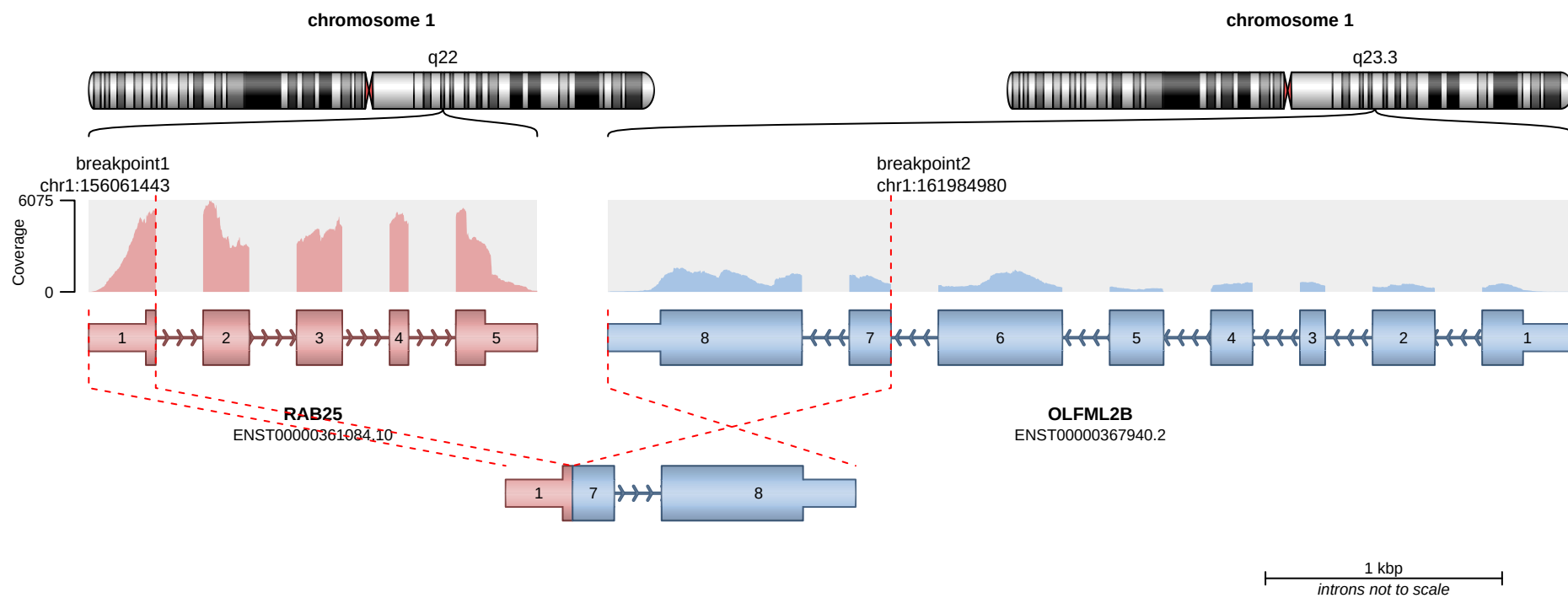
RETAINED PROTEIN DOMAINS reading frame unclear



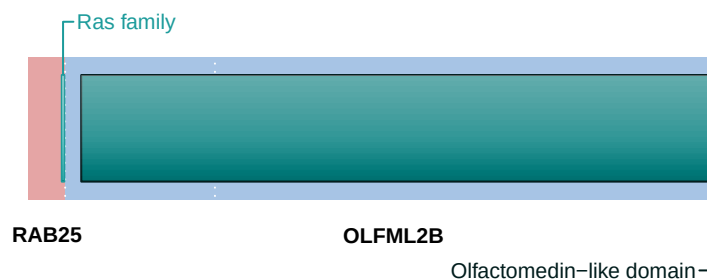
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 1

— translocation — deletion
— duplication — inversion



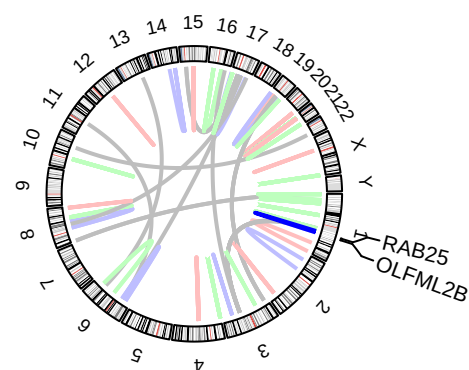
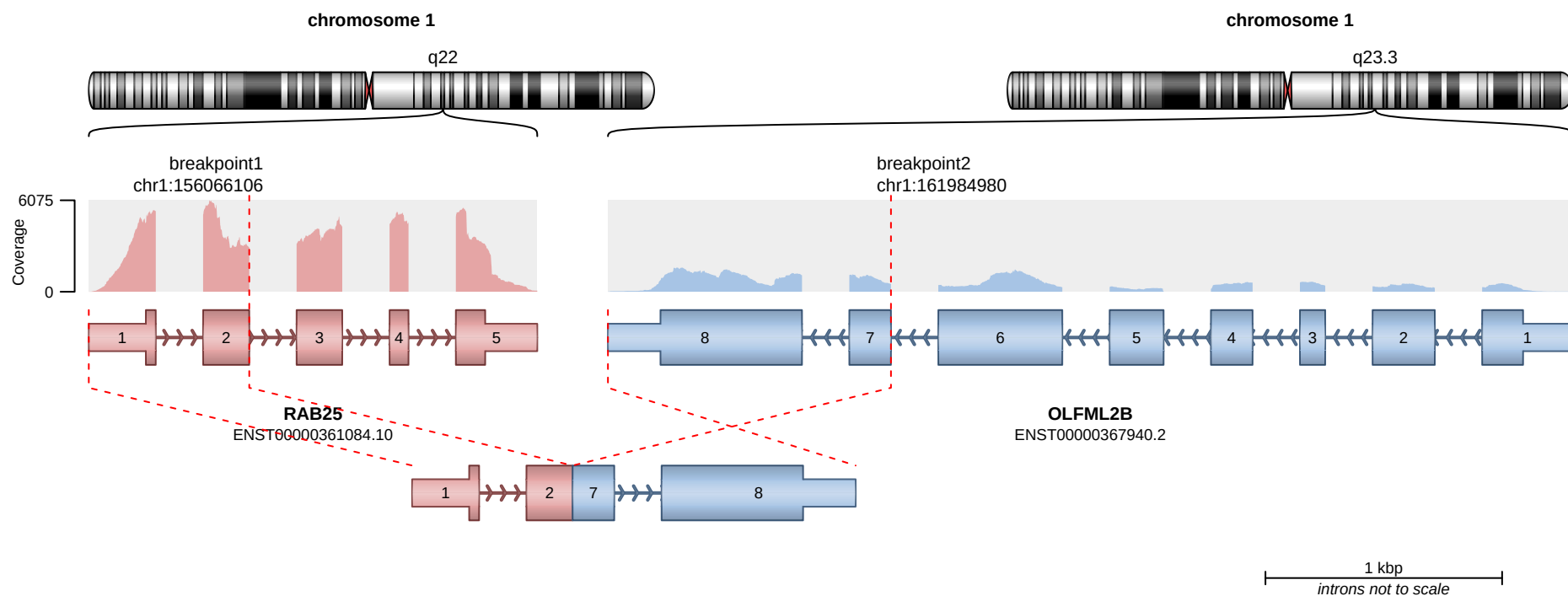
RETAINED PROTEIN DOMAINS reading frame unclear



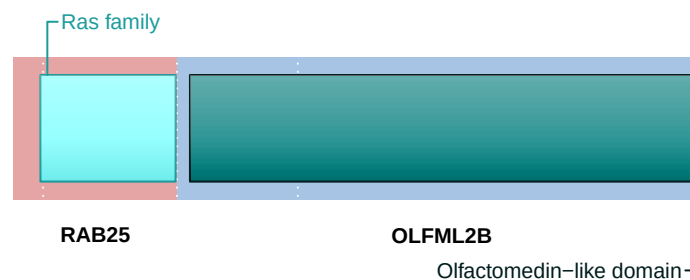
SUPPORTING READ COUNT

Split reads = 17
Discordant mates = 1

translocation deletion
duplication inversion



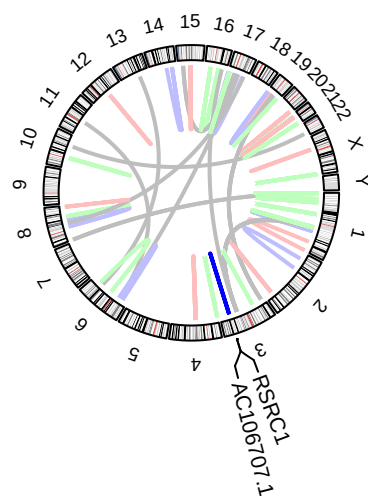
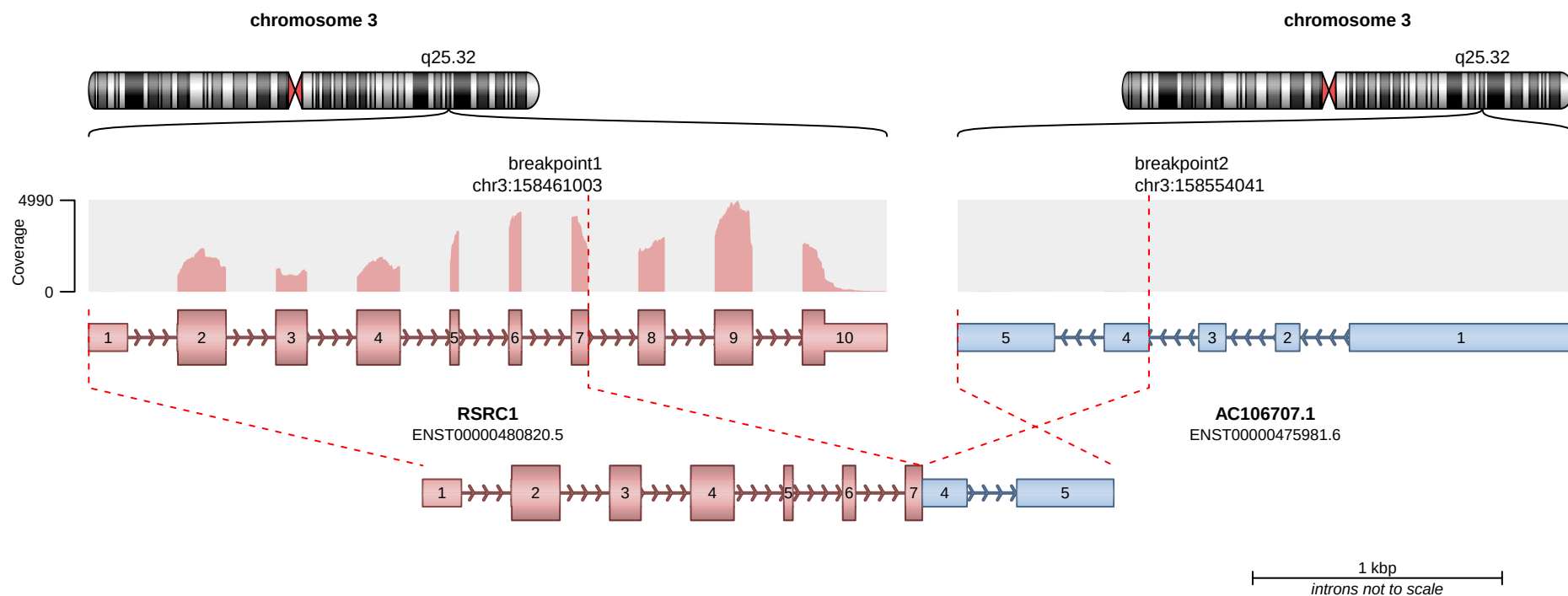
RETAINED PROTEIN DOMAINS reading frame unclear



SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 1

— translocation — deletion
— duplication — inversion

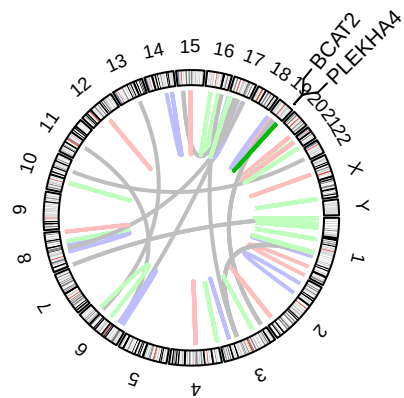
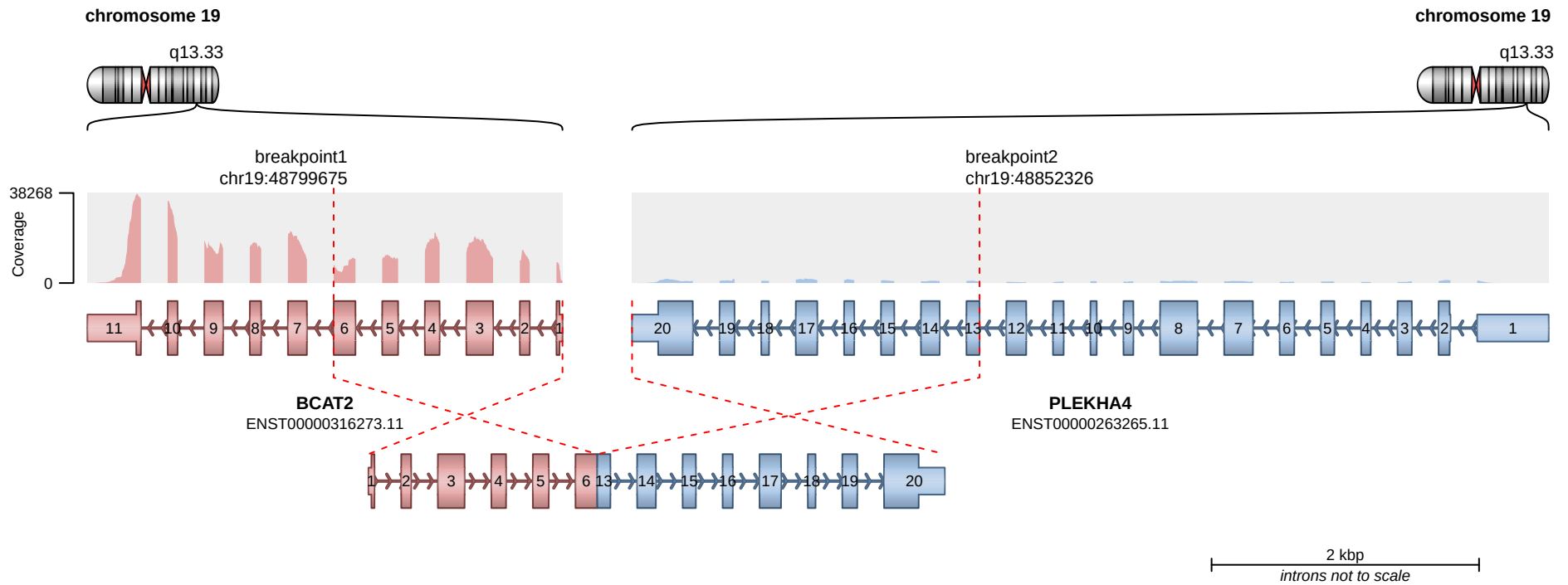


— translocation — deletion
— duplication — inversion

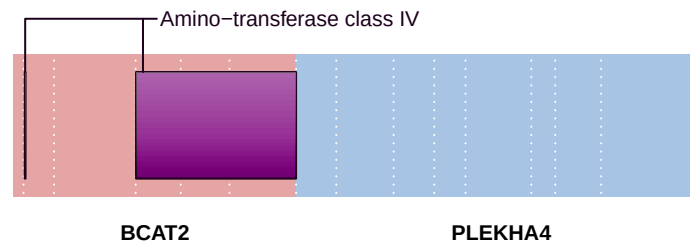
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 16
Discordant mates = 0



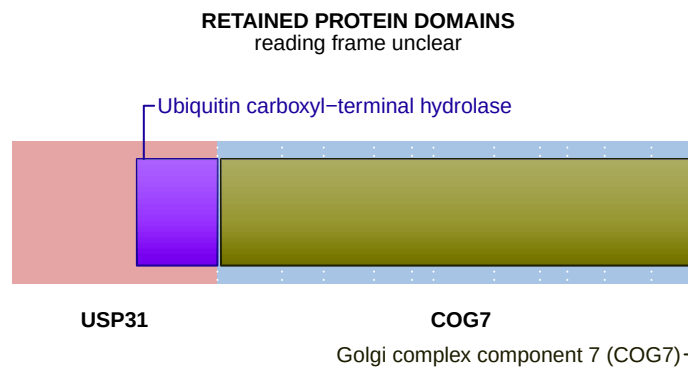
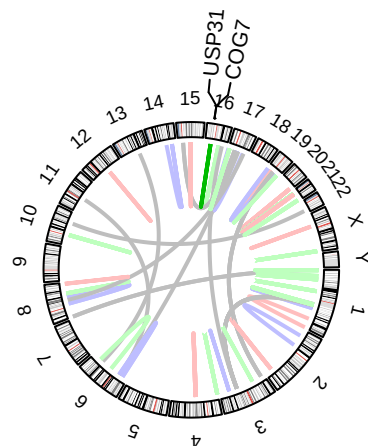
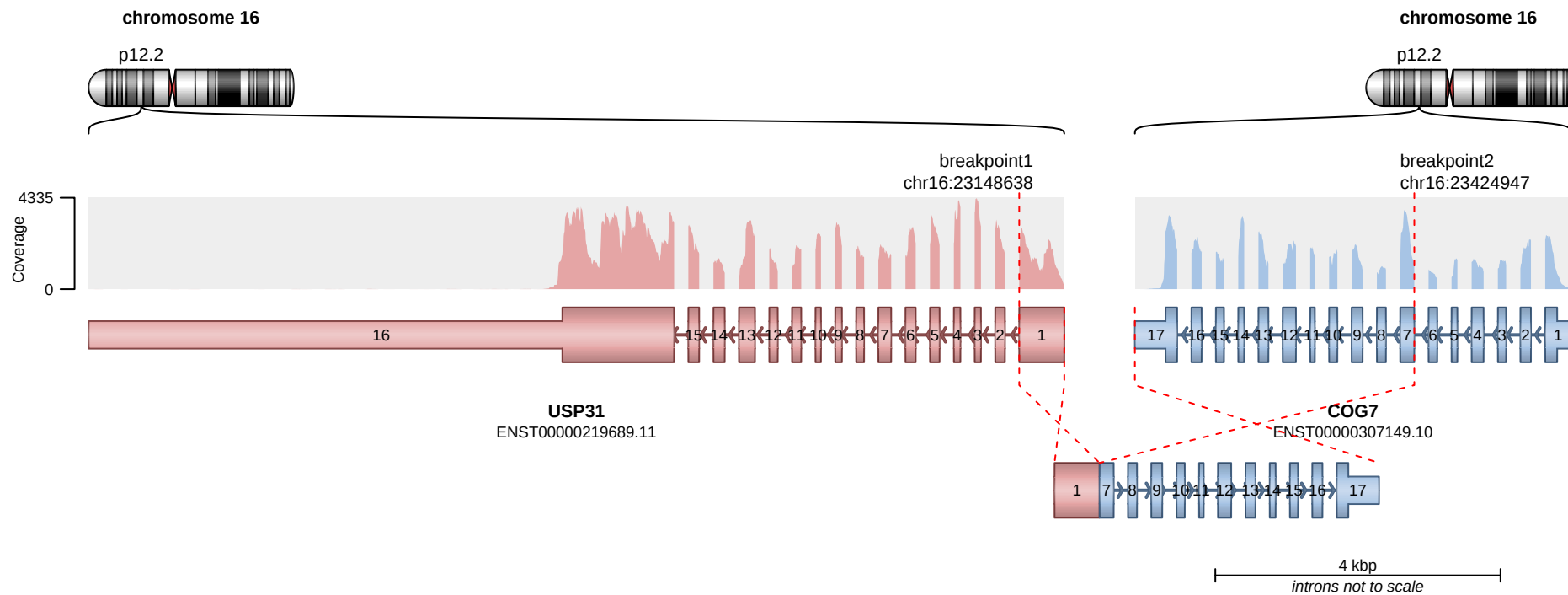
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 15
Discordant mates = 3

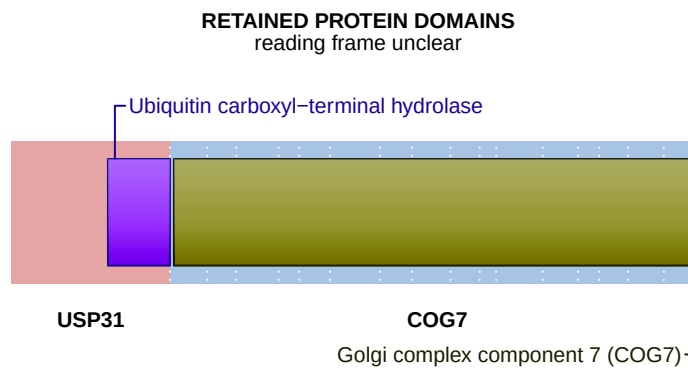
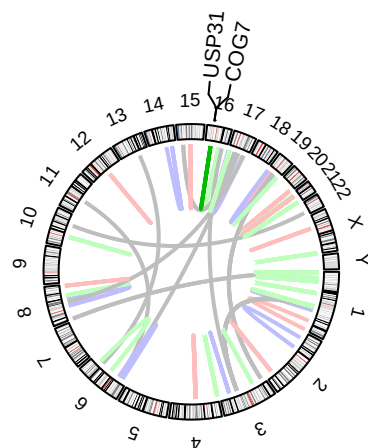
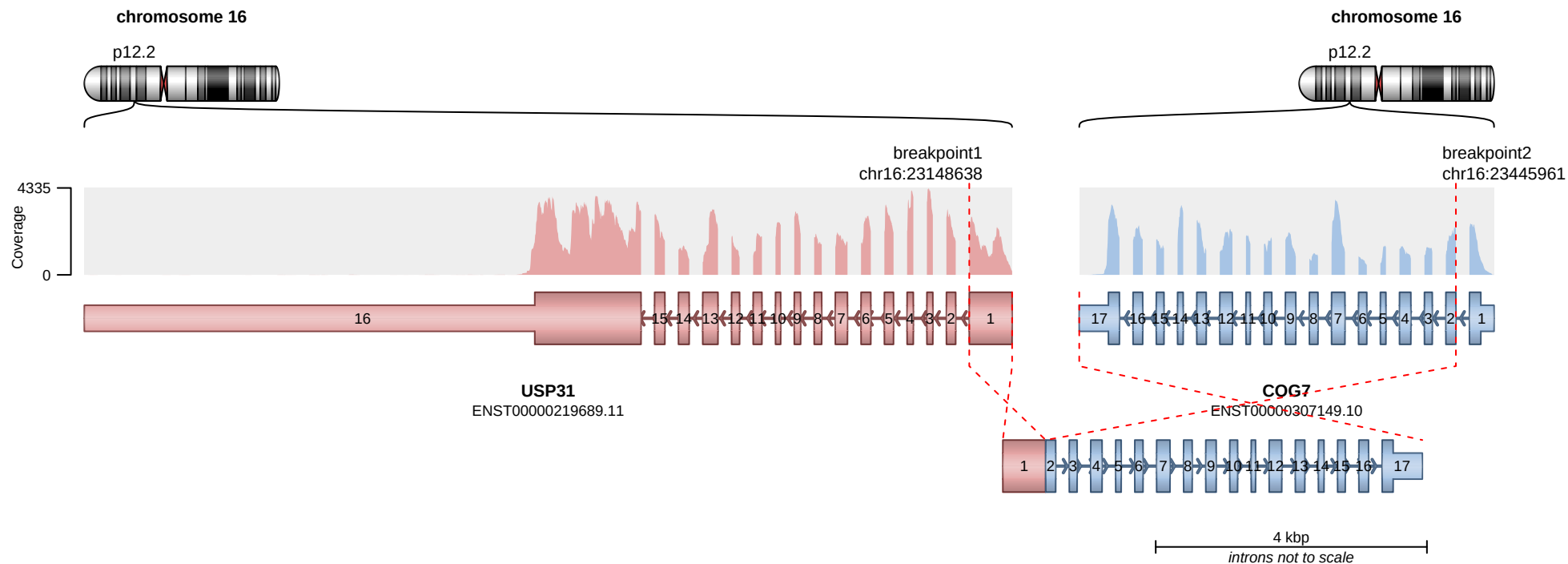
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 15
Discordant mates = 2

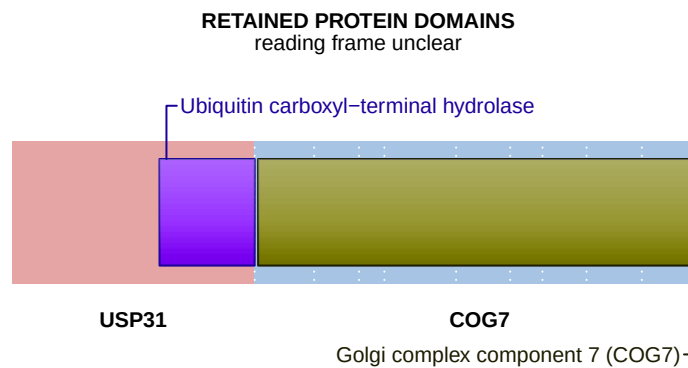
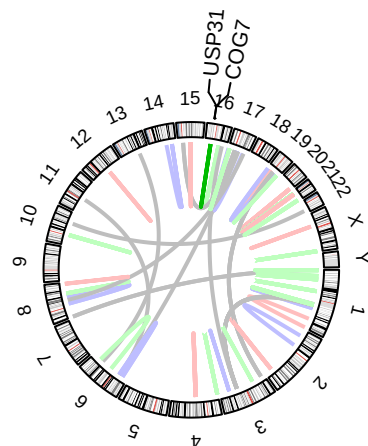
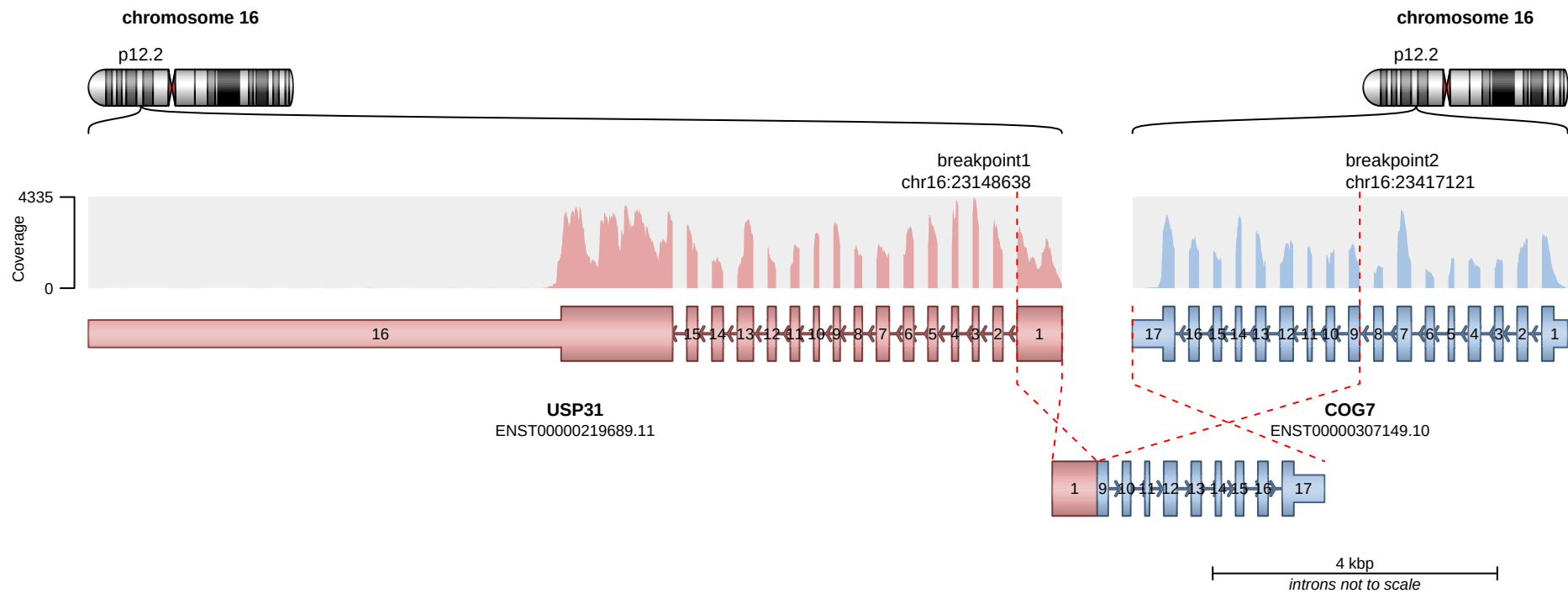
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 2

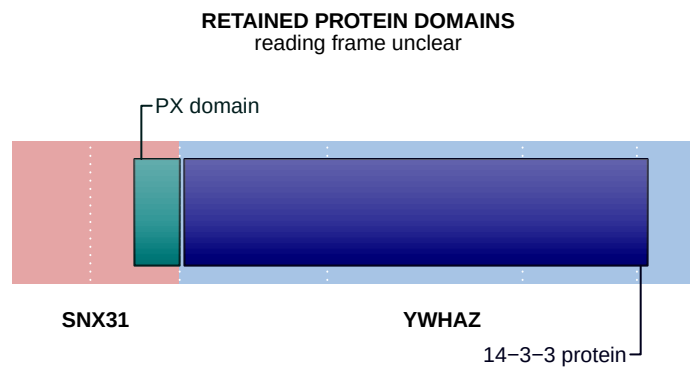
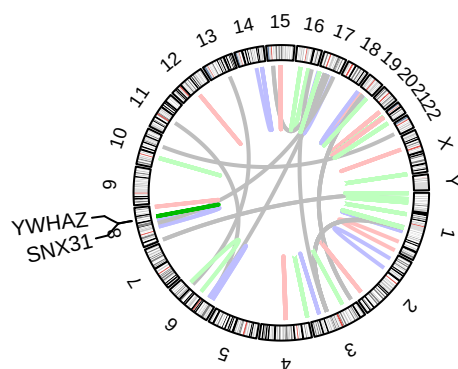
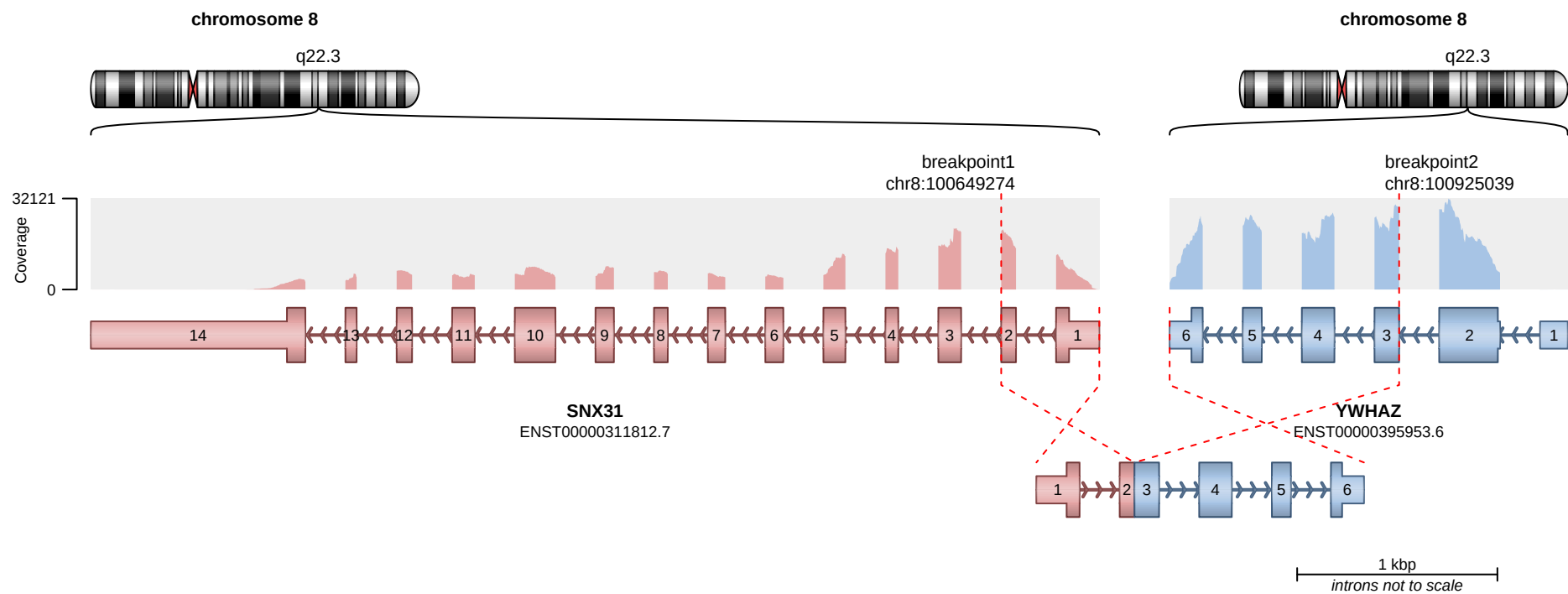
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

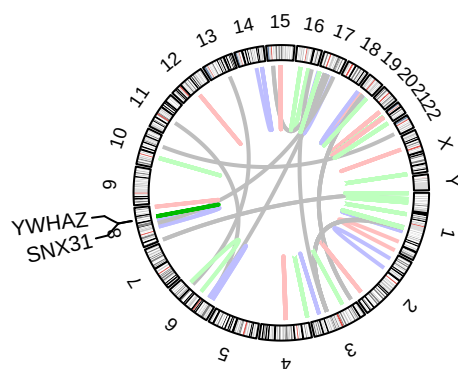
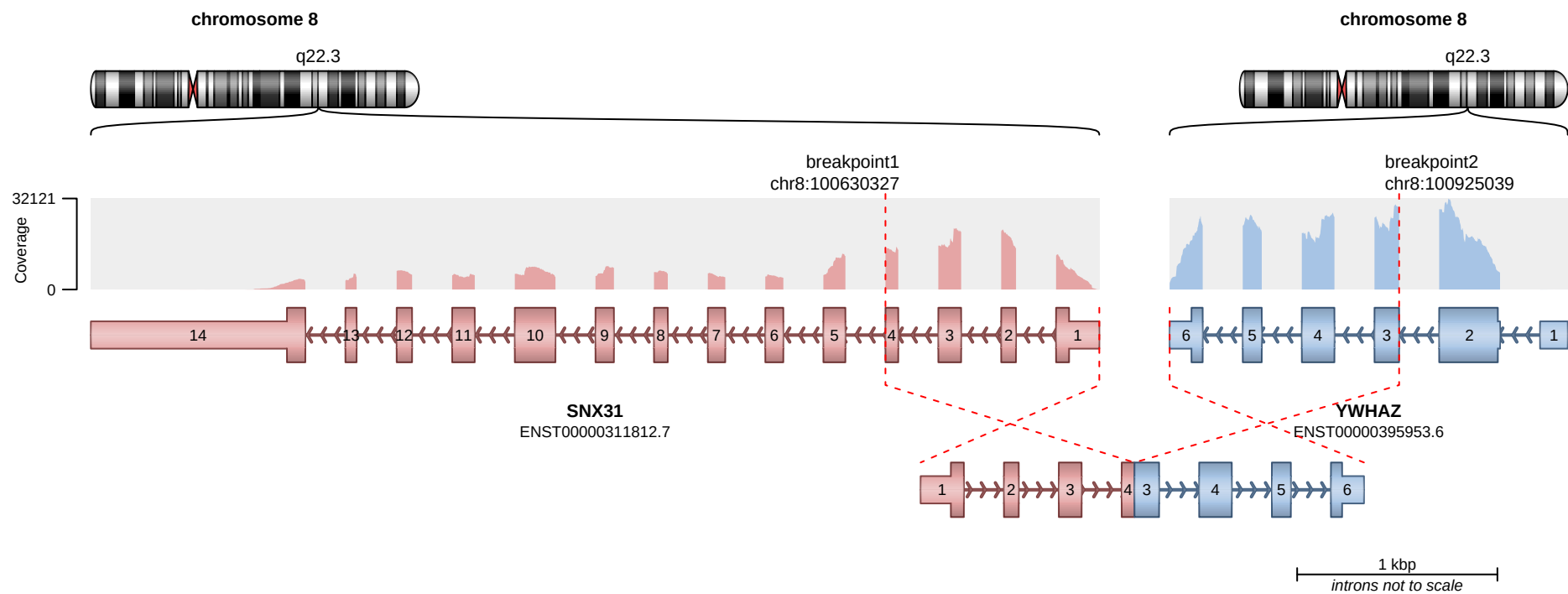
— translocation — deletion
— duplication — inversion



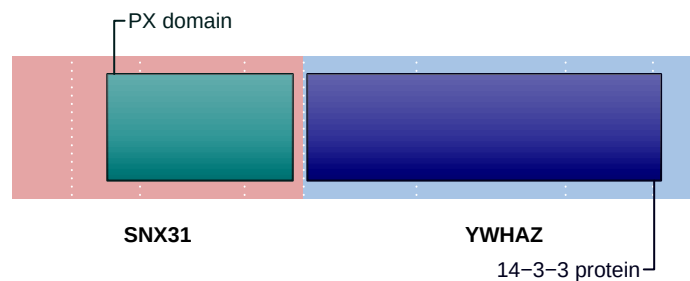
SUPPORTING READ COUNT

Split reads = 15
Discordant mates = 1

— translocation — deletion
— duplication — inversion



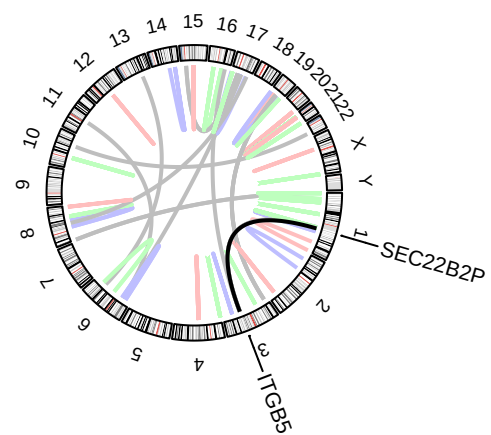
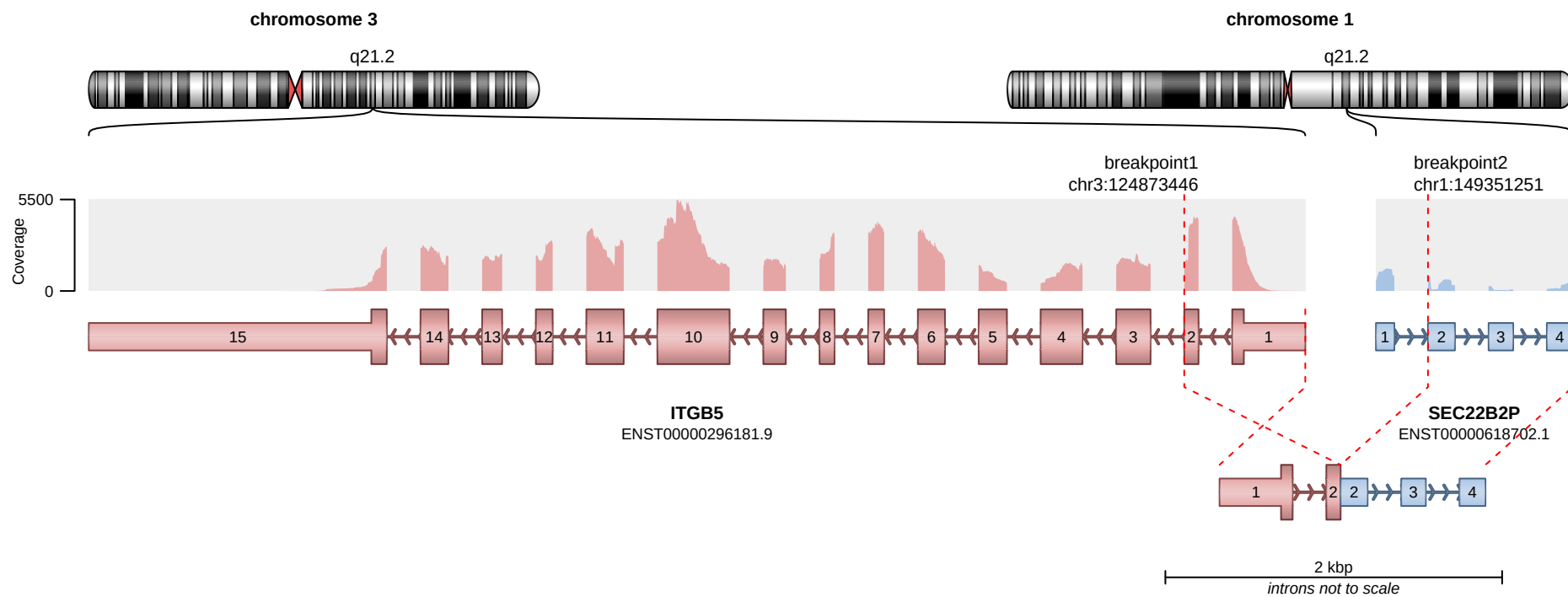
RETAINED PROTEIN DOMAINS
reading frame unclear



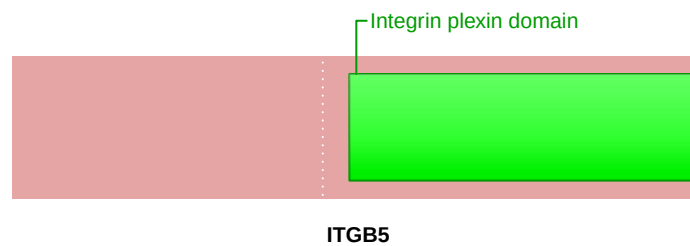
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

— translocation — deletion
— duplication — inversion



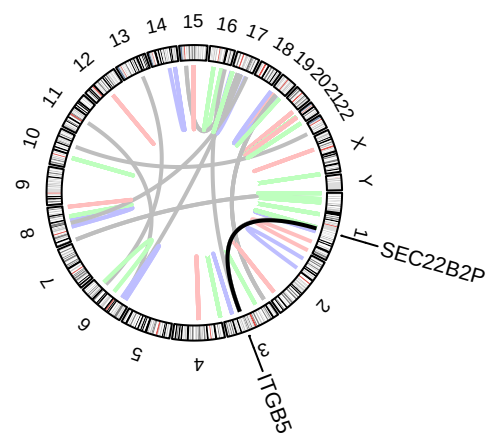
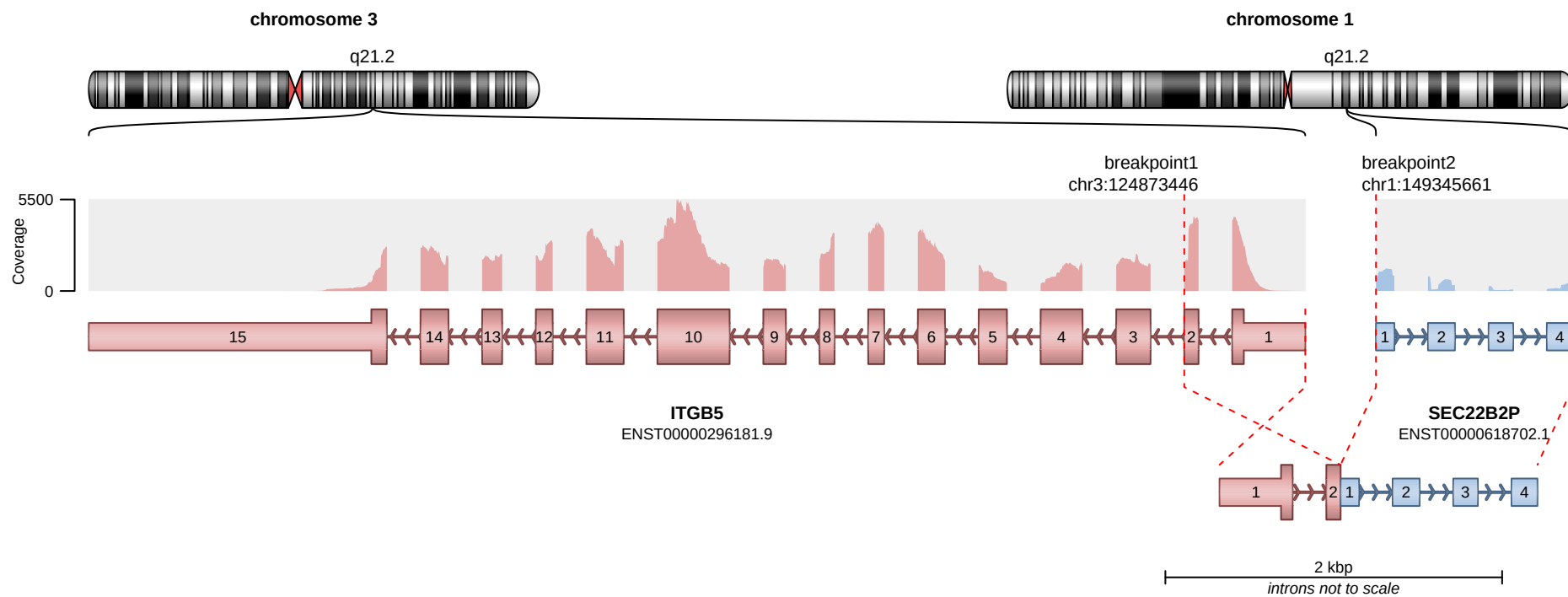
RETAINED PROTEIN DOMAINS
reading frame unclear



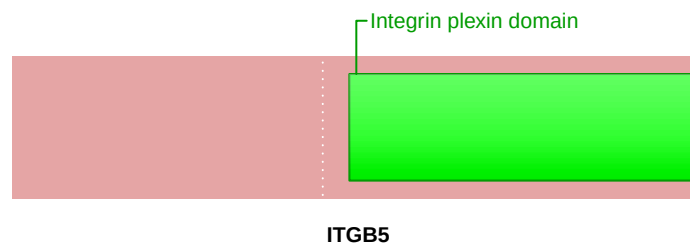
SUPPORTING READ COUNT

Split reads = 15
Discordant mates = 0

— translocation — deletion
— duplication — inversion



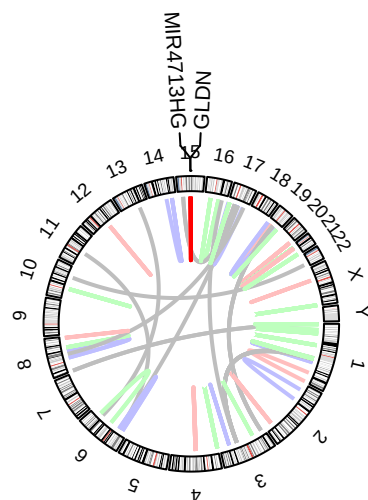
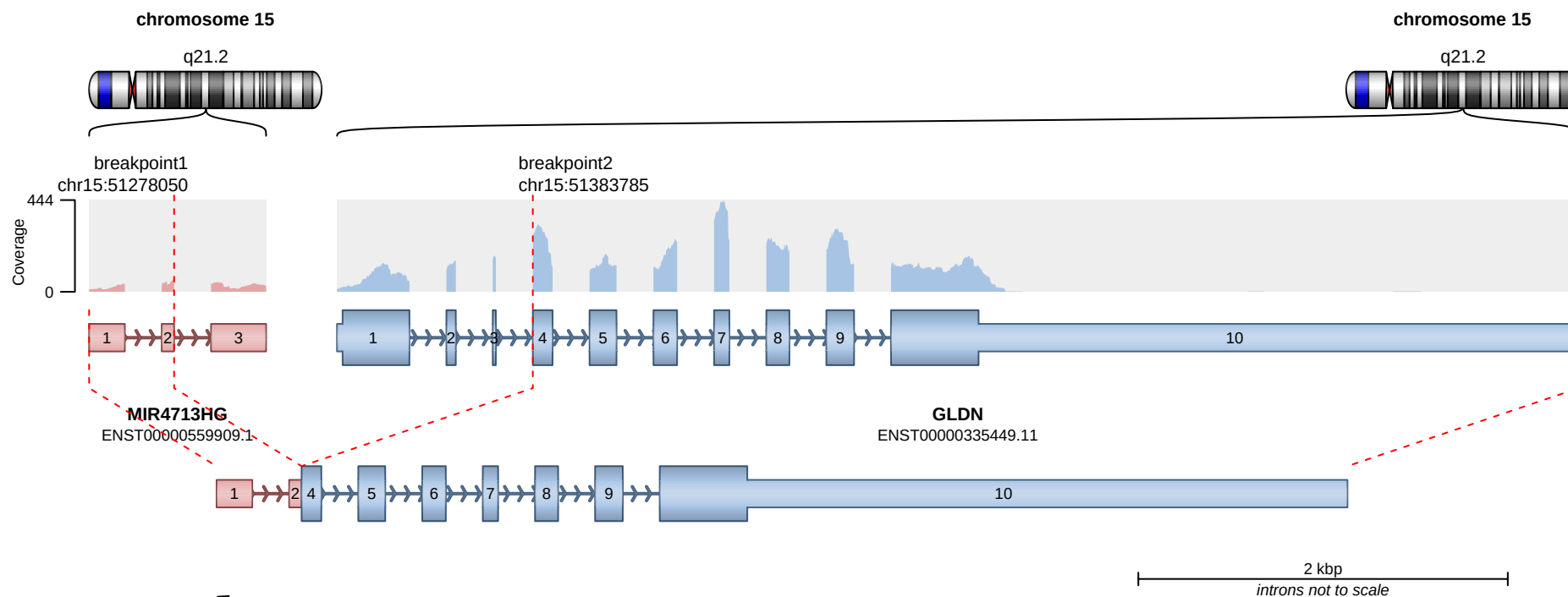
RETAINED PROTEIN DOMAINS
reading frame unclear



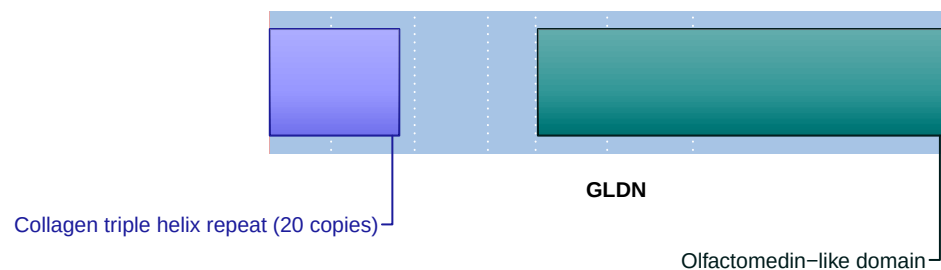
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

— translocation — deletion
— duplication — inversion



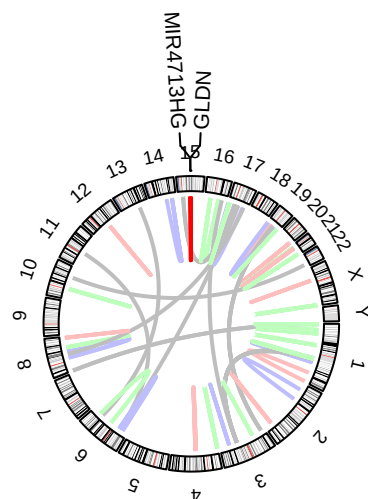
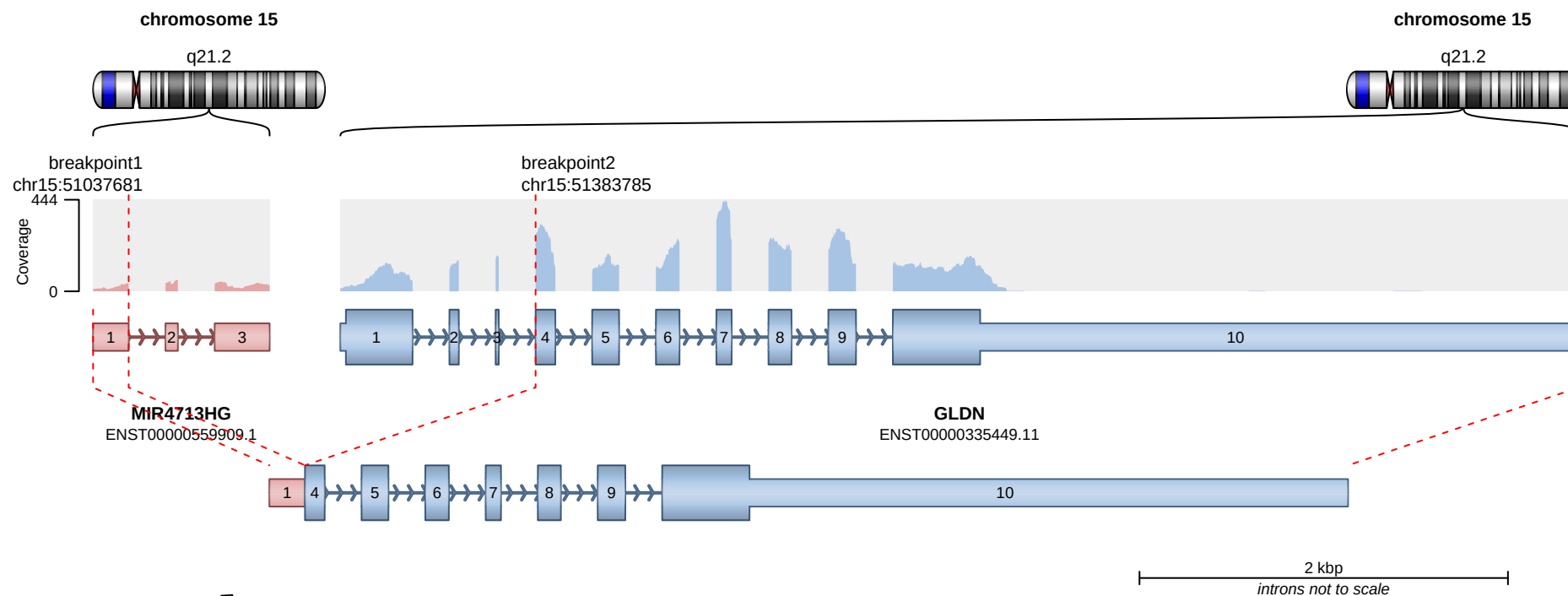
RETAINED PROTEIN DOMAINS reading frame unclear



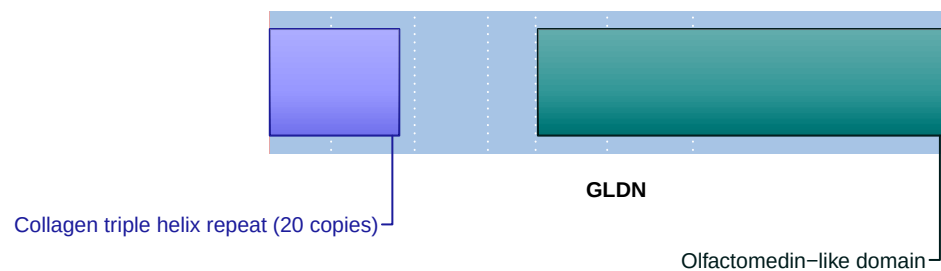
SUPPORTING READ COUNT

Split reads = 14
Discordant mates = 1

— translocation — deletion
— duplication — inversion



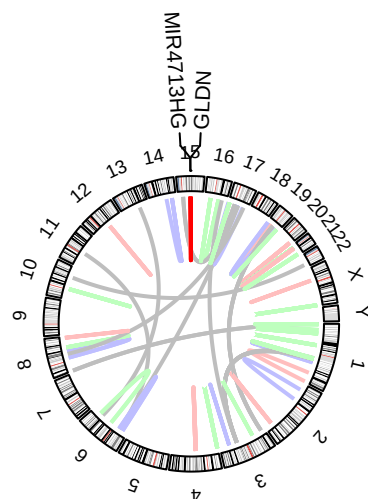
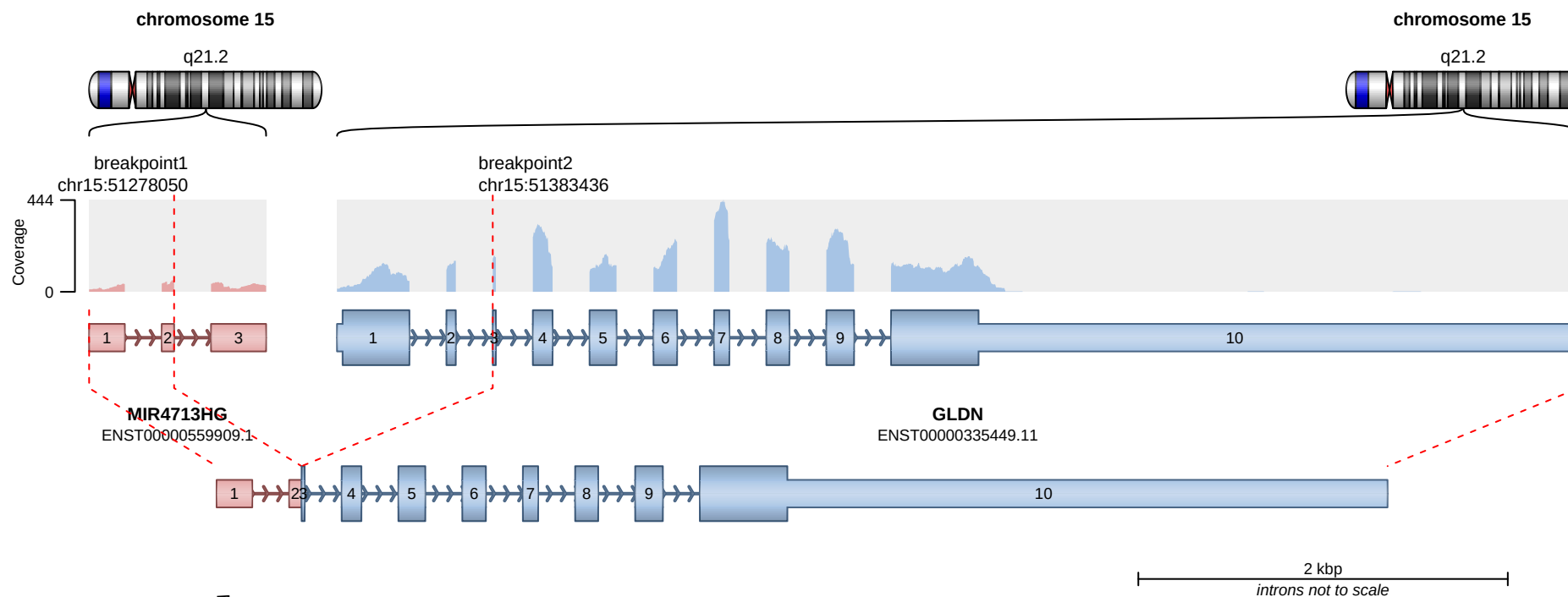
RETAINED PROTEIN DOMAINS reading frame unclear



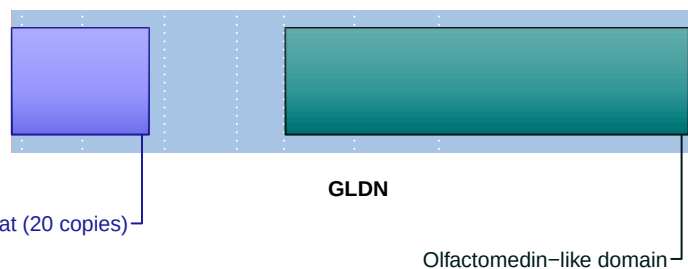
SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 1

— translocation — deletion
— duplication — inversion



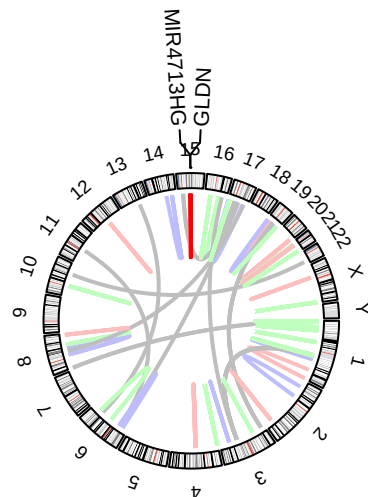
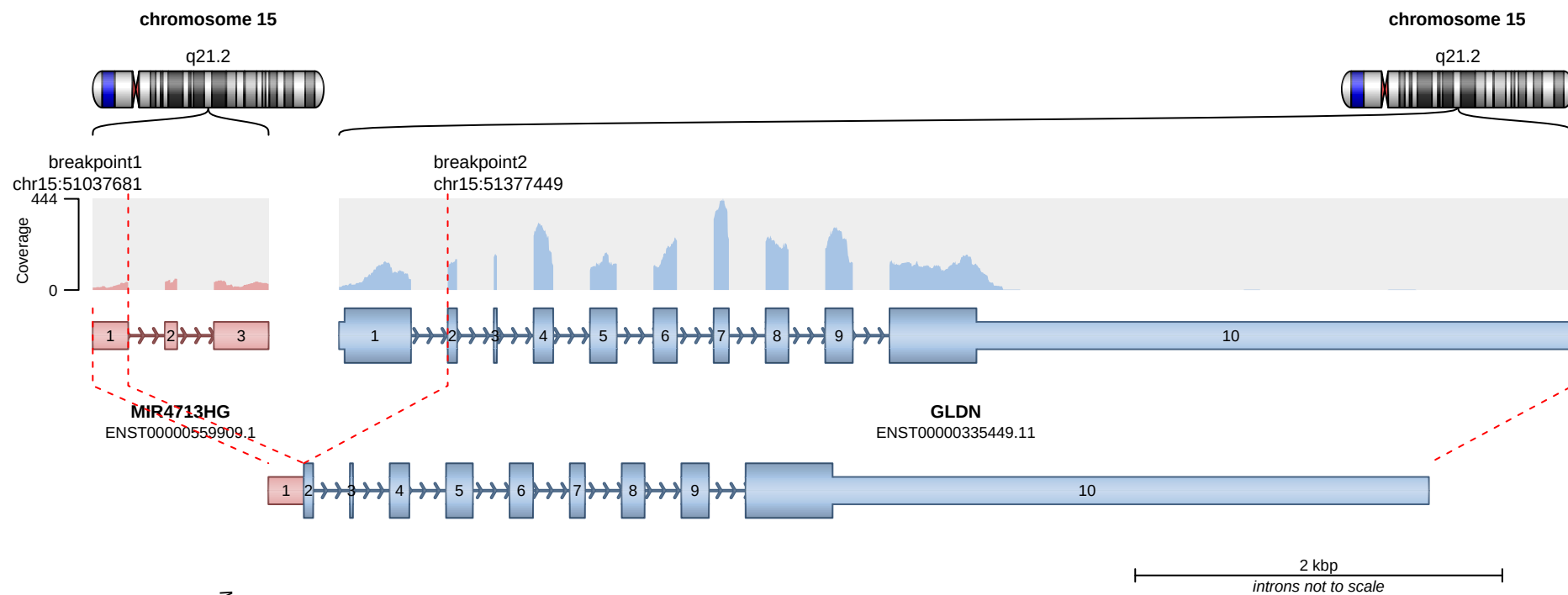
RETAINED PROTEIN DOMAINS reading frame unclear



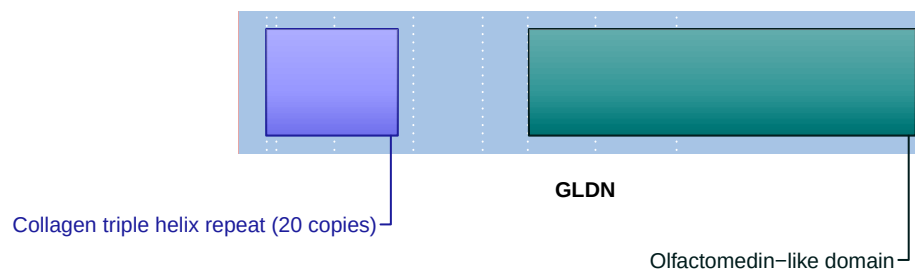
SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 1

translocation deletion
duplication inversion



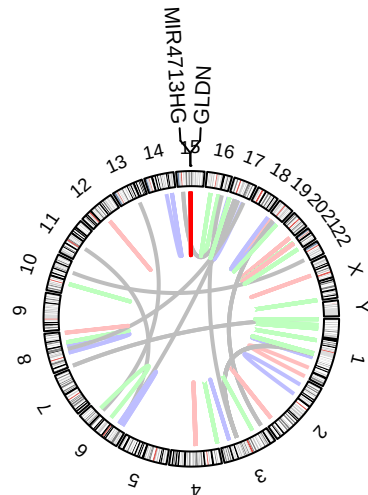
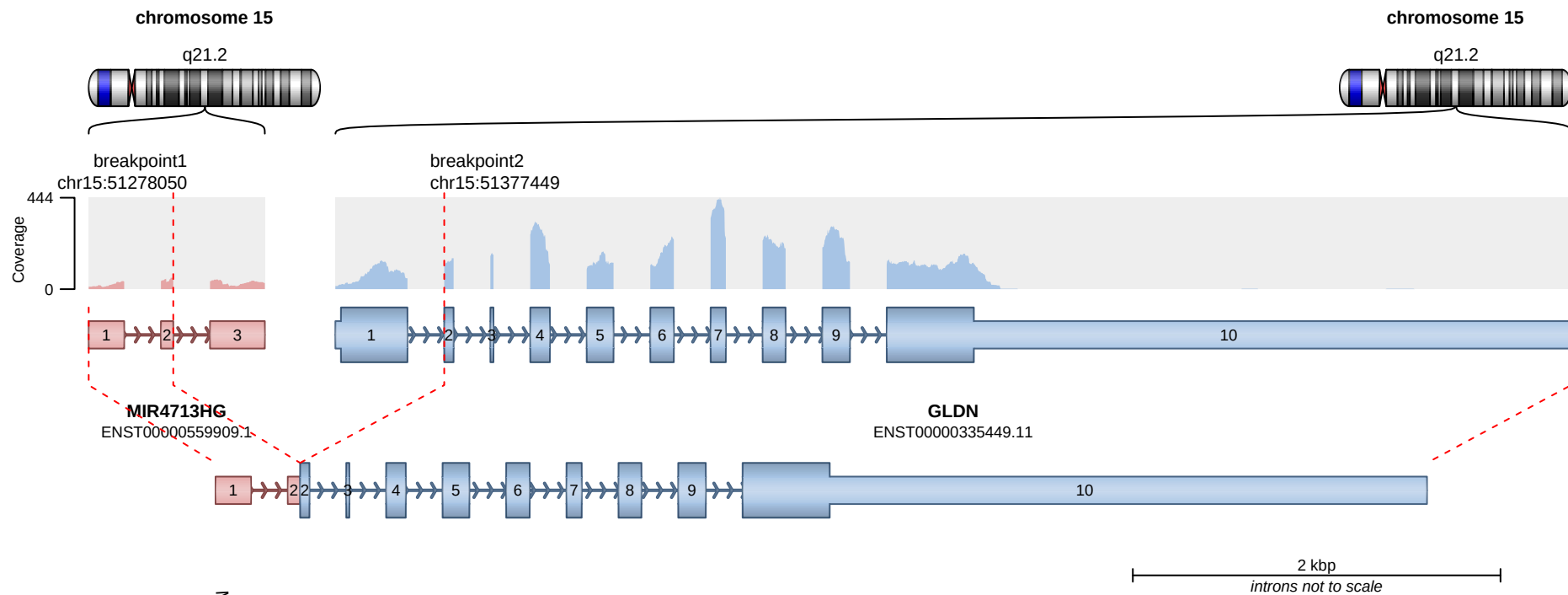
RETAINED PROTEIN DOMAINS reading frame unclear



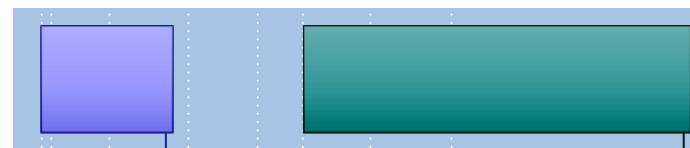
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 1

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS reading frame unclear



GLDN

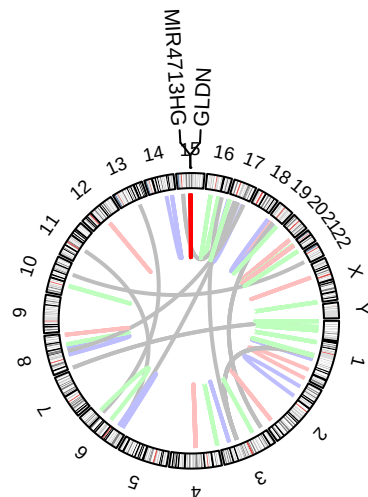
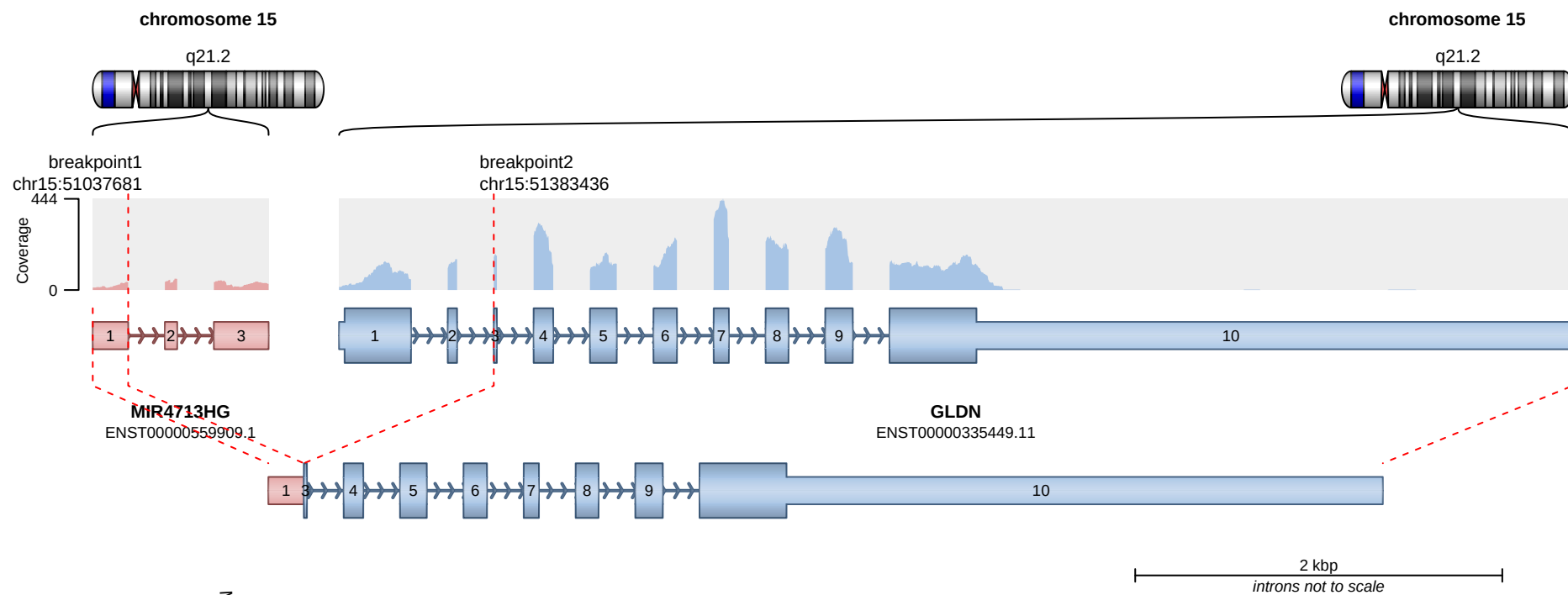
Collagen triple helix repeat (20 copies)

Olfactomedin-like domain

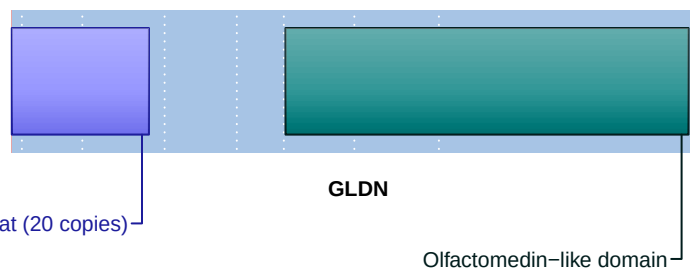
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 1

— translocation — deletion
— duplication — inversion



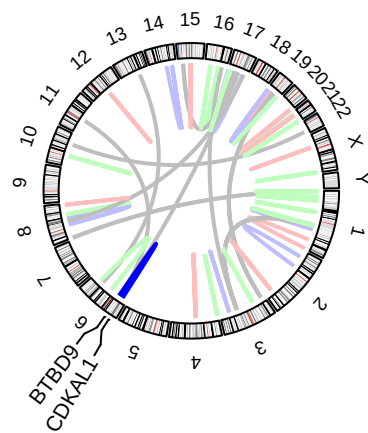
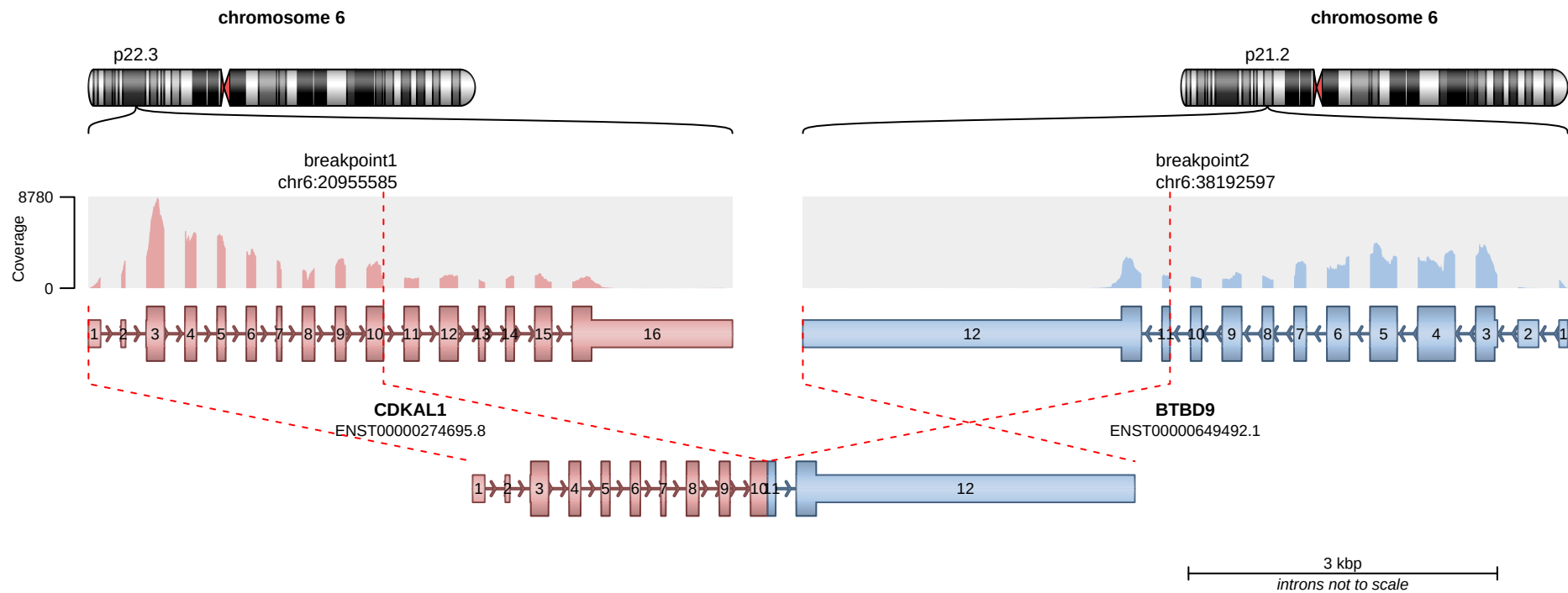
RETAINED PROTEIN DOMAINS reading frame unclear



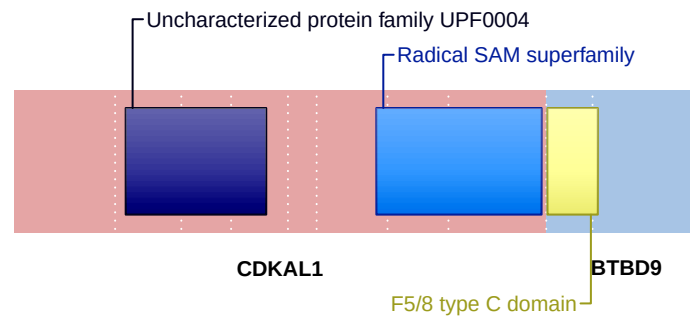
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

translocation deletion
duplication inversion



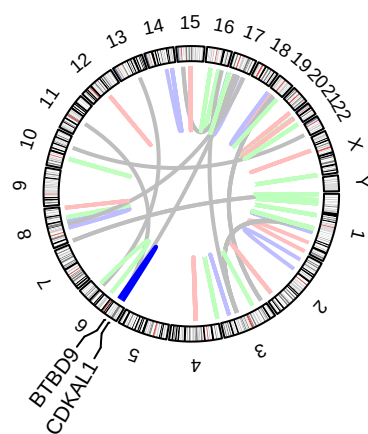
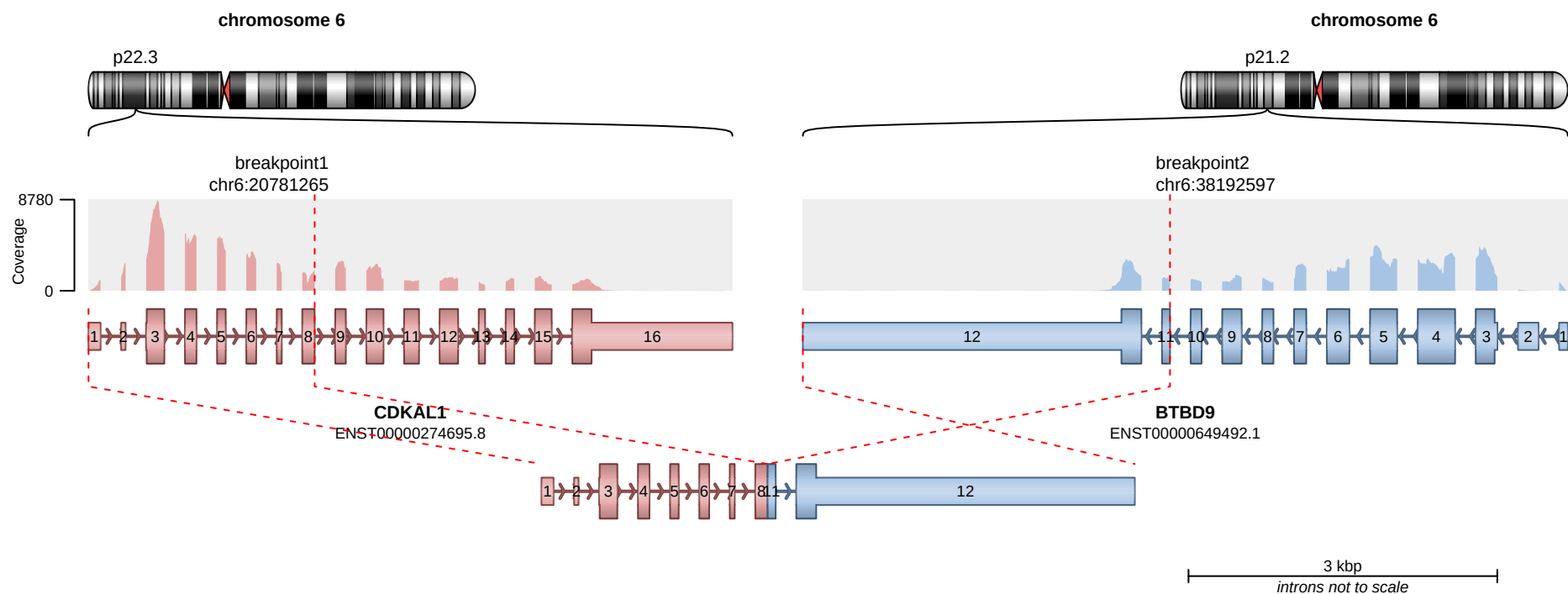
RETAINED PROTEIN DOMAINS reading frame unclear



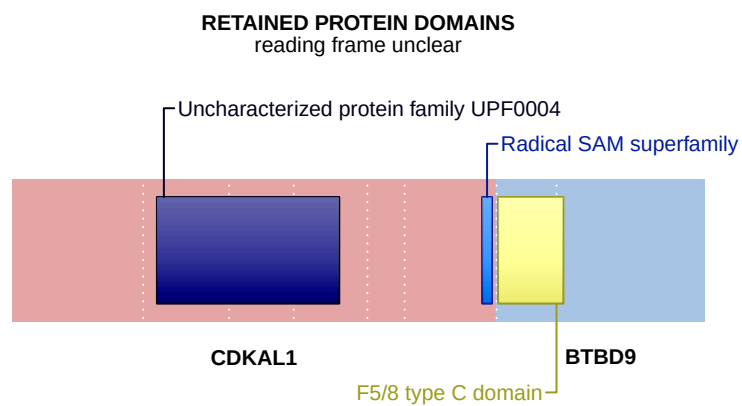
SUPPORTING READ COUNT

Split reads = 14
Discordant mates = 0

— translocation — deletion
— duplication — inversion

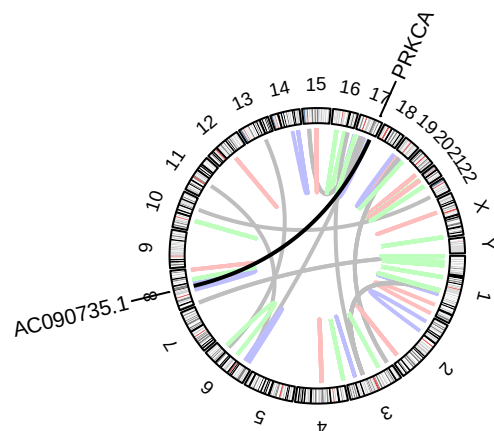
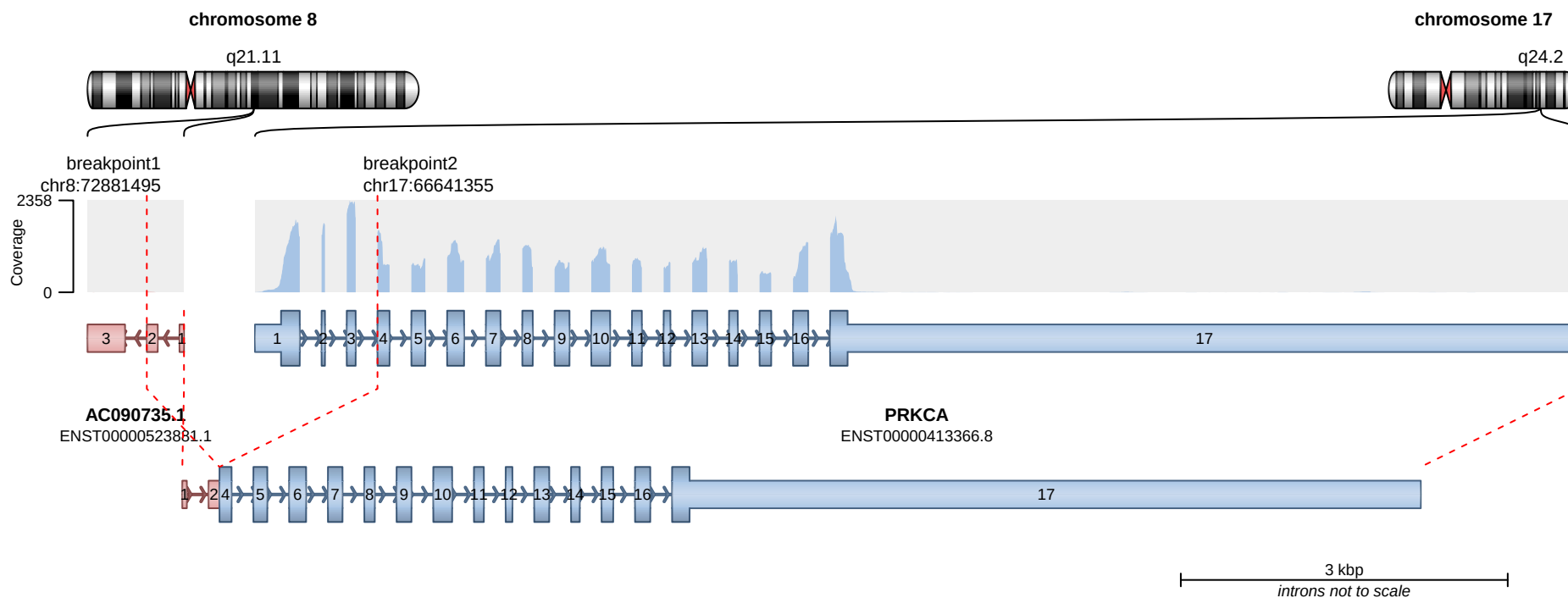


— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



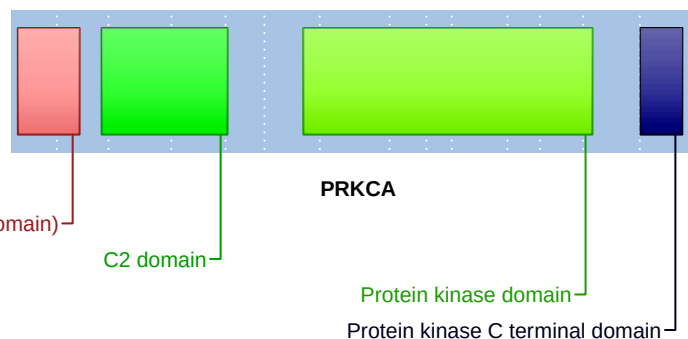
Phorbol esters/diacylglycerol binding domain (C1 domain)

C2 domain

Protein kinase domain

Protein kinase C terminal domain

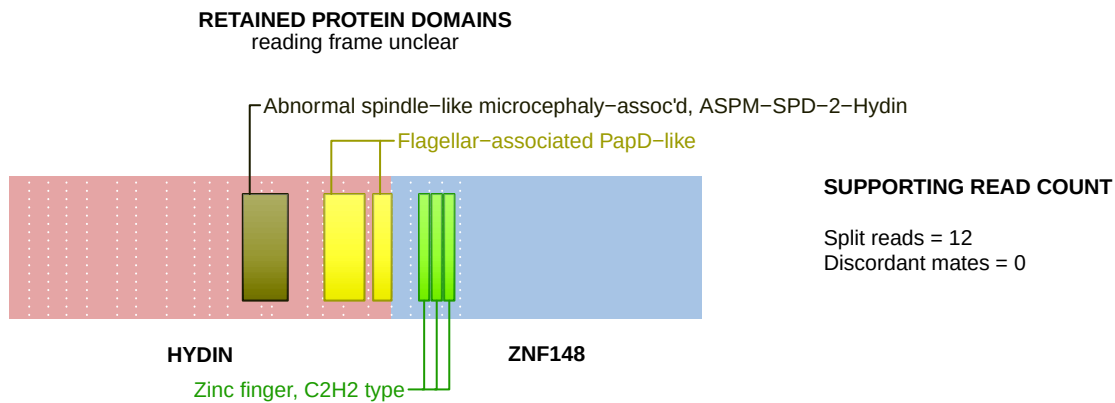
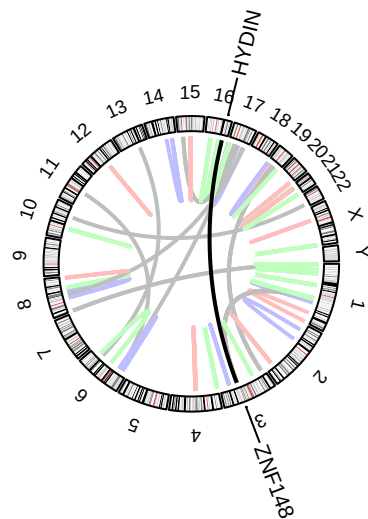
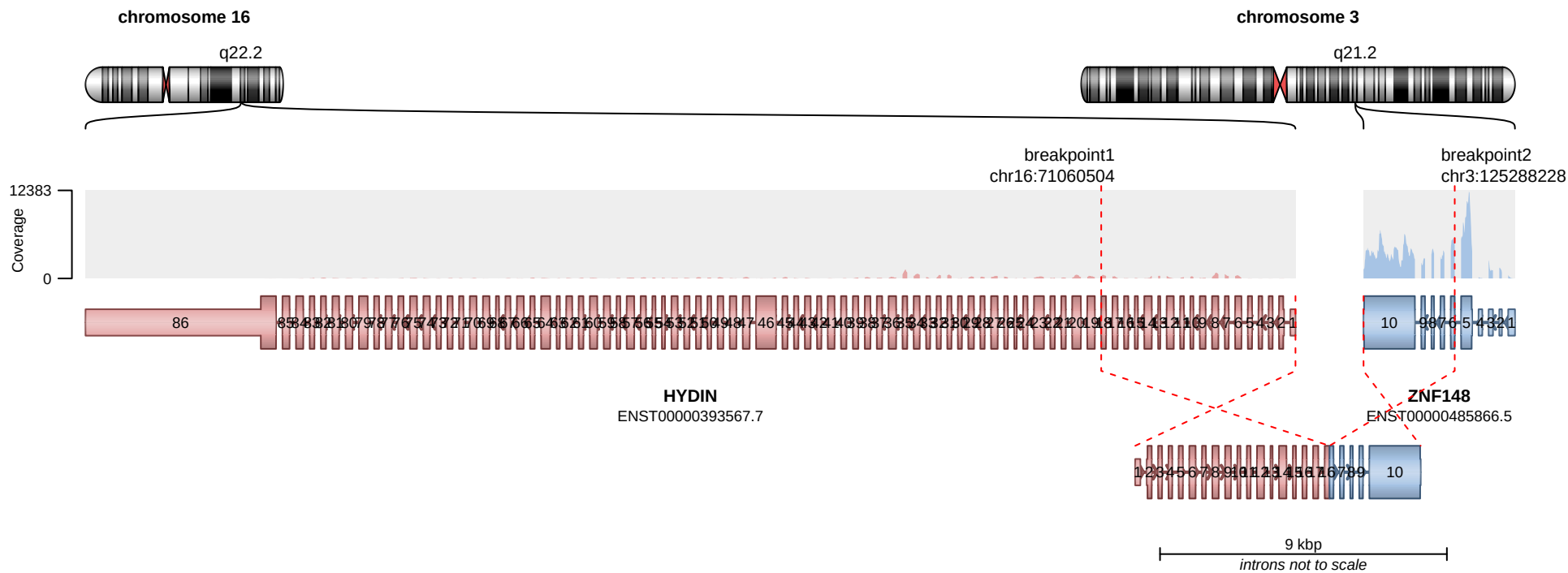
RETAINED PROTEIN DOMAINS
reading frame unclear



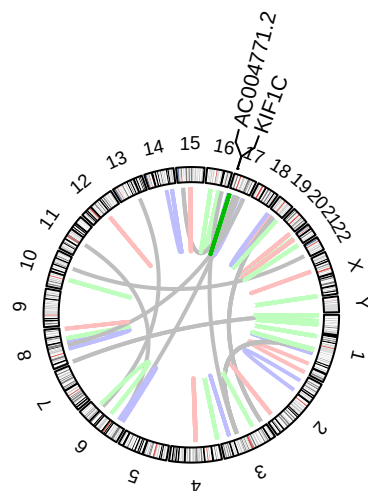
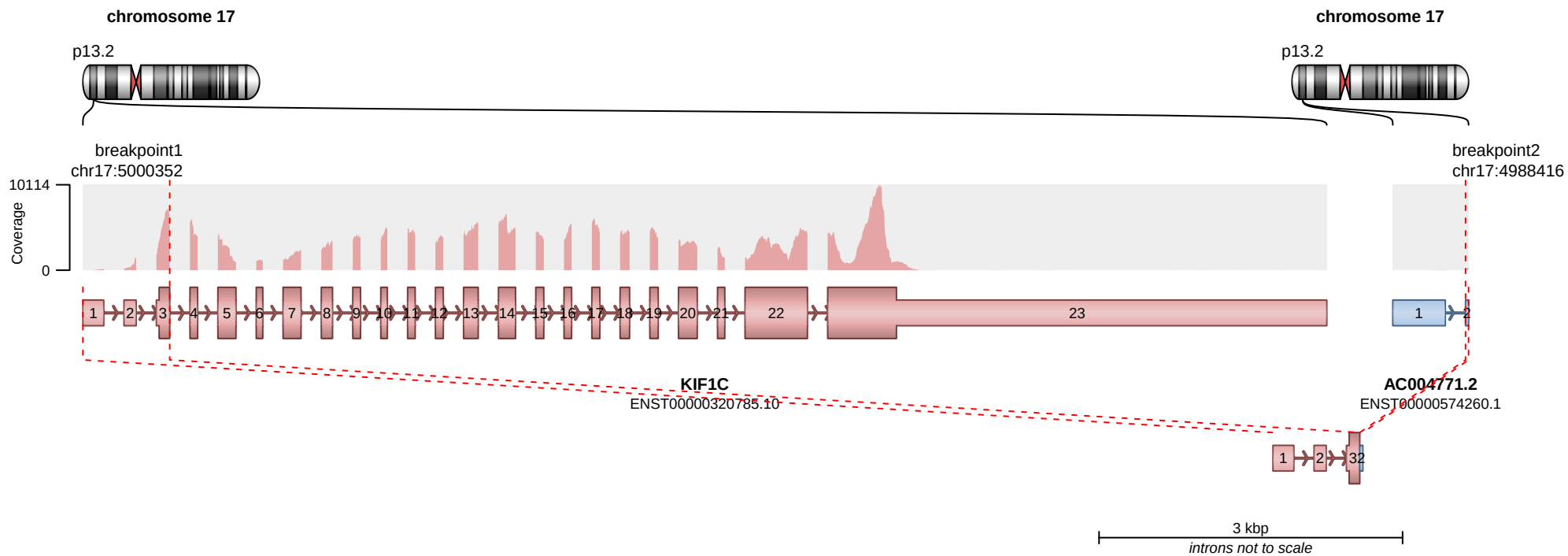
SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 0

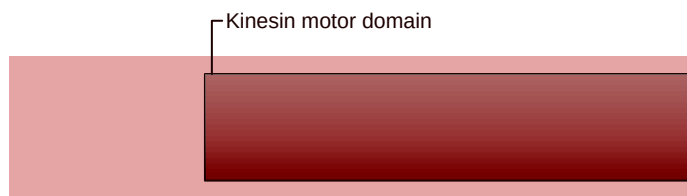
— translocation — deletion
— duplication — inversion



— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS reading frame unclear

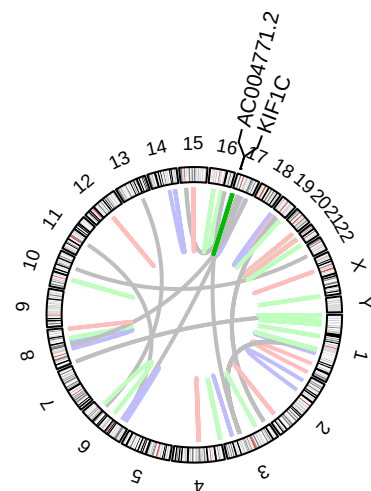
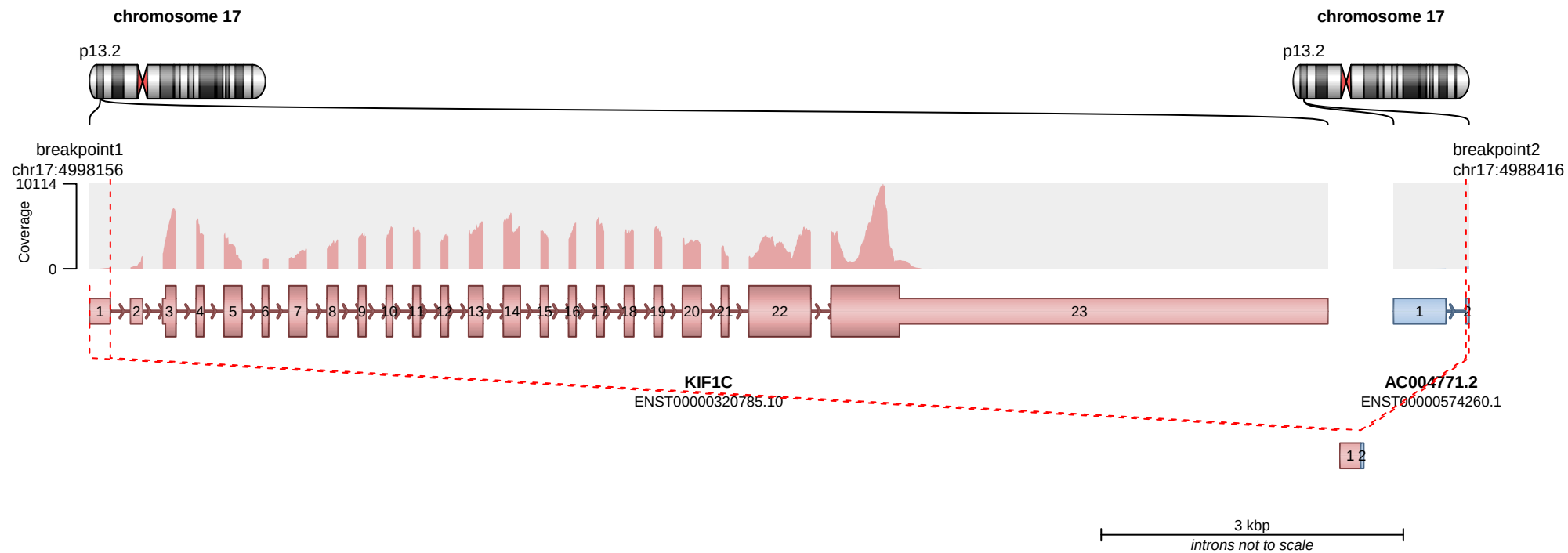


KIF1C

SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 0

— translocation — deletion
— duplication — inversion

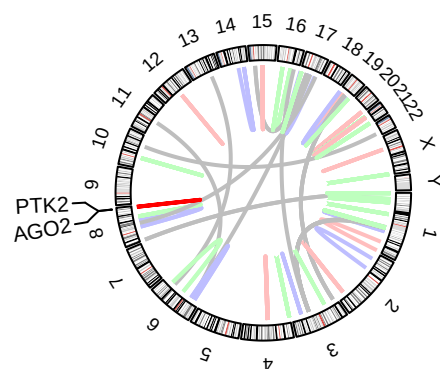
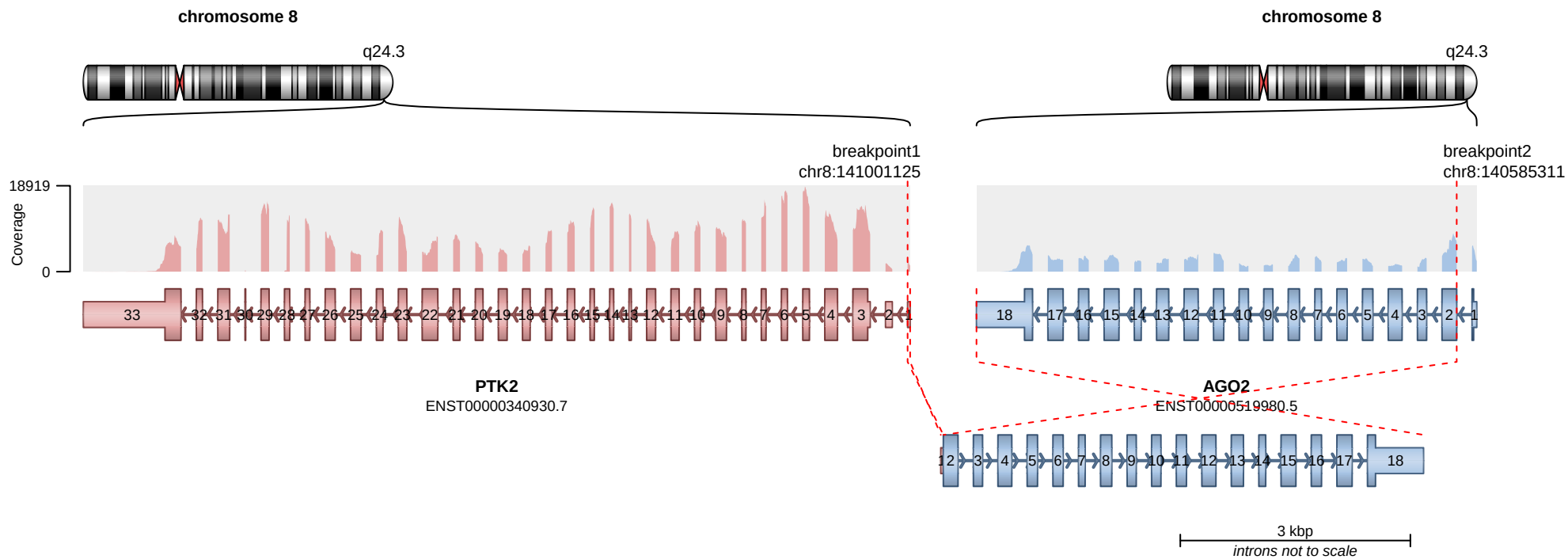


No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

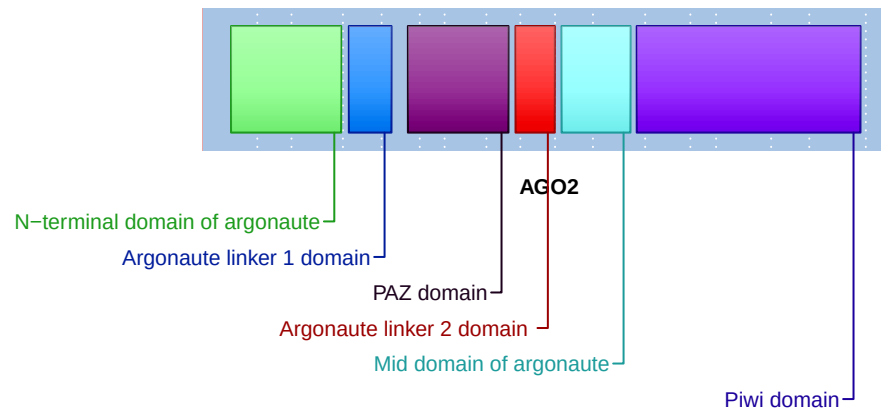
Split reads = 7
Discordant mates = 0

— translocation — deletion
— duplication — inversion



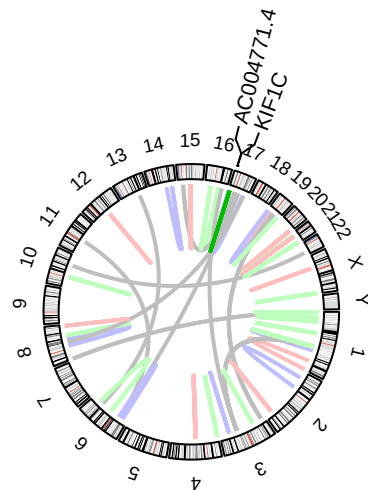
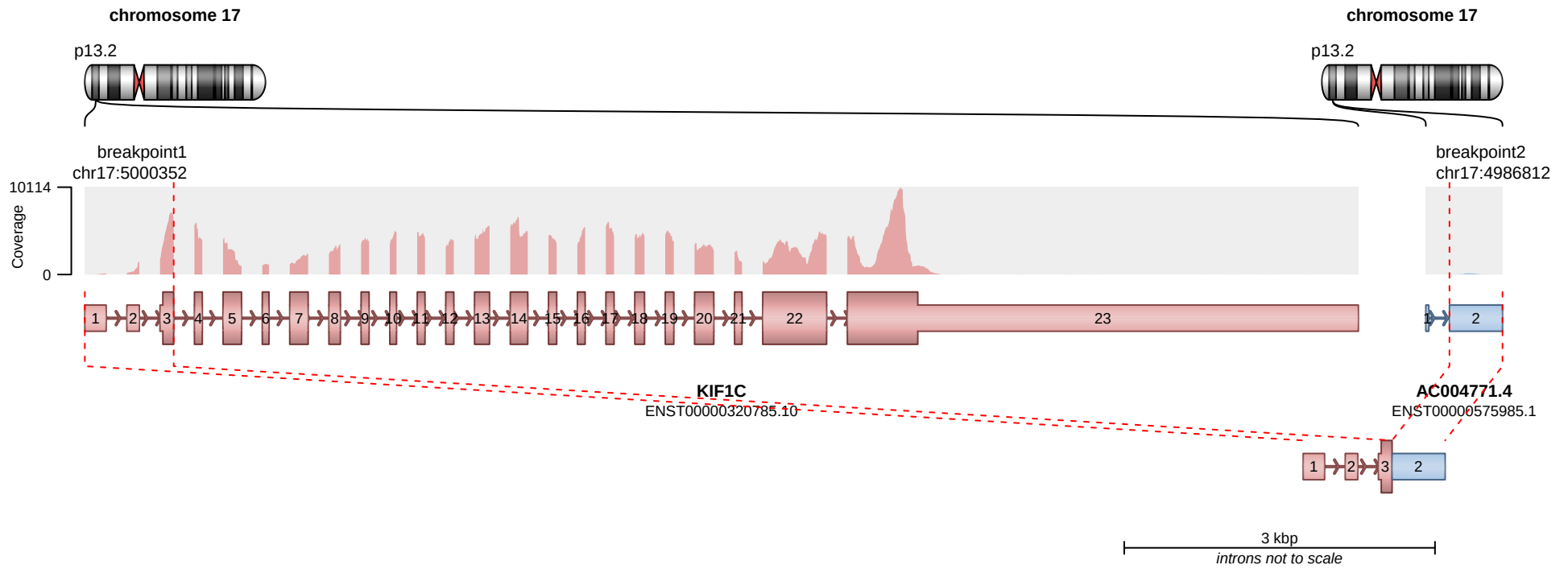
— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS reading frame unclear

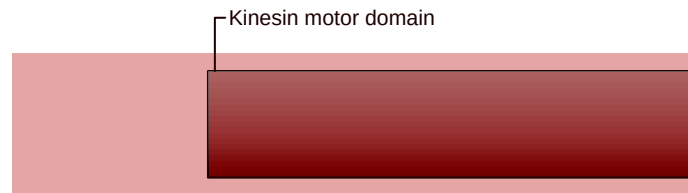


SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 0



RETAINED PROTEIN DOMAINS
reading frame unclear

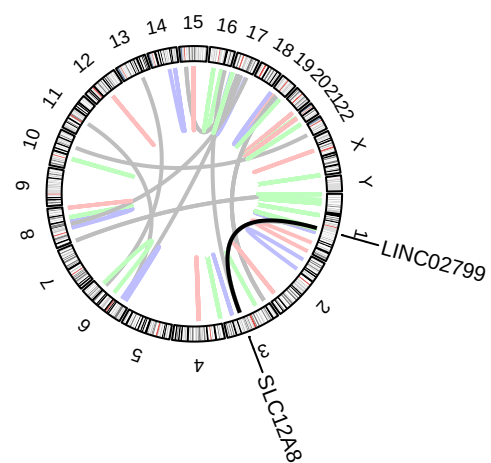
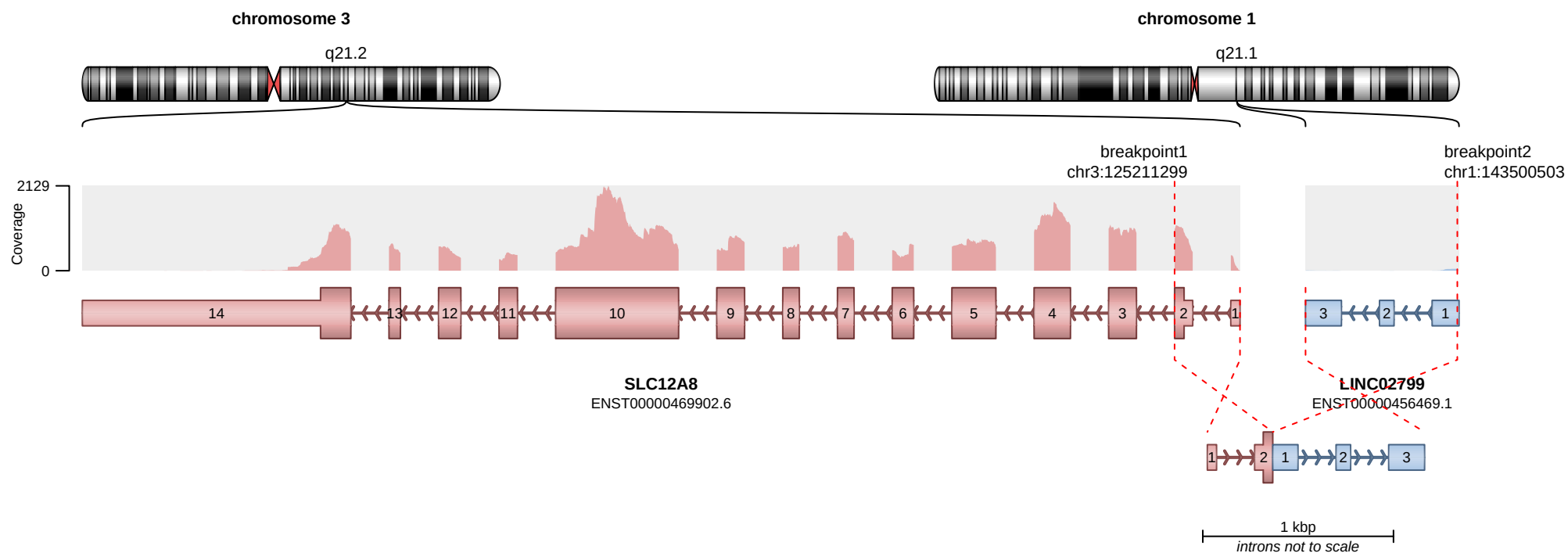


KIF1C

SUPPORTING READ COUNT

Split reads = 11
Discordant mates = 0

— translocation — deletion
— duplication — inversion

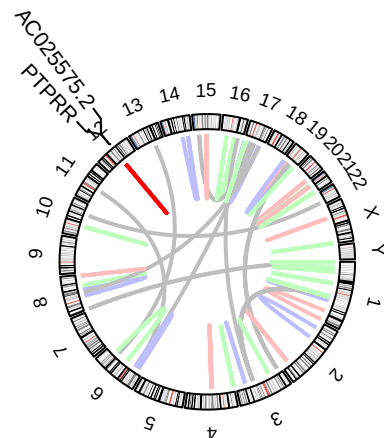
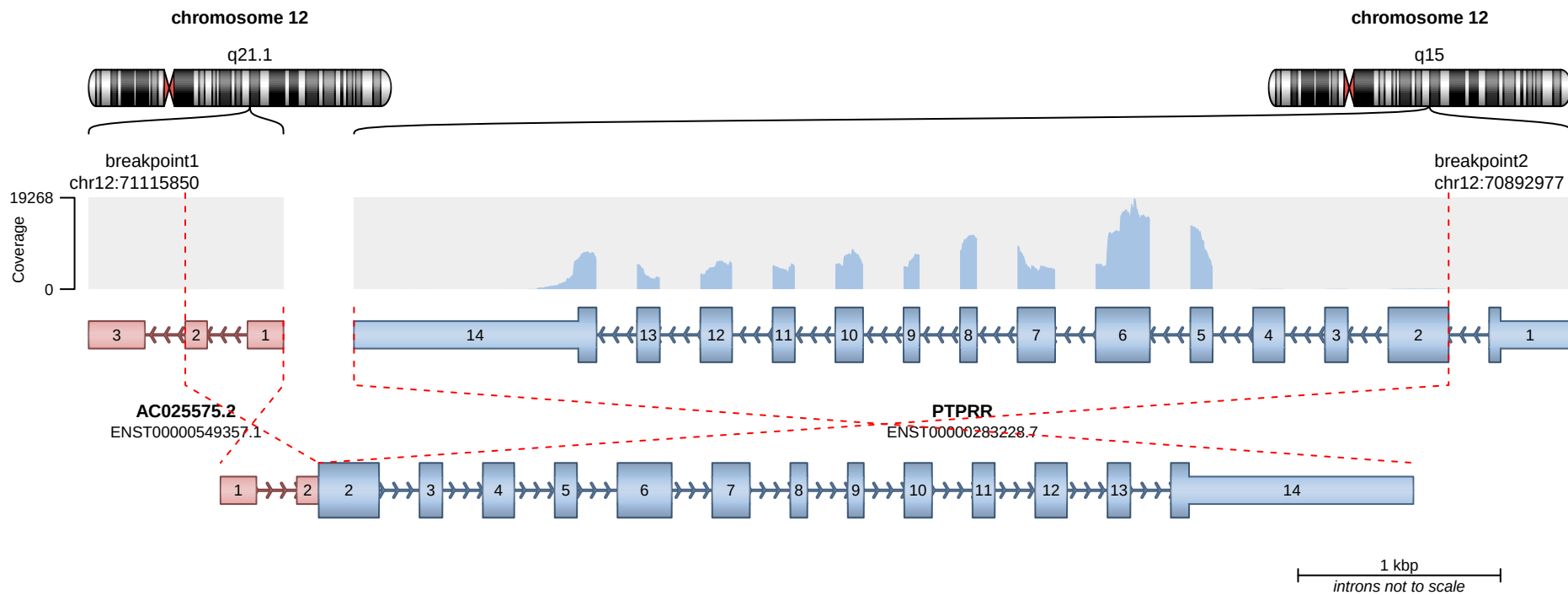


— translocation — deletion
— duplication — inversion

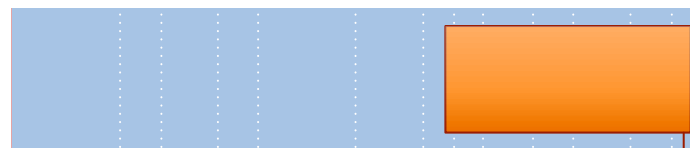
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 11
Discordant mates = 0



RETAINED PROTEIN DOMAINS
reading frame unclear



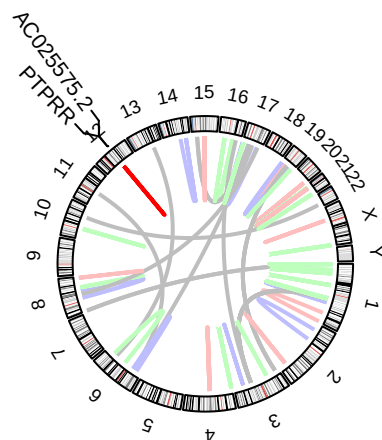
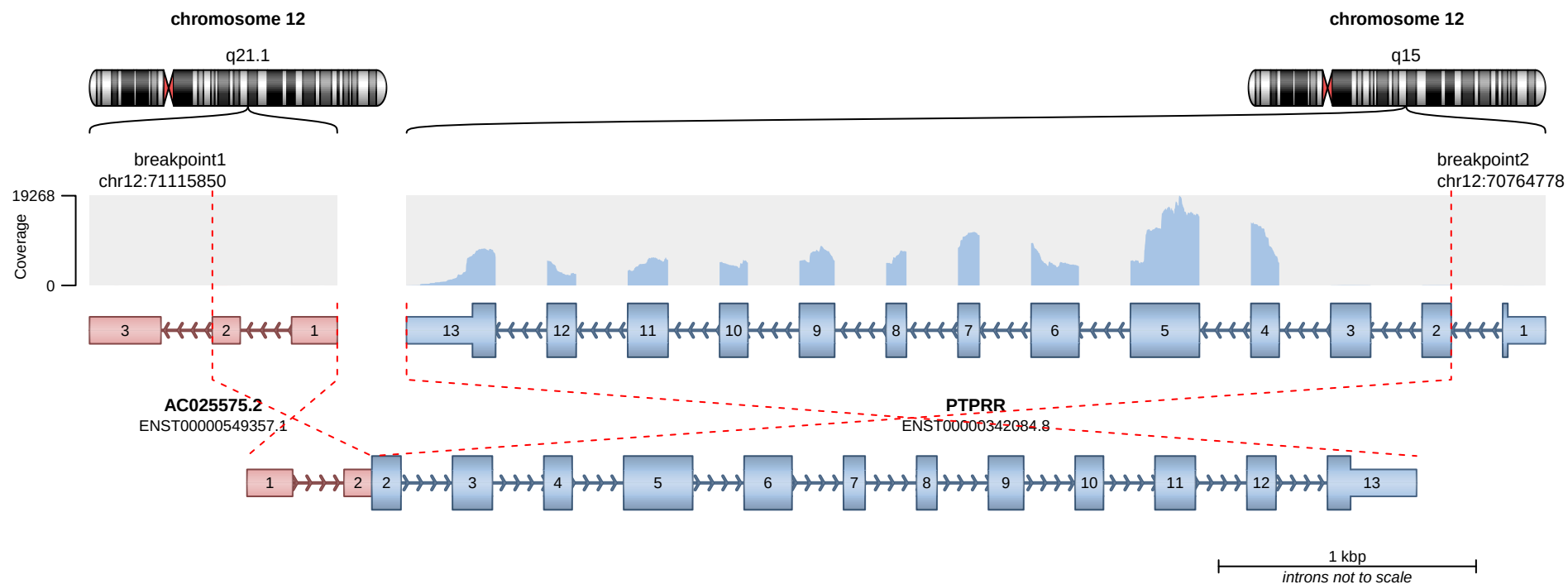
PTPRR

Protein-tyrosine phosphatase

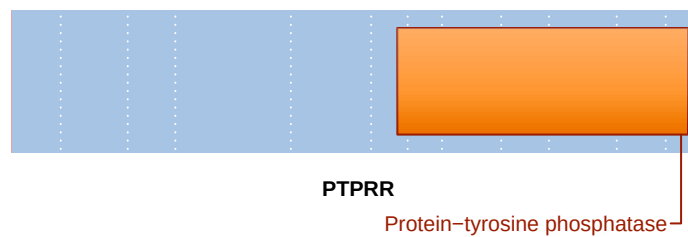
SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 0

— translocation — deletion
— duplication — inversion



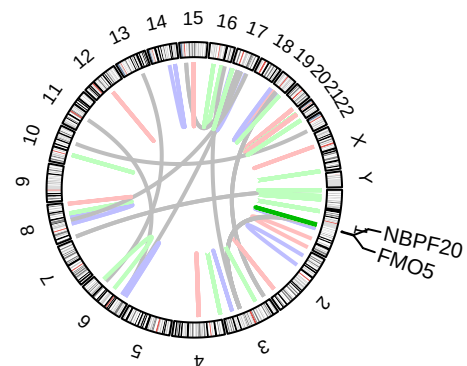
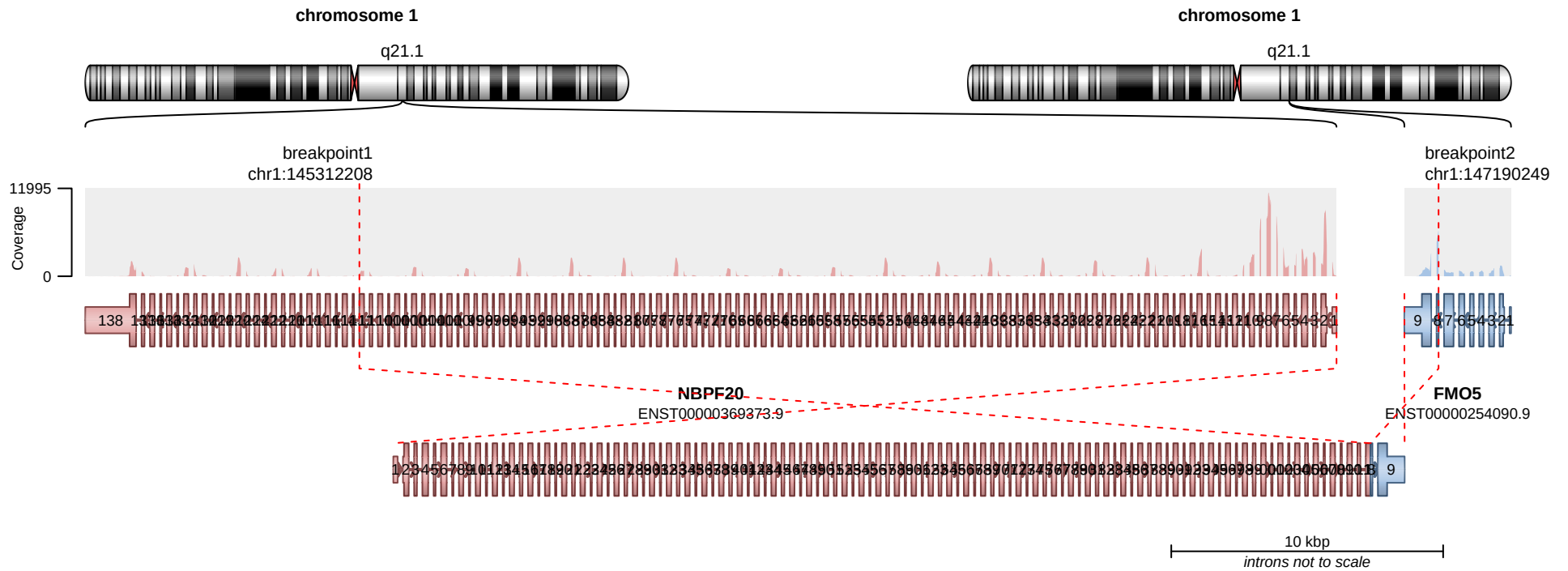
RETAINED PROTEIN DOMAINS
reading frame unclear



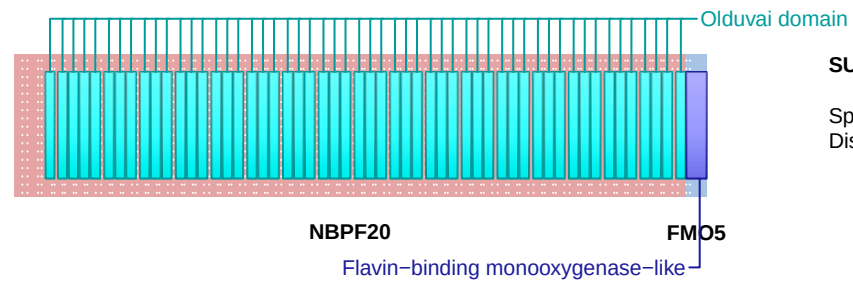
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



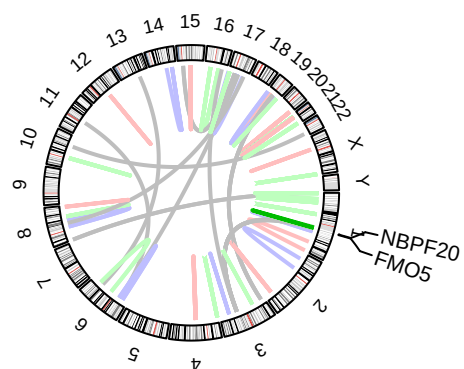
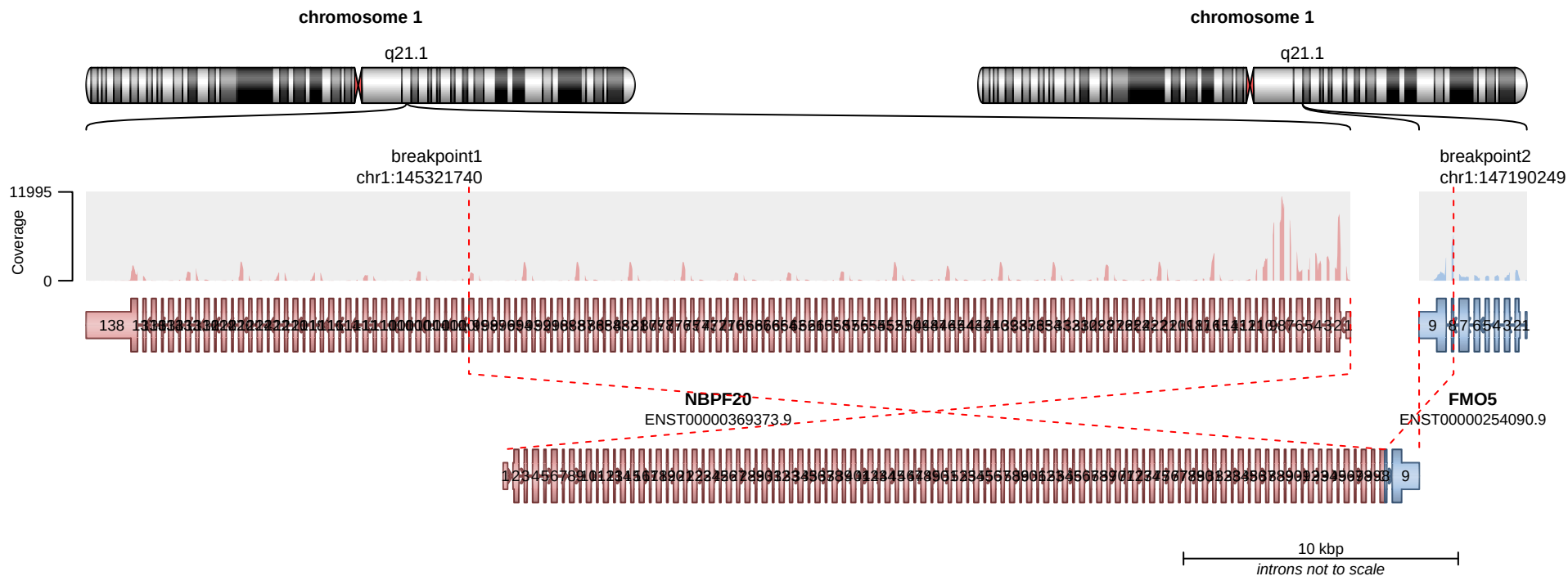
RETAINED PROTEIN DOMAINS reading frame unclear



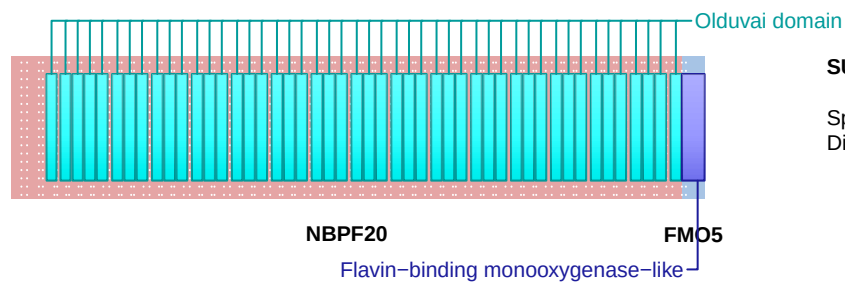
SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 0

— translocation — deletion
— duplication — inversion



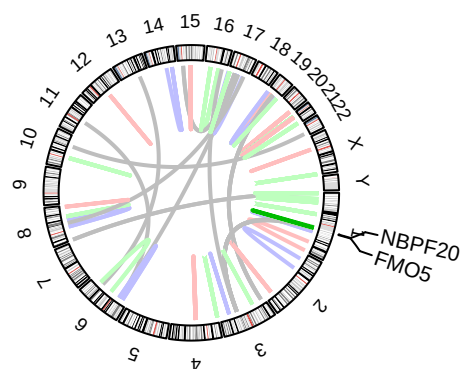
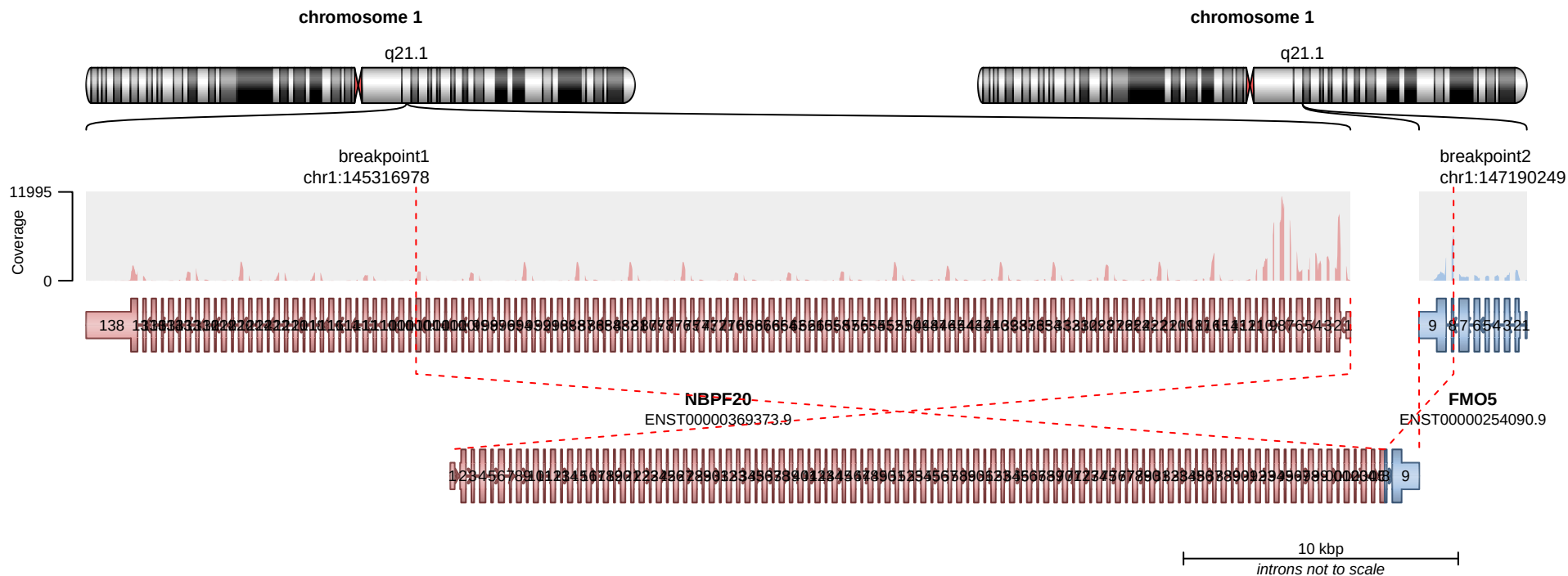
RETAINED PROTEIN DOMAINS reading frame unclear



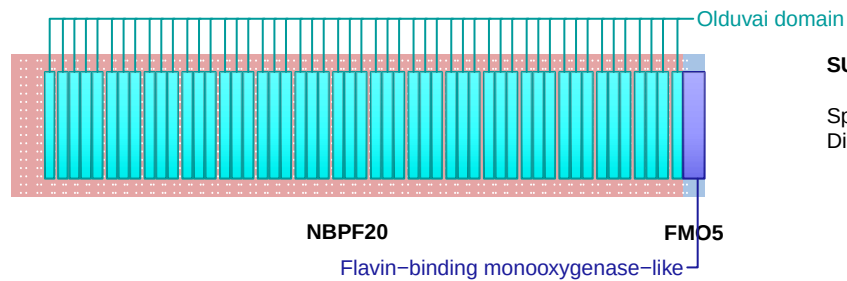
SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 0

— translocation — deletion
— duplication — inversion



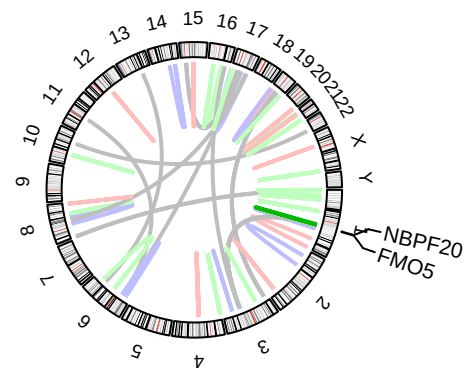
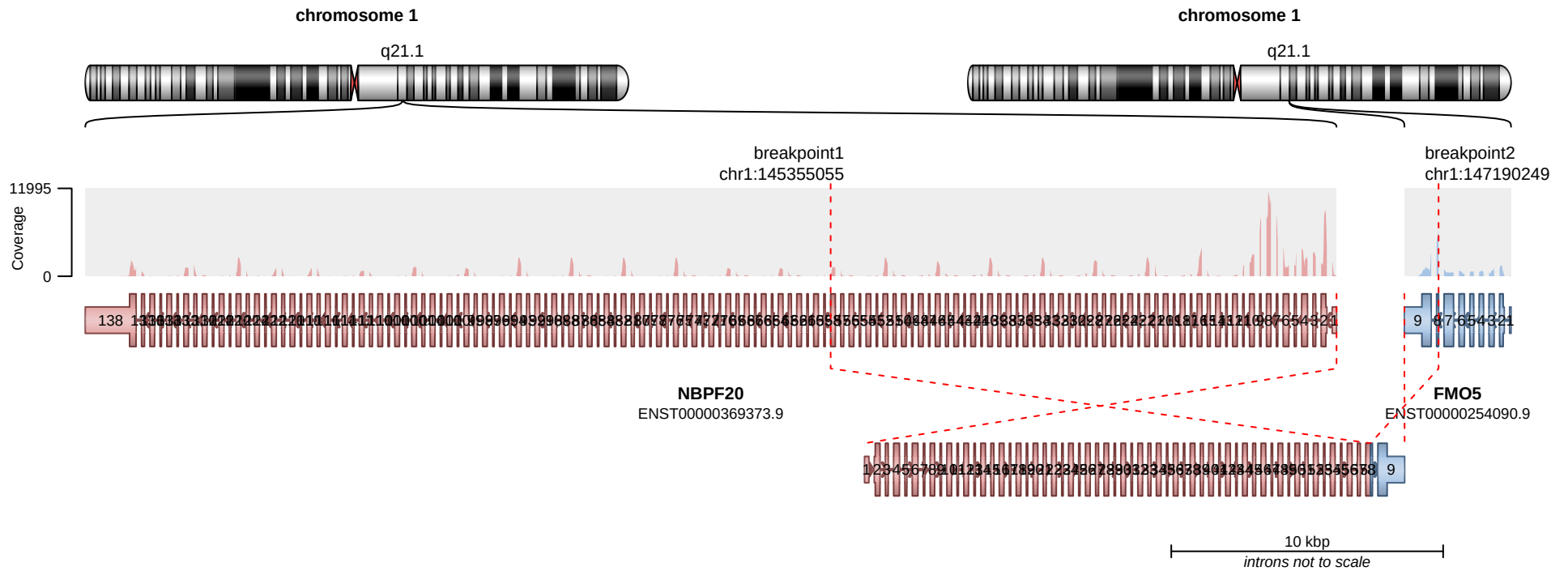
RETAINED PROTEIN DOMAINS reading frame unclear



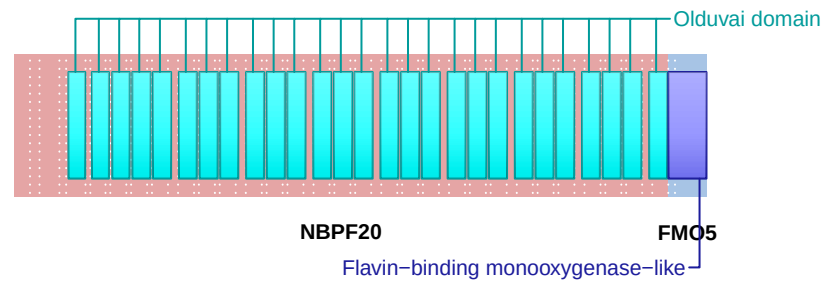
SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 0

— translocation — deletion
— duplication — inversion



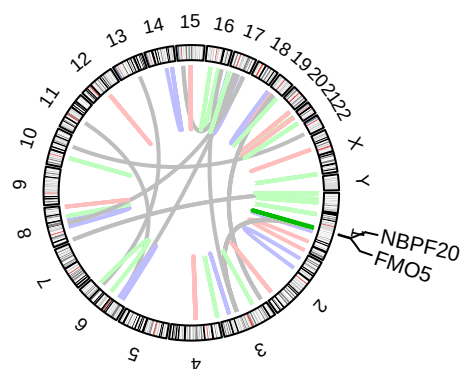
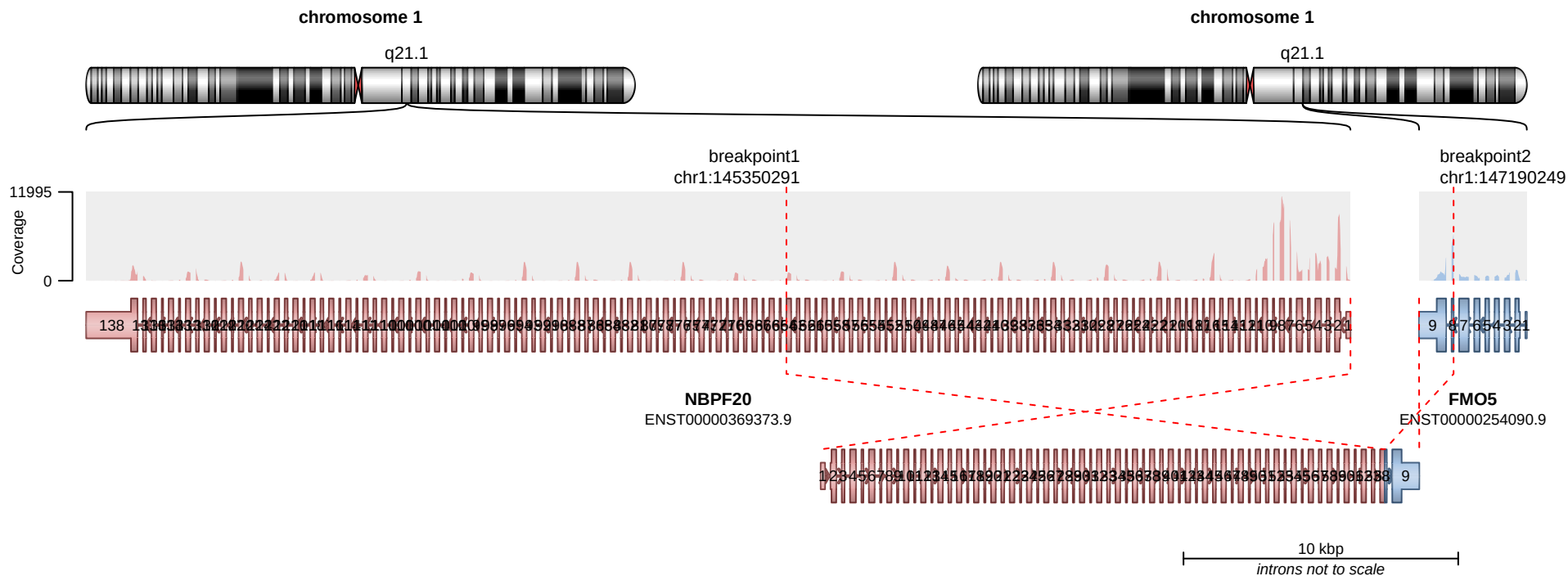
RETAINED PROTEIN DOMAINS reading frame unclear



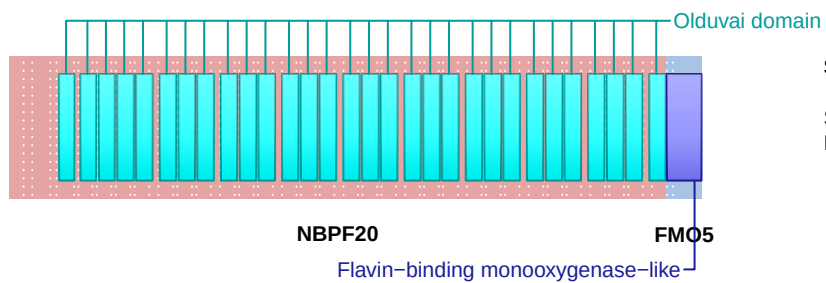
SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 0

— translocation — deletion
— duplication — inversion



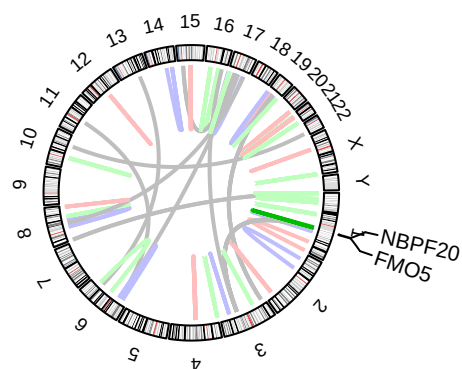
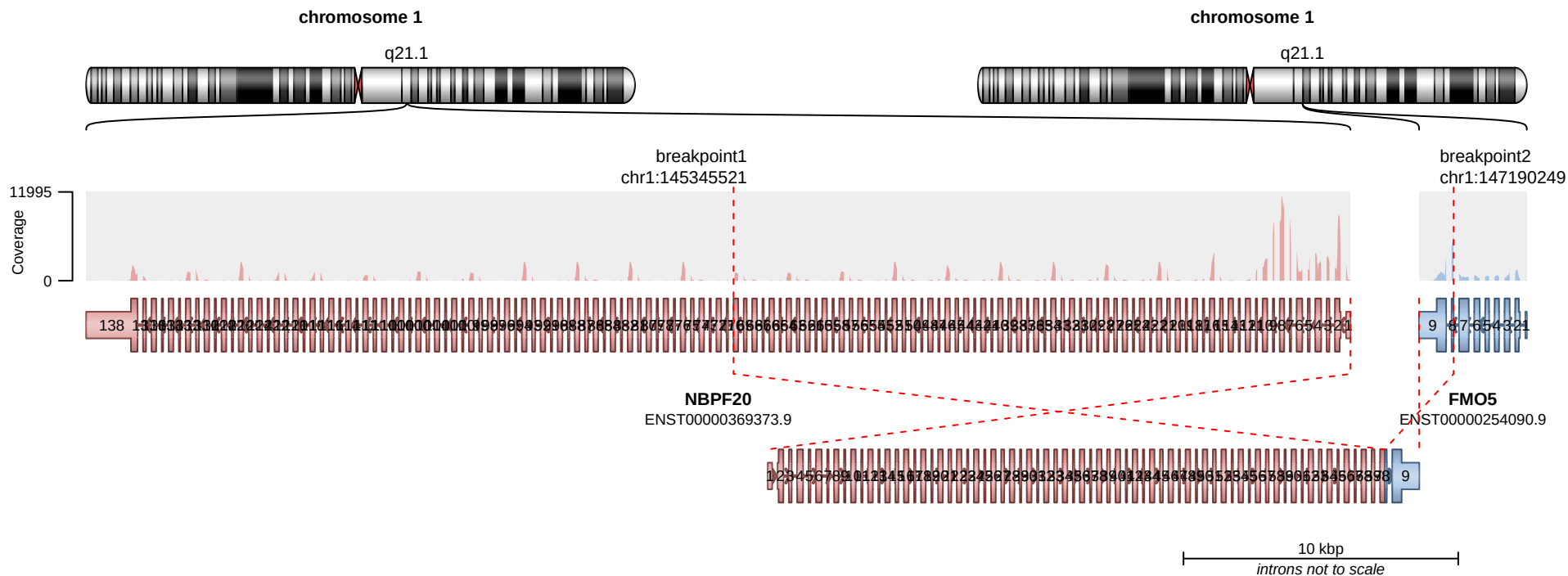
RETAINED PROTEIN DOMAINS reading frame unclear



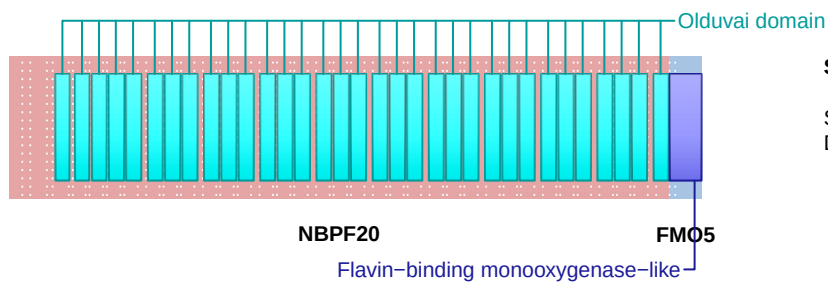
SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 0

— translocation — deletion
— duplication — inversion



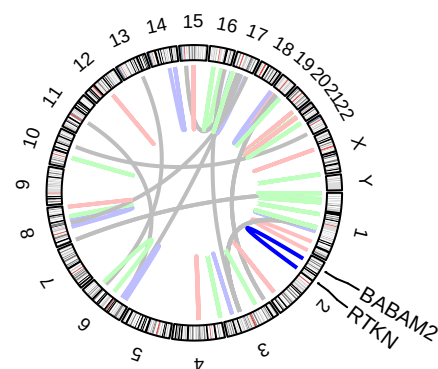
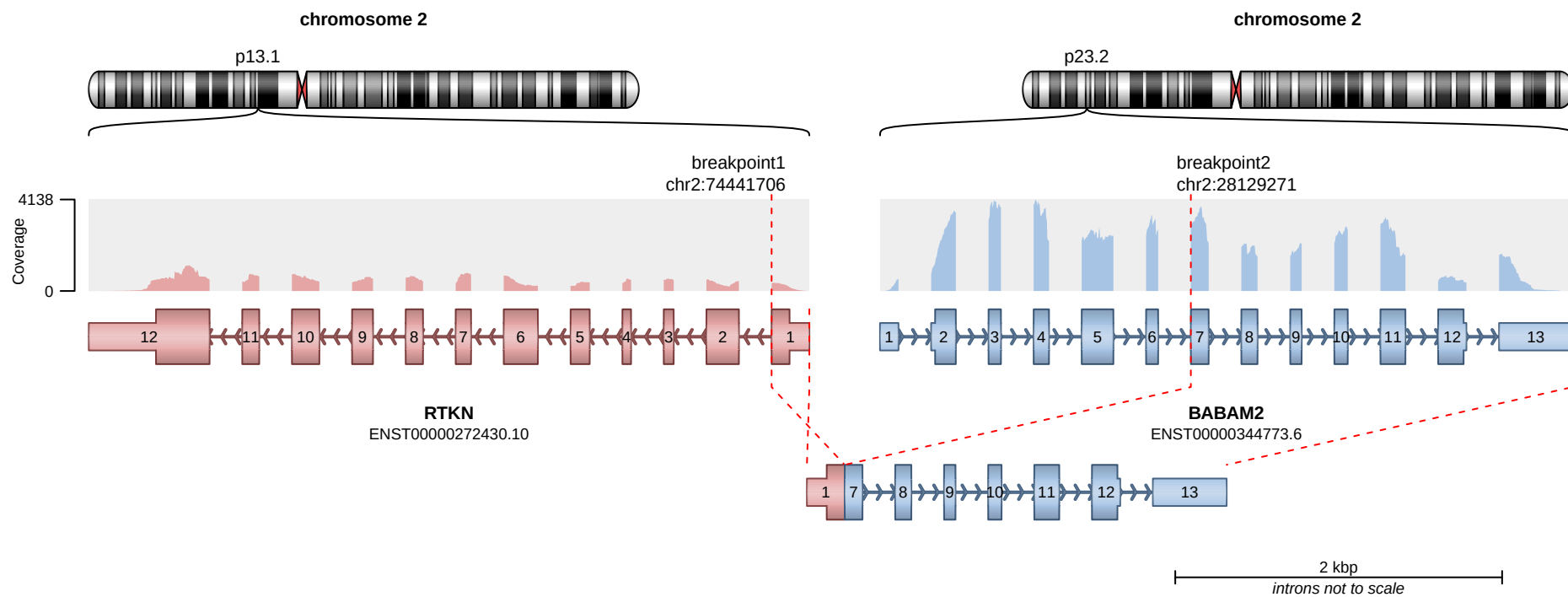
RETAINED PROTEIN DOMAINS reading frame unclear



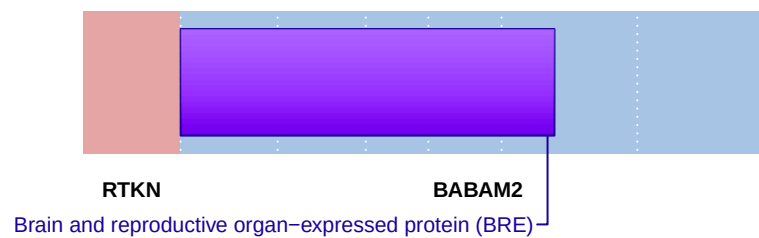
SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 0

— translocation — deletion
— duplication — inversion



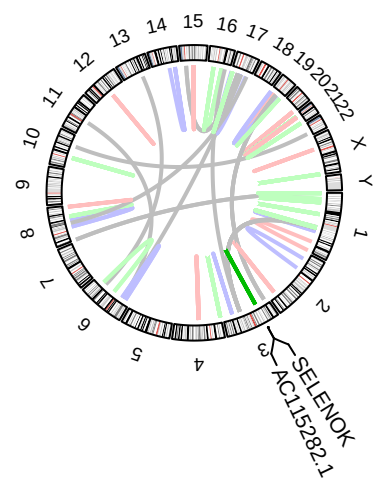
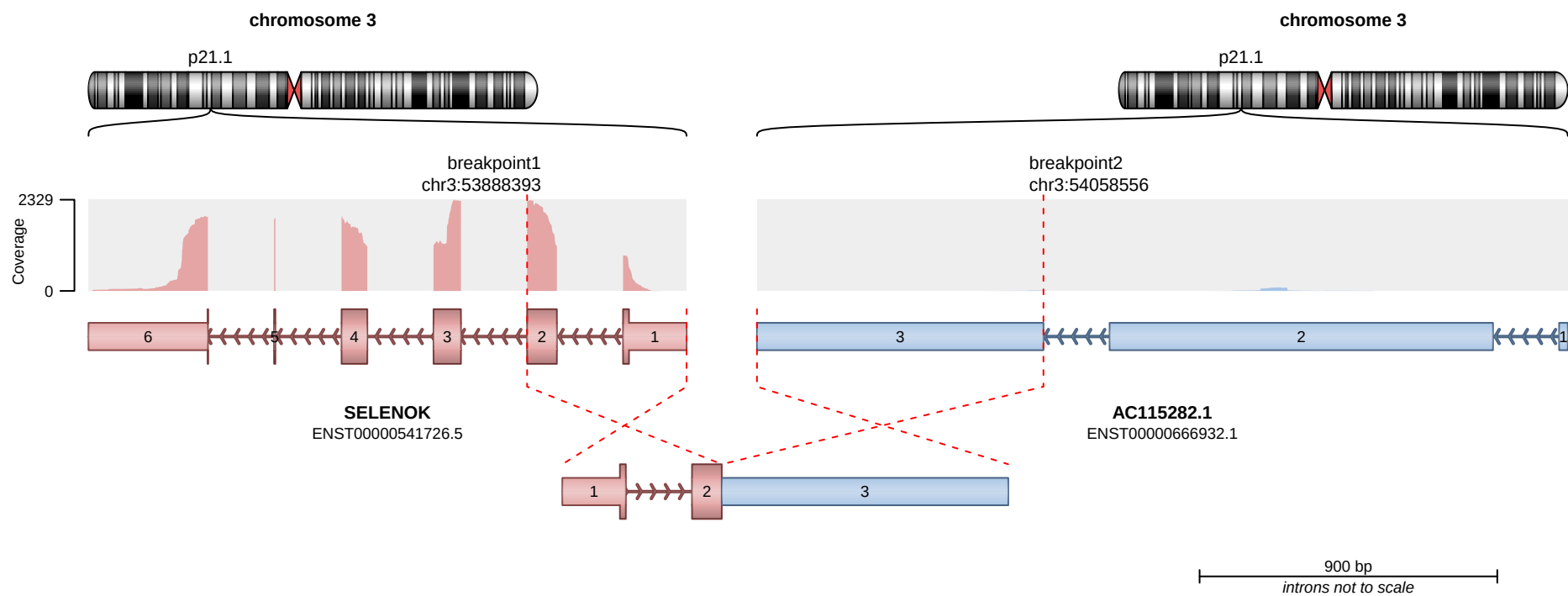
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 0

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

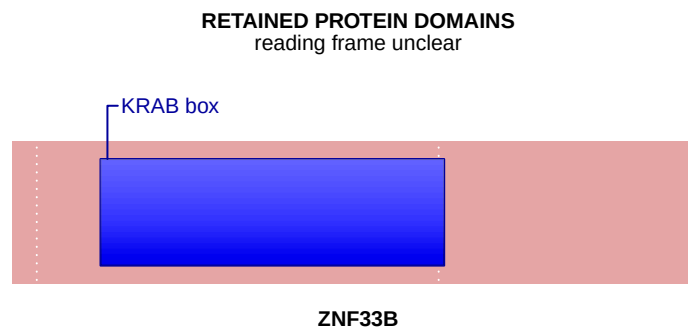
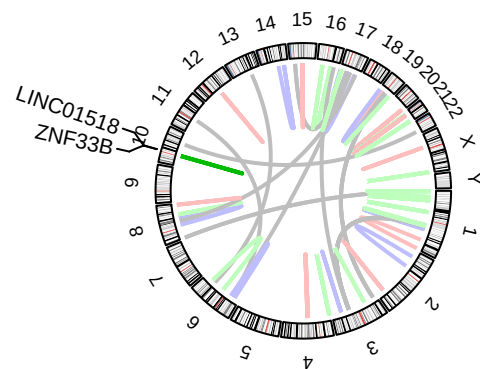
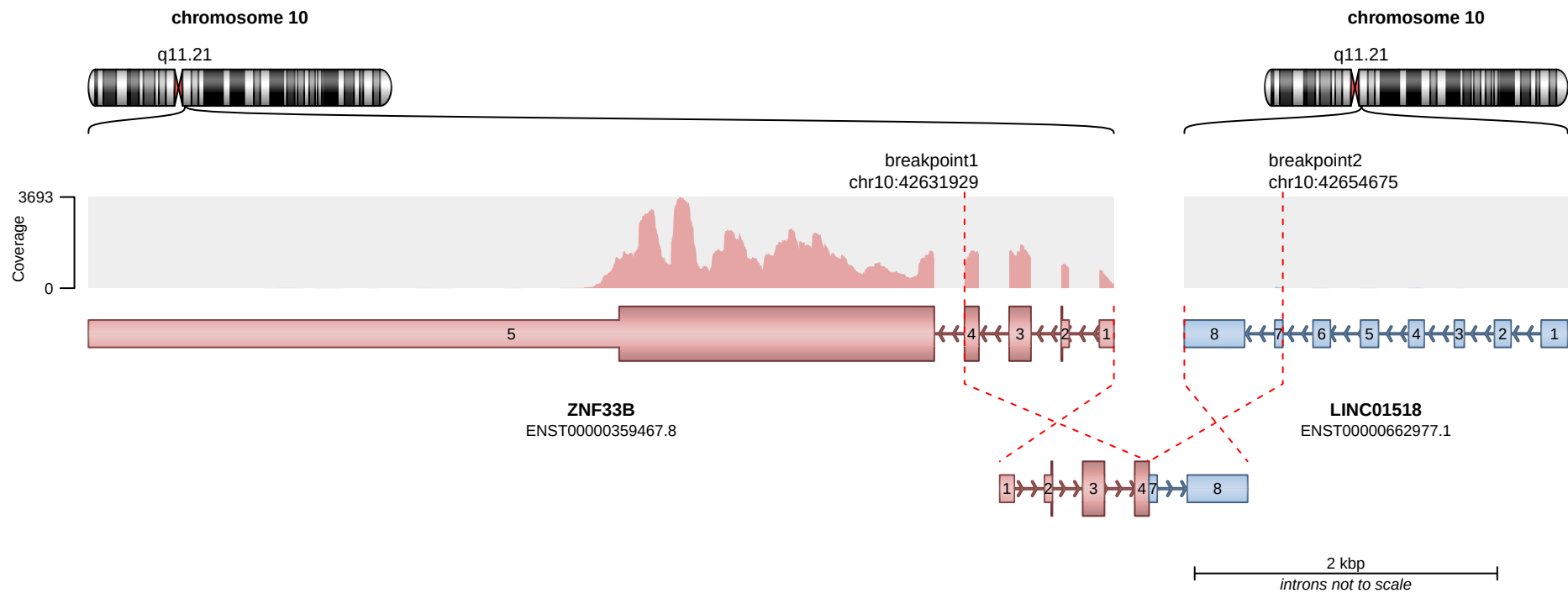


SELENOK

SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 0

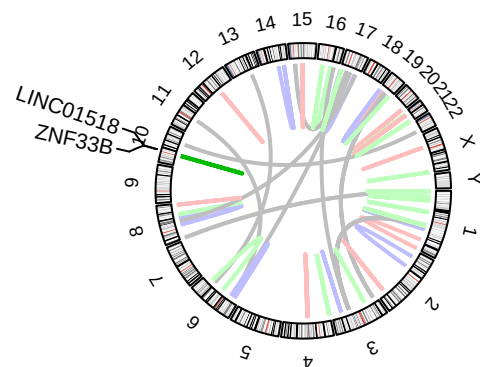
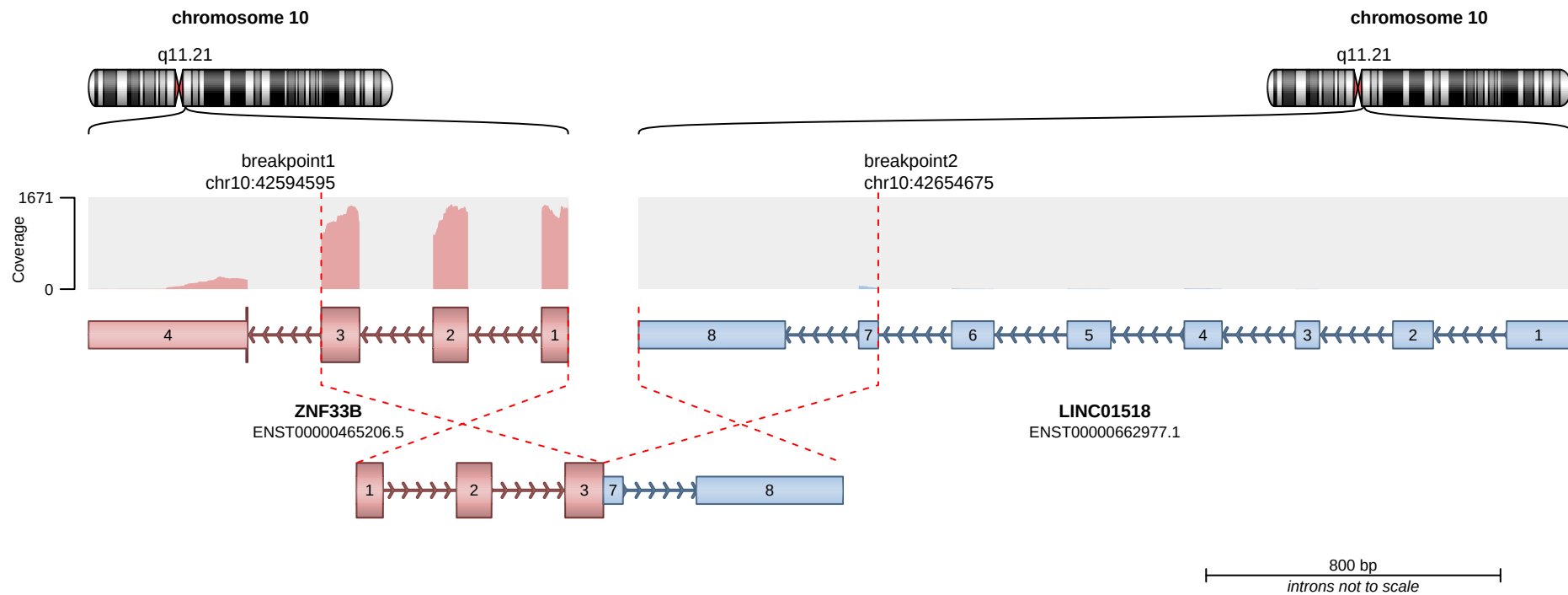
— translocation — deletion
— duplication — inversion



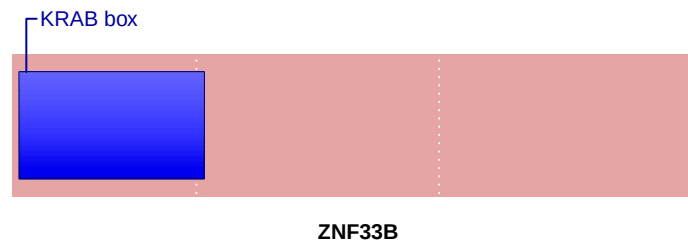
SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 0

— translocation — deletion
— duplication — inversion



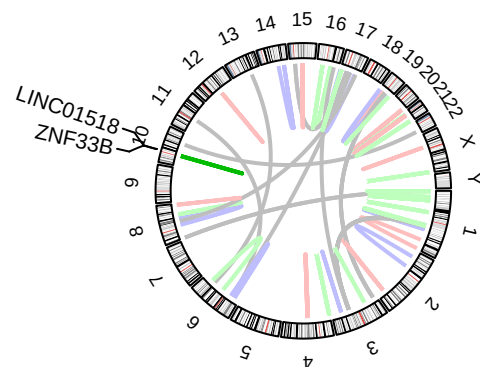
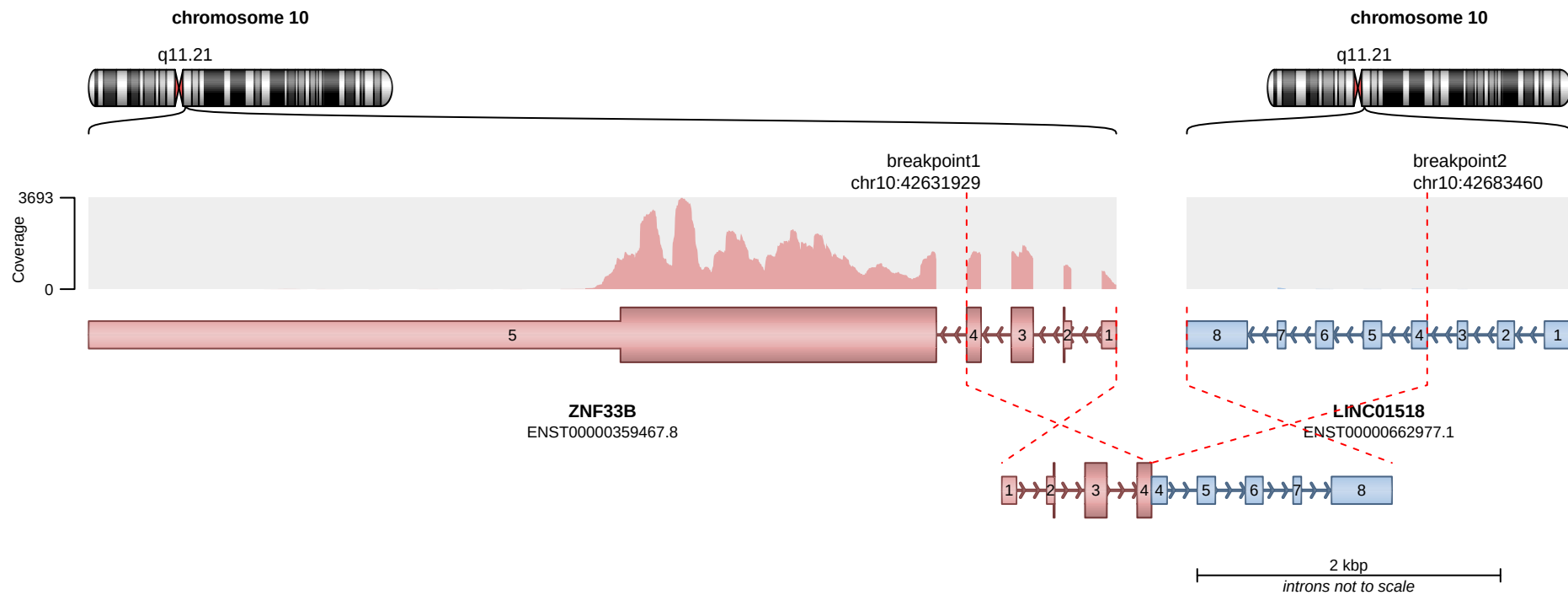
RETAINED PROTEIN DOMAINS reading frame unclear



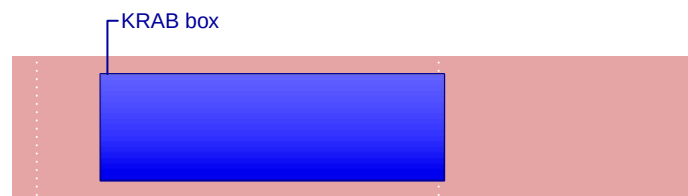
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS
reading frame unclear



ZNF33B

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion