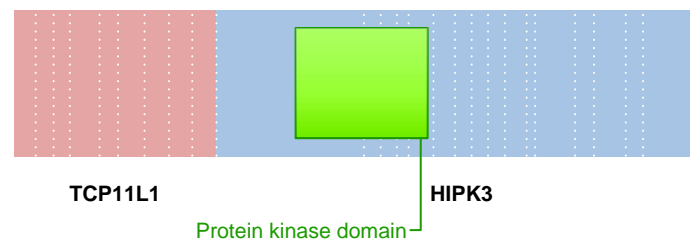


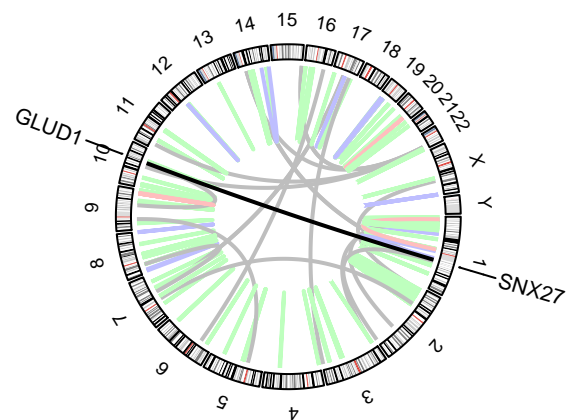
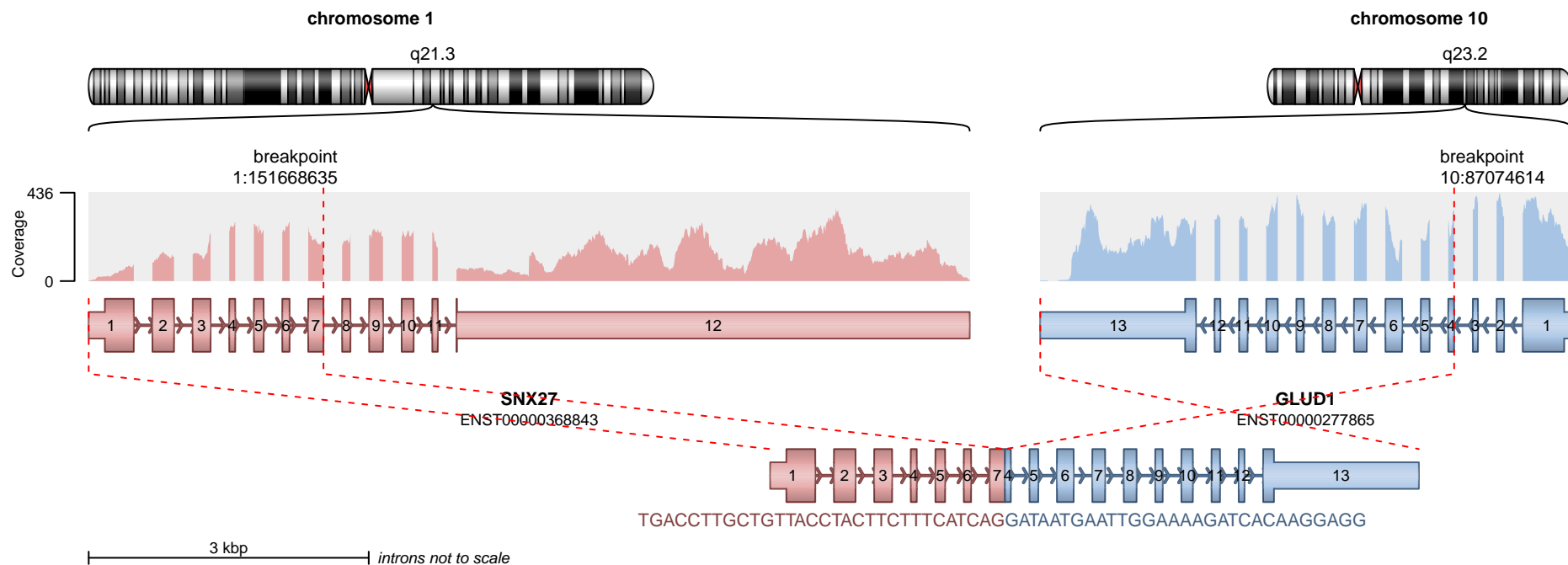
RETAINED PROTEIN DOMAINS in-frame fusion



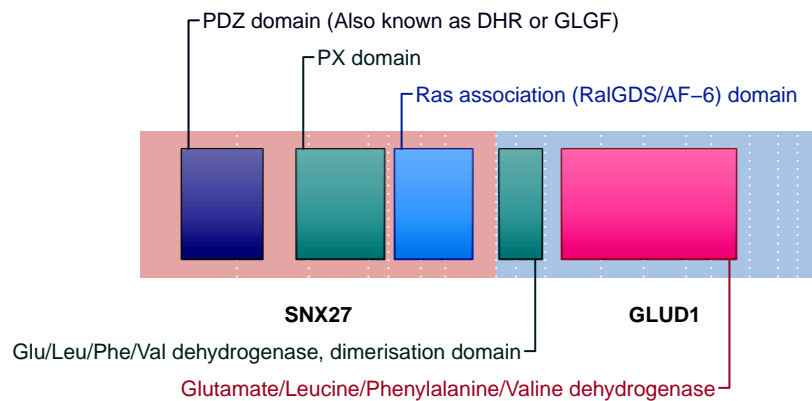
SUPPORTING READ COUNT

Split reads = 8
Discordant mates = 0

translocation
duplication
deletion
inversion



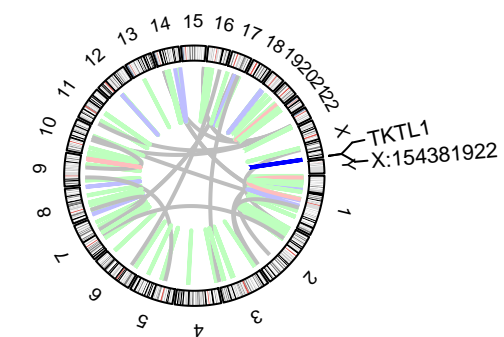
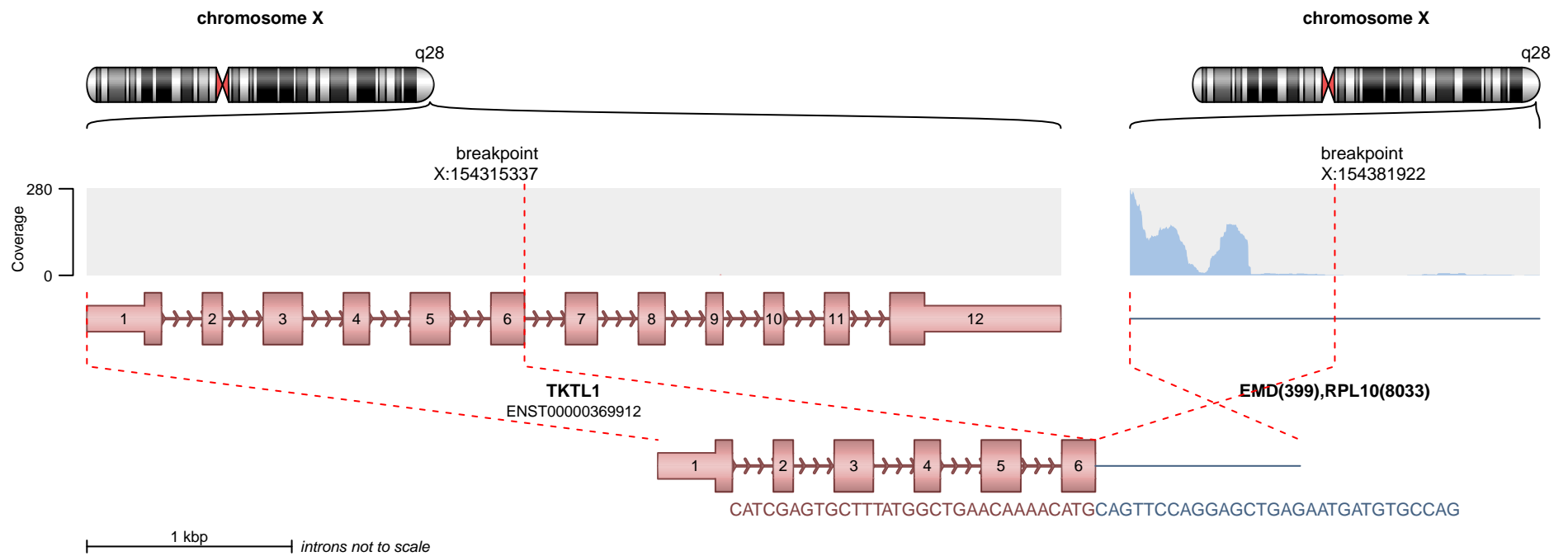
RETAINED PROTEIN DOMAINS in-frame fusion



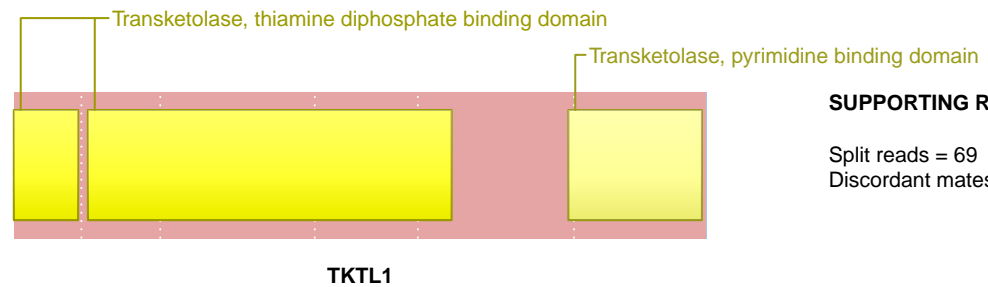
SUPPORTING READ COUNT

Split reads = 79
Discordant mates = 13

translocation deletion
duplication inversion



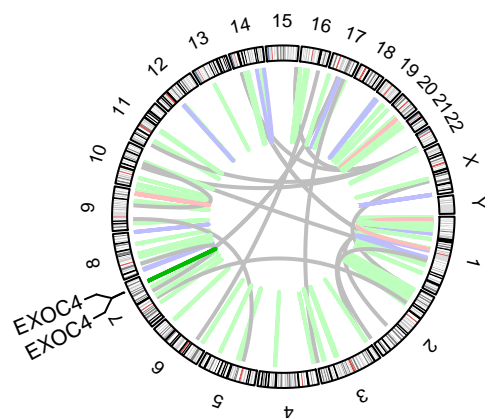
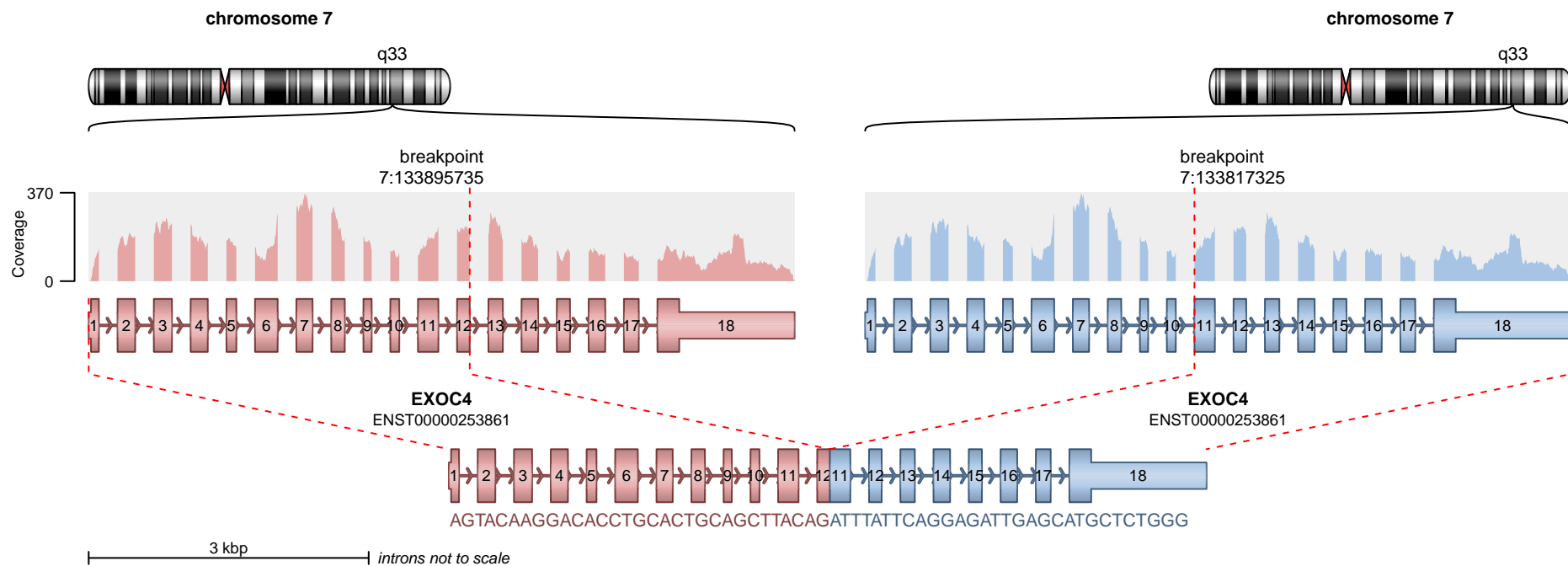
RETAINED PROTEIN DOMAINS out-of-frame fusion



SUPPORTING READ COUNT

Split reads = 69
Discordant mates = 8

translocation deletion
duplication inversion



translocation
duplication
deletion
inversion

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads = 72
Discordant mates = 2