Progress Report

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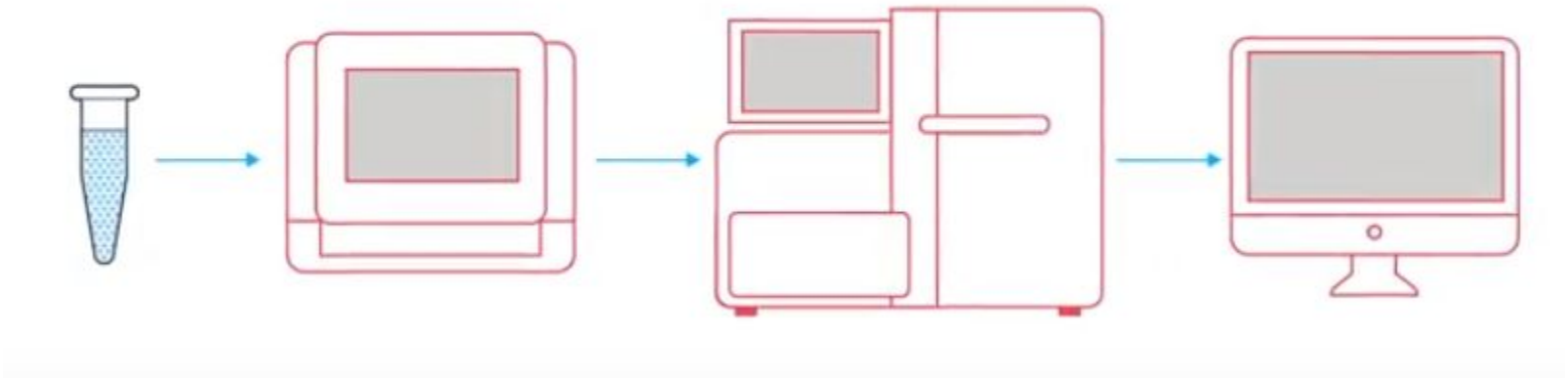
Experimental Process of 10X Genomics



Input
Start with hundreds to thousands of cells

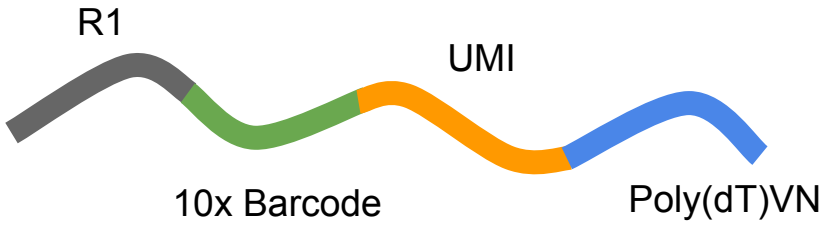
Chromium System
Automated barcoding & library construction

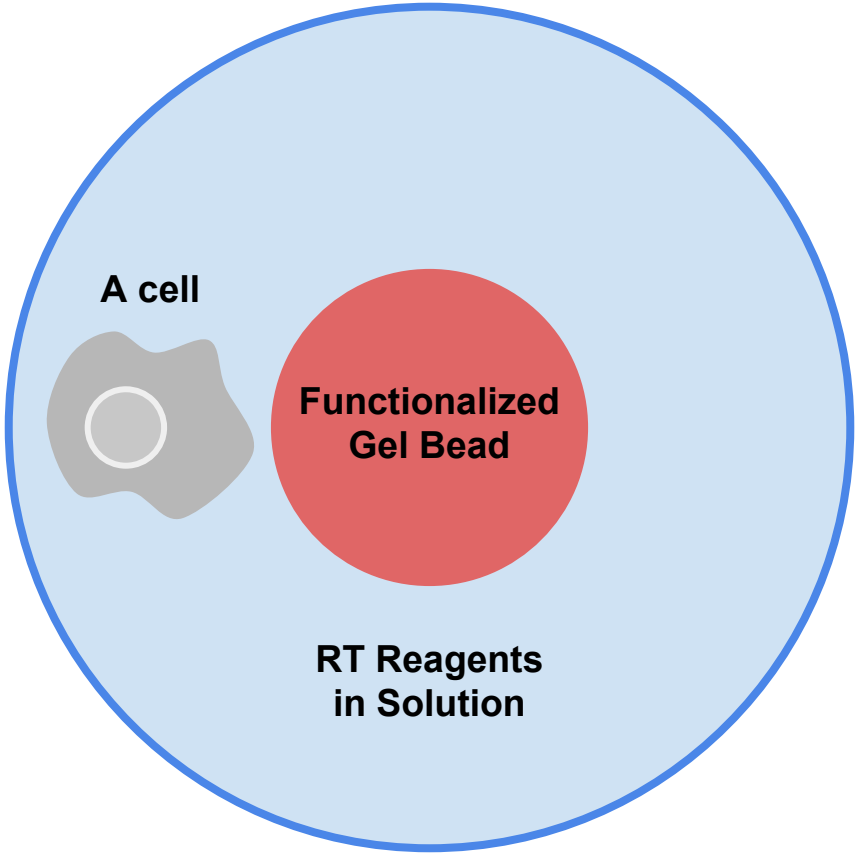
Sequencer
Use existing short-read sequencer

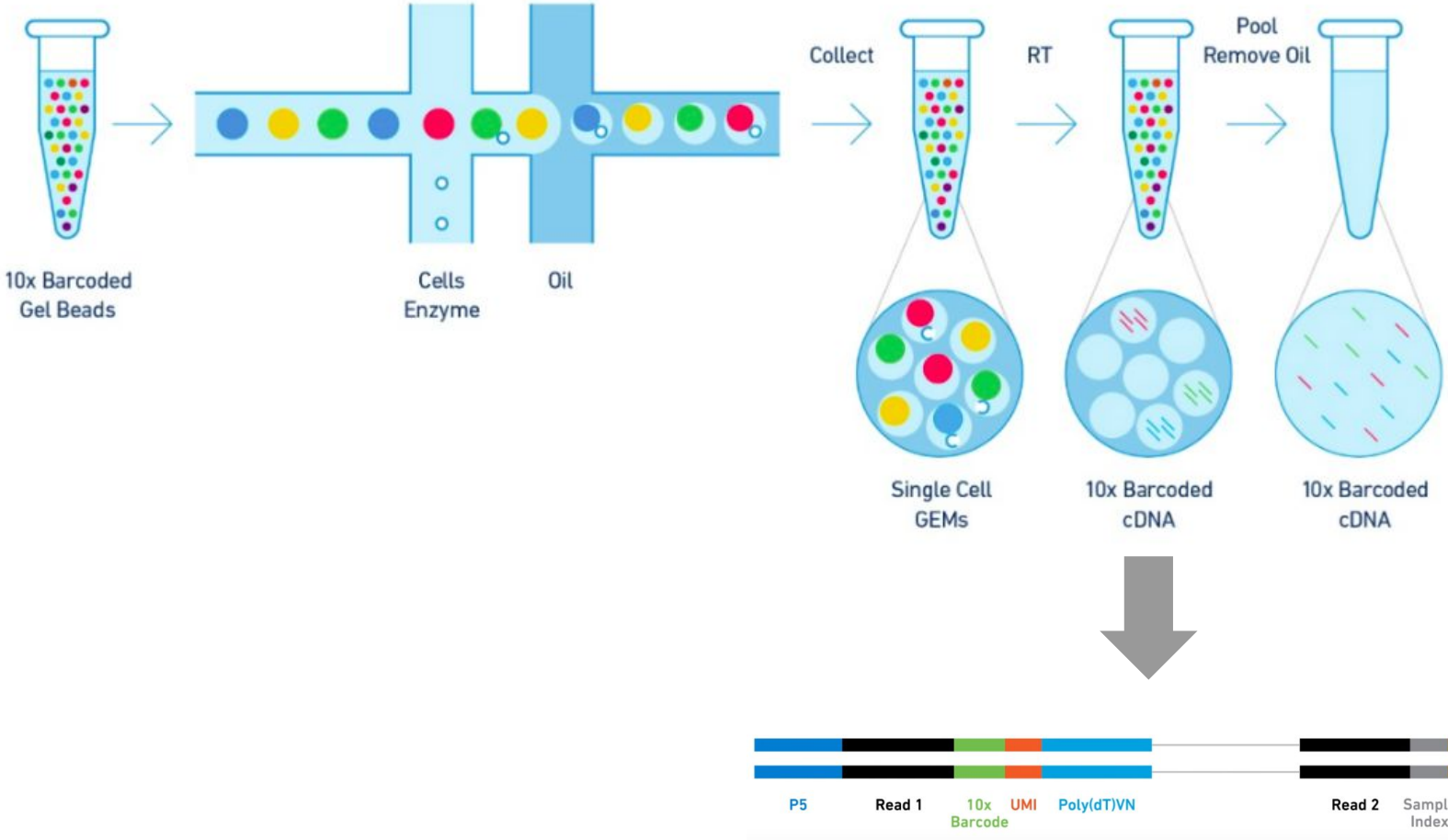
10x Software Tools
Turn-key analysis & visualization

Gel bead in Emulsion droplet (GEM)

Encapsulates each tiny micro-reaction within the Chromium System






10x Barcoded
Gel Beads
Cells
Enzyme
Oil
Collect
RT
Pool
Remove Oil
Single Cell
GEMs
10x Barcoded
cDNA
10x Barcoded
cDNA
P5
Read 1
10x
Barcode
UMI
Poly(dT)VN
Read 2
Sample
Index
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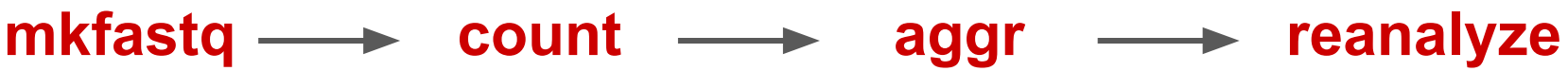
Analyzing Process of 10X Genomics

Single-Library Analysis with cellranger count

- Run **cellranger mkfastq** on the **Illumina BCL output folder** to generate **FASTQ files**.
- Run **cellranger count** on each library that was demultiplexed by cellranger mkfastq
- Optionally, run **cellranger aggr** to aggregate multiple libraries from a single experiment that were analyzed by cellranger count
- Optionally run **cellranger reanalyze** to re-run the secondary analysis on a library or aggregated set of libraries (i.e., PCA, t-SNE, and clustering).



Illumina

Binary base call format (BCL)

Illumina bcl2fastq

FASTQ File

Bowtie / Tophat / Cufflinks / Cuffdiff Pipeline

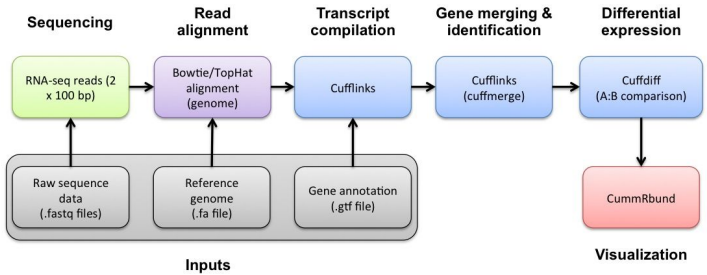
Bowtie / TopHat

SAM/BAM File

Cufflinks

Cuffdiff

Bowtie/Tophat/Cufflinks/Cuffdiff RNA-Seq Pipeline



Tophat/Cufflinks Workflow