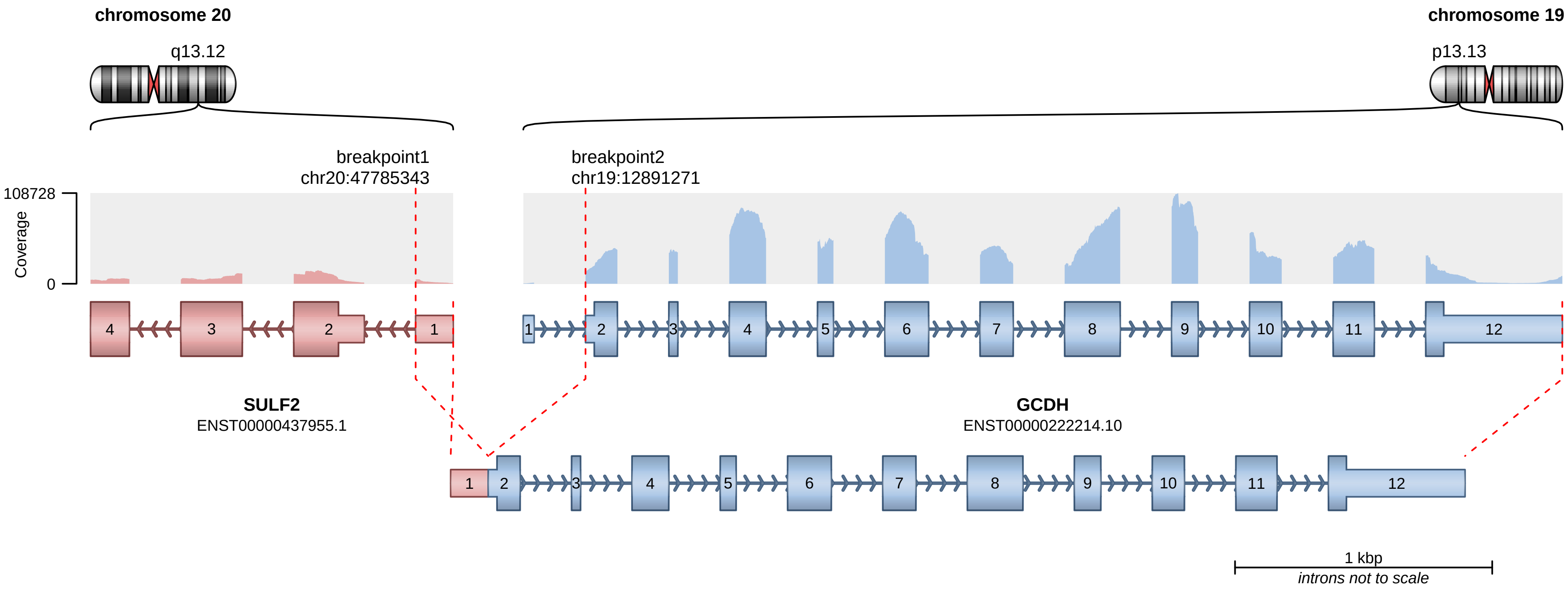
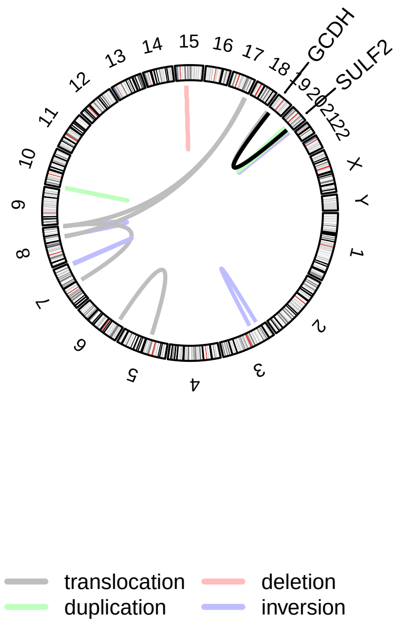
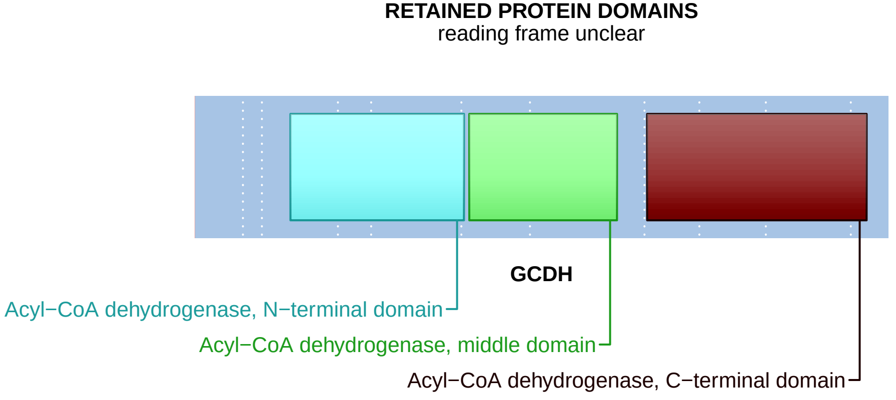
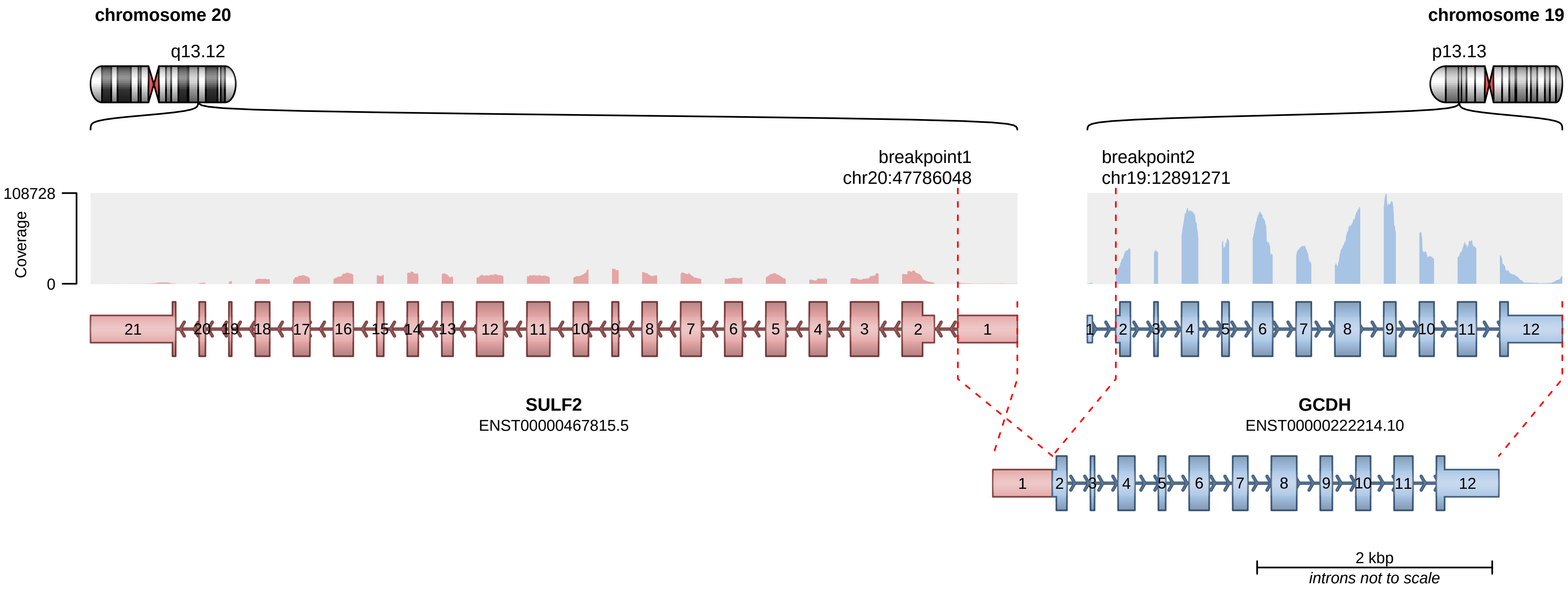


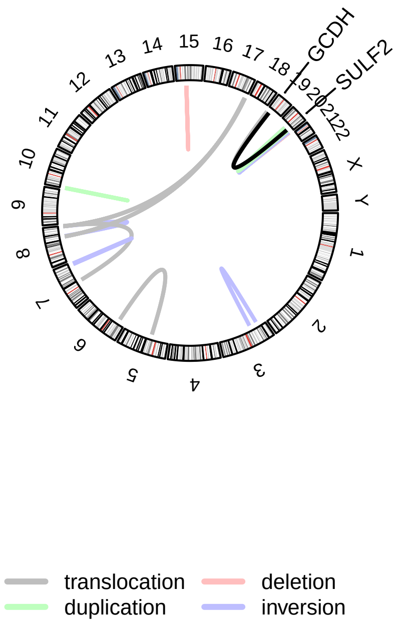




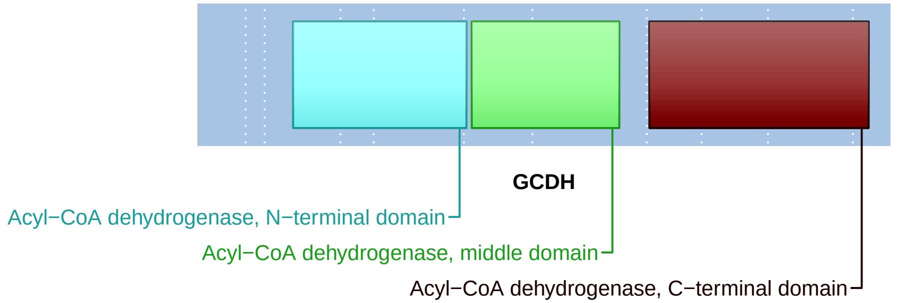
SUPPORTING READ COUNT

Split reads = 2414
Discordant mates = 6



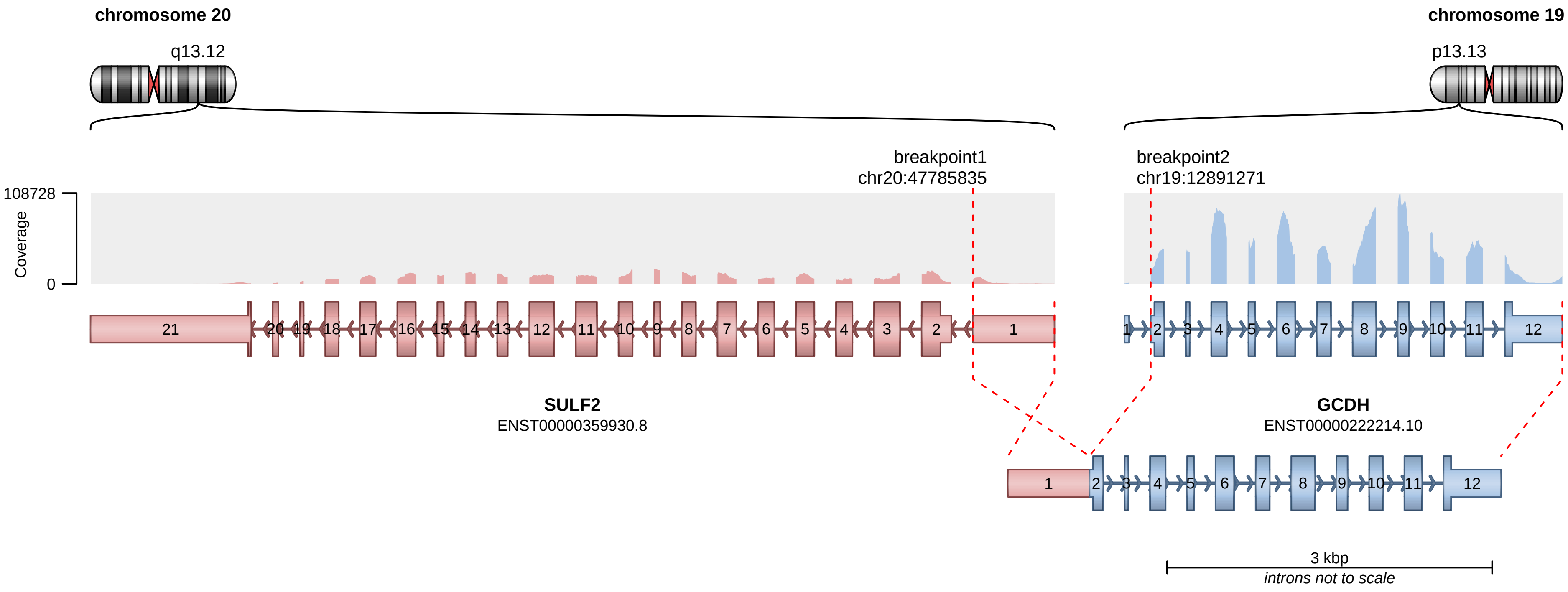


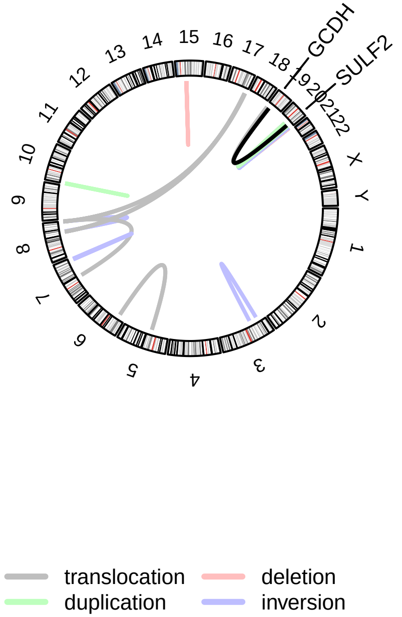
RETAINED PROTEIN DOMAINS
reading frame unclear



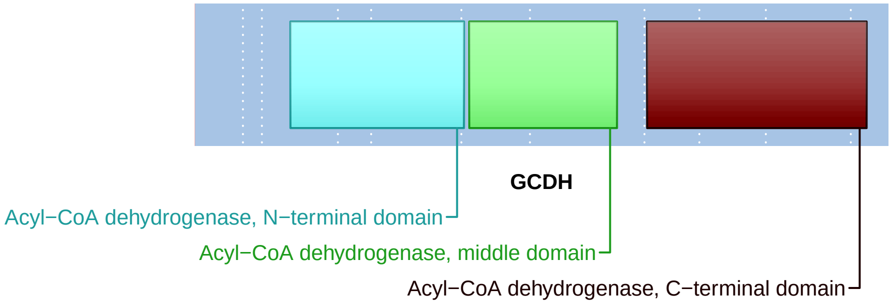
SUPPORTING READ COUNT

Split reads = 334
Discordant mates = 1



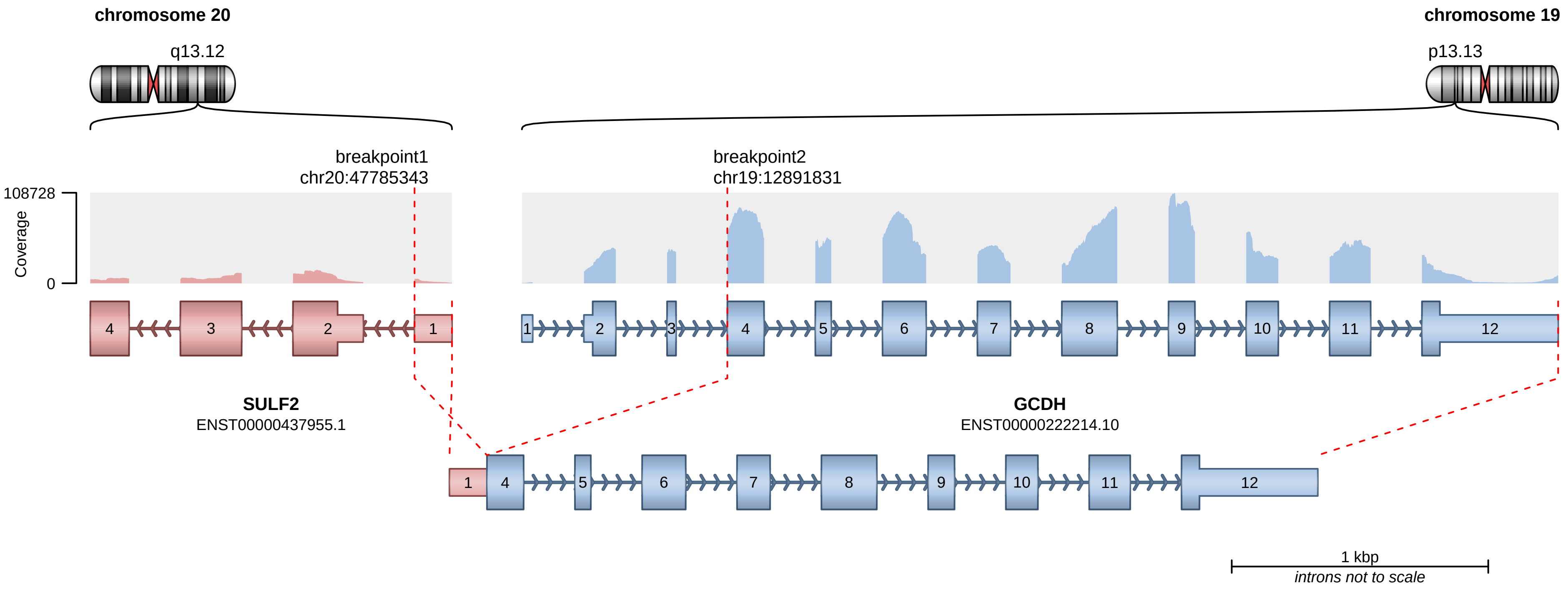


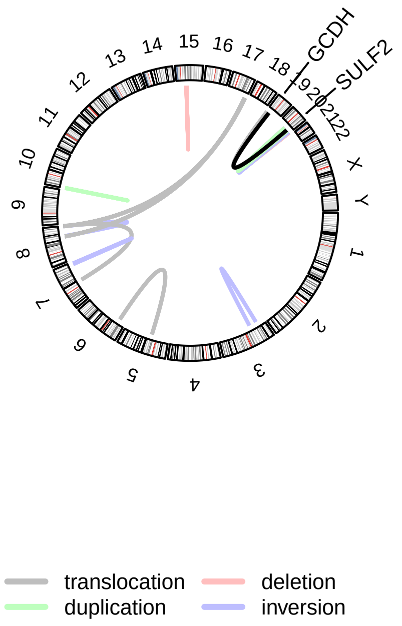
RETAINED PROTEIN DOMAINS
reading frame unclear

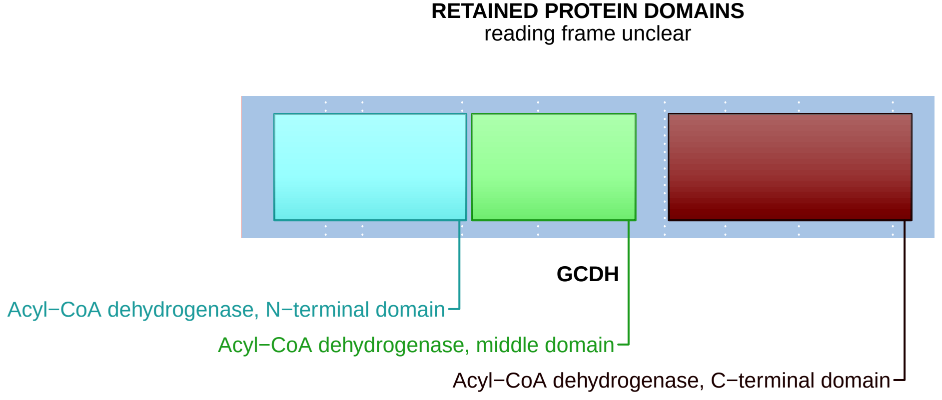


SUPPORTING READ COUNT

Split reads = 204
Discordant mates = 6

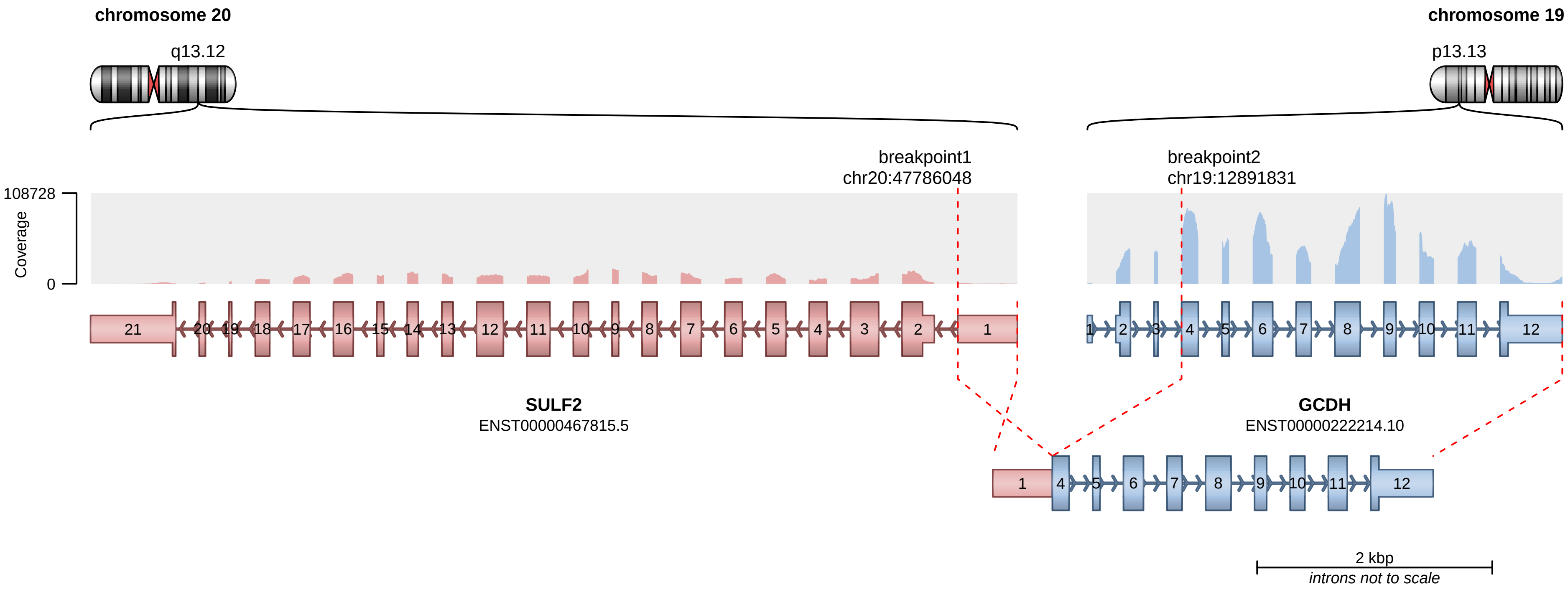


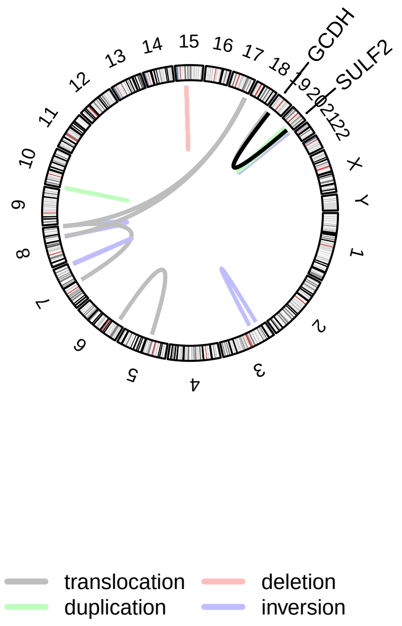




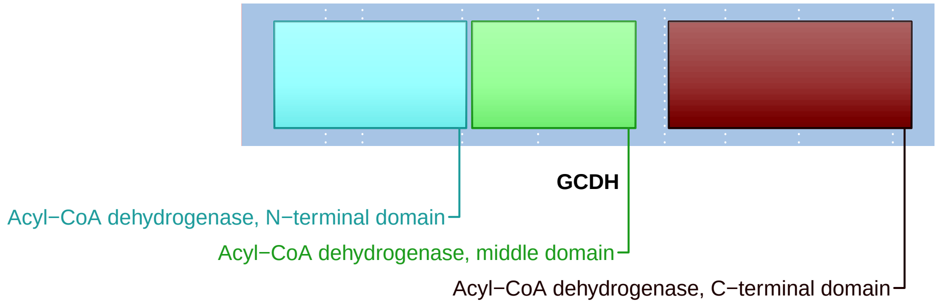
SUPPORTING READ COUNT

Split reads = 32
Discordant mates = 1



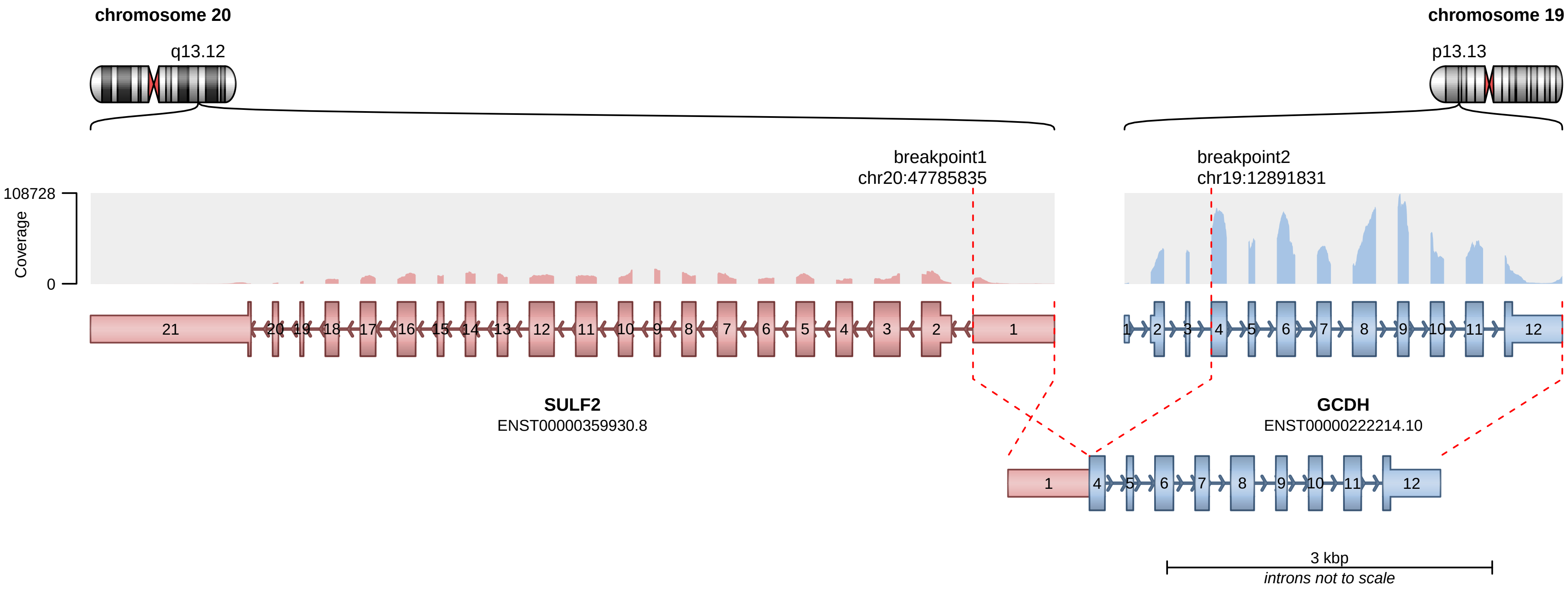


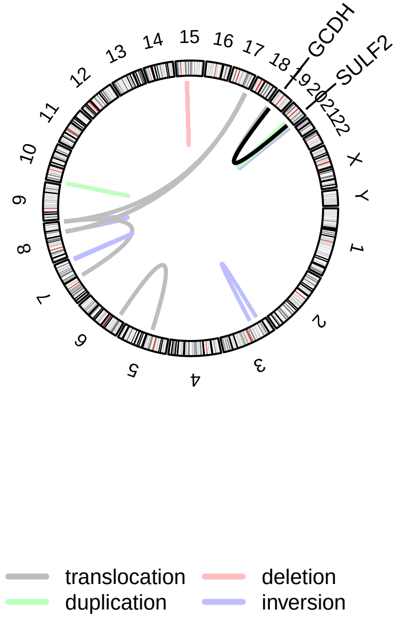
RETAINED PROTEIN DOMAINS
reading frame unclear



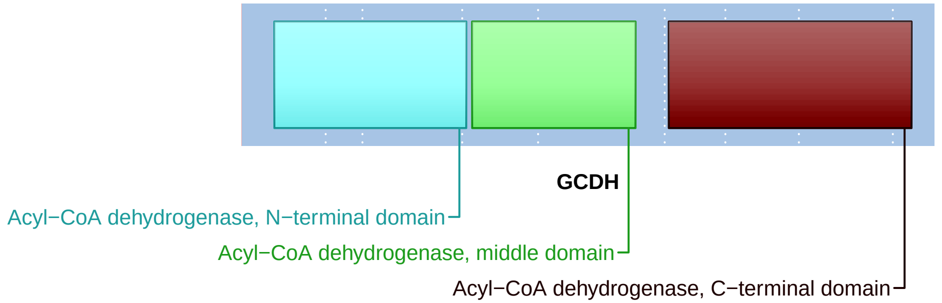
SUPPORTING READ COUNT

Split reads = 21
Discordant mates = 0



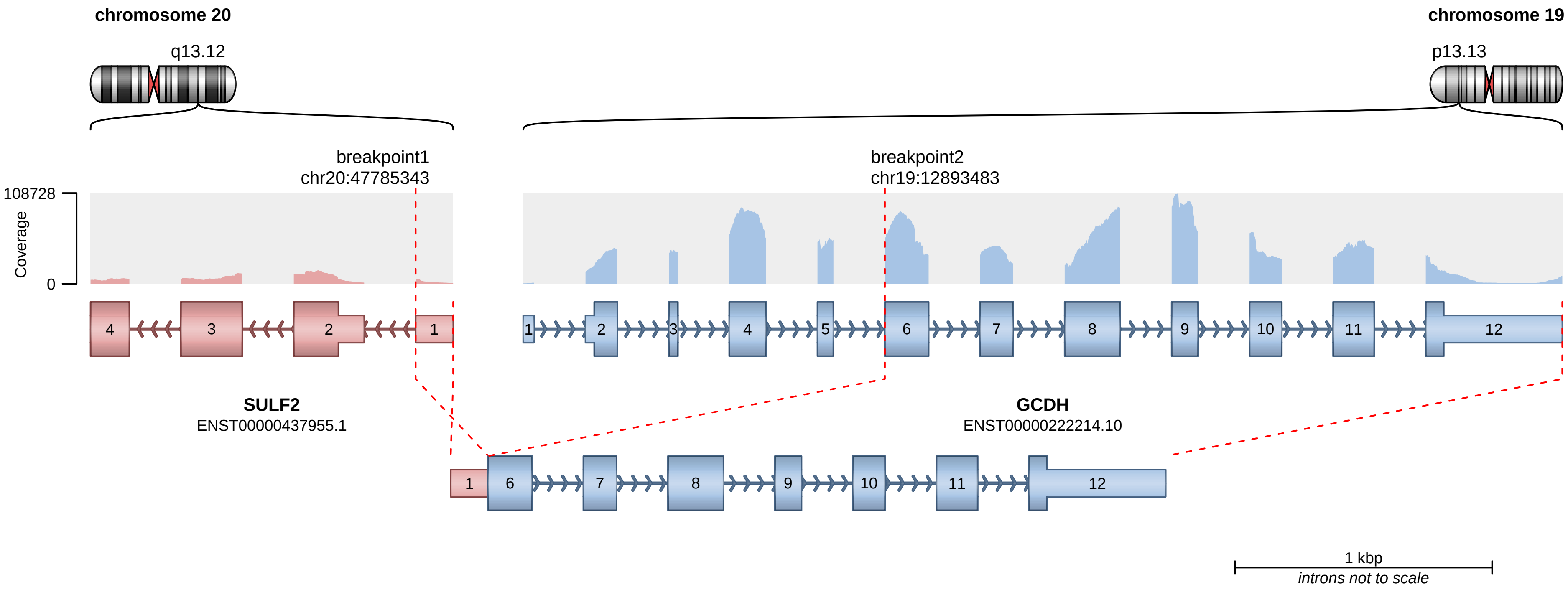


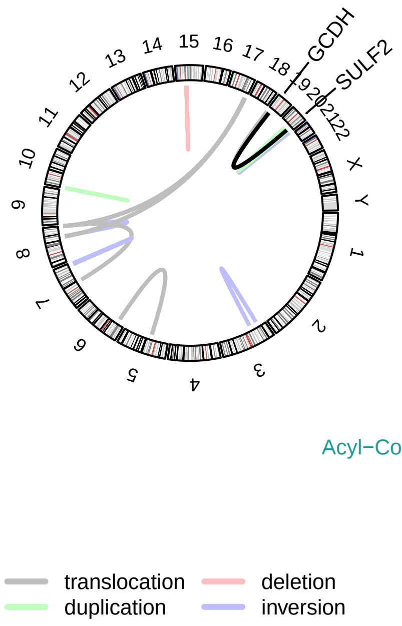
RETAINED PROTEIN DOMAINS
reading frame unclear



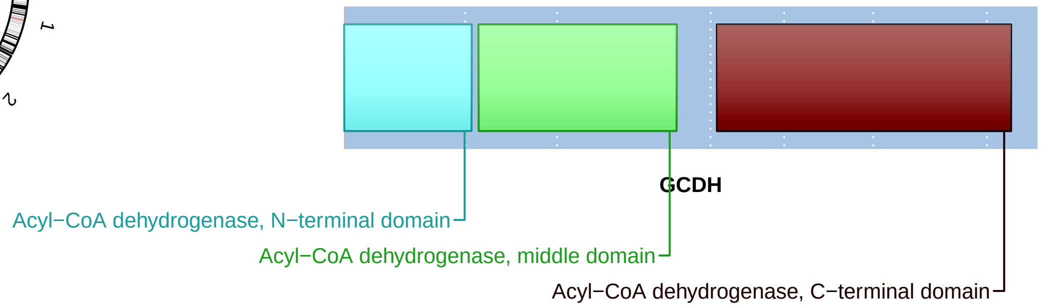
SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 1



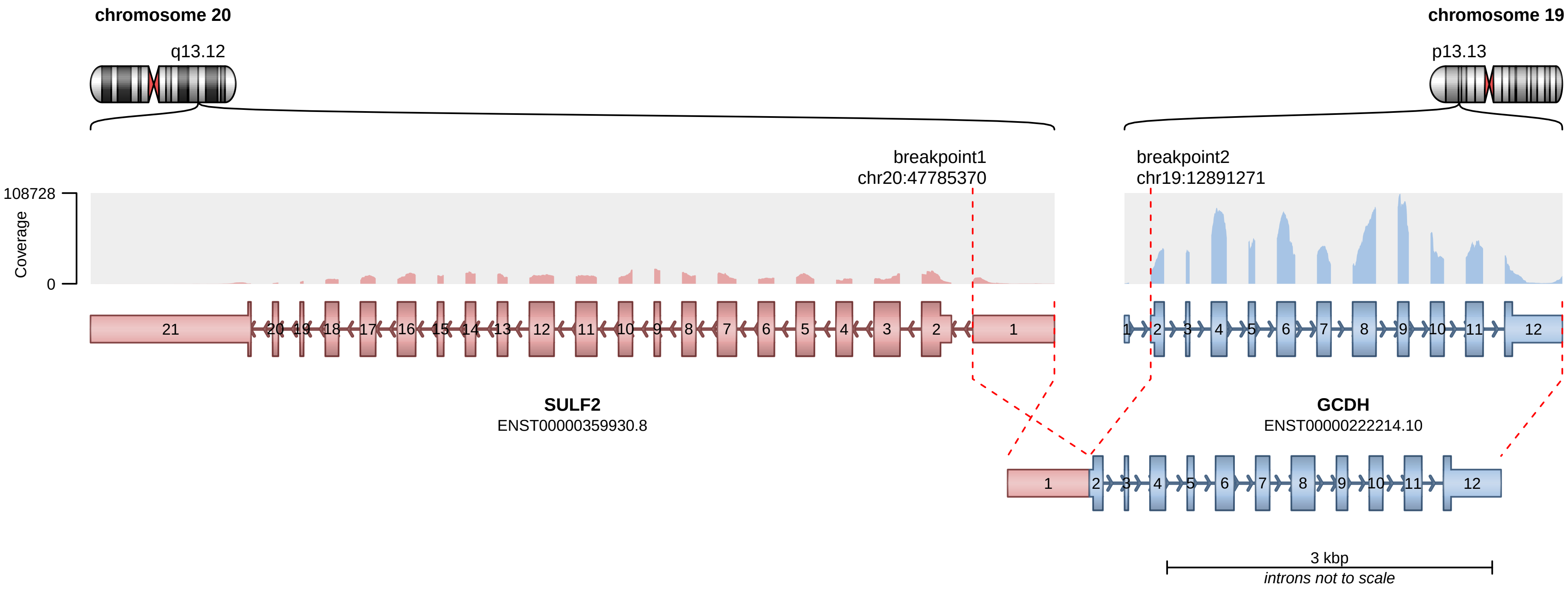


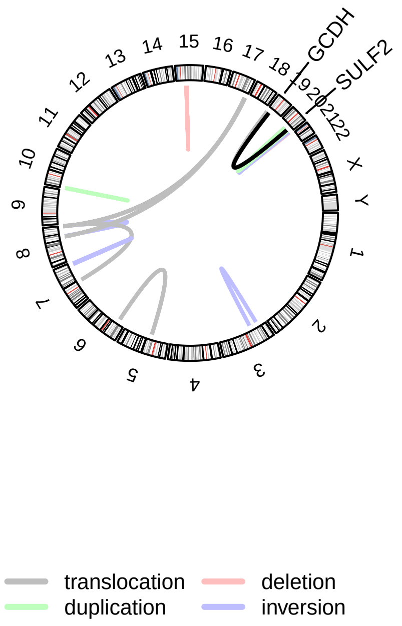
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

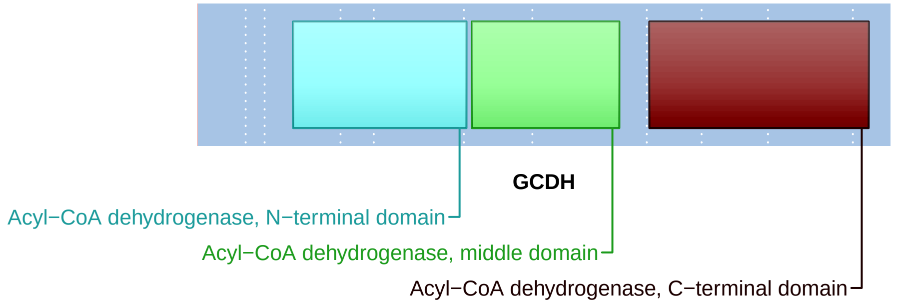
Split reads = 7
Discordant mates = 0





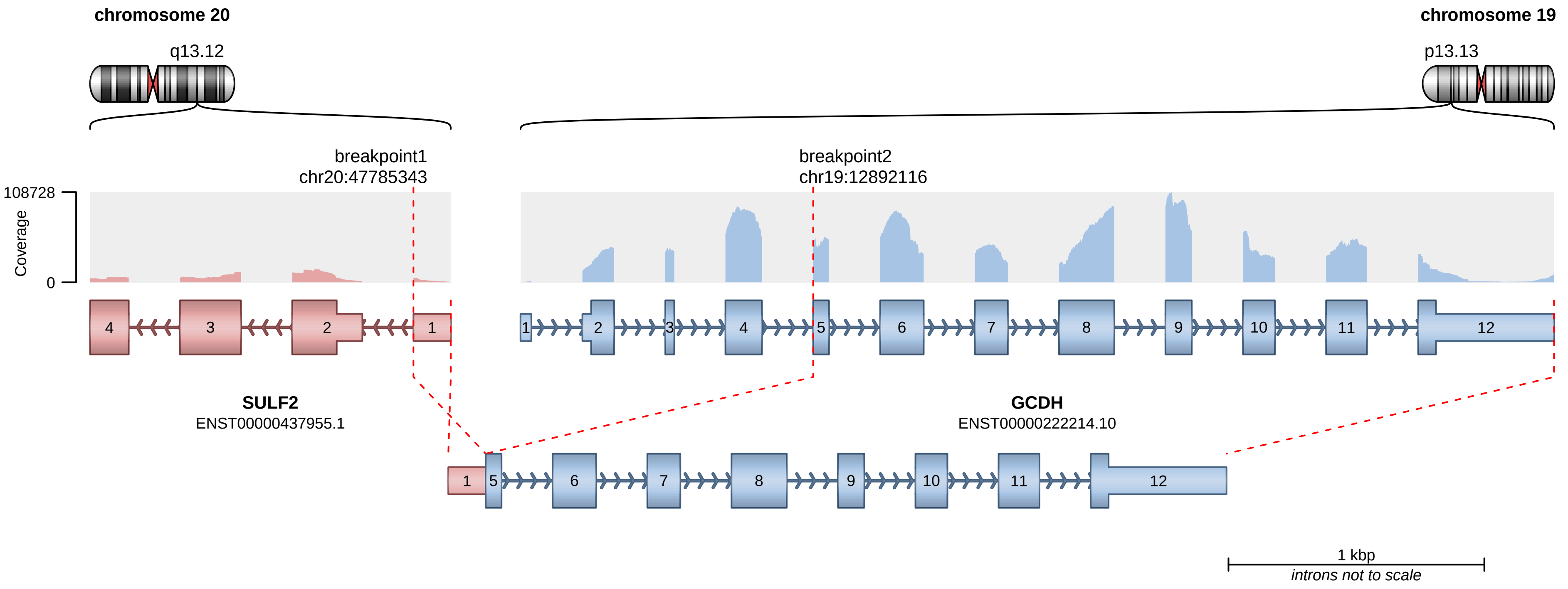
RETAINED PROTEIN DOMAINS

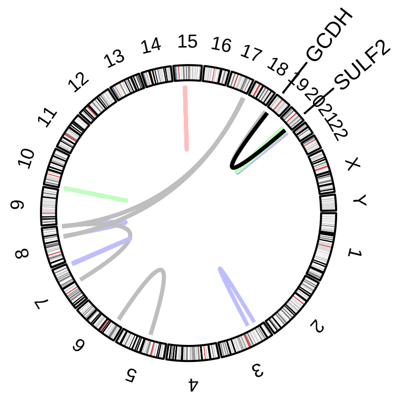
reading frame unclear

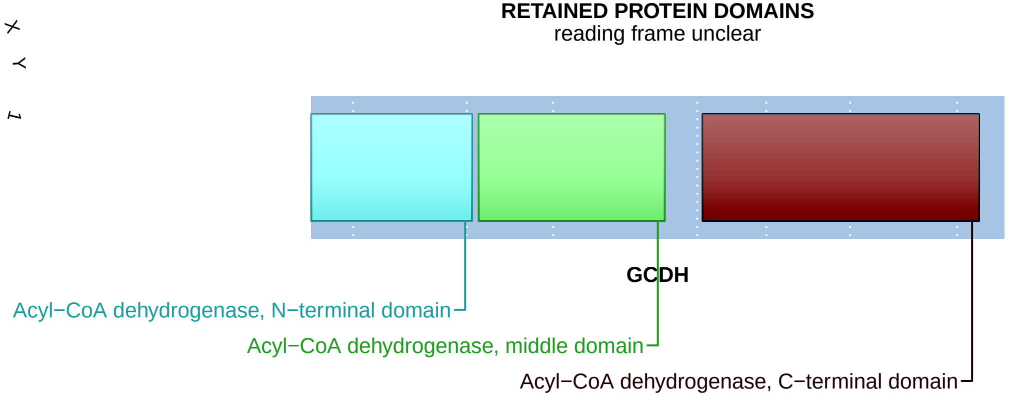


SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 6

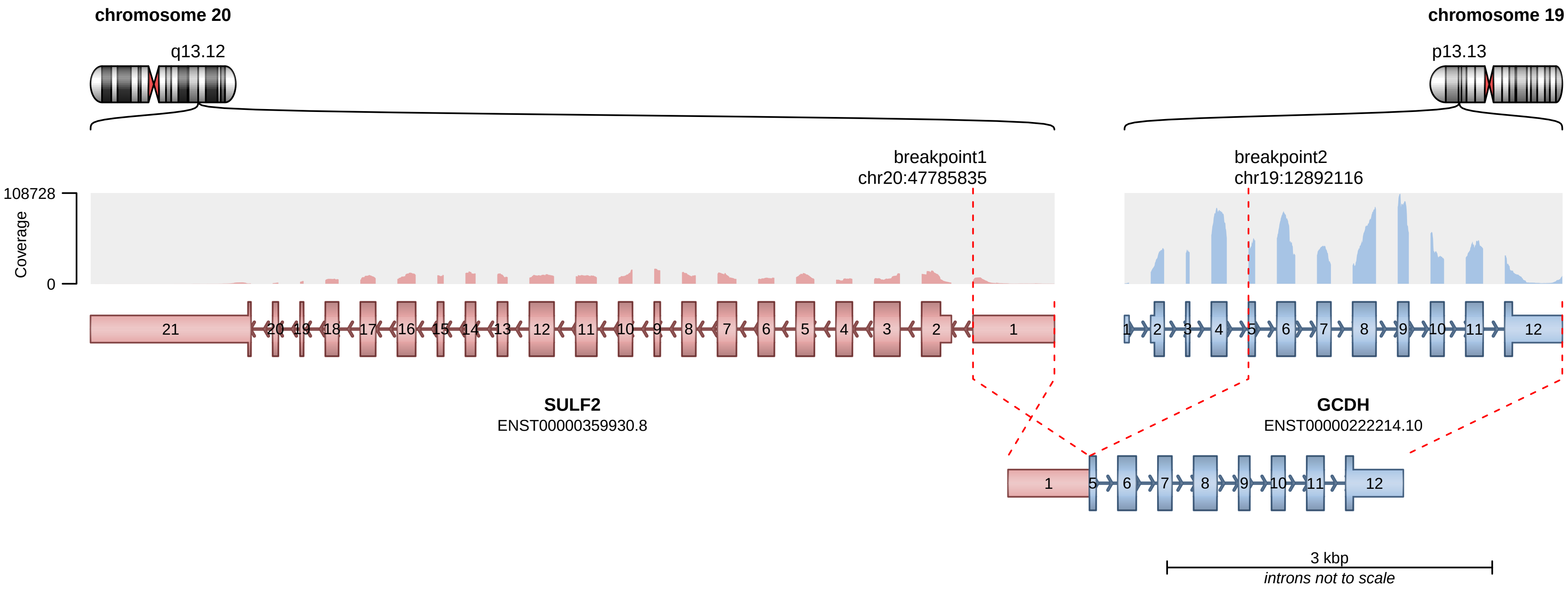


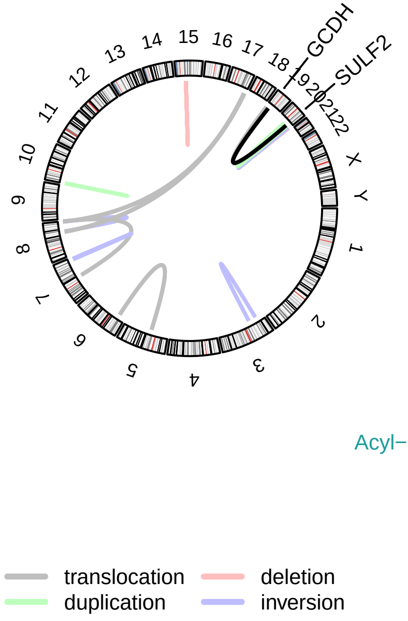




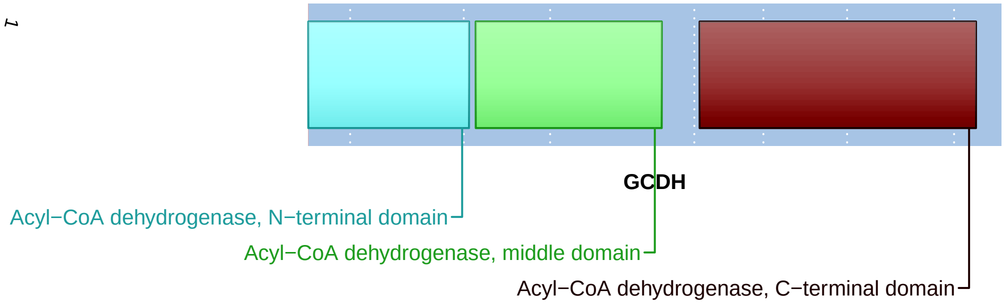
SUPPORTING READ COUNT

Split reads = 6
Discordant mates = 0



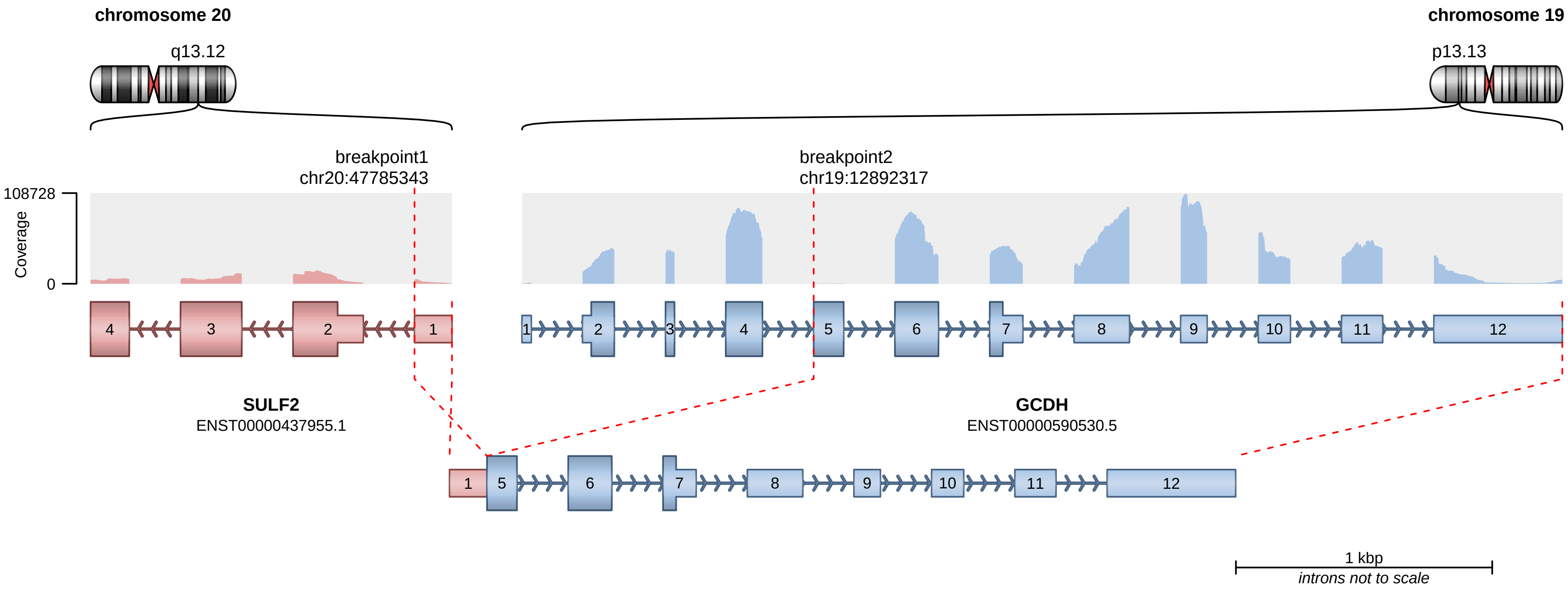


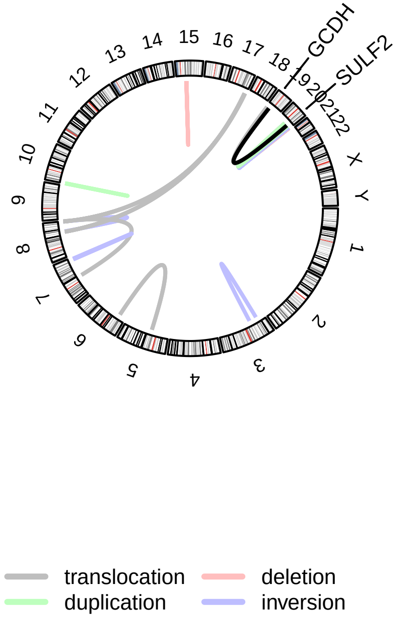
RETAINED PROTEIN DOMAINS
reading frame unclear

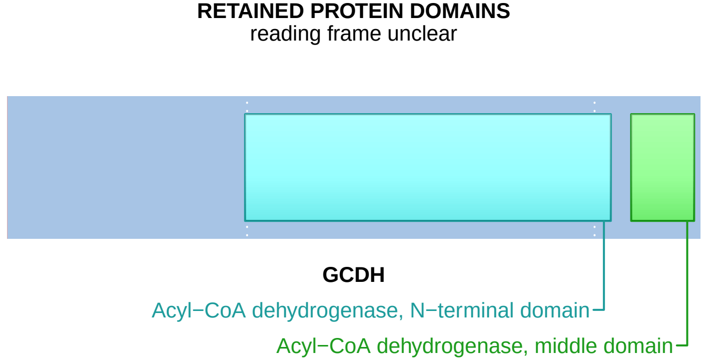


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

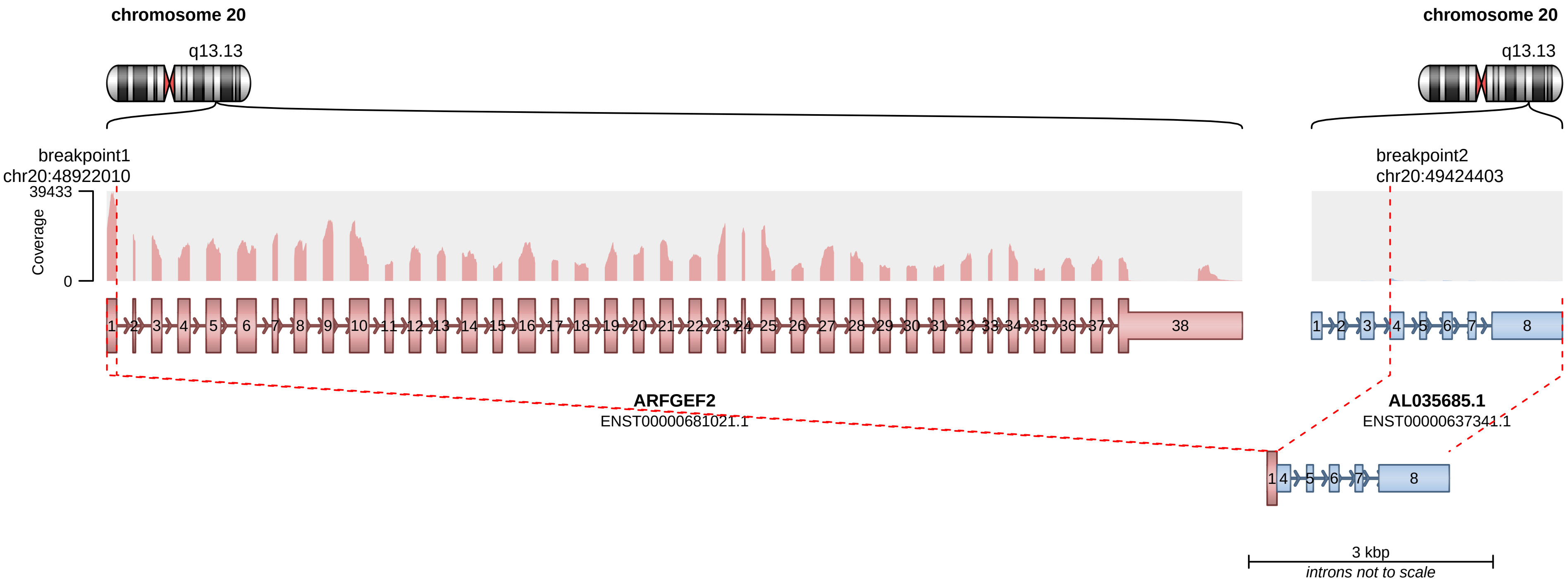


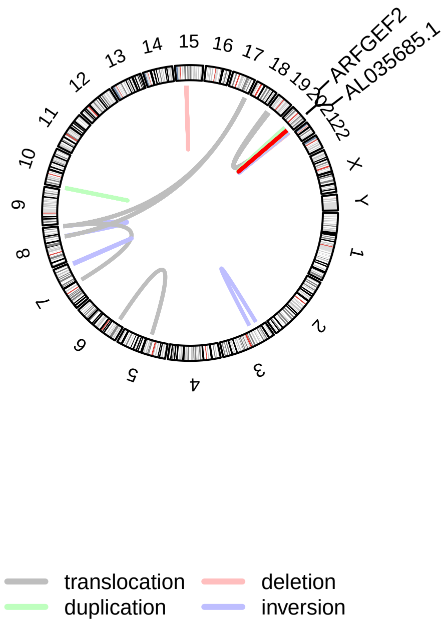




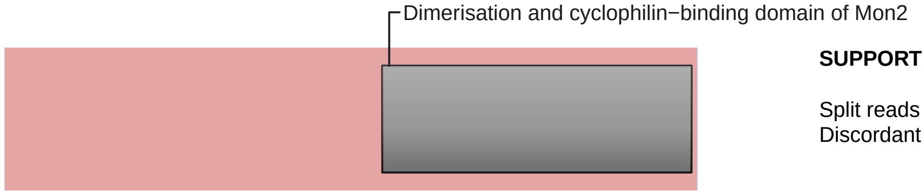
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0





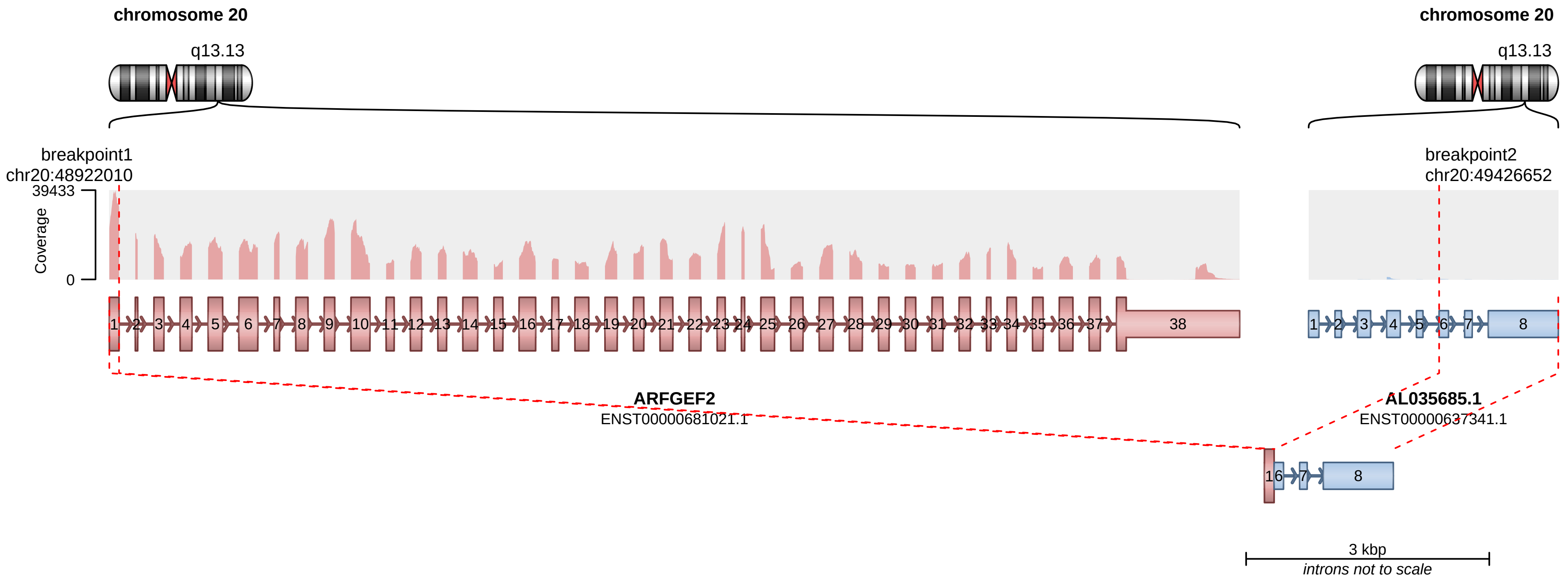
RETAINED PROTEIN DOMAINS
reading frame unclear

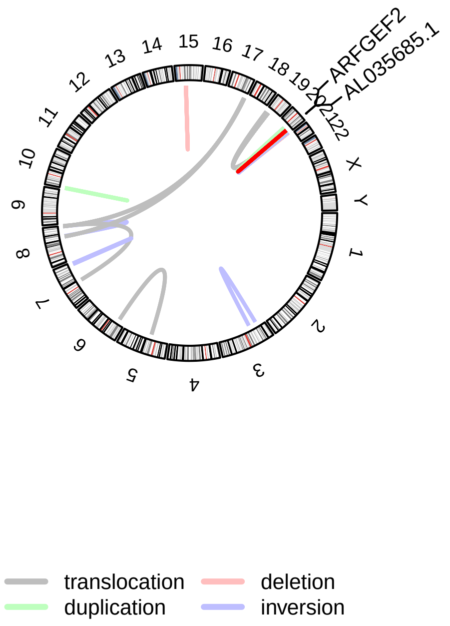


ARFGEF2

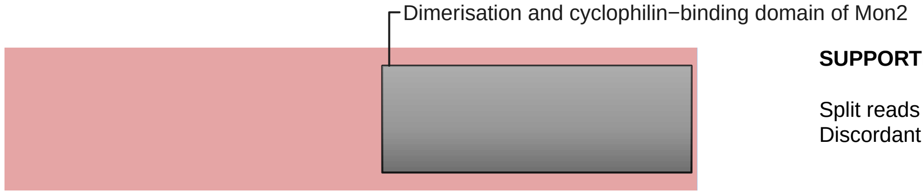
SUPPORTING READ COUNT

Split reads = 735
Discordant mates = 1





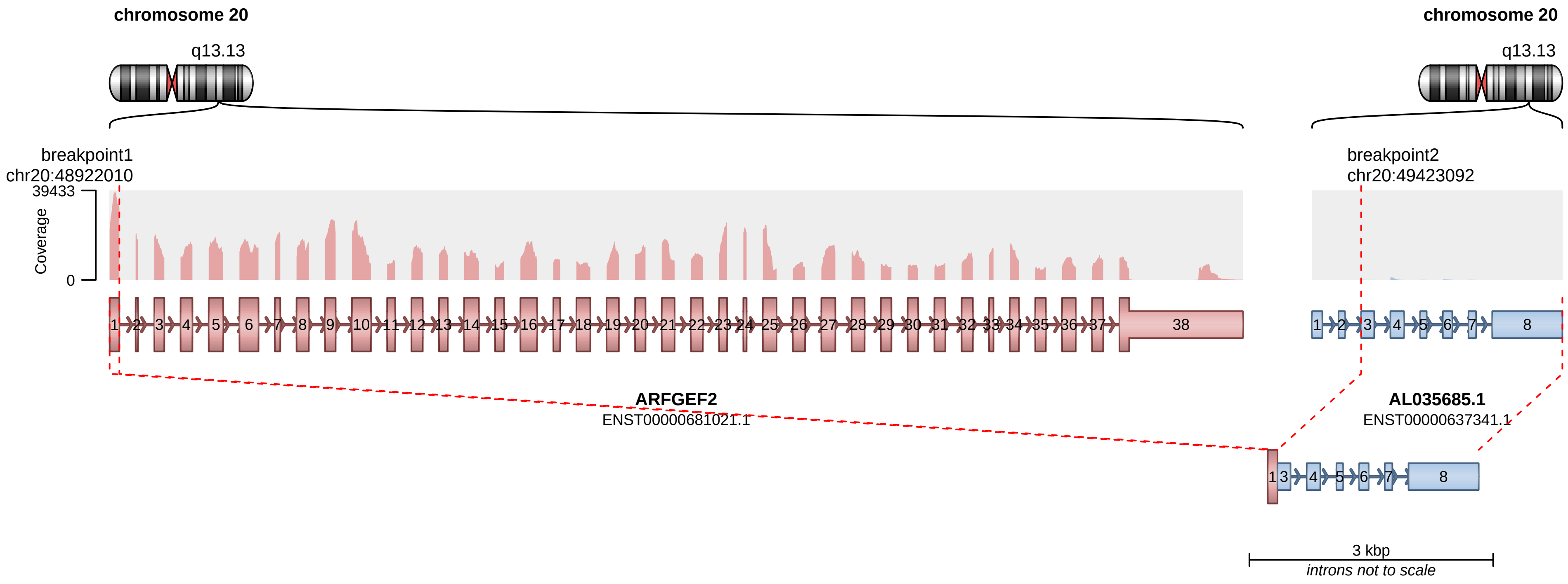
RETAINED PROTEIN DOMAINS
reading frame unclear

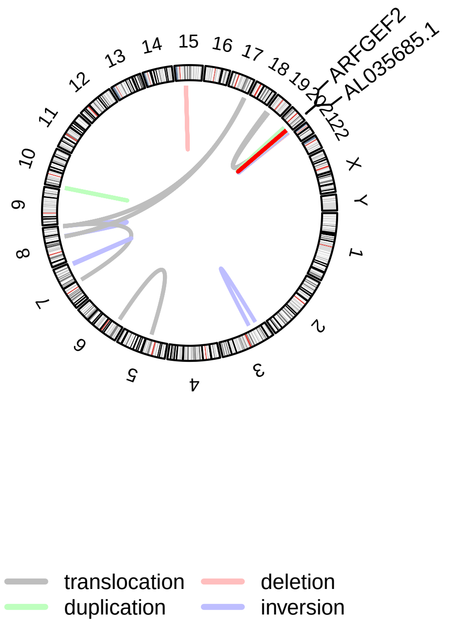


ARFGEF2

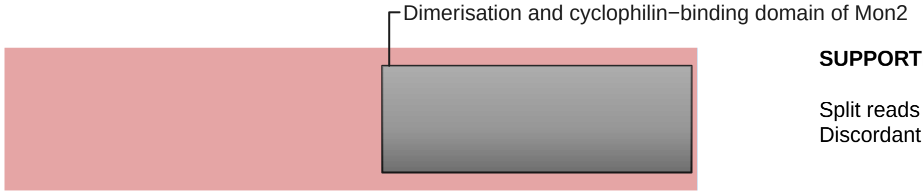
SUPPORTING READ COUNT

Split reads = 121
Discordant mates = 1





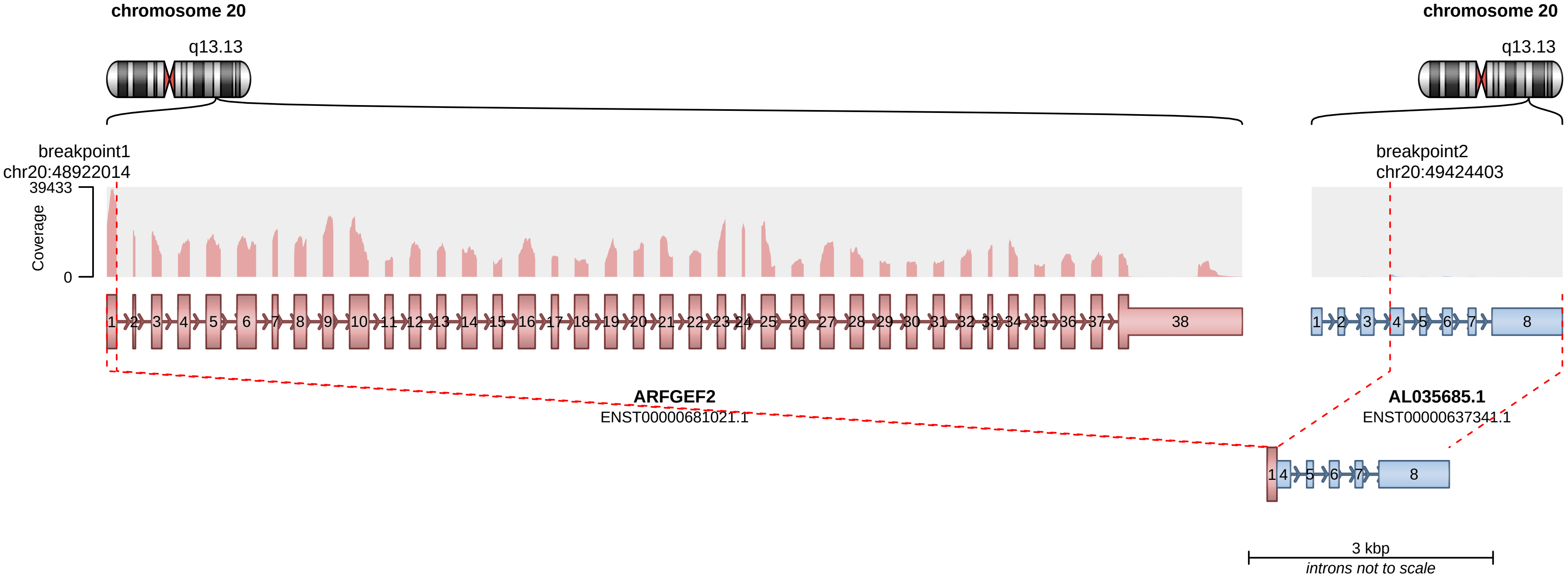
RETAINED PROTEIN DOMAINS
reading frame unclear

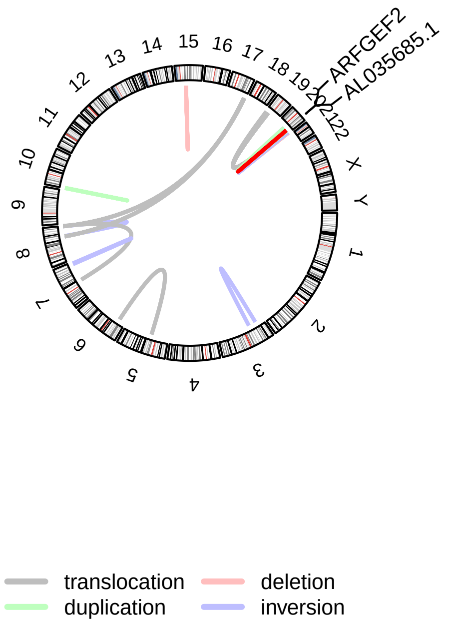


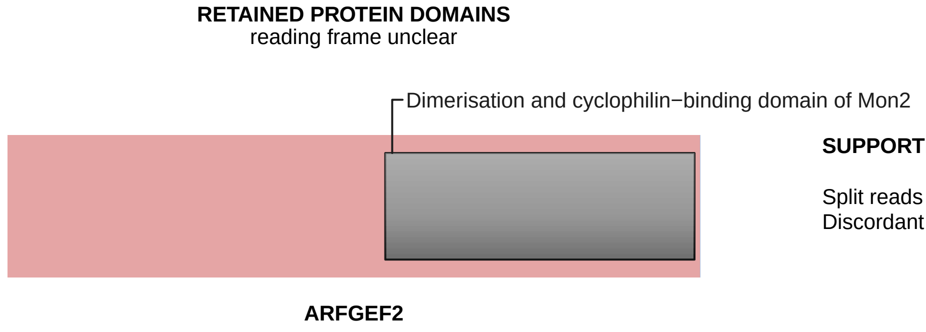
ARFGEF2

SUPPORTING READ COUNT

Split reads = 20
Discordant mates = 1

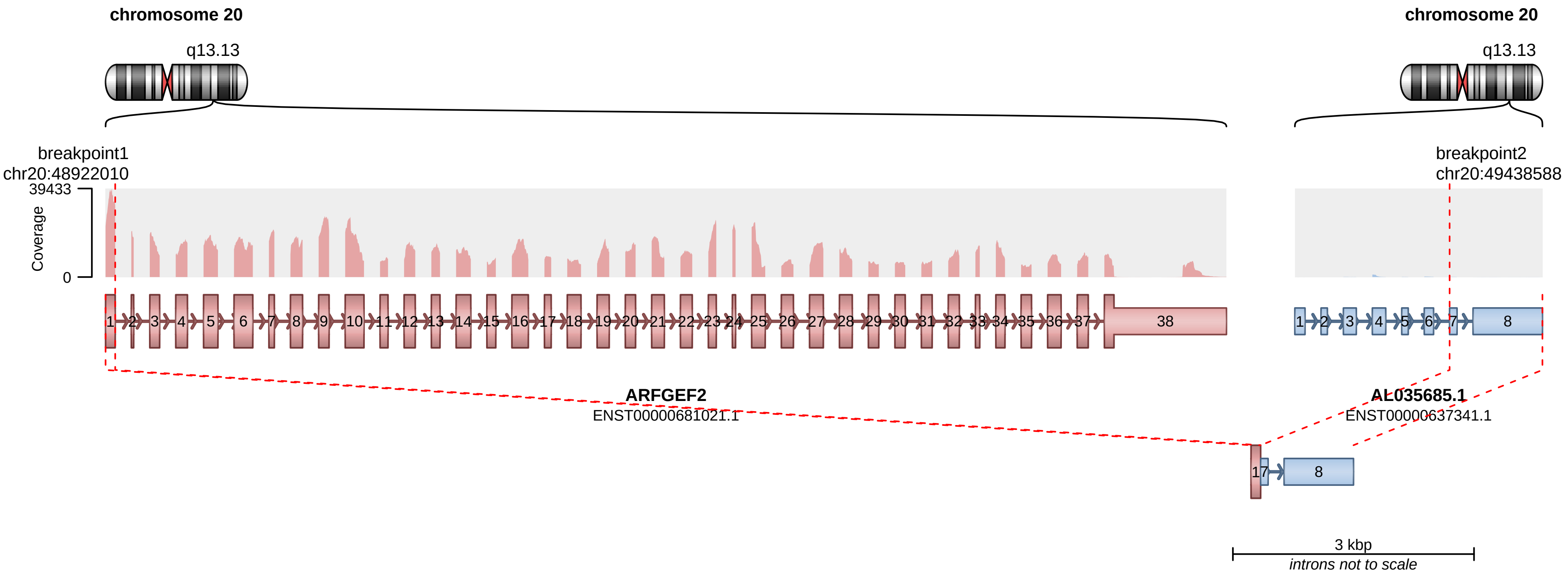


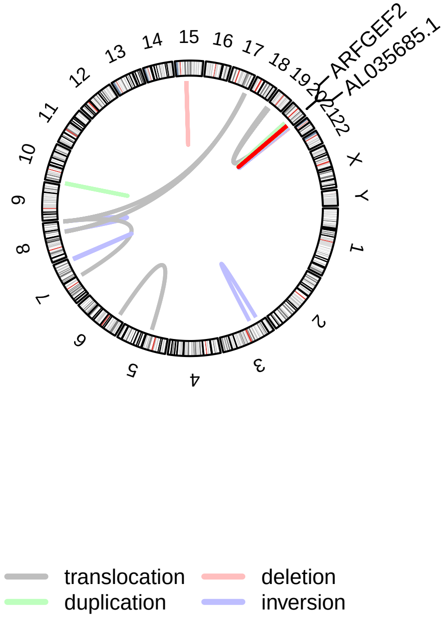




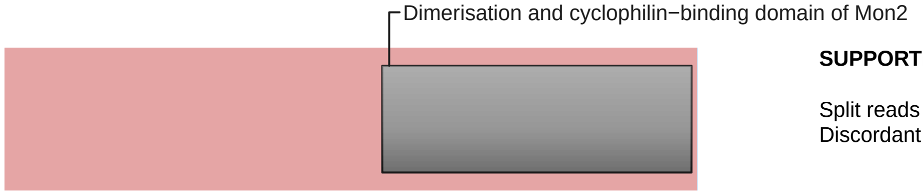
SUPPORTING READ COUNT

Split reads = 13
Discordant mates = 1





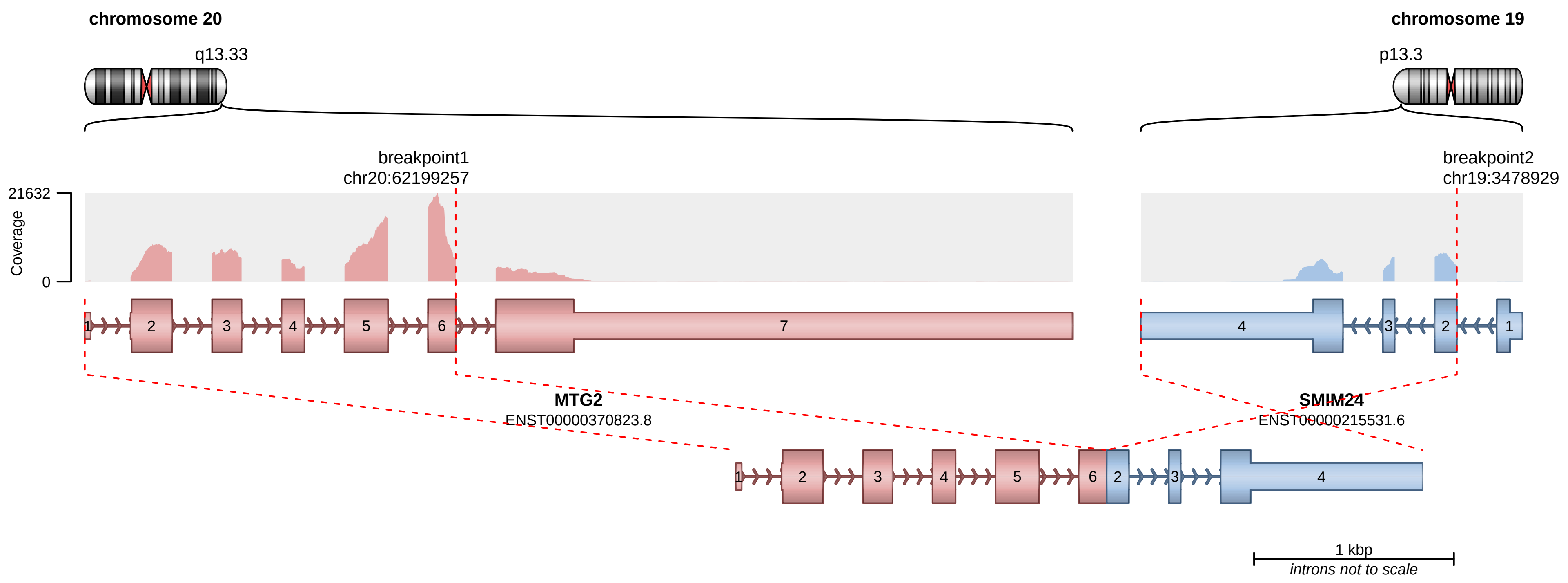
RETAINED PROTEIN DOMAINS
reading frame unclear

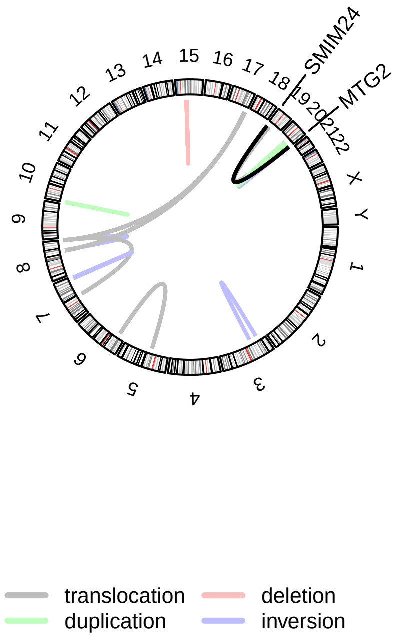


ARFGEF2

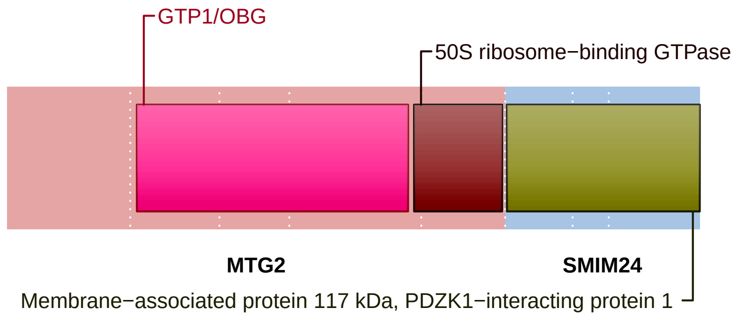
SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0



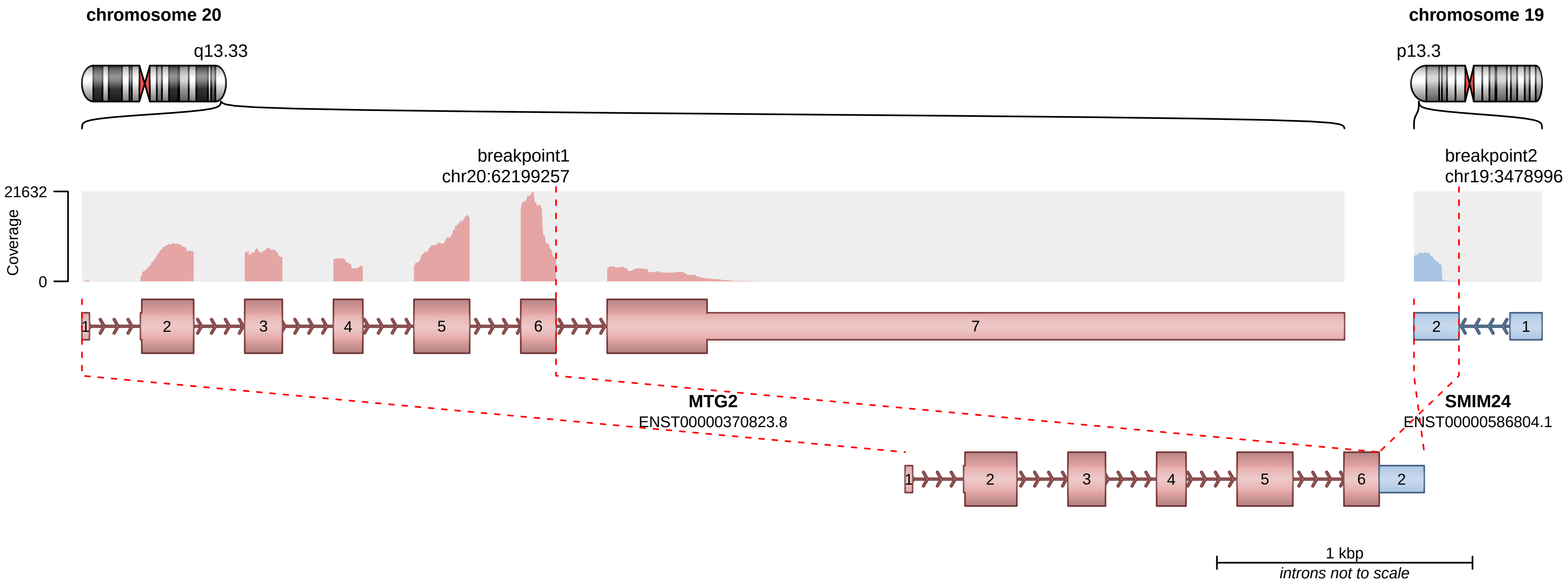


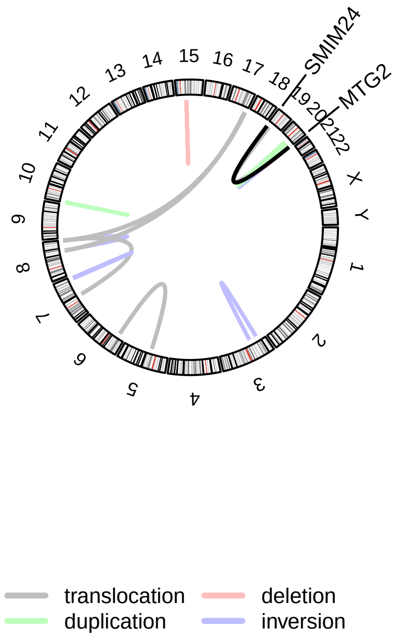
RETAINED PROTEIN DOMAINS
reading frame unclear



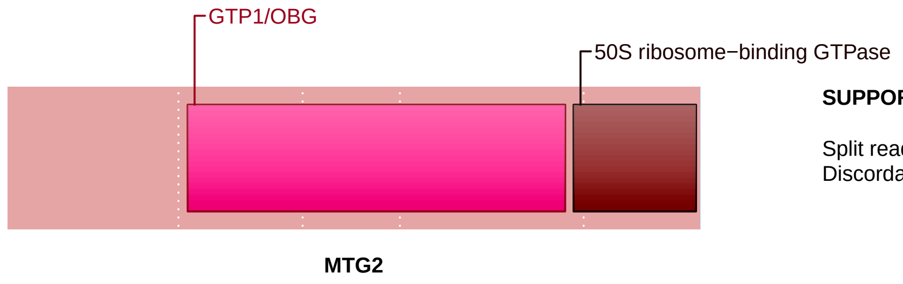
SUPPORTING READ COUNT

Split reads = 713
Discordant mates = 2



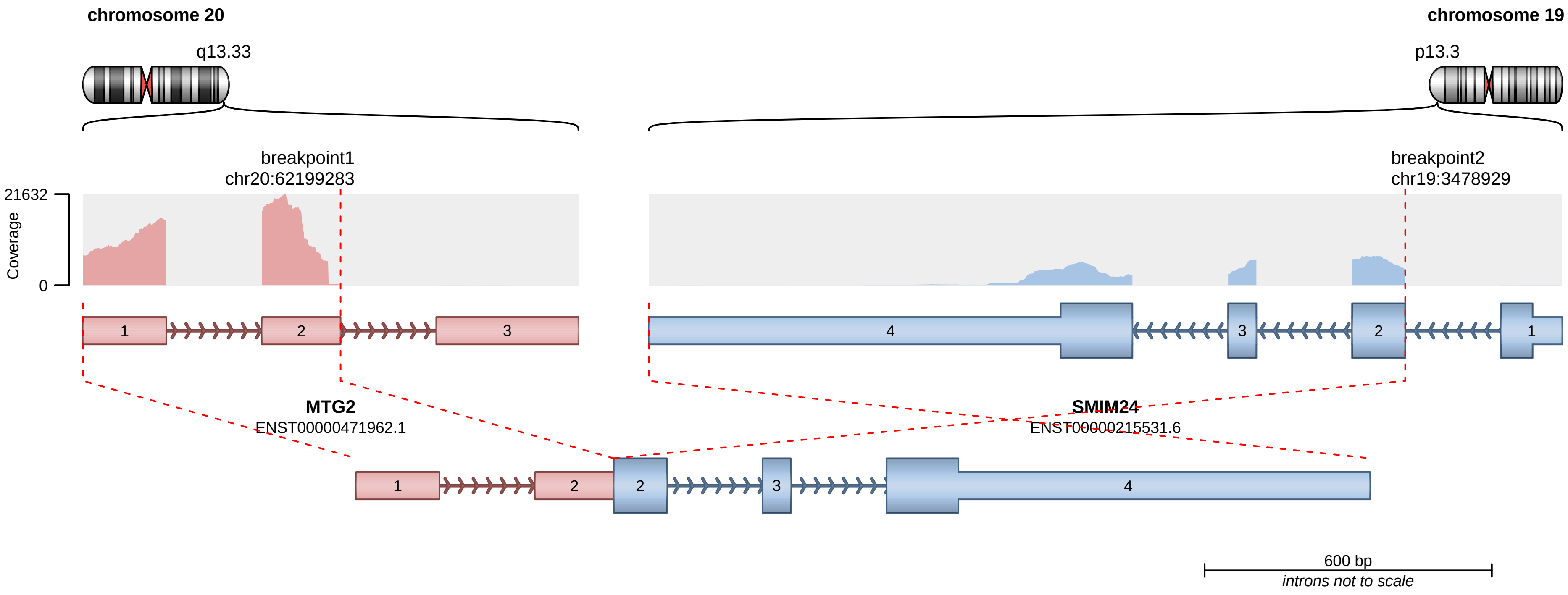


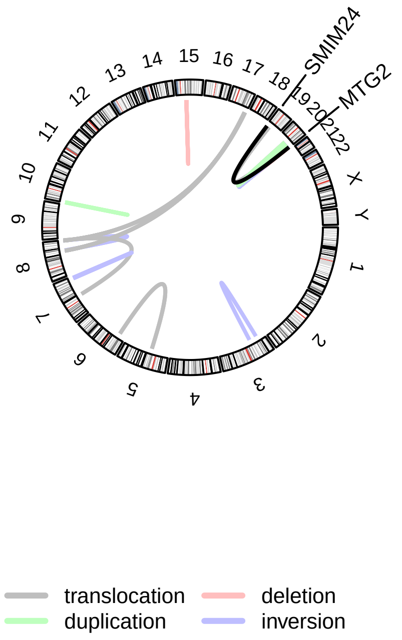
RETAINED PROTEIN DOMAINS
reading frame unclear



SUPPORTING READ COUNT

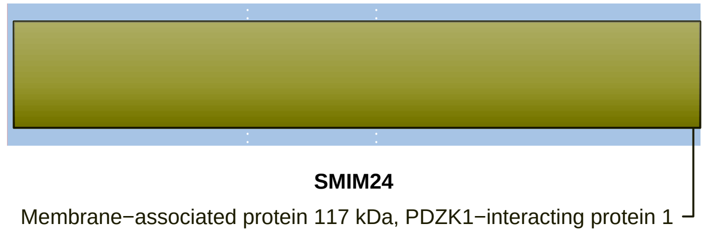
Split reads = 9
Discordant mates = 2





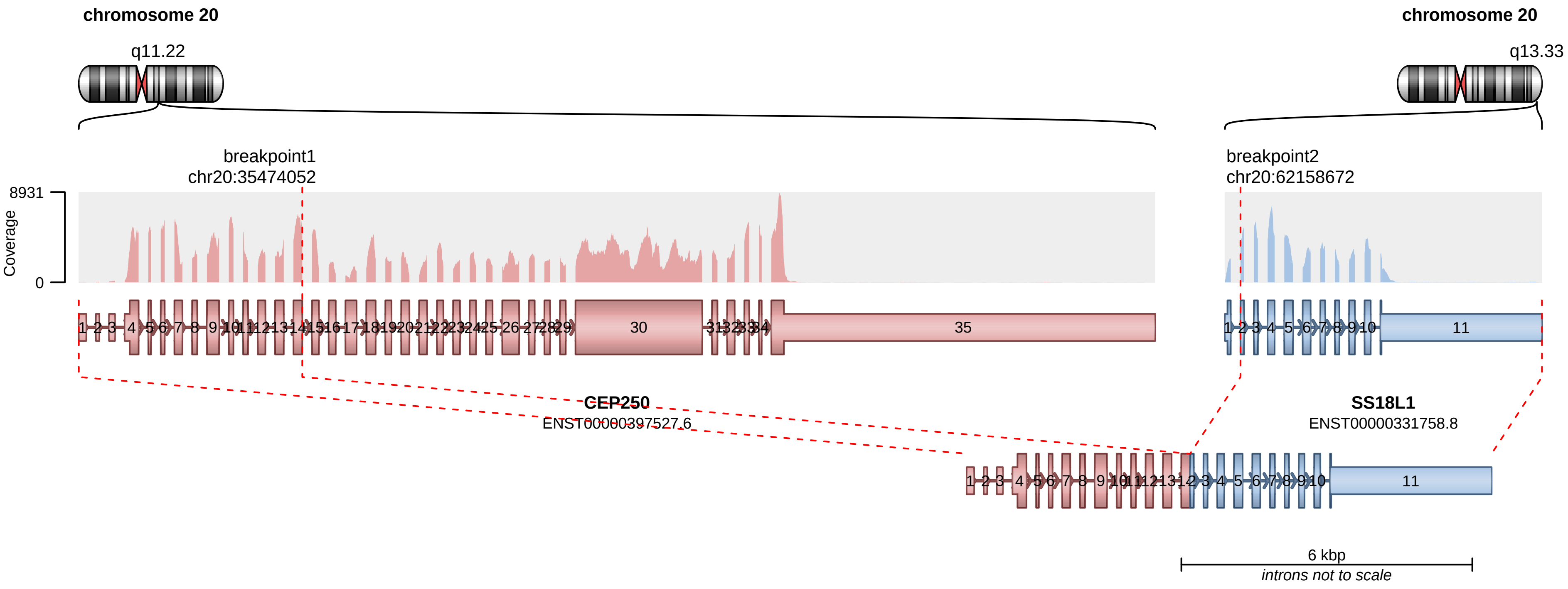
RETAINED PROTEIN DOMAINS

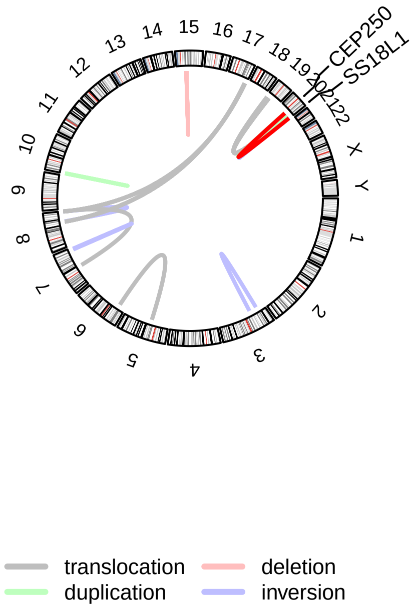
reading frame unclear



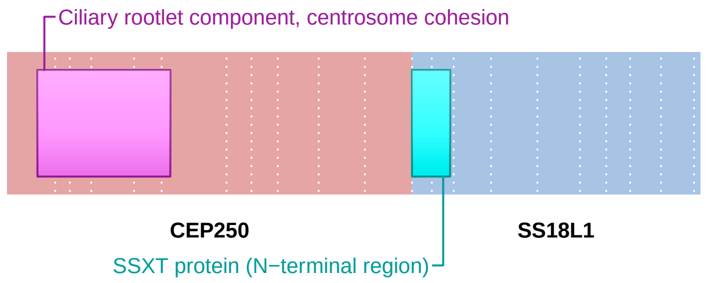
SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 2



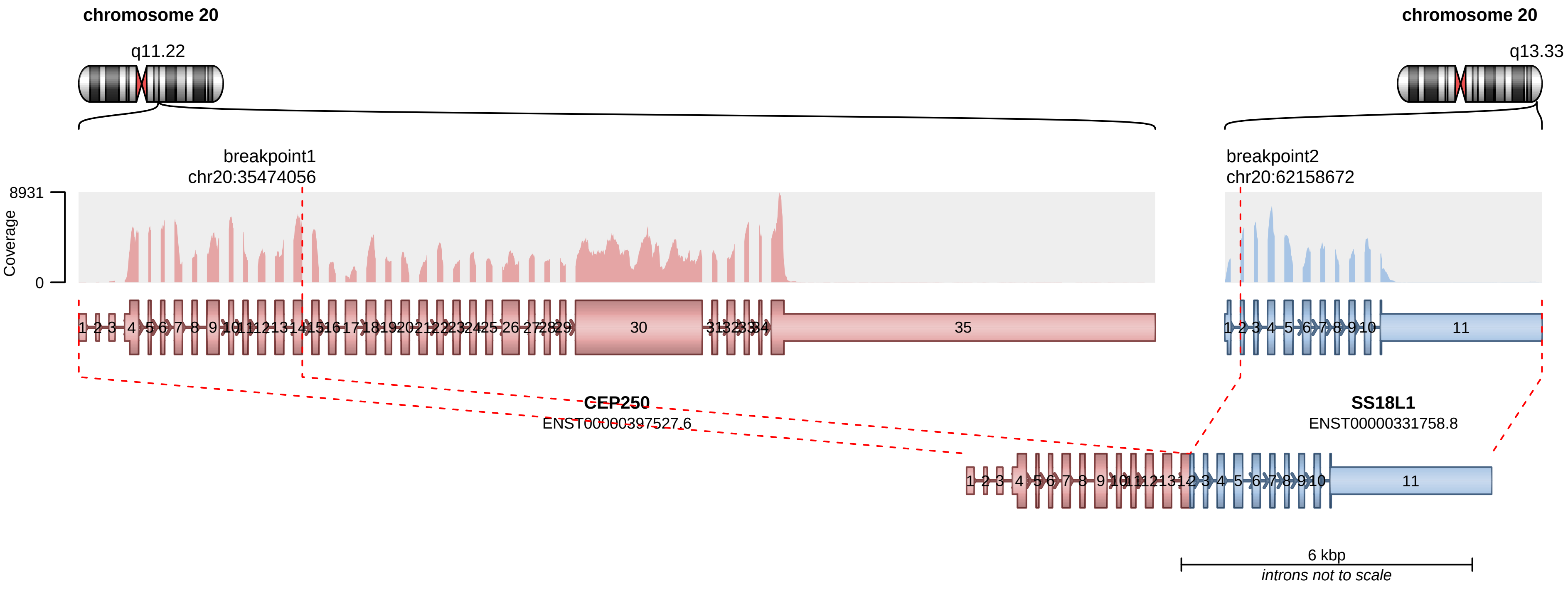


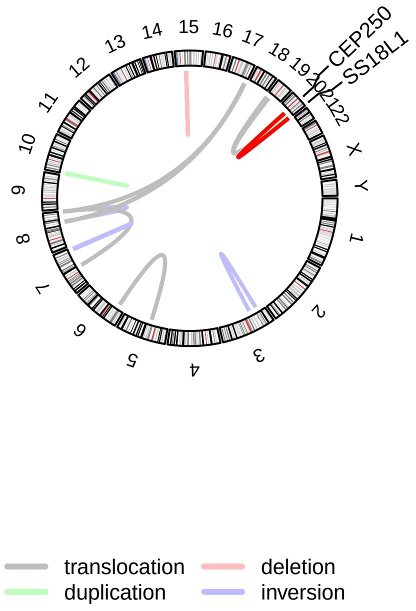
RETAINED PROTEIN DOMAINS
reading frame unclear

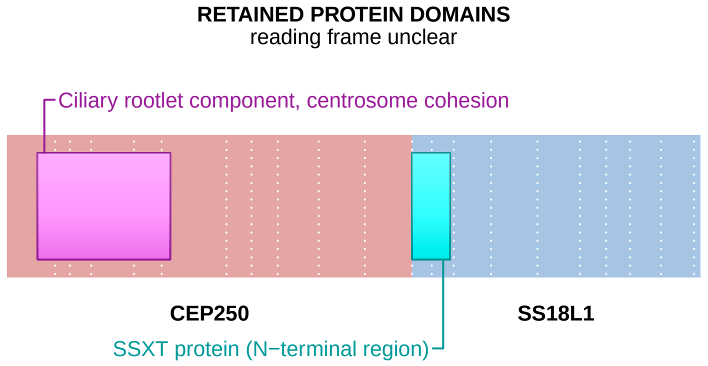


SUPPORTING READ COUNT

Split reads = 330
Discordant mates = 3

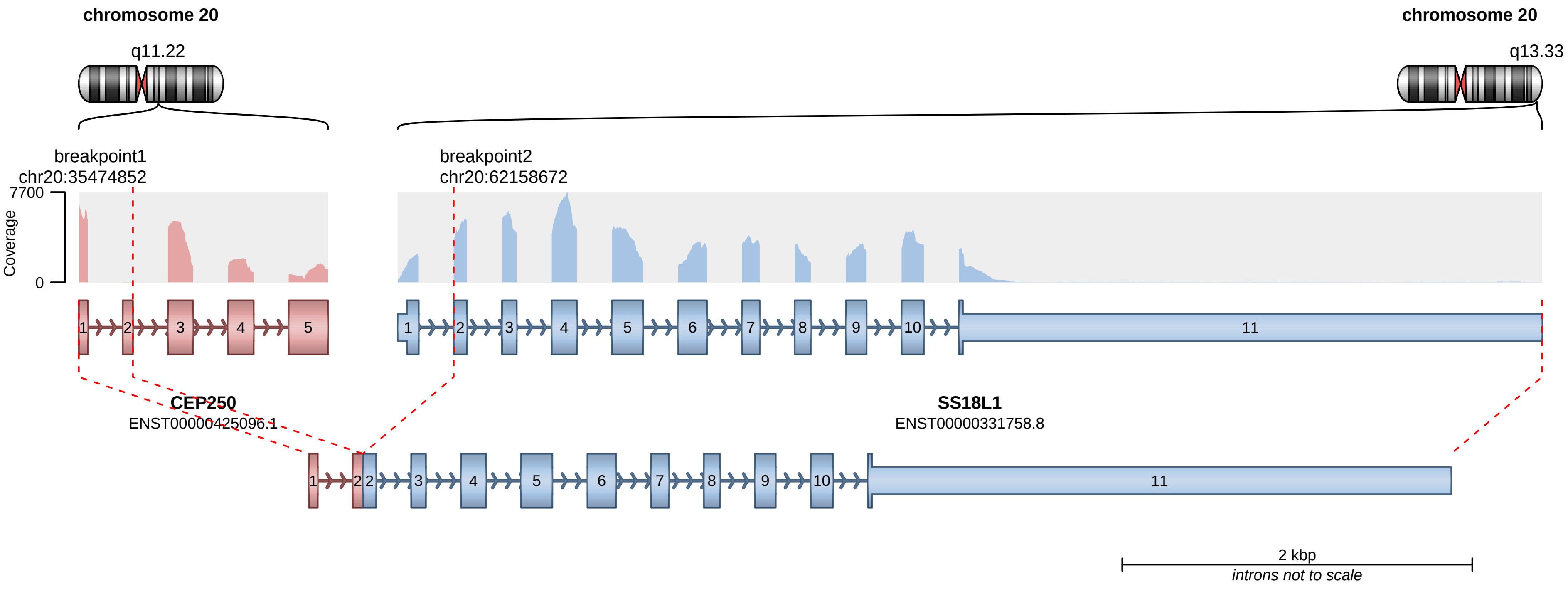


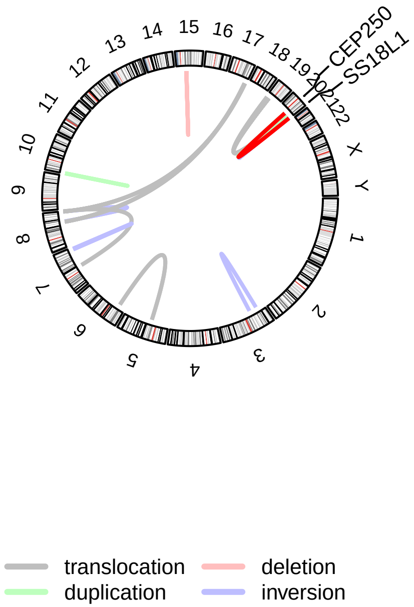




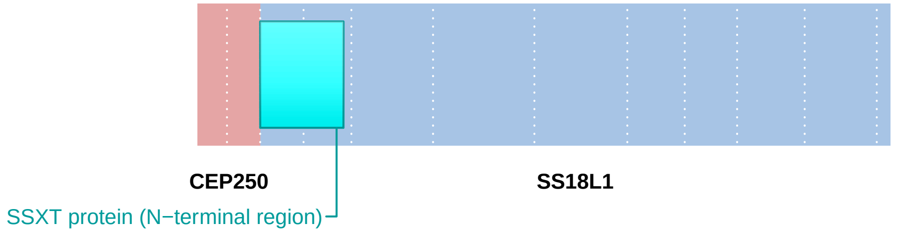
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 3



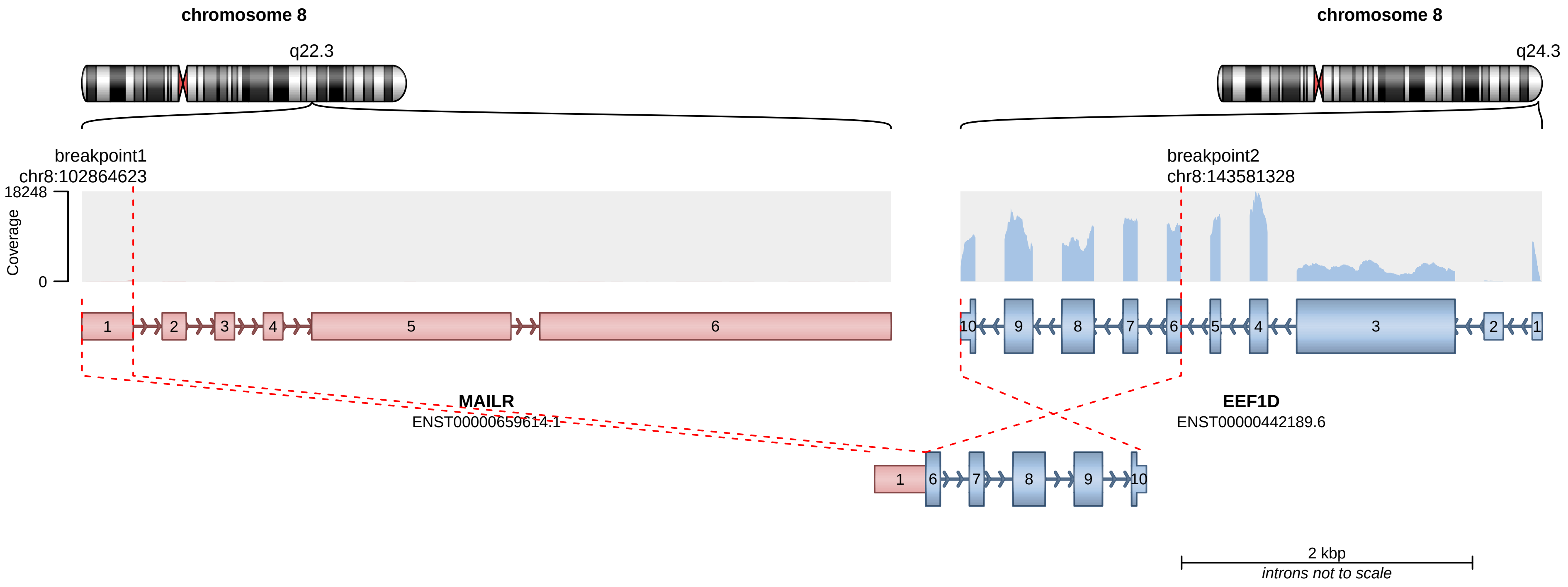


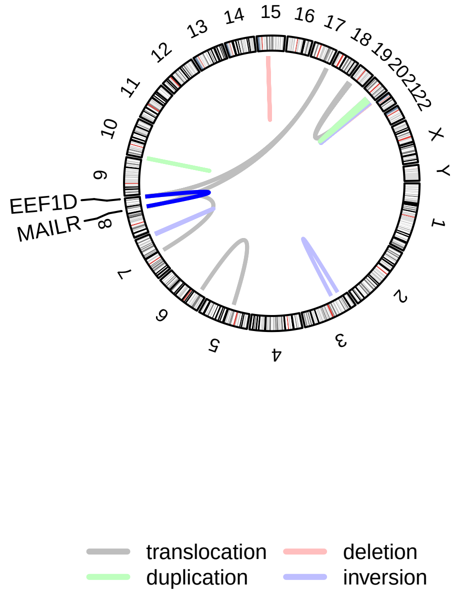
RETAINED PROTEIN DOMAINS
reading frame unclear

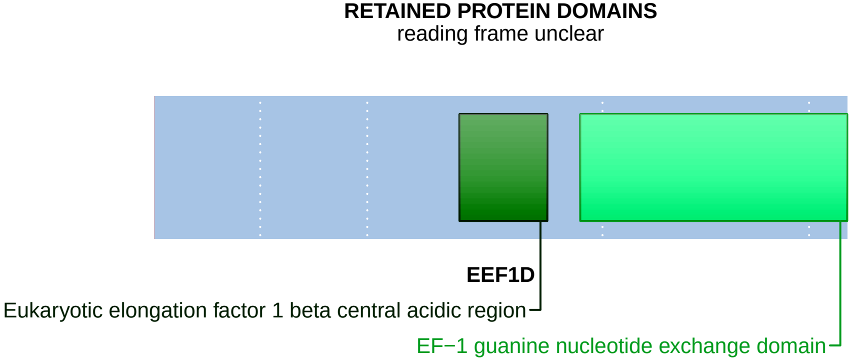


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 3

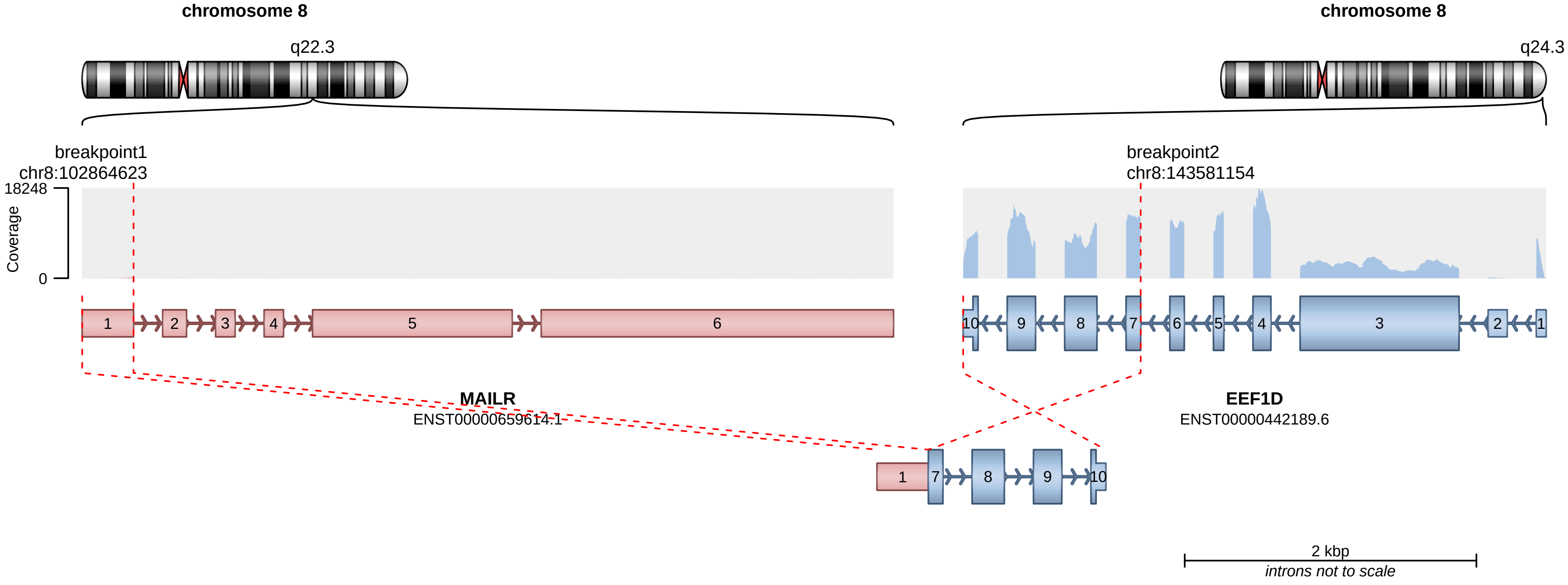


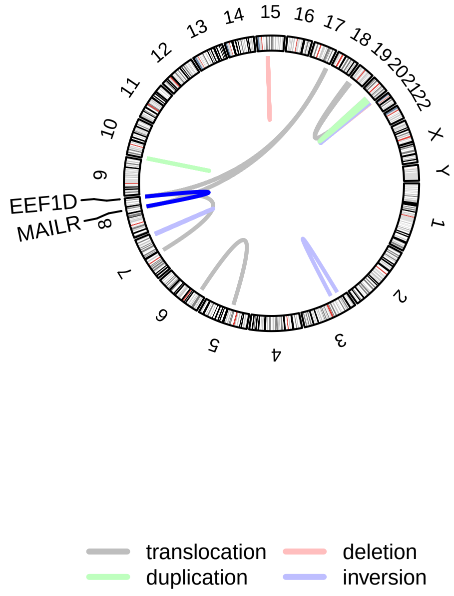


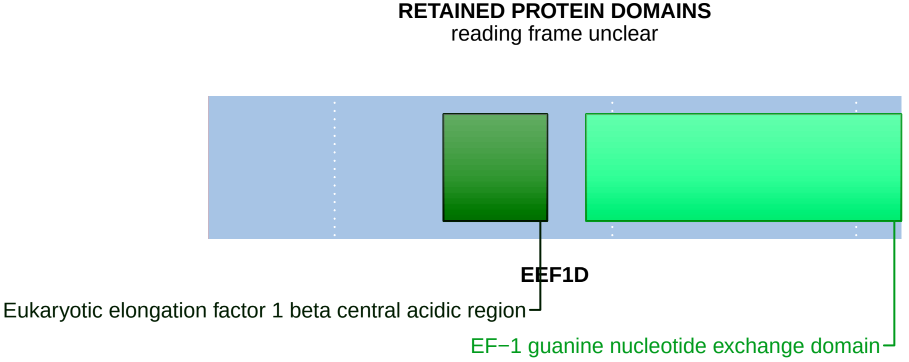


SUPPORTING READ COUNT

Split reads = 138
Discordant mates = 2

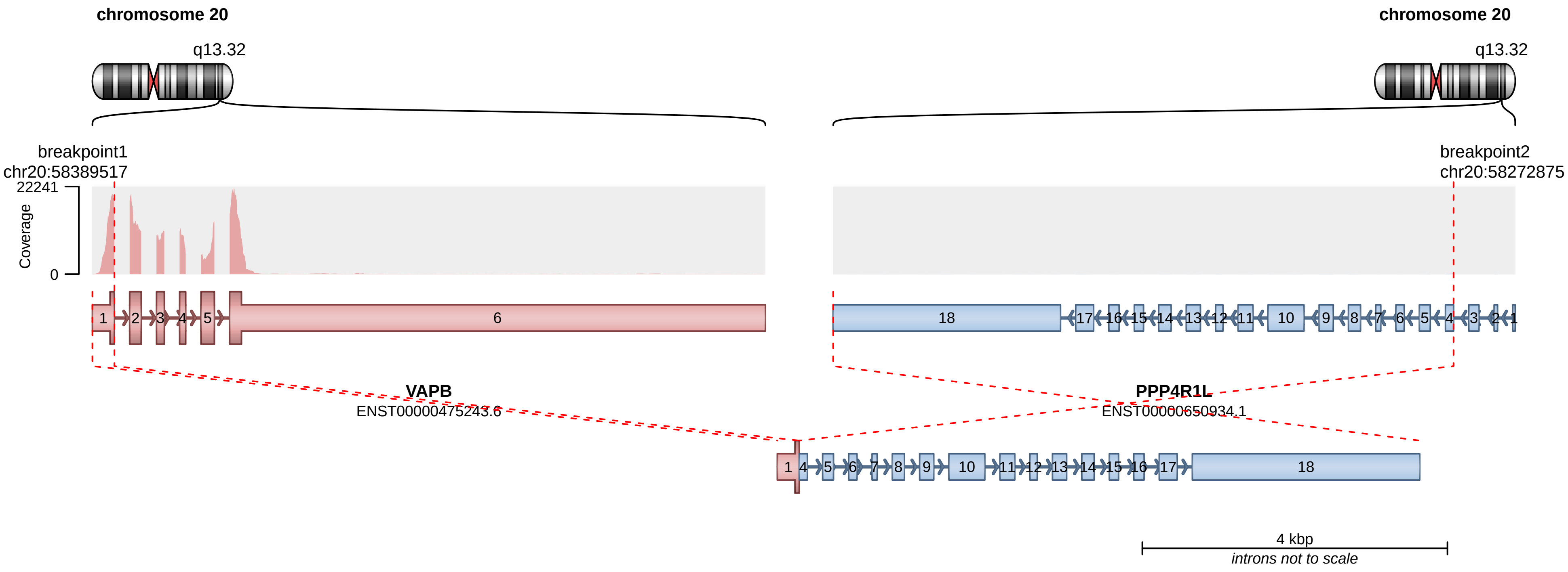


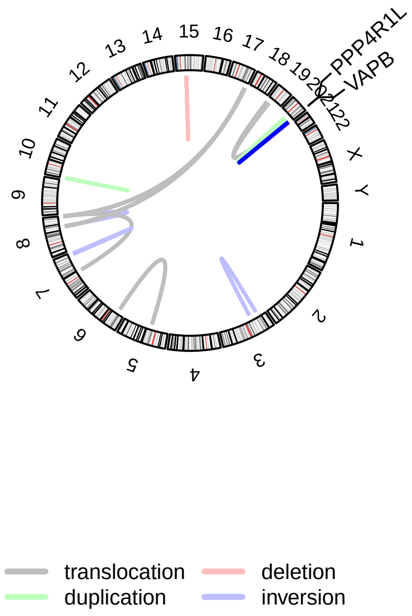




SUPPORTING READ COUNT

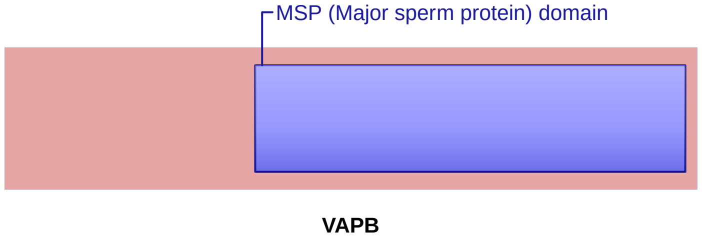
Split reads = 4
Discordant mates = 1





RETAINED PROTEIN DOMAINS

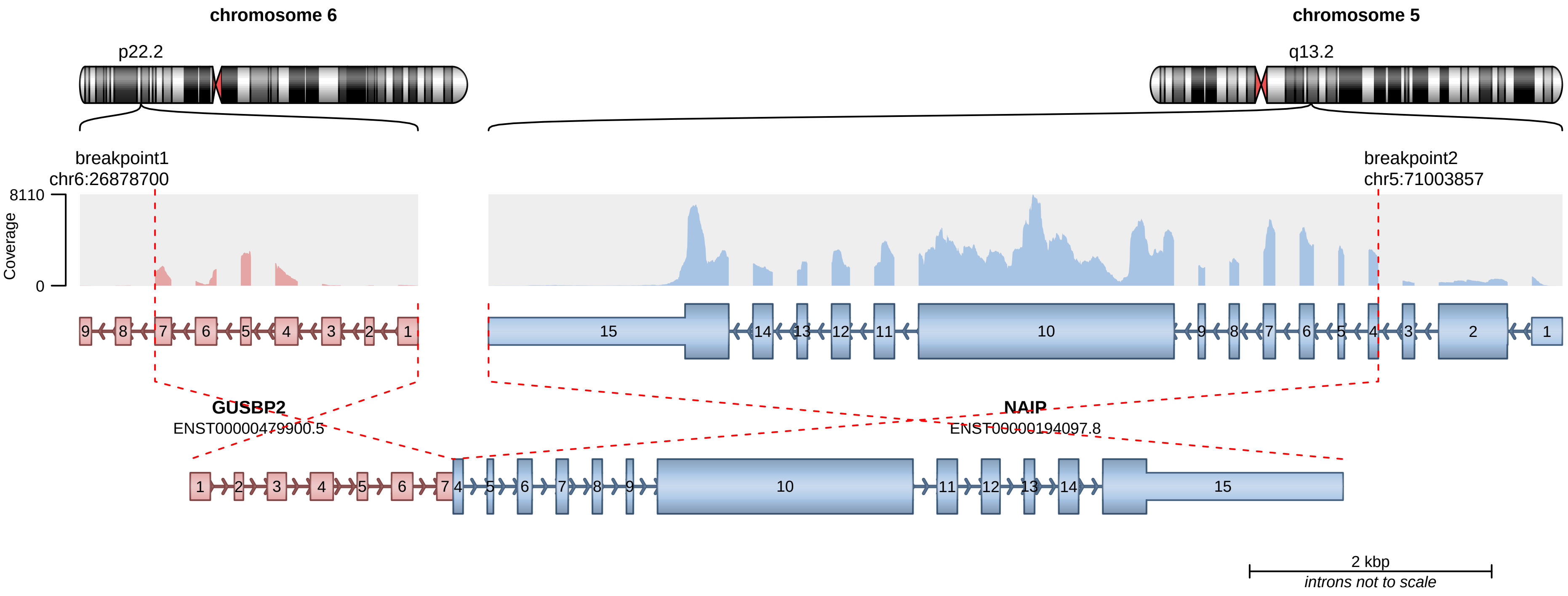
reading frame unclear

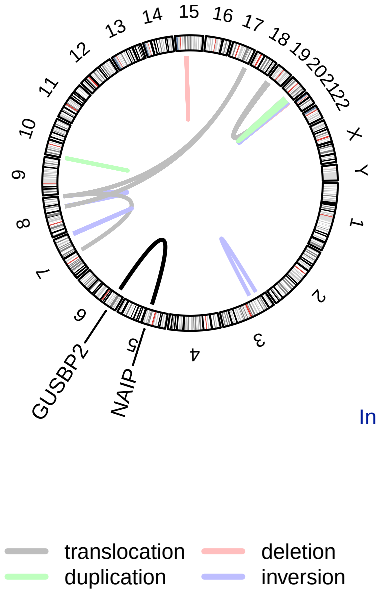


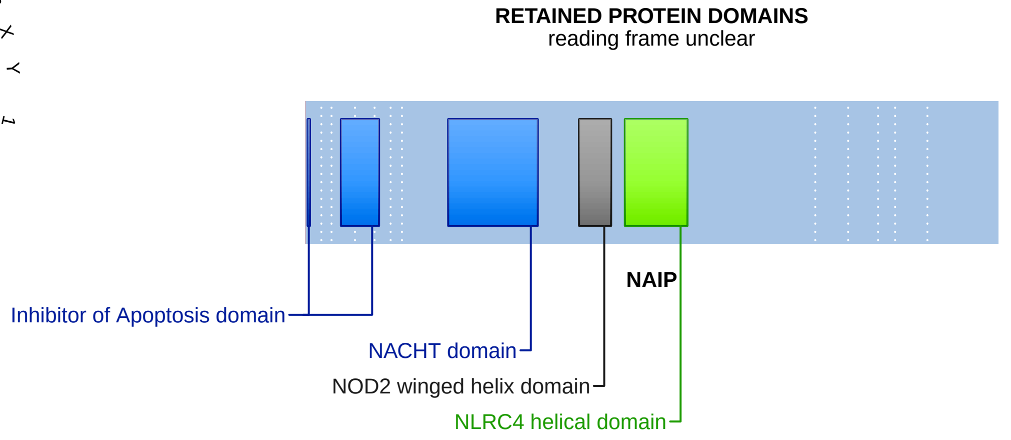
SUPPORTING READ COUNT

Split reads = 101

Discordant mates = 1

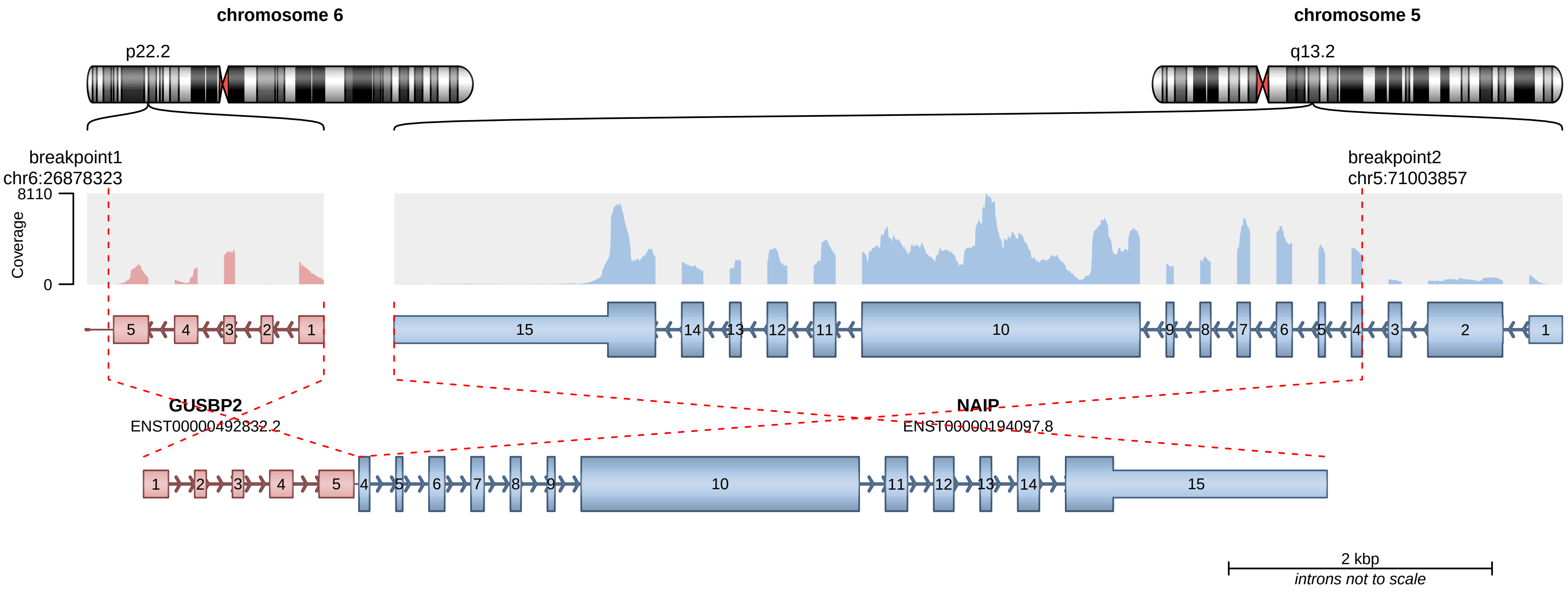


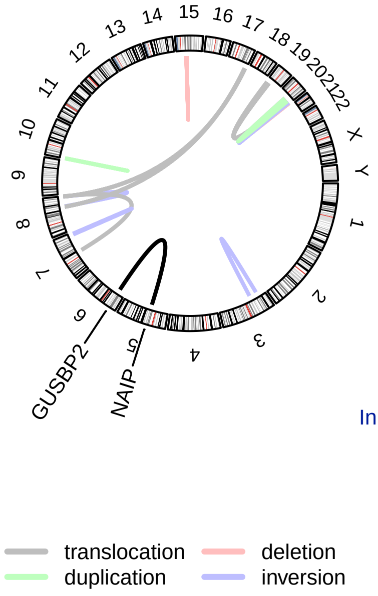


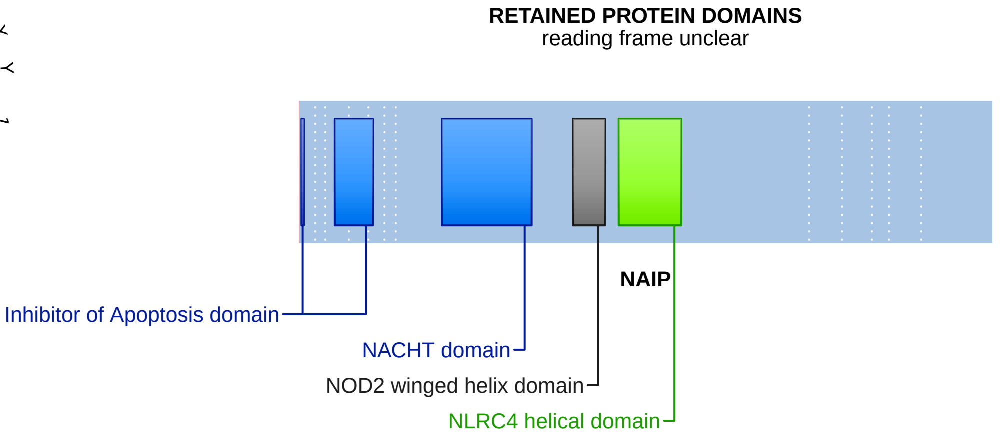


SUPPORTING READ COUNT

Split reads = 85
Discordant mates = 0

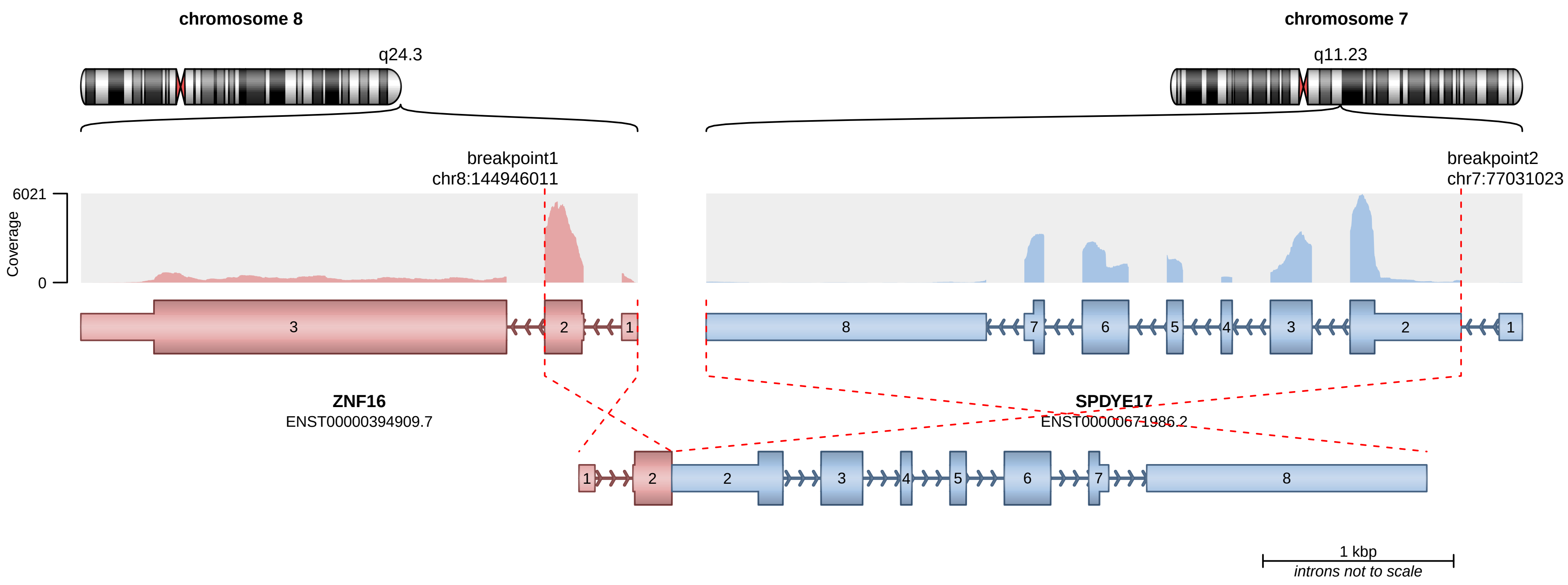


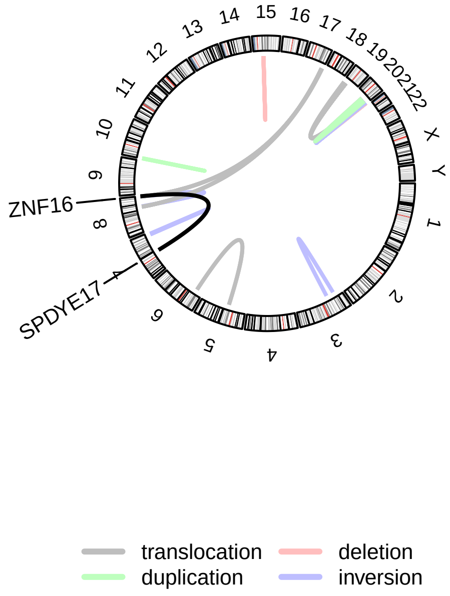




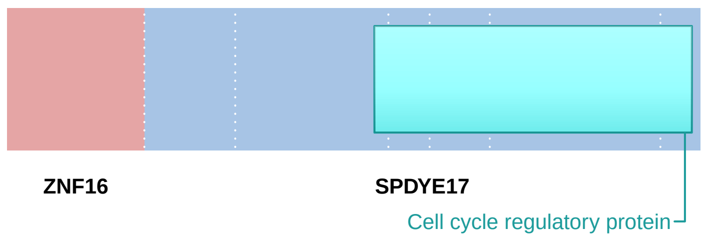
SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 0



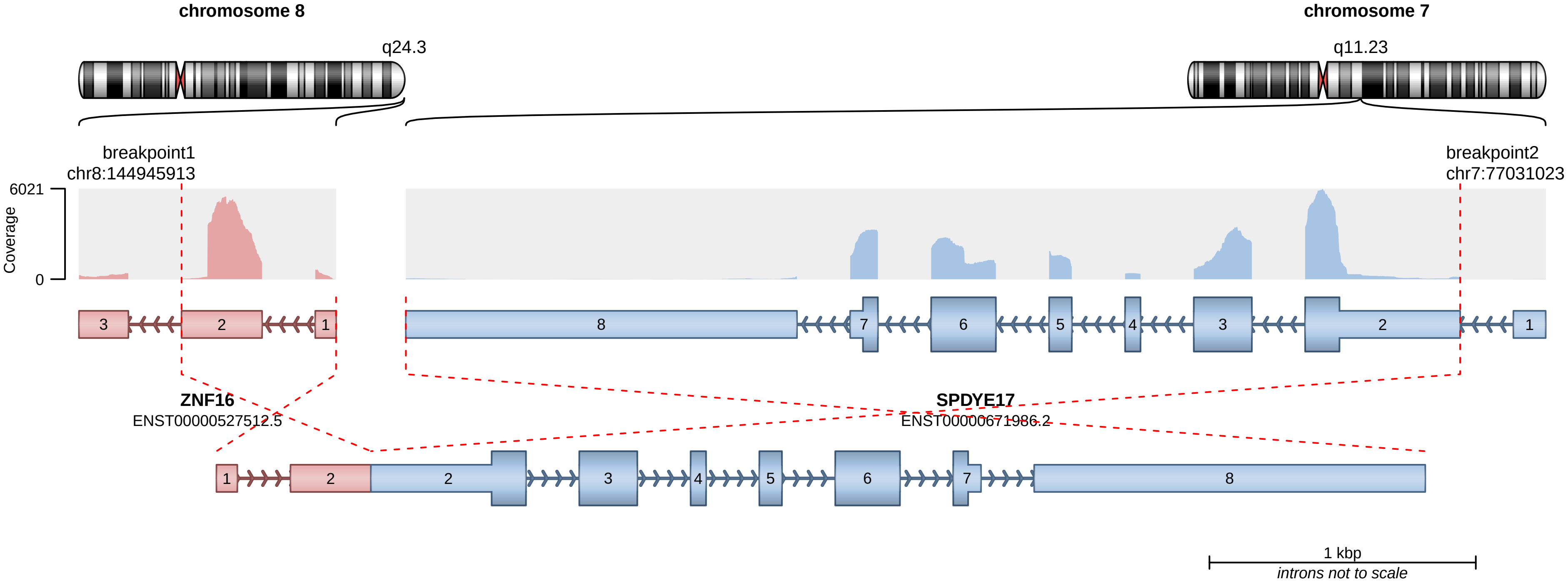


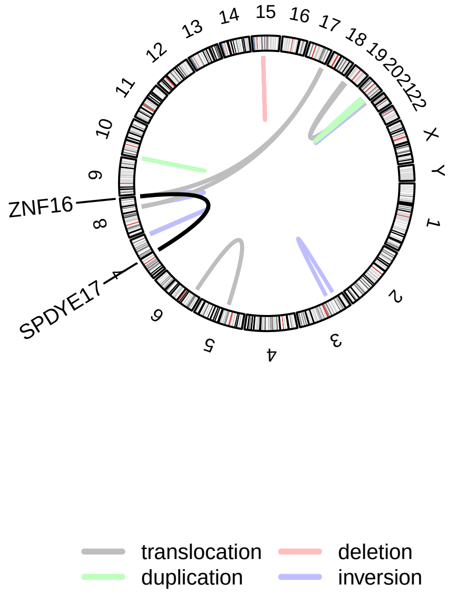
RETAINED PROTEIN DOMAINS
reading frame unclear

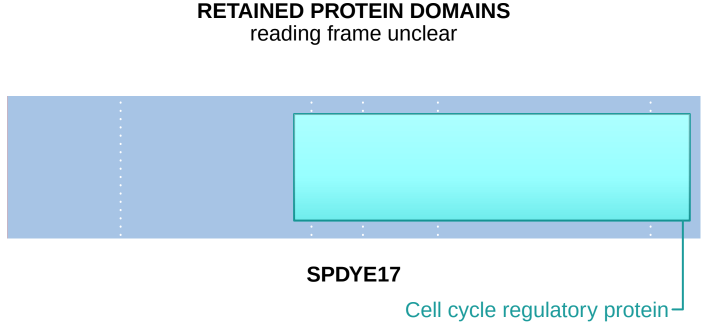


SUPPORTING READ COUNT

Split reads = 83
Discordant mates = 0

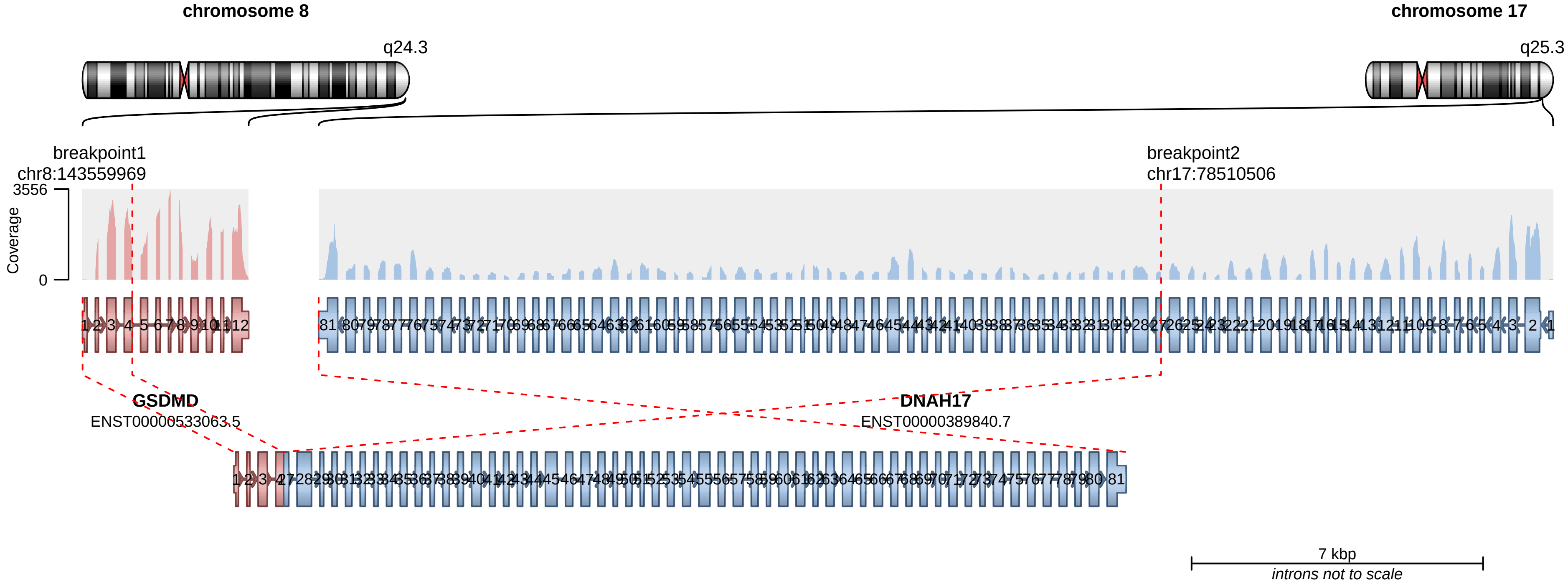


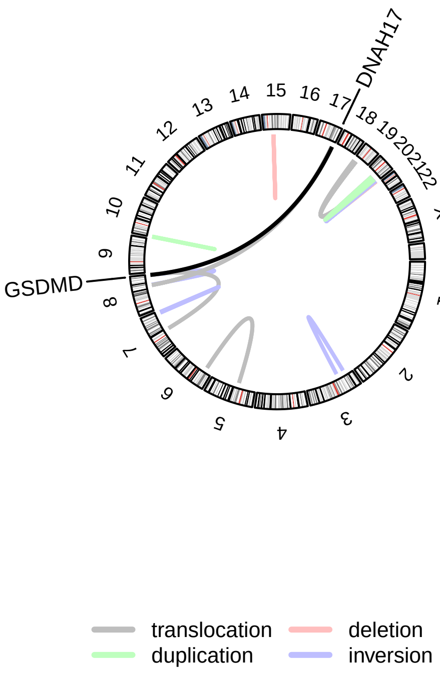


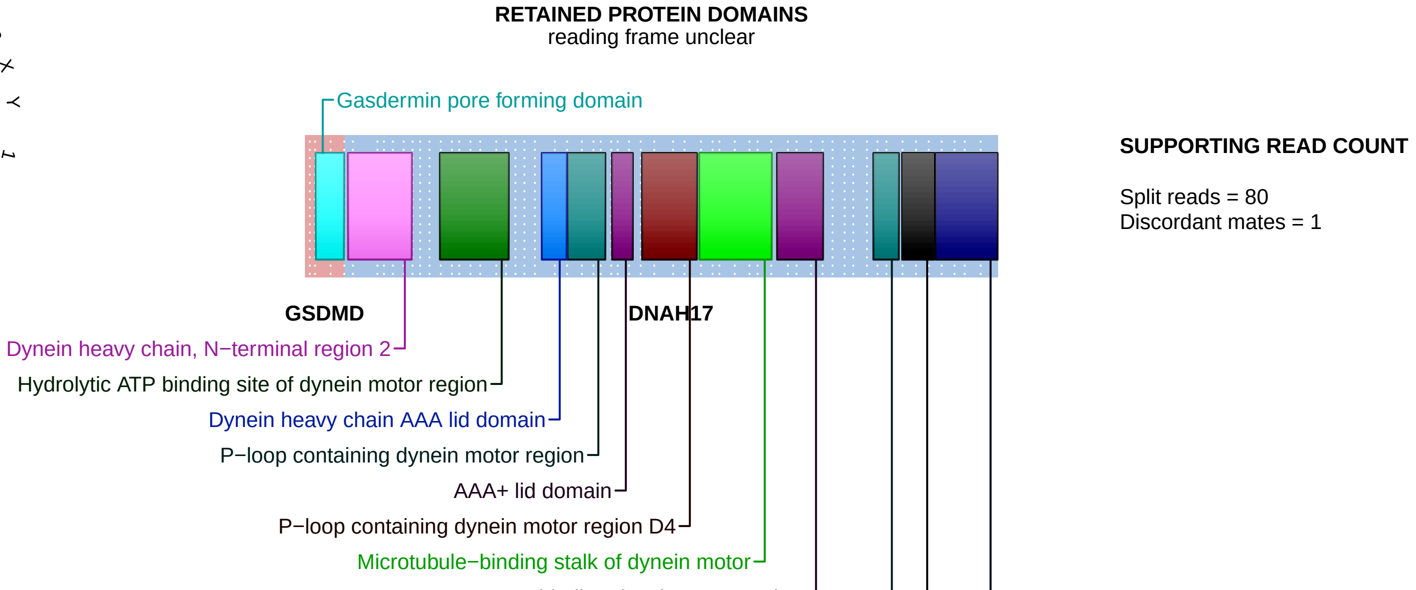

RETAINED PROTEIN DOMAINS
reading frame unclear

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

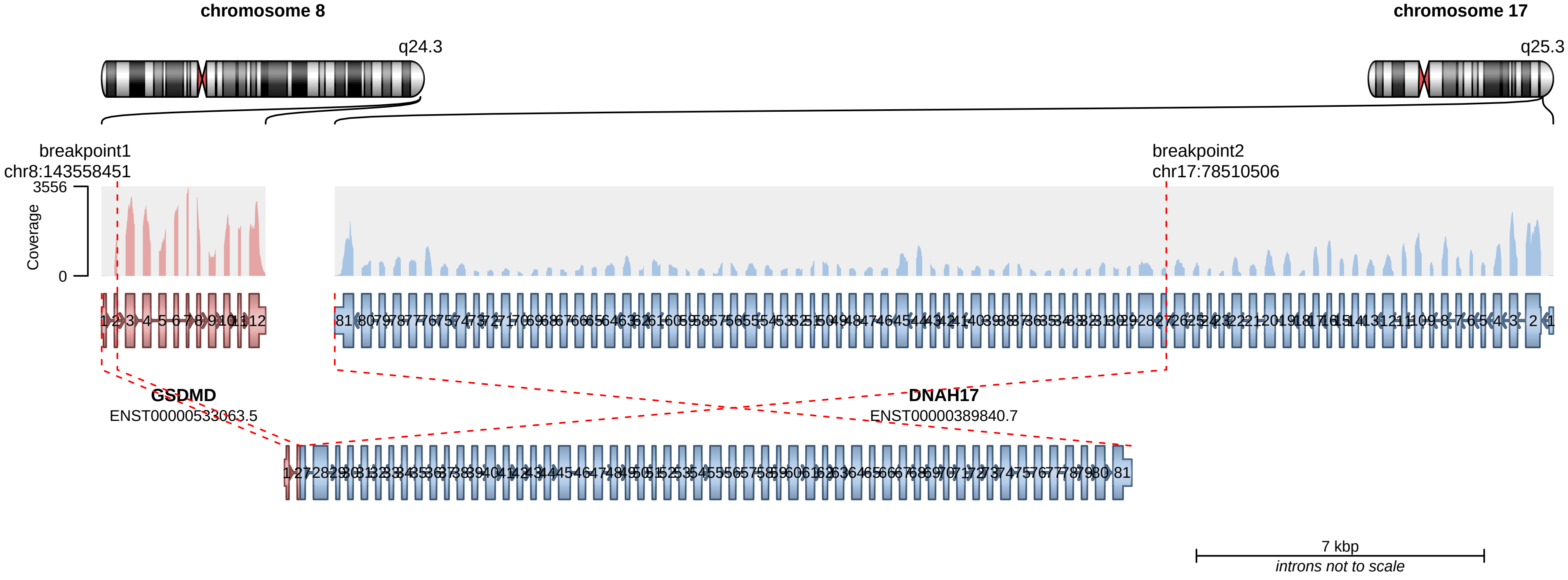


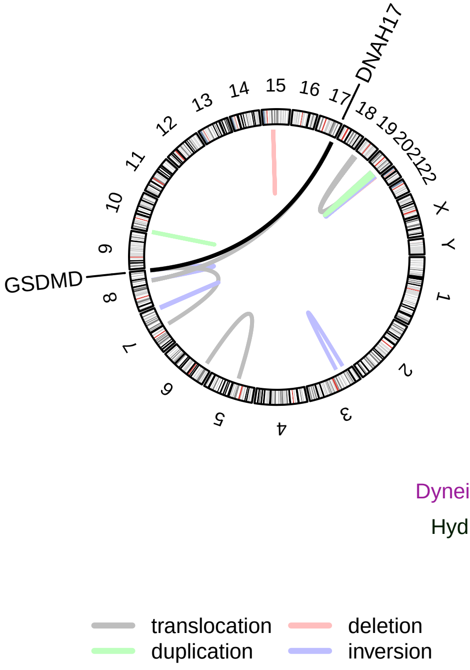


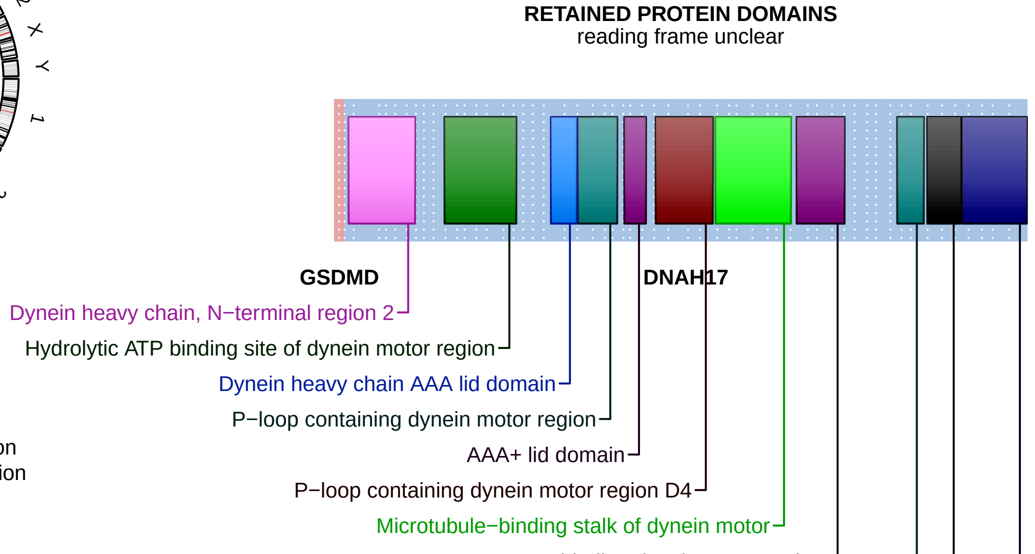


SUPPORTING READ COUNT

Split reads = 80
Discordant mates = 1

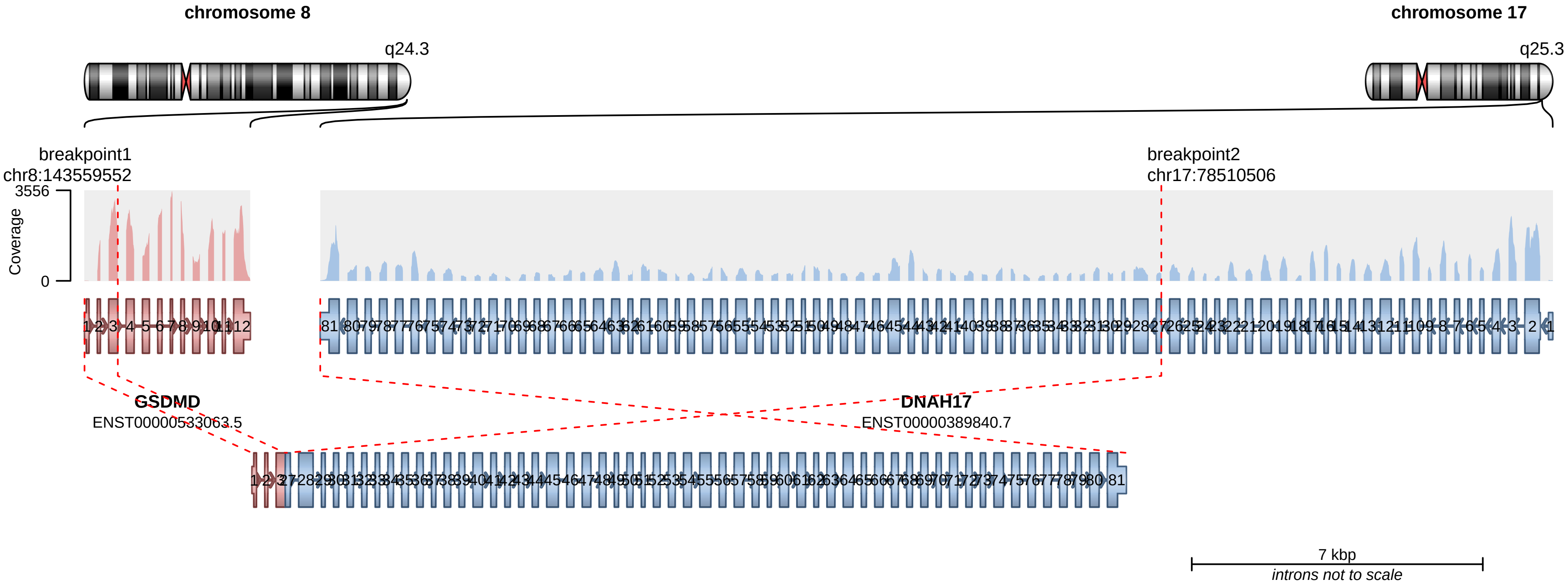


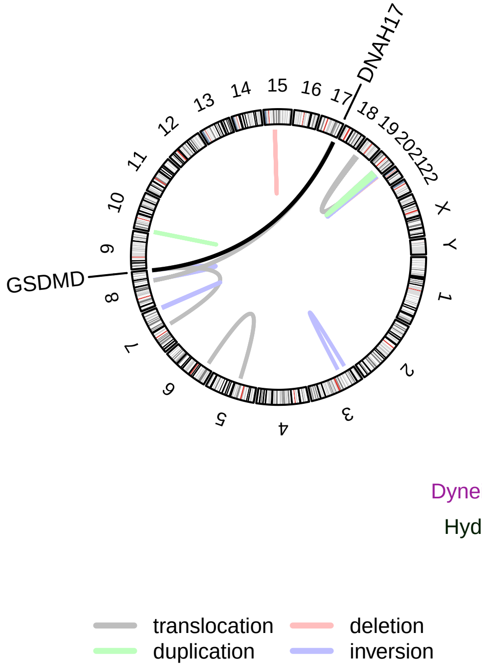


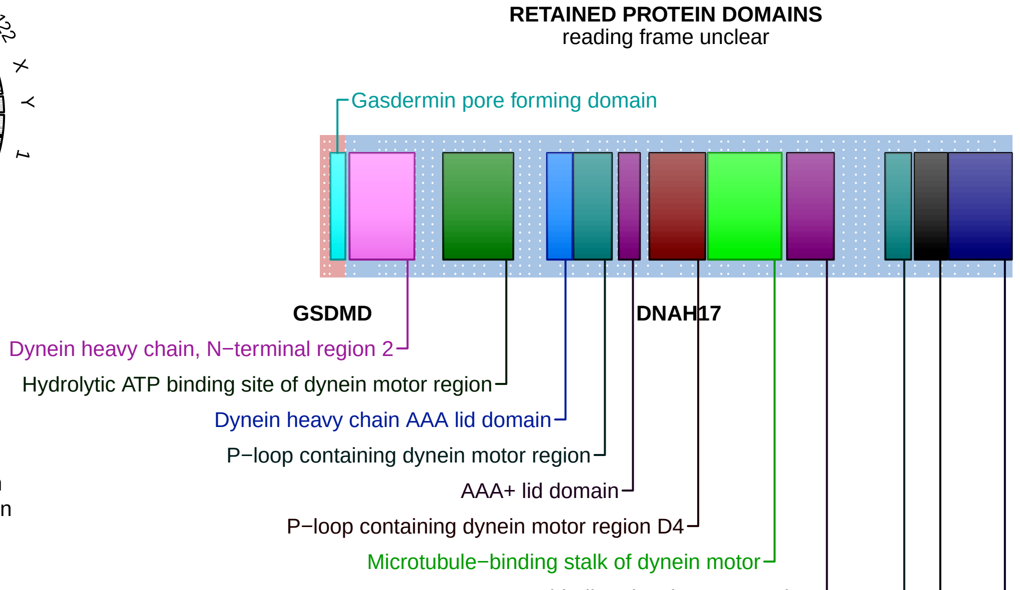


SUPPORTING READ COUNT

Split reads = 53
Discordant mates = 0

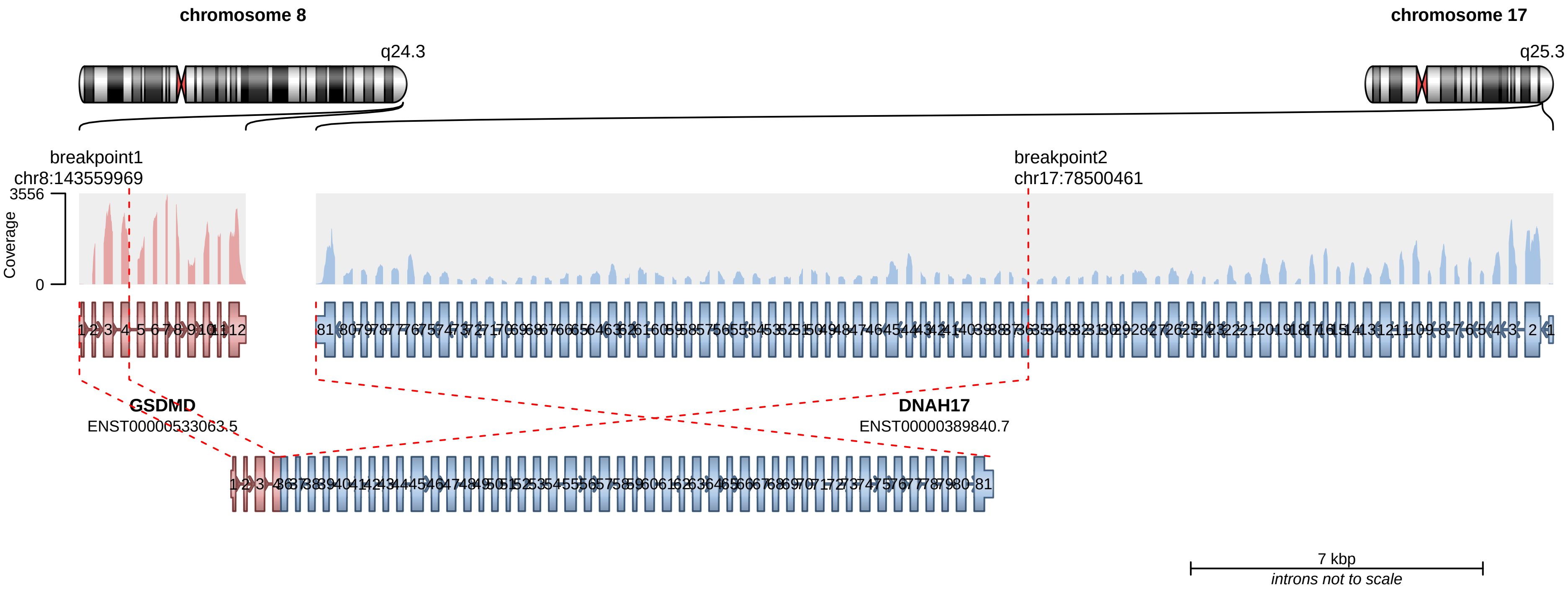


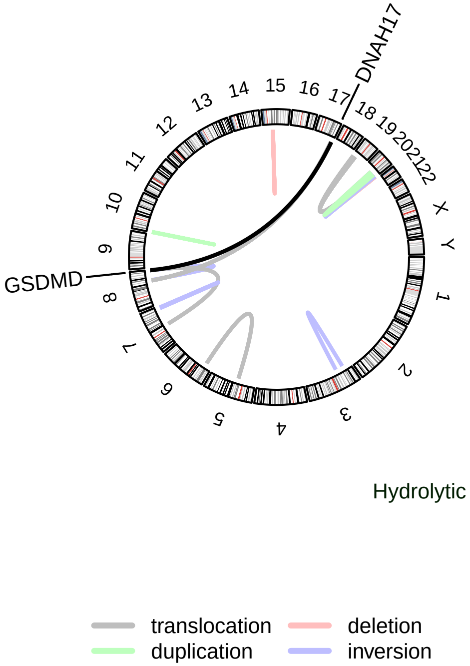




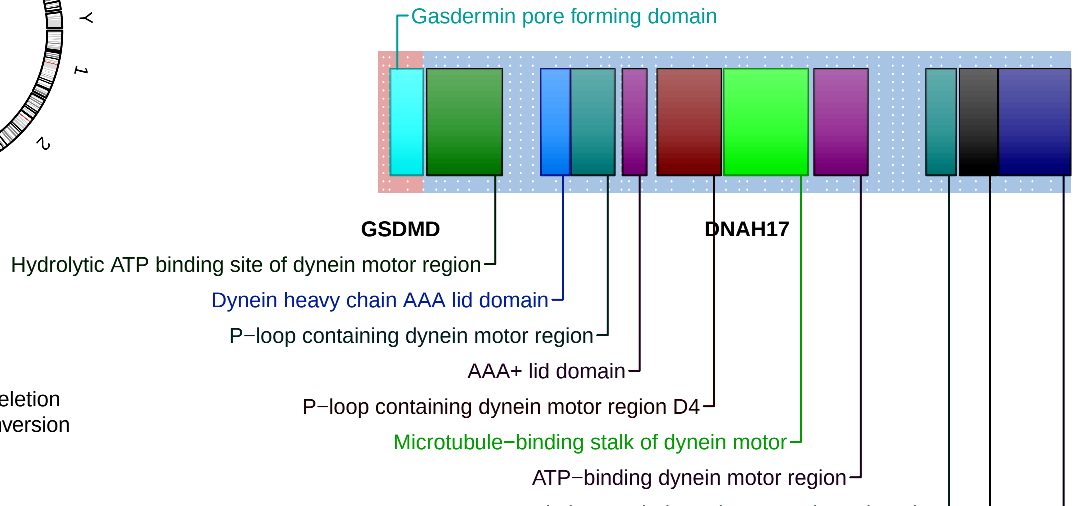
SUPPORTING READ COUNT

Split reads = 7
Discordant mates = 0



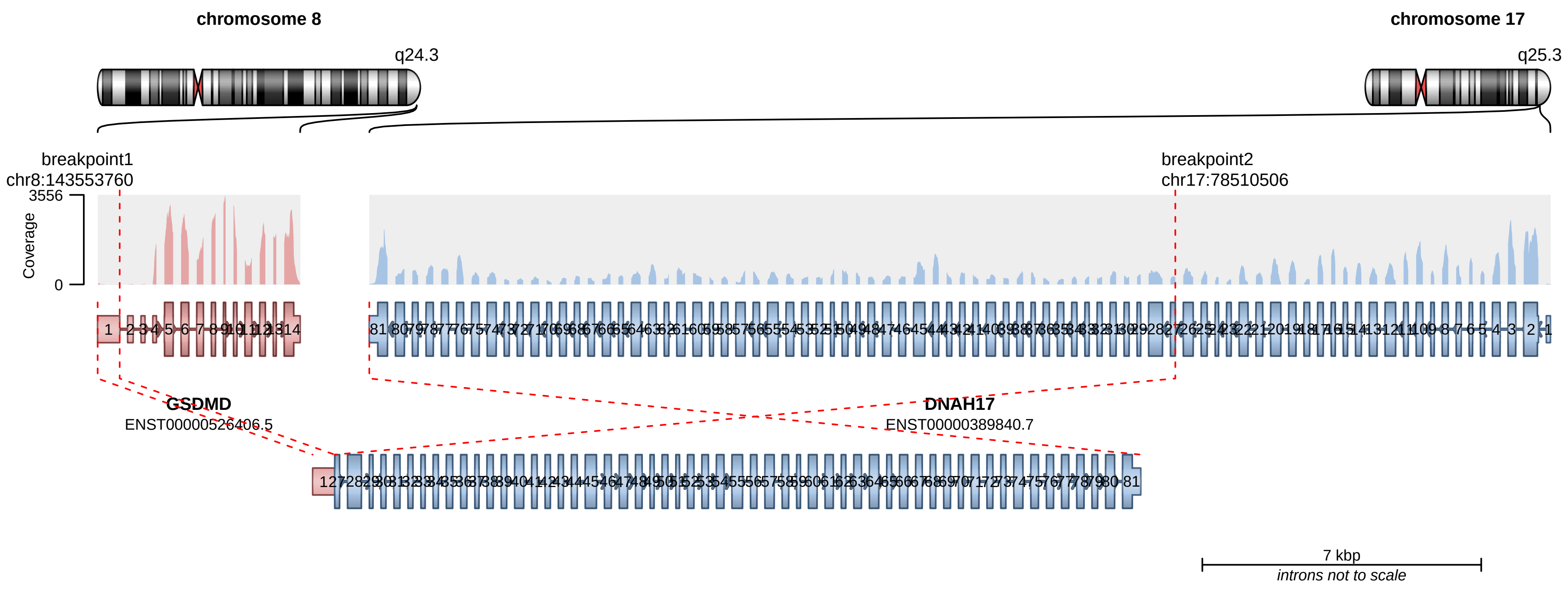


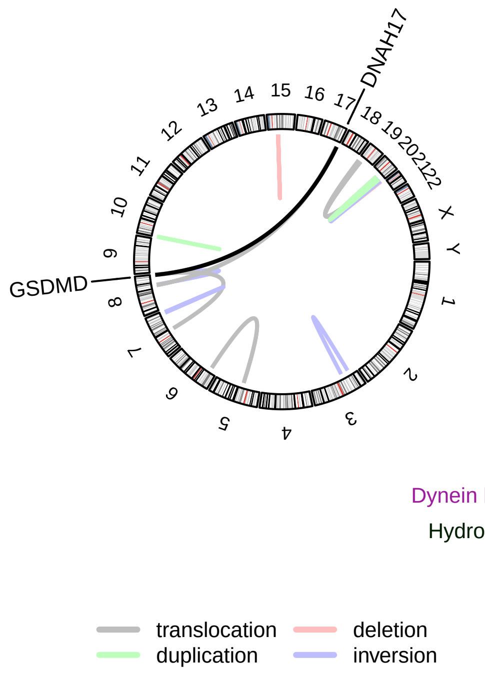
RETAINED PROTEIN DOMAINS
reading frame unclear

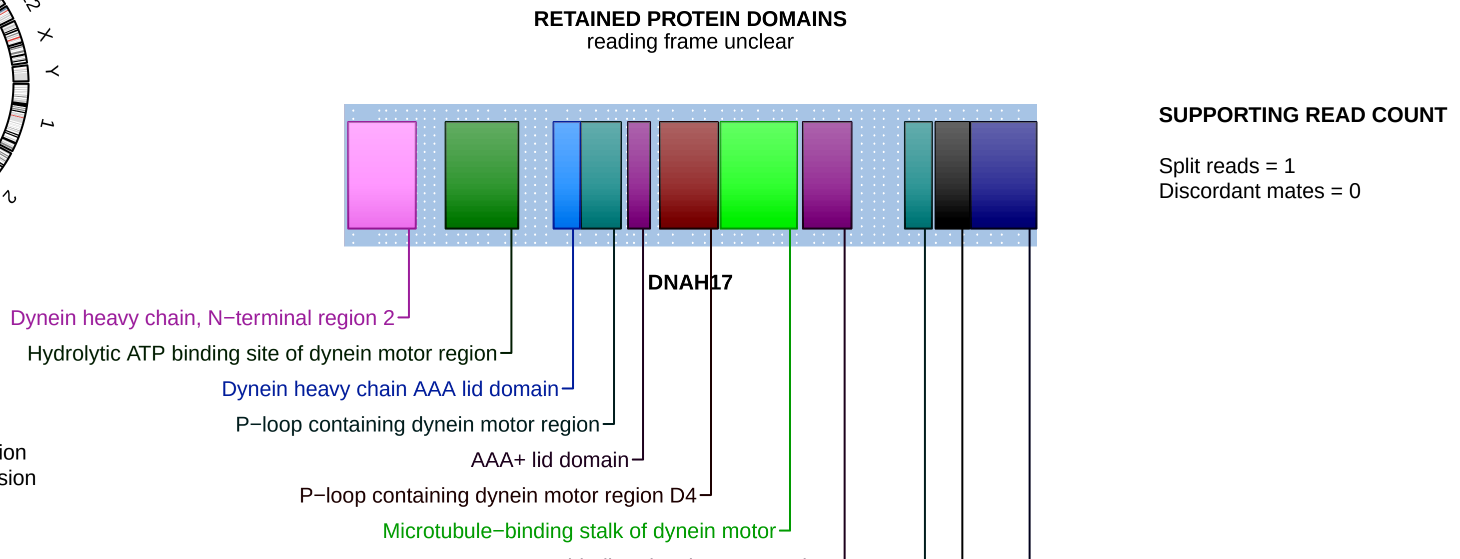


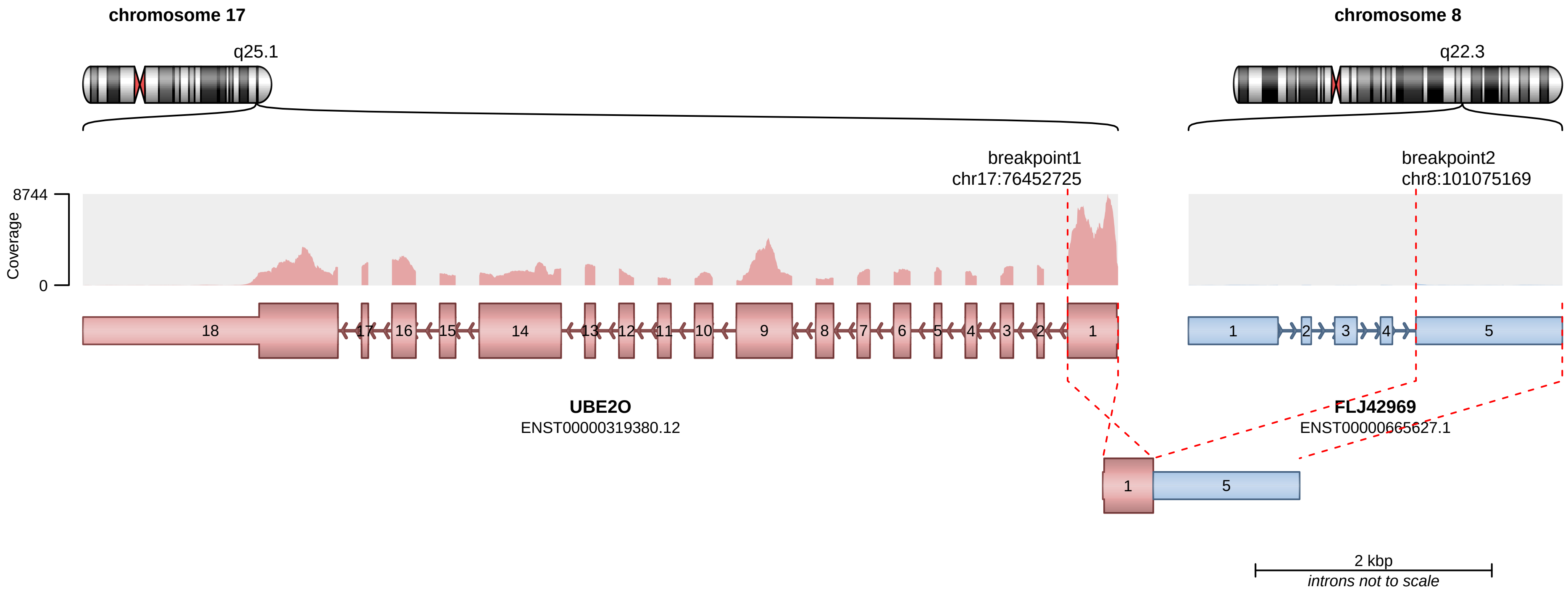
SUPPORTING READ COUNT

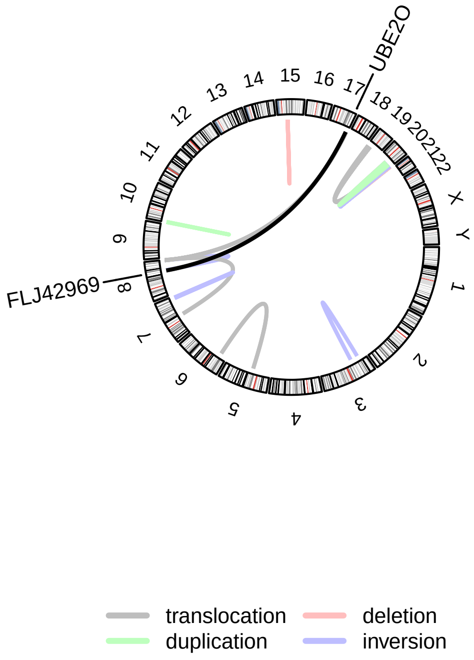
Split reads = 2
Discordant mates = 0


chromosome 8
q24.3
chromosome 17
q25.3
breakpoint1
chr8:143553760
3556
Coverage
0
breakpoint2
chr17:78510506
GSDMD
ENST00000526406.5
DNAH17
ENST00000389840.7
7 kbp
introns not to scale


DNAH17
GSDMD
translocation
duplication
deletion
inversion


RETAINED PROTEIN DOMAINS
reading frame unclear
DNAH17
Dynein heavy chain, N−terminal region 2
Hydrolytic ATP binding site of dynein motor region
Dynein heavy chain AAA lid domain
P−loop containing dynein motor region
AAA+ lid domain
P−loop containing dynein motor region D4
Microtubule−binding stalk of dynein motor
SUPPORTING READ COUNT
Split reads = 1
Discordant mates = 0

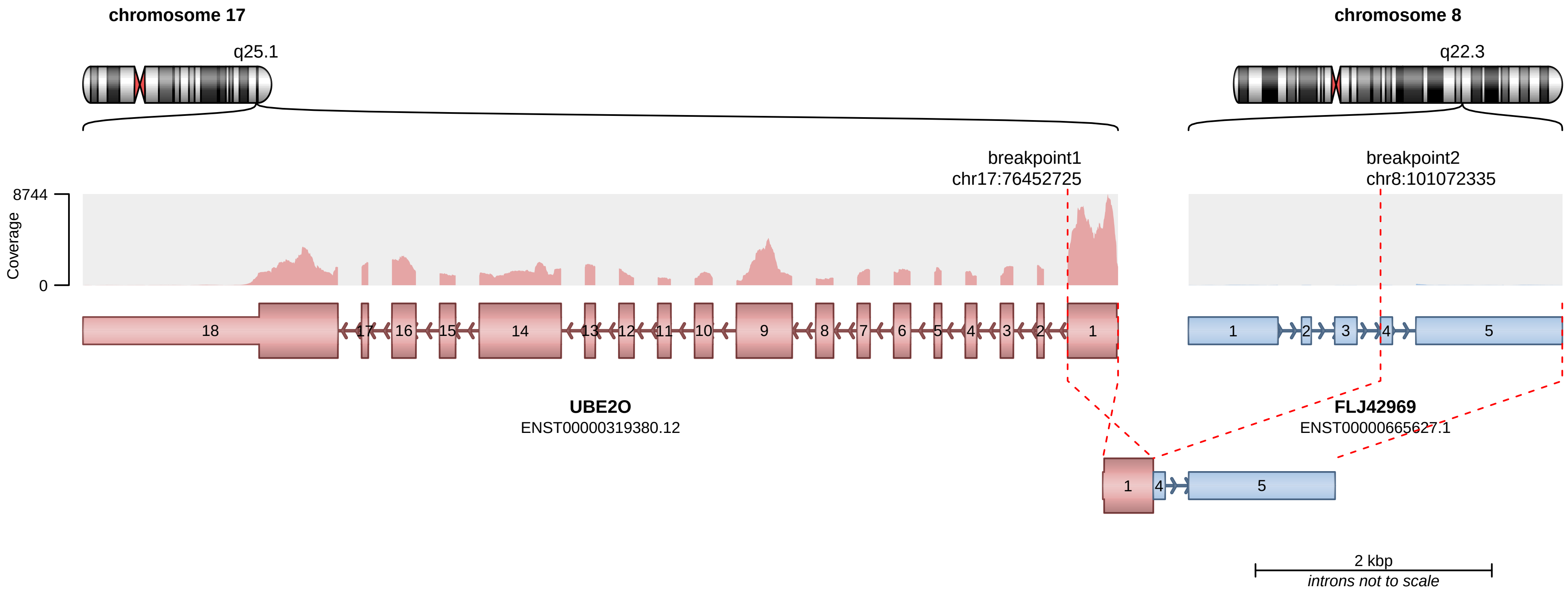


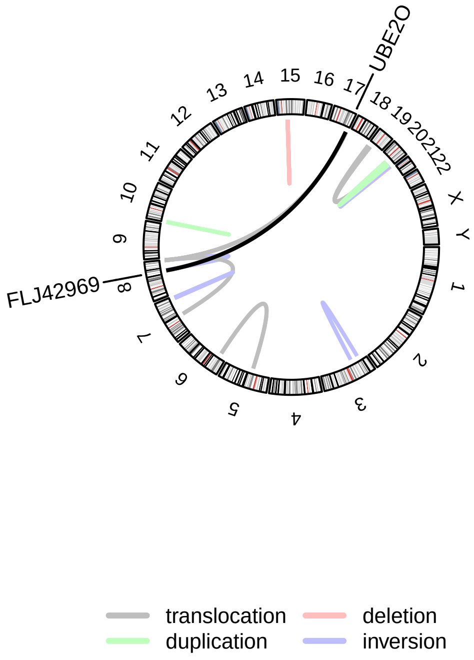


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 71
Discordant mates = 0

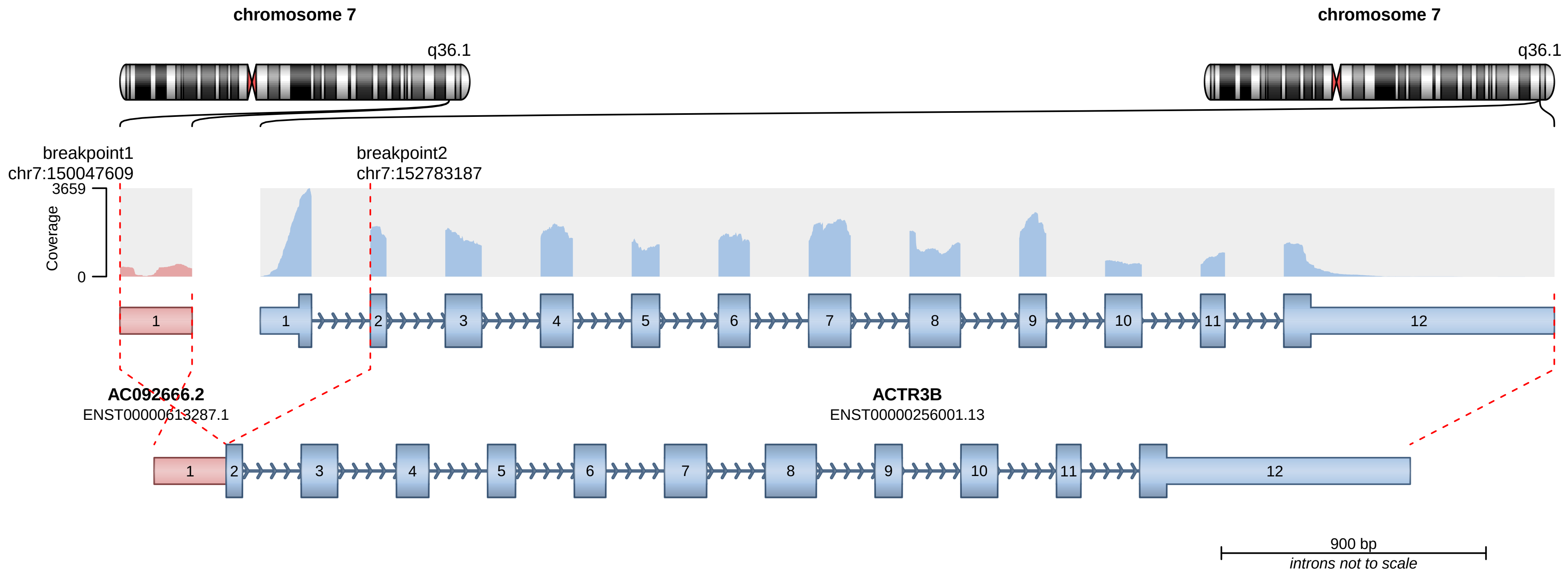


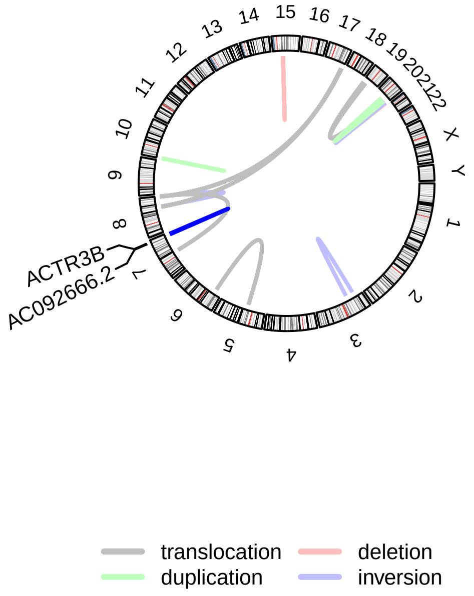


No protein domains retained in fusion.

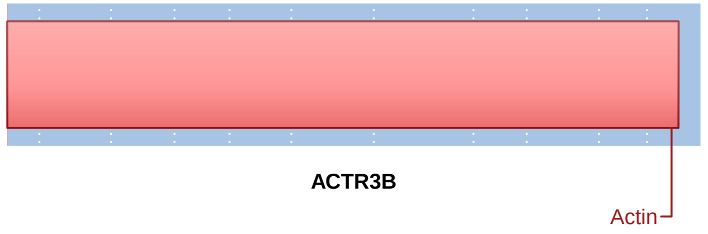
SUPPORTING READ COUNT

Split reads = 5
Discordant mates = 0



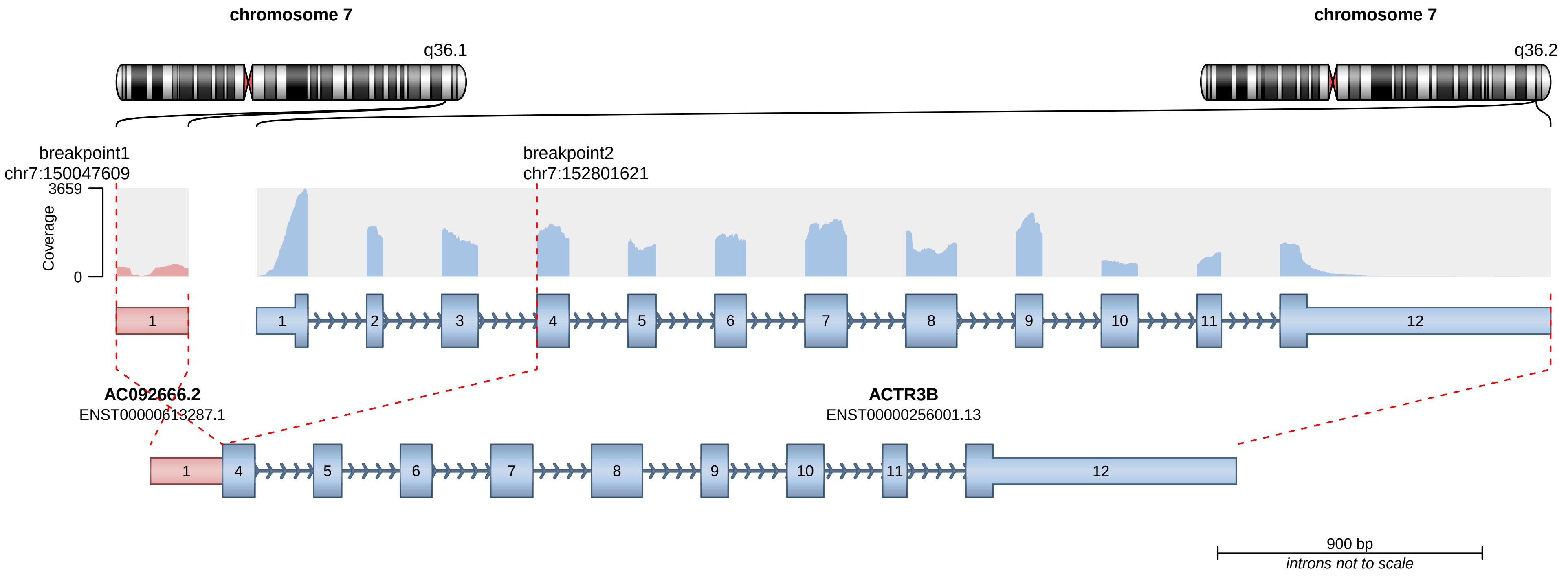


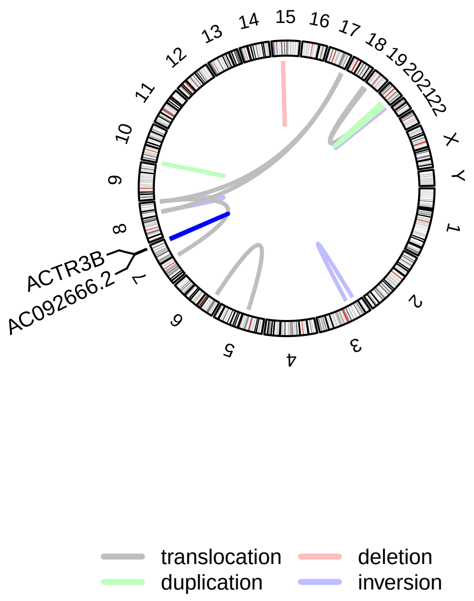
RETAINED PROTEIN DOMAINS
reading frame unclear



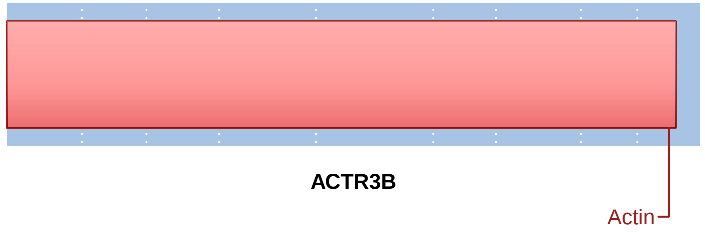
SUPPORTING READ COUNT

Split reads = 60
Discordant mates = 0



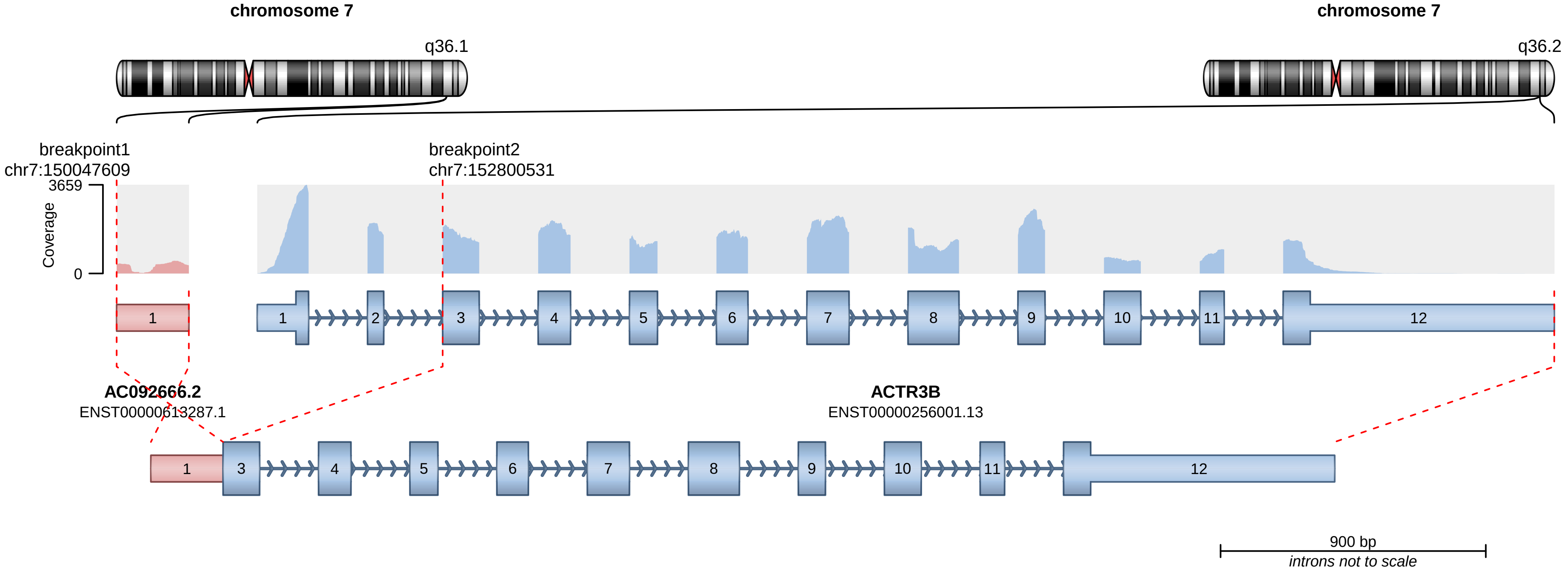


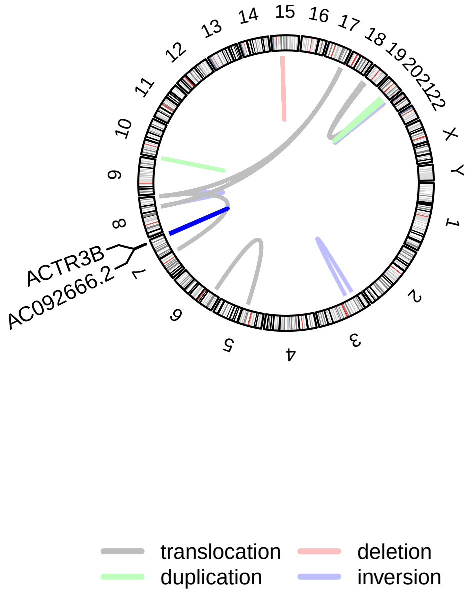
RETAINED PROTEIN DOMAINS
reading frame unclear

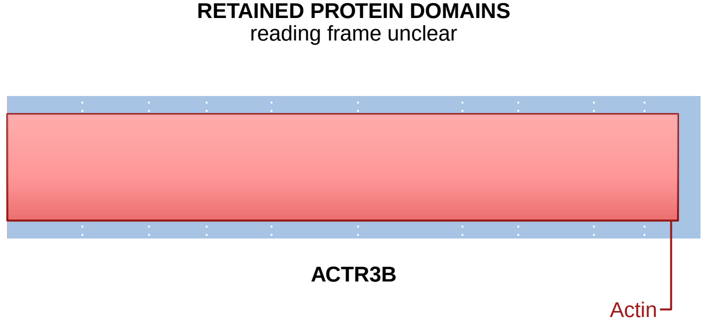


SUPPORTING READ COUNT

Split reads = 43
Discordant mates = 0

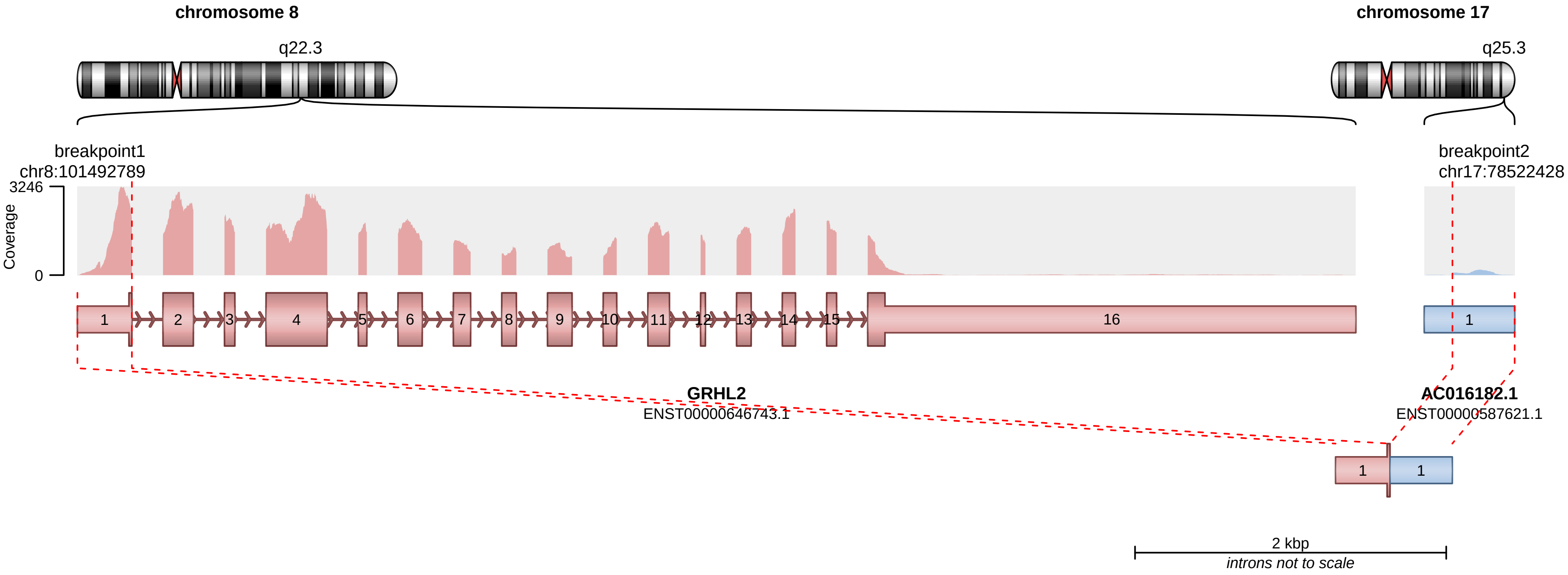


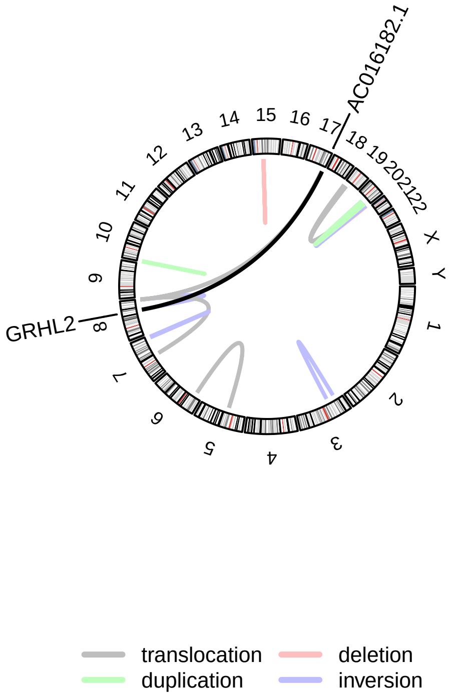




SUPPORTING READ COUNT

Split reads = 4
Discordant mates = 0

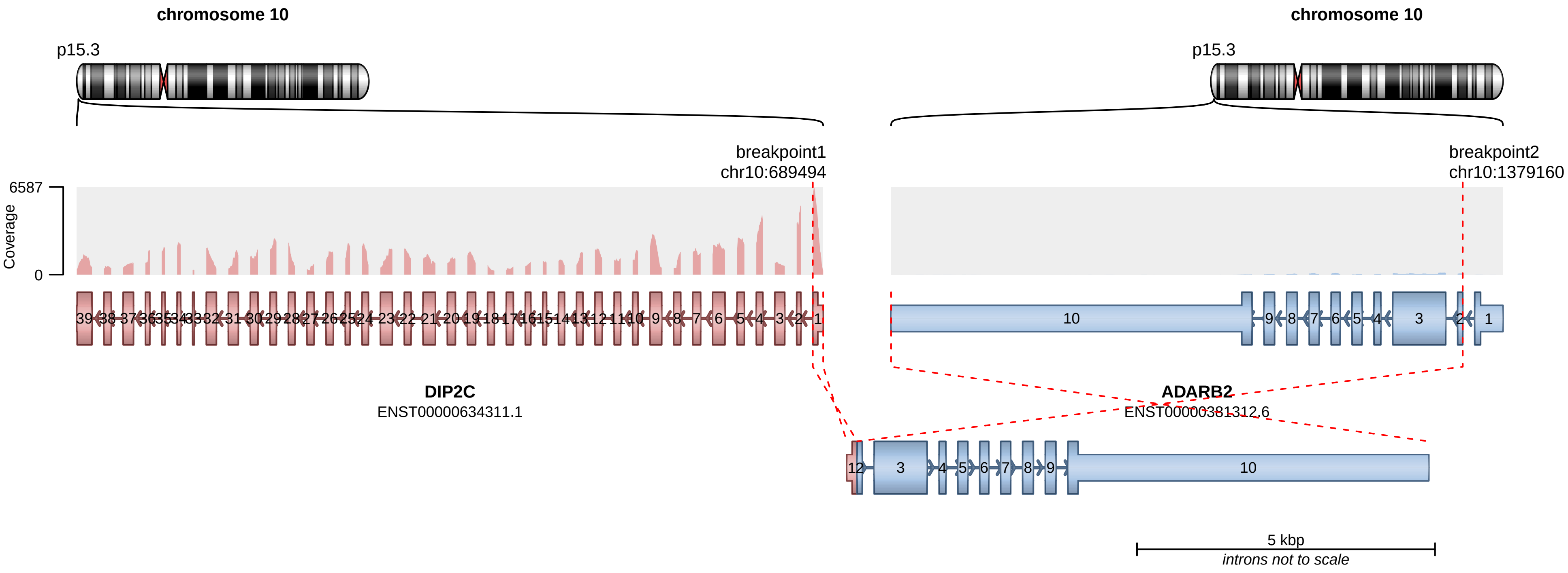


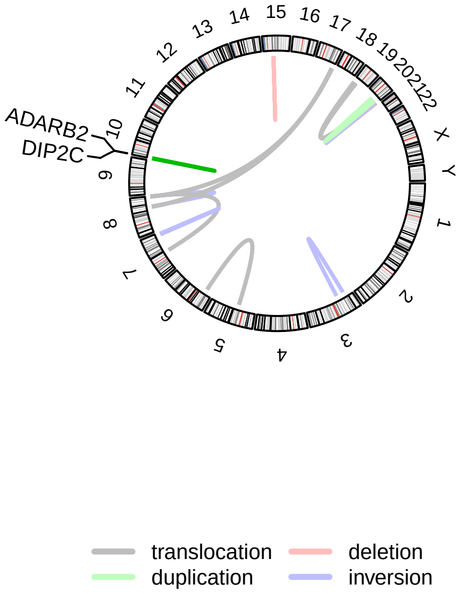


No protein domains retained in fusion.

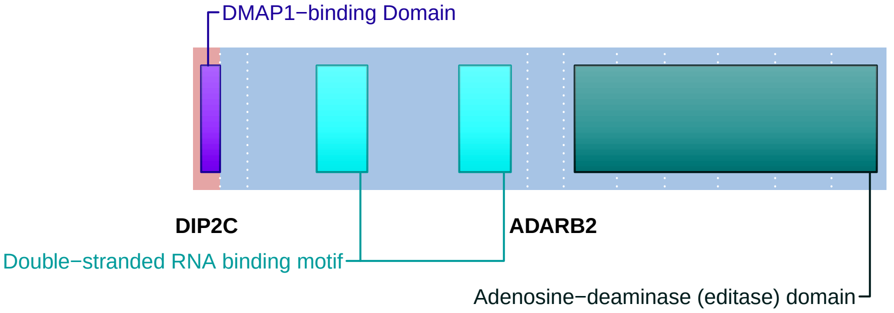
SUPPORTING READ COUNT

Split reads = 54
Discordant mates = 0



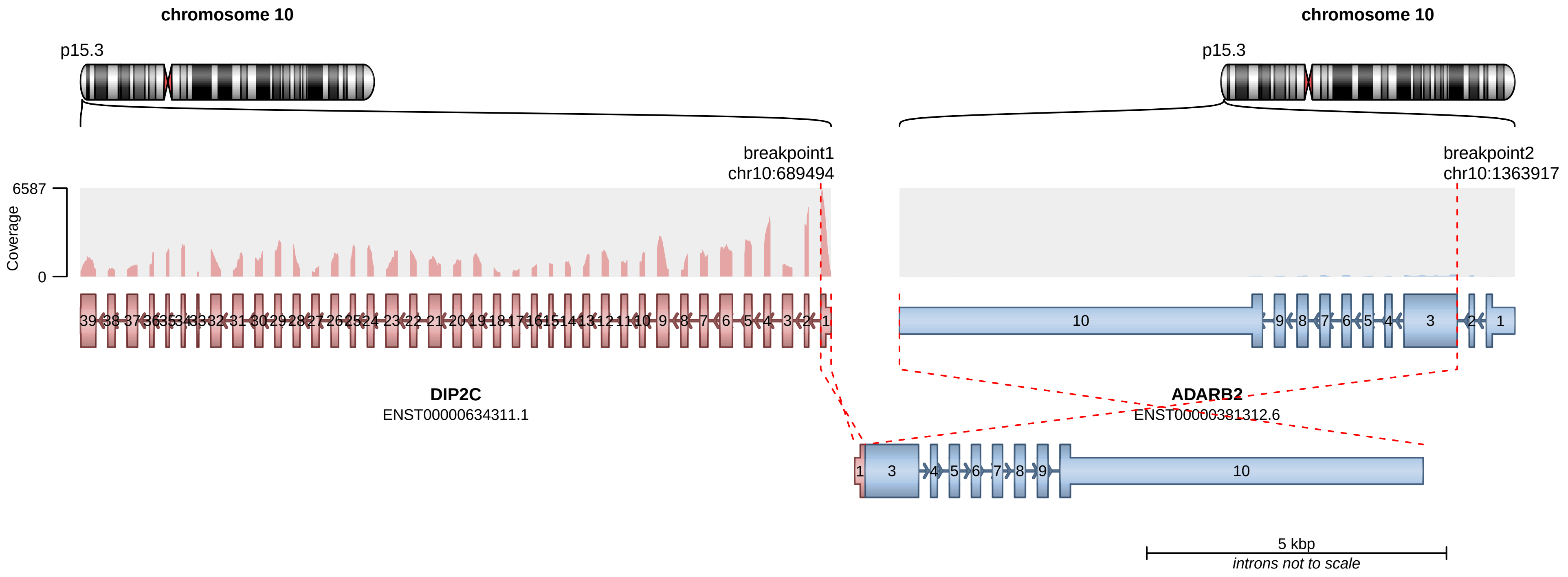


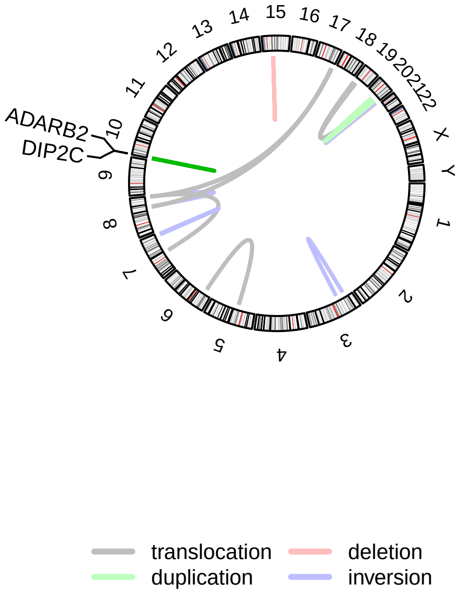
RETAINED PROTEIN DOMAINS
reading frame unclear

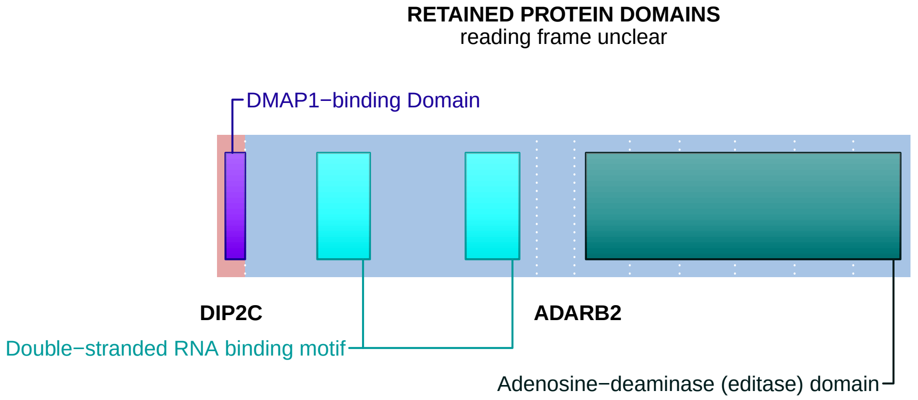


SUPPORTING READ COUNT

Split reads = 39
Discordant mates = 0

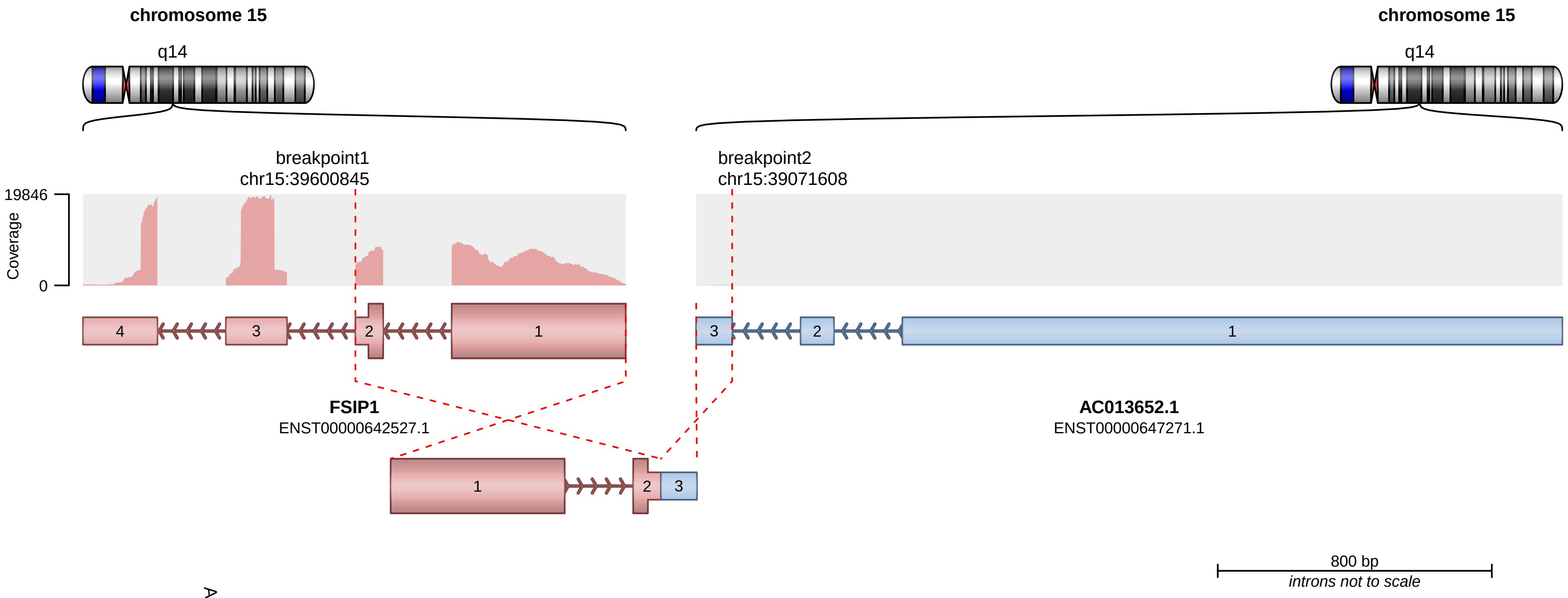


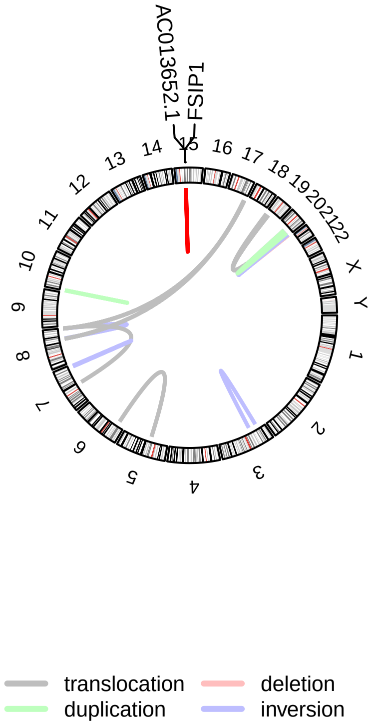




SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

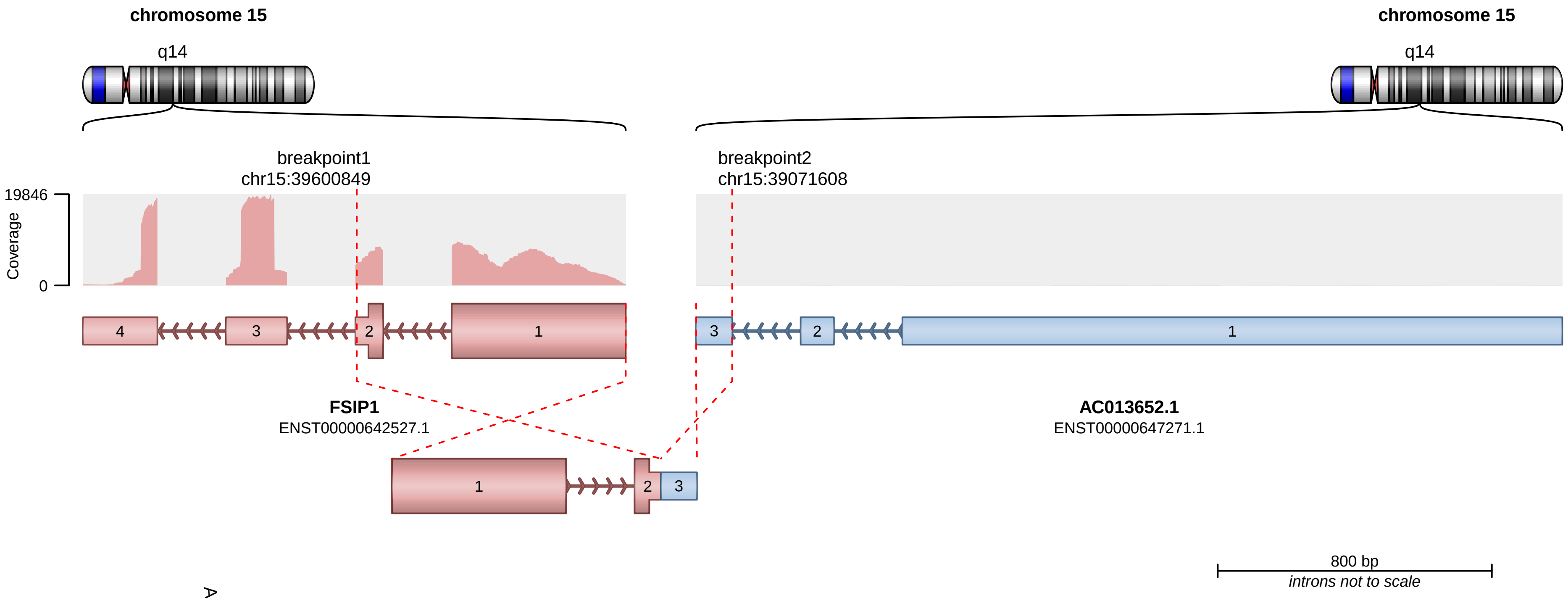


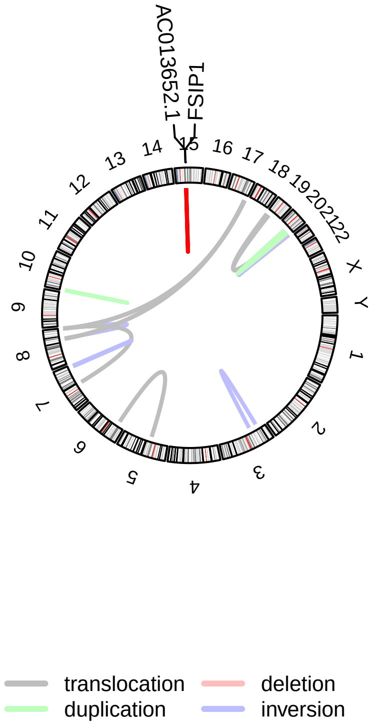


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 29
Discordant mates = 1

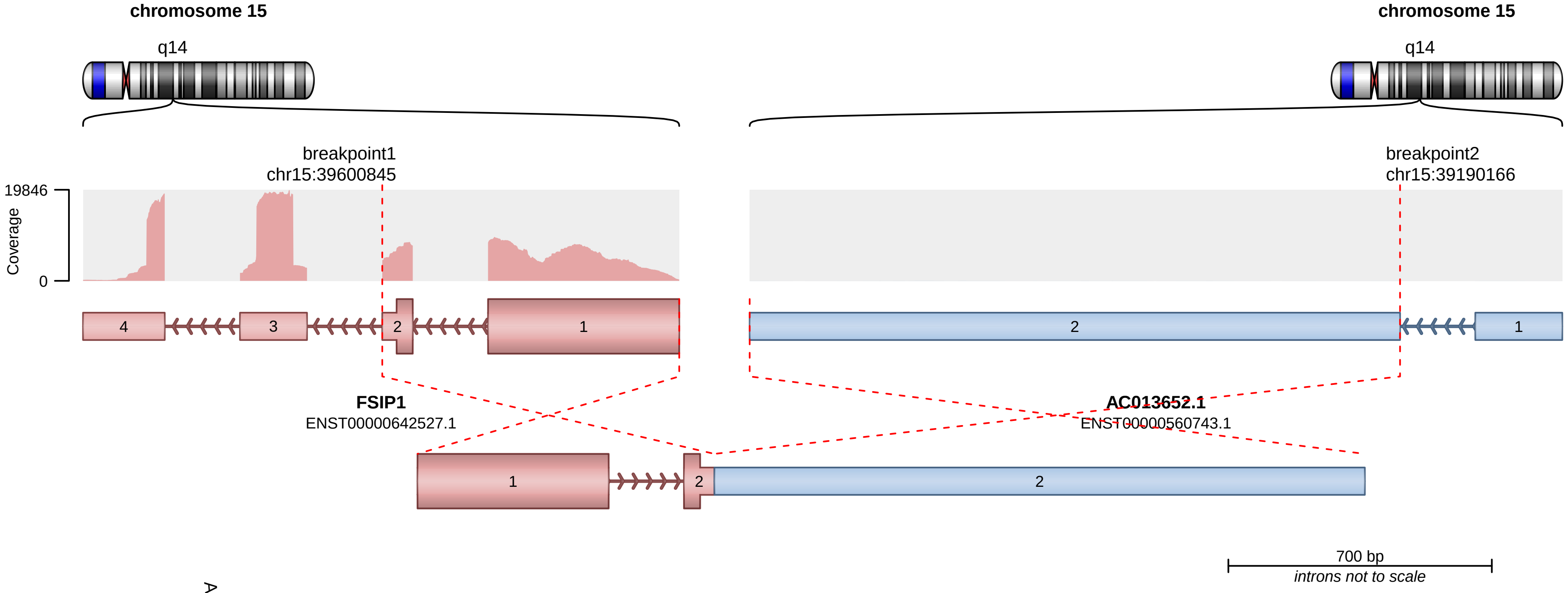


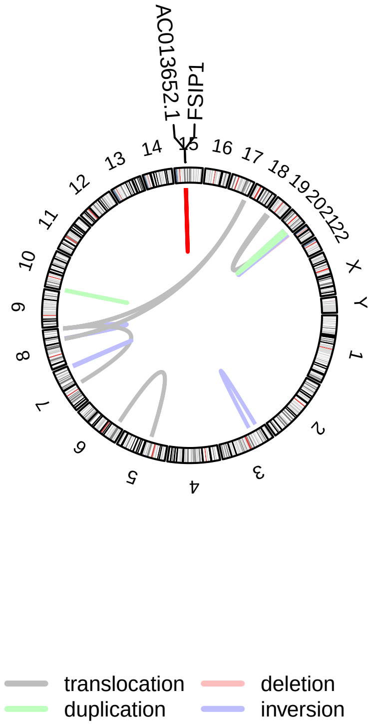


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 15
Discordant mates = 1

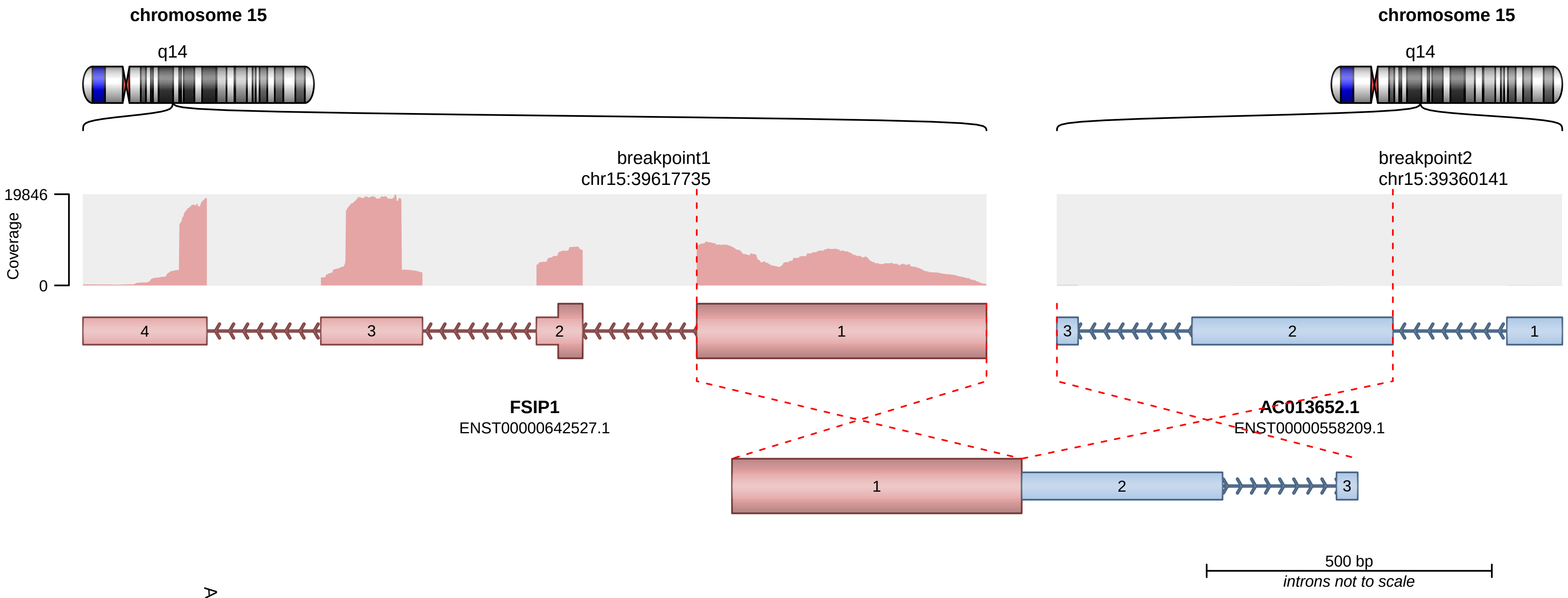


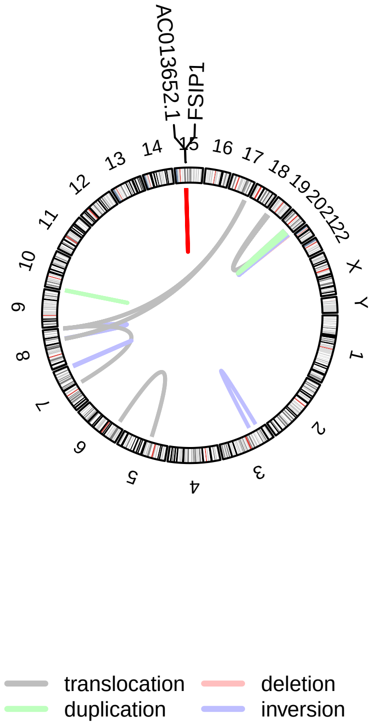


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 1

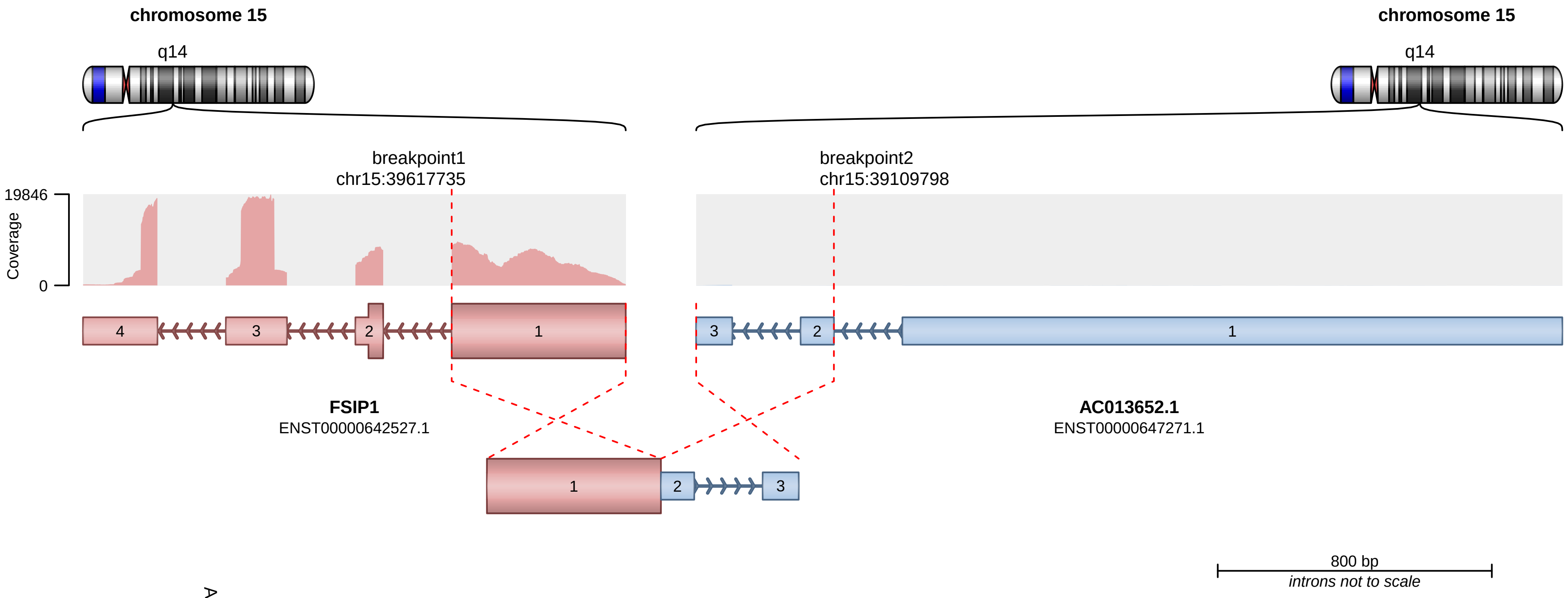


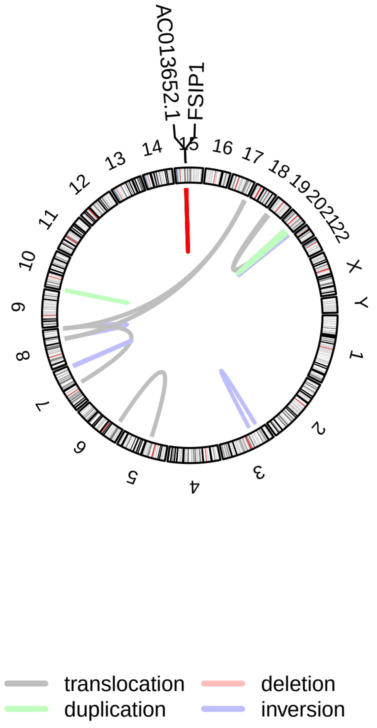


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

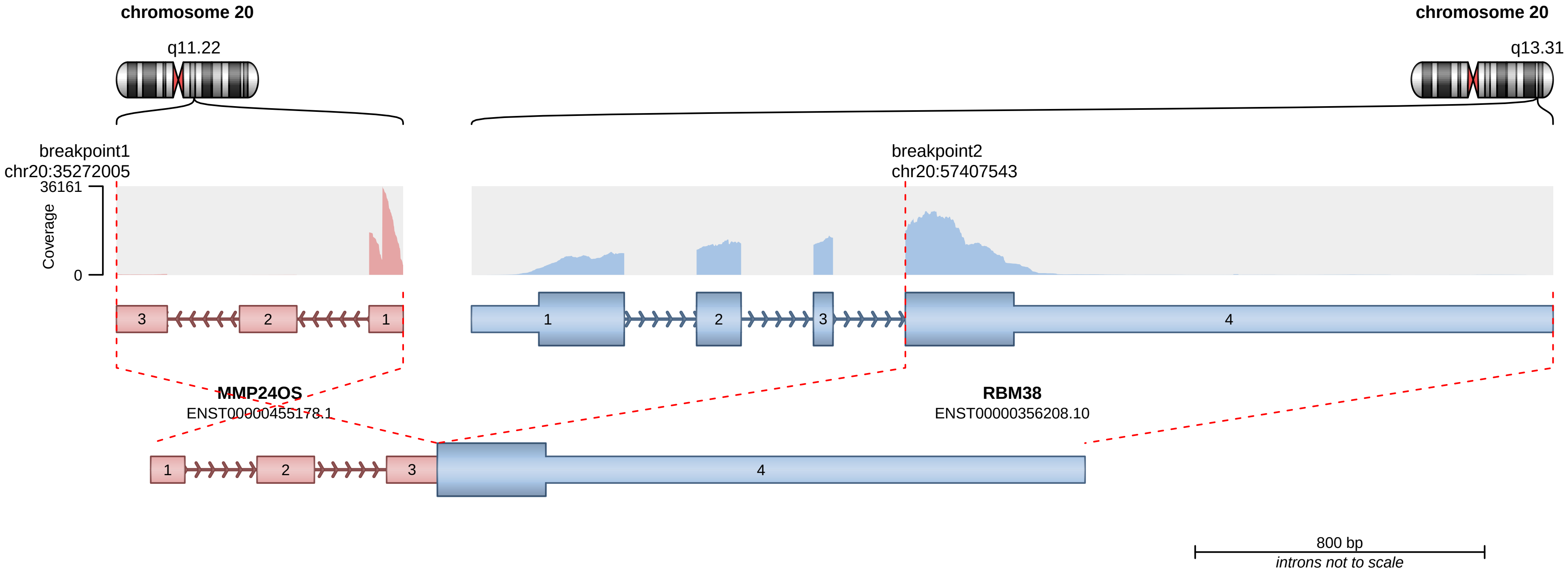


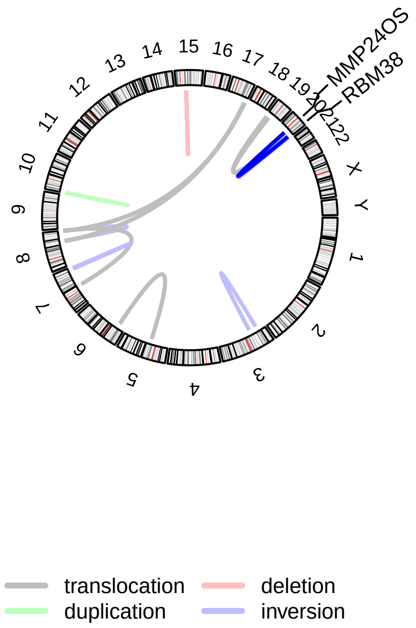


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

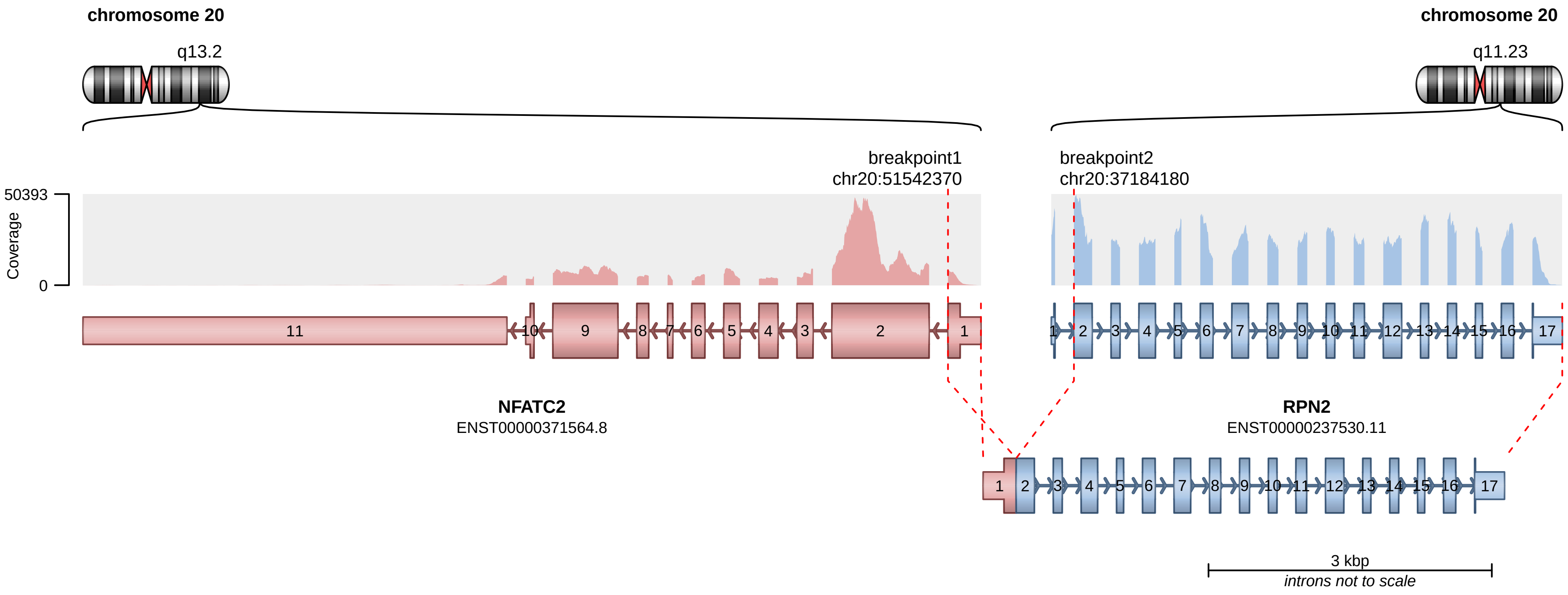


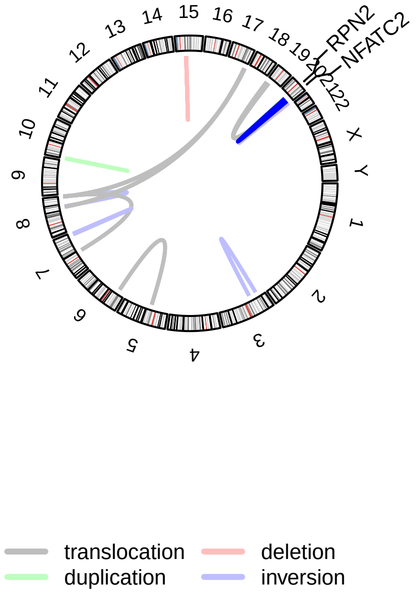


No protein domains retained in fusion.

SUPPORTING READ COUNT

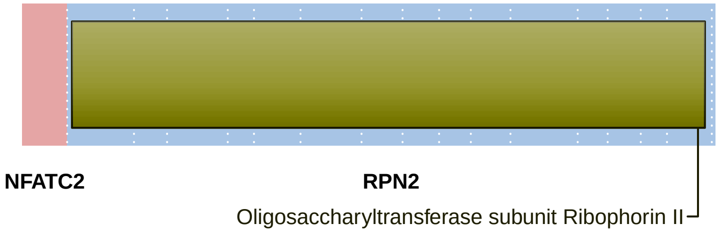
Split reads = 24
Discordant mates = 0





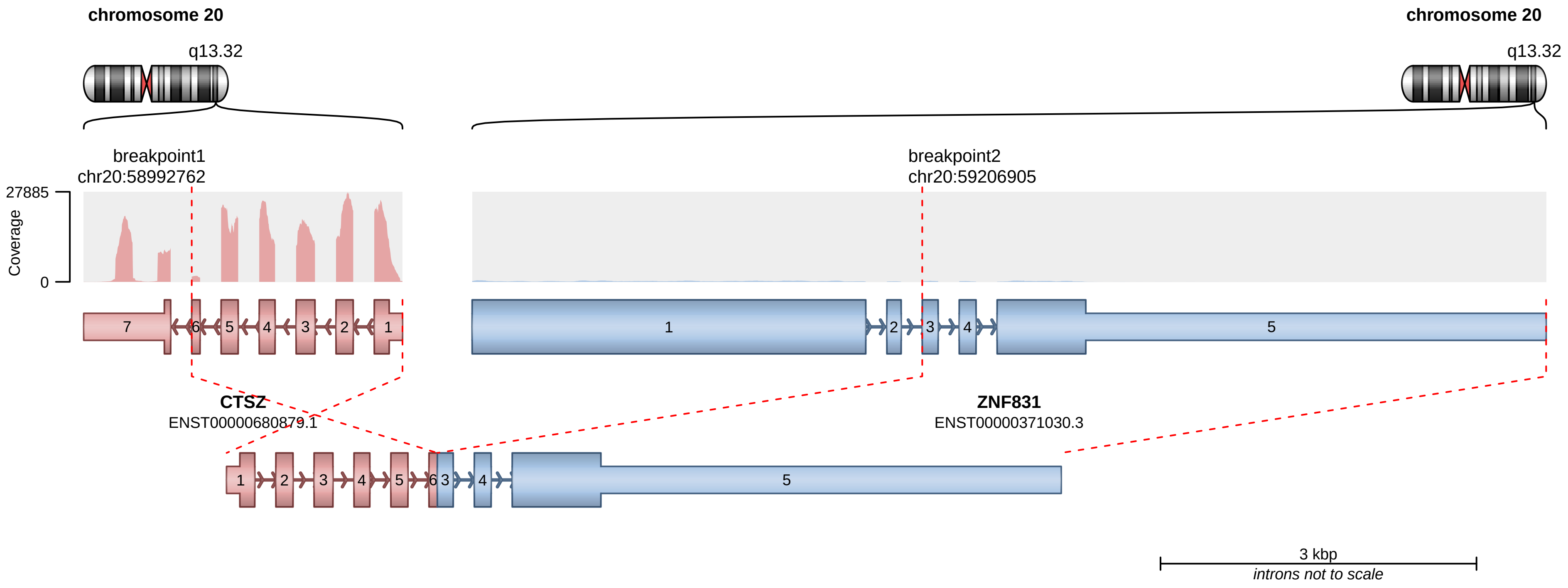
RETAINED PROTEIN DOMAINS

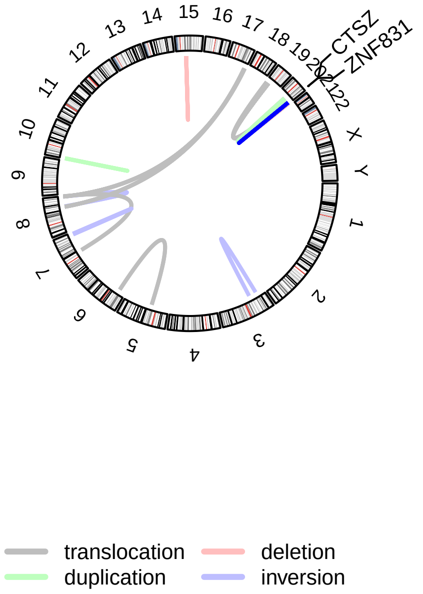
reading frame unclear

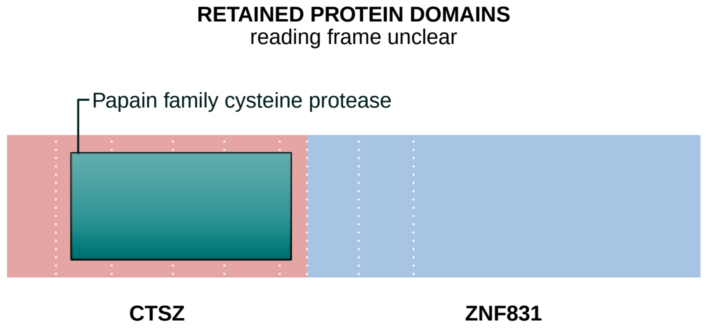


SUPPORTING READ COUNT

Split reads = 22
Discordant mates = 0

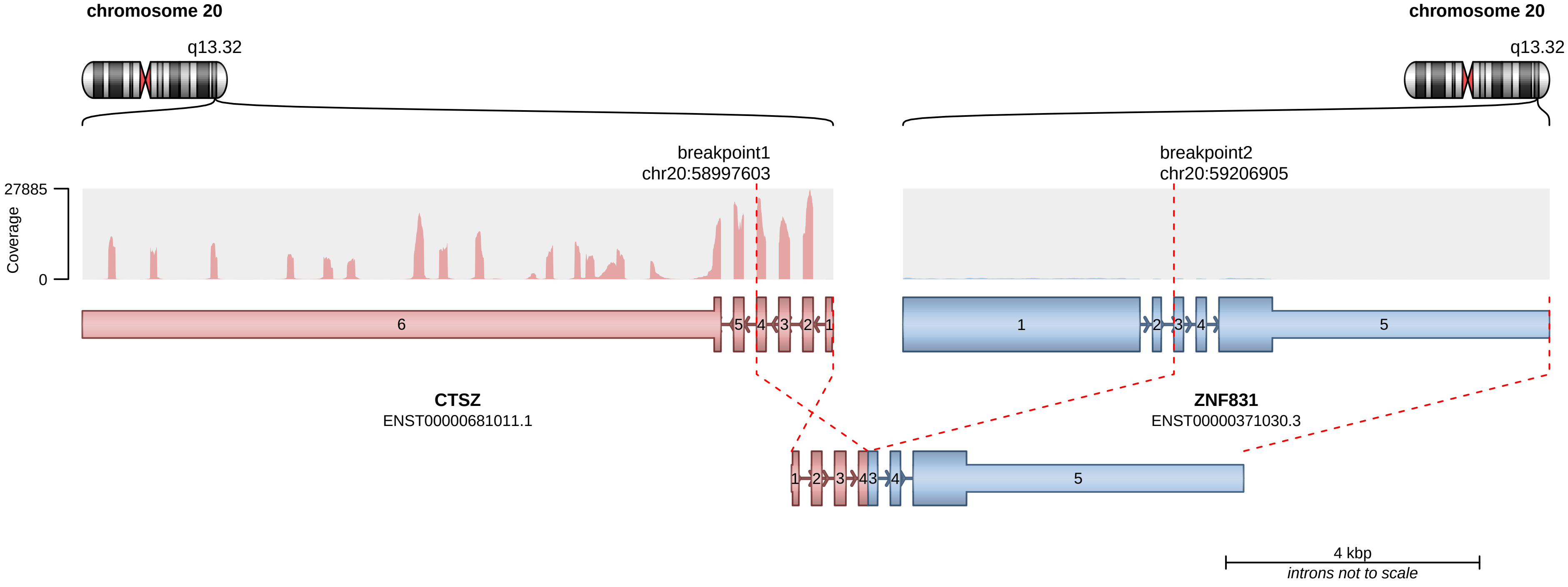


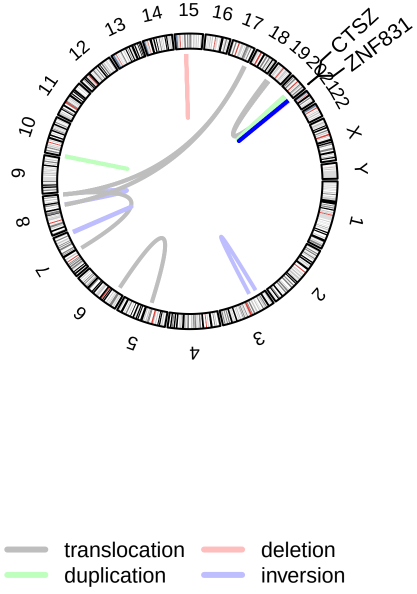




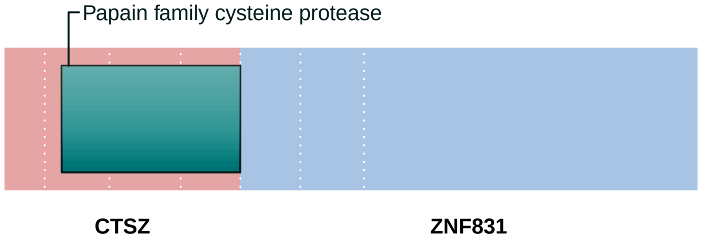
SUPPORTING READ COUNT

Split reads = 18
Discordant mates = 0



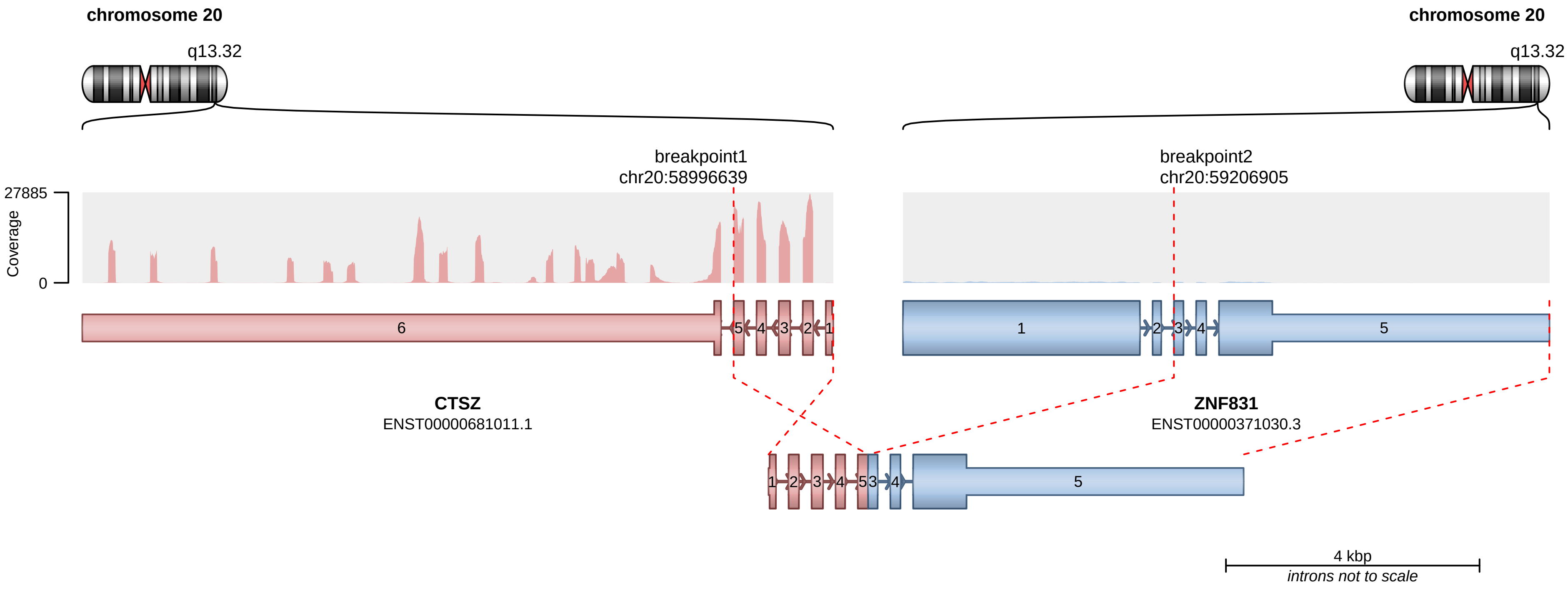


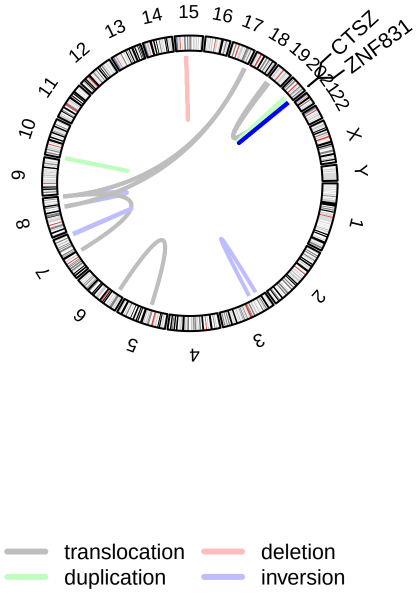
RETAINED PROTEIN DOMAINS
reading frame unclear



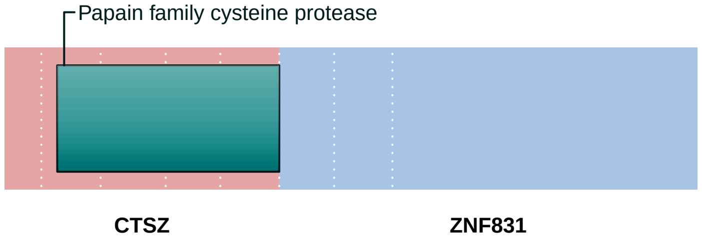
SUPPORTING READ COUNT

Split reads = 10
Discordant mates = 0



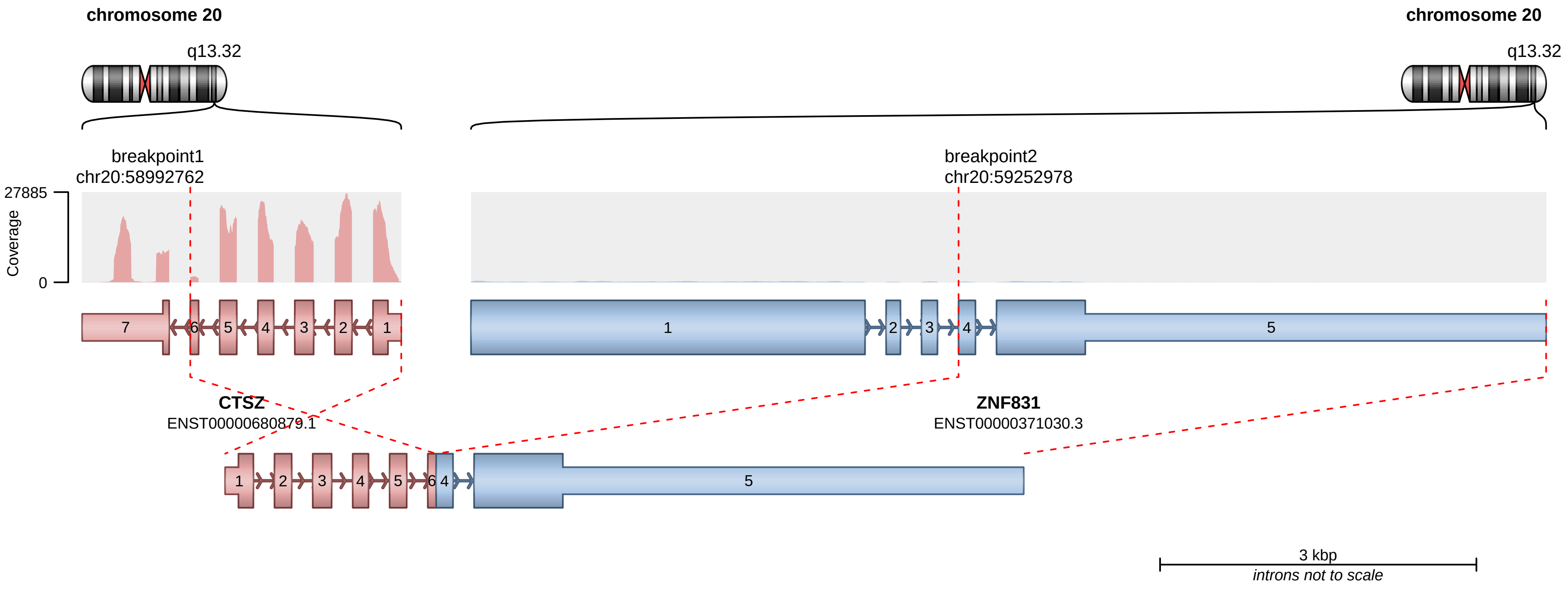


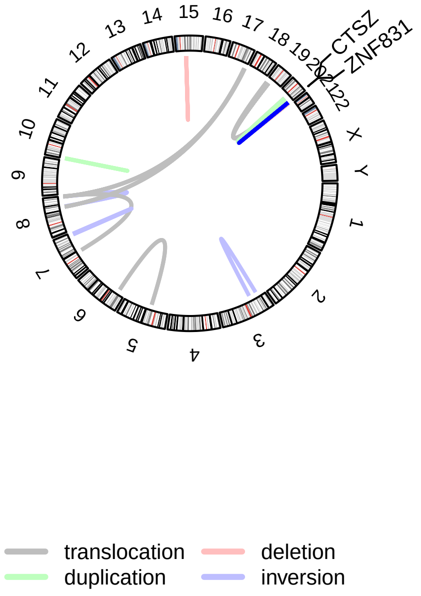
RETAINED PROTEIN DOMAINS
reading frame unclear



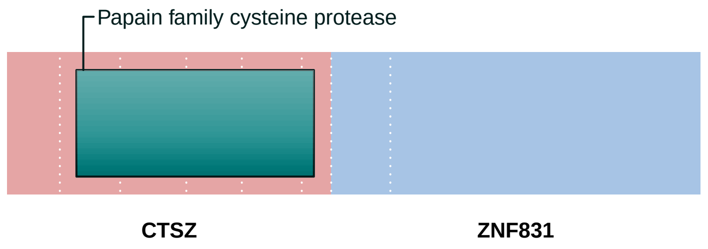
SUPPORTING READ COUNT

Split reads = 3
Discordant mates = 0



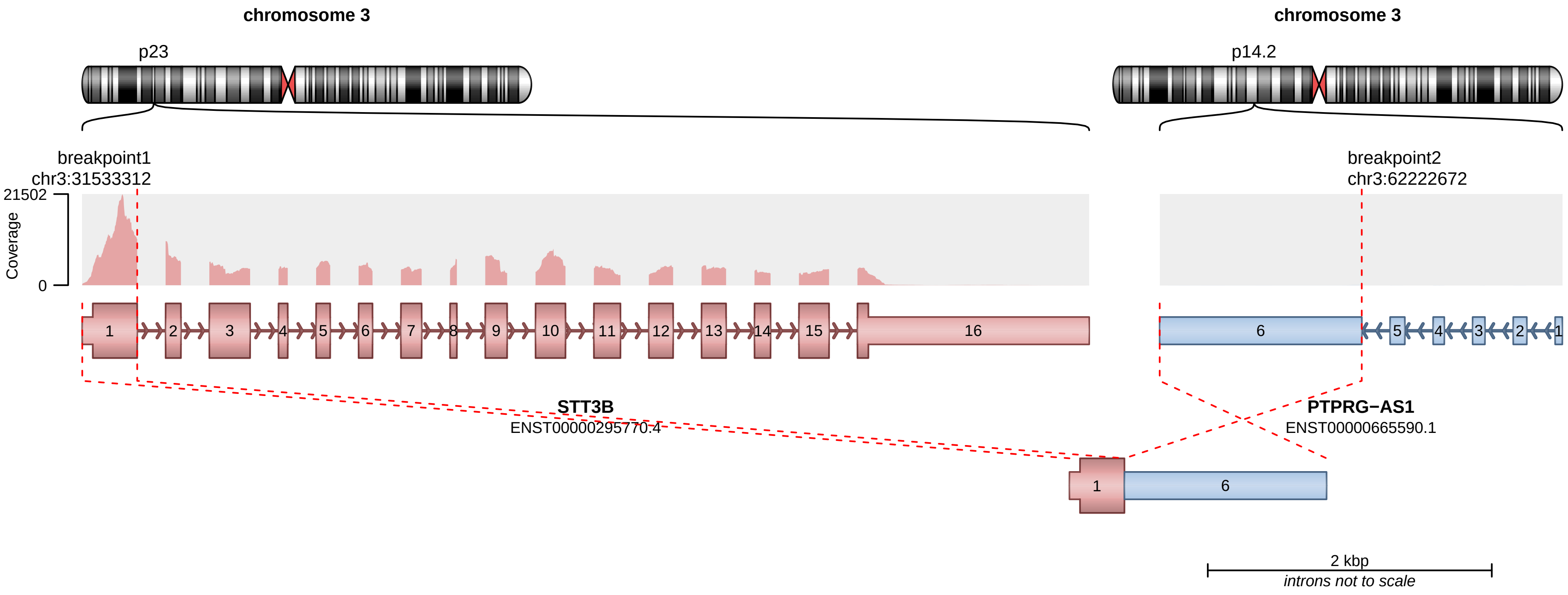


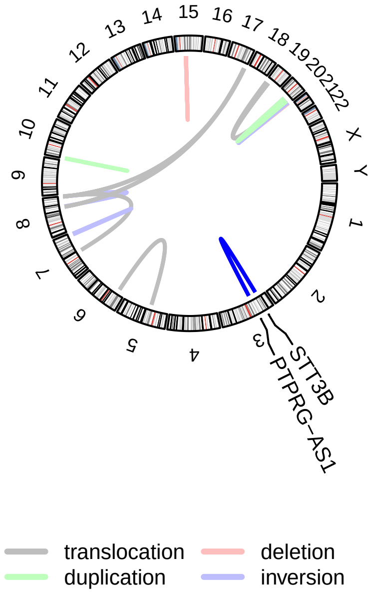
RETAINED PROTEIN DOMAINS
reading frame unclear

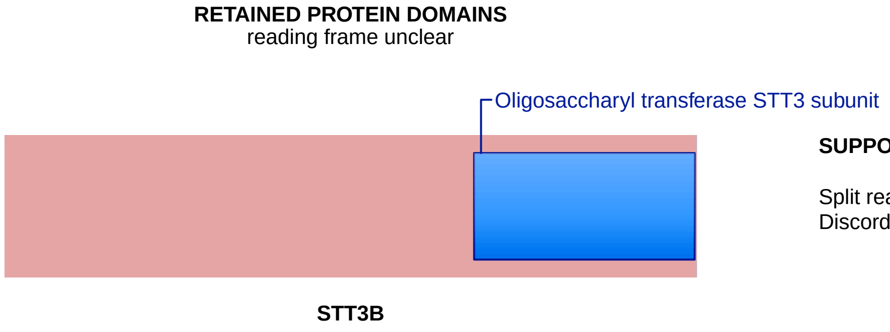


SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0

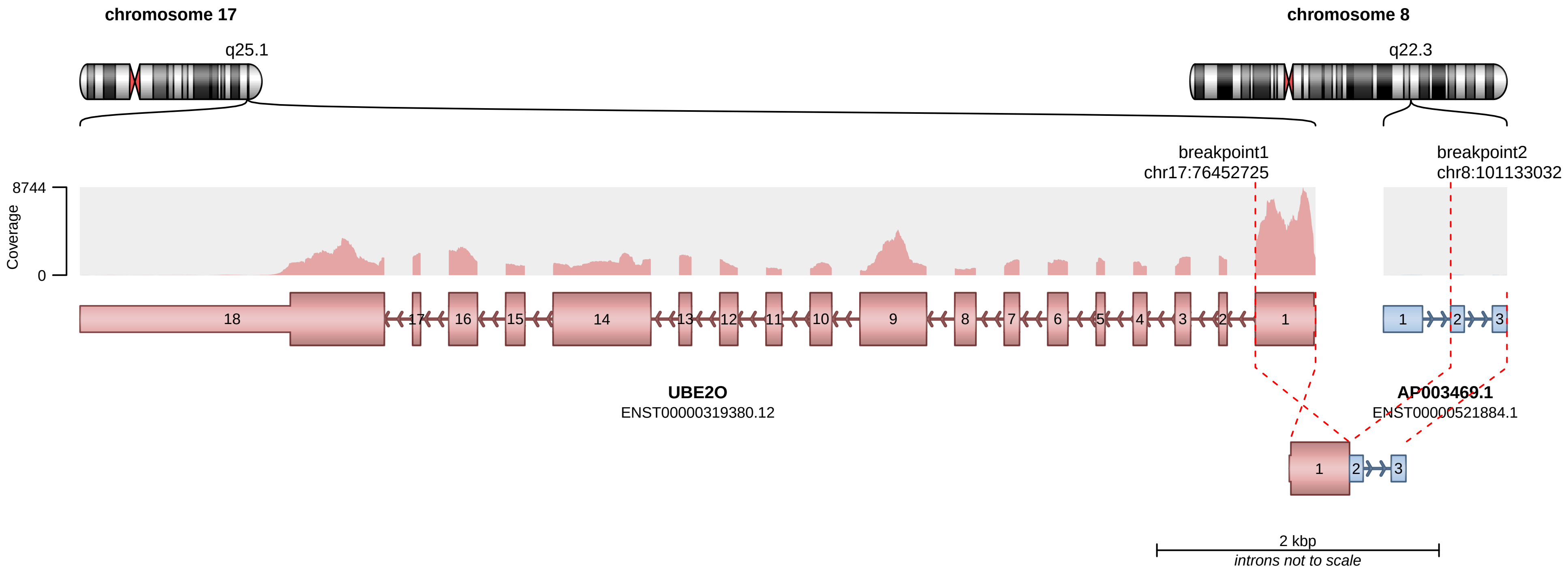


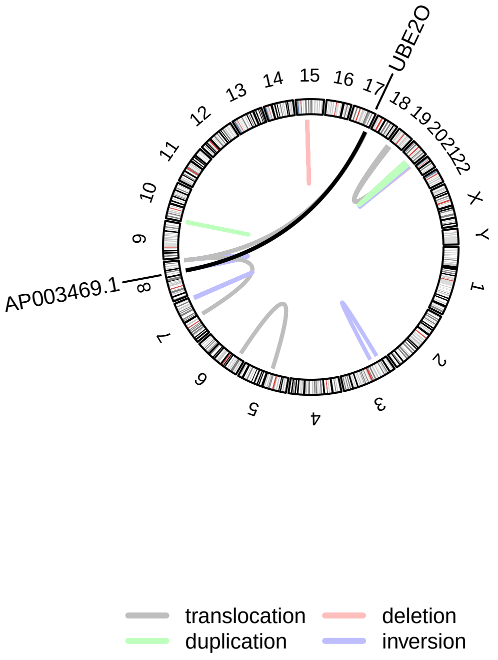




SUPPORTING READ COUNT

Split reads = 15
Discordant mates = 0

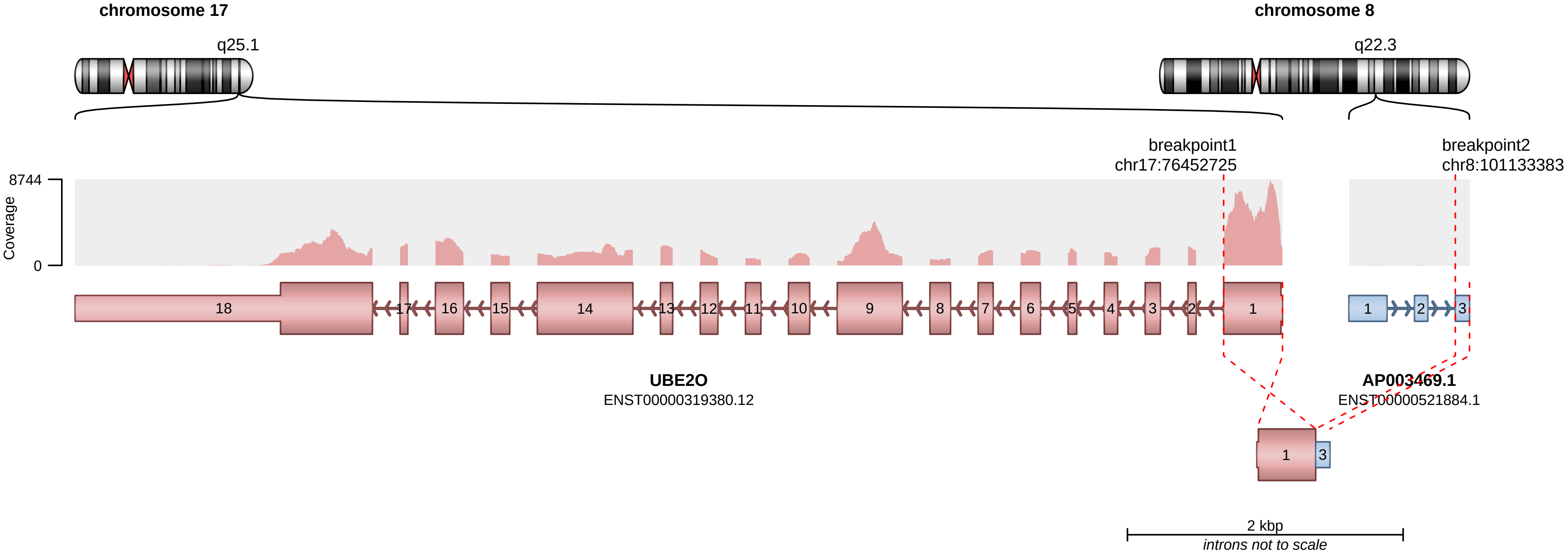


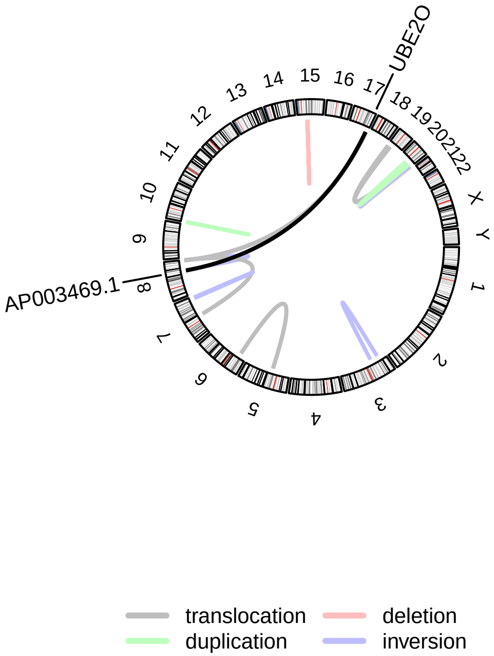


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 14
Discordant mates = 0

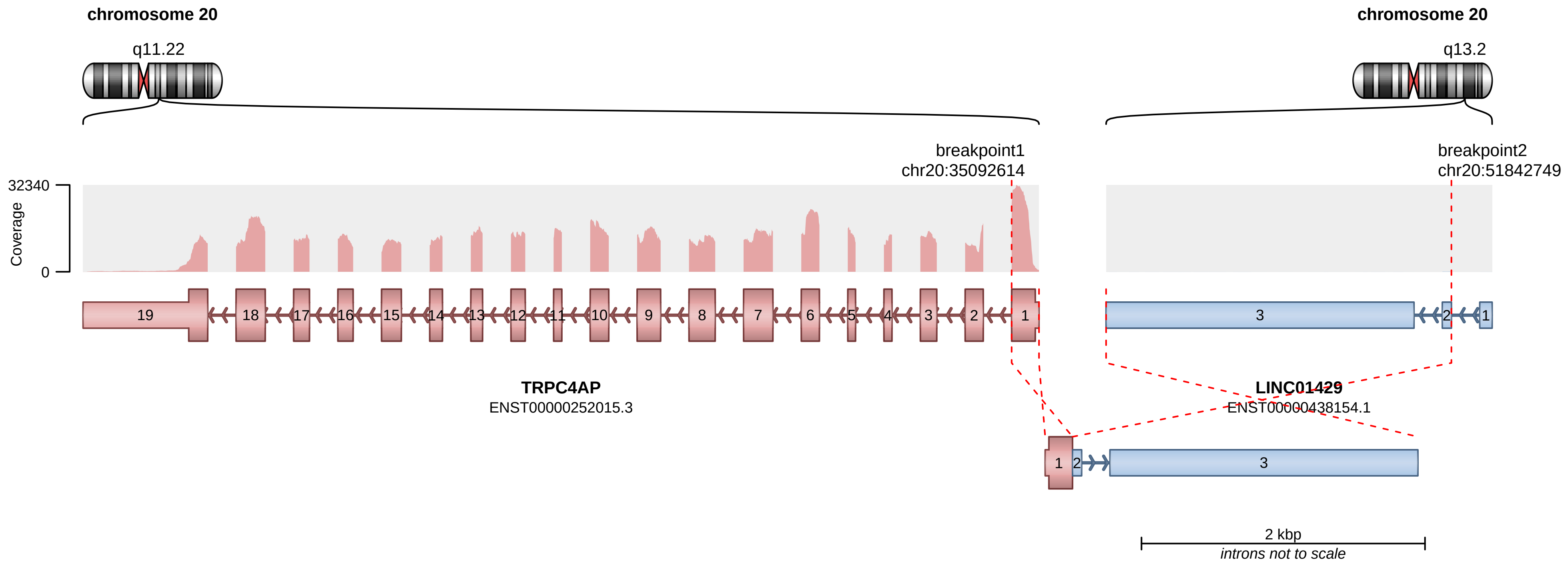


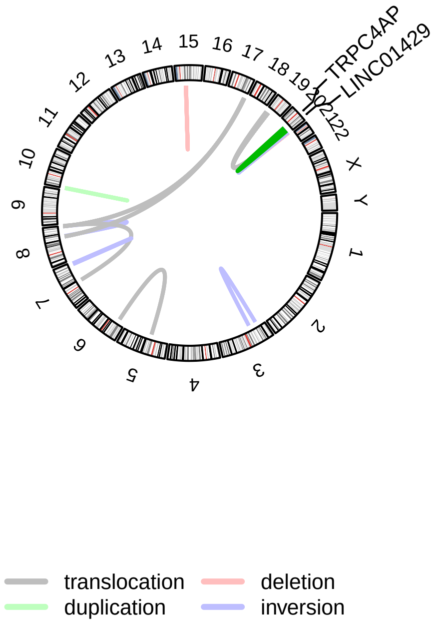


No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 0





No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 1
Discordant mates = 0