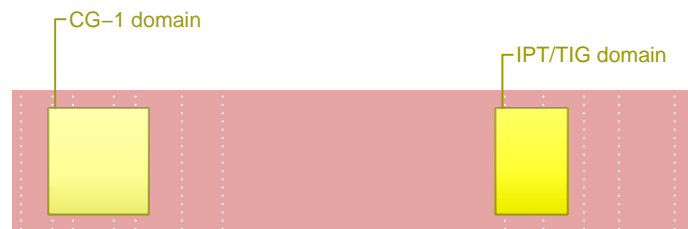


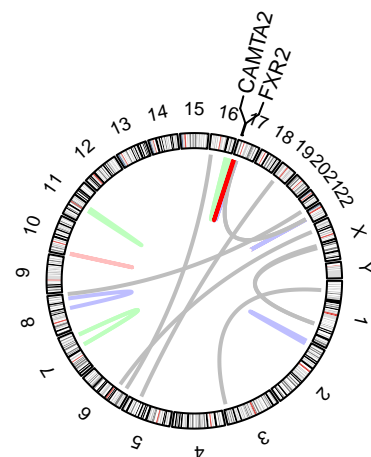
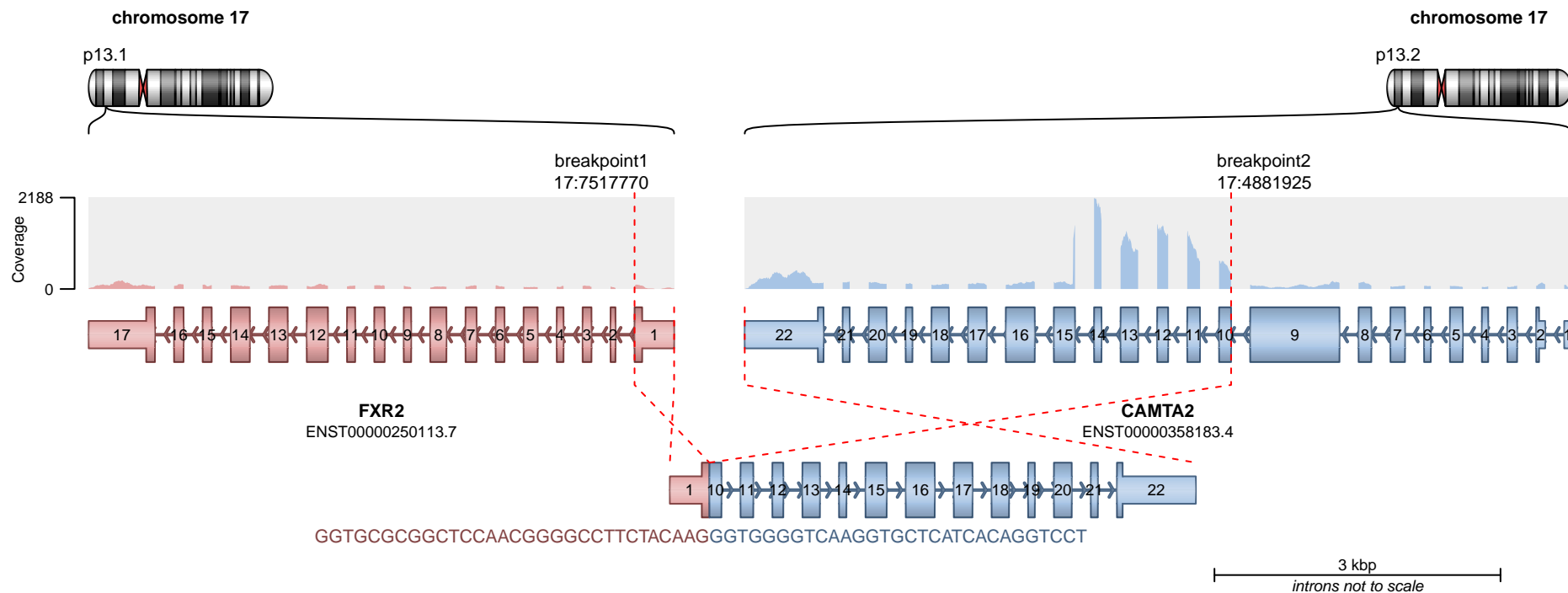
RETAINED PROTEIN DOMAINS out-of-frame fusion



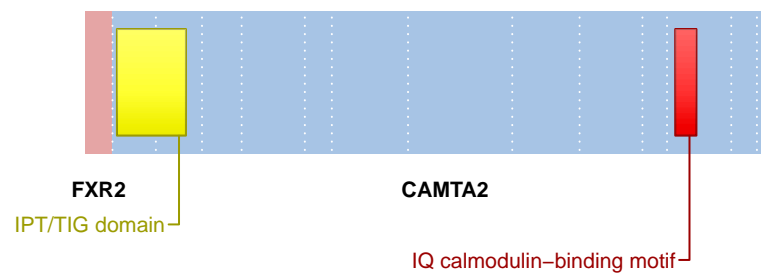
SUPPORTING READ COUNT

Split reads at breakpoint1 = 300
Split reads at breakpoint2 = 269
Discordant mates = 169

— translocation — deletion
— duplication — inversion



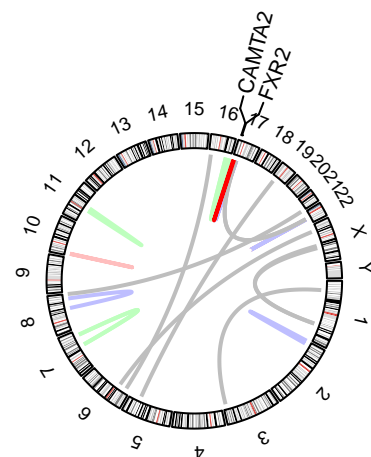
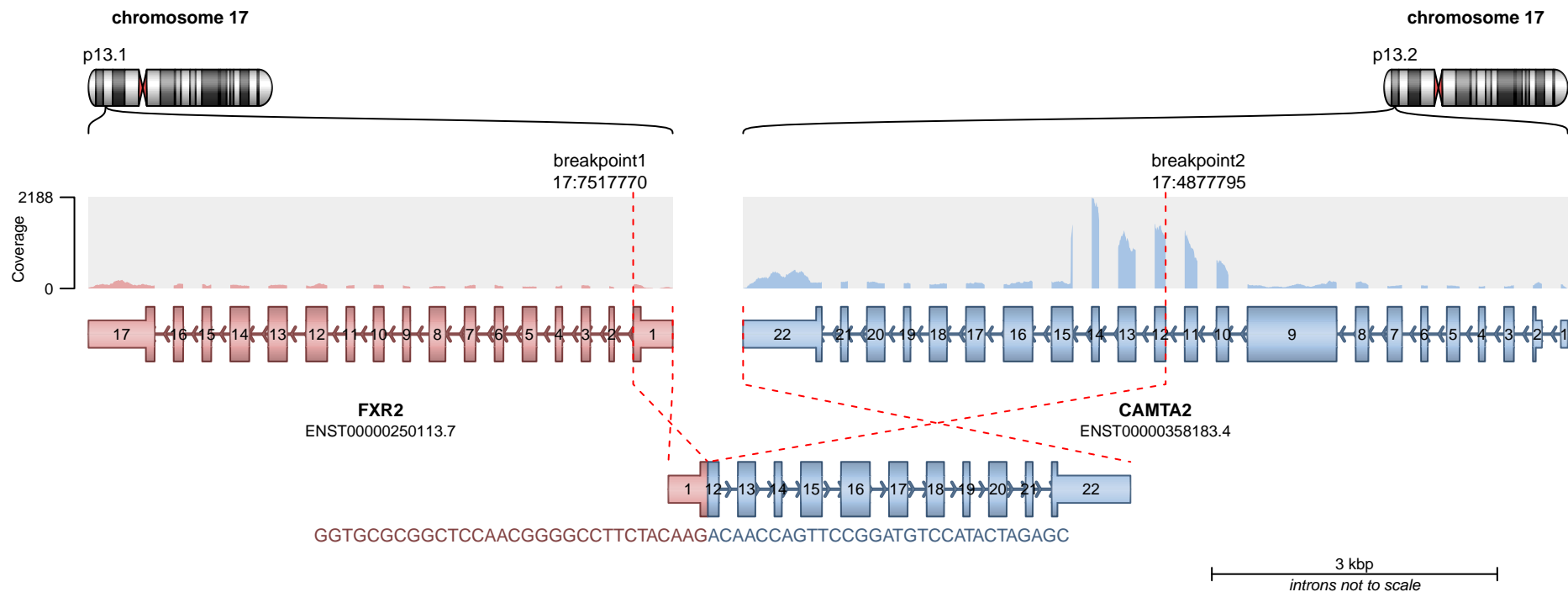
RETAINED PROTEIN DOMAINS in-frame fusion



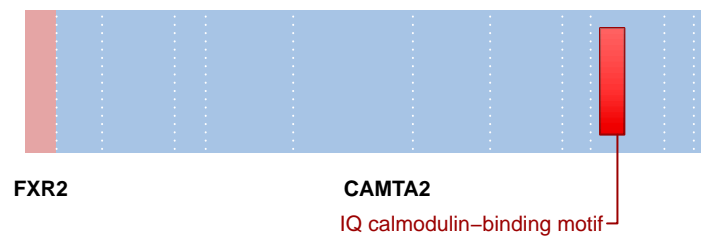
SUPPORTING READ COUNT

Split reads at breakpoint1 = 12
Split reads at breakpoint2 = 69
Discordant mates = 15

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS out-of-frame fusion



SUPPORTING READ COUNT

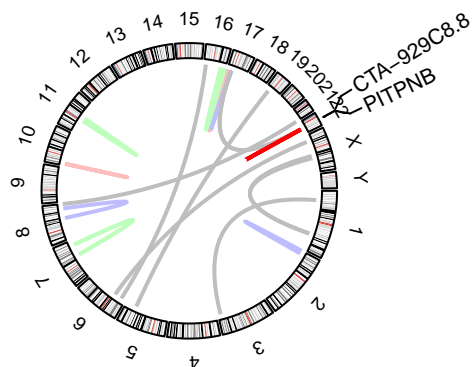
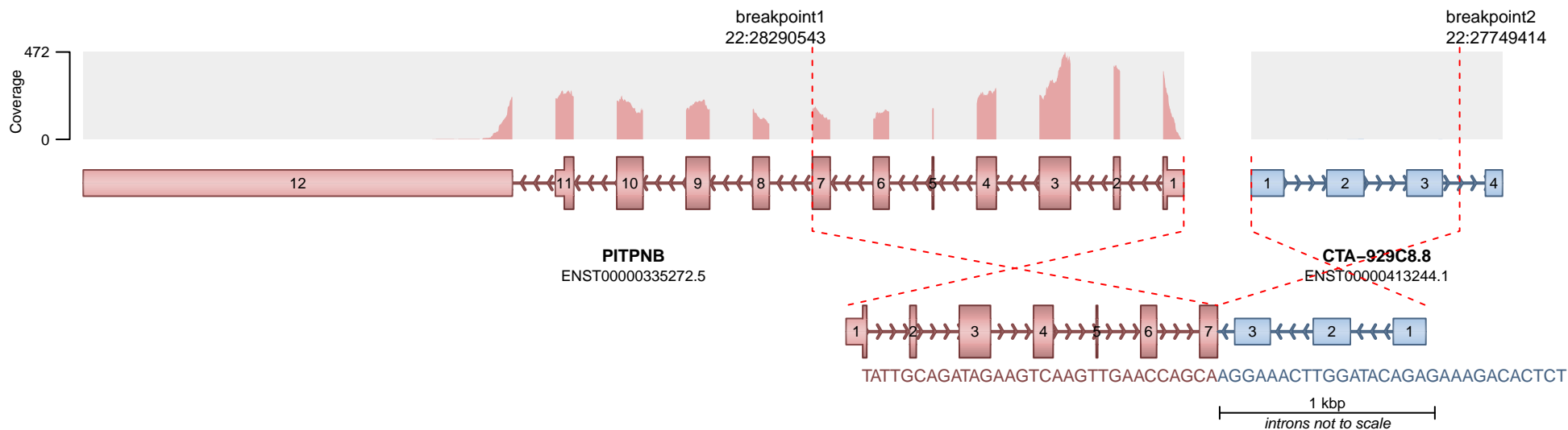
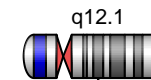
Split reads at breakpoint1 = 0
Split reads at breakpoint2 = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion

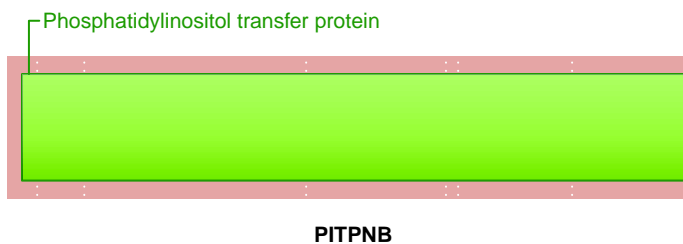
chromosome 22



chromosome 22



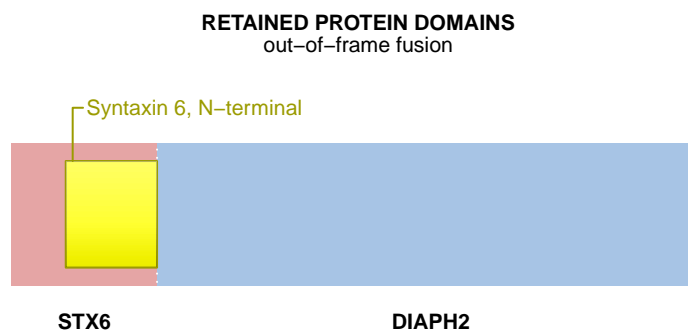
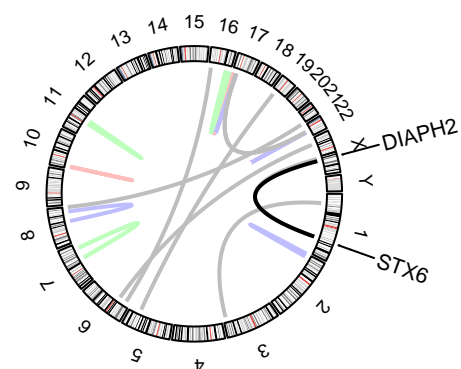
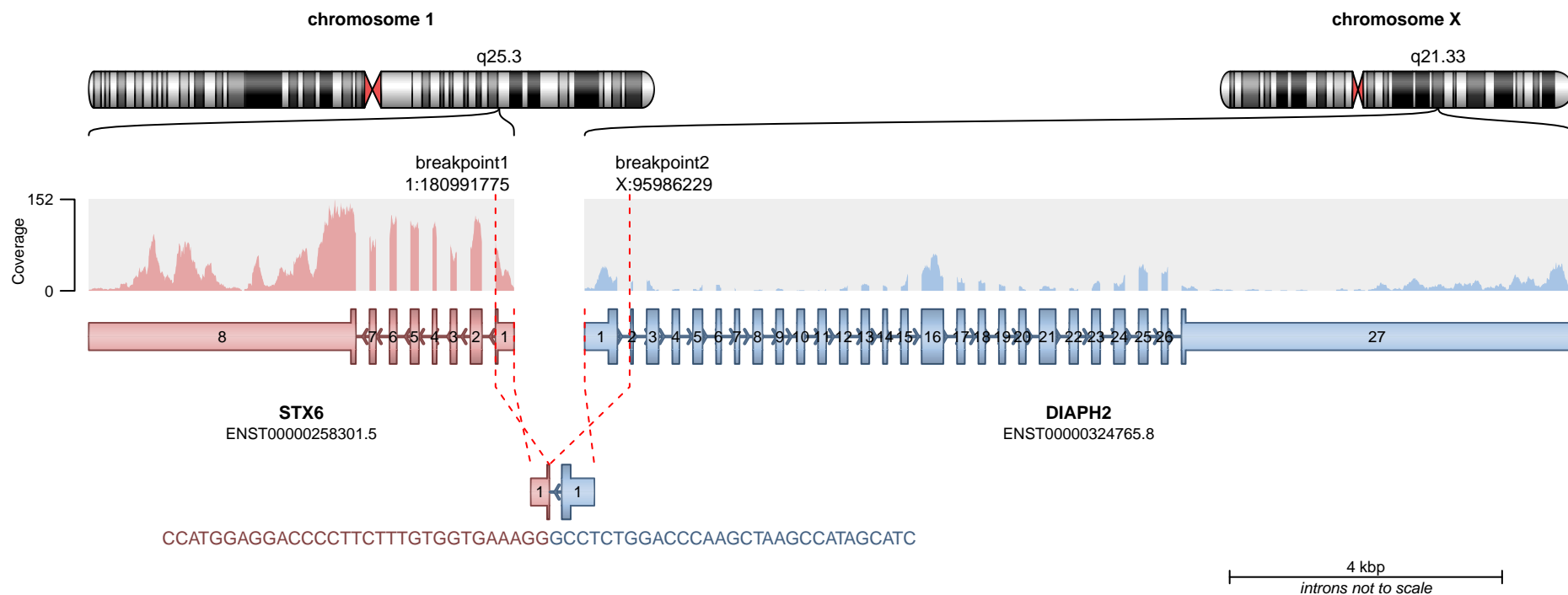
RETAINED PROTEIN DOMAINS
out-of-frame fusion



SUPPORTING READ COUNT

Split reads at breakpoint1 = 5
Split reads at breakpoint2 = 7
Discordant mates = 3

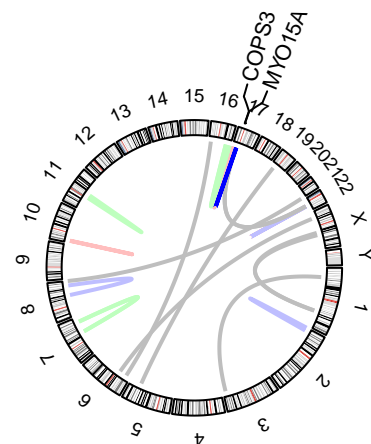
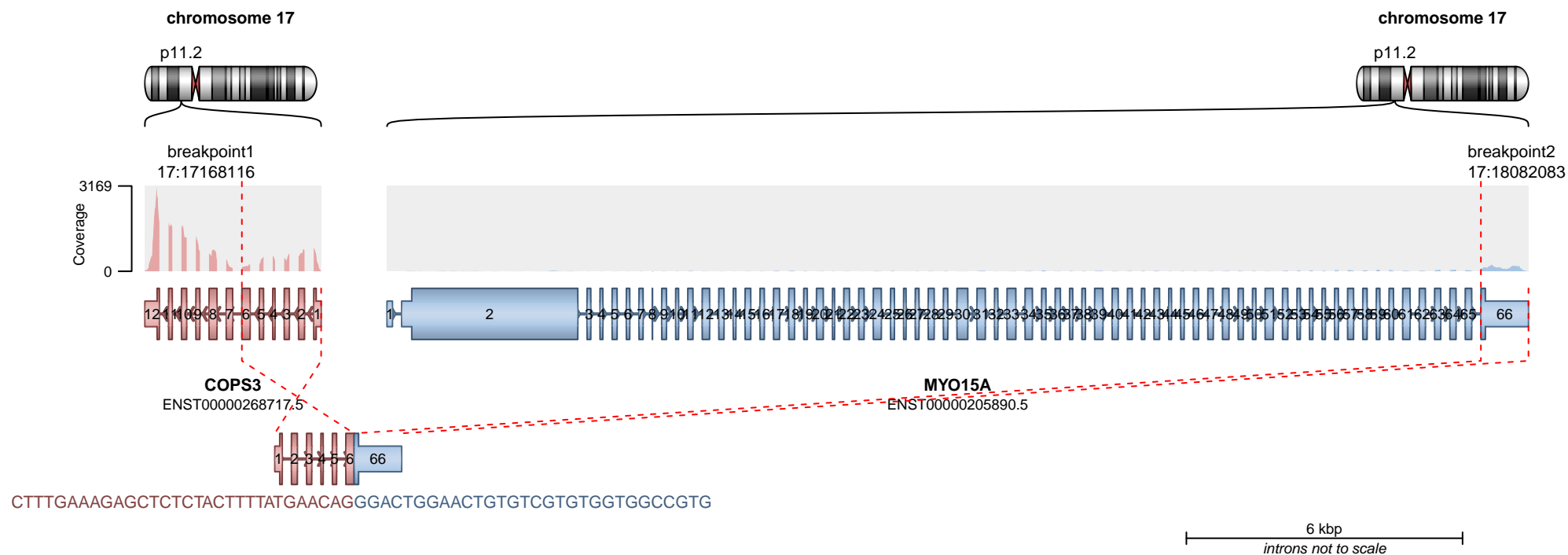
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

Split reads at breakpoint1 = 1
Split reads at breakpoint2 = 5
Discordant mates = 3

translocation deletion
duplication inversion

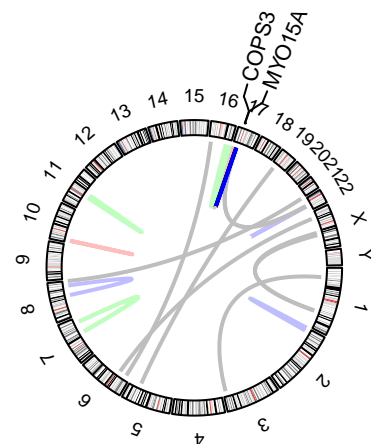
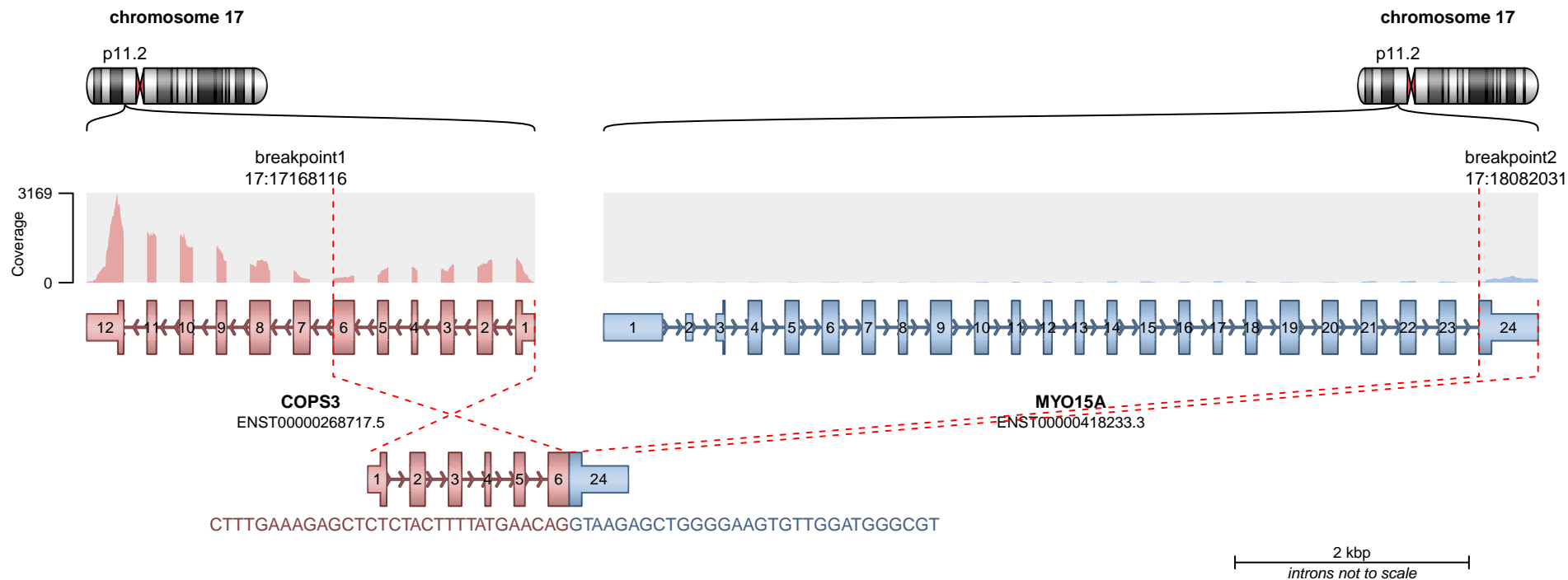


— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 1
Split reads at breakpoint2 = 5
Discordant mates = 3

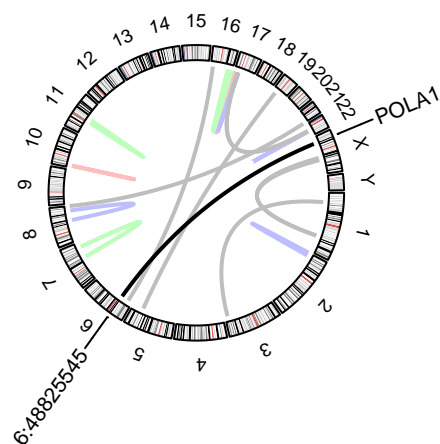
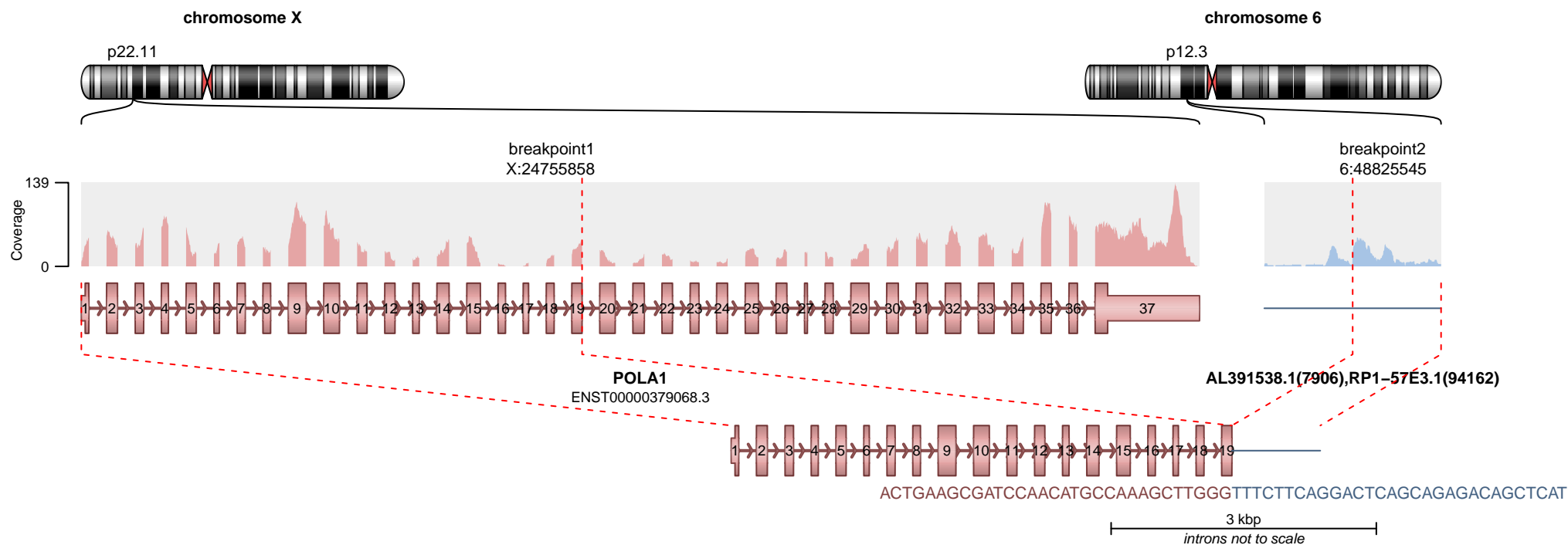


No protein domains retained in fusion.

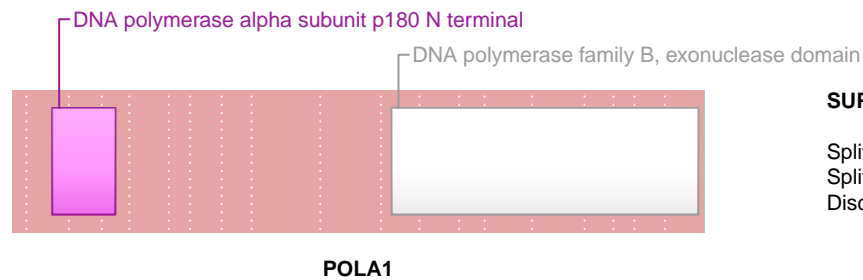
SUPPORTING READ COUNT

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

— translocation — deletion
— duplication — inversion



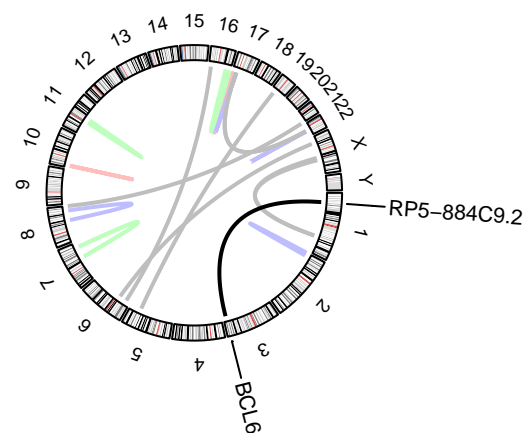
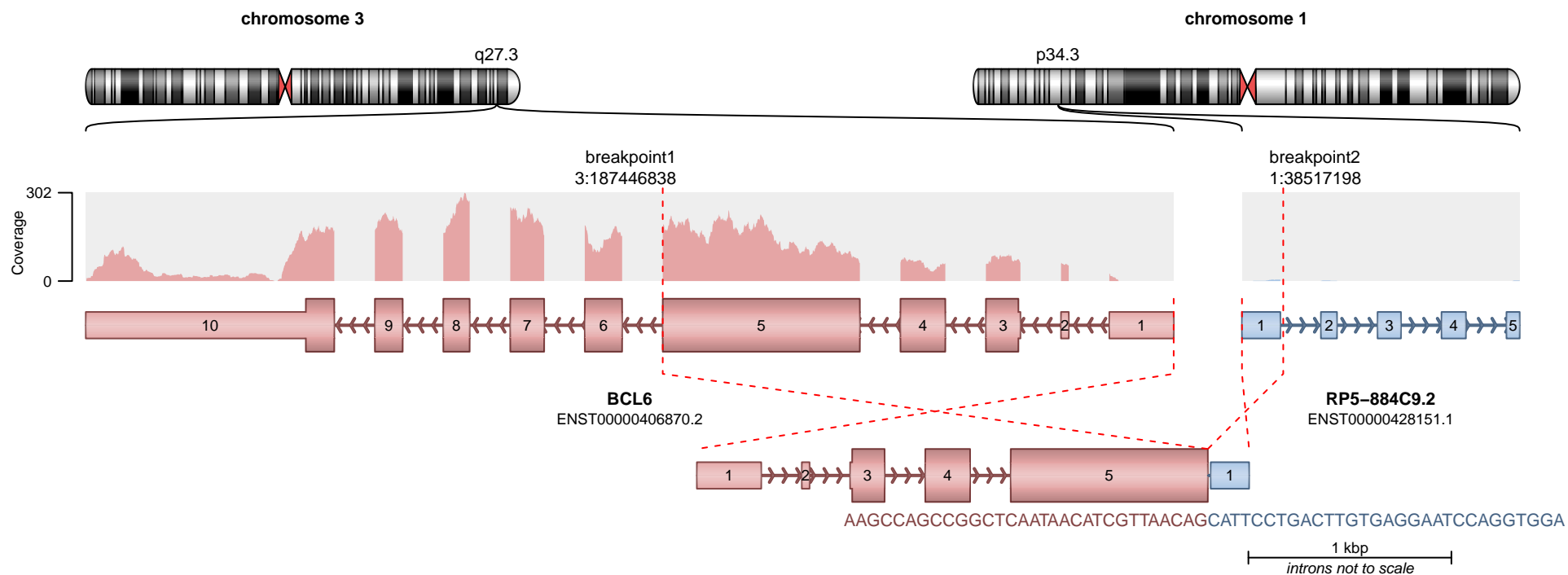
RETAINED PROTEIN DOMAINS out-of-frame fusion



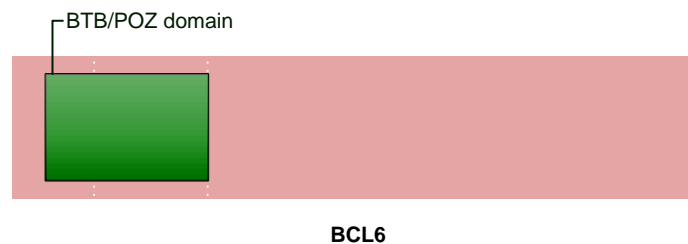
SUPPORTING READ COUNT

Split reads at breakpoint1 = 1
Split reads at breakpoint2 = 7
Discordant mates = 1

— translocation — deletion
— duplication — inversion



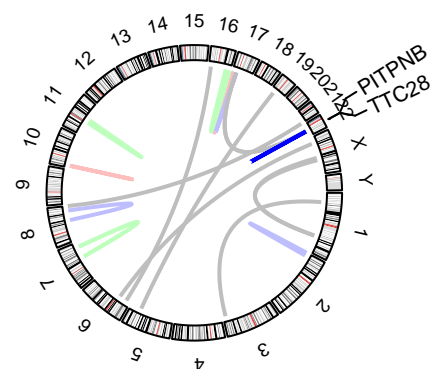
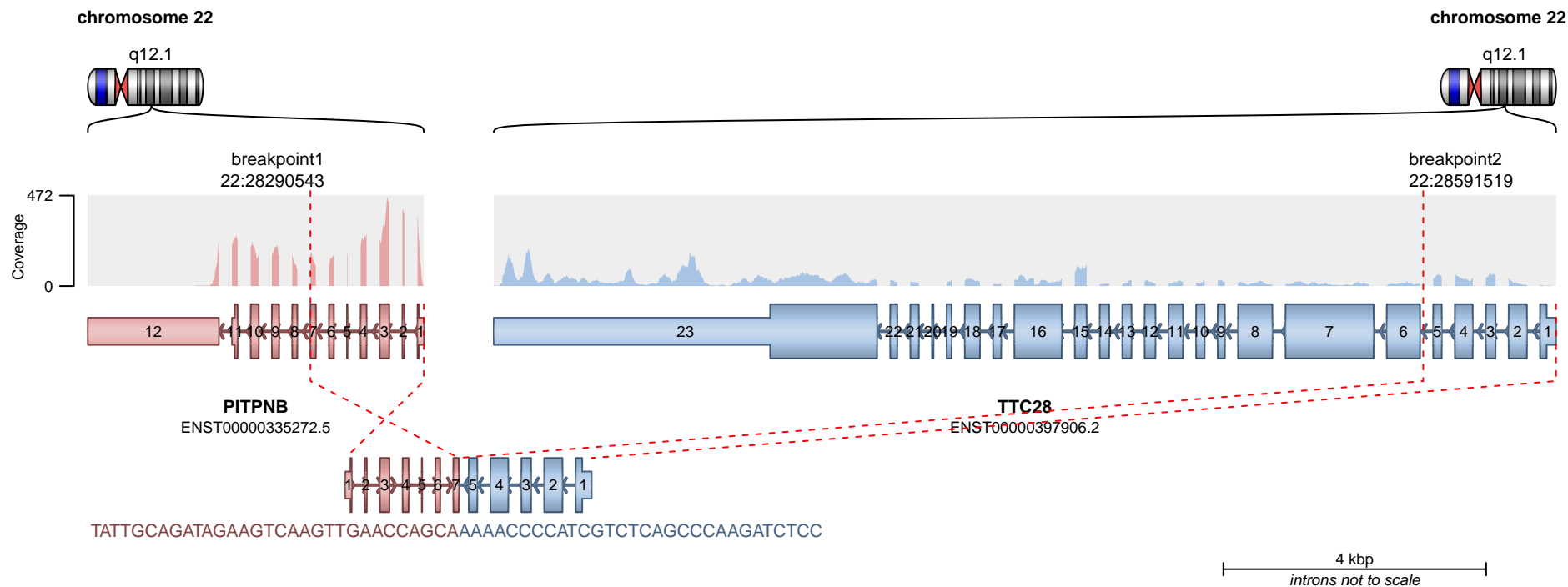
RETAINED PROTEIN DOMAINS out-of-frame fusion



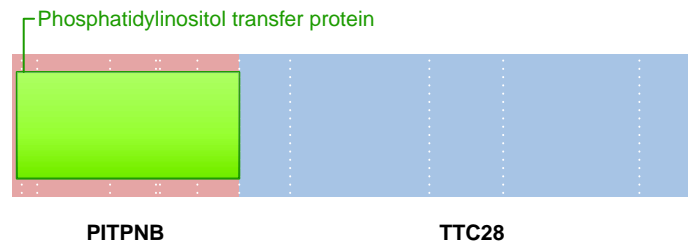
SUPPORTING READ COUNT

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

— translocation — deletion
— duplication — inversion



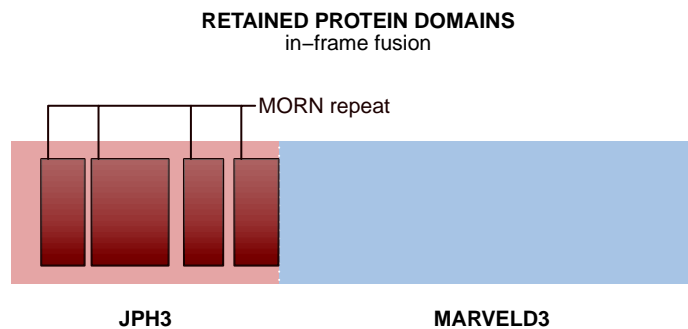
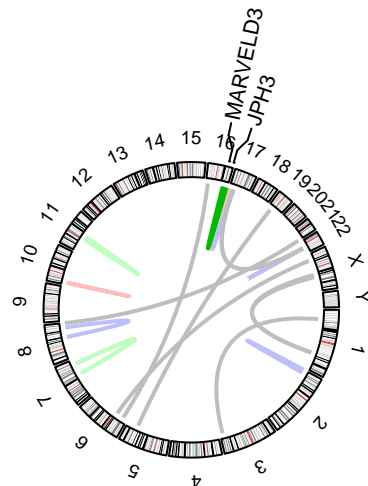
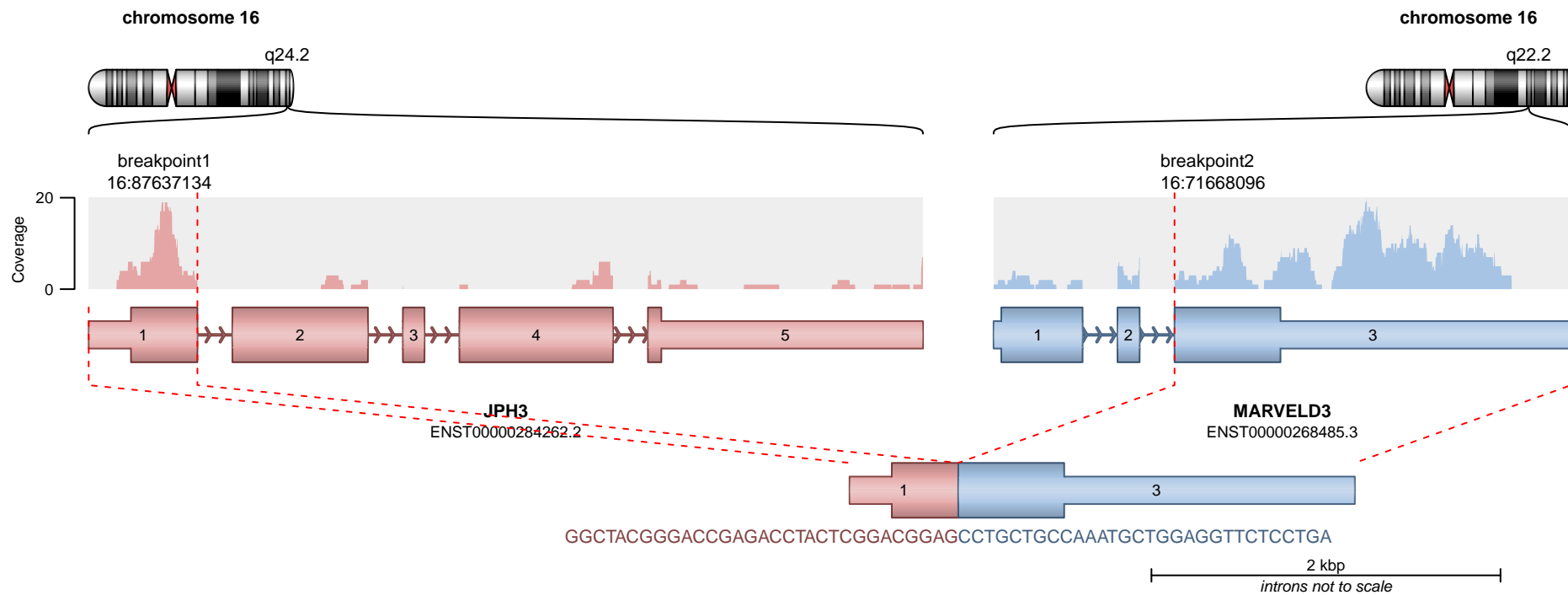
RETAINED PROTEIN DOMAINS out-of-frame fusion



SUPPORTING READ COUNT

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

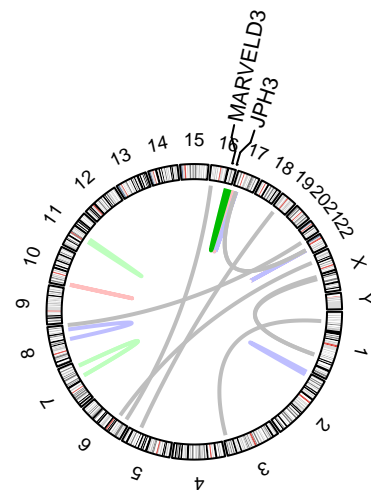
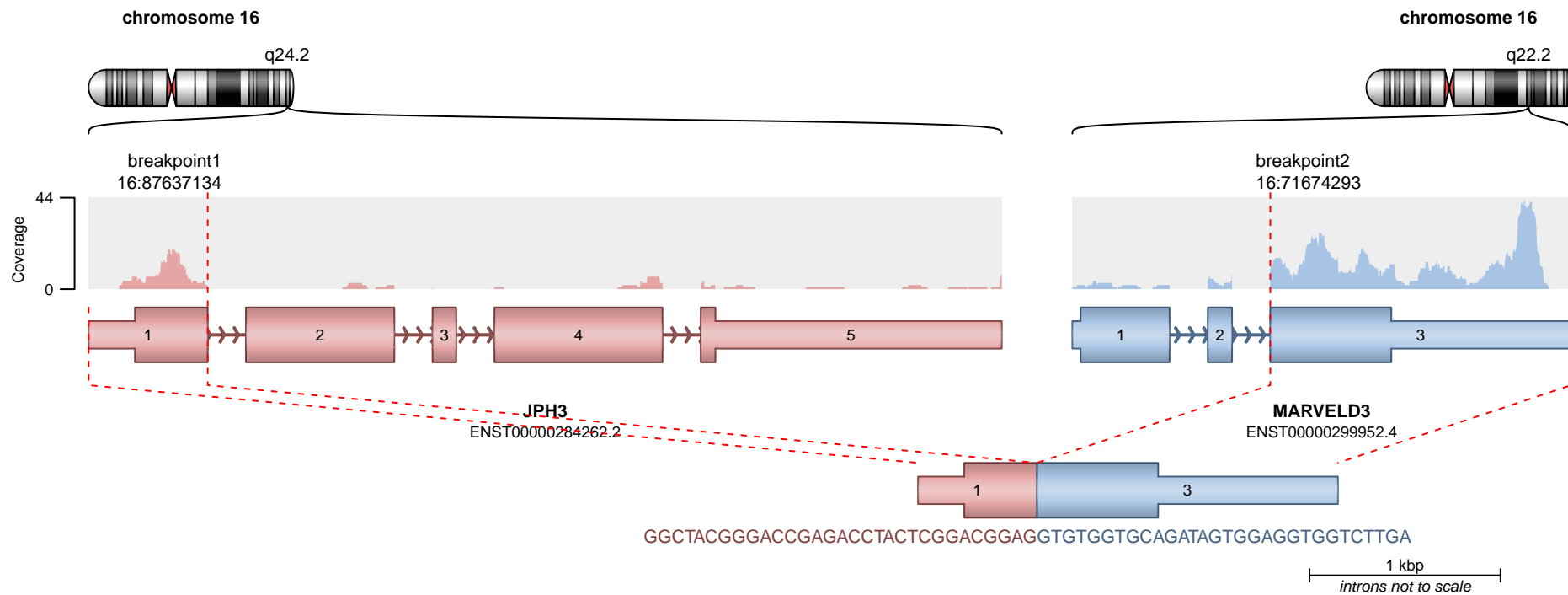
— translocation — deletion
— duplication — inversion



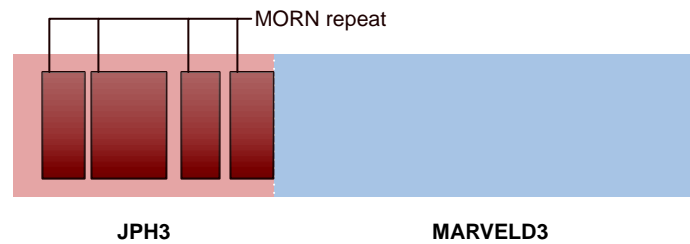
SUPPORTING READ COUNT

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

— translocation — deletion
— duplication — inversion



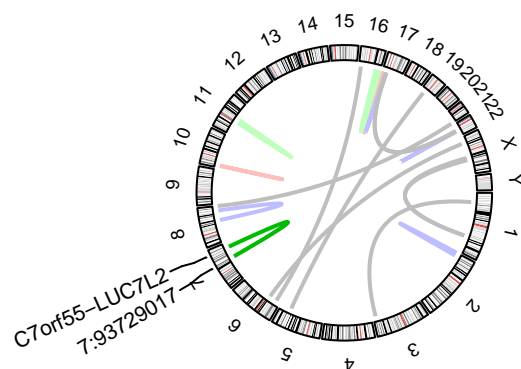
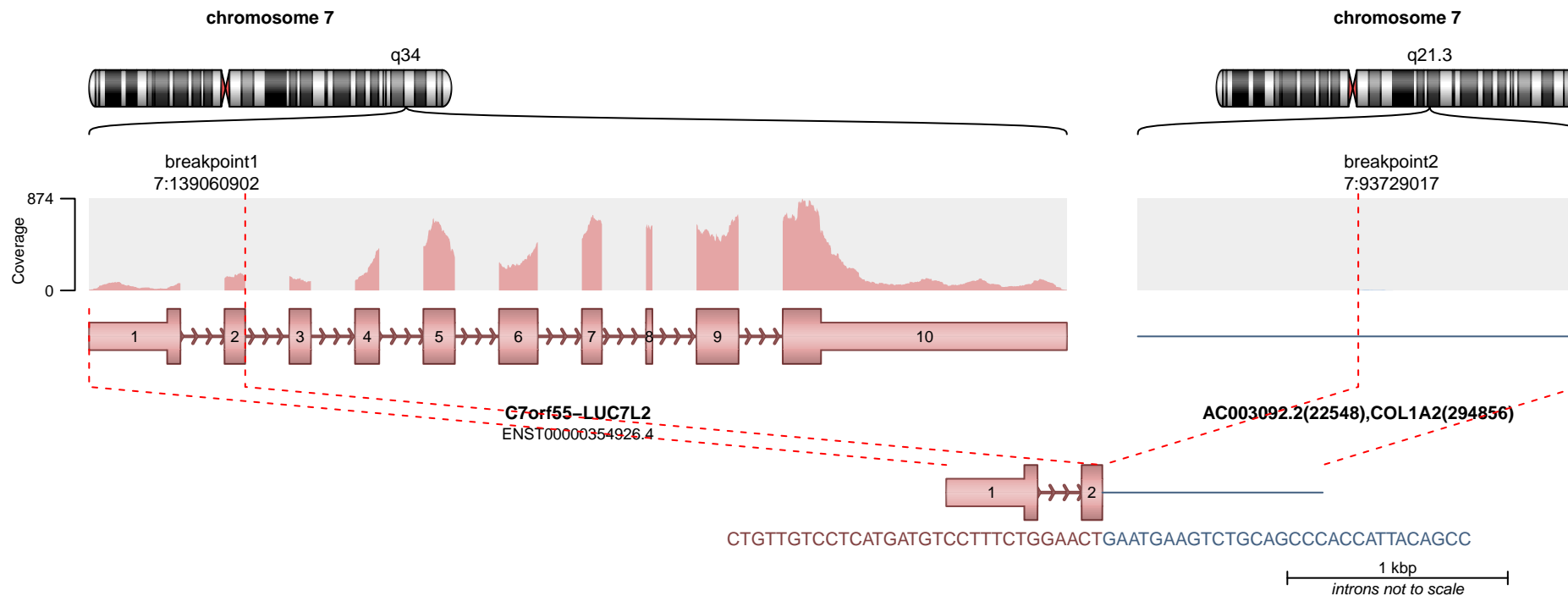
RETAINED PROTEIN DOMAINS in-frame fusion



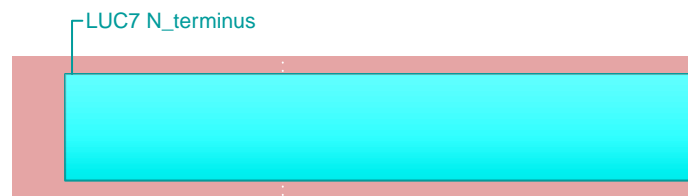
SUPPORTING READ COUNT

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

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS out-of-frame fusion

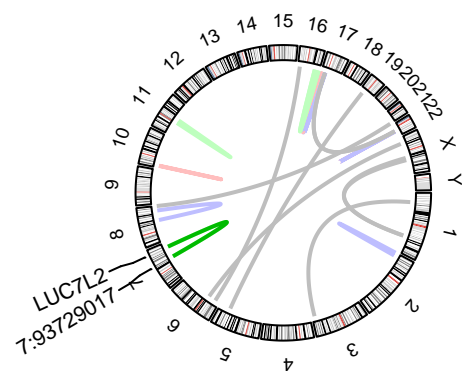
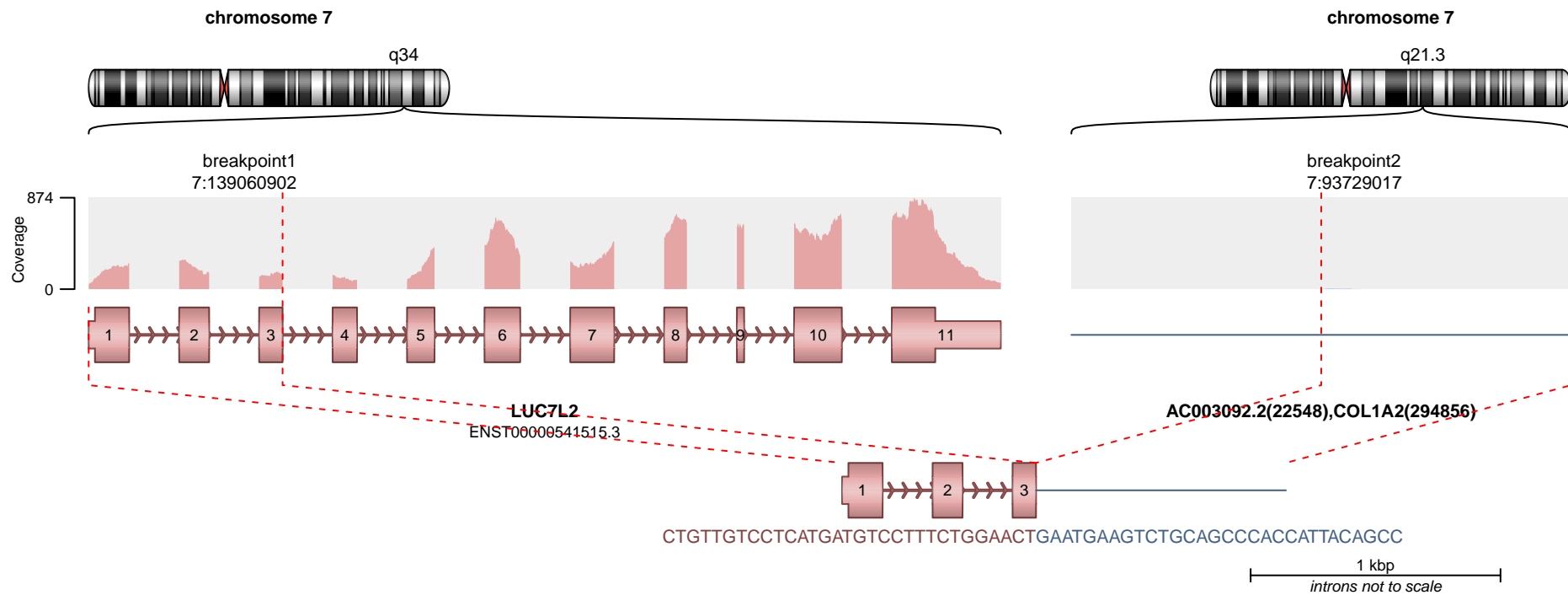


C7orf55-LUC7L2

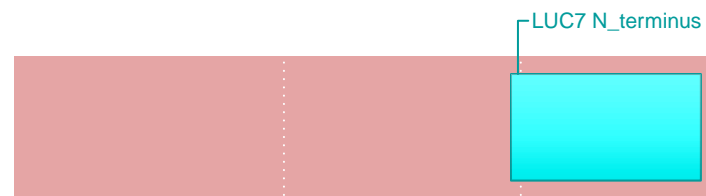
SUPPORTING READ COUNT

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

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS
out-of-frame fusion

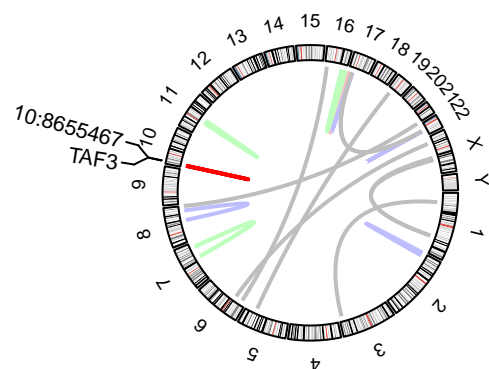
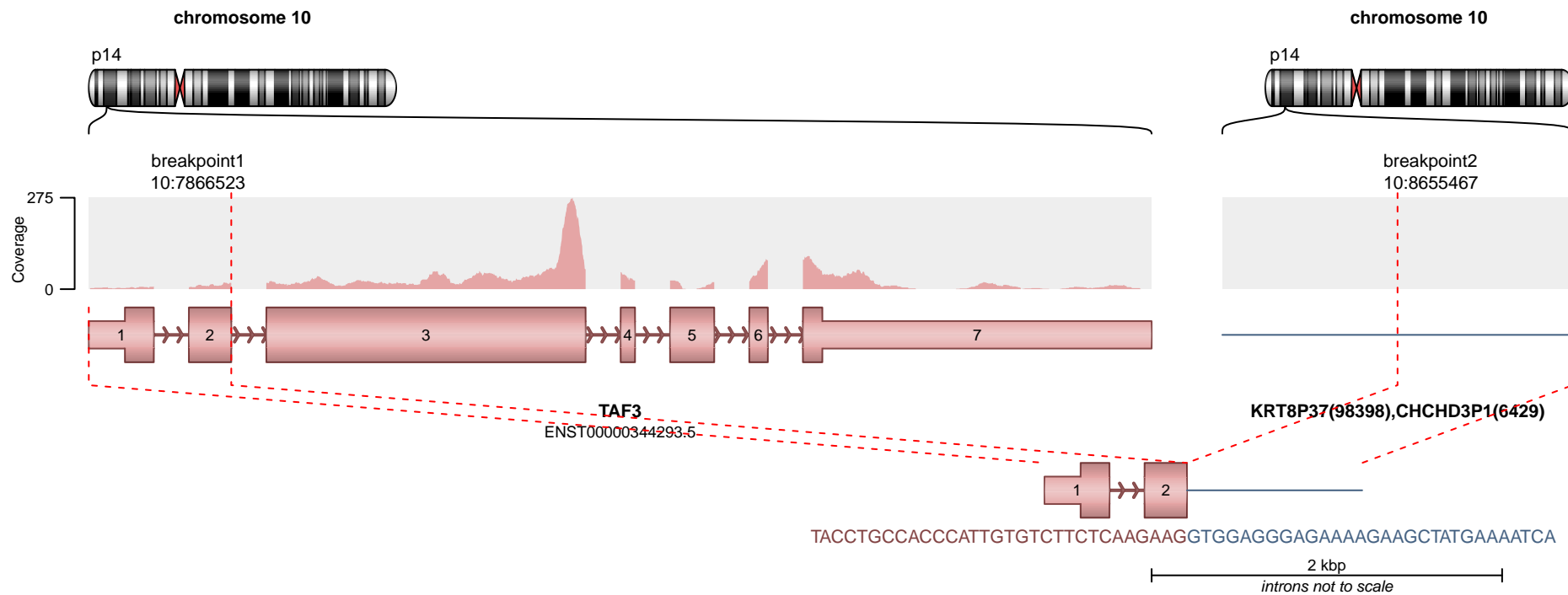


LUC7L2

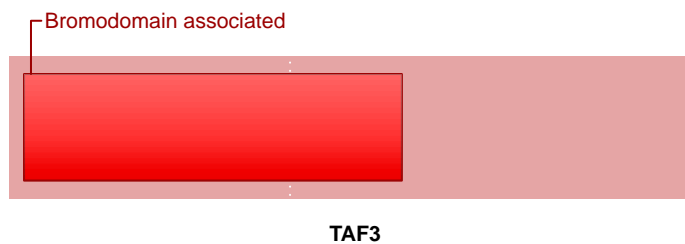
SUPPORTING READ COUNT

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

— translocation — deletion
— duplication — inversion

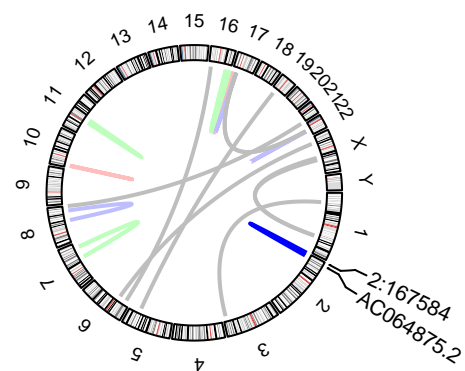
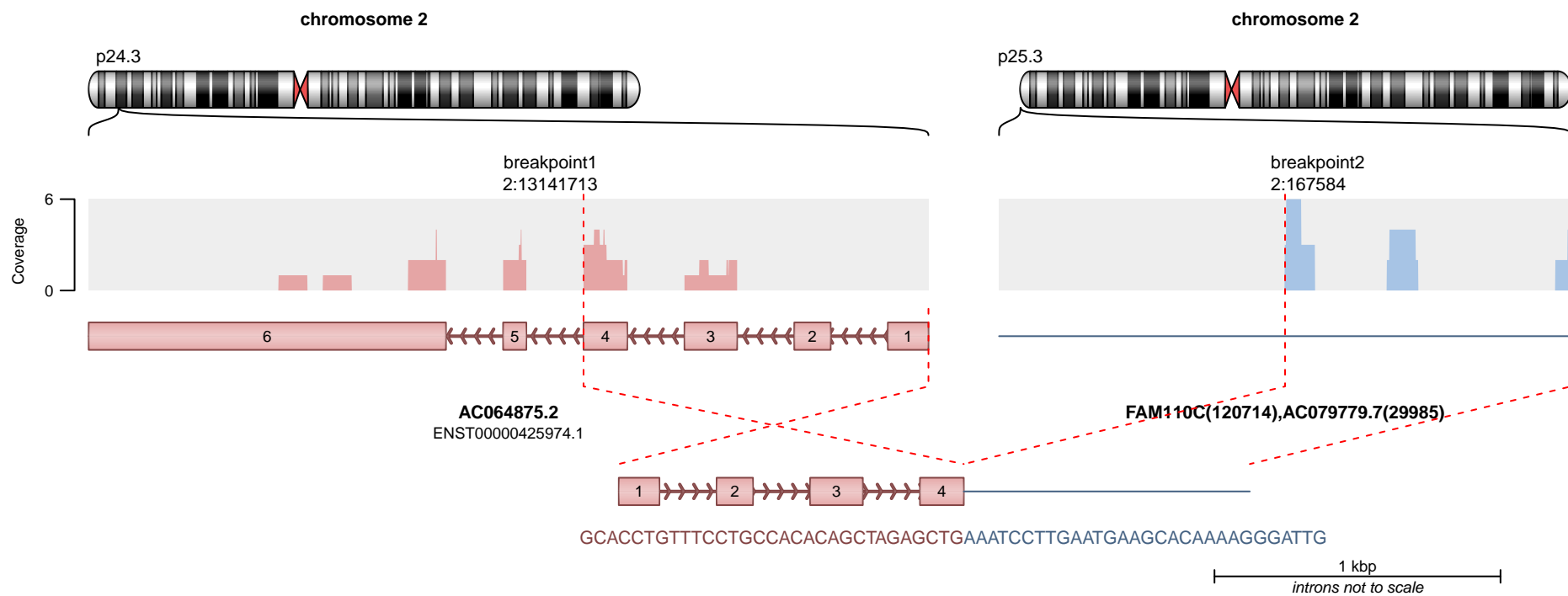


RETAINED PROTEIN DOMAINS out-of-frame fusion



SUPPORTING READ COUNT

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

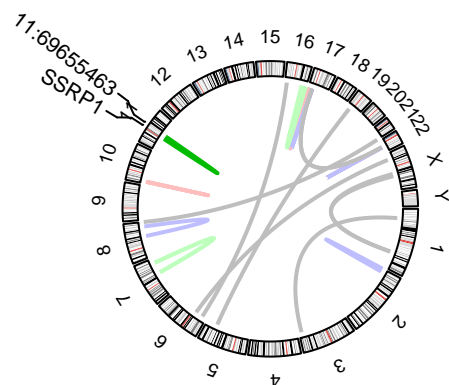
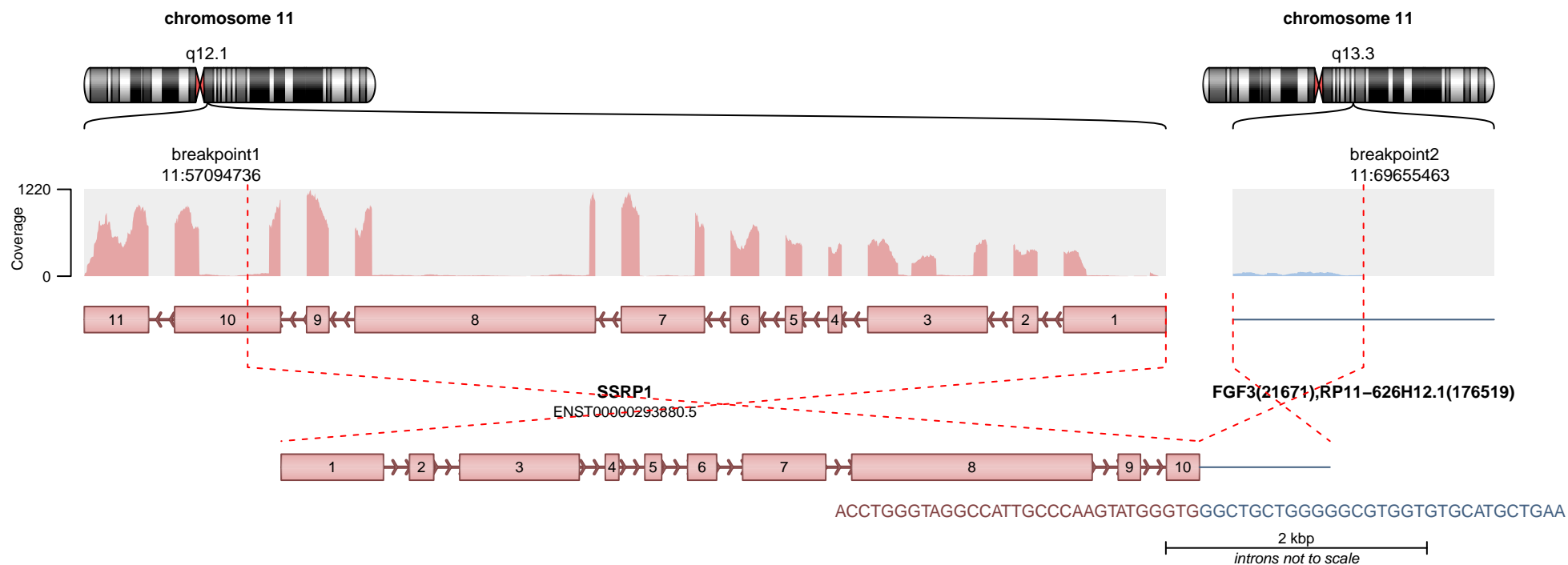


Genes are not protein-coding.

SUPPORTING READ COUNT

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

— translocation — deletion
— duplication — inversion

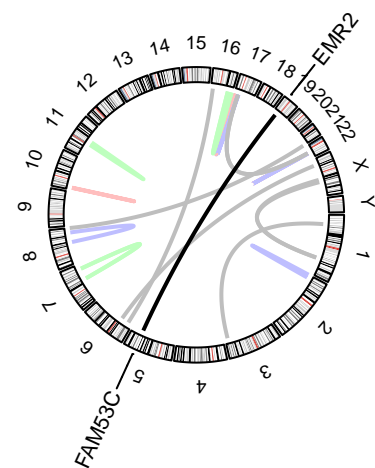
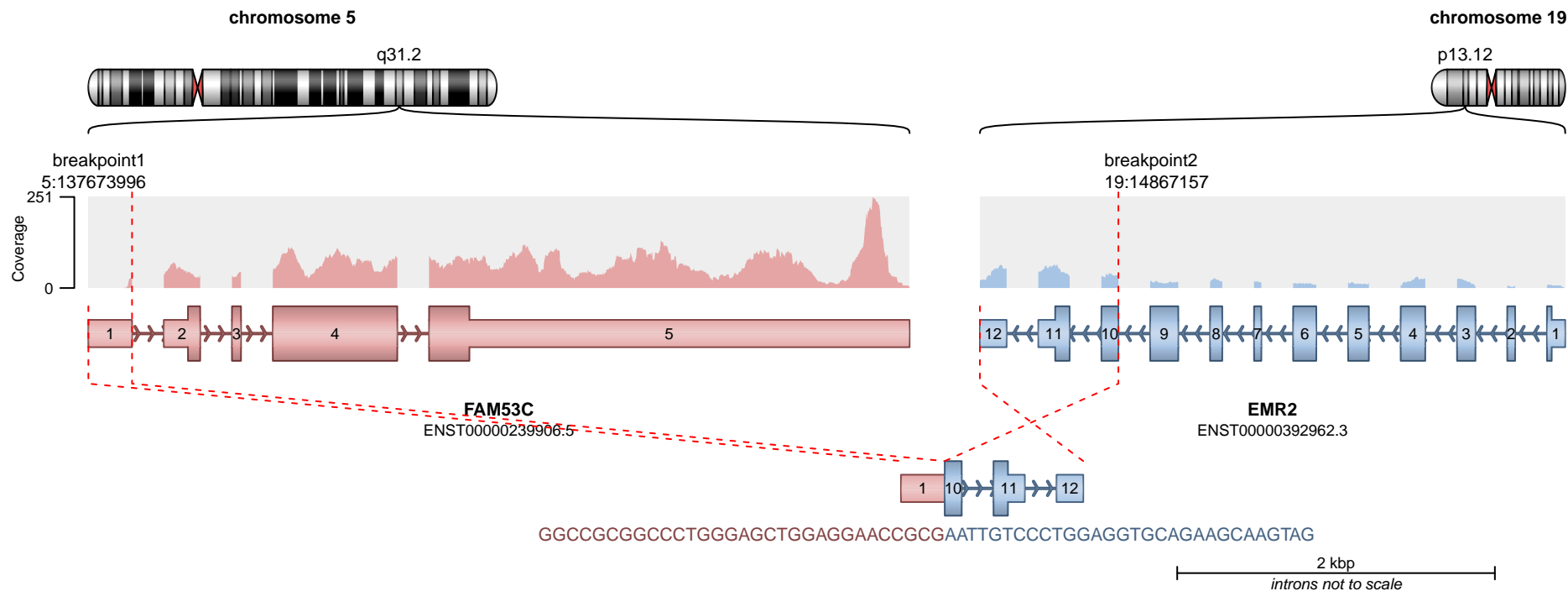


— translocation — deletion
— duplication — inversion

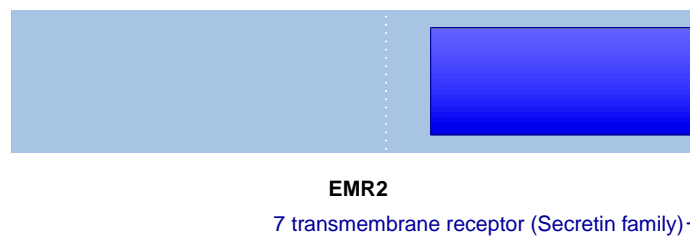
Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 3
Split reads at breakpoint2 = 9
Discordant mates = 2



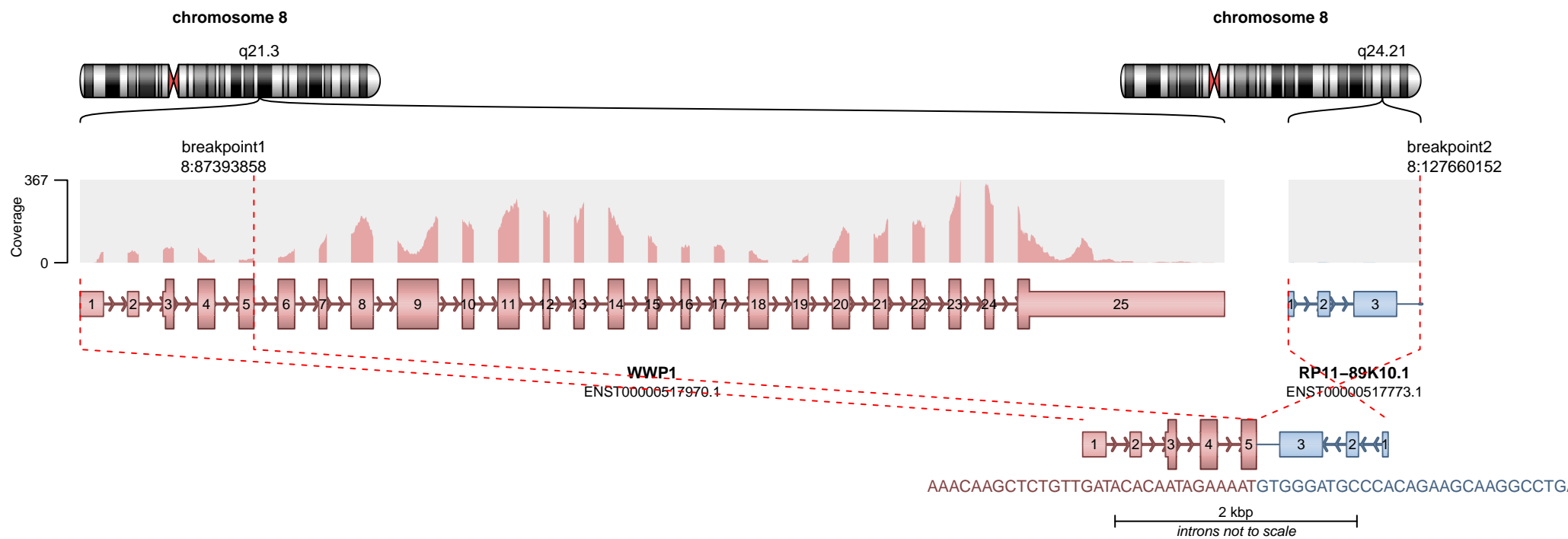
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

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

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS out-of-frame fusion

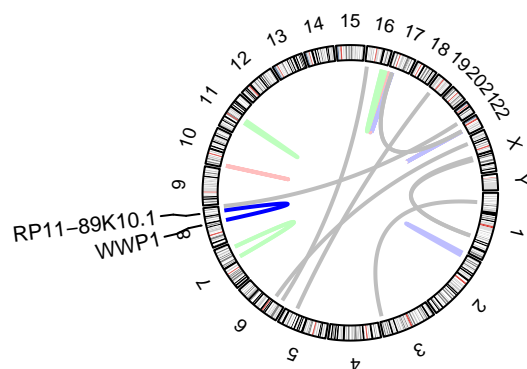


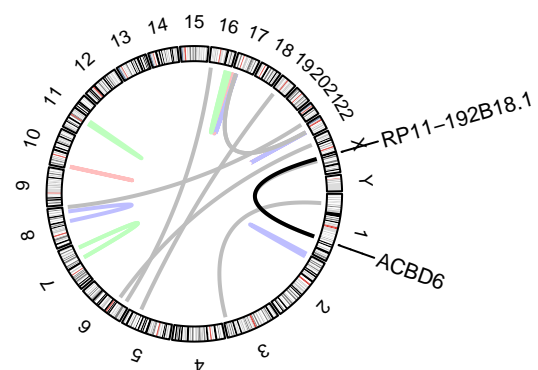
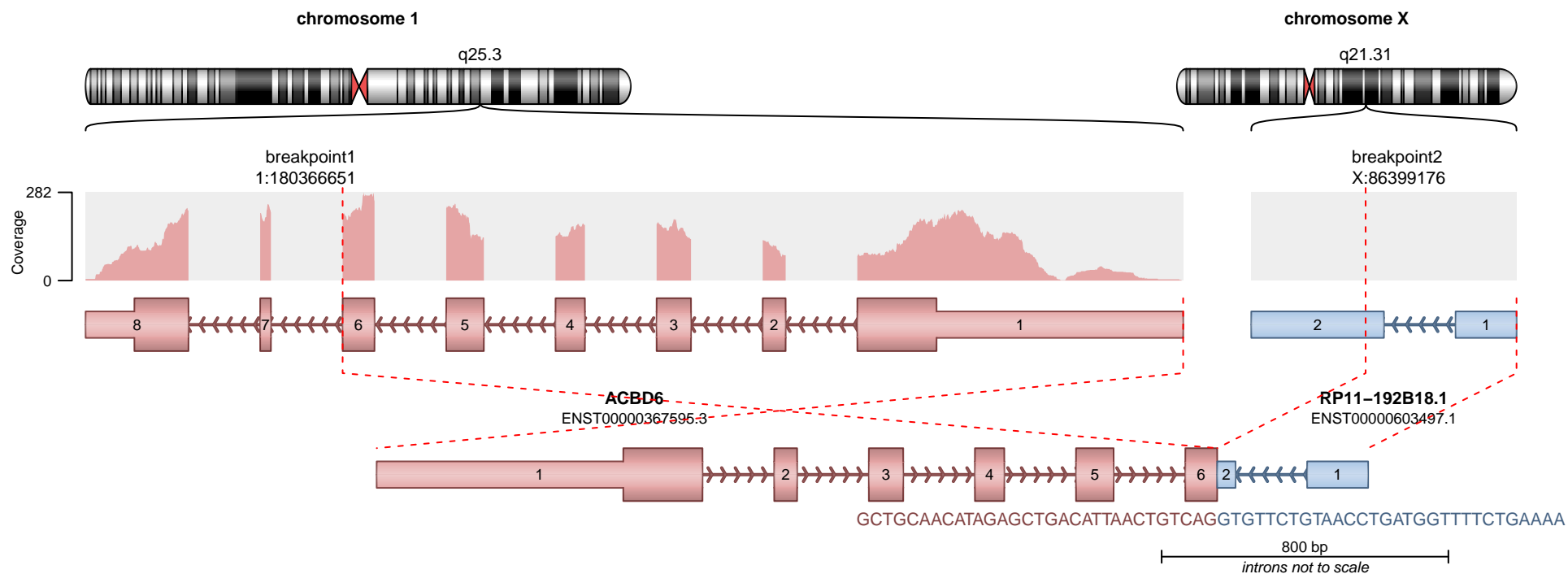
WWP1

SUPPORTING READ COUNT

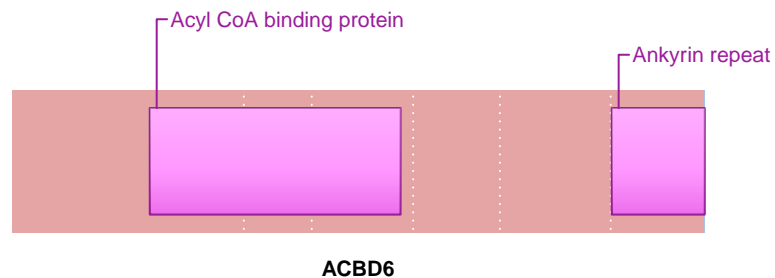
Split reads at breakpoint1 = 0
Split reads at breakpoint2 = 3
Discordant mates = 0

— translocation — deletion
— duplication — inversion





RETAINED PROTEIN DOMAINS out-of-frame fusion



SUPPORTING READ COUNT

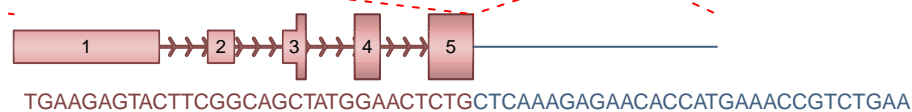
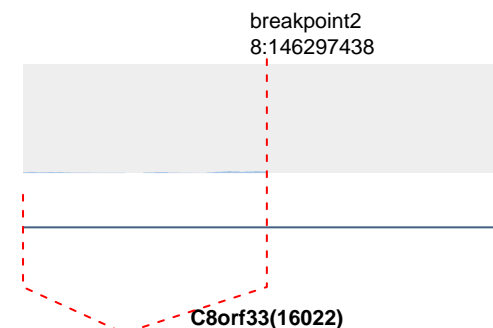
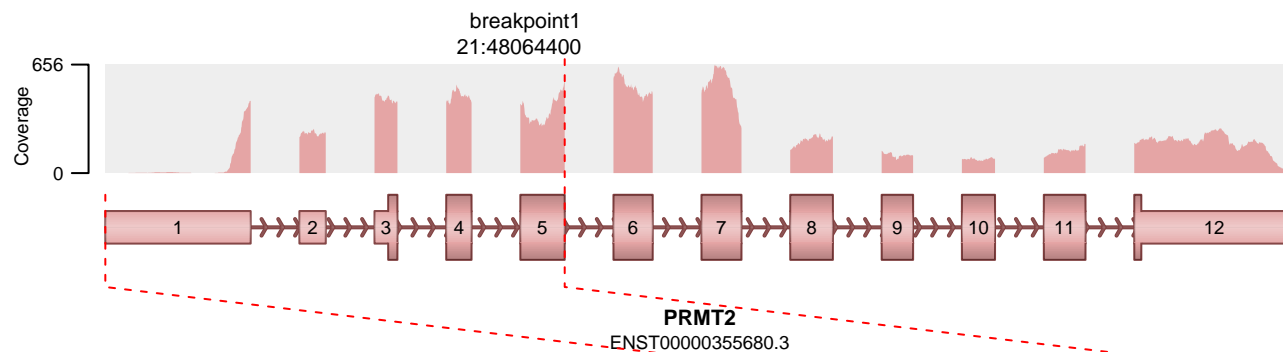
Split reads at breakpoint1 = 3
Split reads at breakpoint2 = 0
Discordant mates = 0

— translocation — deletion
— duplication — inversion

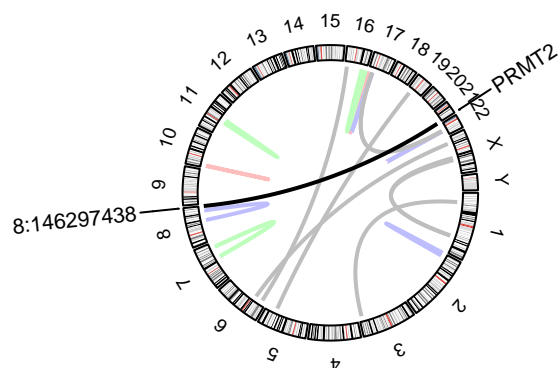
chromosome 21



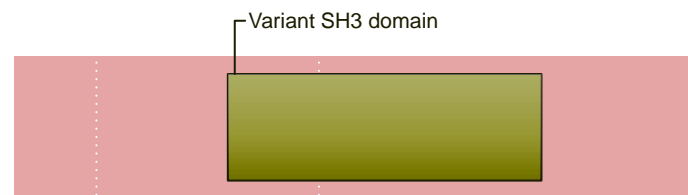
chromosome 8



1 kbp
introns not to scale



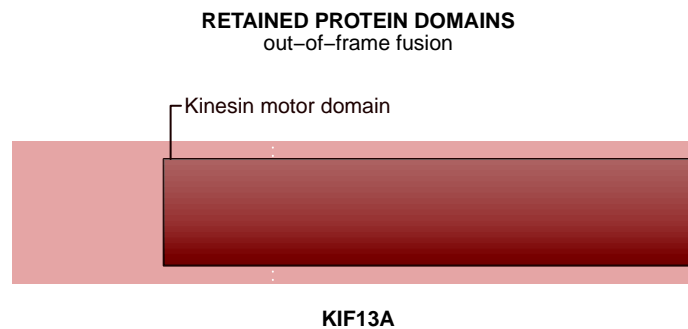
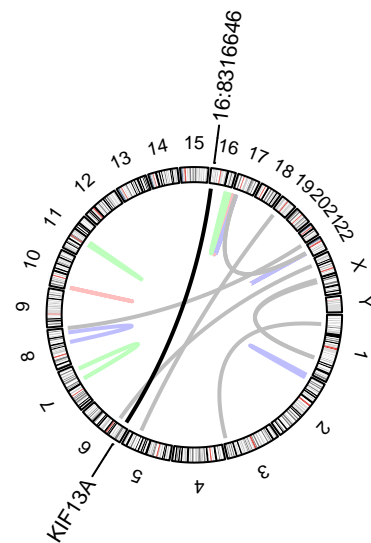
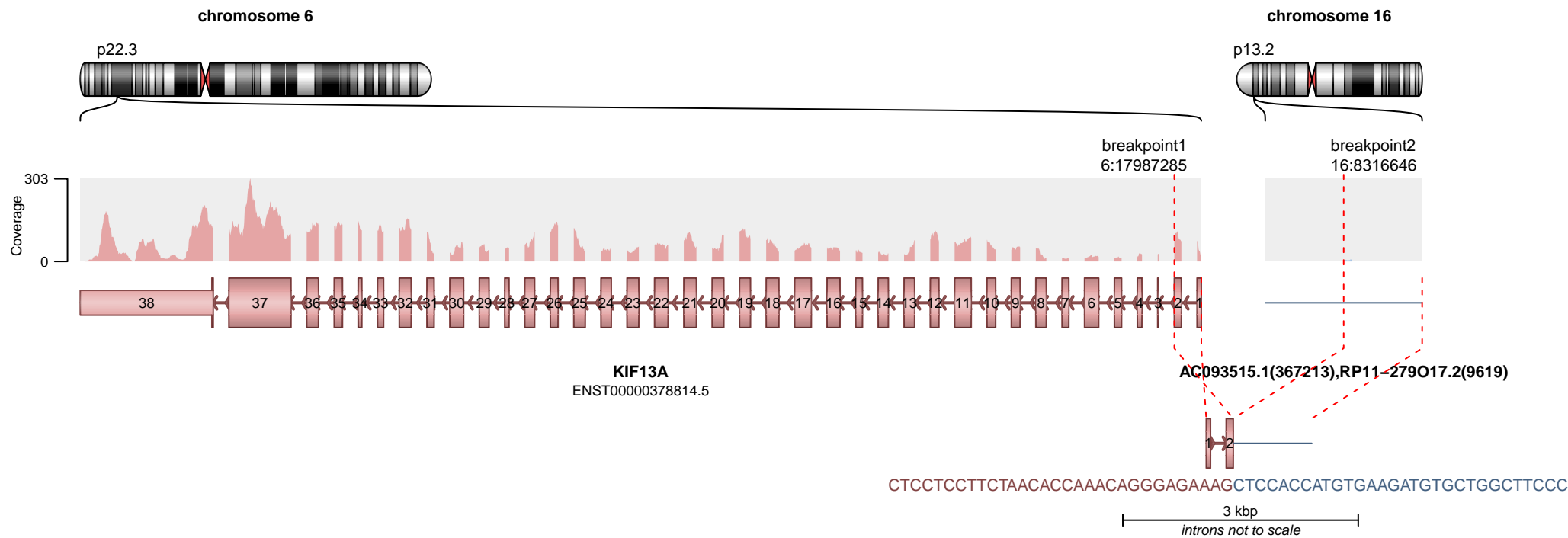
RETAINED PROTEIN DOMAINS
out-of-frame fusion



SUPPORTING READ COUNT

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

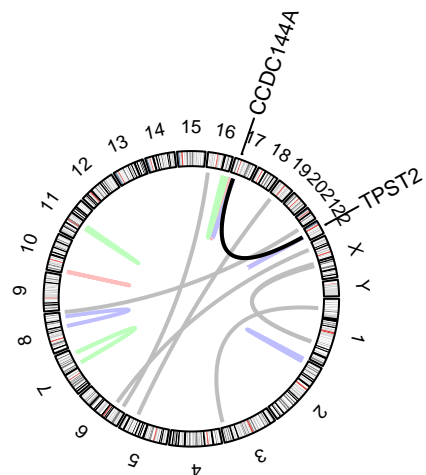
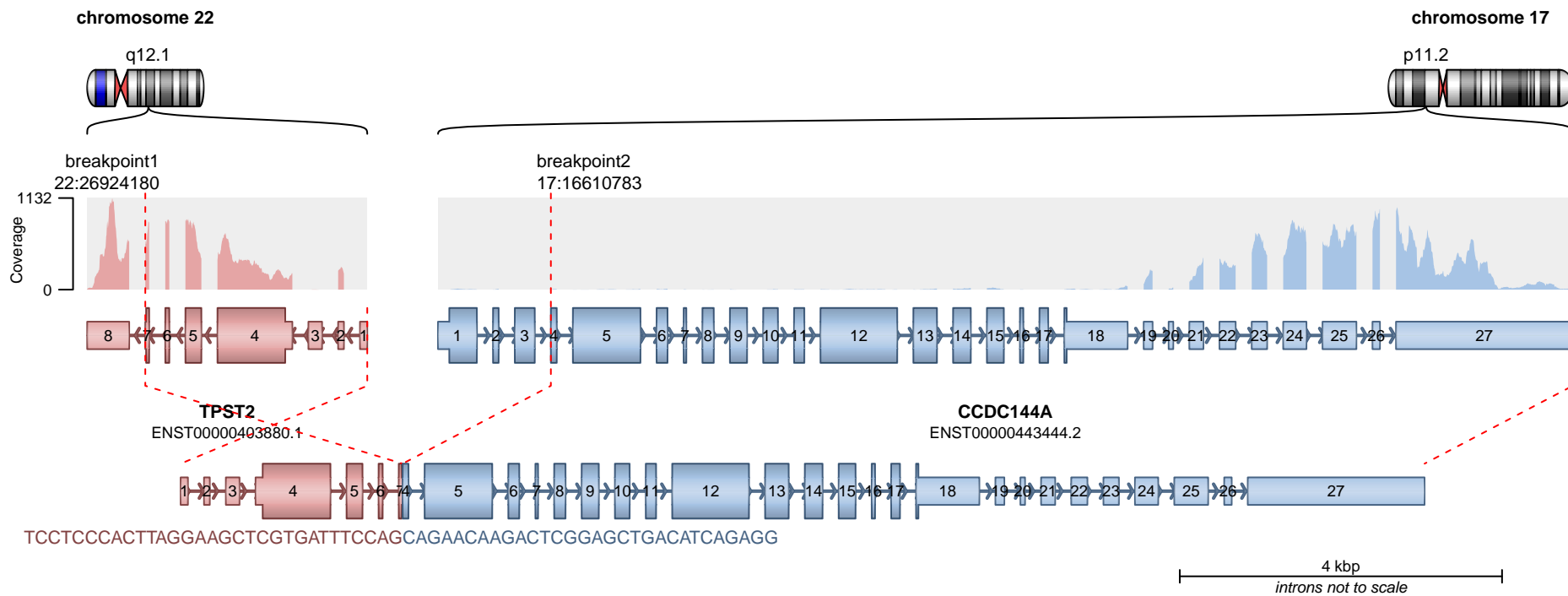
— translocation — deletion
— duplication — inversion



SUPPORTING READ COUNT

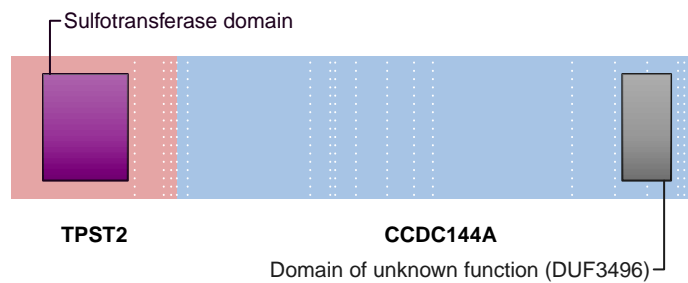
Split reads at breakpoint1 = 0
Split reads at breakpoint2 = 2
Discordant mates = 0

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS

stop codon before fusion junction

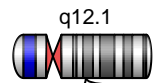


SUPPORTING READ COUNT

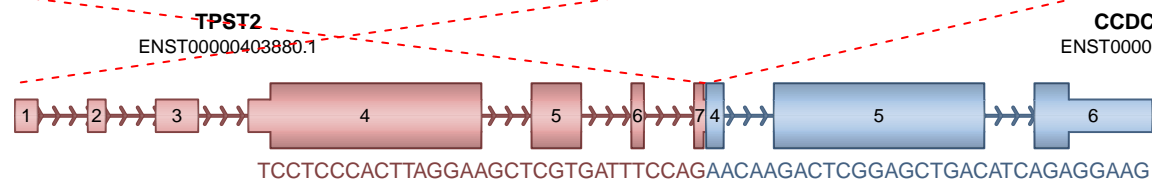
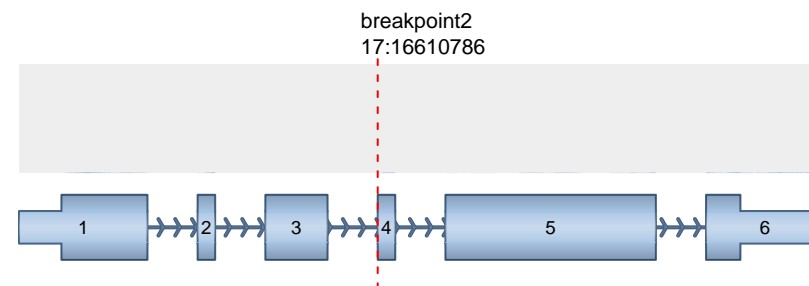
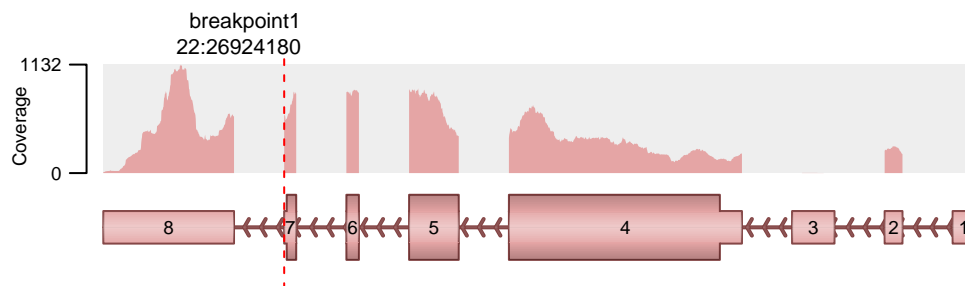
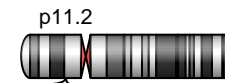
Split reads at breakpoint1 = 2
Split reads at breakpoint2 = 0
Discordant mates = 0

— translocation — deletion
— duplication — inversion

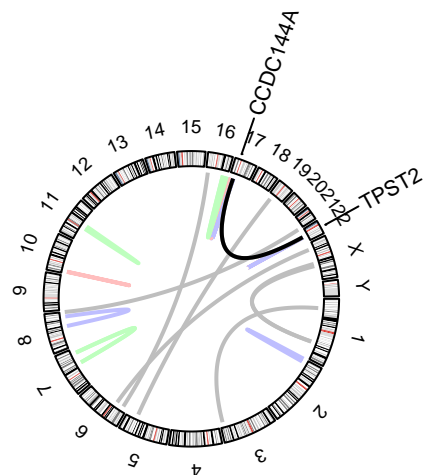
chromosome 22



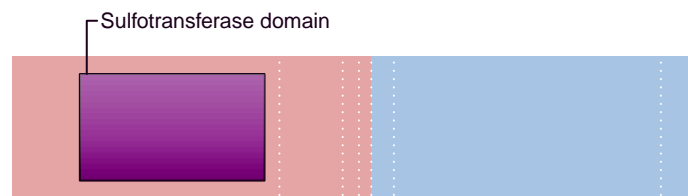
chromosome 17



1 kbp
introns not to scale



RETAINED PROTEIN DOMAINS
stop codon before fusion junction



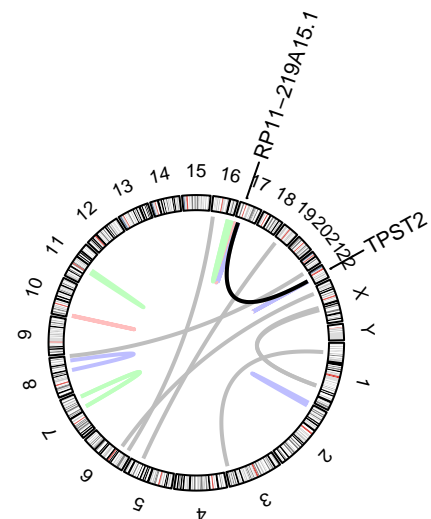
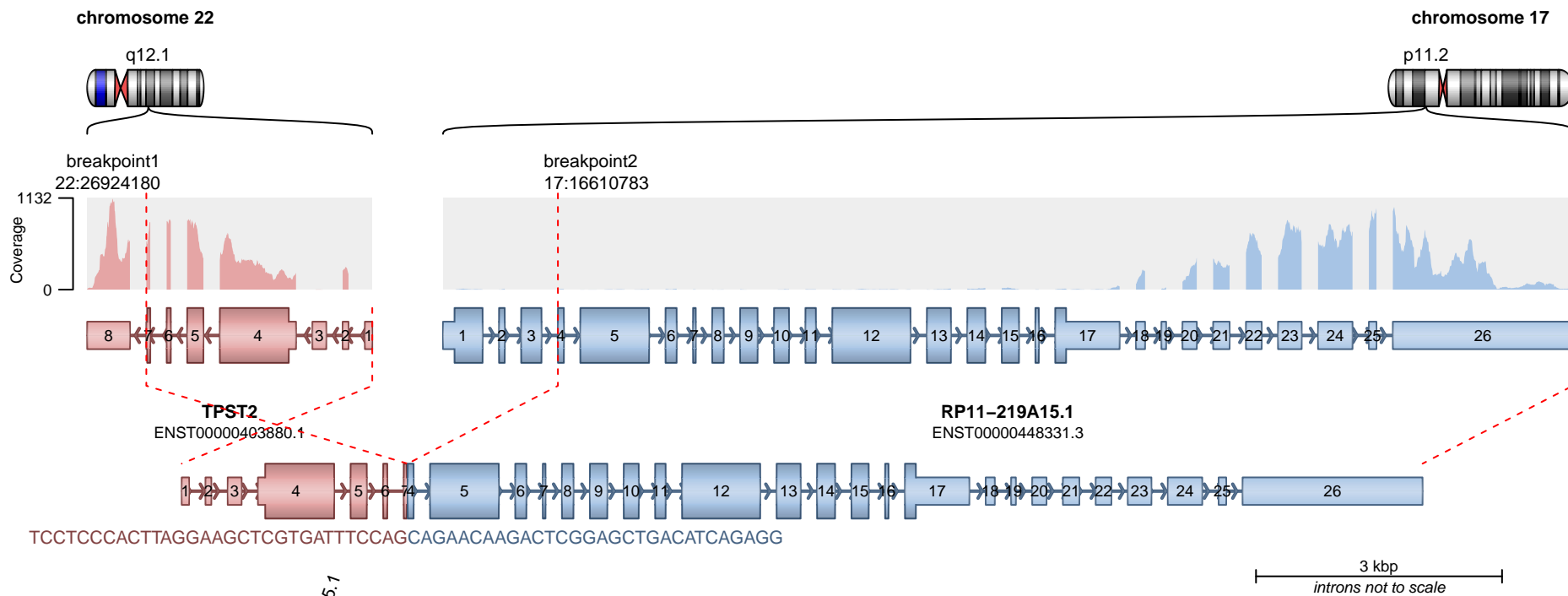
TPST2

CCDC144A

SUPPORTING READ COUNT

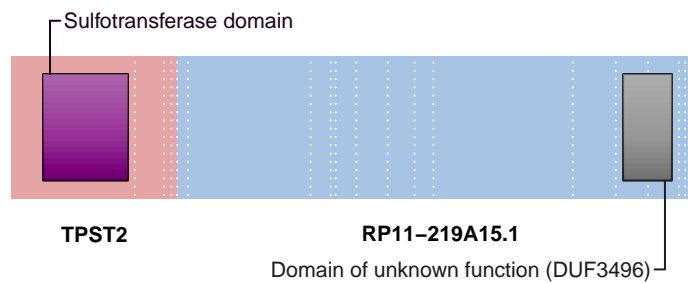
Split reads at breakpoint1 = 0
Split reads at breakpoint2 = 1
Discordant mates = 0

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS

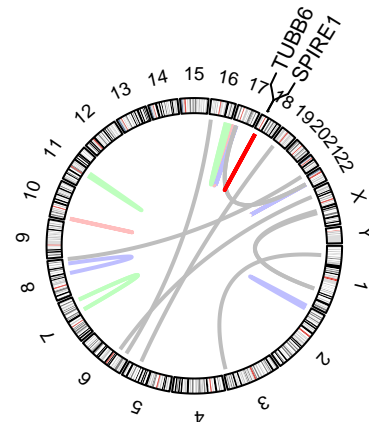
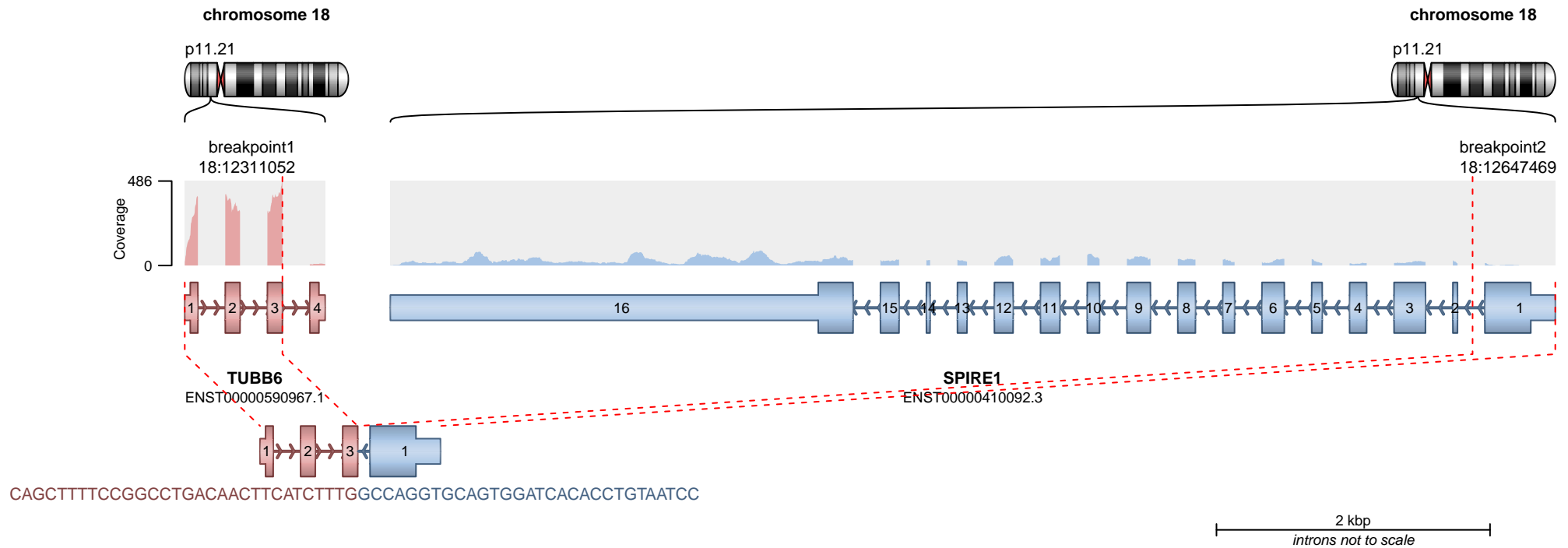
stop codon before fusion junction



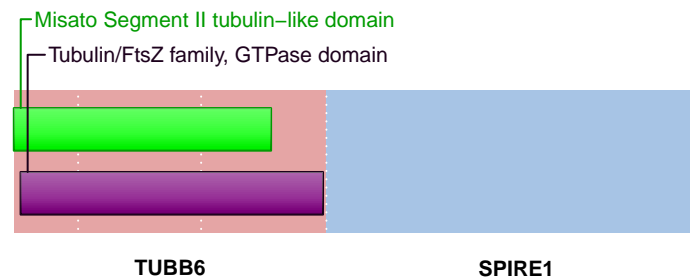
SUPPORTING READ COUNT

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

— translocation — deletion
— duplication — inversion



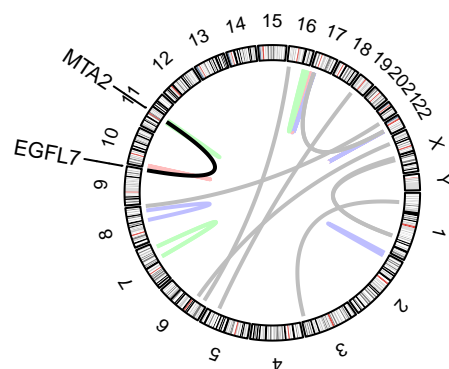
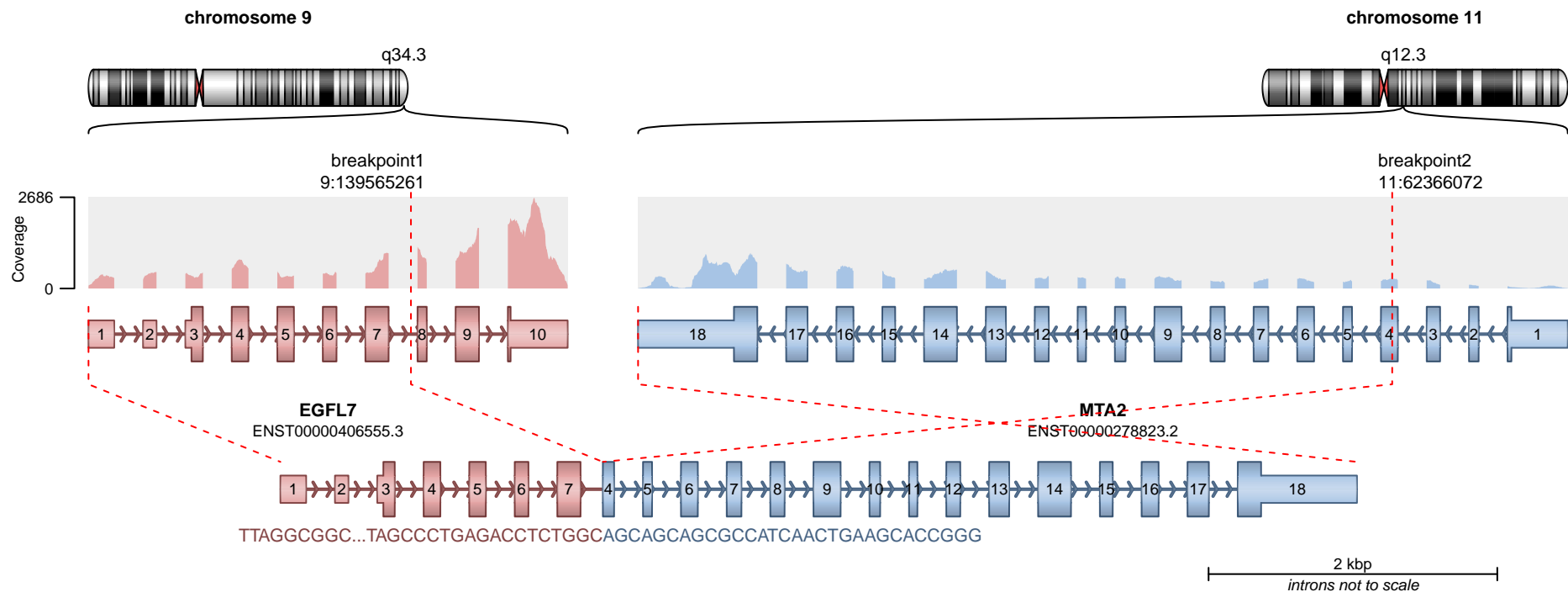
RETAINED PROTEIN DOMAINS out-of-frame fusion



SUPPORTING READ COUNT

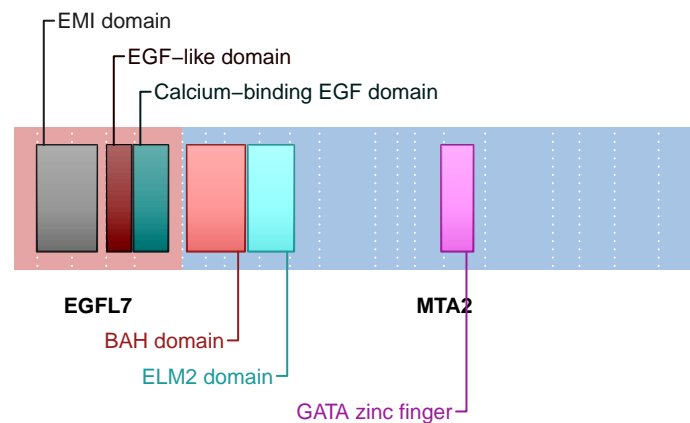
Split reads at breakpoint1 = 1
Split reads at breakpoint2 = 3
Discordant mates = 1

— translocation — deletion
— duplication — inversion



RETAINED PROTEIN DOMAINS

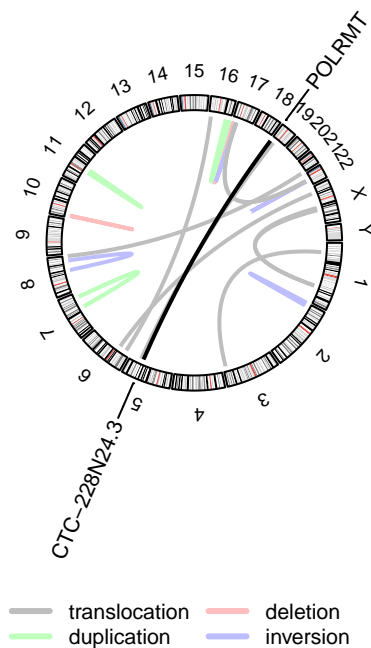
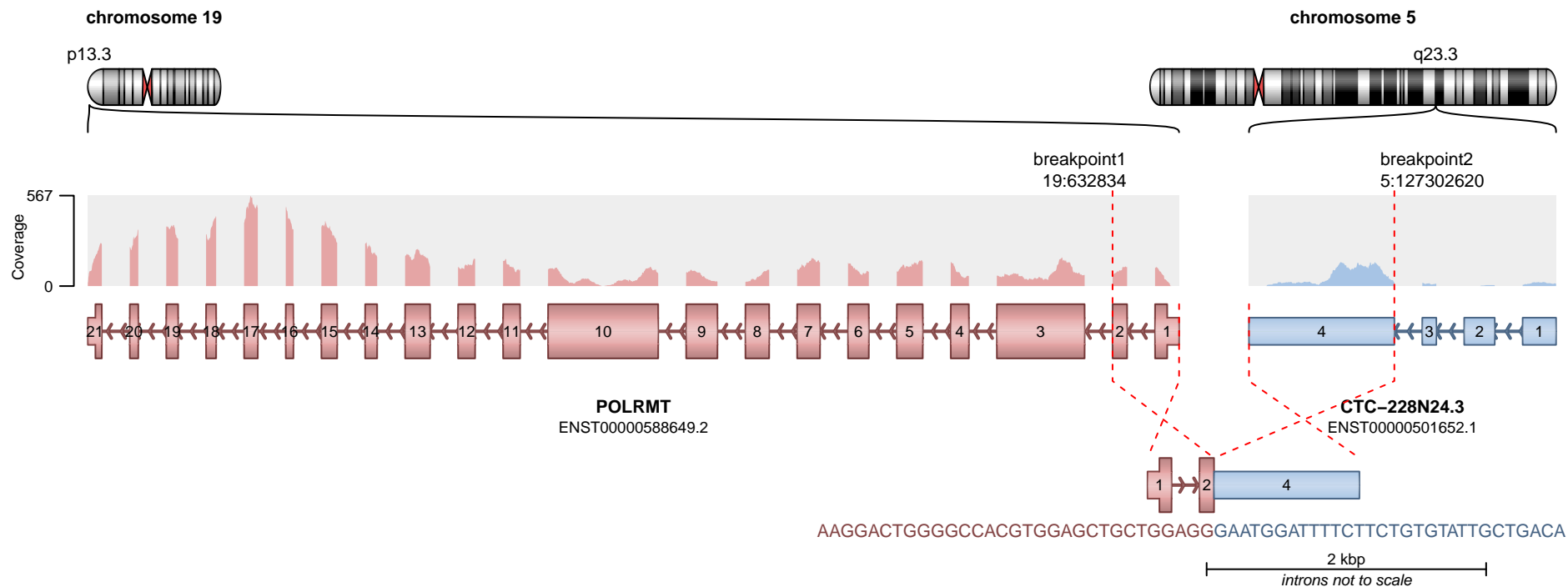
reading frame unclear



SUPPORTING READ COUNT

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

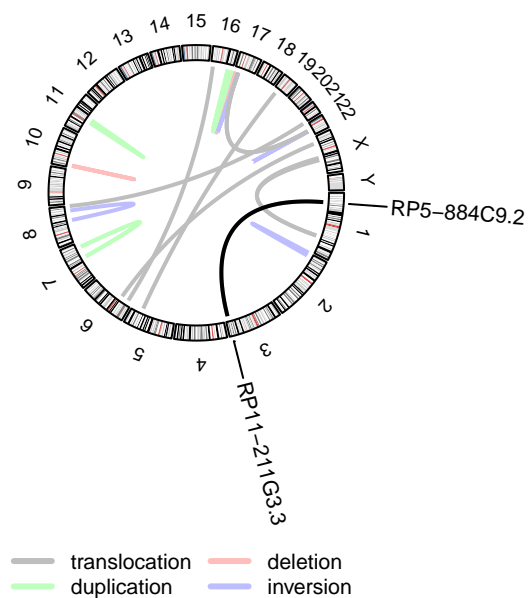
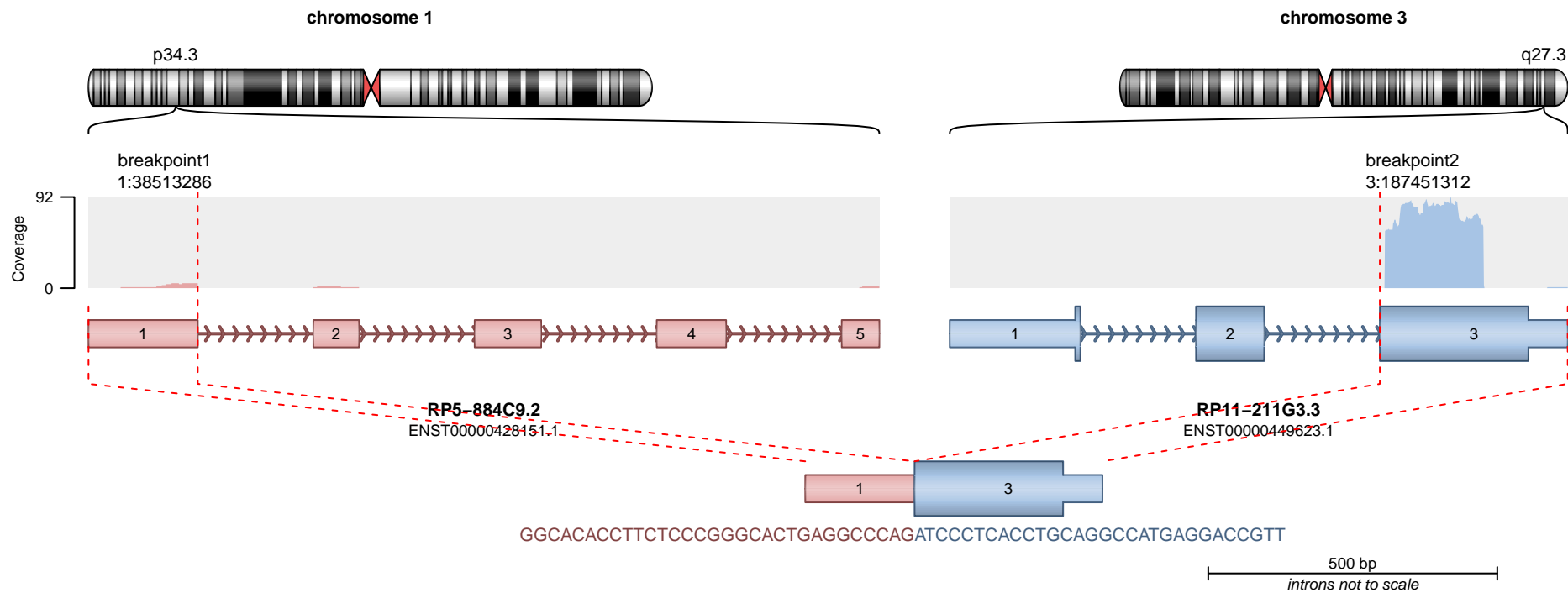
— translocation — deletion
— duplication — inversion



No protein domains retained in fusion.

SUPPORTING READ COUNT

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



No protein domains retained in fusion.

SUPPORTING READ COUNT

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