RNA-seq to study HIV Infection in cells

Jason Laird

Bioinformatics Scientist

Feb 2022

Research Technology Team

Delilah Maloney
High Performance Computing Specialist

Kyle Monahan
Senior Data Science Specialist

Shawn Doughty
Manager, Research Computing

Jason Laird
Bioinformatics Scientist

Chris Barnett
Senior Geospatial Analyst

Tom Phimmasen
Senior Data Consultant

Patrick Florance
Director, Academic Data Services

Jake Perl
Digital Humanities NLP Specialist

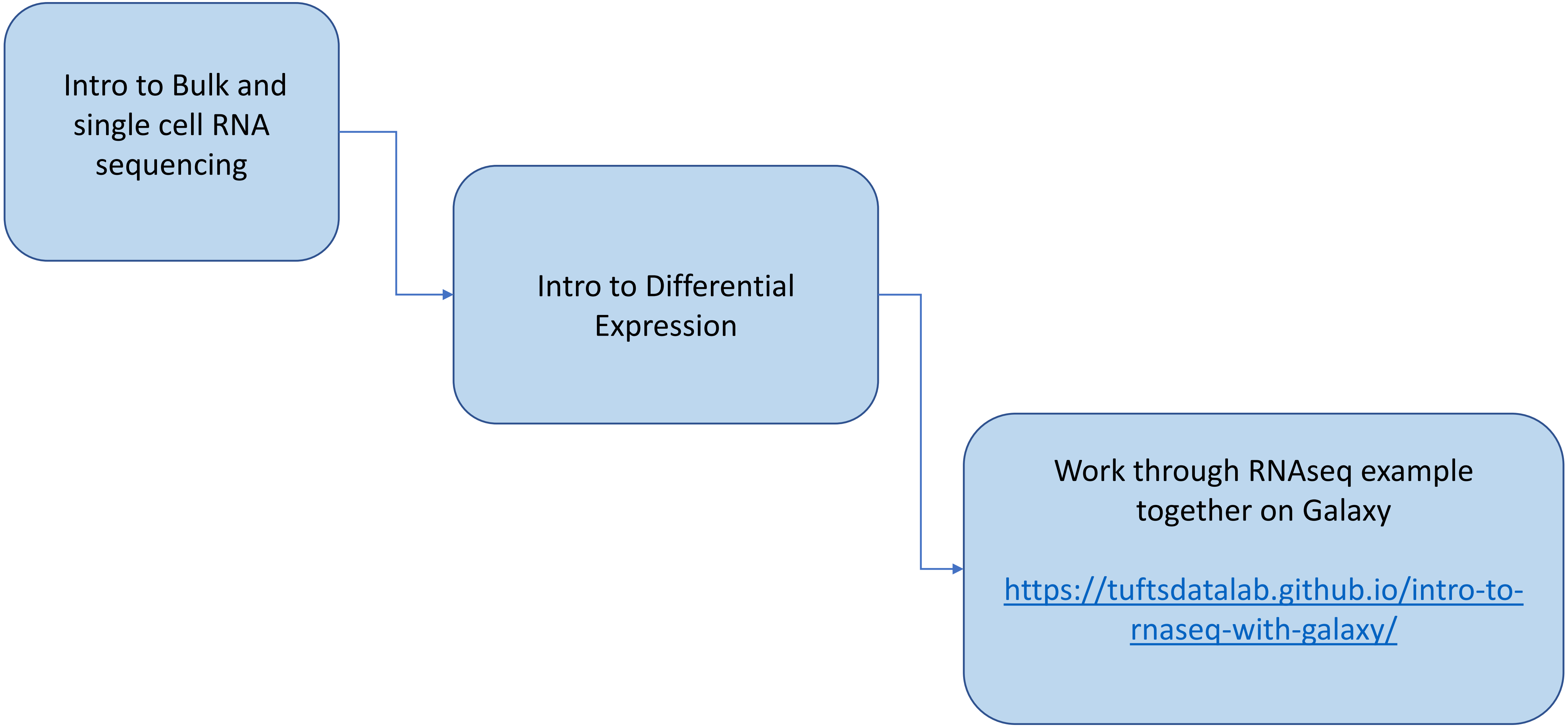
Carolyn Talmadge
Senior GIS Specialist

Uku-Kaspar Uustalu
Data Science Specialist

- ✓ Consultation on Projects and Grants
- ✓ High Performance Compute Cluster
- ✓ Workshops

https://it.tufts.edu/research-technology

Outline



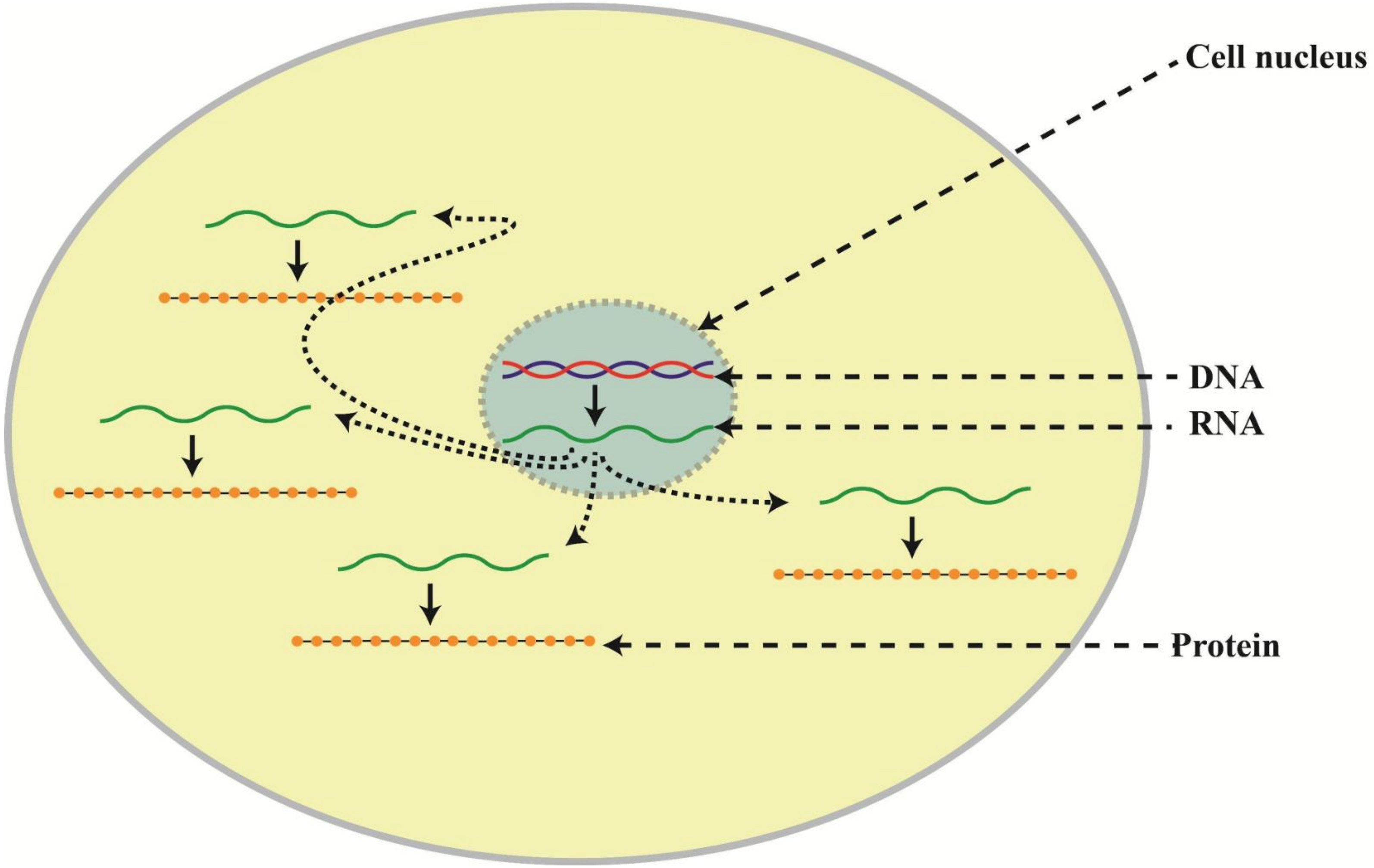
Intro to Bulk and single cell RNA sequencing

Intro to Differential Expression

Work through RNAseq example together on Galaxy

https://tuftsdatalab.github.io/intro-to-rnaseq-with-galaxy/

DNA and RNA in a cell

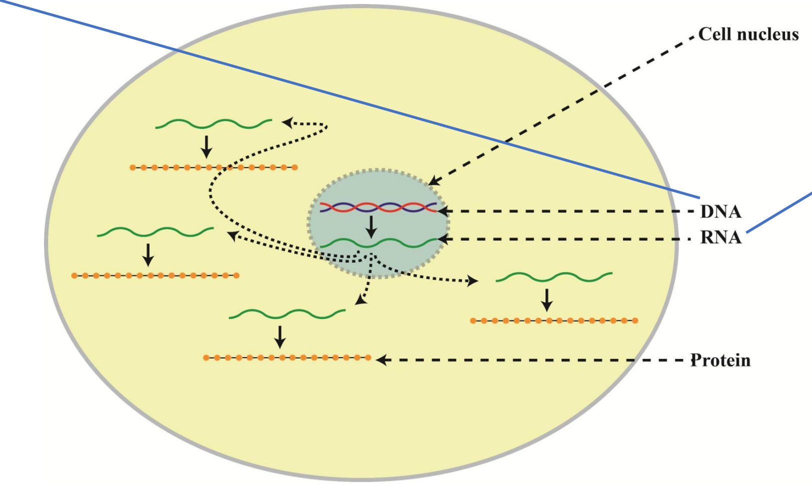


https://i0.wp.com/science-explained.com/wp-content/uploads/2013/08/Cell.jpg

Two common analyses

DNA Sequencing

- Fixed number of copies of a gene per cell
- Analysis goal:
  Variant calling and interpretation



RNA Sequencing

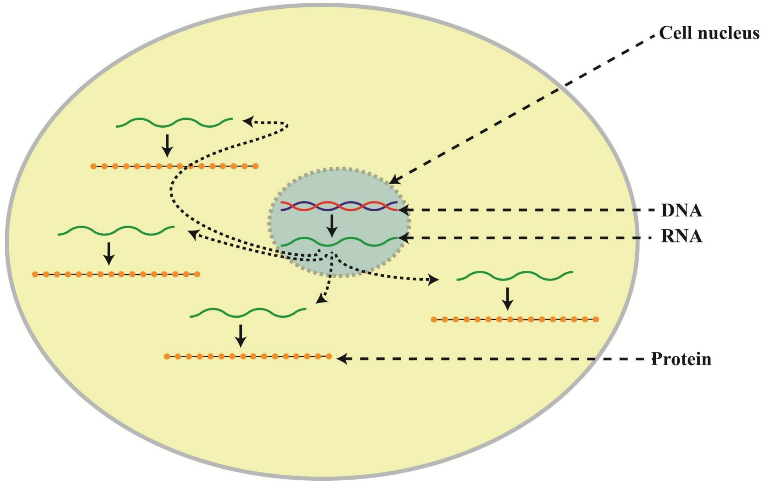
- Number of copies of a gene transcript per cell depends on gene expression
- Analysis goal:
  - Bulk : Differential expression
  - Single cell : Quantify different cell populations

https://i0.wp.com/science-explained.com/wp-content/uploads/2013/08/Cell.jpg

Today we will cover RNA sequencing

DNA Sequencing

- Fixed n er of es of a gene per cell
- Analysis go
  Variant c interpretation



RNA Sequencing

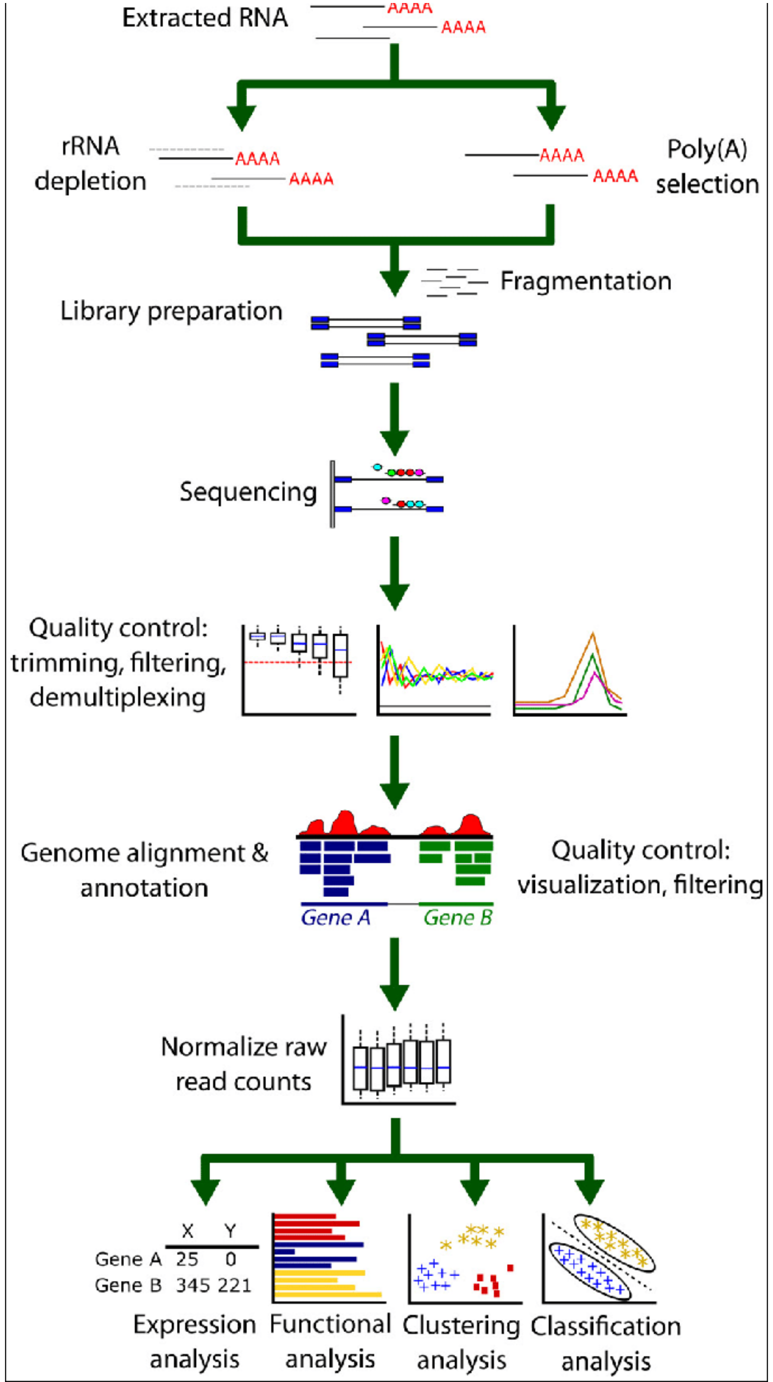
- Number of copies of a gene transcript per cell depends on gene expression
- Analysis goal:
  - Bulk : Differential expression
  - Single cell : Quantify different cell populations

https://i0.wp.com/science-explained.com/wp-content/uploads/2013/08/Cell.jpg

“Bulk” RNA seq workflow

Library prep and sequencing

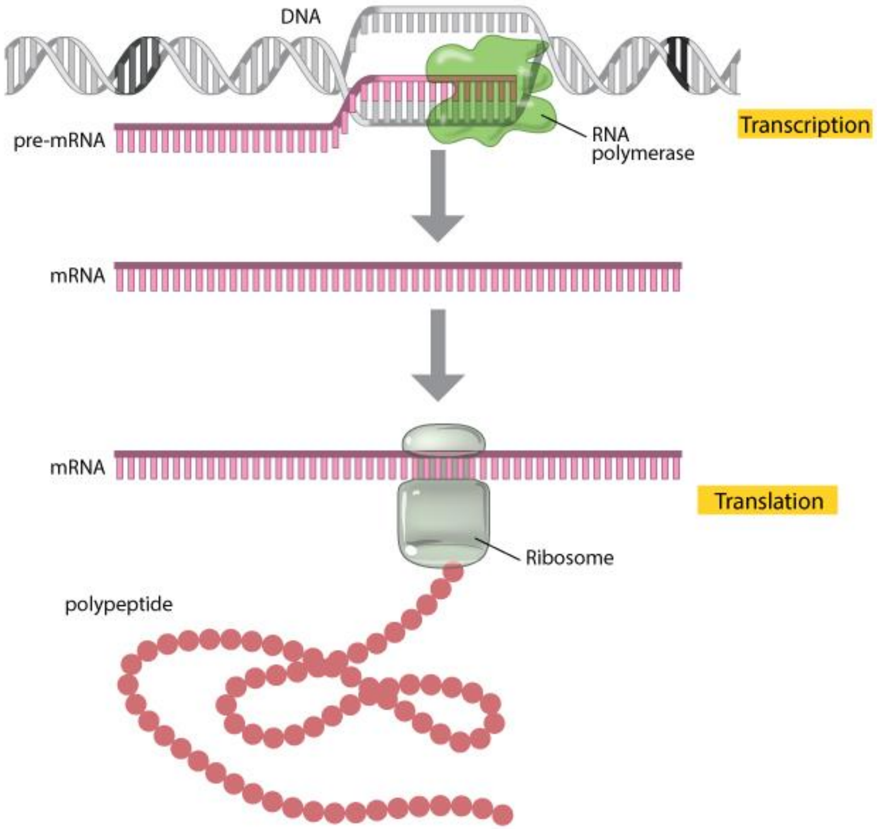
Bioinformatics



Good resource: [Griffiths et al Plos Comp Bio 2015](#)

Ribosomal RNA and Messenger RNA

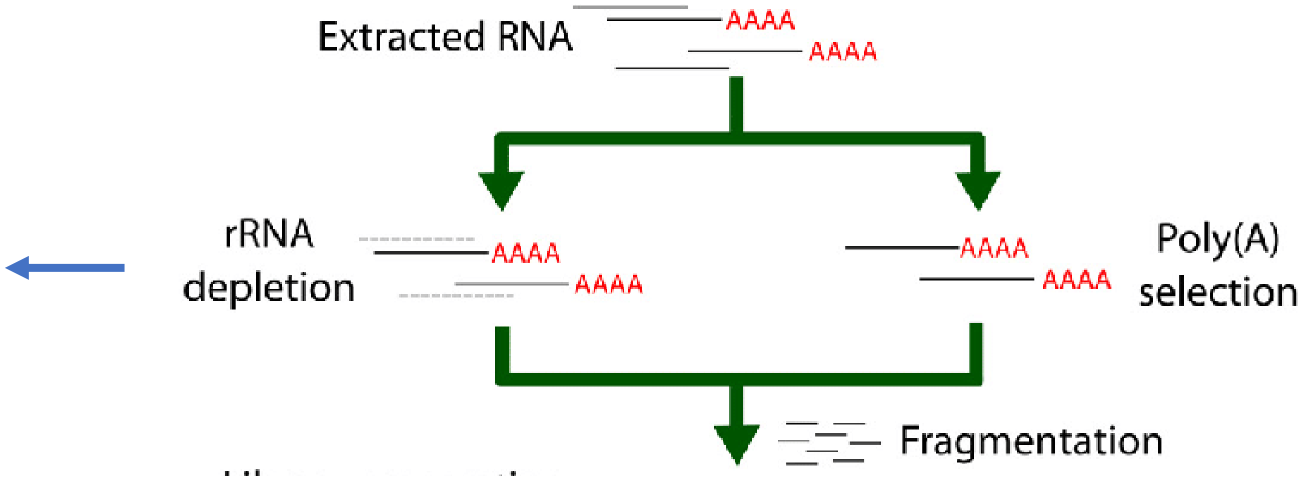
- Messenger RNA (mRNA) is translated into protein
- Ribosomal RNA (rRNA) is used to construct the ribosome which translates mRNA into protein



https://www.nature.com/scitable/topicpage/translation-dna-to-mrna-to-protein-393/

RNA seq library prep and sequencing

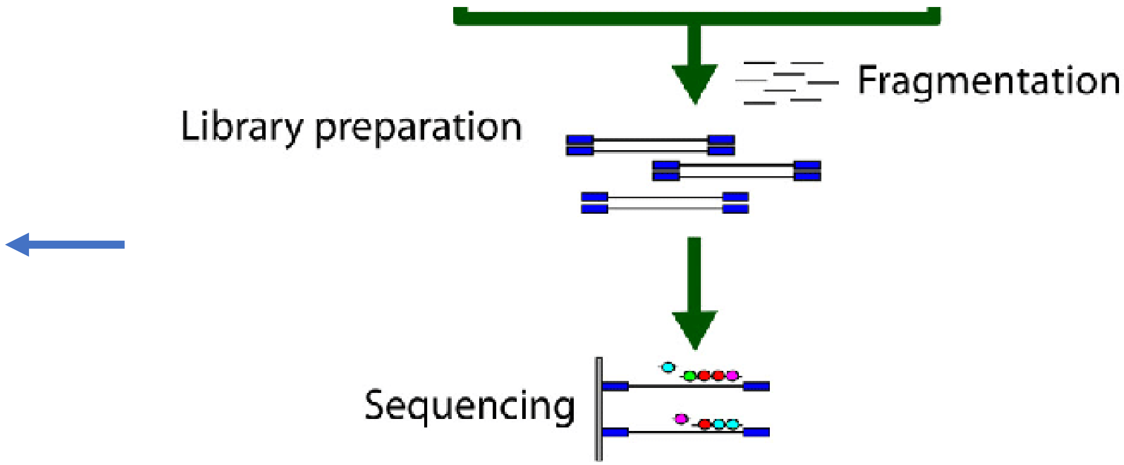
- In humans, ~95%–98% of all RNA molecules are rRNAs
- Need to enrich for mRNA
- To do that we can
  - Deplete all rRNA
  - Select for RNA with Poly A tails



Good resource: Griffiths et al Plos Comp Bio 2015

RNA seq library prep and sequencing

- Random priming to produce fragments and reverse transcription
- Double stranded cDNA synthesis
- Sequencing adapter ligation
- To determine the read sequence:
    - Add fluorescently labelled nucleotides
    - Each time they attach to a base they emit a colored light signal
    - That signal is used to figure out which base is where in the sequence

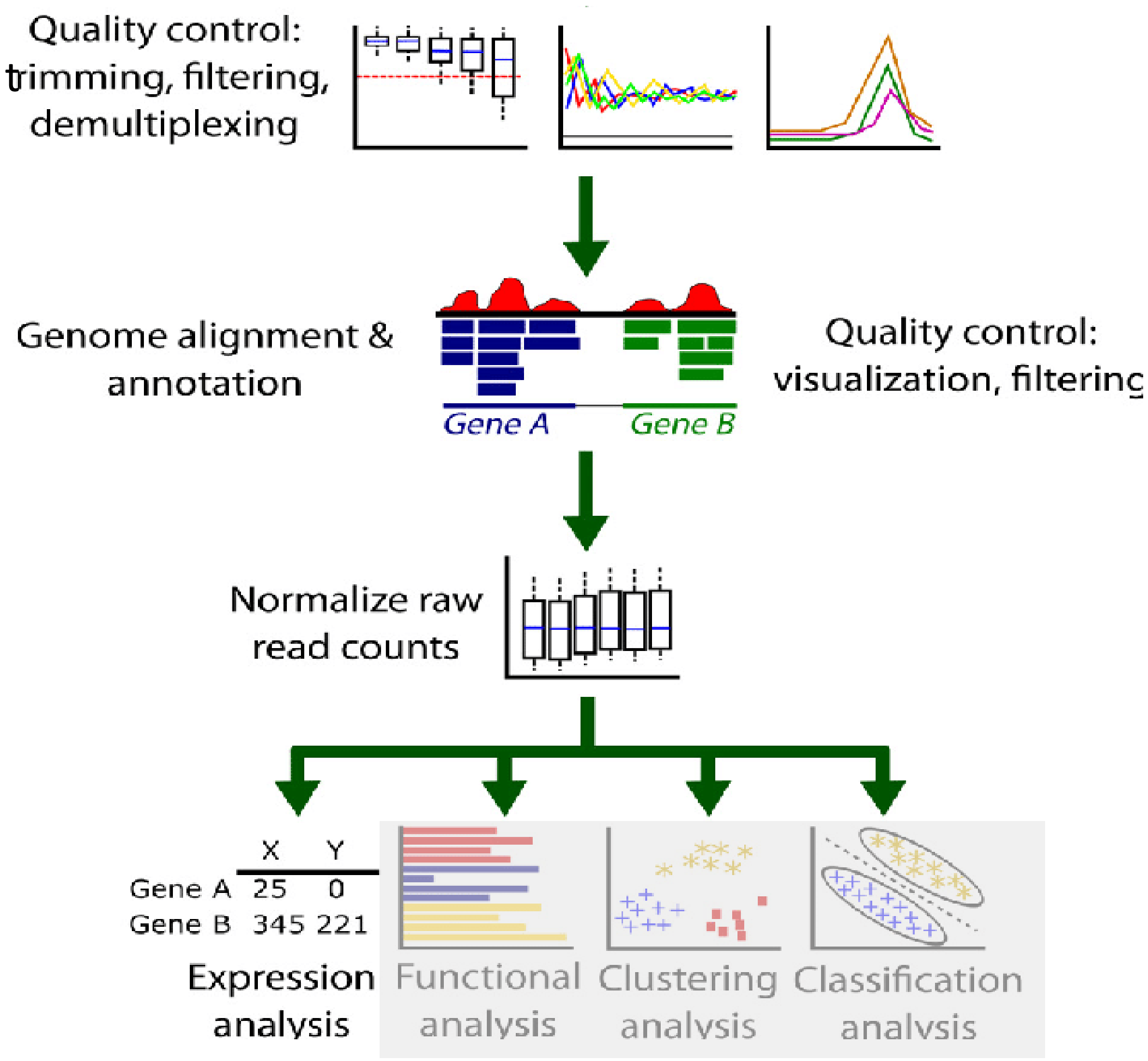


Resources:
[Illumina Sequencing by Synthesis]
[Griffiths et al Plos Comp Bio 2015]

RNA seq bioinformatics

Goal of Differential Expression

"How can we detect genes for which the counts of reads change between conditions **more systematically** than as expected by chance"



Quality control: trimming, filtering, demultiplexing

Genome alignment & annotation

Quality control: visualization, filtering

Normalize raw read counts

	X	Y
Gene A	25	0
Gene B	345	221

Expression analysis

Functional analysis

Clustering analysis

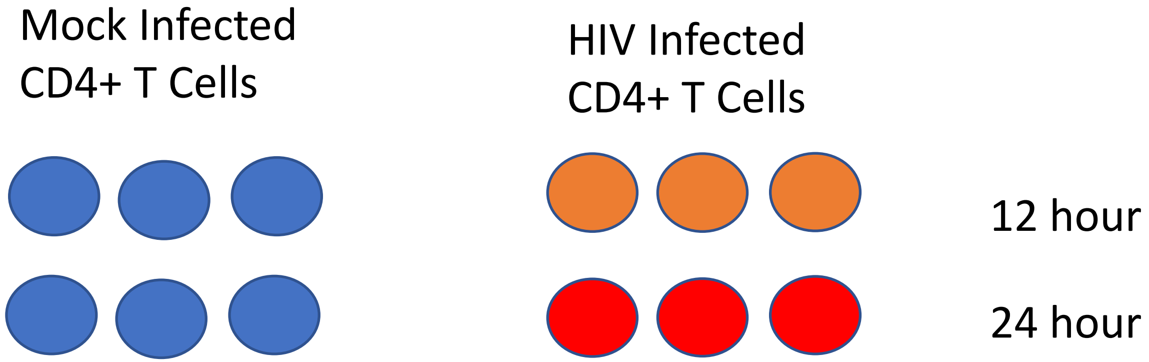
Classification analysis

Oshlack et al. 2010. From RNA-seq reads to differential expression results. Genome Biology 2010, 11:220

Our dataset

Next-Generation Sequencing Reveals HIV-1-Mediated Suppression of T Cell Activation and RNA Processing and Regulation of Noncoding RNA Expression in a CD4$^+$ T Cell Line

Stewart T. Chang, Pavel Sova, Xinxia Peng, Jeffrey Weiss, G. Lynn Law, Robert E. Palermo, Michael G. Katze



Mock Infected CD4+ T Cells

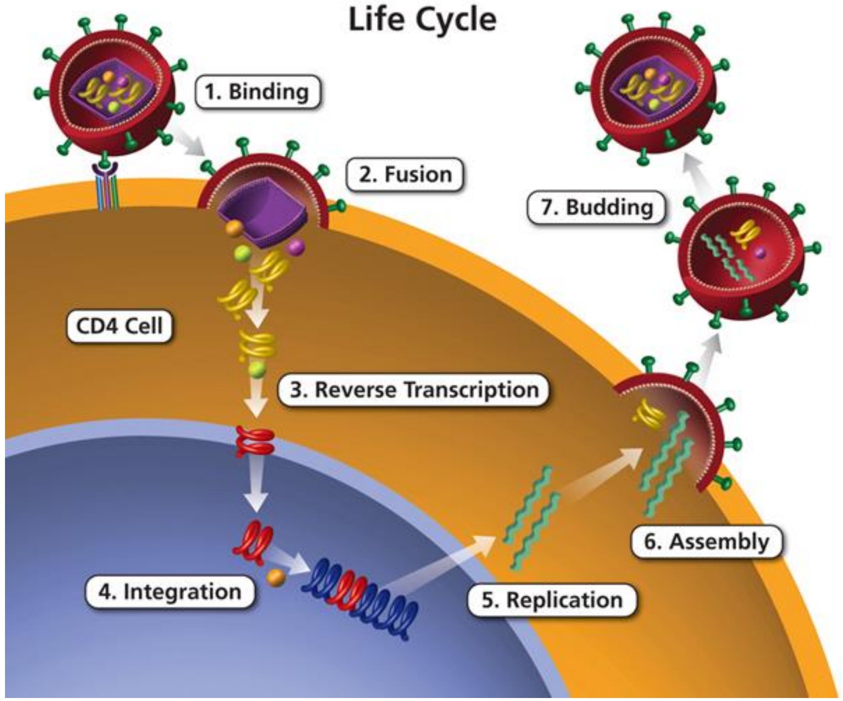
HIV Infected CD4+ T Cells

12 hour

24 hour

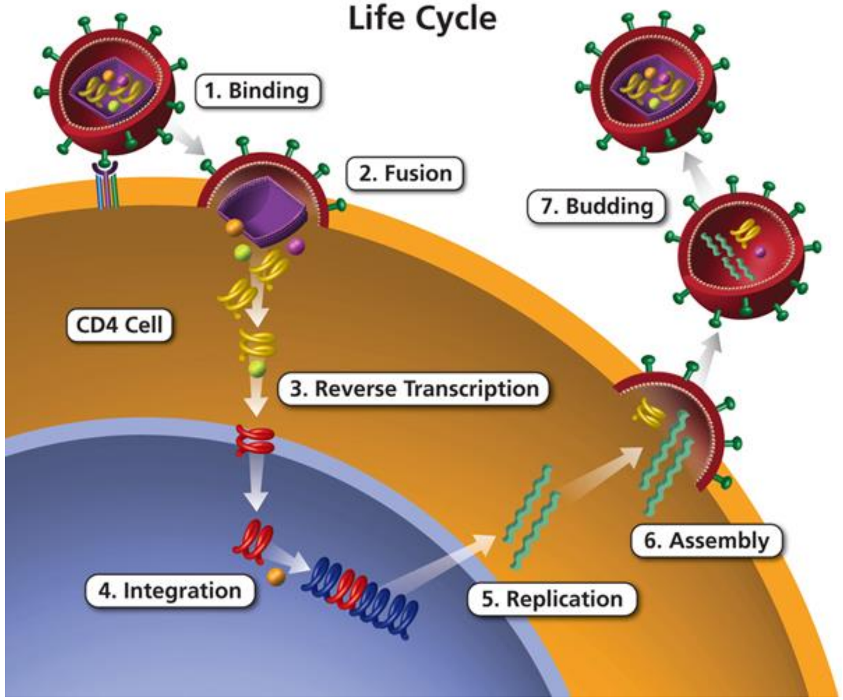
https://www.ncbi.nlm.nih.gov/pubmed/21933919

HIV lifecycle

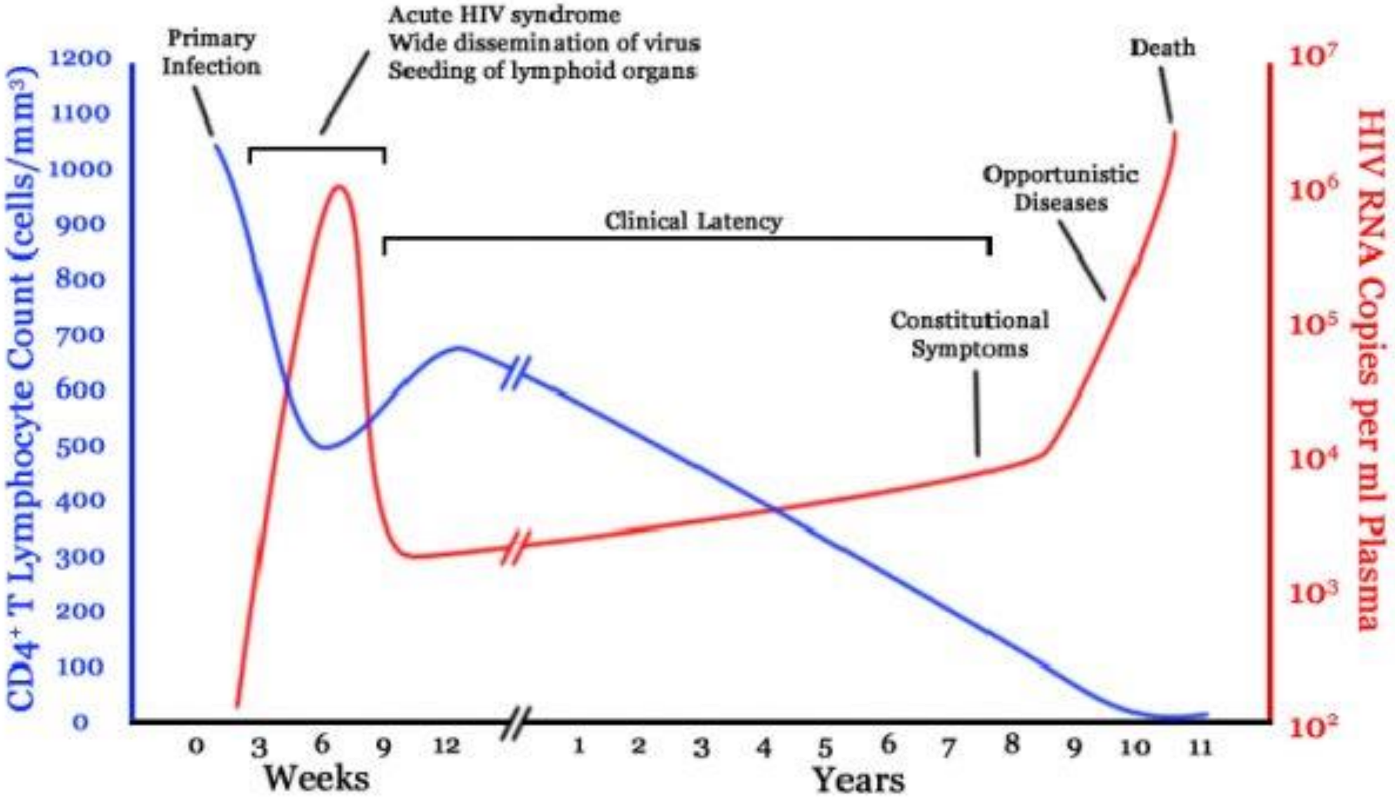


https://aidsinfo.nih.gov/understanding-hiv-aids/glossary/1596/life-cycle

HIV lifecycle



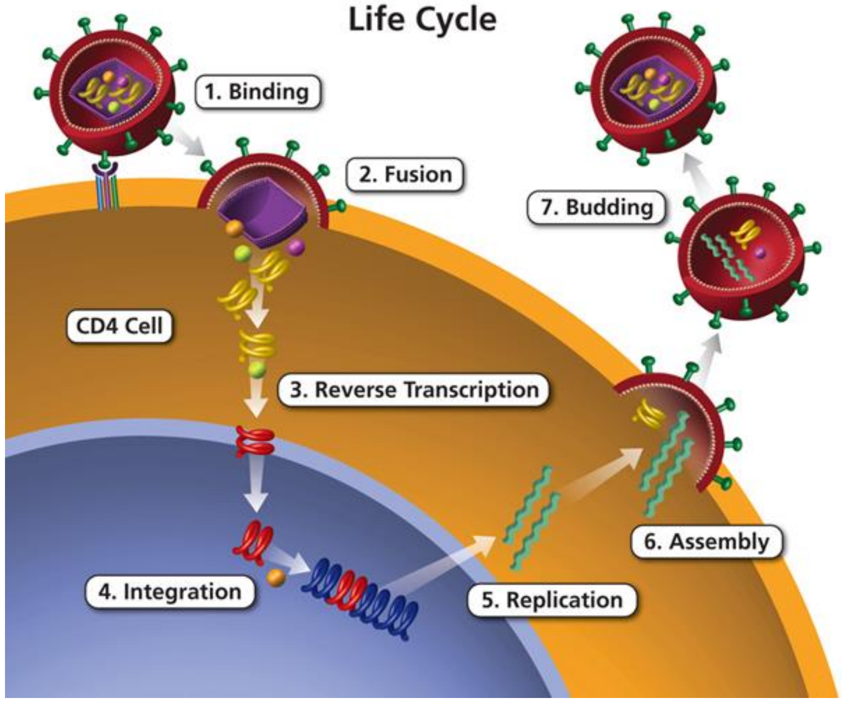
HIV infection in a human host

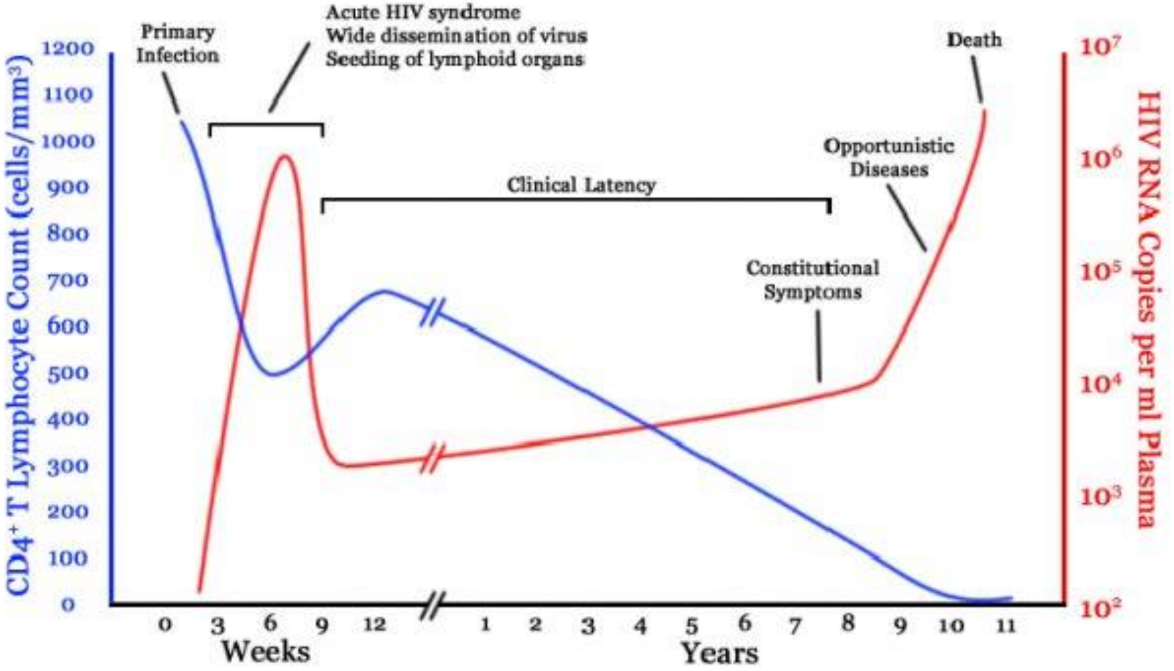


https://aidsinfo.nih.gov/understanding-hiv-aids/glossary/1596/life-cycle

The study question

What changes take place in the first 12-24 hours of HIV infection in terms of gene expression of host cell and viral replication levels?



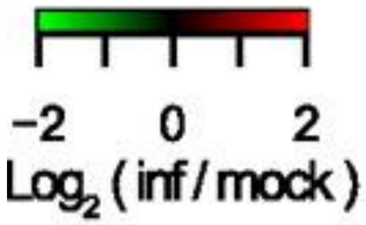


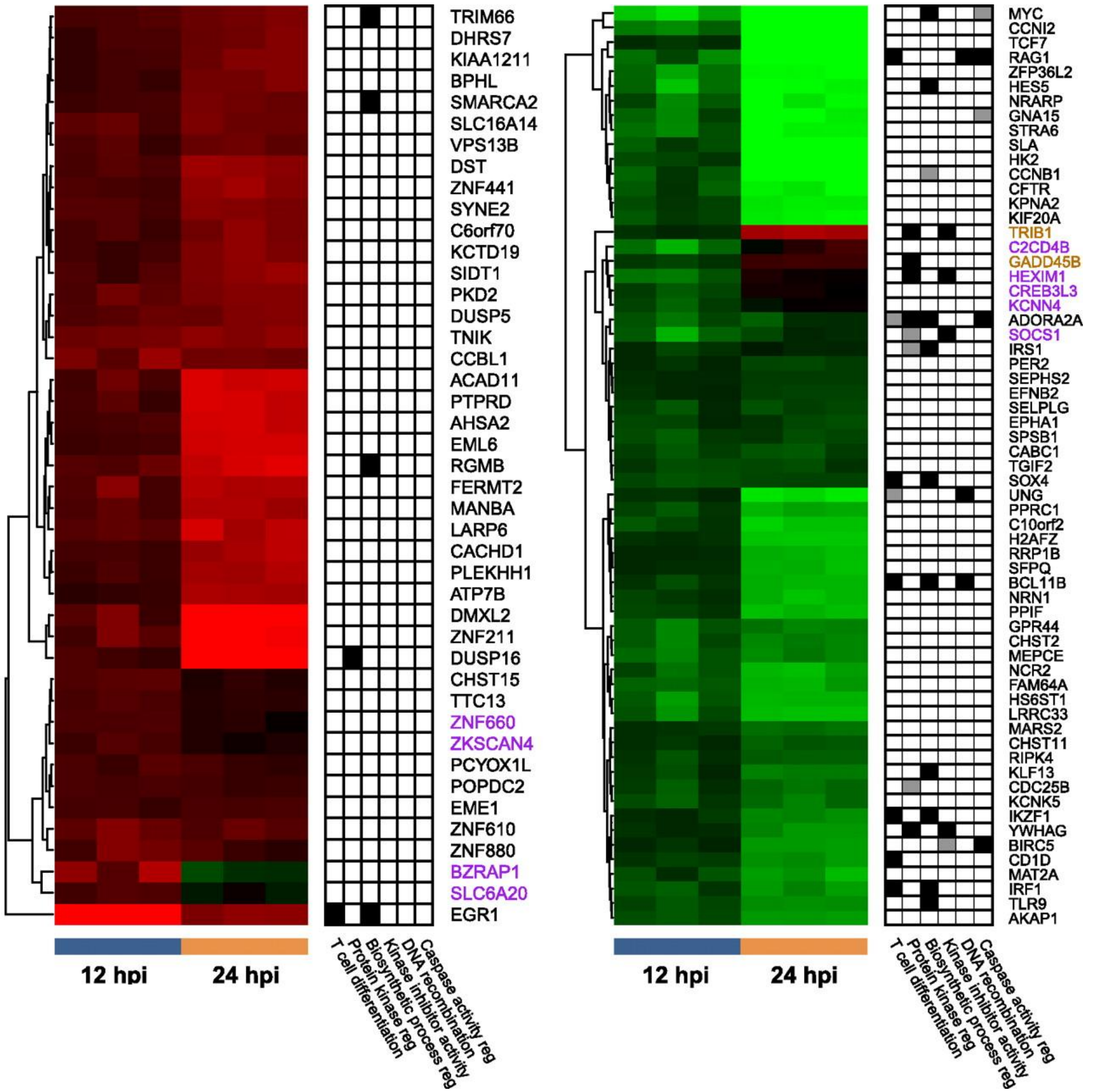
https://aidsinfo.nih.gov/understanding-hiv-aids/glossary/1596/life-cycle

Study findings

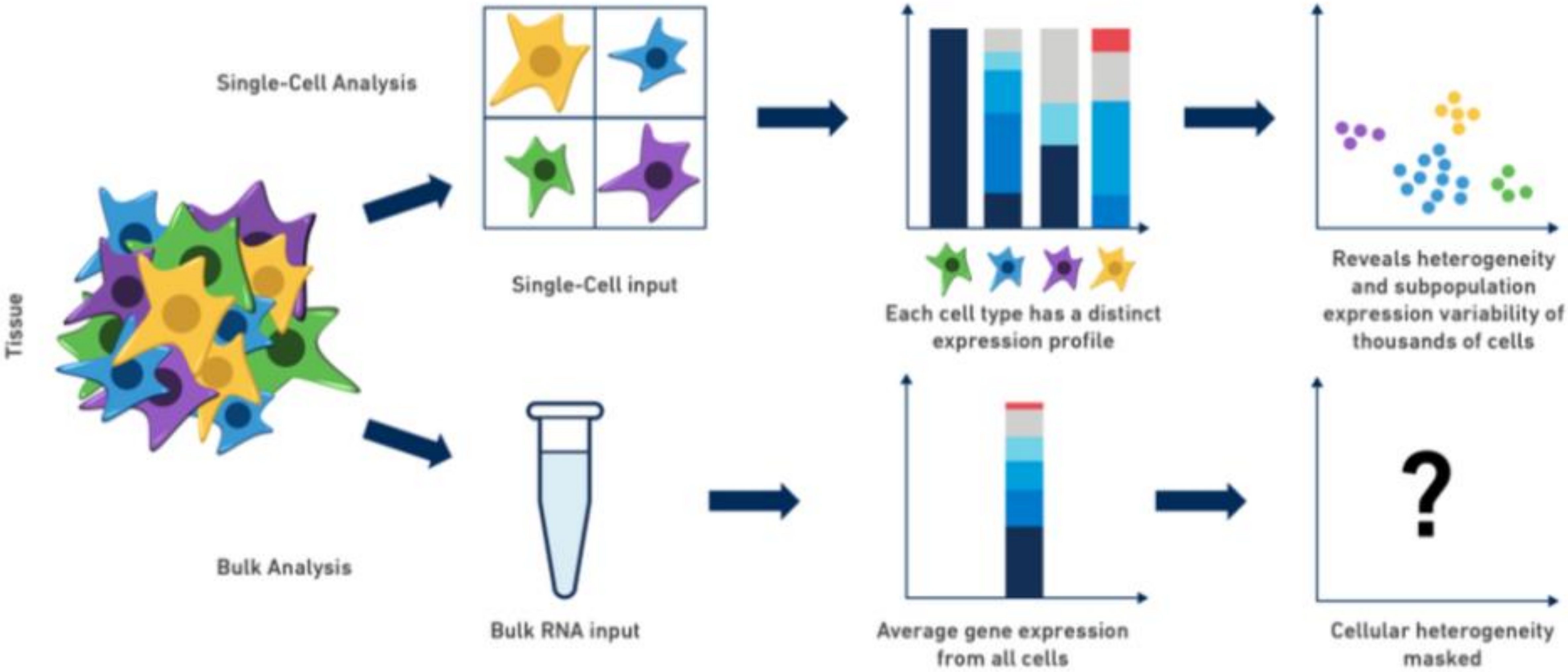
Using RNAseq, authors demonstrate:

- 20% of reads mapped to HIV at 12 hr, 40% at 24hr
- Downregulation of T cell differentiation genes at 12hr
- ‘Large-scale disruptions to host transcription’ at 24hr



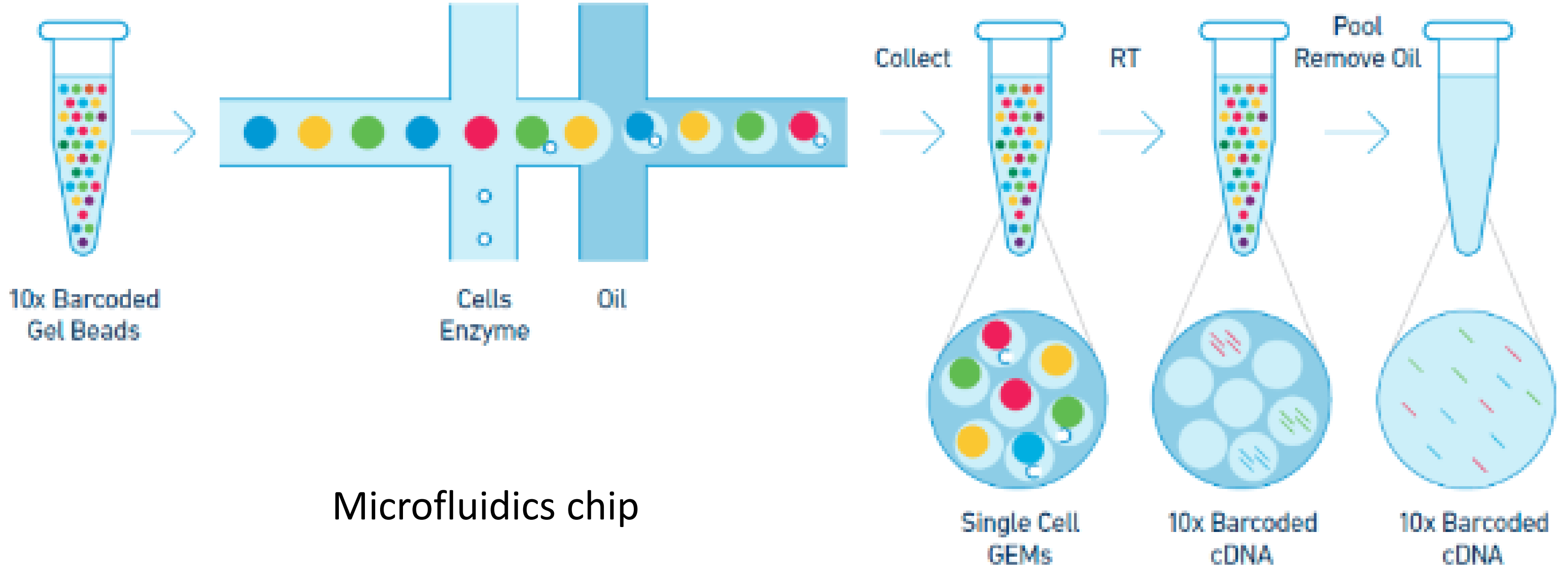


Bulk vs Single Cell RNA Sequencing


Single-Cell Analysis
Single-Cell input
Each cell type has a distinct expression profile
Reveals heterogeneity and subpopulation expression variability of thousands of cells
Tissue
Bulk Analysis
Bulk RNA input
Average gene expression from all cells
?
Cellular heterogeneity masked

https://www.10xgenomics.com/blog/single-cell-rna-seq-an-introductory-overview-and-tools-for-getting-started

10x single cell technology

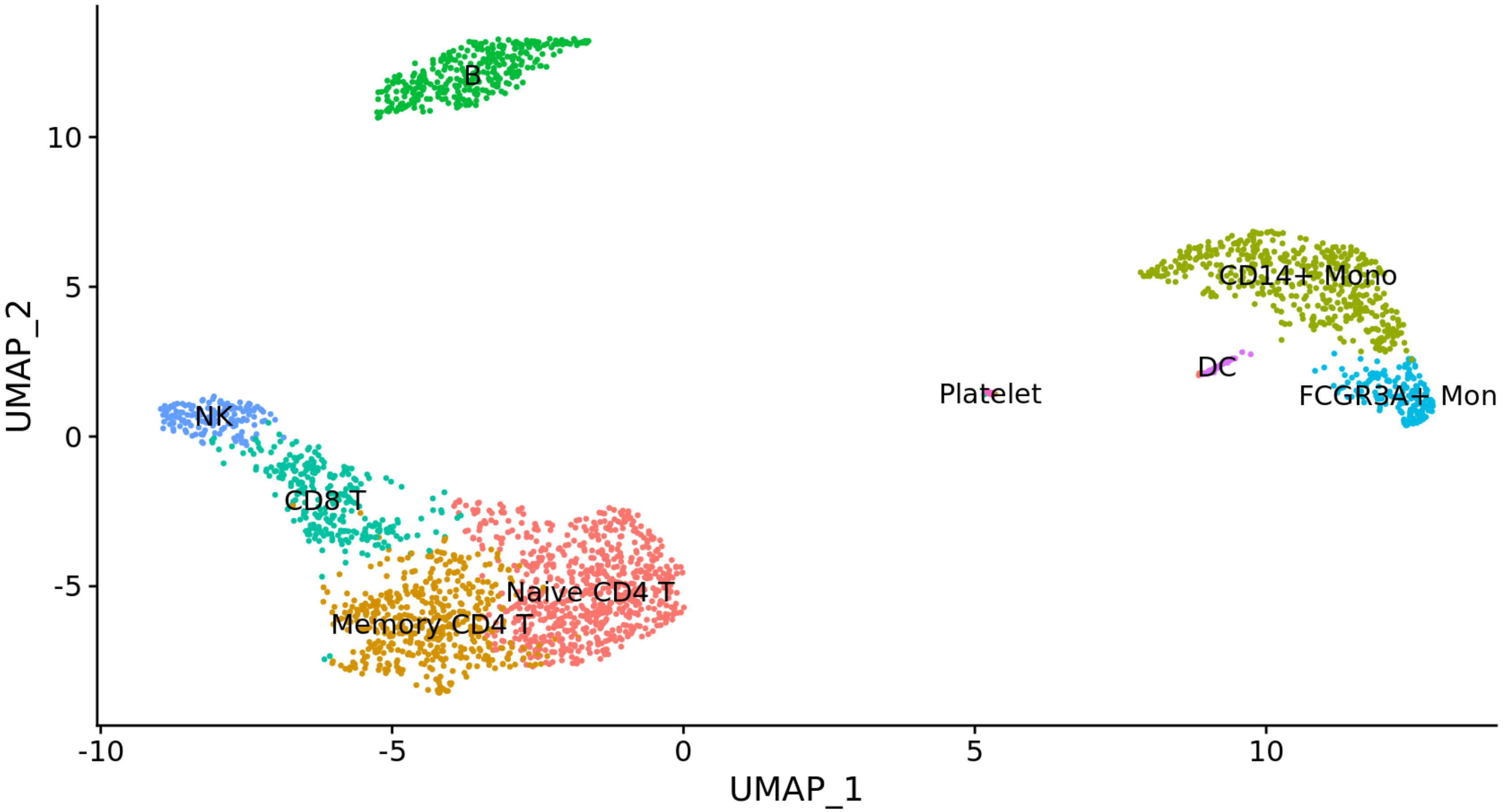


Microfluidics chip

Bulk sequencing

https://github.com/hbctraining/scRNA-seq

scRNA cell subsets in PBMC

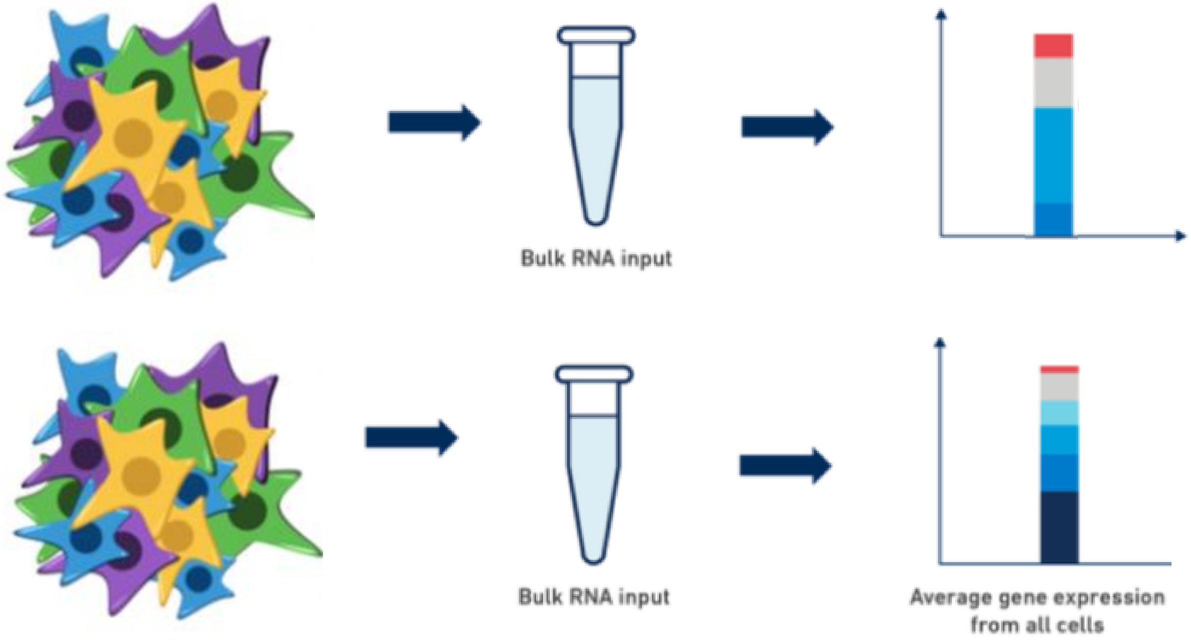


https://satijalab.org/seurat/v3.2/pbmc3k_tutorial.html

Bulk RNAseq for Differential Expression is OK!

Uninfected

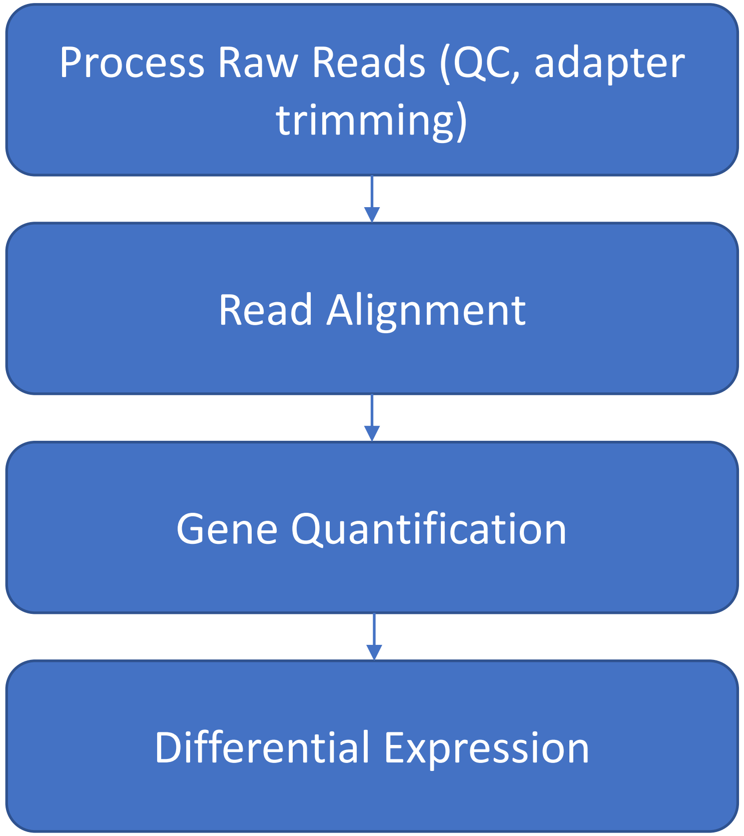
HIV+



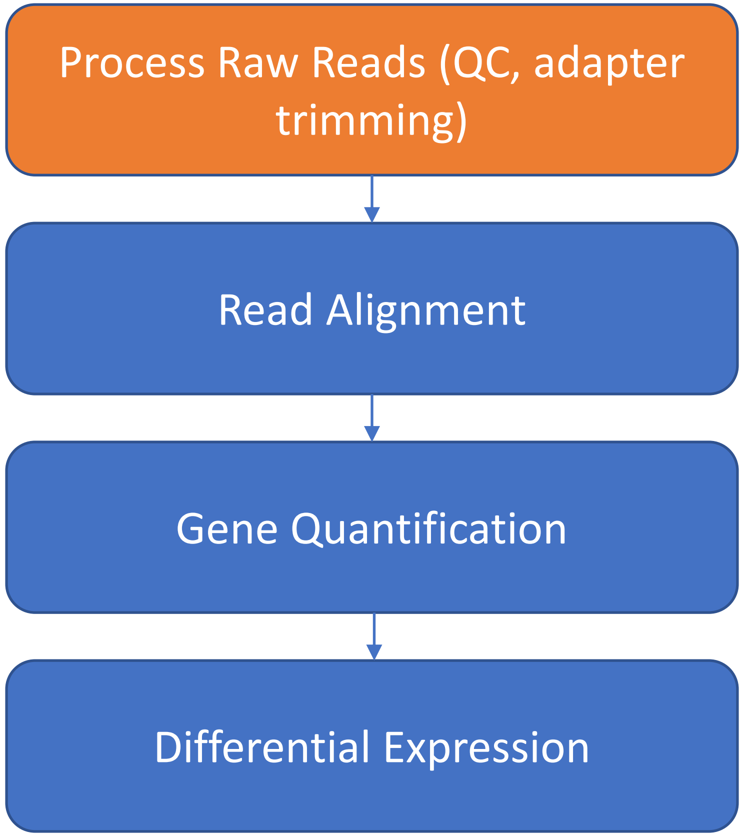
Compare relative gene expression between conditions

https://www.10xgenomics.com/blog/single-cell-rna-seq-an-introductory-overview-and-tools-for-getting-started

Our (bulk) RNAseq Workflow



Quality control on Raw Reads



Process Raw Reads (QC, adapter trimming)

Read Alignment

Gene Quantification

Differential Expression

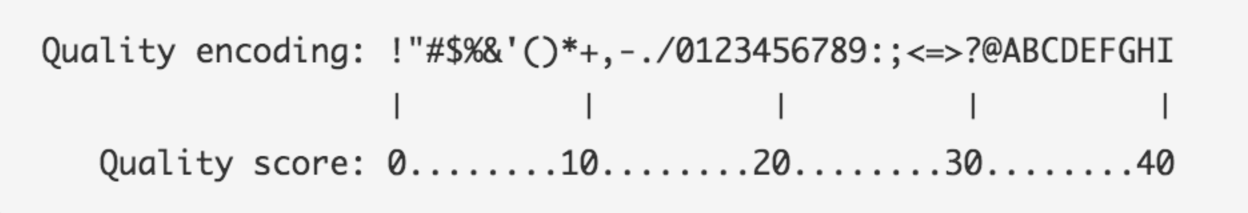
Raw reads in Fastq format

```
@SRR098401.109756285
GACTCACGTAACTTTAAACTCTAACAGAAATATACTA…
+
CAEFGDG?BCGGGEEDGGHGHGDFHEIEGGDDDD…
```

1. Sequence identifier
2. Sequence
3. + (optionally lists the sequence identifier again)
4. Quality string

Base Quality Scores

The symbols we see in the read quality string are an encoding of the quality score:



```
Quality encoding: !"#$%&'()*+,-./0123456789:;<=>?@ABCDEFGHI
                  |         |         |         |         |
   Quality score: 0........10........20........30........40
```

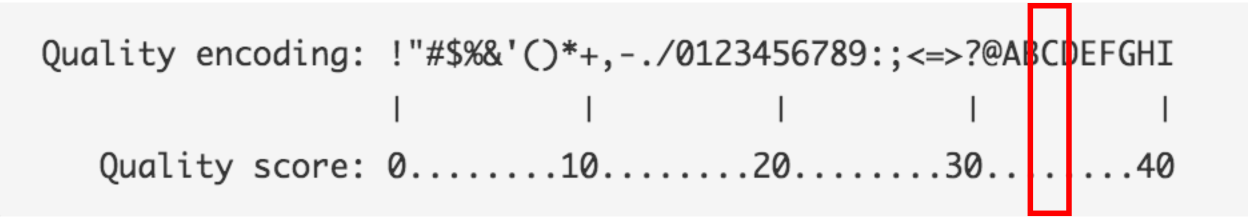
A quality score is a prediction of the probability of an error in base calling:

Quality Score	Probability of Incorrect Base Call	Inferred Base Call Accuracy
10 (Q10)	1 in 10	90%
20 (Q20)	1 in 100	99%
30 (Q30)	1 in 1000	99.9%

https://www.illumina.com/science/education/sequencing-quality-scores.html

Base Quality Scores

The symbols we see in the read quality string are an encoding of the quality score:



```
Quality encoding: !"#$%&'()*+,-./0123456789:;<=>?@ABCDEFGHI
                  |         |         |         |         |
   Quality score: 0........10........20........30........40
```

A quality score is a prediction of the probability of an error in base calling:

Quality Score	Probability of Incorrect Base Call	Inferred Base Call Accuracy
10 (Q10)	1 in 10	90%
20 (Q20)	1 in 100	99%
30 (Q30)	1 in 1000	99.9%

Back to our read:

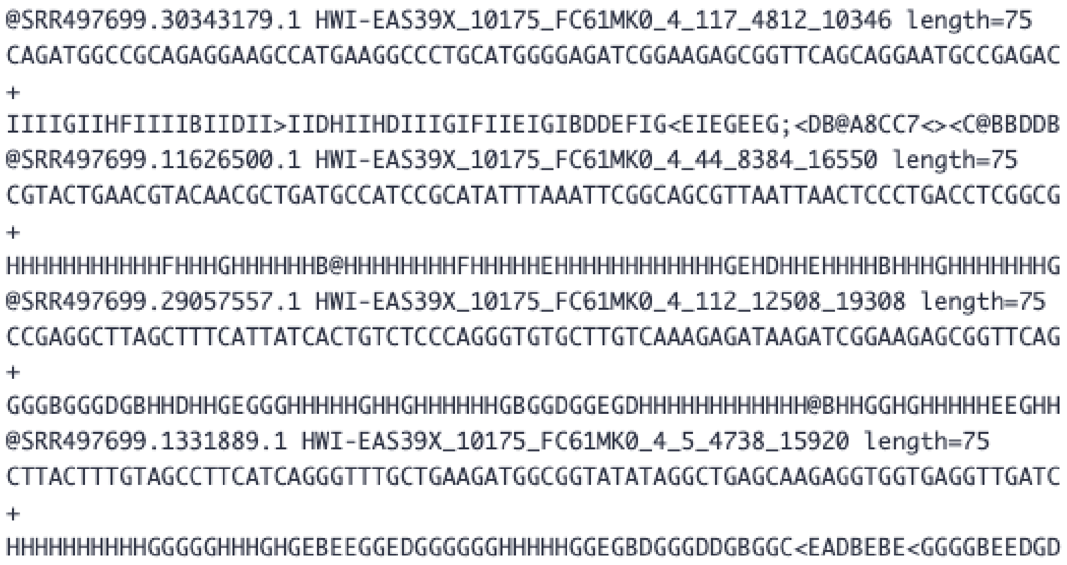
```
@SRR098401.109756285
GACTCACGTAACTTTAAACTCTAACAGAAATATACTA…
+
CAEFGDG?BCGGGEEDGGHGHGDFHEIEGGDDDD…
```

C –> Q = 34 -> Probability < 1/1000 of an error

https://www.illumina.com/science/education/sequencing-quality-scores.html

Raw read quality control

Fastq File



```
@SRR497699.30343179.1 HWI-EAS39X_10175_FC61MK0_4_117_4812_10346 length=75
CAGATGGCCGCAGAGGAAGCCATGAAGGCCCTGCATGGGGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGAC
+
IIIIGIIHFIIIIBIIDII>IIDHIIHDIIIGIFIIEIGIBDDEFIG<EIEGEEG;<DB@A8CC7<><C@BBDDB
@SRR497699.11626500.1 HWI-EAS39X_10175_FC61MK0_4_44_8384_16550 length=75
CGTACTGAACGTACAACGCTGATGCCATCCGCATATTTAAATTCGGCAGCGTTAATTAACTCCCTGACCTCGGCG
+
HHHHHHHHHHHFHHHGHHHHHHB@HHHHHHHHFHHHHHEHHHHHHHHHHHHGEHDHHEHHHHBHHHGHHHHHHHG
@SRR497699.29057557.1 HWI-EAS39X_10175_FC61MK0_4_112_12508_19308 length=75
CCGAGGCTTAGCTTTCATTATCACTGTCTCCCAGGGTGTGCTTGTCAAAGAGATAAGATCGGAAGAGCGGTTCAG
+
GGGBGGGDGBHHDHHGEGGGHHHHHGHHGHHHHHHGBGGDGGEGDHHHHHHHHHHHH@BHHGGHGHHHHHEEGHH
@SRR497699.1331889.1 HWI-EAS39X_10175_FC61MK0_4_5_4738_15920 length=75
CTTACTTTGTAGCCTTCATCAGGGTTTGCTGAAGATGGCGGTATATAGGCTGAGCAAGAGGTGGTGAGGTTGATC
+
HHHHHHHHHHGGGGGHHHGHGEBEEGGEDGGGGGGHHHHHGGEGBDGGGDDGBGGC<EADBEBE<GGGGBEEDGD
```

…

FastQC Tool

Metrics

- Sequence Quality
- GC content
- Per base sequence content
- Adapters in Sequence

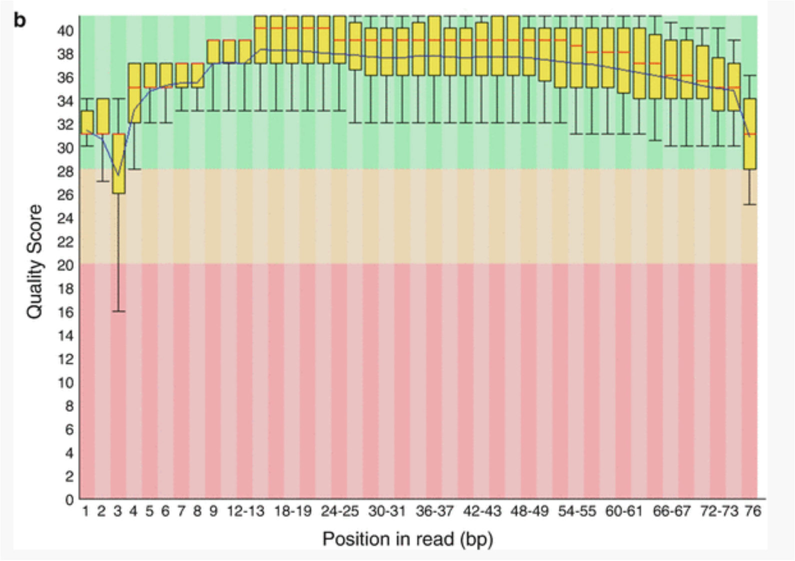
FastQC Results

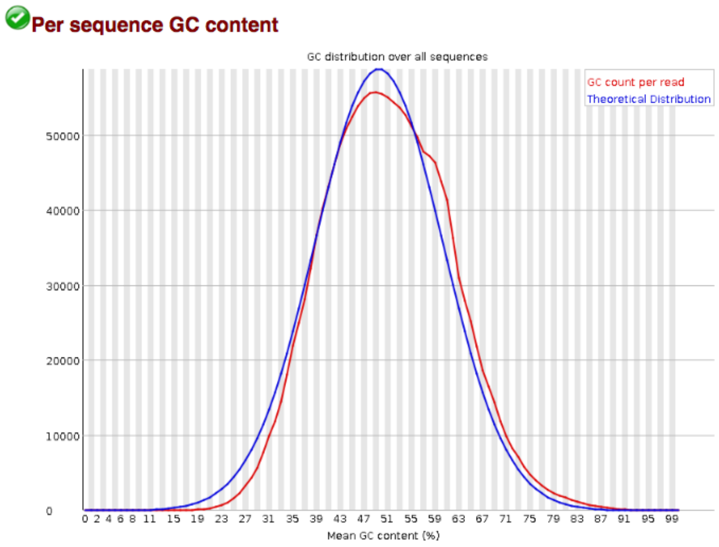
- Sequence Quality
  - Ensure quality scores fall mostly within green bin

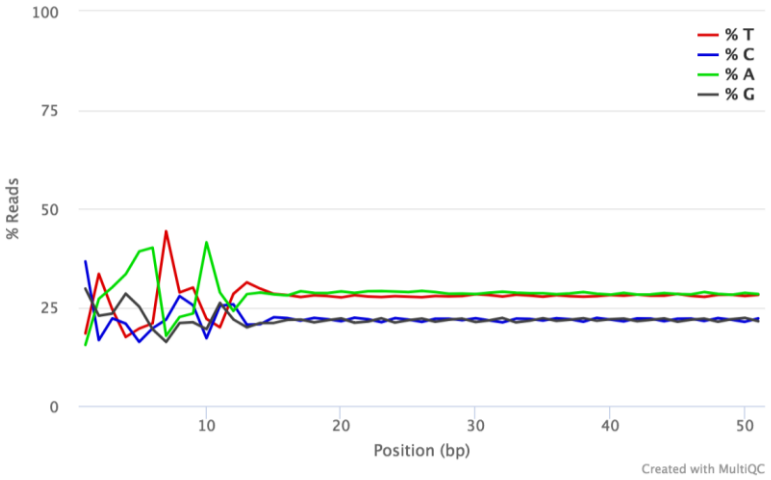
- GC content
  - Ensure normal distribution (bell curve shape) otherwise could indicate contaminant/overrepresented sequence

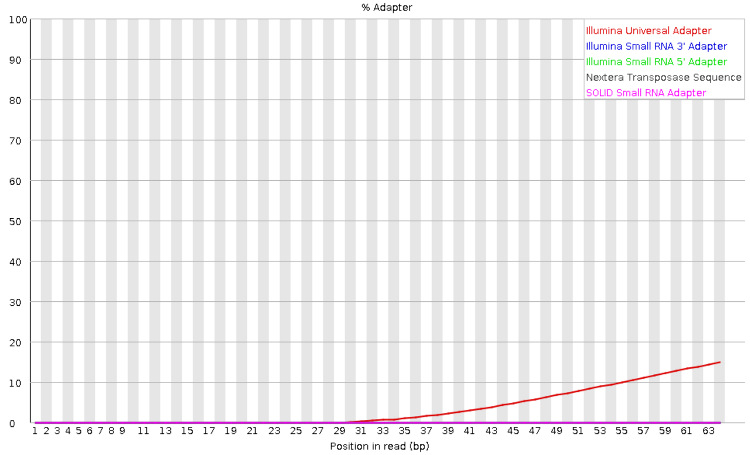
- Per base sequence content
  - Random Priming will make the first 12 bases look off, but ensure that pattern is not seen throughout read

- Adapters in Sequence
  - Check for adapter presence



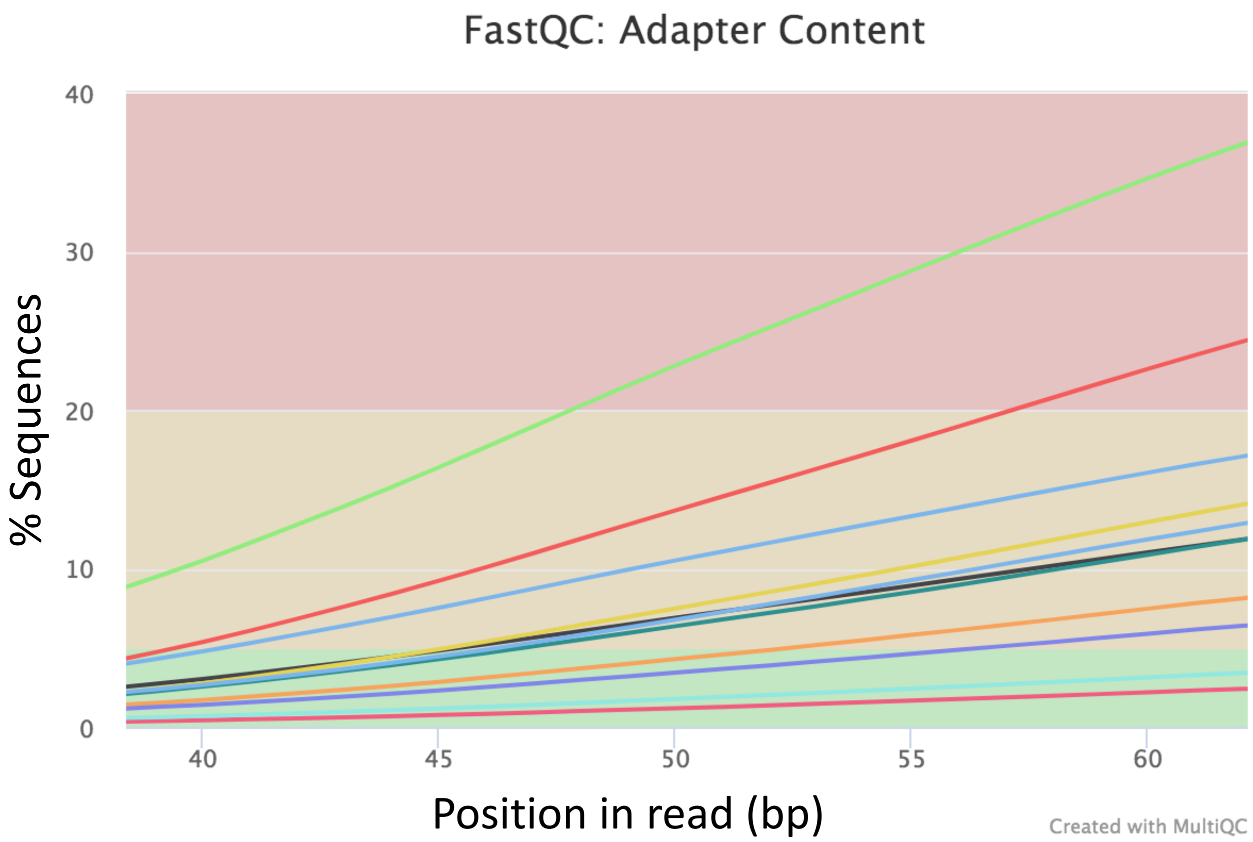






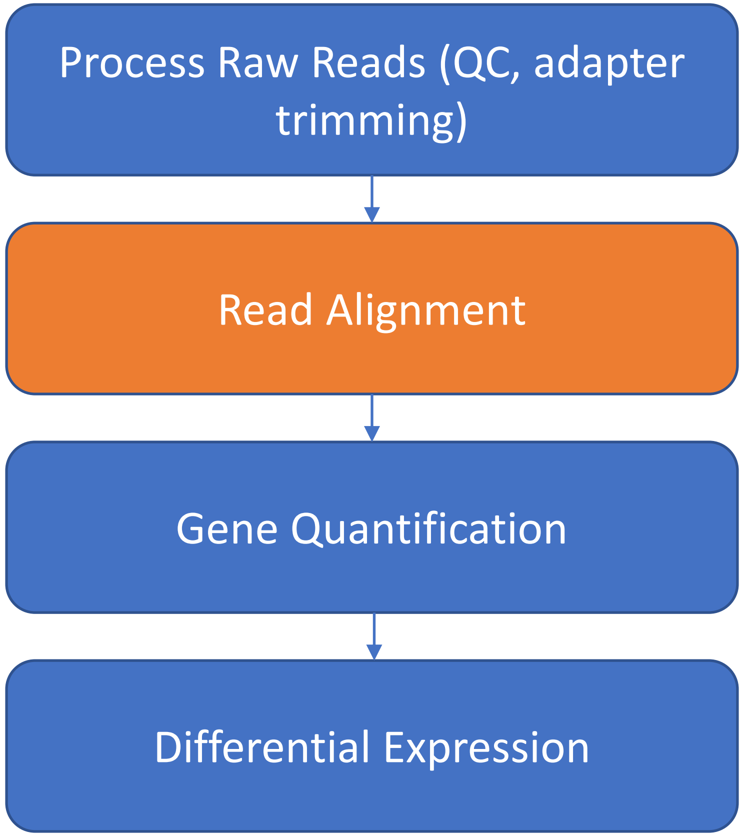
FastQC -> MultiQC

Should view all samples at once to notice abnormalities for our dataset.



We'll use a tool called "Trim Galore!" to trim adapters and remove low quality bases/reads.

Workflow



Process Raw Reads (QC, adapter trimming)

Read Alignment

Gene Quantification

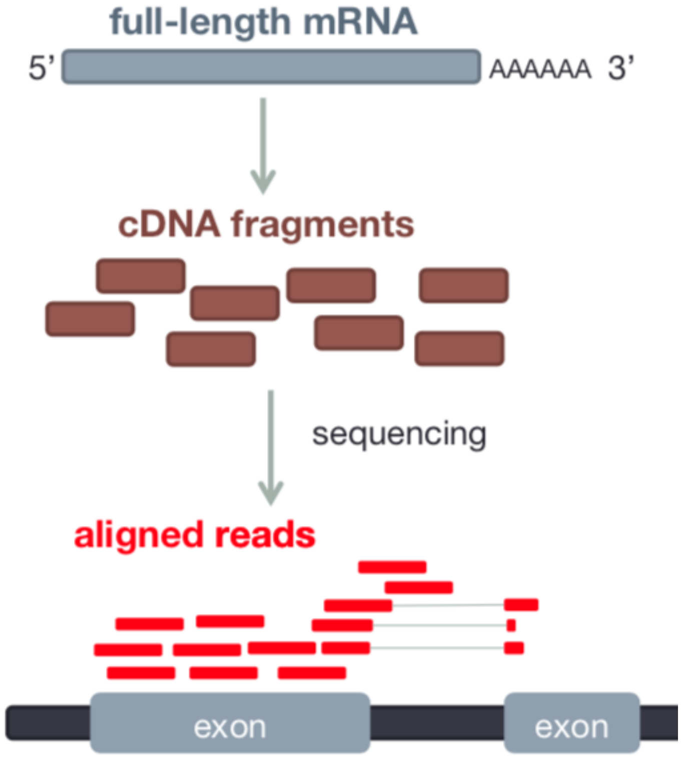
Differential Expression

Read Alignment

- RNAseq data originates from spliced mRNA (no introns)

- When aligning to the genome, our aligner must find a spliced alignment for reads

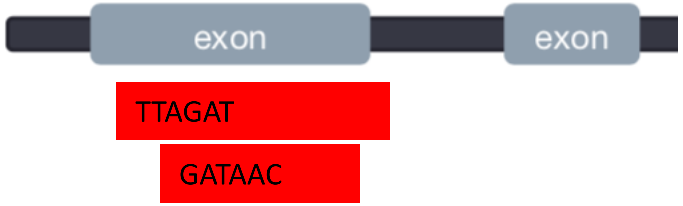
- We use a tool called STAR (Spliced Transcripts Alignment to a Reference) that has a exon-aware mapping algorithm.



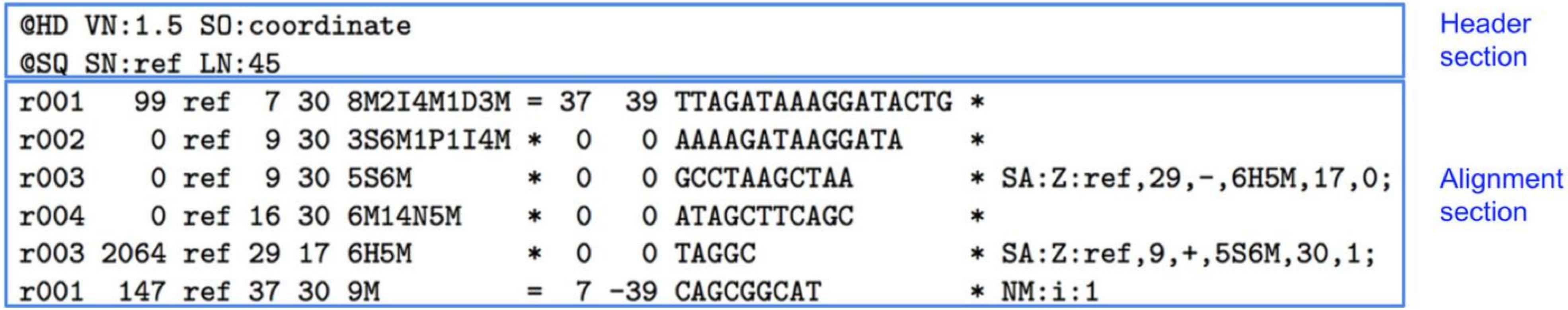
Reference sequence

Dobin et al Bioinformatics 2013

Sequence Alignment Map (SAM)


Reference seq

Reads


```
@HD VN:1.5 SO:coordinate
@SQ SN:ref LN:45
r001    99 ref  7 30 8M2I4M1D3M = 37  39 TTAGATAAAGGATACTG *
r002     0 ref  9 30 3S6M1P1I4M *  0   0 AAAAGATAAGGATA    *
r003     0 ref  9 30 5S6M       *  0   0 GCCTAAGCTAA       * SA:Z:ref,29,-,6H5M,17,0;
r004     0 ref 16 30 6M14N5M    *  0   0 ATAGCTTCAGC       *
r003  2064 ref 29 17 6H5M       *  0   0 TAGGC             * SA:Z:ref,9,+,5S6M,30,1;
r001   147 ref 37 30 9M         =  7 -39 CAGCGGCAT         * NM:i:1
```

CIGAR: summary of alignment, e.g. match, gap, insertion, deletion

Mapping Quality

Position

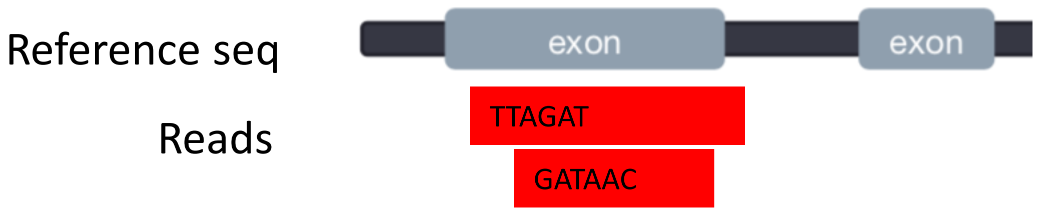
Ref Sequence name

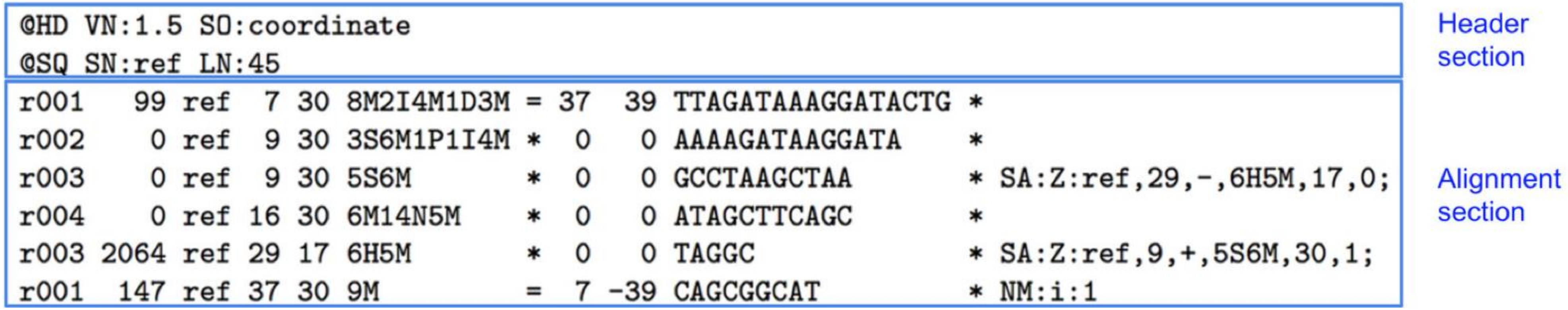
Flag: indicates alignment information e.g. paired, aligned, etc
https://broadinstitute.github.io/picard/explain-flags.html

Read ID

www.samformat.info

Sequence Alignment Map (SAM)





```
@HD VN:1.5 SO:coordinate
@SQ SN:ref LN:45
r001   99 ref  7 30 8M2I4M1D3M = 37  39 TTAGATAAAGGATACTG *
r002    0 ref  9 30 3S6M1P1I4M *  0   0 AAAAGATAAGGATA    *
r003    0 ref  9 30 5S6M       *  0   0 GCCTAAGCTAA       * SA:Z:ref,29,-,6H5M,17,0;
r004    0 ref 16 30 6M14N5M    *  0   0 ATAGCTTCAGC       *
r003 2064 ref 29 17 6H5M       *  0   0 TAGGC             * SA:Z:ref,9,+,5S6M,30,1;
r001  147 ref 37 30 9M         =  7 -39 CAGCGGCAT         * NM:i:1
```

Header section

Alignment section

Paired end info

Sequence

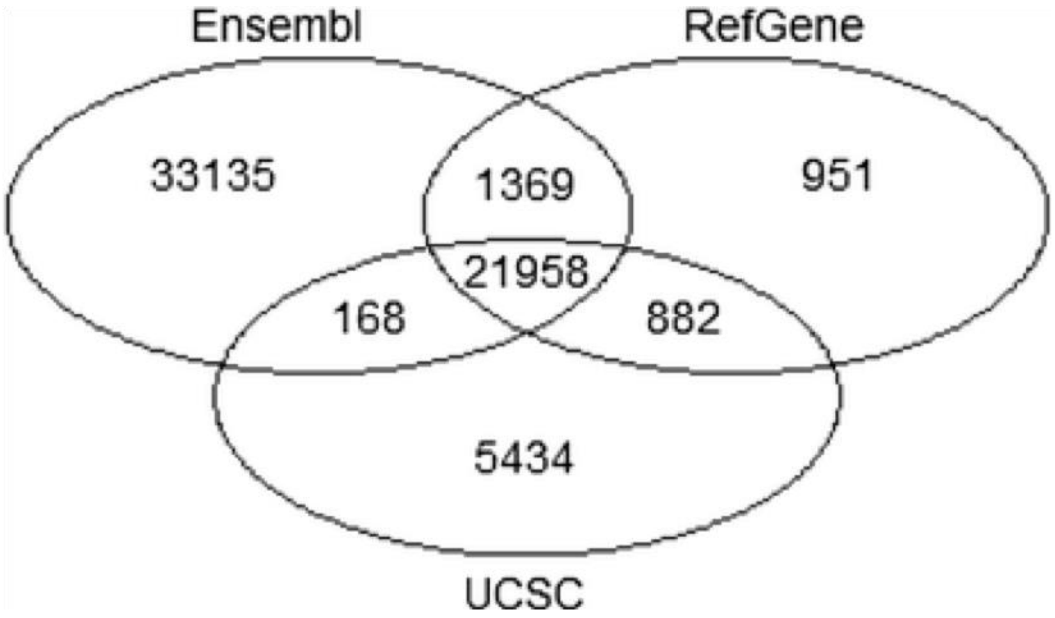
Quality Score

Optional Fields

www.samformat.info

Genome Annotation Standards

- STAR can use an annotation file gives the location and structure of genes in order to improve alignment in known splice junctions
- Annotation is dynamic and there are at least three major sources of annotation
- The intersection among RefGene, UCSC, and Ensembl annotations shows high overlap. RefGene has the fewest unique genes, while more than 50% of genes in Ensembl are unique
- Be consistent with your choice of annotation source!



Zhao et al Bioinformatics 2015

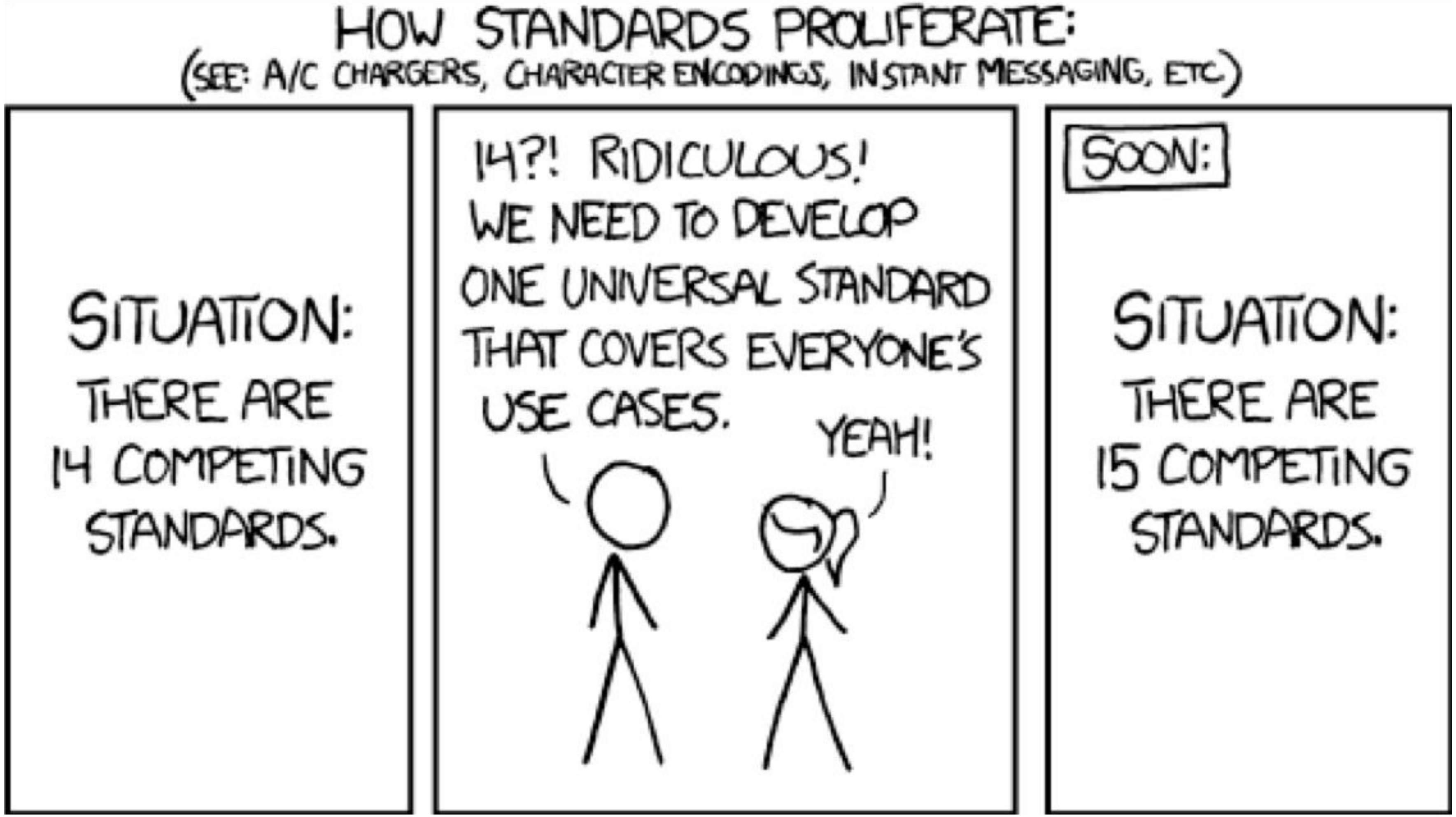
Gene Annotation Format (GTF)

In order to count genes, we need to know where they are located in the reference sequence
STAR uses a Gene Transfer Format (GTF) file for gene annotation

Chrom	Source	Feature type	Start	Stop	(Score)	Strand	Frame	Attribute
chr5	hg38_refGene	exon	138465492	138466068	.	+	.	gene_id "EGR1";
chr5	hg38_refGene	CDS	138465762	138466068	.	+	0	gene_id "EGR1";
chr5	hg38_refGene	start_codon	138465762	138465764	.	+	.	gene_id "EGR1";
chr5	hg38_refGene	CDS	138466757	138468078	.	+	2	gene_id "EGR1";
chr5	hg38_refGene	exon	138466757	138469315	.	+	.	gene_id "EGR1";
chr5	hg38_refGene	stop_codon	138468079	138468081	.	+	.	gene_id "EGR1";

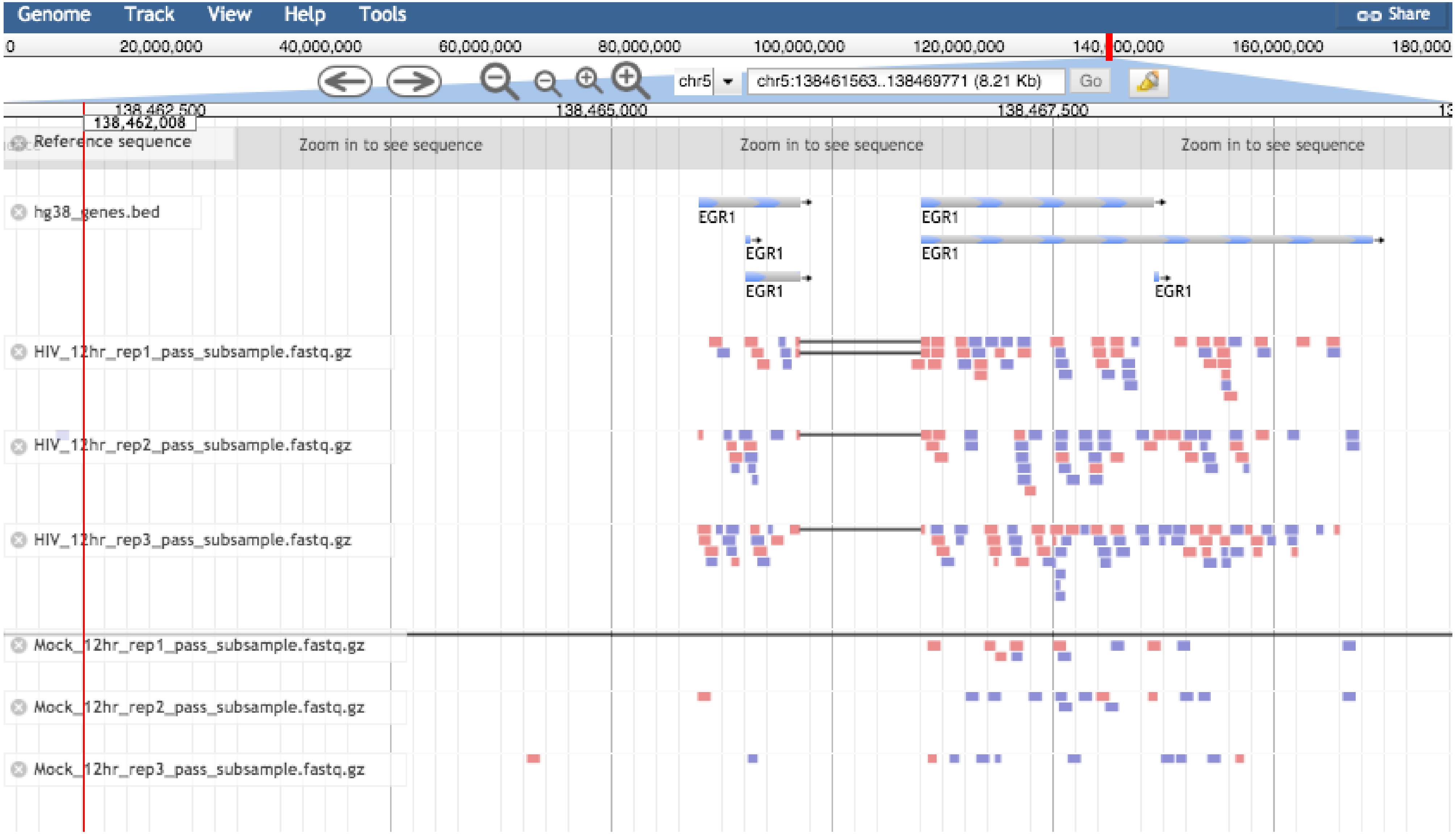
https://useast.ensembl.org/info/website/upload/gff.html

A note on standards

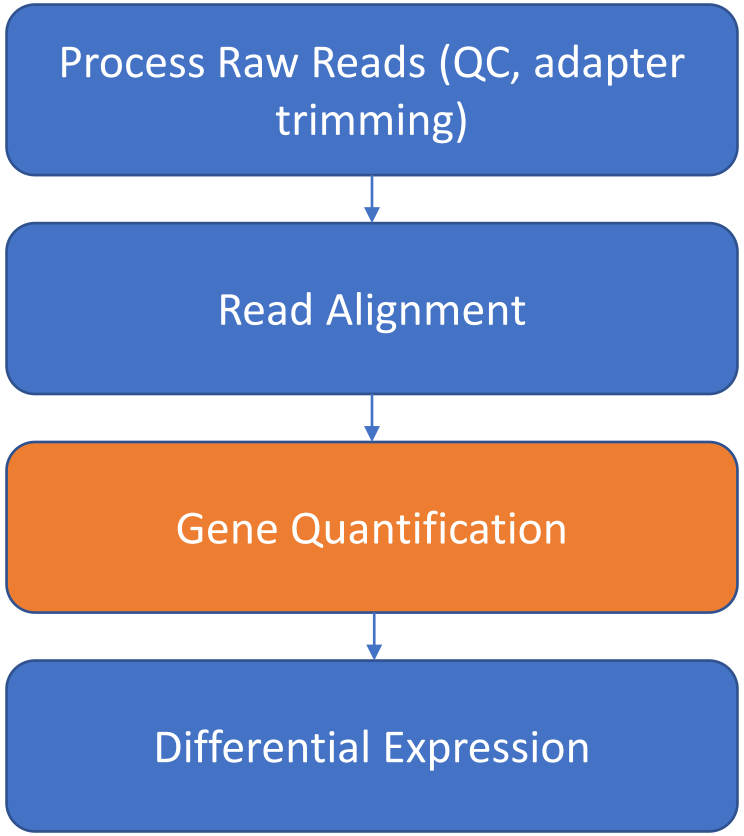

HOW STANDARDS PROLIFERATE:
(SEE: A/C CHARGERS, CHARACTER ENCODINGS, INSTANT MESSAGING, ETC)
SITUATION: THERE ARE 14 COMPETING STANDARDS.
14?! RIDICULOUS! WE NEED TO DEVELOP ONE UNIVERSAL STANDARD THAT COVERS EVERYONE'S USE CASES.
YEAH!
SOON:
SITUATION: THERE ARE 15 COMPETING STANDARDS.

https://xkcd.com/927/

Visualizing reads with JBrowse



Workflow



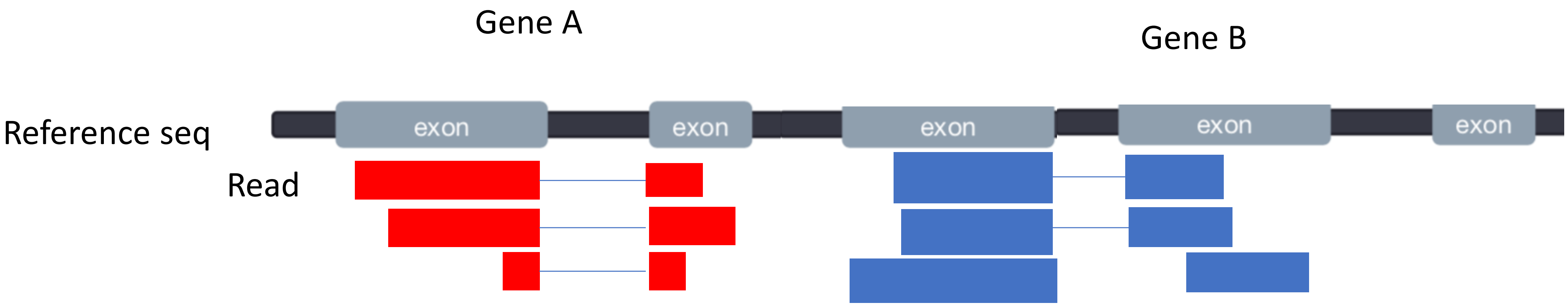
Process Raw Reads (QC, adapter trimming)

Read Alignment

Gene Quantification

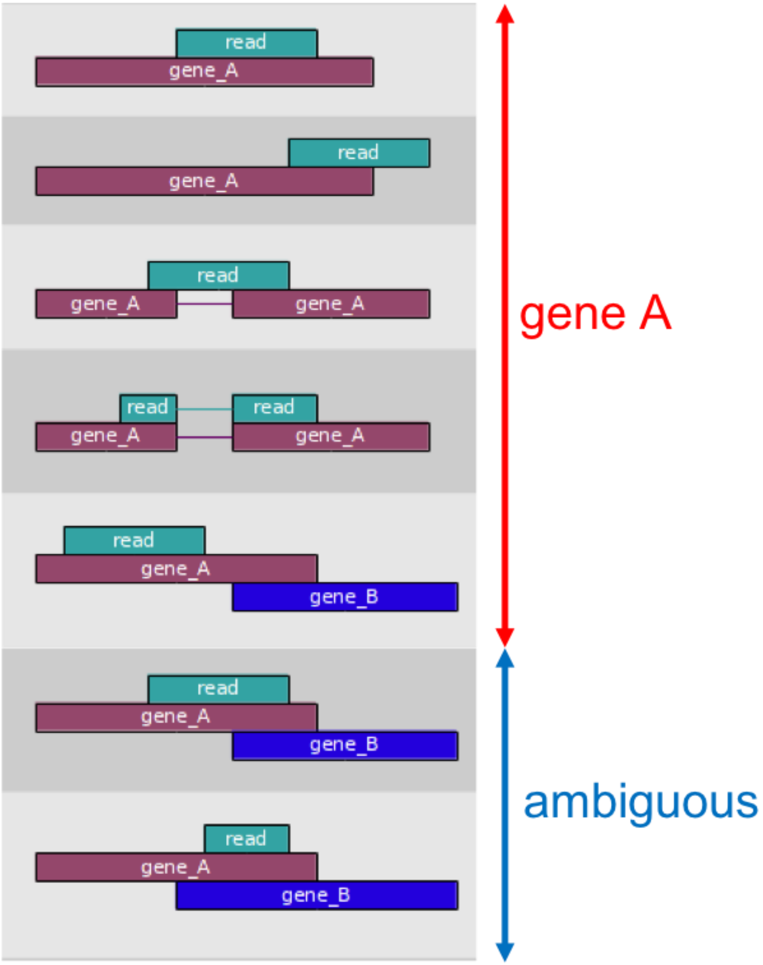
Differential Expression

Counting reads for each gene



Counting reads: featurecounts

- The mapped coordinates of each read are compared with the features in the GTF file
- Reads that overlap with a gene by >=1 bp are counted as belonging to that feature
- Ambiguous reads will be discarded

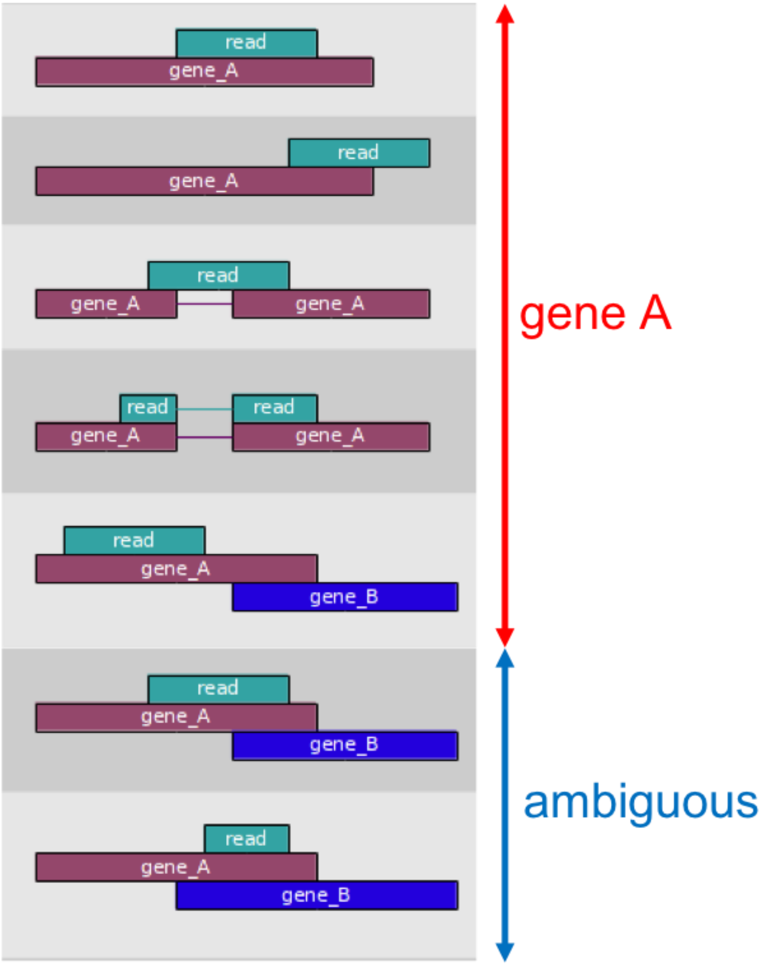


Counting reads: featurecounts

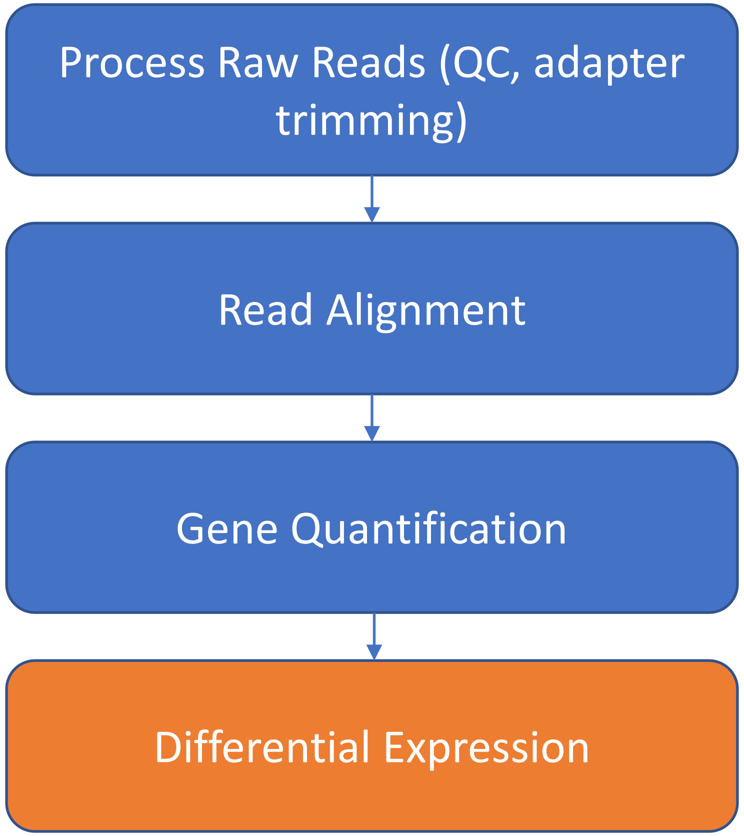
- The mapped coordinates of each read are compared with the features in the GTF file
- Reads that overlap with a gene by >=1 bp are counted as belonging to that feature
- Ambiguous reads will be discarded

Result is a gene count matrix:

Gene	Sample 1	Sample 2	Sample 3	Sample 4
A	1000	1000	100	10
B	10	1	5	6
C	10	1	10	20



Workflow



Process Raw Reads (QC, adapter trimming)

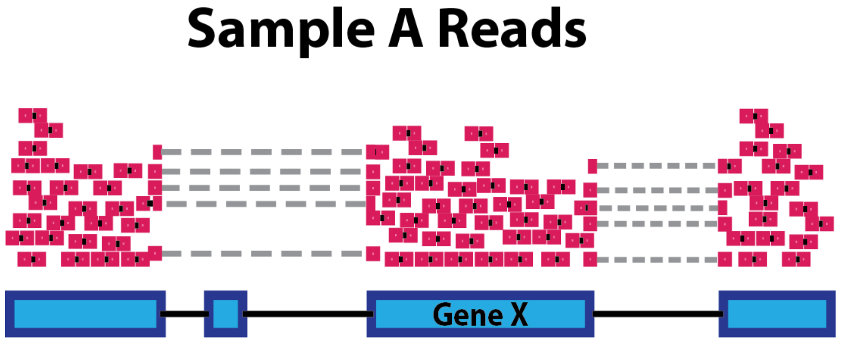
Read Alignment

Gene Quantification

Differential Expression

Normalization

- Raw Count != Expression strength
- Normalization:
  - Eliminates factors that are not of interest for our experiment
  - Enables accurate comparison between samples or genes

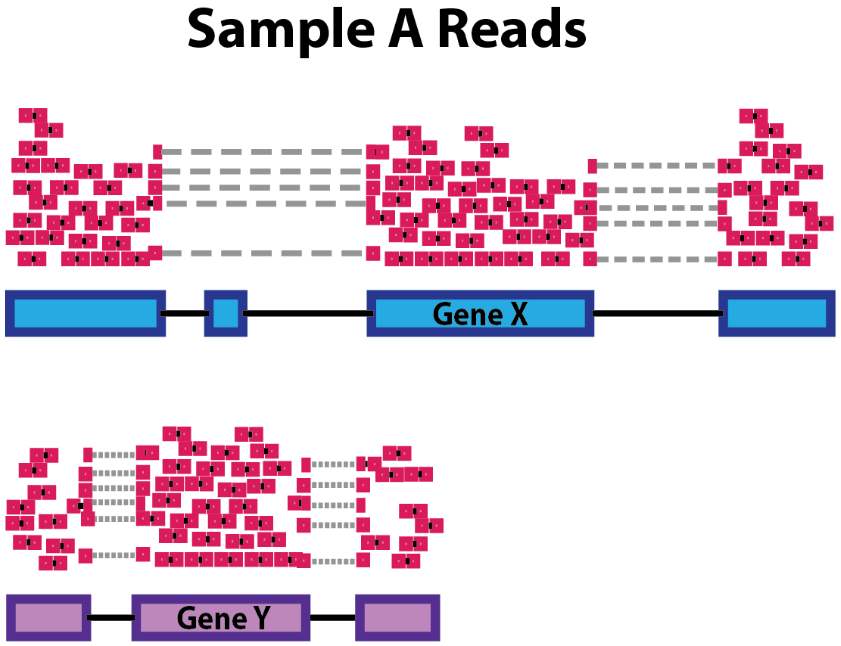


Adapted from https://hbctraining.github.io/DGE_workshop

Normalization

The number of reads mapped to a gene depends on

- **Gene Length**

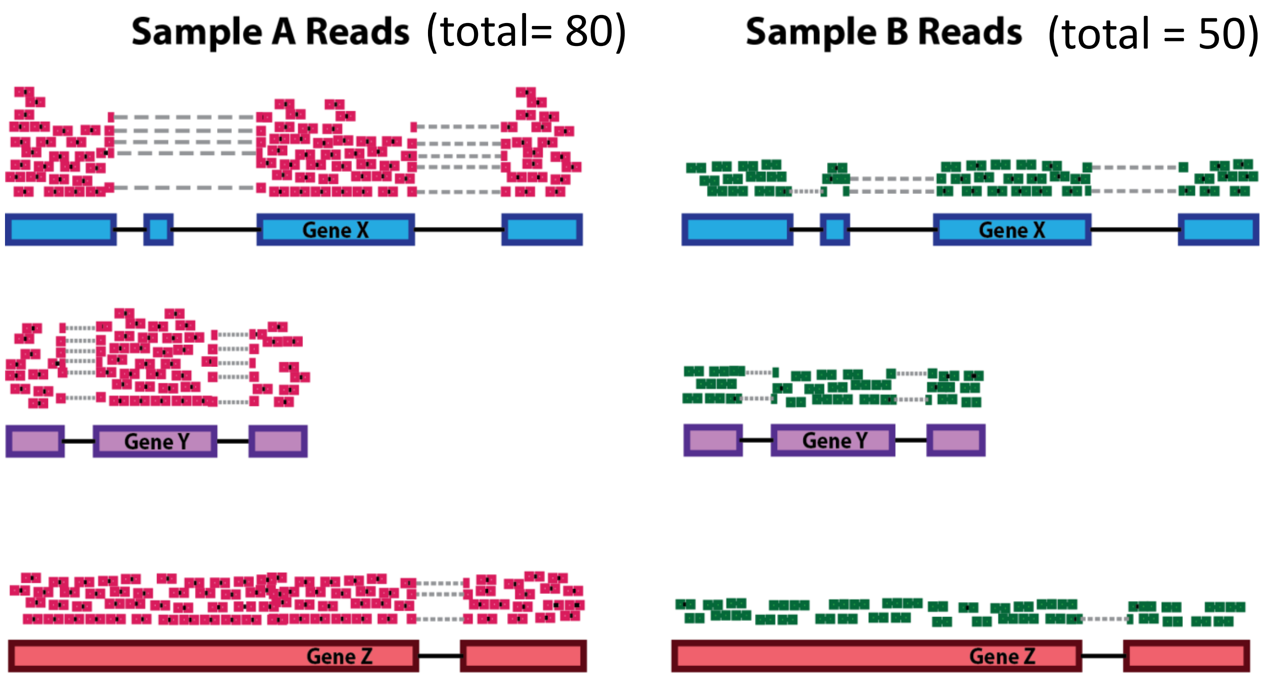


Adapted from https://hbctraining.github.io/DGE_workshop

Normalization

The number of reads mapped to a gene depends on

- Gene Length
- **Sequencing depth**

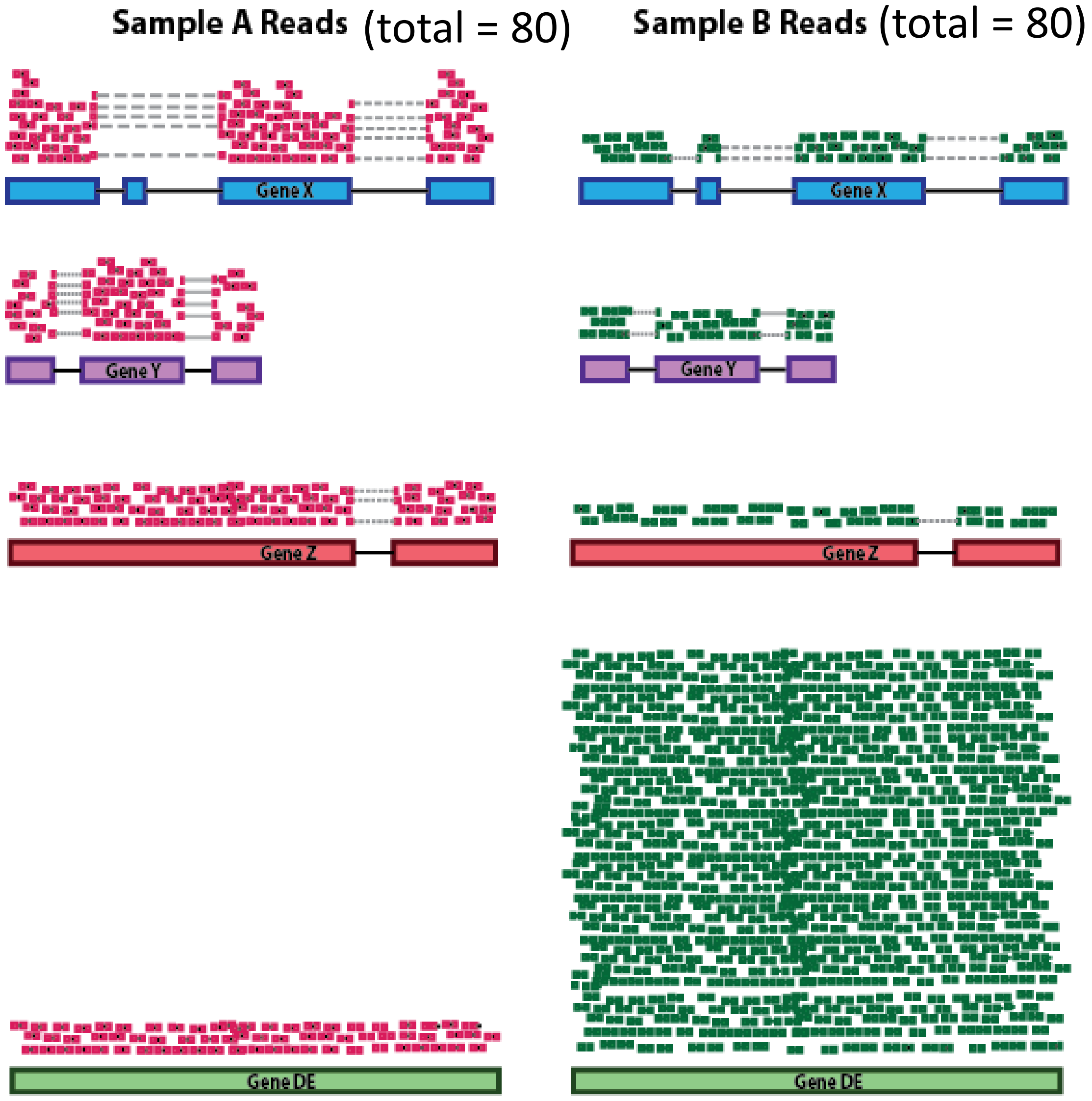


Adapted from https://hbctraining.github.io/DGE_workshop

Normalization

The number of reads mapped to a gene depends on

- Gene Length
- Sequencing depth
- **The expression level of other genes in the sample (RNA Composition)**



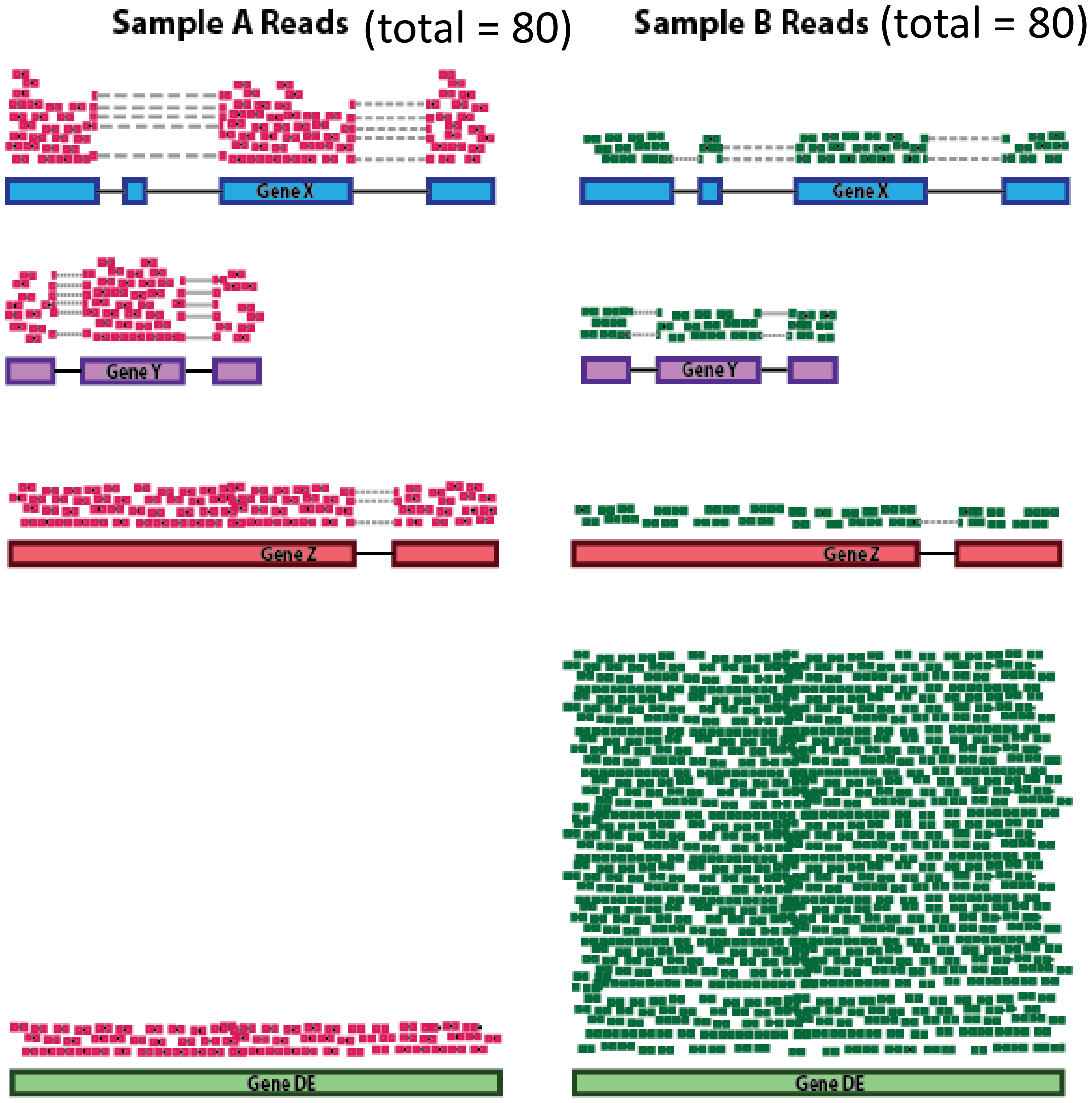
Adapted from https://hbctraining.github.io/DGE_workshop

Normalization

The number of reads mapped to a gene depends on

- Gene Length
- **Sequencing depth**
- **The expression level of other genes in the sample (RNA Composition)**

DESeq2 Median of Ratios

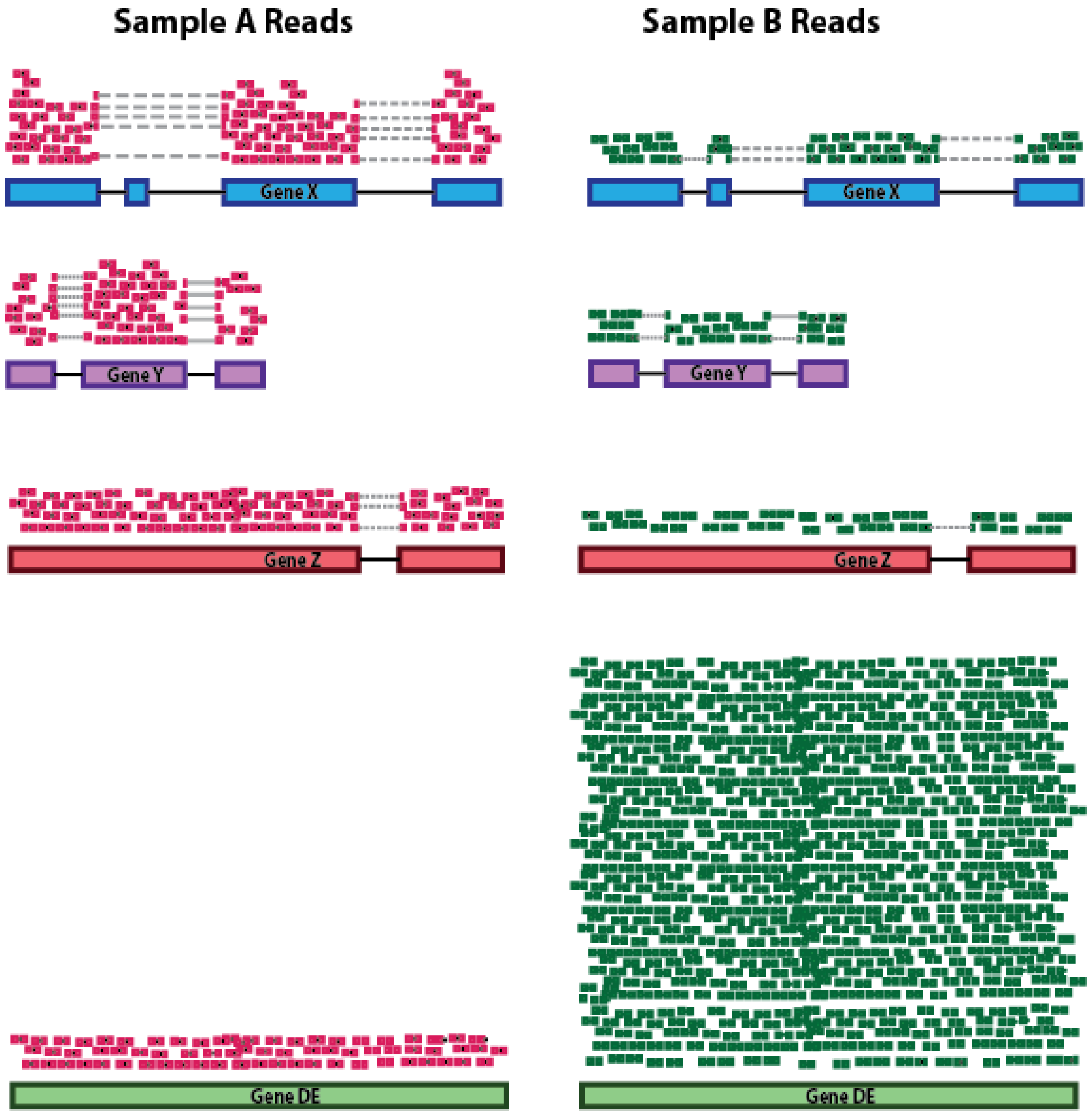


Adapted from https://hbctraining.github.io/DGE_workshop

Normalization: DESeq2 Median of Ratios

Gene	Sample A	Sample B
X	26	10
Y	26	10
Z	26	10
DE	2	50

Total = 80 80



Normalization: DESeq2 Median of Ratios

1. Take a row-wise average to produce an average sample (geometric mean) $\sqrt[n]{x_1 x_2 \cdots x_n}$

Gene	Sample A	Sample B
X	26	10
Y	26	10
Z	26	10
DE	2	50

Avg. Sample
16
16
16
10

Normalization: DESeq2 Median of Ratios

1. Take a row-wise average to produce an average sample (geometric mean) $\sqrt[n]{x_1 x_2 \cdots x_n}$

Gene	Sample A	Sample B
X	26	10
Y	26	10
Z	26	10
DE	2	50

→

Avg. Sample
16
16
16
10

2. Divide all rows by the Average Sample for that gene (**Ratio**)

Gene	Sample A/Avg.	Sample B /Avg.
X	26/16 = 1.6	10/16 = 0.6
Y	1.6	0.6
Z	1.6	0.6
DE	0.2	5

Normalization: DESeq2 Median of Ratios

1. Take a row-wise average to produce an average sample (geometric mean) $\sqrt[n]{x_1 x_2 \cdots x_n}$

Gene	Sample A	Sample B
X	26	10
Y	26	10
Z	26	10
DE	2	50

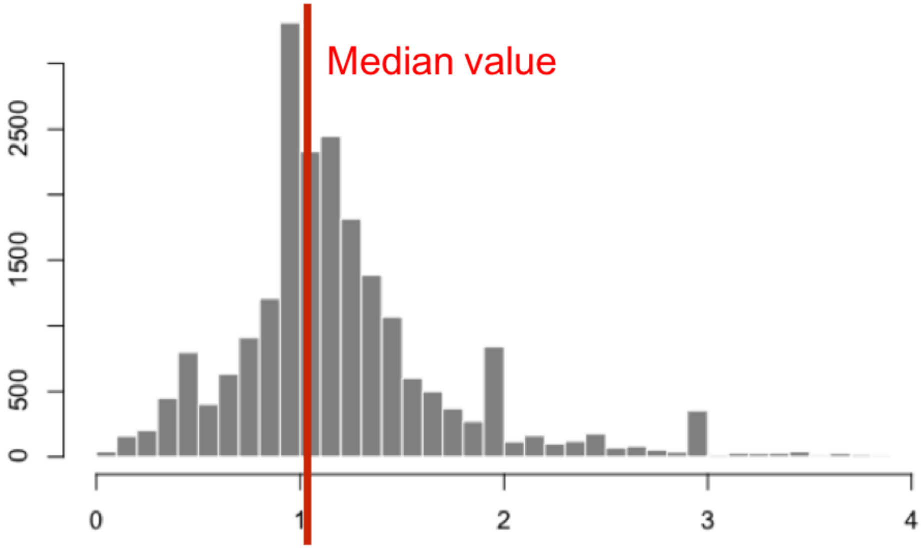
Avg. Sample
16
16
16
16

2. Divide all rows by the Average Sample for that gene (**Ratio**)

Gene	Sample A/Avg.	Sample B /Avg.
X	26/16 = 1.6	10/16 = 0.6
Y	1.6	0.6
Z	1.6	0.6
DE	0.2	5

3. Take the **median** of each column. Should be ~1 for all

Size factor	1.6	0.6



Normalization: DESeq2 Median of Ratios

1. Take a row-wise average to produce an average sample (geometric mean) $\sqrt[n]{x_1 x_2 \cdots x_n}$

Gene	Sample A	Sample B
X	26	10
Y	26	10
Z	26	10
DE	2	50

→

Avg. Sample
16
16
16
16

2. Divide all rows by the Average Sample for that gene (**Ratio**)

Gene	Sample A/Avg.	Sample B /Avg.
X	26/16 = 1.6	10/16 = 0.6
Y	1.6	0.6
Z	1.6	0.6
DE	0.2	5

3. Take the **median** of each column. Should be ~1 for all

Size factor	1.6	0.6

4. Divide all counts by sample specific size factor

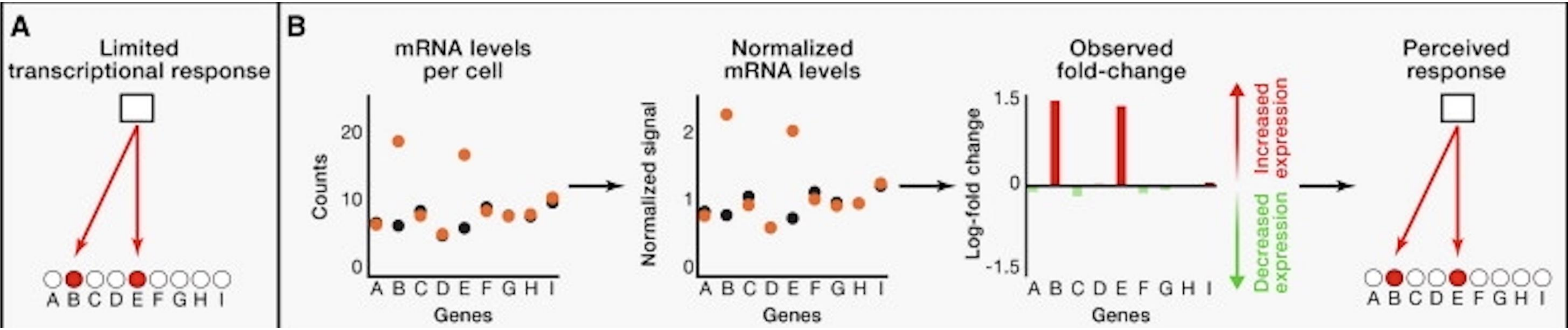
Gene	Sample A / S_A	Sample B / S_B
X	16.3	16.7
Y	16.3	16.7
Z	16.3	16.7
DE	1.3	83.3

Normalized counts for non-DE genes are similar!

```
estimateSizeFactors(dds)
```

Assumption of DESeq2 Median of Ratios

Median of Ratios method assumes that most genes are not Differentially Expressed between samples.

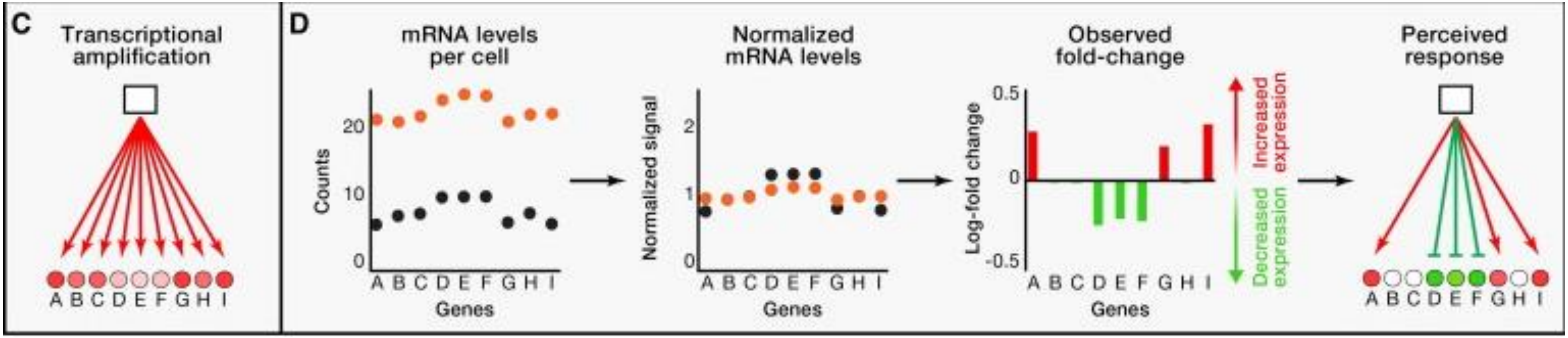


Loven et al “Revisiting Global Gene Expression Analysis” Cell 2012 https://doi.org/10.1016/j.cell.2012.10.012

Assumption of DESeq2 Median of Ratios

Median of Ratios method assumes that most genes are not Differentially Expressed between samples.

<u>COUNTER EXAMPLE</u>



- Late stage cell death (total RNA DOWN)
- High c-Myc cells (total RNA UP)

Known quantity spike-in transcripts (ERCC) can be used to normalize in these cases.

Loven et al “Revisiting Global Gene Expression Analysis” Cell 2012 https://doi.org/10.1016/j.cell.2012.10.012

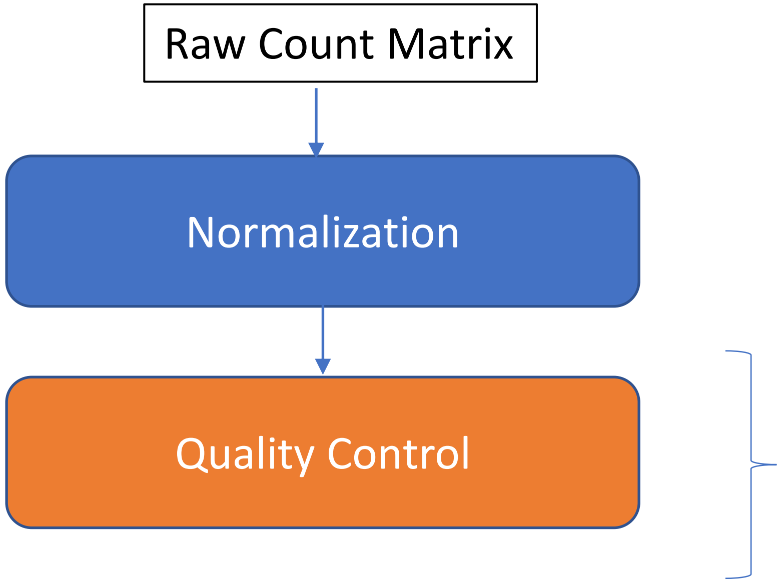
Normalization methods

Normalization method	Description	Accounted factors	Recommended use
CPM (counts per million)	$\frac{\mathrm{K_i}}{Total\ Reads\ per\ Sample/10^6}$	sequencing depth	Comparison between replicates of the sample group
R/FPKM (reads/fragments per kilobase of exon per million reads/fragments mapped)	$\frac{\mathrm{K_i}}{Gene\ Length/10^3 * \ Total\ Reads\ per\ Sample/10^6}$	sequencing depth and gene length	Comparison between genes in a sample
DESeq2's **median of ratios** [1]	$\mathrm{K_i}$ divided by sample-specific size factors	sequencing depth and RNA composition	**Differential Expression** between samples

Similar to DESeq2: EdgeR, limma-voom

Adapted from https://hbctraining.github.io/DGE_workshop

Quality Control Visualizations



Examine sources of variation in the data

- Principal Component Analysis
- Hierarchical Clustering

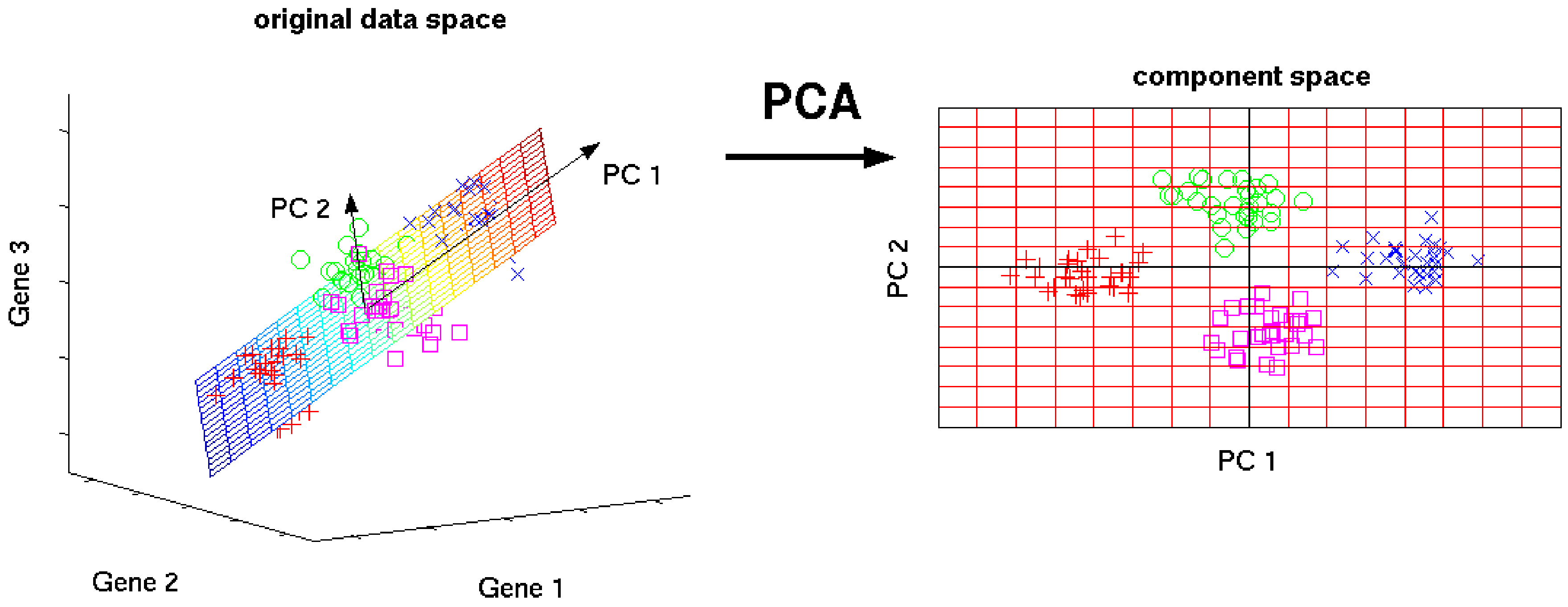
(Log2 + 1) Transformed, Normalized Count Table

Gene	Sample A	Sample B	Sample C
1	1	1.6	0.5
2	2.2	-0.2	1
3	-1	1	3.1

Principle Component Analysis

Dimension reduction technique
Example: 3 gene dimensions -> 2 PC

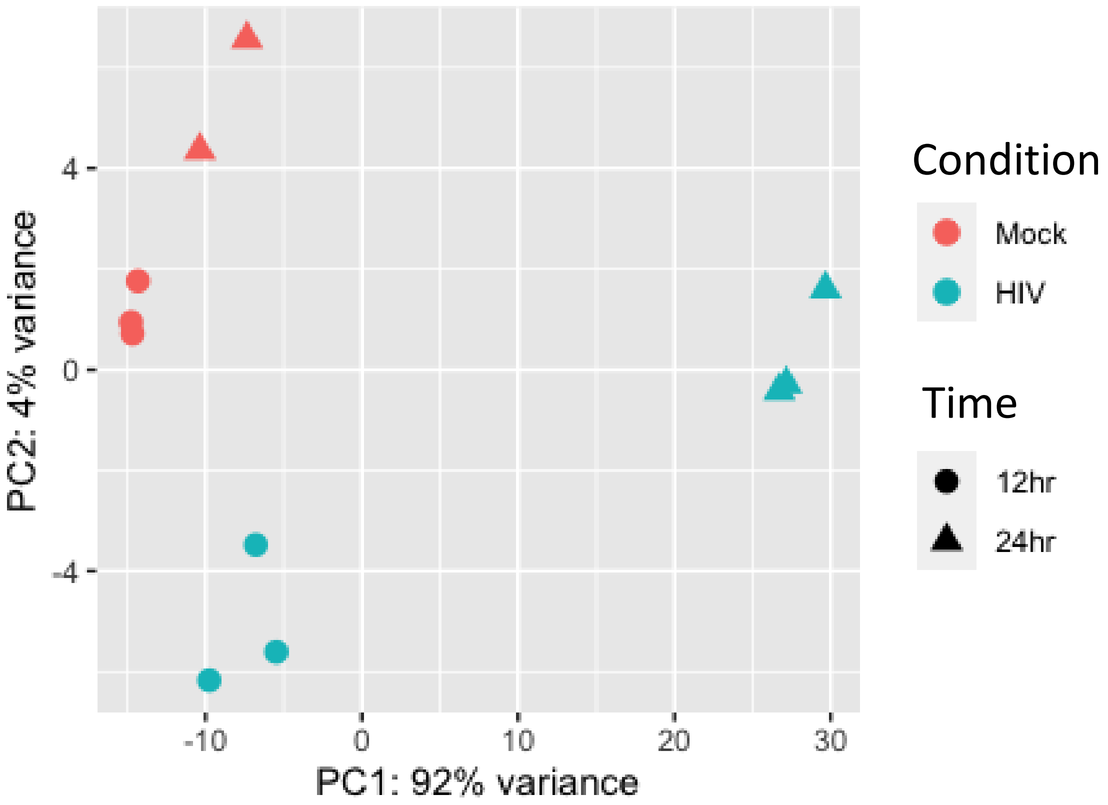
Gene	Mock_12h	Mock_12h	Mock_24h	Mock_24h	HIV_12h	HIV_12h	HIV_24h	HIV_24h
Gene 1	8.9	8.9	8.9	9.0	8.9	8.9	9.0	6.8
Gene 2	0.6	-1.0	0.6	-1.0	0.6	-1.0	0.6	3.8
Gene 3	4.1	11.9	4.1	-0.5	4.1	8.7	4.0	4.4



Do your samples cluster as expected?

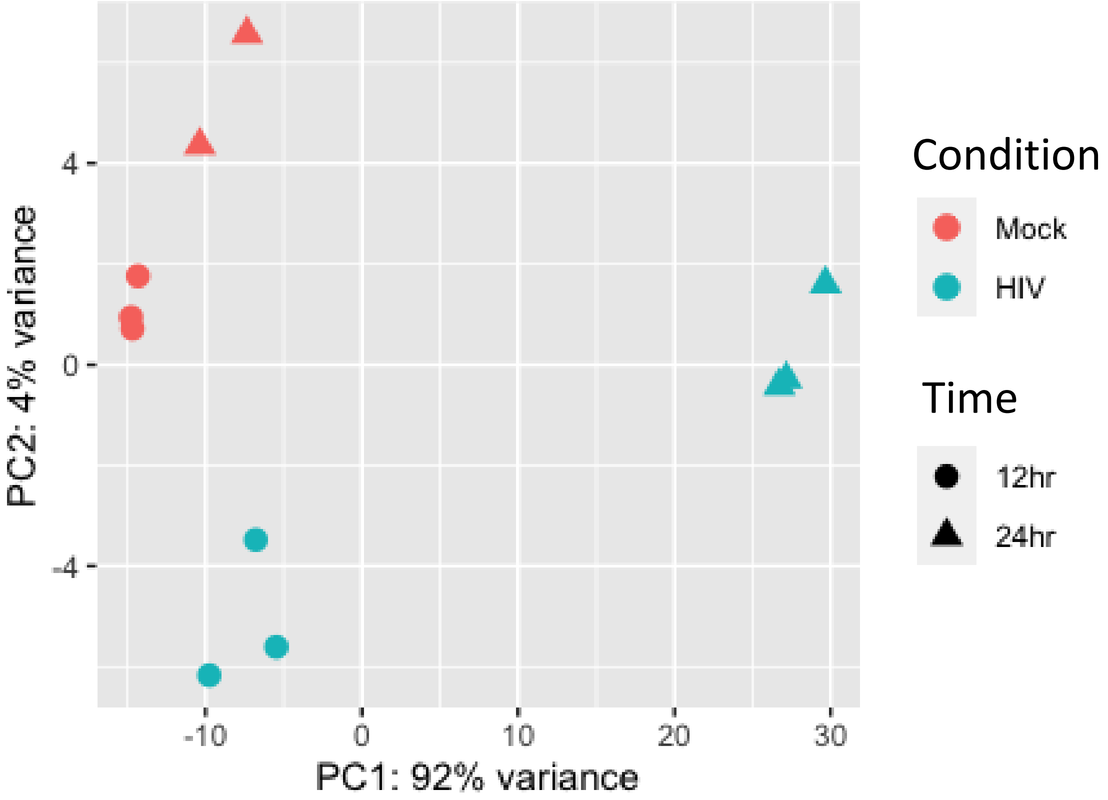
What are the major sources of variation in the data?

Principle Component Analysis



- ✓ Do your samples cluster as expected?
- ✓ What are the major sources of variation in the data?

Principle Component Analysis



- ✓ Do your samples cluster as expected?
- ✓ What are the major sources of variation in the data?
- ✓ Is there a batch effect?

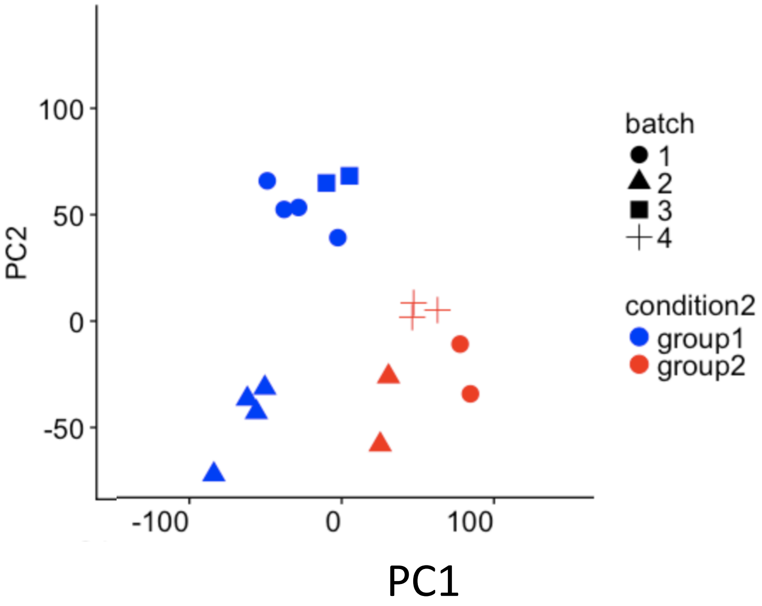
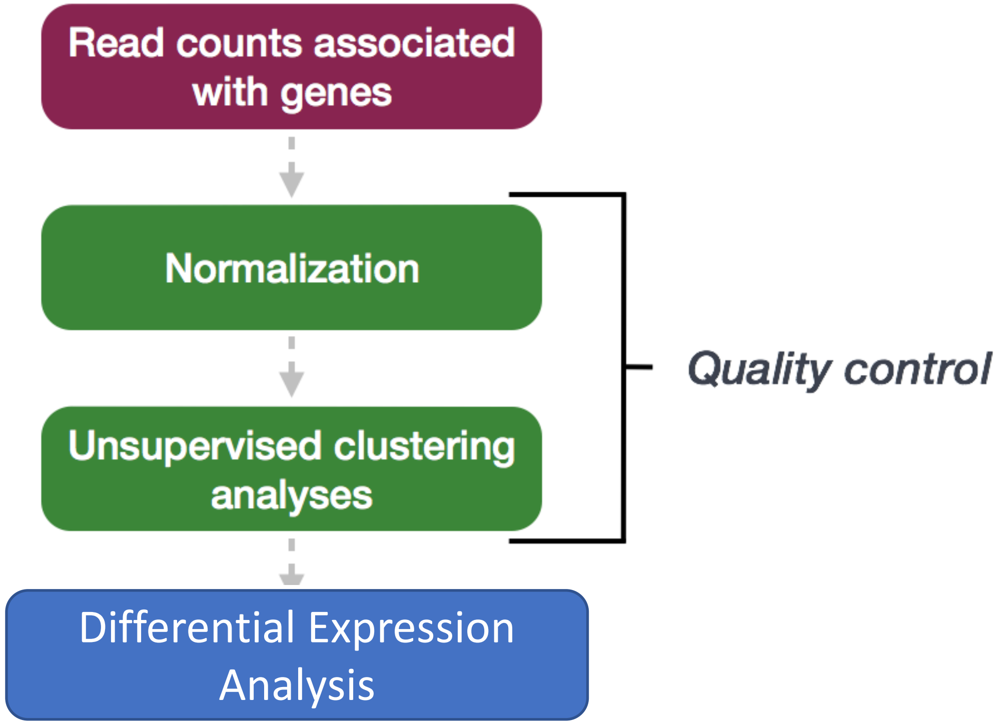


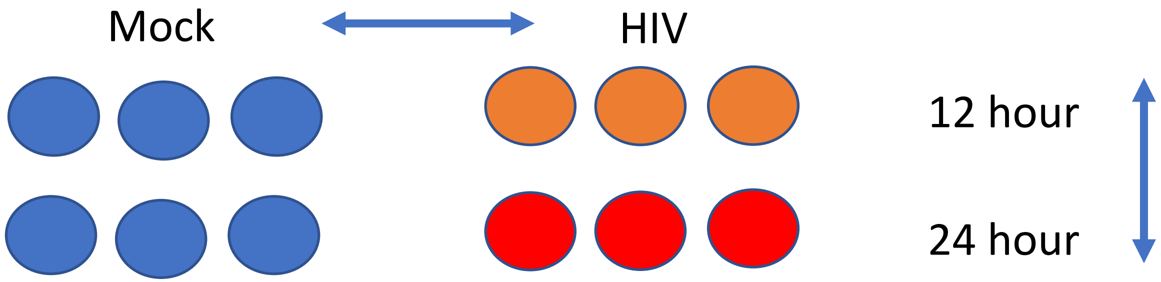
Image https://support.bioconductor.org/p/111491/

Differential Expression with DESeq2


Read counts associated with genes
Normalization
Unsupervised clustering analyses
Quality control
Differential Expression Analysis

https://hbctraining.github.io/DGE_workshop

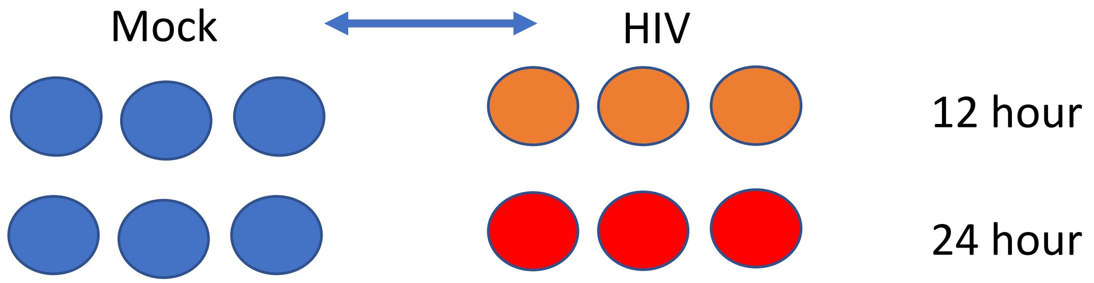
Multi-factor experiment design



Factor 1:
Infection status (Mock or HIV)

Factor 2:
Time (12 or 24 hr)

Multi-factor experiment design

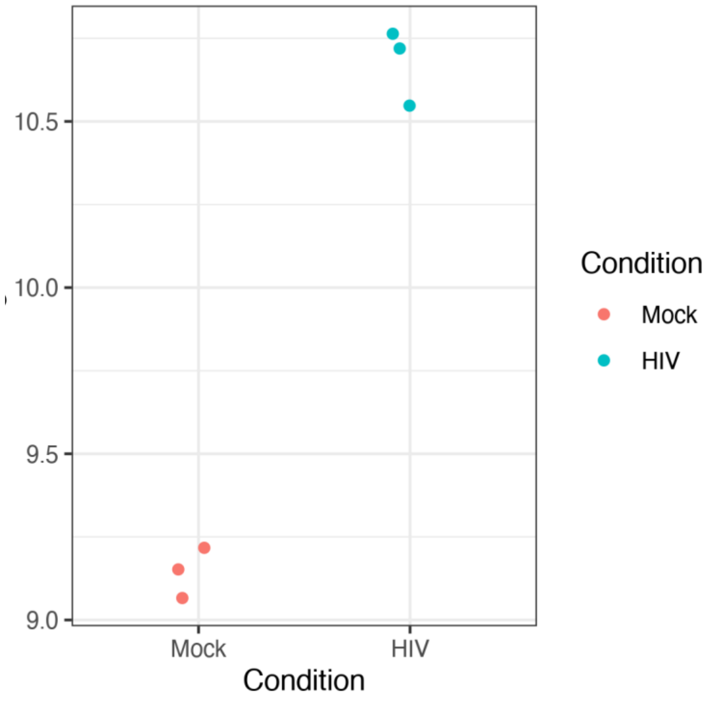


- Differential Expression compares two conditions
- We'll choose Infection status at 12 hr (Mock or HIV) for comparison
- We could also choose time, or a combination of multiple factors

Step 1: Modeling gene expression values

All leading DE tools use **regression models** to estimate the fold change between conditions for **each gene**

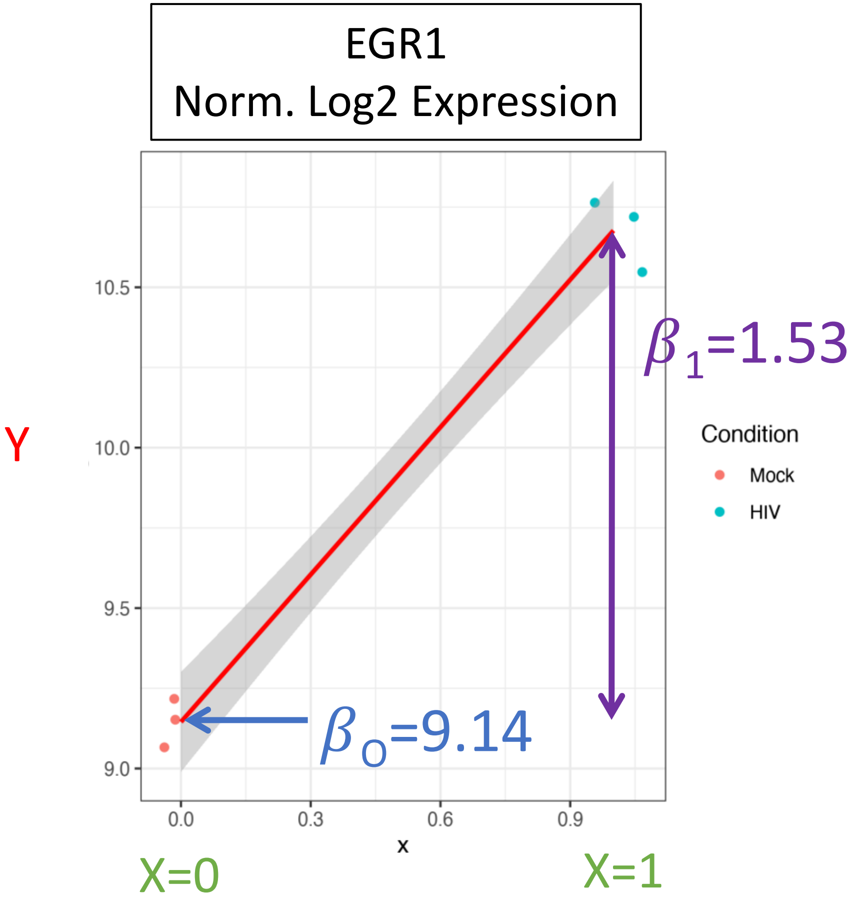
EGR1
Norm. Log2 Expression



(12hr)

Step 1: Modeling gene expression values

All leading DE tools use **regression models** to estimate the fold change between conditions for **each gene**
Example, simple linear regression:



Intercept

Condition (0-Mock, 1-HIV)

$$Y = \beta_o + \beta_1 X + e$$

Log2 Expression Values

Slope: difference between Mock /HIV

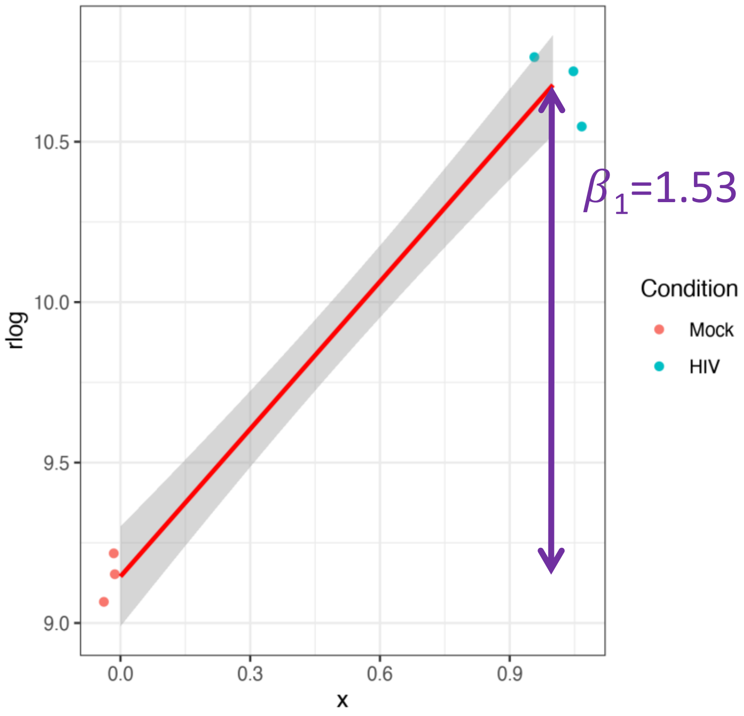
Error

DESeq2 uses a Generalized Linear Model with a Negative Binomial error Distribution, which has been shown to be best fit for RNAseq data.

Love, M.I., Huber, W. & Anders, S. Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. *Genome Biol* **15,** 550 (2014).

Step 2: Hypothesis Testing

EGR1
Norm. Log2 Expression



Is EGR1 differentially expressed?

Yes! $p << 0.05$

$$H_O : \beta_1 = 0 \quad \text{vs.} \quad H_A : \beta_1 \neq 0$$

H_o: there is no systematic difference between the average read count values for Mock vs. HIV

- Statistical test – Wald test (similar to t-test) on β_1
- $Z = \beta_1 / SE_{\beta 1}$
- Z-statistic is compared to the normal distribution and probability of getting a statistic at least as extreme is computed

DESeq2 Results table

GeneID	Base mean	log2FoldChange	StdErr	P-value	P-adj
EGR1	1273	1.55	0.13	1.19e-77	1.52e-73
MYC	5226	-1.53	0.14	1.63e-36	1.03e-32

- Mean of normalized counts – averaged over all samples from two conditions (HIV, Mock)
- Log of the fold change between two conditions
- StdErr – Standard error of coefficient (e.g. b_1)
- P-value – the probability that the Wald statistic is as extreme as observed if H_O were true
- P-adj – accounting for multiple testing correction

References

DESeq2 vignette (R/Rstudio):
http://www.bioconductor.org/packages/release/bioc/vignettes/DESeq2/inst/doc/DESeq2.html#differential-expression-analysis

HBC Training (Command line/R):
https://hbctraining.github.io/DGE_workshop

Galaxy Training:
https://galaxyproject.org/tutorials/rb_rnaseq/

Next: Introduction To Galaxy