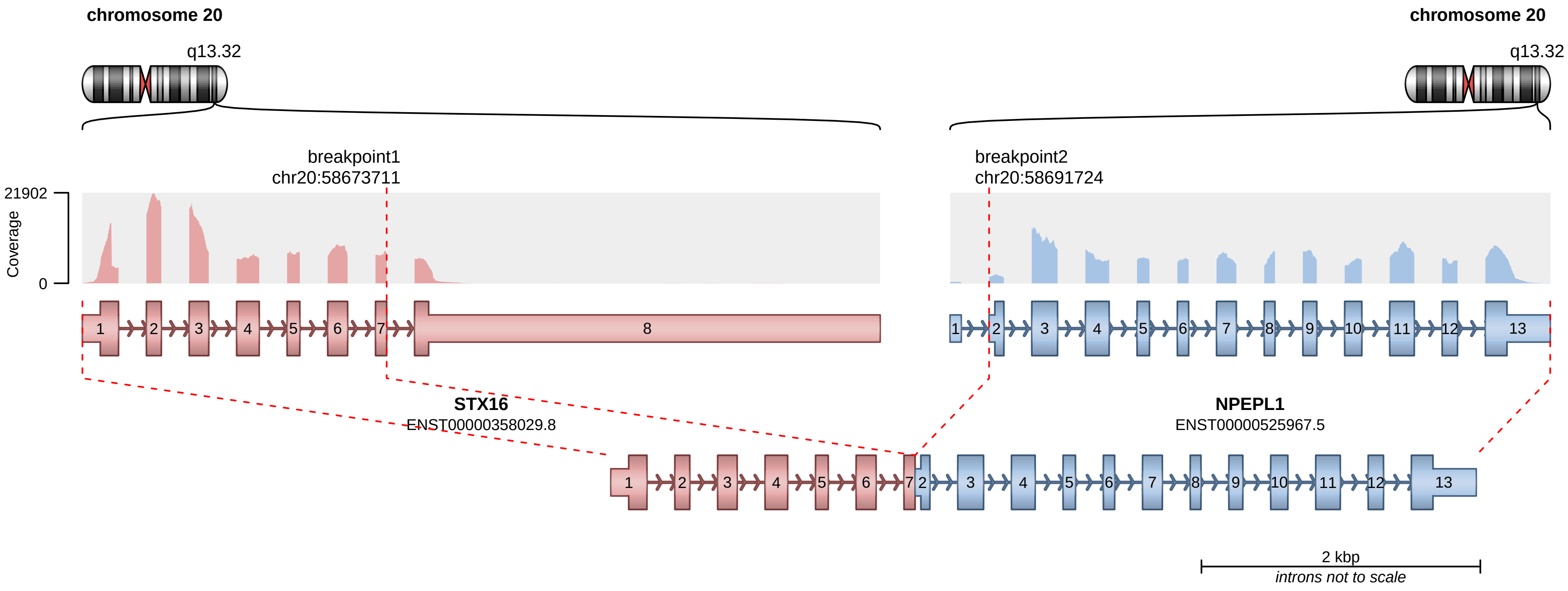
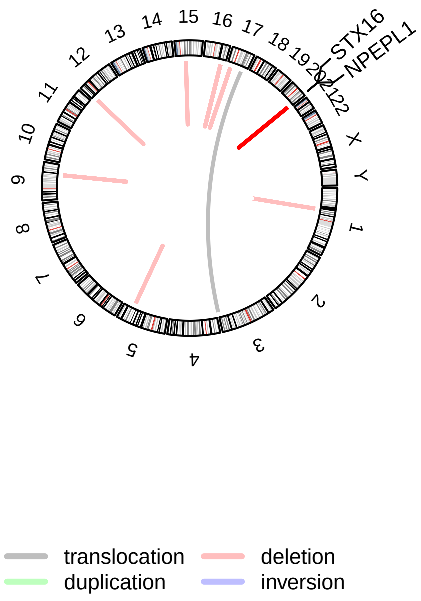
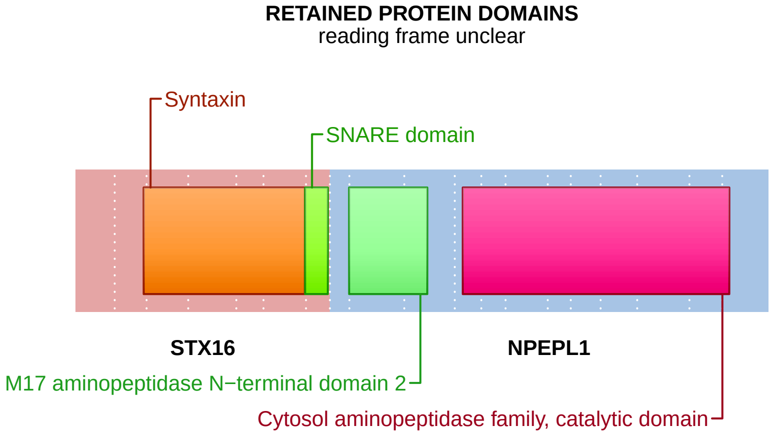
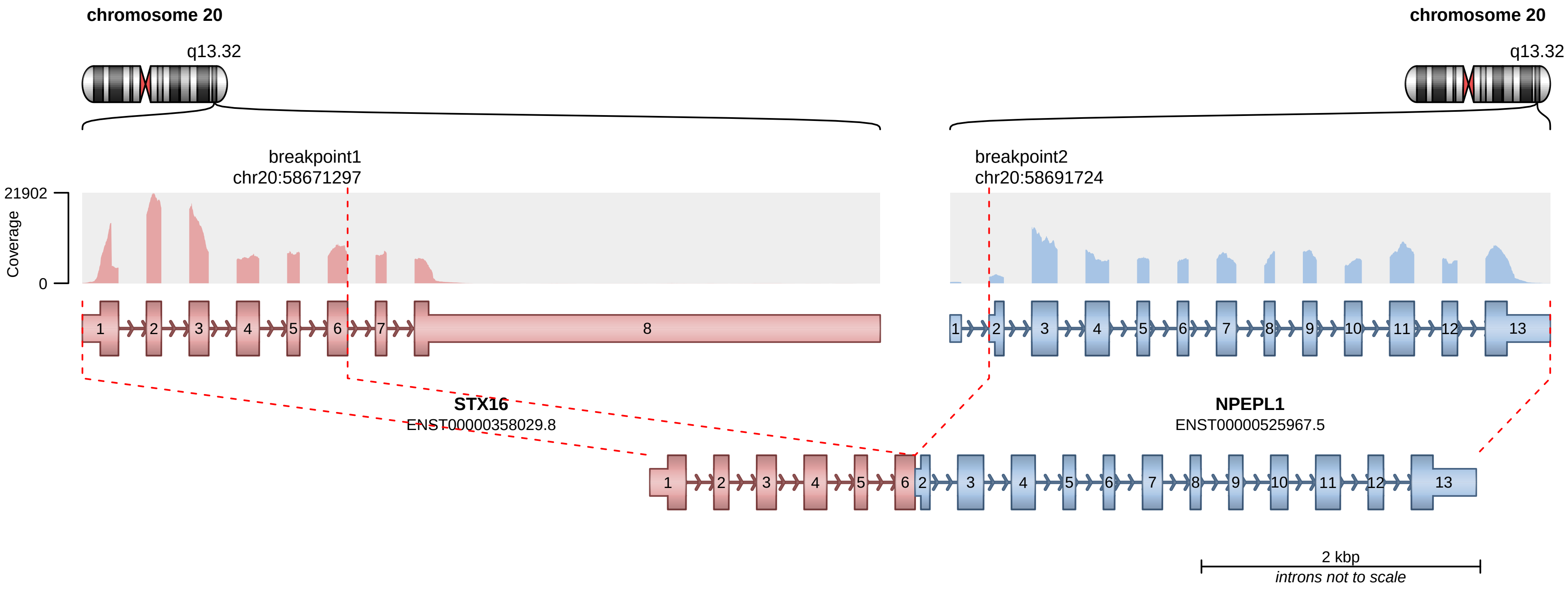


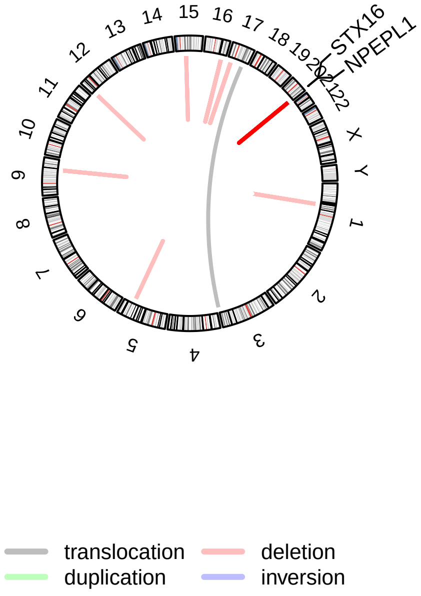




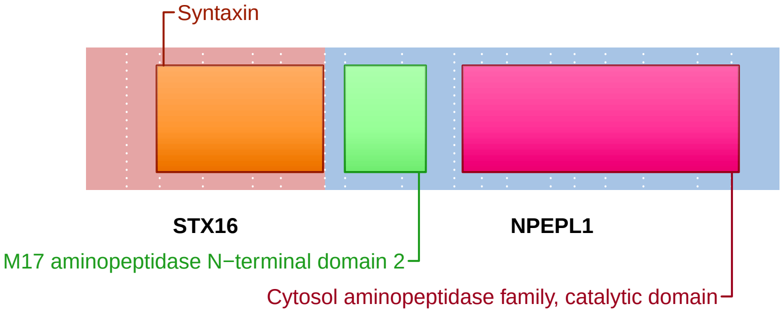
SUPPORTING READ COUNT

Split reads = 235
Discordant mates = 6



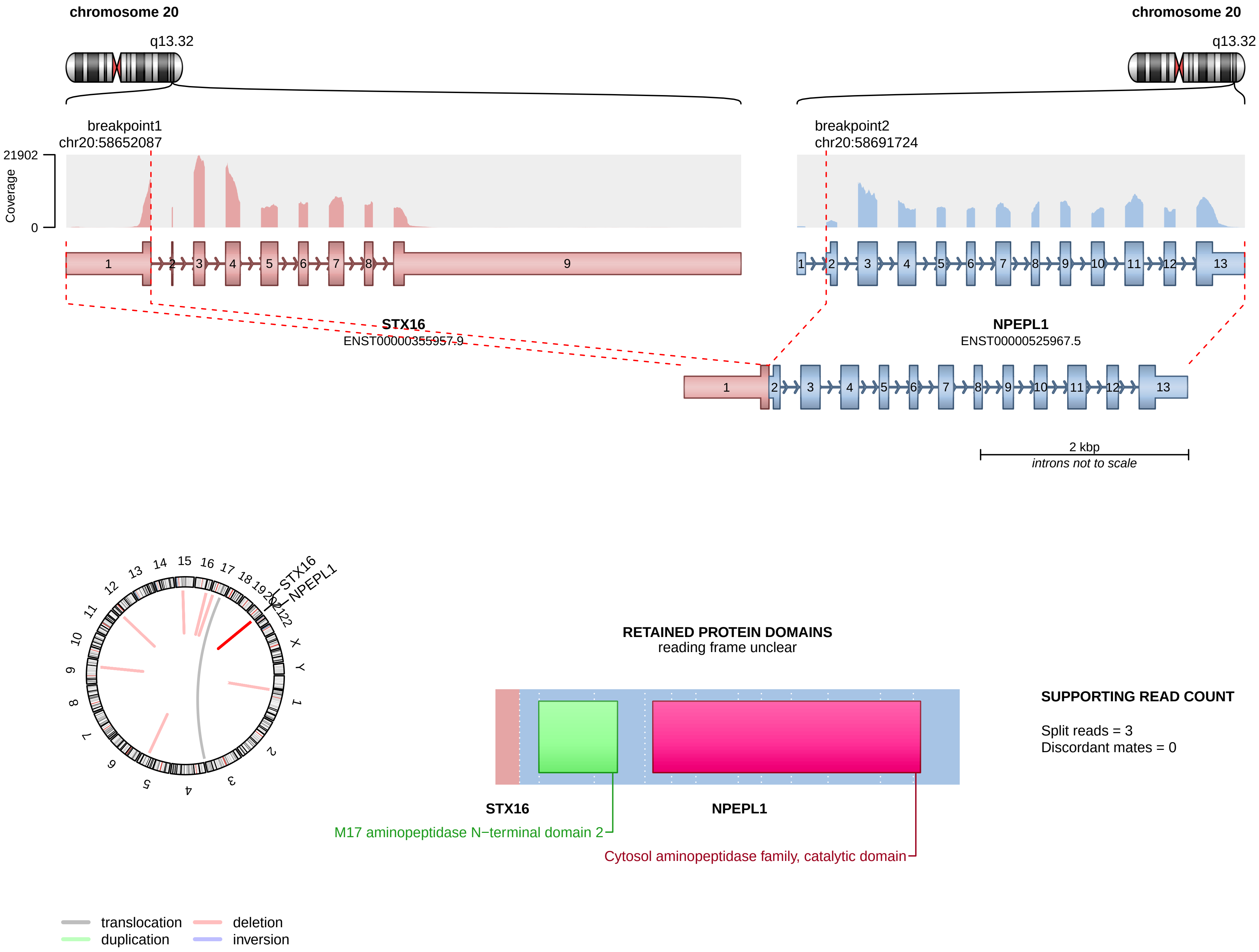


RETAINED PROTEIN DOMAINS
reading frame unclear



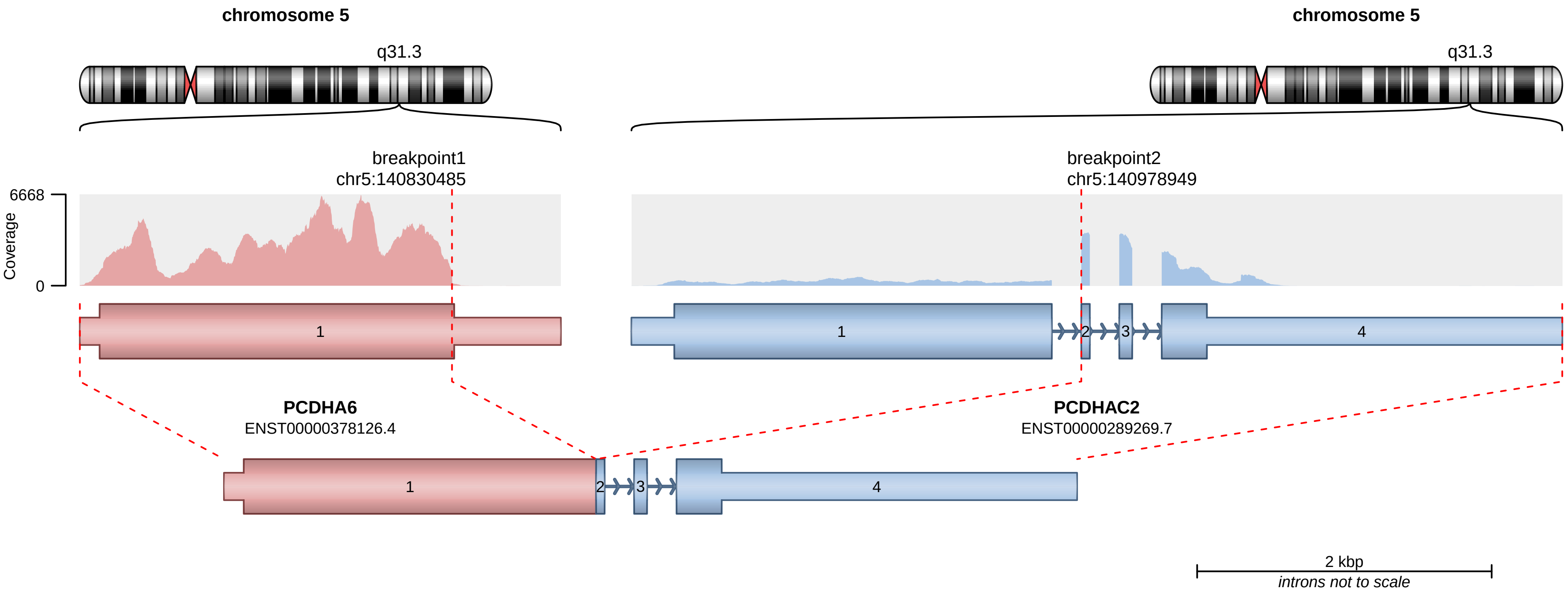
SUPPORTING READ COUNT

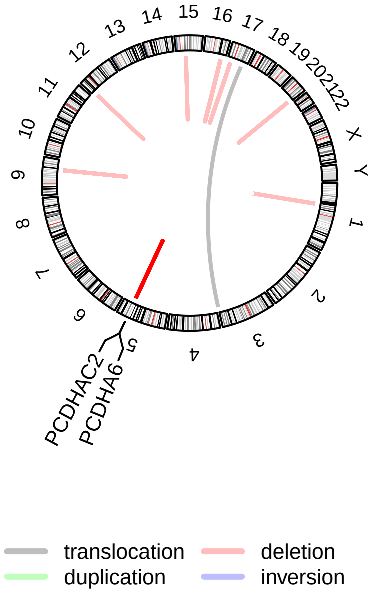
Split reads = 3
Discordant mates = 2

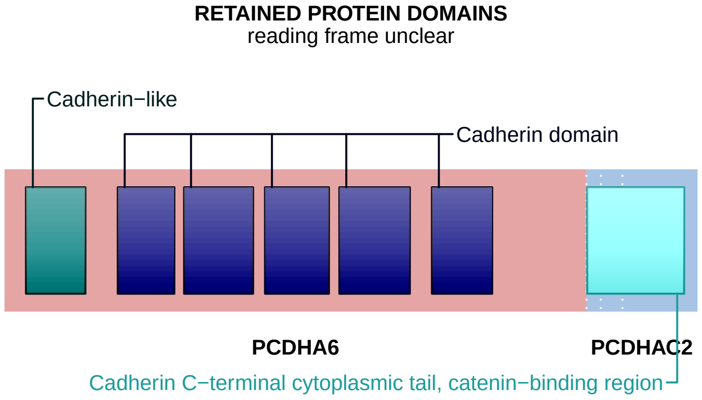


SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0

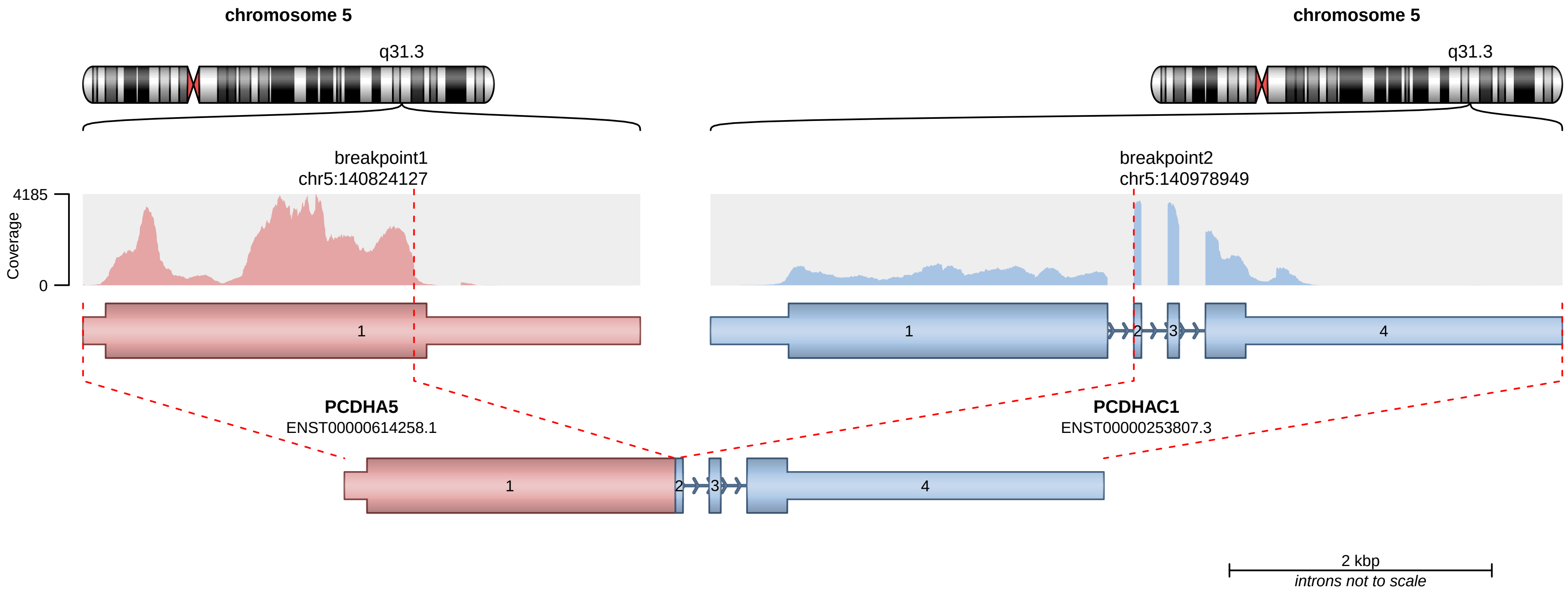


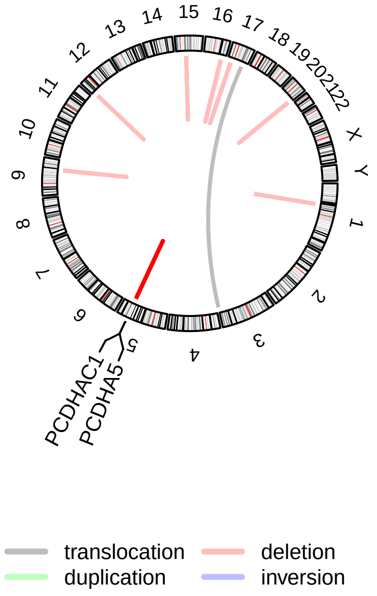


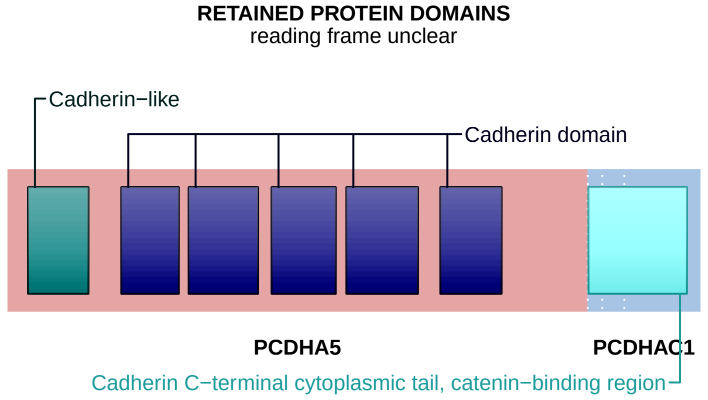


SUPPORTING READ COUNT

Split reads = 212
Discordant mates = 2

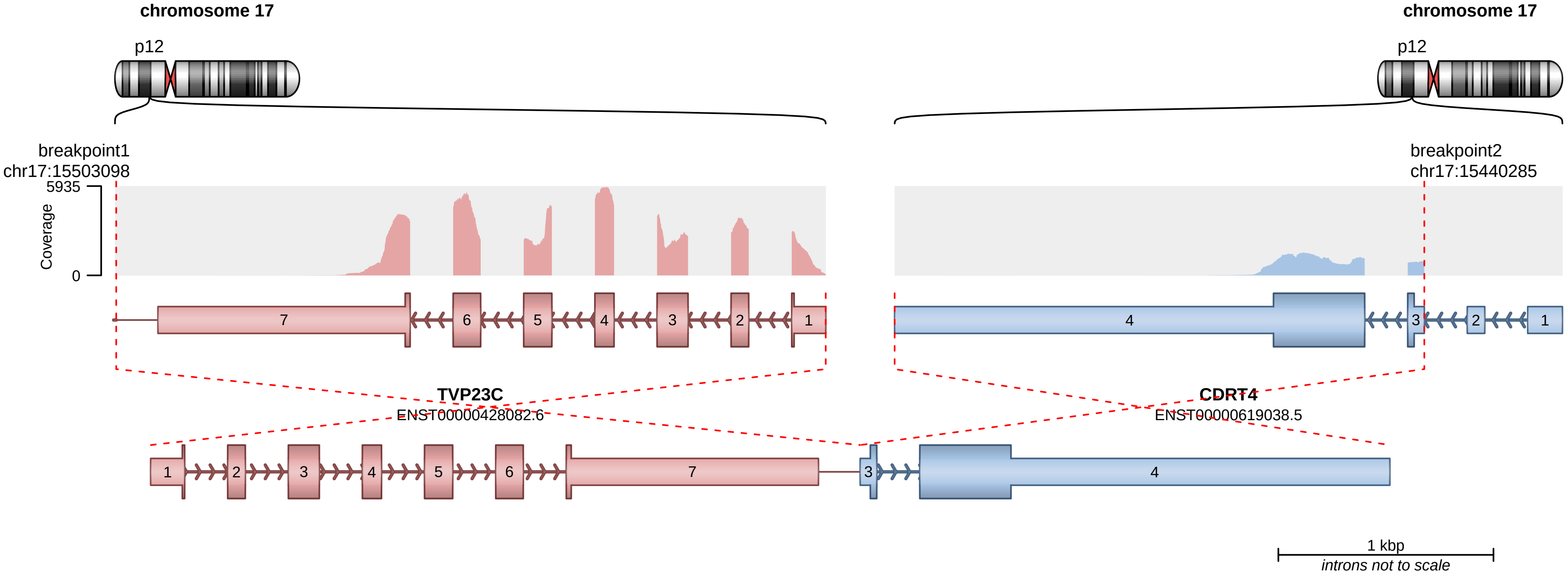


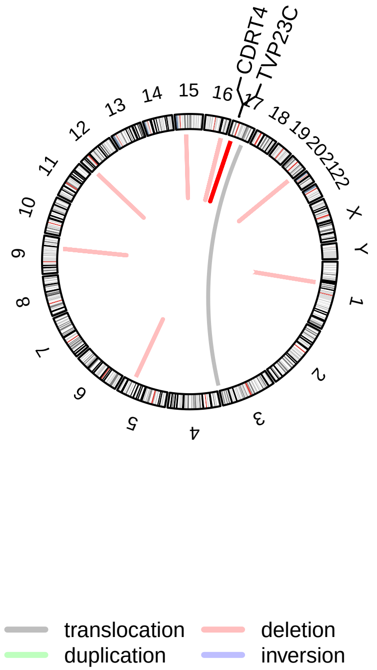


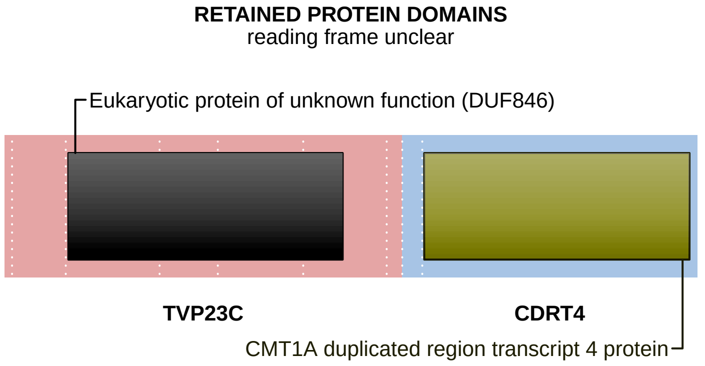


SUPPORTING READ COUNT

Split reads = 169
Discordant mates = 4

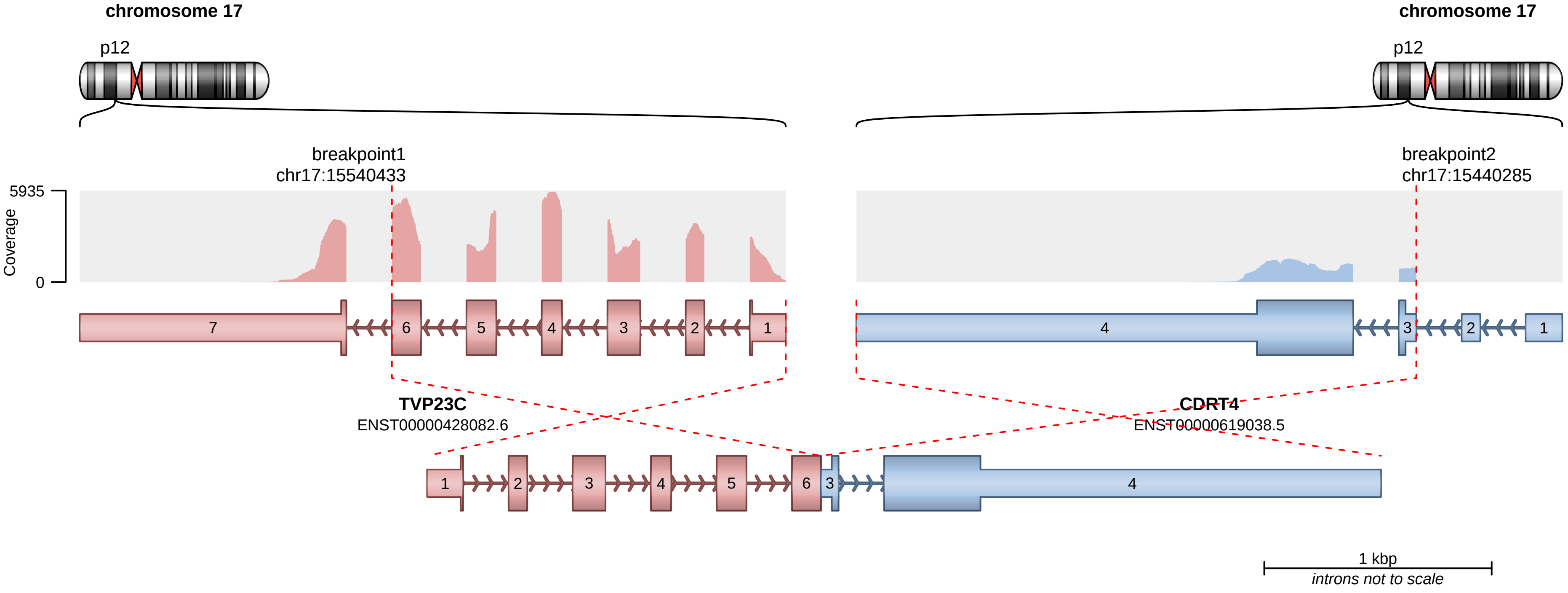


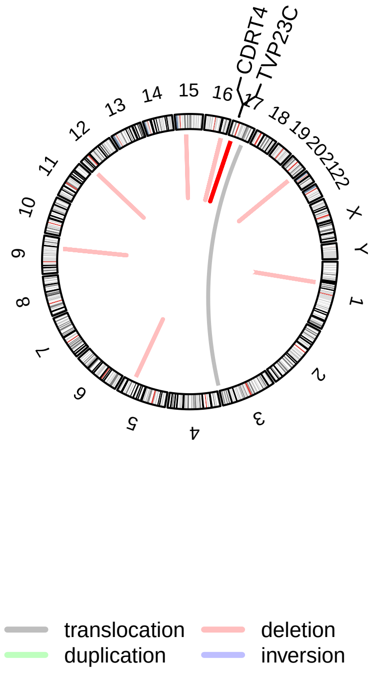




SUPPORTING READ COUNT

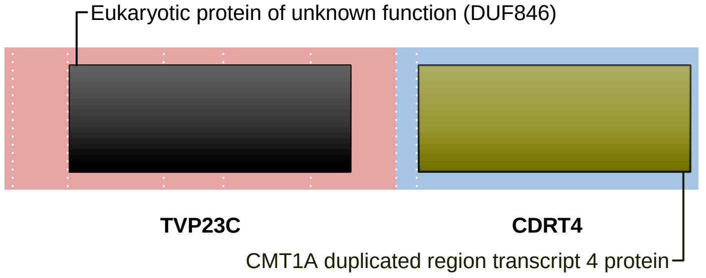
Split reads = 117
Discordant mates = 1





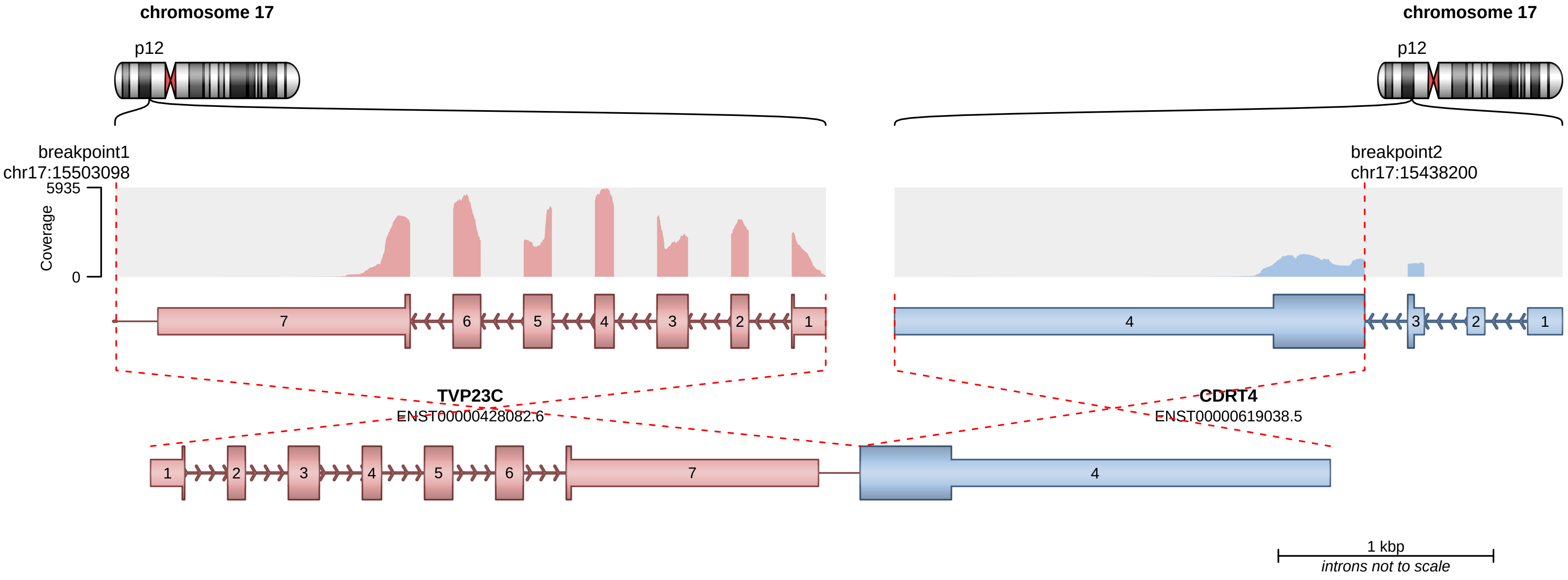
RETAINED PROTEIN DOMAINS

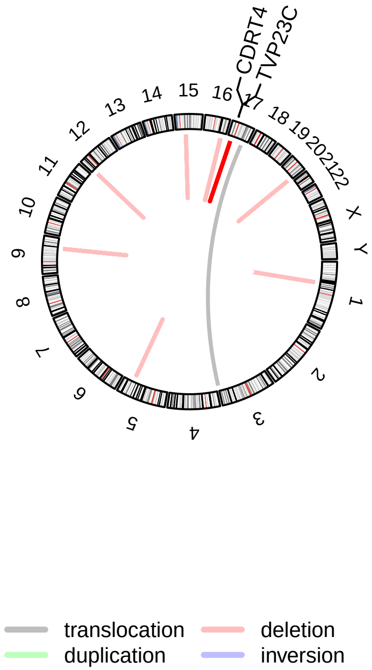
reading frame unclear



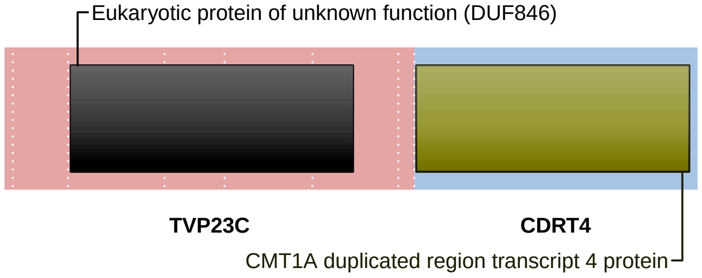
SUPPORTING READ COUNT

Split reads = 57
Discordant mates = 0



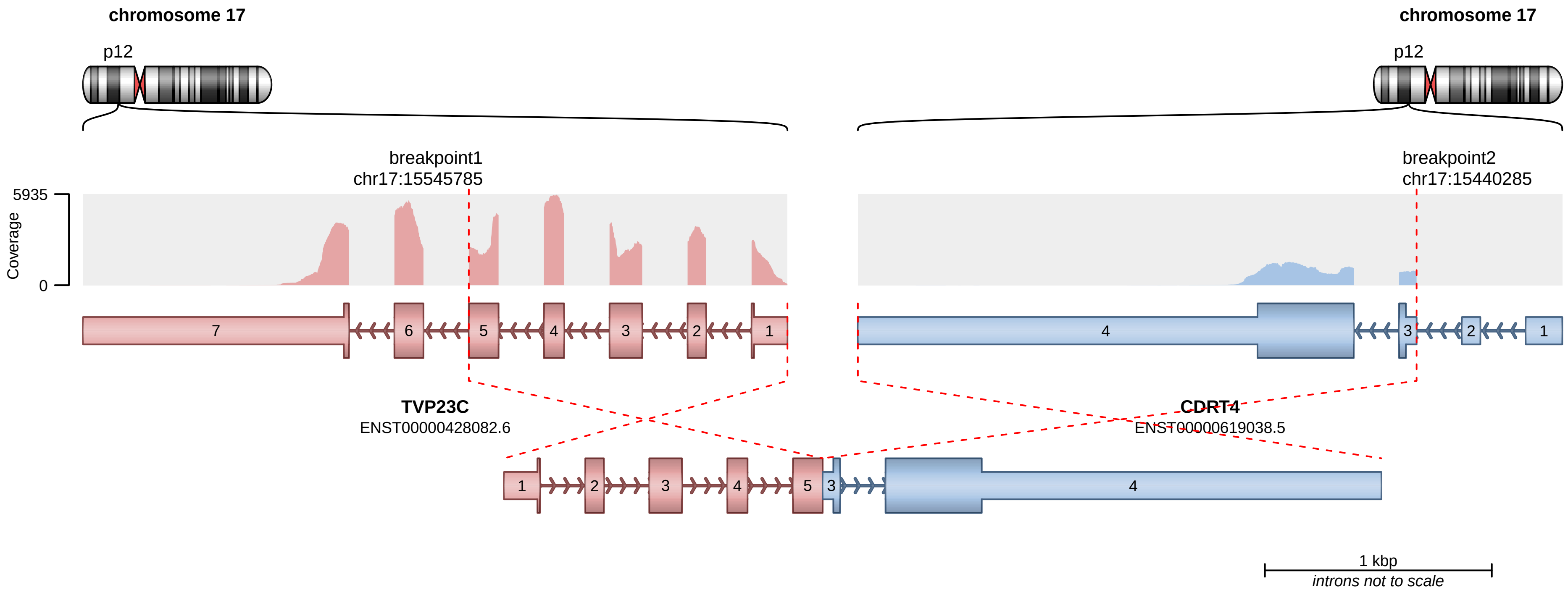


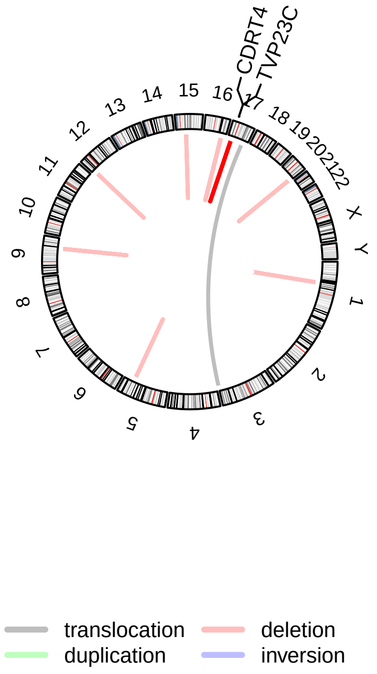
RETAINED PROTEIN DOMAINS
reading frame unclear

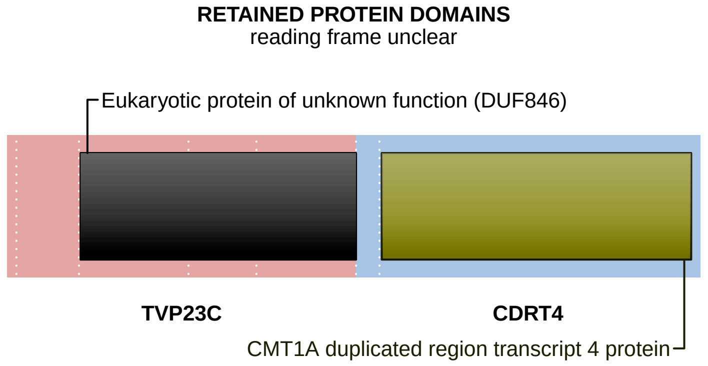


SUPPORTING READ COUNT

Split reads = 47
Discordant mates = 0

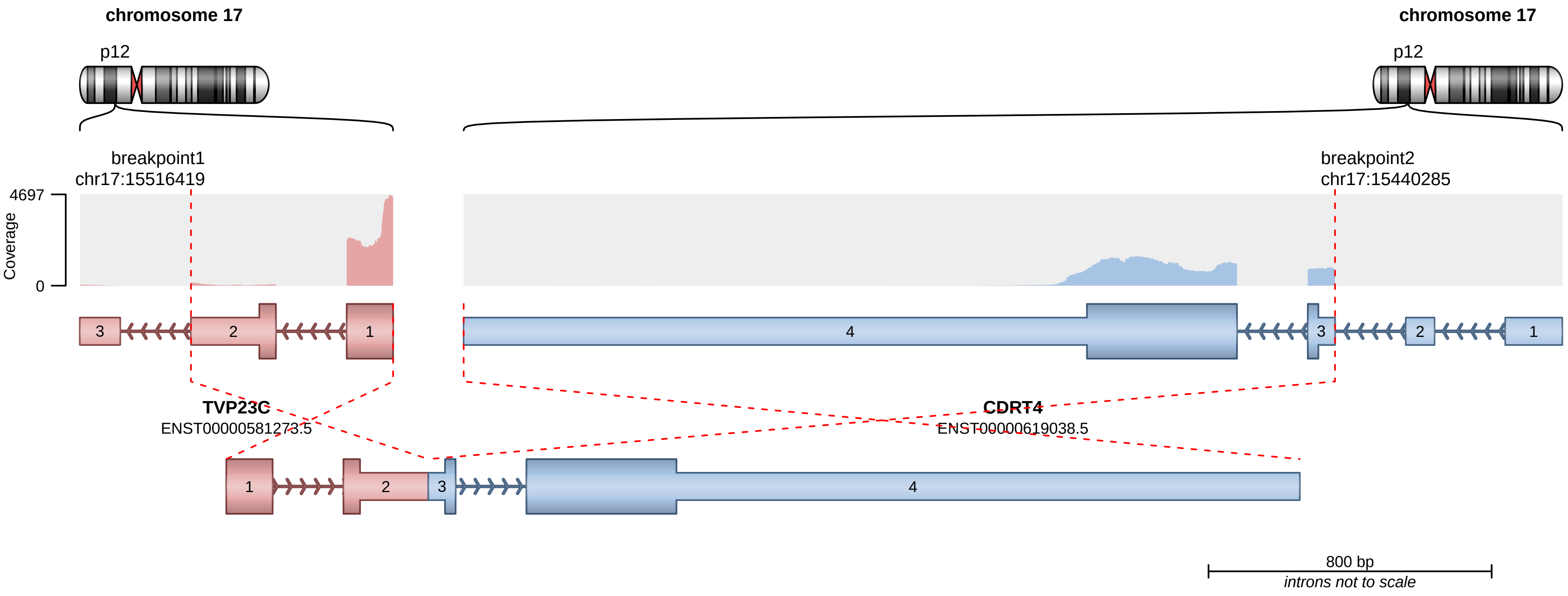


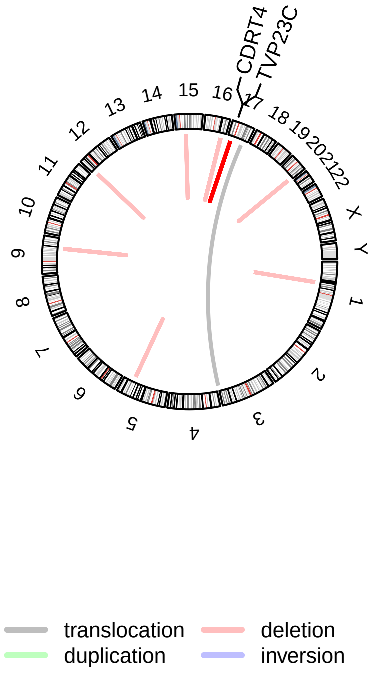


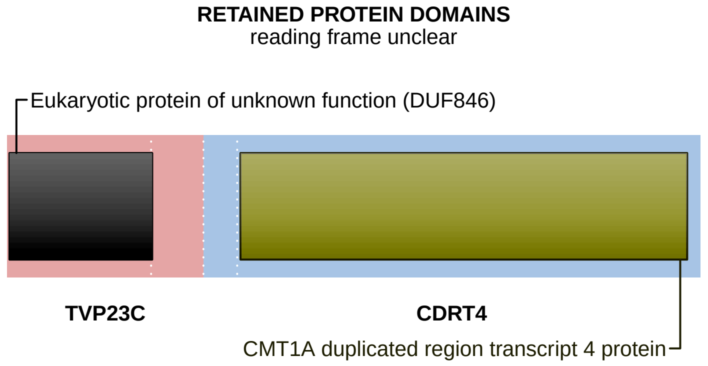


SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 0

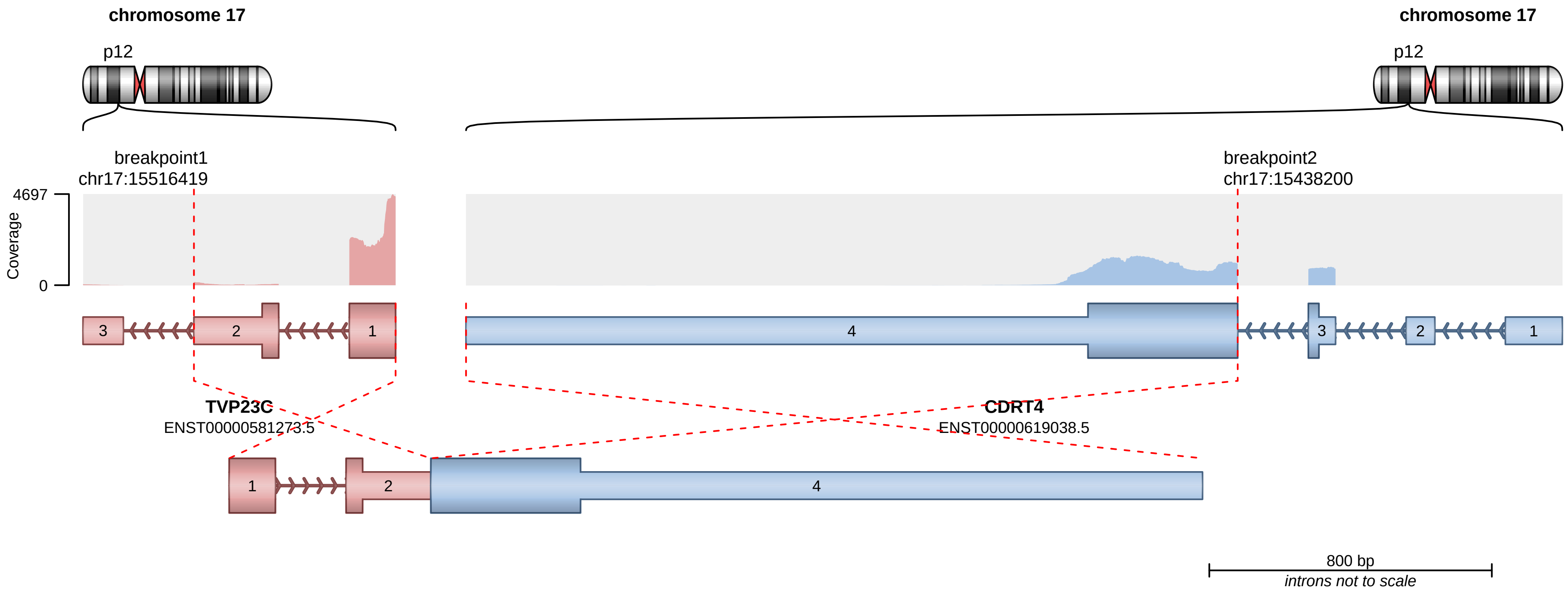


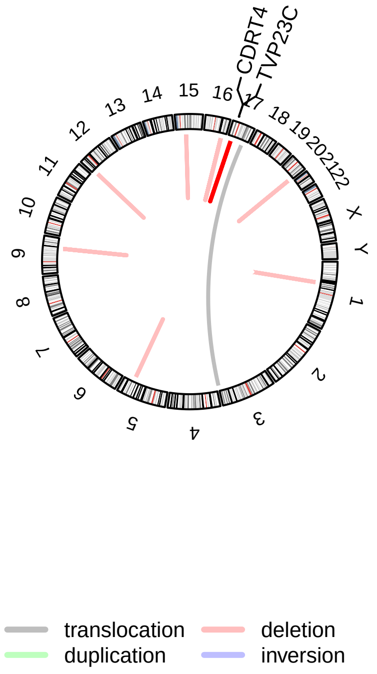




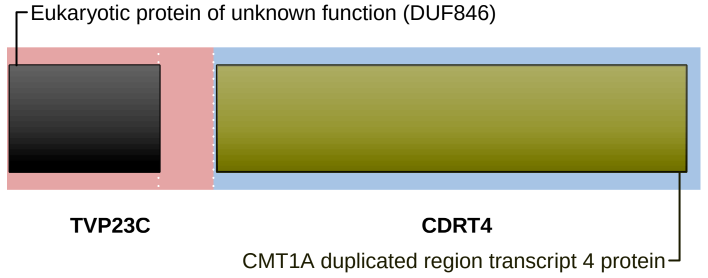
SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 0



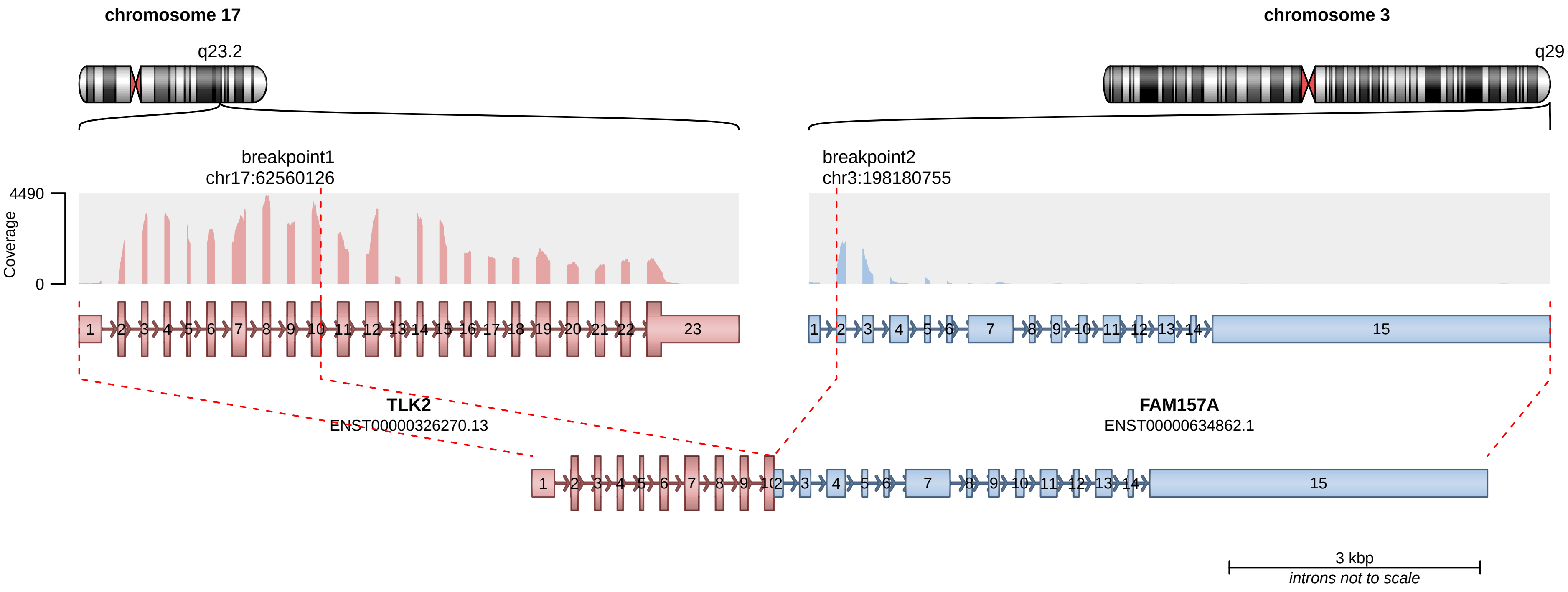


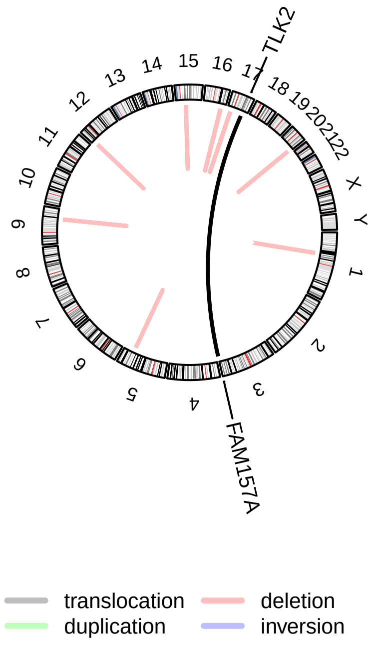
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

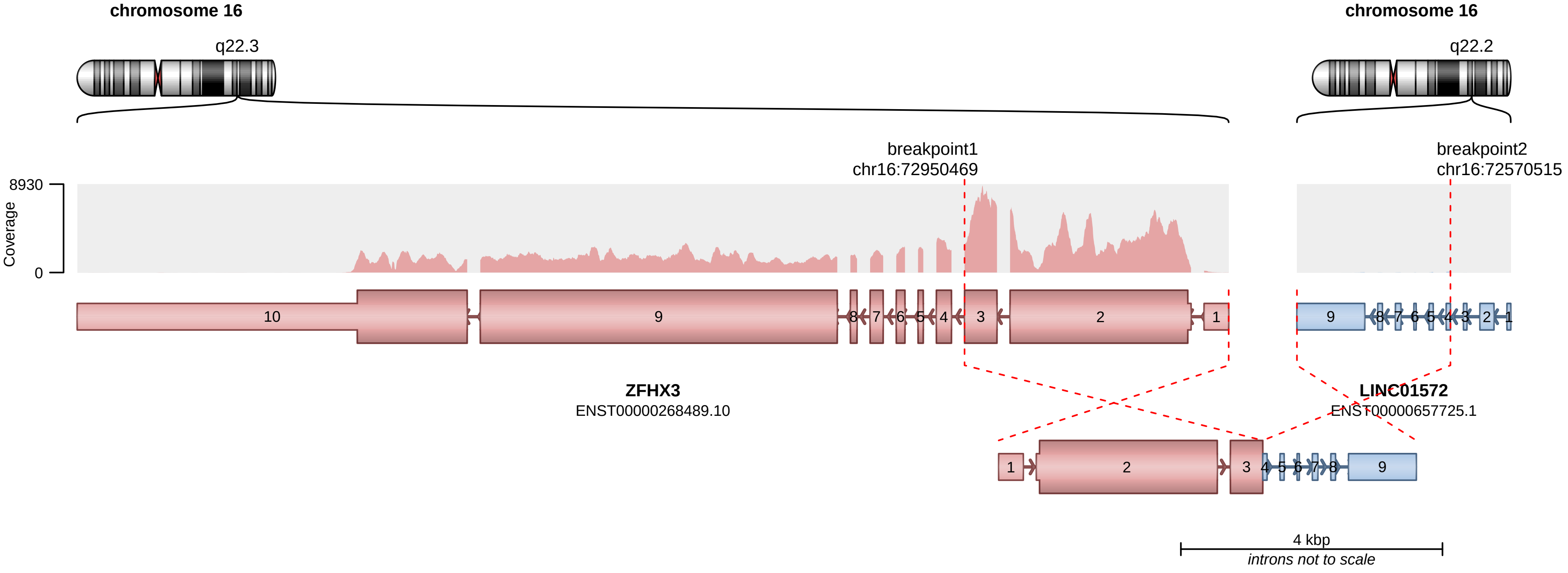


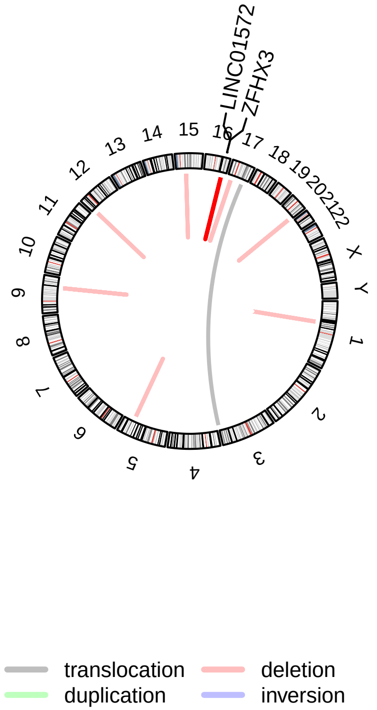


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 83
Discordant mates = 2



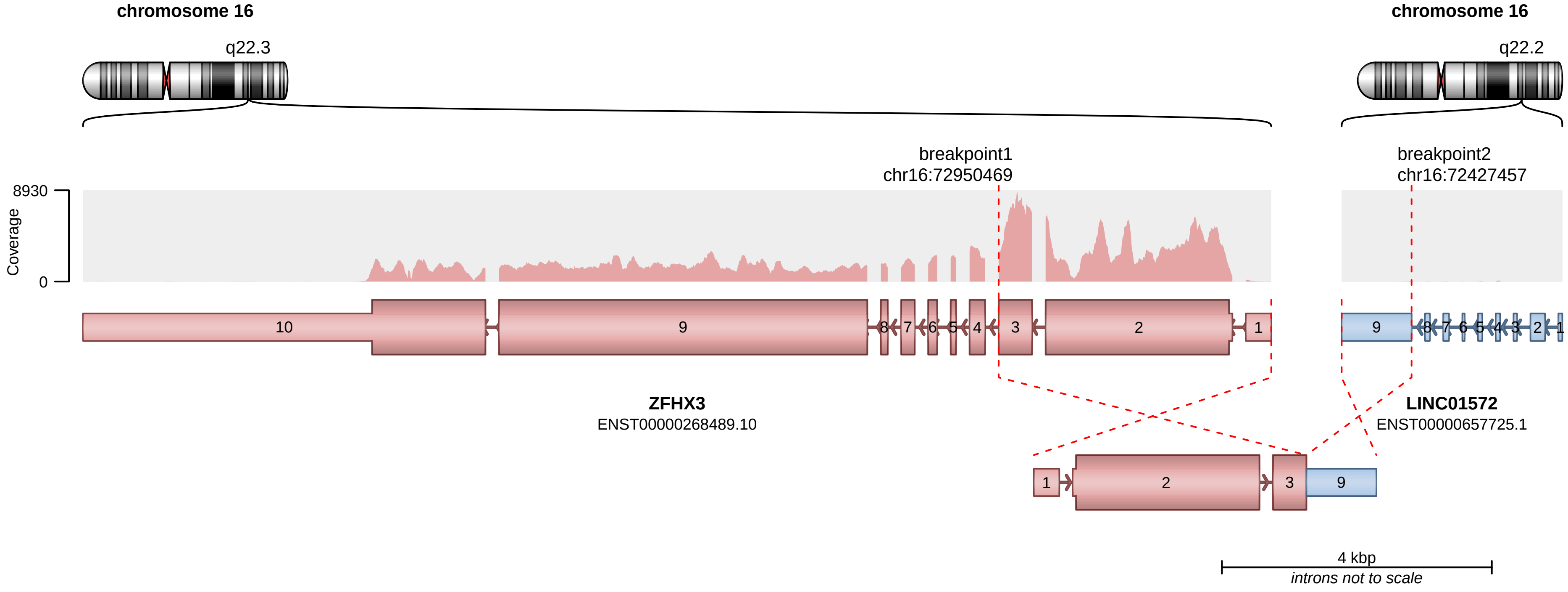


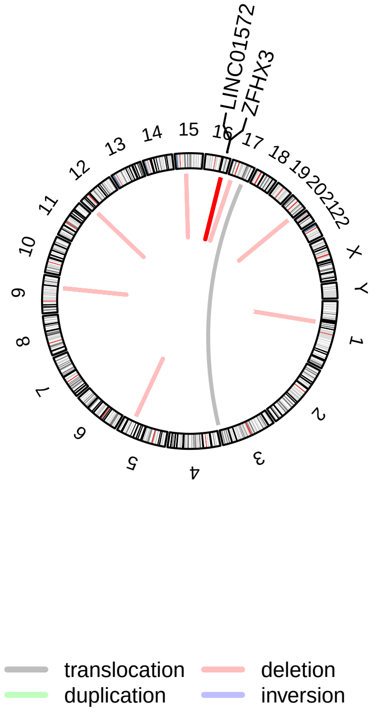
RETAINED PROTEIN DOMAINS
reading frame unclear

ZFHX3

SUPPORTING READ COUNT

Split reads = 62
Discordant mates = 2



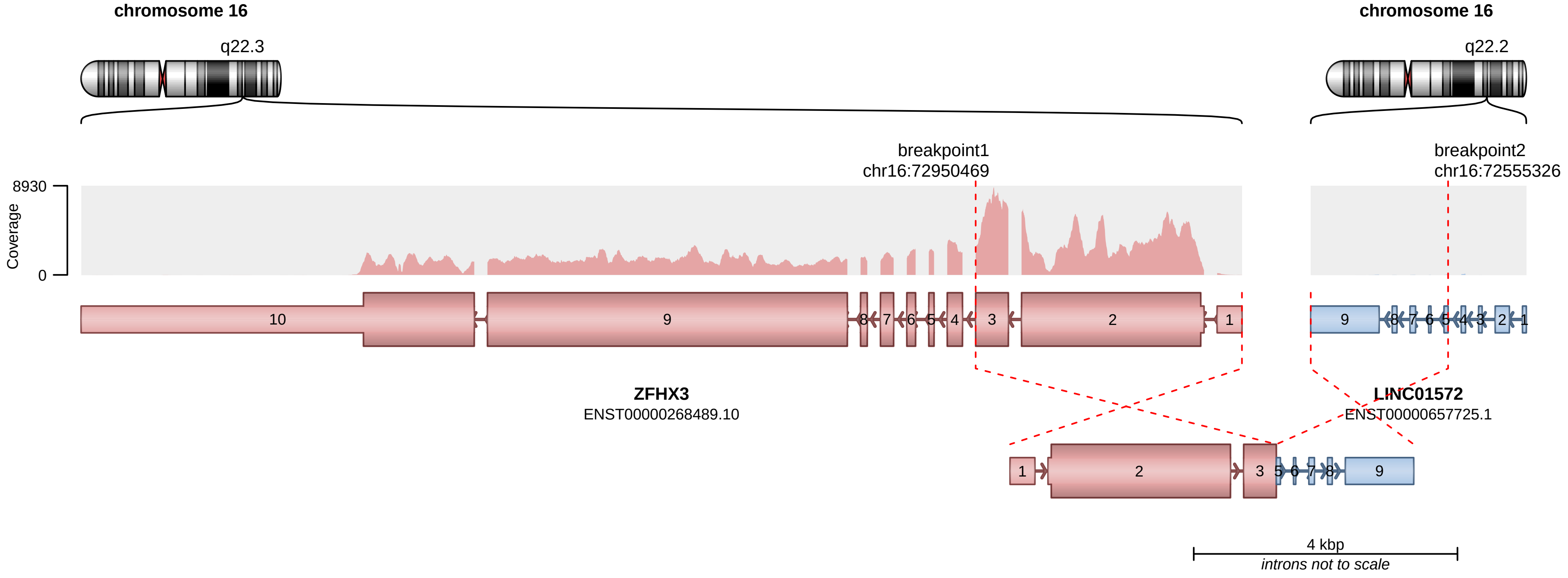


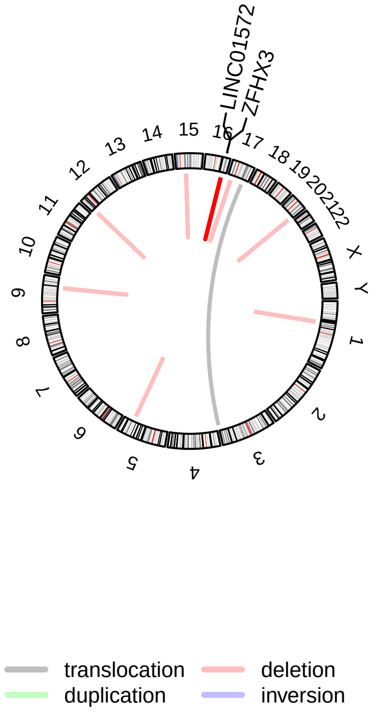
RETAINED PROTEIN DOMAINS
reading frame unclear

ZFHX3

SUPPORTING READ COUNT

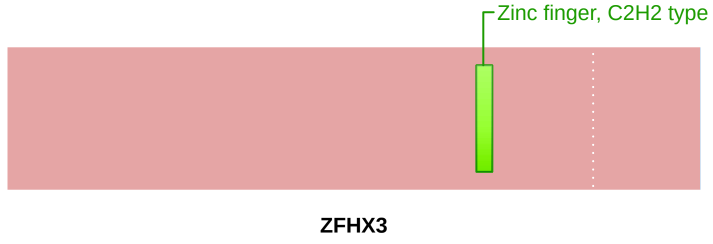
Split reads = 9
Discordant mates = 0





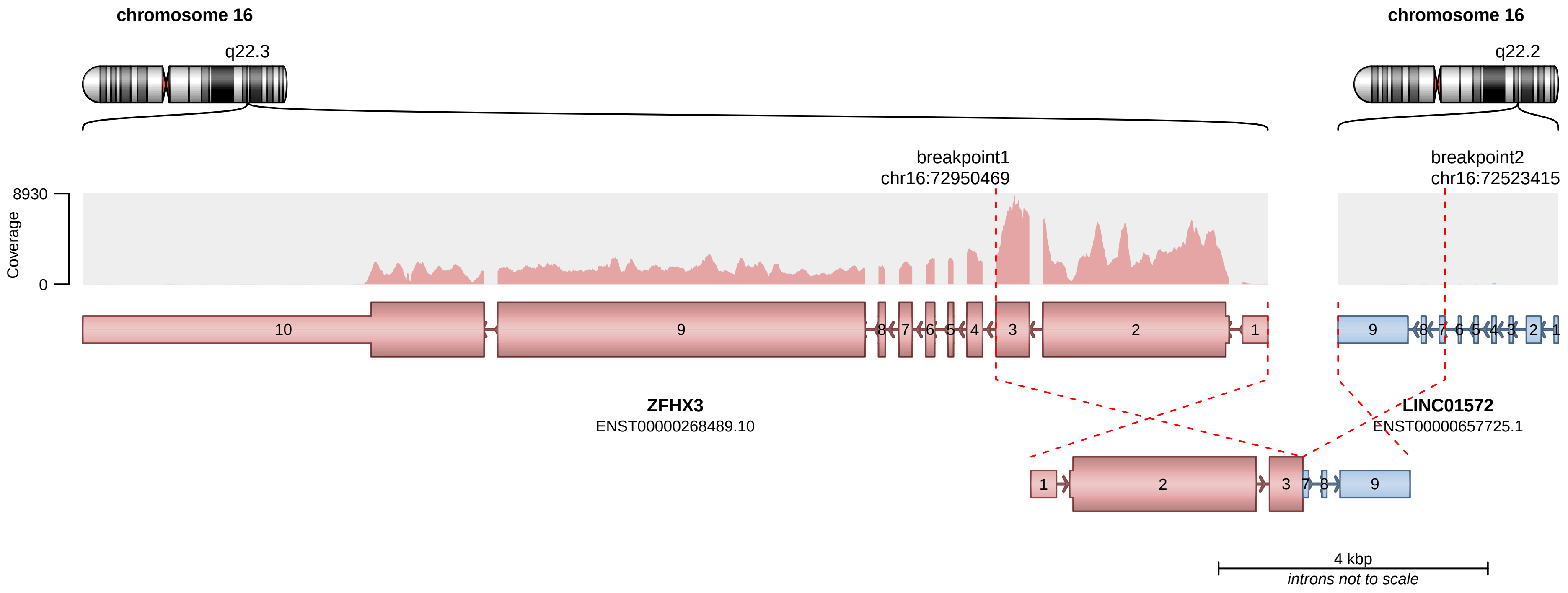
RETAINED PROTEIN DOMAINS

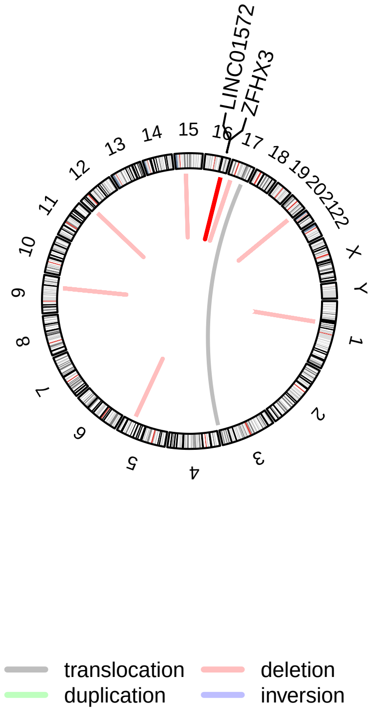
reading frame unclear



SUPPORTING READ COUNT

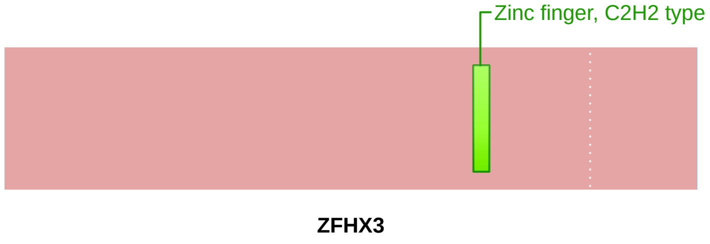
Split reads = 8
Discordant mates = 2





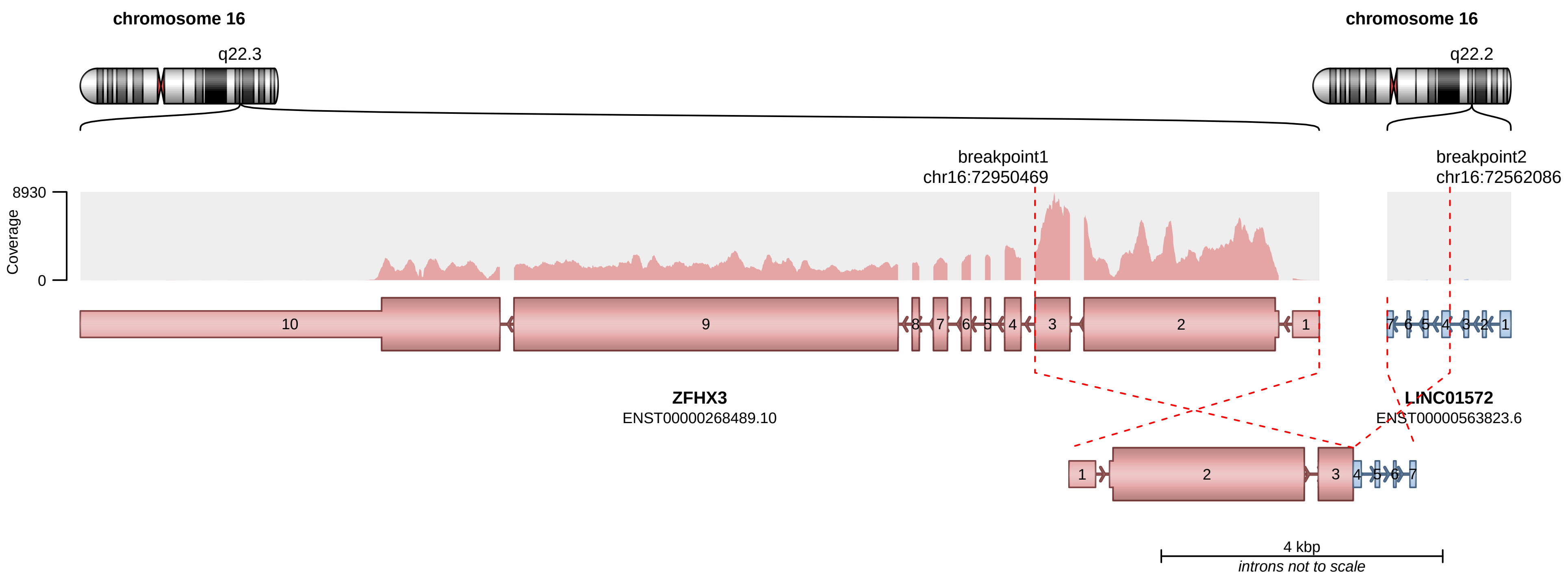
RETAINED PROTEIN DOMAINS

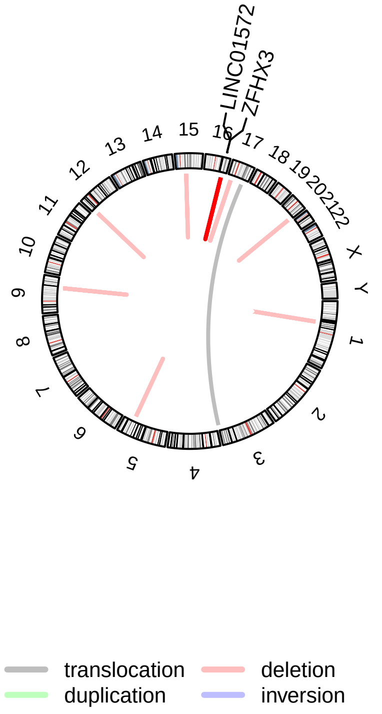
reading frame unclear

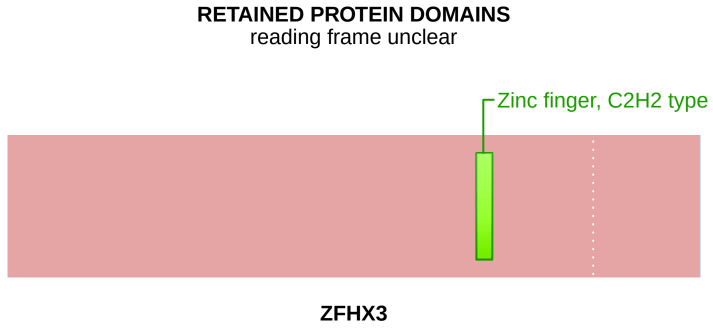


SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 2

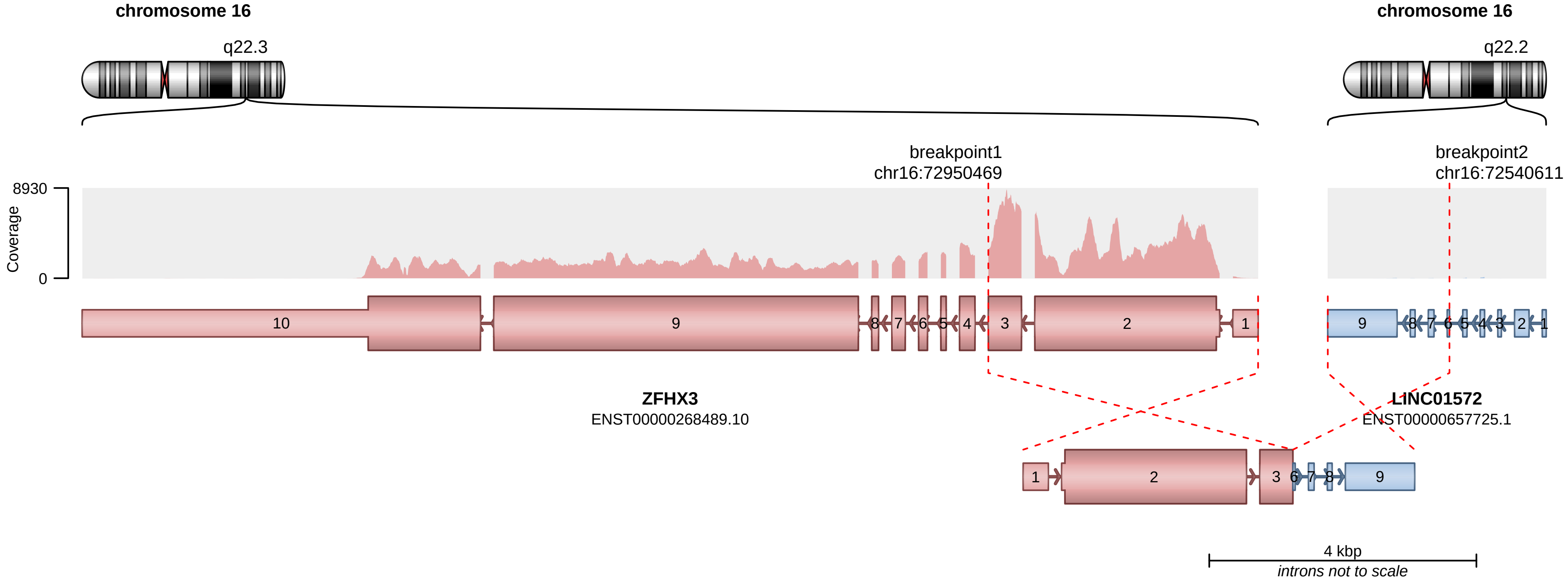


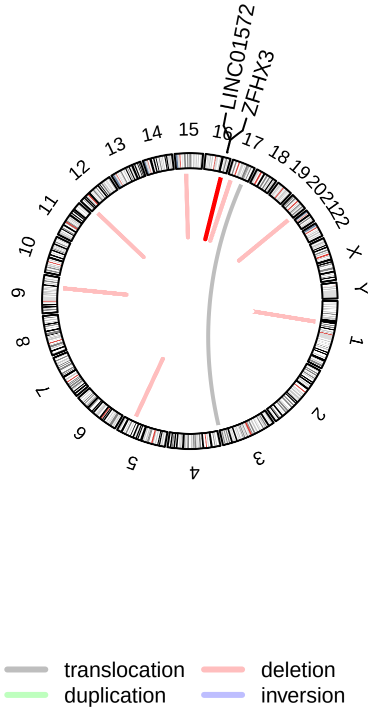




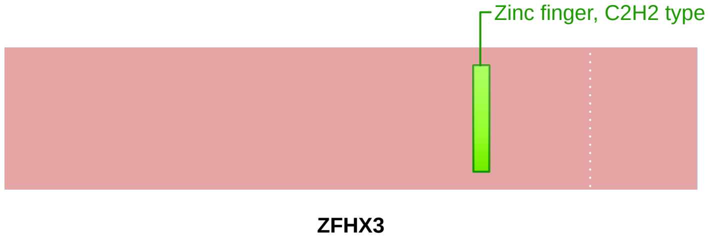
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 2



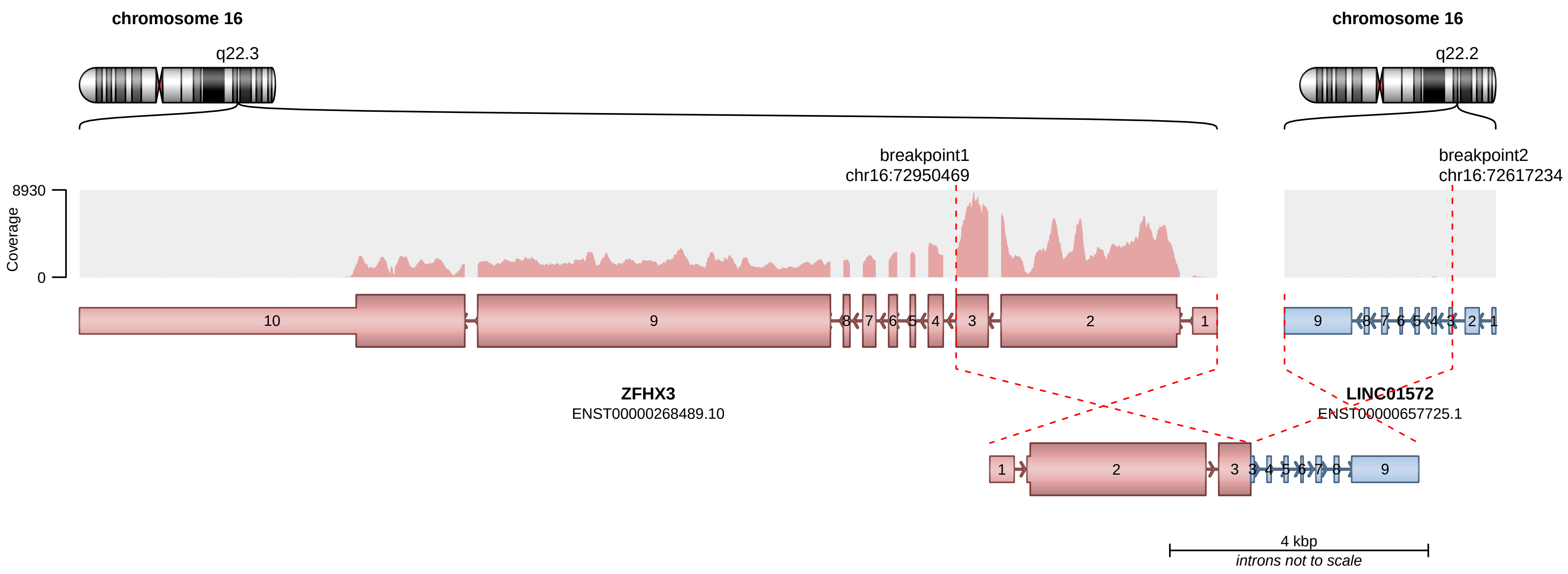


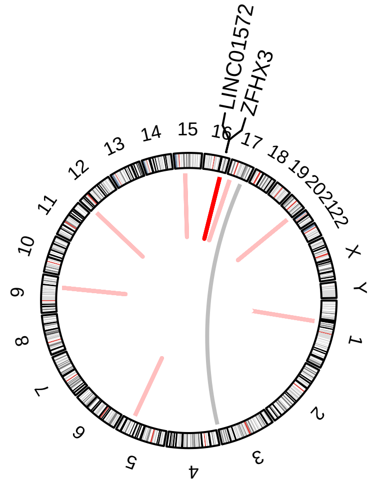
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 2





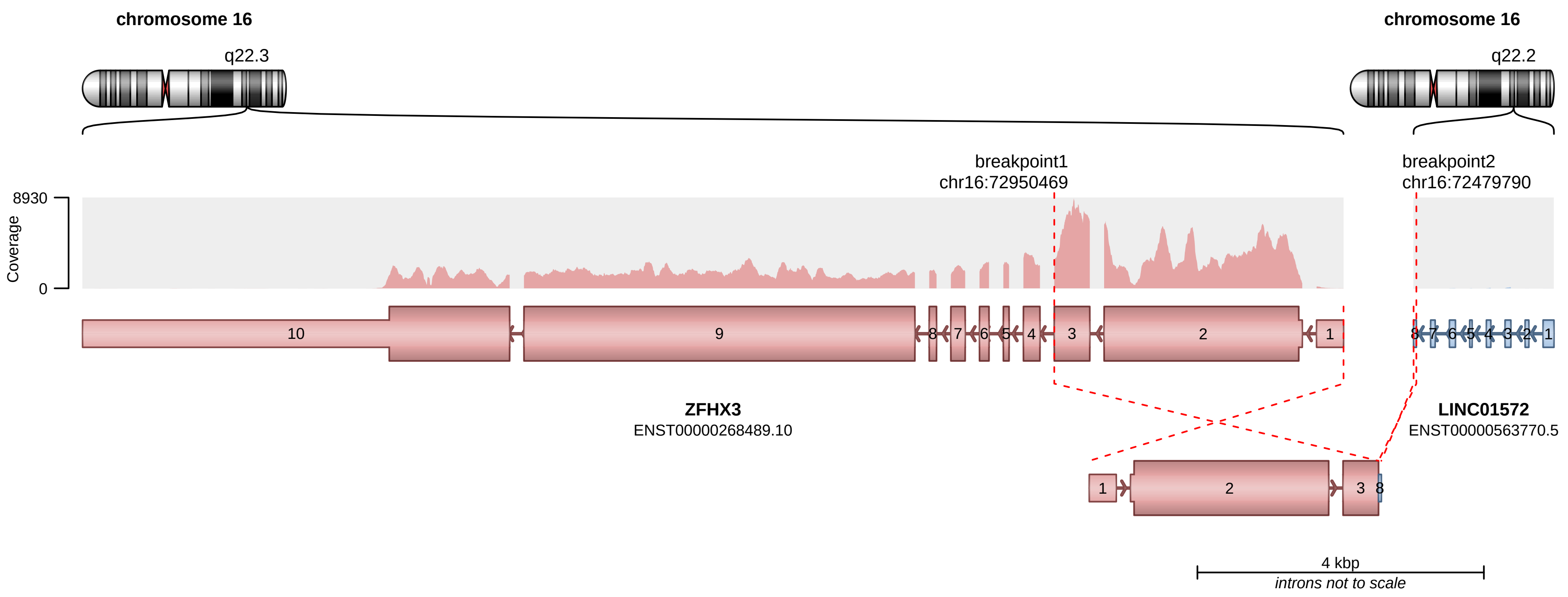
RETAINED PROTEIN DOMAINS
reading frame unclear

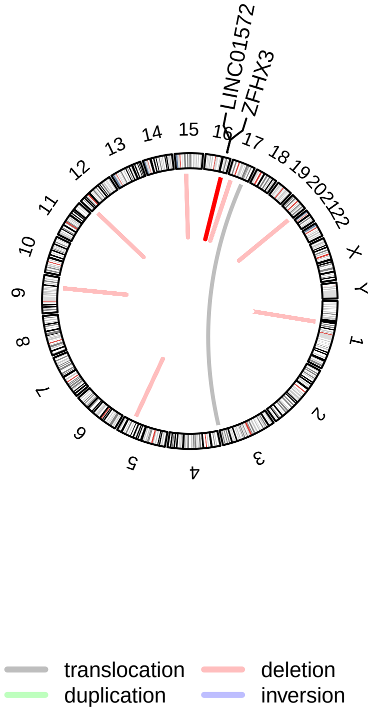
ZFHX3

SUPPORTING READ COUNT

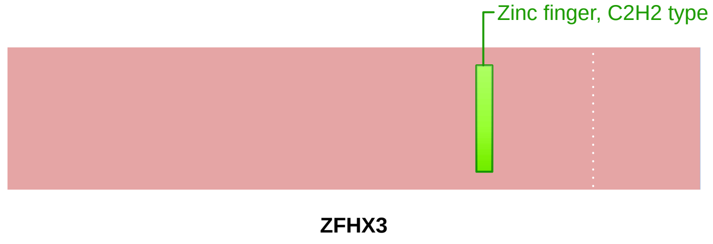
Split reads = 2
Discordant mates = 2

▬ translocation ▬ deletion
▬ duplication ▬ inversion



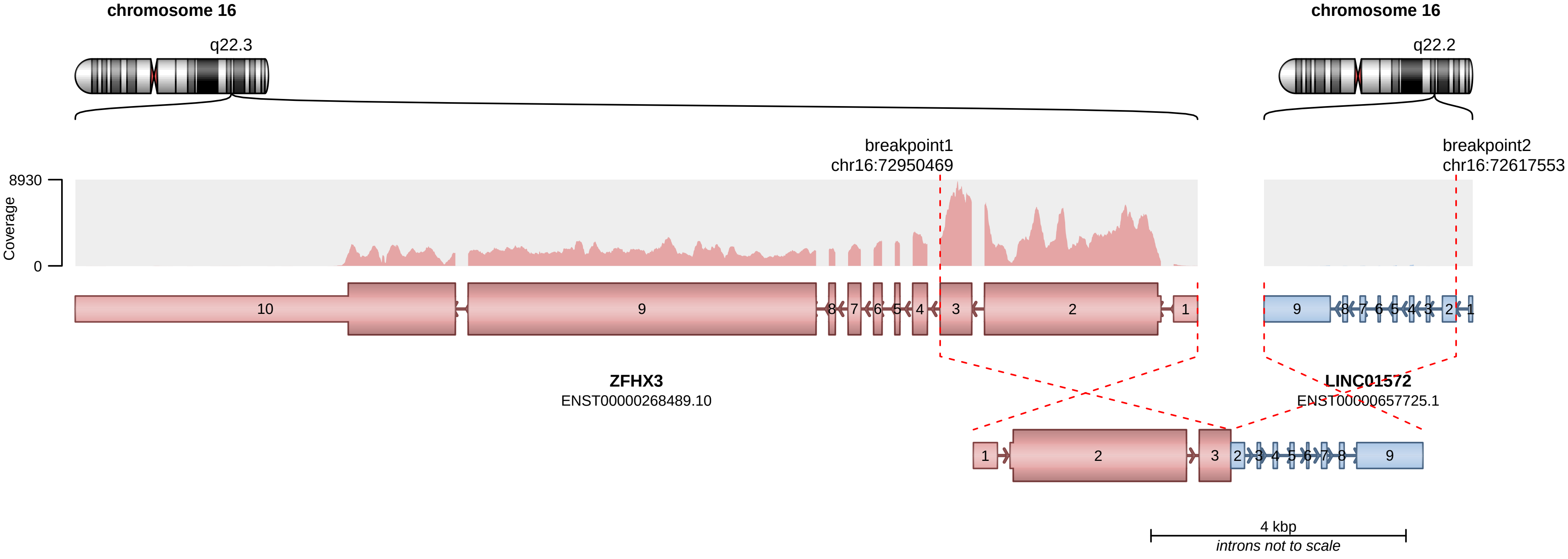


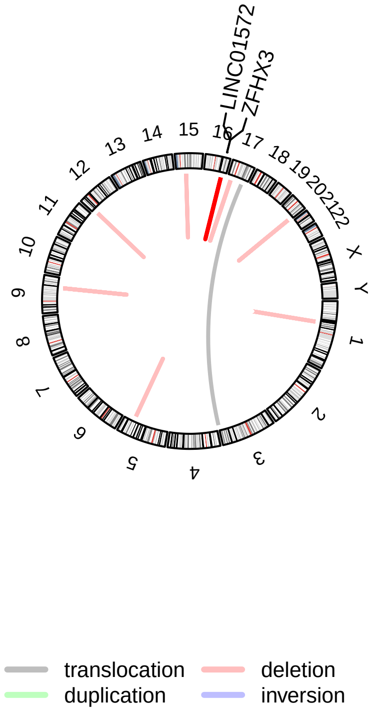
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 2
Discordant mates = 0



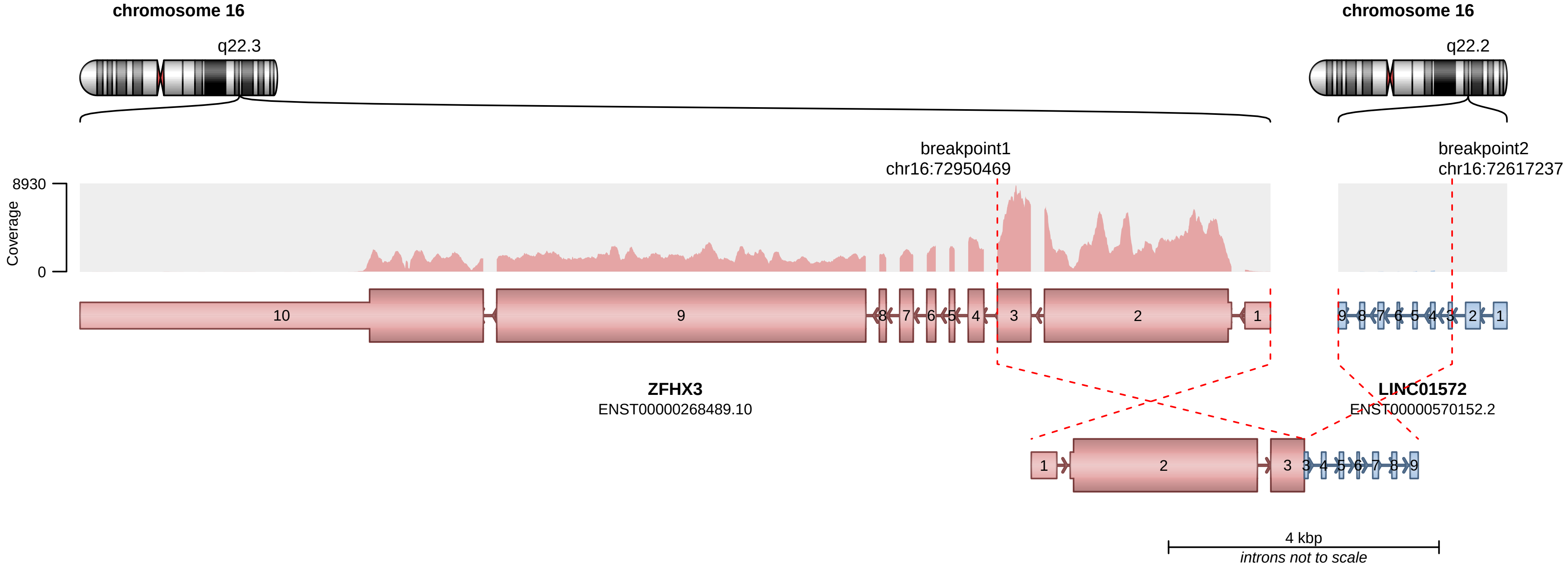


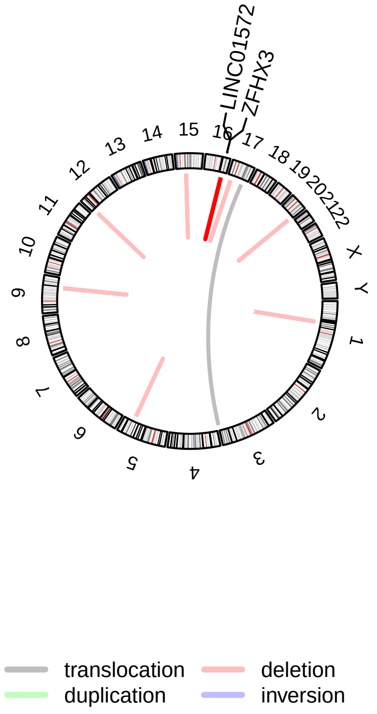
RETAINED PROTEIN DOMAINS
reading frame unclear

ZFHX3

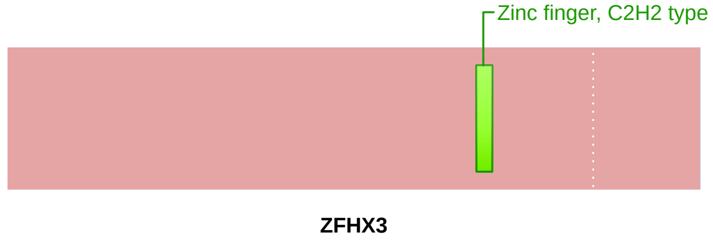
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 2



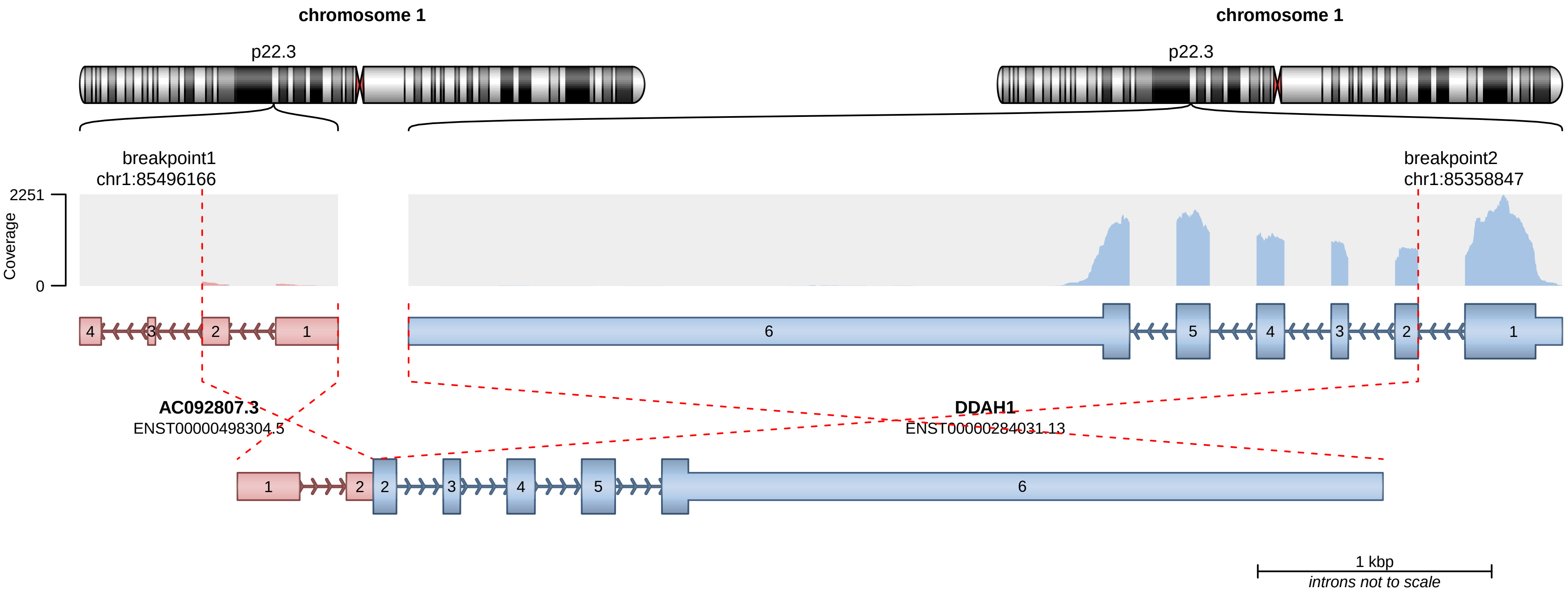


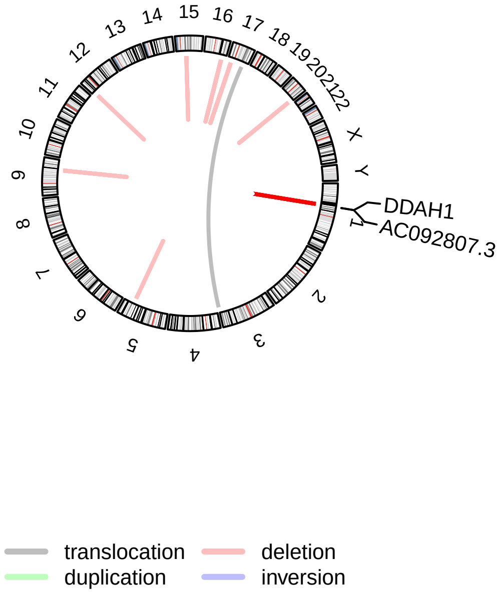
RETAINED PROTEIN DOMAINS
reading frame unclear



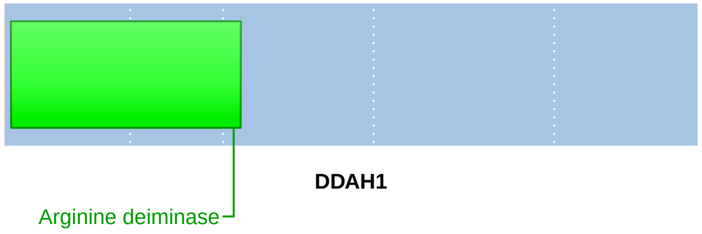
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 2



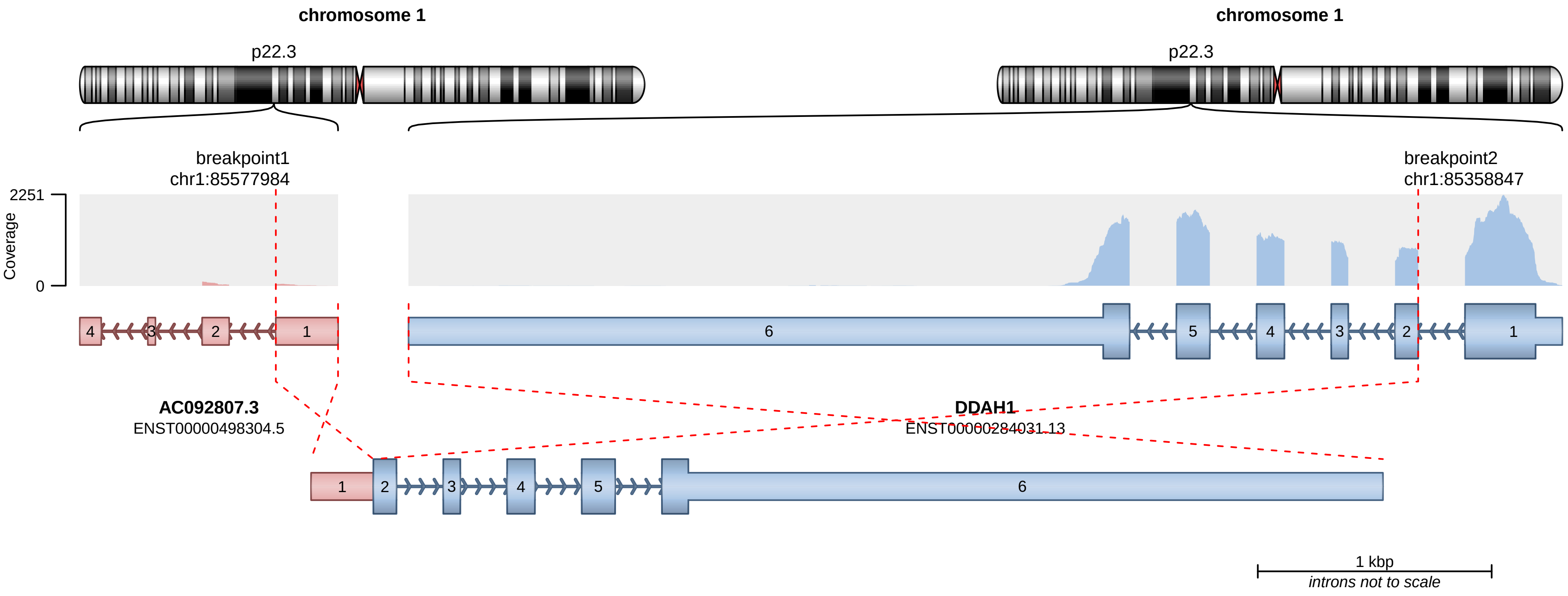


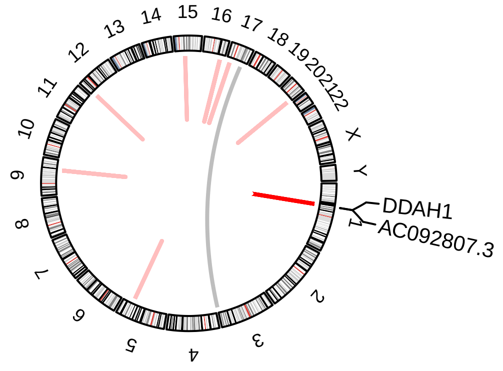
RETAINED PROTEIN DOMAINS
reading frame unclear

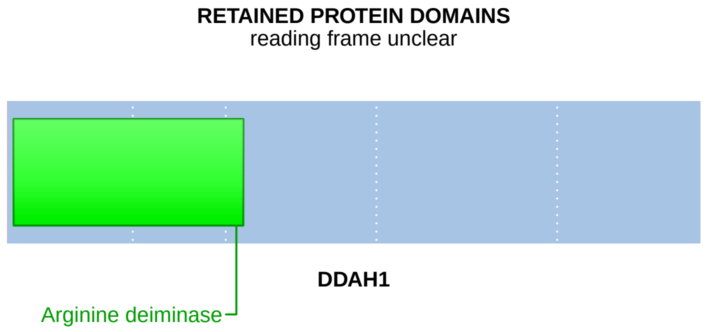


SUPPORTING READ COUNT

Split reads = 23
Discordant mates = 0

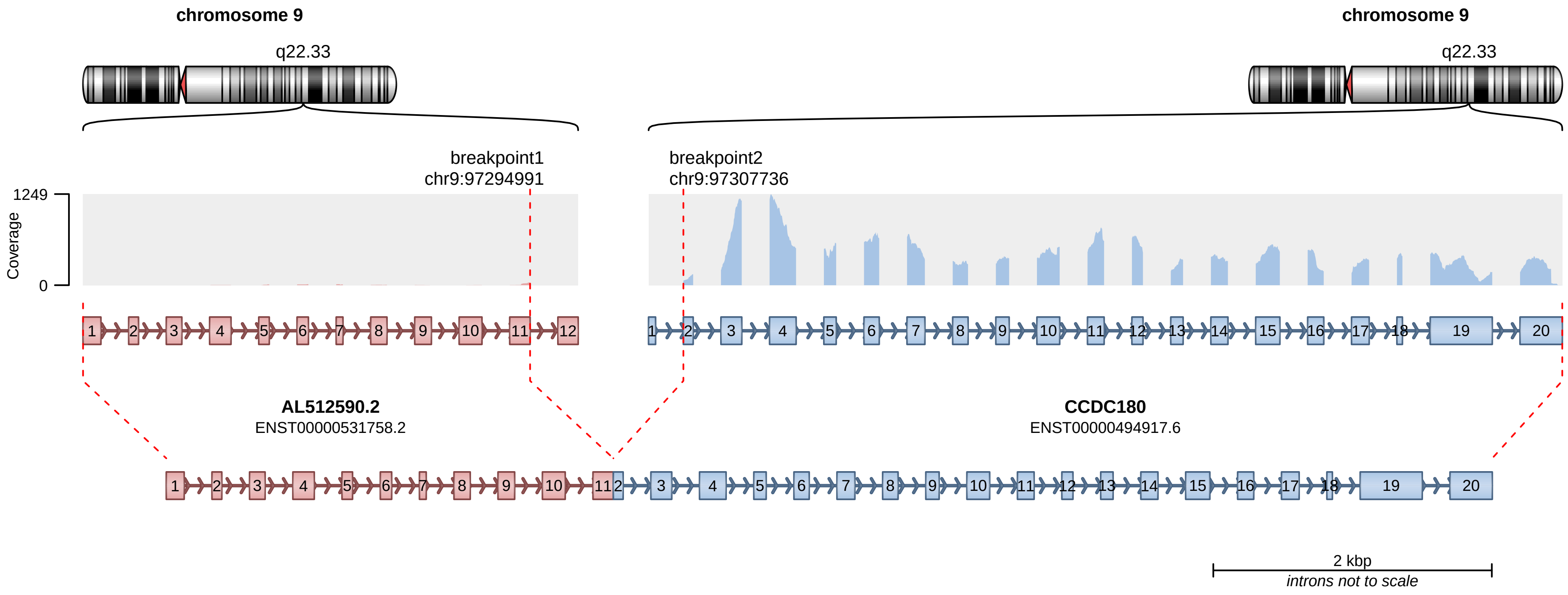


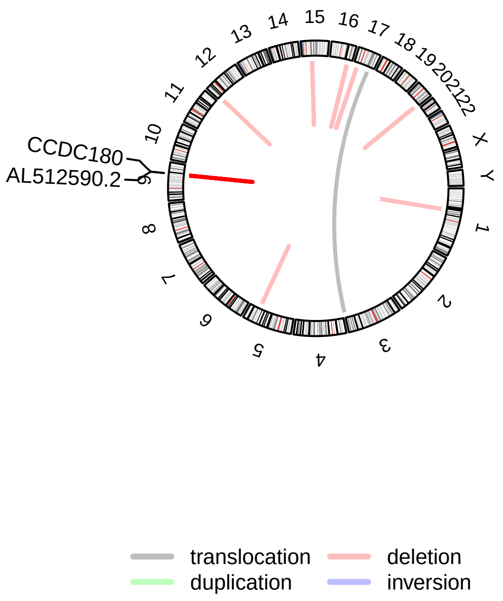




SUPPORTING READ COUNT

Split reads = 14
Discordant mates = 0

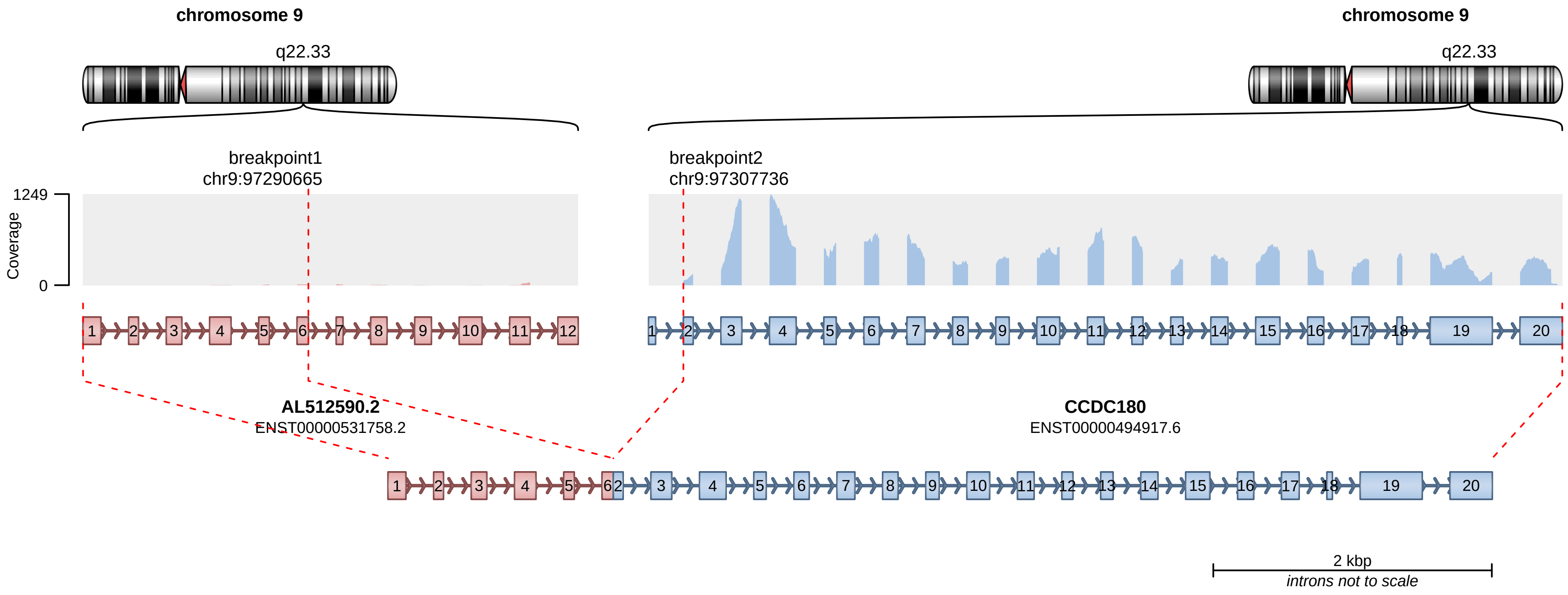


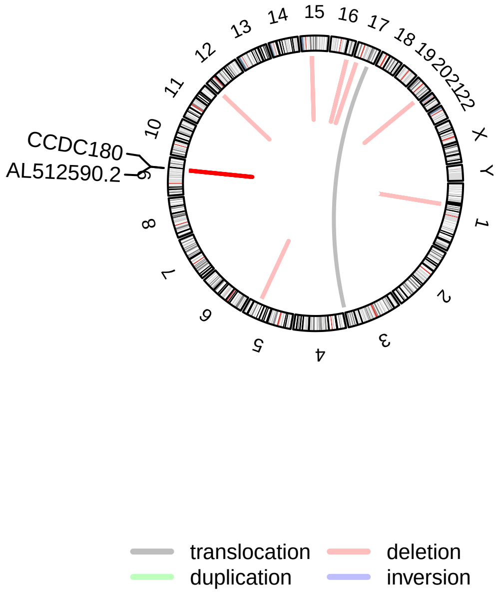


Genes are not protein−coding.

SUPPORTING READ COUNT

Split reads = 16
Discordant mates = 1

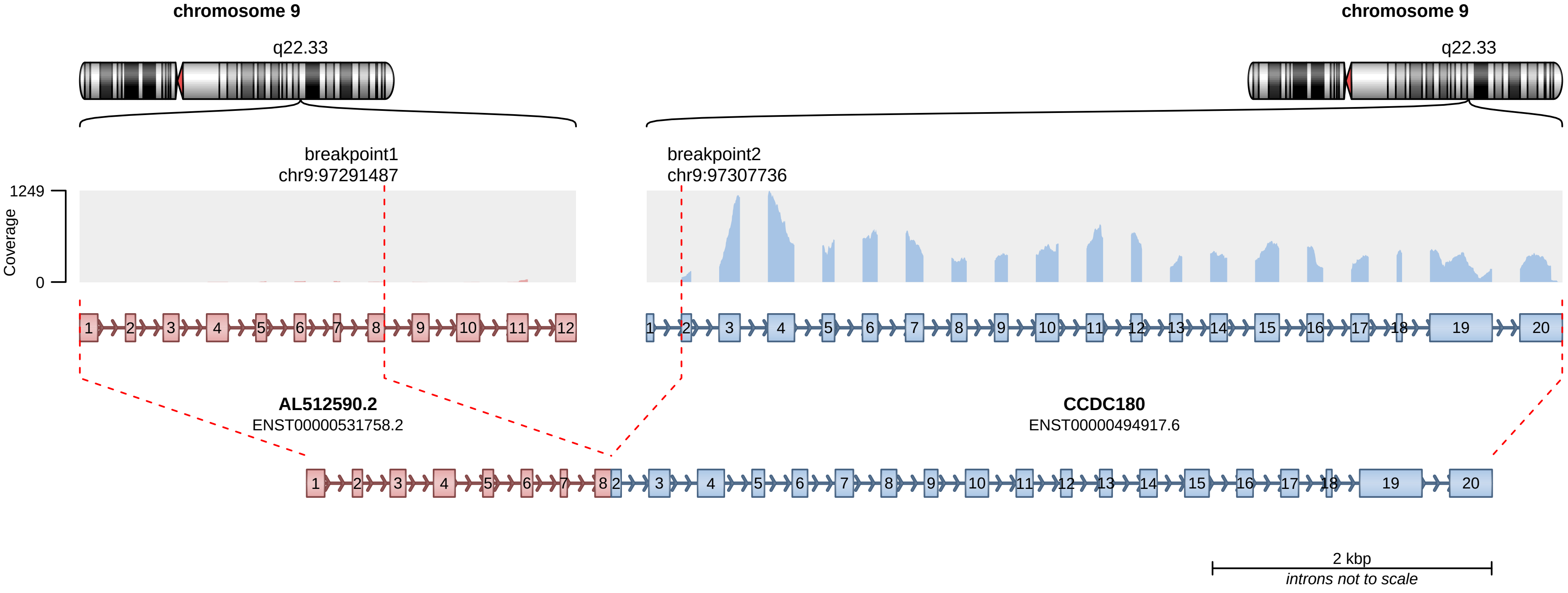


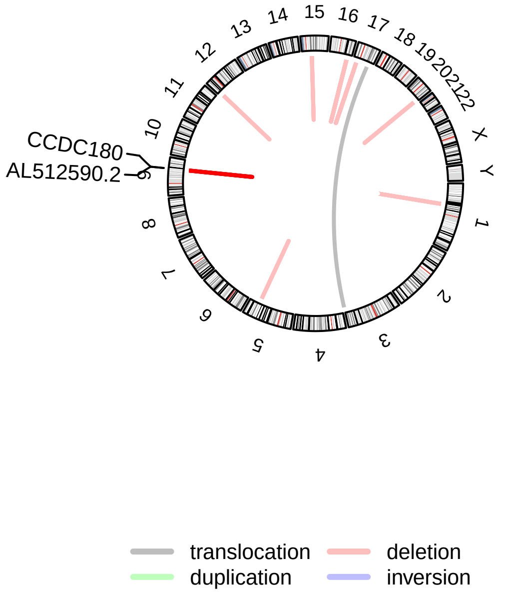


Genes are not protein−coding.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

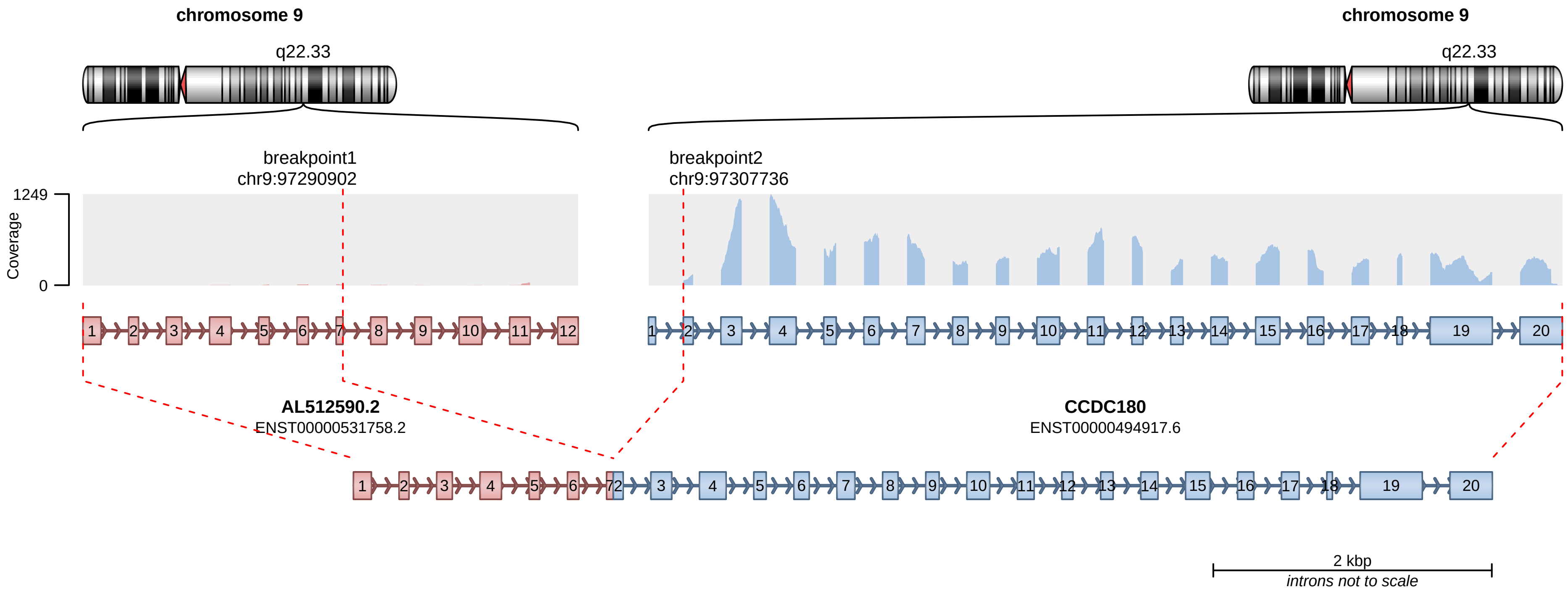


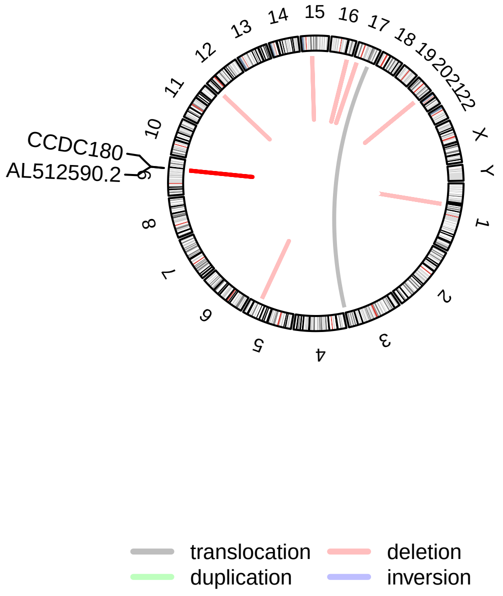


Genes are not protein−coding.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

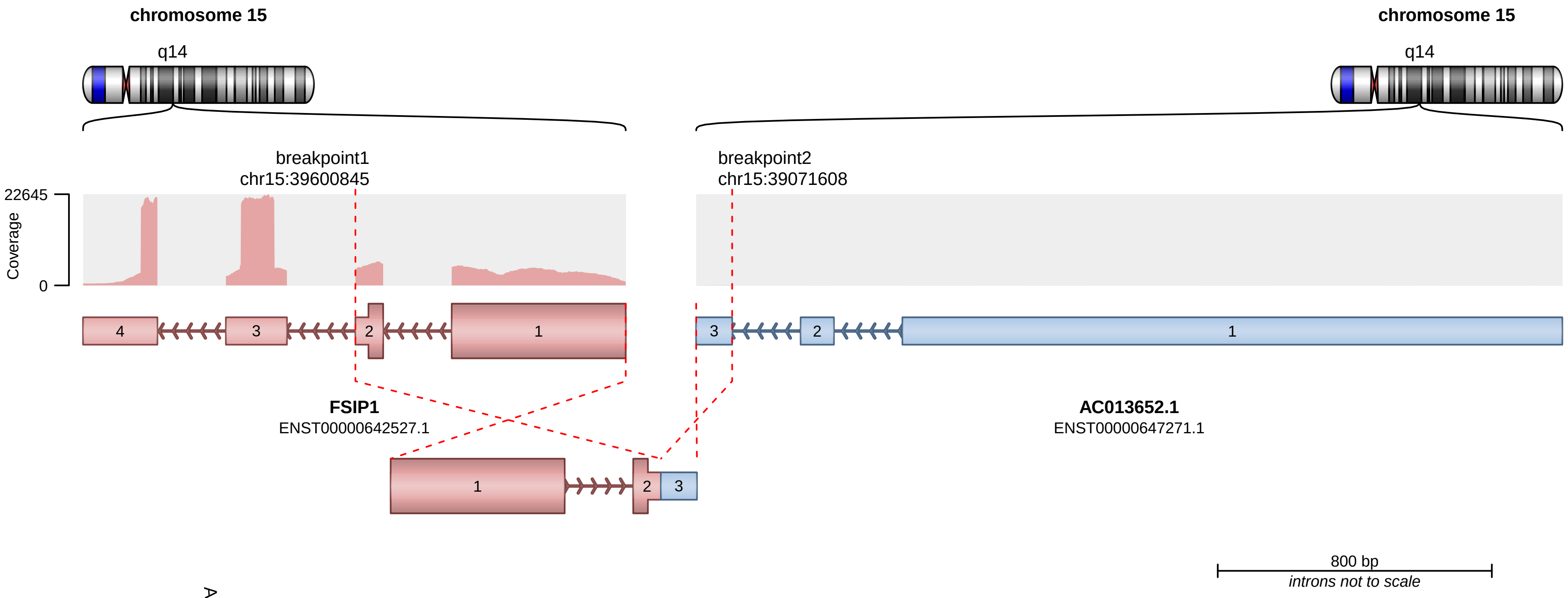


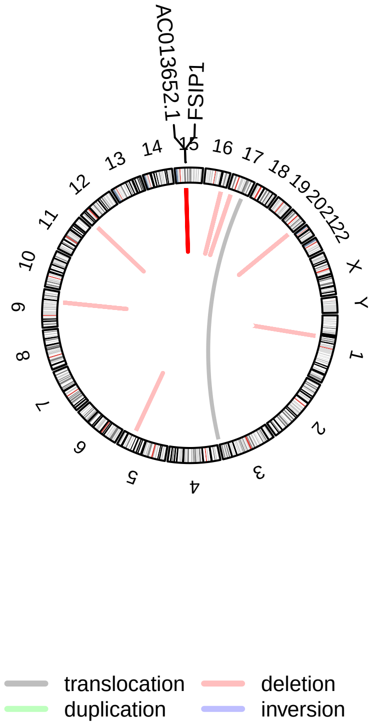


Genes are not protein−coding.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

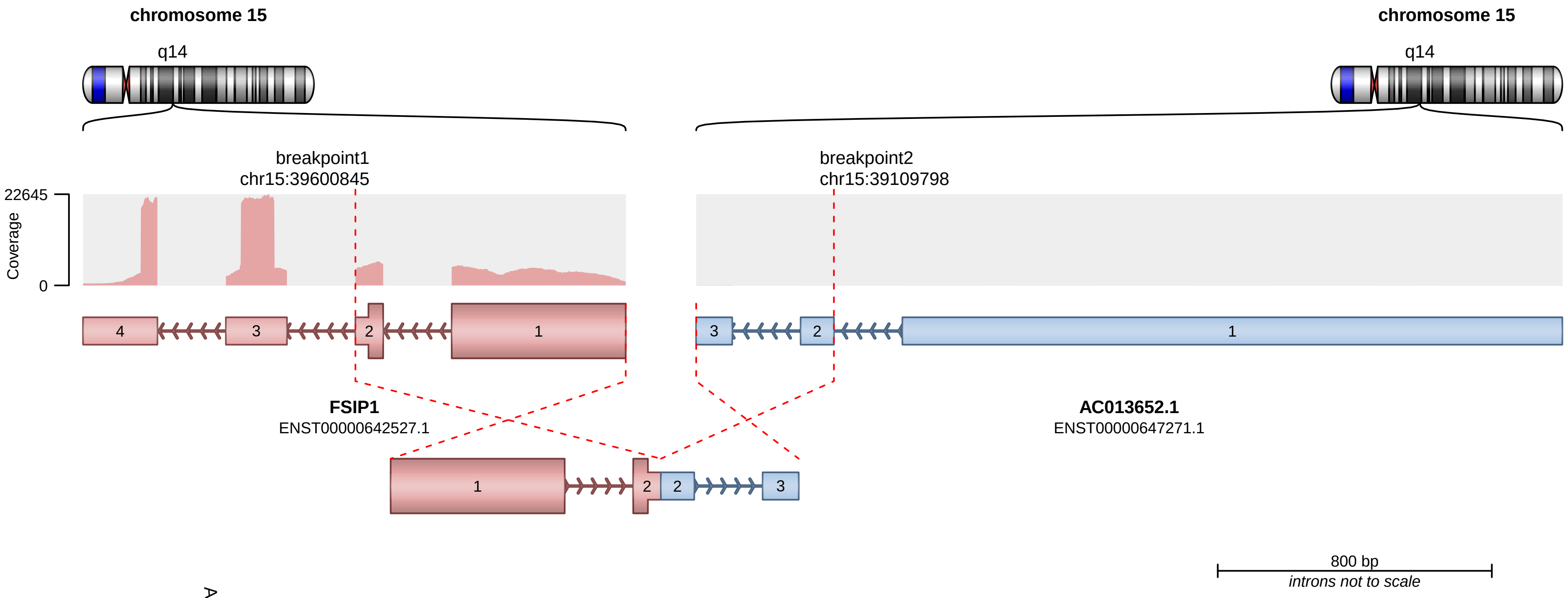


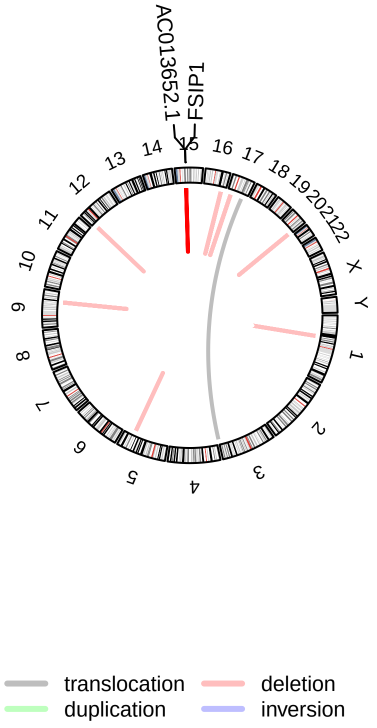


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 13
Discordant mates = 3

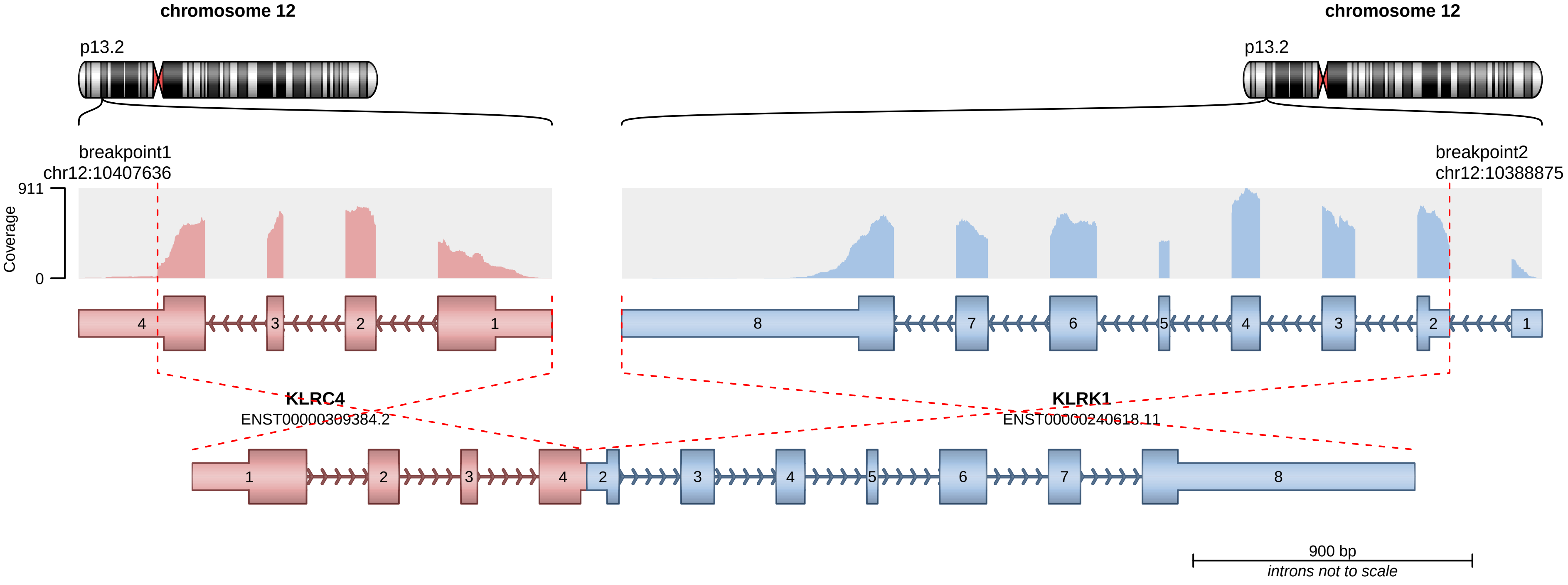


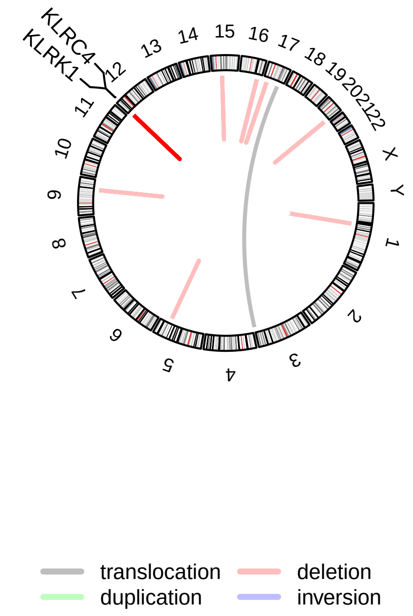


No protein domains retained in fusion.

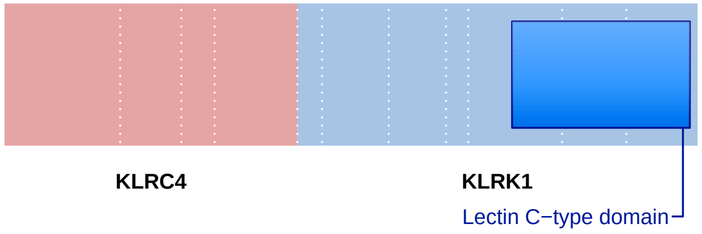
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 3





RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 0