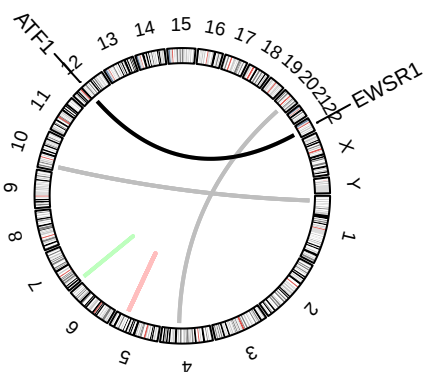
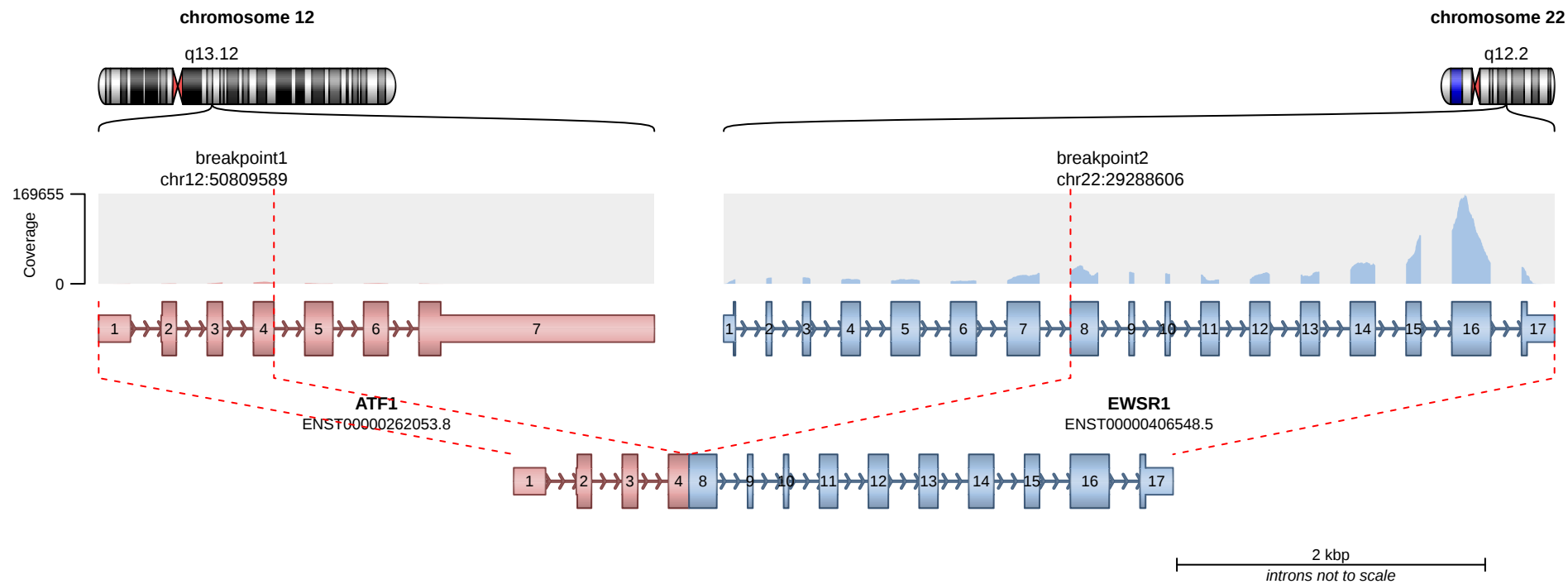
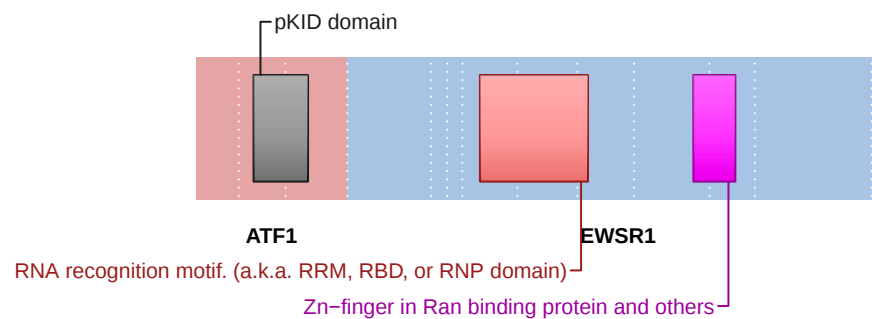




RETAINED PROTEIN DOMAINS reading frame unclear



SUPPORTING READ COUNT

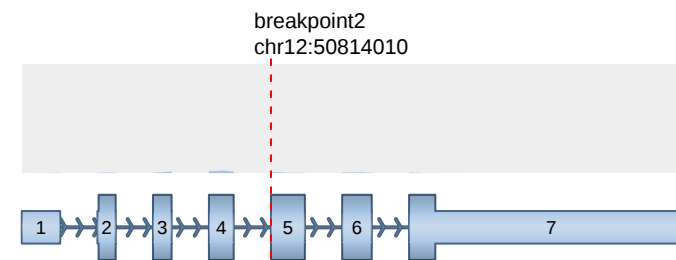
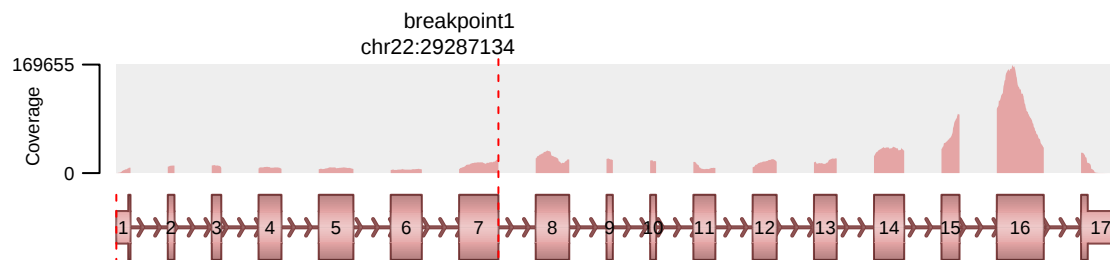
Split reads = 683
Discordant mates = 0

— translocation — deletion
— duplication — inversion

chromosome 22



chromosome 12

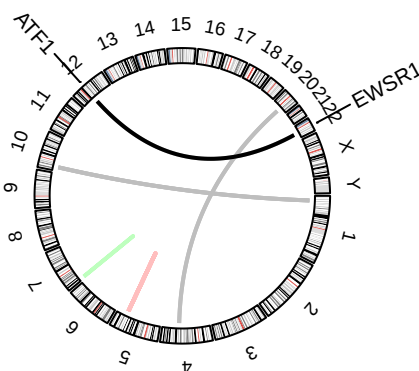


EWSR1
ENST00000406548.5

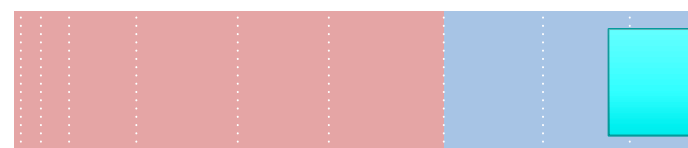
ATF1
ENST00000262053.8



2 kbp
introns not to scale



RETAINED PROTEIN DOMAINS
reading frame unclear



EWSR1

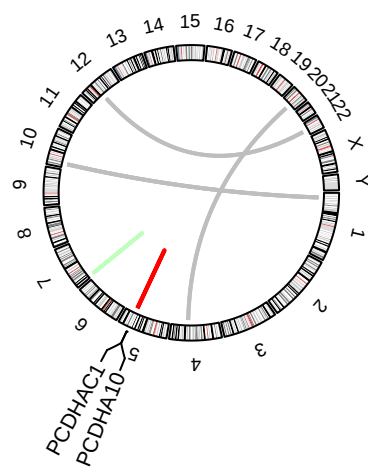
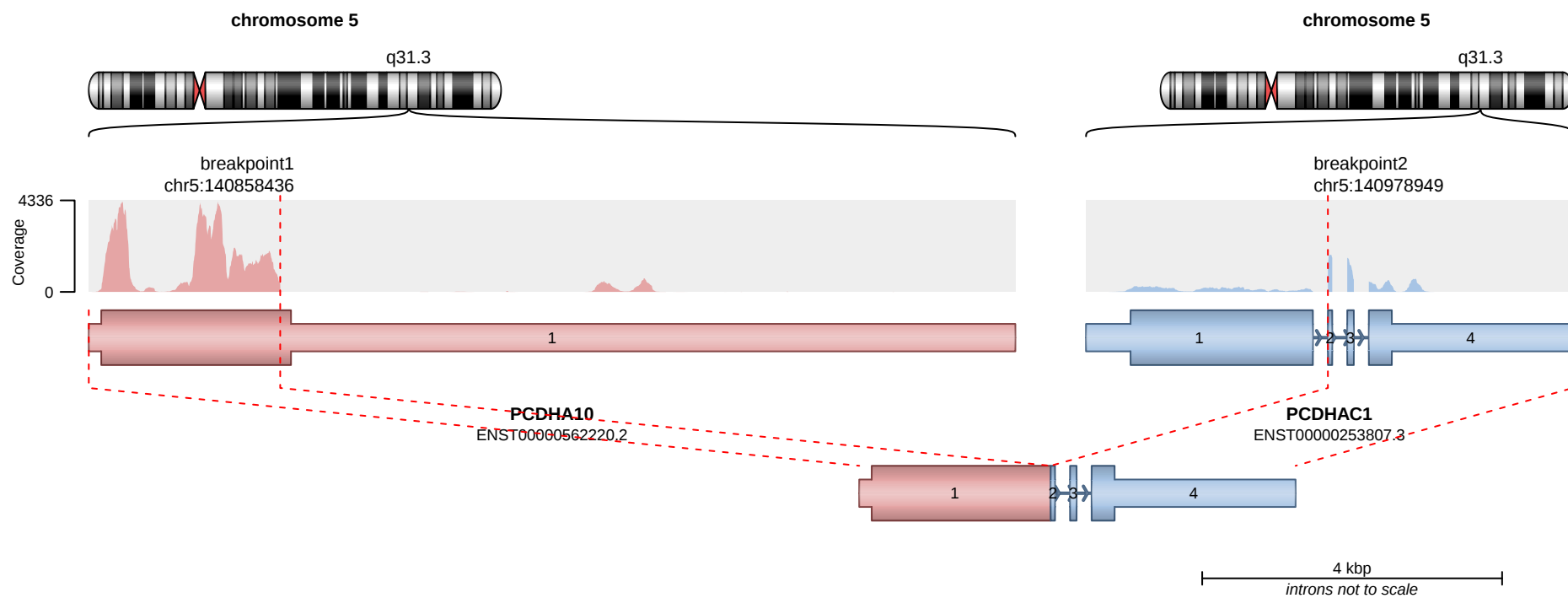
ATF1

bZIP transcription factor

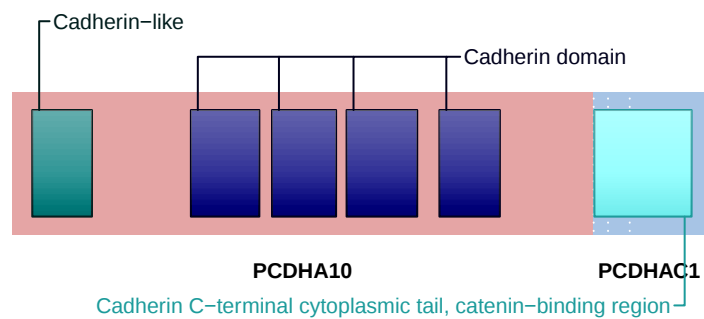
SUPPORTING READ COUNT

Split reads = 579
Discordant mates = 0

— translocation — deletion
— duplication — inversion



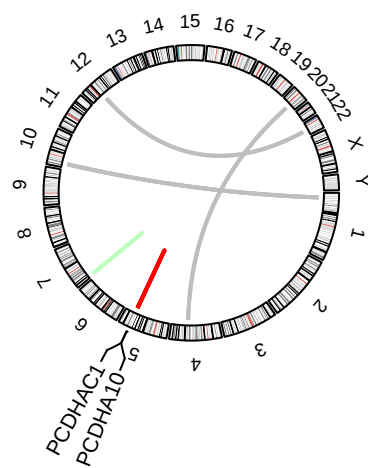
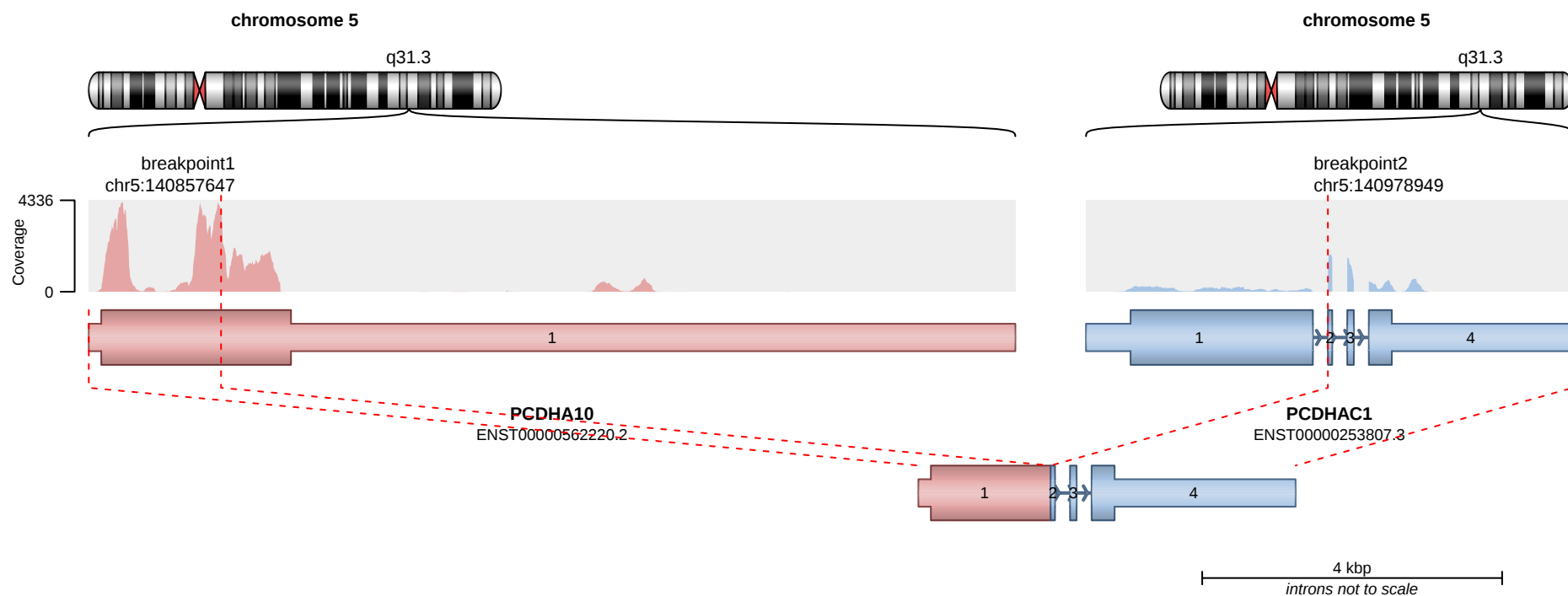
RETAINED PROTEIN DOMAINS reading frame unclear



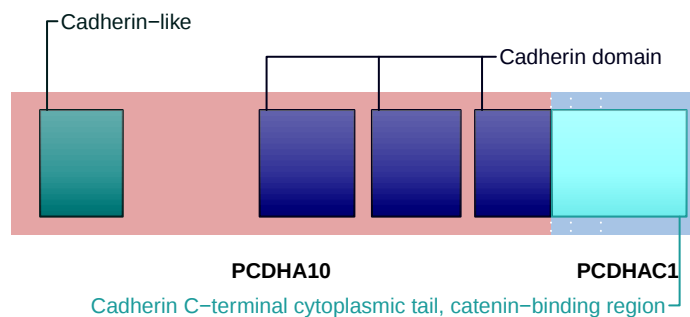
SUPPORTING READ COUNT

Split reads = 105
Discordant mates = 0

— translocation — deletion
— duplication — inversion



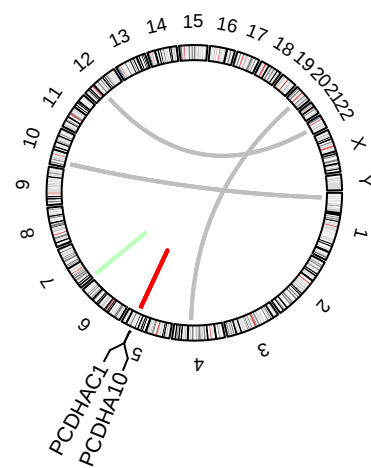
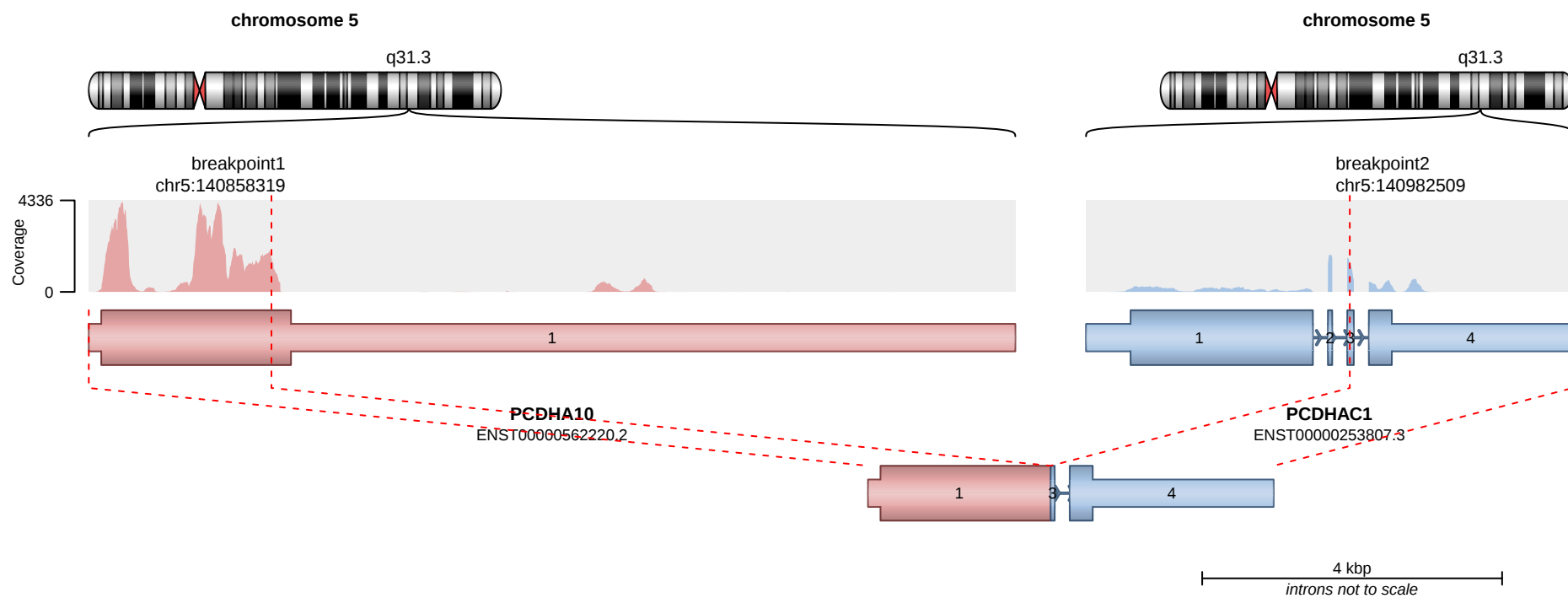
RETAINED PROTEIN DOMAINS reading frame unclear



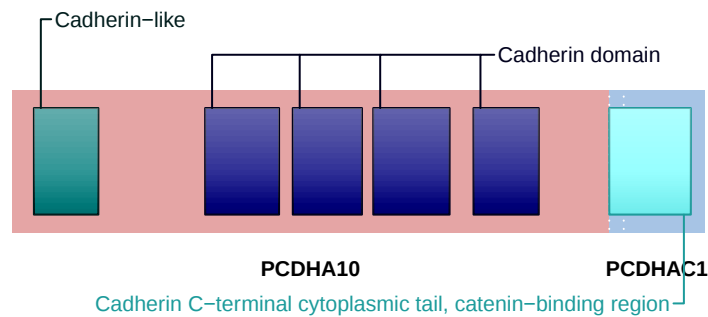
SUPPORTING READ COUNT

Split reads = 11
Discordant mates = 0

— translocation — deletion
— duplication — inversion



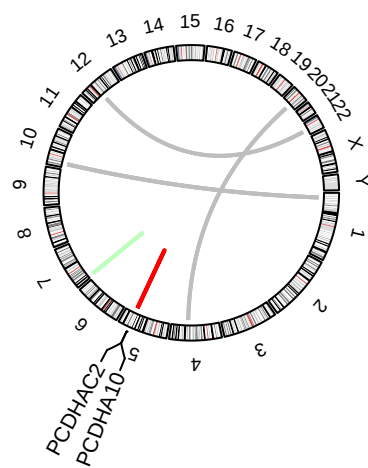
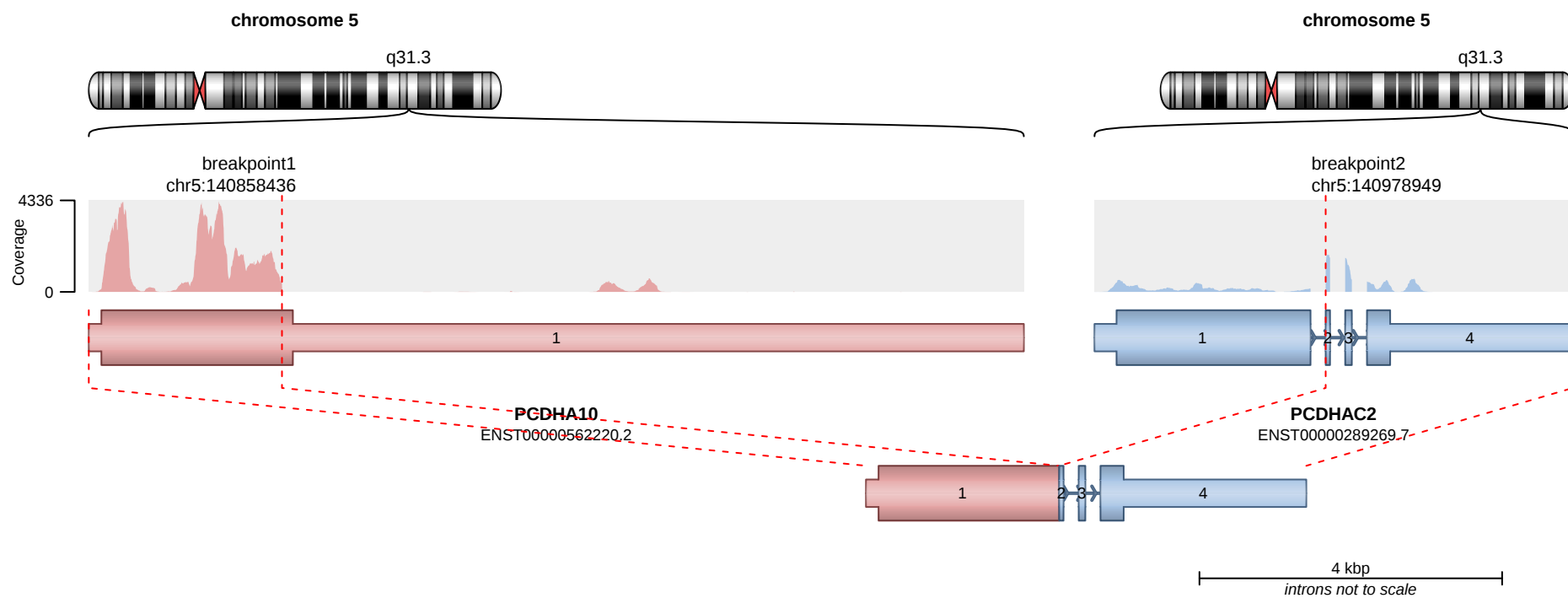
RETAINED PROTEIN DOMAINS reading frame unclear



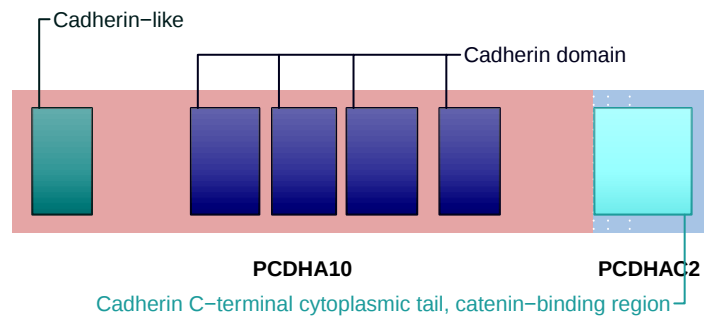
SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 0

— translocation — deletion
— duplication — inversion



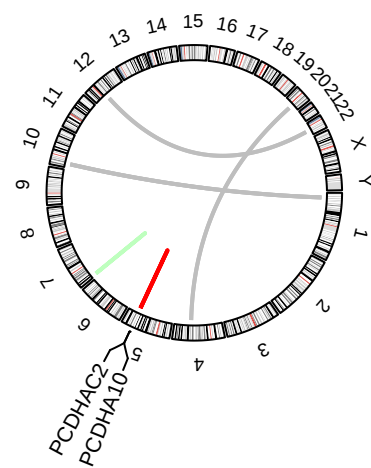
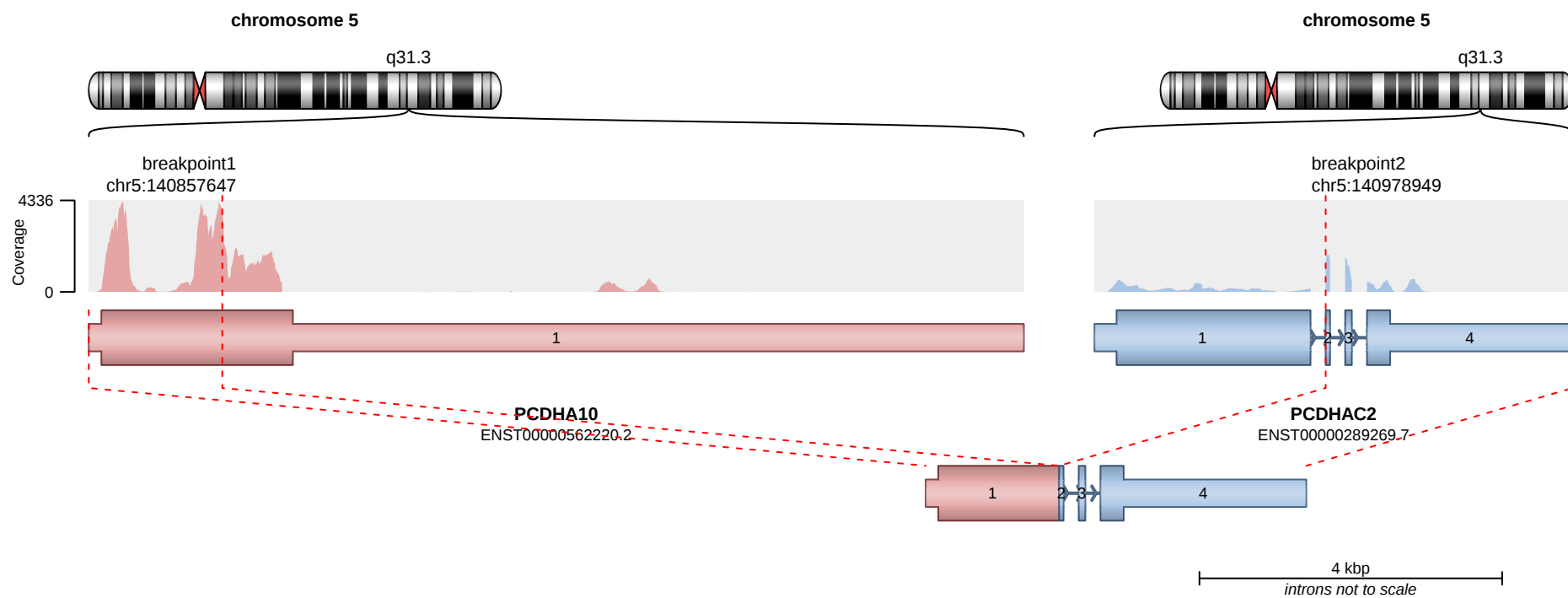
RETAINED PROTEIN DOMAINS reading frame unclear



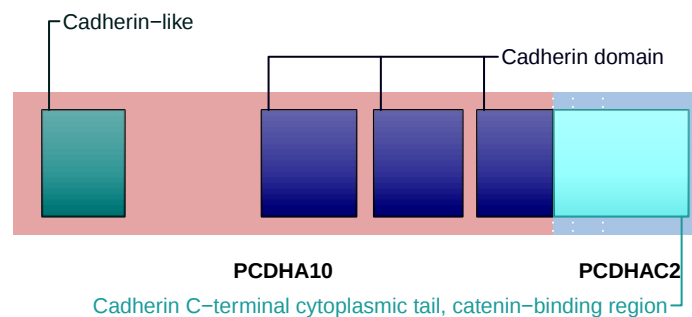
SUPPORTING READ COUNT

Split reads = 105
Discordant mates = 0

— translocation — deletion
— duplication — inversion



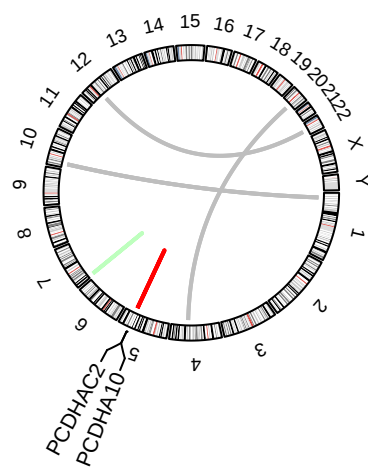
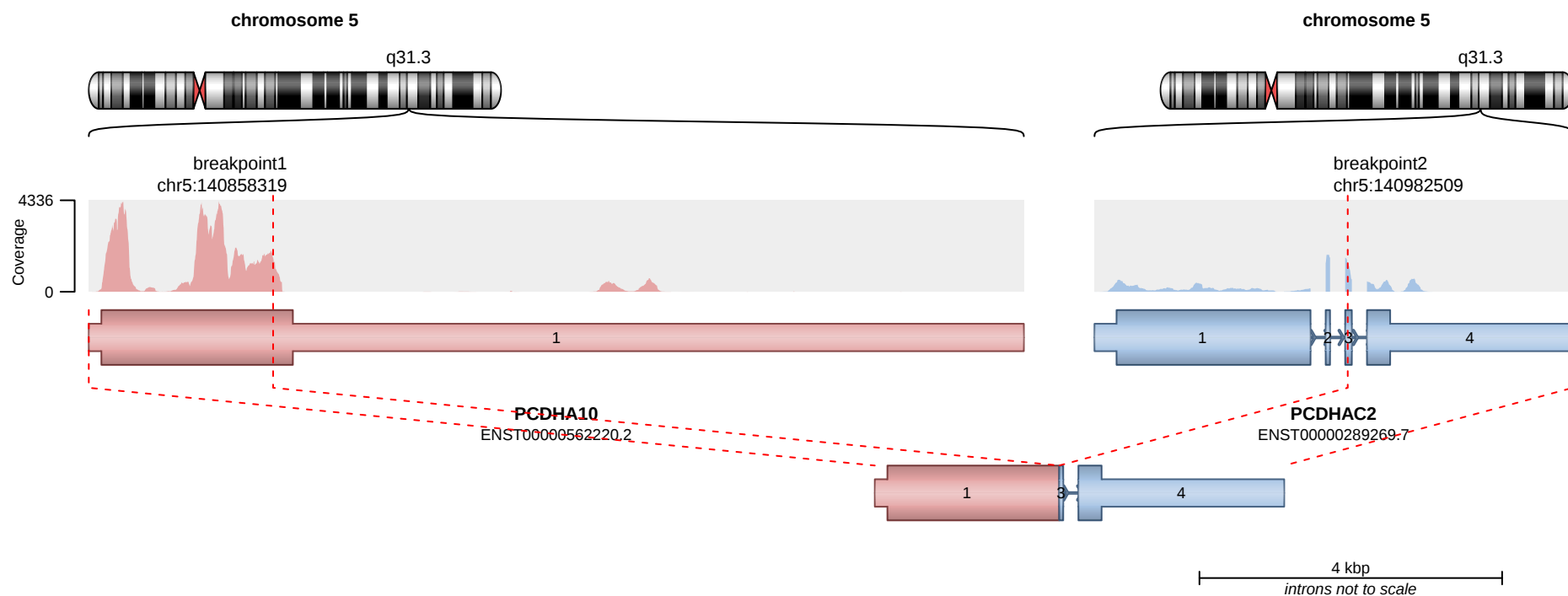
RETAINED PROTEIN DOMAINS reading frame unclear



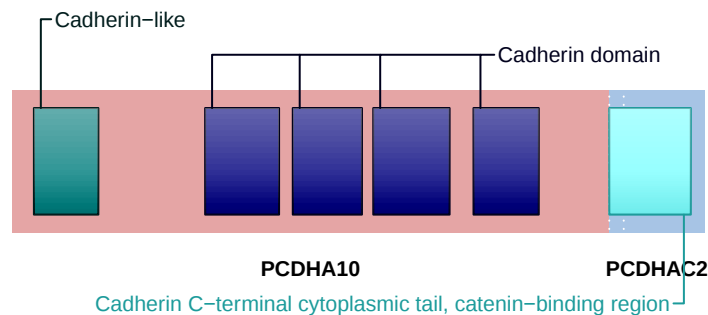
SUPPORTING READ COUNT

Split reads = 11
Discordant mates = 0

— translocation — deletion
— duplication — inversion



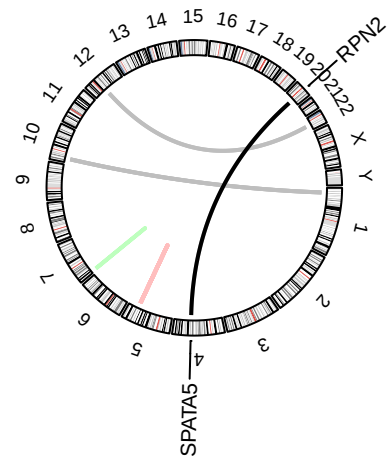
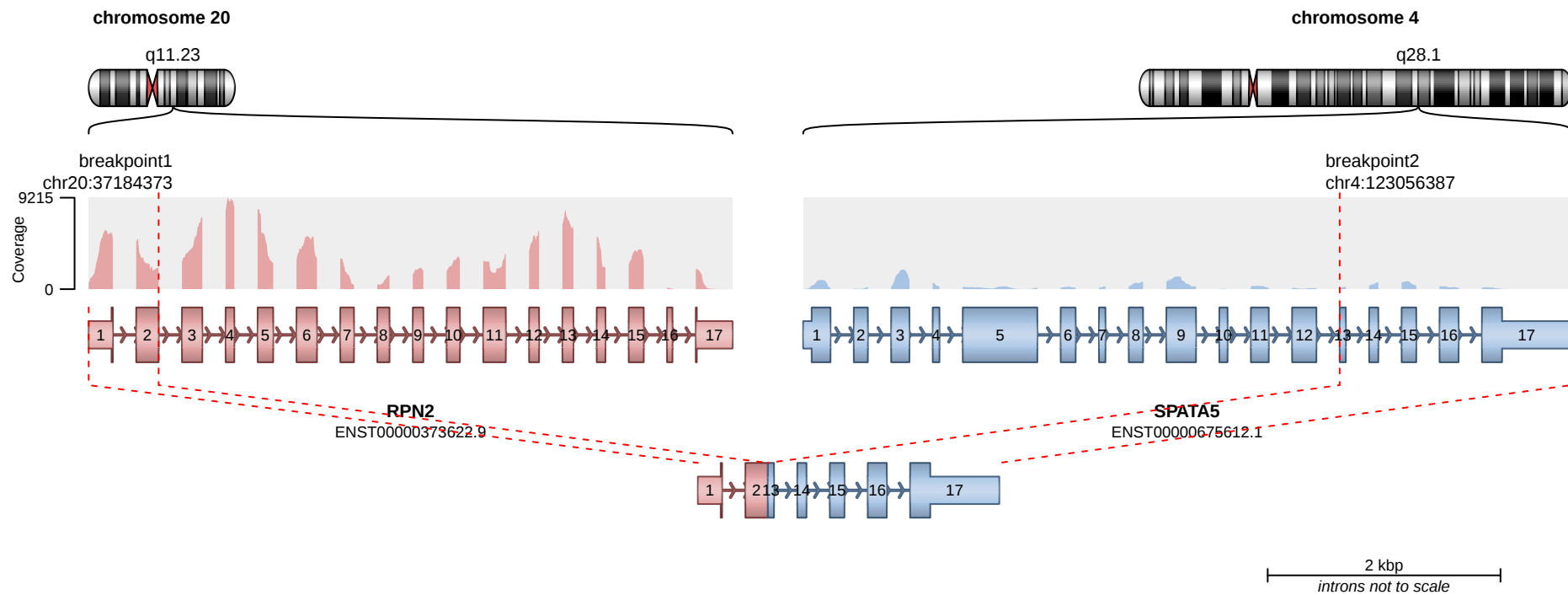
RETAINED PROTEIN DOMAINS reading frame unclear



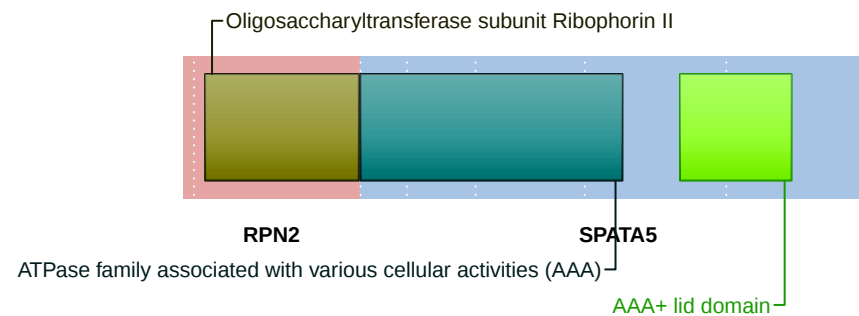
SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 0

— translocation — deletion
— duplication — inversion



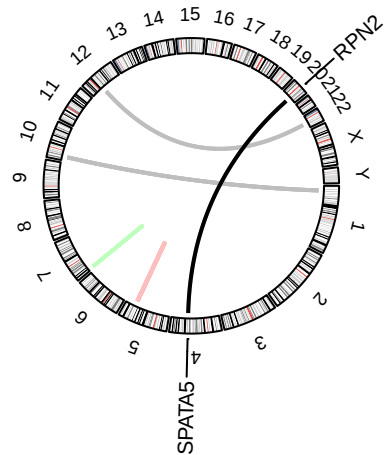
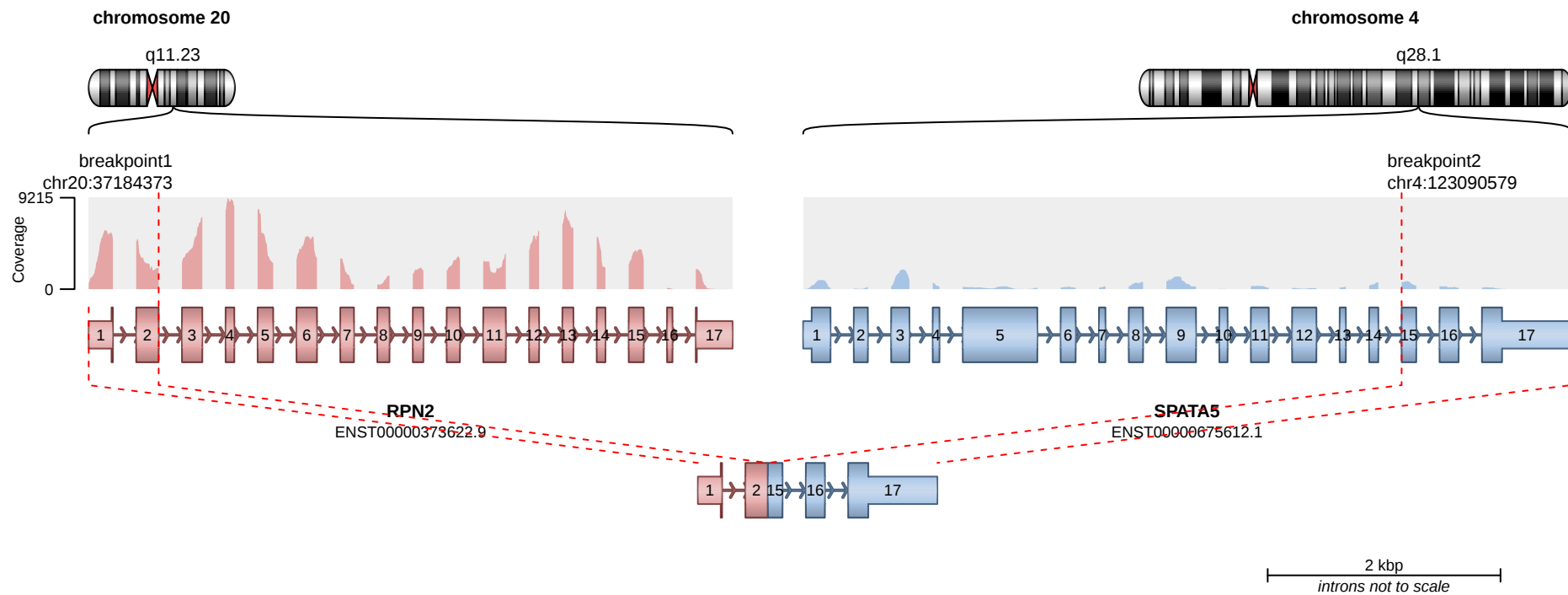
RETAINED PROTEIN DOMAINS reading frame unclear



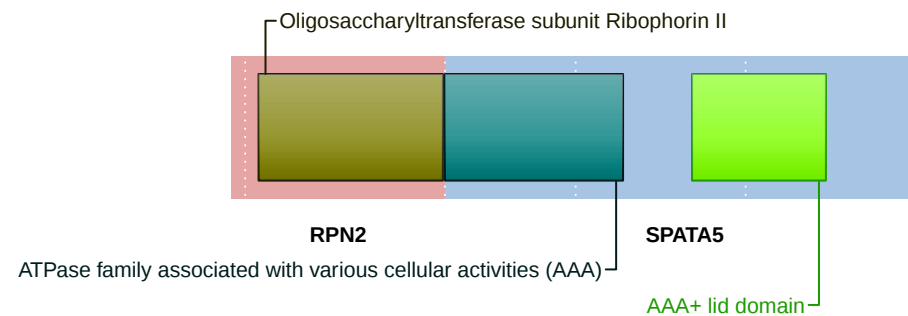
SUPPORTING READ COUNT

Split reads = 46
Discordant mates = 0

— translocation — deletion
— duplication — inversion



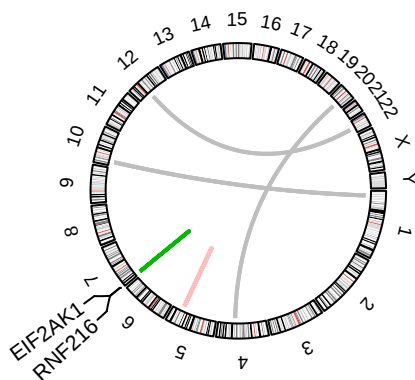
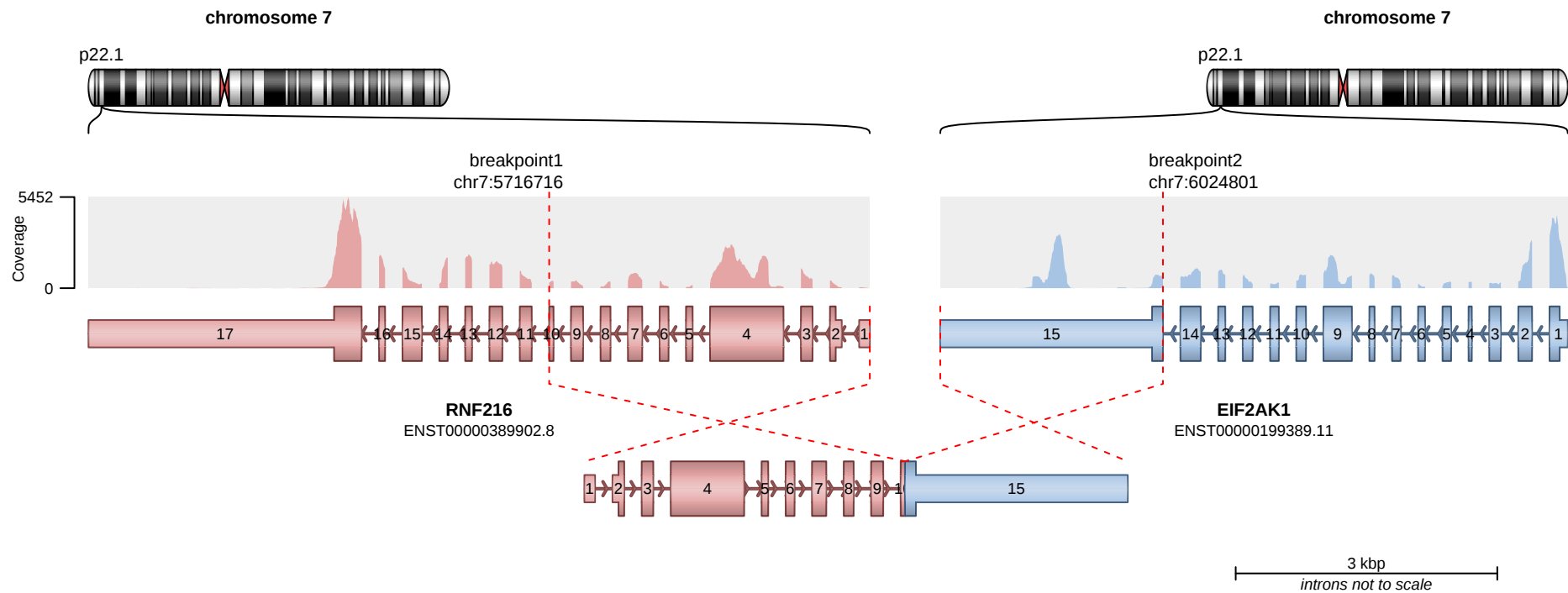
RETAINED PROTEIN DOMAINS reading frame unclear



SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

— translocation — deletion
— duplication — inversion



— translocation — deletion
— duplication — inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 17
Discordant mates = 0