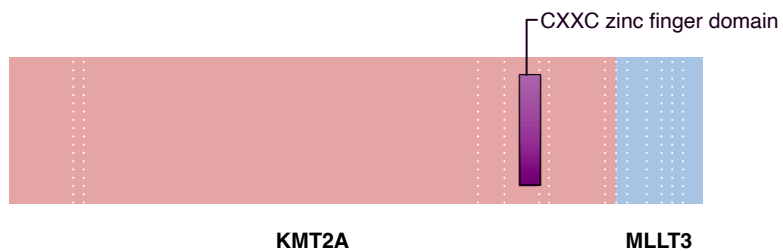


### RETAINED PROTEIN DOMAINS in-frame fusion



### SUPPORTING READ COUNT

Split reads in KMT2A = 2

Split reads in MLLT3 = 1

Discordant mates = 3