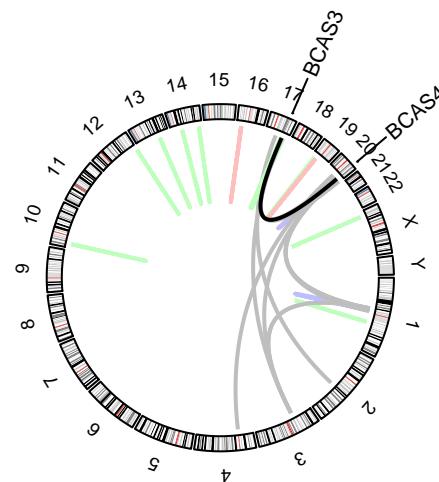
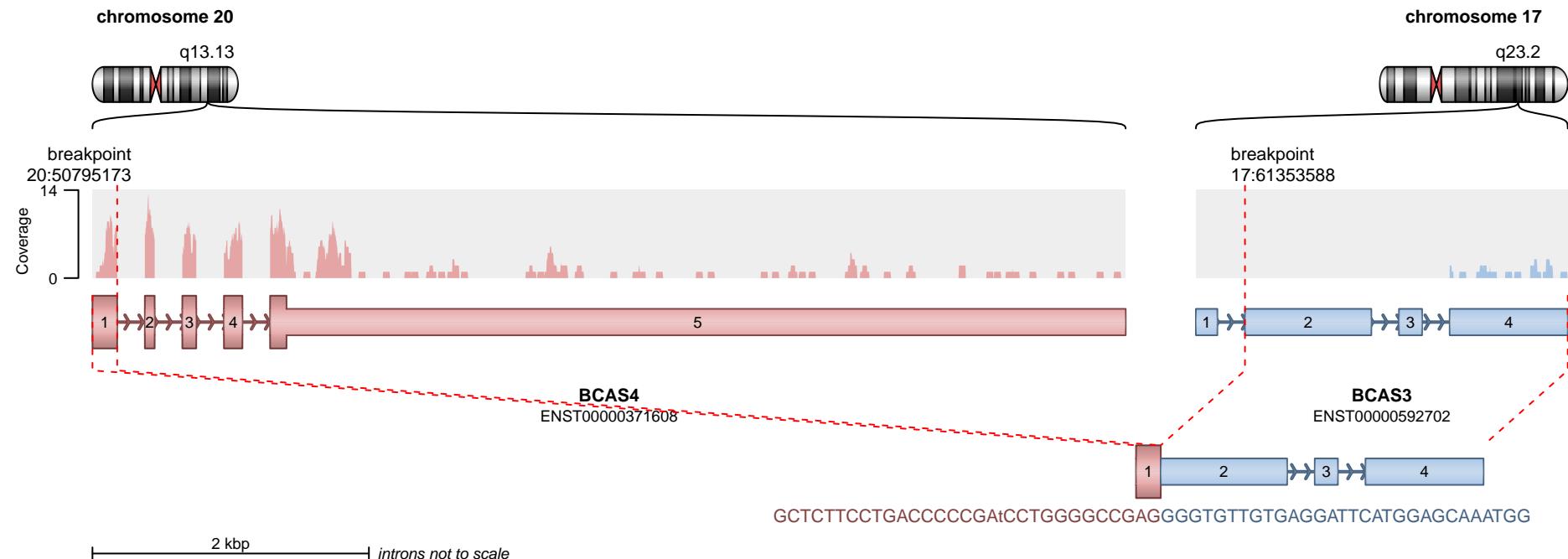


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 17
Discordant mates = 136

— translocation — deletion
— duplication — inversion

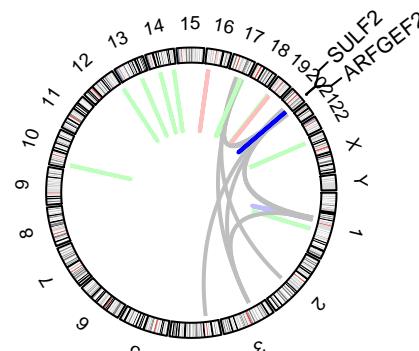
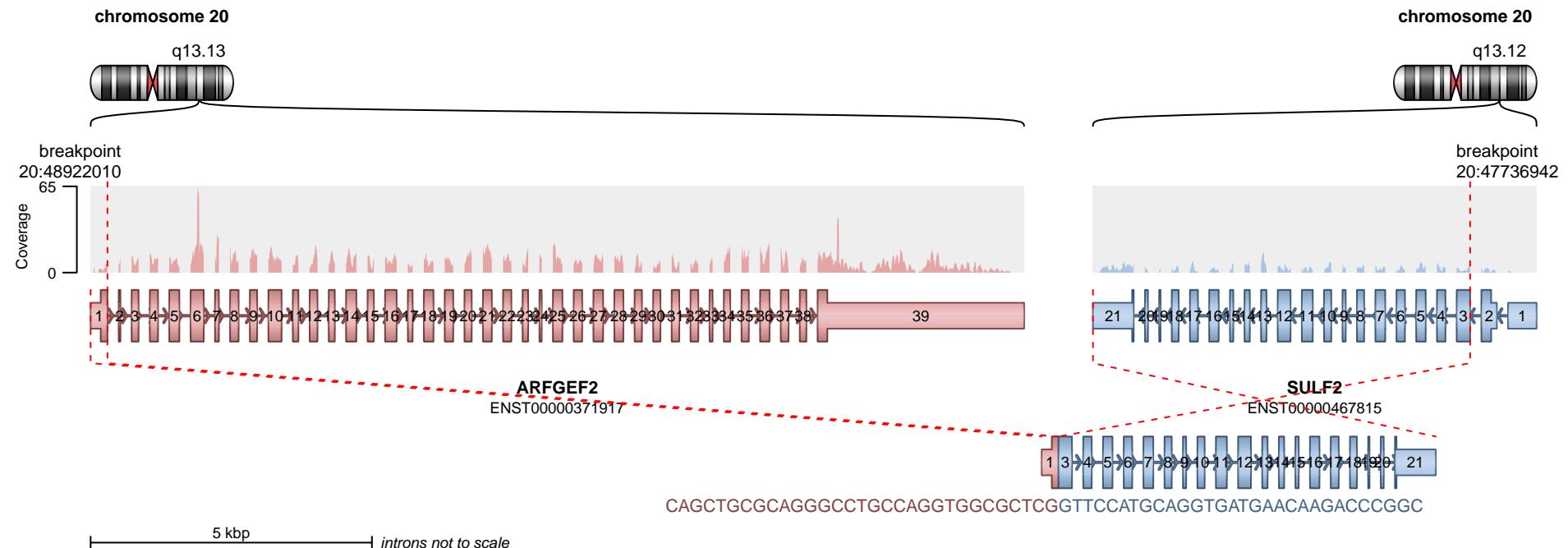


No protein domains retained in fusion.

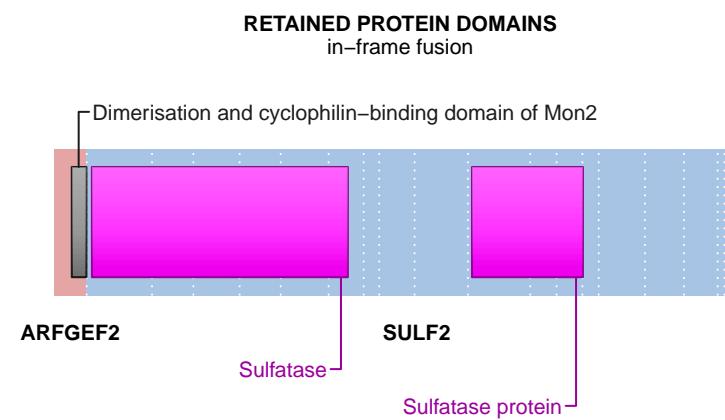
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 164

— translocation — deletion
— duplication — inversion

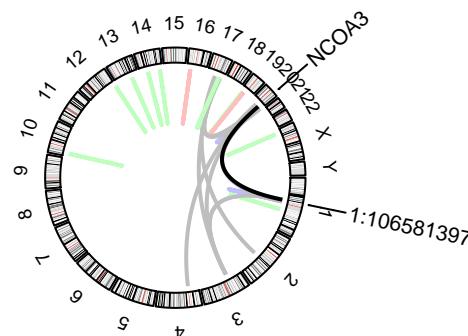
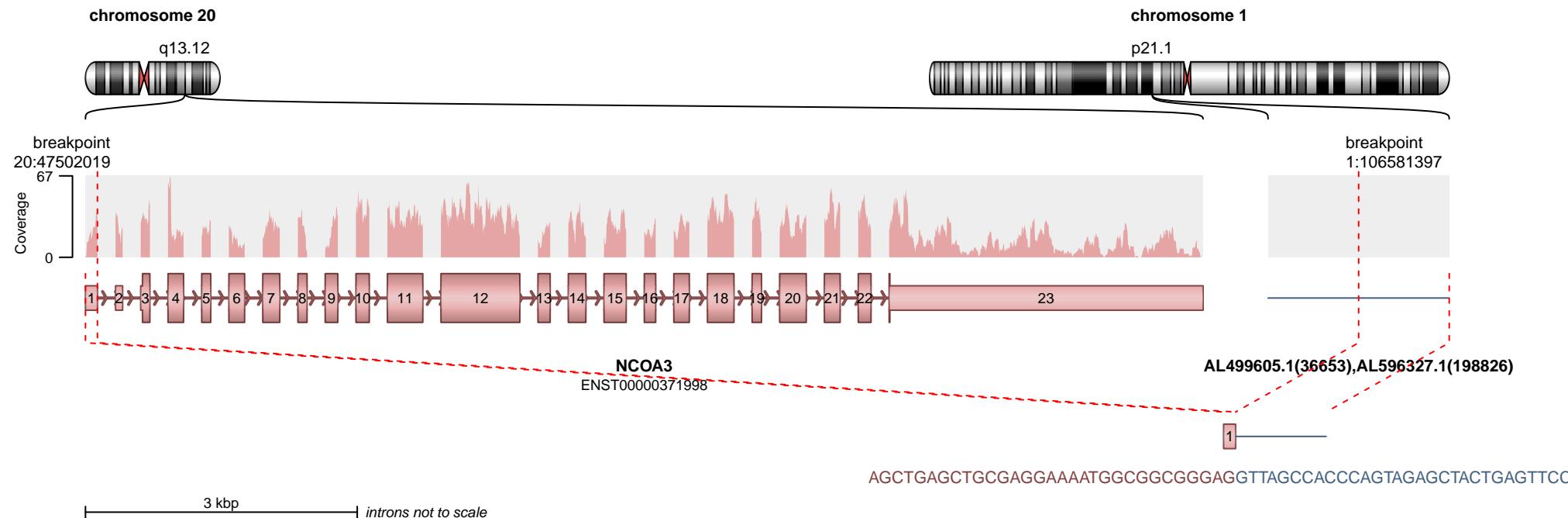


— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 14
Discordant mates = 12

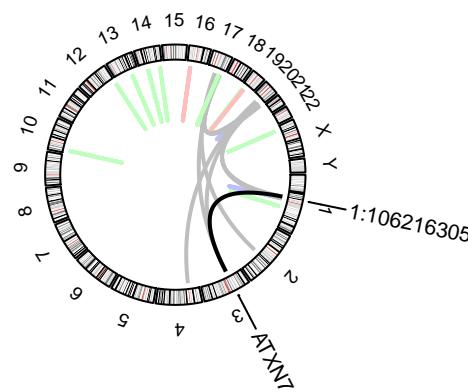
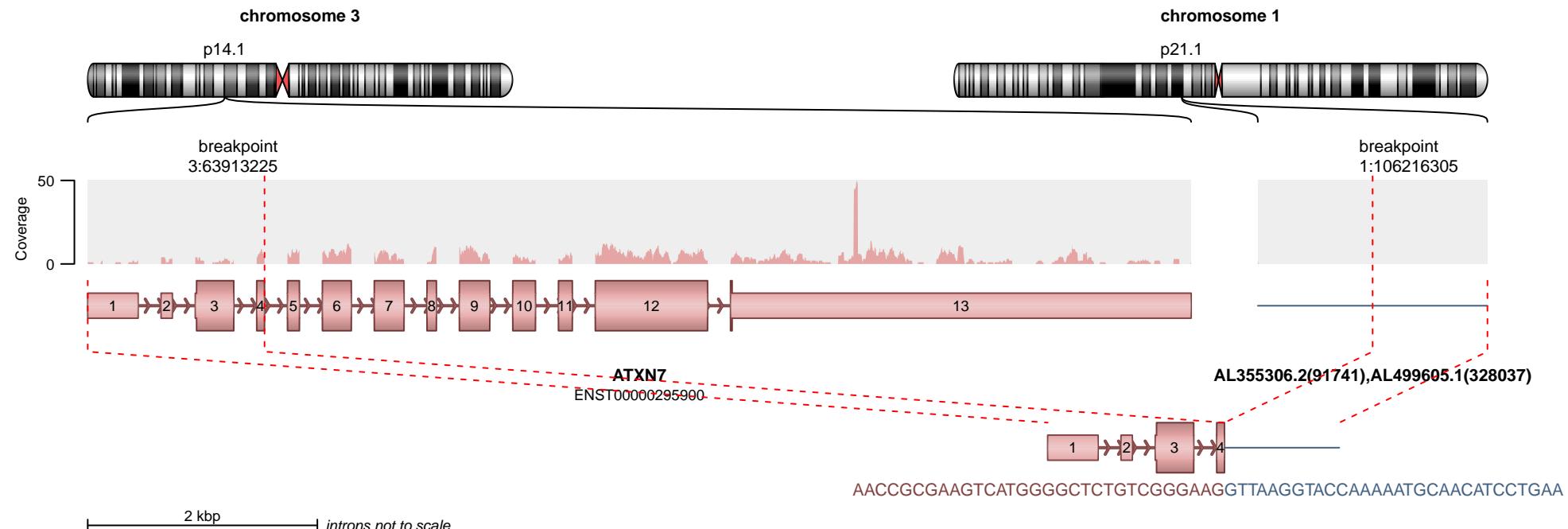


No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 10

— translocation — deletion
— duplication — inversion

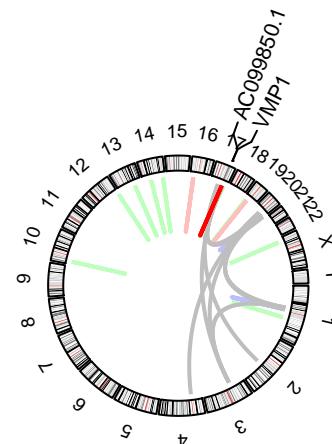
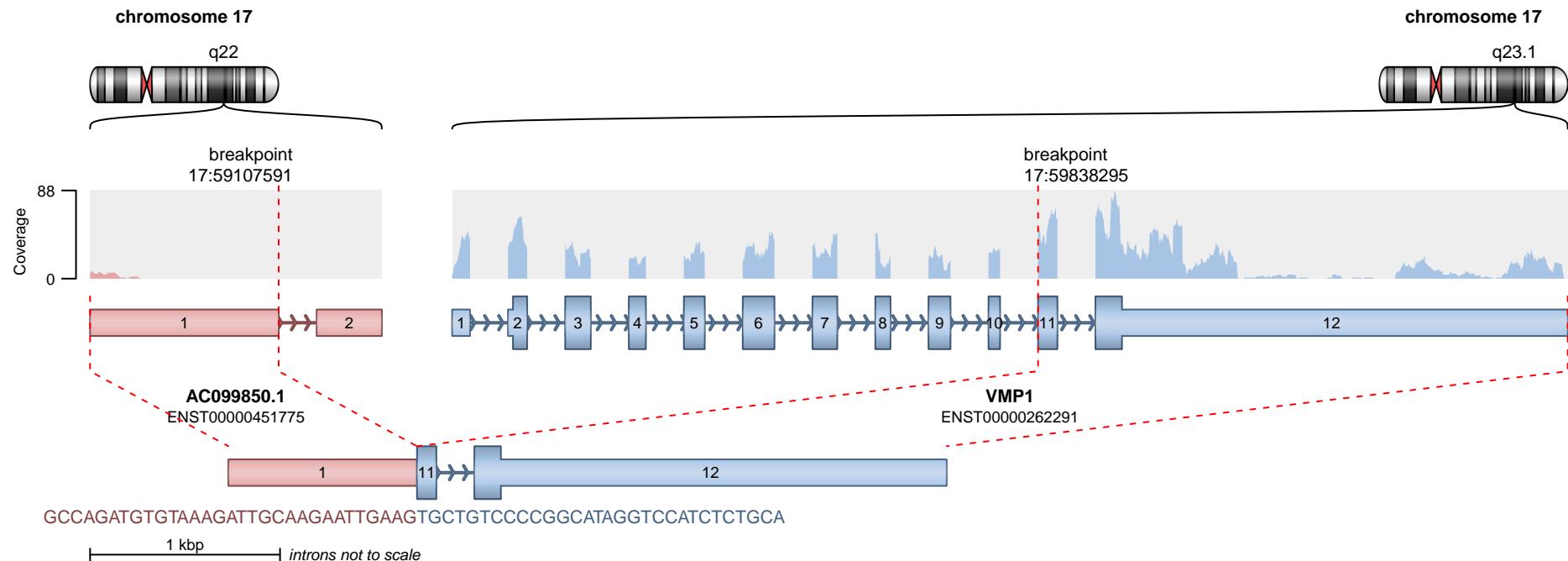


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 13

— translocation — deletion
— duplication — inversion



No protein domains retained in fusion.

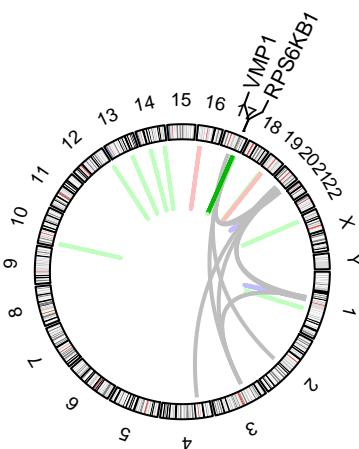
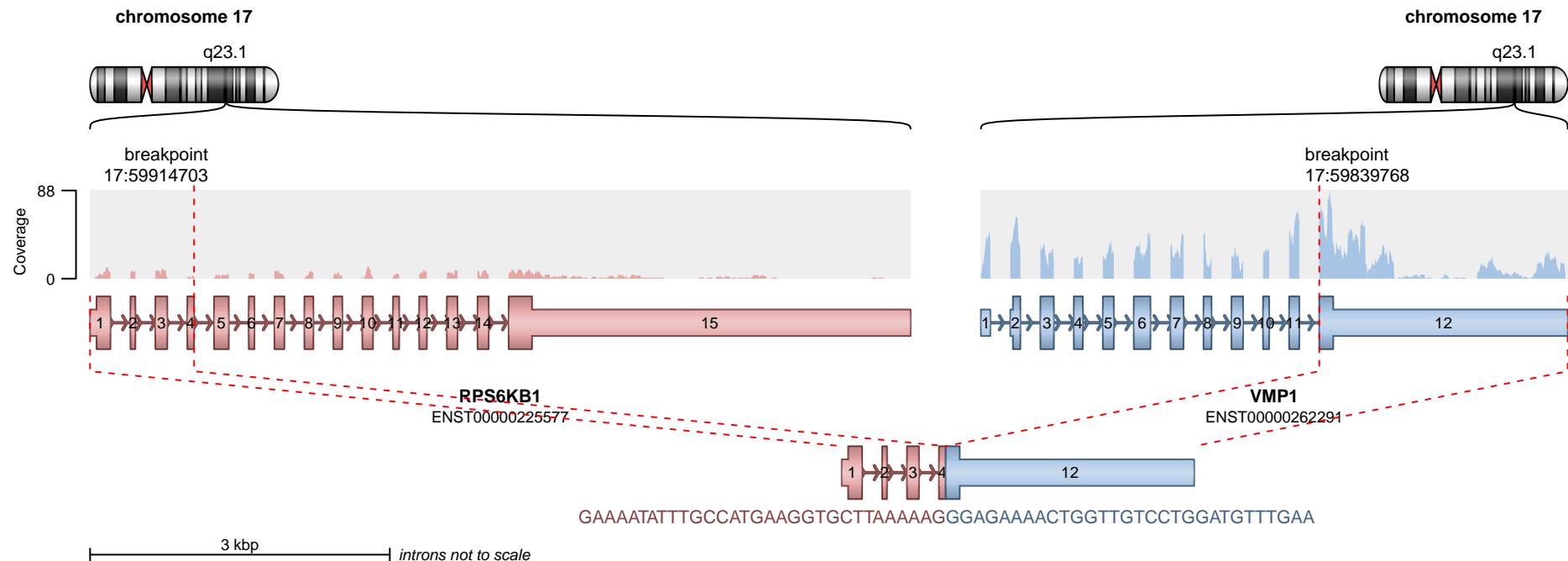
SUPPORTING READ COUNT

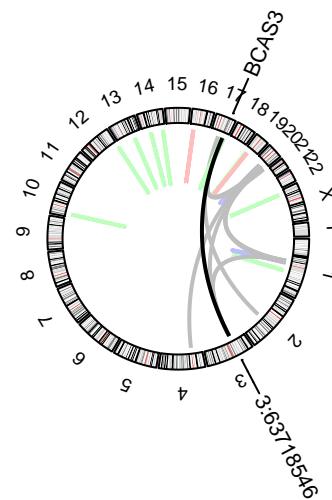
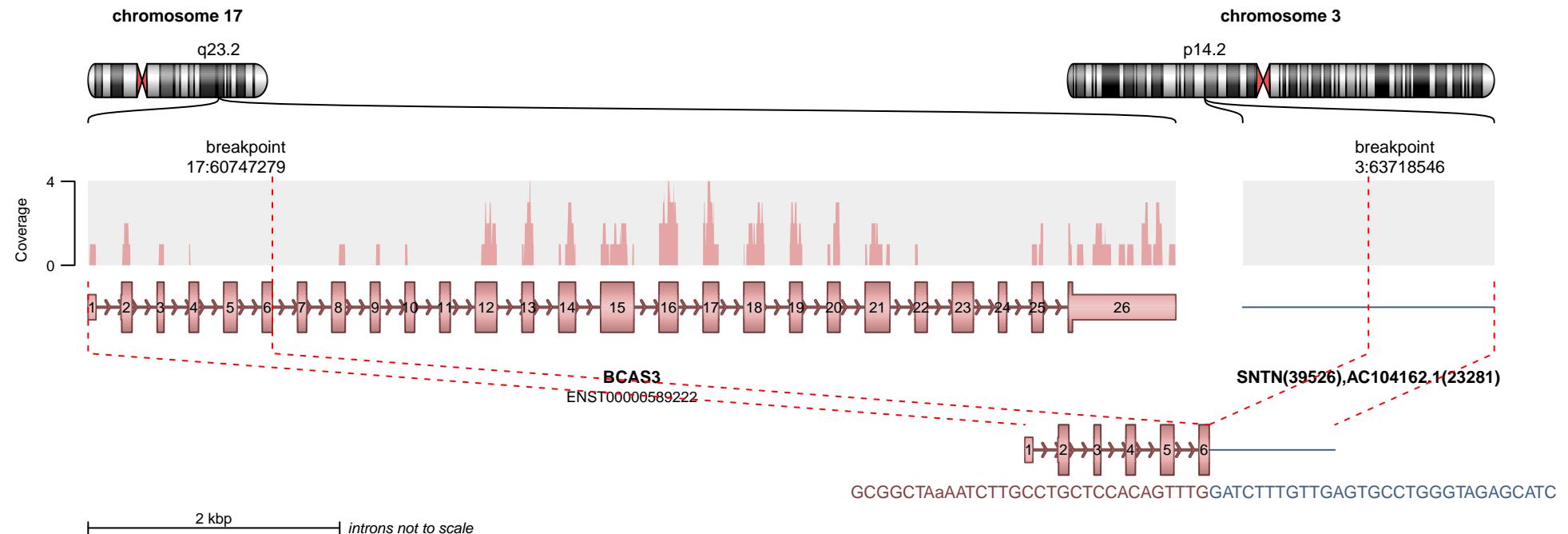
Split reads = 4
Discordant mates = 6

— translocation — deletion
— duplication — inversion

chromosome 17

q23.1



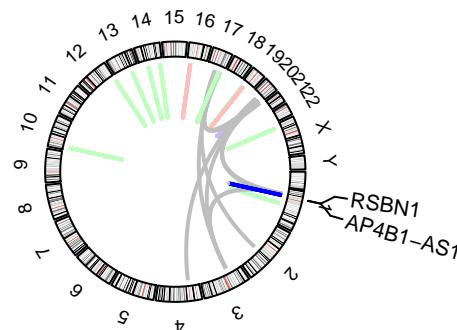
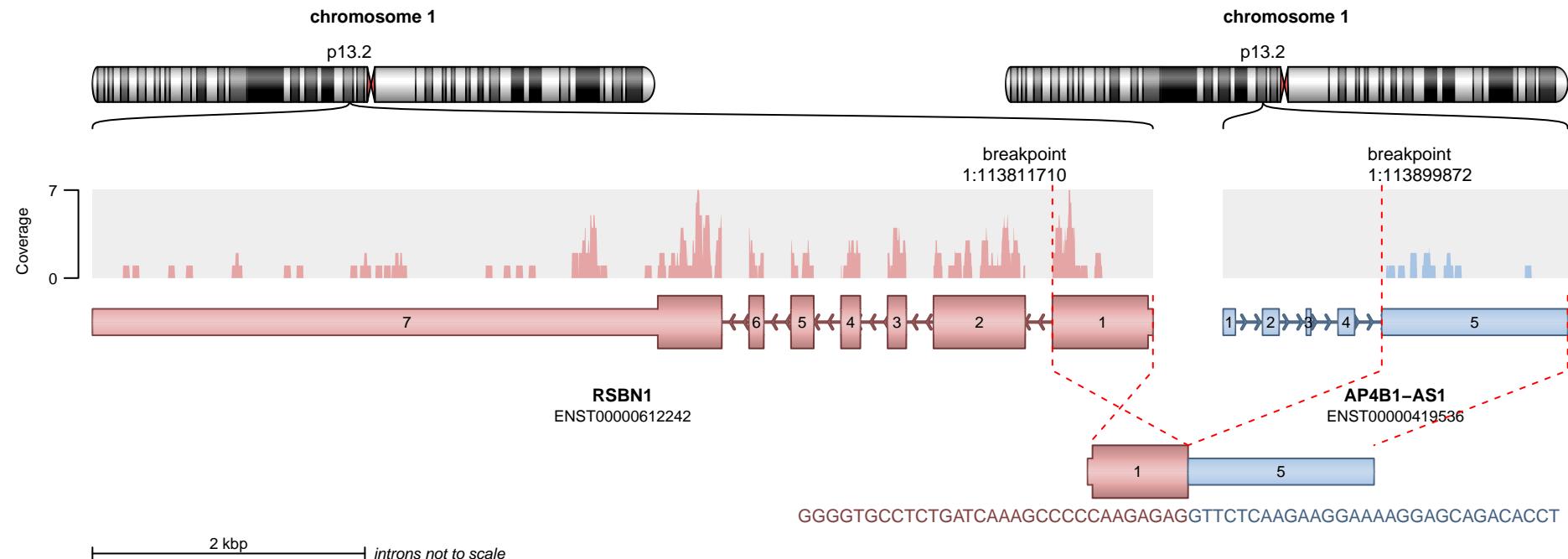


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 3

— translocation — deletion
— duplication — inversion

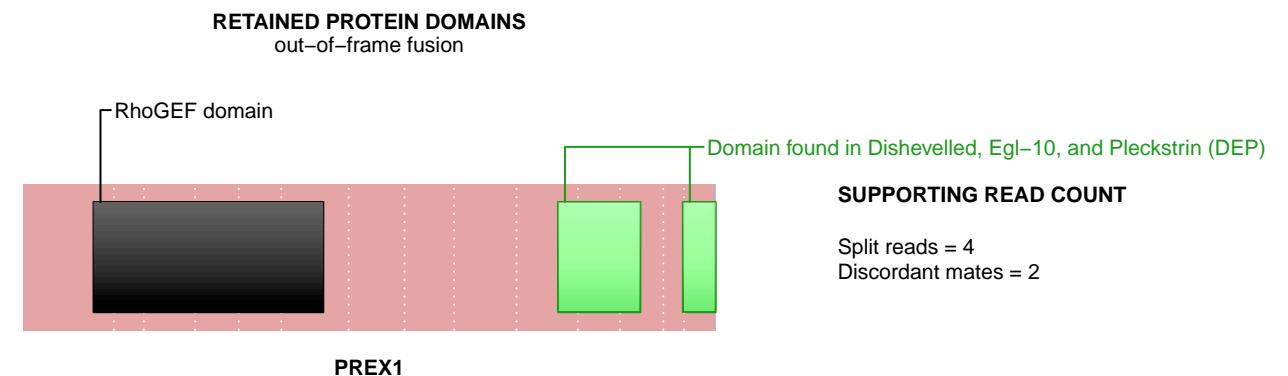
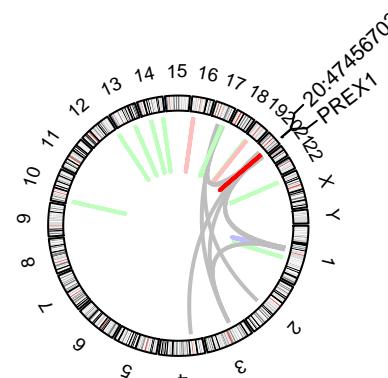
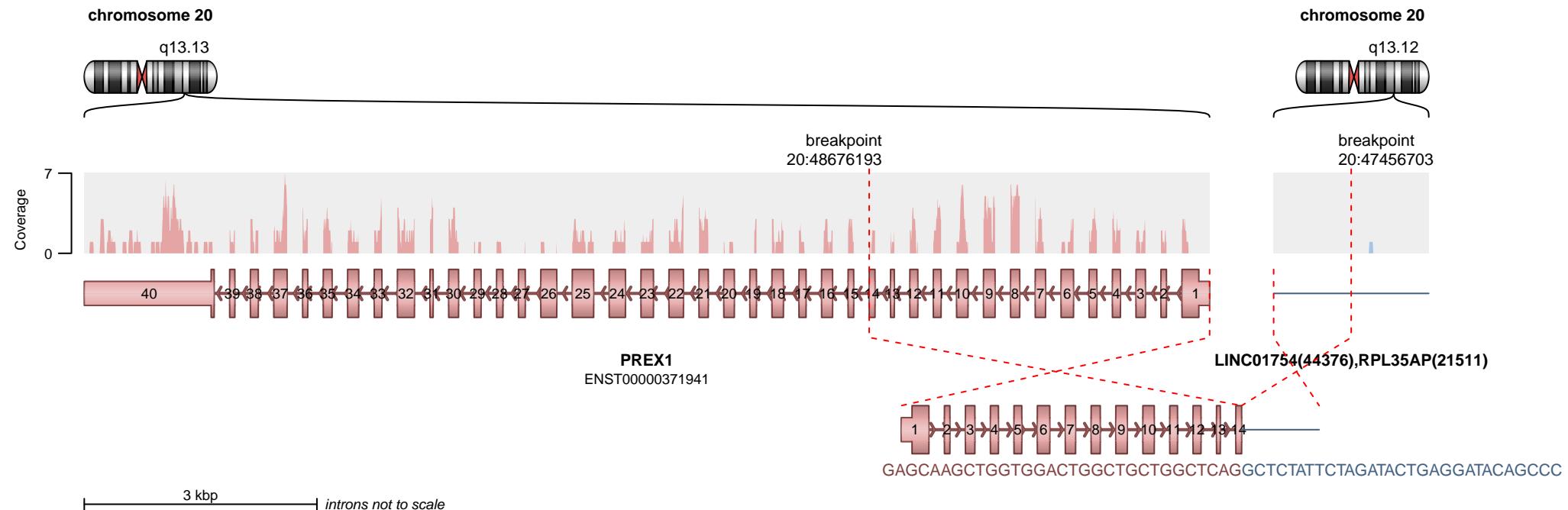


No protein domains retained in fusion.

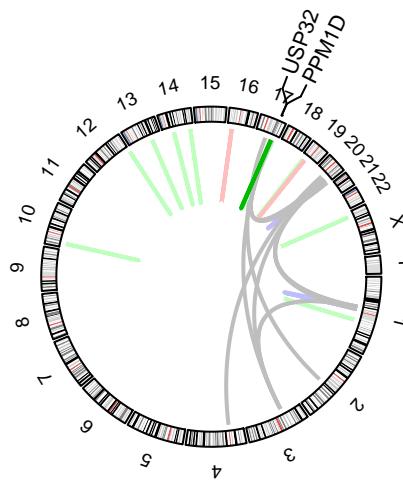
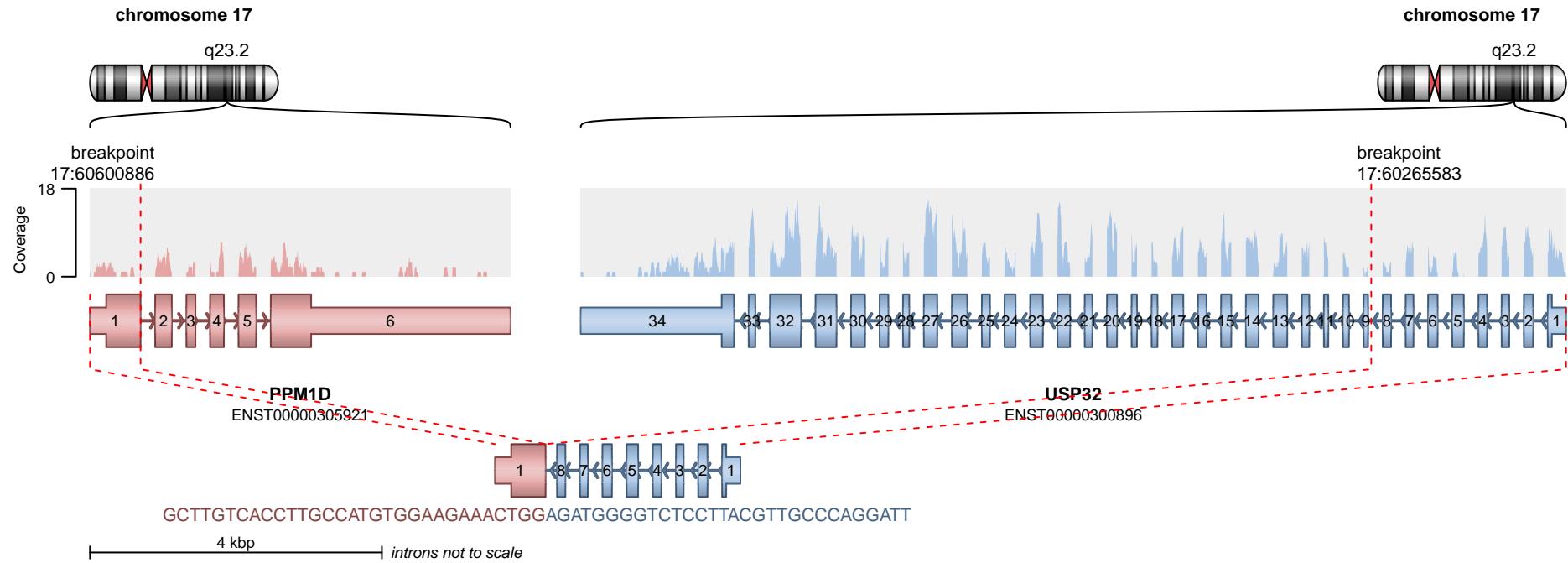
SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 2

— translocation — deletion
— duplication — inversion

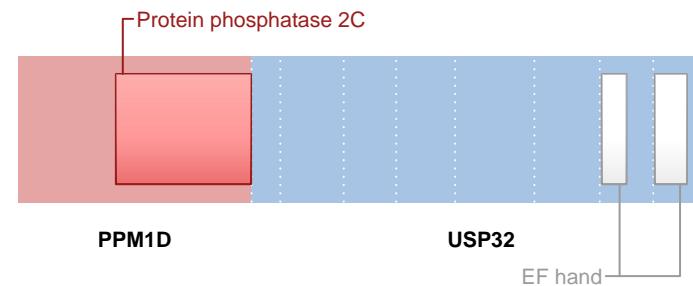


— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS out-of-frame fusion

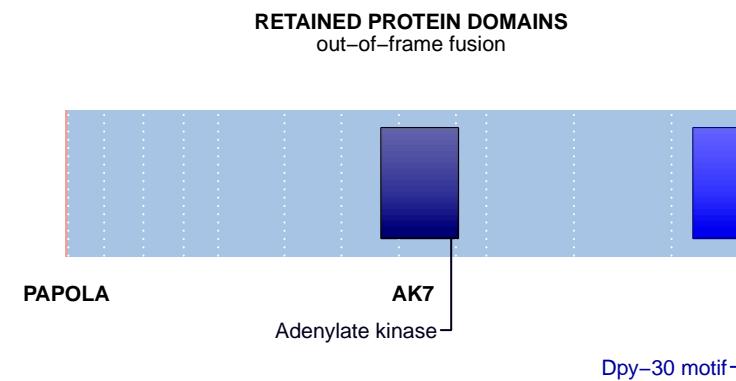
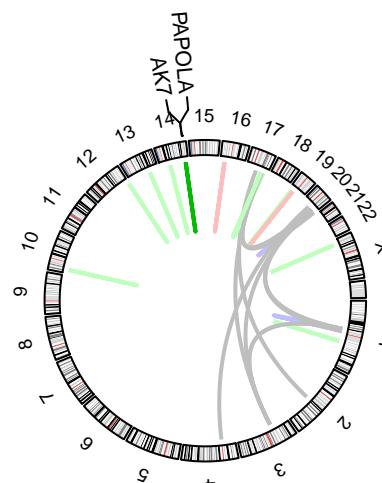
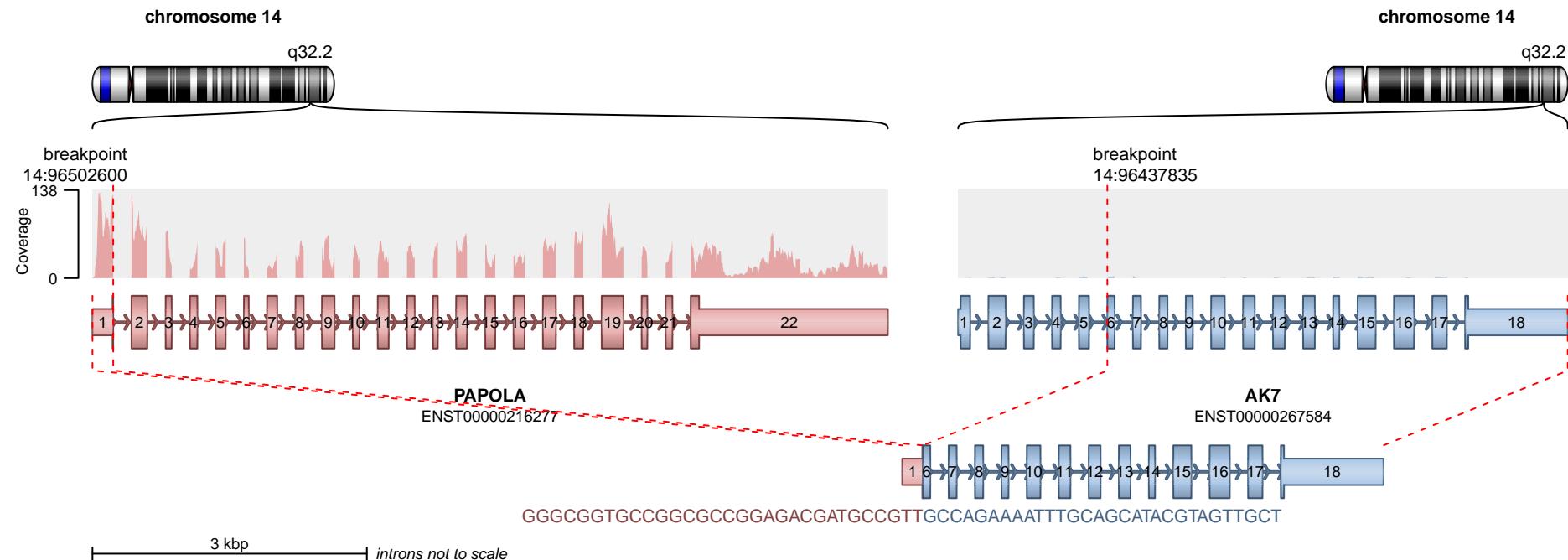
out-of-frame fusion



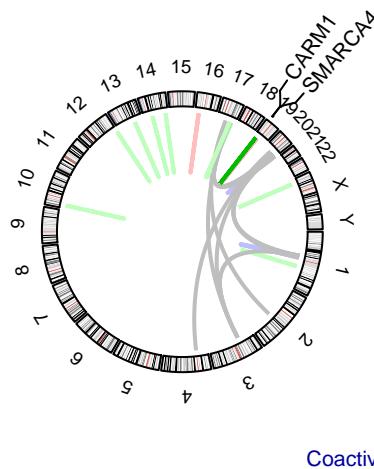
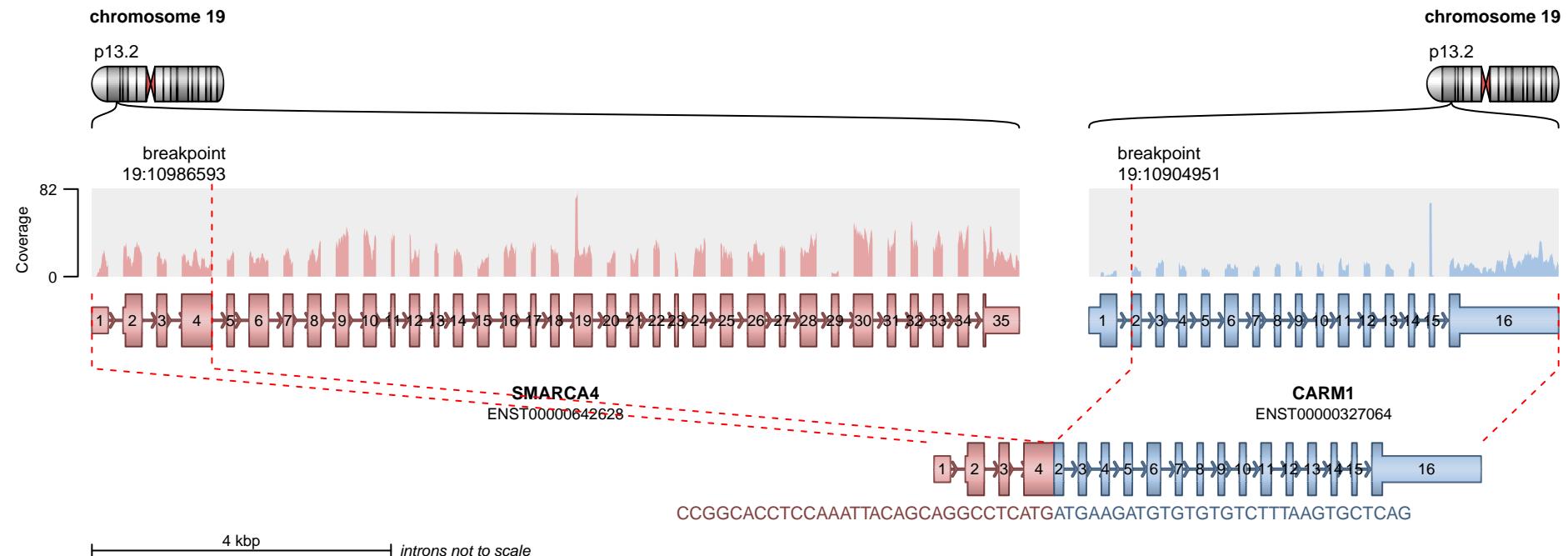
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 3

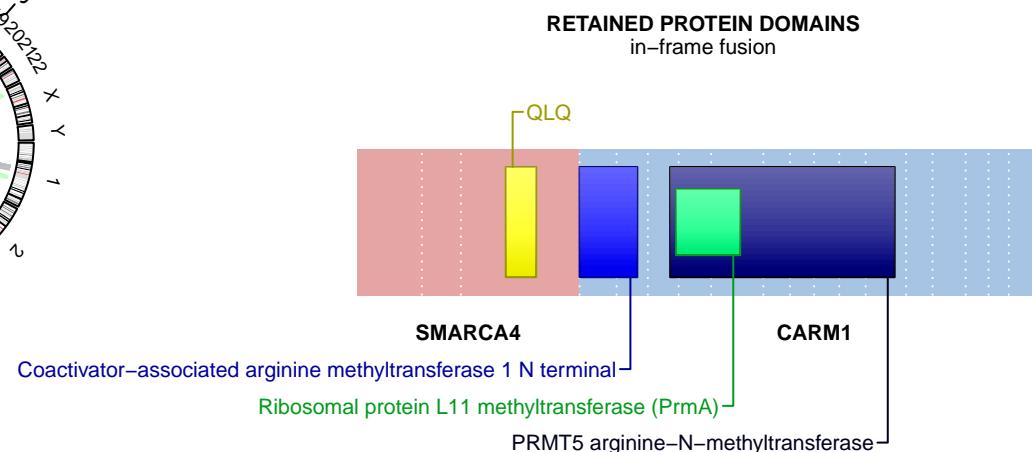
— translocation — deletion
— duplication — inversion



— translocation — deletion
— duplication — inversion

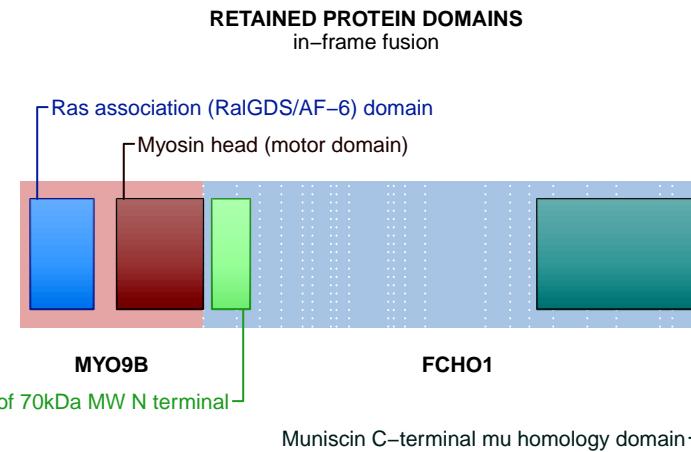
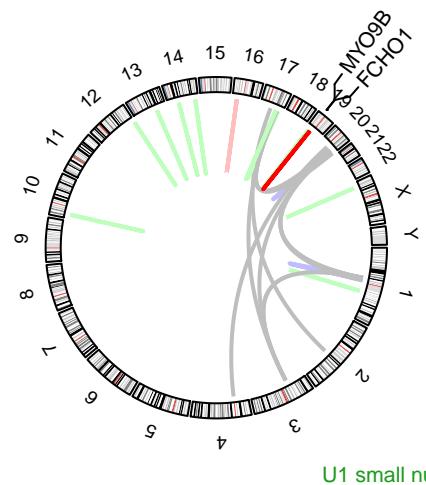
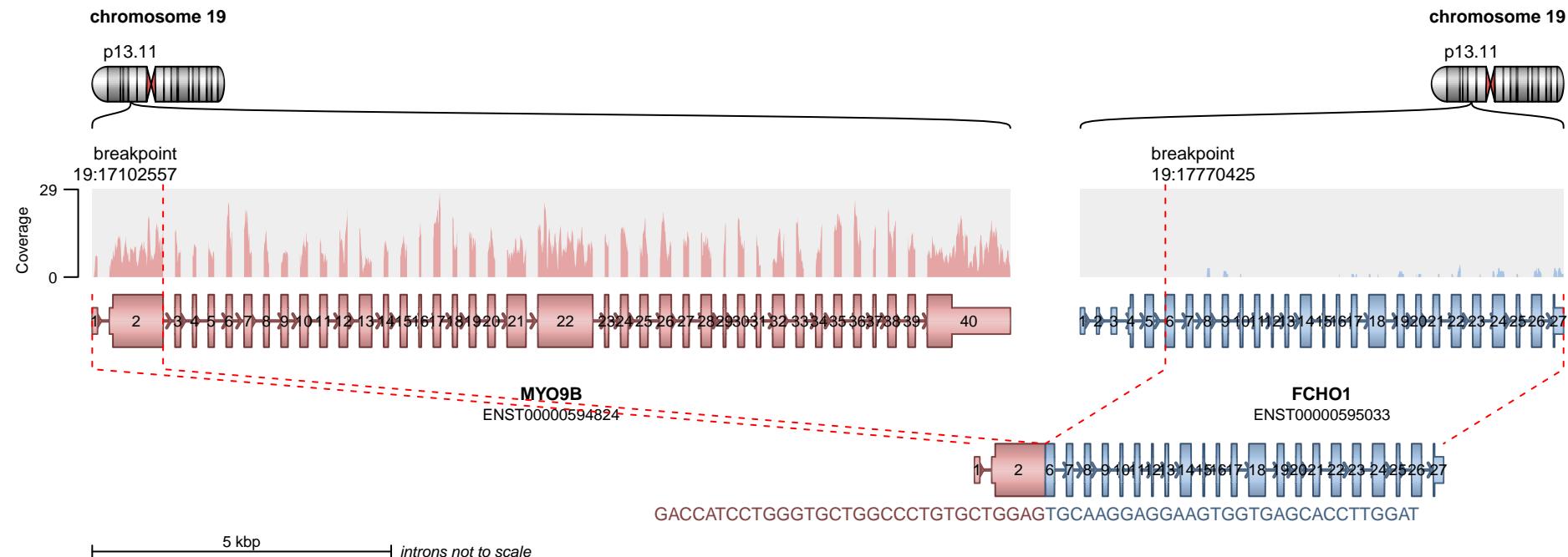


— translocation — deletion
— duplication — inversion

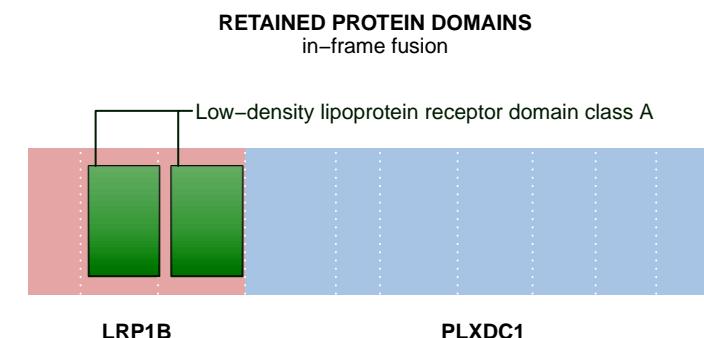
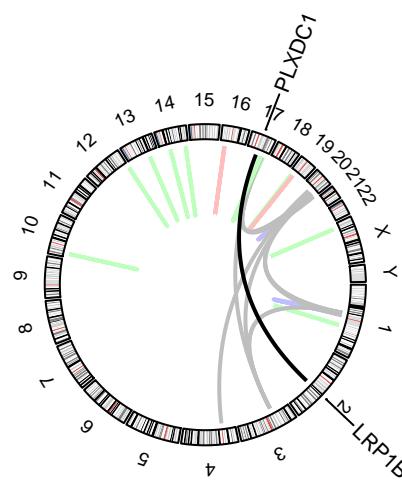
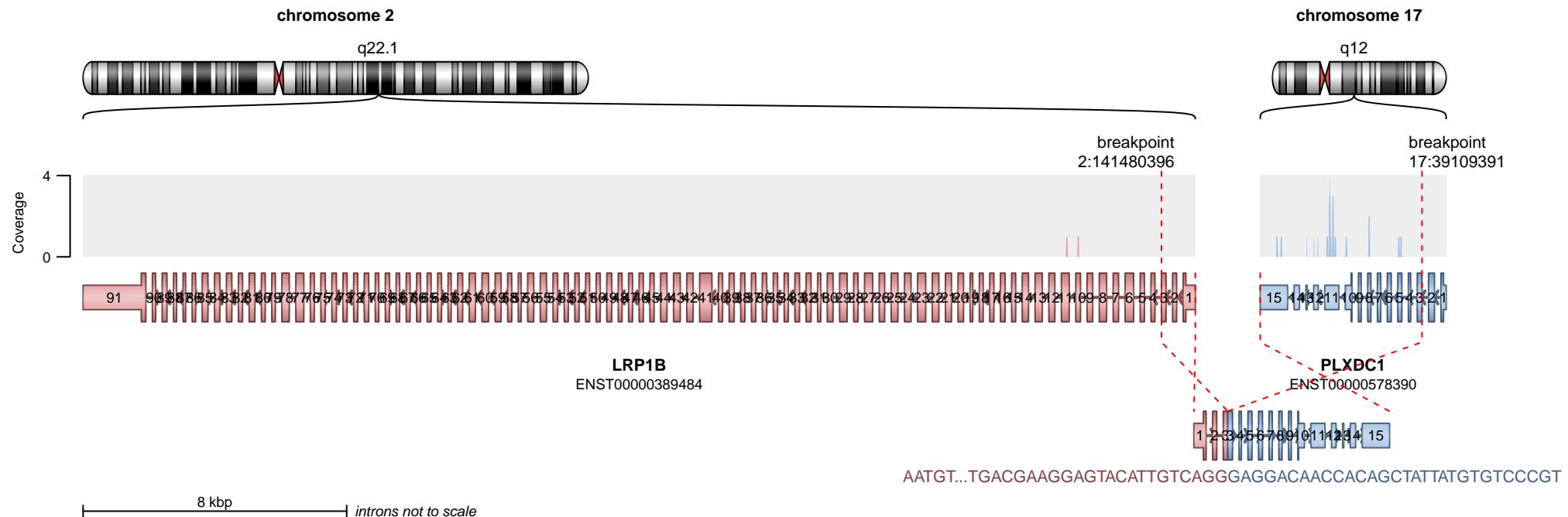


SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 3



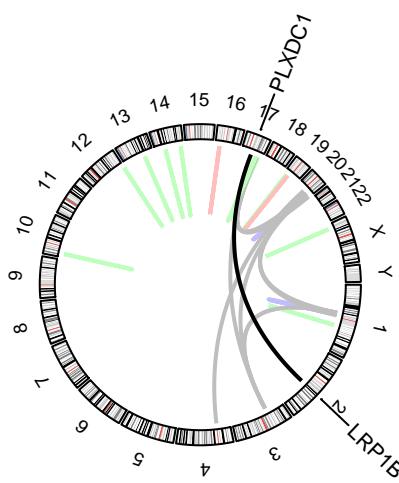
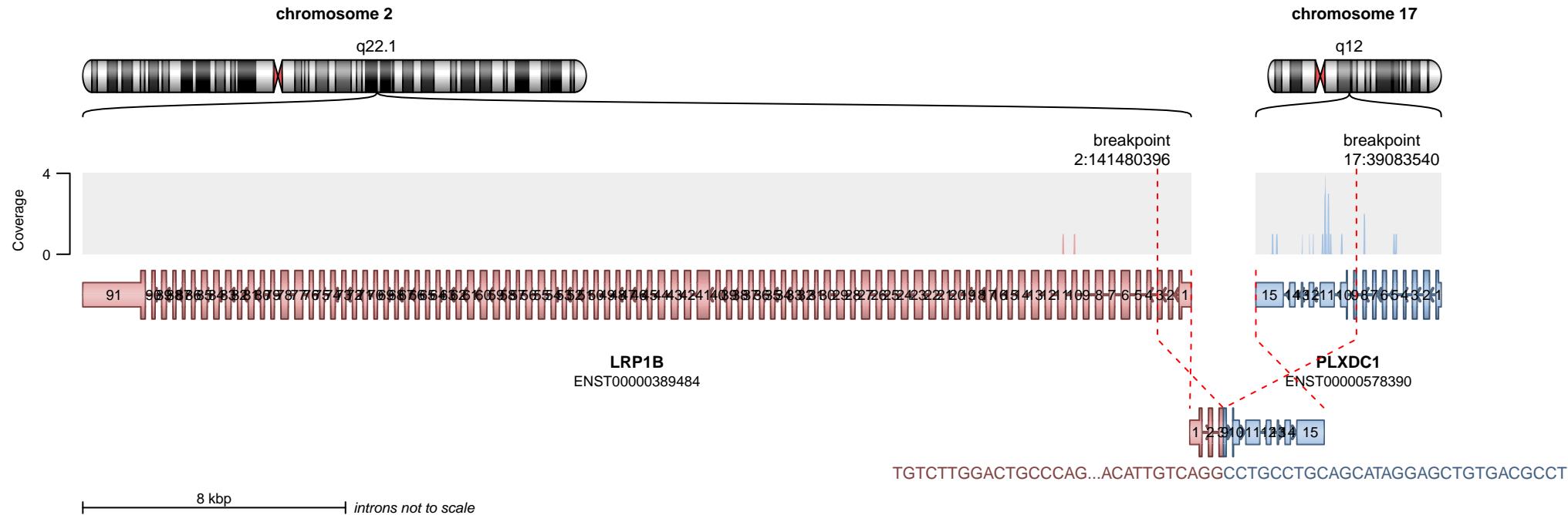
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 3

— translocation — deletion
— duplication — inversion



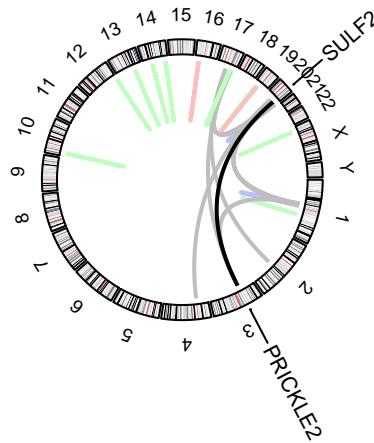
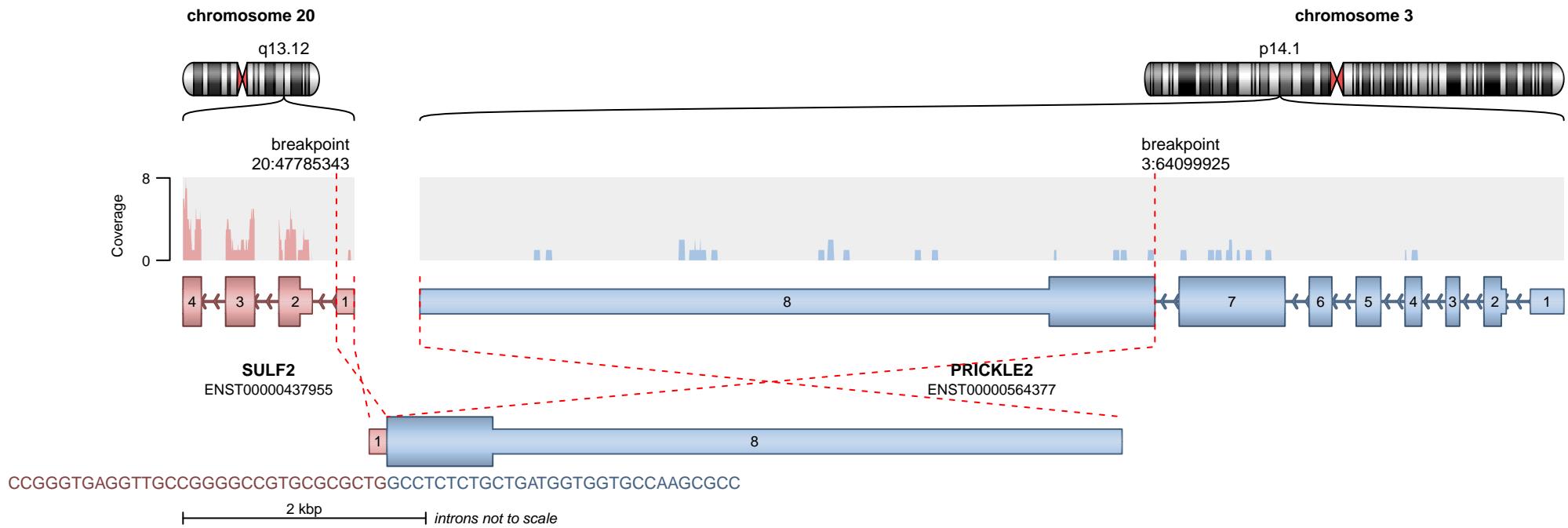
RETAINED PROTEIN DOMAINS in-frame fusion

— Low-density lipoprotein receptor domain class A

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion

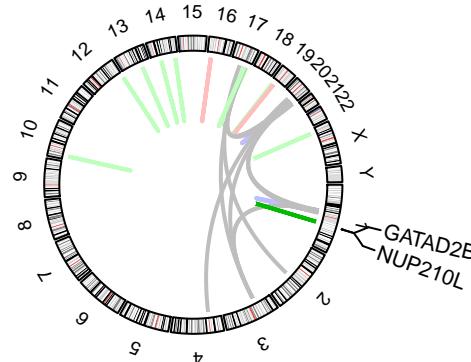
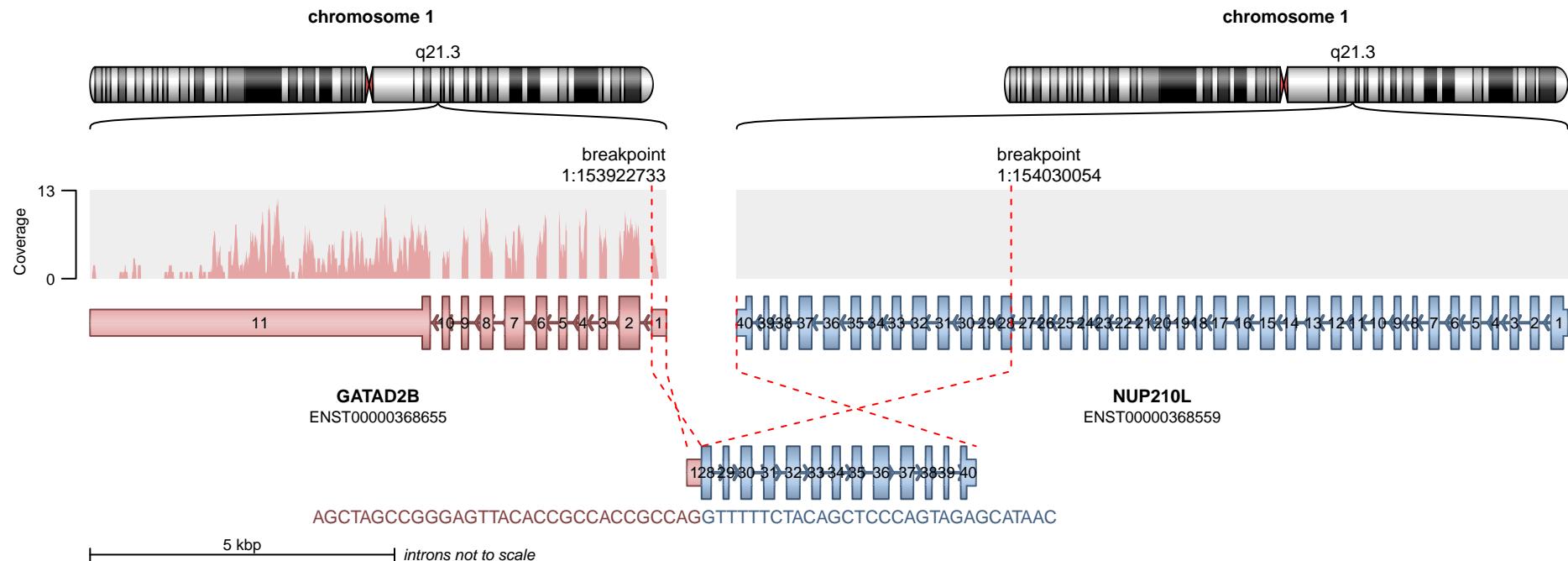


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 3

— translocation — deletion
— duplication — inversion

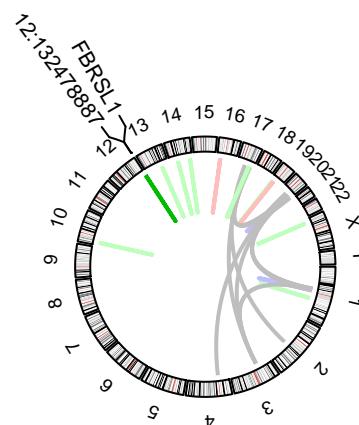
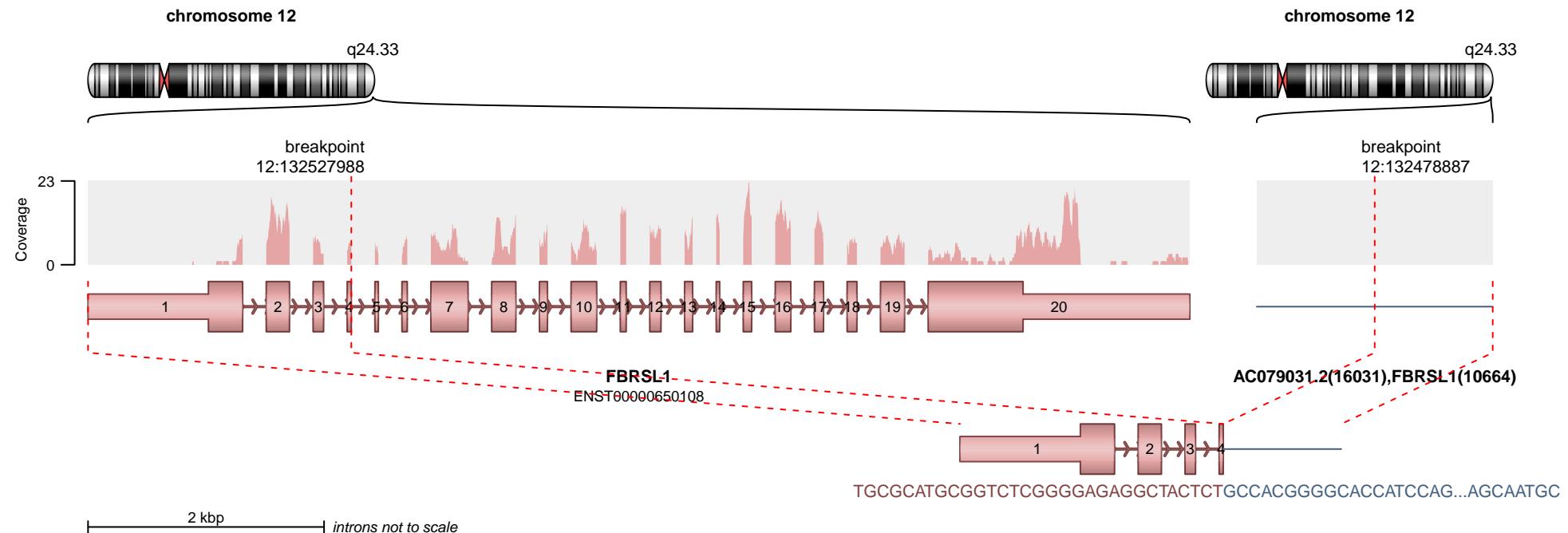


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 3

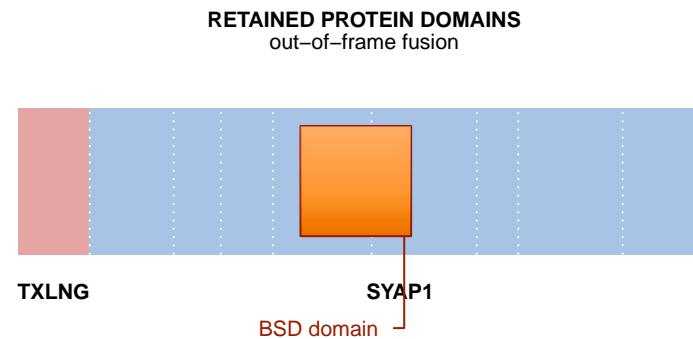
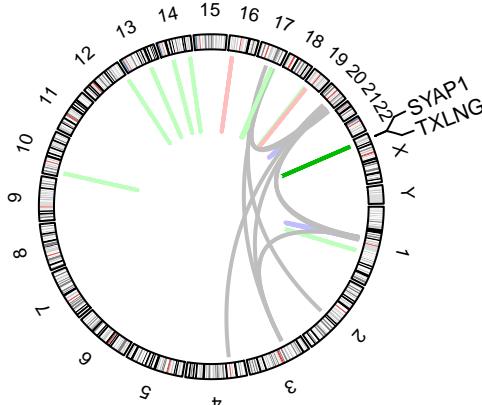
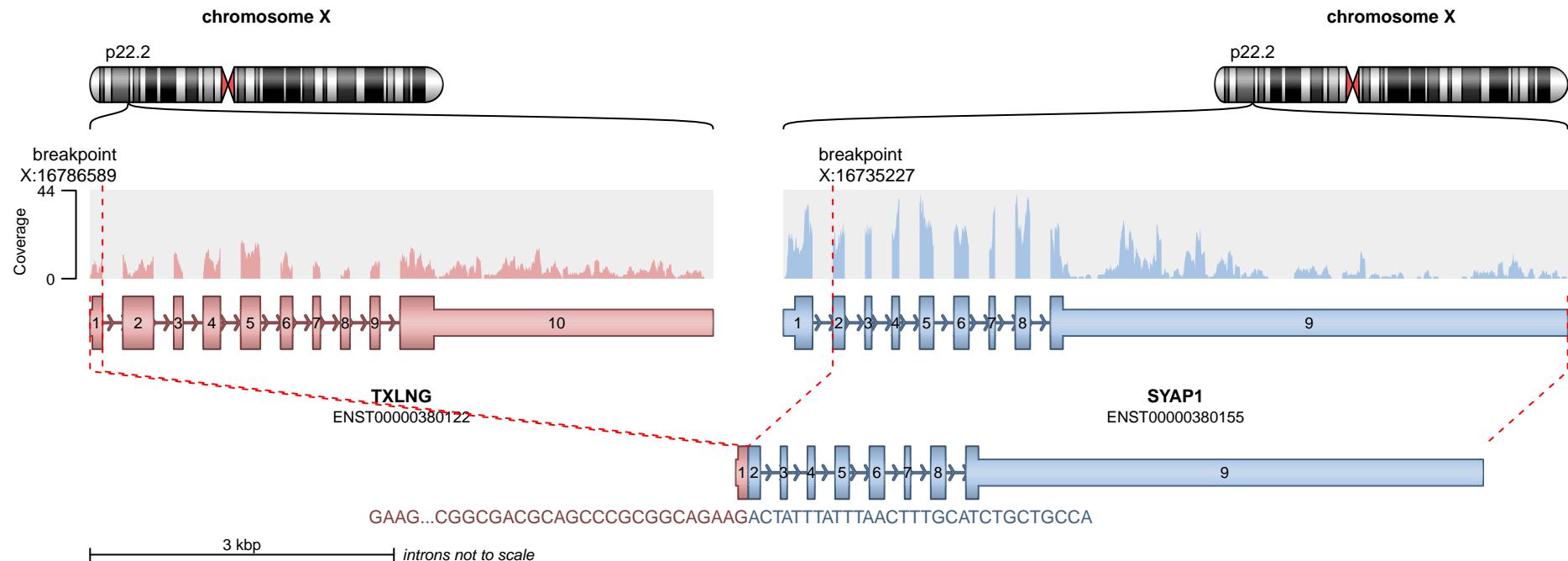


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 3

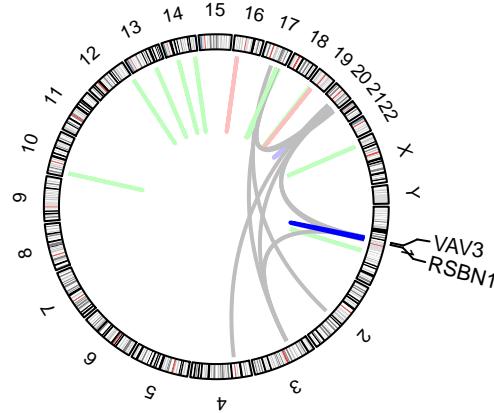
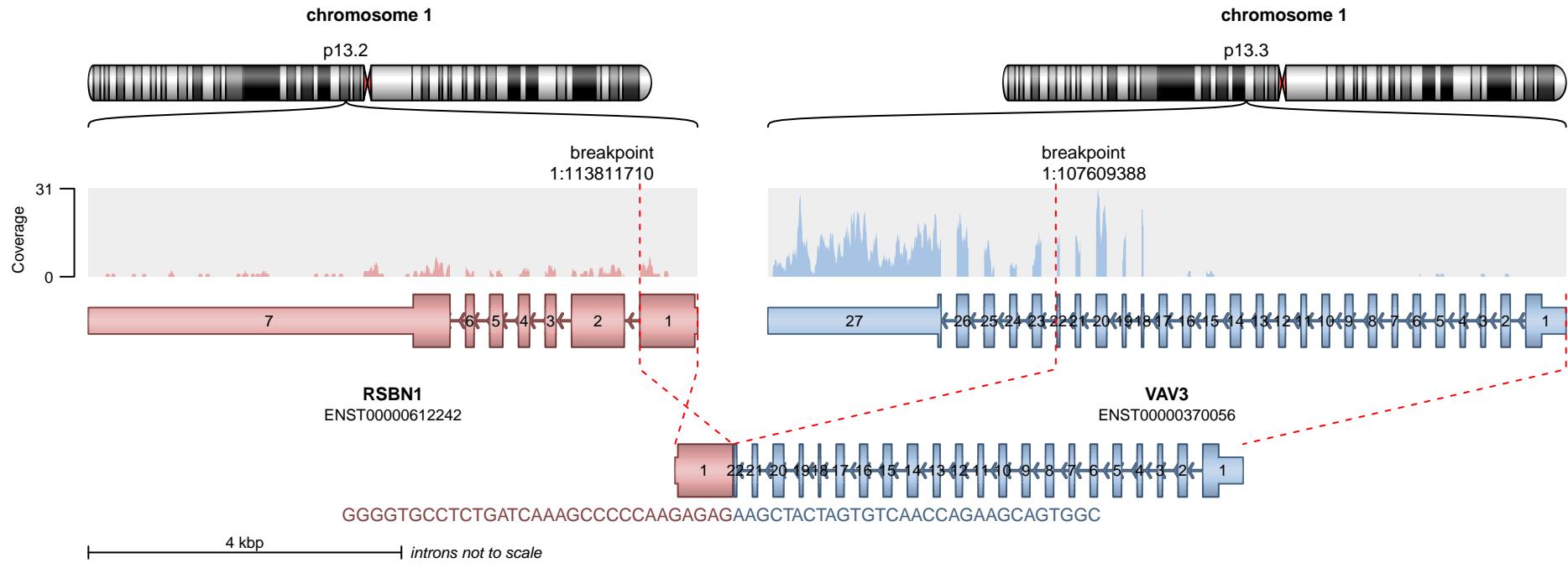
— translocation — deletion
— duplication — inversion



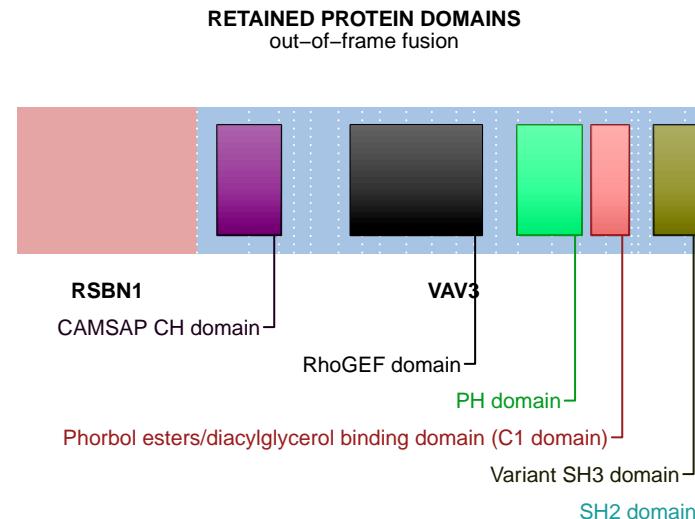
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 1

— translocation — deletion
— duplication — inversion

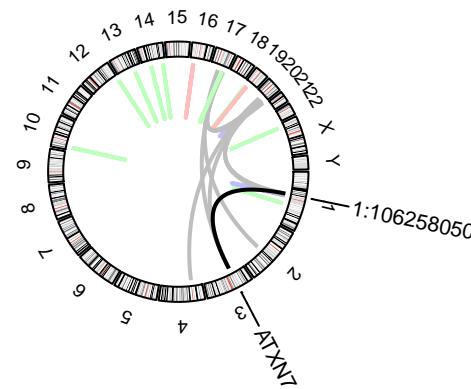
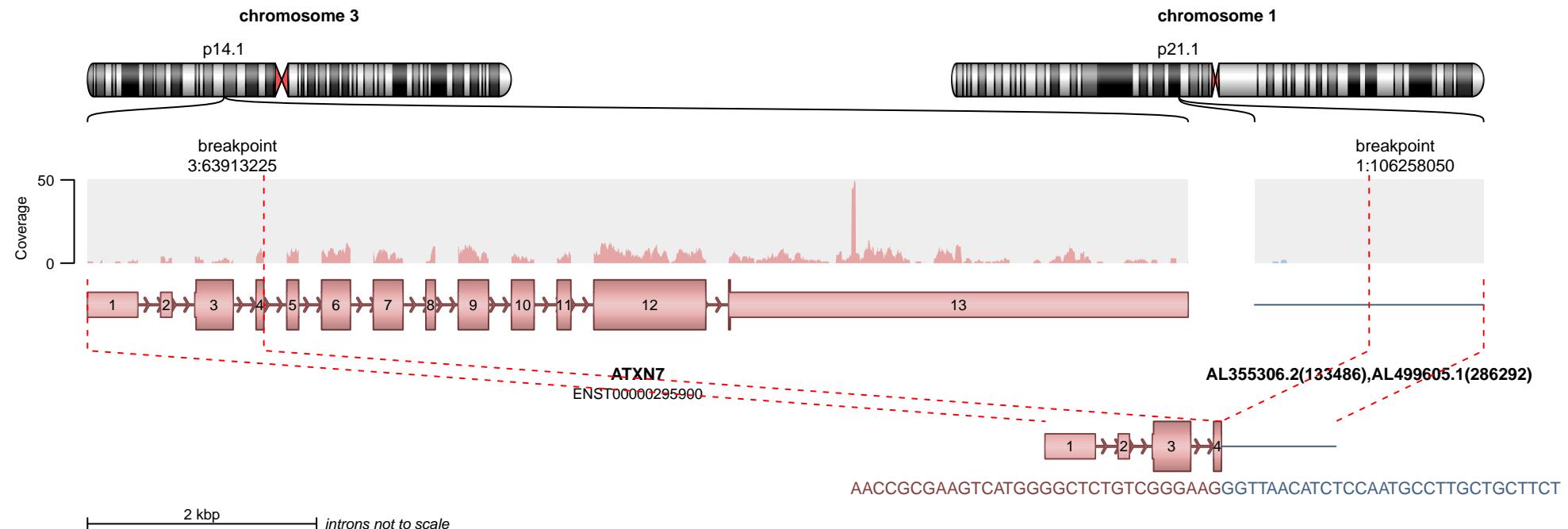


— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 2

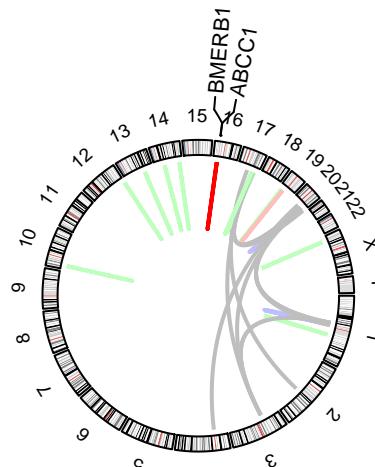
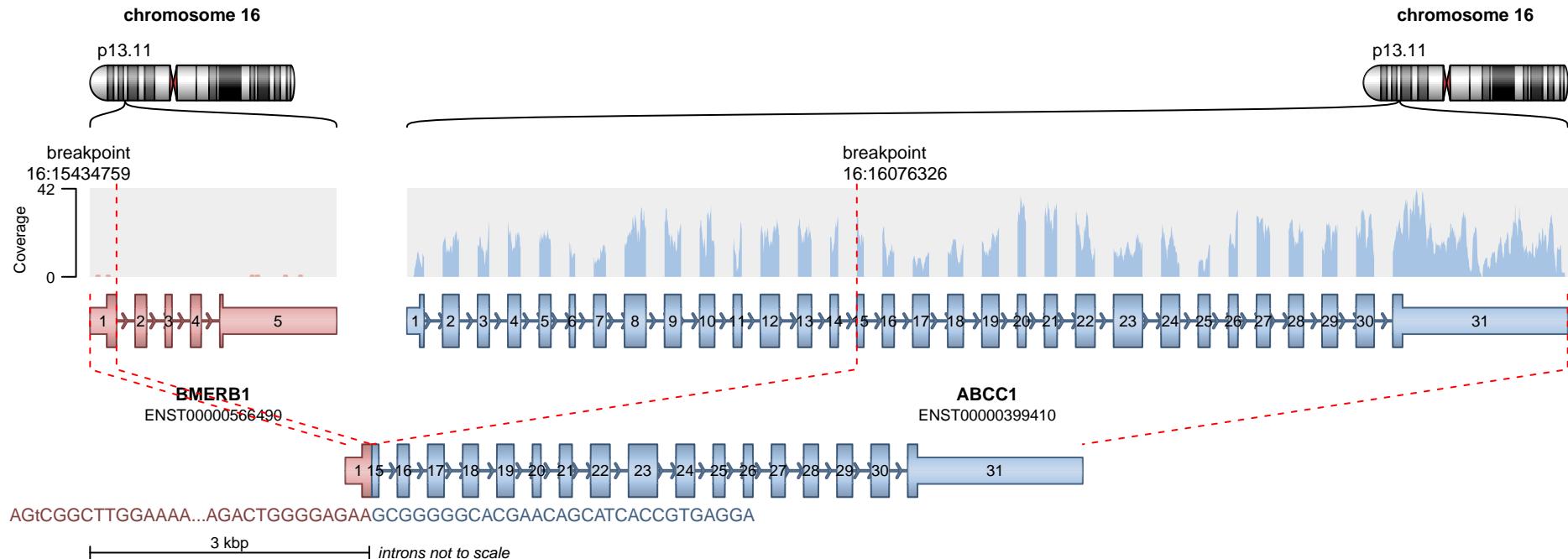


No protein domains retained in fusion.

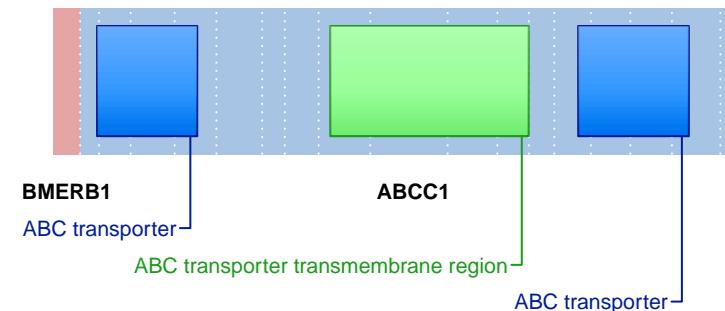
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

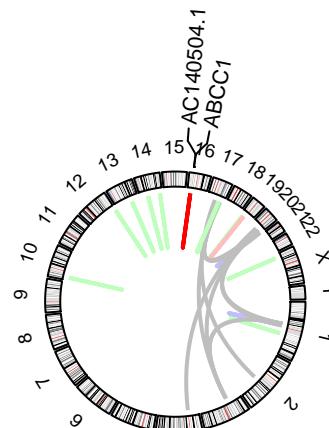
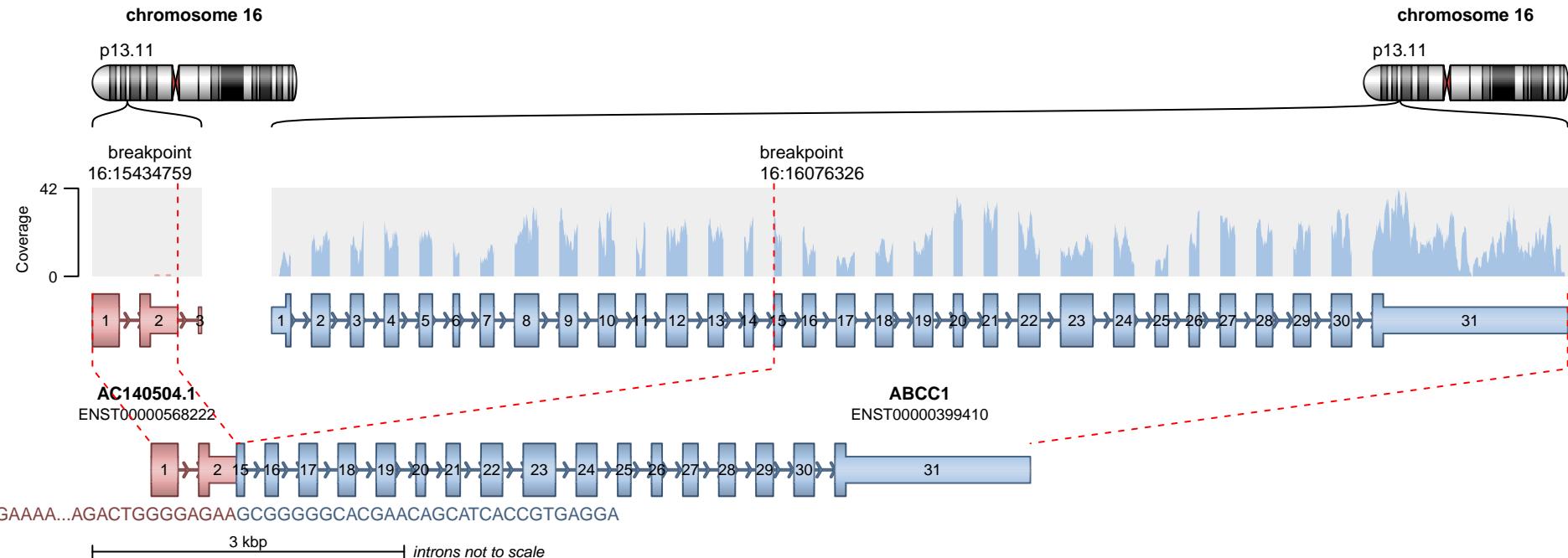
— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS in-frame fusion

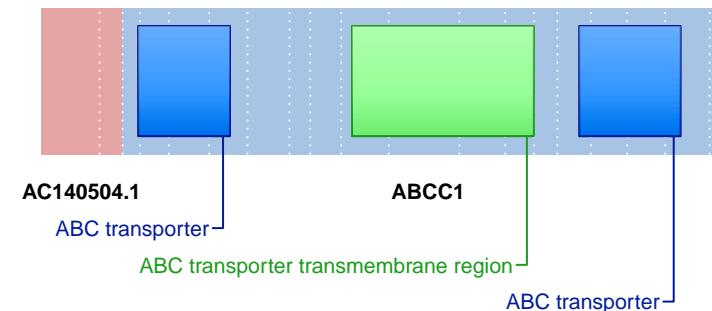


— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS

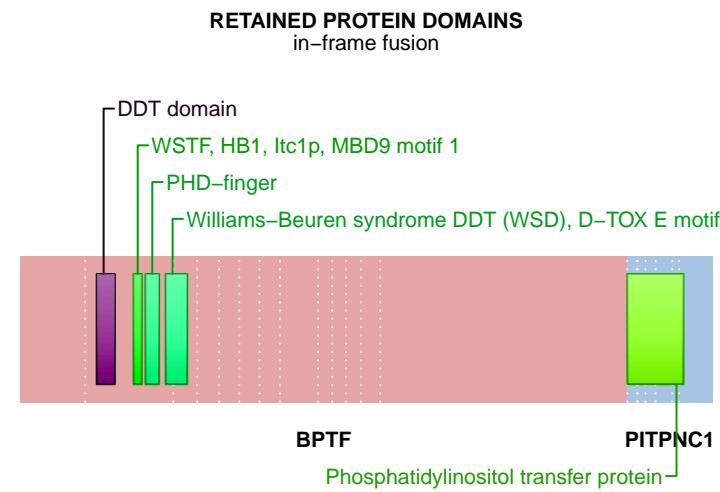
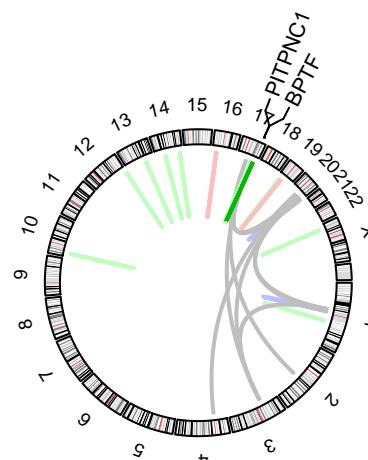
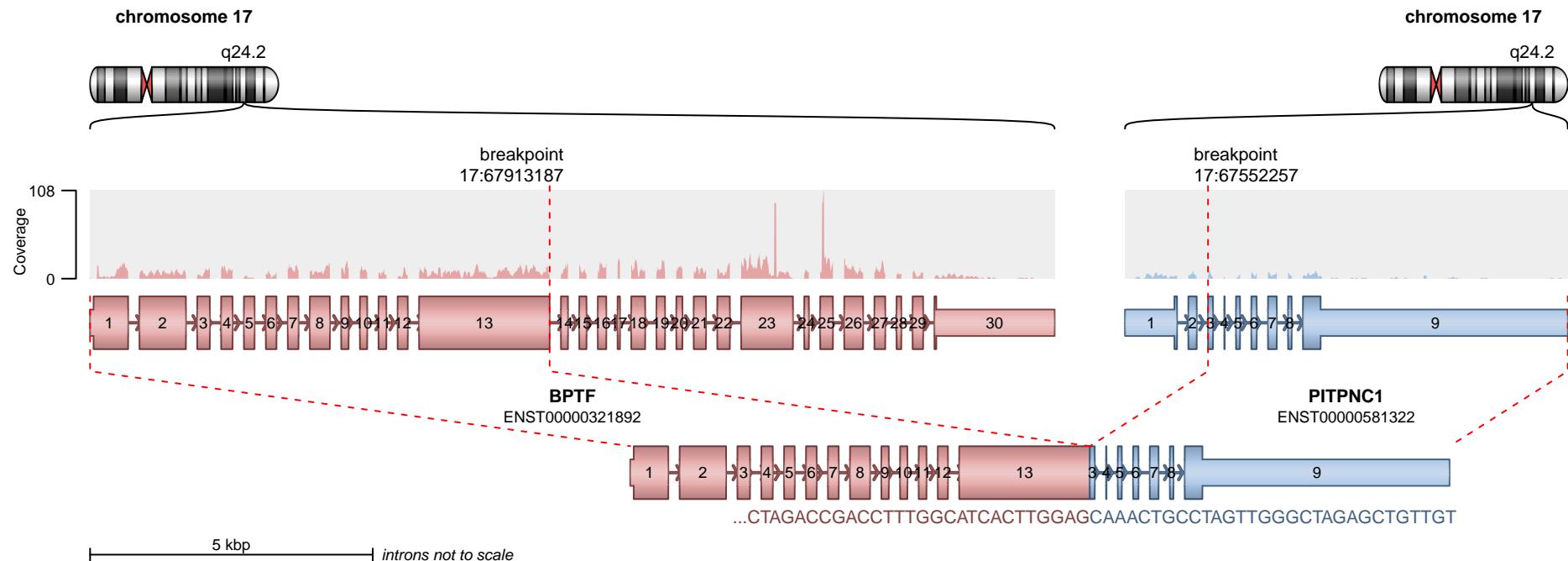
reading frame unclear



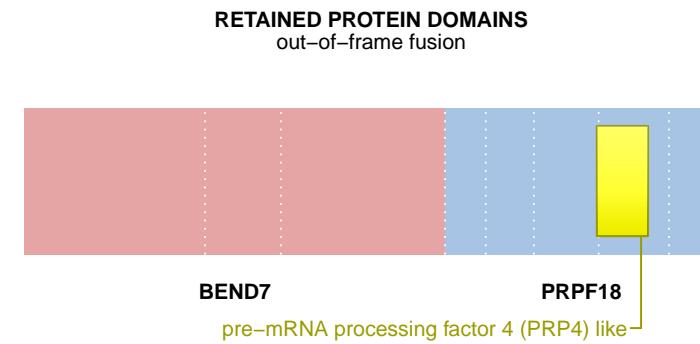
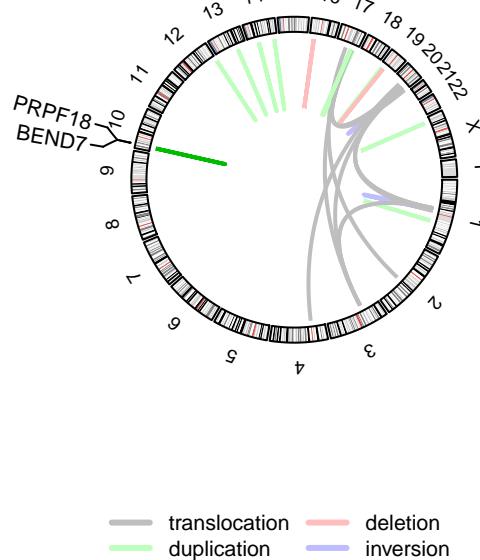
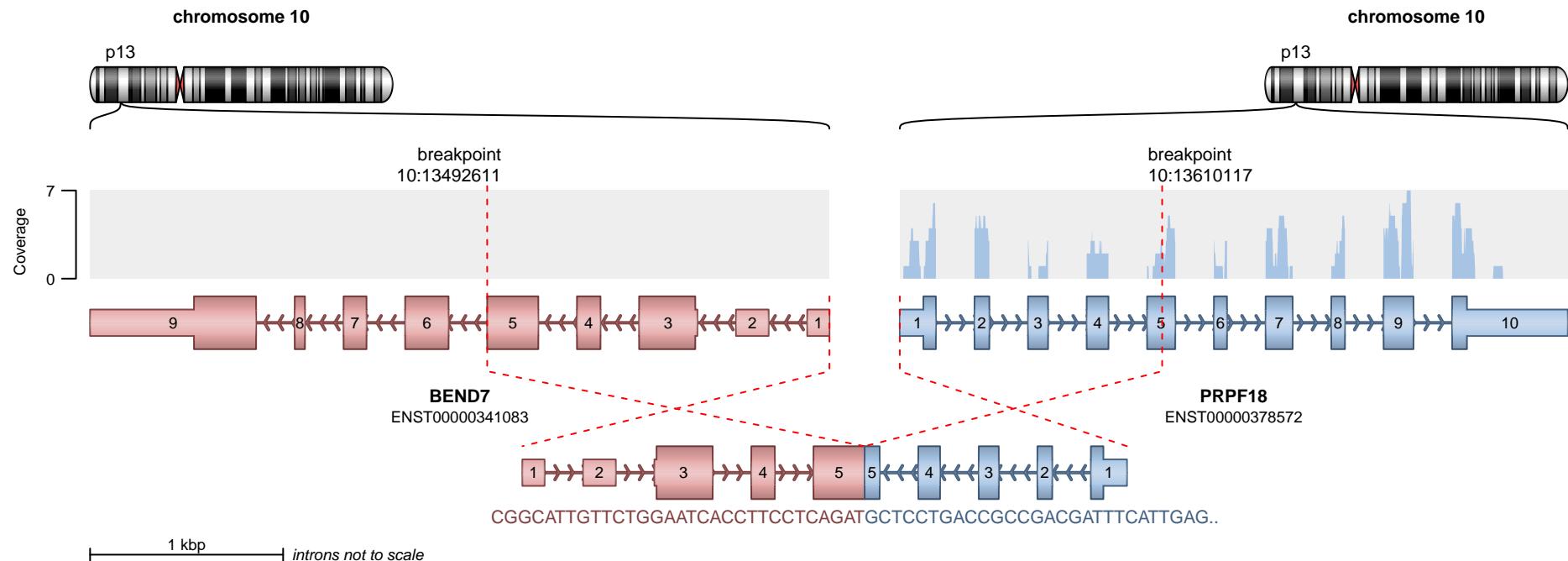
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

— translocation — deletion
— duplication — inversion

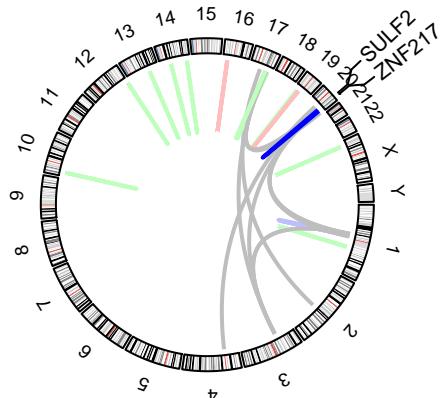
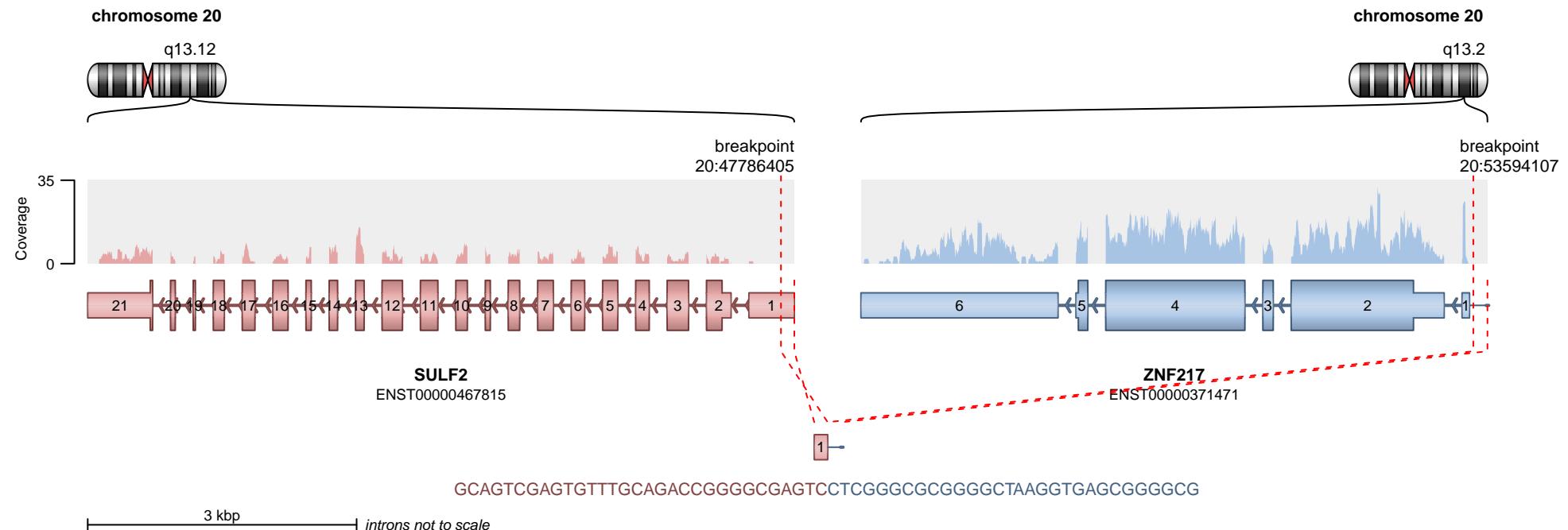


— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

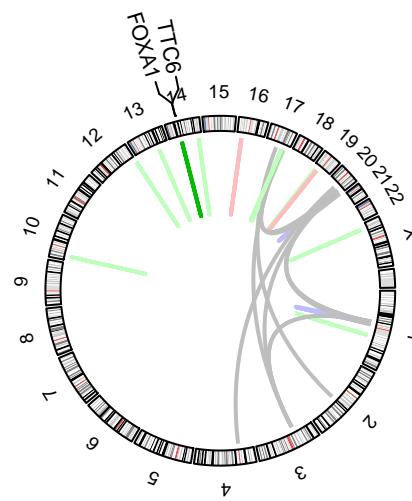
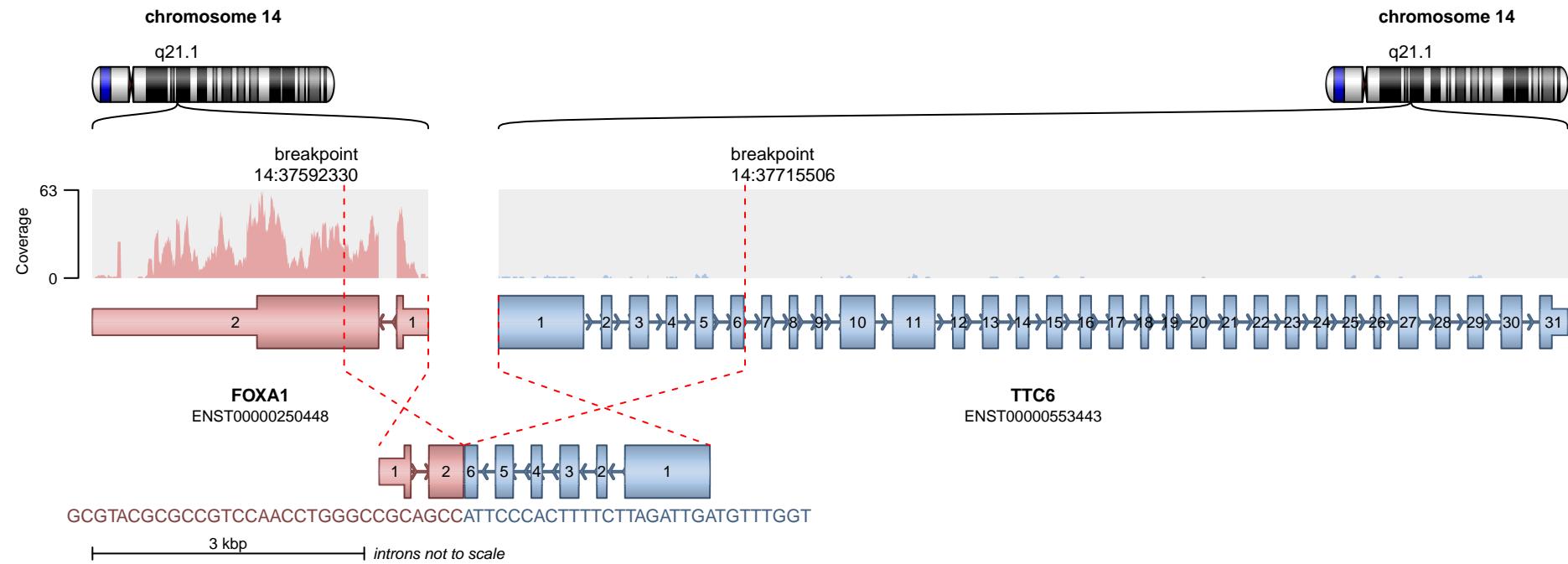


No coding regions retained in fusion transcript.

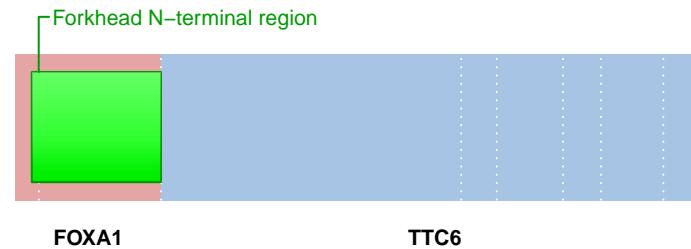
SUPPORTING READ COUNT

Split reads = 9
Discordant mates = 15

— translocation — deletion
— duplication — inversion



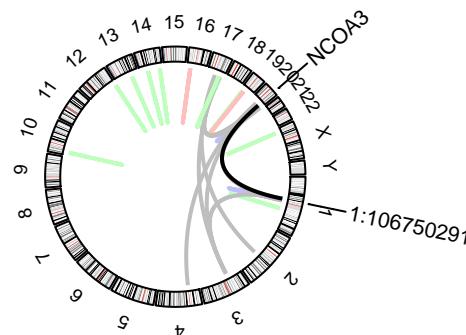
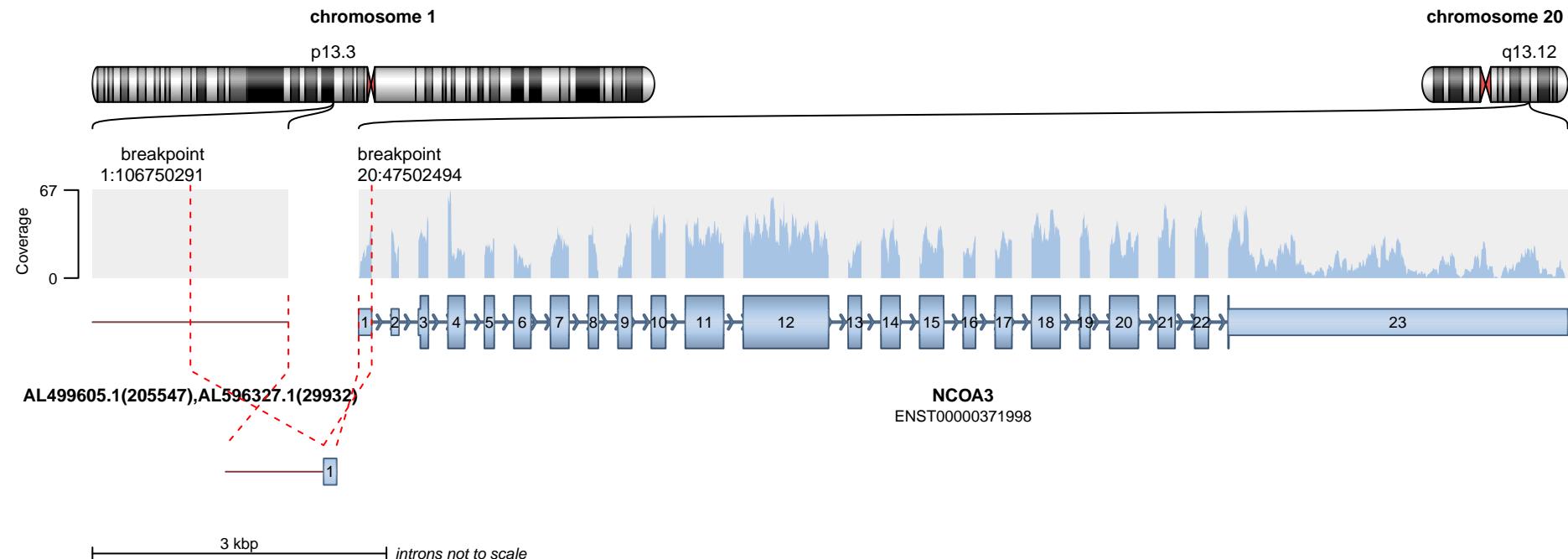
RETAINED PROTEIN DOMAINS out-of-frame fusion



SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 18

— translocation — deletion
— duplication — inversion

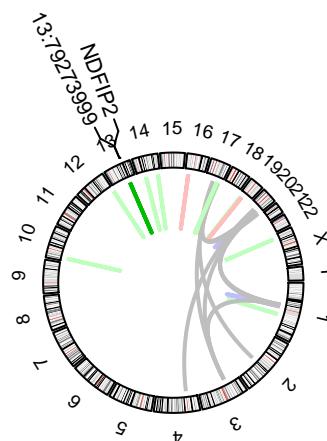
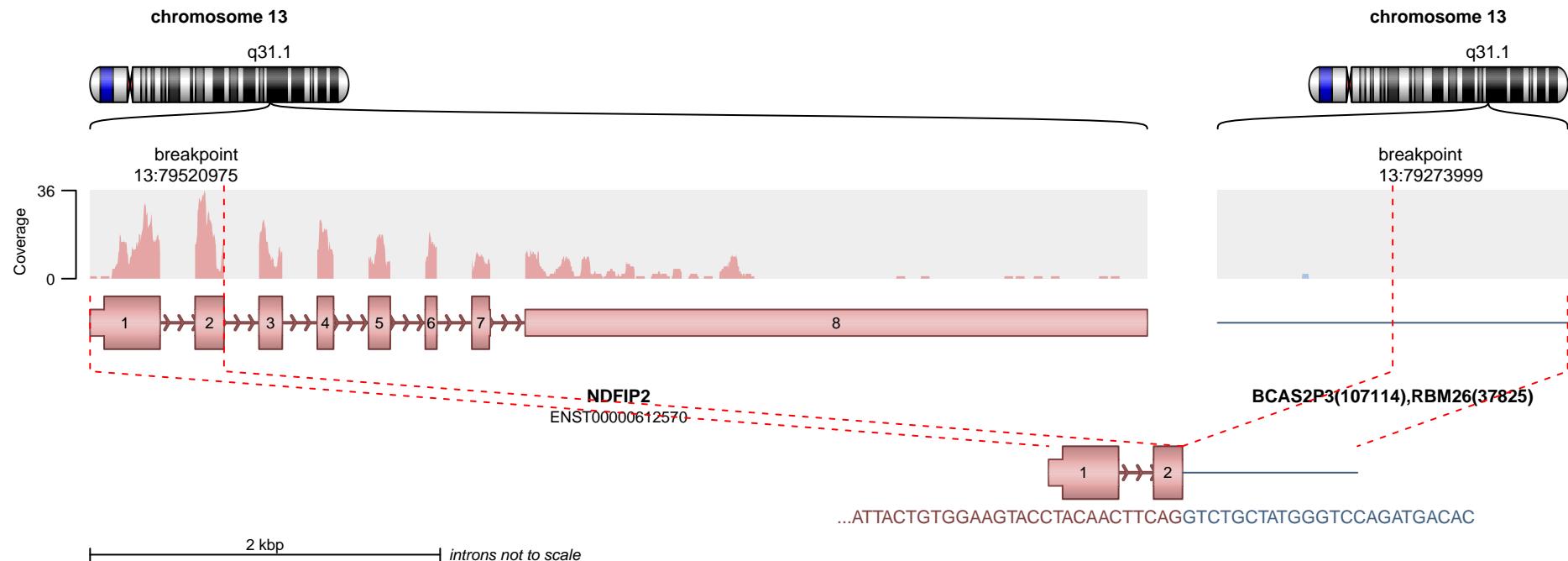


No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 5

— translocation — deletion
— duplication — inversion

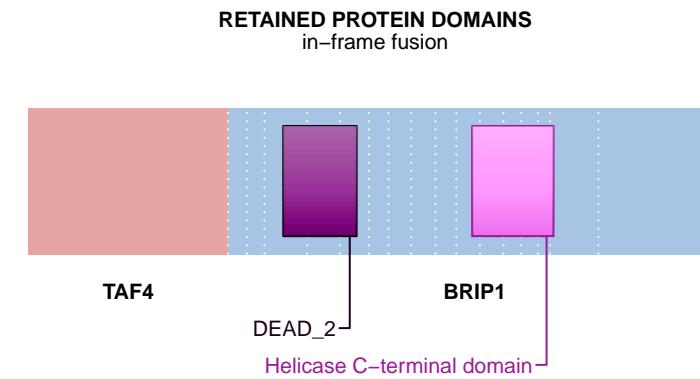
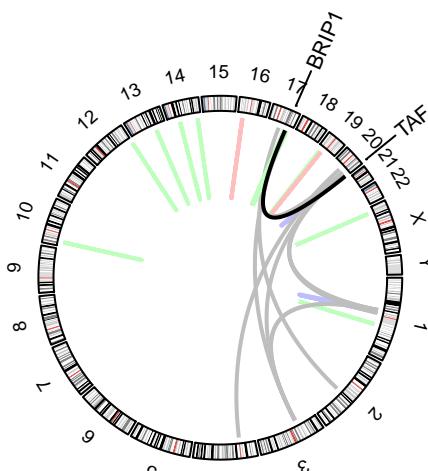
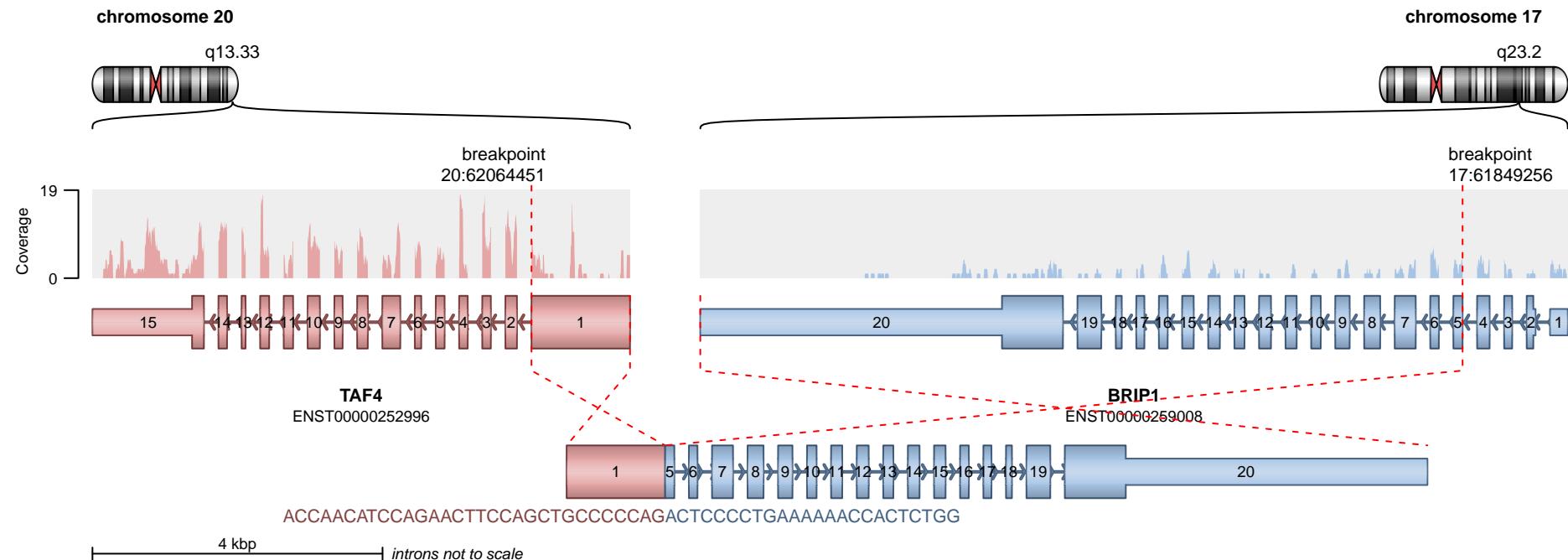


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

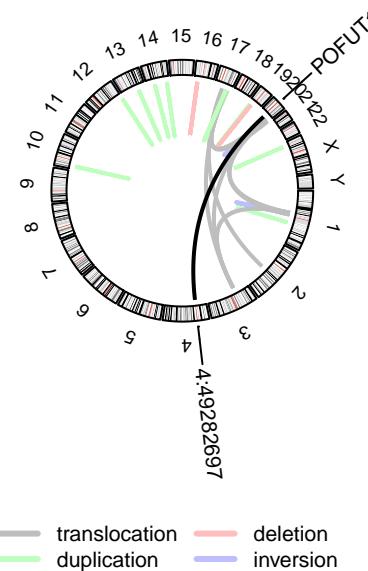
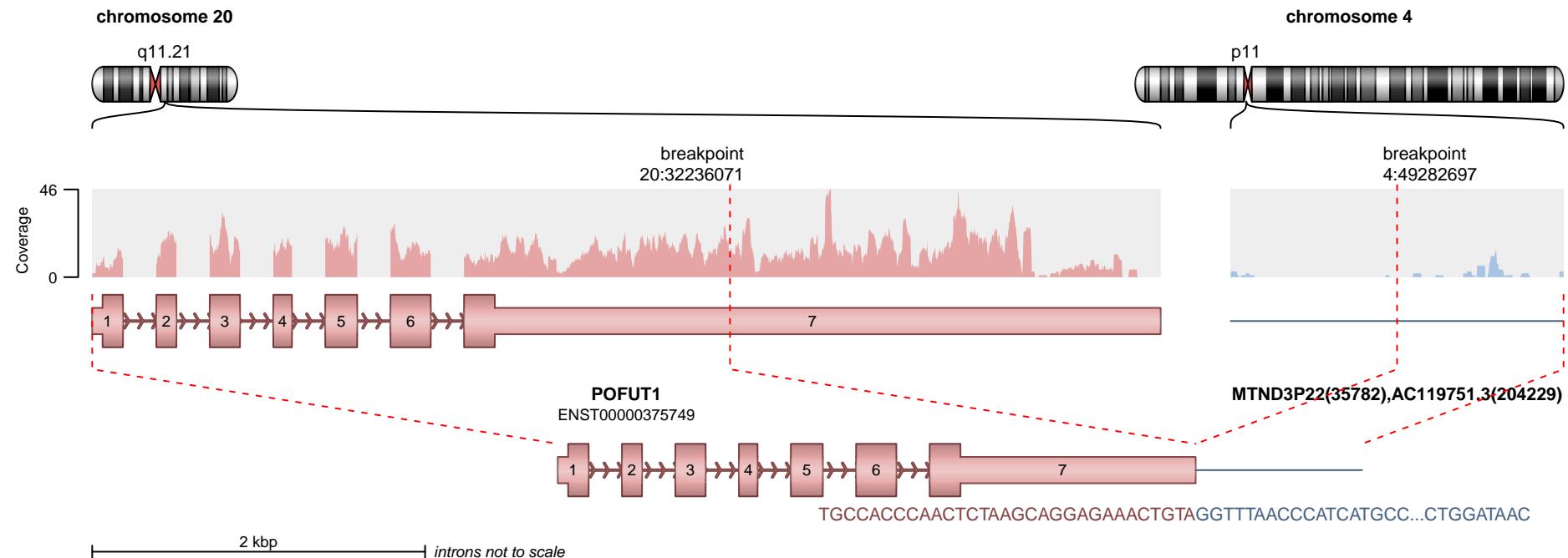
Split reads = 2
Discordant mates = 0



SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

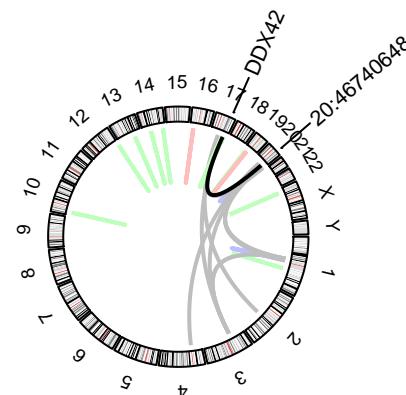
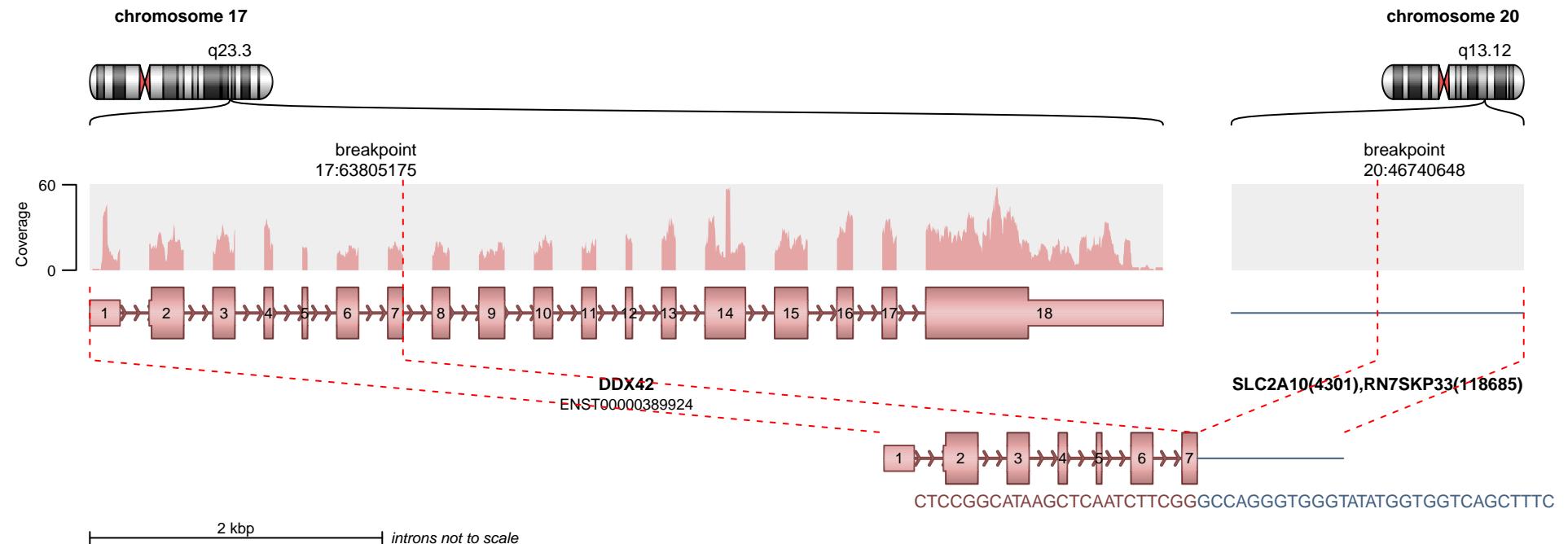
— translocation — deletion
— duplication — inversion



No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

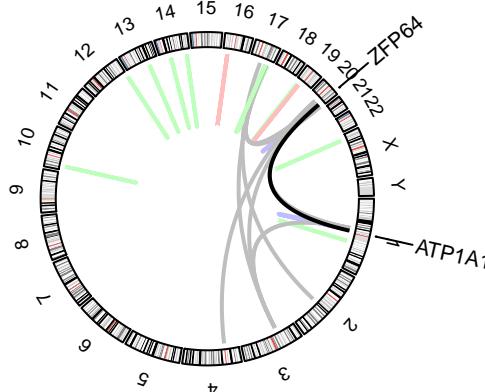
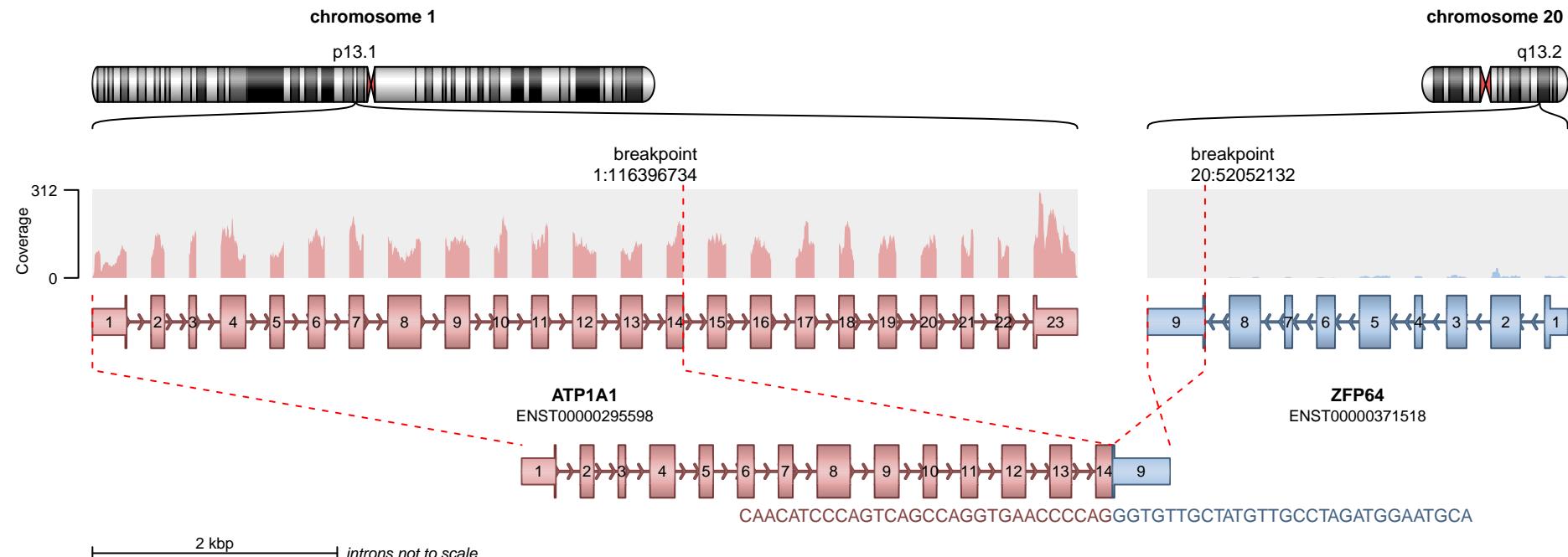


No protein domains retained in fusion.

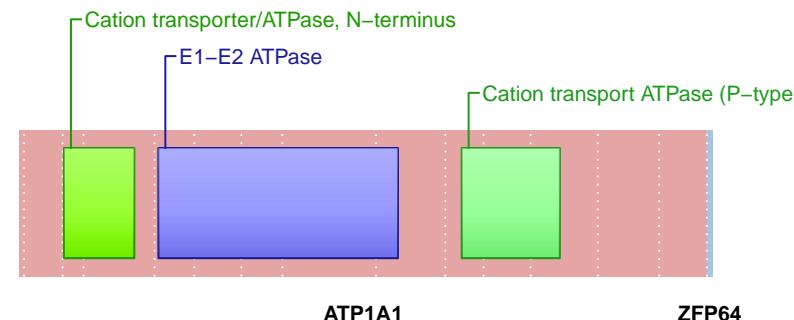
SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

— translocation — deletion
— duplication — inversion



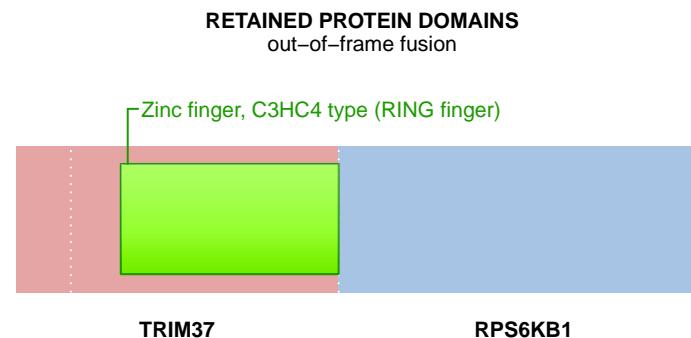
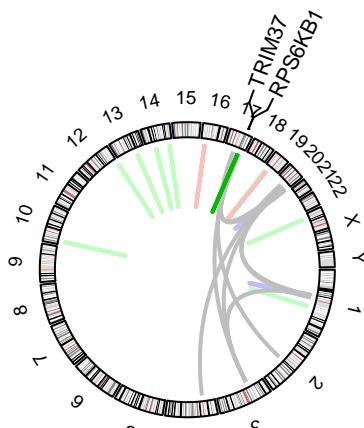
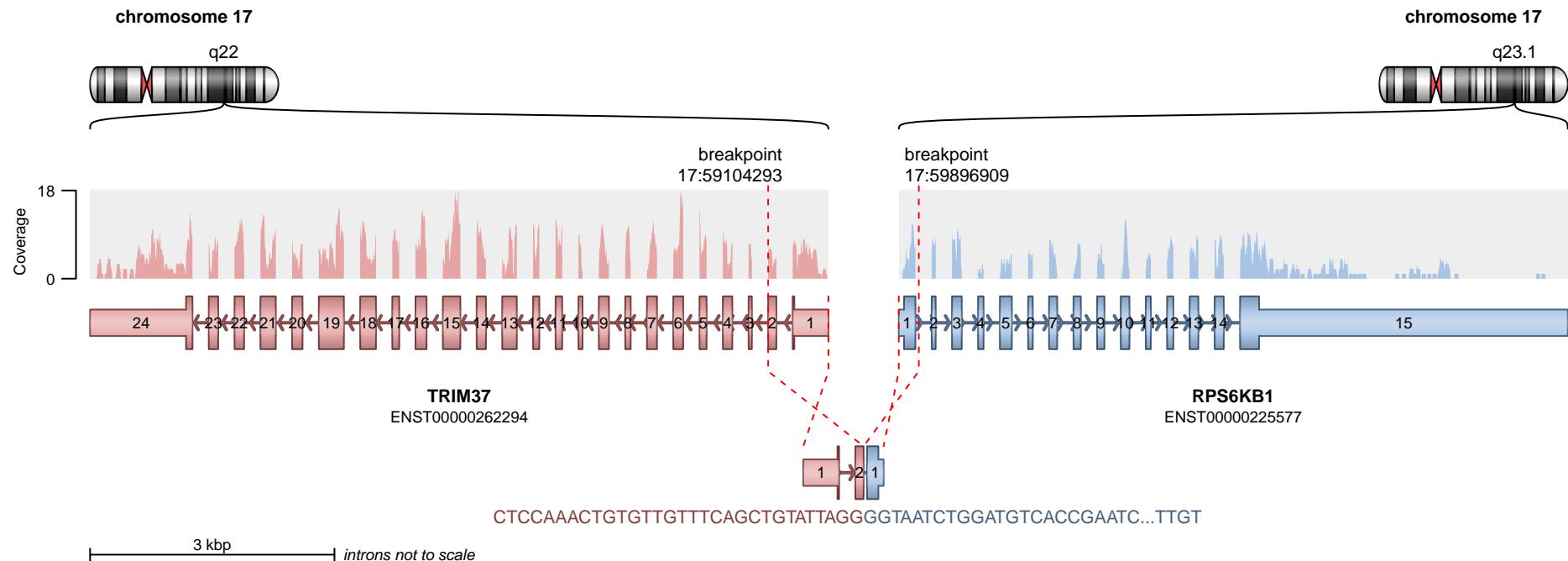
RETAINED PROTEIN DOMAINS out-of-frame fusion



SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0

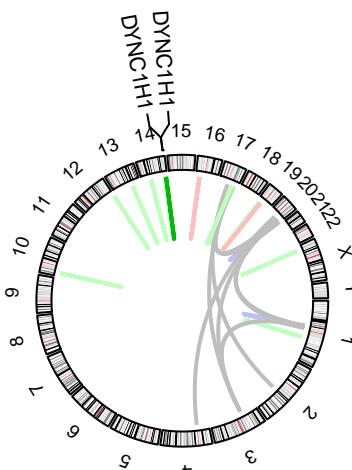
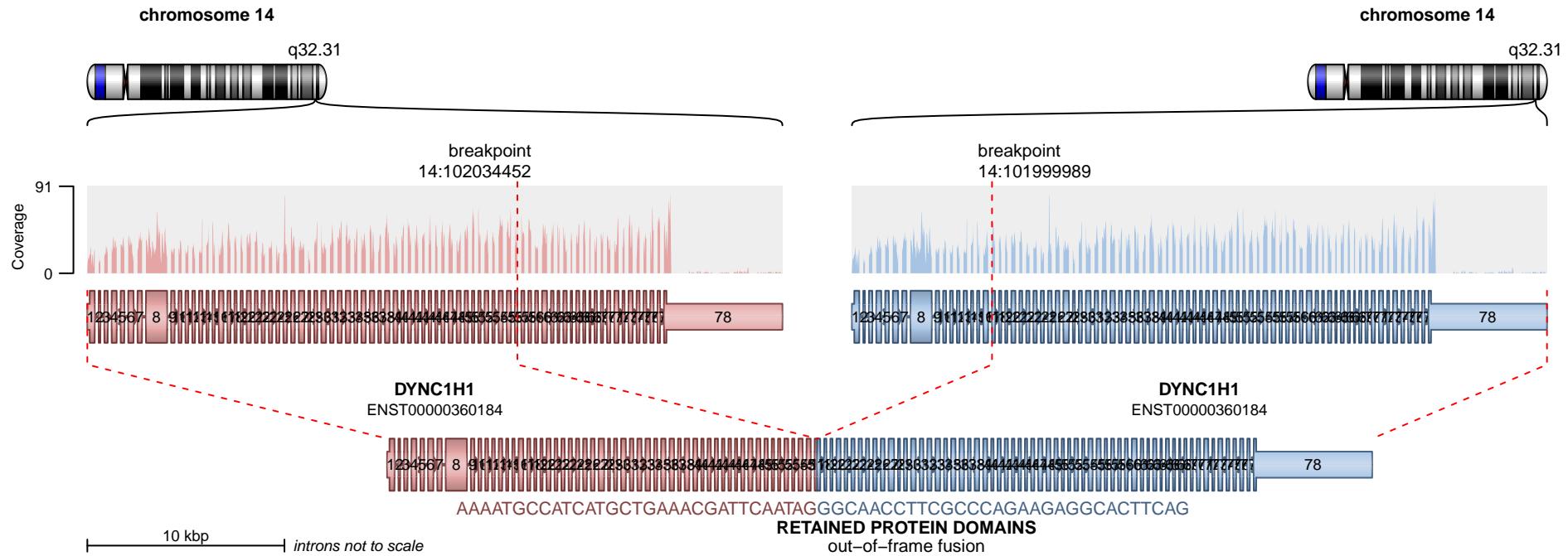
— translocation — deletion
— duplication — inversion



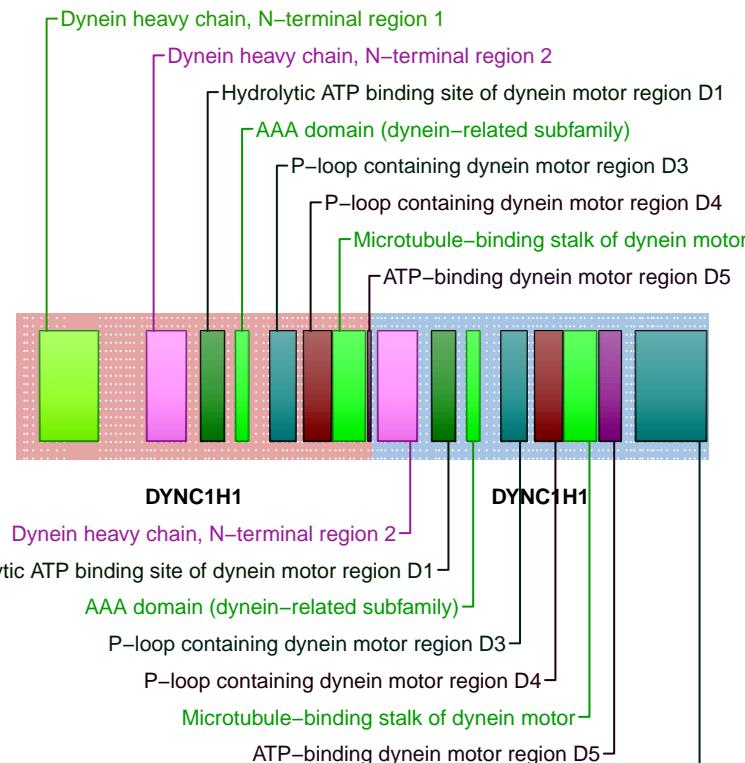
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

— translocation — deletion
— duplication — inversion



— translocation — deletion
— duplication — inversion

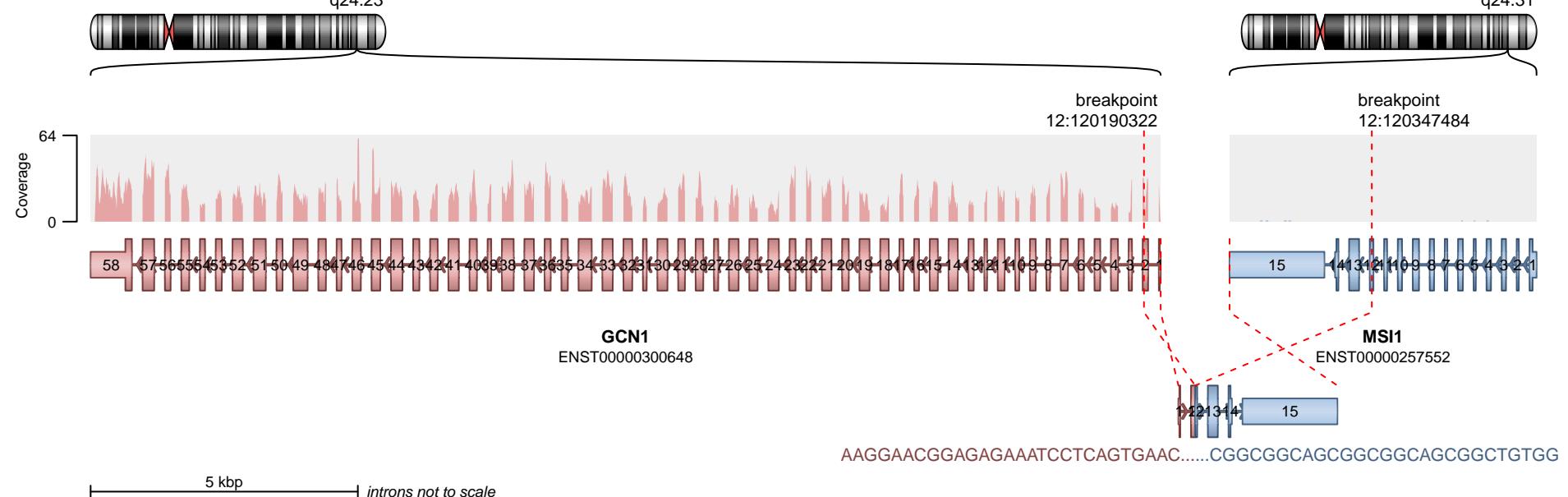


SUPPORTING READ COUNT

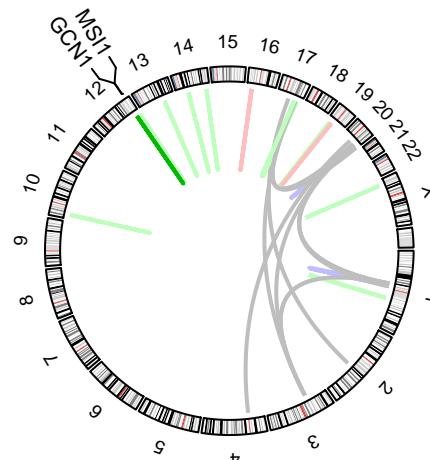
Split reads = 6
Discordant mates = 4

chromosome 12

q24.23

**chromosome 12**

q24.31

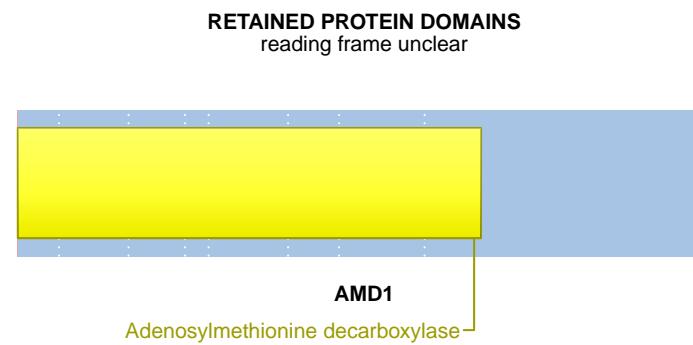
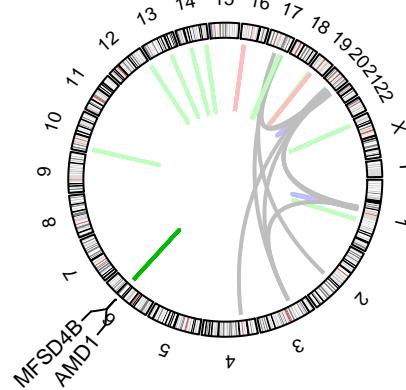
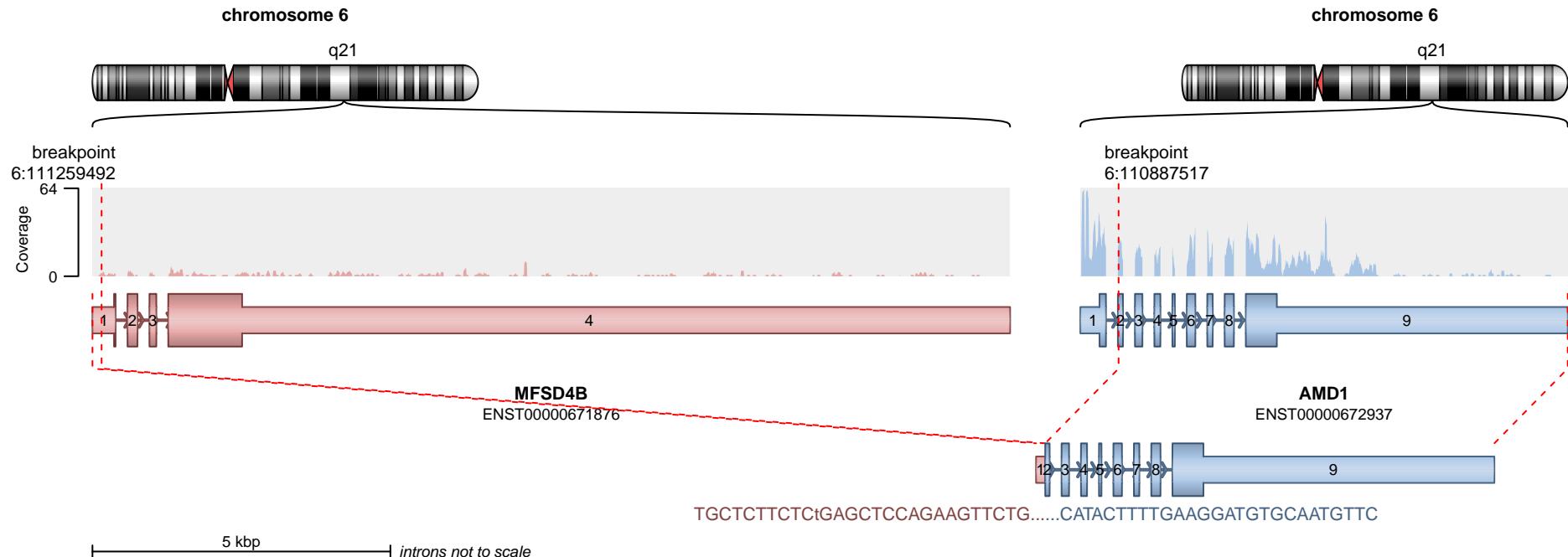


No protein domains retained in fusion.

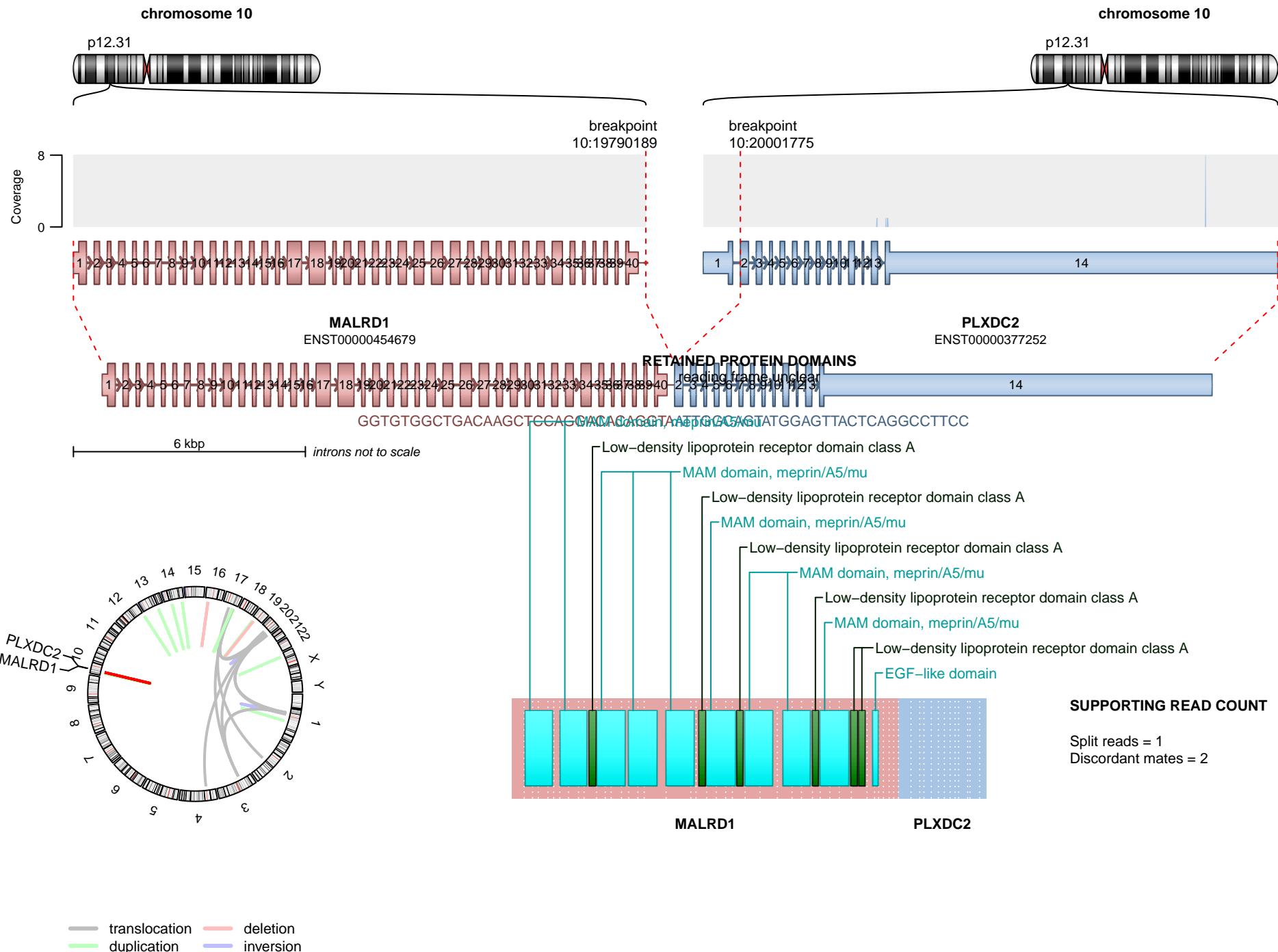
SUPPORTING READ COUNT

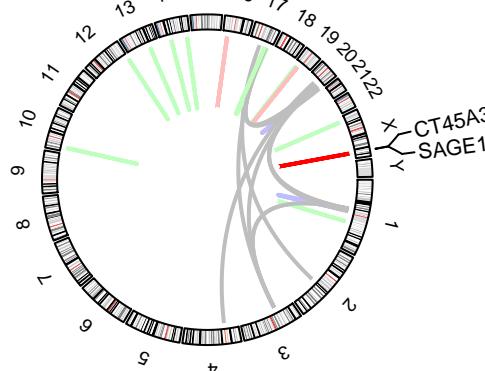
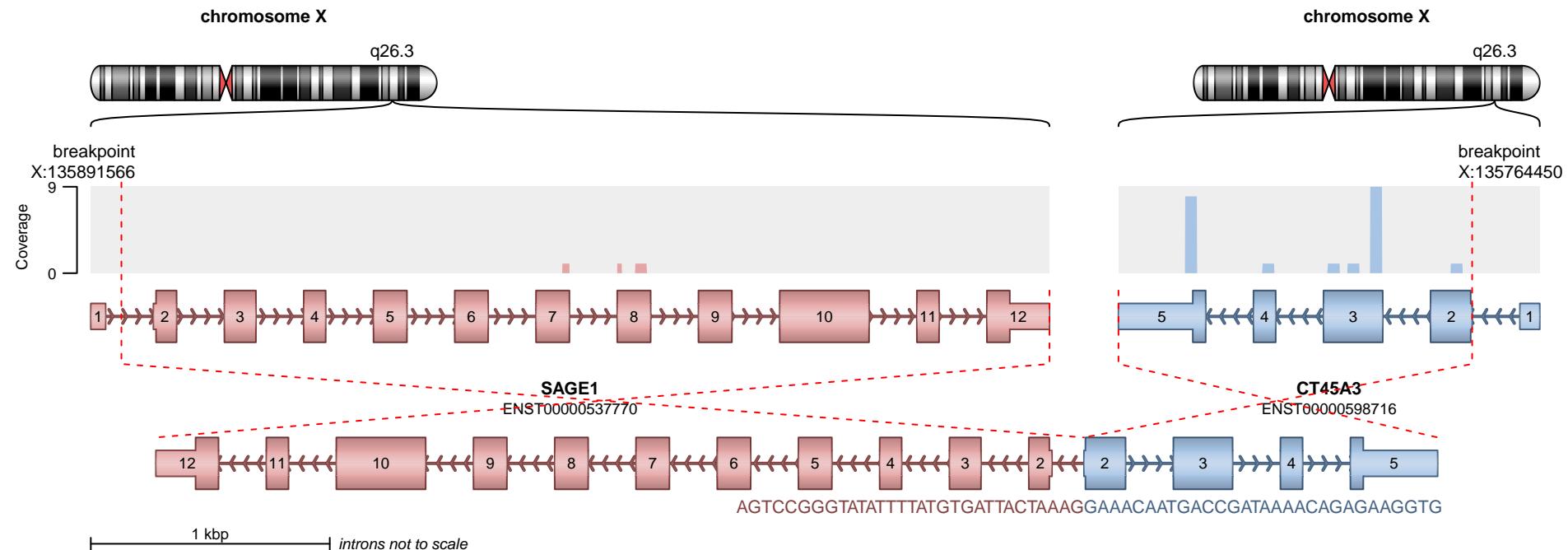
Split reads = 0
Discordant mates = 7

— translocation — deletion
— duplication — inversion



— translocation — deletion
— duplication — inversion



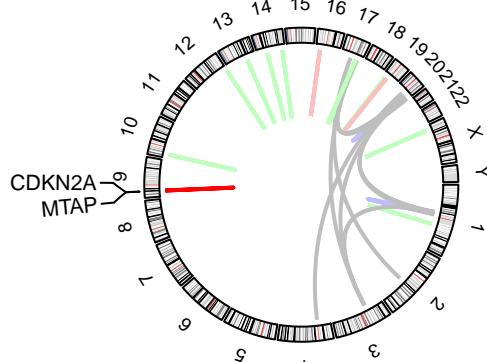
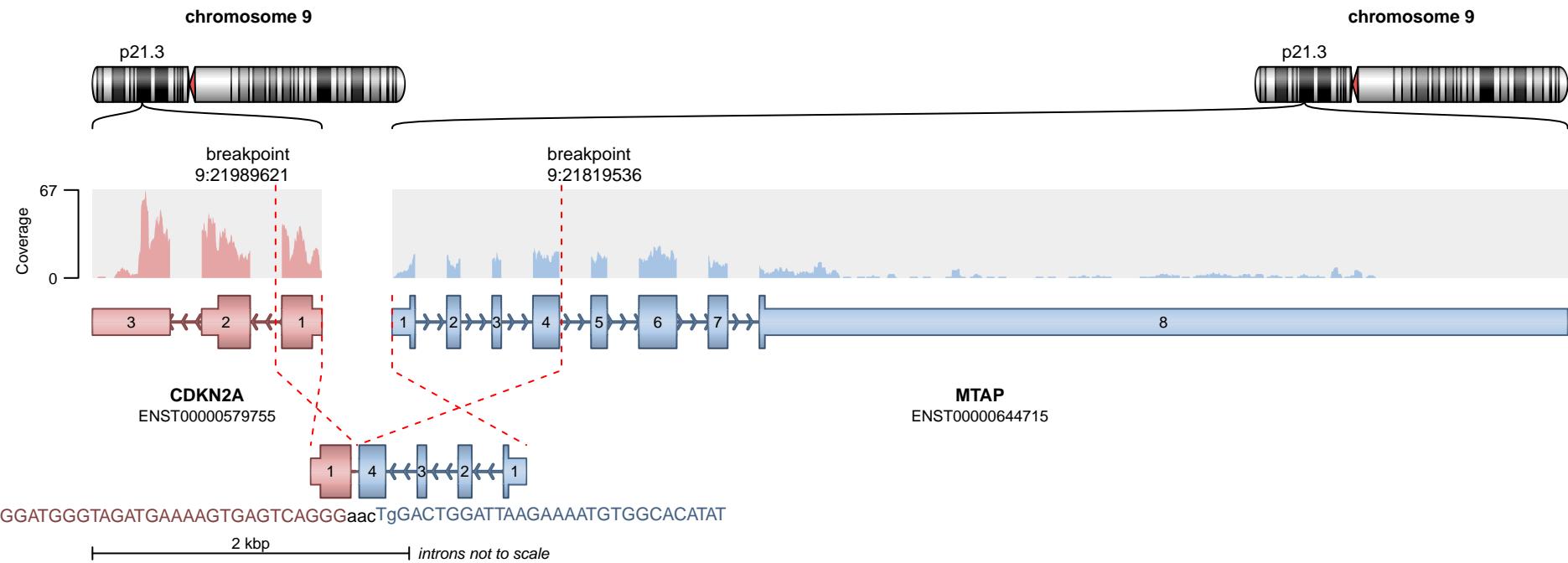


No protein domains retained in fusion.

SUPPORTING READ COUNT

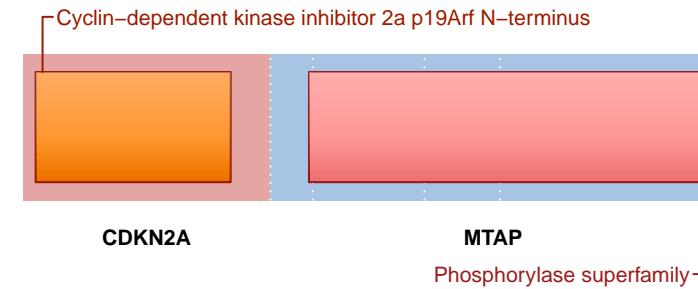
Split reads = 1
Discordant mates = 1

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS

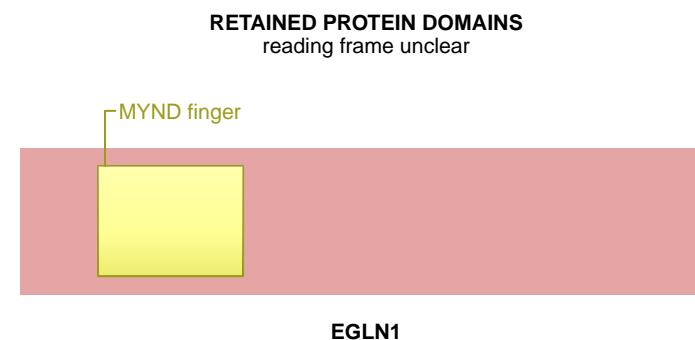
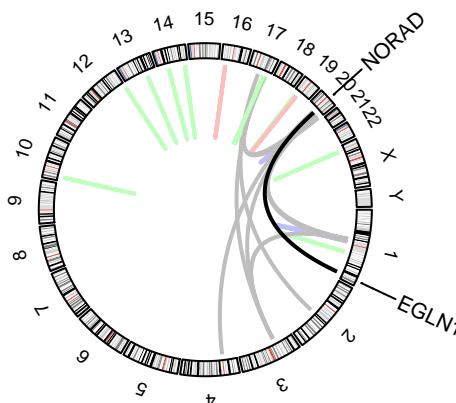
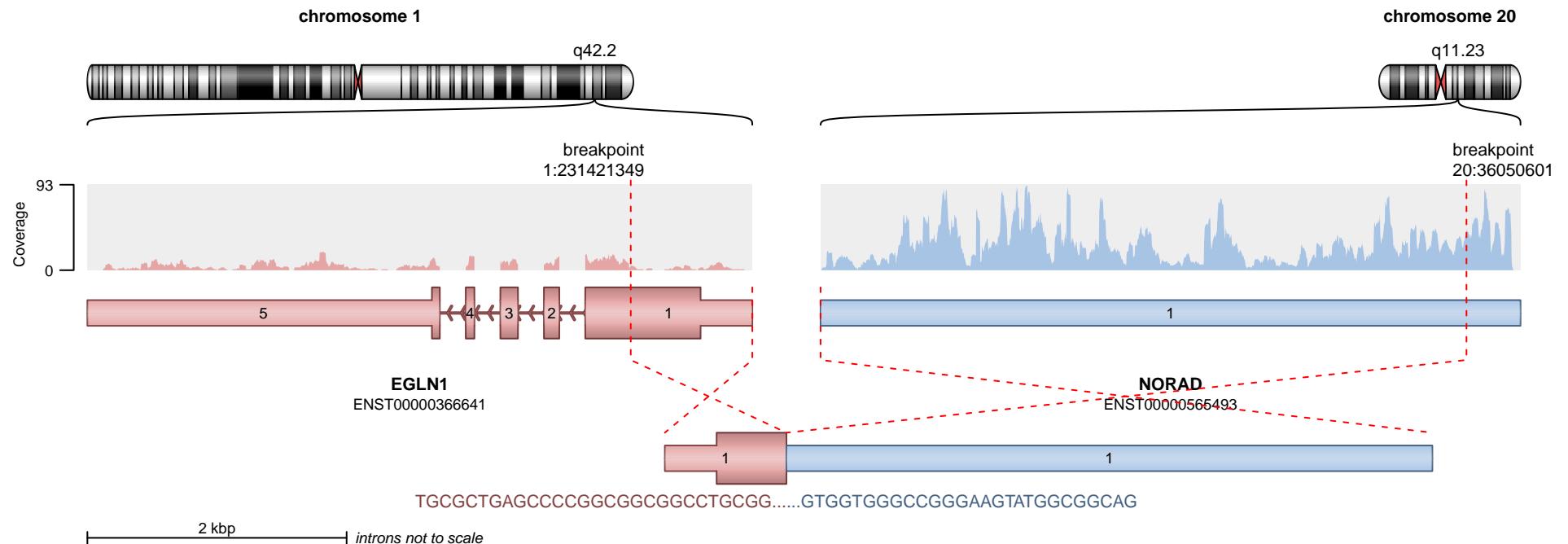
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads = 0
Discordant mates = 2

— translocation — deletion
— duplication — inversion