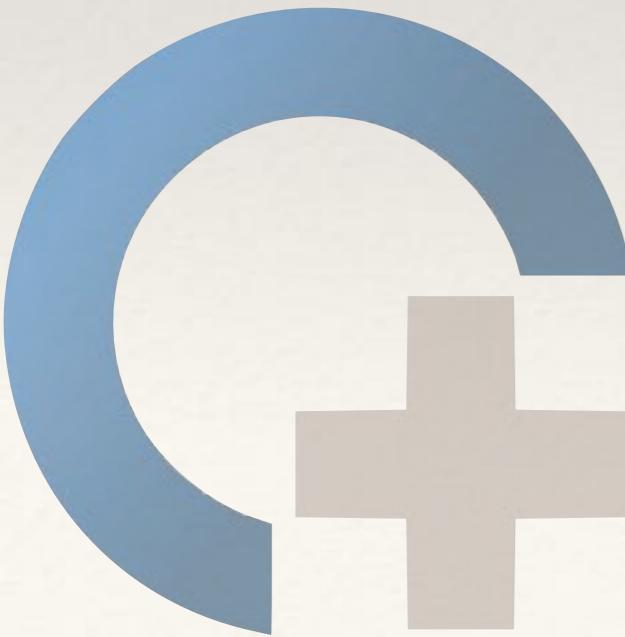


*UiO IN-BIOS*5000/9000

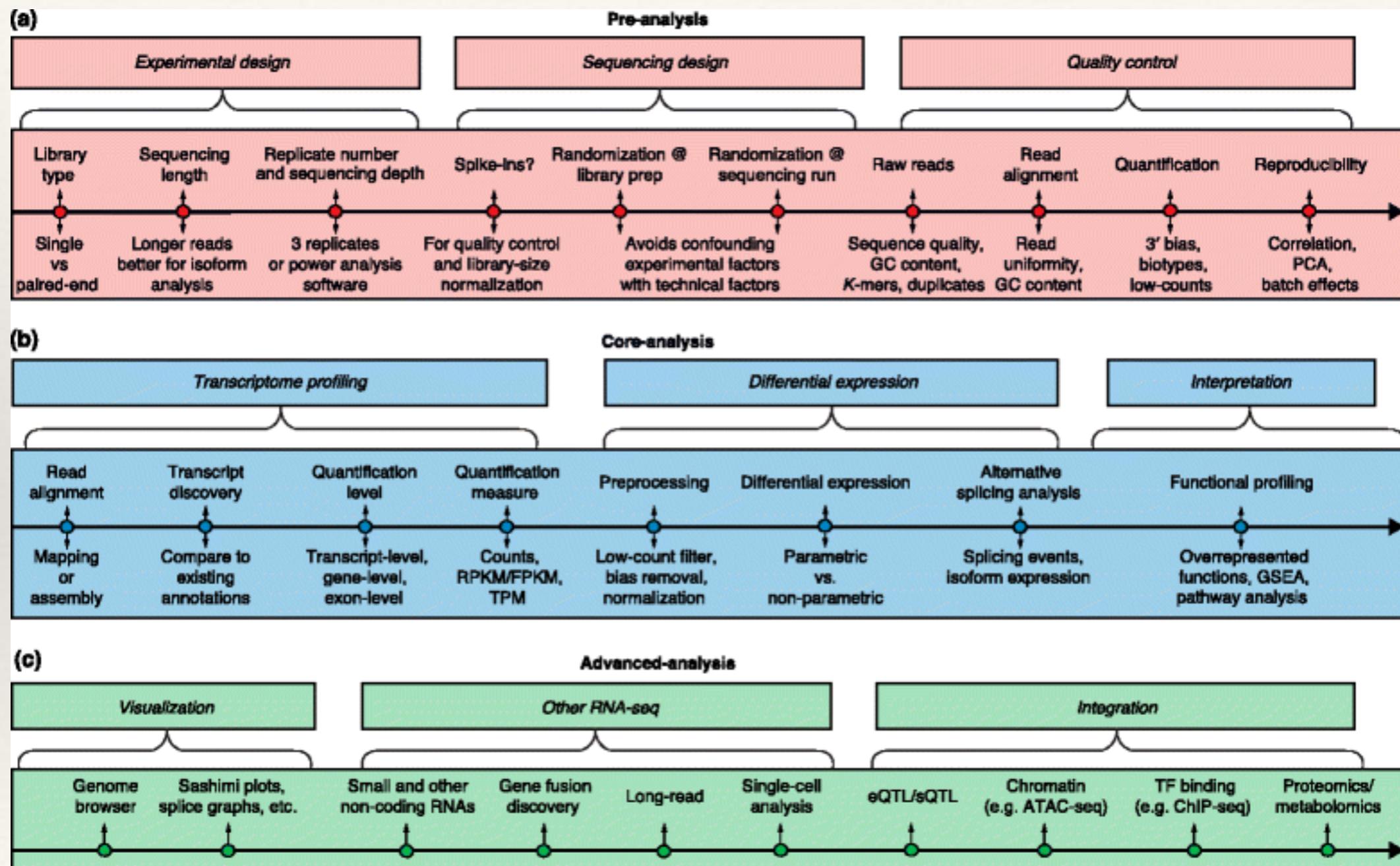
Experimental Design - from a HTS perspective

Arvind Sundaram
Oct 29, 2024

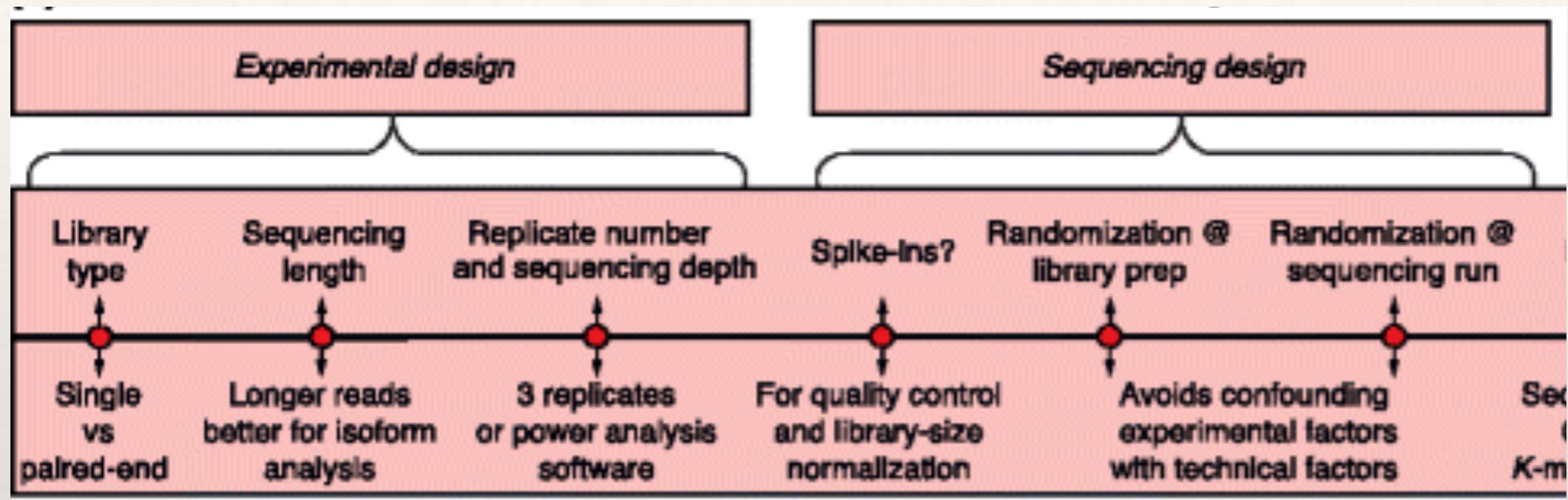
Norwegian Sequencing Centre
OUS, Ullevål, Oslo



RNA seq analysis pipeline



Experimental design



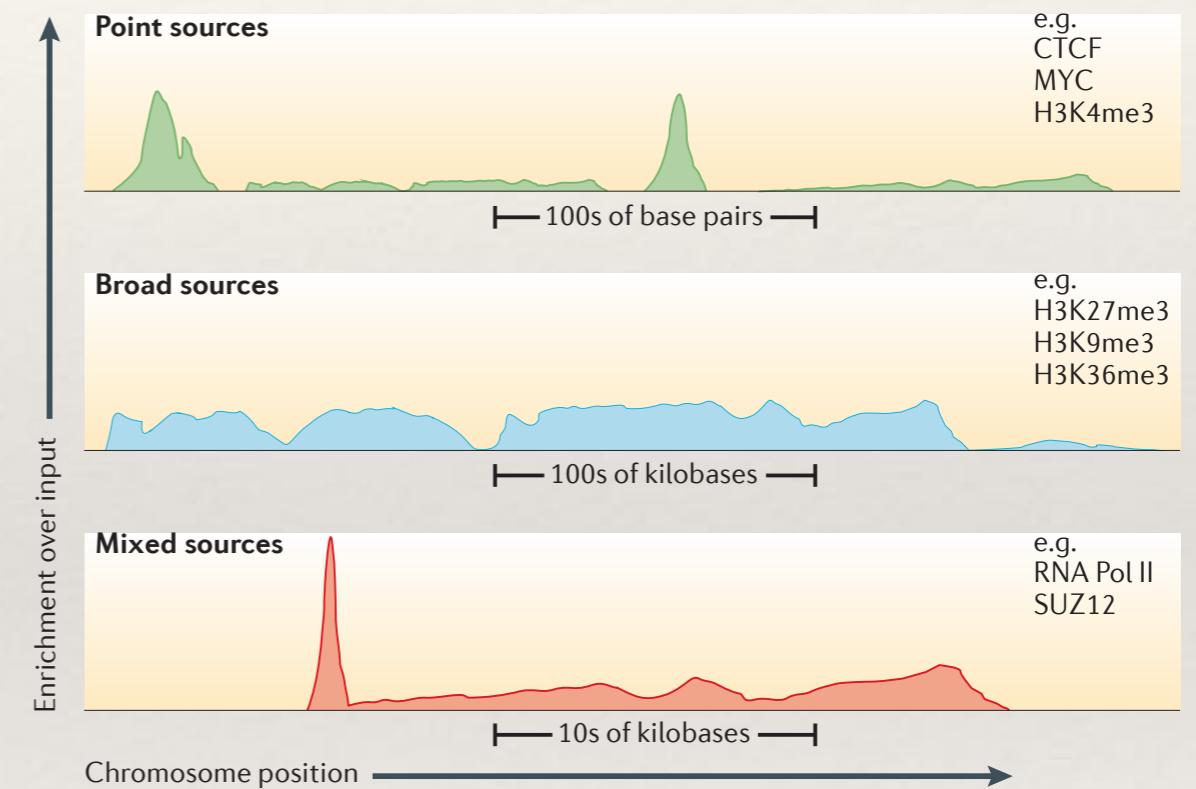
Design of the experiment and sequencing plan have a direct effect on downstream analyses and interpretation of data

Experimental design

- ❖ Biological question
- ❖ Platform choice
- ❖ Technology variation
 - ❖ Technical bias
 - ❖ Run/Lane bias
 - ❖ Index/barcode bias
 - ❖ Duplicates
 - ❖ Error rates
 - ❖ Sample variation
 - ❖ PCR amplification?
 - ❖ Sequencing depth
 - ❖ Data analysis
 - ❖ Species-specific information
 - ❖ Is there a genome sequence available??
 - ❖ Genome size (c-value)
 - ❖ genomesize.com

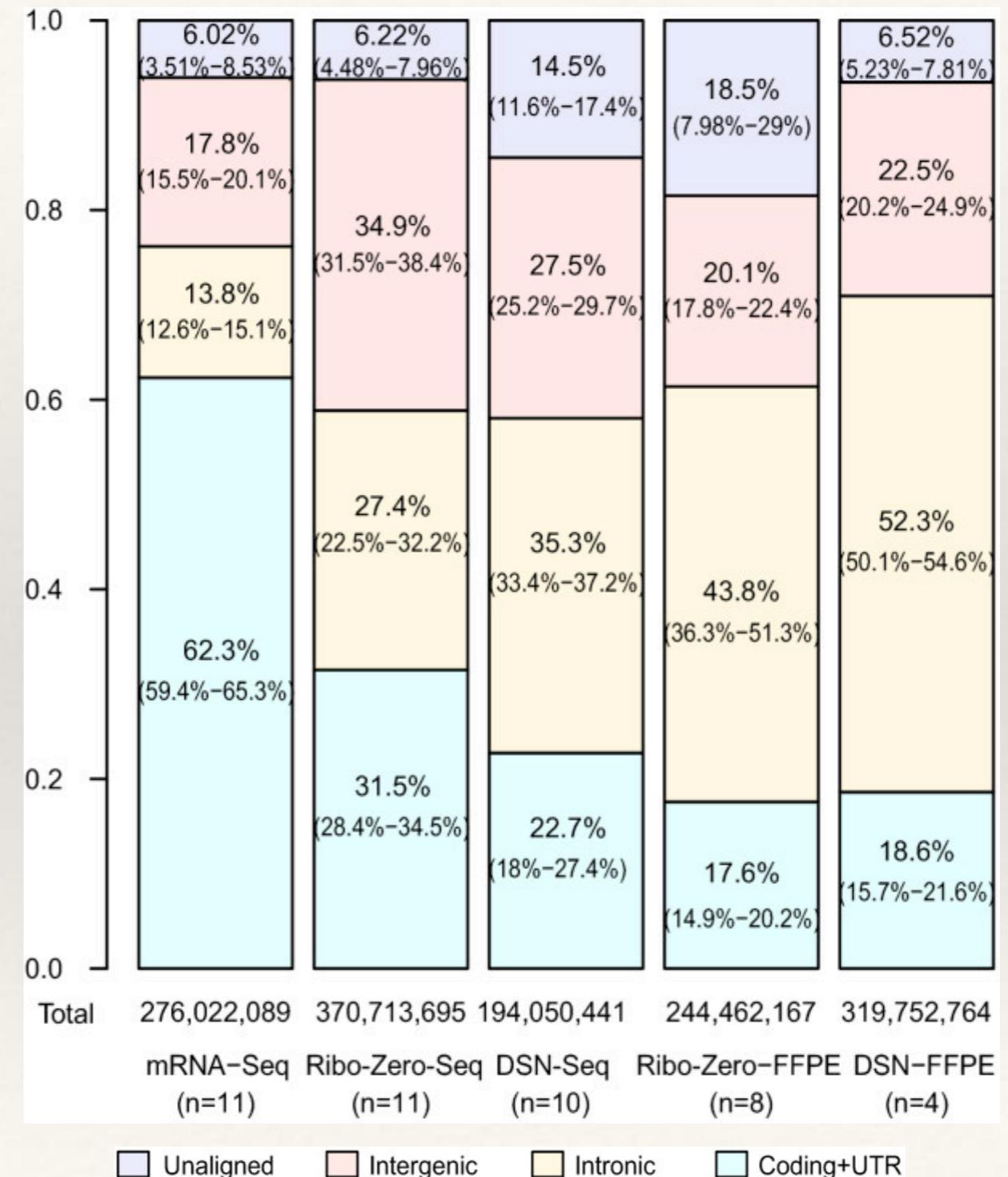
Biological question

- ❖ Know your targets
 - ❖ Whole genome
 - ❖ Targeted (re)seq
 - ❖ Exome
 - ❖ ChIP-seq
 - ❖



Biological question

- ❖ Know your targets
 - ❖ Whole genome
 - ❖ Targeted (re)seq
 - ❖ Exome
 - ❖ ChIP-seq
 - ❖ RNA-seq
 - ❖ rRNA depleted?
 - ❖ polyA enriched?
 - ❖ microRNA



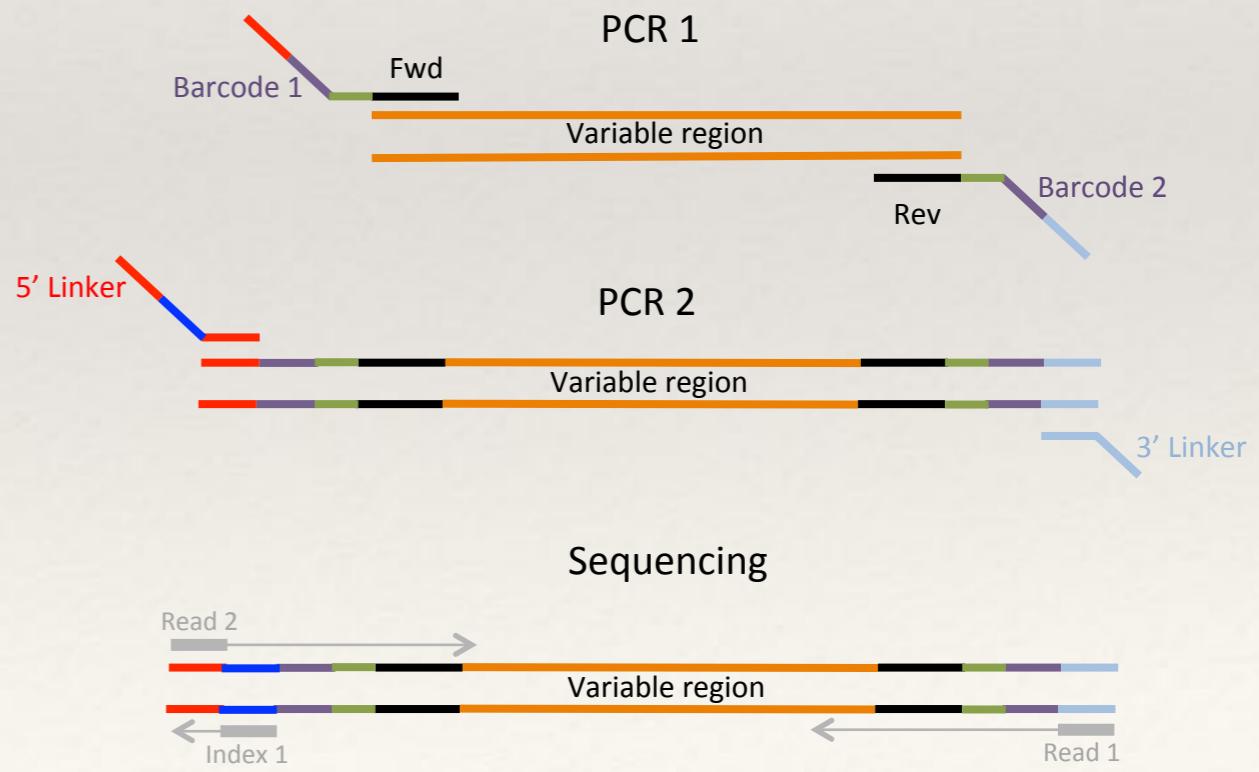
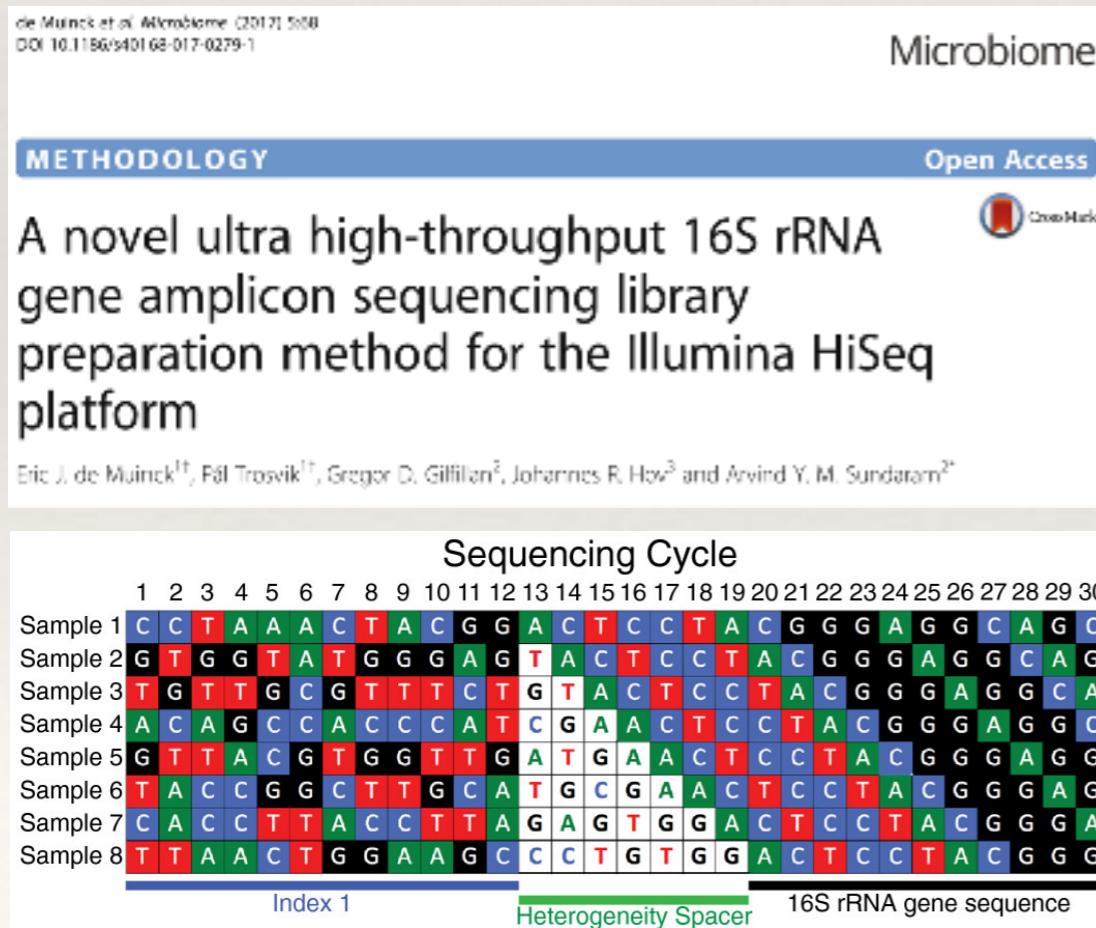
Experimental design

- ❖ Short or long fragments
- ❖ Short or long reads
- ❖ Single or paired end
- ❖ Multiplexing
 - ❖ single or dual index
 - ❖ more barcodes?
- ❖ Library prep method
 - ❖ Depth required
 - ❖ Coverage required
- ❖ Replicates
 - ❖ biological
 - ❖ technical

Indexing

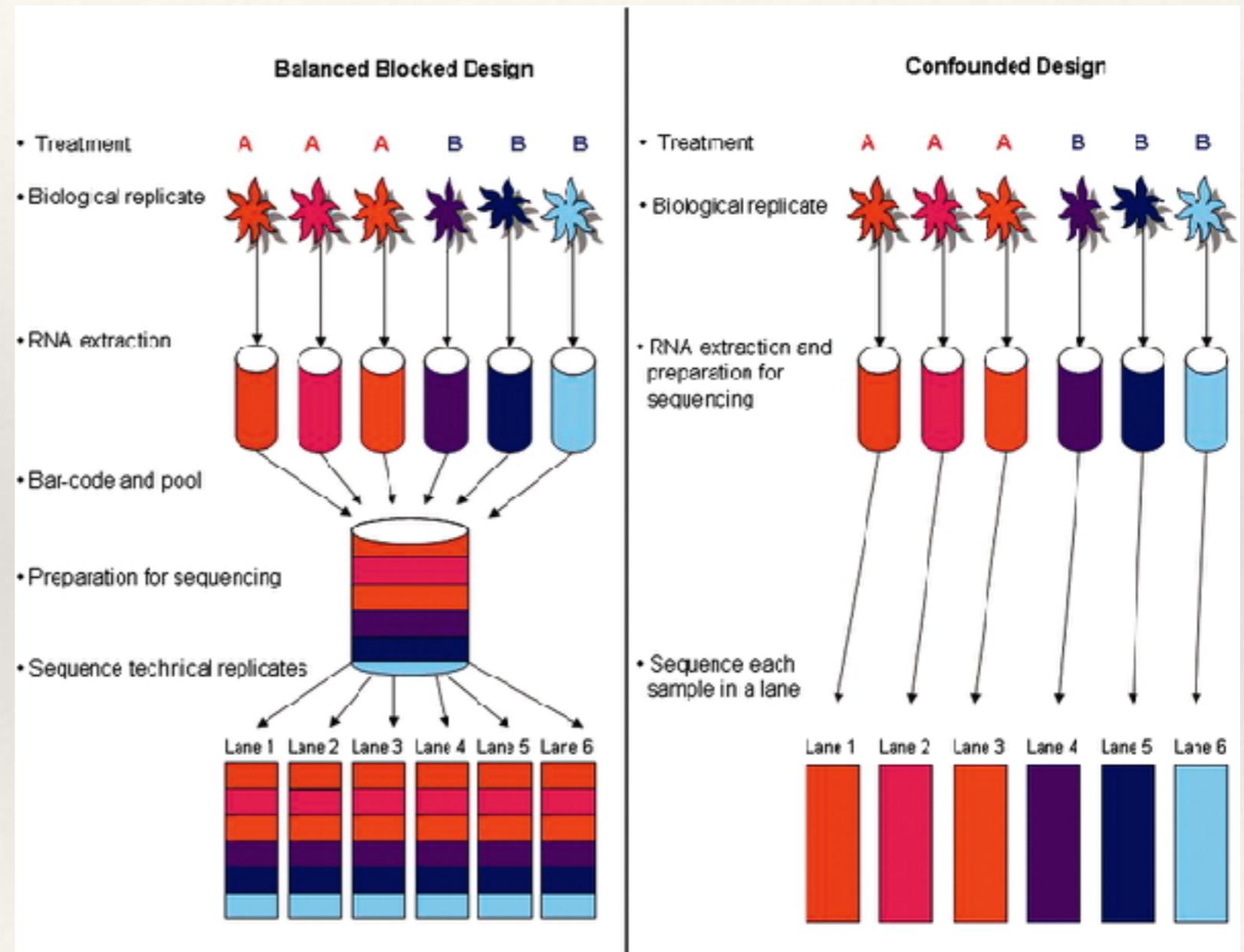
- ❖ Dual index possible
- ❖ Dual internal barcodes possible
 - ❖ multiplex up to 4000 samples.

de Muinck et al. Microbiome (2017) 5:68
DOI 10.1186/s40168-017-0279-1



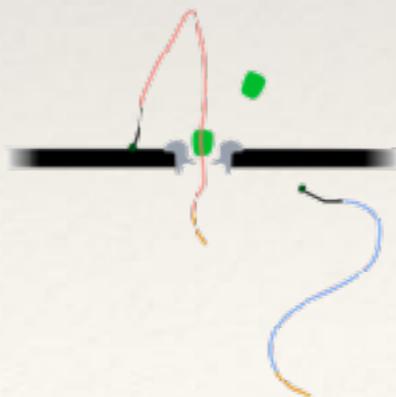
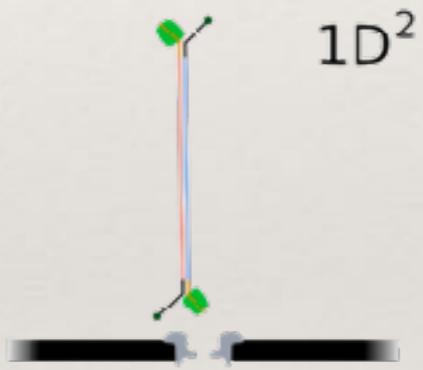
Technical bias

- ❖ Lane / flowcell bias
- ❖ Index / barcode bias
- ❖ Batch effect
- ❖ Randomisation is key

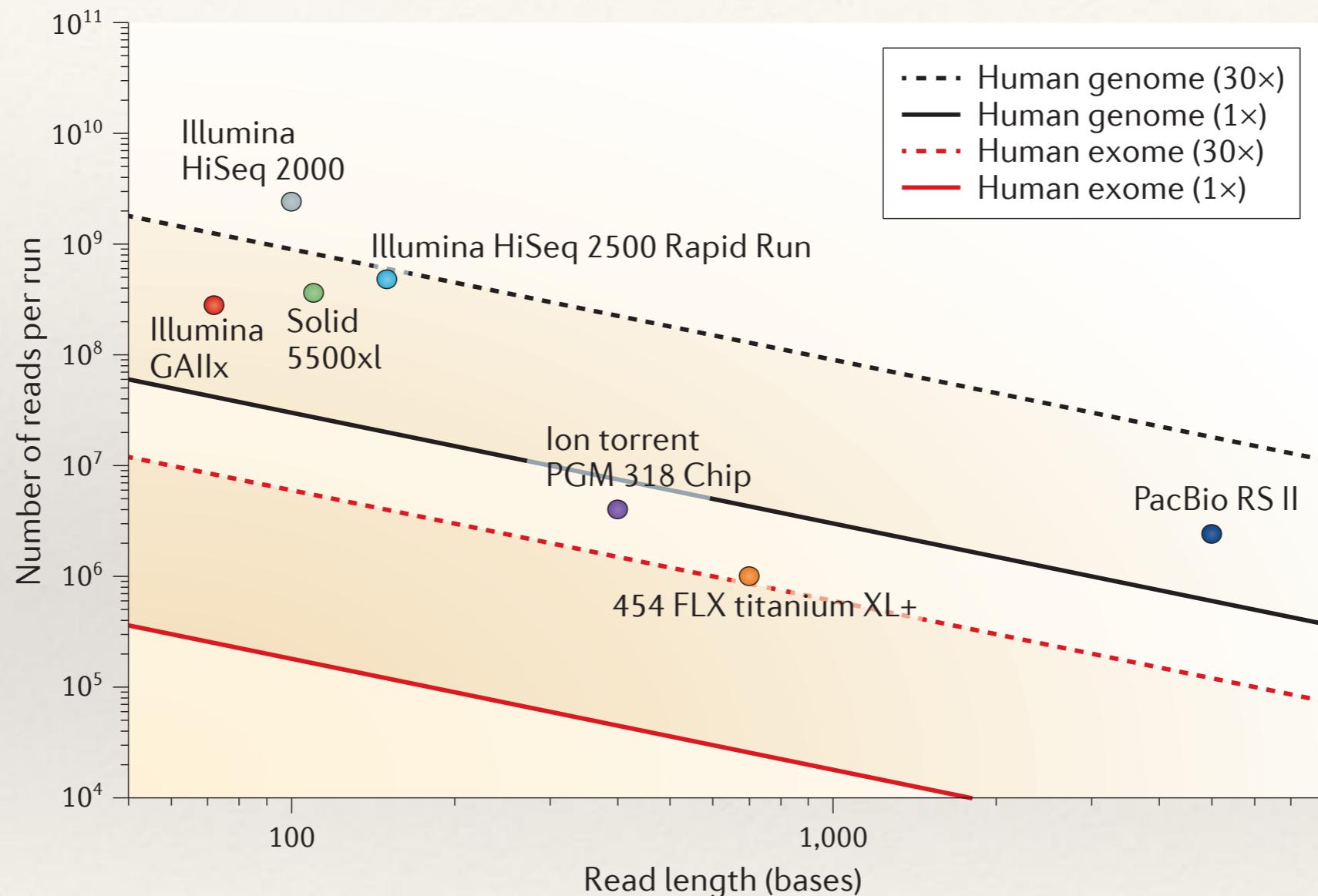


Error rates

- ❖ Illumina has low error rates
- ❖ Pacbio and Oxford Nanopore have relatively high error rates
 - ❖ Cyclic sequencing can reduce the error rate in Pacbio
 - ❖ 1D² sequencing can reduce the error rate in Oxford Nanopore
- ❖ Deep sequencing is used to correct for errors

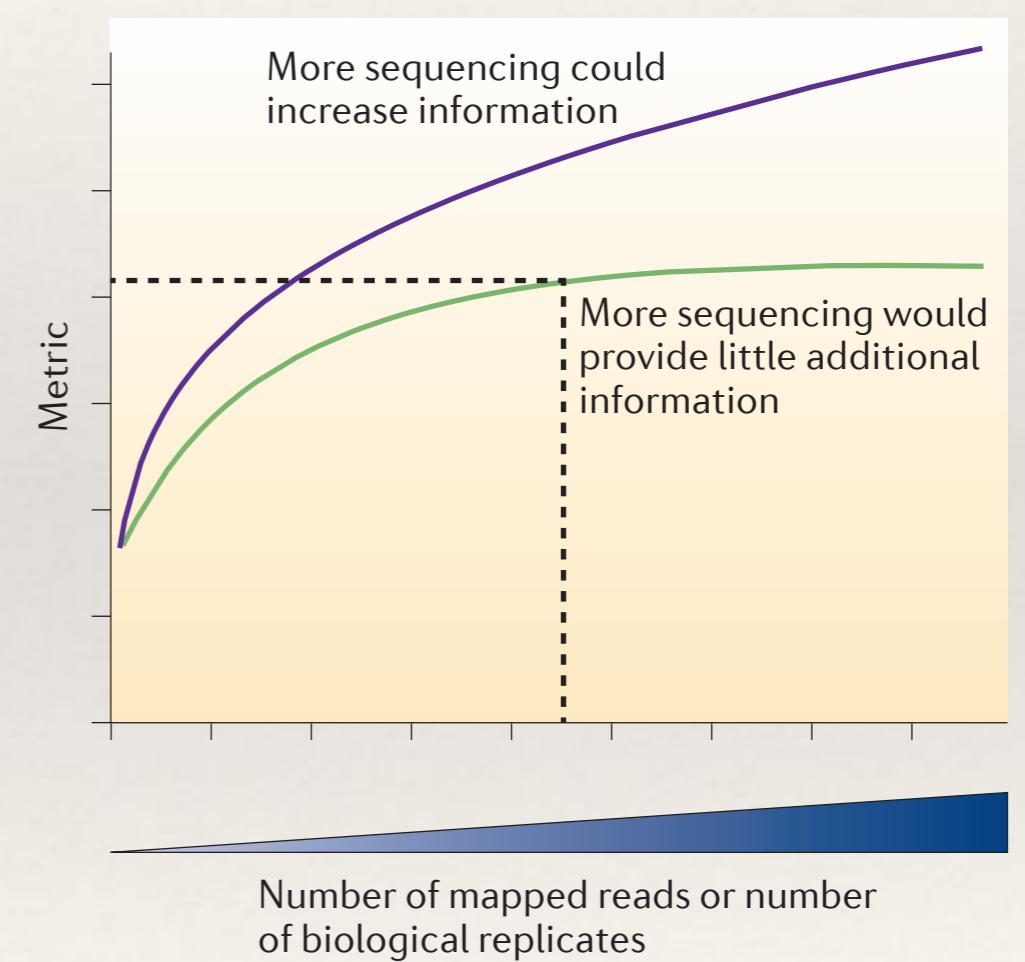
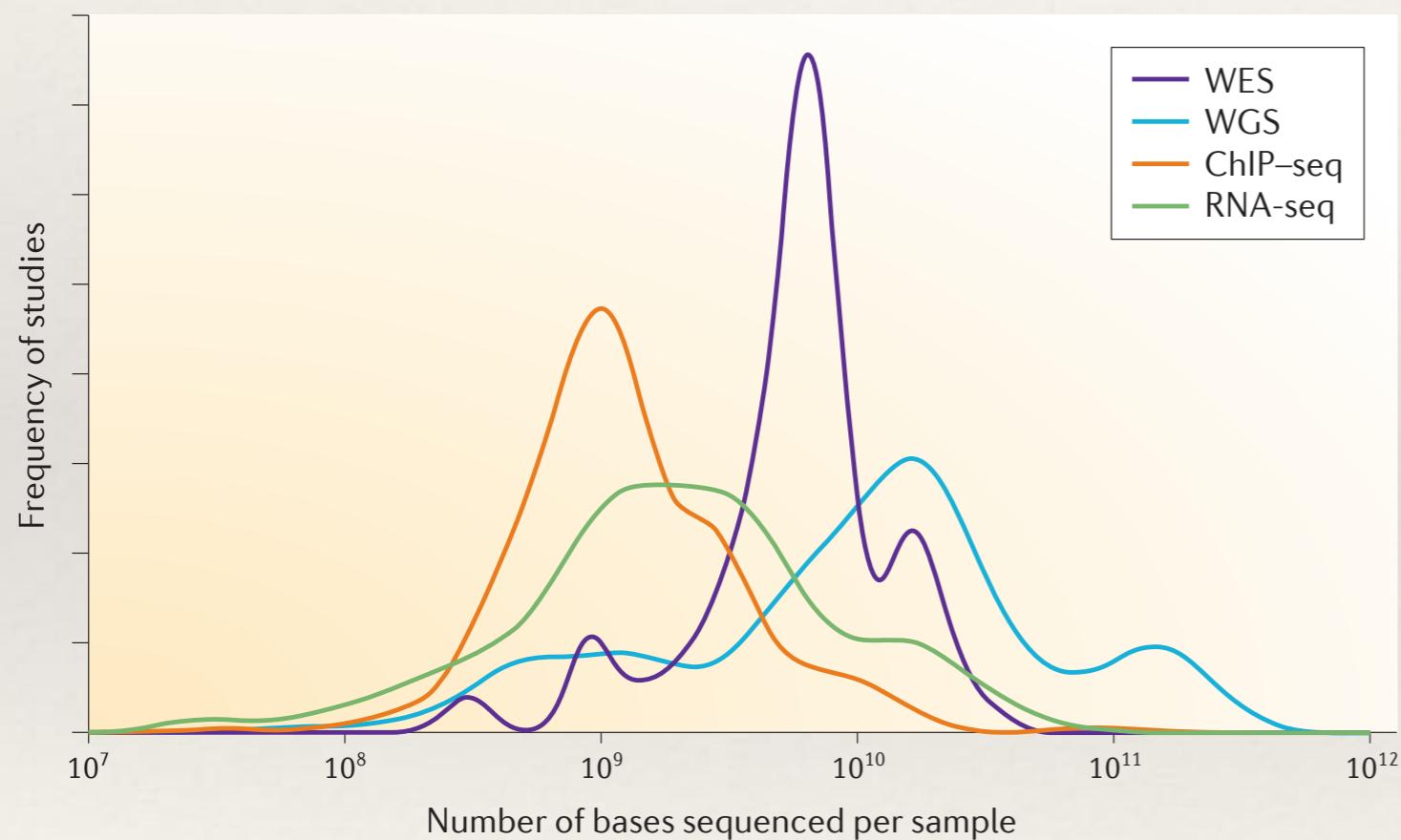


Sequencing depth and coverage

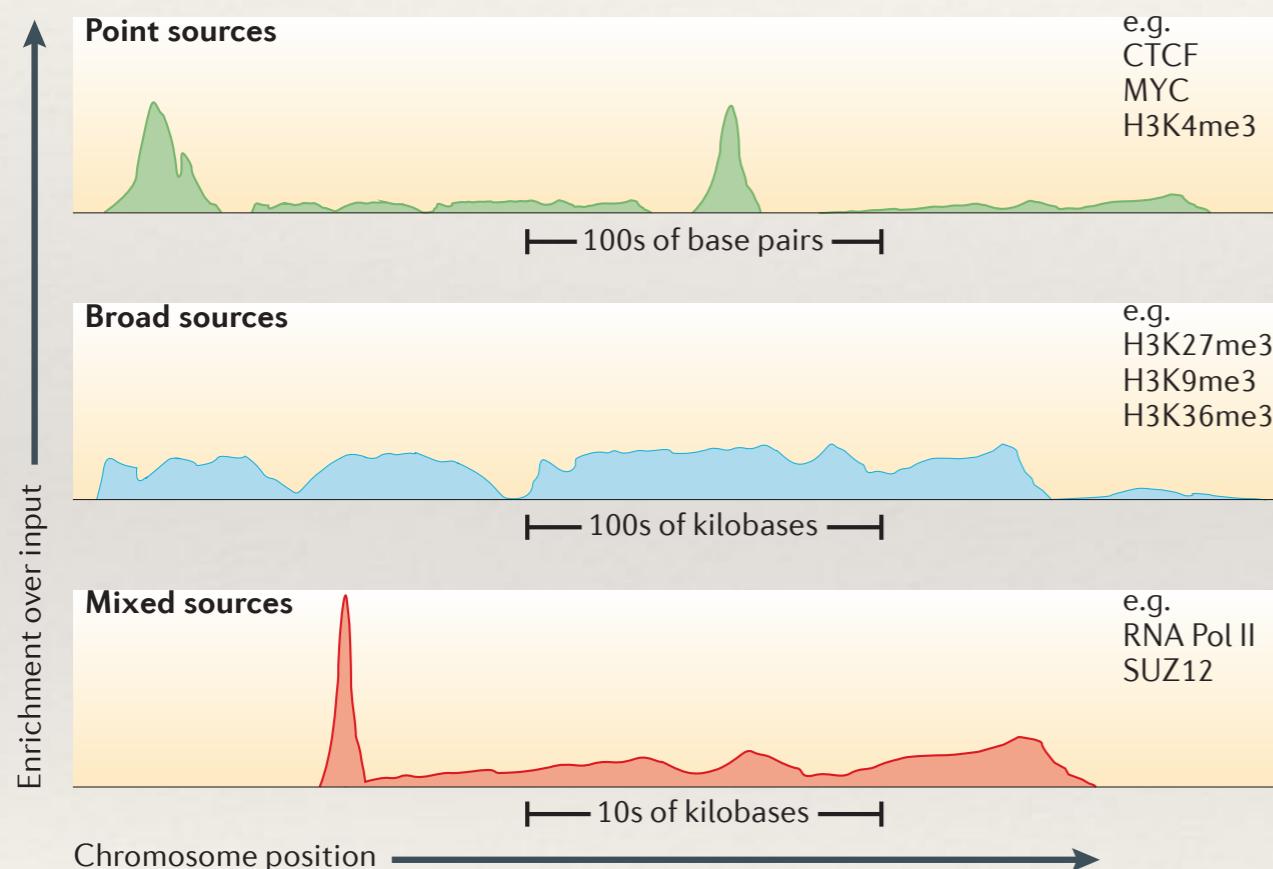


GAIix, Genome Analyzer Iix; PacBio, Pacific Biosciences; PGM, personal genome machine.

Sequencing depth and coverage



Sequencing depth and coverage



Techniques	Read counts in representative studies
DNaseI-seq and FAIRE-seq	20–50 million
CLIP-seq	7.5 million; 36 million
iCLIP and PAR-CLIP	8 million; 14 million
ChIP and CHART	26 million
4C	1–2 million
ChIA-PET	20 million
5C	25 million
Hi-C	>100 million
MeDIP-seq	60 million
CAP-seq	>20 million
ChIP-seq	>10 million per sample (point source); >20 million per sample (broad source)

Replicates and Depth

- ❖ Sound experimental design
- ❖ Number of replicates
 - ❖ Biological variation
 - ❖ Technical replicates - not so important
- ❖ Sequencing depth

Table 1 Statistical power to detect differential expression varies with effect size, sequencing depth and number of replicates

Effect size (fold change)	Replicates per group		
	3	5	10
1.25	17 %	25 %	44 %
1.5	43 %	64 %	91 %
2	87 %	98 %	100 %
Sequencing depth (millions of reads)			
3	19 %	29 %	52 %
10	33 %	51 %	80 %
15	38 %	57 %	85 %

Replicates vs Depth

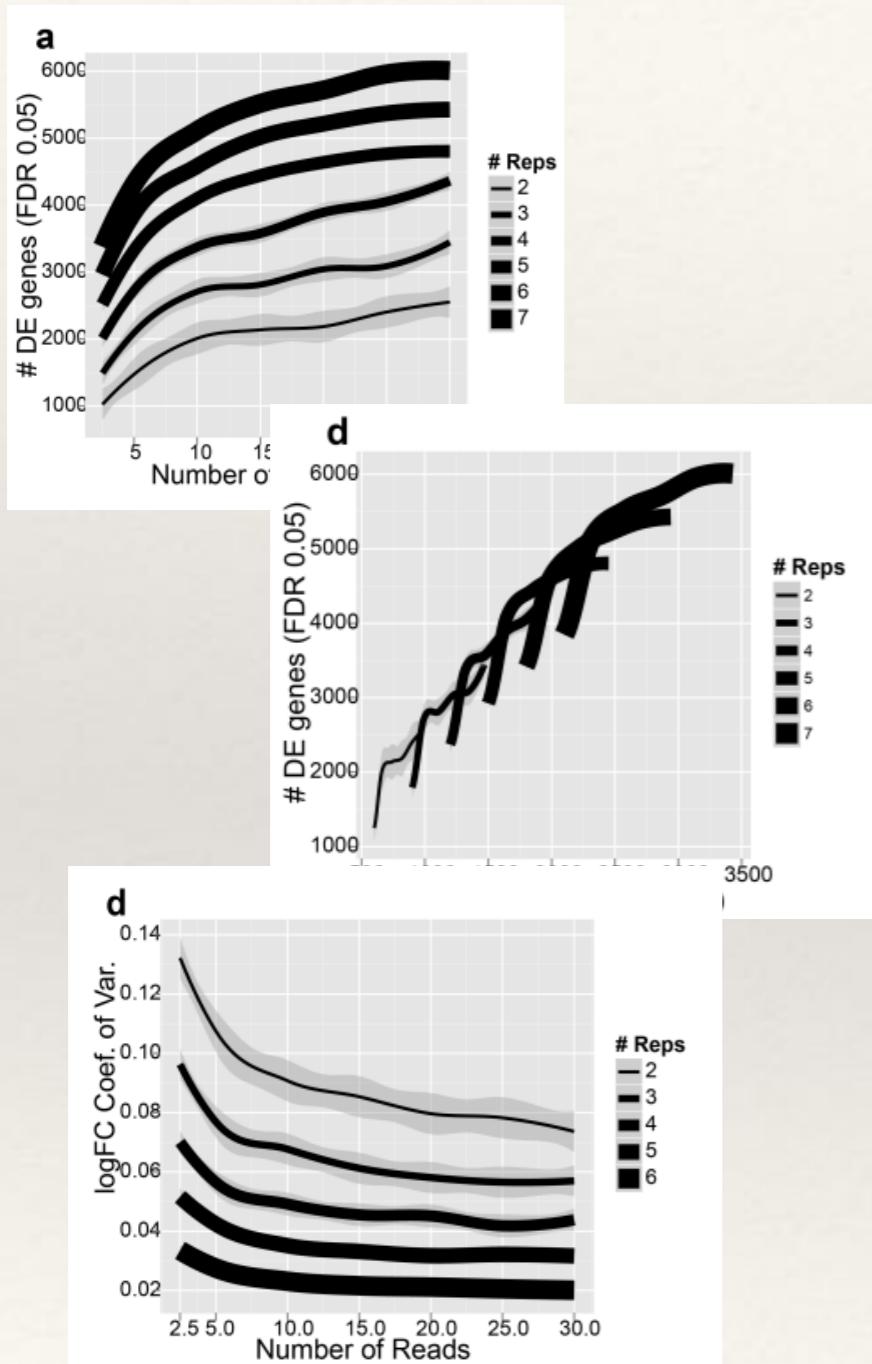


Table 1. Cost efficiency for power to detect DE genes (cost per 1% power given each experimental design where the variables are). Assumptions made during calculations are described in Methods. * indicates lowest cost per 1% power in each replication level. Units are in dollars.

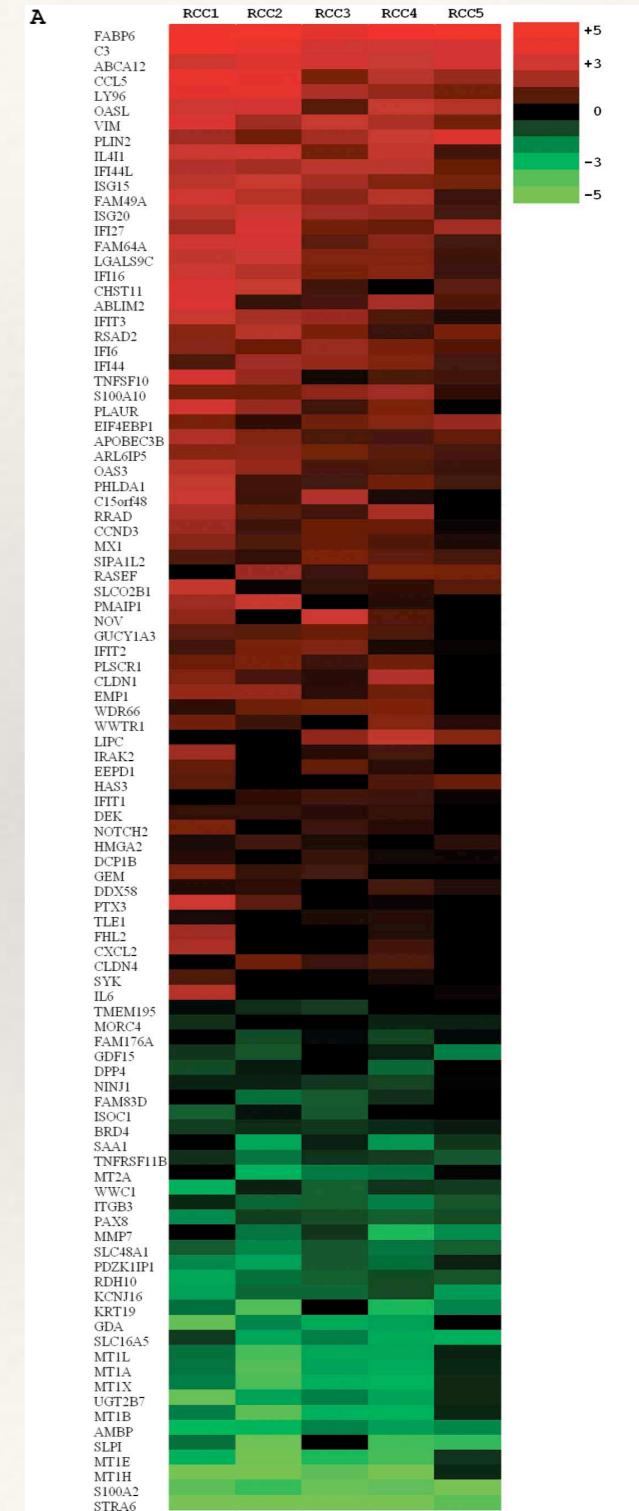
Relative Cost	2.5M	5M	10M	15M	20M	25M	30M
2 replicates	24.2	17.2	14.4*	15.8	16.7	17.0	17.8
3 replicates	23.4	17.2	15.3*	16.3	17.1	18.5	19.4
4 replicates	23.1	17.7	16.5*	17.5	18.6	19.8	21.2
5 replicates	23.8	19.0	18.1*	19.4	21.0	22.8	24.9
6 replicates	25.0	20.7	20.6*	22.4	24.6	27.0	29.4
7 replicates	26.8	23.0*	23.5	26.0	28.7	31.5	34.3

Depth: example

- ❖ RNA sequencing
 - ❖ Highly expressed known transcripts
 - ❖ Novel isoforms
 - ❖ Low expressed / rare transcripts



More depth



Design prior to sequencing

- ❖ Sources of variation
 - ❖ Dynamic range - Not all samples get sequenced the same way
 - ❖ Technical variation - biases inherent to the technology
 - ❖ Biological variation
- ❖ Controlling for variation
 - ❖ Randomisation
 - ❖ Blocking: Pool and sequence across several lanes
 - ❖ Replication

Pre-processing

- ❖ Remove sequencing adapters
 - ❖ Trim / remove low quality reads
 - ❖ Remove sequencing spike-ins (PhiX for Illumina), if any
- Make sure paired end data is always paired and in correct order!

Simple truth

To consult the statistician after an experiment is finished is often merely to ask him (her) to conduct a post mortem examination. He (she) can perhaps say what the experiment died of.

- Ronald Fischer