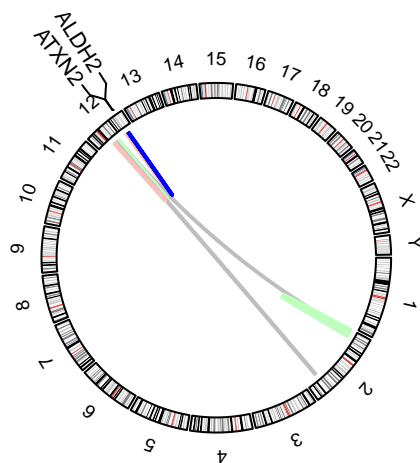
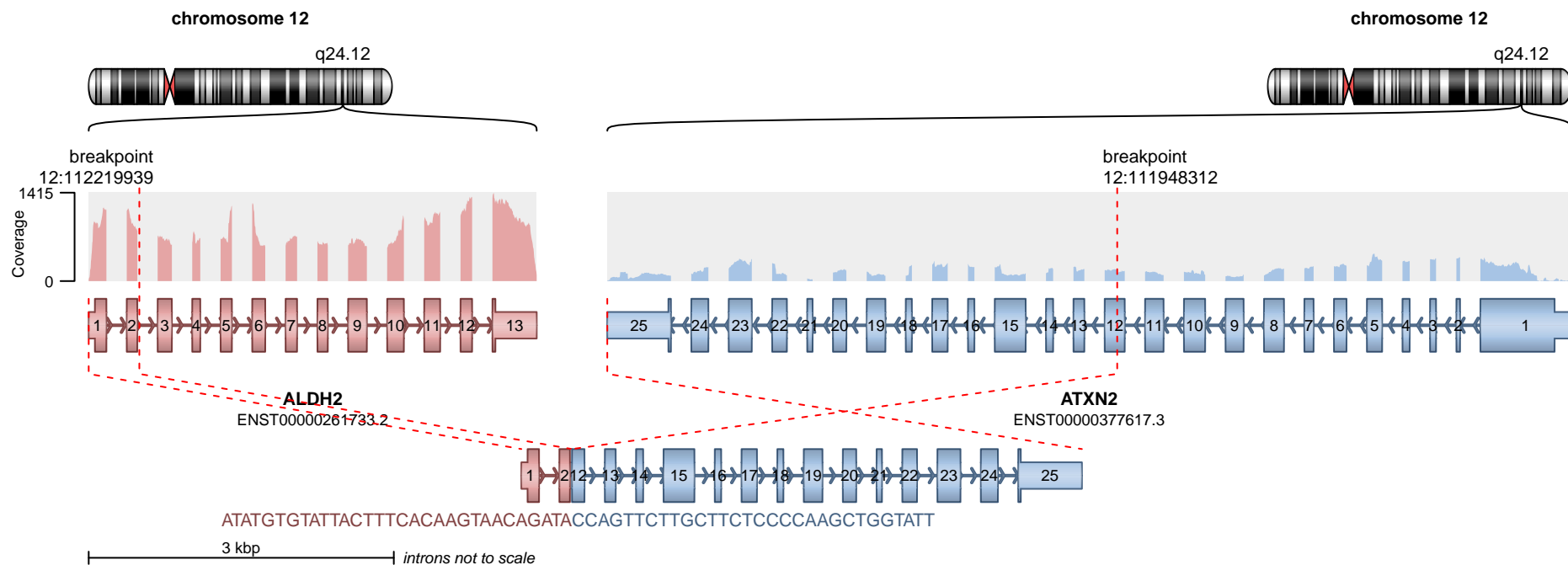


— translocation — deletion
— duplication — inversion

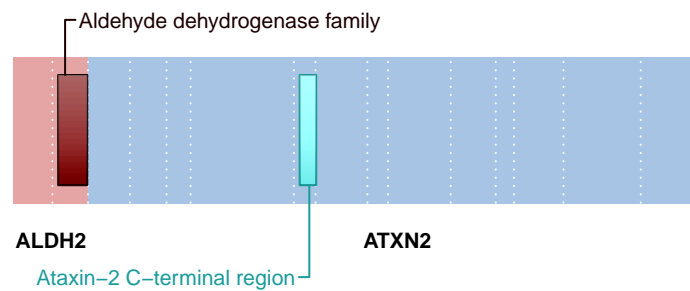
Genes are not protein-coding.

SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 62



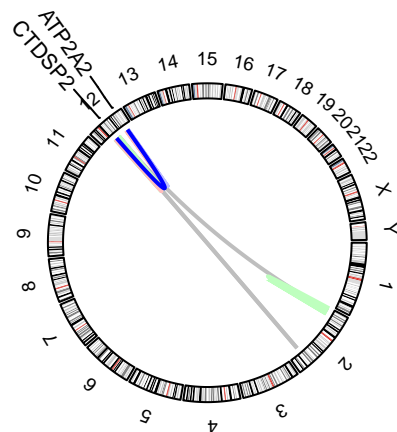
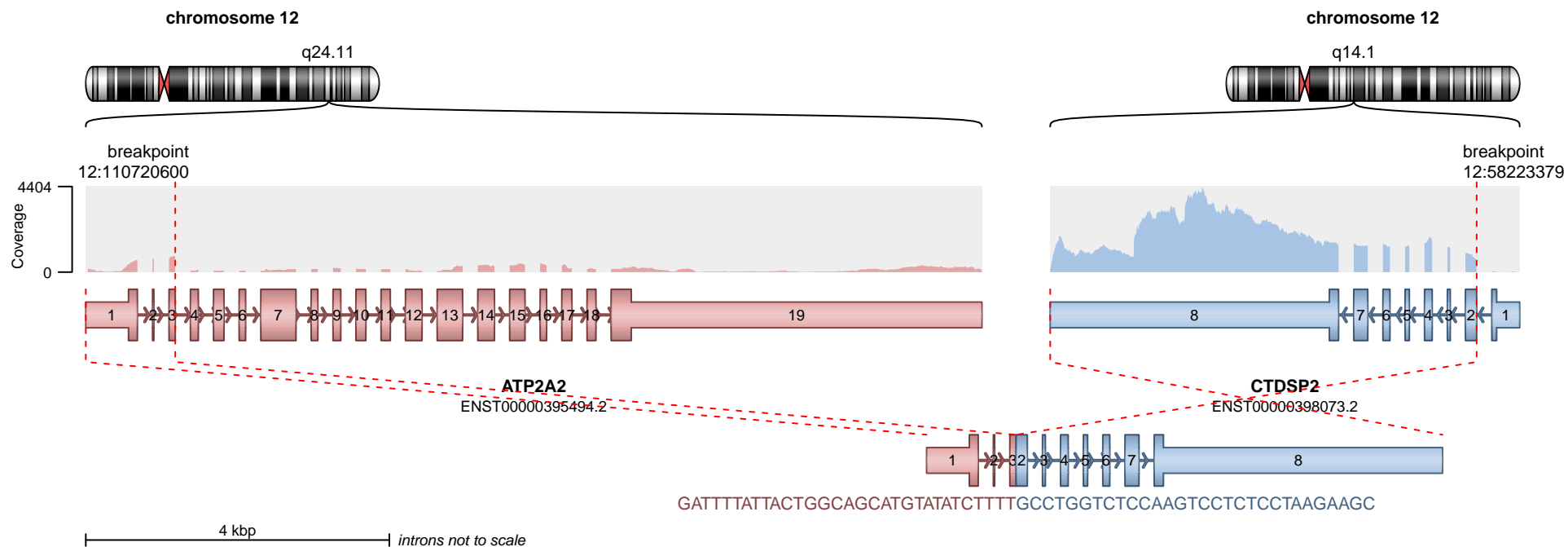
RETAINED PROTEIN DOMAINS out-of-frame fusion



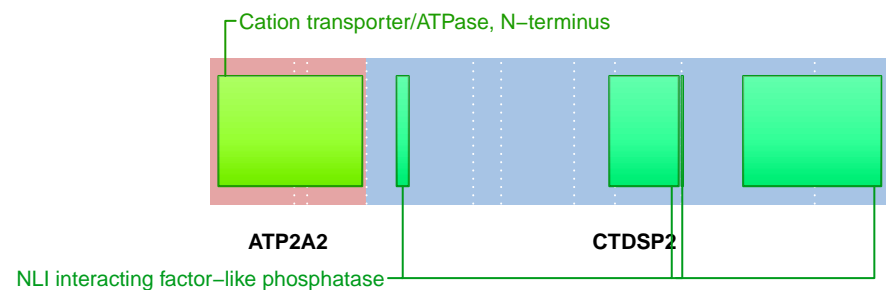
SUPPORTING READ COUNT

Split reads = 37
Discordant mates = 17

translocation deletion
duplication inversion



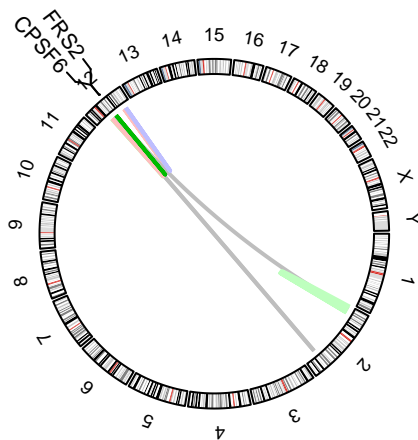
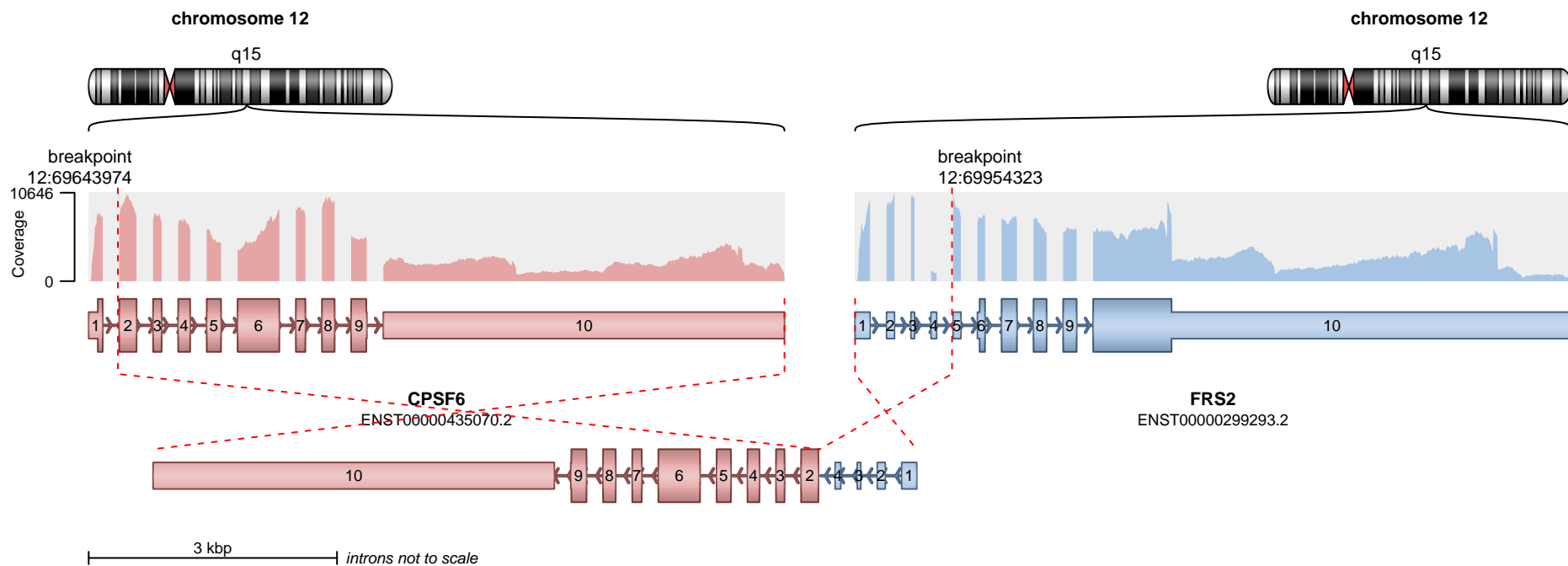
RETAINED PROTEIN DOMAINS out-of-frame fusion



SUPPORTING READ COUNT

Split reads = 264
Discordant mates = 238

translocation deletion
duplication inversion

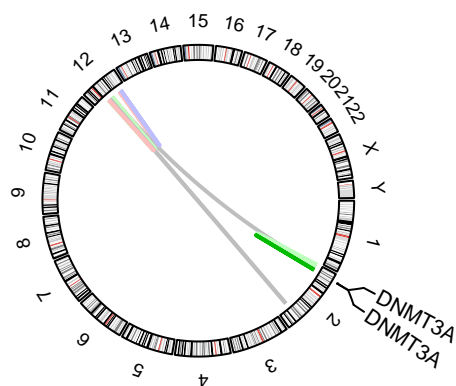
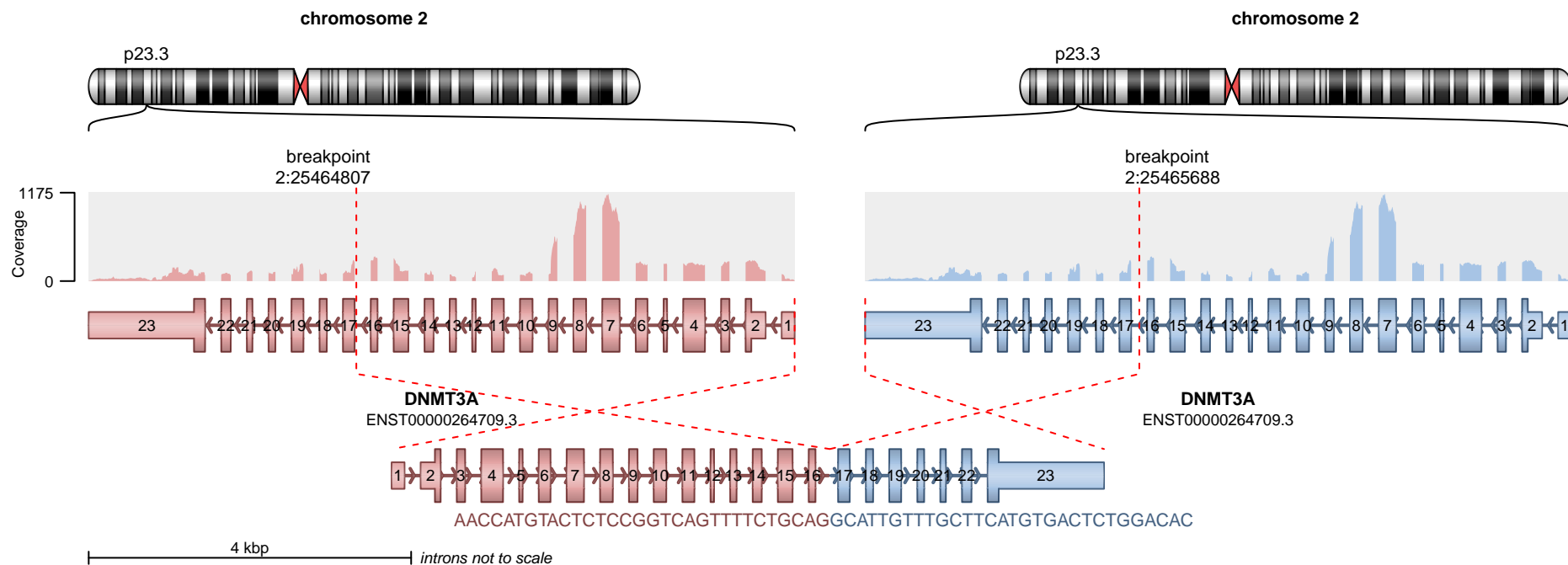


translocation deletion
duplication inversion

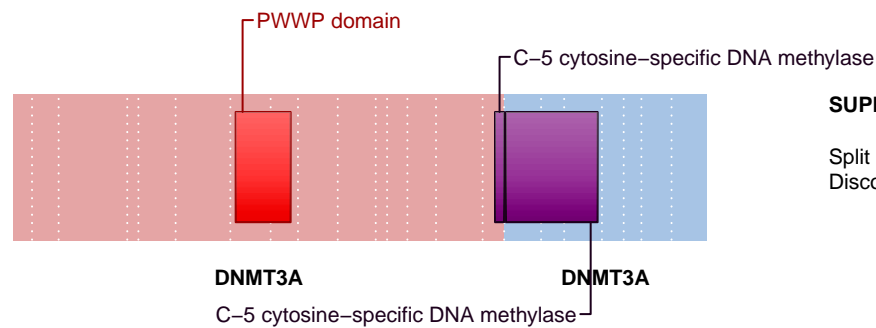
No coding regions due to antisense transcription.

SUPPORTING READ COUNT

Split reads = 31
Discordant mates = 110



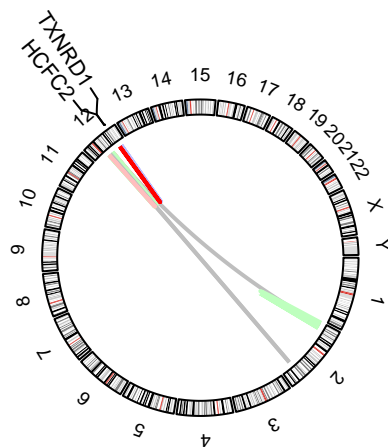
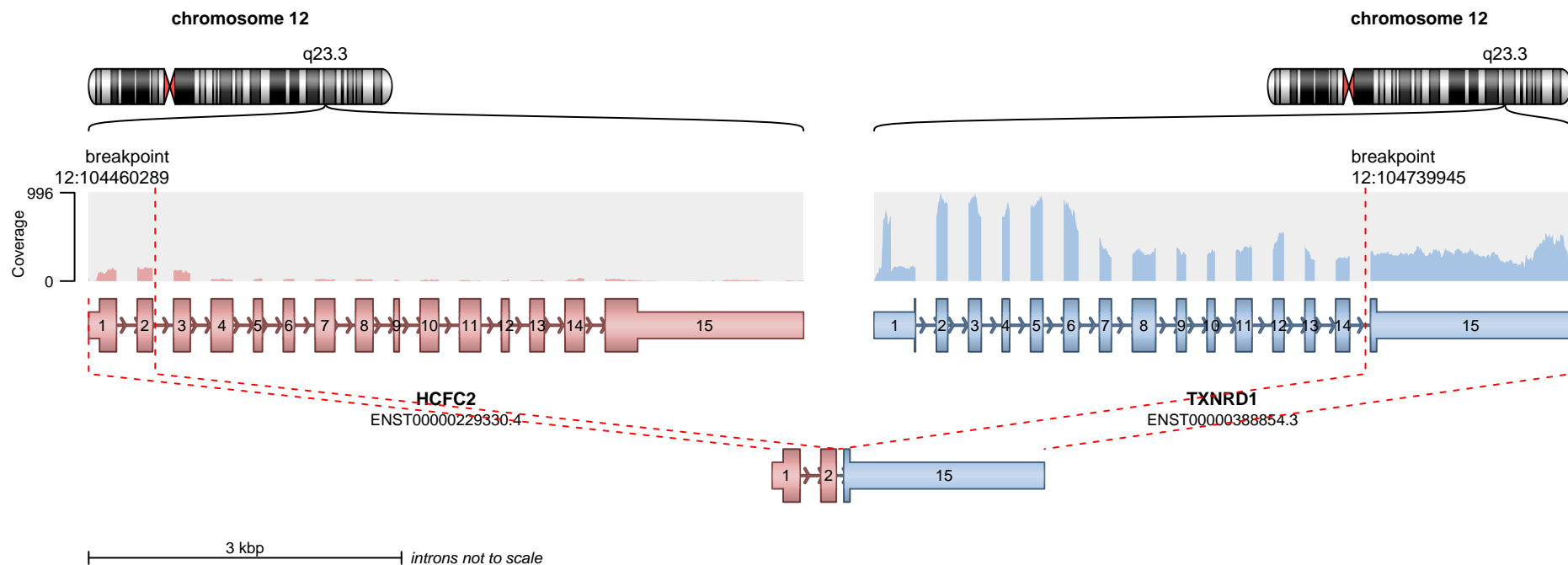
RETAINED PROTEIN DOMAINS reading frame unclear



SUPPORTING READ COUNT

Split reads = 18
Discordant mates = 14

translocation deletion
duplication inversion

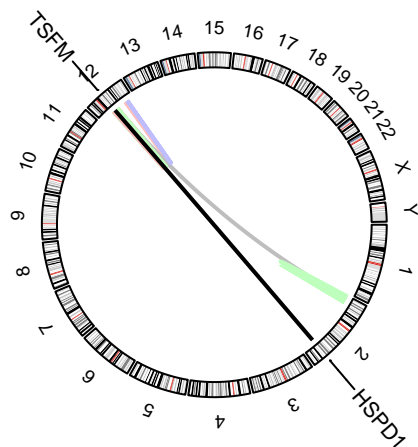
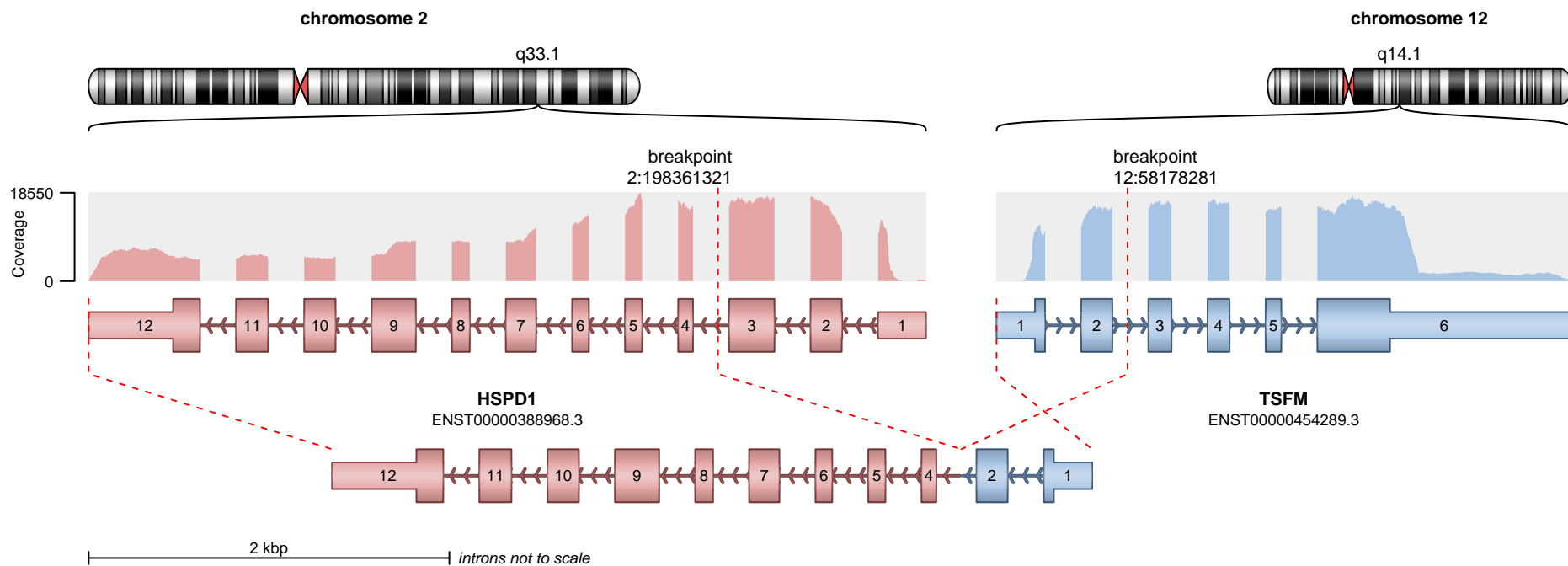


translocation deletion
duplication inversion

No coding regions due to antisense transcription.

SUPPORTING READ COUNT

Split reads = 27
Discordant mates = 26

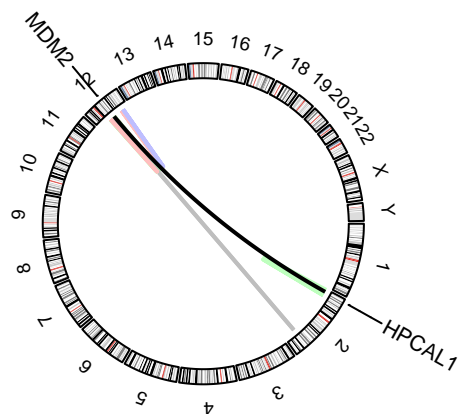
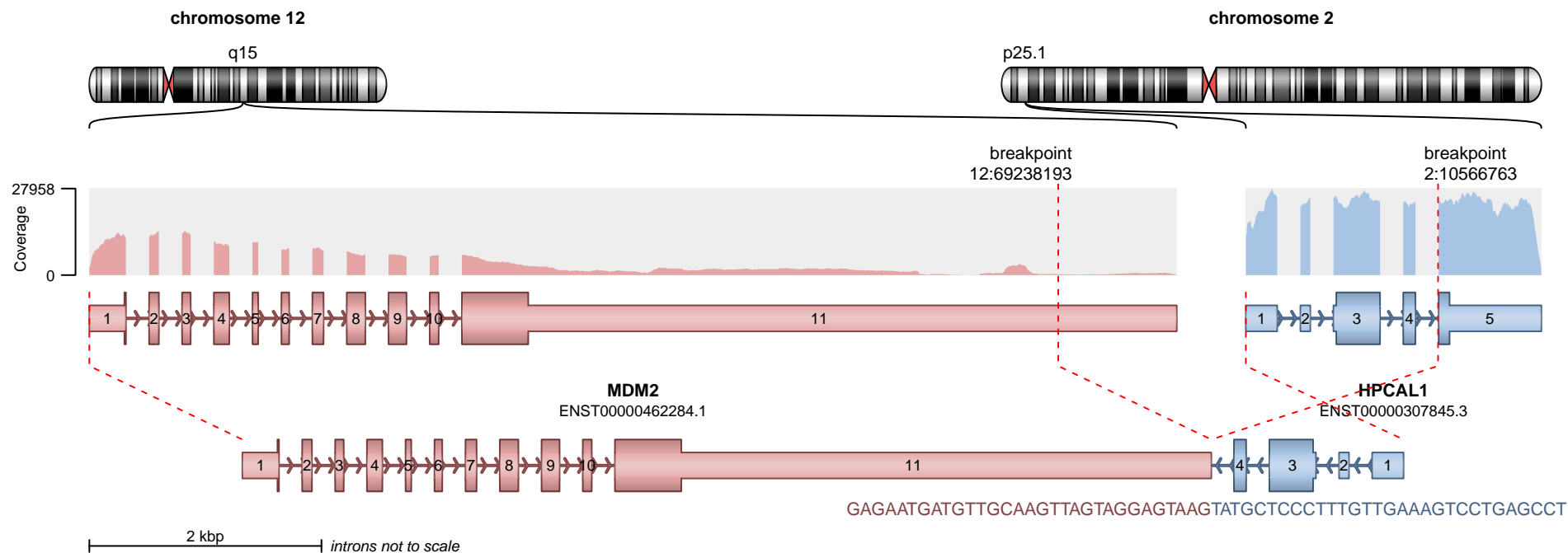


translocation deletion
duplication inversion

No coding regions due to antisense transcription.

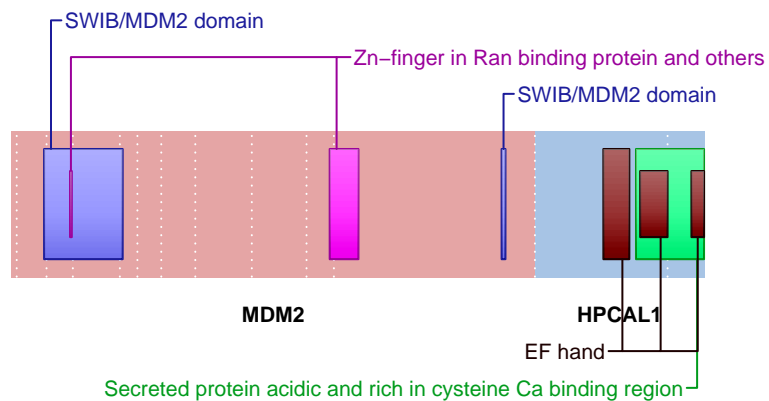
SUPPORTING READ COUNT

Split reads = 31
Discordant mates = 23



RETAINED PROTEIN DOMAINS

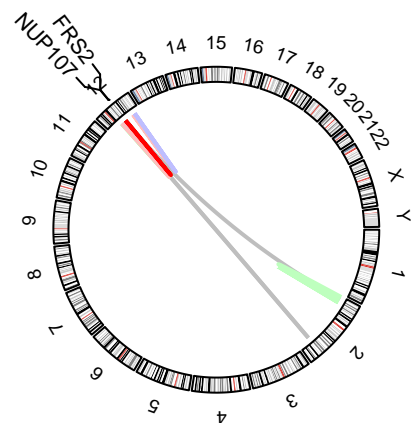
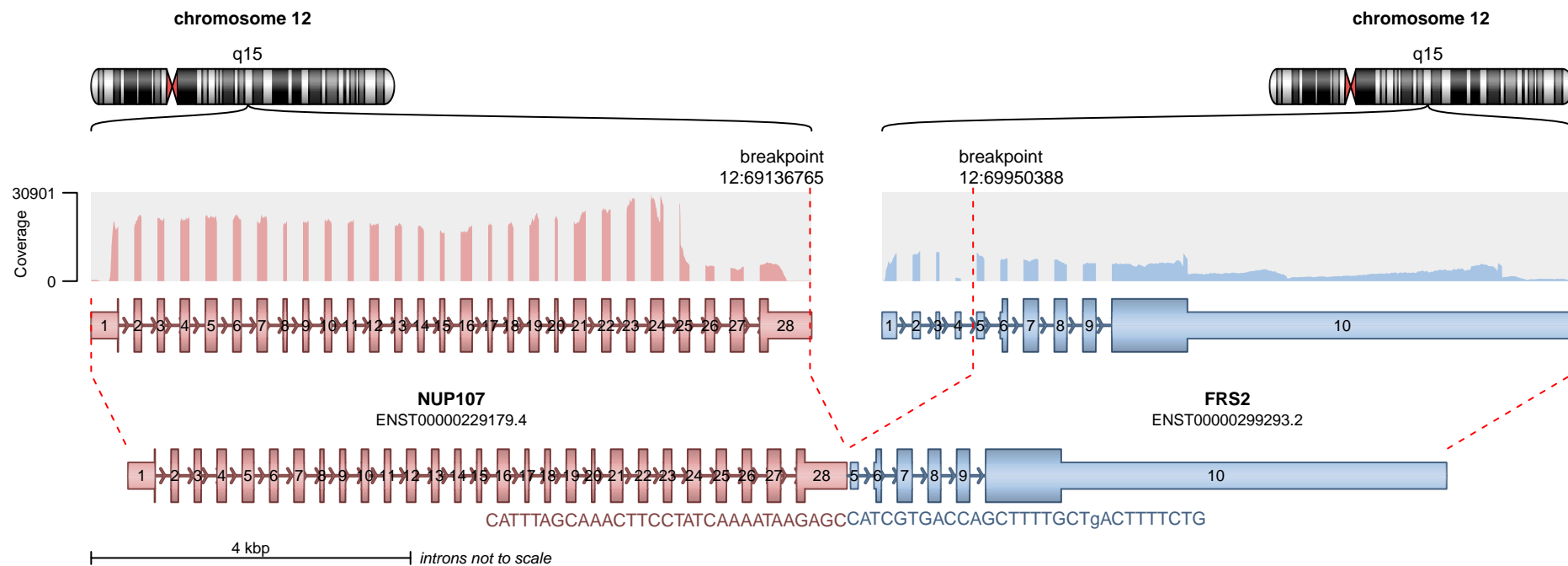
reading frame unclear



SUPPORTING READ COUNT

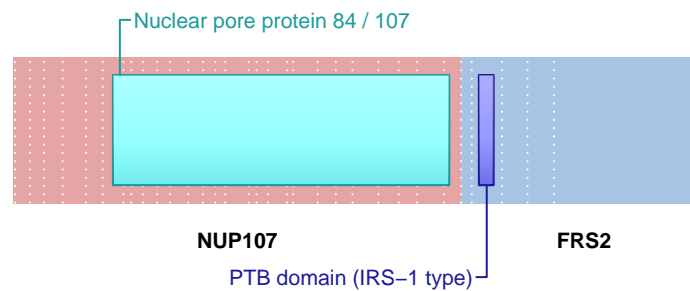
Split reads = 39
Discordant mates = 38

translocation deletion
duplication inversion



RETAINED PROTEIN DOMAINS

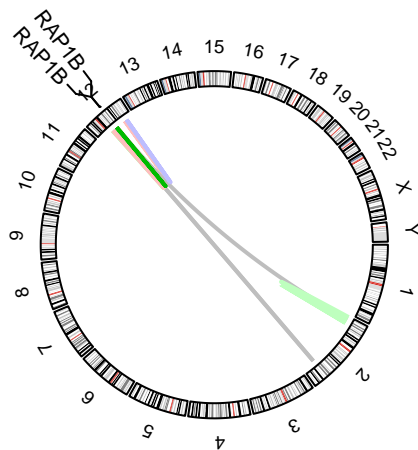
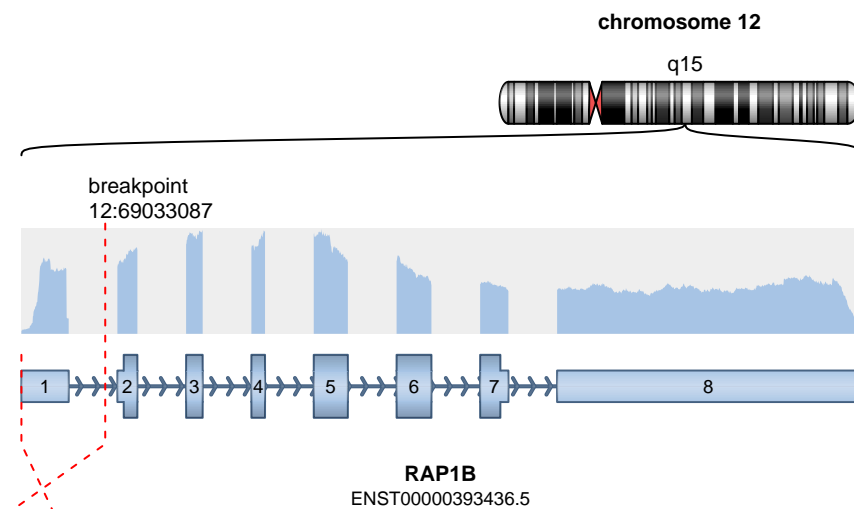
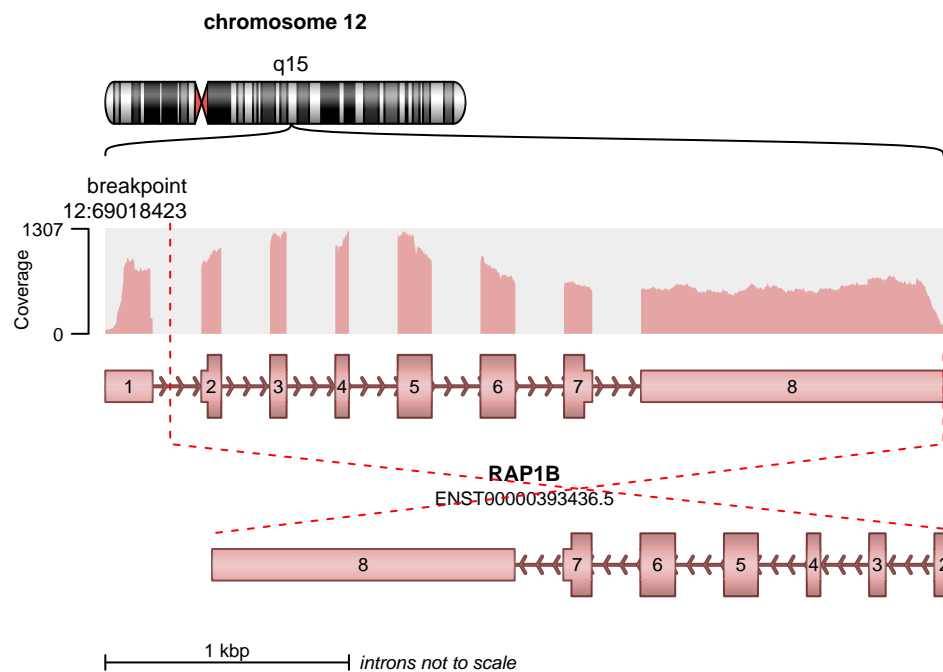
reading frame unclear



SUPPORTING READ COUNT

Split reads = 15
Discordant mates = 13

translocation deletion
duplication inversion

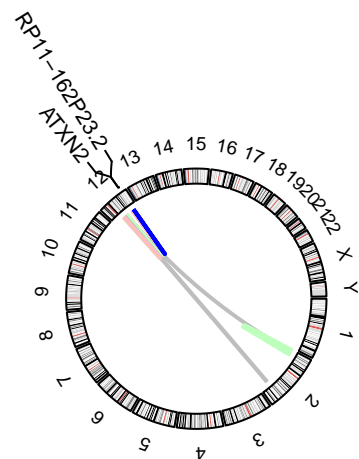
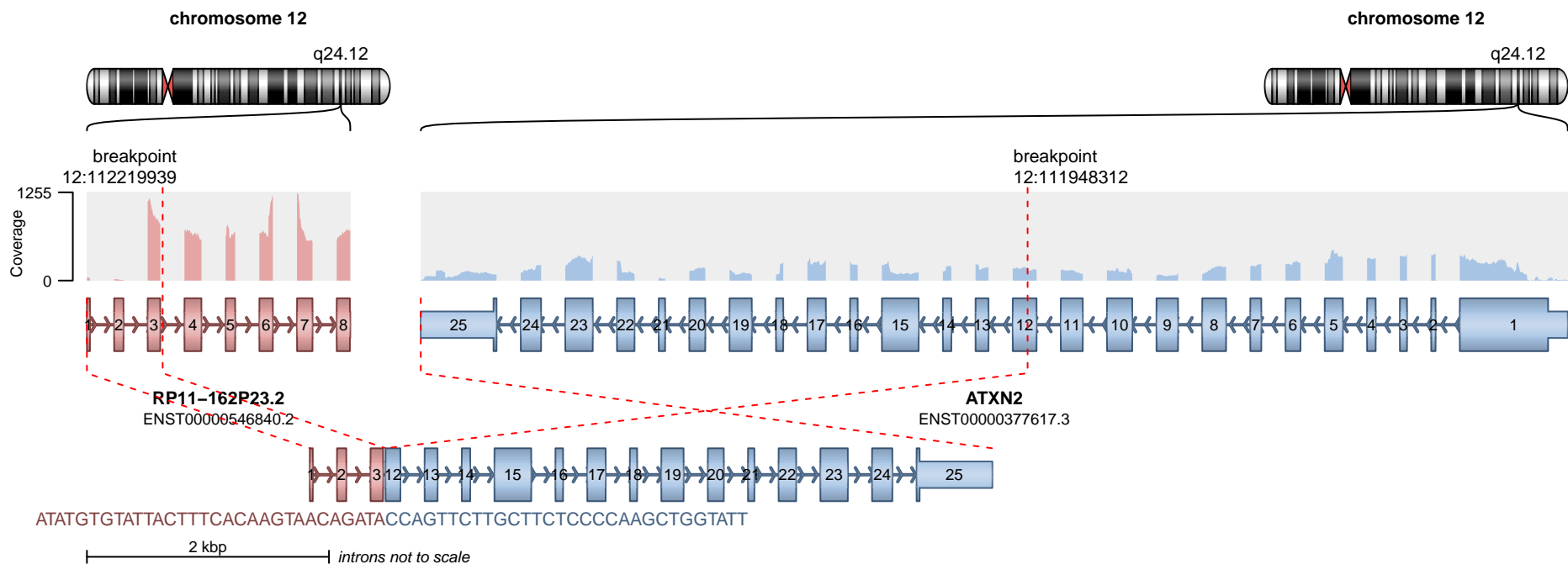


No coding regions due to antisense transcription.

SUPPORTING READ COUNT

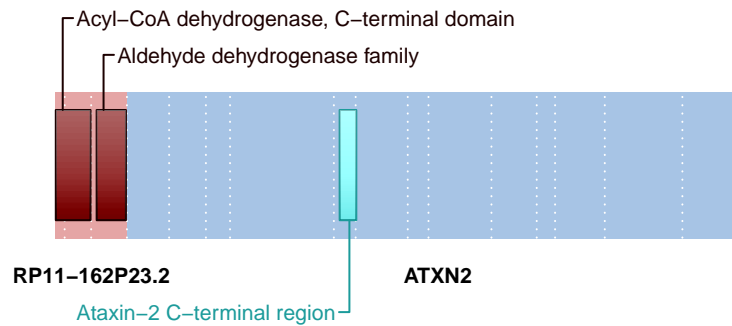
Split reads = 10
Discordant mates = 7

translocation deletion
duplication inversion



RETAINED PROTEIN DOMAINS

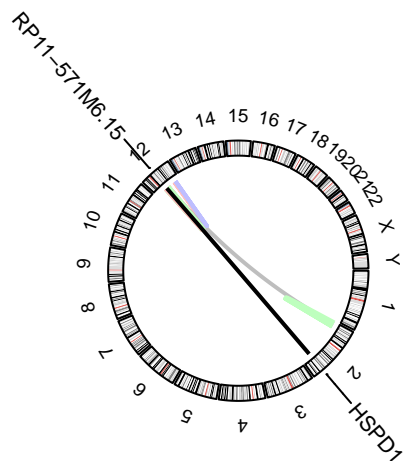
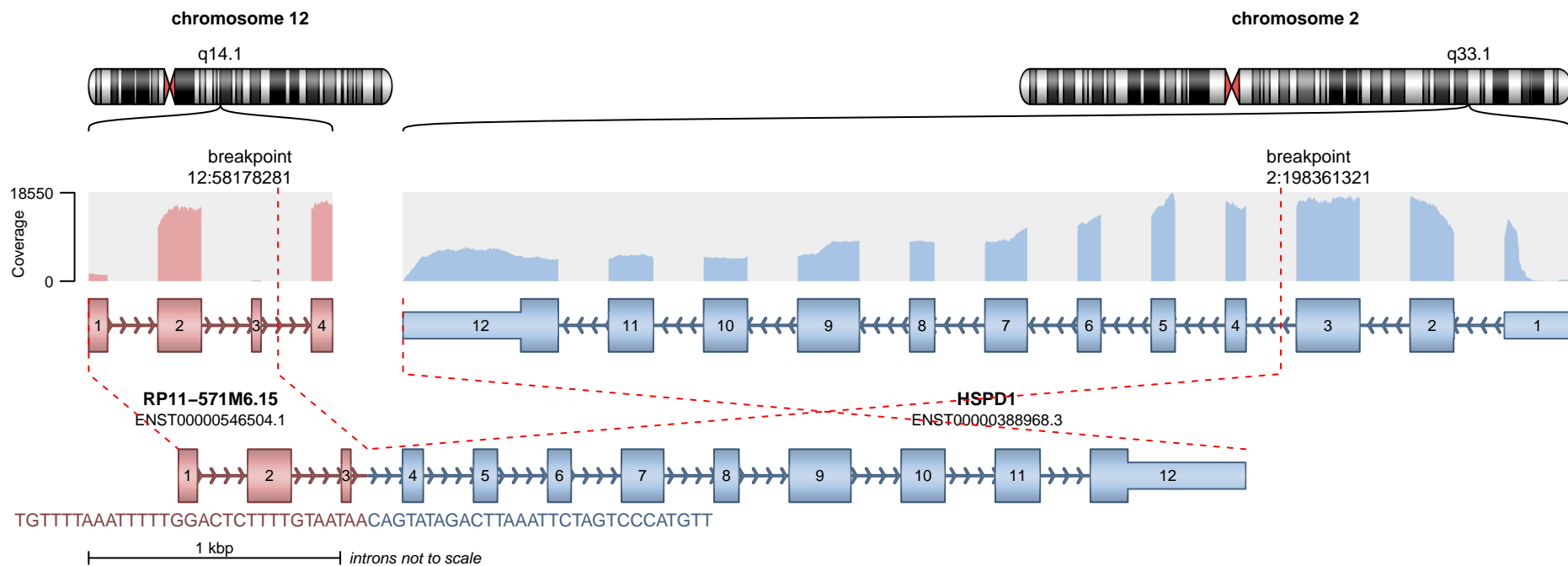
reading frame unclear



SUPPORTING READ COUNT

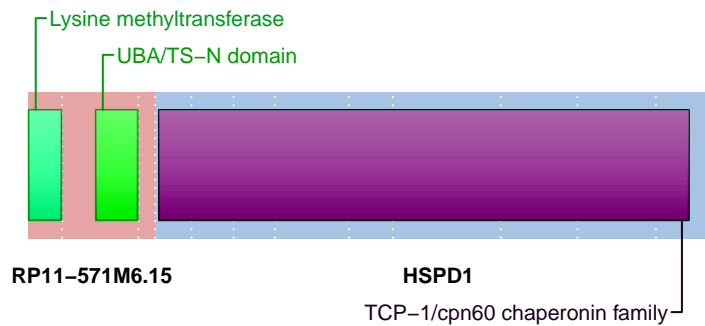
Split reads = 36
Discordant mates = 17

translocation deletion
duplication inversion



RETAINED PROTEIN DOMAINS

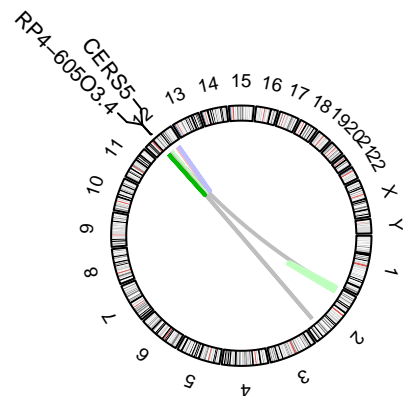
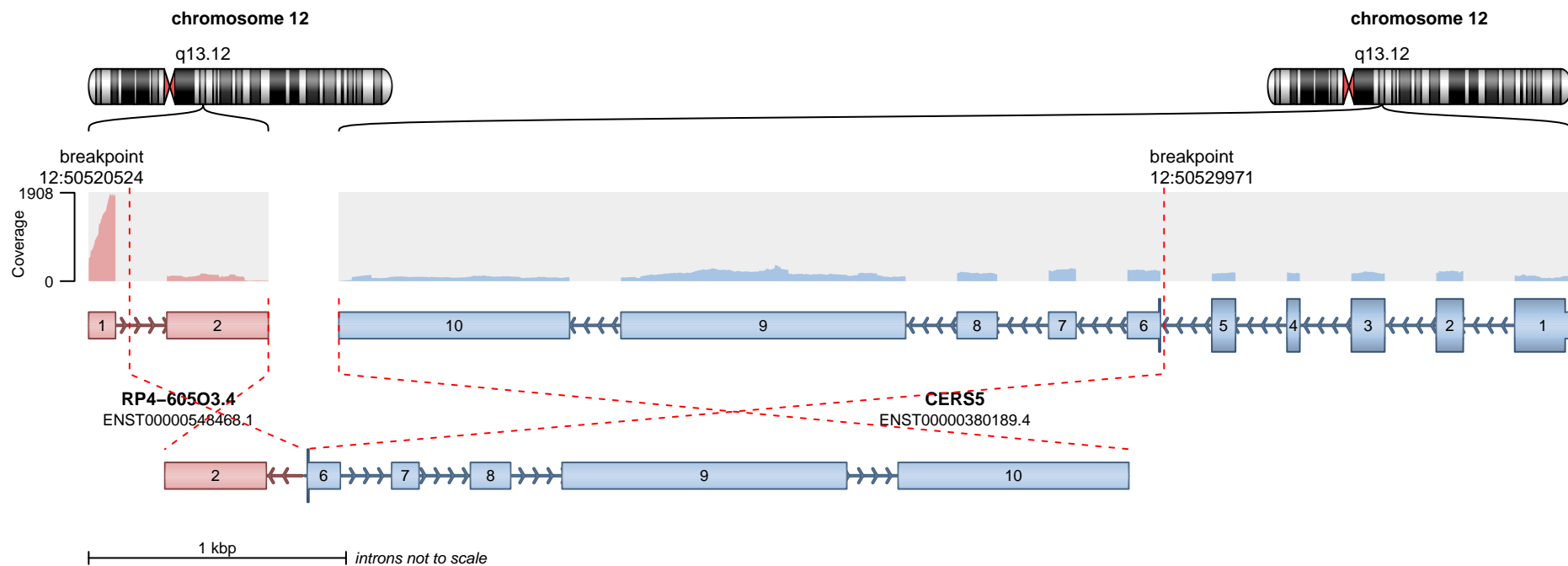
reading frame unclear



SUPPORTING READ COUNT

Split reads = 31
Discordant mates = 24

translocation deletion
duplication inversion

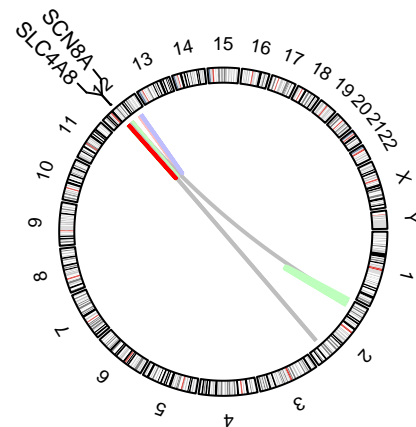
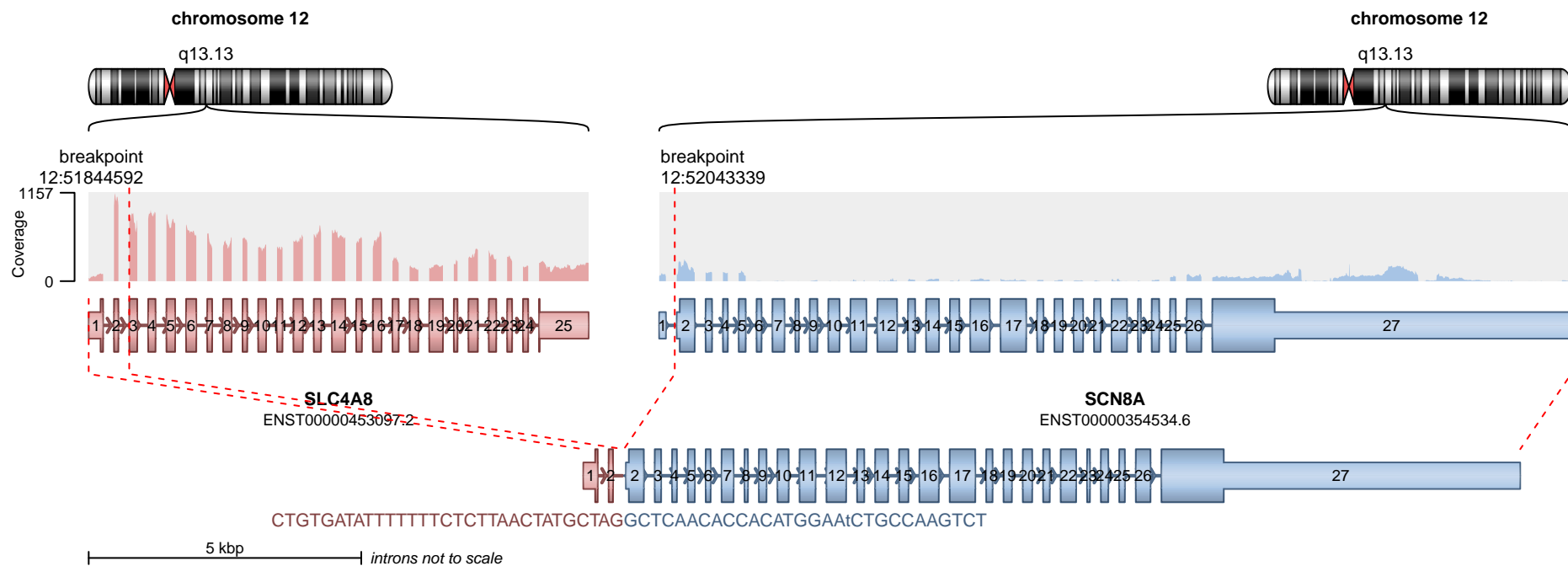


translocation deletion
duplication inversion

No coding regions due to antisense transcription.

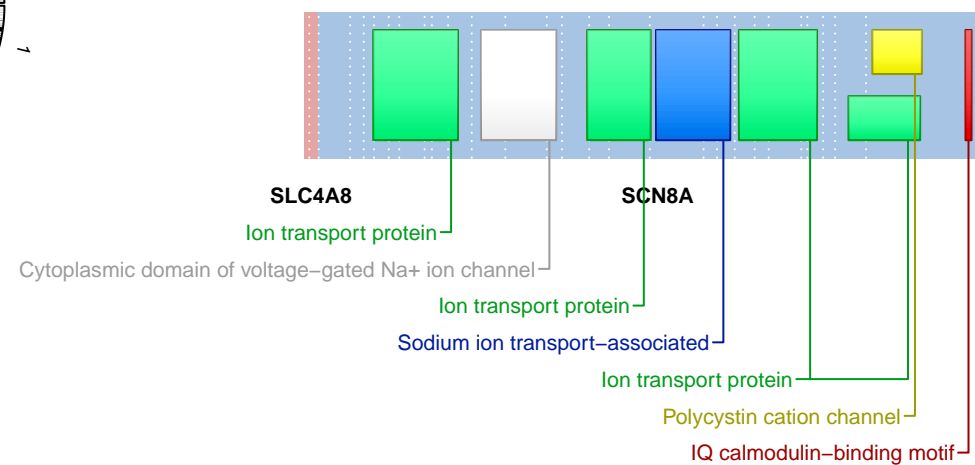
SUPPORTING READ COUNT

Split reads = 34
Discordant mates = 14



— translocation — deletion
— duplication — inversion

RETAINED PROTEIN DOMAINS reading frame unclear



SUPPORTING READ COUNT

Split reads = 20
Discordant mates = 16