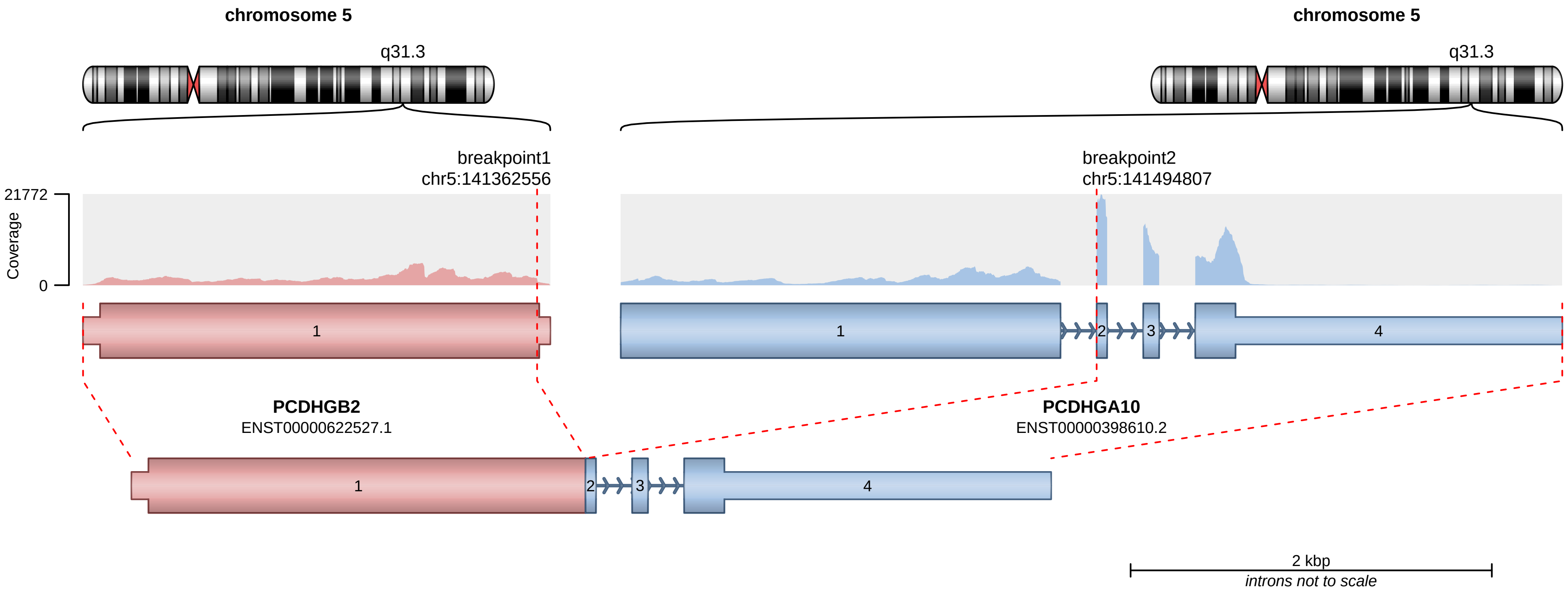
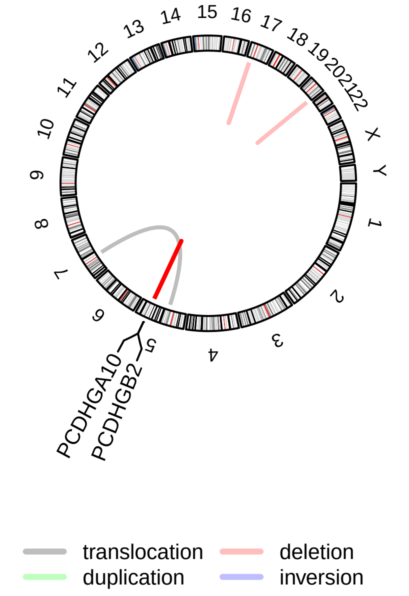
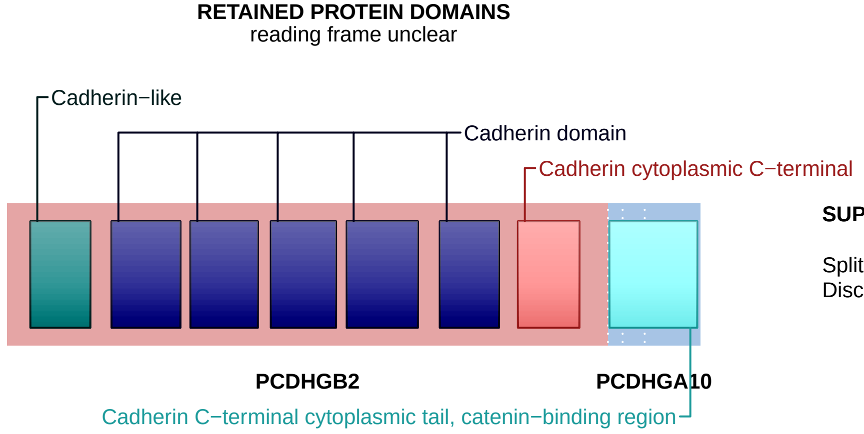
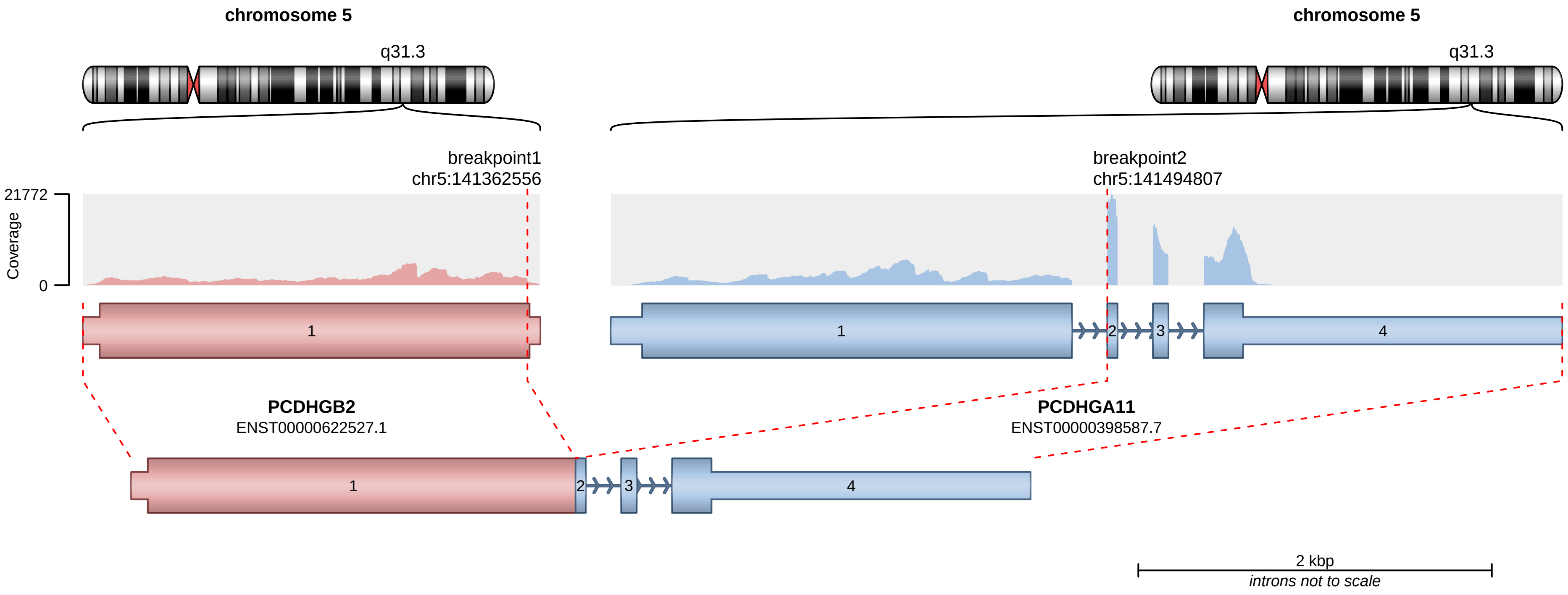


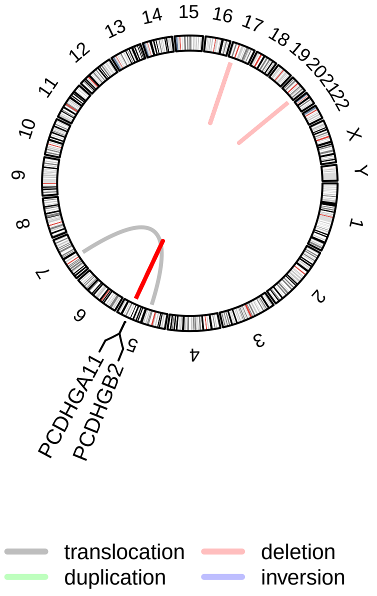


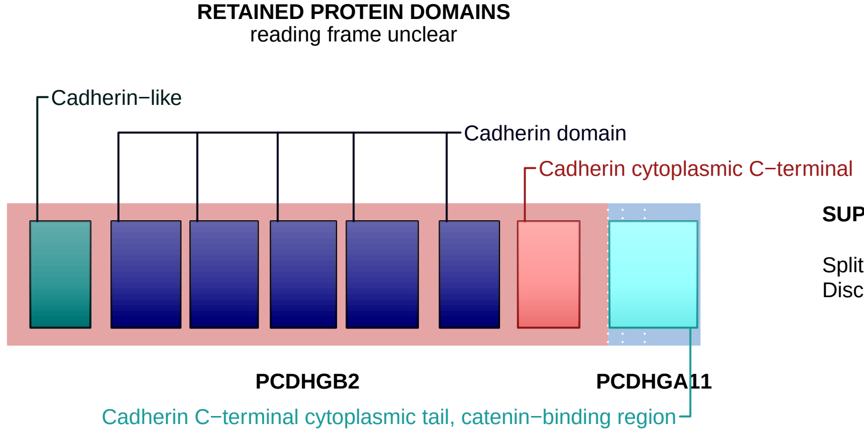


SUPPORTING READ COUNT

Split reads = 257
Discordant mates = 0

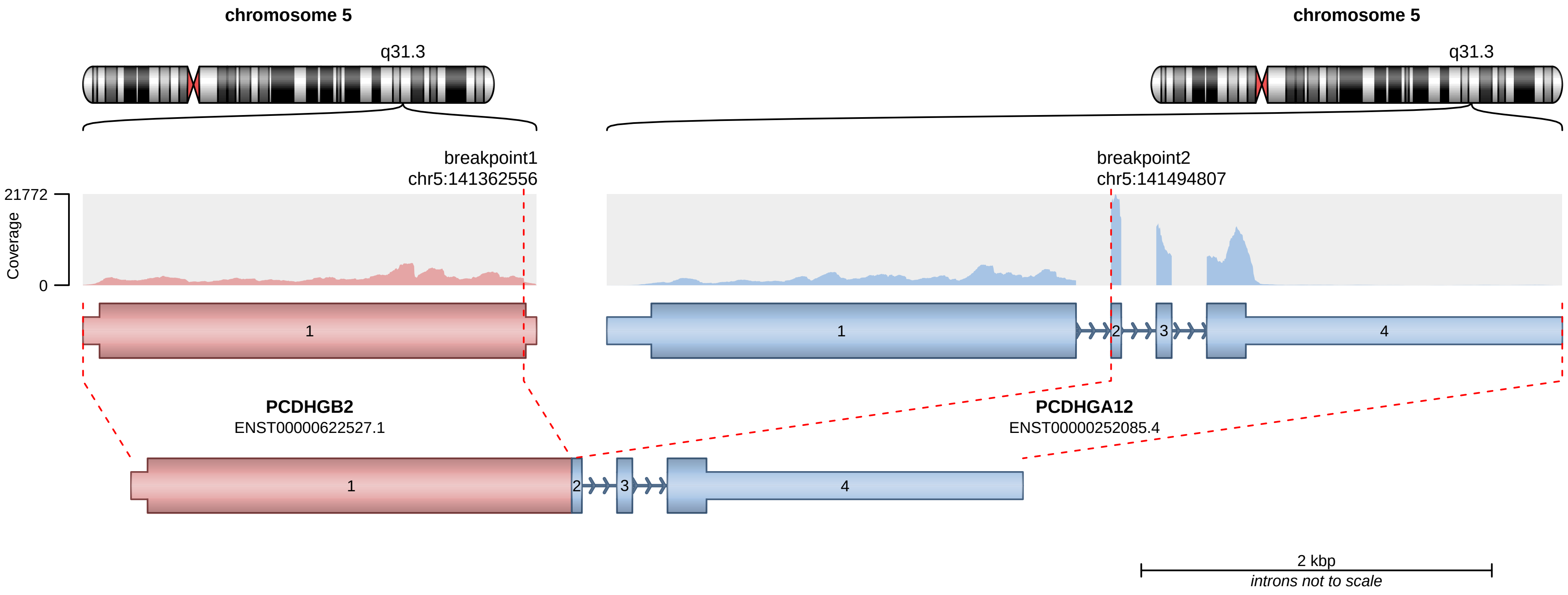


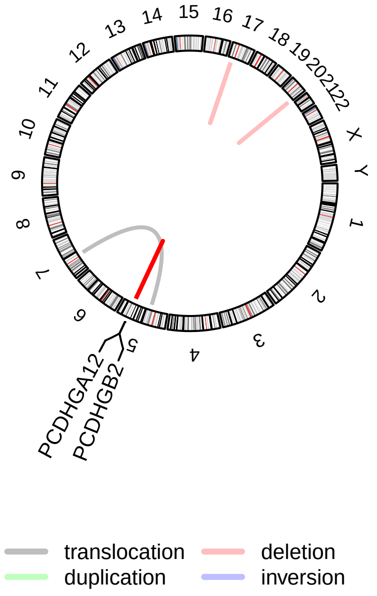




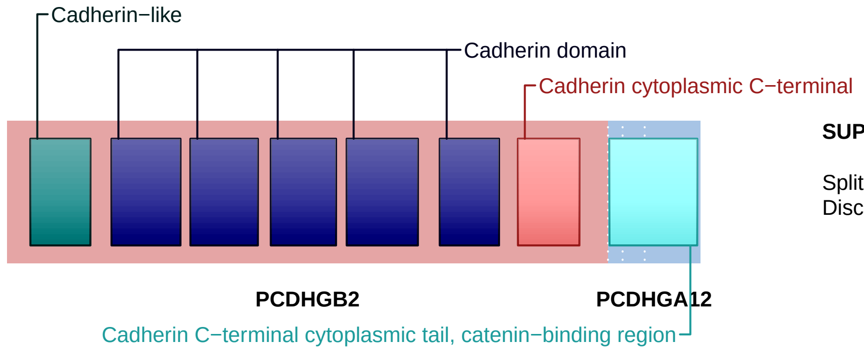
SUPPORTING READ COUNT

Split reads = 257
Discordant mates = 0



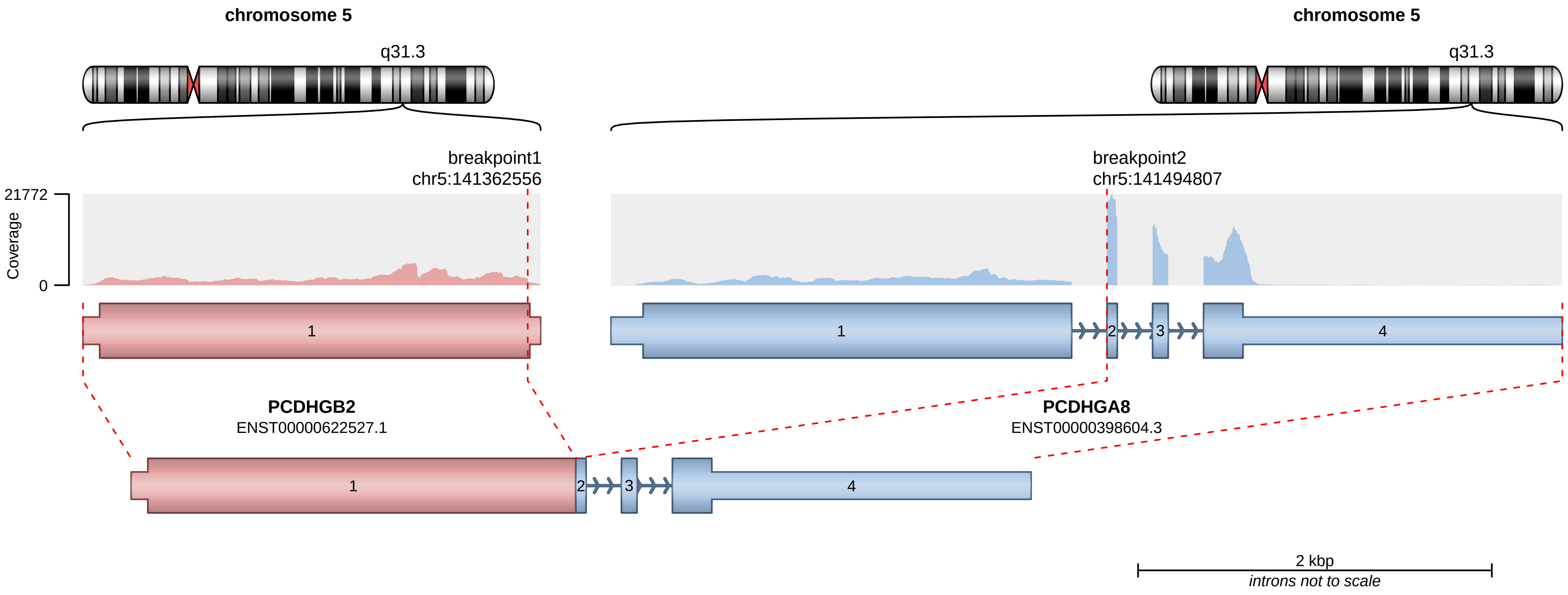


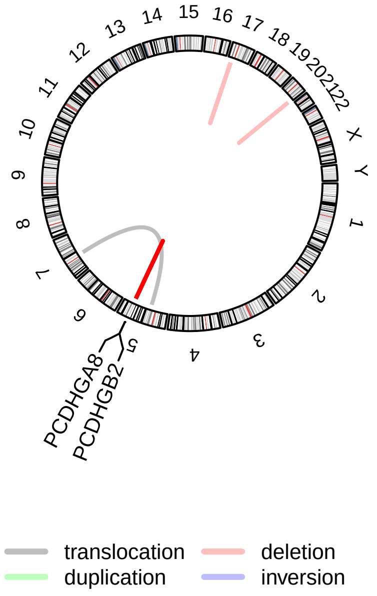
RETAINED PROTEIN DOMAINS
reading frame unclear



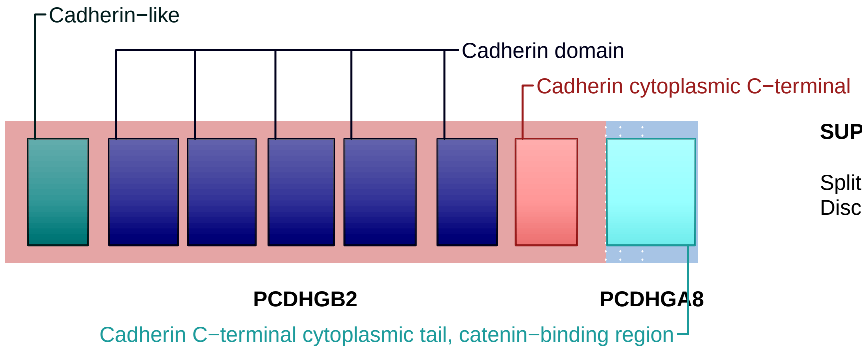
SUPPORTING READ COUNT

Split reads = 257
Discordant mates = 0



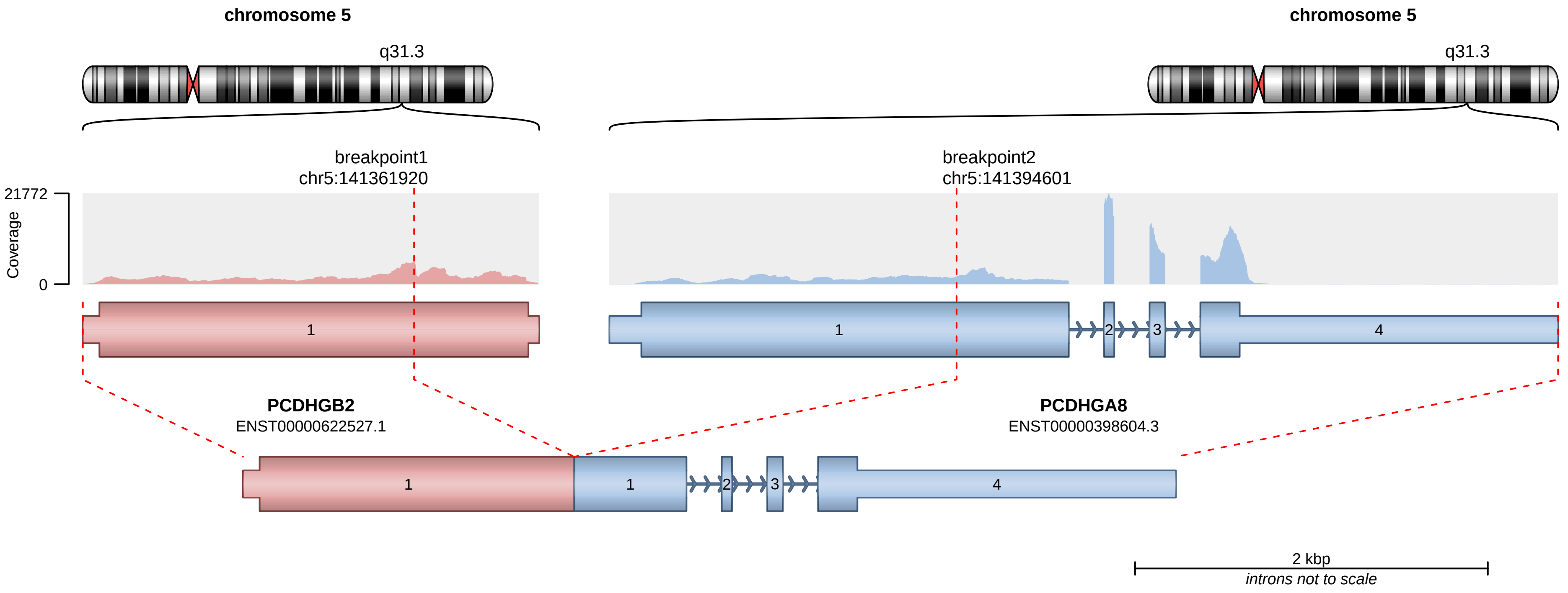


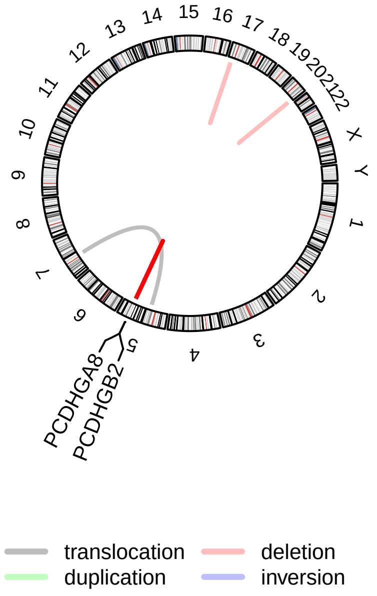
RETAINED PROTEIN DOMAINS
reading frame unclear

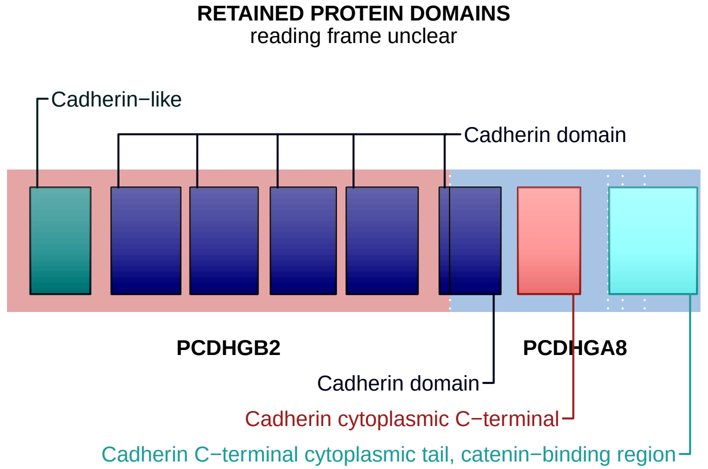


SUPPORTING READ COUNT

Split reads = 257
Discordant mates = 0

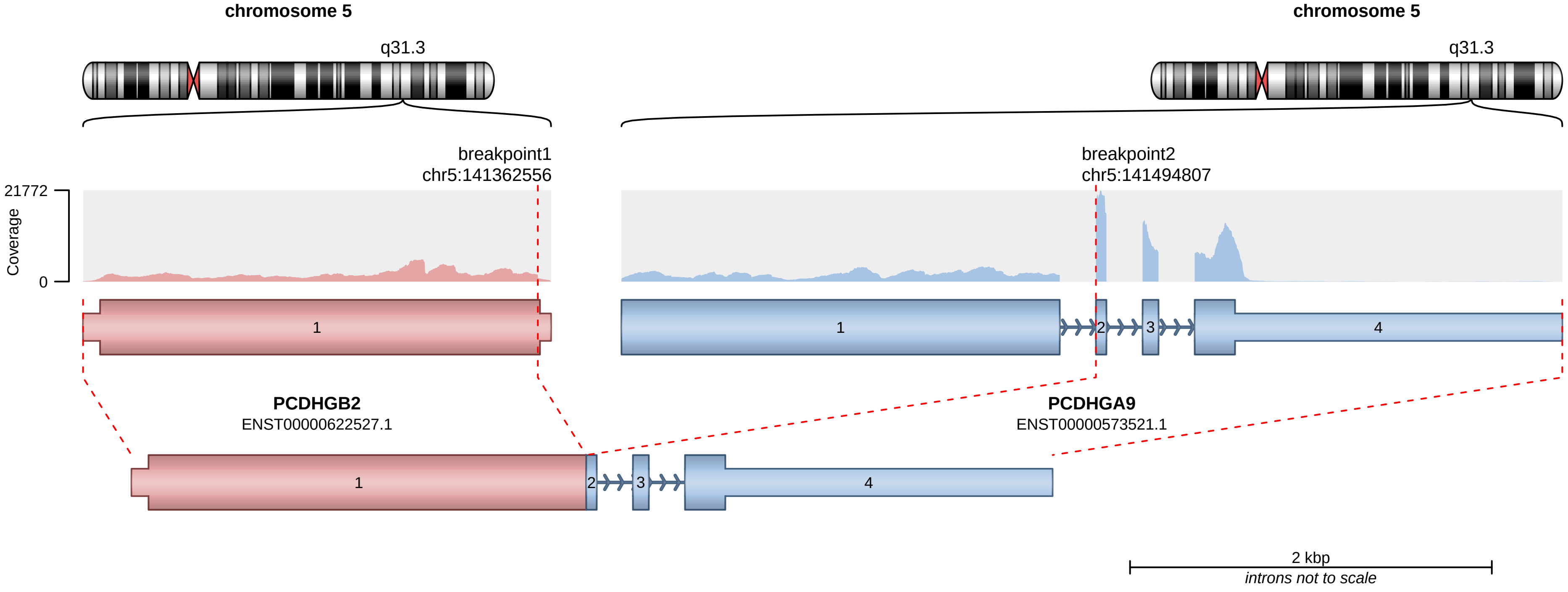


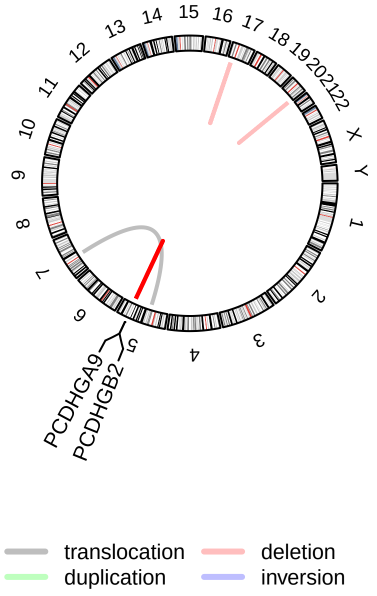




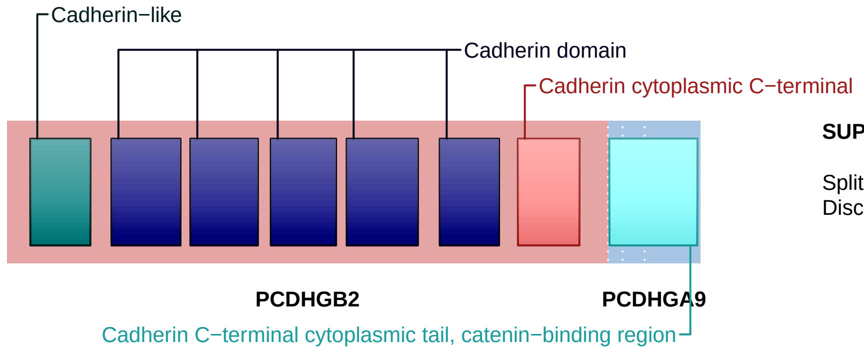
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0



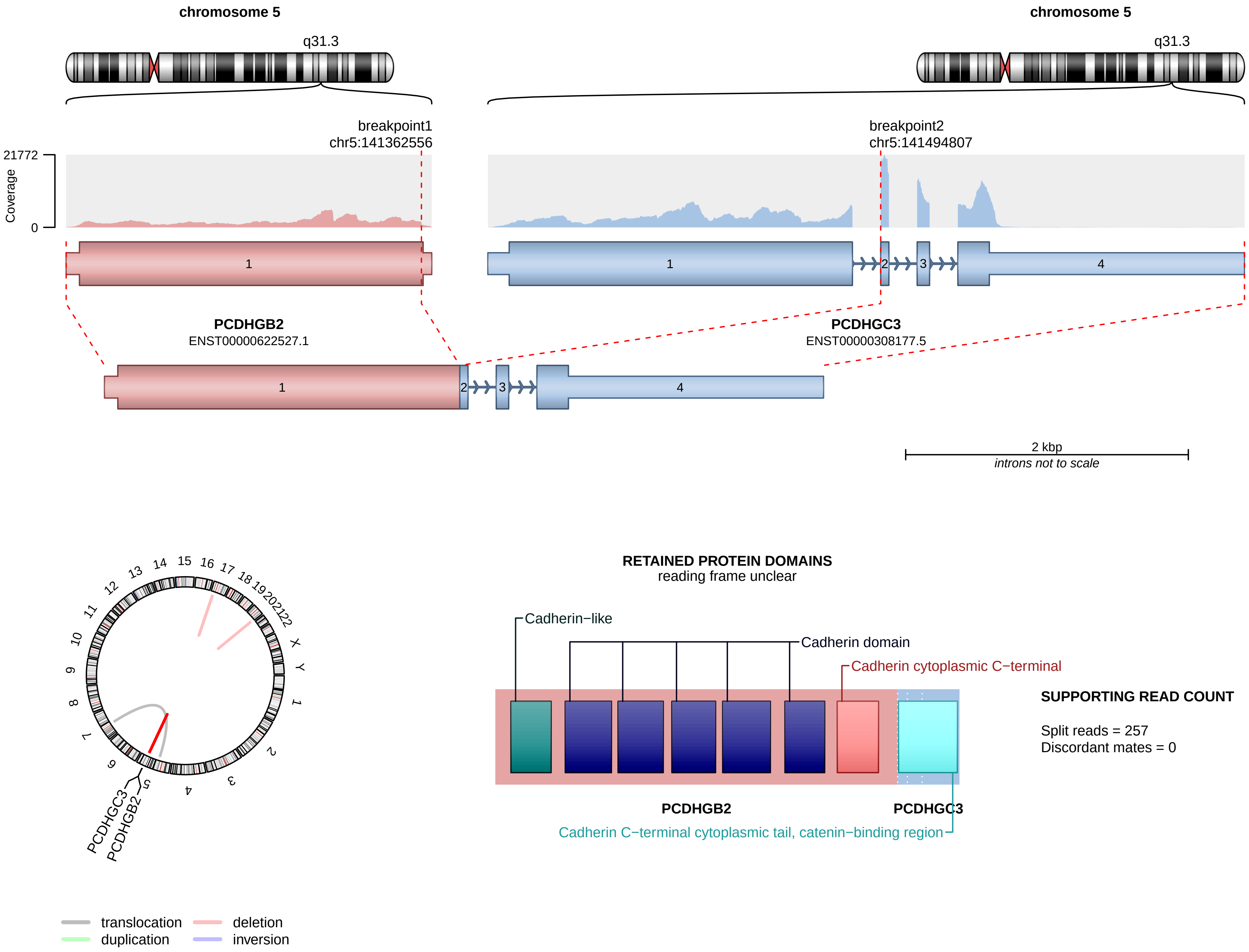


RETAINED PROTEIN DOMAINS
reading frame unclear



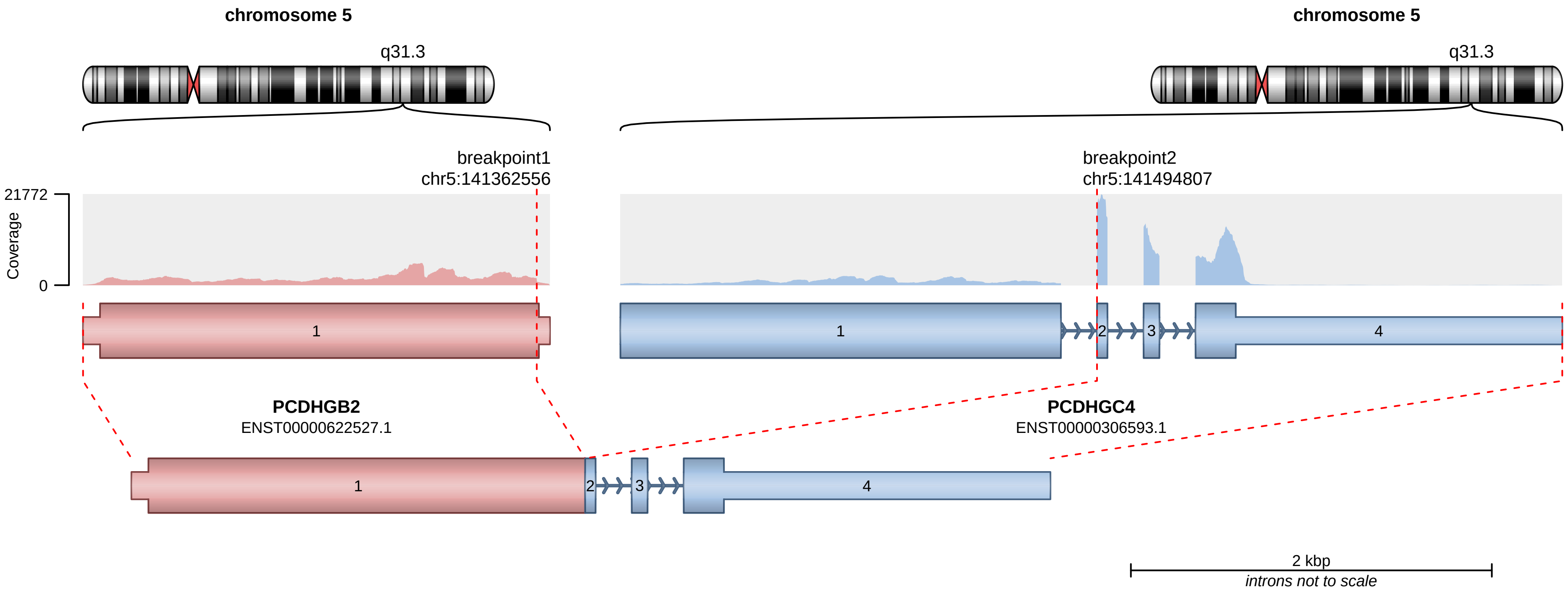
SUPPORTING READ COUNT

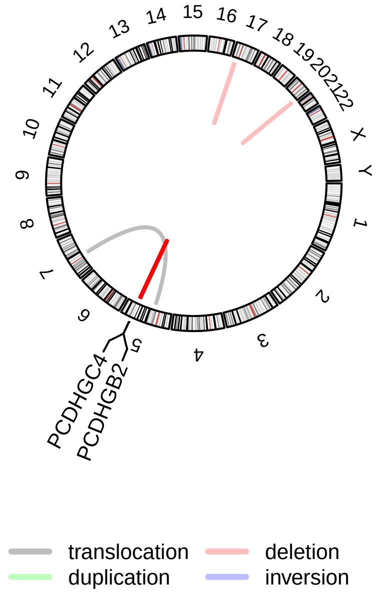
Split reads = 257
Discordant mates = 0

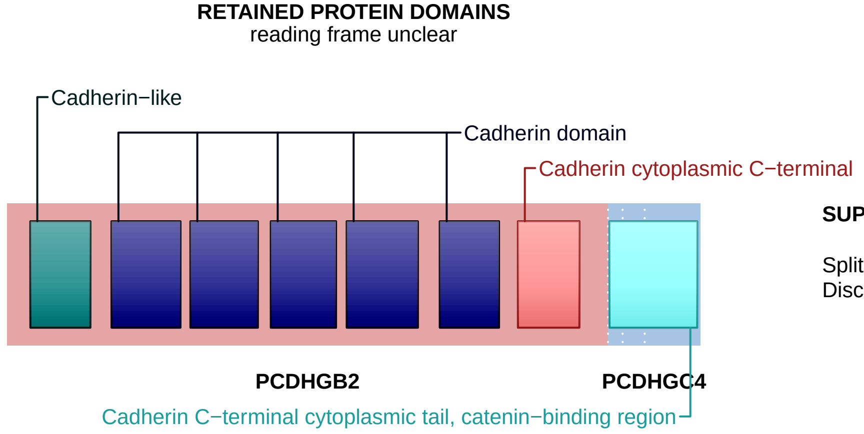


SUPPORTING READ COUNT

Split reads = 257
Discordant mates = 0

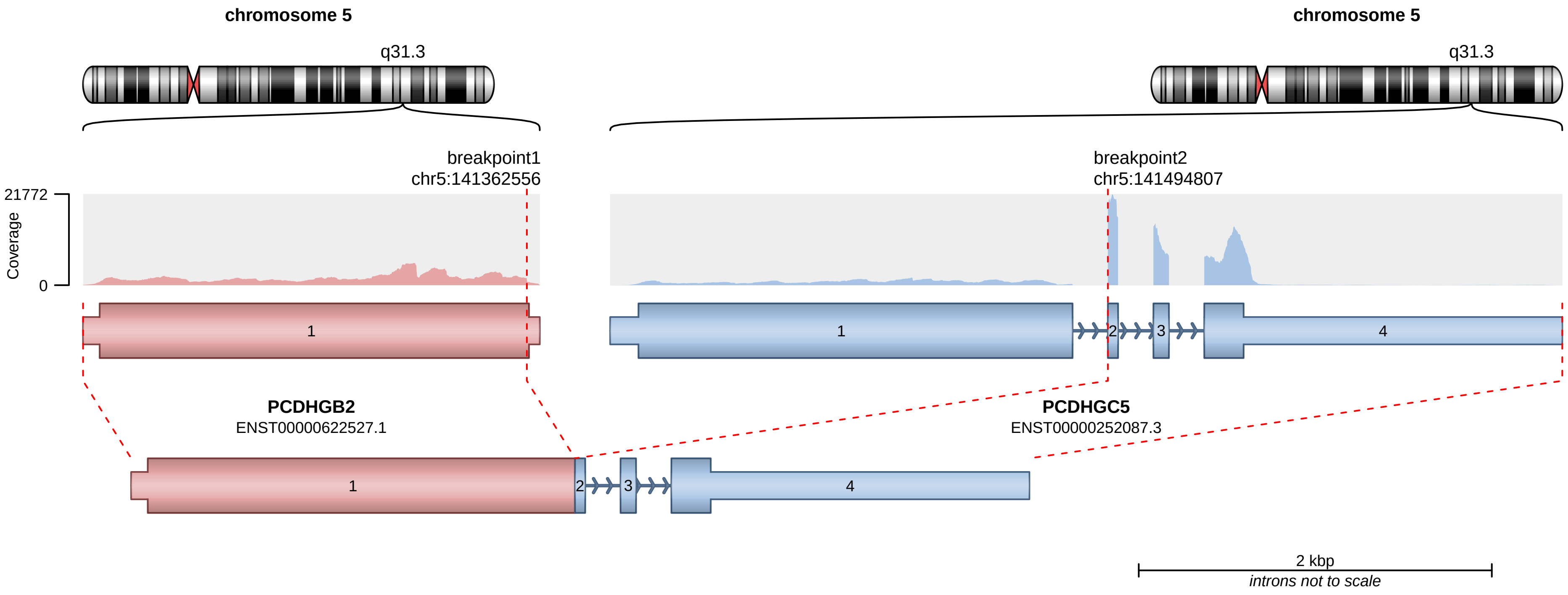


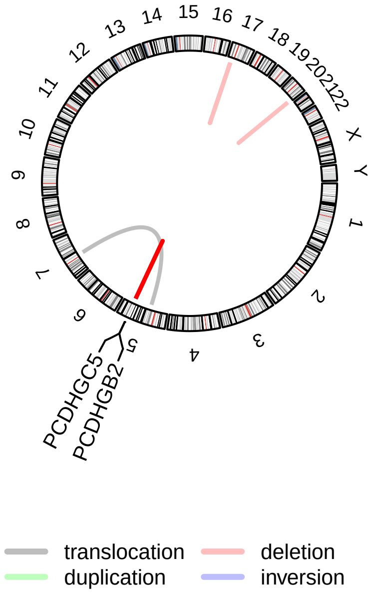




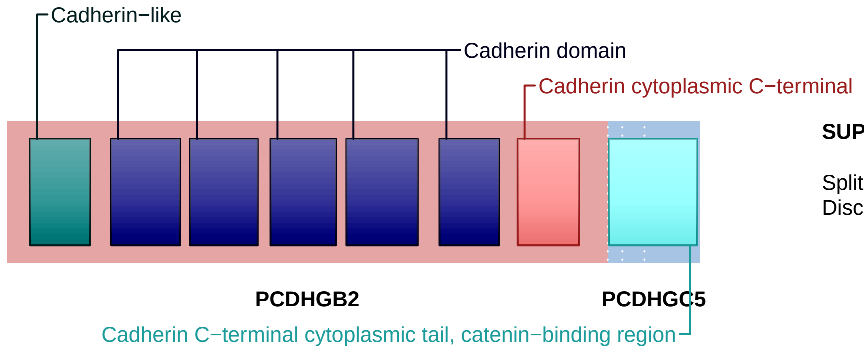
SUPPORTING READ COUNT

Split reads = 257
Discordant mates = 0



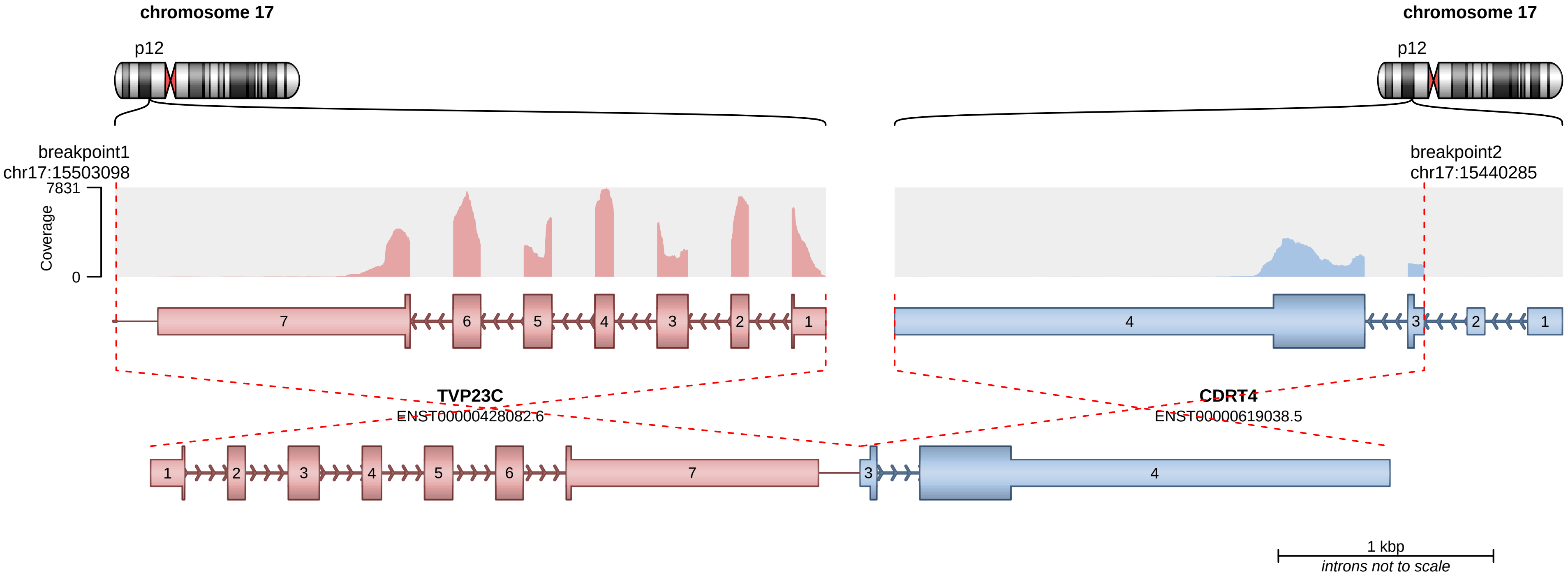


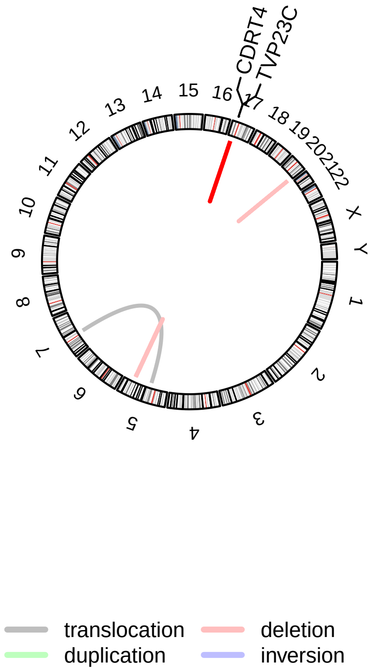
RETAINED PROTEIN DOMAINS
reading frame unclear



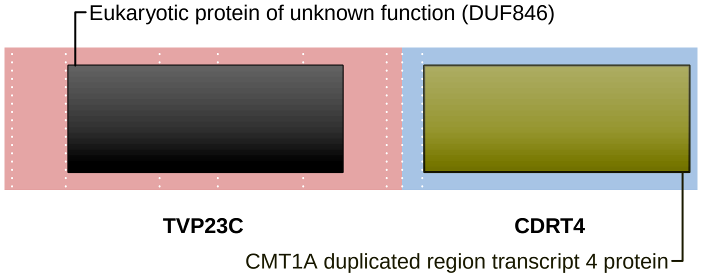
SUPPORTING READ COUNT

Split reads = 257
Discordant mates = 0



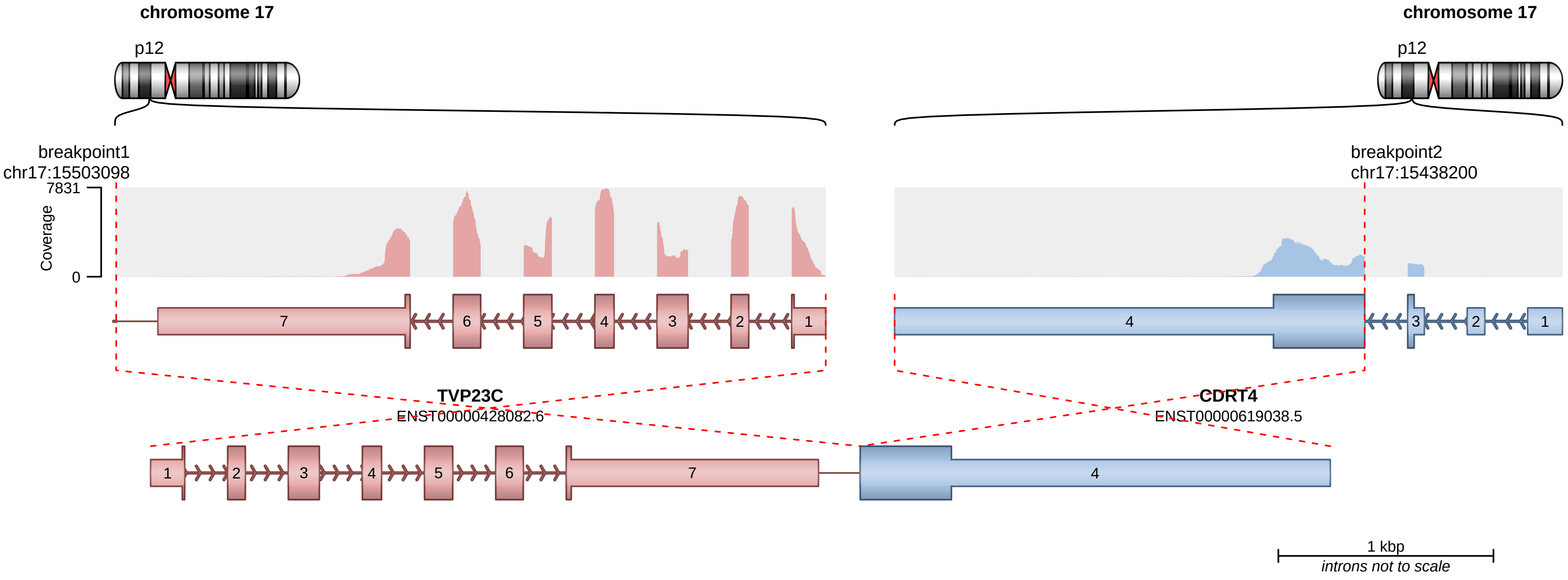


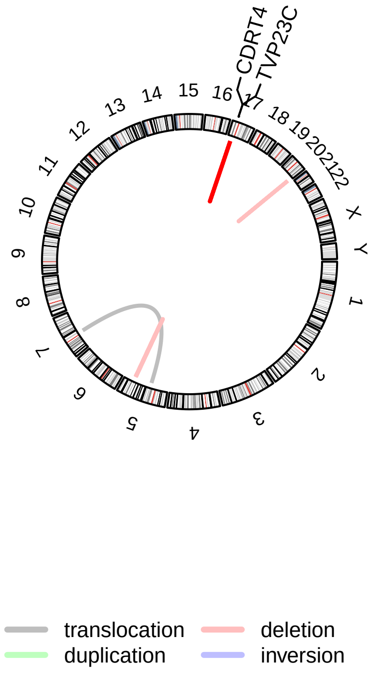
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

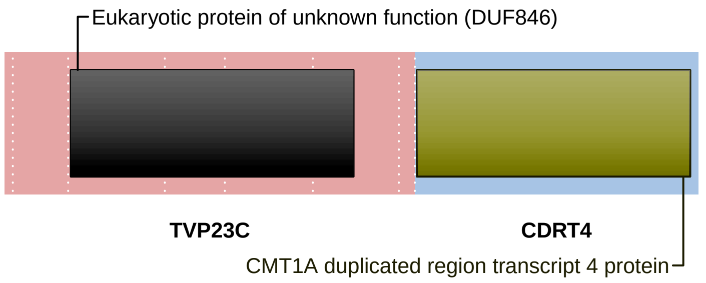
Split reads = 165
Discordant mates = 0





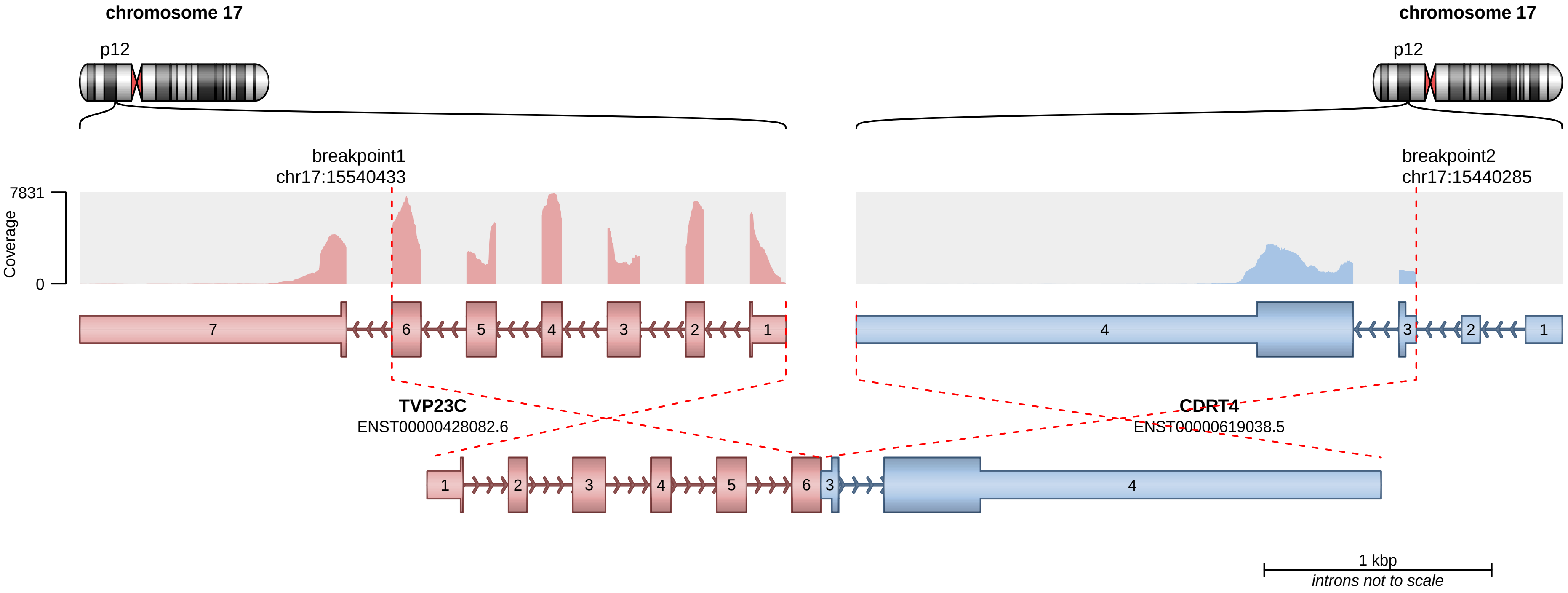
RETAINED PROTEIN DOMAINS

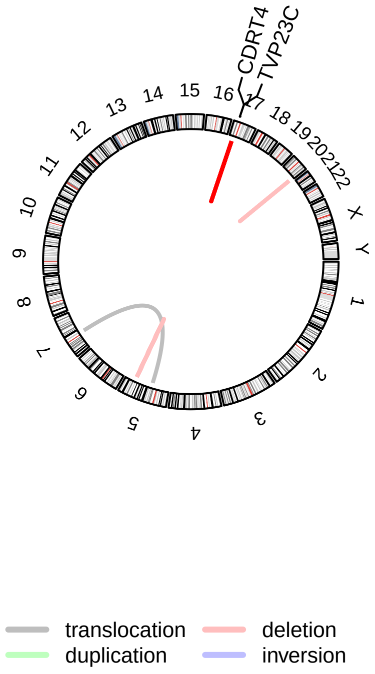
reading frame unclear



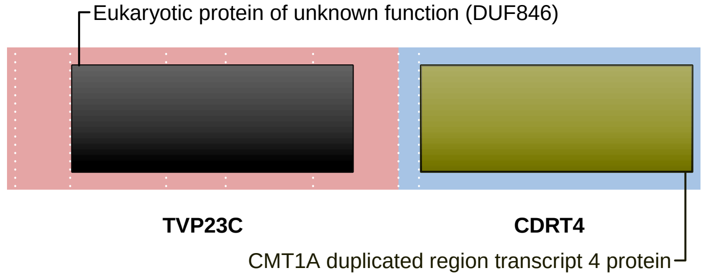
SUPPORTING READ COUNT

Split reads = 114
Discordant mates = 0



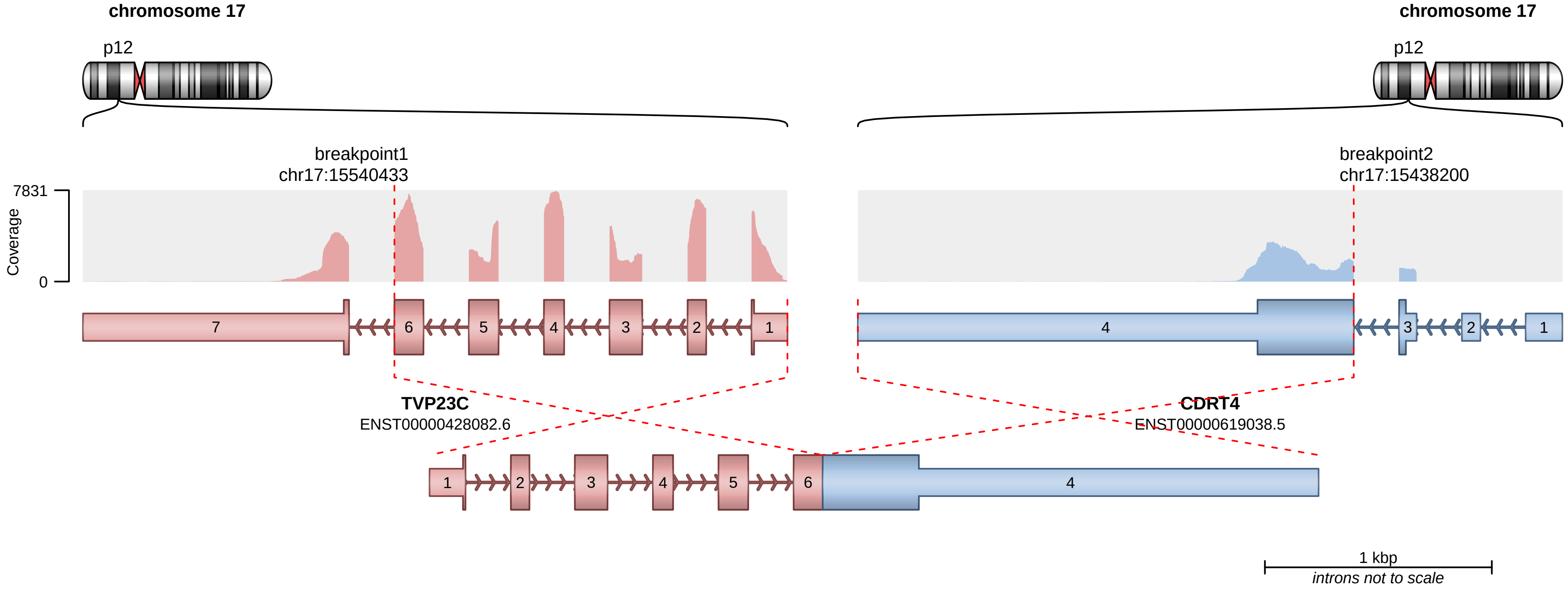


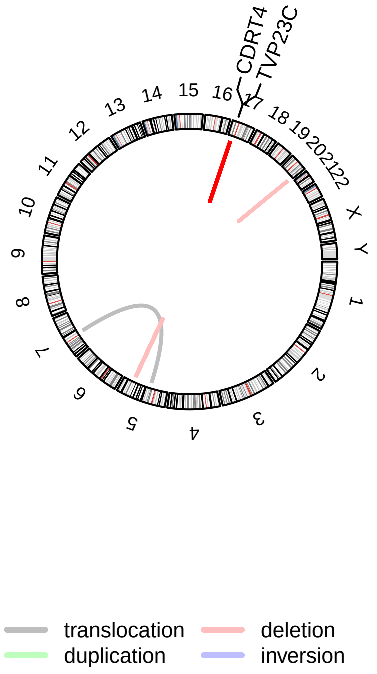
RETAINED PROTEIN DOMAINS
reading frame unclear

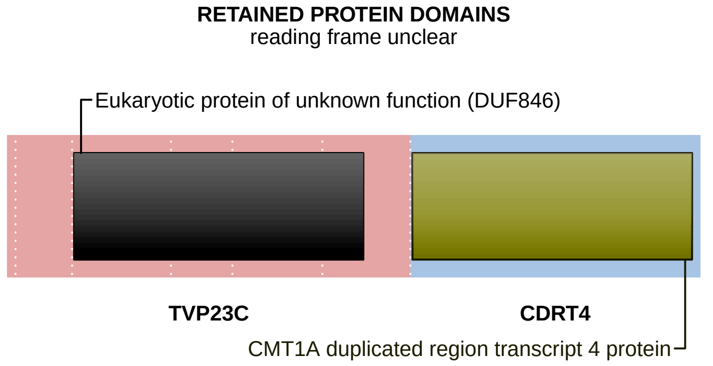


SUPPORTING READ COUNT

Split reads = 44
Discordant mates = 0

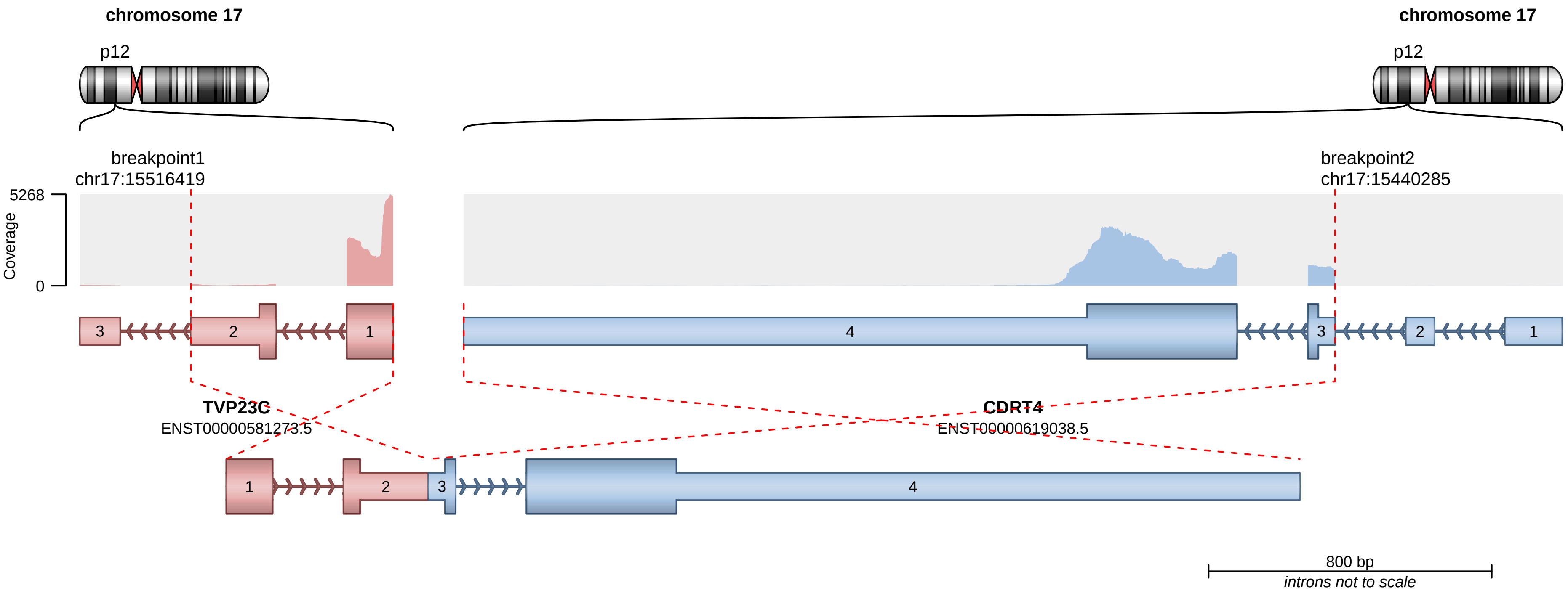


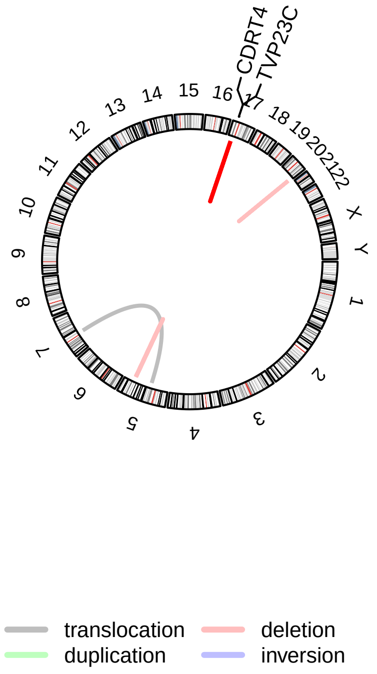




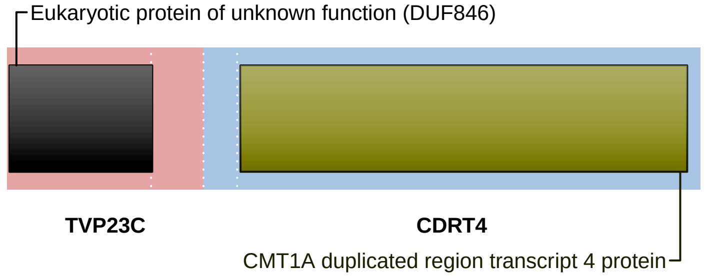
SUPPORTING READ COUNT

Split reads = 38
Discordant mates = 0



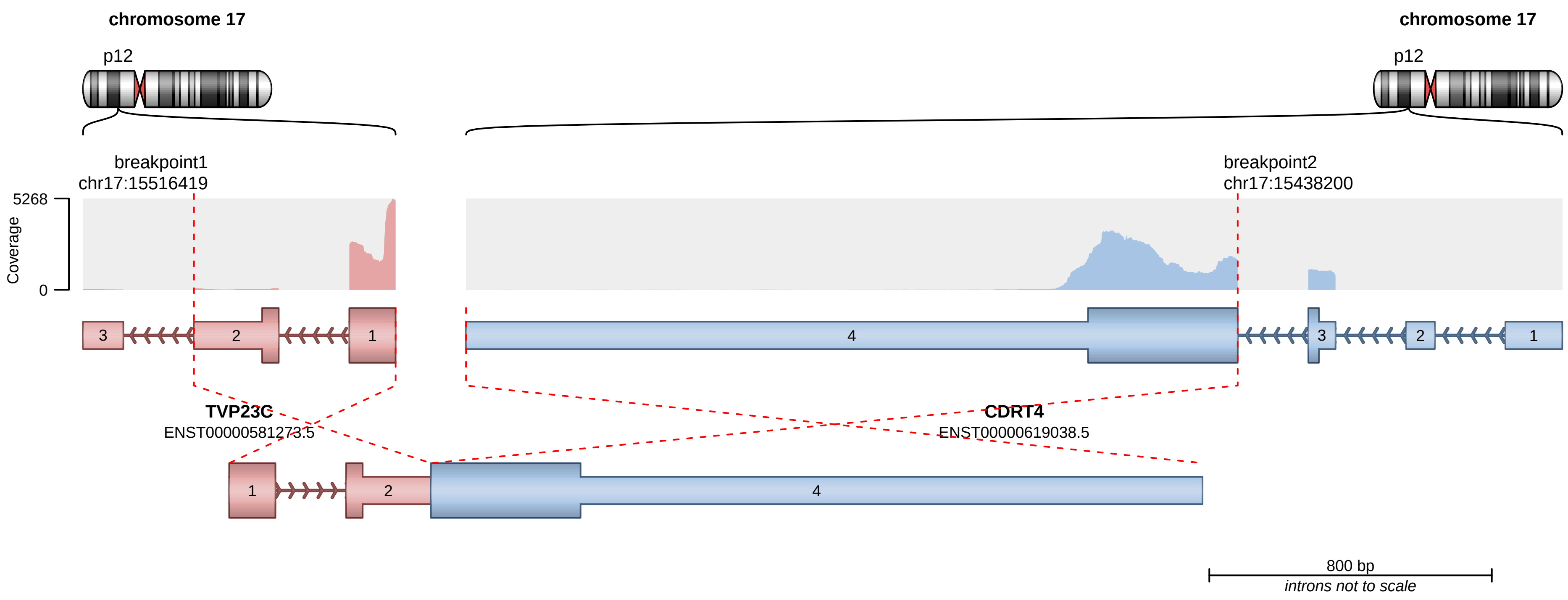


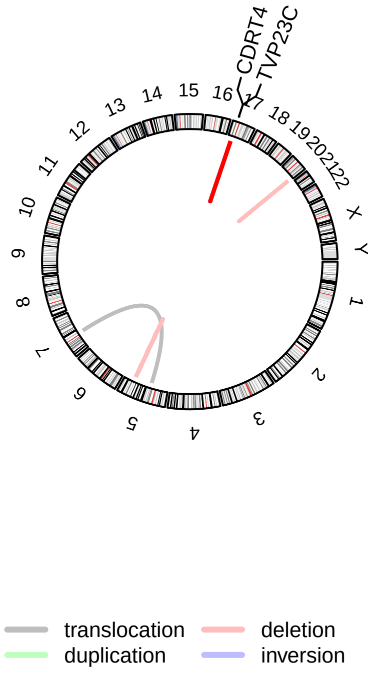
RETAINED PROTEIN DOMAINS
reading frame unclear

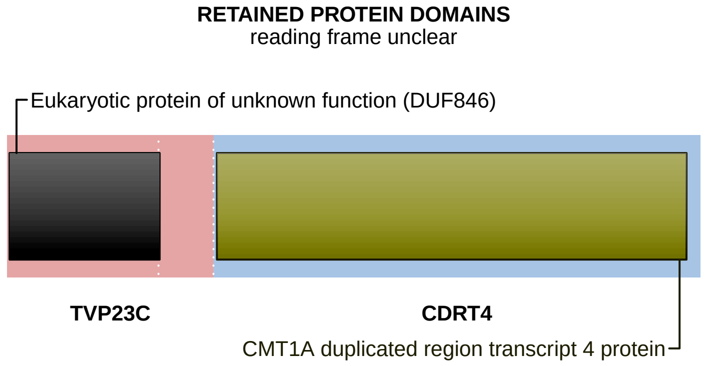


SUPPORTING READ COUNT

Split reads = 12
Discordant mates = 0

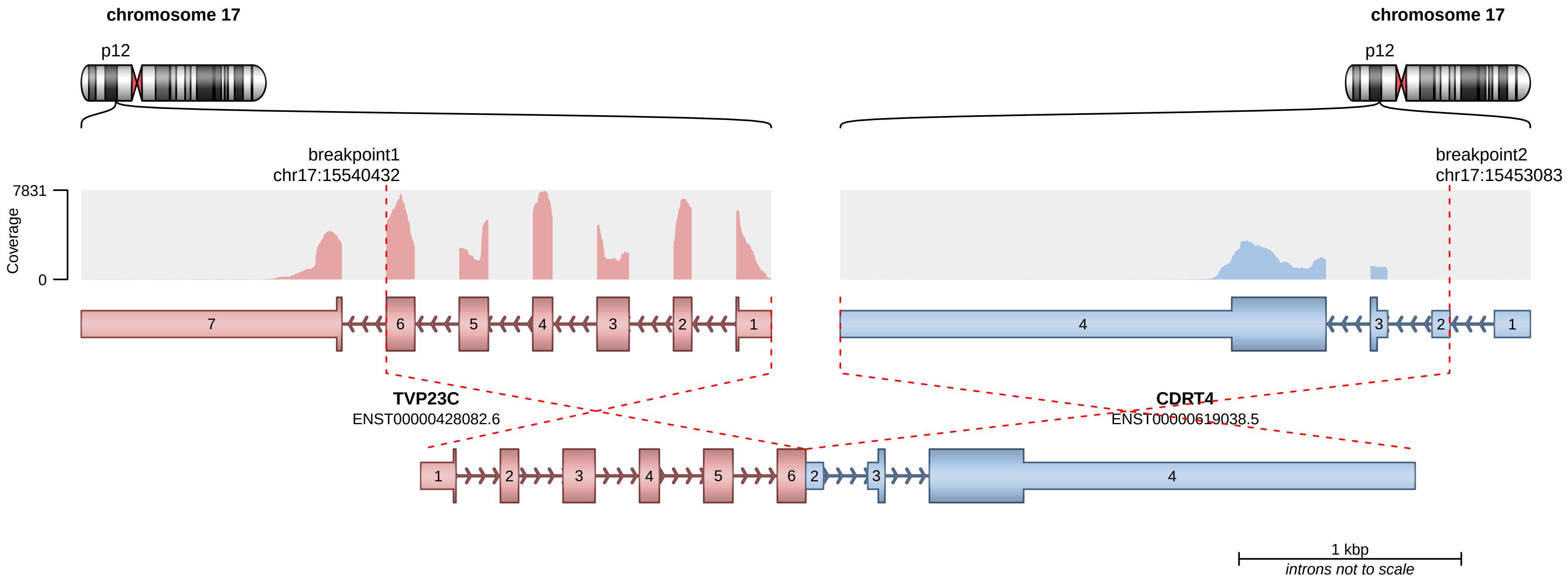


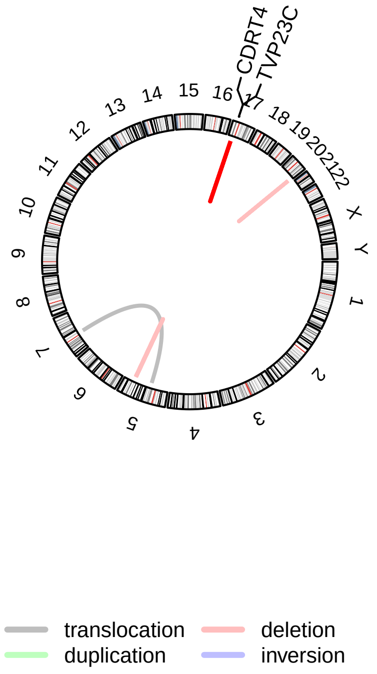




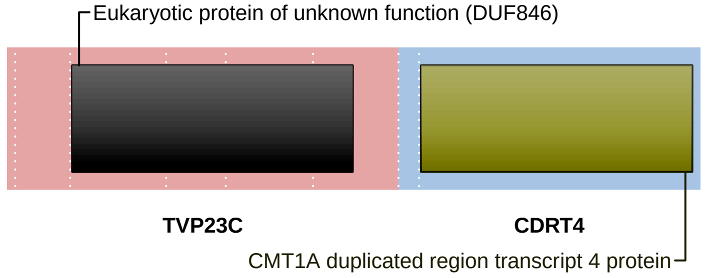
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0



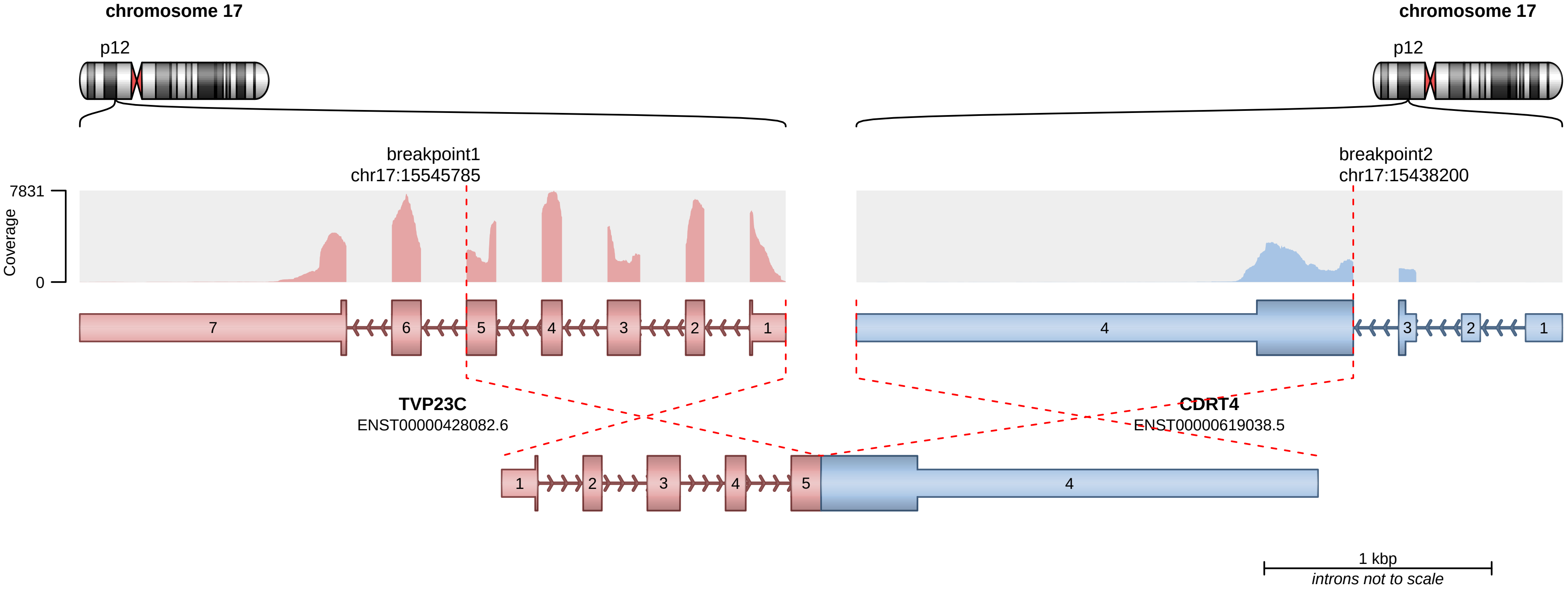


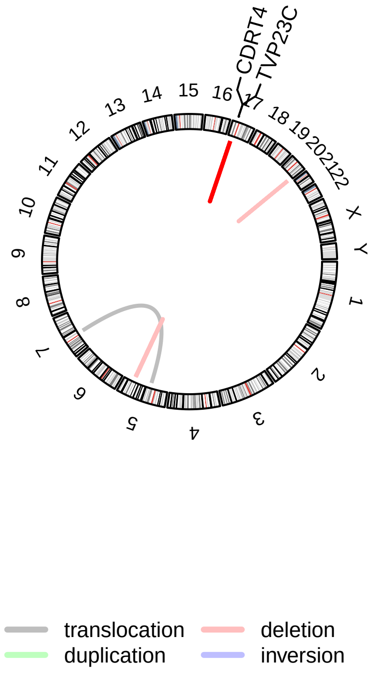
RETAINED PROTEIN DOMAINS
reading frame unclear



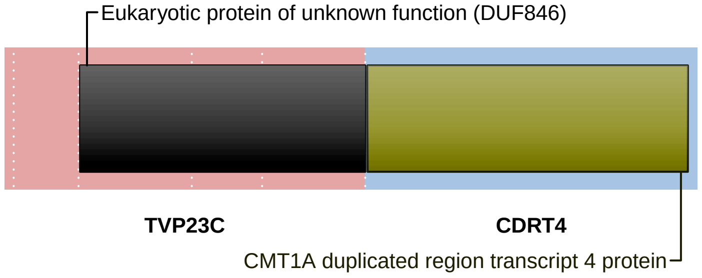
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0



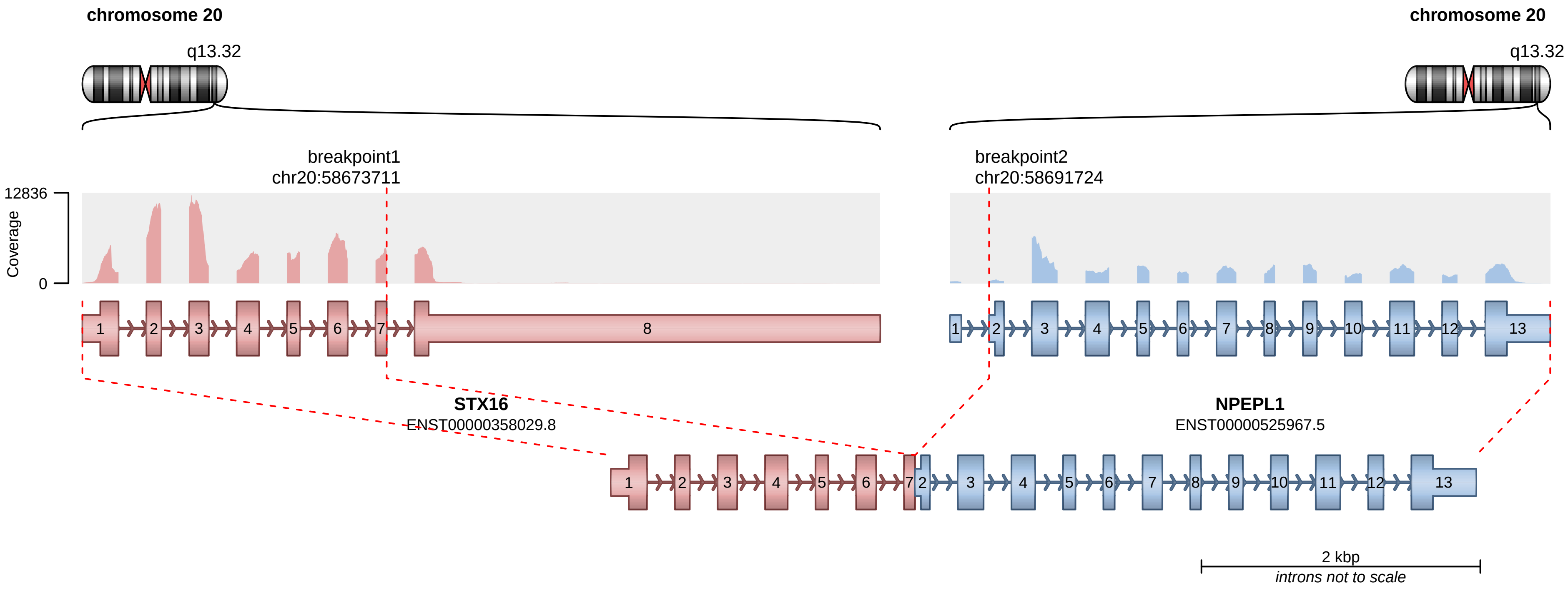


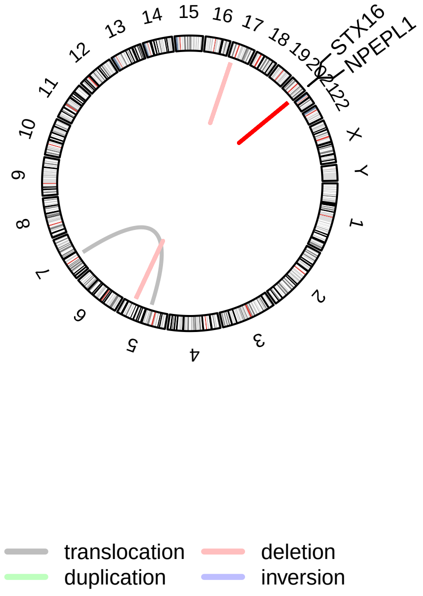
RETAINED PROTEIN DOMAINS
reading frame unclear

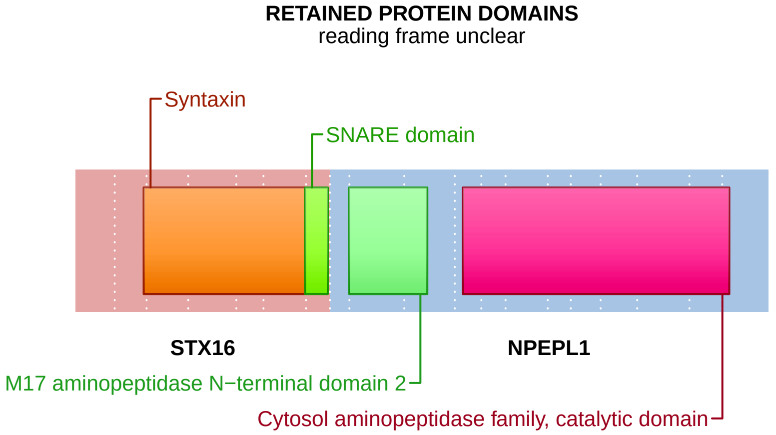


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

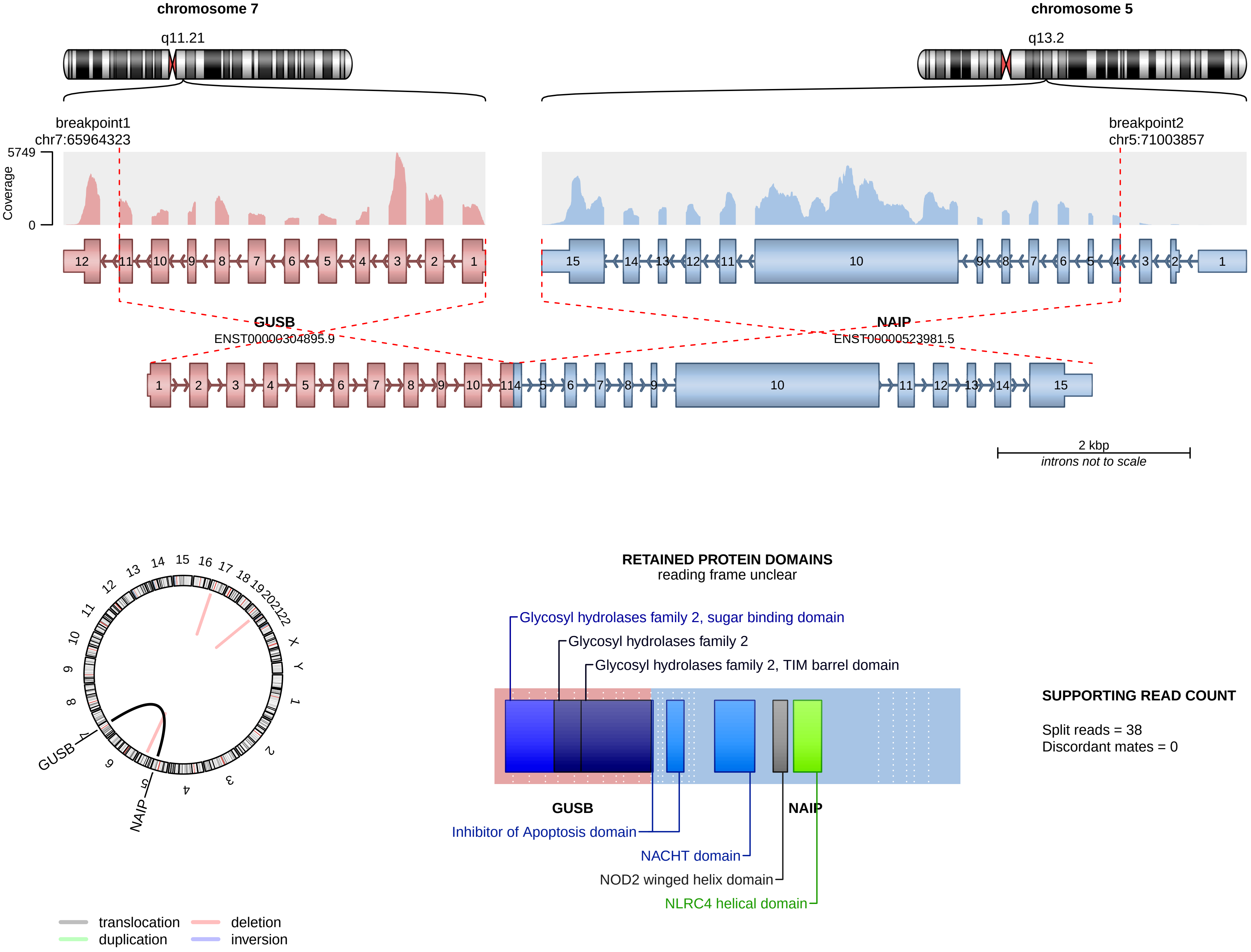


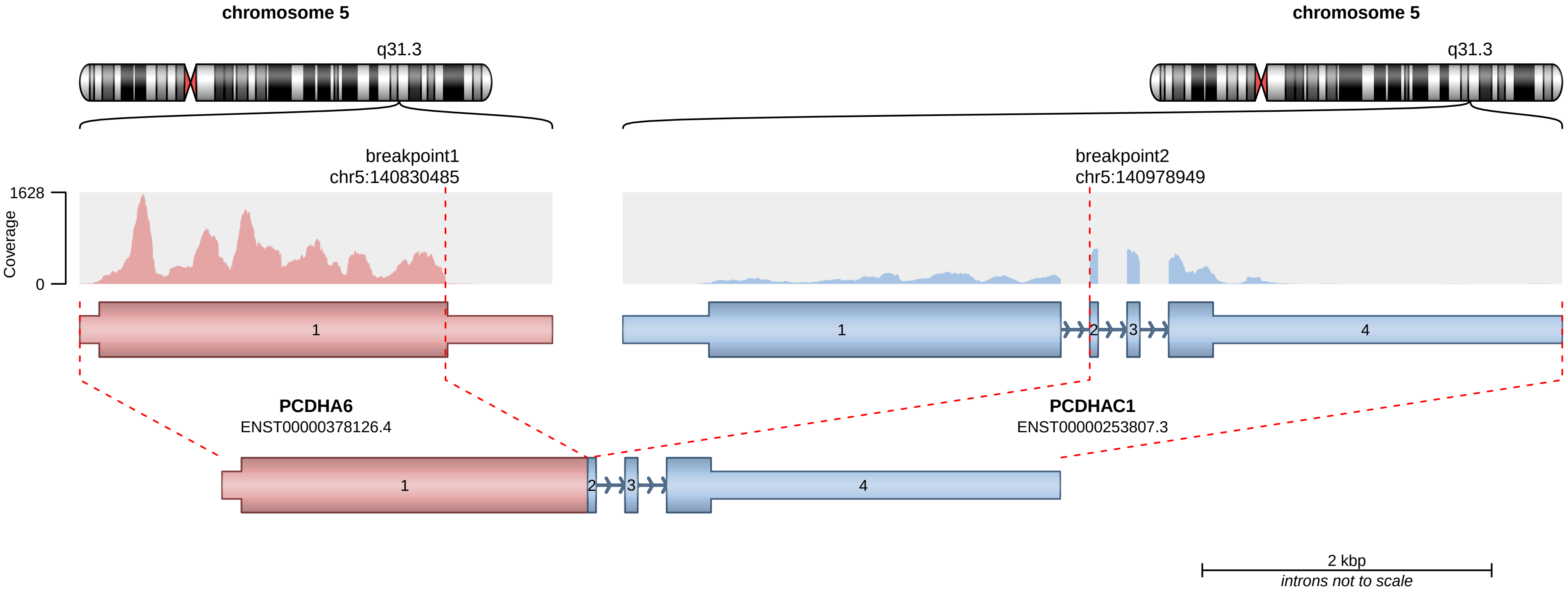


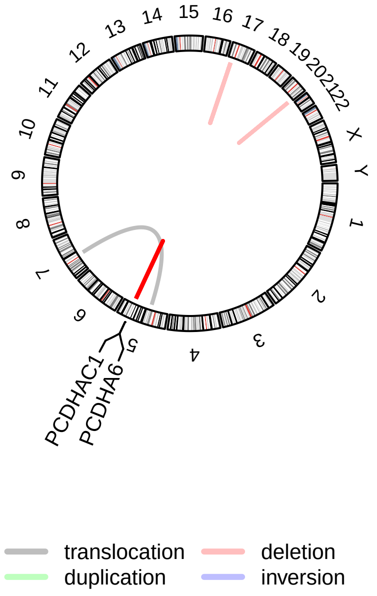


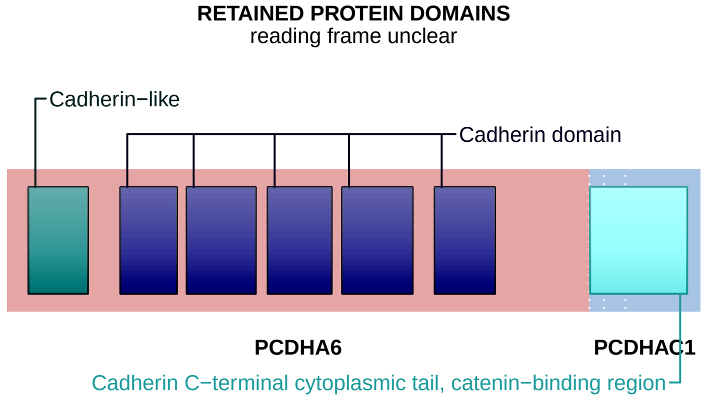
SUPPORTING READ COUNT

Split reads = 85
Discordant mates = 1


chromosome 7
q11.21
chromosome 5
q13.2
breakpoint1
chr7:65964323
breakpoint2
chr5:71003857
5749
Coverage
0
GUSB
ENST00000304895.9
NAIP
ENST00000523981.5
2 kbp
introns not to scale
RETAINED PROTEIN DOMAINS
reading frame unclear
Glycosyl hydrolases family 2, sugar binding domain
Glycosyl hydrolases family 2
Glycosyl hydrolases family 2, TIM barrel domain
GUSB
NAIP
Inhibitor of Apoptosis domain
NACHT domain
NOD2 winged helix domain
NLRC4 helical domain
SUPPORTING READ COUNT
Split reads = 38
Discordant mates = 0
GUSB
NAIP
translocation
deletion
duplication
inversion

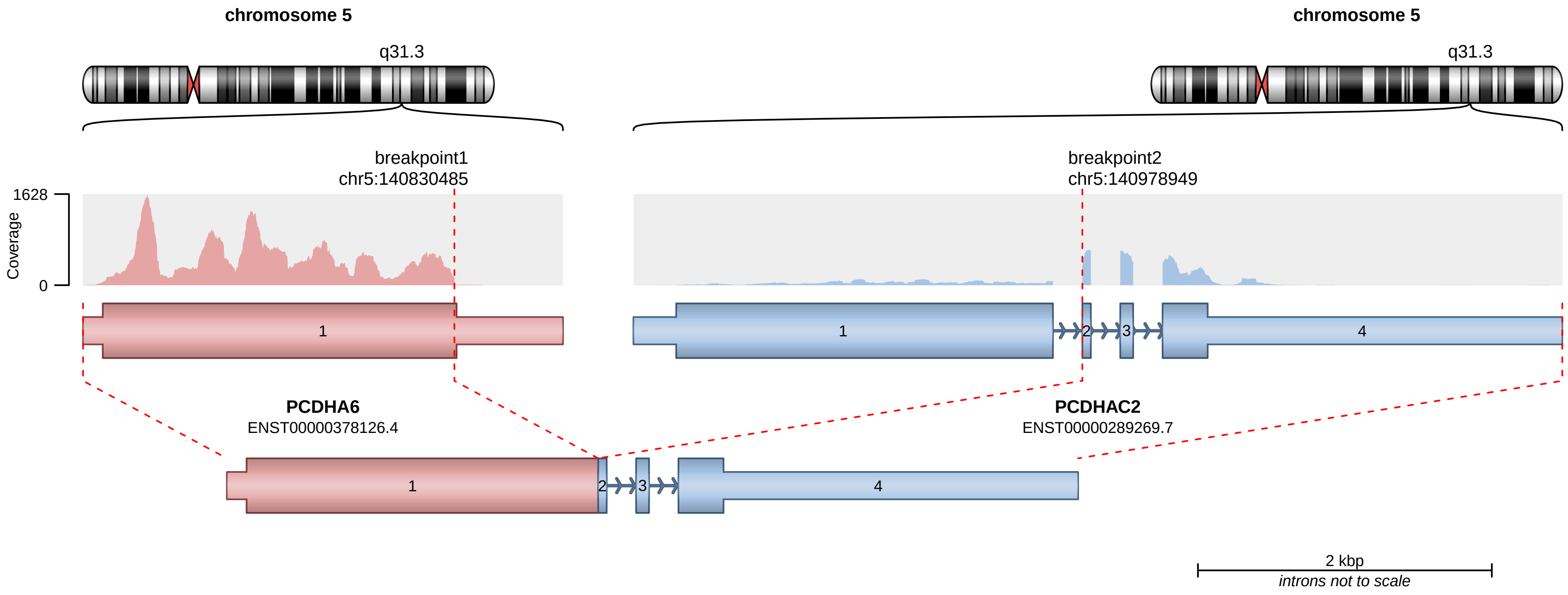


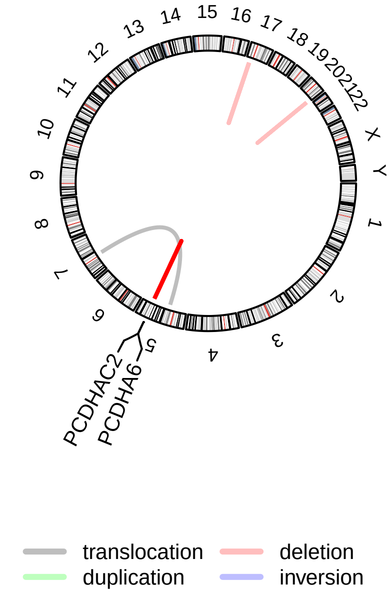


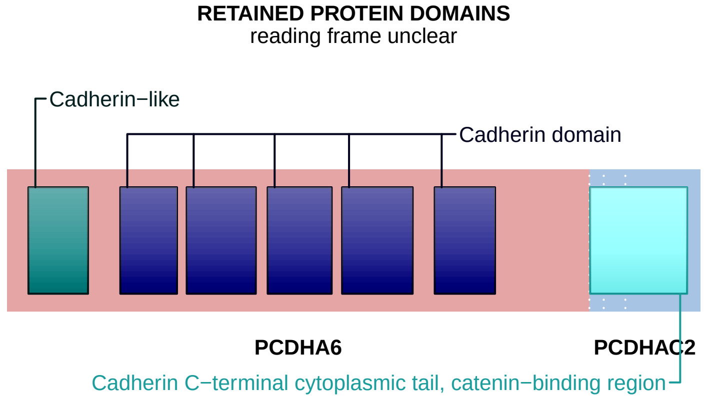


SUPPORTING READ COUNT

Split reads = 30
Discordant mates = 0

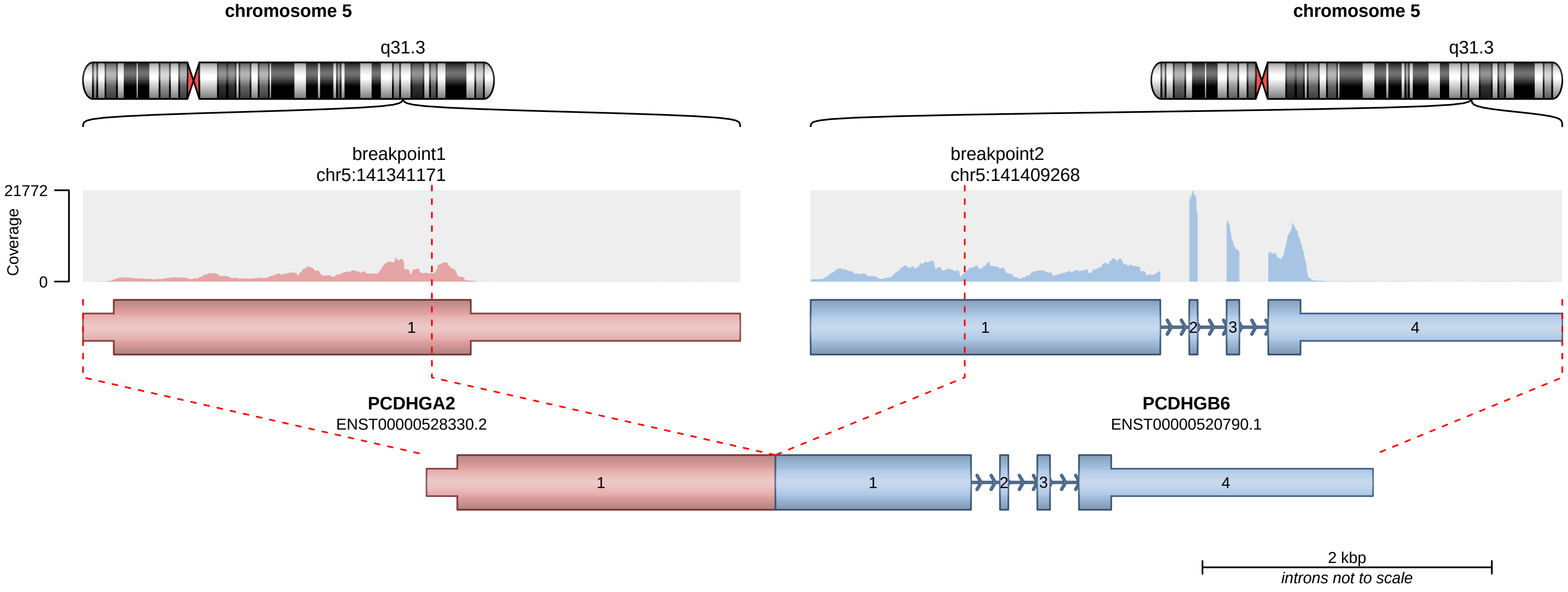


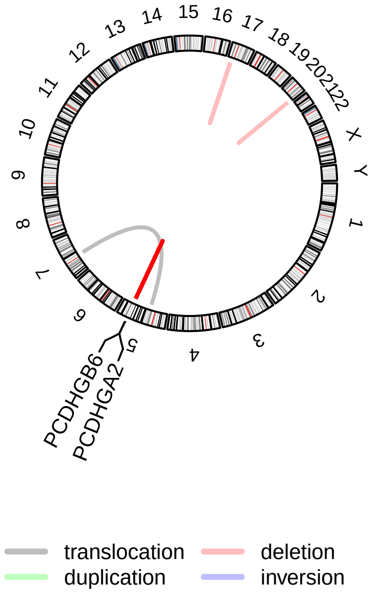




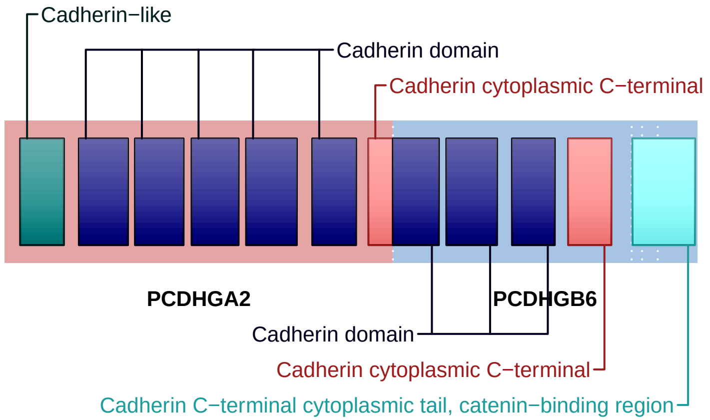
SUPPORTING READ COUNT

Split reads = 30
Discordant mates = 0





RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0