What we need to know about NGS in Hi-C

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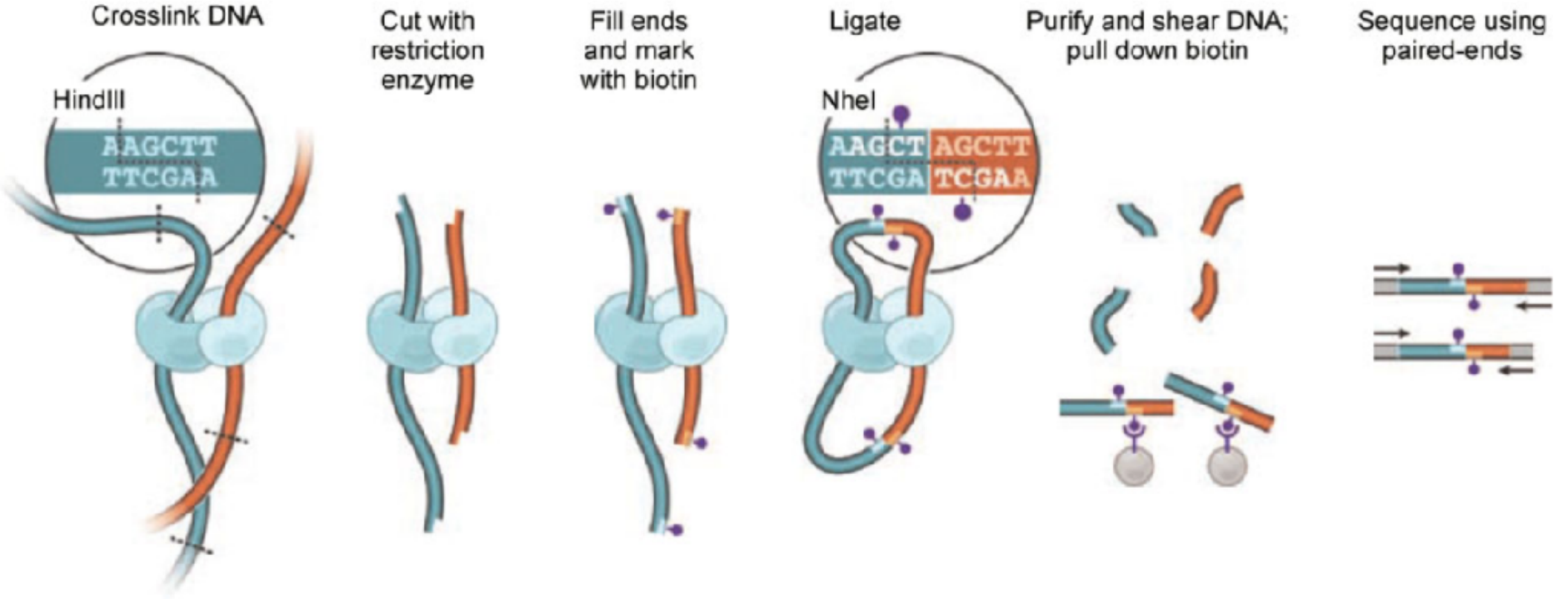
Structural Genomics Group (CNAG-CRG)

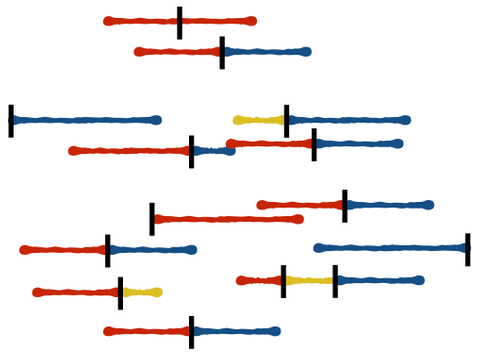
Illumina official video

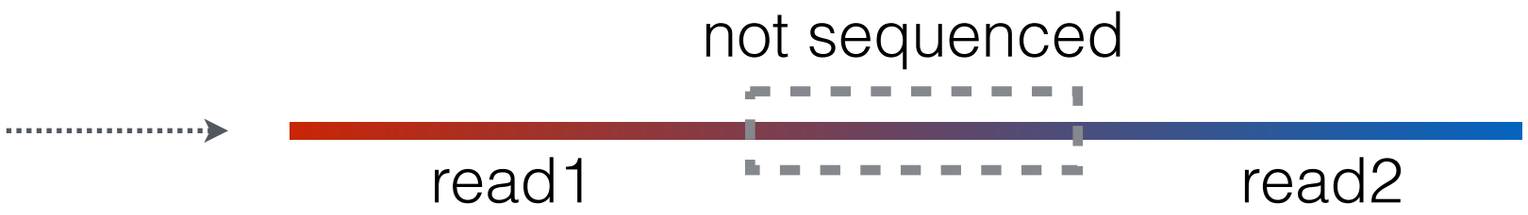
Hi-C experiment



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

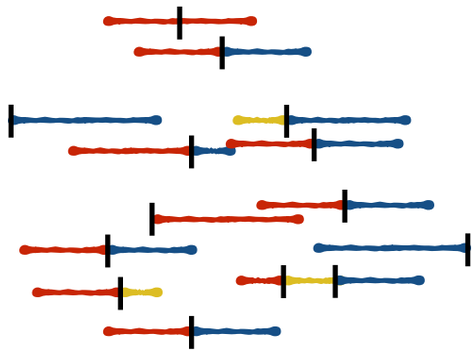
HiC mapping

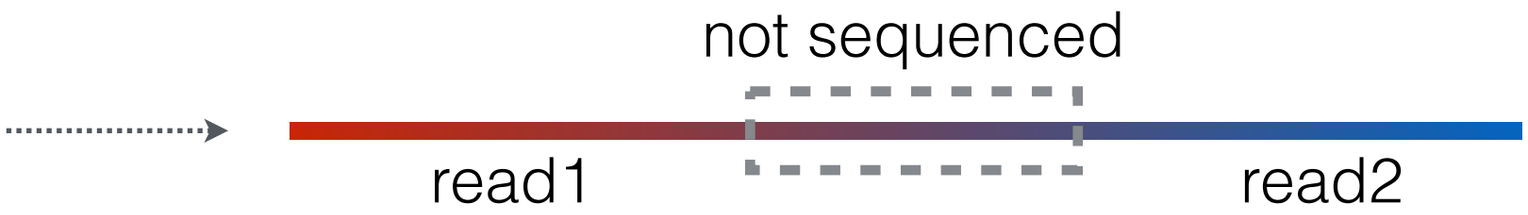




Iterative mapping

HiC mapping

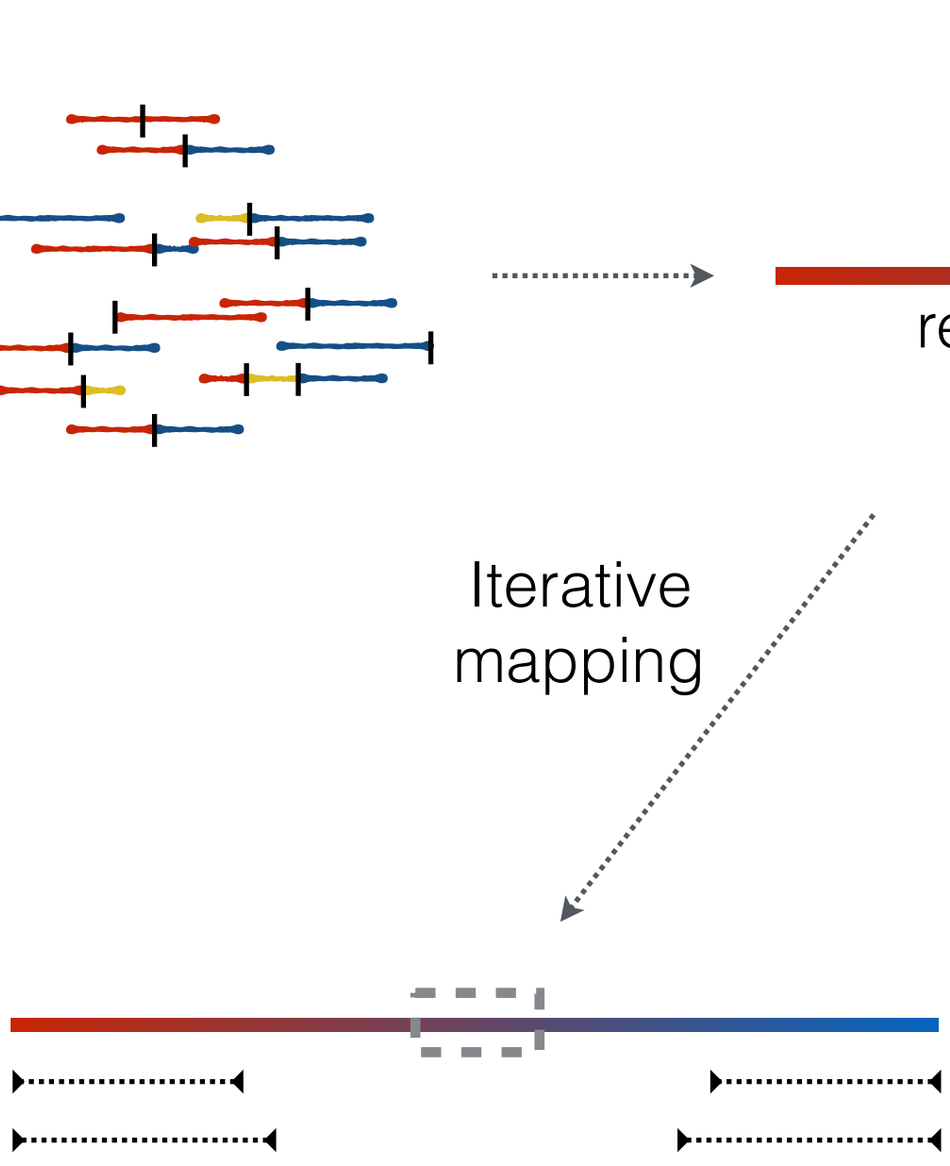




Iterative mapping

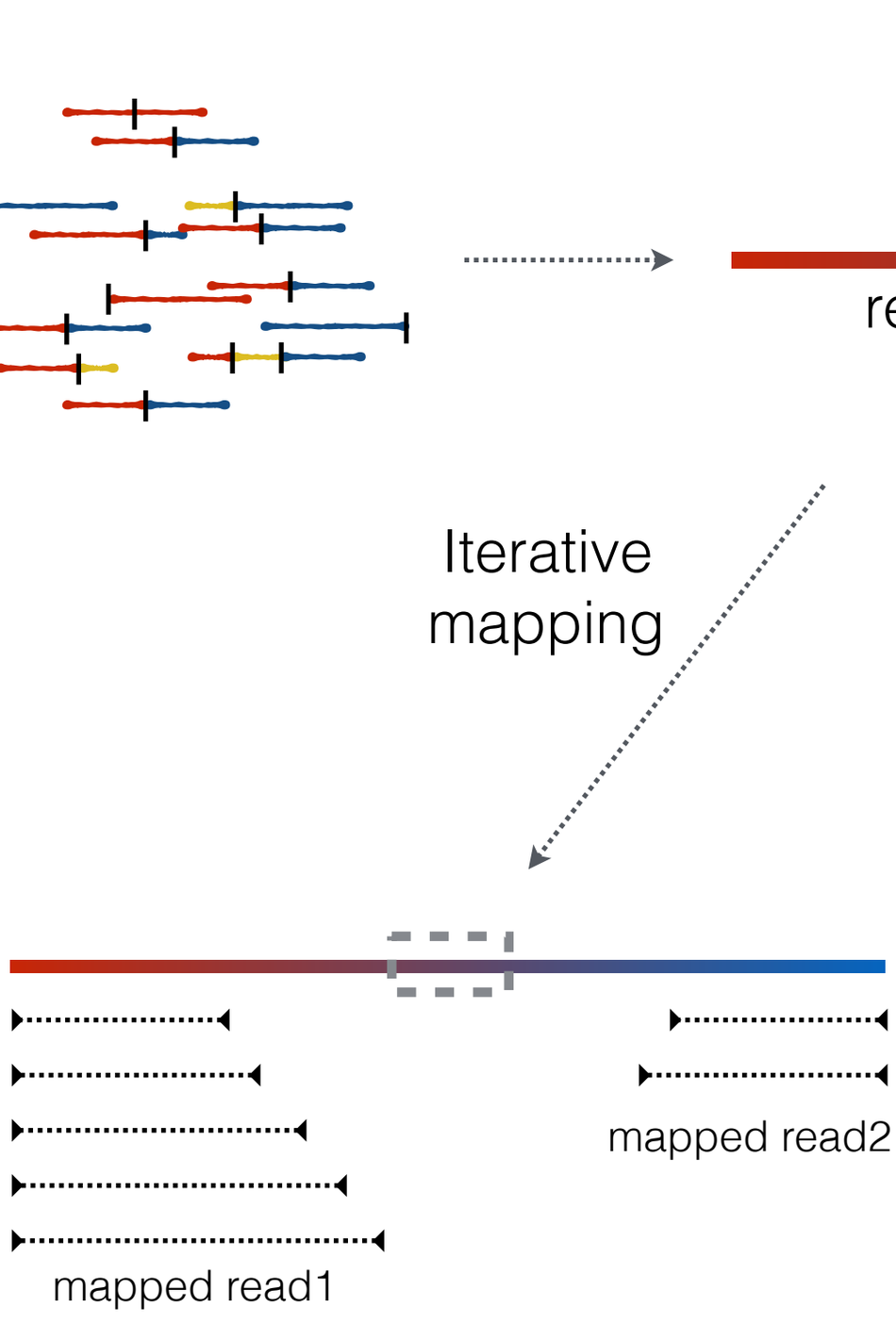
HiC mapping

Iterative mapping

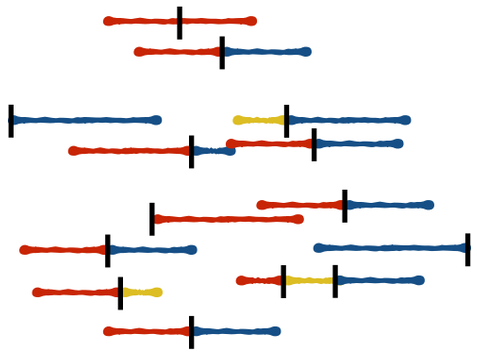


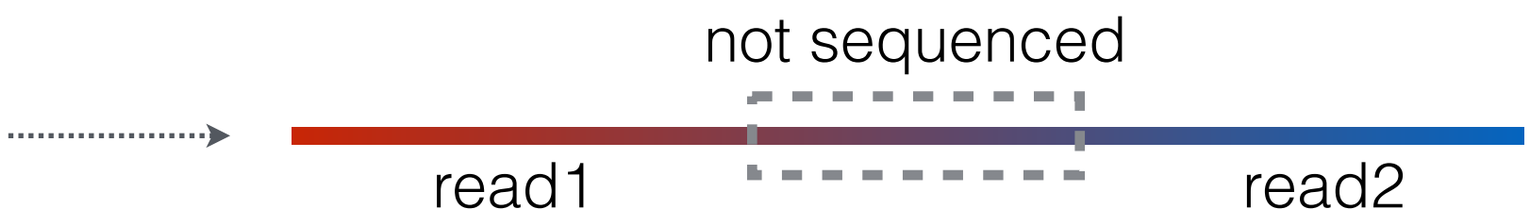
HiC mapping

Iterative mapping



HiC mapping

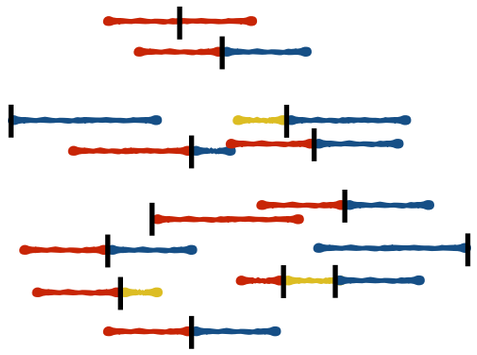


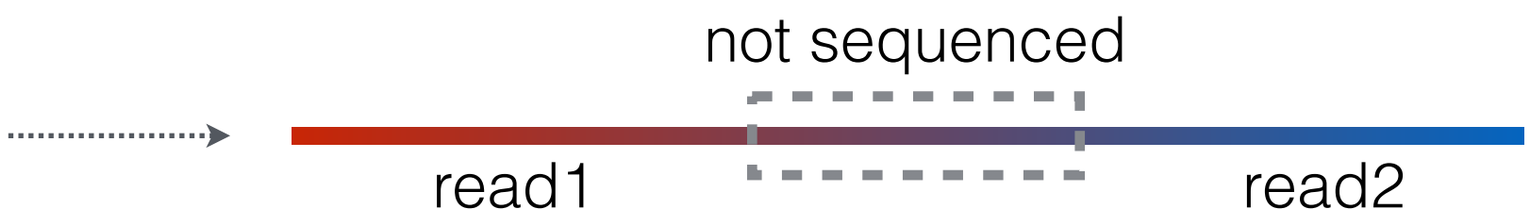


Iterative mapping

fragment based mapping

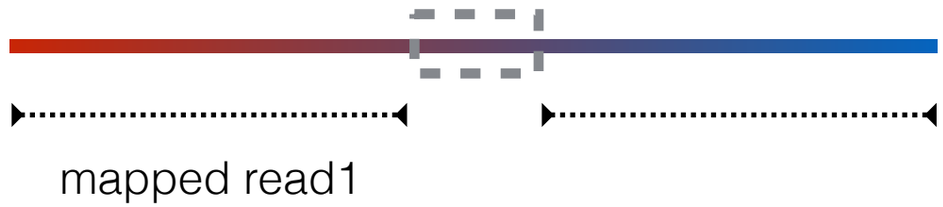
HiC mapping



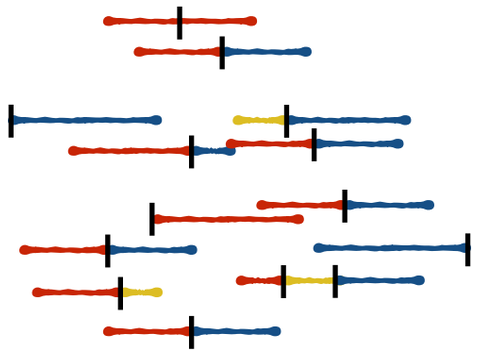


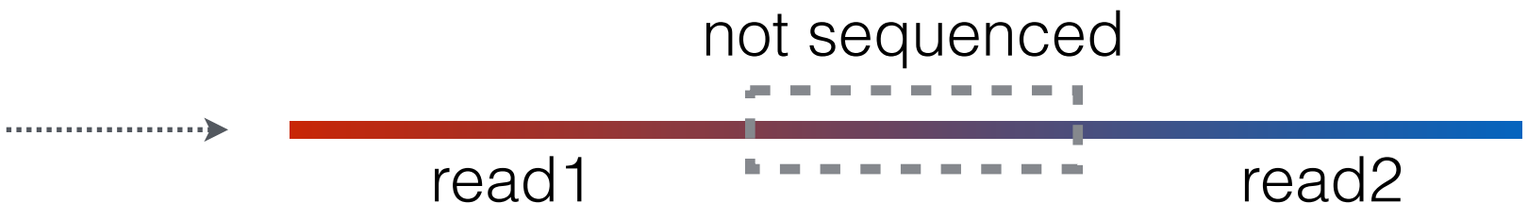
Iterative mapping

fragment based mapping

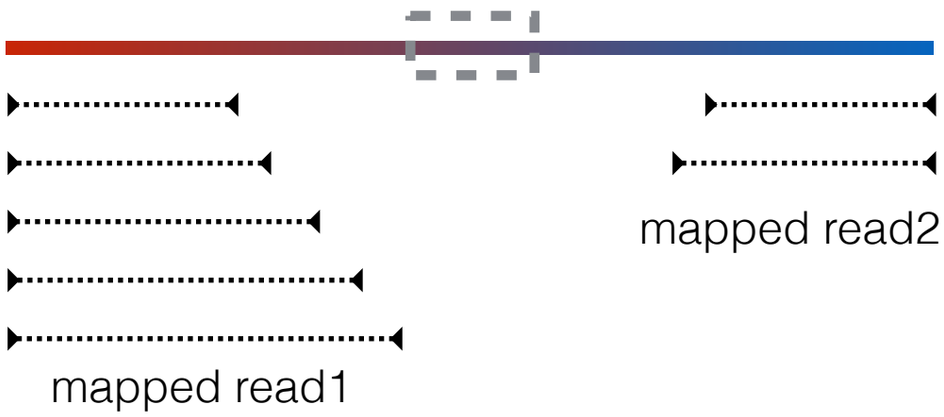


HiC mapping

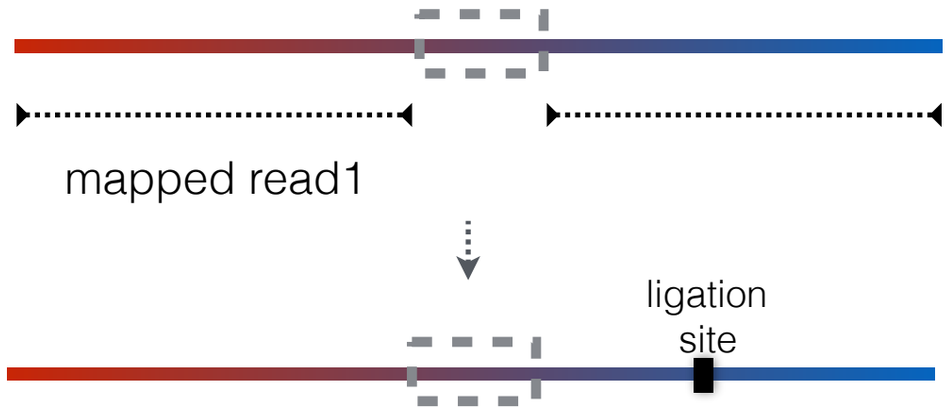




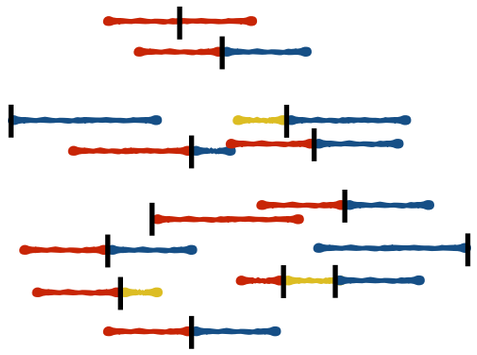
Iterative mapping

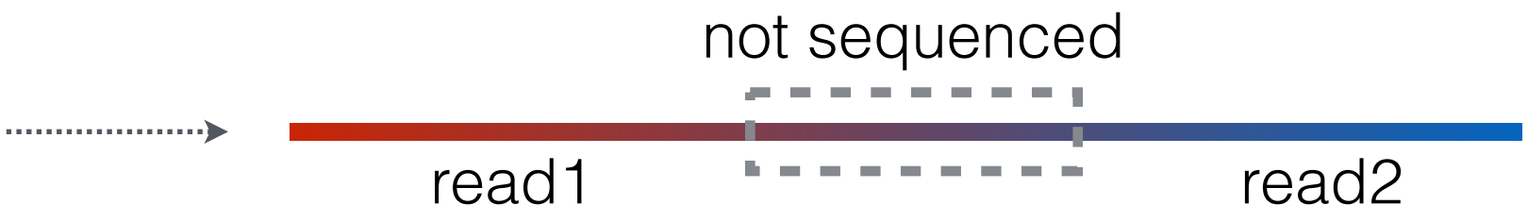


fragment based mapping



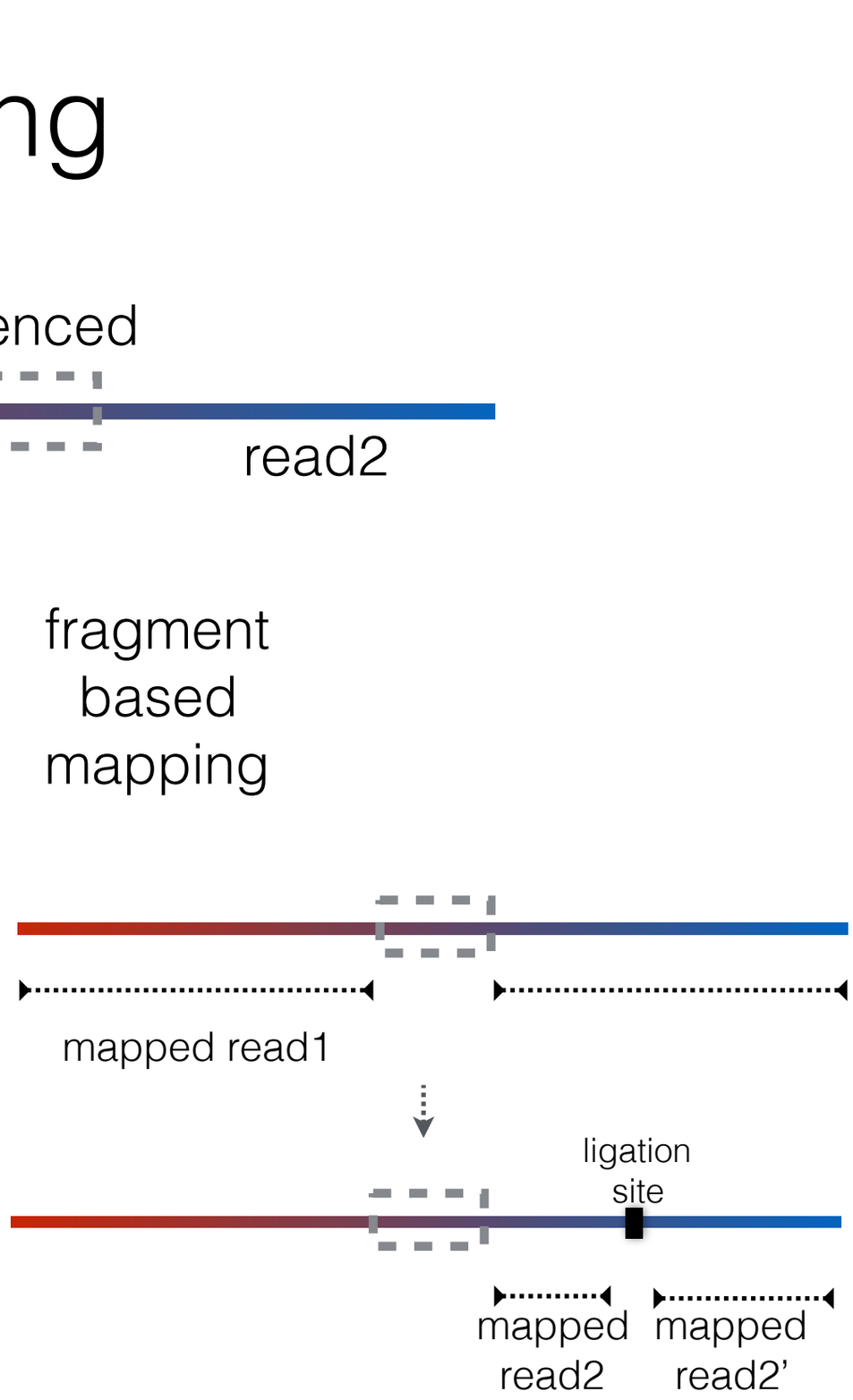
HiC mapping



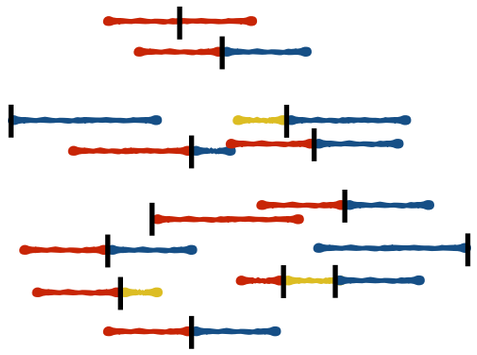


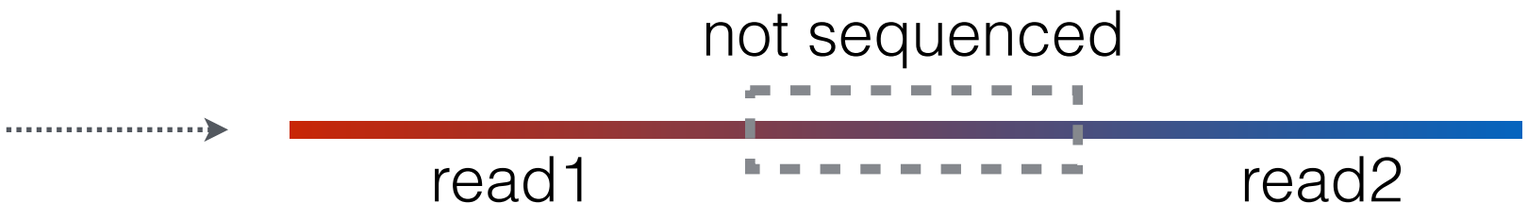
Iterative mapping

fragment based mapping



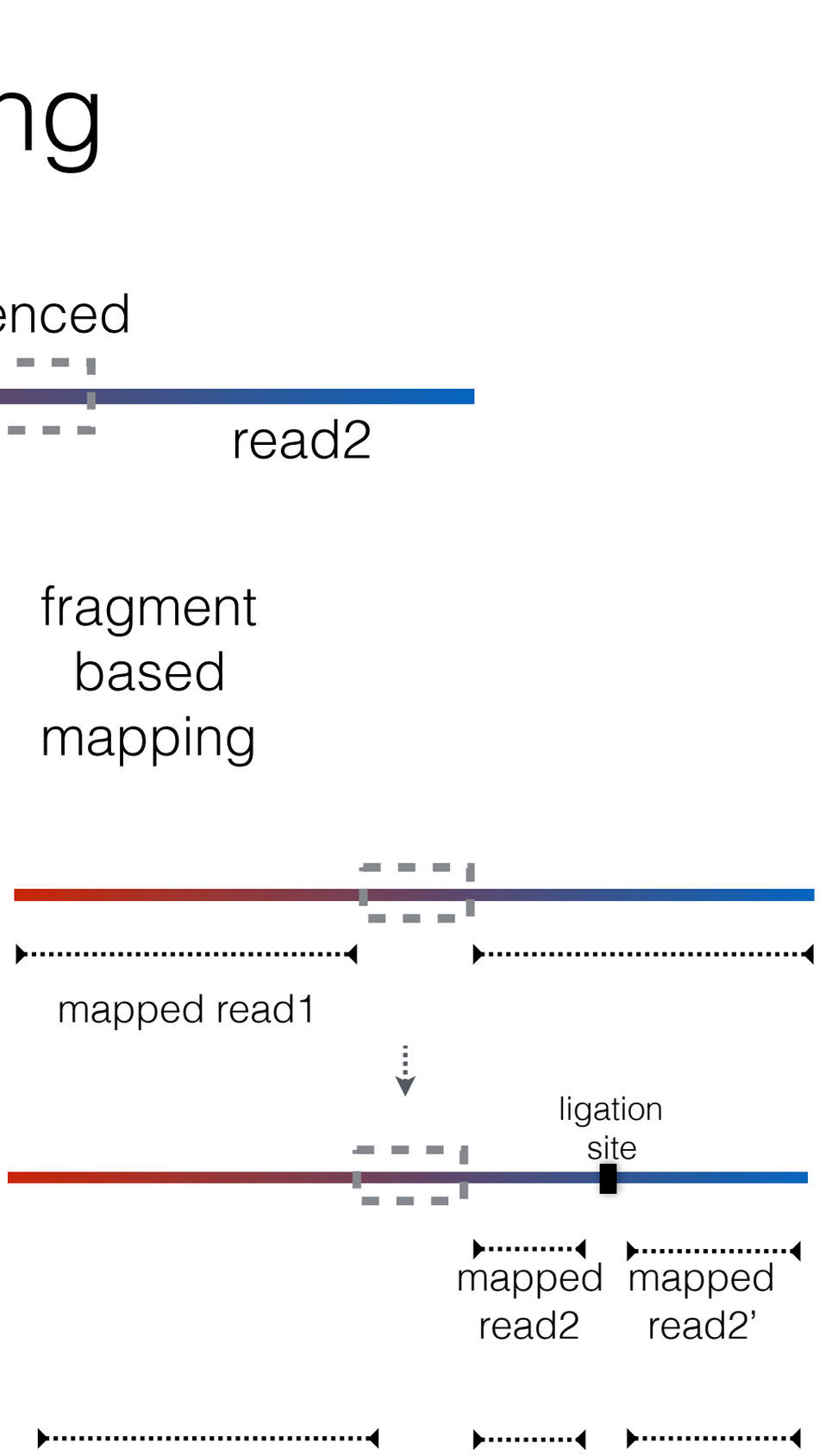
HiC mapping



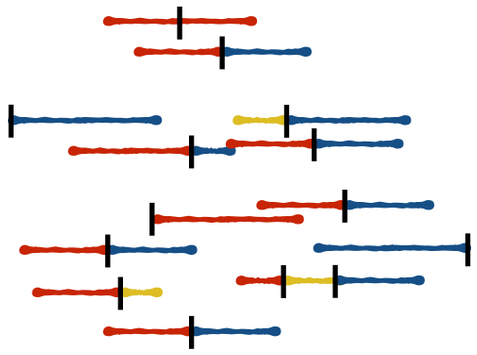


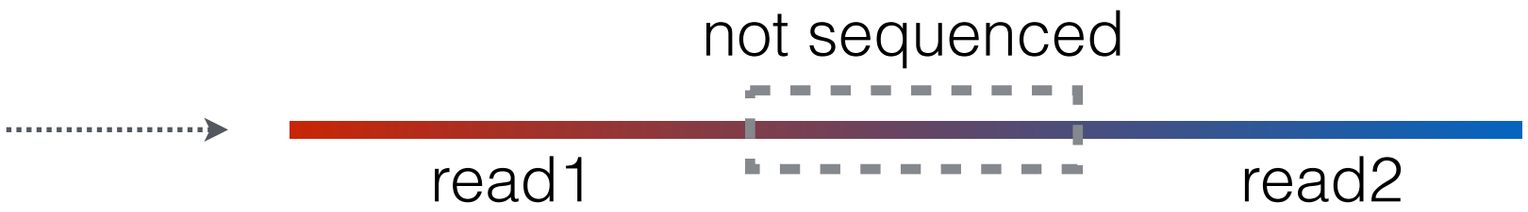
Iterative mapping

fragment based mapping



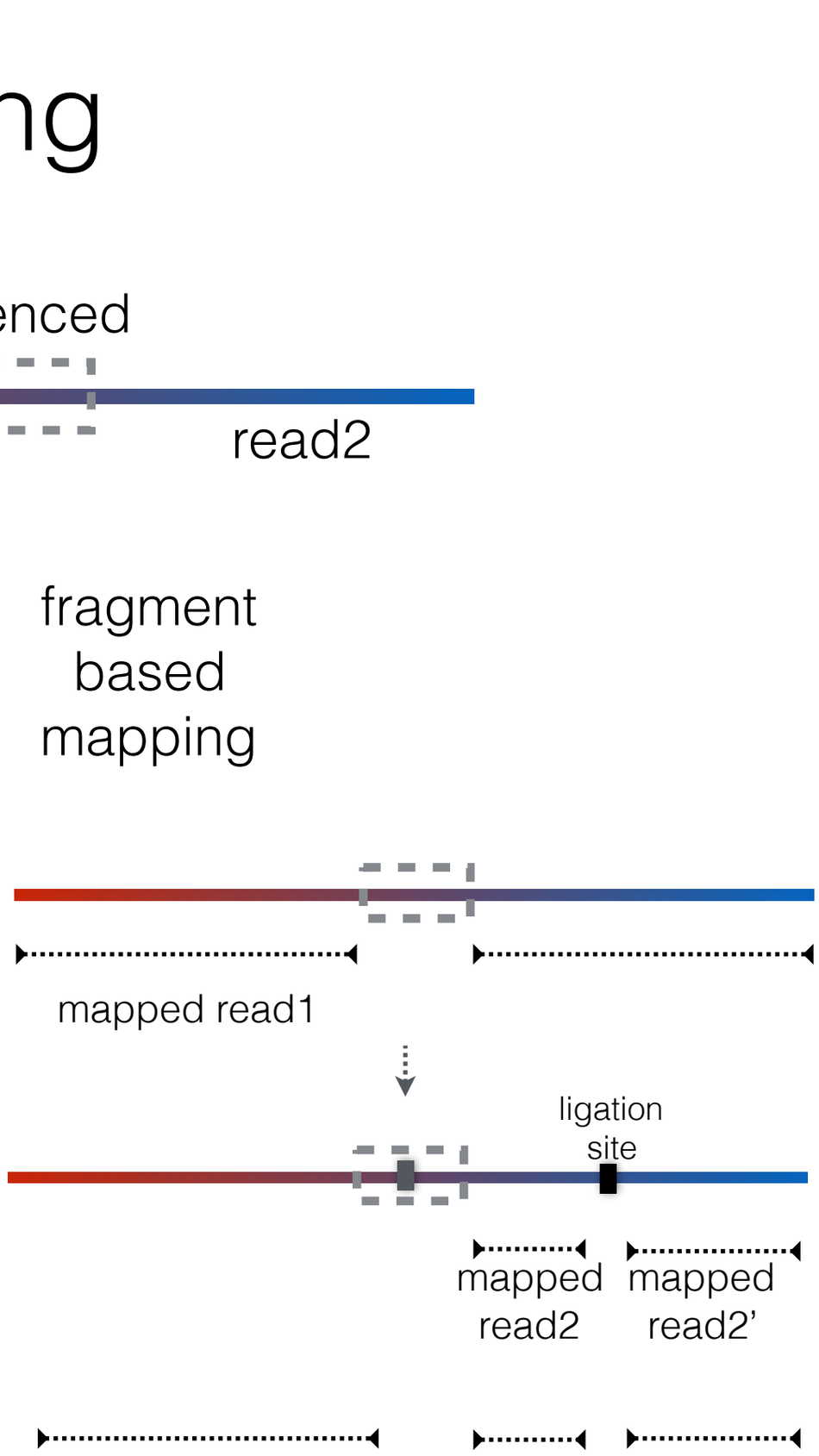
HiC mapping



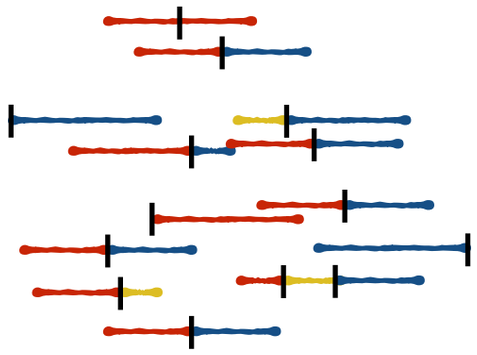


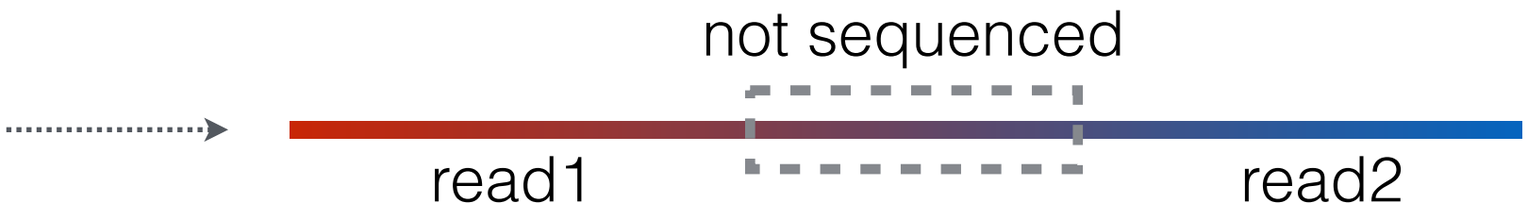
Iterative mapping

fragment based mapping



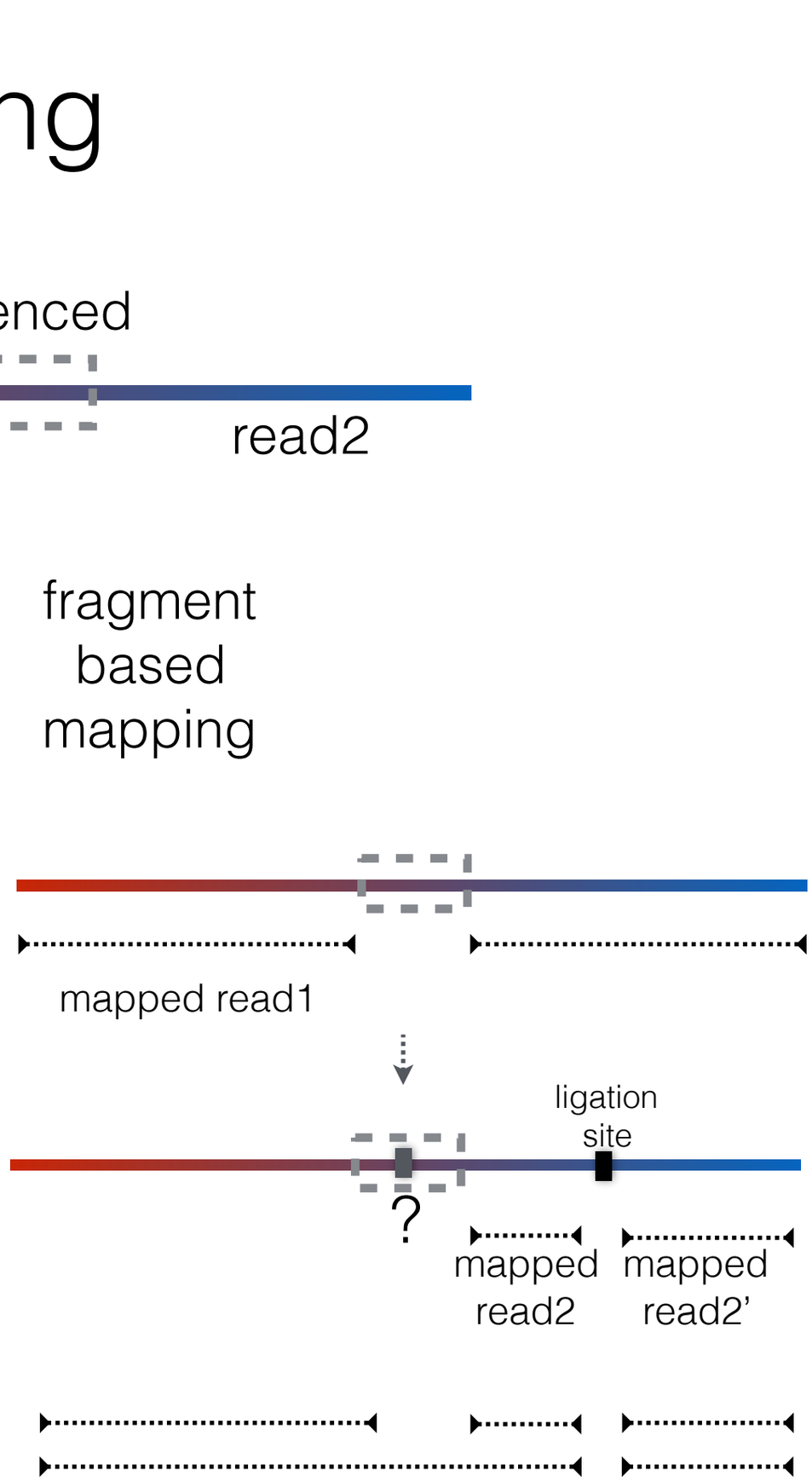
HiC mapping





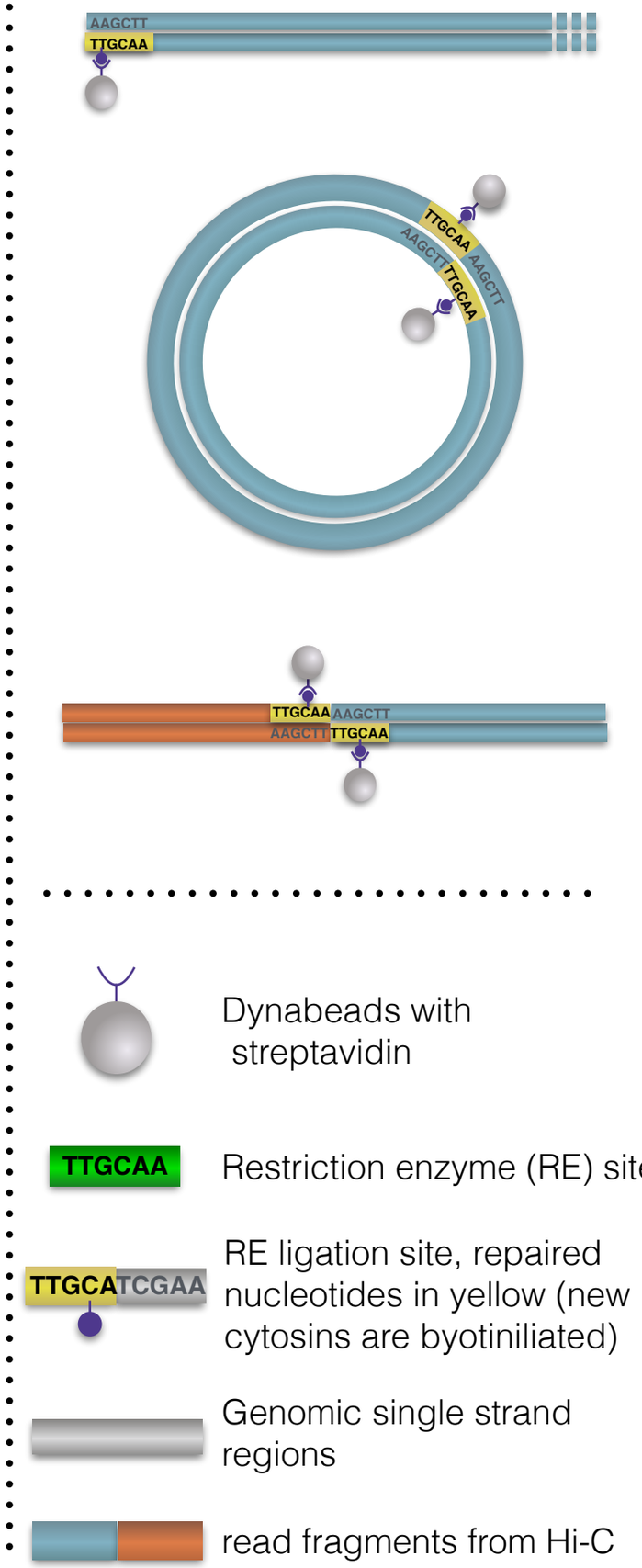
Iterative mapping

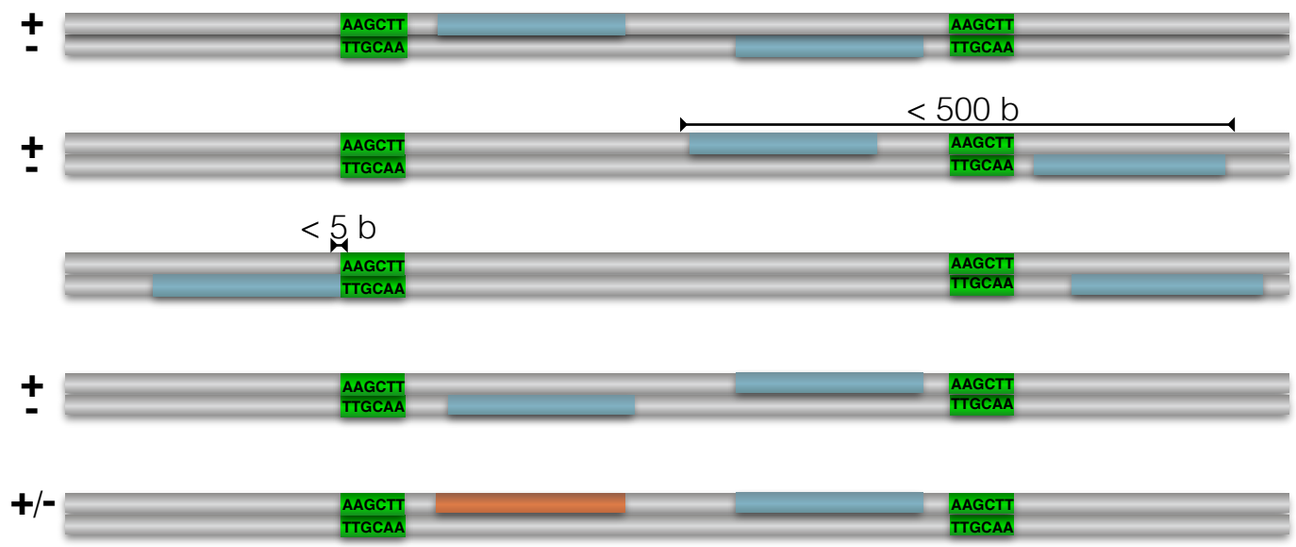
fragment based mapping

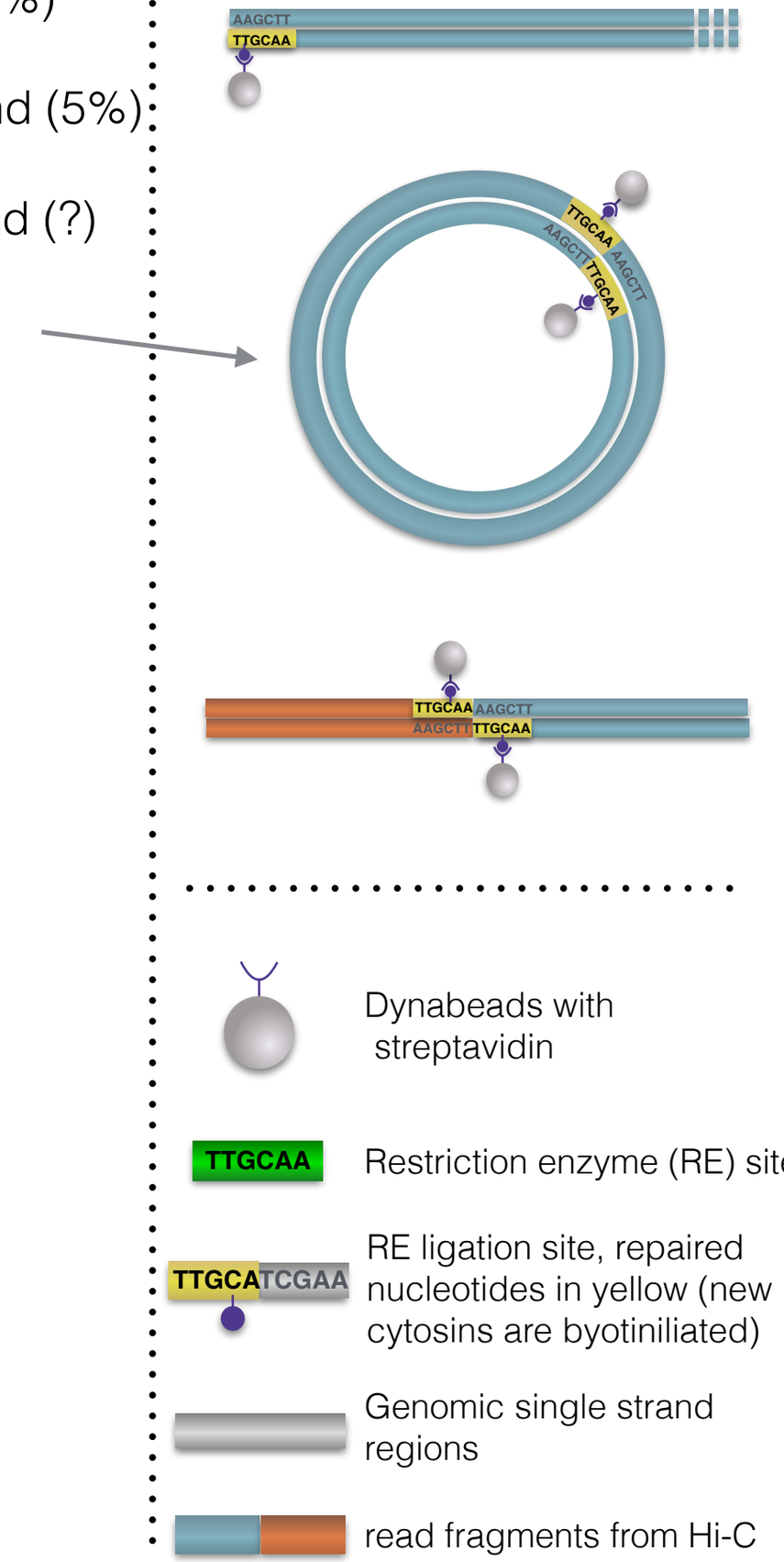


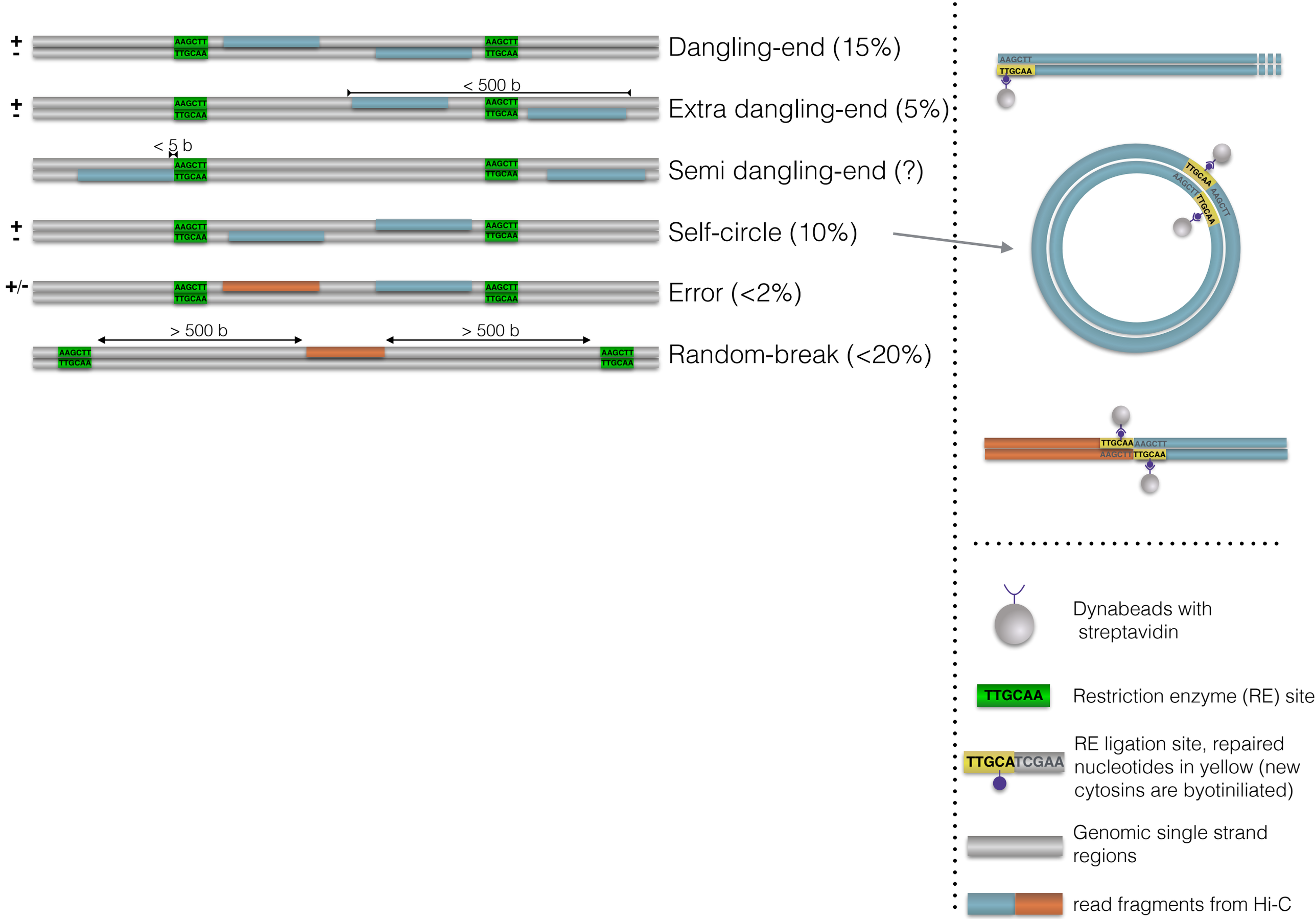
How much do we map?

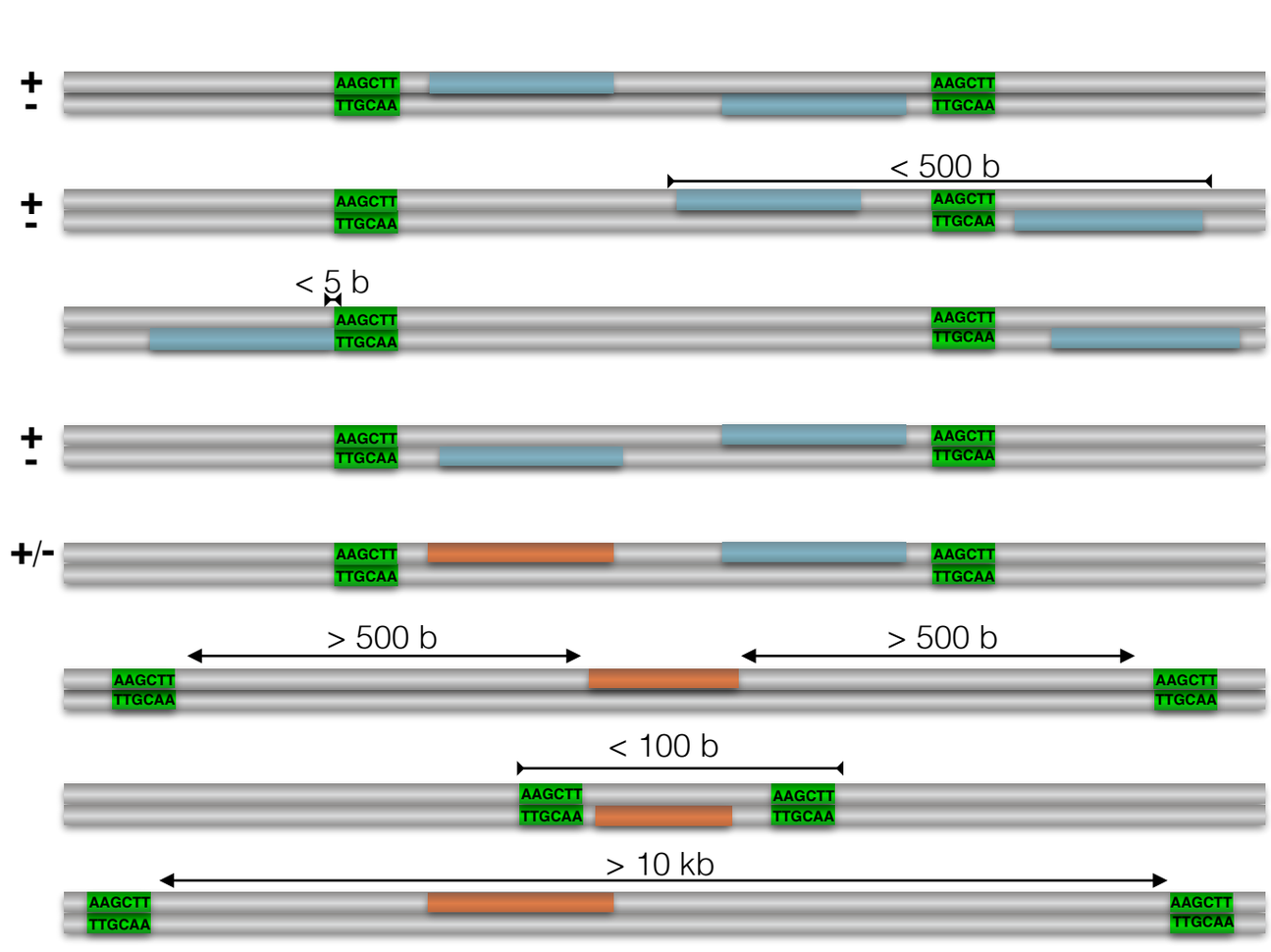
- 80-90% each end => 64-81% intersection
- 1% multiple contacts
- many of these will be lost in the filtering…

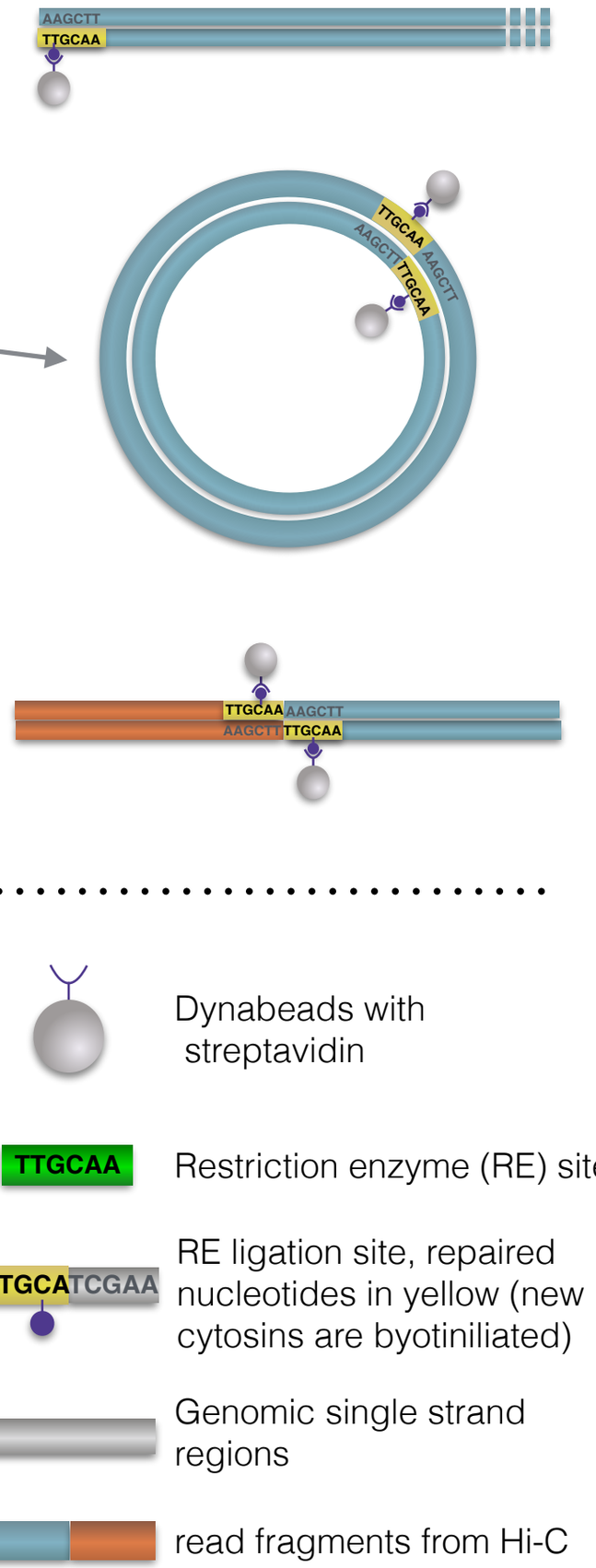

AAGCTT
TTGCAA
TTGCAA
AAGCTT
AAGCTT
TTGCAA
TTGCAA
AAGCTT
AAGCTT
TTGCAA
Dynabeads with streptavidin
TTGCAA
Restriction enzyme (RE) site
TTGCATCGAA
RE ligation site, repaired nucleotides in yellow (new cytosins are byotiniliated)
Genomic single strand regions
read fragments from Hi-C


+
-
AAGCTT
TTGCAA
AAGCTT
TTGCAA
Dangling-end (15%)
< 500 b
Extra dangling-end (5%)
< 5 b
Semi dangling-end (?)
Self-circle (10%)
+/-
Error (<2%)


AAGCTT
TTGCAA
TTGCAA
AAGCTT
AAGCTT
TTGCAA
TTGCAA
AAGCTT
AAGCTT
TTGCAA
Dynabeads with
streptavidin
TTGCAA
Restriction enzyme (RE) site
TTGCATCGAA
RE ligation site, repaired
nucleotides in yellow (new
cytosins are byotiniliated)
Genomic single strand
regions
read fragments from Hi-C


+
-
AAGCTT
TTGCAA
Dangling-end (15%)
< 500 b
Extra dangling-end (5%)
< 5 b
Semi dangling-end (?)
Self-circle (10%)
+/-
Error (<2%)
> 500 b
> 500 b
Random-break (<20%)
TTGCAA
AAGCTT
Dynabeads with streptavidin
Restriction enzyme (RE) site
TTGCATCGAA
RE ligation site, repaired nucleotides in yellow (new cytosins are byotiniliated)
Genomic single strand regions
read fragments from Hi-C


+
-
AAGCTT
TTGCAA
Dangling-end (15%)
< 500 b
Extra dangling-end (5%)
< 5 b
Semi dangling-end (?)
Self-circle (10%)
+/-
Error (<2%)
> 500 b
Random-break (<20%)
< 100 b
Too short (<1%)
> 10 kb
Too large (<1%)


AAGCTT
TTGCAA
TTGCAA
AAGCTT
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AAGCTT
Dynabeads with streptavidin
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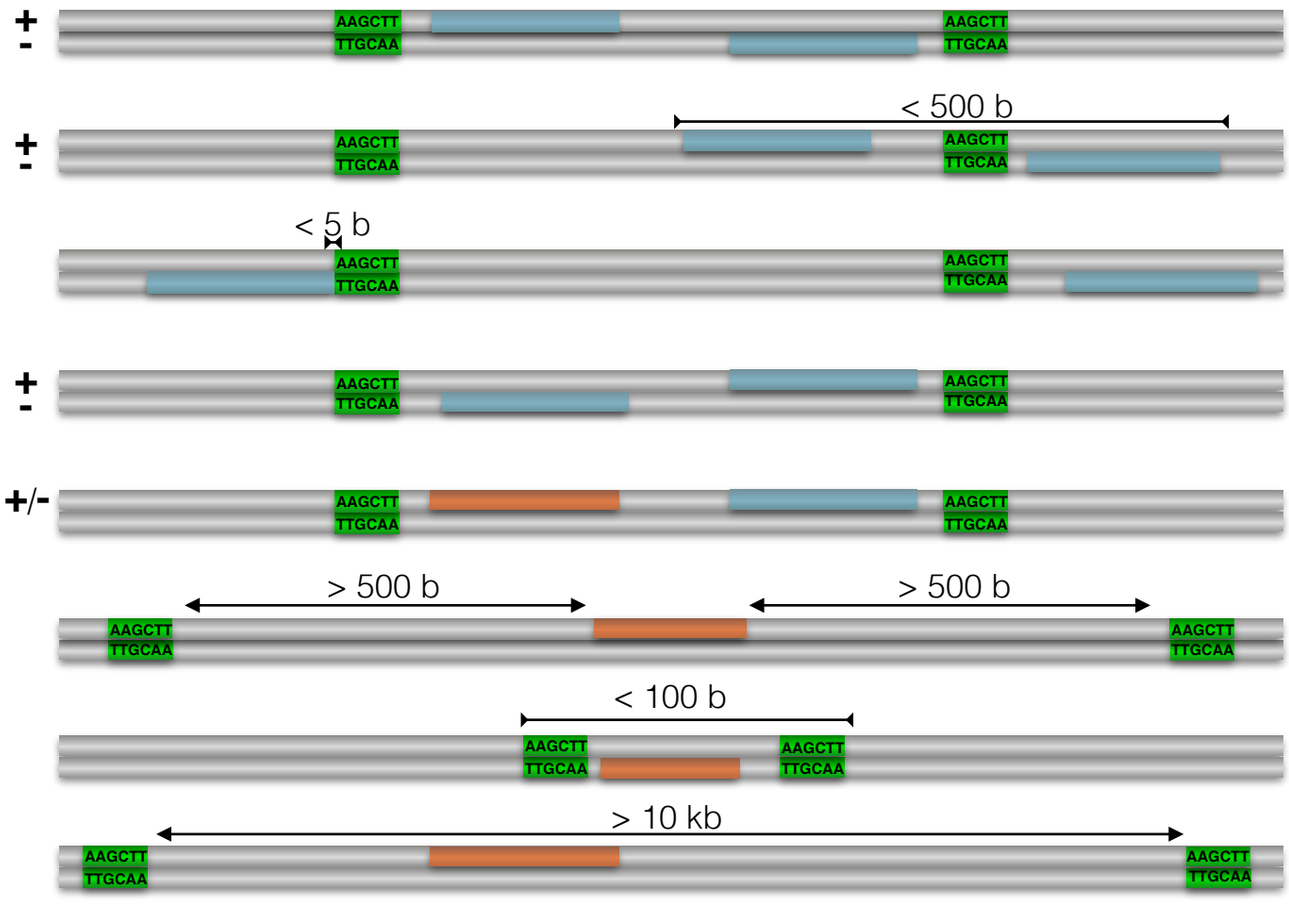
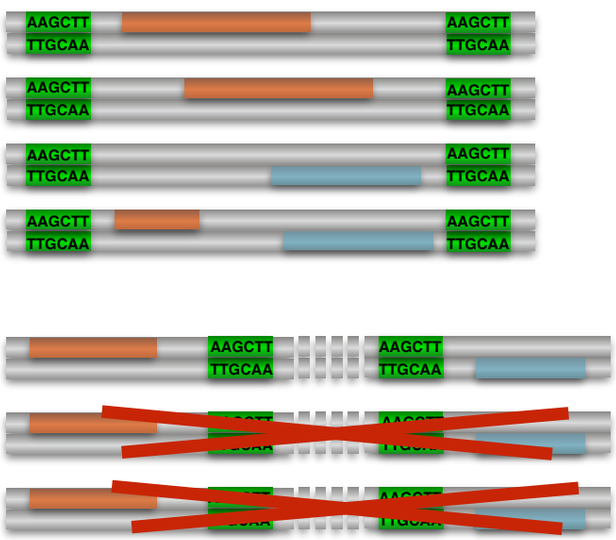
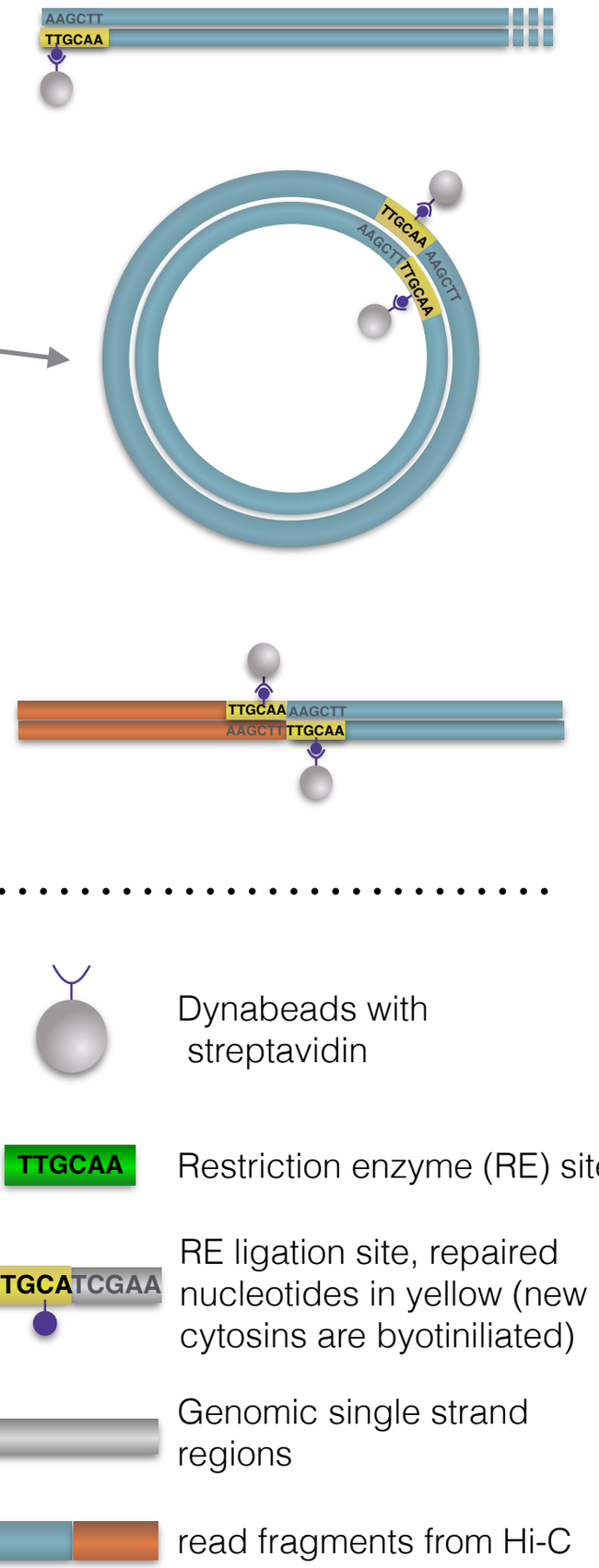
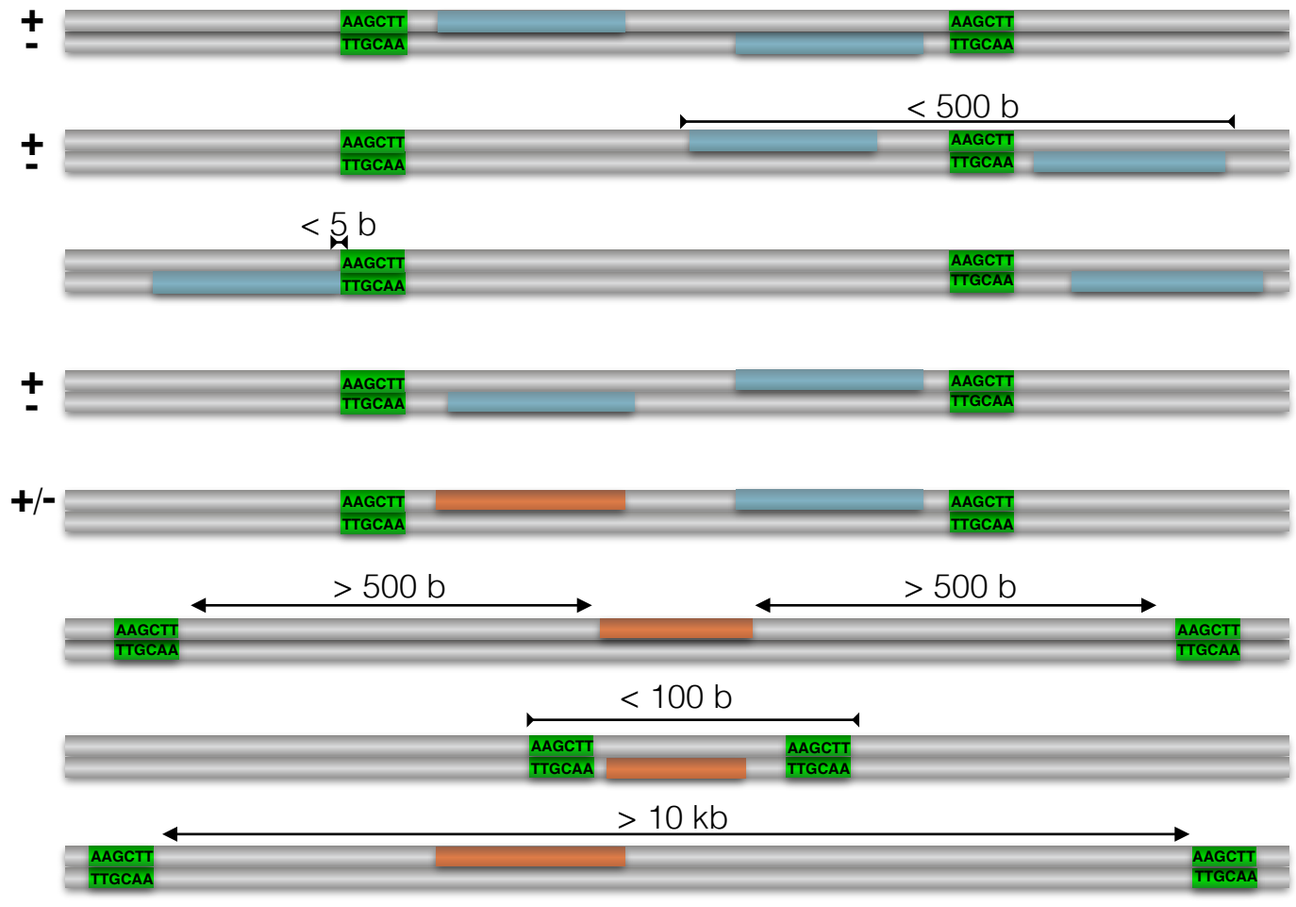
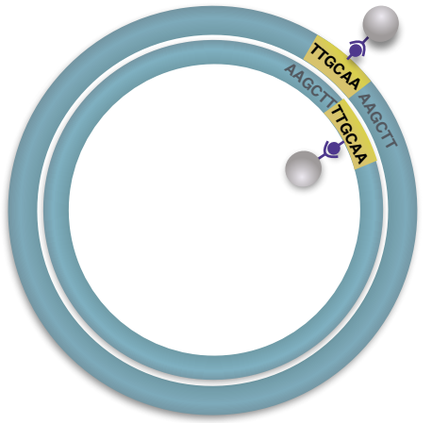

+
-
AAGCTT
TTGCAA
Dangling-end (15%)
< 500 b
Extra dangling-end (5%)
< 5 b
Semi dangling-end (?)
Self-circle (10%)
+/-
Error (<2%)
> 500 b
Random-break (<20%)
< 100 b
Too short (<1%)
> 10 kb
Too large (<1%)

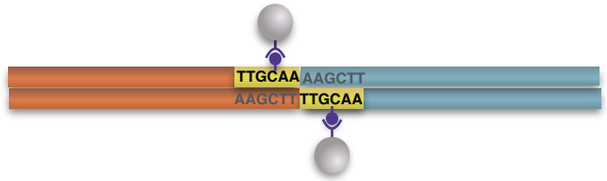

Over-represented (<1%)
Duplicated (20%)

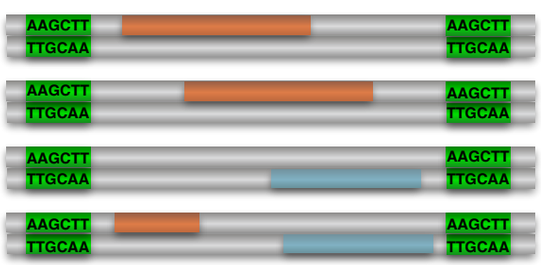

AAGCTT
TTGCAA
Dynabeads with streptavidin
TTGCAA
Restriction enzyme (RE) site
TTGCATCGAA
RE ligation site, repaired nucleotides in yellow (new cytosins are byotiniliated)
Genomic single strand regions
read fragments from Hi-C

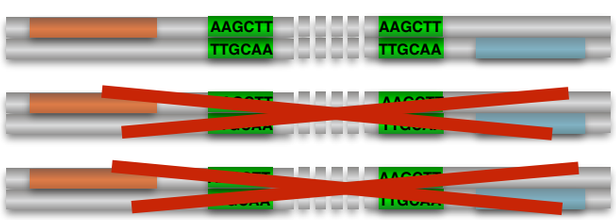

+
-
AAGCTT
TTGCAA
Dangling-end (15%)
< 500 b
Extra dangling-end (5%)
< 5 b
Semi dangling-end (?)
Self-circle (10%)
+/-
Error (<2%)
> 500 b
> 500 b
Random-break (<20%)
< 100 b
Too short (<1%)
> 10 kb
Too large (<1%)

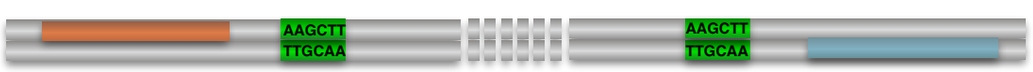

AAGCTT
TTGCAA

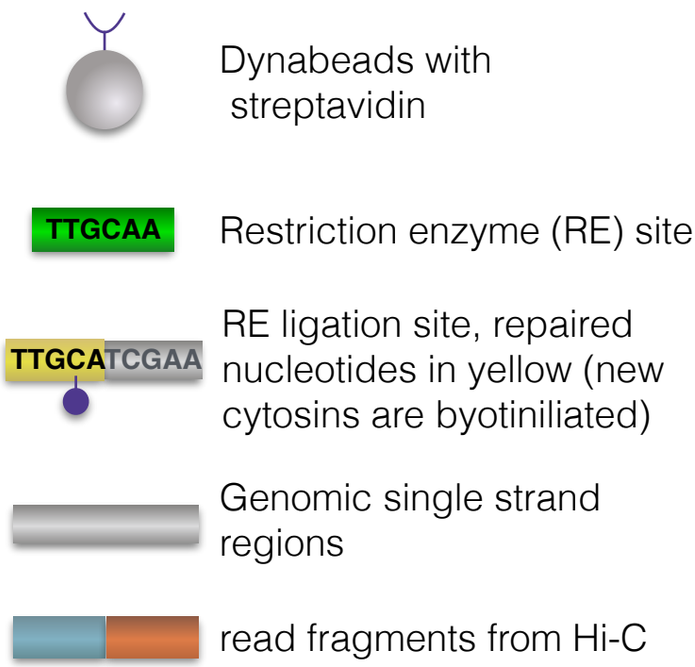

TTGCAA
AAGCTT
AAGCTT
TTGCAA


TTGCAA
AAGCTT
AAGCTT
TTGCAA


AAGCTT
TTGCAA
Over-represented (<1%)


AAGCTT
TTGCAA
Duplicated (20%)


AAGCTT
TTGCAA
Valid pair
(60% of intersection,
<50% of the total)


Dynabeads with
streptavidin
TTGCAA
Restriction enzyme (RE) site
TTGCATCGAA
RE ligation site, repaired
nucleotides in yellow (new
cytosins are byotiniliated)
Genomic single strand
regions
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