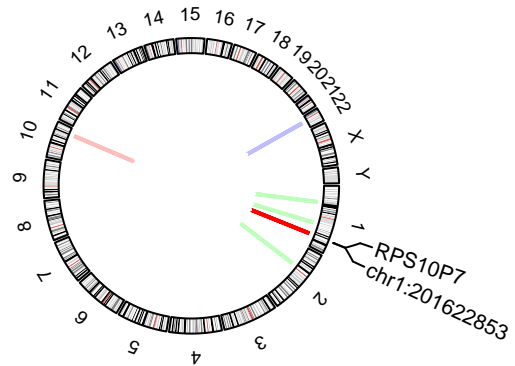
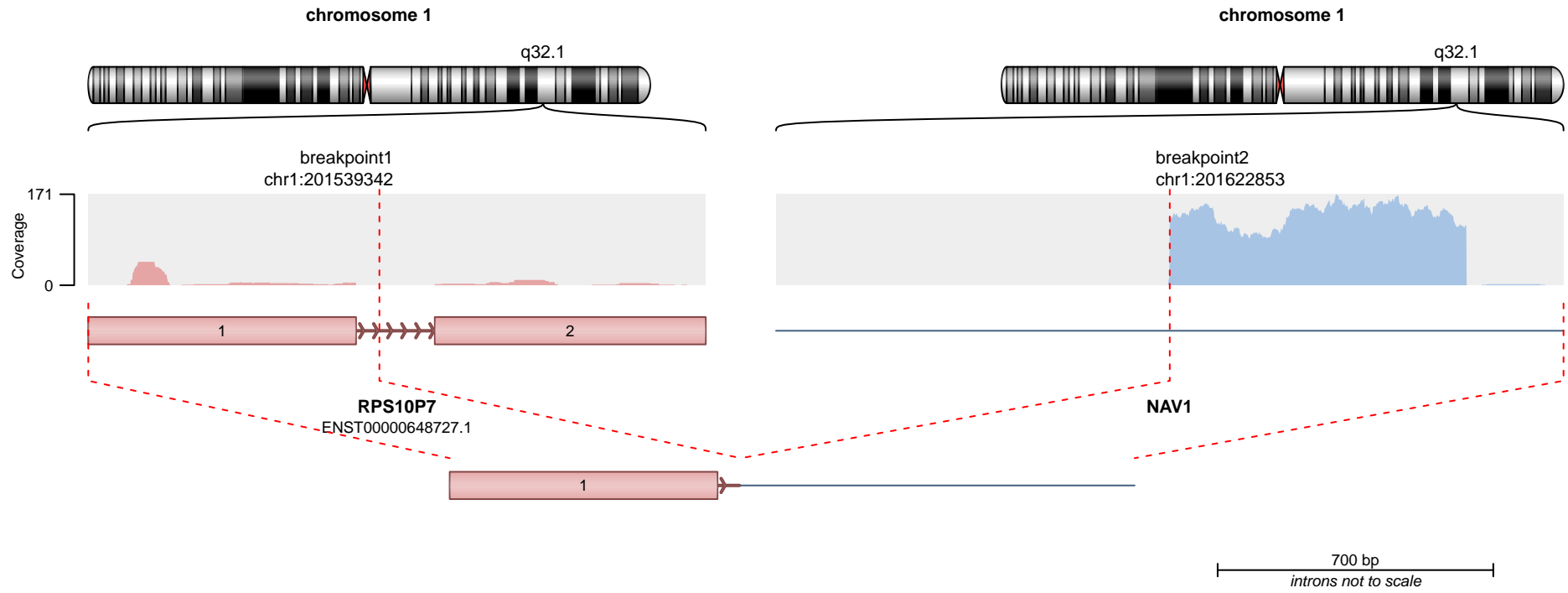


# Patient\_8



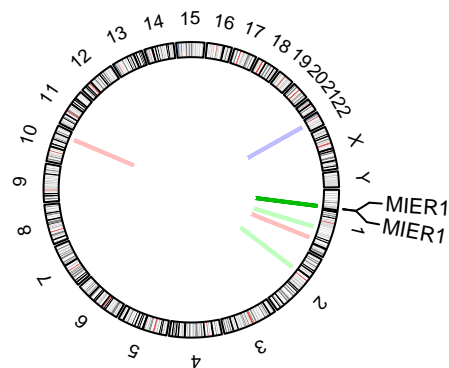
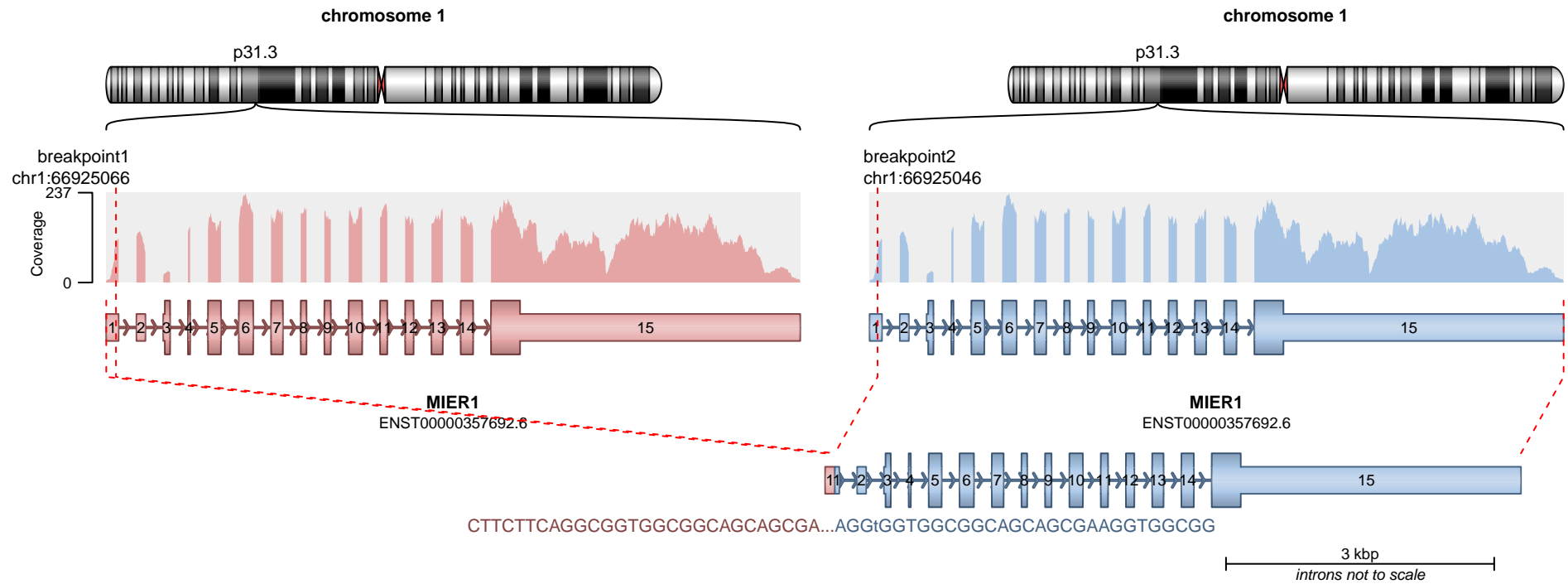
— translocation  
 — duplication  
 — deletion  
 — inversion

Genes are not protein-coding.

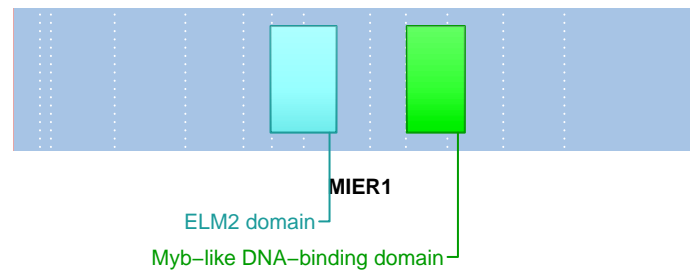
## SUPPORTING READ COUNT

Split reads at breakpoint1 = 11  
 Split reads at breakpoint2 = 18  
 Discordant mates = 7

# Patient\_8



## RETAINED PROTEIN DOMAINS reading frame unclear

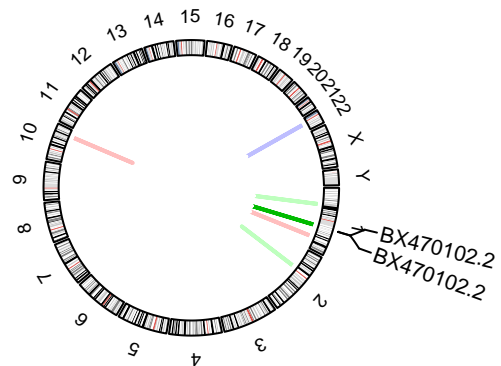
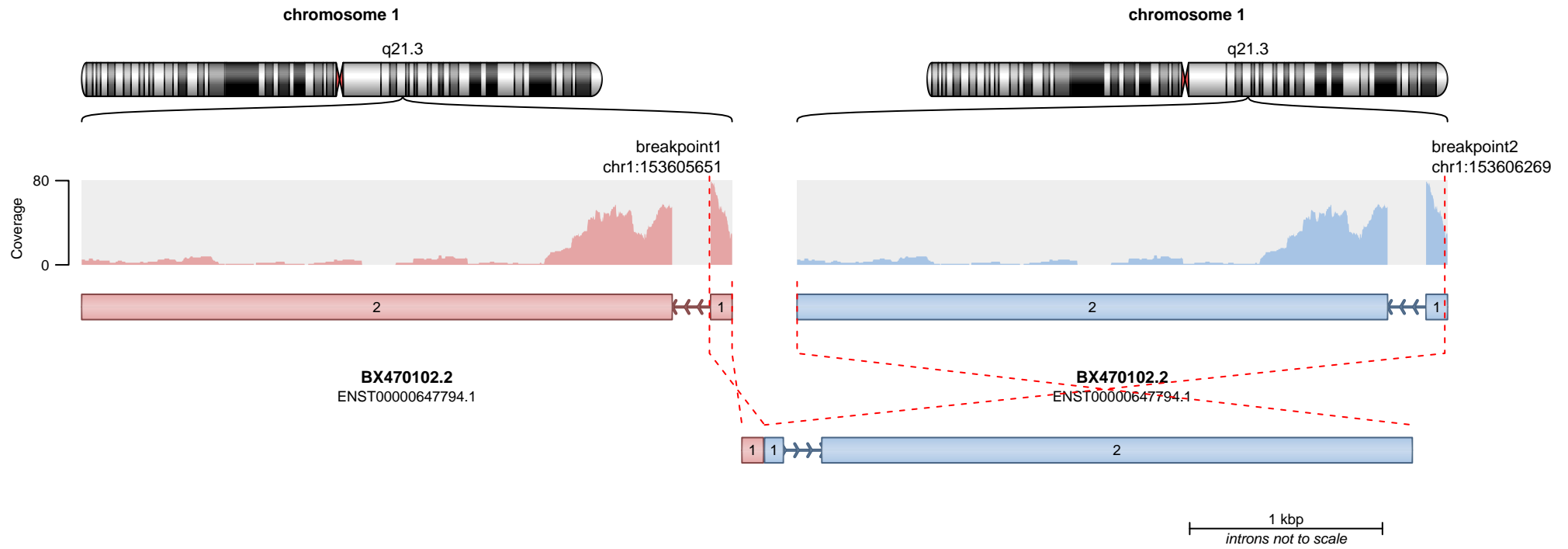


## SUPPORTING READ COUNT

Split reads at breakpoint1 = 1  
Split reads at breakpoint2 = 11  
Discordant mates = 0

translocation  
deletion  
duplication  
inversion

# Patient\_8



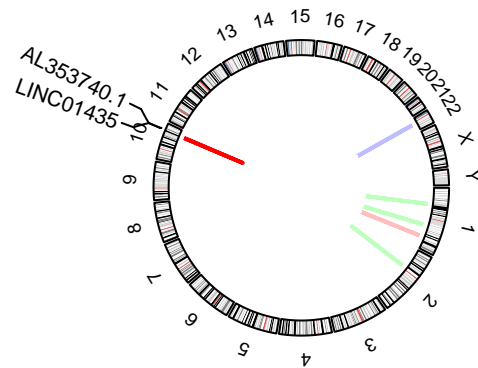
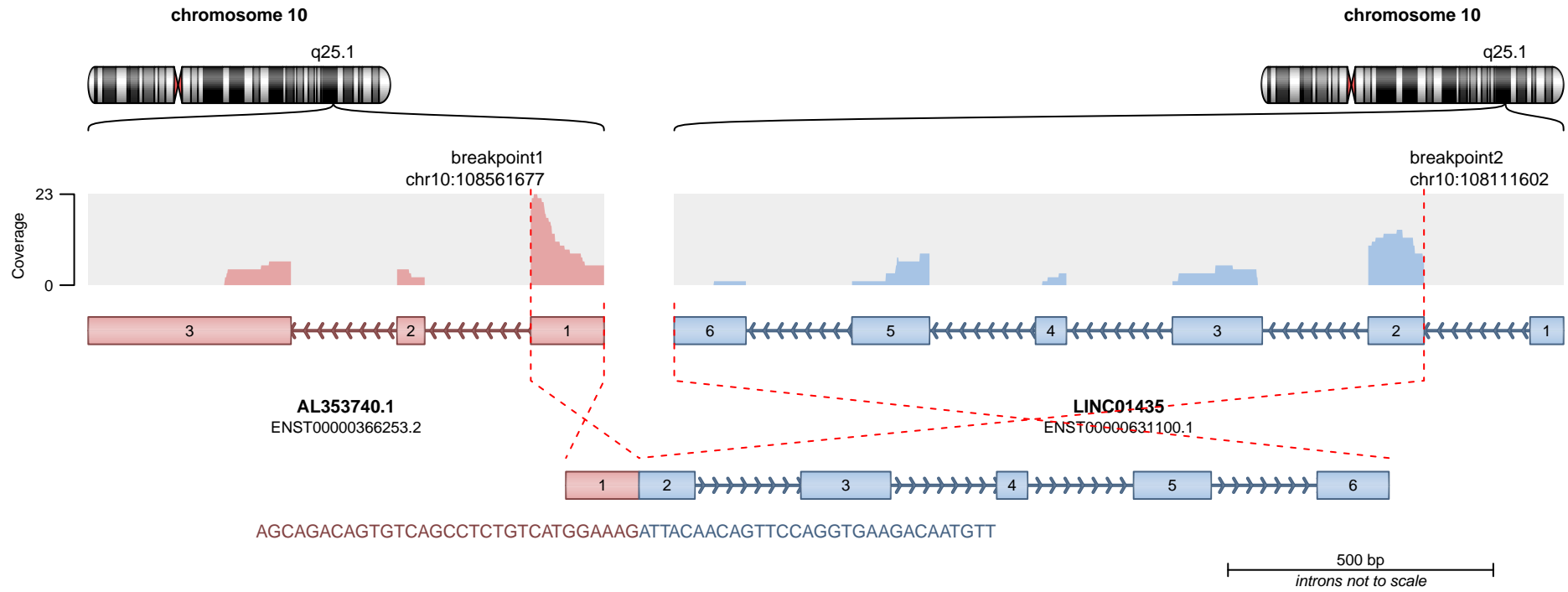
translocation deletion  
duplication inversion

Genes are not protein-coding.

## SUPPORTING READ COUNT

Split reads at breakpoint1 = 0  
Split reads at breakpoint2 = 2  
Discordant mates = 5

# Patient\_8



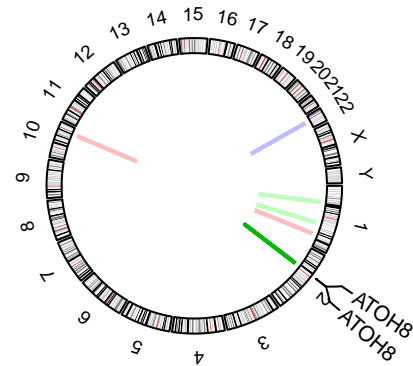
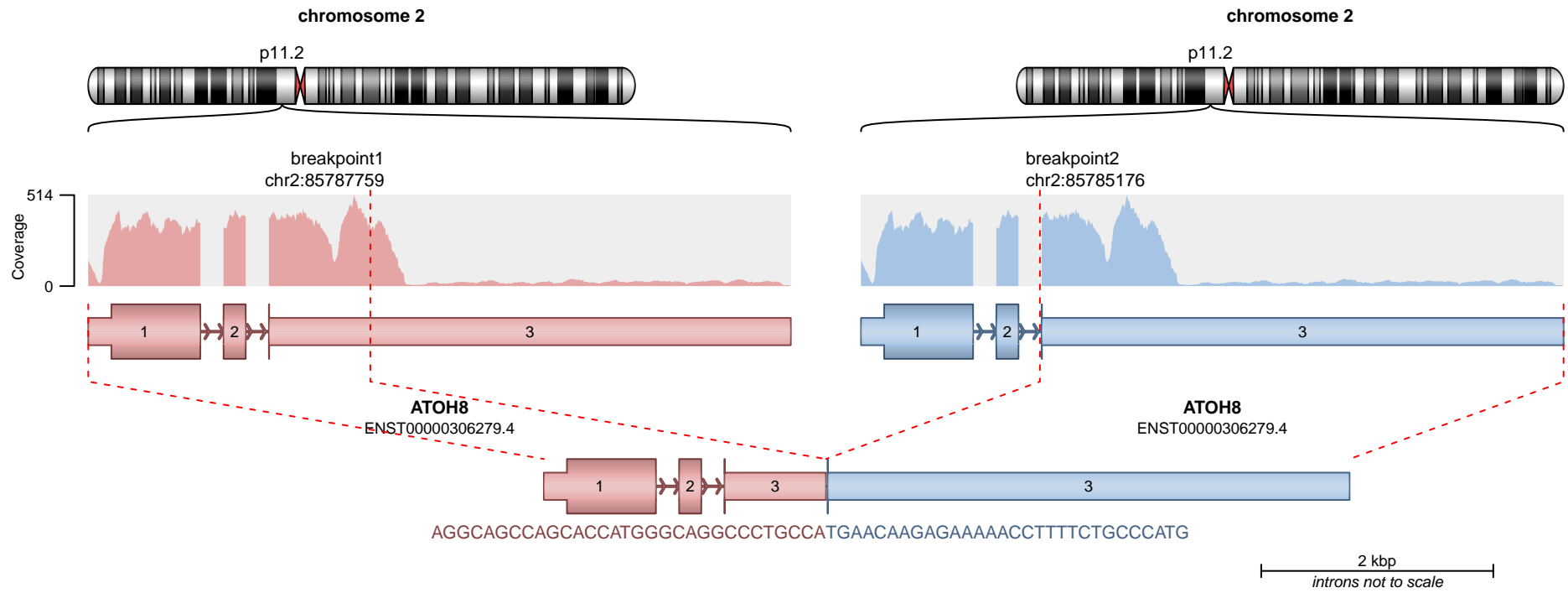
translocation deletion  
duplication inversion

Genes are not protein-coding.

## SUPPORTING READ COUNT

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

# Patient\_8



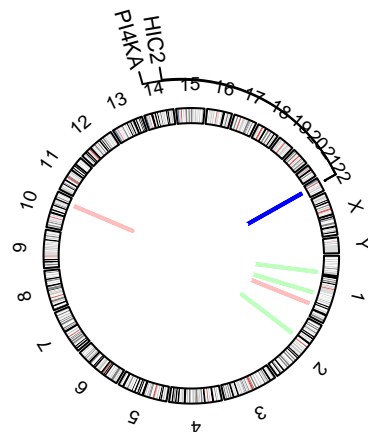
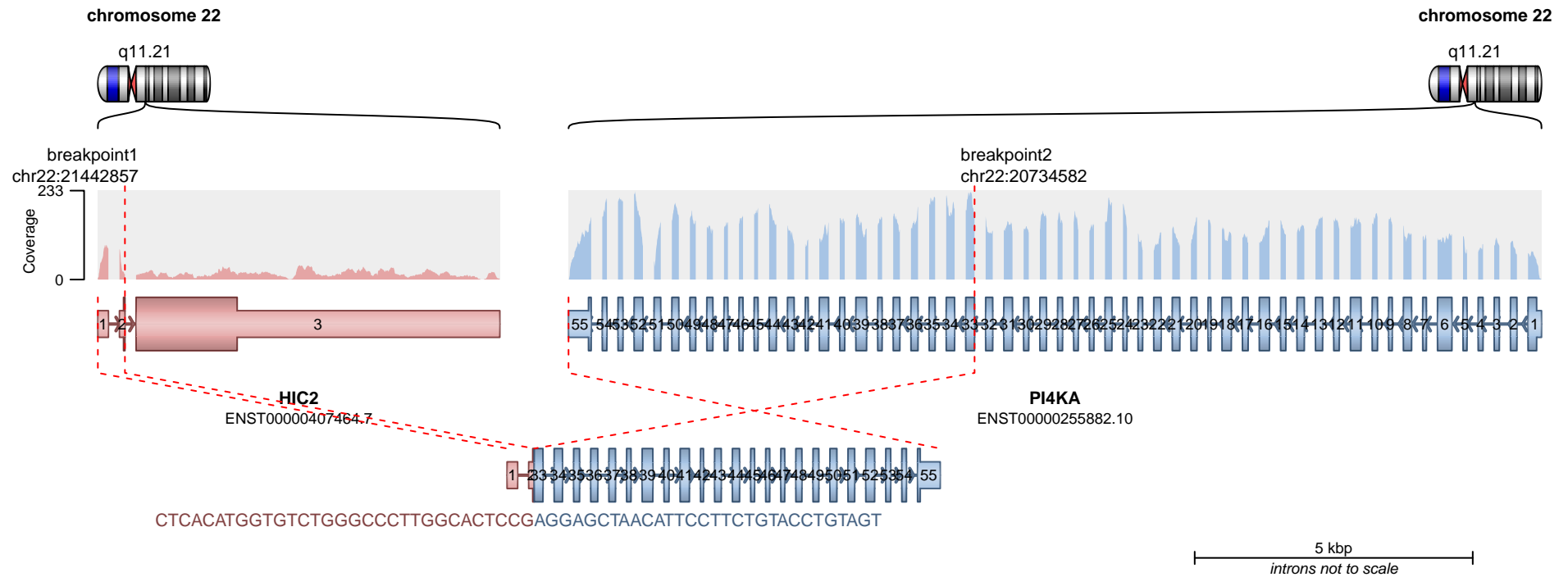
No protein domains retained in fusion.

## SUPPORTING READ COUNT

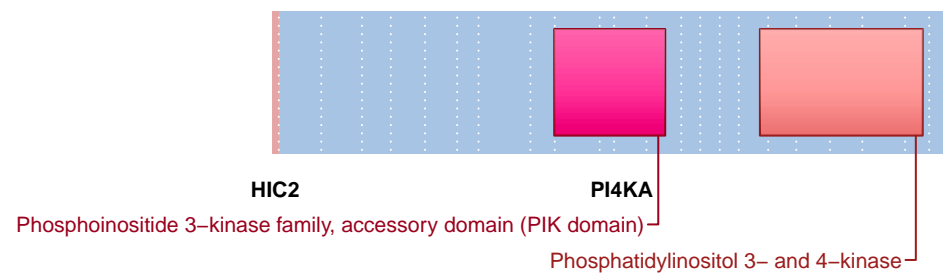
Split reads at breakpoint1 = 0  
Split reads at breakpoint2 = 2  
Discordant mates = 1

translocation deletion  
duplication inversion

# Patient\_8



## RETAINED PROTEIN DOMAINS out-of-frame fusion

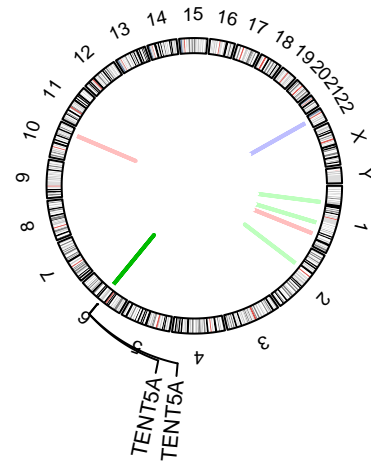
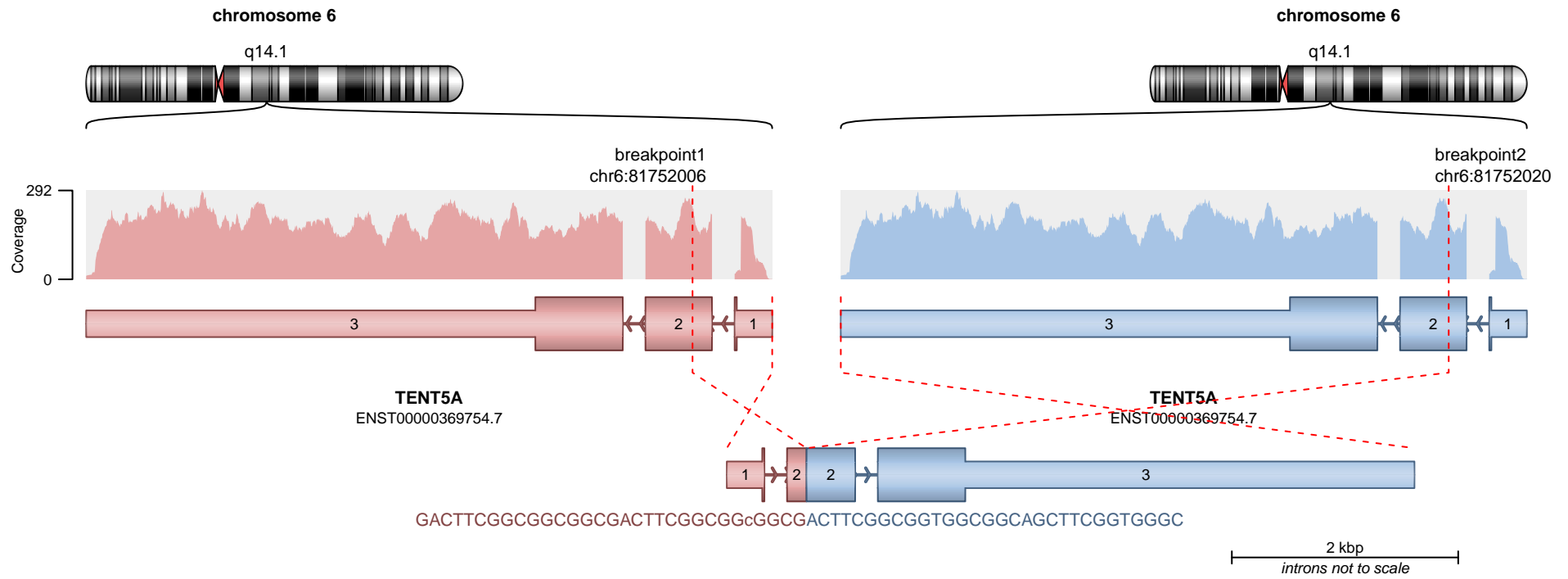


## SUPPORTING READ COUNT

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

translocation  
deletion  
duplication  
inversion

# Patient\_8



translocation  
deletion  
duplication  
inversion

No protein domains retained in fusion.

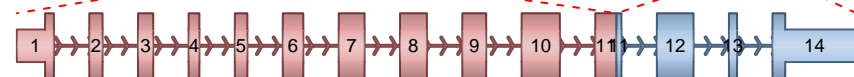
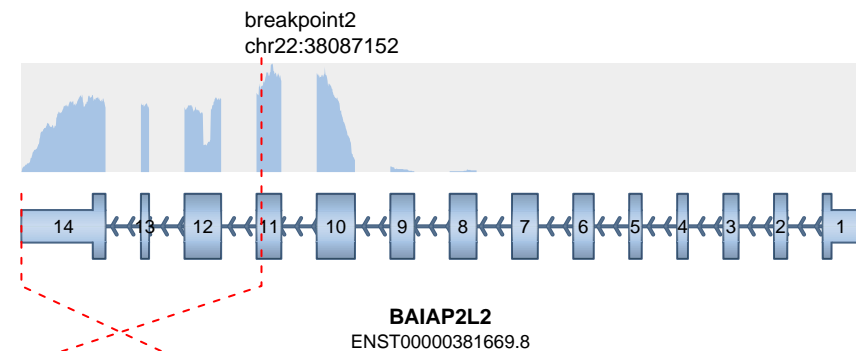
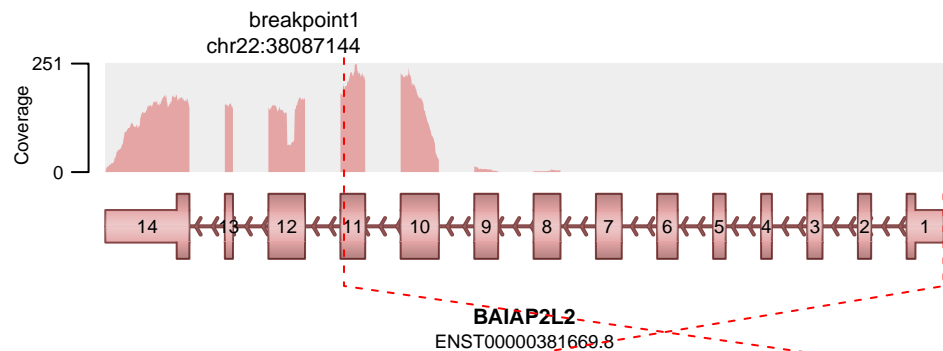
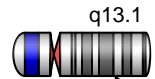
## SUPPORTING READ COUNT

Split reads at breakpoint1 = 1  
Split reads at breakpoint2 = 10  
Discordant mates = 0

# Patient\_8

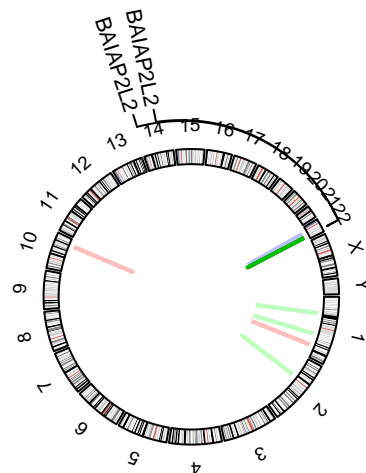
chromosome 22

chromosome 22

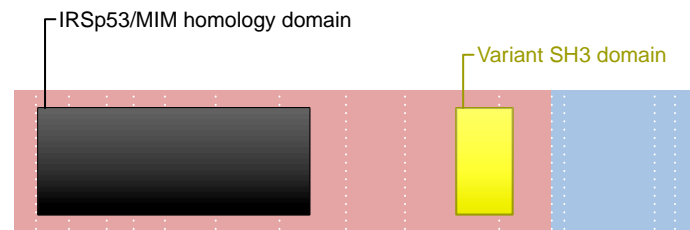


CTCCATGTCCCCATGACACCCATGACaCCCATGAACCCCGGGAACGAGCTGCCTTCAG\_

2 kbp  
introns not to scale



## RETAINED PROTEIN DOMAINS in-frame fusion



BAIAP2L2

BAIAP2L2

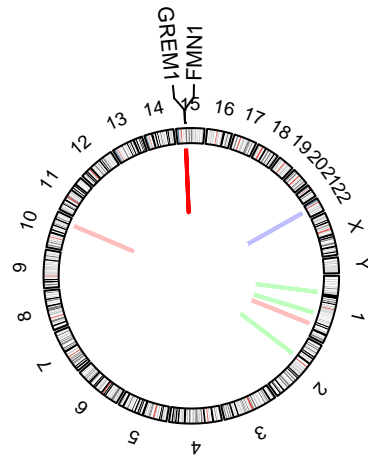
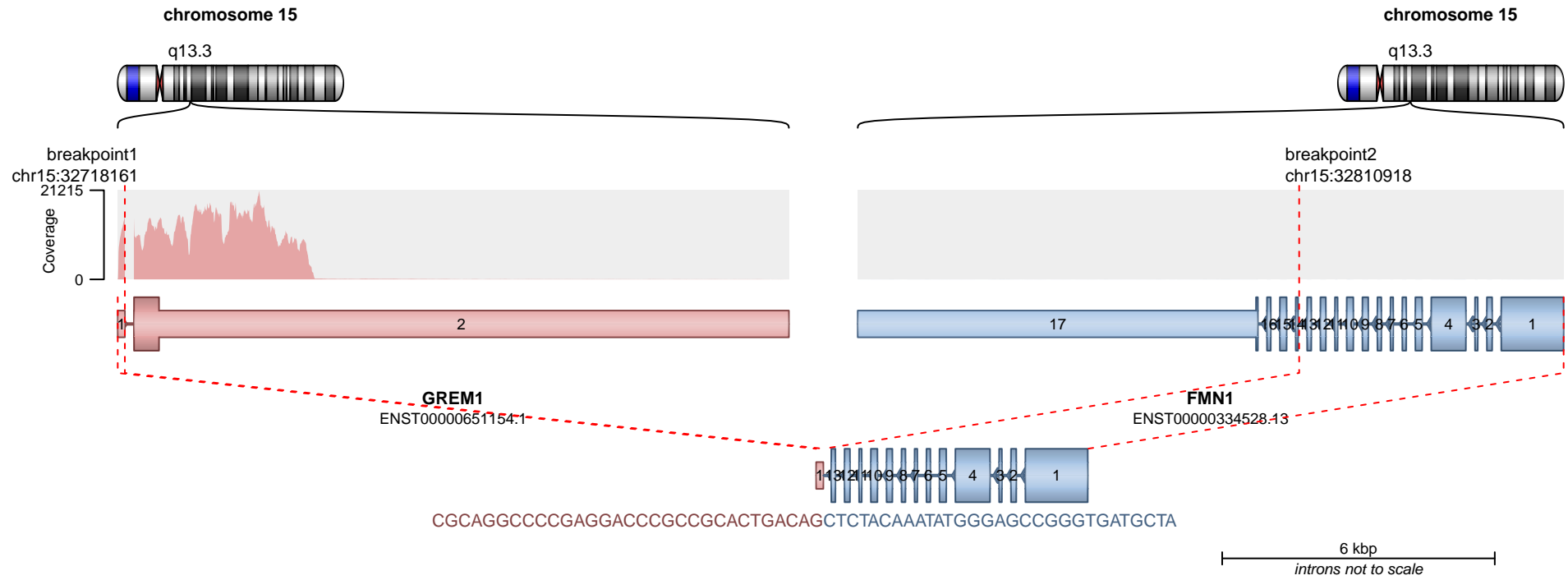
## SUPPORTING READ COUNT

Split reads at breakpoint1 = 6  
Split reads at breakpoint2 = 3  
Discordant mates = 0

translocation deletion  
duplication inversion



# Patient\_8



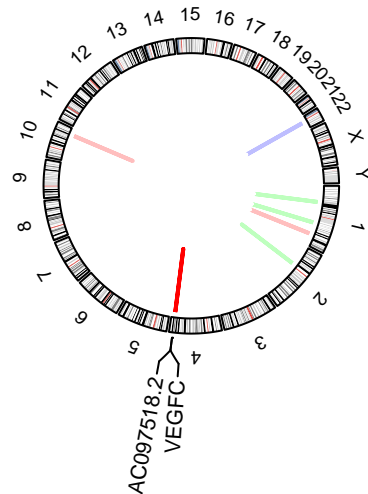
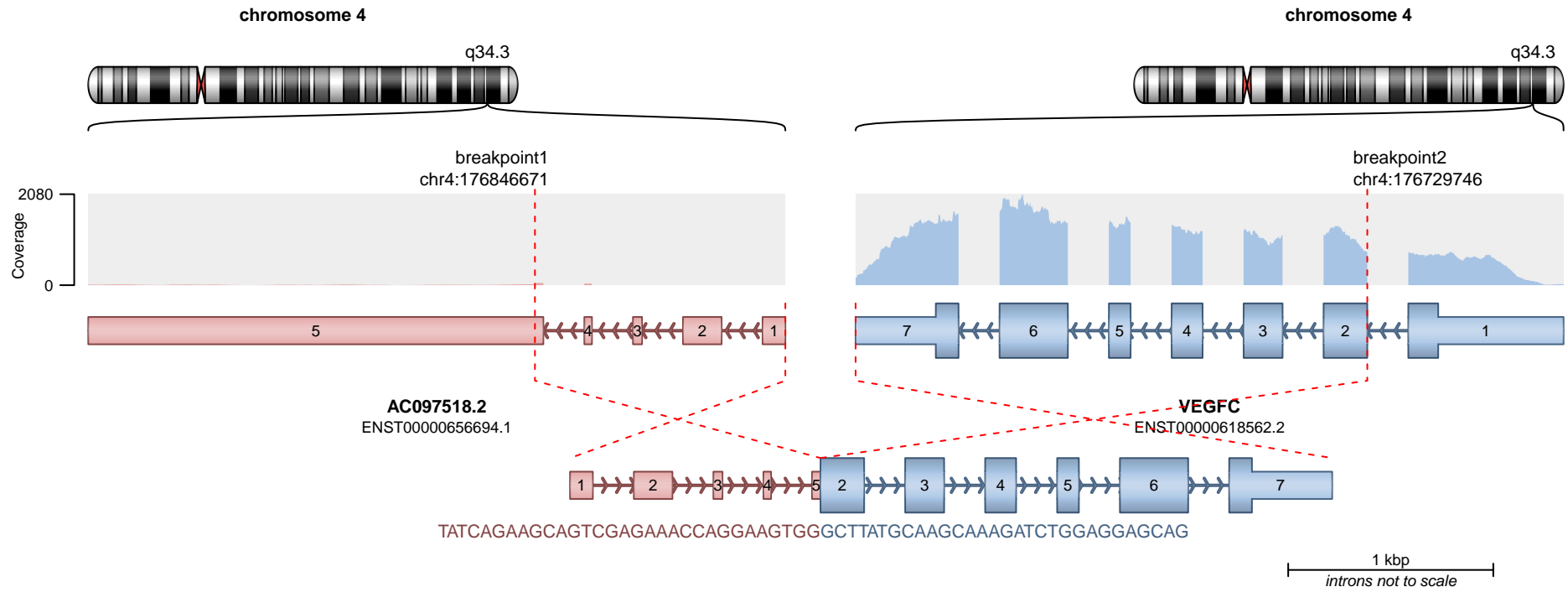
No coding regions due to antisense transcription.

## SUPPORTING READ COUNT

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

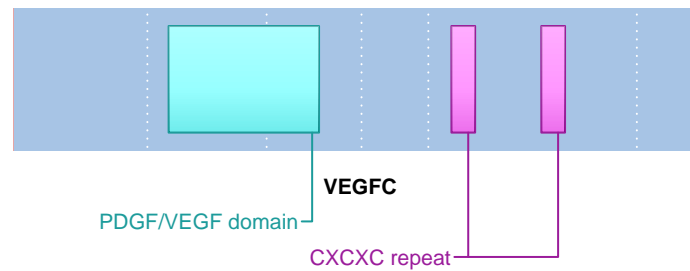
translocation deletion  
duplication inversion

# Patient\_8



translocation  
deletion  
duplication  
inversion

## RETAINED PROTEIN DOMAINS reading frame unclear



## SUPPORTING READ COUNT

Split reads at breakpoint1 = 1  
Split reads at breakpoint2 = 0  
Discordant mates = 4