



Canadian Bioinformatics Workshops

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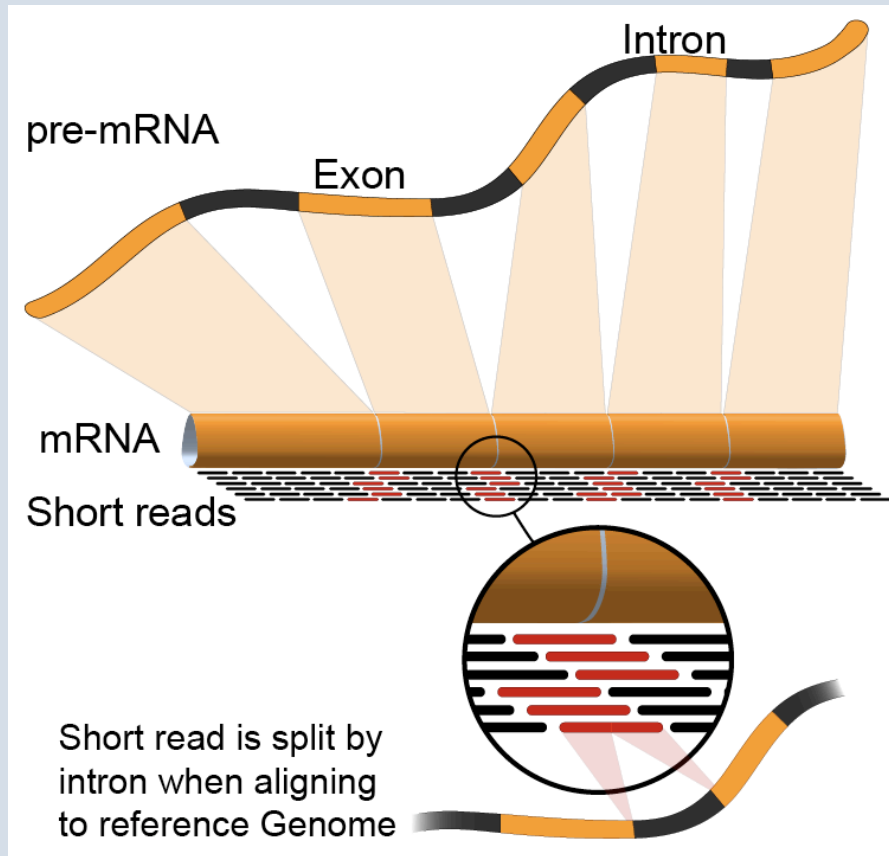
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Module 1

Introduction to RNA sequencing (lecture)

Malachi Griffith & Obi Griffith
Informatics for RNA-seq Analysis
June 8-9, 2015



Learning objectives of the course

- Module 0: Introduction to cloud computing
- **Module 1: Introduction to RNA sequencing**
- Module 2: RNA-seq alignment and visualization
- Module 3: Expression and Differential Expression
- Module 4: Isoform discovery and alternative expression

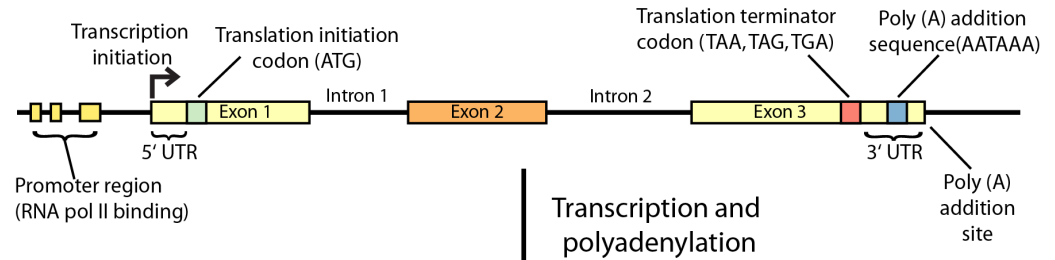
- Tutorials
 - Provide a working example of an RNA-seq analysis pipeline
 - Run in a ‘reasonable’ amount of time with modest computer resources
 - Self contained, self explanatory, portable

Learning objectives of module 1

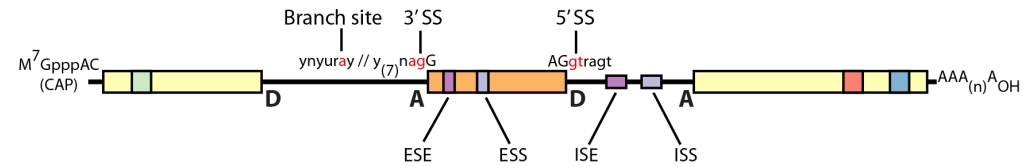
- Introduction to the theory and practice of RNA sequencing (RNA-seq) analysis
 - Rationale for sequencing RNA
 - Challenges specific to RNA-seq
 - General goals and themes of RNA-seq analysis work flows
 - Common technical questions related to RNA-seq analysis
 - Getting help outside of this course
 - Introduction to the RNA-seq hands on tutorial

Gene expression

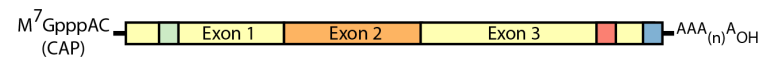
Double-stranded genomic DNA template



Single-stranded pre-mRNA (nuclear RNA)



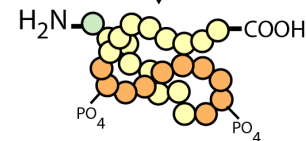
Mature mRNA



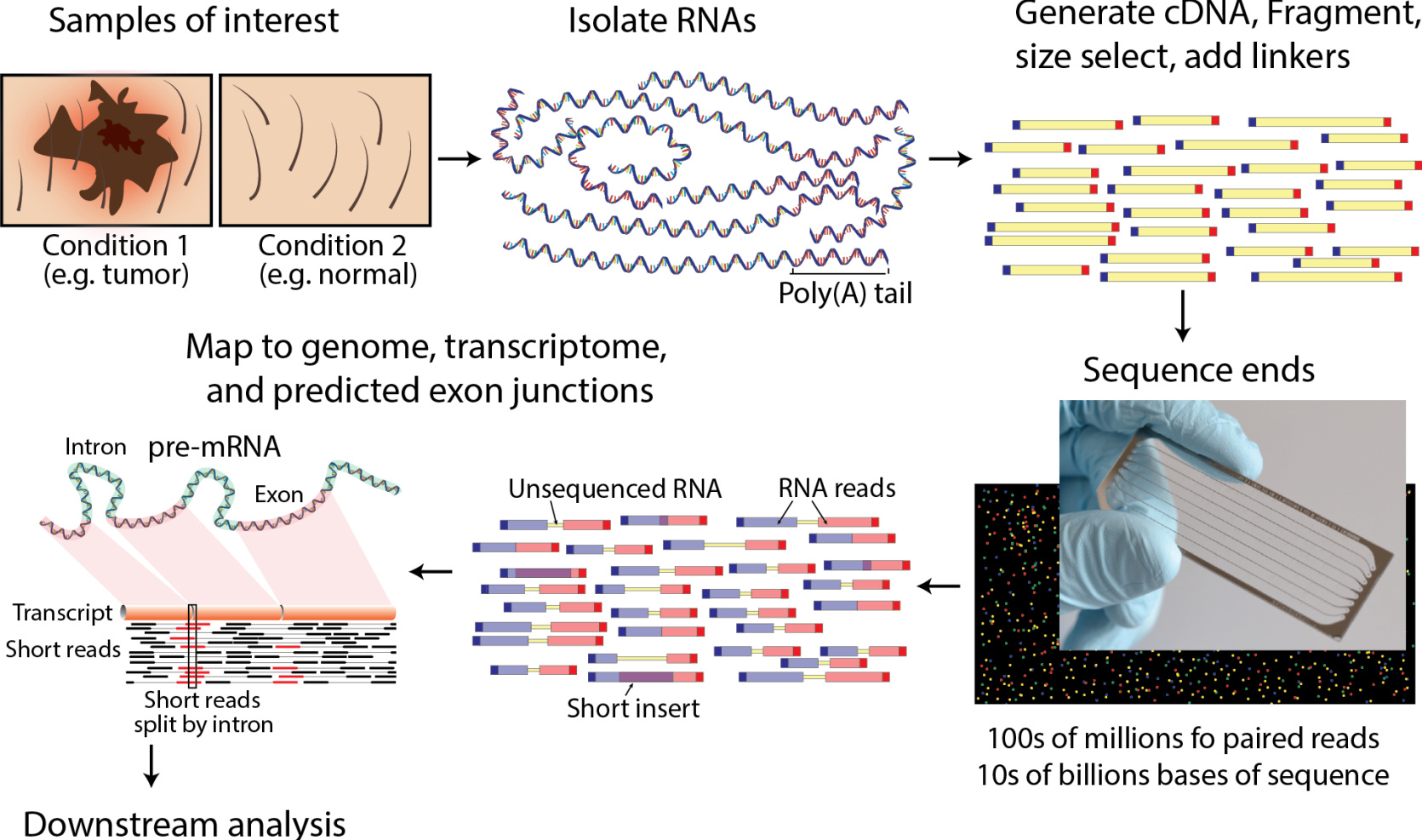
Protein (amino acid sequence)



Folding, posttranslational modification, subcellular localization, etc.



RNA sequencing



Why sequence RNA (versus DNA)?

- Functional studies
 - Genome may be constant but an experimental condition has a pronounced effect on gene expression
 - e.g. Drug treated vs. untreated cell line
 - e.g. Wild type versus knock out mice
- Predicting transcript sequence from genome sequence is difficult
 - Gene annotation is revolutionized by RNA-seq
- Some molecular features can only be observed at the RNA level
 - Alternative isoforms, fusion transcripts, RNA editing

Why sequence RNA (versus DNA)?

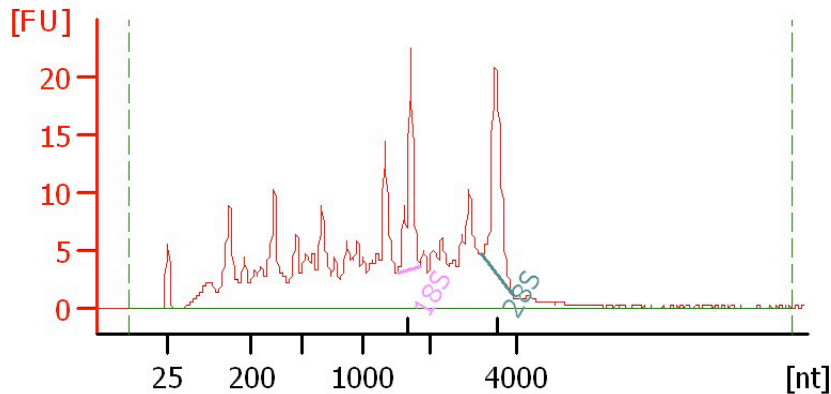
- Interpreting mutations that do not have an obvious effect on protein sequence
 - ‘Regulatory’ mutations that affect what mRNA isoform is expressed and how much
- Prioritizing protein coding somatic mutations (often heterozygous)
 - If the gene is not expressed, a mutation in that gene would be less interesting
 - If the gene is expressed but only from the wild type allele, this might suggest loss-of-function (haploinsufficiency)
 - If the mutant allele itself is expressed, this might suggest a candidate drug target

Challenges

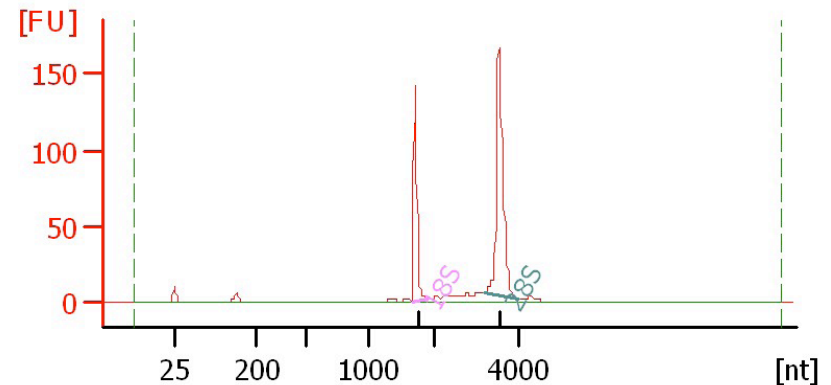
- Sample
 - Purity?, quantity?, quality?
- RNAs consist of small exons that may be separated by large introns
 - Mapping reads to genome is challenging
- The relative abundance of RNAs vary wildly
 - $10^5 - 10^7$ orders of magnitude
 - Since RNA sequencing works by random sampling, a small fraction of highly expressed genes may consume the majority of reads
 - Ribosomal and mitochondrial genes
- RNAs come in a wide range of sizes
 - Small RNAs must be captured separately
 - PolyA selection of large RNAs may result in 3' end bias
- RNA is fragile compared to DNA (easily degraded)

Agilent example / interpretation

- https://github.com/griffithlab/rnaseq_tutorial/wiki/Resources/Agilent_Trace_Examples.pdf
- ‘RIN’ = RNA integrity number
 - 0 (bad) to 10 (good)



RIN = 6.0



RIN = 10

Design considerations

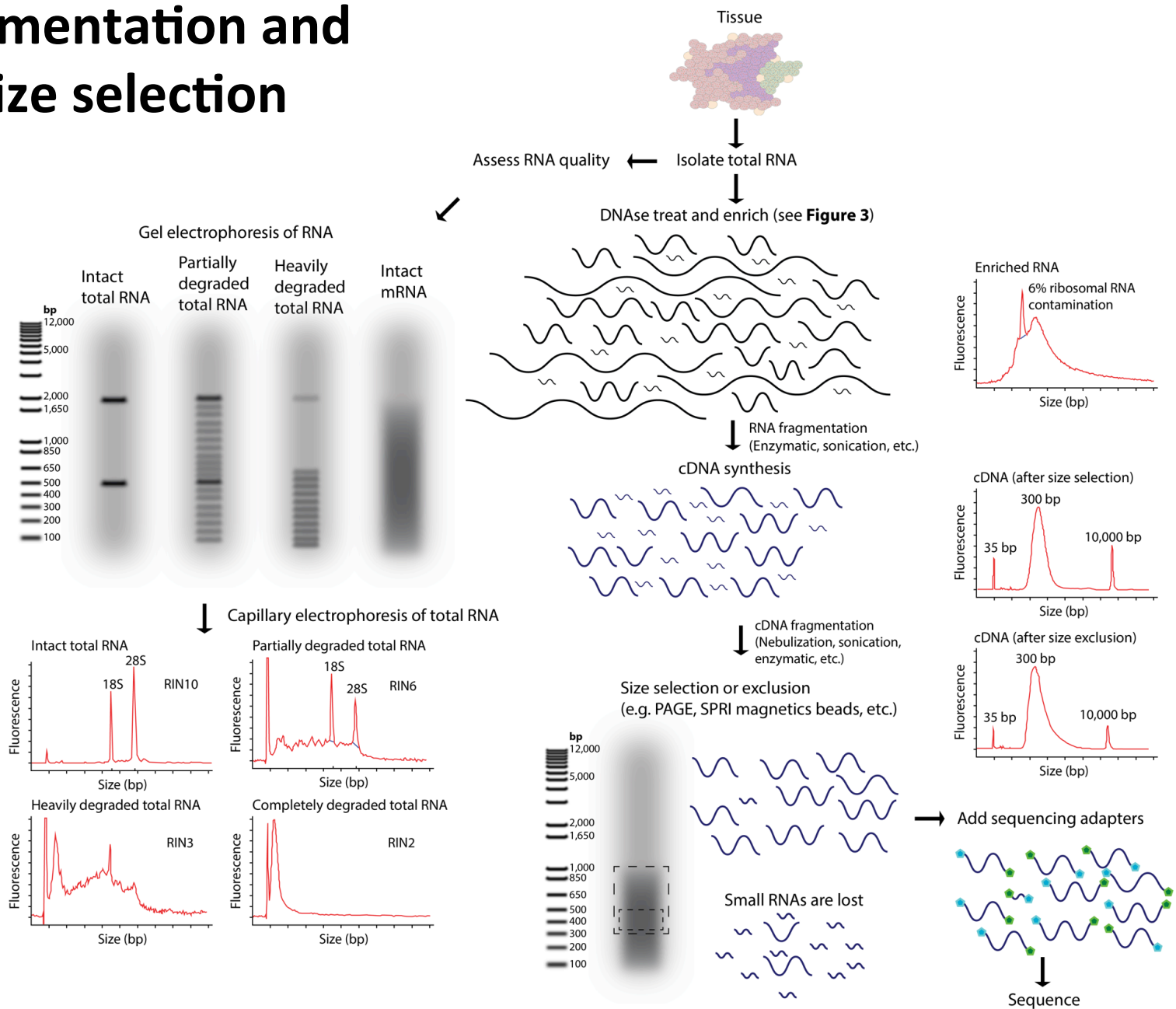
- Standards, Guidelines and Best Practices for RNA-seq
 - The ENCODE Consortium
 - Download from the Course Wiki
 - Meta data to supply, replicates, sequencing depth, control experiments, reporting standards, etc.
- https://github.com/griffithlab/rnaseq_tutorial/wiki/Resources/ENCODE_RNAseq_standards_v1.0.pdf

There are many RNA-seq library construction strategies

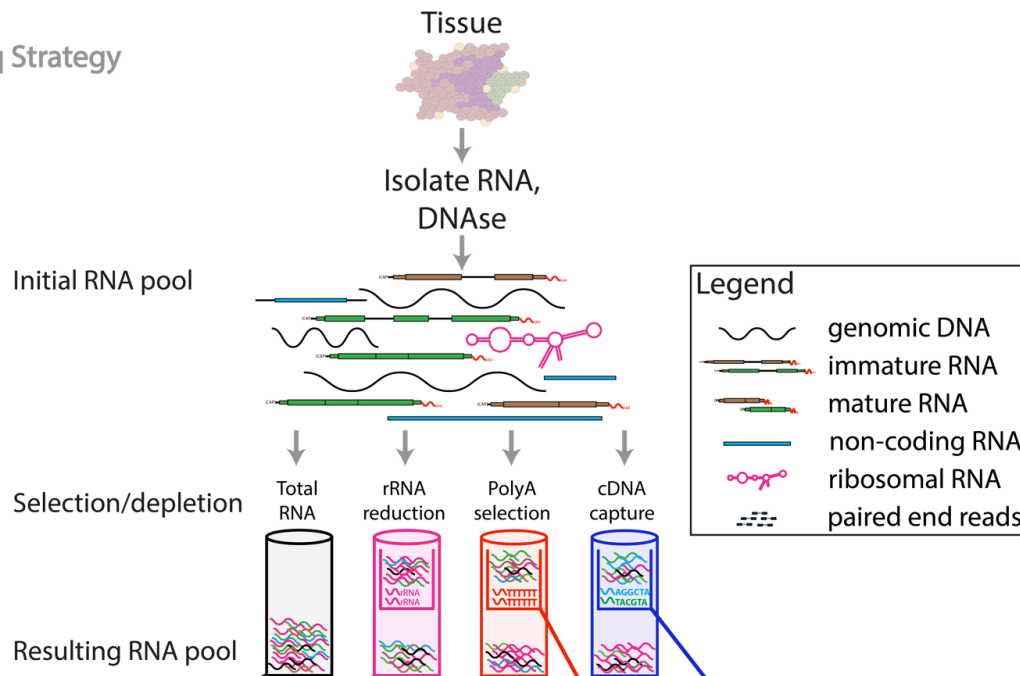
- Total RNA versus polyA+ RNA?
- Ribo-reduction?
- Size selection (before and/or after cDNA synthesis)
 - Small RNAs (microRNAs) vs. large RNAs?
 - A narrow fragment size distribution vs. a broad one?
- Linear amplification?
- Stranded vs. un-stranded libraries
- Exome captured vs. un-captured
- Library normalization?

- These details can affect analysis strategy
 - Especially comparisons between libraries

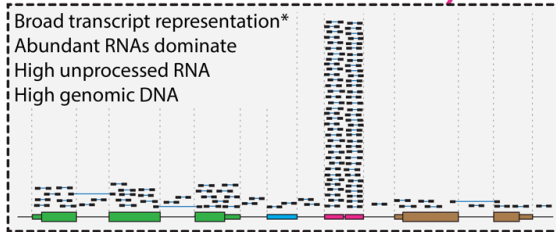
Fragmentation and size selection



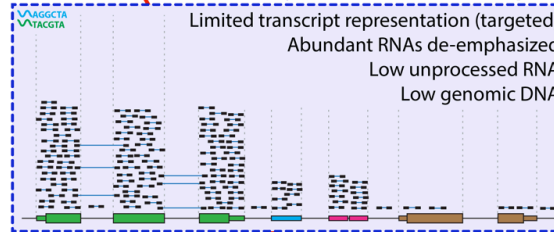
RNA sequence selection/depletion



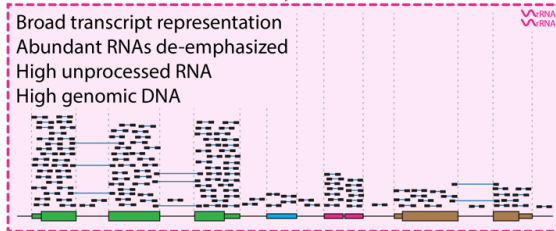
A. Total RNA



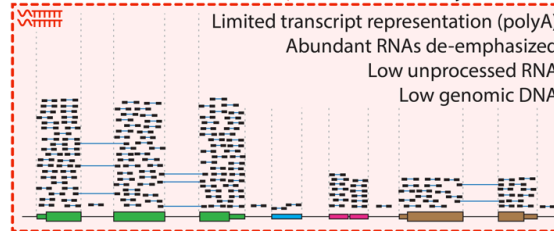
D. cDNA capture



B. rRNA reduction



C. PolyA selection



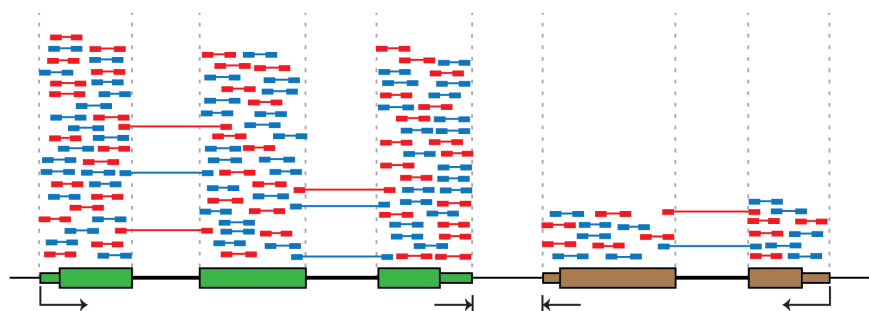
Expected Alignments

Stranded vs. unstranded

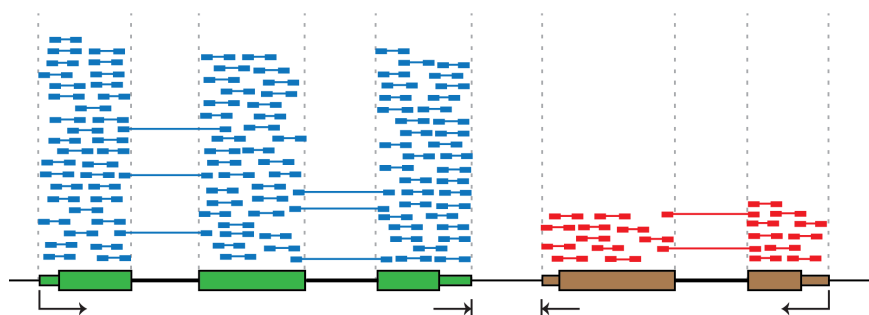
A. Depiction of cDNA fragments from an unstranded library

Legend

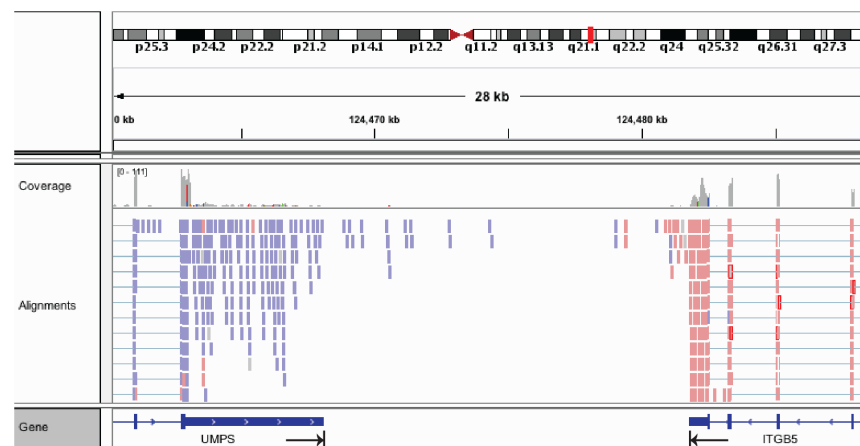
- Transcription start site and direction
- ⌞ PolyA site (transcription end)
- Read sequenced from positive strand (forward)
- Read sequenced from negative strand (reverse)



B. Depiction of cDNA fragments from a stranded library

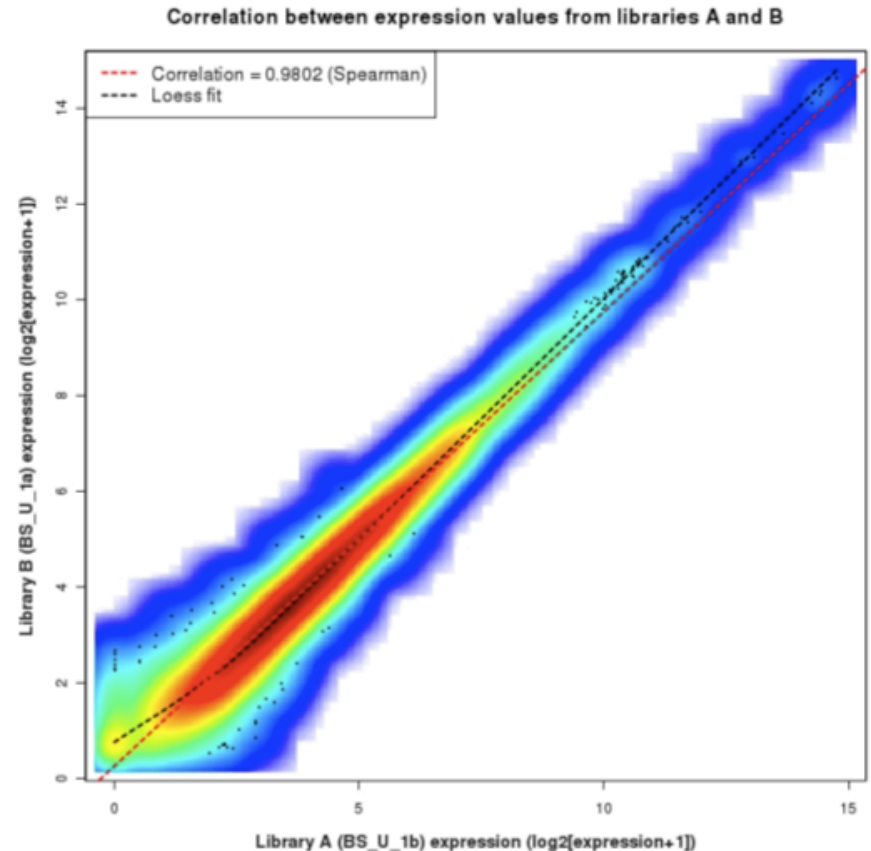


C. Viewing strand of aligned reads in IGV



Replicates

- Technical Replicate
 - Multiple instances of sequence generation
 - Flow Cells, Lanes, Indexes
- Biological Replicate
 - Multiple isolations of cells showing the same phenotype, stage or other experimental condition
 - Some example concerns/challenges:
 - Environmental Factors, Growth Conditions, Time
 - Correlation Coefficient 0.92-0.98



Common analysis goals of RNA-Seq analysis (what can you ask of the data?)

- Gene expression and differential expression
- Alternative expression analysis
- Transcript discovery and annotation
- Allele specific expression
 - Relating to SNPs or mutations
- Mutation discovery
- Fusion detection
- RNA editing

General themes of RNA-seq workflows

- Each type of RNA-seq analysis has distinct requirements and challenges but also a common theme:
 1. Obtain raw data (convert format)
 2. Align/assemble reads
 3. Process alignment with a tool specific to the goal
 - e.g. ‘cufflinks’ for expression analysis, ‘defuse’ for fusion detection, etc.
 4. Post process
 - Import into downstream software (R, Matlab, Cytoscape, Ingenuity, etc.)
 5. Summarize and visualize
 - Create gene lists, prioritize candidates for validation, etc.

BioStar exercise

- Go to the BioStar website:
 - <http://www.biostars.org/>
 - If you do not already have an OpenID (e.g. Google, Yahoo, etc.)
 - Login -> ‘get one’
- Login and set up your user profile
- Tasks:
 - Find a question that seems useful and ‘vote it up’
 - Answer a question [optional]
 - Search for a topic area of interest and ask a question that has not already been asked [optional]

Common questions: Should I remove duplicates for RNA-seq?

- Maybe... more complicated question than for DNA
- Concern.
 - Duplicates may correspond to biased PCR amplification of particular fragments
 - For highly expressed, short genes, duplicates are expected even if there is no amplification bias
 - Removing them may reduce the dynamic range of expression estimates
- If you do remove them, assess duplicates at the level of paired-end reads (fragments) not single end reads

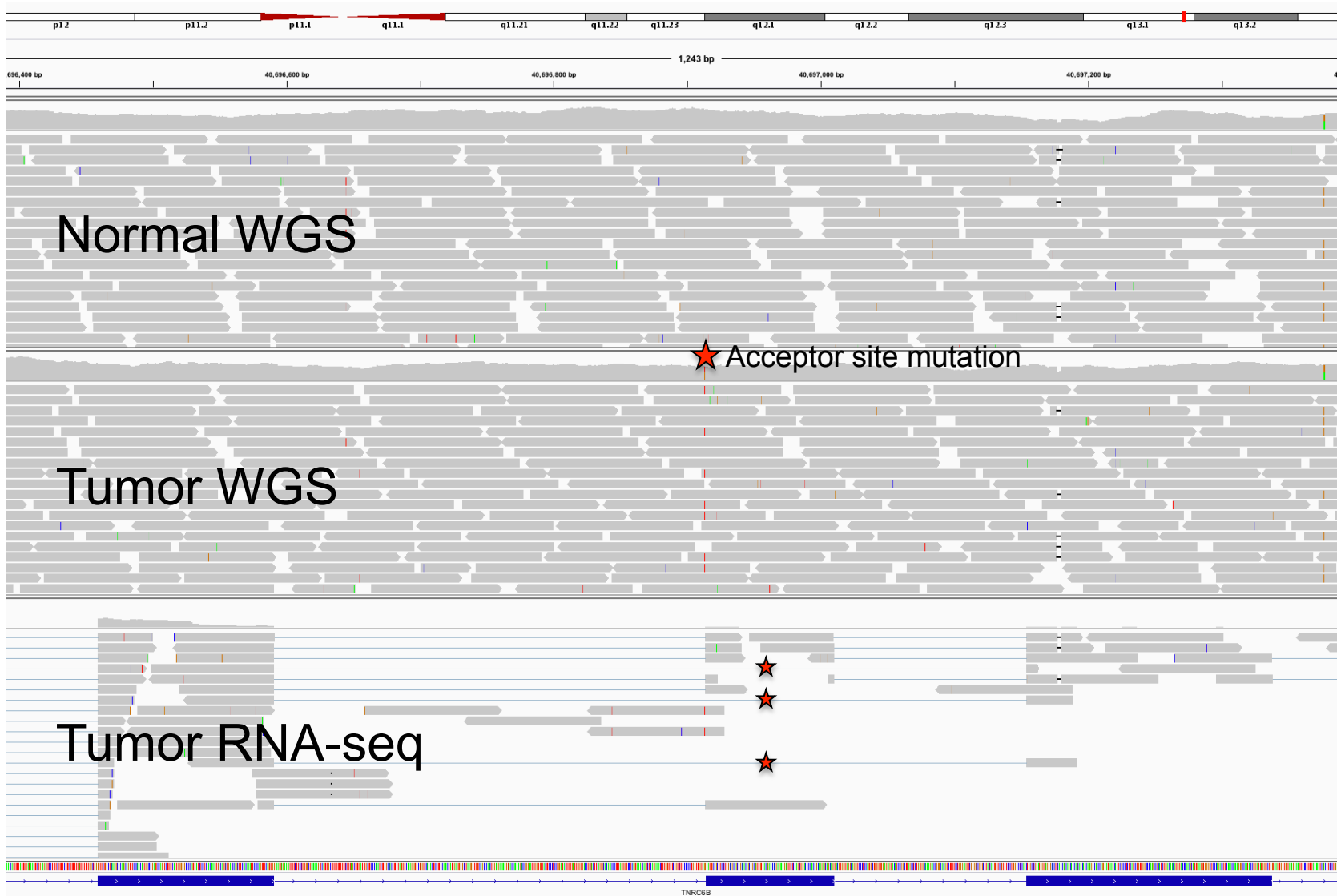
Common questions: How much library depth is needed for RNA-seq?

- Depends on a number of factors:
 - Question being asked of the data. Gene expression? Alternative expression? Mutation calling?
 - Tissue type, RNA preparation, quality of input RNA, library construction method, etc.
 - Sequencing type: read length, paired vs. unpaired, etc.
 - Computational approach and resources
- Identify publications with similar goals
- Pilot experiment
- Good news: 1-2 lanes of recent Illumina HiSeq data should be enough for most purposes

Common questions: What mapping strategy should I use for RNA-seq?

- Depends on read length
- < 50 bp reads
 - Use aligner like BWA and a genome + junction database
 - Junction database needs to be tailored to read length
 - Or you can use a standard junction database for all read lengths and an aligner that allows substring alignments for the junctions only (e.g. BLAST ... slow).
 - Assembly strategy may also work (e.g. Trans-ABYSS)
- > 50 bp reads
 - Spliced aligner such as Bowtie/TopHat

Visualization of spliced alignment of RNA-seq data

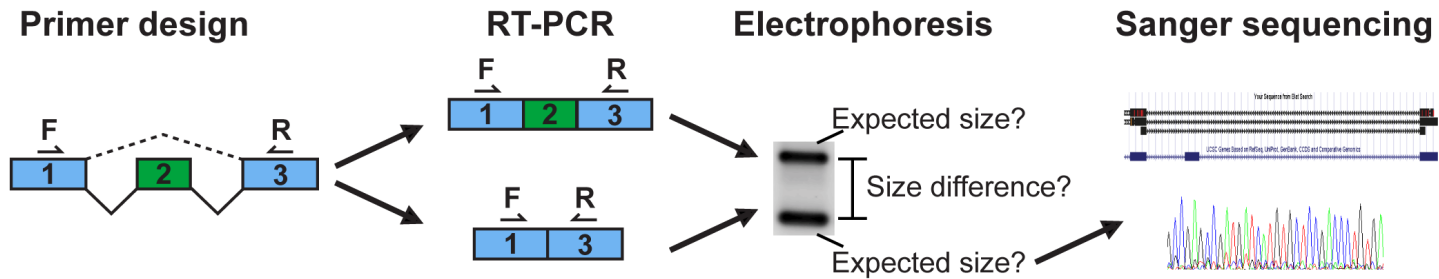


IGV screenshot

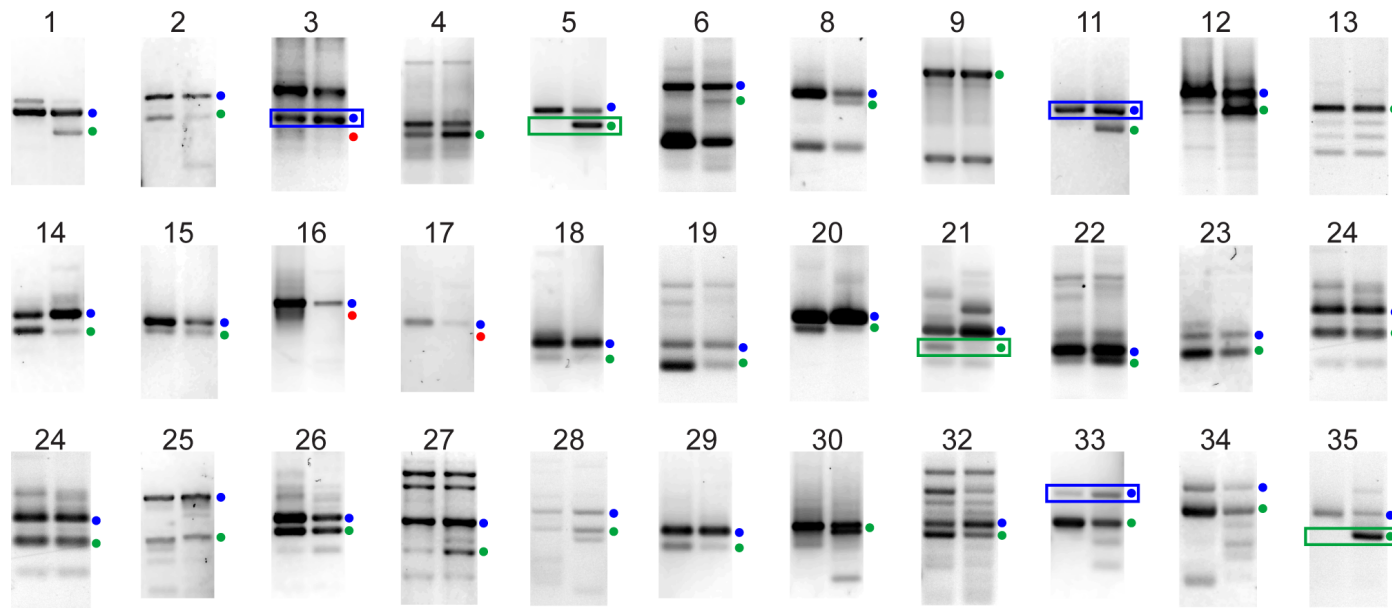
Common questions: how reliable are expression predictions from RNA-seq?

- Are novel exon-exon junctions real?
 - What proportion validate by RT-PCR and Sanger sequencing?
- Are differential/alternative expression changes observed between tissues accurate?
 - How well do DE values correlate with qPCR?
- 384 validations
 - qPCR, RT-PCR, Sanger sequencing
- See ALEXA-Seq publication for details:
 - Also includes comparison to microarrays
 - Griffith et al. *Alternative expression analysis by RNA sequencing*. Nature Methods. 2010 Oct;7(10):843-847.

Validation (qualitative)

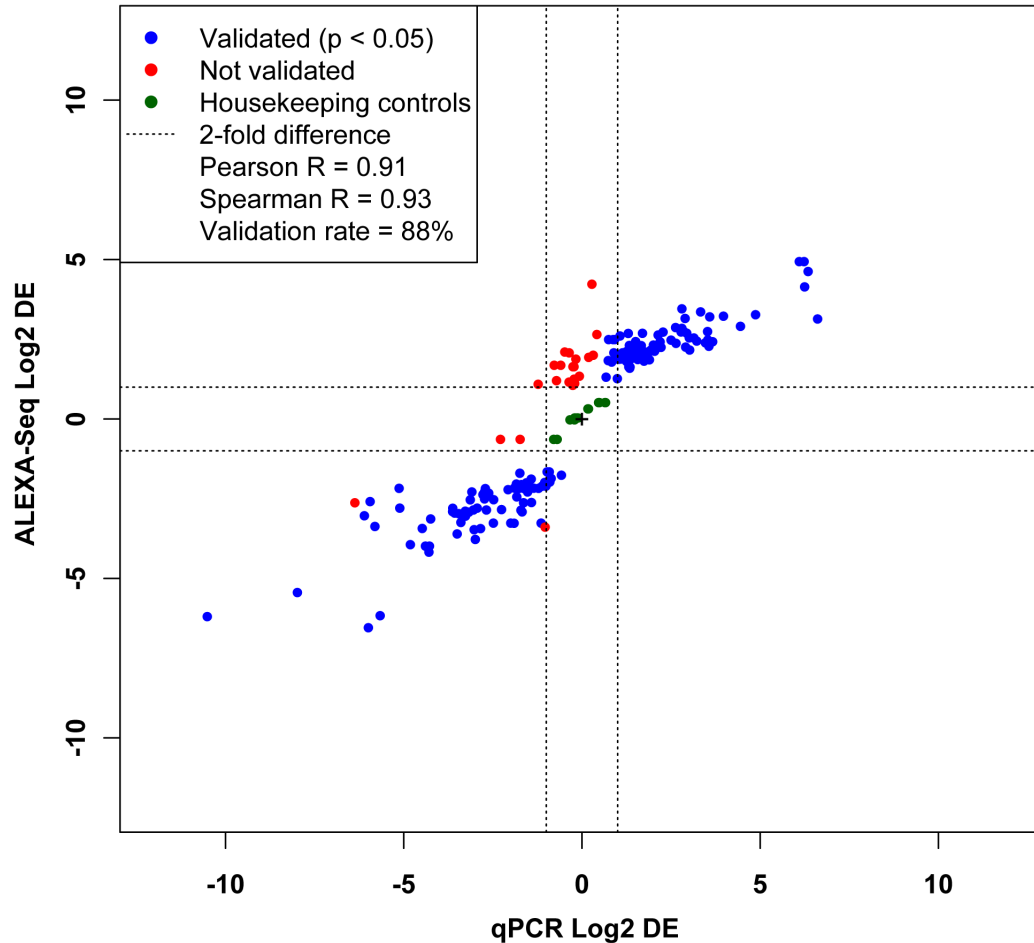
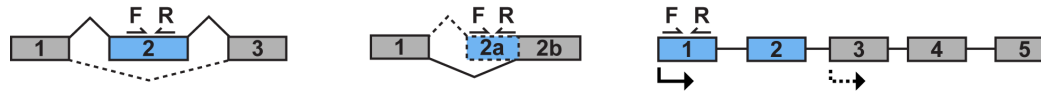


● Canonical isoform ● Alternative isoform ● Failure (missing band)



33 of 192 assays shown. Overall validation rate = 85%

Validation (quantitative)



qPCR of 192
exons identified
as alternatively
expressed by
ALEXA-Seq

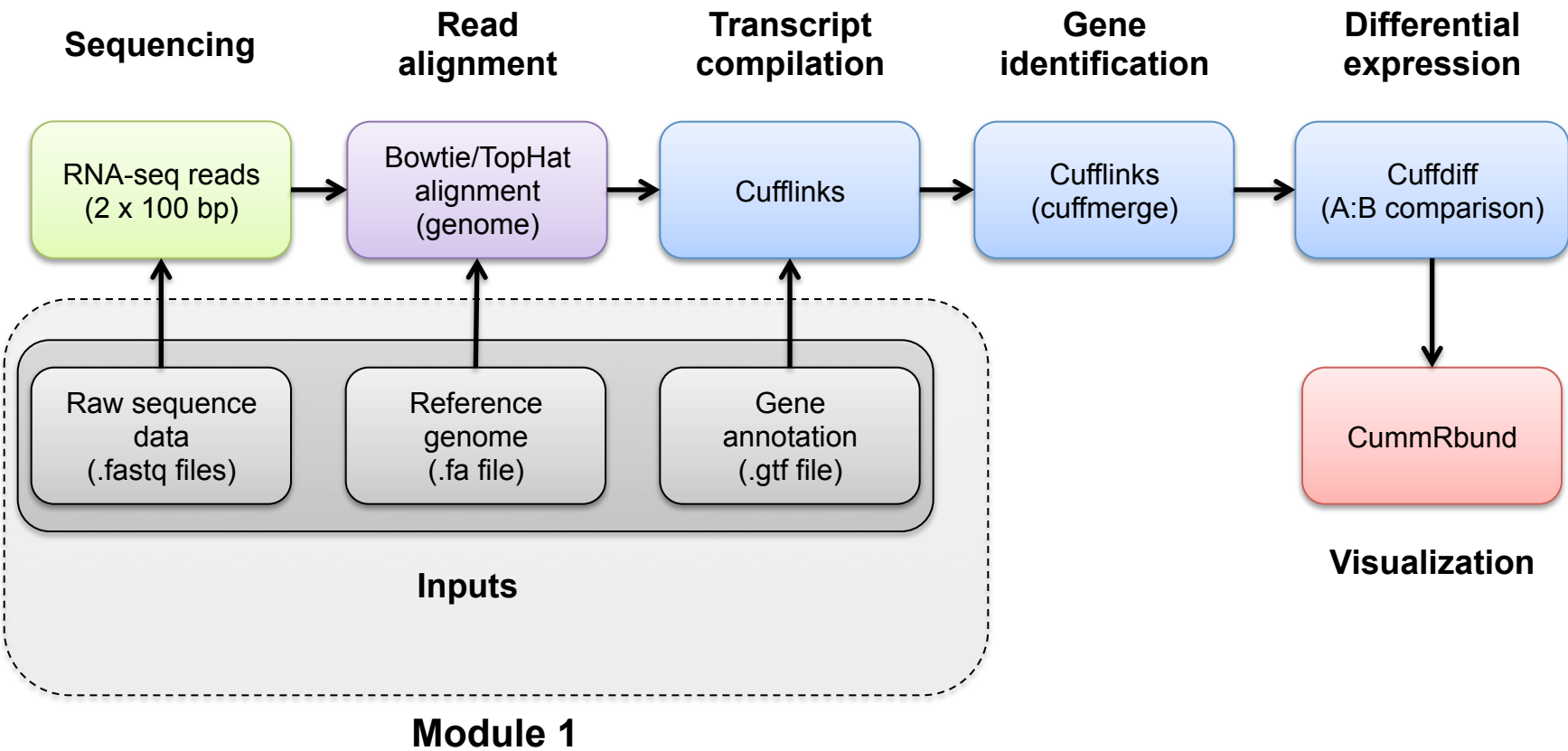
Validation rate = 88%

Common questions: What if I don't have a reference genome for my species?

- Have you considered sequencing the genome of your species?
- If that is not practical or you simply prefer a transcript discovery approach that does not rely on prior knowledge of the genome or transcriptome there are some tools available ...
 - Unfortunately de novo transcriptome assembly is beyond the scope of this workshop
 - The good news is that the skills you learn here will help you figure out how to install and run those tools yourself

Introduction to tutorial (Module 1)

Bowtie/TopHat/Cufflinks/Cuffdiff RNA-seq Pipeline



We are on a Coffee Break & Networking Session

