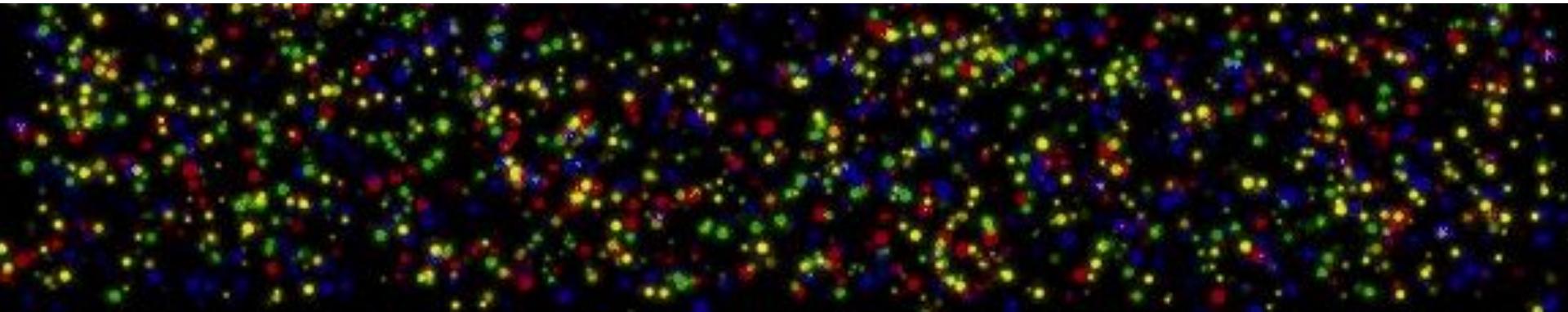
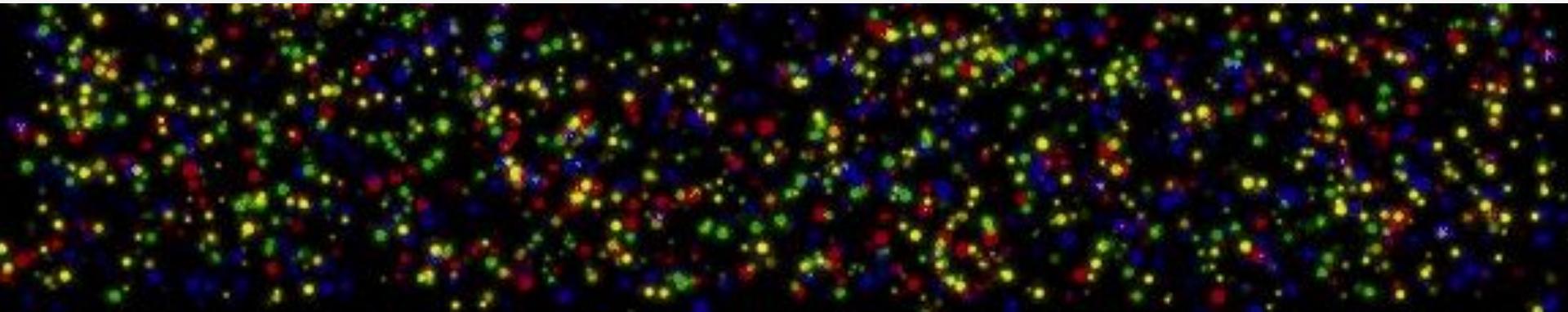


Intro to RNAseq technology and data



Mary-Ann Blätke
JJ Szymanski

Intro to RNAseq technology and data



- Get familiar with jargon of RNAseq/HTS (paired-end, cluster density, fastq, index, etc)
- Understand Illumina's "Sequencing by Synthesis" (SBS) technology
- Set priorities when planning a sequencing experiment
- Understand the basics of library prep for HTS

Paired-end

Flow cell

**Clustering
density**

Q30

fastq

NextSeq

Single-end

fasta

SBS

Library

Read depth

HiSeq

Read length

Indicies

The birthplace of high-throughput sequencing (HTS)

David Klenerman



Shankar Balasubramanian

Sequencing circa 2012



Roche 454 'pyroseq'



Life Technologies SOLiD

Life Technologies
Ion Torrent



Ion Torrent



Illumina

The year of sequencing

In 2007, the next-generation sequencing technologies have come into their own with an impressive array of successful applications. Kelly Rae Chi reports.

SPECIAL FEATURE | METHOD OF THE YEAR

CREATING THE GENOME ANALYZER

When John West started as CEO of Solexa Ltd. in August of 2004, the longest stretch of DNA that the company could sequence was only six bases long. "That was a little bit intimidating," recalls West, now the vice president and general manager of Illumina's DNA sequencing business unit following the acquisition of Solexa Ltd. by Illumina. "The problem was we never had a commercial platform to be able to sequence it on."

The next-generation sequencing platform they developed and commercialized by June 2006, West says, has been a huge success.

Since the commercial release of the platform they have sold 100 instruments and increased the scale or what they have tackled using the technology—from a 5,300-base-pair viral genome to a 150-million-base-pair human X chromosome. But the machine was a challenge to develop. The developers had to bring together key elements of chemistry, people and technology to make it work.

By the time Solexa Ltd. announced its plans to merge with Lynx

Therapeutics in August 2004, a lot of the core sequencing-by-synthesis chemistry and molecular biology had already been done, West says. The early chemistry work, done by Solexa Ltd. in the United Kingdom, led to the creation of a reversible terminator nucleotide and a polymerase that would incorporate it. Solexa Ltd. and Lynx Therapeutics had bought cluster technology for solid phase amplification together from the Swiss company Manteia SA, and did some instrumentation design.



Illumina's (Solexa) Genome Analyzer.

Still, the company was in a state of flux in late 2004 and needed to figure out how to combine the chemistry and technology into a complete system. The researchers needed to meet and brainstorm, operating on an eight-hour time difference between the two branches, one in the UK and one in the US. Ligation chemistry developed by Lynx Therapeutics was an option. There were differing opinions about which chemistry, ligation or polymerase would work best, but ultimately they took a gamble on the Solexa polymerase because it could complete reactions faster. "It was risky at the time because it wasn't all proven," West remembers. "We basically put all our eggs in one basket."

And it worked. It became easier, with the cluster technology and polymerase chemistry, to increase the sequence lengths. By February 2005, they increased the read length to 25 bases. They sequenced the 5,300-base-pair virus PHIX174 genome, the same genome

that Sanger first sequenced. In October 2005, they sequenced an 180,000-base-pair bacterial artificial chromosome.

Illumina acquired Solexa, Inc. in January of last year, and commercial sales increased, West says. In 2007, the company completed sequencing the human X chromosome and has since moved on to sequencing the human genome using paired-end sequencing. "I think [2007] has been a great year for us," West says. KRC

The Transcriptional Landscape of the Yeast Genome Defined by RNA Sequencing

Ugrappa Nagalakshmi,^{1*} Zhong Wang,^{1*} Karl Waern,¹ Chong Shou,² Debasish Raha,¹ Mark Gerstein,^{2,3} Michael Snyder^{1,2,†}

The identification of untranslated regions, introns, and coding regions within an organism remains challenging. We developed a quantitative sequencing-based method called RNA-Seq for mapping transcribed regions, in which complementary DNA fragments are subjected to high-throughput sequencing and mapped to the genome. We applied RNA-Seq to generate a high-resolution transcriptome map of the yeast genome and demonstrated that most (74.5%) of the nonrepetitive sequence of the yeast genome is transcribed. We confirmed many known and predicted introns and demonstrated that others are not actively used. Alternative initiation codons and upstream open reading frames also were identified for many yeast genes. We also found unexpected 3'-end heterogeneity and the presence of many overlapping genes. These results indicate that the yeast transcriptome is more complex than previously appreciated.

Illumina sequencing



MiniSeq System

MiSeq Series

NextSeq Series

HiSeq Series

HiSeq X Series

NovaSeq Series

Data output

Instrument cost

Per base cost

NovaSeq



MiniSeq



MiSeq



NextSeq



- well-suited for a lab
- not sufficient for transcriptomics
- Applications include:
 - ✓ amplicon sequencing (16S)
 - ✓ bacterial genome seq
 - ✓ QC of RNAseq libraries

0.4 - 1.1 billion reads
150bp paired-end
24 hr run time

- best fit for a large core facility
- requires a dedicated technician
- complicated set-up
- Applications include:
 - ✓ Just about anything

Democratization of sequencing



MiniSeq System

MiSeq Series

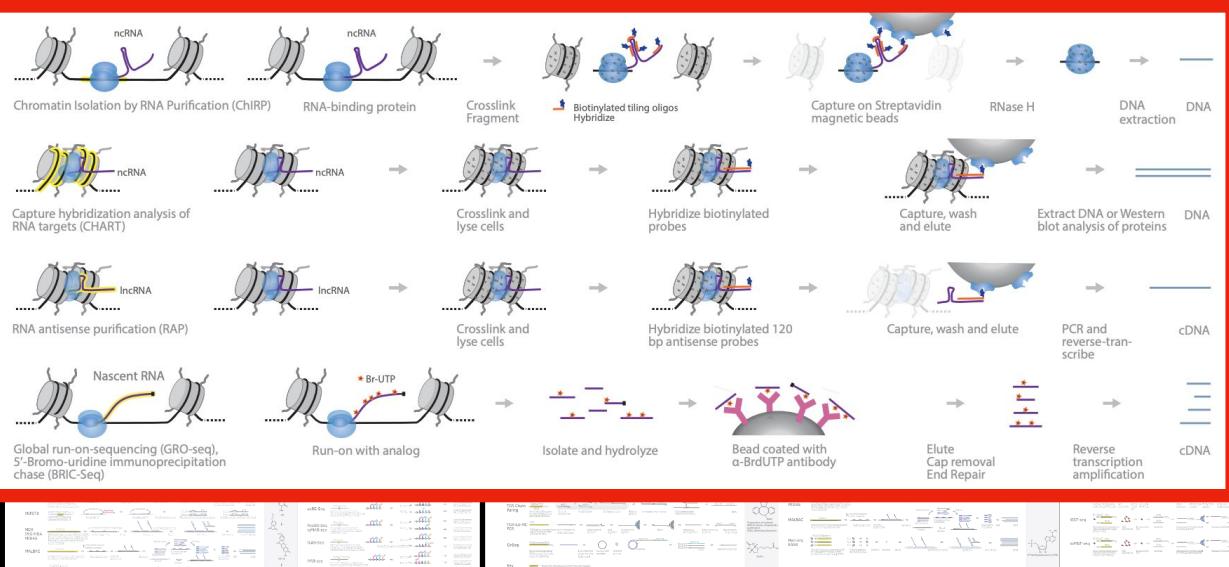
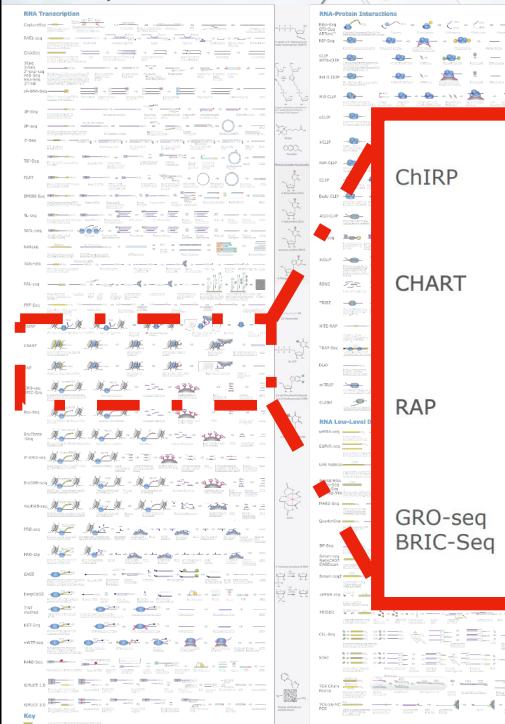
NextSeq Series

HiSeq Series

HiSeq X Series

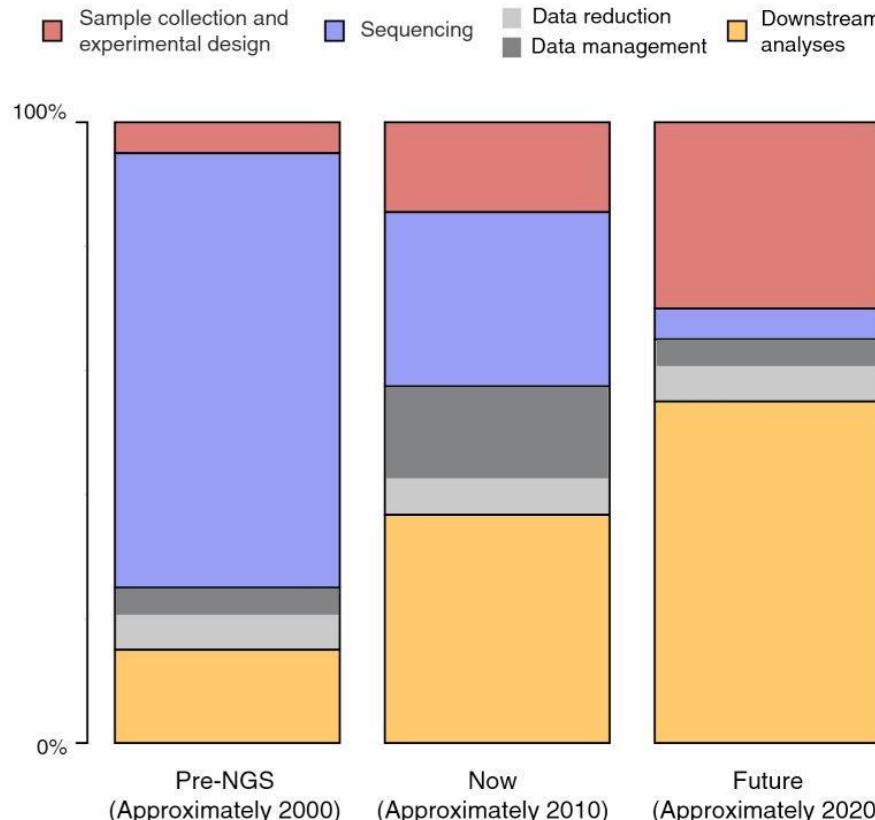
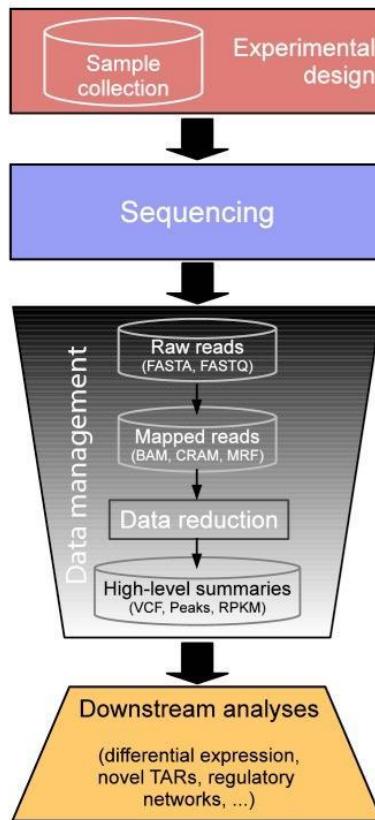
NovaSeq Series

Democratization of sequencing

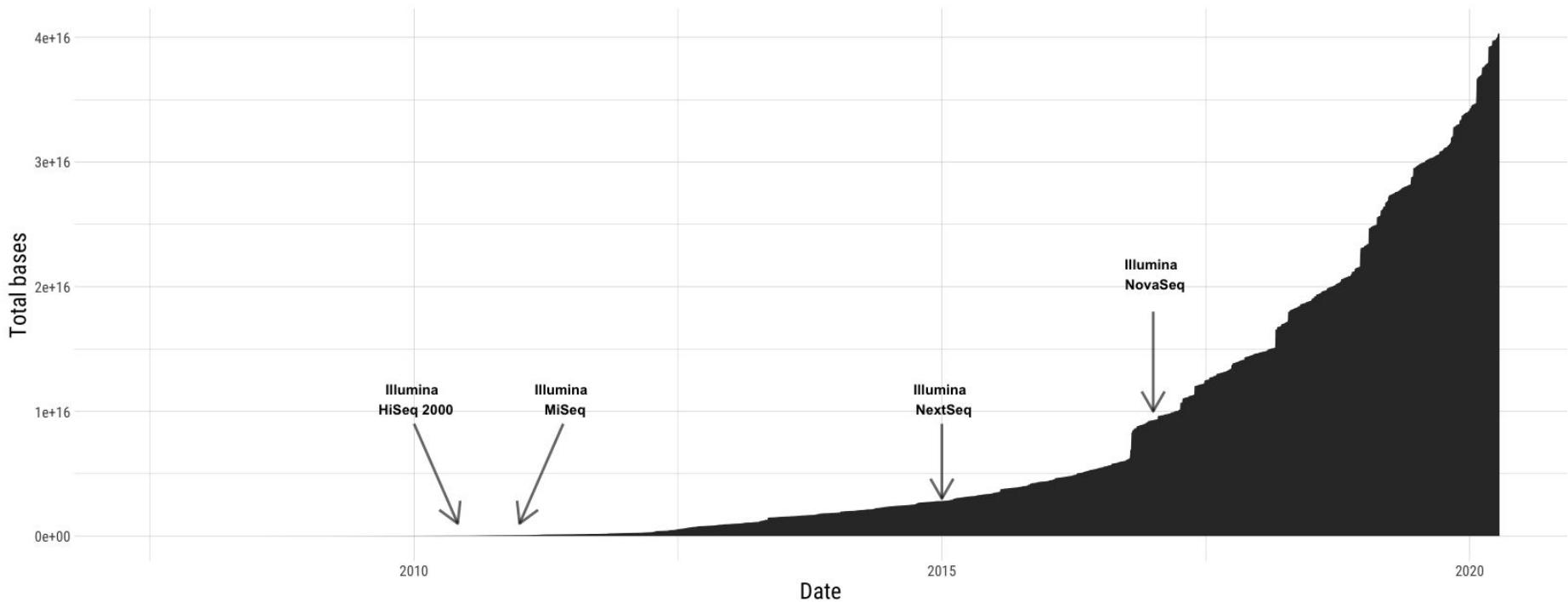


bit.ly/4ALLUSEQ

A shift in how time and money are spent on genomics experiments



NCBI Sequence Read Archive (SRA)



Illumina sequencing



MiniSeq System

MiSeq Series

NextSeq Series

HiSeq Series

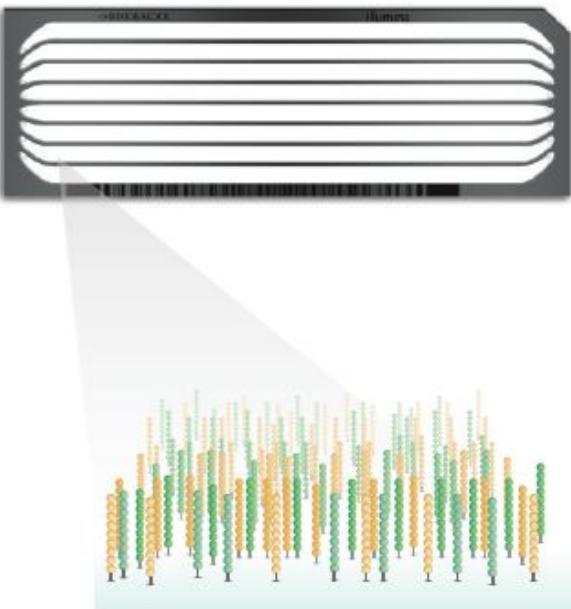
HiSeq X Series

NovaSeq Series

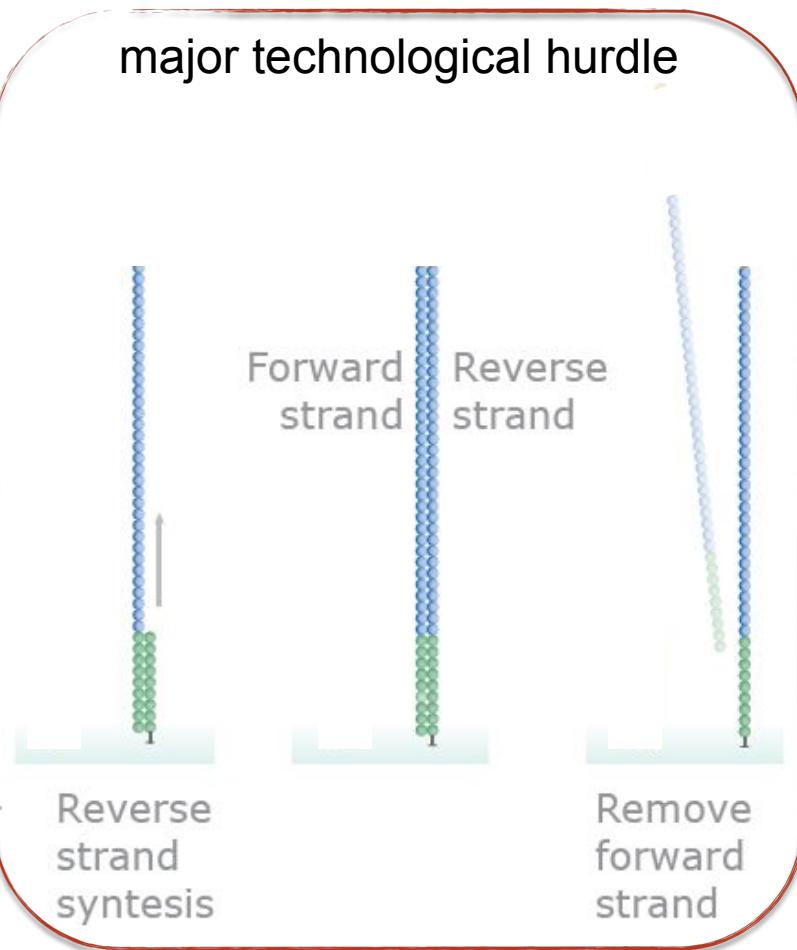
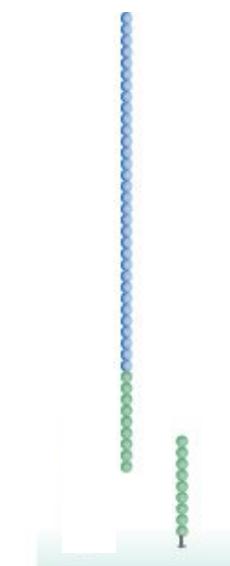
'Sequencing By Synthesis' (SBS) technology

Sequencing by Synthesis

major technological hurdle



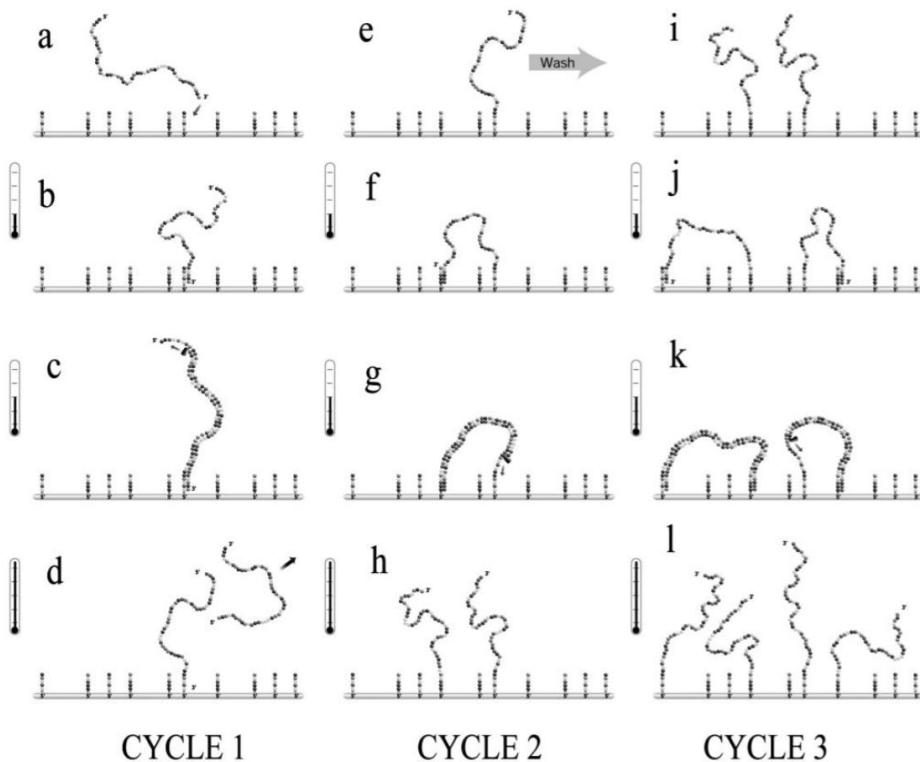
Adapter hybridizes to flowcell



Solid Phase DNA Amplification: A Simple Monte Carlo Lattice Model

Jean-Francois Mercier,* Gary W. Slater,* and Pascal Mayer[†]

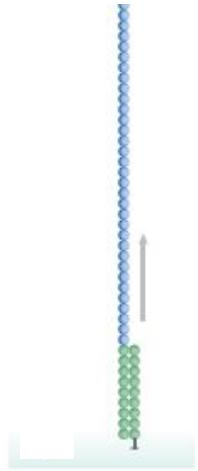
*Department of Physics, University of Ottawa, Ottawa, Ontario, Canada; and [†]Manteia Predictive Medicine S.A., Coinsins, Switzerland



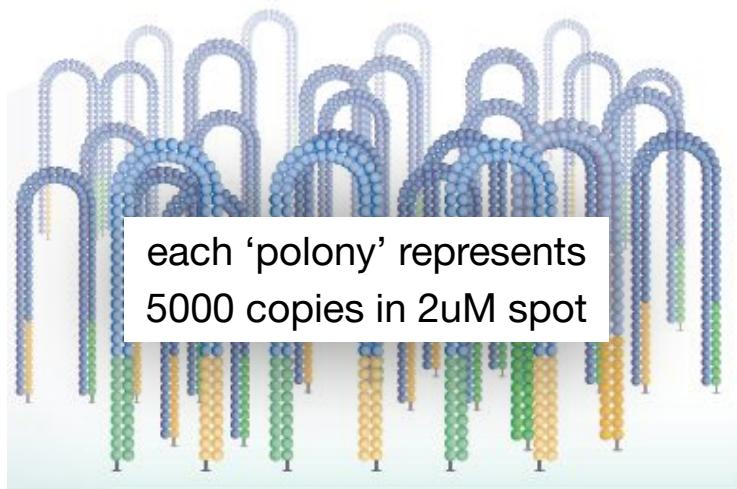
“solid phase DNA amplification leads to the growth of a colony of molecules attached to the surface and located in the same region.”

This characteristic could easily be exploited in the design of DNA microarrays.”

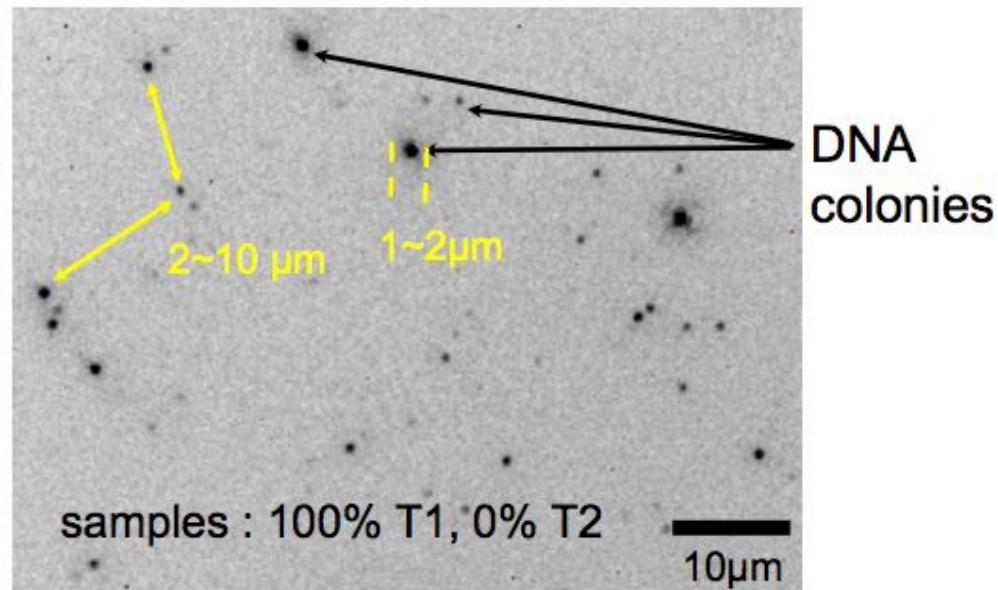
Sequencing by Synthesis (SBS)



PCR colony (aka, 'polony') size and distribution can be precisely controlled

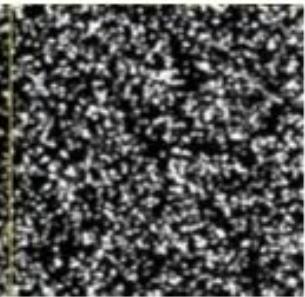


Thousands of molecules are amplified in parallel

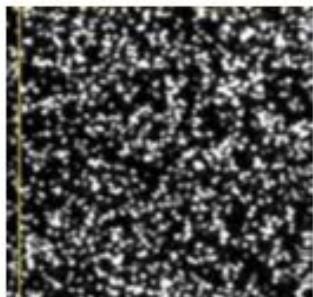


Mayer et al., Presentation 1998

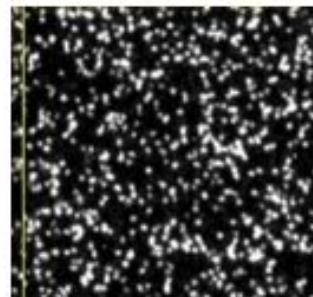
Clustering density is key to data output and quality



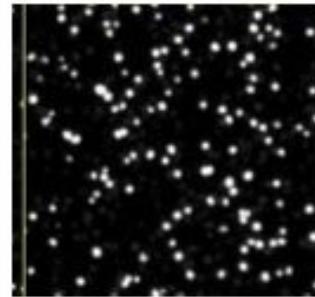
20pM



10pM



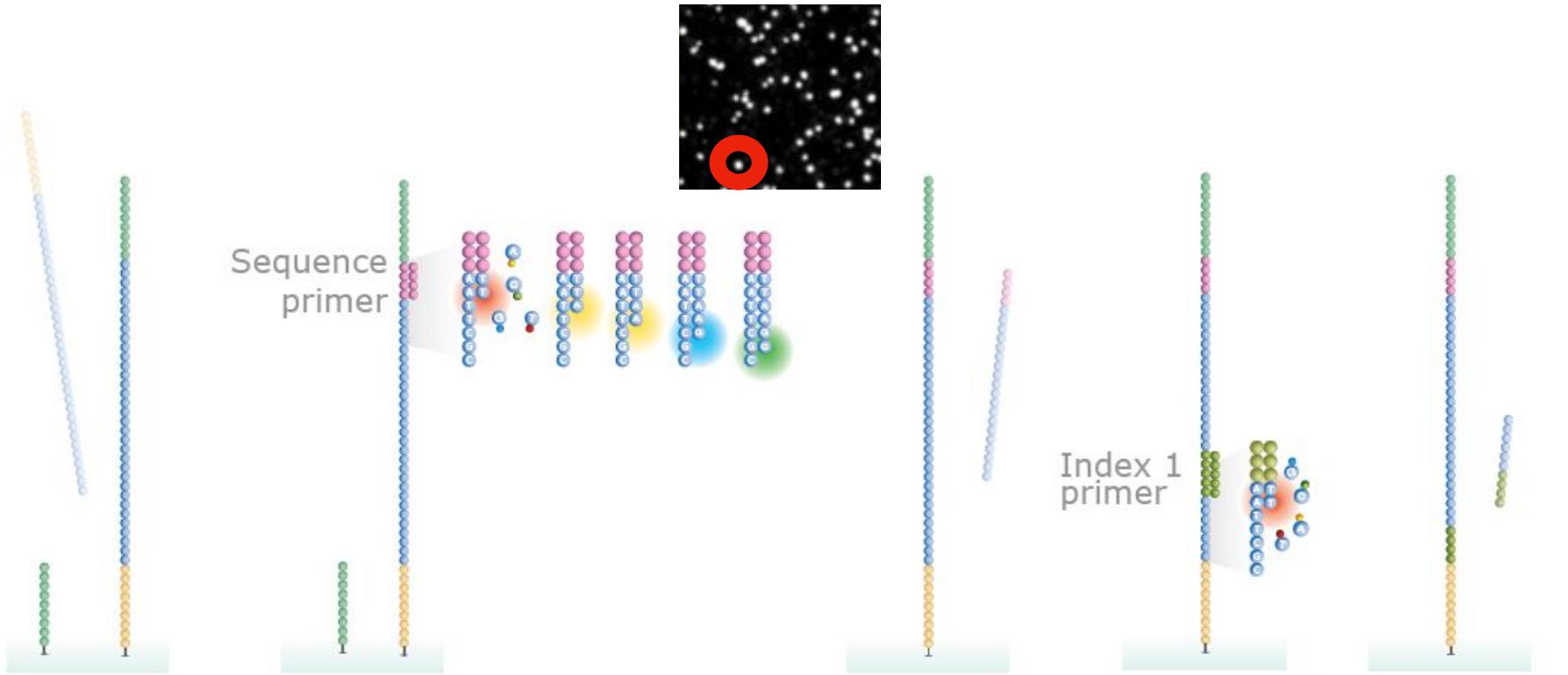
5pM



1pM

HiSeq: 950-1050K clusters/mm²

NextSeq: 170-220K clusters/mm²



The reverse strand is cleaved and washed away

With each cycle, four fluorescently tagged nucleotides compete for addition to the growing chain. Only one is incorporated based on the sequence of the template.

The read product is washed away

Sequence Index 1

The read product is washed away

bit.ly/Illumina_SBS

High-throughput sequencing data is stored in .fastq format

Fast

Header >VIT_201s0011g03530.1
Sequence AATTAAGCATAAATACTCACTCTTACCCCTTATTTCTTATCTCTCATCACTTTGGTGCAGAAG
Header >VIT_201s0011g03540.1
Sequence CAGGTAGCGTGAAGTTAACCTAGCGTTAGACAAACAGCTGTAGTCACGCCAACAAACACC
Header >VIT_201s0011g03550.1
Sequence CATGCAAAGCTGAACCGCATGCTGTGATTGGTGGTAAGTGGTAGTTGAGTAAATTGACAGTGAA
GCCGAAATGGTAAAAGACTAAGGCTAGAAGTAGAATACCACTGTTCTCATCAGTGGGCCA

a

Fastq

Label: @FORJUSP02AJWD1
Sequence: CCGTCAATTCAATTAAAGTTAACCTTGGCCGTACTCCCCAGGCGGT
Q scores (as ASCII chars): +AAAAA@:::?:?@:@:FFAAAAACAA:@:BB@:@?A?
Base=T, Q=':'=25

These are just
text files!

ASCII characters

!	"	#	\$	%	&	'	()	*	+	,	-	.	/	0	1	2	3	4	5	6	7	8	9	:	<	=	>	?	@	A	B	C	D	E	F	G	H	I	
0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40

Quality score

Fastq

Label

Sequence

Q scores (as ASCII chars)

Base=T, Q=':'=25

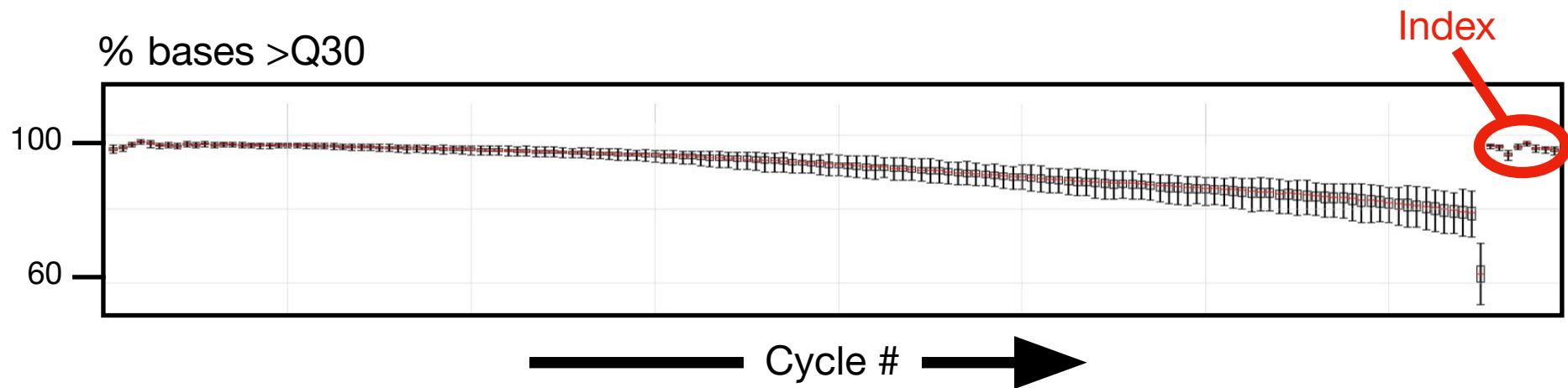
```
@FORJUSP02AJWD1
CCGTCATTCAATTAAAGTTAACCTTGCAGCGTACTCCCCAGGGCGGT
+
AAAAAAA:::99@:::?:?@:@:FFAAAAACCAA:::BB@@?A?

```

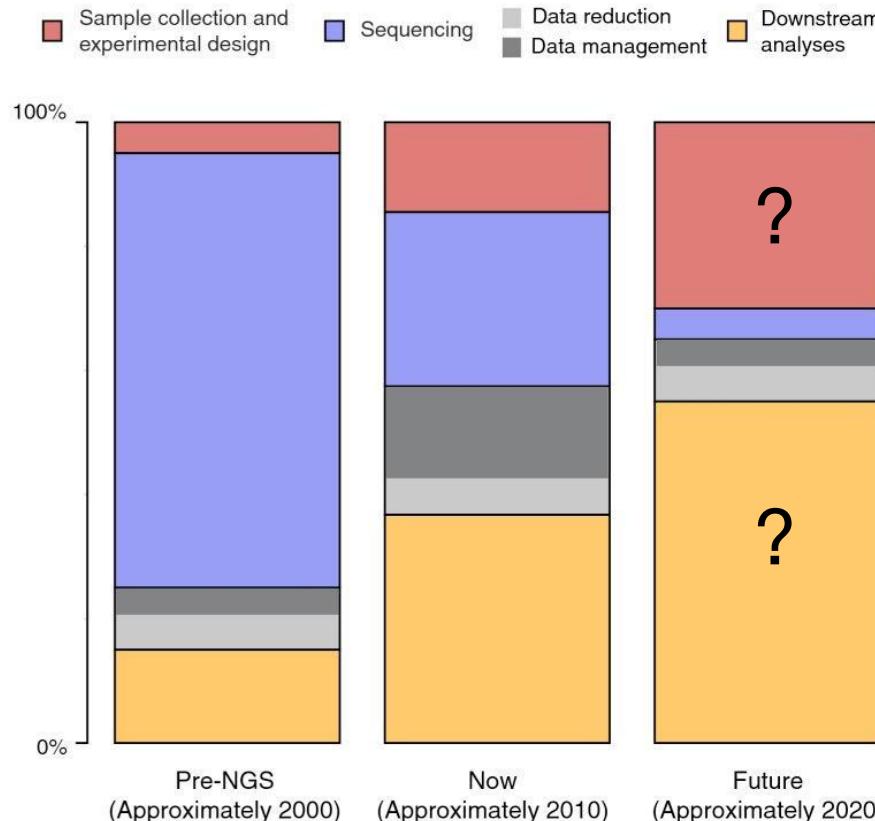
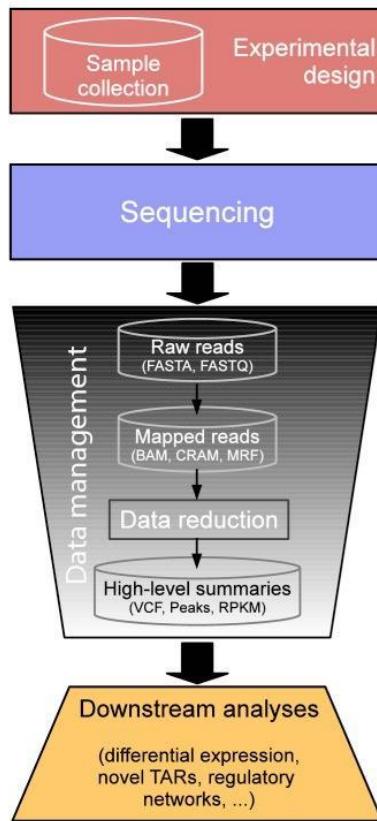
1/1000

1/10000

Illumina sequences are short for a reason



A shift in how time and money are spent on genomics experiments



Costs associated with bulk* sequencing

Library Preparation



Sequencing



TruSeq kit	cat#	cost
stranded total RNA LT (w/ RiboZero)	RS-122-2201	\$5,067
stranded mRNA LT	RS-122-2101	\$2,430

all kits process 48 samples

cycles	cat#	cost
300	FC-404-2004	\$4,222
150	FC-404-2002	\$2,635
75	FC-404-2005	\$1,374

24 samples
library prep = \$51/sample
sequencing = \$58/sample
data output = 15M reads/sample

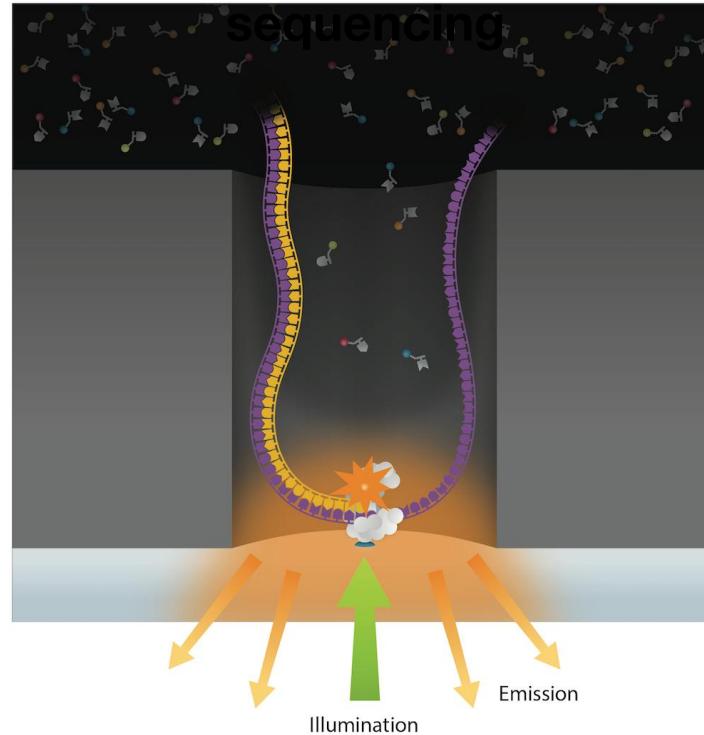
*Costs associated with scRNAseq are much more complicated

Long read sequencing

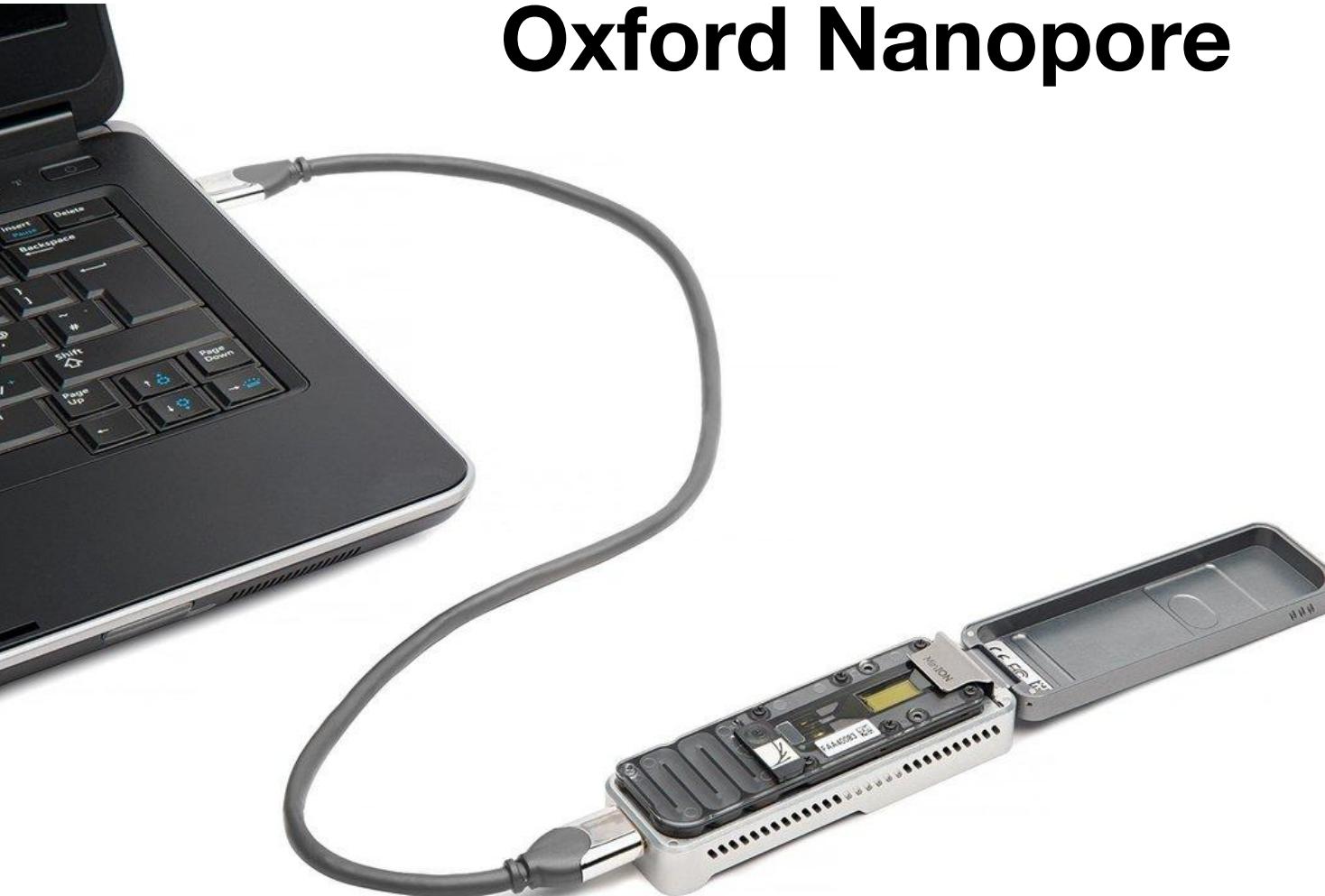
PacBio Sequel 2



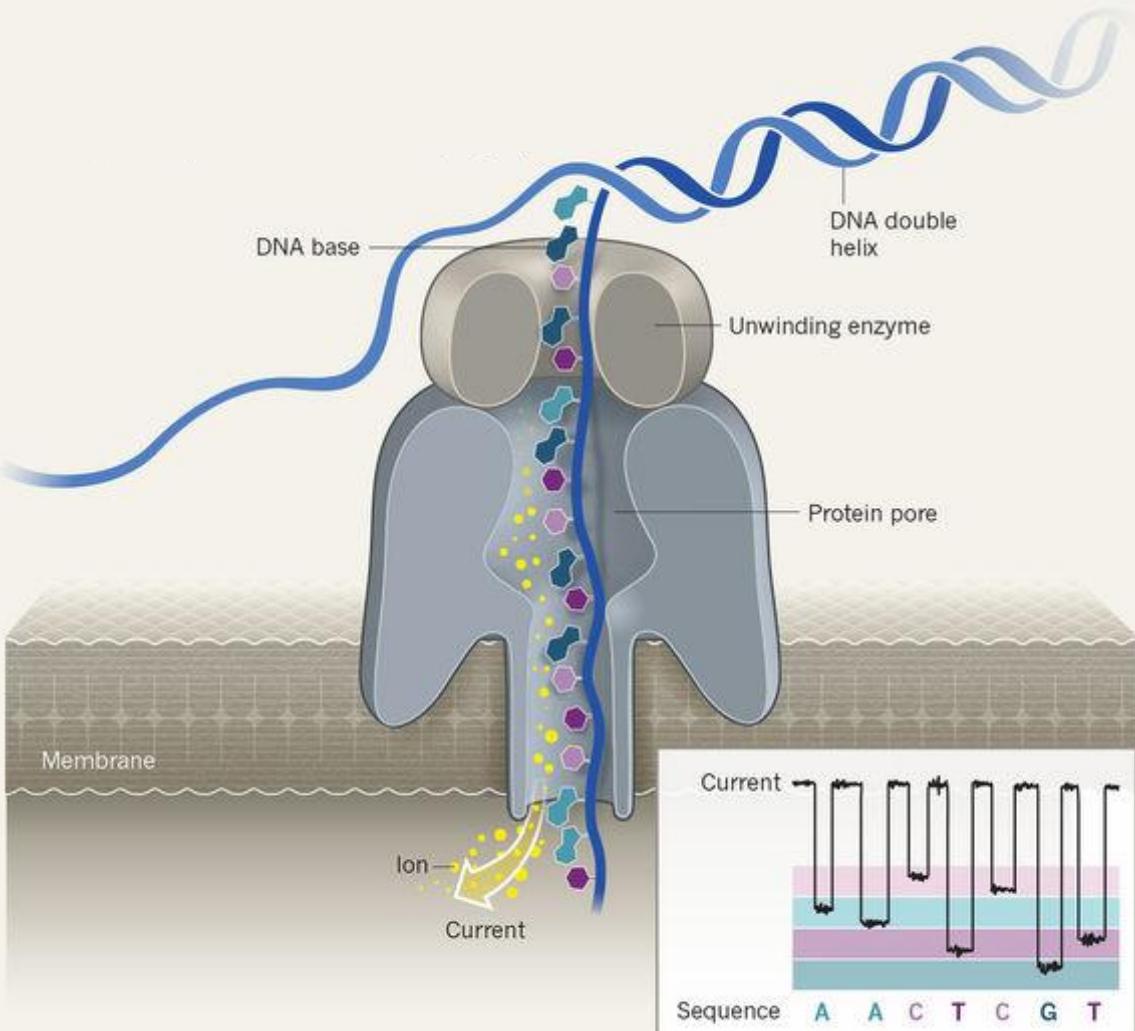
SMRT



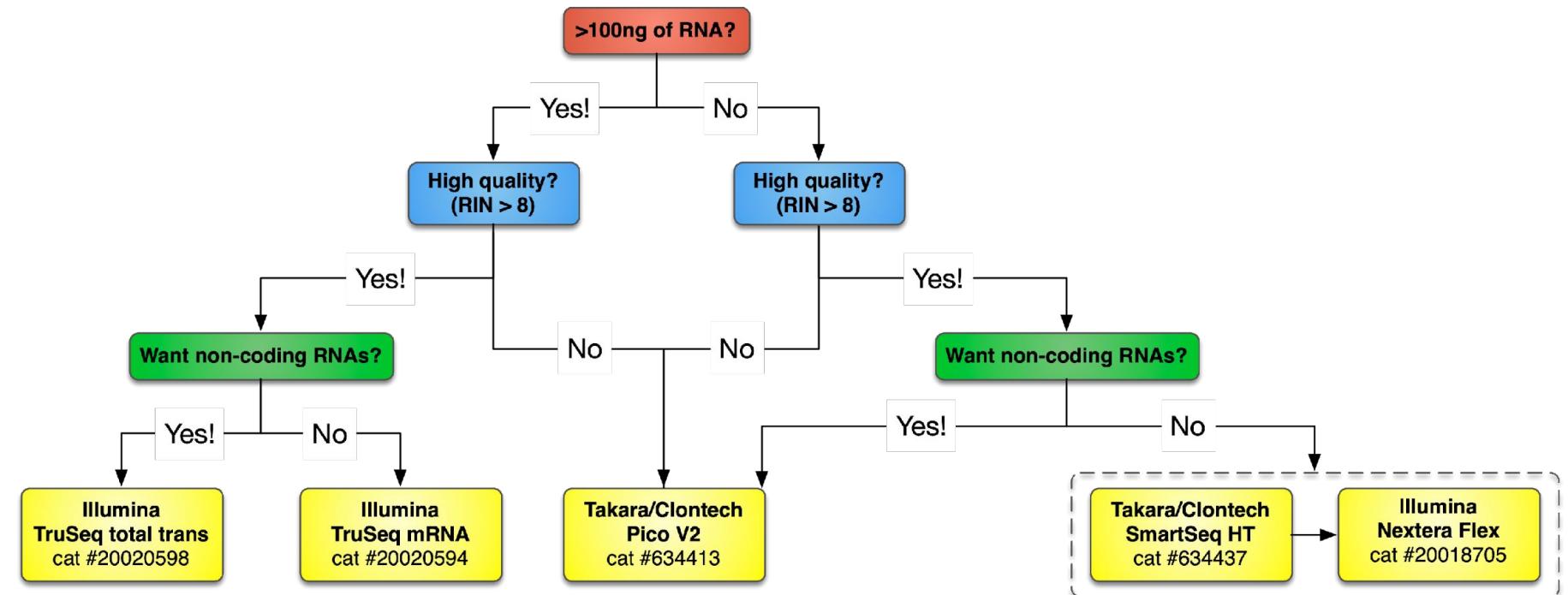
Oxford Nanopore



Nanopore Sequencing



Decision tree for RNAseq library prep



Standard total trans.
100ng-1ug input
\$106/sample

Standard mRNA-seq
100ng-1ug input
\$51/sample

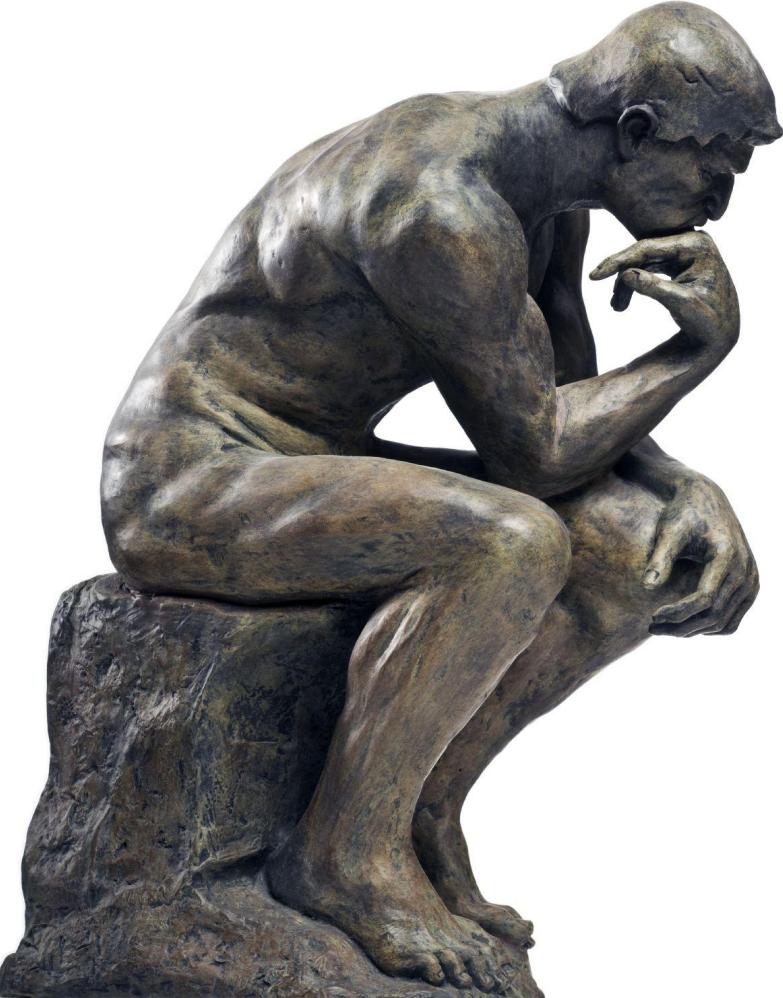
Low input total trans.
250pg-1ng input
\$70/sample

Low input mRNA-seq
10pg-1ng input
\$45/sample for HT + \$47/sample for Flex = ~\$90/sample

The End

Library preparation

- All sequencing experiments begin by using molecular techniques at the bench to construct a catalog or library of oligonucleotides present in a sample.
- Reagents and steps of library prep are organized in kits, and choice of kit will depend on what you want to do/ask.
- Steps may differ depending on end goal, but many features of library prep are shared (*e.g.*, DNA as output, fragmentation, adapter ligation, barcoding of samples)
- QC is critical before, during and after library prep.
- Major technological advances in library prep protocols/kits for special applications (*e.g.*, FFPE-seq, low-input, single cell sequencing)
- The length of library prep (1-3 days), low volume pipetting and chemistry, make this step particularly prone to error and batch effects



Experiment planning

- Study design
- Library prep and sequencing
- Analysis

RNaseq FAQs

Analysis

1. How do I check the quality of my reads?
2. Which aligner should I use?
3. Am I using the proper statistical methods?
4. What are the best ways to visualize results?



RNaseq FAQs

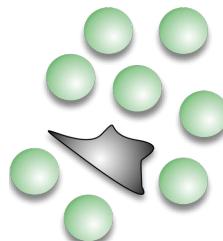
study design

1. Independent evaluation that your experiment worked?
2. Controls will depend on the Q's
3. What insight is to be gained from each treatment/condition?
4. Signal to noise ratio for your cell type

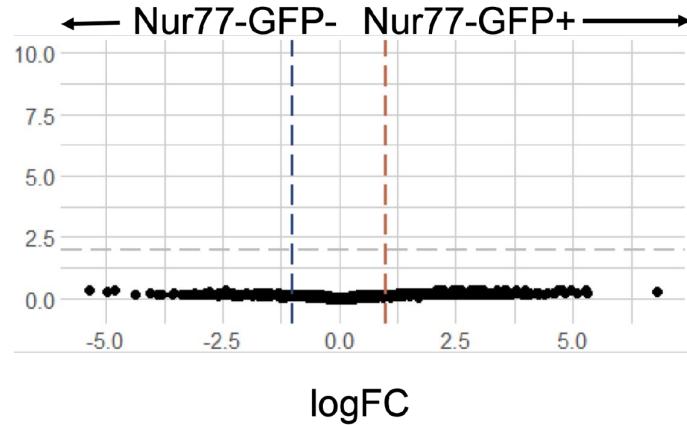


Signal to noise

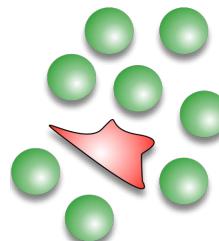
Condition A



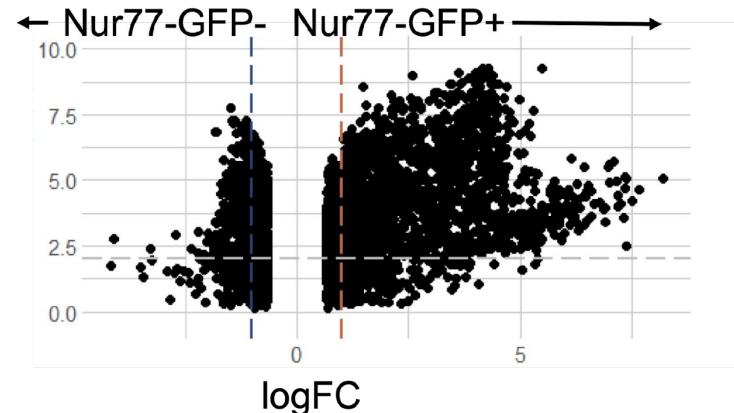
Single sorted
DEGs: 0



Condition B

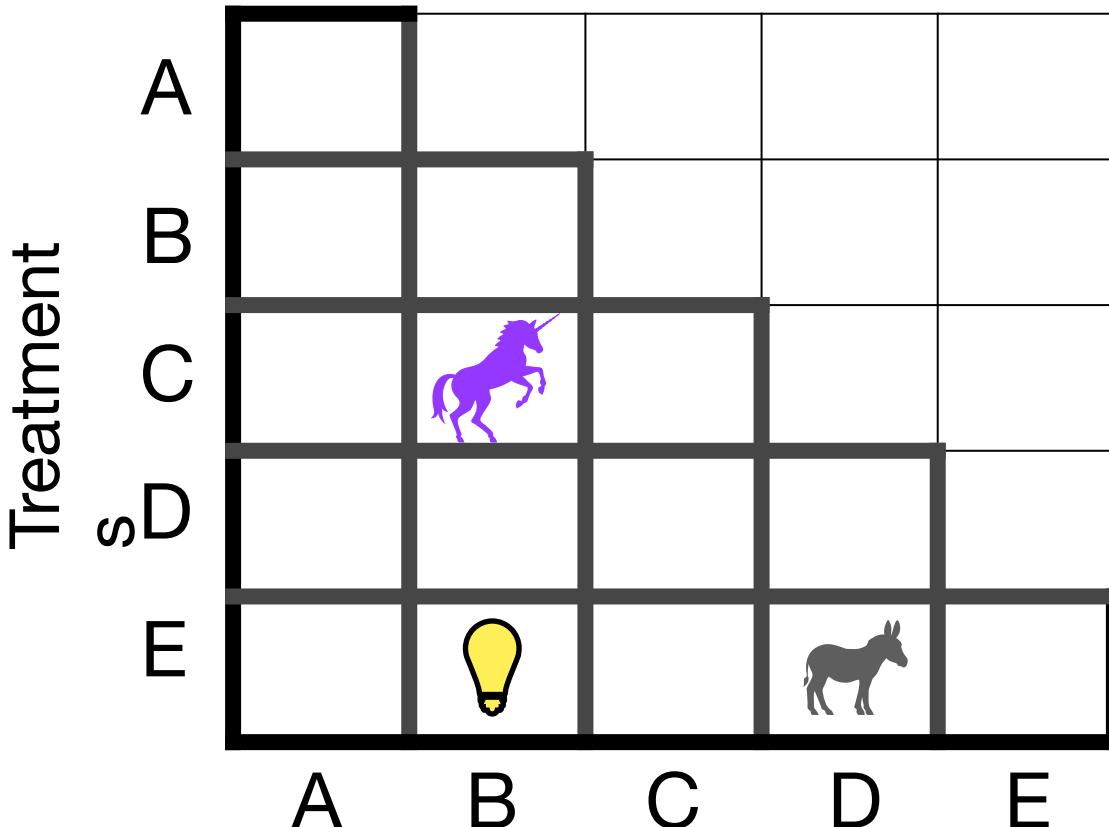


Double sorted
DEGs: 1096



Data courtesy of Lindsey Shallberg (Hunter lab)

What insight is to be gained from each treatment or condition?



Total number of pairwise comparisons

$$(a)(a-1)/2$$

$$(5)(5-1)/2 = 10$$

RNAseq FAQs

sequencing

1. How many replicates are needed?
2. How deep should I sequence (reads)?
3. How much will it cost?



MiniSeq System



MiSeq Series



NextSeq Series



HiSeq Series



HiSeq X Series



NovaSeq Series

Deeper sequencing or more replicates?

BIOINFORMATICS

DISCOVERY NOTE

Vol. 30 no. 3 2014, pages 301–304
doi:10.1093/bioinformatics/btt688

Gene expression

Advance Access publication December 6, 2013

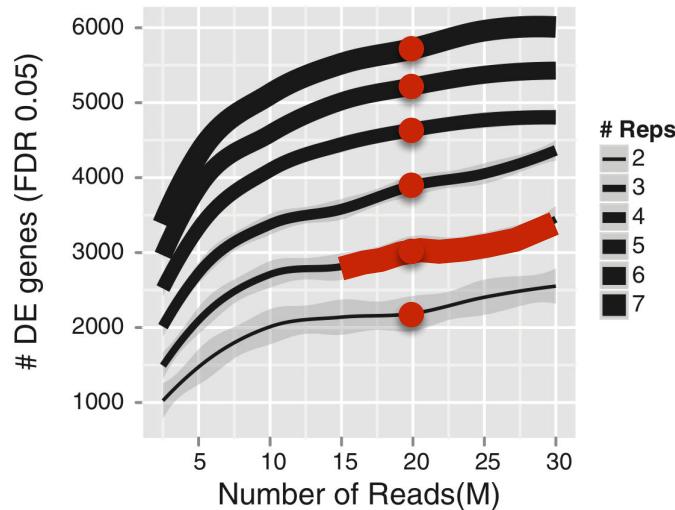
RNA-seq differential expression studies: more sequence or more replication?

Yuwen Liu^{1,2}, Jie Zhou^{1,3} and Kevin P. White^{1,2,3,*}

¹Institute of Genomics and Systems Biology, ²Committee on Development, Regeneration, and Stem Cell Biology and

³Department of Human Genetics, University of Chicago, Chicago, IL 60637, USA

Associate Editor: Janet Kelso



Deeper sequencing or more replicates?

BIOINFORMATICS

DISCOVERY NOTE

Vol. 30 no. 3 2014, pages 301–304
doi:10.1093/bioinformatics/btt688

Gene expression

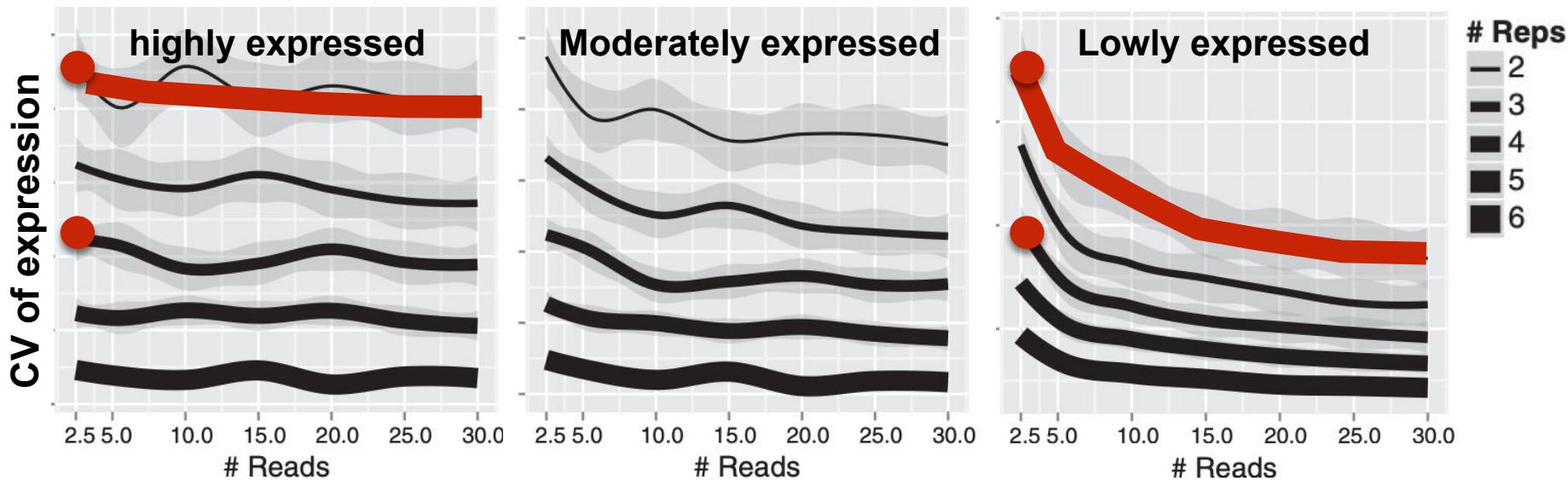
Advance Access publication December 6, 2013

RNA-seq differential expression studies: more sequence or more replication?

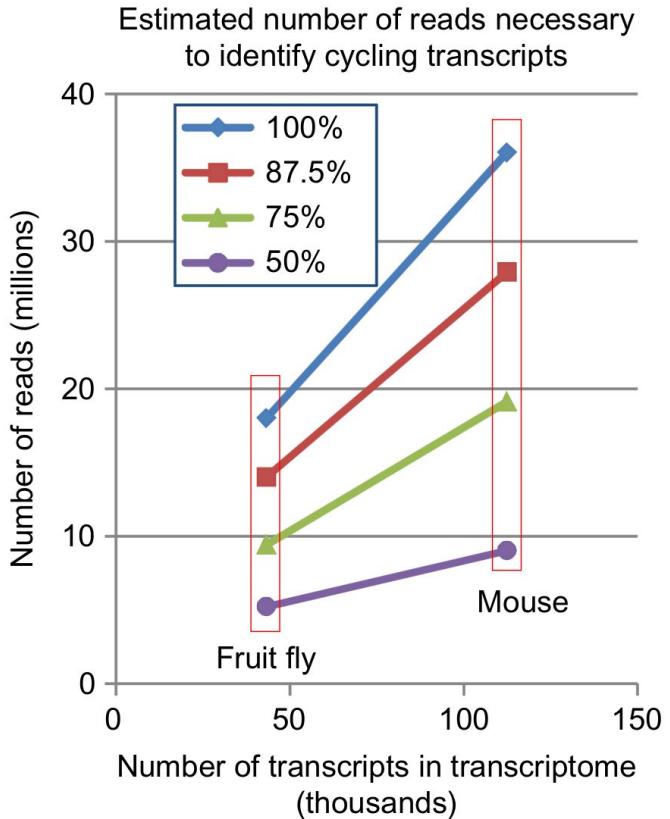
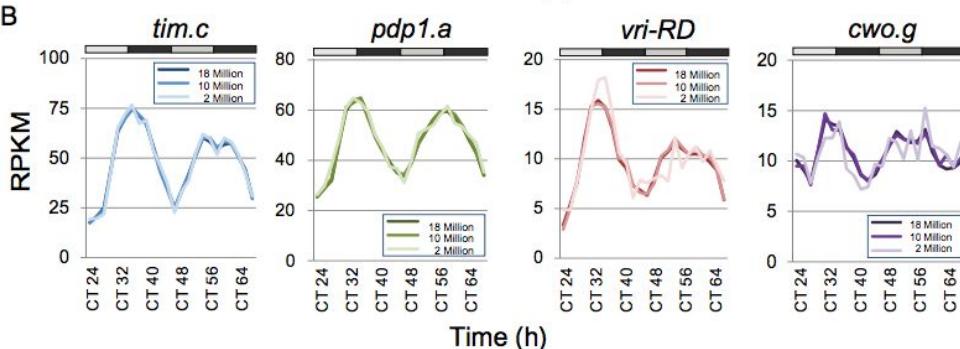
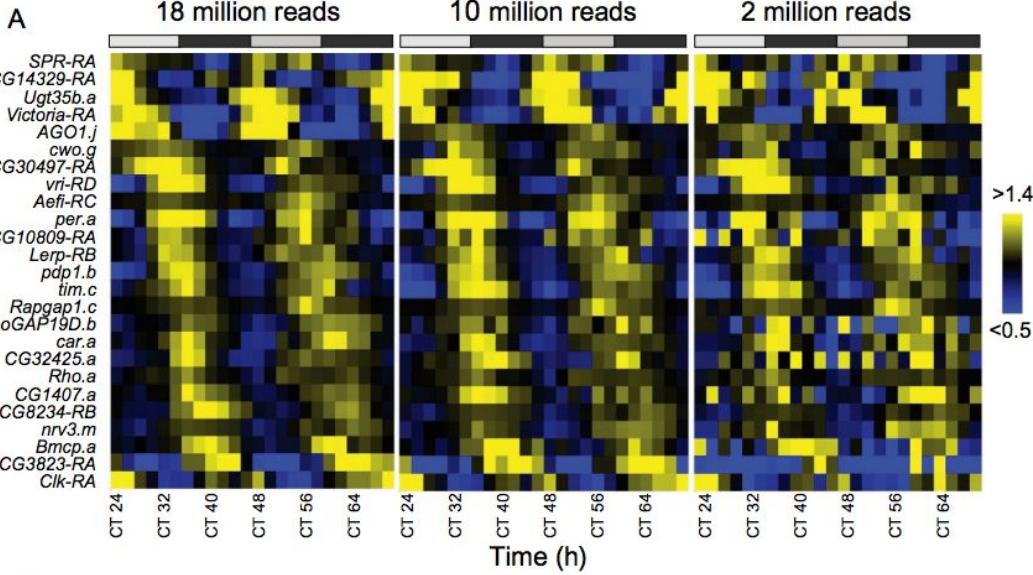
Yuwen Liu^{1,2}, Jie Zhou^{1,3} and Kevin P. White^{1,2,3,*}

¹Institute of Genomics and Systems Biology, ²Committee on Development, Regeneration, and Stem Cell Biology and

³Department of Human Genetics, University of Chicago, Chicago, IL 60637, USA



low sequencing depth can still reveal biology



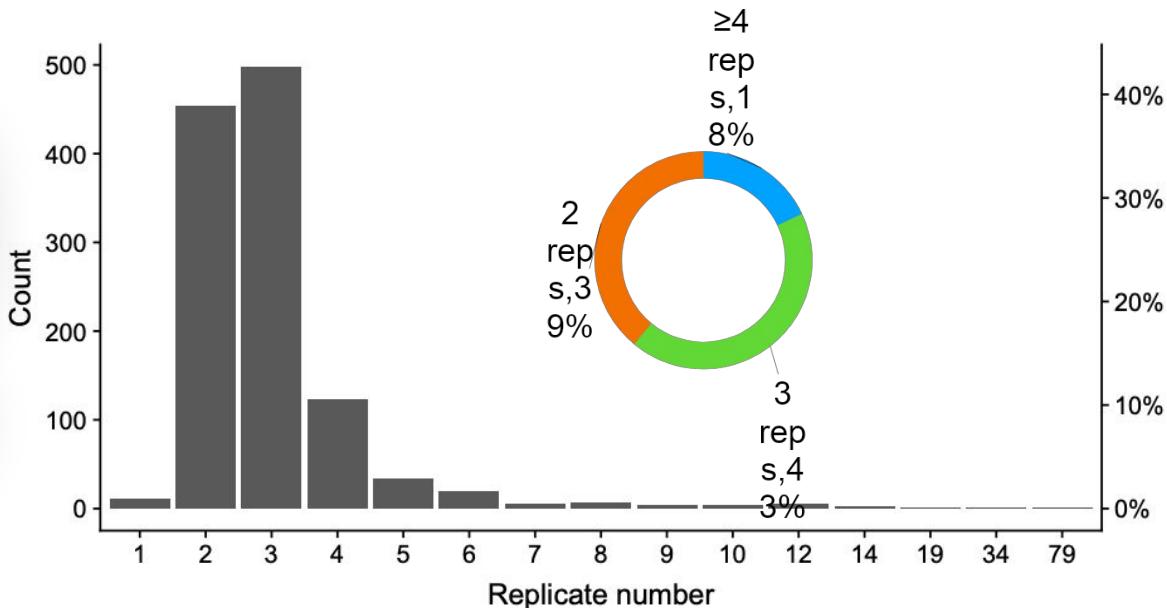
How many biological replicates are needed in an RNA-seq experiment and which differential expression tool should you use?

TABLE 2. A summary of the recommendations of this paper

			Tool recommended for: (# good replicates per condition) ^d				
		Agreement with other tools ^a	WT vs. WT FPR ^b	Fold-change threshold (T) ^c	≤3	≤12	>12
DESeq	Consistent	Pass		0	-	-	Yes
				0.5	-	Yes	Yes
				2.0	Yes	Yes	Yes
EBSeq	Consistent	Pass		0	-	-	Yes
				0.5	-	Yes	Yes
				2.0	Yes	Yes	Yes
edgeR (exact)	Consistent	Pass		0	-	-	Yes
				0.5	Yes	Yes	Yes
				2.0	Yes	Yes	Yes
Limma	Consistent	Pass		0	-	-	Yes
				0.5	-	Yes	Yes
				2.0	Yes	Yes	Yes
cuffdiff	Consistent	Fail					
DESeq2	Consistent	Fail					
BaySeq	Inconsistent	Pass					
edgeR (GLM)	Inconsistent	Pass					
DEGSeq	Inconsistent	Fail					
NOISeq	Inconsistent	Fail					
PoissonSeq	Inconsistent	Fail					
SAMSeq	Inconsistent	Fail					

How many replicates are ‘standard’?

Mined public data from 1167 studies were investigators named samples ‘rep1’, ‘replicate 1’, ‘rep_1’, etc,



Your budget is better spent sequencing more replicates rather than fewer reps more deeply

How ‘bout read length?

