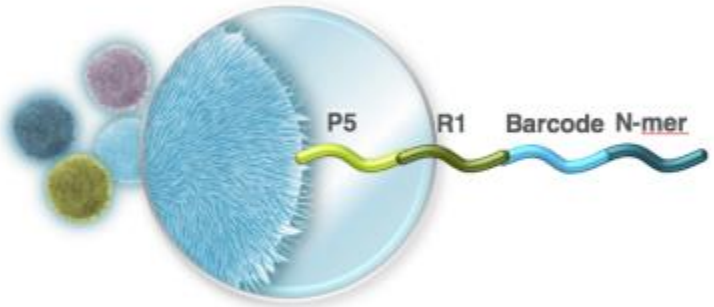
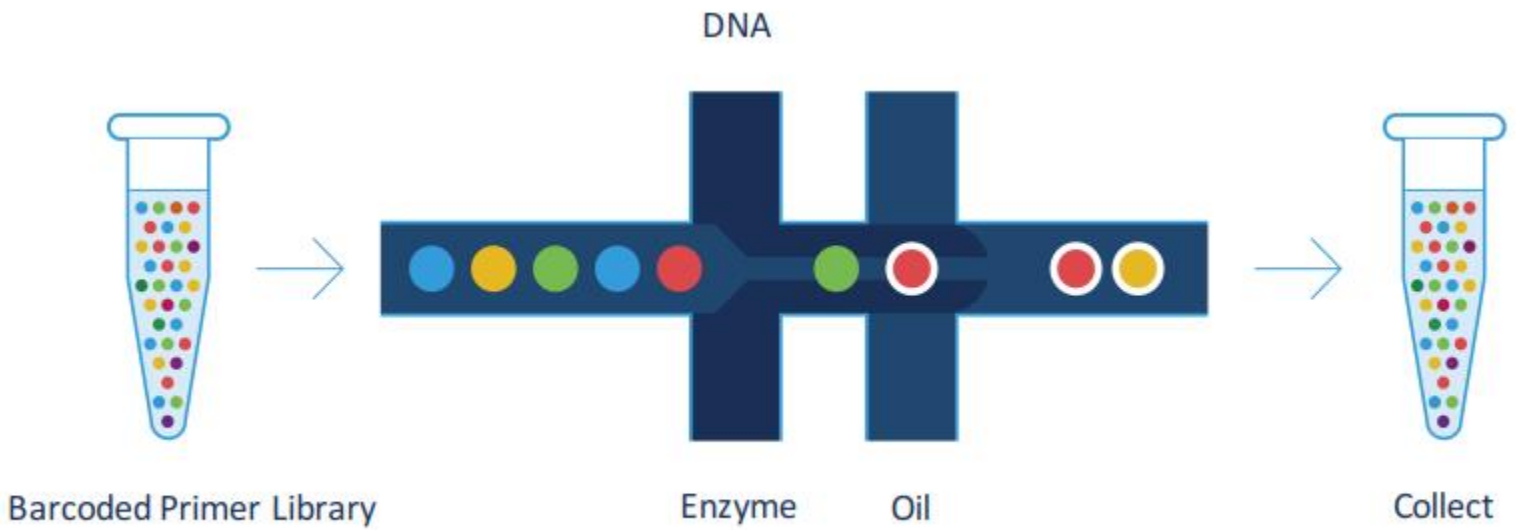


3 Components:

1. Gel Beads
2. Genomic DNA with Enzyme Mix
3. Partitioning Oil

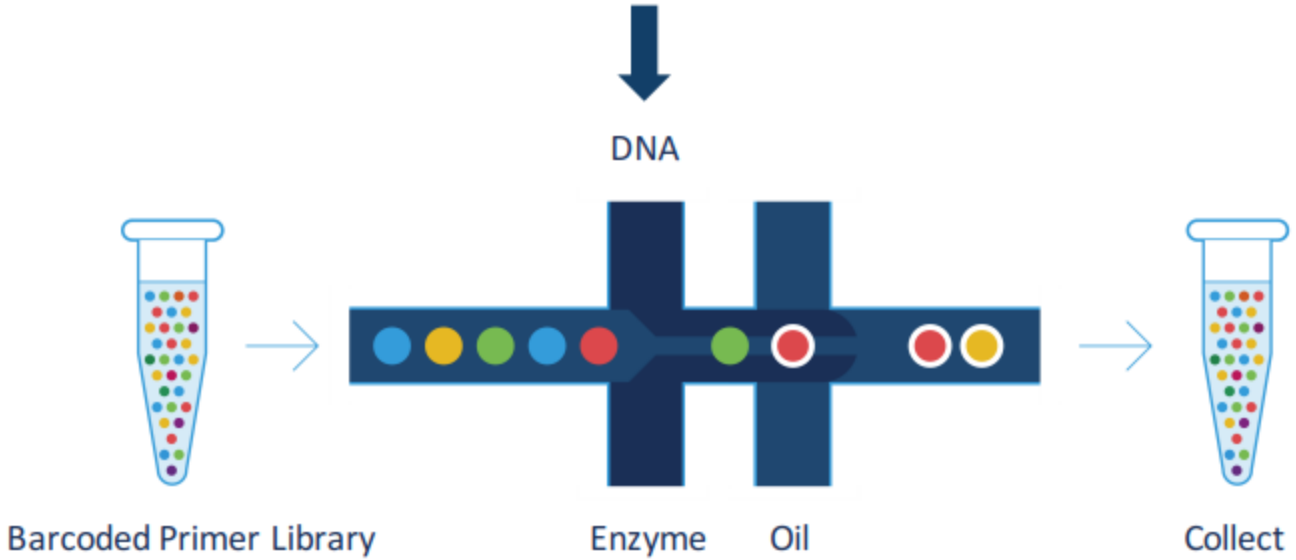


All graphics from 10X Genomics

Start with:

HMW gDNA, 100Kb+ molecules

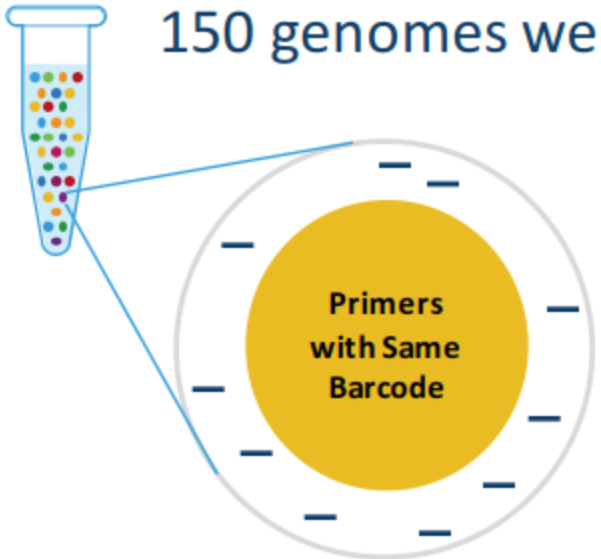
1.0 ng input DNA = 300 copies of the genome



0.5ng DNA = **150** copies of the genome,

partitioned into > 1M GEMs

All graphics from 10X Genomics



150 genomes went into 1M partitions

Each GEM contains:

- One barcode (many copies)
- 1/6000 of the genome (500 Kb)
- At 50Kb length, 10 molecules

Chance that 2 molecules covering a locus are in same GEM:

1 in 6000

Percent unique barcodes at any genomic locus:

99.98%

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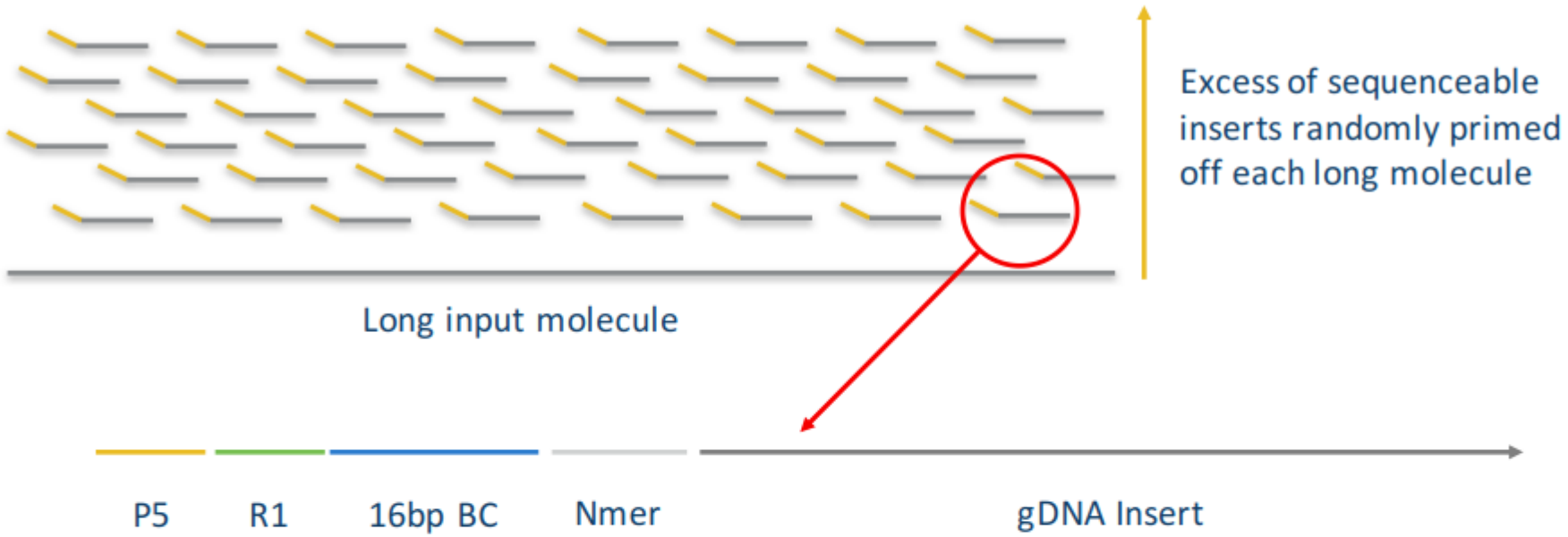


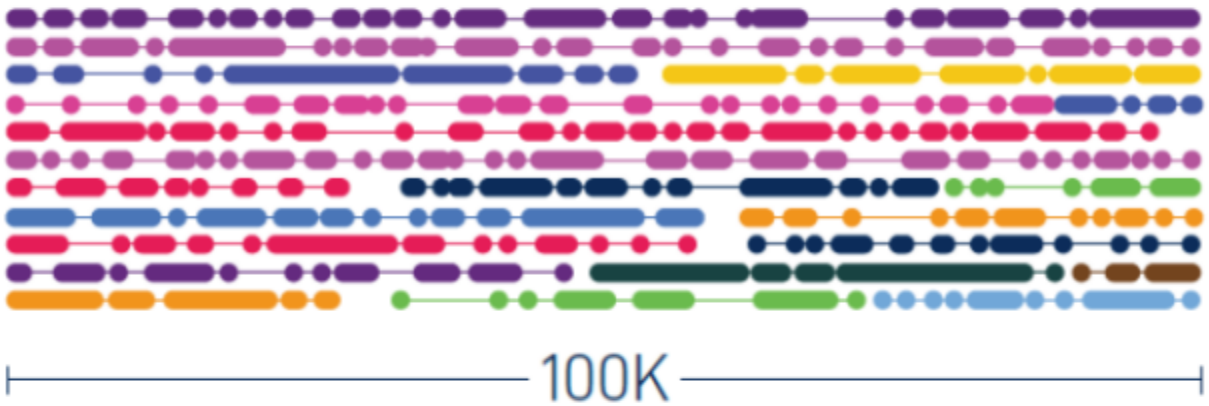
At 30X read coverage, ~35 library fragments
will end up sequenced from each 50Kb input molecule

35 *x* 2 *x* 150bp ≈ 10Kb, or 0.2X read coverage per molecule

Reads from the same input molecule are called “Linked-Reads”

All graphics from 10X Genomics

- Long-range information from short reads
  - Partition long input molecules into GEMs (***G**elbead-in-**Em**ulsion*)
  - Gelbeads carry barcode oligos that are incorporated in sequencing library
  - Use barcodes to link short reads back to original long input molecules



- Resulting barcoded reads are called ***Linked-Reads***
- Let's walk through an example…

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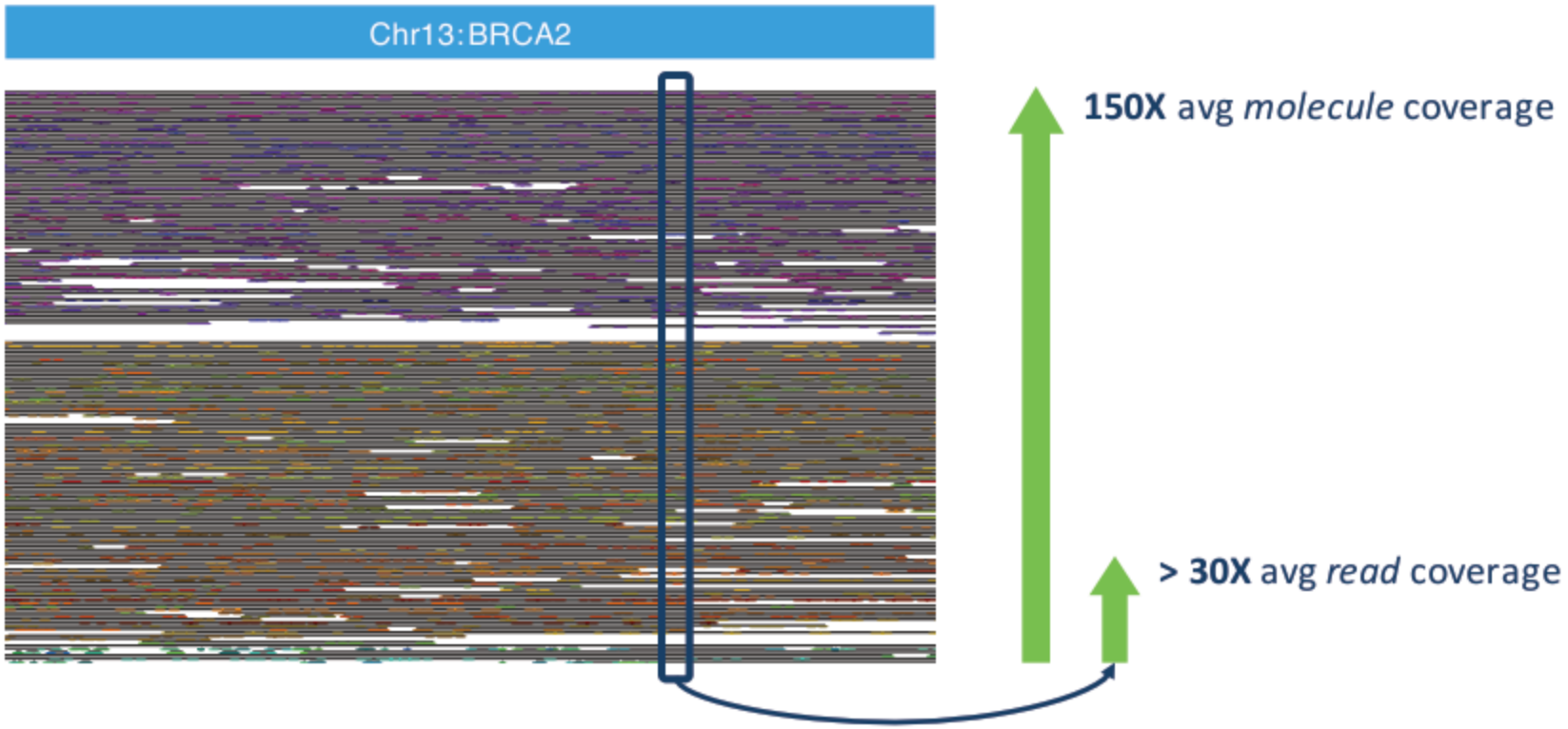

At recommended loading, any given genomic locus will have

~150 molecules spanning it, and an average read depth of >30X

(150X molecule depth) *x* (0.2X read/m) = 30X read depth

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