High Throughput Sequencing the Multi-Tool of Life Sciences

Lutz Froenicke

DNA Technologies and Expression Analysis Cores

UCD Genome Center

Outline

- Who are we and what are we doing?
- Overview HTS sequencing technologies
- How does Illumina sequencing work? Sequencing library and run QC
- How does RNA-seq work?
- PacBio and Nanopore Sequencing
- Some cutting edge technologies & applications

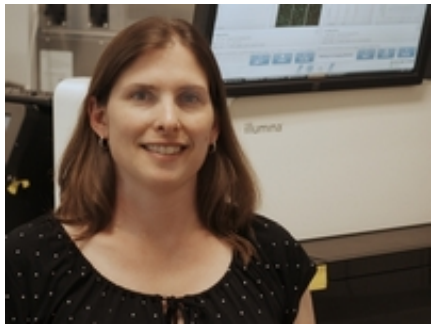
DNA Technologies & Expression Analysis Cores

- HT Sequencing Illumina
- Long-Read & Linked-Read Sequencing
  PacBio, Oxoford Nanopore, 10X Genomics
- HMW DNA isolation
- Illumina microarray (genotyping)
- Single-cell RNA-seq

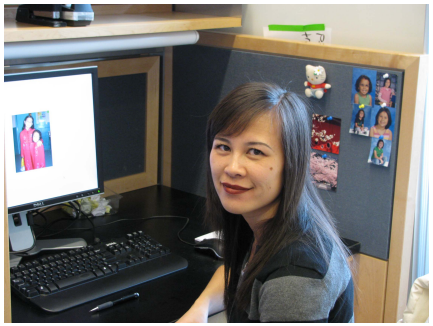
- Consultations → Experimental Design
  (Bioinformatics Core & DNA Tech Core)

- introducing new technologies to the campus
- shared equipment
- teaching (workshops)

The DNA Tech Core Team

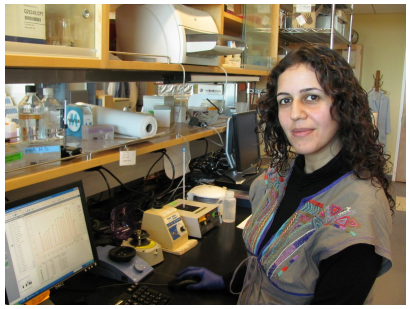


Emily

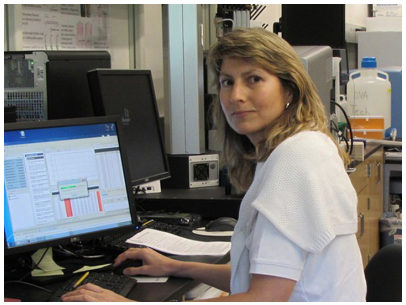


Oanh

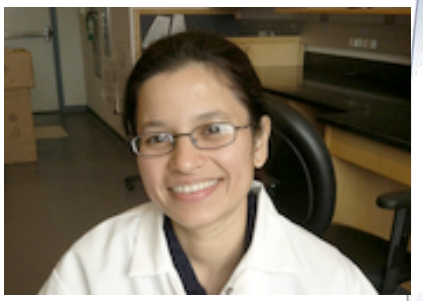
Diana



Siranoosh

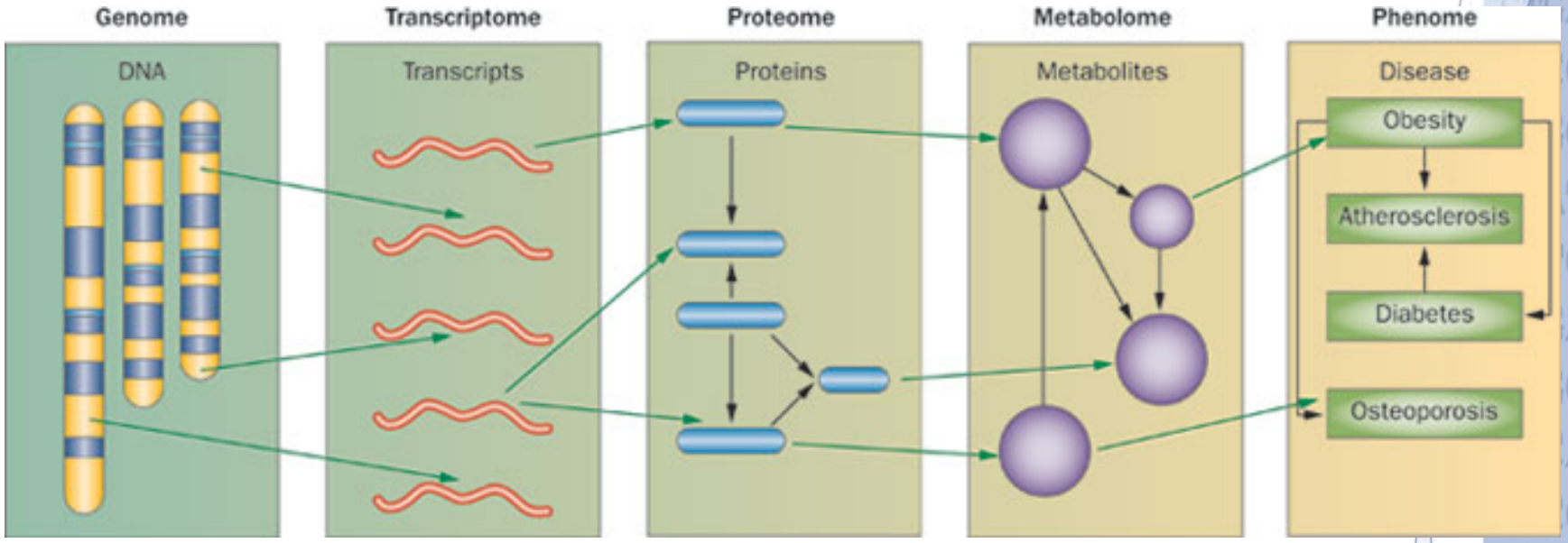


Vanessa



Ruta

The UCD GENOME CENTER



DNA Tech & Expression Analysis Proteomics Core Metabolomics Core

"DNA makes RNA and RNA makes protein"

the Central Dogma of Molecular Biology; simplified from Francis Crick 1958

nature REVIEWS CARDIOLOGY

MacLellan, W. R. *et al.* (2012) Systems-based approaches to cardiovascular disease *Nat. Rev. Cardiol.* doi:10.1038/nrcardio.2011.208

Complementary Approaches

Illumina	PacBio CLR	PacBio HiFi	PromethION Nanopore
Still-imaging of clusters (~1000 clonal molecules)	Video recordings fluorescence of single molecules	Video recordings fluorescence of single molecules	Recording of electric current through pores
Short reads - 2x300 bp Miseq	Up to 70 kb, N50 25 kb	Up to 20 kb, N50 18	Up to 100 kb, N50 30 kb
Repeats are mostly not analyzable	spans retro elements	accurate enough to assemble through REs	spans retro elements
High output - up to 2.4 Tb per lane	up to 100 Gb per SMRT-cell	up to 25 Gb HiFi data per cell	Up to 100 Gb per flowcell
High accuracy (< 0.5 %)	Raw data error rate 15 %	CCS data < 0.1%	Raw data error rate 8 %
Considerable base composition bias	No base composition bias	No base composition bias, but still mononucleotide repeat problem	Some systematic errors,
Very affordable	Costs 3 to 5 times higher	Costs 3 to 5 times higher	Costs 2x higher
De novo assemblies of thousands of scaffolds	“Near perfect” genome assemblies	“Near perfect” genome assemblies; lowest error rate	“Near perfect” genome assemblies with suppl. data; highest contiguity

High Throughput Short Read Sequencing: Illumina

- Whole genome sequencing & Exome sequencing:
  Variant detection (small variants SNPs and indels)
  Copy number variation (CNVs; prenatal diagnostics)

- Genotyping by sequencing

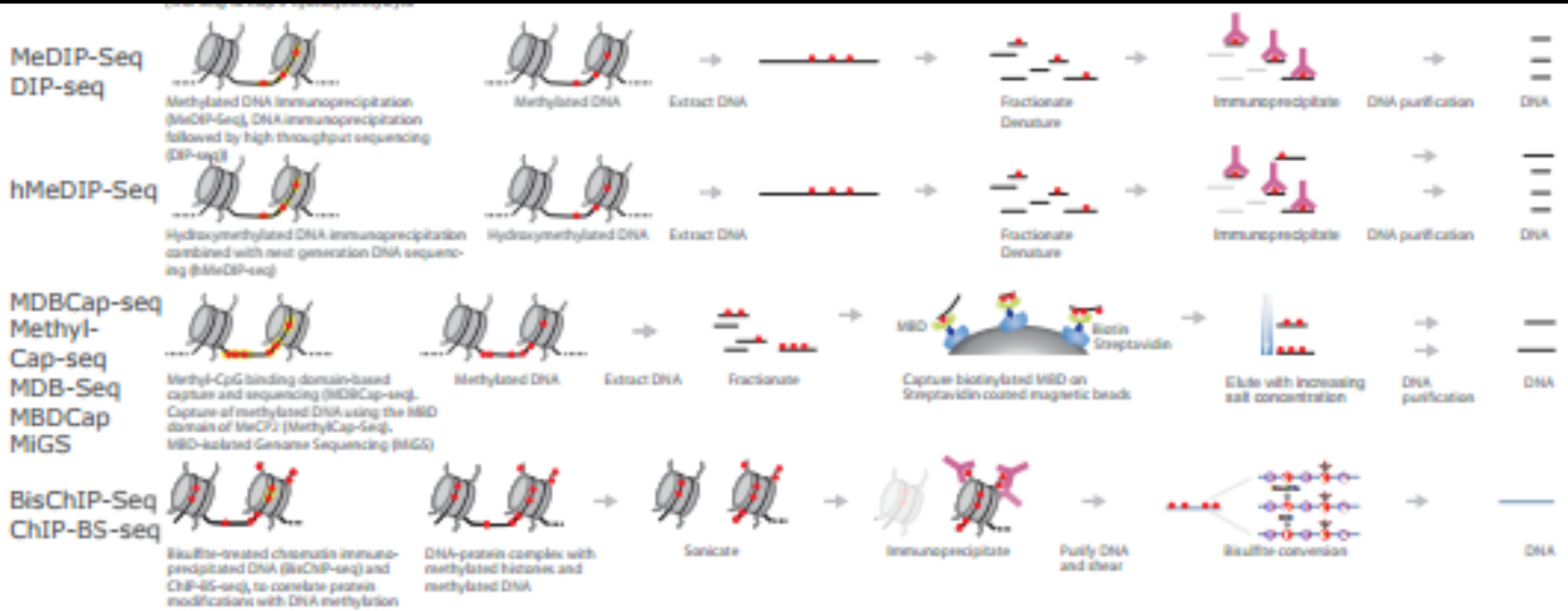
- Genome assemblies: small genomes

- Metagenomics

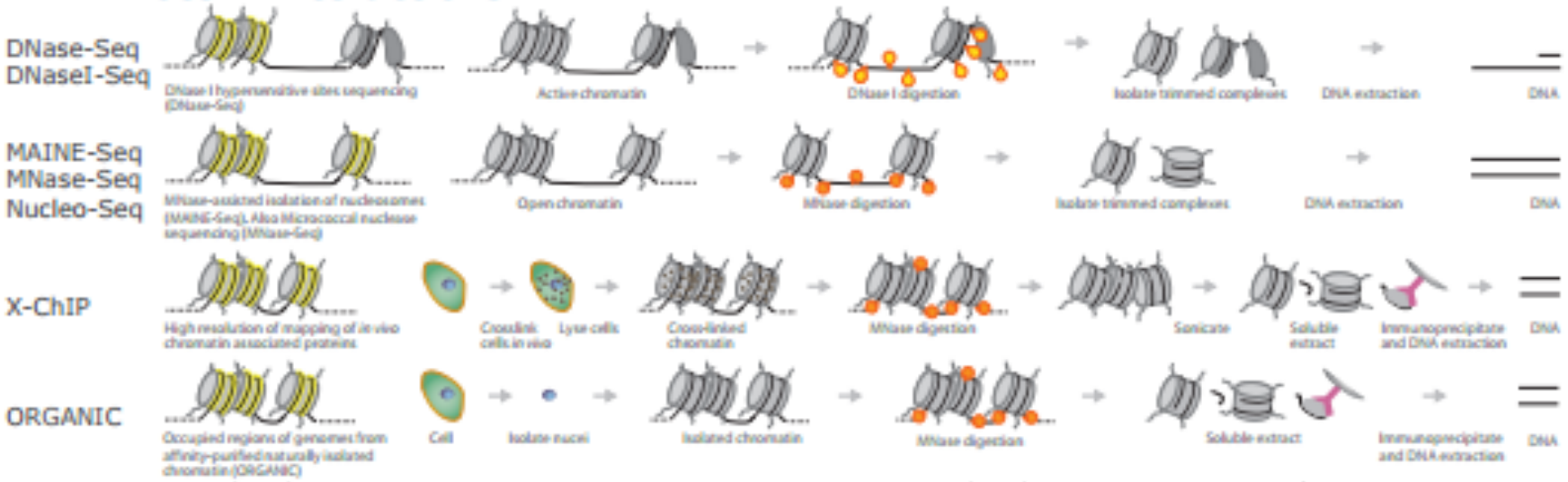
- RNA-seq: gene expression, transcript expression
- Small RNA-seq
- Single-cell RNA-seq

- Epigenetics: Methyl-Seq:
- ChIP-Seq (detecting molecular interactions)

- 3D Organization of the nucleus (Hi-C)



DNA-Protein Interactions



Long Read Sequencing: PacBio and Nanopore

- Whole genome sequencing : Highest quality genome assemblies, Structural variant detection

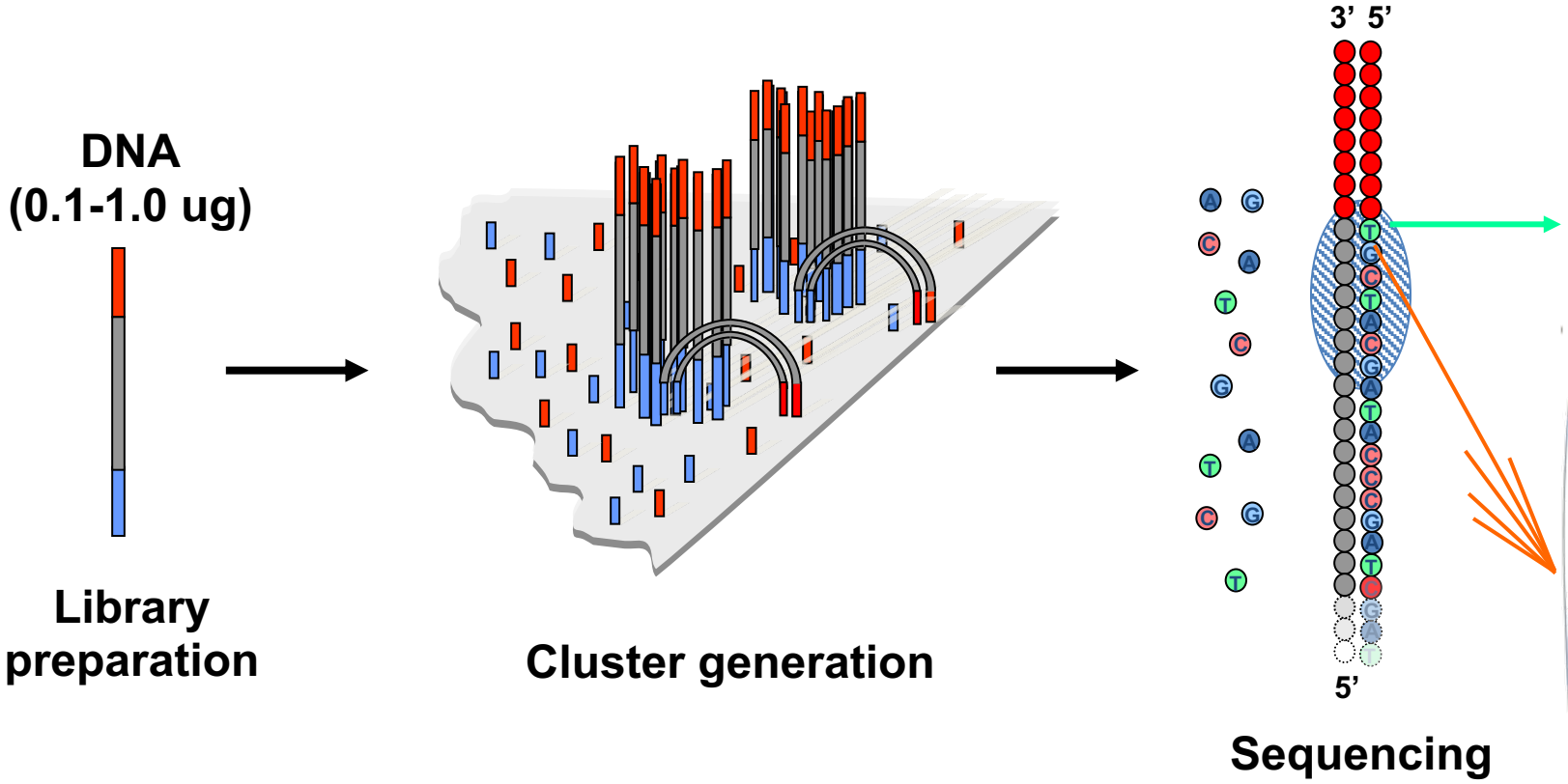
- RNA-sequencing:
- full transcript data, Iso-form detection and quantification
- Direct RNA-seq identifies base modifications (Nanopore)

- Metagenomics

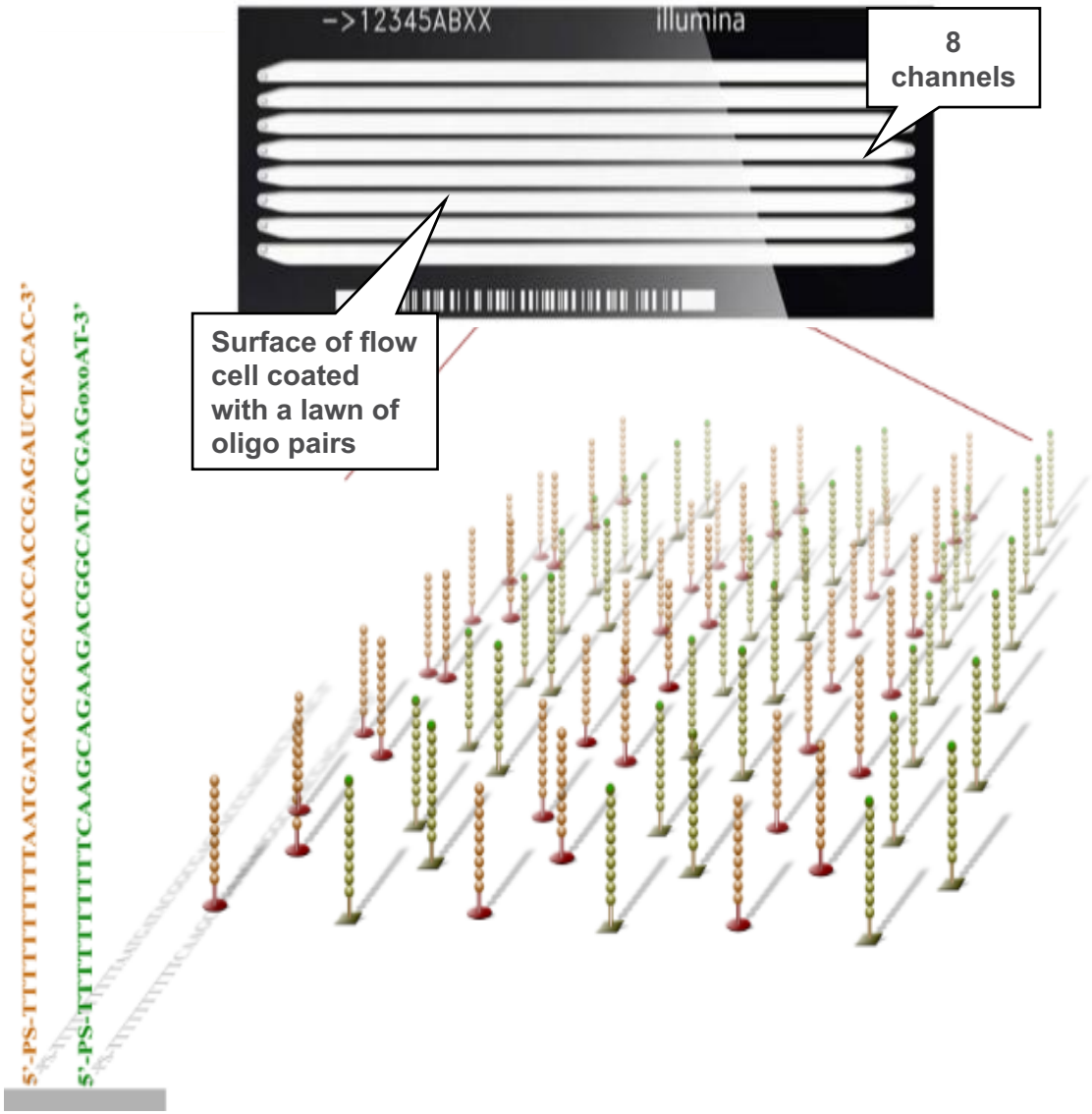
- Epigenetics (Nanopore: any modified bases, PacBio bacteria)

Illumina Sequencing Technology

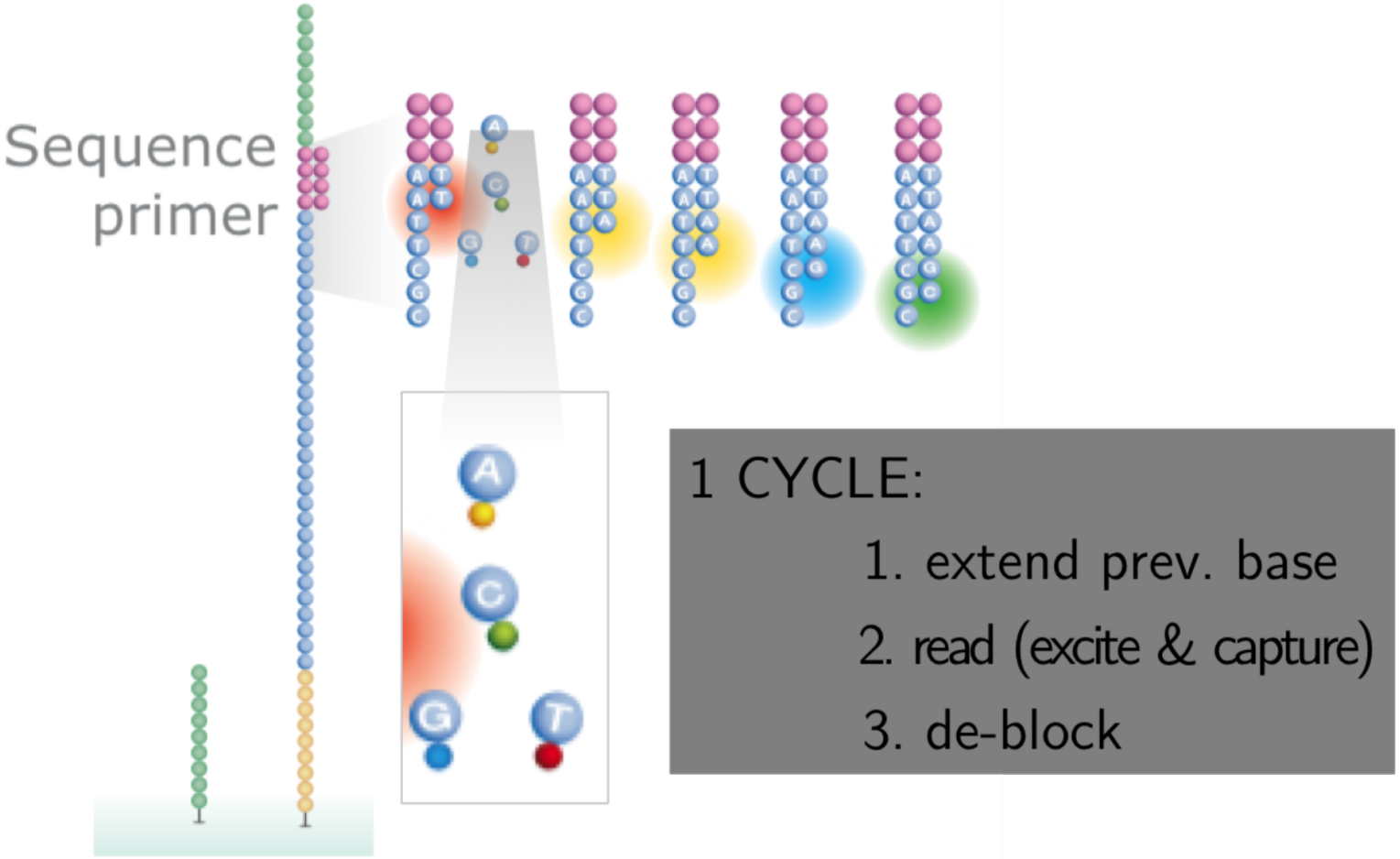
Sequencing By Synthesis (SBS) Technology



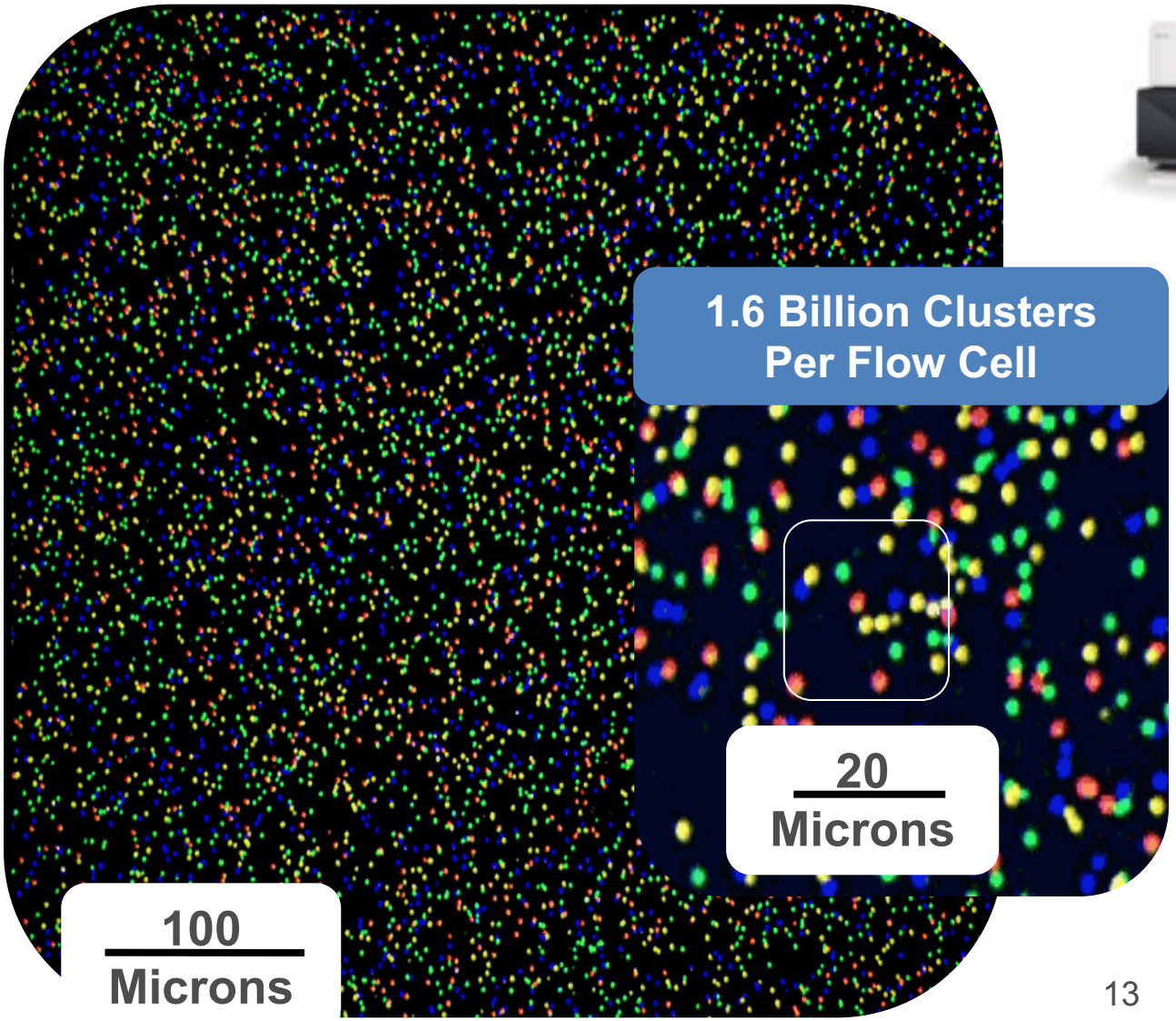
TruSeq Chemistry: Flow Cell



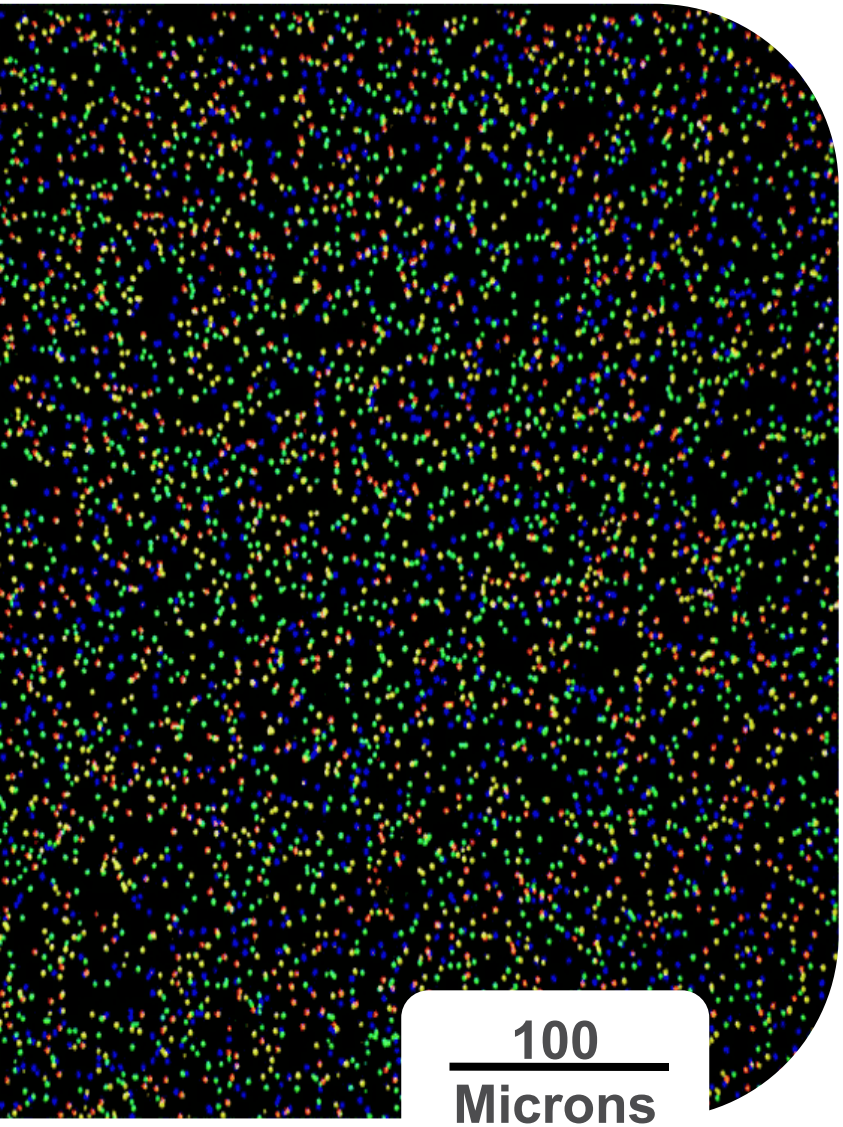
Illumina's sequencing is based on **fluorophore-labelled dNTPs** with **reversible** terminator elements that will become incorporated and excited by a laser one at a time.

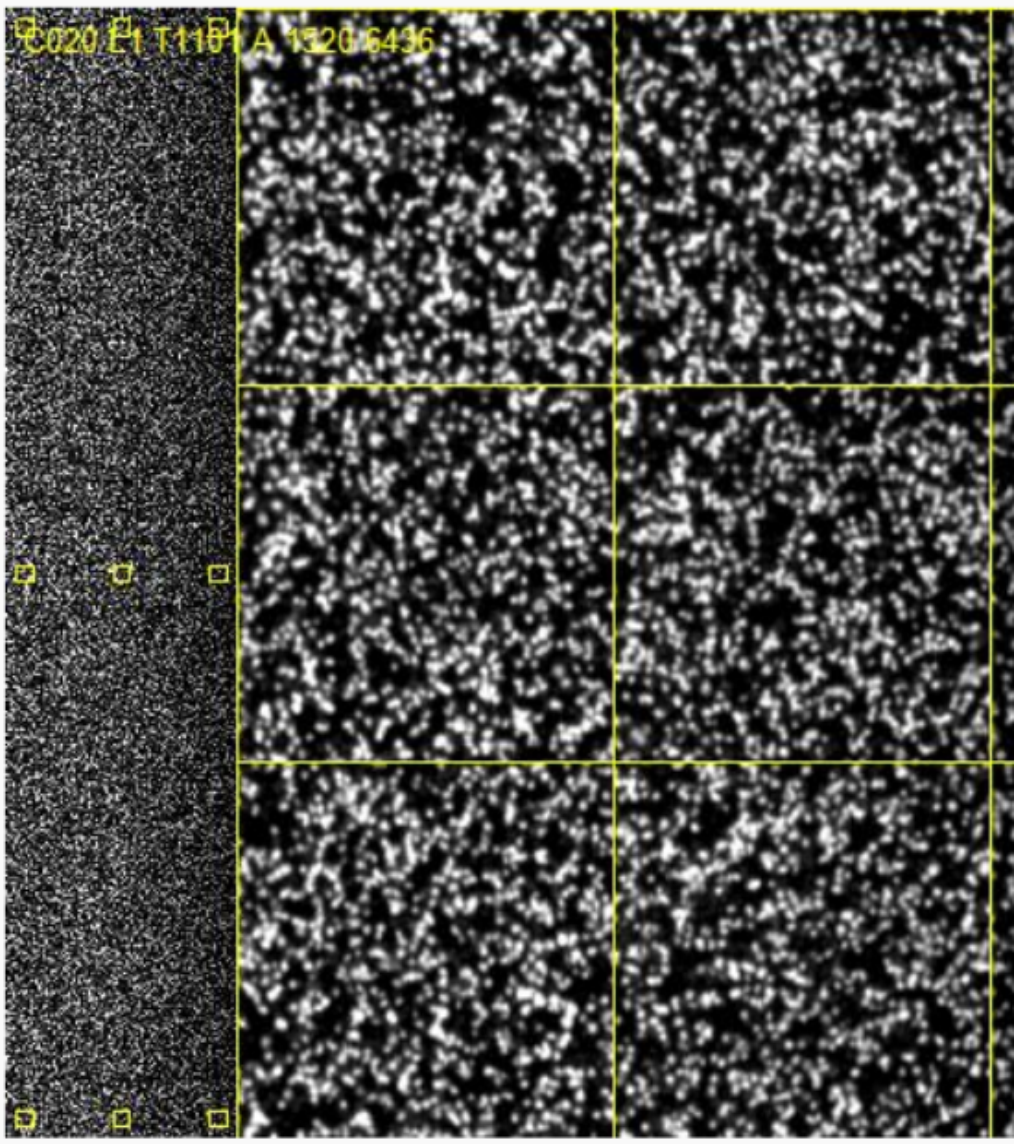


False colored and merged four channel flowcell images

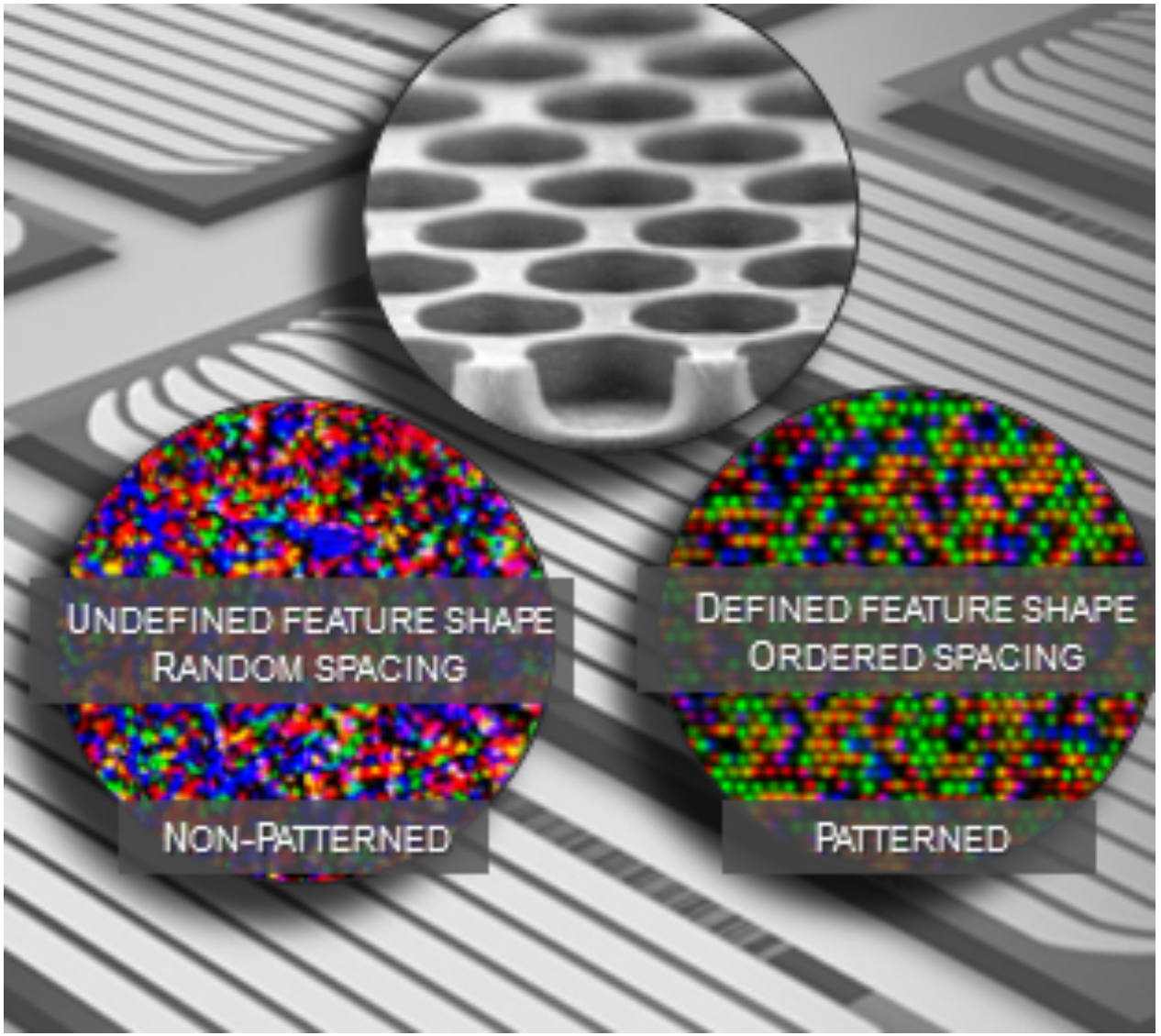


B&W imaging

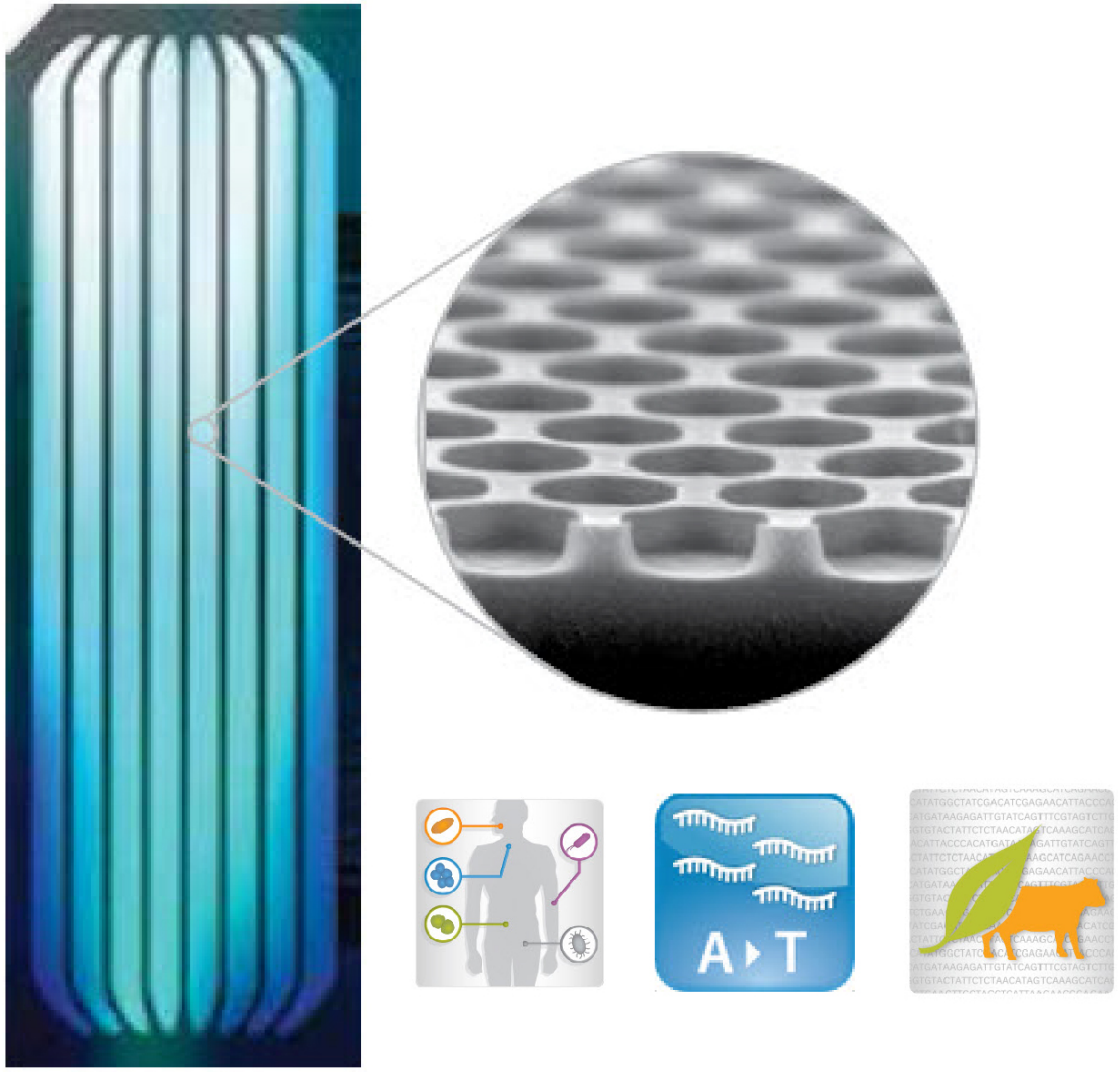




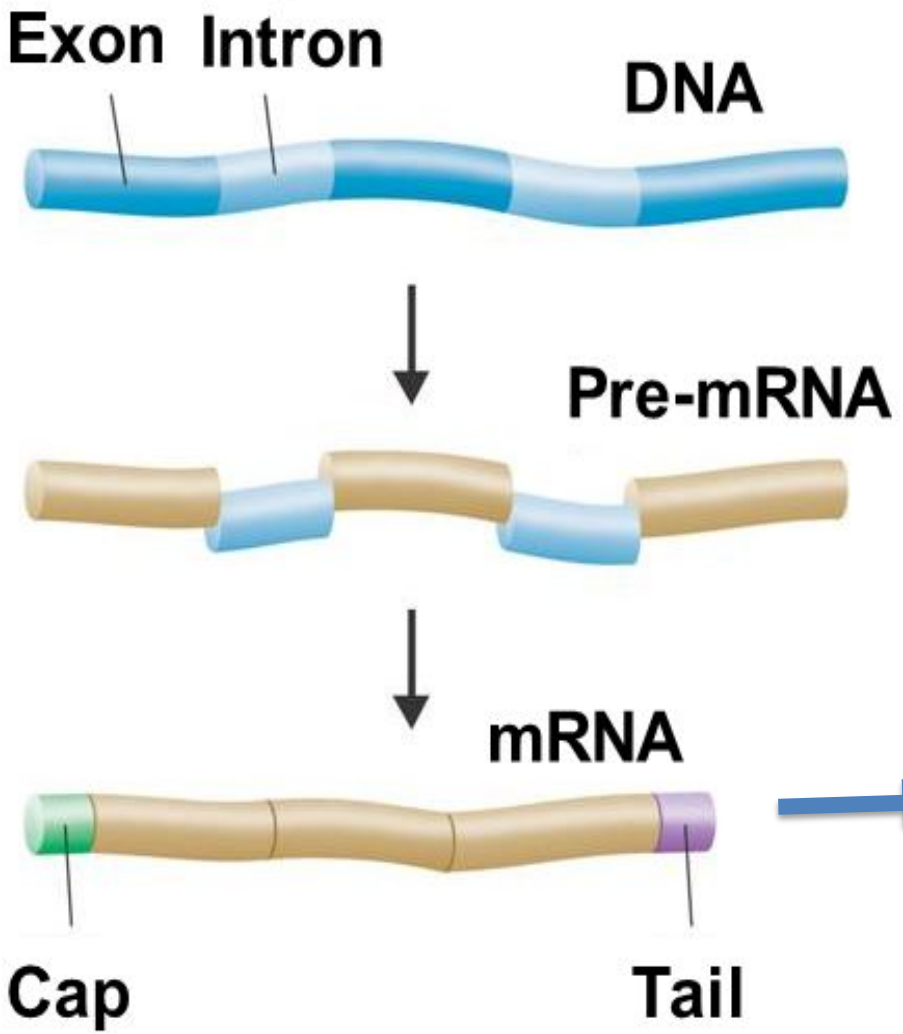
Patterned Flowcell



Hiseq 4000: 478 million nanowells per lane

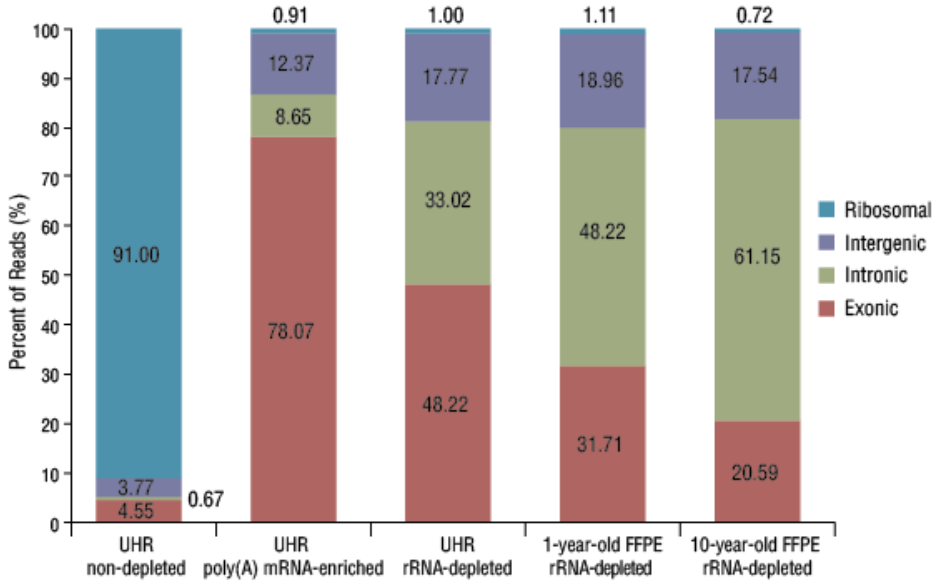


transcription and processing in nucleus



transport through nuclear pore

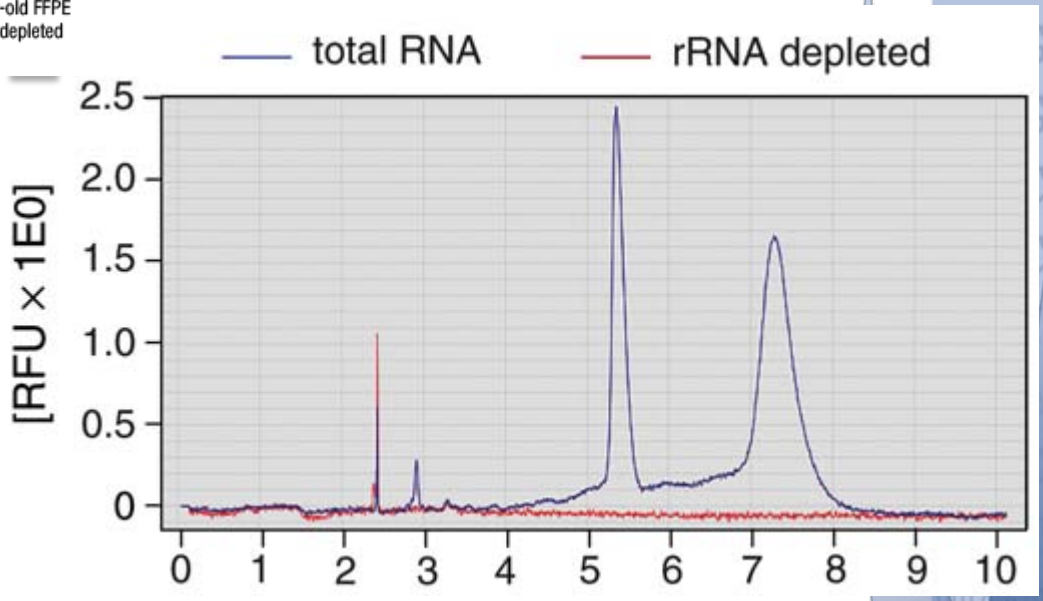
mRNA makes up only about 2% of a total RNA sample



- more than 90% rRNA content

- multiple other non-coding RNA species

Bioanalyzer trace before and after ribo-depletion

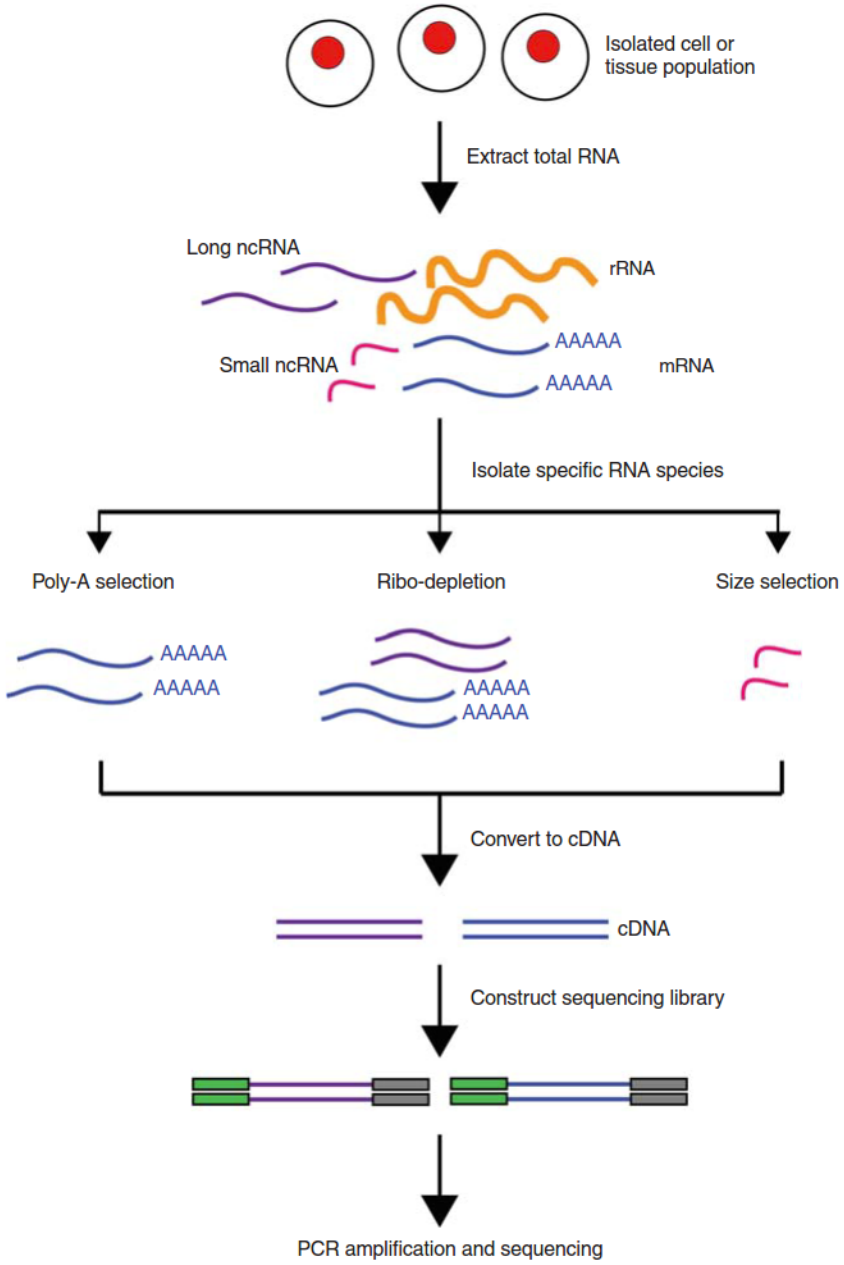


RNA-Seq library prep procedure

1. RNA-sample QC, quantification, and normalization
2. Removal of ribosomal RNA sequences:
   via positive or negative selection: Poly-A enrichment or ribo-depletion
3. Fragment RNA:
   heating in Mg++ containing buffer – chemical fragmentation has little bias
4. First-strand synthesis:
   random hexamer primed reverse transcription
5. RNAse-H digestion:
   - creates nicks in RNA strand; the nicks prime 2nd-strand synthesis
   - dUTP incorporated into 2nd strand only
6. A-tailing and adapter ligation exactly as for DNA-Seq libraries
7. PCR amplification of only the first strand to achieve strand-specific libraries - archeal polymerases will not use dUTP containing DNA as template

Illumina sequencing workflow

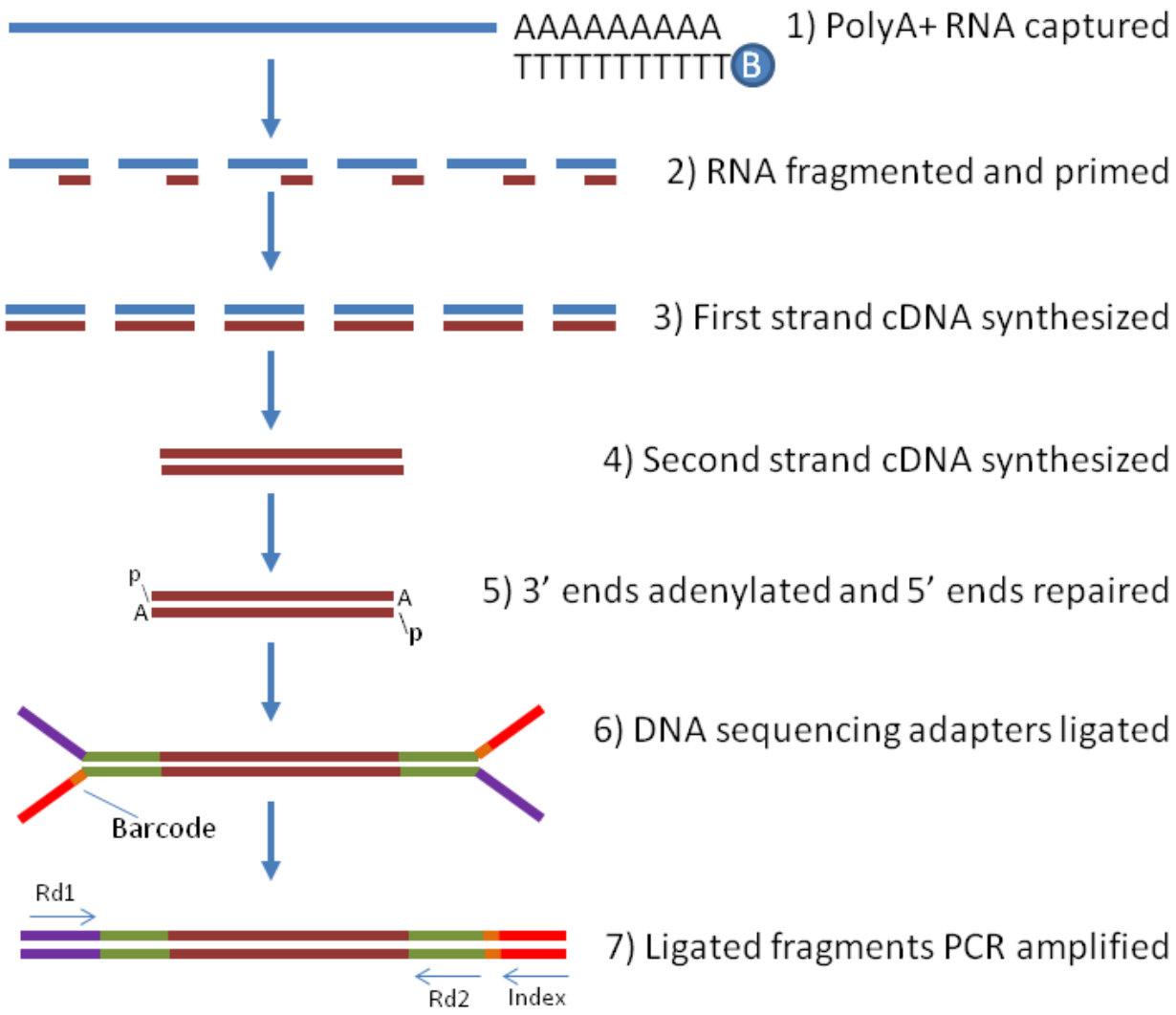
- Library Construction
- Cluster Formation
- Sequencing
- Data Analysis



RNA-seq?

Sorry – Illumina and PacBio are only sequencing DNA.

Conventional RNA-Seq library preparation w. Poly-A capture



What will go wrong ?

- cluster identification
- bubbles
- synthesis errors:

```
ClusterCluster
ClustsrCluster
ClusterCluster
ClusterCluster
CllsterCluster
```

What will go wrong ?

- synthesis errors:

```
ClusterCluster
ClustsrCluster
ClusterCluster
ClusterCluster
CllsterCluster
```

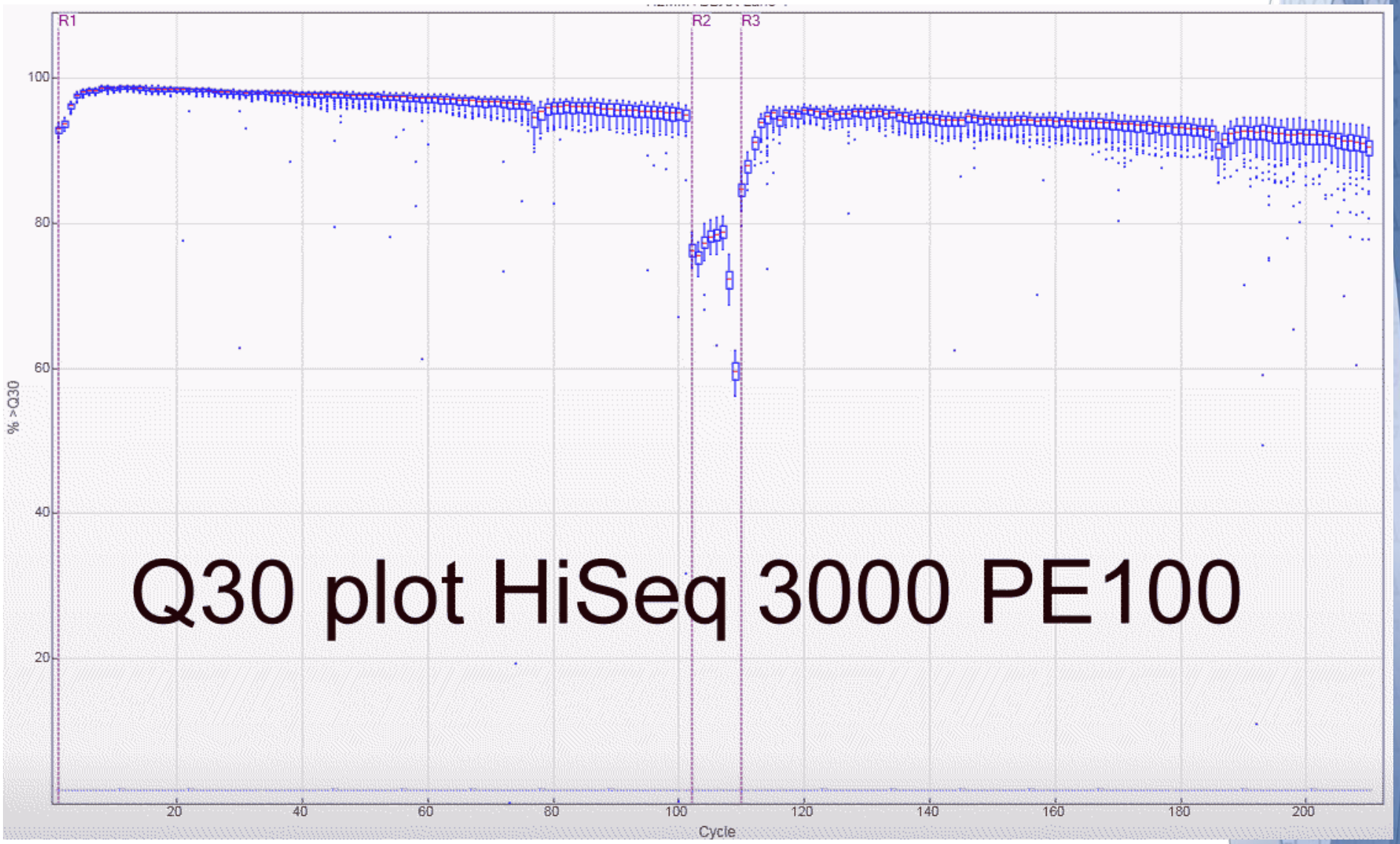
```
ClsterClusterC
ClusterCluster
ClusterCluster
CllusterCluste
ClusterCluster
```

Phasing & Pre-Phasing problems

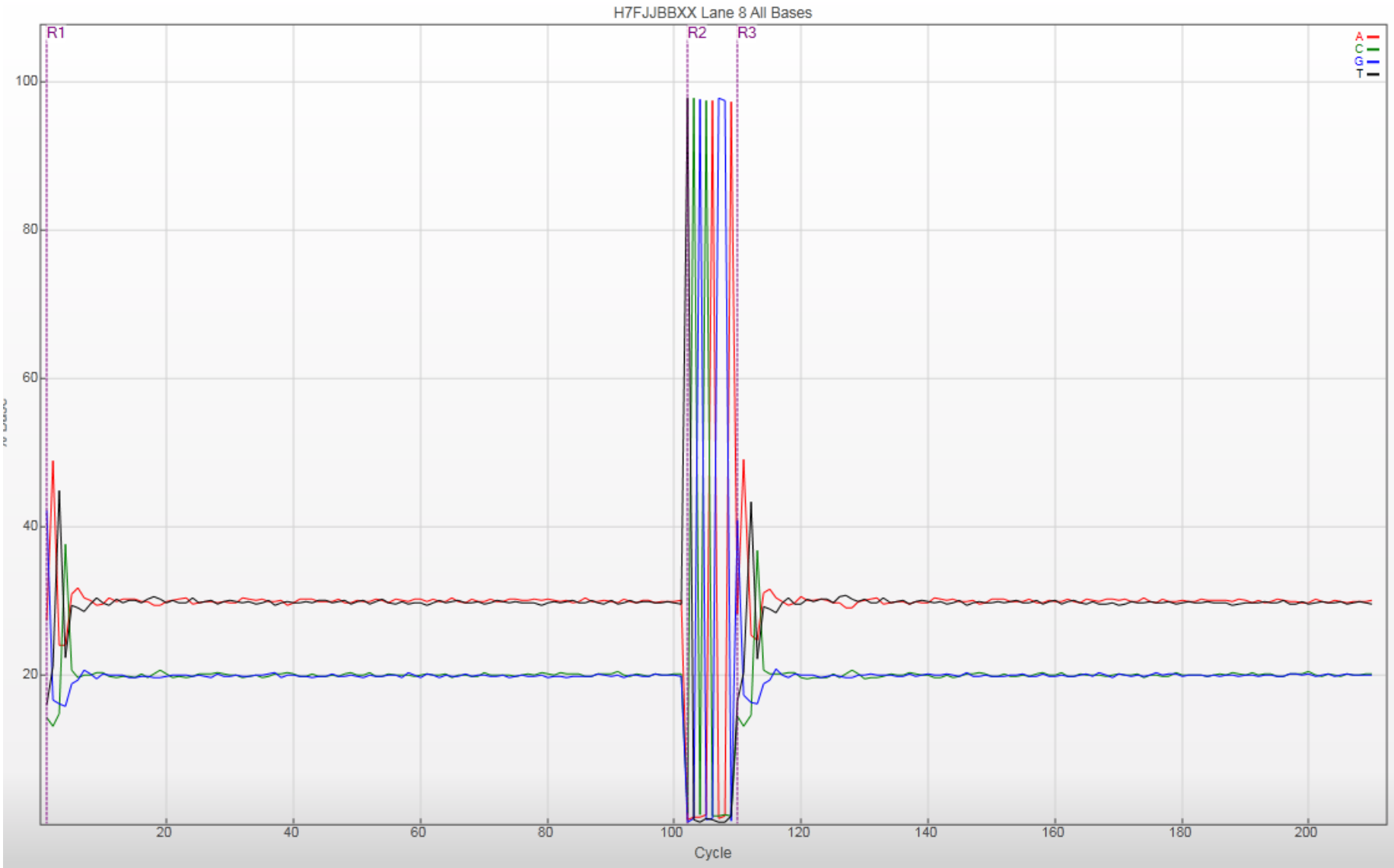
The first lines of your data

```
@700593F:586:HTWJJBCXX:1:1107:2237:10031 2:N:0:GGAGAACA
NNNNNNNNNNNNNNNNNNNNNAGGCCAGCCATAGAACGCTCCCGGCTTCACGGACGT
CATATAGTCAGGCACGAGGTCGGCGCCGAGTTCGTCACGCTCGTTGACGACCGCCCAT
ACCGCTTGATTTGCGGGGTTGATCGCTAGCGCGGTCGGATTGCGAATGCCCGAGGCAT
ACGTCCGATGGGCCCCGCTGGCGCGGTCCACTTCCCATACAACCGCGCGTTCCTCTTC
CAGCGCCATGCCGCGTT
+
@@@@@@@@@@@@@@@@@@@@@@@@IHHFIIIIIHIIIIIIIIEHIIIIIHHFHIIIIII
IIGHHHHIHHIIIIEHIIHIHIHIGIIHHDHIIIIIHHHHEEHIHIHCG/EH@GHHII
GIHHIIHHIIIICHGHHIHIIHHIIIIIHIHIIHIGIIIGIEH?H?HHHIGHIIIGHI
GHIDHH@AHHIHIH=HI=GHGHHGD
```

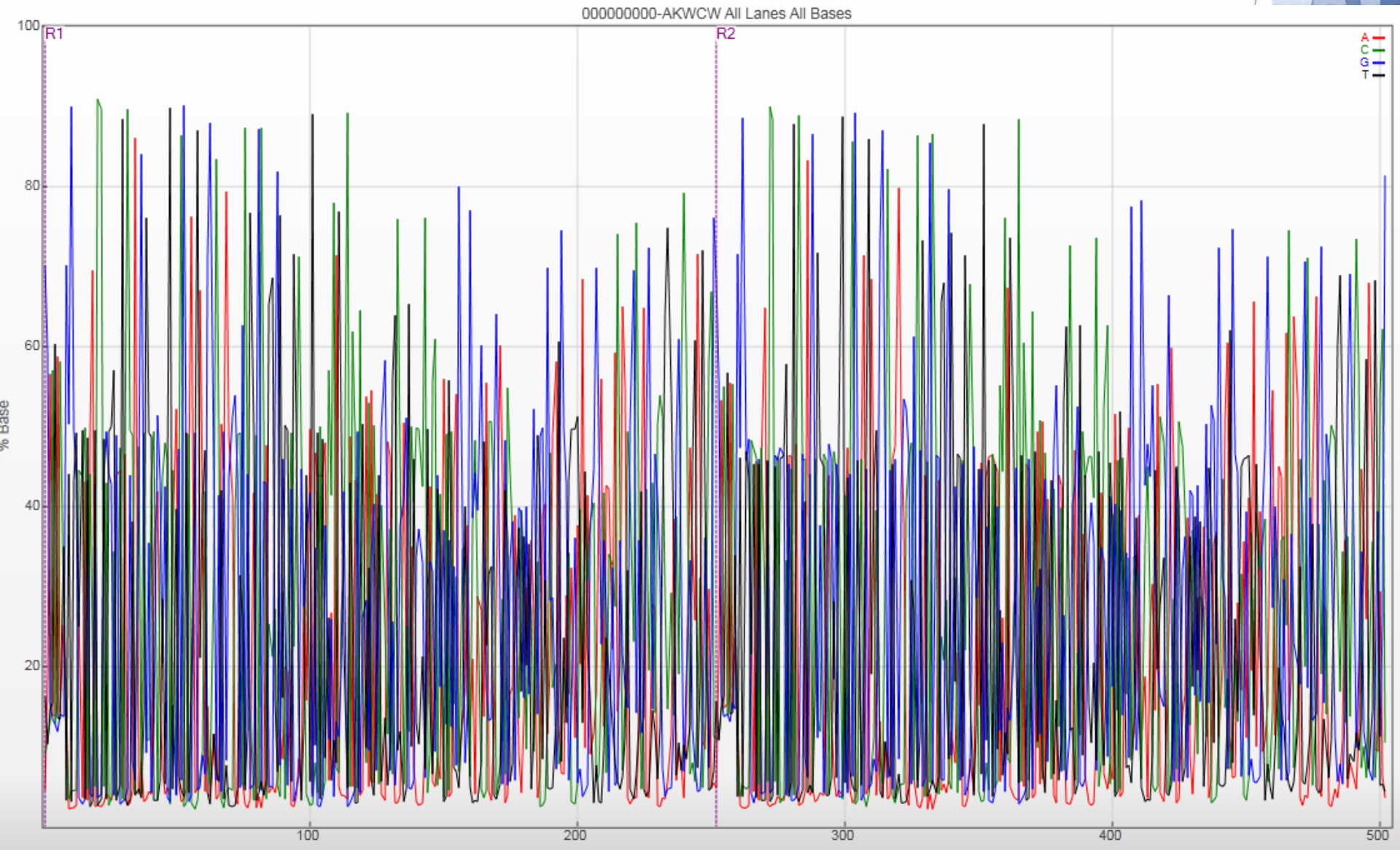
Illumina SAV viewer



base composition



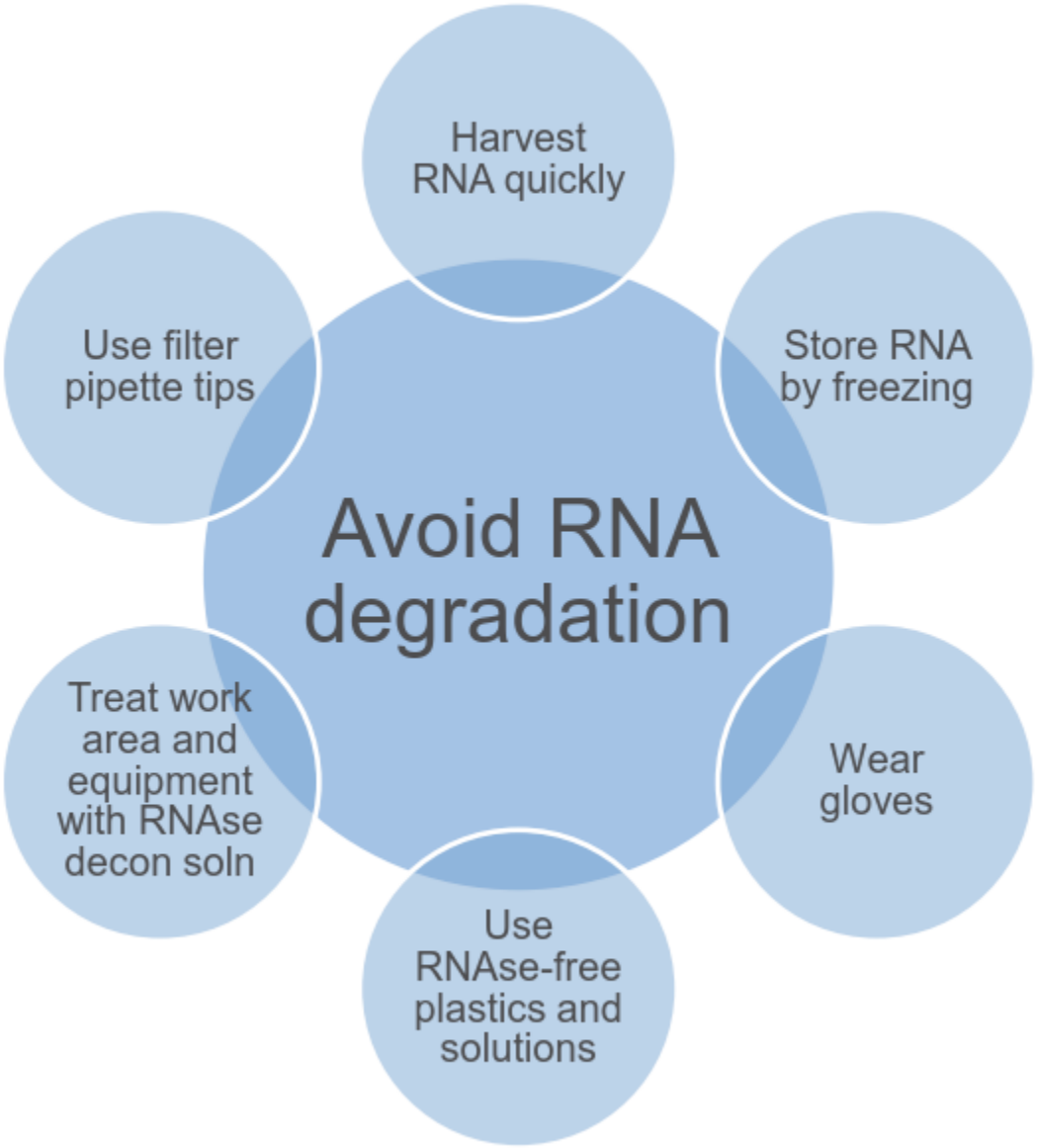
amplicon


000000000-AKWCW All Lanes All Bases
R1
R2
A
C
G
T
100
80
60
40
20
% Base
100
200
300
400
500

RNA is not that fragile

Actually: Avoid DEPC-treated reagents -- remnants can inhibit enzymes

RNA Handling Best Practices



- 18S (2500b) , 28S (4000b)

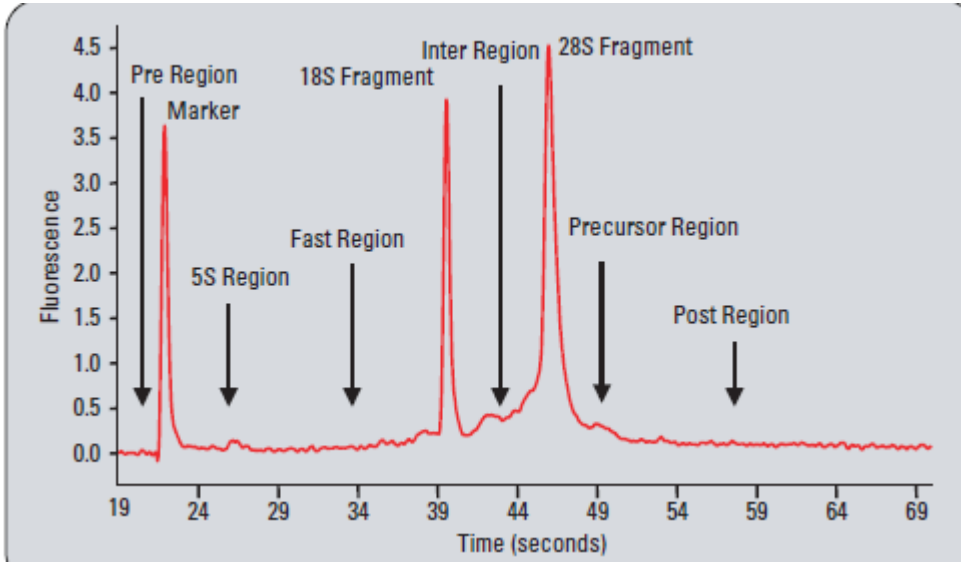
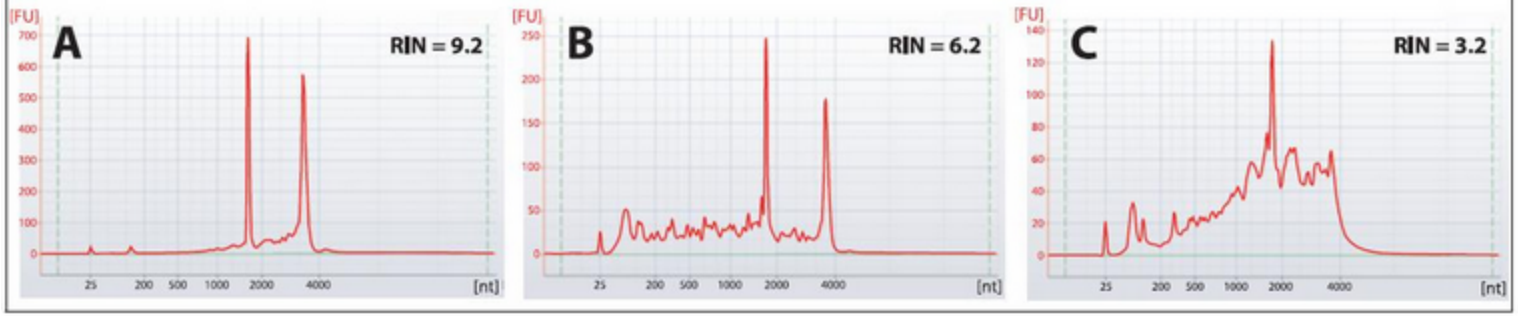
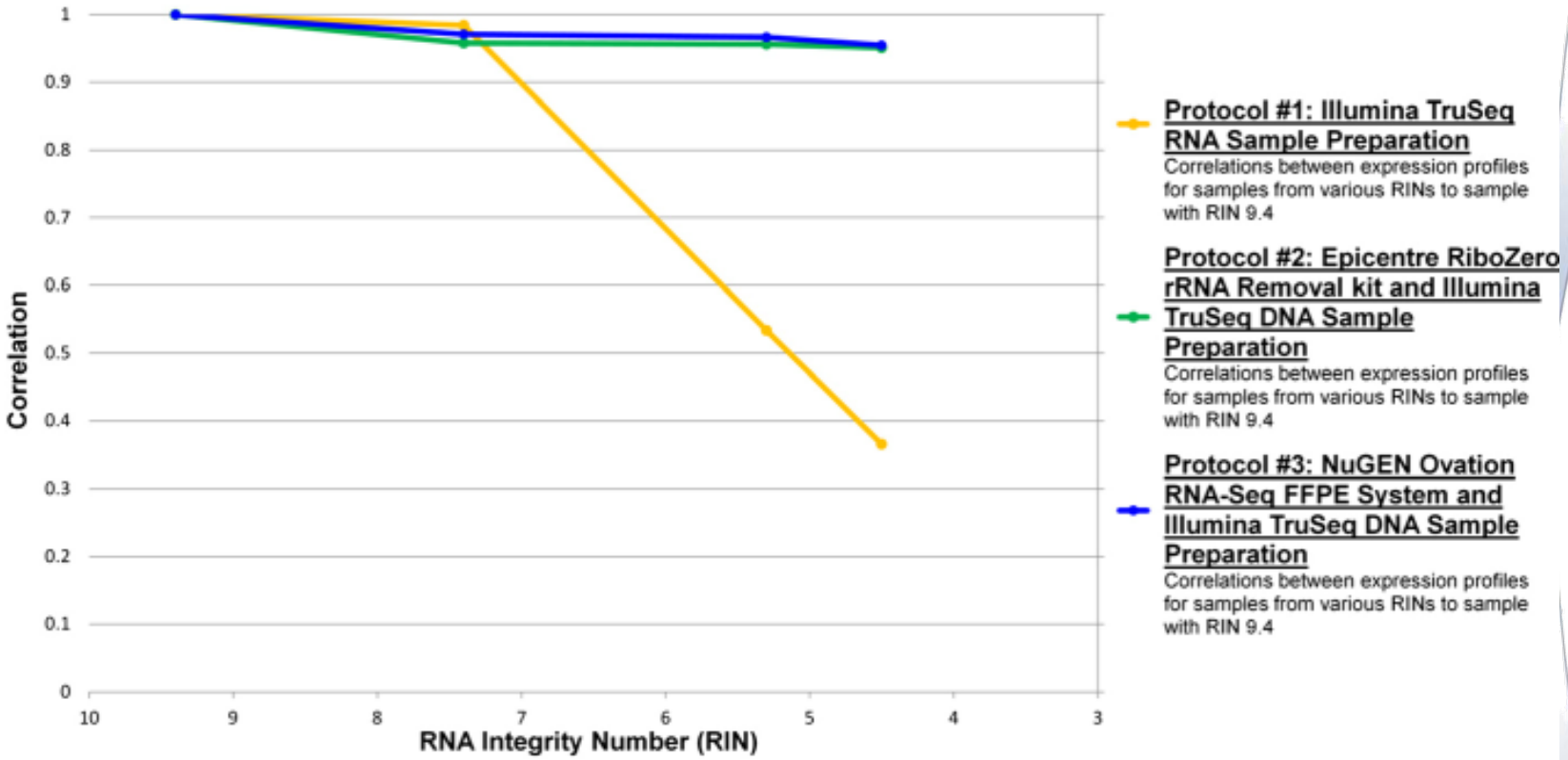


Figure 2.1 Example Agilent Bioanalyzer Electropherograms from three different total RNAs of varying integrity. Panel [A] represents a highly intact total RNA (RIN = 9.2), panel [B] represents a moderately intact total RNA (RIN = 6.2), and panel [C] represents a degraded total RNA sample (RIN = 3.2).



RNA integrity <> reproducibility



Chen et al. 2014

Quantitation & QC methods

- Intercalating dye methods (PicoGreen, Qubit, etc.):

Specific to dsDNA, accurate at low levels of DNA
Great for pooling of indexed libraries to be sequenced in one lane
Requires standard curve generation, many accurate pipetting steps

- Bioanalyzer:

Quantitation is good for rough estimate
Invaluable for library QC
High-sensitivity DNA chip allows quantitation of low DNA levels

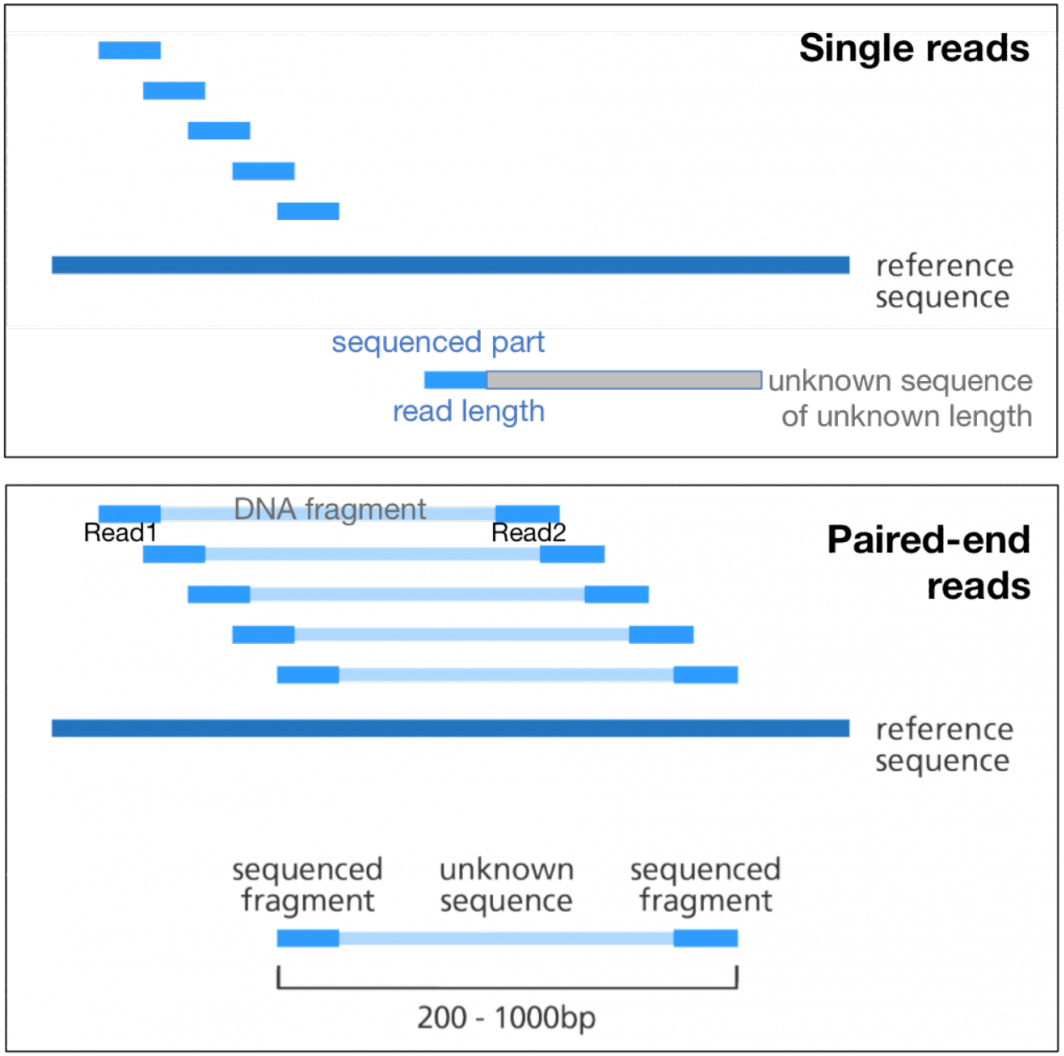
- qPCR

Most accurate quantitation method
More labor-intensive
Must be compared to a control

Recommended RNA input

Library prep kit	Starting material
mRNA (TruSeq)	100 ng – 4 µg total RNA
Directional mRNA (TruSeq)	1 – 5 µg total RNA or 50 ng mRNA
Apollo324 library robot (strand specific)	100 ng mRNA
Small RNA (TruSeq)	100 ng -1 µg total RNA
Ribo depletion (Epicentre)	500 ng – 5 µg total RNA
SMARTer™ Ultra Low RNA (Clontech)	100 pg – 10 ng
Ovation RNA seq V2, Single Cell RNA seq (NuGen)	10 ng – 100 ng

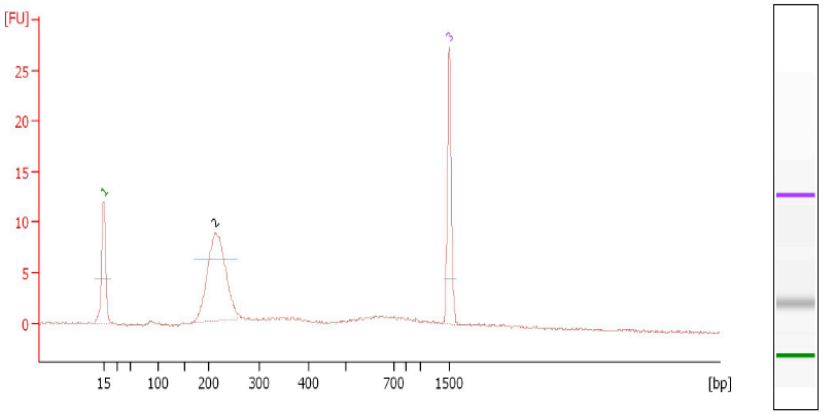
https://www.yourgenome.org/facts/how-do-you-put-a-genome-back-together-after-sequencing



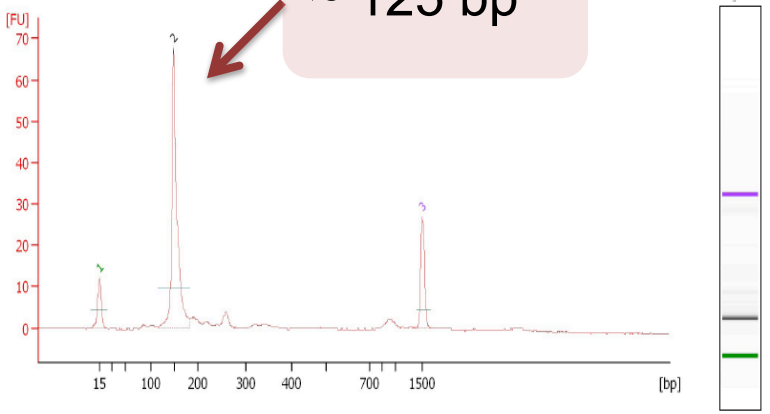
Single reads are the cheaper. Paired-end (PE) reads are helpful for:

- **alignment** along repetitive regions
- chromosomal **rearrangements** and gene fusion detection
- *de novo* genome and transcriptome **assembly**
- precise information about the size of the original fragment (**insert size**)
- PCR duplicate identification

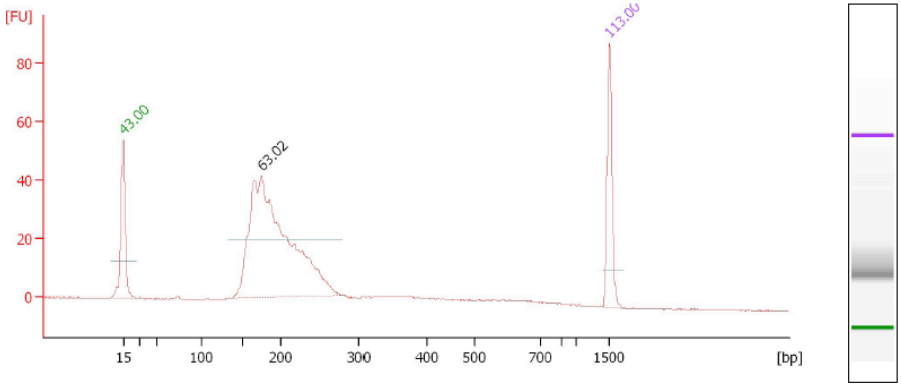
Library QC by Bioanalyzer



Beautiful

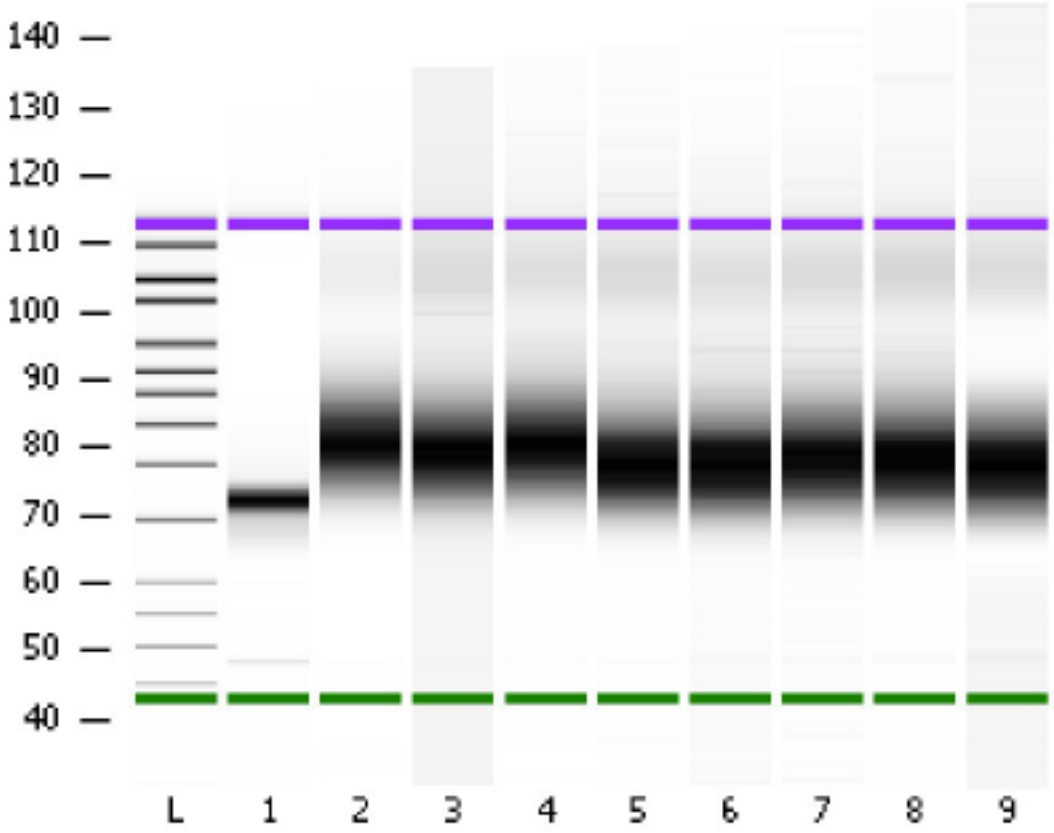


100% Adapters

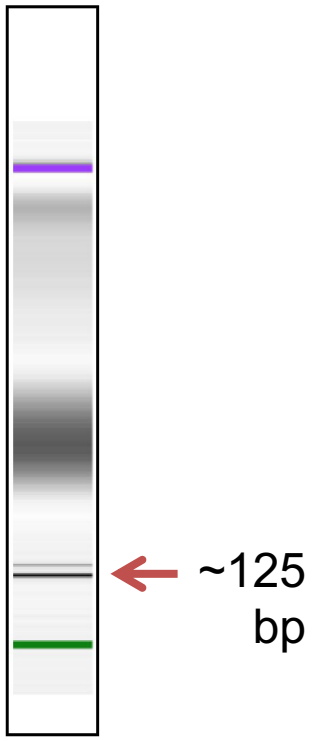


Beautiful

Library QC



Examples for successful libraries



Adapter contamination at ~125 bp

Considerations in choosing an RNA-Seq method

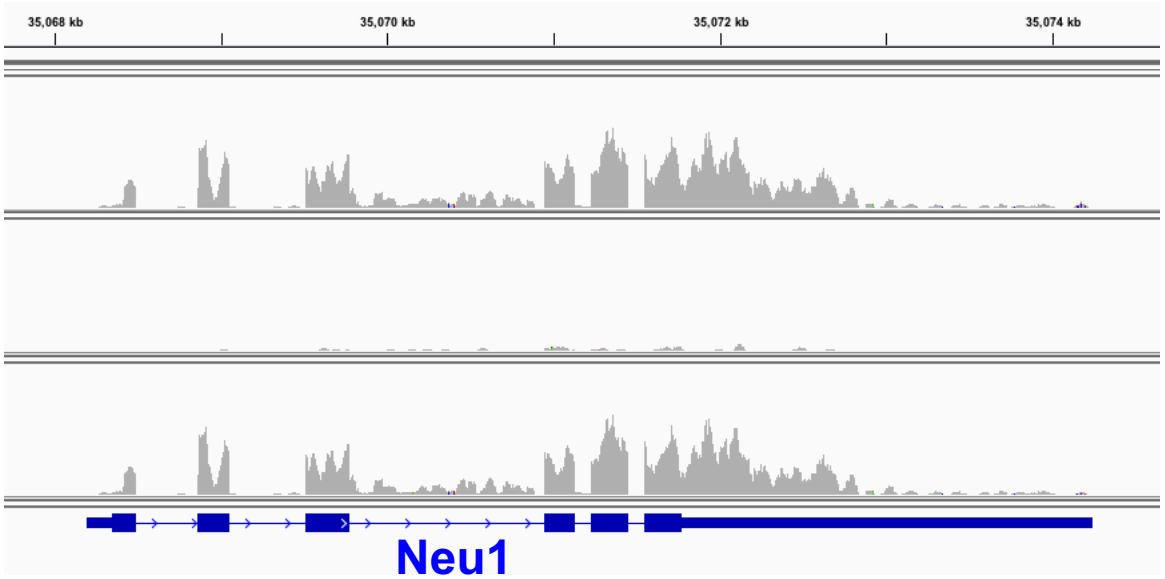
- Transcript type:
  - mRNA, extent of degradation
  - small/micro RNA
- Strandedness:
  - un-directional ds cDNA library
  - directional library
- Input RNA amount:
  - 0.1-4ug original total RNA
  - linear amplification from 0.5-10ng RNA
- Complexity:
  - original abundance
  - cDNA normalization for uniformity
- Boundary of transcripts:
  - identify 5’ and/or 3’ ends
  - poly-adenylation sites
  - Degradation, cleavage sites

strand-specific information

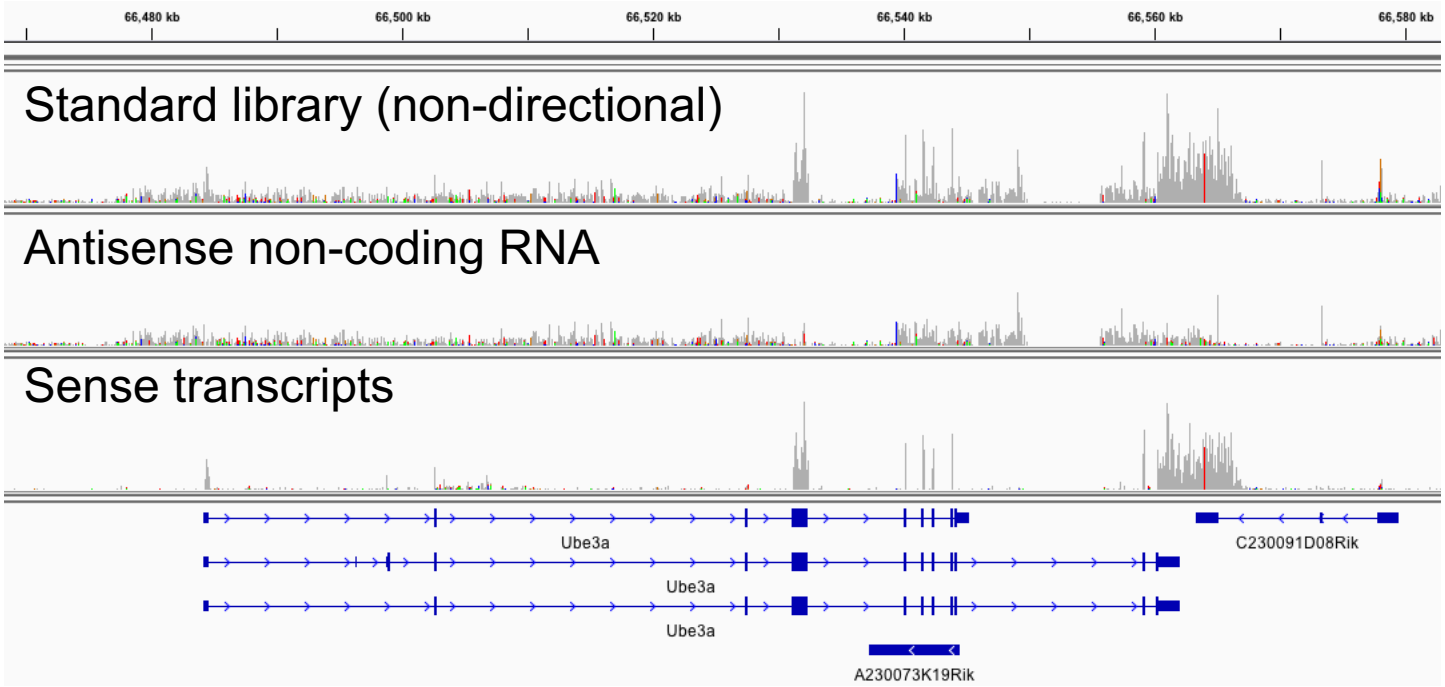
Standard library (non-directional)

antisense

sense



Strand-specific RNA-seq

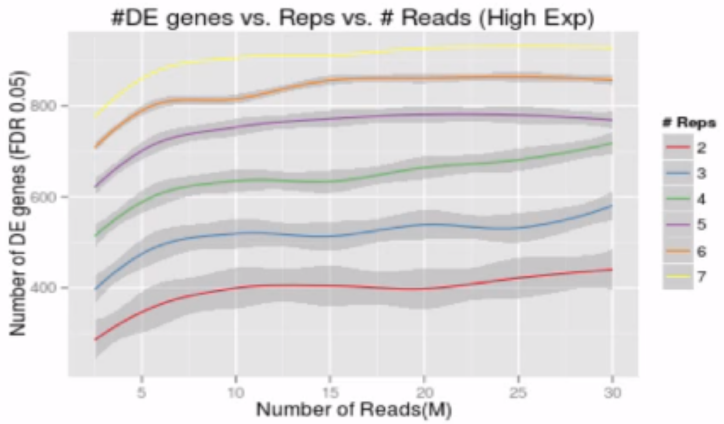


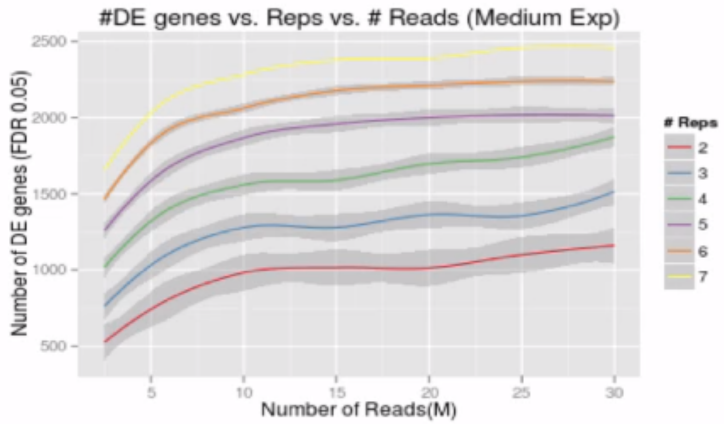
- Informative for non-coding RNAs and antisense transcripts
- Essential when NOT using polyA selection (mRNA)
- No disadvantage to preserving strand specificity

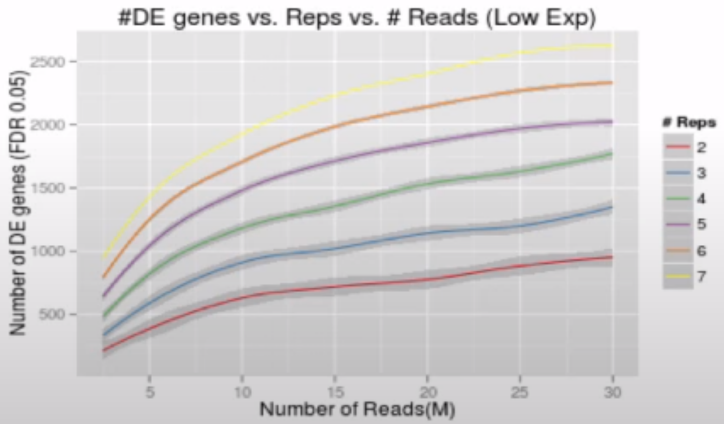
RNA-seq for DGE

- Differential Gene Expression (DGE)
  - 50 bp single end reads
  - 30 million reads per sample (eukaryotes)
    - 10 mill. reads > 80% of annotated genes
    - 30 mill. . reads > 90% of annotated genes
  - 10 million reads per sample (bacteria)

Experimental Design







For high expressers: Increasing sequencing depth has little effect on increasing number of DE genes detected, while biological replicates are clearly more beneficial.

For low expressers: Both sequencing depth and biological replicates increases power to detect DE genes.

Liu et al. (2014) RNA-Seq differential expression studies: more sequence or more replication?, Bioinformatics, 30(3):1-4

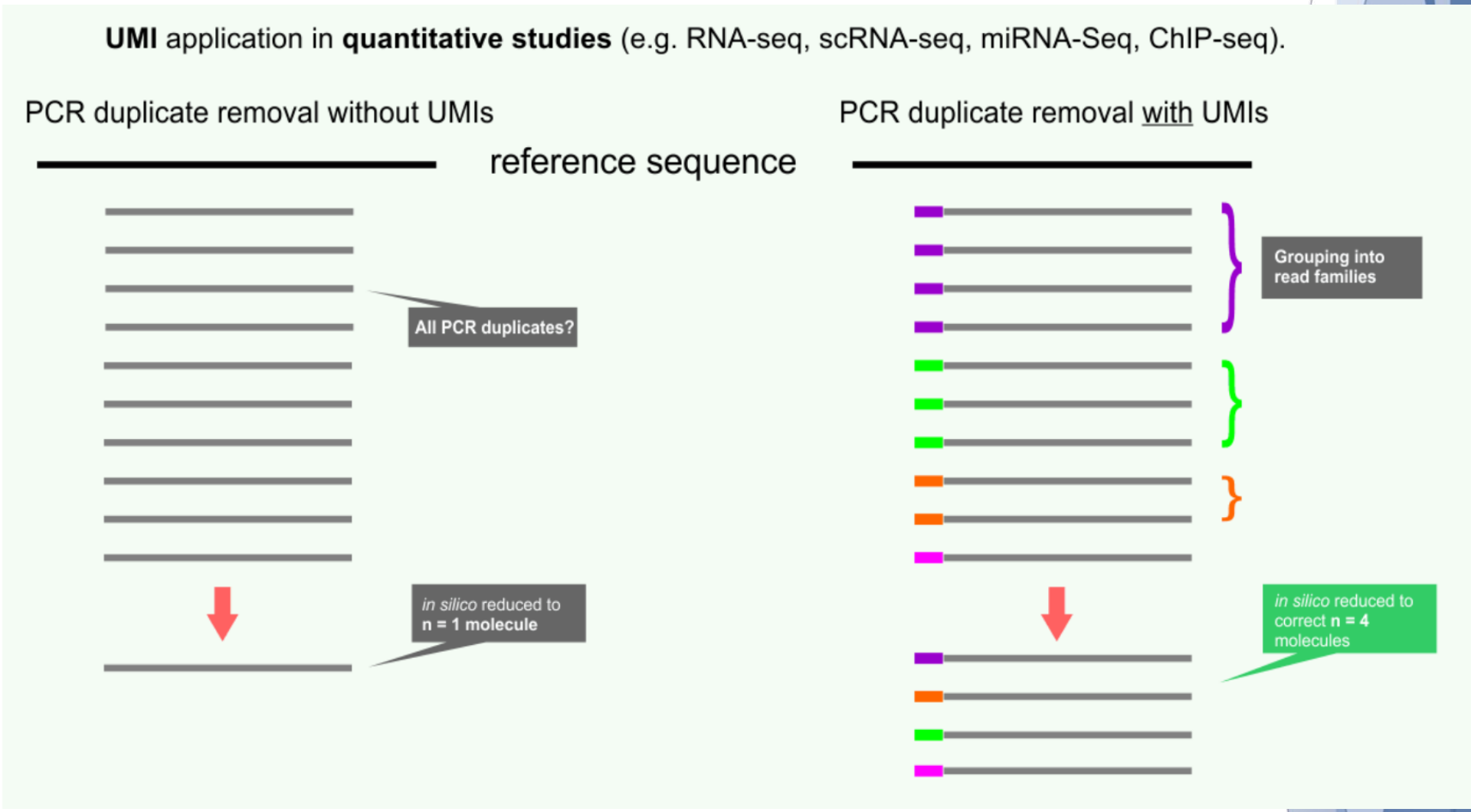
Image credit: Kevin Knudtson

RNA-seq reproducibility

- Two big studies multi-center studies (2014)
- High reproducibility of data given:

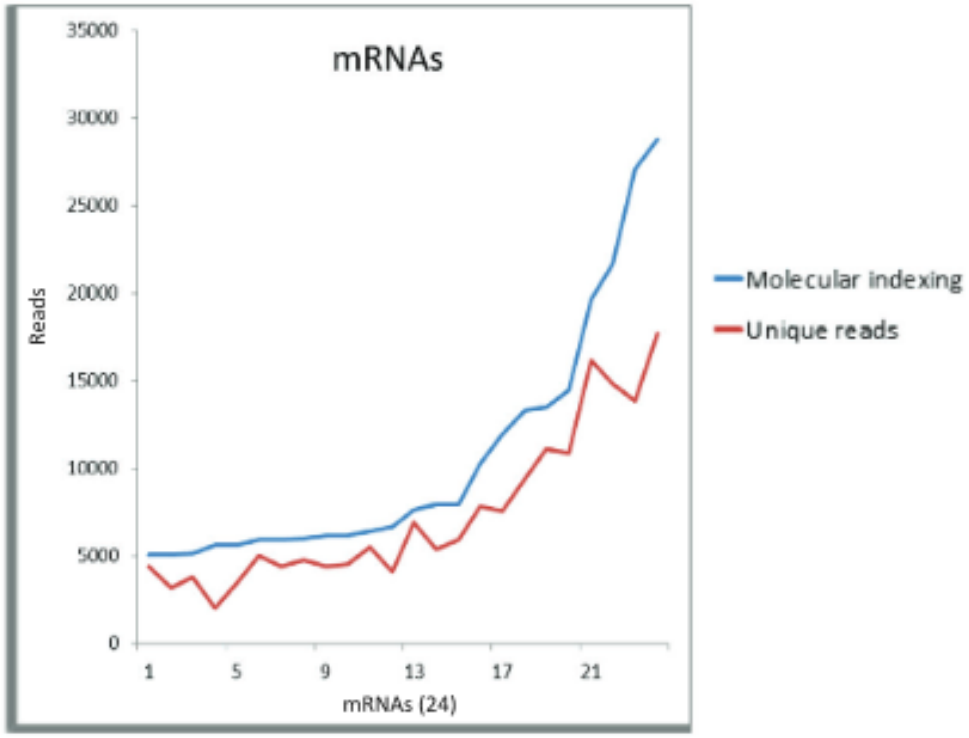
  - same library prep kits, same protocols
  - same RNA–samples
  - RNA isolation protocols have to be identical
  - robotic library preps?

UMIs – Unique Molecular Identifiers
Molecular indexing for precision counts

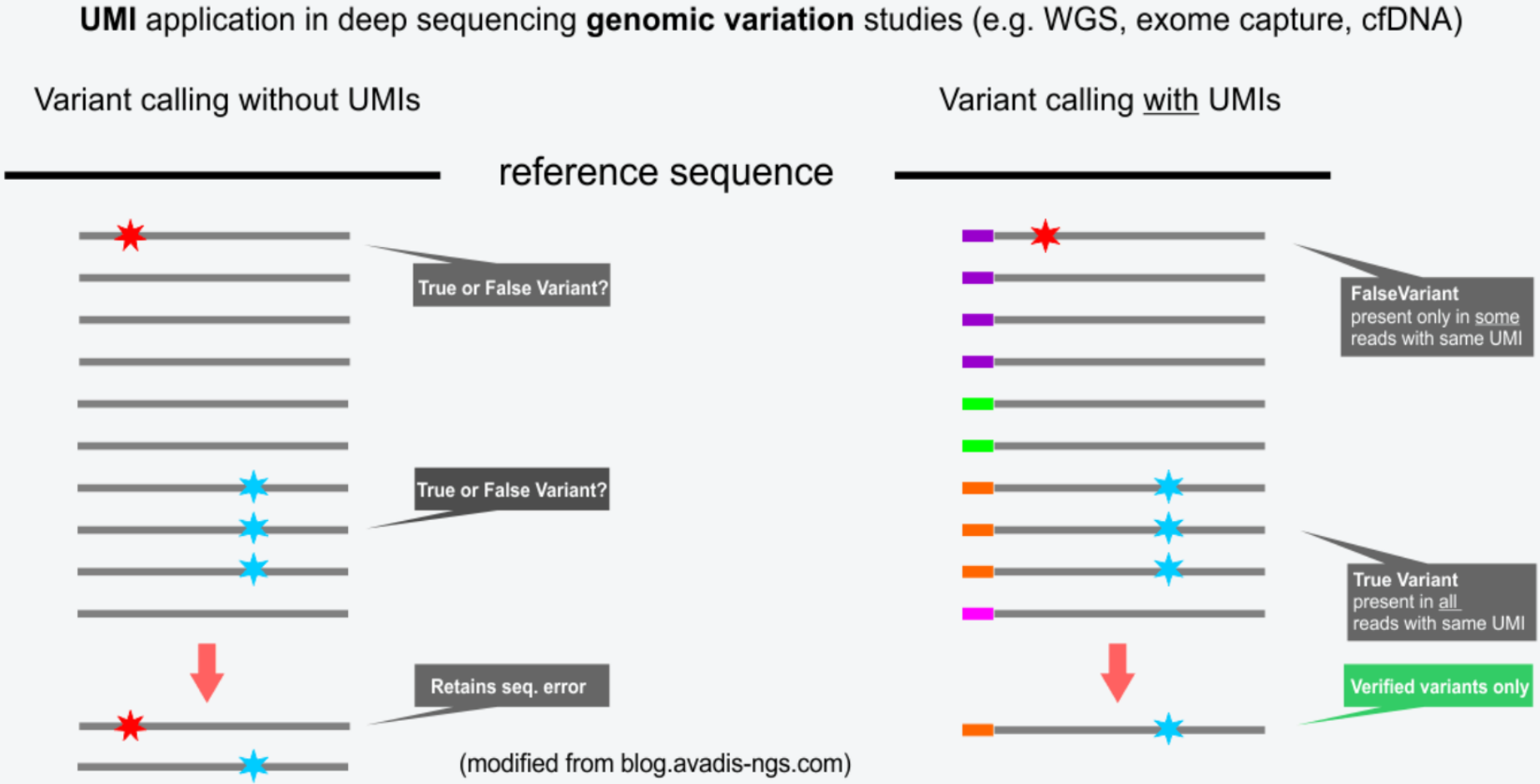


Molecular indexing – for precision counts

B



UMIs – Unique Molecular Identifiers
Molecular indexing for low abundance variants



3’-Tag-Seq

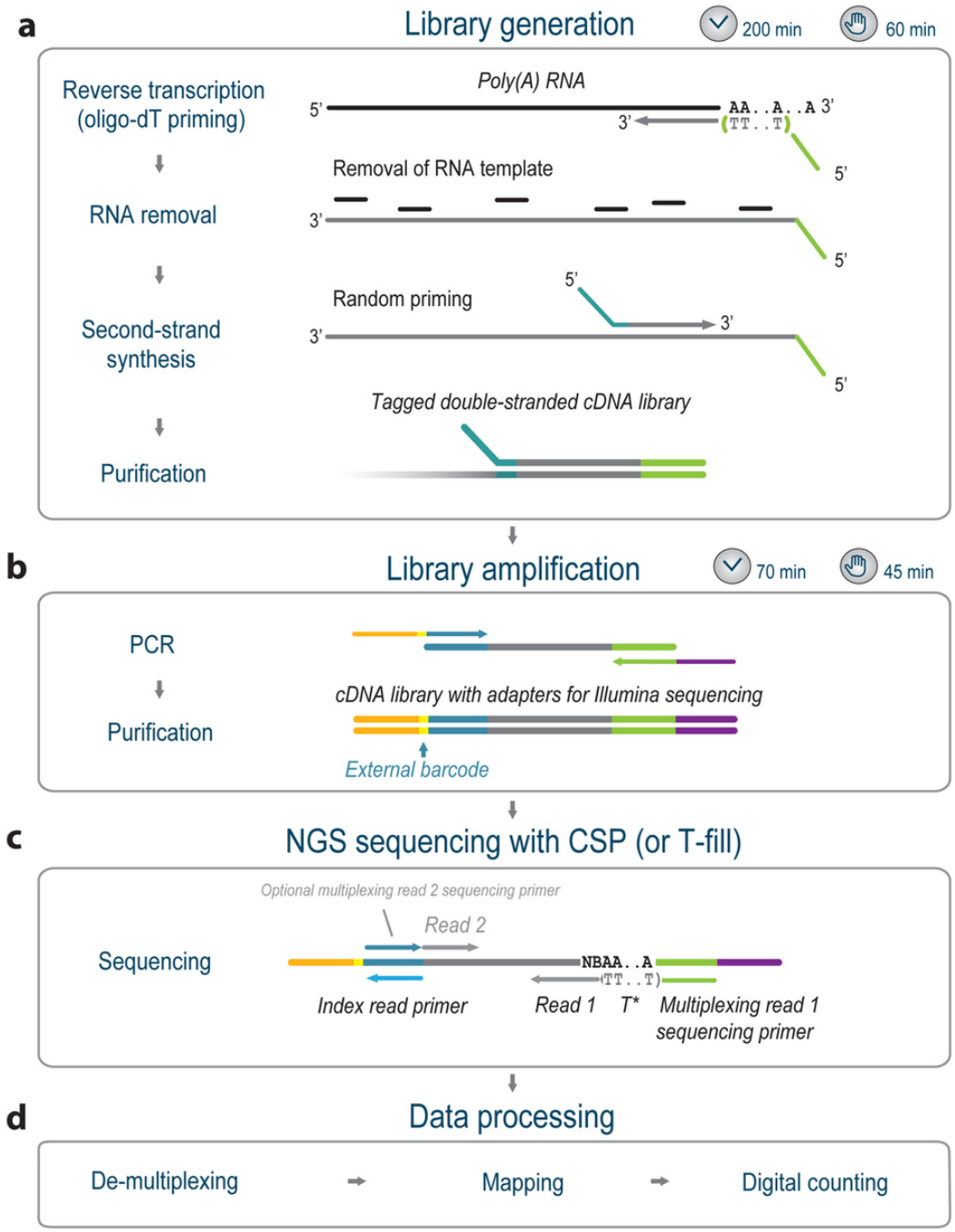
- In contrast to full length RNA-seq
- Sequencing 1/10 for the average transcript
- Less dependent on RNA integrity
- Microarray-like data

- Options:

- **BRAD-Seq : 3’ Digital Gene Expression**

- **Lexogen Quant-Seq**

Lexogen Quant-Seq



- we include UMIs

Other RNA-seq objectives

- Transcriptome assembly:
  - 300 bp paired end plus
  - 100 bp paired end
- Long non coding RNA studies:
  - 100 bp paired end
  - 60-100 million reads
- Splice variant studies:
  - 100 bp paired end
  - 60-100 million reads

RNA-seq targeted sequencing:

- Capture-seq (Mercer et al. 2014)
- Nimblegen and Illumina

- Low quality DNA (FFPE)
- Lower read numbers 10 million reads
- Targeting lowly expressed genes.

Typical RNA-seq drawbacks

- Very much averaged data:
  Data from mixed cell types & mixed cell cycle stages

- Hundreds of differentially expressed genes
  (which changes started the cascade?)

higher resolution desired

→ beyond steady-state RNA-seq

mechanisms influencing the mRNA steady-state

- Transcription rates
- Transport rates
- miRNAs and siRNAs influence both translation and degradation
- RNA modifications (e.g. methylated RNA bases, m^6A, m^5C, pseudouridine, …)
- RNA degradation pathways
- (differential translation into proteins)

beyond steady-state RNA-seq

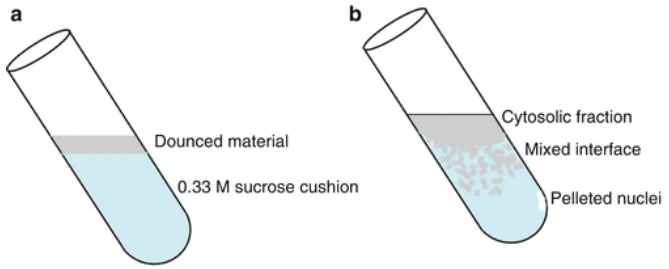
- GRO-Seq; PRO-Seq; nuclear RNA-Seq:
  what is currently transcribed

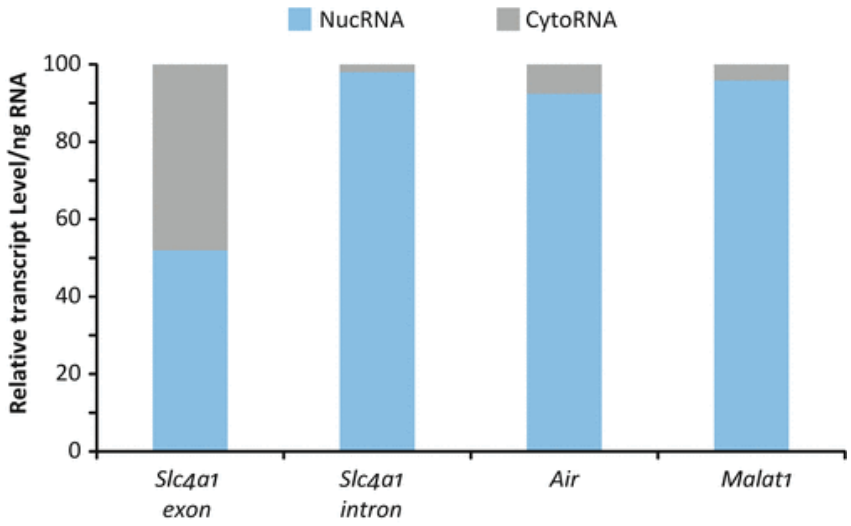
- Ribosomal Profiling:
  what is currently translated

- Degradome Sequencing:
  what is … ?

nucRNA-seq

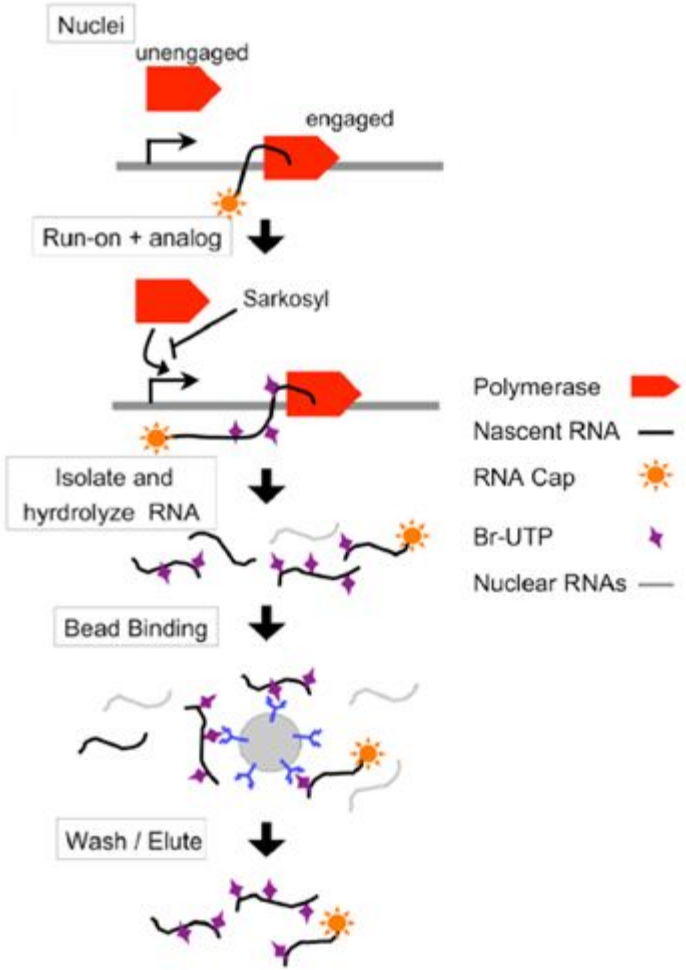
- Fractioning of nuclei and cytosol
- Studying active transcription





Dhaliwal et al. 2016

GRO-Seq



Core *et al, Science*, 2008

2008: GRO - without the seq

- Global Run-On – sequencing
- pulse-chase experiments (Br-UTP)
- uses isolated nuclei
- sarcosyl prevents binding of polymerase (only transcription in progress will be seq.)

- measures active transcription rather than steady state

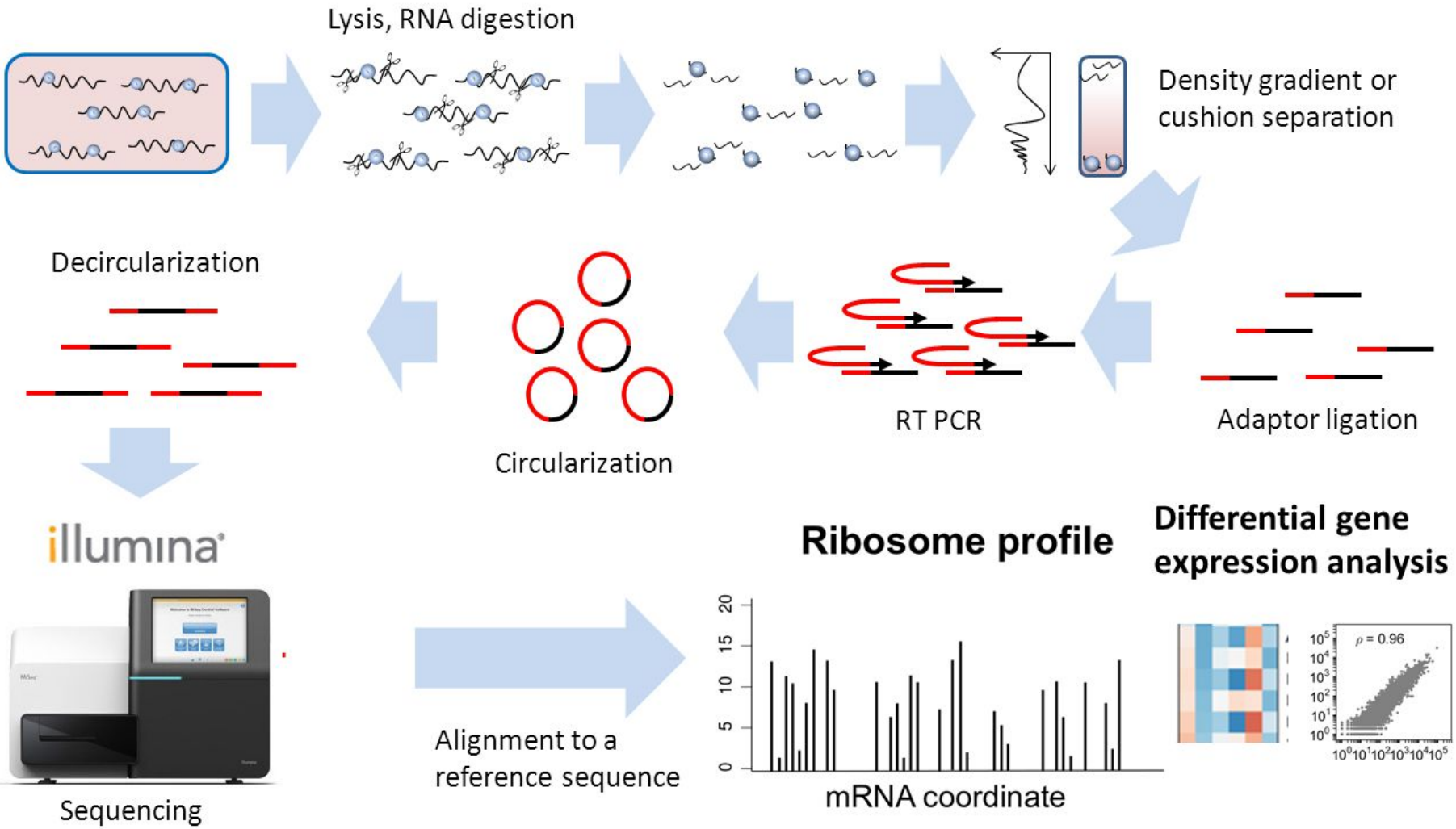
- Maps position and orientation

- Earliest changes identify primary targets
- Detection of novel transcripts including non-coding and enhancer RNAs

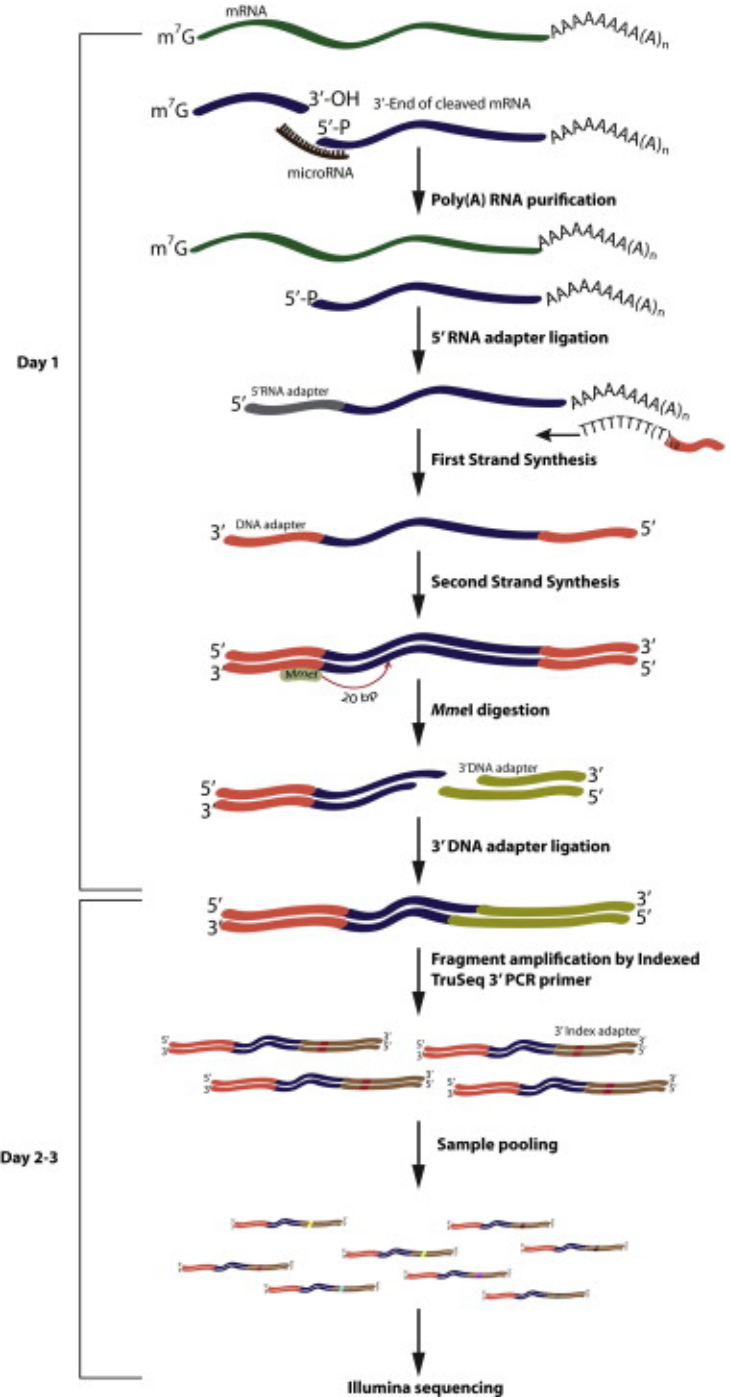
Baranov 2014

Ribosomal profiling (ribo-seq)

Ingolia et al (2009) Science 324: 218-23



Degradome Sequencing

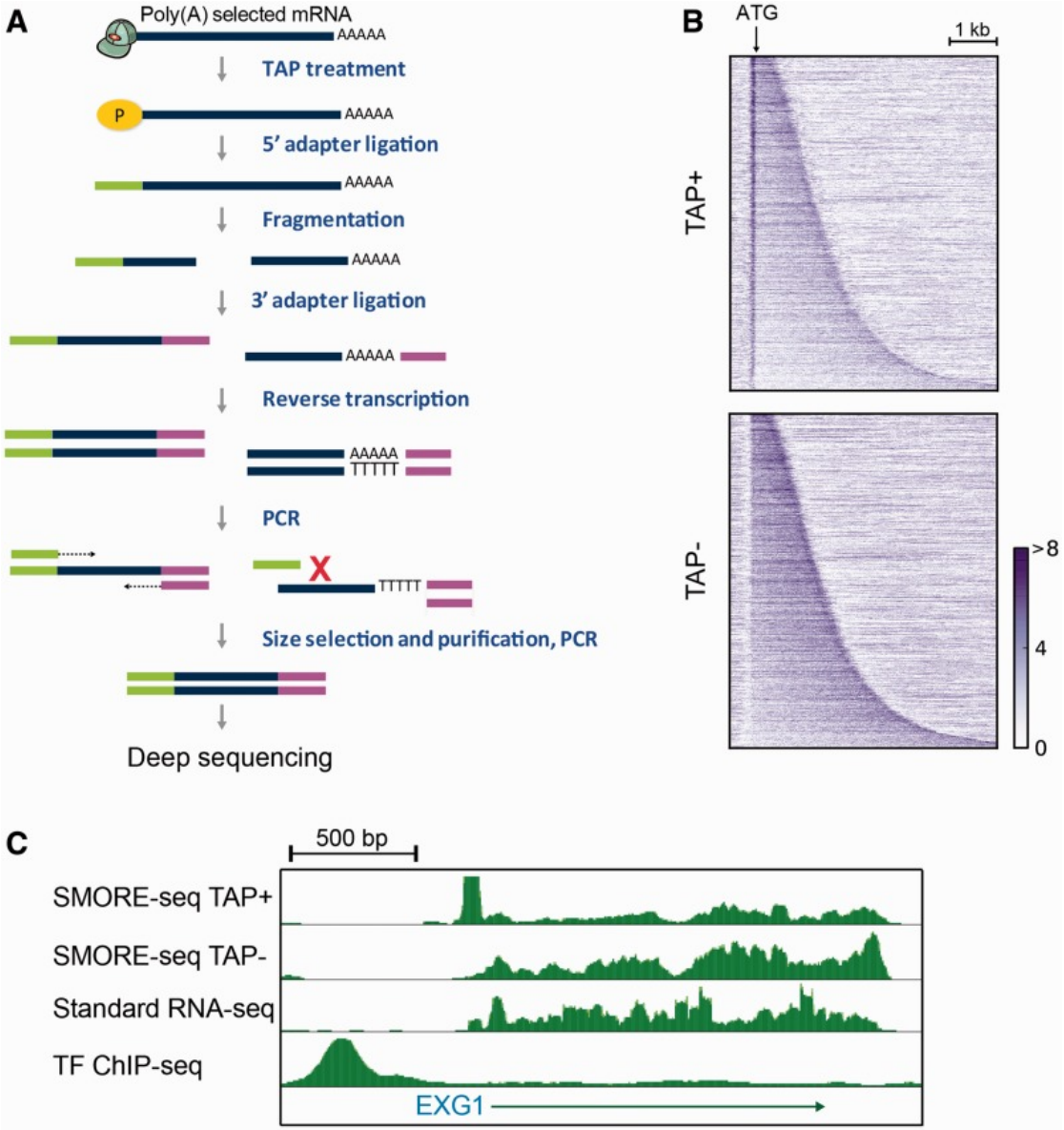


PARE-Seq

(Parallel Analysis of RNA Ends)

Zhai et al . 2013

Degradome Sequencing



SMORE-Seq

Park et al . 2014

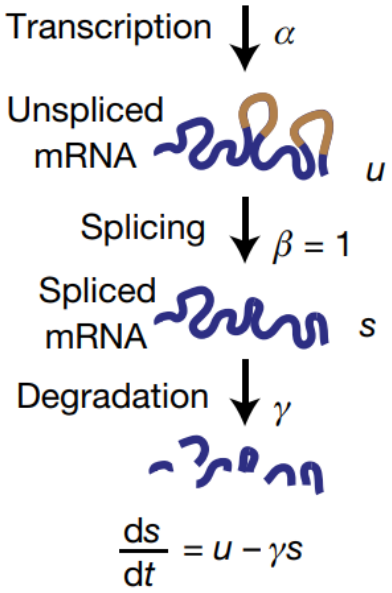
RNA velocity (2018)

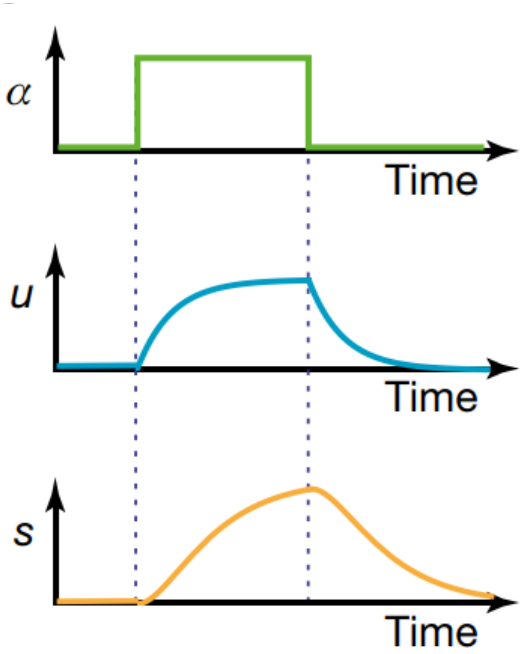
LETTER

https://doi.org/10.1038/s41586-018-0414-6

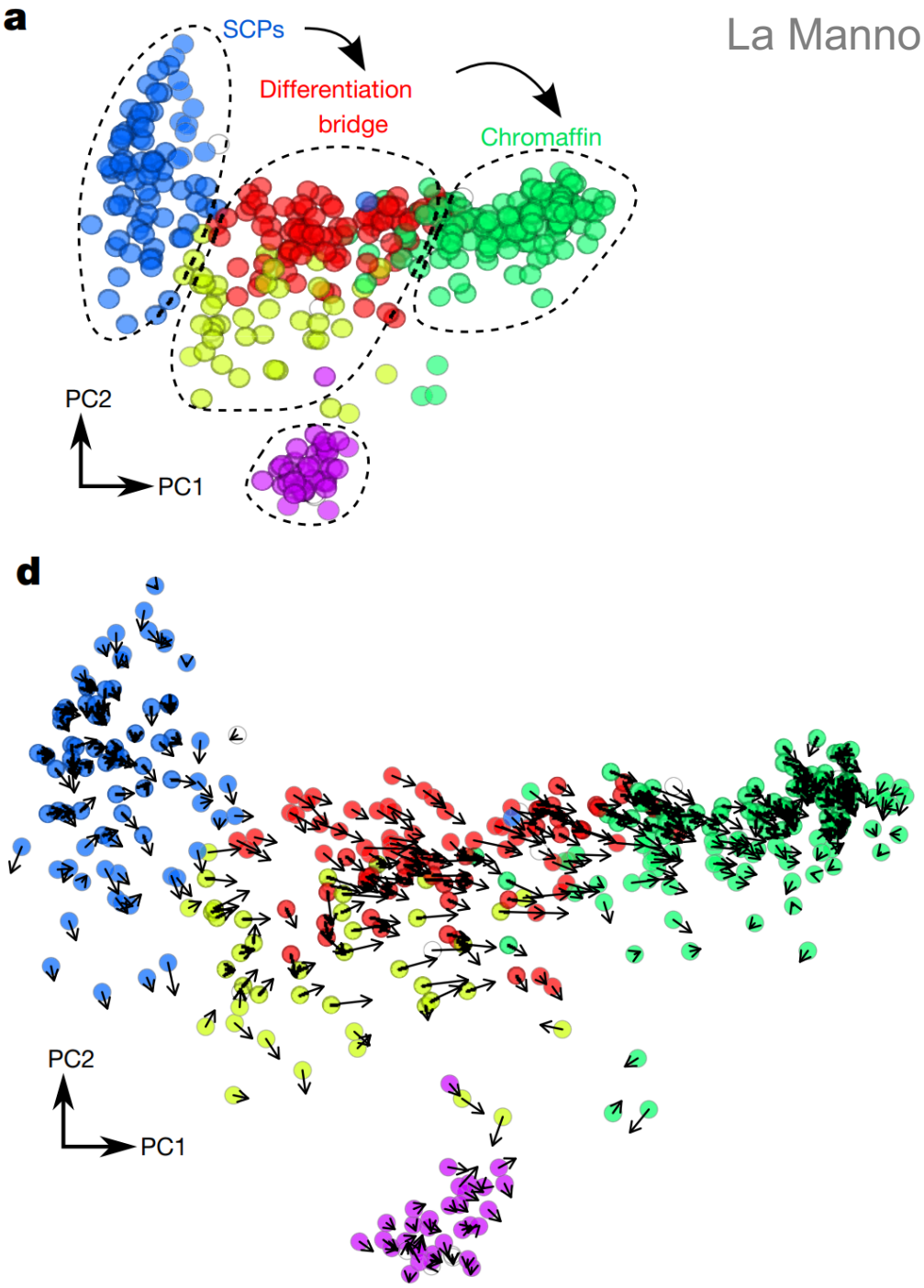
RNA velocity of single cells

Gioele La Manno[1,2], Ruslan Soldatov[3], Amit Zeisel[1,2], Emelie Braun[1,2], Hannah Hochgerner[1,2], Viktor Petukhov[3,4], Katja Lidschreiber[5], Maria E. Kastriti[6], Peter Lönnerberg[1,2], Alessandro Furlan[1], Jean Fan[3], Lars E. Borm[1,2], Zehua Liu[3], David van Bruggen[1], Jimin Guo[3], Xiaoling He[7], Roger Barker[7], Erik Sundström[8], Gonçalo Castelo-Branco[1], Patrick Cramer[5,9], Igor Adameyko[6], Sten Linnarsson[1,2]* & Peter V. Kharchenko[3,10]*





La Manno et al. 2018



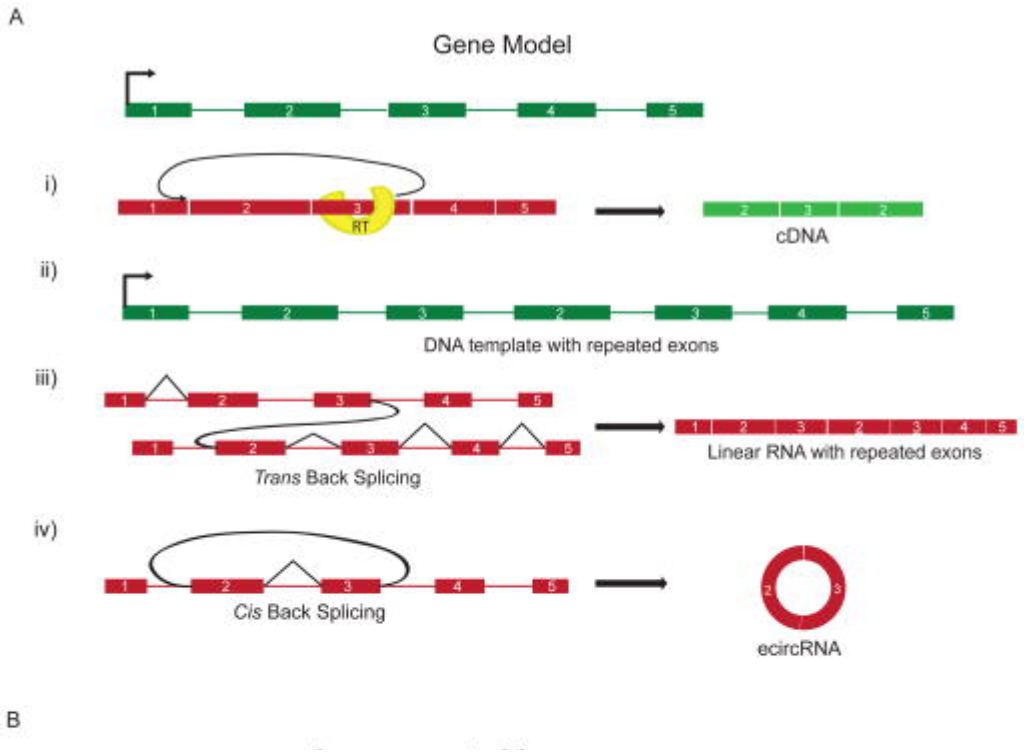
Circular RNA (circRNA)

- Evolutionary conserved
- Eukaryotes
- Spliced (back-spliced)
- Some tissues contain more circRNA than mRNA
- Sequencing after exonuclease digestion (RNAse R)

- Interpretation of ribo-depletion RNA-seq data ????

Role of circRNAs ?

Back-splicing and other mechanisms



- miRNA sponge
- protein expression regulators:
  mRNA traps
  (blocking translation)
- Interactions with RNA binding proteins

Jeck and Sharpless, 2014

PACIFIC BIOSCIENCES™

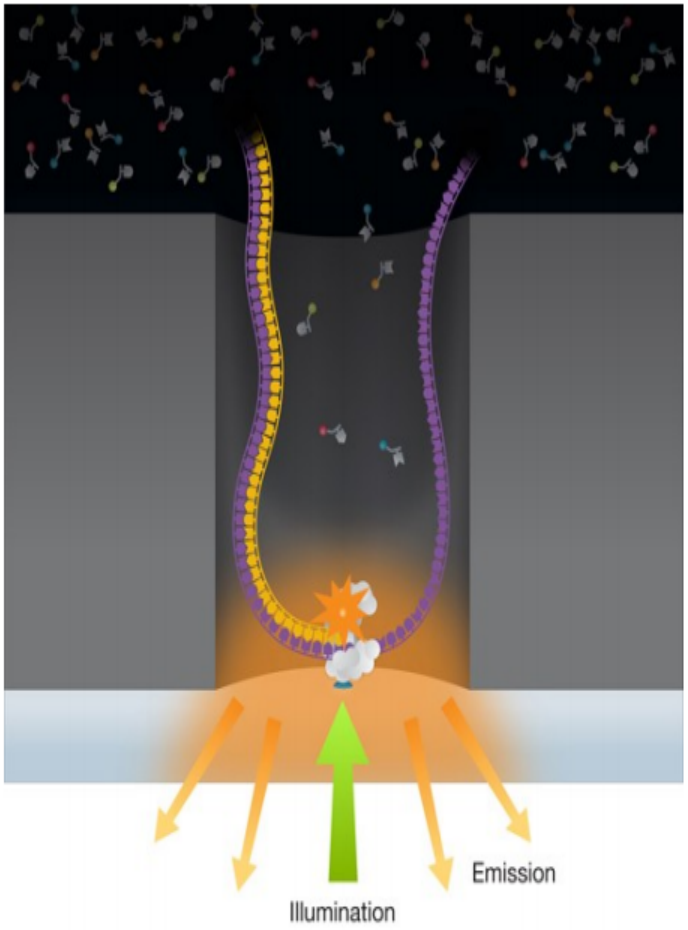
http://pacificbiosciences.com

THIRD GENERATION DNA SEQUENCING

Single Molecule Real Time (SMRT™) sequencing
Sequencing of single DNA molecule by single polymerase
Very long reads: average reads over 8 kb, up to 30 kb
High error rate (~13%).
Complementary to short accurate reads of Illumina

Third Generation Sequencing : Single Molecule Sequencing

Pacific Biosciences

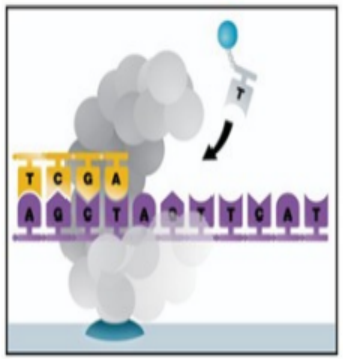


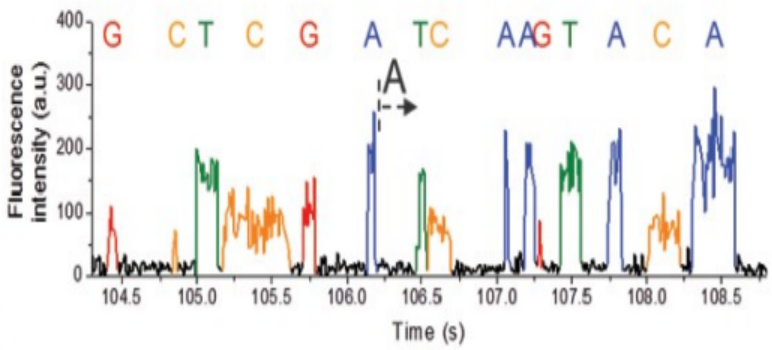
4 nucleotides with different fluorescent dye simultaneous present

2-3 nucleotides/sec
2-3 Kb (up to 50) read length
6 TB data in 30 minutes

laser damages polymerase

70 nm aperture
“Zero Mode Waveguide”

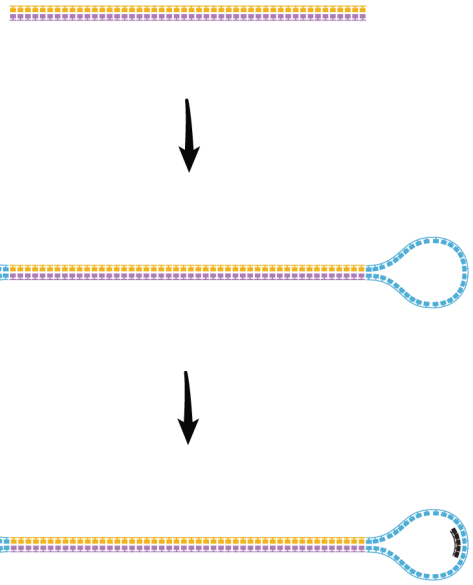




Start with high-quality double stranded DNA

Ligate SMRTbell adapters and size select

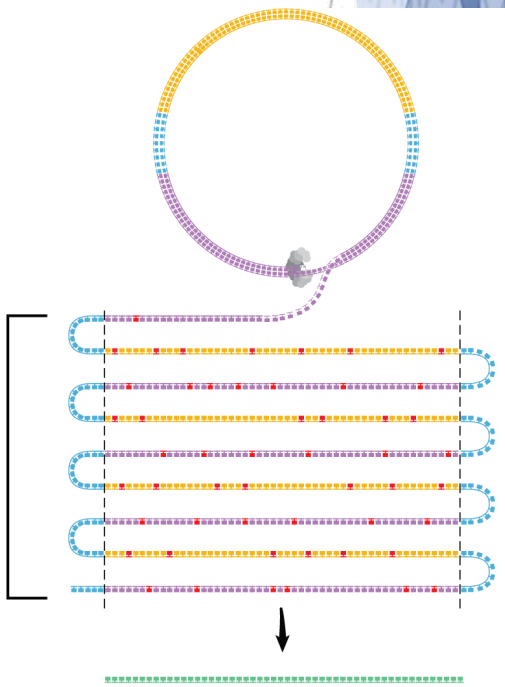
Anneal primers and bind DNA polymerase



Circularized DNA is sequenced in repeated passes

The polymerase reads are trimmed of adapters to yield subreads

Consensus is called from subreads

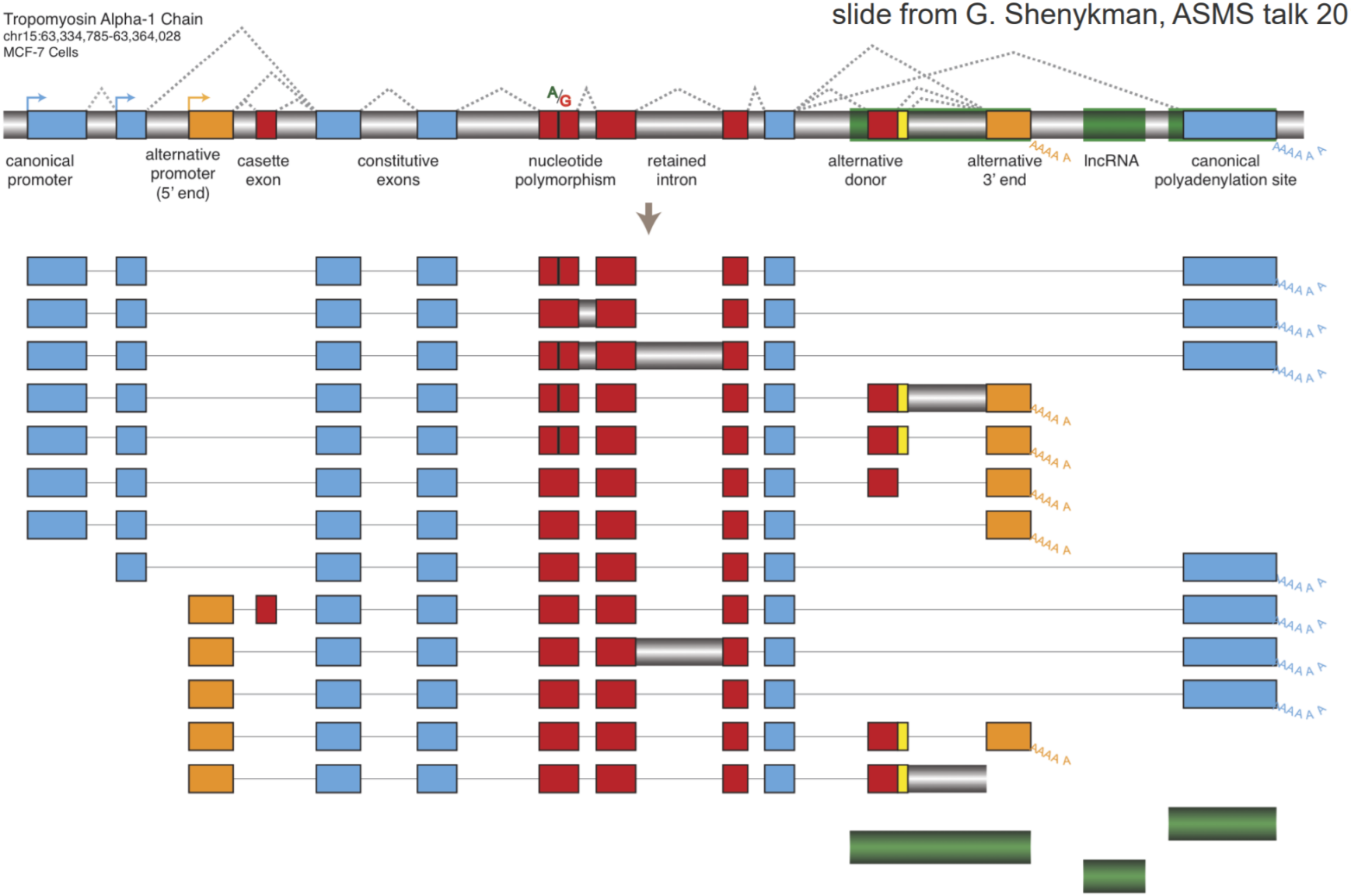


HiFi READ

(>99% accuracy)

A Single Gene Locus ➔ Many Transcripts

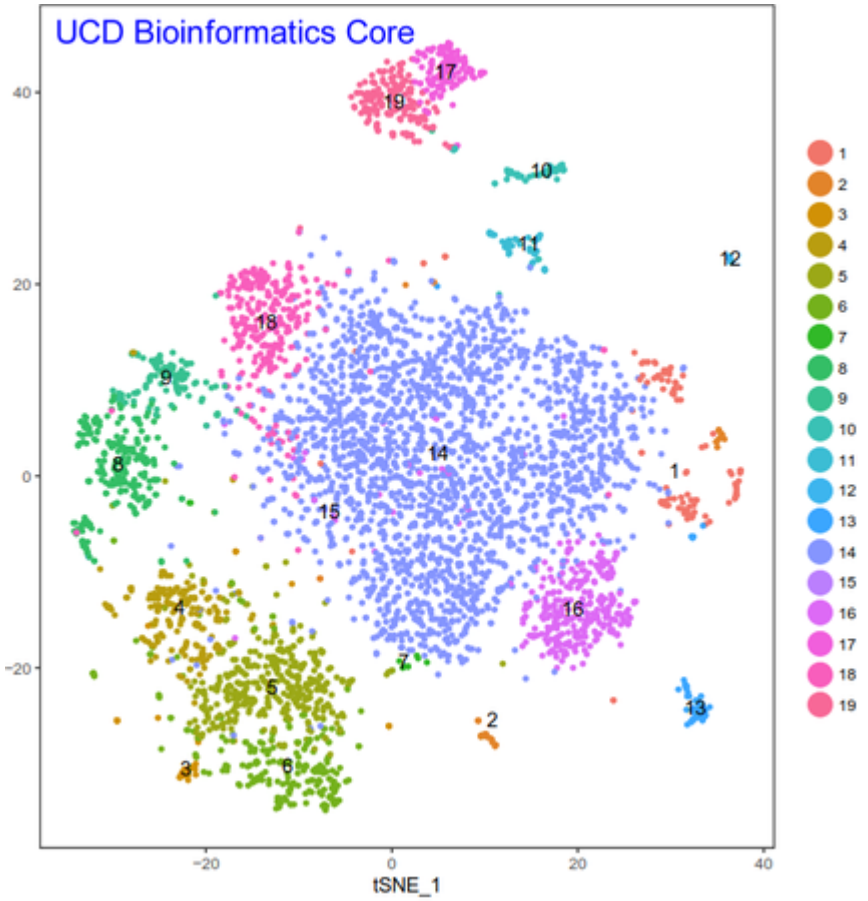
slide from G. Shenykman, ASMS talk 2014



Iso-Seq Pacbio

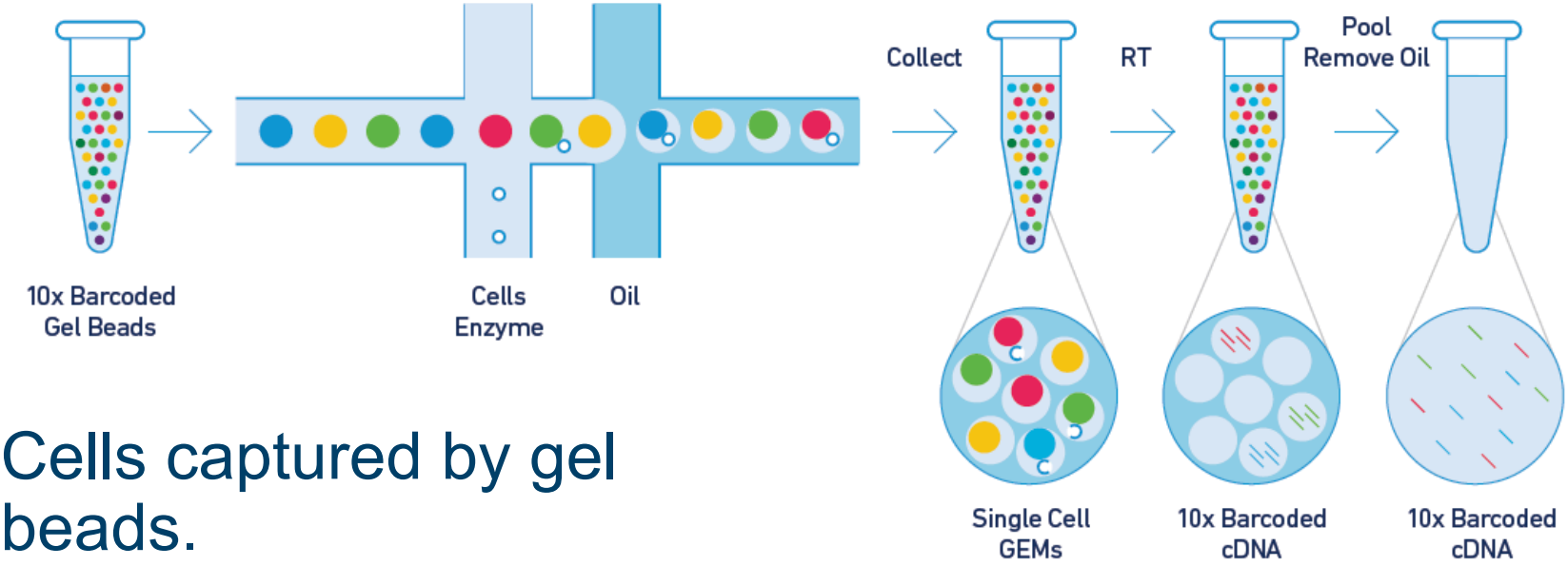
- Sequence full length transcripts
  → no assembly
- High accuracy (except very long transcripts)
- More than 95% of genes show alternate splicing
- On average more than 5 isoforms/gene
- Precise delineation of transcript isoforms (PCR artifacts? chimeras?)

scRNA-seq (single cells)



- Gene expression profiling of individual cells.
- Resulting data can distinguish cell types and cell cycle stages - no longer a mix
- Allows the analysis of low abundance cell types

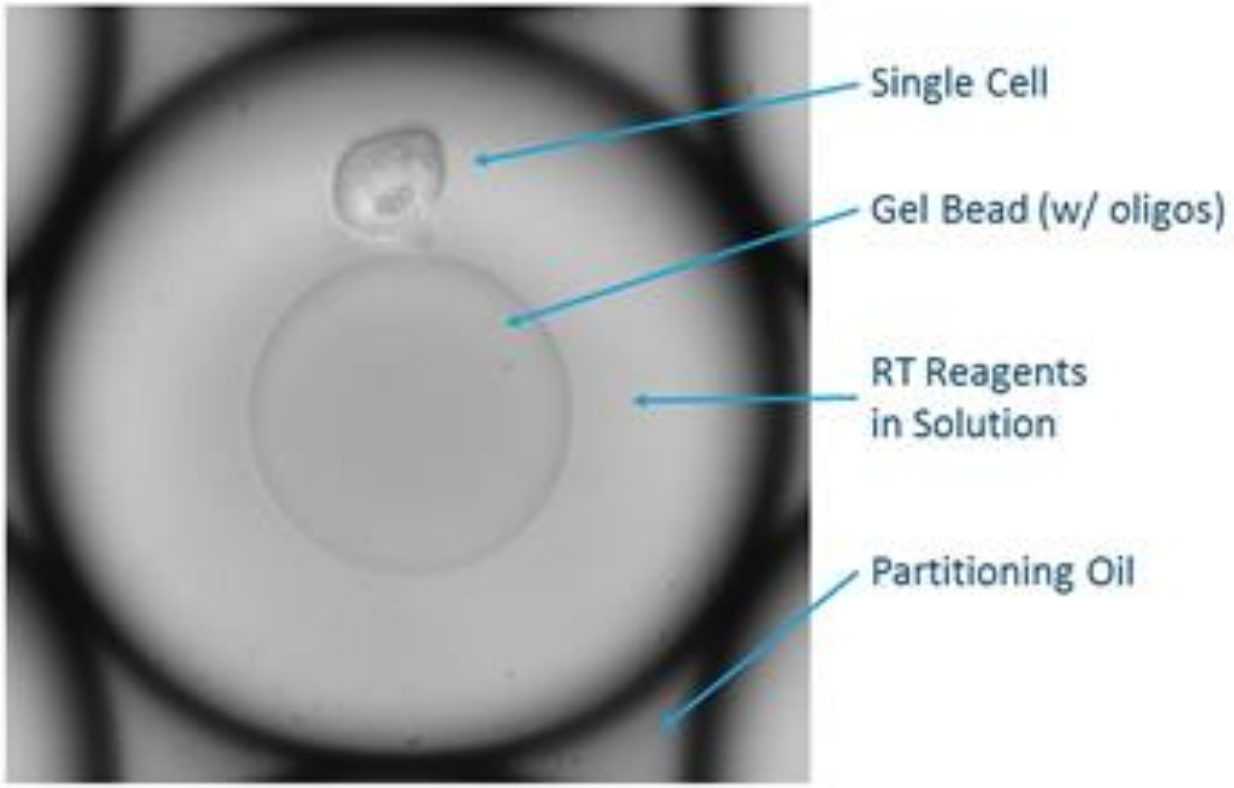
cDNA preparation



- Cells captured by gel beads.
- 10X barcode added to transcript.
- cDNA amplification.
- Transcriptional profiling of individual cells due to unique barcodes / UMIs.

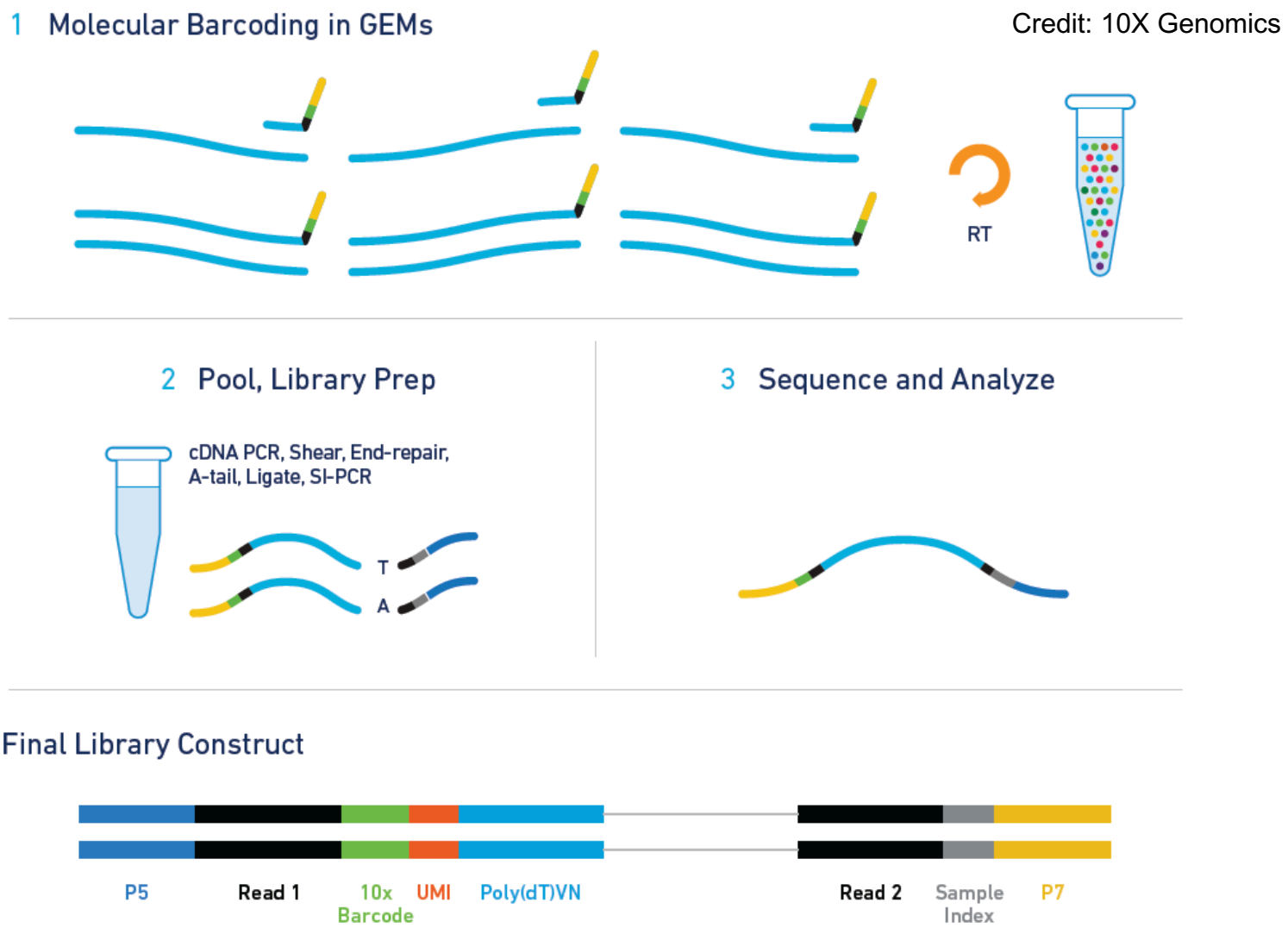
Cell partitioning into GEMs

- GEM

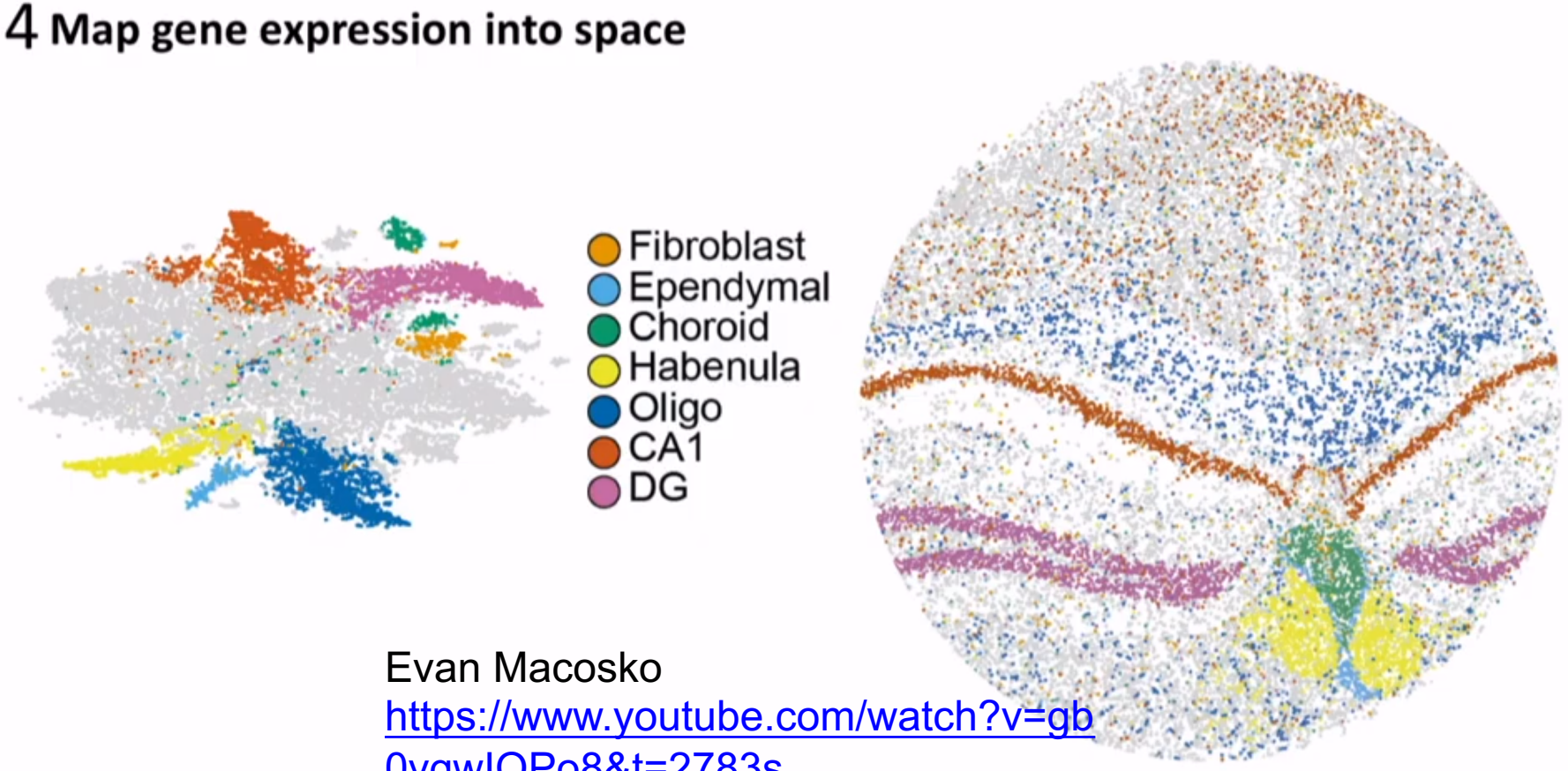


Credit: 10X Genomics

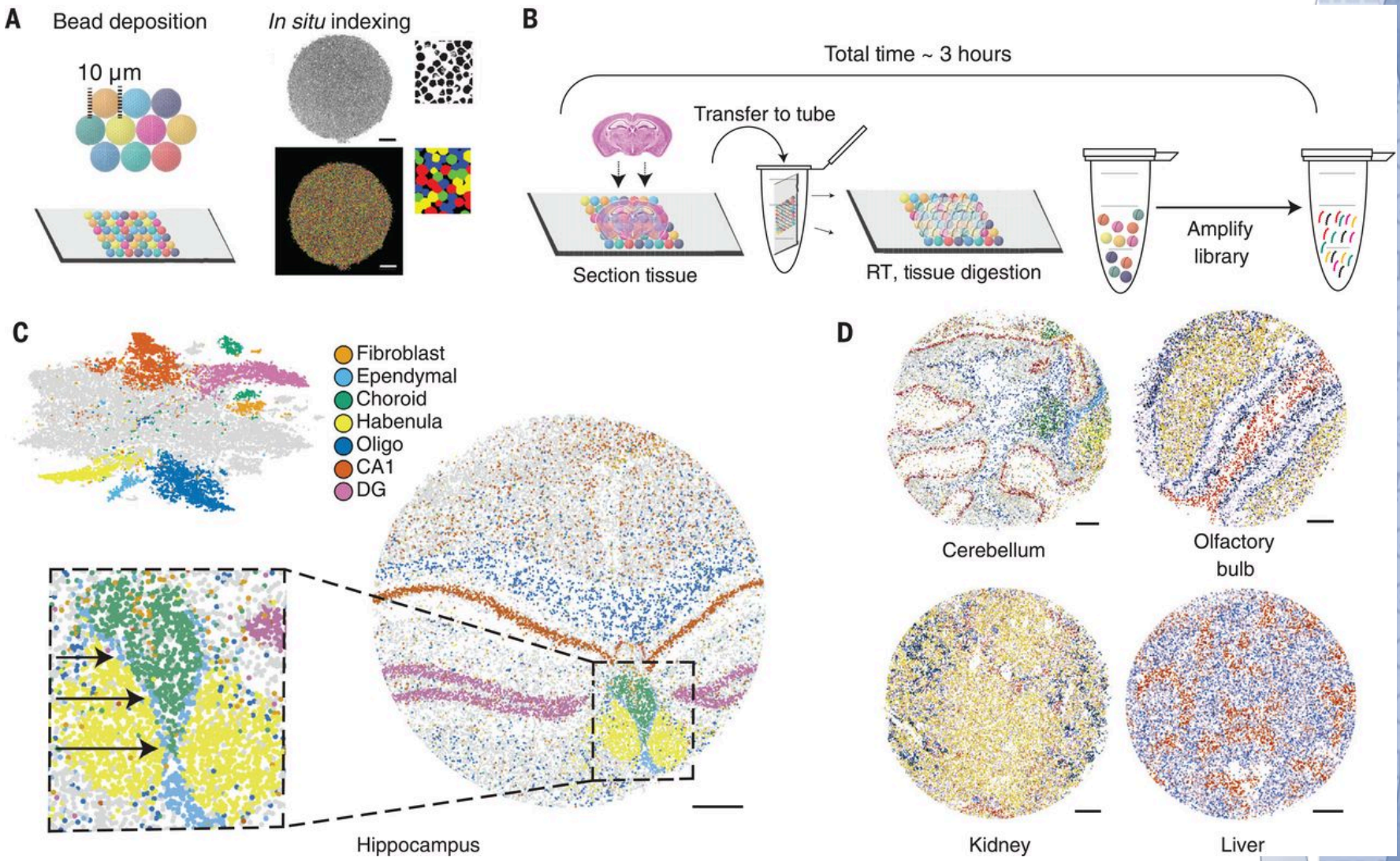
Library preparation



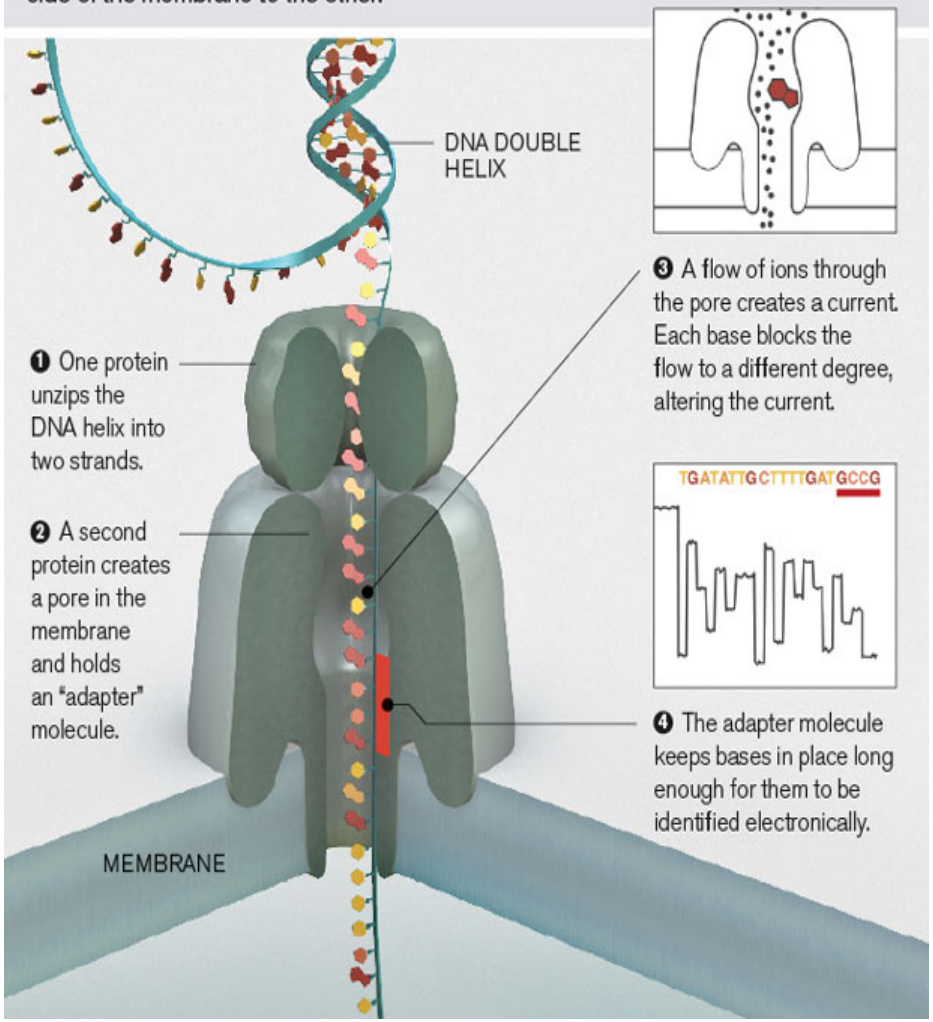
Spatial Transcriptomics (10XGenomics Visium; Slide-Seq)



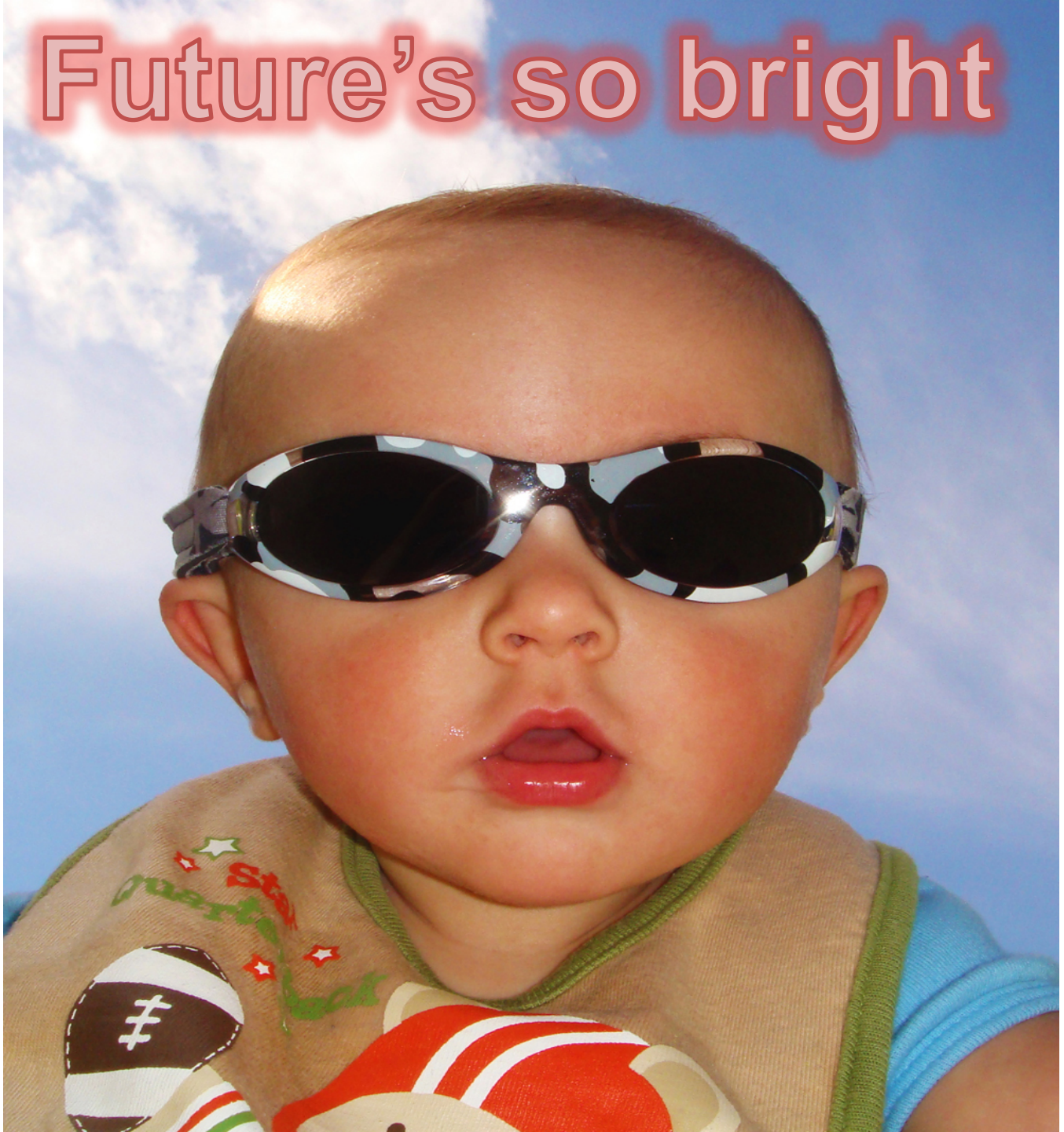
Evan Macosko
https://www.youtube.com/watch?v=gb0vgwIQPo8&t=2783s


A
Bead deposition
10 μm
In situ indexing
B
Total time ~ 3 hours
Transfer to tube
Section tissue
RT, tissue digestion
Amplify library
C
Fibroblast
Ependymal
Choroid
Habenula
Oligo
CA1
DG
Hippocampus
D
Cerebellum
Olfactory bulb
Kidney
Liver

DNA can be sequenced by threading it through a microscopic pore in a membrane. Bases are identified by the way they affect ions flowing through the pore from one side of the membrane to the other.



Future's so bright



Thank you!