Ligated rearrangements will generate novel anomalous pairs, 1-read pairs and junction reads
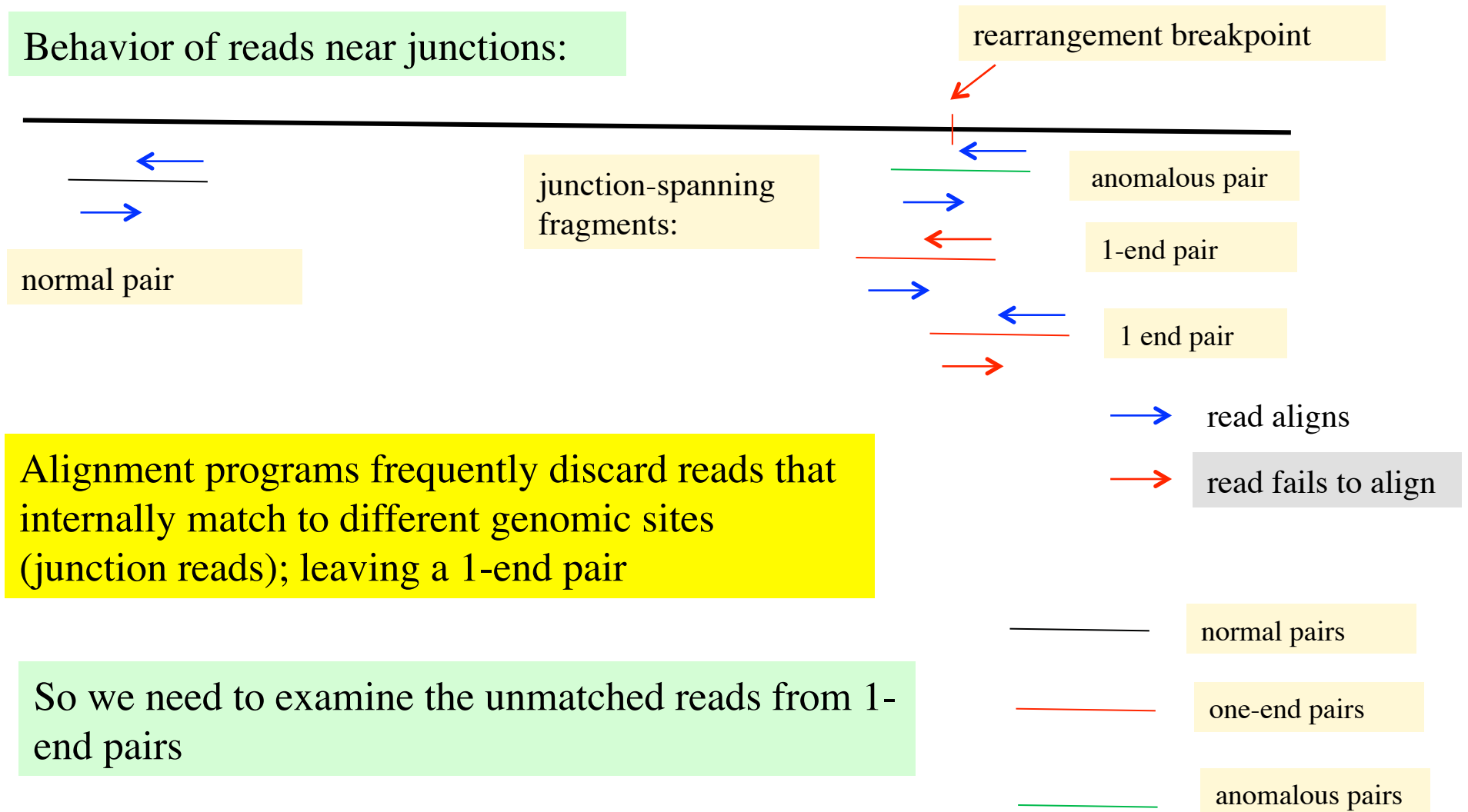
Behavior of reads near junctions:

rearrangement breakpoint

junction-spanning fragments:

anomalous pair

1-end pair

normal pair

1 end pair

read aligns

read fails to align

Alignment programs frequently discard reads that internally match to different genomic sites (junction reads); leaving a 1-end pair

normal pairs

one-end pairs

So we need to examine the unmatched reads from 1-end pairs

anomalous pairs