## What we need to know about NGS in $\mathrm{Hi}-\mathrm{C}$

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## Hi-C experiment



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

## HiC mapping


not sequenced
read1
read2

Iterative
mapping


## HiC mapping


not sequenced
－ロー・ーローロ！
read1
read2


## HiC mapping



## HiC mapping



> Iterative
> mapping

mapped read1

## HiC mapping



## HiC mapping


mapped read1

## HiC mapping



## HiC mapping


mapped read1


## HiC mapping



mapped read1


## HiC mapping



mapped read1


## HiC mapping


mapped read1


## How much do we map?

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



Extra dangling-end (5\%):
Semi dangling-end (?)


Self-circle (10\%) $\longrightarrow$


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 $\mathrm{Hi}-\mathrm{C}$





