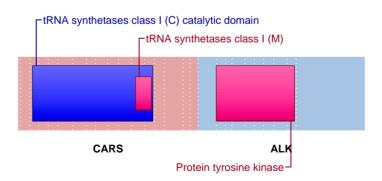


introns not to scale

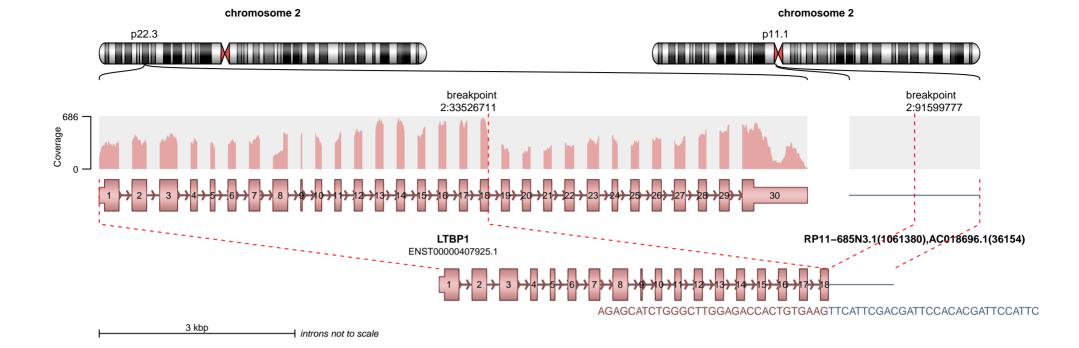
RETAINED PROTEIN DOMAINS

in-frame fusion

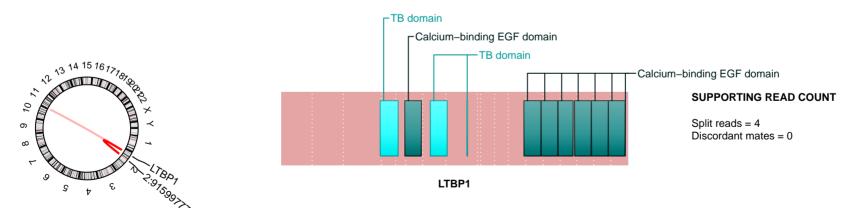


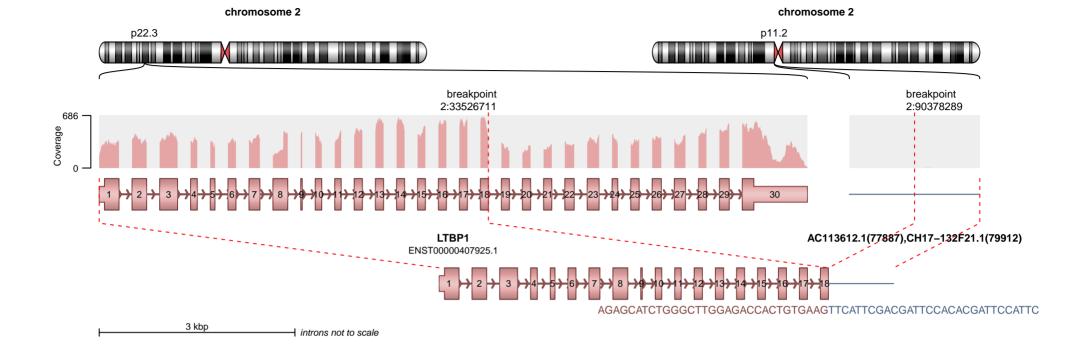
SUPPORTING READ COUNT

Split reads = 13 Discordant mates = 3











out-of-frame fusion

