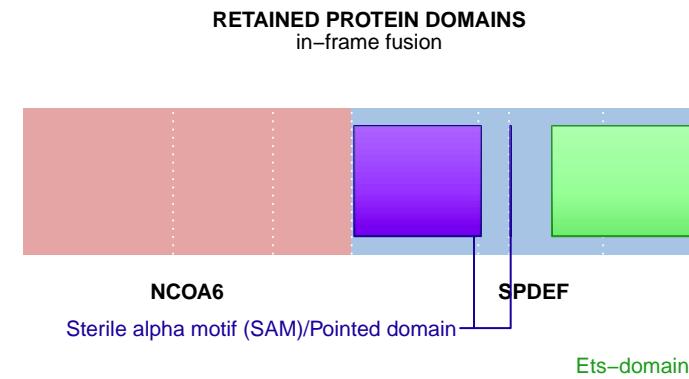
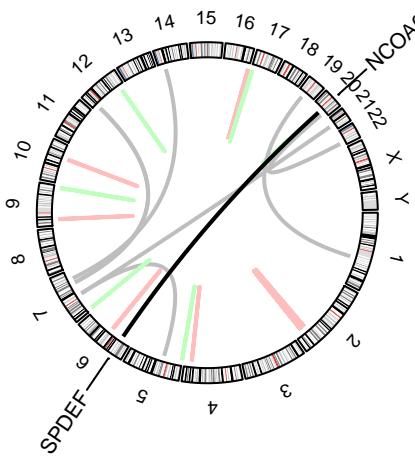
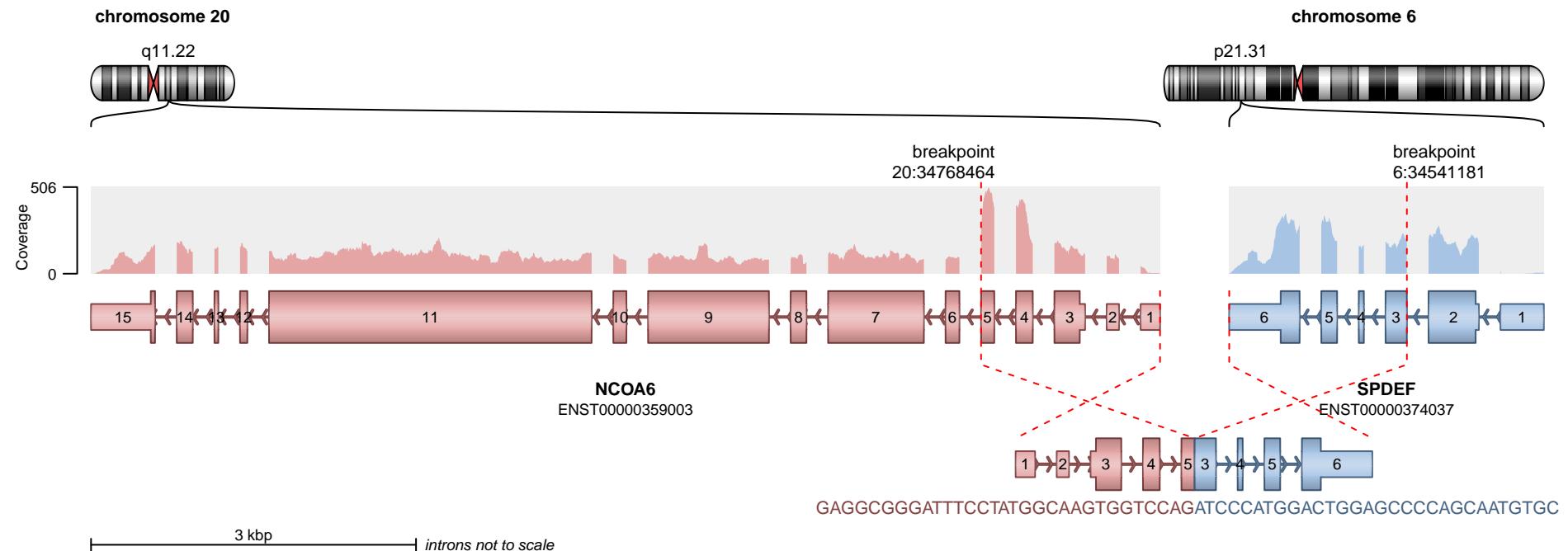


SUPPORTING READ COUNT

Split reads = 122
Discordant mates = 58

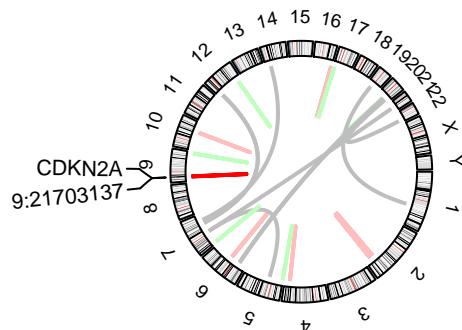
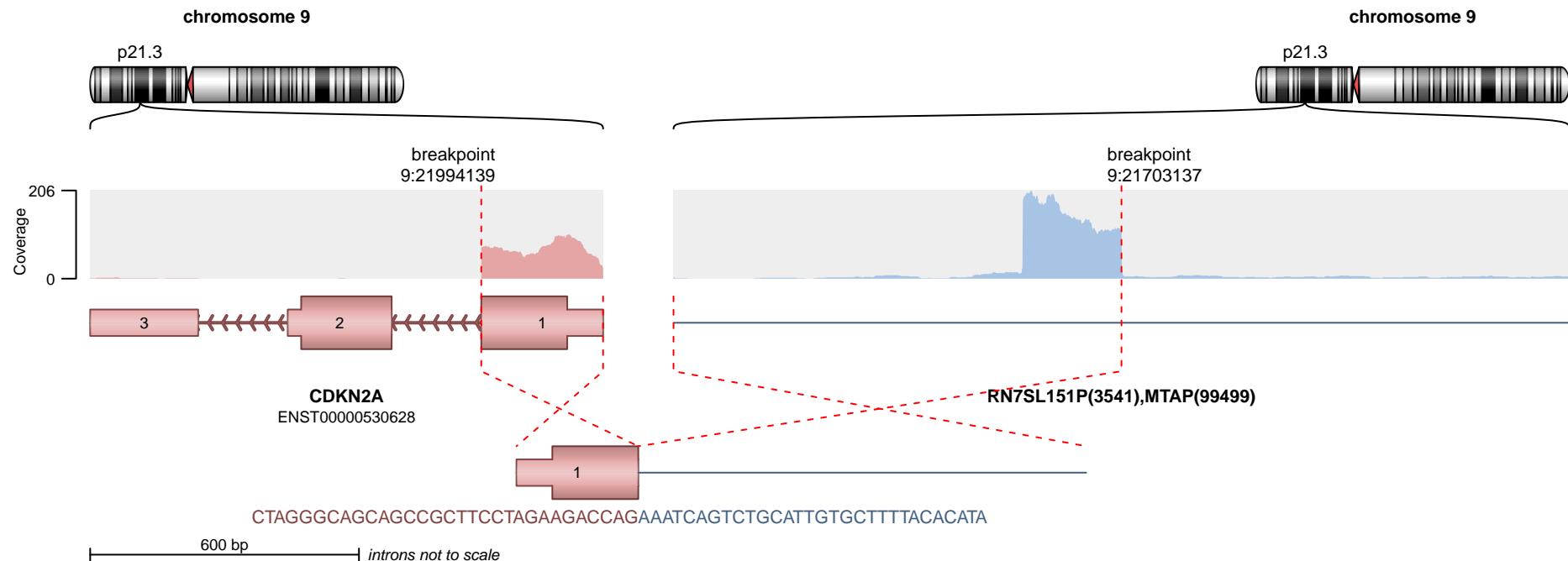
— translocation — deletion
— duplication — inversion



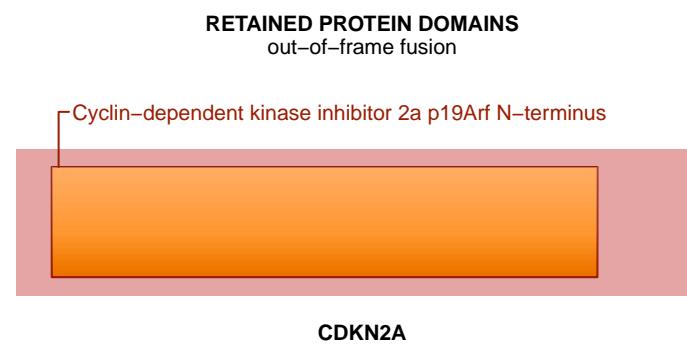
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

— translocation — deletion
— duplication — inversion

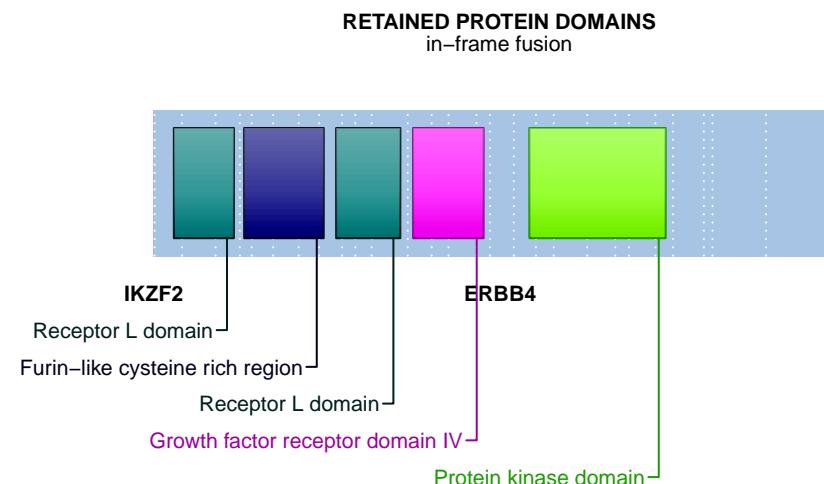
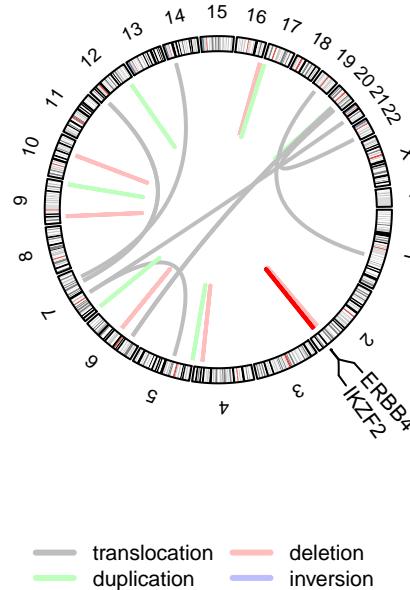
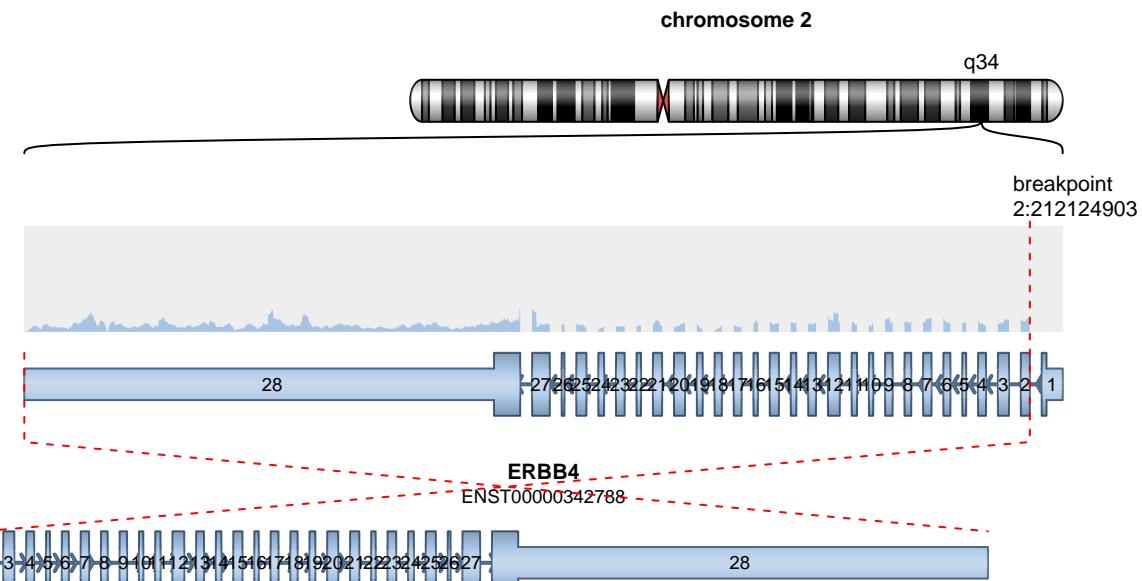
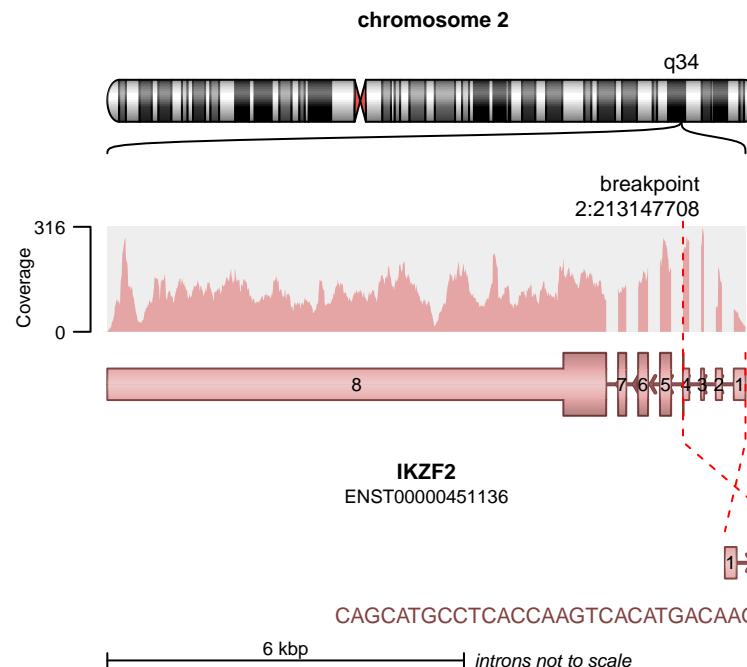


— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

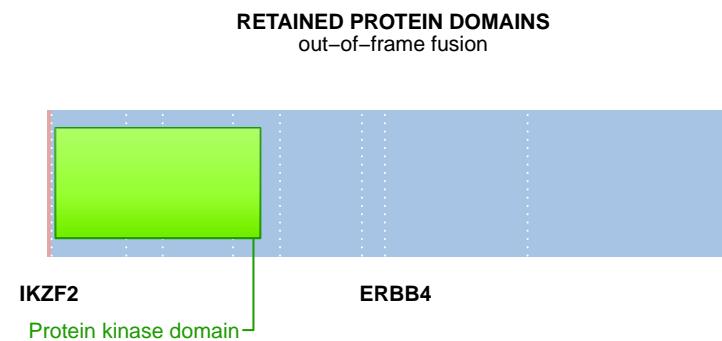
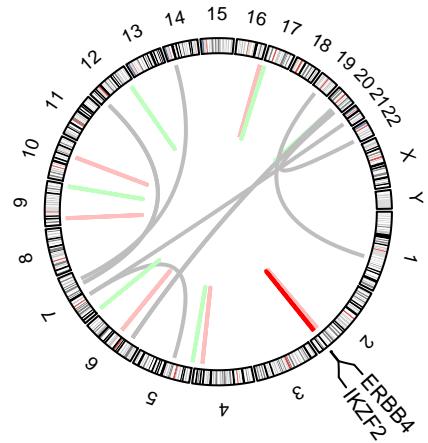
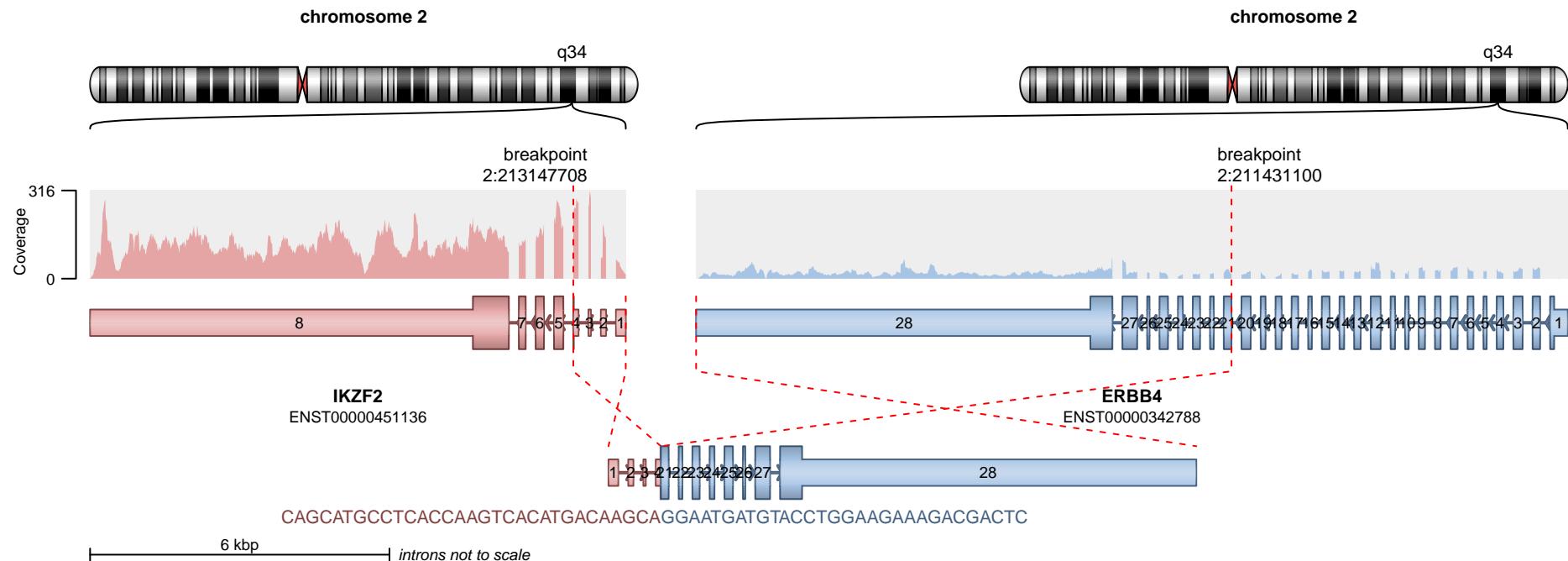
Split reads = 26
Discordant mates = 20



SUPPORTING READ COUNT

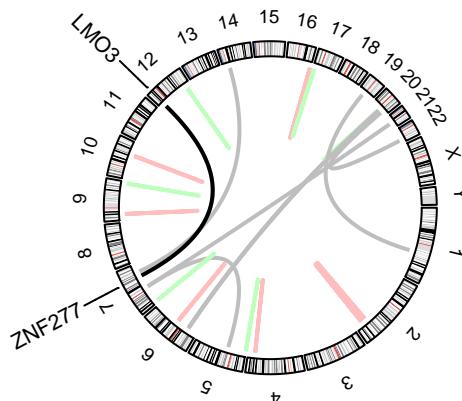
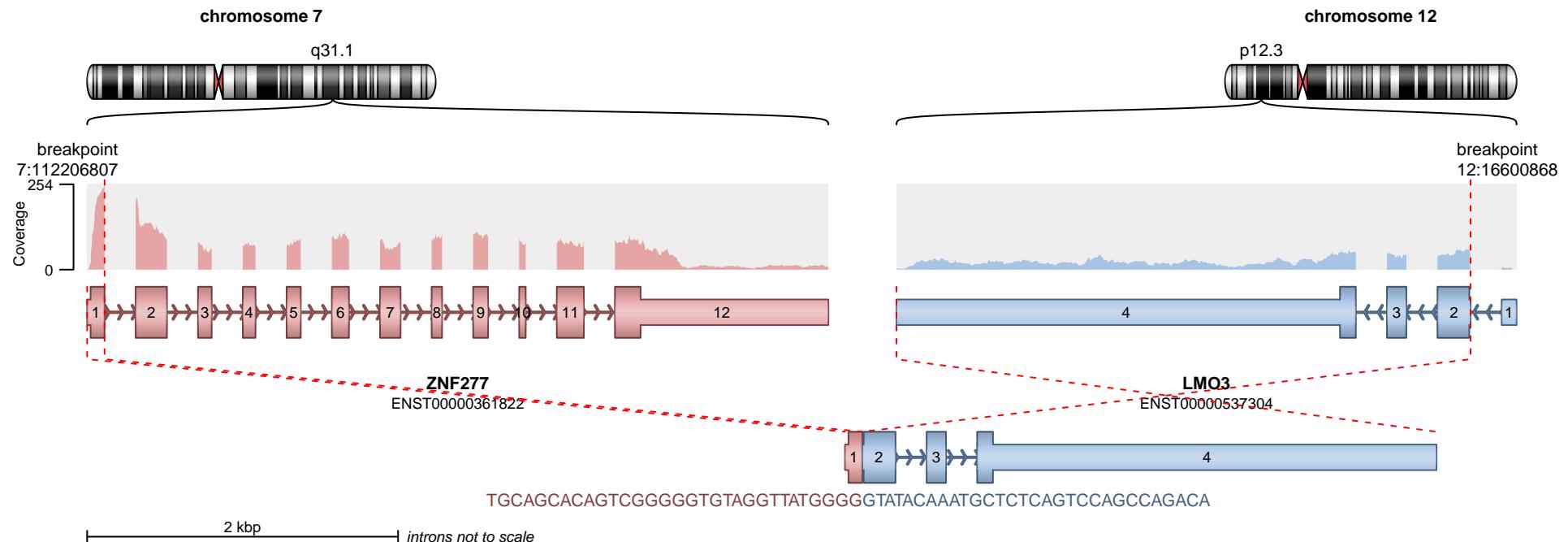
Split reads = 21

Discordant mates = 14

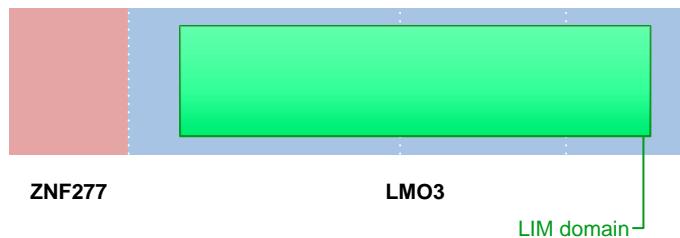


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



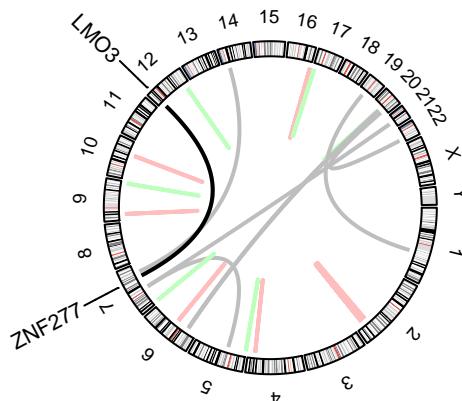
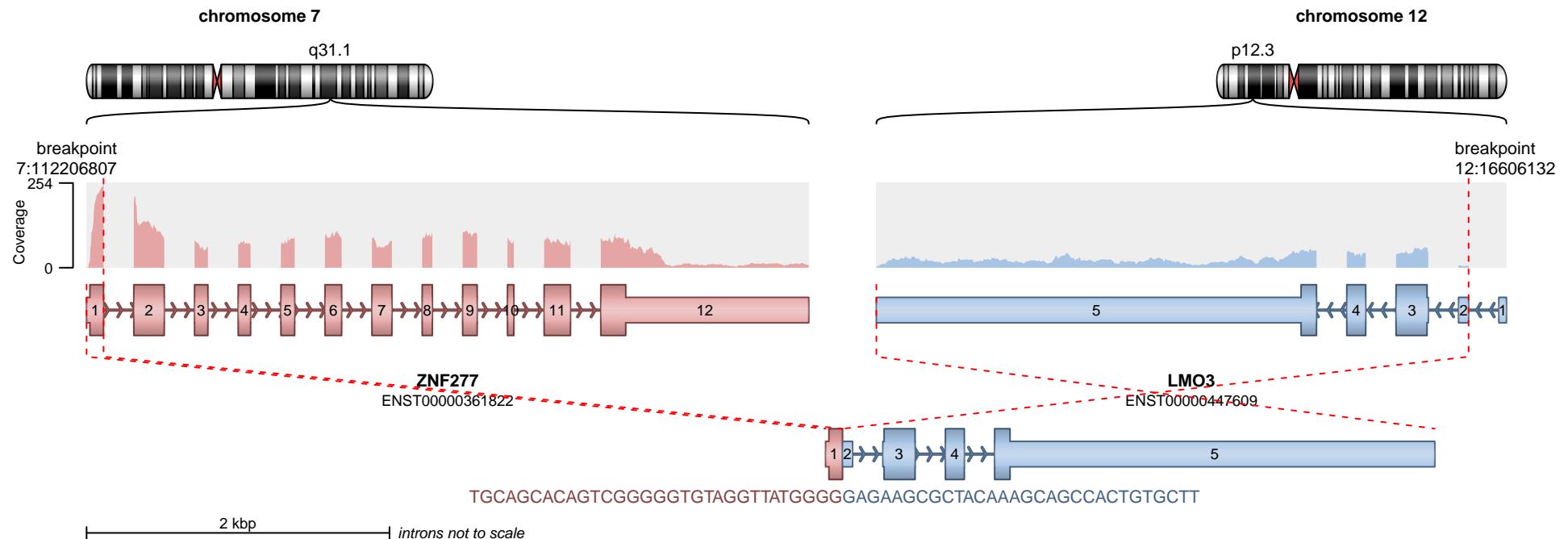
RETAINED PROTEIN DOMAINS in-frame fusion



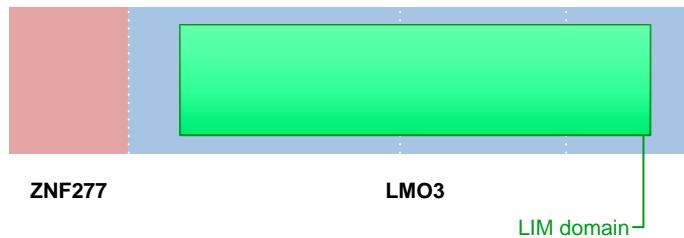
SUPPORTING READ COUNT

Split reads = 22
Discordant mates = 4

— translocation — deletion
— duplication — inversion



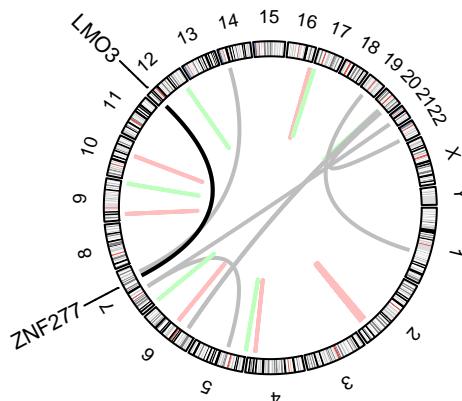
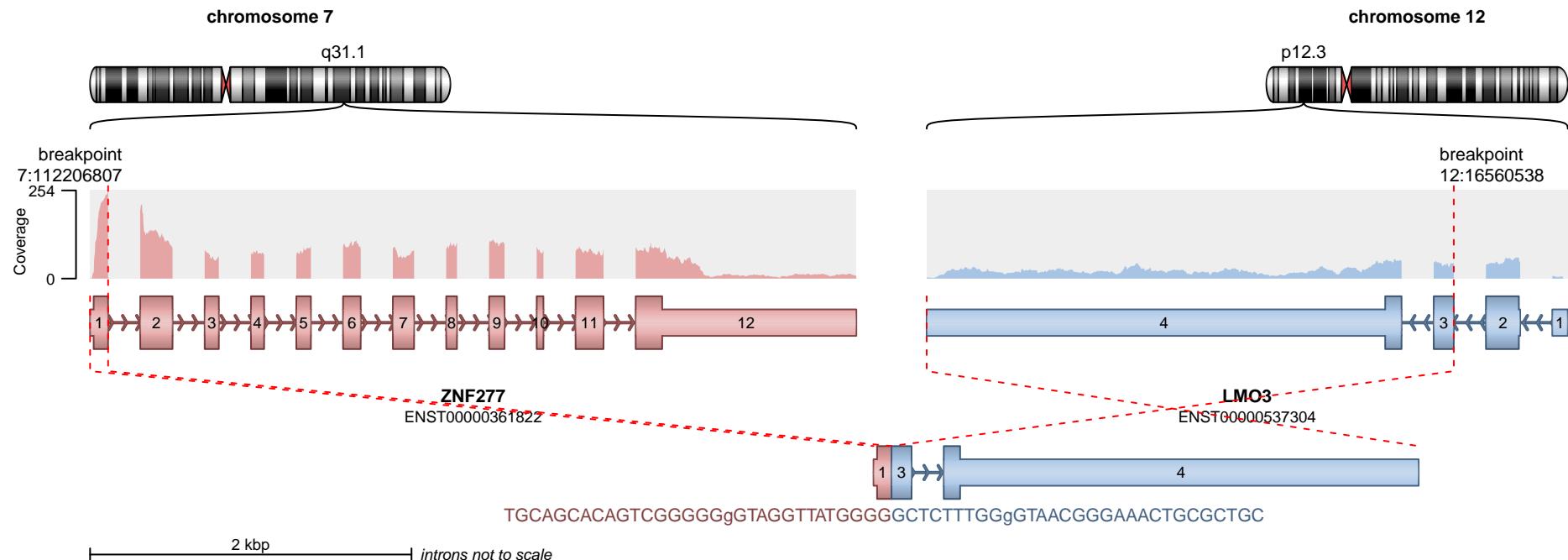
RETAINED PROTEIN DOMAINS out-of-frame fusion



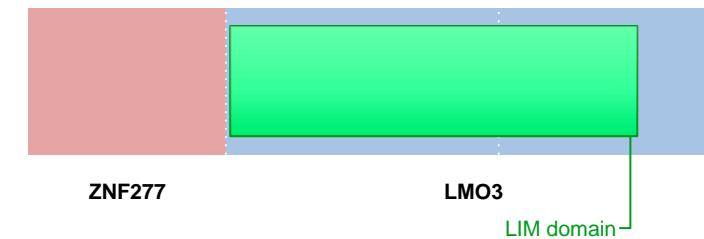
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 4

— translocation — deletion
— duplication — inversion



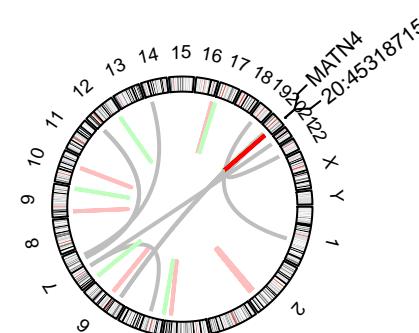
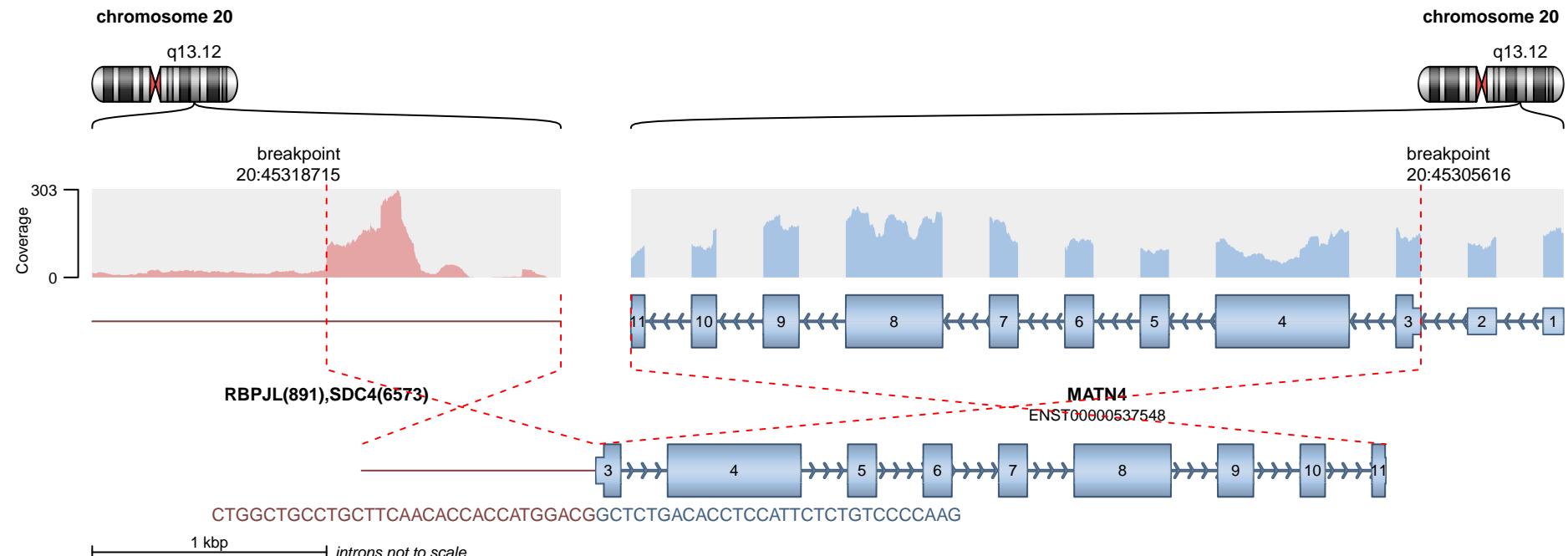
RETAINED PROTEIN DOMAINS out-of-frame fusion



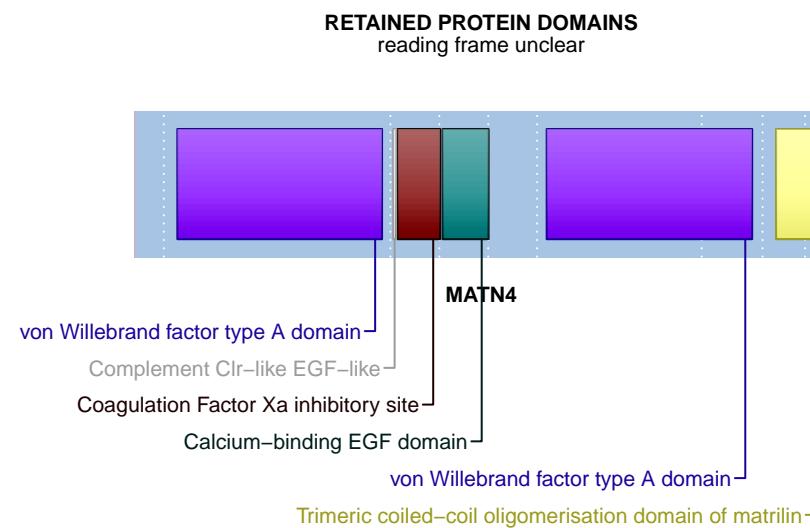
SUPPORTING READ COUNT

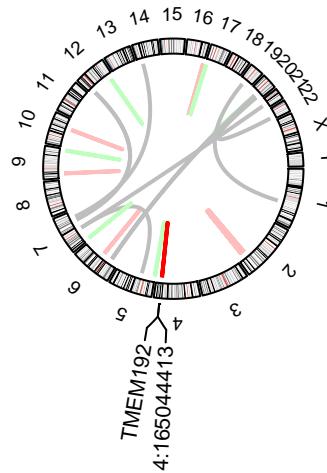
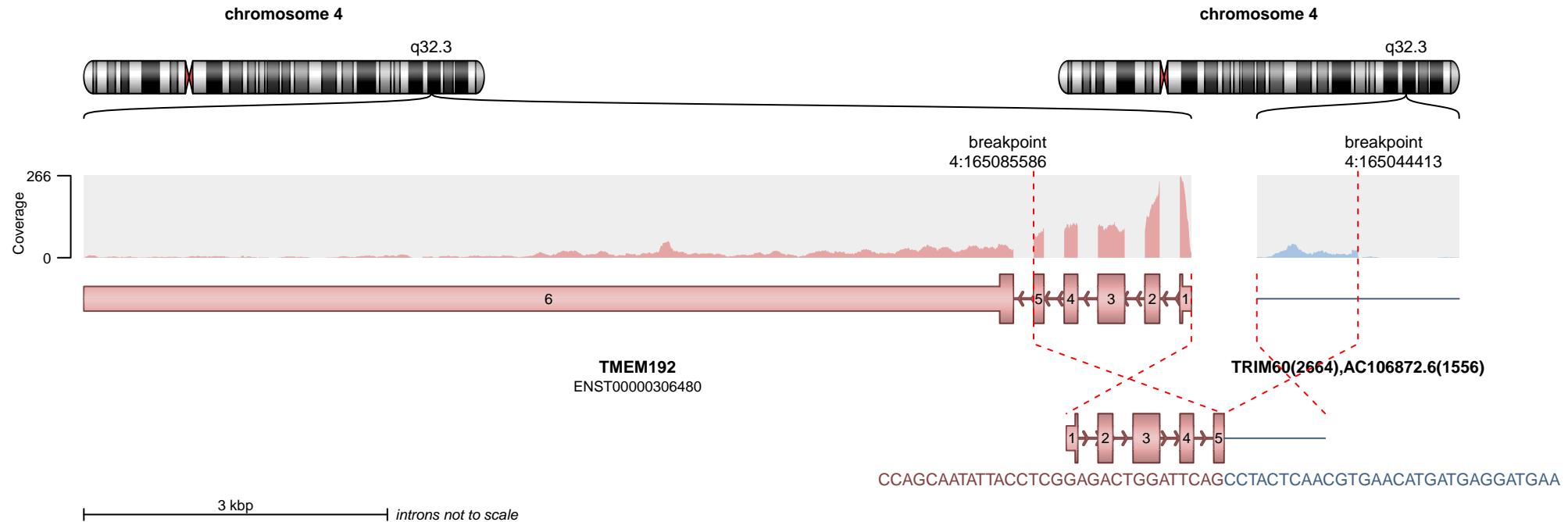
Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



— translocation — deletion
— duplication — inversion



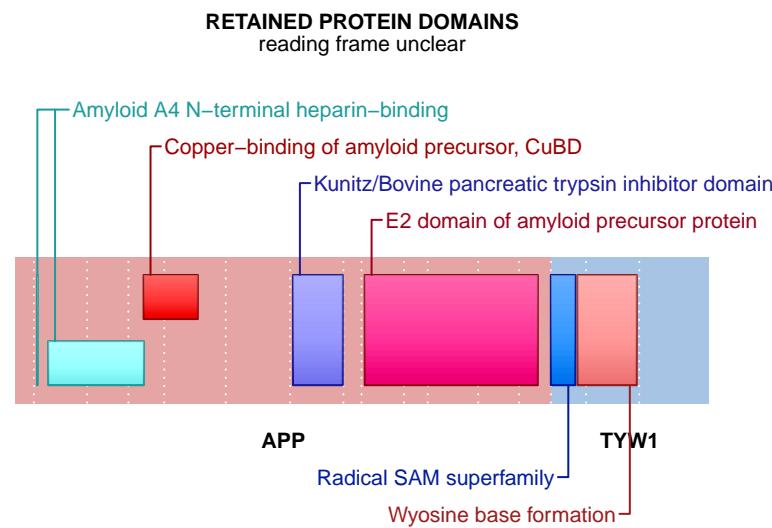
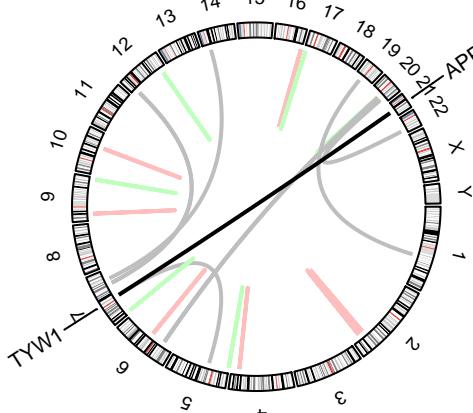
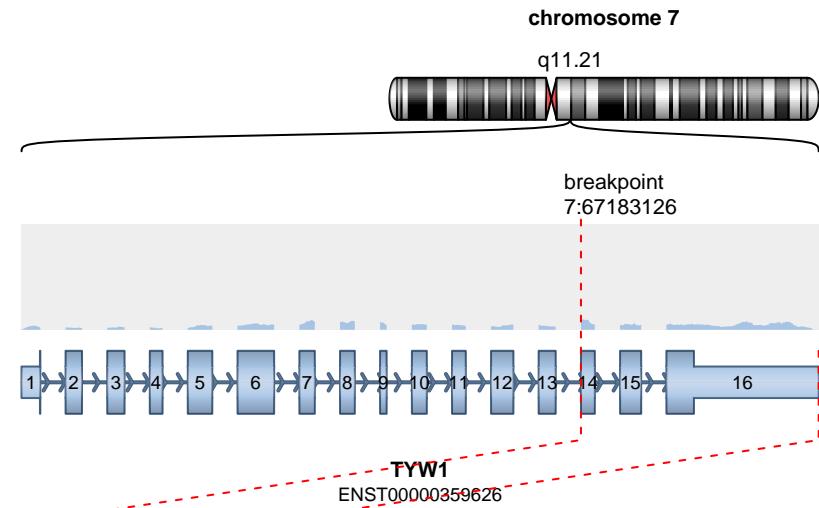
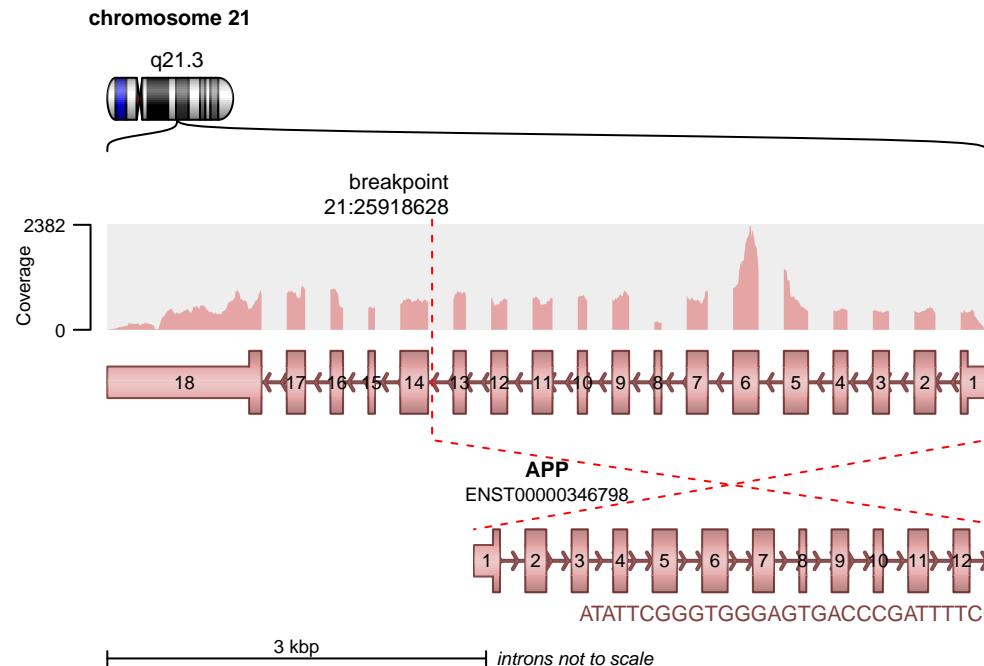


No protein domains retained in fusion

SUPPORTING READ COUNT

Split reads = 15
Discordant mates = 6

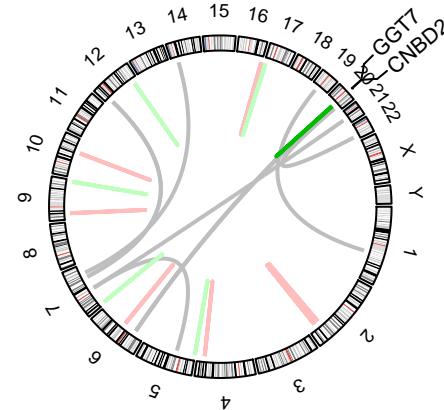
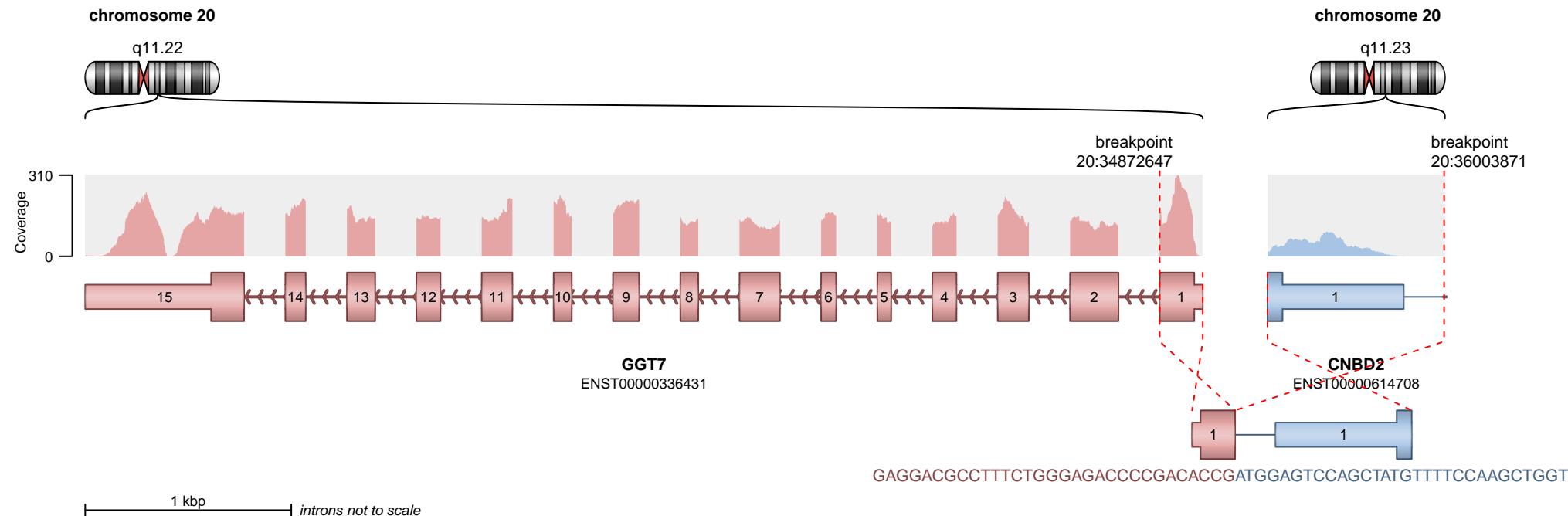
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 16
Discordant mates = 2

— translocation — deletion
— duplication — inversion

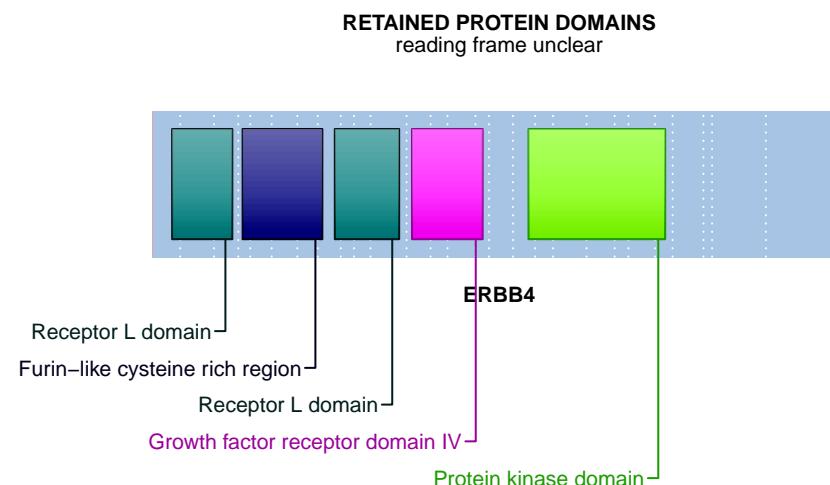
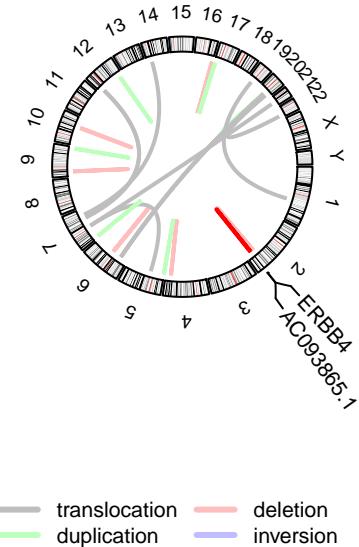
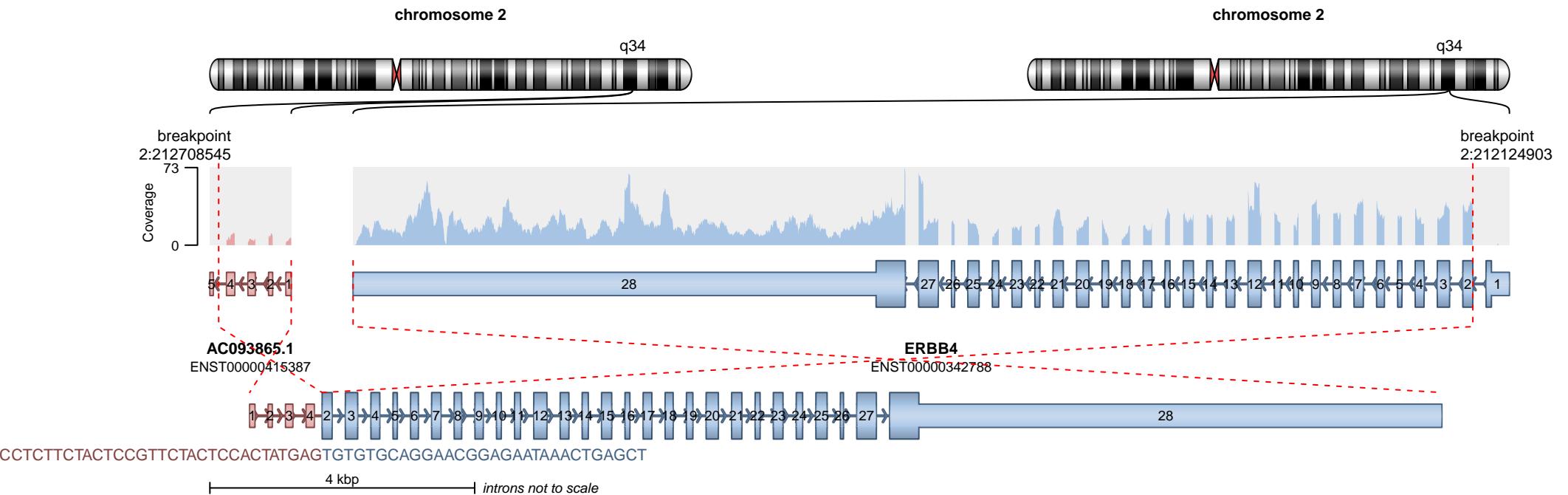


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 9

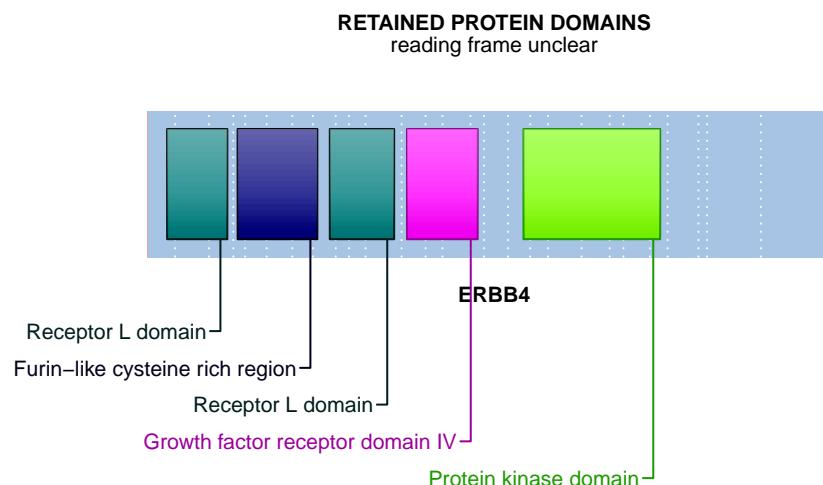
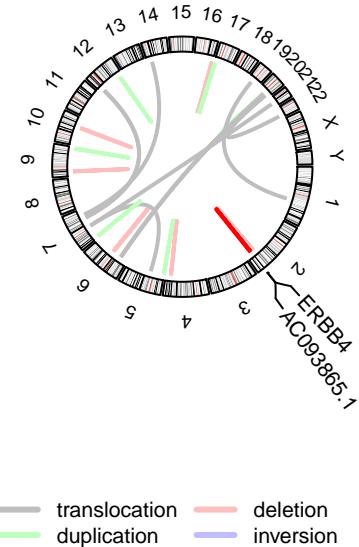
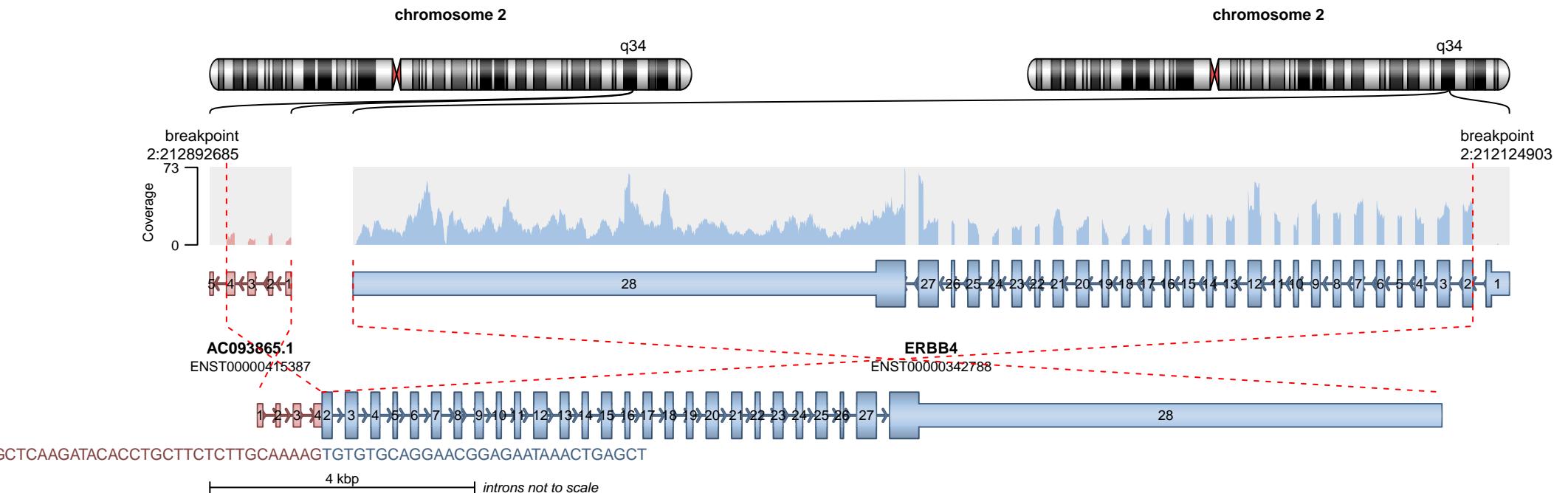
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

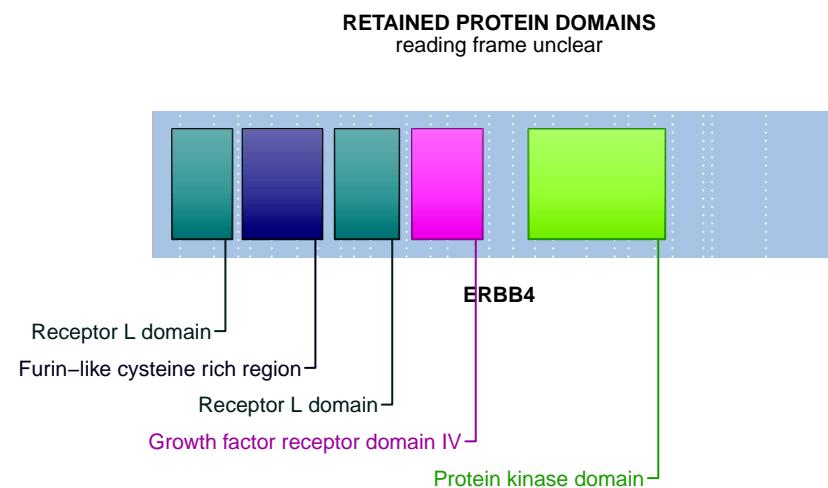
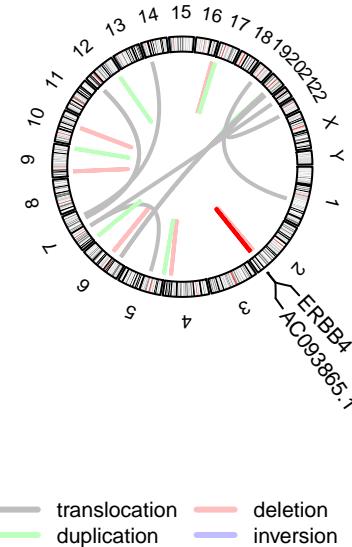
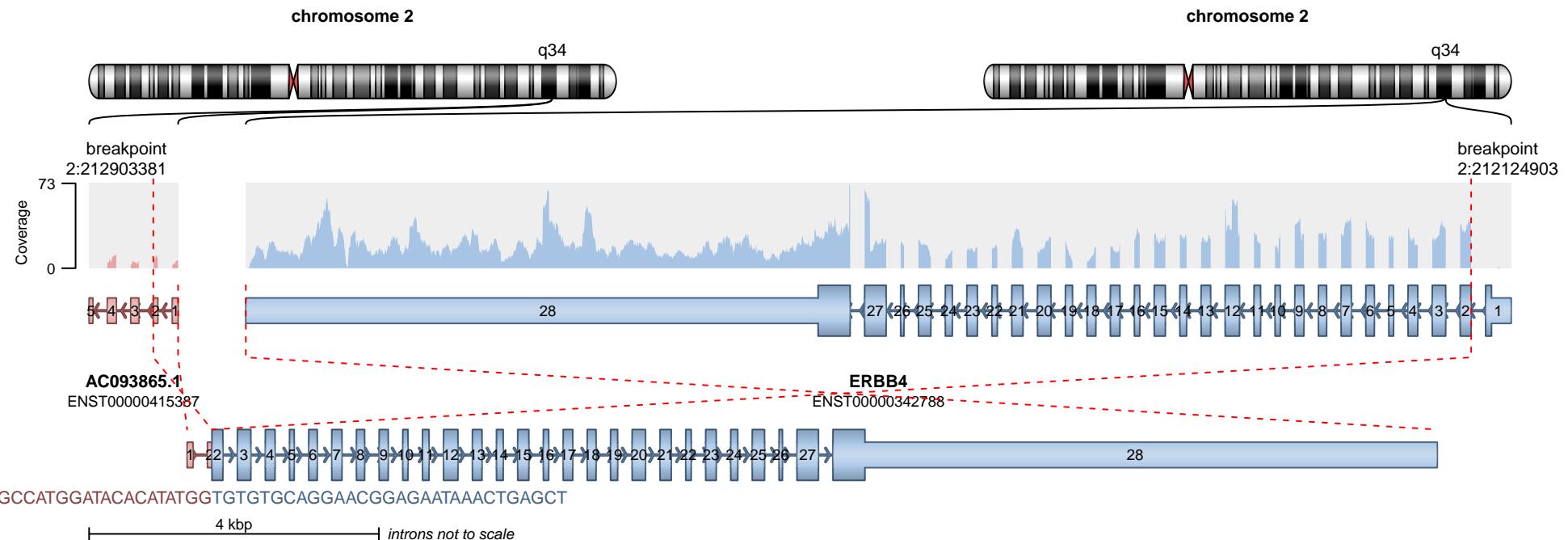
Split reads = 2

Discordant mates = 2



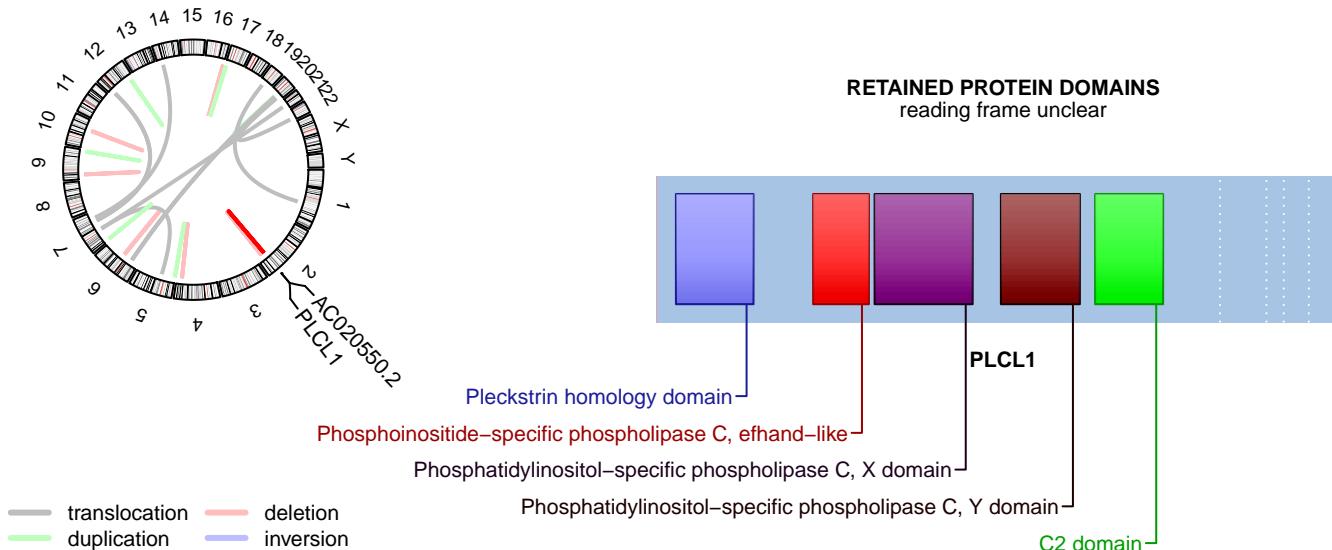
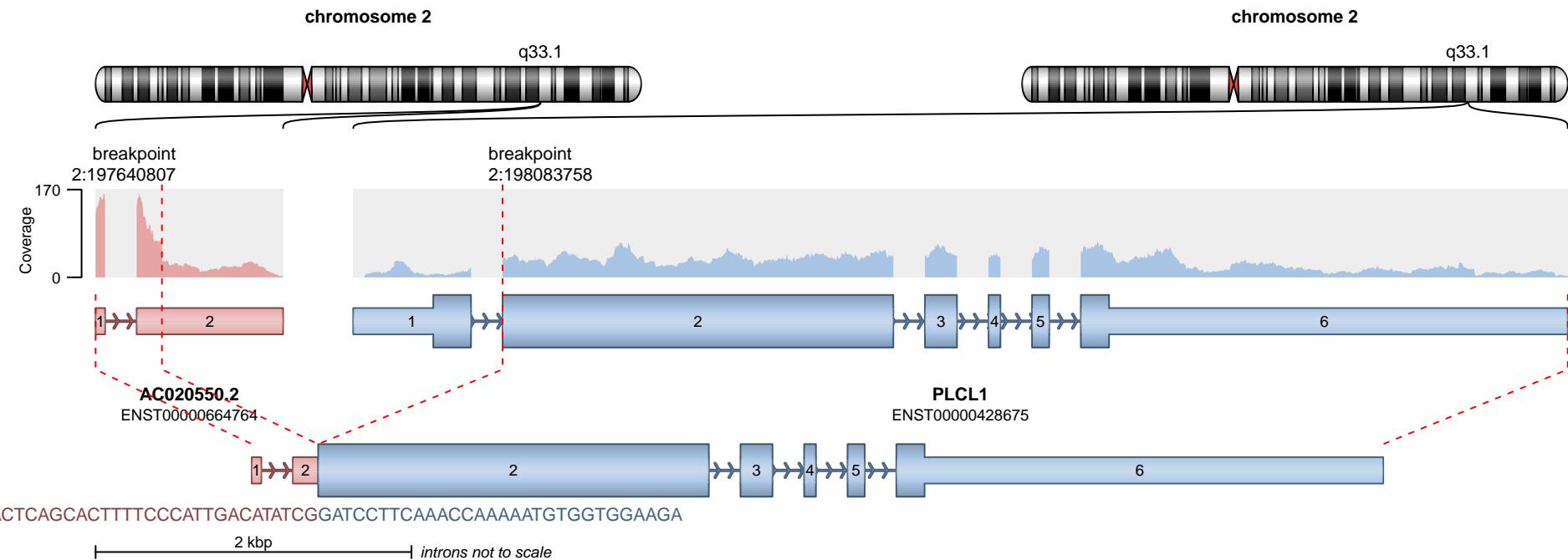
SUPPORTING READ COUNT

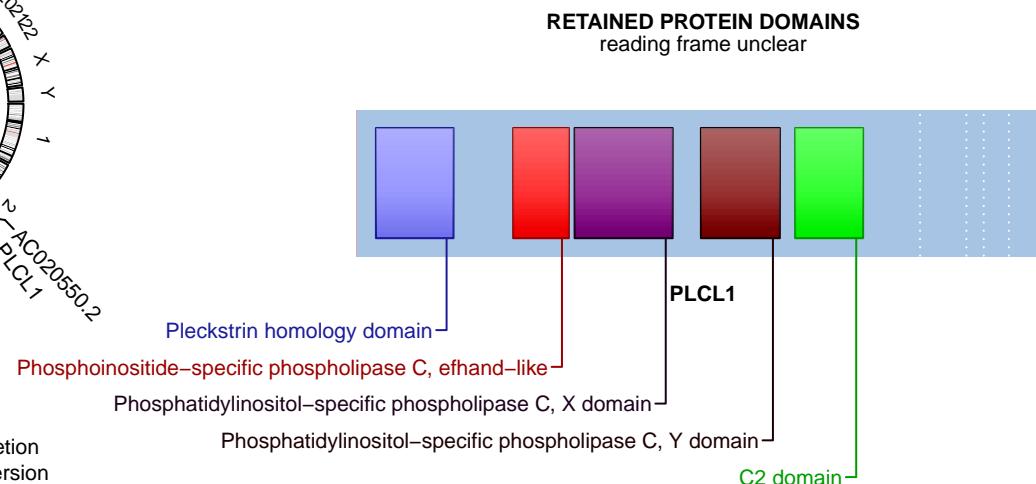
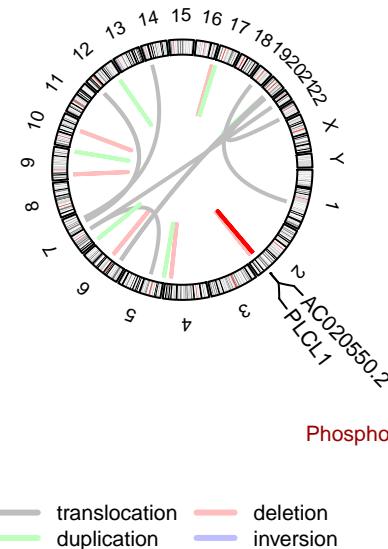
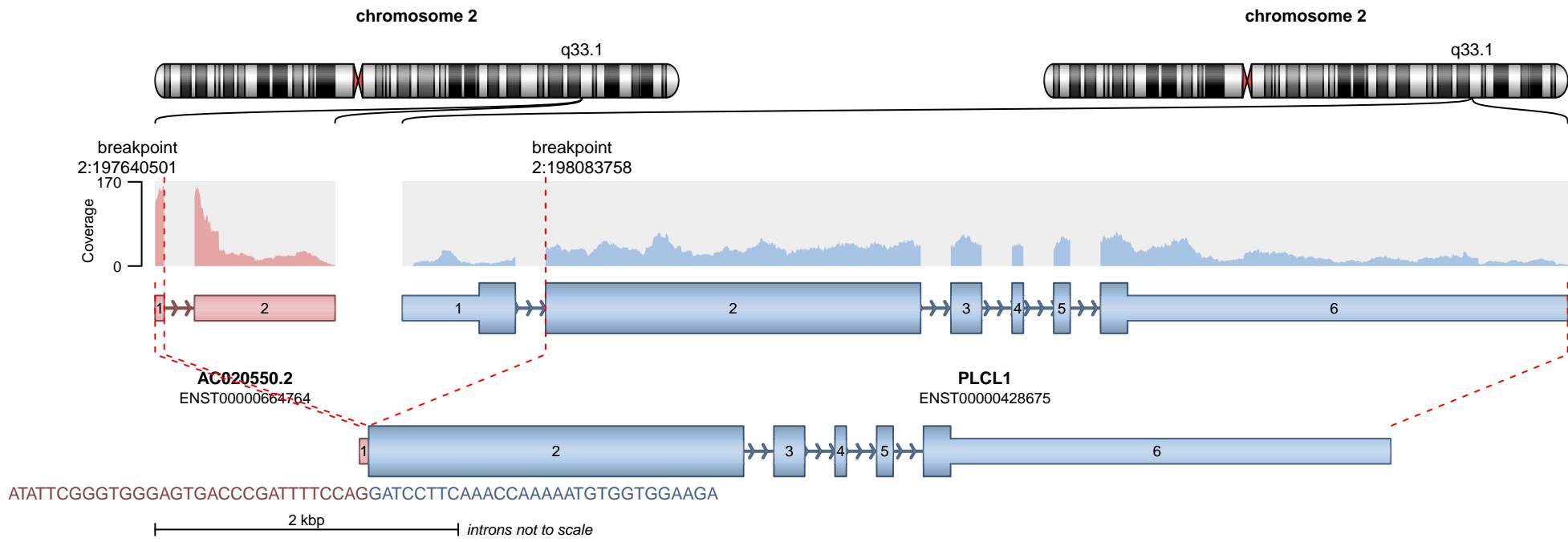
Split reads = 1
Discordant mates = 2



SUPPORTING READ COUNT

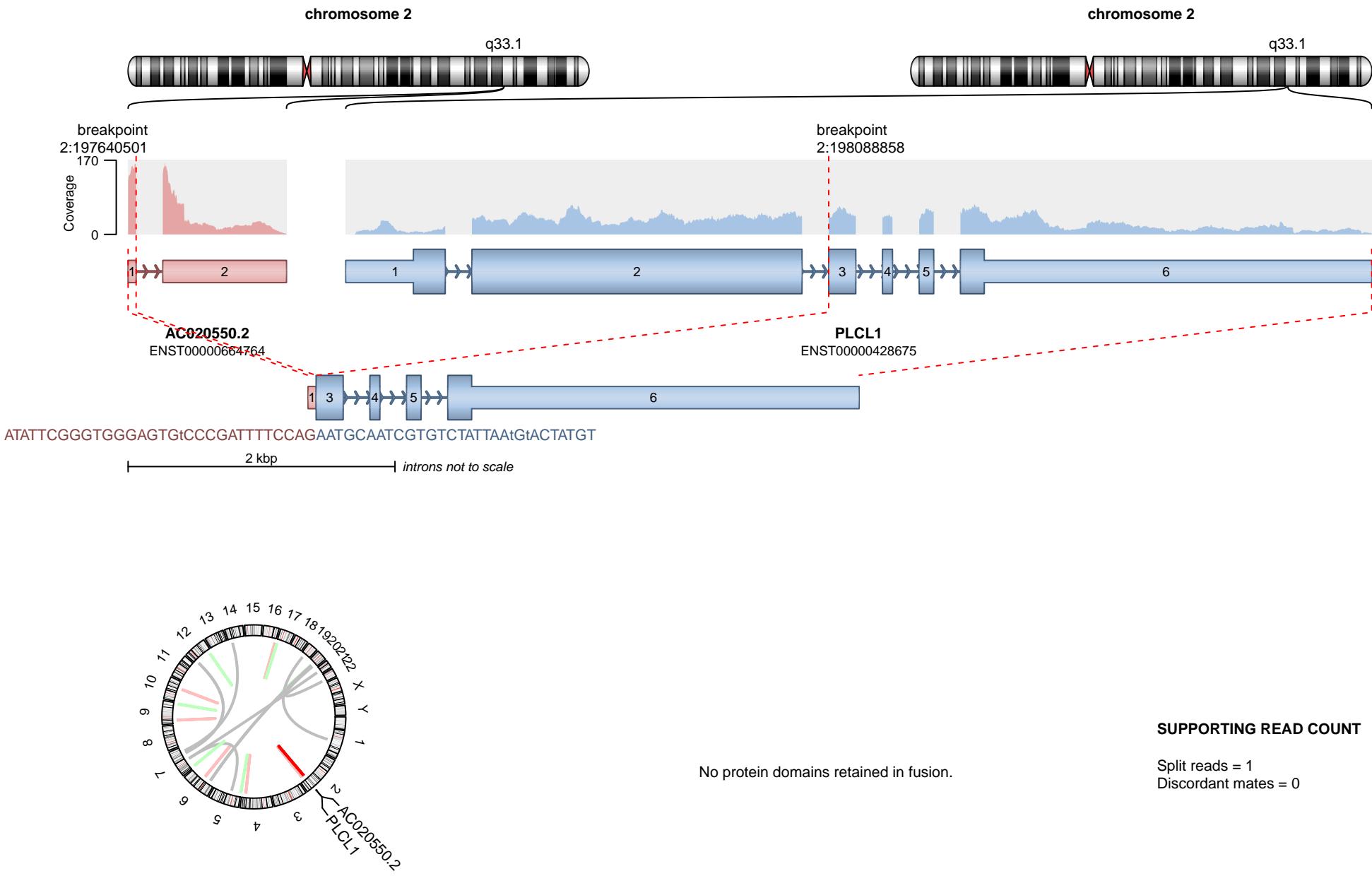
Split reads = 1
Discordant mates = 1



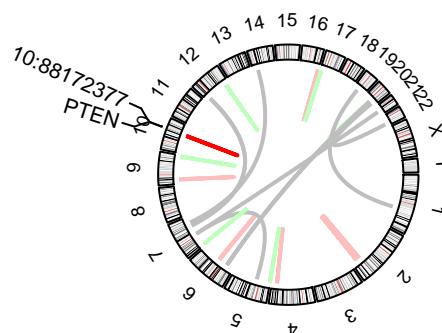
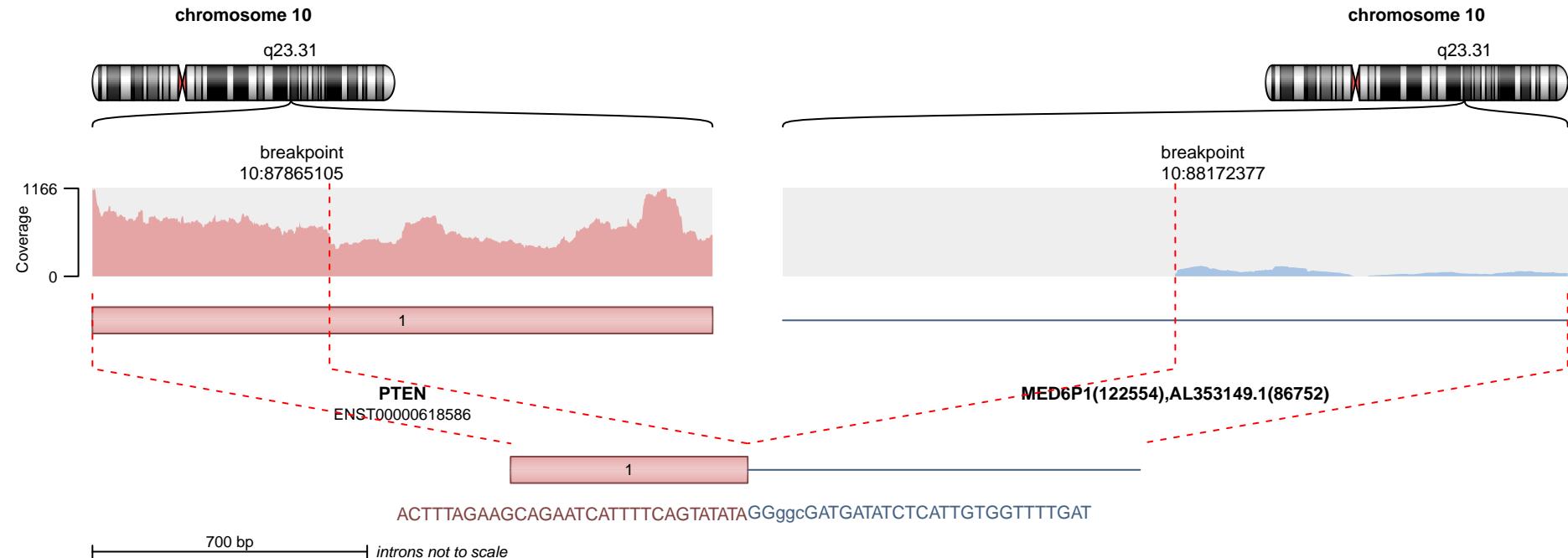


SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0



— translocation — deletion
— duplication — inversion

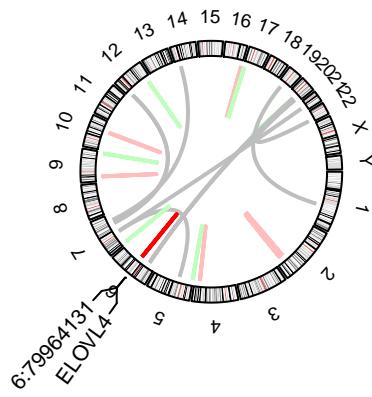
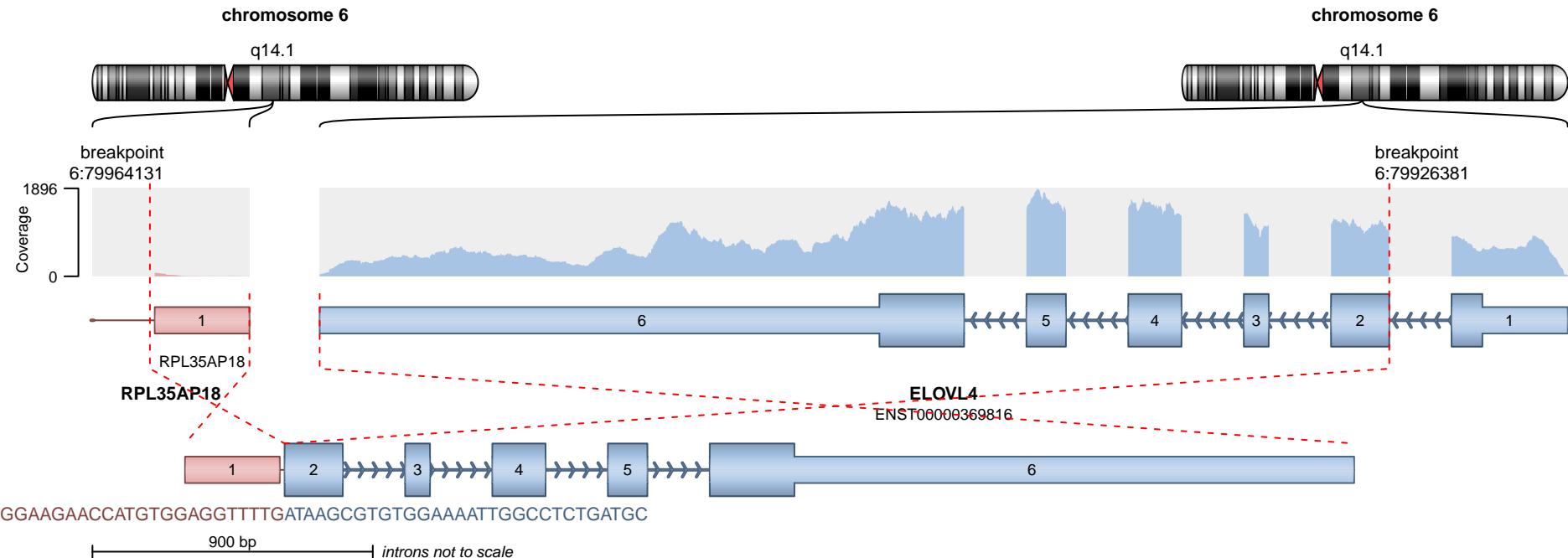


Genes are not protein-coding.

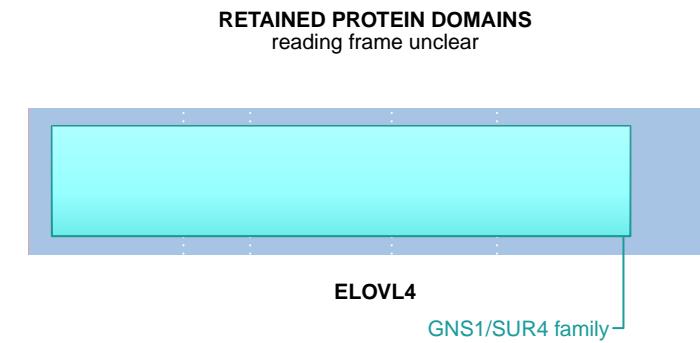
SUPPORTING READ COUNT

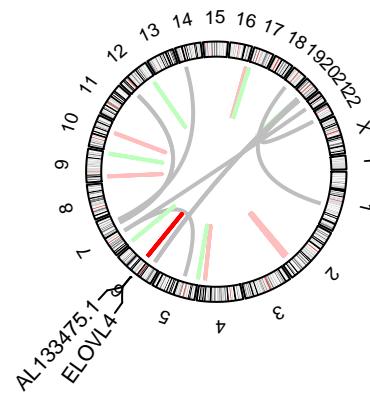
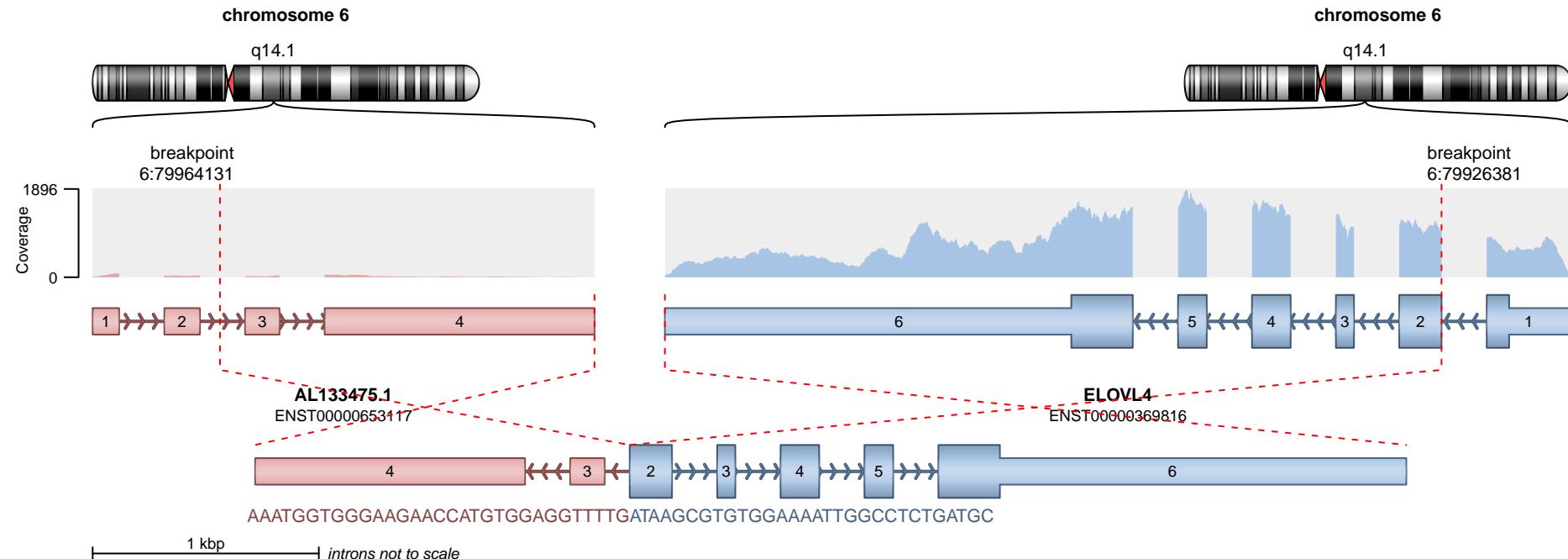
Split reads = 28
Discordant mates = 35

— translocation — deletion
— duplication — inversion

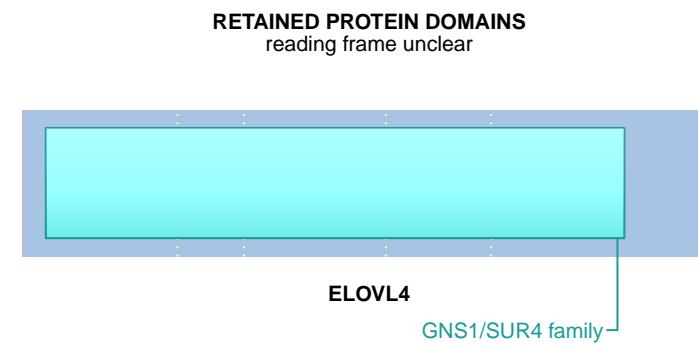


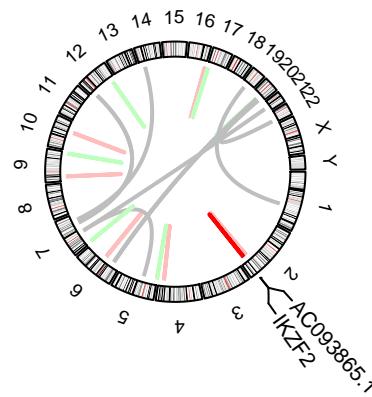
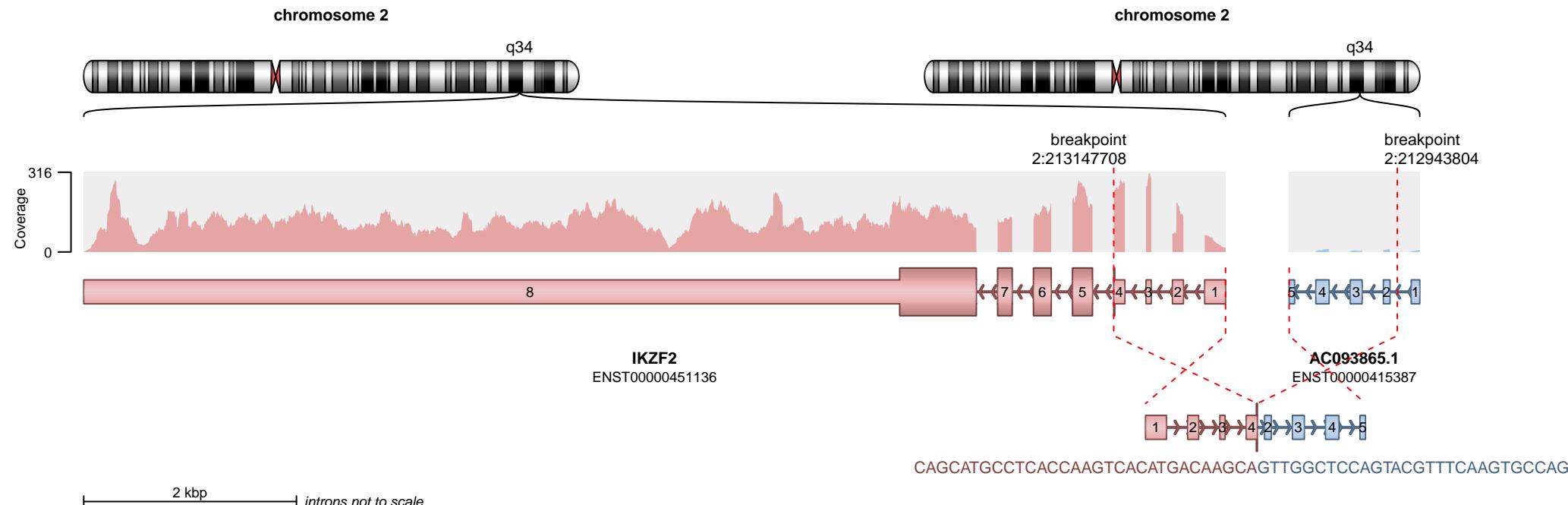
— translocation — deletion
— duplication — inversion





— translocation — deletion
— duplication — inversion



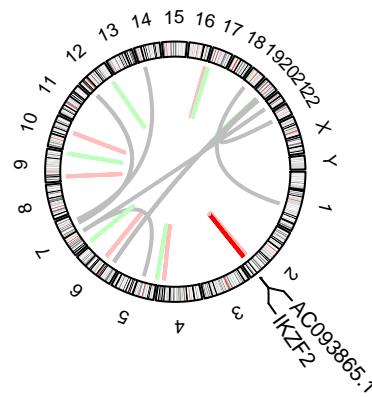
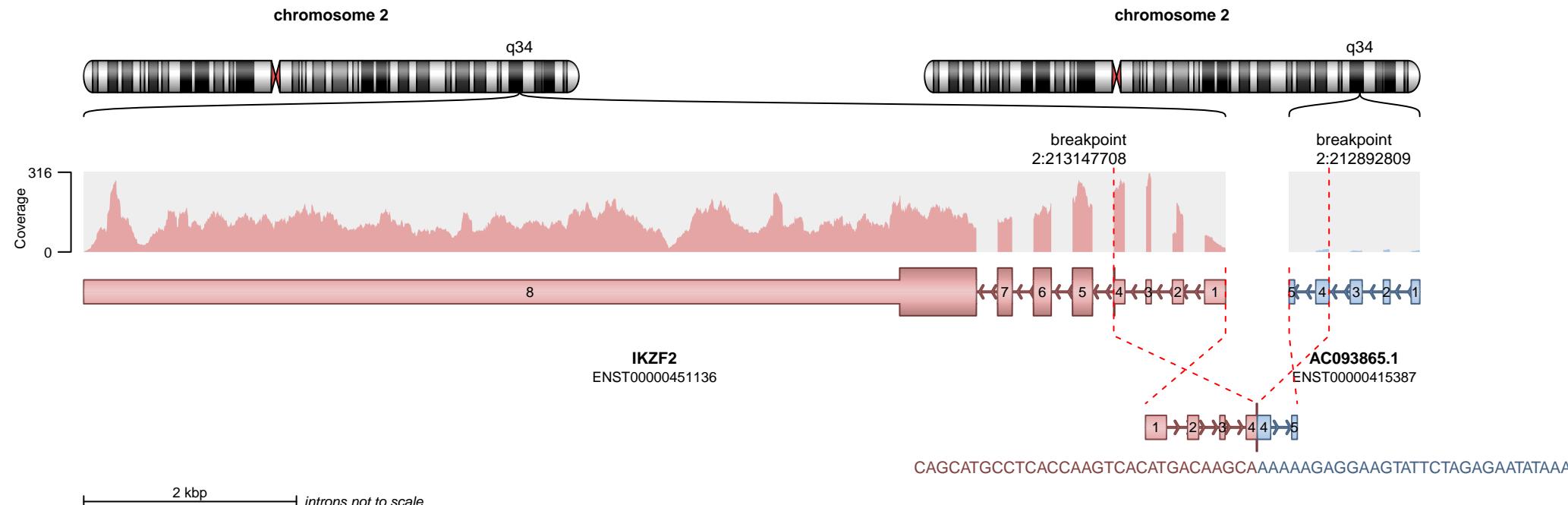


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 4

— translocation — deletion
— duplication — inversion

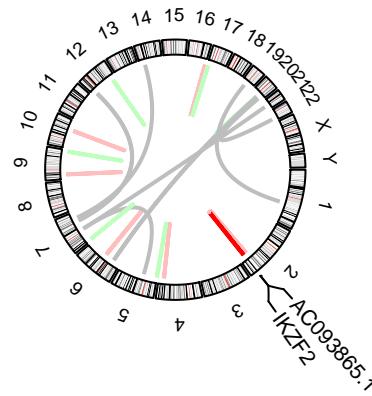
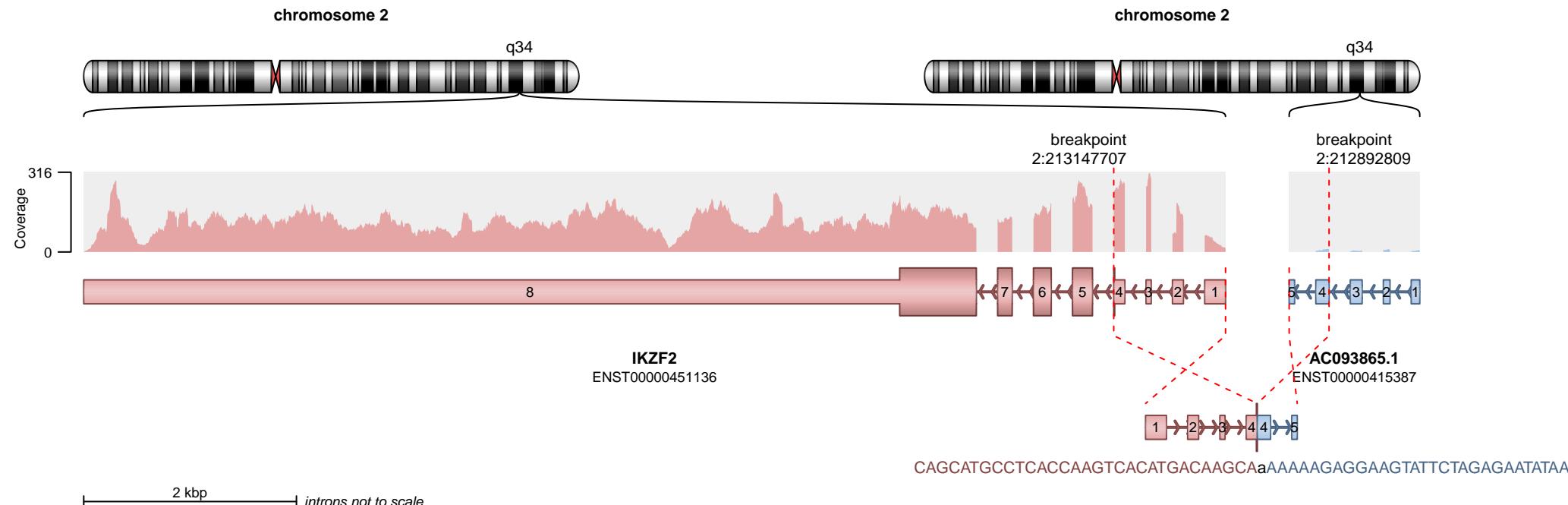


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 2

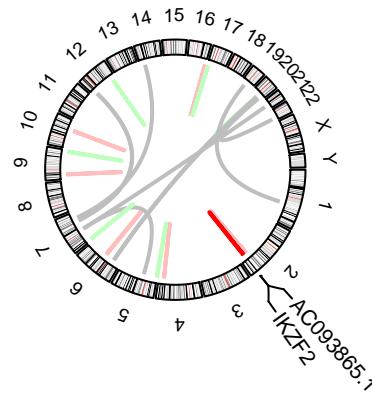
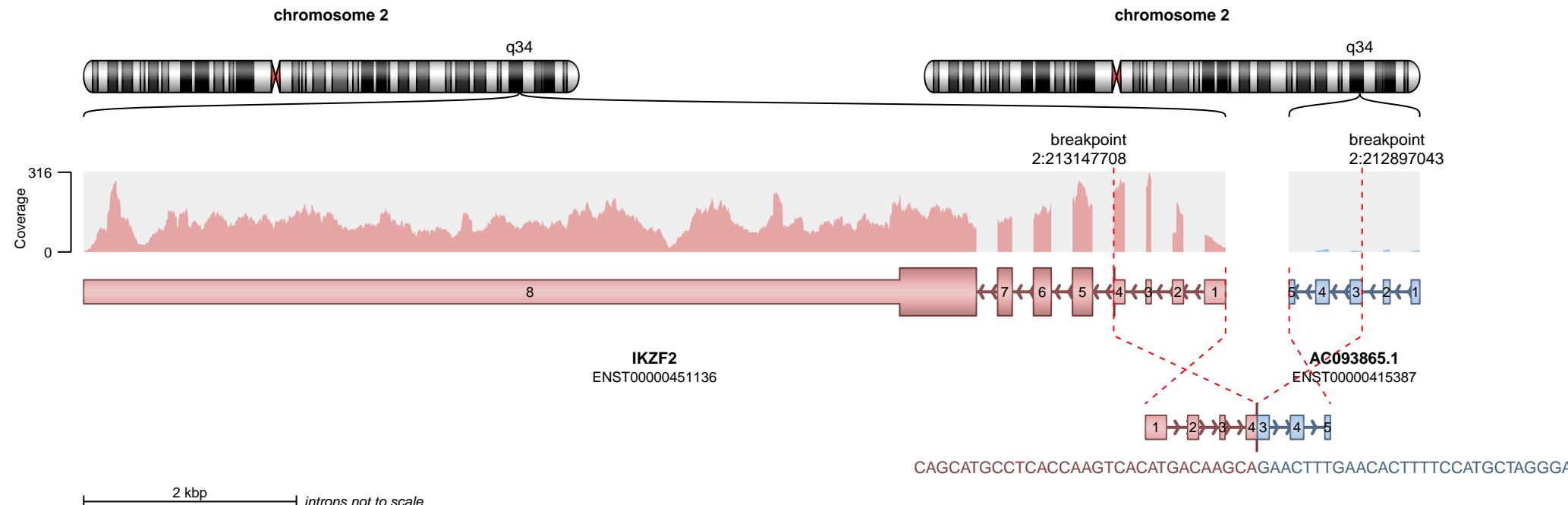


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 2

— translocation — deletion
— duplication — inversion

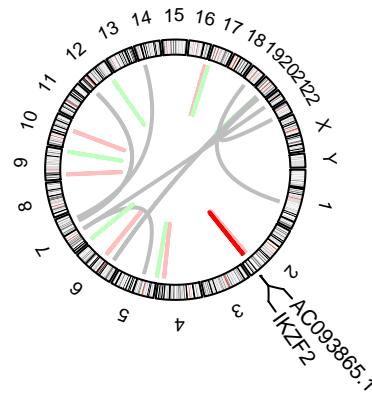
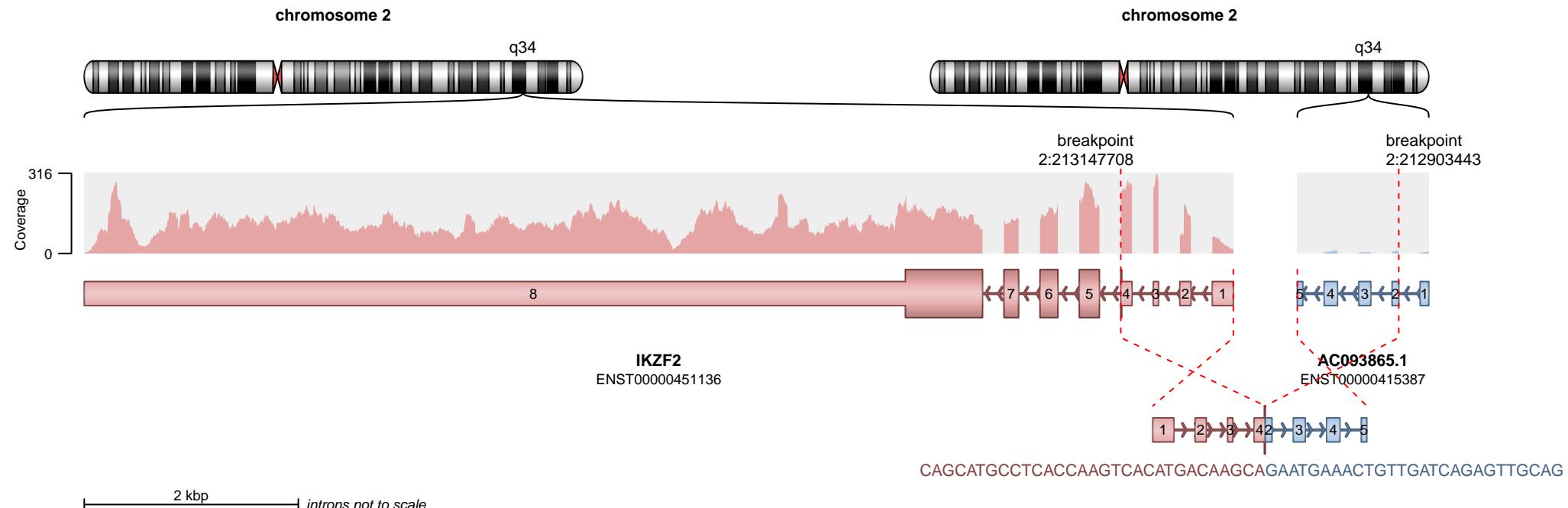


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 2

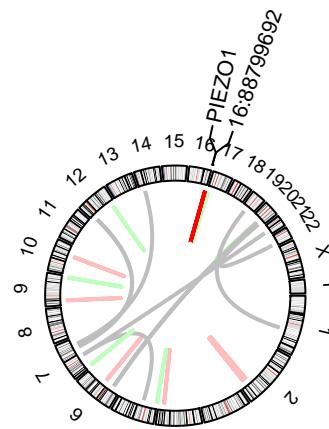
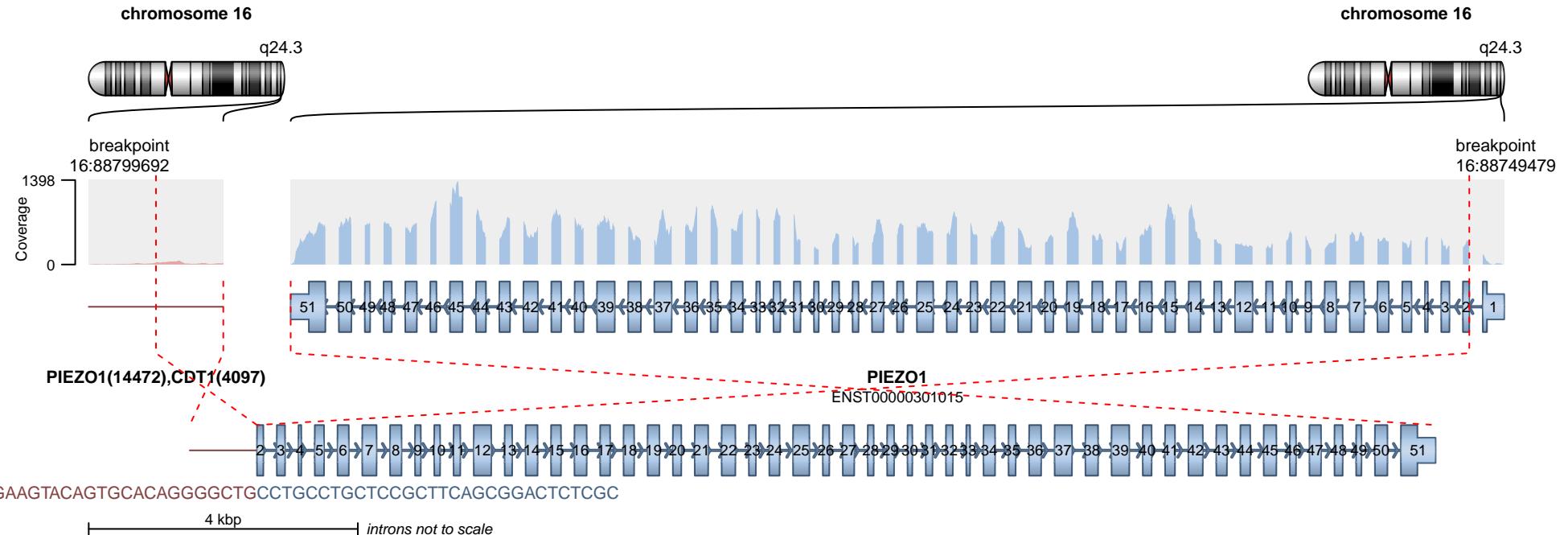


translocation
deletion
duplication
inversion

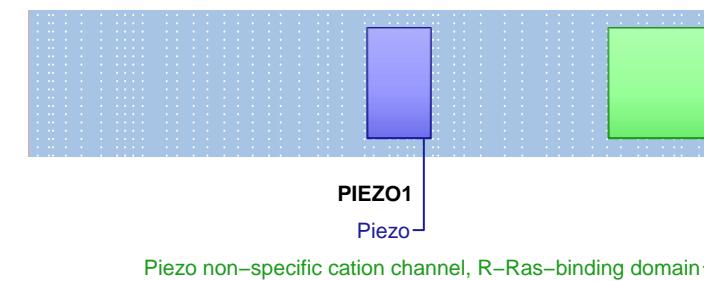
No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 2



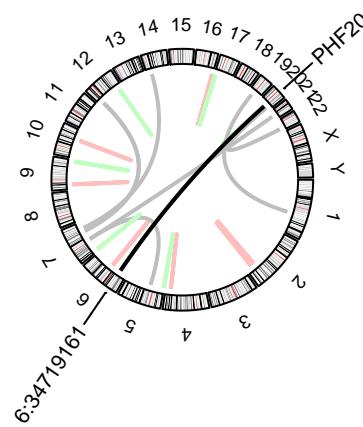
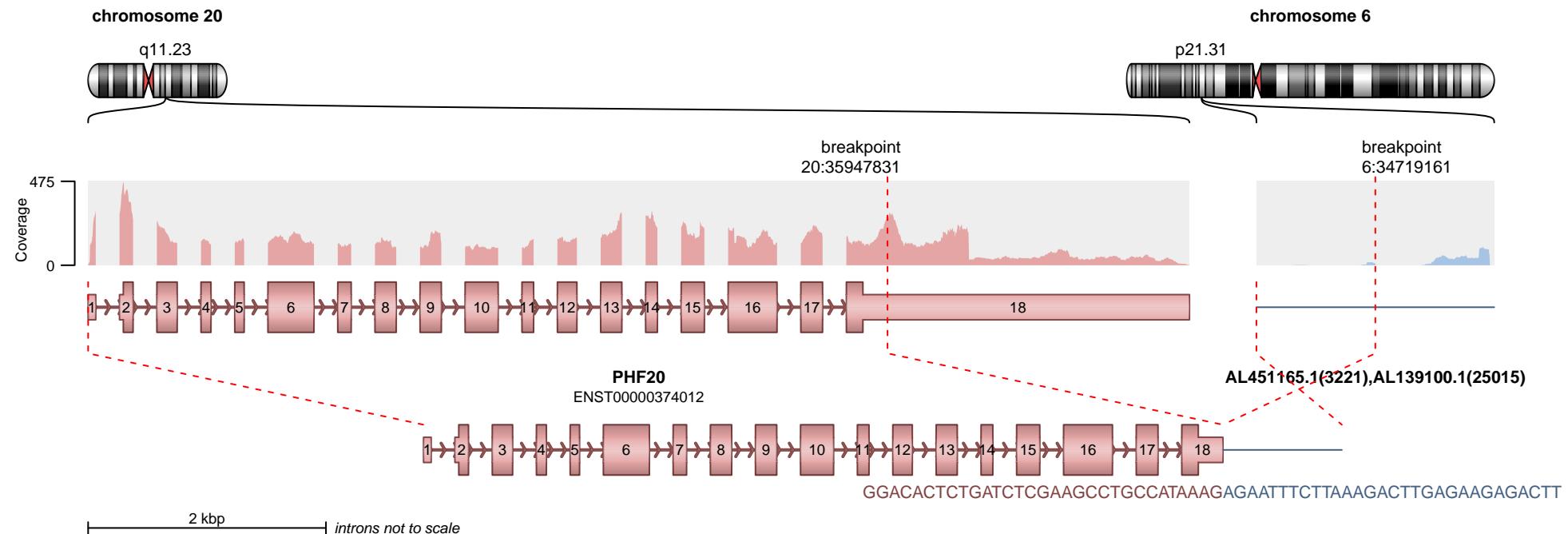
RETAINED PROTEIN DOMAINS reading frame unclear



SUPPORTING READ COUNT

Split reads = 9
Discordant mates = 1

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS

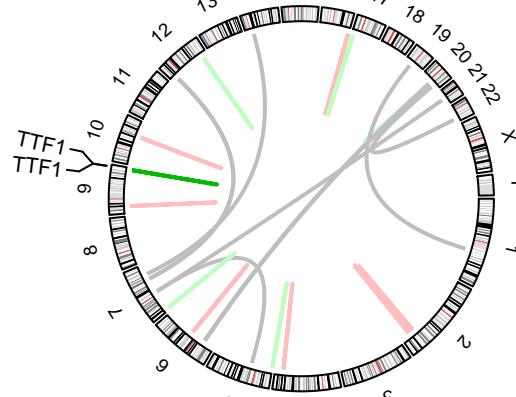
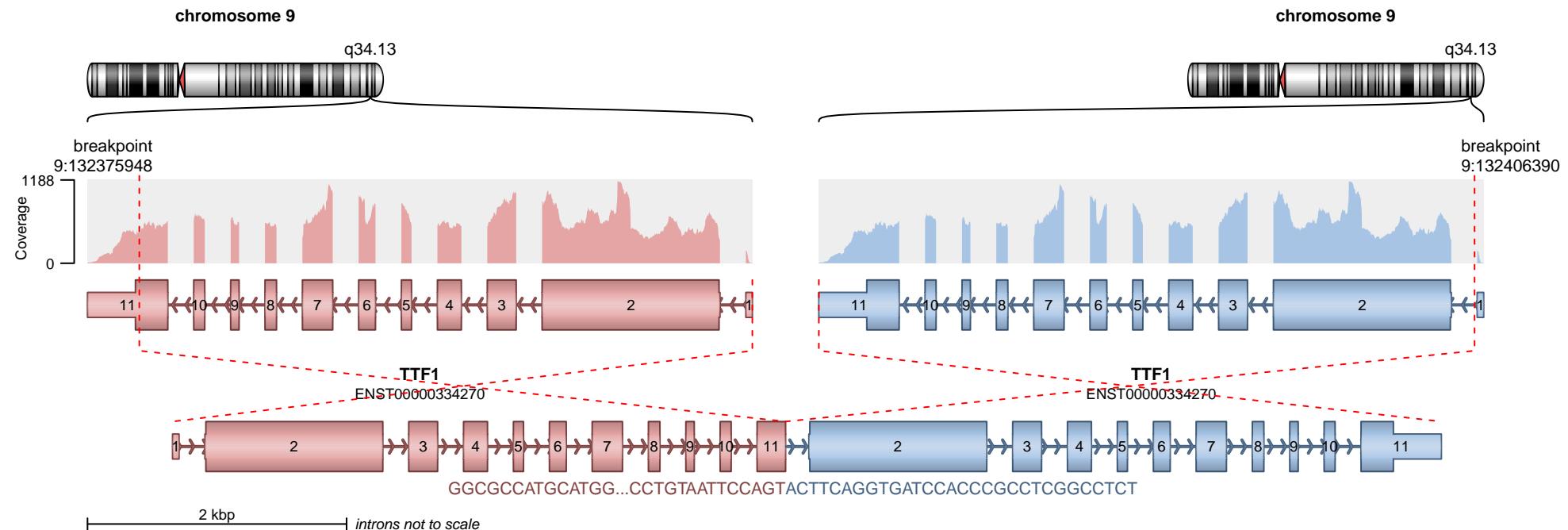
reading frame unclear

The diagram illustrates the domain architecture of a protein. It features a central vertical column of 12 light blue rectangles representing domains, flanked by two columns of 12 light red rectangles each. A horizontal dashed line extends from the top of the central column to the top of the flanking columns. An arrow points from the text "Protein of unknown function (DUF3776)" to the first rectangle in the central column.

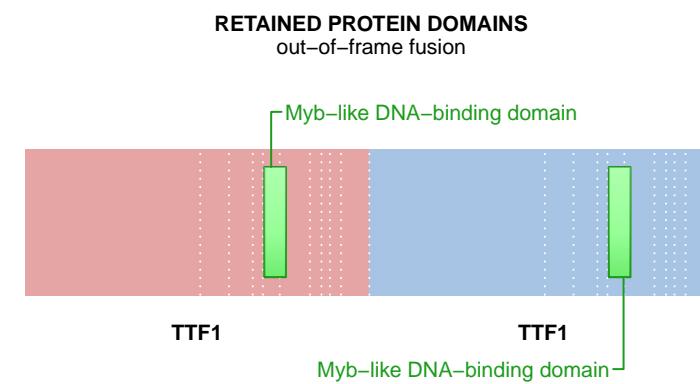
SUPPORTING READ COUNT

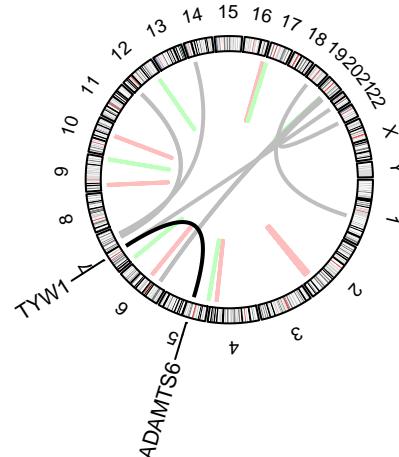
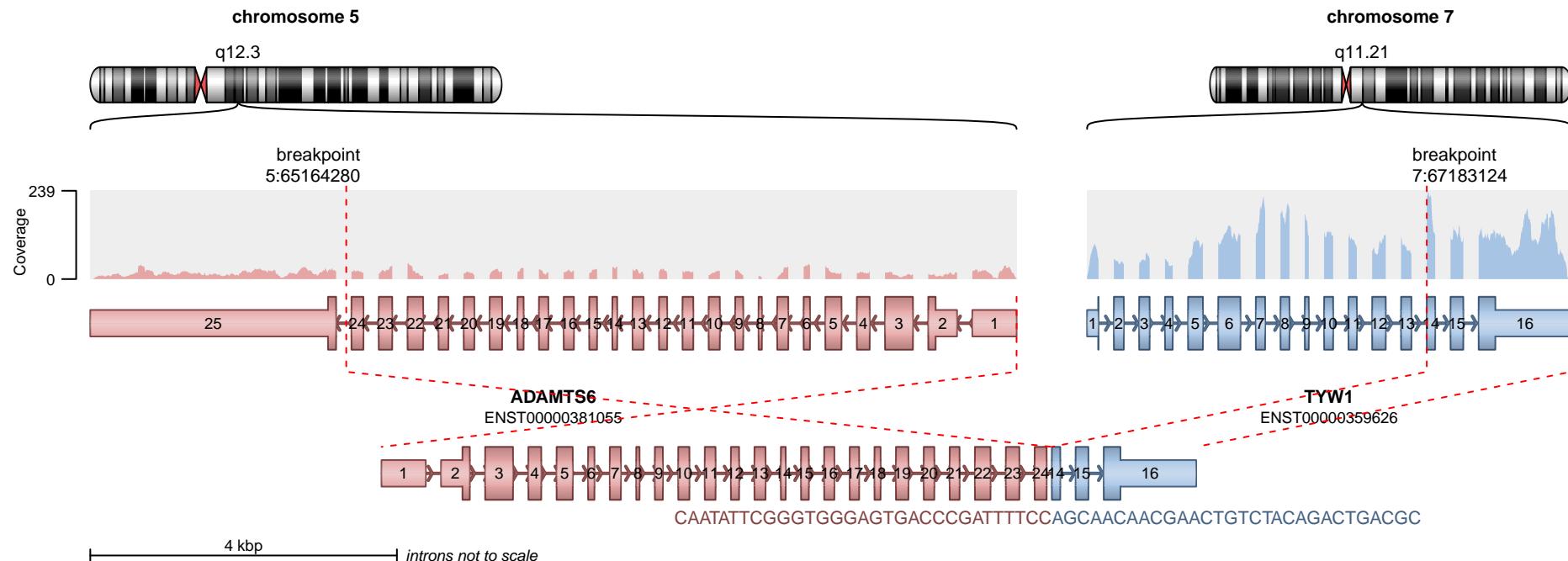
Split reads = 6
Discordant mates = 0

— translocation — deletion
— duplication — inversion

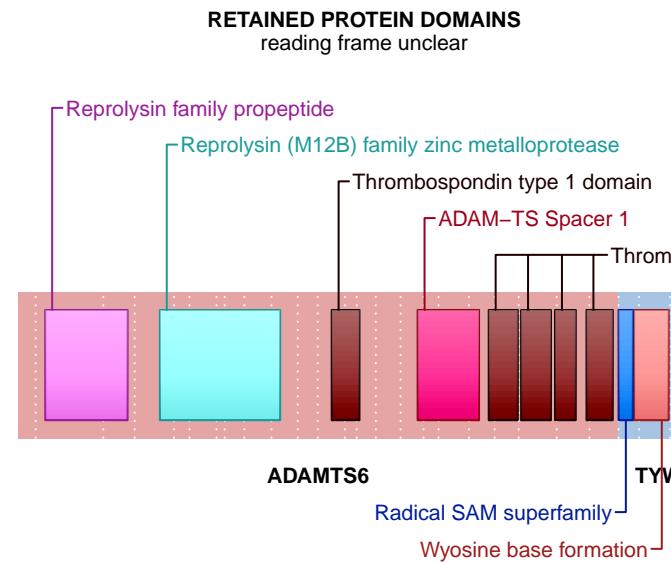


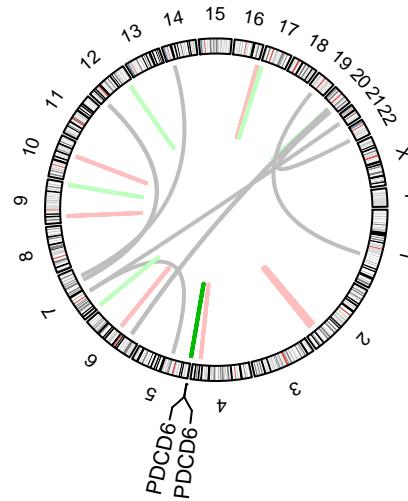
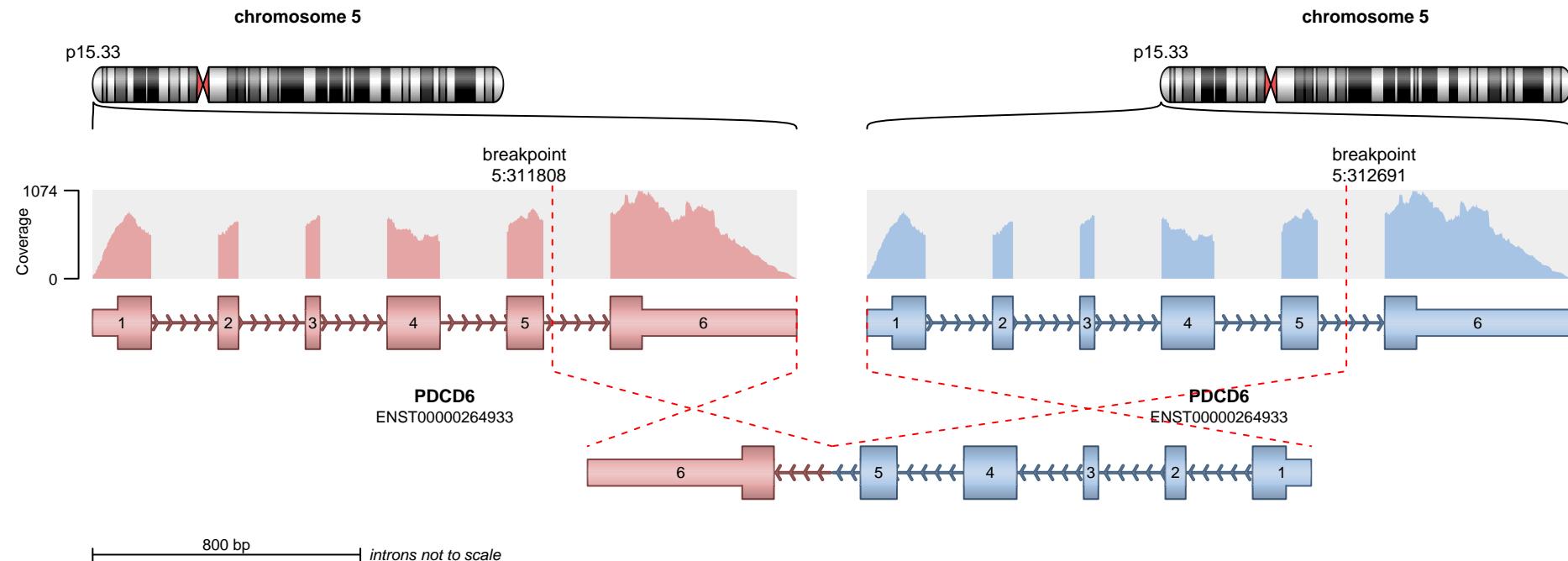
— translocation — deletion
— duplication — inversion





— translocation — deletion
— duplication — inversion



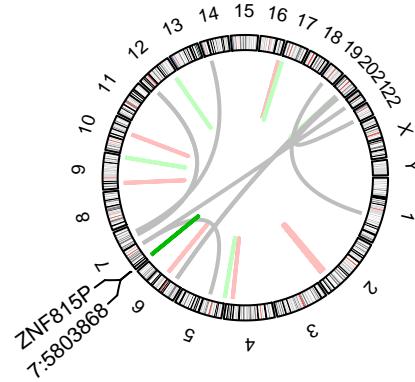
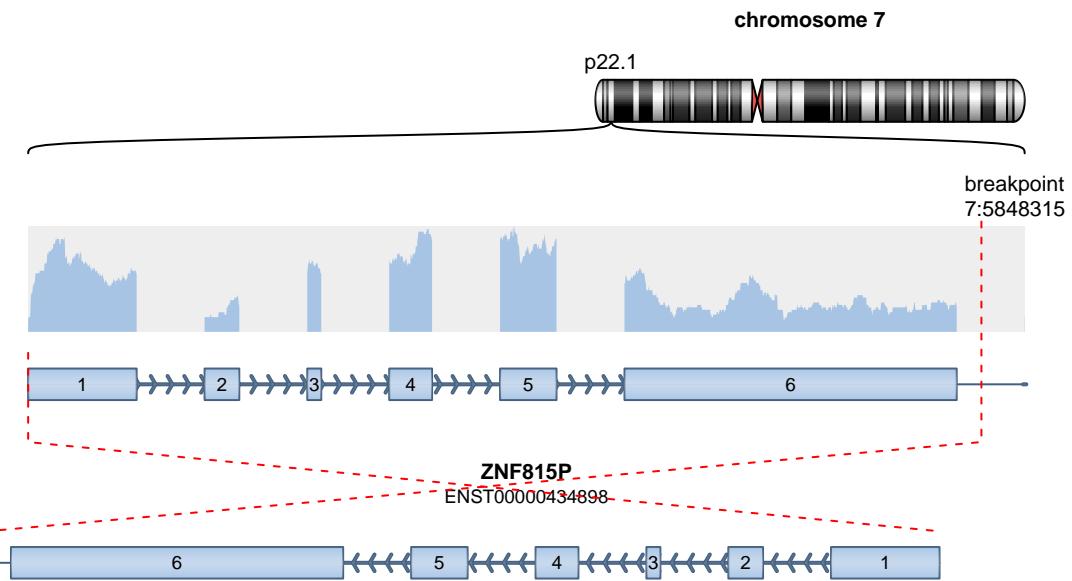
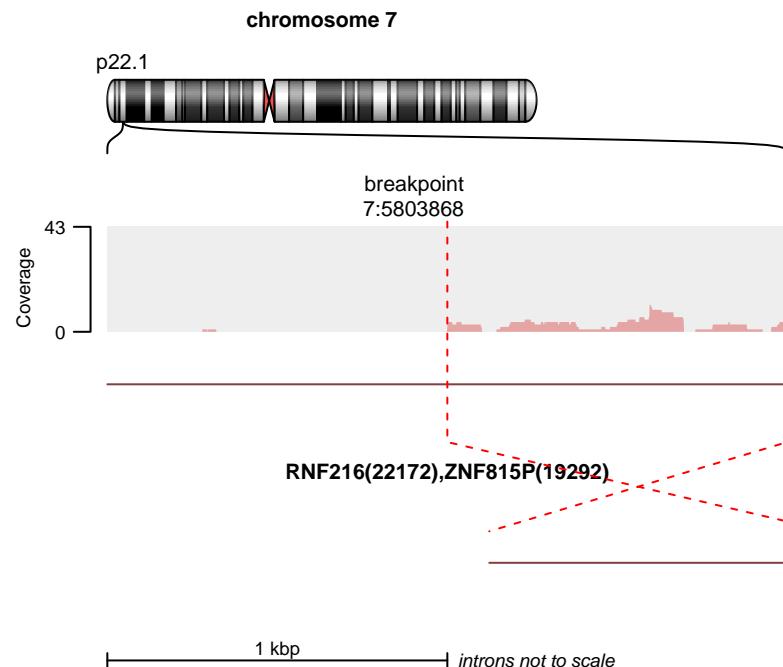


— translocation — deletion
— duplication — inversion

No coding regions due to antisense transcription.

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 2

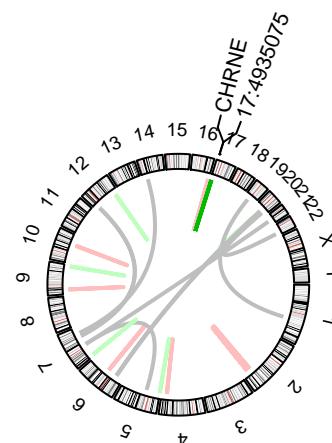
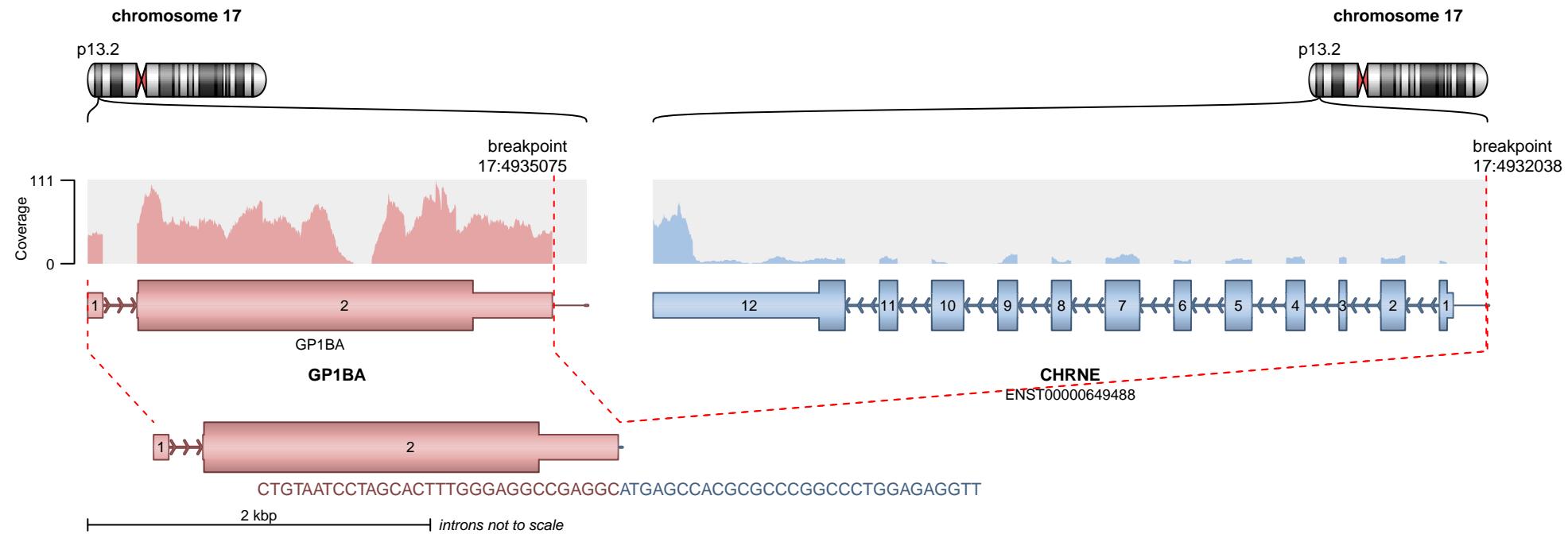


Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 3

— translocation — deletion
— duplication — inversion

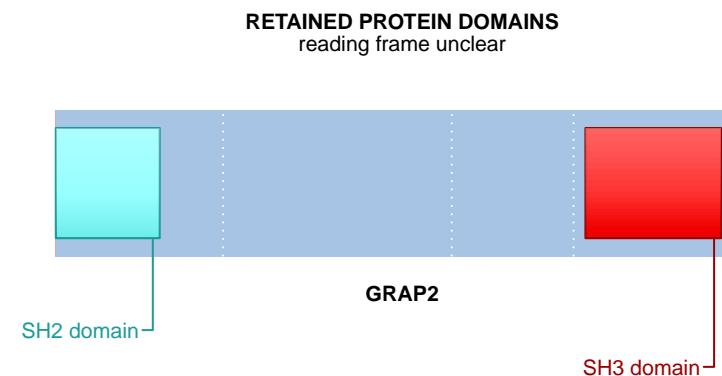
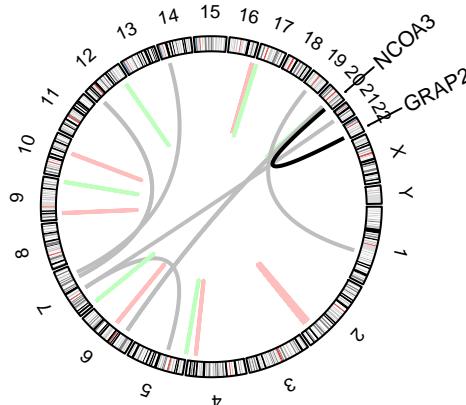
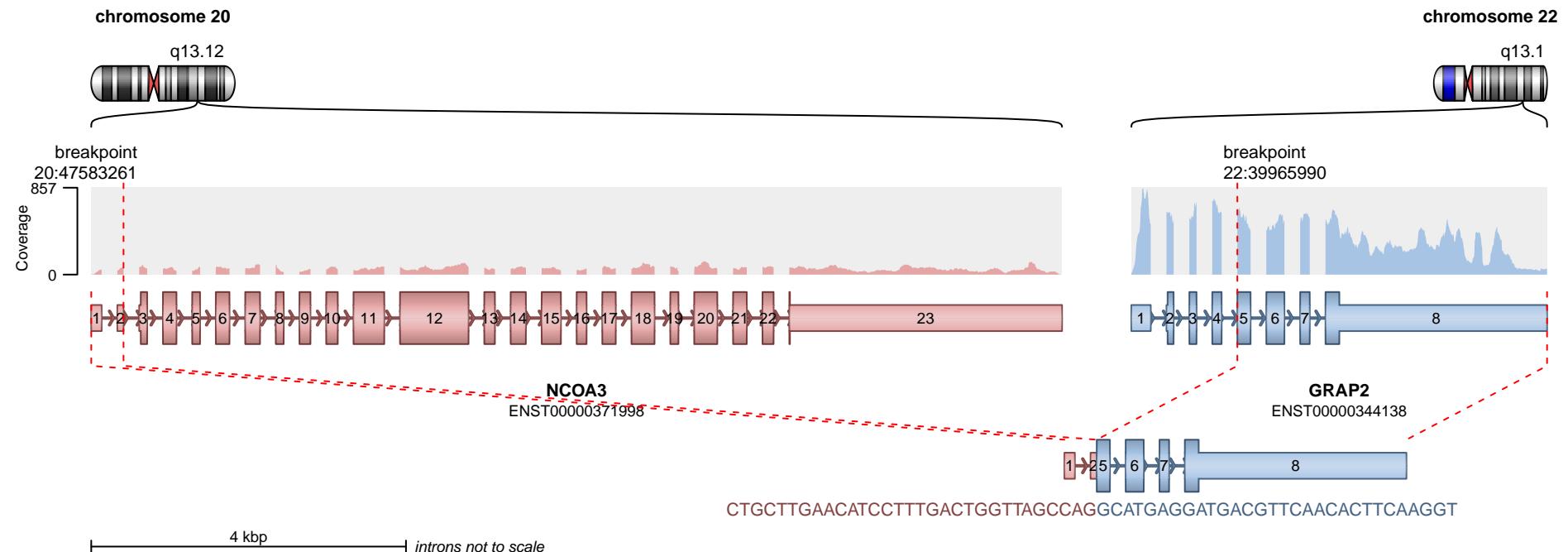


No coding regions retained in fusion transcript.

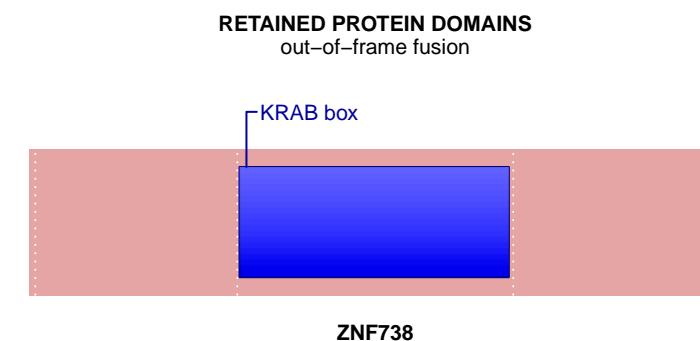
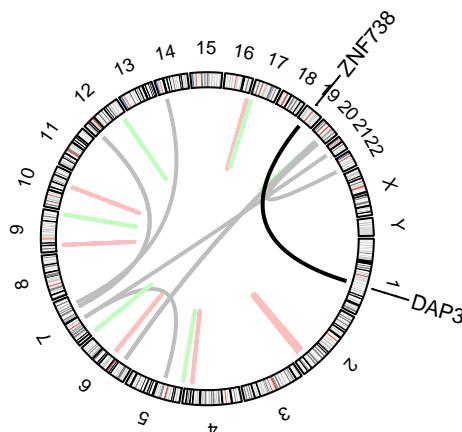
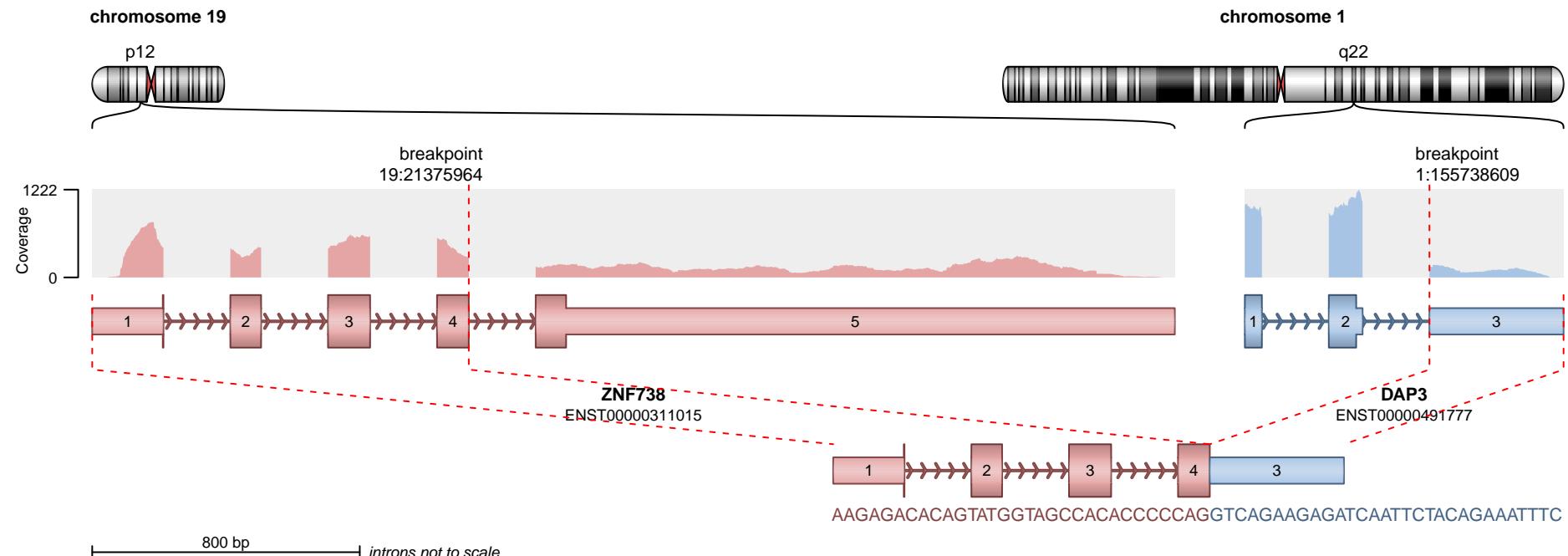
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 3

— translocation — deletion
— duplication — inversion



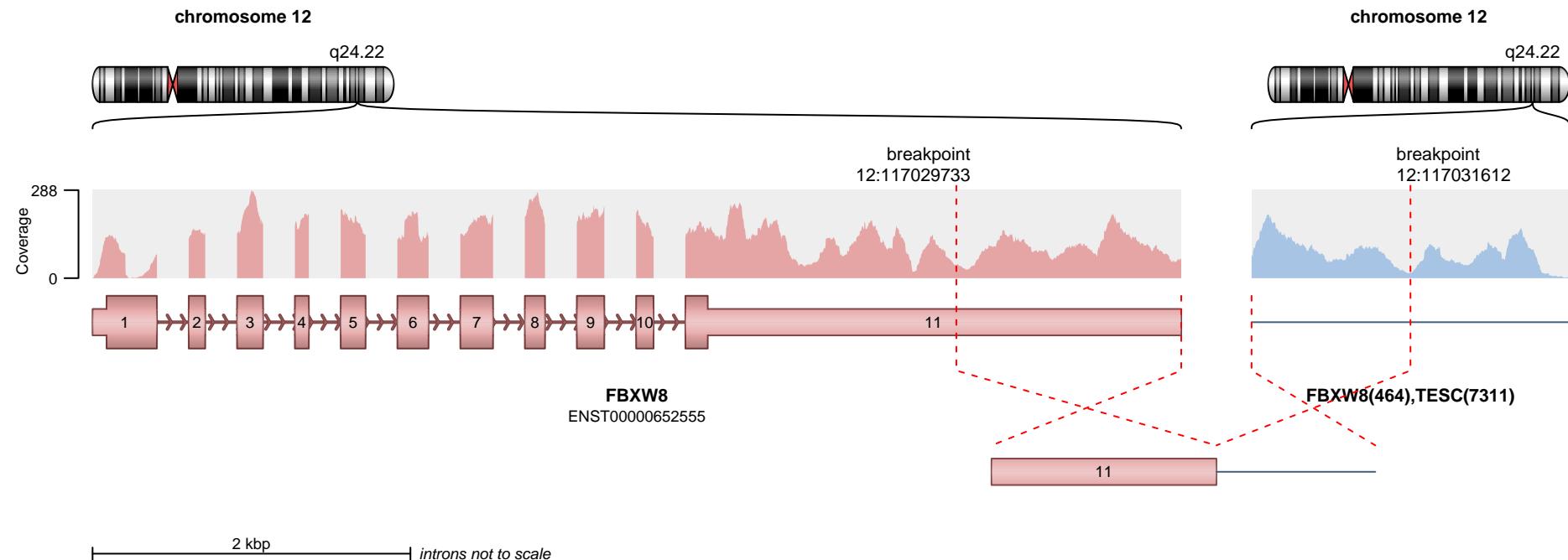
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

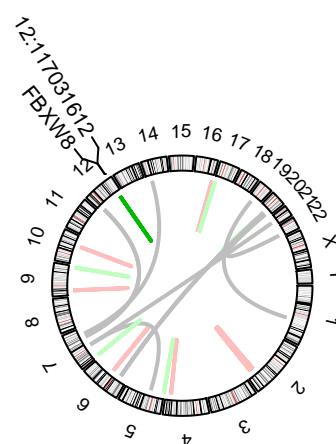
— translocation — deletion
— duplication — inversion



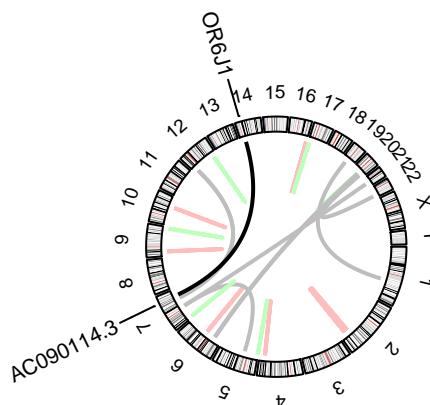
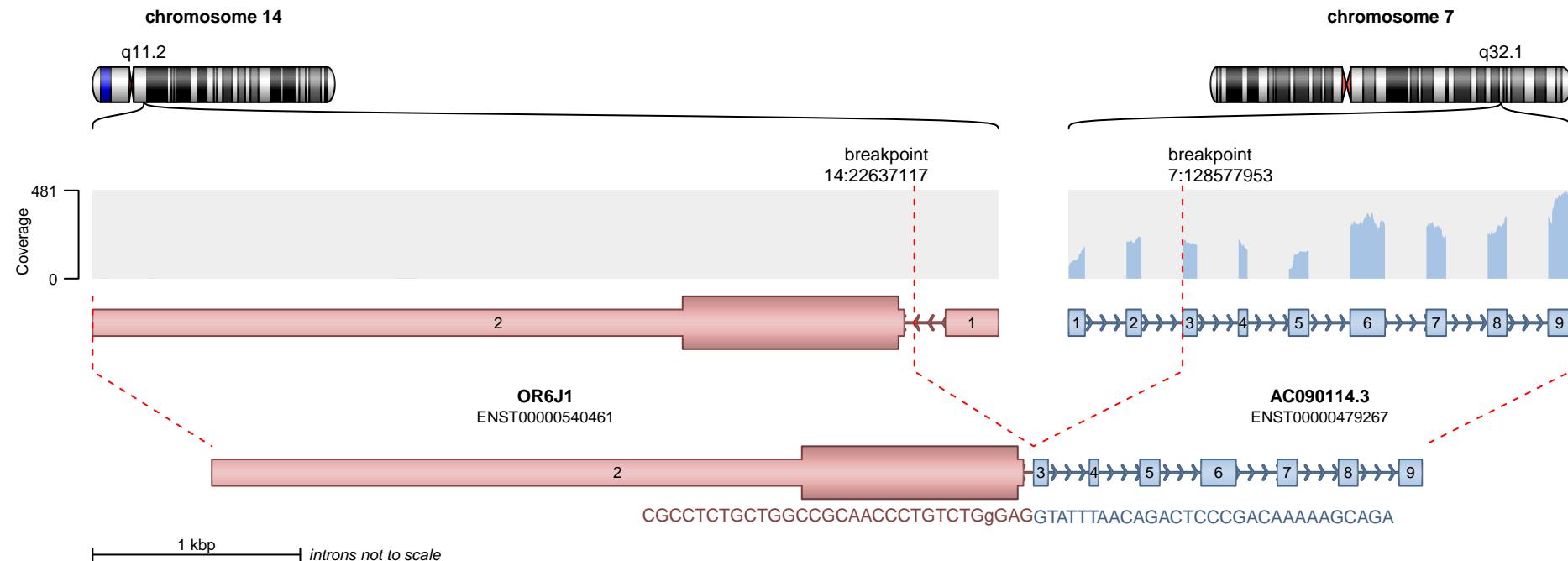
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 2

No coding regions retained in fusion transcript.



— translocation — deletion
— duplication — inversion

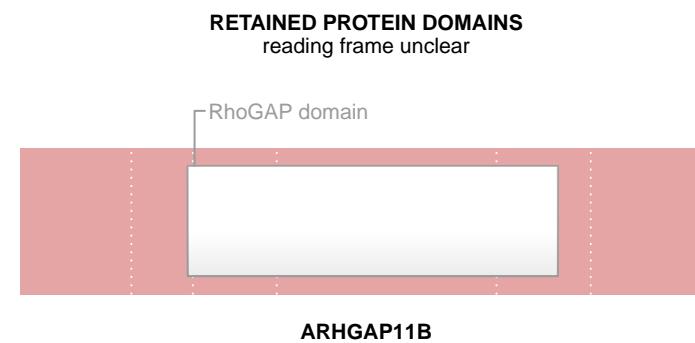
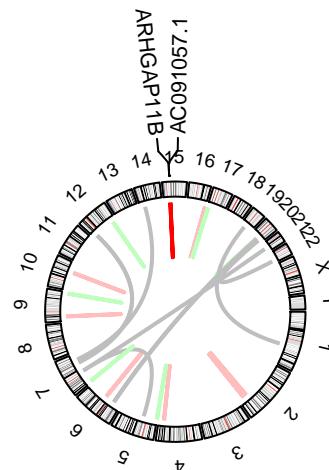
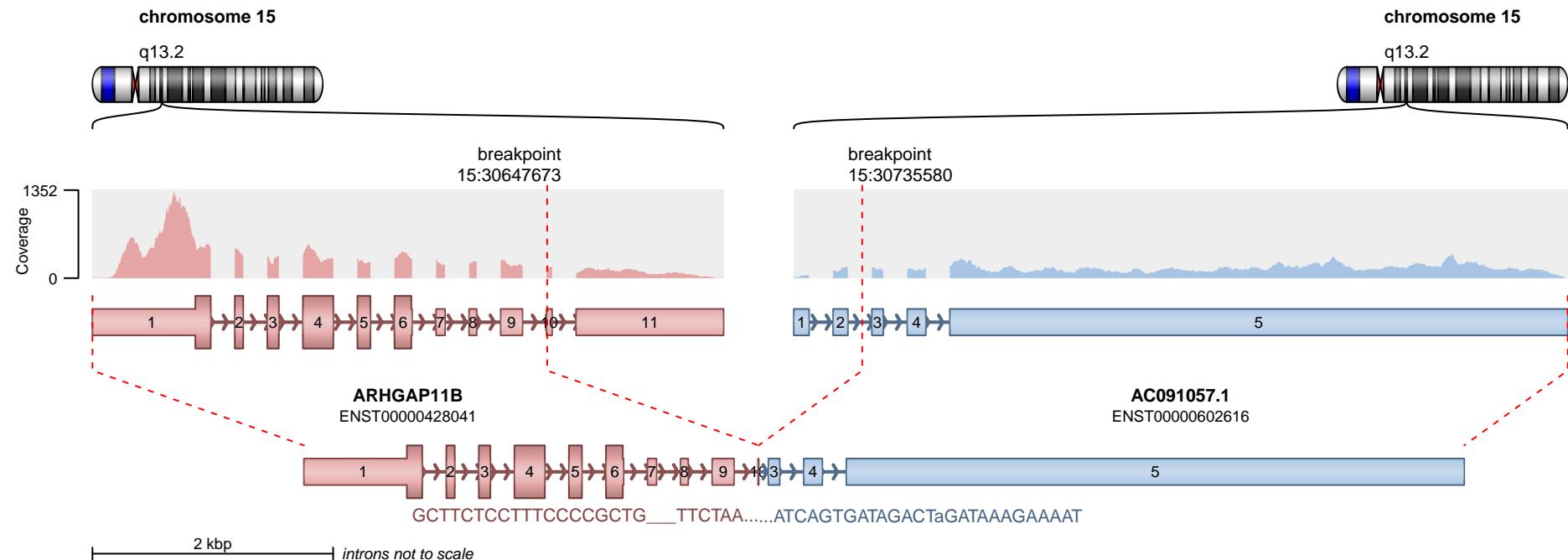


No coding regions due to antisense transcription.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 2

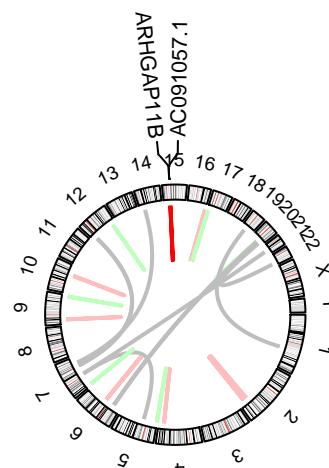
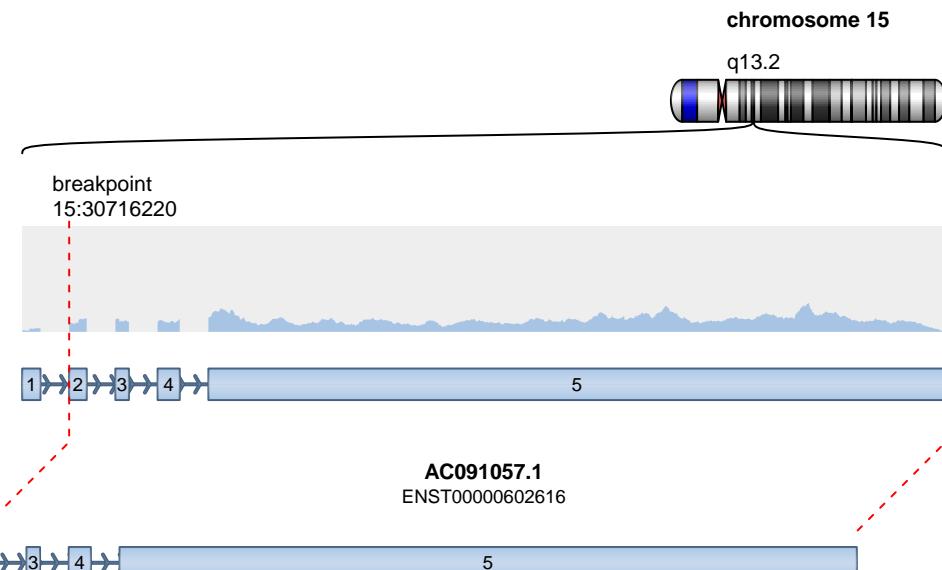
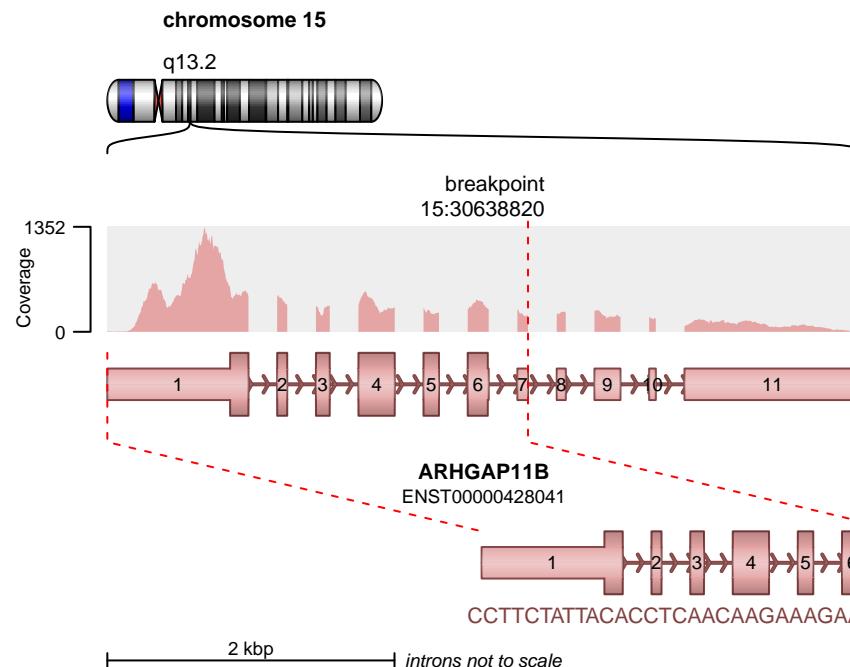
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

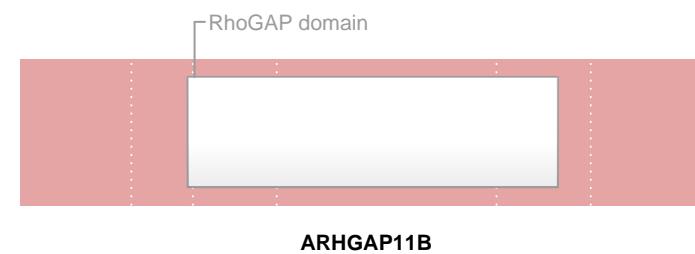
Split reads = 0
Discordant mates = 16

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS

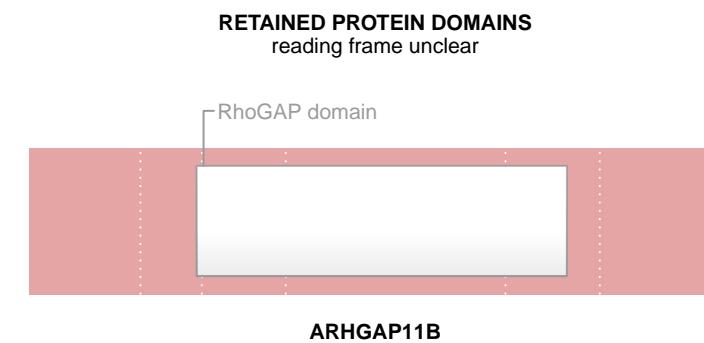
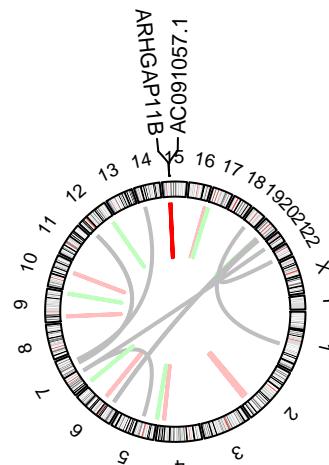
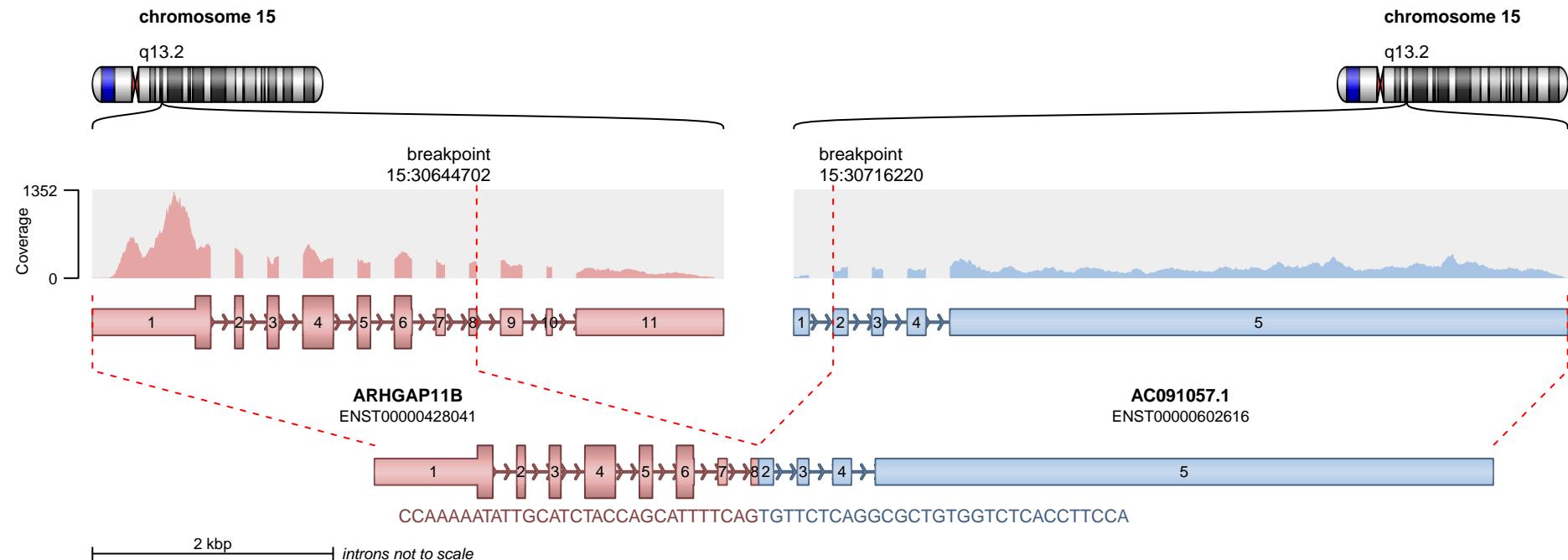
reading frame unclear



SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 0

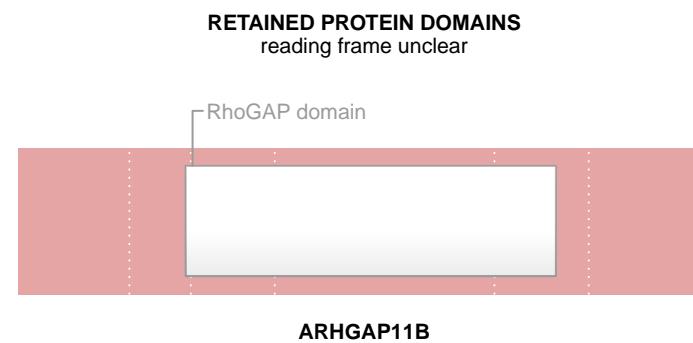
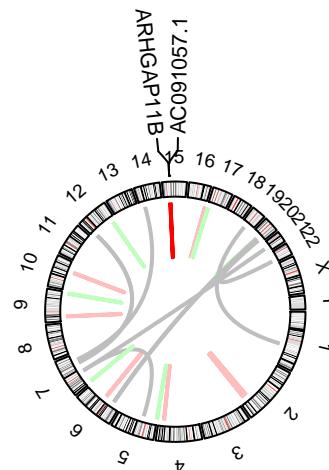
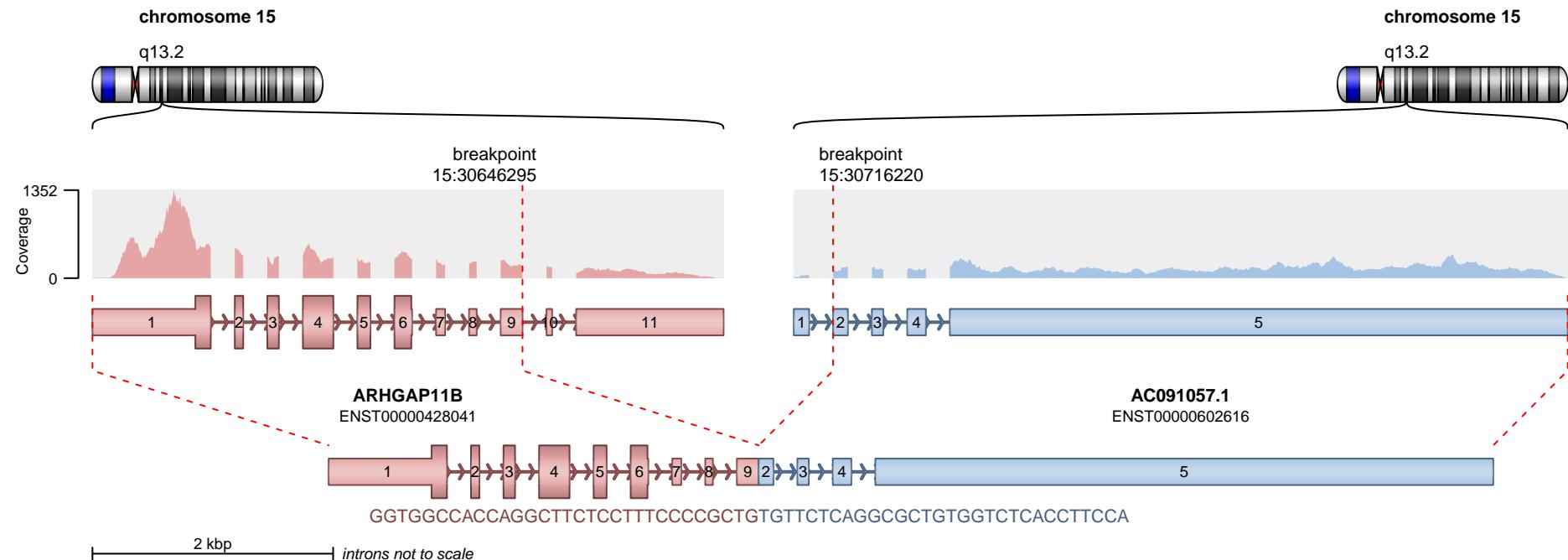
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 0

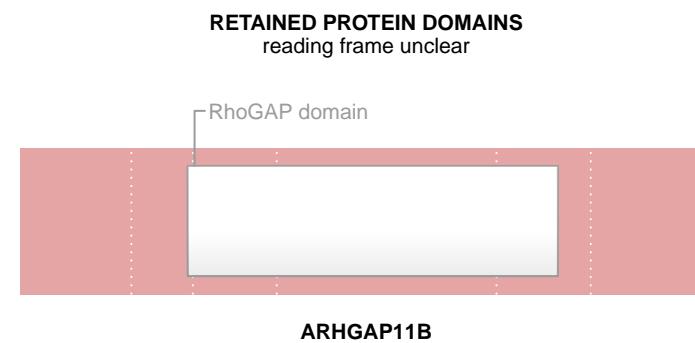
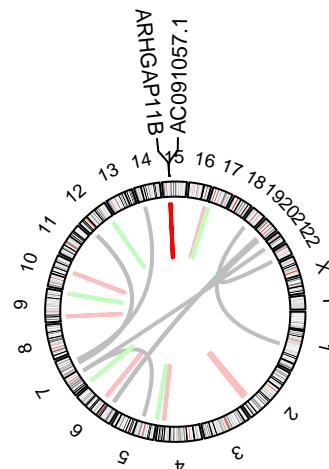
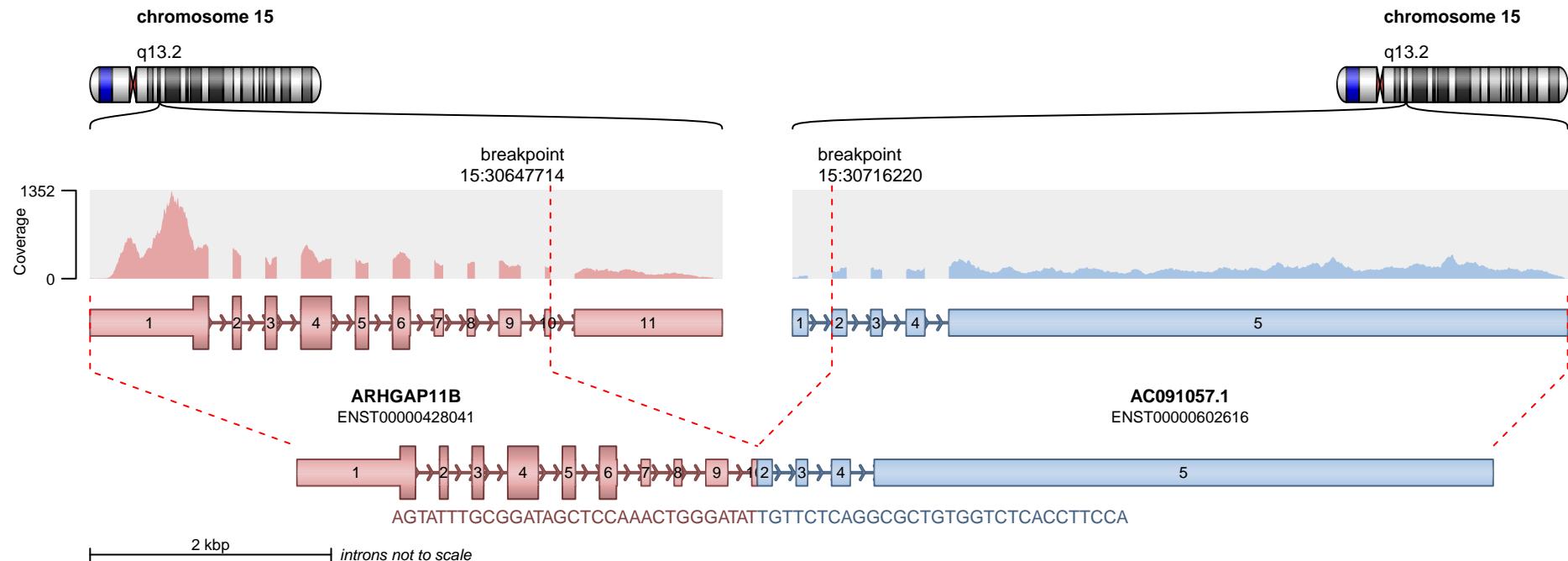
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 0

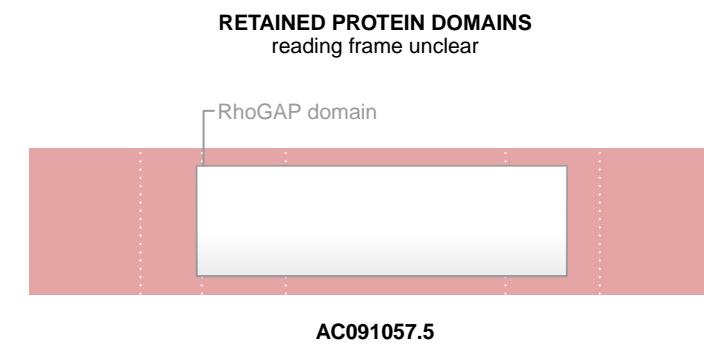
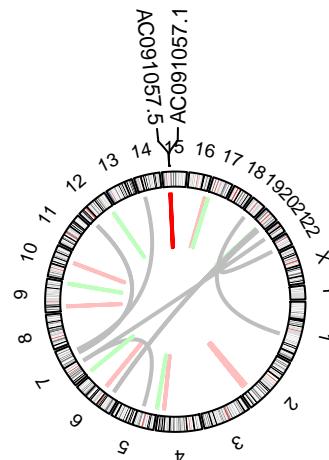
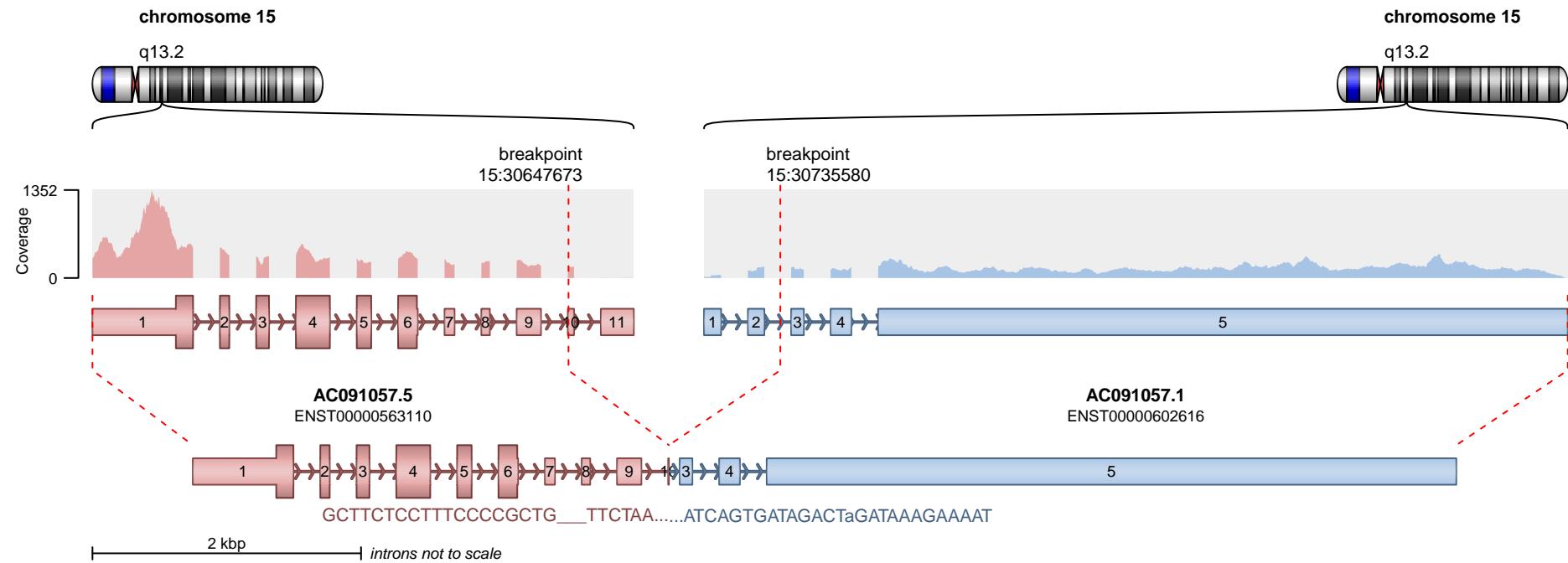
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 0

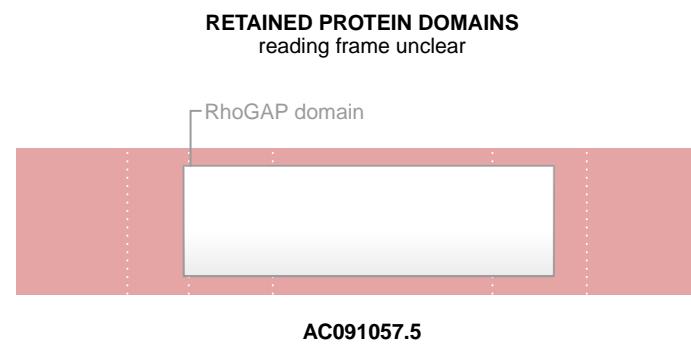
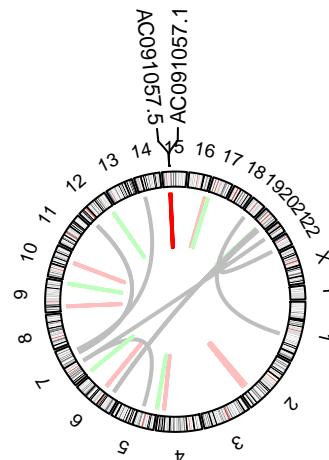
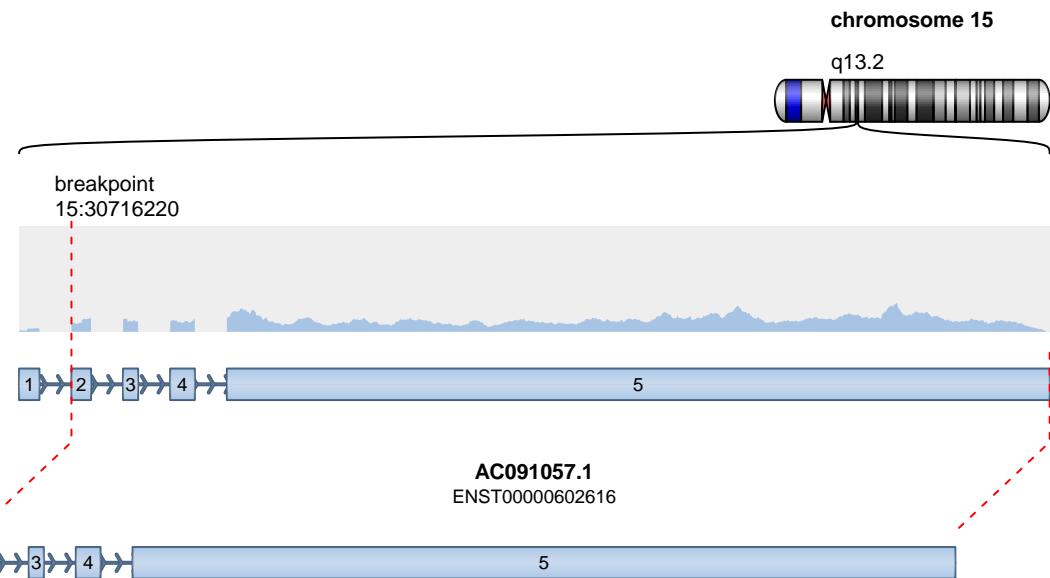
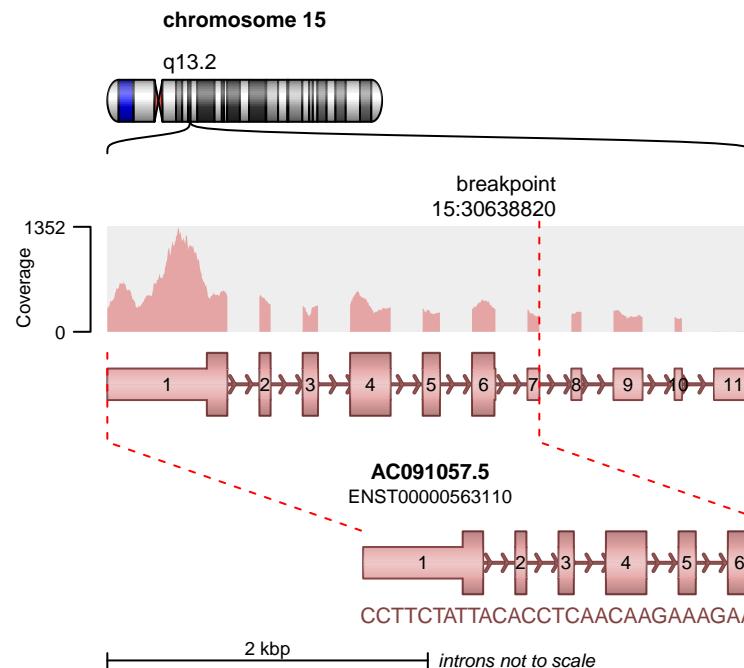
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 16

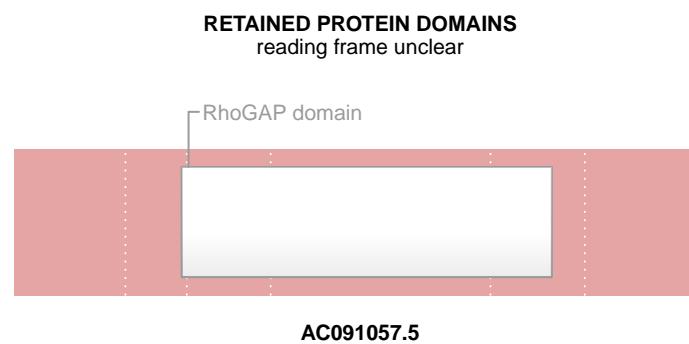
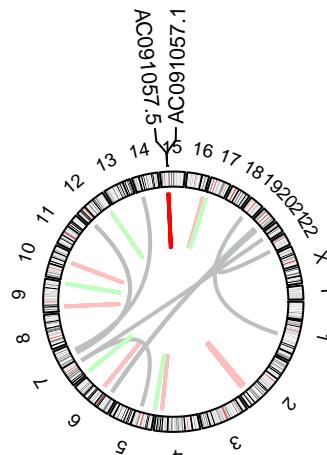
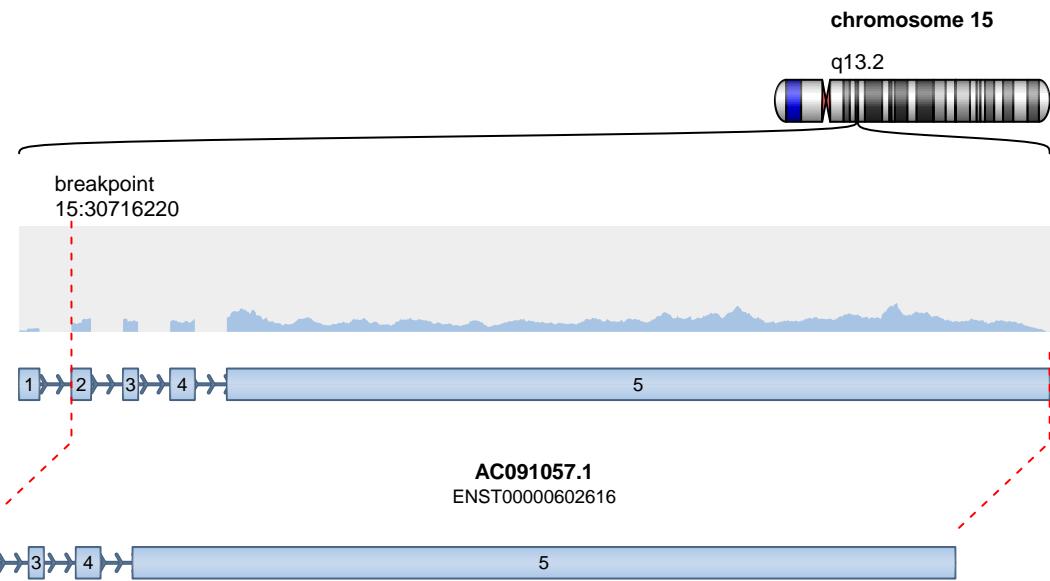
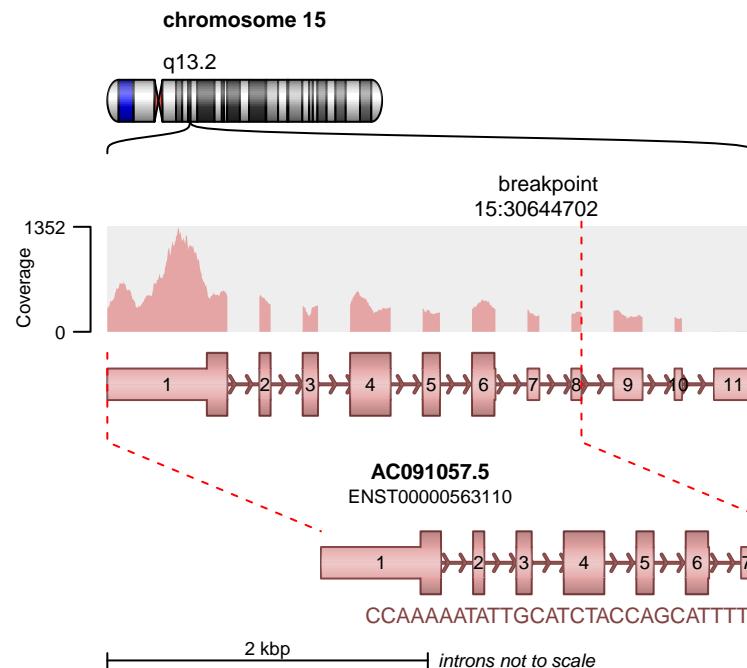
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 0

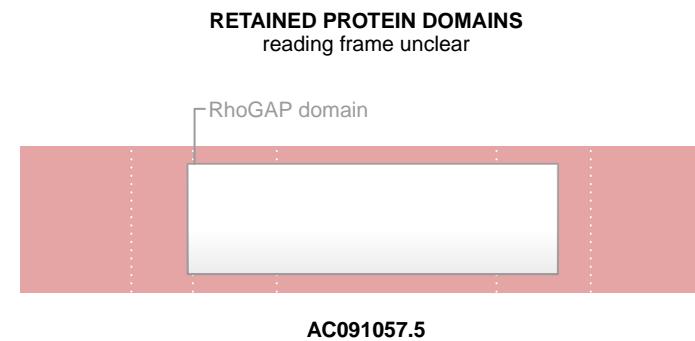
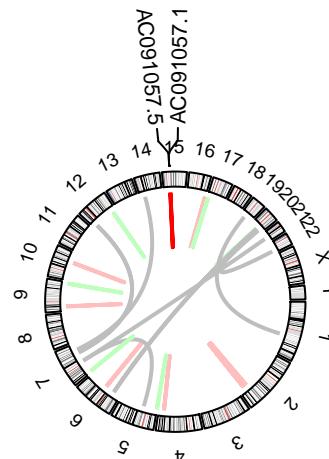
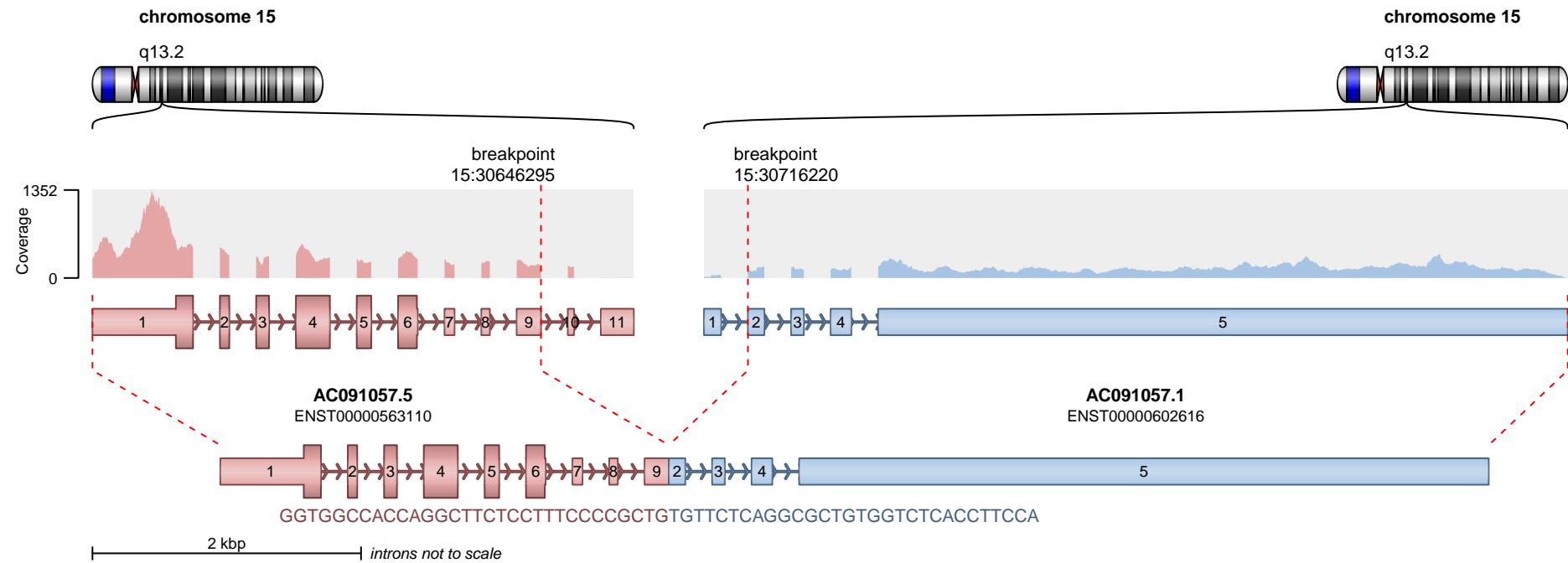
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 0

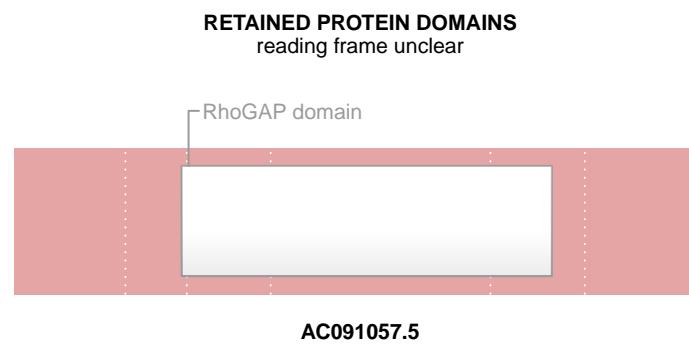
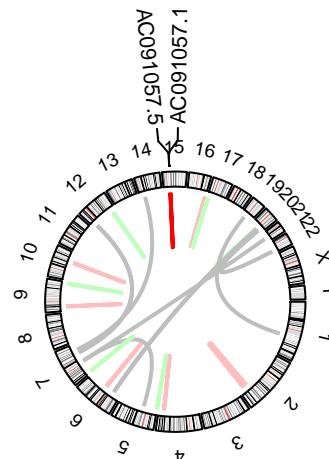
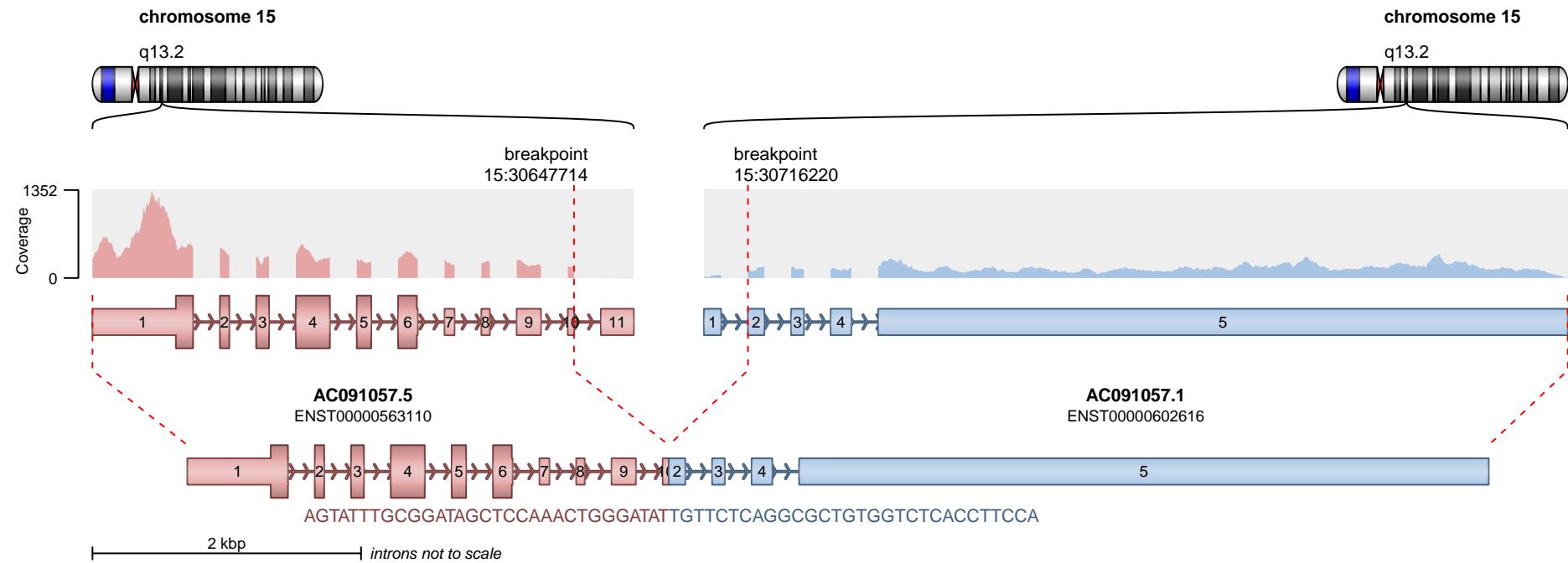
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 0

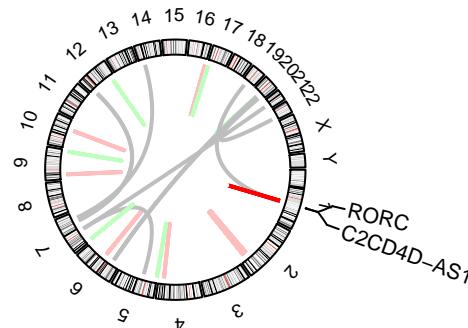
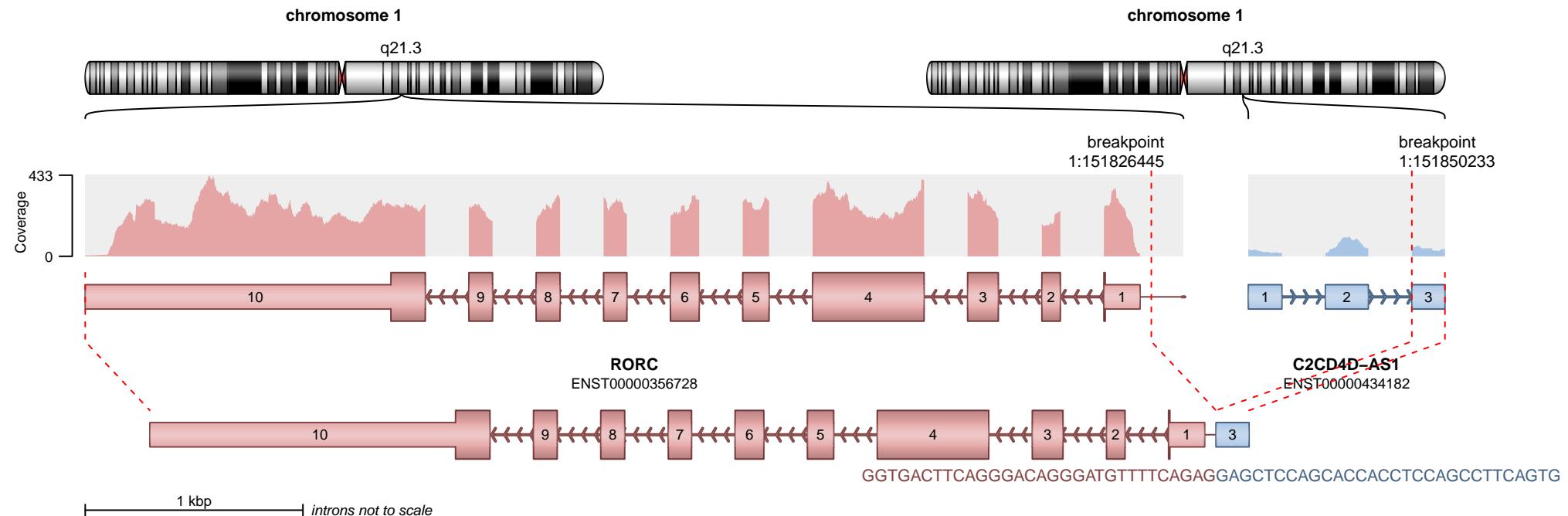
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 0

— translocation — deletion
— duplication — inversion

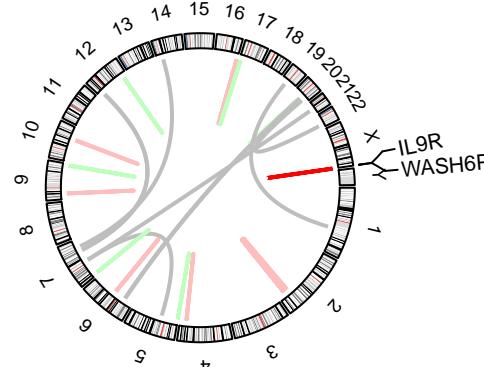
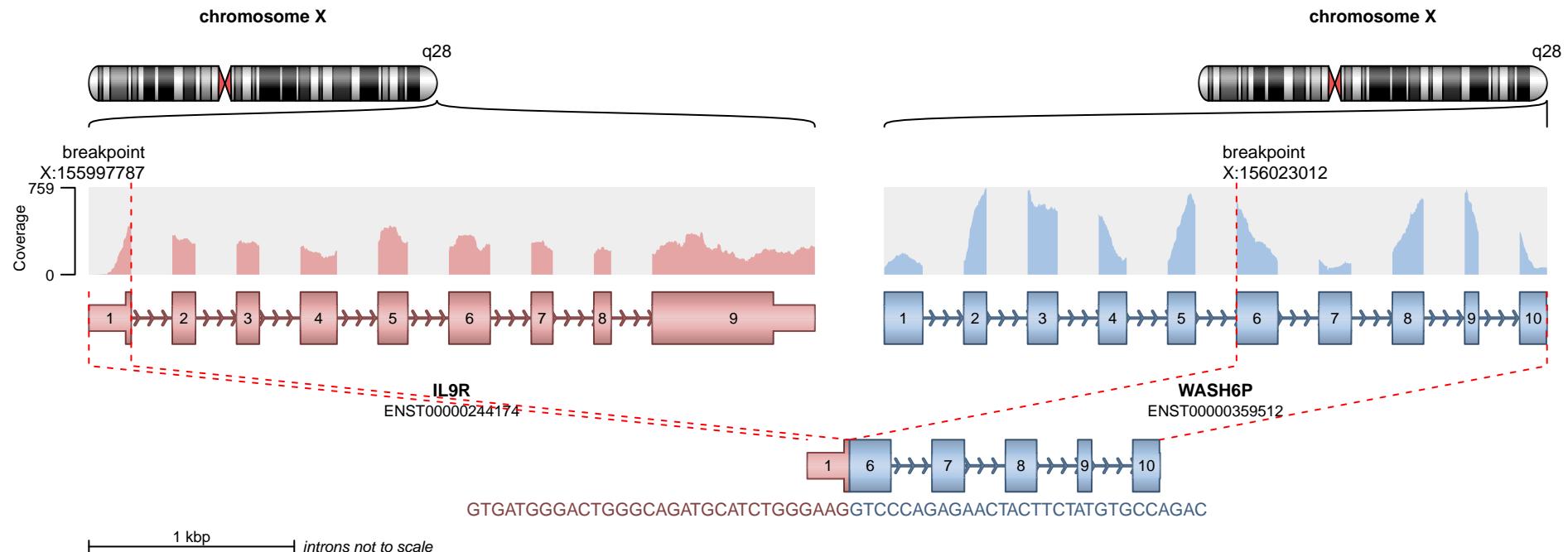


No coding regions due to antisense transcription.

SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 6

— translocation — deletion
— duplication — inversion

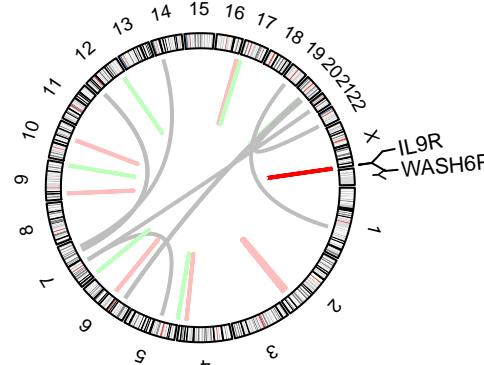
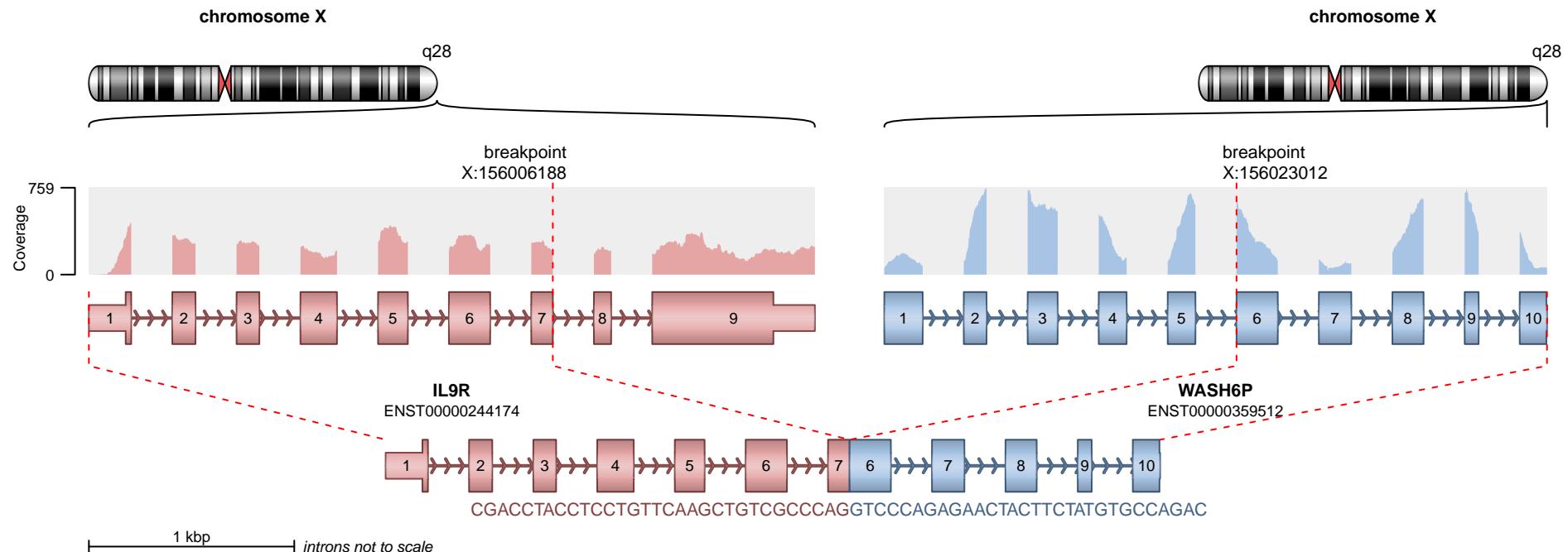


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 1

— translocation — deletion
— duplication — inversion

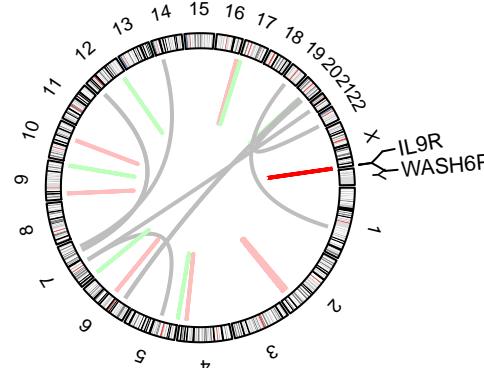
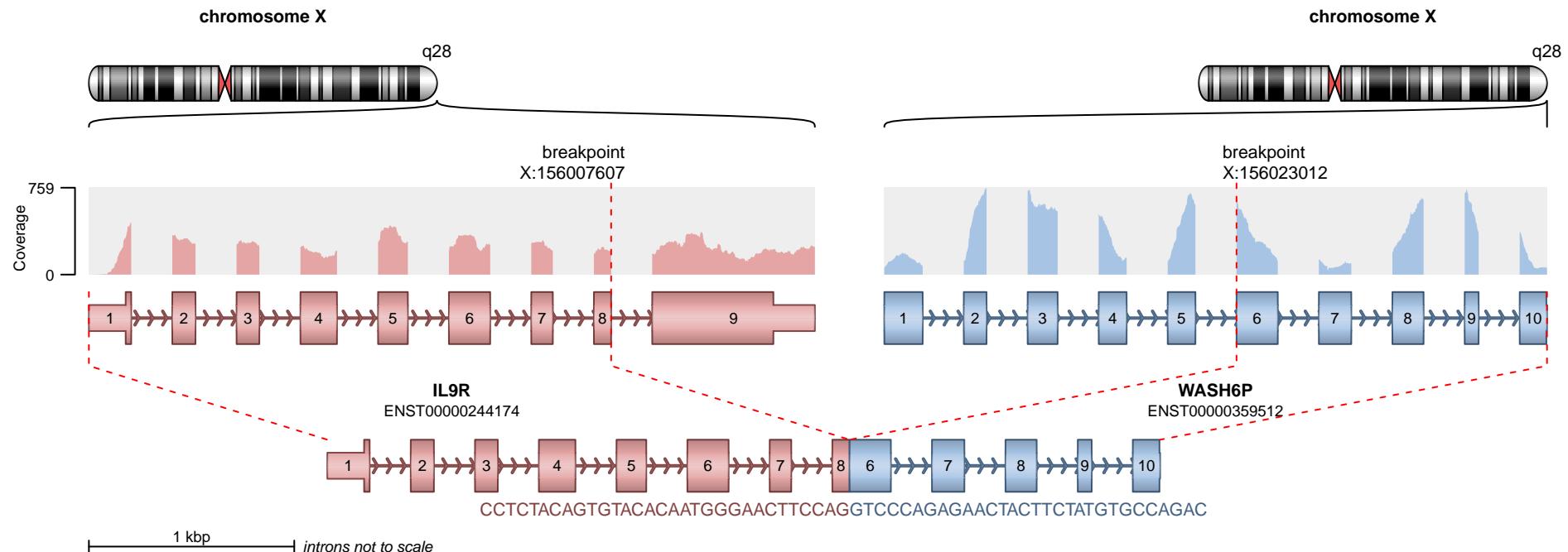


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 5

— translocation — deletion
— duplication — inversion

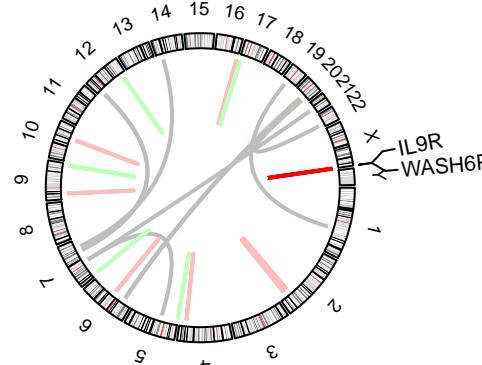
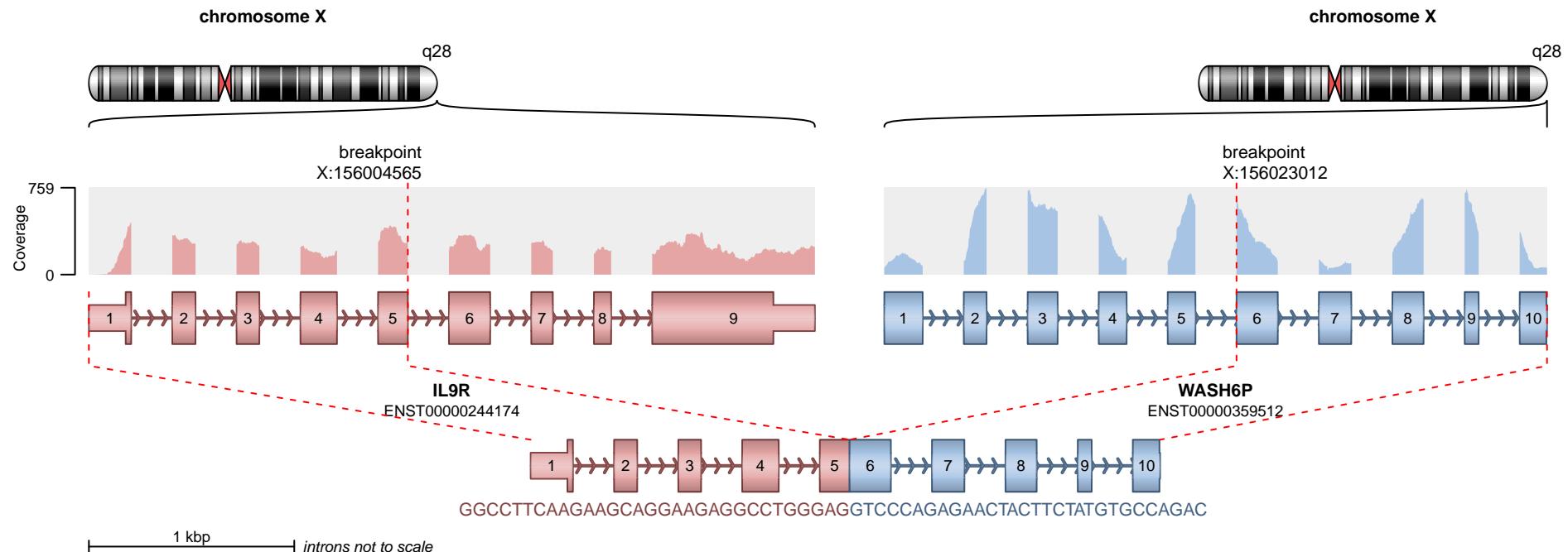


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 5

— translocation — deletion
— duplication — inversion

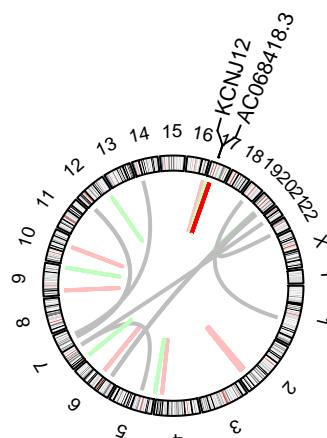
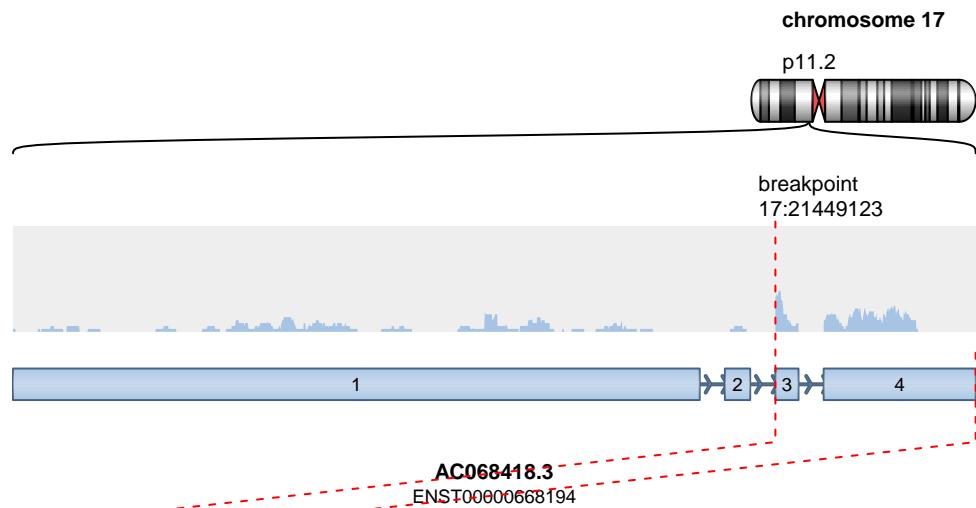
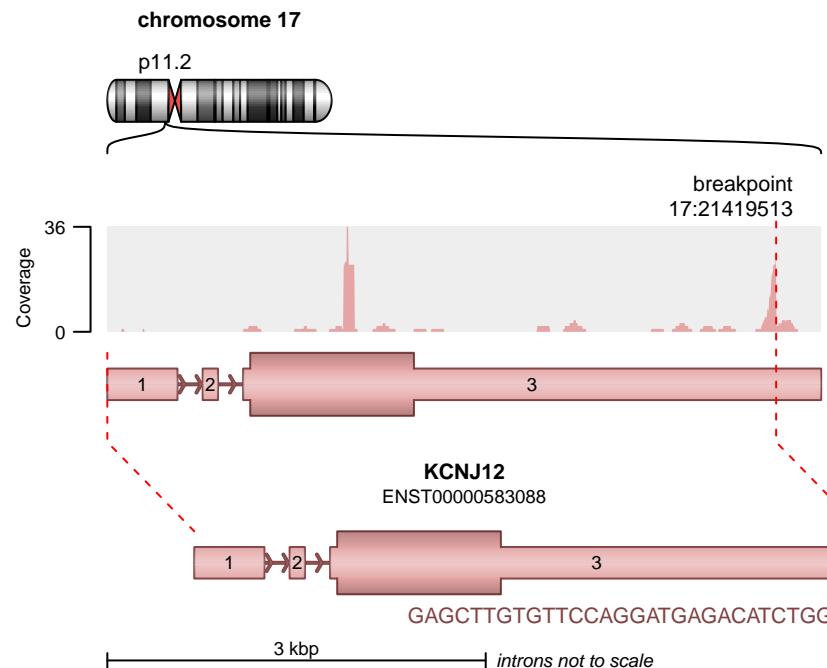


No protein domains retained in fusion.

SUPPORTING READ COUNT

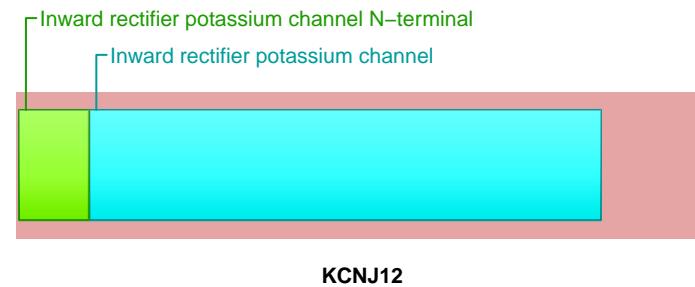
Split reads = 1
Discordant mates = 3

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS

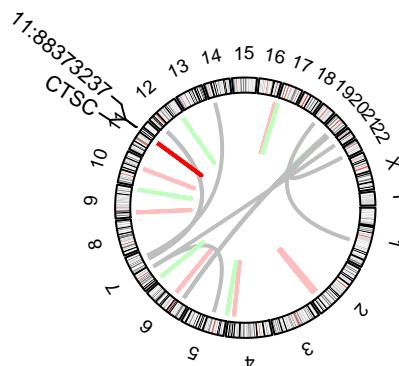
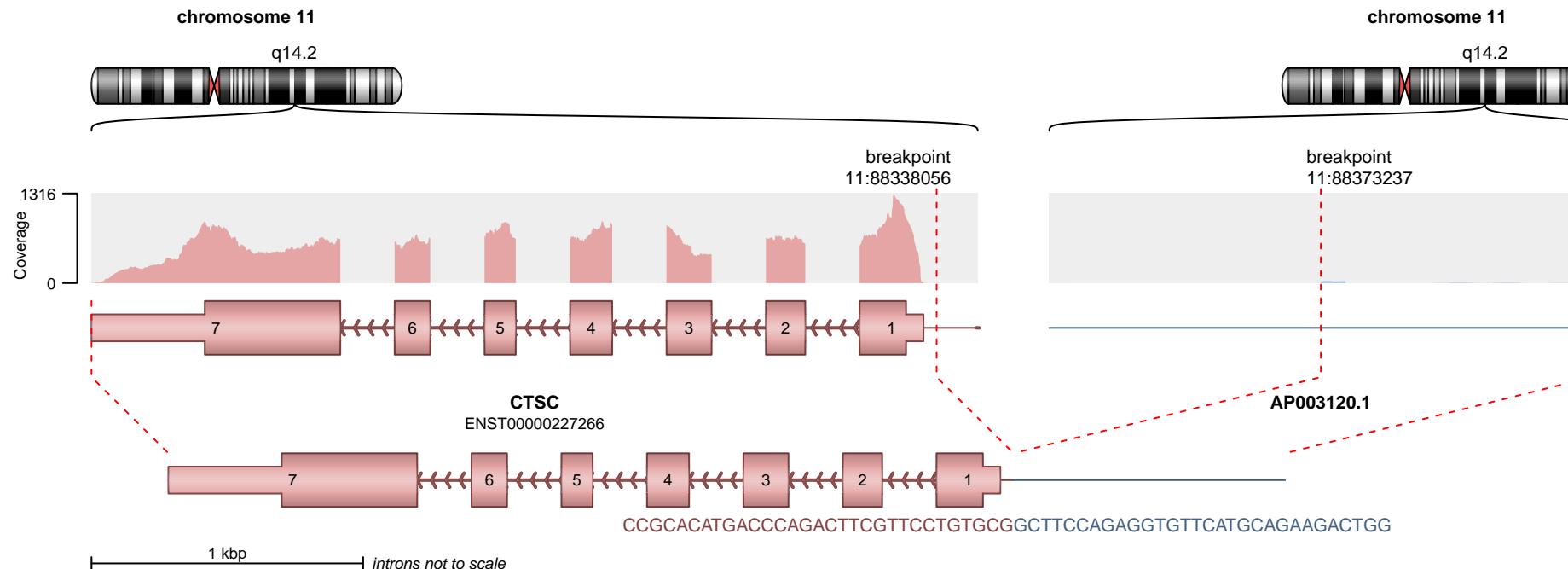
reading frame unclear



SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 2

— translocation — deletion
— duplication — inversion

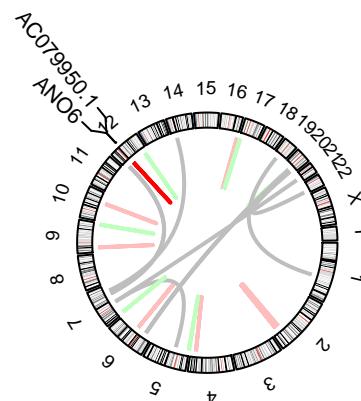
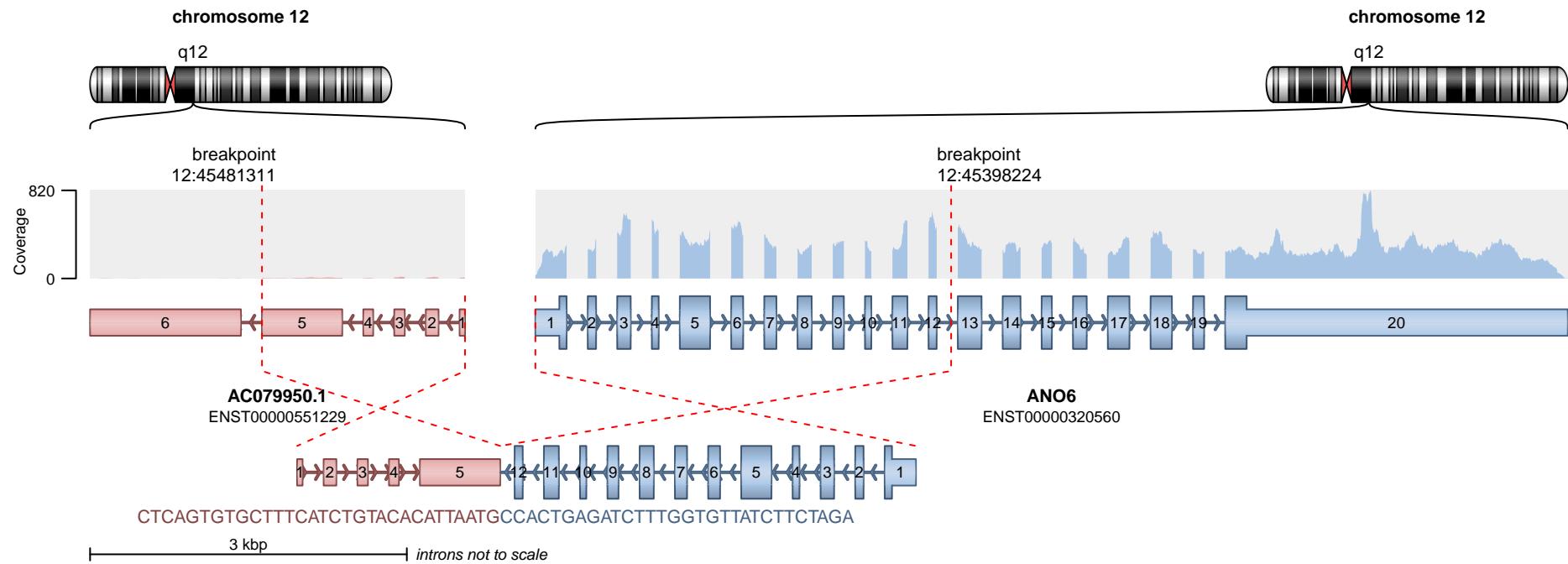


No coding regions due to antisense transcription.

SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 2

— translocation — deletion
— duplication — inversion

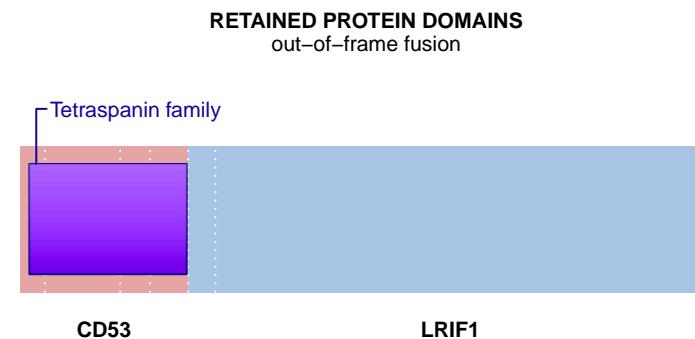
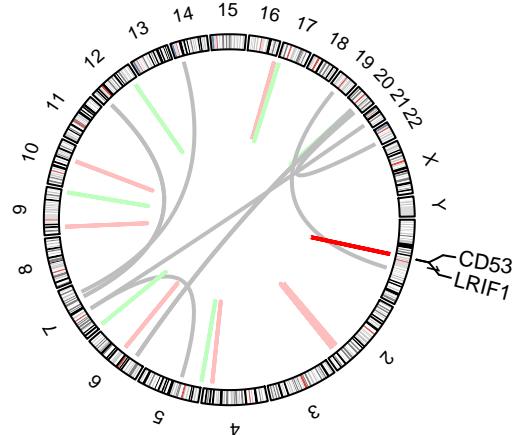
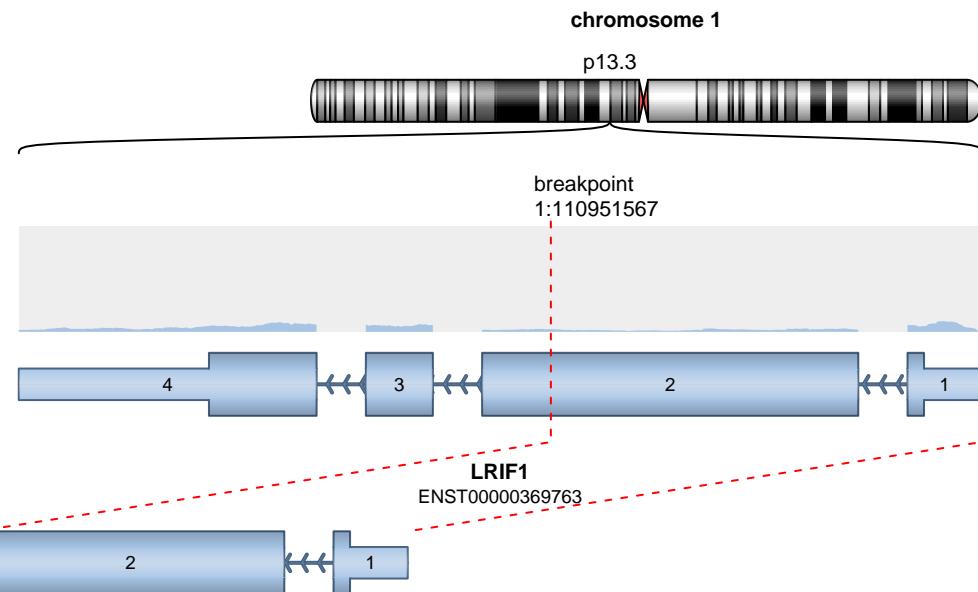
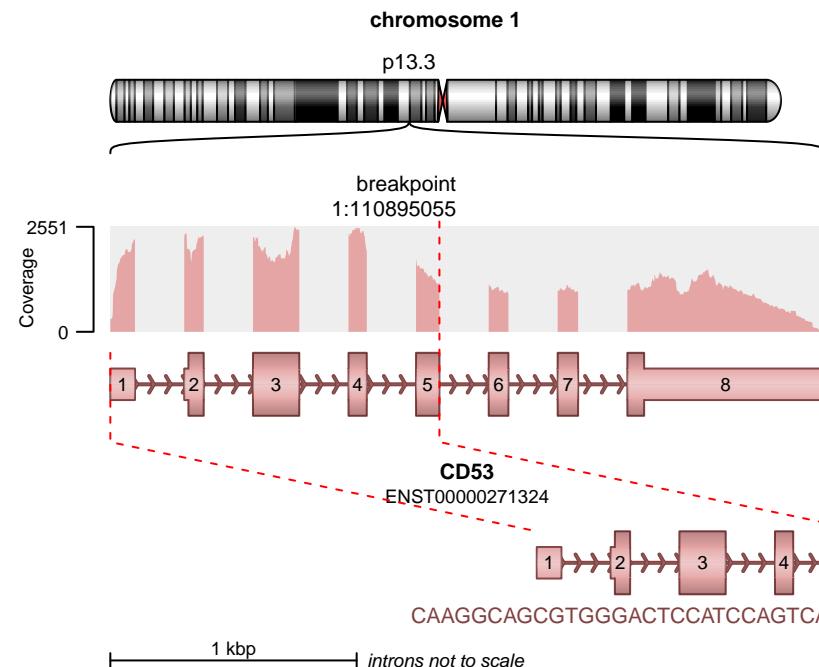


No coding regions due to antisense transcription.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 6

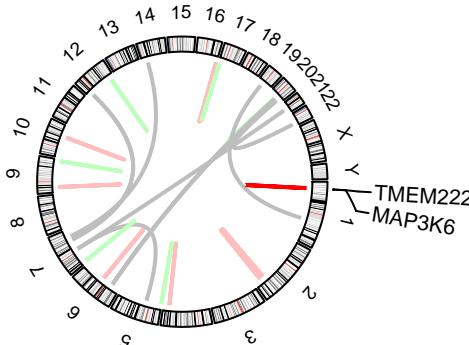
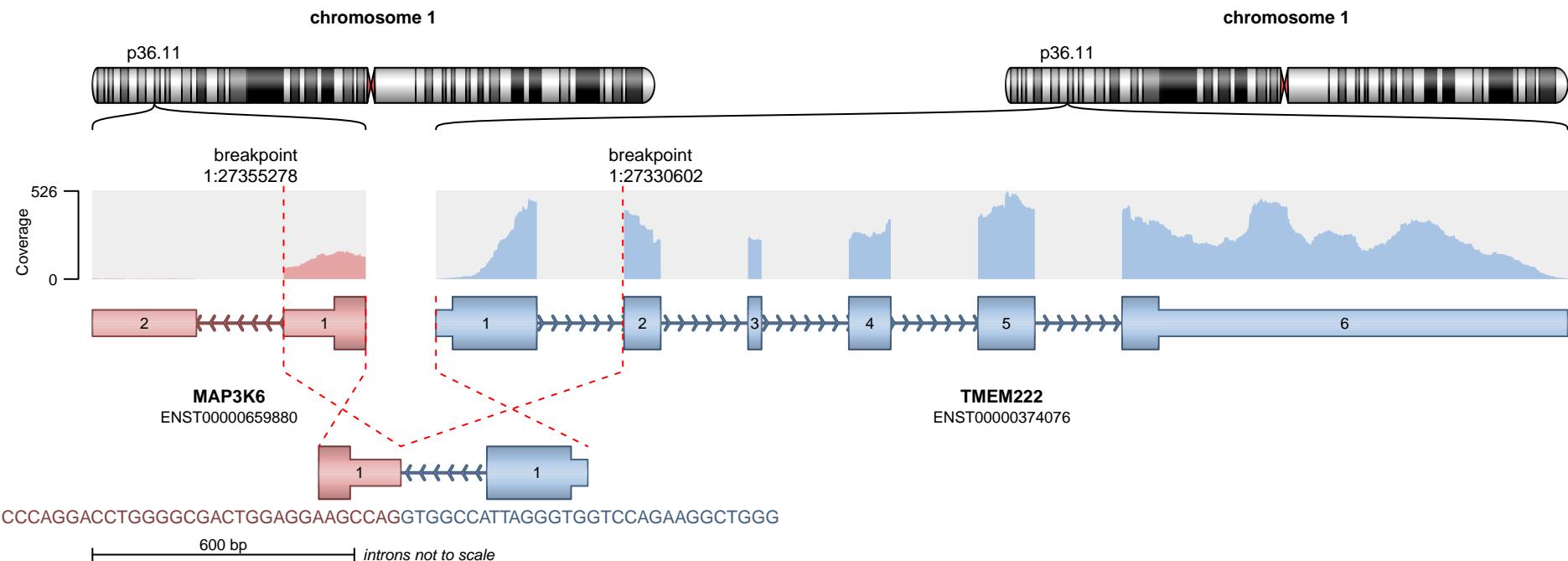
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

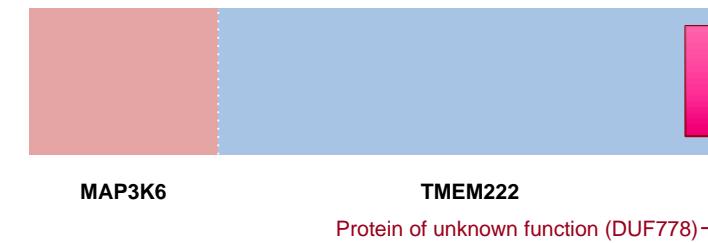
Split reads = 1
Discordant mates = 5

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS

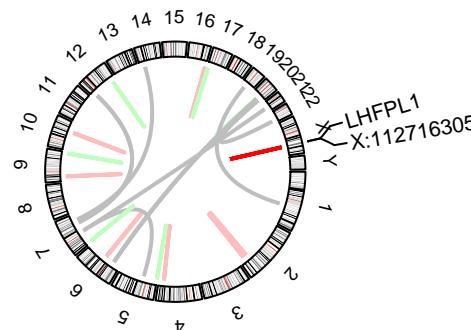
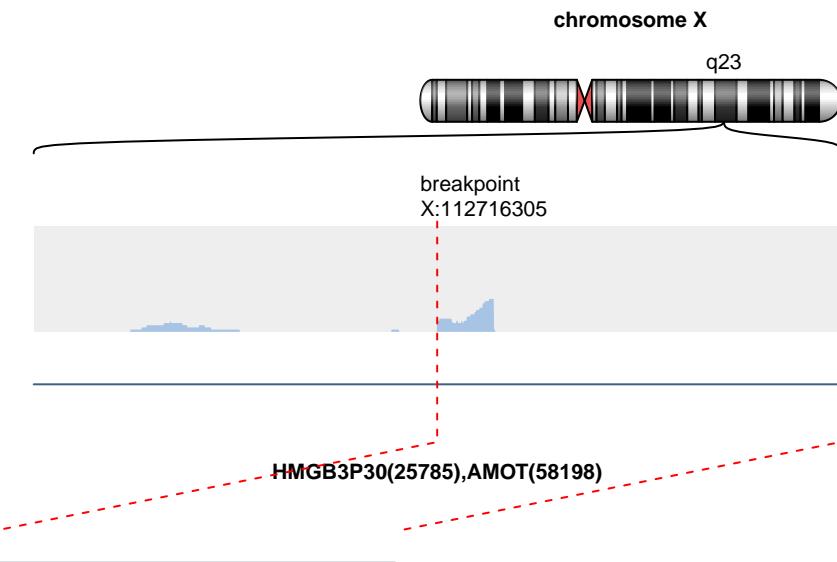
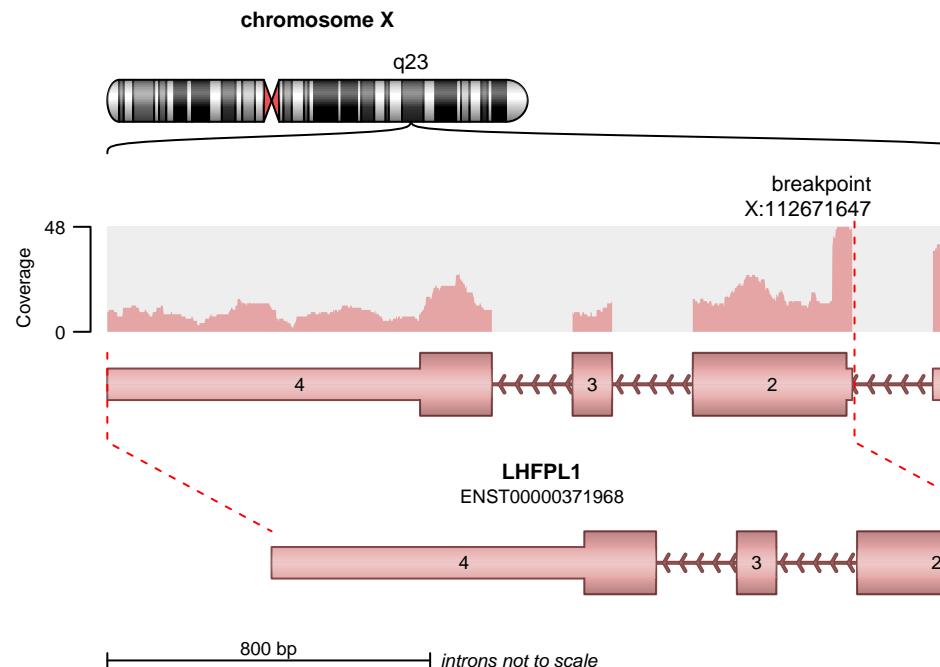
reading frame unclear



SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 2

— translocation — deletion
— duplication — inversion

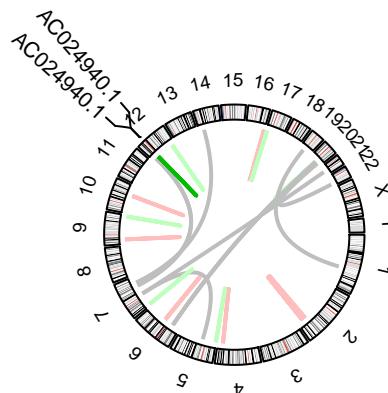
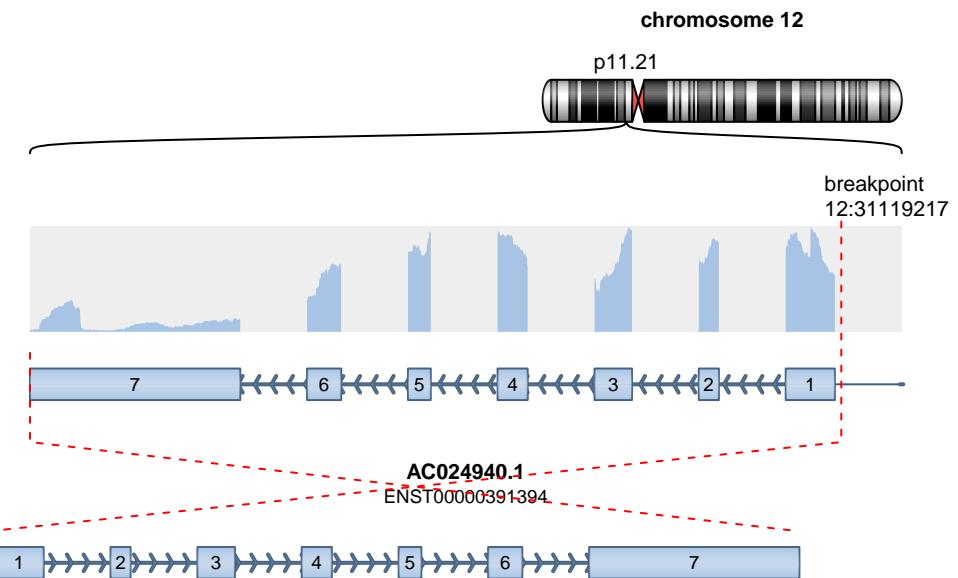
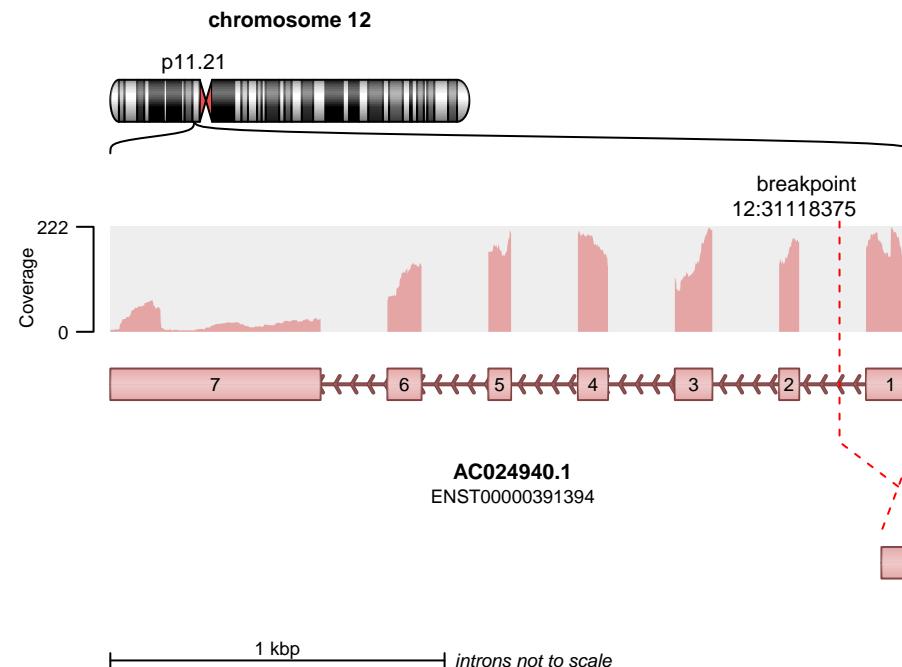


No coding regions due to antisense transcription.

SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 1

— translocation — deletion
— duplication — inversion

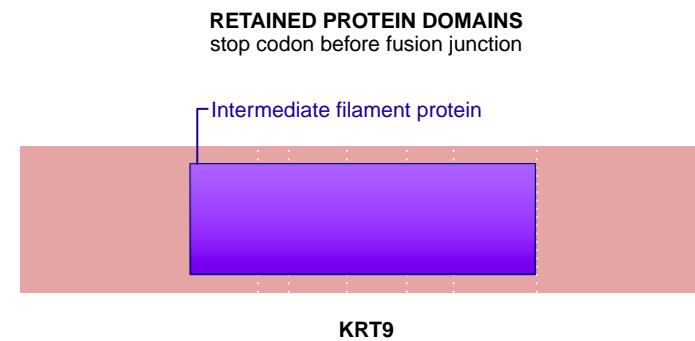
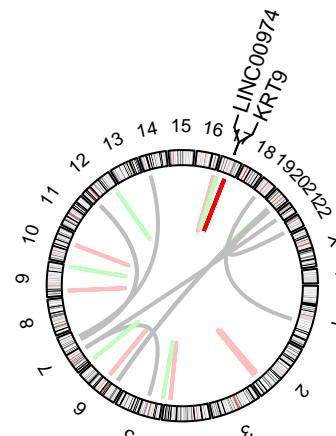
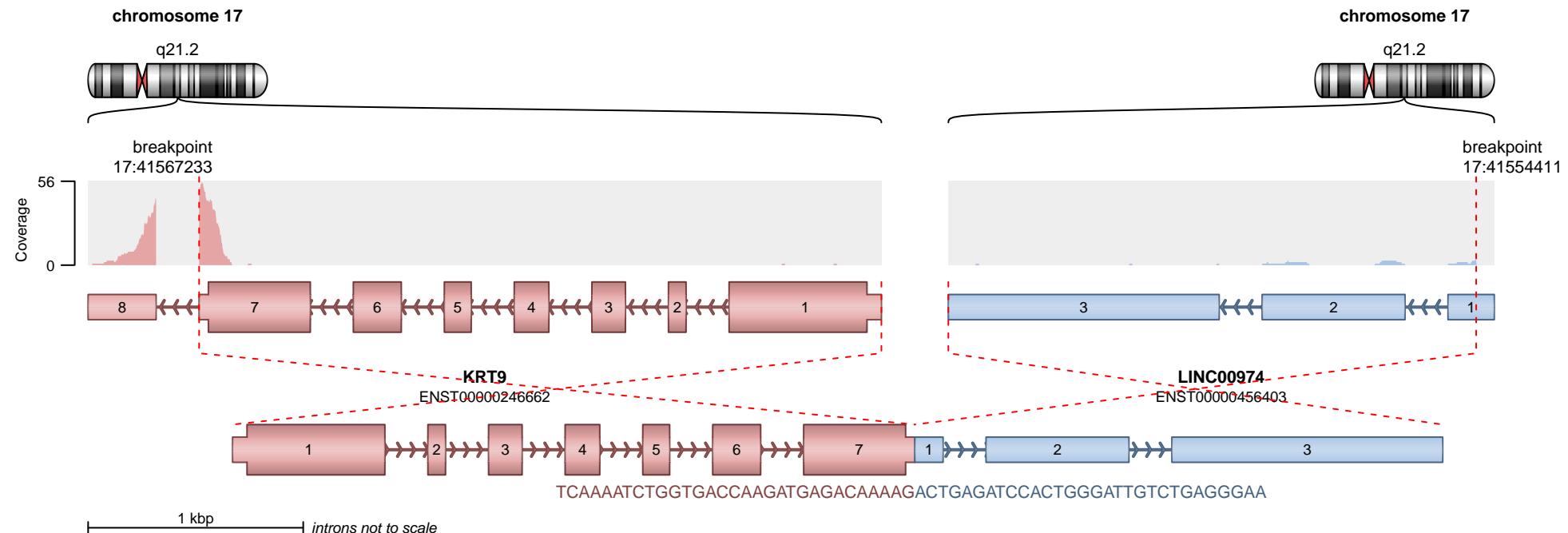


Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

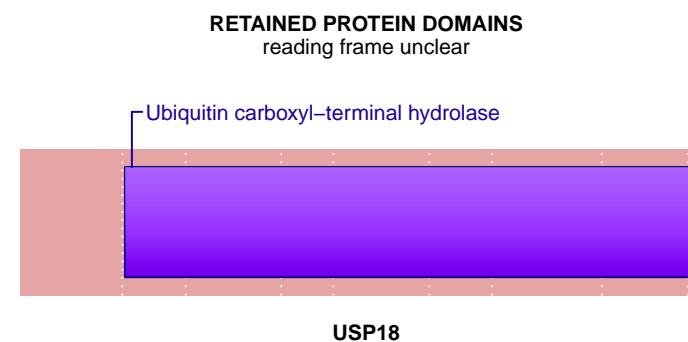
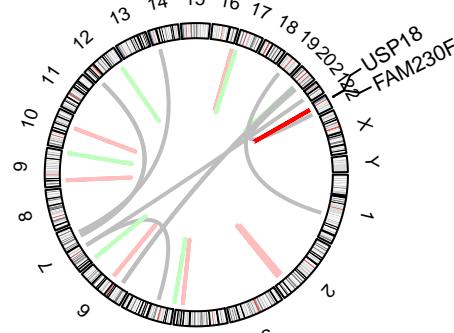
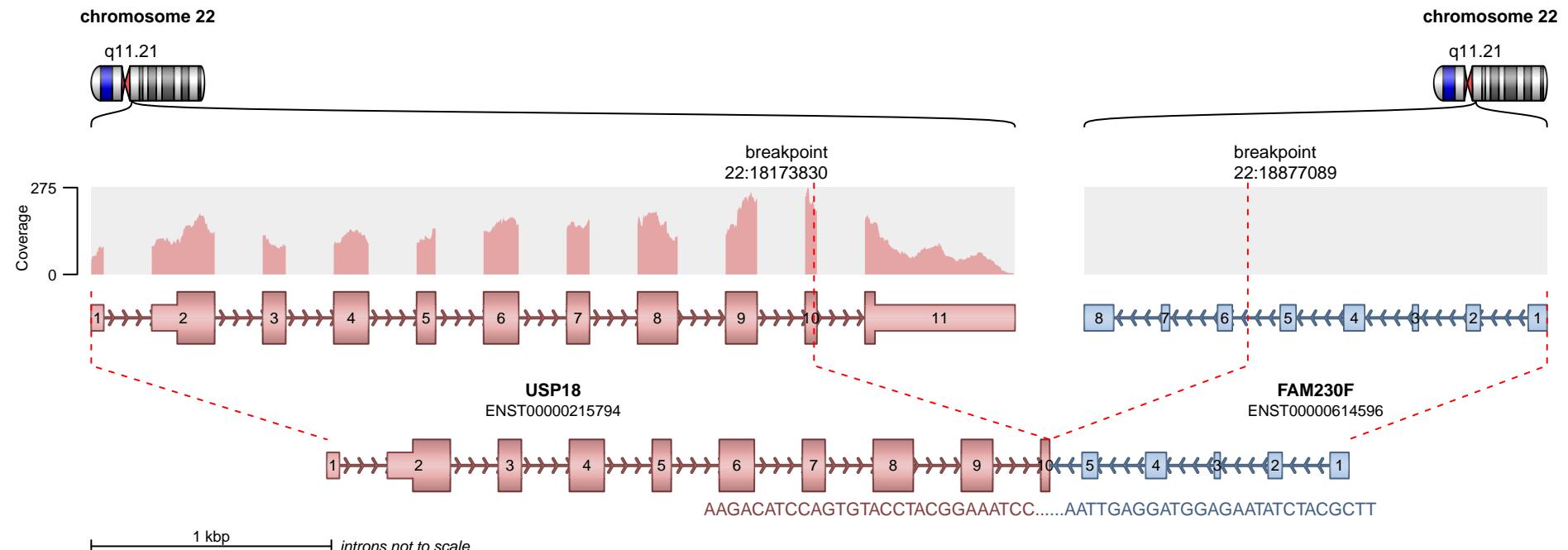
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 2

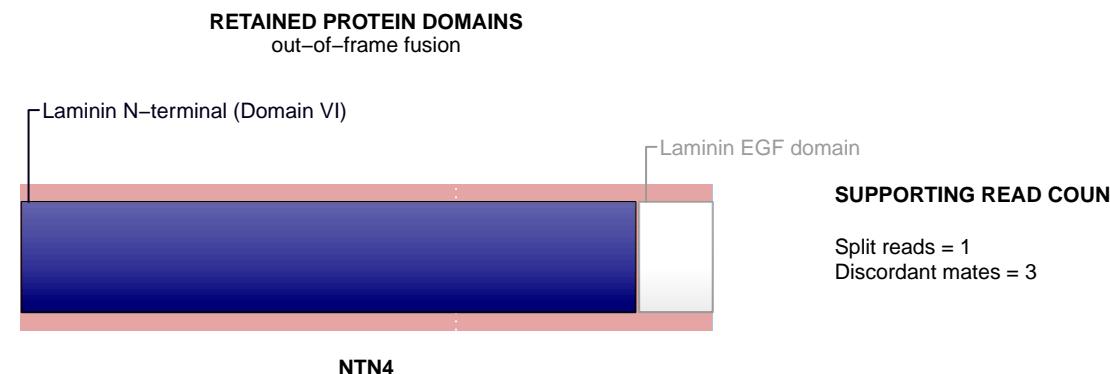
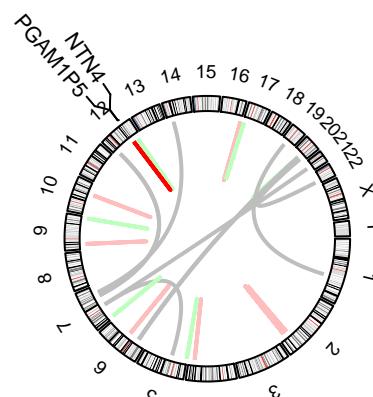
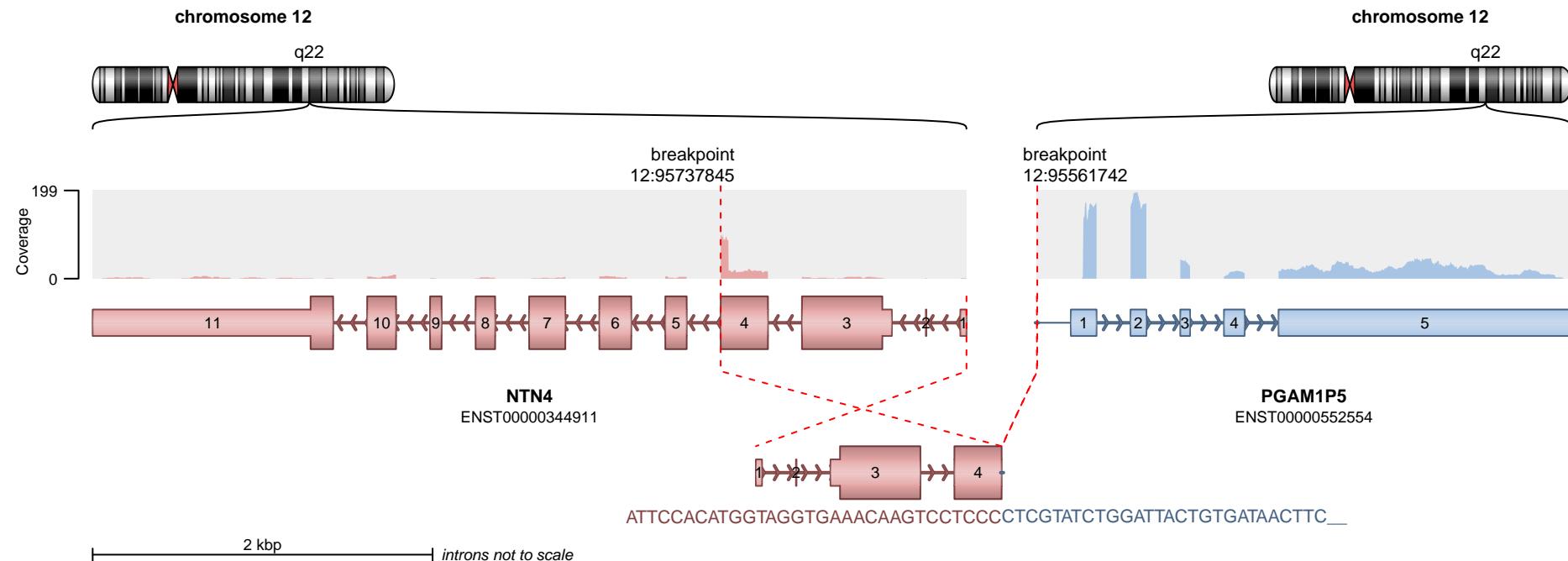
— translocation — deletion
— duplication — inversion



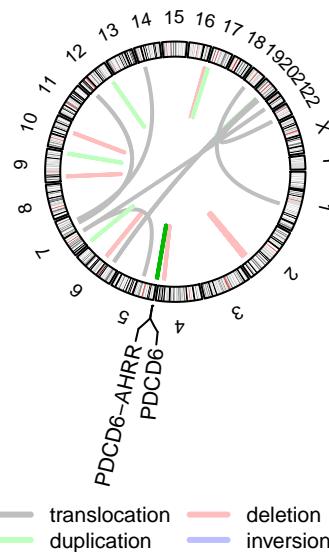
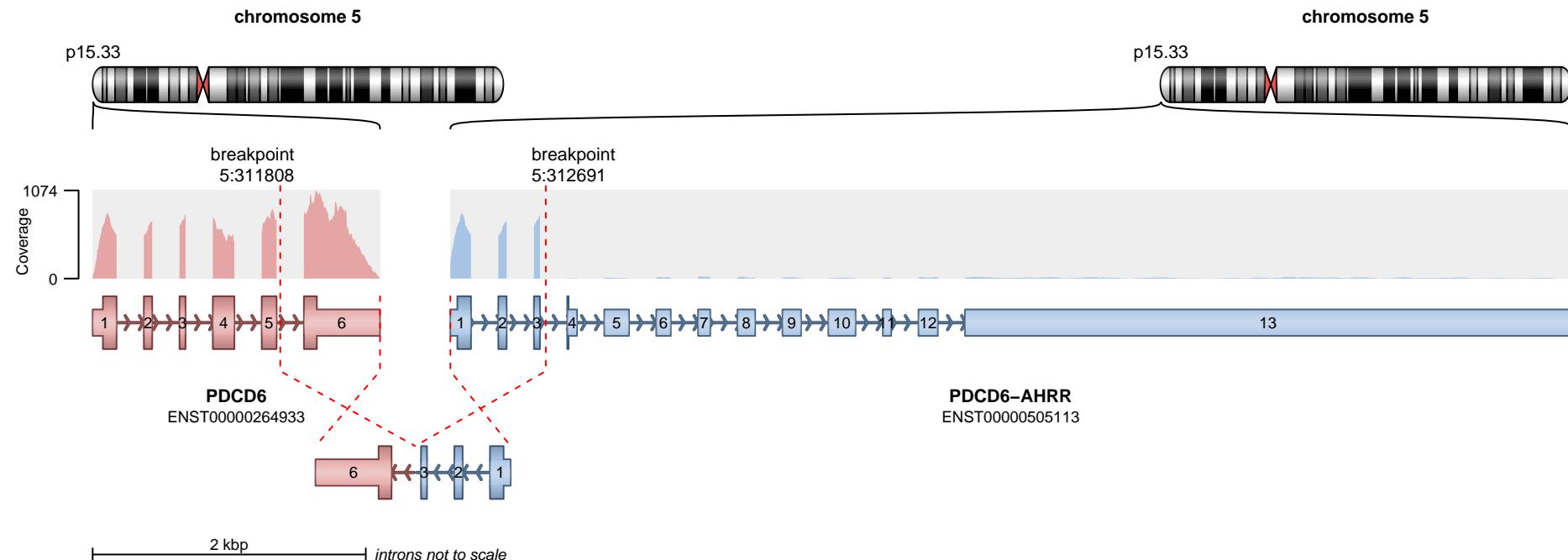
SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 4

— translocation — deletion
— duplication — inversion



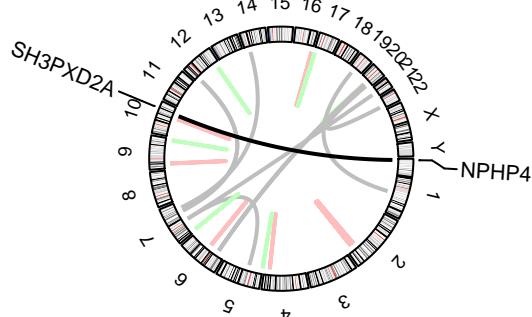
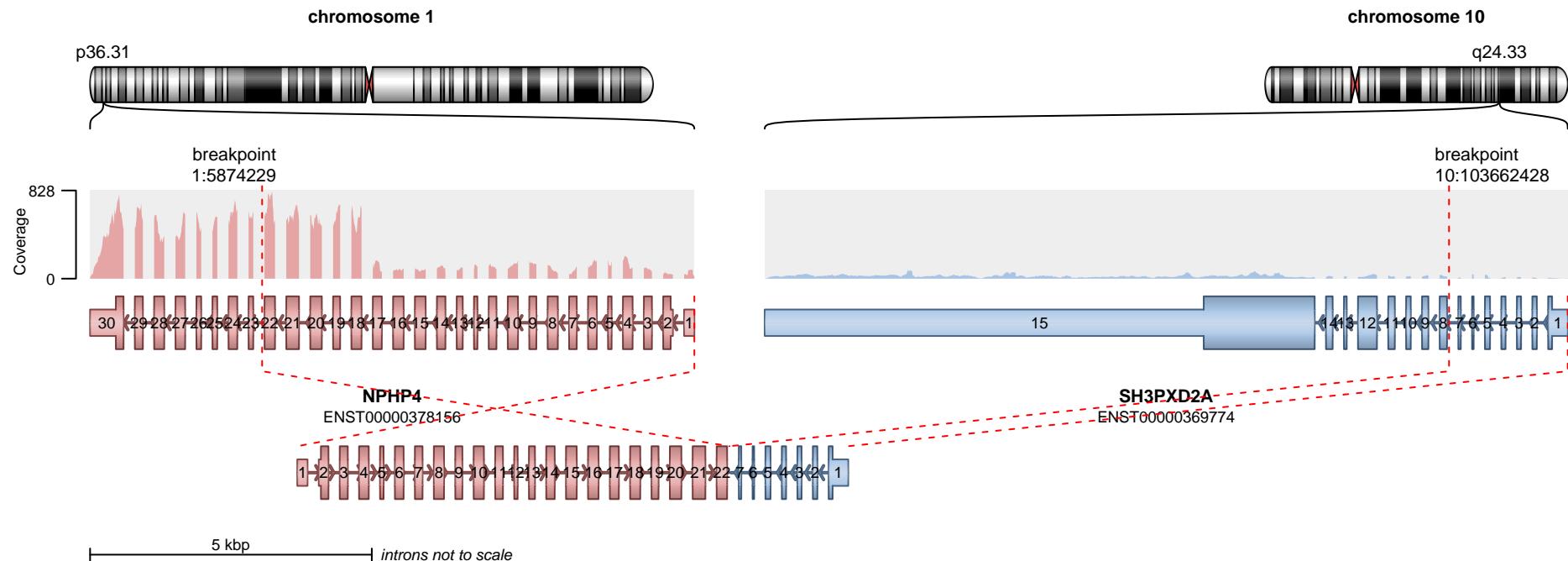
— translocation — deletion
— duplication — inversion



No coding regions due to antisense transcription.

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 2

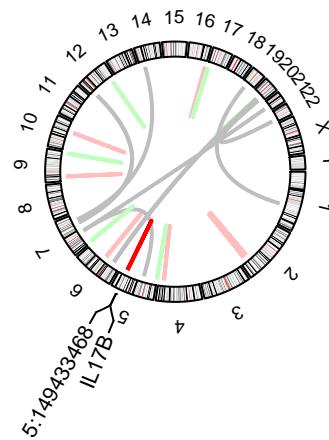
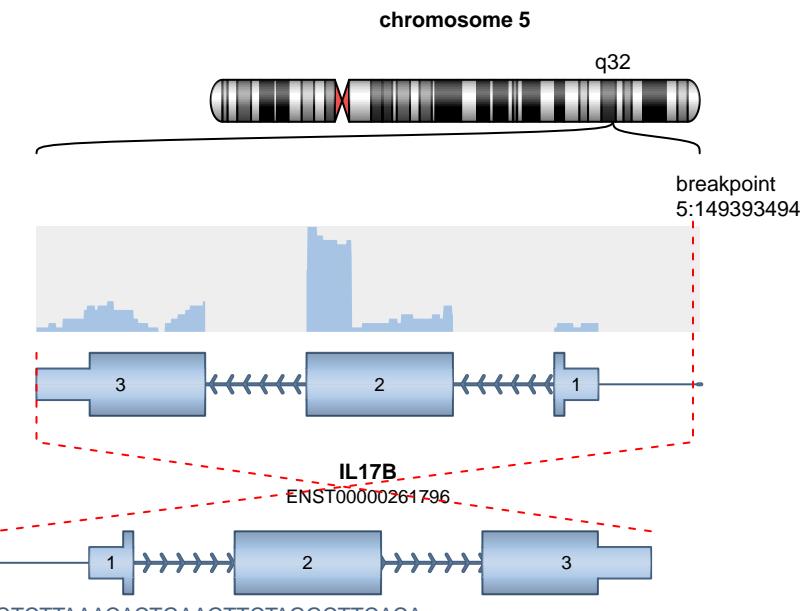
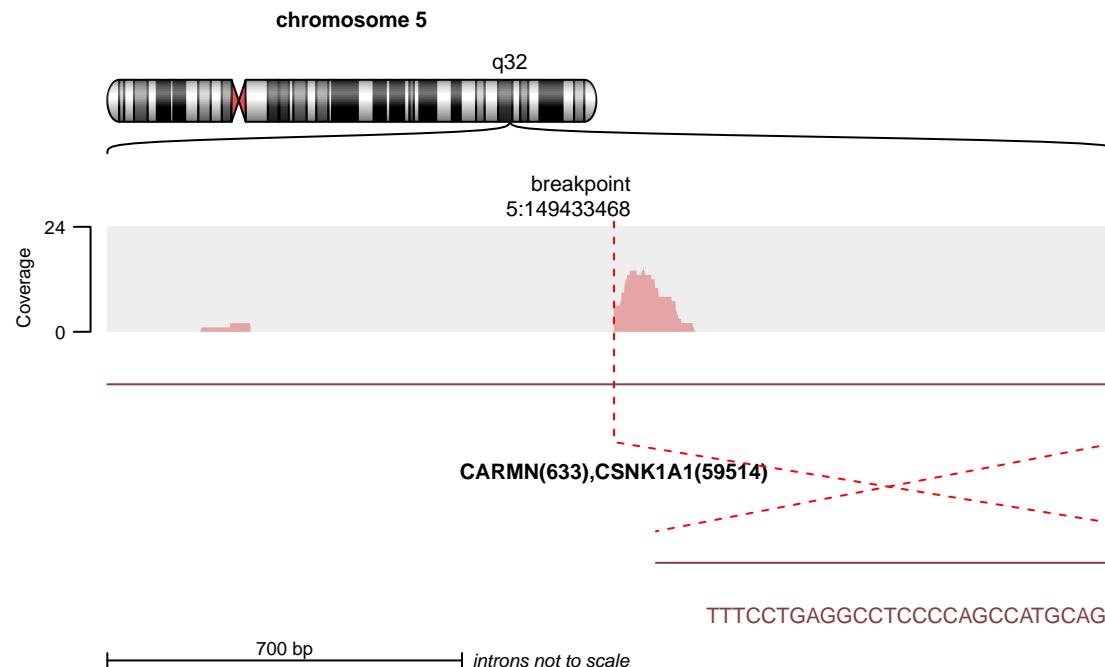


No coding regions due to antisense transcription.

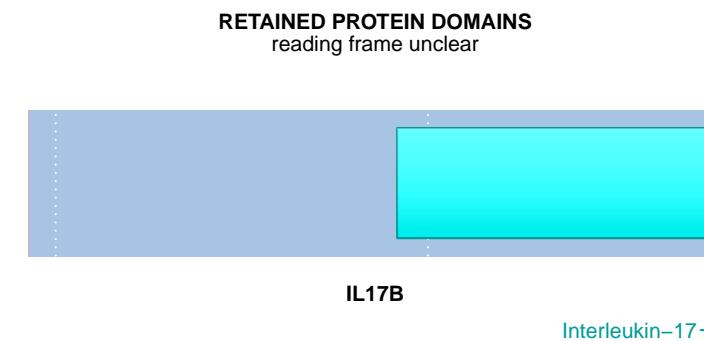
SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 3

— translocation — deletion
— duplication — inversion

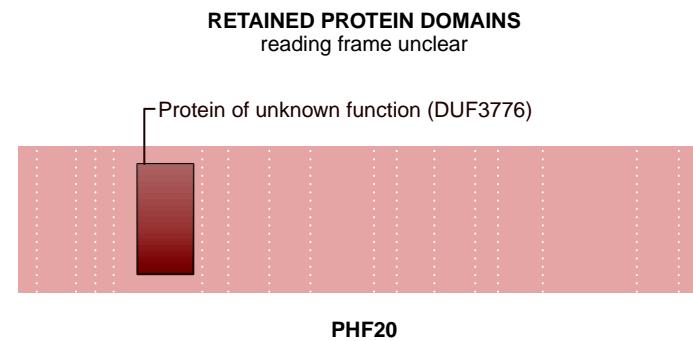
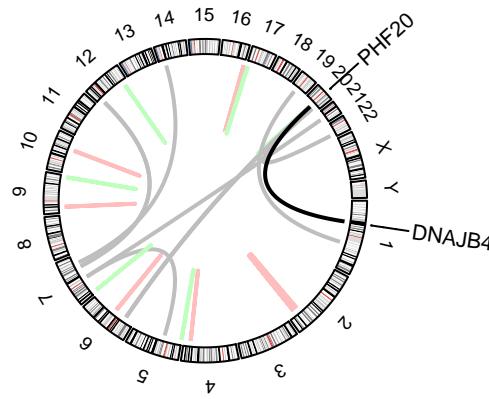
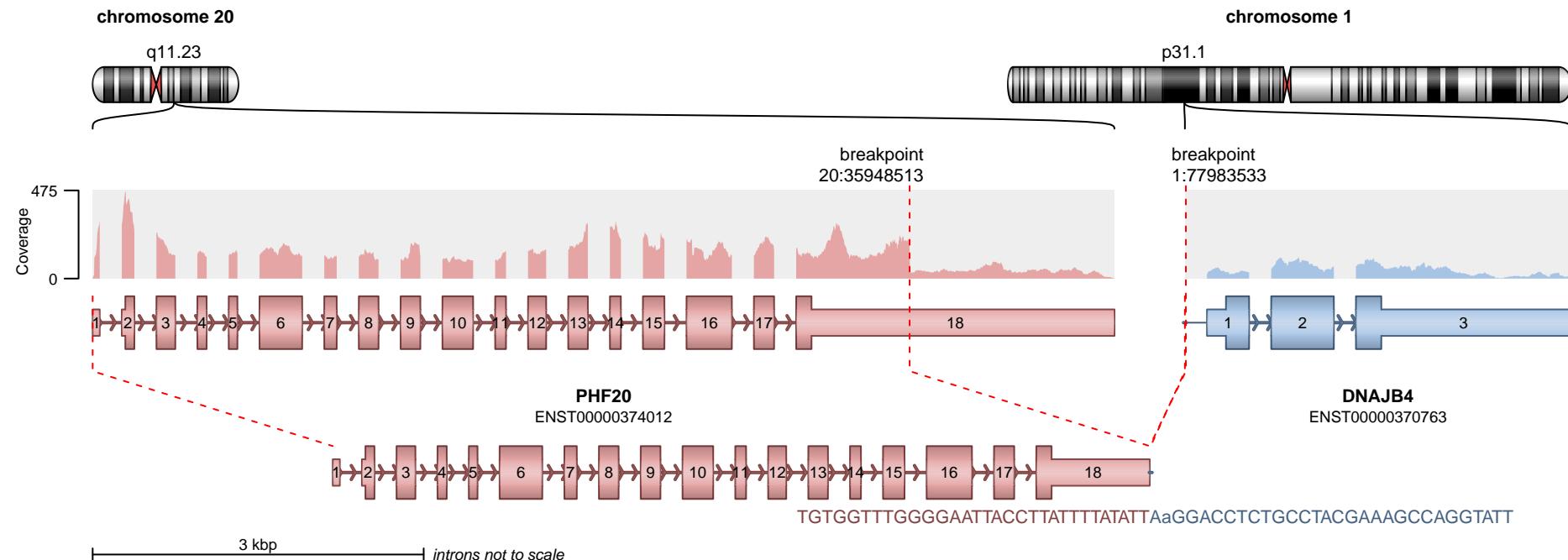


— translocation — deletion
— duplication — inversion

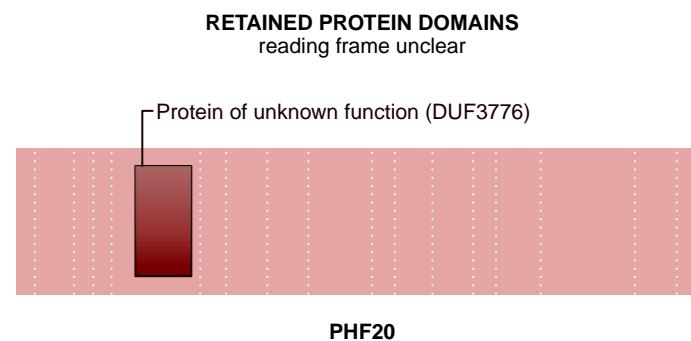
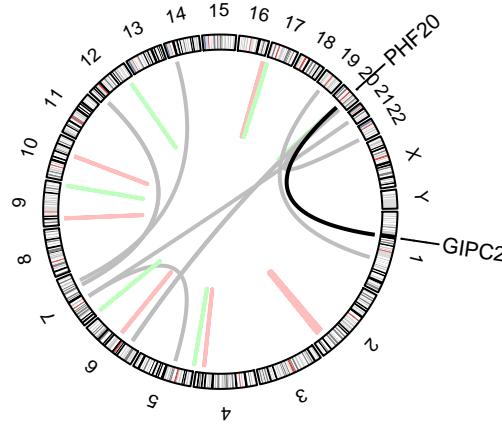
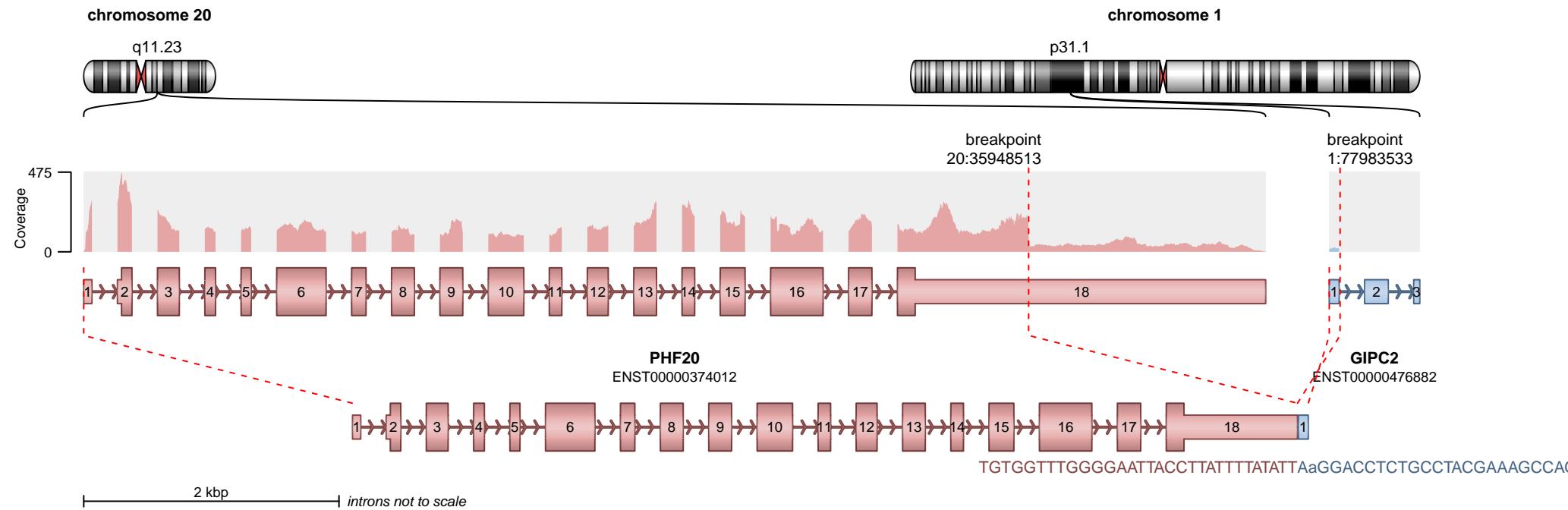


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 1



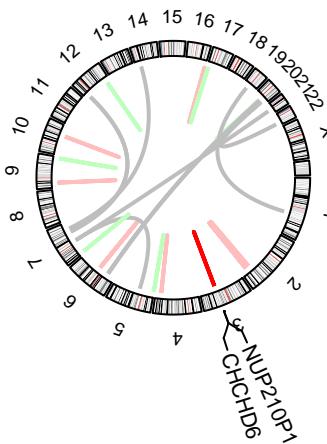
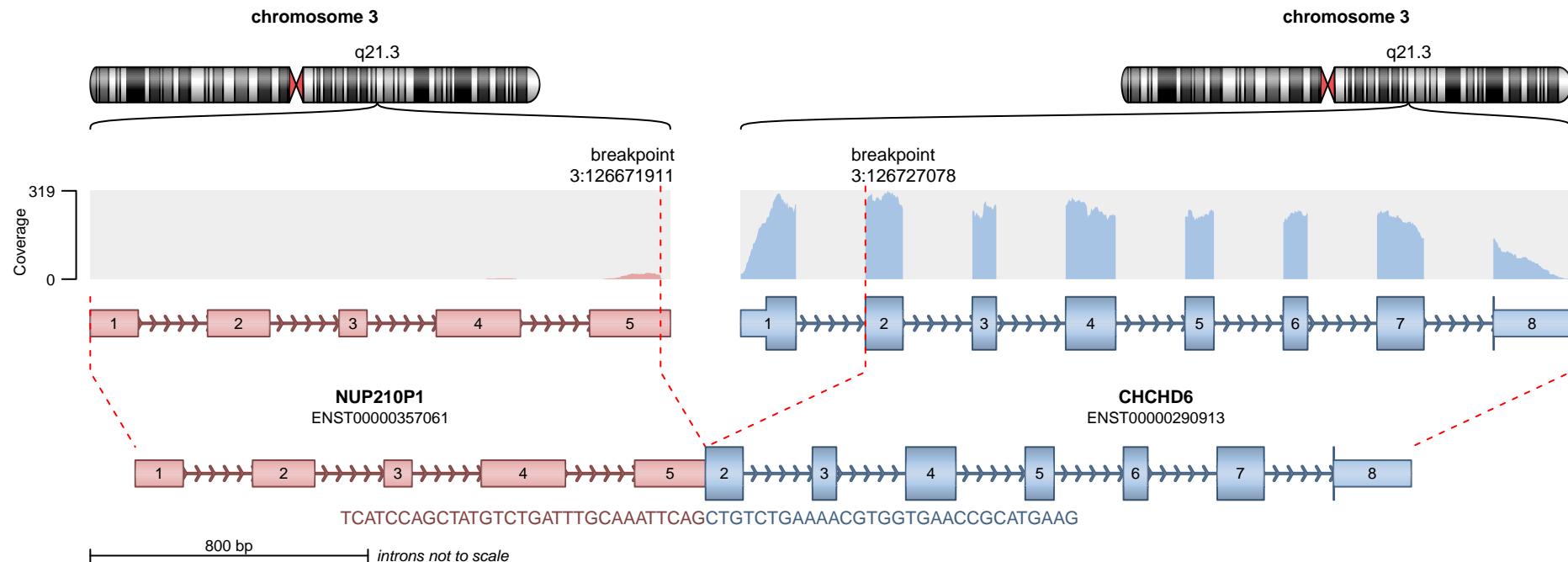
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

— translocation — deletion
— duplication — inversion

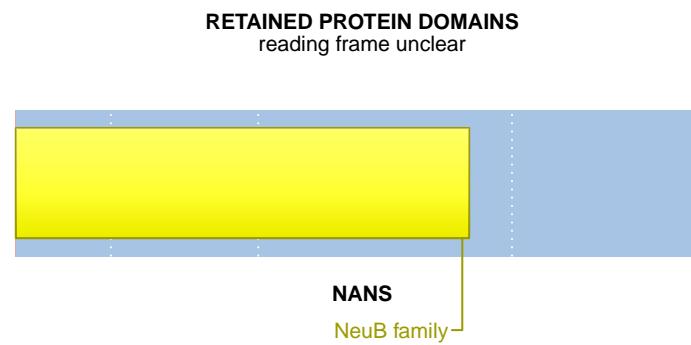
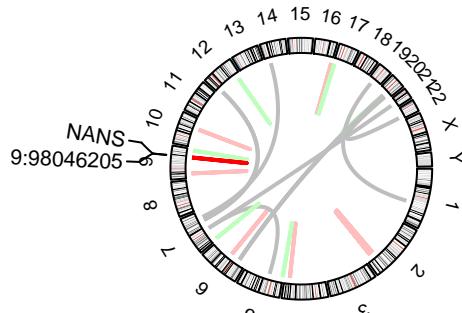
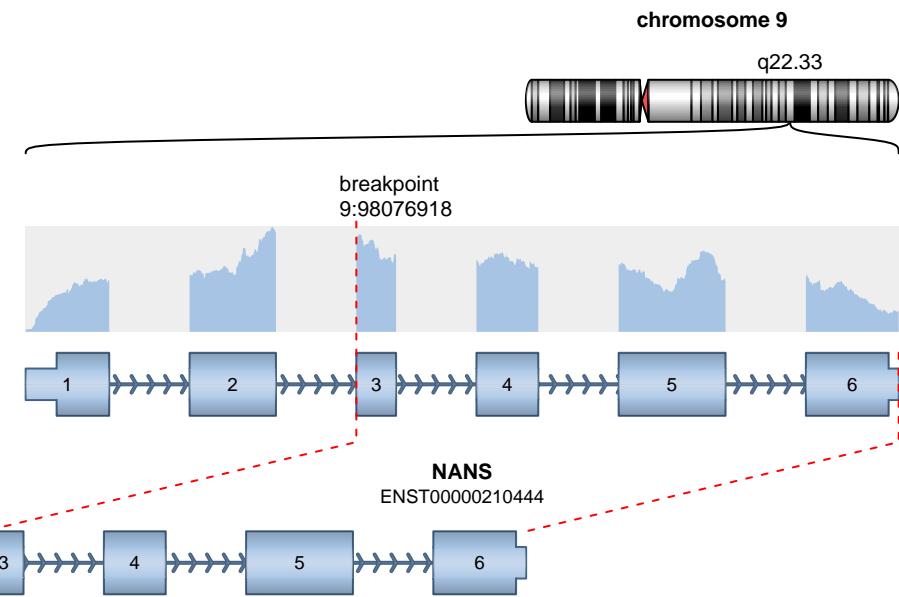
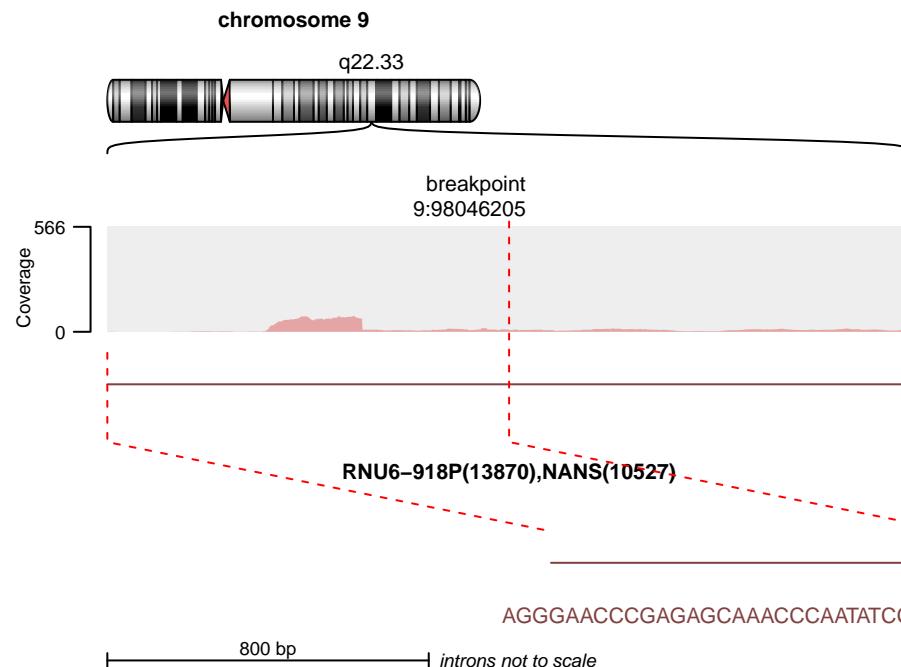


— translocation — deletion
— duplication — inversion

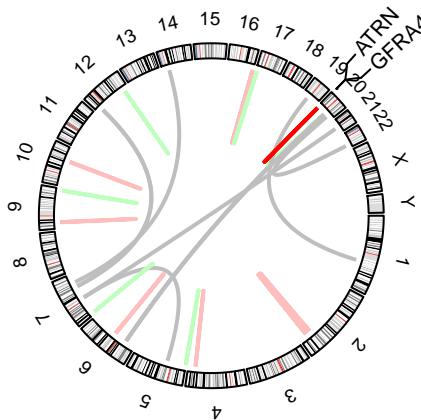
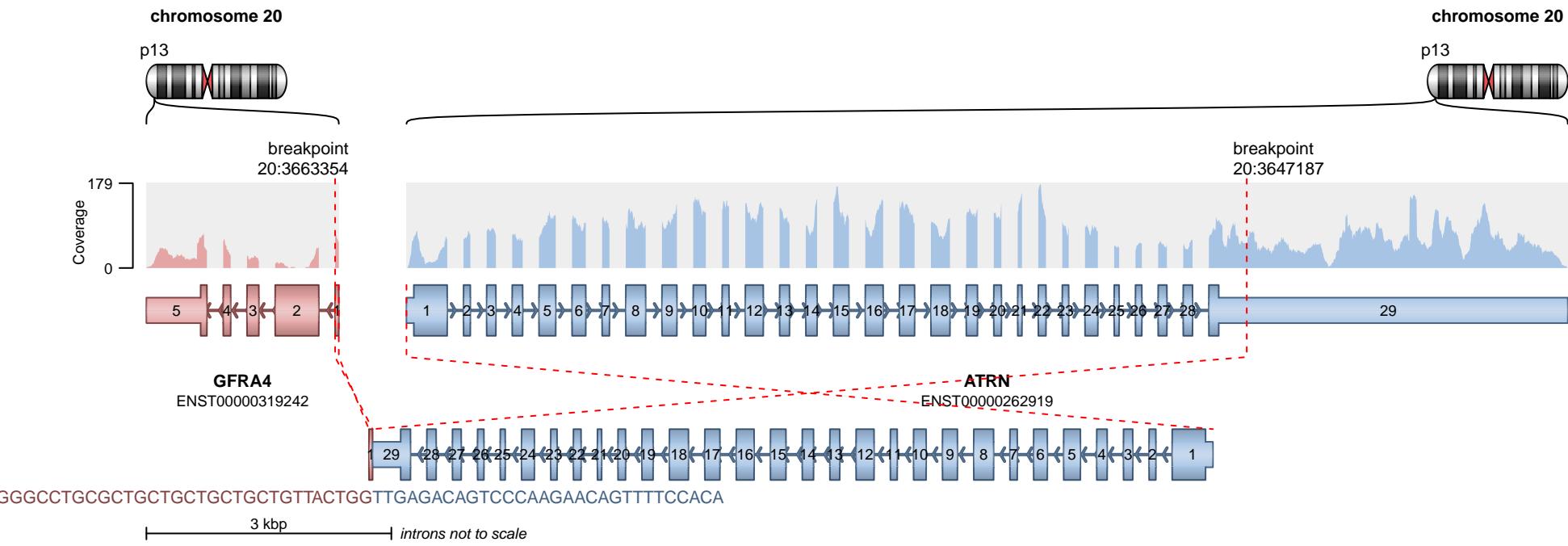
No protein domains retained in fusion.

SUPPORTING READ COUNT

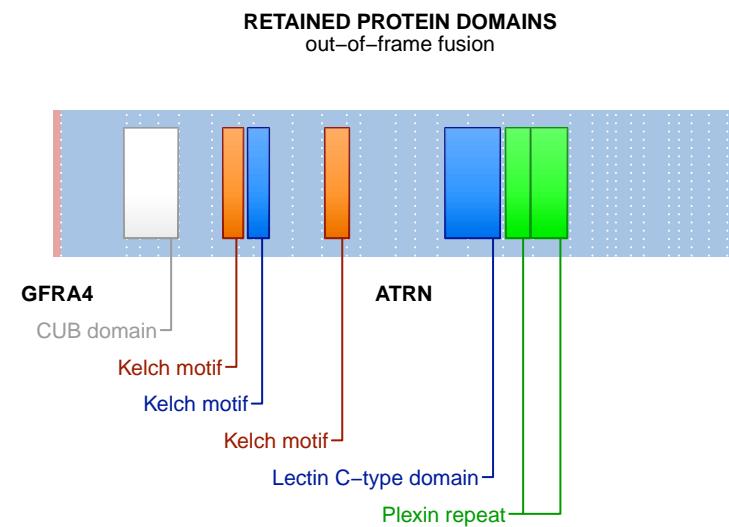
Split reads = 2
Discordant mates = 1



— translocation — deletion
— duplication — inversion

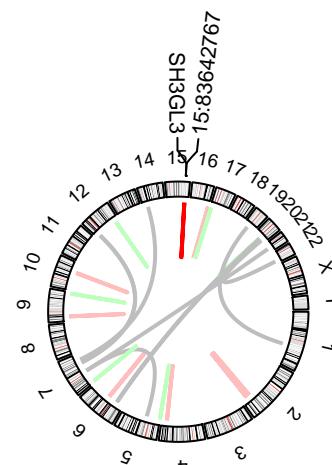
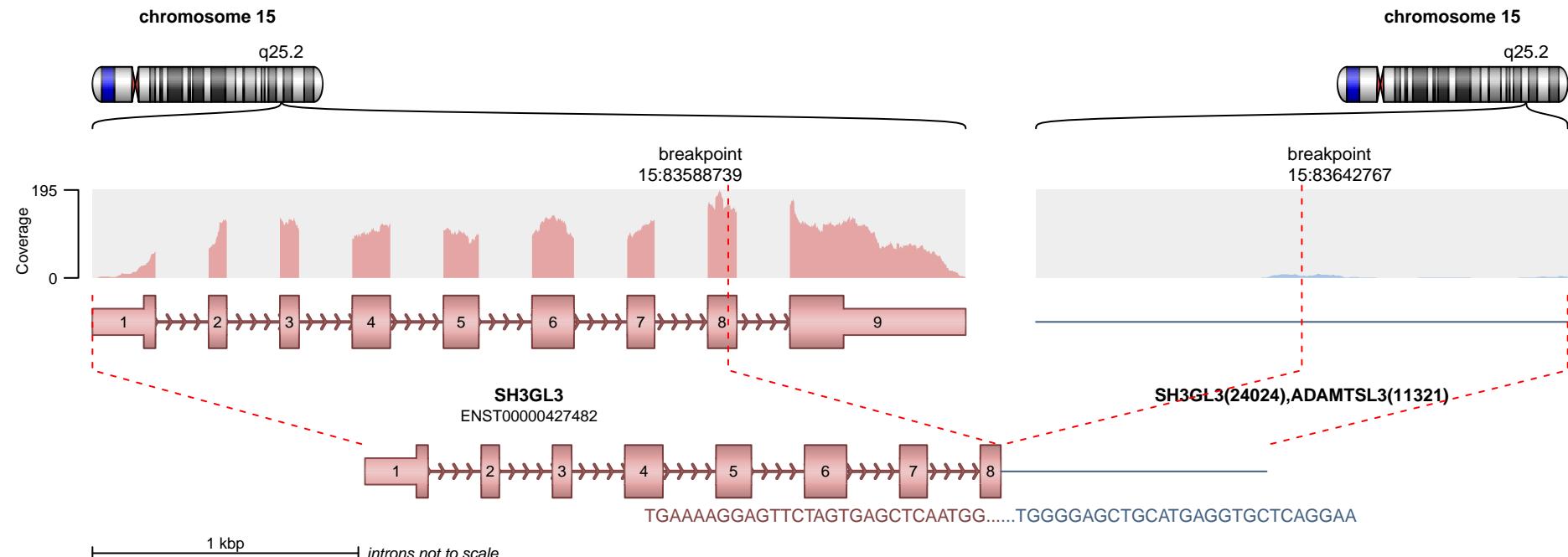


— translocation — deletion
— duplication — inversion

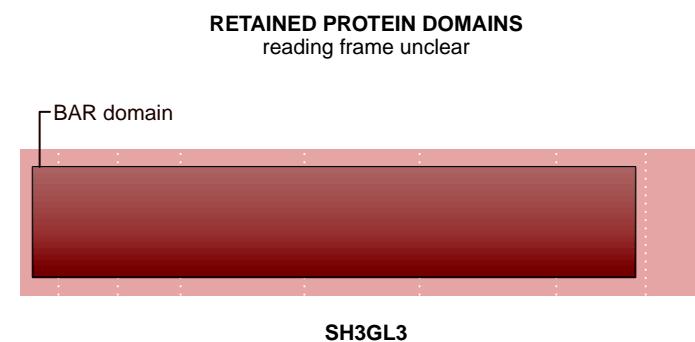


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 1

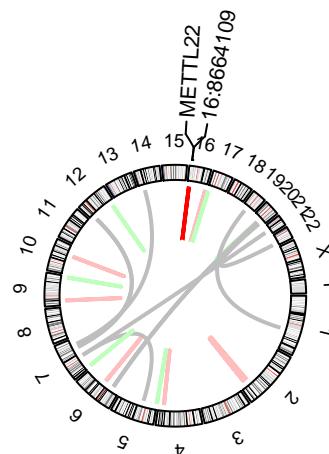
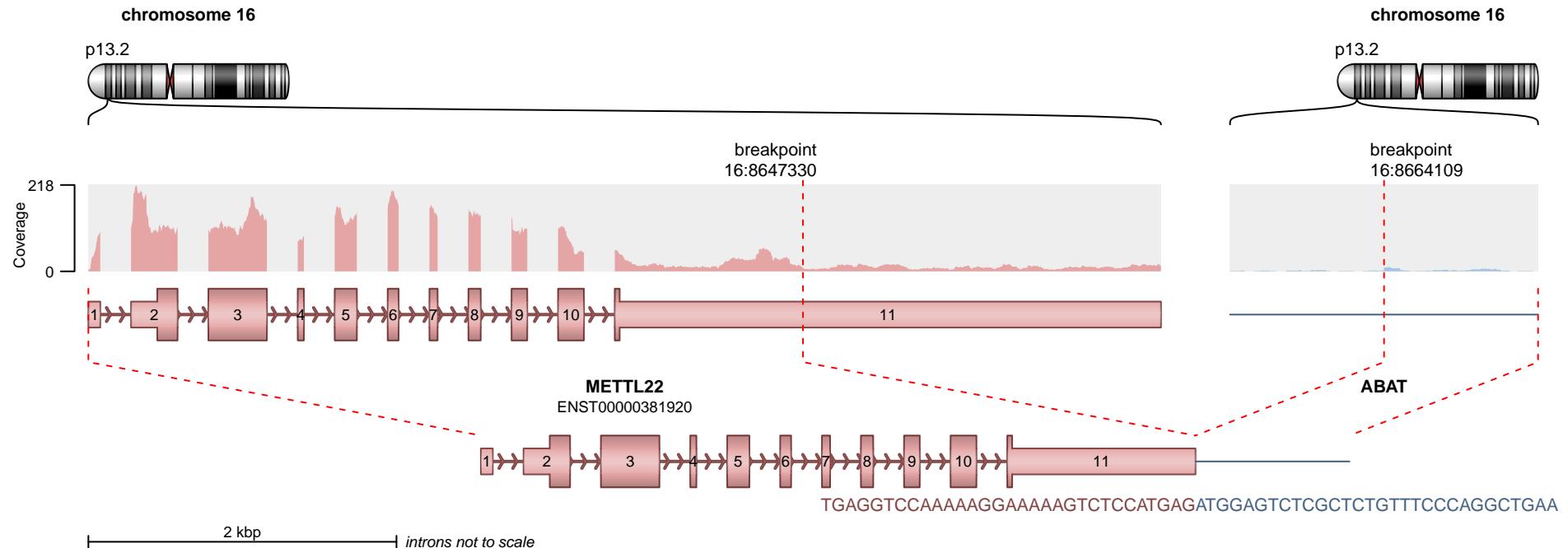


— translocation — deletion
— duplication — inversion

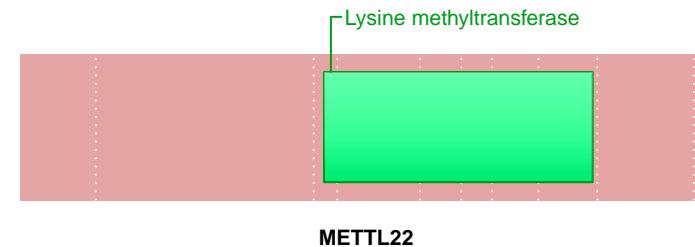


SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 3



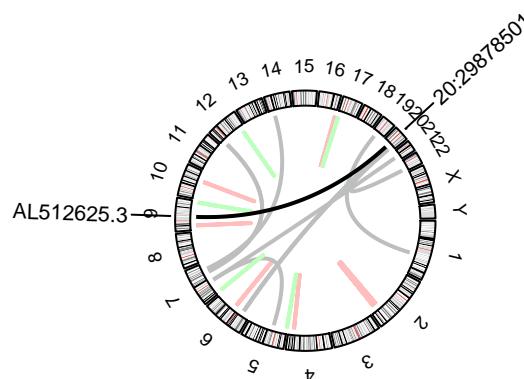
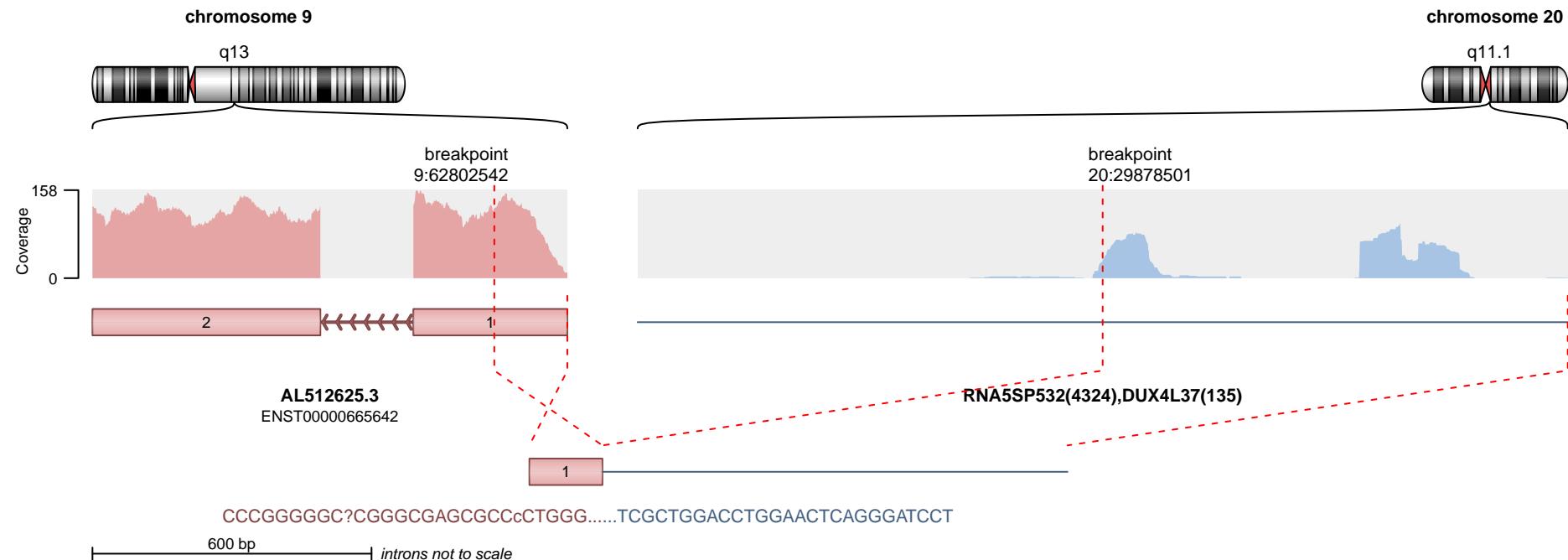
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 2

— translocation — deletion
— duplication — inversion

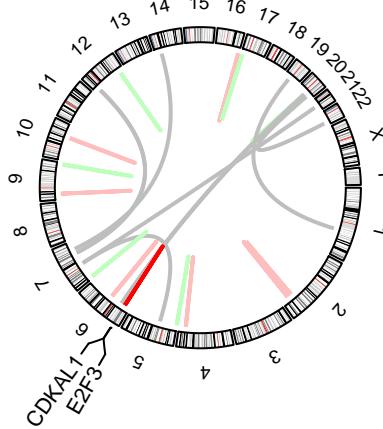
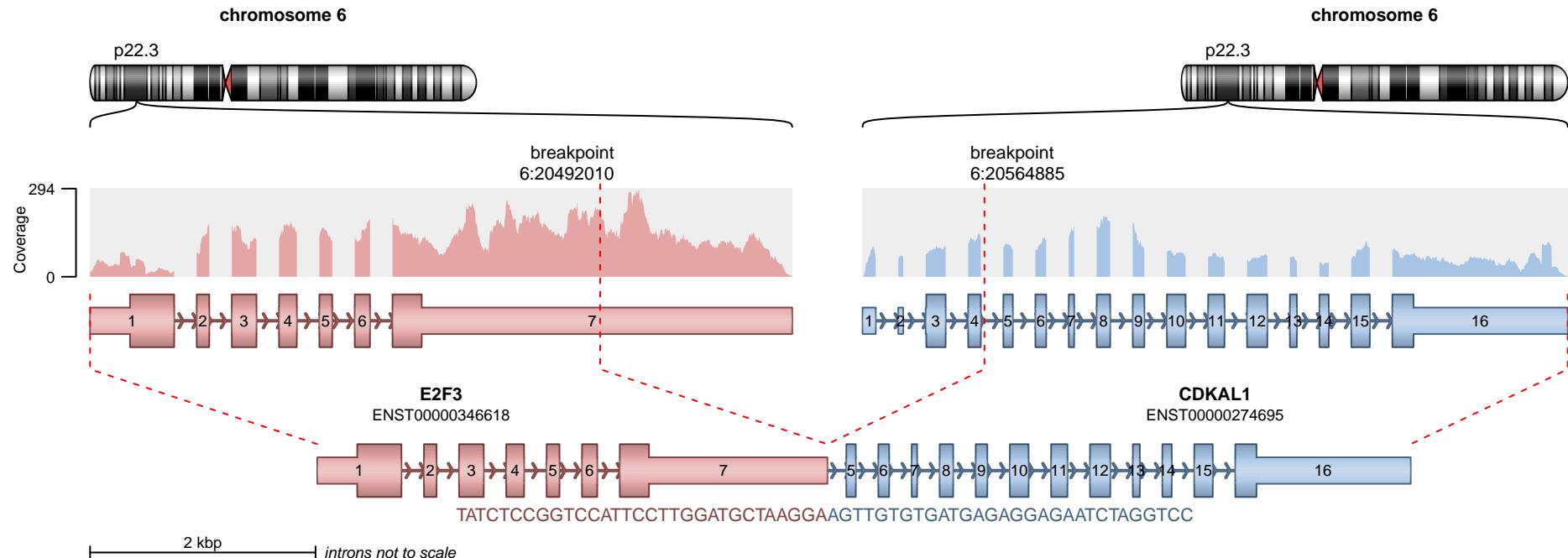


Genes are not protein-coding.

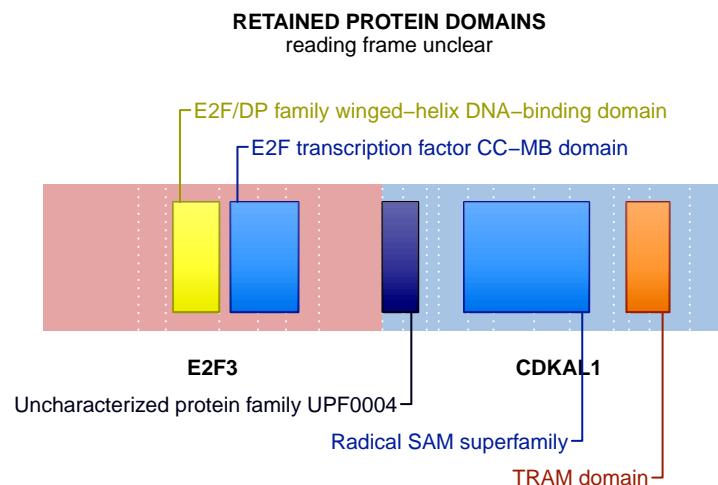
SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 3

— translocation — deletion
— duplication — inversion

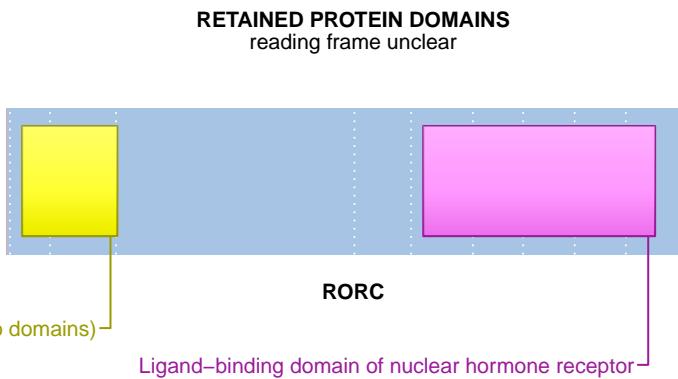
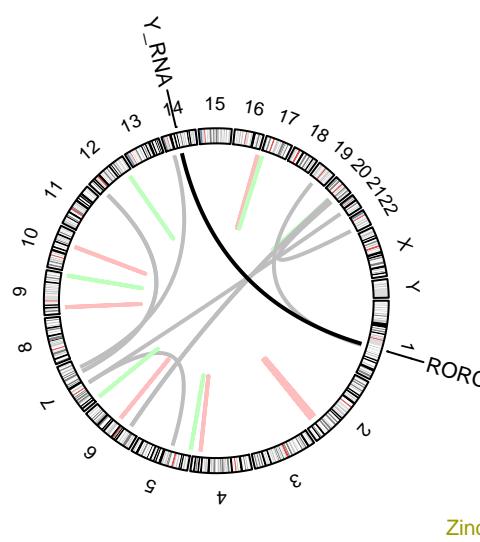
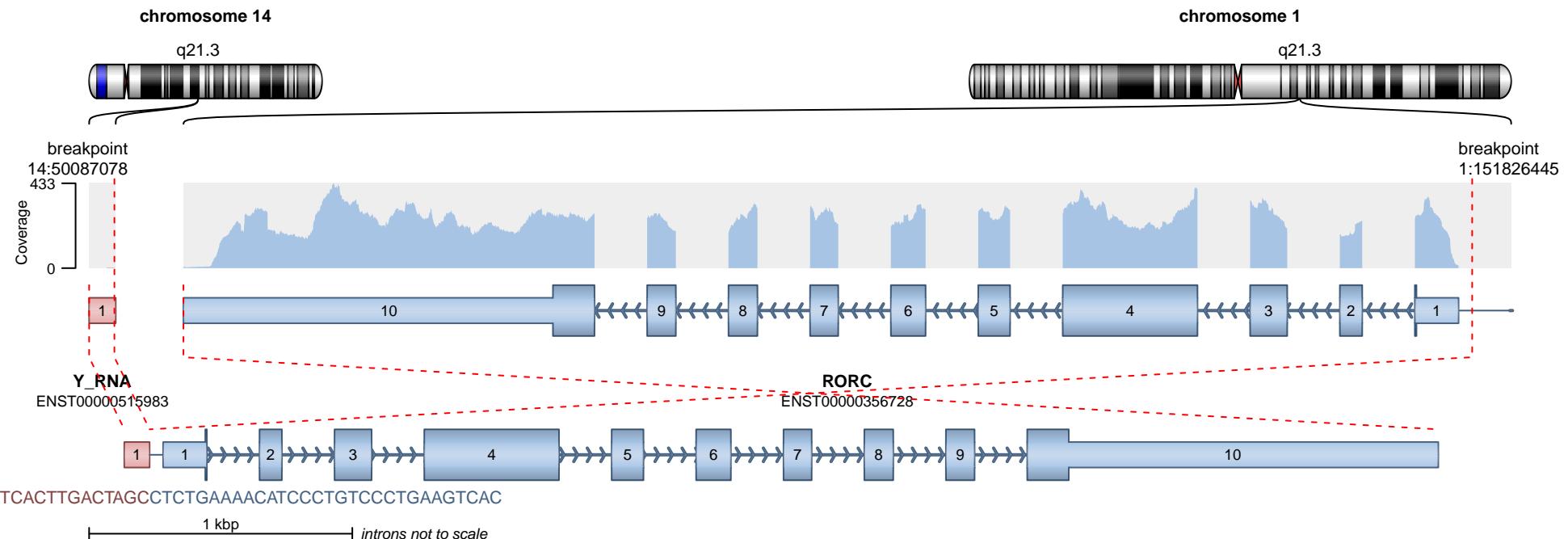


— translocation
— duplication
— deletion
— inversion

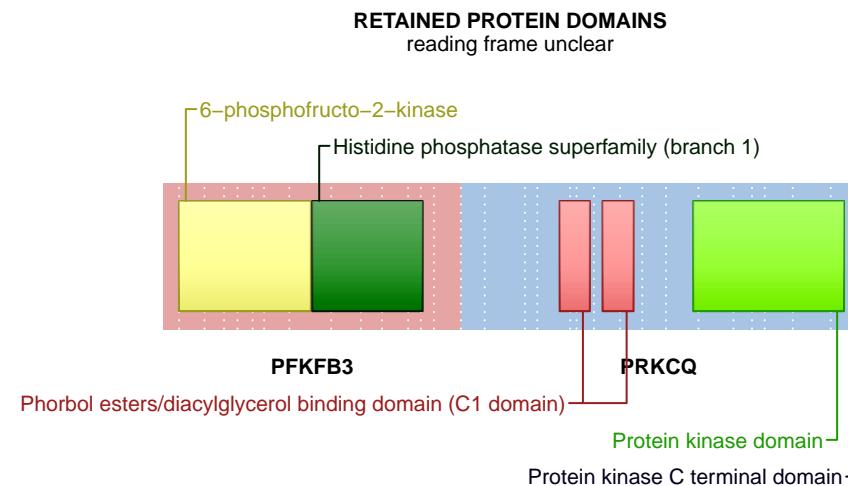
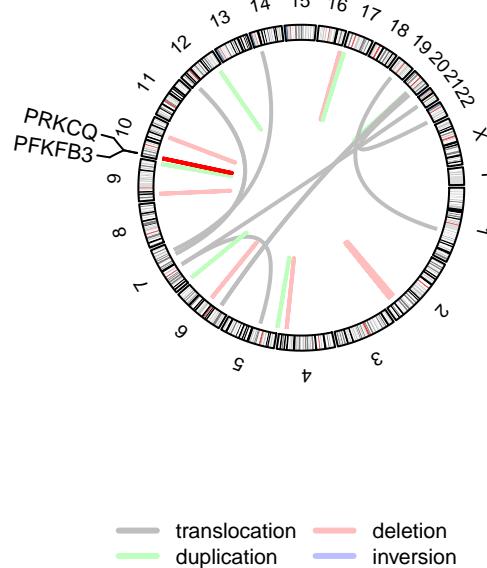
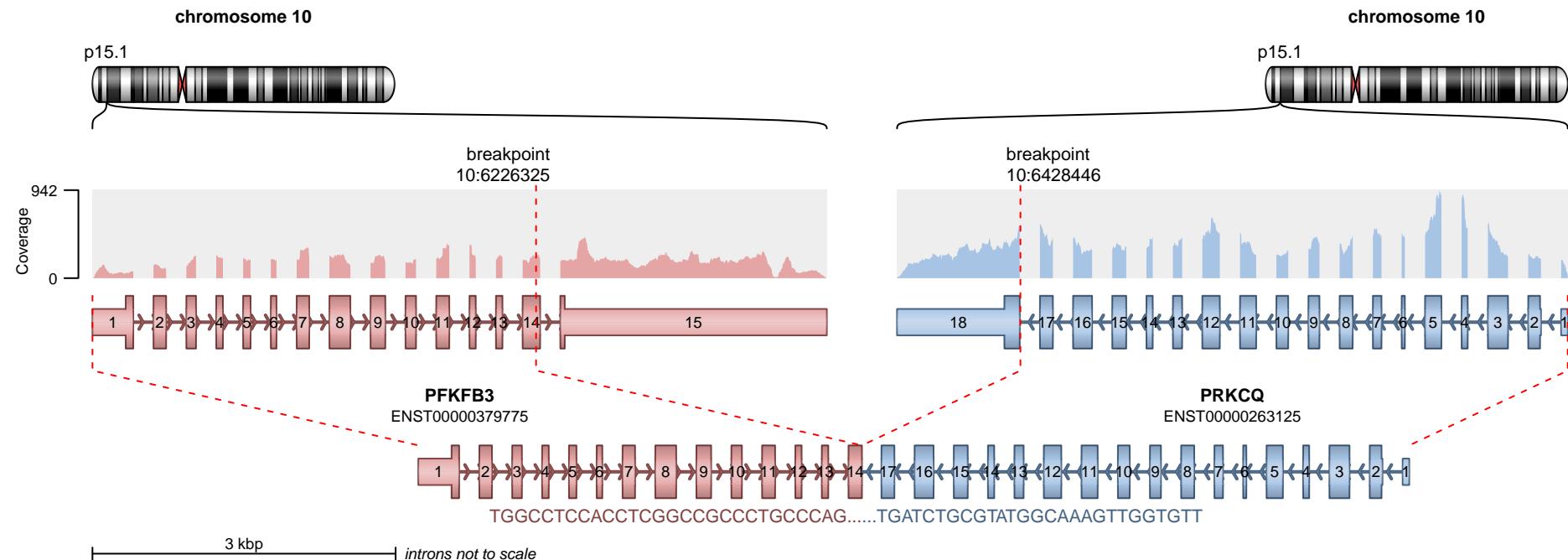


SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

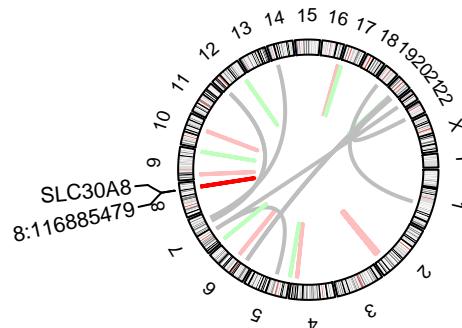
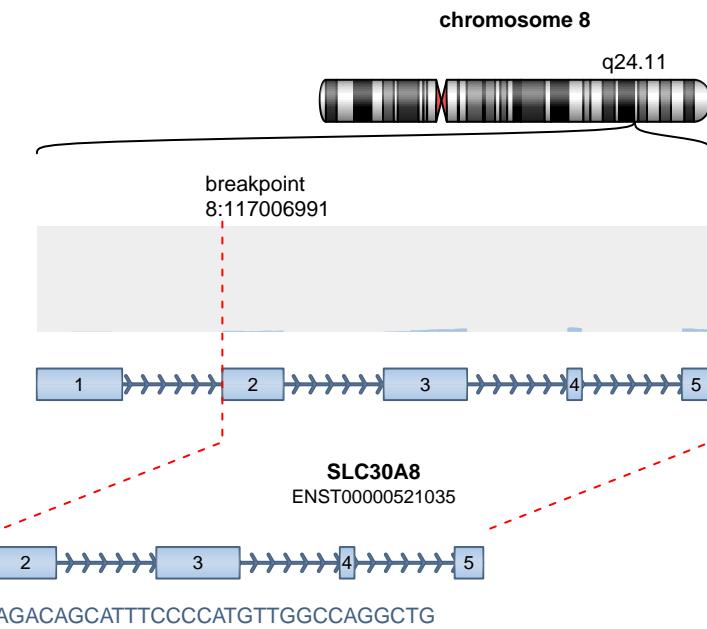
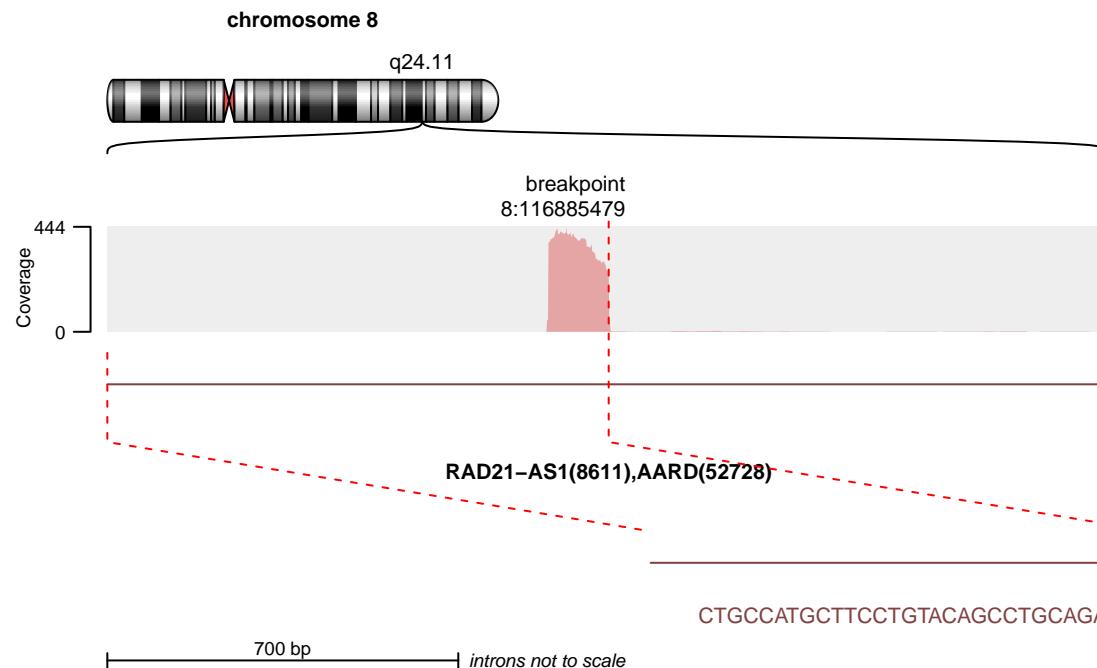


— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 3

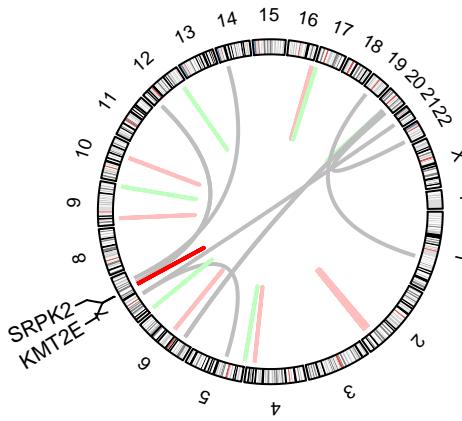
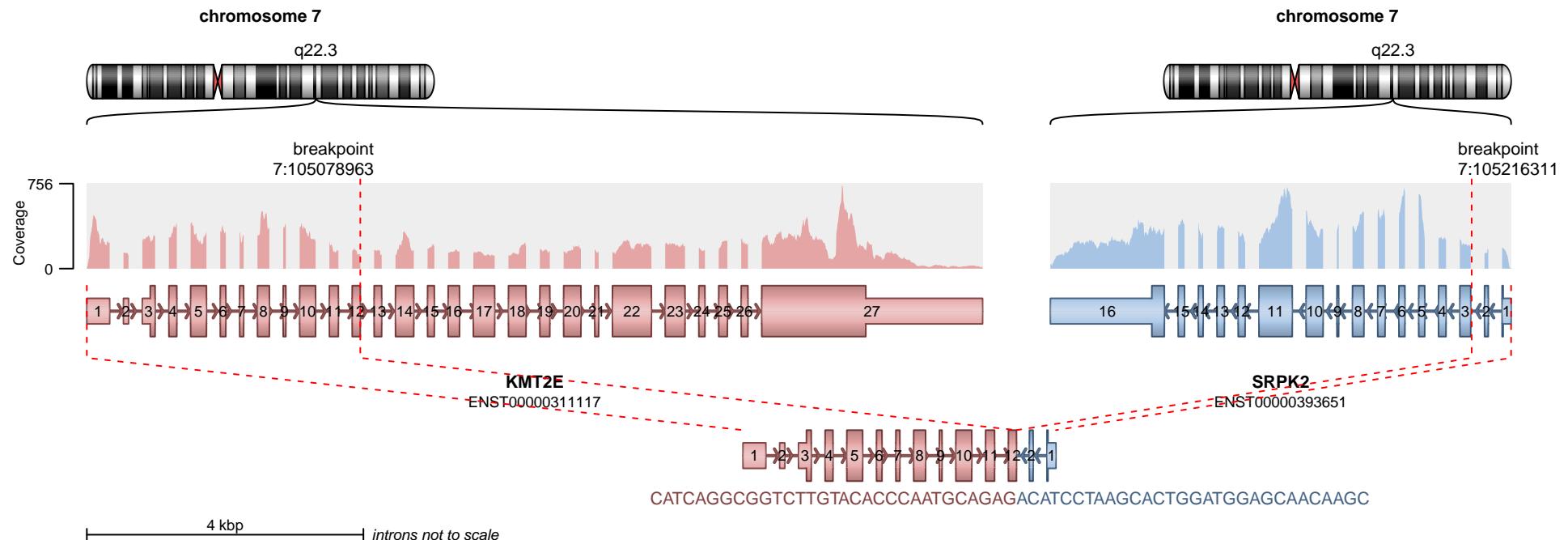


Genes are not protein-coding.

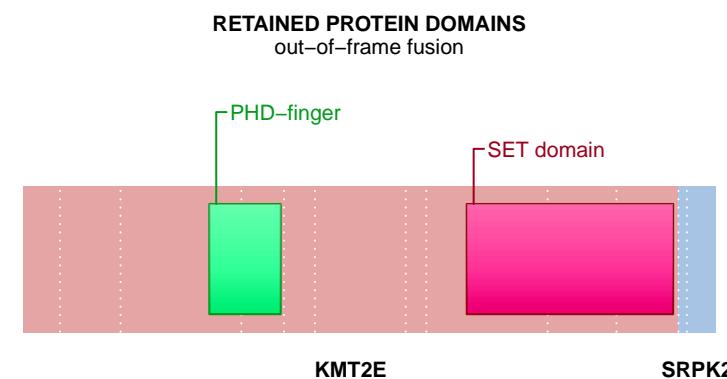
SUPPORTING READ COUNT

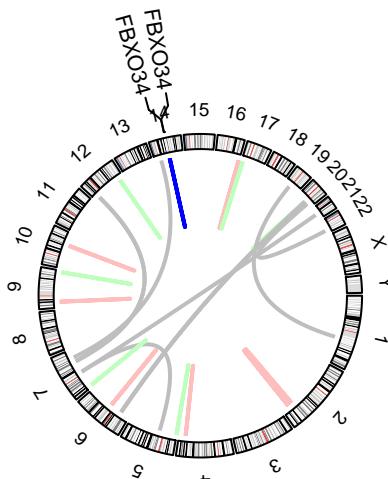
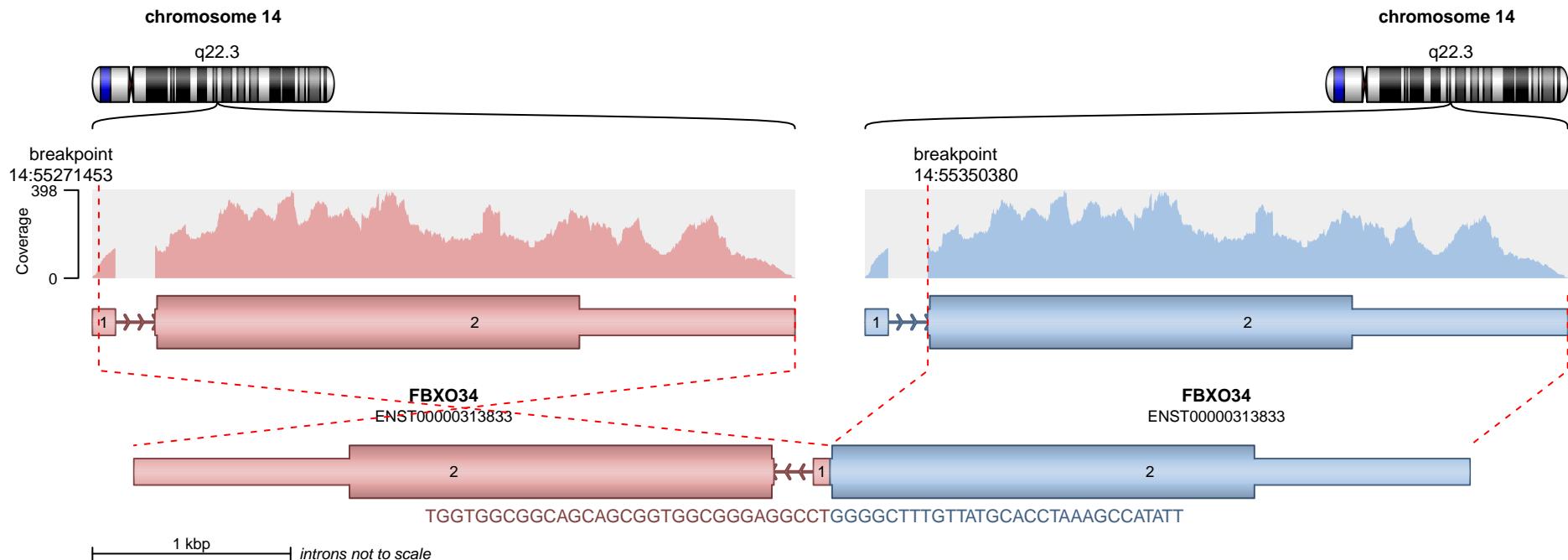
Split reads = 2
Discordant mates = 0

— translocation — deletion
— duplication — inversion



— translocation — deletion
— duplication — inversion



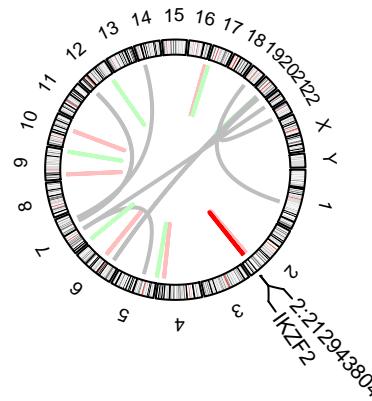
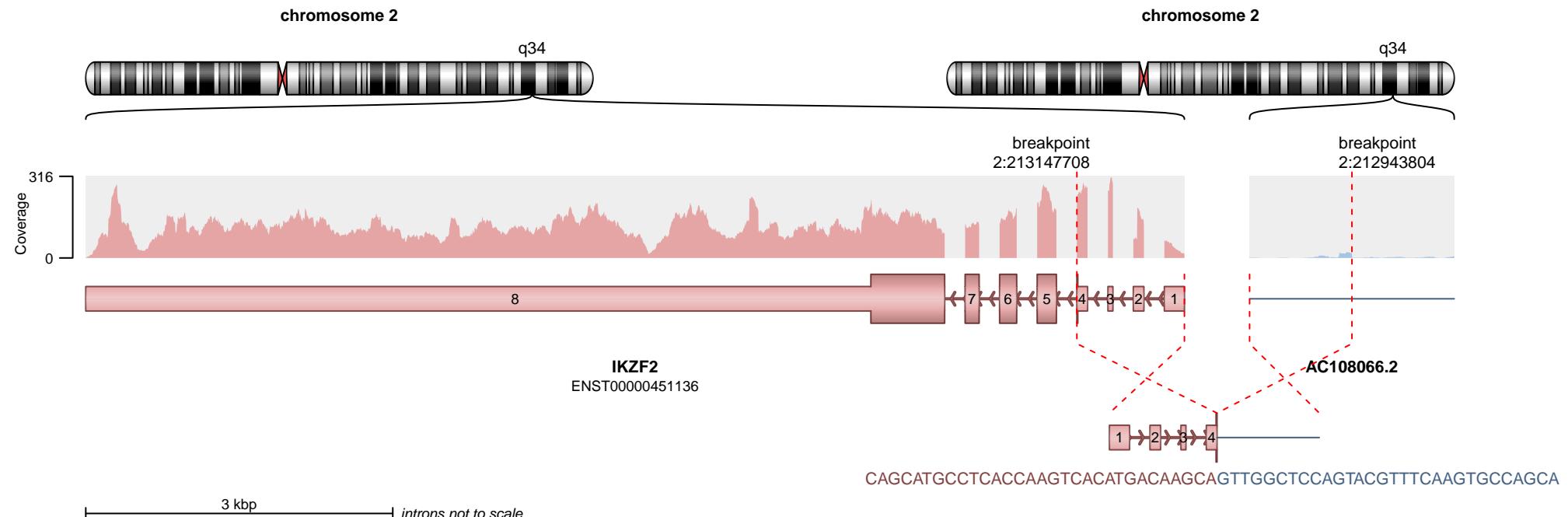


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

— translocation — deletion
— duplication — inversion

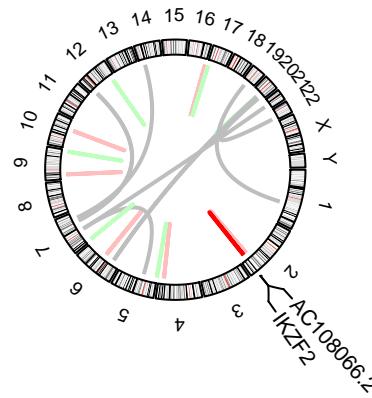
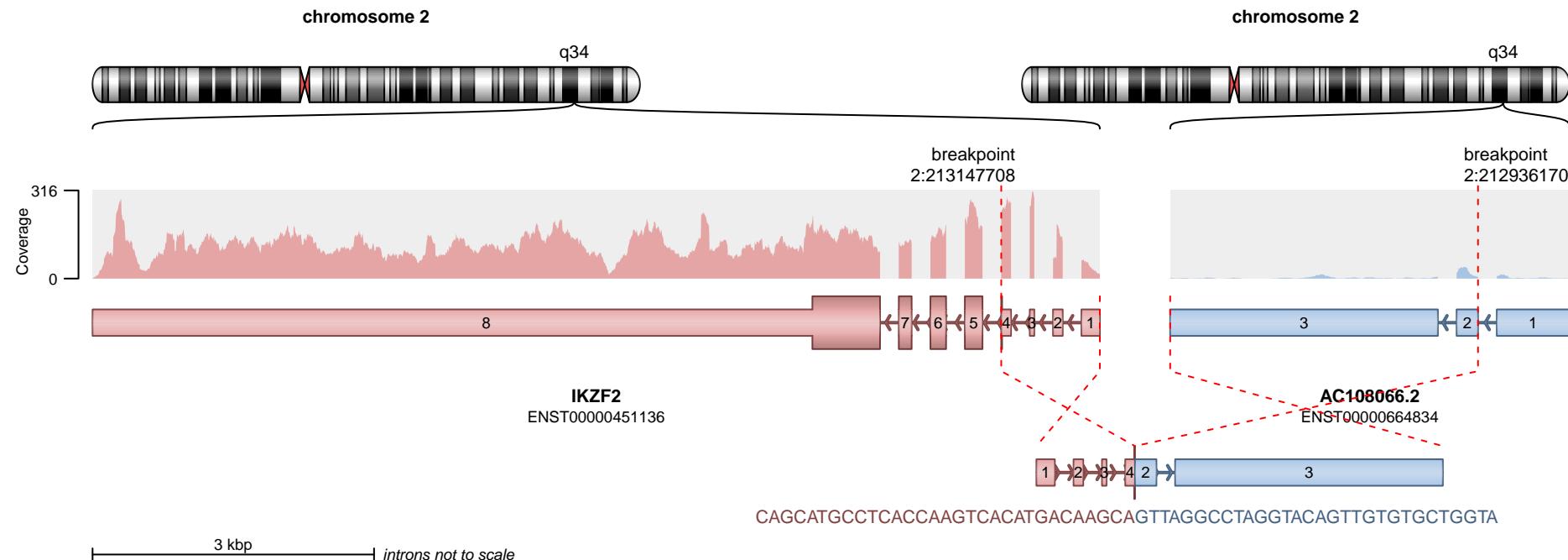


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

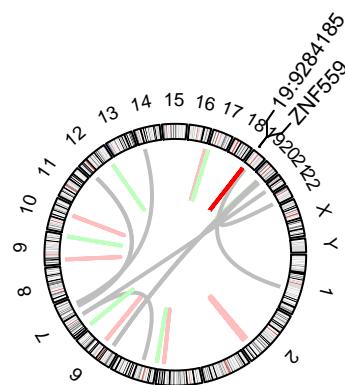
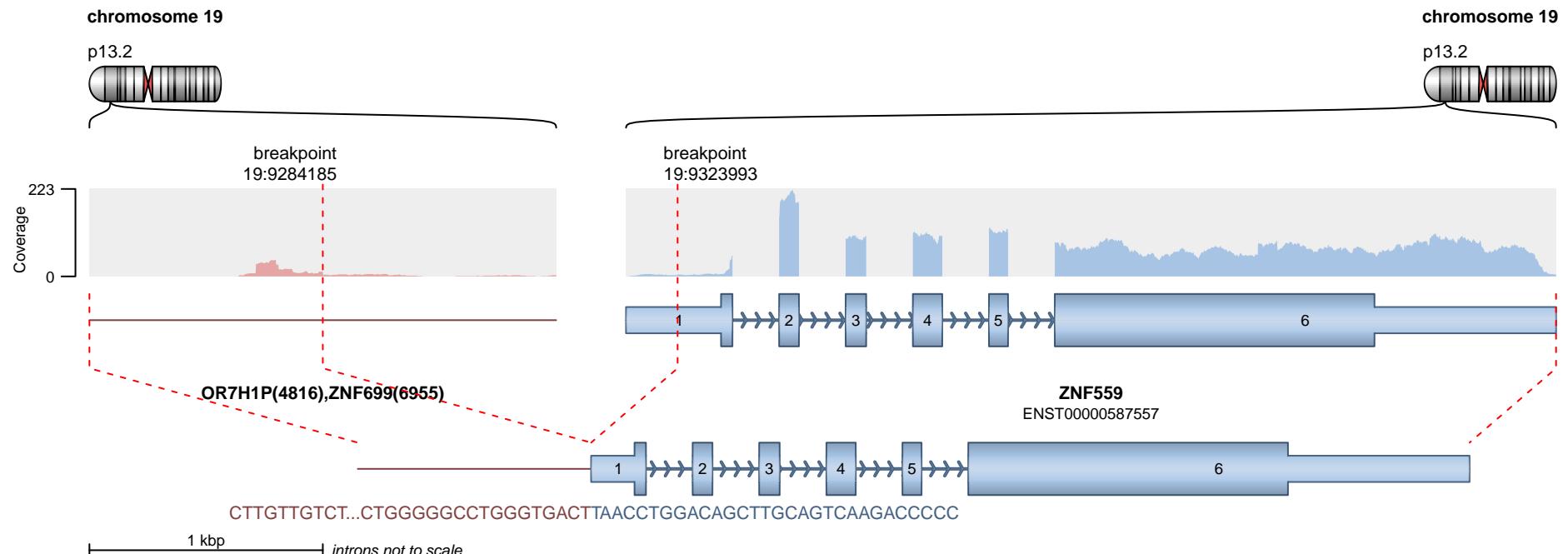


No protein domains retained in fusion.

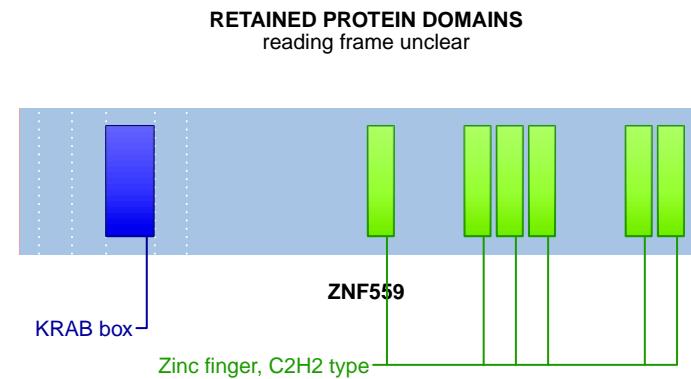
SUPPORTING READ COUNT

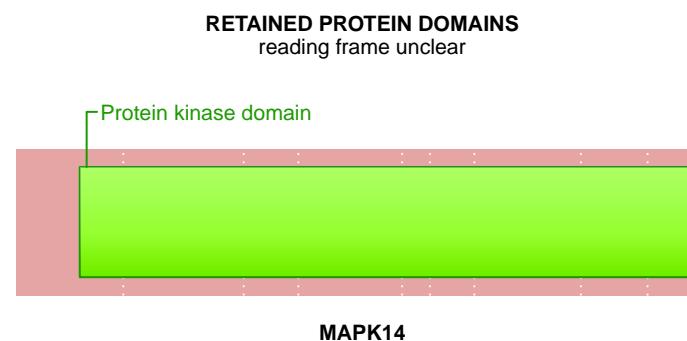
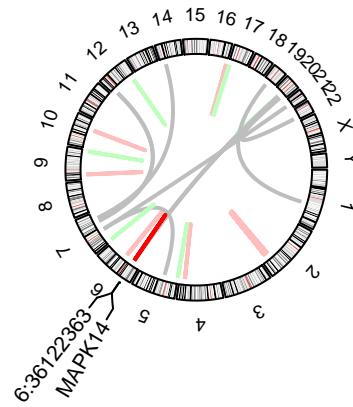
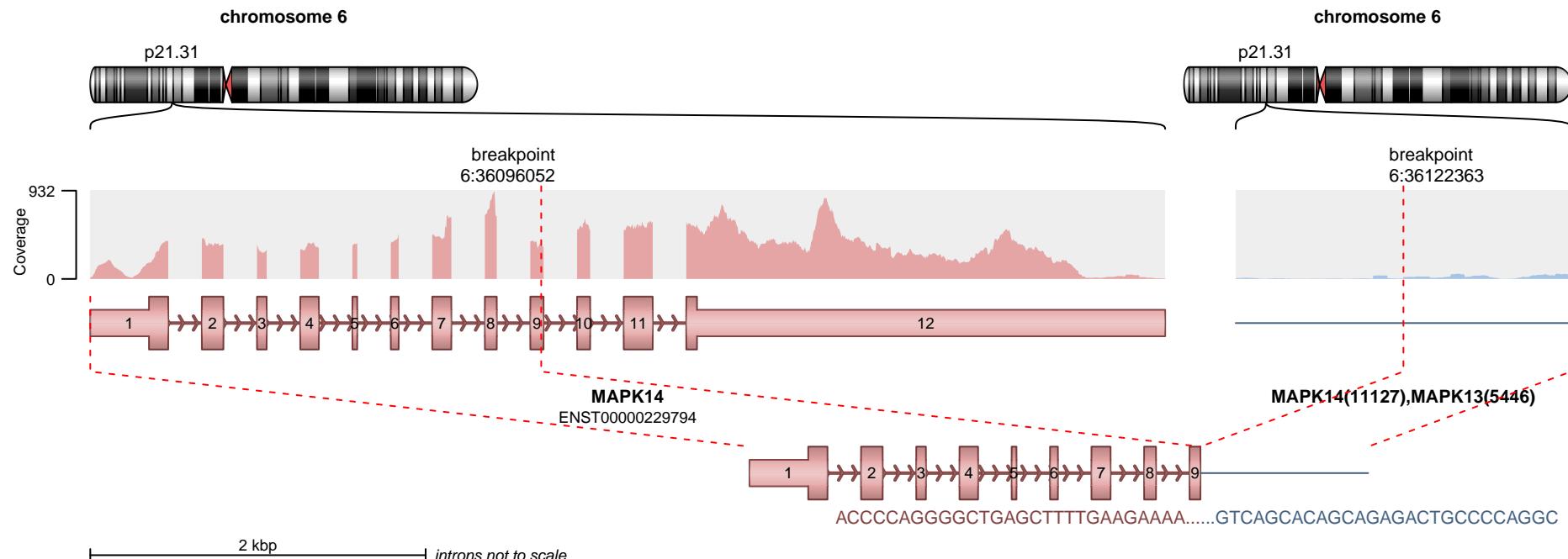
Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



— translocation — deletion
— duplication — inversion

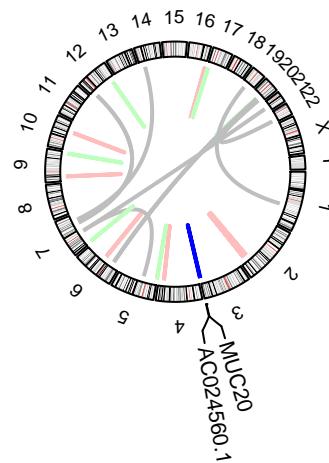
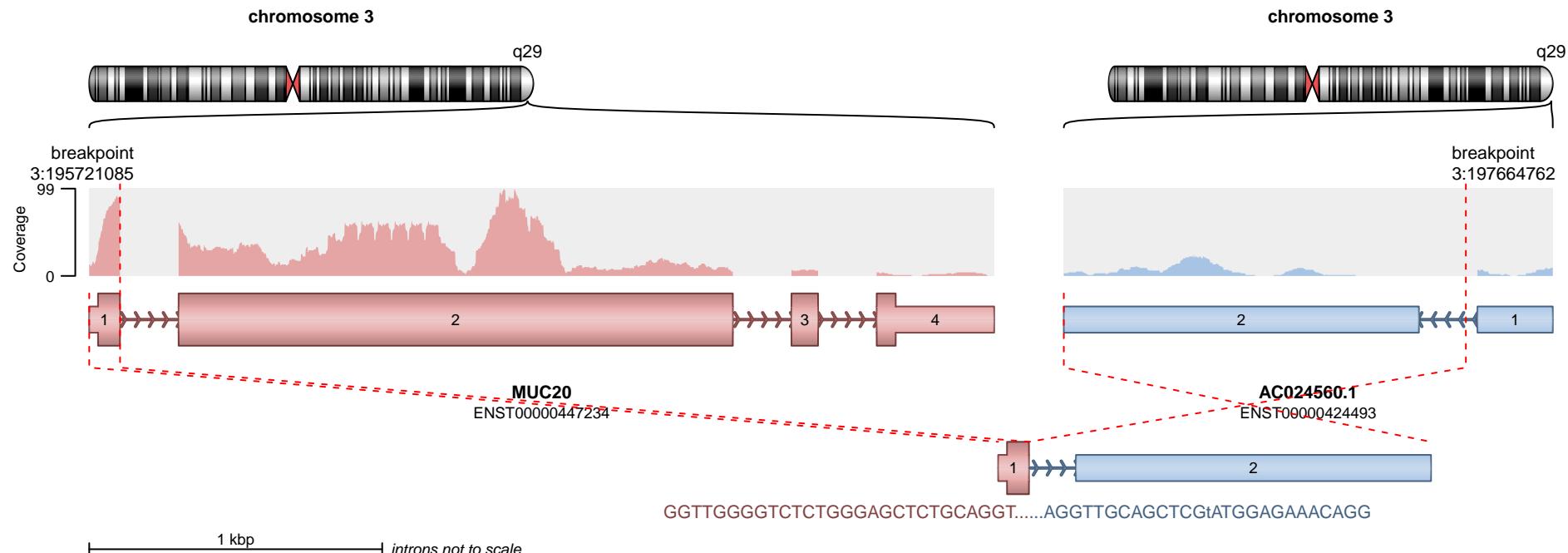




SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 2

— translocation — deletion
— duplication — inversion

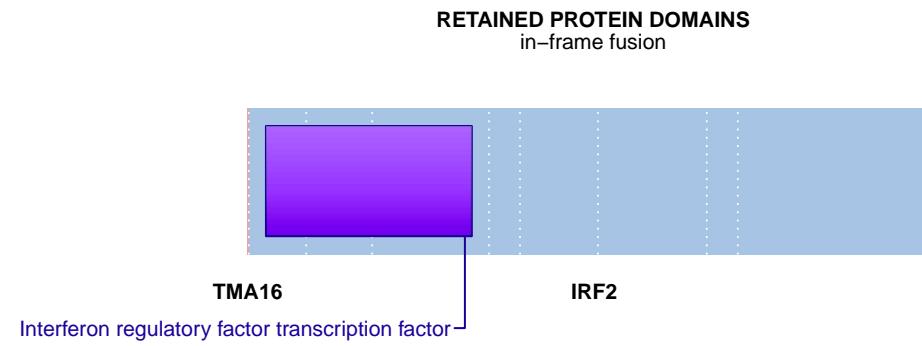
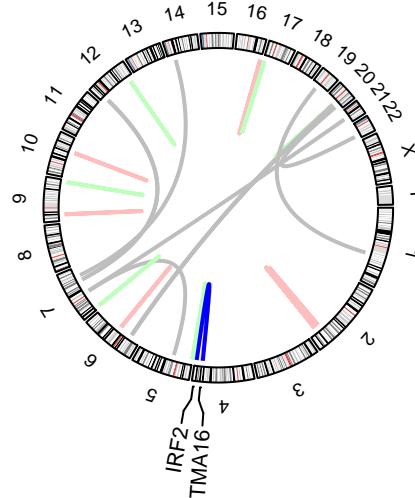
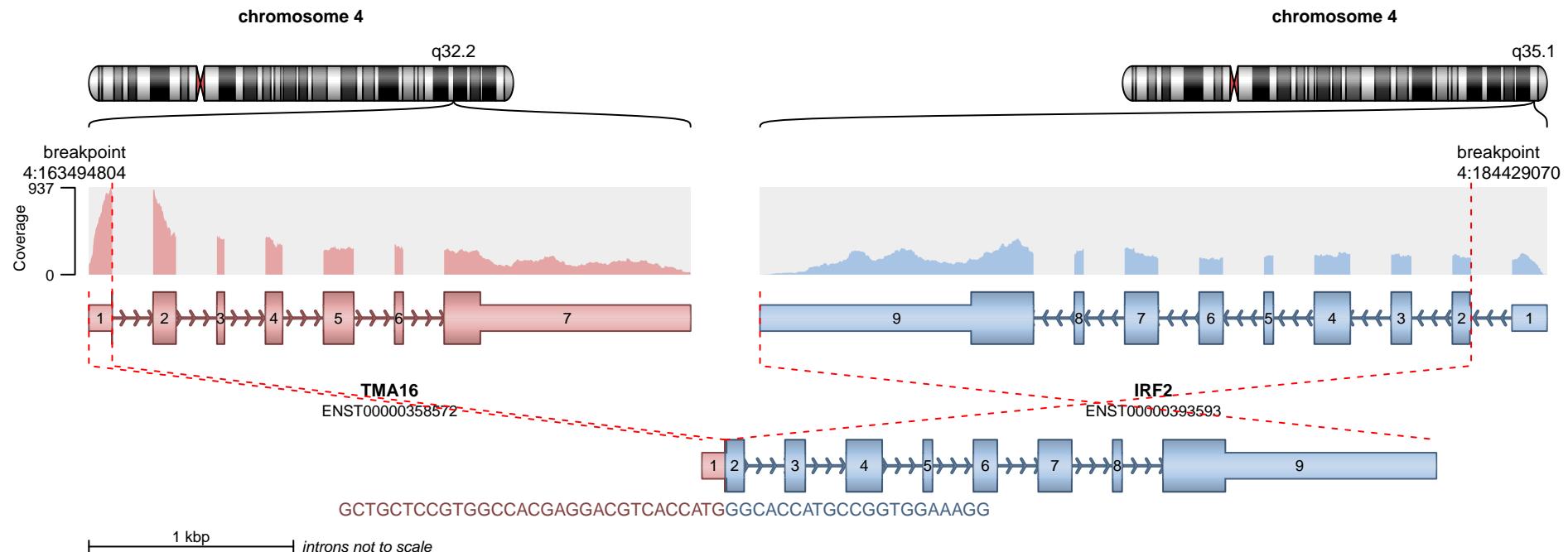


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

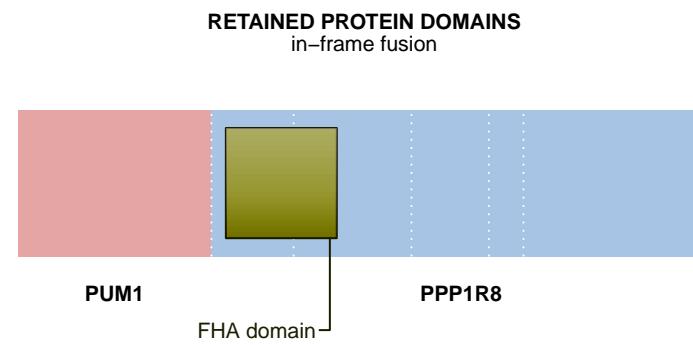
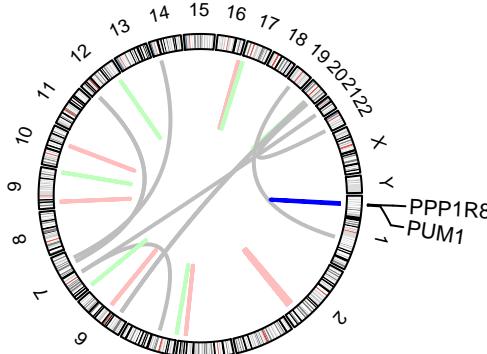
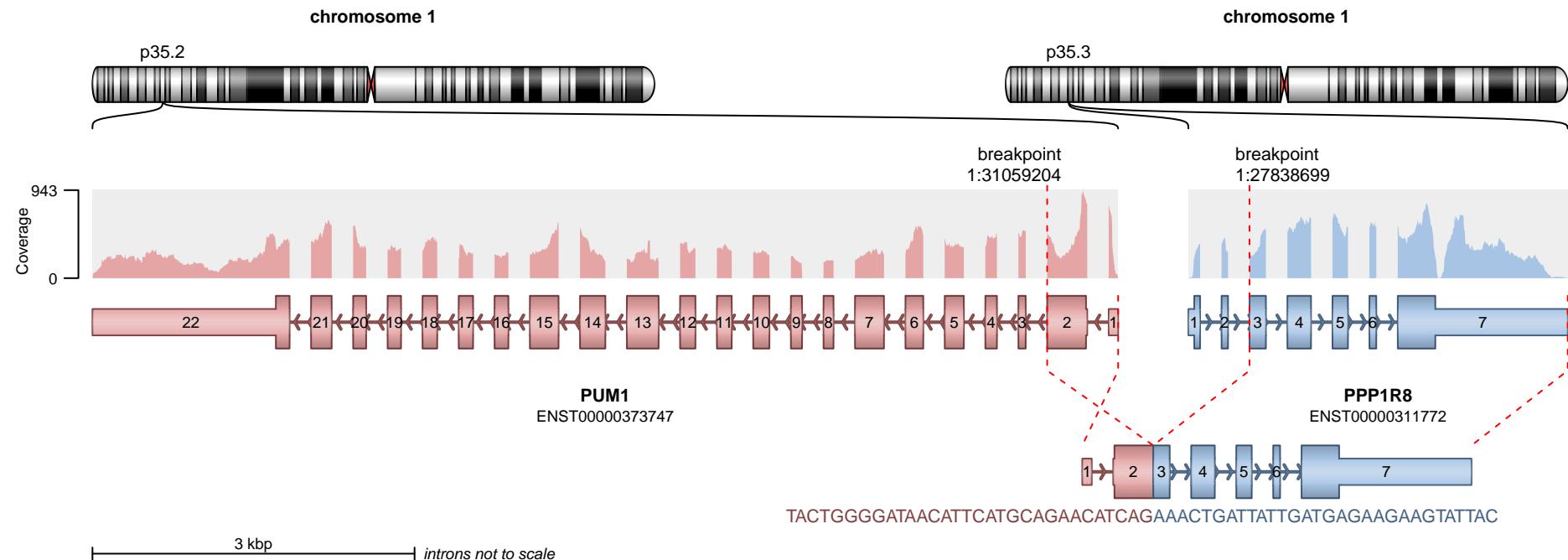
Split reads = 0
Discordant mates = 2



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

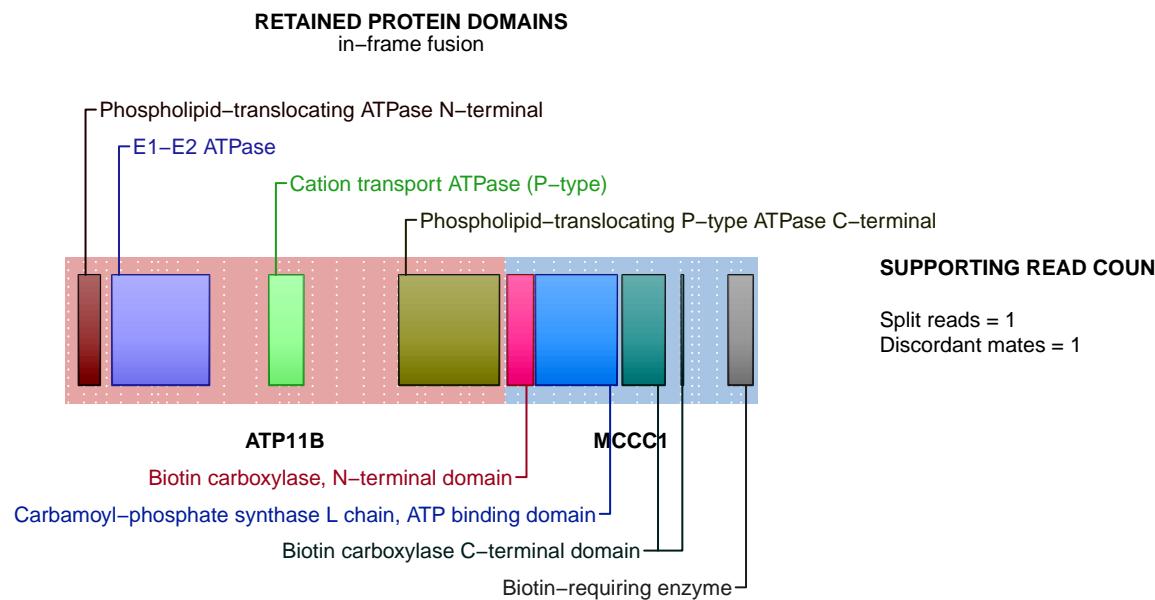
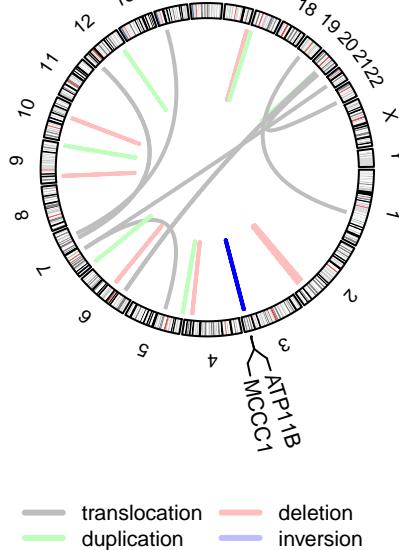
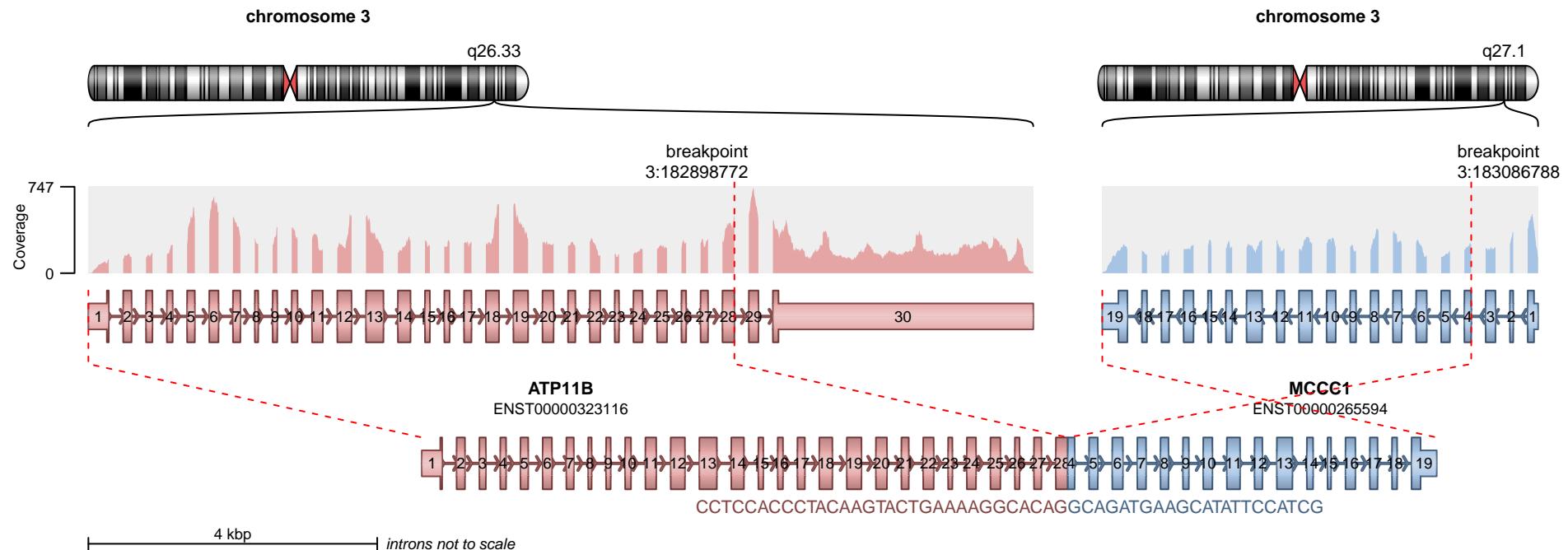
— translocation — deletion
— duplication — inversion

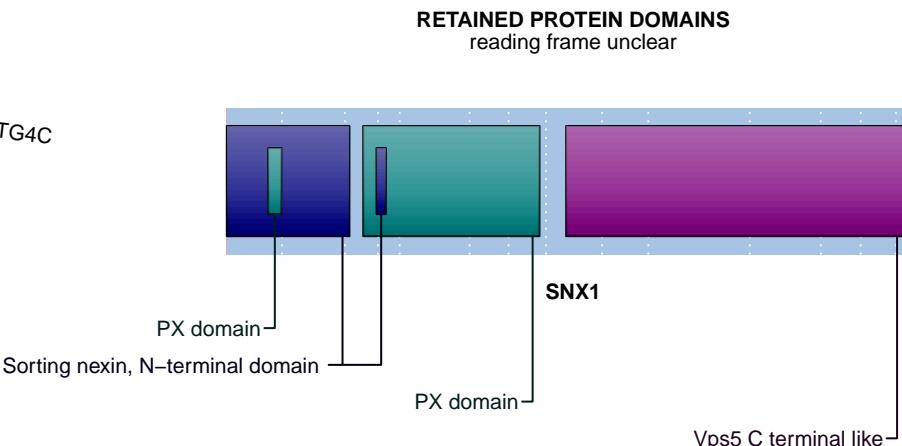
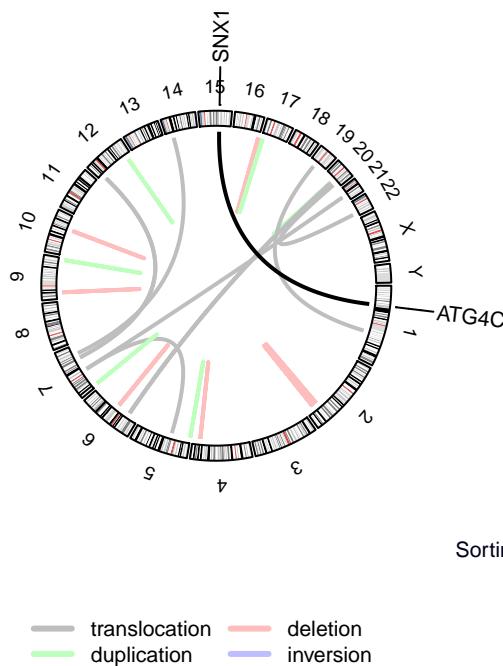
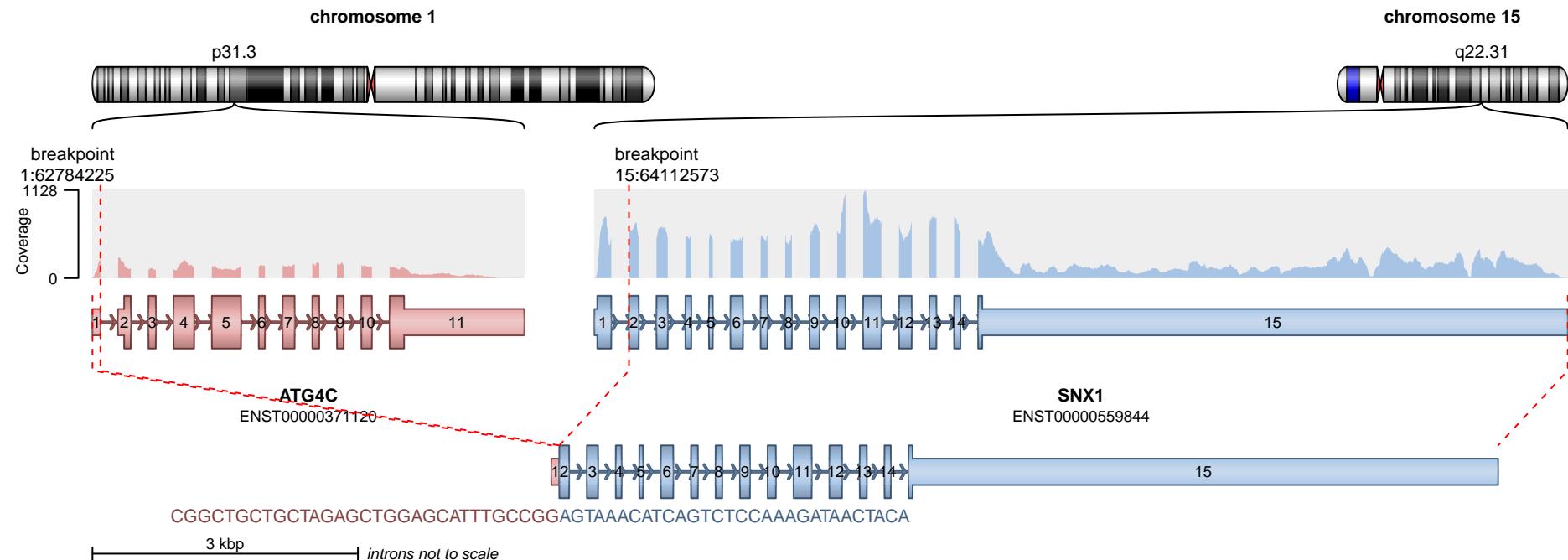


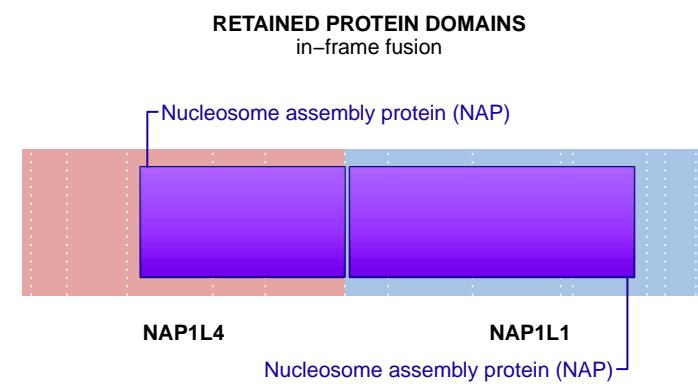
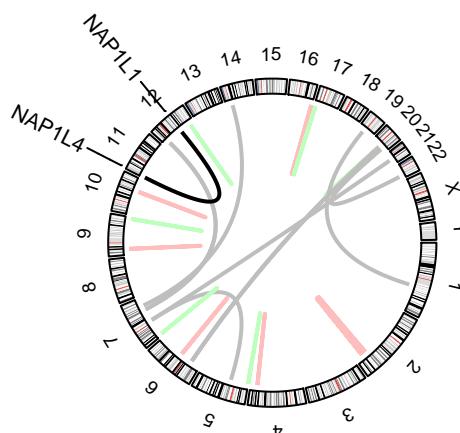
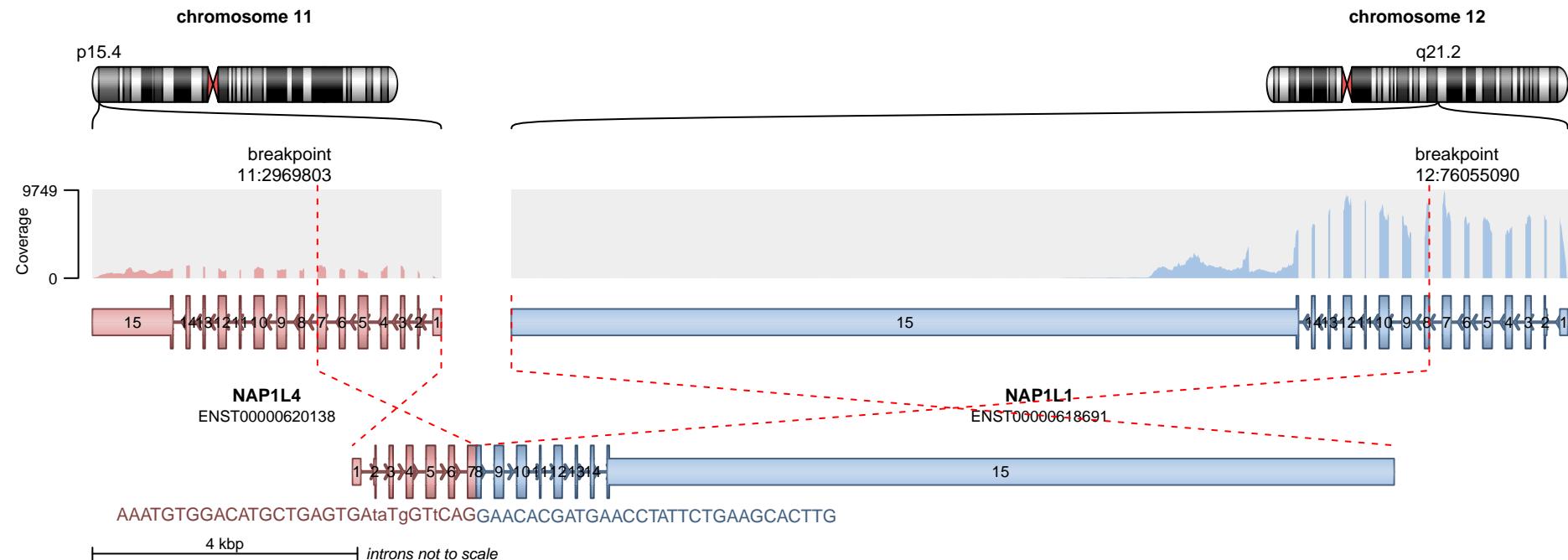
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

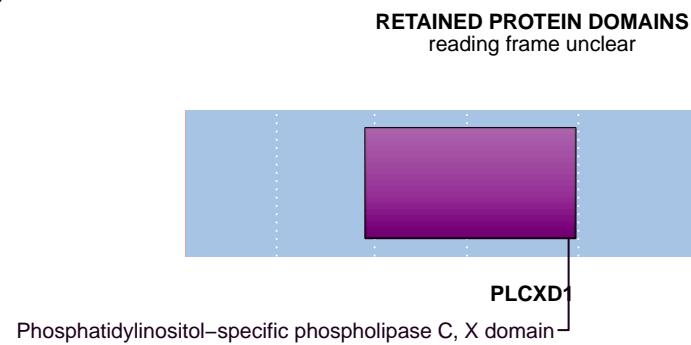
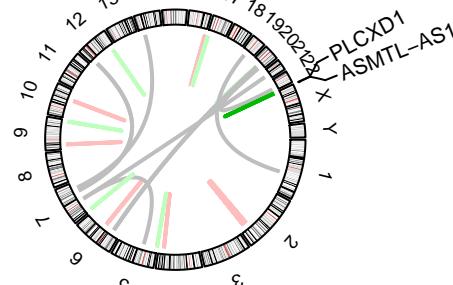
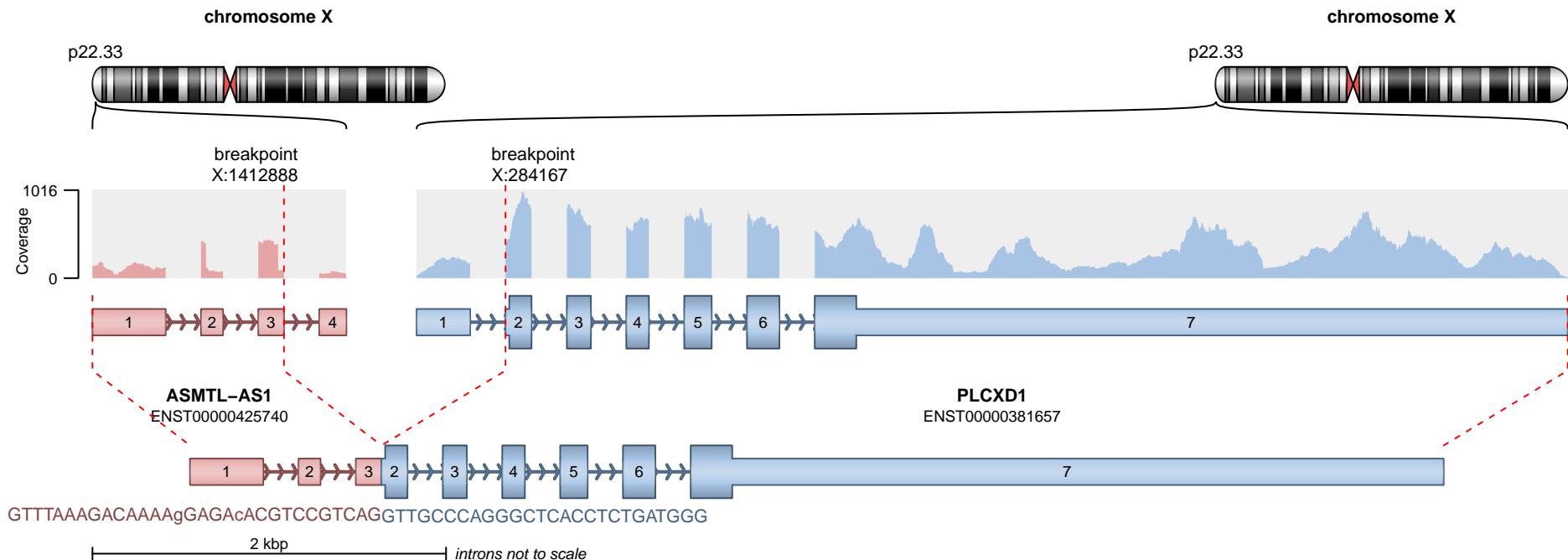
— translocation — deletion
— duplication — inversion







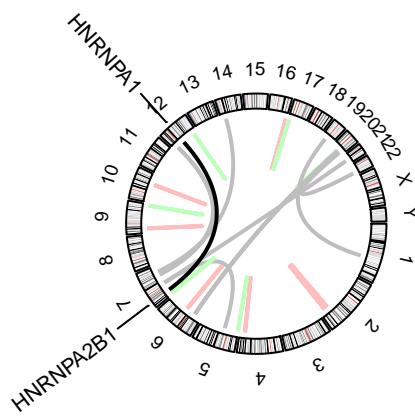
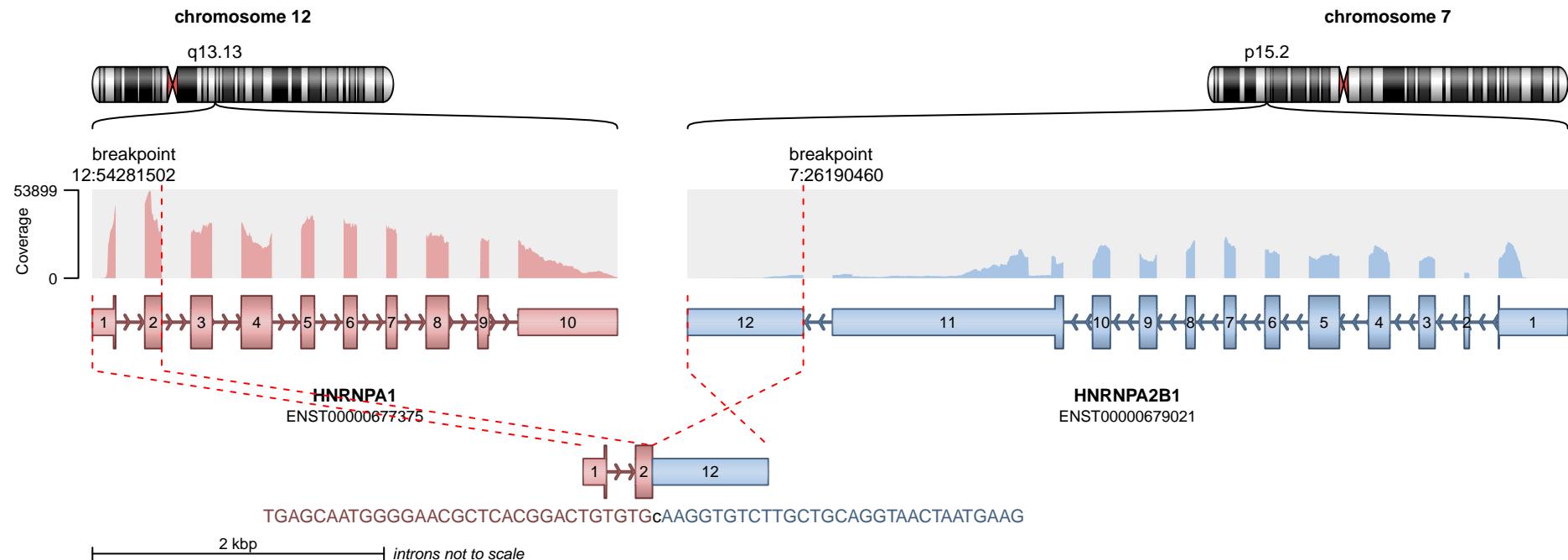
— translocation — deletion
— duplication — inversion



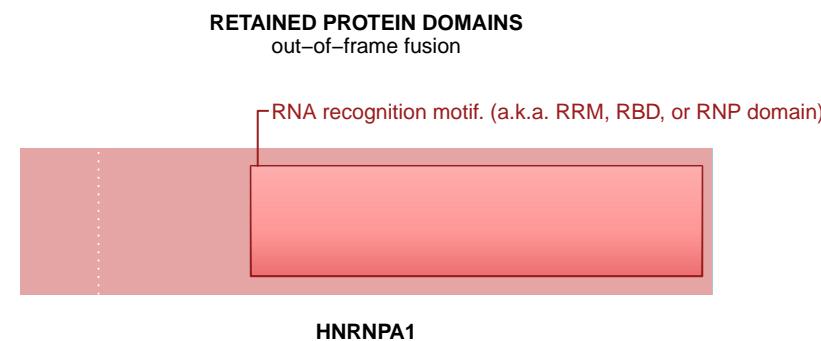
SUPPORTING READ COUNT

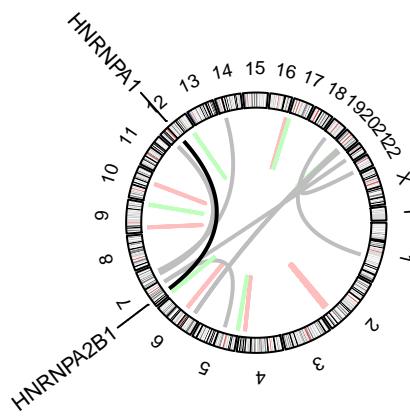
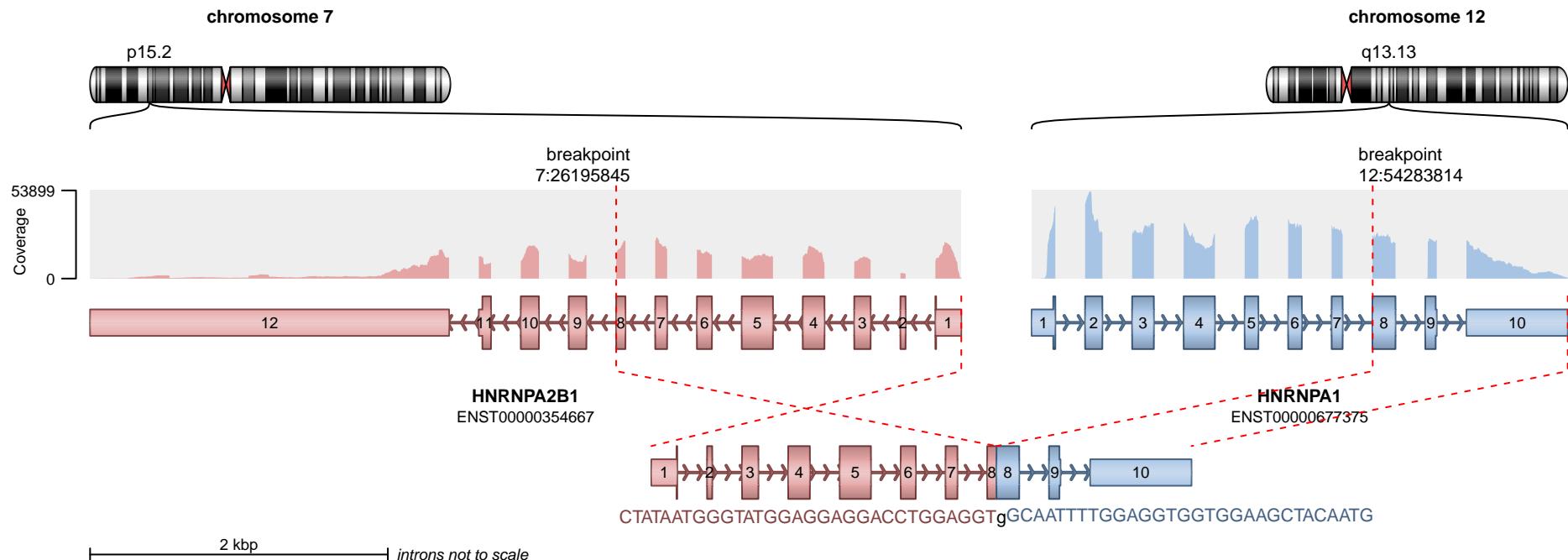
Split reads = 1
Discordant mates = 1

— translocation — deletion
— duplication — inversion

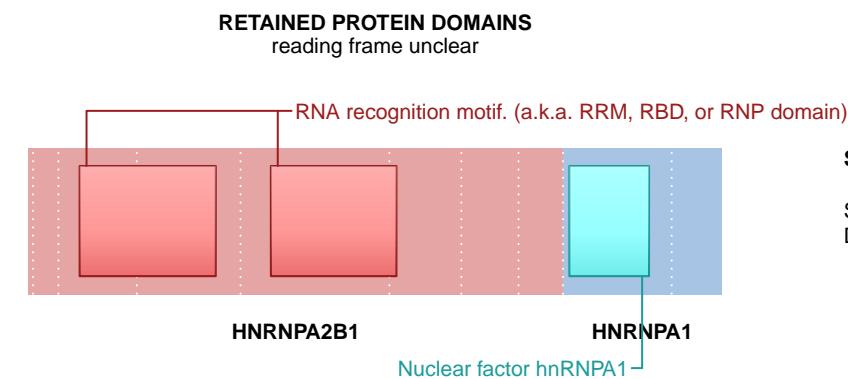


— translocation — deletion
— duplication — inversion



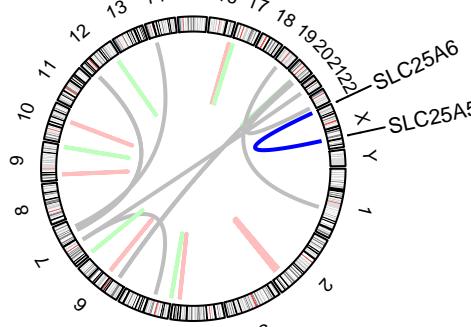
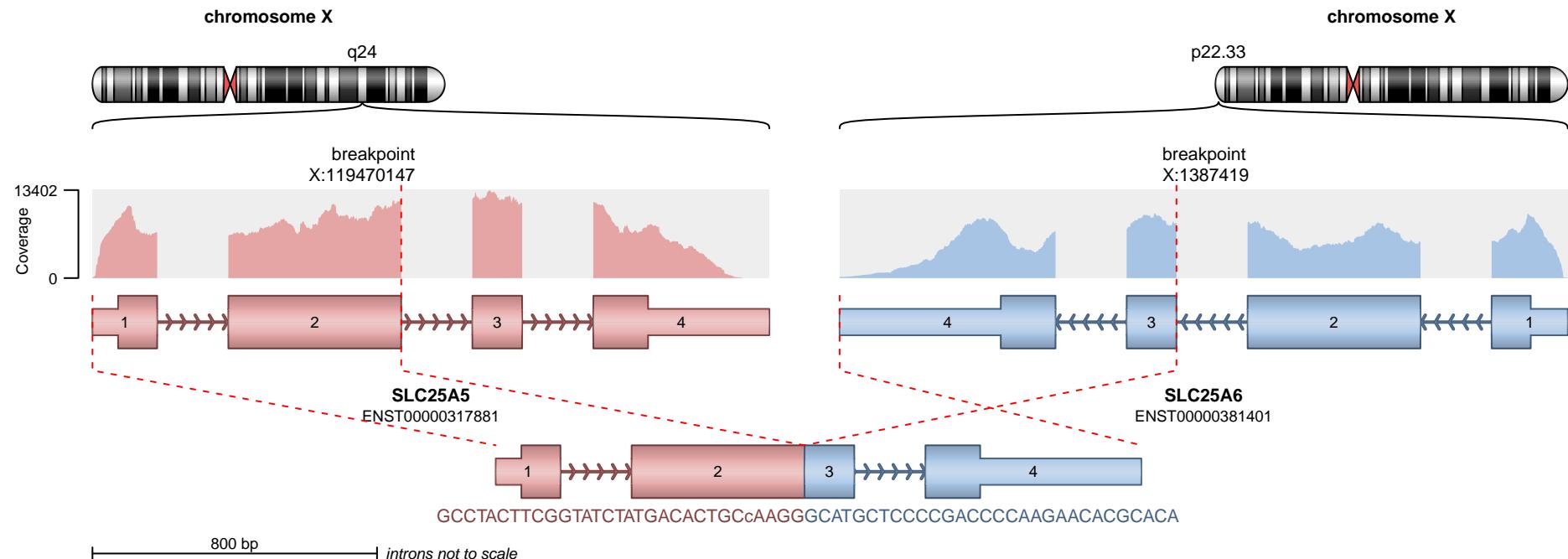


— translocation — deletion
— duplication — inversion

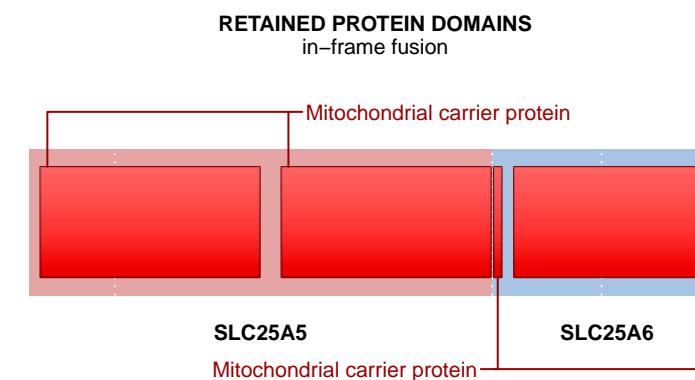


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0