Other applications of RNA-Seq data

# A non-comprehensive list...

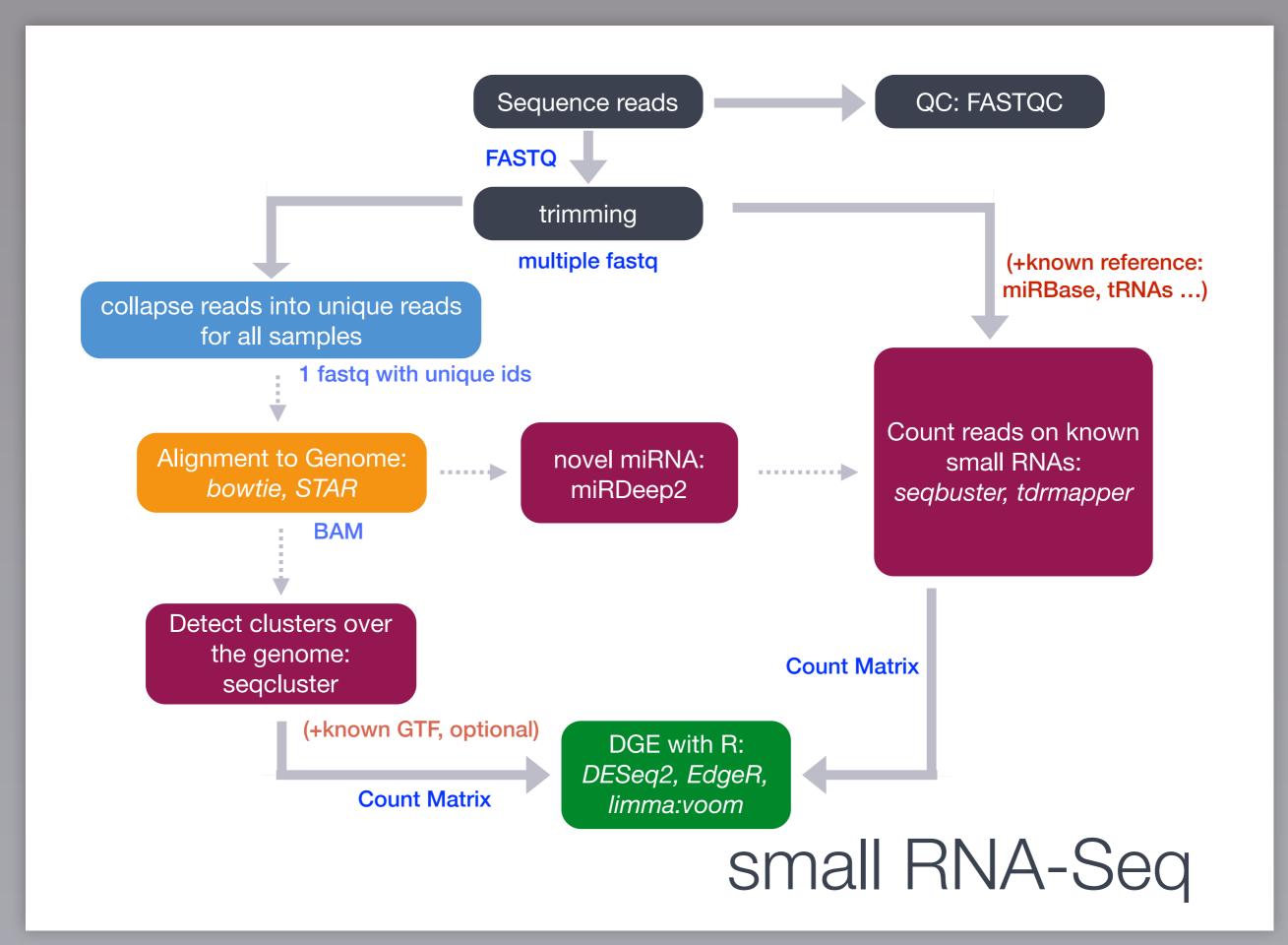
- Evaluating/comparing expression of small RNA
- Identifying the protein interaction sites on RNA molecules:

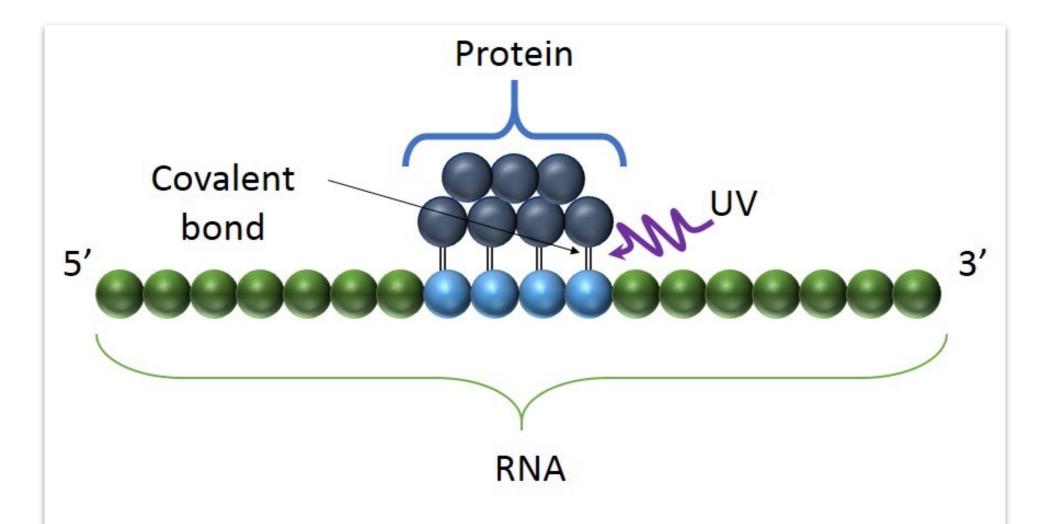
HITS-CLIP, PAR-CLIP, ICLIP

Identifying translation status of genes:

Ribo-Seq (Ribosomal Profiling)

Understanding expression profiles of cells starting with single cells

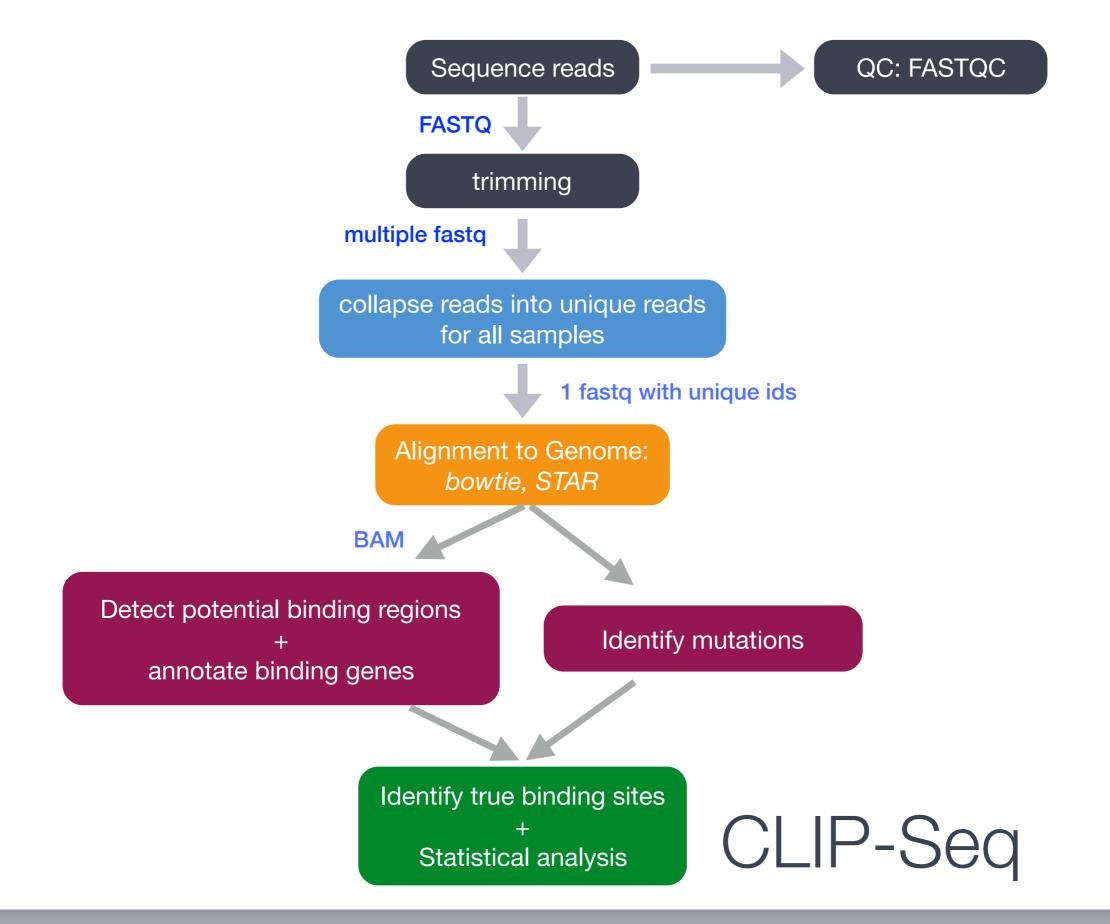


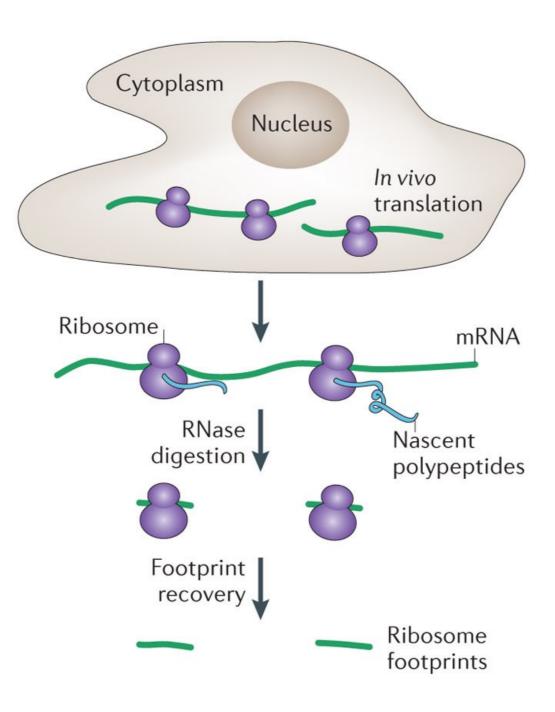


**Figure 1: Basic principle of CLIP.** Covalent bonds are formed between proximal proteins and RNA upon exposure to ultraviolet light. These bonds only occur at the sites of direct contact and preserve RNA-protein interactions.

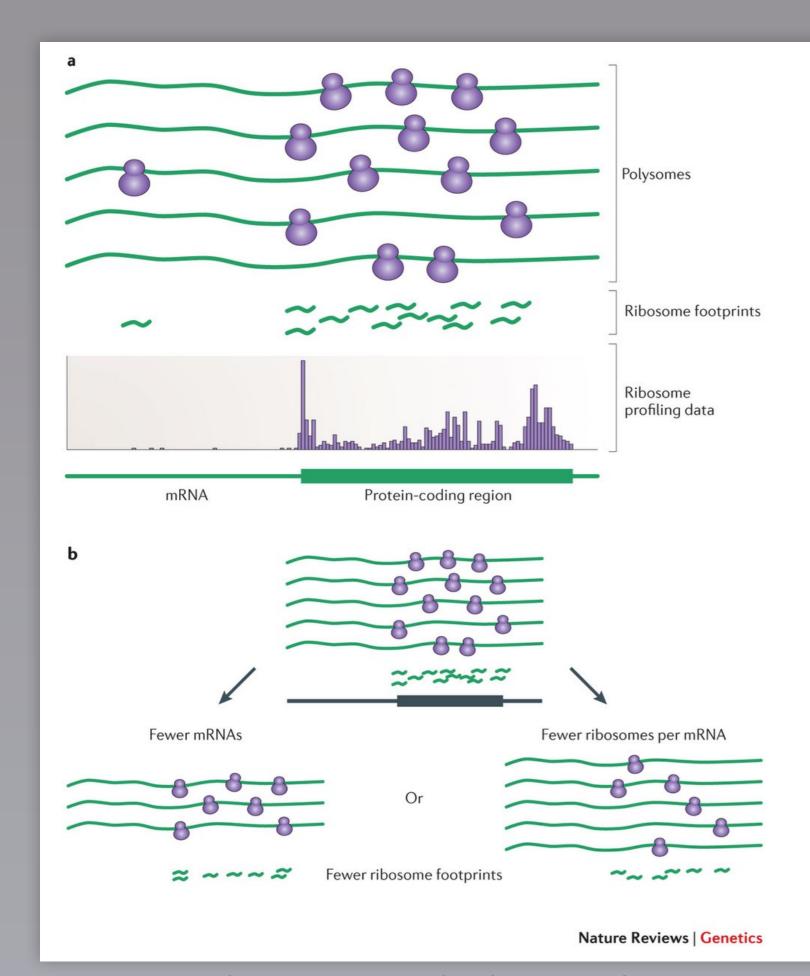
https://en.wikipedia.org/wiki/CLIP#/media/File:Basic\_Principle\_of\_CLIP.jpg

CLIP-Seq





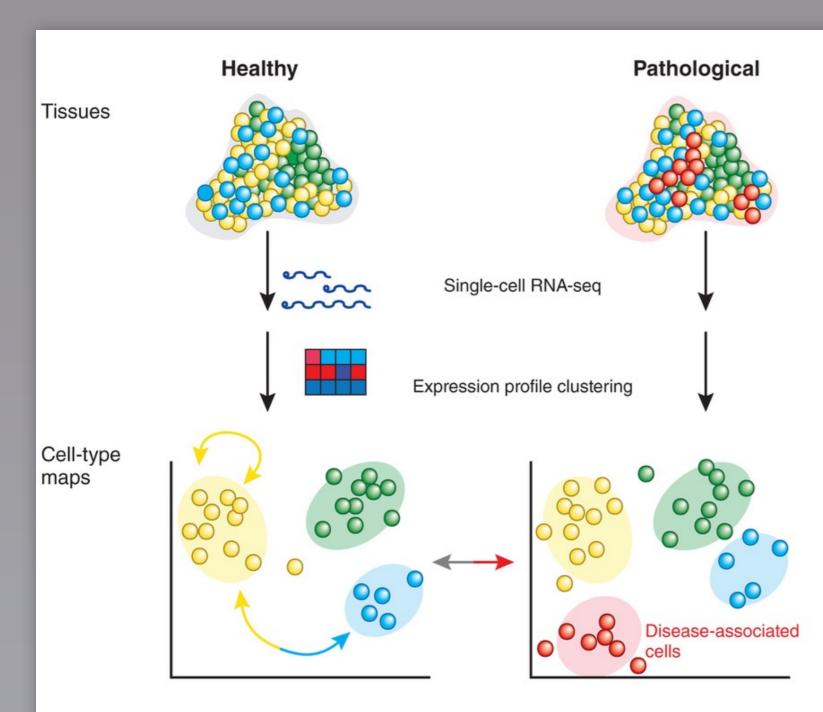
# Ribo-Seq



Ribo-Seq

Sequence reads **FASTQ** Quality control (+reference genome index) **FASTQ** (+known GTF, optional) Alignment to Genome: Tophat2, STAR multiple BAMs (+known GTF) Count reads associated with genes: htseq-count, featureCounts **Count Matrix** DGE with R: DESeq2, EdgeR, limma:voom

Ribo-Seq



## Types of analyses



## Within cell type

- · Stochasticity, variability of transcription
- Regulatory network inference
- Allelic expression patterns
- Scaling laws of transcription



#### Between cell types

- Identify biomarkers
- (Post)-transcriptional differences



#### Between tissues

- Cell-type compositions
- Altered transcription in matched cell types

scRNA-Seq

Sequence reads **FASTQ** Quality control (+reference genome index) **FASTQ** (+known GTF, optional) Alignment to Genome: Tophat2, STAR multiple BAMs (+known GTF) Count reads associated with genes: htseq-count, featureCounts **Count Matrix** Statistical Analysis:

Clustering, differential gene expression, count imputation, etc.

scRNA-Seq