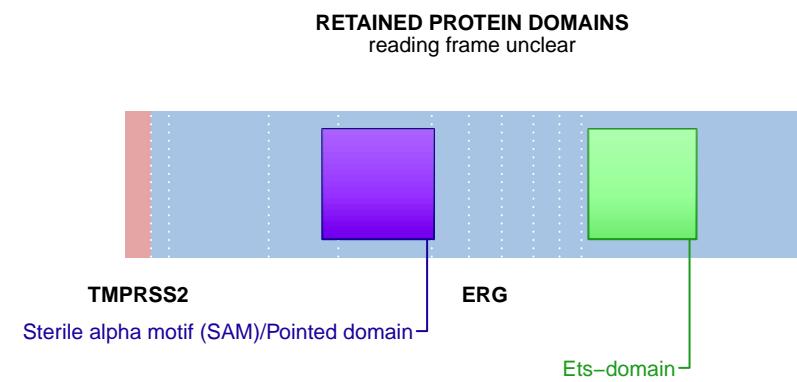
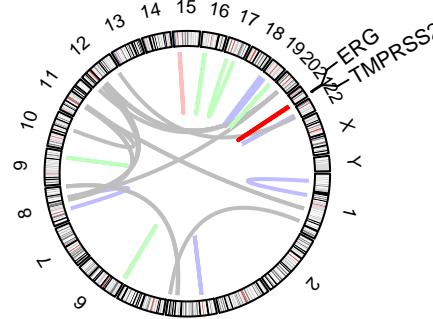
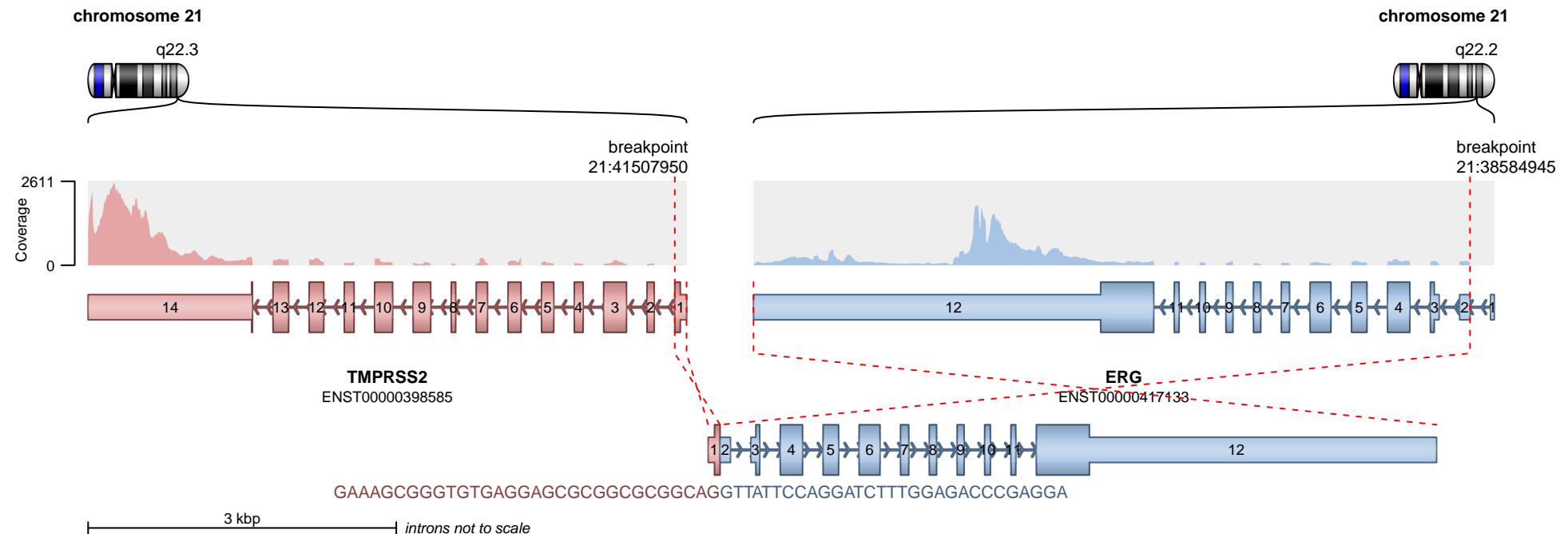


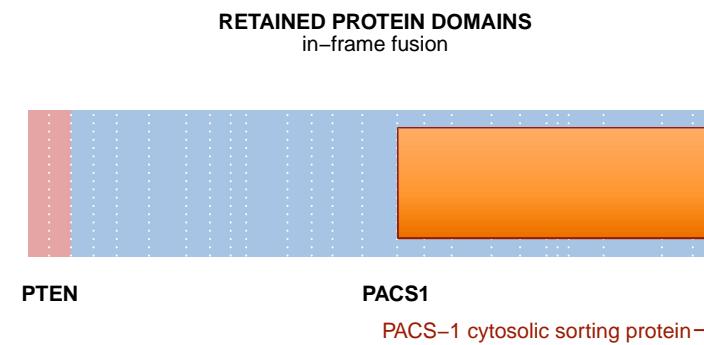
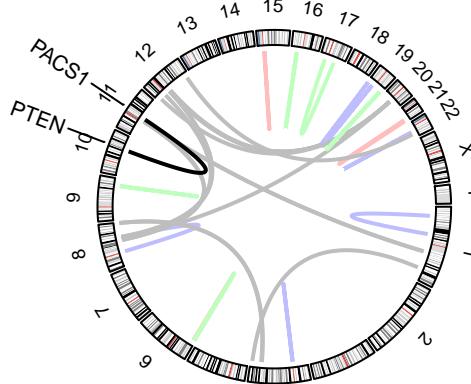
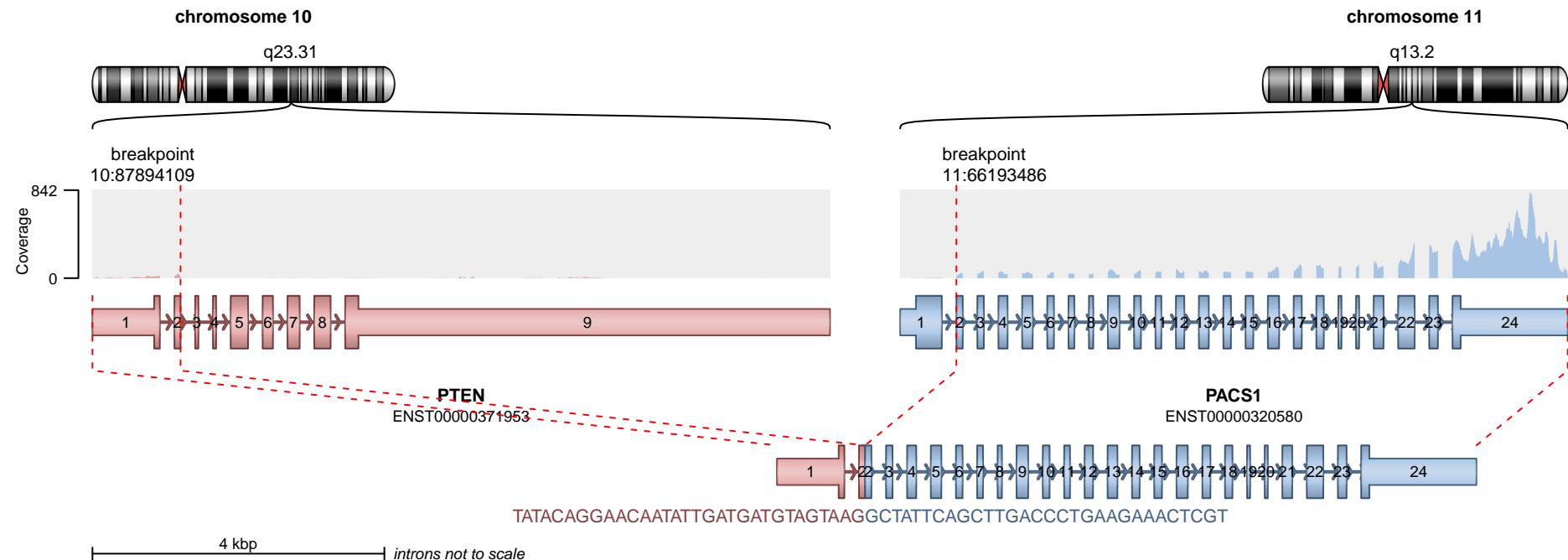
SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 75

— translocation — deletion
— duplication — inversion



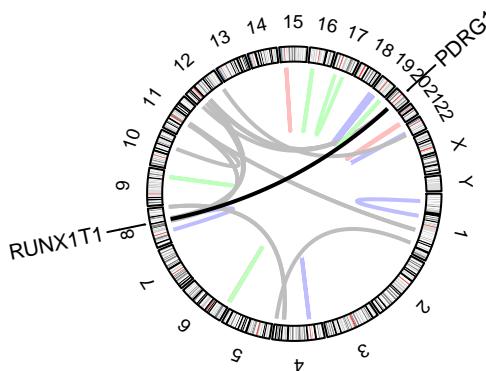
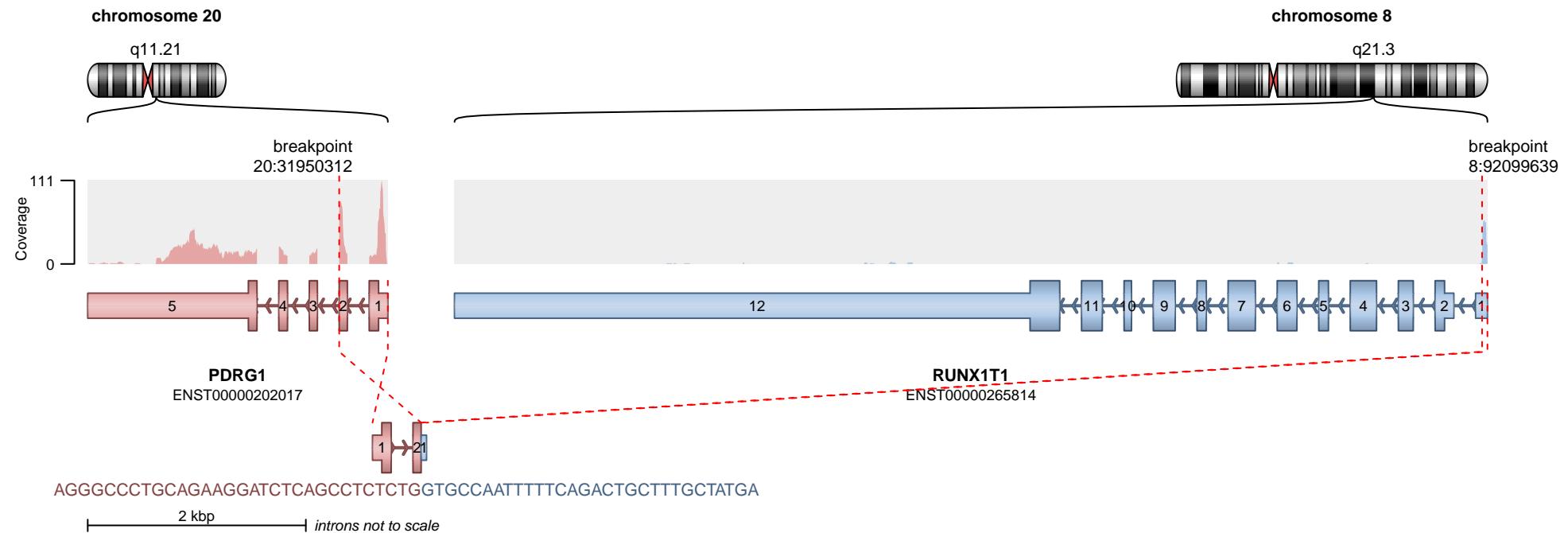
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 37

— translocation — deletion
— duplication — inversion

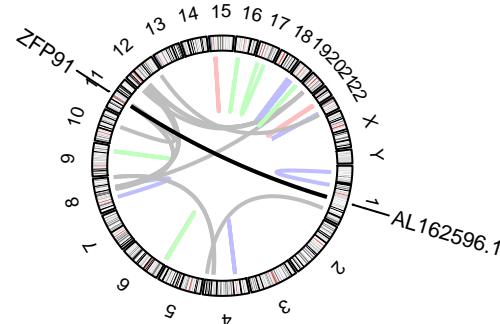
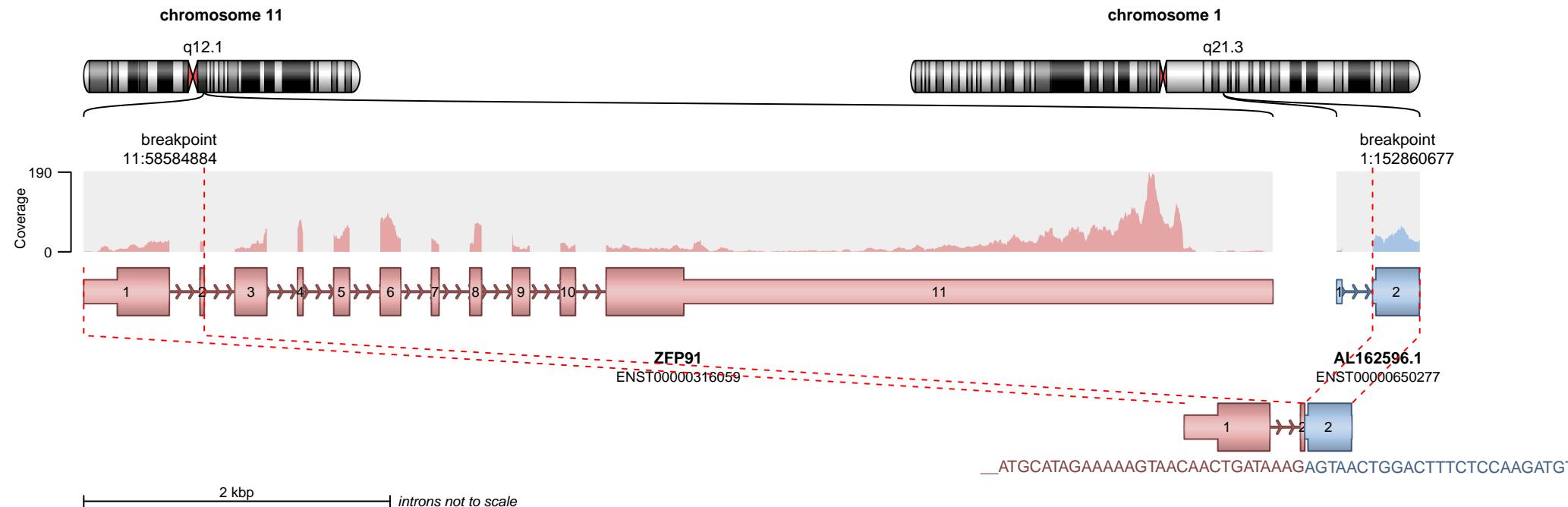


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 35

— translocation — deletion
— duplication — inversion

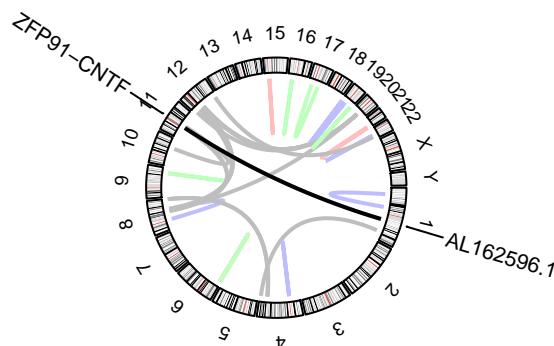
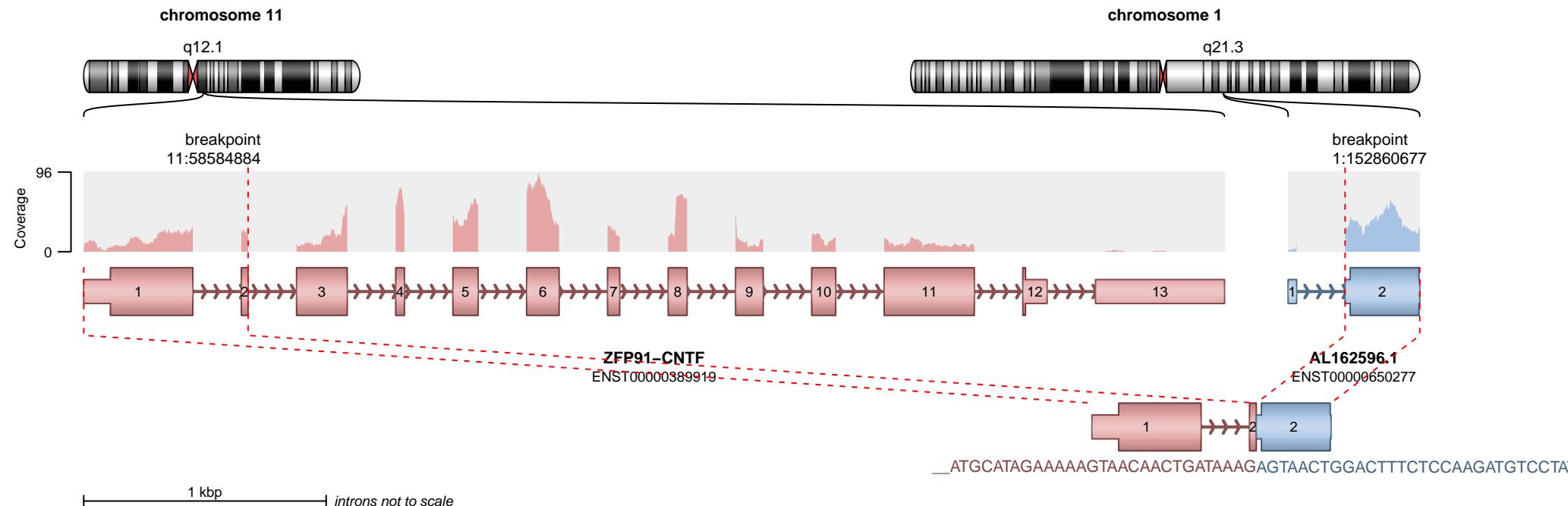


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 33

— translocation — deletion
— duplication — inversion

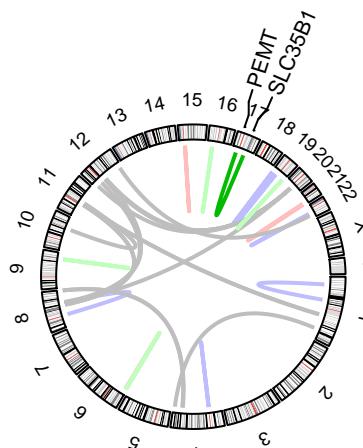
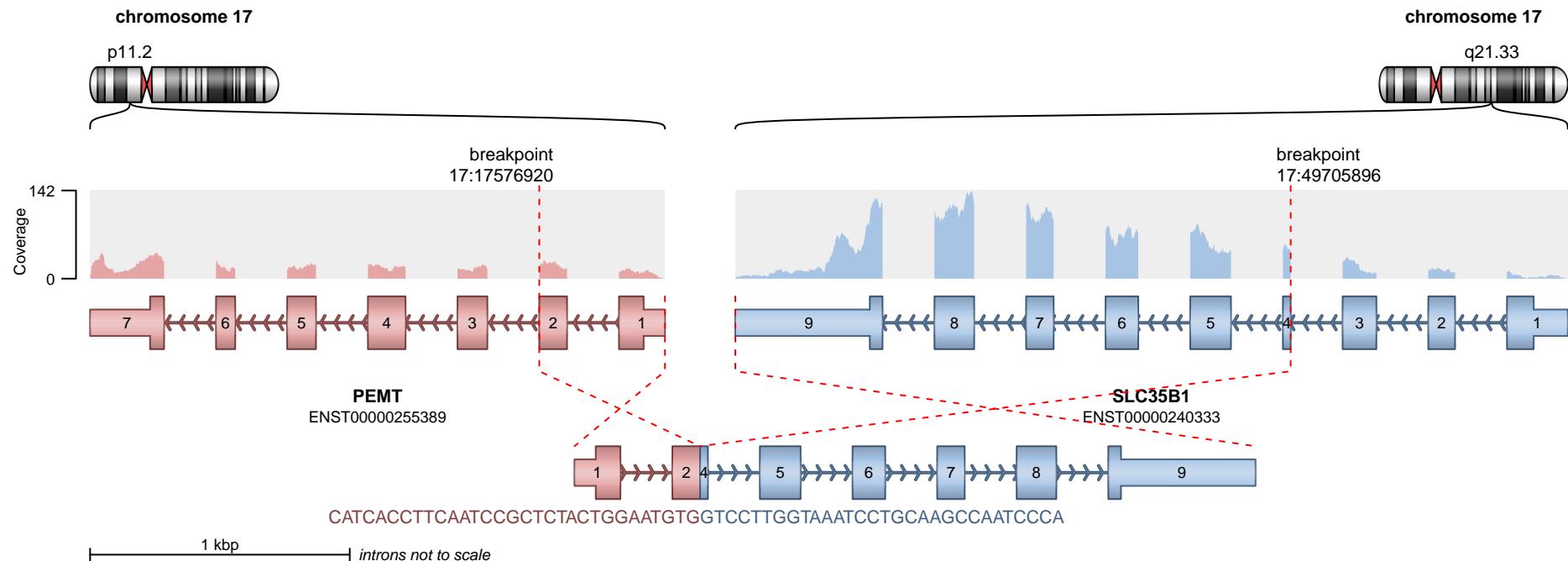


No protein domains retained in fusion.

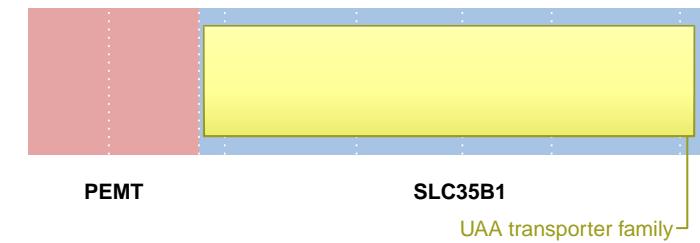
SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 33

— translocation — deletion
— duplication — inversion



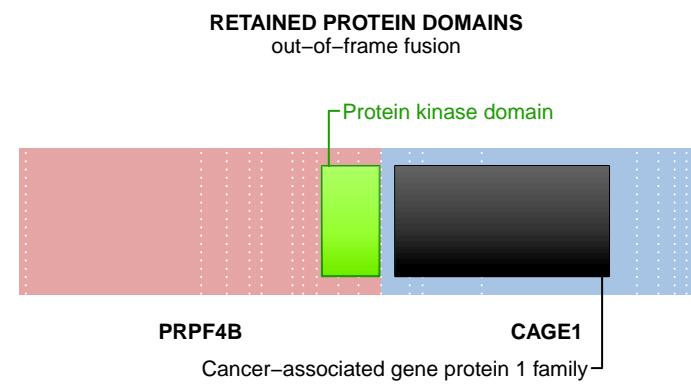
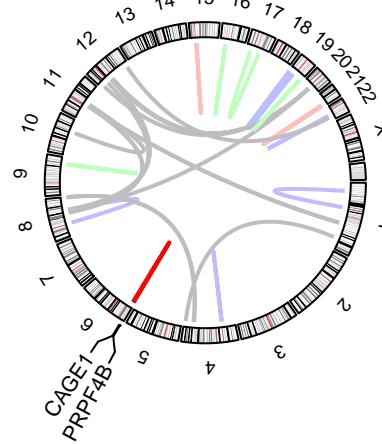
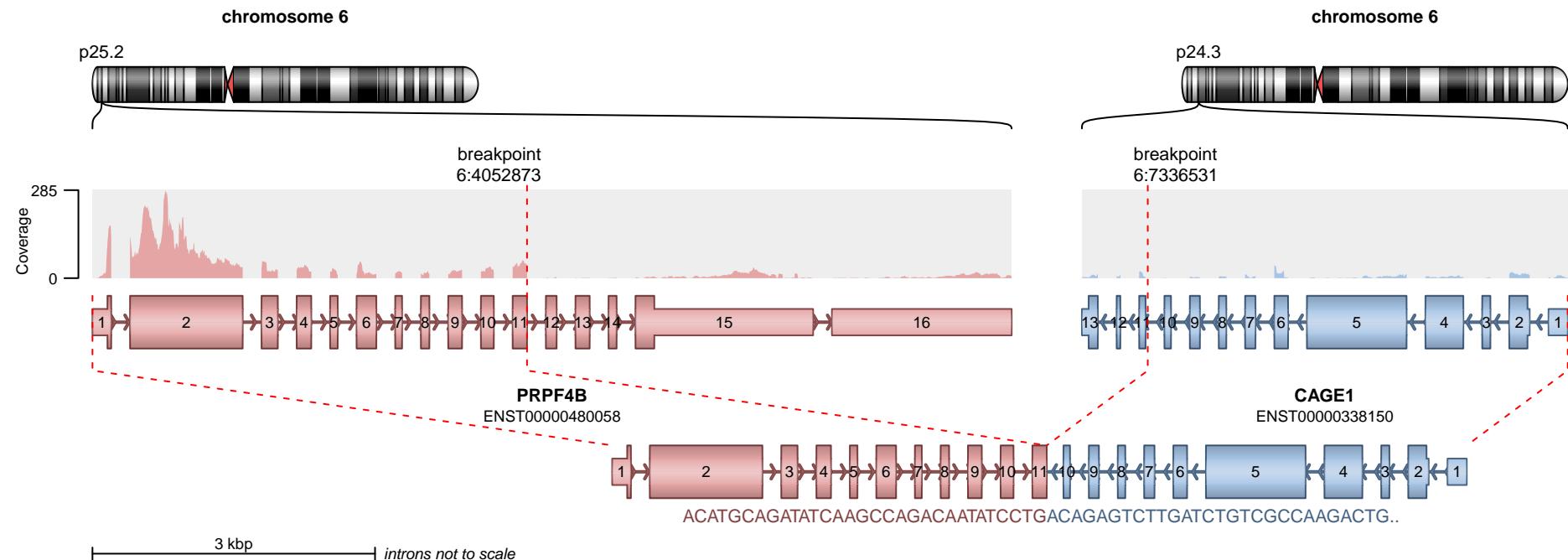
RETAINED PROTEIN DOMAINS
in-frame fusion



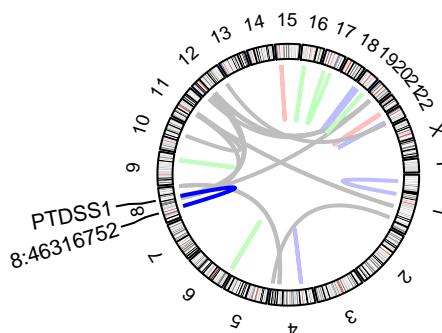
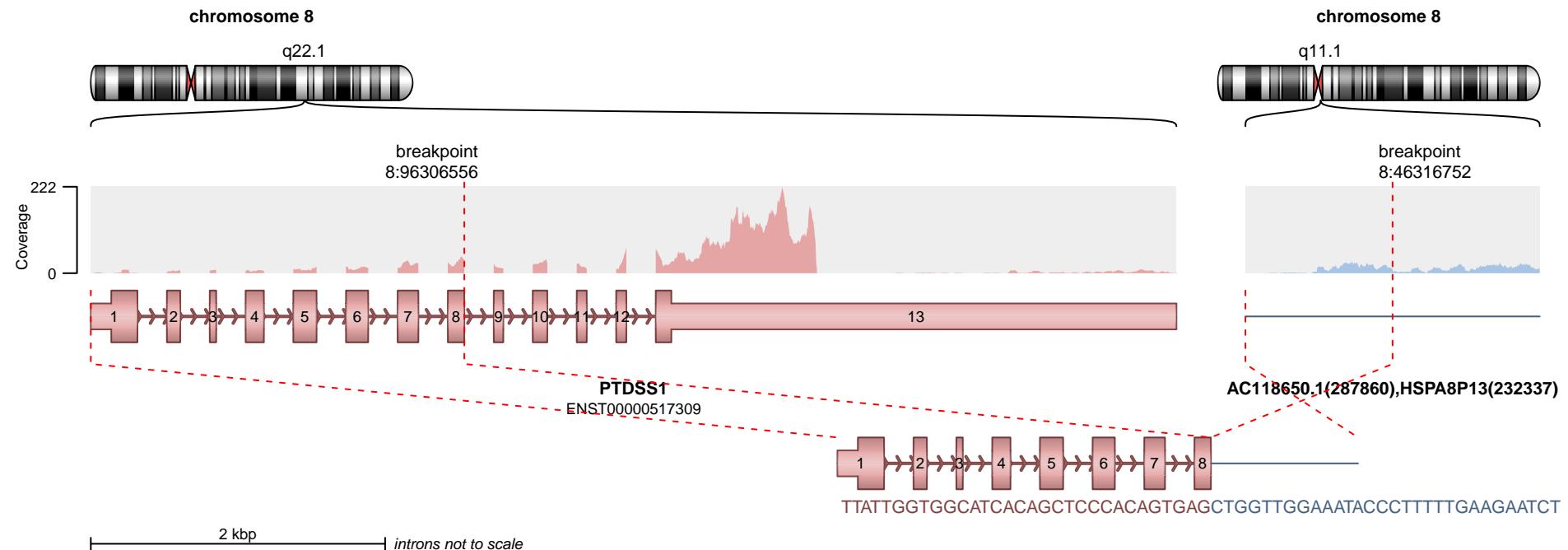
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 22

— translocation — deletion
— duplication — inversion



— translocation — deletion
— duplication — inversion

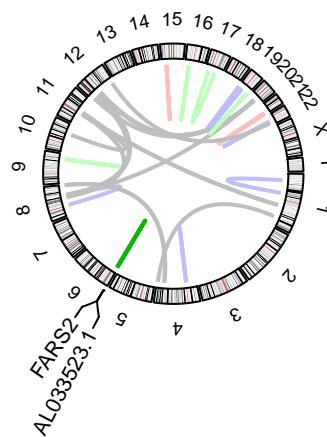
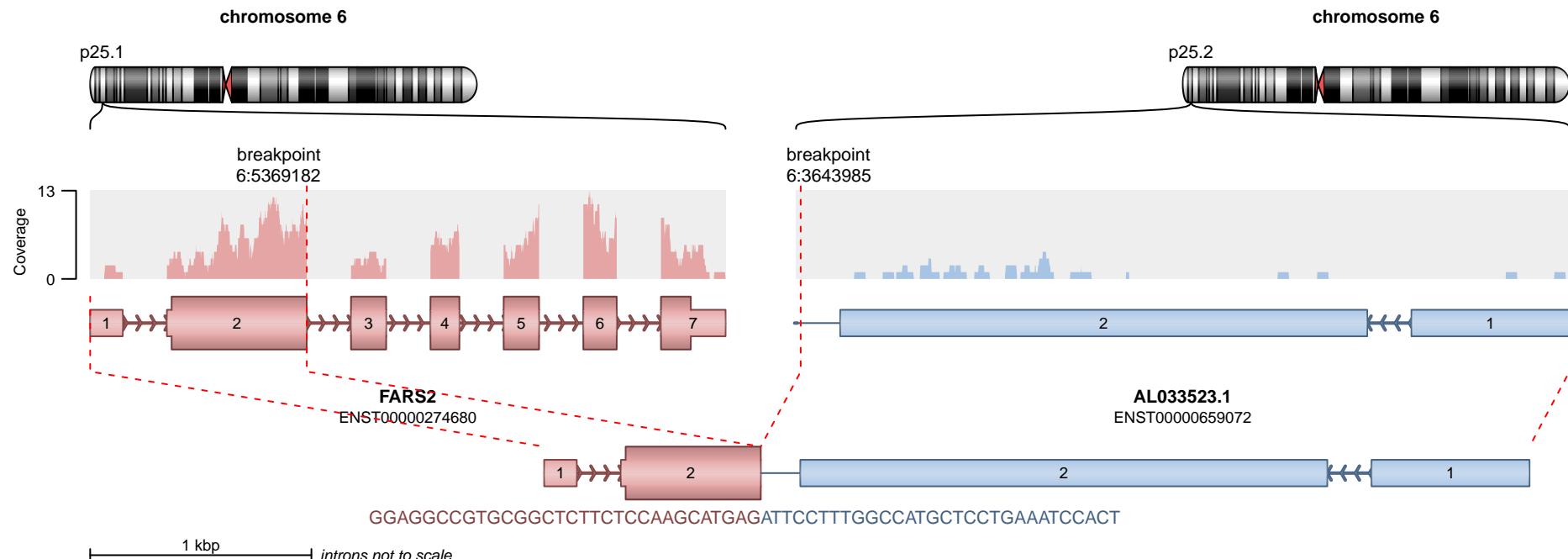


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 9

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS out-of-frame fusion

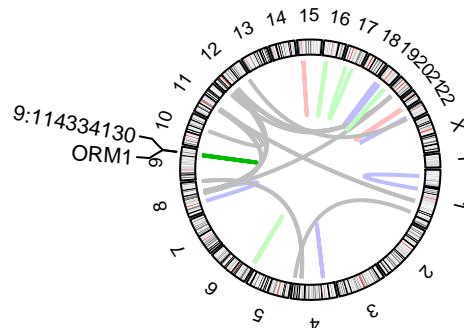
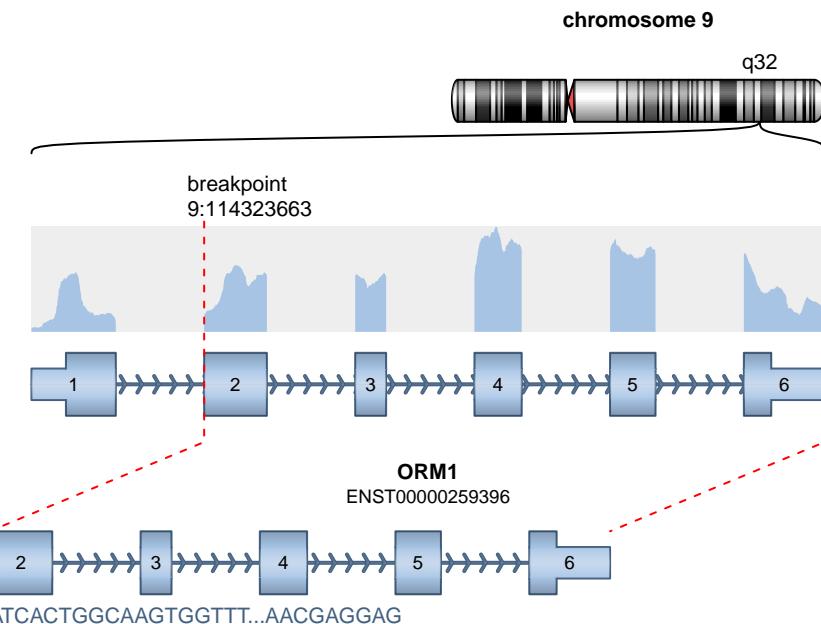
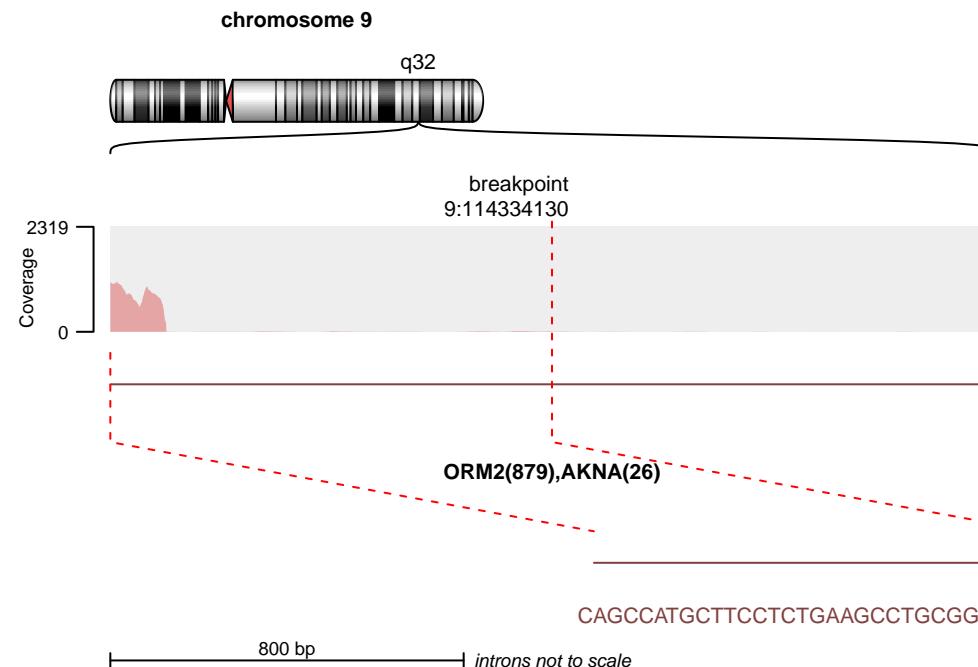
tRNA synthetases class II core domain (F)

FARS2

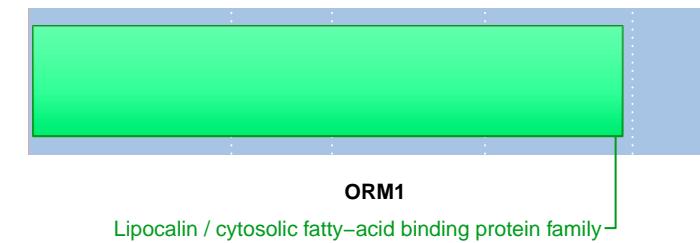
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 9

— translocation — deletion
— duplication — inversion



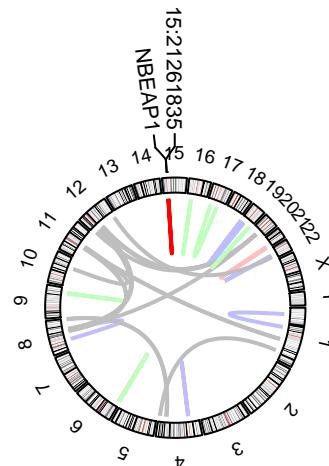
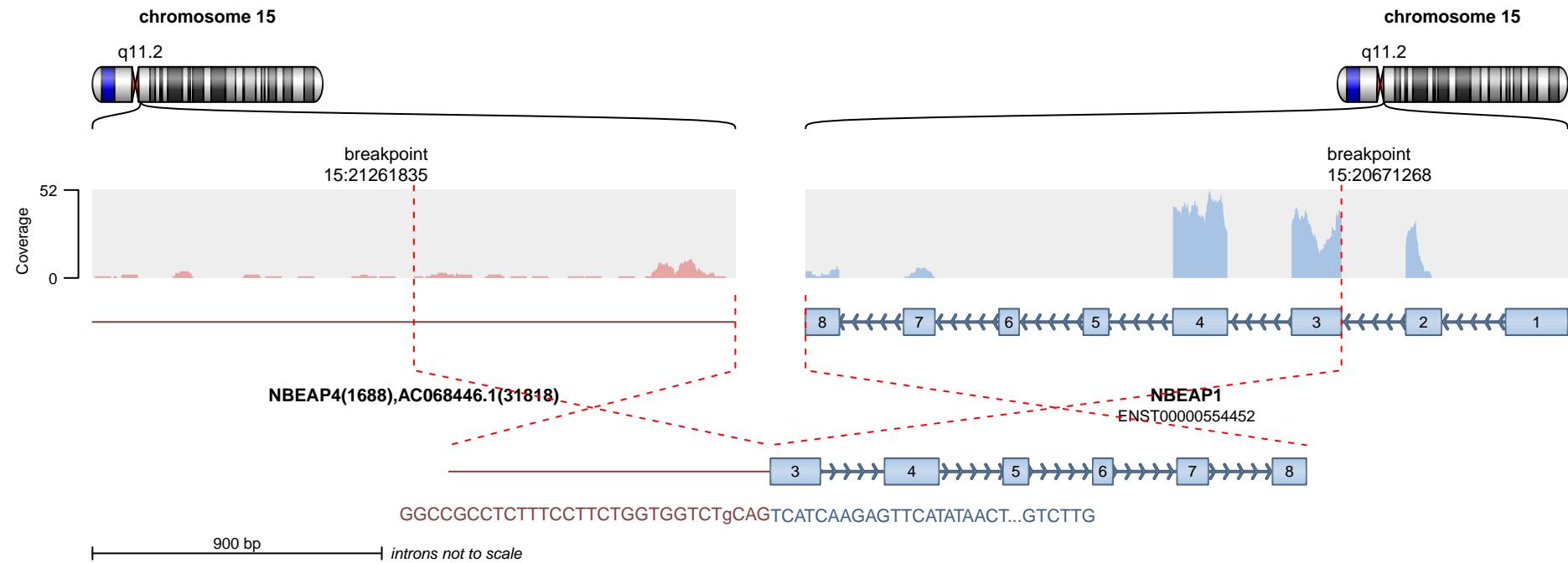
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 9

— translocation — deletion
— duplication — inversion



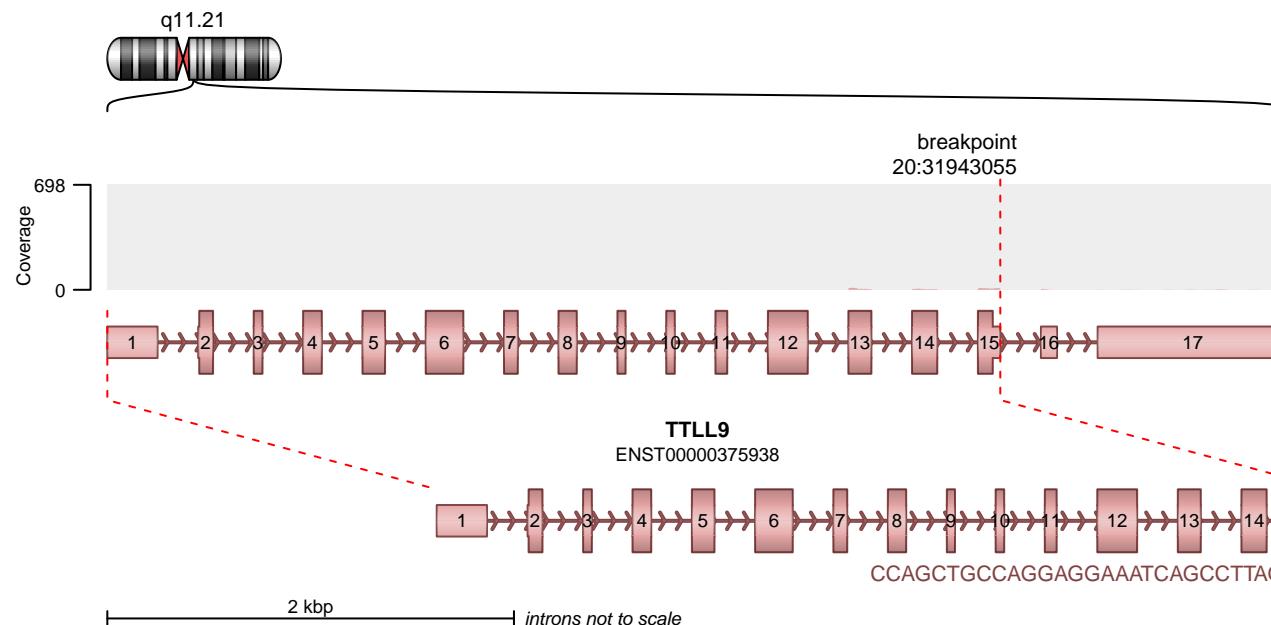
Genes are not protein-coding.

SUPPORTING READ COUNT

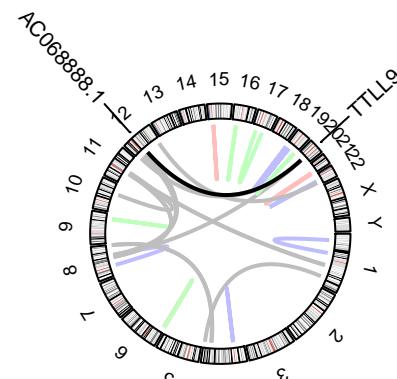
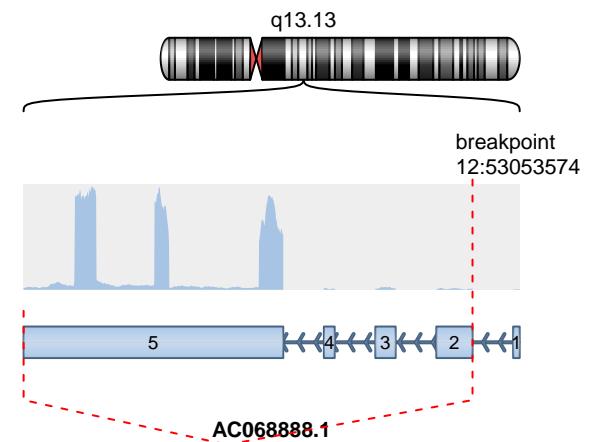
Split reads = 1
Discordant mates = 7

— translocation — deletion
— duplication — inversion

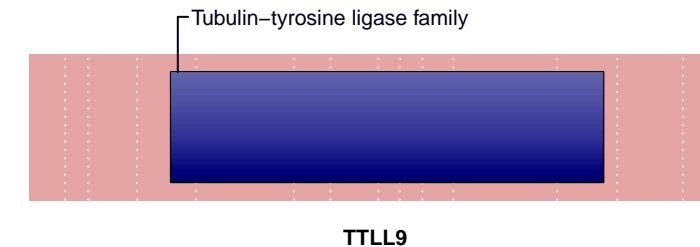
chromosome 20



chromosome 12



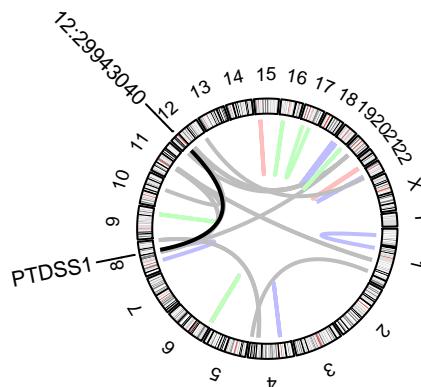
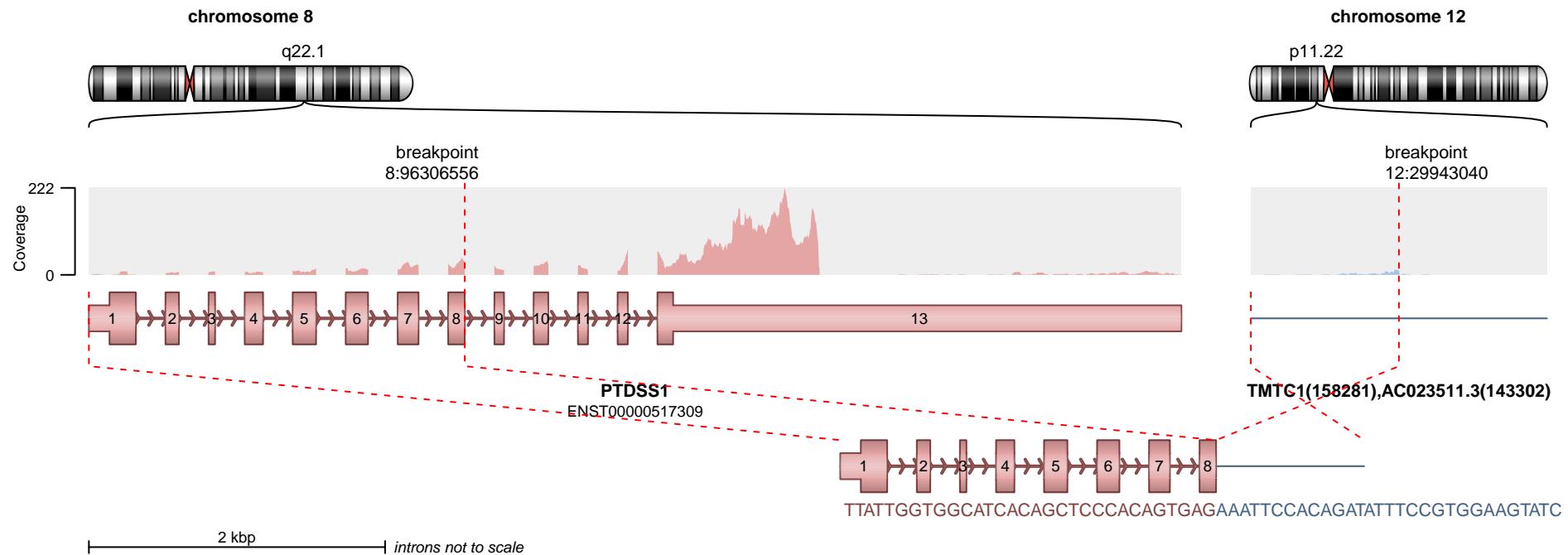
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 5

— translocation — deletion
— duplication — inversion

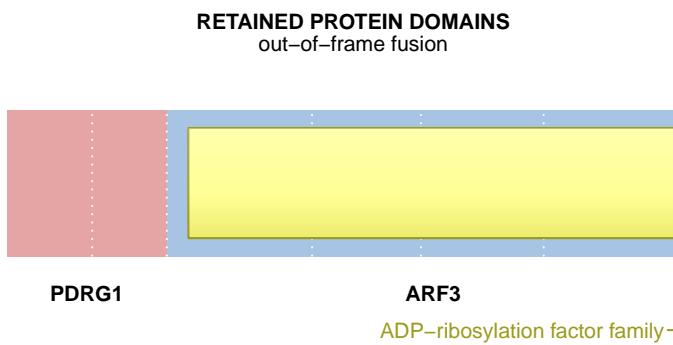
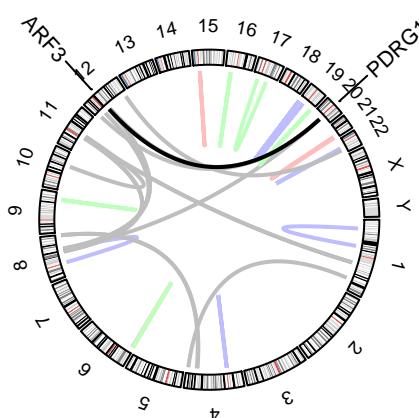
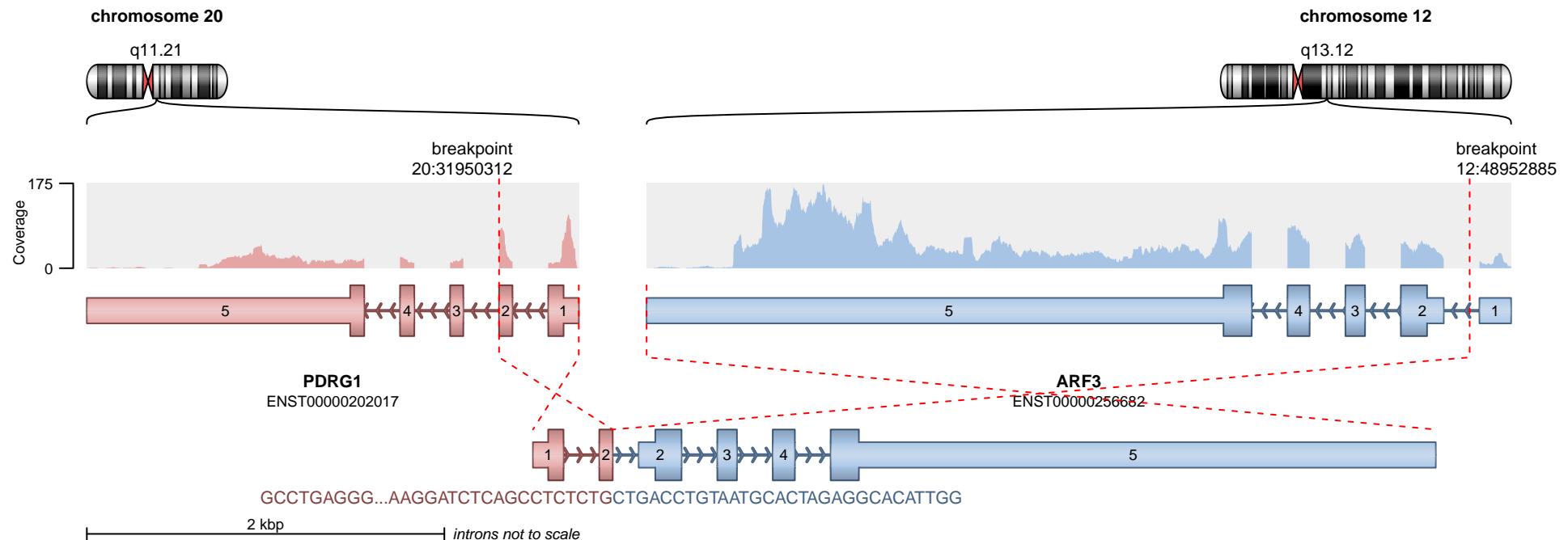


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 5

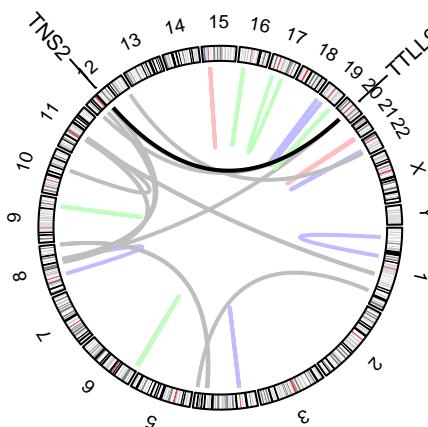
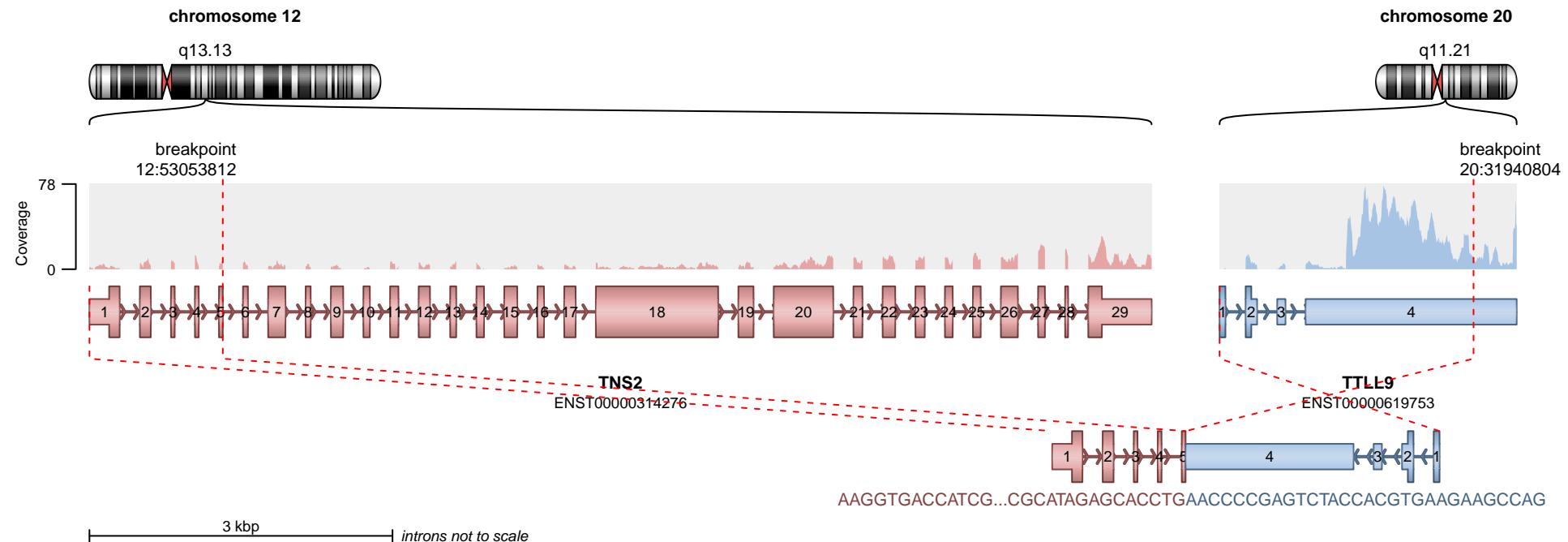
— translocation — deletion
— duplication — inversion



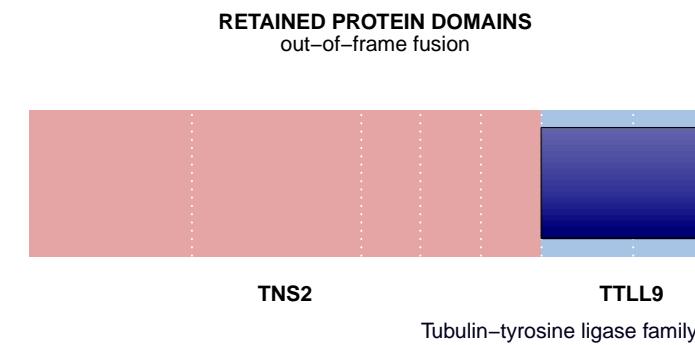
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 3

— translocation — deletion
— duplication — inversion

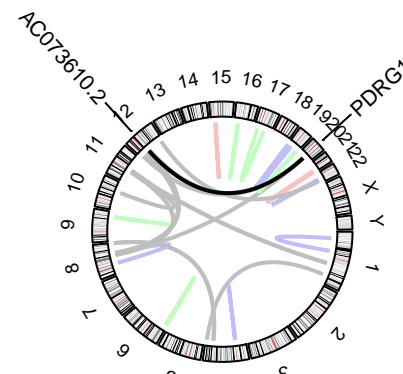
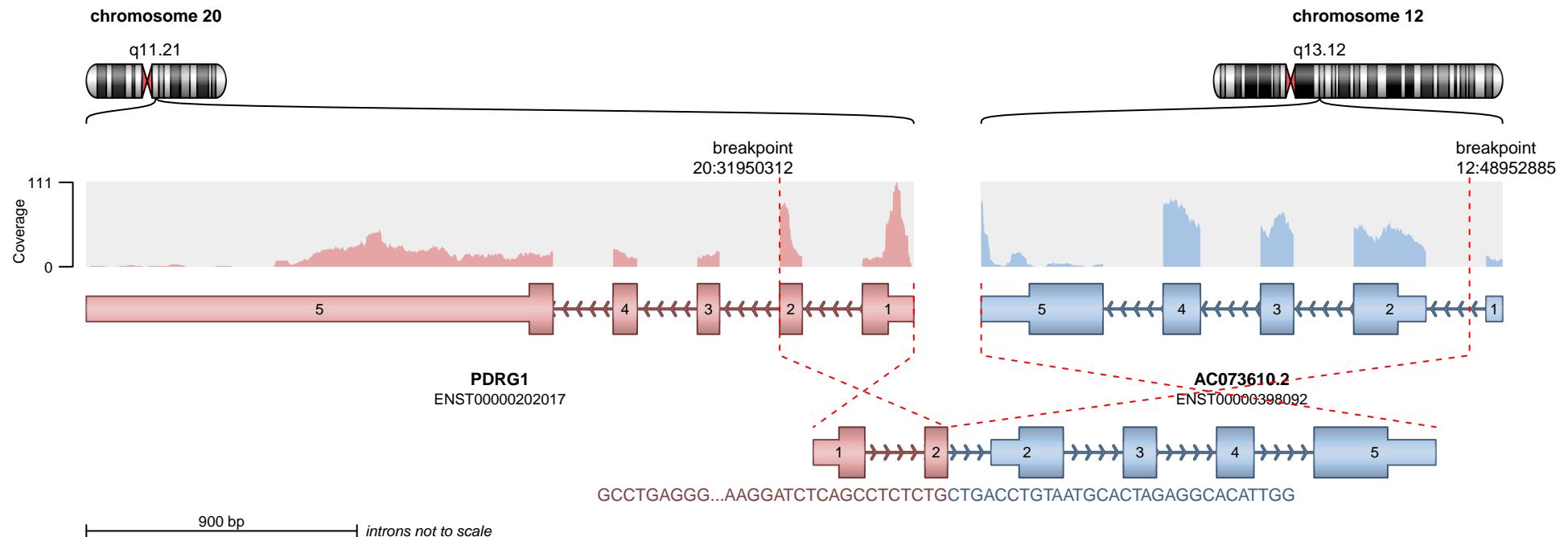


— translocation — deletion
— duplication — inversion

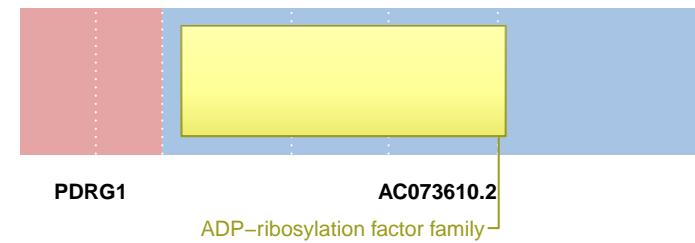


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 3



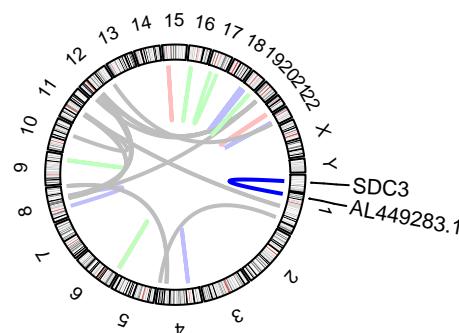
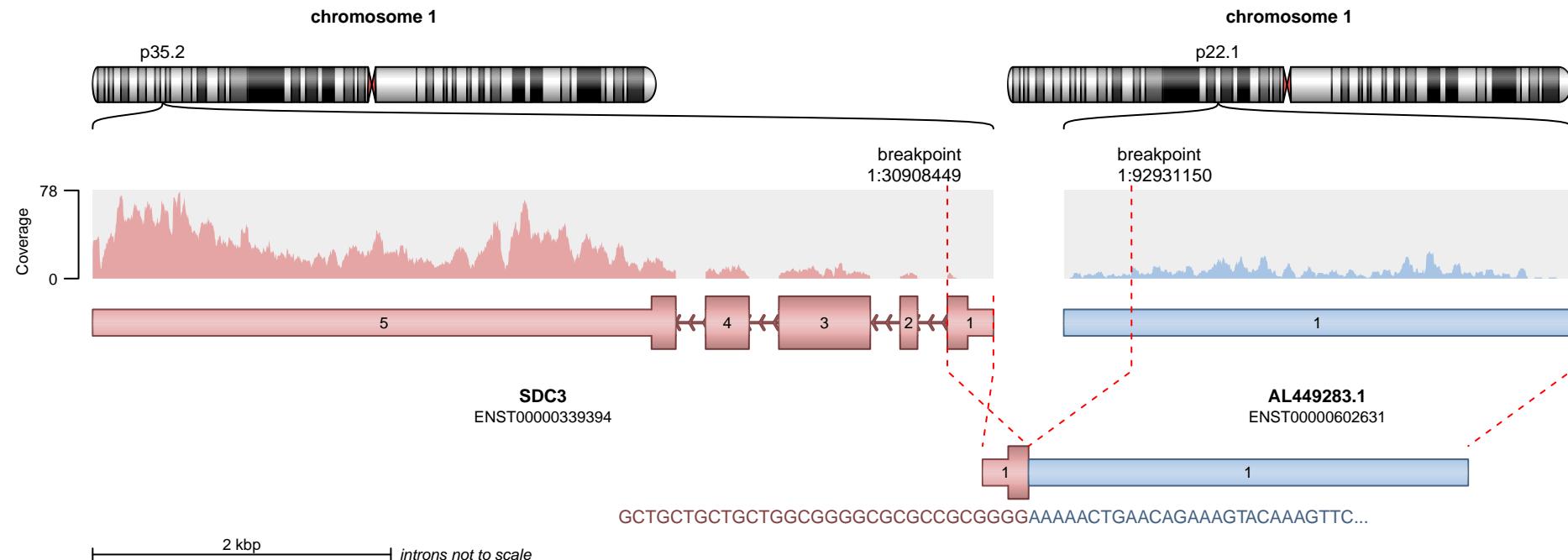
RETAINED PROTEIN DOMAINS out-of-frame fusion



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 3

— translocation — deletion
— duplication — inversion

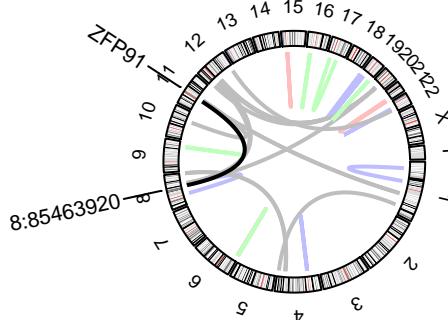
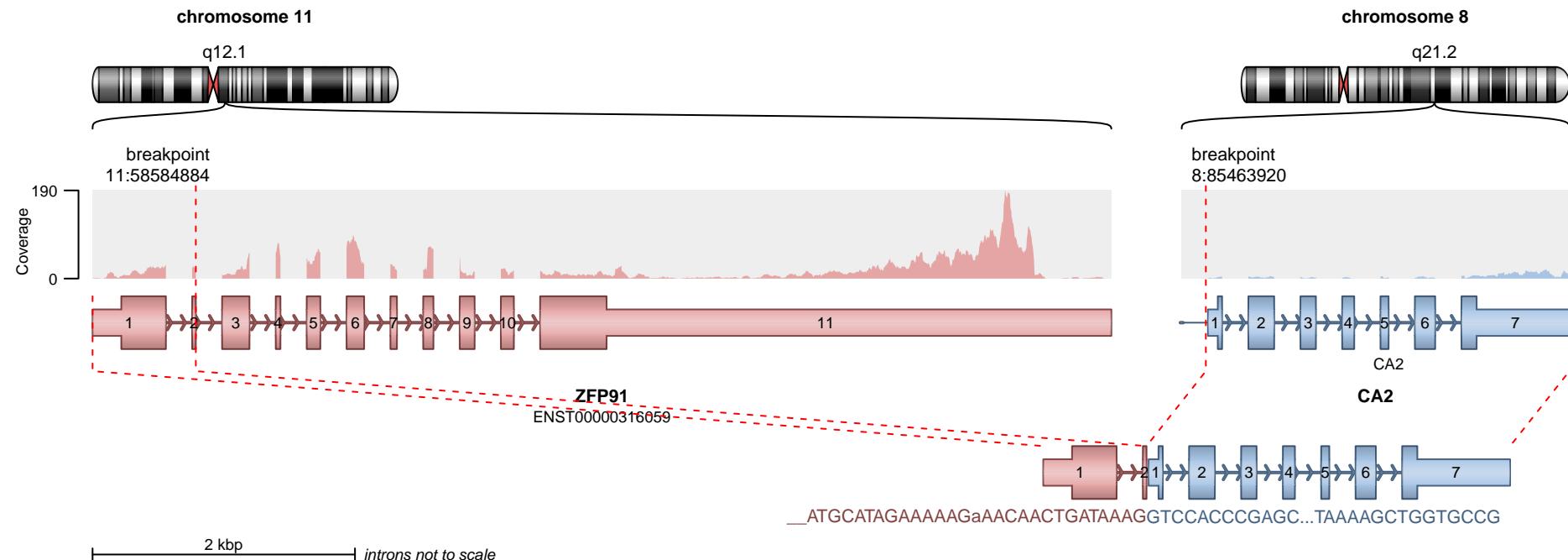


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

— translocation — deletion
— duplication — inversion

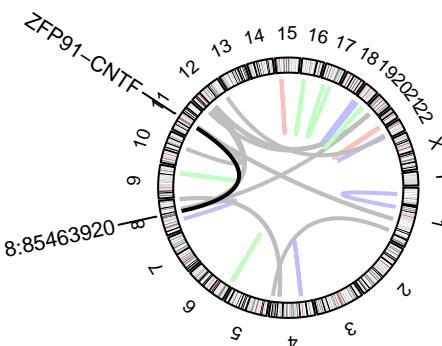
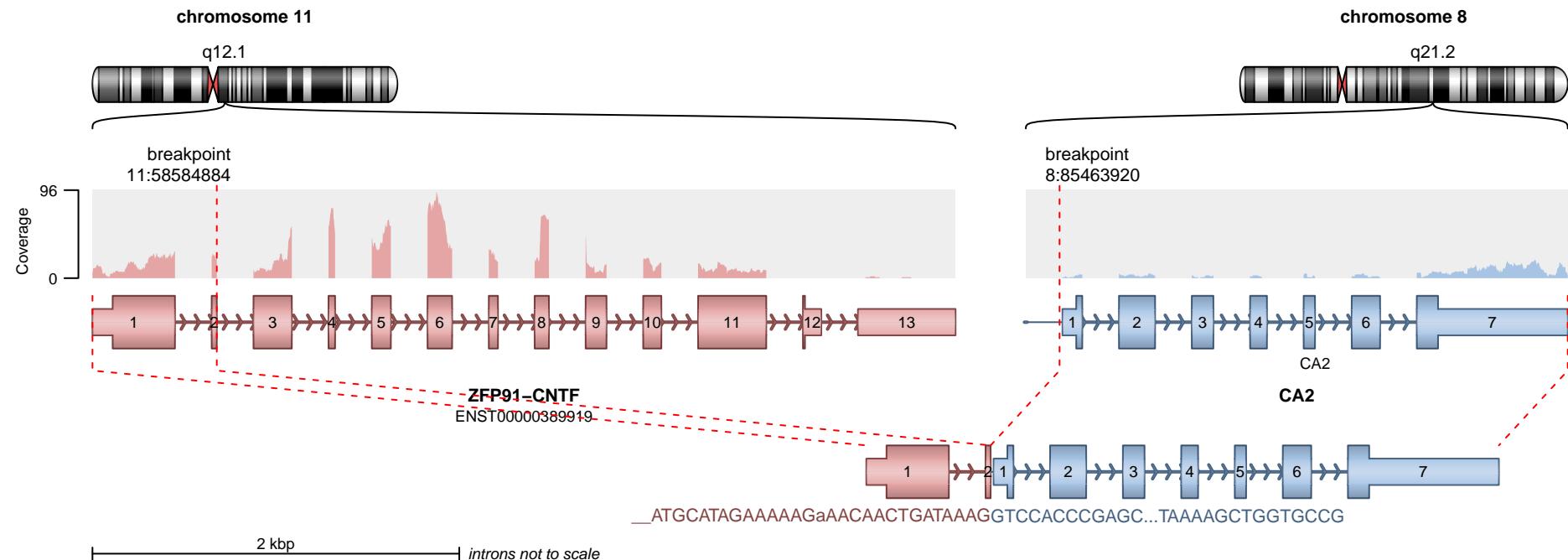


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

— translocation — deletion
— duplication — inversion

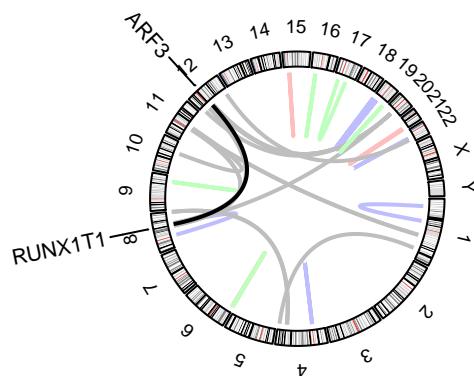
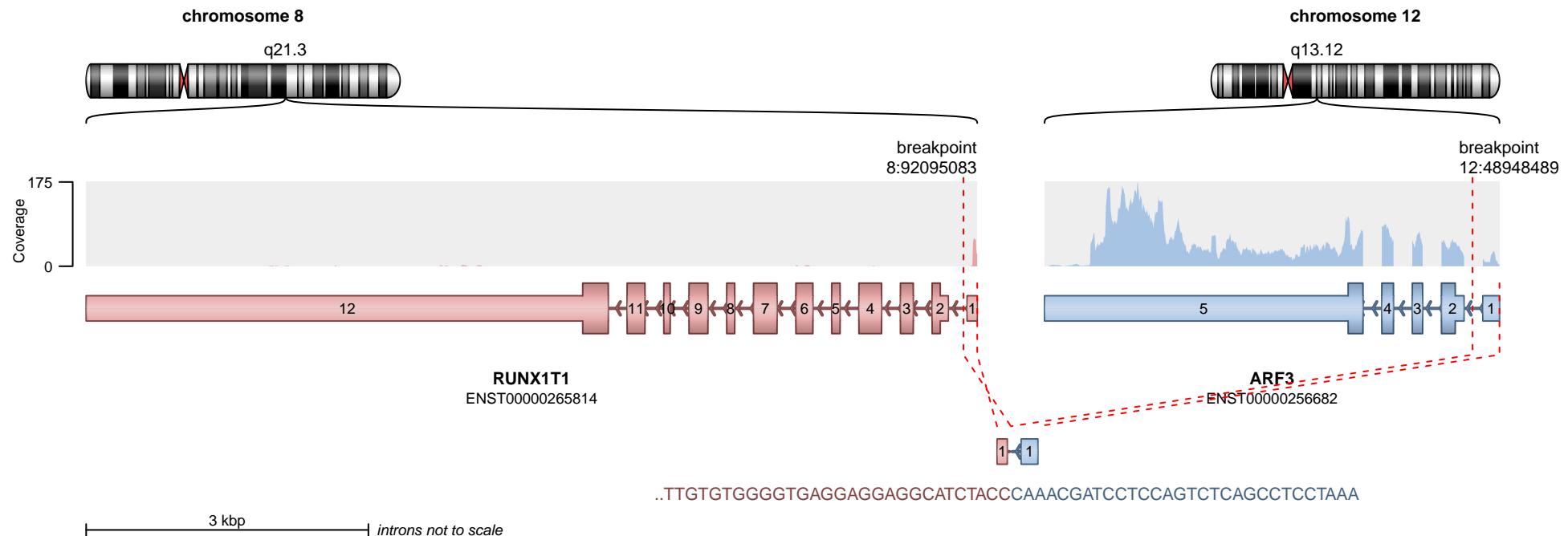


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

— translocation — deletion
— duplication — inversion

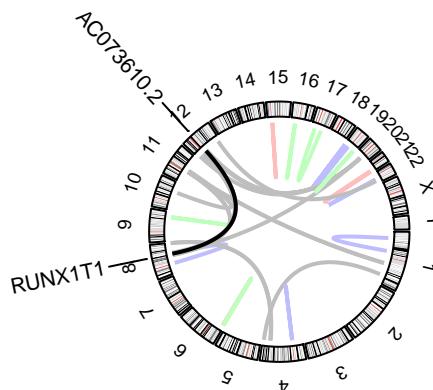
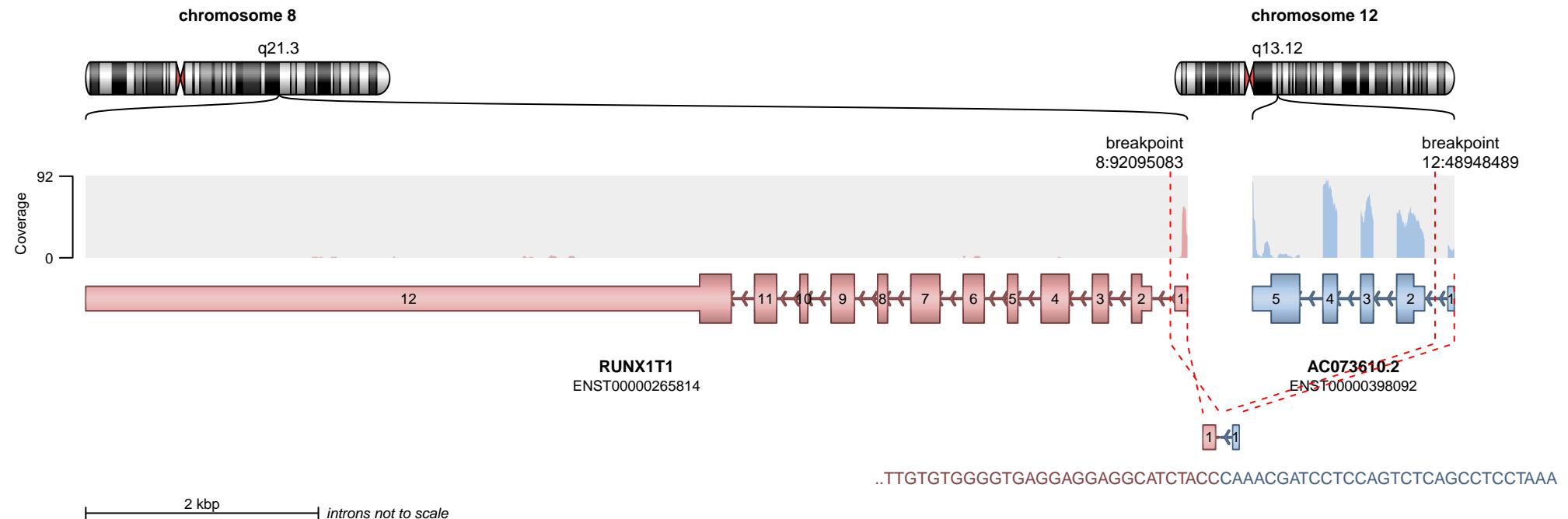


No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 7

— translocation — deletion
— duplication — inversion

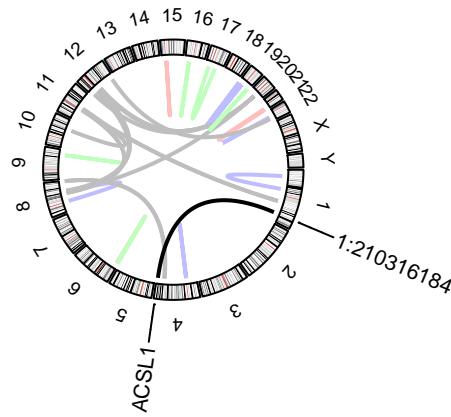
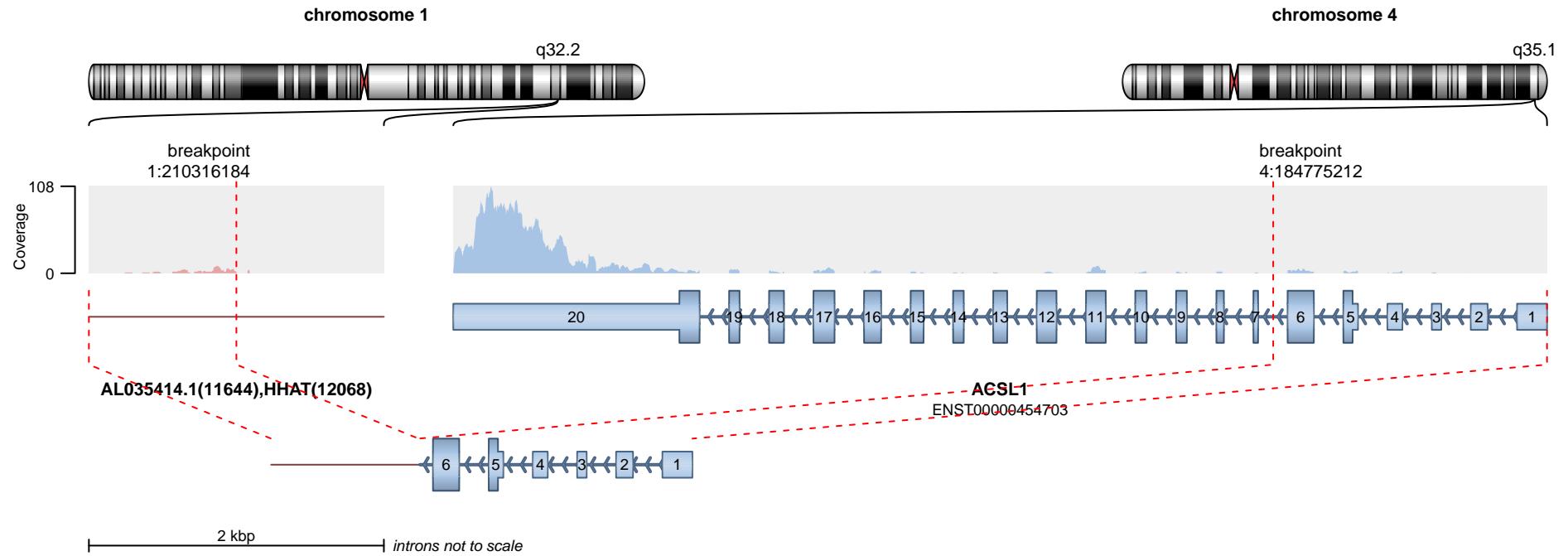


No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 7

— translocation — deletion
— duplication — inversion

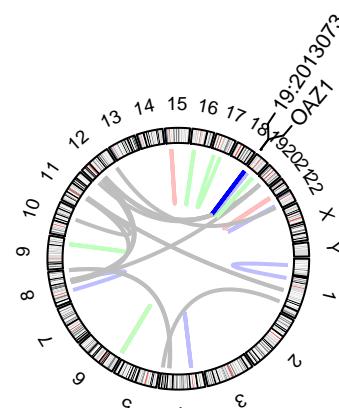
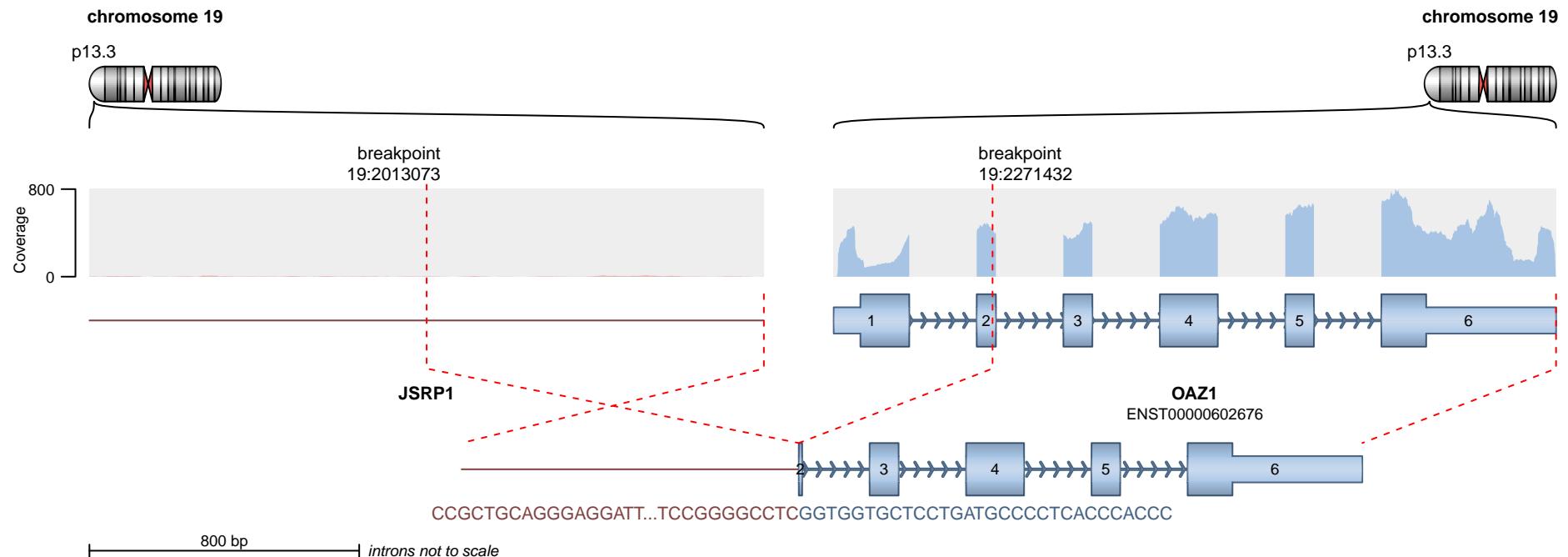


No coding regions due to antisense transcription.

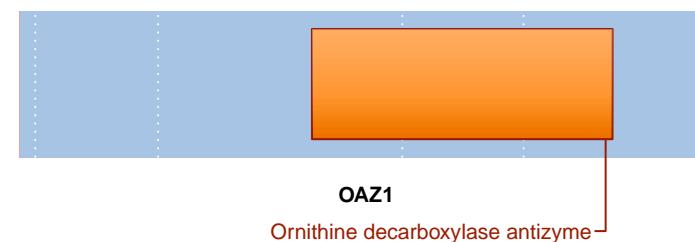
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 5

— translocation — deletion
— duplication — inversion



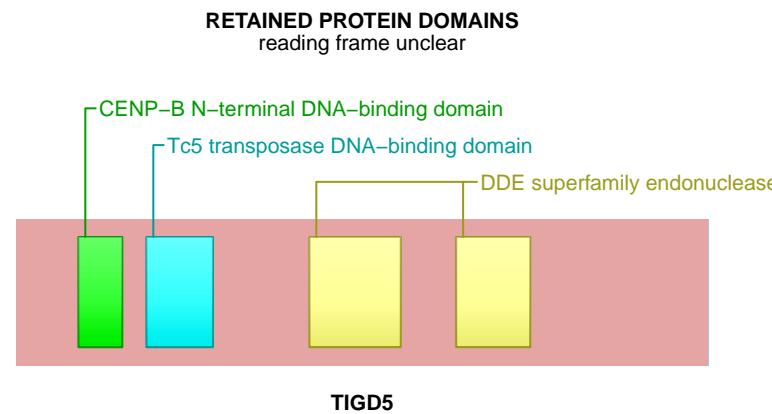
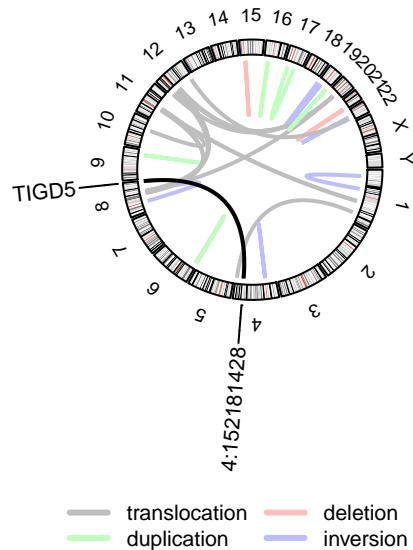
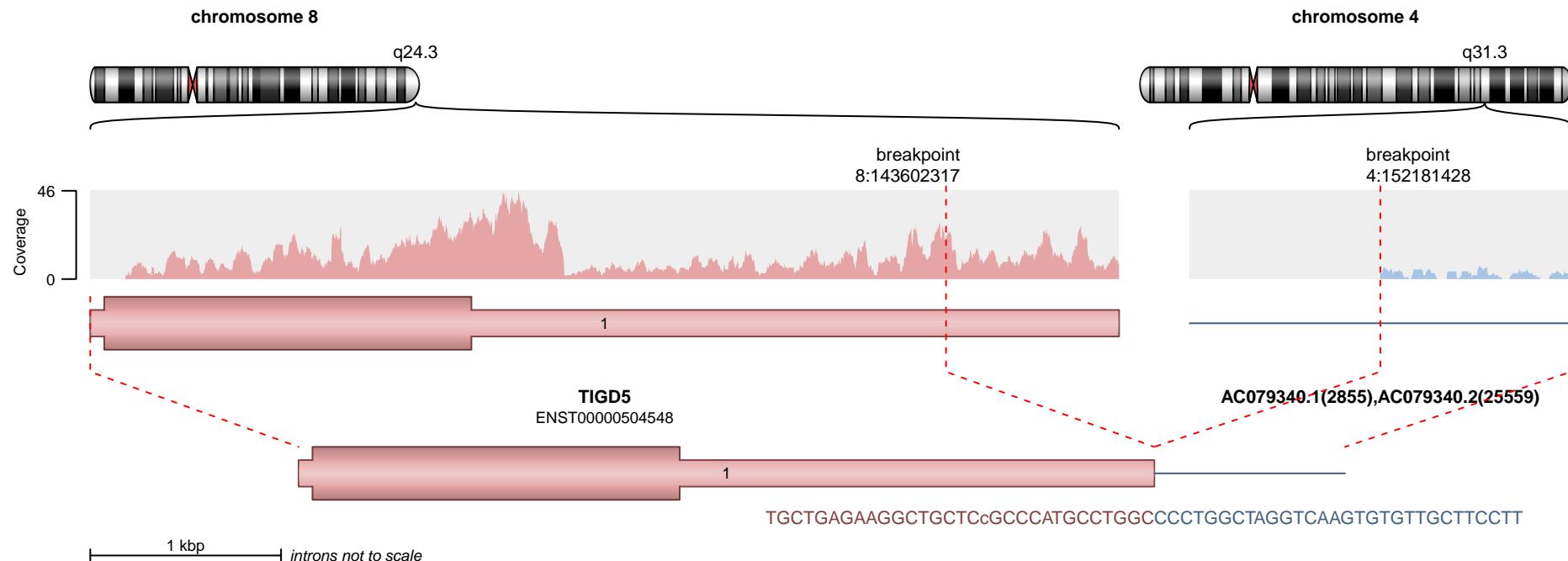
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

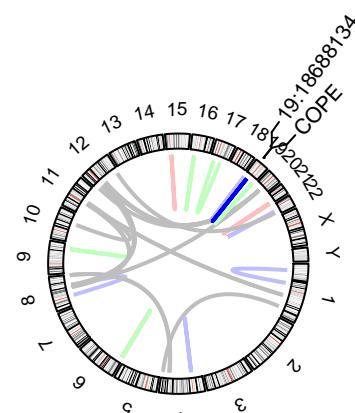
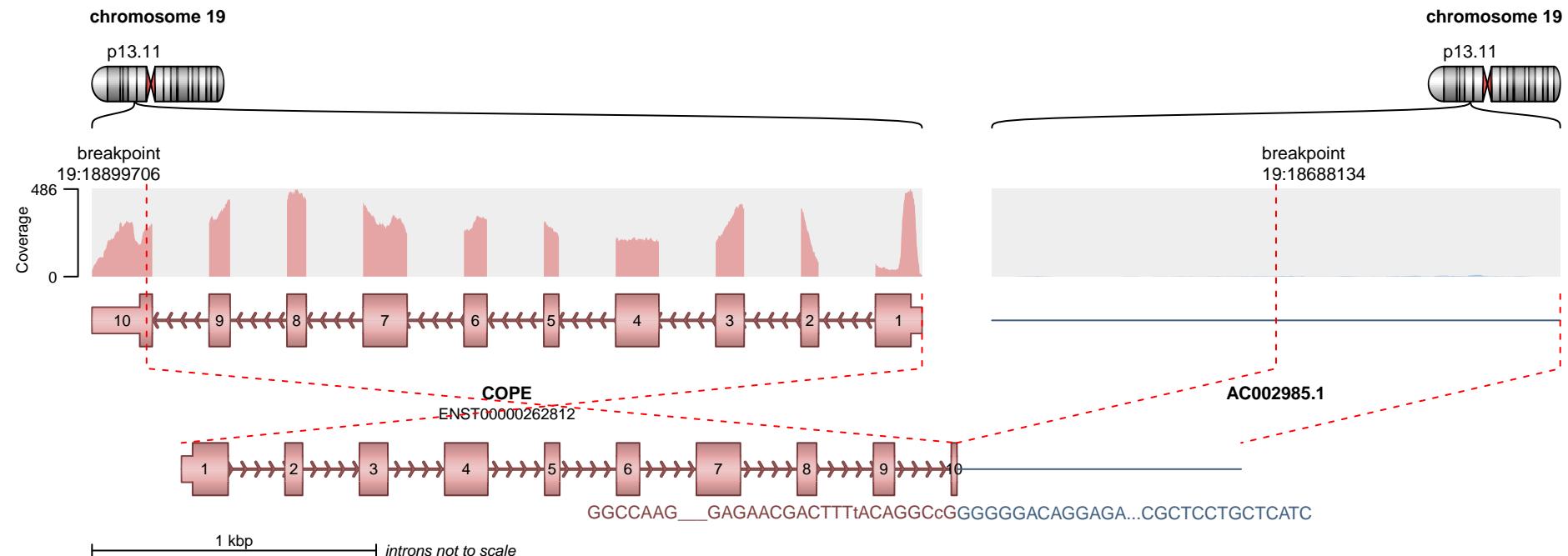
Split reads = 1
Discordant mates = 6

— translocation — deletion
— duplication — inversion

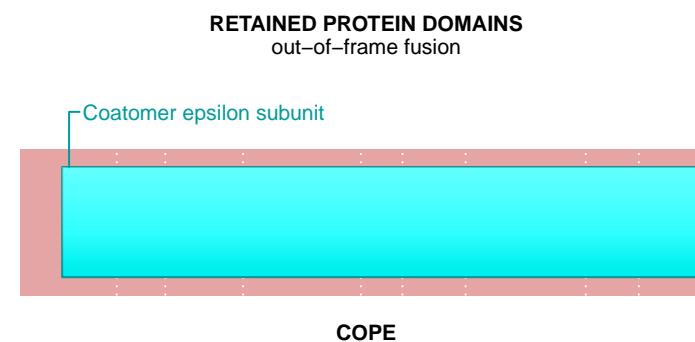


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 5

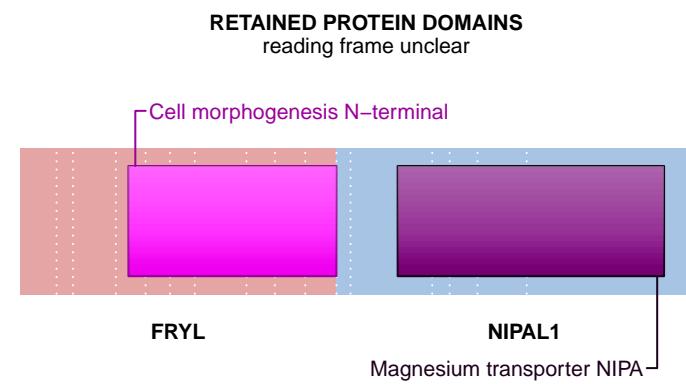
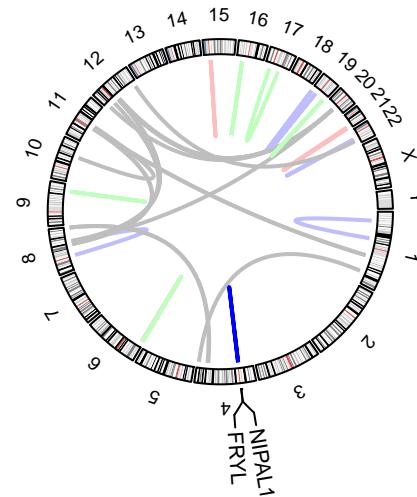
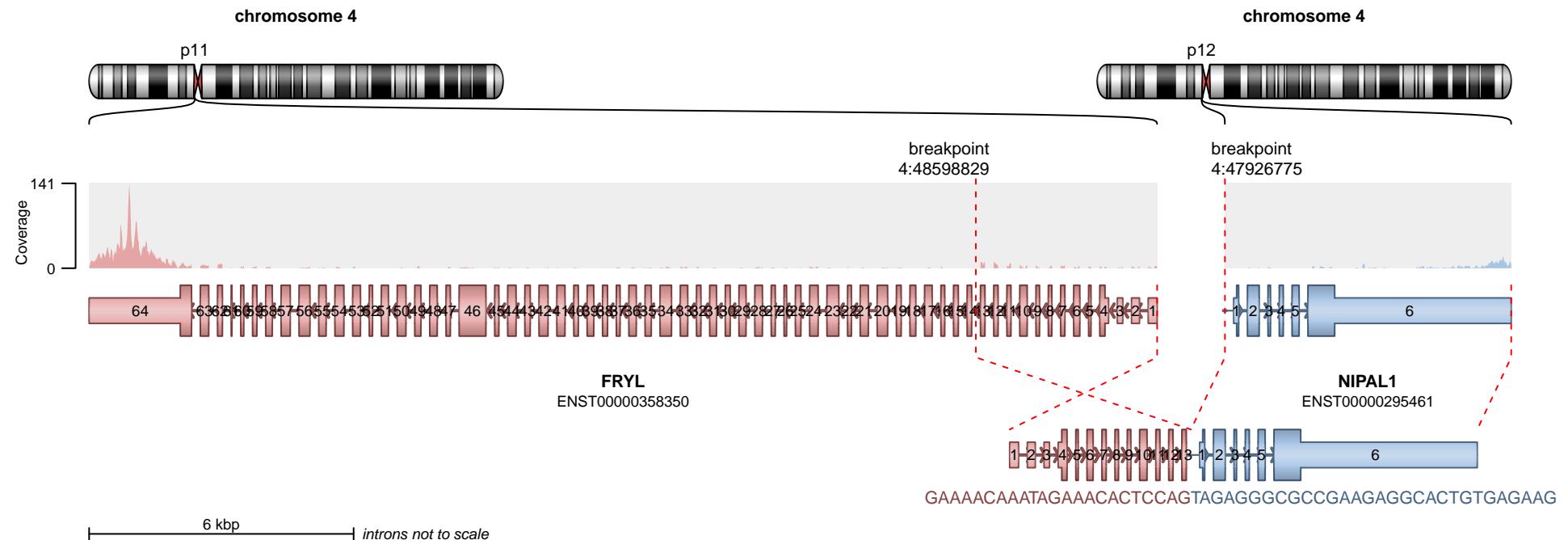


— translocation — deletion
— duplication — inversion



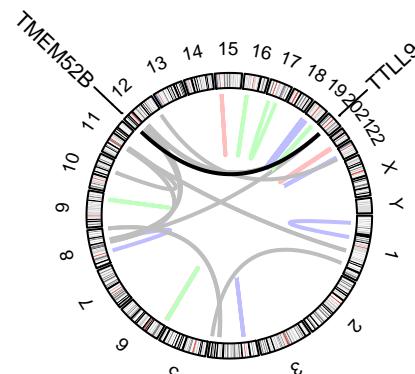
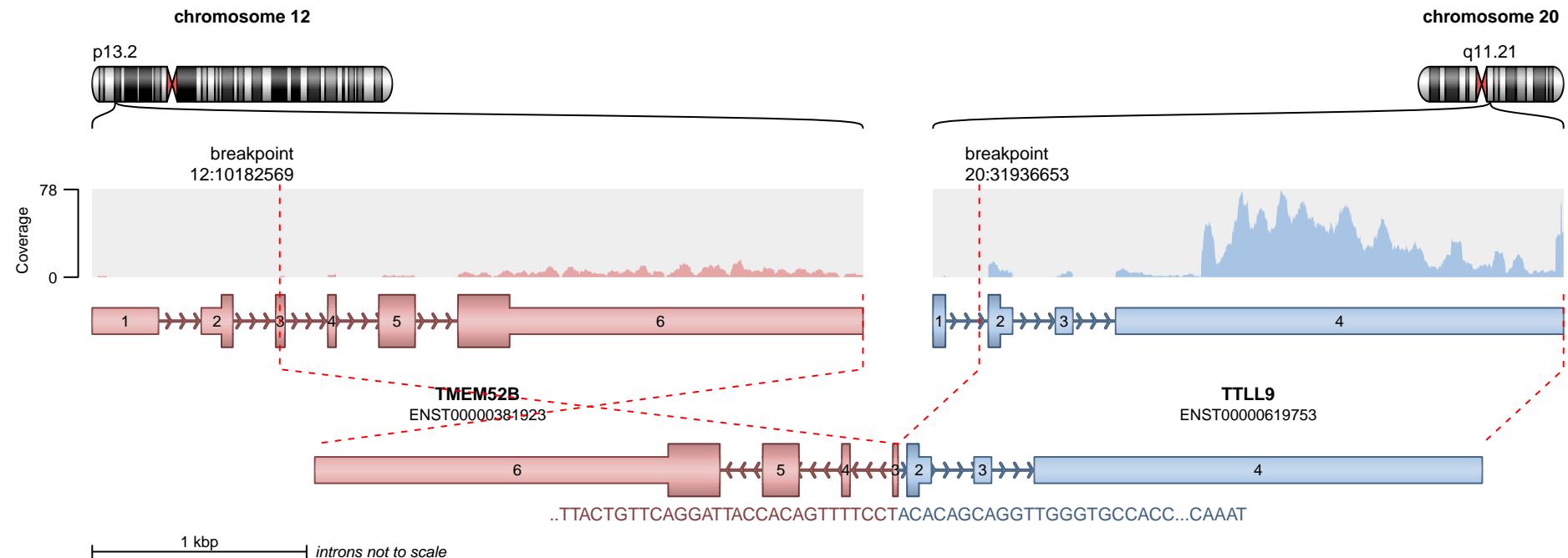
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 5



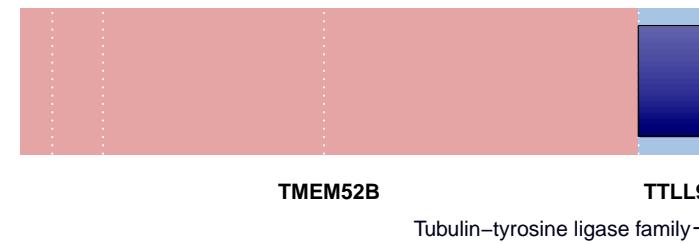
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 4



RETAINED PROTEIN DOMAINS

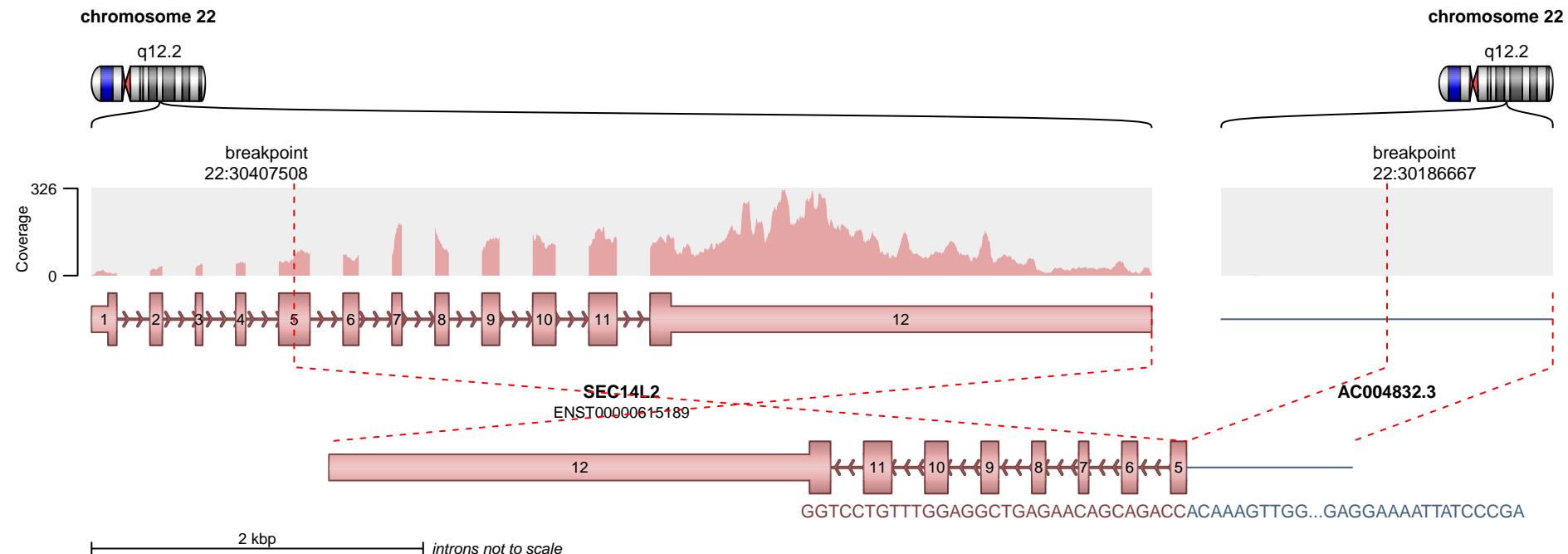
reading frame unclear



SUPPORTING READ COUNT

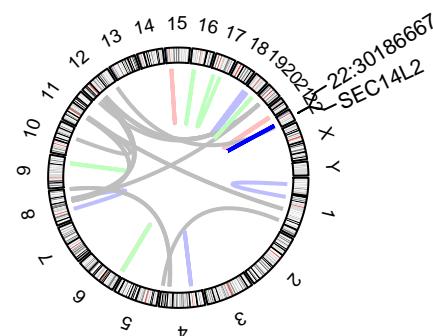
Split reads = 1
Discordant mates = 4

— translocation — deletion
— duplication — inversion



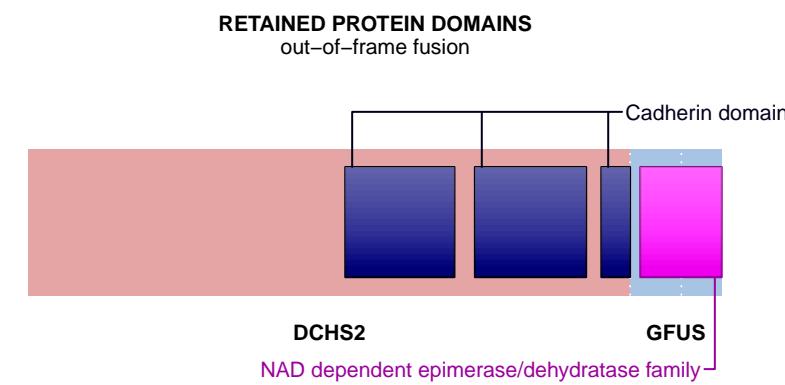
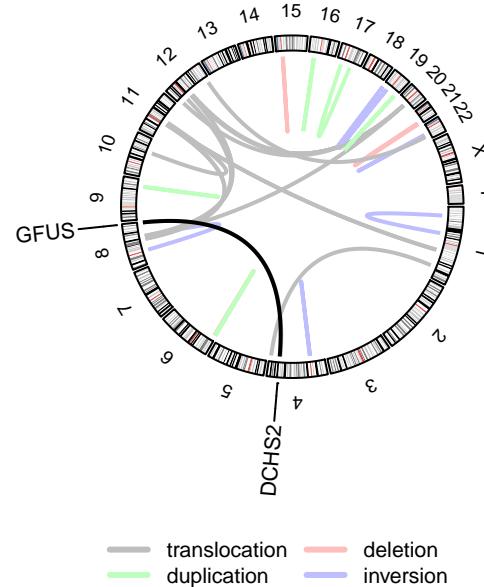
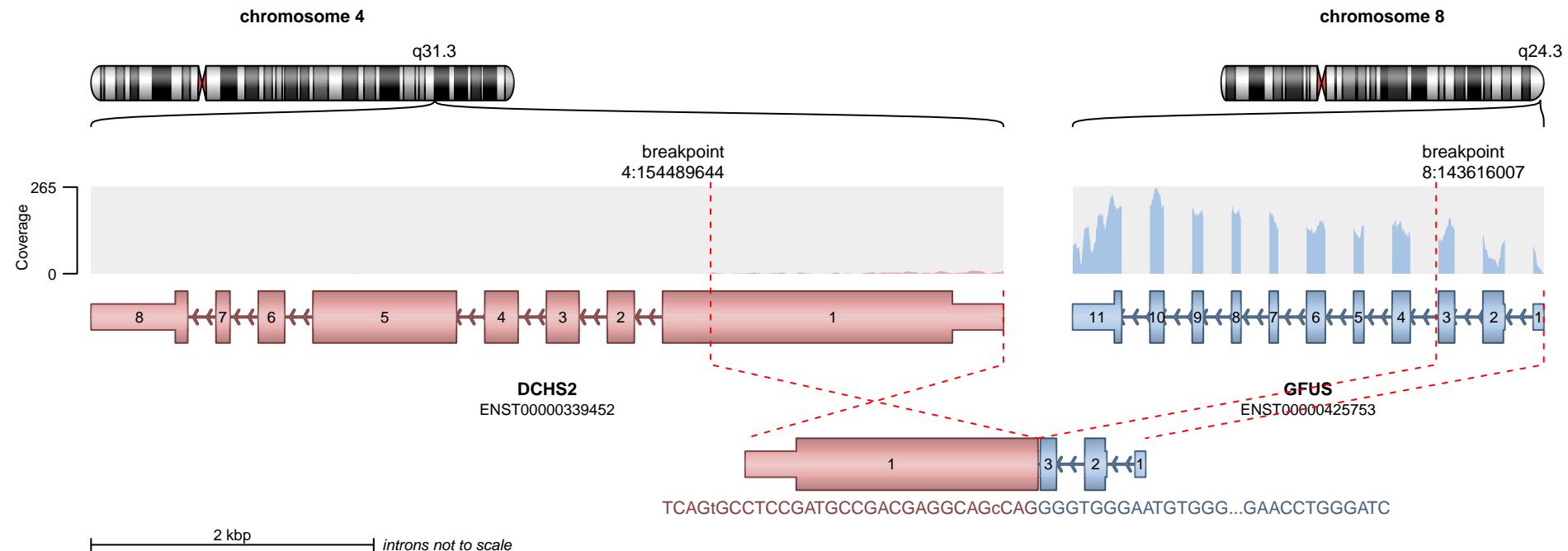
SUPPORTING READ COUNT

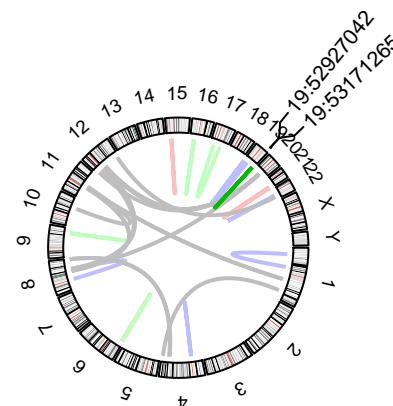
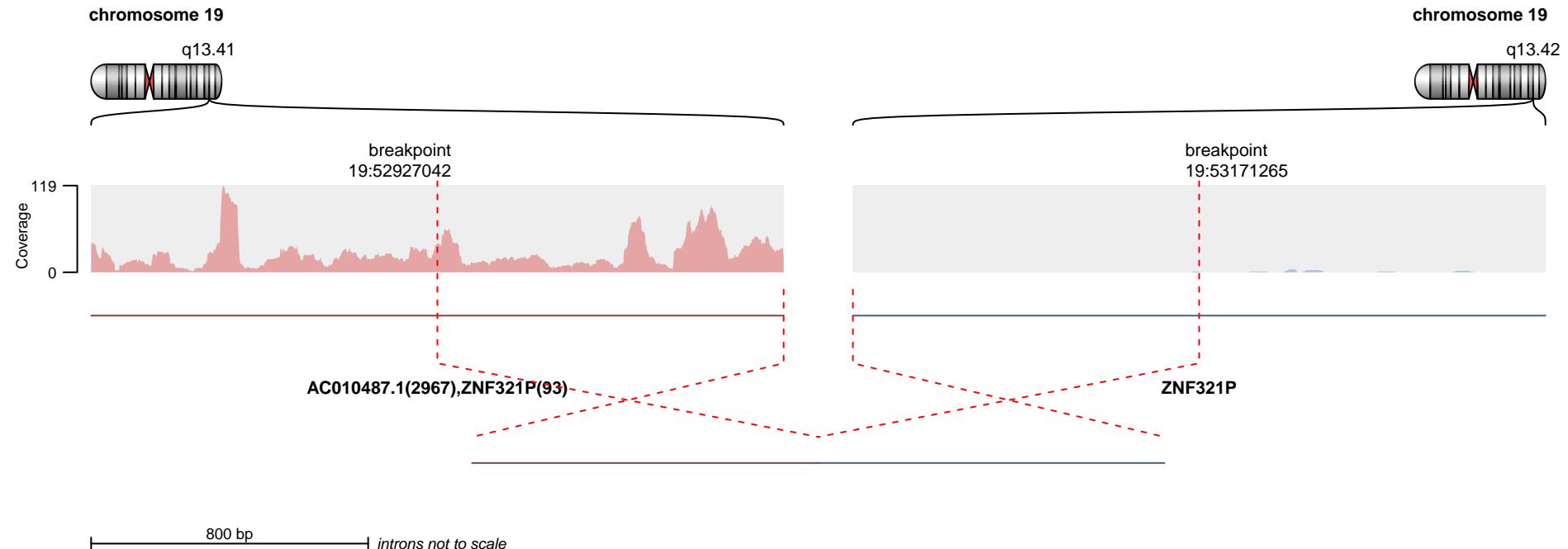
Split reads = 1
Discordant mates = 4



No coding regions due to antisense transcription.

— translocation — deletion
— duplication — inversion



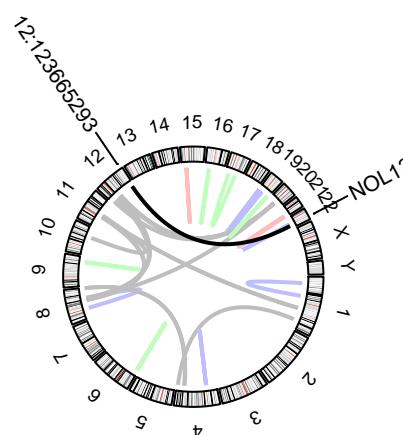
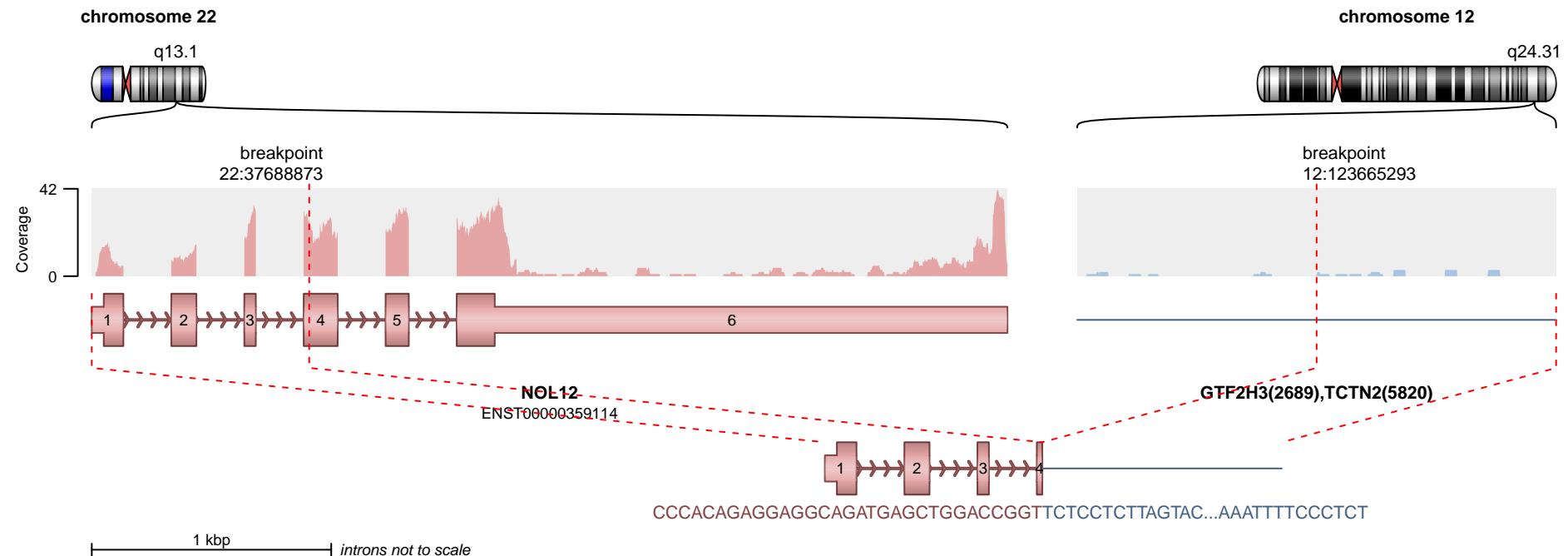


Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 2

— translocation — deletion
— duplication — inversion

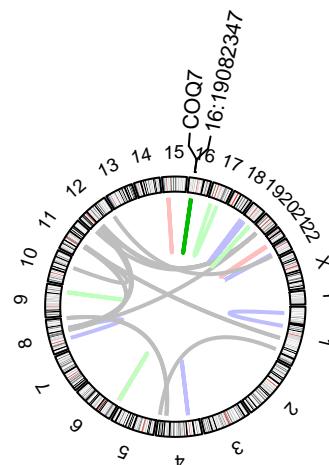
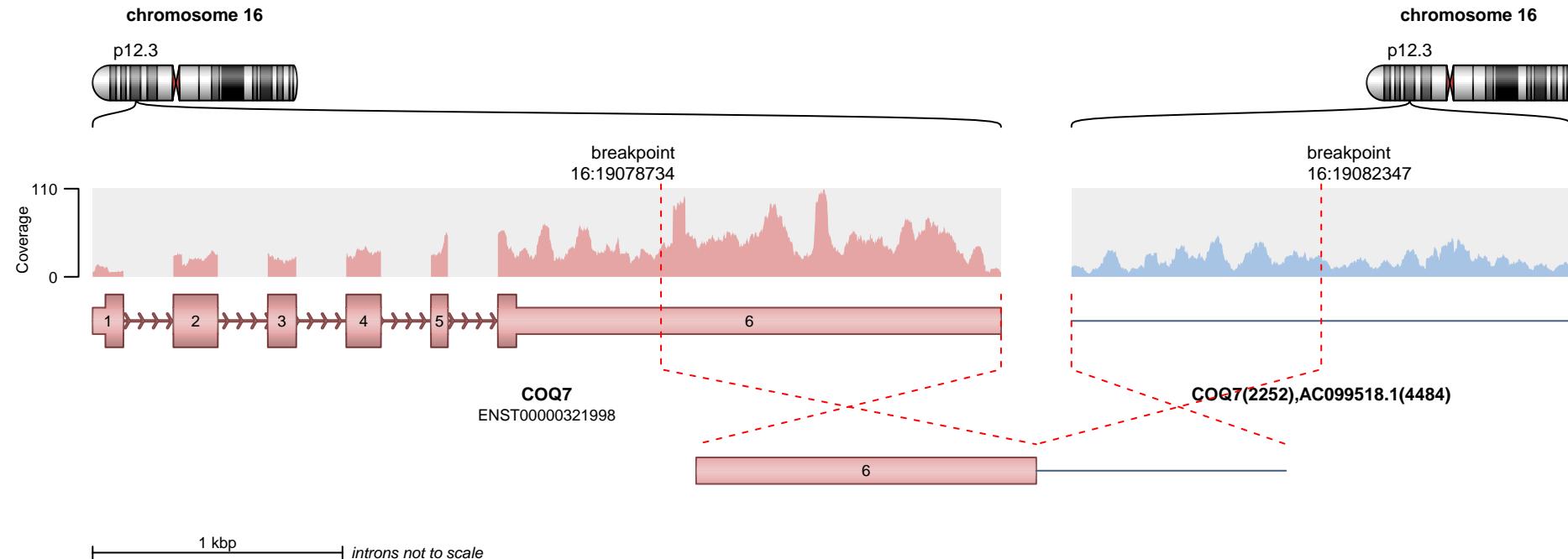


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

— translocation — deletion
— duplication — inversion

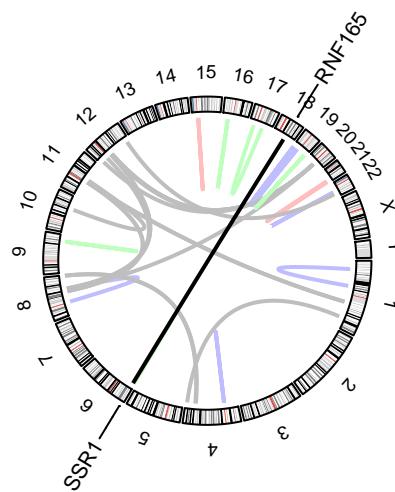
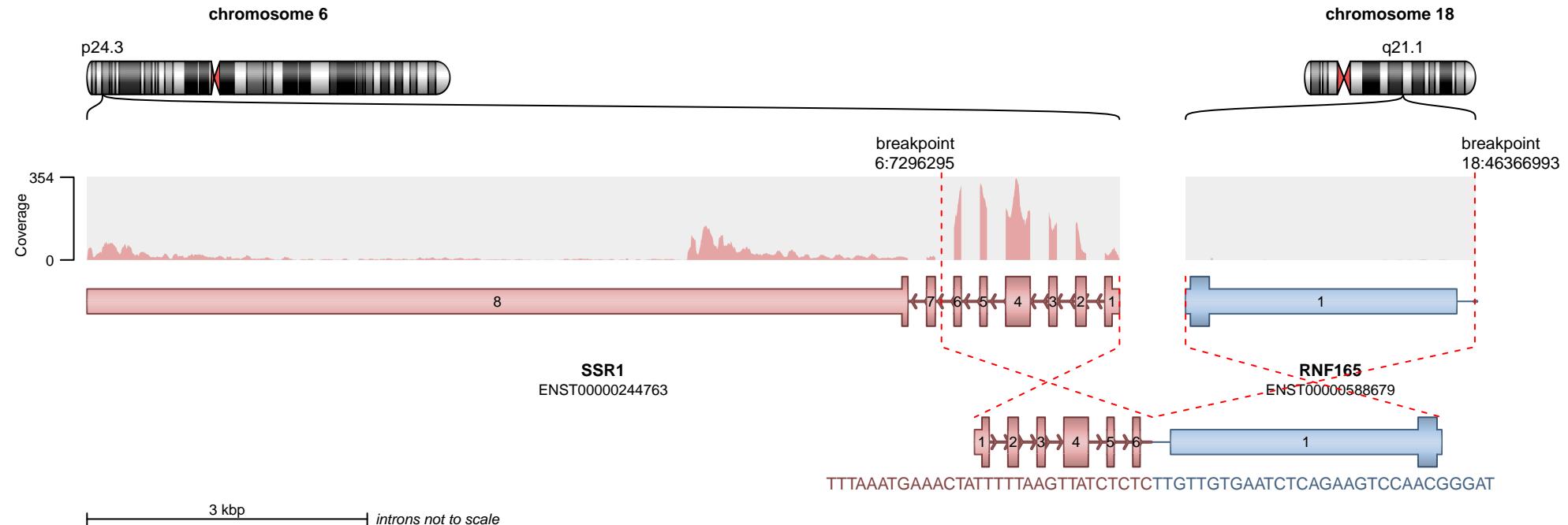


No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

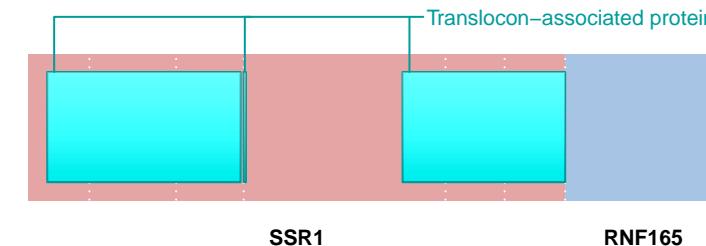
Split reads = 1
Discordant mates = 1

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS

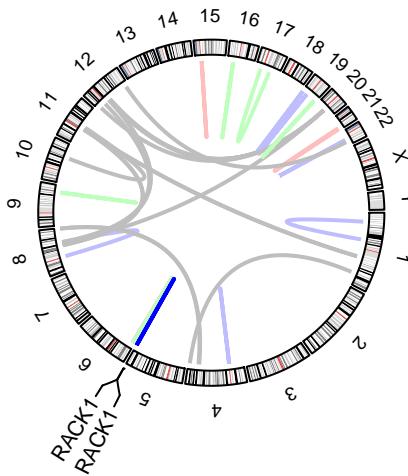
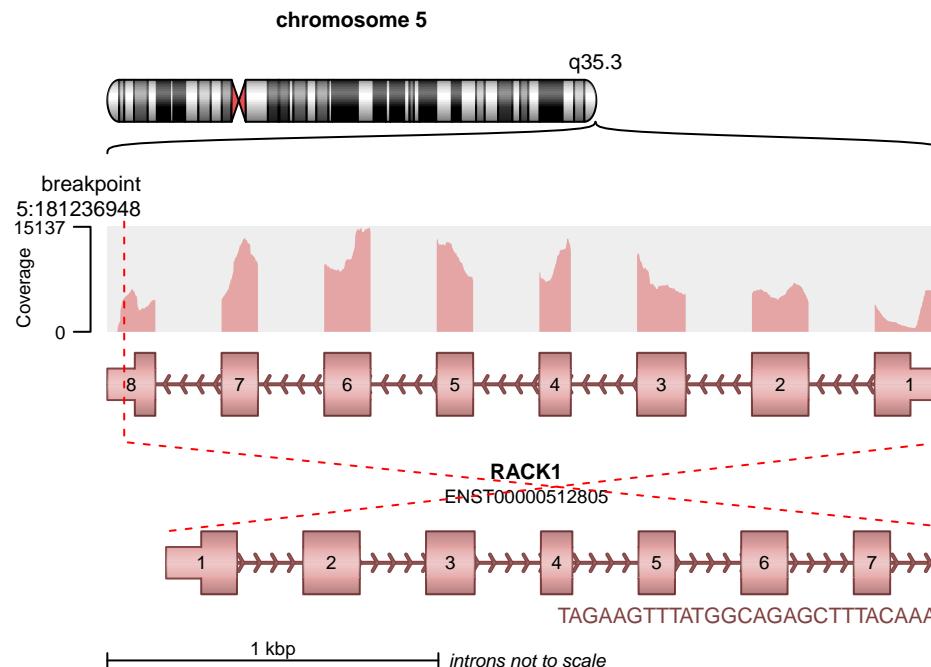
reading frame unclear



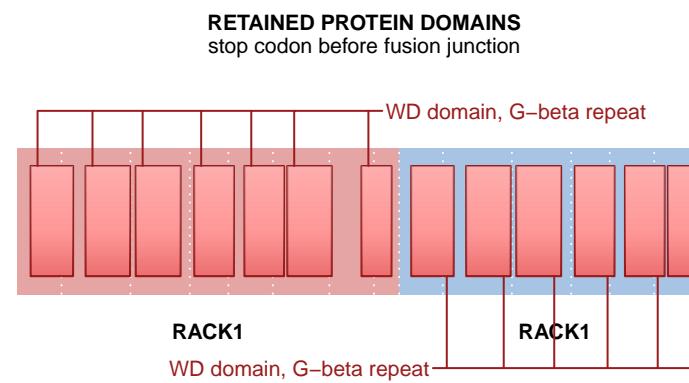
SUPPORTING READ COUNT

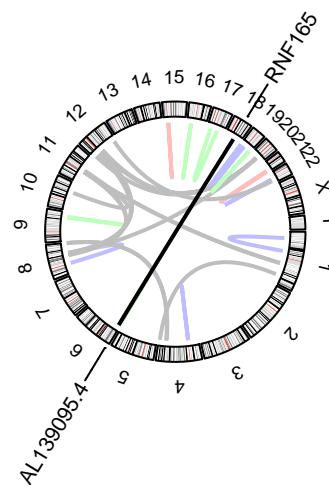
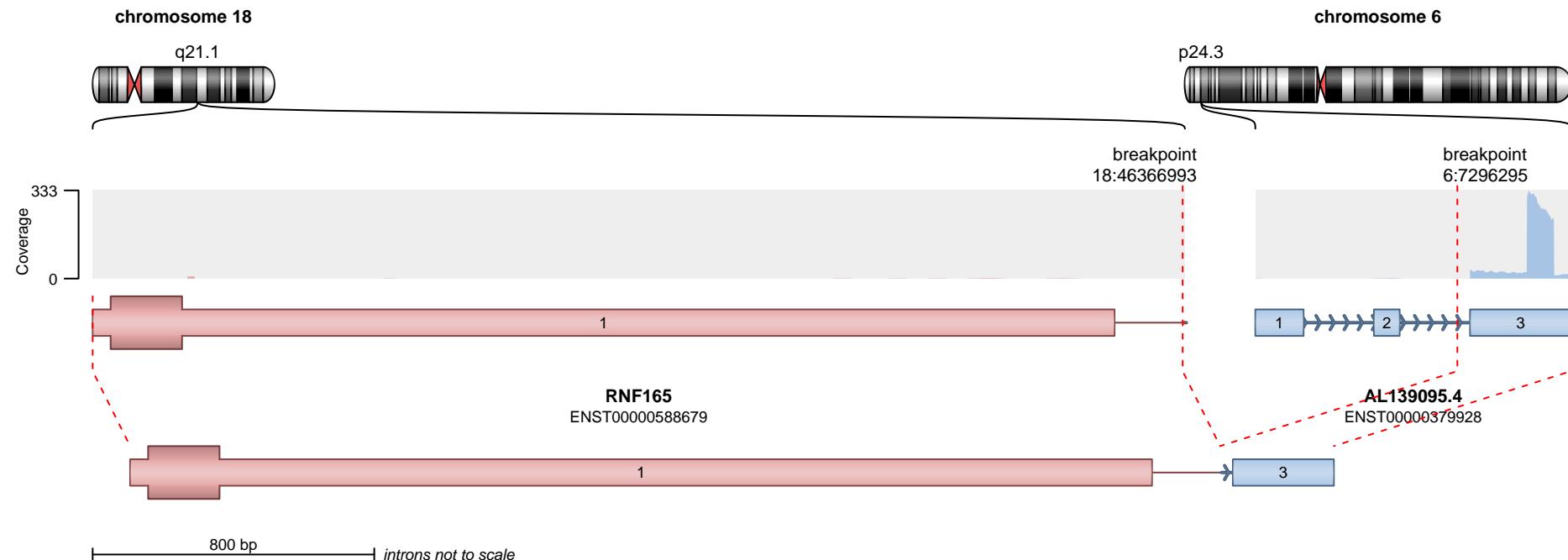
Split reads = 2
Discordant mates = 180

— translocation — deletion
— duplication — inversion



— translocation — deletion
— duplication — inversion



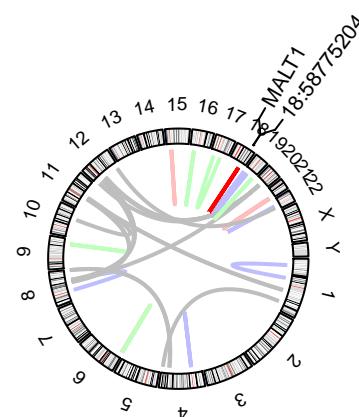
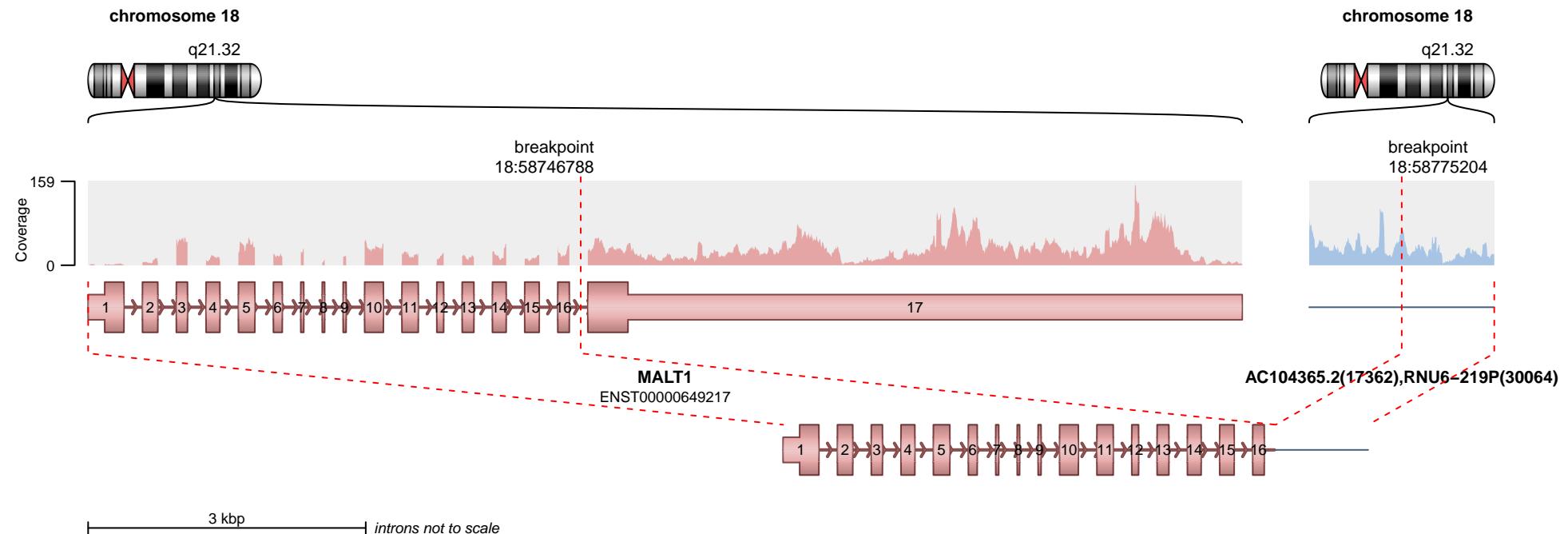


No coding regions due to antisense transcription.

SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 43

— translocation — deletion
— duplication — inversion

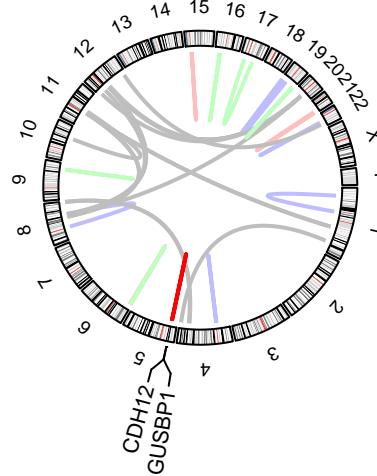
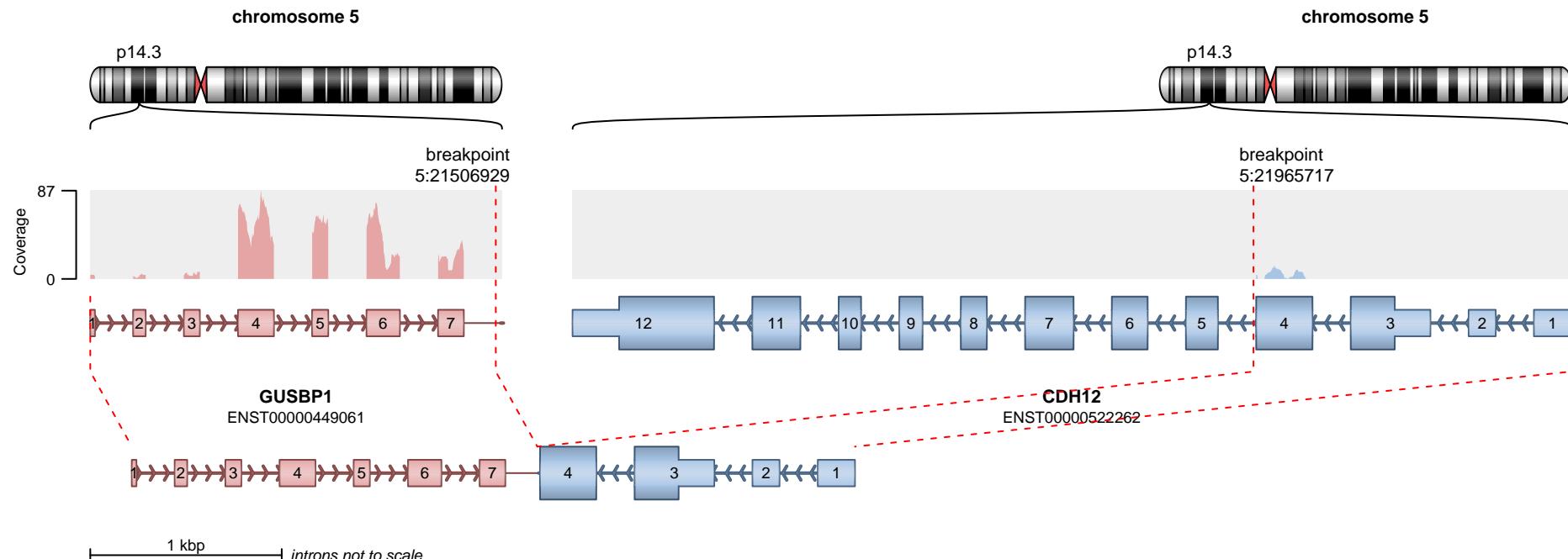


No coding regions due to antisense transcription.

SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 17

— translocation — deletion
— duplication — inversion

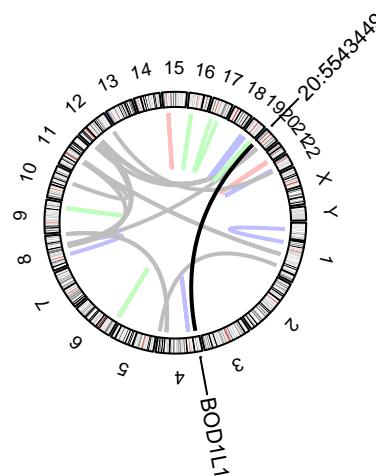
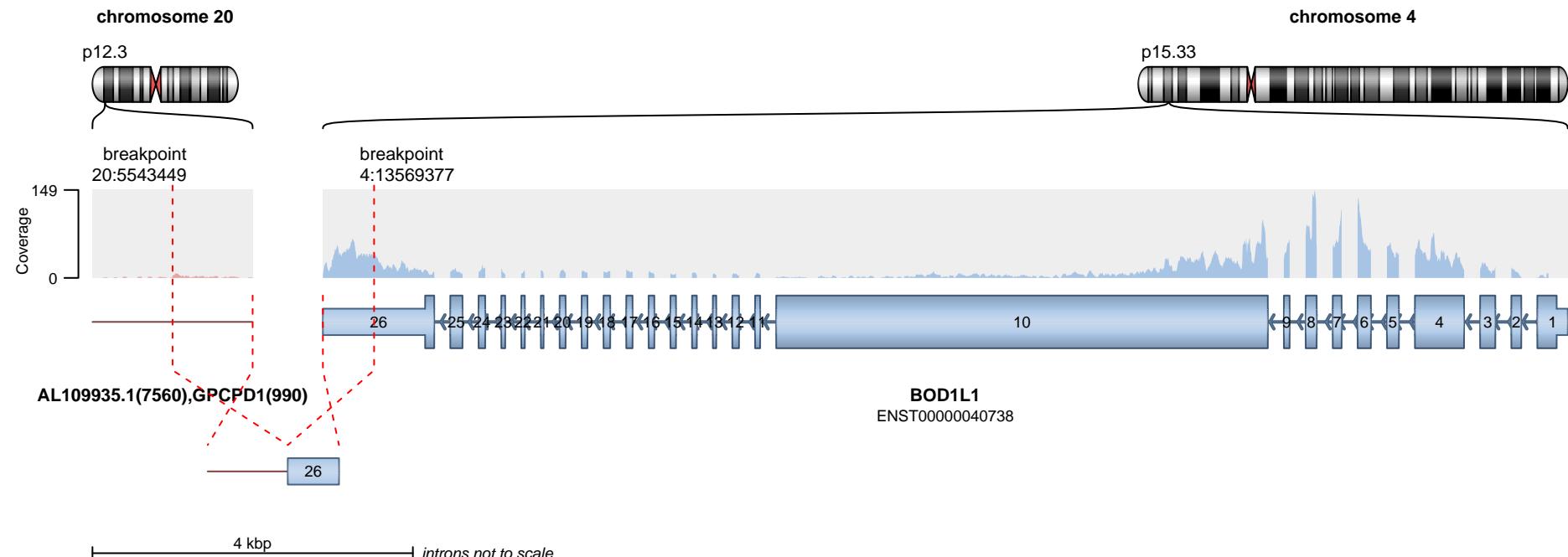


— translocation — deletion
— duplication — inversion

No coding regions due to antisense transcription.

SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 16

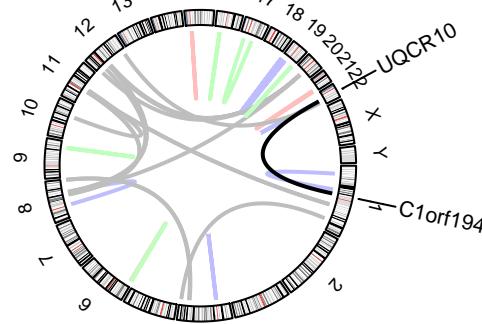
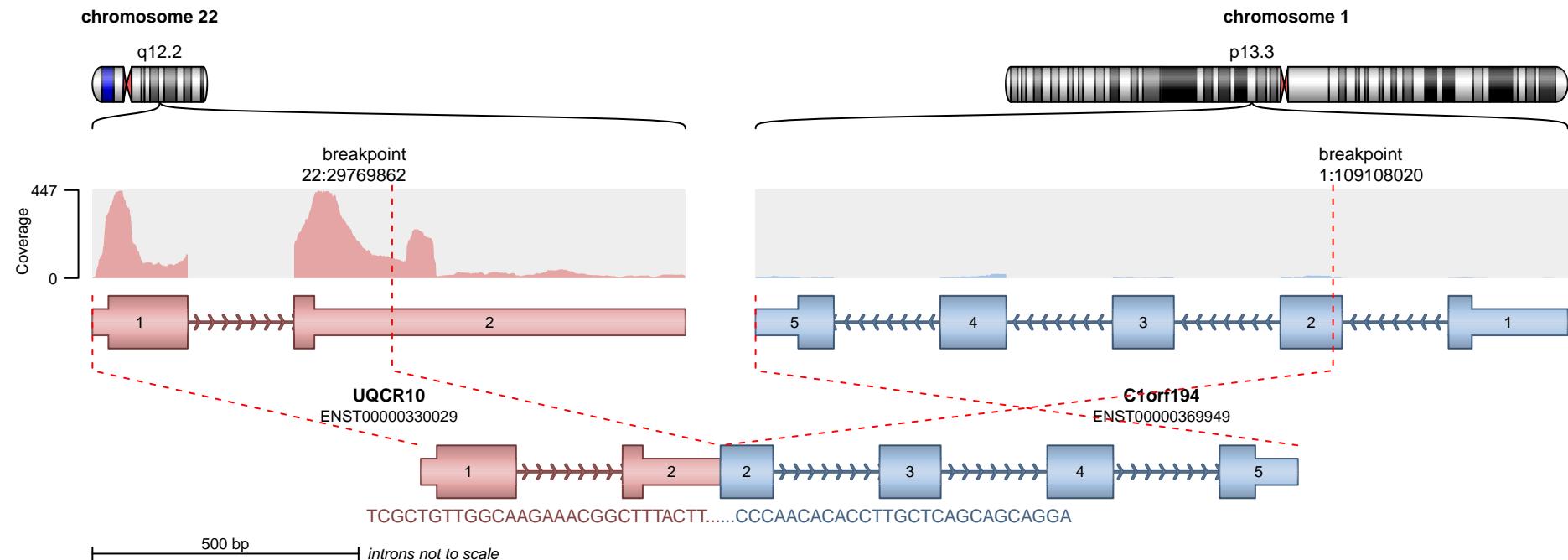


No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

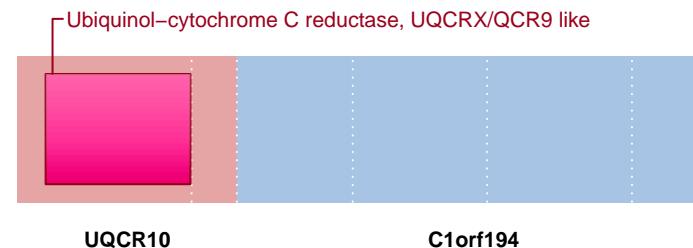
Split reads = 0
Discordant mates = 13

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS

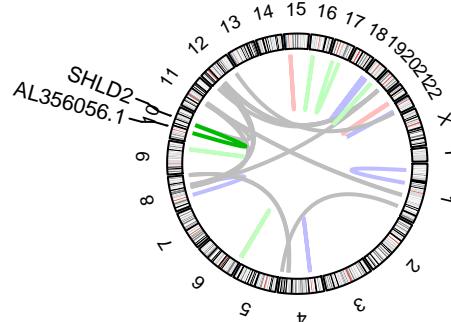
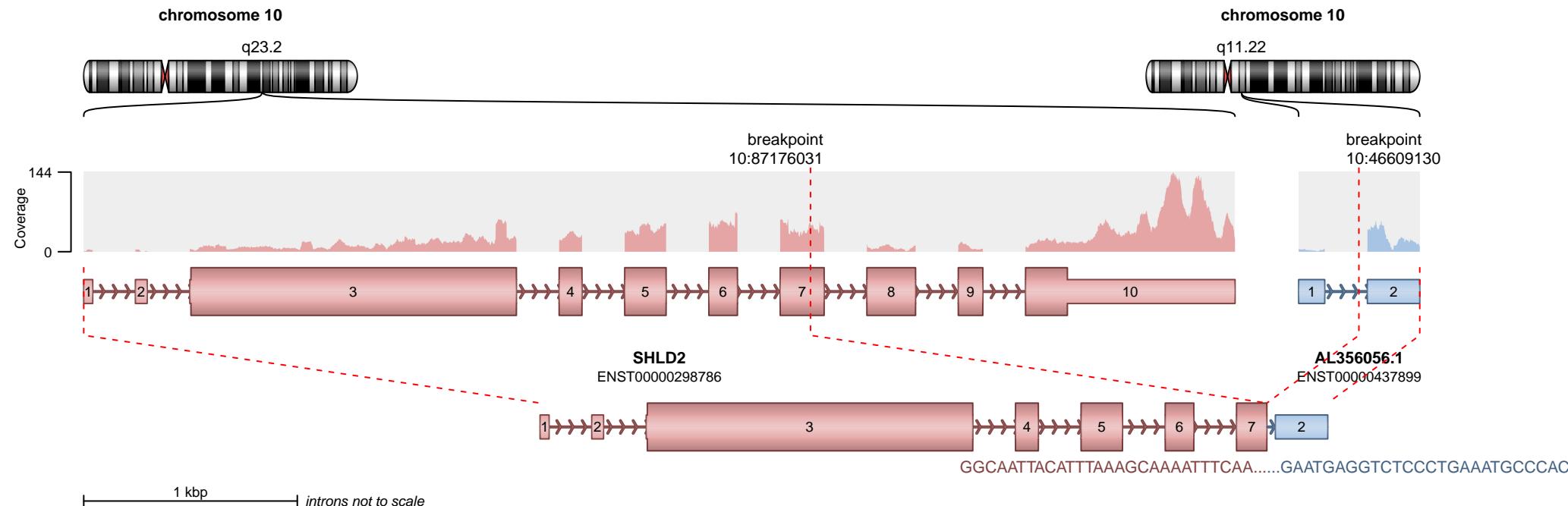
reading frame unclear



SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 12

— translocation — deletion
— duplication — inversion

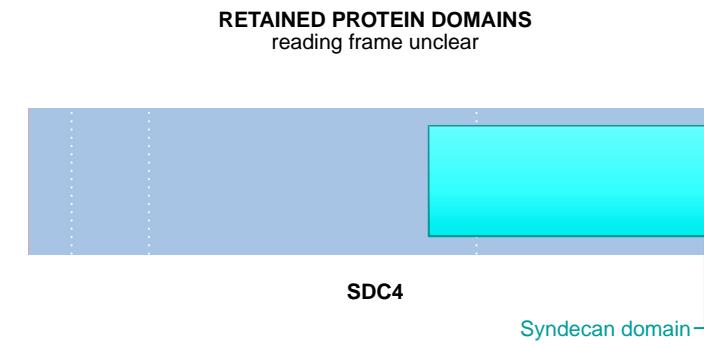
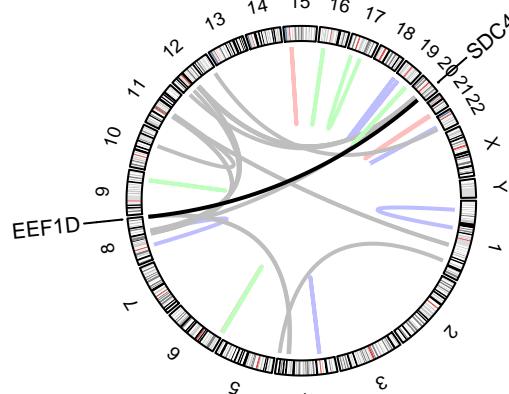
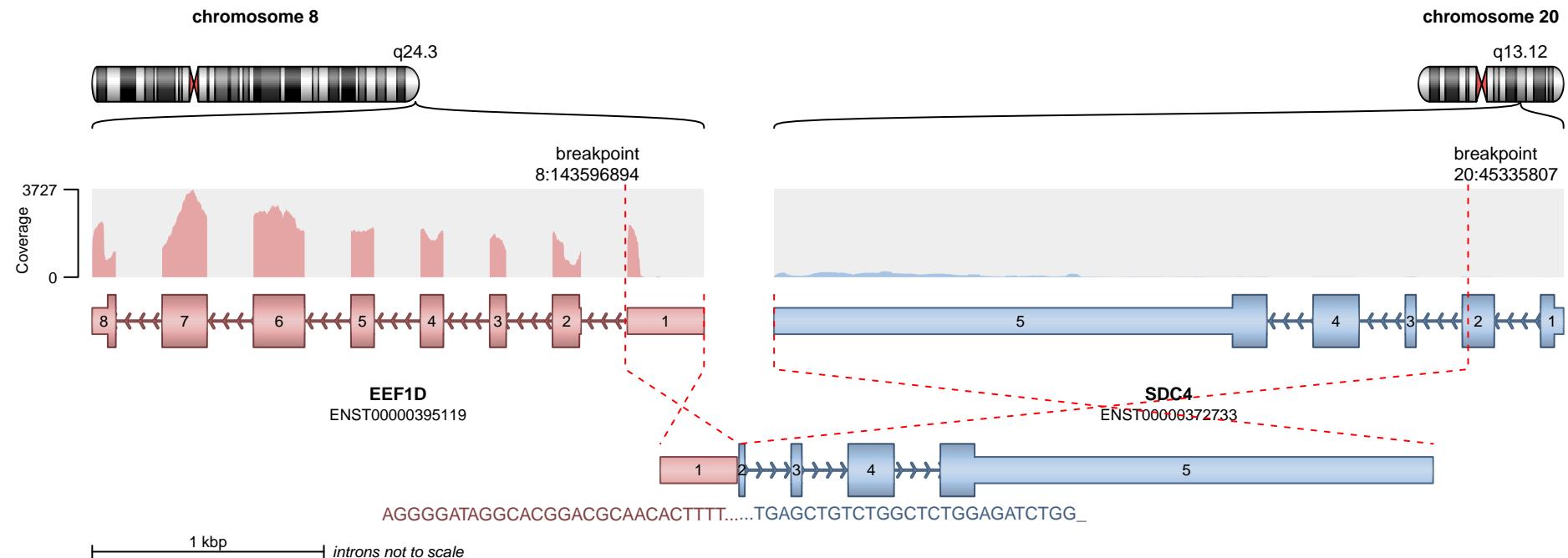


No protein domains retained in fusion.

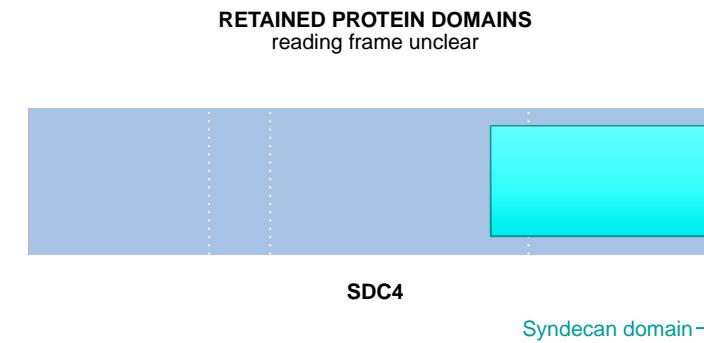
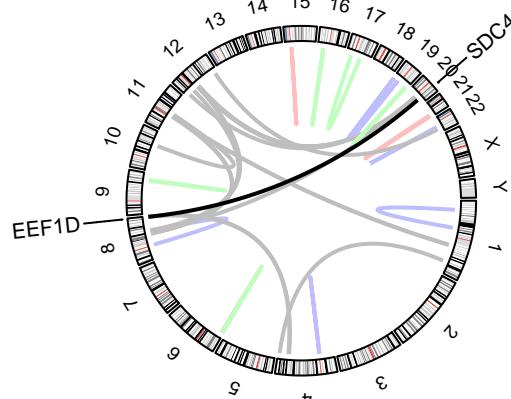
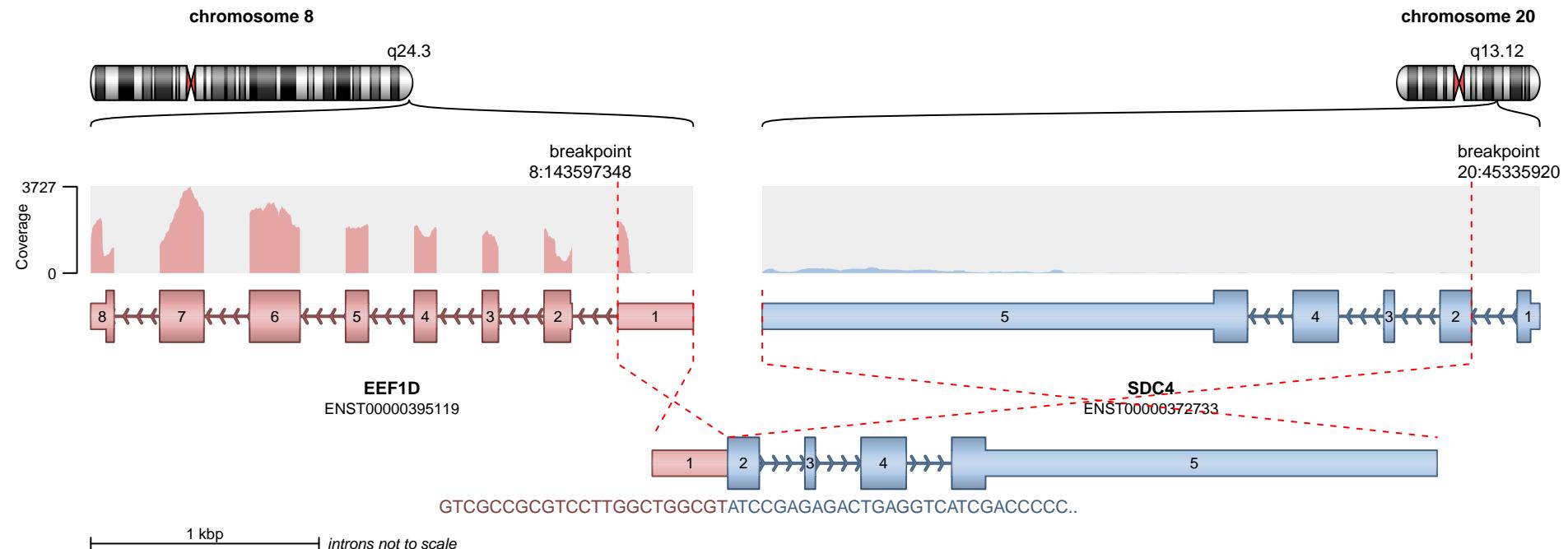
SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 8

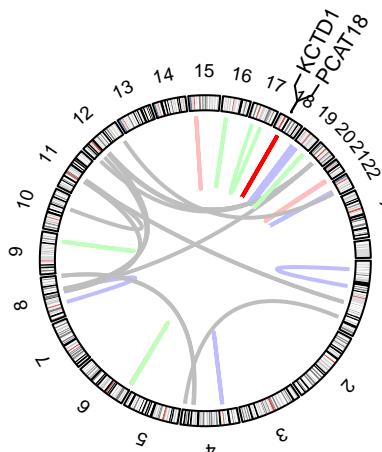
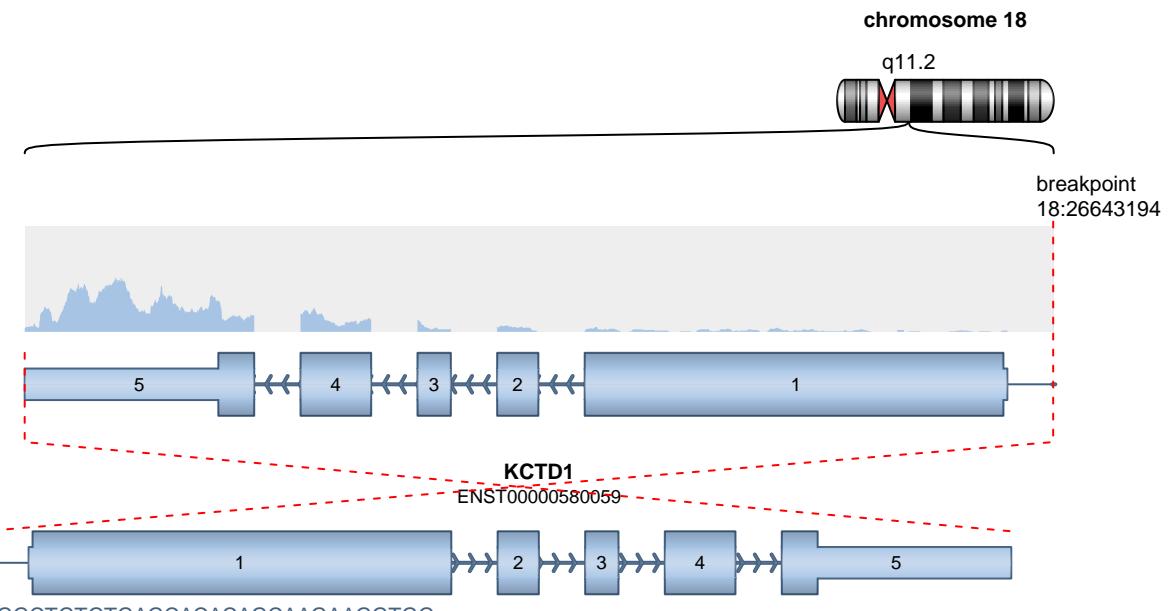
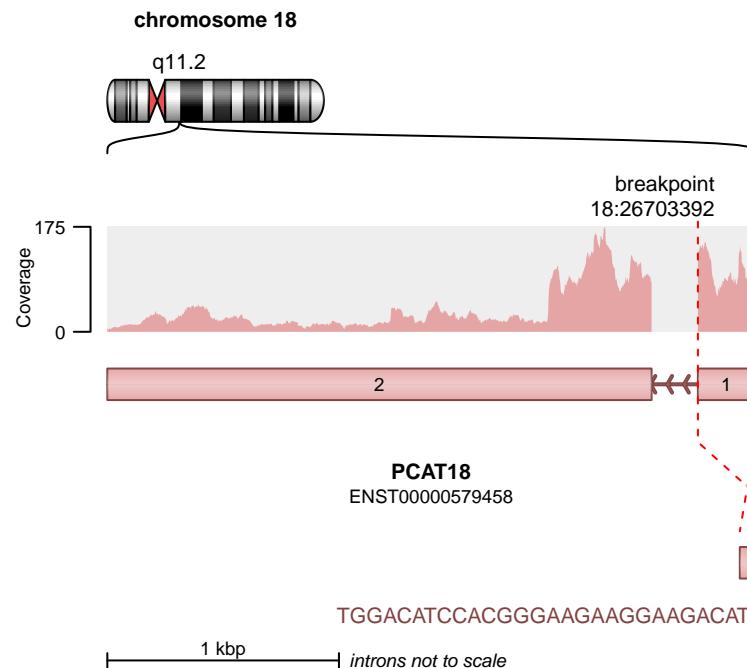
— translocation — deletion
— duplication — inversion



— translocation — deletion
— duplication — inversion



— translocation — deletion
— duplication — inversion

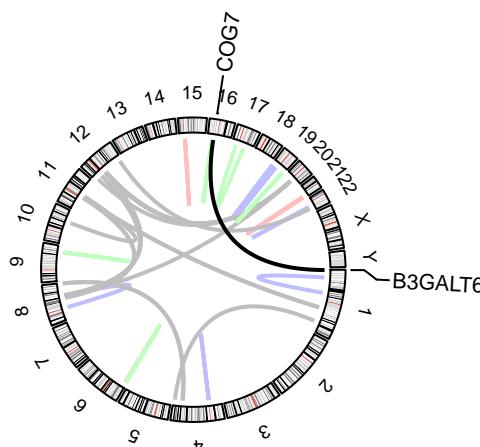
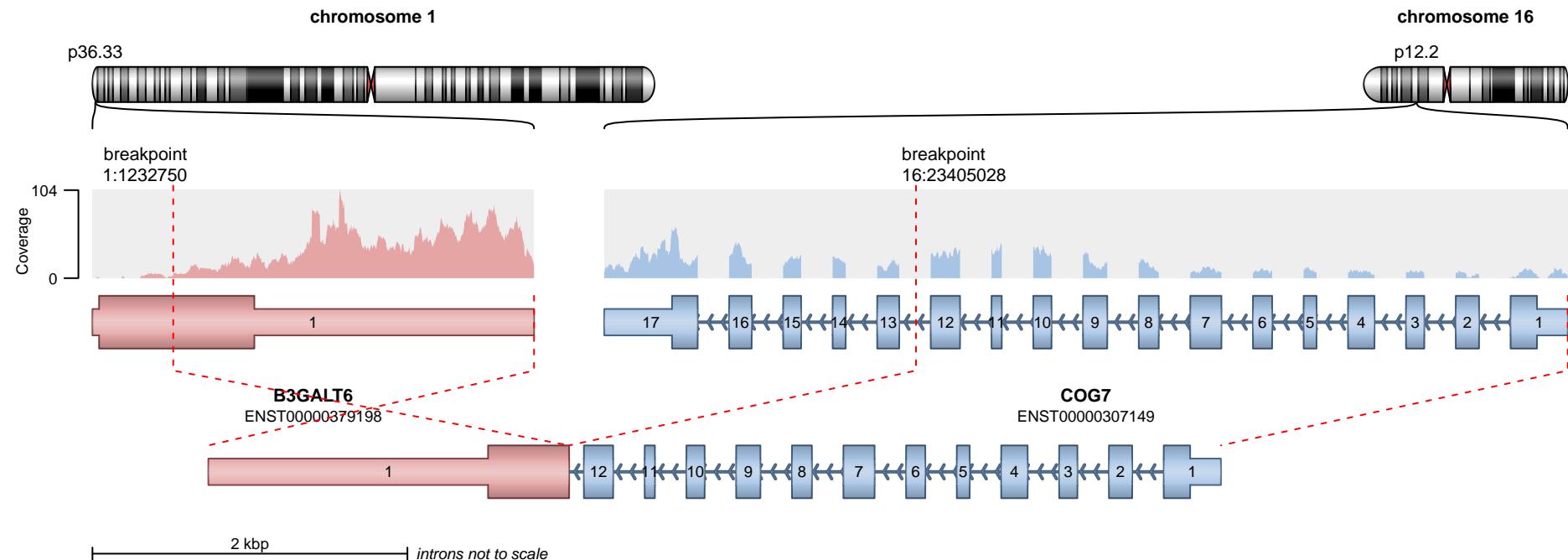


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 6

— translocation — deletion
— duplication — inversion

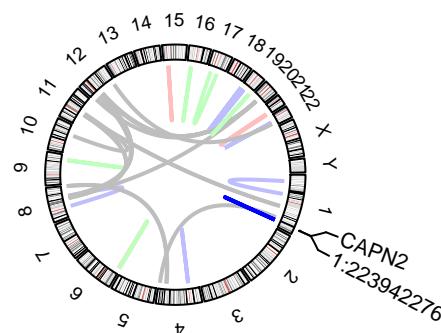
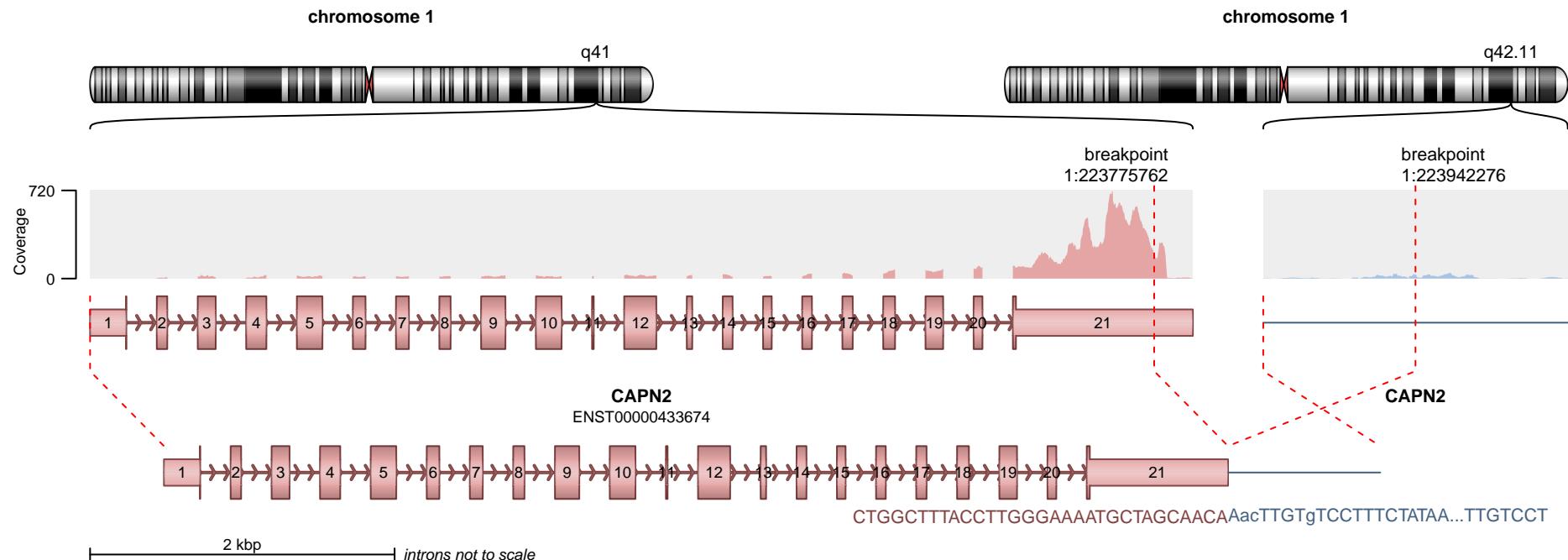


No coding regions due to antisense transcription.

SUPPORTING READ COUNT

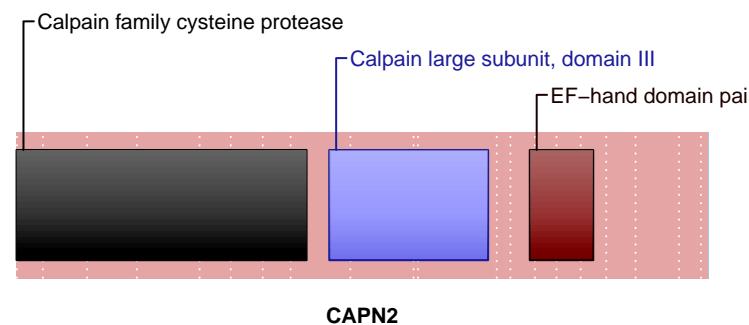
Split reads = 0
Discordant mates = 5

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS

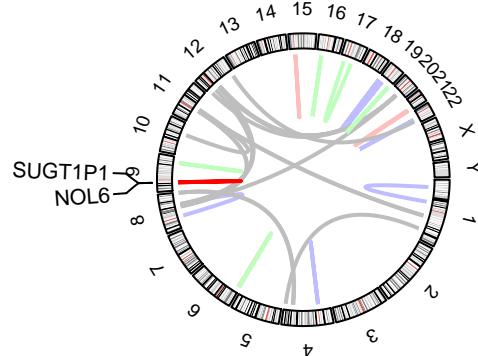
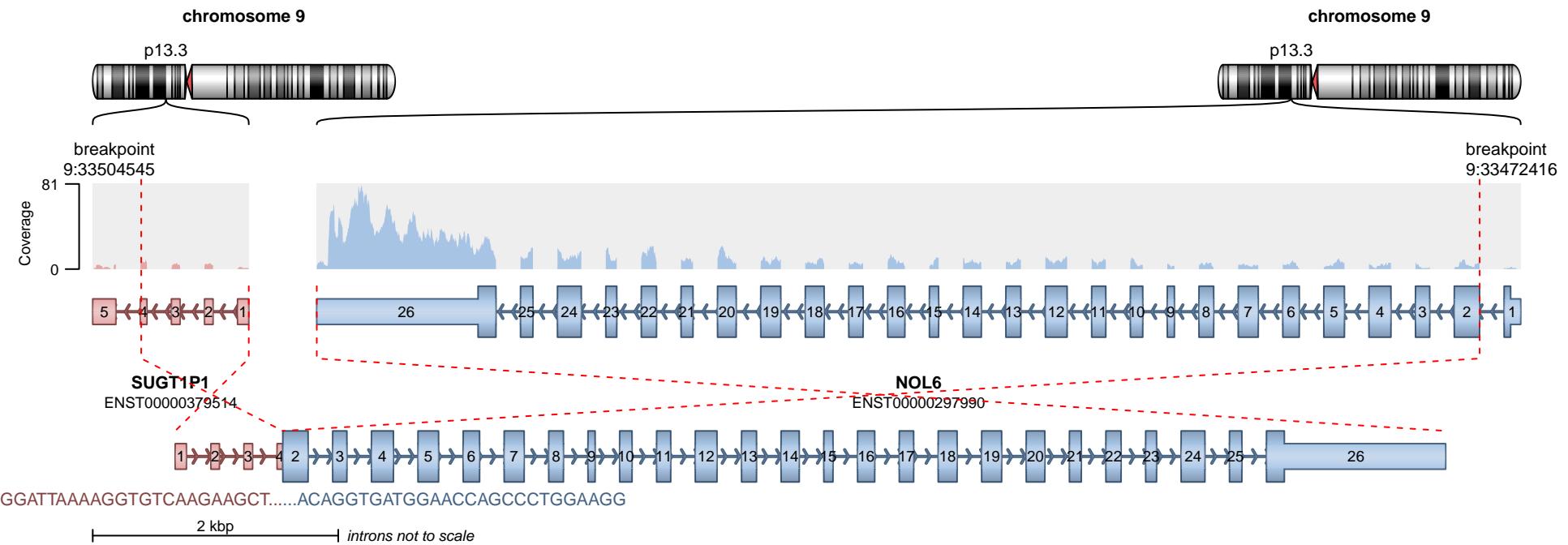
reading frame unclear



SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0

— translocation — deletion
— duplication — inversion

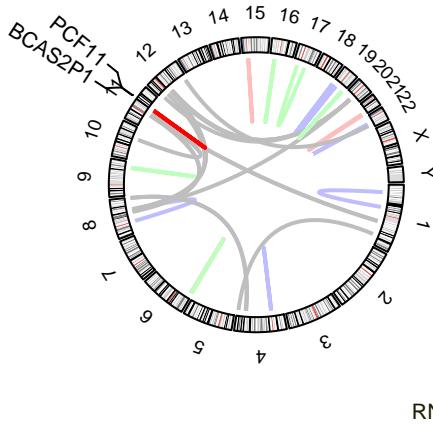
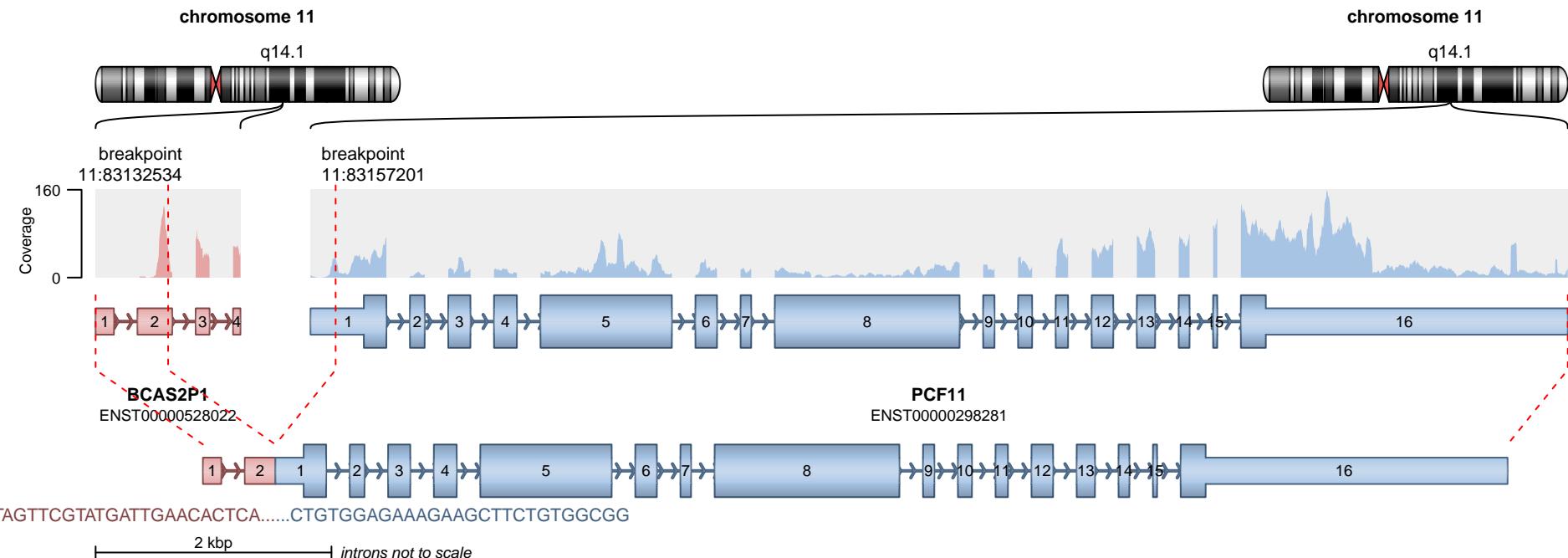


No protein domains retained in fusion.

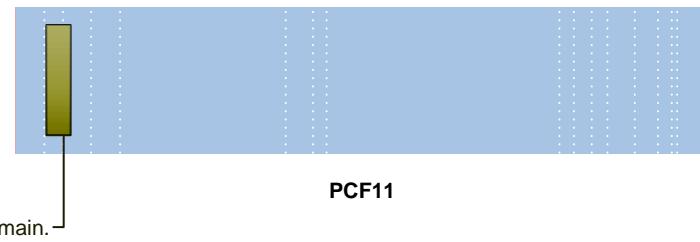
SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 5

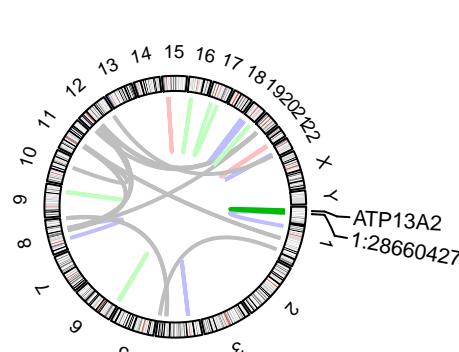
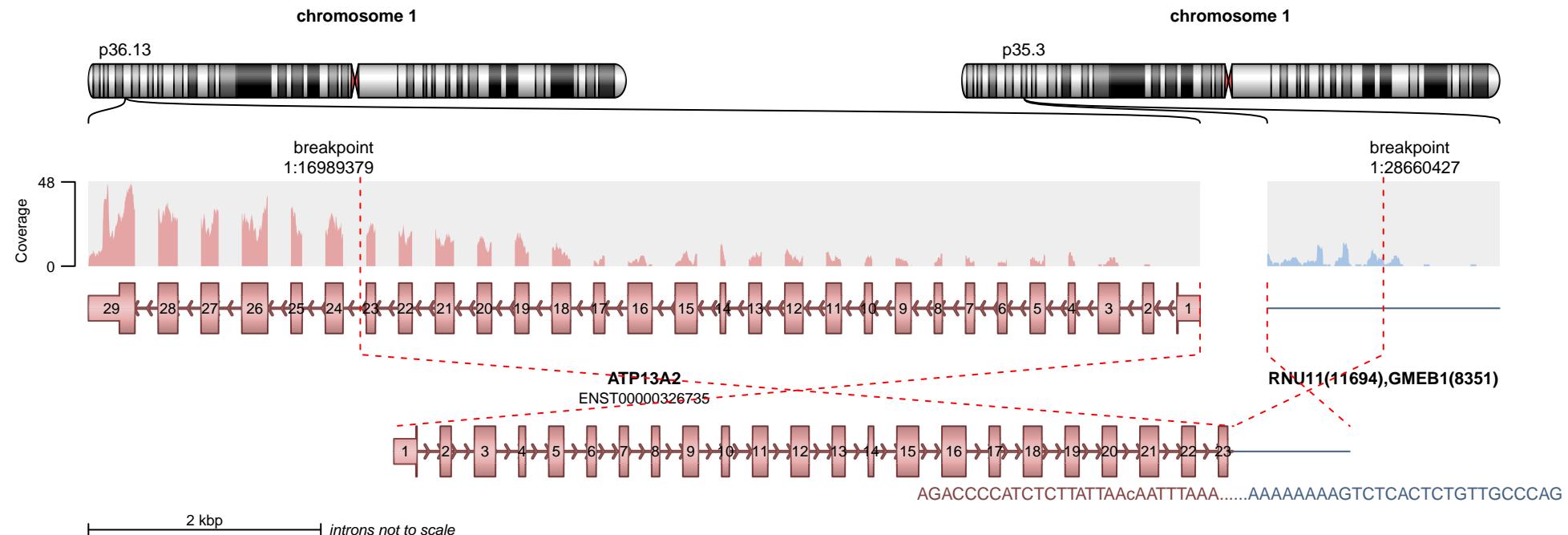
— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS
reading frame unclear

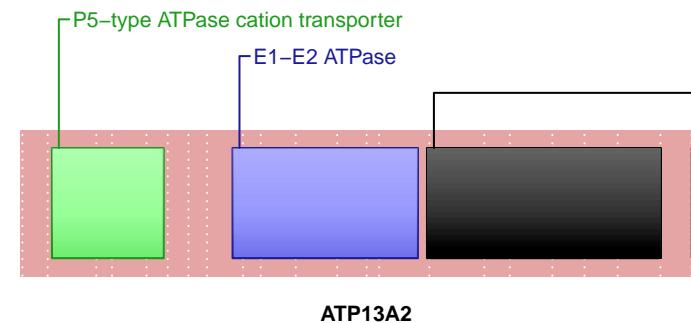


— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS

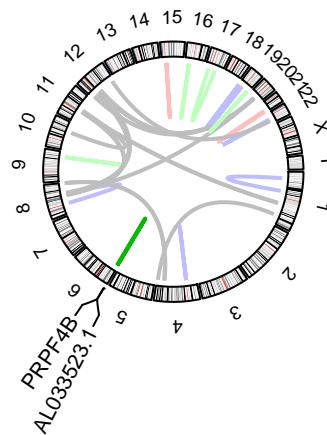
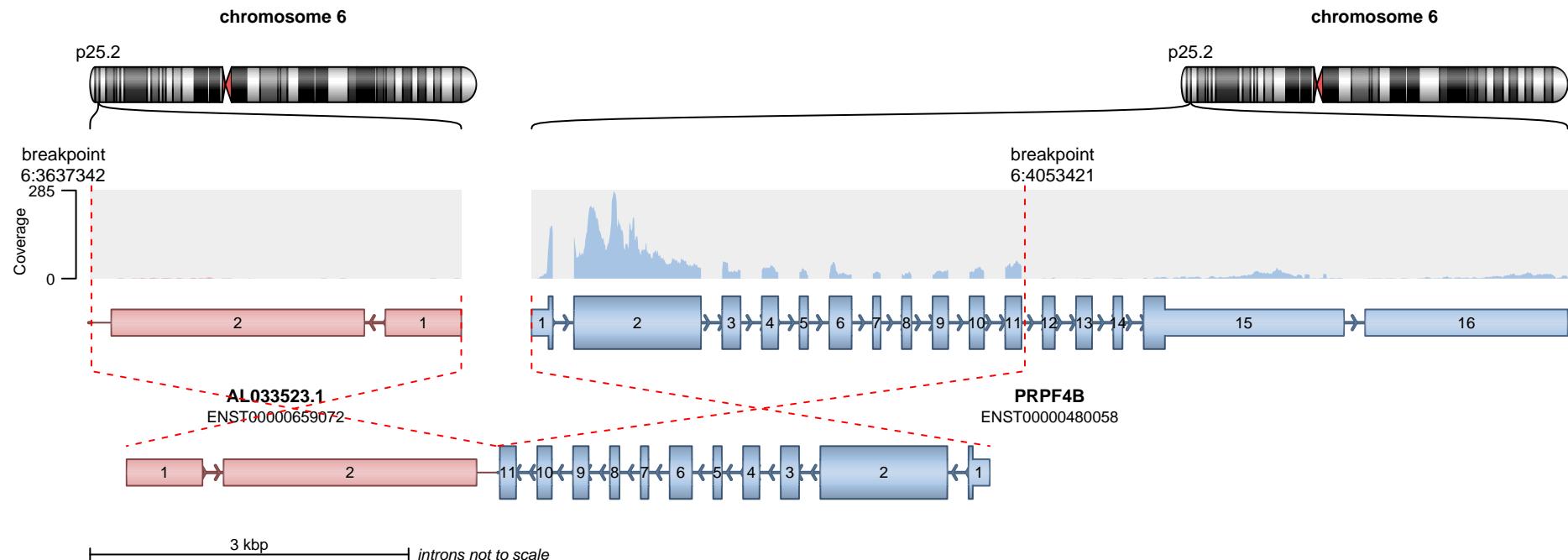
reading frame unclear



SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 4

— translocation — deletion
— duplication — inversion

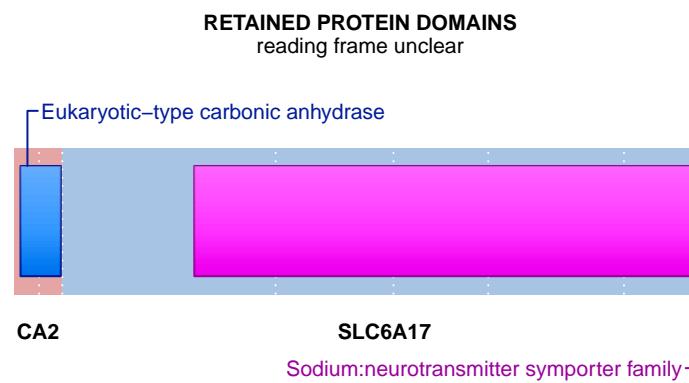
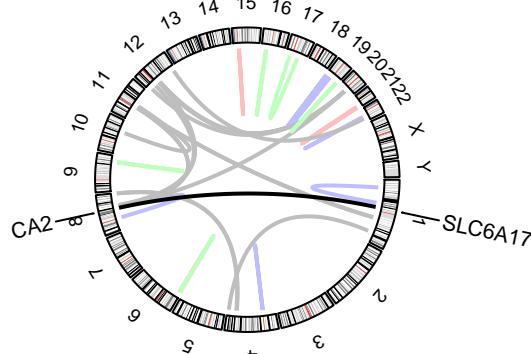
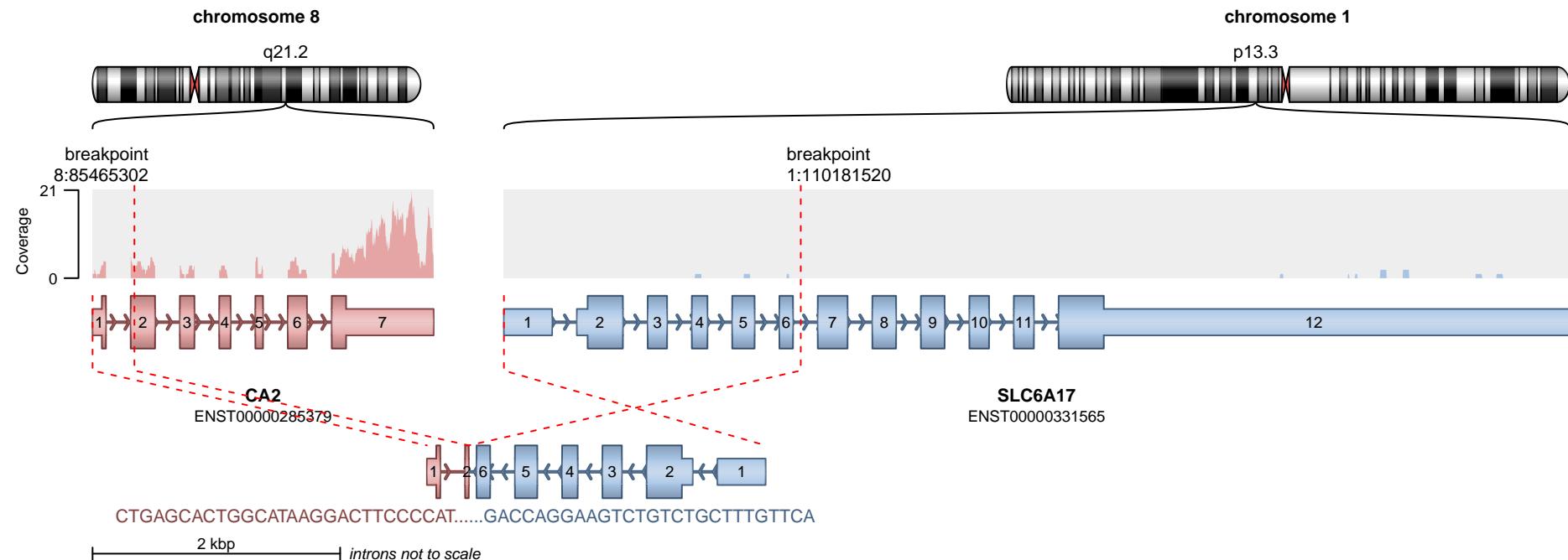


No coding regions due to antisense transcription.

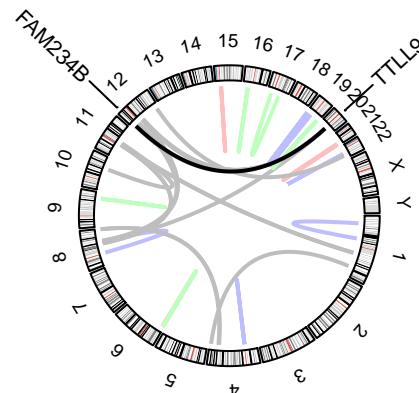
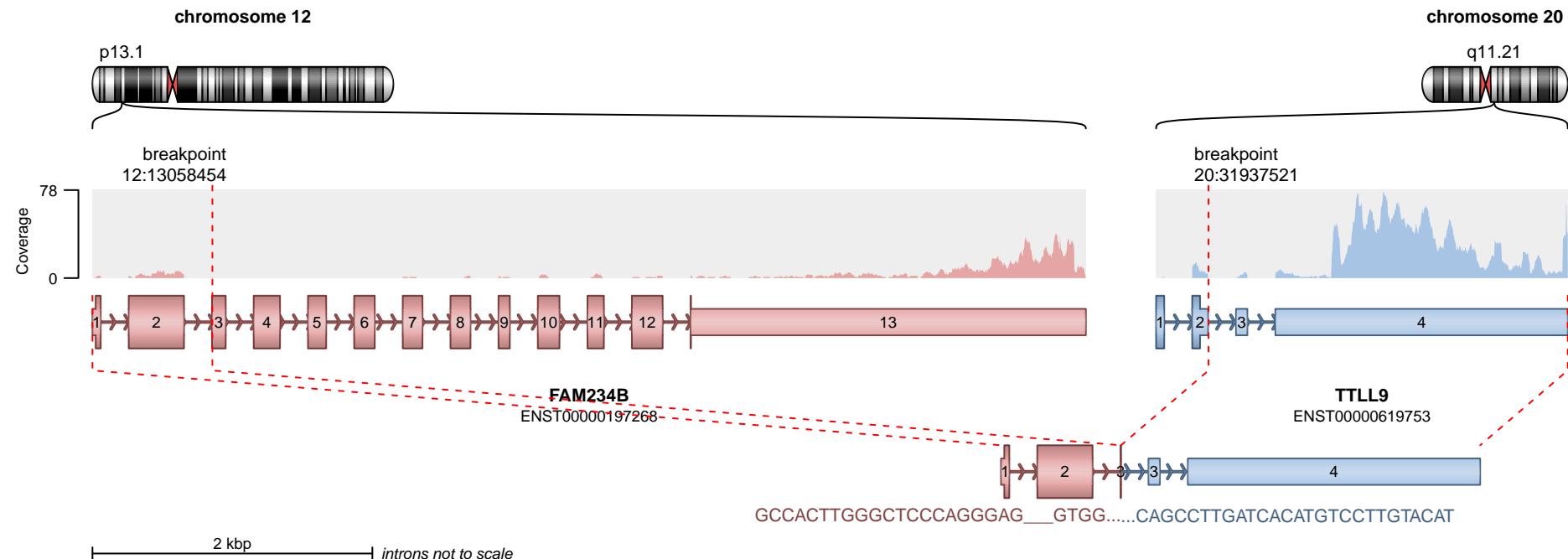
SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 4

— translocation — deletion
— duplication — inversion



— translocation — deletion
— duplication — inversion

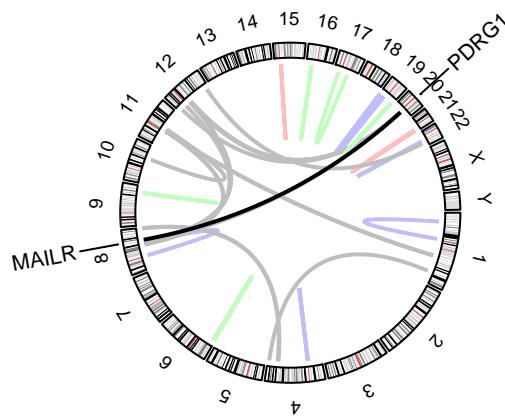
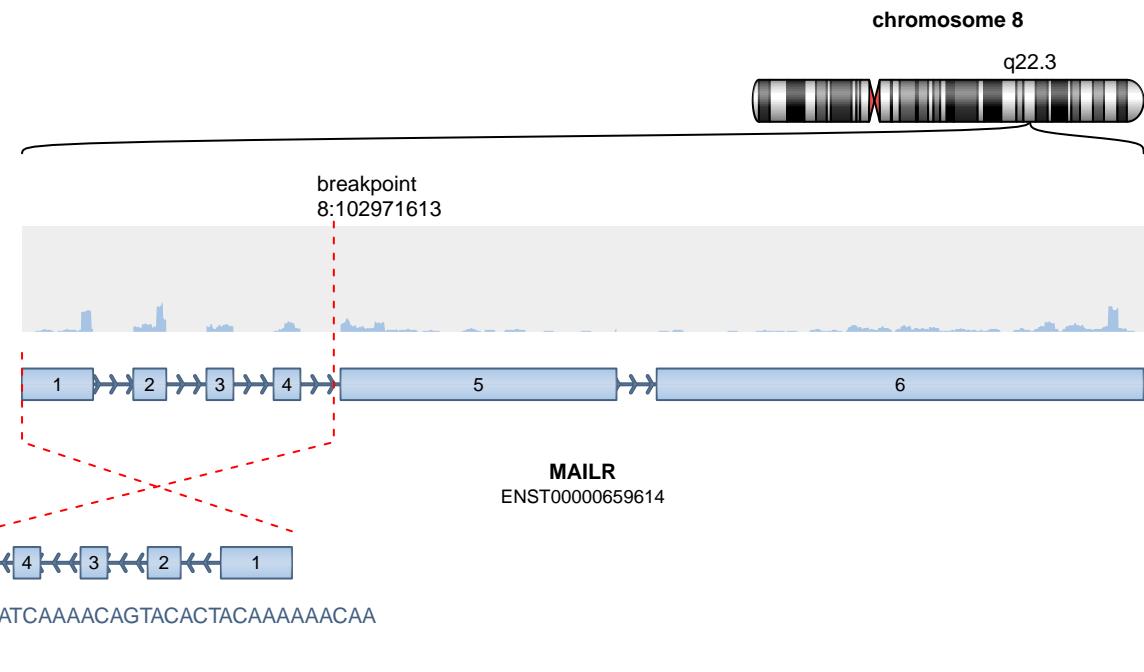
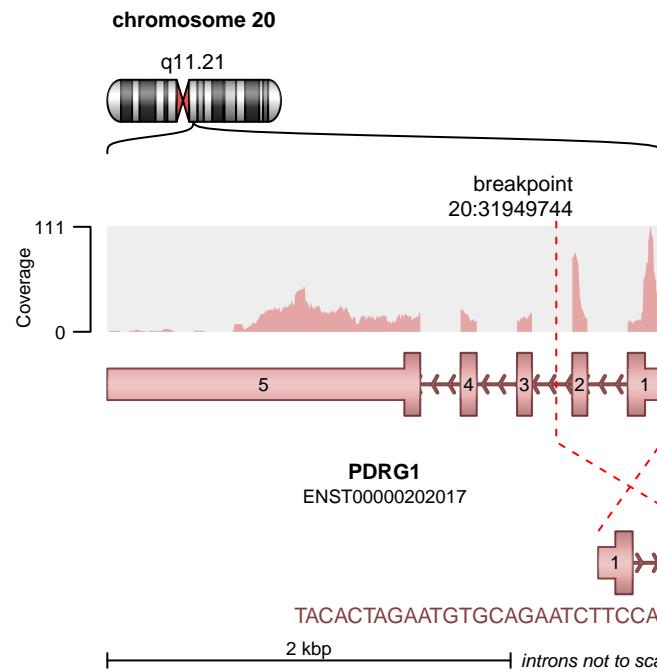


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 4

— translocation — deletion
— duplication — inversion

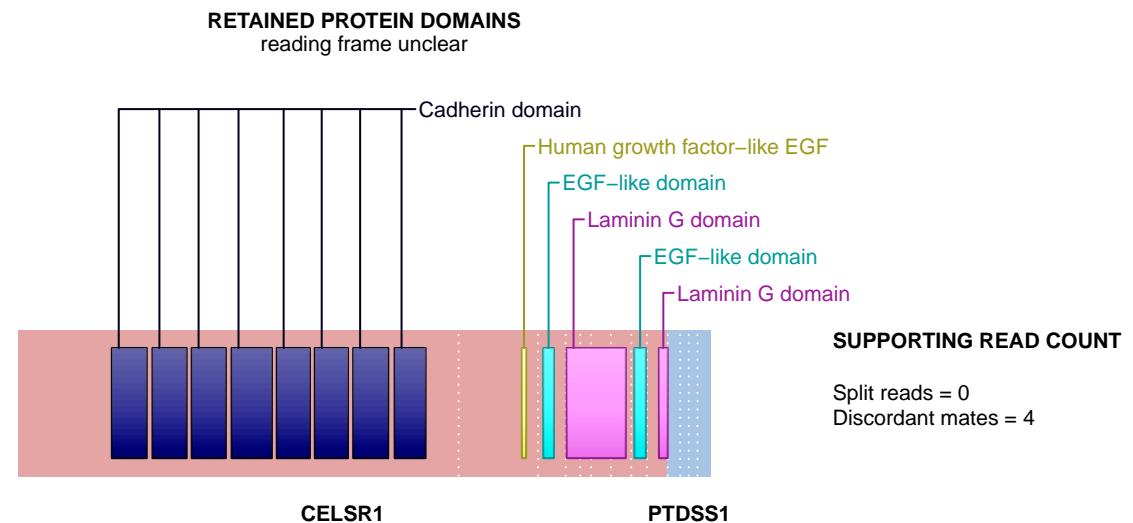
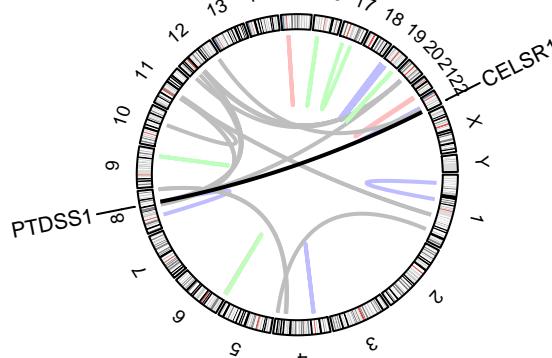
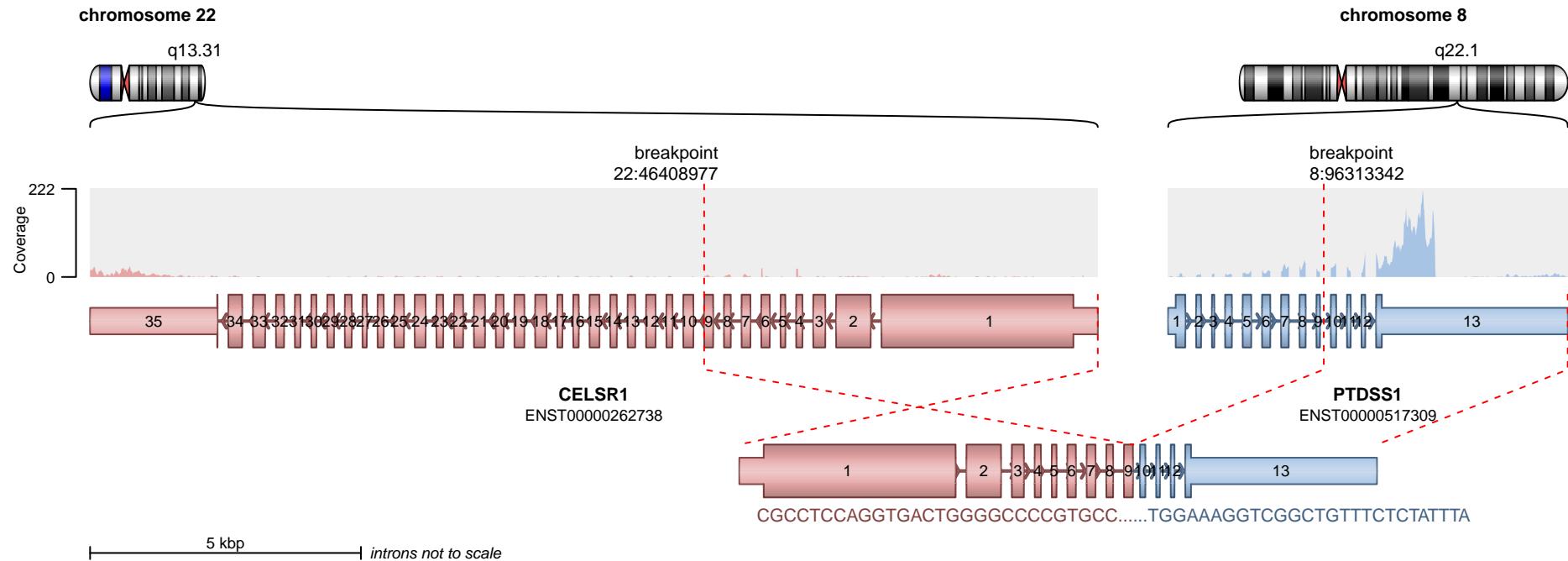


No protein domains retained in fusion.

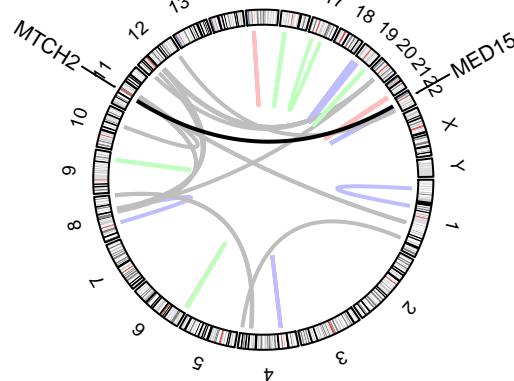
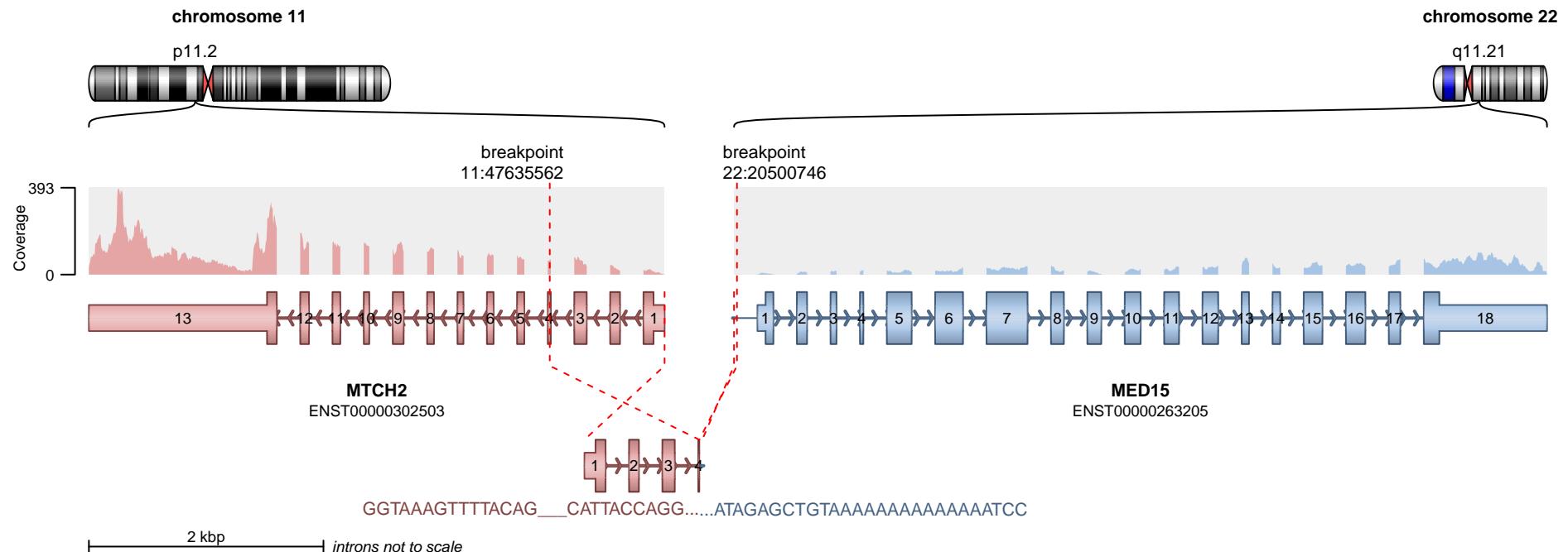
SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 4

— translocation — deletion
— duplication — inversion



— translocation — deletion
— duplication — inversion

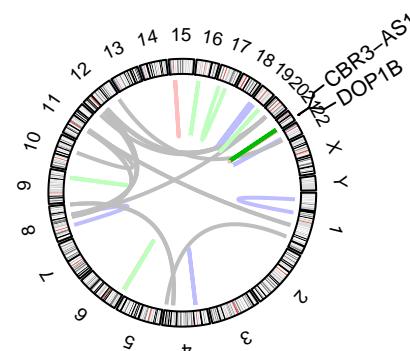
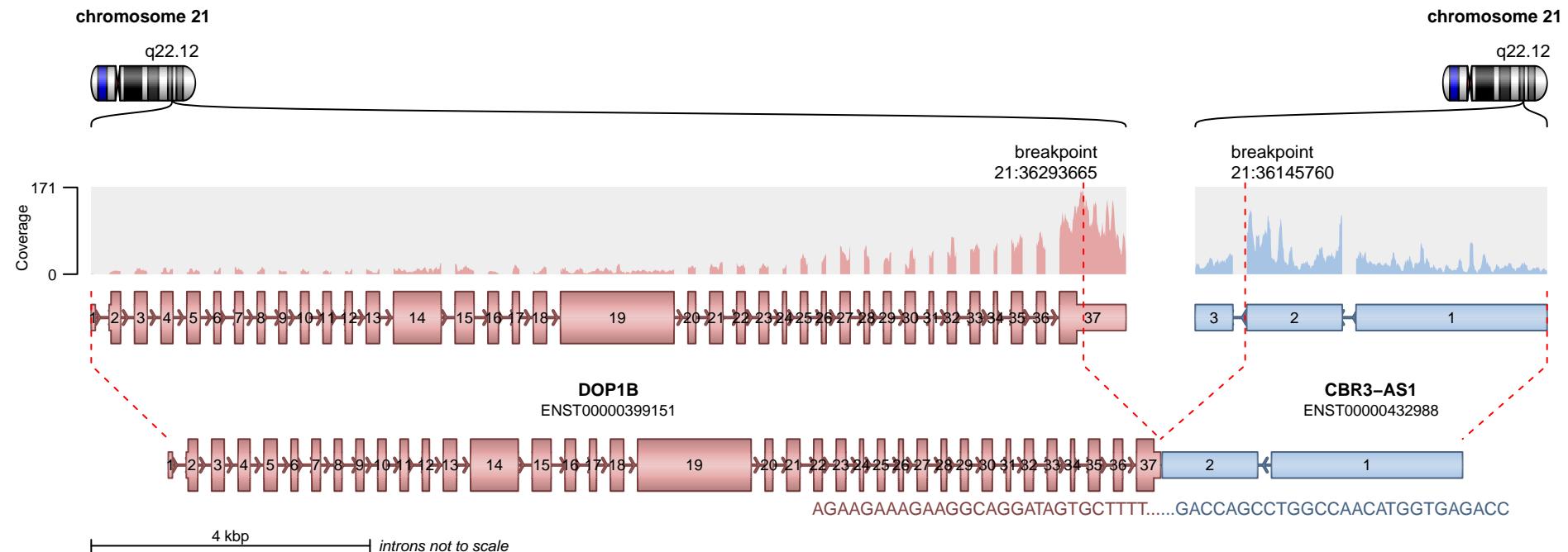


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 4

— translocation — deletion
— duplication — inversion

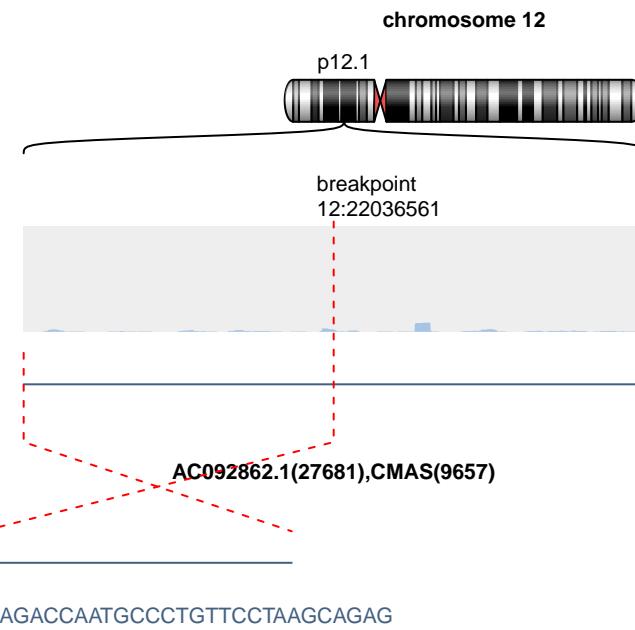
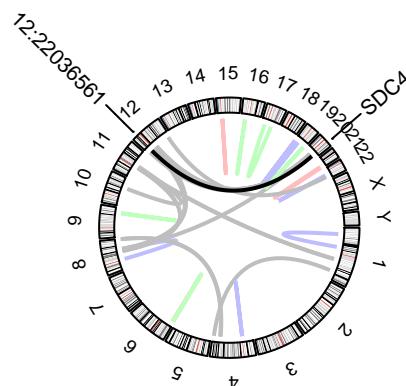
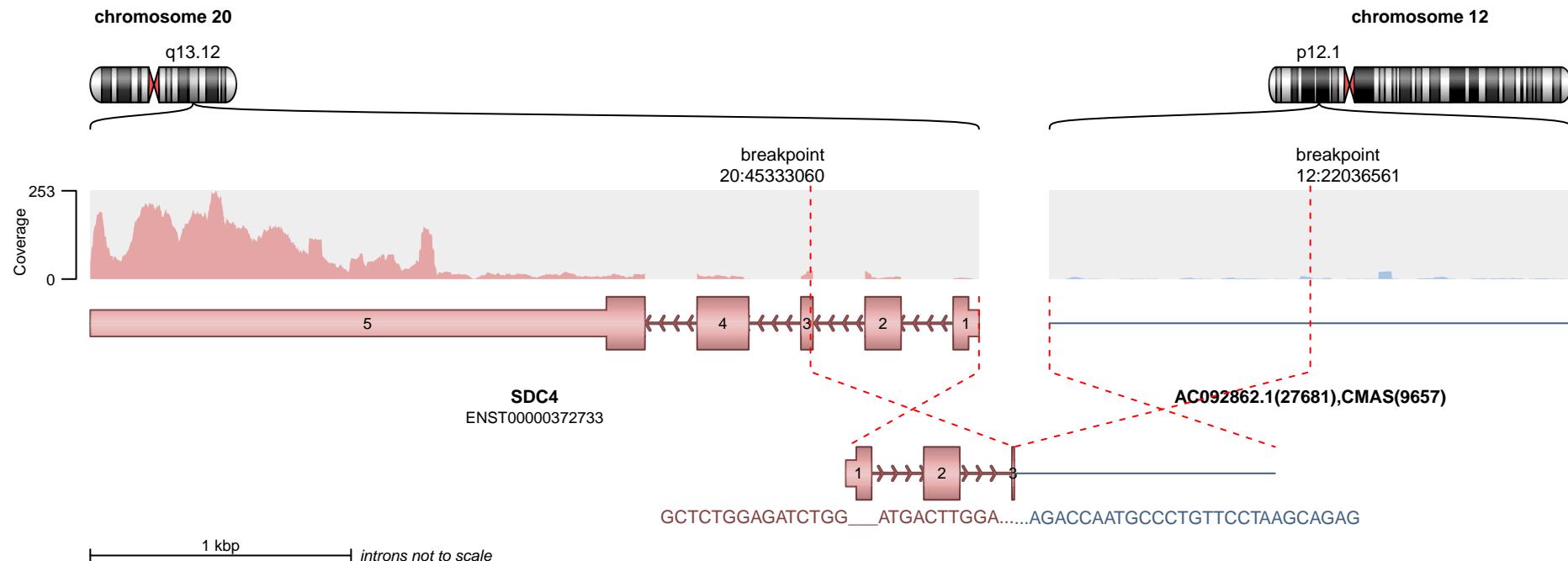


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 4

— translocation — deletion
— duplication — inversion

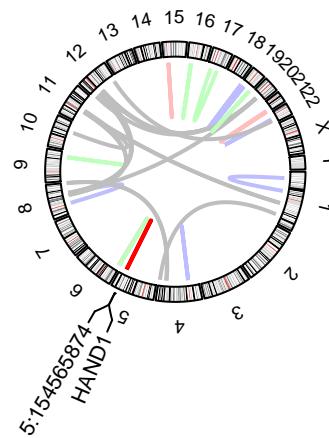
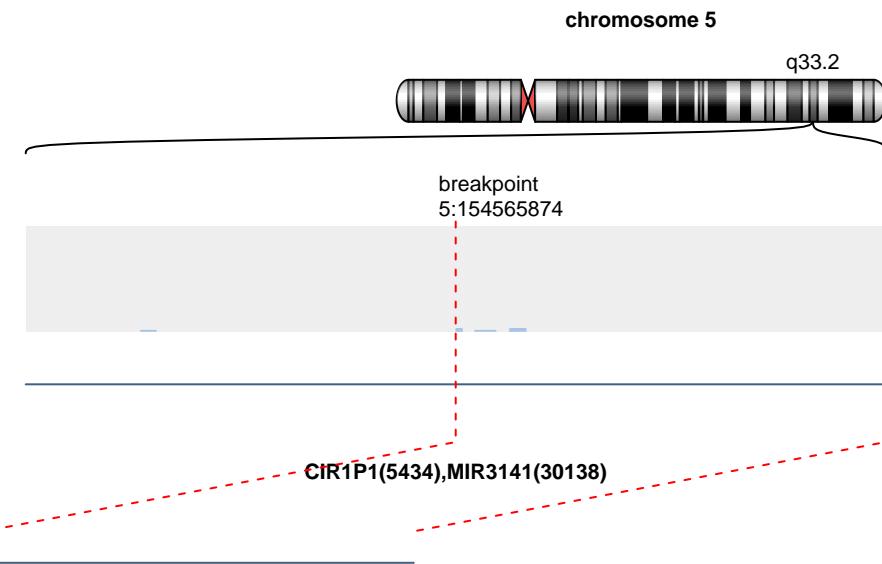
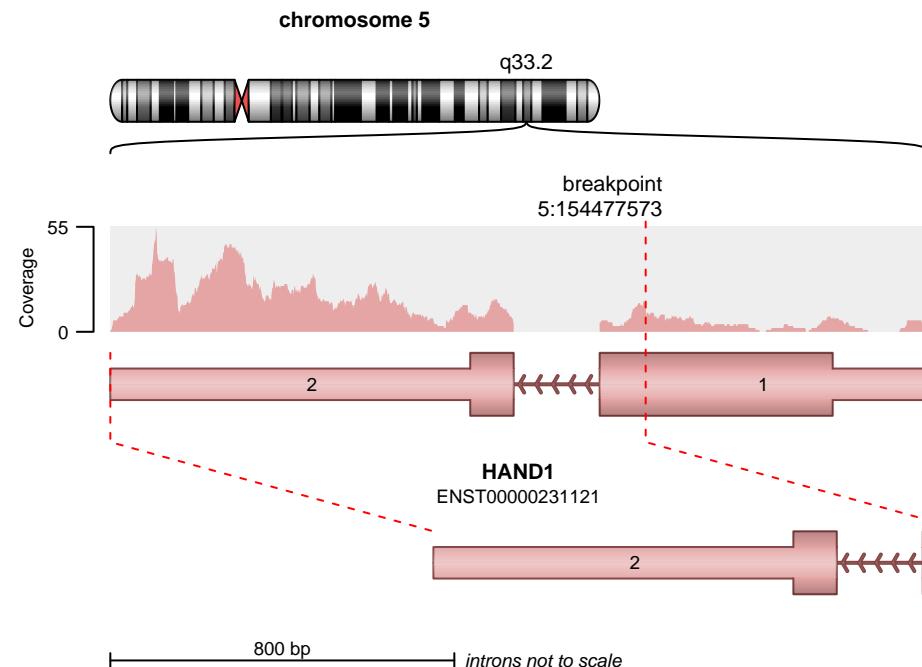


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 3

— translocation — deletion
— duplication — inversion

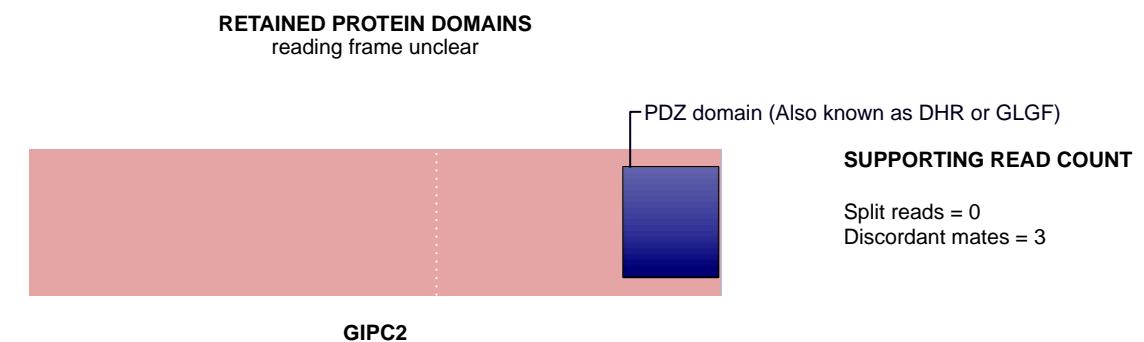
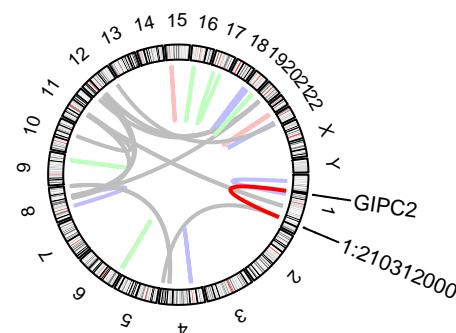
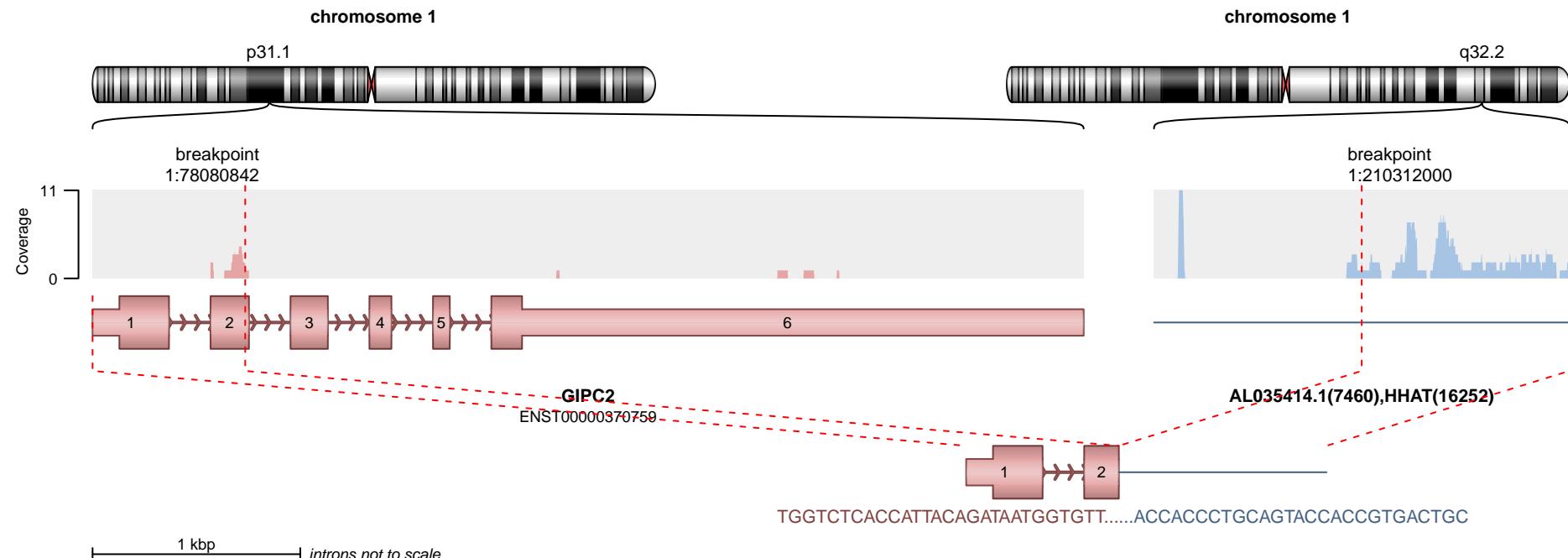


No coding regions due to antisense transcription.

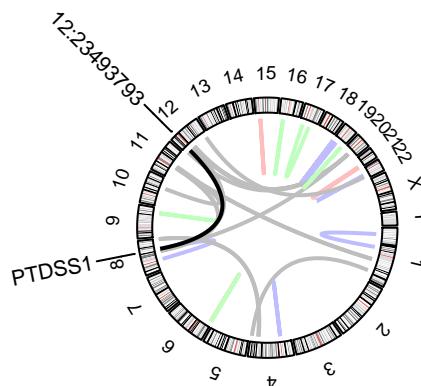
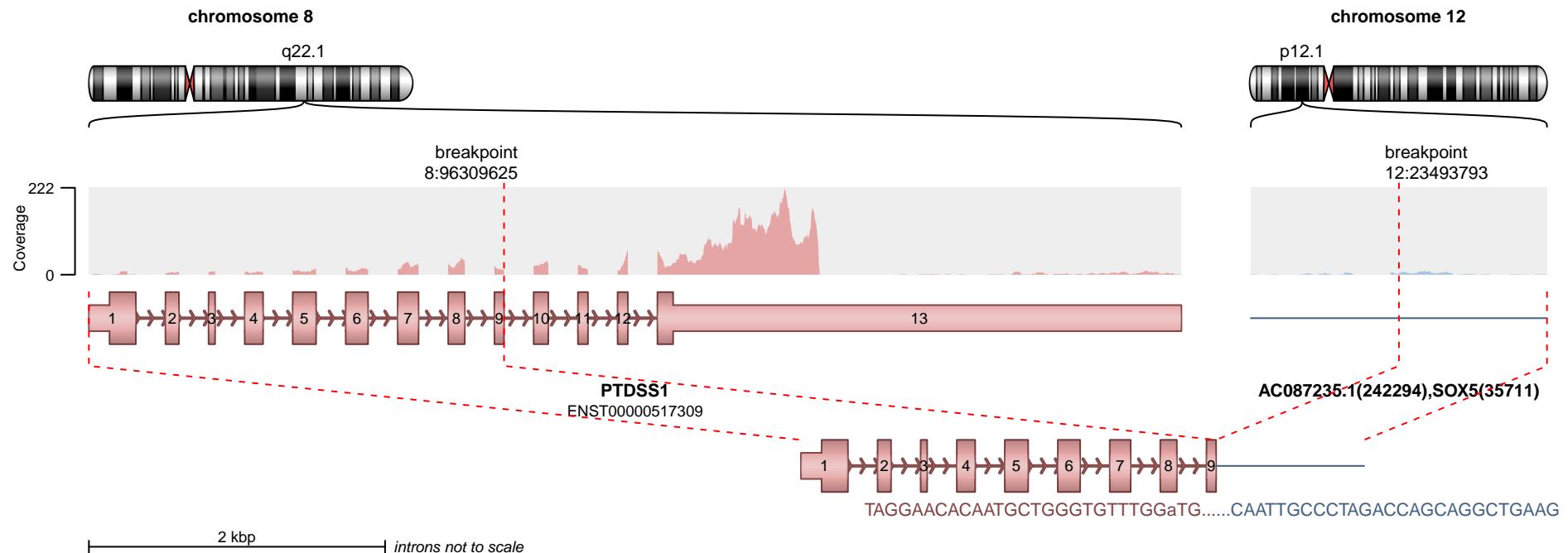
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 1

— translocation — deletion
— duplication — inversion



— translocation — deletion
— duplication — inversion

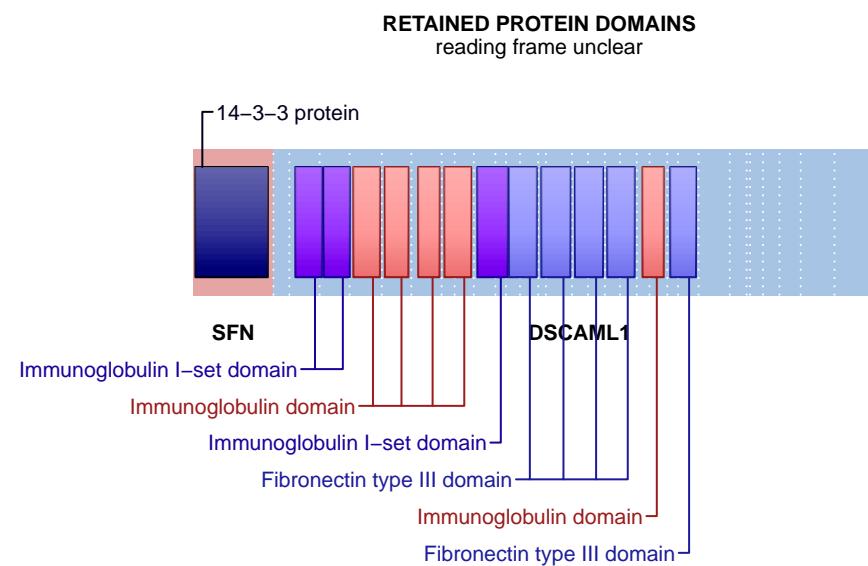
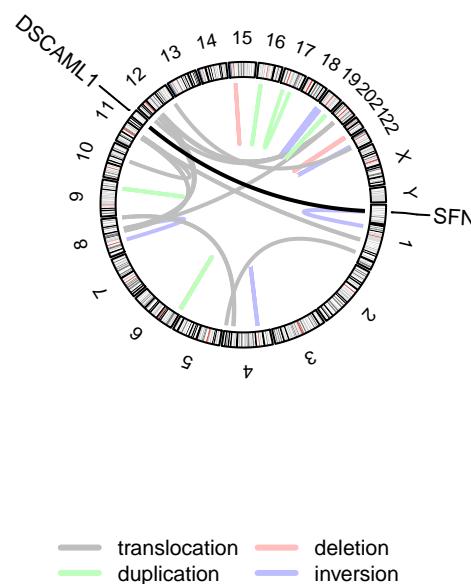
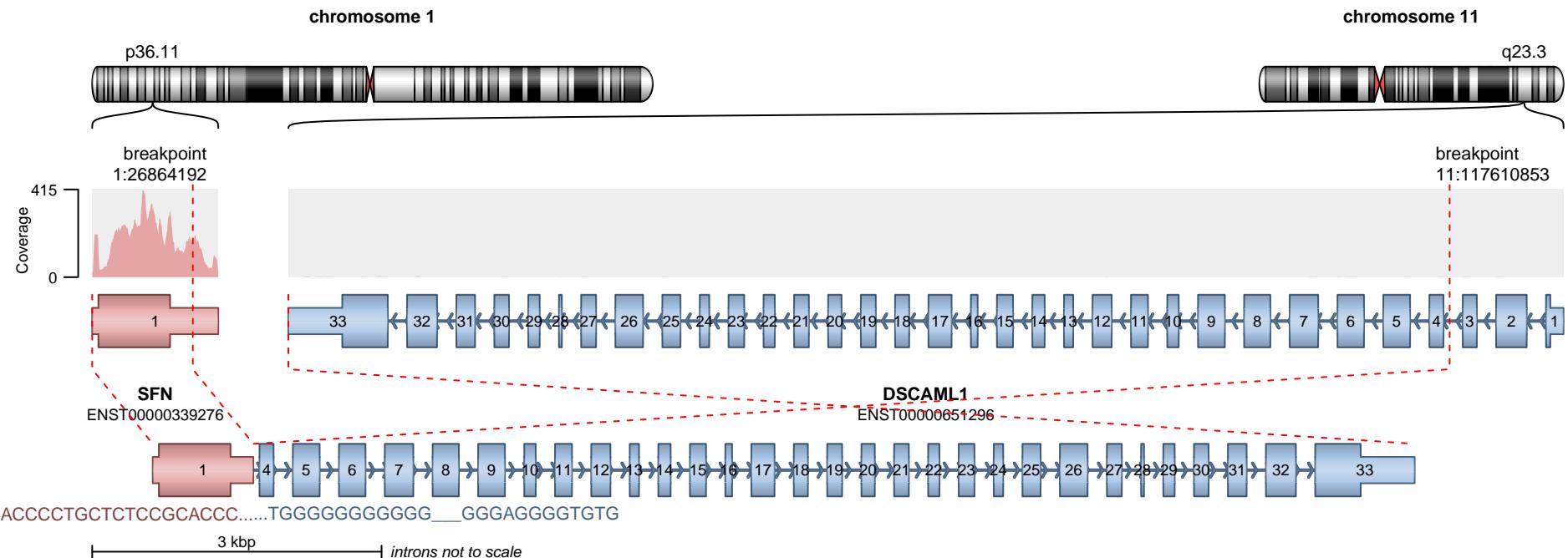


No protein domains retained in fusion.

SUPPORTING READ COUNT

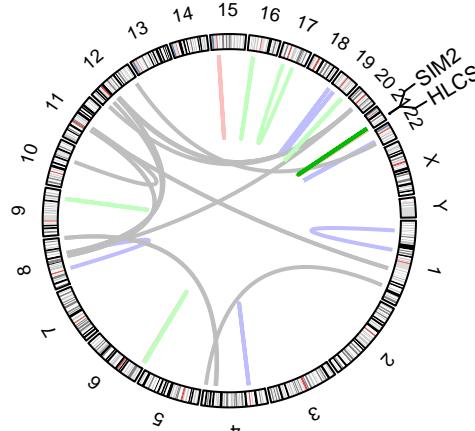
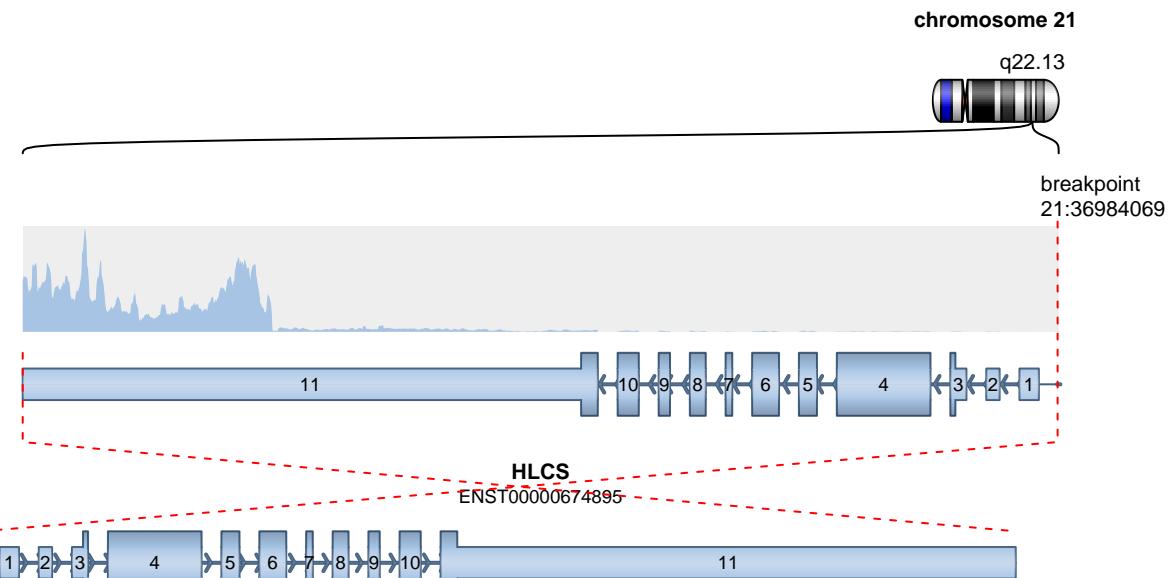
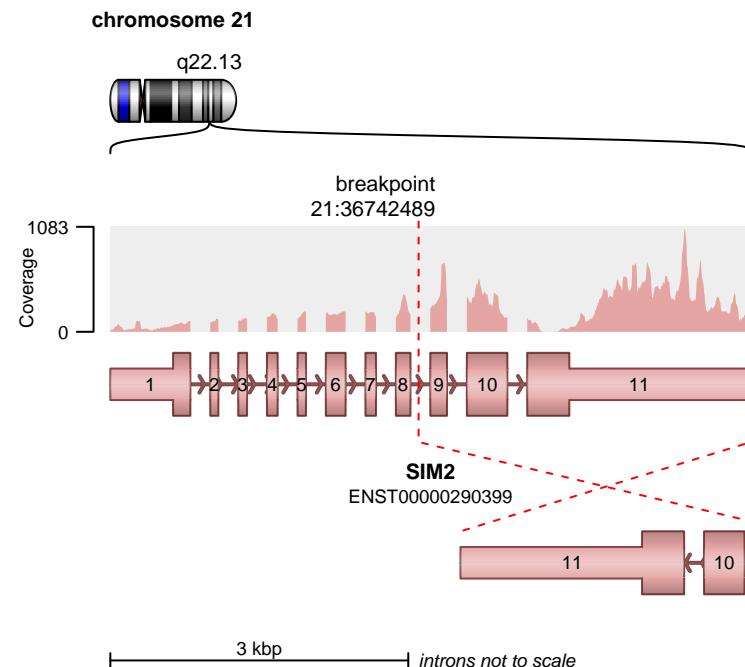
Split reads = 0
Discordant mates = 3

— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 3

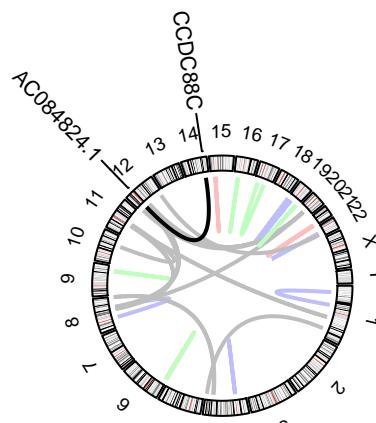
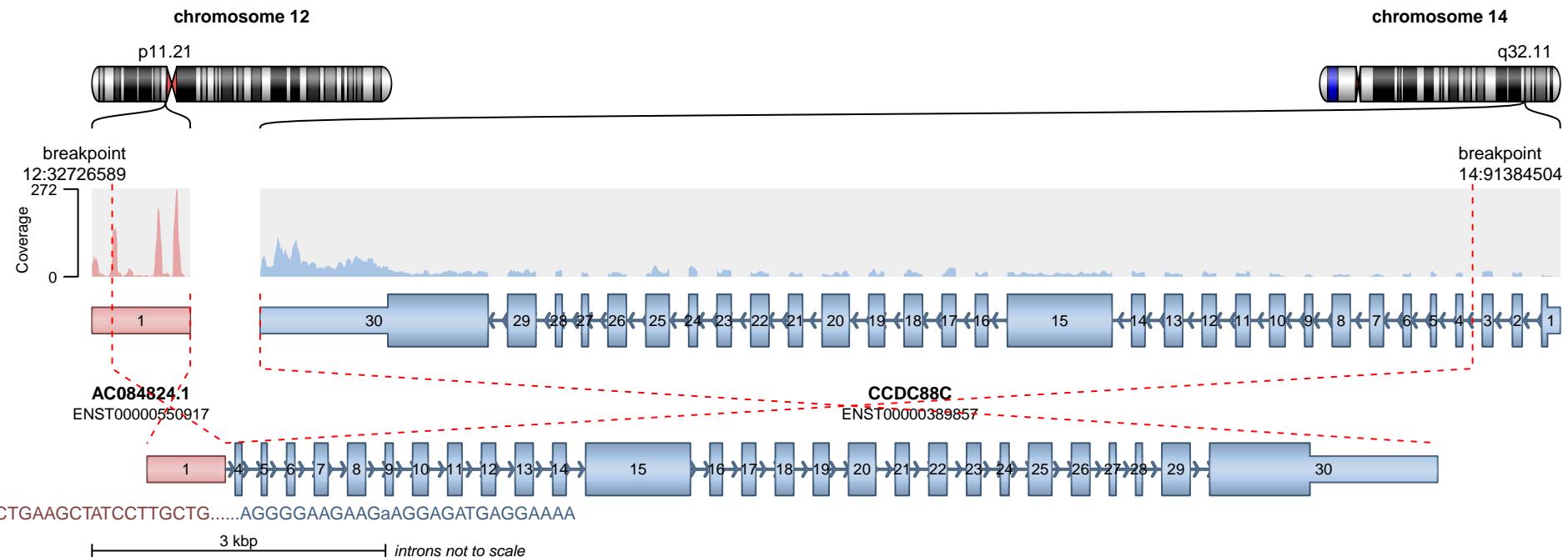


No coding regions due to antisense transcription.

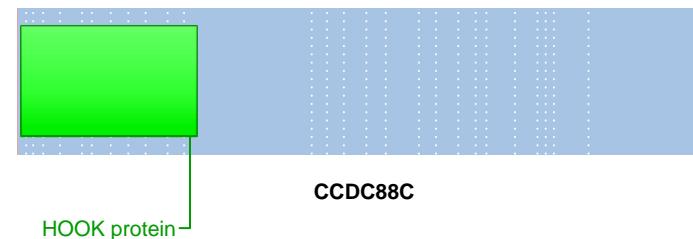
SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 3

— translocation — deletion
— duplication — inversion



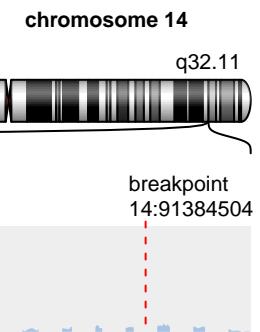
RETAINED PROTEIN DOMAINS
reading frame unclear

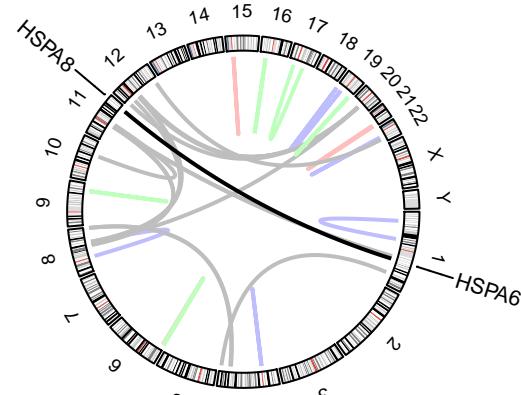
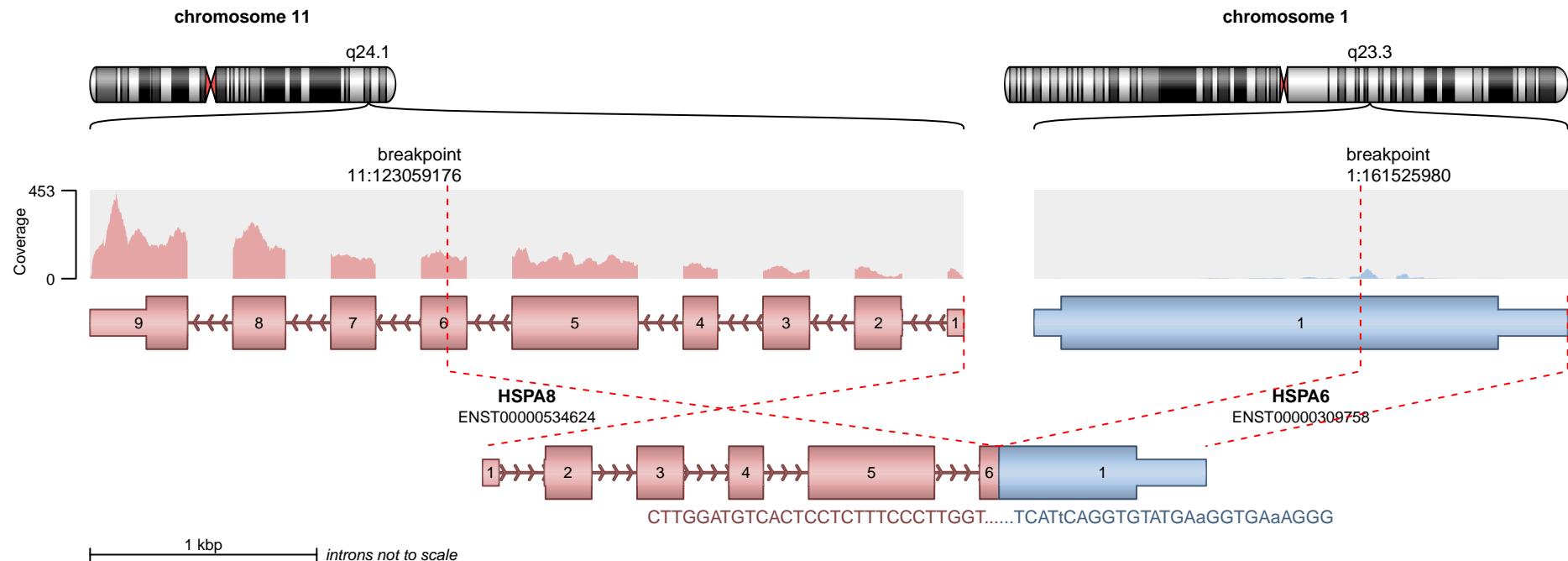


SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 3

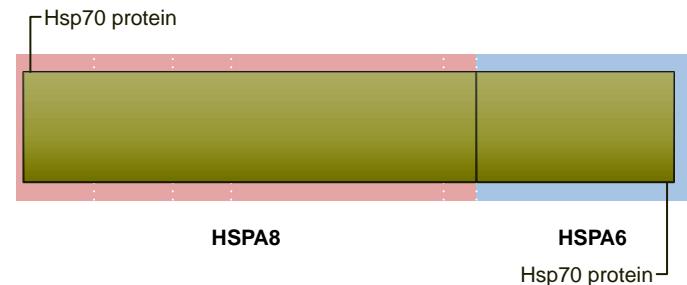
— translocation — deletion
— duplication — inversion





RETAINED PROTEIN DOMAINS

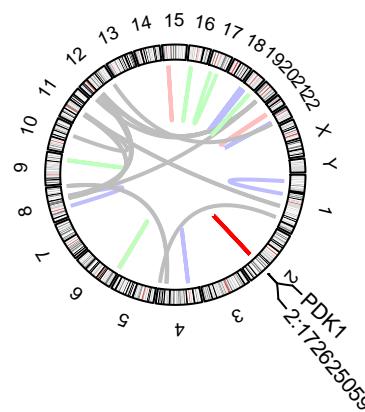
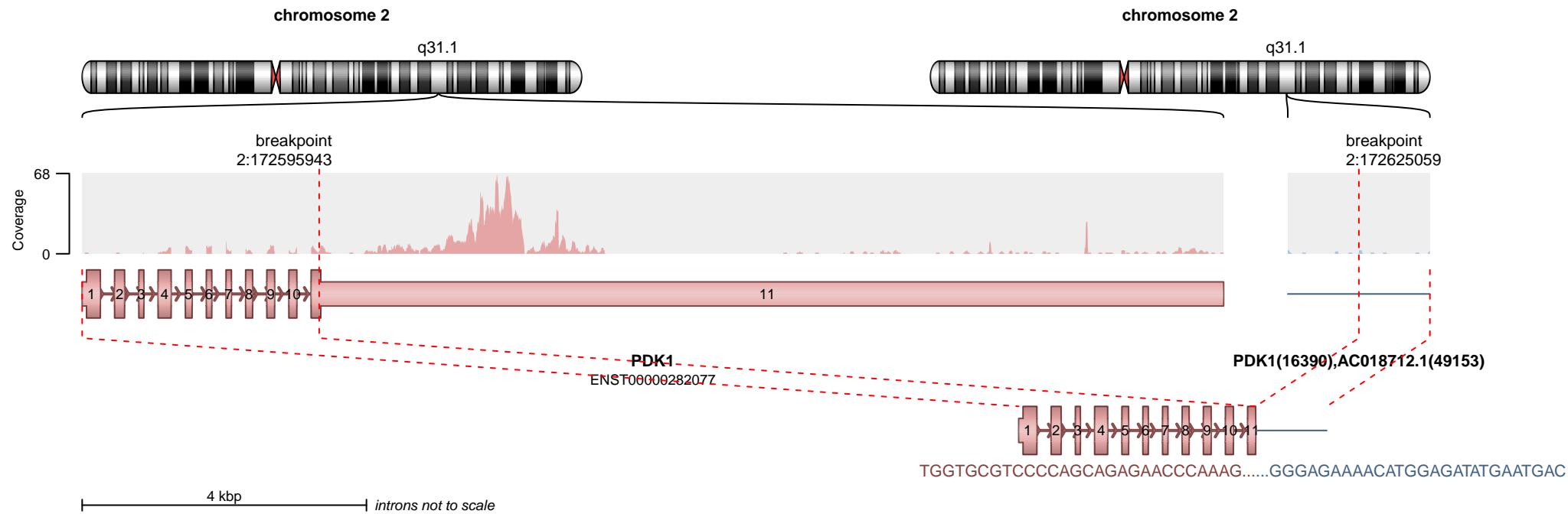
reading frame unclear



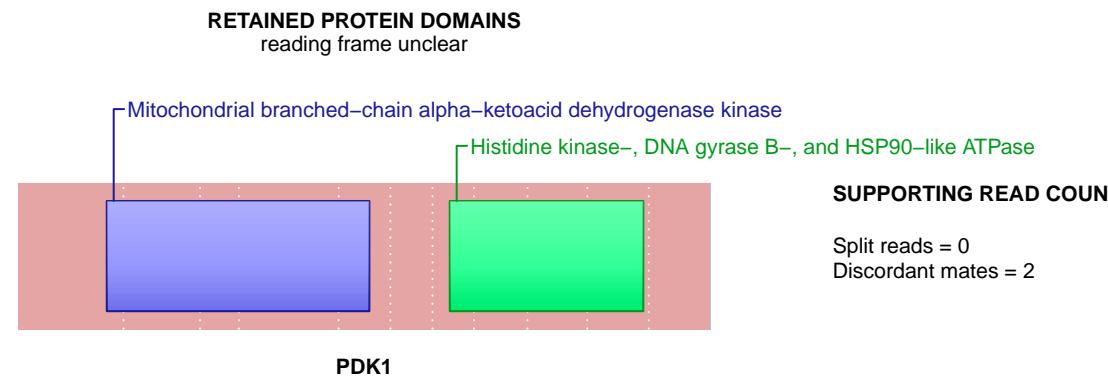
SUPPORTING READ COUNT

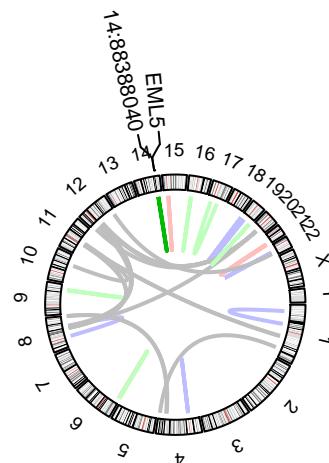
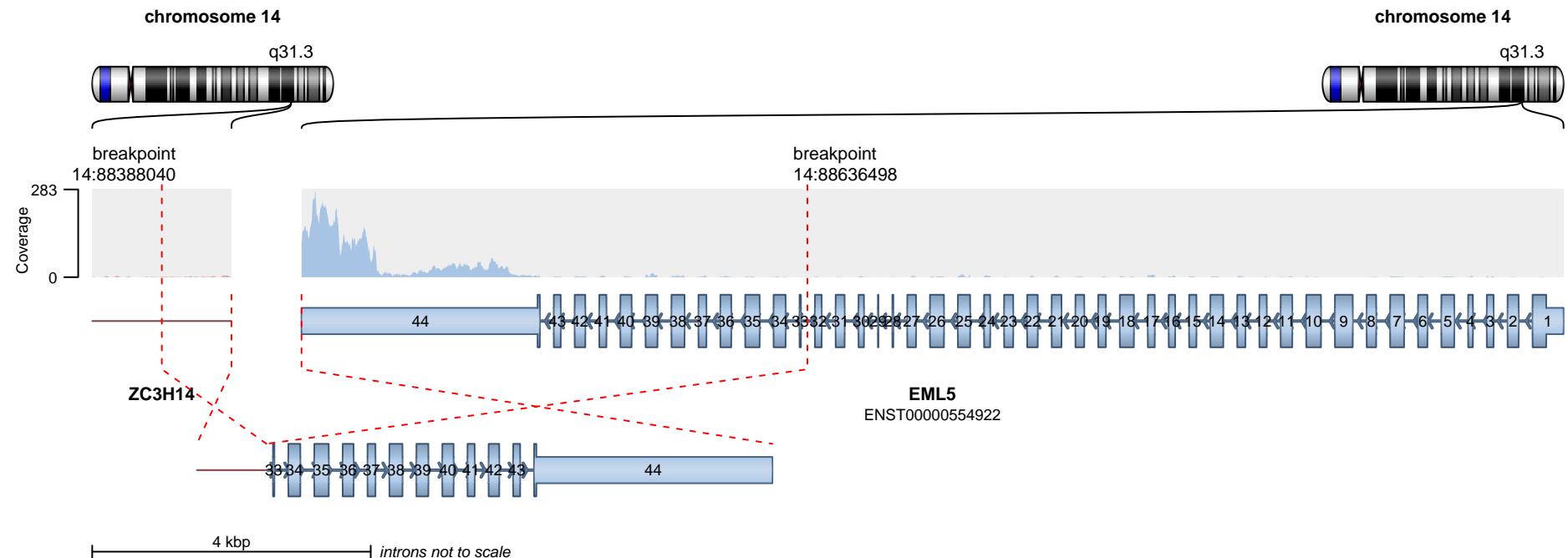
Split reads = 0
Discordant mates = 3

— translocation — deletion
— duplication — inversion



— translocation — deletion
— duplication — inversion



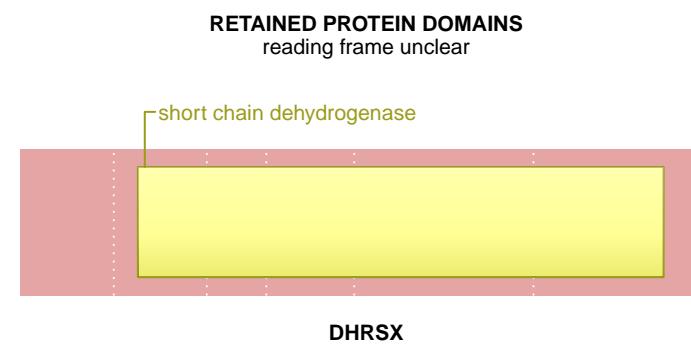
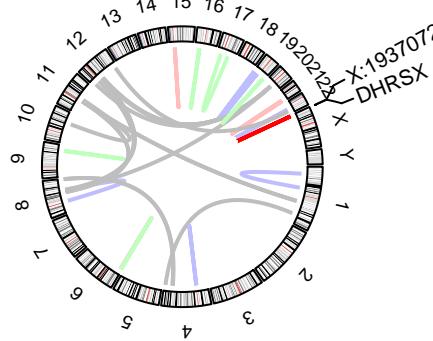
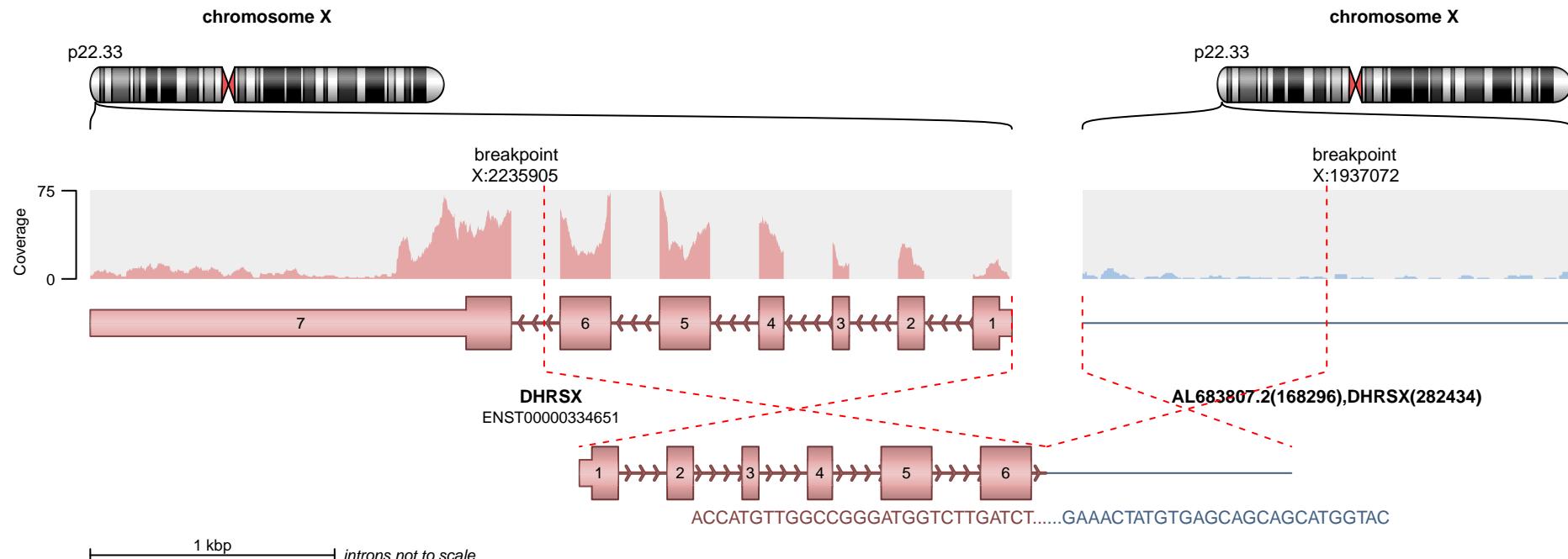


No coding regions due to antisense transcription.

SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 2

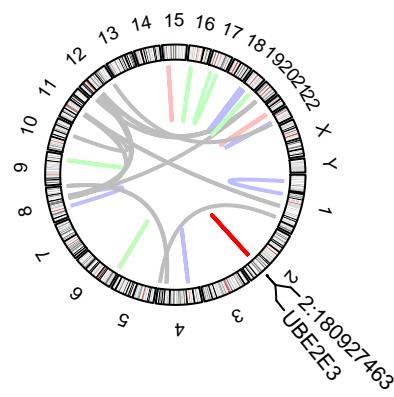
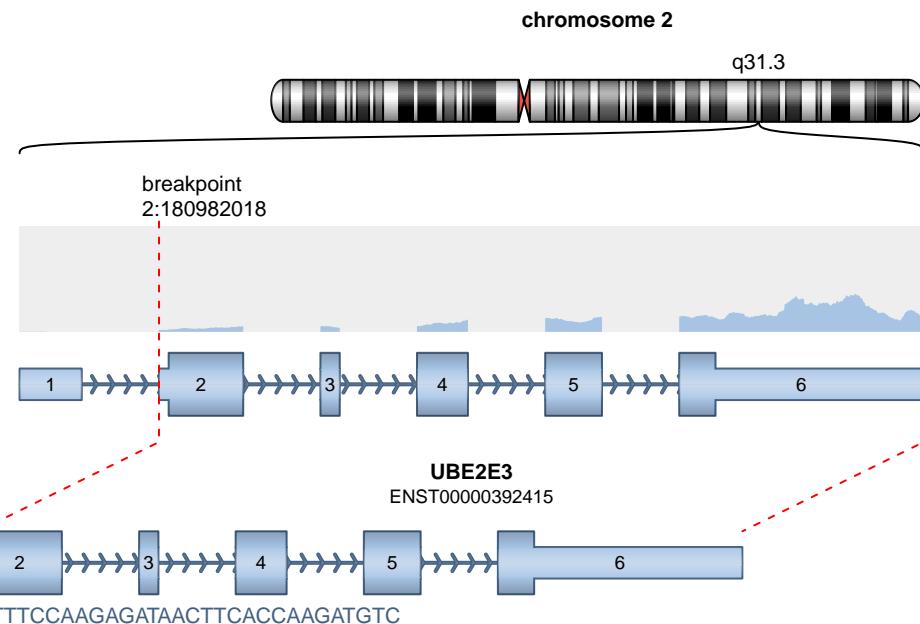
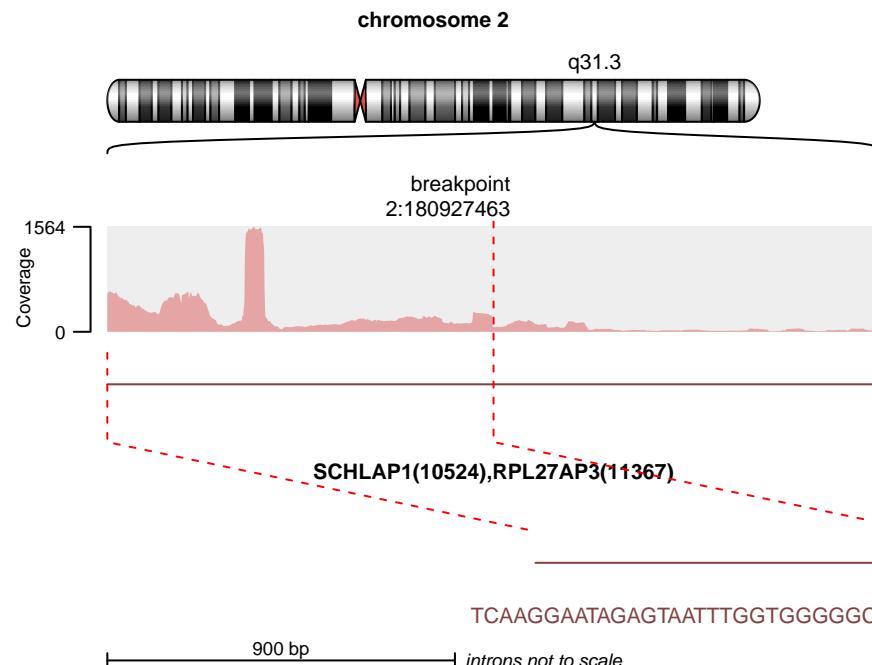
— translocation — deletion
— duplication — inversion



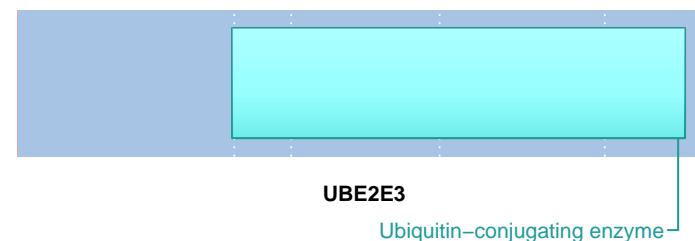
SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 2

— translocation — deletion
— duplication — inversion



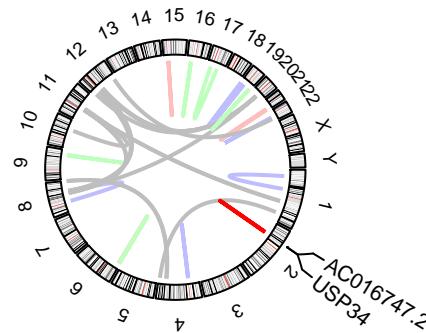
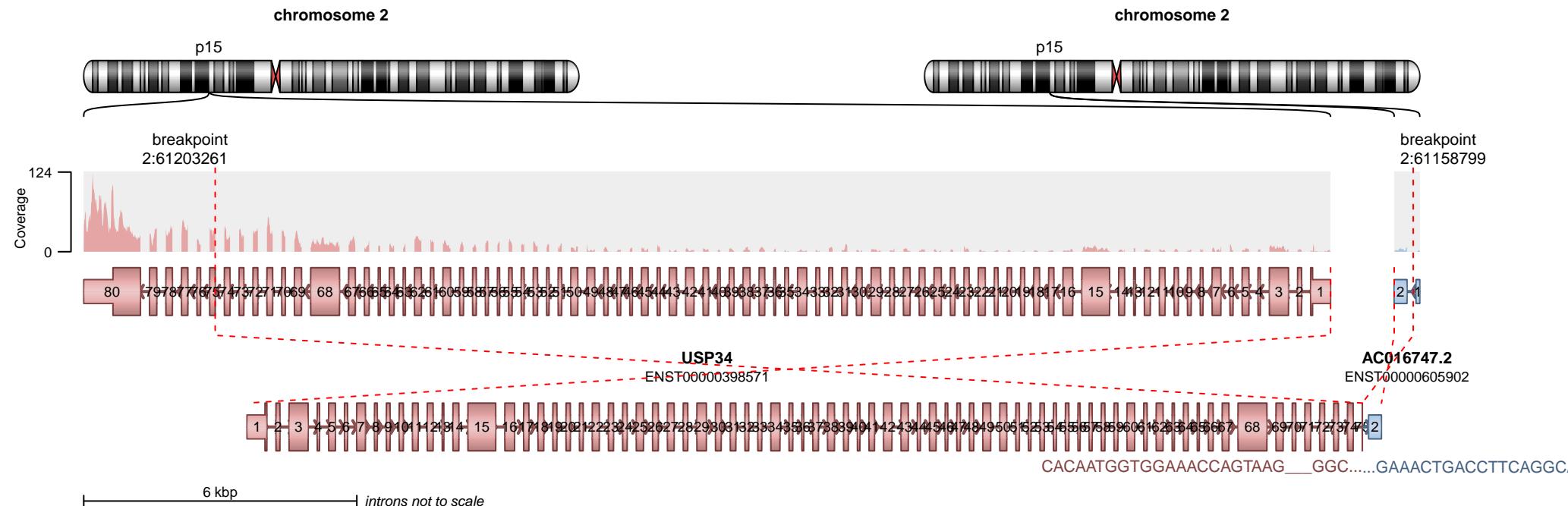
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

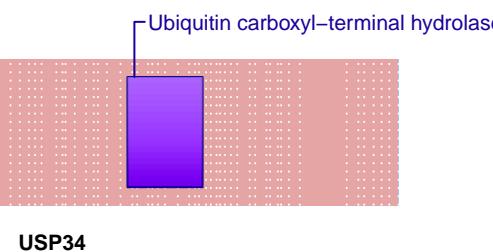
Split reads = 1
Discordant mates = 1

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS

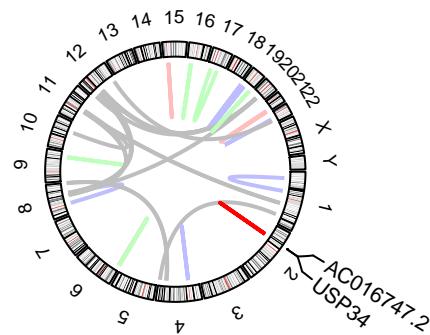
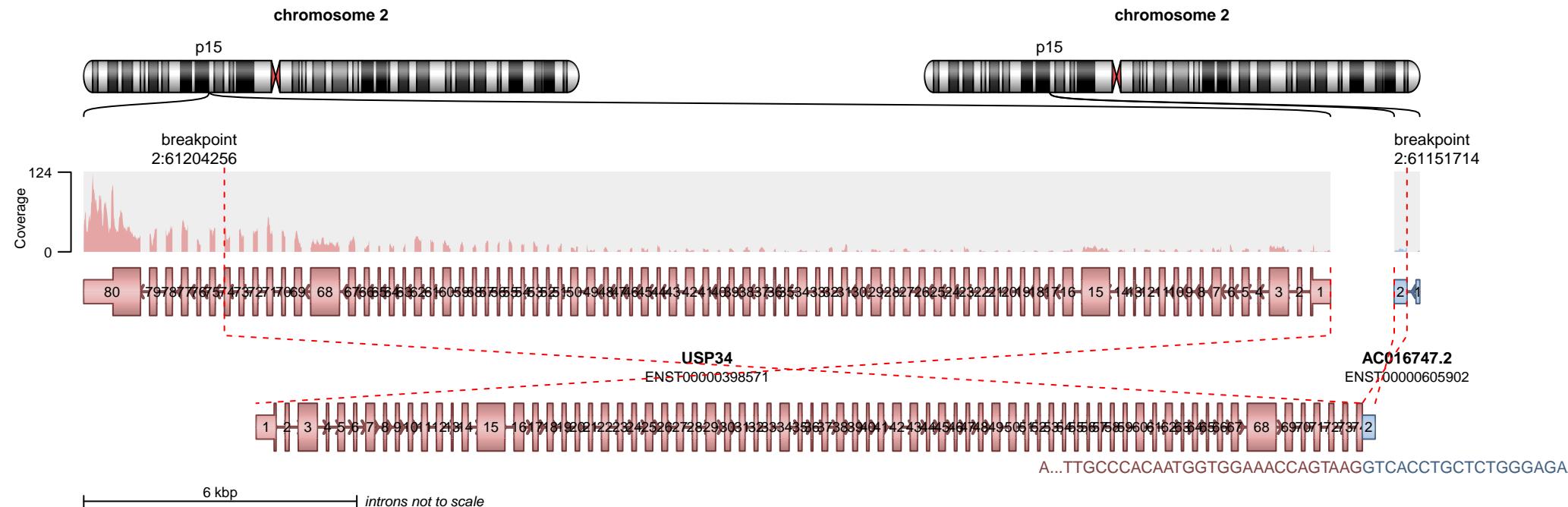
reading frame unclear



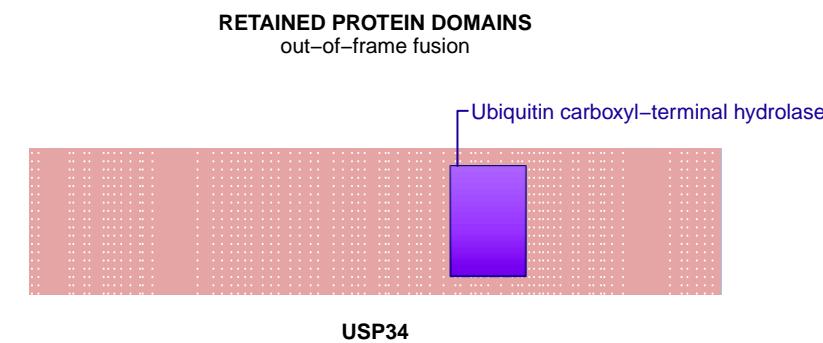
SUPPORTING READ COUNT

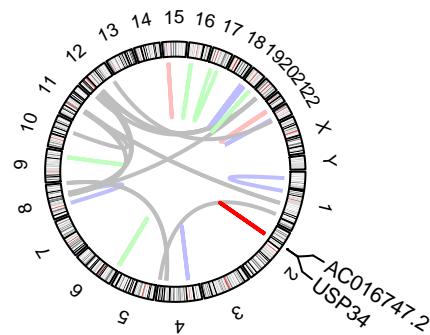
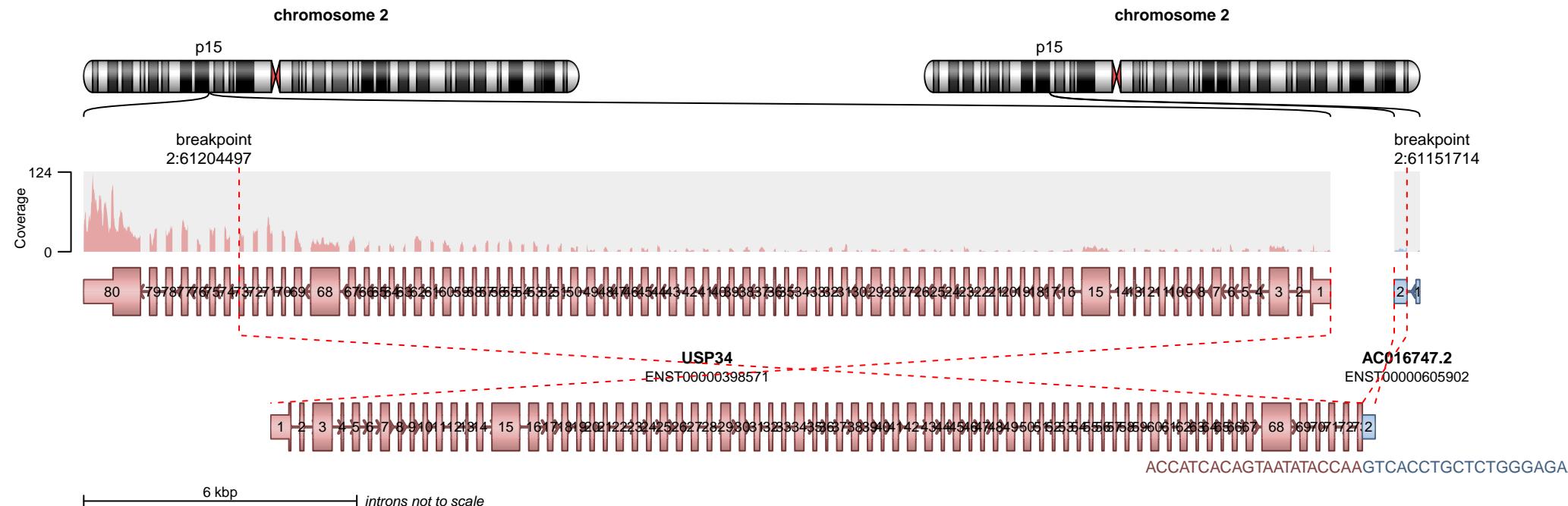
Split reads = 0
Discordant mates = 2

— translocation — deletion
— duplication — inversion

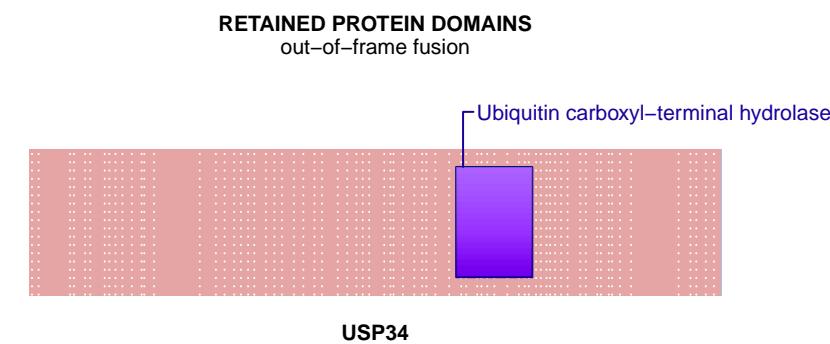


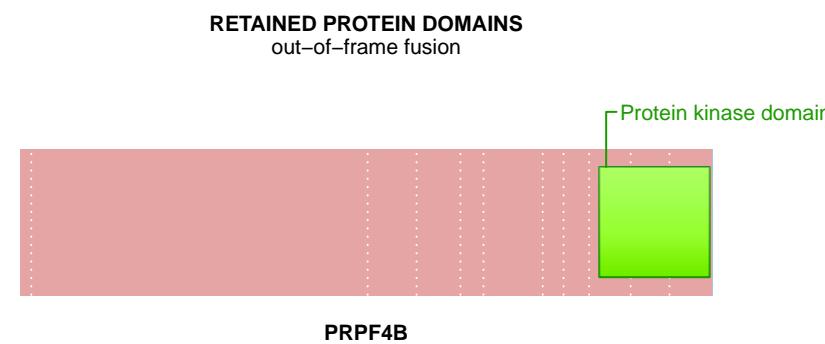
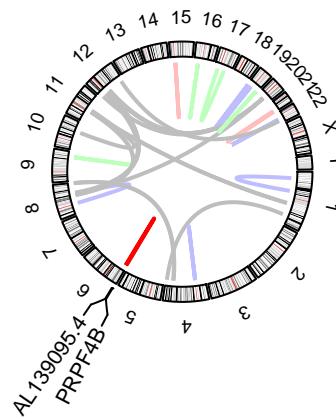
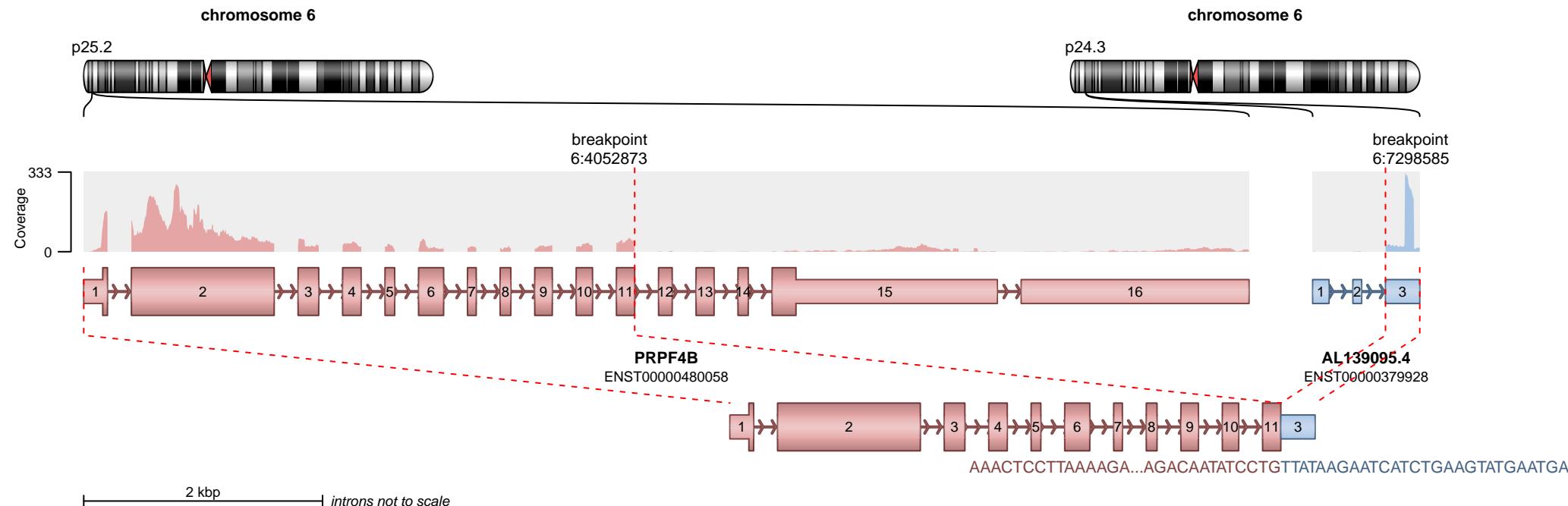
— translocation — deletion
— duplication — inversion



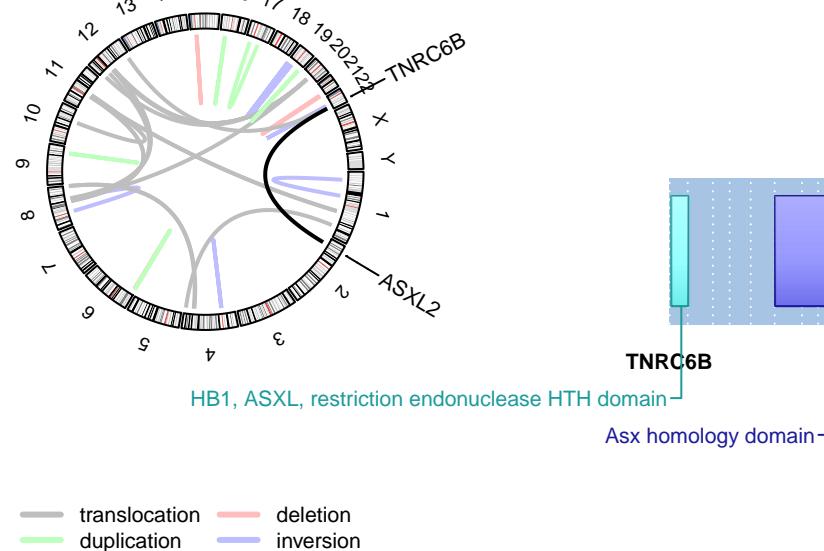
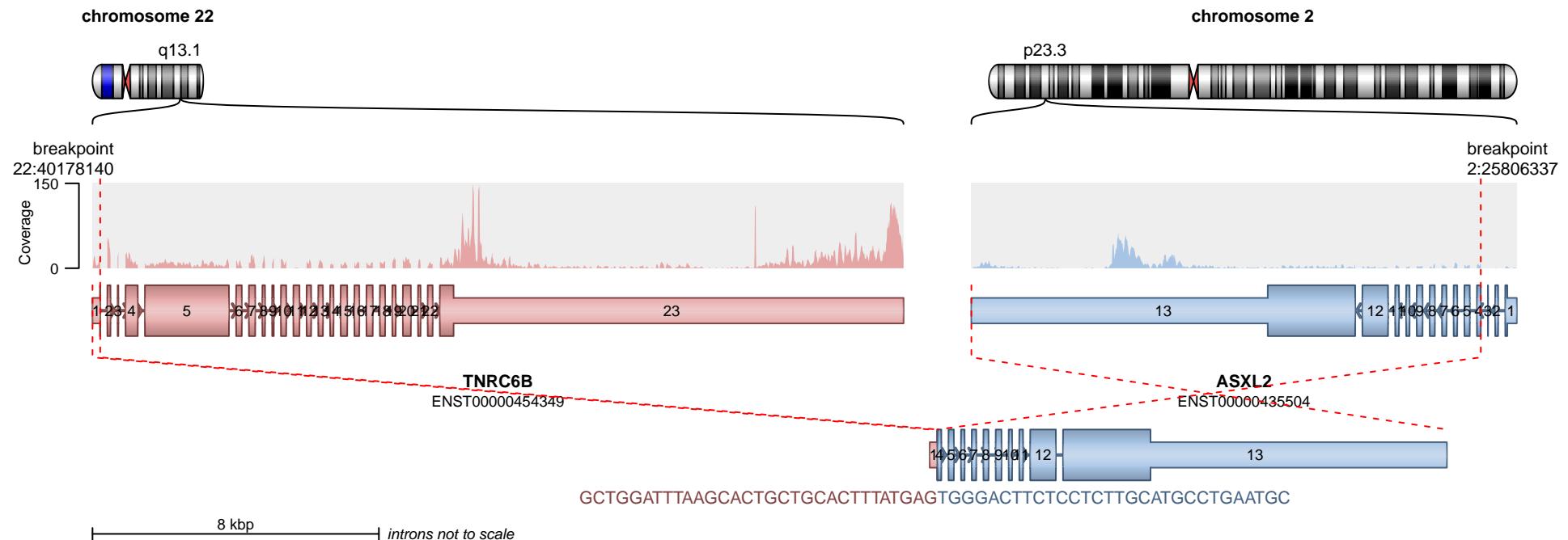


— translocation — deletion
— duplication — inversion





— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS in-frame fusion

PHD domain of transcriptional enhancer, Asx

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1