TADbit

Hi-C contact matrices: filtering

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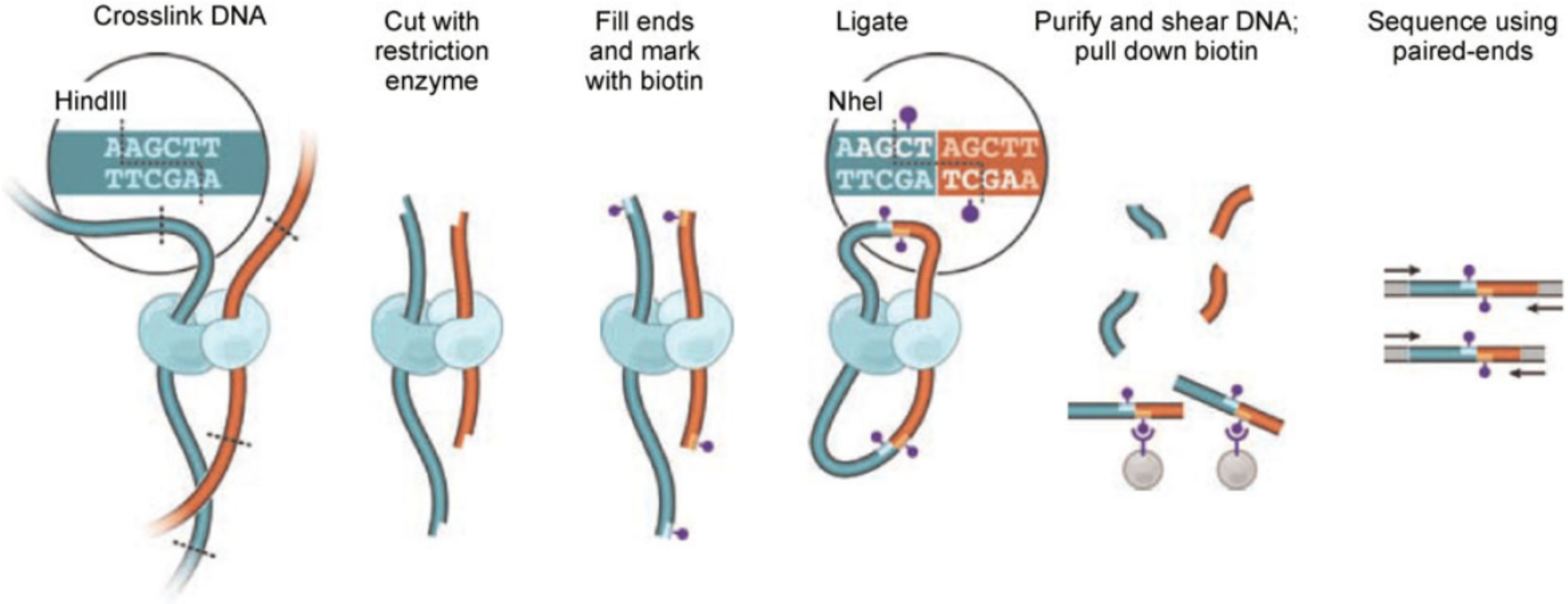
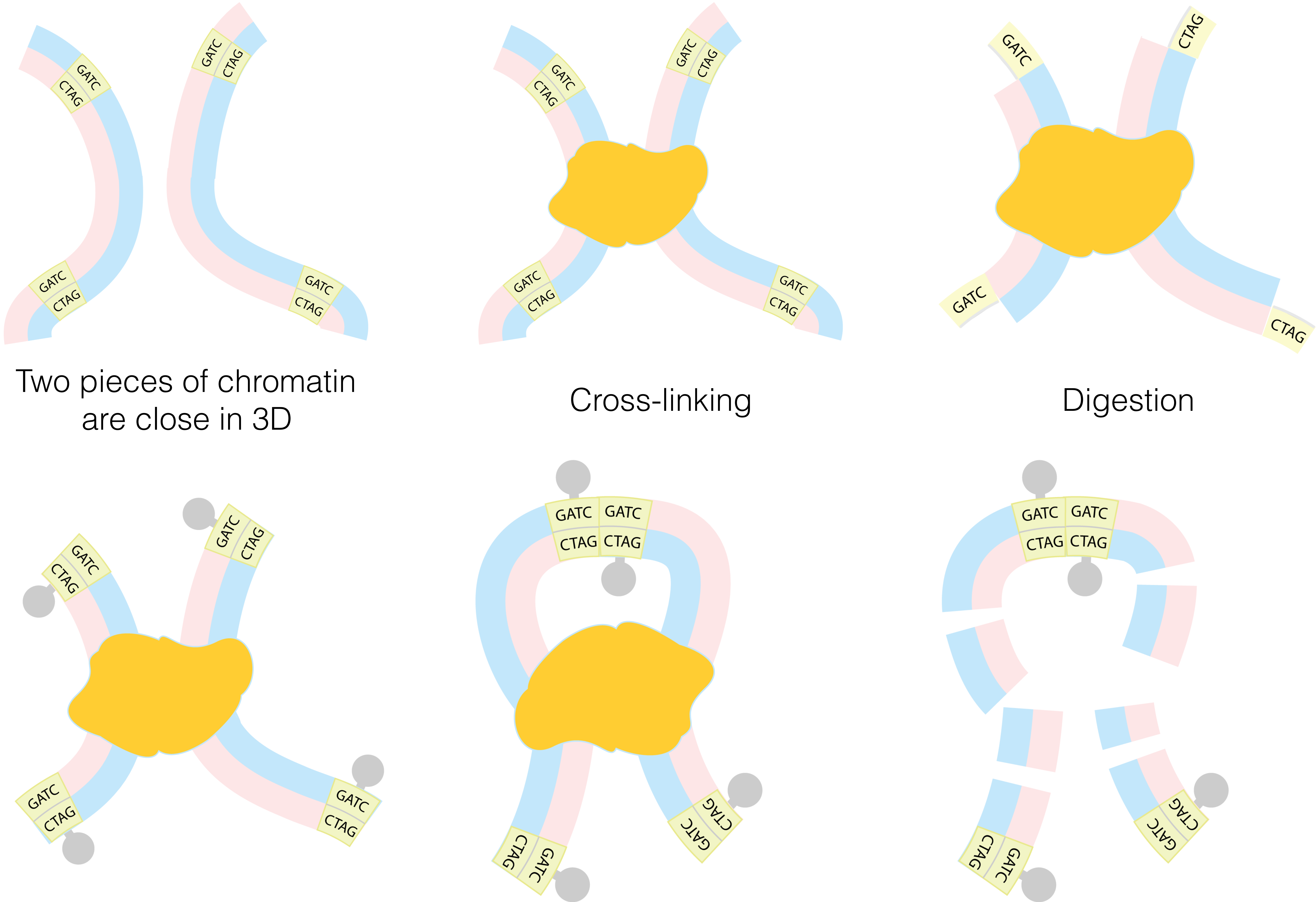
Hi-C experiment


Crosslink DNA
HindIII
AAGCTT
TTCGAA
Cut with restriction enzyme
Fill ends and mark with biotin
Ligate
NheI
AAGCT AGCTT
TTCGA TCGAA
Purify and shear DNA; pull down biotin
Sequence using paired-ends

Lieberman-Aiden, E. … Dekker, J. (2009). Science, 326(5950),

Hi-C experiment



Two pieces of chromatin are close in 3D

Cross-linking

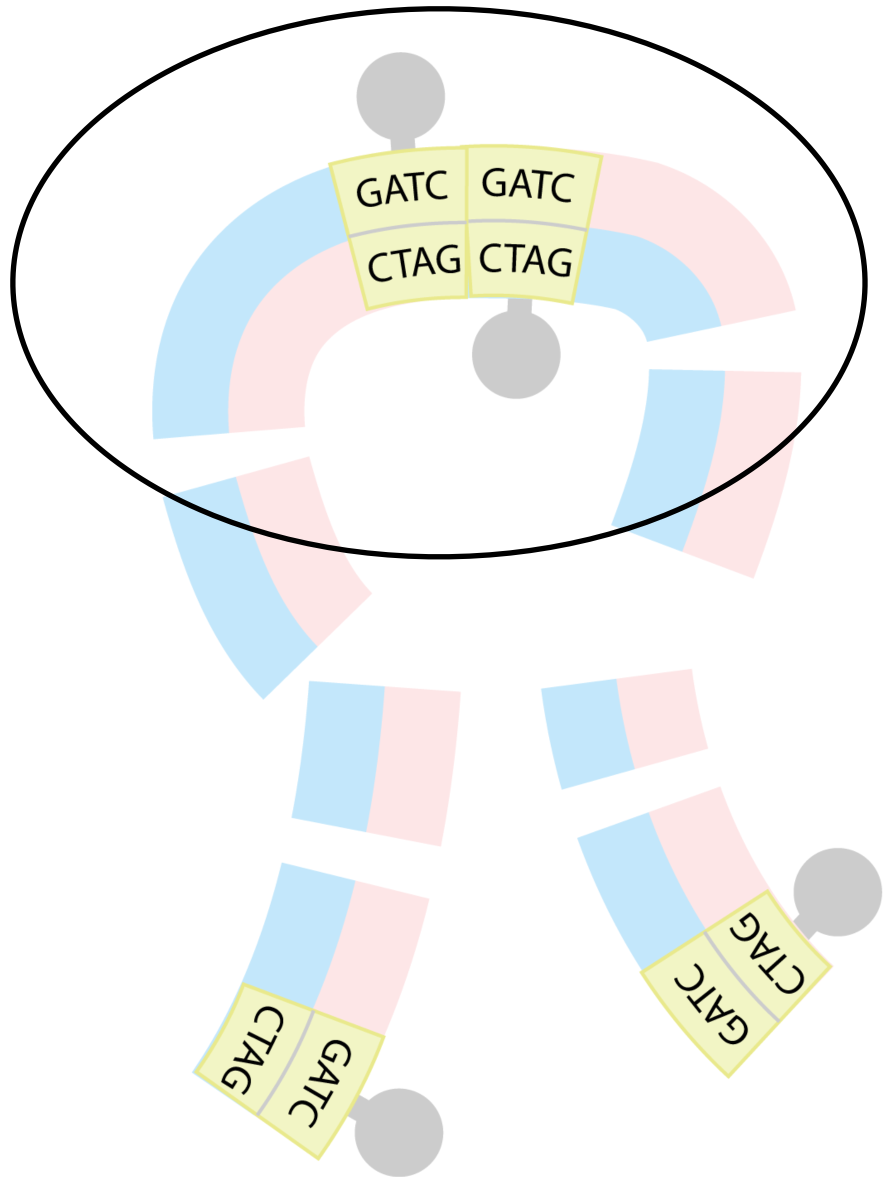
Digestion

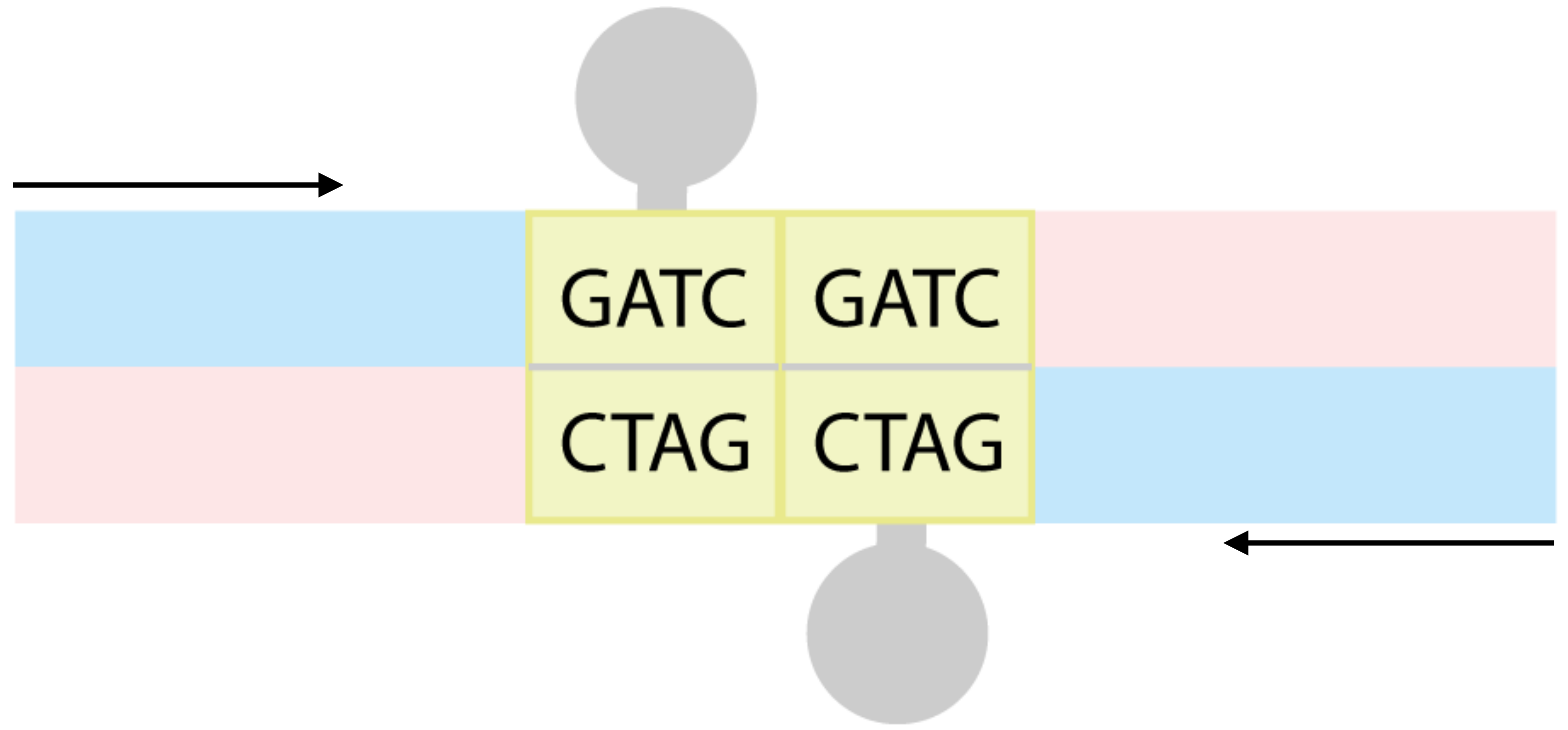
Biotinylation

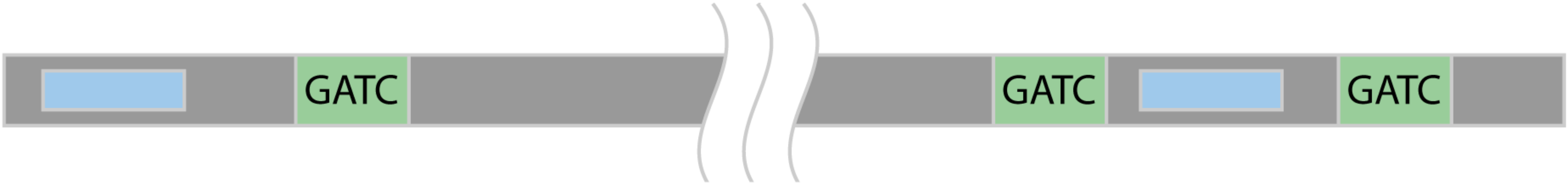
Ligation

Shearing

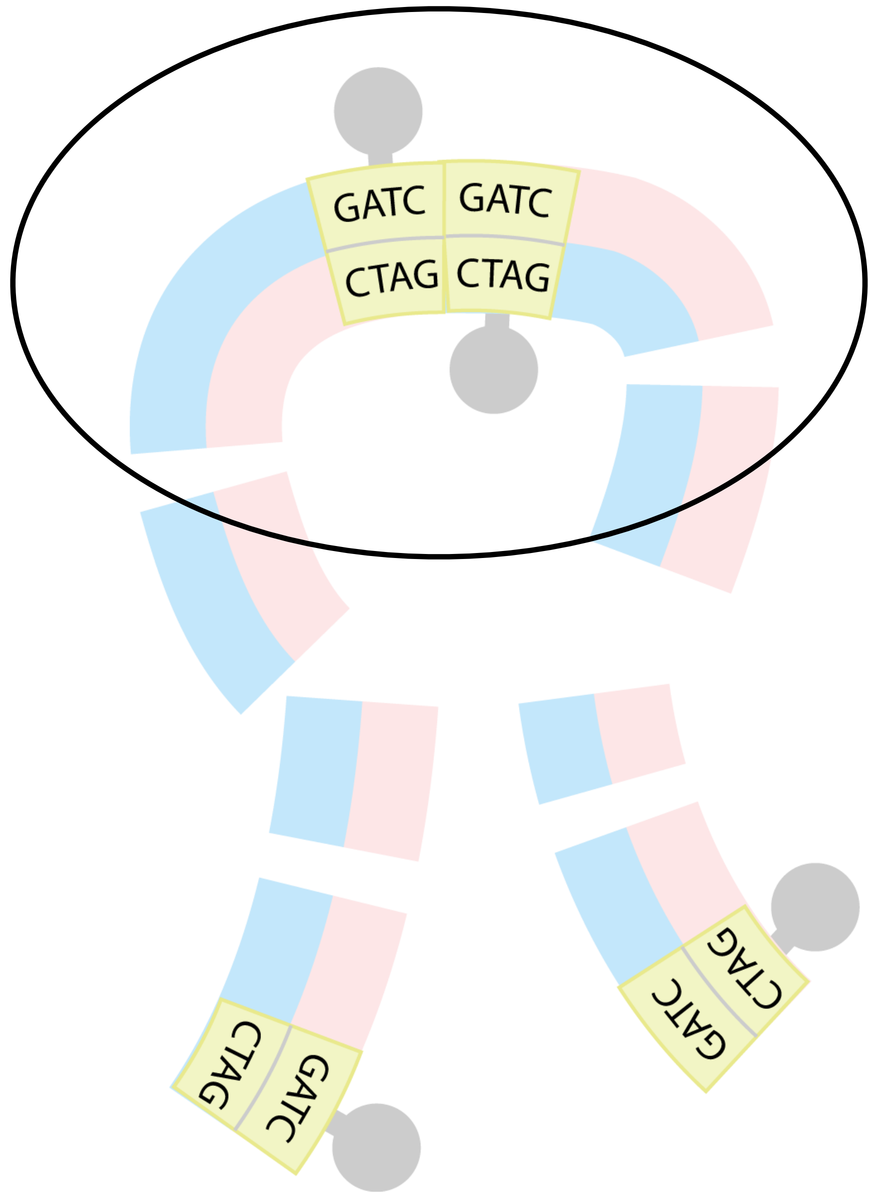
Valid pair

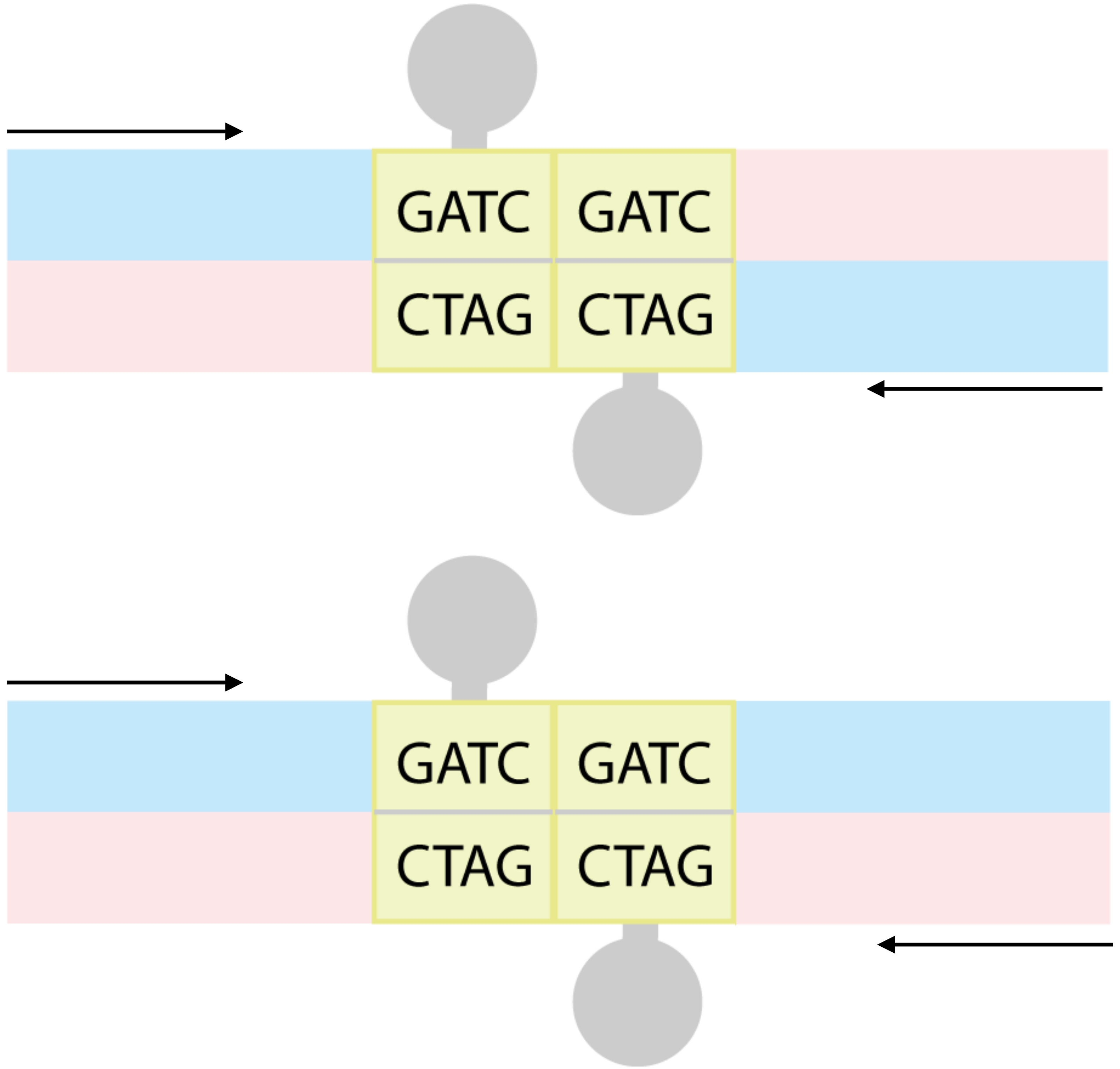

GATC
GATC
CTAG
CTAG
CTAG
GATC
CTAG
GATC

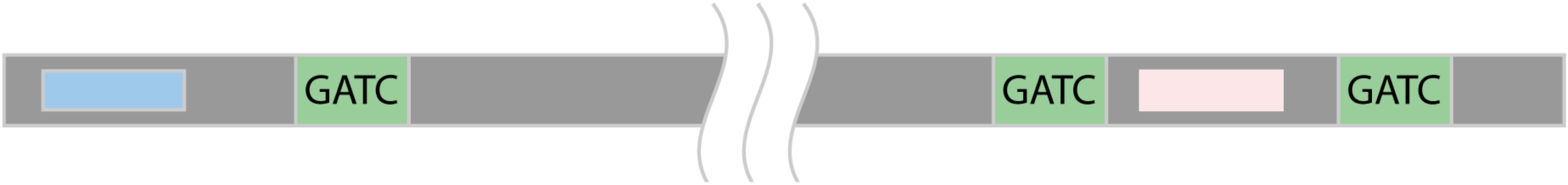

GATC
GATC
CTAG
CTAG


GATC
GATC
GATC

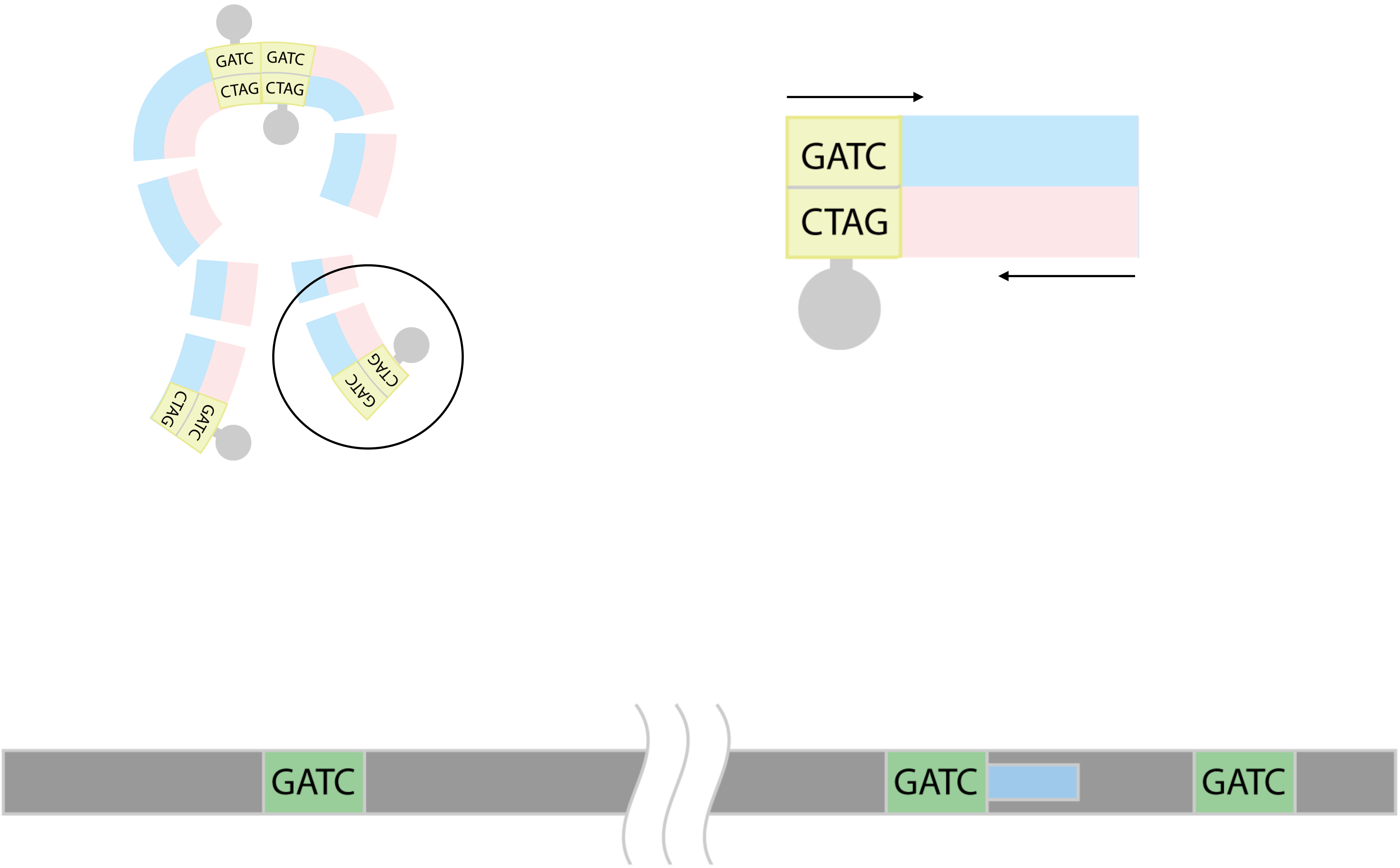
Valid pair (~36% of the mapped read-pairs)



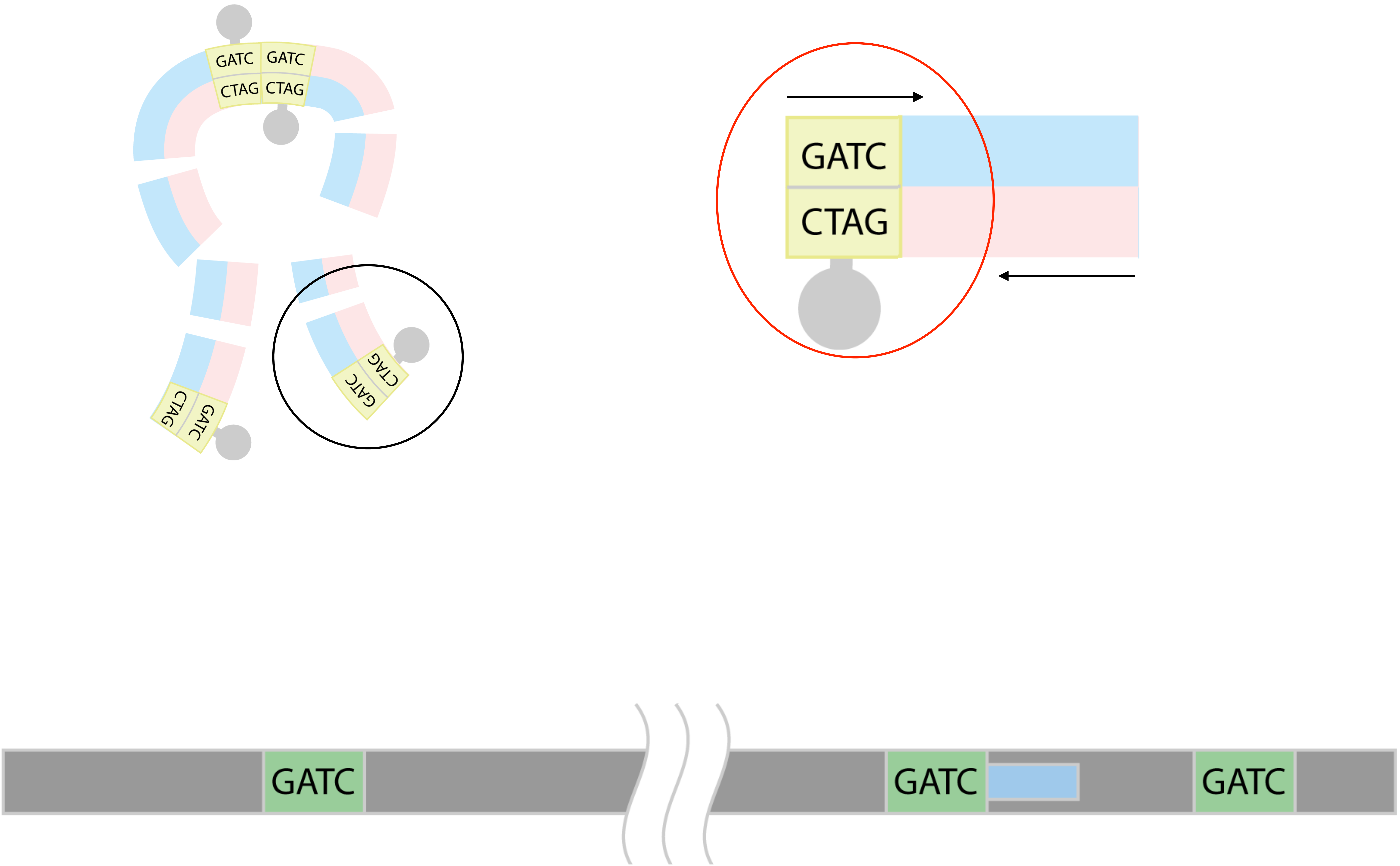




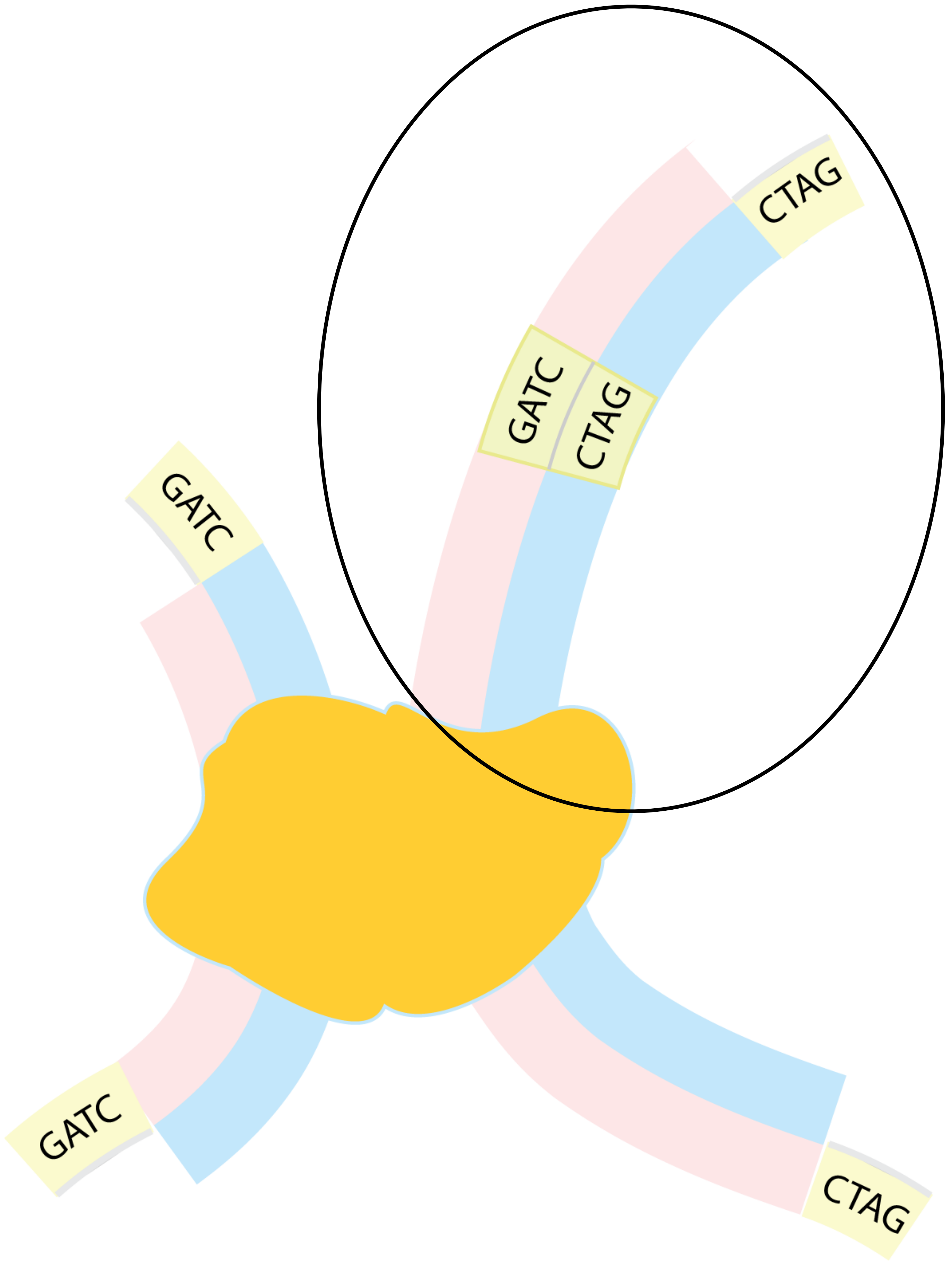
Dangling-end (~15%)

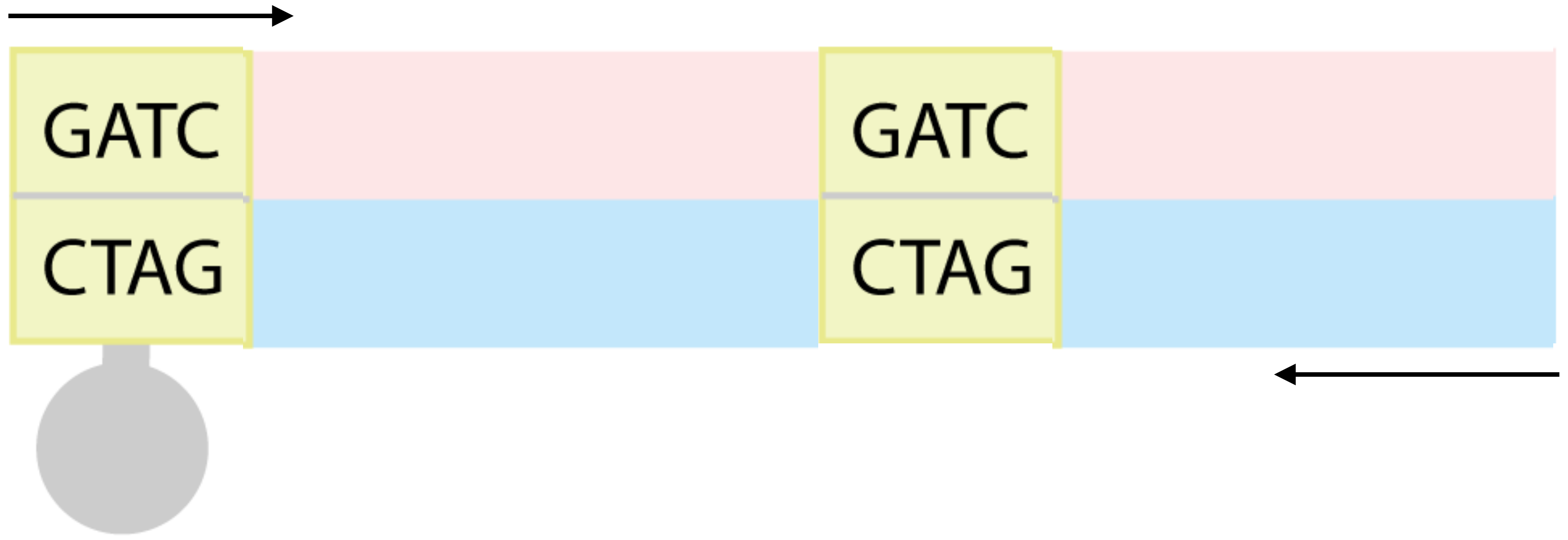


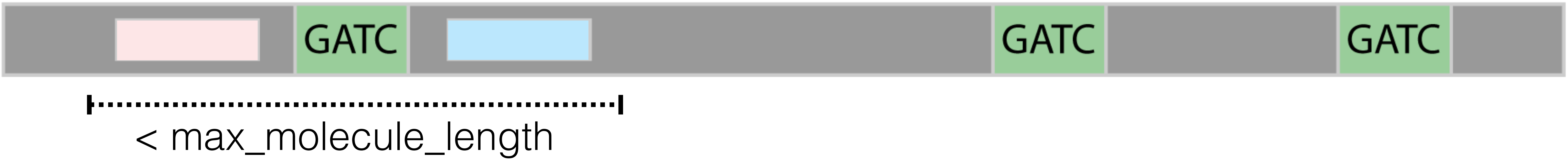
Dangling-end (~15%)



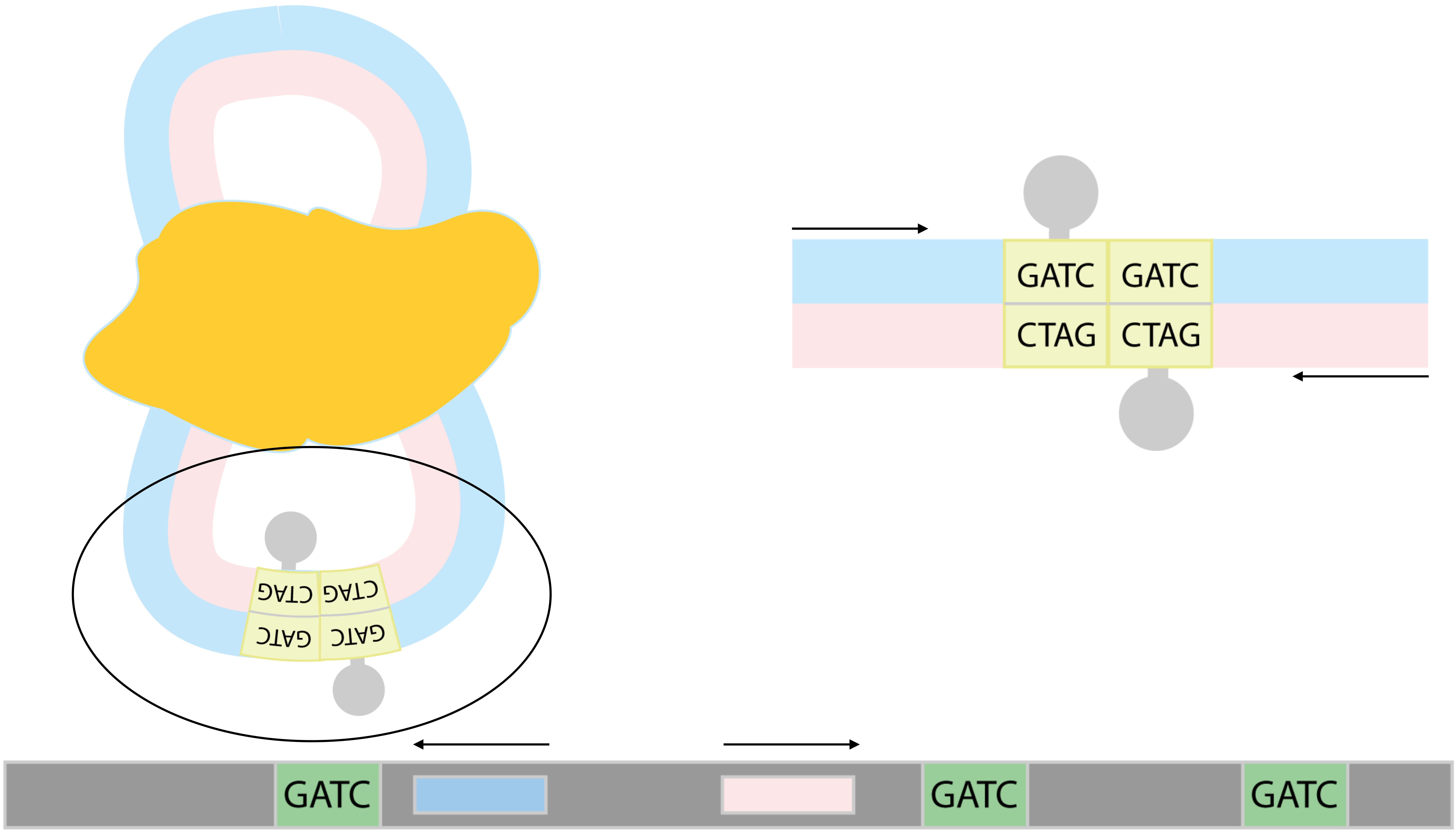
Extra dangling-end (~5%)



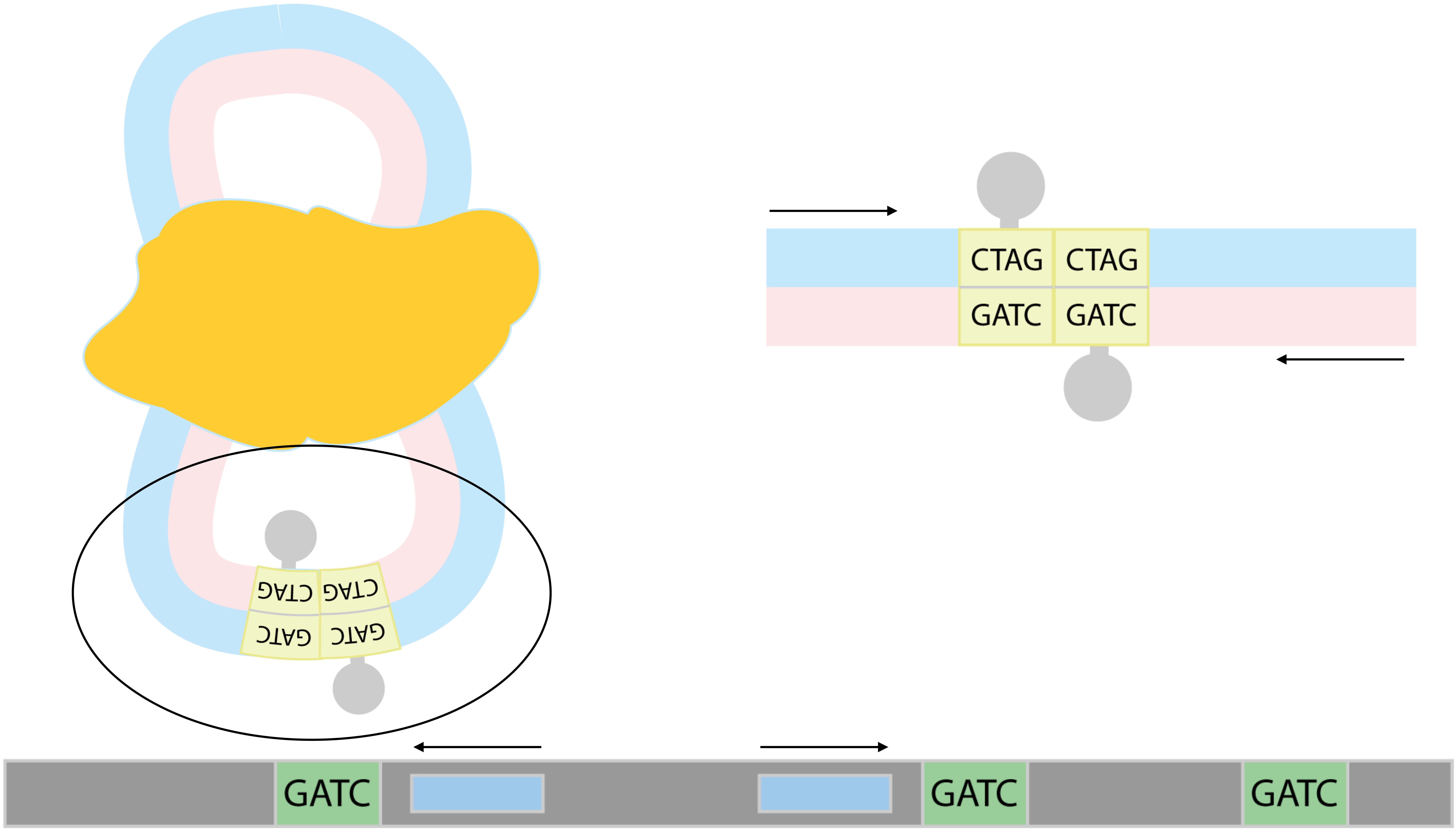




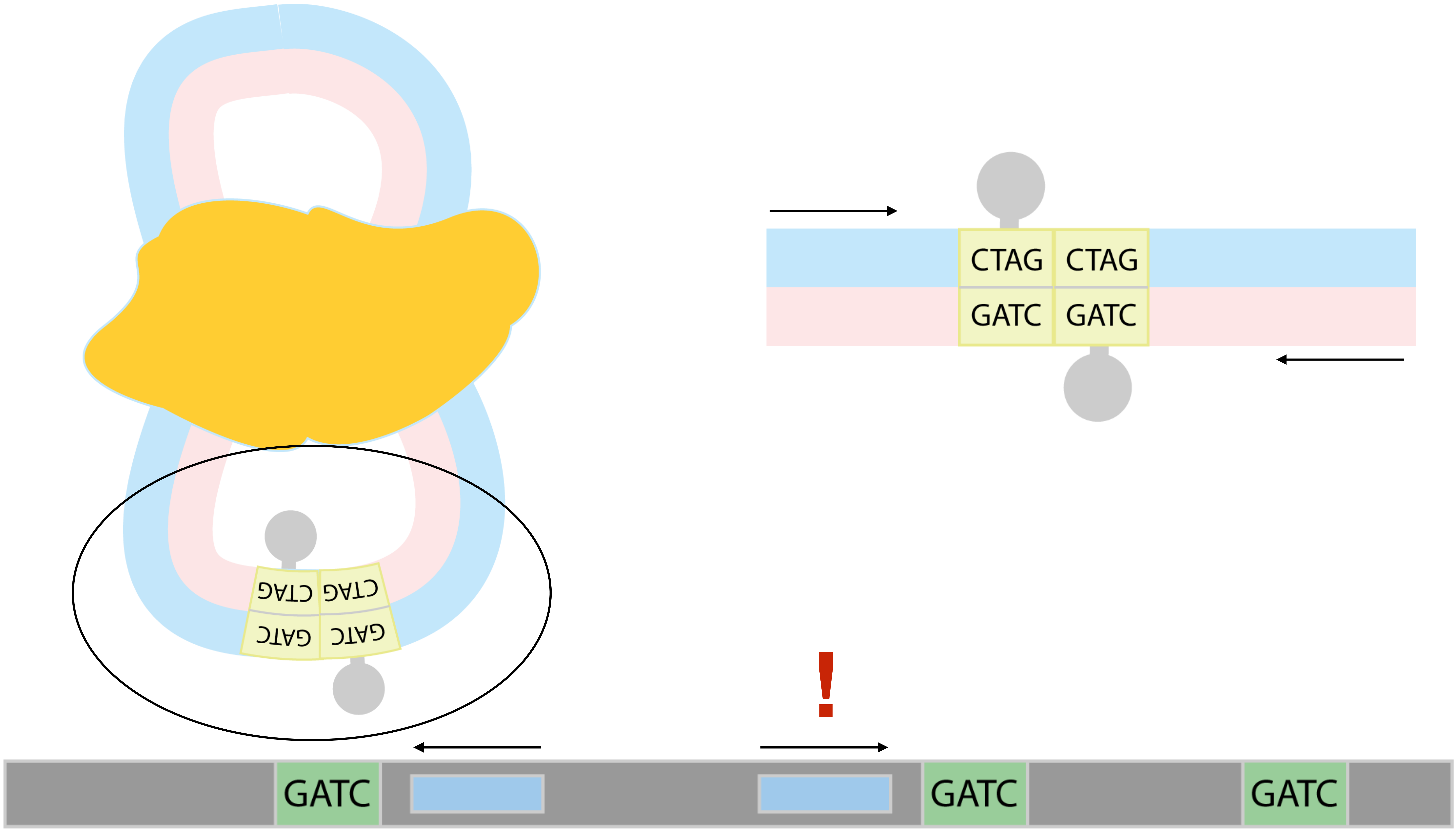
Self-circle (~10%)



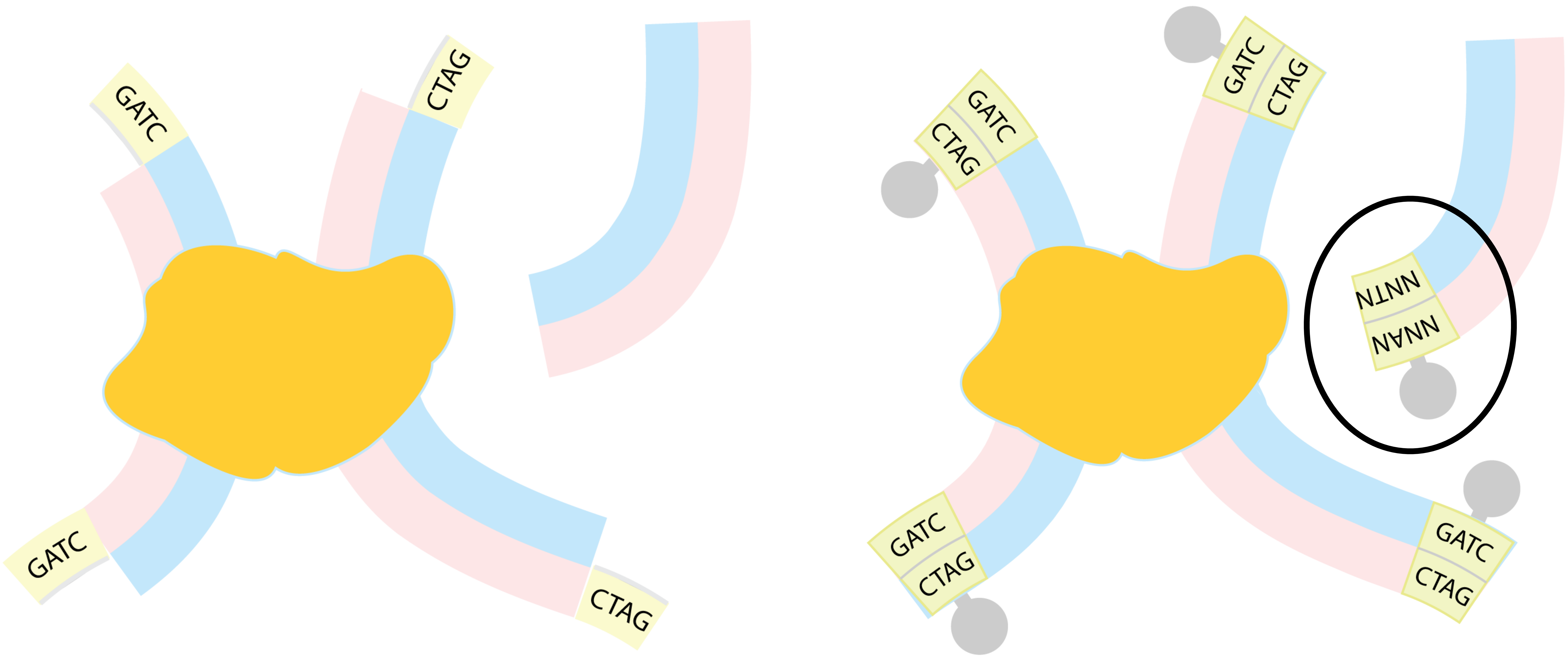
Error (<2%)

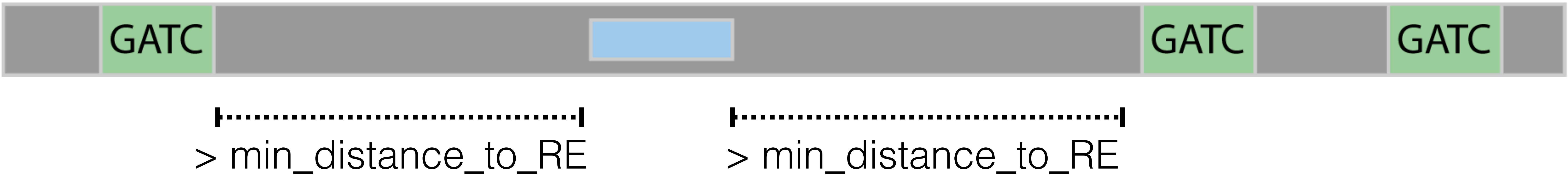


Error (<2%)



Random break (~20%)

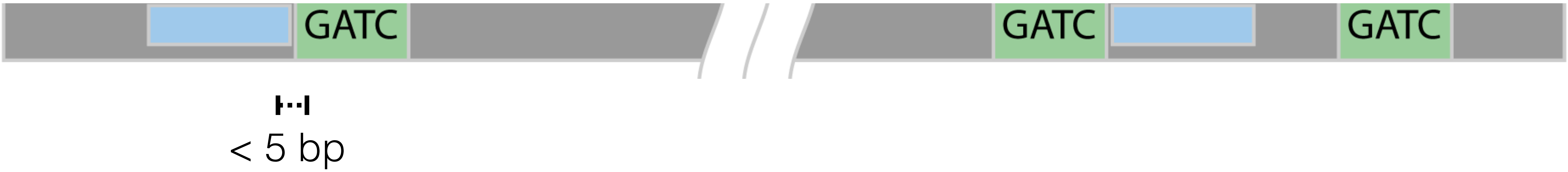




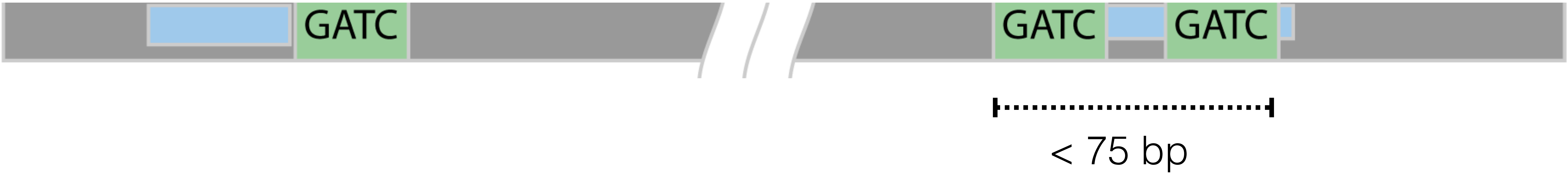
> min_distance_to_RE

> min_distance_to_RE

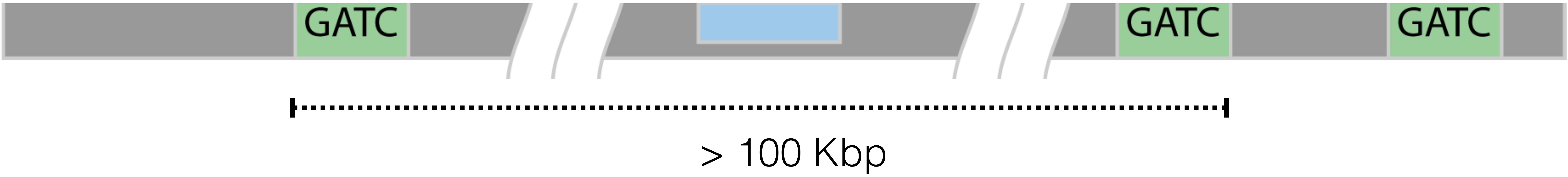
Too close from RE sites (~2%)



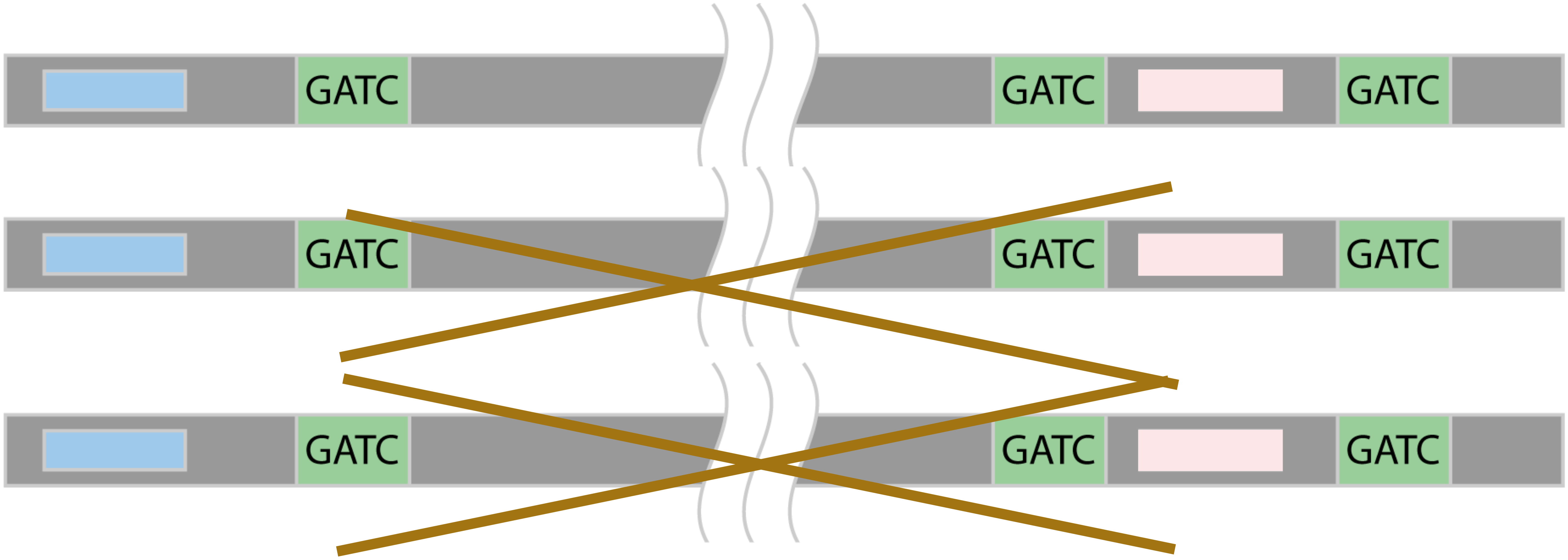
Too short (<1%)



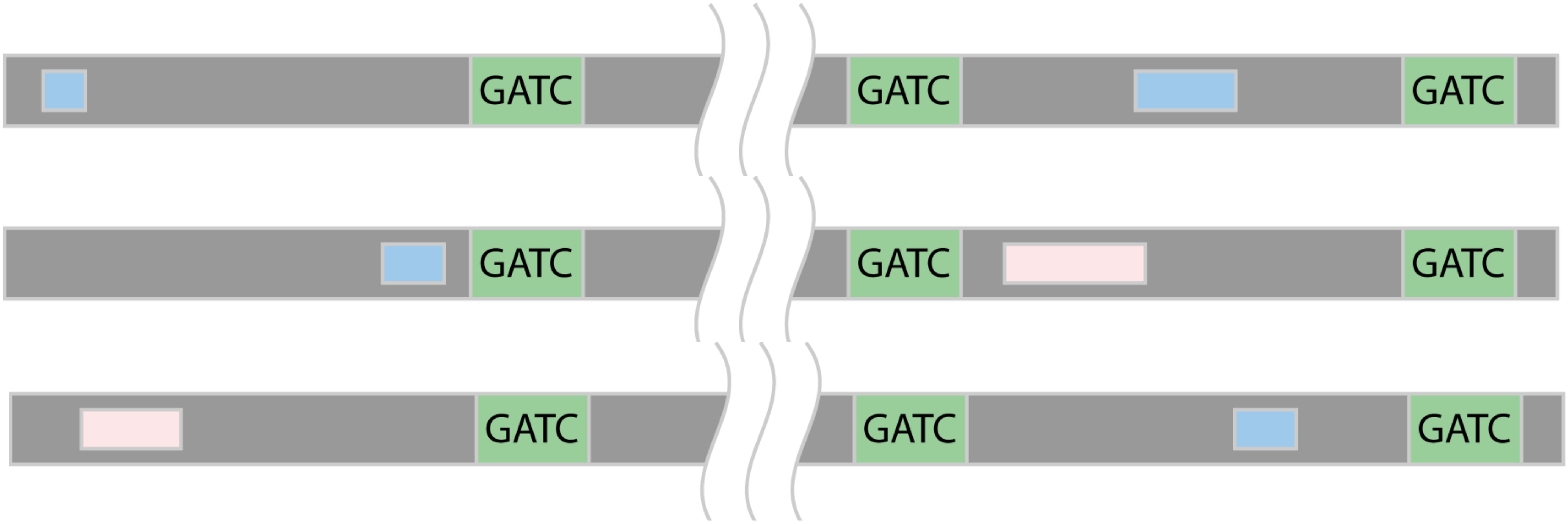
Too large (<1%)



Duplicated (~20%)



Over represented (<1%)



How much do we map?

- Valid reads: 80-90% each end => 64-81% intersection => 60% of the intersection, 36% of the total

- 1% multiple contacts

- many of the reads will be lost in the filtering…