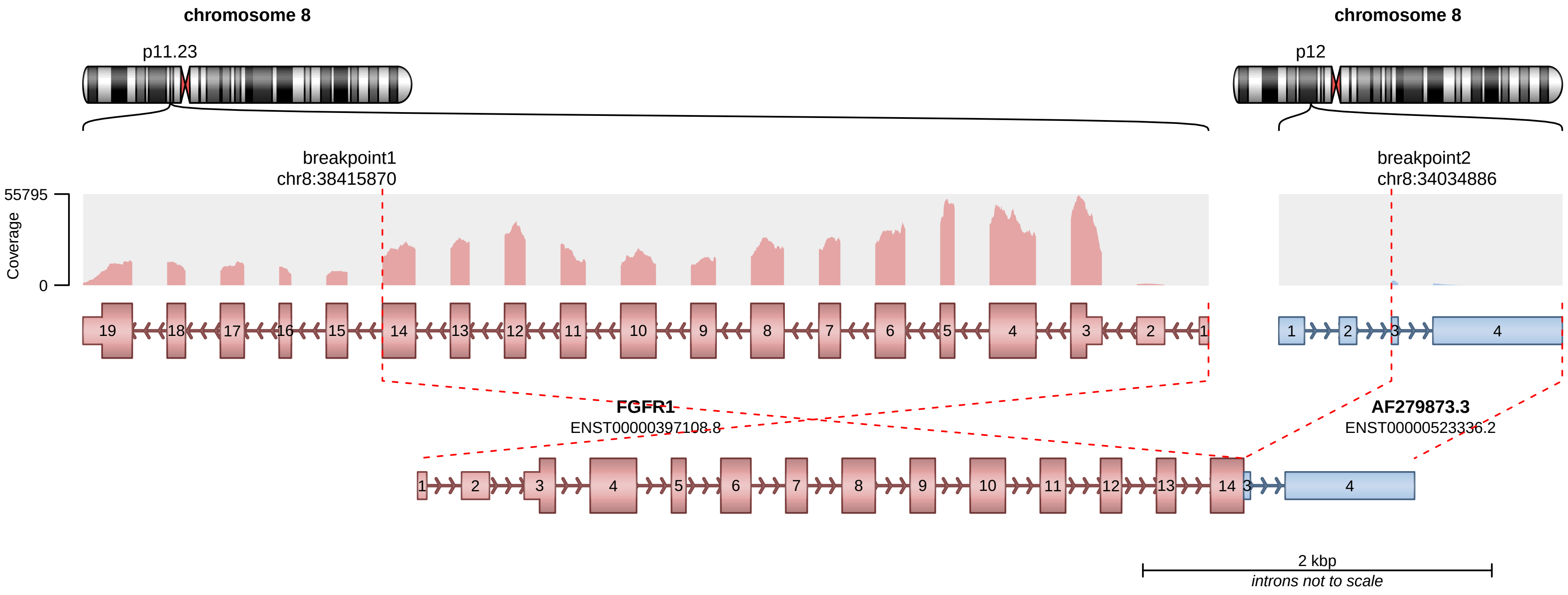
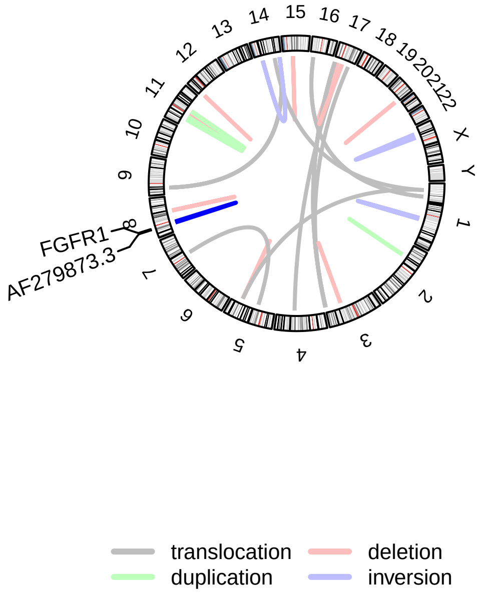
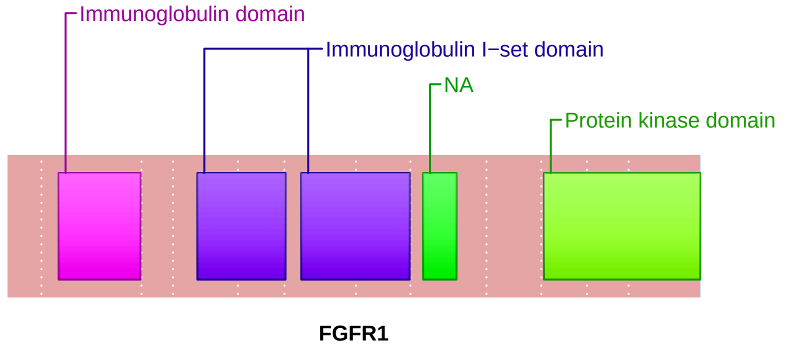


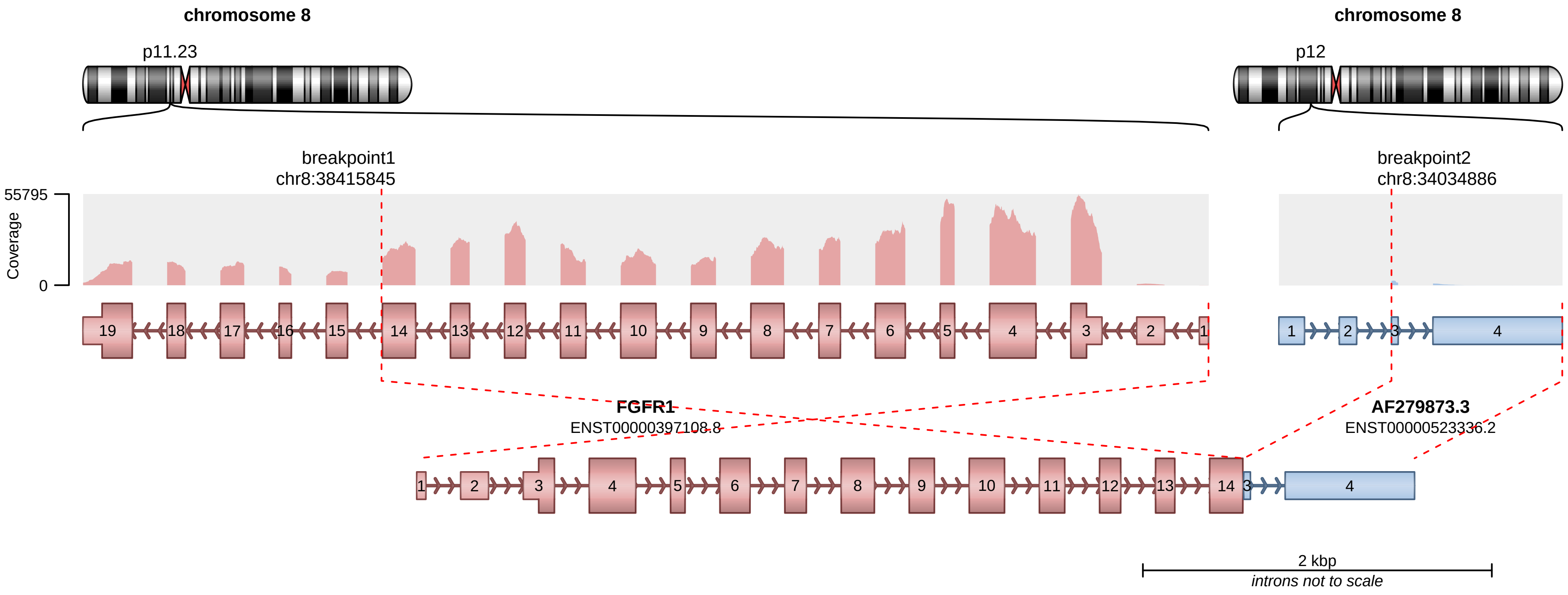


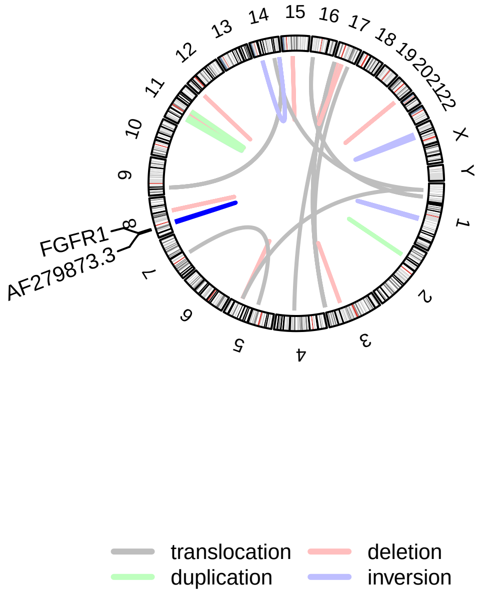
**RETAINED PROTEIN DOMAINS**
reading frame unclear

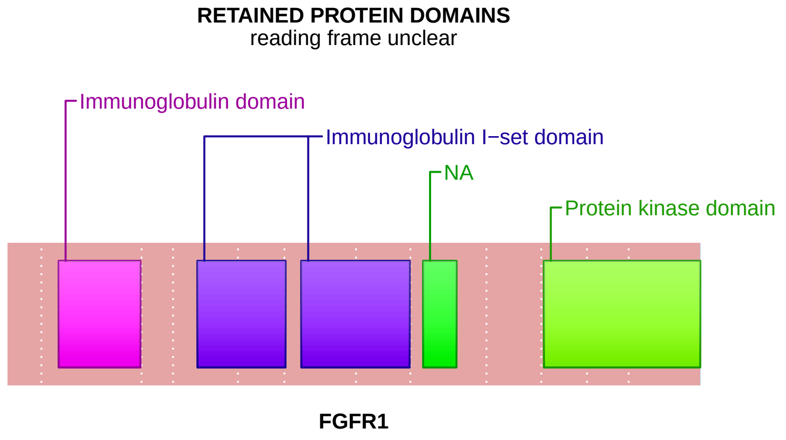


**SUPPORTING READ COUNT**

Split reads = 2269
Discordant mates = 45

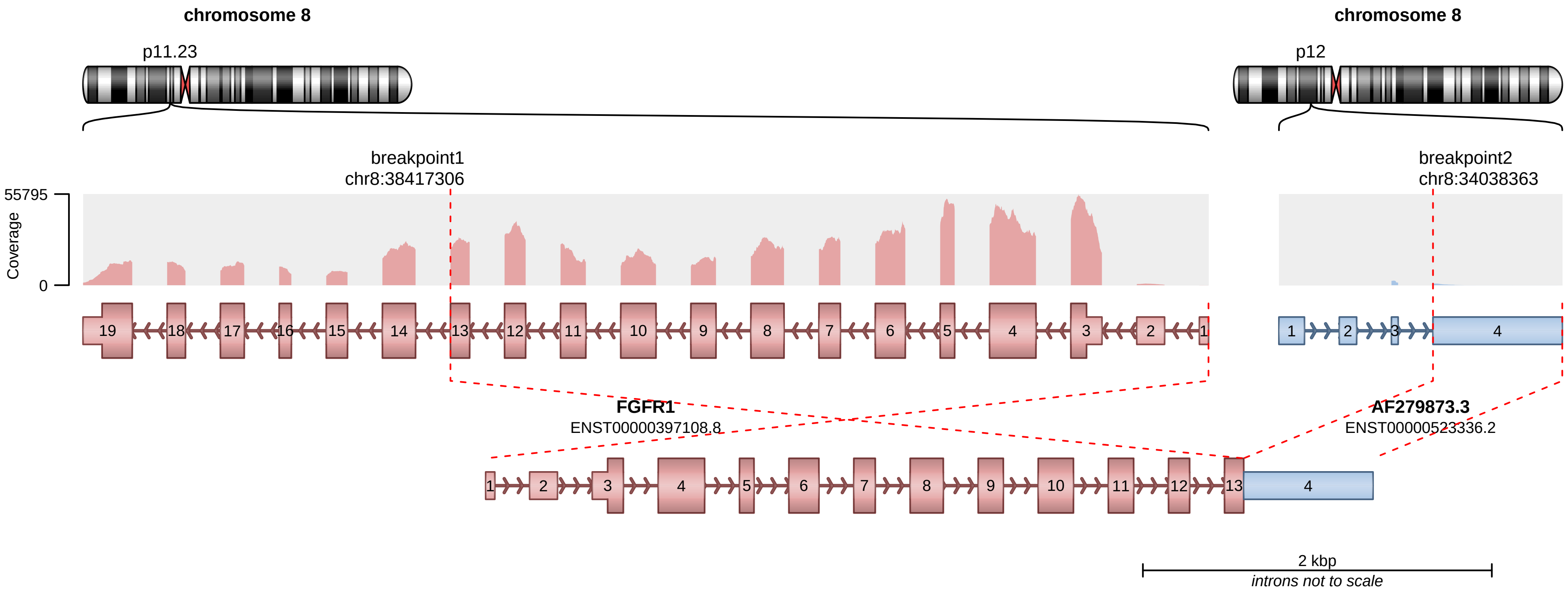


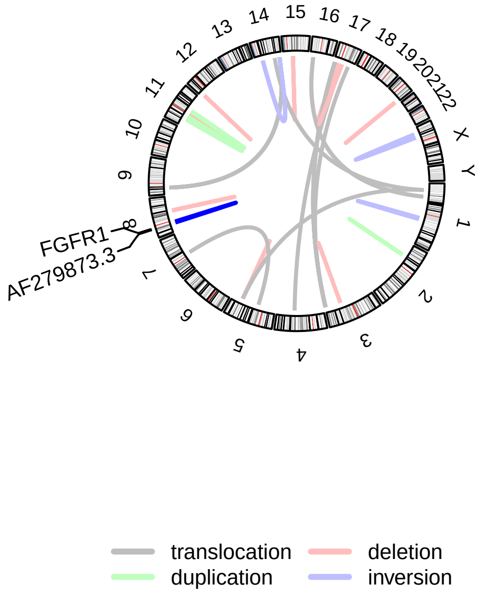




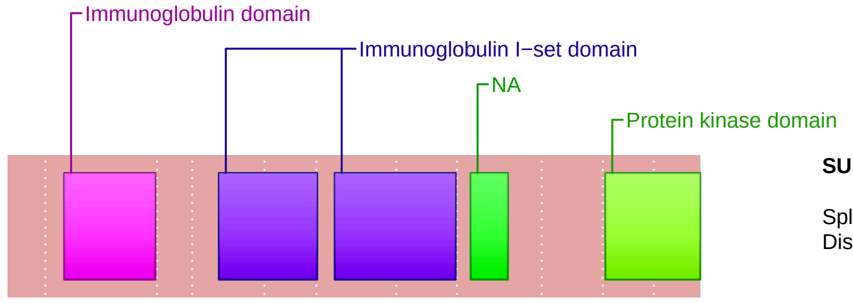
**SUPPORTING READ COUNT**

Split reads = 33
Discordant mates = 46





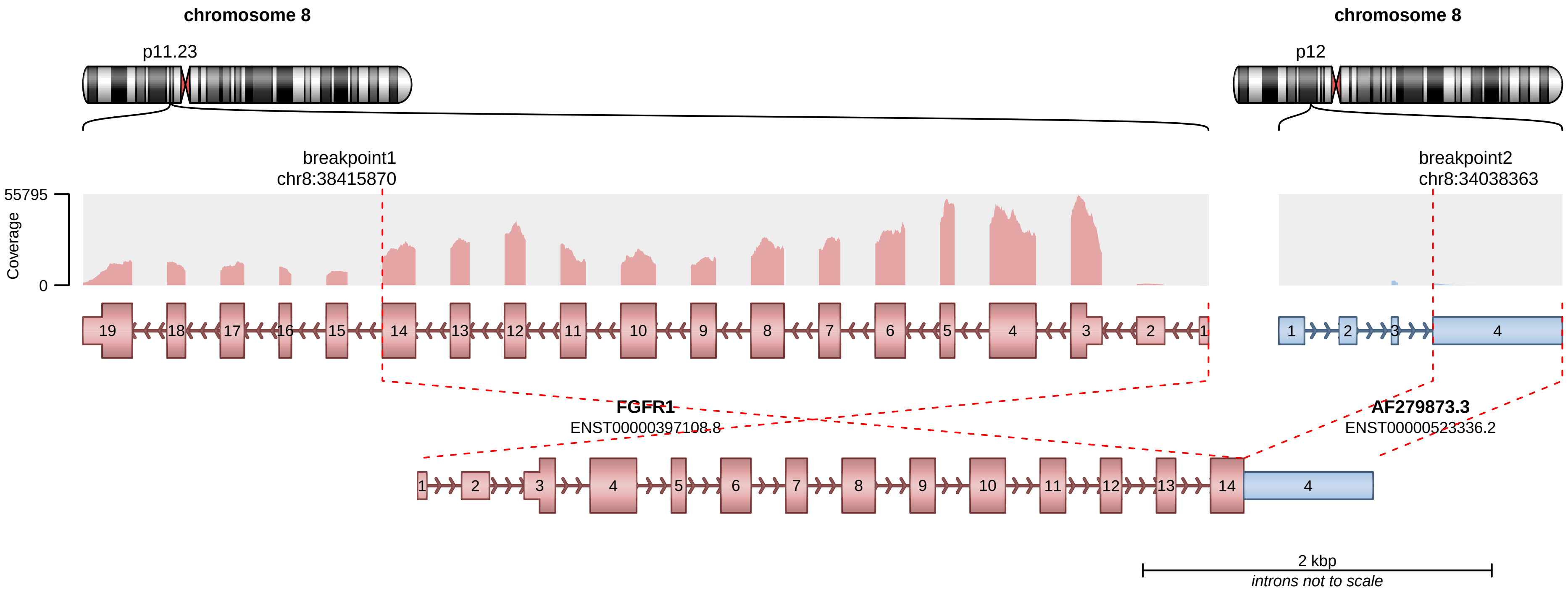
**RETAINED PROTEIN DOMAINS**
reading frame unclear

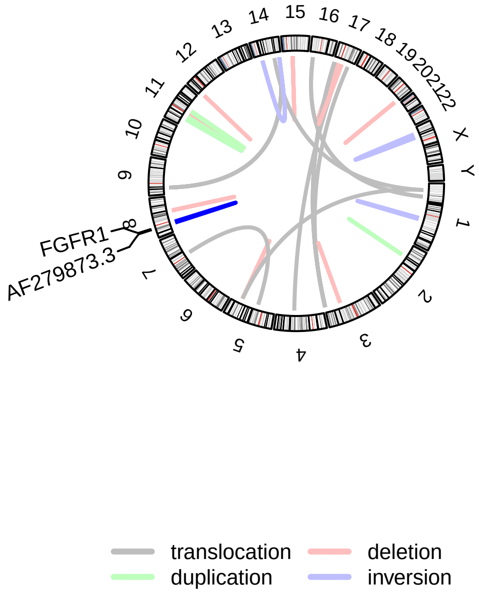


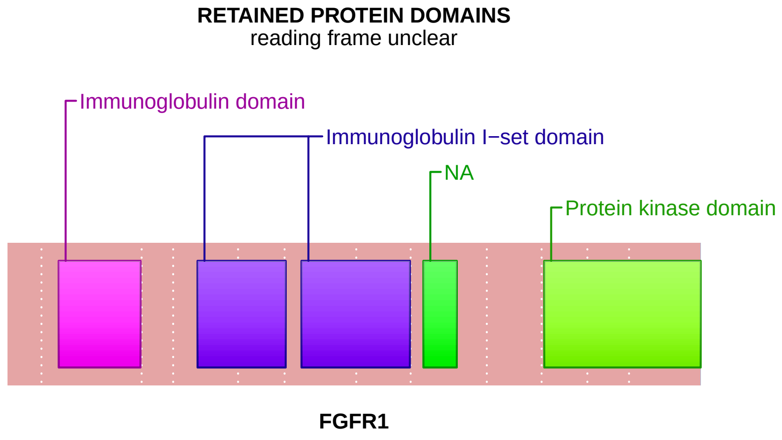
**FGFR1**

**SUPPORTING READ COUNT**

Split reads = 10
Discordant mates = 0

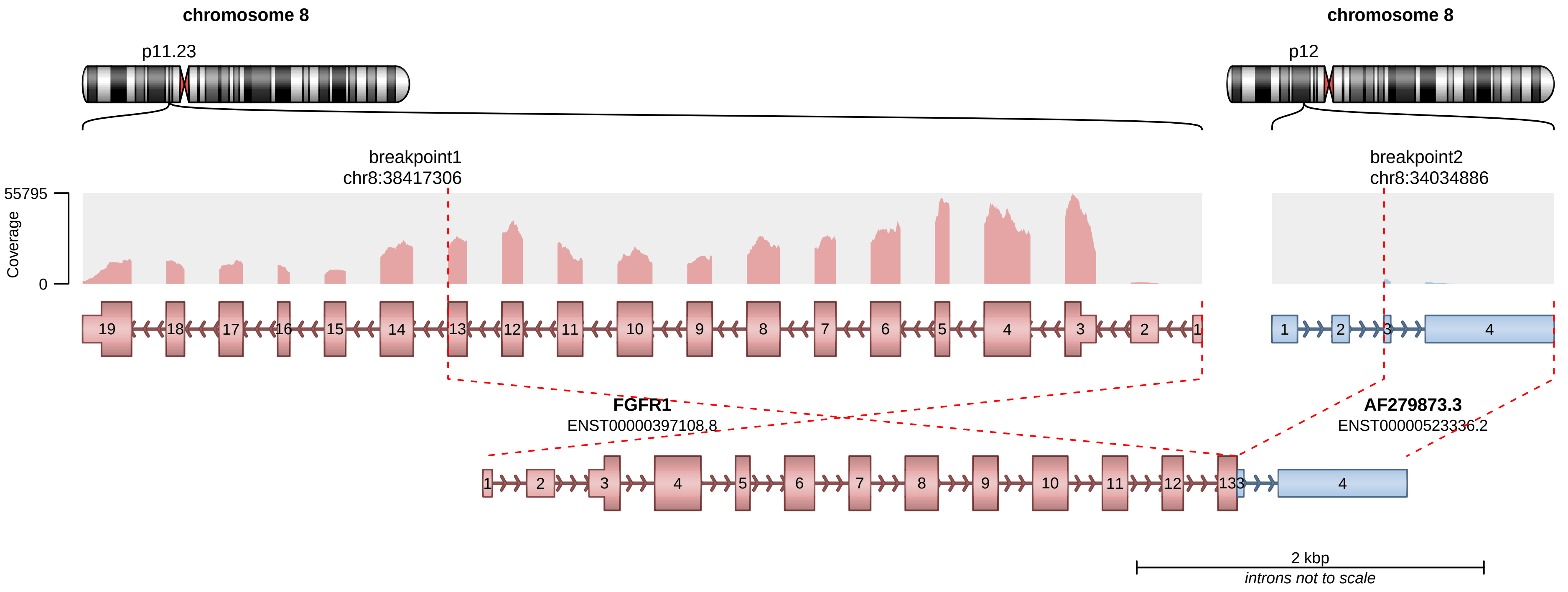


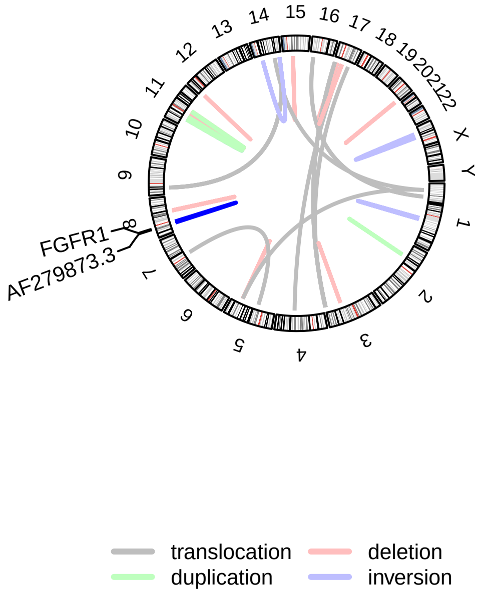


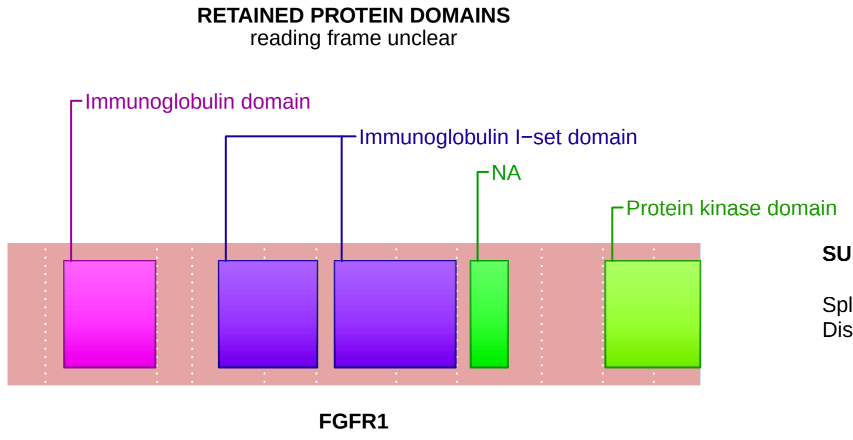


**SUPPORTING READ COUNT**

Split reads = 1
Discordant mates = 14

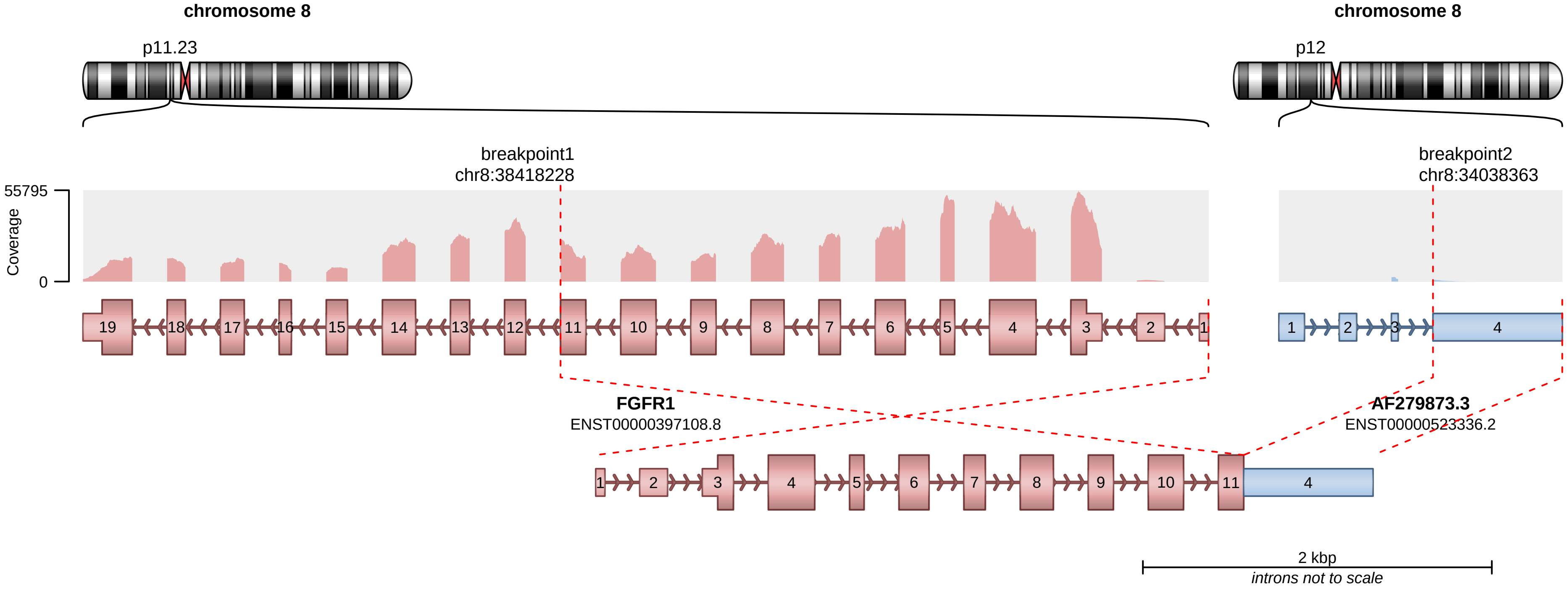


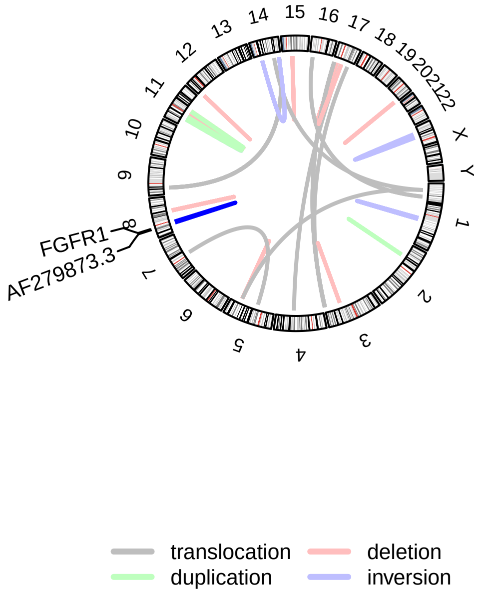


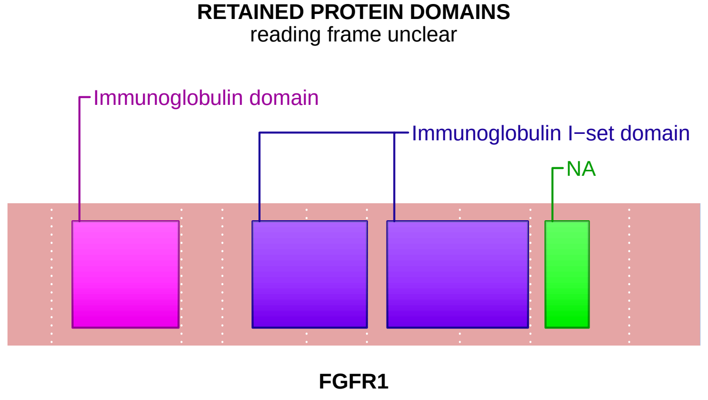


**SUPPORTING READ COUNT**

Split reads = 2
Discordant mates = 1

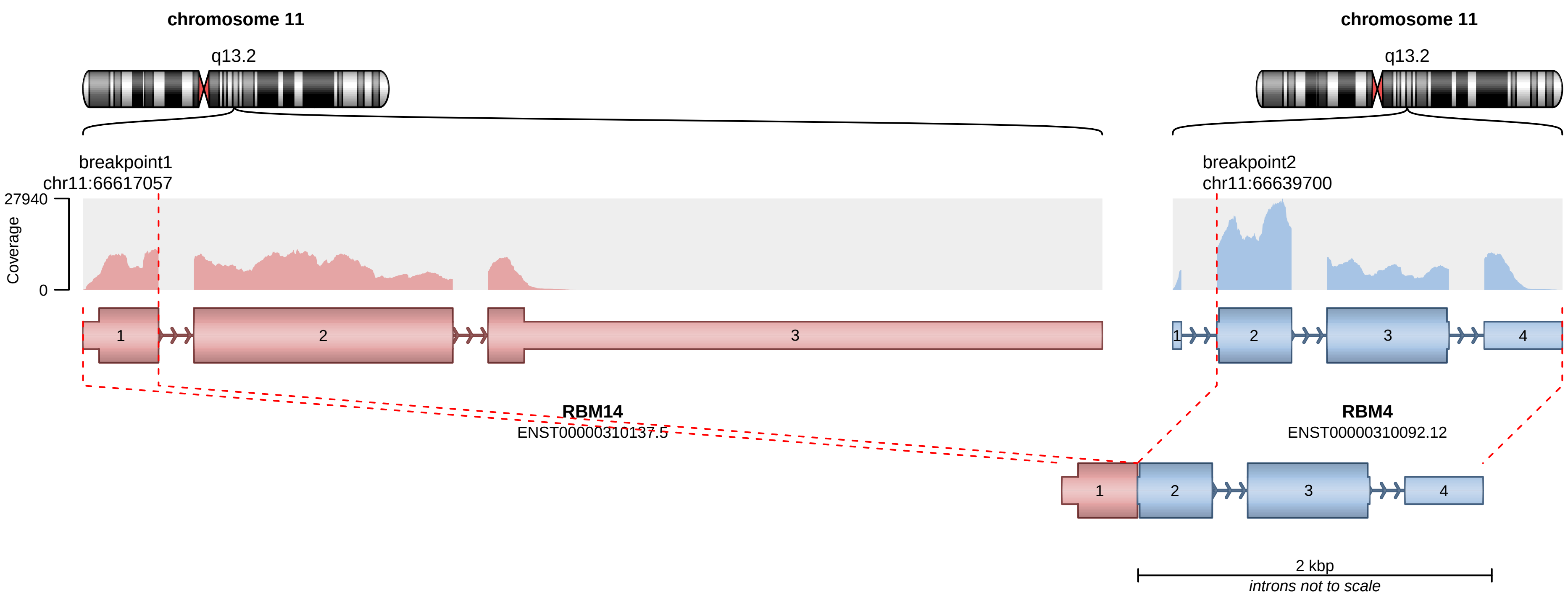


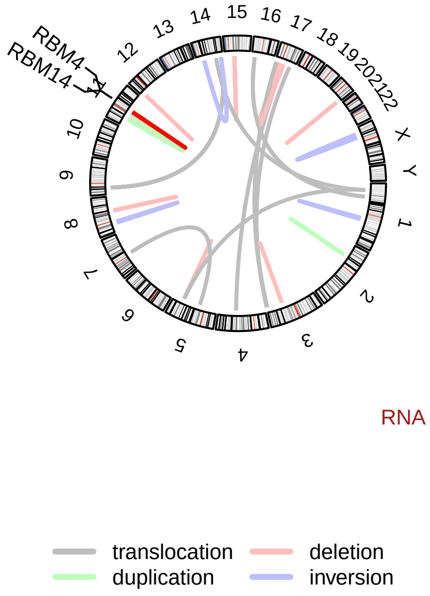


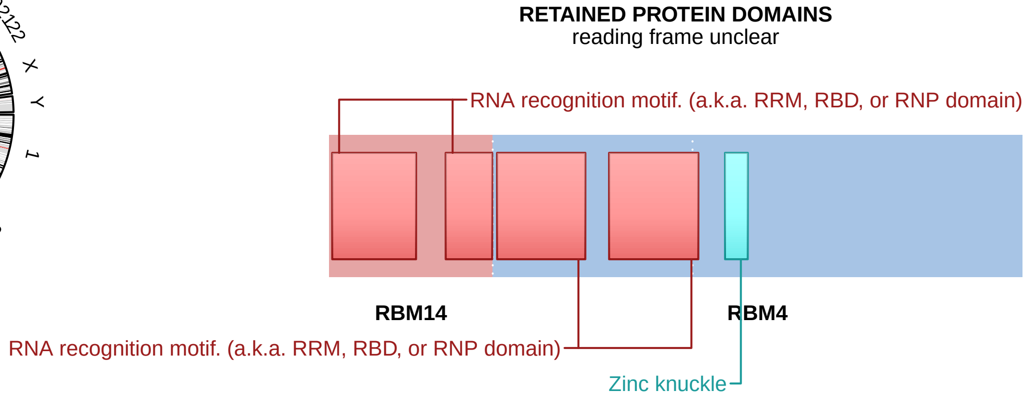


**SUPPORTING READ COUNT**

Split reads = 1
Discordant mates = 0

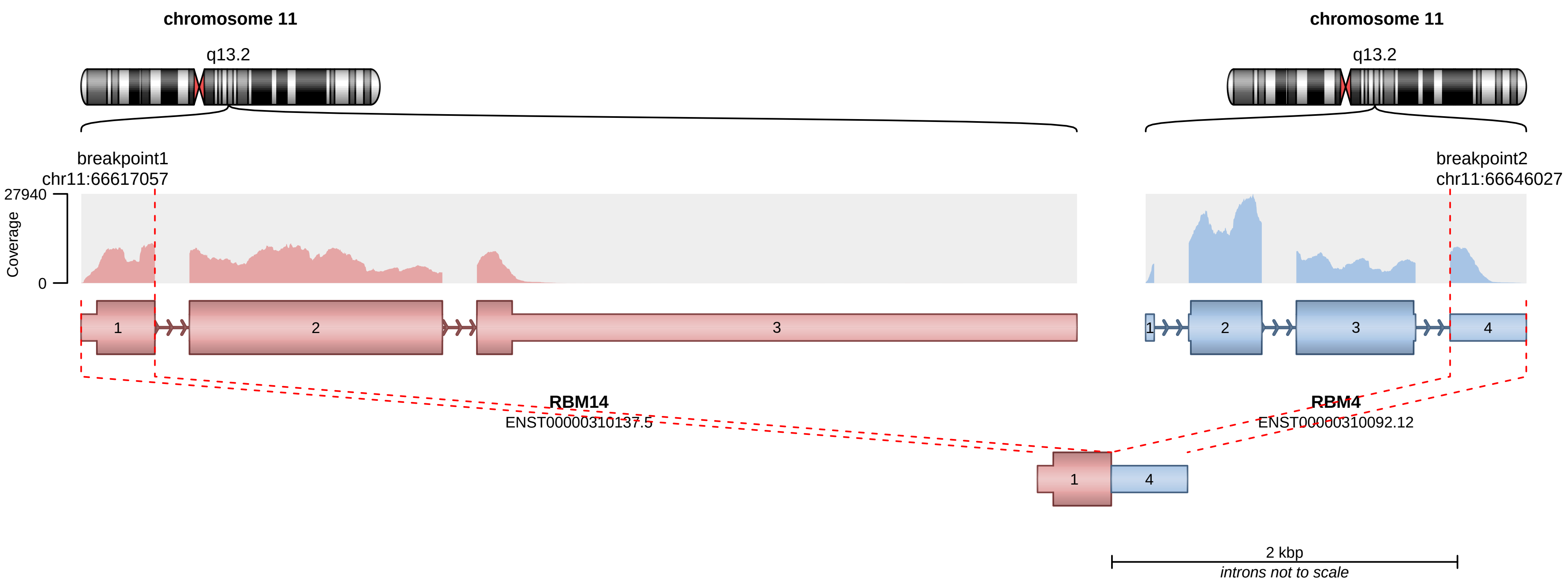


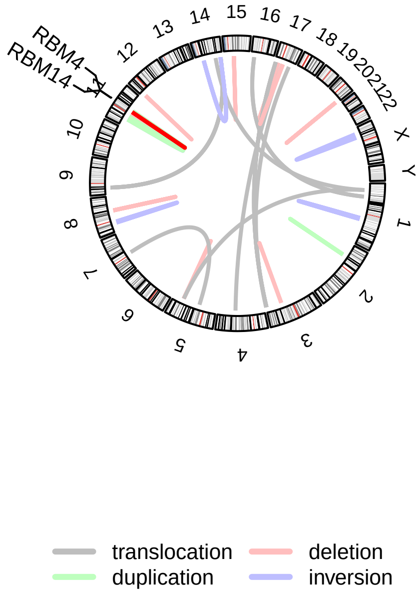




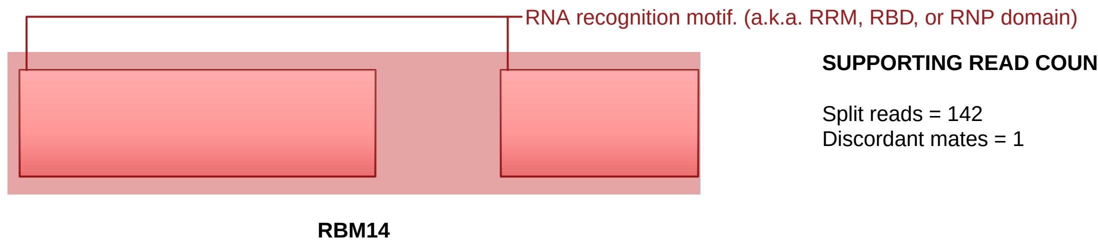
**SUPPORTING READ COUNT**

Split reads = 958
Discordant mates = 12



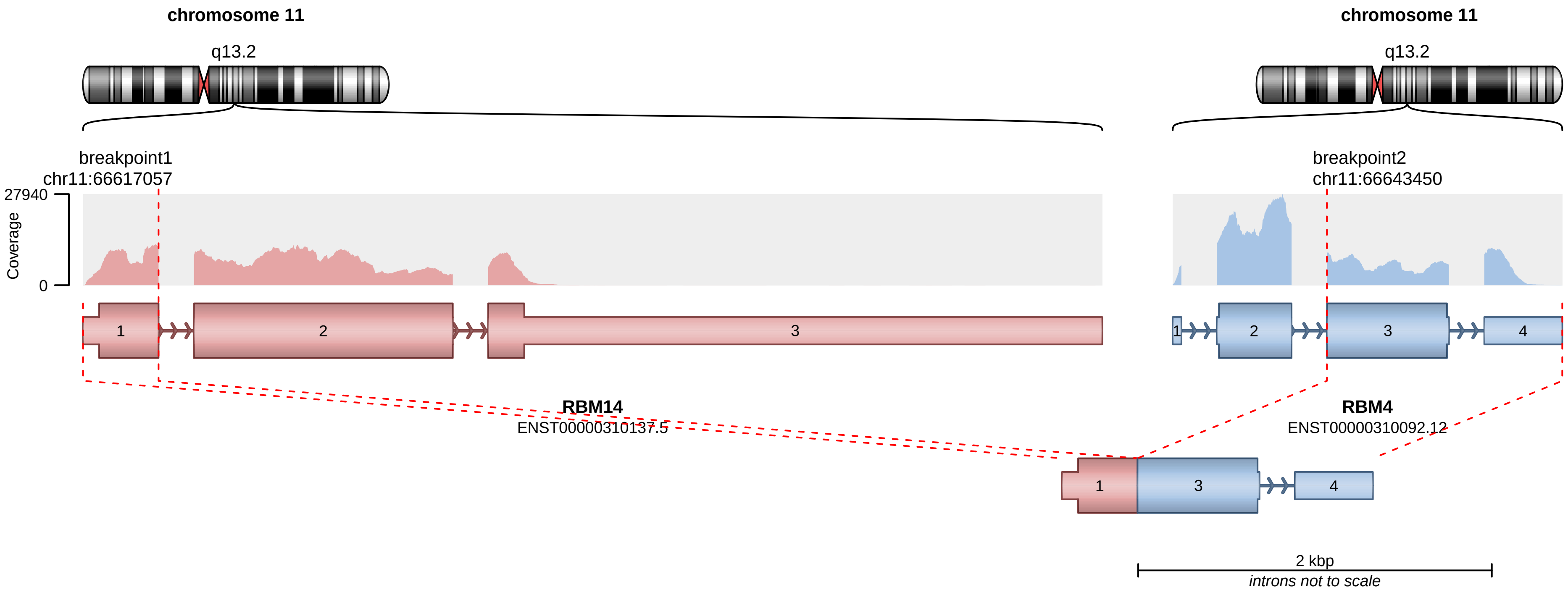


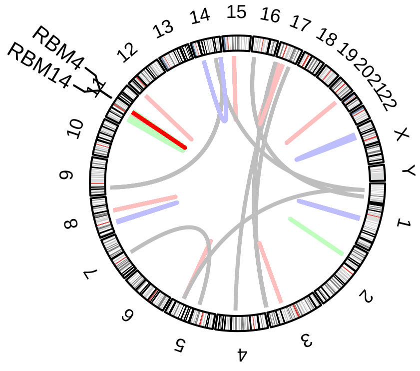
**RETAINED PROTEIN DOMAINS**
reading frame unclear



**SUPPORTING READ COUNT**

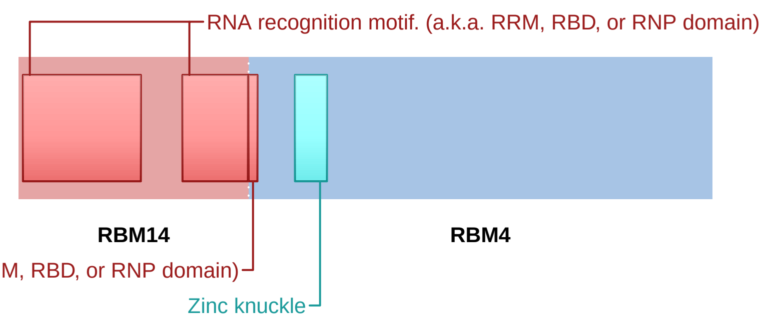
Split reads = 142
Discordant mates = 1





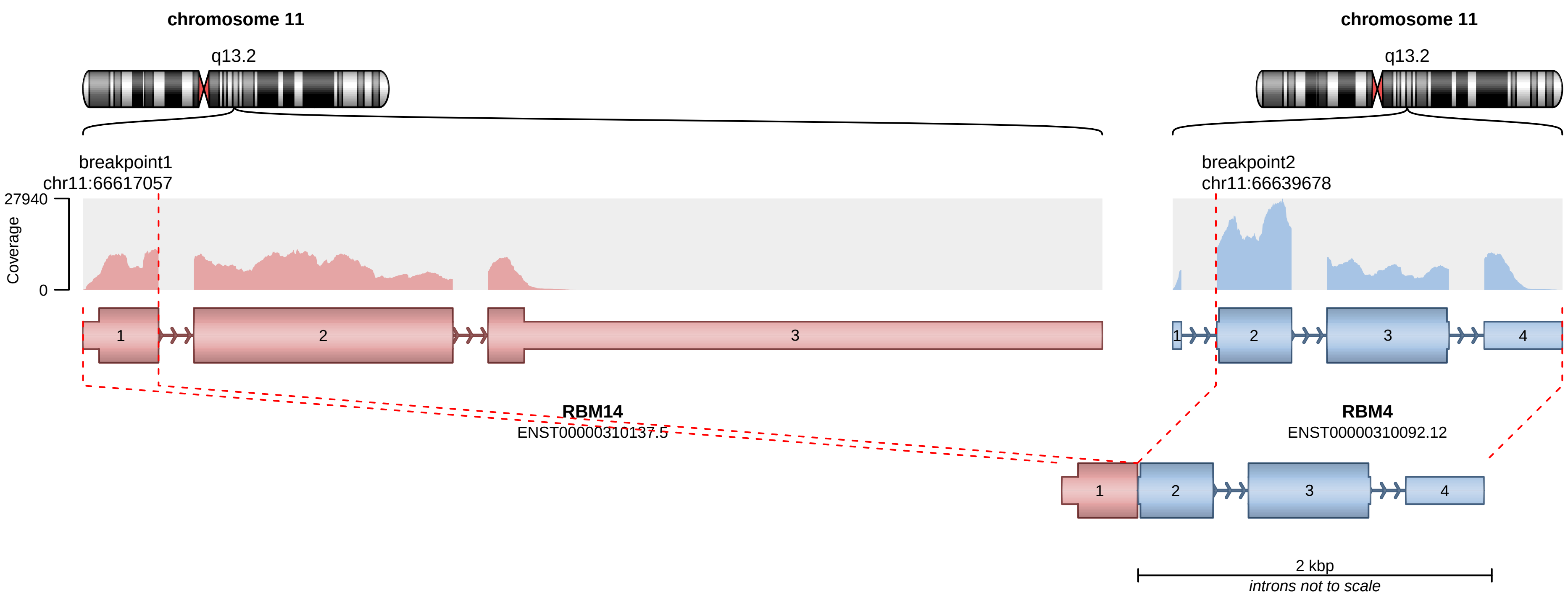
translocation
deletion
duplication
inversion

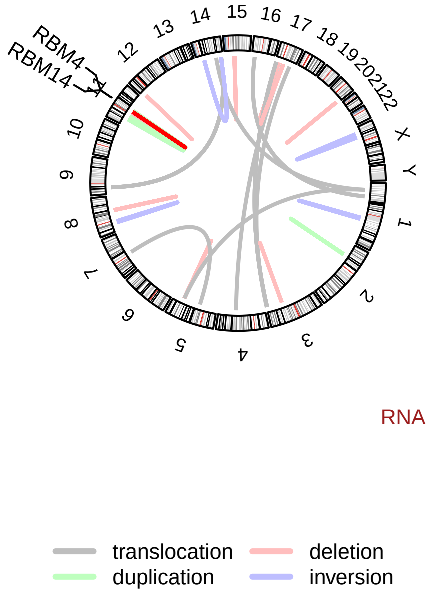
**RETAINED PROTEIN DOMAINS**
reading frame unclear

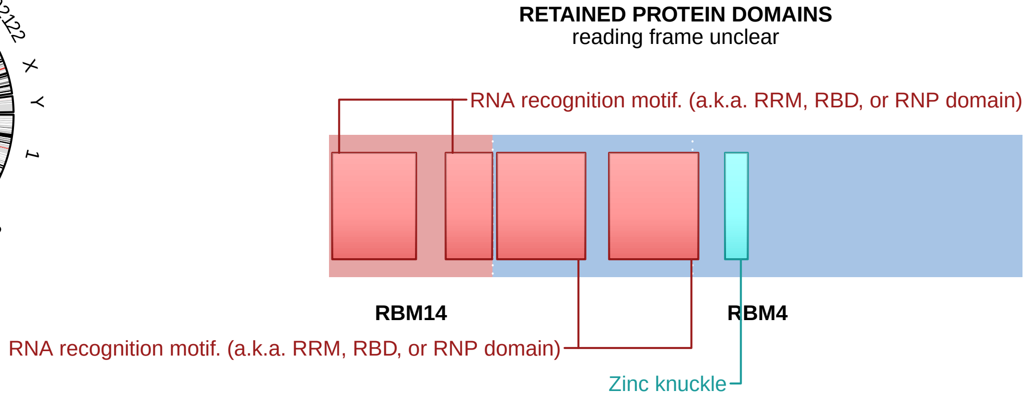


**SUPPORTING READ COUNT**

Split reads = 18
Discordant mates = 1

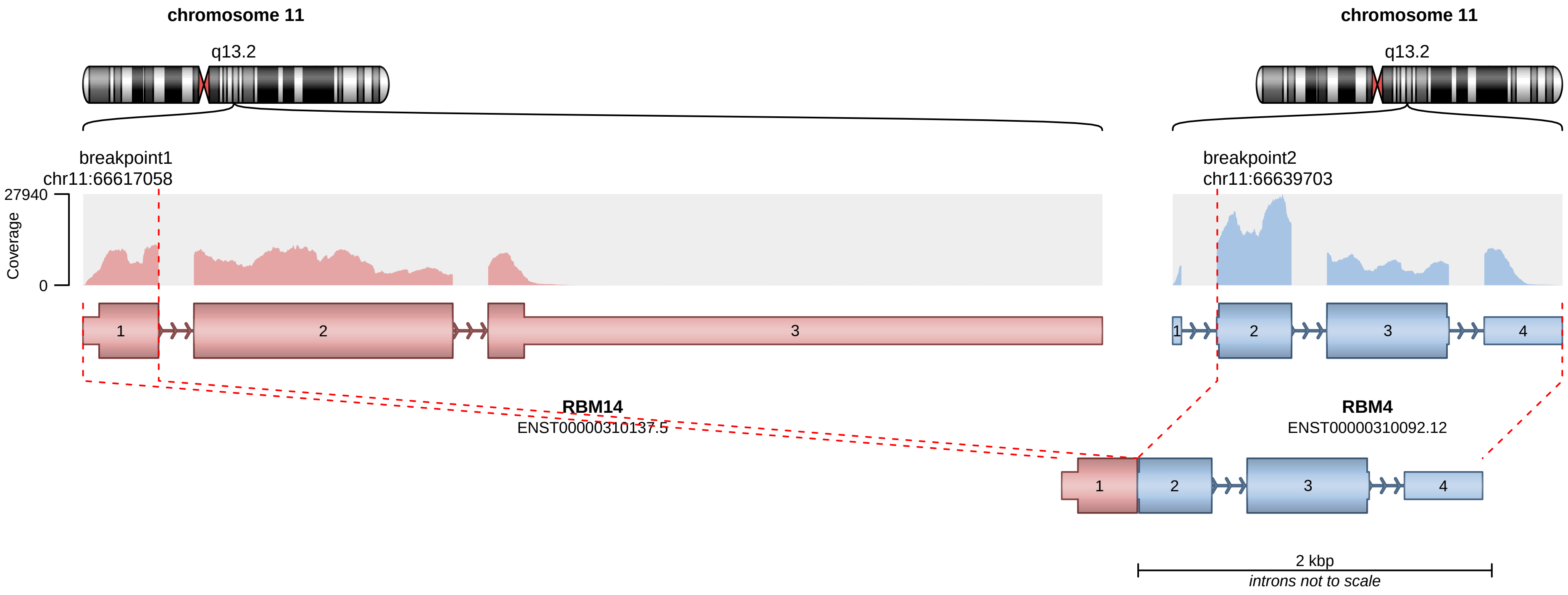


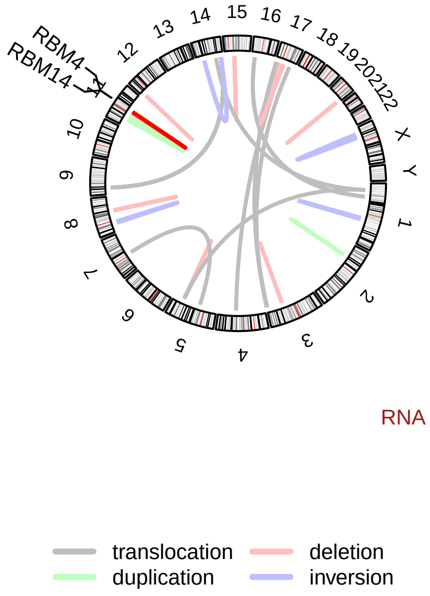




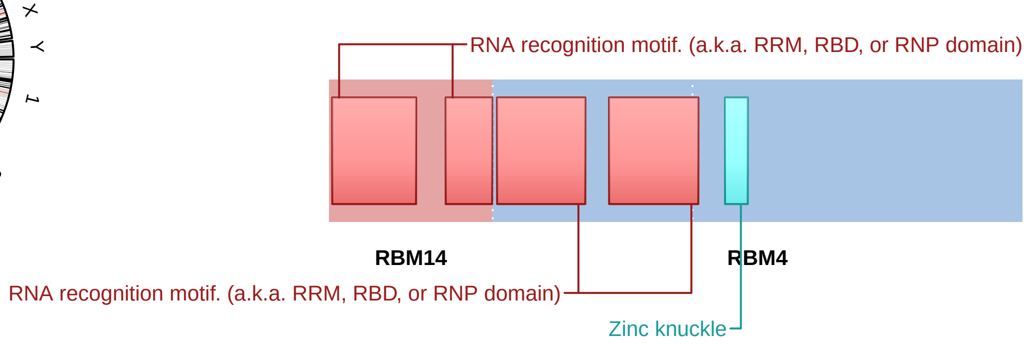
**SUPPORTING READ COUNT**

Split reads = 12
Discordant mates = 12



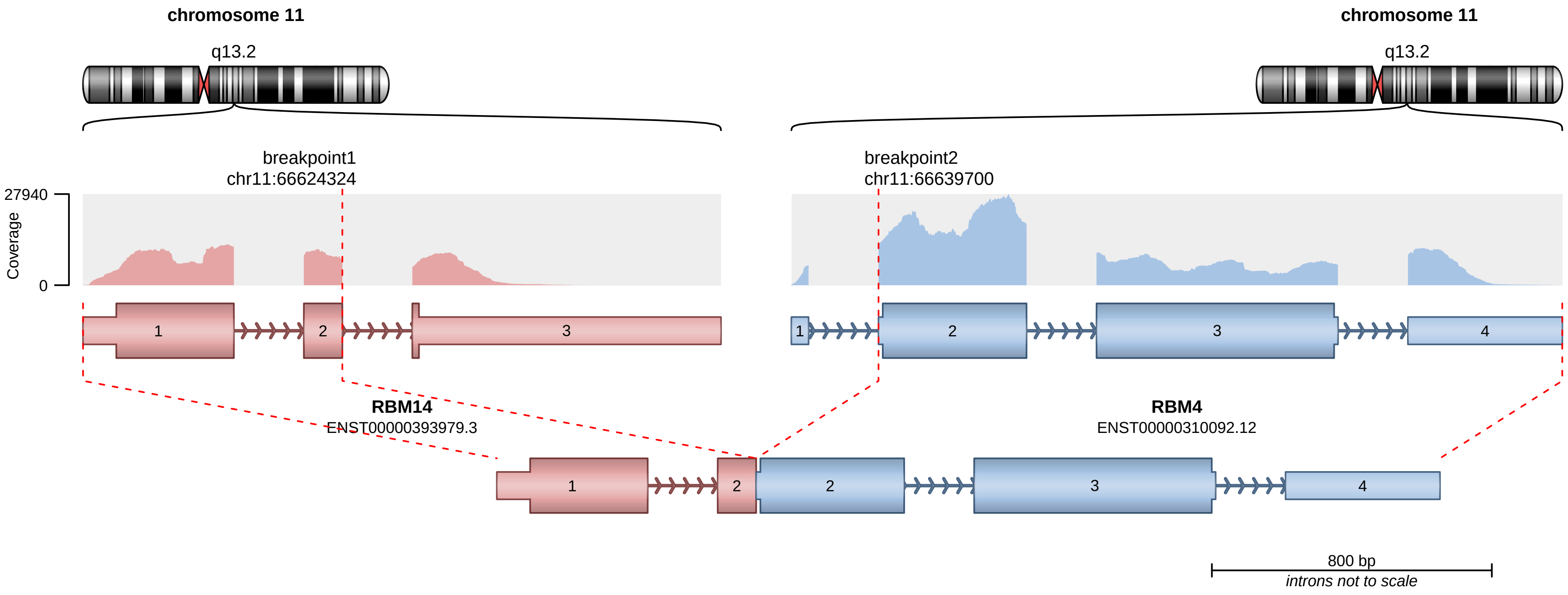


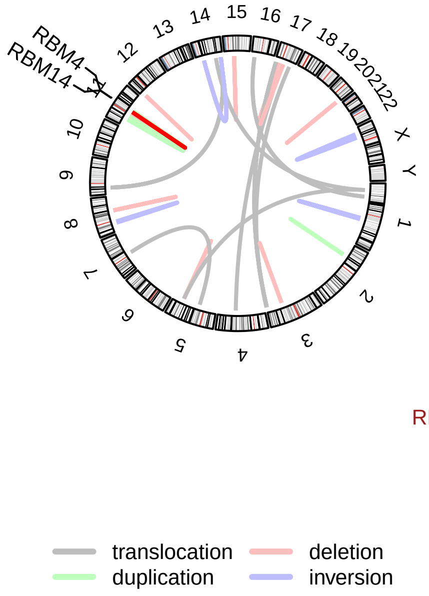
**RETAINED PROTEIN DOMAINS**
reading frame unclear

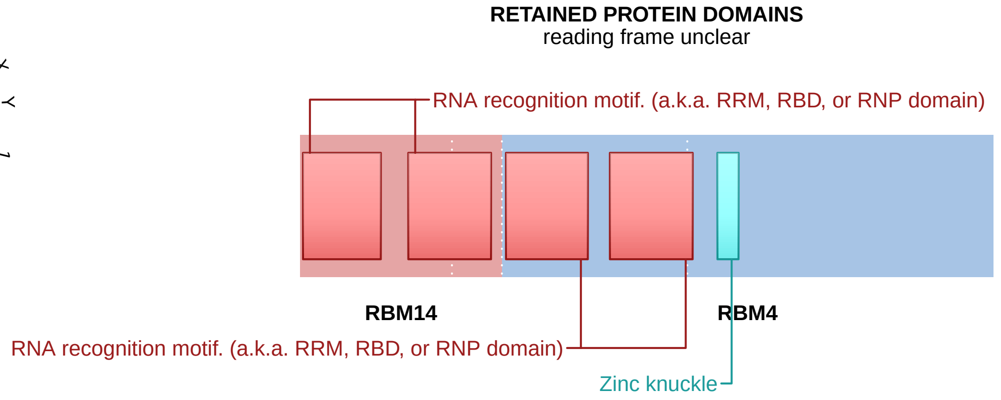


**SUPPORTING READ COUNT**

Split reads = 4
Discordant mates = 7

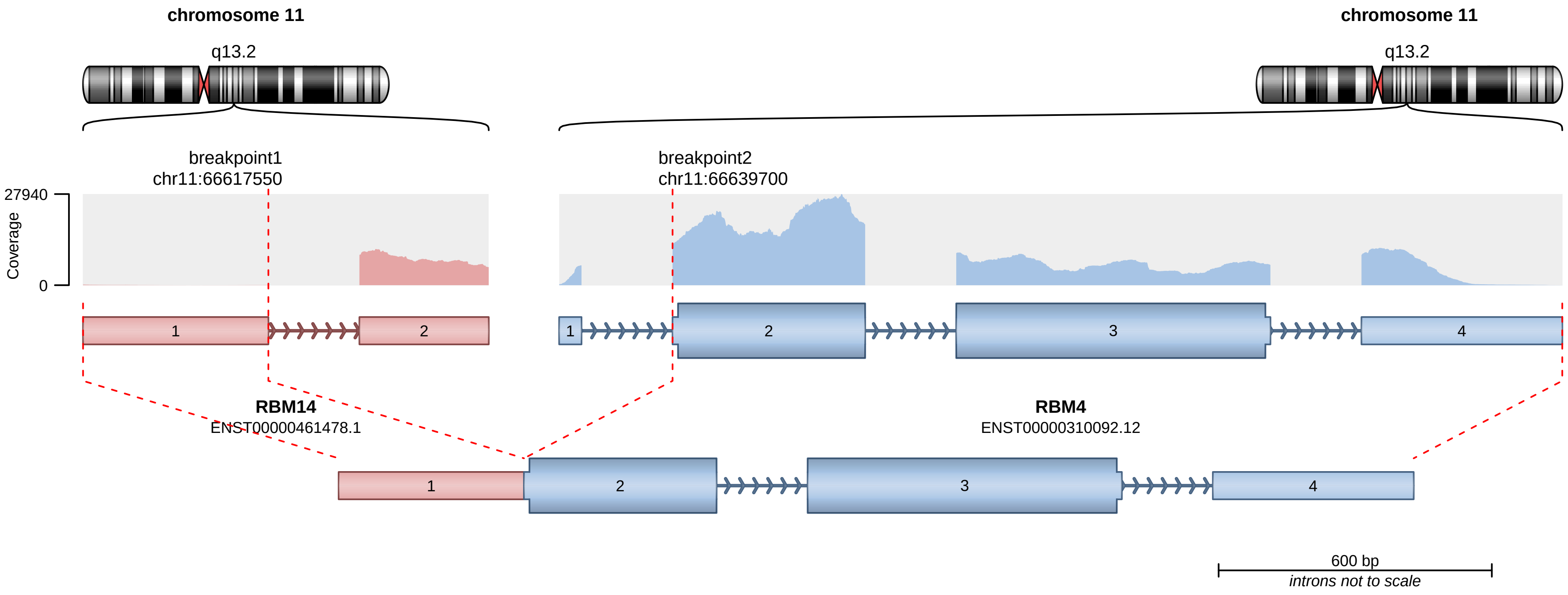


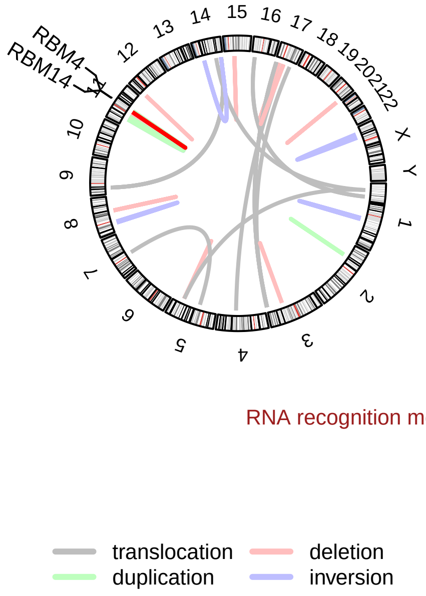


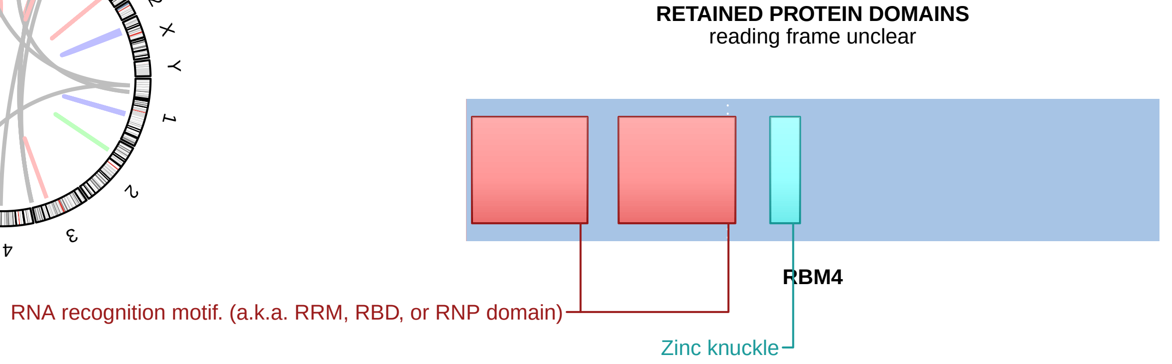


**SUPPORTING READ COUNT**

Split reads = 2
Discordant mates = 13

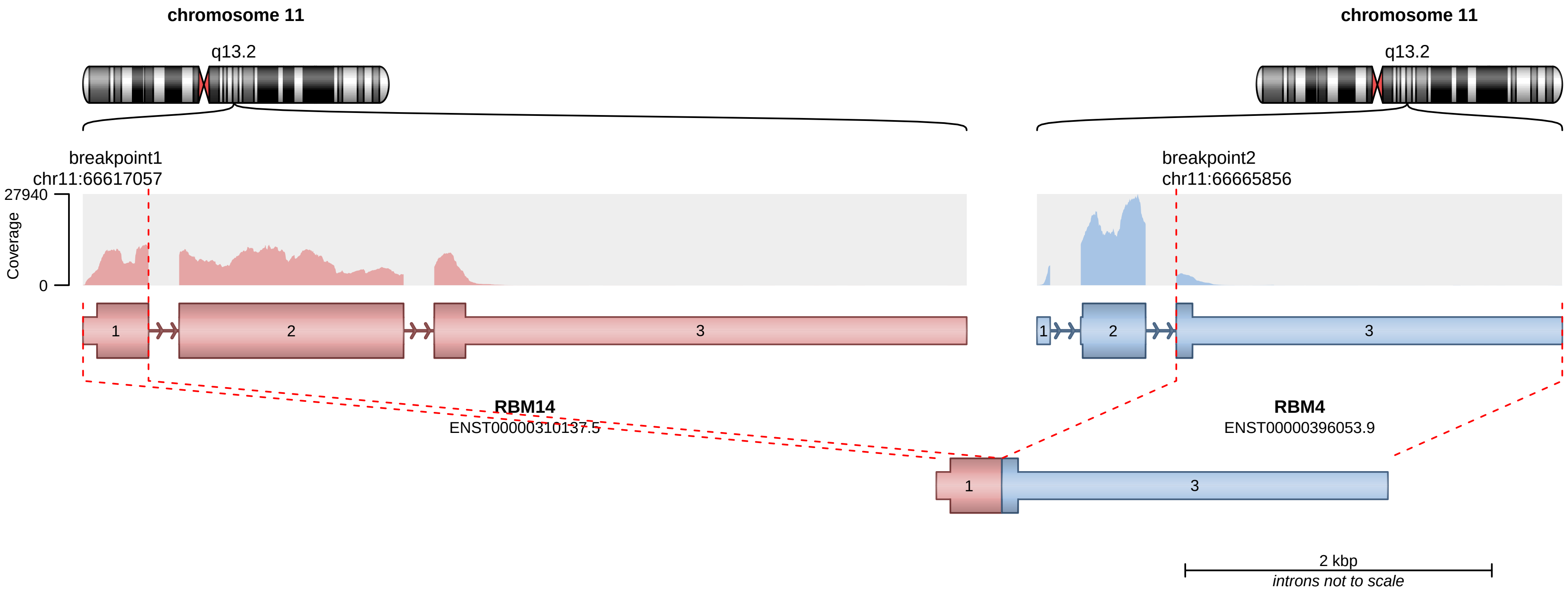


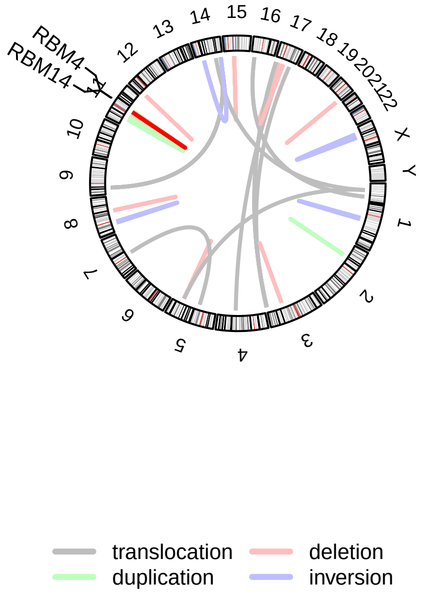


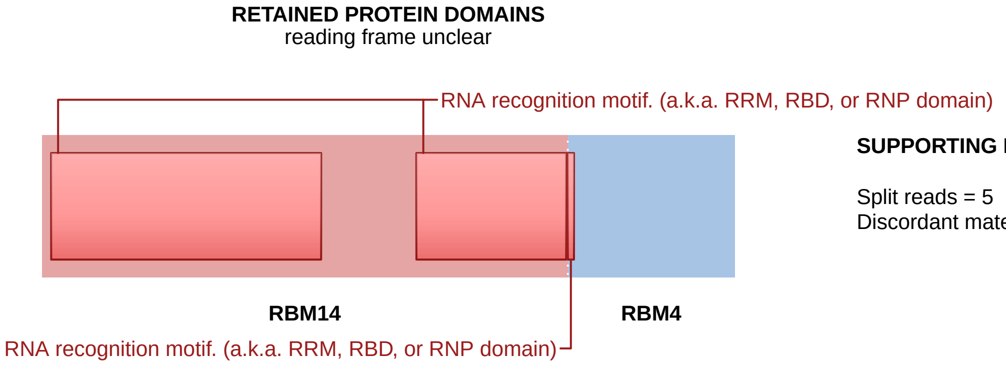


**SUPPORTING READ COUNT**

Split reads = 2
Discordant mates = 12

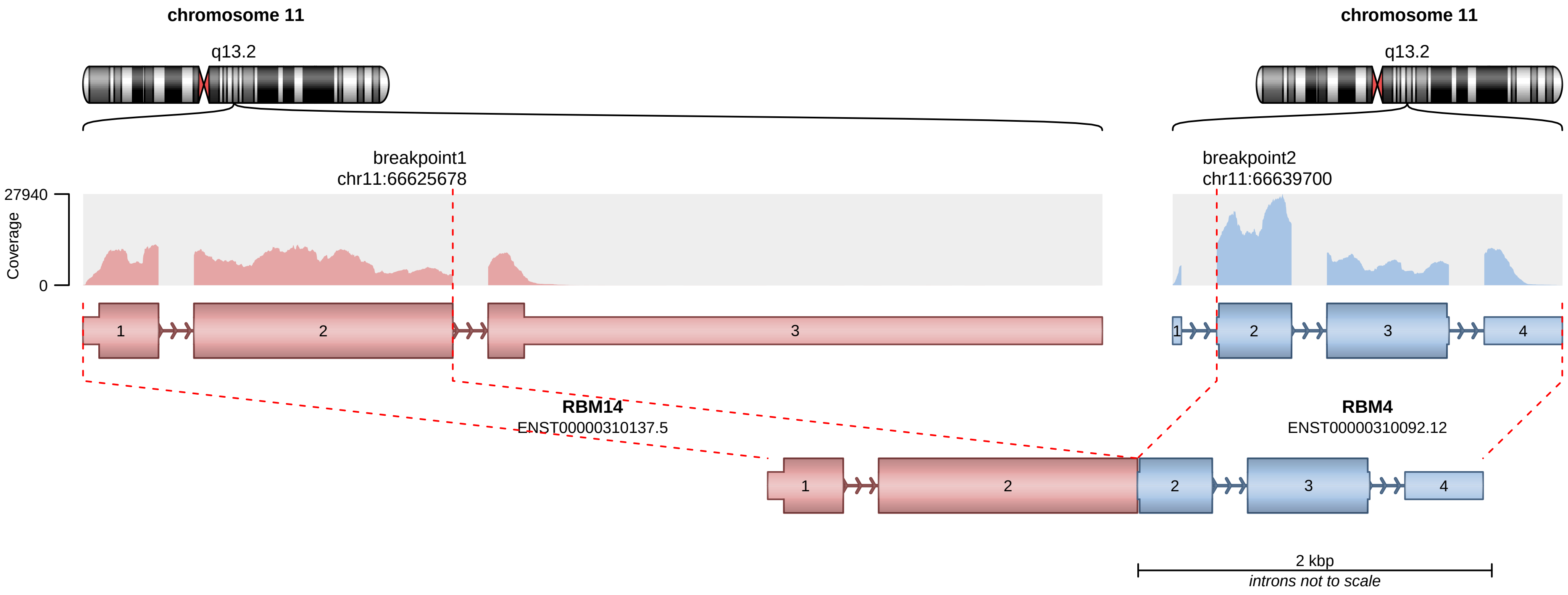


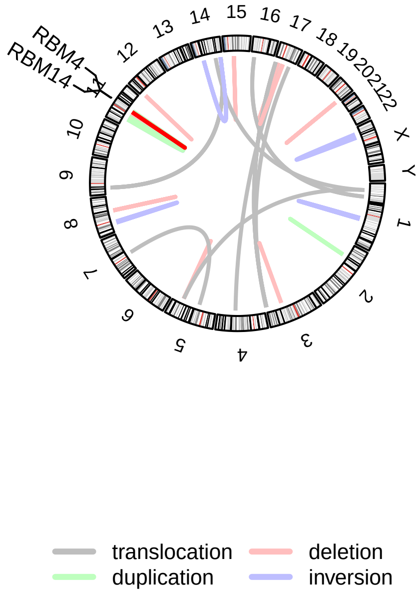


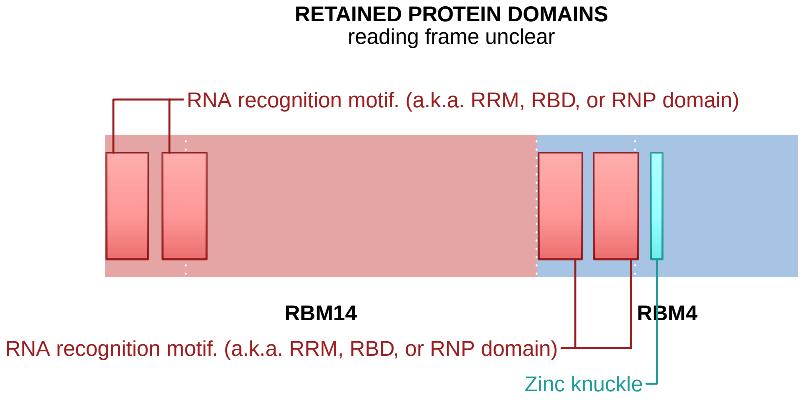


**SUPPORTING READ COUNT**

Split reads = 5
Discordant mates = 0

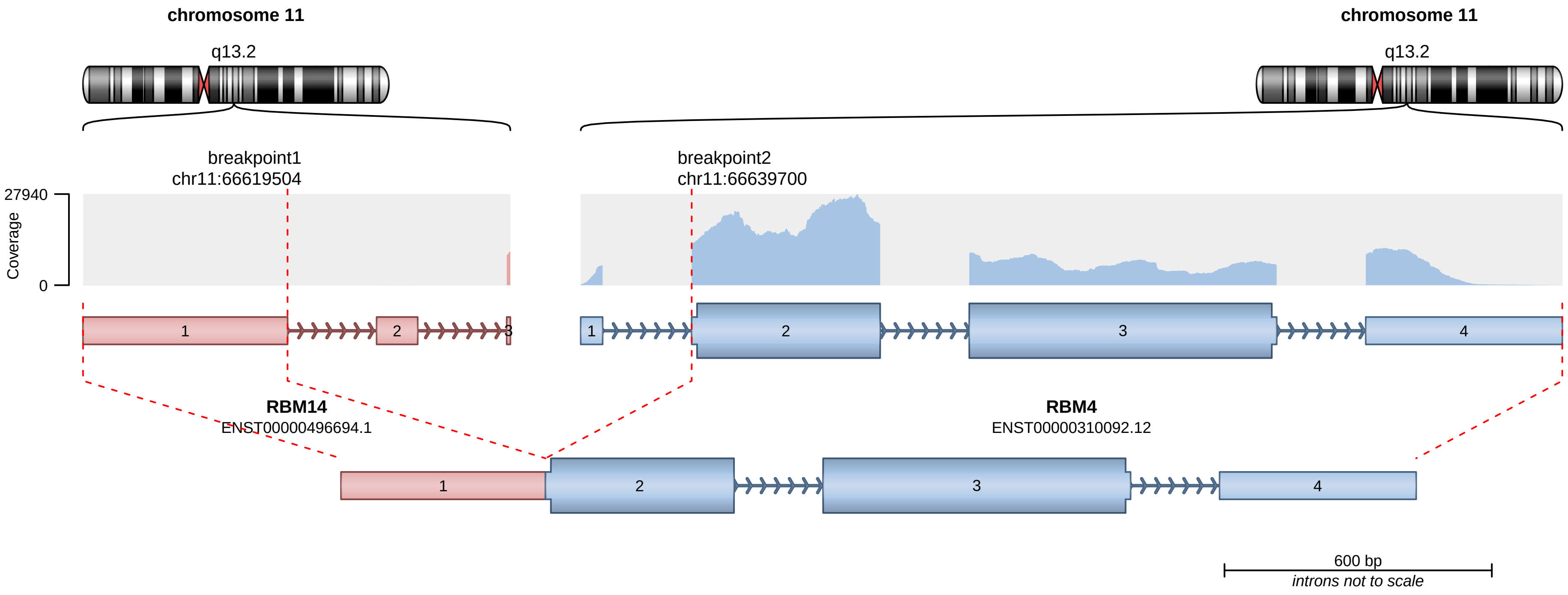


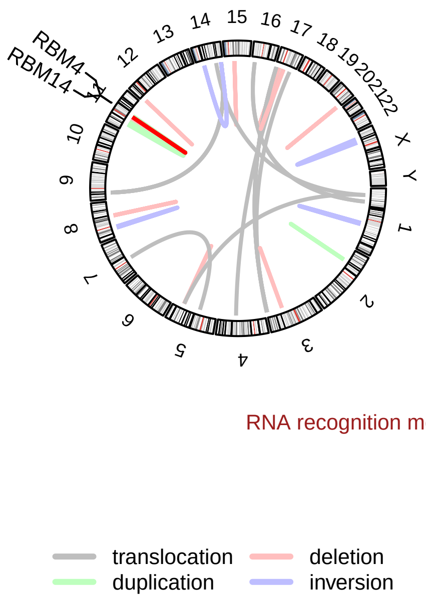


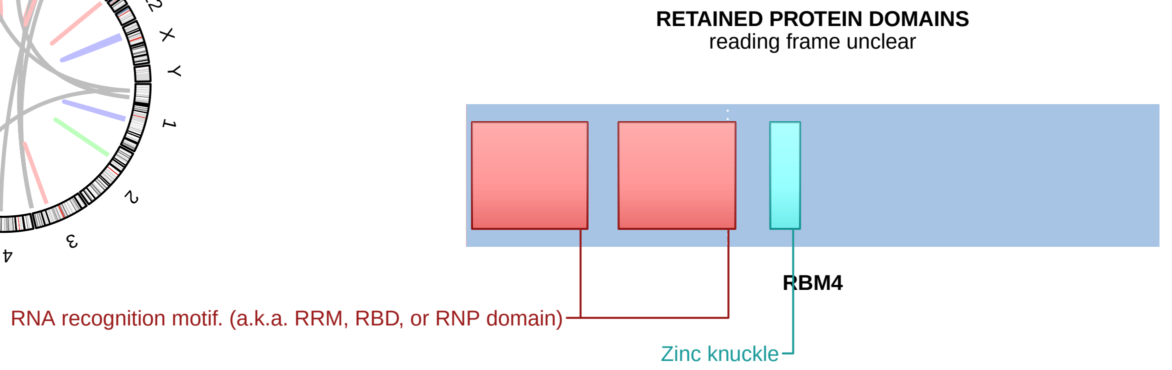


**SUPPORTING READ COUNT**

Split reads = 1
Discordant mates = 13

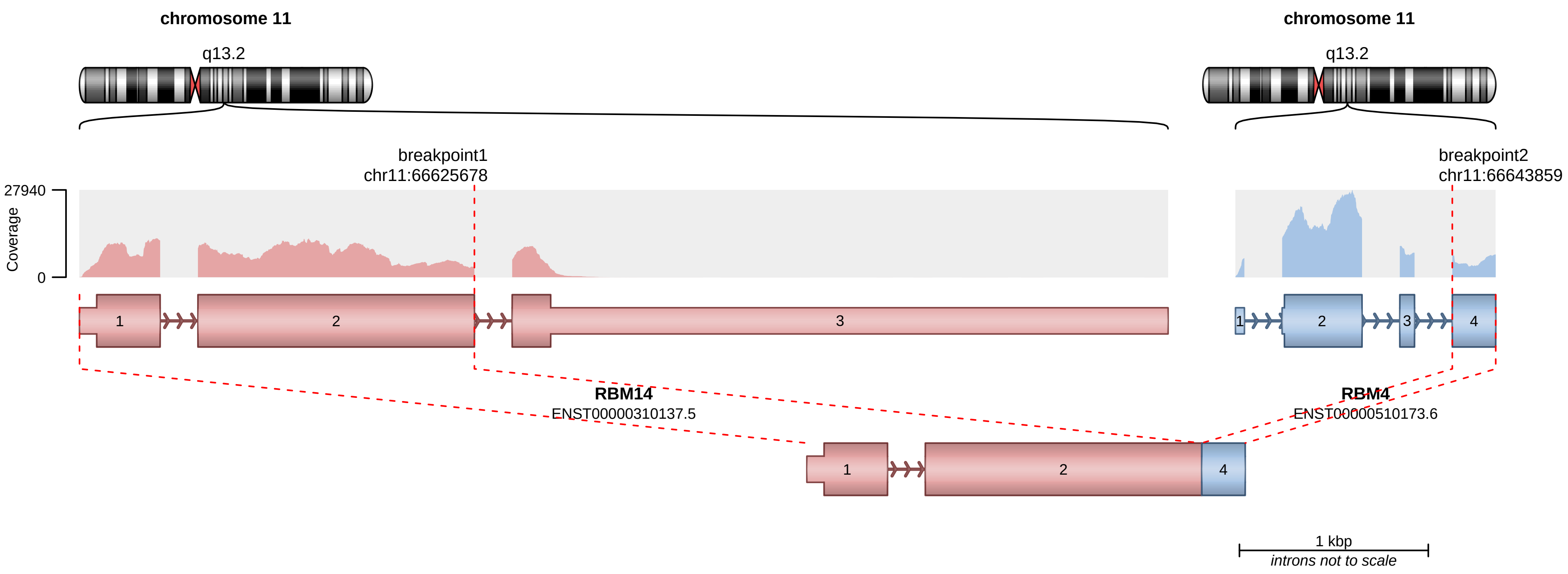


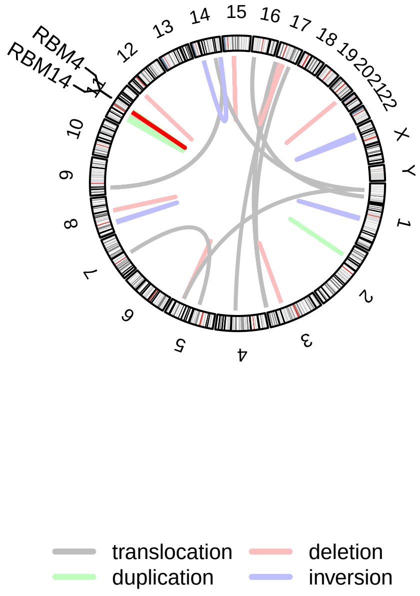


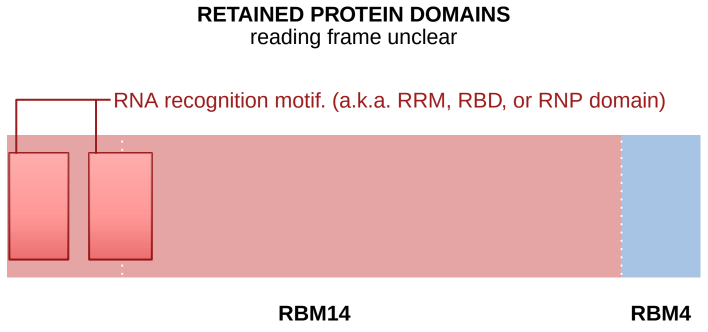


**SUPPORTING READ COUNT**

Split reads = 1
Discordant mates = 13

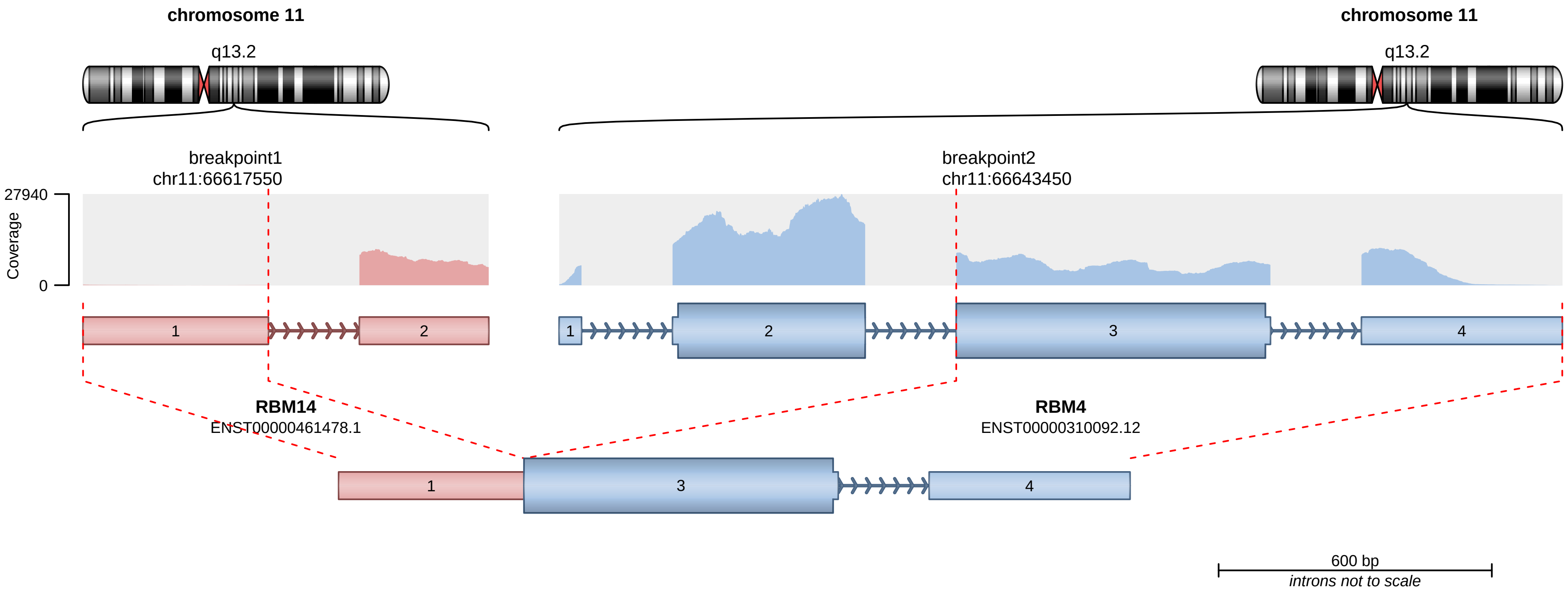


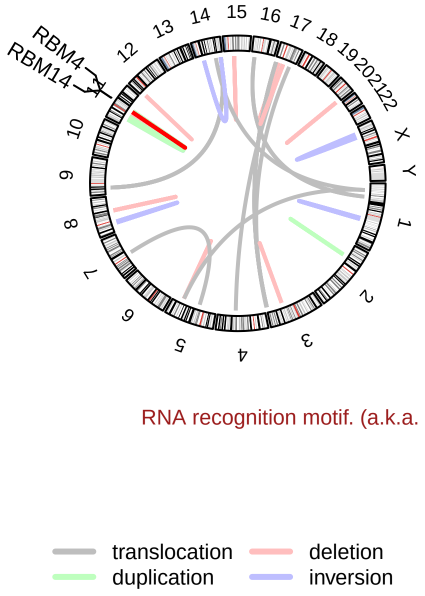




**SUPPORTING READ COUNT**

Split reads = 1
Discordant mates = 2

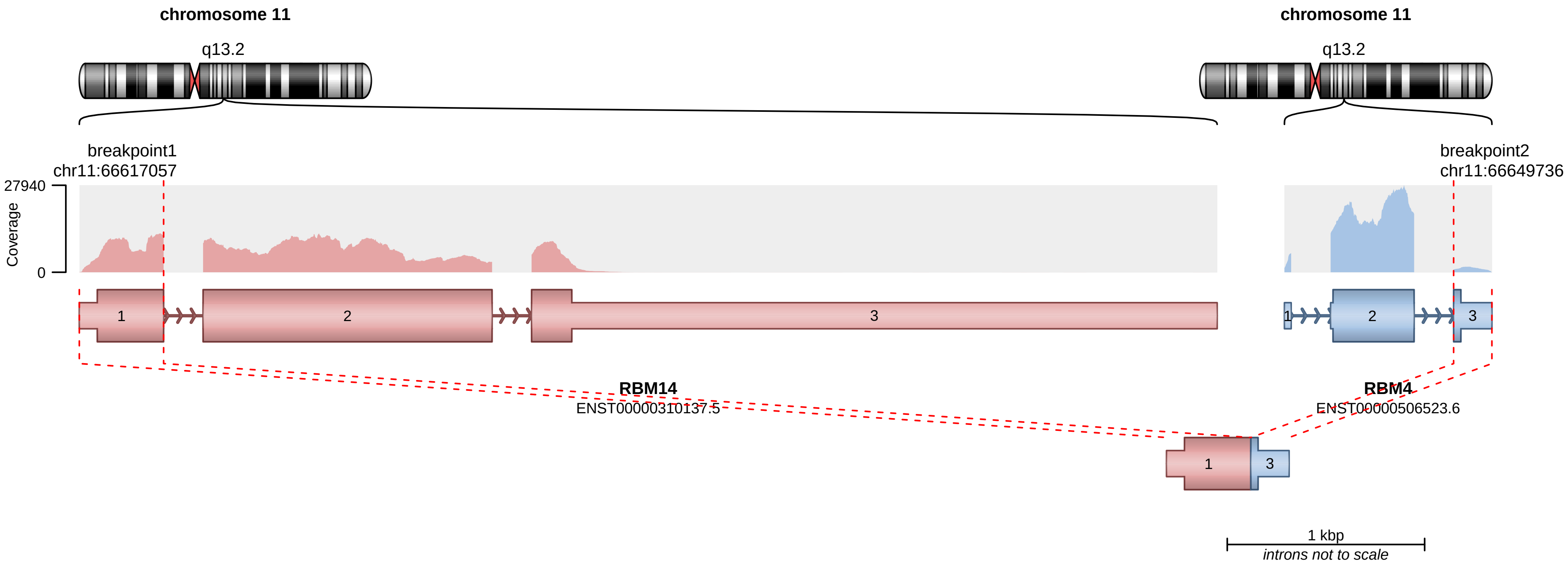


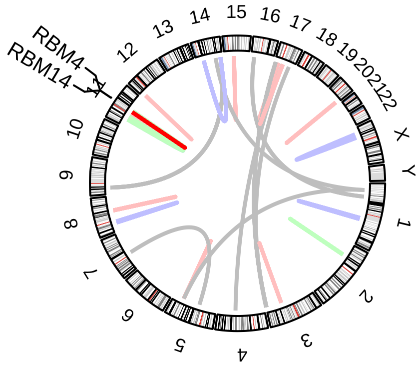


**RETAINED PROTEIN DOMAINS**
reading frame unclear

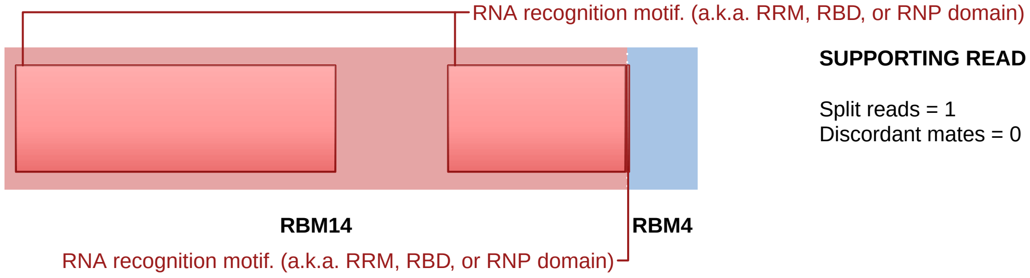
**SUPPORTING READ COUNT**

Split reads = 1
Discordant mates = 1



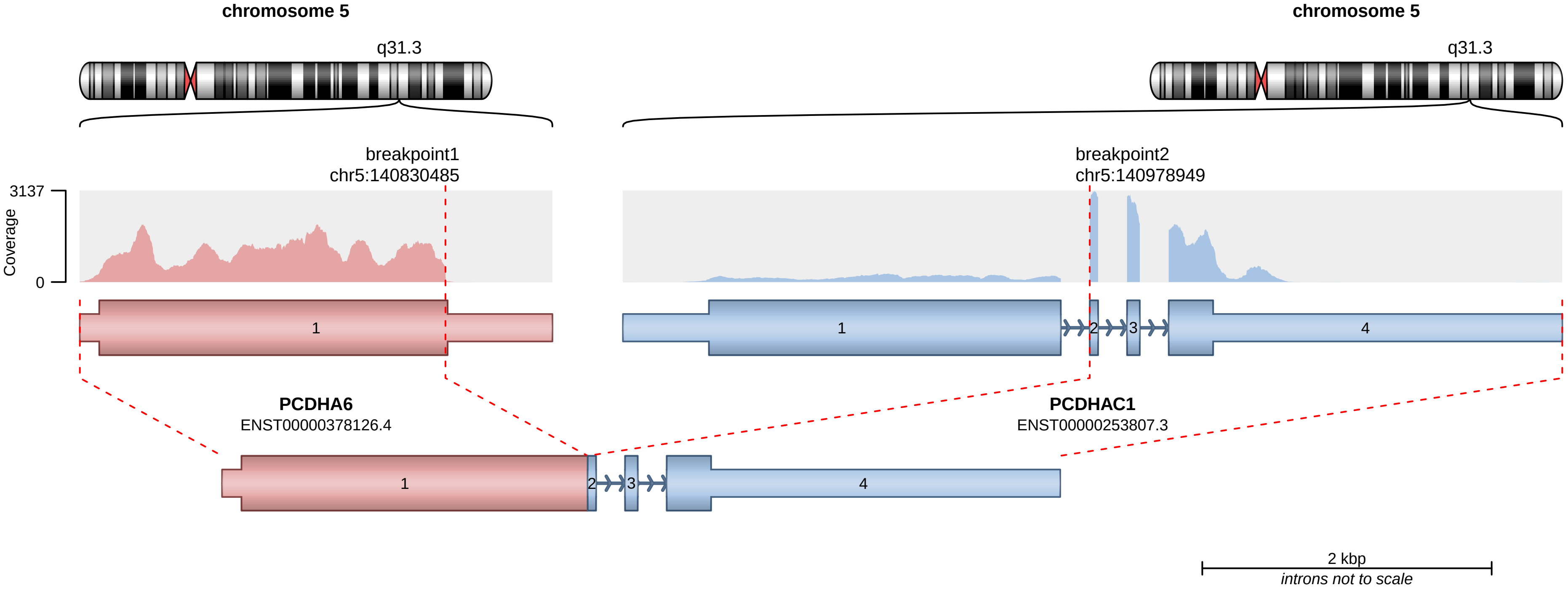


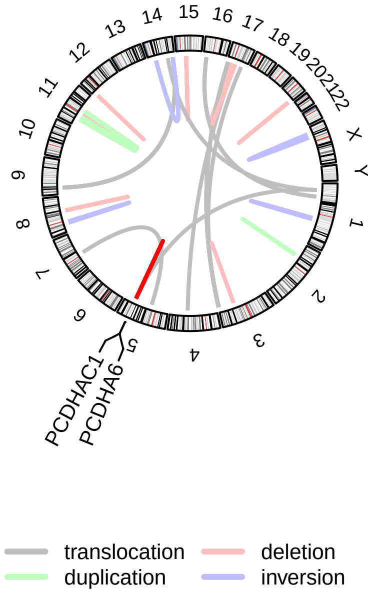
**RETAINED PROTEIN DOMAINS**
reading frame unclear



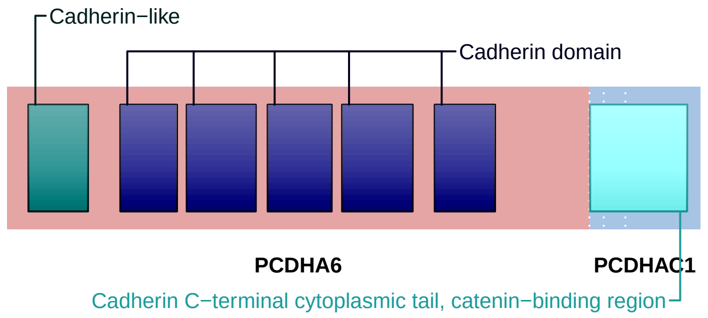
**SUPPORTING READ COUNT**

Split reads = 1
Discordant mates = 0



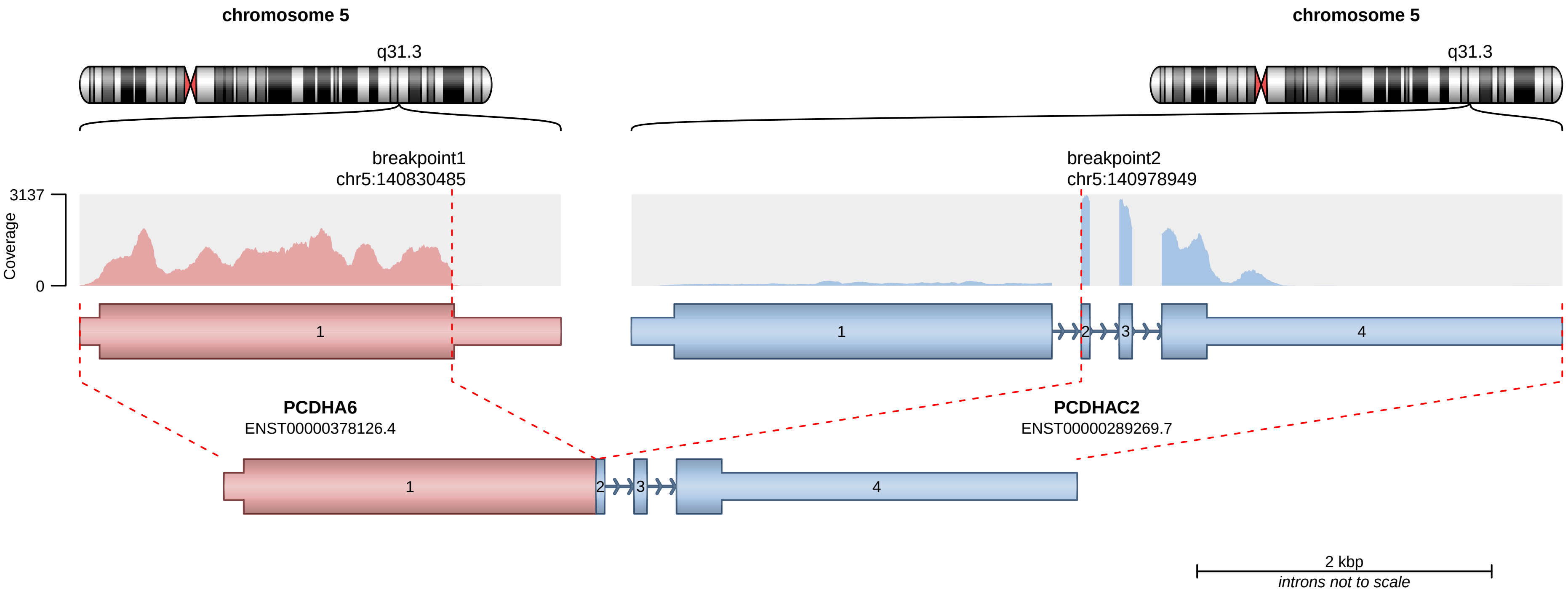


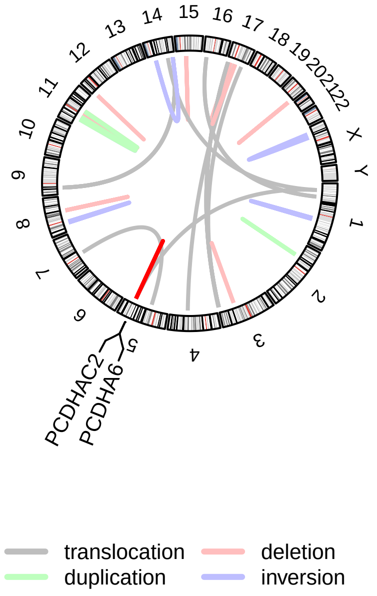
**RETAINED PROTEIN DOMAINS**
reading frame unclear



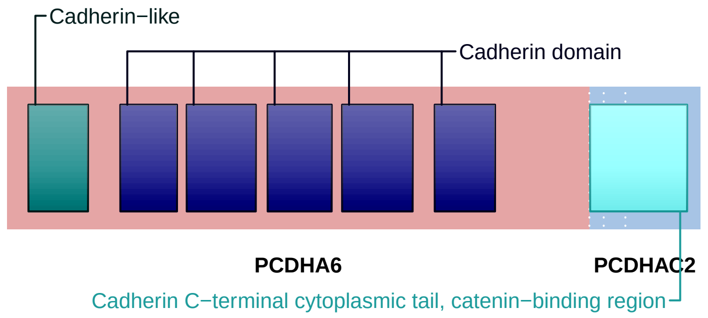
**SUPPORTING READ COUNT**

Split reads = 221
Discordant mates = 2



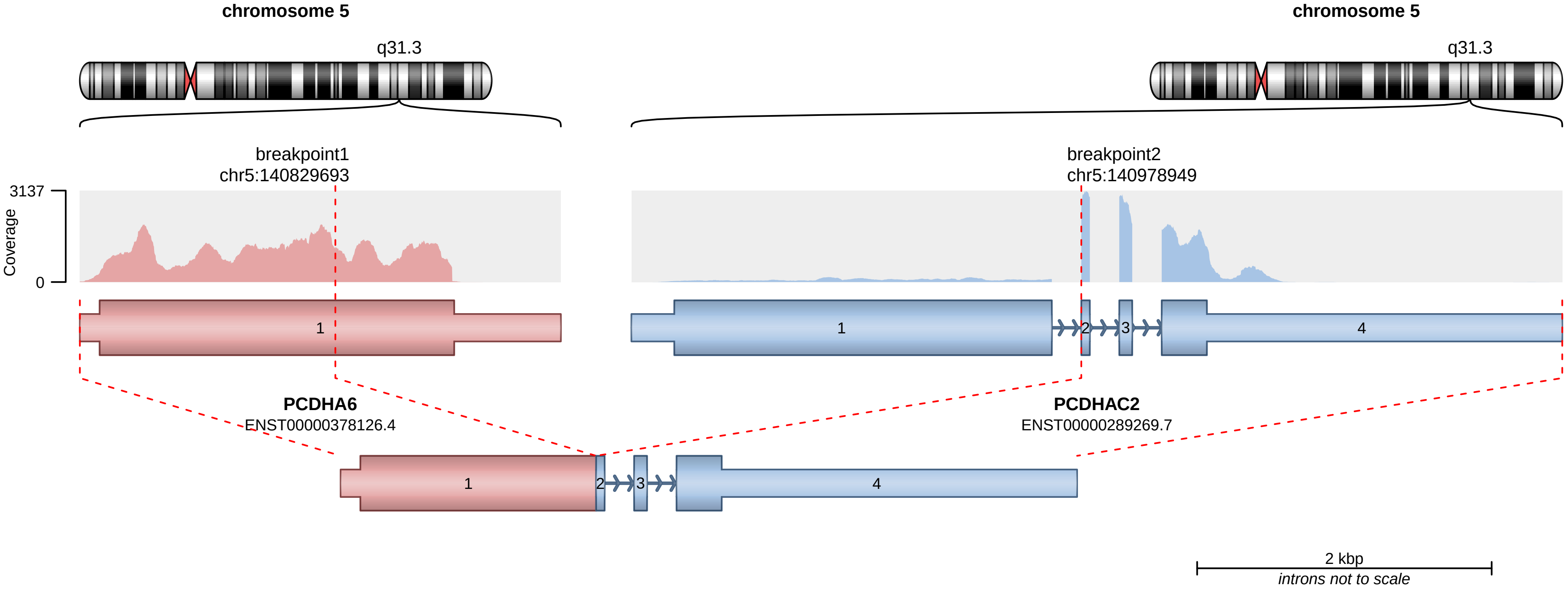


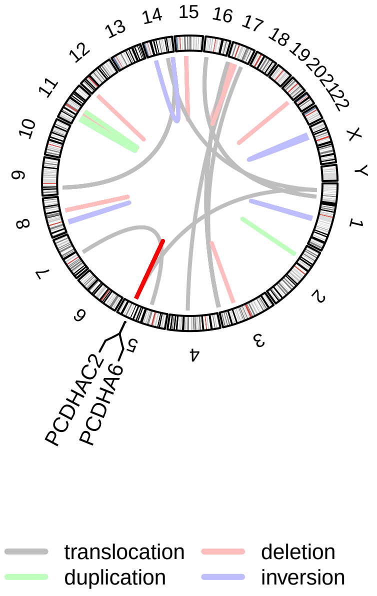
**RETAINED PROTEIN DOMAINS**
reading frame unclear

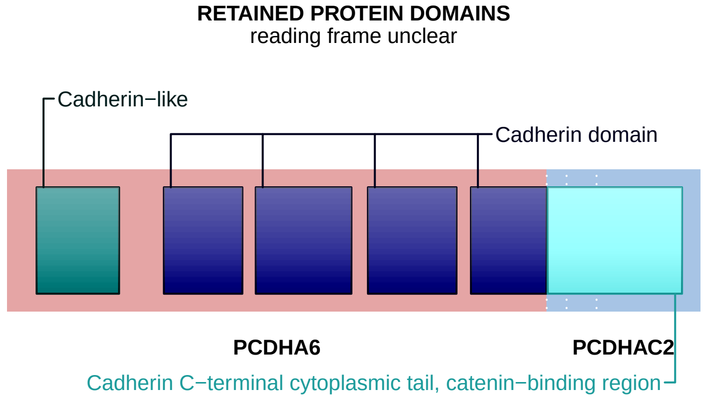


**SUPPORTING READ COUNT**

Split reads = 221
Discordant mates = 2

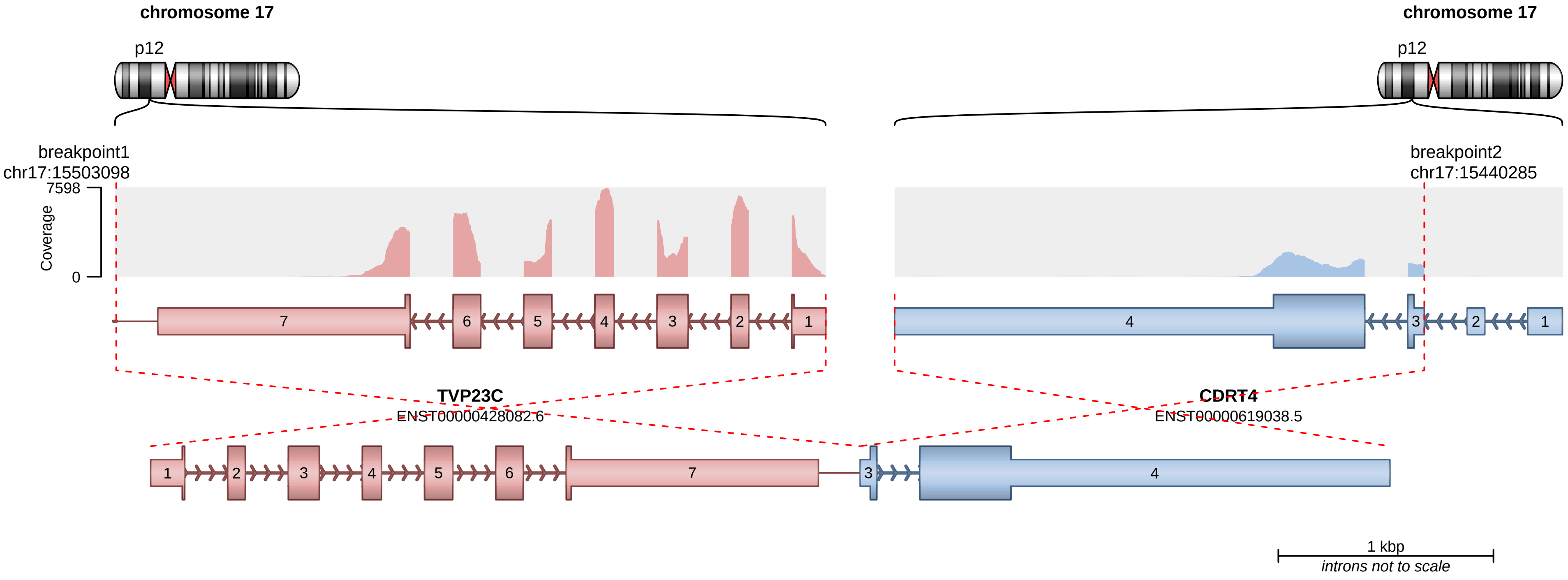


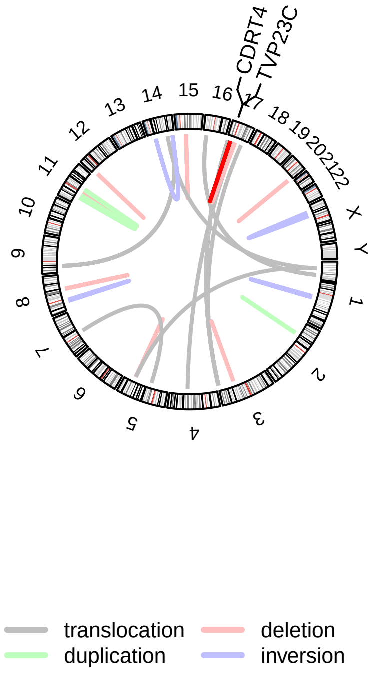


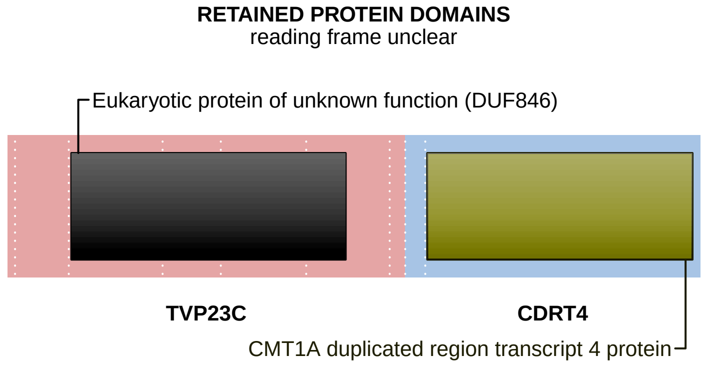


**SUPPORTING READ COUNT**

Split reads = 58
Discordant mates = 1

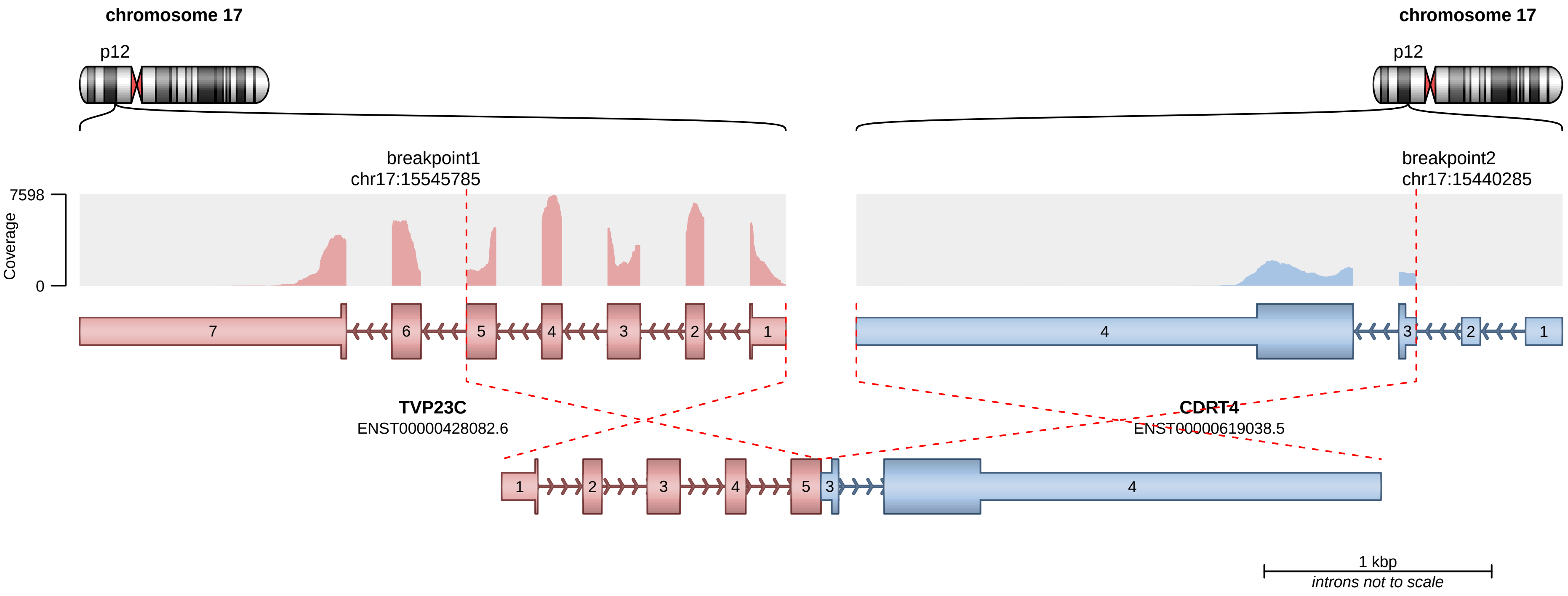


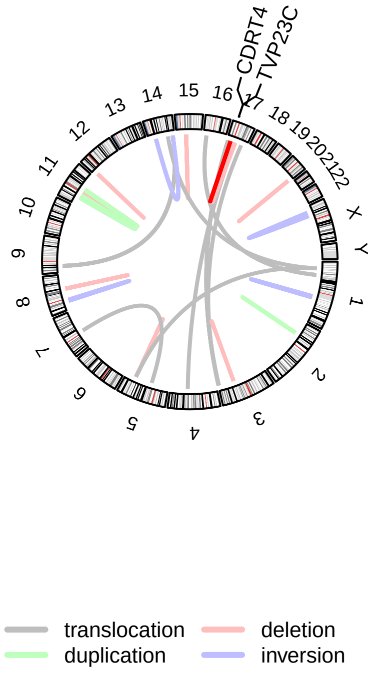


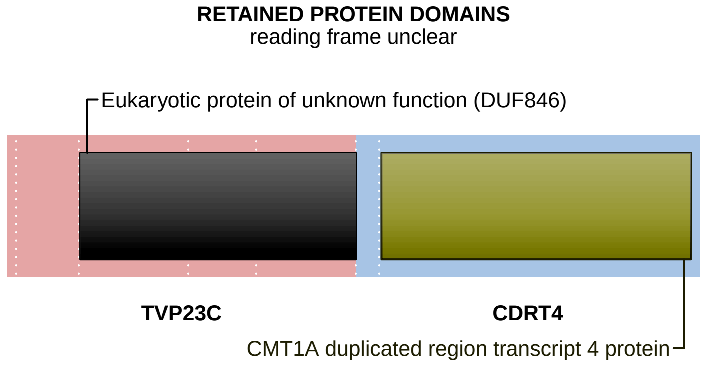


**SUPPORTING READ COUNT**

Split reads = 179
Discordant mates = 4

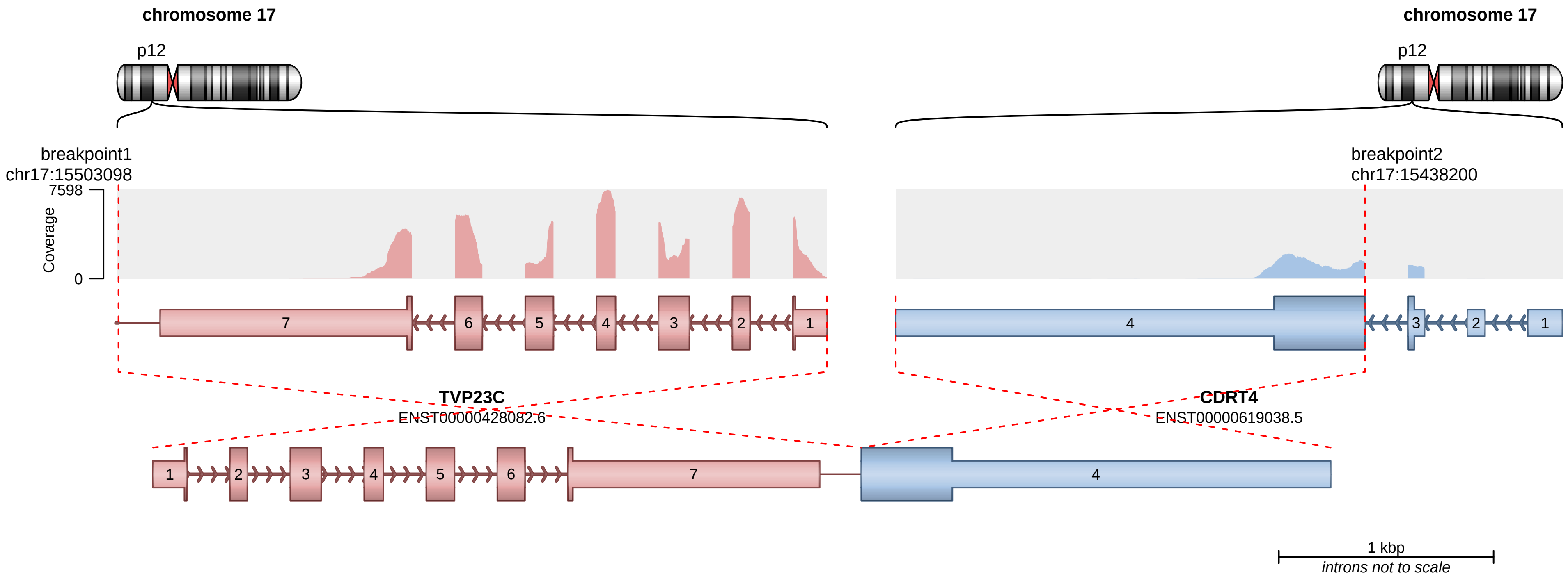


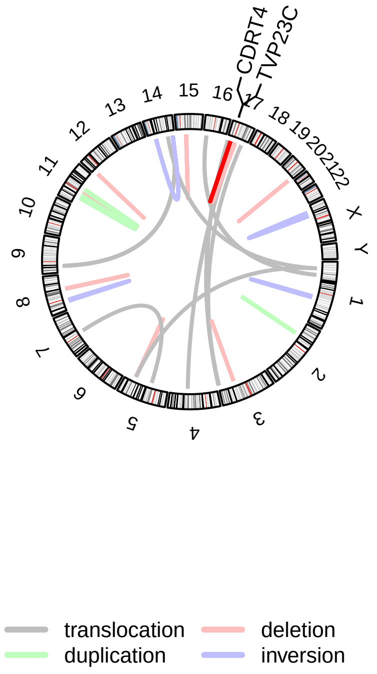


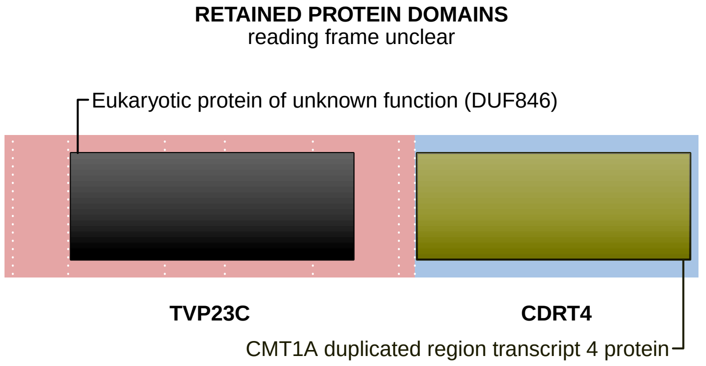


**SUPPORTING READ COUNT**

Split reads = 104
Discordant mates = 3

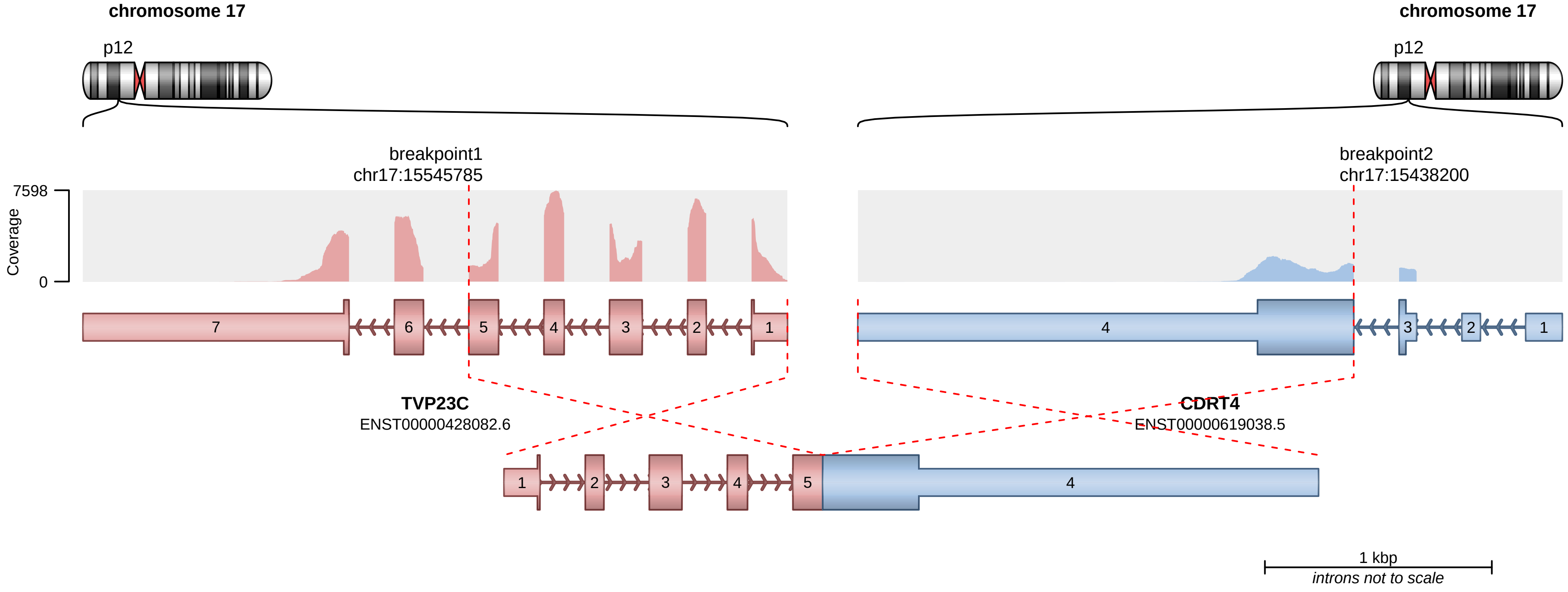


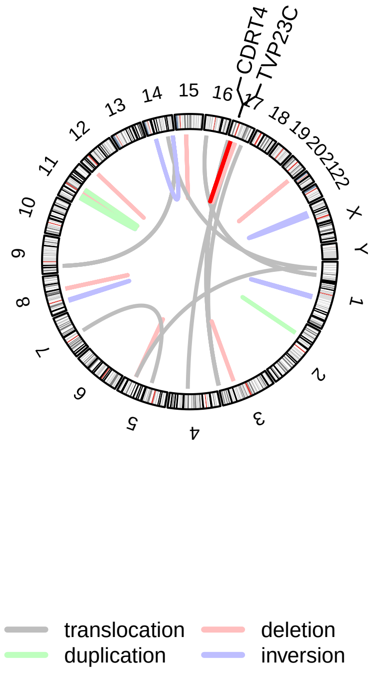




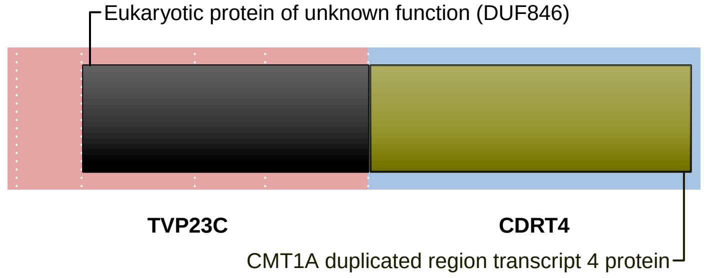
**SUPPORTING READ COUNT**

Split reads = 73
Discordant mates = 1



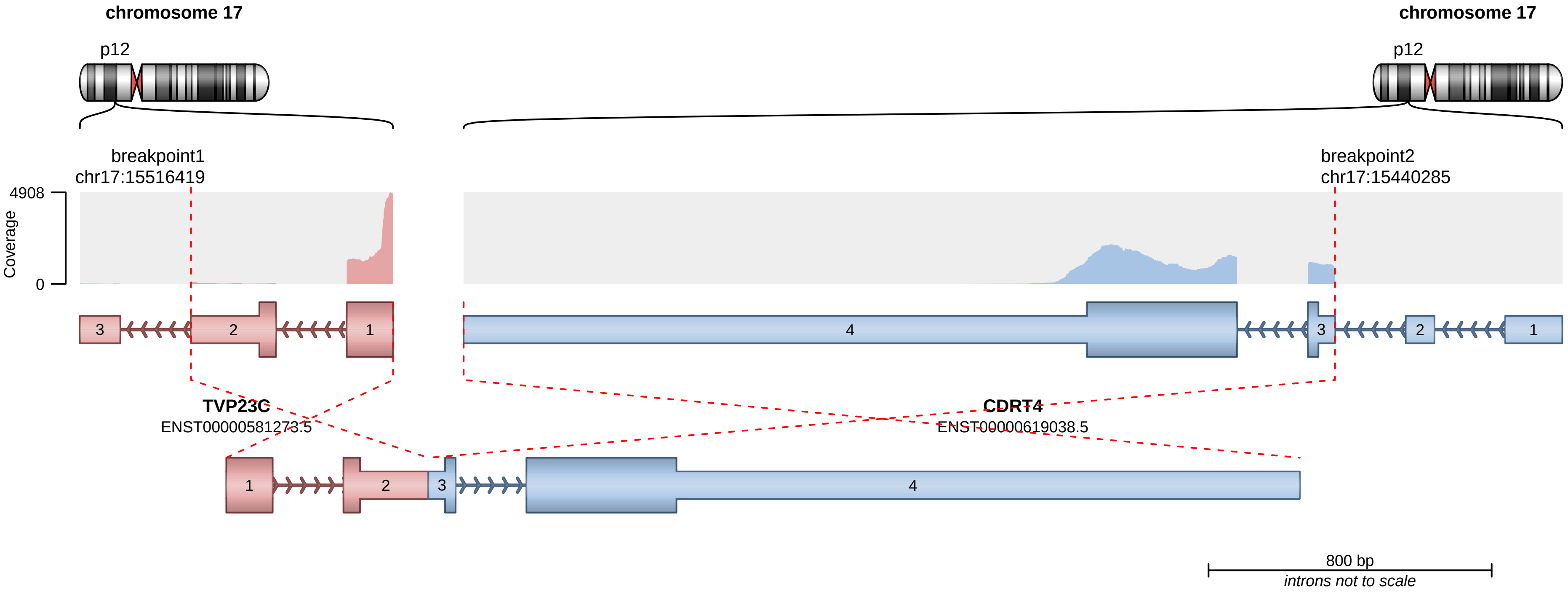


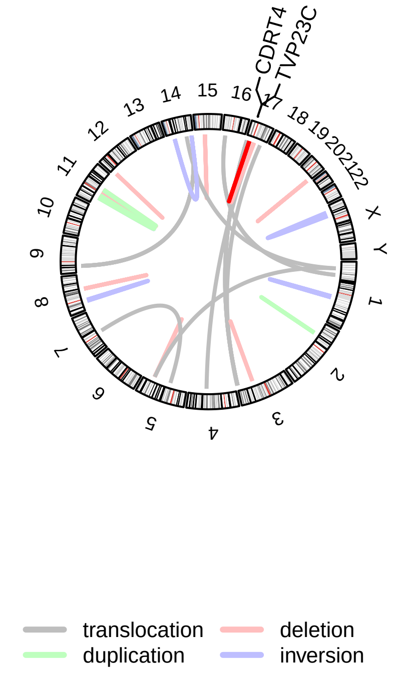
**RETAINED PROTEIN DOMAINS**
reading frame unclear



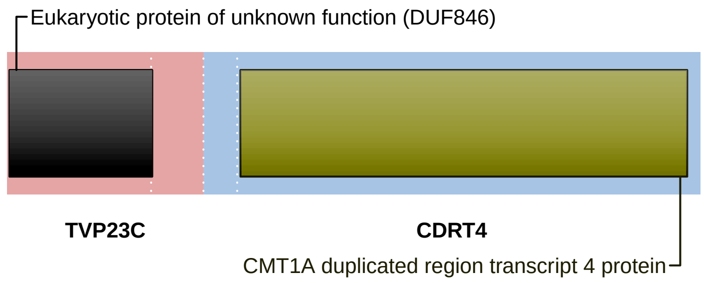
**SUPPORTING READ COUNT**

Split reads = 26
Discordant mates = 1



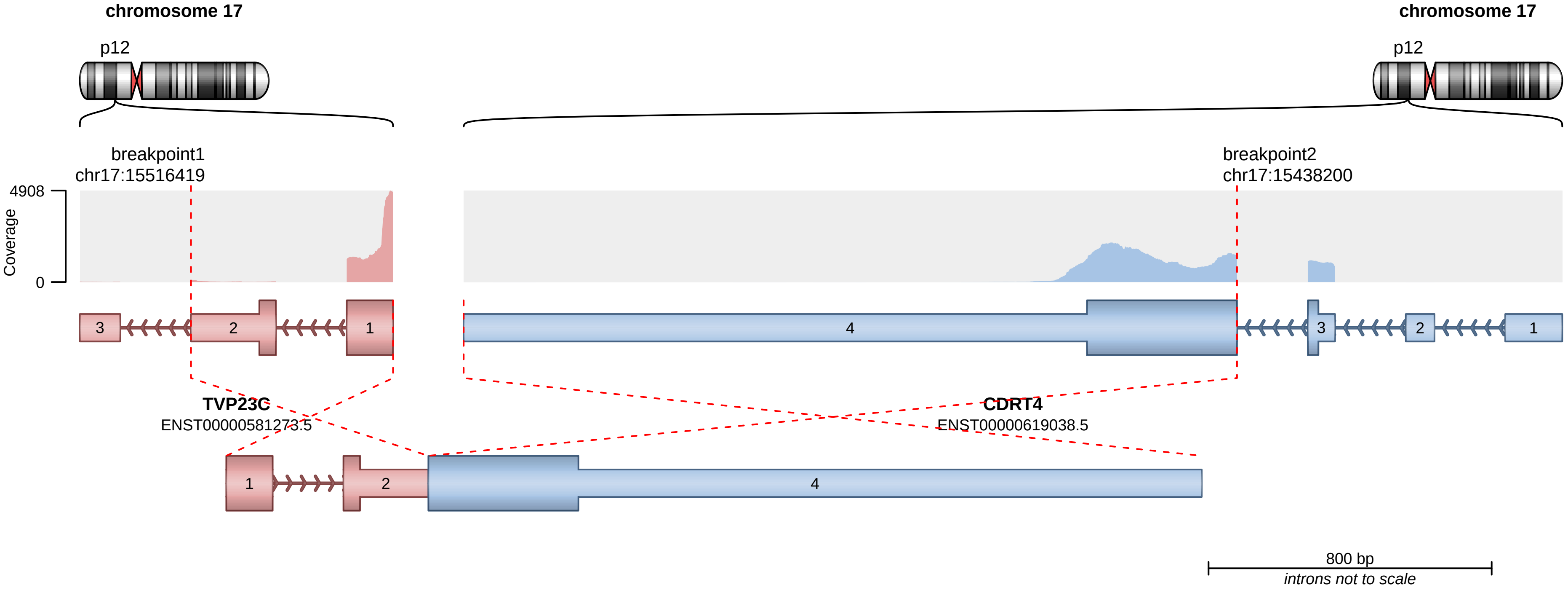


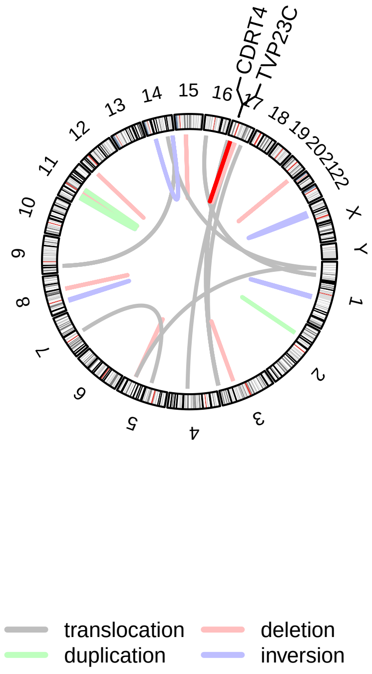
**RETAINED PROTEIN DOMAINS**
reading frame unclear

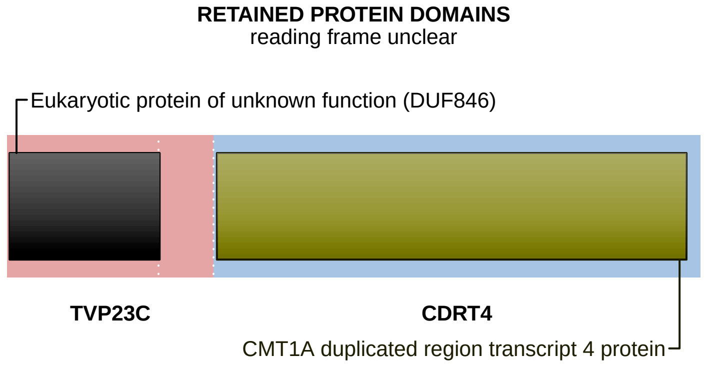


**SUPPORTING READ COUNT**

Split reads = 21
Discordant mates = 3

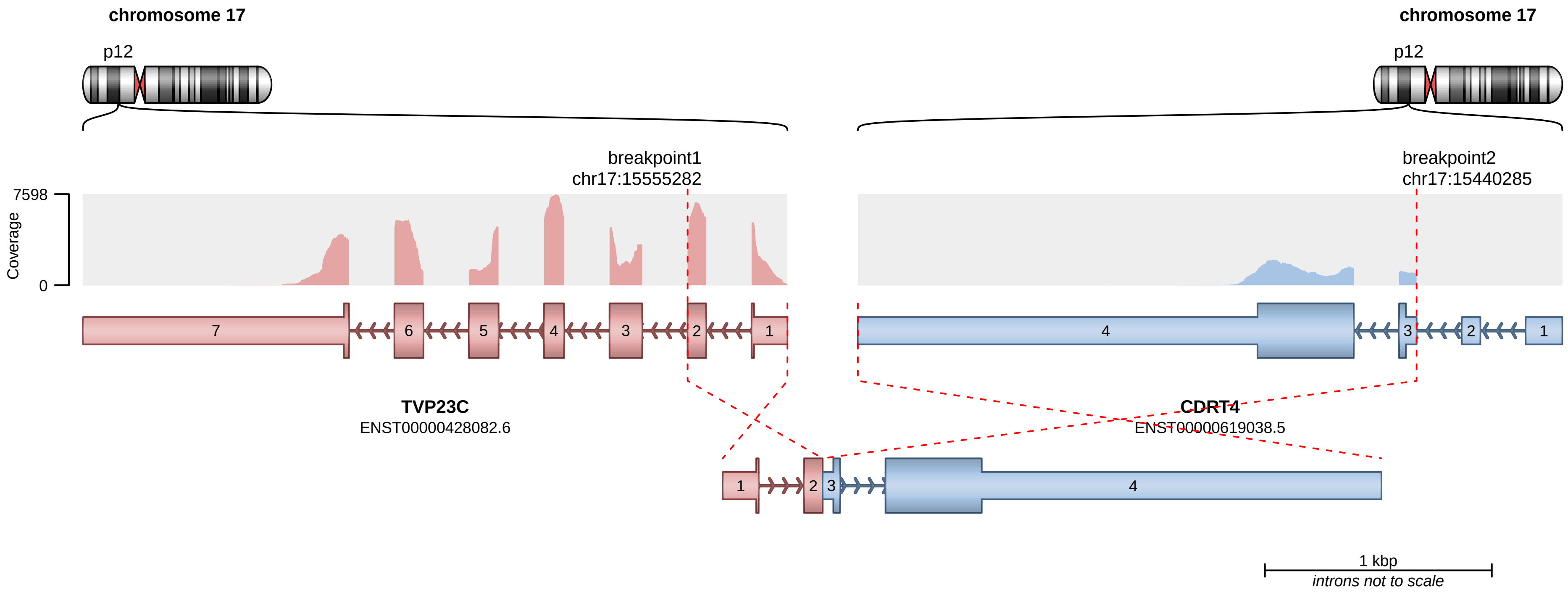


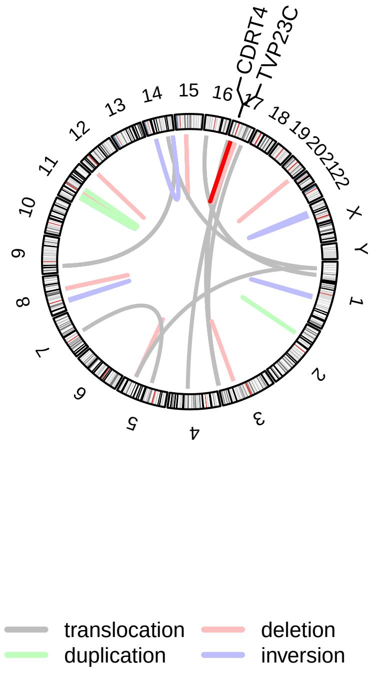




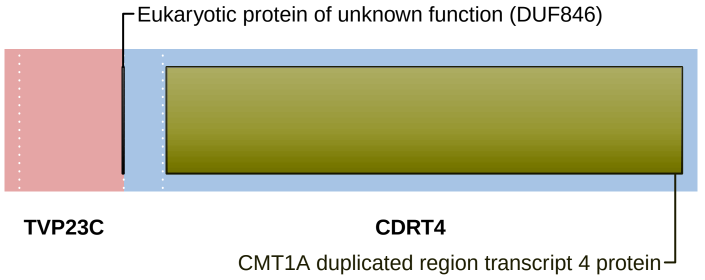
**SUPPORTING READ COUNT**

Split reads = 3
Discordant mates = 1



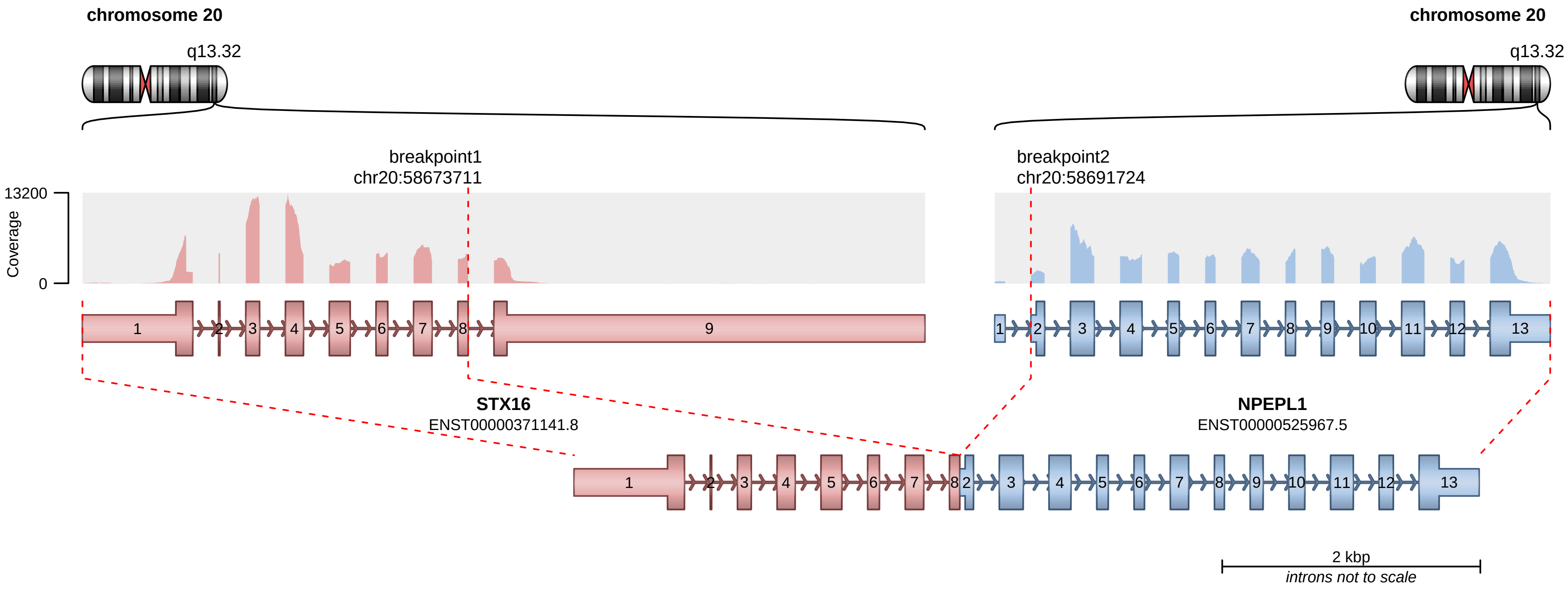


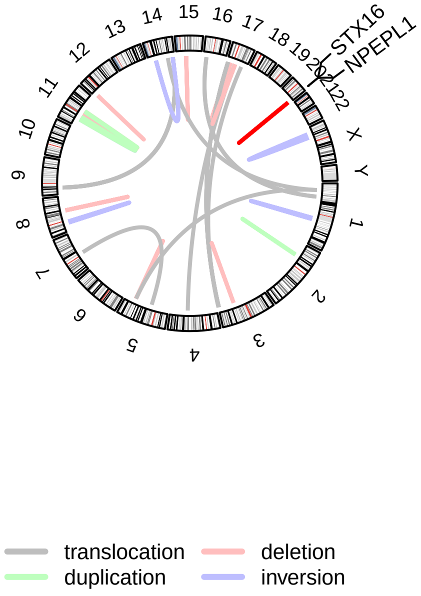
**RETAINED PROTEIN DOMAINS**
reading frame unclear

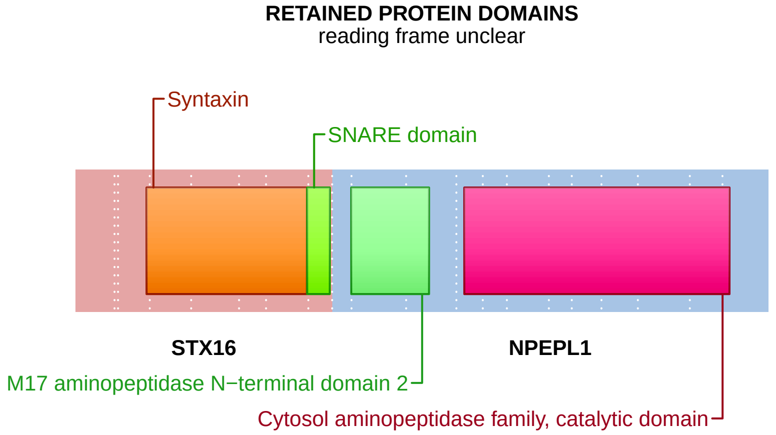


**SUPPORTING READ COUNT**

Split reads = 1
Discordant mates = 0

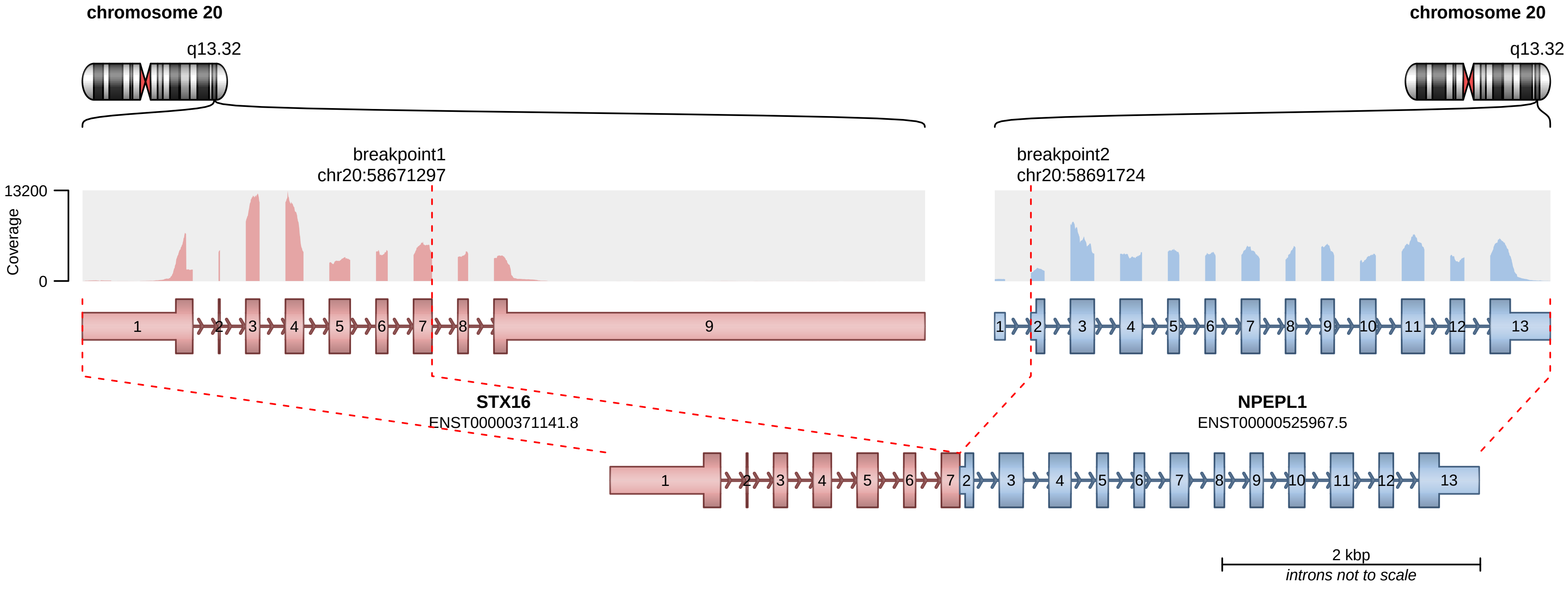


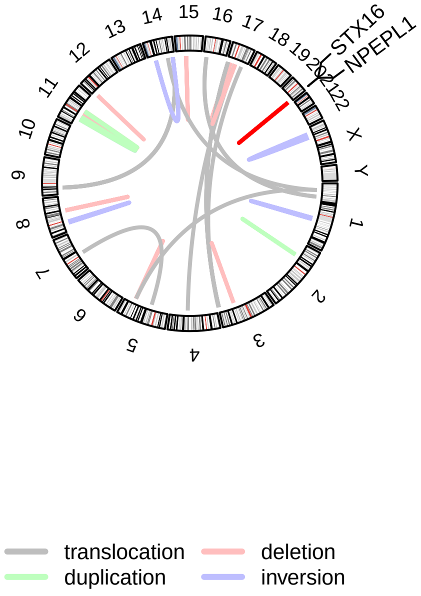


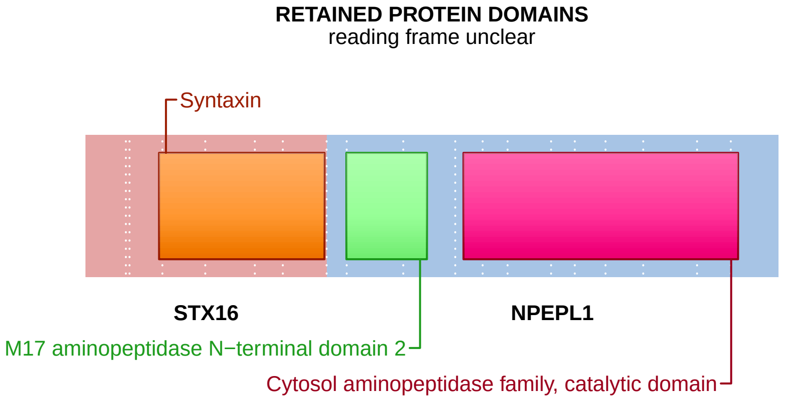


**SUPPORTING READ COUNT**

Split reads = 159
Discordant mates = 1

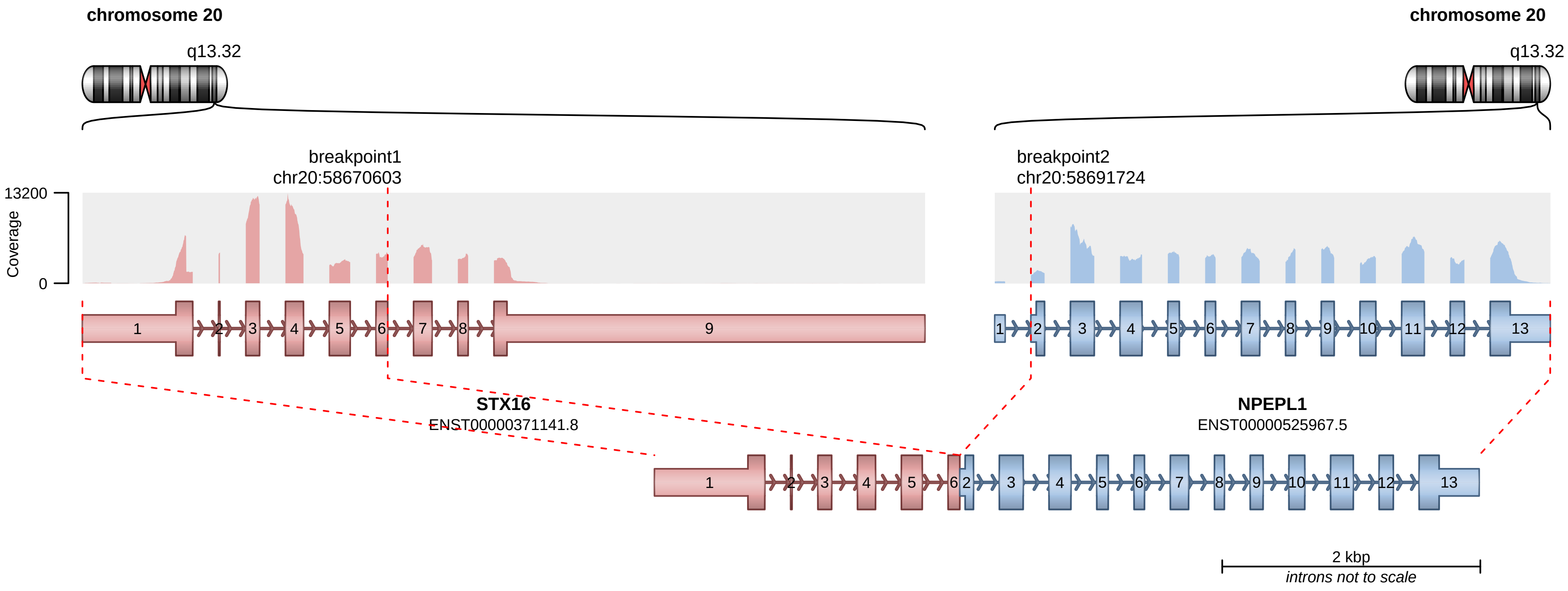


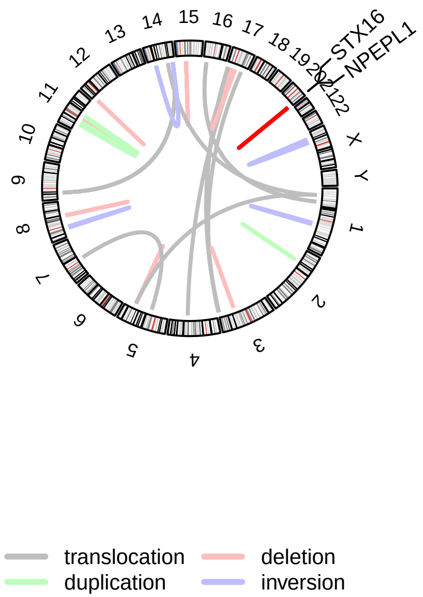


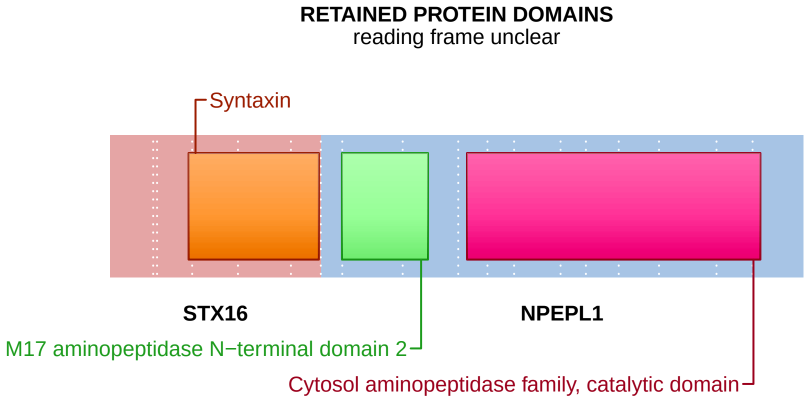


**SUPPORTING READ COUNT**

Split reads = 1
Discordant mates = 0

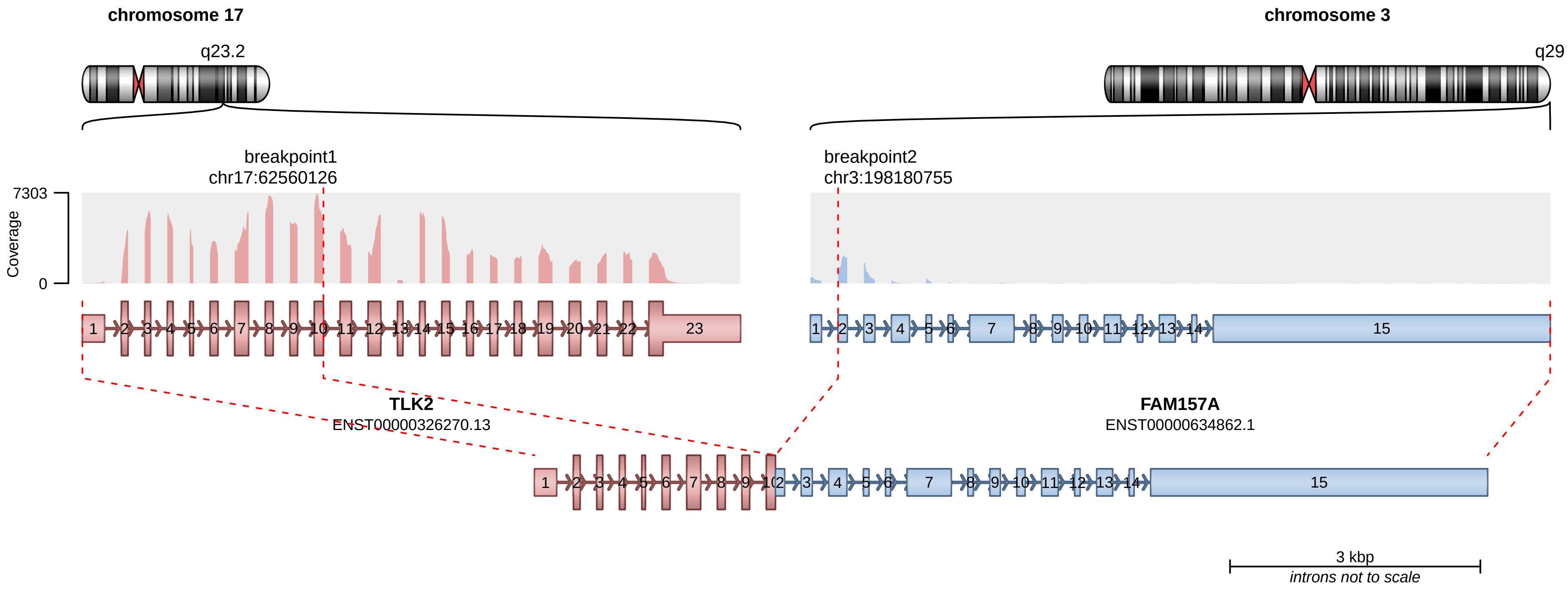


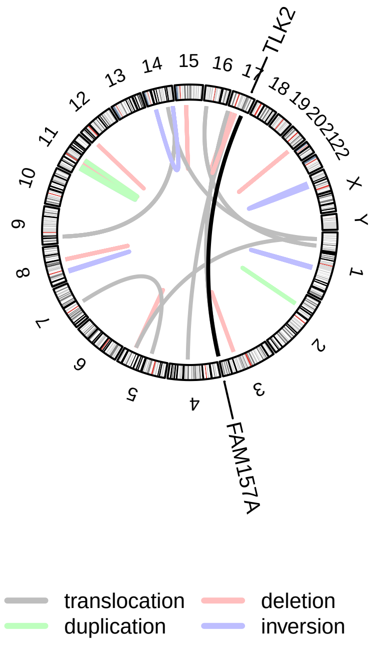




**SUPPORTING READ COUNT**

Split reads = 1
Discordant mates = 0

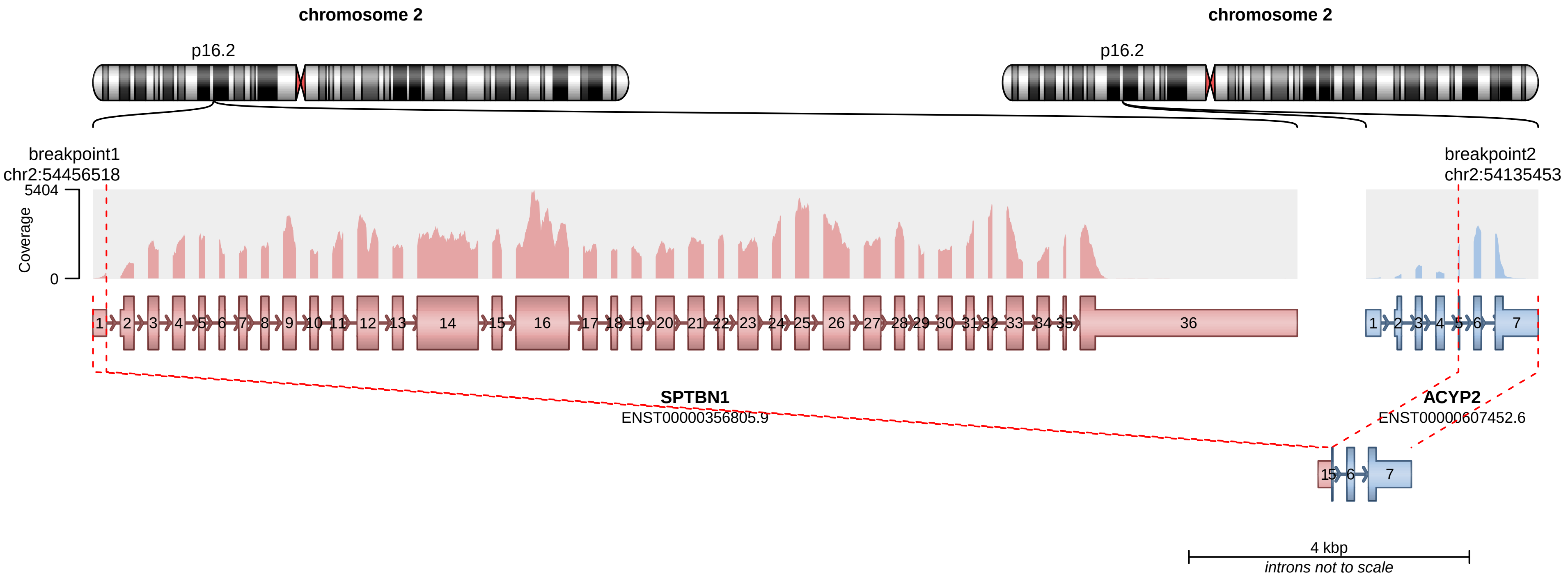


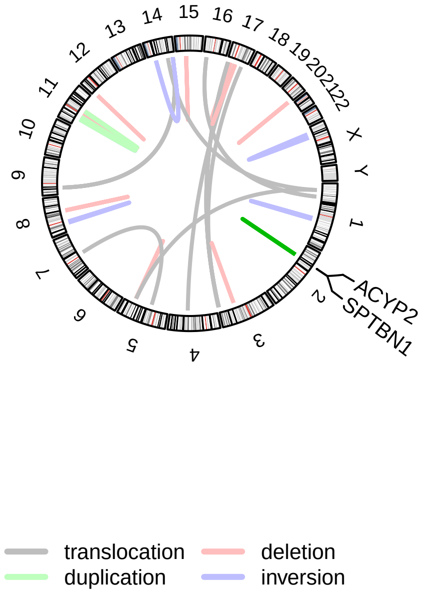


No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 124
Discordant mates = 0

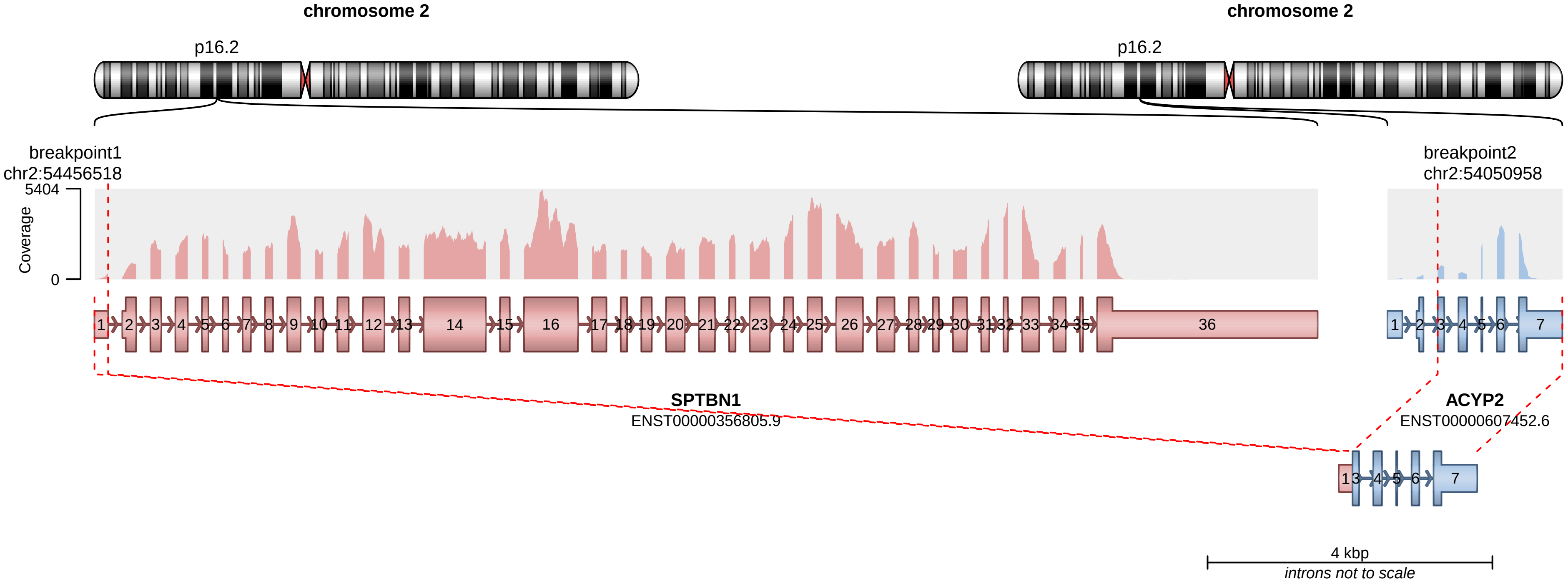


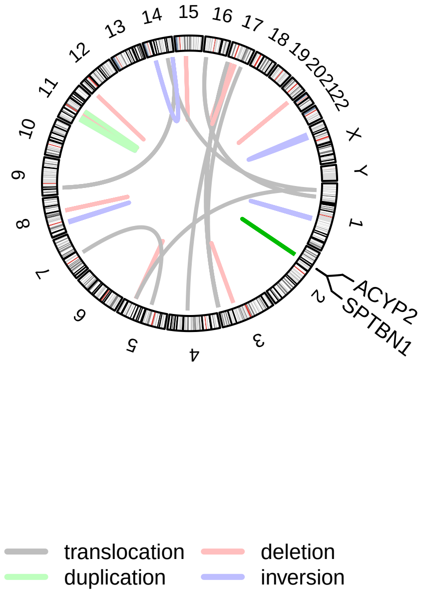


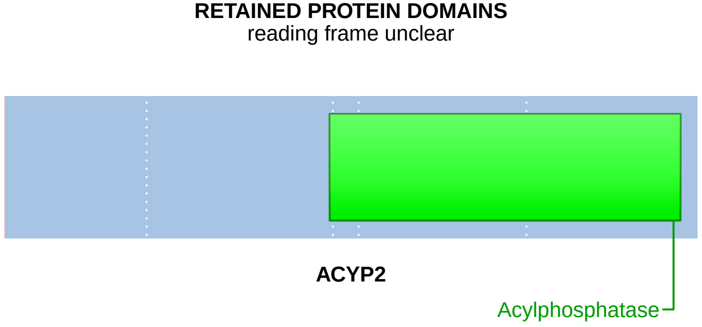
**RETAINED PROTEIN DOMAINS**
reading frame unclear

**SUPPORTING READ COUNT**

Split reads = 114
Discordant mates = 4

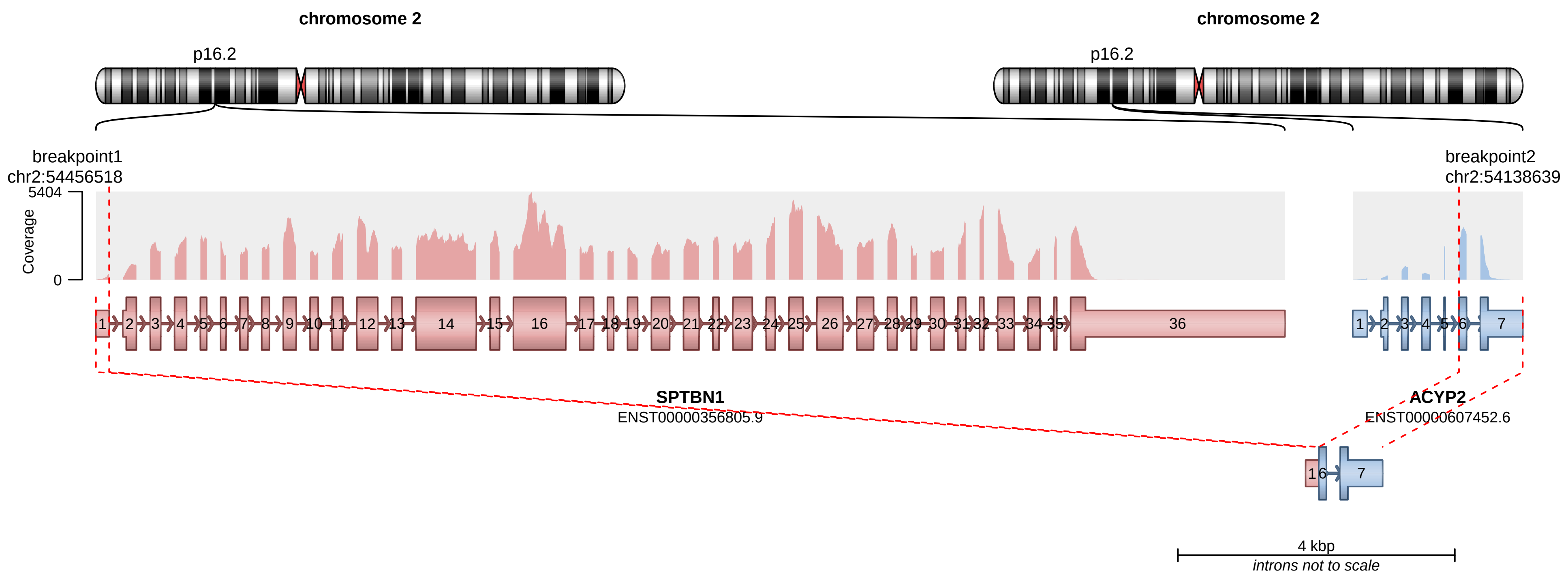


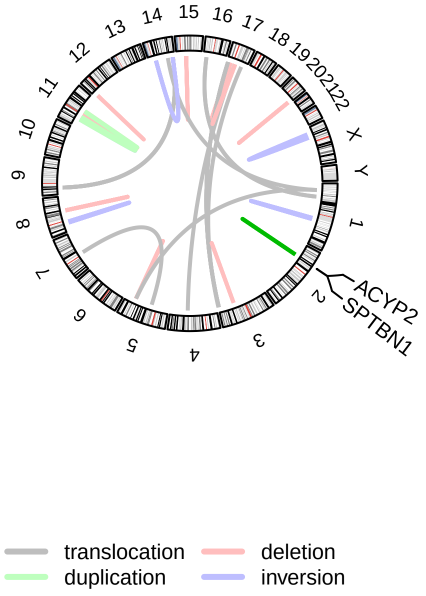




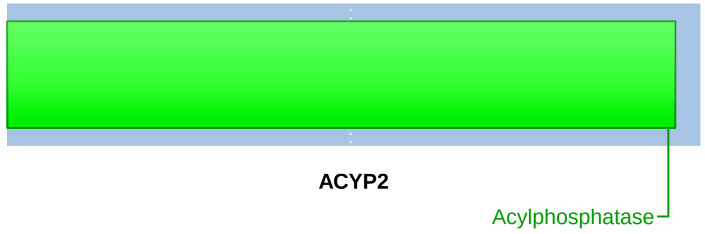
**SUPPORTING READ COUNT**

Split reads = 69
Discordant mates = 5



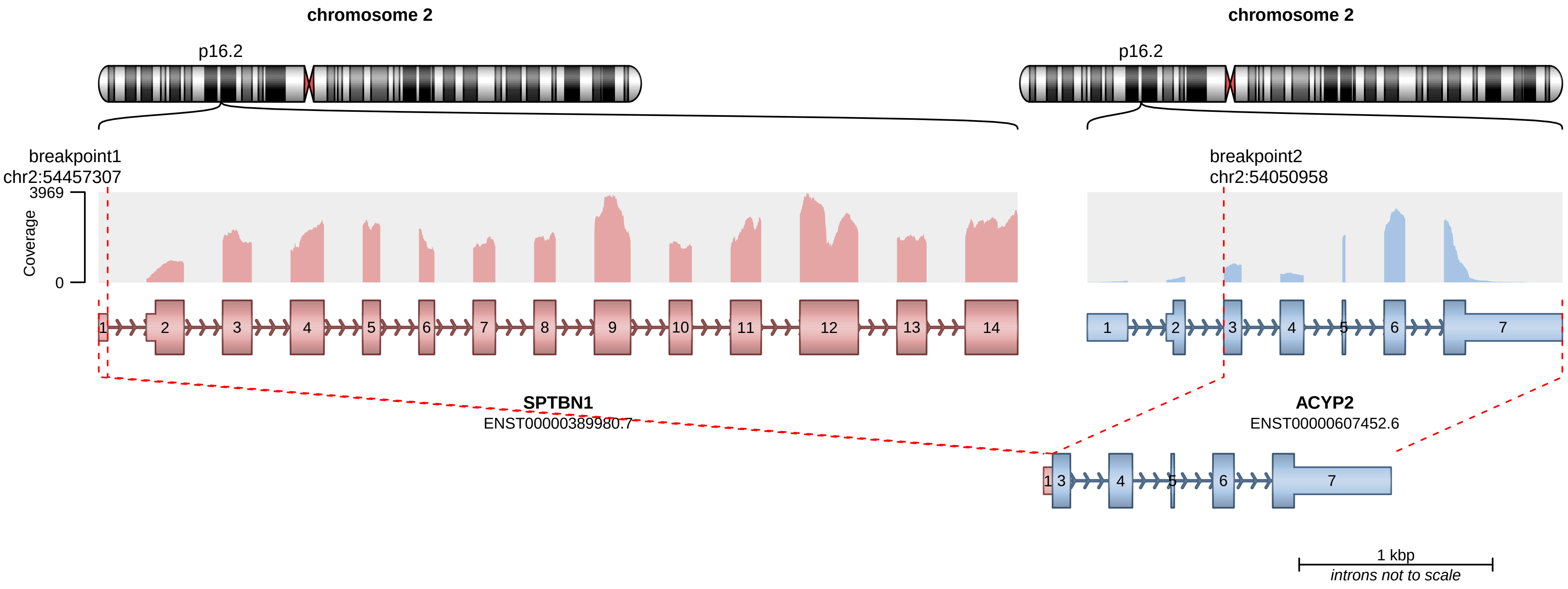


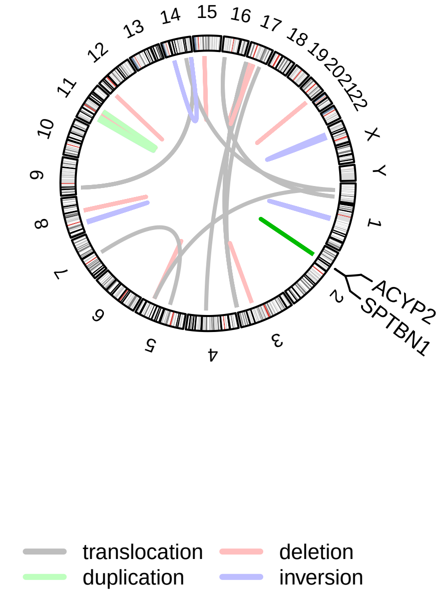
**RETAINED PROTEIN DOMAINS**
reading frame unclear



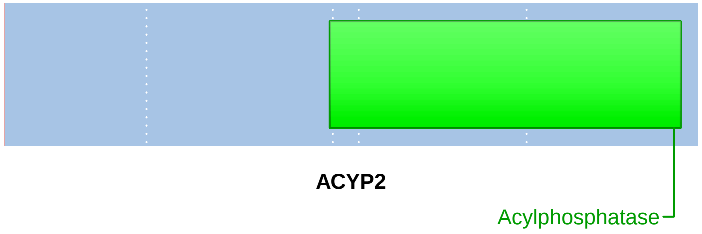
**SUPPORTING READ COUNT**

Split reads = 6
Discordant mates = 3



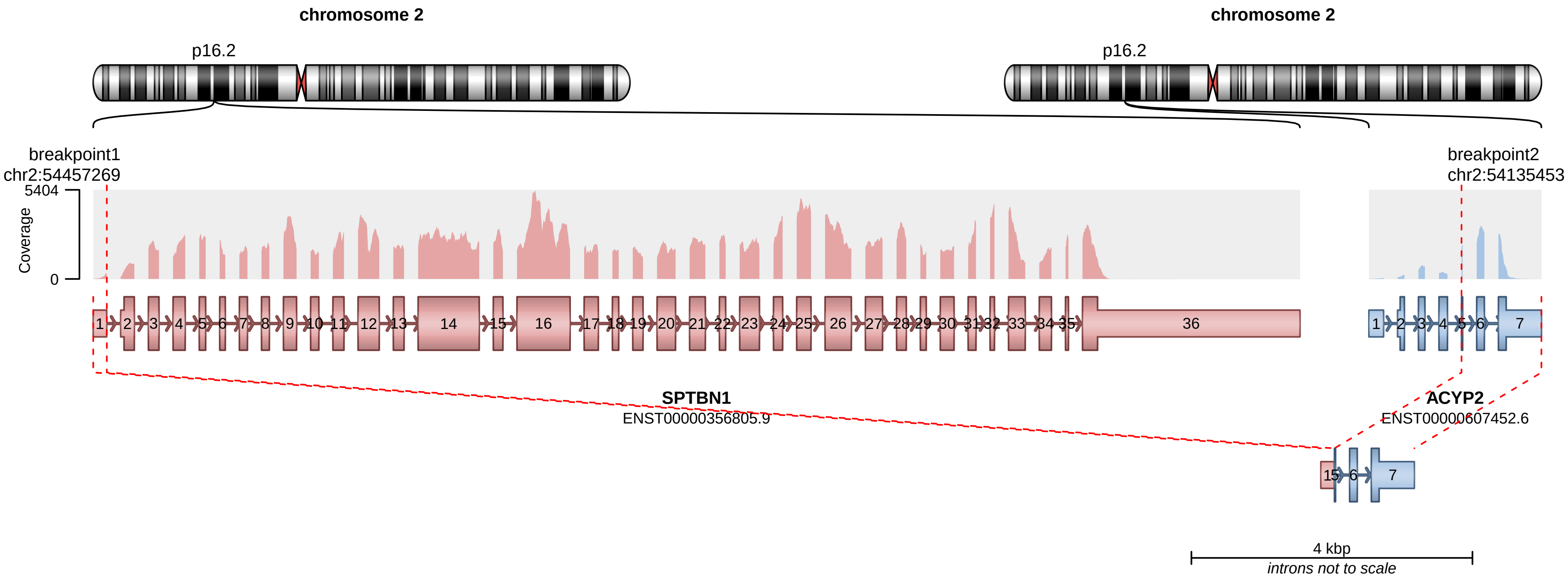


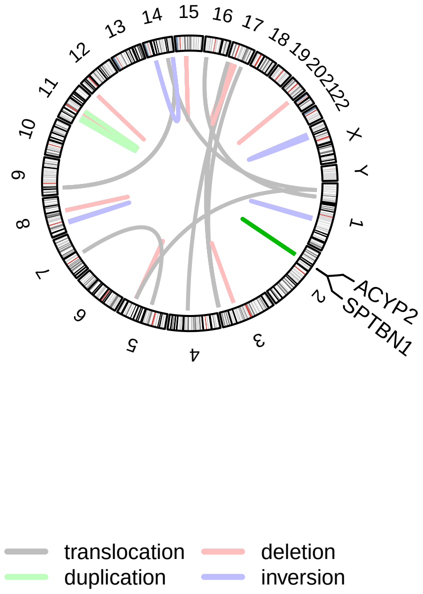
**RETAINED PROTEIN DOMAINS**
reading frame unclear

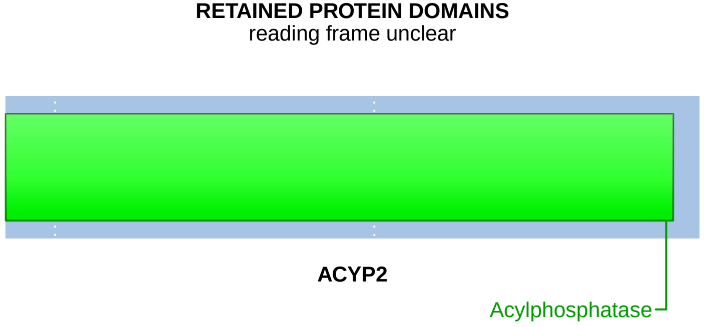


**SUPPORTING READ COUNT**

Split reads = 3
Discordant mates = 5

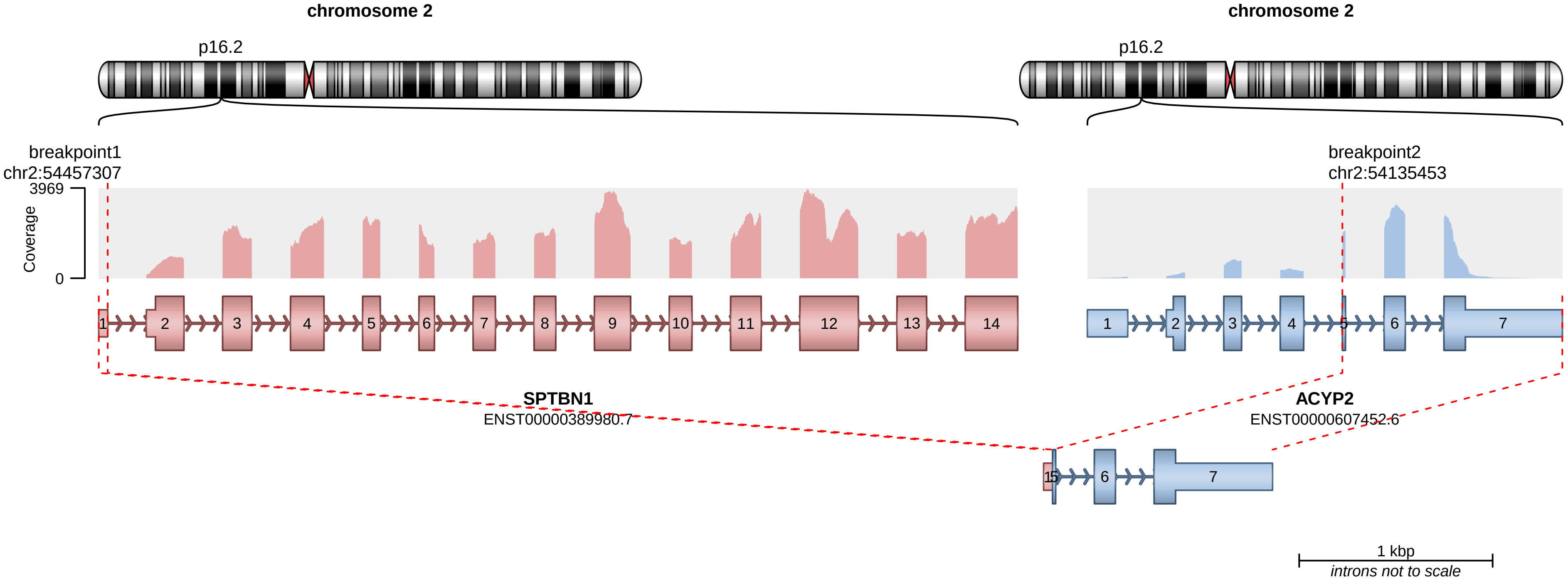


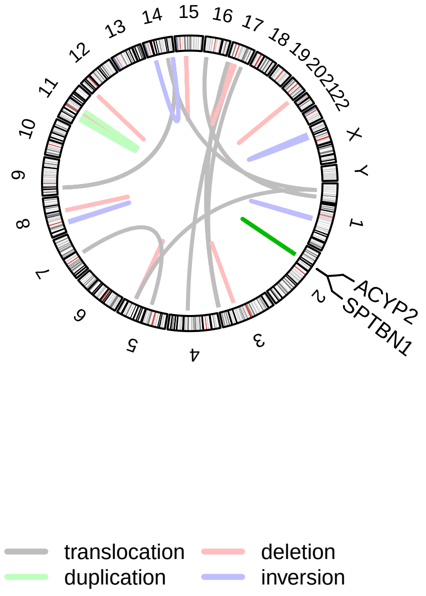




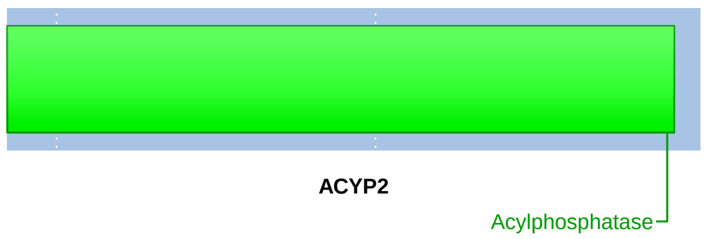
**SUPPORTING READ COUNT**

Split reads = 3
Discordant mates = 4



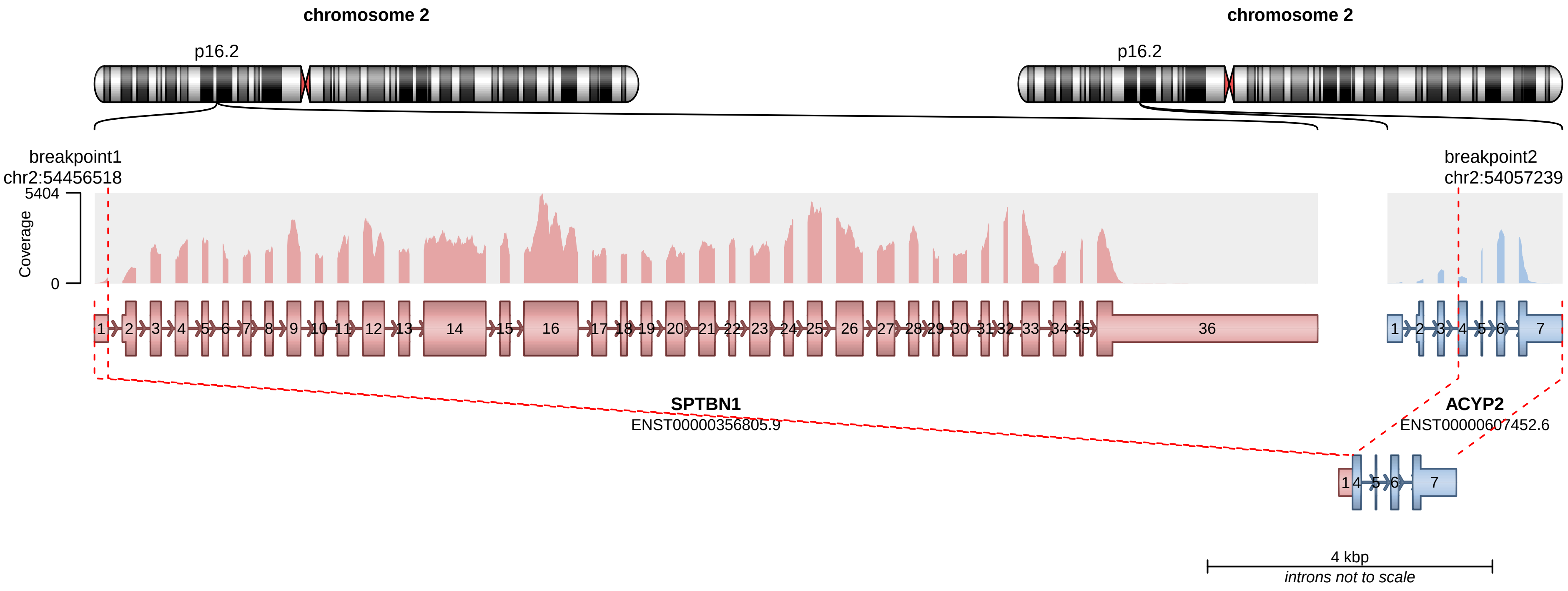


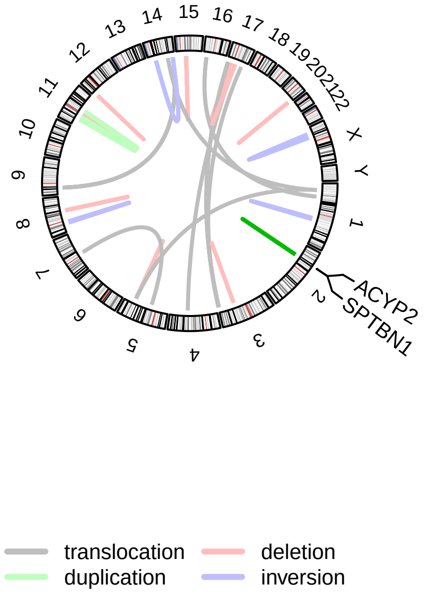
**RETAINED PROTEIN DOMAINS**
reading frame unclear

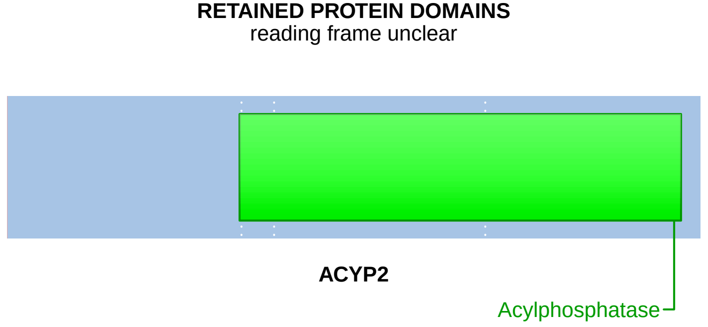


**SUPPORTING READ COUNT**

Split reads = 1
Discordant mates = 4

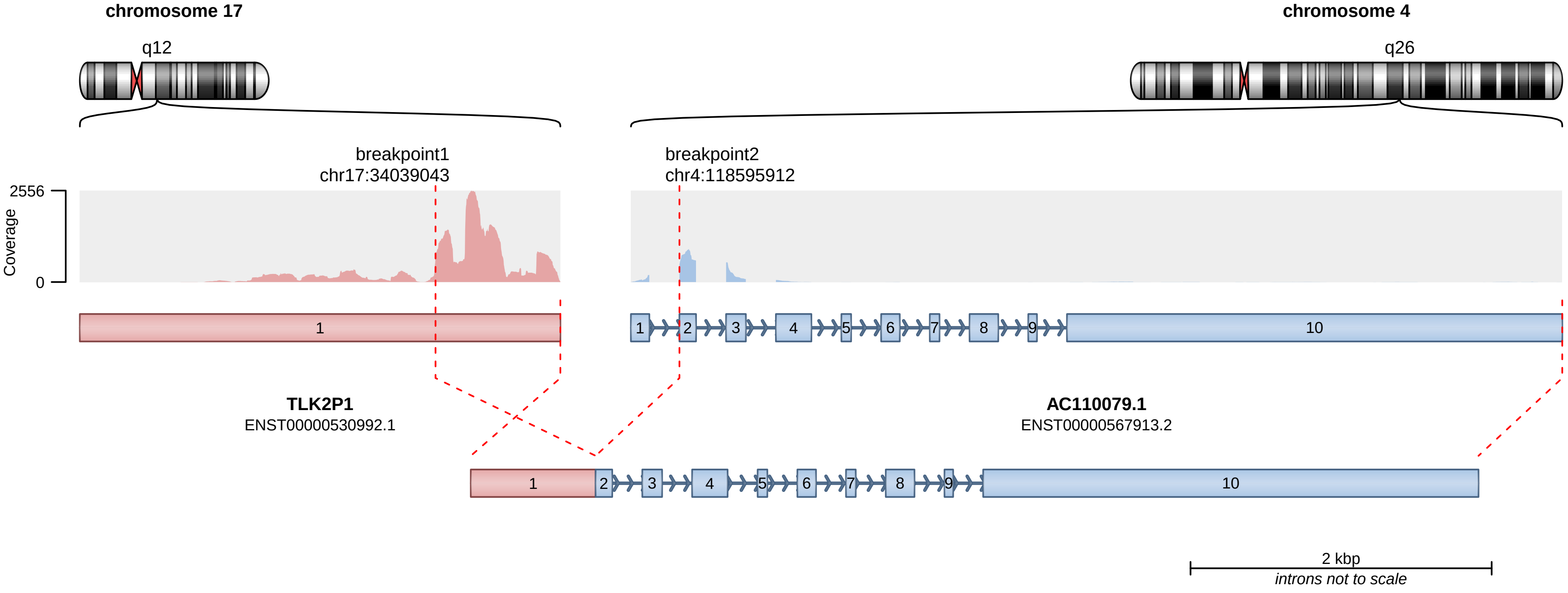


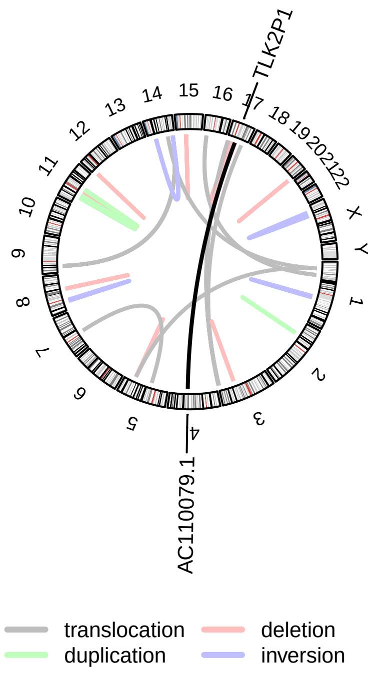




**SUPPORTING READ COUNT**

Split reads = 1
Discordant mates = 4

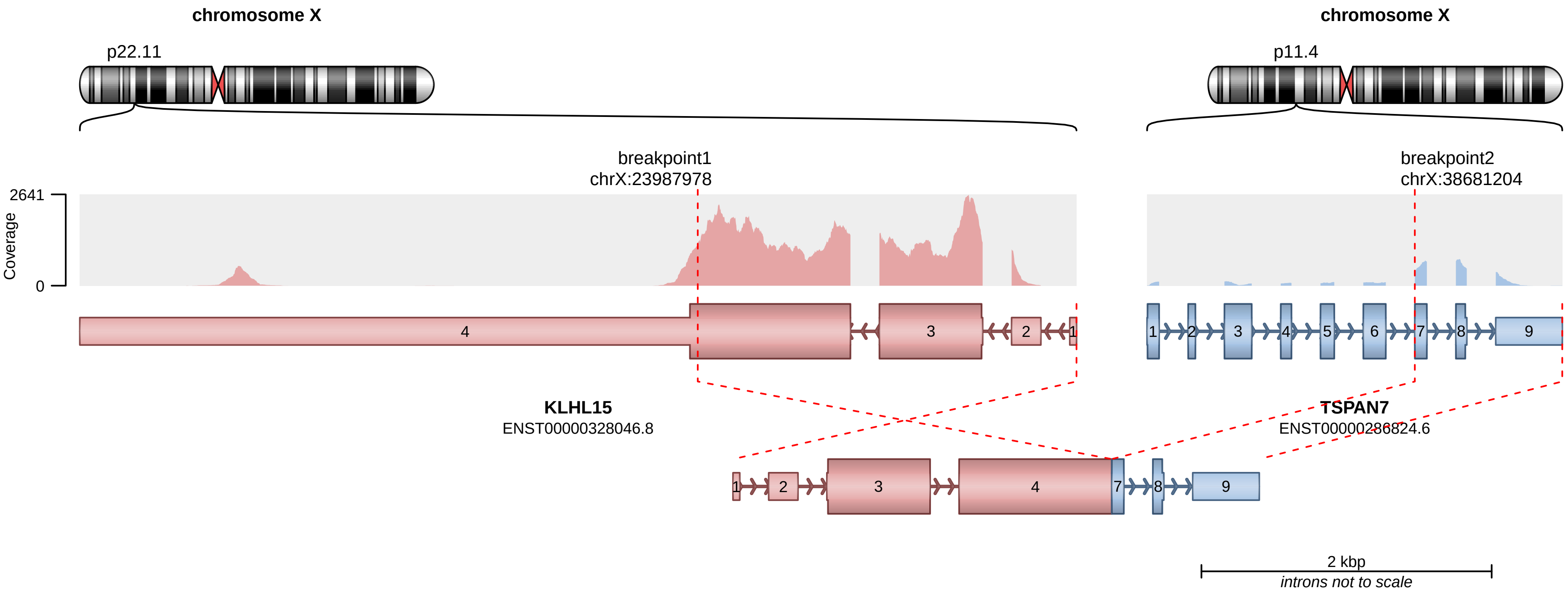


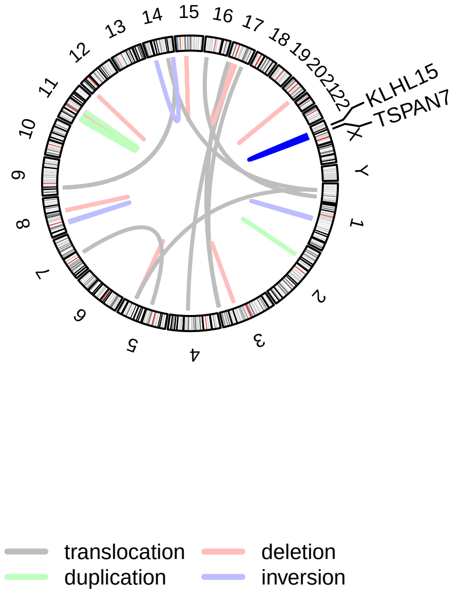


Genes are not protein−coding.

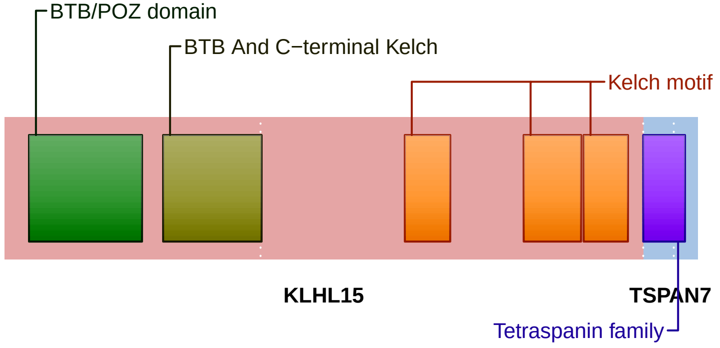
**SUPPORTING READ COUNT**

Split reads = 79
Discordant mates = 0



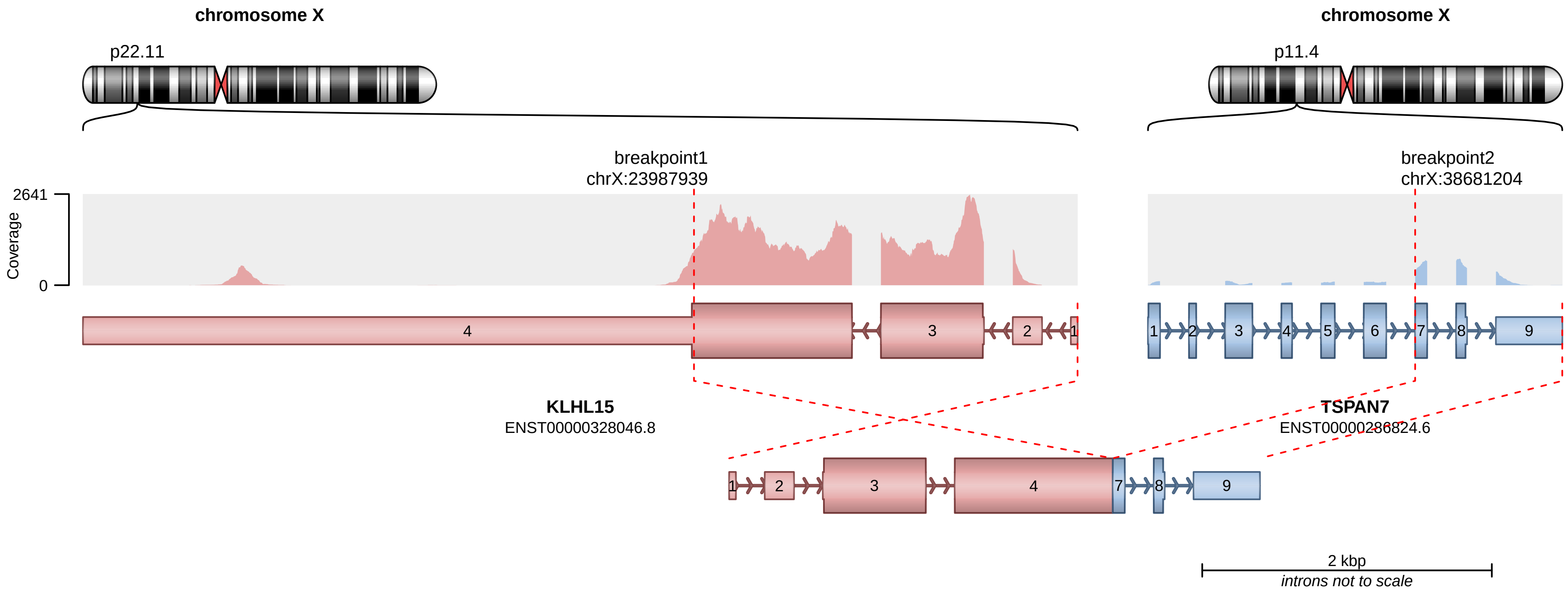


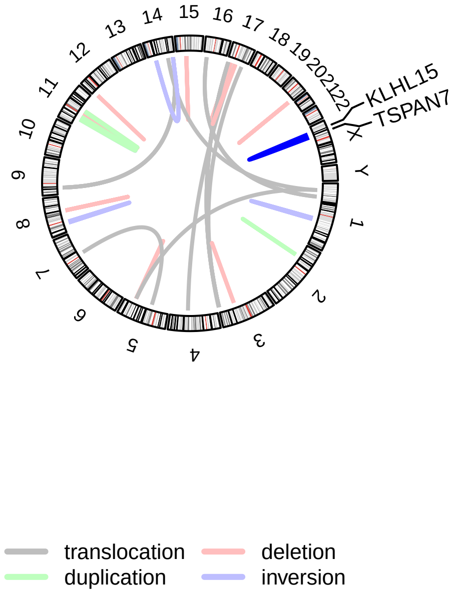
**RETAINED PROTEIN DOMAINS**
reading frame unclear

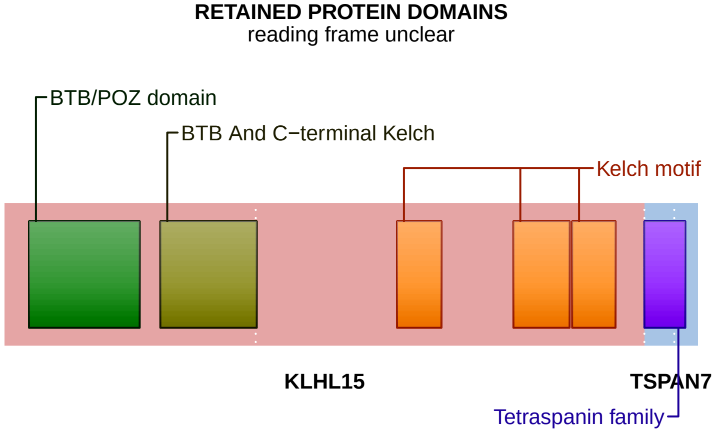


**SUPPORTING READ COUNT**

Split reads = 66
Discordant mates = 0

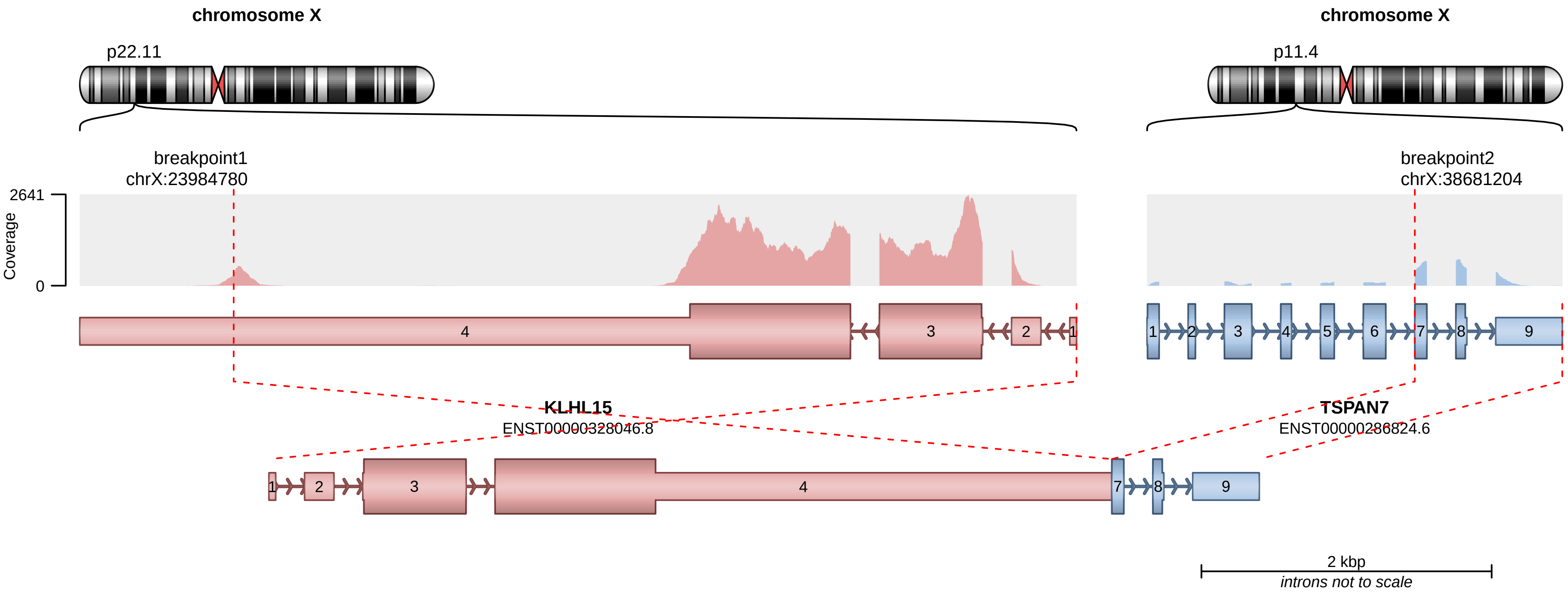


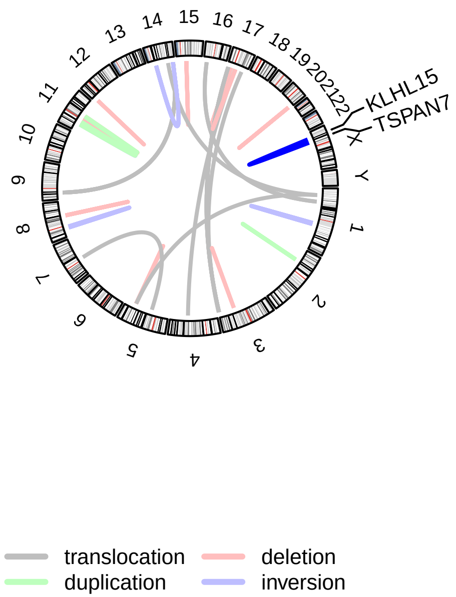


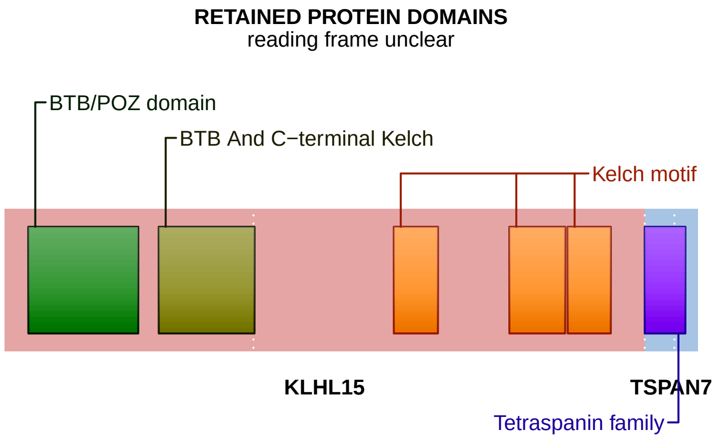


**SUPPORTING READ COUNT**

Split reads = 22
Discordant mates = 2

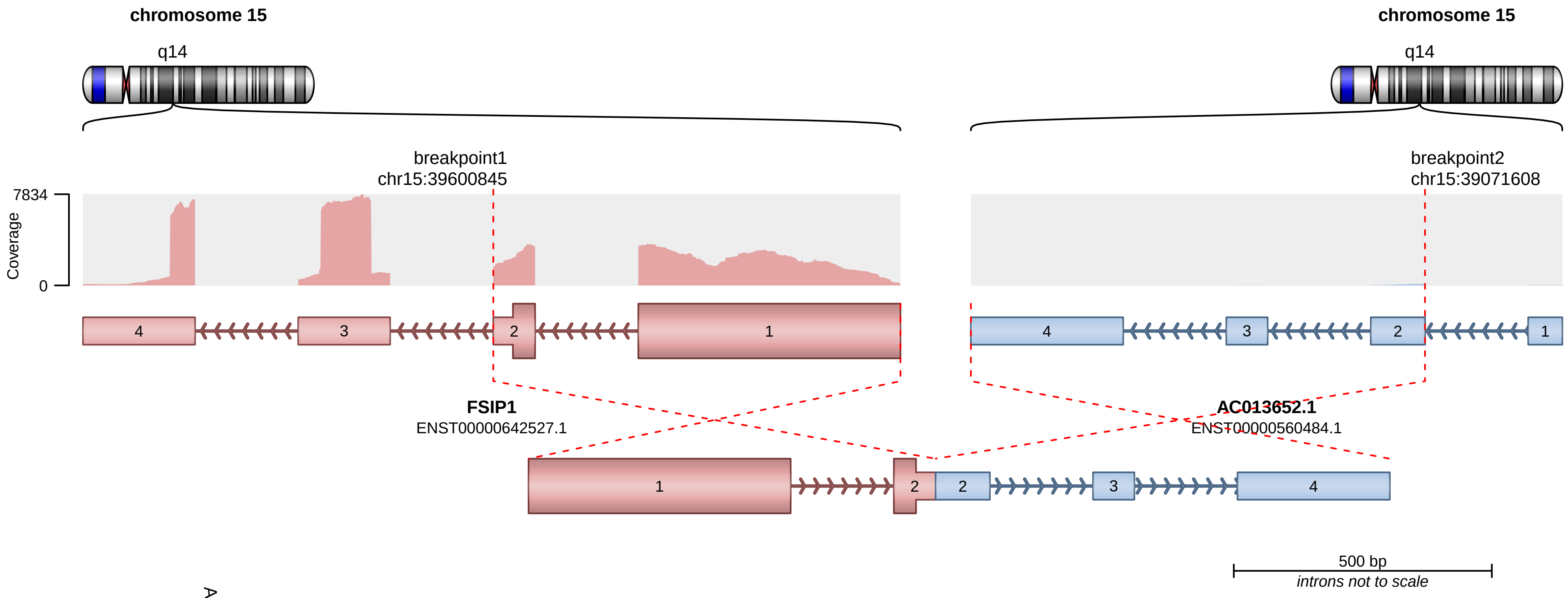


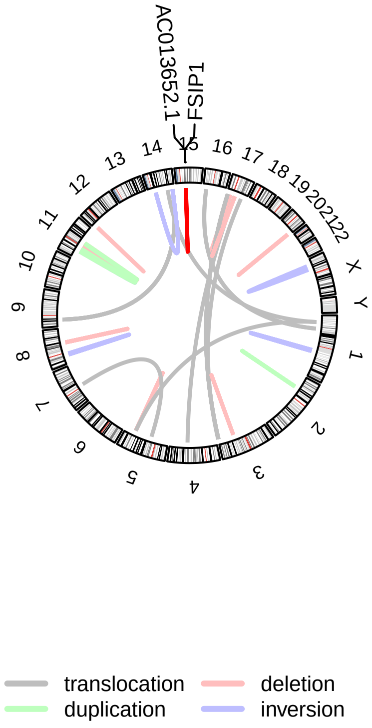




**SUPPORTING READ COUNT**

Split reads = 19
Discordant mates = 3

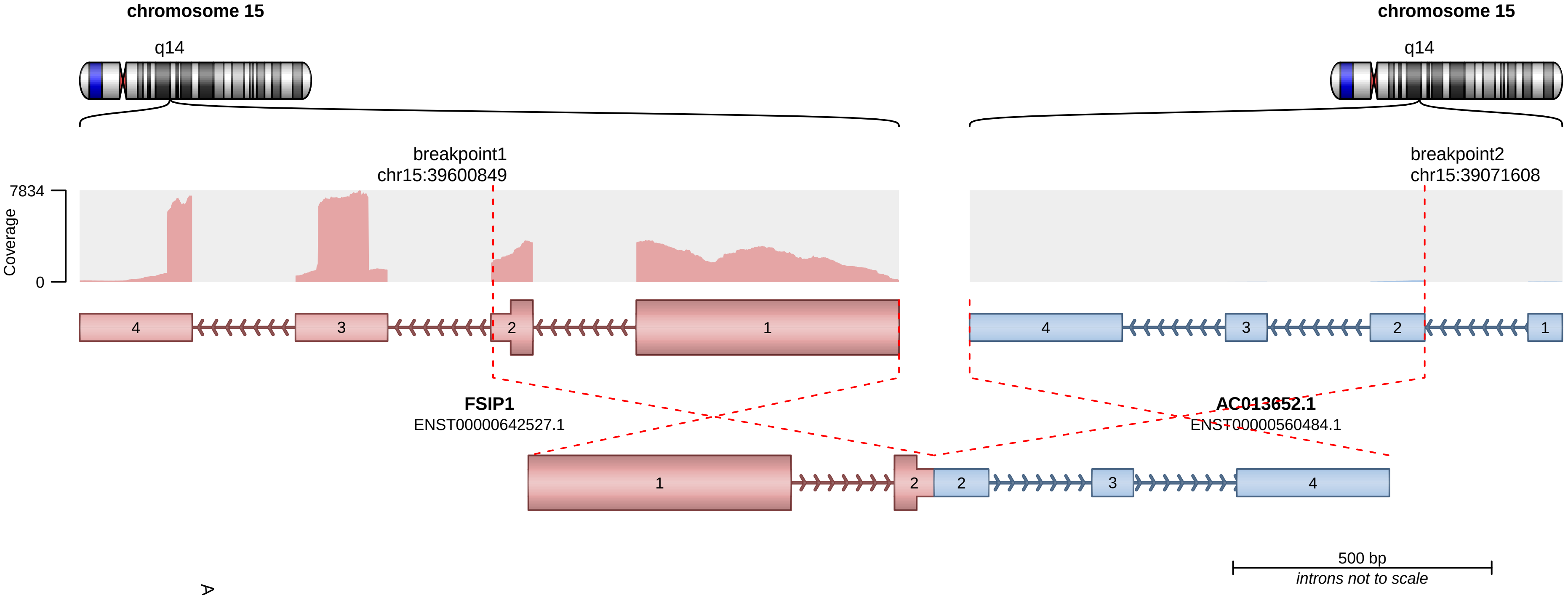


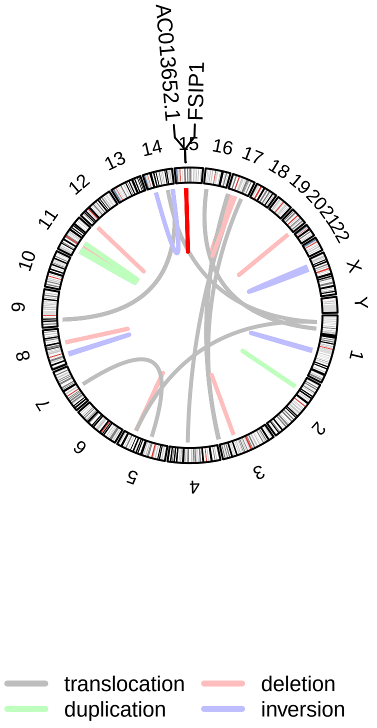


No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 56
Discordant mates = 3

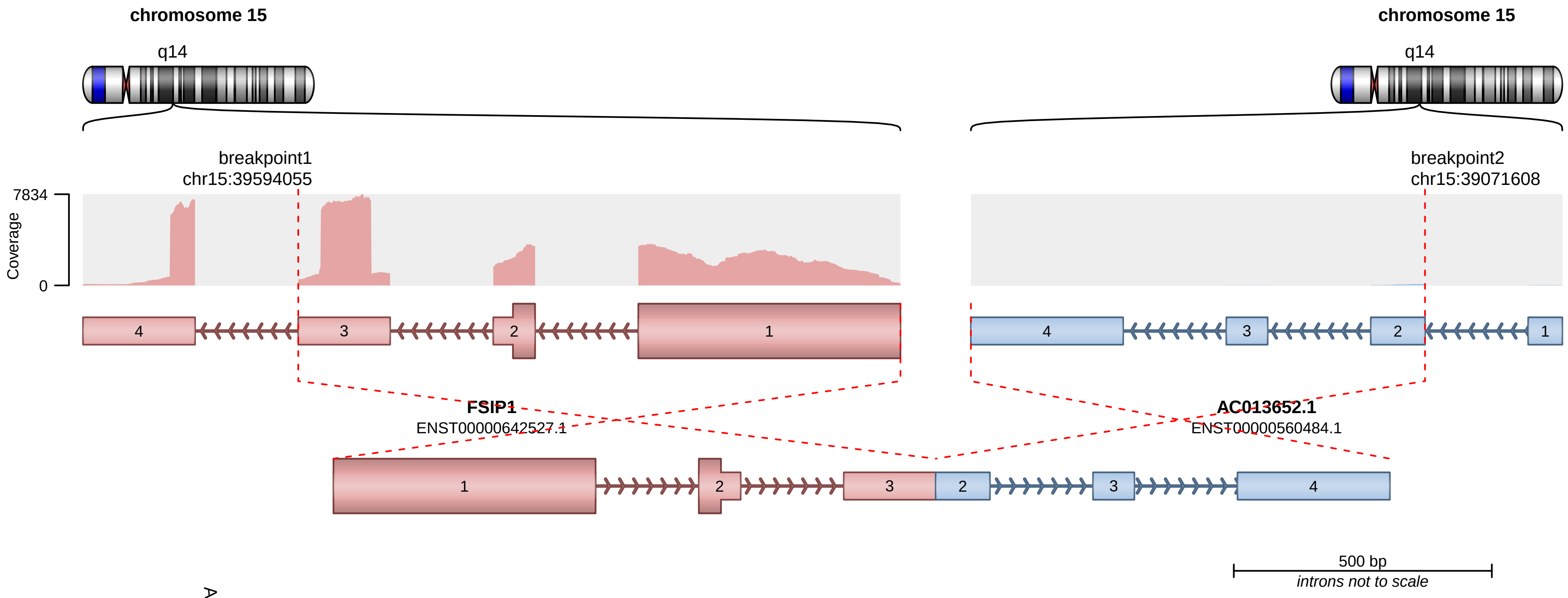


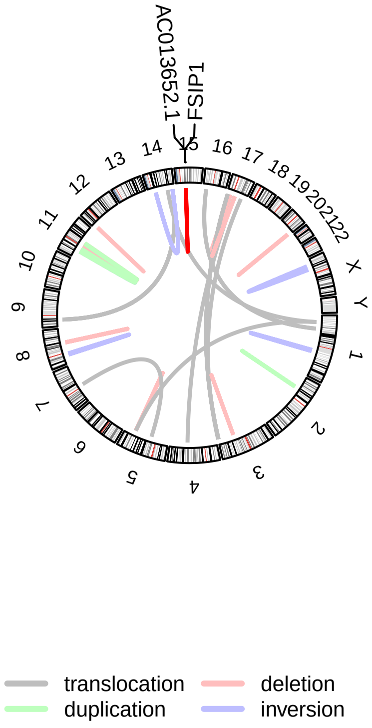


No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 15
Discordant mates = 3

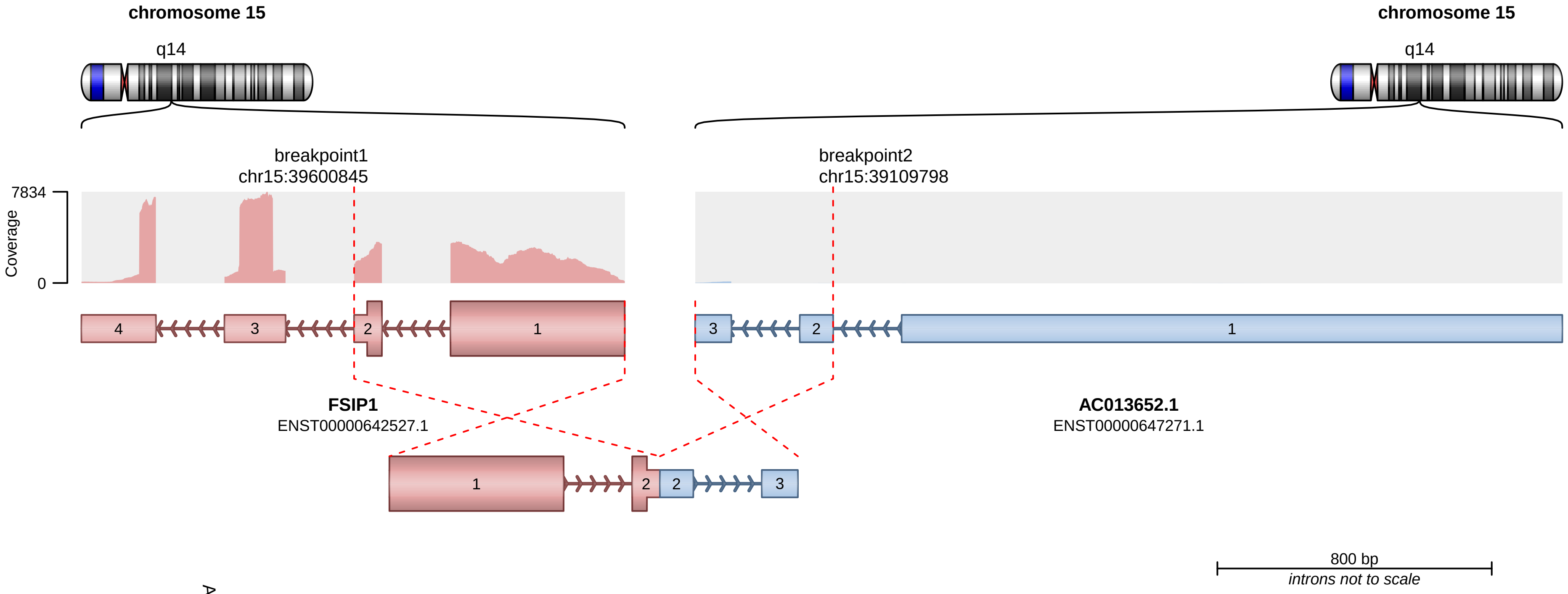


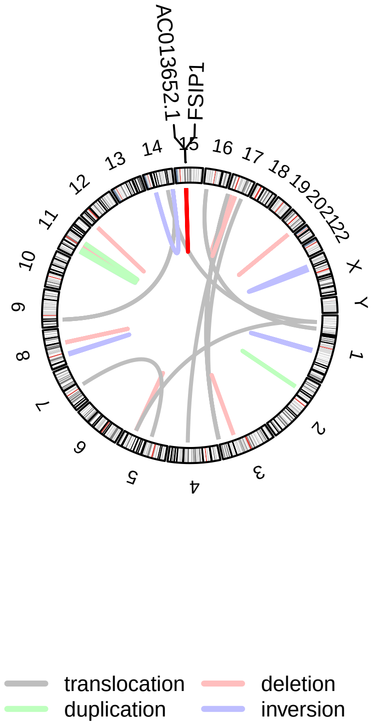


No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 2
Discordant mates = 3

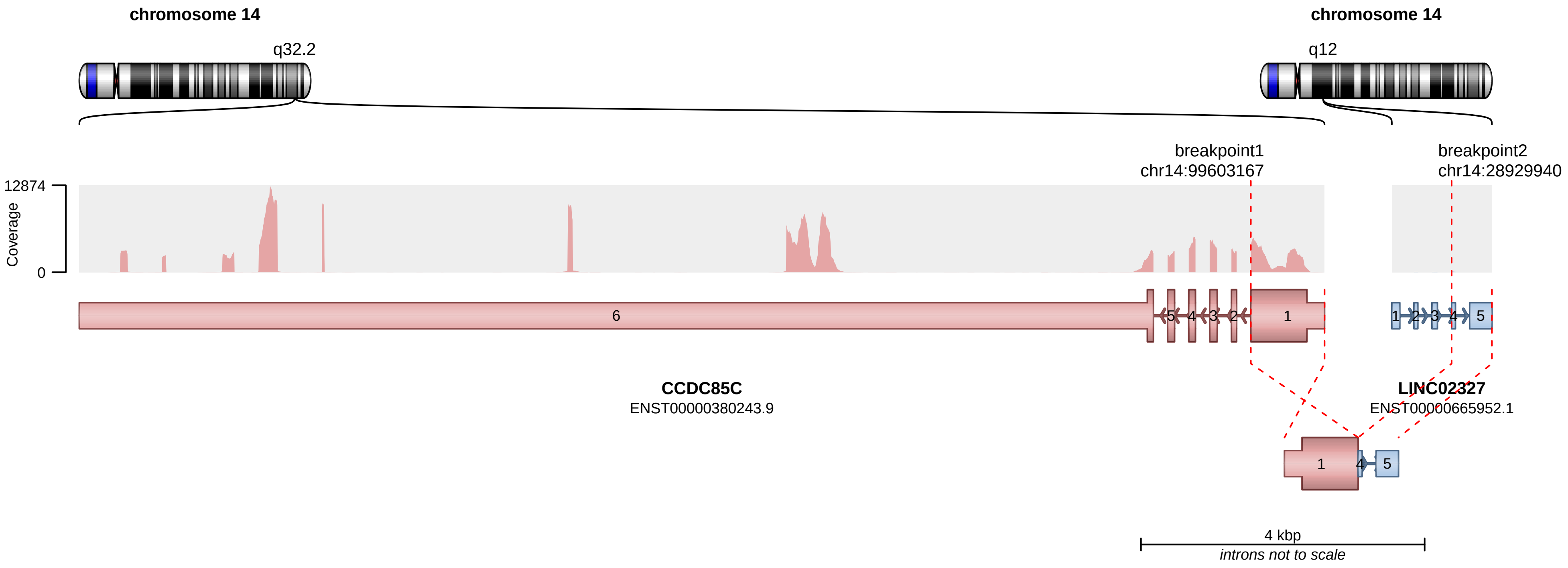


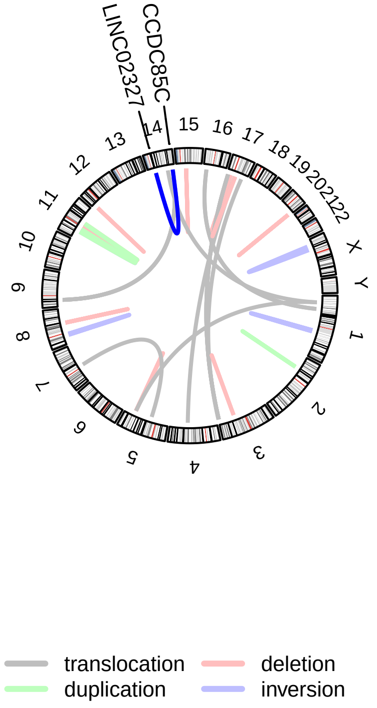


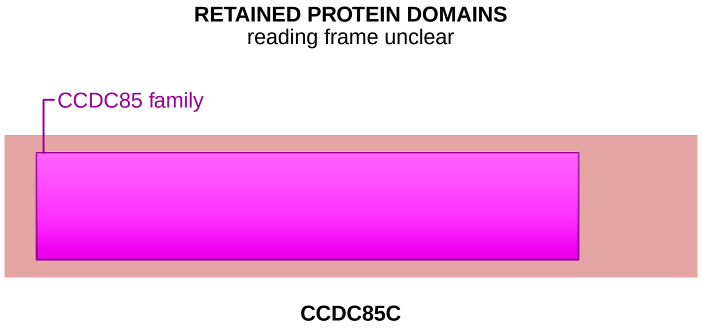
No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 1
Discordant mates = 3

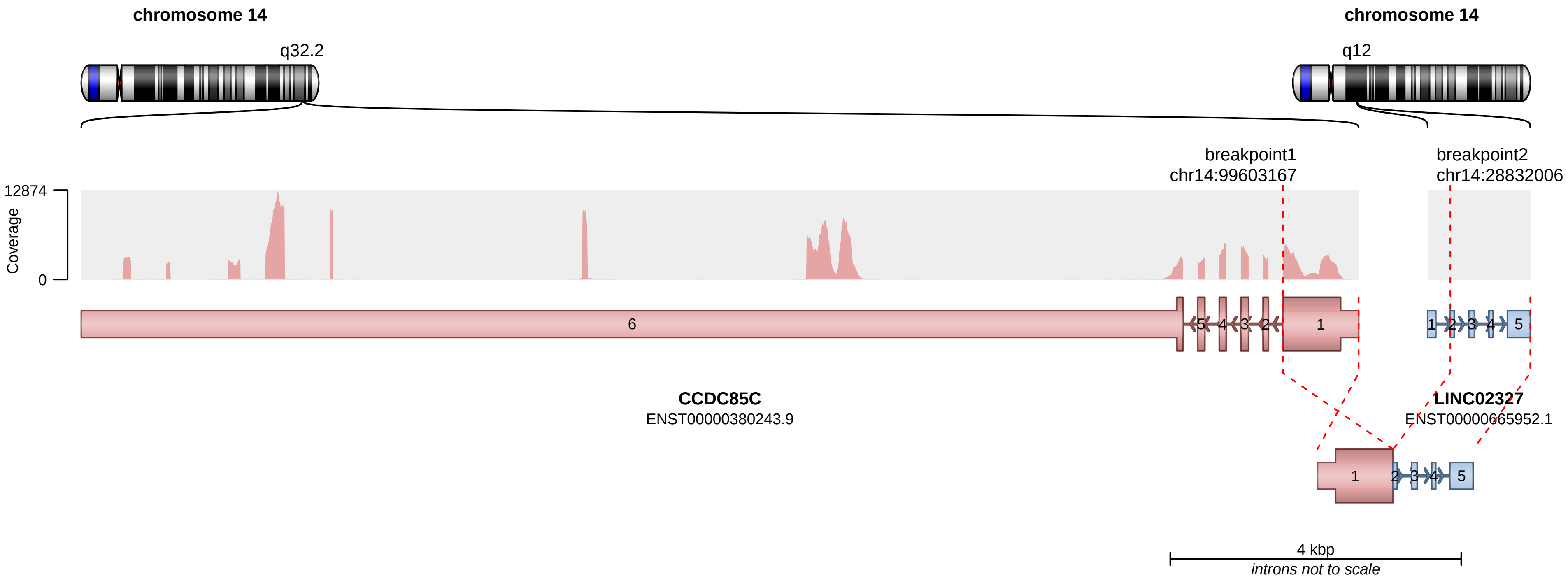


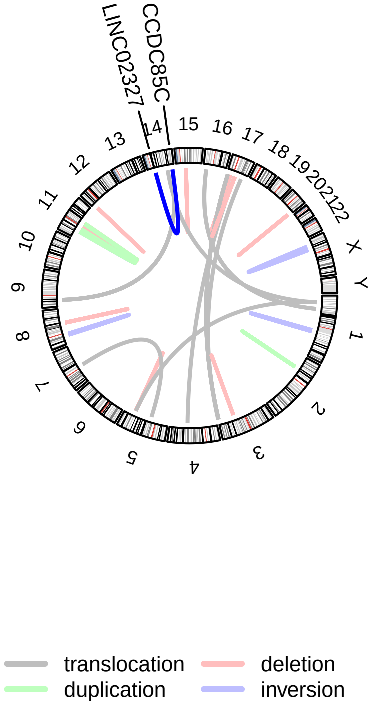




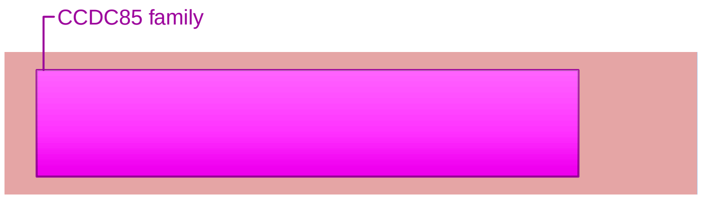
**SUPPORTING READ COUNT**

Split reads = 52
Discordant mates = 0





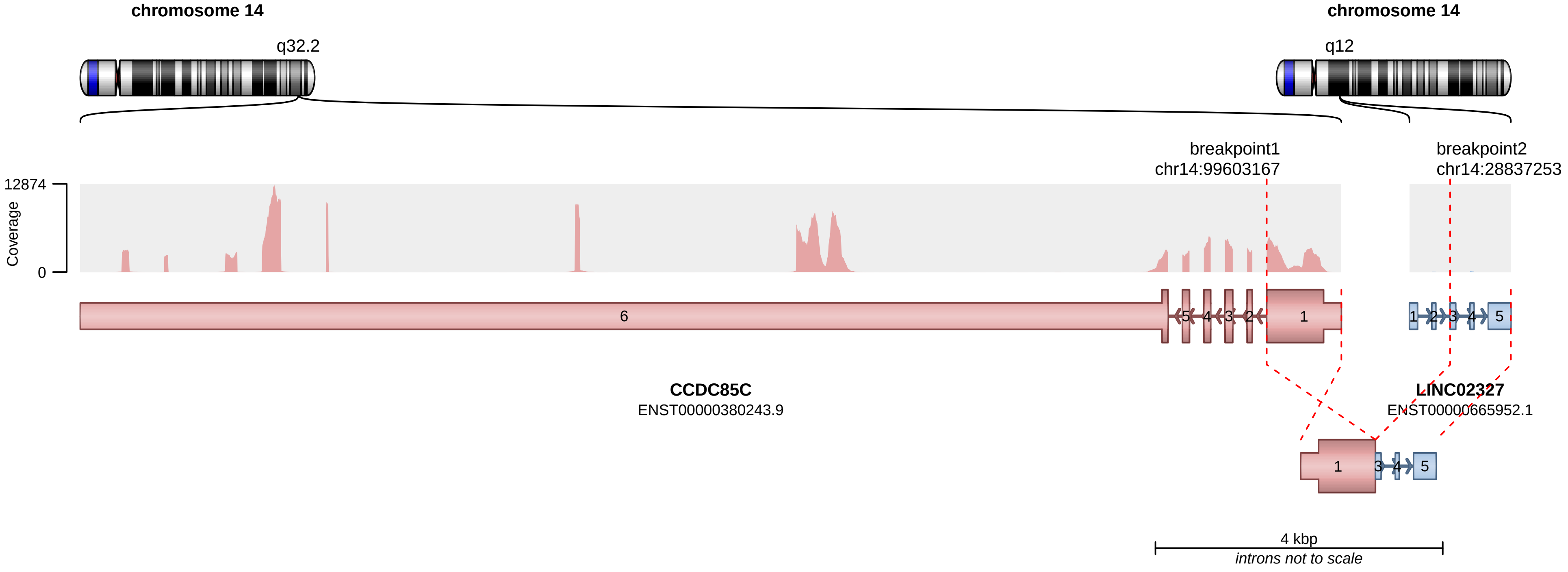
**RETAINED PROTEIN DOMAINS**
reading frame unclear

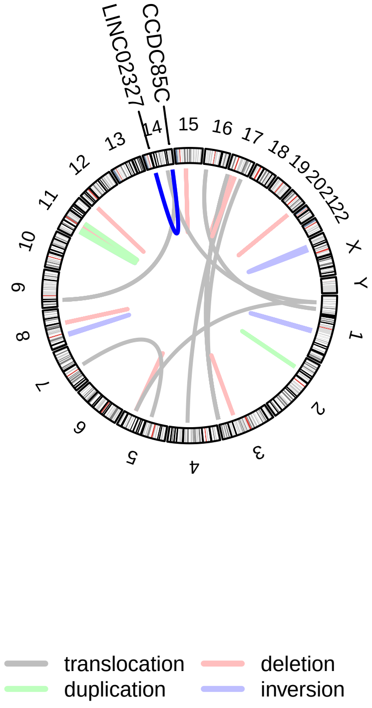


**CCDC85C**

**SUPPORTING READ COUNT**

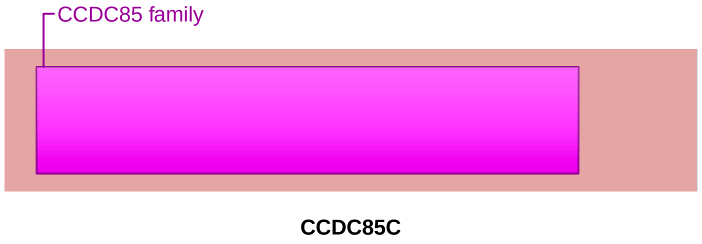
Split reads = 36
Discordant mates = 0





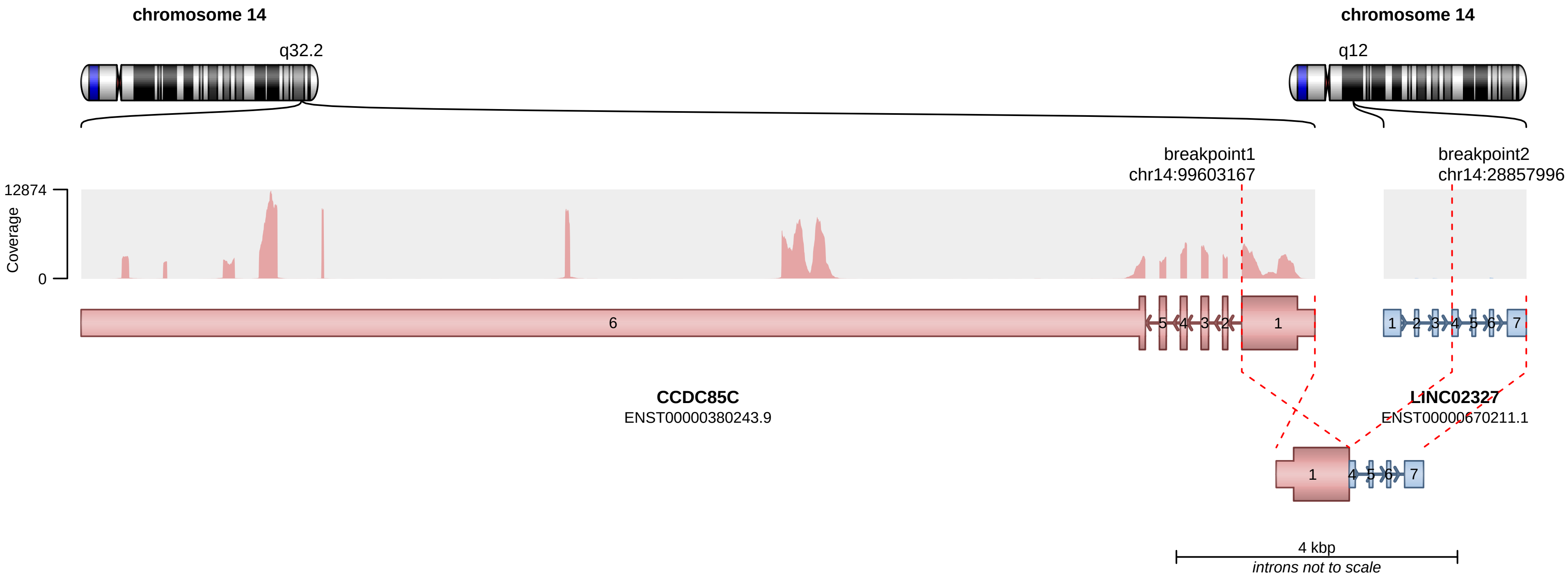
## RETAINED PROTEIN DOMAINS

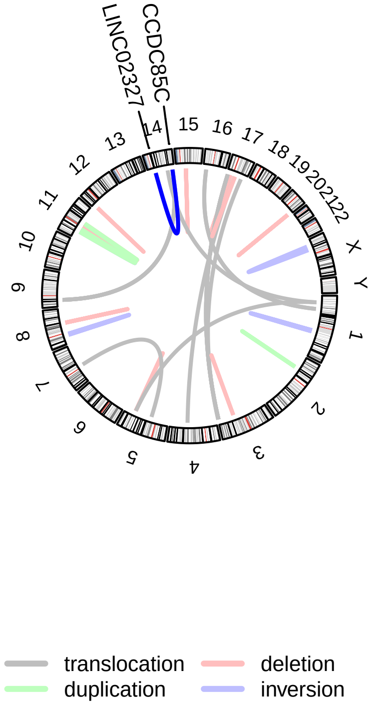
reading frame unclear



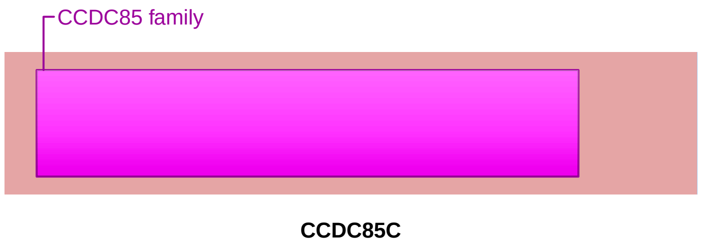
**SUPPORTING READ COUNT**

Split reads = 22
Discordant mates = 0



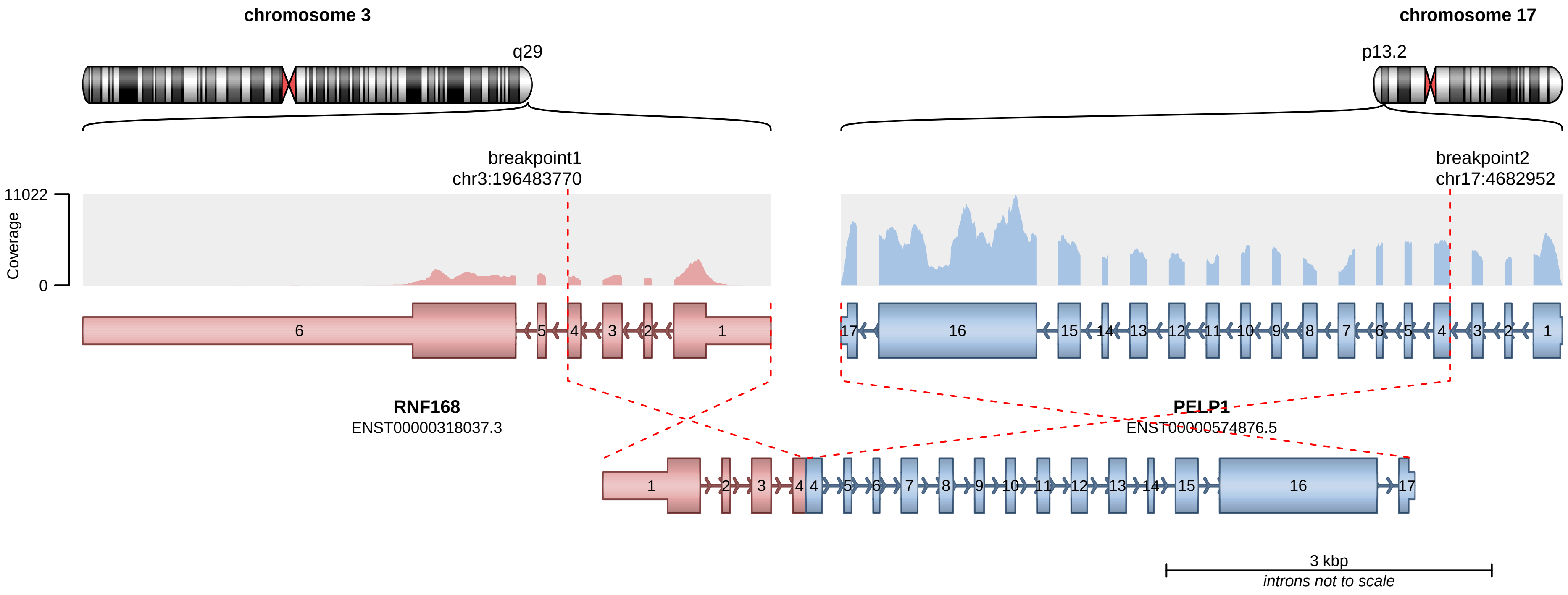


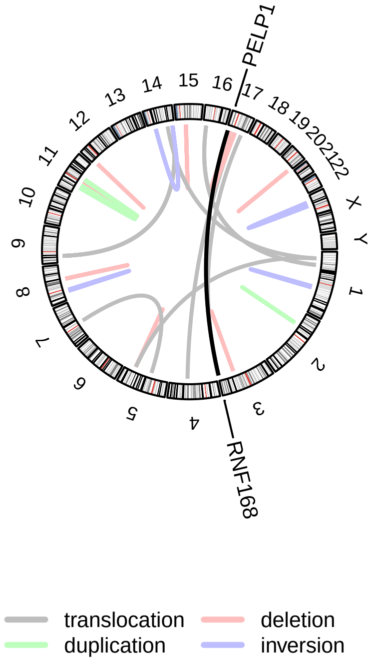
**RETAINED PROTEIN DOMAINS**
reading frame unclear

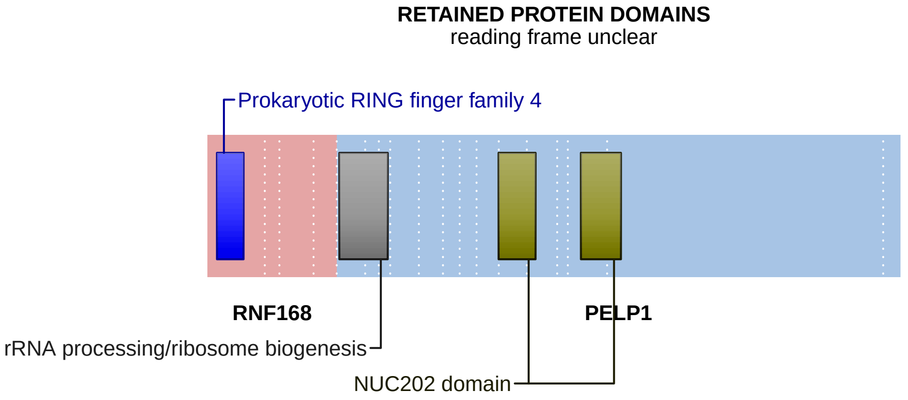


**SUPPORTING READ COUNT**

Split reads = 2
Discordant mates = 0

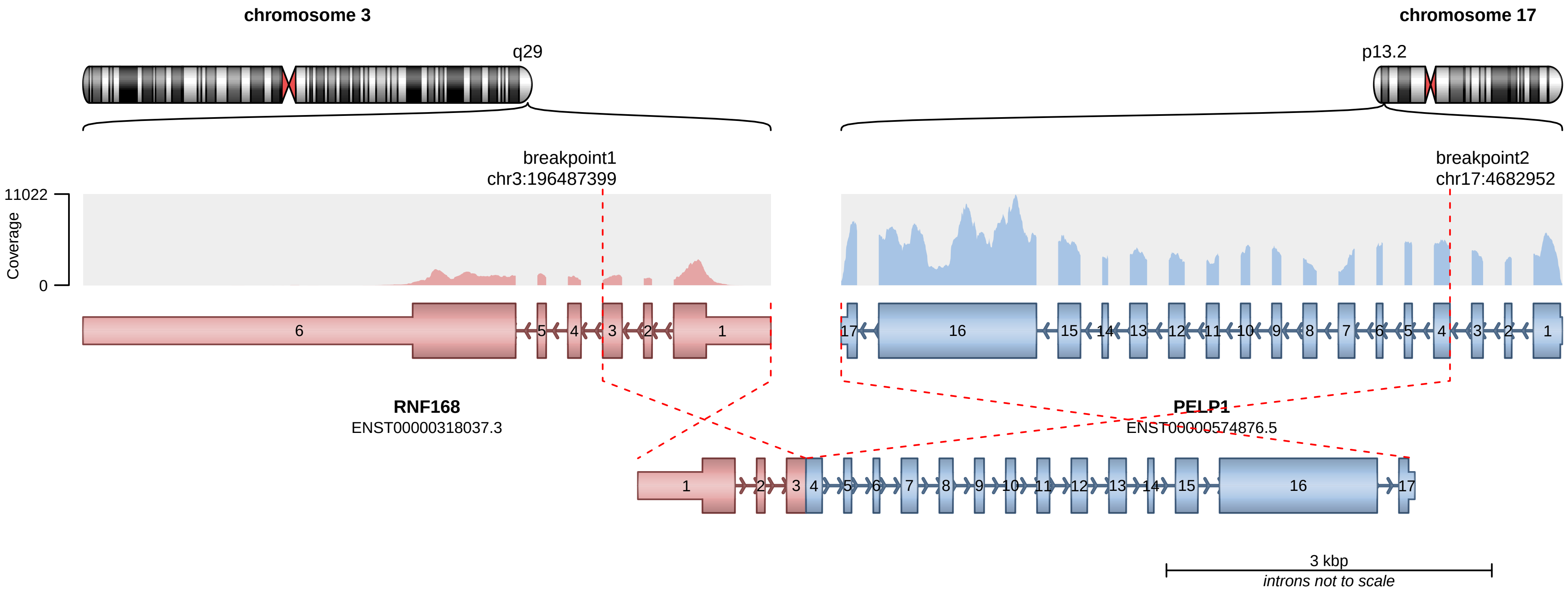


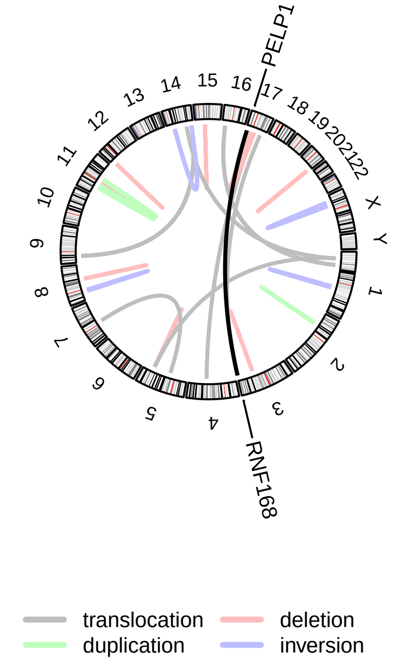


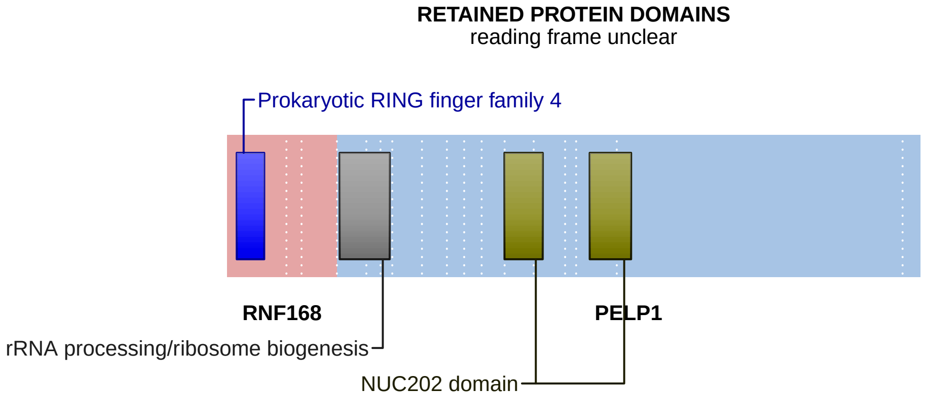


**SUPPORTING READ COUNT**

Split reads = 49
Discordant mates = 0

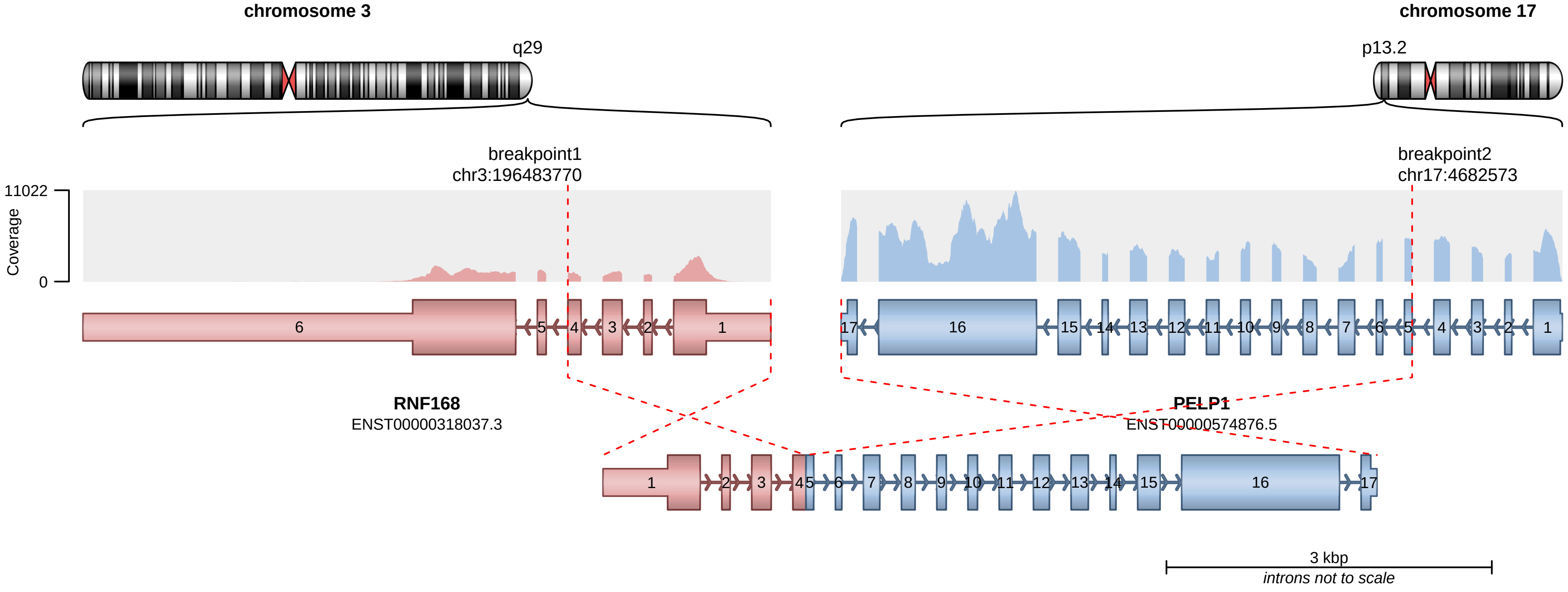


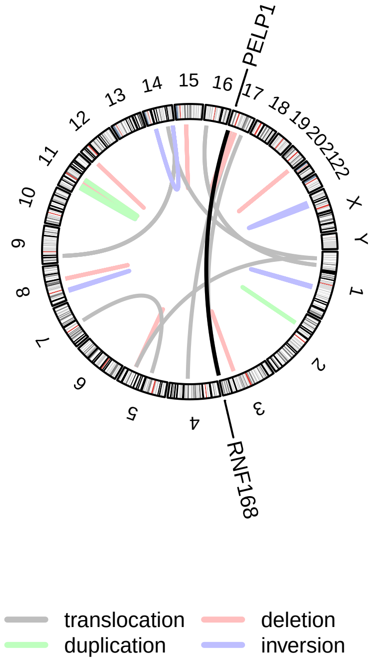




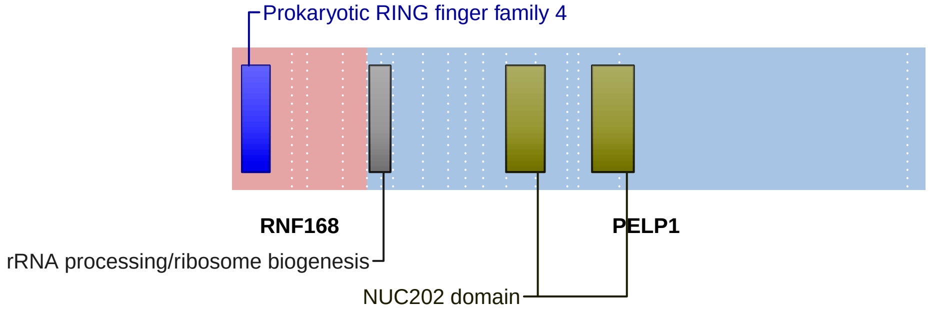
**SUPPORTING READ COUNT**

Split reads = 4
Discordant mates = 0



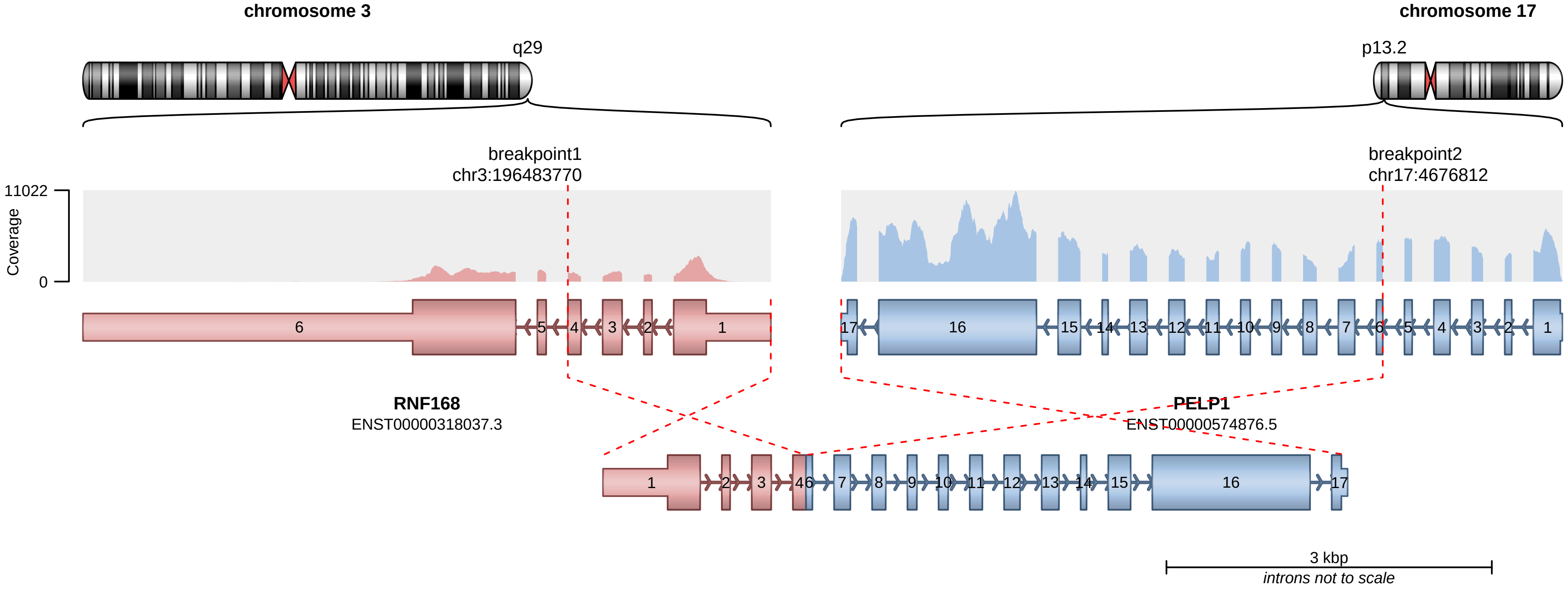


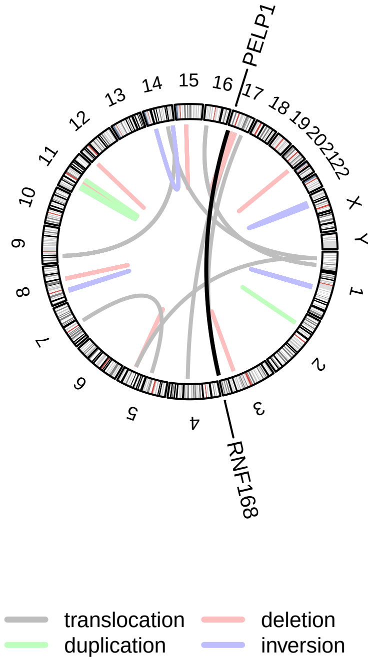
**RETAINED PROTEIN DOMAINS**
reading frame unclear

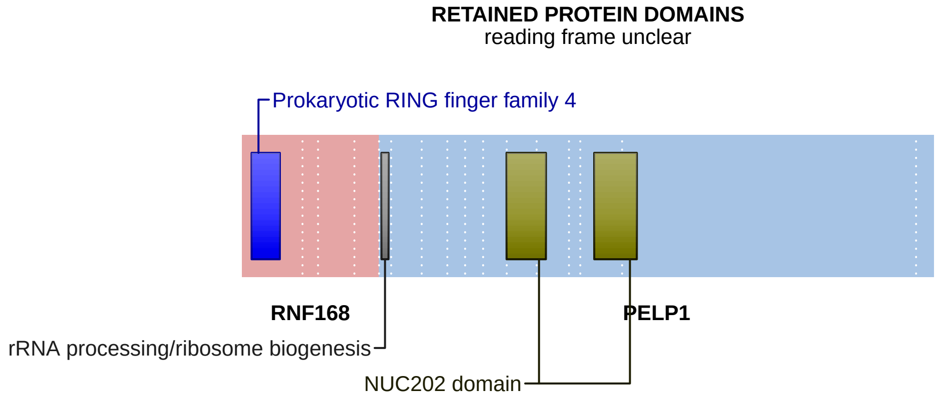


**SUPPORTING READ COUNT**

Split reads = 1
Discordant mates = 0

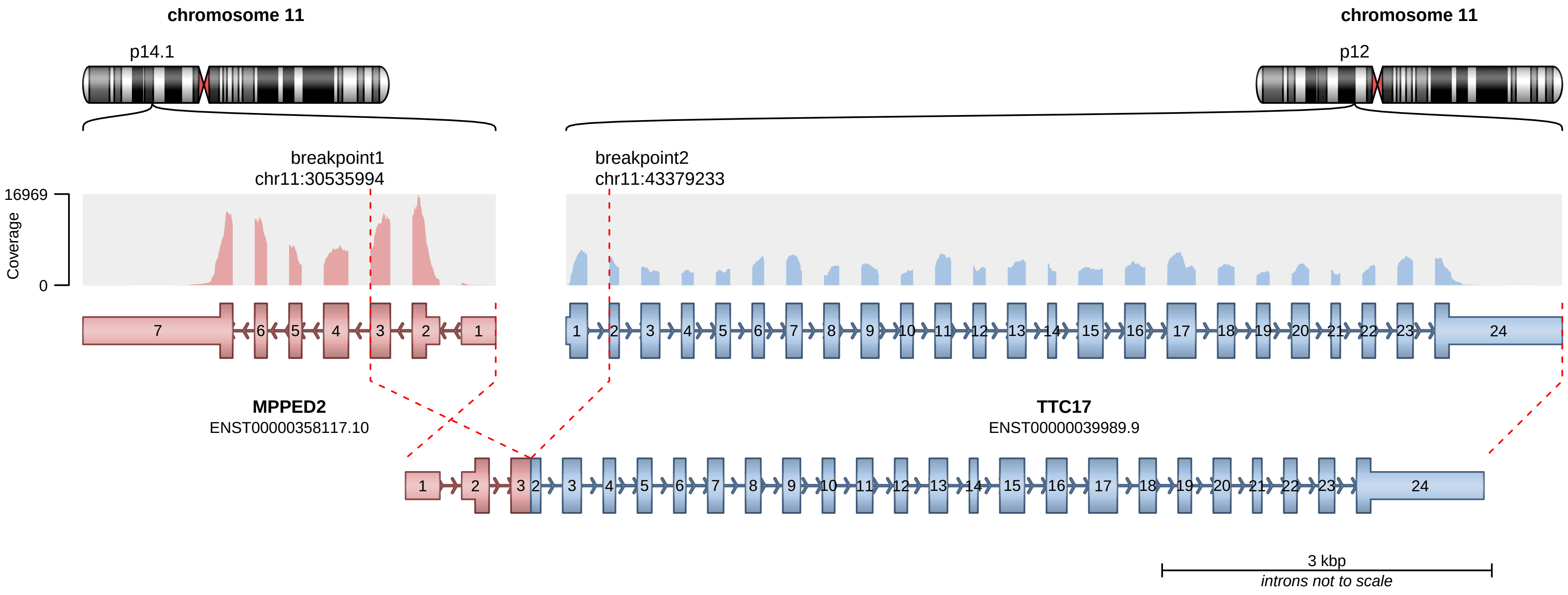


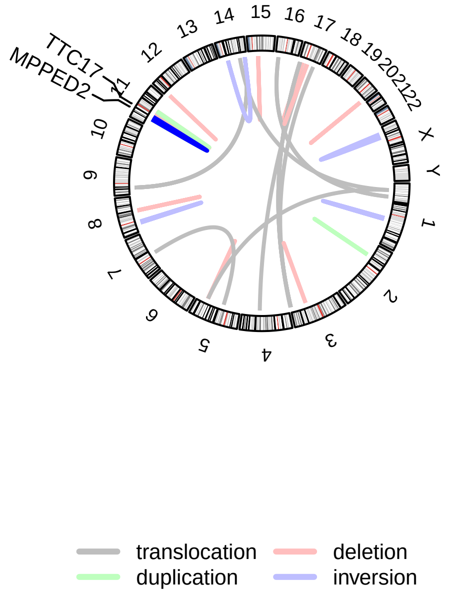


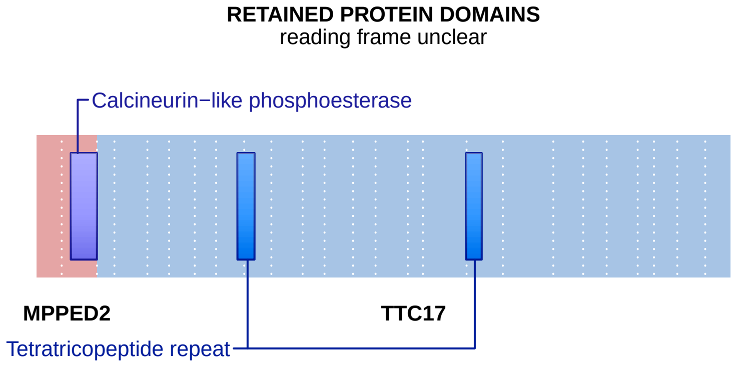


**SUPPORTING READ COUNT**

Split reads = 1
Discordant mates = 0

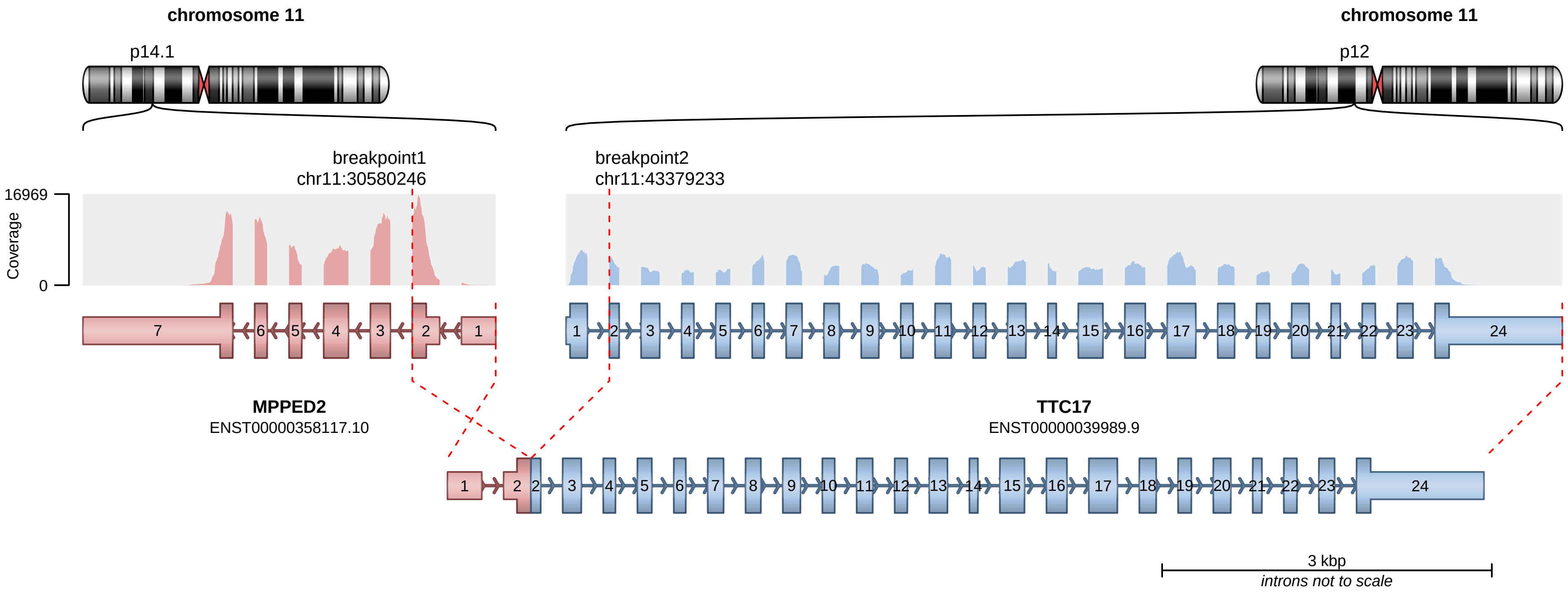


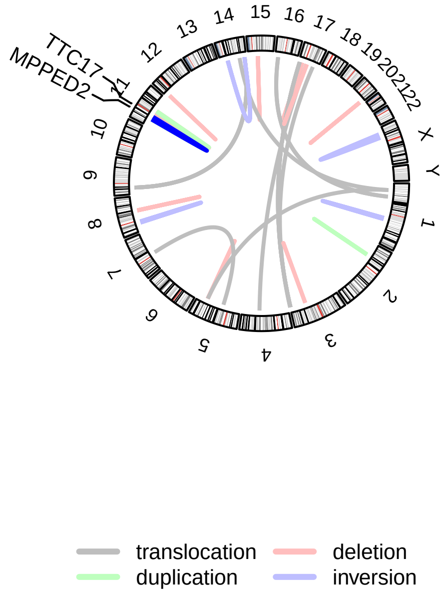


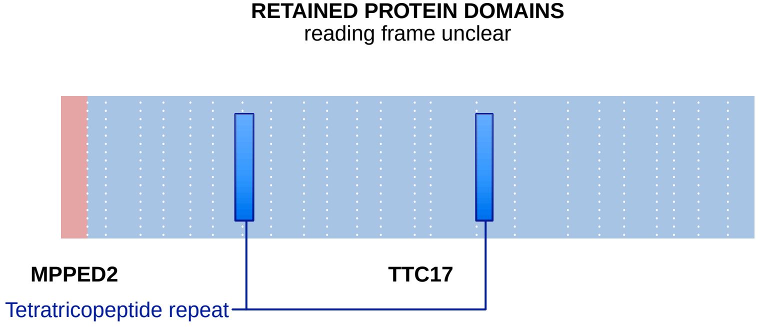


**SUPPORTING READ COUNT**

Split reads = 35
Discordant mates = 1

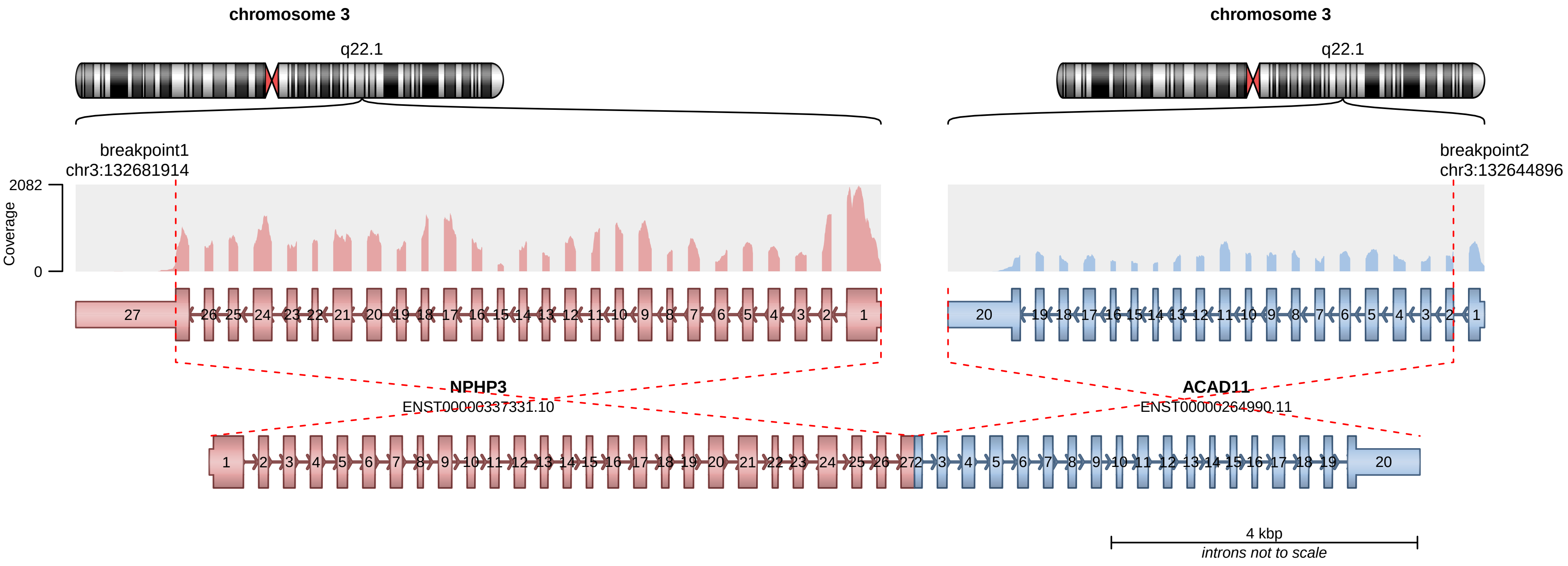


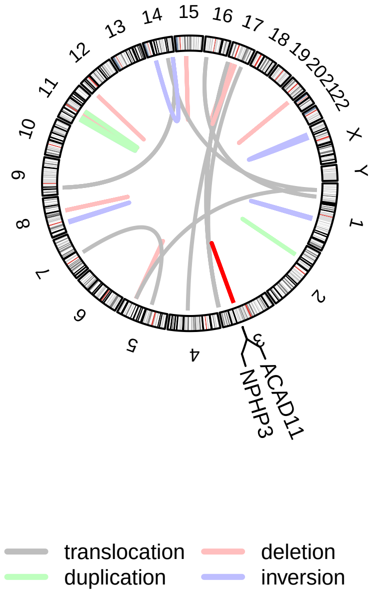




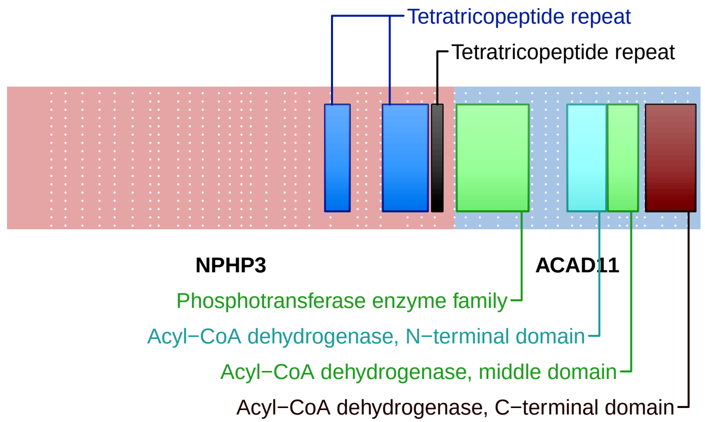
**SUPPORTING READ COUNT**

Split reads = 8
Discordant mates = 0



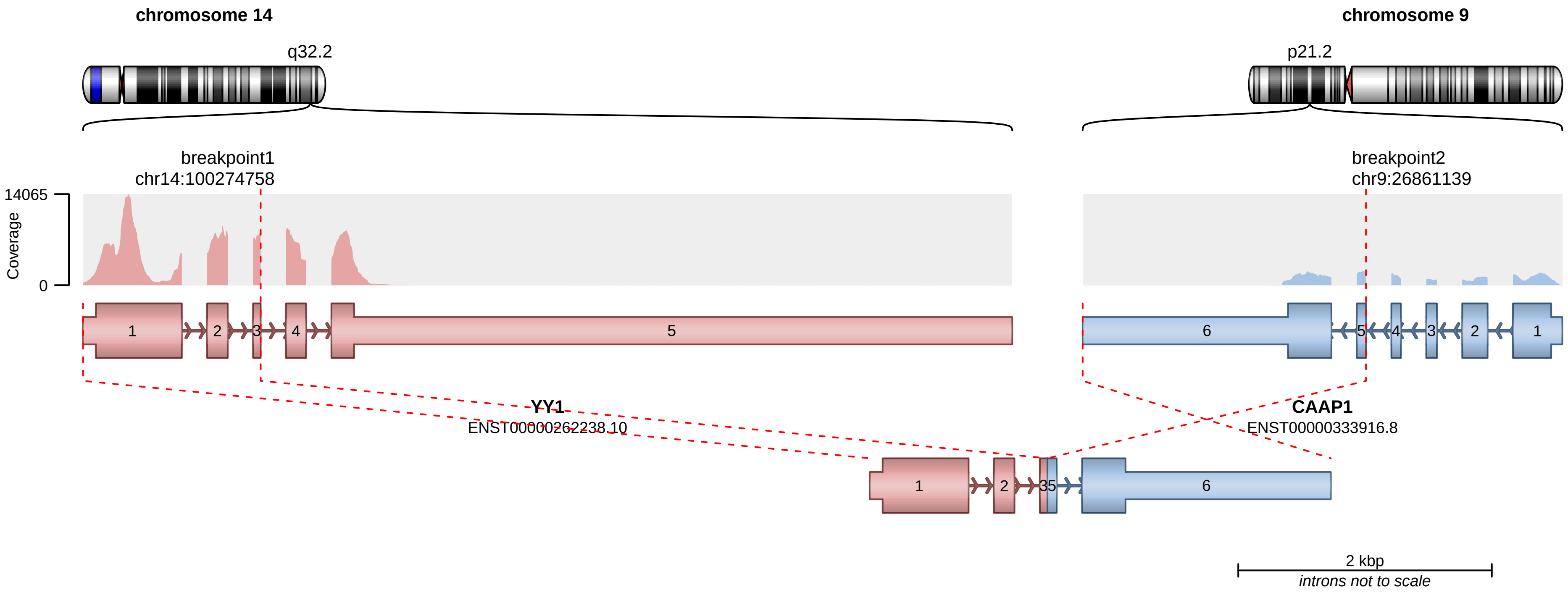


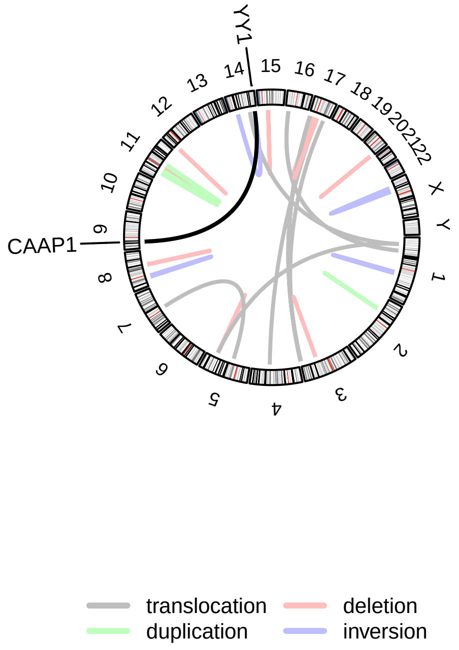
**RETAINED PROTEIN DOMAINS**
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 34
Discordant mates = 0

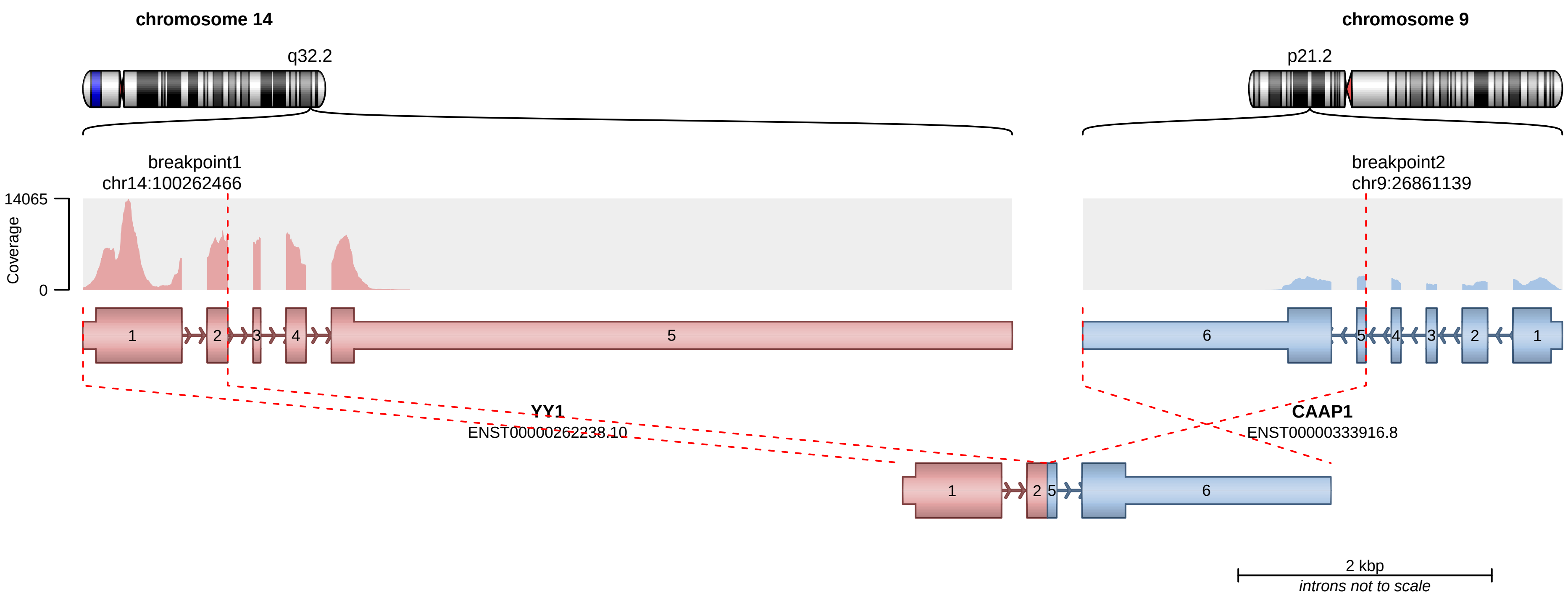


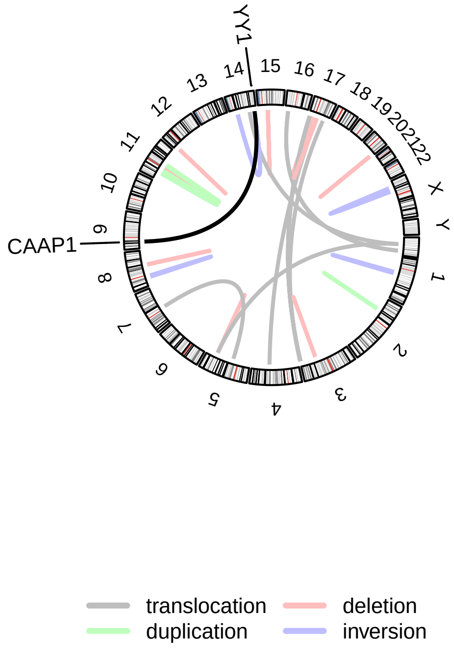


No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 33
Discordant mates = 0

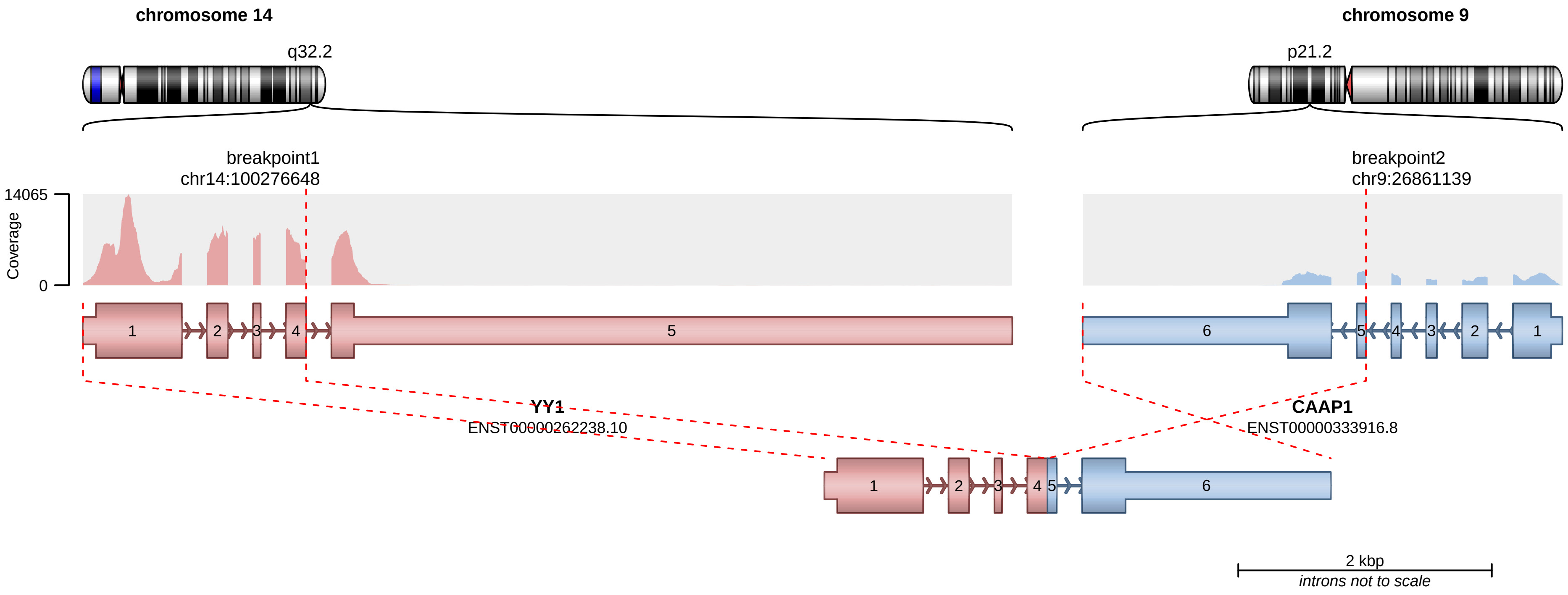


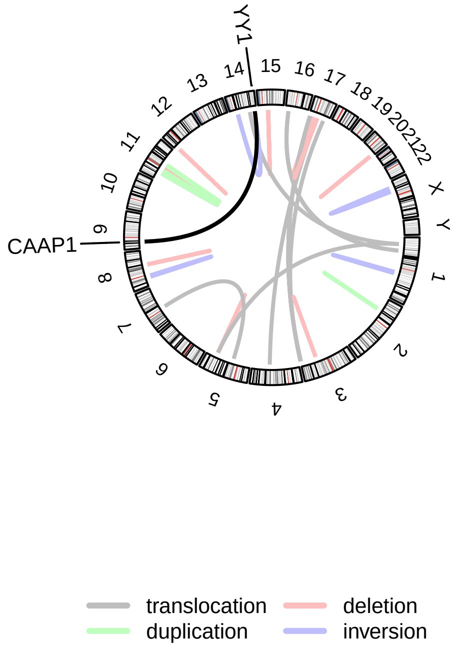


No protein domains retained in fusion.

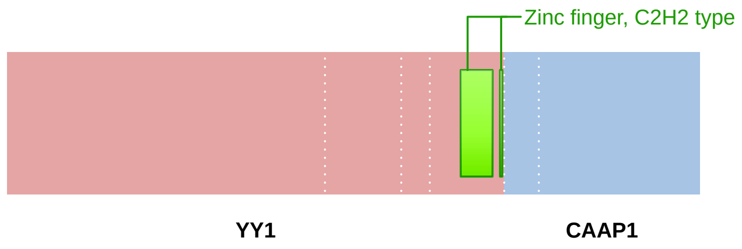
**SUPPORTING READ COUNT**

Split reads = 26
Discordant mates = 0



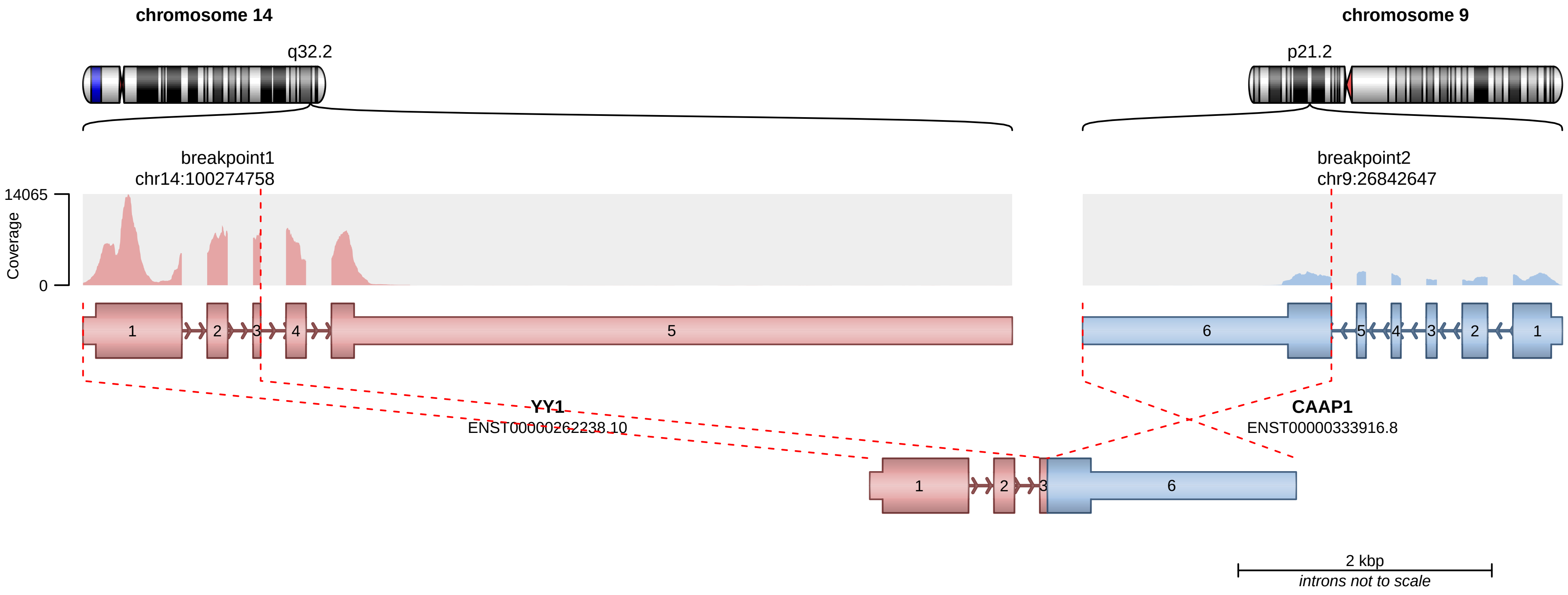


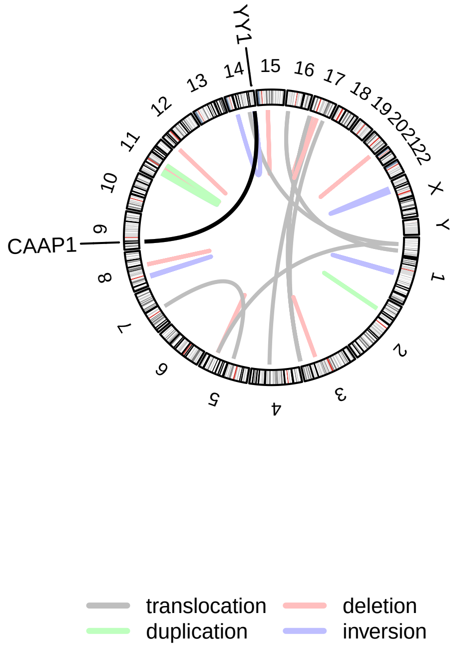
**RETAINED PROTEIN DOMAINS**
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 5
Discordant mates = 0

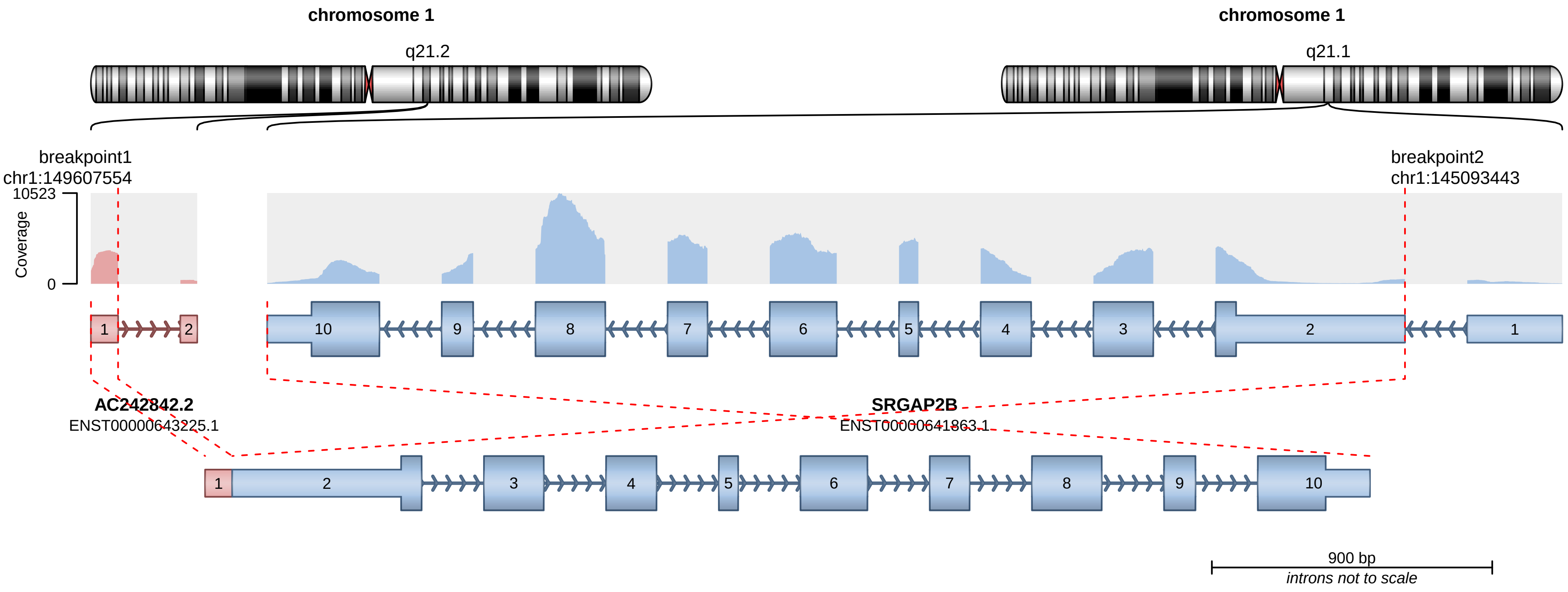


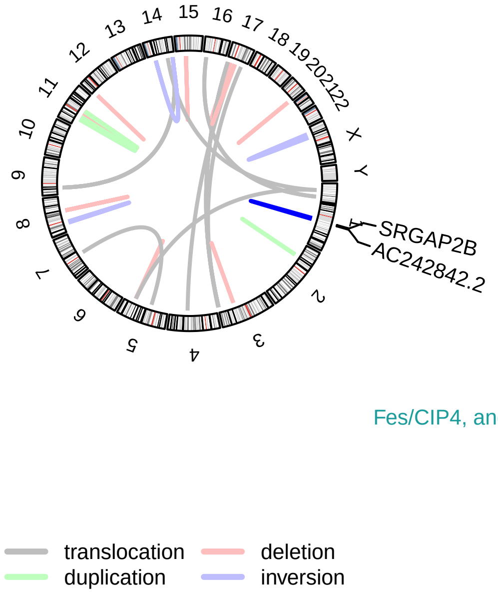


No protein domains retained in fusion.

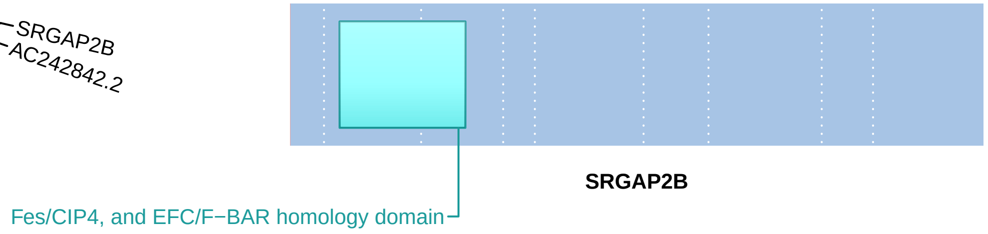
**SUPPORTING READ COUNT**

Split reads = 4
Discordant mates = 0



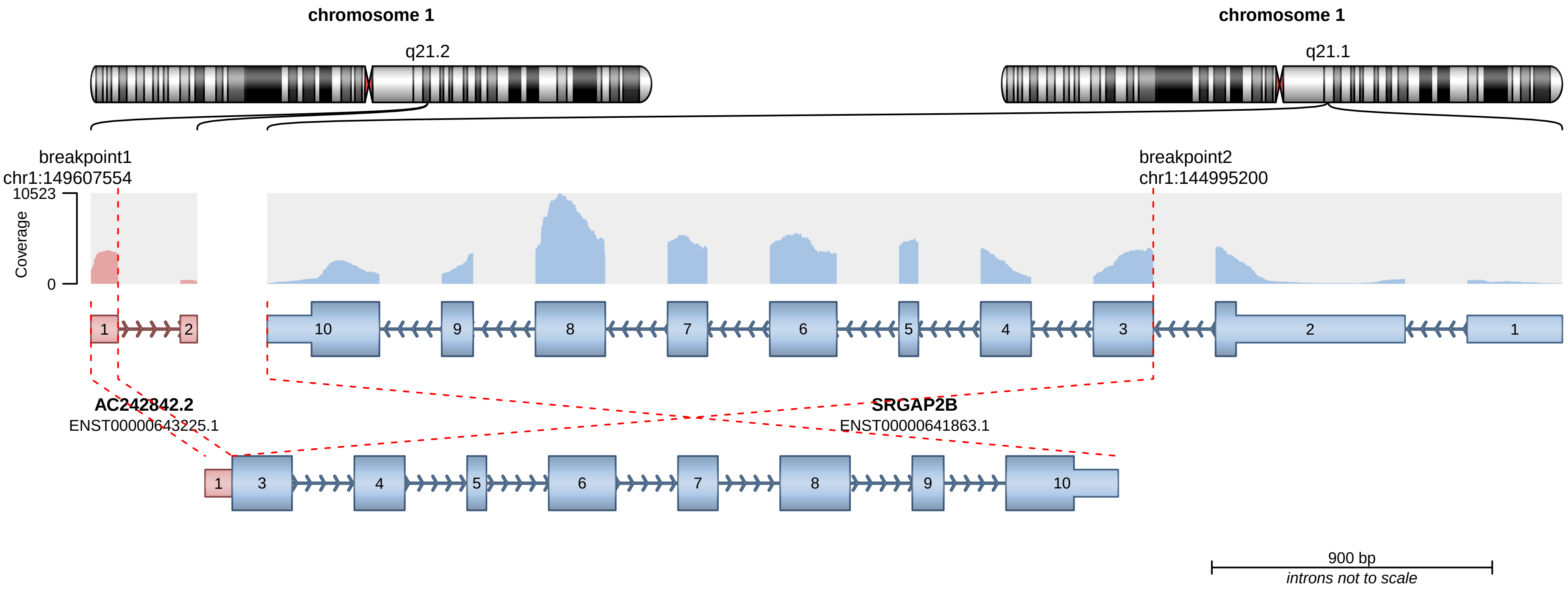


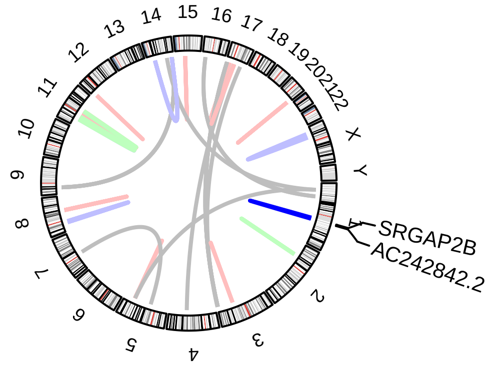
**RETAINED PROTEIN DOMAINS**
reading frame unclear



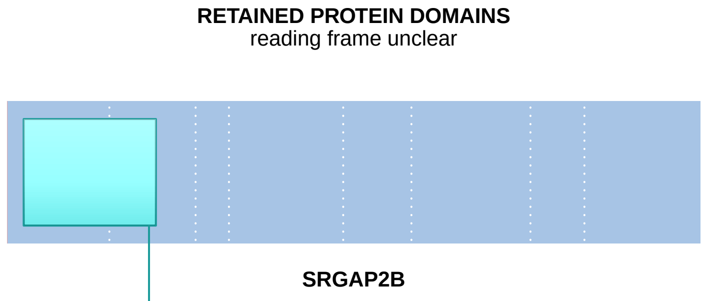
**SUPPORTING READ COUNT**

Split reads = 32
Discordant mates = 0



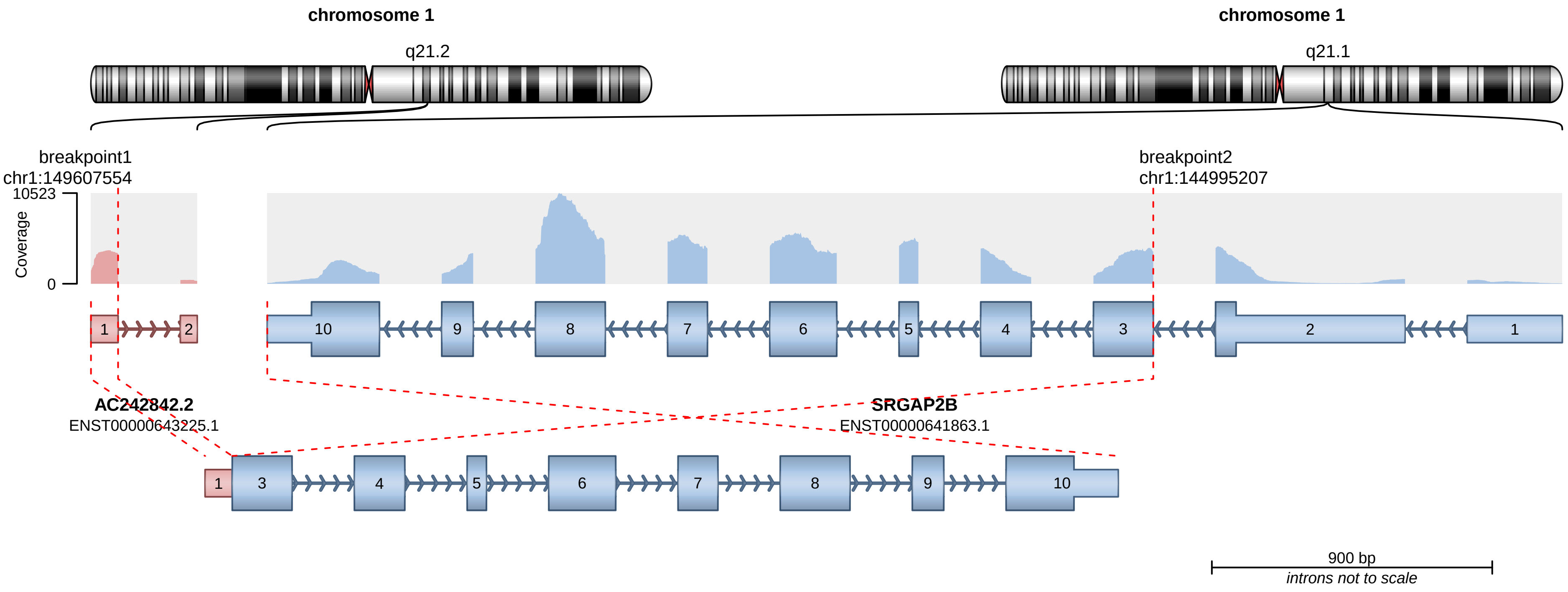


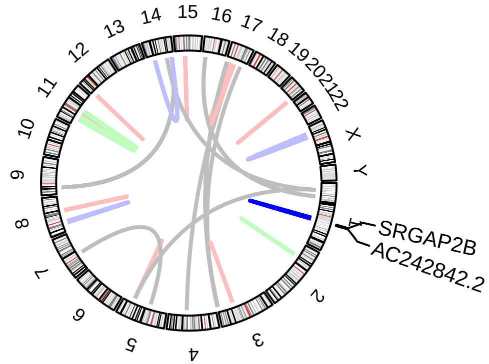
**RETAINED PROTEIN DOMAINS**
reading frame unclear



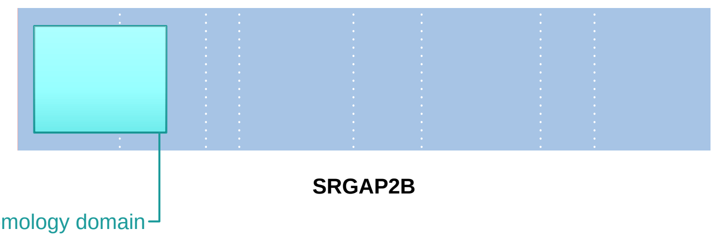
**SUPPORTING READ COUNT**

Split reads = 12
Discordant mates = 0



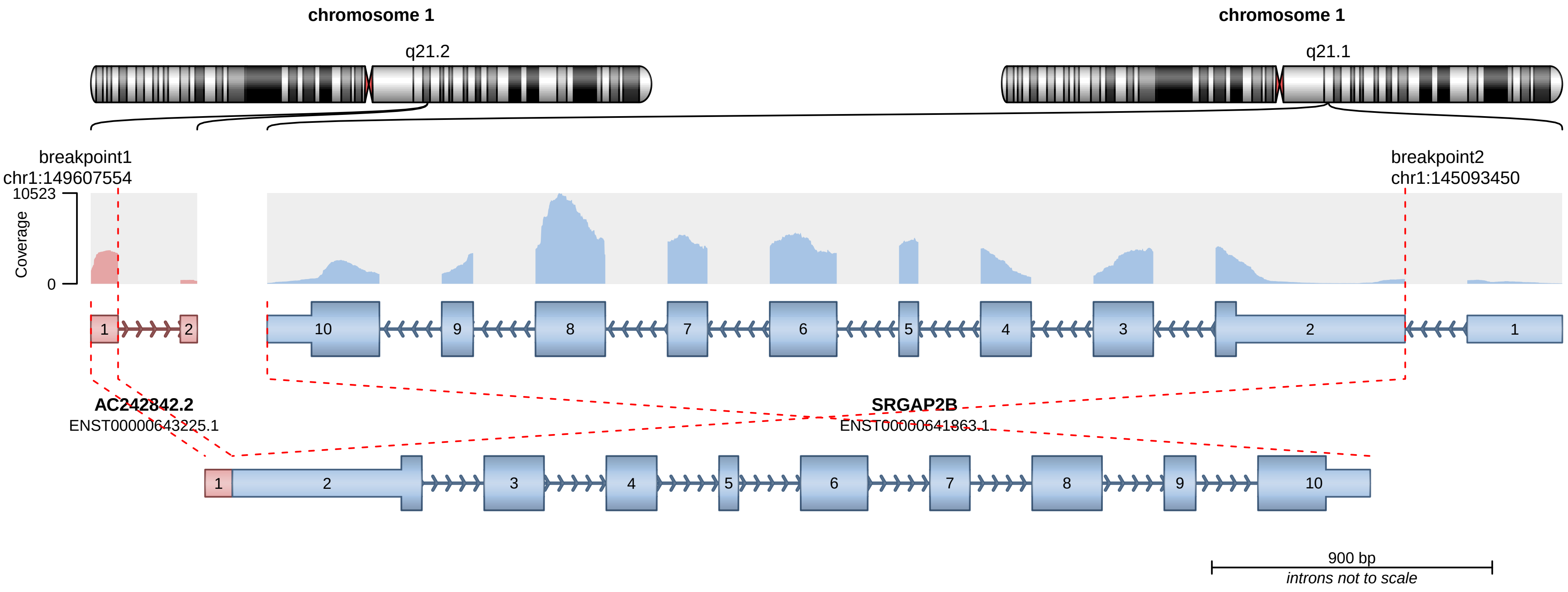


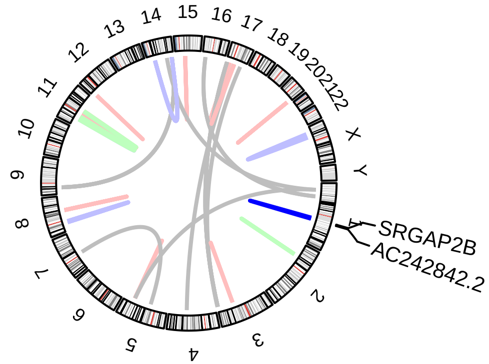
**RETAINED PROTEIN DOMAINS**
reading frame unclear



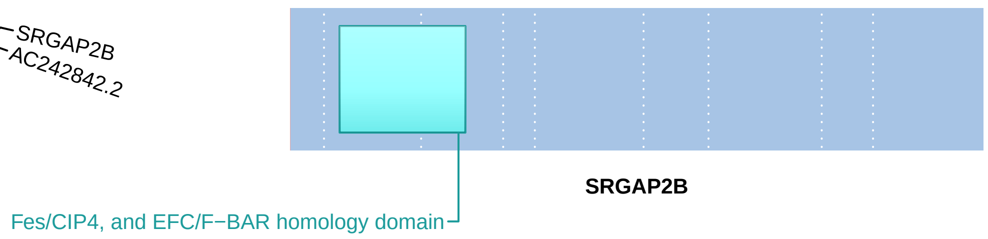
**SUPPORTING READ COUNT**

Split reads = 11
Discordant mates = 0





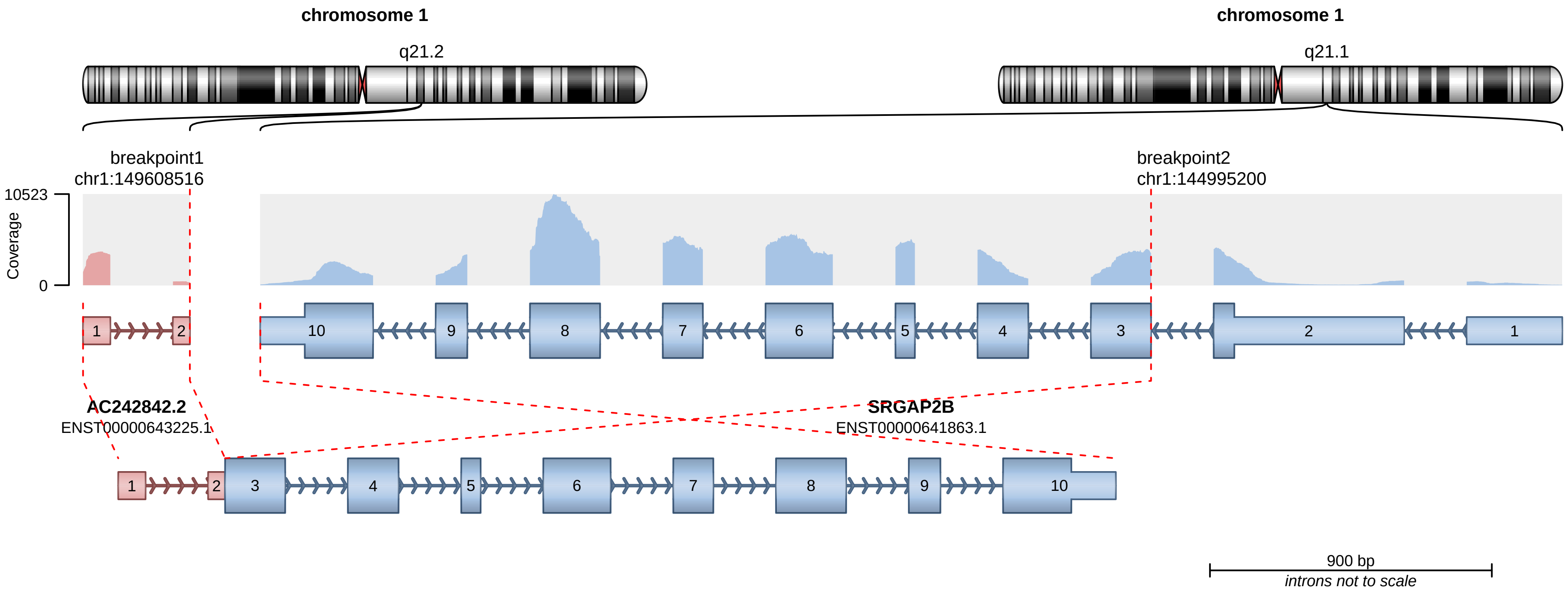
**RETAINED PROTEIN DOMAINS**
reading frame unclear

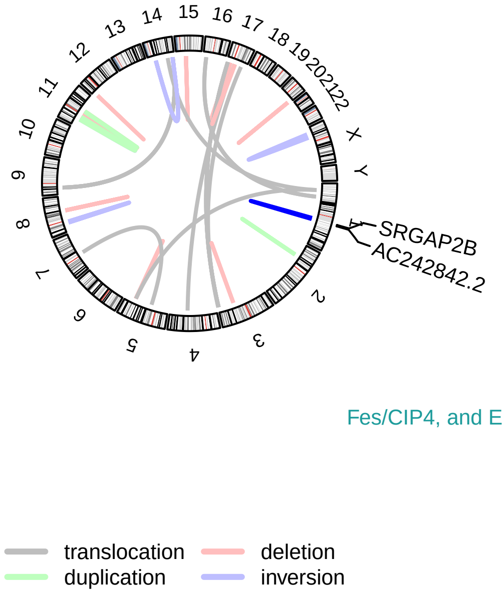


**SUPPORTING READ COUNT**

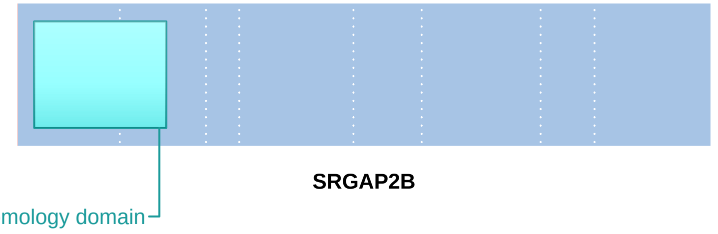
Split reads = 6
Discordant mates = 0

translocation
duplication
deletion
inversion



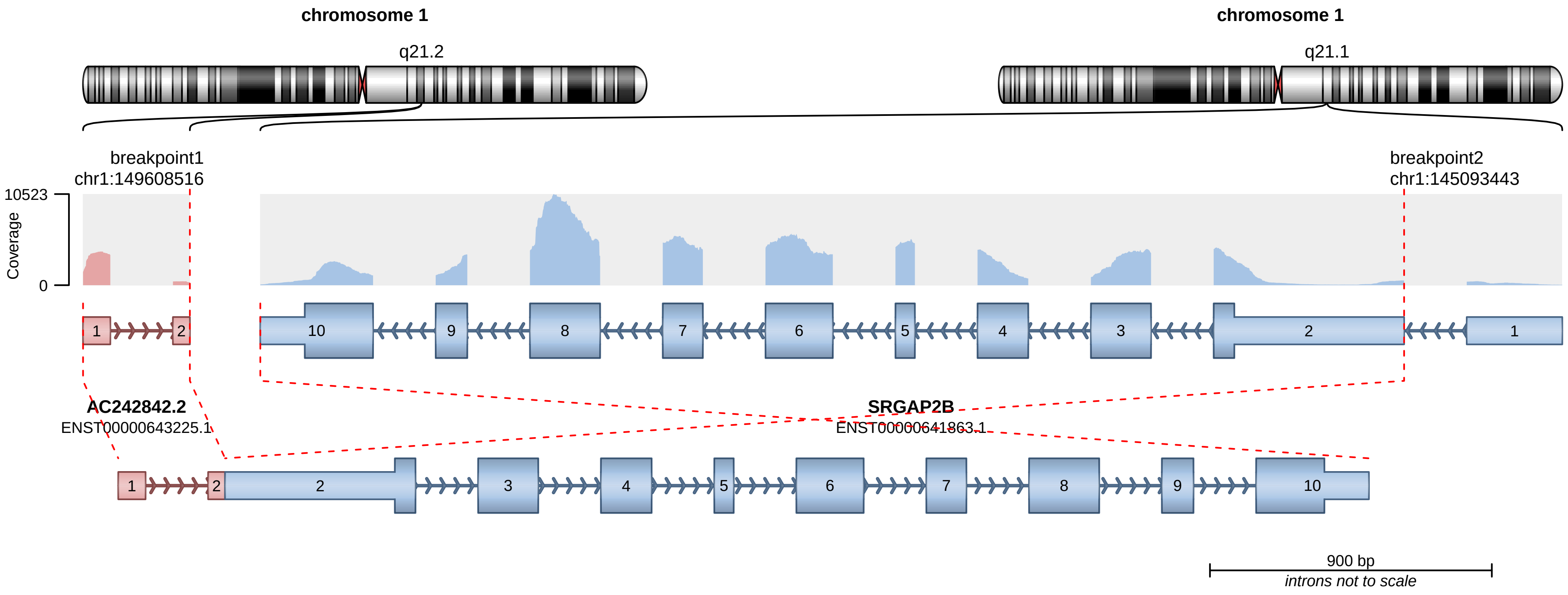


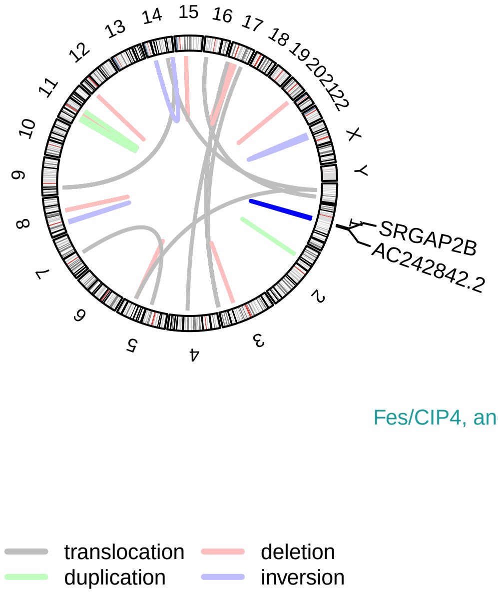
**RETAINED PROTEIN DOMAINS**
reading frame unclear



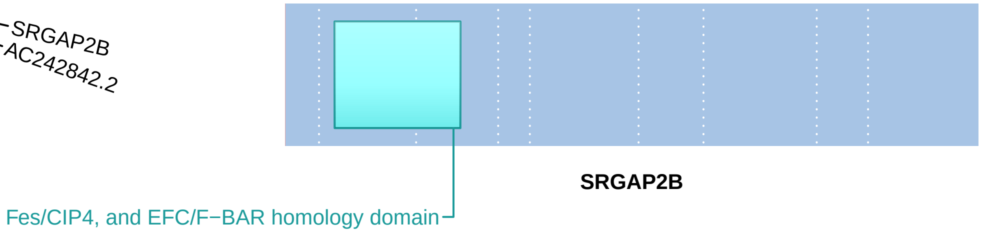
**SUPPORTING READ COUNT**

Split reads = 5
Discordant mates = 0



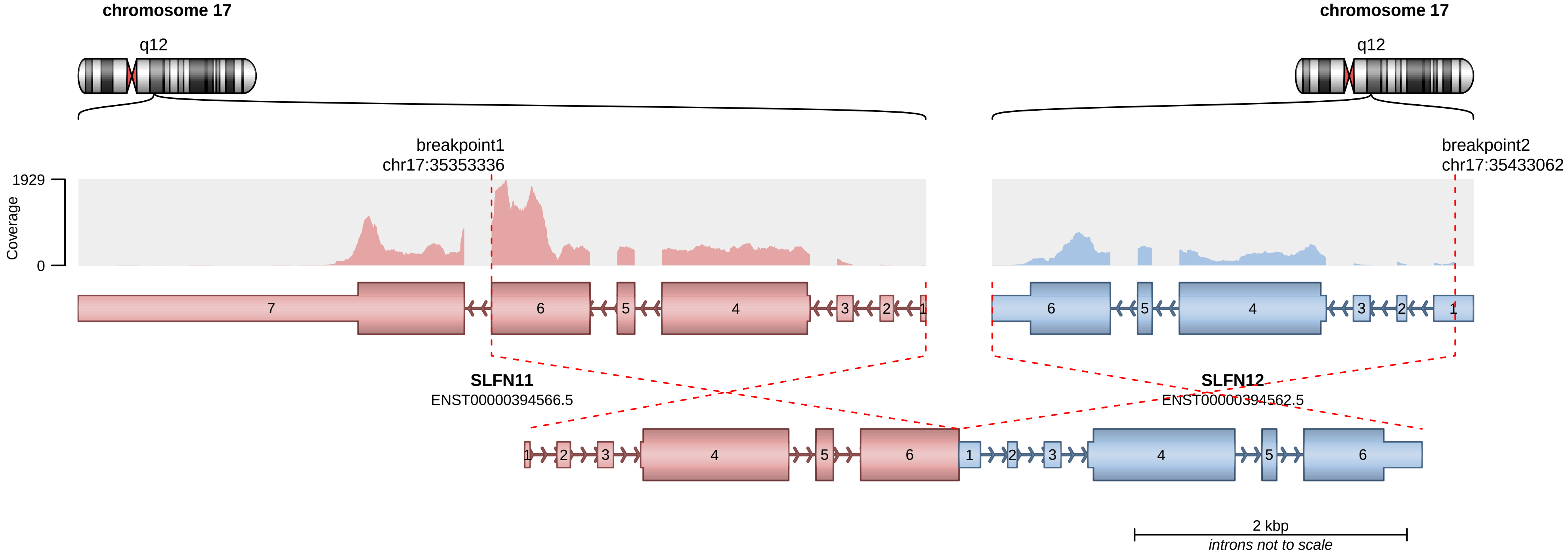


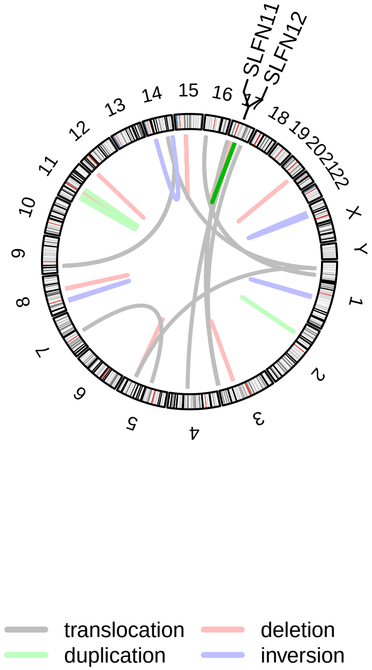
**RETAINED PROTEIN DOMAINS**
reading frame unclear



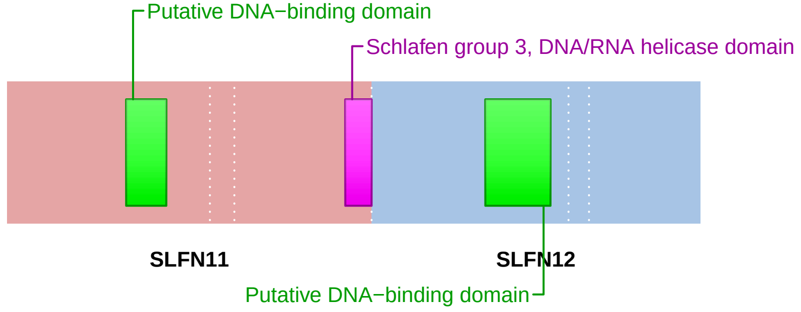
**SUPPORTING READ COUNT**

Split reads = 1
Discordant mates = 0



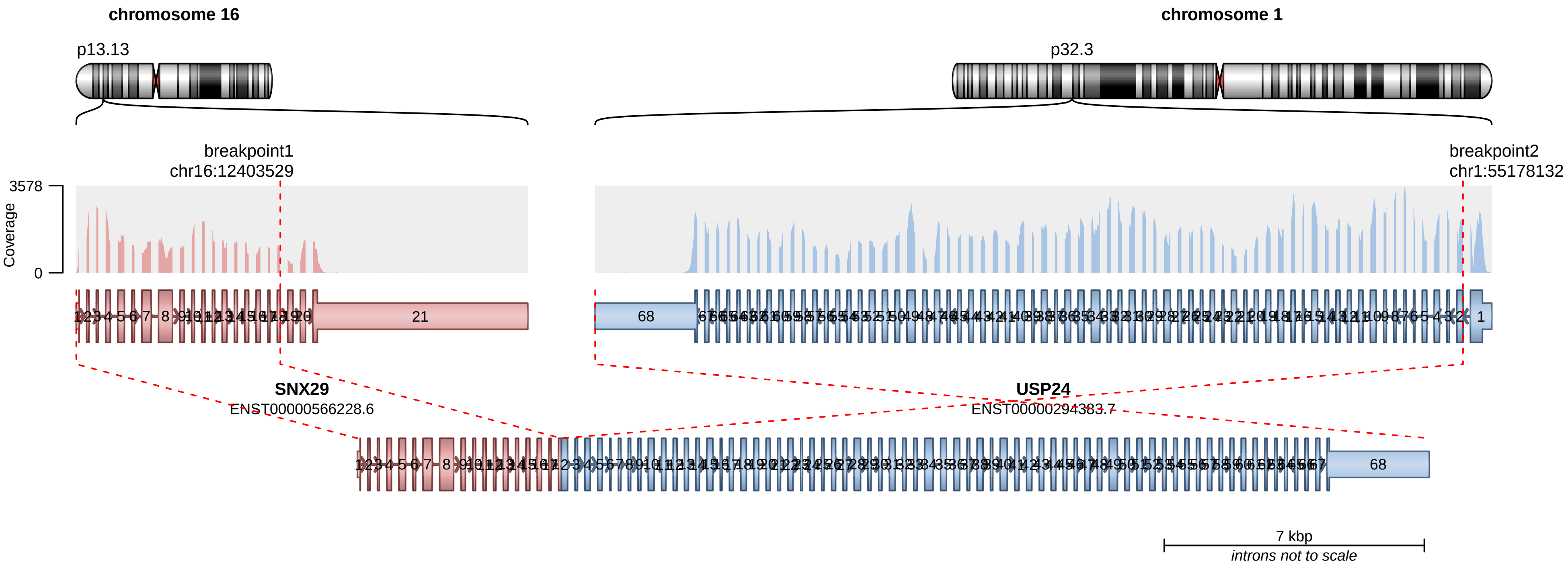


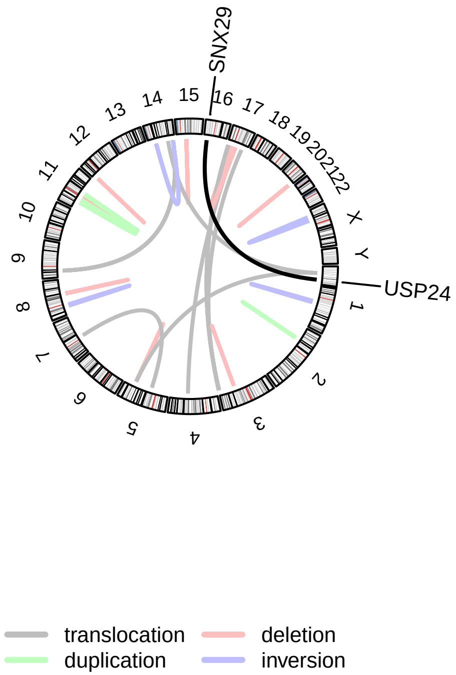
**RETAINED PROTEIN DOMAINS**
reading frame unclear

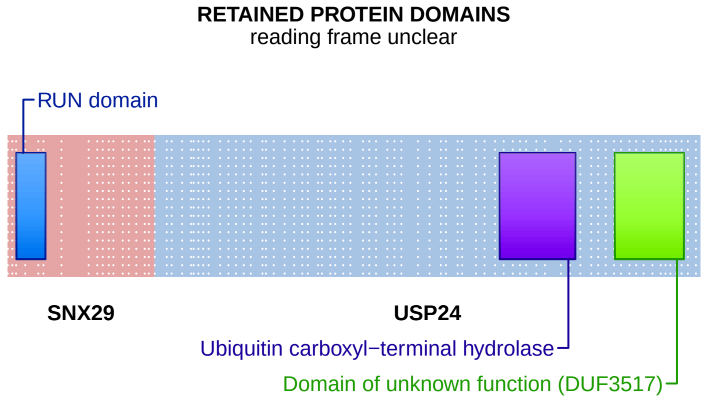


**SUPPORTING READ COUNT**

Split reads = 30
Discordant mates = 0

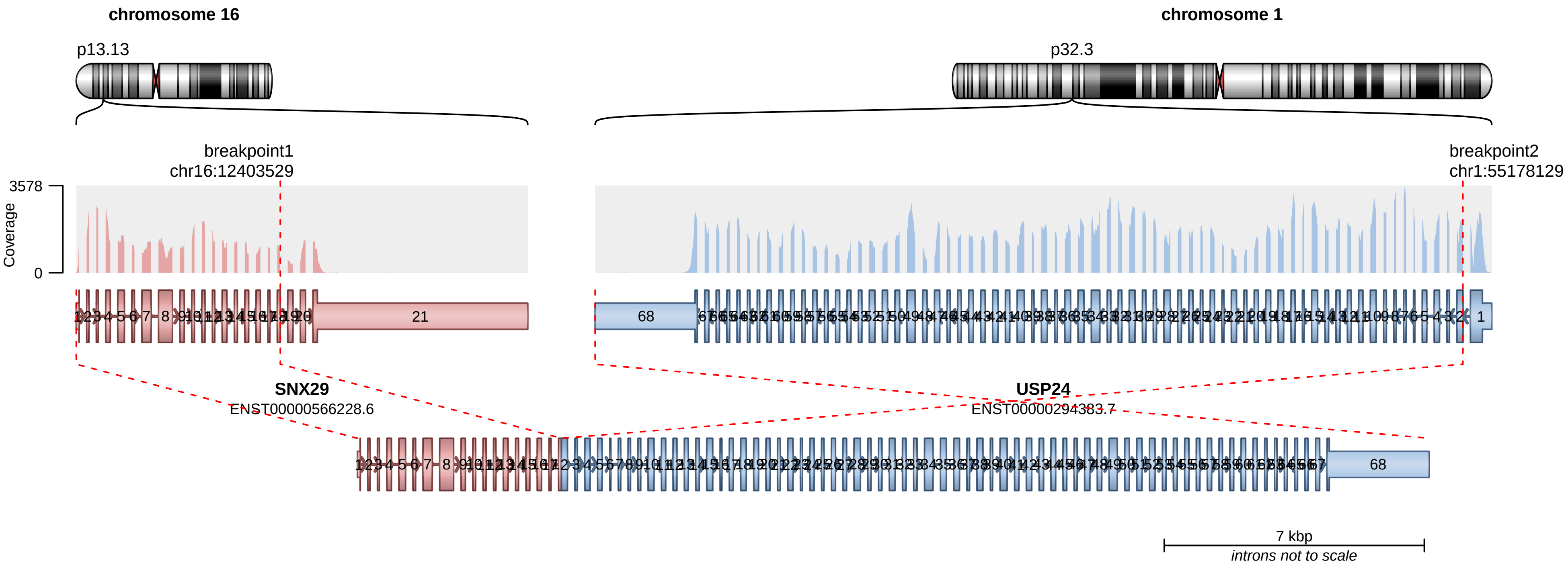


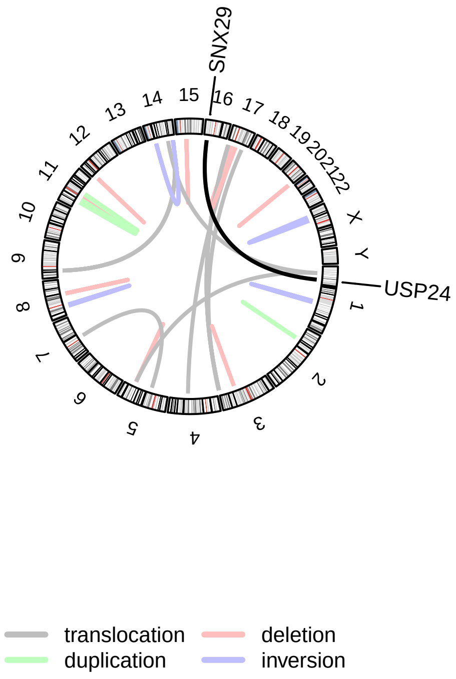




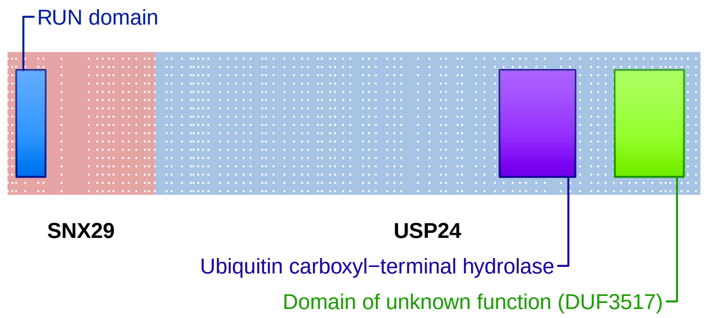
**SUPPORTING READ COUNT**

Split reads = 29
Discordant mates = 1



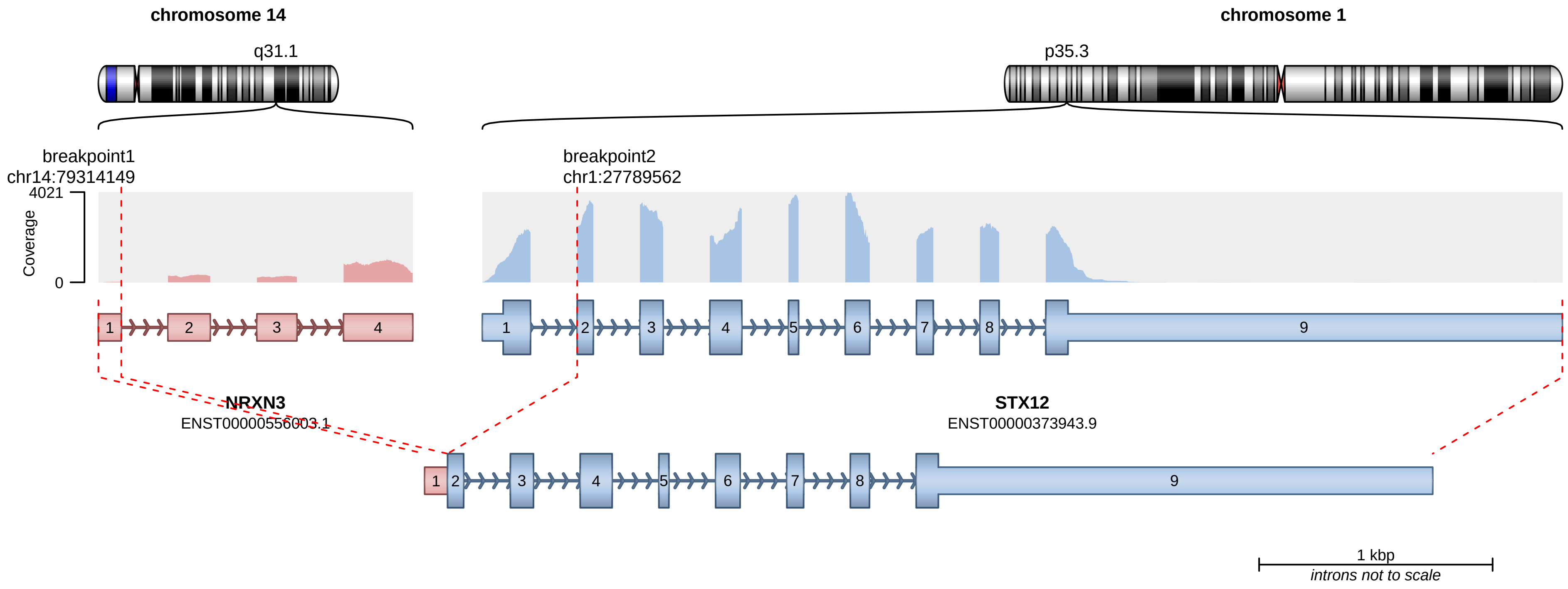


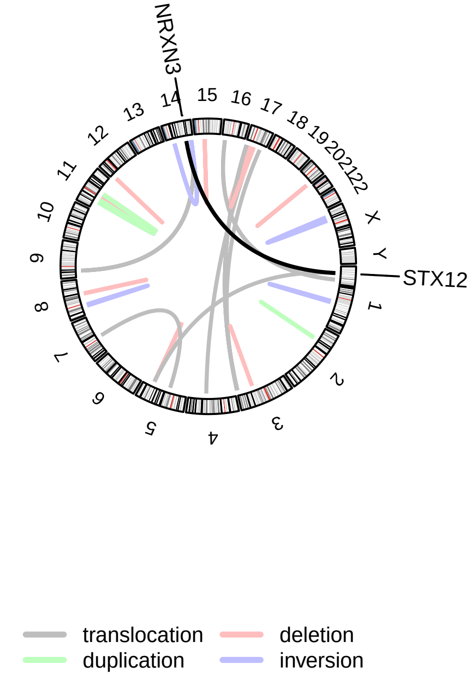
**RETAINED PROTEIN DOMAINS**
reading frame unclear

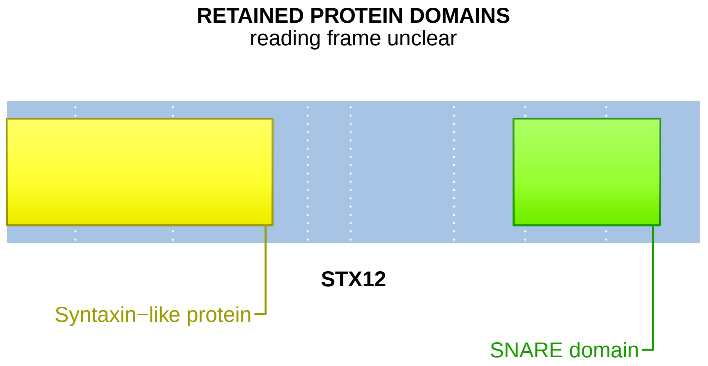


**SUPPORTING READ COUNT**

Split reads = 17
Discordant mates = 1

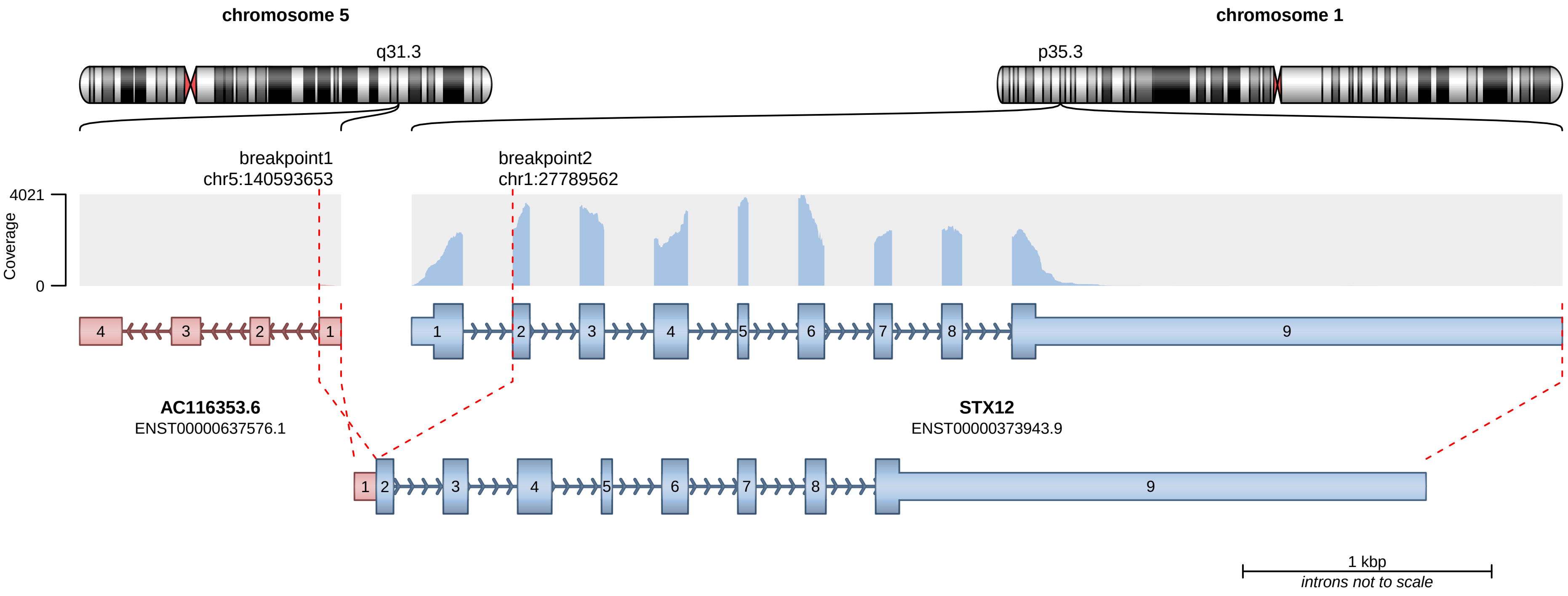


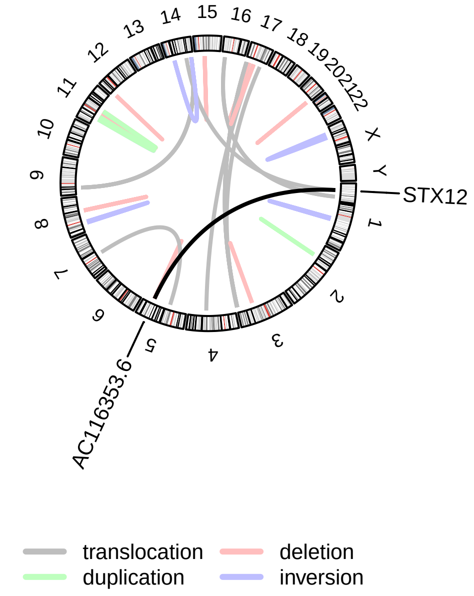


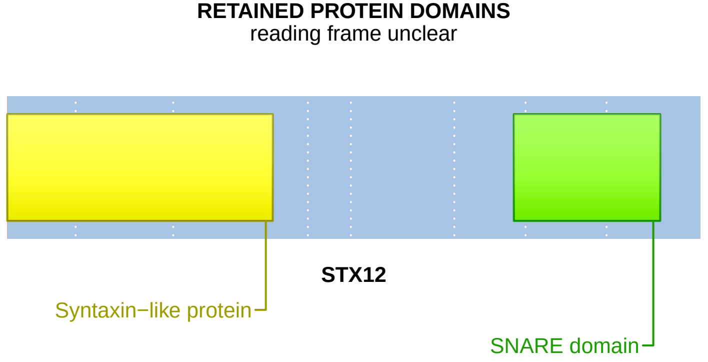


**SUPPORTING READ COUNT**

Split reads = 28
Discordant mates = 0

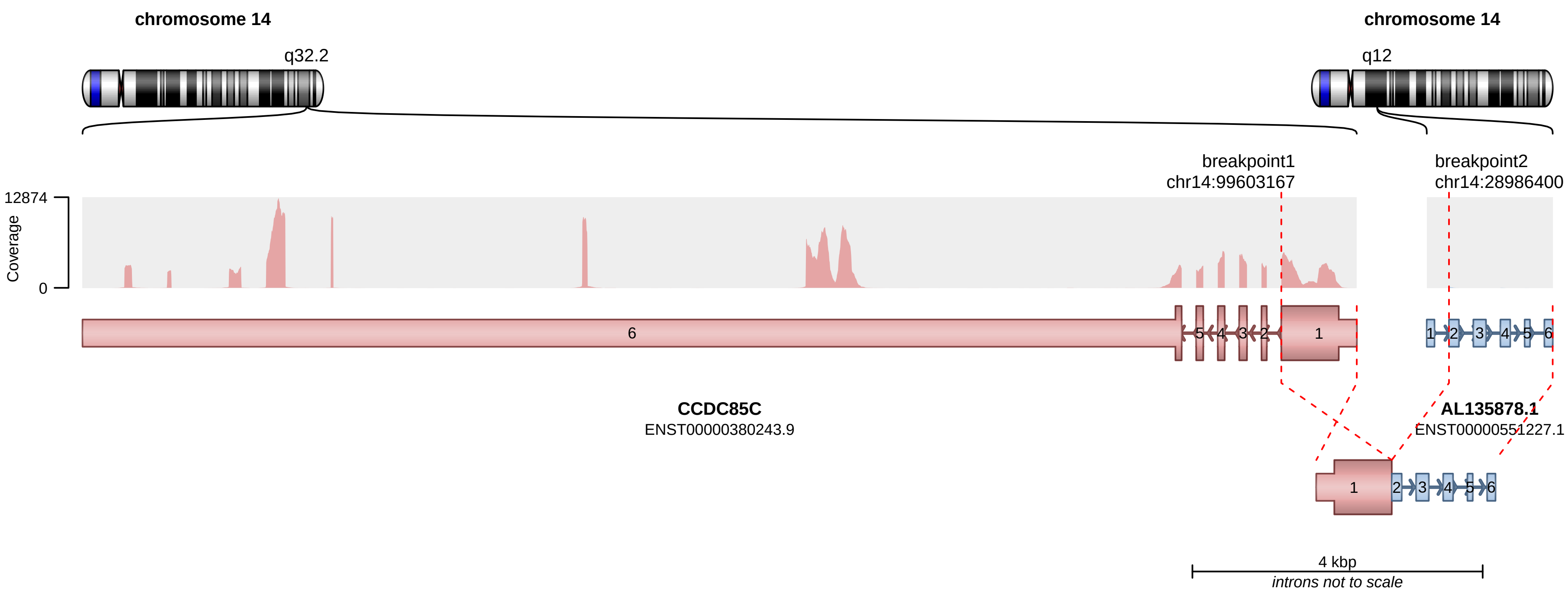


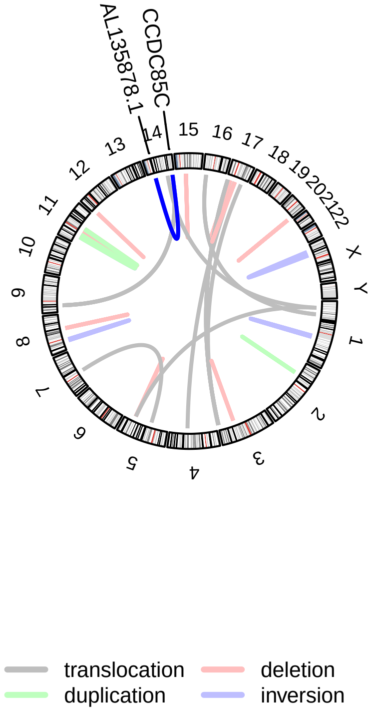


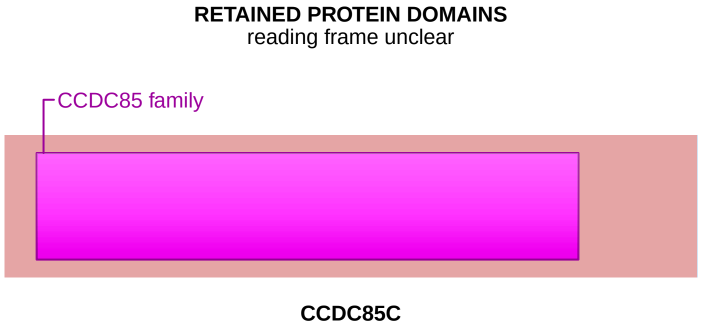


**SUPPORTING READ COUNT**

Split reads = 23
Discordant mates = 0

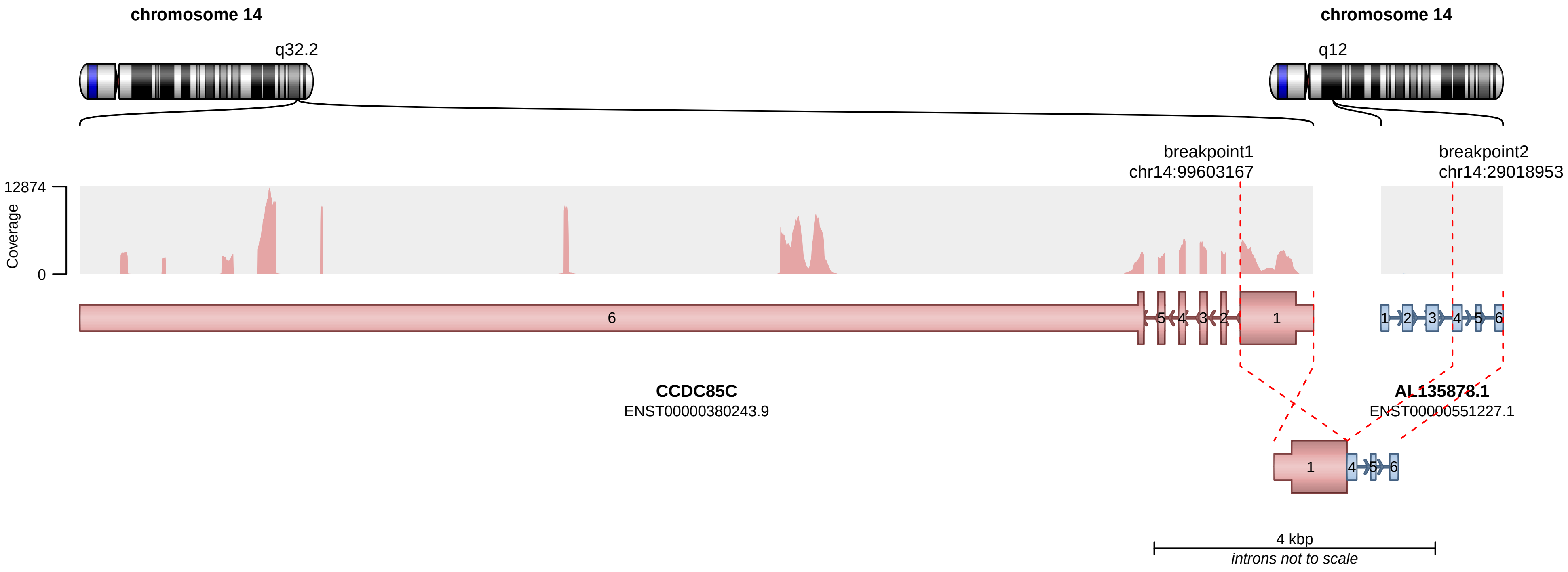


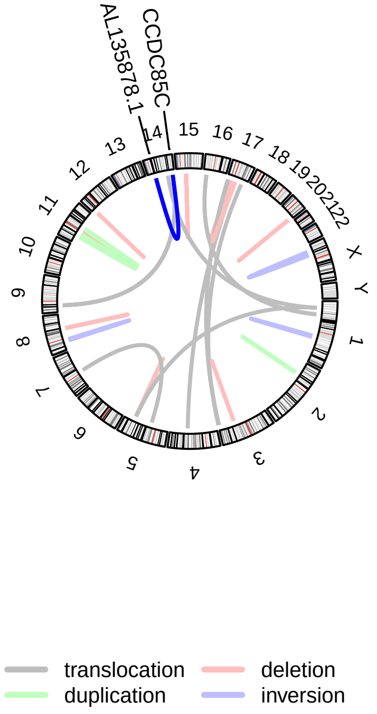


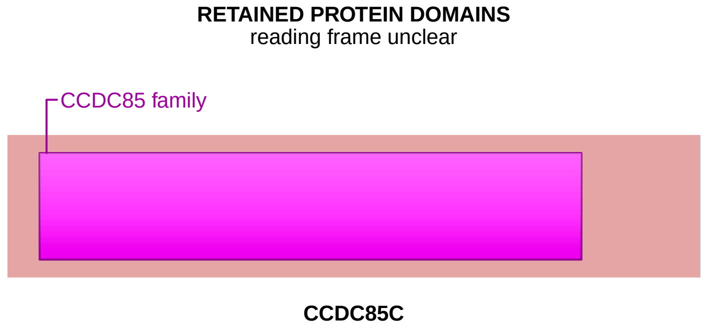


**SUPPORTING READ COUNT**

Split reads = 18
Discordant mates = 0

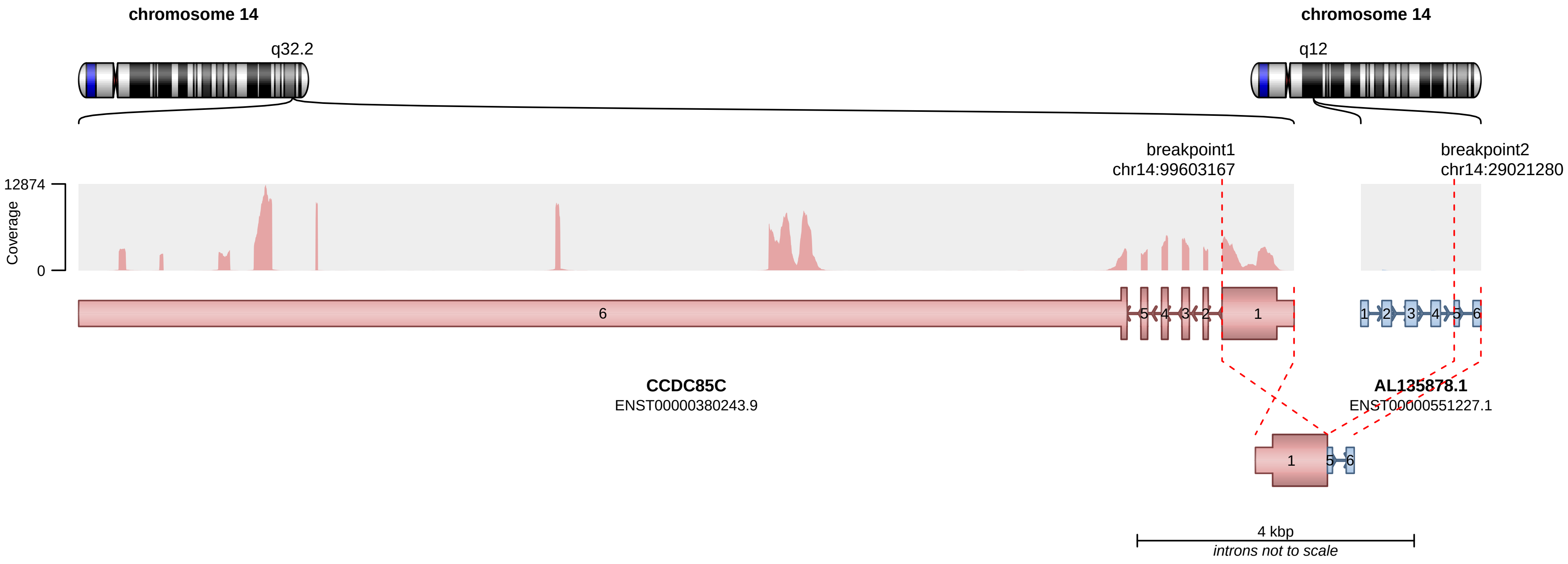


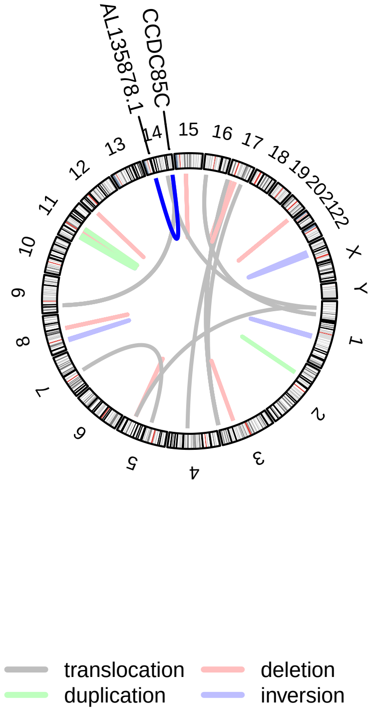




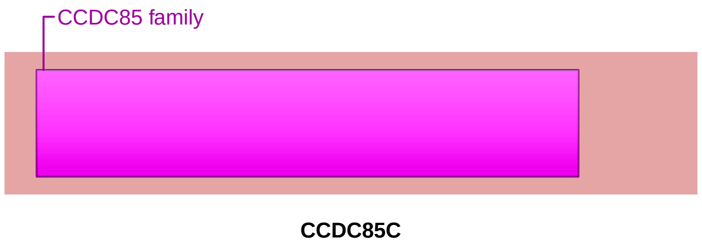
**SUPPORTING READ COUNT**

Split reads = 13
Discordant mates = 0



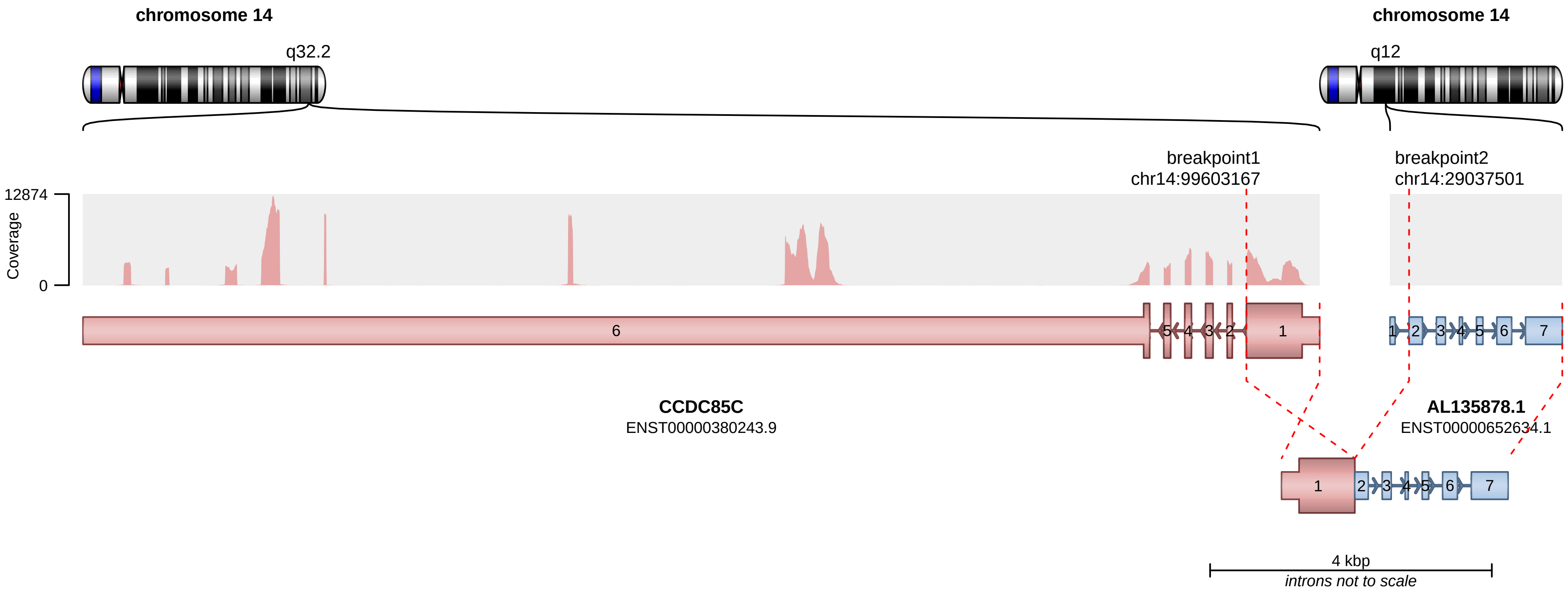


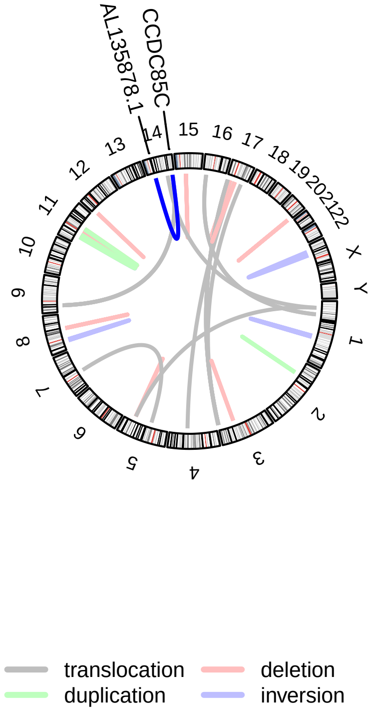
**RETAINED PROTEIN DOMAINS**
reading frame unclear



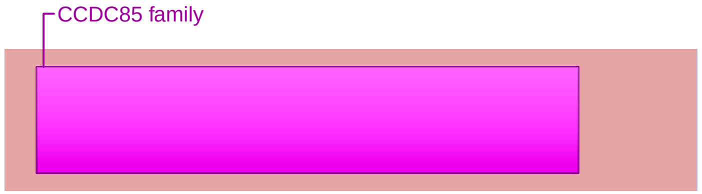
**SUPPORTING READ COUNT**

Split reads = 4
Discordant mates = 0





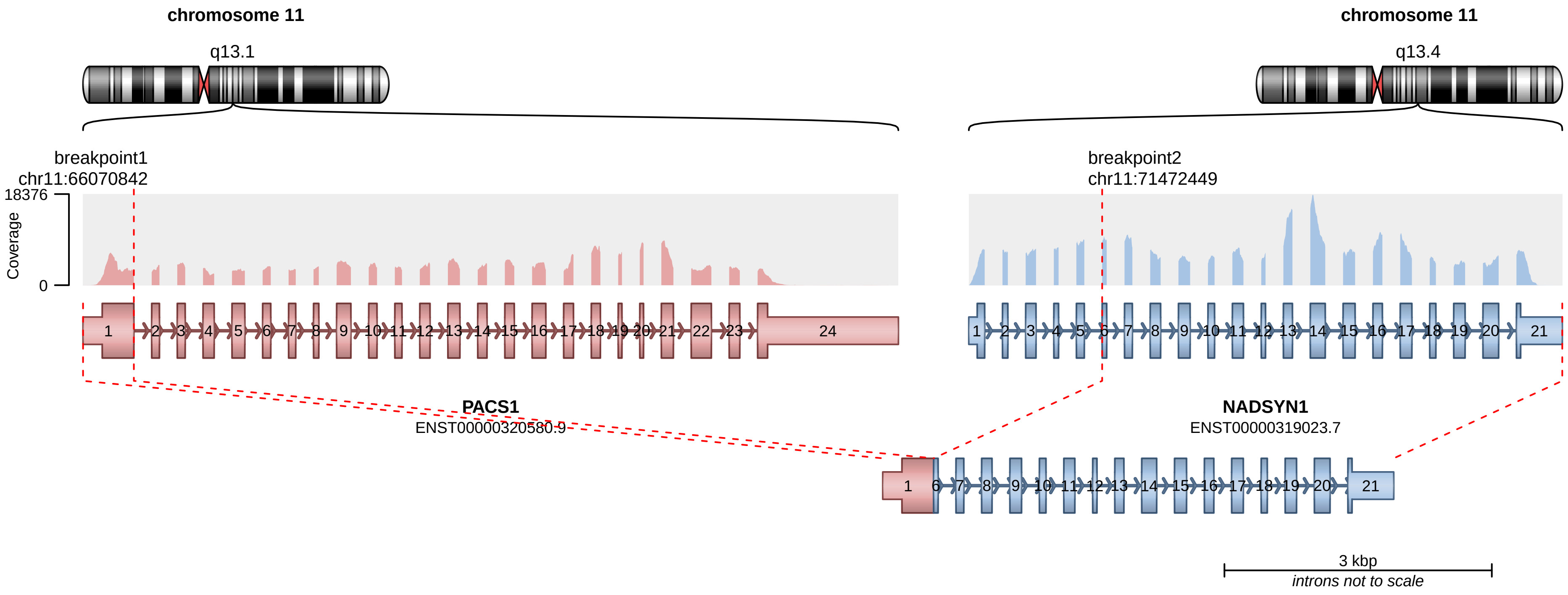
**RETAINED PROTEIN DOMAINS**
reading frame unclear

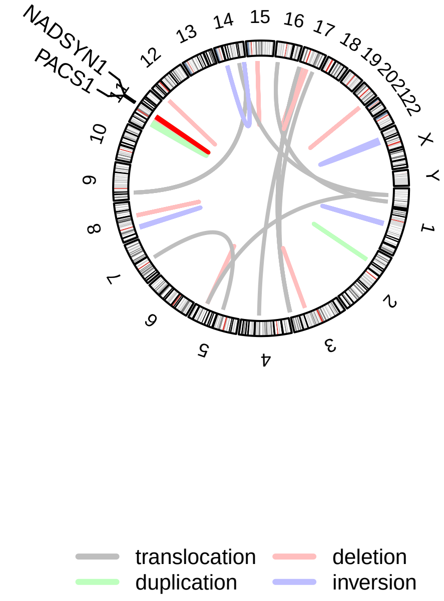


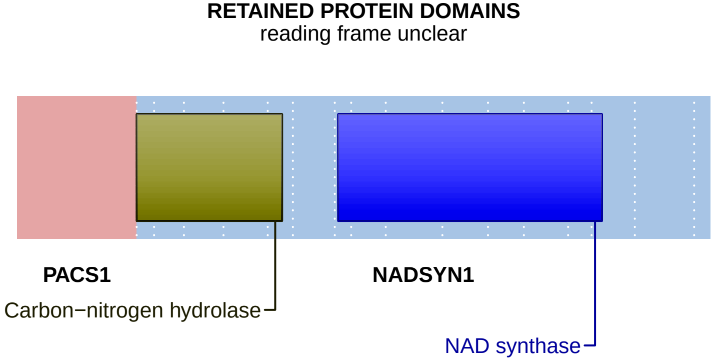
**CCDC85C**

**SUPPORTING READ COUNT**

Split reads = 1
Discordant mates = 0

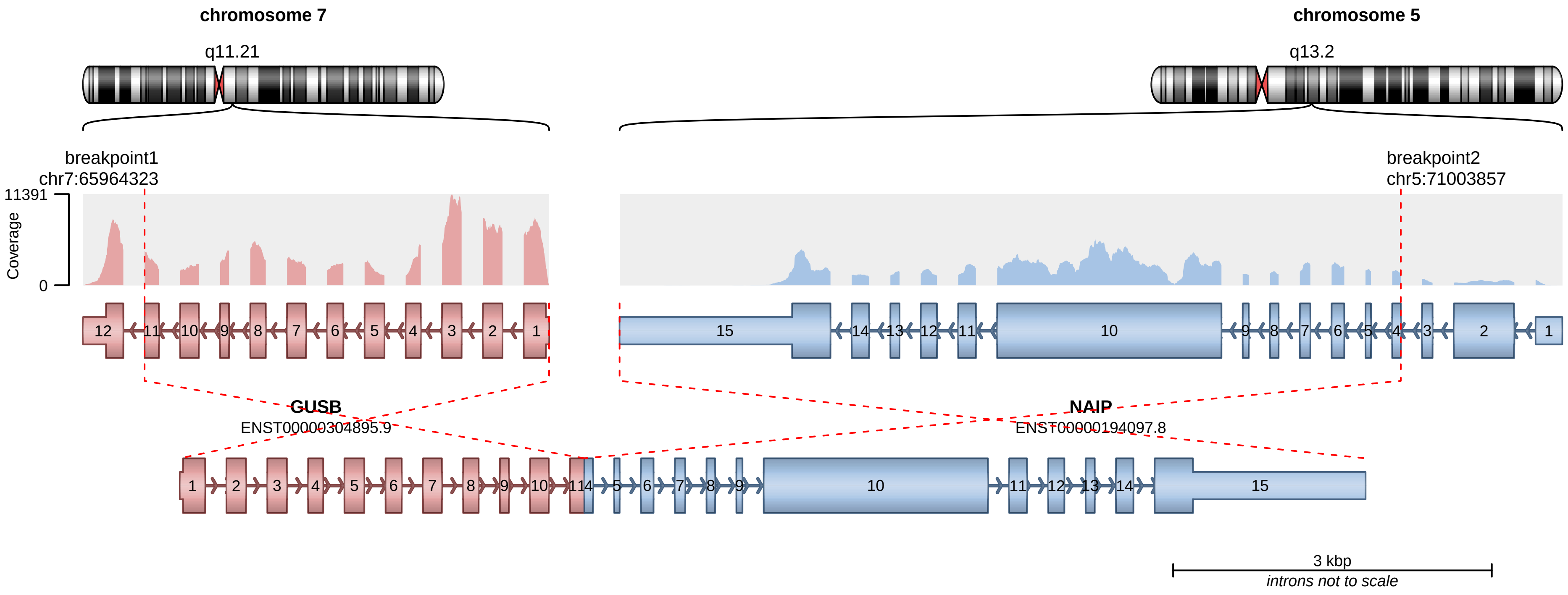


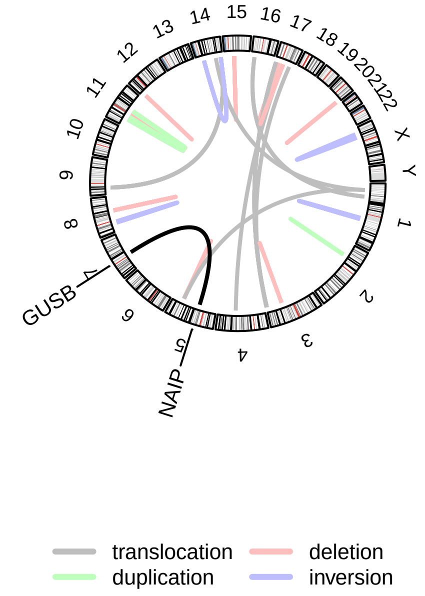


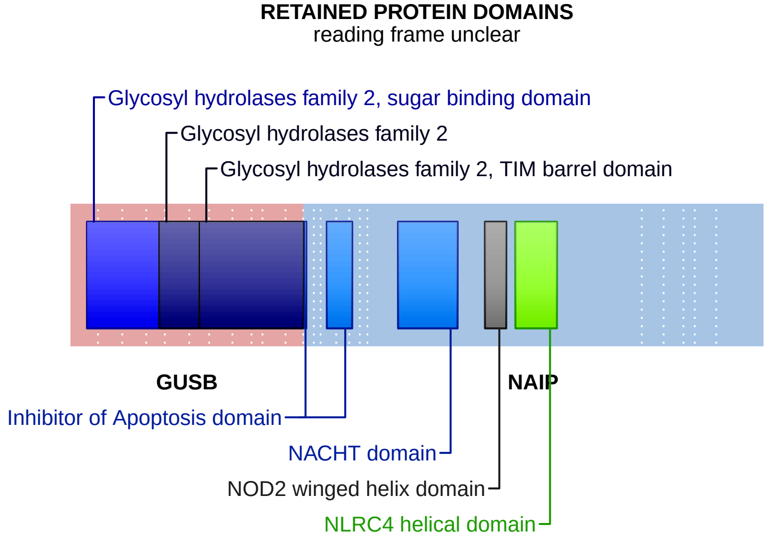


**SUPPORTING READ COUNT**

Split reads = 18
Discordant mates = 0

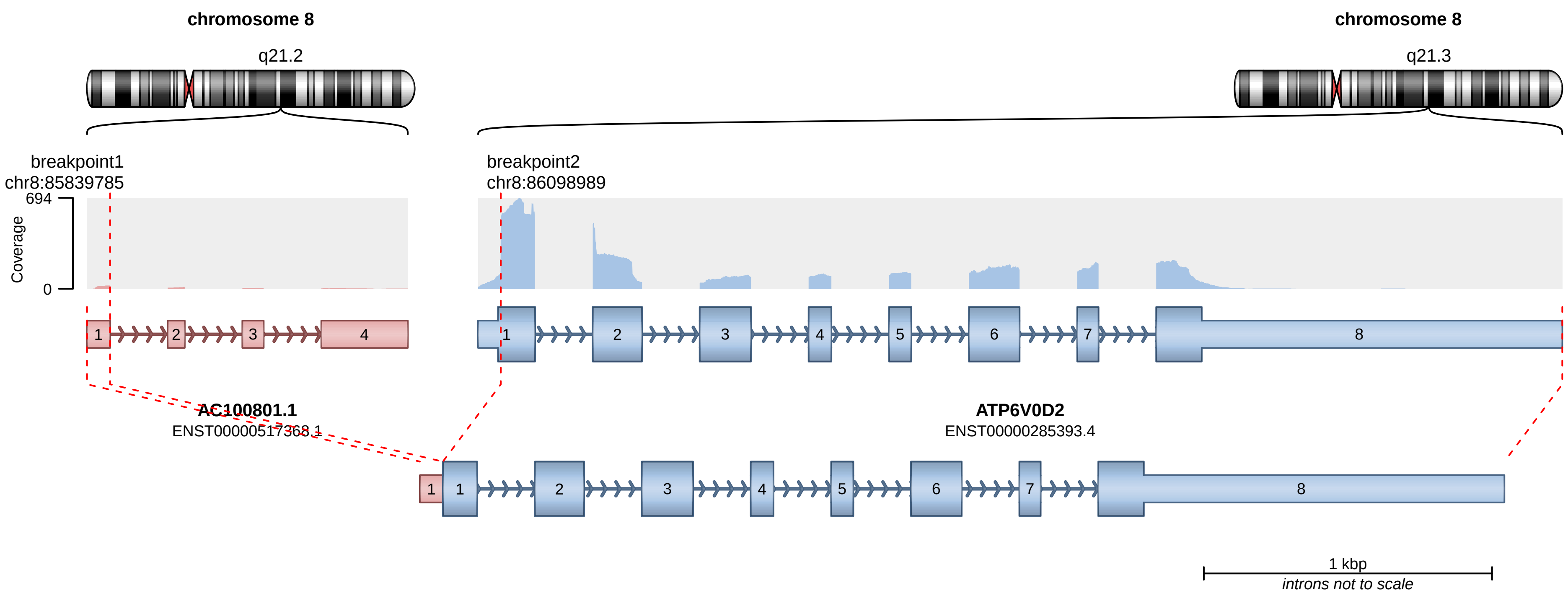


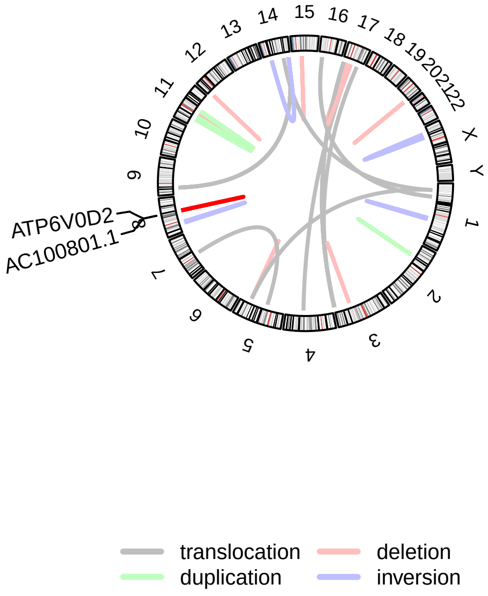




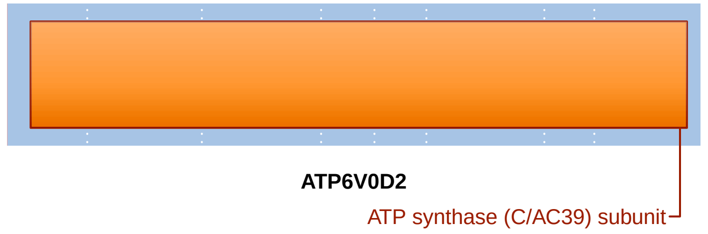
**SUPPORTING READ COUNT**

Split reads = 17
Discordant mates = 0



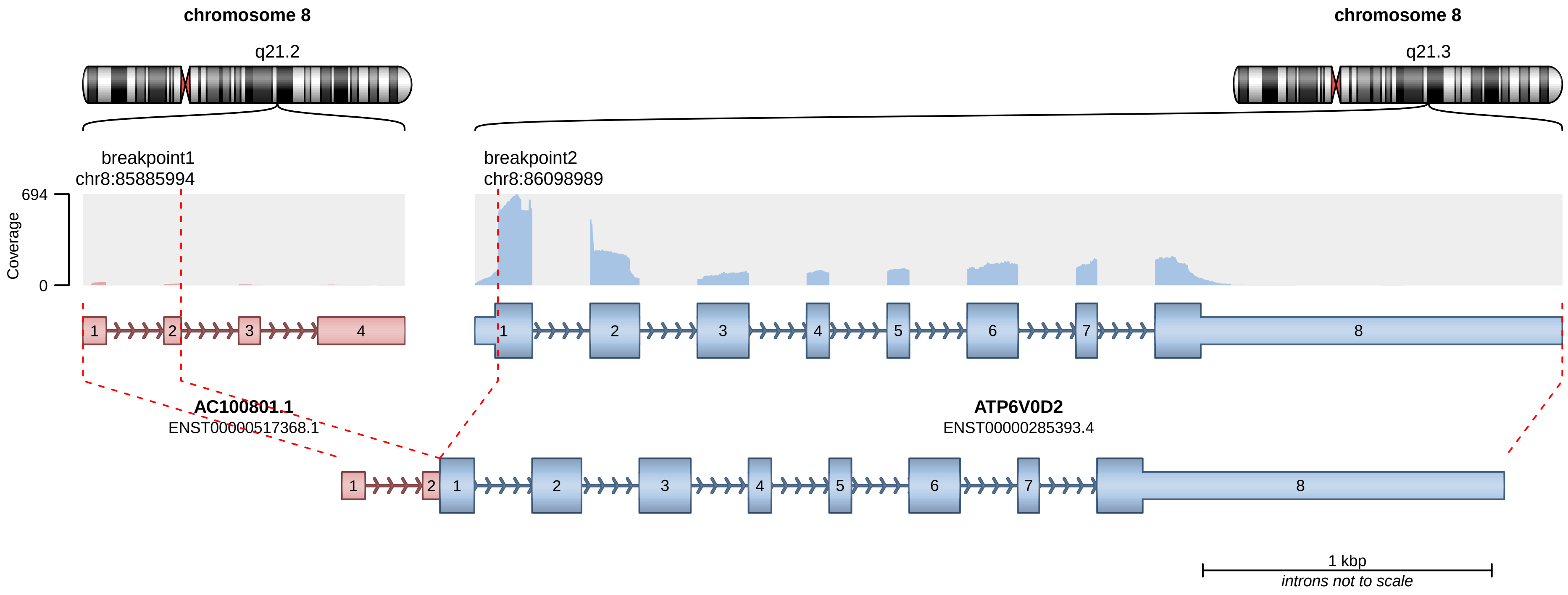


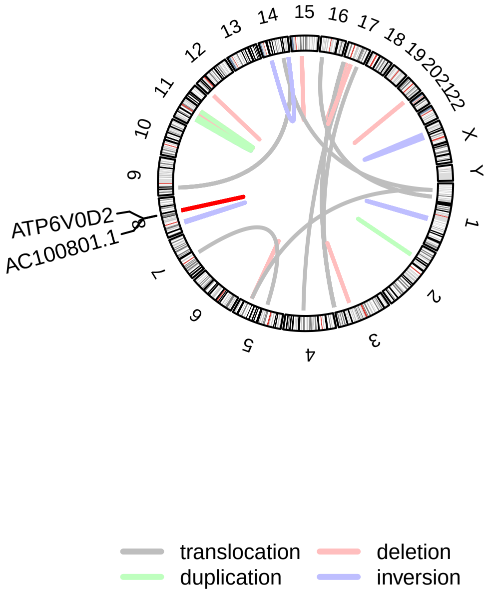
**RETAINED PROTEIN DOMAINS**
reading frame unclear



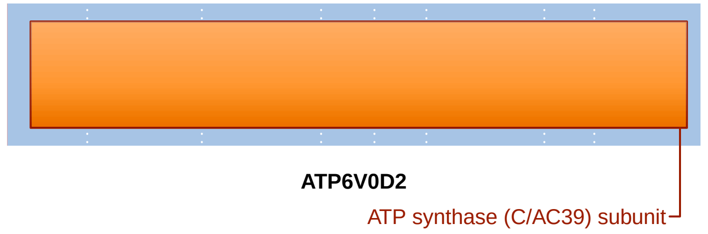
**SUPPORTING READ COUNT**

Split reads = 14
Discordant mates = 0



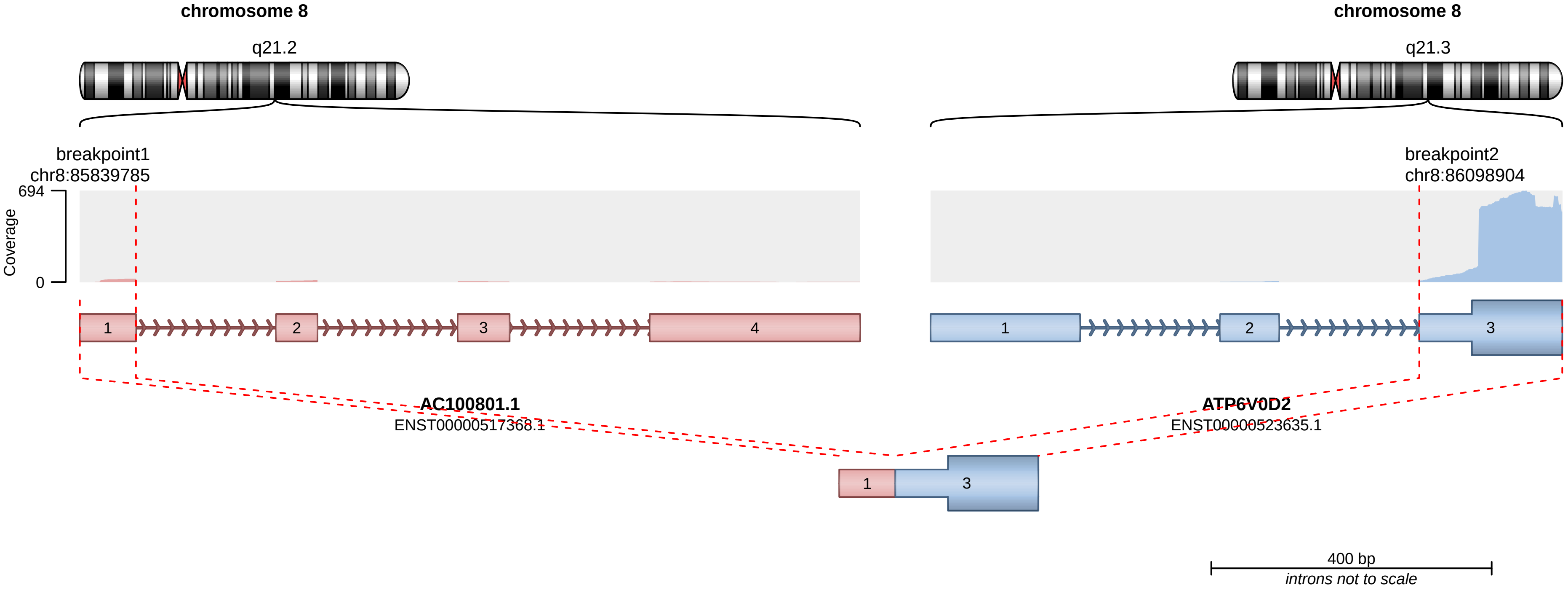


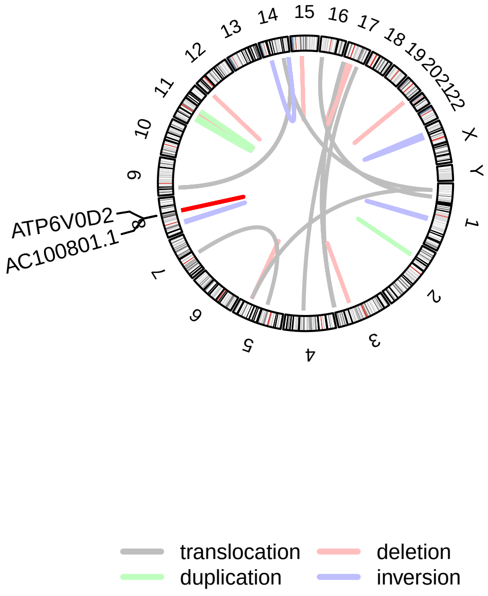
**RETAINED PROTEIN DOMAINS**
reading frame unclear



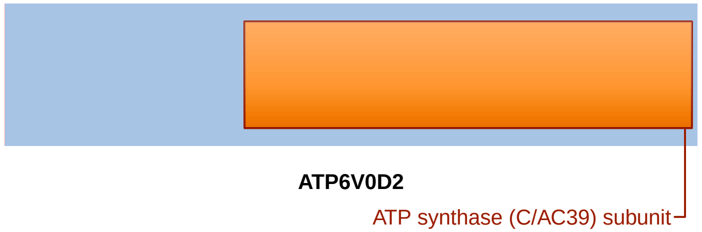
**SUPPORTING READ COUNT**

Split reads = 3
Discordant mates = 0



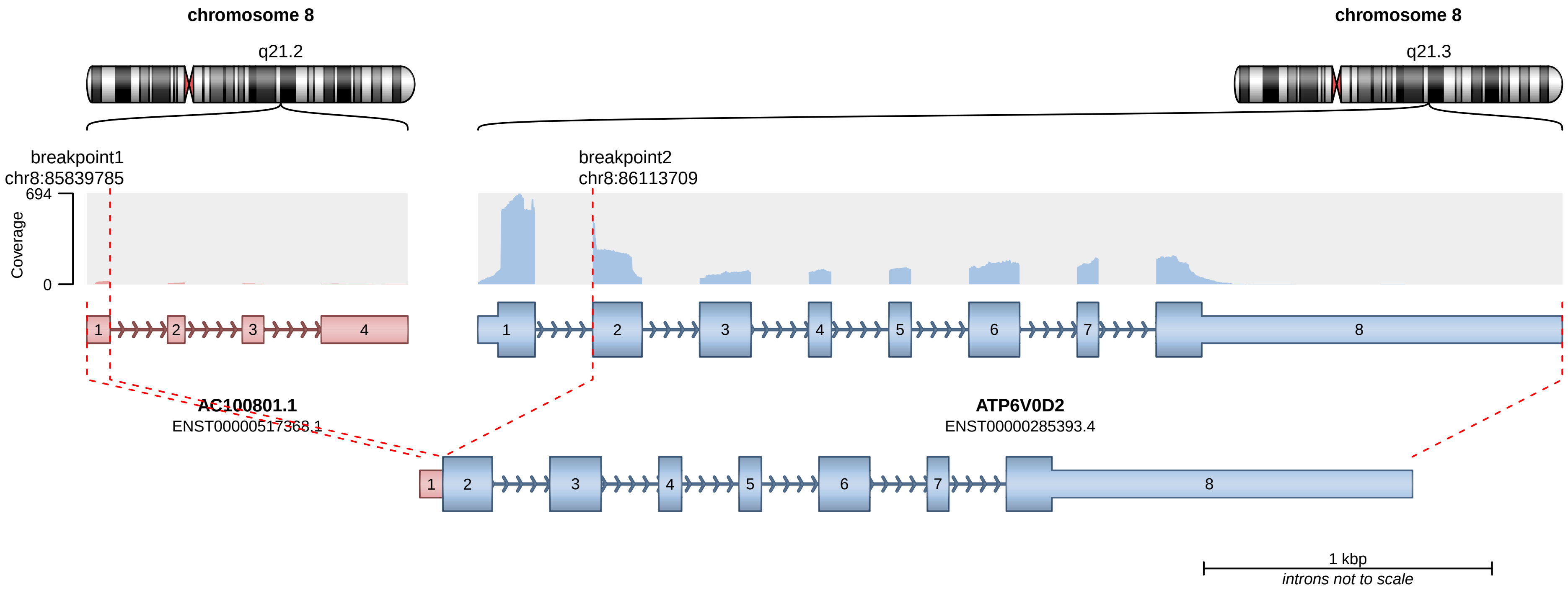


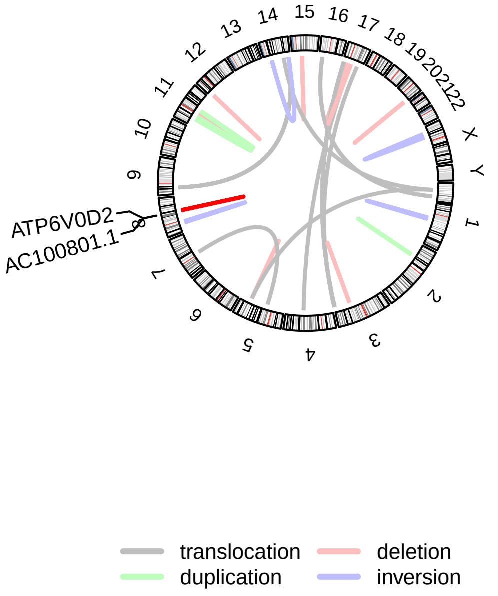
**RETAINED PROTEIN DOMAINS**
reading frame unclear

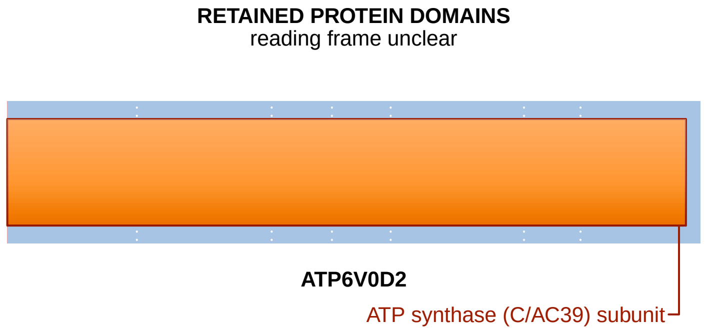


**SUPPORTING READ COUNT**

Split reads = 2
Discordant mates = 0

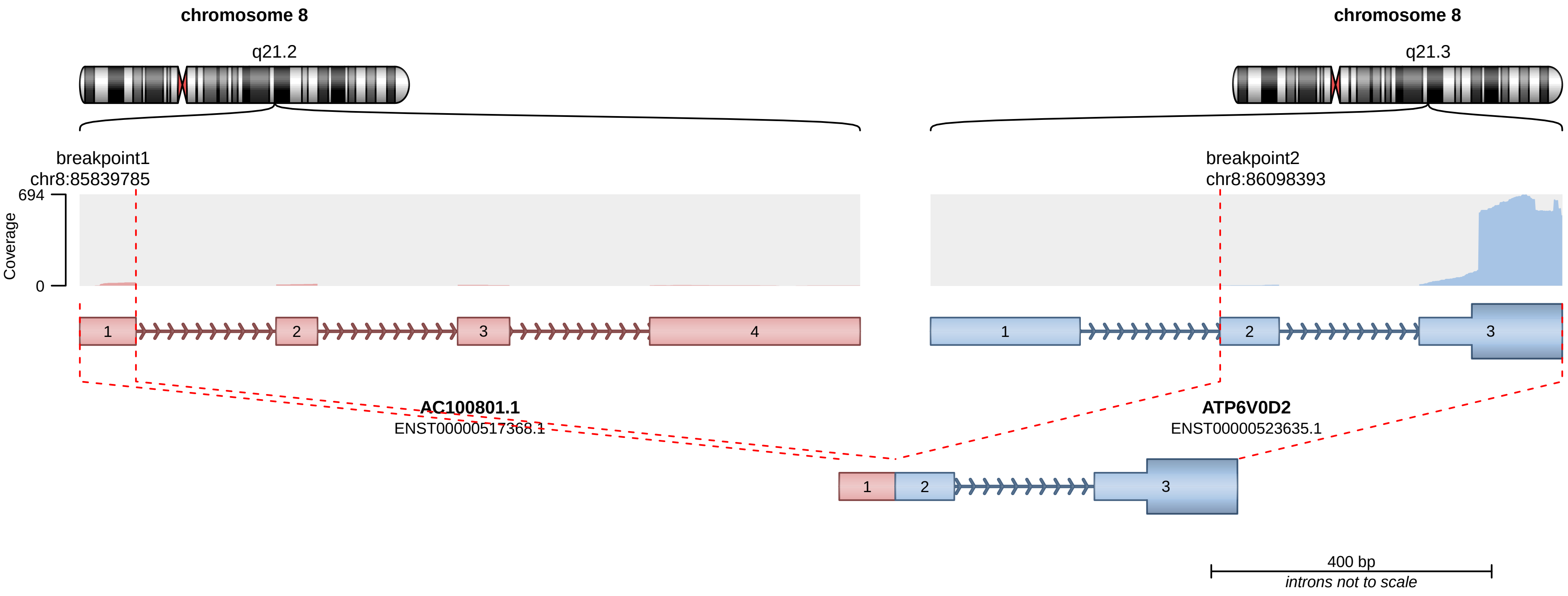


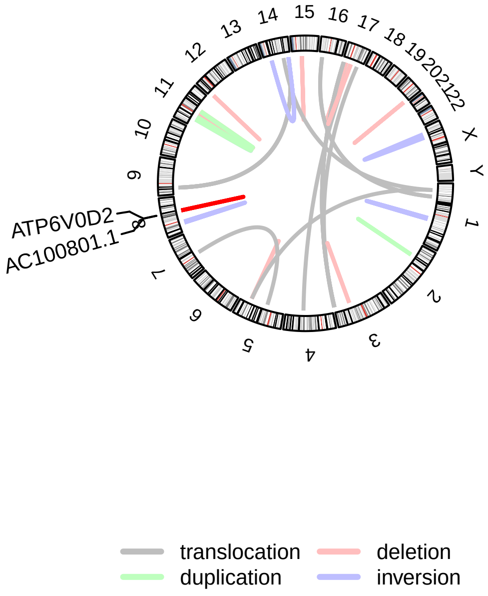




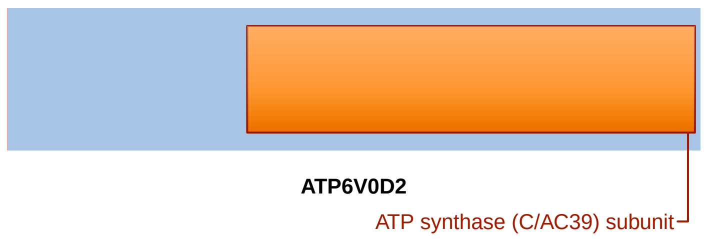
**SUPPORTING READ COUNT**

Split reads = 1
Discordant mates = 0



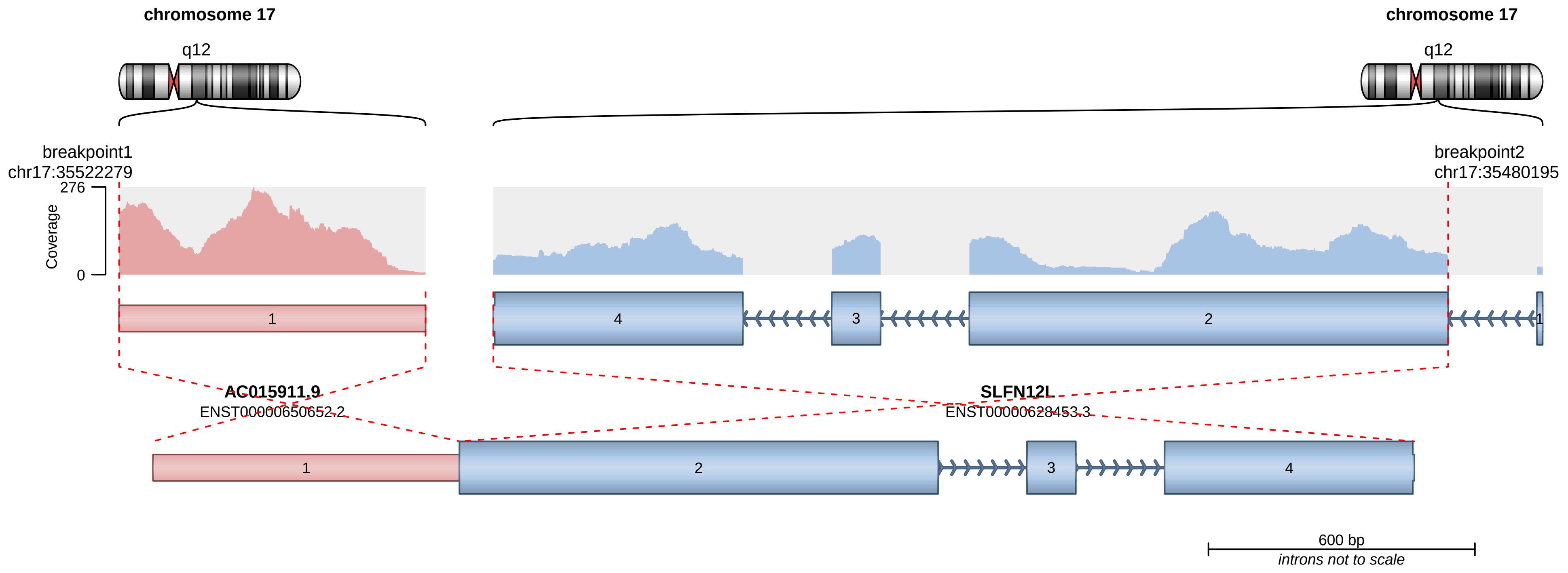


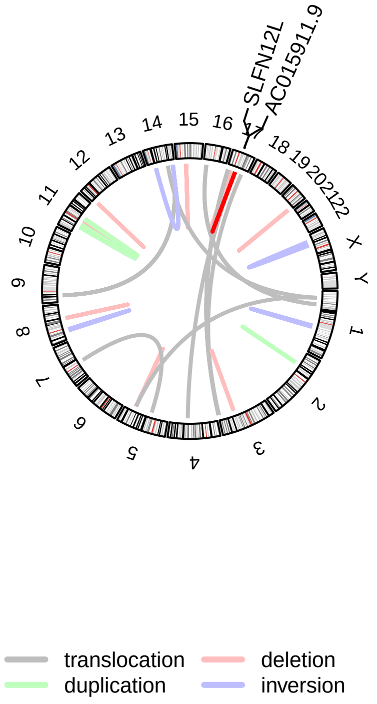
**RETAINED PROTEIN DOMAINS**
reading frame unclear



**SUPPORTING READ COUNT**

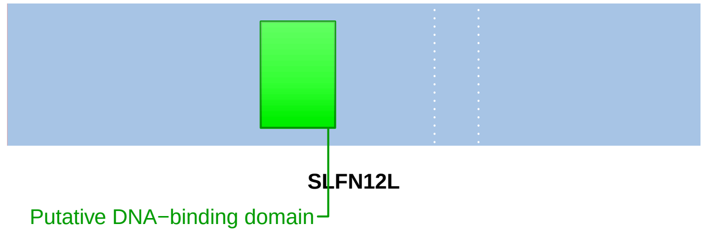
Split reads = 1
Discordant mates = 0





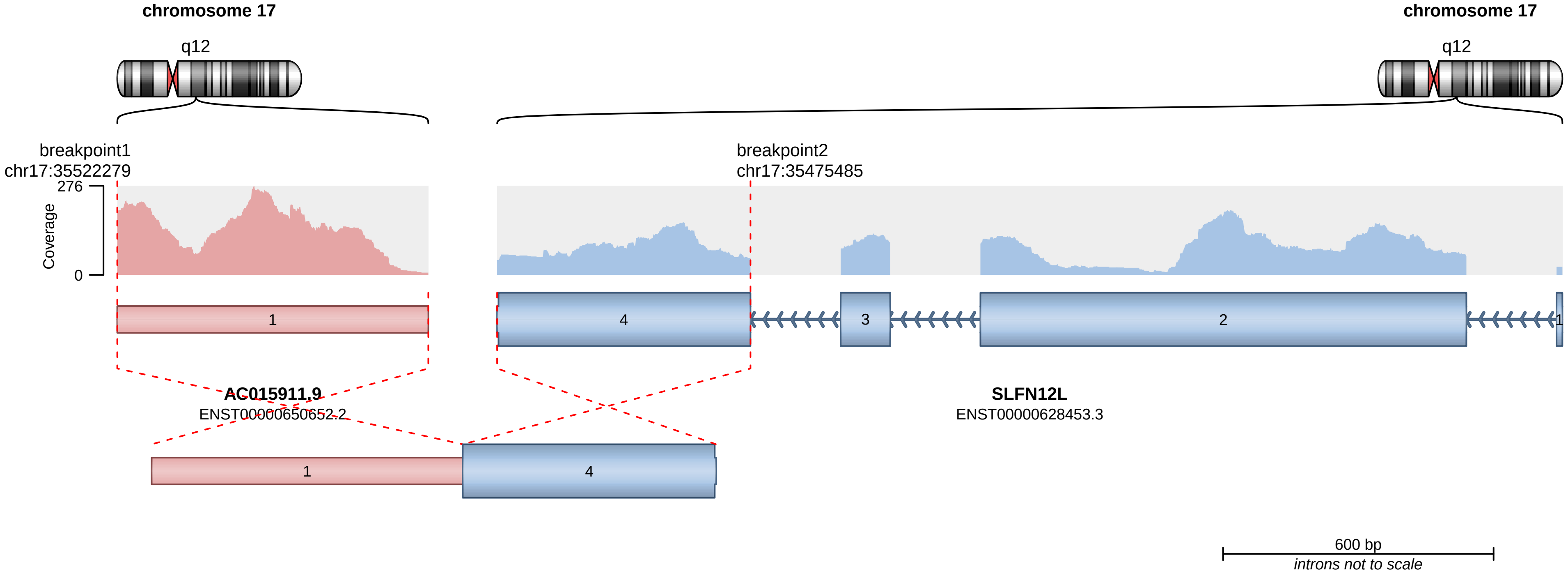
### RETAINED PROTEIN DOMAINS

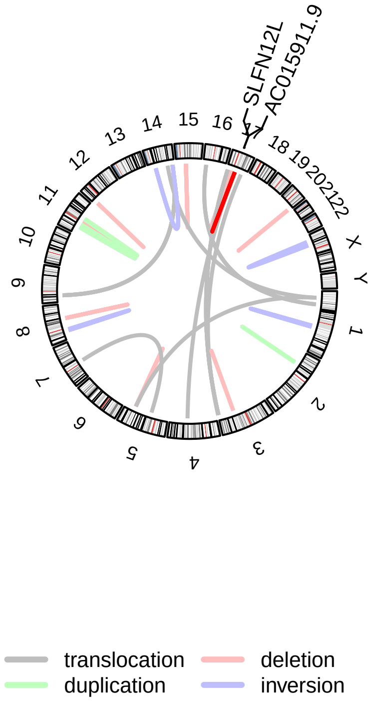
reading frame unclear



**SUPPORTING READ COUNT**

Split reads = 13
Discordant mates = 1

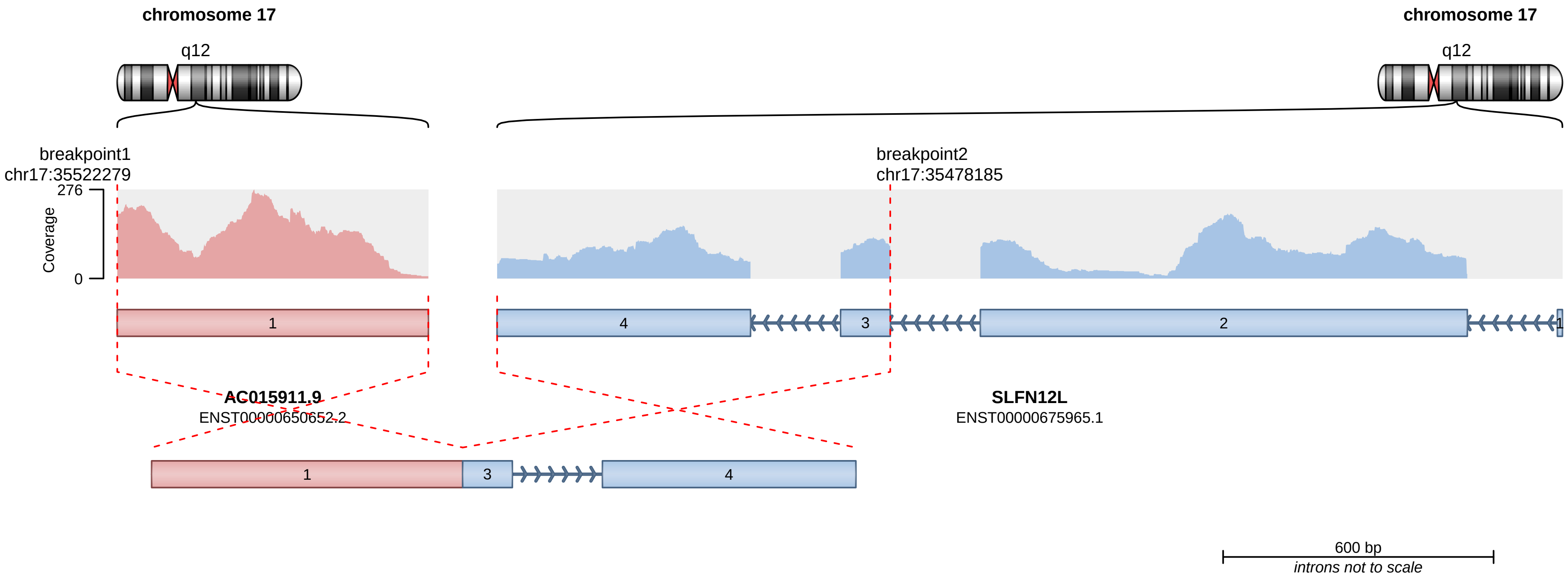


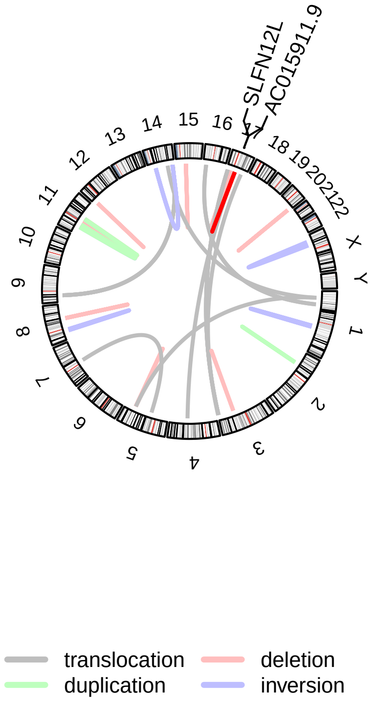


No protein domains retained in fusion.

**SUPPORTING READ COUNT**

Split reads = 1
Discordant mates = 1

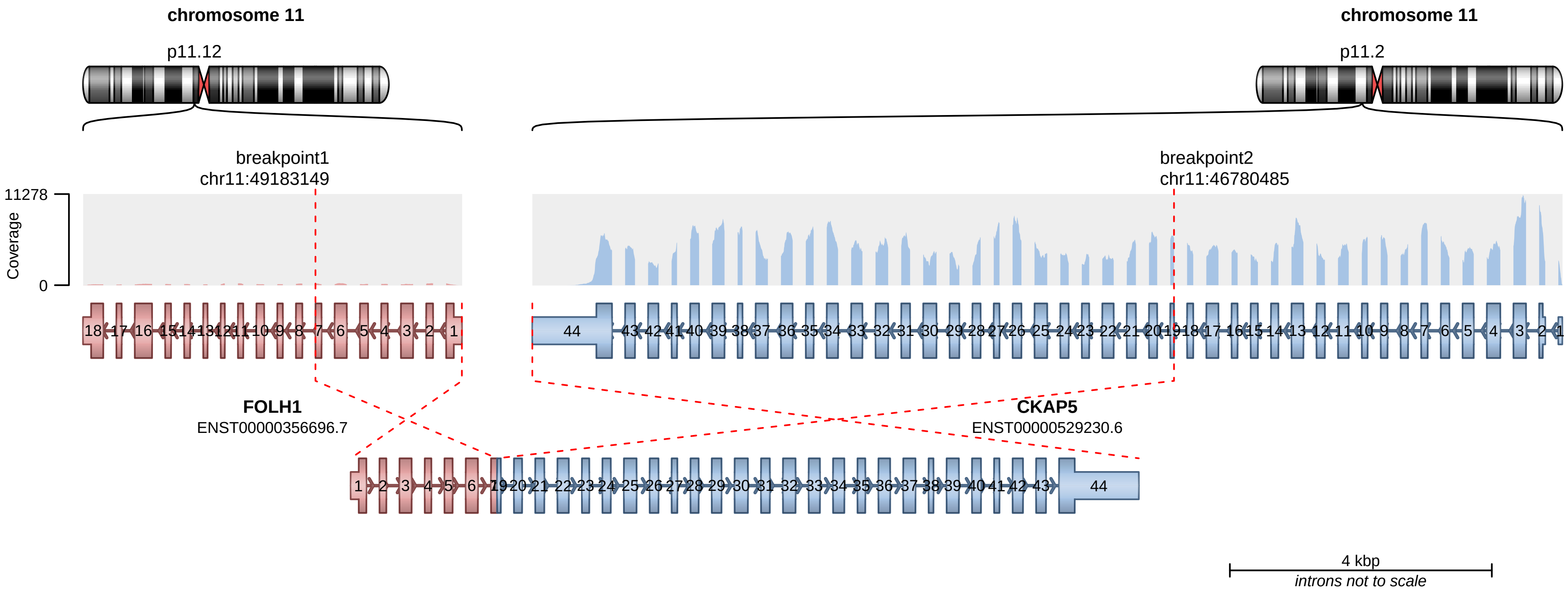


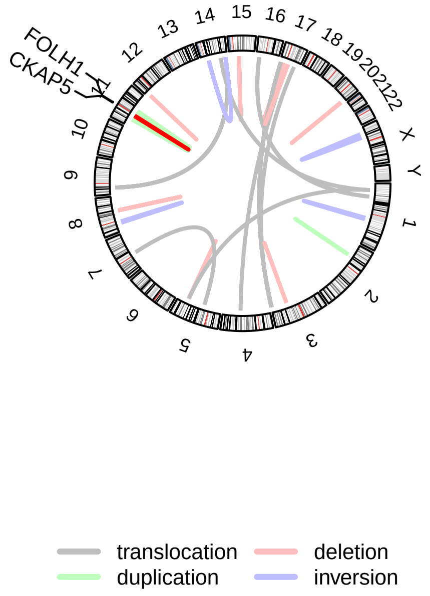


Genes are not protein−coding.

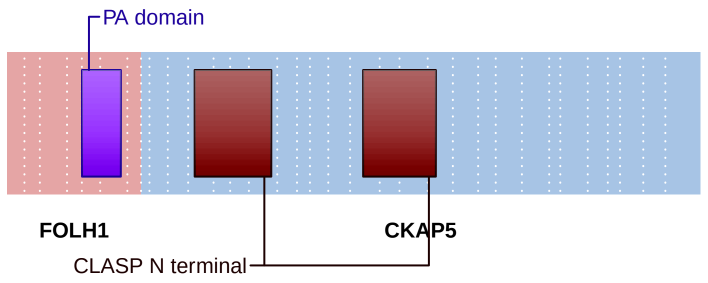
**SUPPORTING READ COUNT**

Split reads = 1
Discordant mates = 1



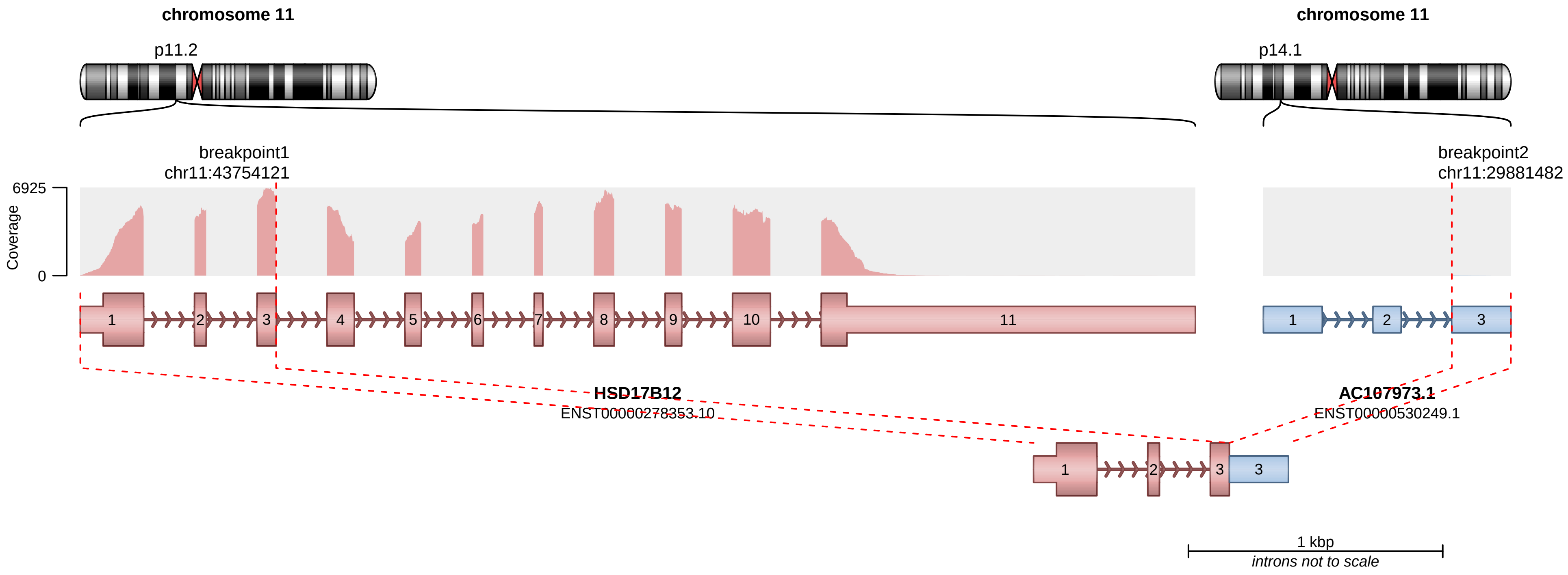


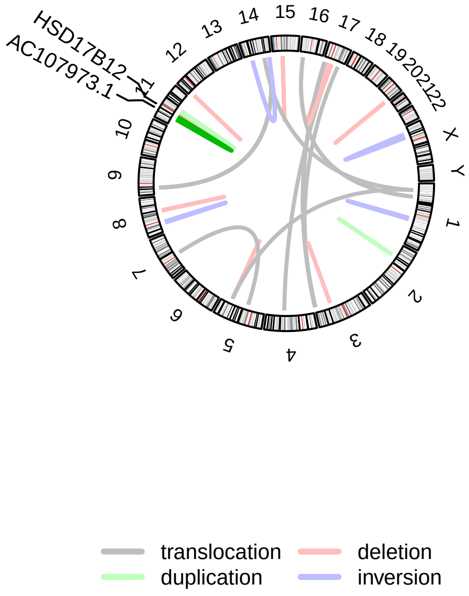
**RETAINED PROTEIN DOMAINS**
reading frame unclear



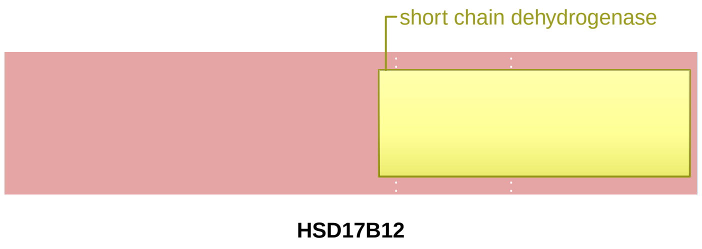
**SUPPORTING READ COUNT**

Split reads = 13
Discordant mates = 1



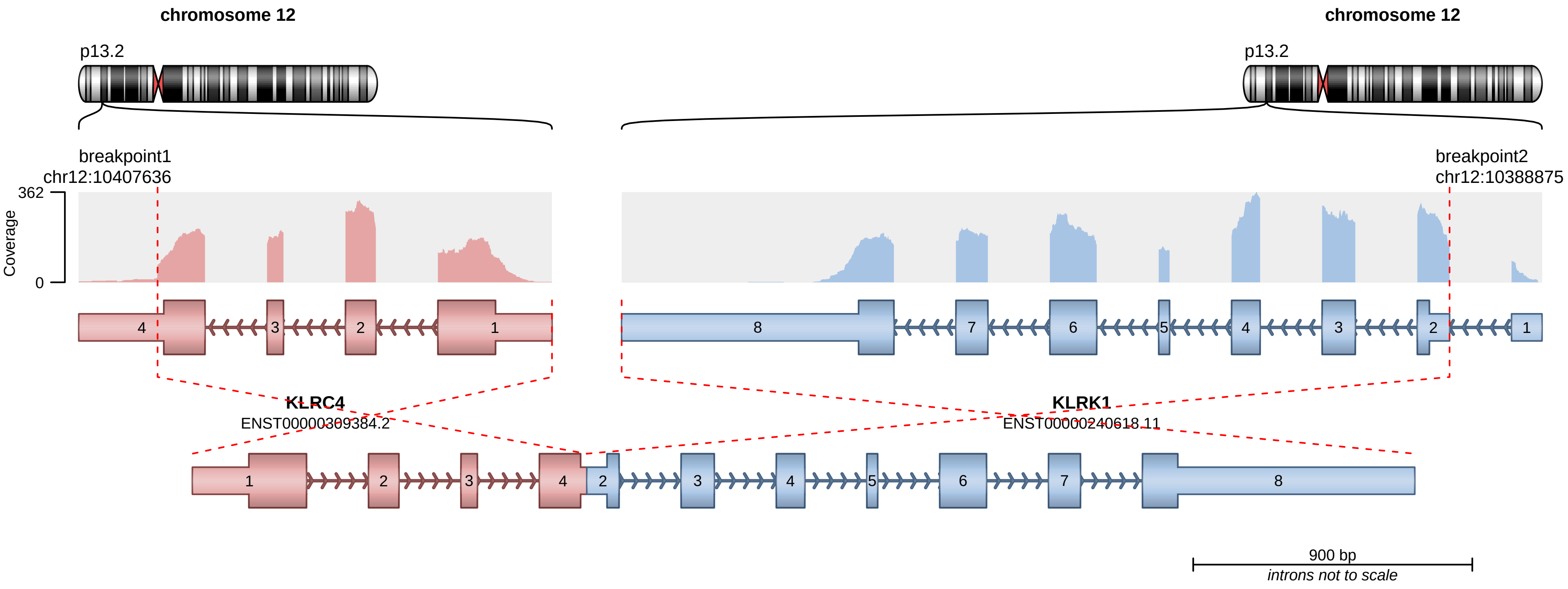


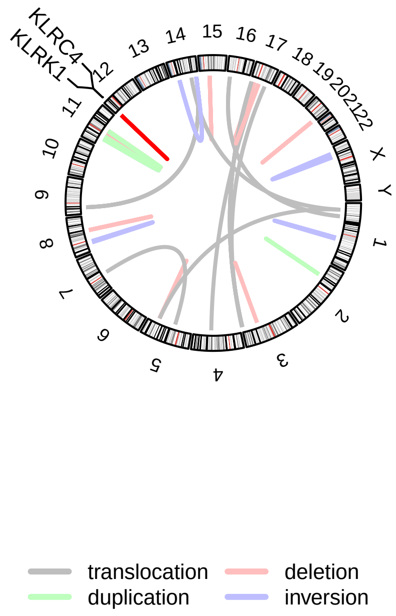
**RETAINED PROTEIN DOMAINS**
reading frame unclear



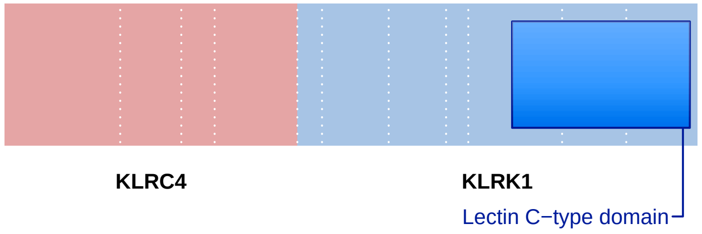
**SUPPORTING READ COUNT**

Split reads = 12
Discordant mates = 1



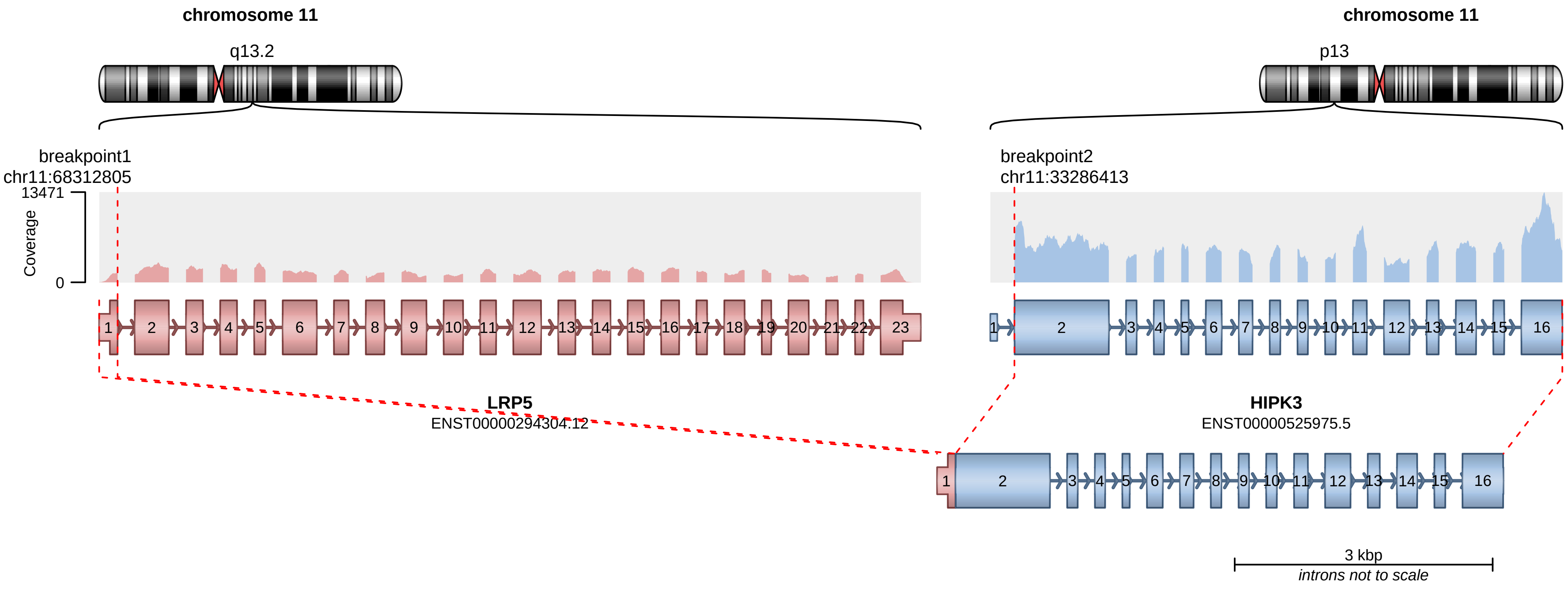


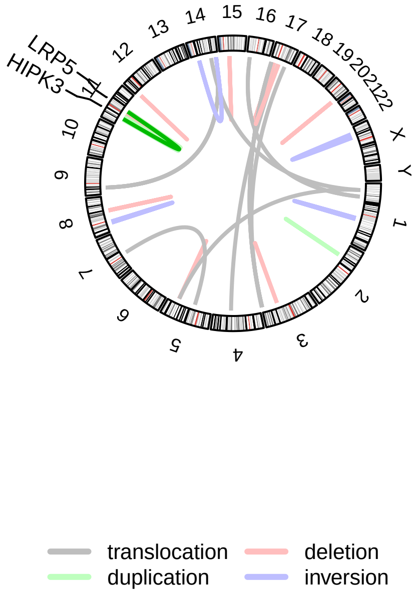
**RETAINED PROTEIN DOMAINS**
reading frame unclear

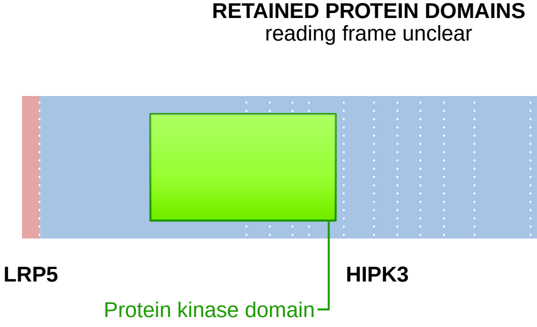


**SUPPORTING READ COUNT**

Split reads = 12
Discordant mates = 0

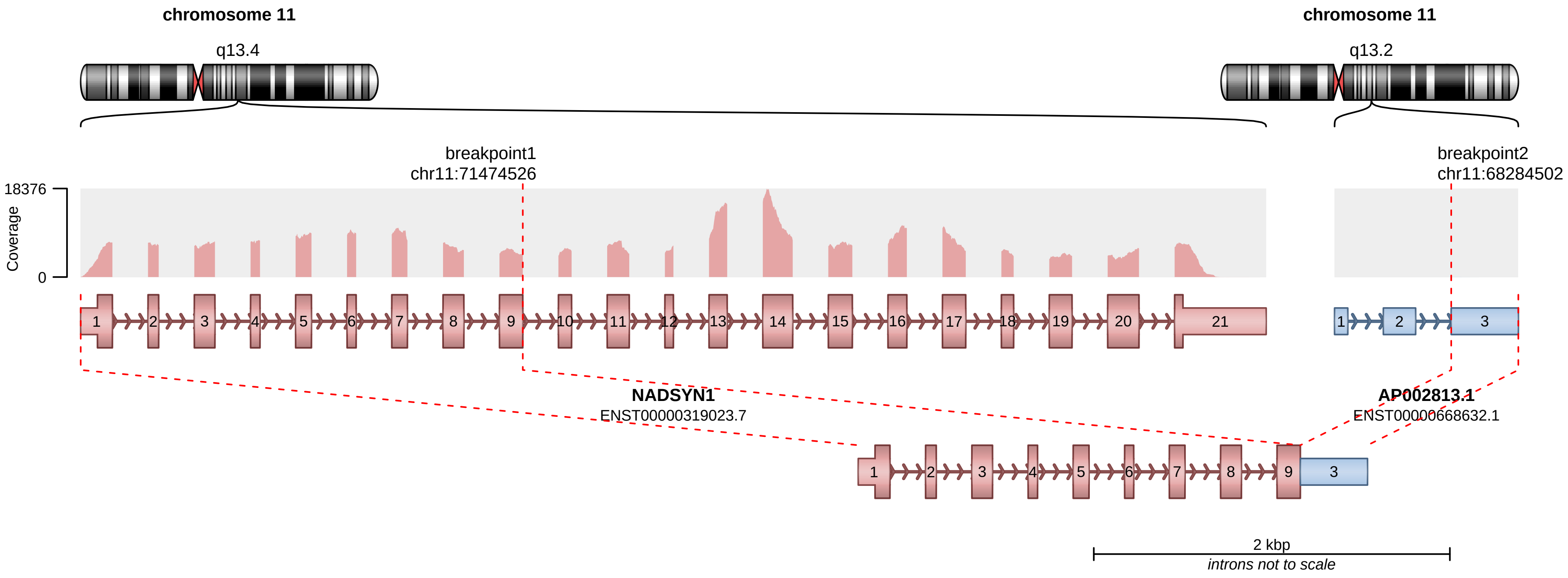


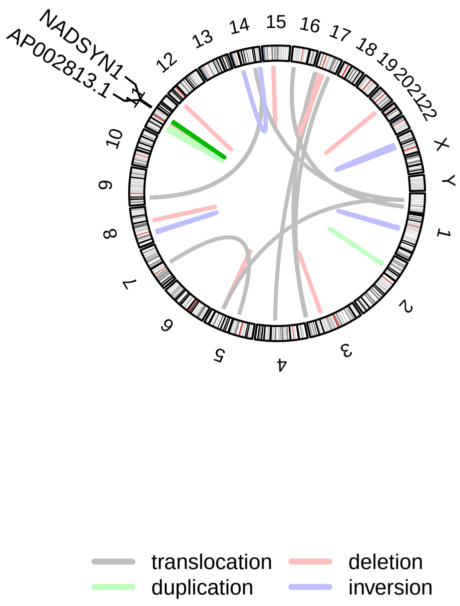




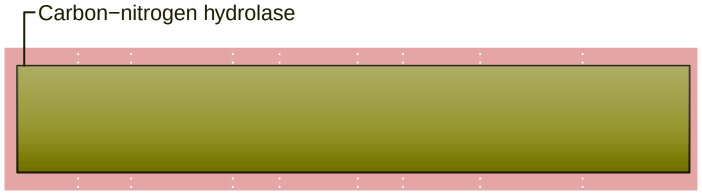
**SUPPORTING READ COUNT**

Split reads = 12
Discordant mates = 0





**RETAINED PROTEIN DOMAINS**
reading frame unclear



**NADSYN1**

**SUPPORTING READ COUNT**

Split reads = 10
Discordant mates = 0