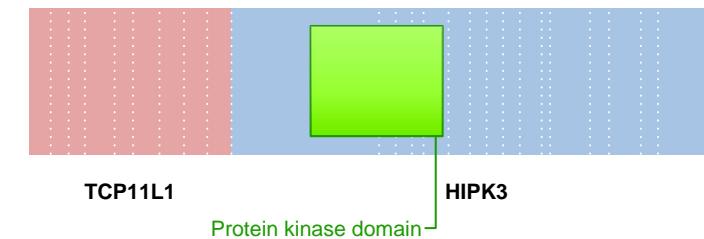
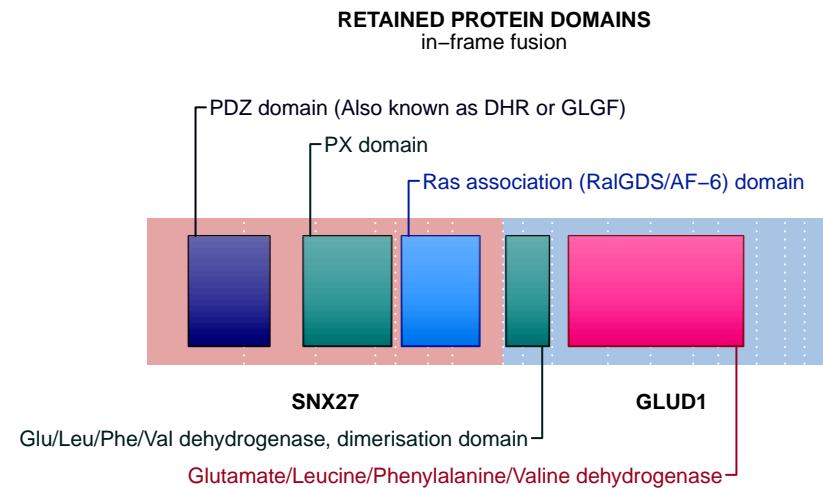
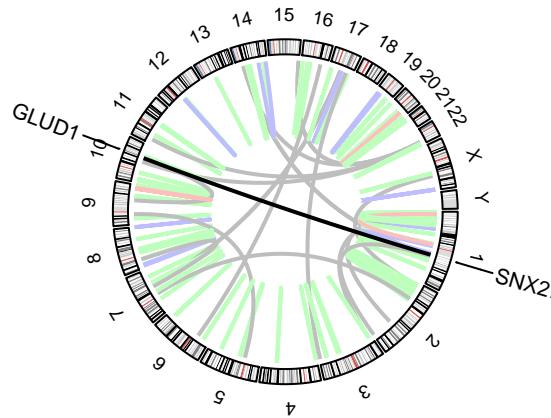
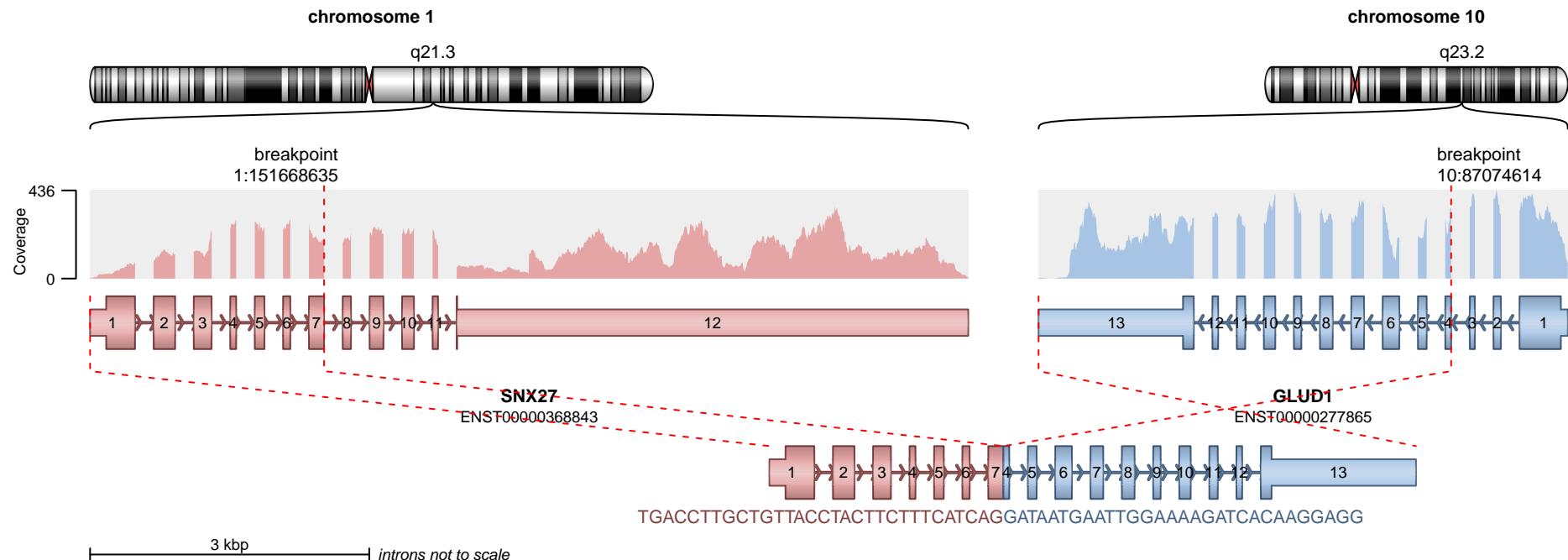


#### RETAINED PROTEIN DOMAINS in-frame fusion



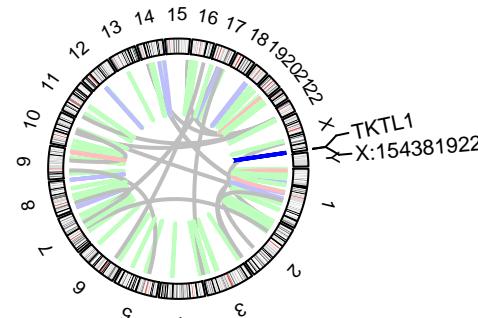
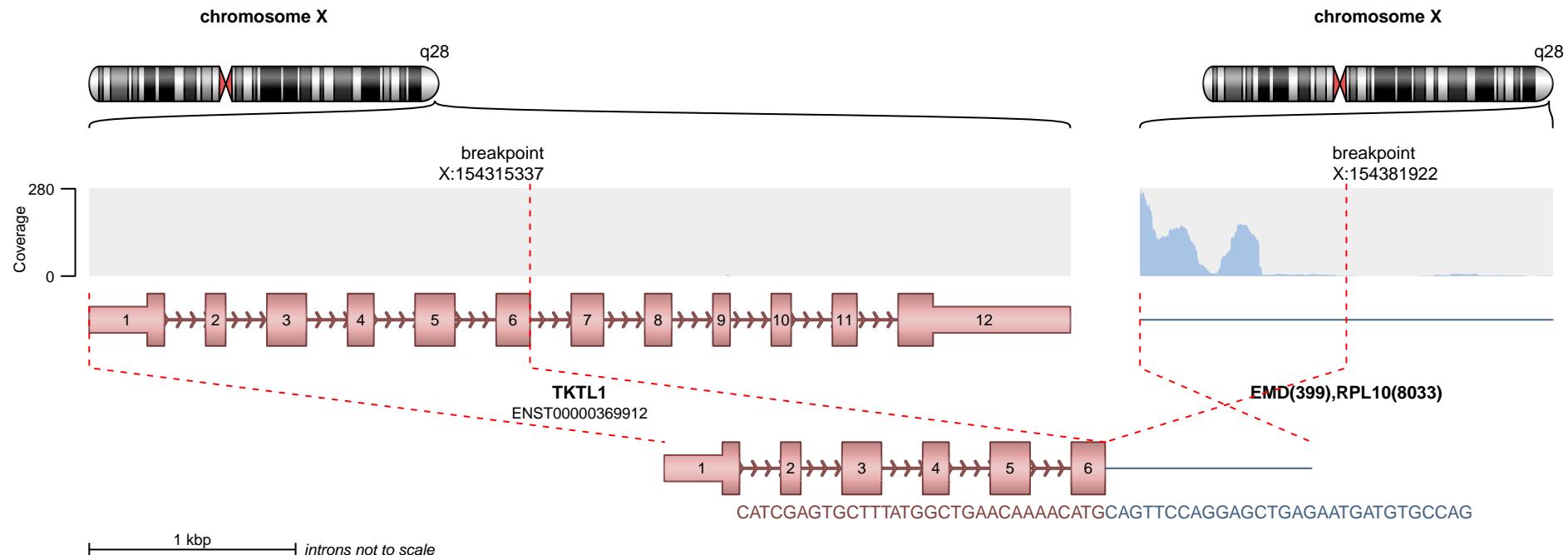
— translocation    — deletion  
— duplication    — inversion



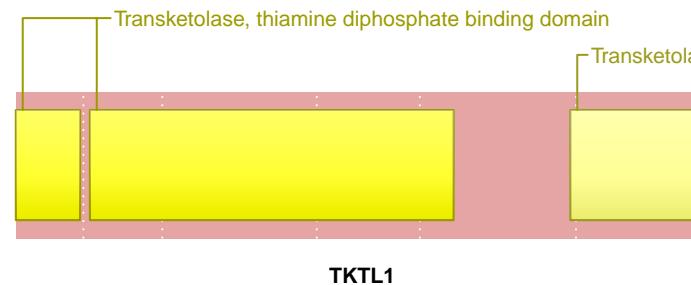
#### SUPPORTING READ COUNT

Split reads = 79  
Discordant mates = 13

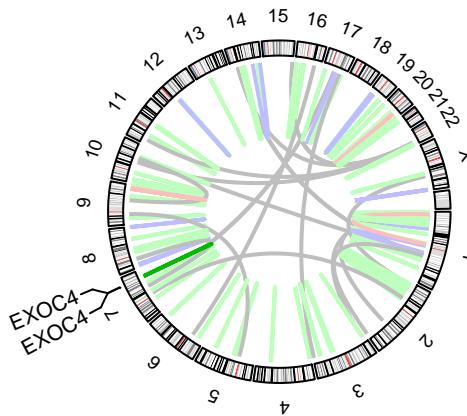
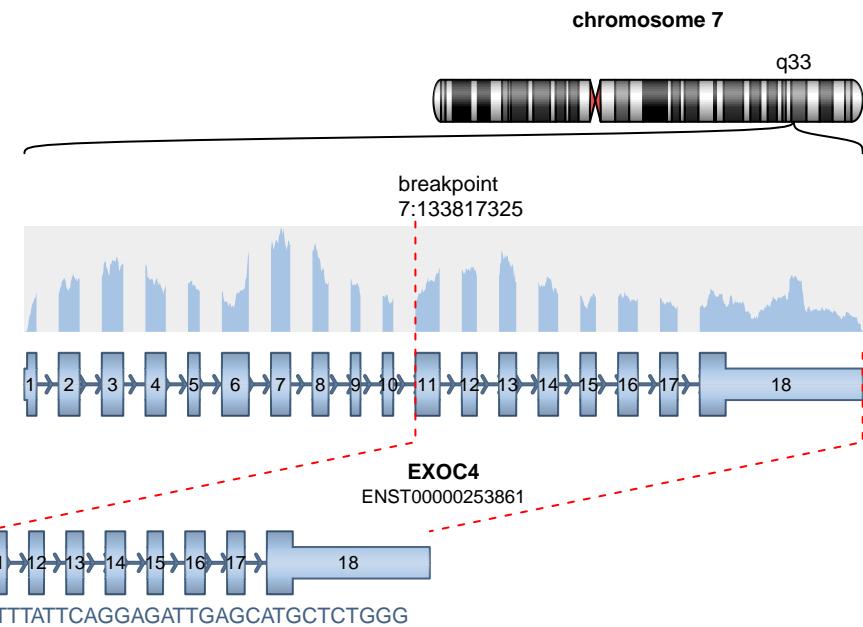
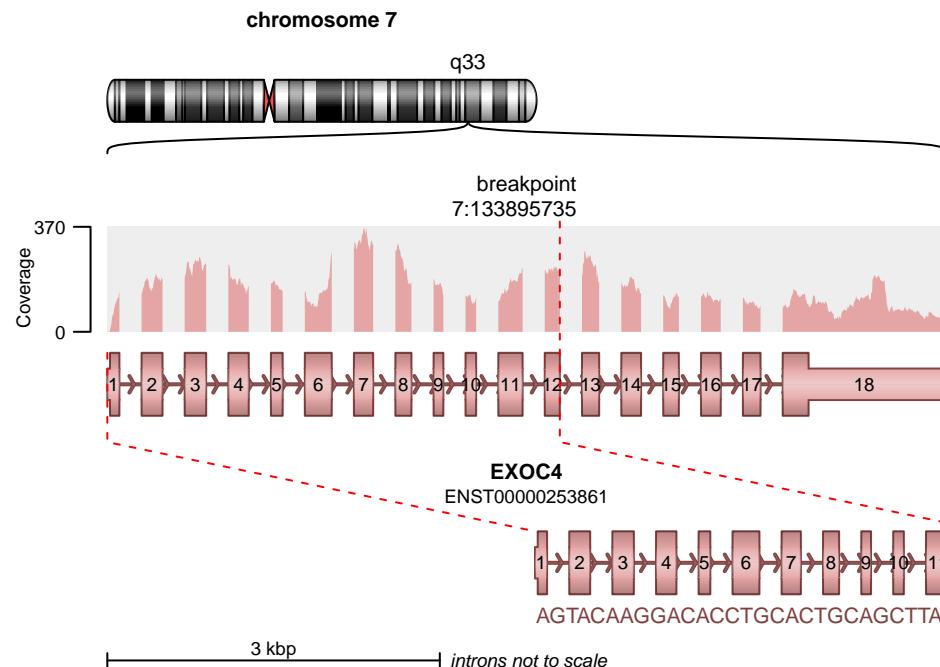
— translocation — deletion  
— duplication — inversion



### RETAINED PROTEIN DOMAINS out-of-frame fusion



— translocation — deletion  
— duplication — inversion



No protein domains retained in fusion.

#### SUPPORTING READ COUNT

Split reads = 72  
Discordant mates = 2

— translocation — deletion  
— duplication — inversion