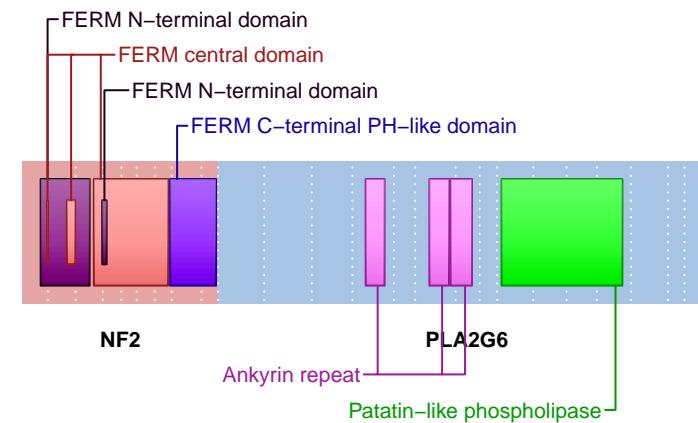


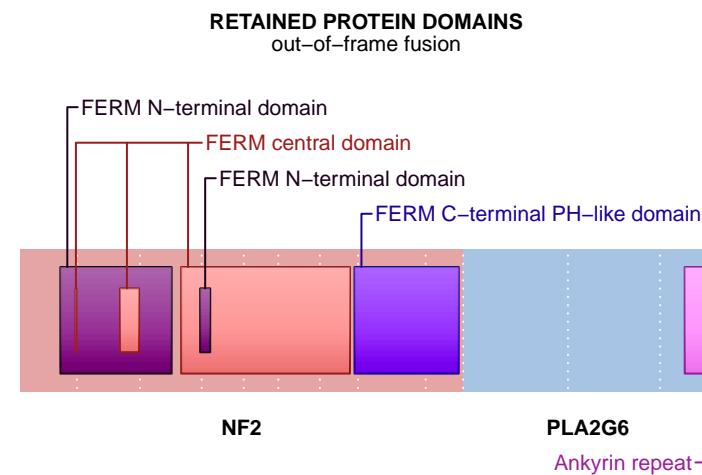
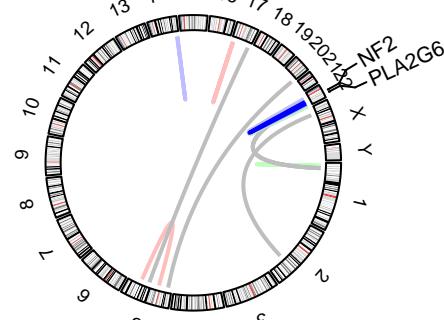
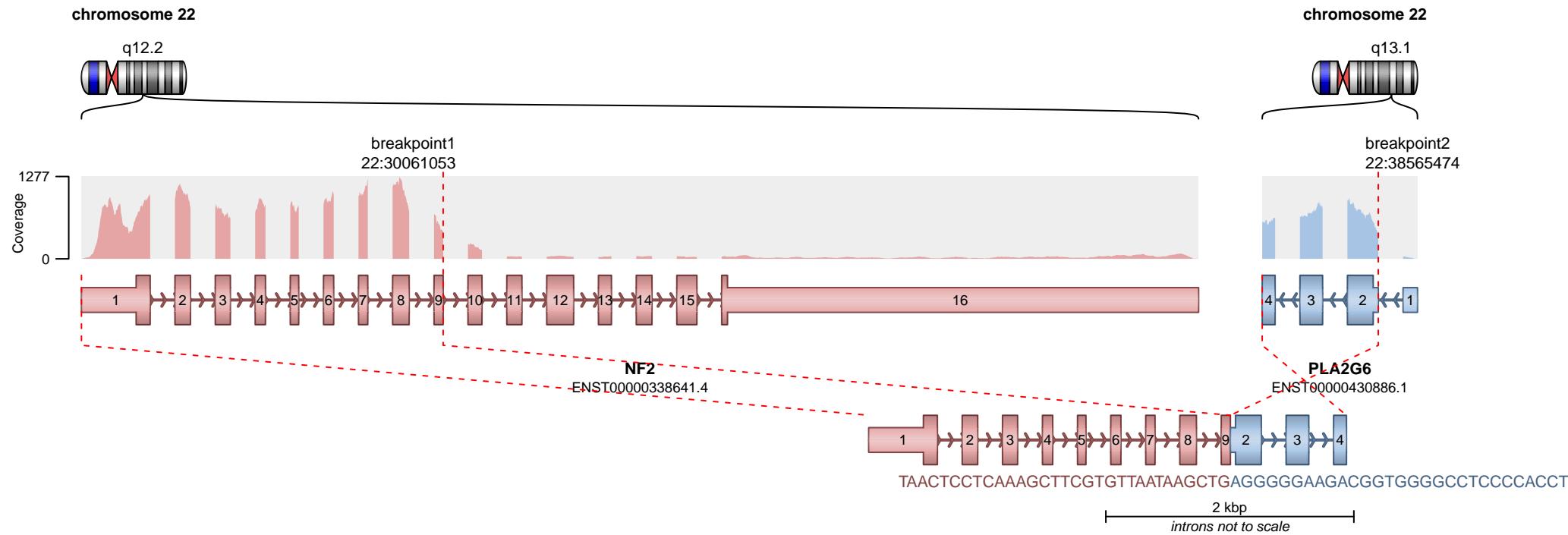
RETAINED PROTEIN DOMAINS in-frame fusion



SUPPORTING READ COUNT

Split reads at breakpoint1 = 119
Split reads at breakpoint2 = 102
Discordant mates = 61

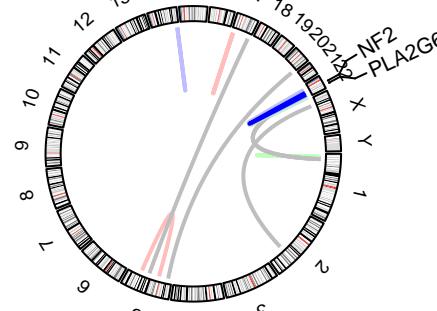
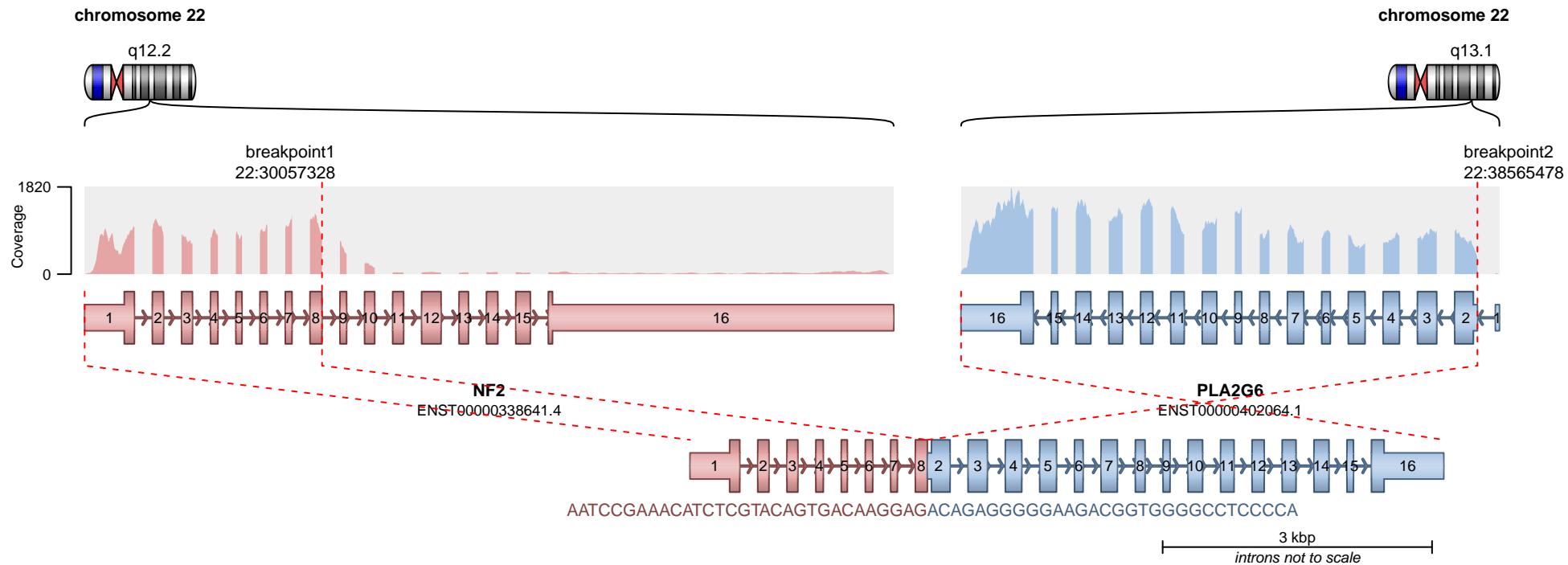
— translocation — deletion
— duplication — inversion



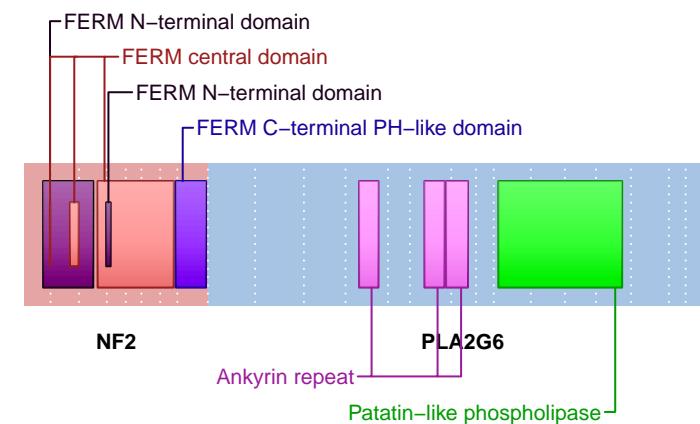
SUPPORTING READ COUNT

Split reads at breakpoint1 = 5
Split reads at breakpoint2 = 2
Discordant mates = 56

— translocation — deletion
— duplication — inversion



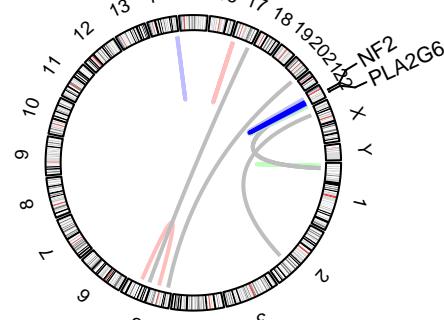
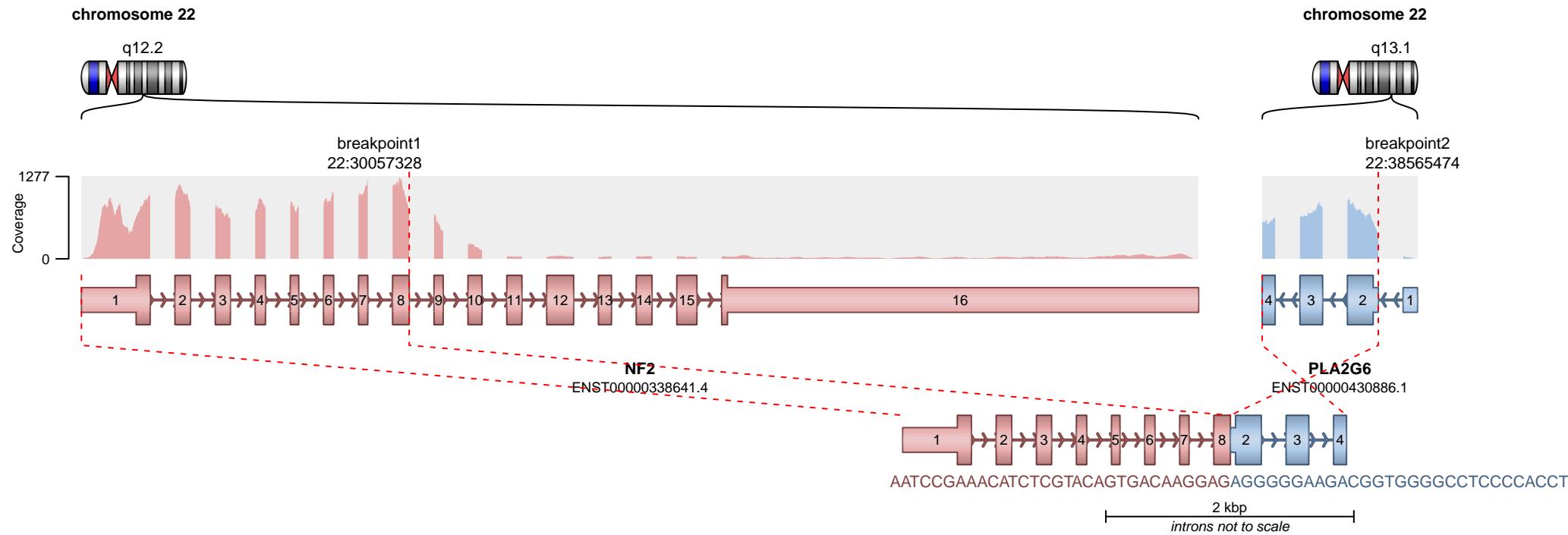
RETAINED PROTEIN DOMAINS in-frame fusion



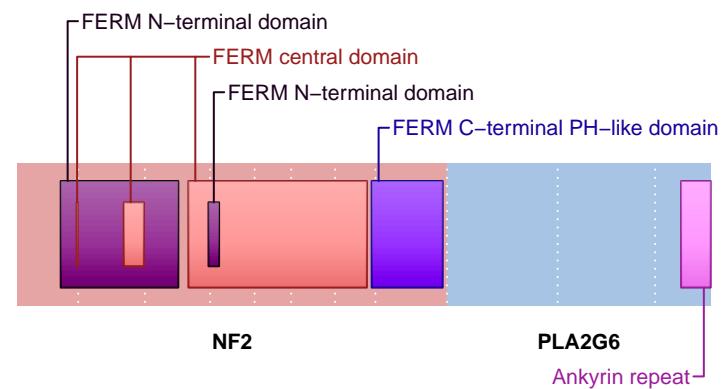
SUPPORTING READ COUNT

Split reads at breakpoint1 = 0
Split reads at breakpoint2 = 1
Discordant mates = 11

— translocation — deletion
— duplication — inversion



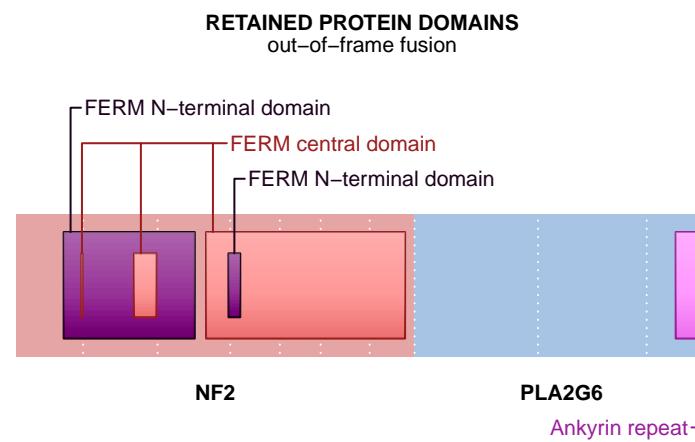
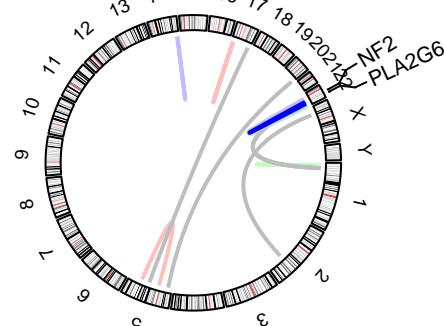
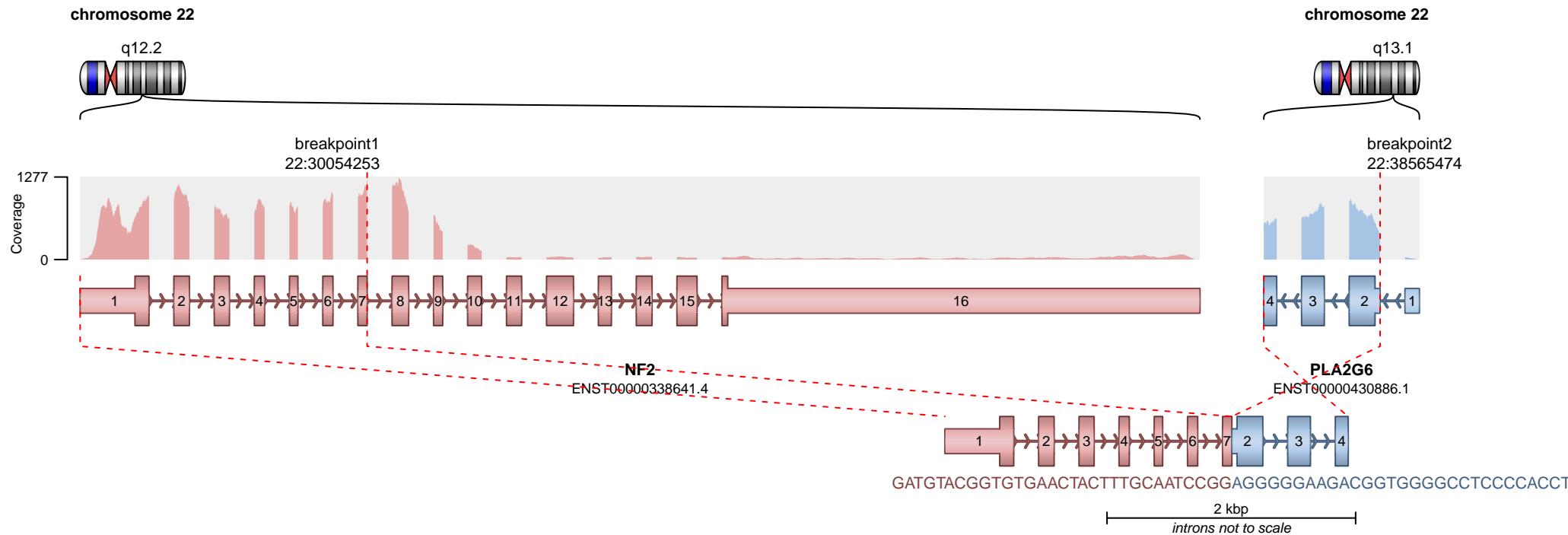
RETAINED PROTEIN DOMAINS out-of-frame fusion



SUPPORTING READ COUNT

Split reads at breakpoint1 = 0
Split reads at breakpoint2 = 1
Discordant mates = 10

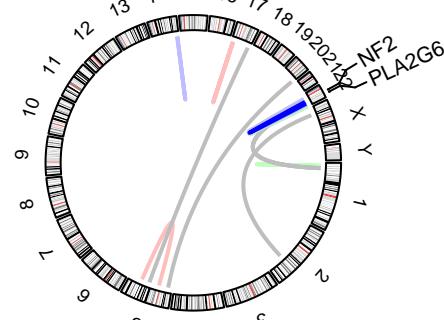
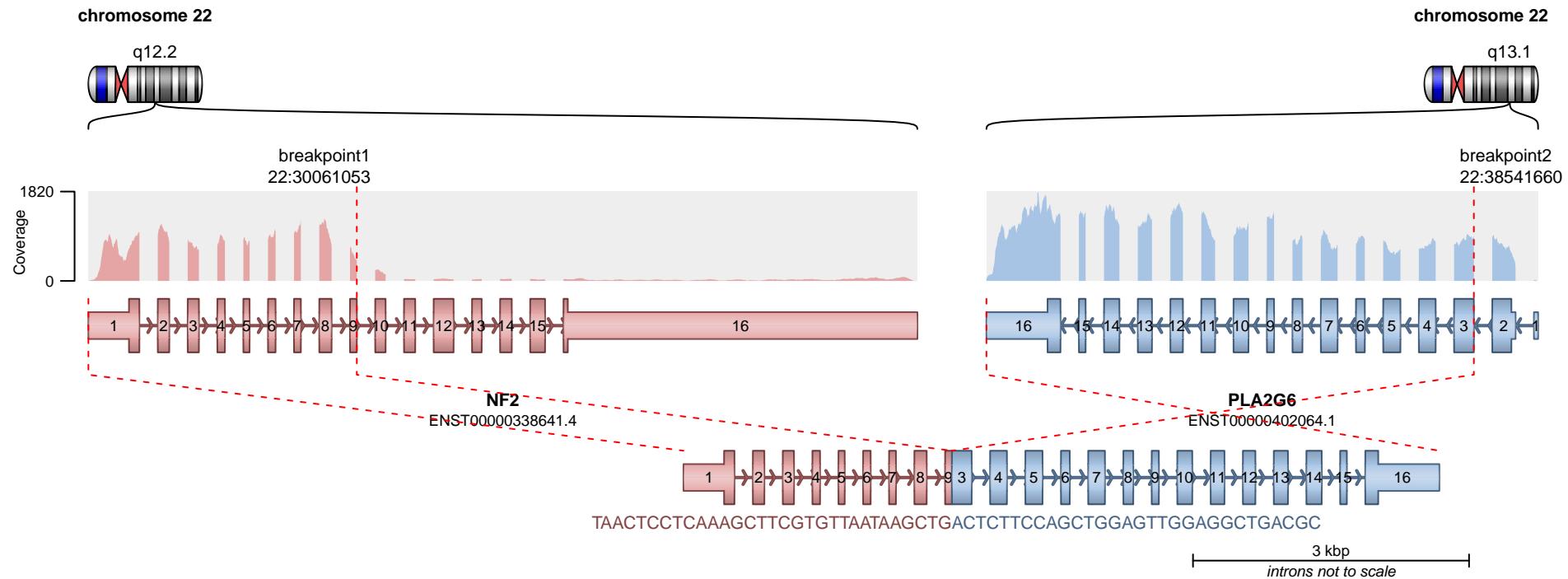
— translocation — deletion
— duplication — inversion



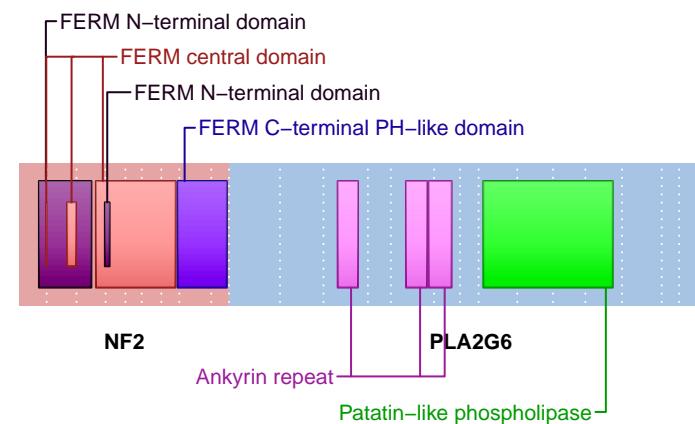
SUPPORTING READ COUNT

Split reads at breakpoint1 = 1
Split reads at breakpoint2 = 0
Discordant mates = 1

— translocation — deletion
— duplication — inversion



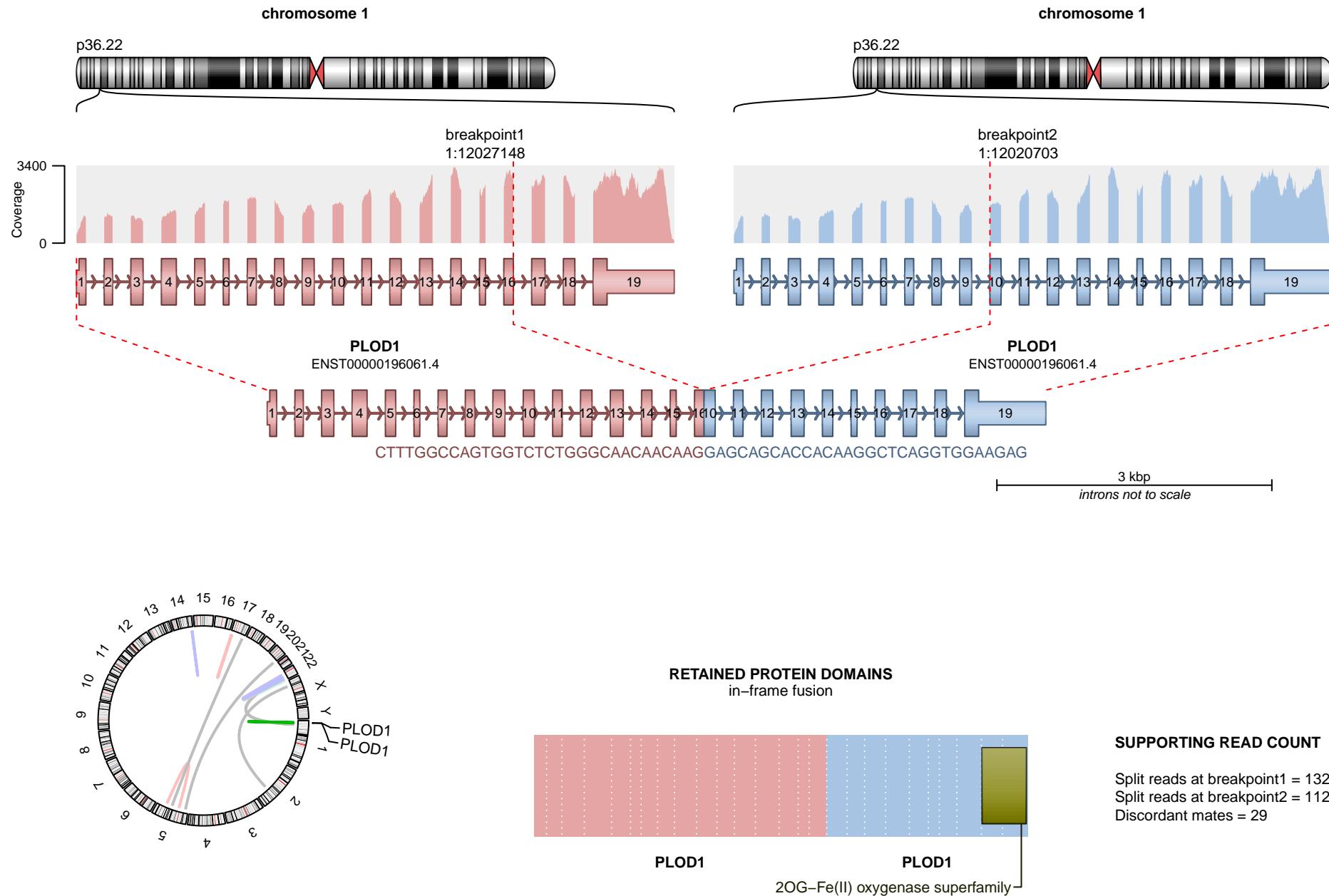
RETAINED PROTEIN DOMAINS out-of-frame fusion



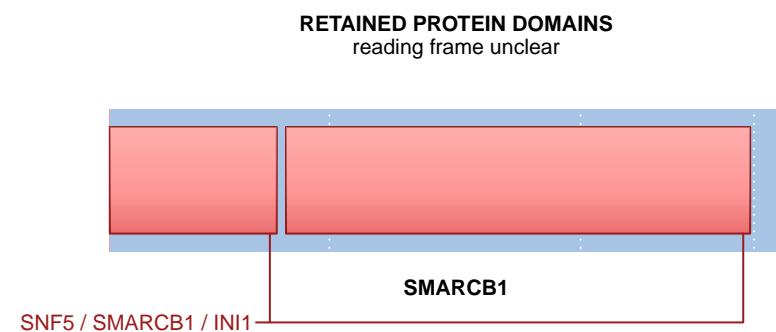
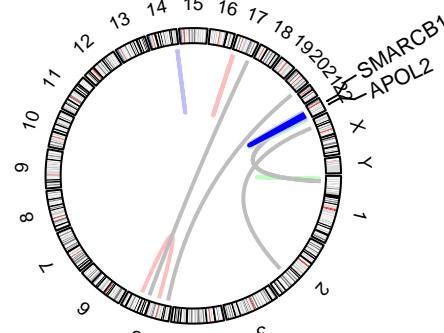
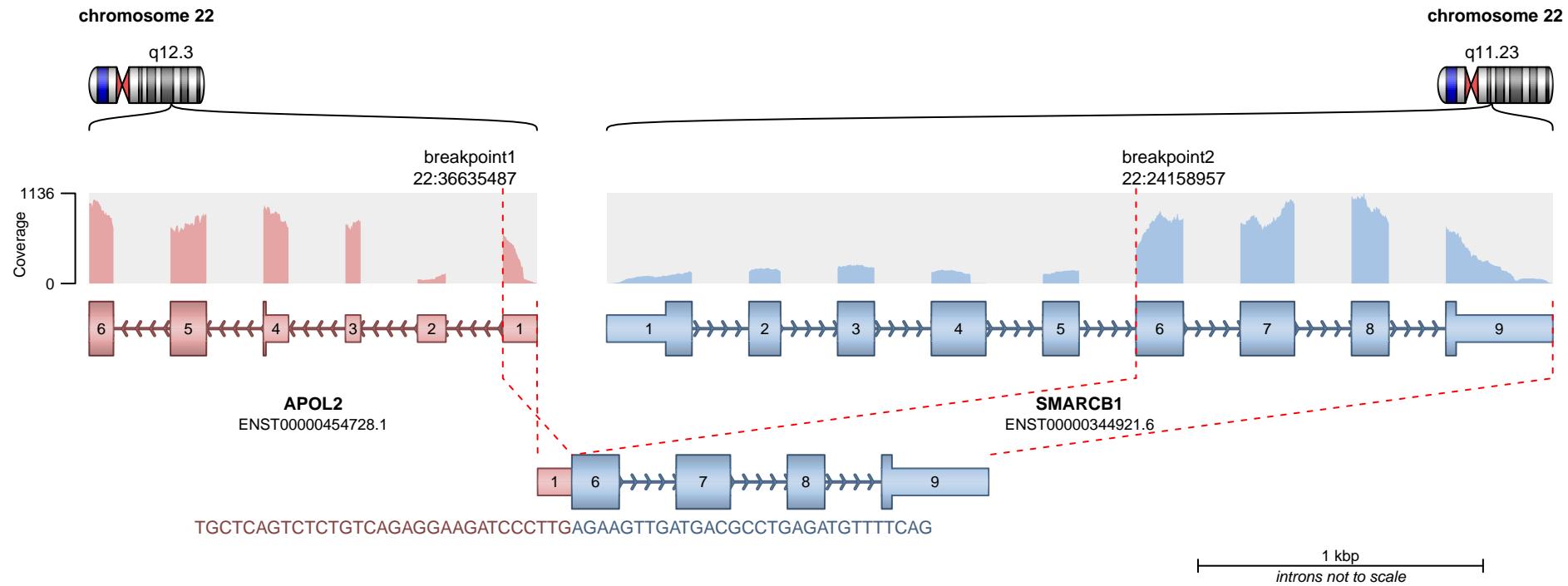
SUPPORTING READ COUNT

Split reads at breakpoint1 = 1
Split reads at breakpoint2 = 0
Discordant mates = 0

— translocation — deletion
— duplication — inversion



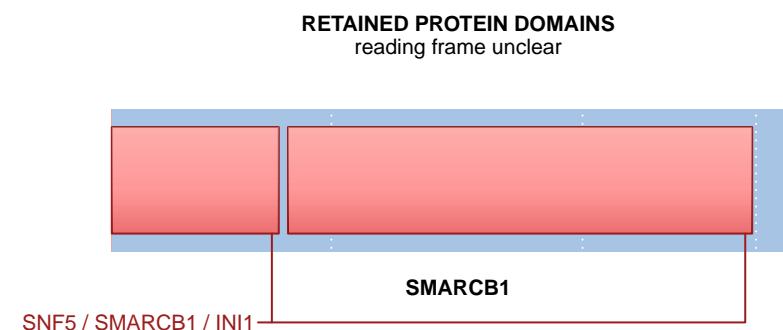
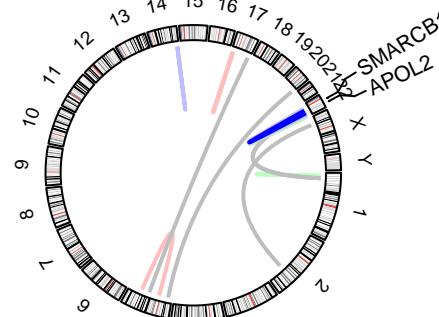
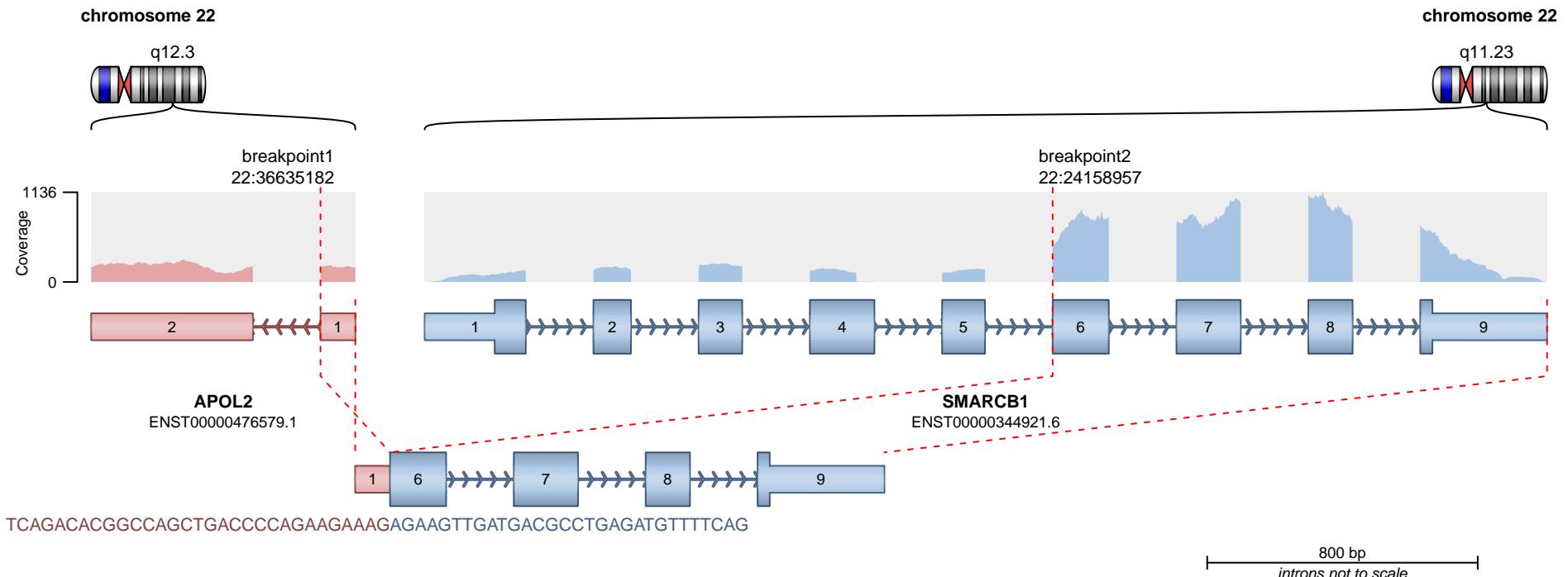
— translocation — deletion
— duplication — inversion



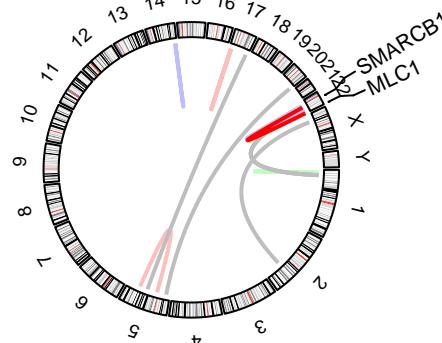
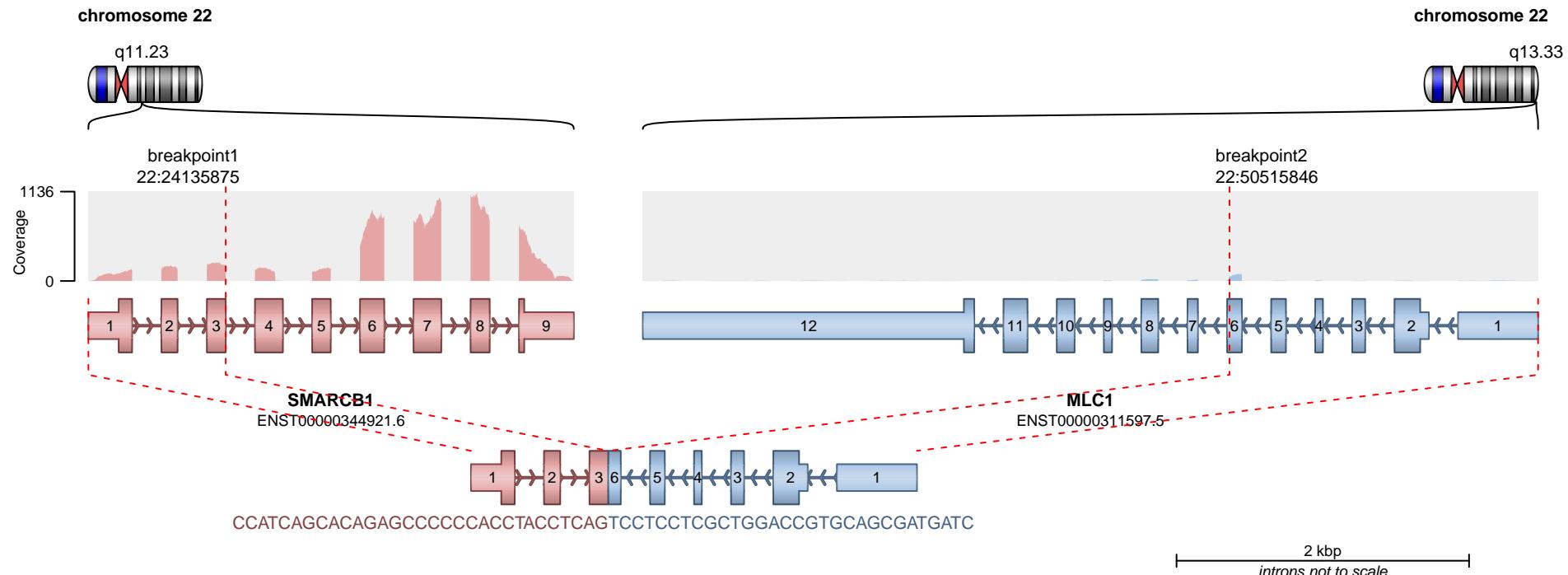
SUPPORTING READ COUNT

Split reads at breakpoint1 = 5
Split reads at breakpoint2 = 149
Discordant mates = 13

— translocation — deletion
— duplication — inversion



— translocation — deletion
— duplication — inversion

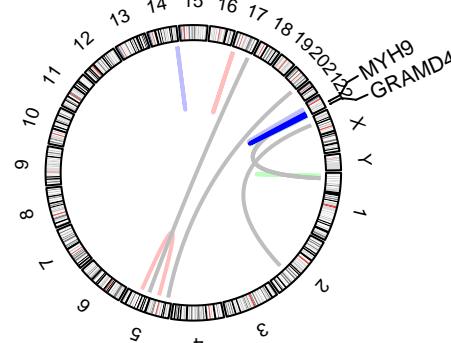
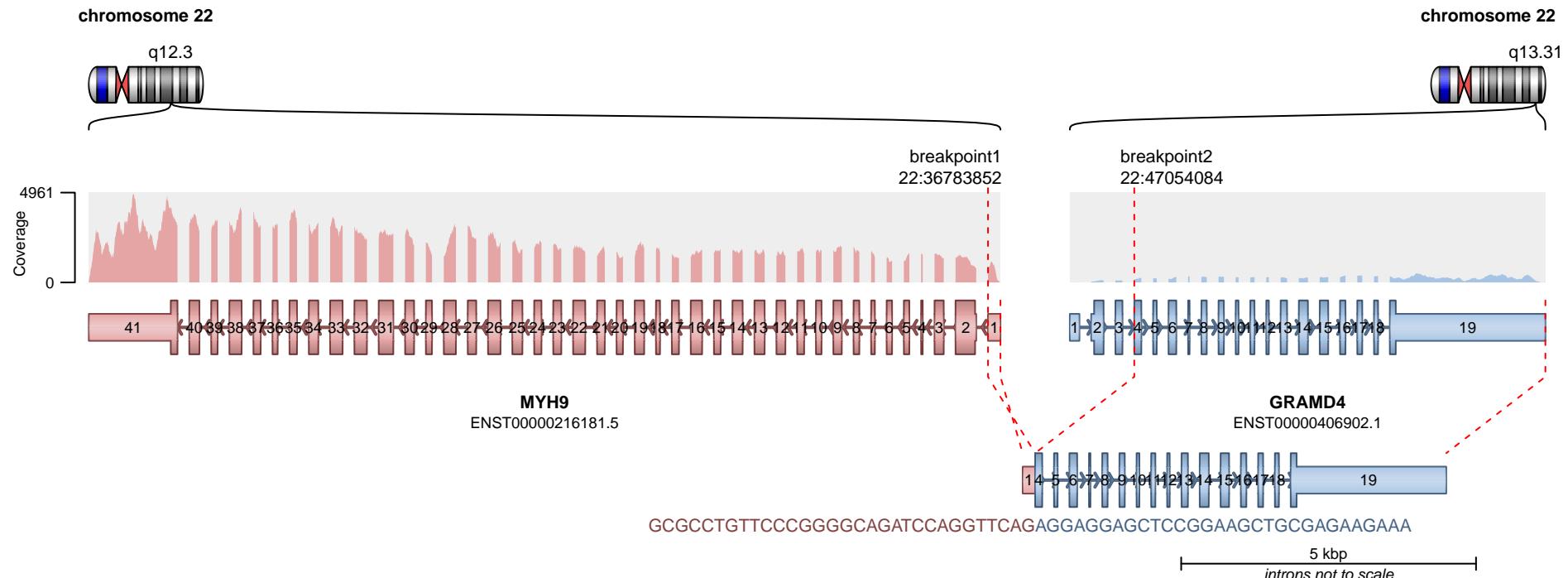


No protein domains retained in fusion.

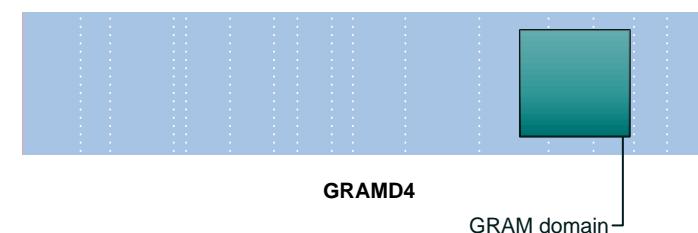
SUPPORTING READ COUNT

Split reads at breakpoint1 = 24
Split reads at breakpoint2 = 26
Discordant mates = 6

— translocation — deletion
— duplication — inversion



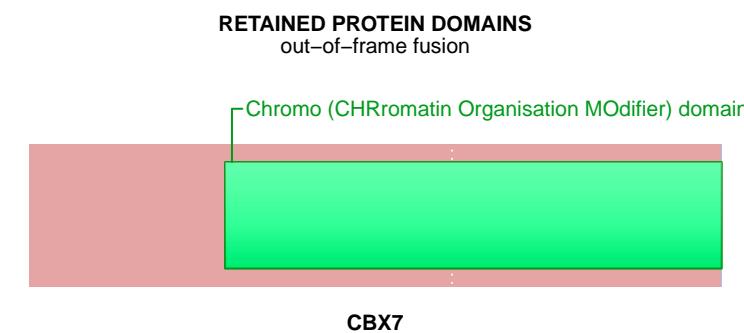
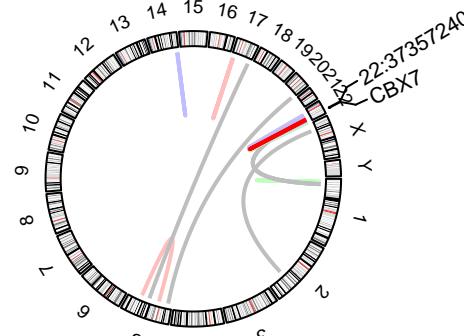
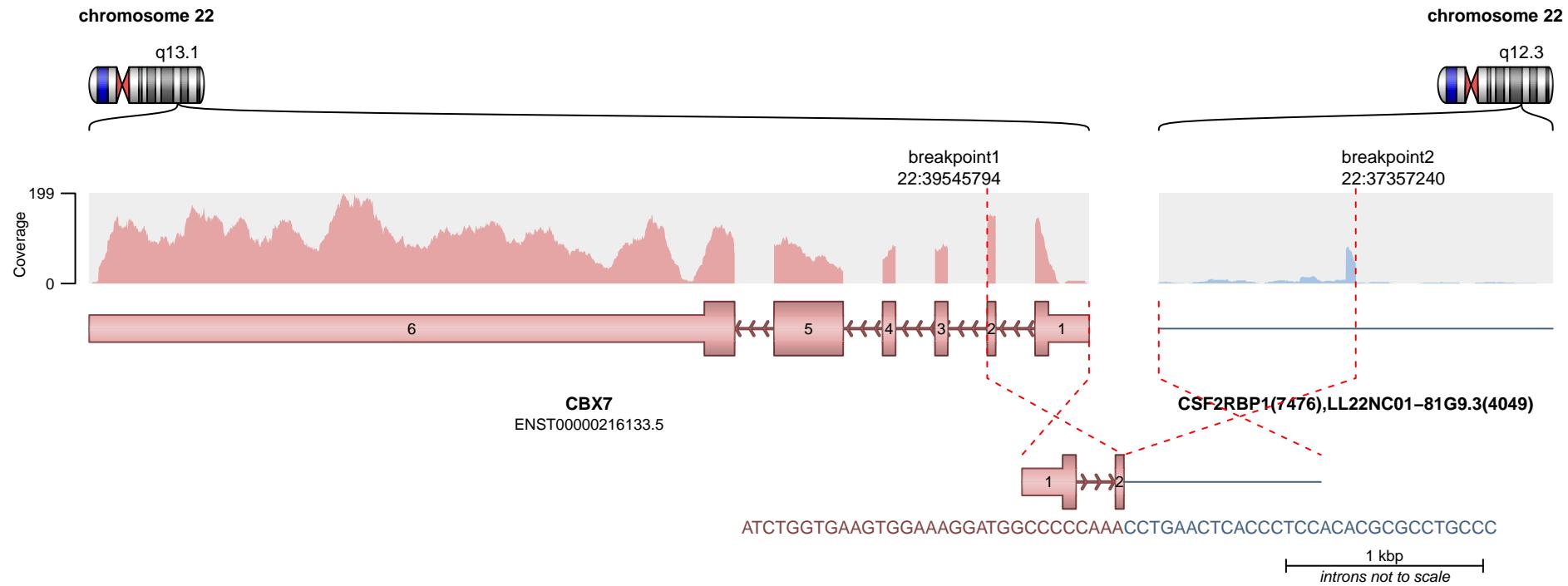
RETAINED PROTEIN DOMAINS
reading frame unclear



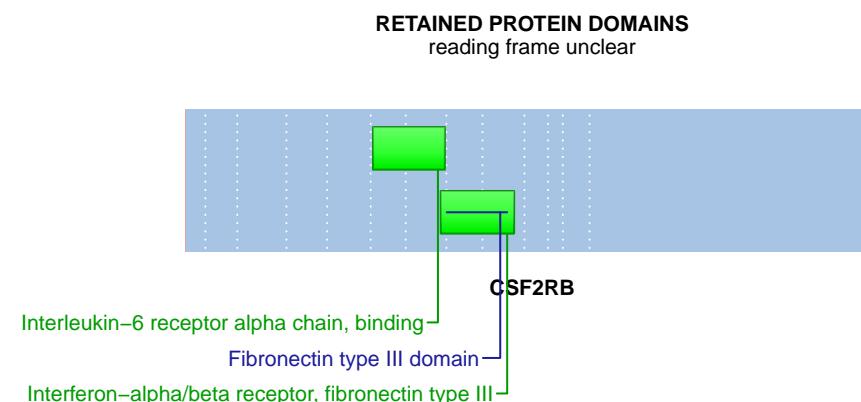
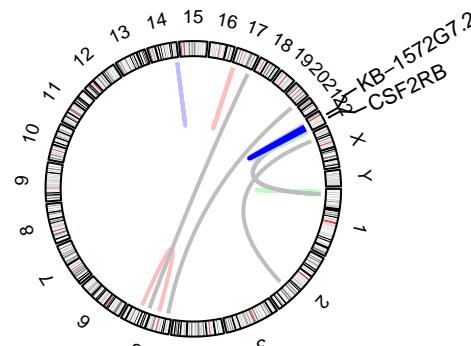
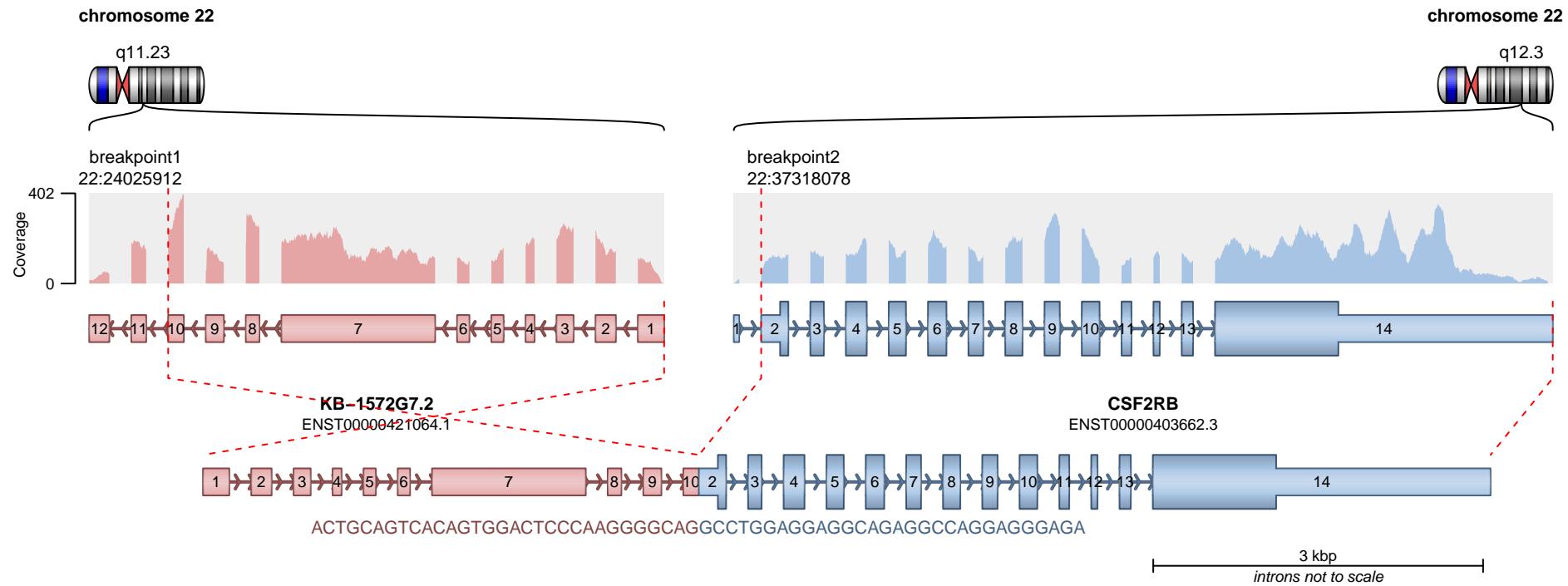
SUPPORTING READ COUNT

Split reads at breakpoint1 = 20
Split reads at breakpoint2 = 22
Discordant mates = 9

— translocation — deletion
— duplication — inversion



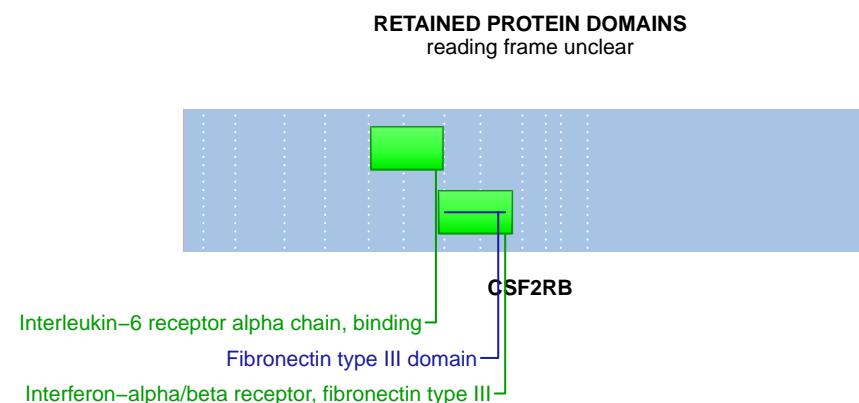
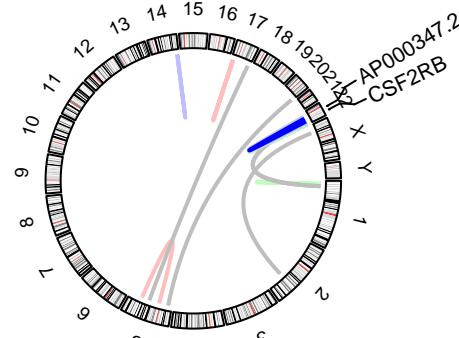
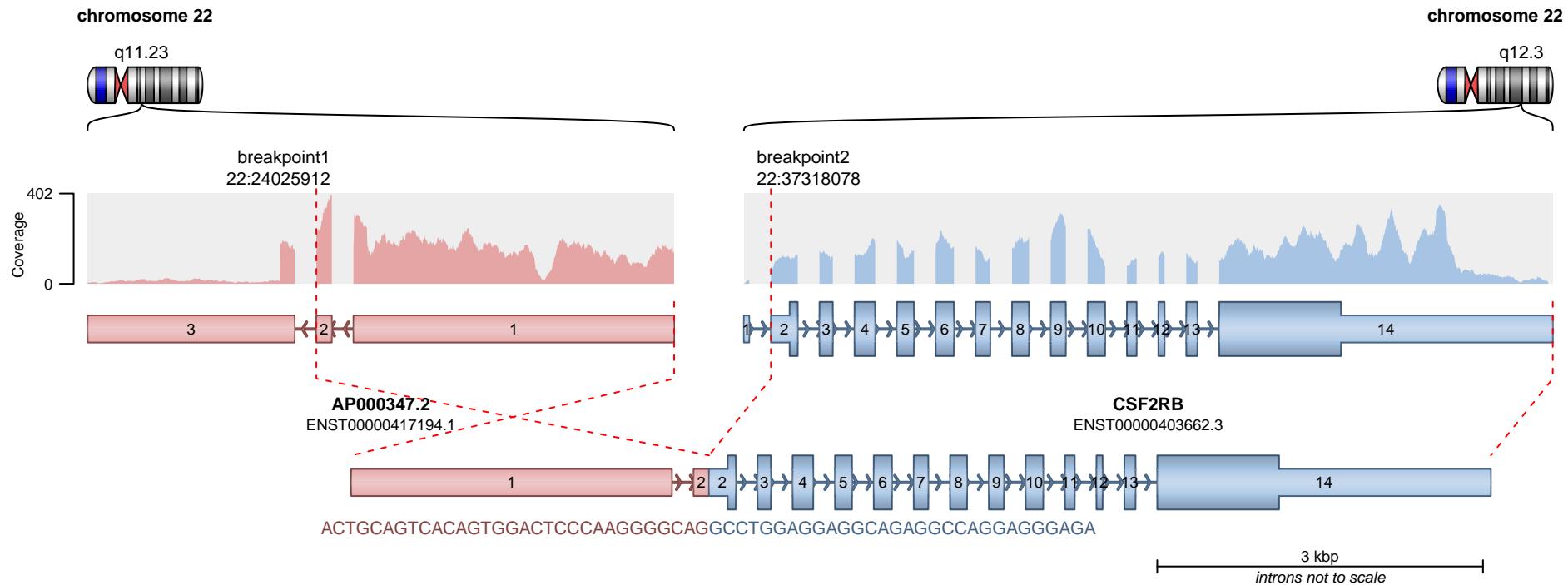
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads at breakpoint1 = 6
Split reads at breakpoint2 = 18
Discordant mates = 7

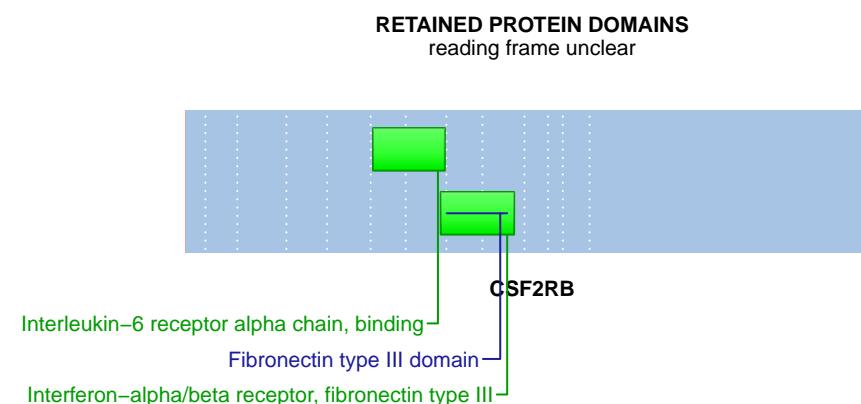
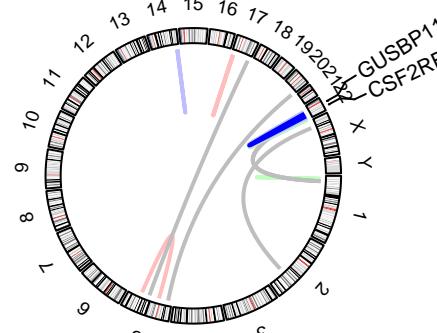
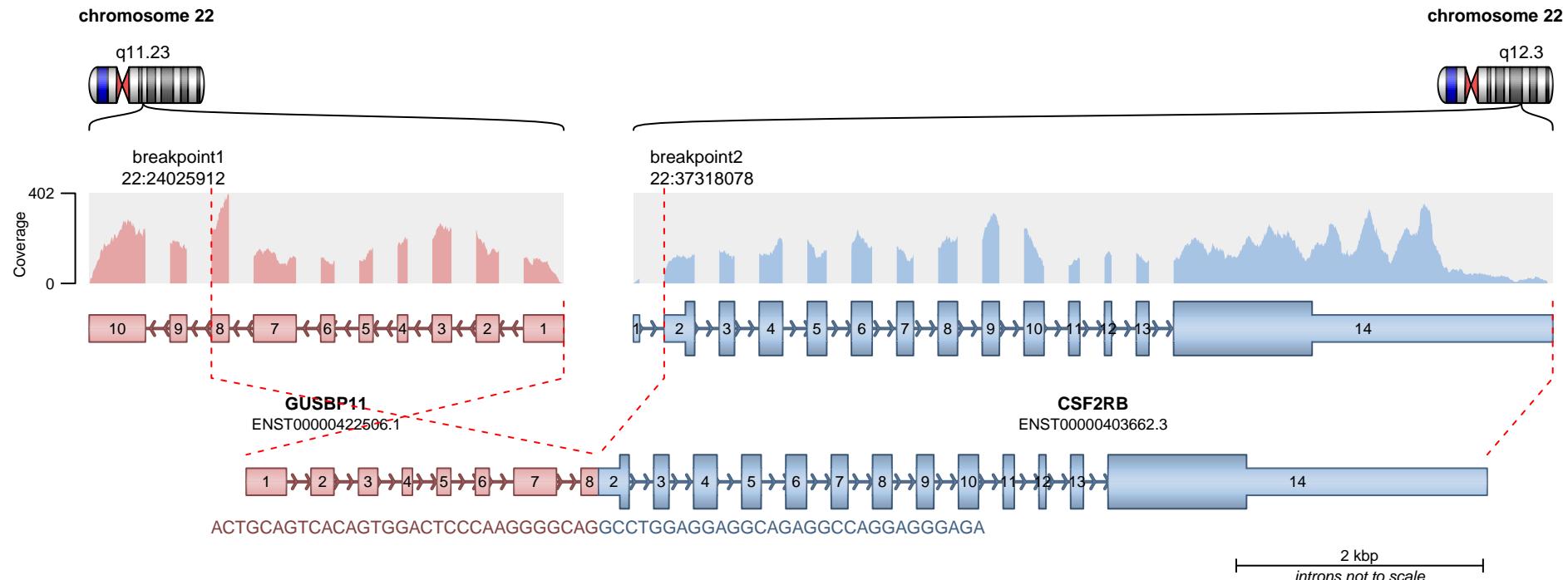
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads at breakpoint1 = 6
Split reads at breakpoint2 = 18
Discordant mates = 7

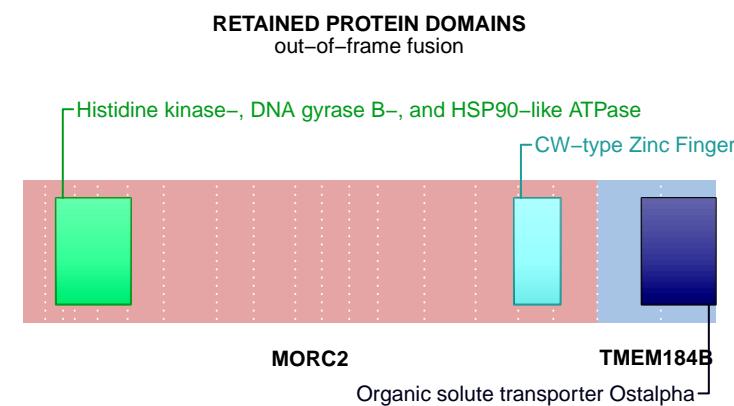
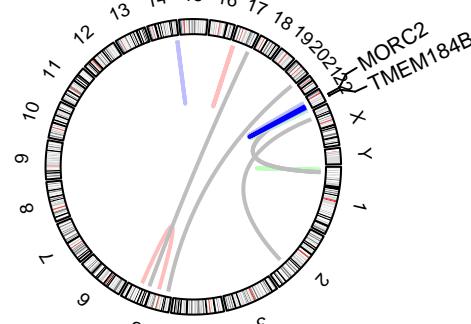
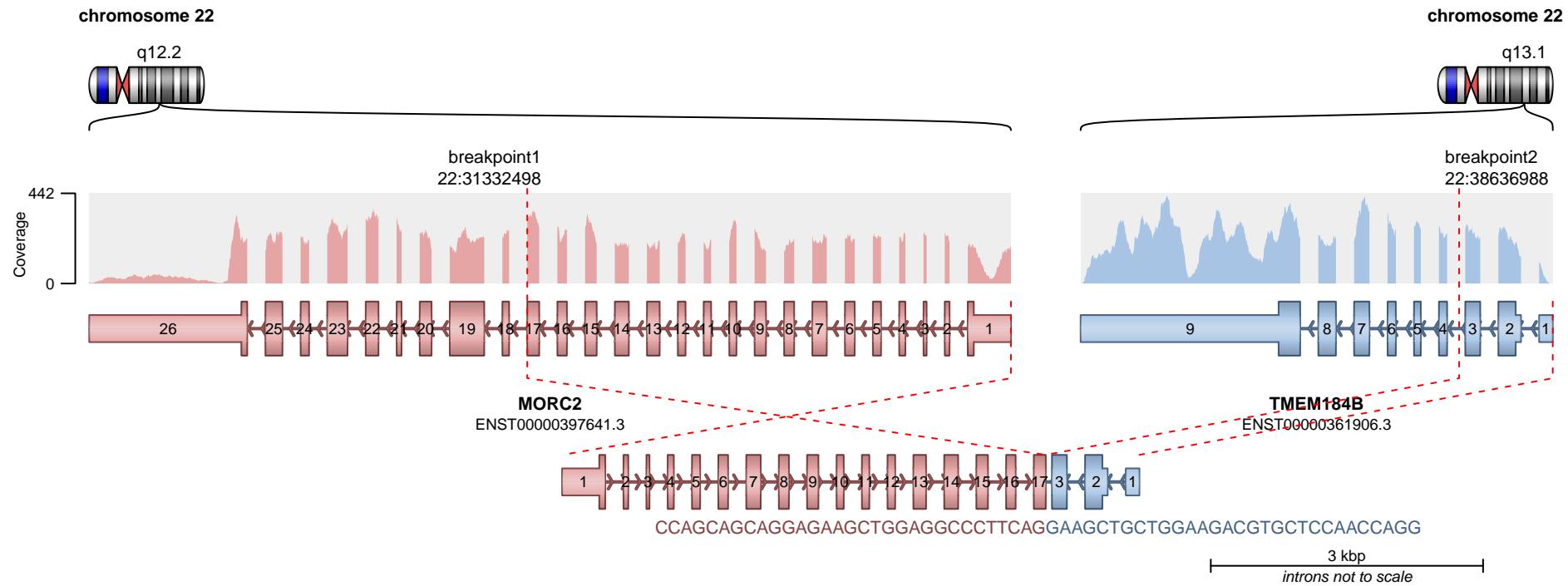
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads at breakpoint1 = 6
Split reads at breakpoint2 = 18
Discordant mates = 7

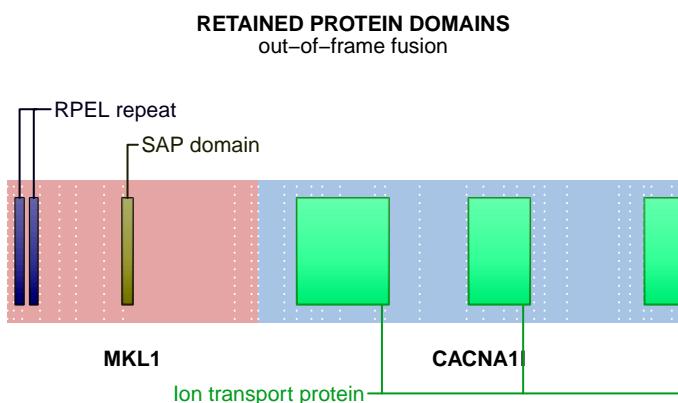
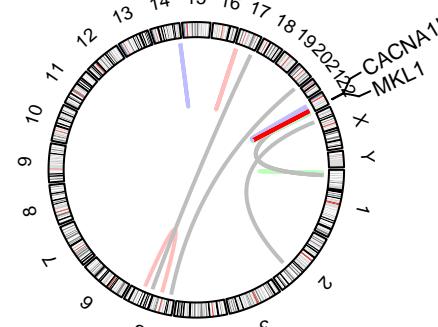
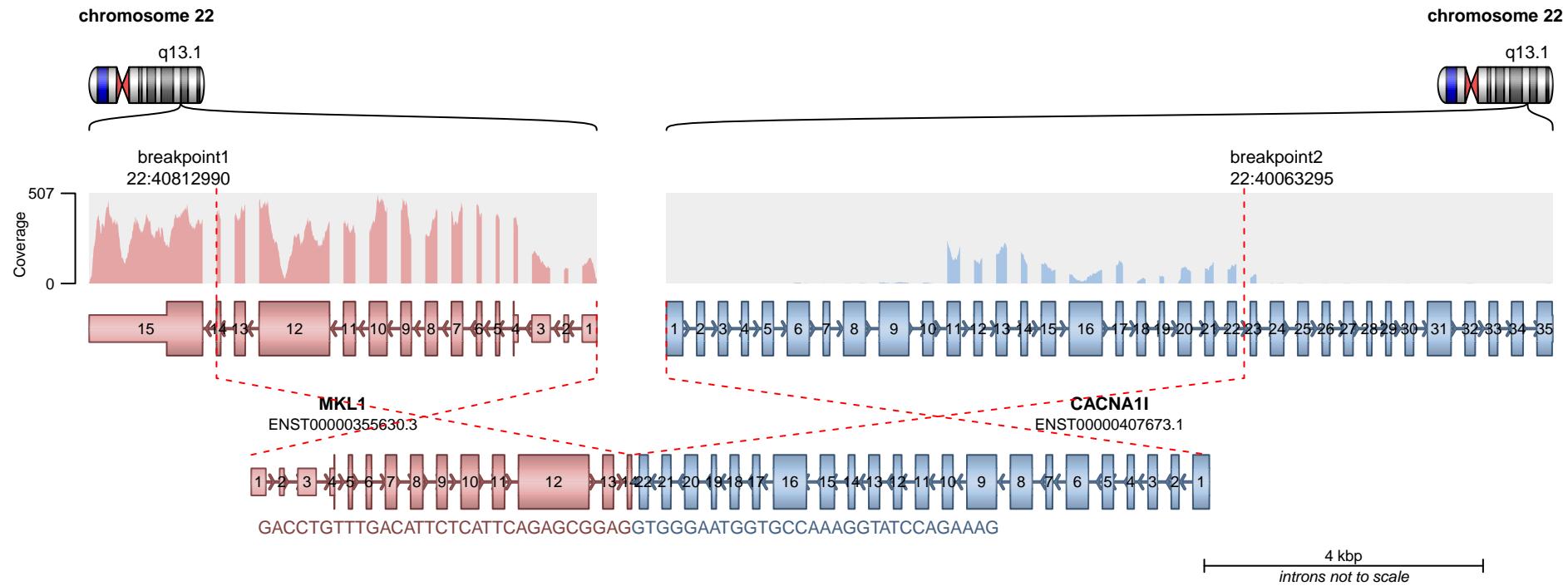
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads at breakpoint1 = 8
Split reads at breakpoint2 = 9
Discordant mates = 11

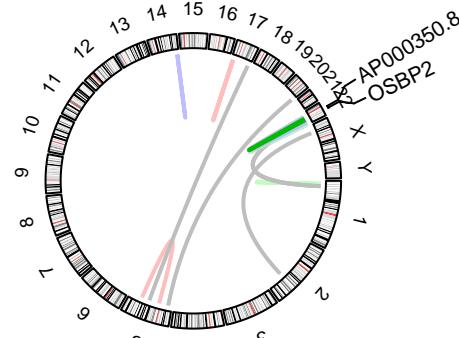
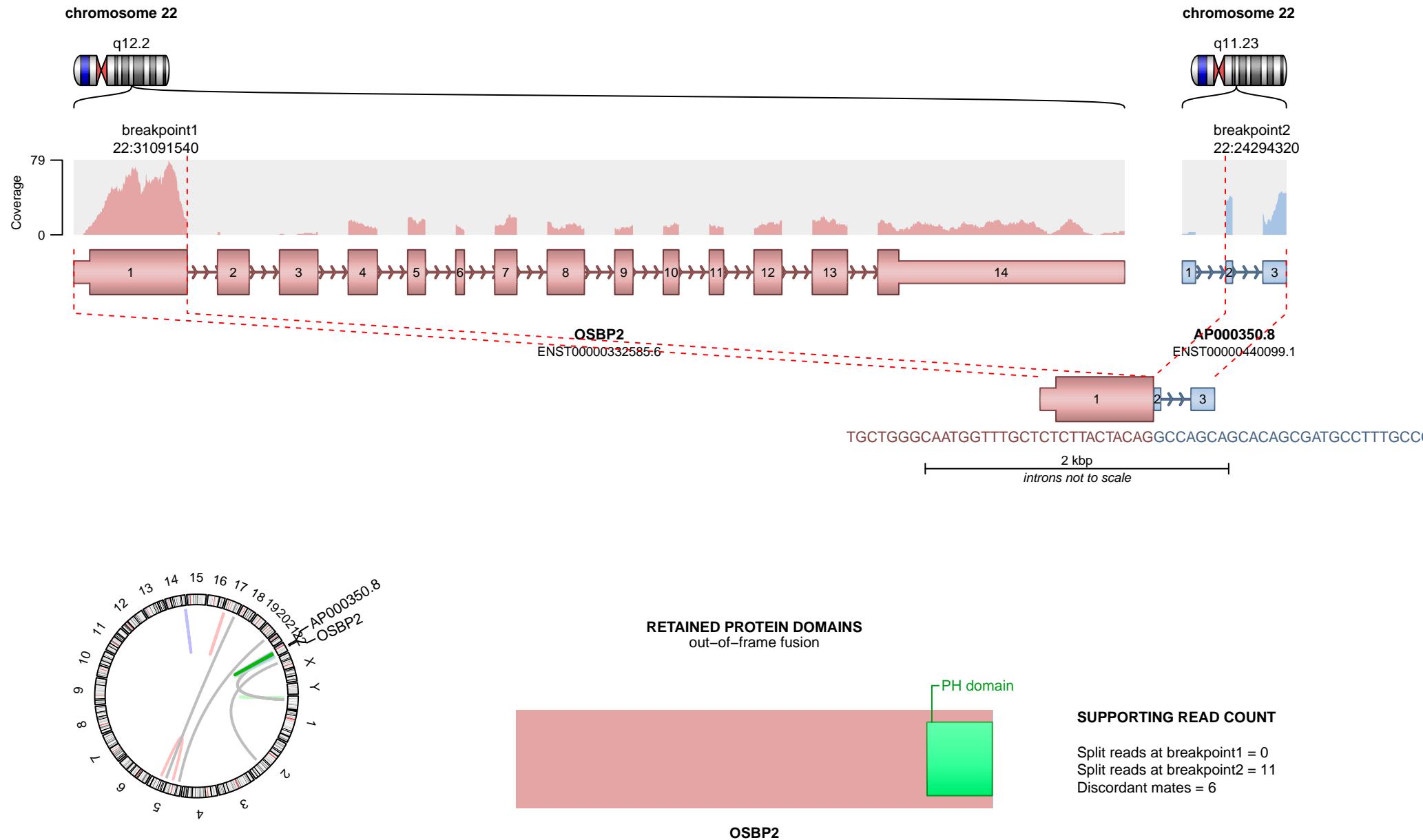
— translocation — deletion
— duplication — inversion



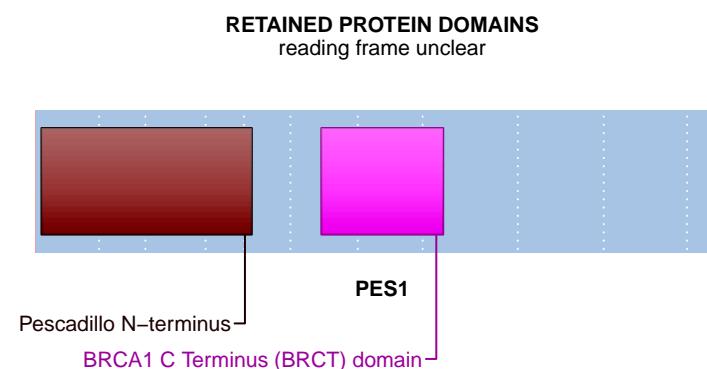
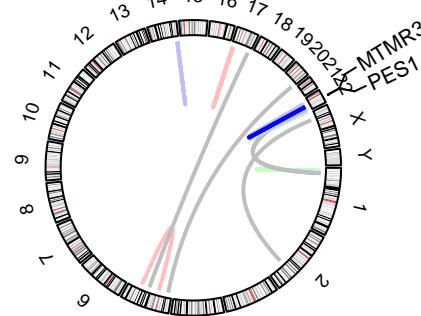
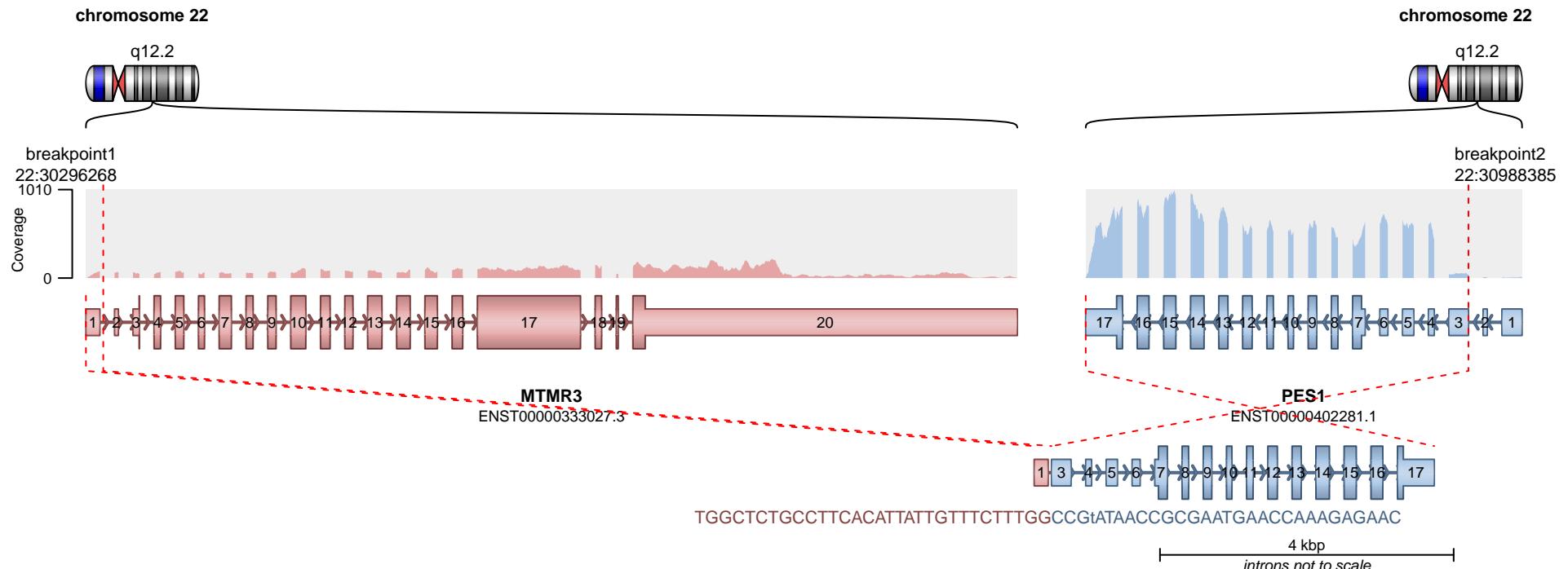
SUPPORTING READ COUNT

Split reads at breakpoint1 = 11
Split reads at breakpoint2 = 5
Discordant mates = 2

— translocation — deletion
— duplication — inversion



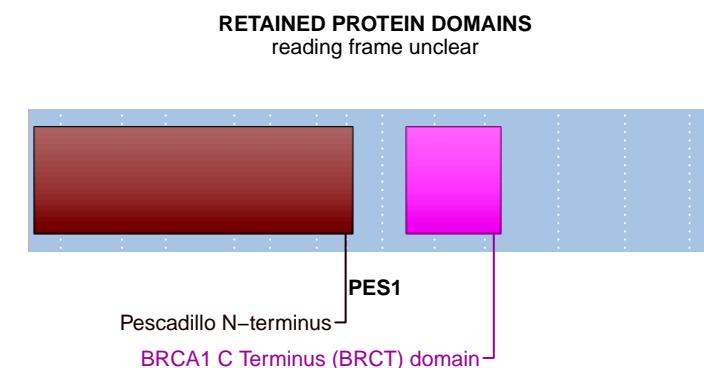
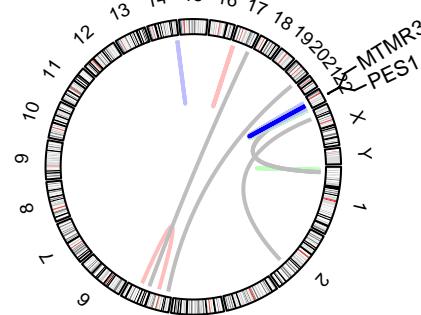
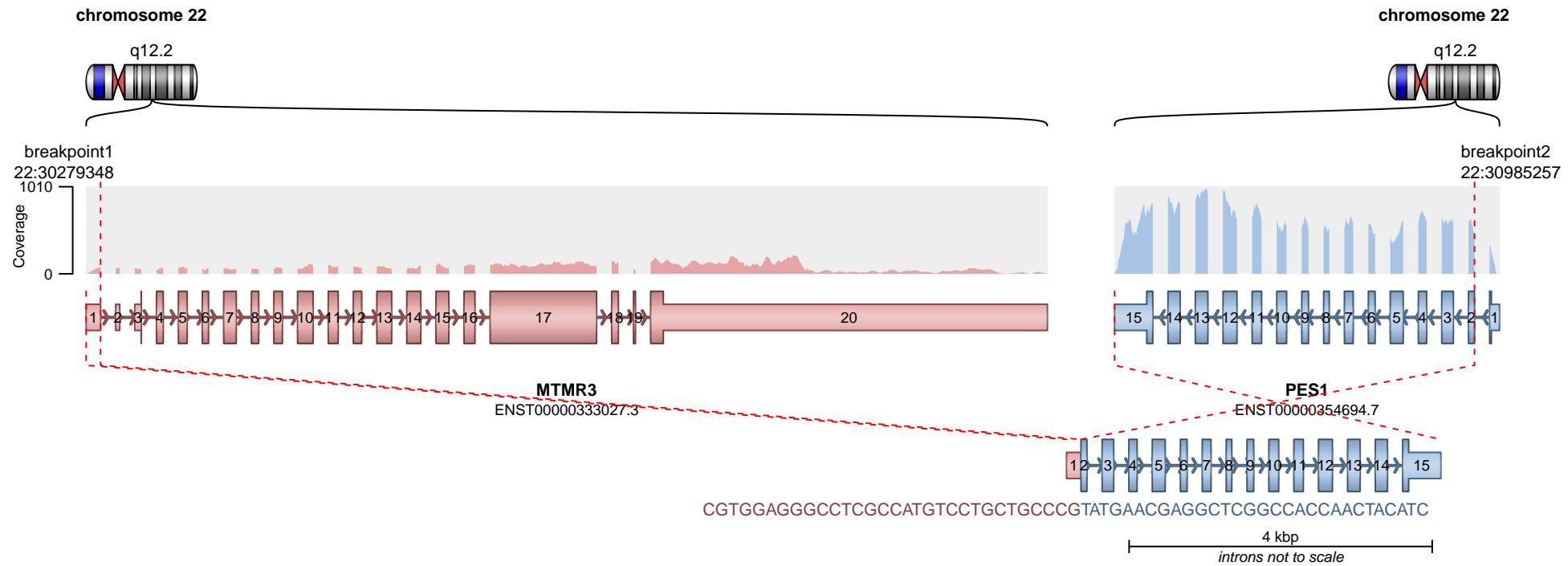
translocation **deletion**
duplication **inversion**



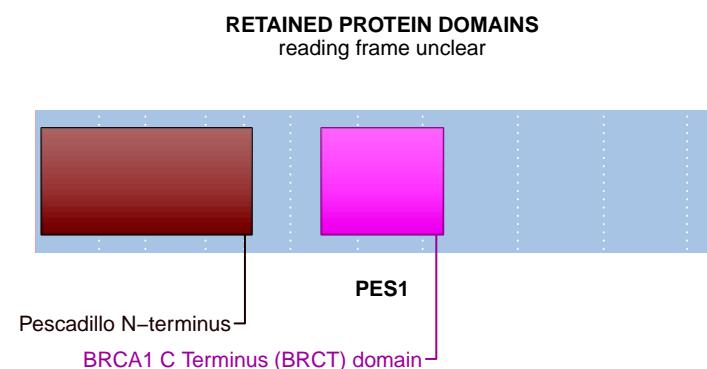
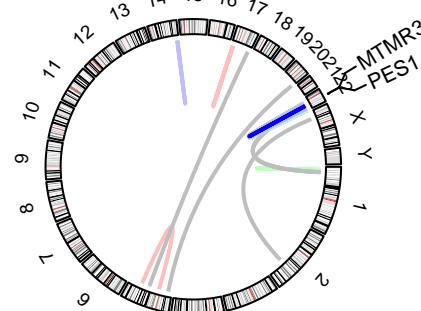
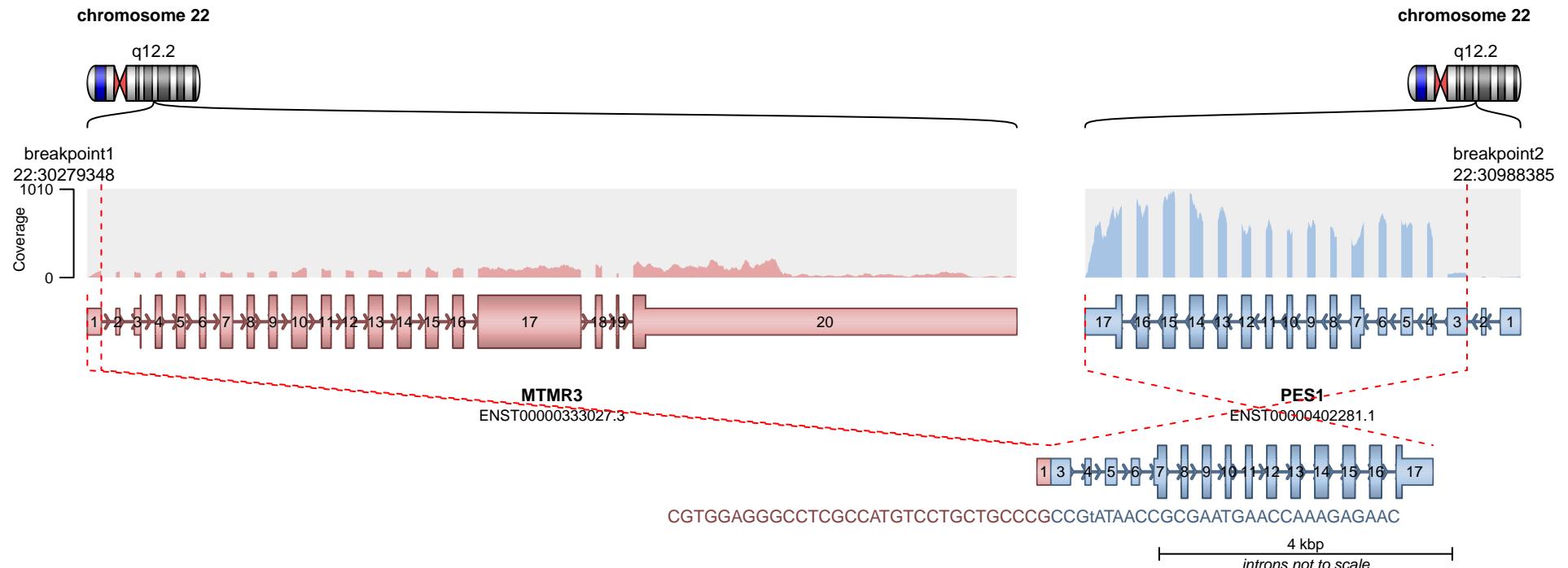
SUPPORTING READ COUNT

Split reads at breakpoint1 = 5
Split reads at breakpoint2 = 5
Discordant mates = 5

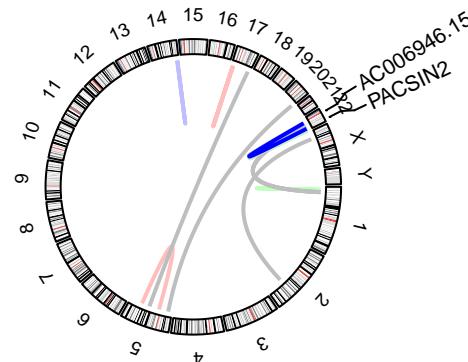
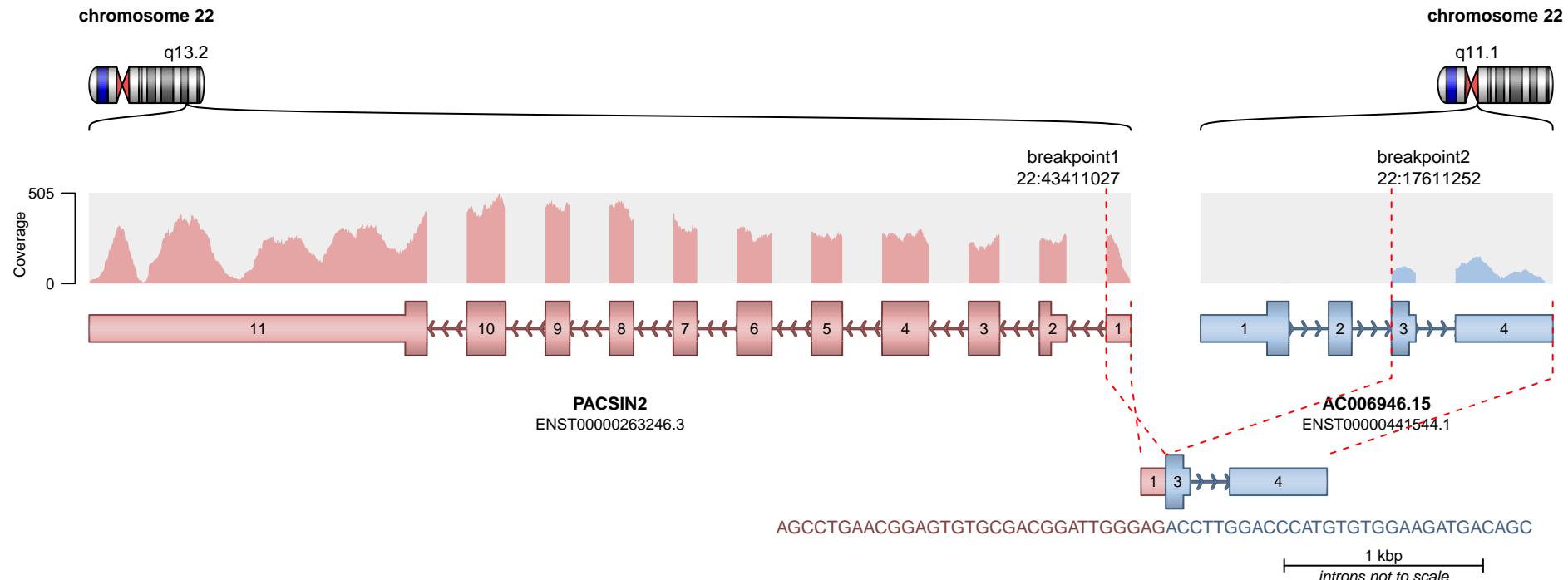
— translocation — deletion
— duplication — inversion



— translocation — deletion
— duplication — inversion



— translocation — deletion
— duplication — inversion

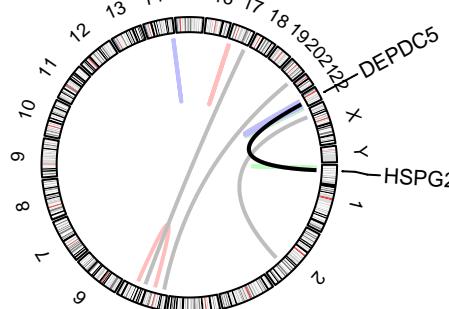
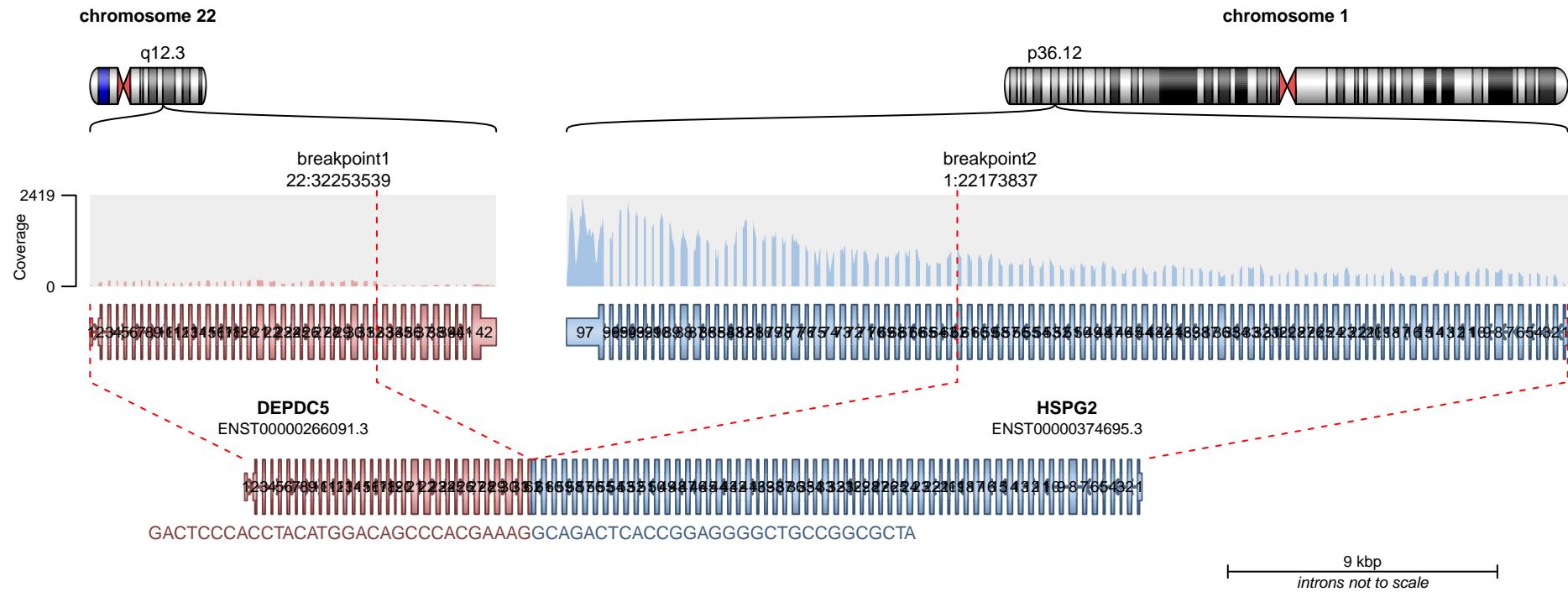


— translocation — deletion
— duplication — inversion

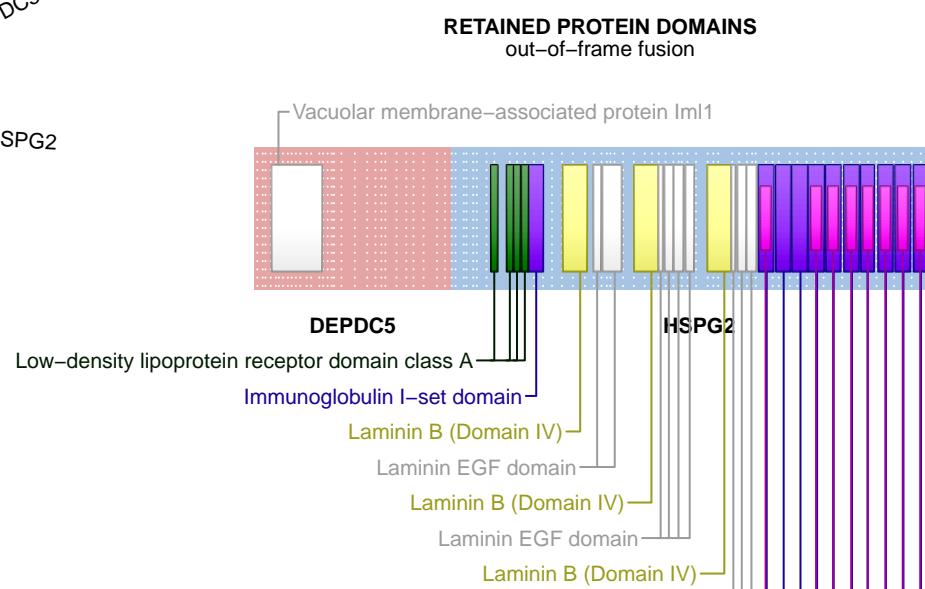
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 1
Split reads at breakpoint2 = 12
Discordant mates = 1

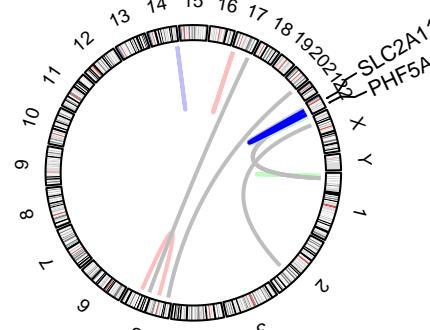
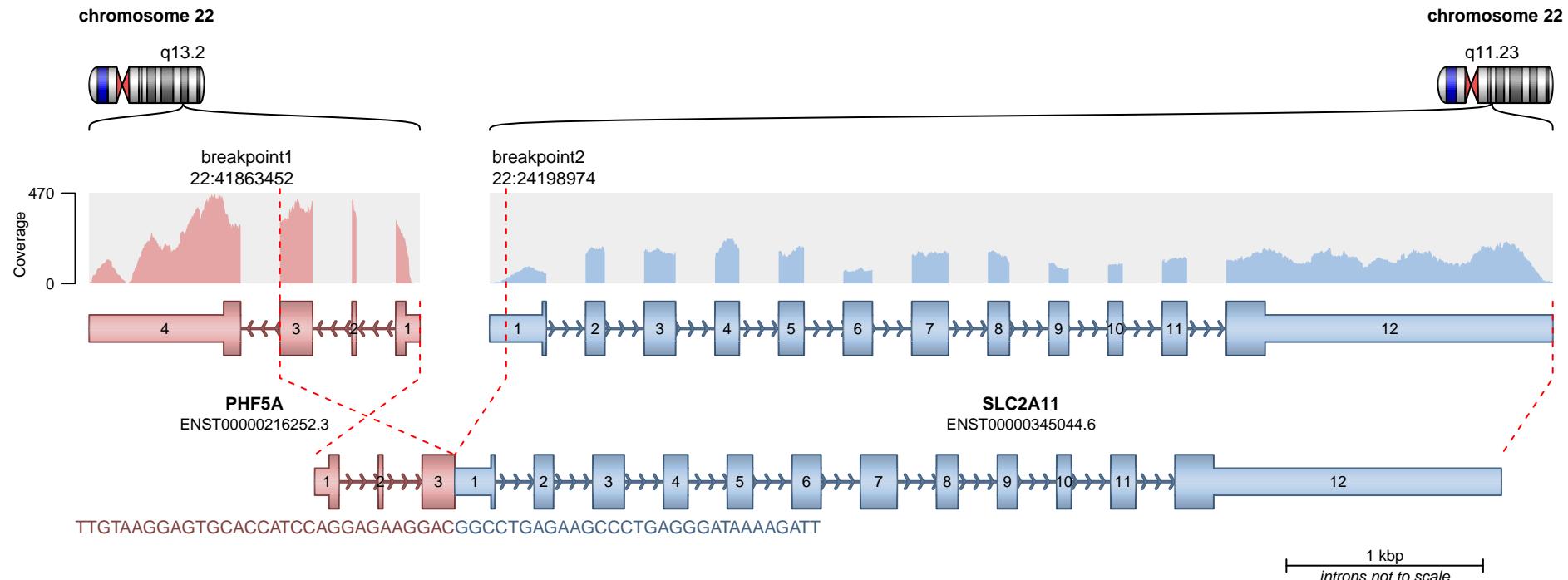


— translocation — deletion
— duplication — inversion

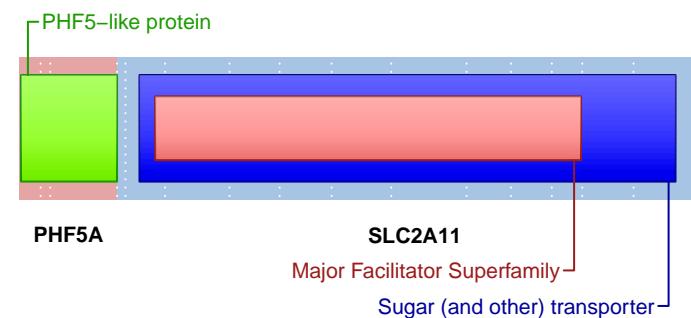


SUPPORTING READ COUNT

Split reads at breakpoint1 = 10
Split reads at breakpoint2 = 2
Discordant mates = 1



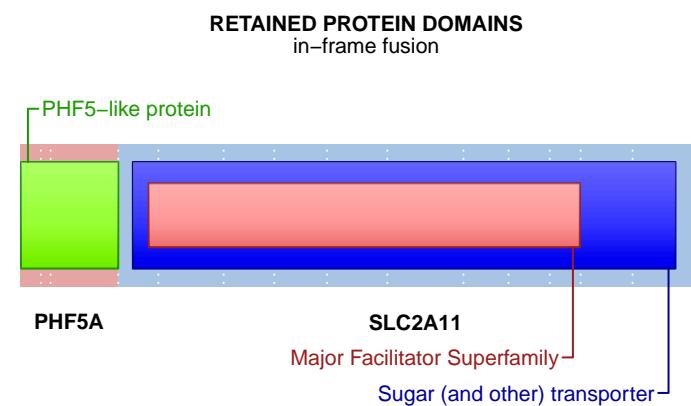
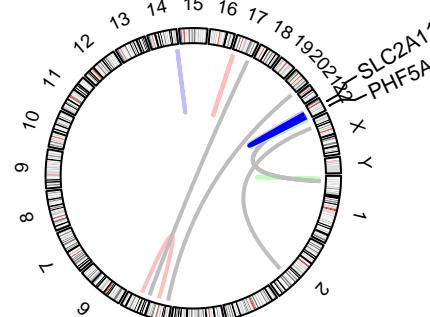
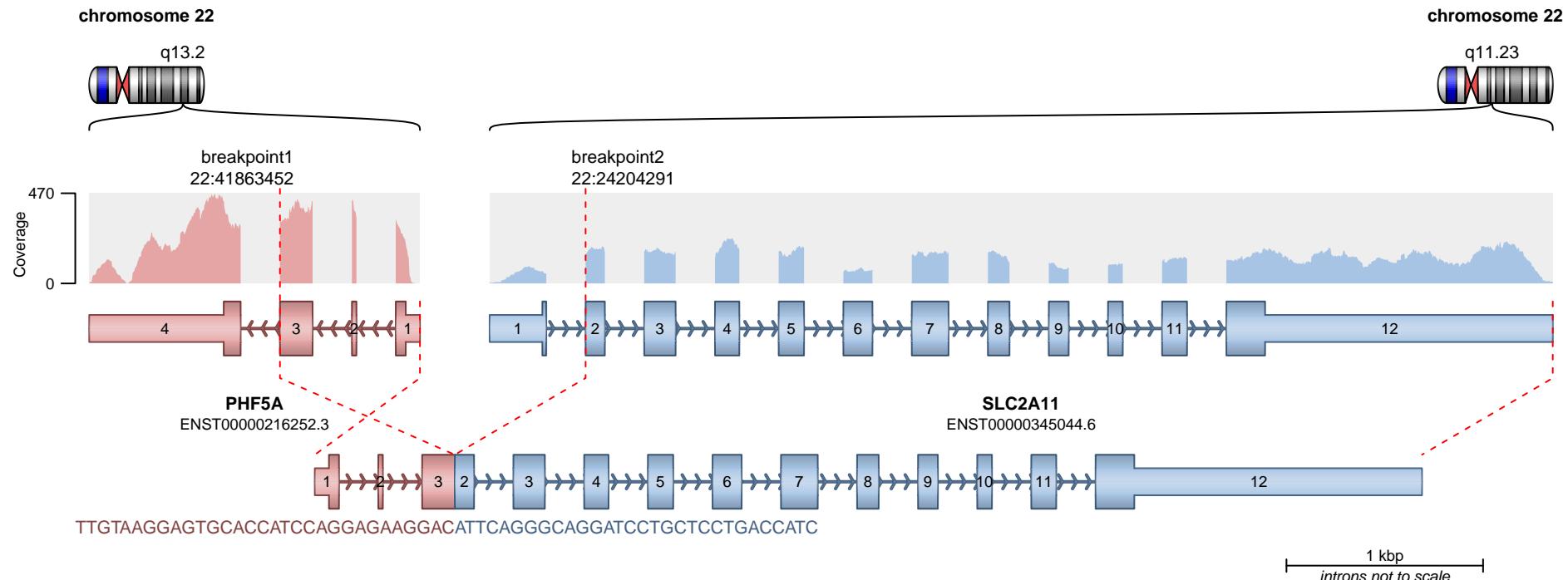
RETAINED PROTEIN DOMAINS out-of-frame fusion



SUPPORTING READ COUNT

Split reads at breakpoint1 = 2
Split reads at breakpoint2 = 5
Discordant mates = 5

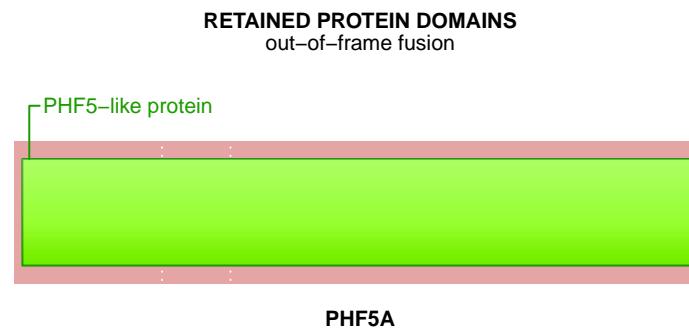
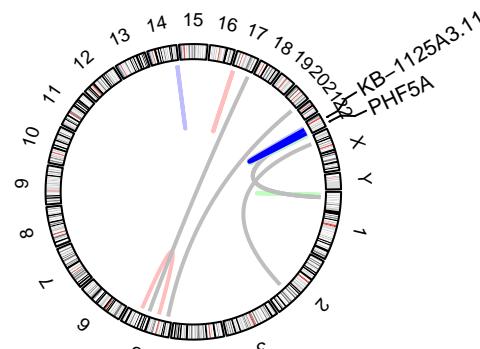
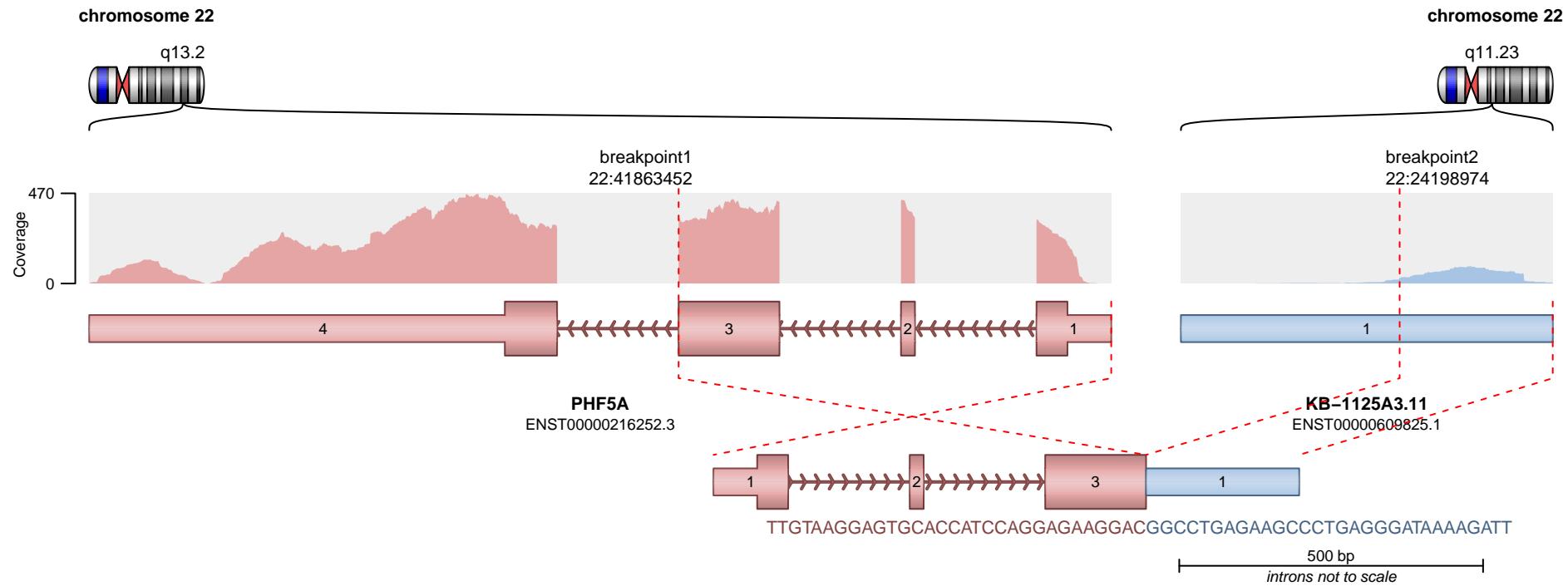
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads at breakpoint1 = 0
Split reads at breakpoint2 = 3
Discordant mates = 0

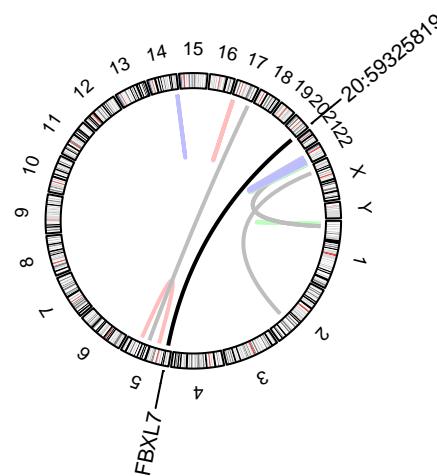
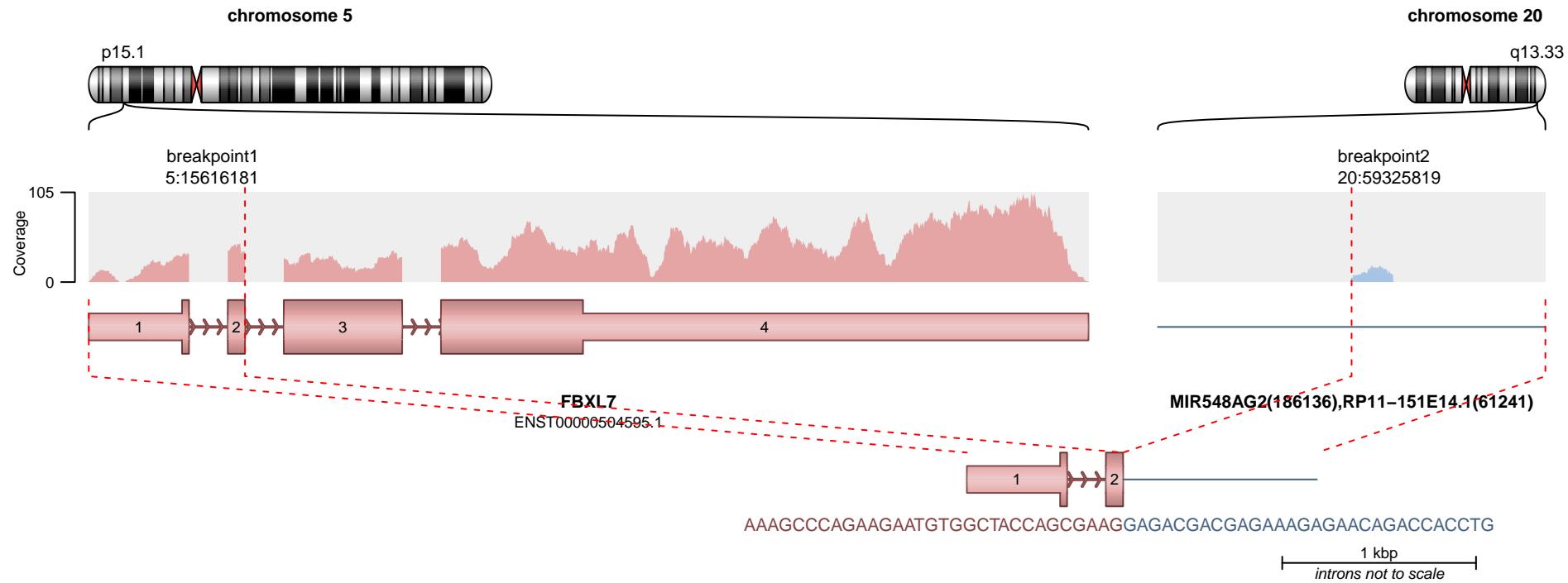
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads at breakpoint1 = 2
Split reads at breakpoint2 = 5
Discordant mates = 4

— translocation — deletion
— duplication — inversion

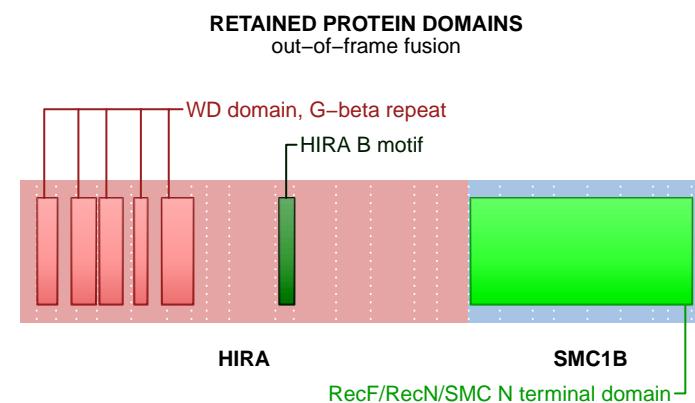
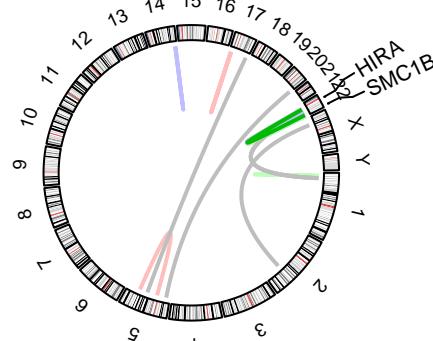
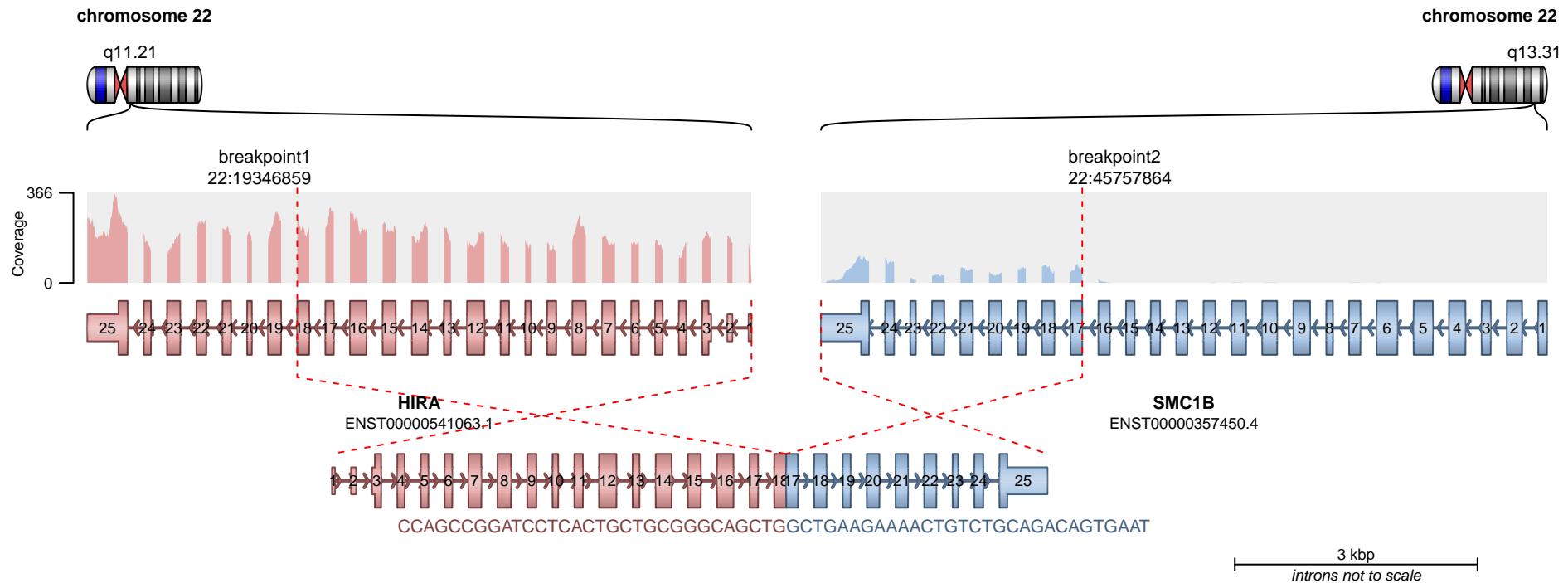


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 6
Split reads at breakpoint2 = 3
Discordant mates = 1

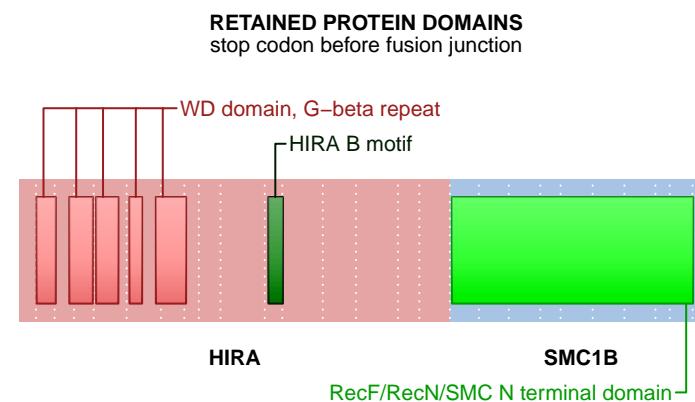
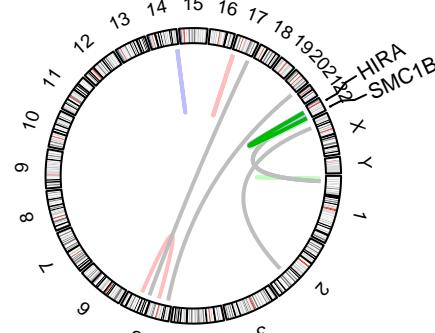
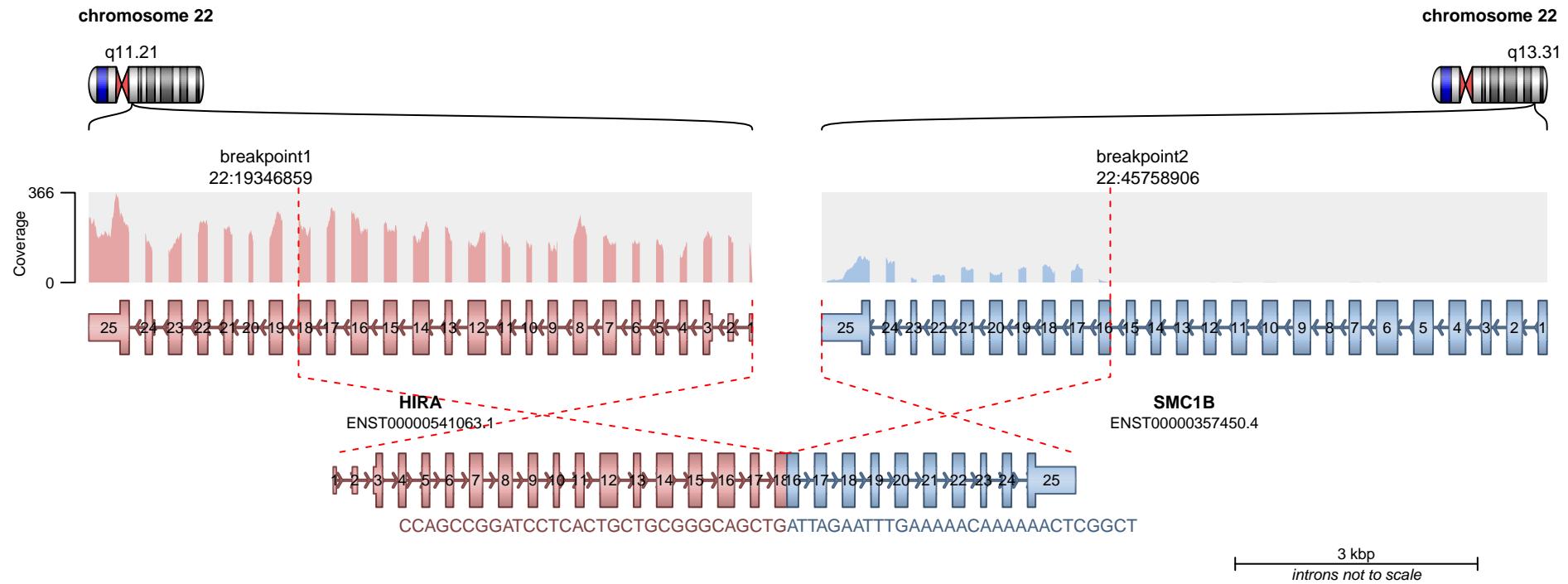
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads at breakpoint1 = 4
Split reads at breakpoint2 = 5
Discordant mates = 1

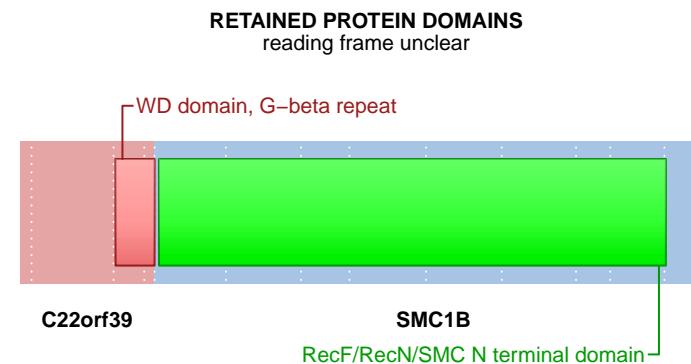
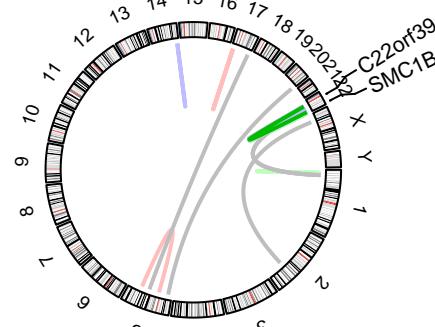
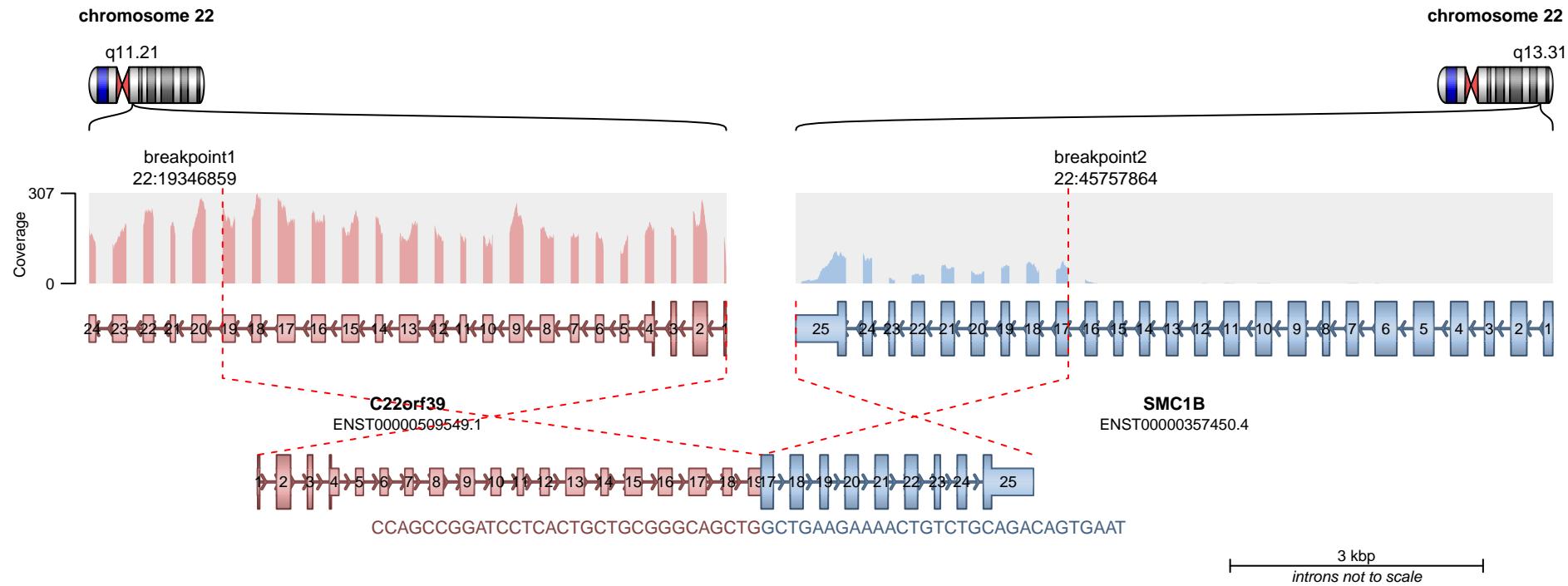
— translocation
— duplication
— deletion
— inversion



SUPPORTING READ COUNT

Split reads at breakpoint1 = 0
Split reads at breakpoint2 = 1
Discordant mates = 3

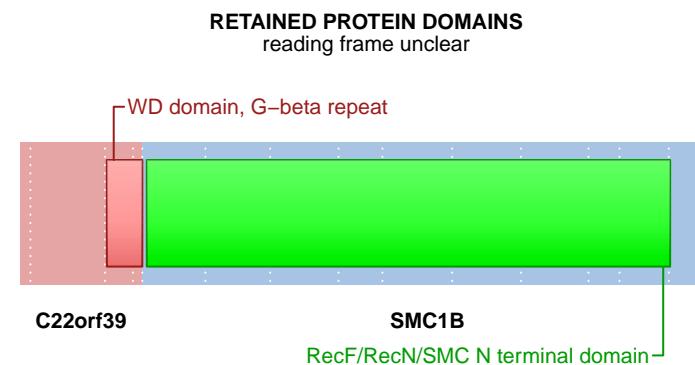
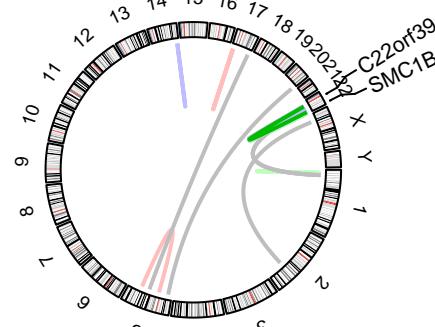
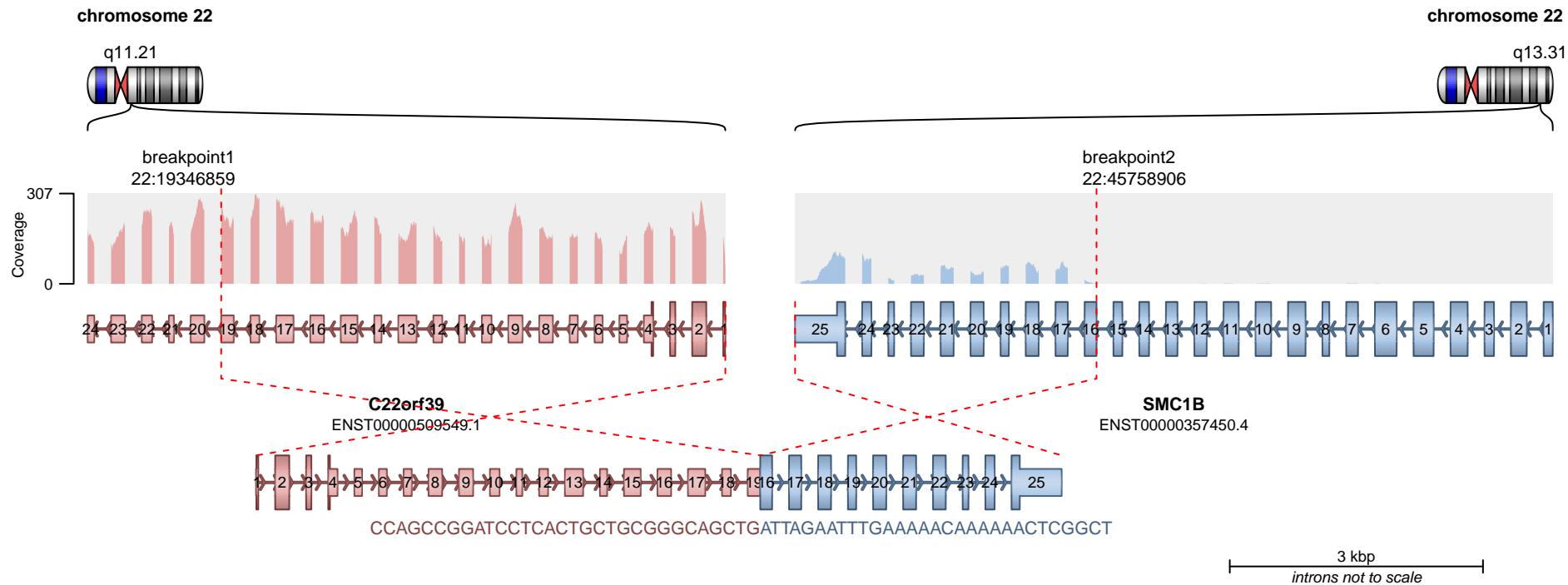
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads at breakpoint1 = 4
Split reads at breakpoint2 = 5
Discordant mates = 1

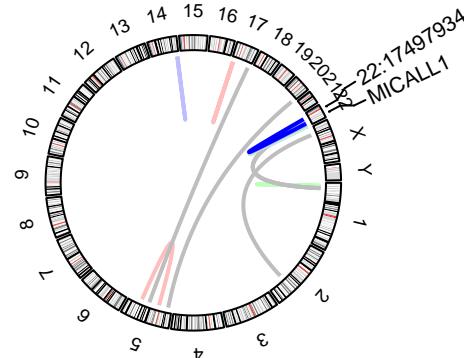
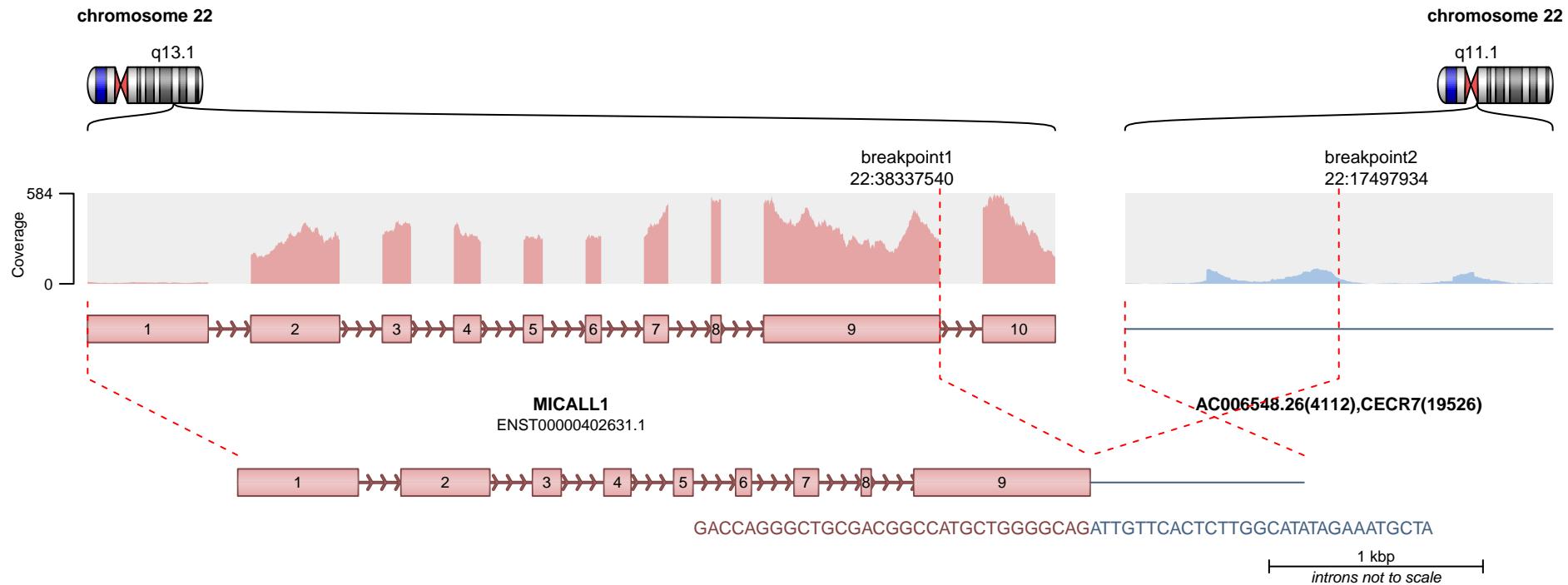
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads at breakpoint1 = 0
Split reads at breakpoint2 = 1
Discordant mates = 3

— translocation — deletion
— duplication — inversion

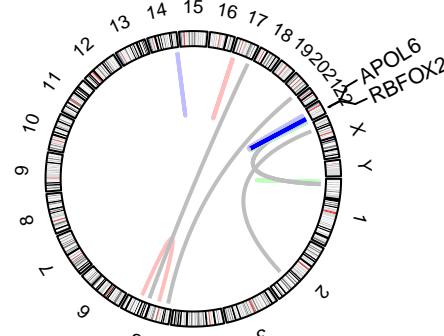
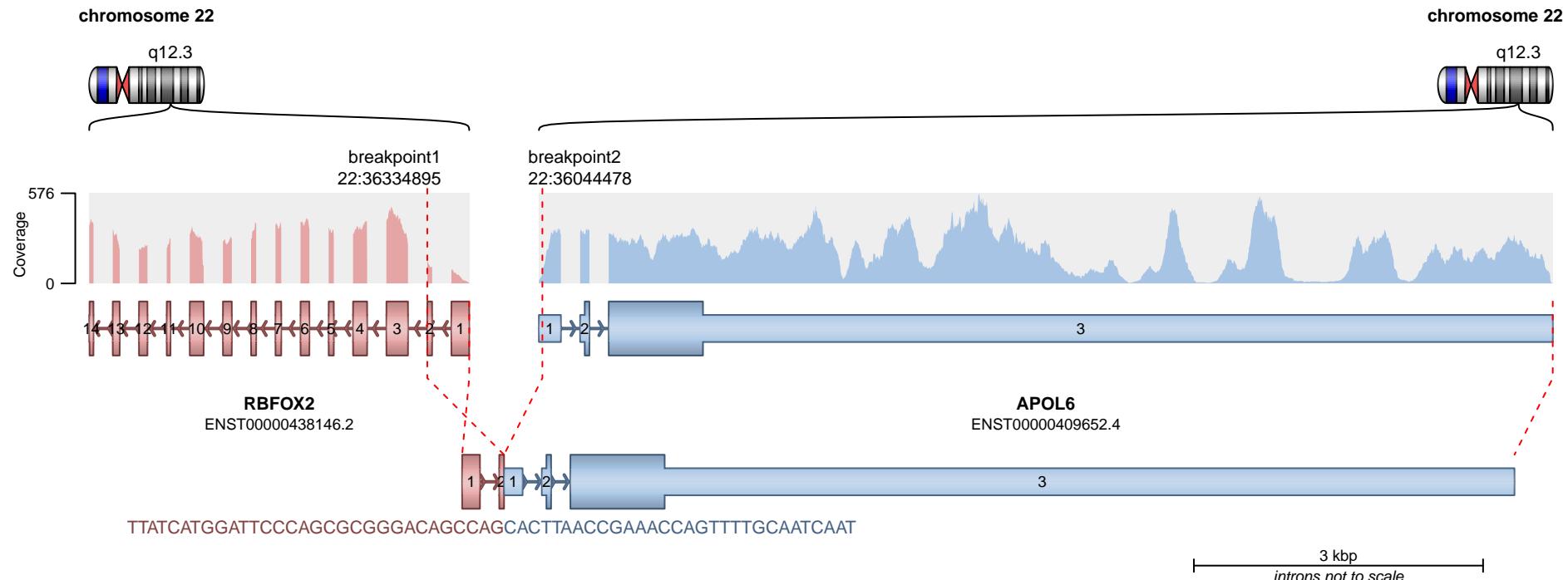


Genes are not protein-coding.

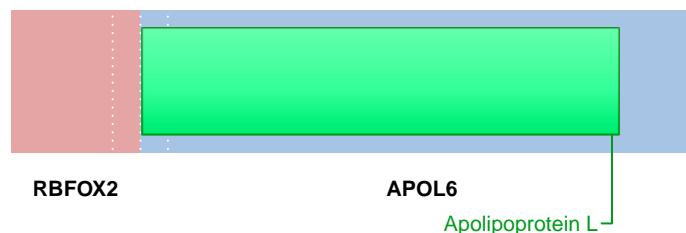
SUPPORTING READ COUNT

Split reads at breakpoint1 = 0
Split reads at breakpoint2 = 4
Discordant mates = 4

— translocation
— deletion
— duplication
— inversion



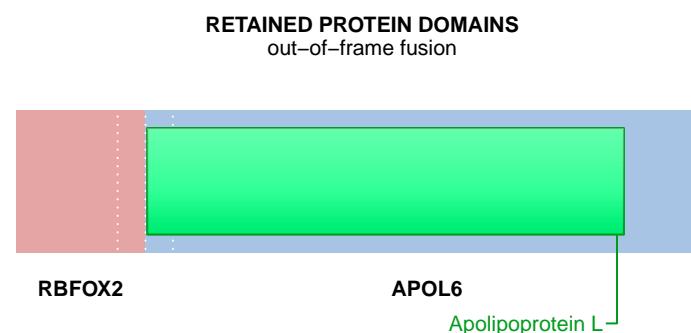
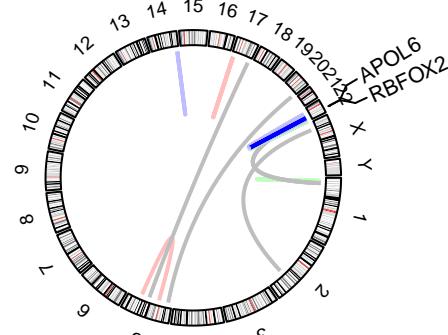
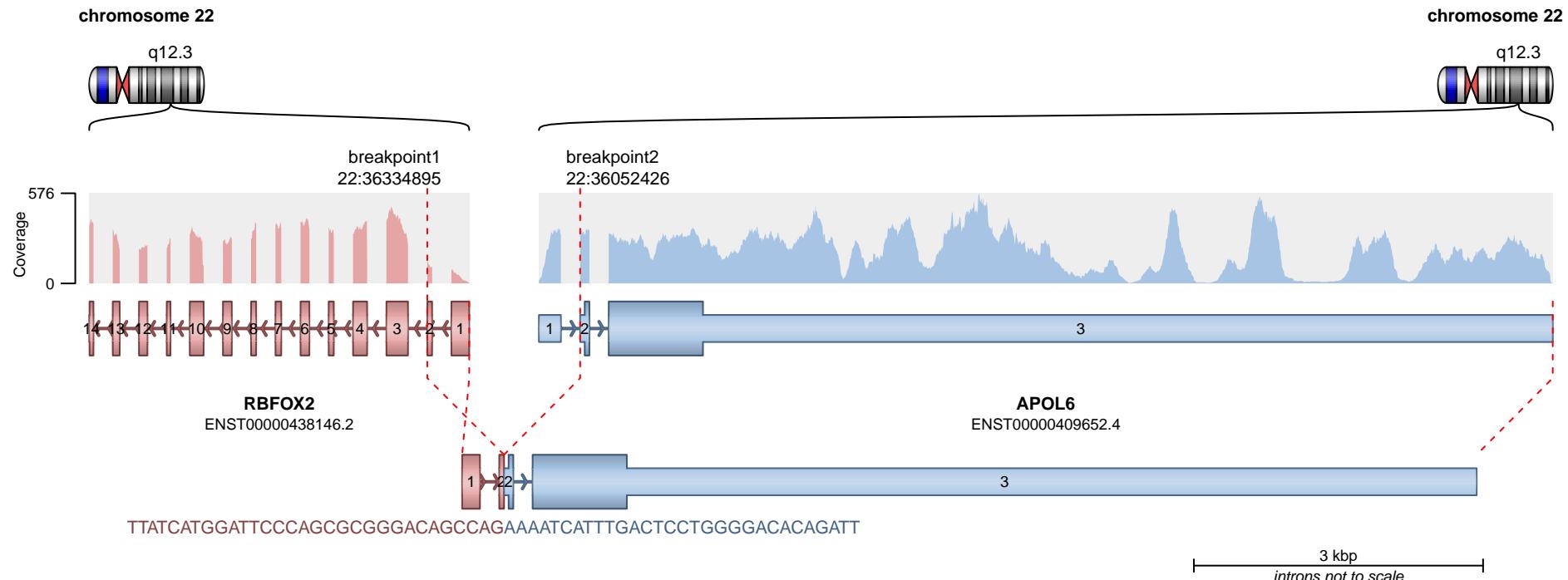
RETAINED PROTEIN DOMAINS in-frame fusion



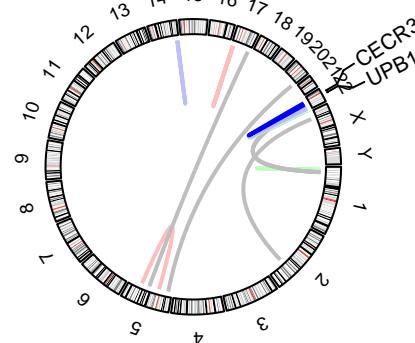
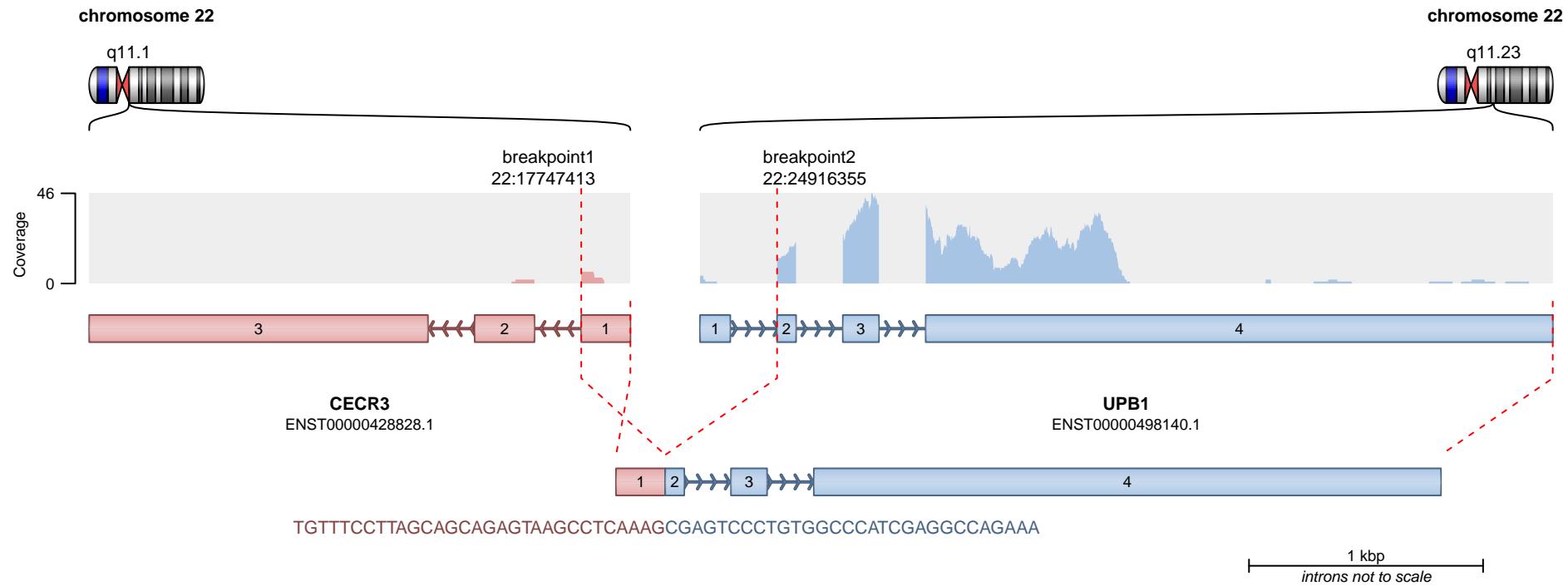
SUPPORTING READ COUNT

Split reads at breakpoint1 = 2
Split reads at breakpoint2 = 4
Discordant mates = 1

— translocation — deletion
— duplication — inversion



— translocation — deletion
— duplication — inversion

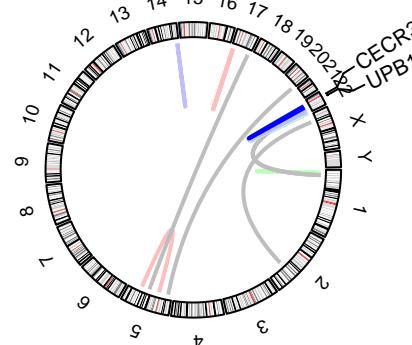
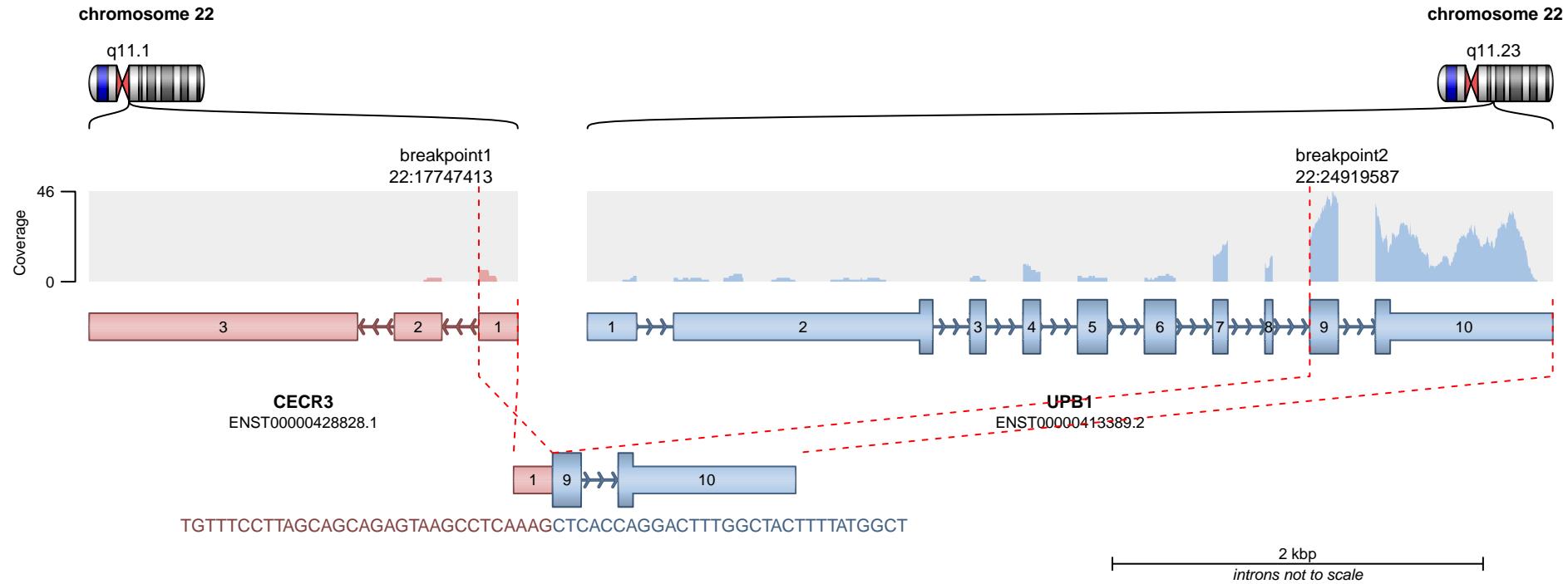


Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 2
Split reads at breakpoint2 = 4
Discordant mates = 0

— translocation — deletion
— duplication — inversion

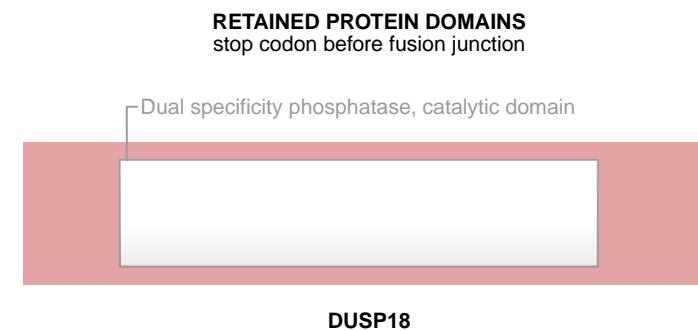
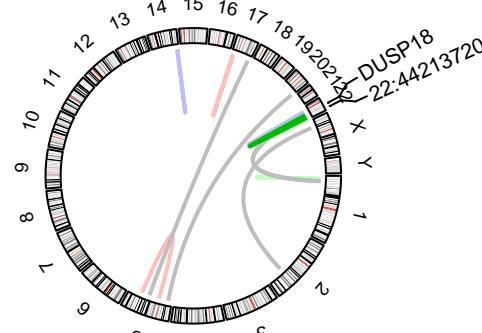
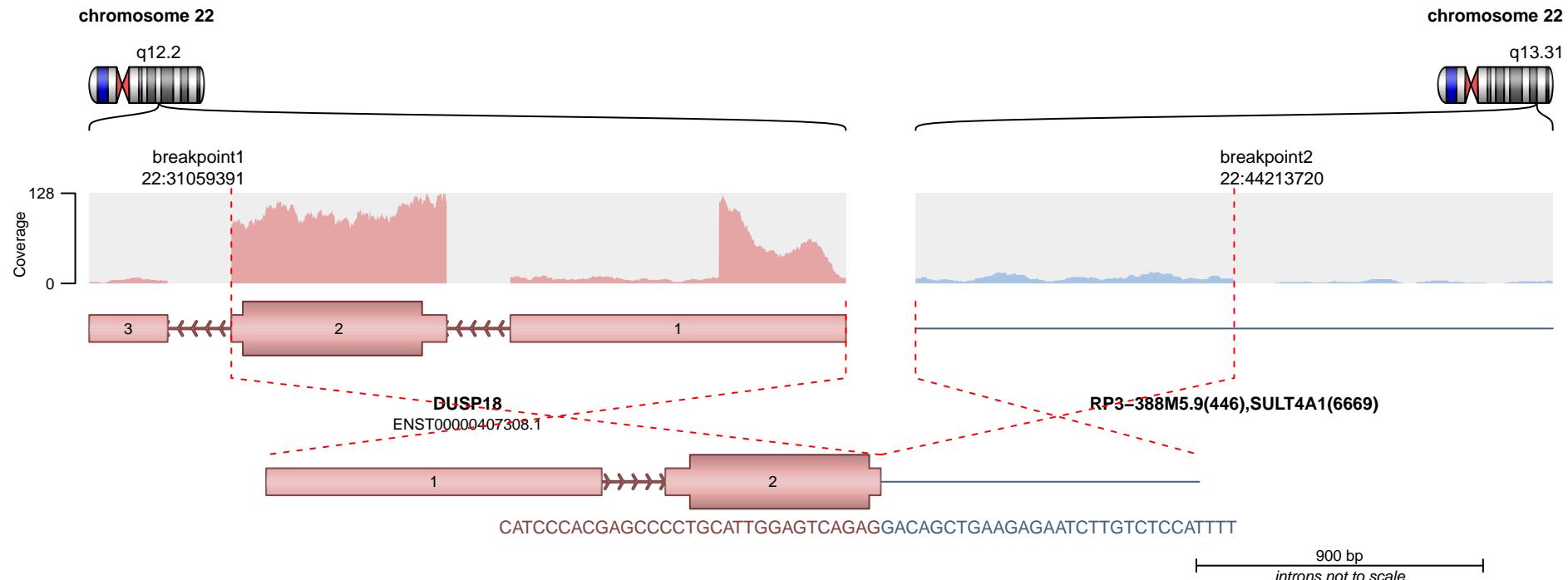


No protein domains retained in fusion.

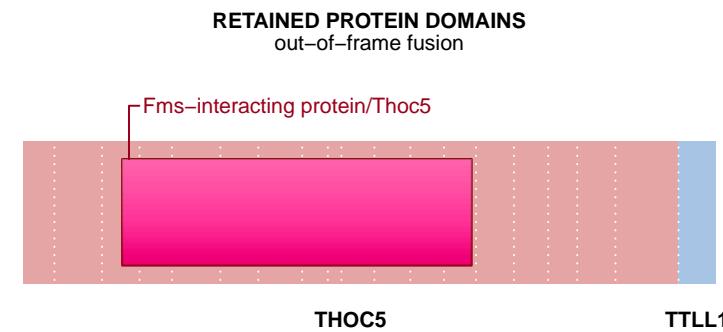
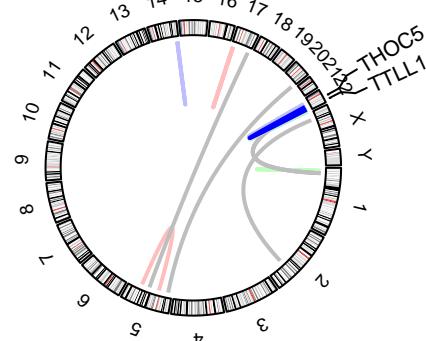
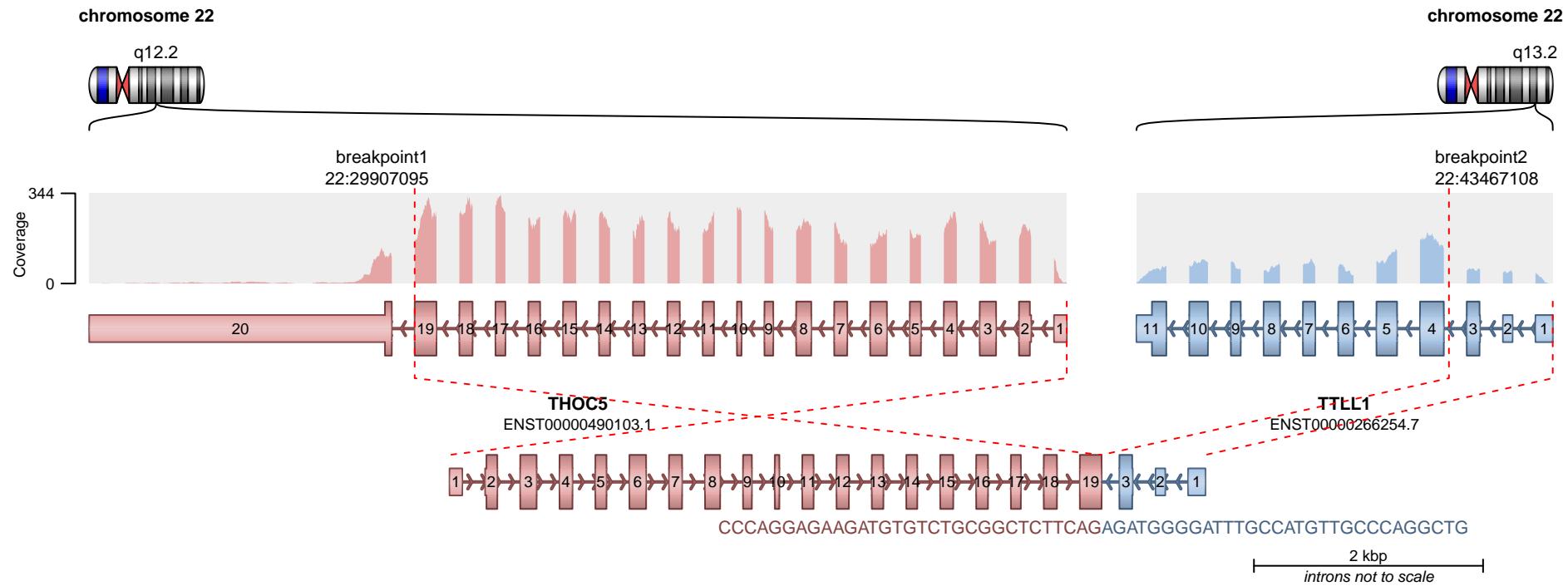
SUPPORTING READ COUNT

Split reads at breakpoint1 = 0
Split reads at breakpoint2 = 0
Discordant mates = 0

— translocation — deletion
— duplication — inversion



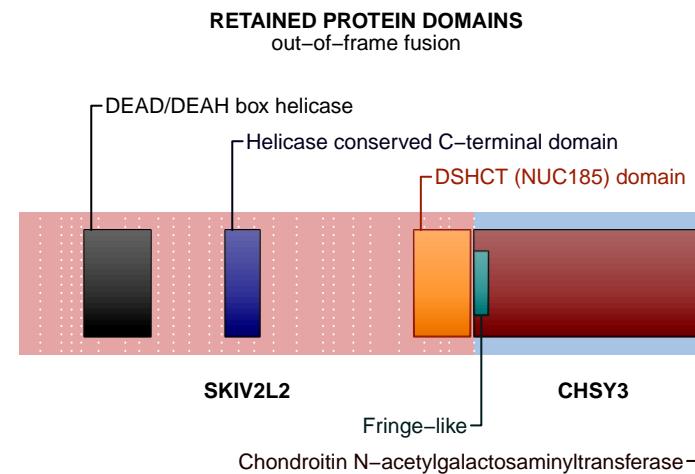
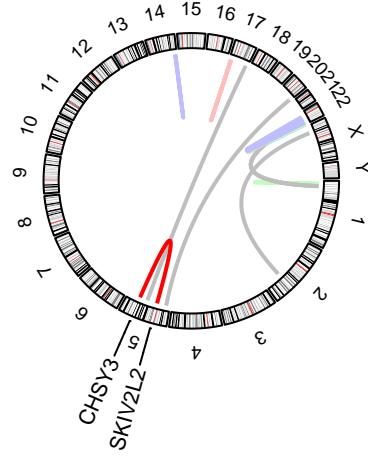
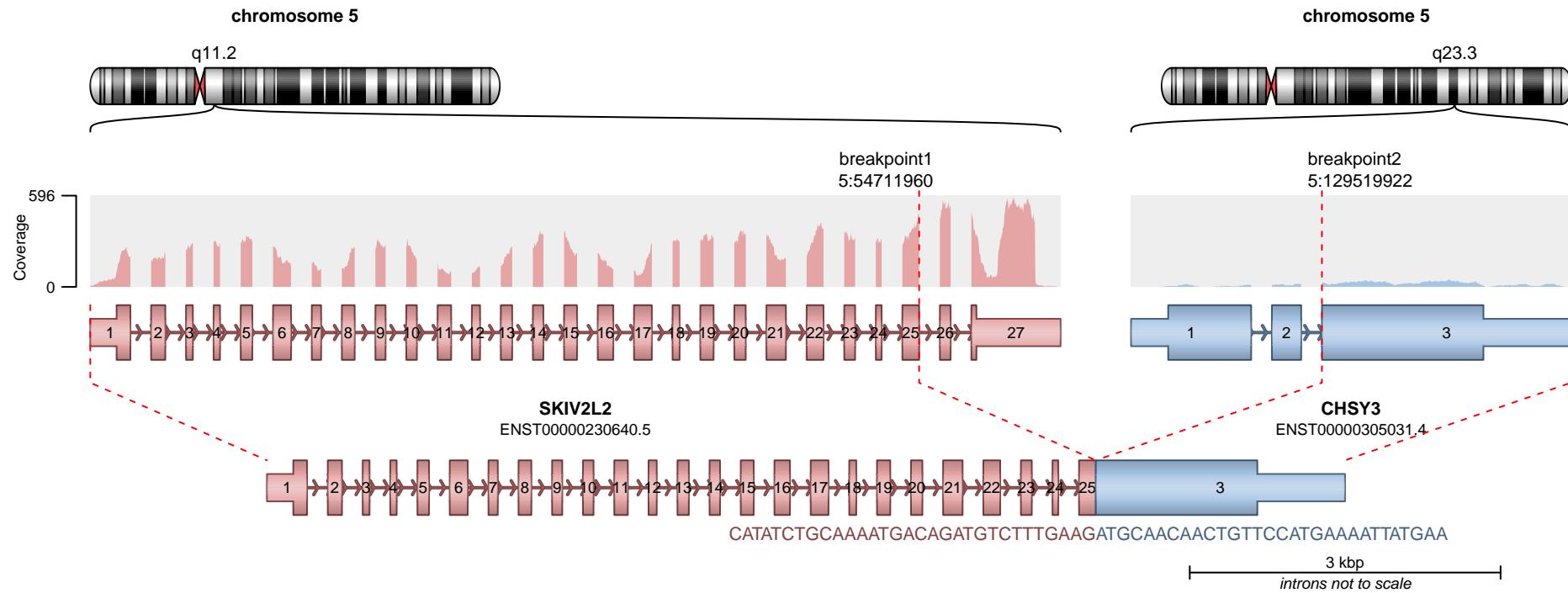
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads at breakpoint1 = 2
Split reads at breakpoint2 = 0
Discordant mates = 4

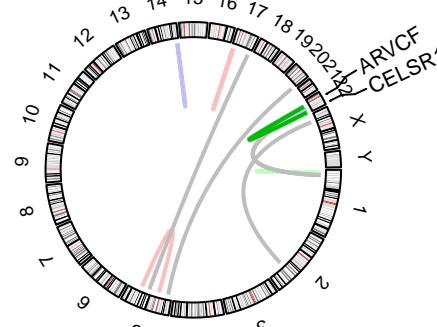
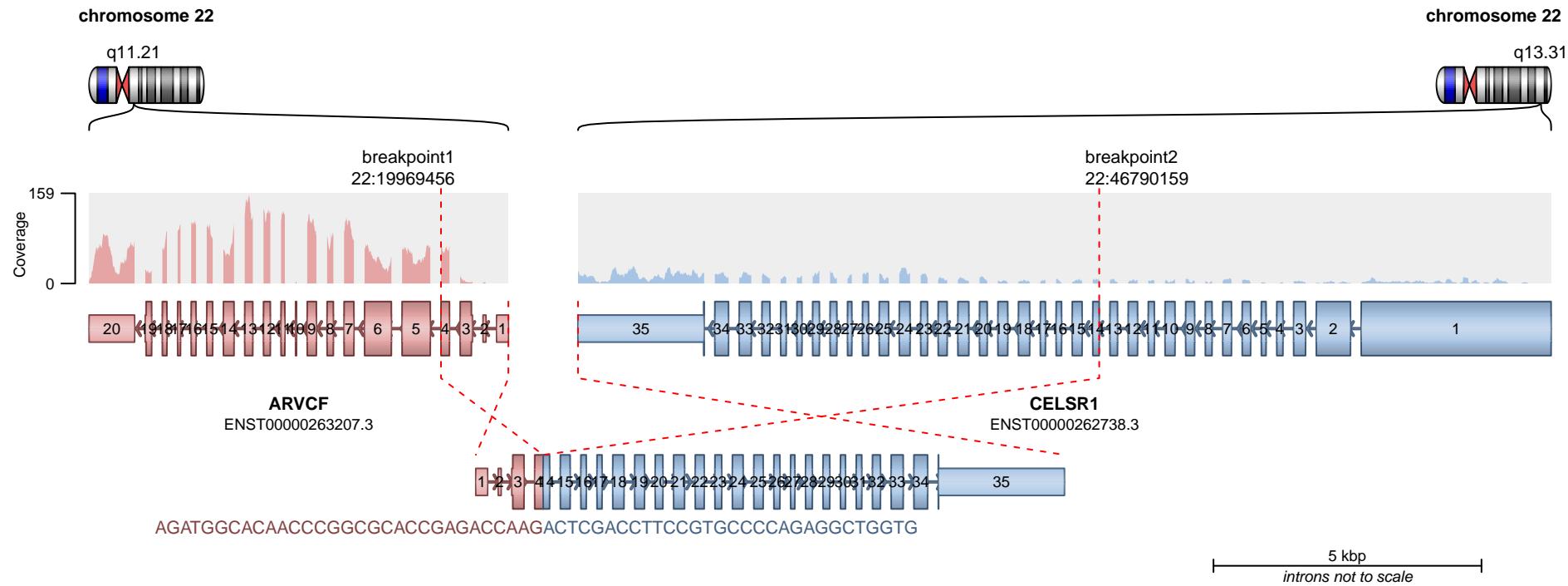
— translocation — deletion
— duplication — inversion



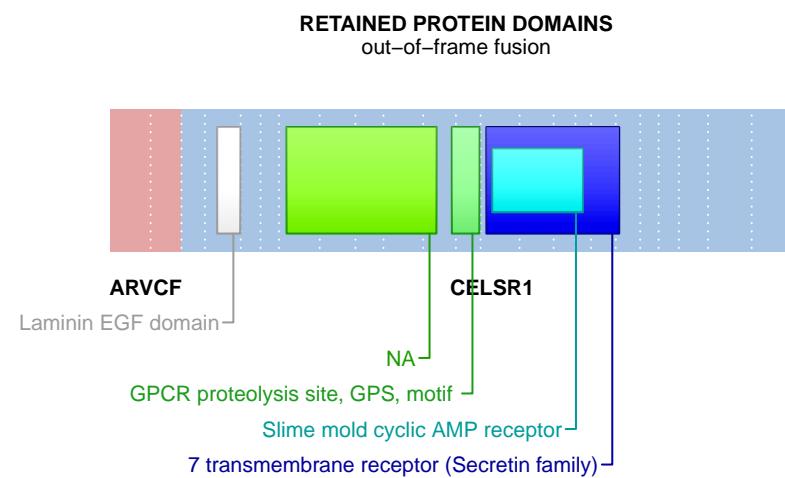
SUPPORTING READ COUNT

Split reads at breakpoint1 = 1
Split reads at breakpoint2 = 4
Discordant mates = 0

— translocation — deletion
— duplication — inversion

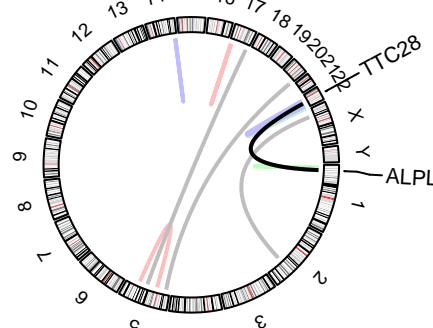
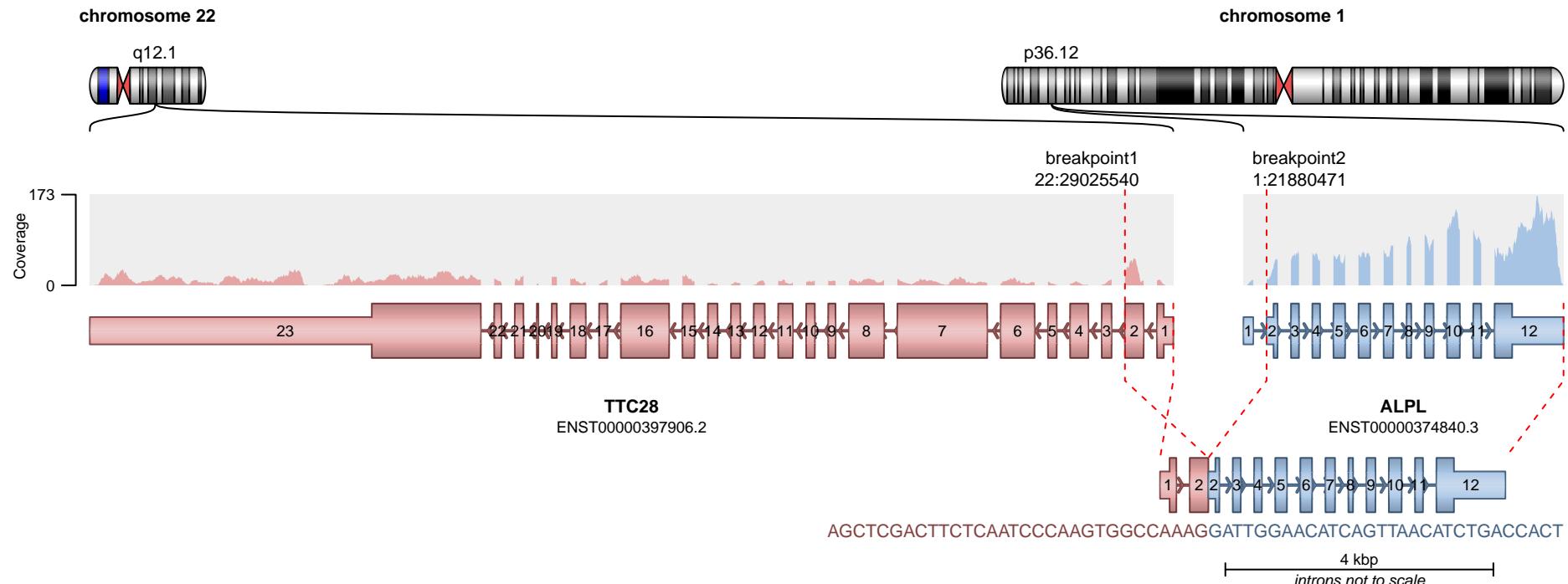


— translocation — deletion
— duplication — inversion

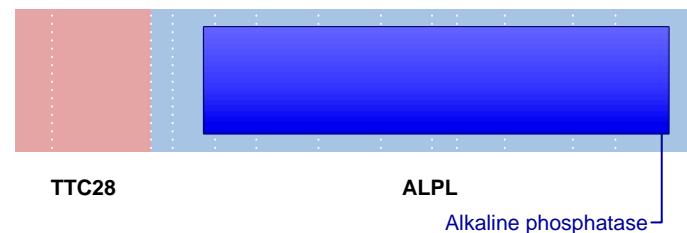


SUPPORTING READ COUNT

Split reads at breakpoint1 = 0
Split reads at breakpoint2 = 2
Discordant mates = 2



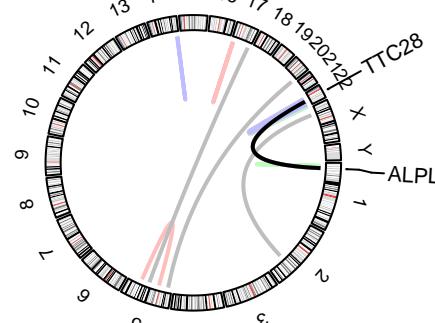
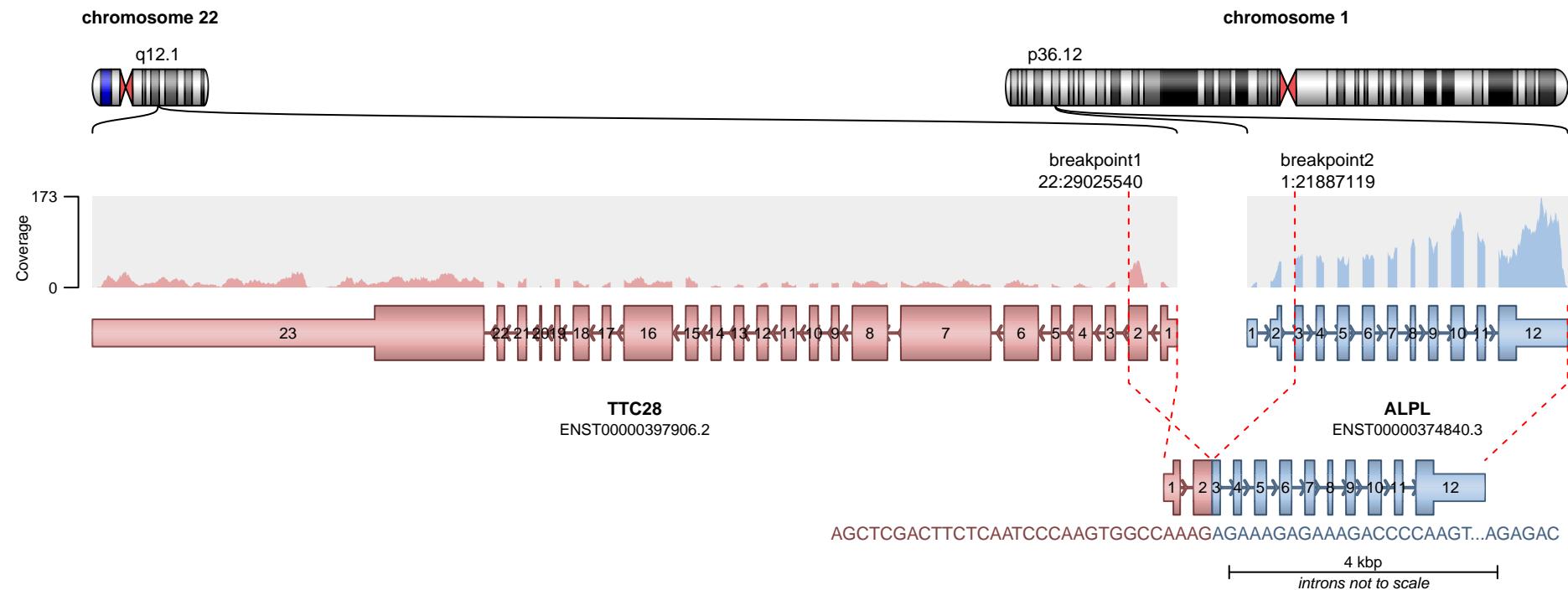
RETAINED PROTEIN DOMAINS out-of-frame fusion



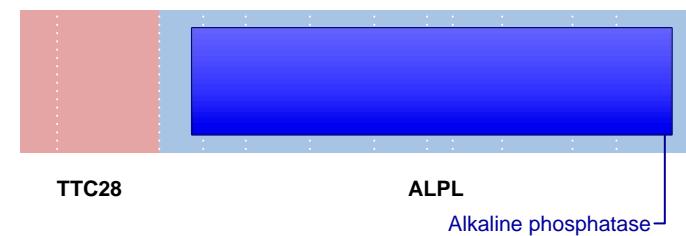
SUPPORTING READ COUNT

Split reads at breakpoint1 = 3
Split reads at breakpoint2 = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



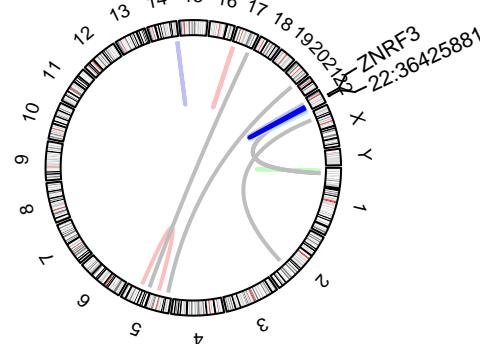
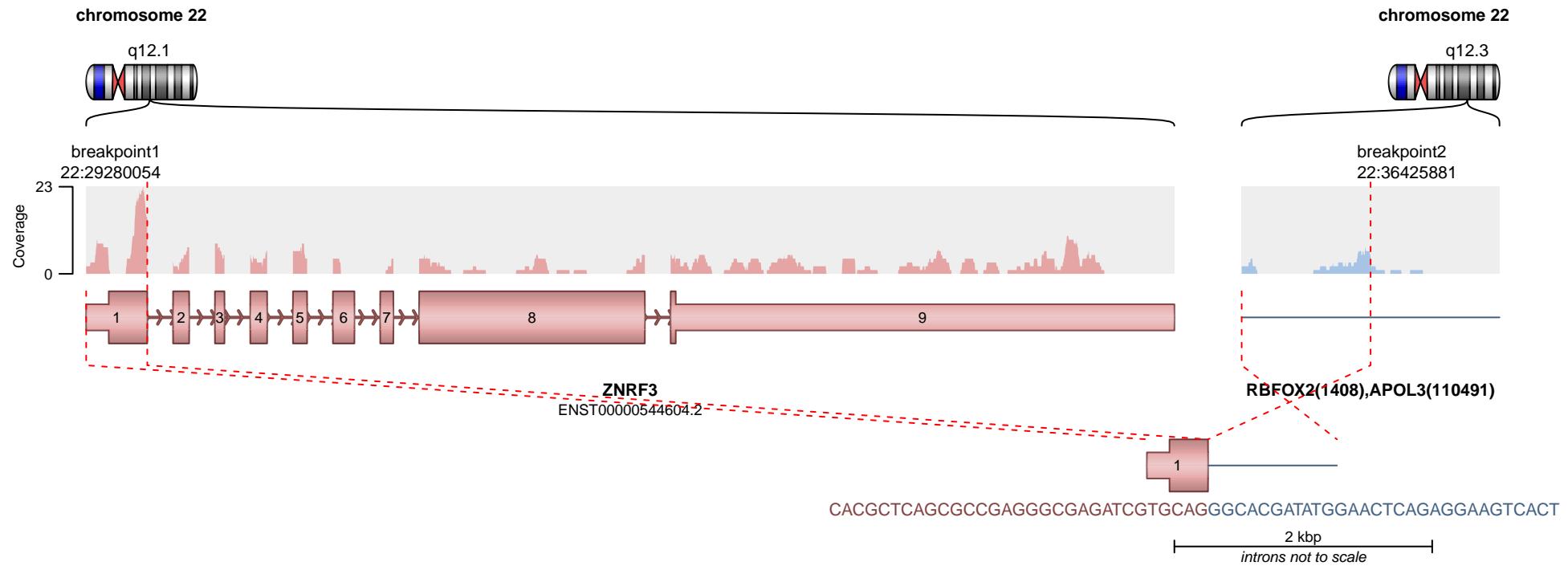
RETAINED PROTEIN DOMAINS out-of-frame fusion



SUPPORTING READ COUNT

Split reads at breakpoint1 = 0
Split reads at breakpoint2 = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion

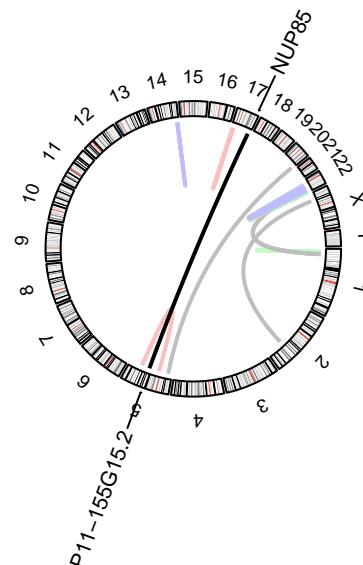
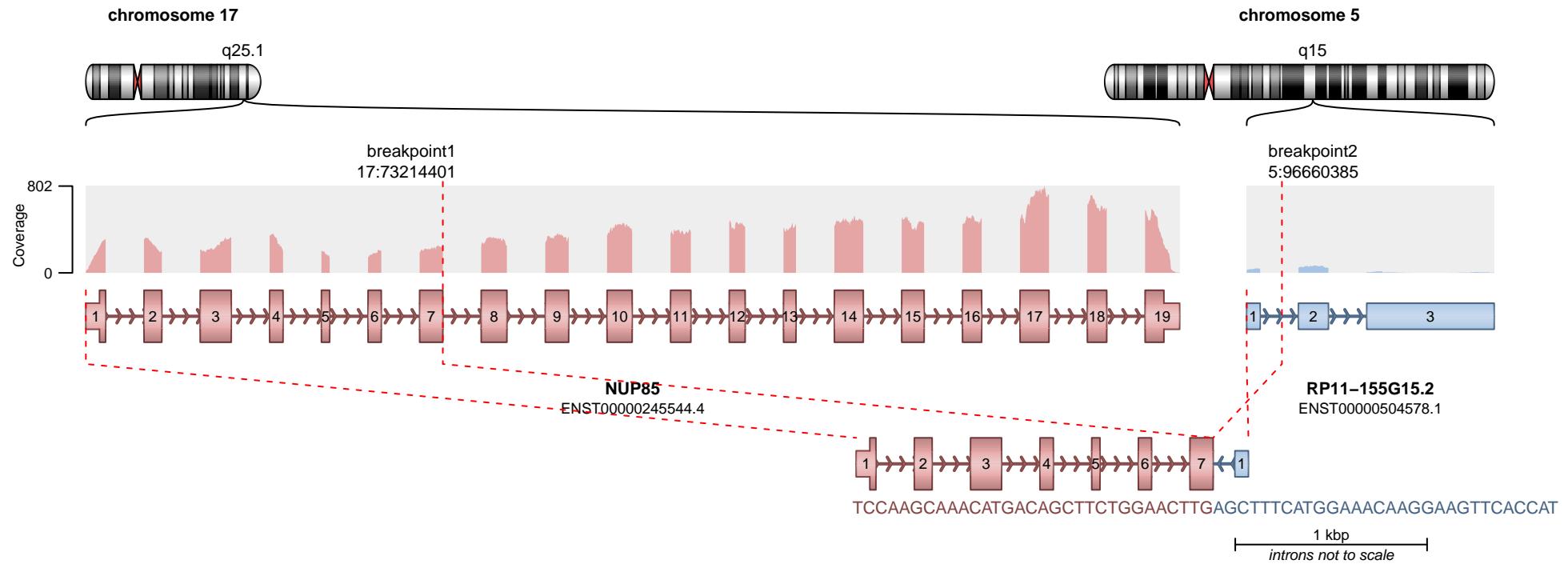


No protein domains retained in fusion.

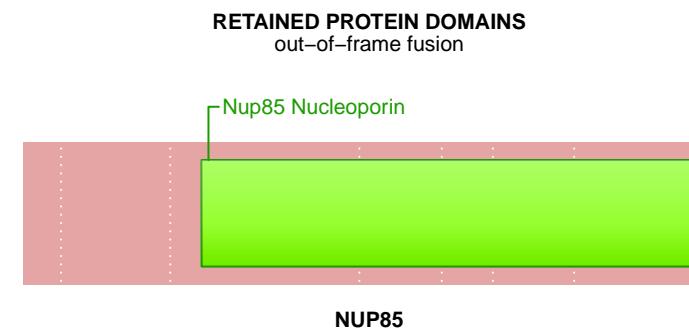
SUPPORTING READ COUNT

Split reads at breakpoint1 = 1
Split reads at breakpoint2 = 2
Discordant mates = 0

— translocation — deletion
— duplication — inversion

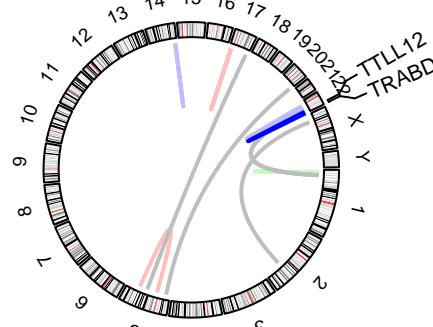
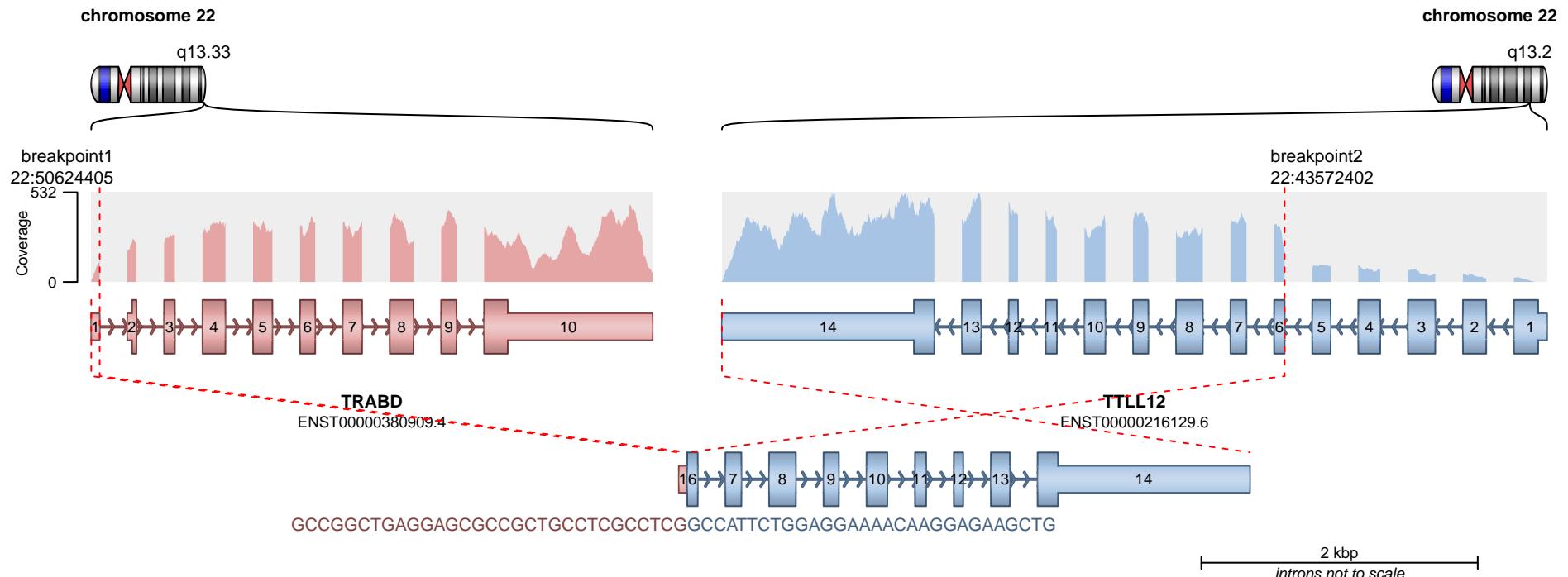


— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads at breakpoint1 = 2
Split reads at breakpoint2 = 1
Discordant mates = 0



RETAINED PROTEIN DOMAINS

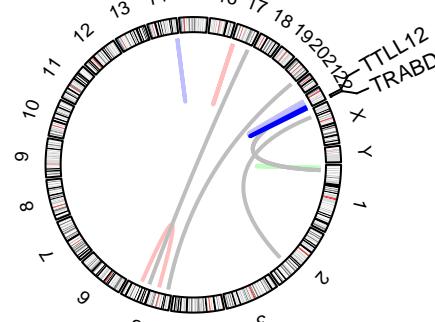
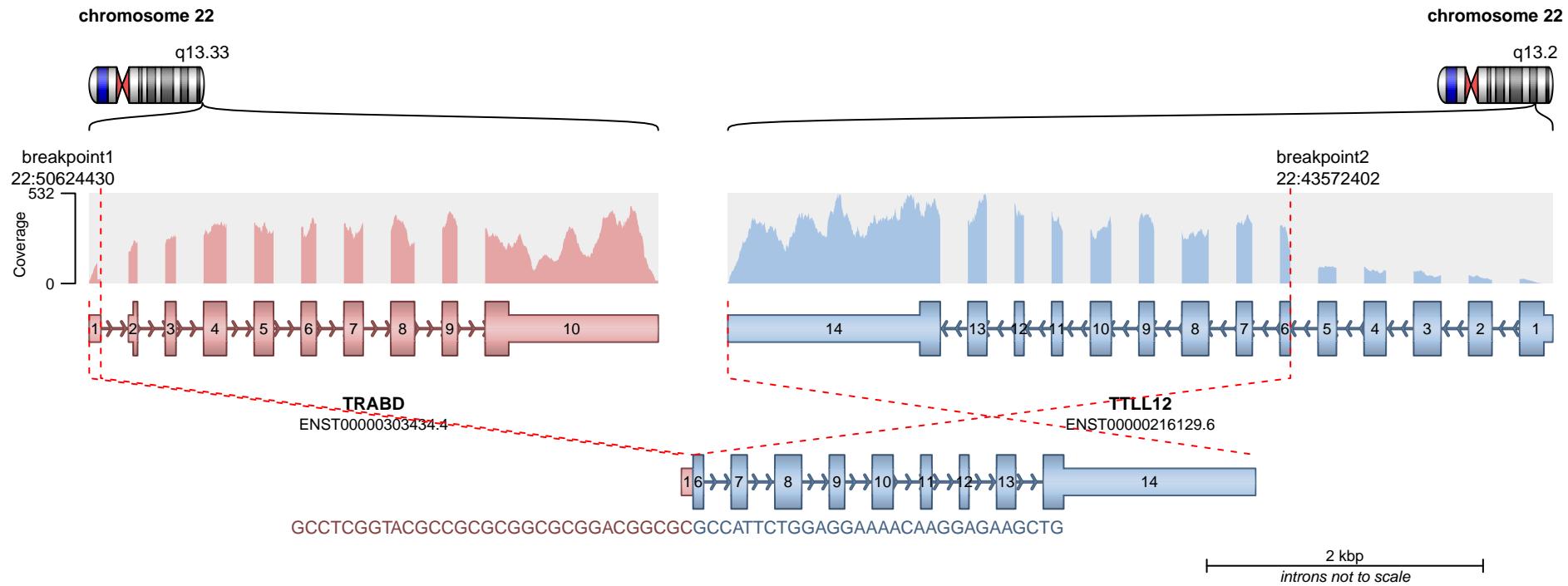
reading frame unclear



SUPPORTING READ COUNT

Split reads at breakpoint1 = 0
Split reads at breakpoint2 = 47
Discordant mates = 0

— translocation — deletion
— duplication — inversion



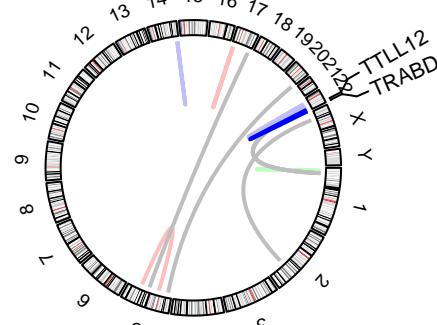
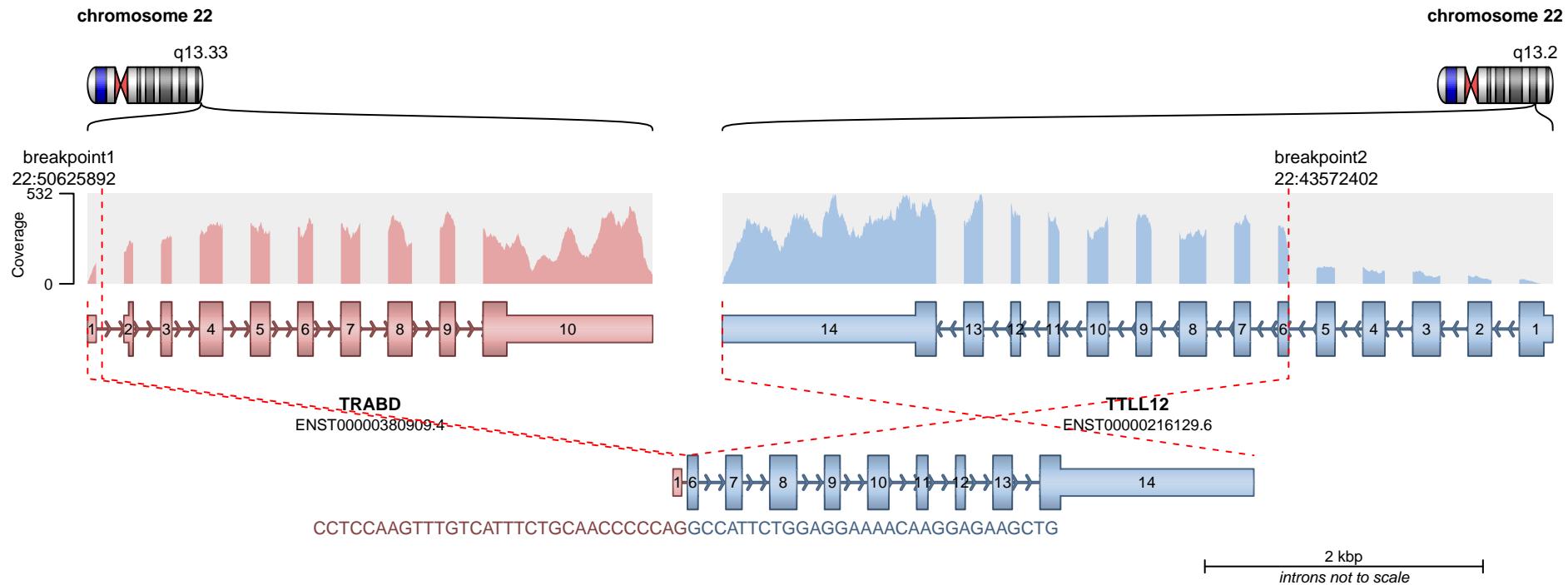
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads at breakpoint1 = 0
Split reads at breakpoint2 = 3
Discordant mates = 0

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS

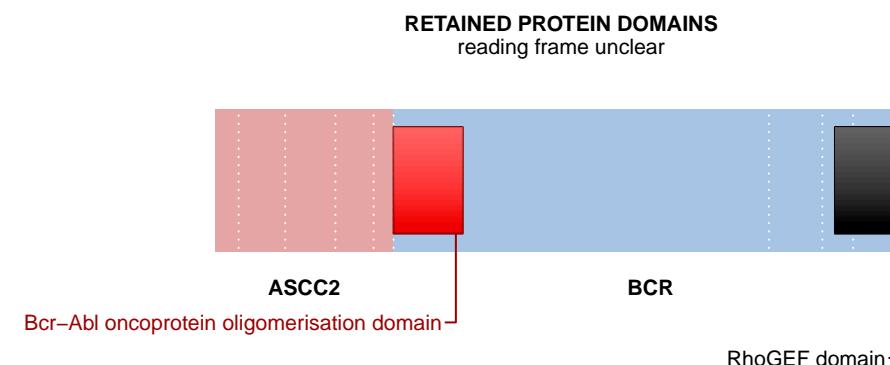
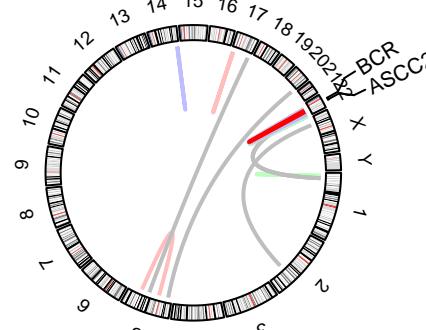
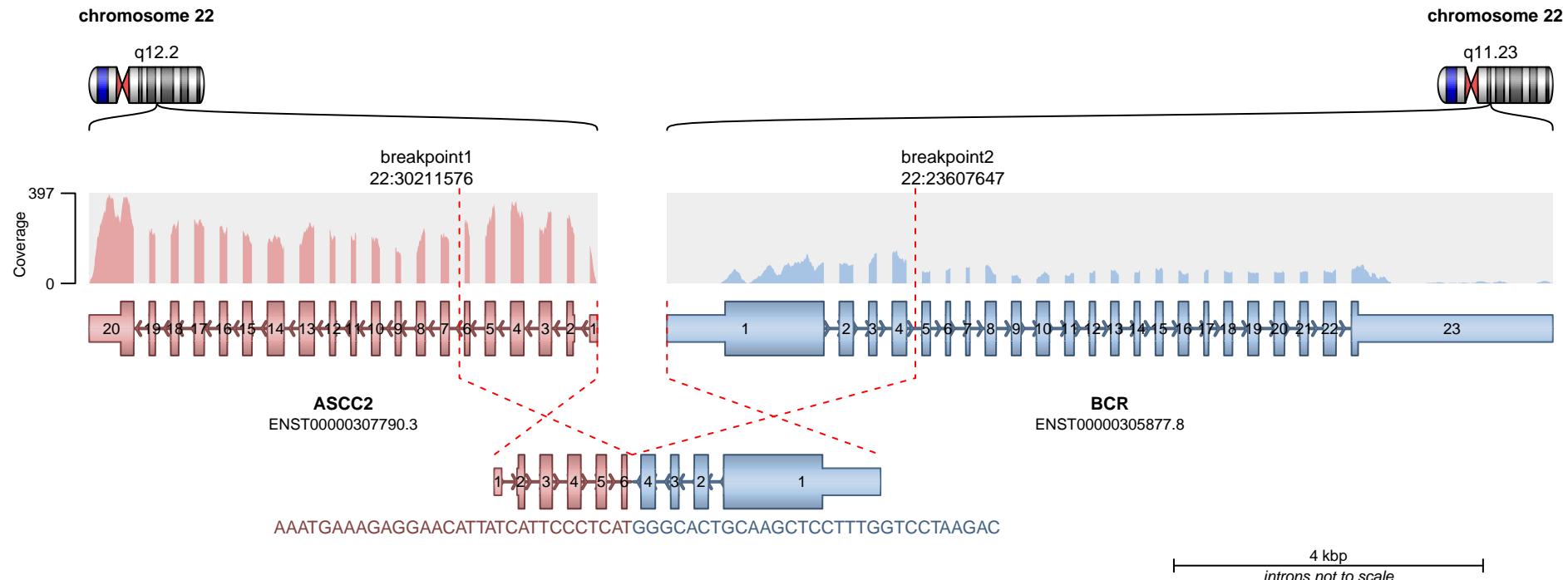
reading frame unclear



SUPPORTING READ COUNT

Split reads at breakpoint1 = 1
Split reads at breakpoint2 = 0
Discordant mates = 1

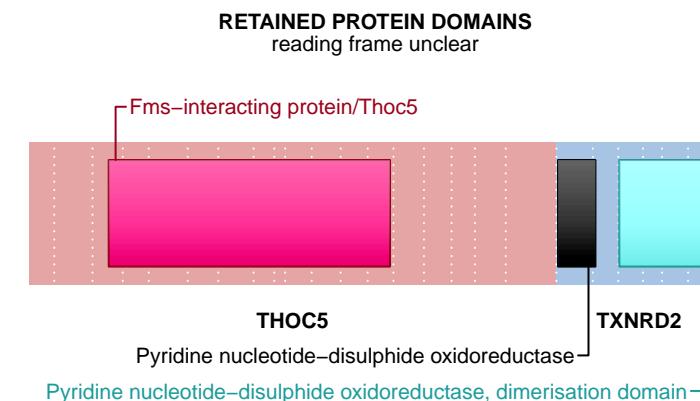
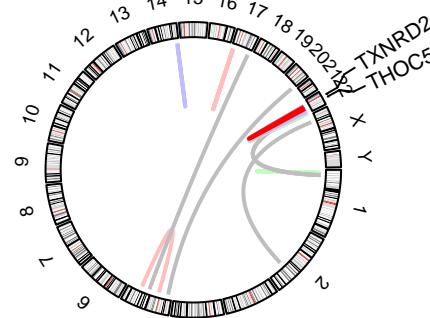
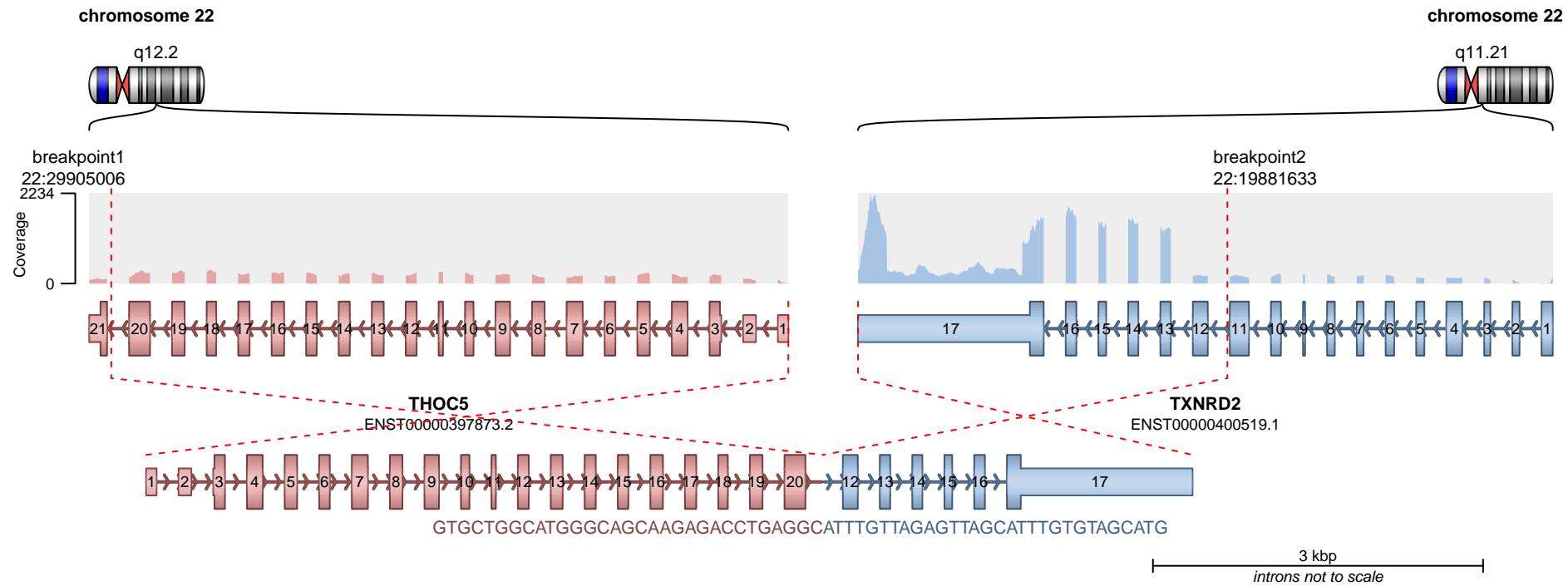
— translocation — deletion
— duplication — inversion



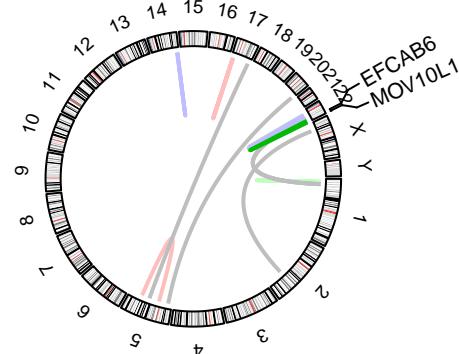
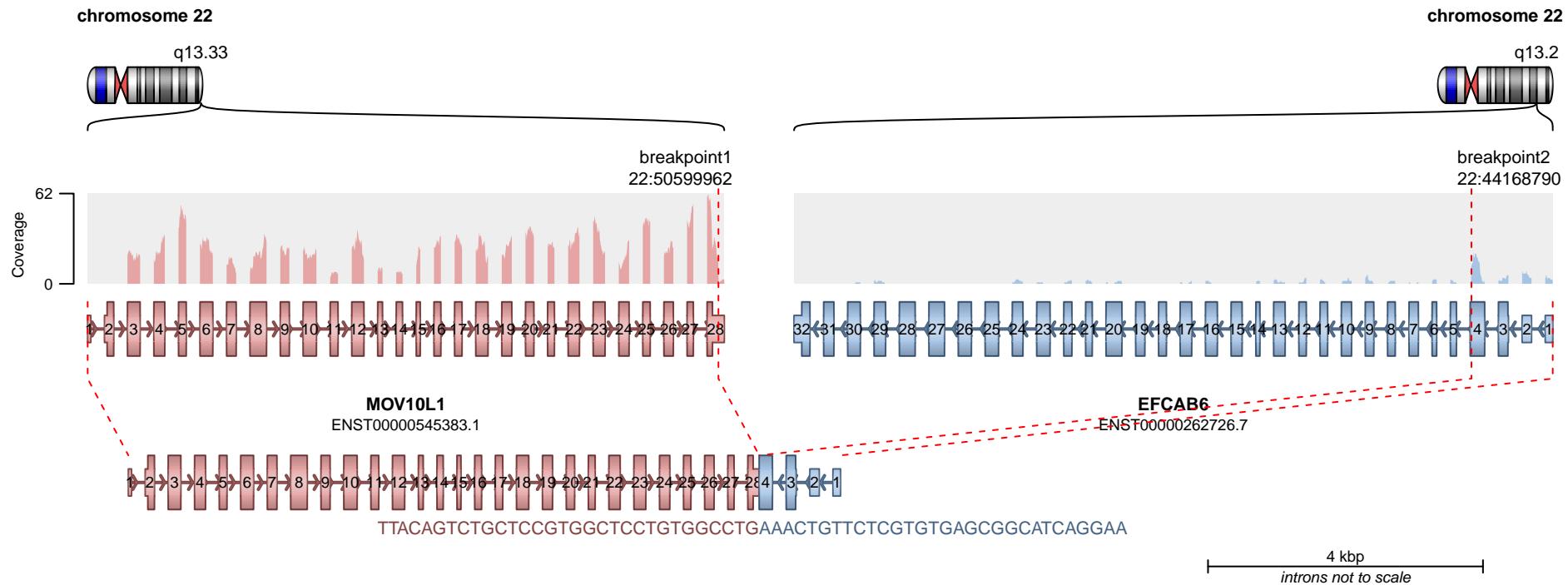
SUPPORTING READ COUNT

Split reads at breakpoint1 = 12
Split reads at breakpoint2 = 22
Discordant mates = 4

— translocation — deletion
— duplication — inversion



— translocation — deletion
— duplication — inversion

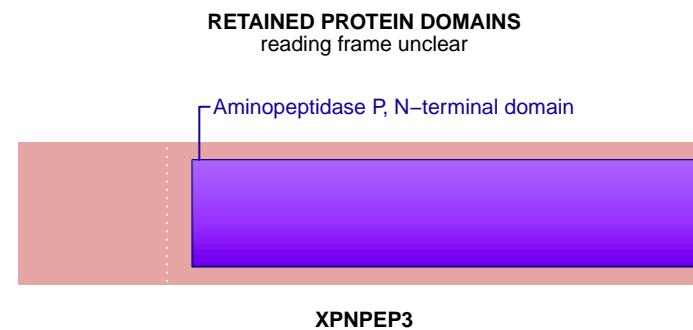
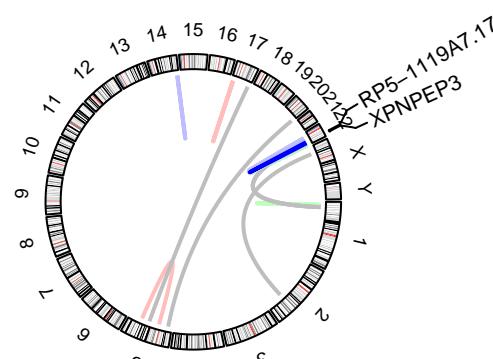
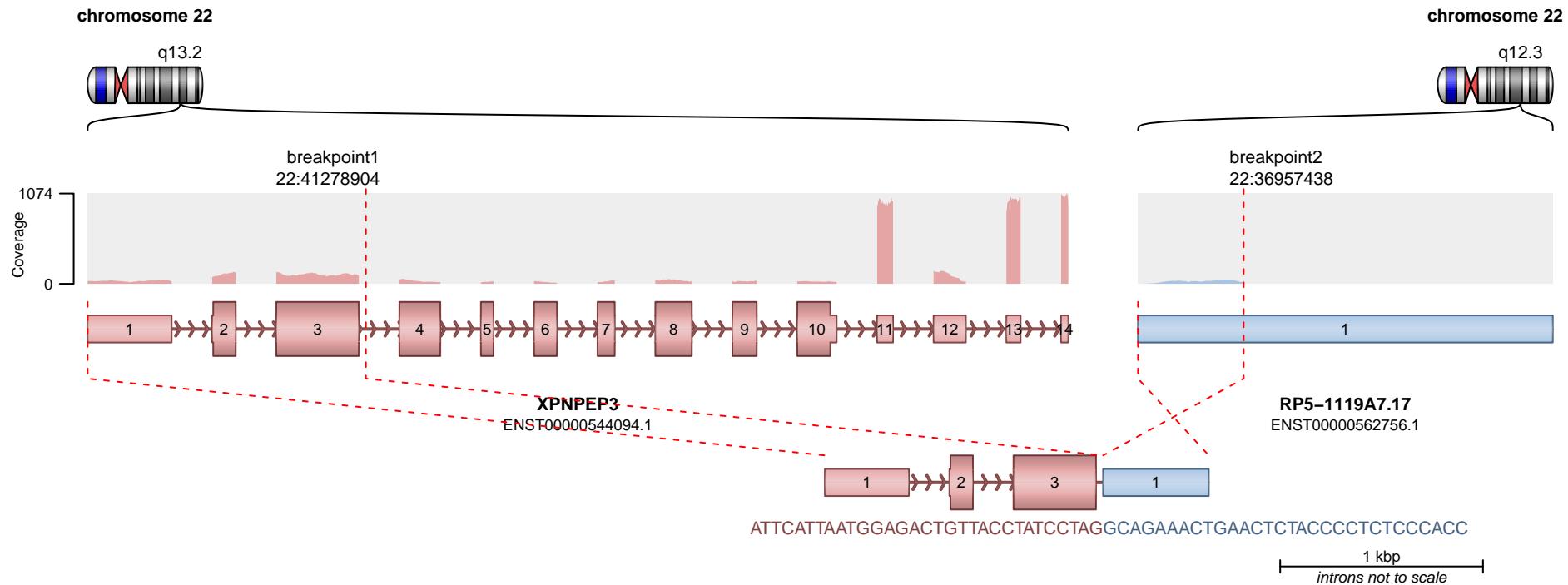


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 7
Split reads at breakpoint2 = 8
Discordant mates = 2

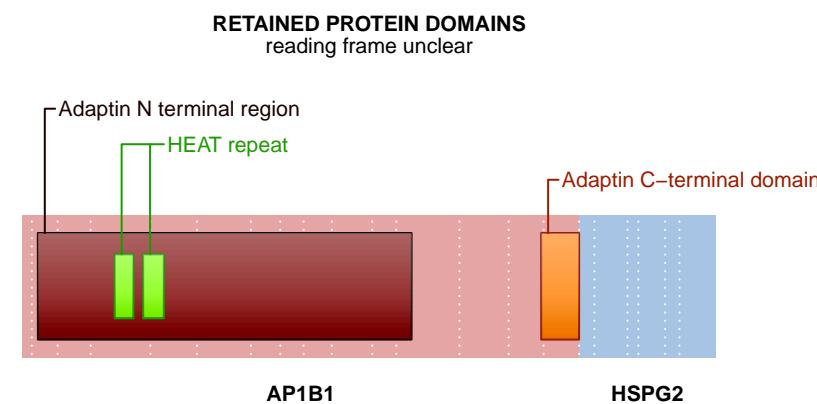
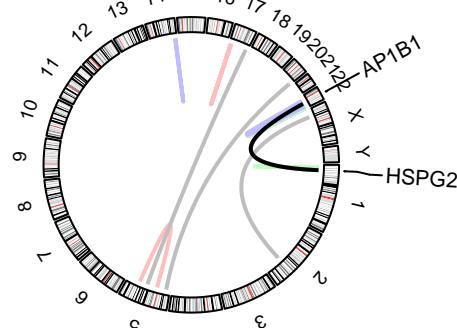
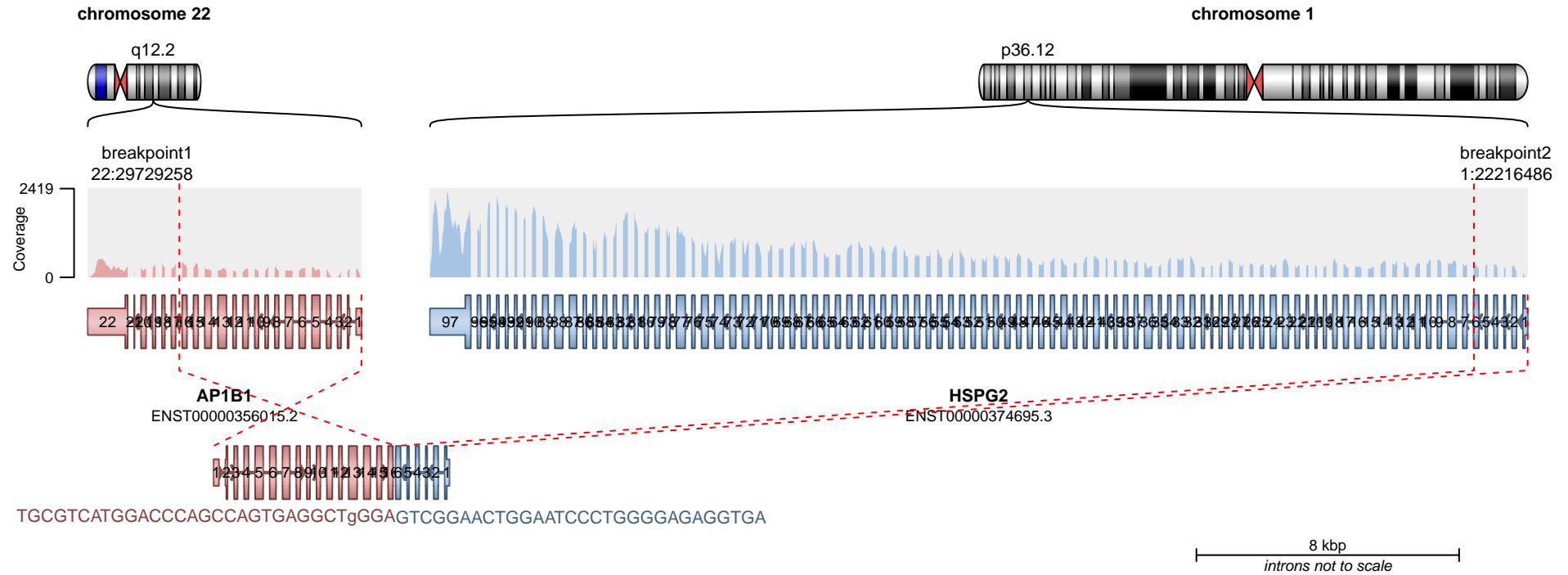
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads at breakpoint1 = 5
Split reads at breakpoint2 = 7
Discordant mates = 0

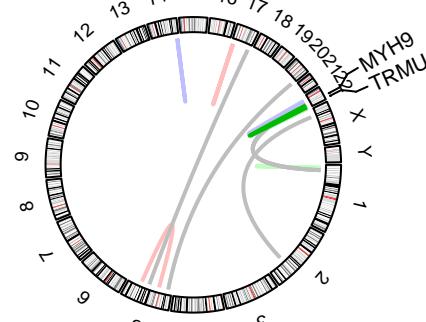
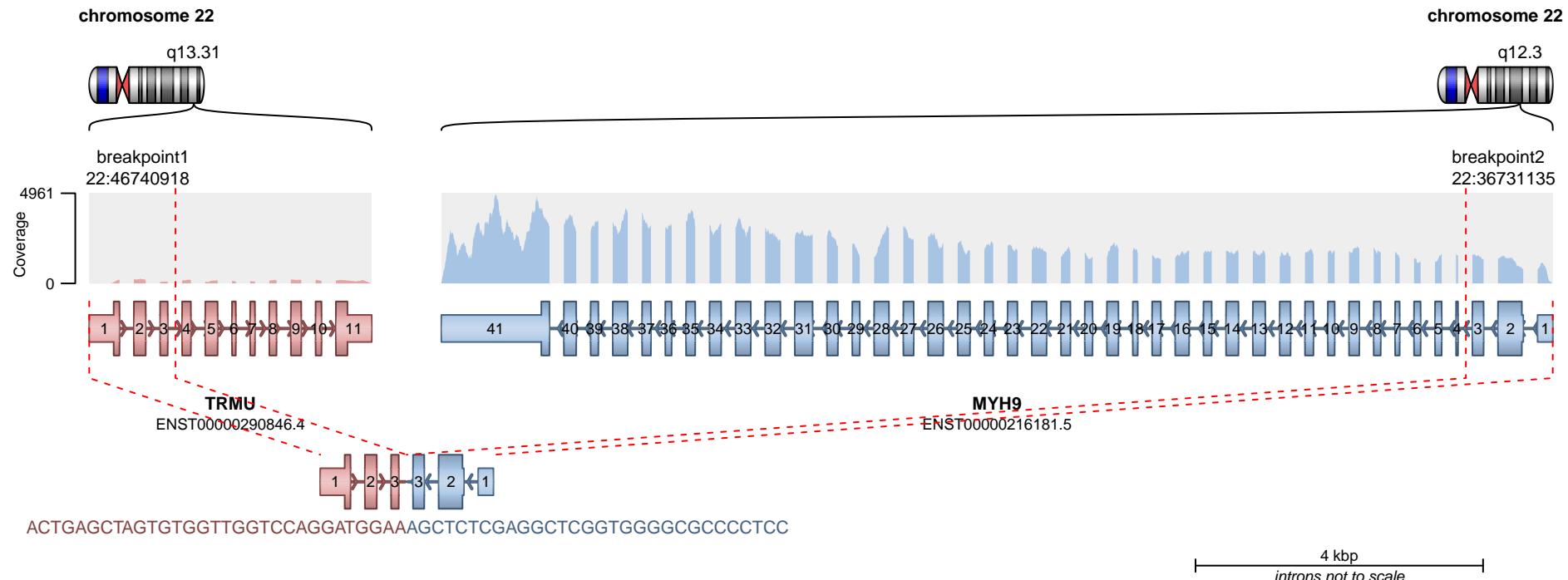
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

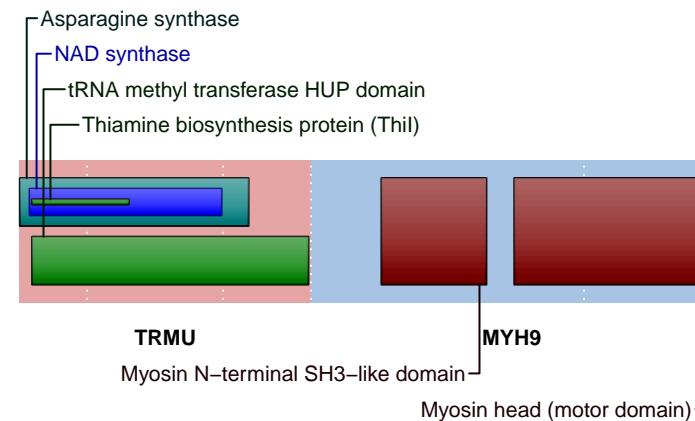
Split reads at breakpoint1 = 7
Split reads at breakpoint2 = 4
Discordant mates = 0

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS

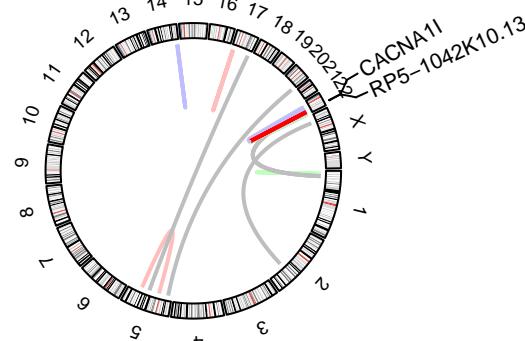
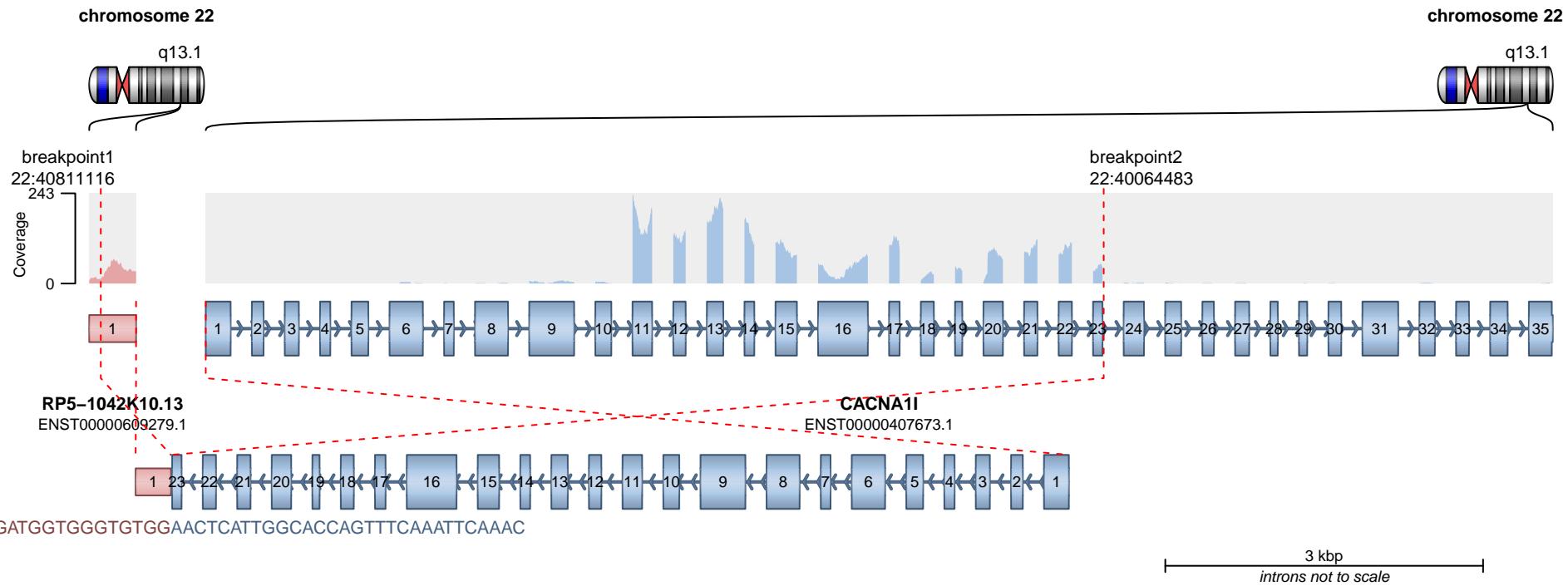
reading frame unclear



SUPPORTING READ COUNT

Split reads at breakpoint1 = 2
Split reads at breakpoint2 = 5
Discordant mates = 4

— translocation — deletion
— duplication — inversion

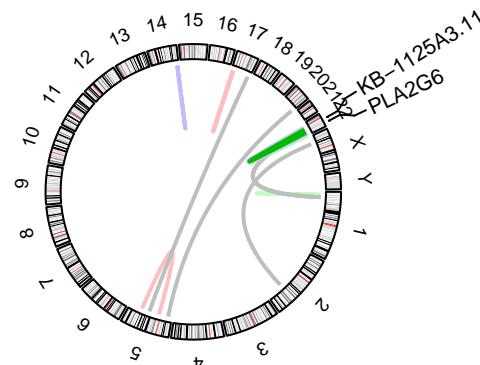
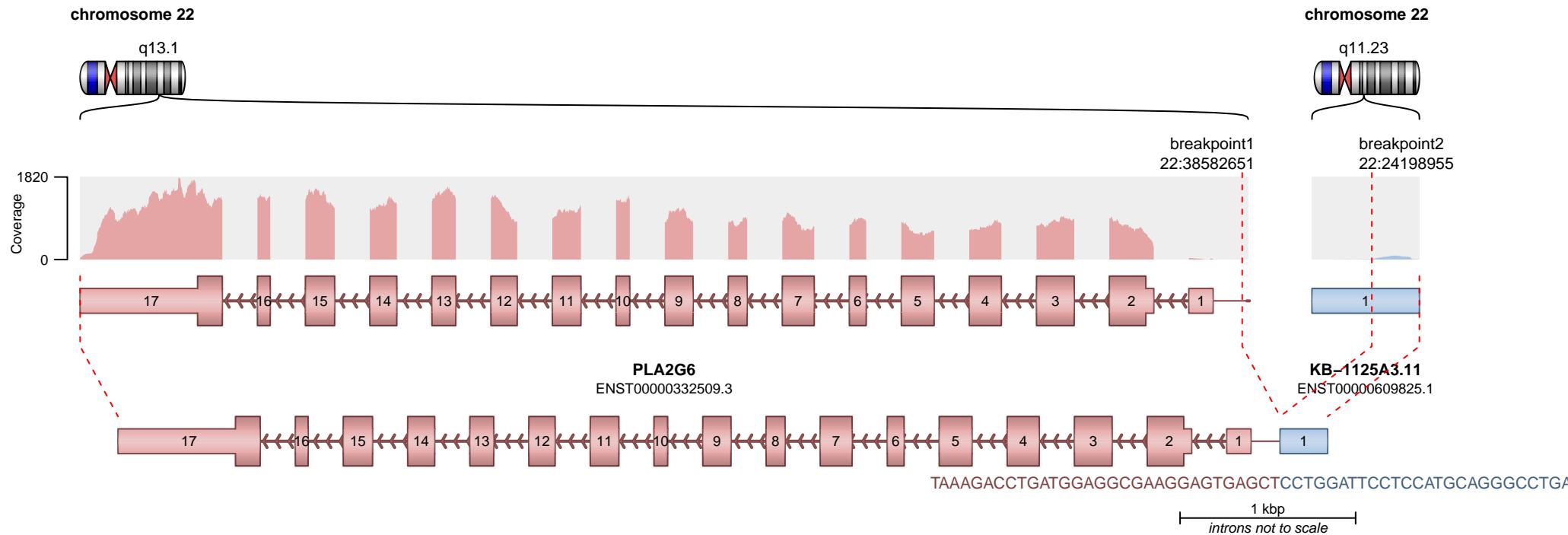


No coding regions due to antisense transcription.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 3
Split reads at breakpoint2 = 4
Discordant mates = 1

— translocation — deletion
— duplication — inversion

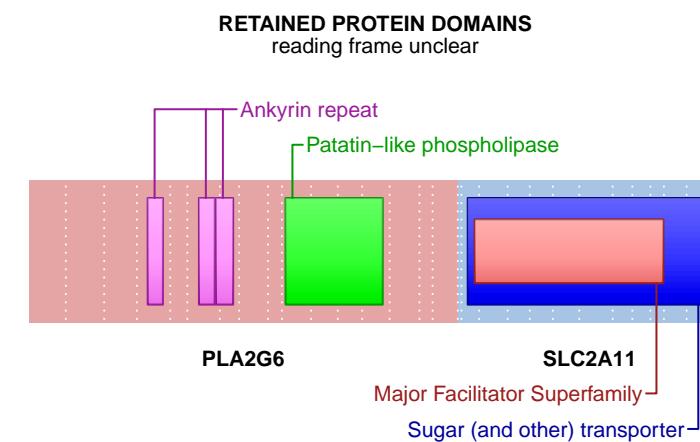
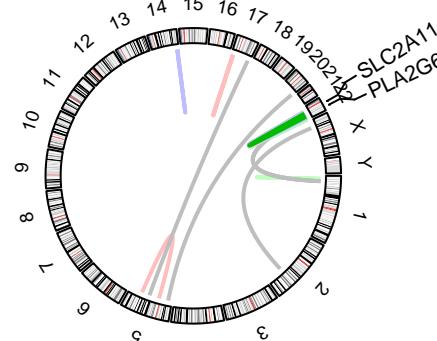
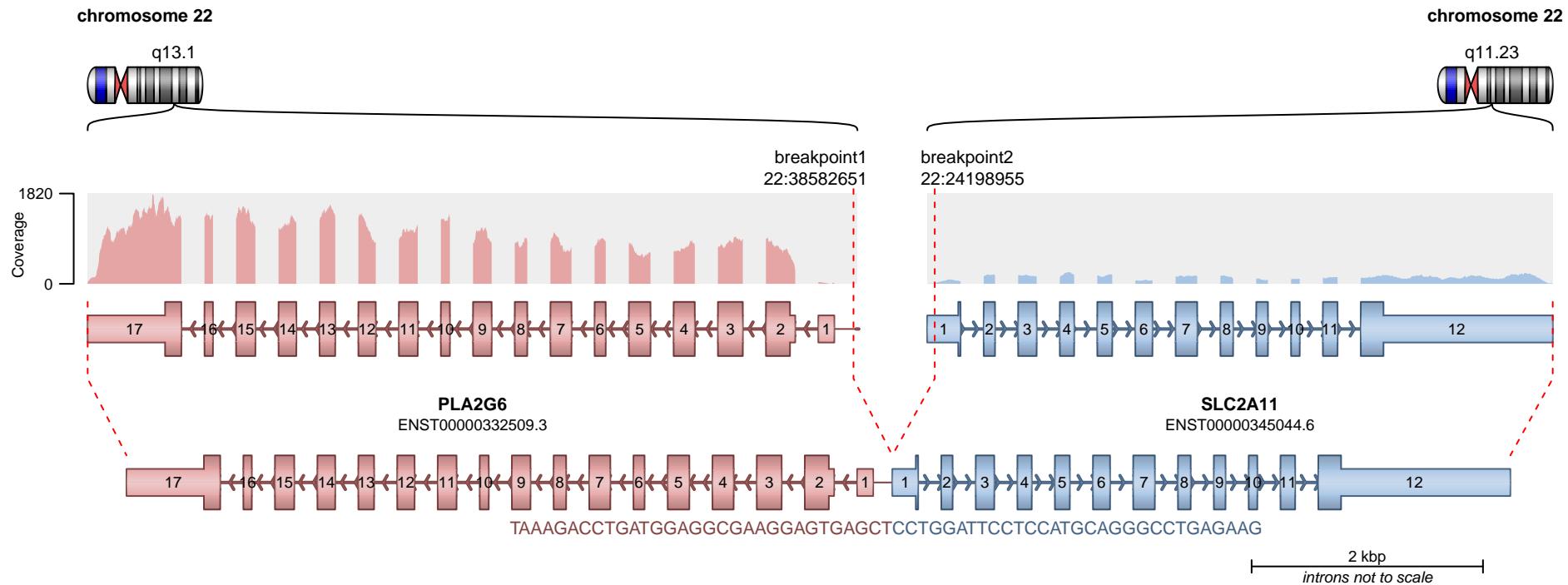


No coding regions due to antisense transcription.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 1
Split reads at breakpoint2 = 2
Discordant mates = 3

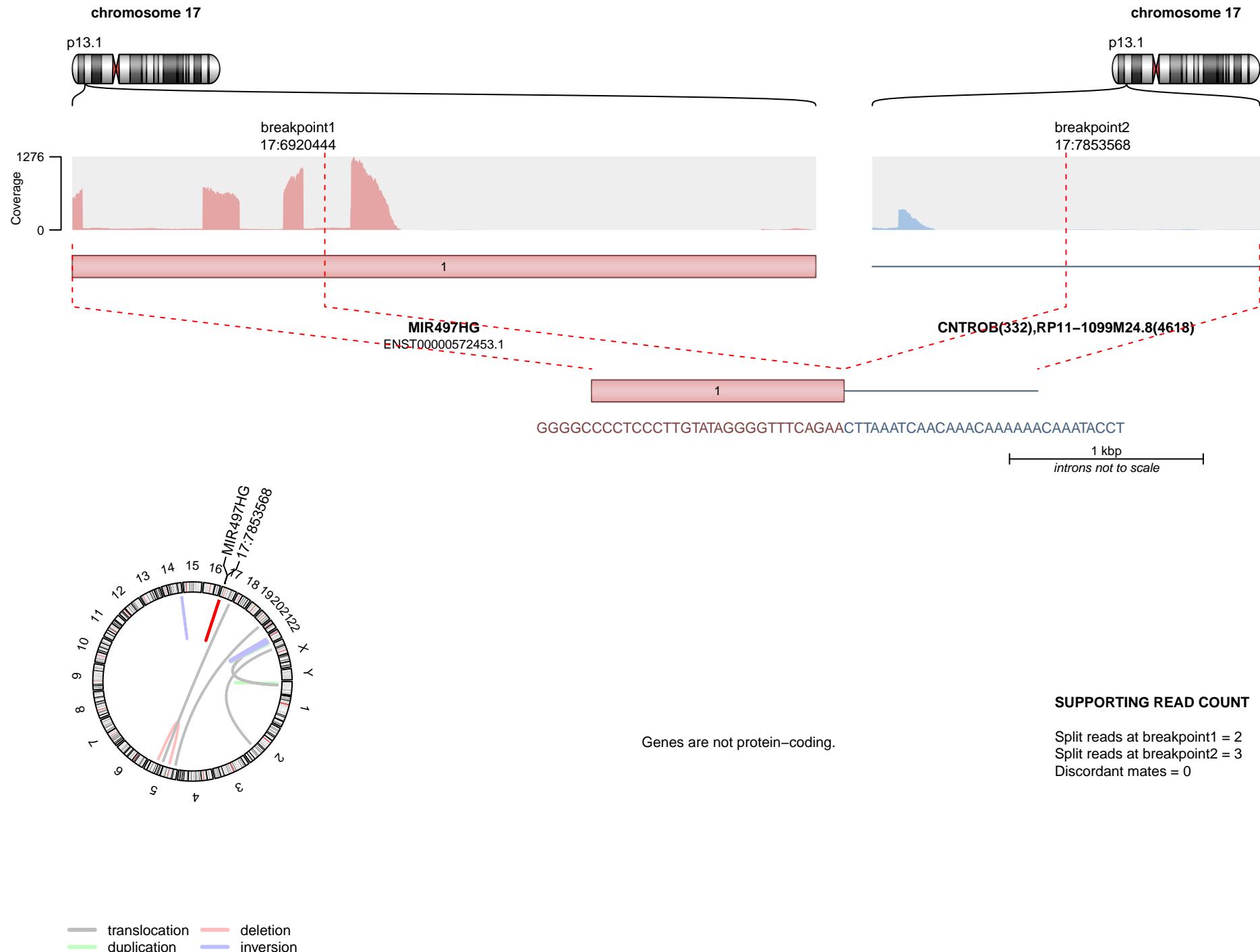
— translocation — deletion
— duplication — inversion

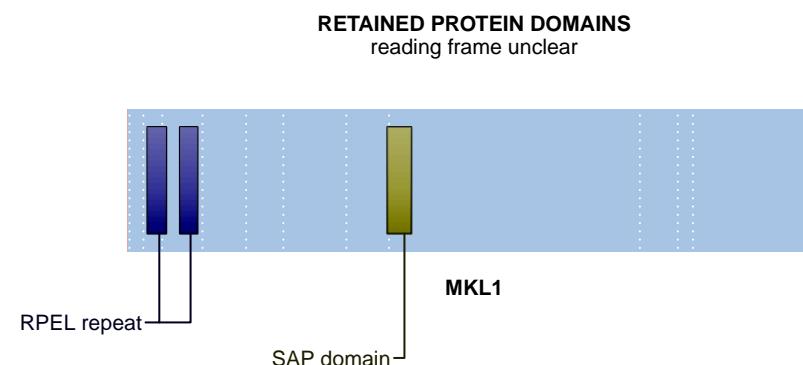
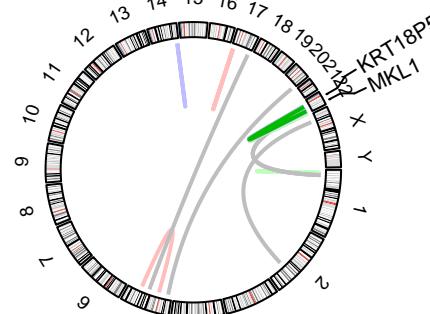
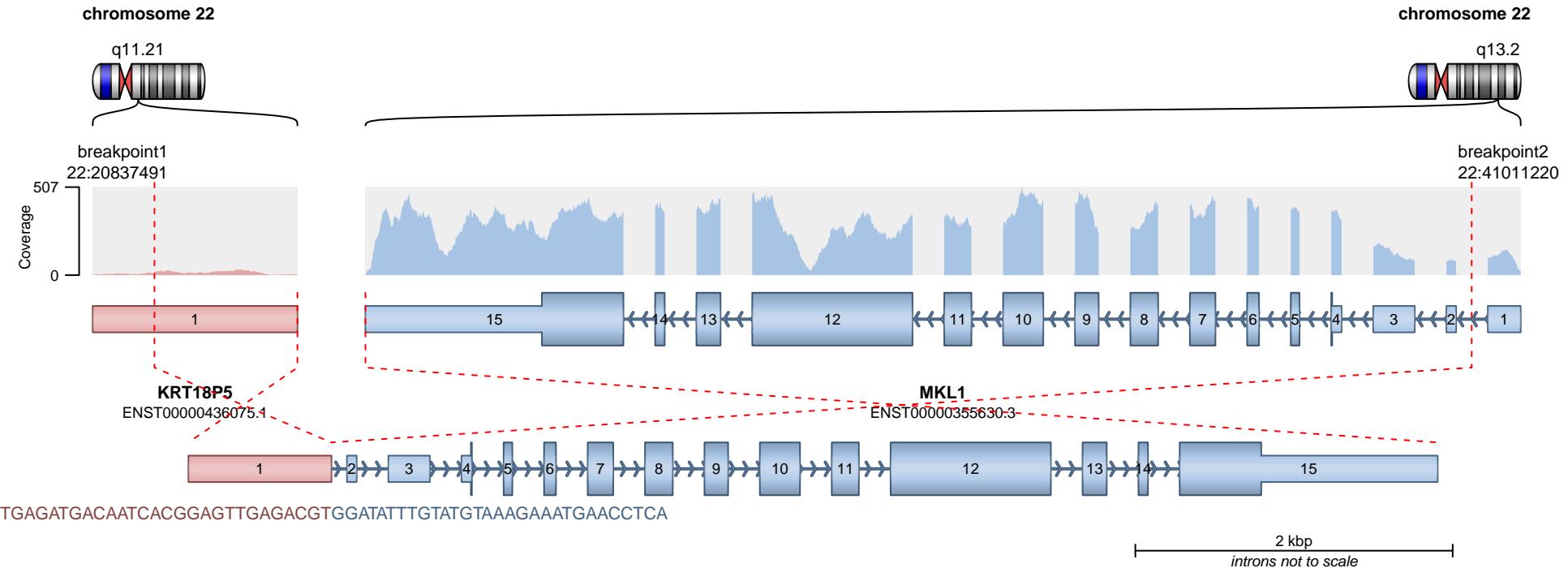


SUPPORTING READ COUNT

Split reads at breakpoint1 = 1
Split reads at breakpoint2 = 2
Discordant mates = 3

— translocation — deletion
— duplication — inversion

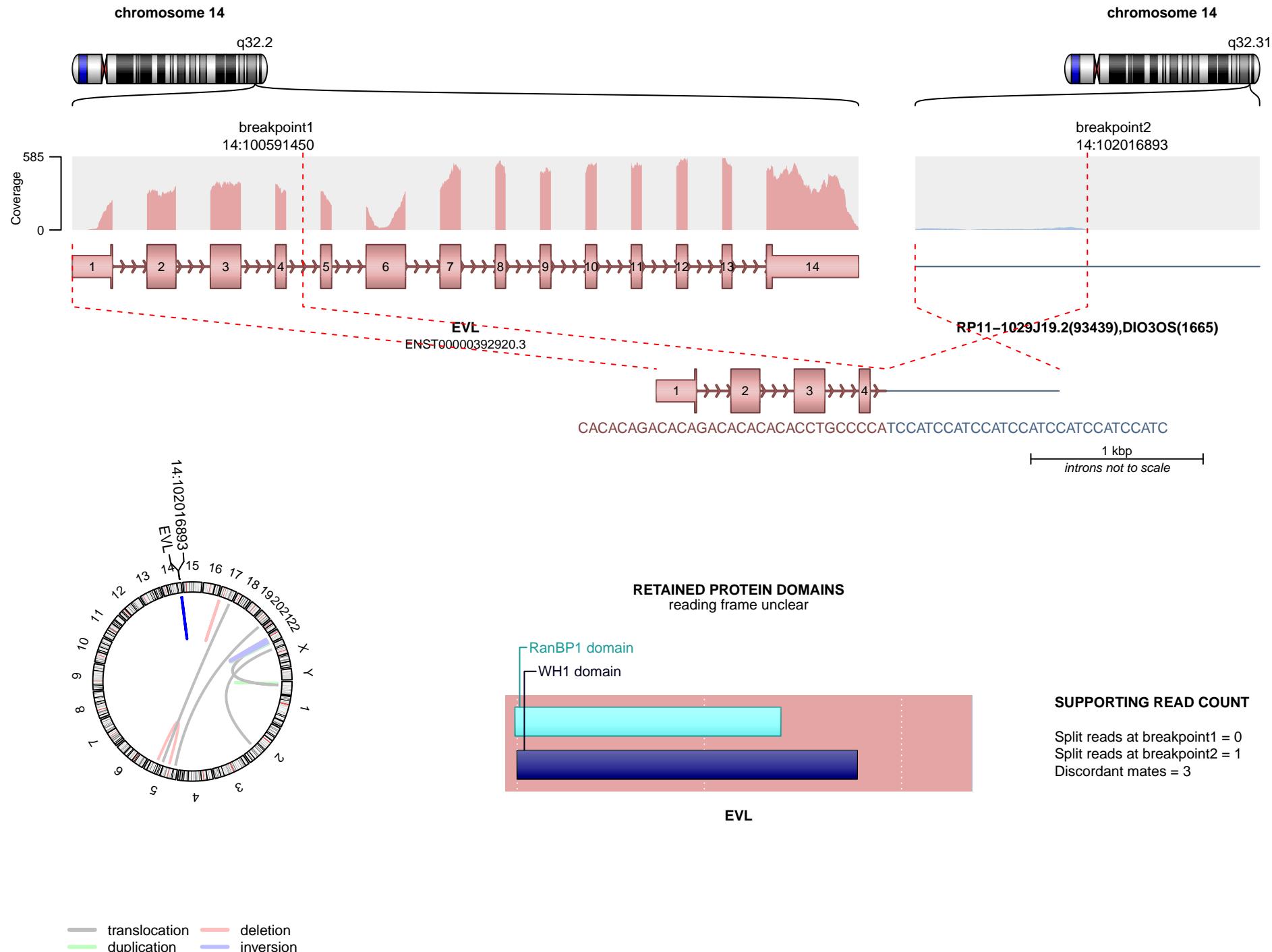


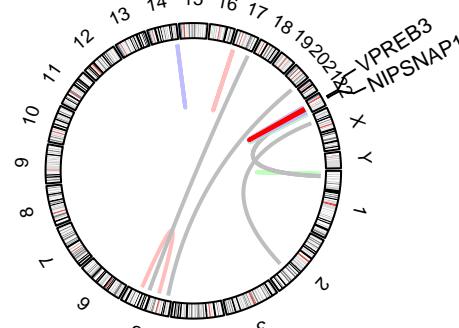
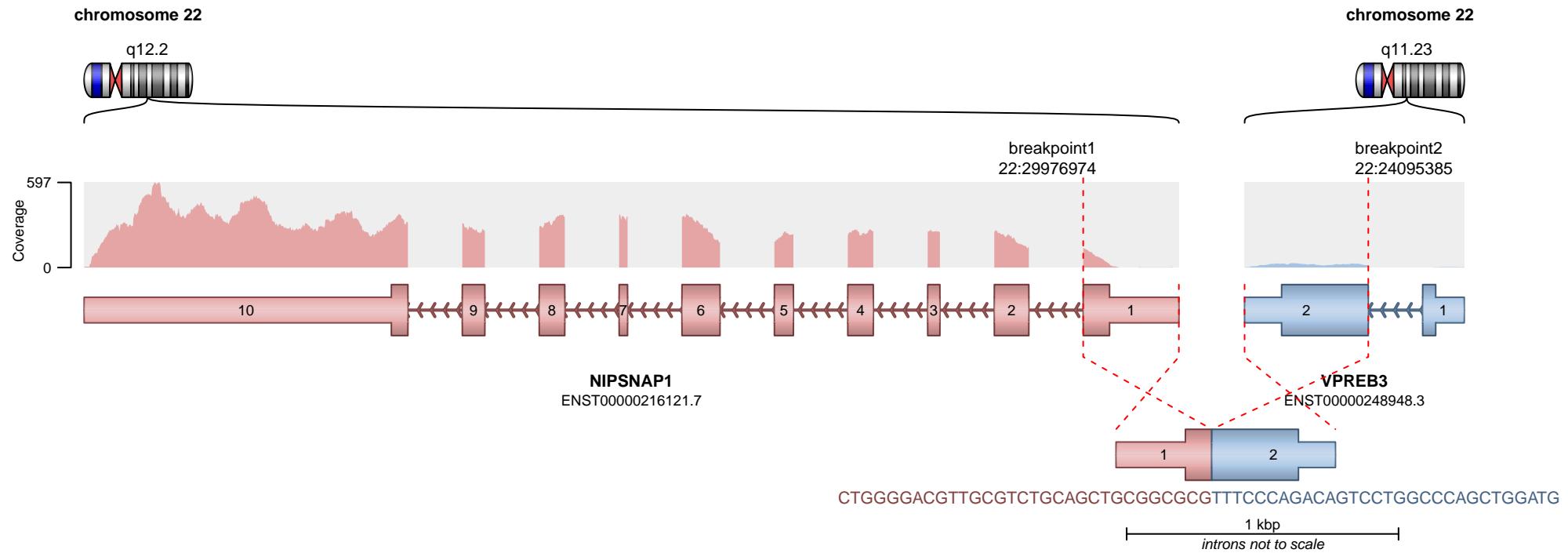


SUPPORTING READ COUNT

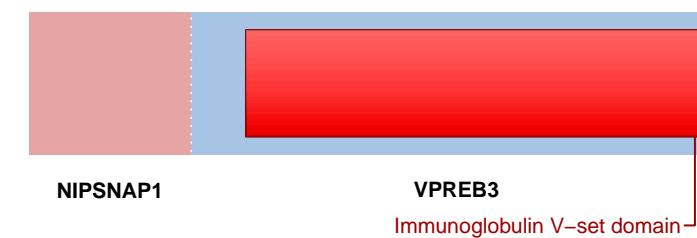
Split reads at breakpoint1 = 2
Split reads at breakpoint2 = 3
Discordant mates = 0

— translocation — deletion
— duplication — inversion





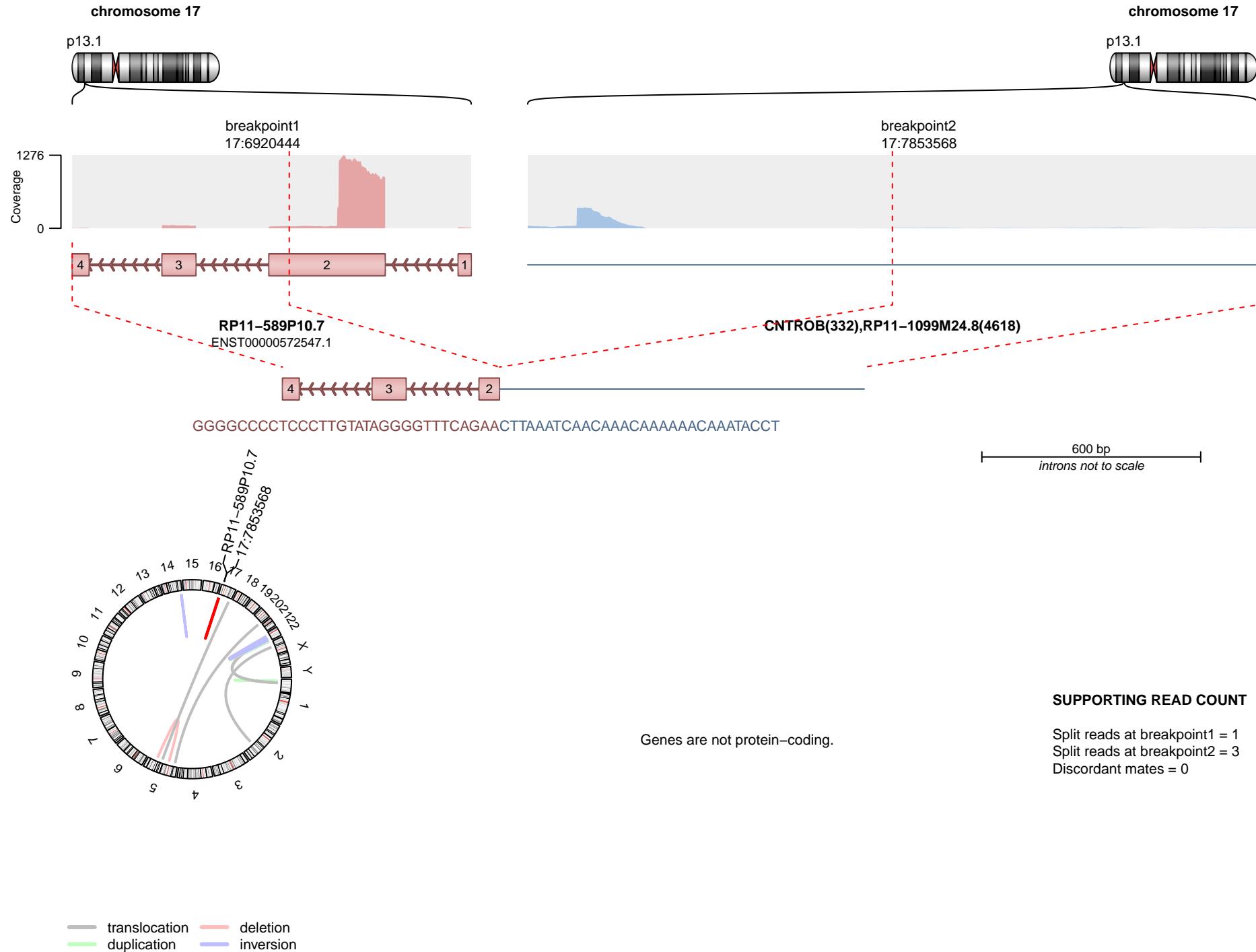
RETAINED PROTEIN DOMAINS out-of-frame fusion

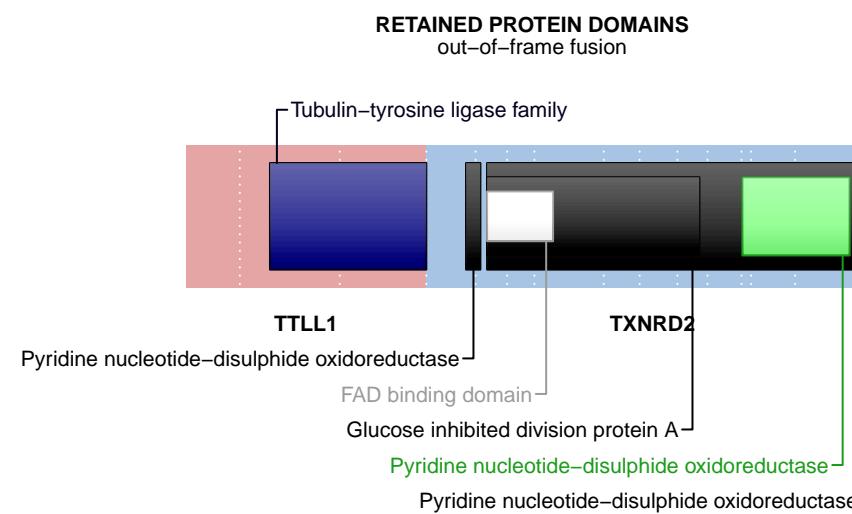
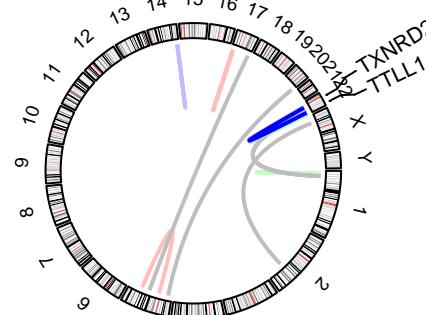
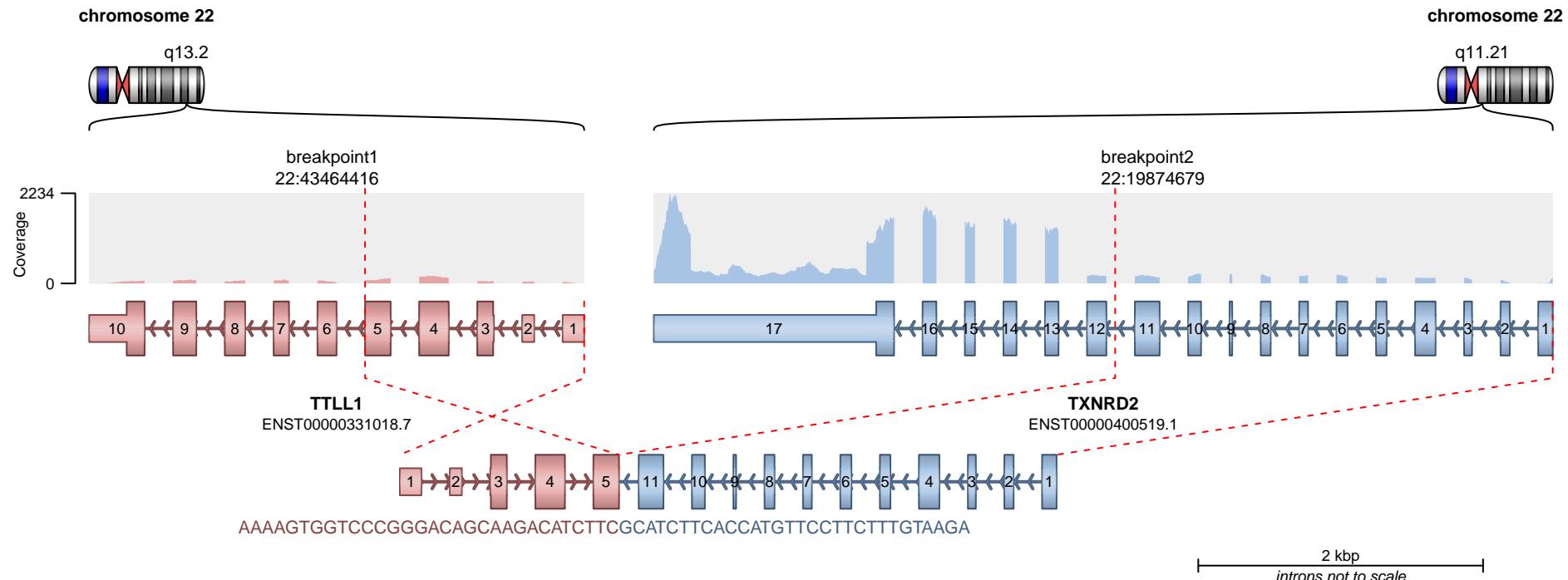


SUPPORTING READ COUNT

Split reads at breakpoint1 = 0
Split reads at breakpoint2 = 4
Discordant mates = 0

— translocation — deletion
— duplication — inversion

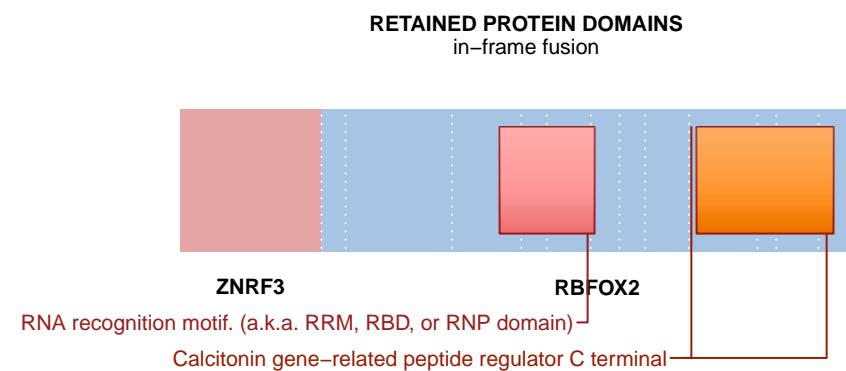
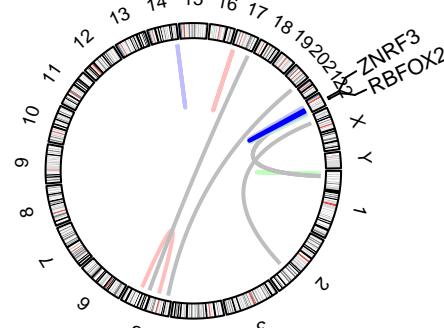
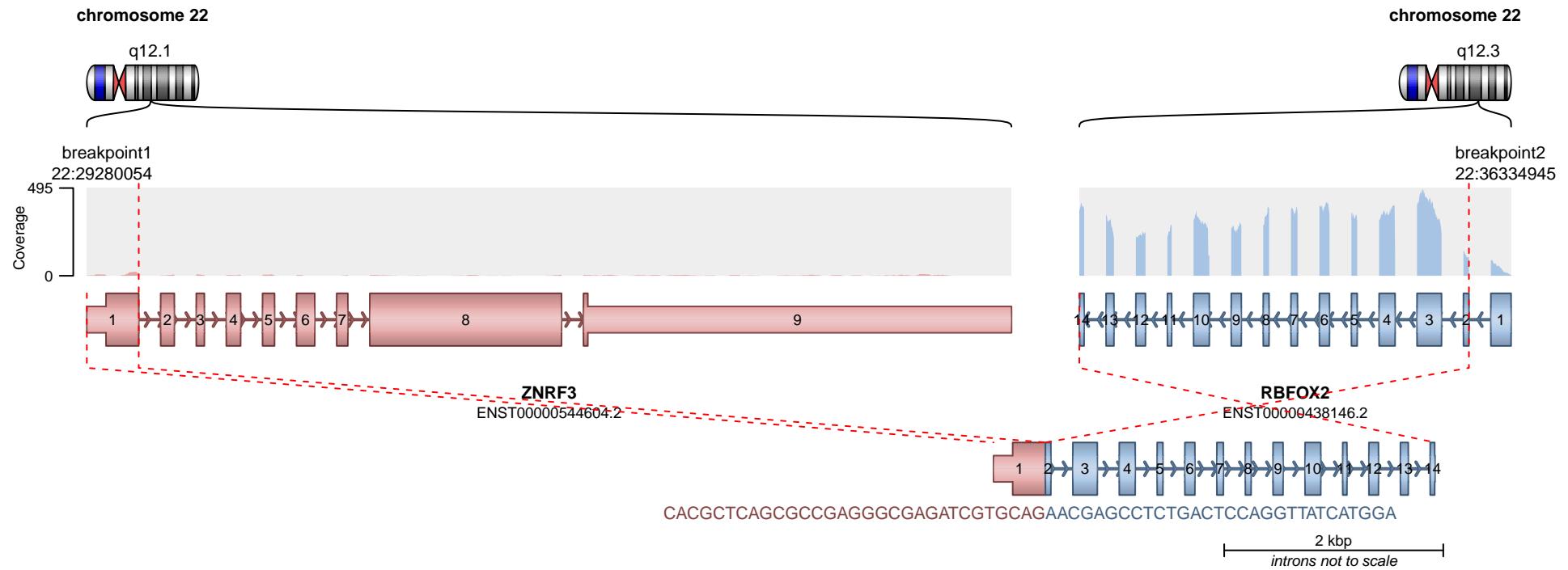




SUPPORTING READ COUNT

Split reads at breakpoint1 = 4
Split reads at breakpoint2 = 0
Discordant mates = 0

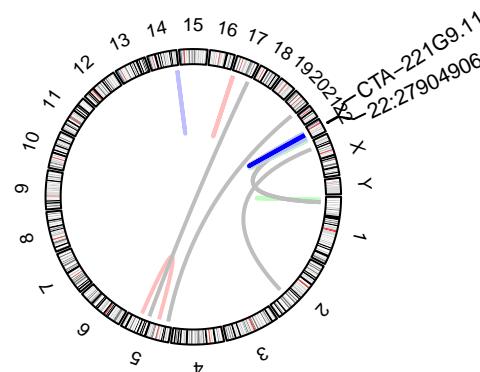
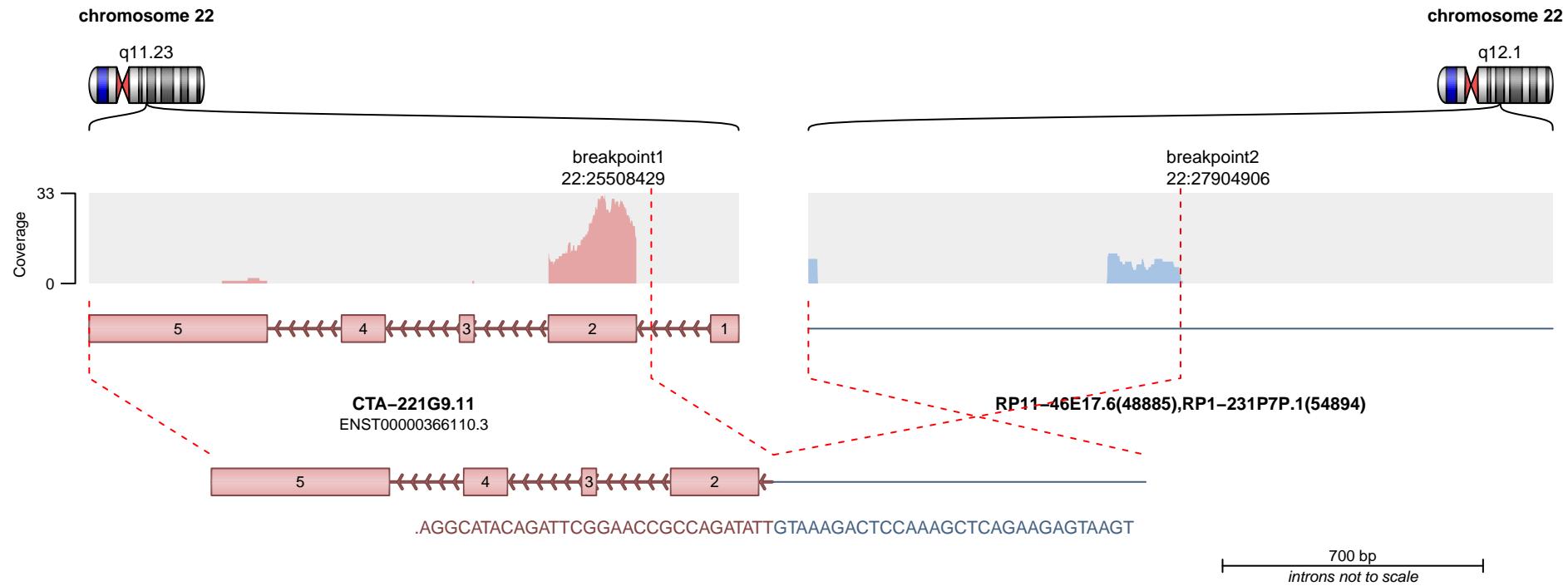
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads at breakpoint1 = 3
Split reads at breakpoint2 = 0
Discordant mates = 0

— translocation — deletion
— duplication — inversion

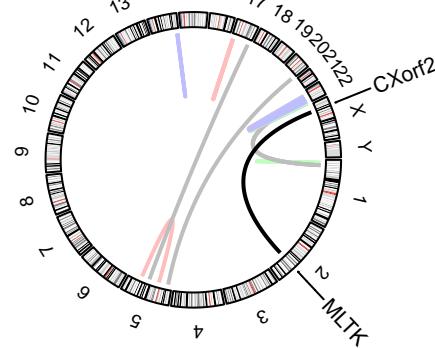
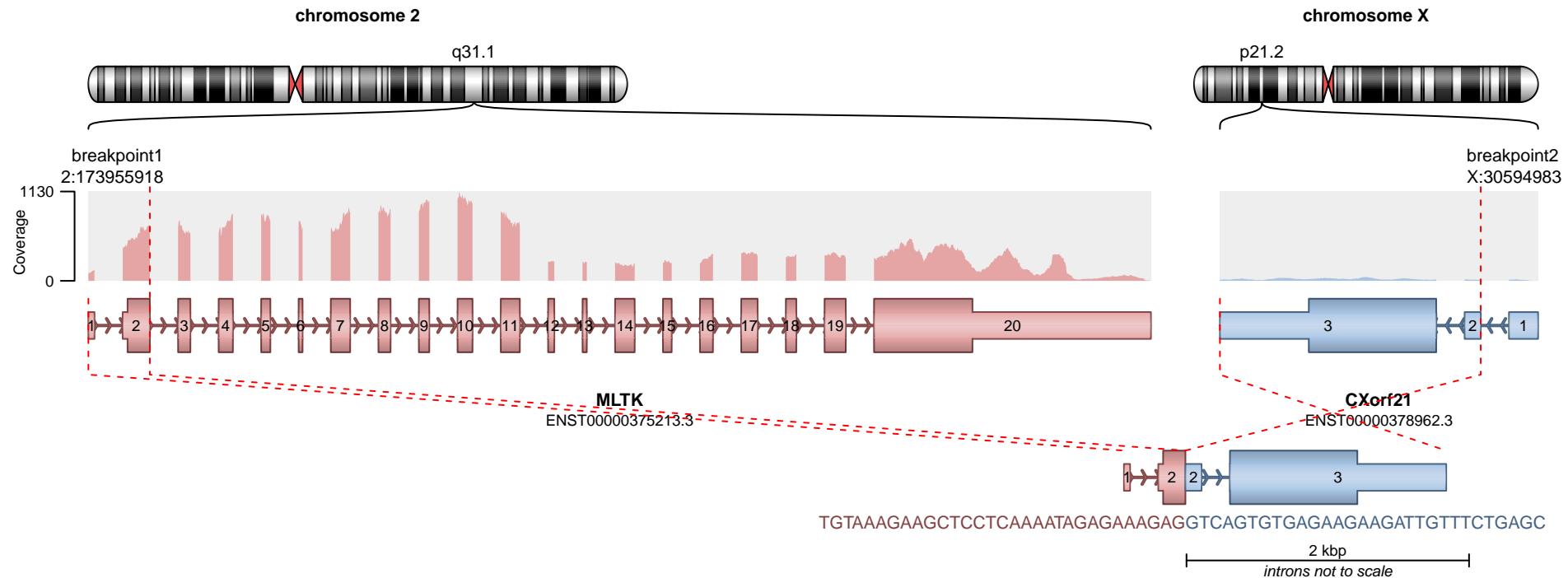


Genes are not protein-coding.

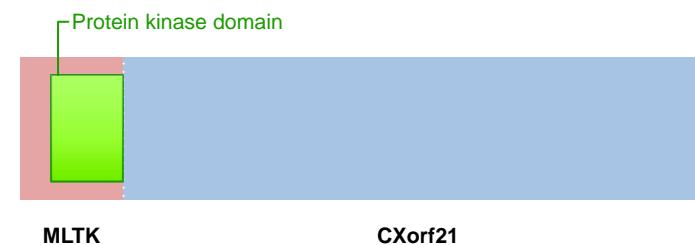
SUPPORTING READ COUNT

Split reads at breakpoint1 = 0
Split reads at breakpoint2 = 2
Discordant mates = 1

— translocation — deletion
— duplication — inversion



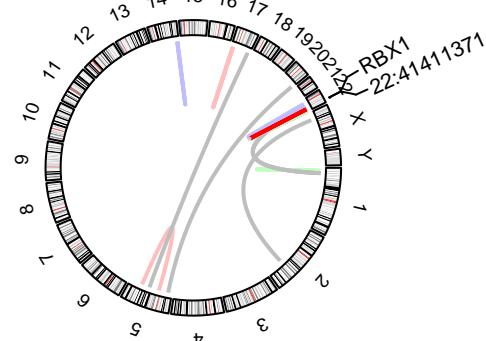
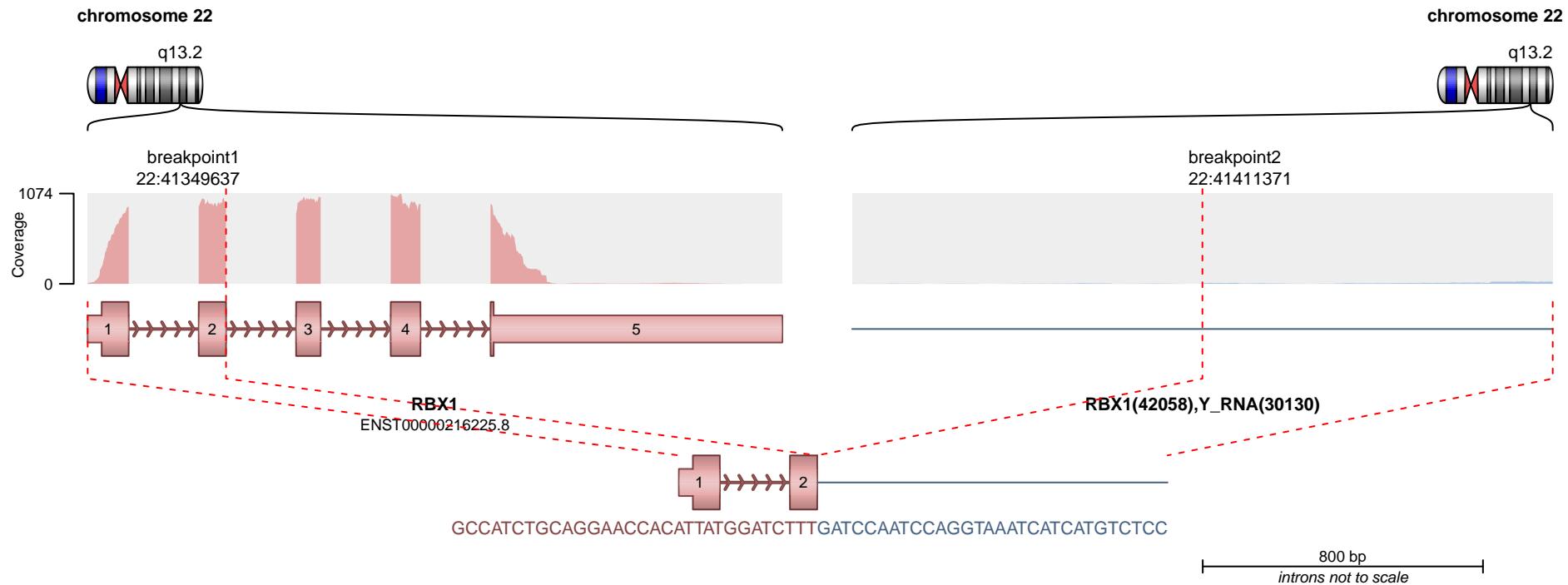
RETAINED PROTEIN DOMAINS out-of-frame fusion



SUPPORTING READ COUNT

Split reads at breakpoint1 = 1
Split reads at breakpoint2 = 1
Discordant mates = 1

— translocation — deletion
— duplication — inversion

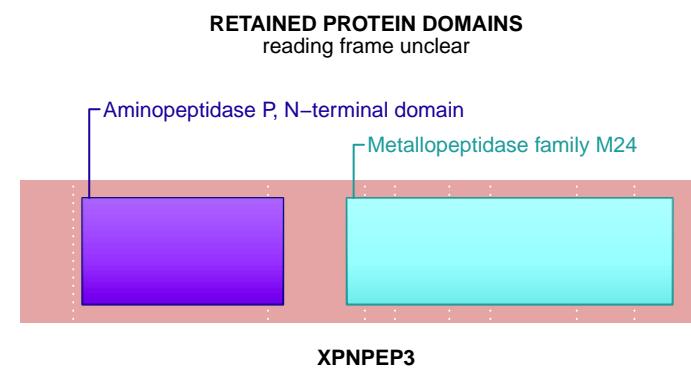
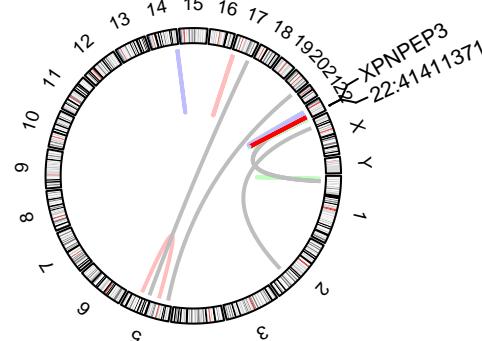
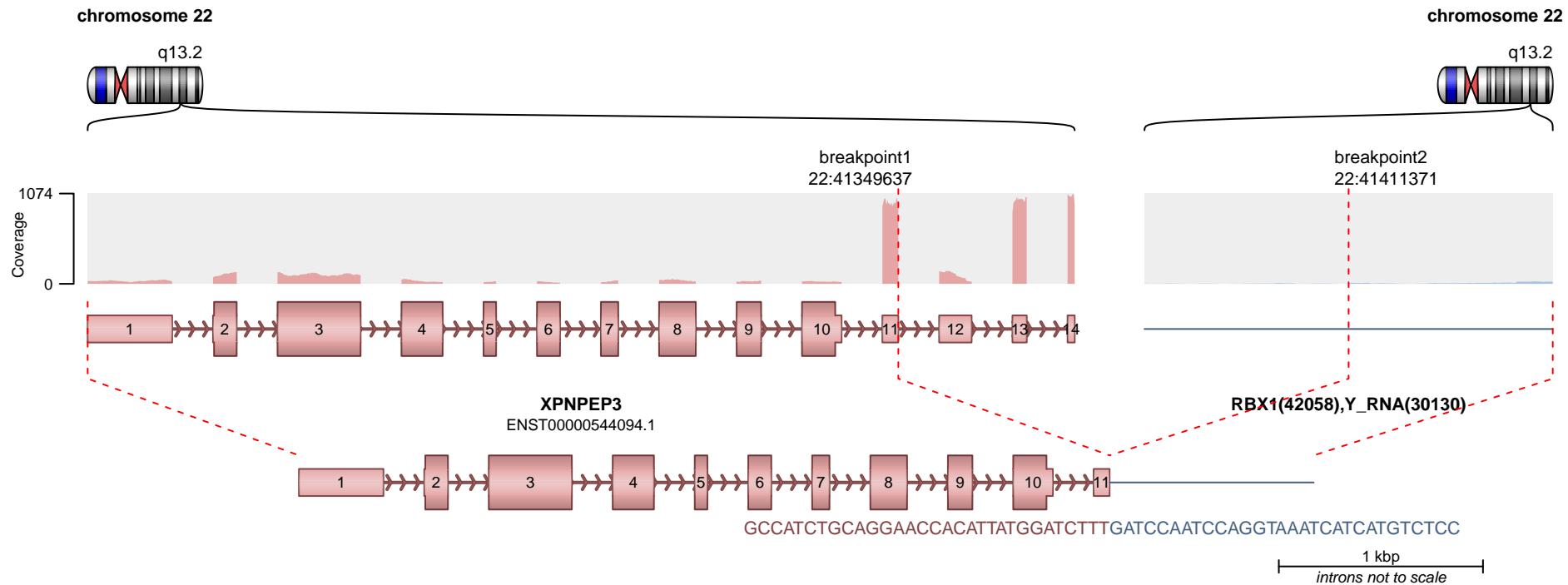


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 6
Split reads at breakpoint2 = 0
Discordant mates = 1

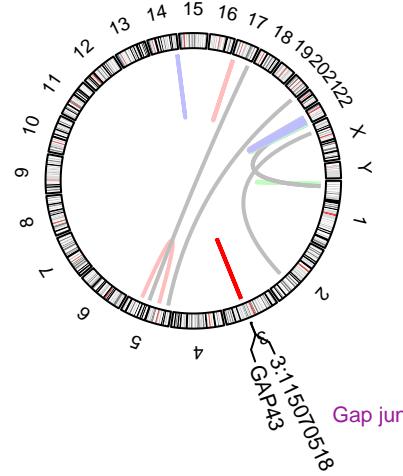
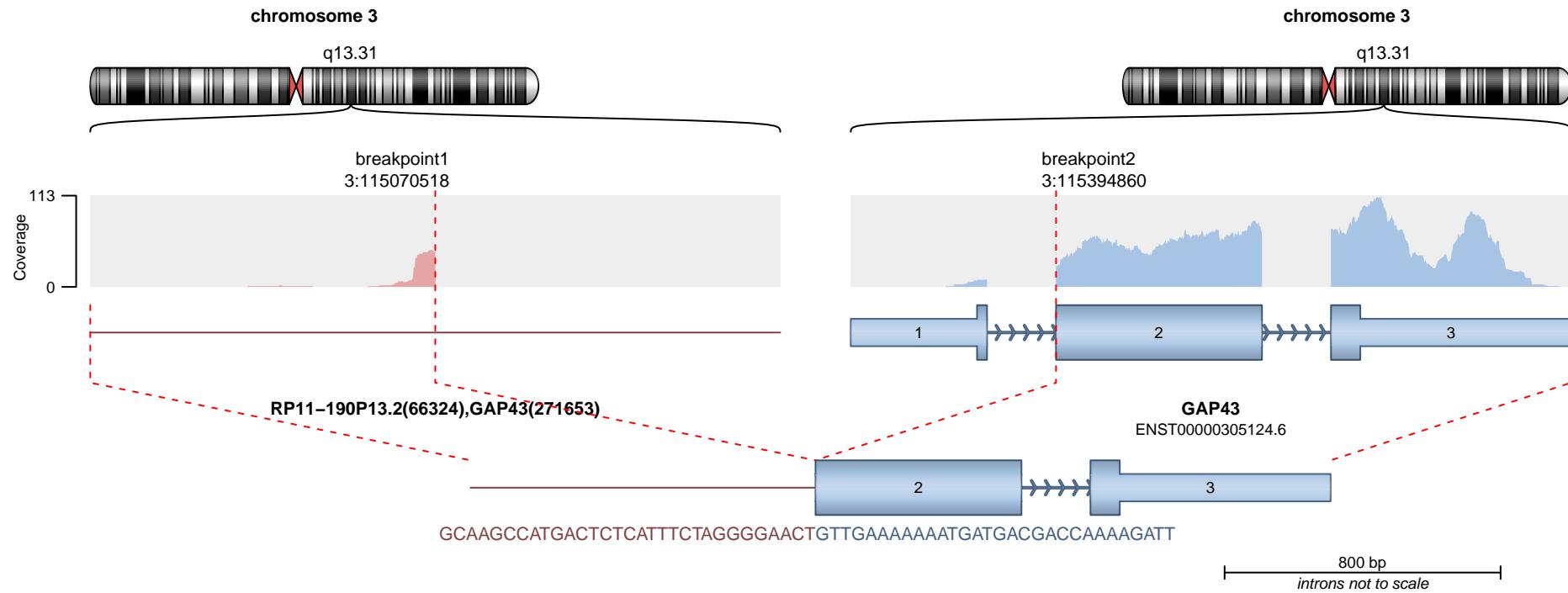
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads at breakpoint1 = 6
Split reads at breakpoint2 = 0
Discordant mates = 1

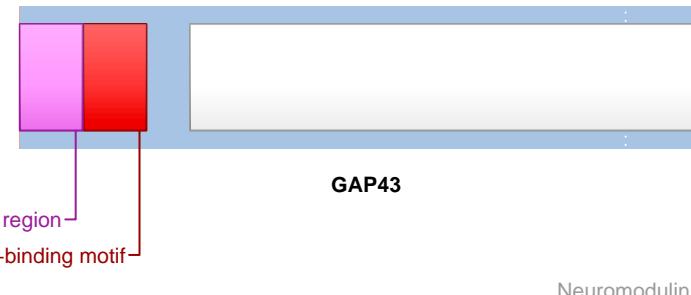
— translocation — deletion
— duplication — inversion



— translocation — deletion
— duplication — inversion

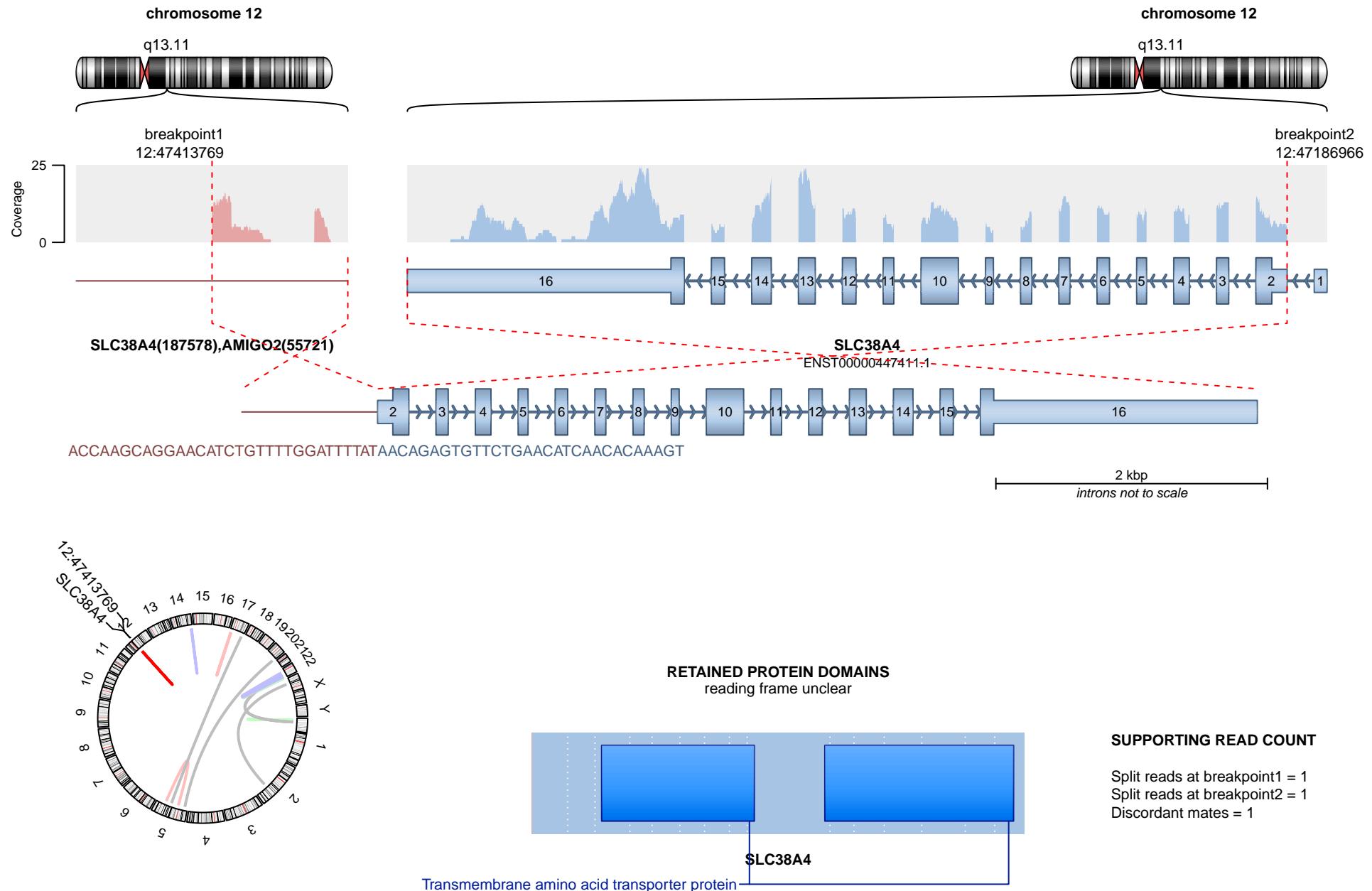
RETAINED PROTEIN DOMAINS

reading frame unclear

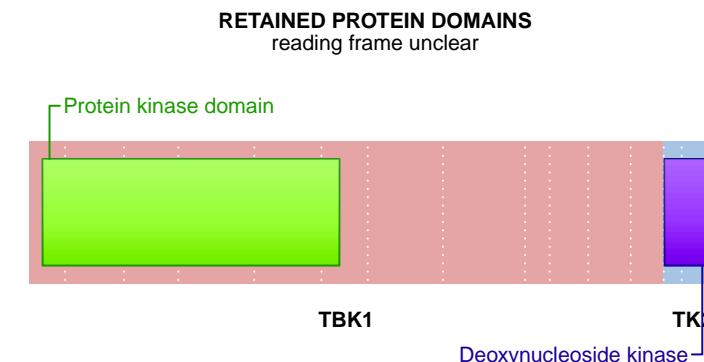
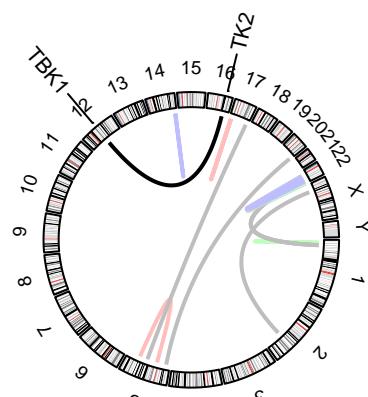
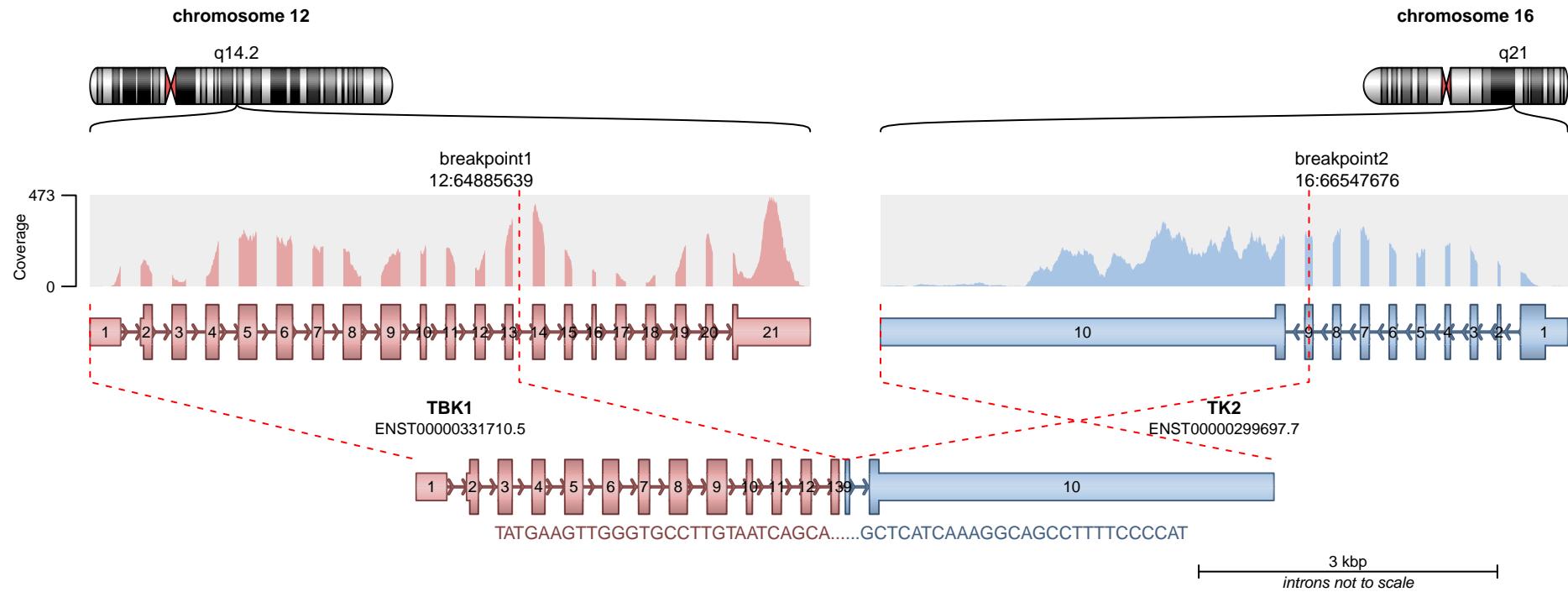


SUPPORTING READ COUNT

Split reads at breakpoint1 = 1
Split reads at breakpoint2 = 5
Discordant mates = 0



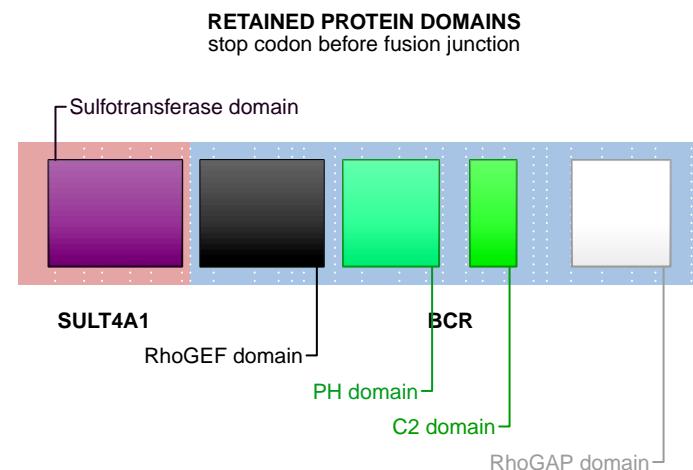
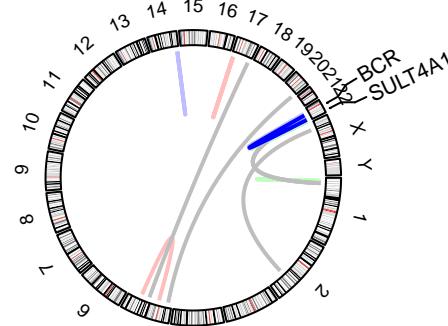
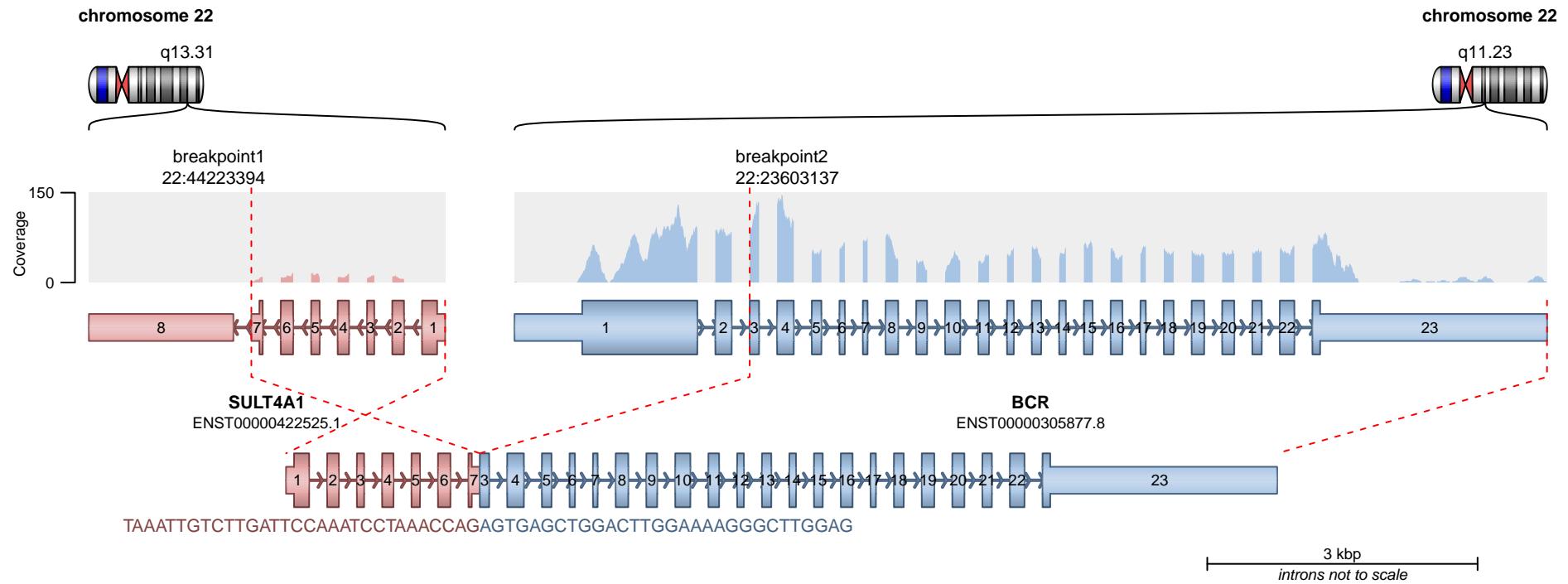
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads at breakpoint1 = 0
Split reads at breakpoint2 = 0
Discordant mates = 2

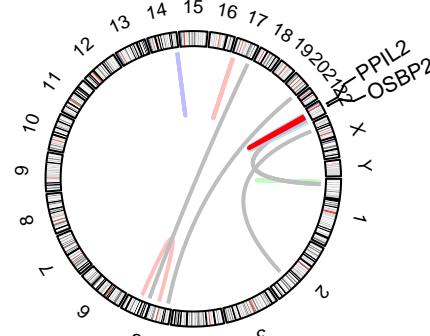
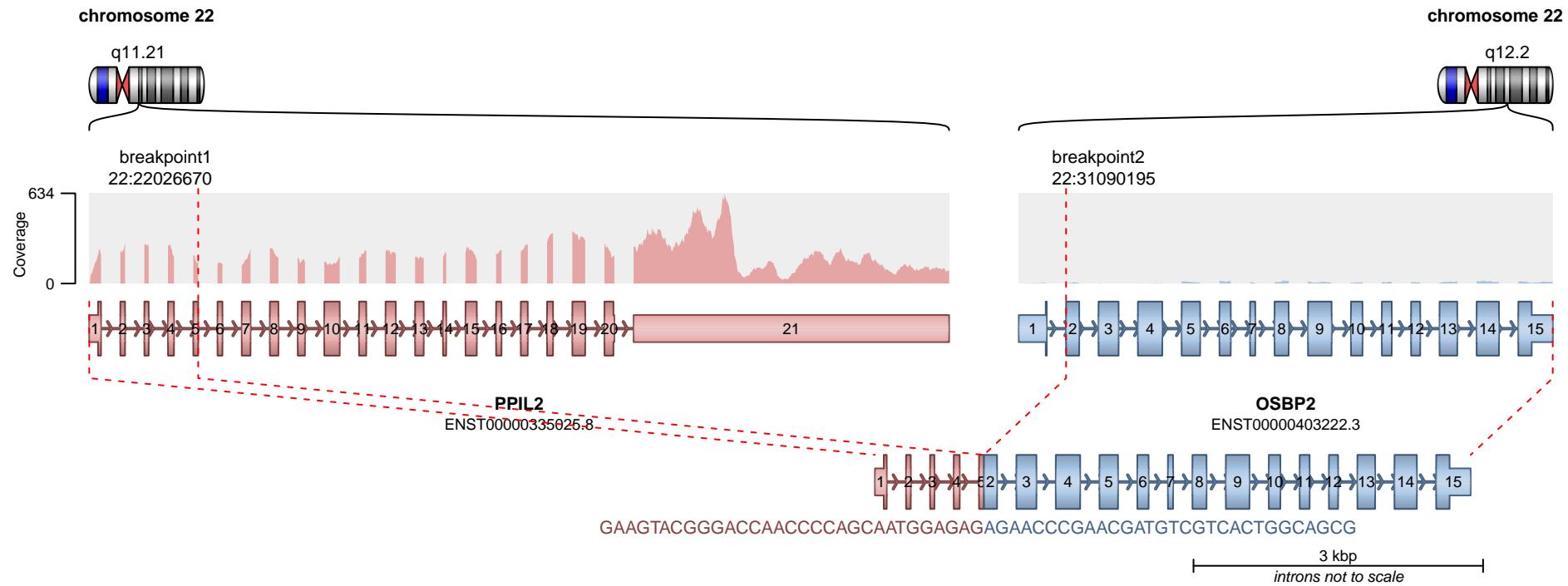
— translocation — deletion
— duplication — inversion



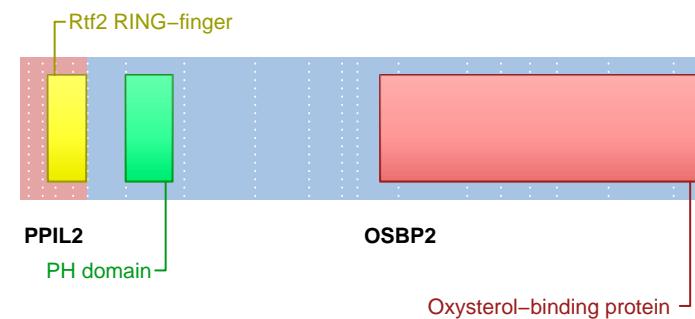
SUPPORTING READ COUNT

Split reads at breakpoint1 = 1
Split reads at breakpoint2 = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



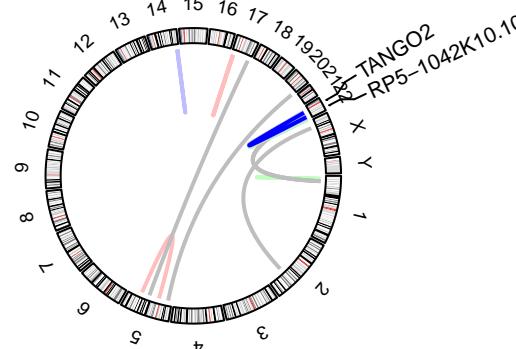
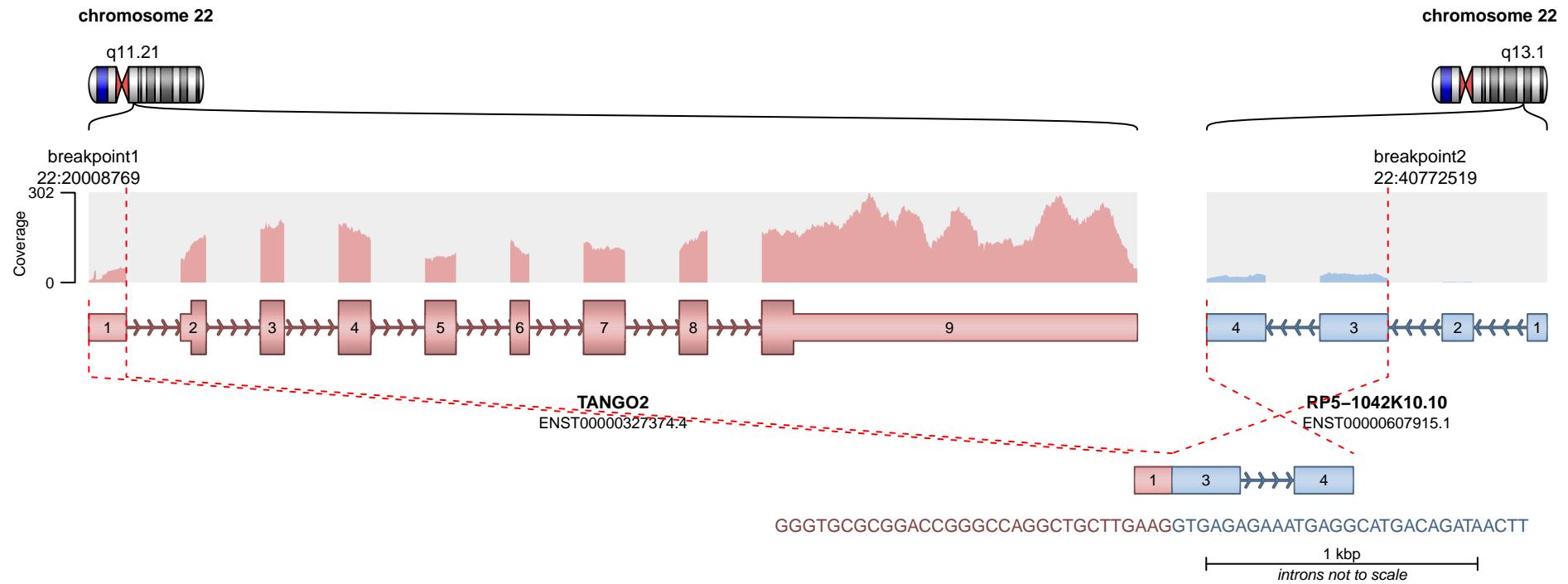
RETAINED PROTEIN DOMAINS in-frame fusion



SUPPORTING READ COUNT

Split reads at breakpoint1 = 2
Split reads at breakpoint2 = 0
Discordant mates = 0

— translocation — deletion
— duplication — inversion

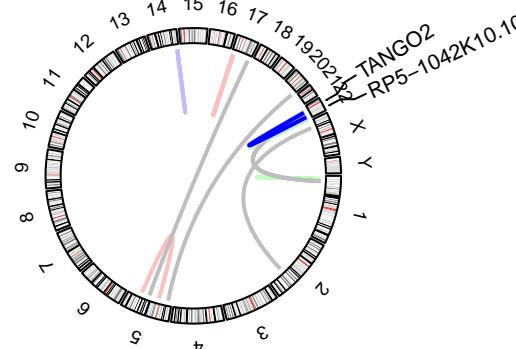
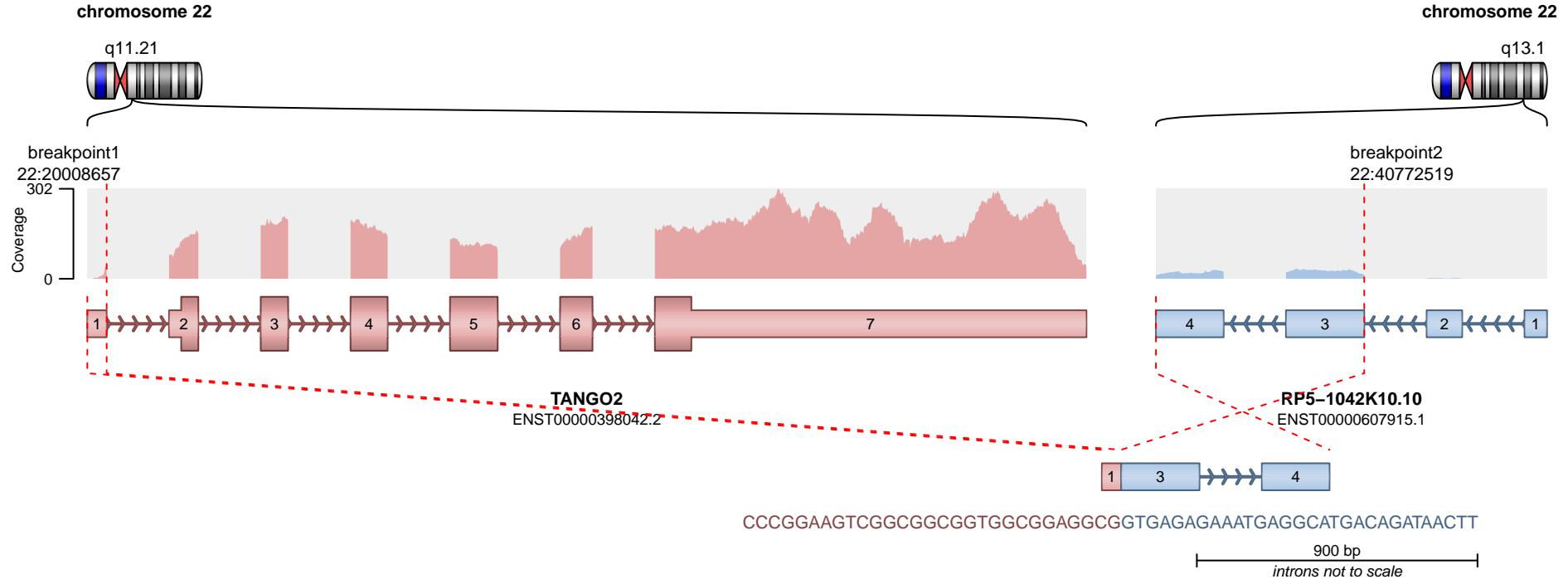


No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 0
Split reads at breakpoint2 = 2
Discordant mates = 0

— translocation — deletion
— duplication — inversion

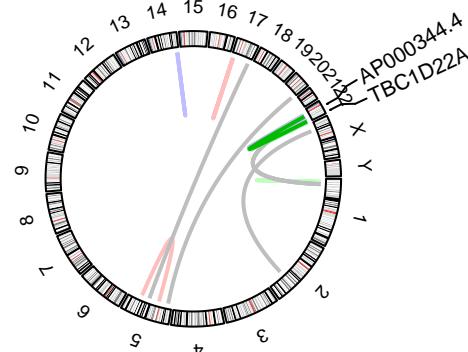
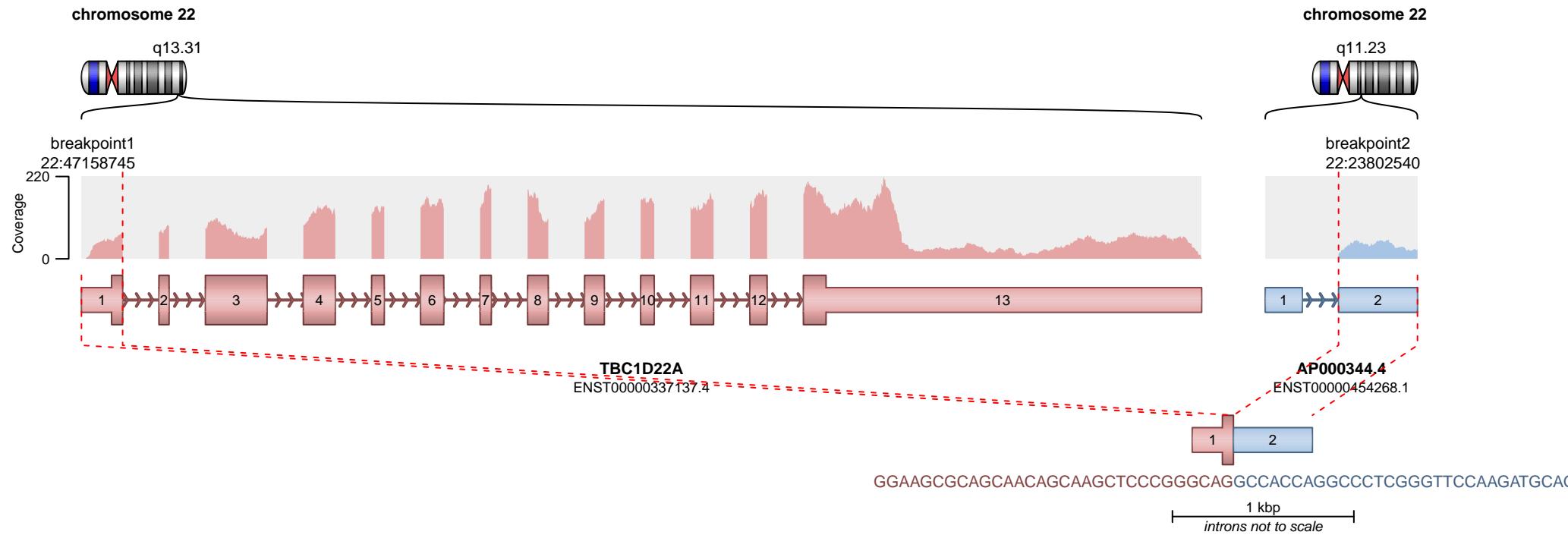


No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 0
Split reads at breakpoint2 = 0
Discordant mates = 0

— translocation — deletion
— duplication — inversion

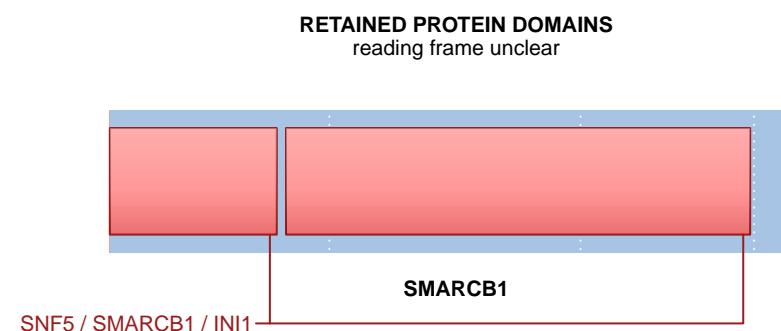
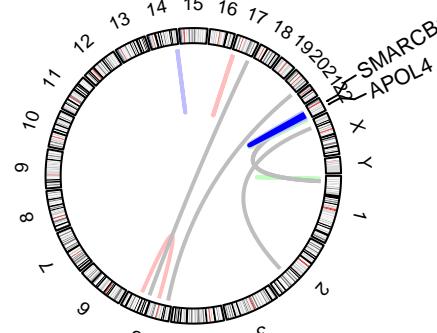
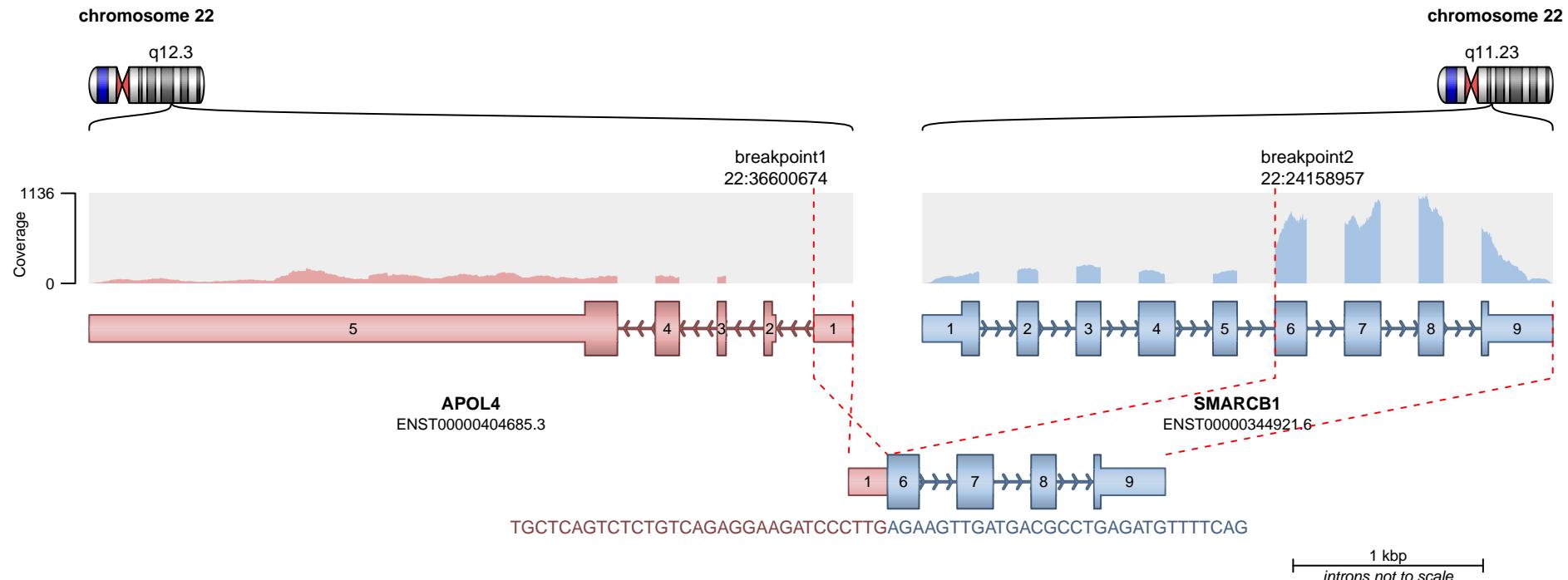


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 1
Split reads at breakpoint2 = 0
Discordant mates = 1

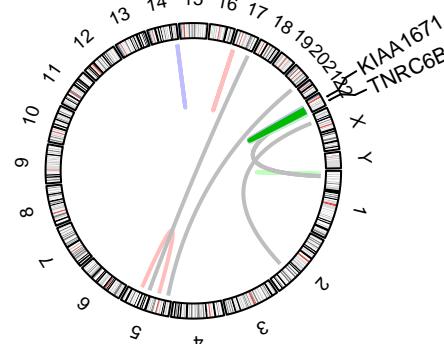
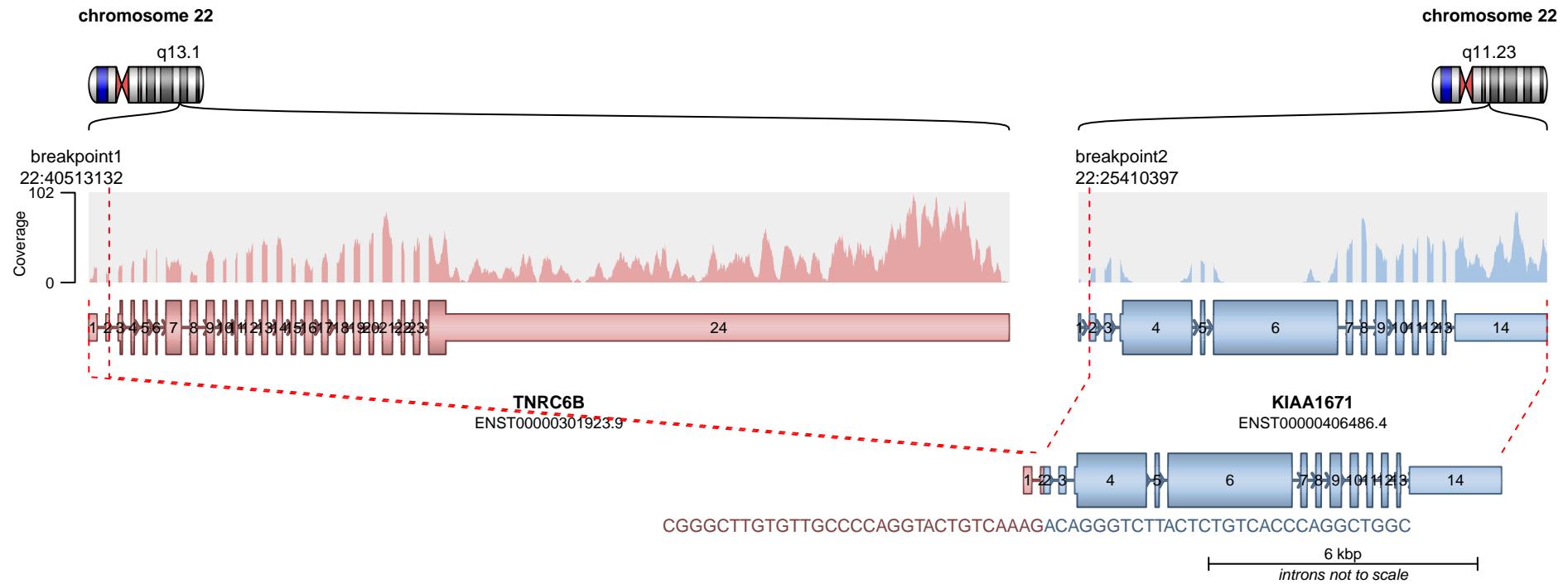
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads at breakpoint1 = 2
Split reads at breakpoint2 = 0
Discordant mates = 0

— translocation — deletion
— duplication — inversion

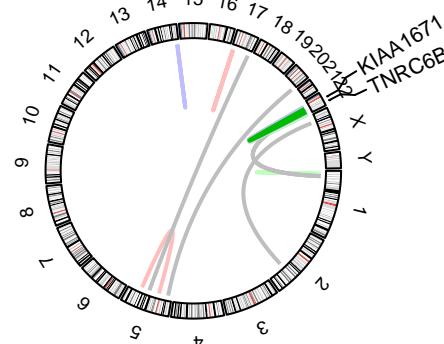
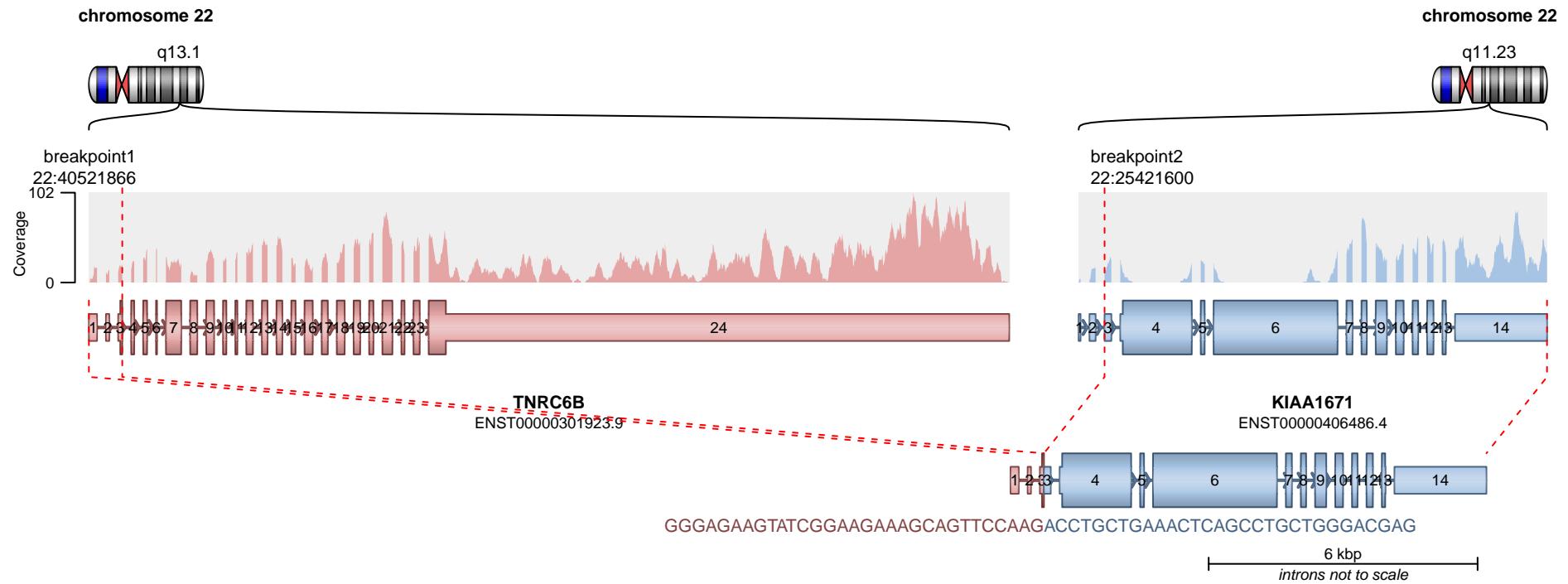


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 0
Split reads at breakpoint2 = 1
Discordant mates = 0

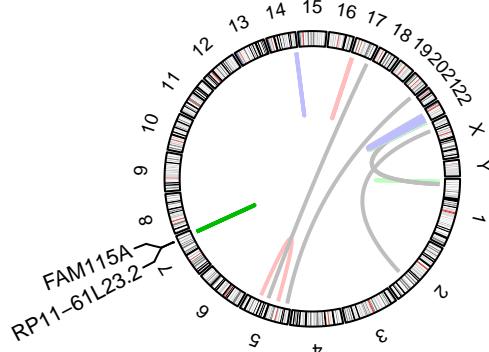
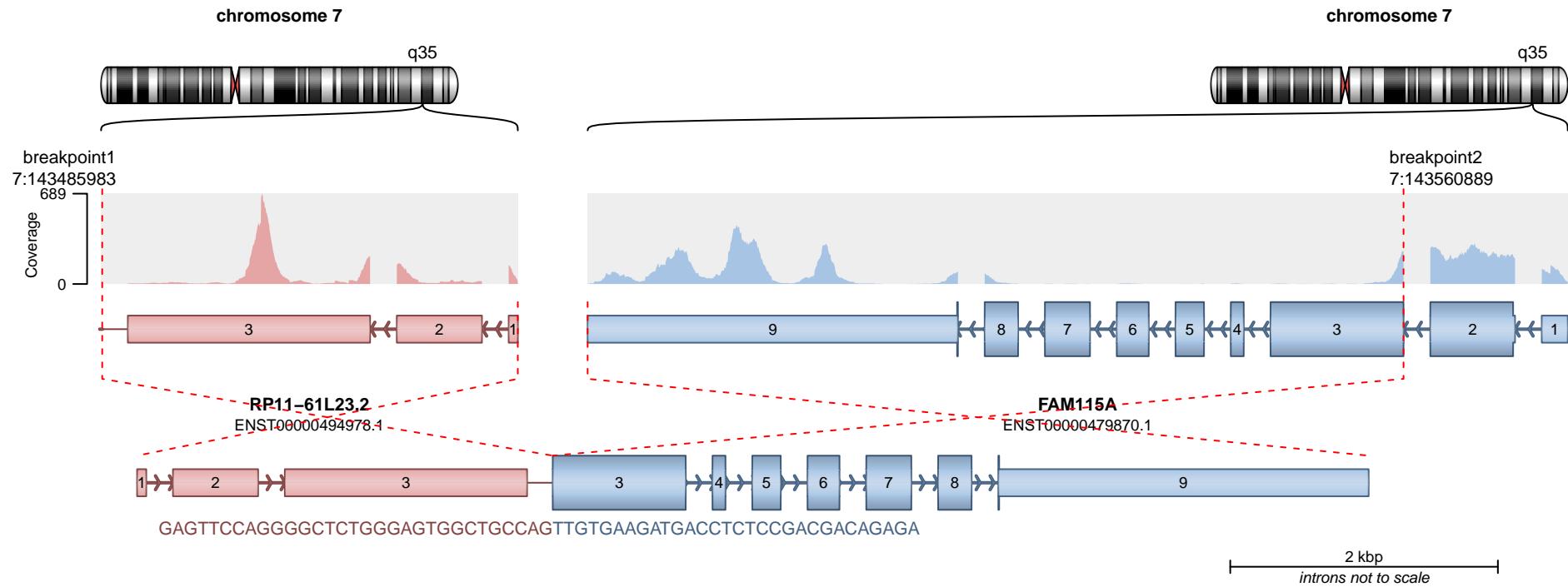


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 0
Split reads at breakpoint2 = 1
Discordant mates = 0



No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 1
Split reads at breakpoint2 = 0
Discordant mates = 0

— translocation — deletion
— duplication — inversion