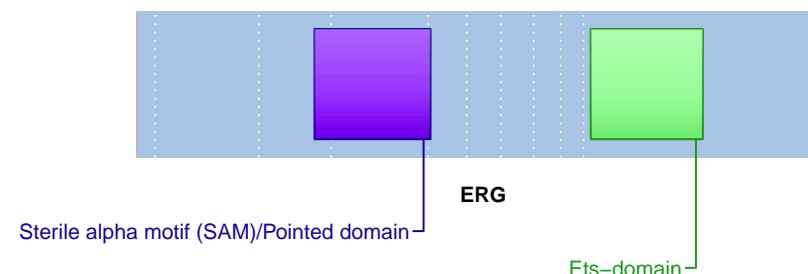


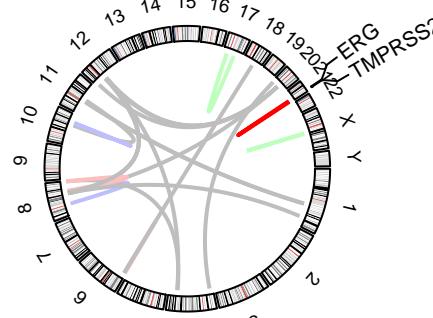
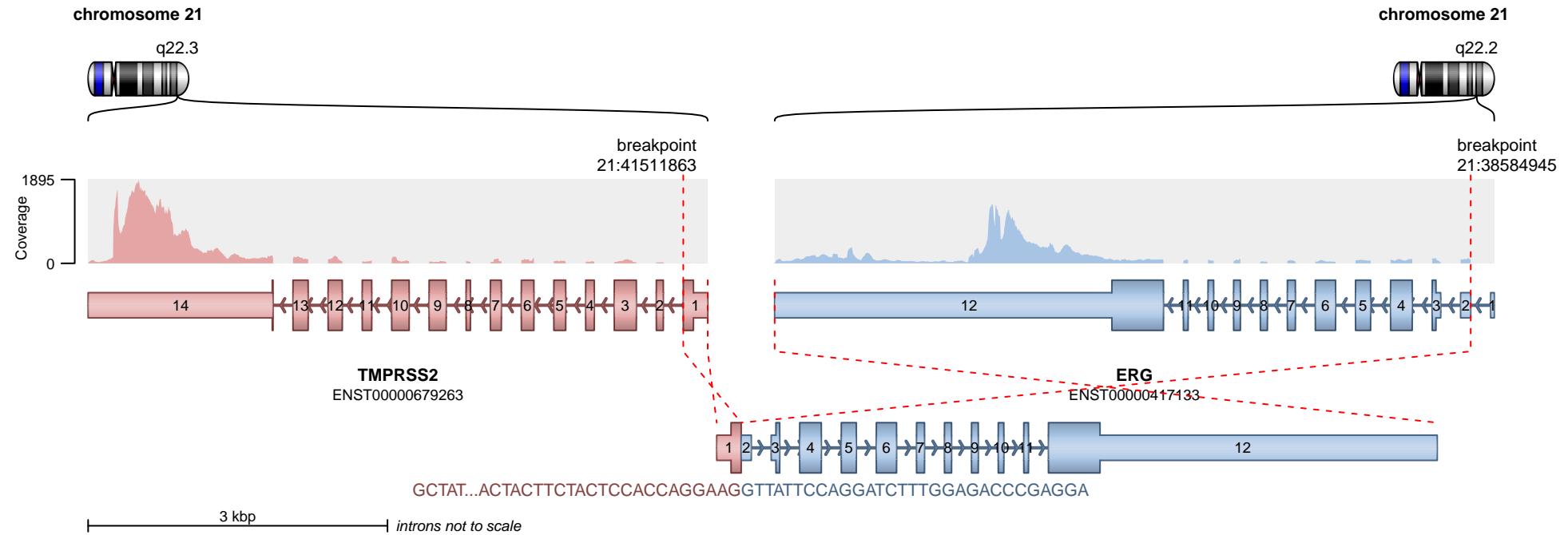
RETAINED PROTEIN DOMAINS reading frame unclear



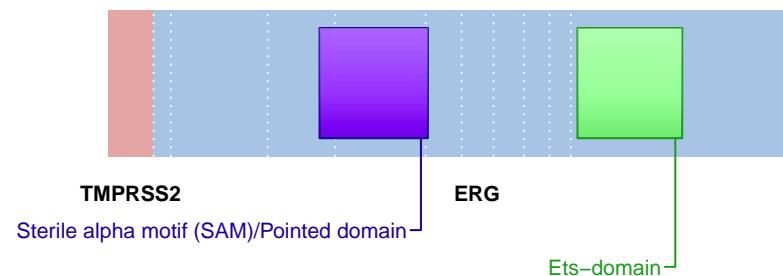
SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 70

— translocation — deletion
— duplication — inversion



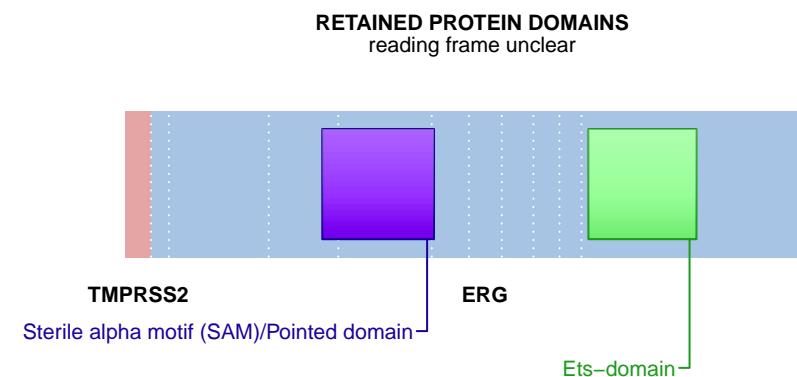
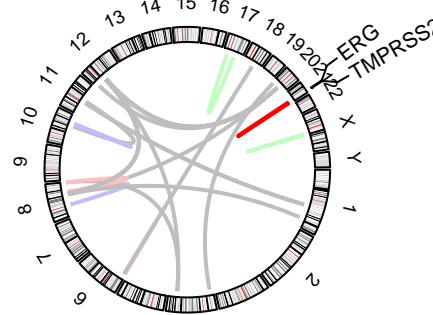
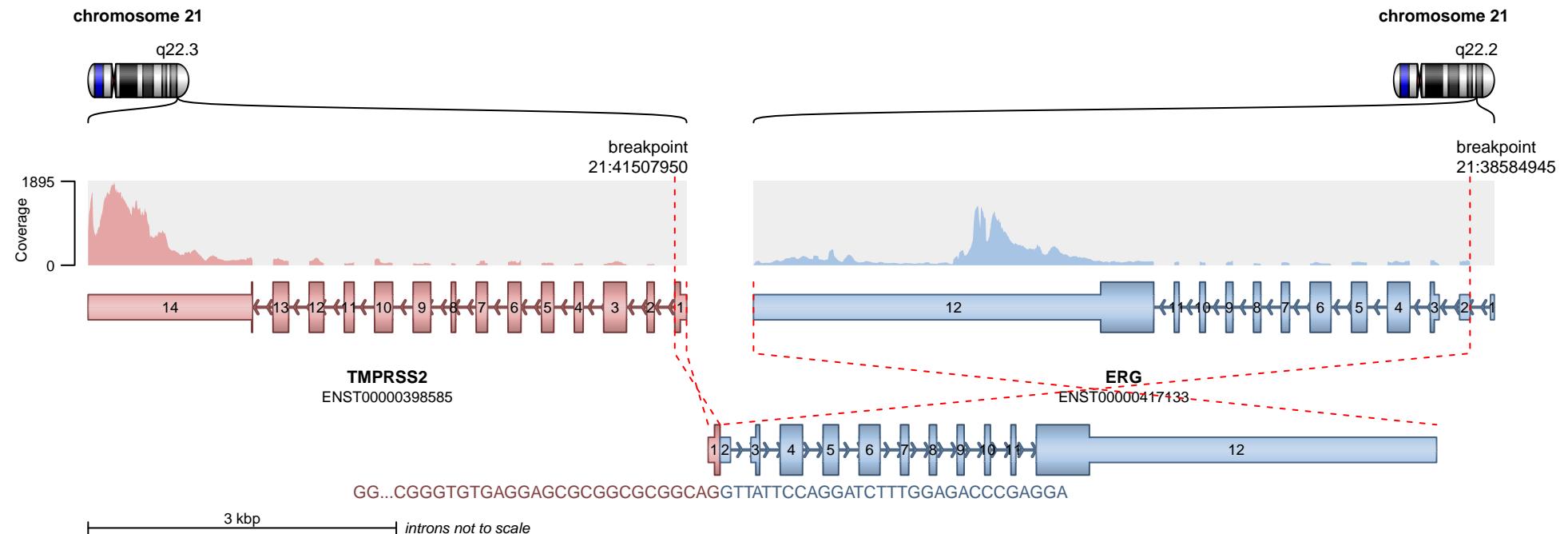
RETAINED PROTEIN DOMAINS out-of-frame fusion



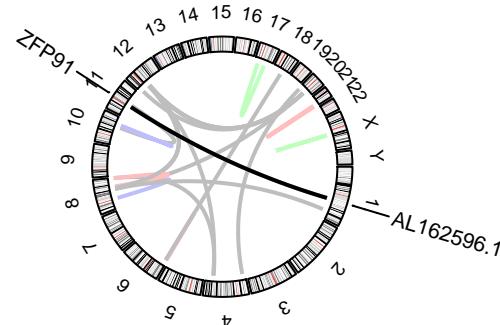
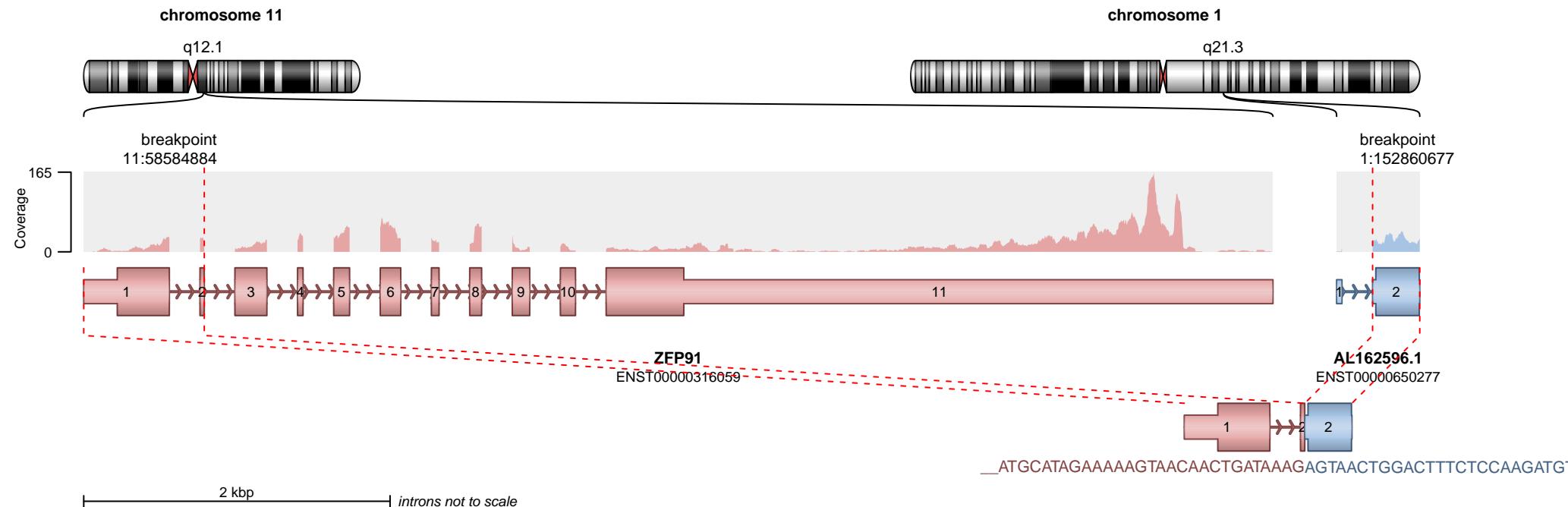
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 3

— translocation — deletion
— duplication — inversion



— translocation — deletion
— duplication — inversion

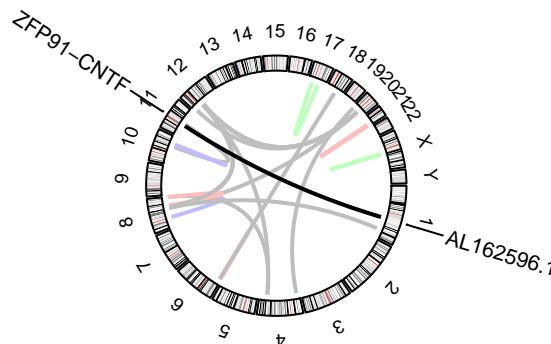
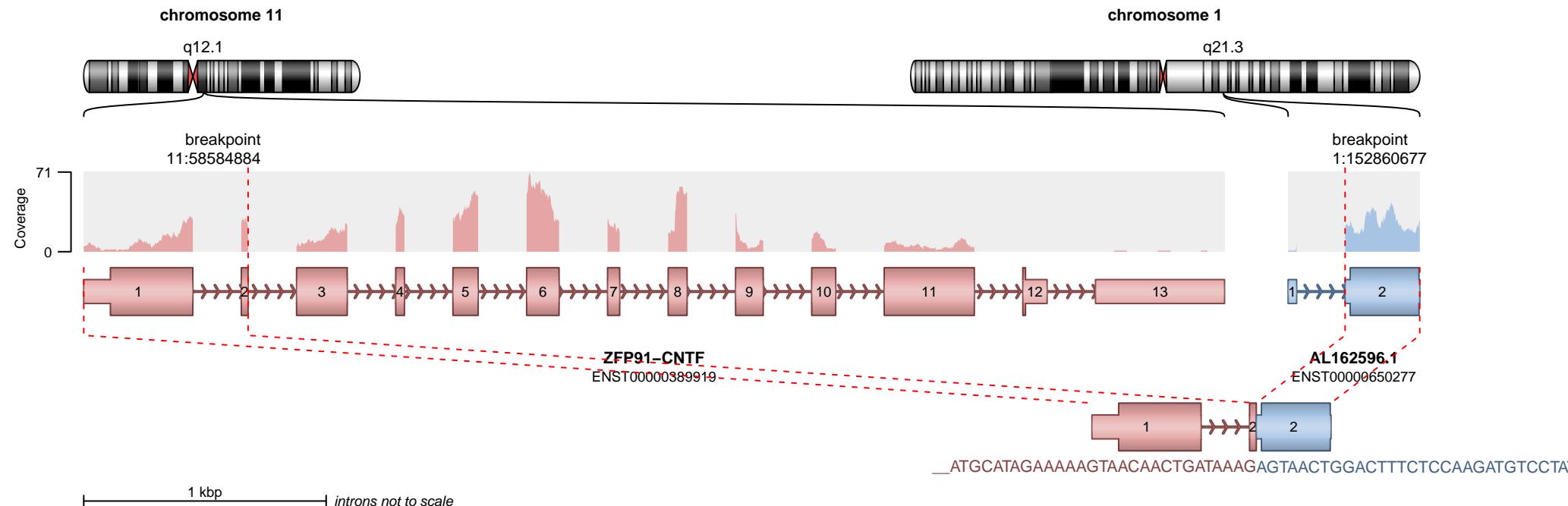


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 11
Discordant mates = 37

— translocation — deletion
— duplication — inversion

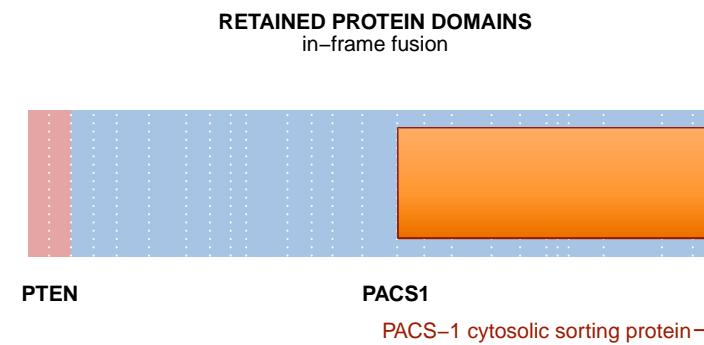
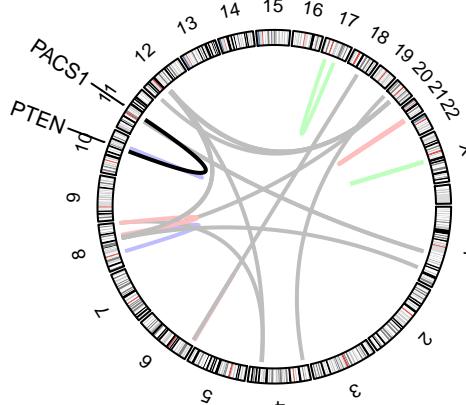
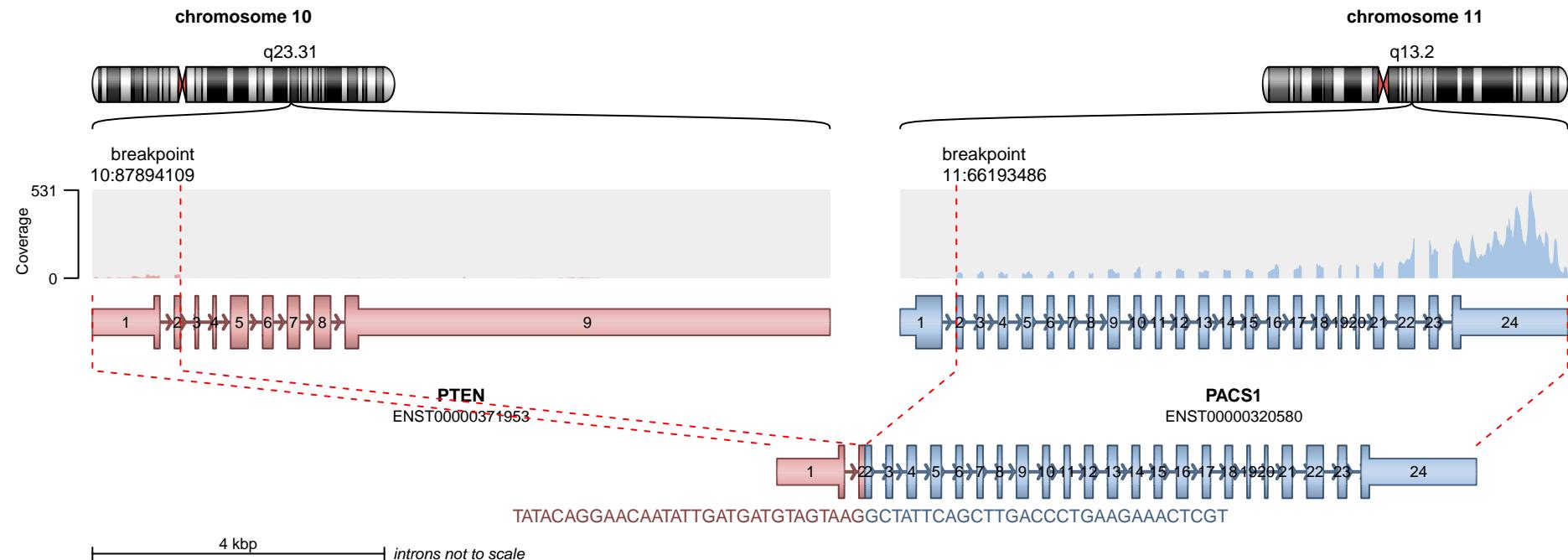


No protein domains retained in fusion.

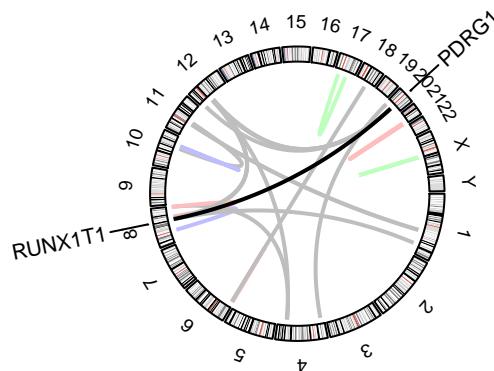
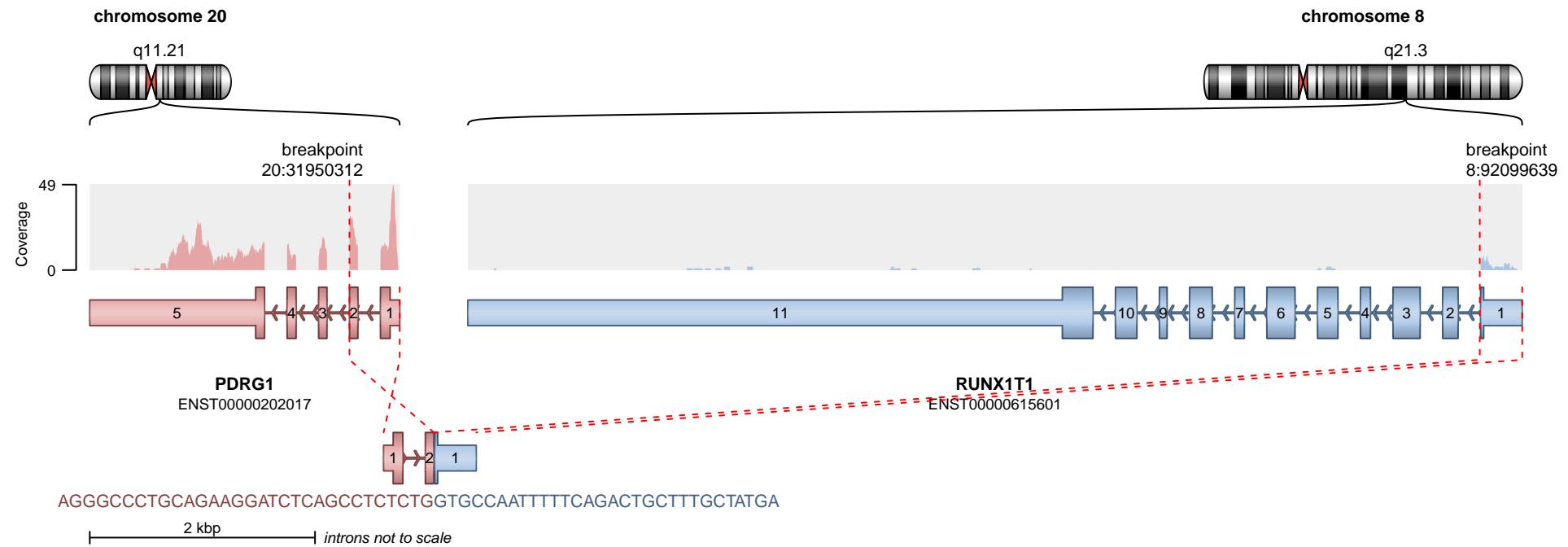
SUPPORTING READ COUNT

Split reads = 11
Discordant mates = 37

— translocation — deletion
— duplication — inversion



— translocation — deletion
— duplication — inversion

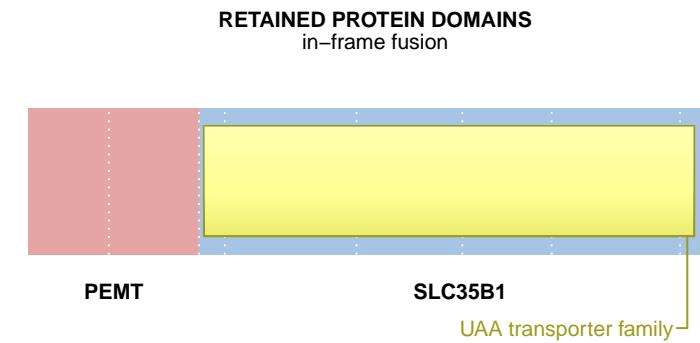
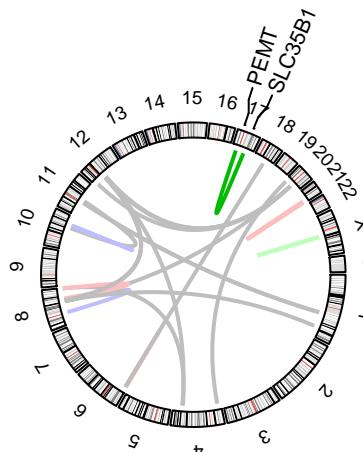
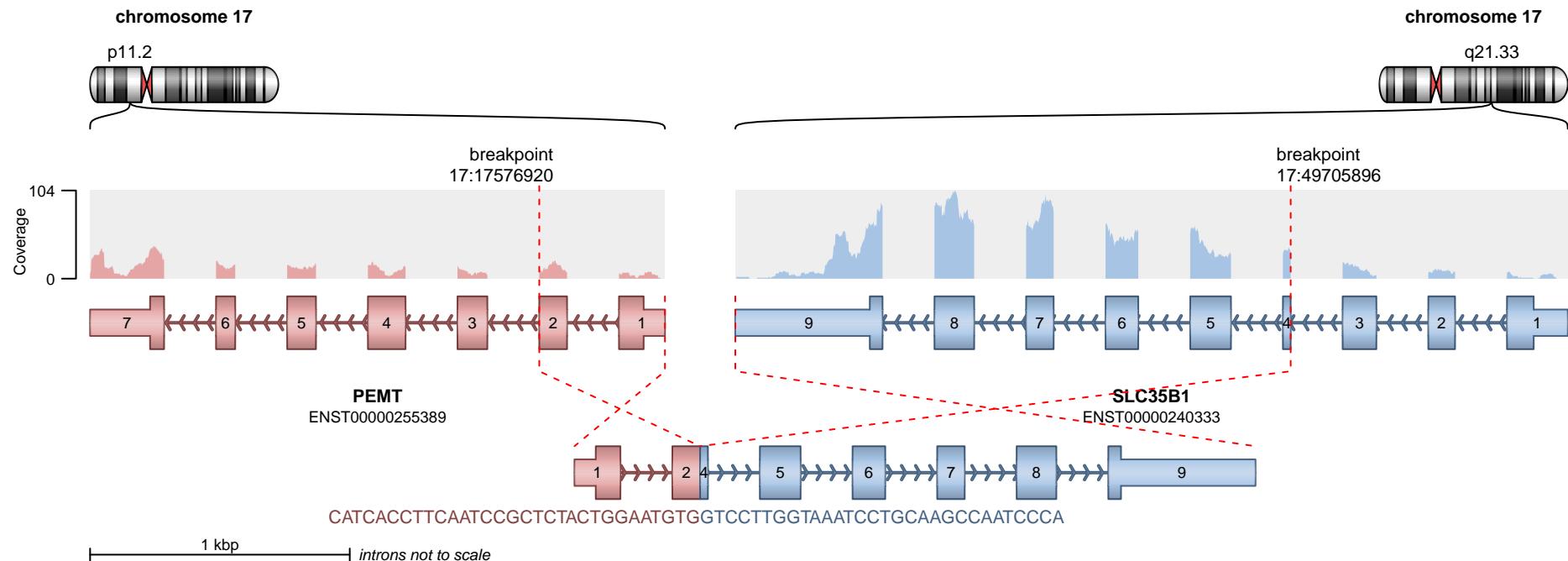


No protein domains retained in fusion.

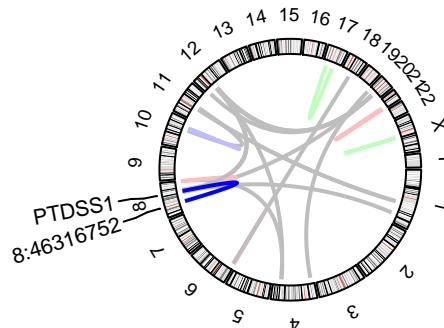
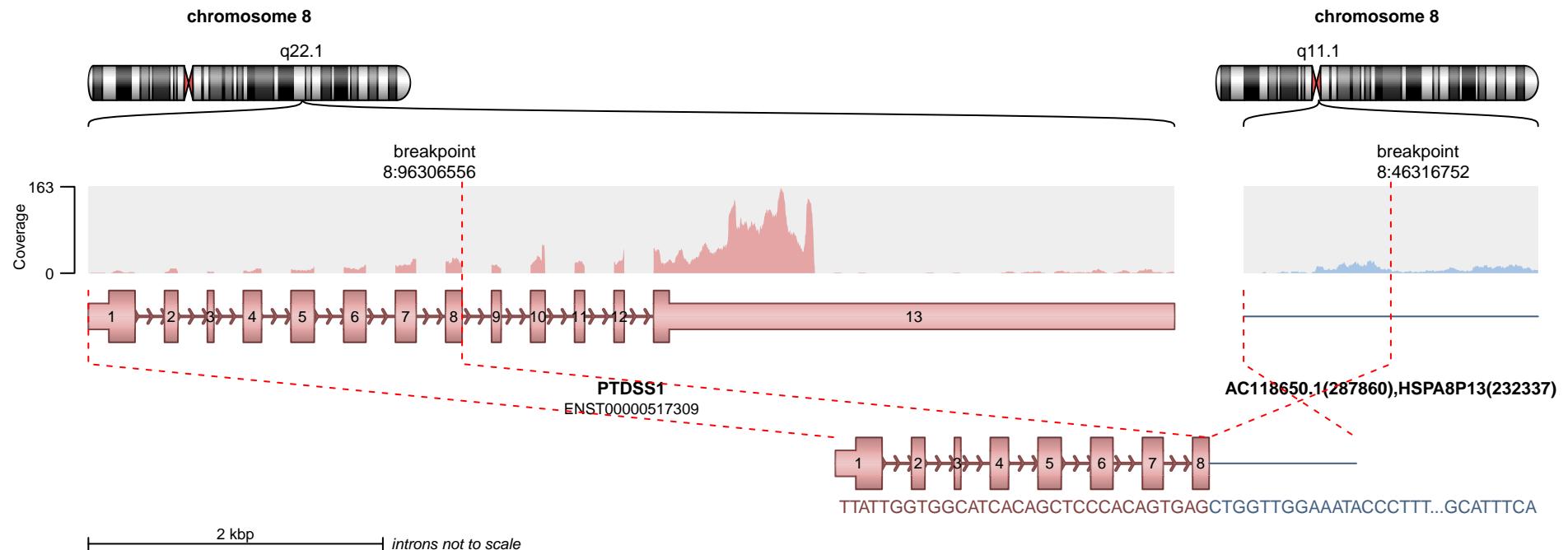
SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 25

— translocation — deletion
— duplication — inversion



— translocation — deletion
— duplication — inversion

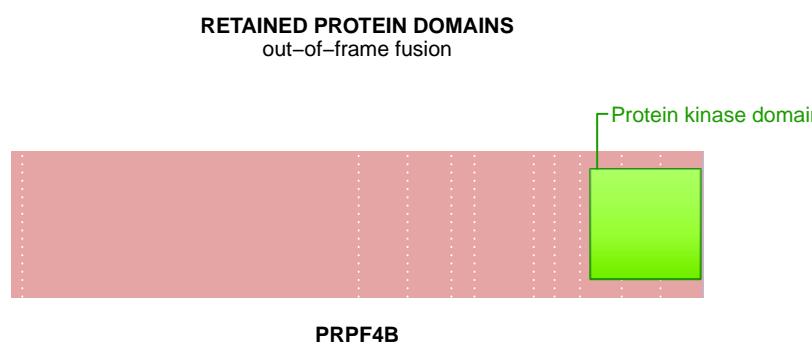
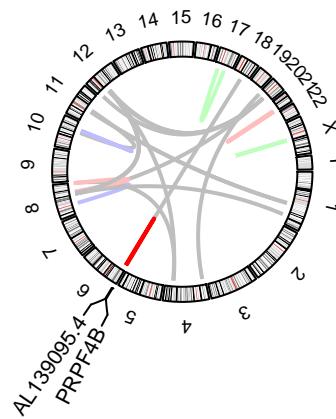
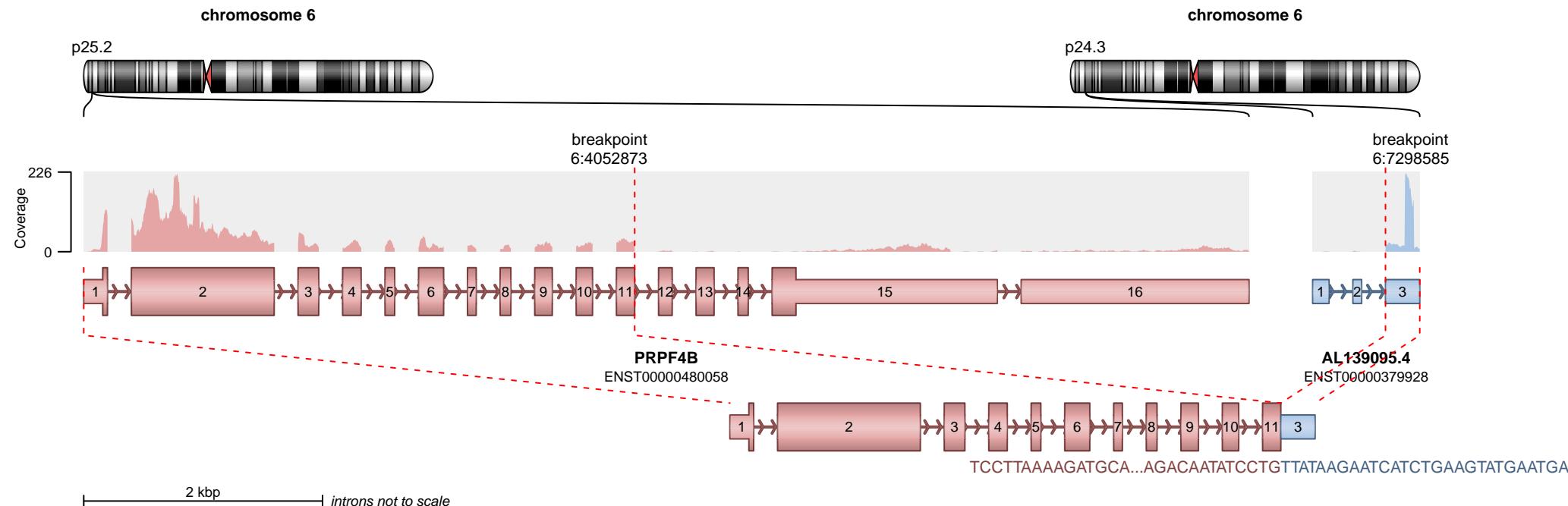


No protein domains retained in fusion.

SUPPORTING READ COUNT

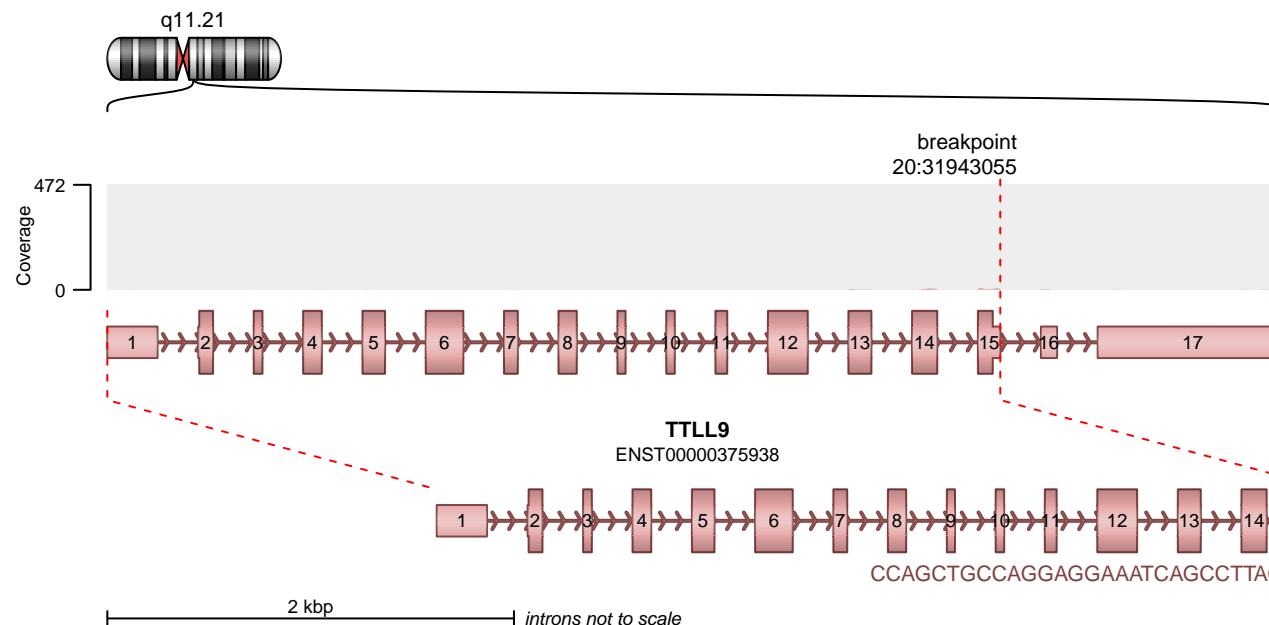
Split reads = 1
Discordant mates = 5

— translocation — deletion
— duplication — inversion

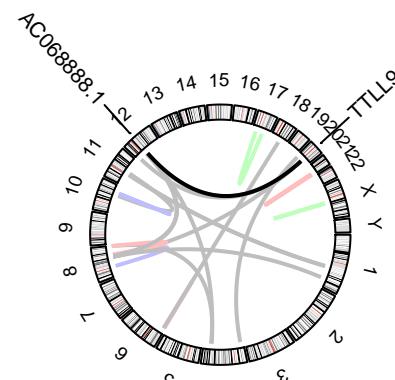
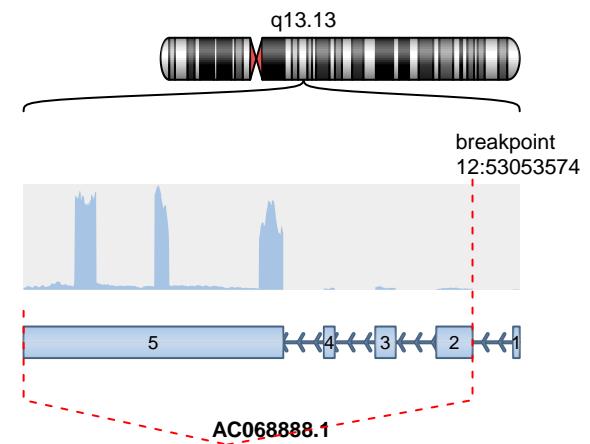


— translocation — deletion
— duplication — inversion

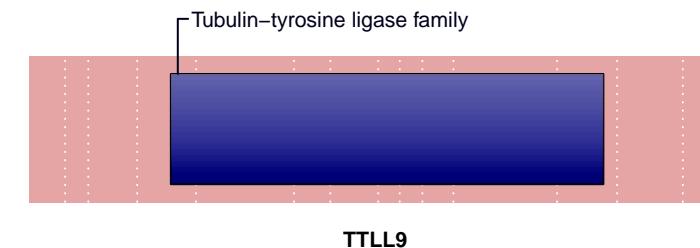
chromosome 20



chromosome 12



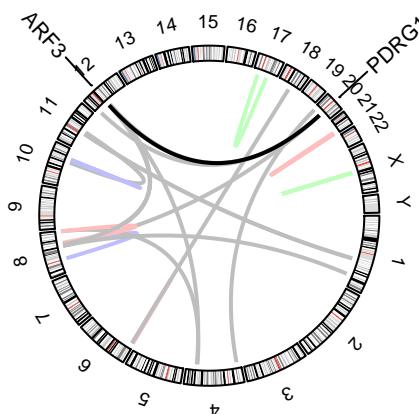
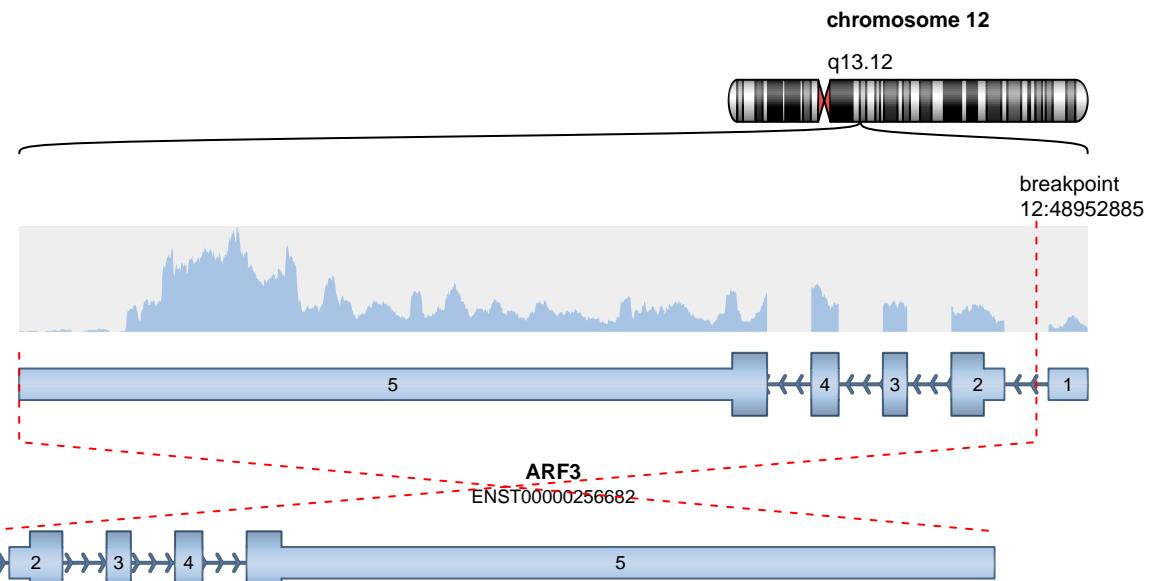
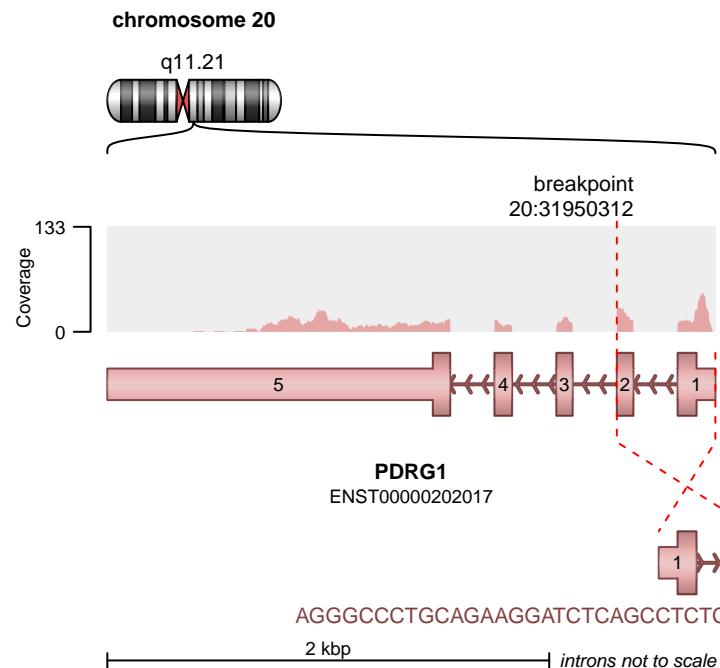
RETAINED PROTEIN DOMAINS
reading frame unclear



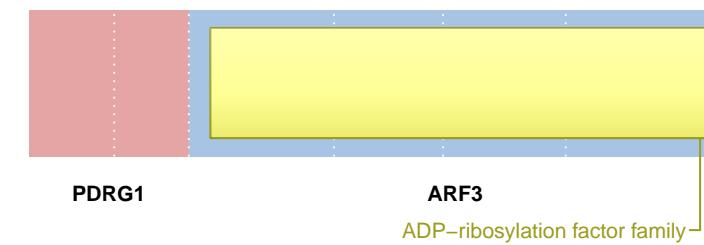
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 3

— translocation — deletion
— duplication — inversion



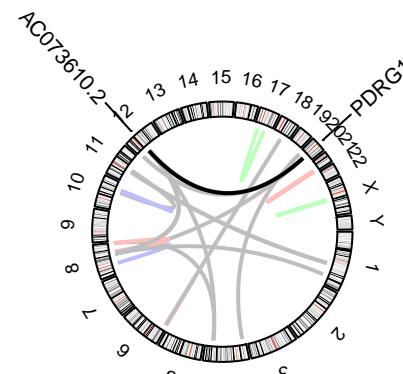
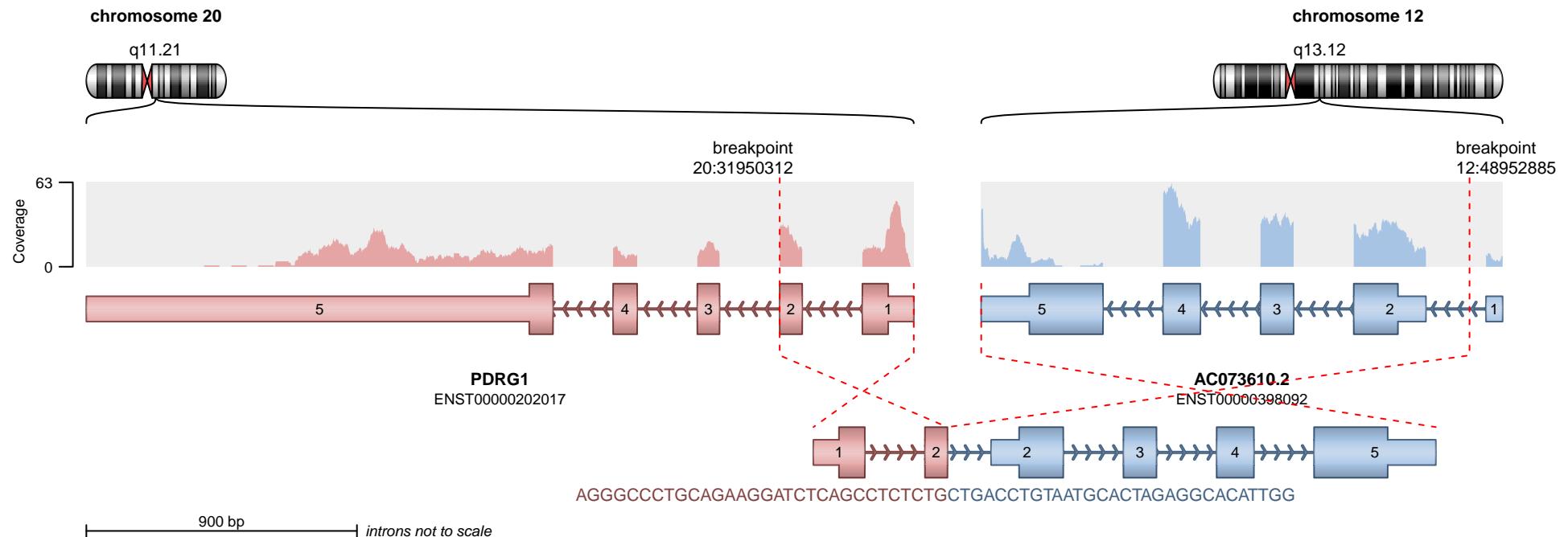
RETAINED PROTEIN DOMAINS out-of-frame fusion



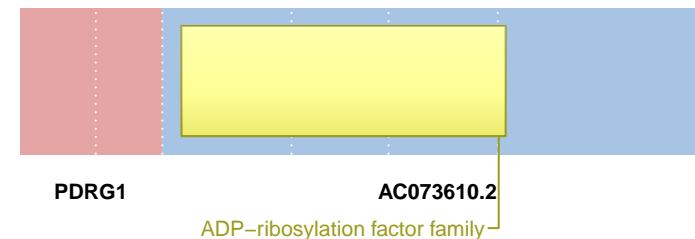
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 1

— translocation — deletion
— duplication — inversion



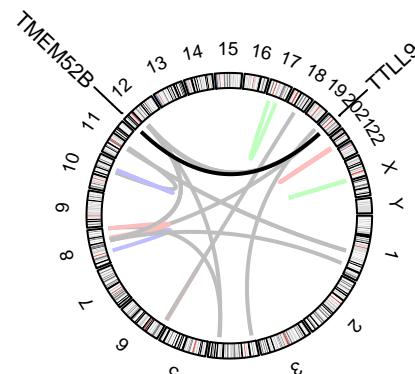
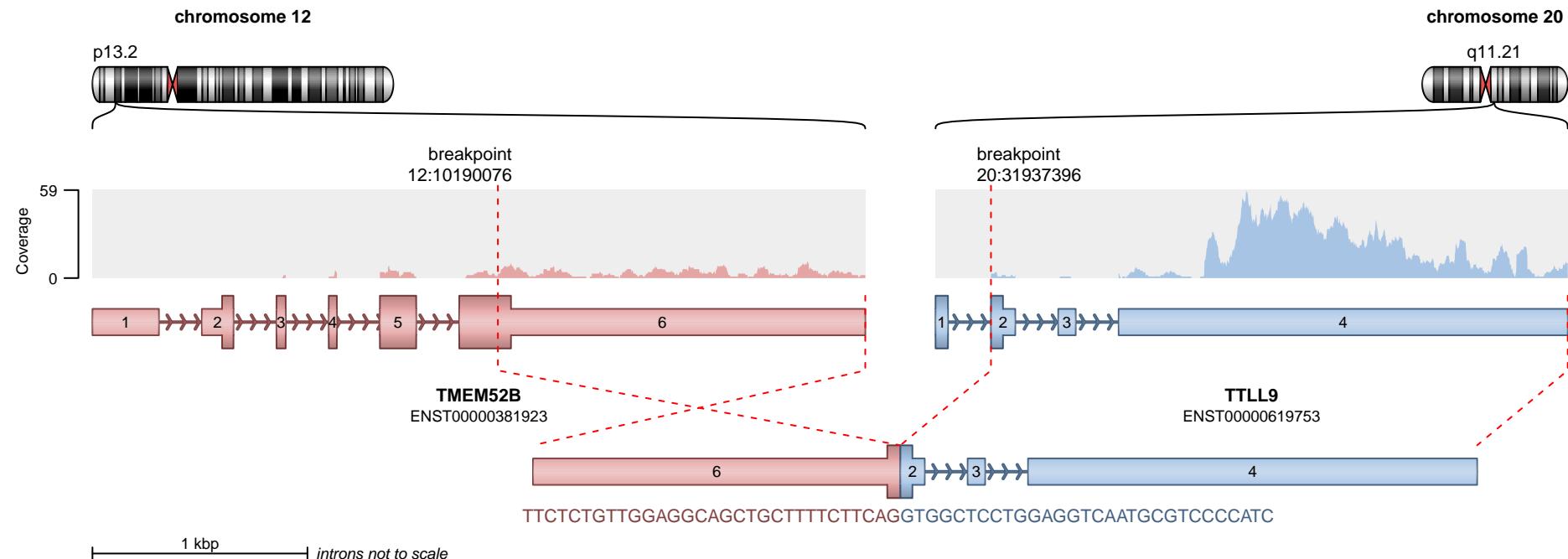
RETAINED PROTEIN DOMAINS out-of-frame fusion



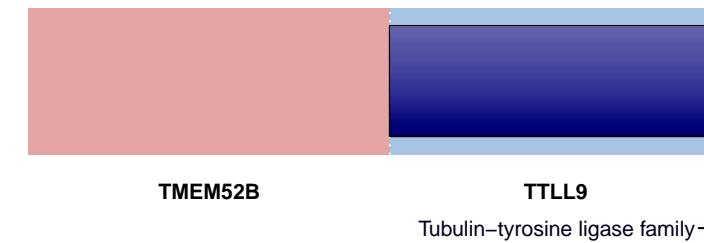
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 1

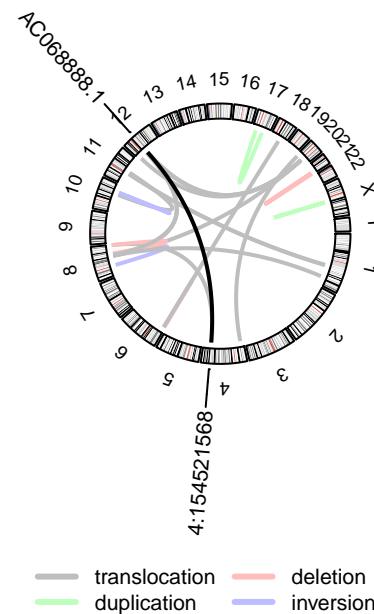
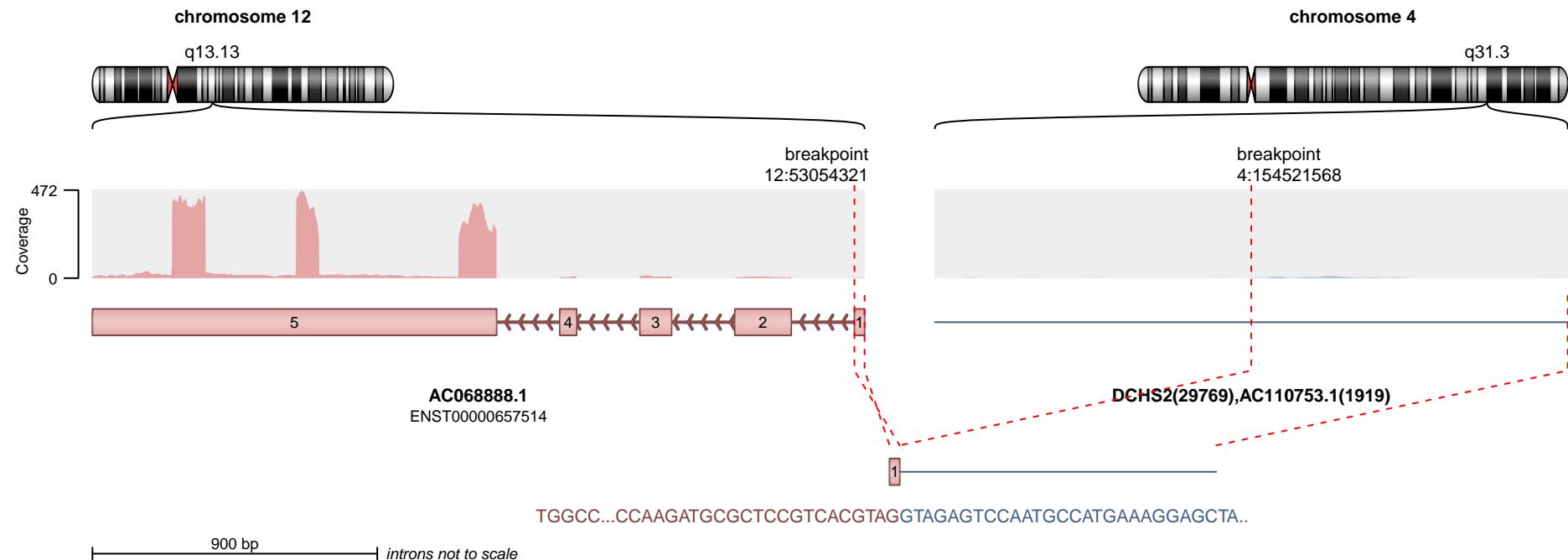
— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS
reading frame unclear



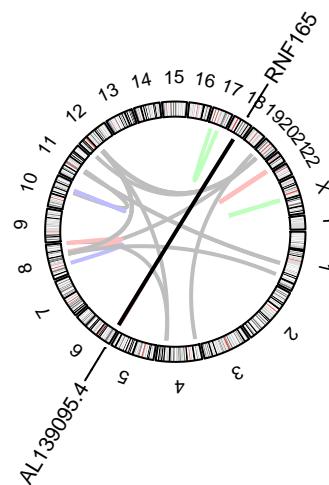
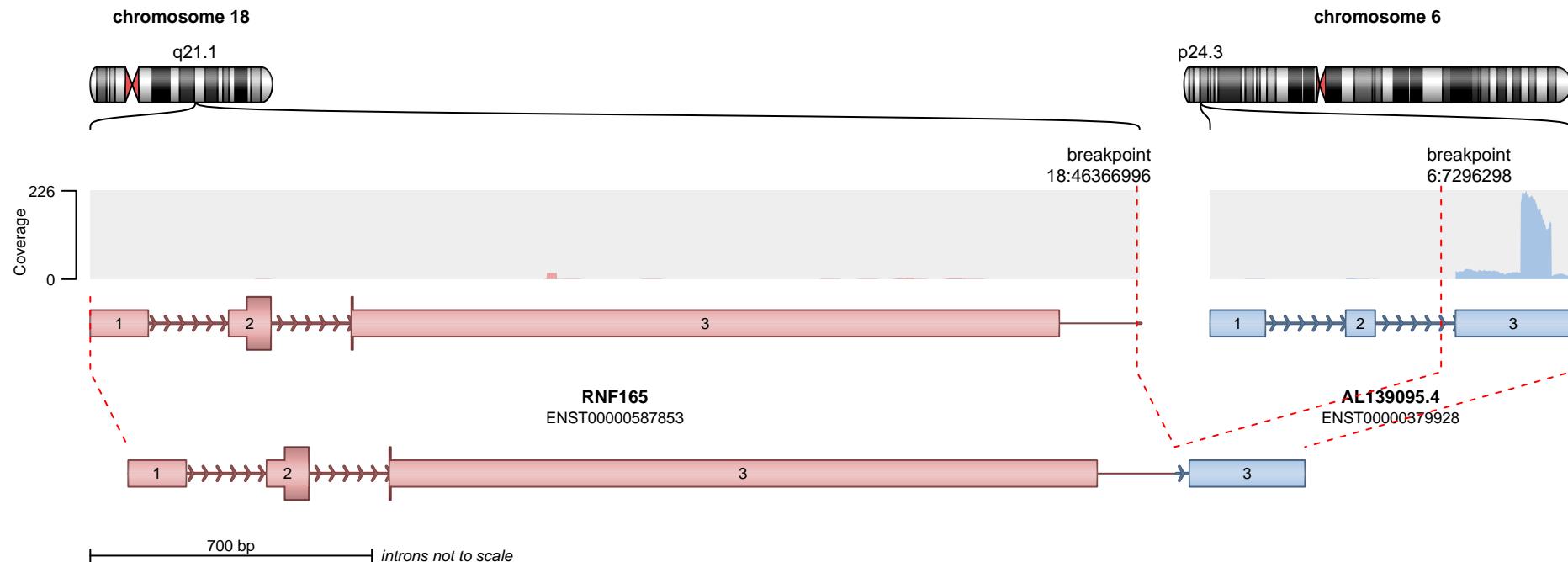
— translocation — deletion
— duplication — inversion



Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

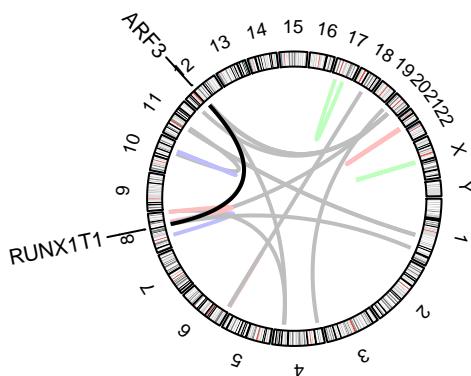
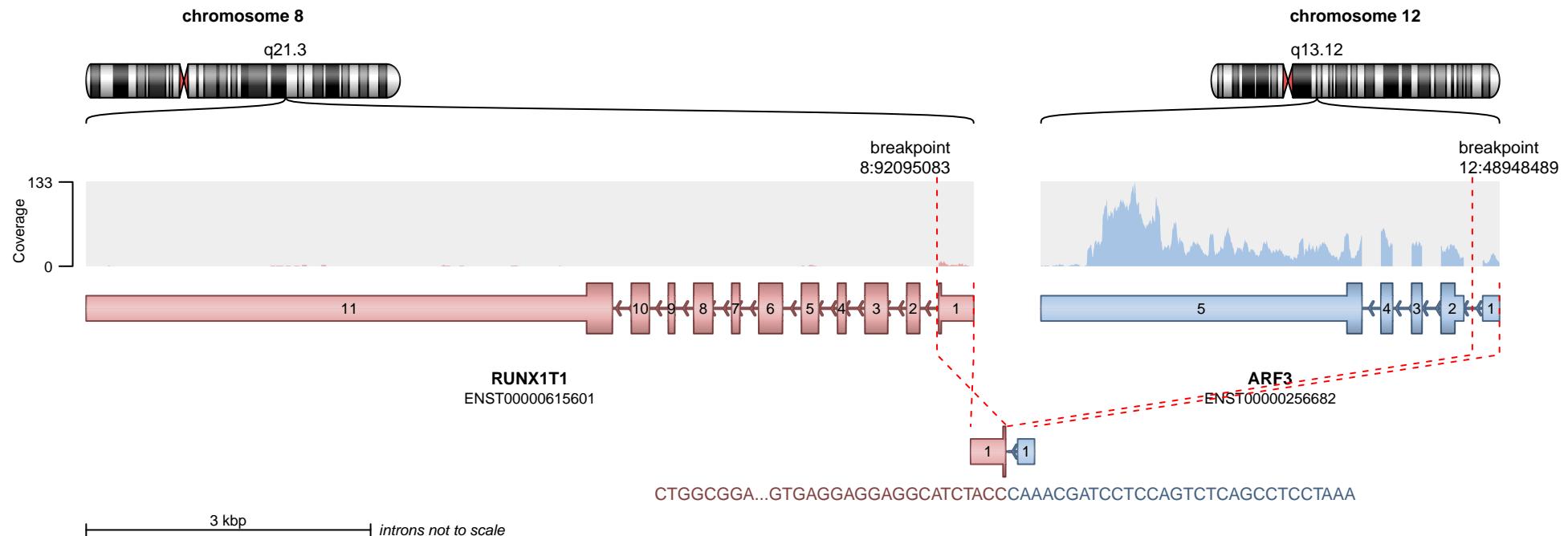


No coding regions due to antisense transcription.

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 33

— translocation — deletion
— duplication — inversion

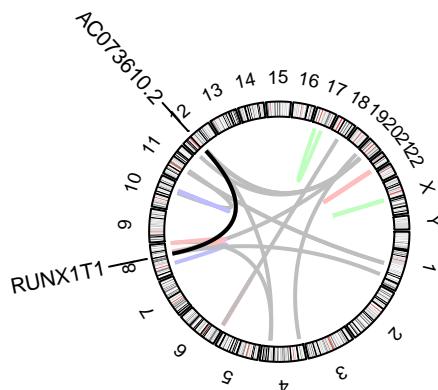
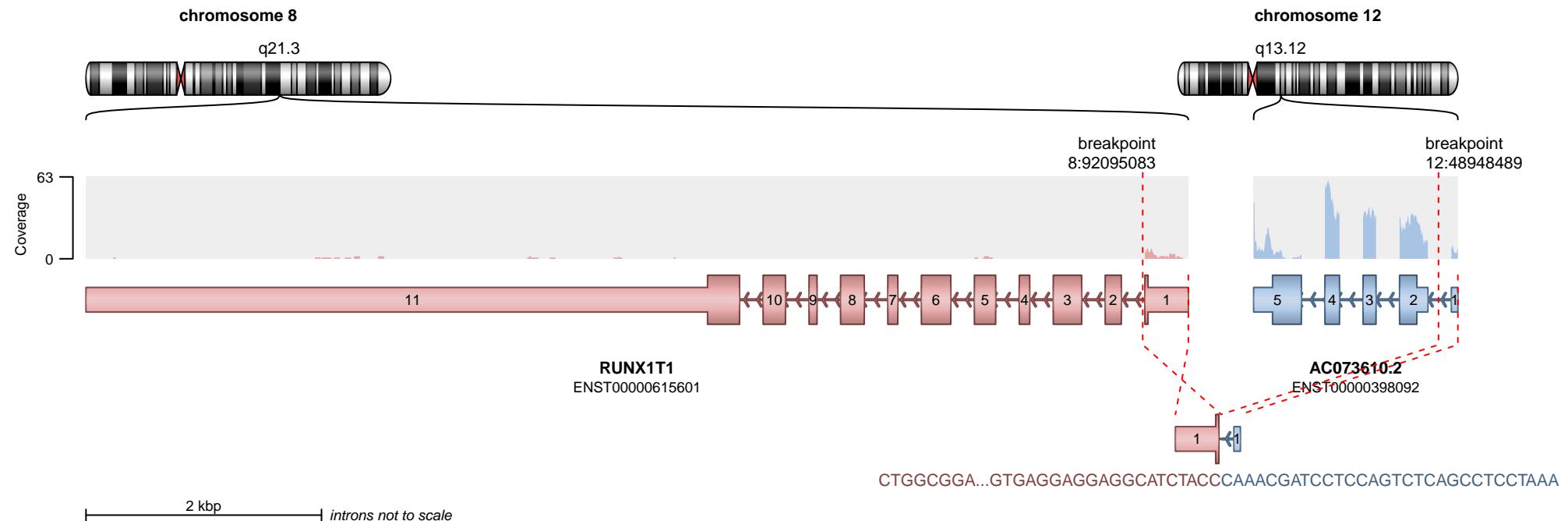


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 9

— translocation — deletion
— duplication — inversion

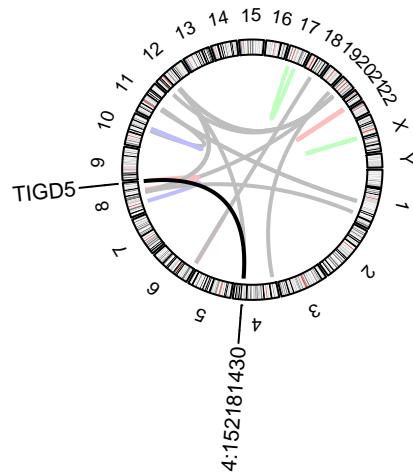
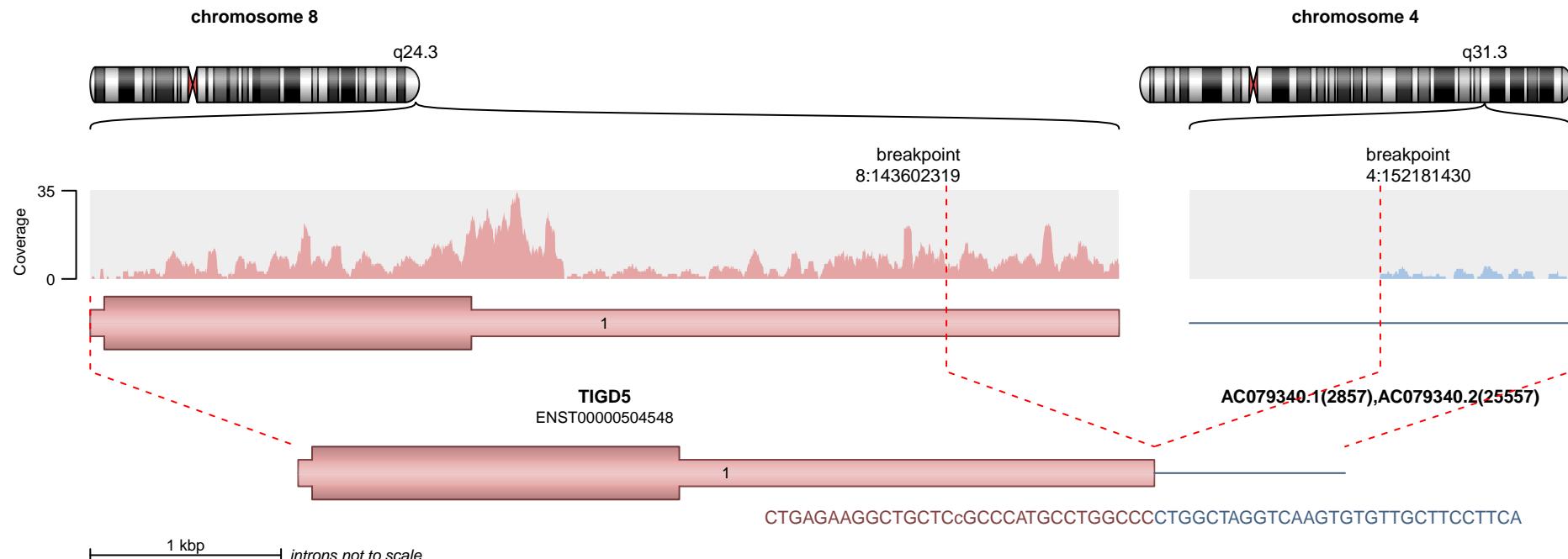


No protein domains retained in fusion.

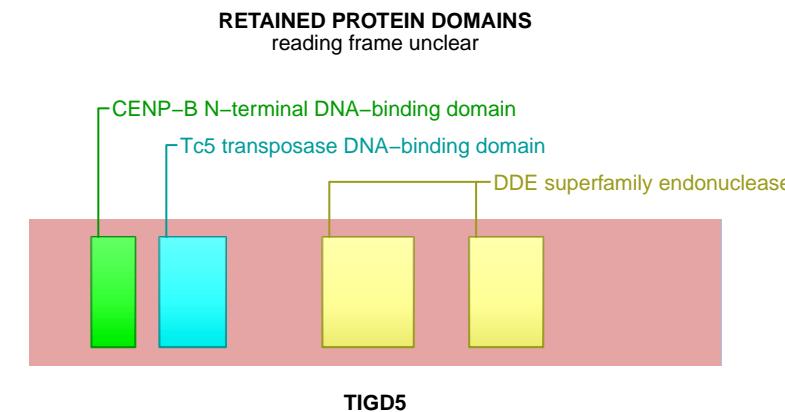
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 9

— translocation — deletion
— duplication — inversion

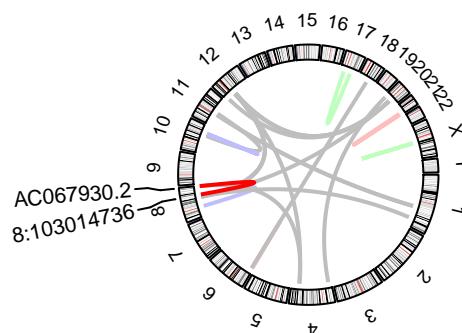
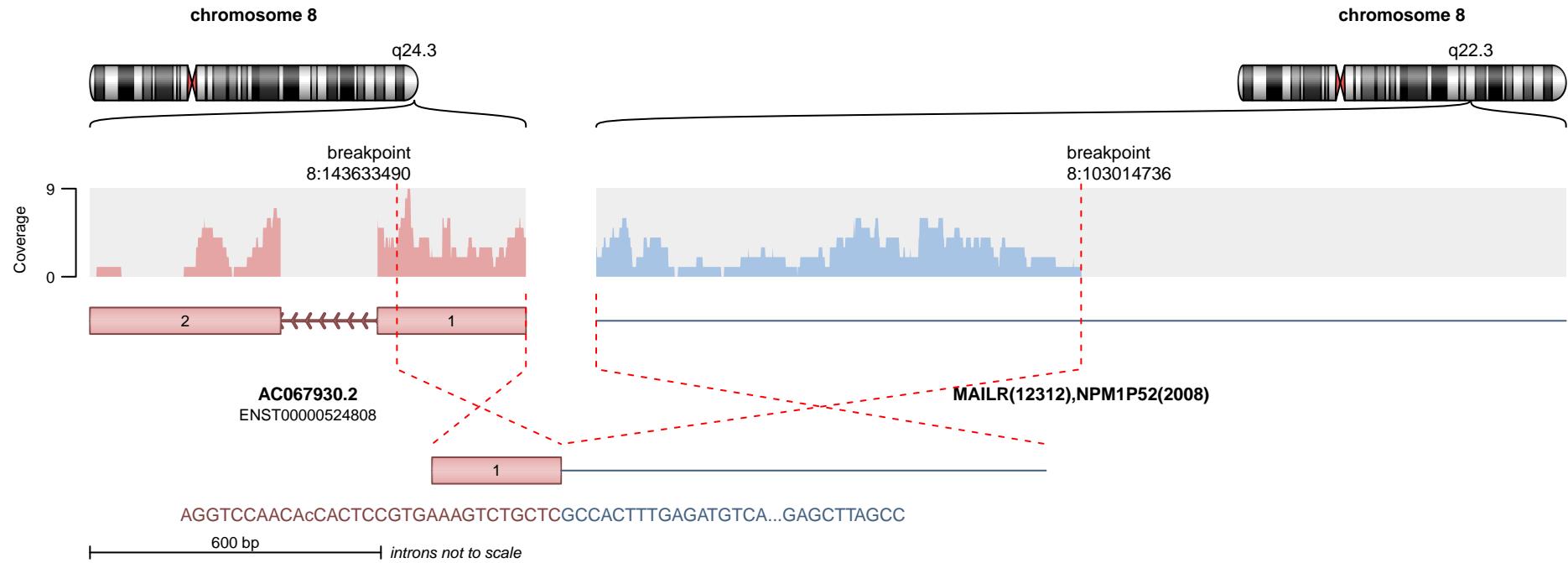


— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 4

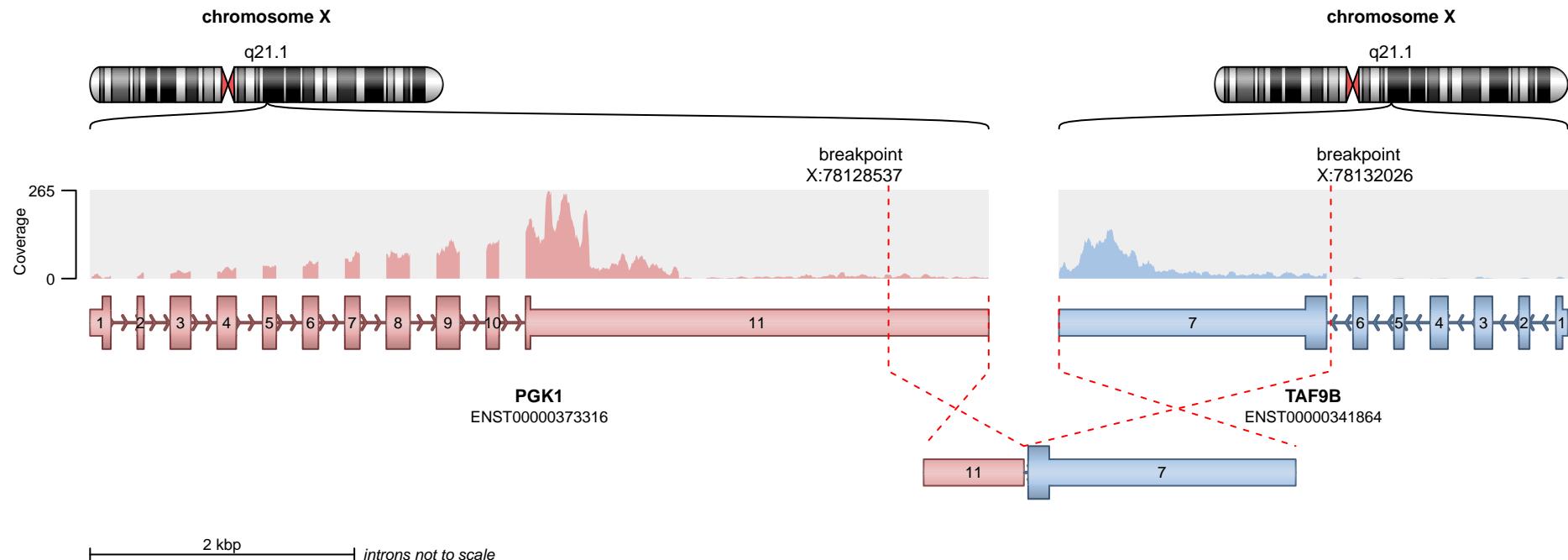


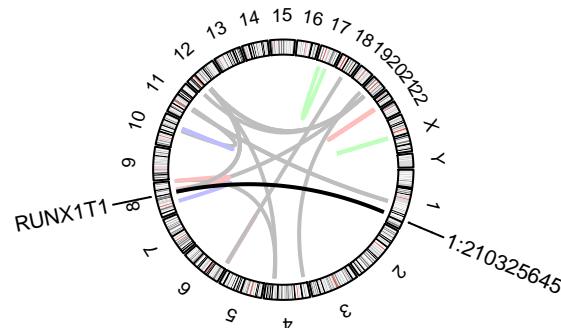
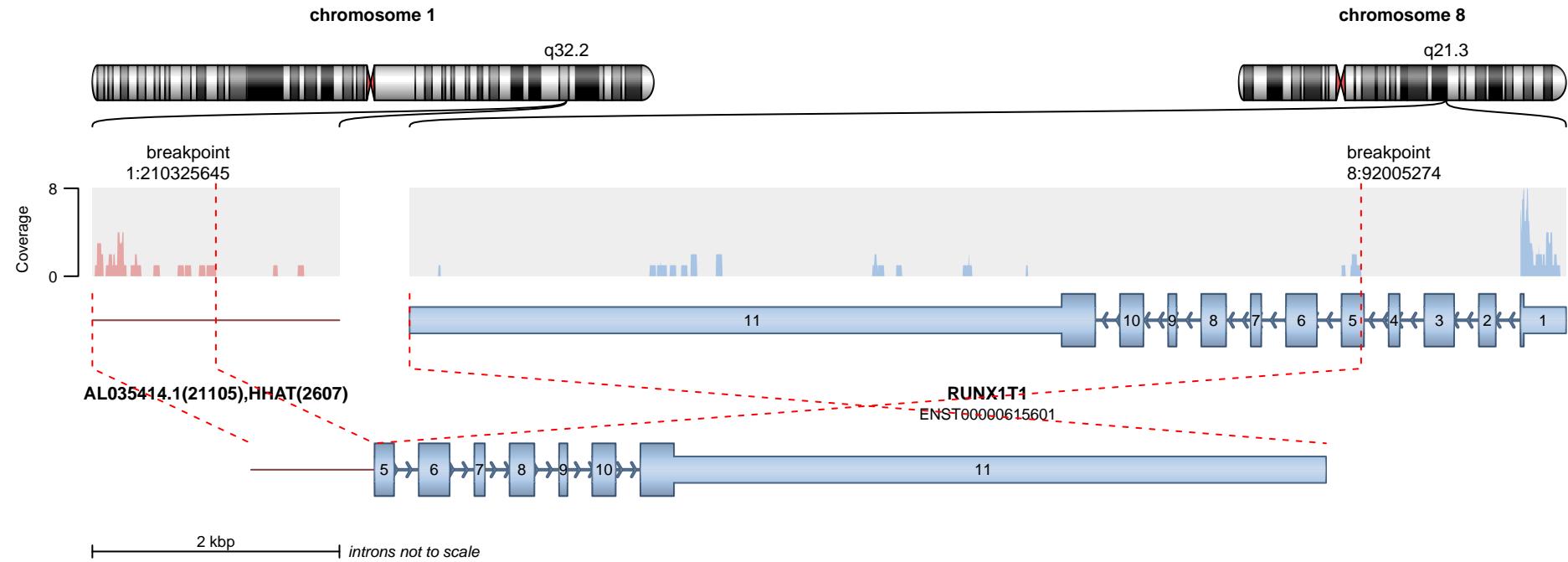
Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 2

— translocation — deletion
— duplication — inversion



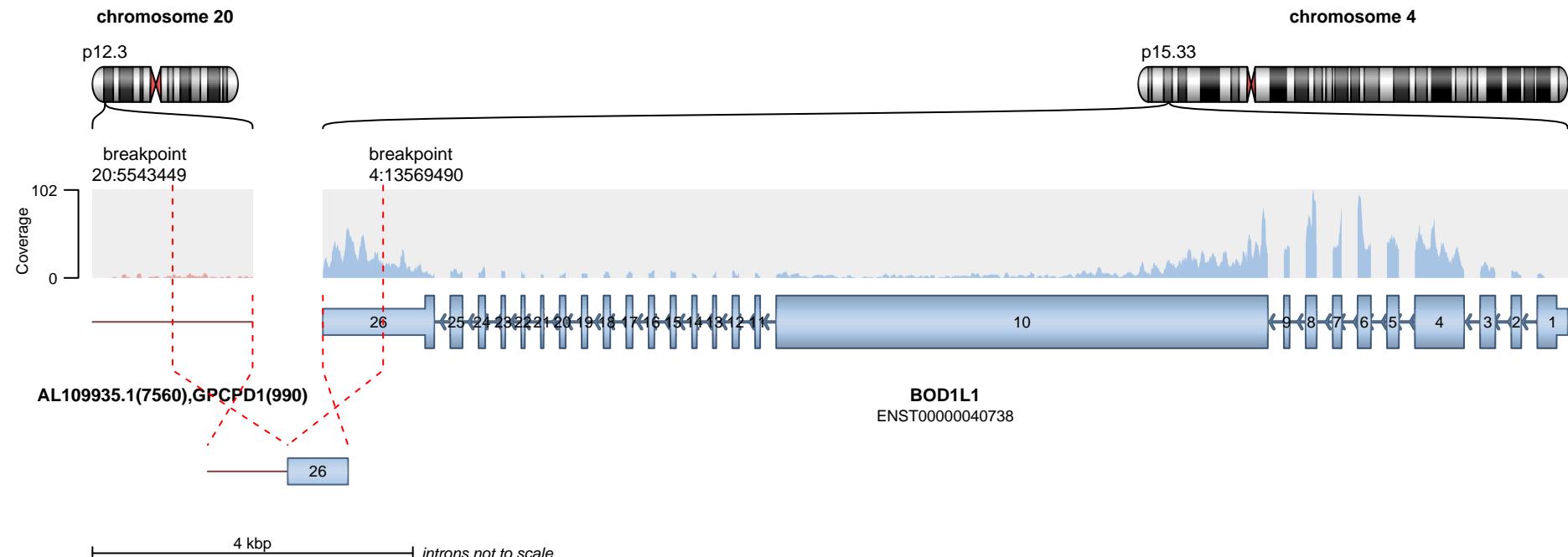


No coding regions due to antisense transcription.

SUPPORTING READ COUNT

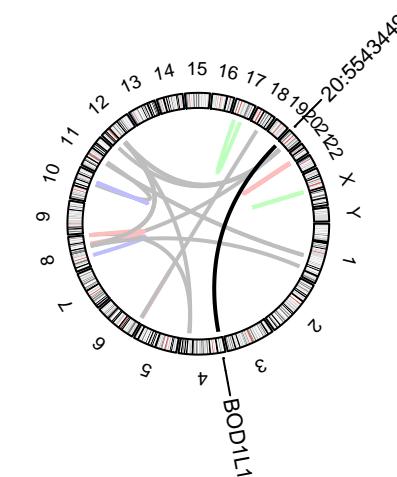
Split reads = 1
Discordant mates = 1

— translocation — deletion
— duplication — inversion

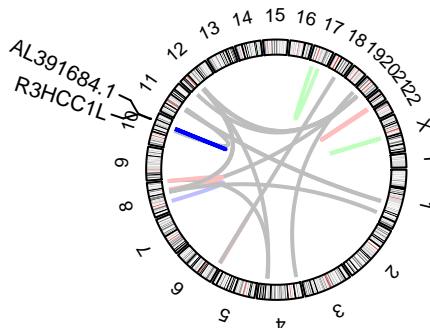
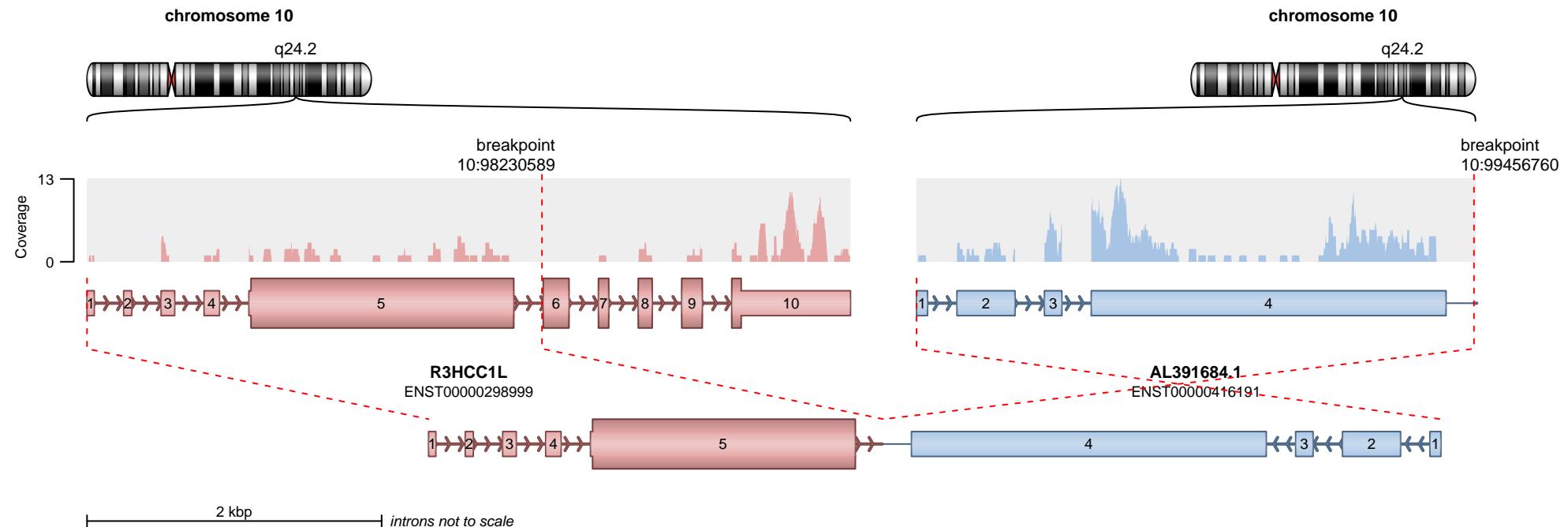


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1



— translocation — deletion
— duplication — inversion

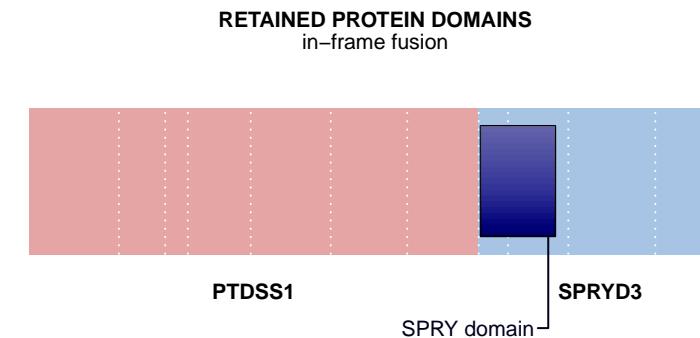
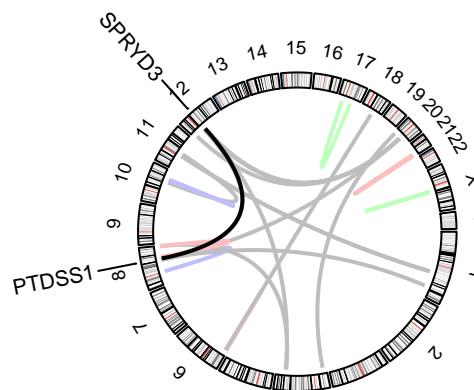
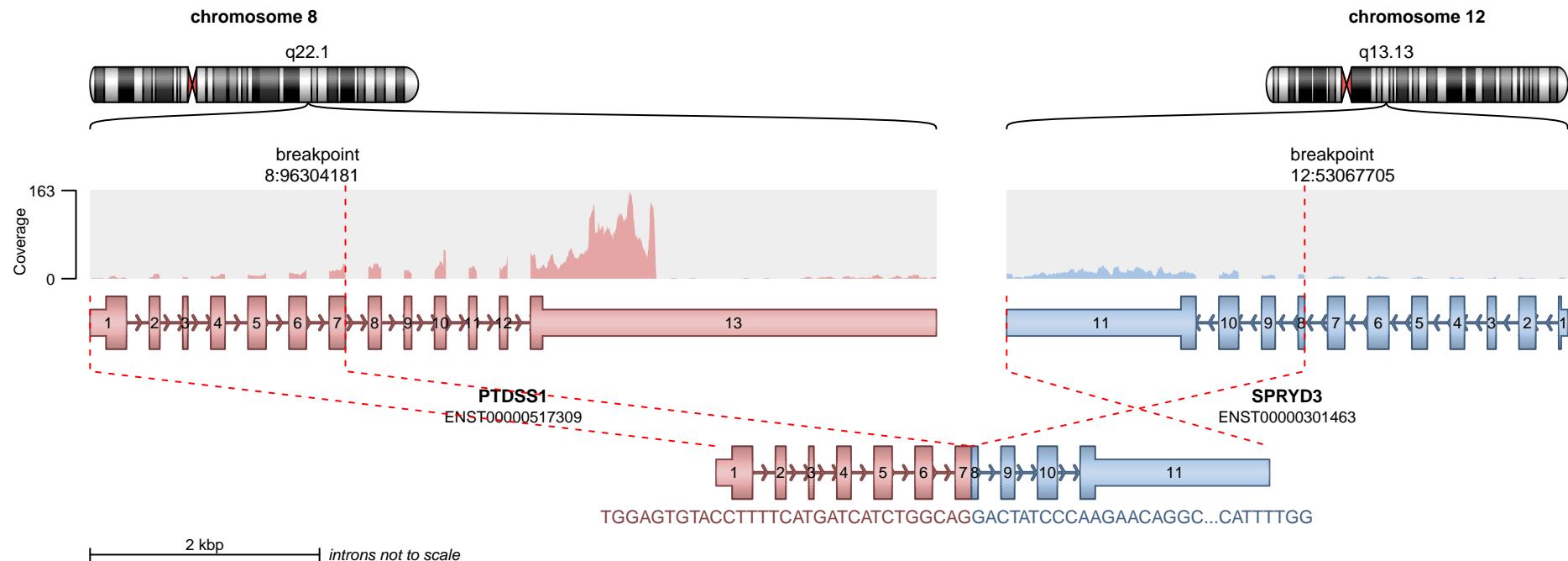


No coding regions due to antisense transcription.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

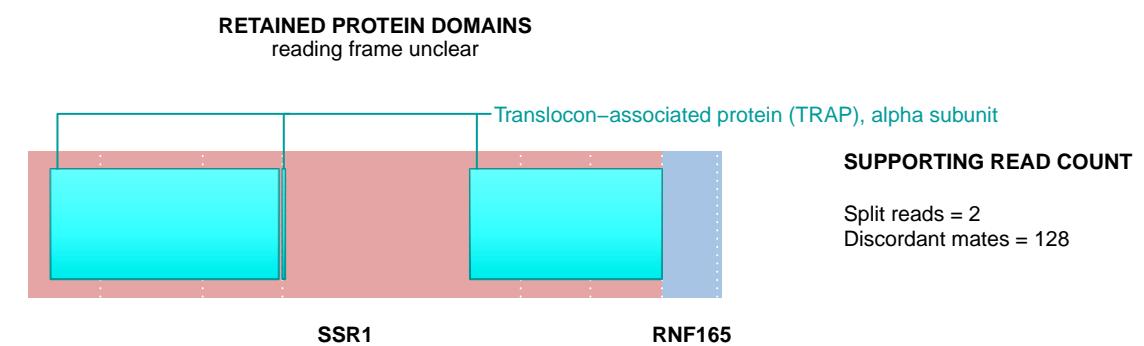
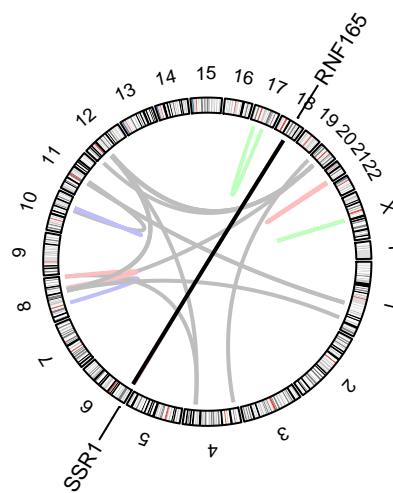
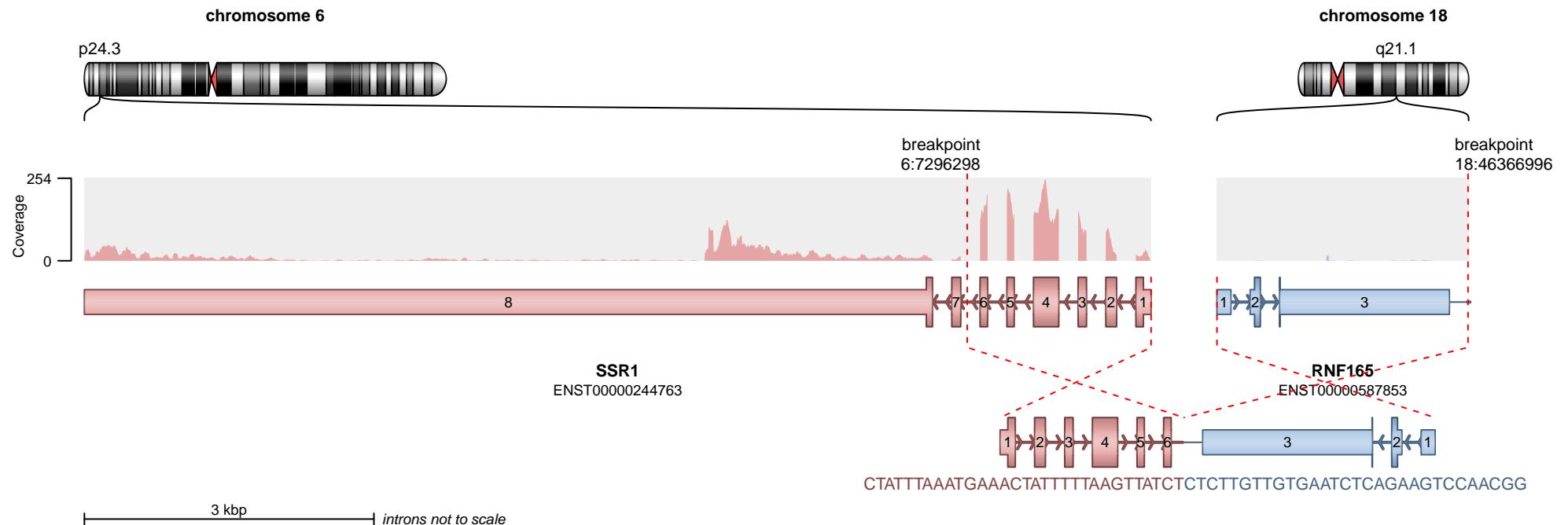
— translocation — deletion
— duplication — inversion



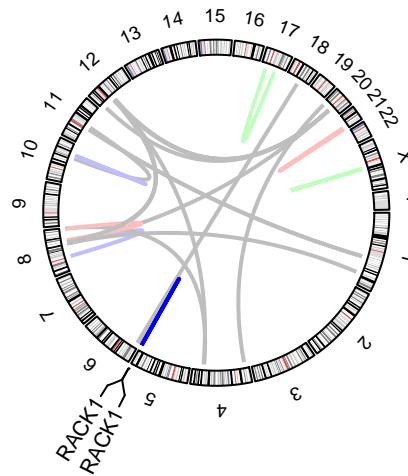
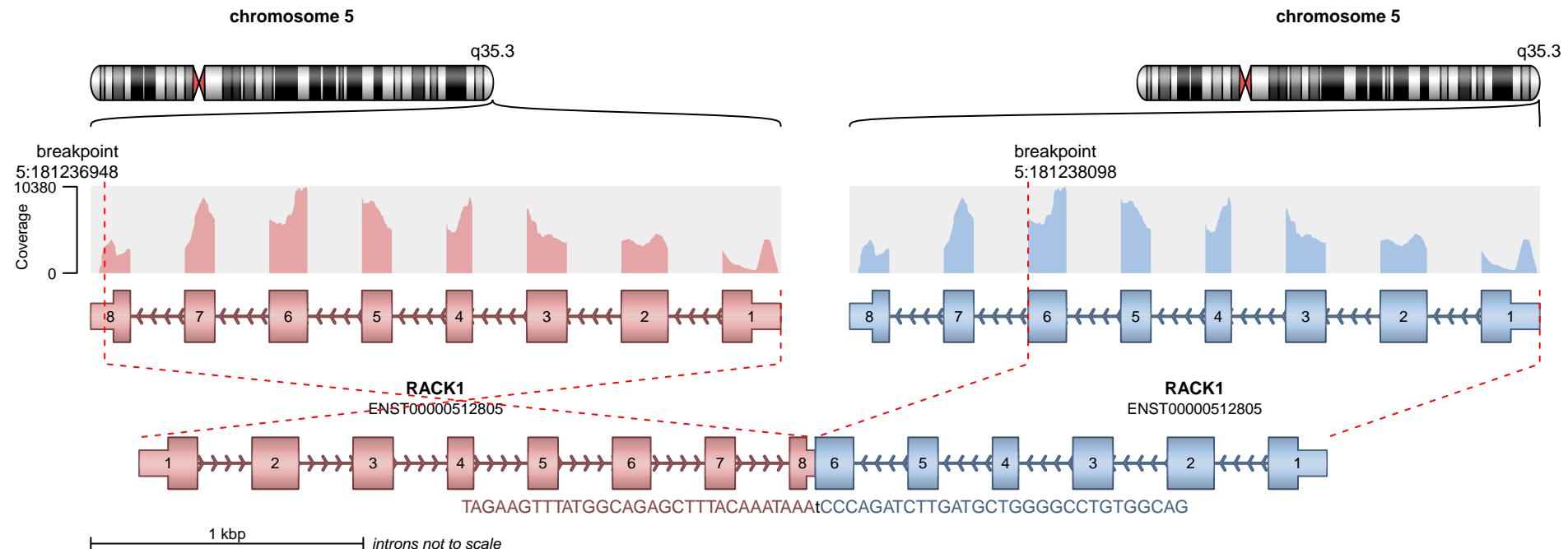
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

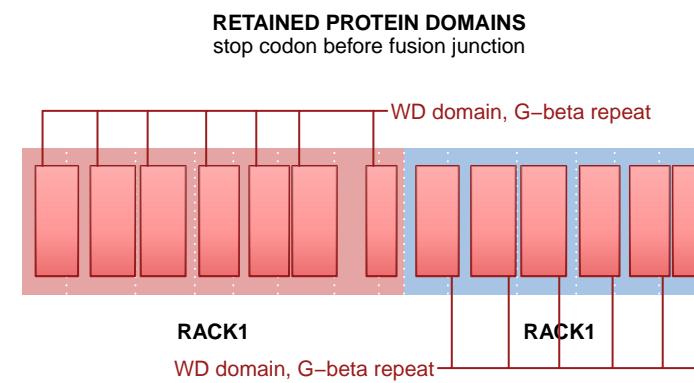
— translocation — deletion
— duplication — inversion



— translocation — deletion
— duplication — inversion

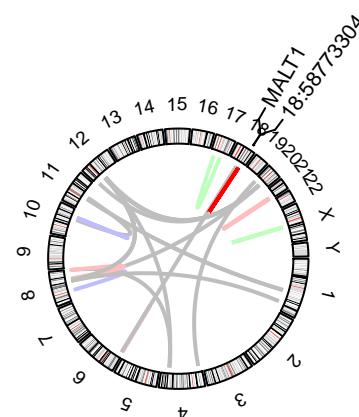
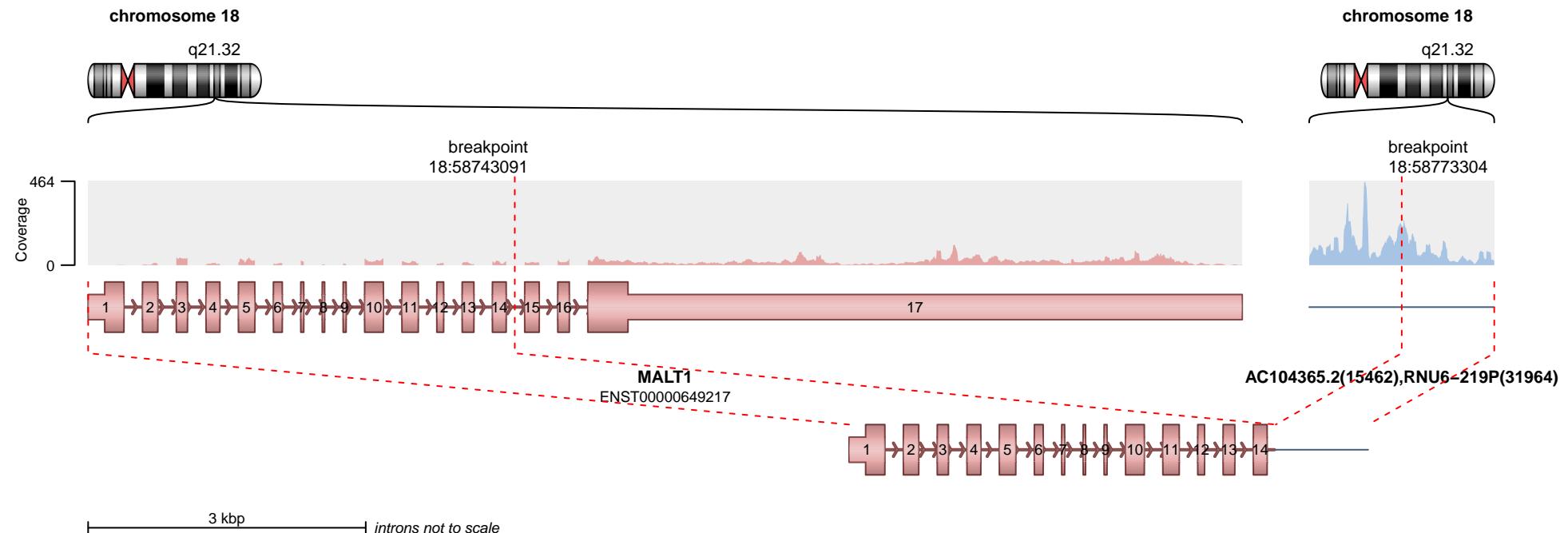


— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 59

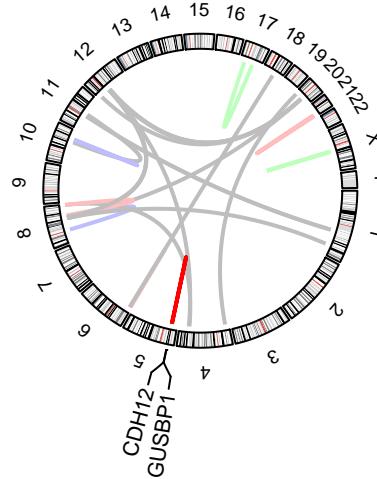
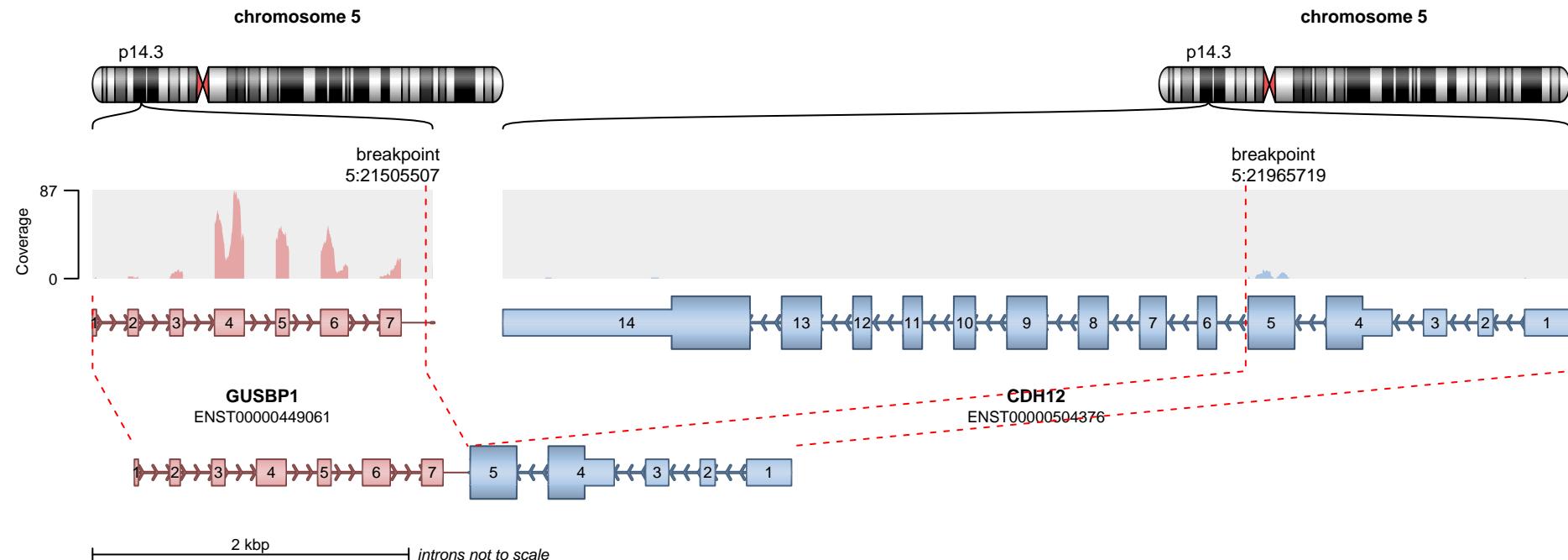


No coding regions due to antisense transcription.

SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 12

— translocation — deletion
— duplication — inversion

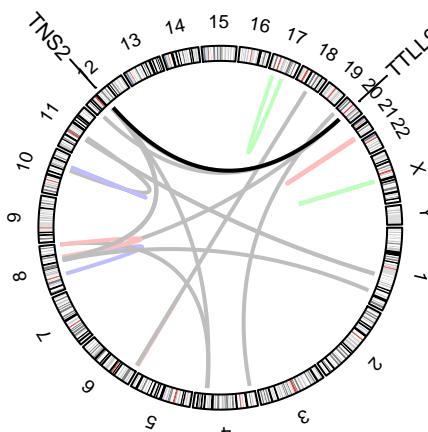
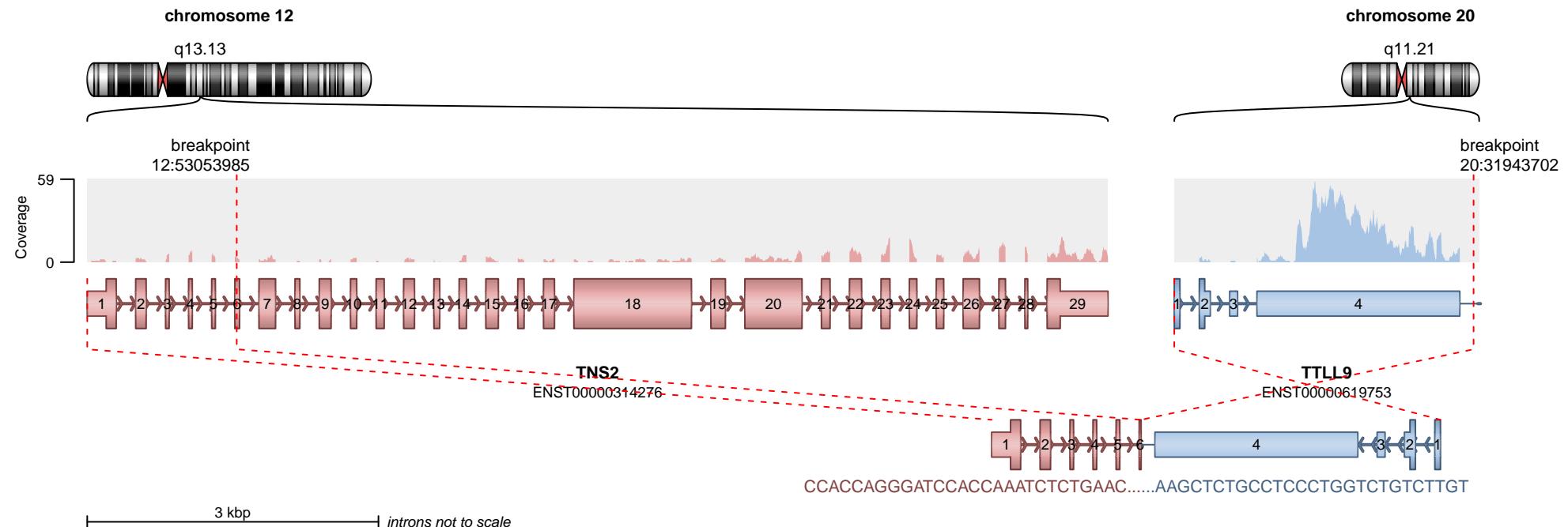


— translocation — deletion
— duplication — inversion

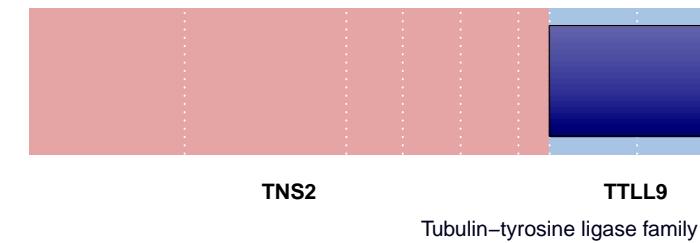
No coding regions due to antisense transcription.

SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 11



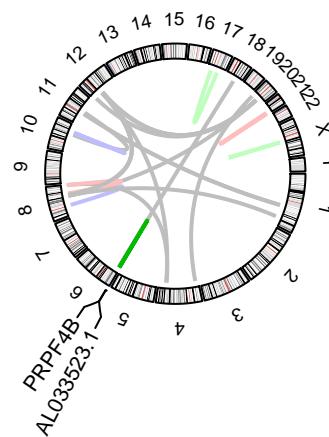
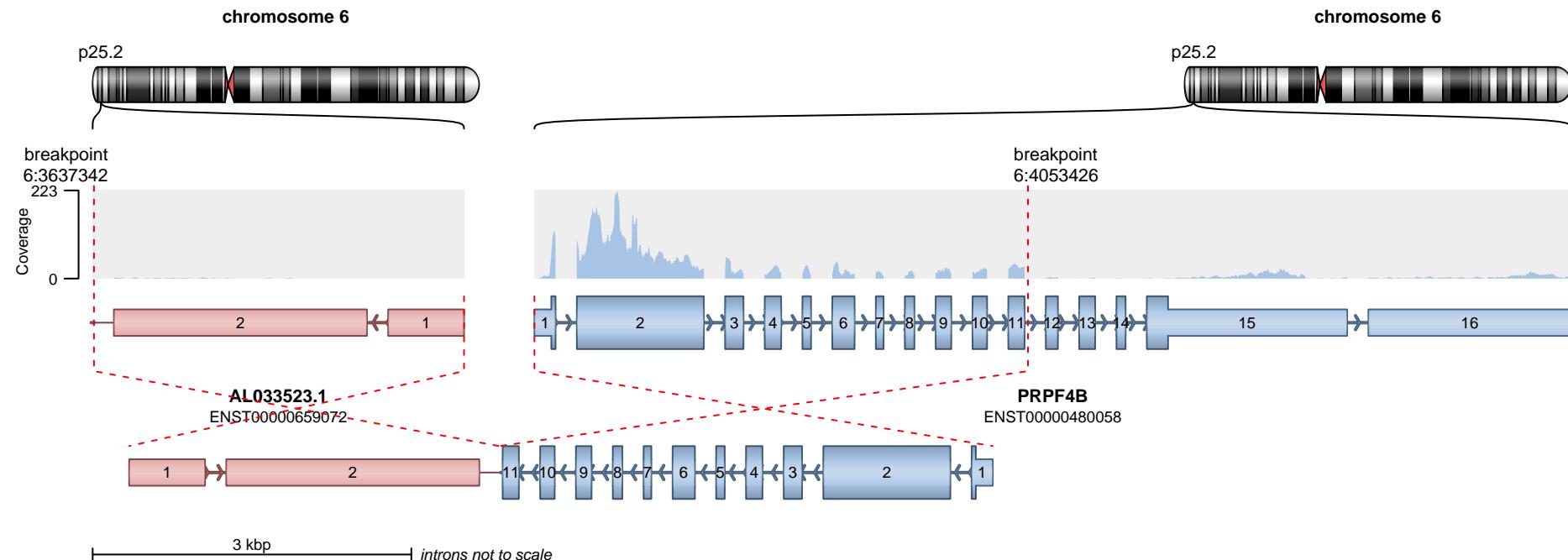
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 8

— translocation — deletion
— duplication — inversion

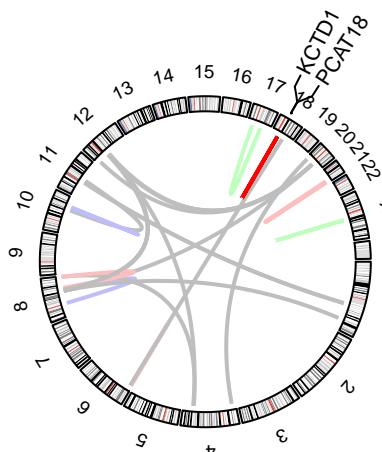
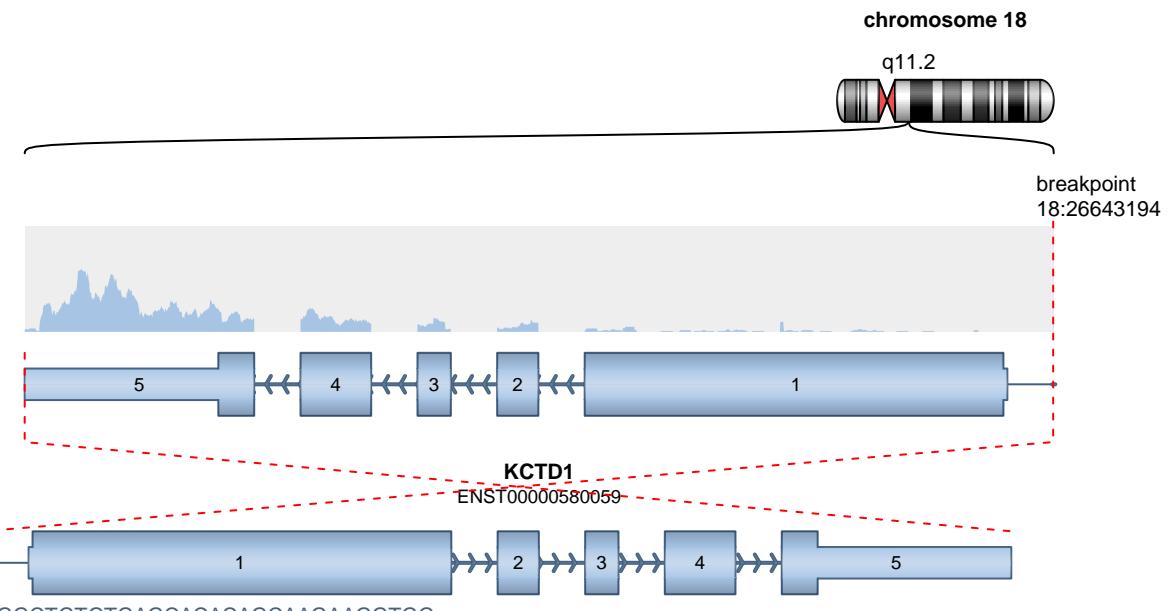
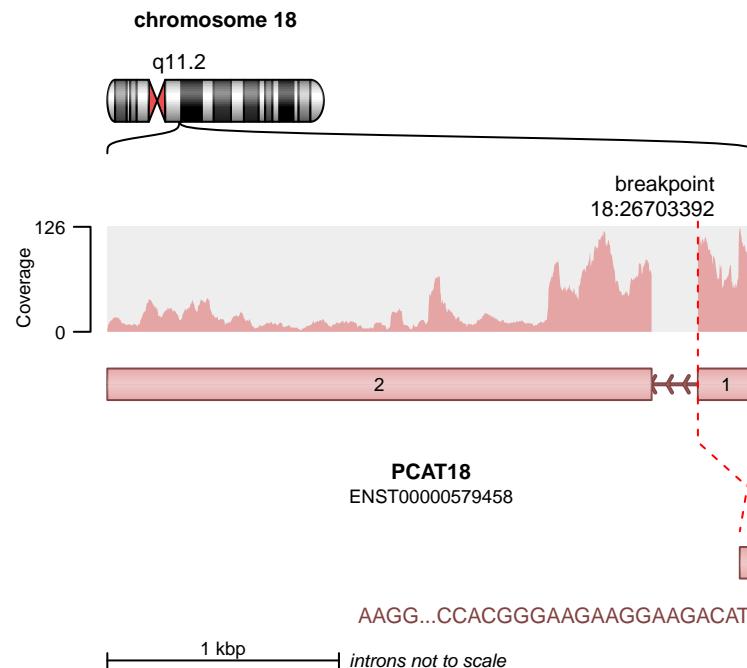


— translocation — deletion
— duplication — inversion

No coding regions due to antisense transcription.

SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 5

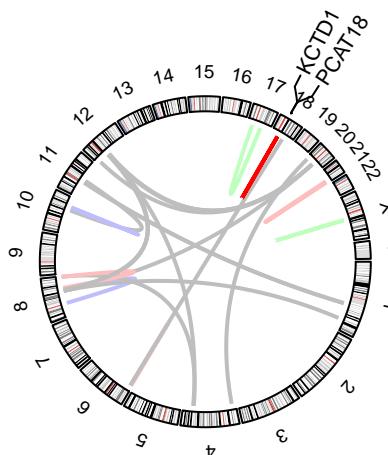
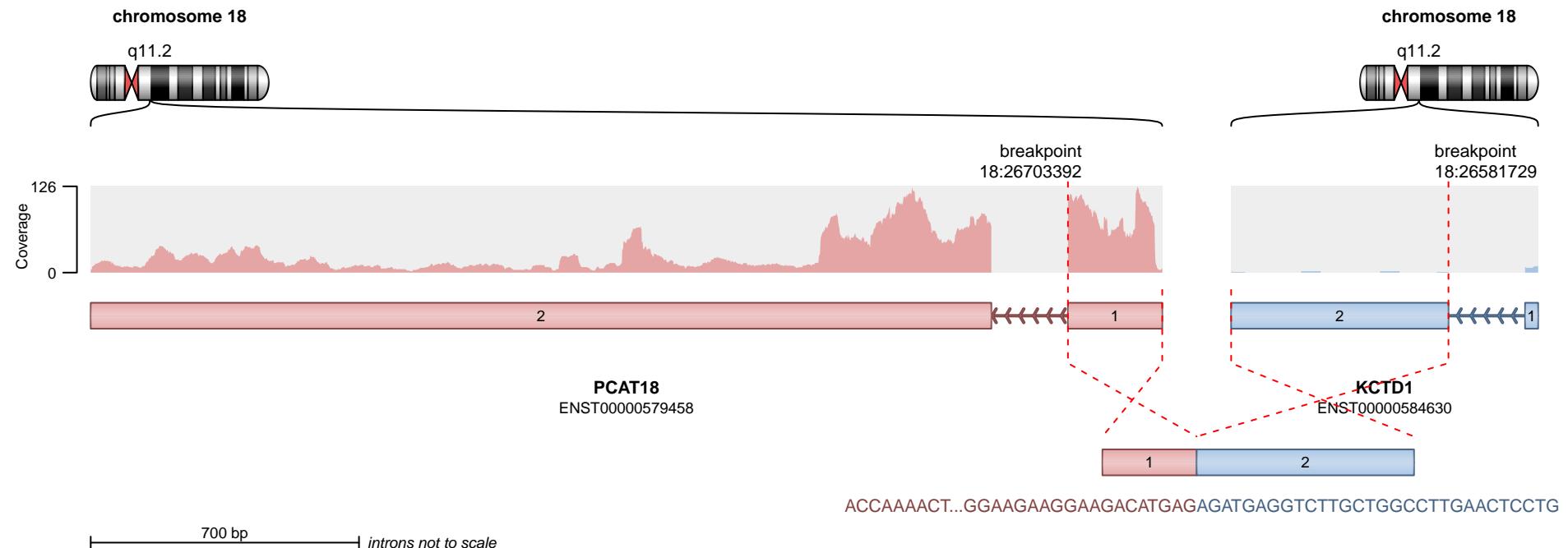


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 4

— translocation — deletion
— duplication — inversion

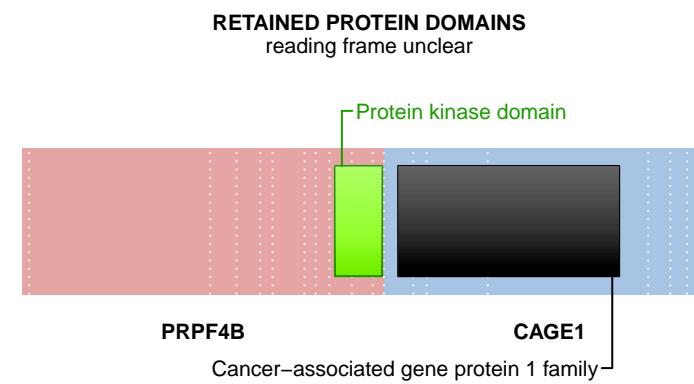
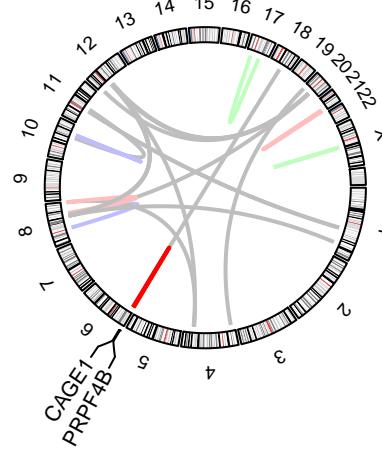
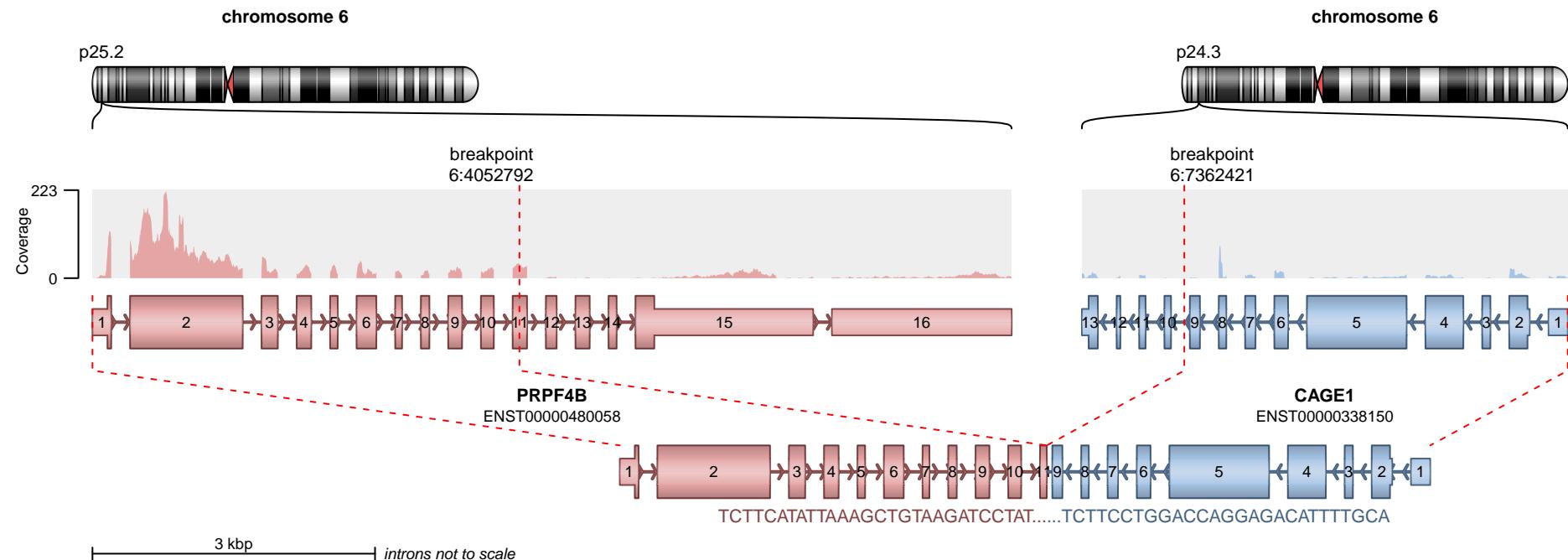


Genes are not protein-coding.

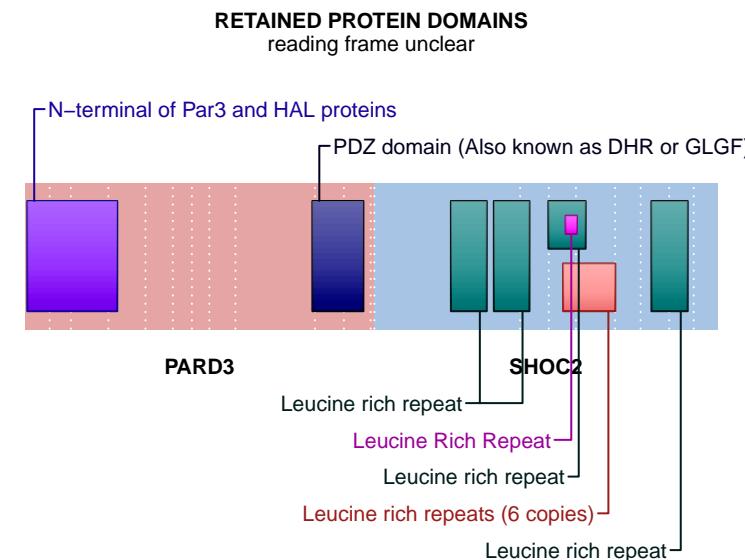
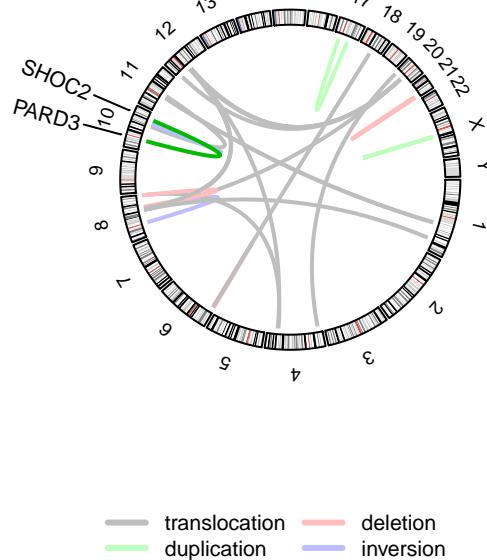
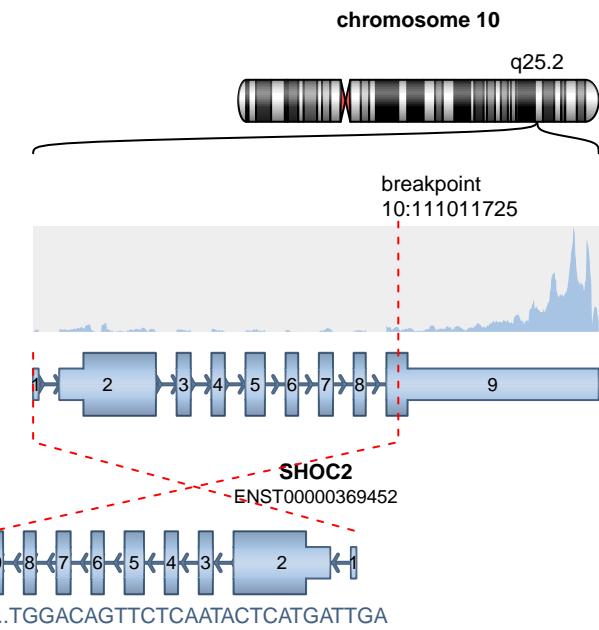
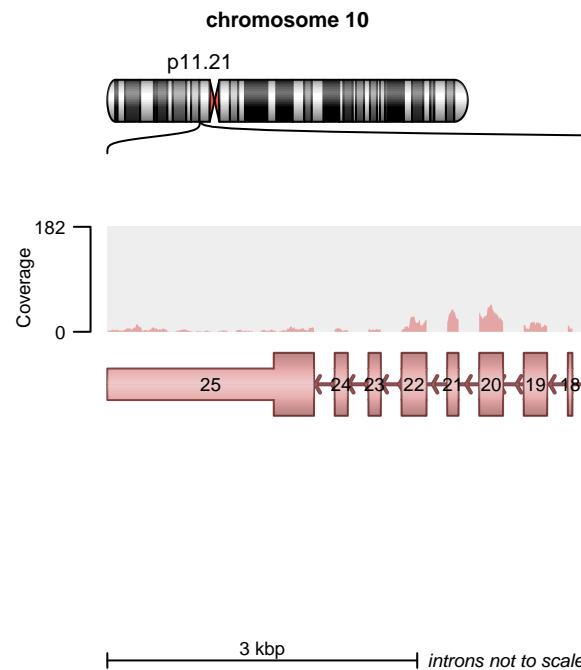
SUPPORTING READ COUNT

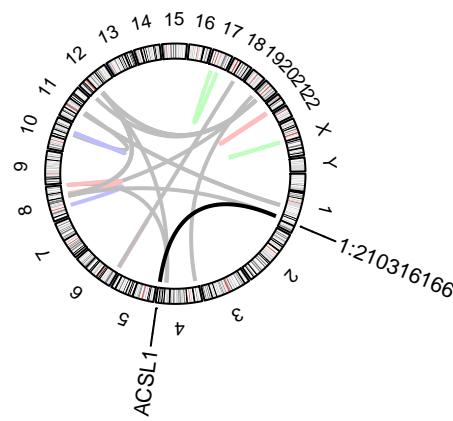
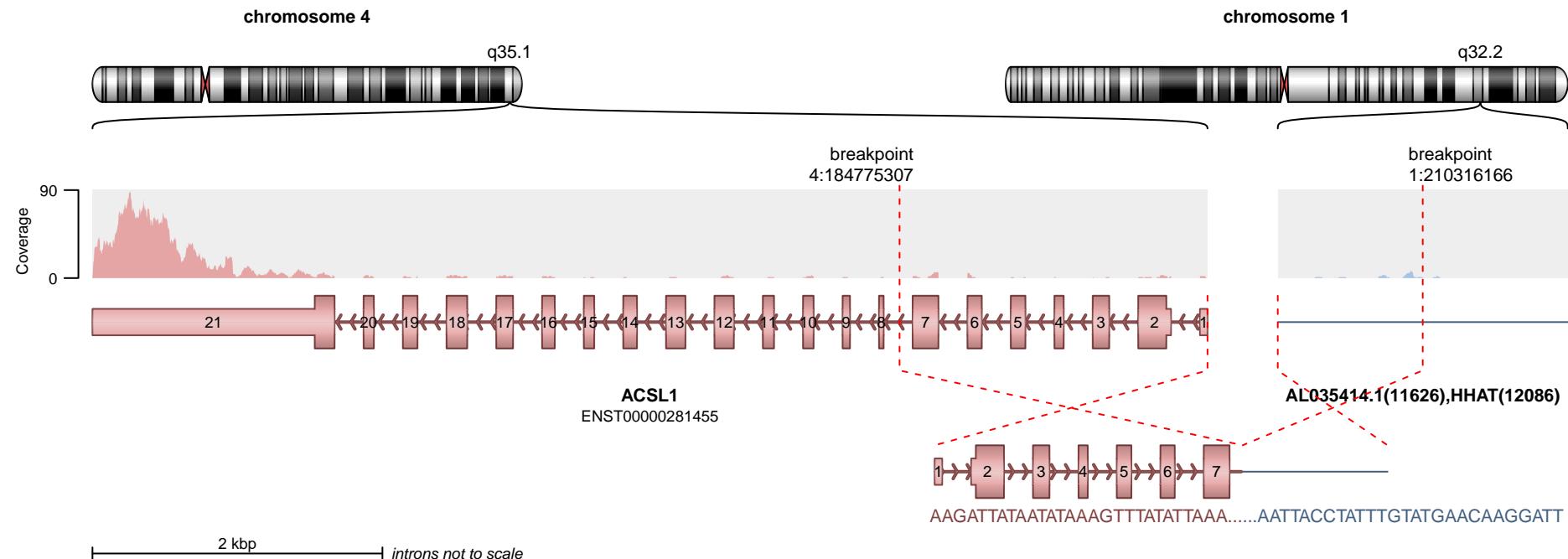
Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



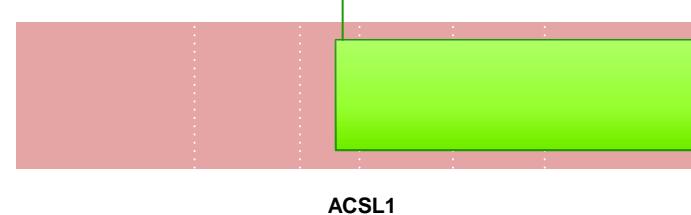
— translocation — deletion
— duplication — inversion



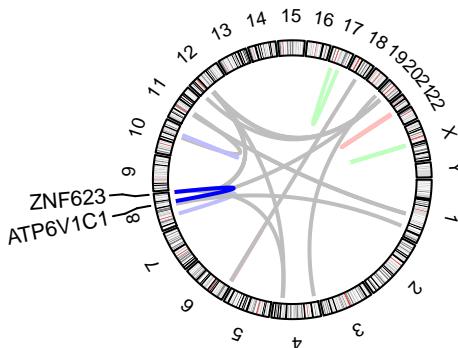
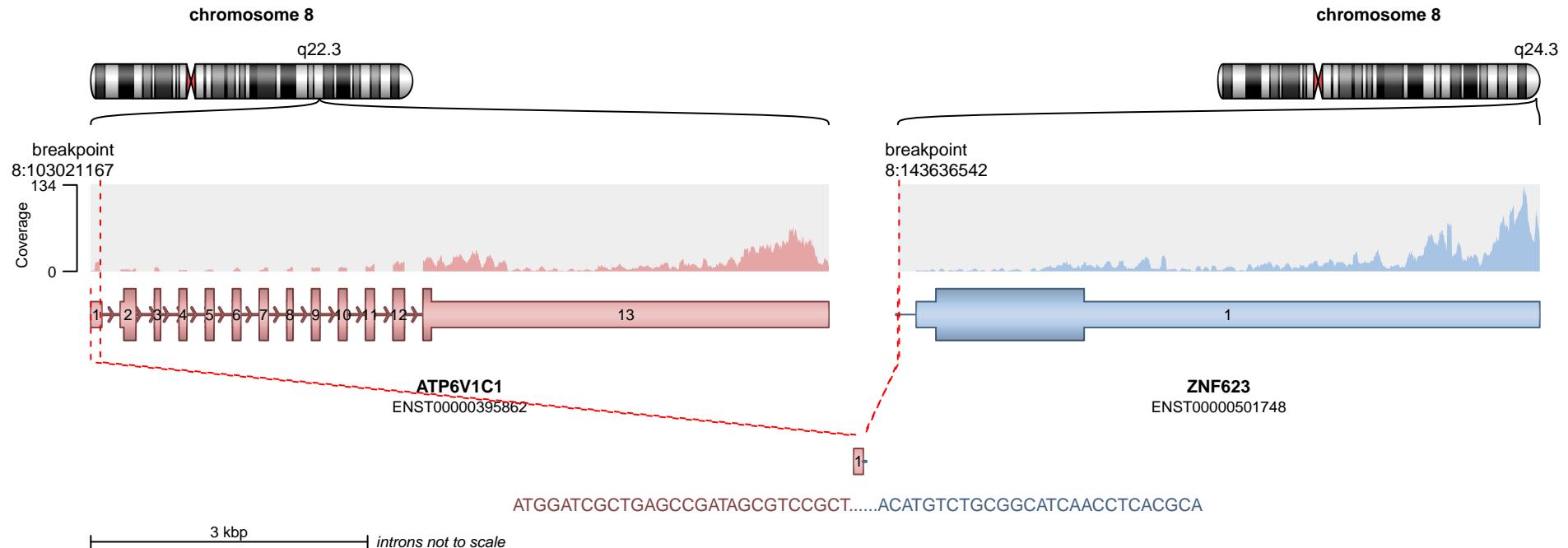


RETAINED PROTEIN DOMAINS
reading frame unclear

AMP-binding enzyme



— translocation — deletion
— duplication — inversion

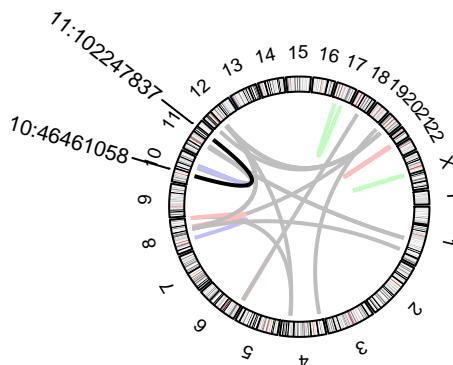
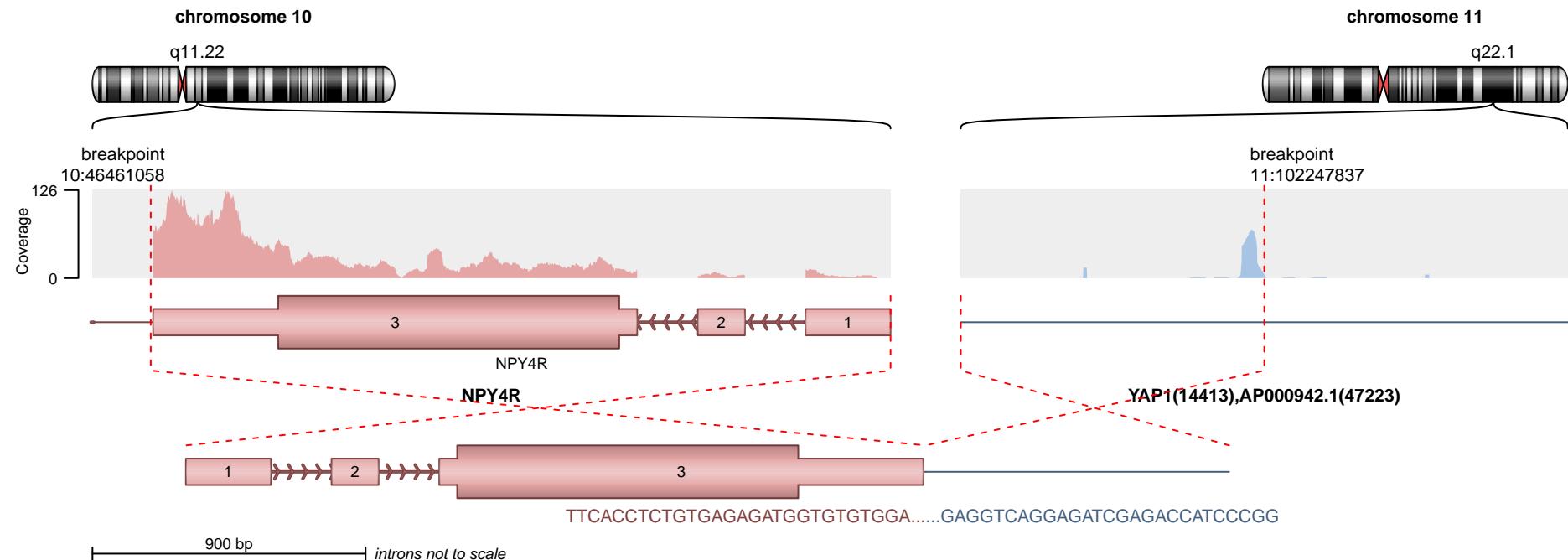


No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 4

— translocation — deletion
— duplication — inversion

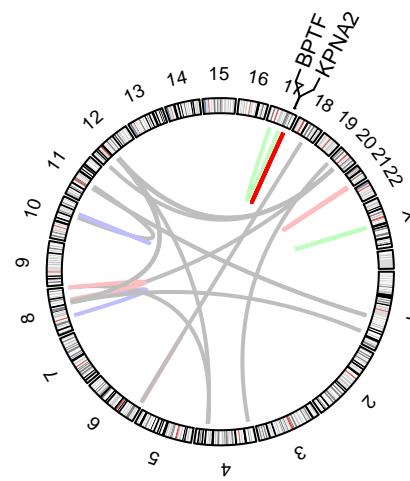
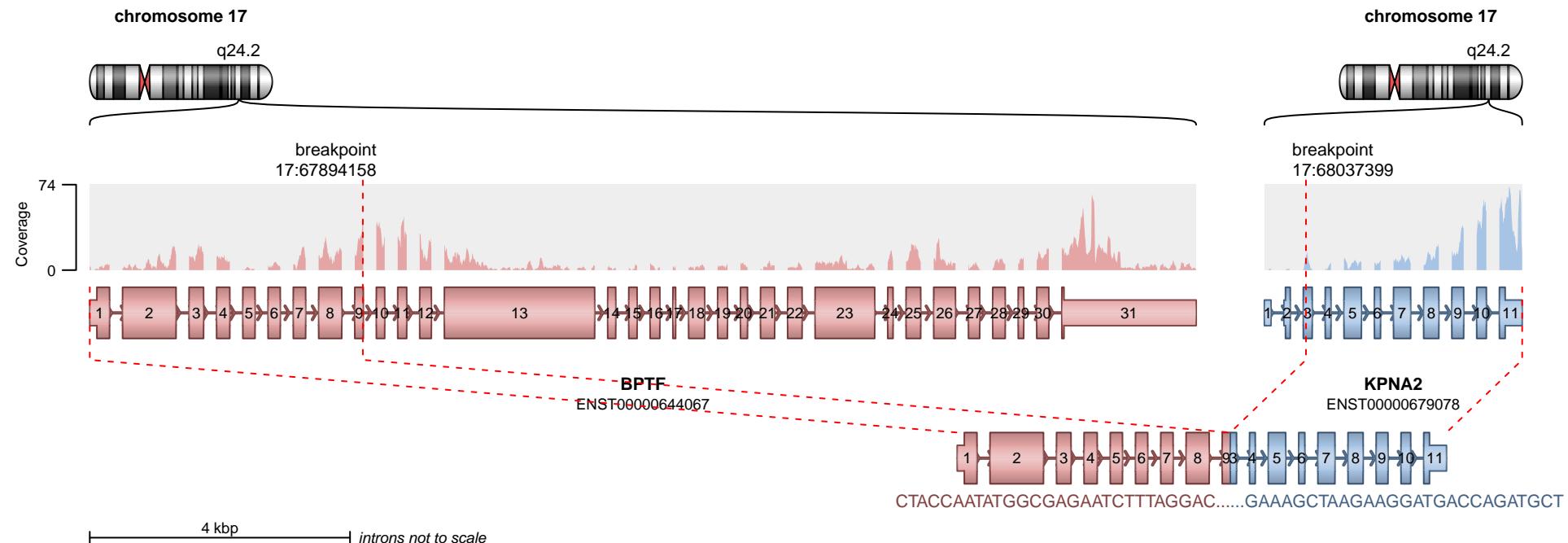


No coding regions retained in fusion transcript.

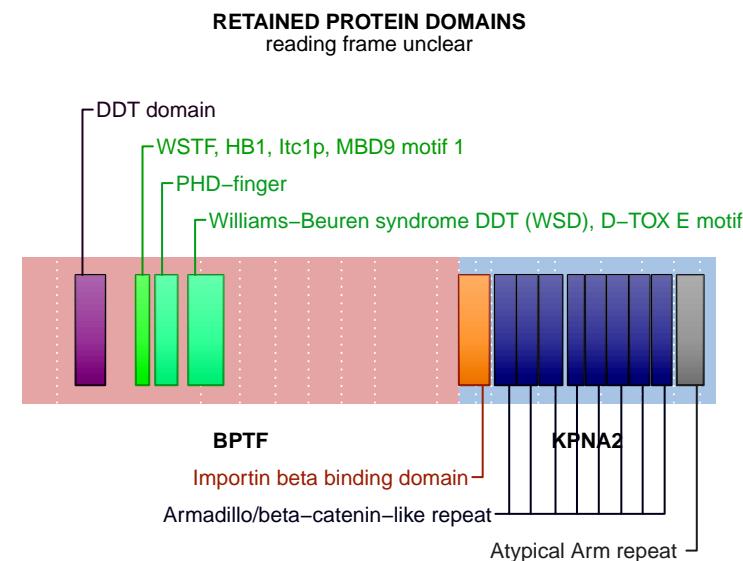
SUPPORTING READ COUNT

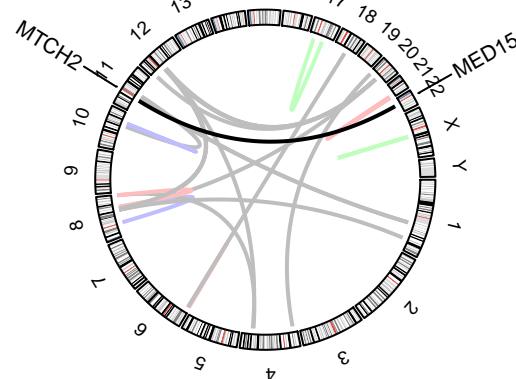
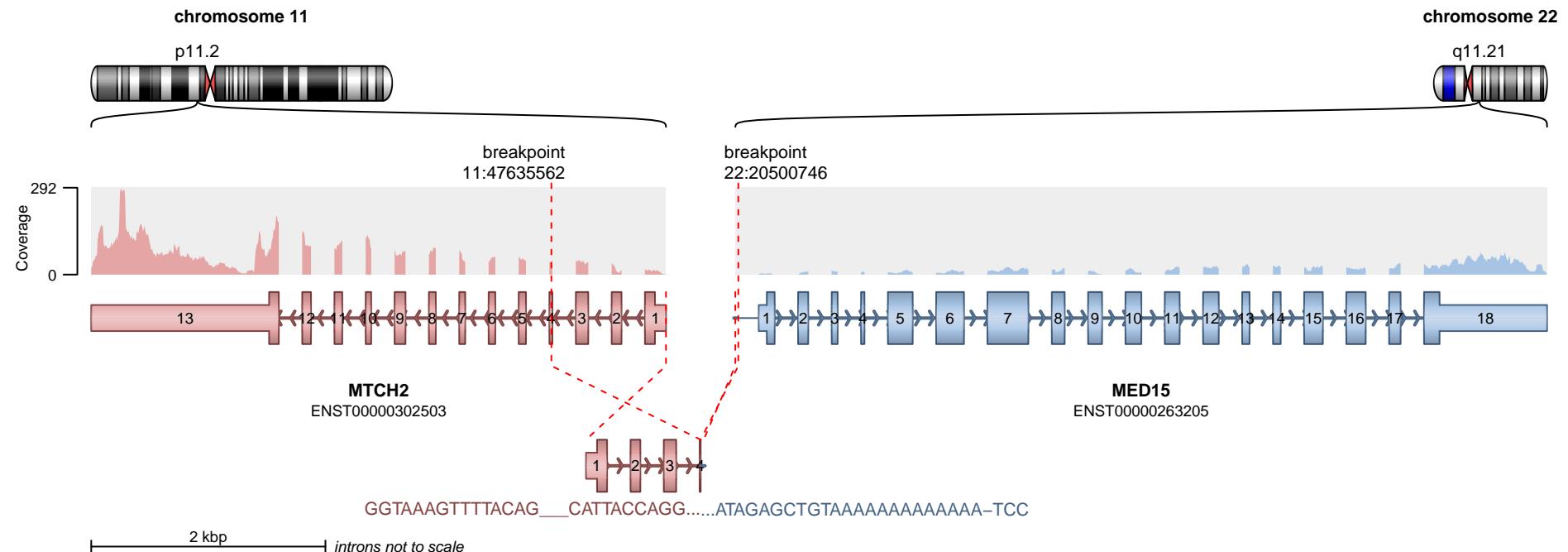
Split reads = 0
Discordant mates = 4

— translocation — deletion
— duplication — inversion



— translocation — deletion
— duplication — inversion



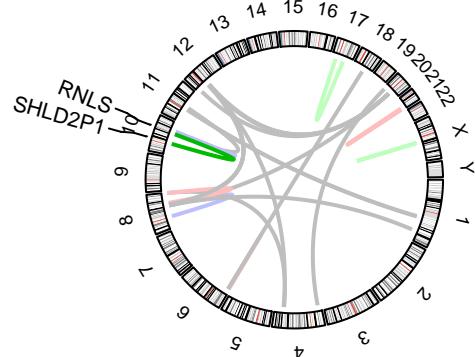
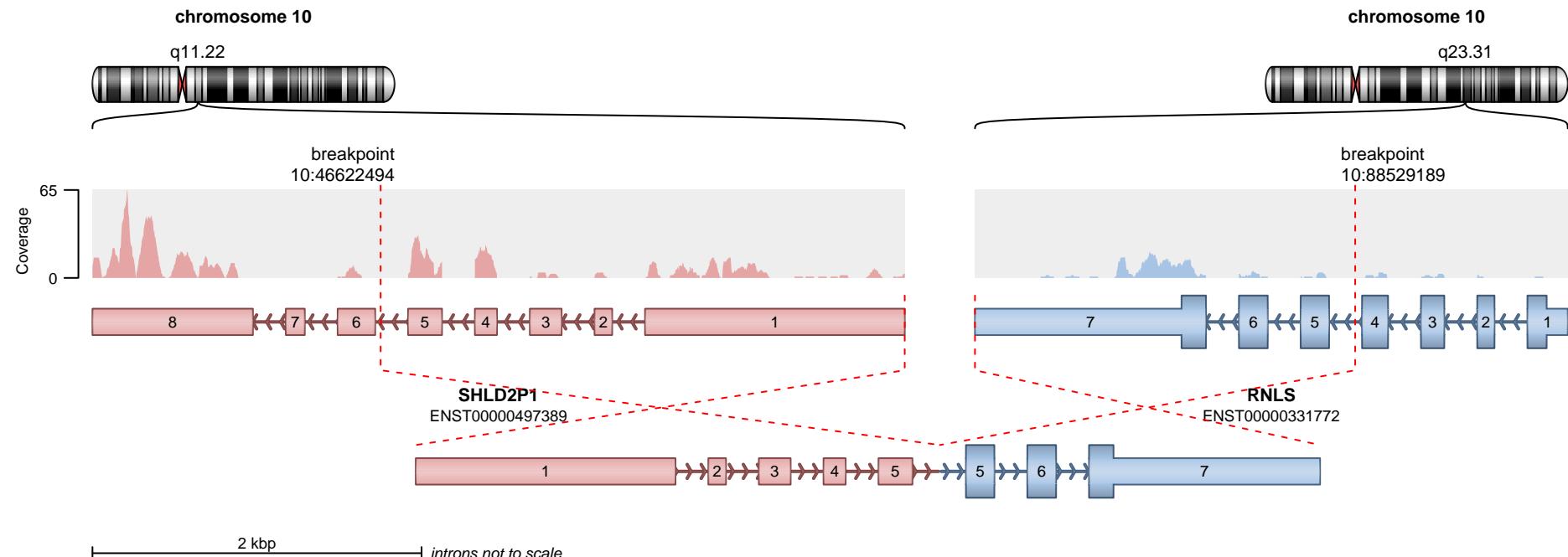


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 4

— translocation — deletion
— duplication — inversion

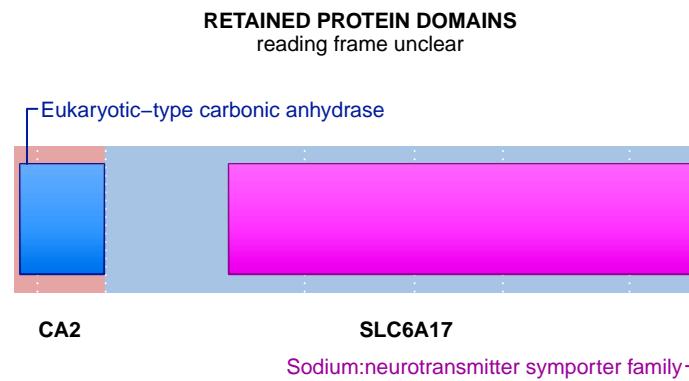
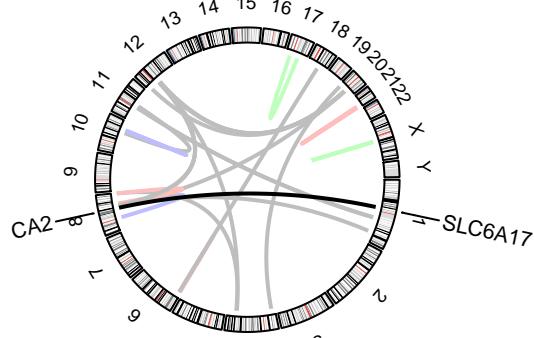
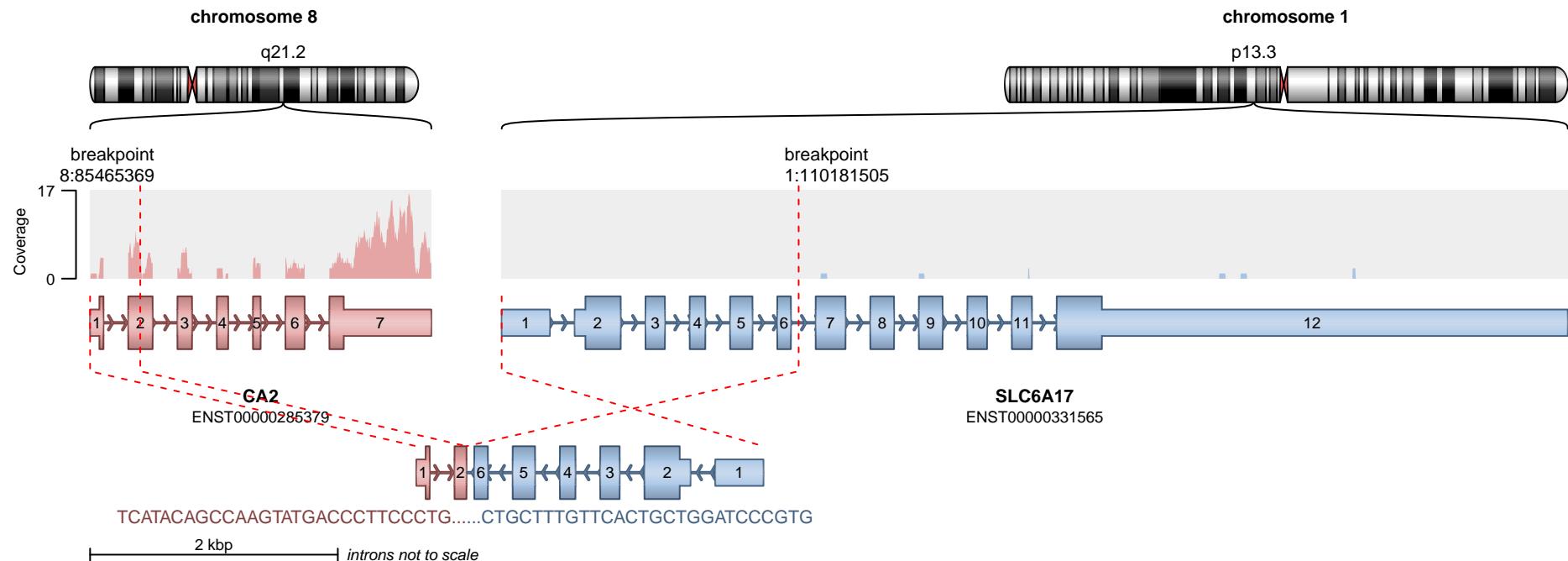


No coding regions due to antisense transcription.

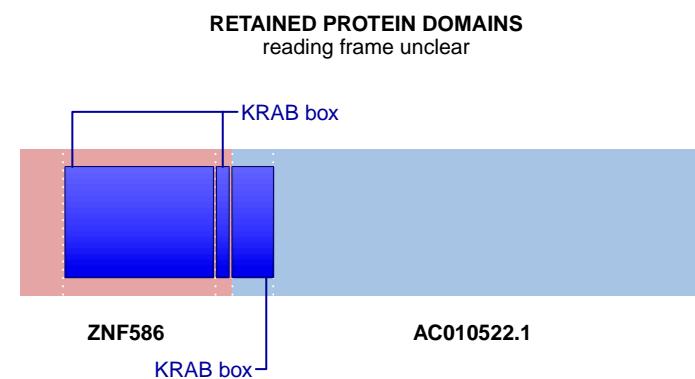
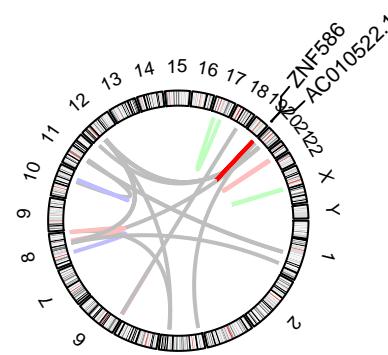
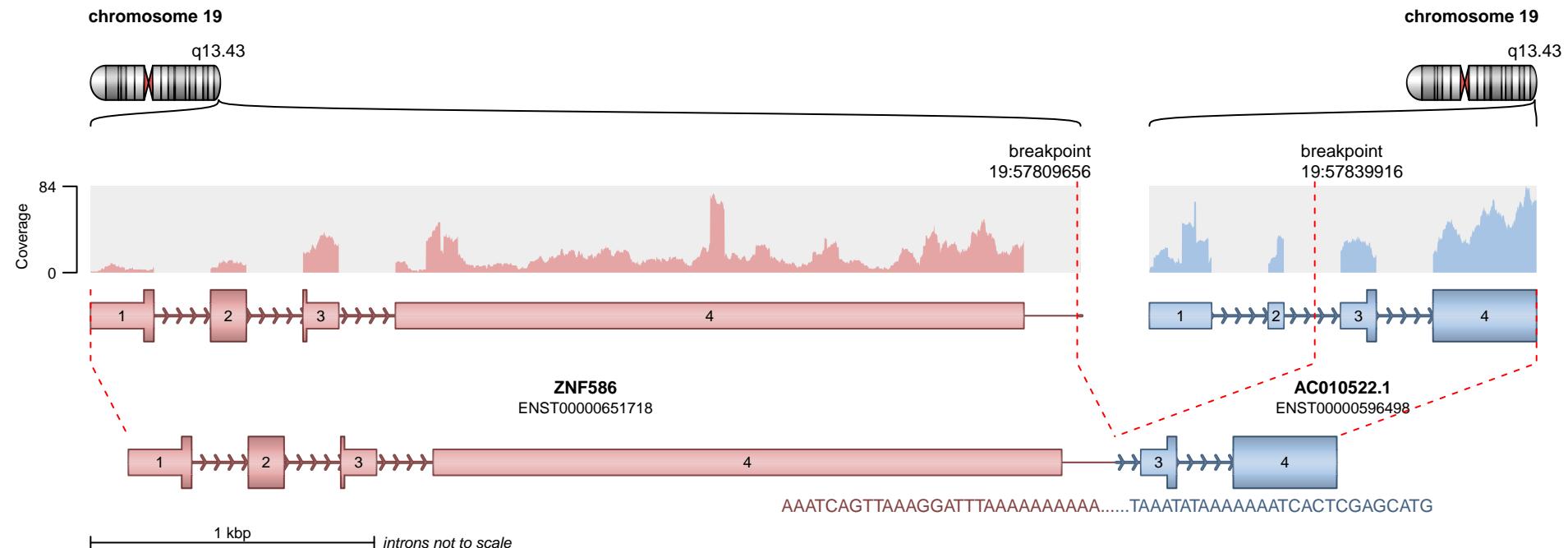
SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 3

— translocation — deletion
— duplication — inversion



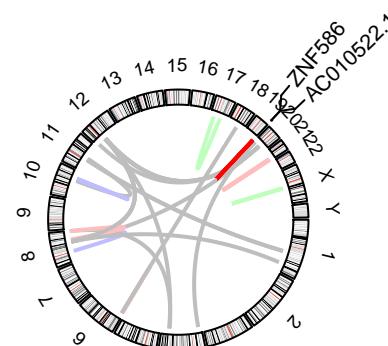
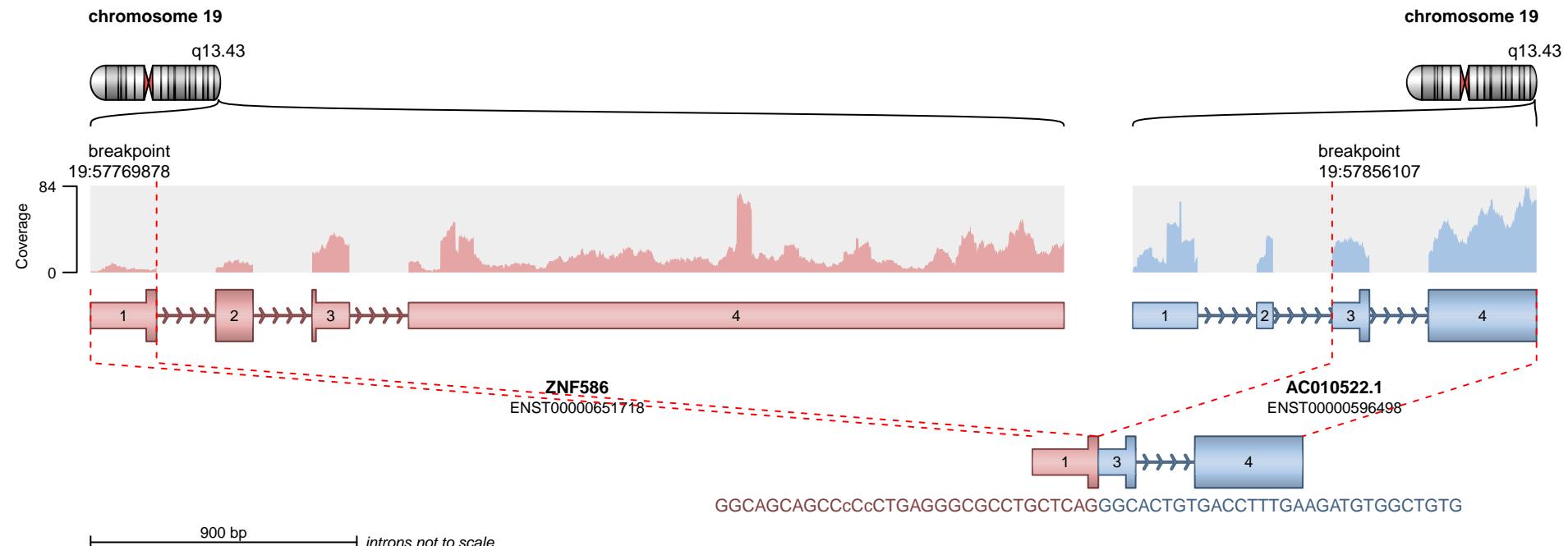
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 3

— translocation — deletion
— duplication — inversion



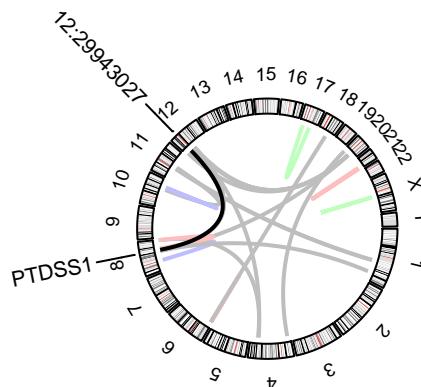
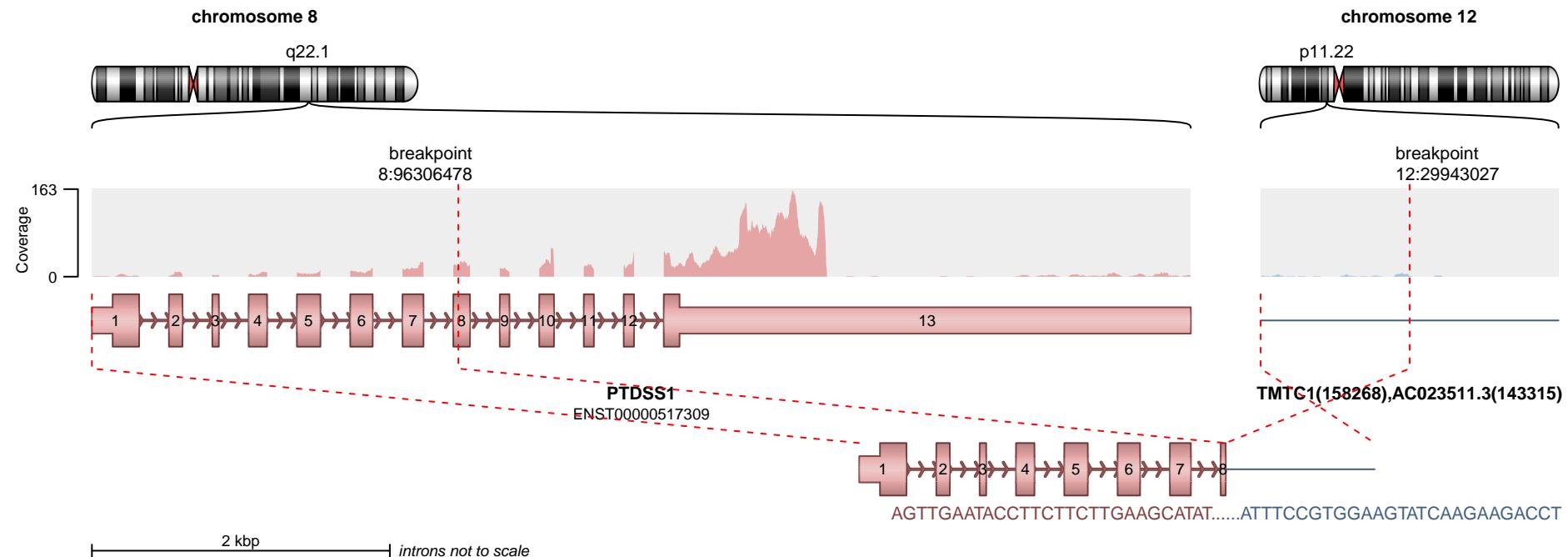
RETAINED PROTEIN DOMAINS in-frame fusion



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion

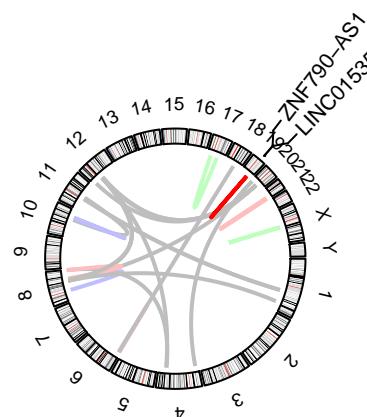
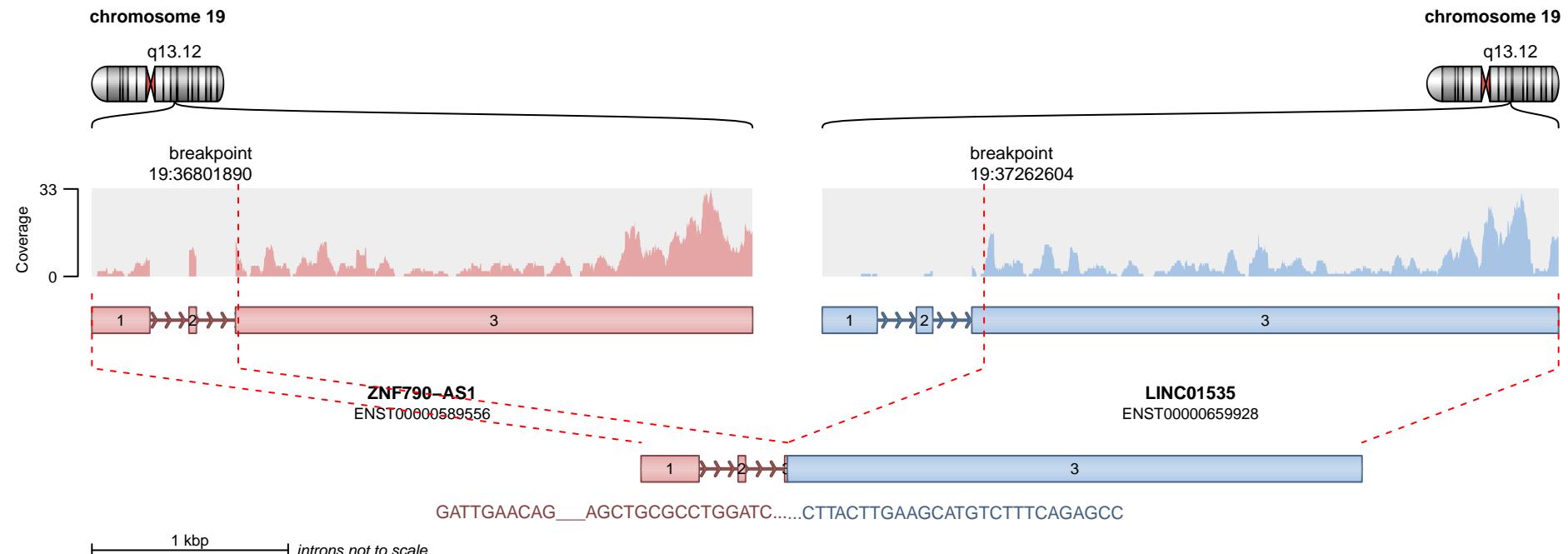


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 3

— translocation — deletion
— duplication — inversion

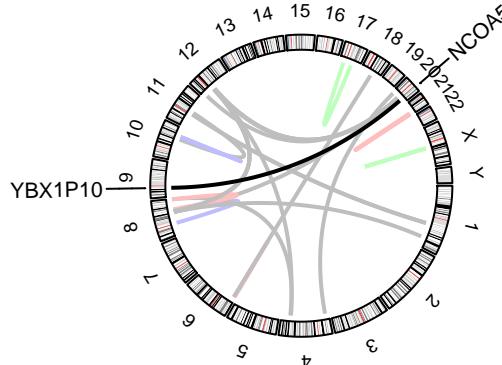
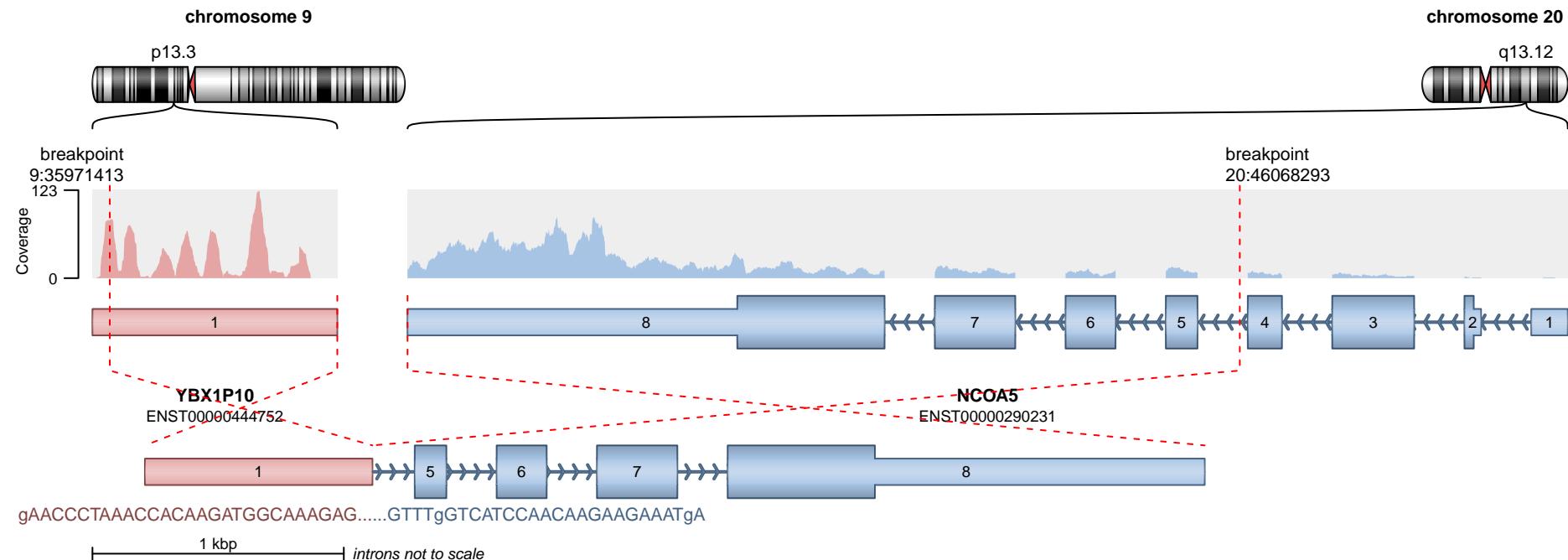


Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 3

— translocation — deletion
— duplication — inversion

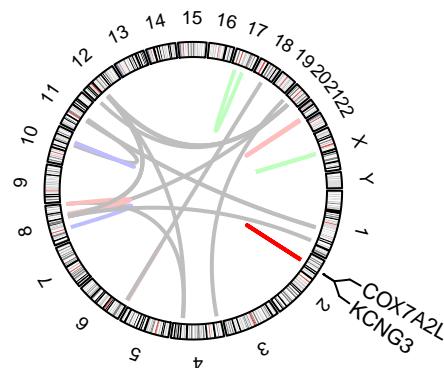
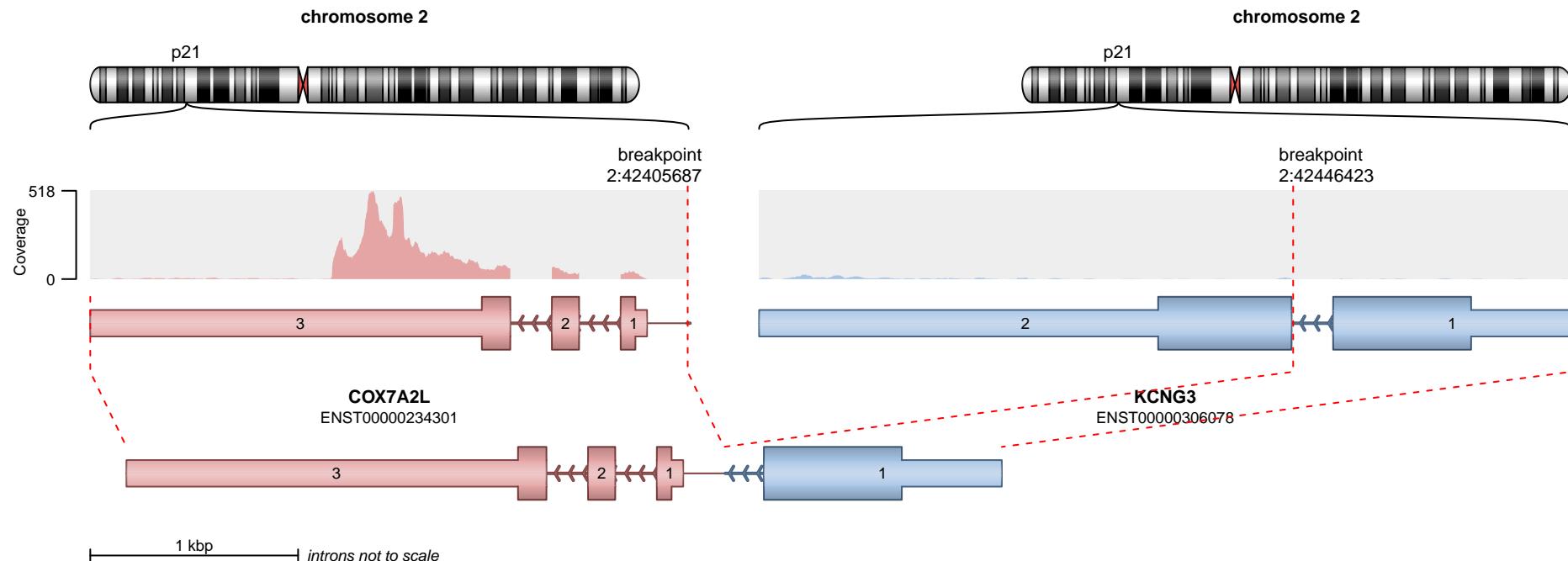


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 2

— translocation — deletion
— duplication — inversion



No coding regions due to antisense transcription.

SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 2

— translocation — deletion
— duplication — inversion