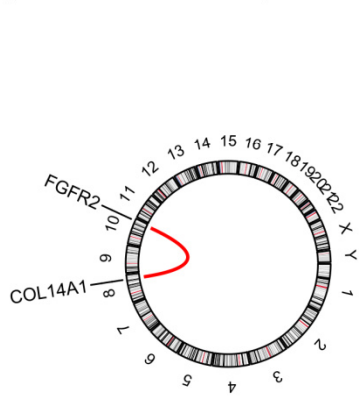
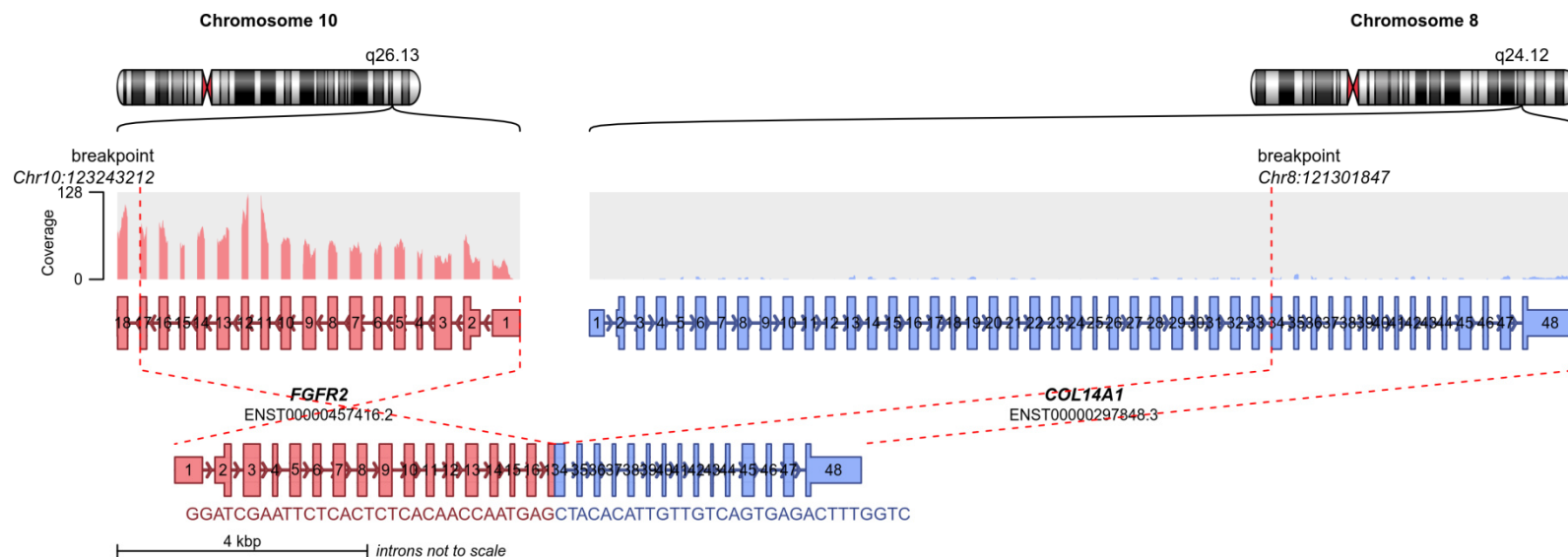
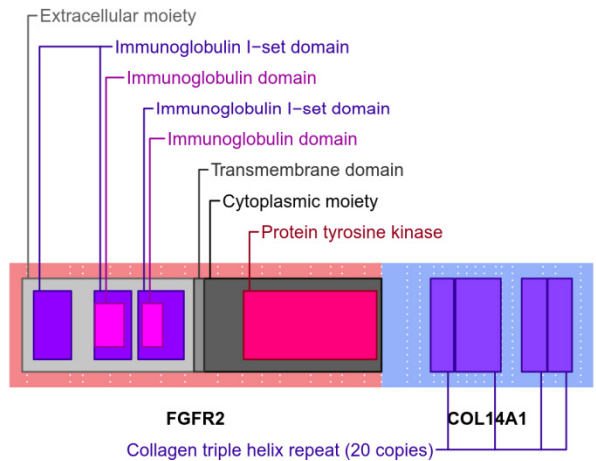


CFPAC-1 (9fc5da43-4f04-4bdc-a5bb-59a1ec219926)



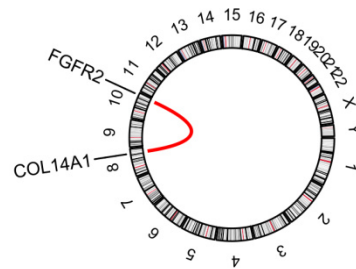
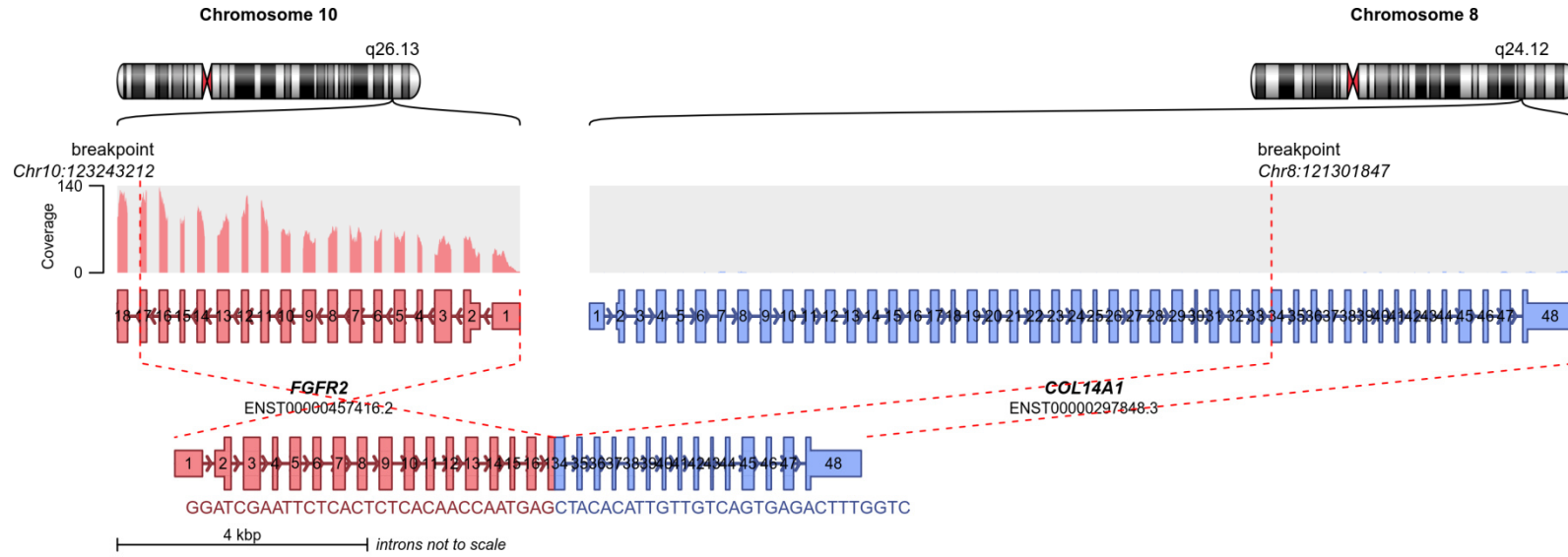
RETAINED PROTEIN DOMAINS



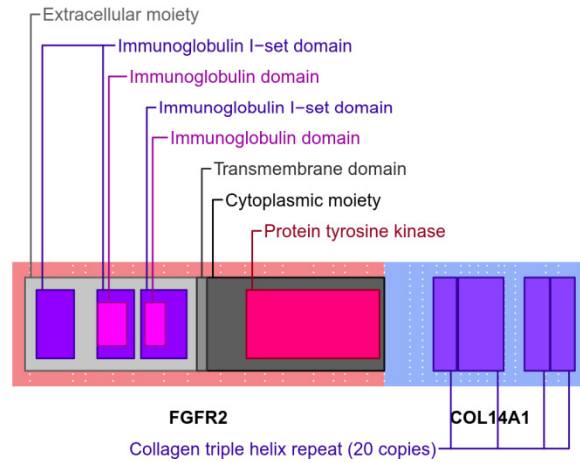
SUPPORTING READ COUNT

Split reads in *FGFR2* = 0
 Split reads in *COL14A1* = 2
 Discordant mates = 1

HPAC (59b5010b-df6b-4d72-9538-350c4cd6062a)



RETAINED PROTEIN DOMAINS



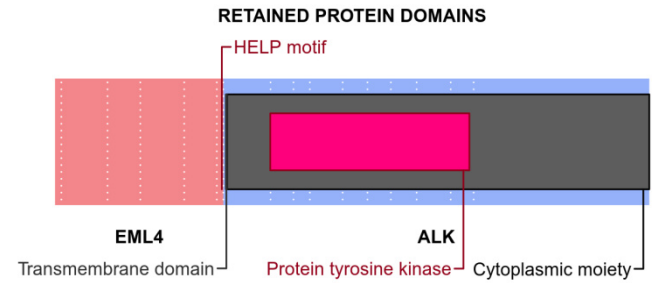
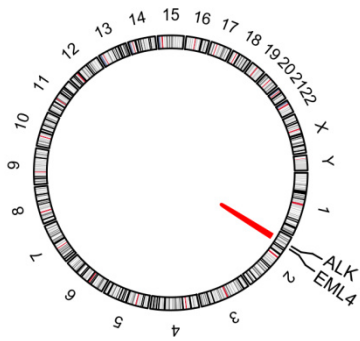
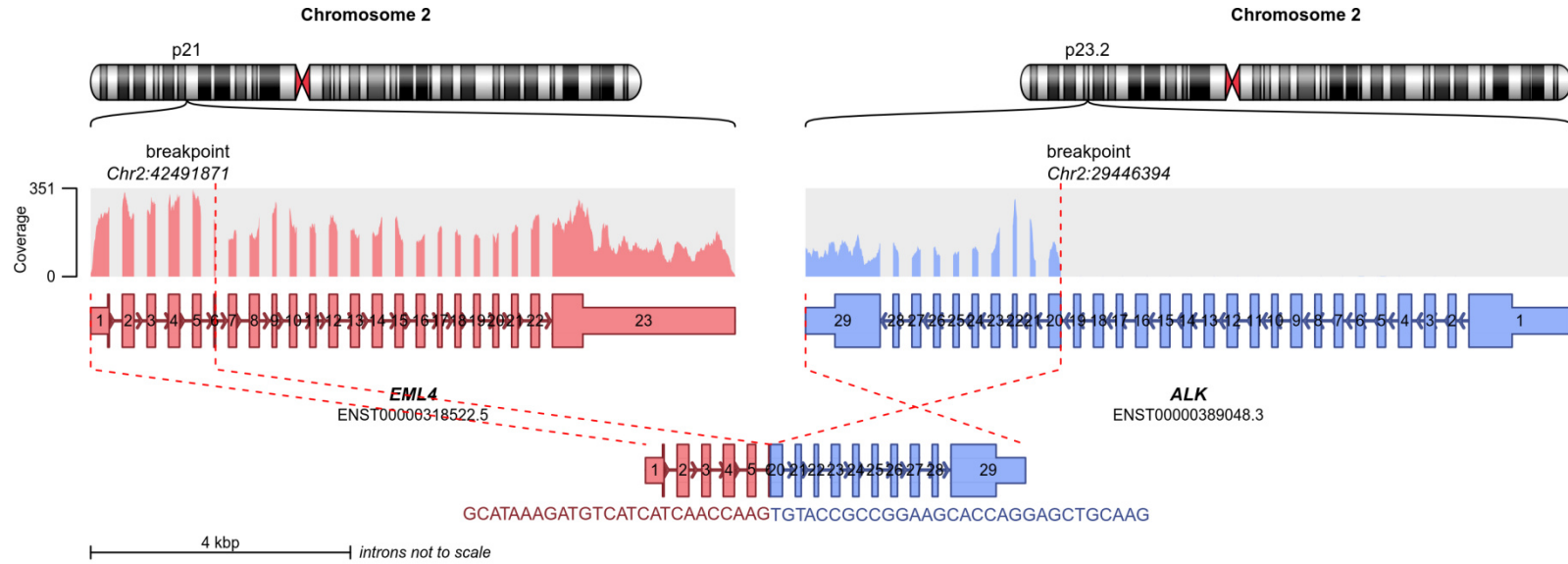
SUPPORTING READ COUNT

Split reads in *FGFR2* = 2

Split reads in *COL14A1* = 0

Discordant mates = 1

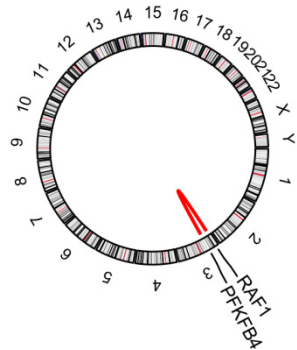
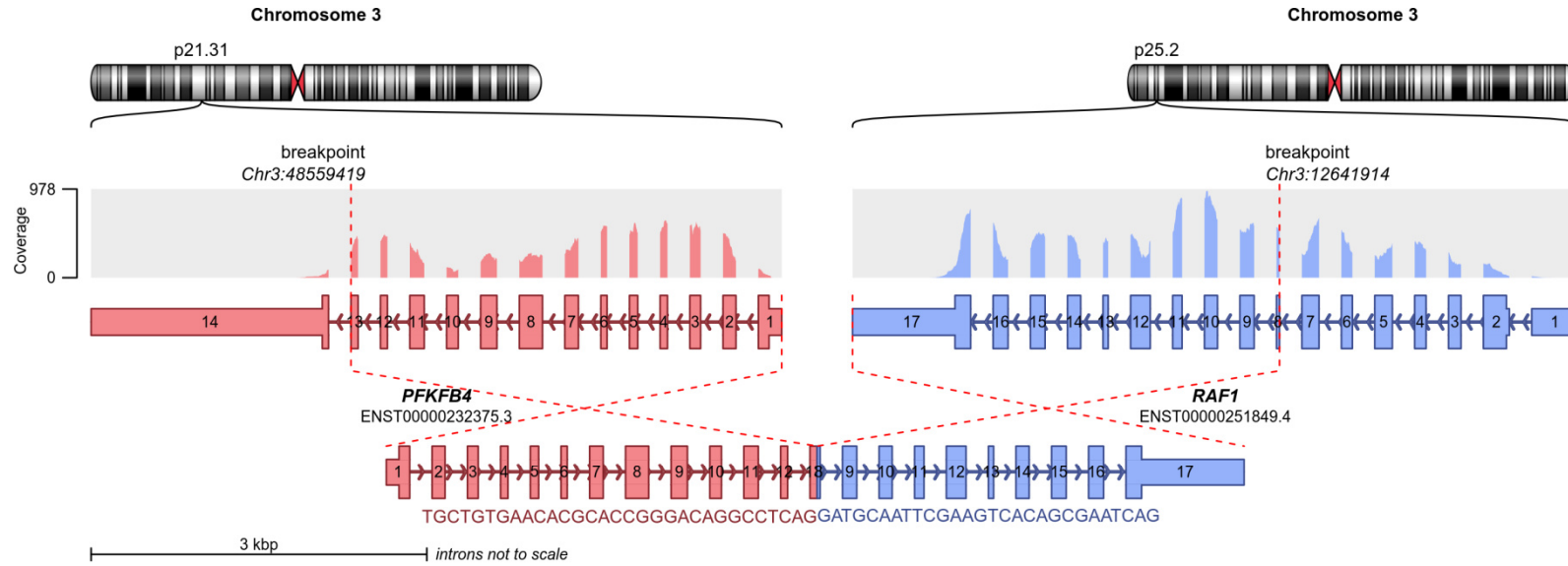
SNU-324 (13924031-19ce-4fcb-b023-5b2e3aefdf77)



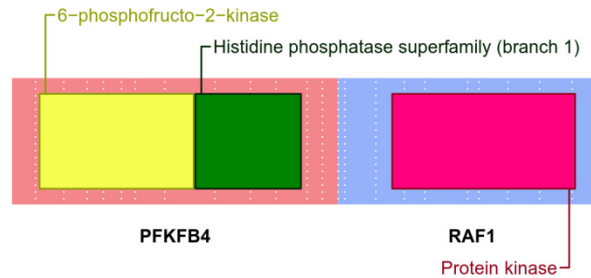
SUPPORTING READ COUNT

- Split reads in *EML4* = 8
- Split reads in *ALK* = 12
- Discordant mates = 24

COMP-002 (EGAF00001725478, EGAF00001745325, EGAF00001745326)



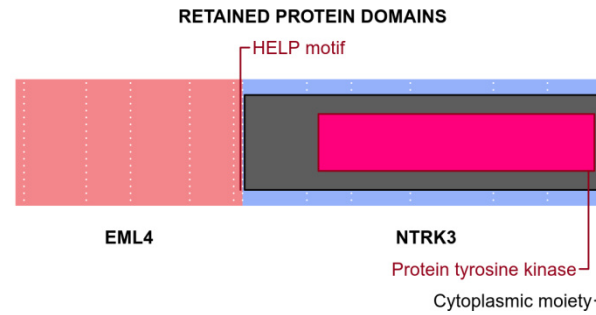
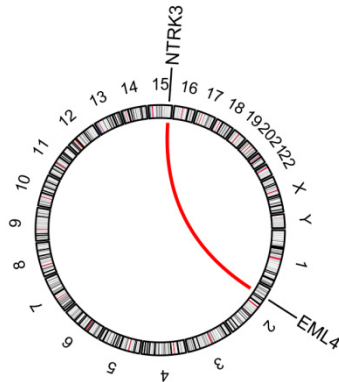
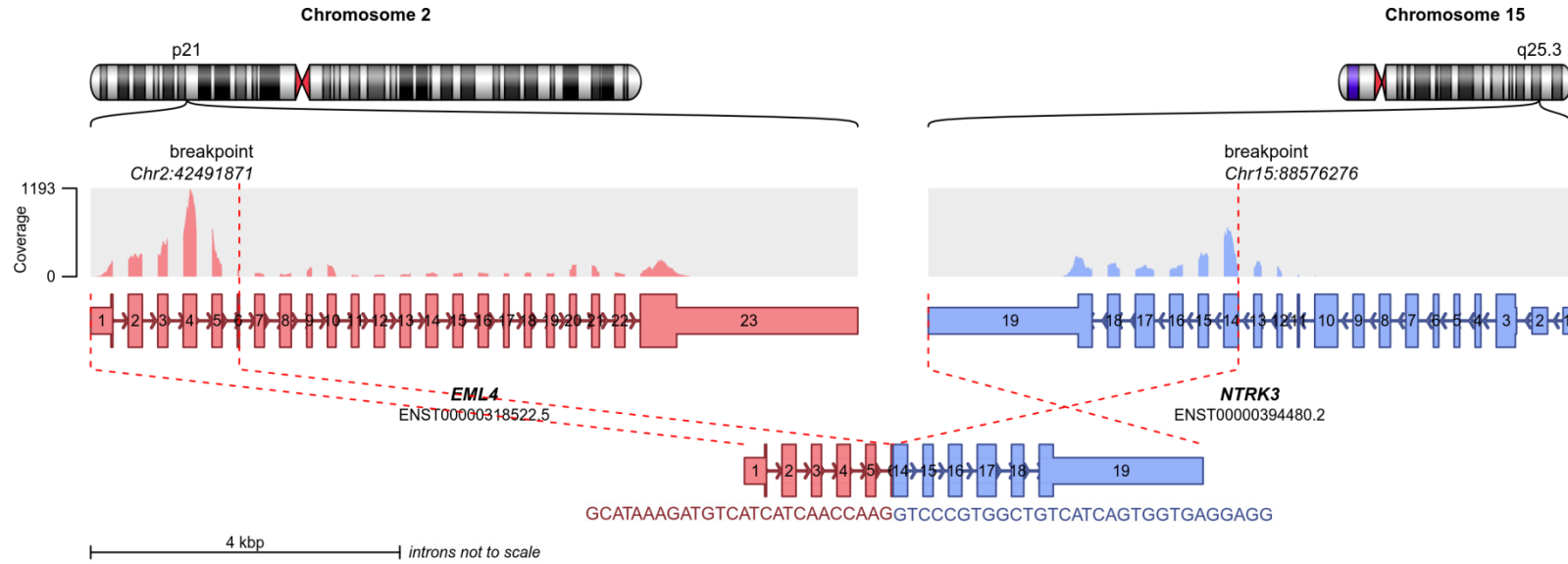
RETAINED PROTEIN DOMAINS



SUPPORTING READ COUNT

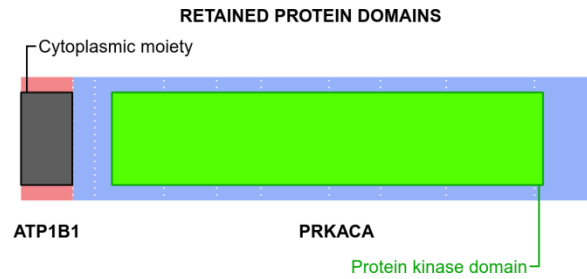
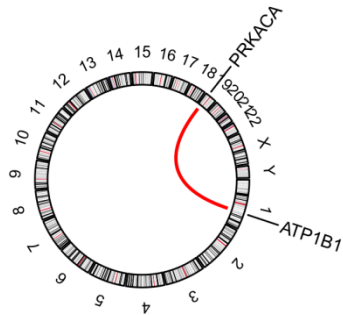
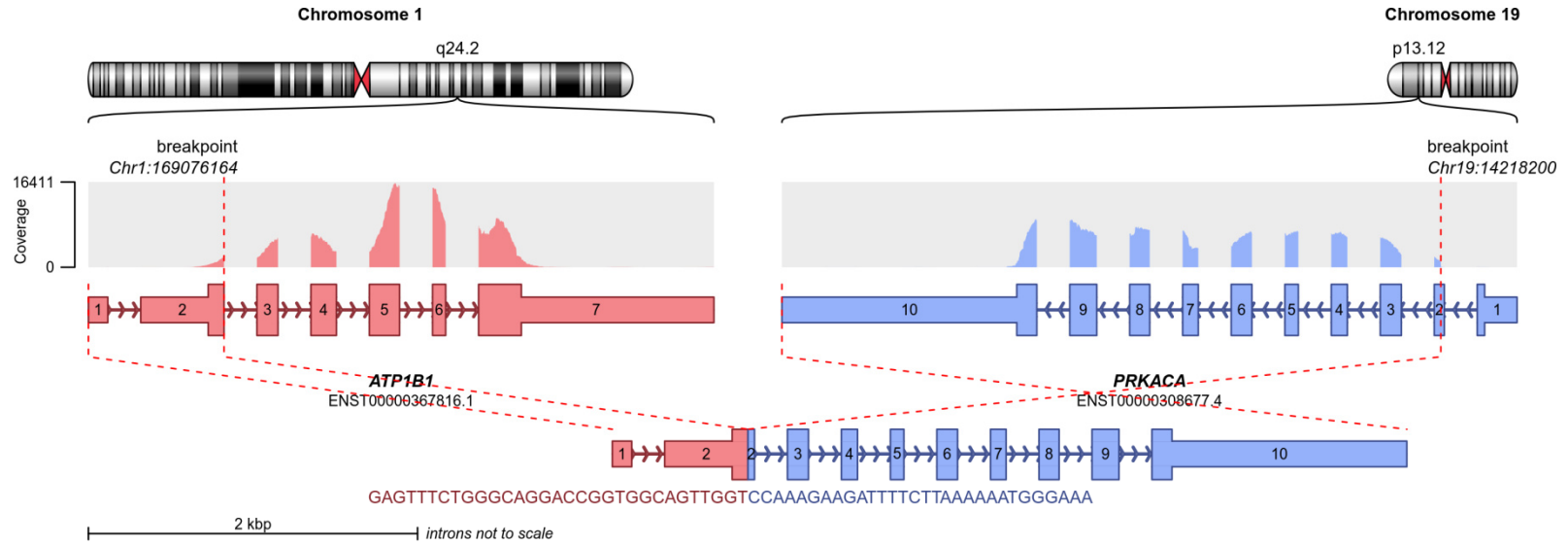
Split reads in *PFKFB4* = 17
 Split reads in *RAF1* = 19
 Discordant mates = 2

COMP-0023 (EGAF00001725495, EGAF00001745371, EGAF00001745372)



SUPPORTING READ COUNT
Split reads in *EML4* = 3
Split reads in *NTRK3* = 13
Discordant mates = 2

COMP-0028 (EGAF00001725498, EGAF00001745377, EGAF00001745378)



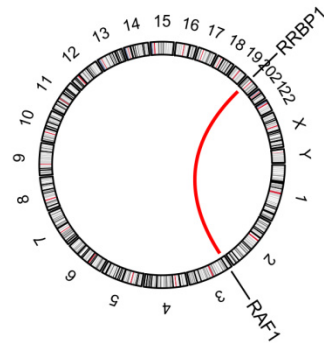
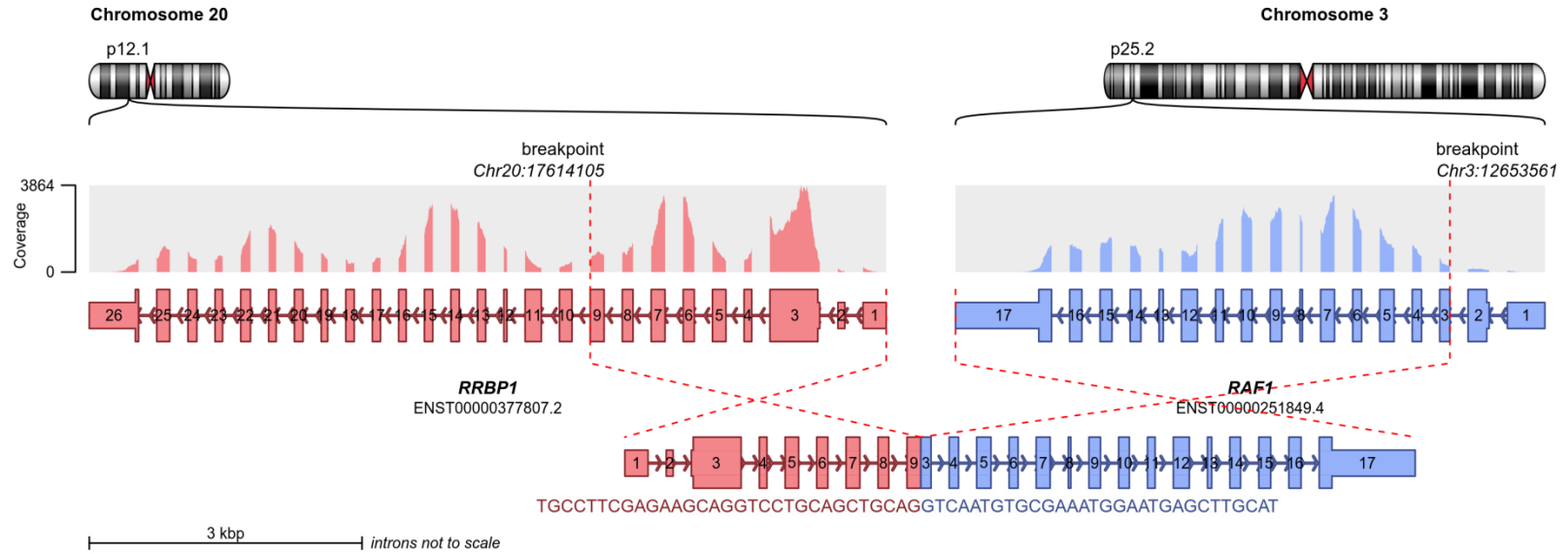
SUPPORTING READ COUNT

Split reads in *ATP1B1* = 15

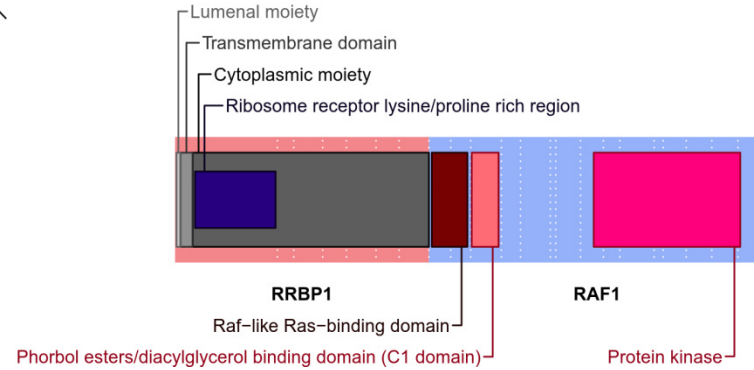
Split reads in *PRKACA* = 150

Discordant mates = 22

COMP-0055 (EGAF00001725520, EGAF00001745345, EGAF00001745346)



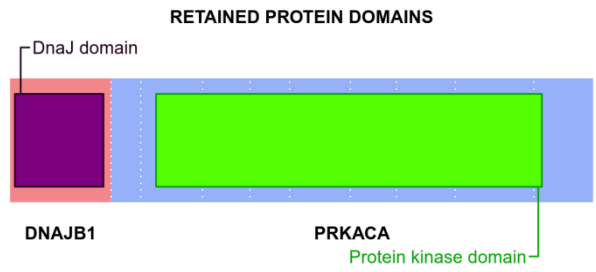
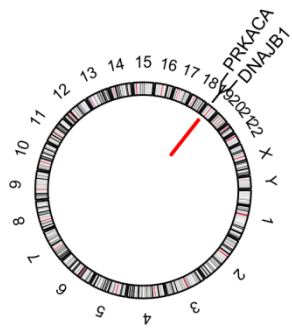
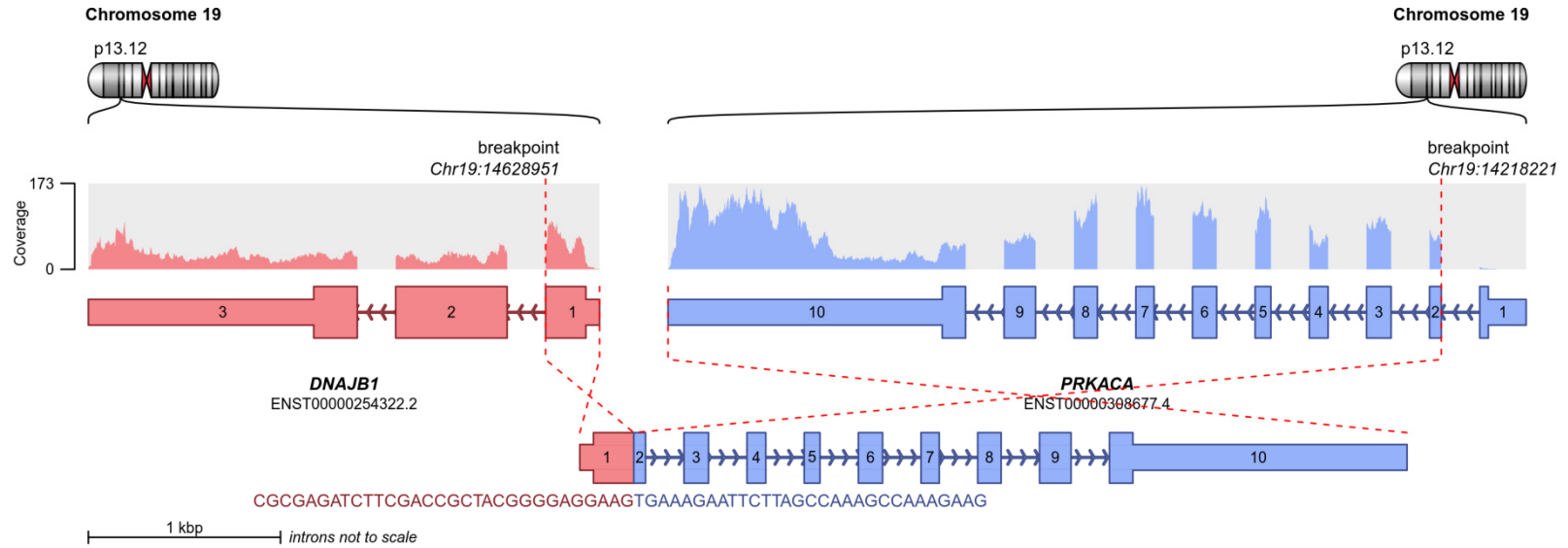
RETAINED PROTEIN DOMAINS



SUPPORTING READ COUNT

Split reads in *RRBP1* = 52
 Split reads in *RAF1* = 46
 Discordant mates = 28

T_05_08_A230b (SRR3308904)



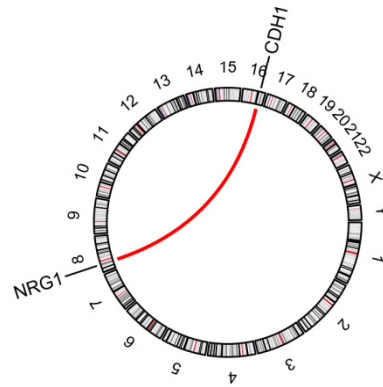
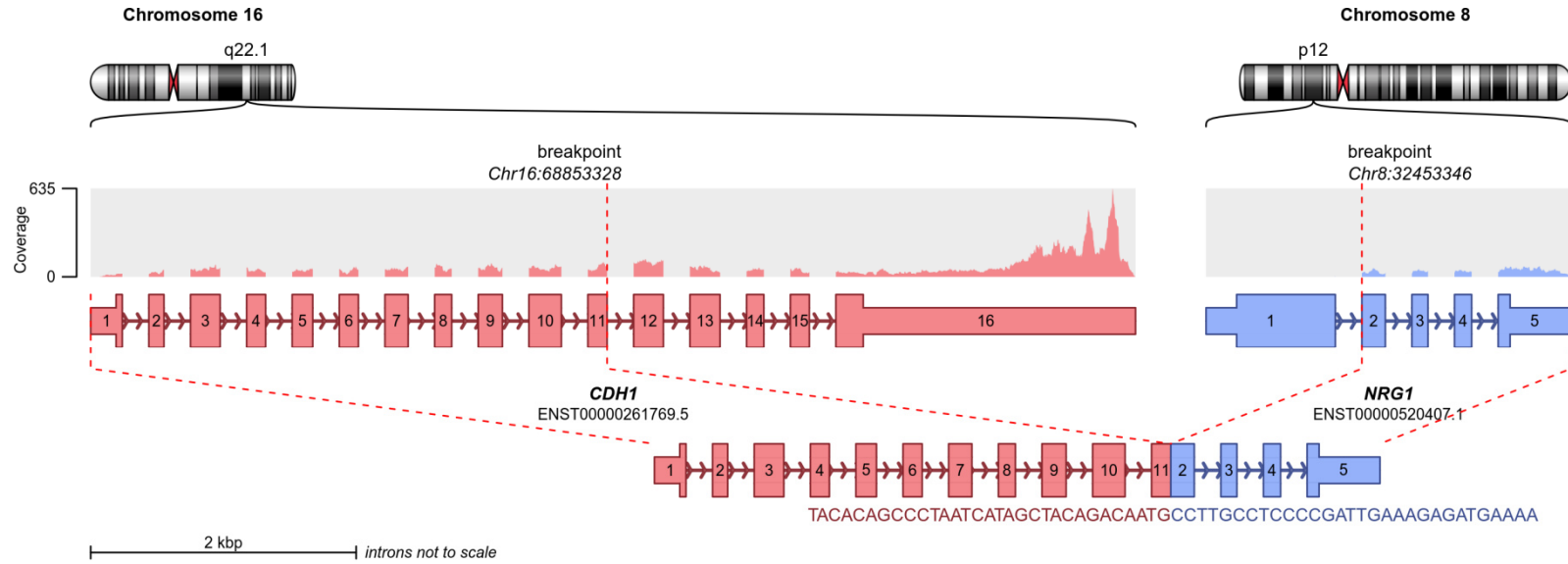
SUPPORTING READ COUNT

Split reads in *DNAJB1* = 3

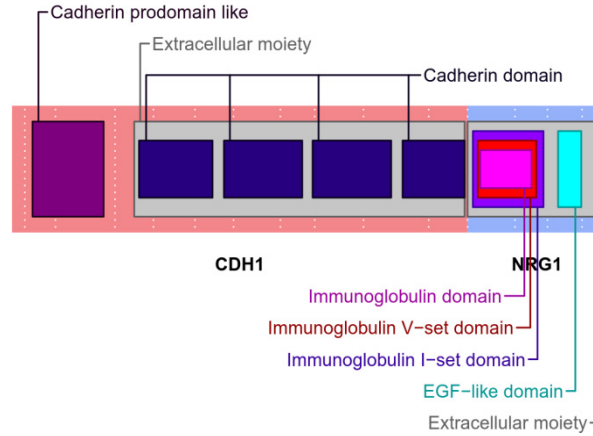
Split reads in *PRKACA* = 9

Discordant mates = 73

T_07_06_A323a (SRR3308914)



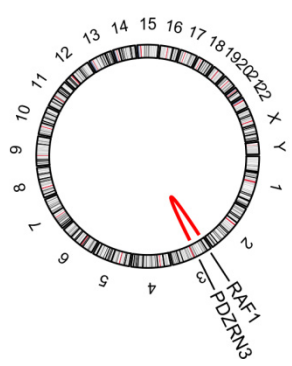
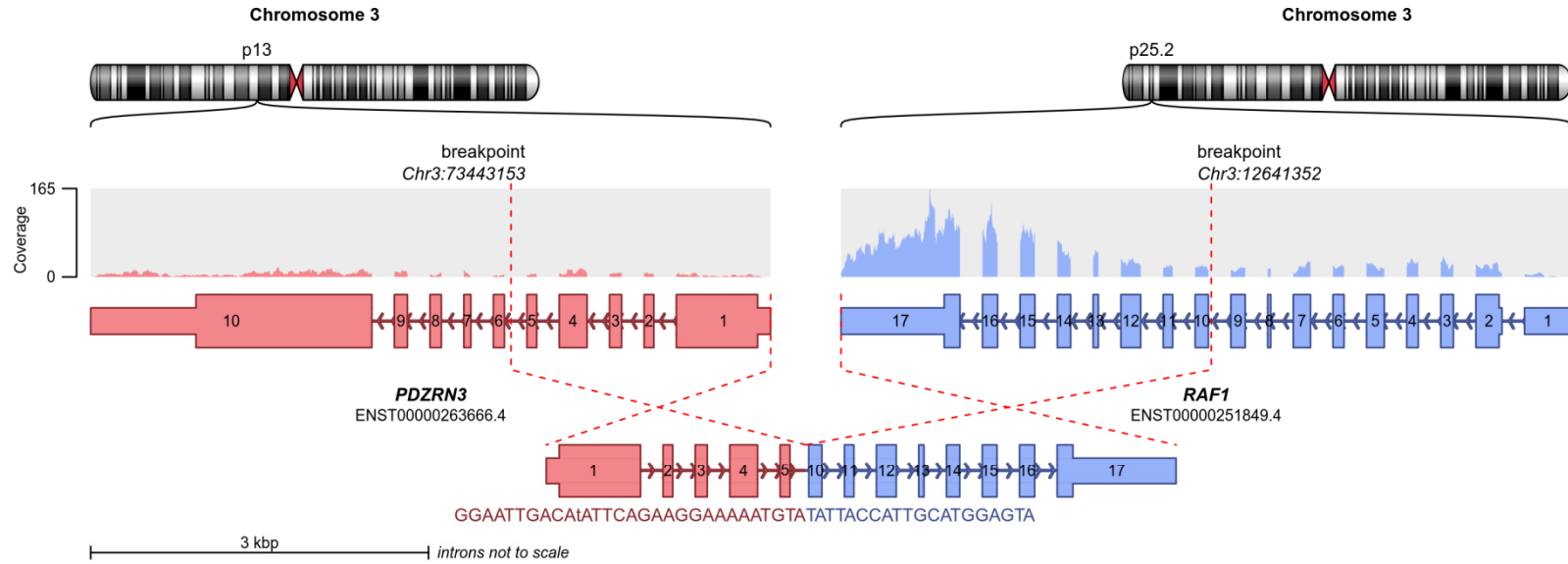
RETAINED PROTEIN DOMAINS



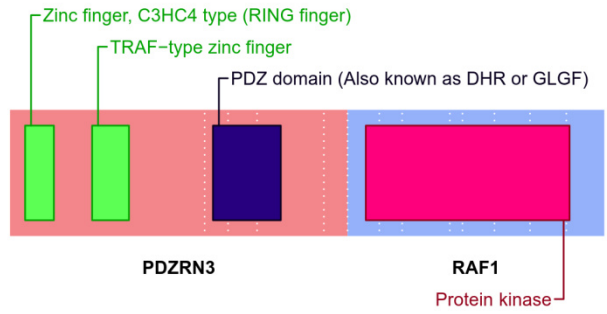
SUPPORTING READ COUNT

Split reads in *CDH1* = 1
 Split reads in *NRG1* = 12
 Discordant mates = 32

T_07_11_A090a (SRR3308887)



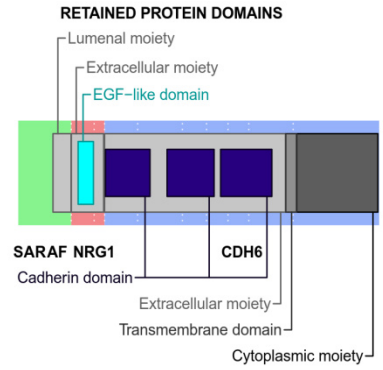
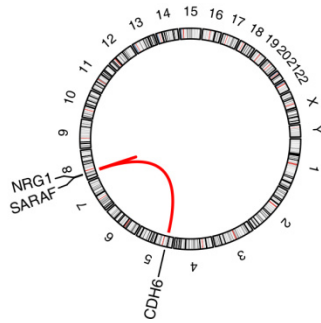
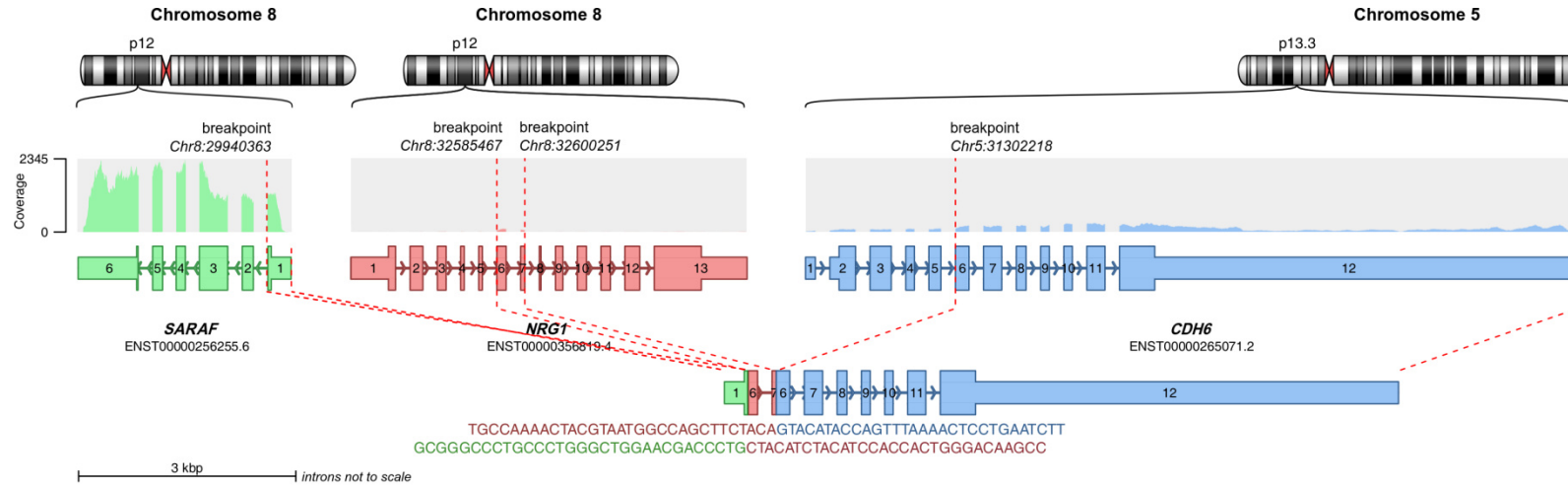
RETAINED PROTEIN DOMAINS



SUPPORTING READ COUNT

Split reads in *PDZRN3* = 0
 Split reads in *RAF1* = 1
 Discordant mates = 5

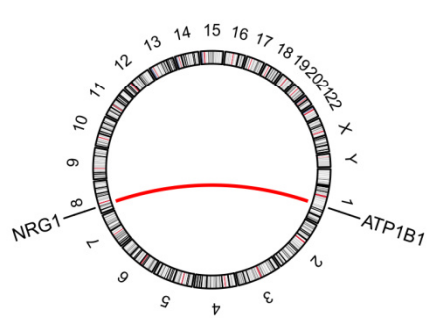
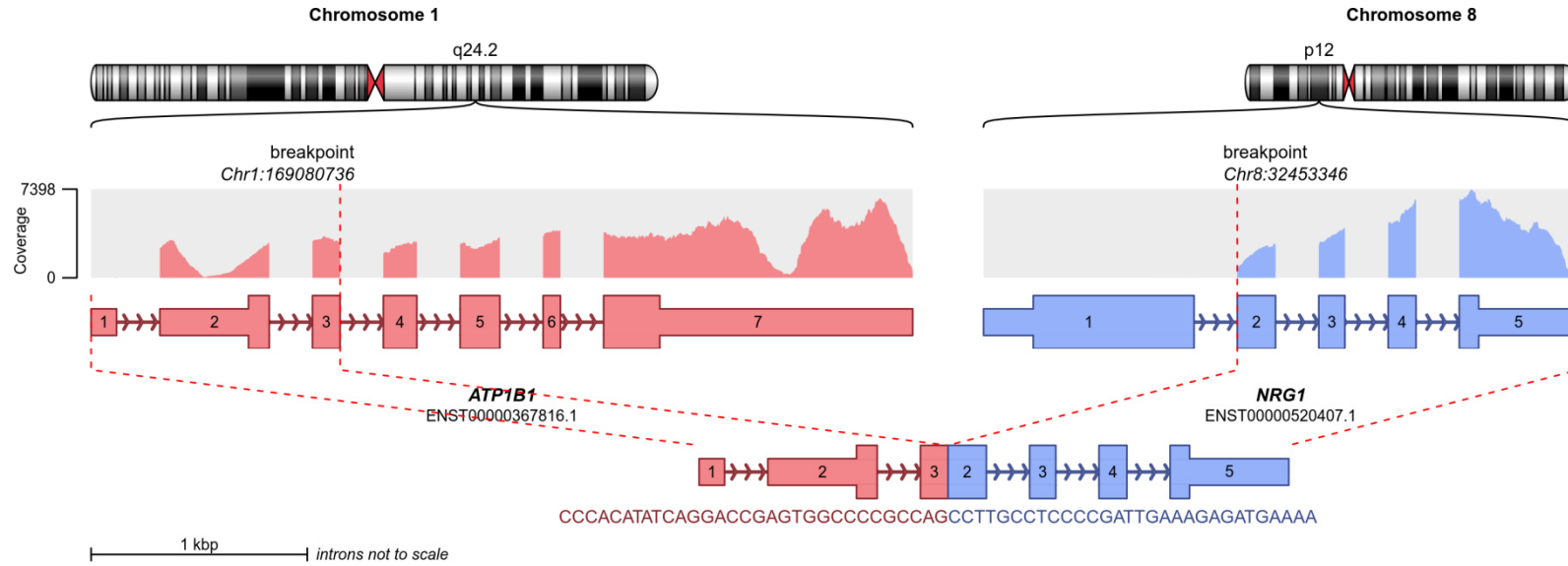
Patient 15 (EGAF00001984744)



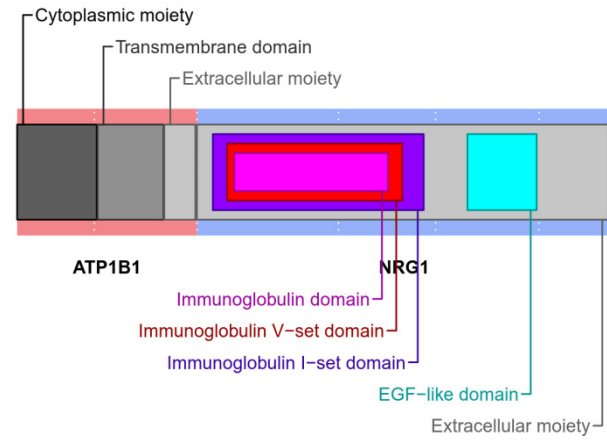
SUPPORTING READ COUNT

Split reads in *SARAF* = 49
 Split reads in *NRG1* = 14-15
 Split reads in *CDH6* = 11
 Discordant mates = 12-13

Patient 14 (EGAF00001984739)



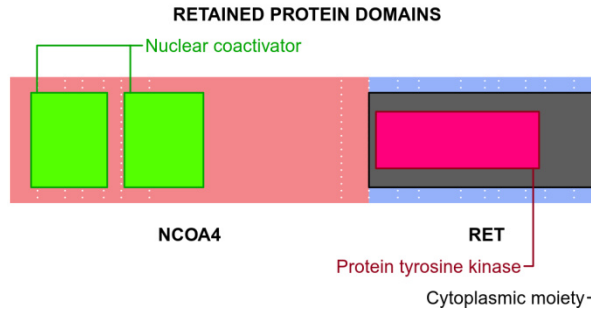
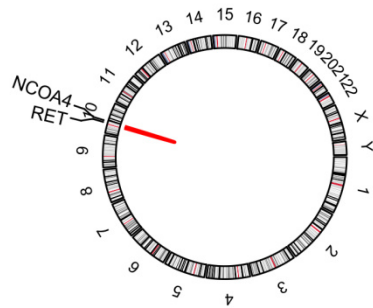
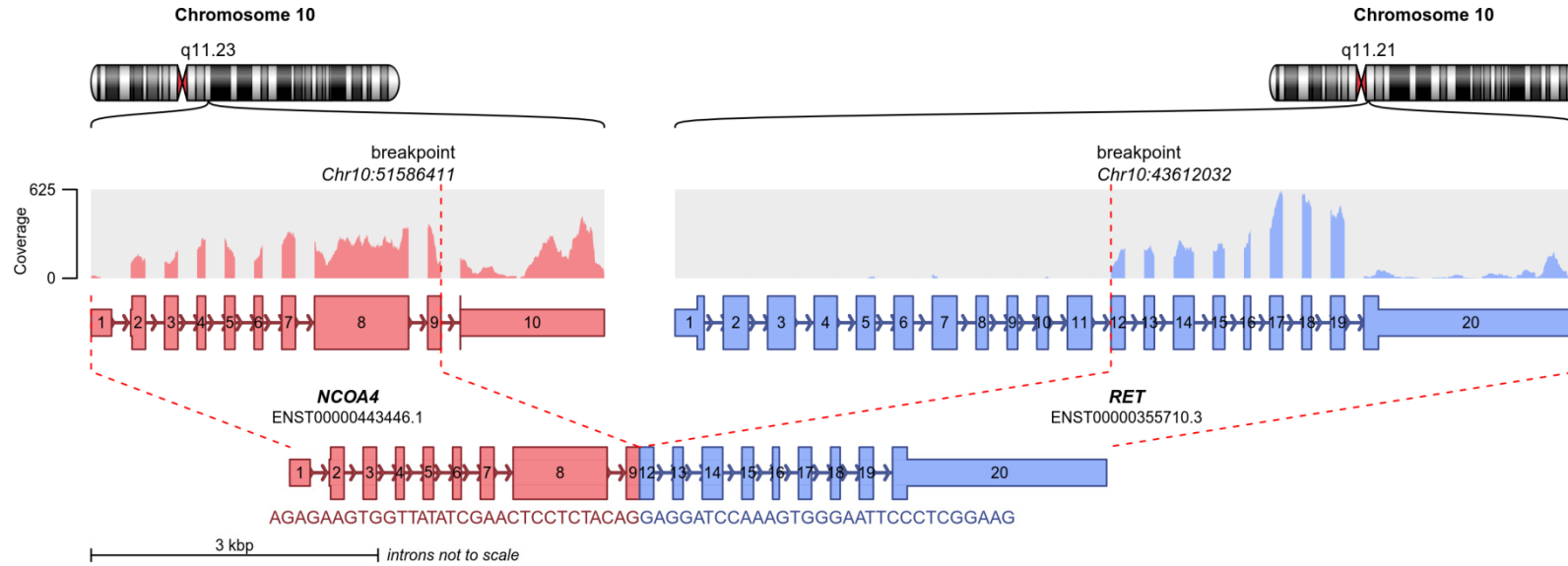
RETAINED PROTEIN DOMAINS



SUPPORTING READ COUNT

Split reads in *ATP1B1* = 160
 Split reads in *NRG1* = 111
 Discordant mates = 38

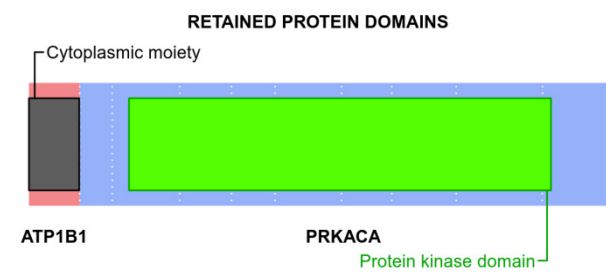
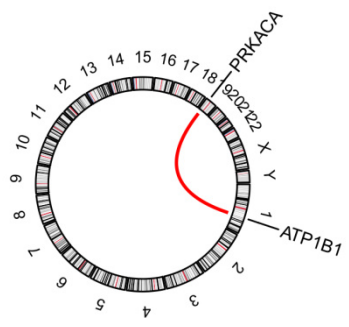
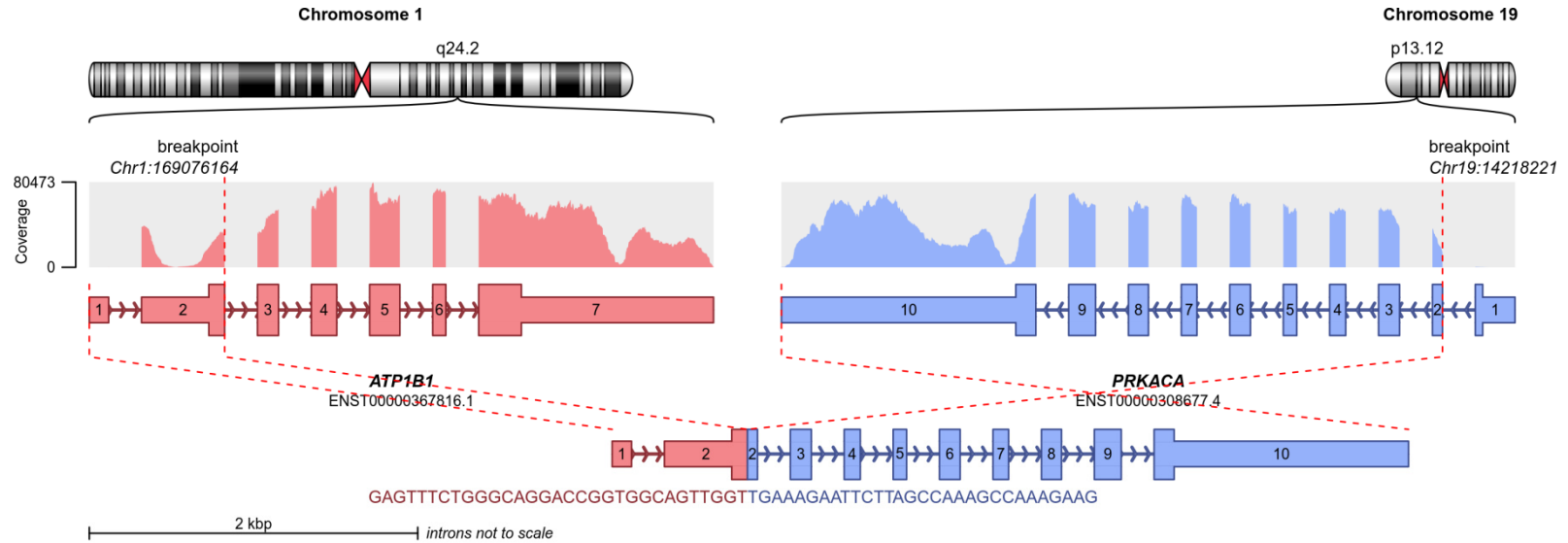
Patient 17 (EGAF00001984730)



SUPPORTING READ COUNT

Split reads in *NCOA4* = 1
 Split reads in *RET* = 0
 Discordant mates = 1

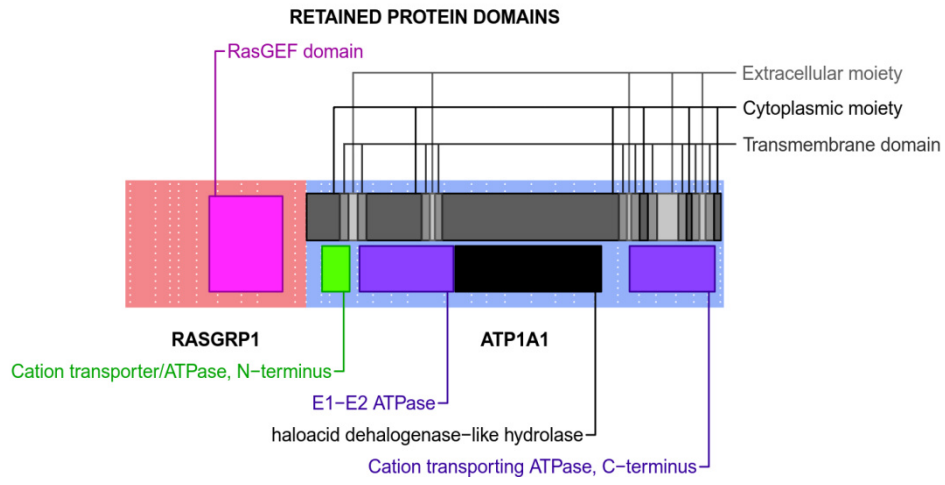
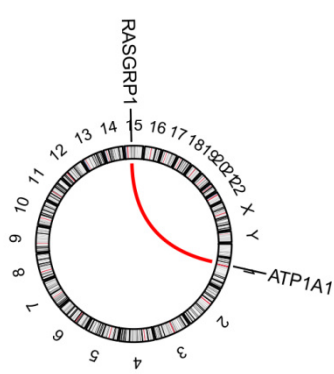
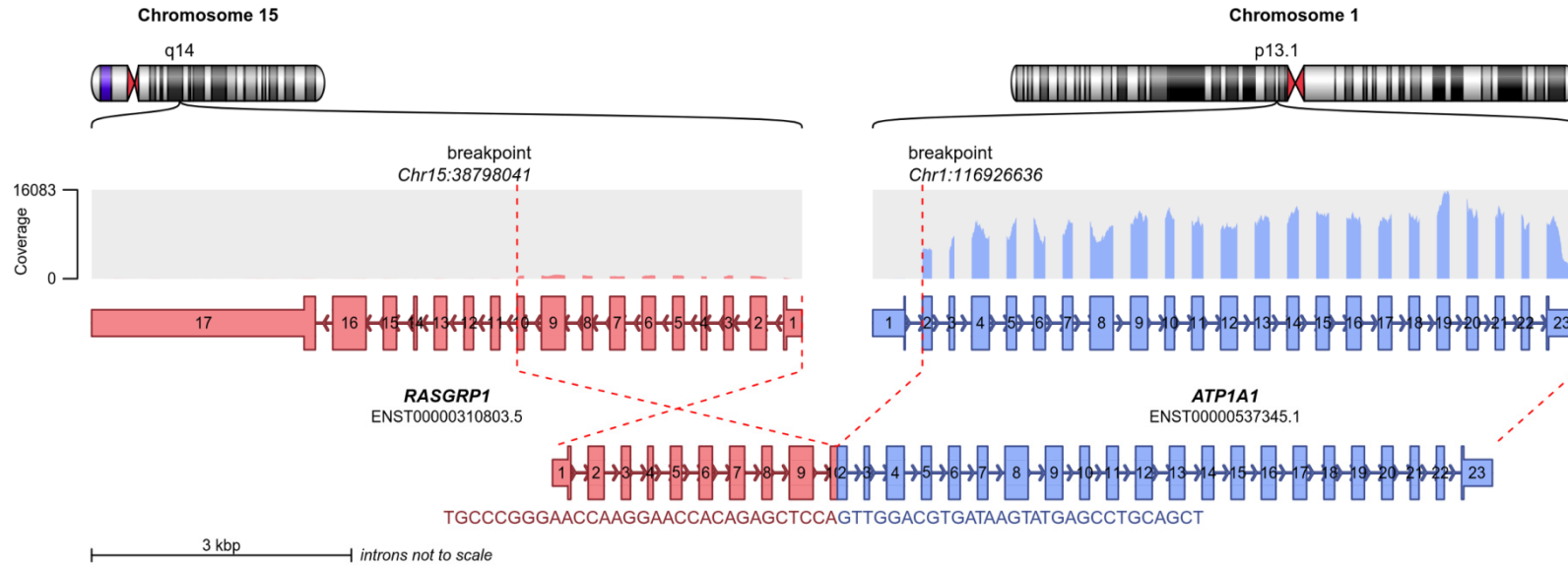
PDCM (EGAF00001984748)



SUPPORTING READ COUNT

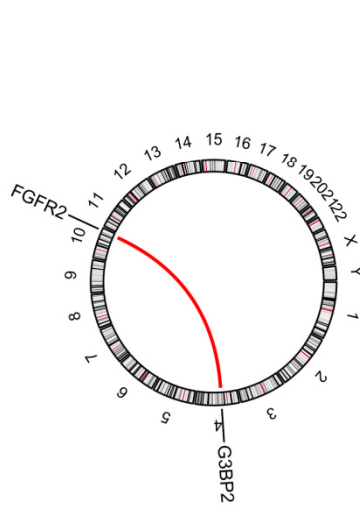
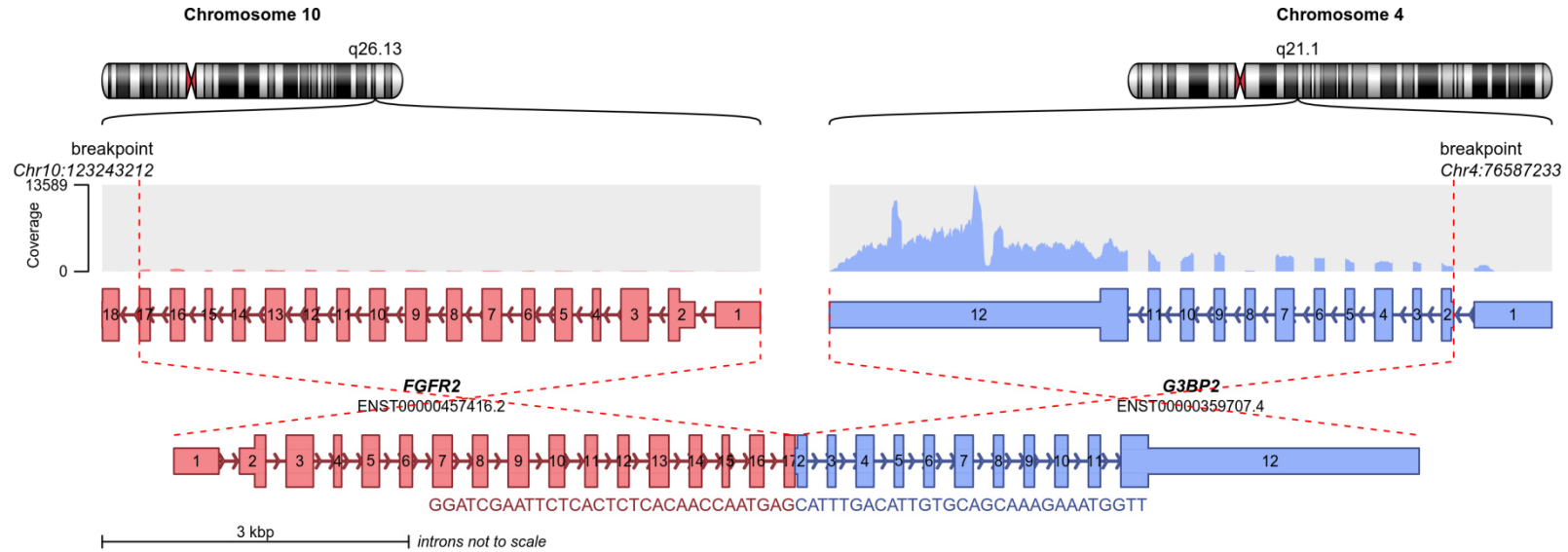
Split reads in *ATP1B1* = 110
 Split reads in *PRKACA* = 303
 Discordant mates = 65

Patient A (EGAF00002486941)

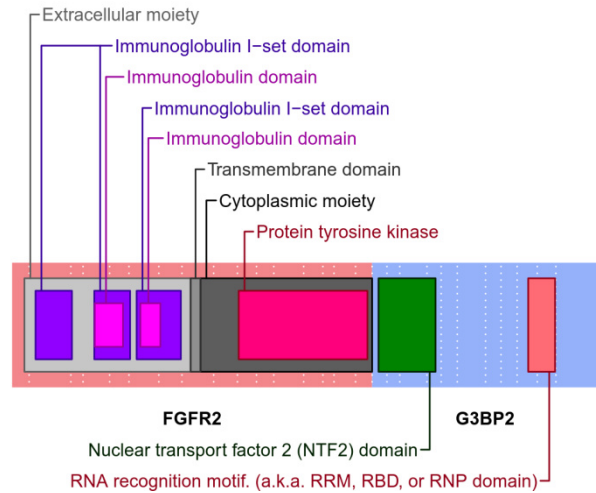


SUPPORTING READ COUNT
 Split reads in *RASGRP1* = 131
 Split reads in *ATP1A1* = 76
 Discordant mates = 36

PDAC009T (ERR1880131, ERR1880132)



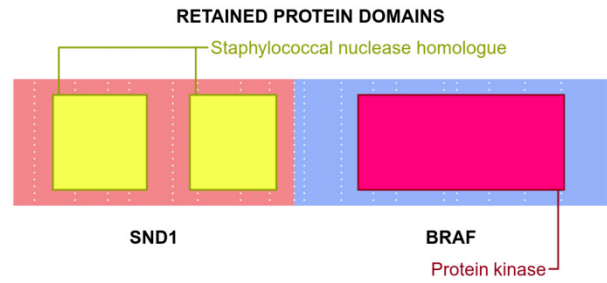
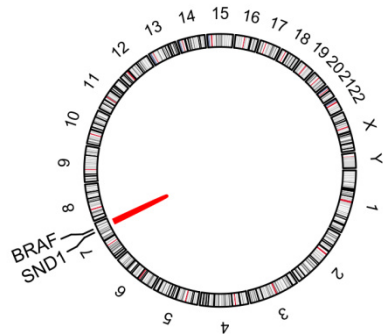
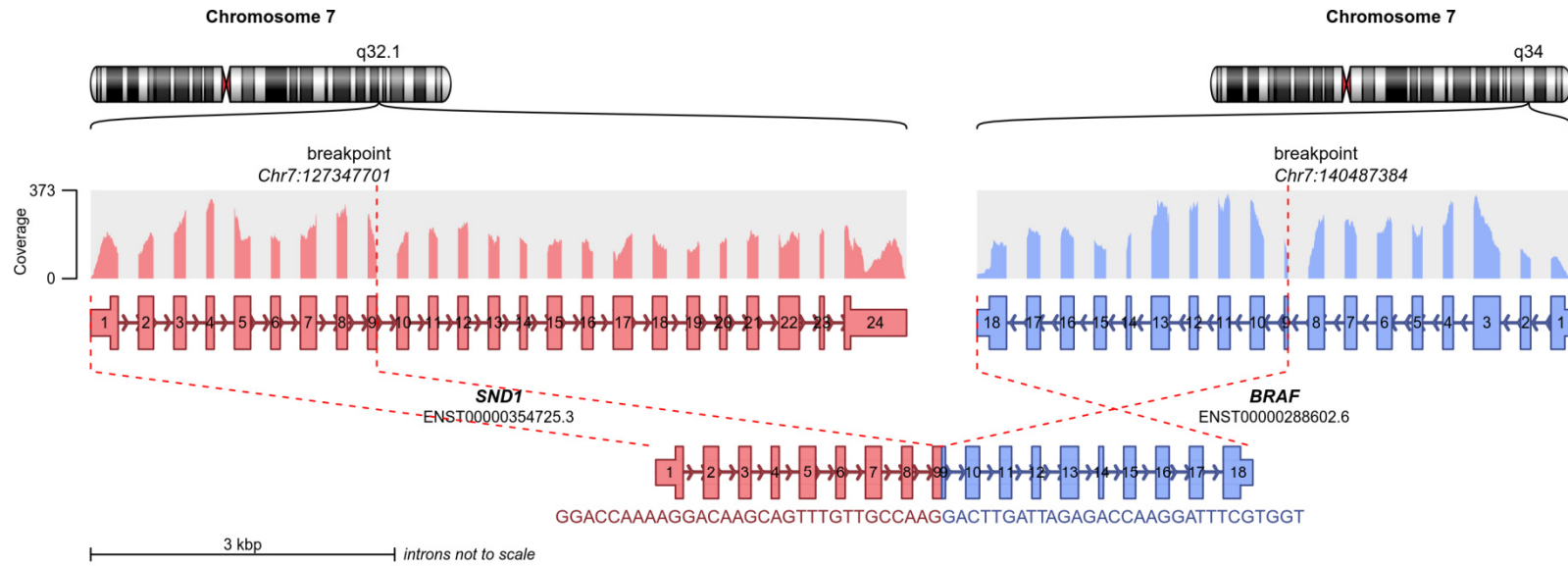
RETAINED PROTEIN DOMAINS



SUPPORTING READ COUNT

Split reads in *FGFR2* = 33
 Split reads in *G3BP2* = 103
 Discordant mates = 300

ICGC_0338 (EGAF00001682709)



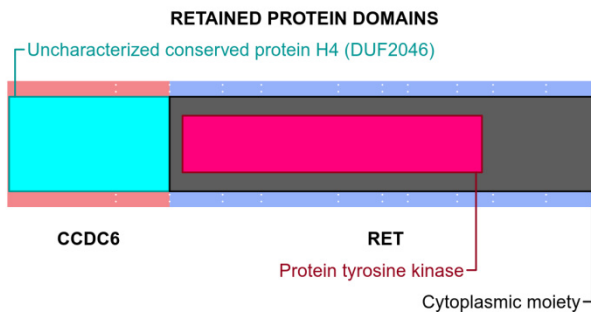
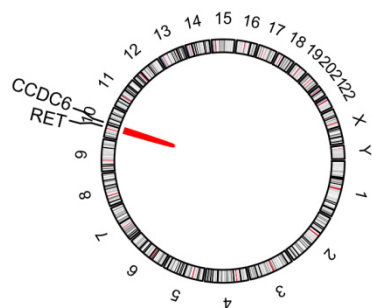
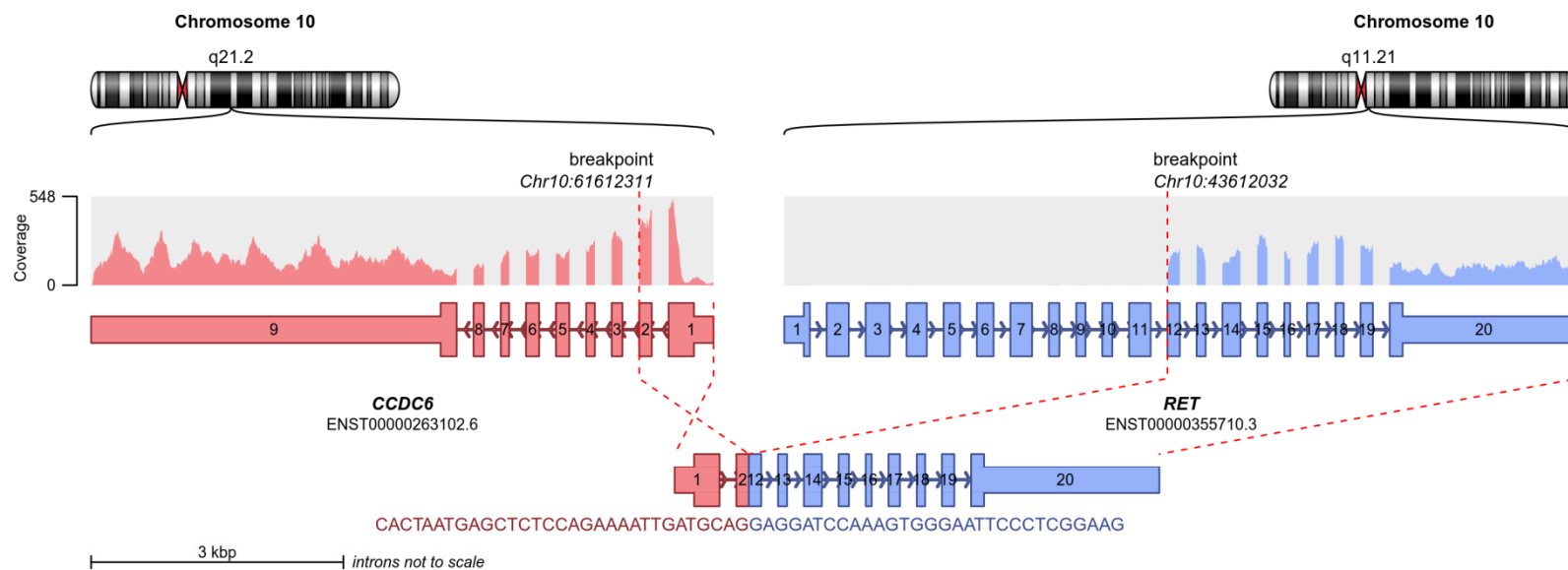
SUPPORTING READ COUNT

Split reads in *SND1* = 33

Split reads in *BRAF* = 49

Discordant mates = 18

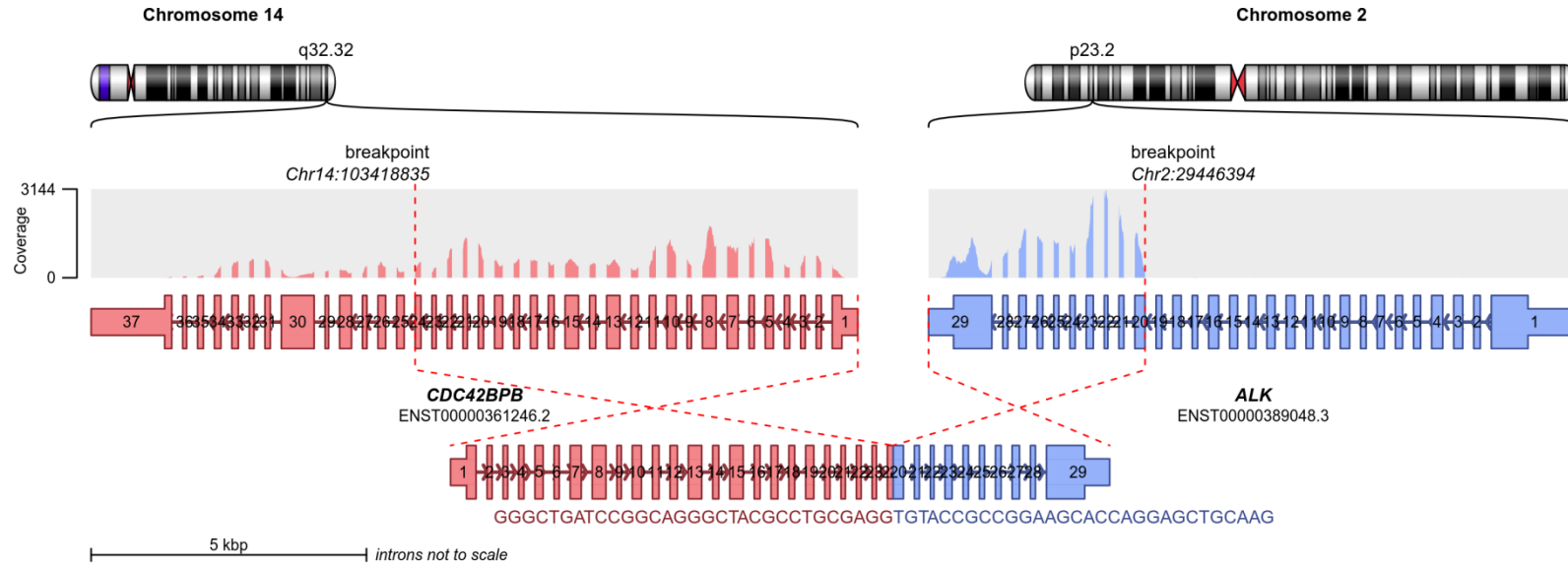
ICGC_0391 (EGAF00001682868)



SUPPORTING READ COUNT

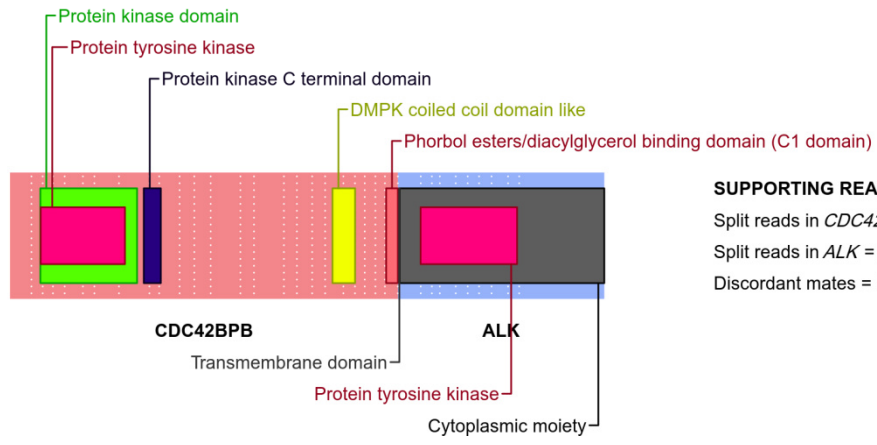
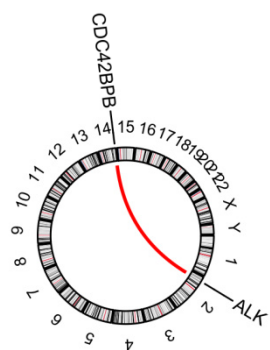
Split reads in **CCDC6** = 51
 Split reads in **RET** = 31
 Discordant mates = 11

PCSI_0572 (EGAF00001844274, EGAF00001879250, EGAF00001879251)



GGGCTGATCCGGCAGGGCTACGCCTGCGAGGTGTACCGCCGAAGCACCAGGAGCTGCAAG

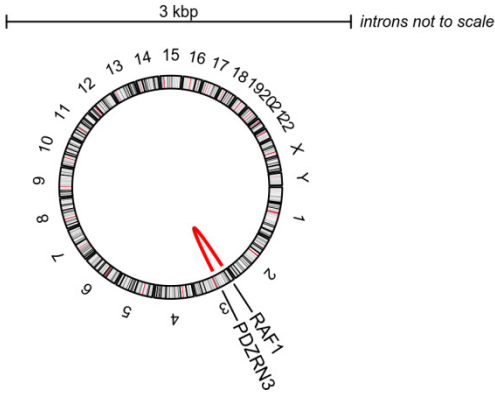
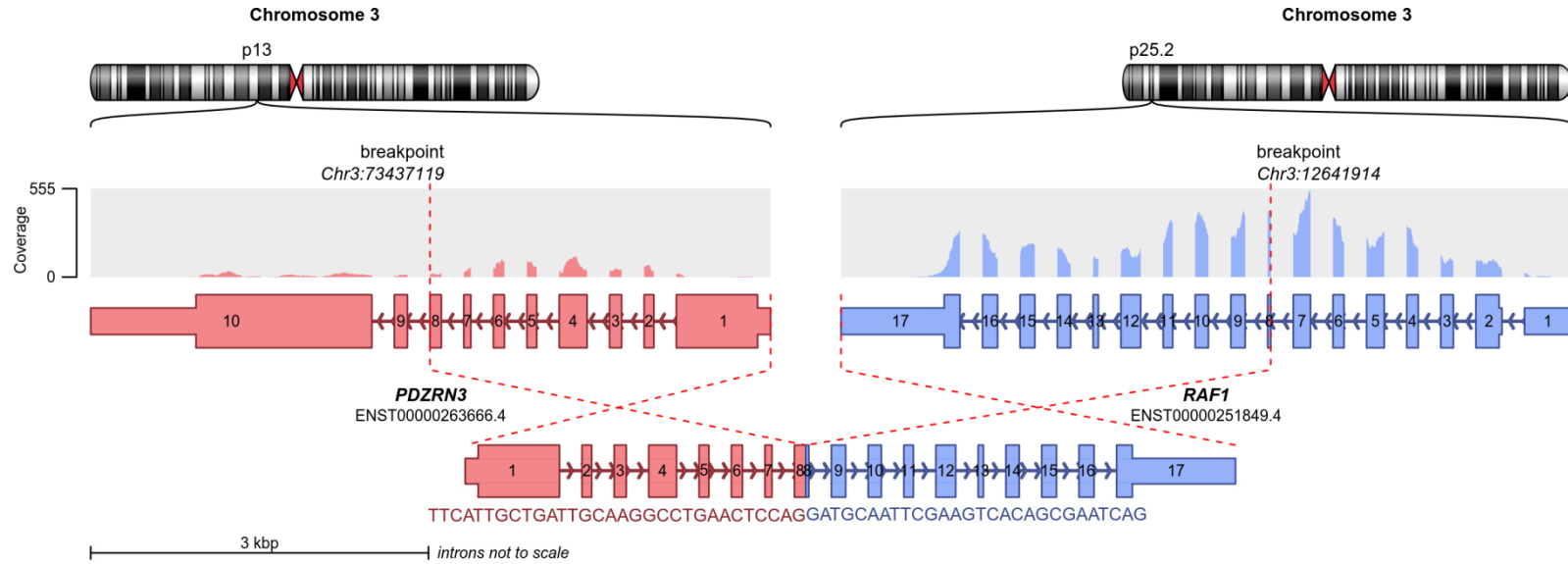
RETAINED PROTEIN DOMAINS



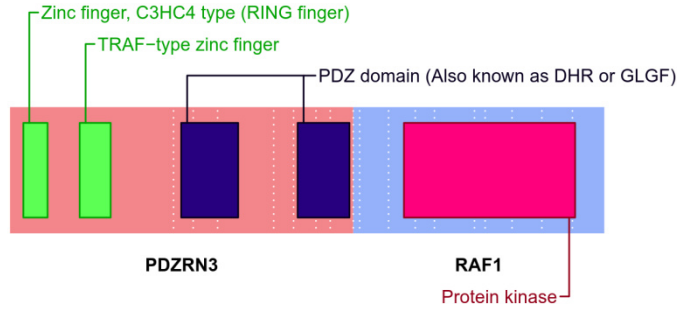
SUPPORTING READ COUNT

Split reads in *CDC42BPB* = 28
 Split reads in *ALK* = 24
 Discordant mates = 6

PCSI_0108 (EGAF00001844288, EGAF00001878986, EGAF00001878987)



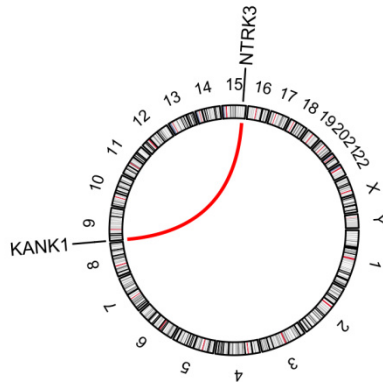
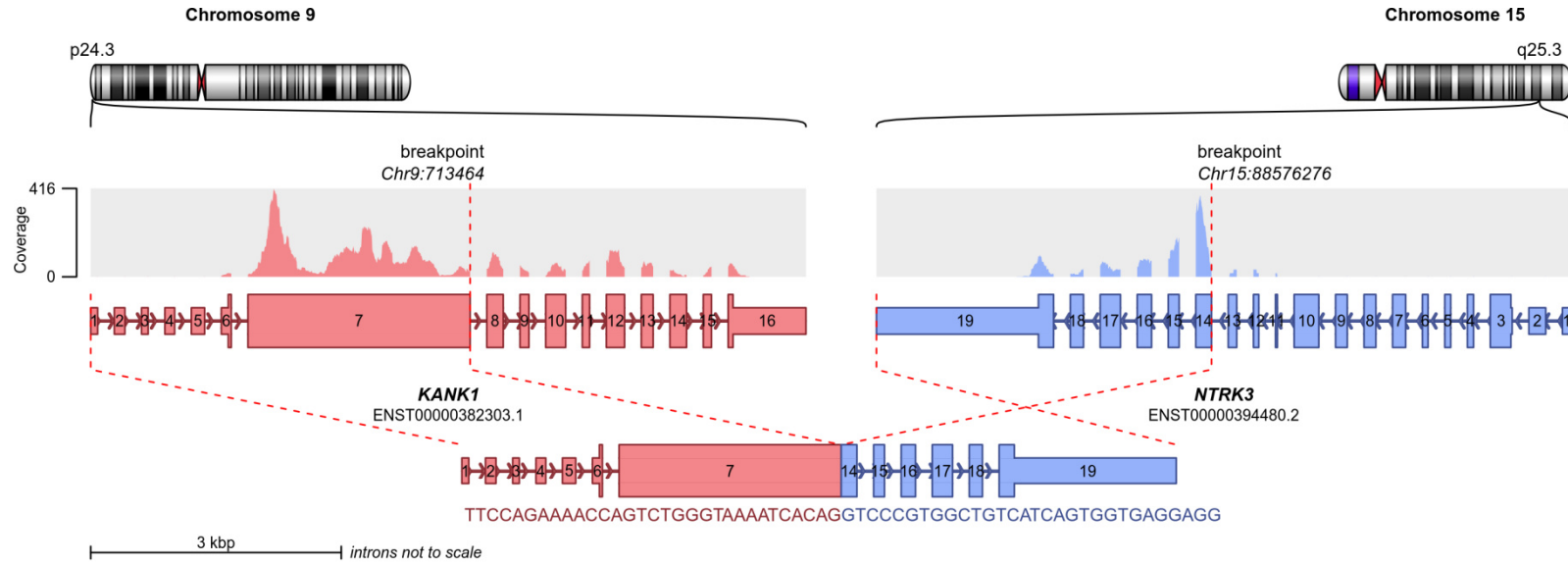
RETAINED PROTEIN DOMAINS



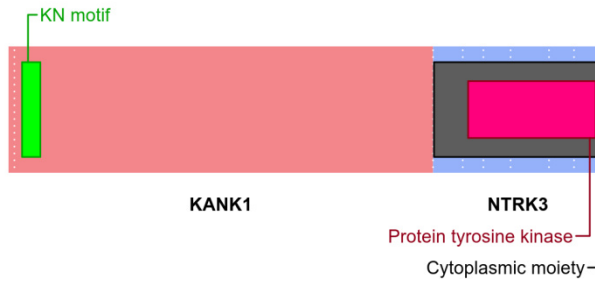
SUPPORTING READ COUNT

Split reads in *PDZRN3* = 0
 Split reads in *RAF1* = 1
 Discordant mates = 1

PCSI_0279 (EGAF00001844342, EGAF00001879056, EGAF00001879057)



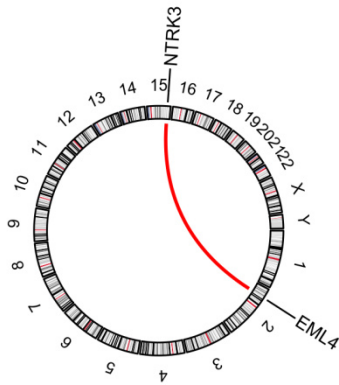
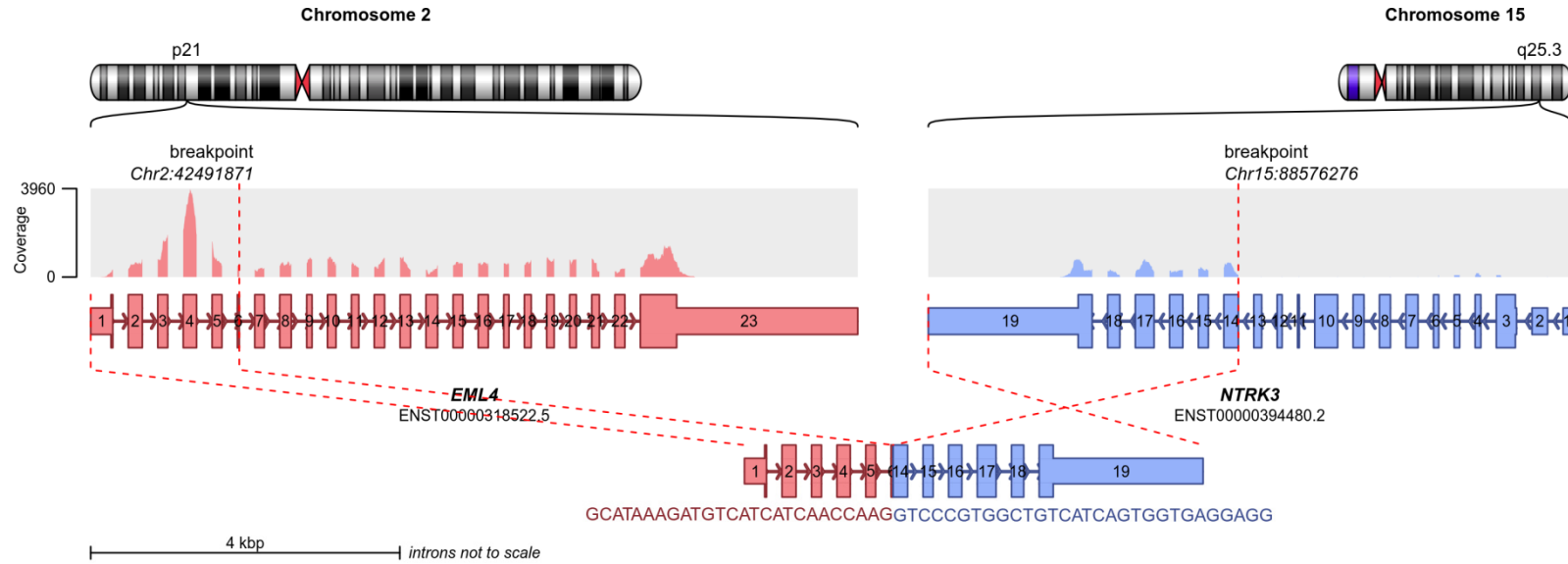
RETAINED PROTEIN DOMAINS



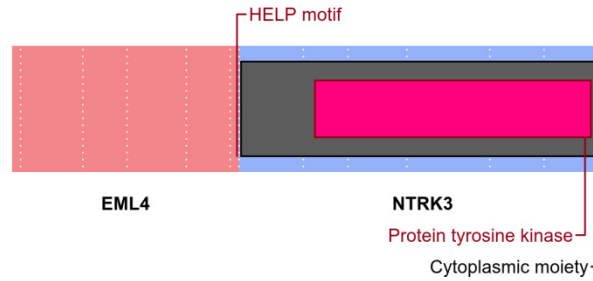
SUPPORTING READ COUNT

- Split reads in **KANK1** = 1
- Split reads in **NTRK3** = 4
- Discordant mates = 2

PCSI_0305 (EGAF00001844367, EGAF00001879088, EGAF00001879089)



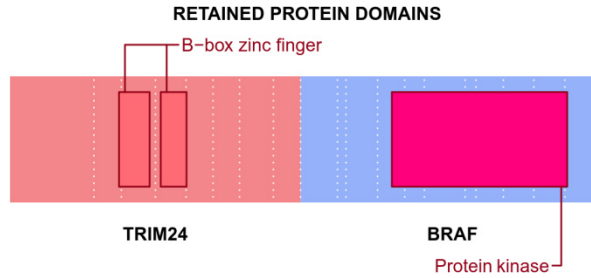
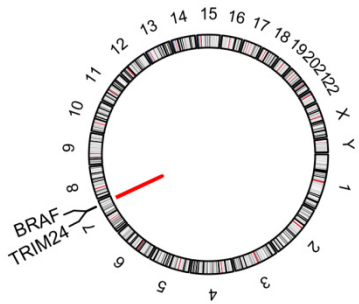
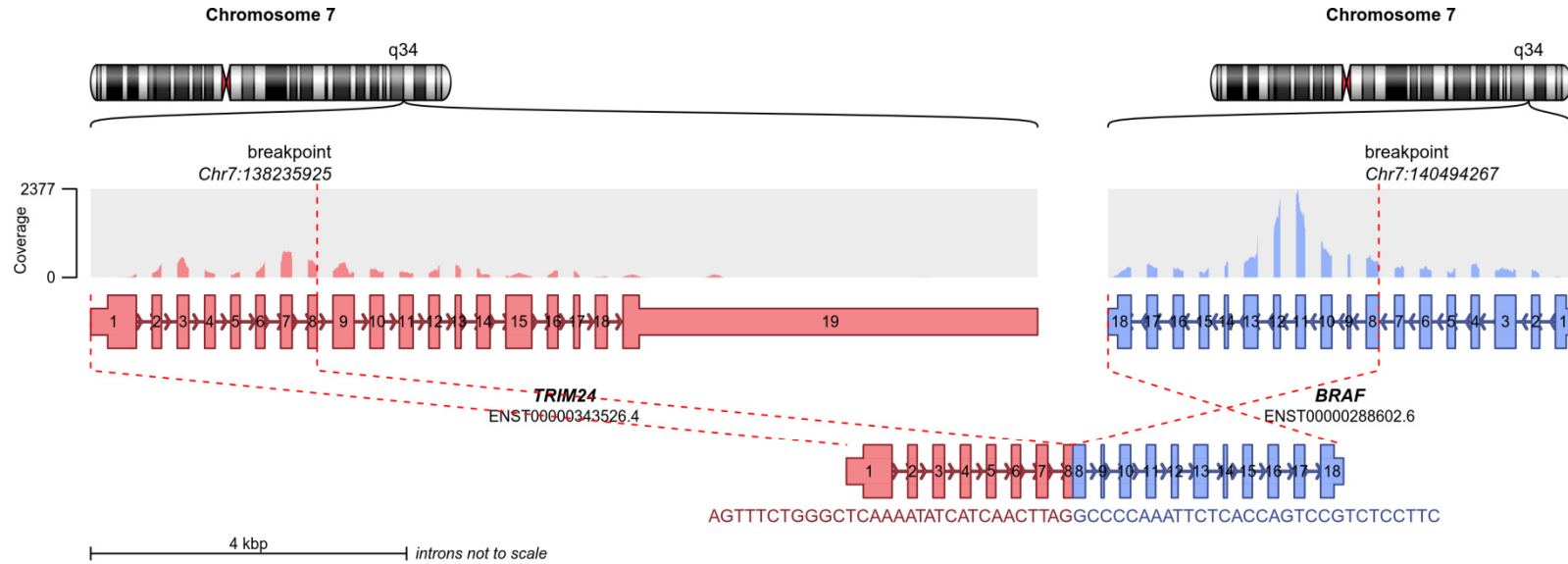
RETAINED PROTEIN DOMAINS



SUPPORTING READ COUNT

Split reads in *EML4* = 3
 Split reads in *NTRK3* = 5
 Discordant mates = 2

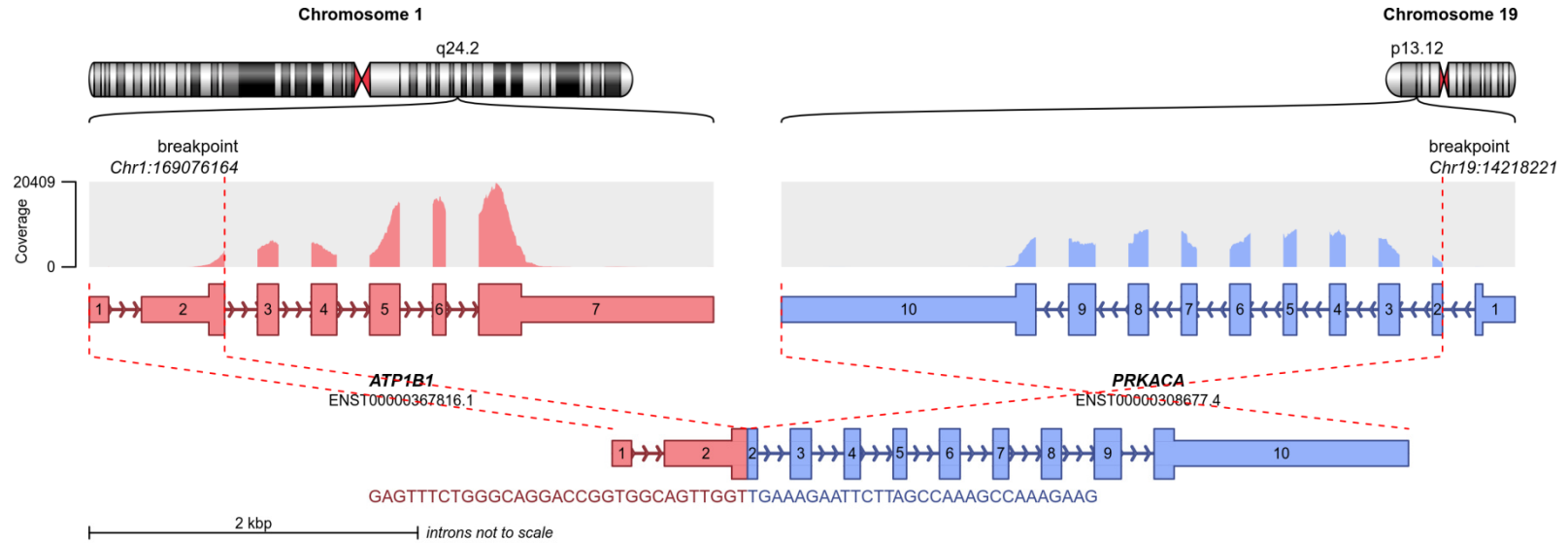
PCSI_0326 (EGAF00001844548, EGAF00001879104, EGAF00001879105)



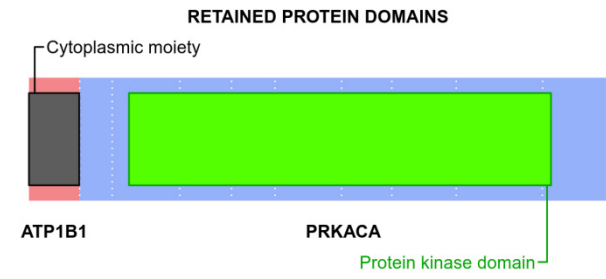
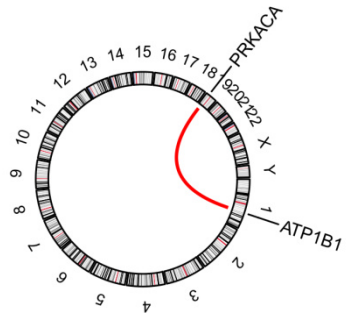
SUPPORTING READ COUNT

Split reads in *TRIM24* = 1
 Split reads in *BRAF* = 1
 Discordant mates = 0

PCSI_0330 (EGAF00001844551, EGAF00001879110, EGAF00001879111)

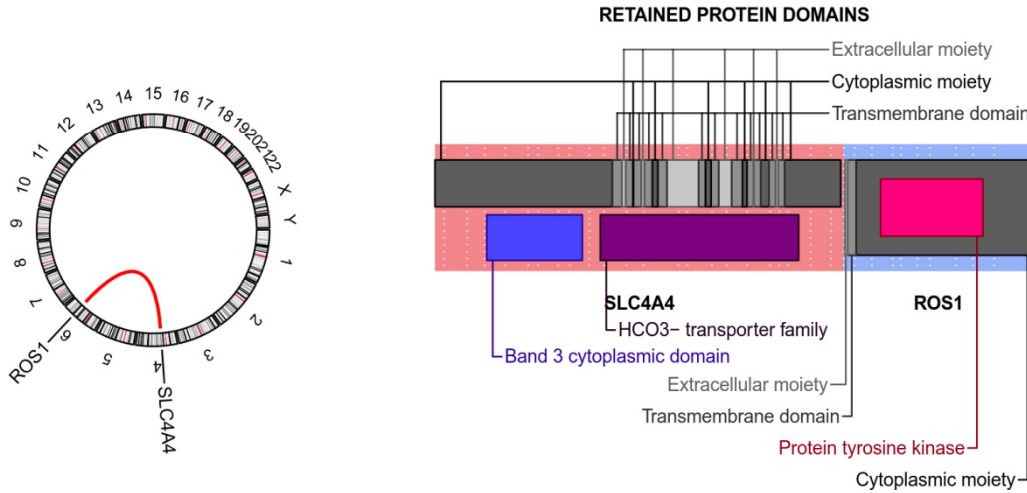
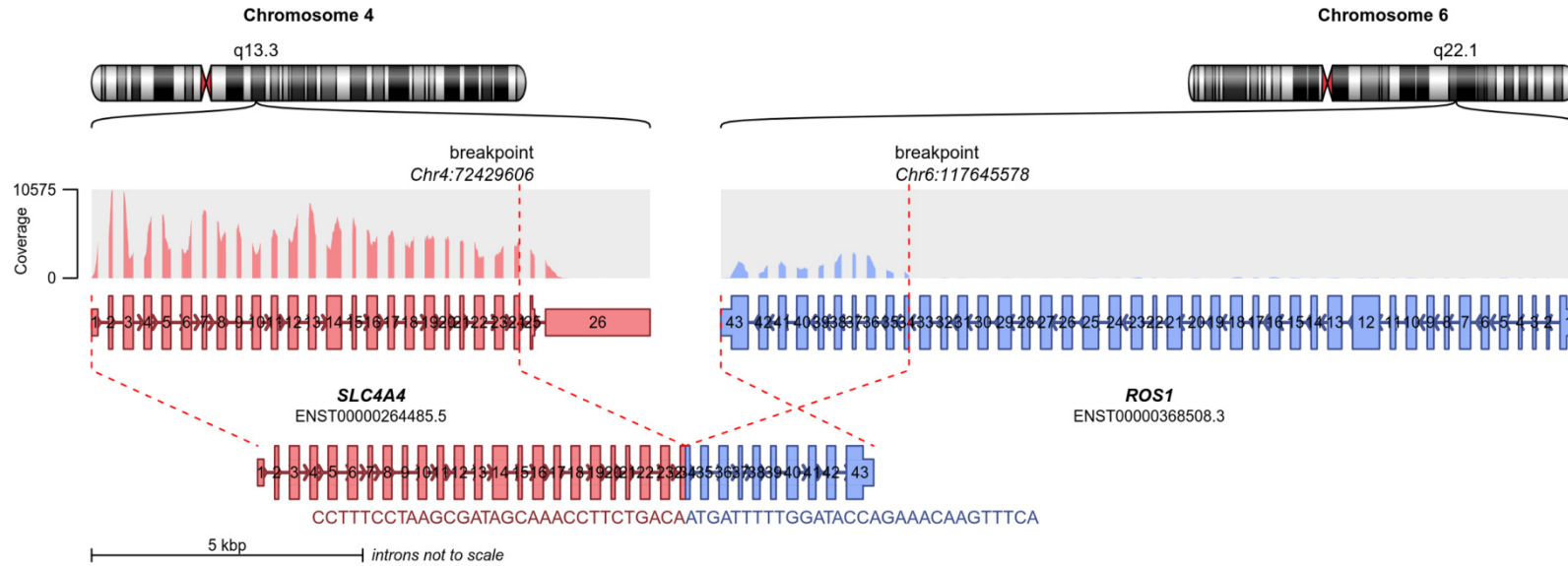


GAGTTTCTGGGCAGGACCGGTGGCAGTTGGTTGAAAGAATTCTTAGCCAAAGCCAAAGAAG



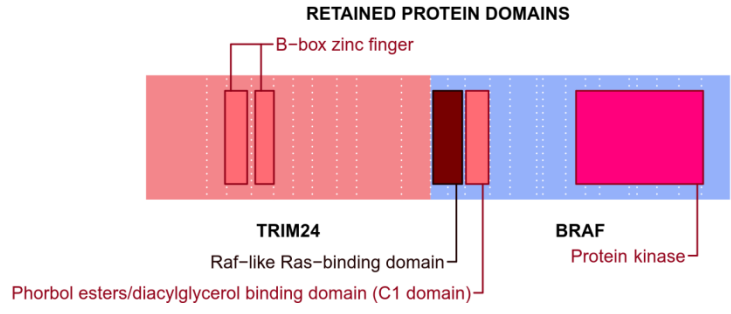
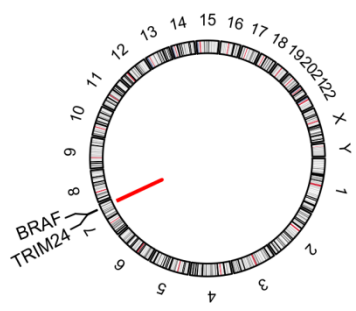
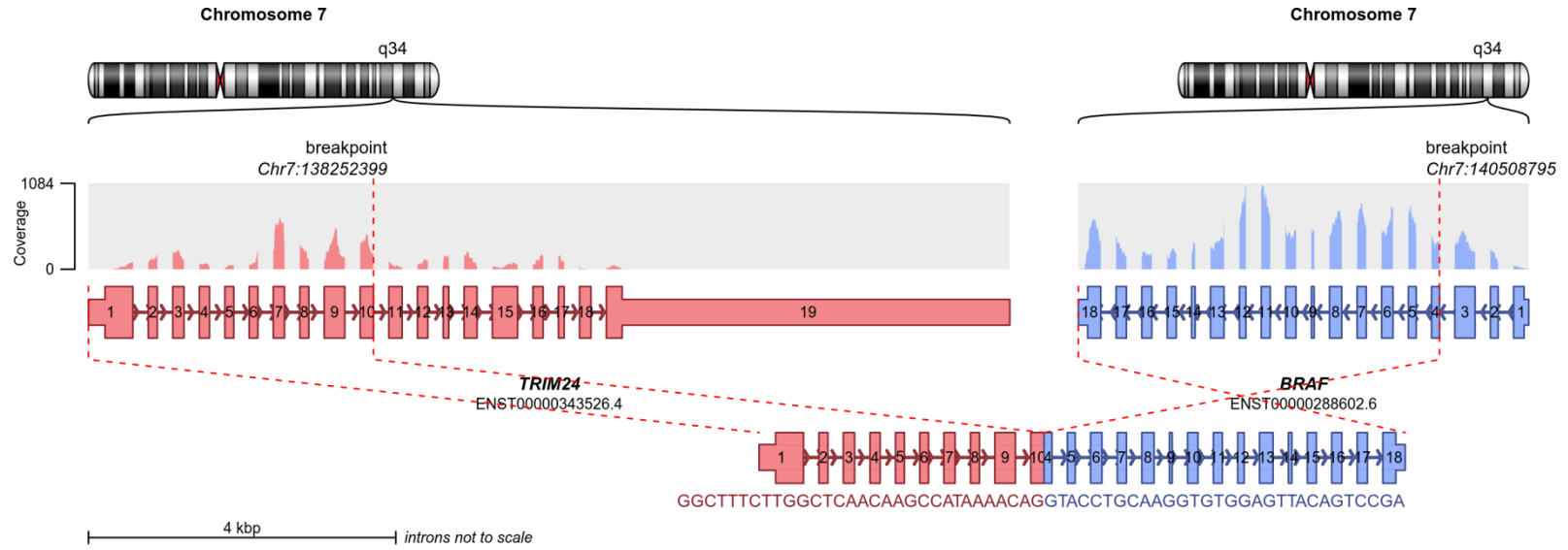
SUPPORTING READ COUNT
 Split reads in *ATP1B1* = 22
 Split reads in *PRKACA* = 71
 Discordant mates = 11

PCSI_0347 (EGAF00001844561, EGAF00001879130, EGAF00001879131)



SUPPORTING READ COUNT
 Split reads in *SLC4A4* = 70
 Split reads in *ROS1* = 69
 Discordant mates = 22

PCSI_0458 (EGAF00001844592, EGAF00001879192, EGAF00001879193)



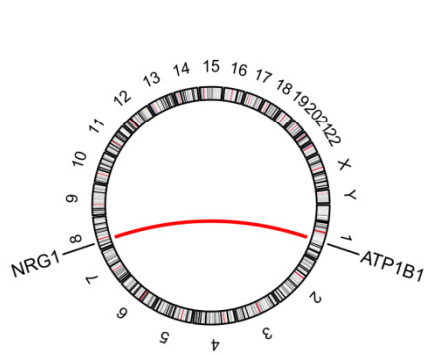
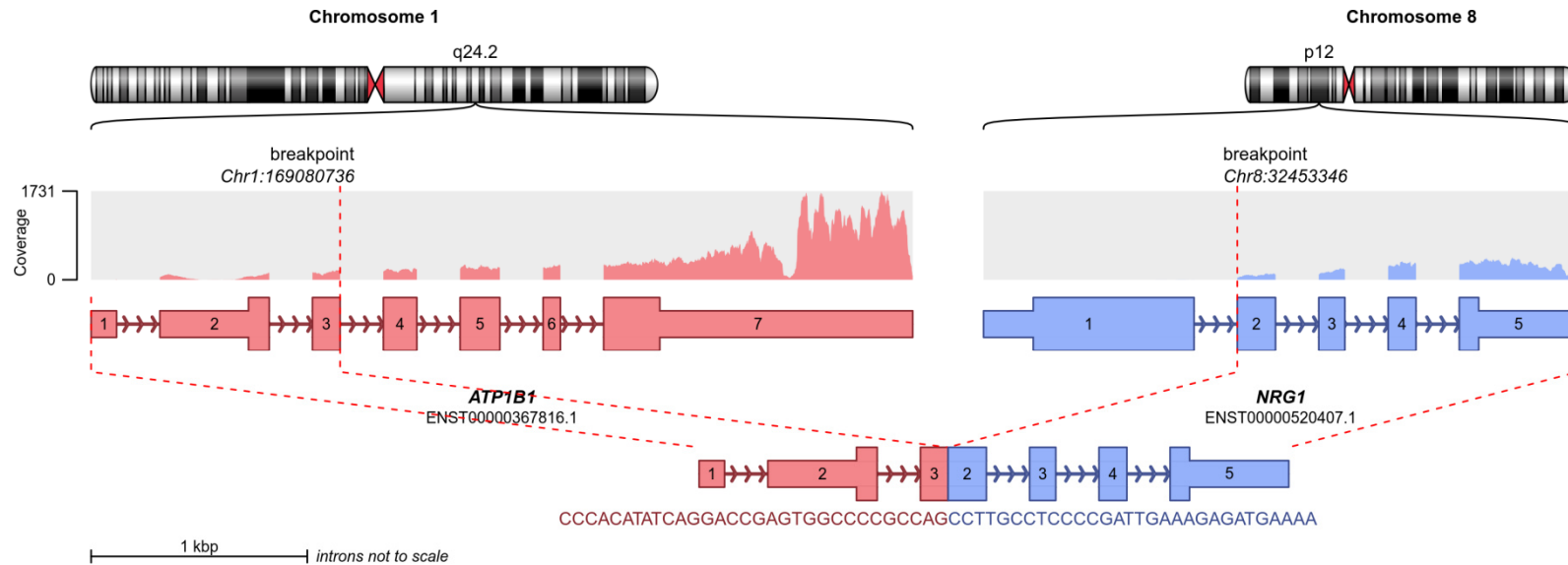
SUPPORTING READ COUNT

Split reads in *TRIM24* = 3

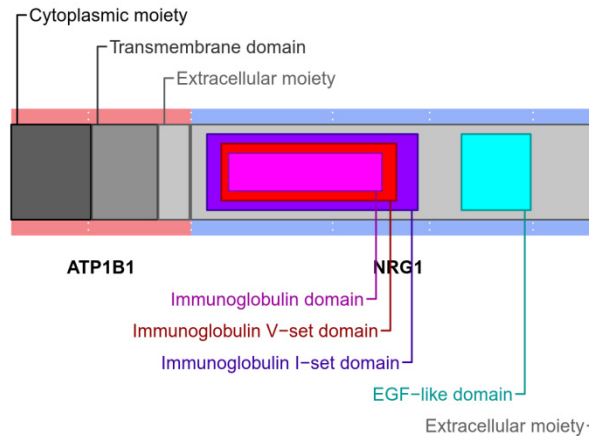
Split reads in *BRAF* = 3

Discordant mates = 1

TCGA-3A-A9I5 (163427ab-f1e7-4d63-91a0-66a0513ac795)



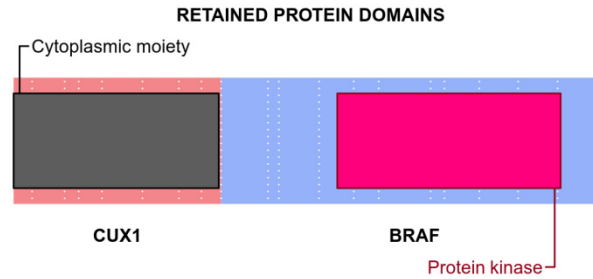
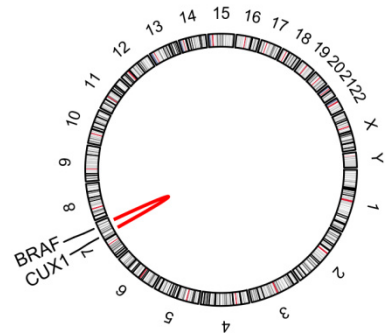
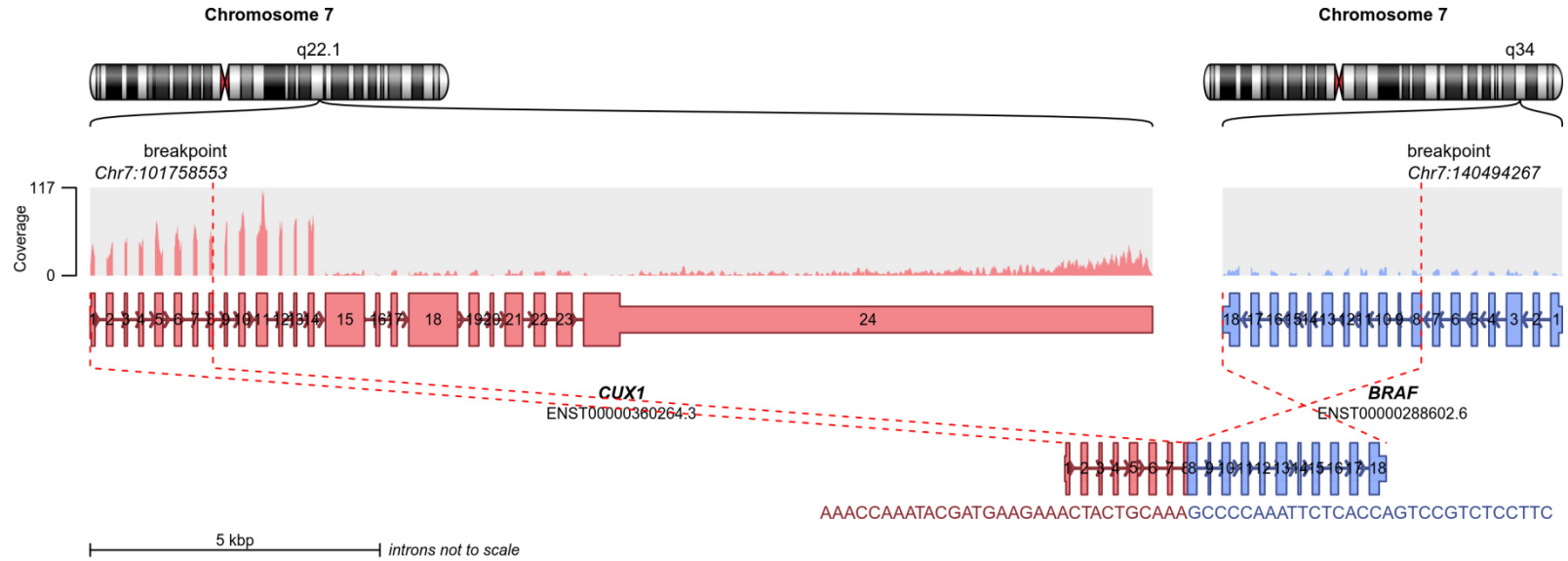
RETAINED PROTEIN DOMAINS



SUPPORTING READ COUNT

Split reads in *ATP1B1* = 9
 Split reads in *NRG1* = 15
 Discordant mates = 70

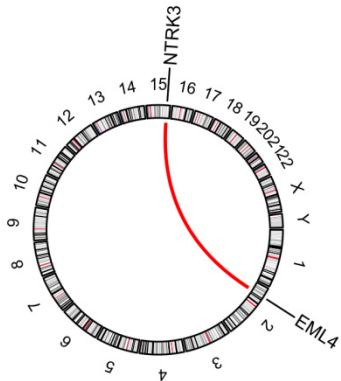
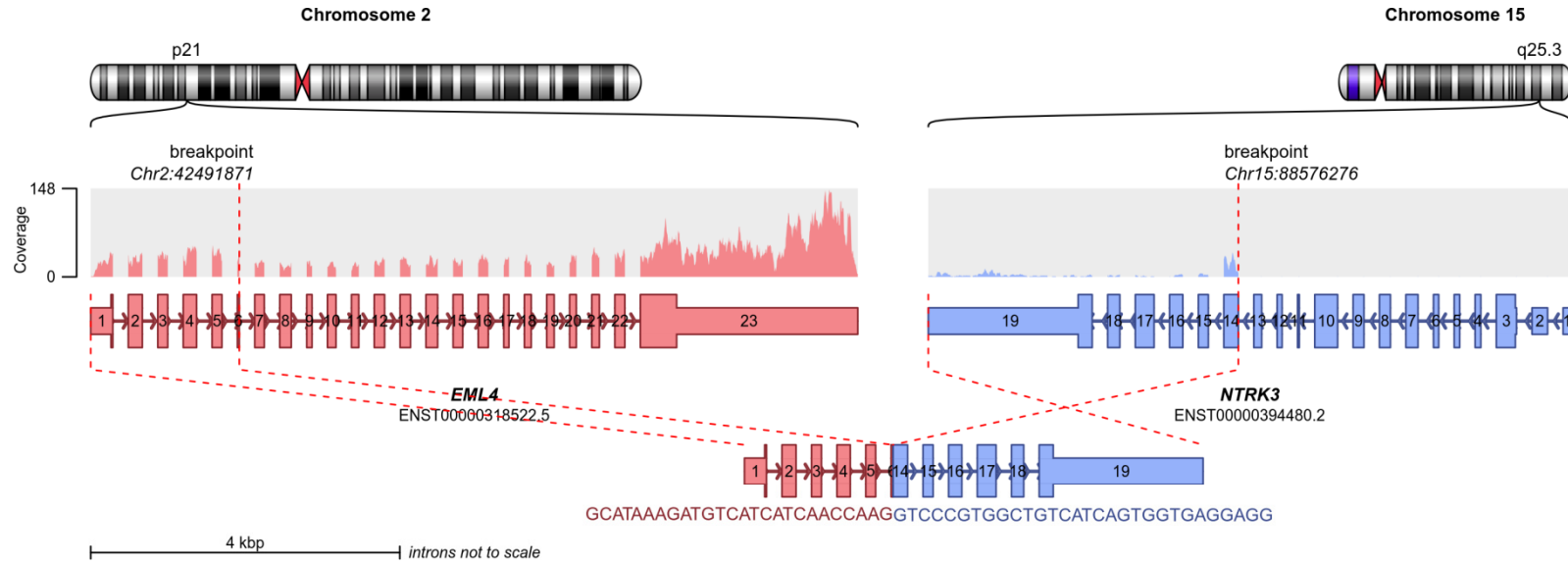
TCGA-F2-A44H (65d99cd1-7601-4dec-a9dd-e6d28880164d)



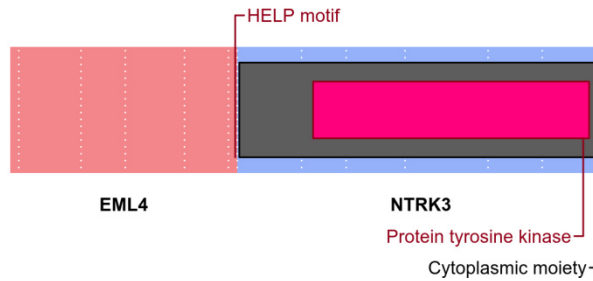
SUPPORTING READ COUNT

Split reads in *CUX1* = 0
 Split reads in *BRAF* = 2
 Discordant mates = 4

TCGA-FB-AAPP (43dc033e-ed48-486d-af91-7bef6ad03cdc)



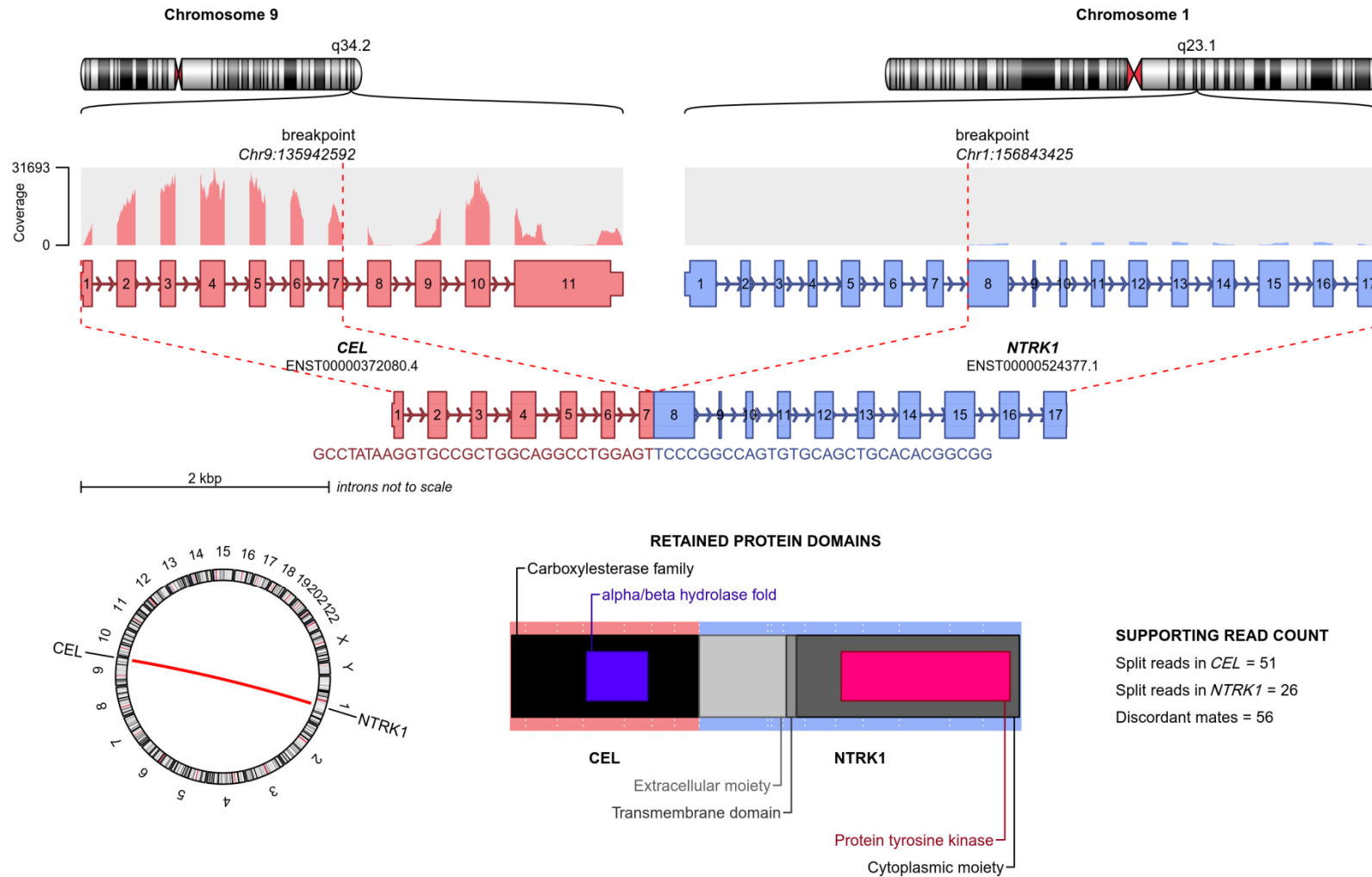
RETAINED PROTEIN DOMAINS



SUPPORTING READ COUNT

Split reads in *EML4* = 1
 Split reads in *NTRK3* = 3
 Discordant mates = 26

TCGA-HZ-7918 (8a2f438c-93cd-43c0-97e1-28176d0b93ef)



Supplemental Figure S6: Putative driver fusions identified by Arriba in pancreatic cancer samples.
 In 30 of 803 RNA-Seq samples from pancreatic cancer patients Arriba identified a potential oncogenic fusion.