

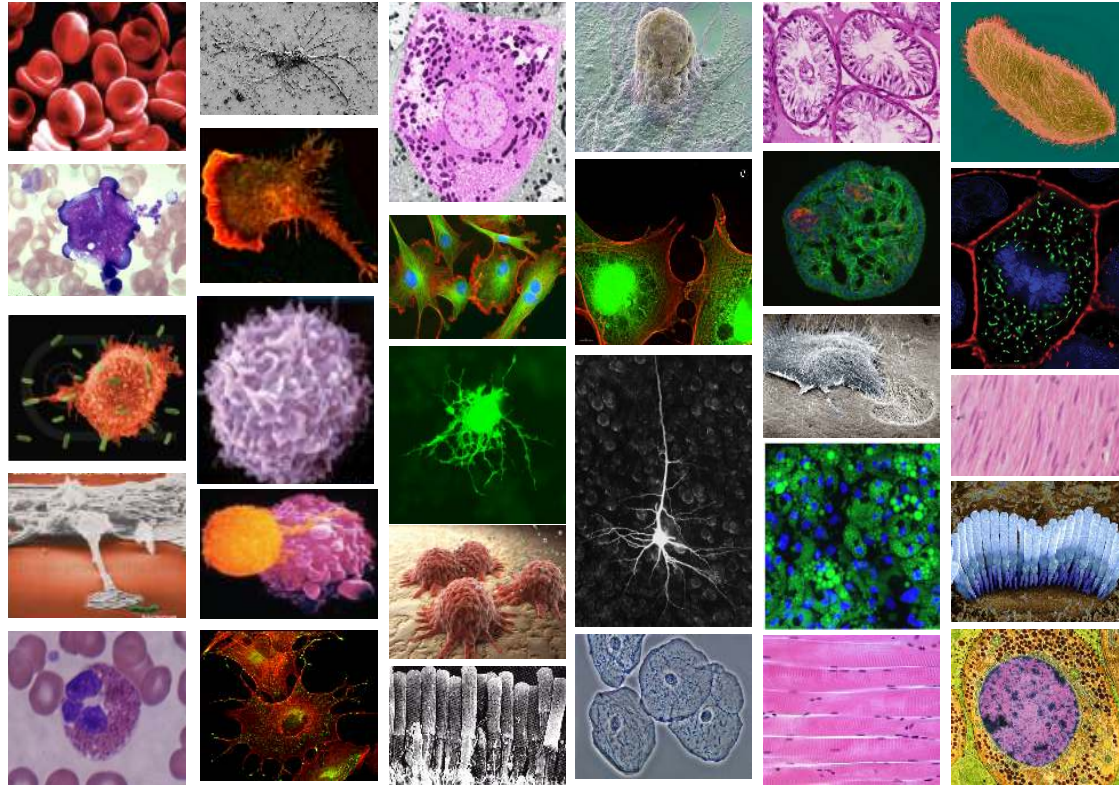
Short read sequence analysis

Manuel Garber
Krumlov 2014

Overview of the session

- Explaining diversity: Transcriptional regulation
 - A short story from our recent work
- Diving into RNA-Seq
 - The different BLA-Seq libraries. A common theme
 - Read mapping (alignment): Placing short reads in the genome
 - Reconstruction: Finding the regions that originated the reads
 - Quantification:
 - Assigning scores to regions
 - Finding regions that are differentially represented between two or more samples.
 - How much depth?!
- RNA-Seq Vignette: non-coding RNA evolution

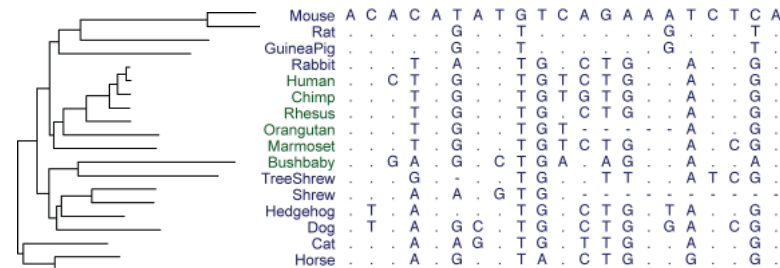
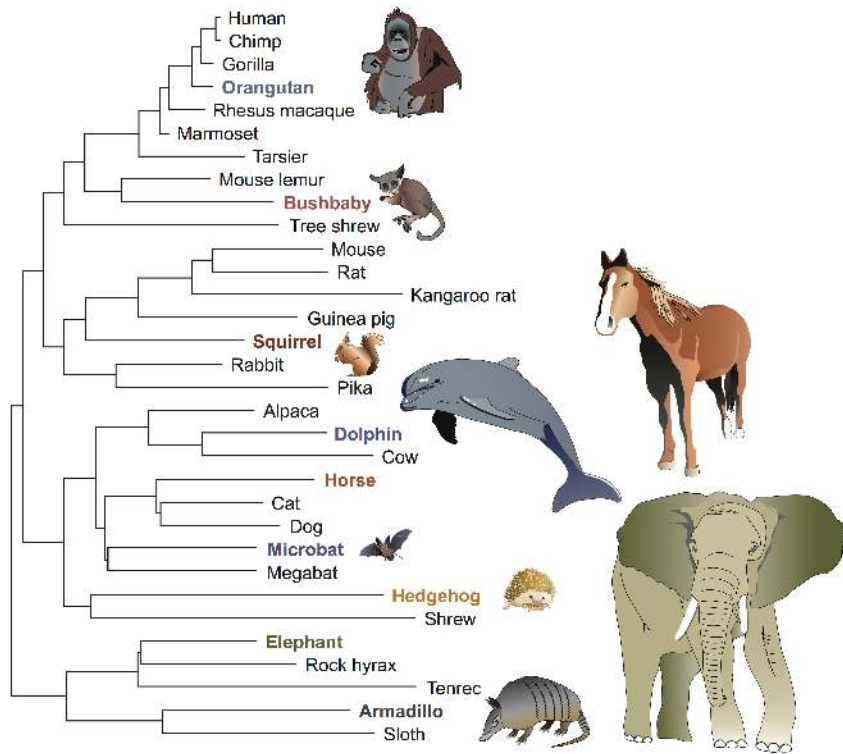
[illegible]



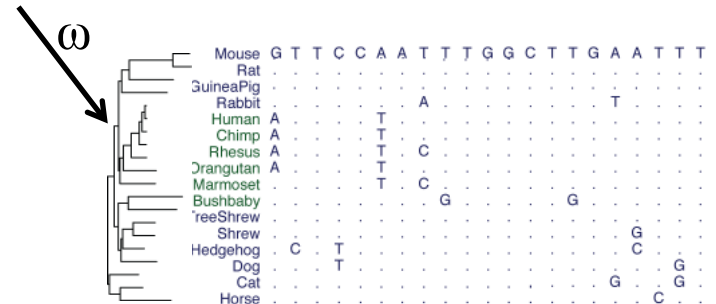
However, all this diversity arises from the same genome sequence!
Proteins are very conserved across vertebrates, what is the driving force of variability?

Sequence-based strategy: Comparative genomics

Technique: Identify regions undergoing selection

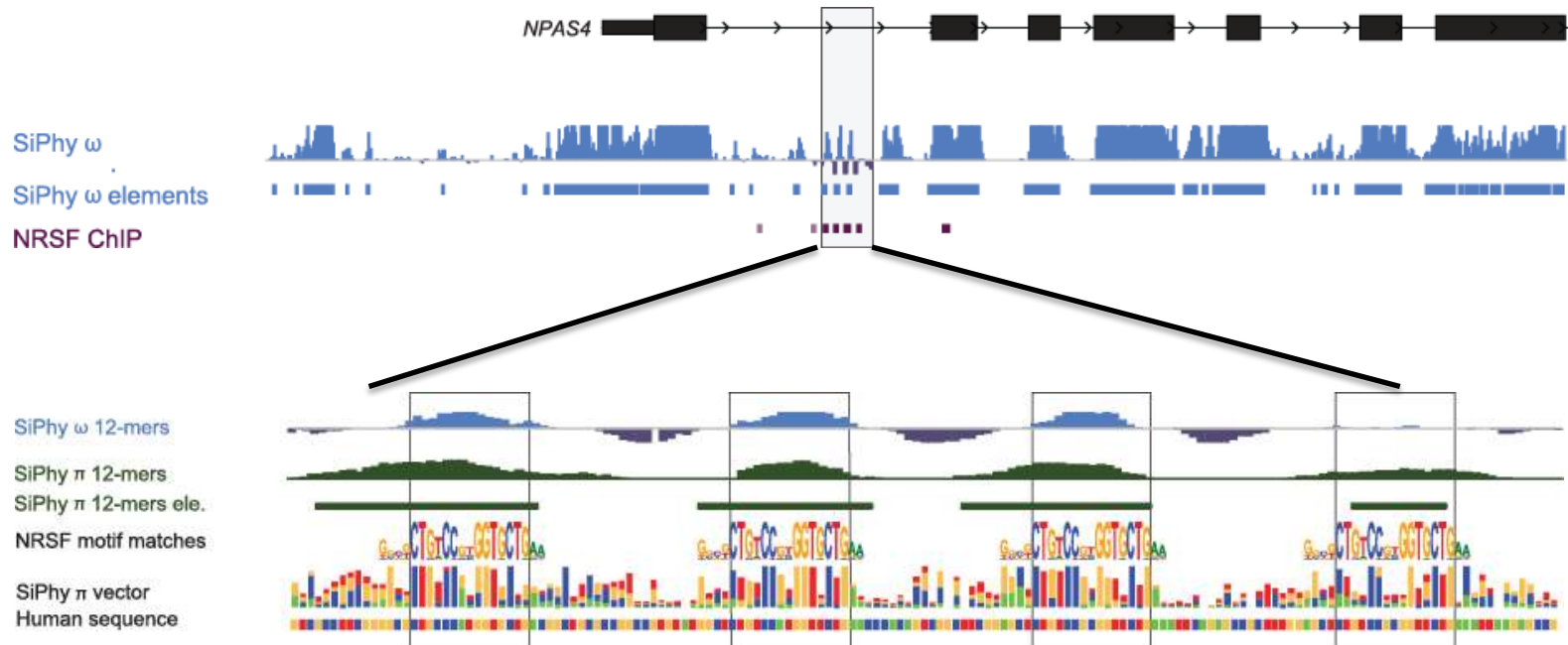


Neutral



Under Selection

In some cases resolution is astonishing

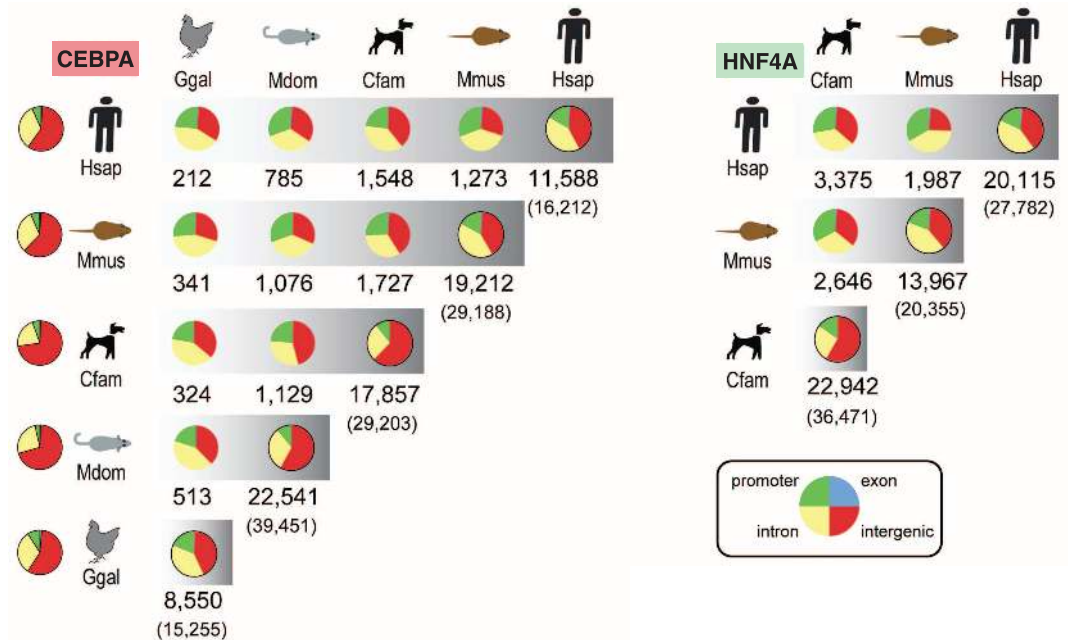


However, most binding is not conserved

REPORTS

Five-Vertebrate ChIP-seq Reveals the Evolutionary Dynamics of Transcription Factor Binding

Dominic Schmidt,^{1,2*} Michael D. Wilson,^{1,2*} Benoit Ballester,^{3*} Petra C. Schwalie,³ Gordon D. Brown,¹ Aileen Marshall,^{1,4} Claudia Kutter,¹ Stephen Watt,¹ Celia P. Martinez-Jimenez,⁵ Sarah Mackay,⁶ Iannis Talianidis,⁵ Paul Flicek,^{3,7}† Duncan T. Odom^{1,2}†



Transcriptional regulation may be a key driver of diversity and definitively of cell type diversity

Enhancers poorly conserved, cell type specific



Chromatin stretch enhancer states drive cell-specific gene regulation and harbor human disease risk variants

Stephen C. J. Parker^{a,1}, Michael L. Stitzel^{a,1}, D. Leland Taylor^a, Jose Miguel Orozco^a, Michael R. Erdos^a, Jennifer A. Akiyama^b, Kelly Lammerts van Bueren^c, Peter S. Chines^a, Narisu Narisu^a, NISC Comparative Sequencing Program^a, Brian L. Black^c, Axel Visel^{b,d}, Len A. Pennacchio^{b,d}, and Francis S. Collins^{a,2}

LETTERS

Histone modifications at human enhancers reflect global cell-type-specific gene expression

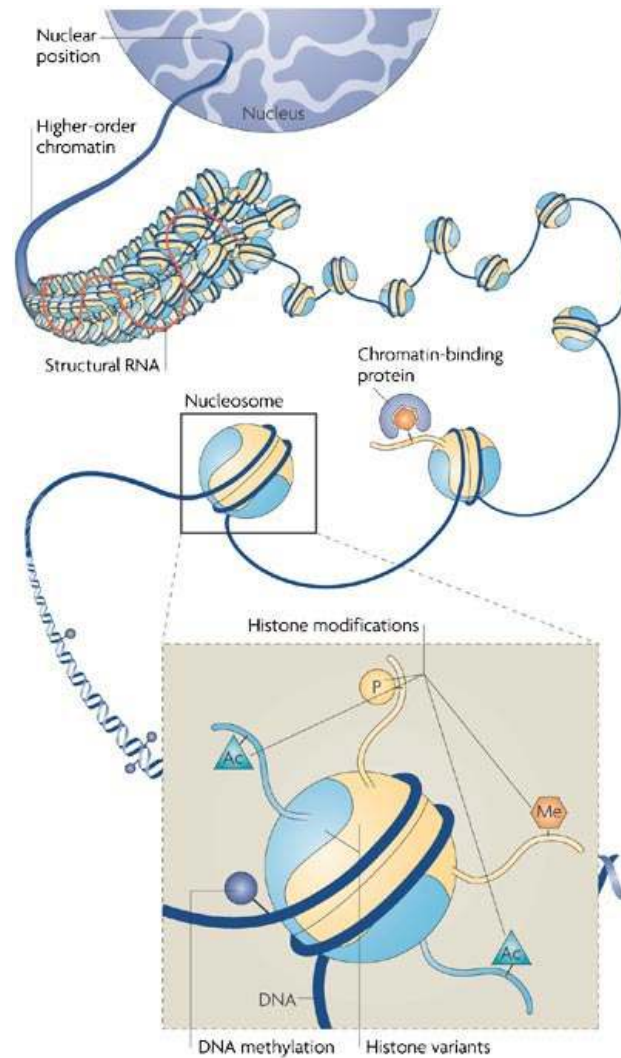
Nathaniel D. Heintzman^{1,2*}, Gary C. Hon^{1,3*}, R. David Hawkins^{1*}, Pouya Kheradpour⁵, Alexander Stark^{5,6}, Lindsey F. Harp¹, Zhen Ye¹, Leonard K. Lee¹, Rhona K. Stuart¹, Christina W. Ching¹, Keith A. Ching¹, Jessica E. Antosiewicz-Bourget⁷, Hui Liu⁸, Xinmin Zhang⁸, Roland D. Green⁸, Victor V. Lobanenkov⁹, Ron Stewart⁷, James A. Thomson^{7,10}, Gregory E. Crawford¹¹, Manolis Kellis^{5,6} & Bing Ren^{1,4}

Enhancer elements are poorly conserved, are cell type specific, How do we find them?

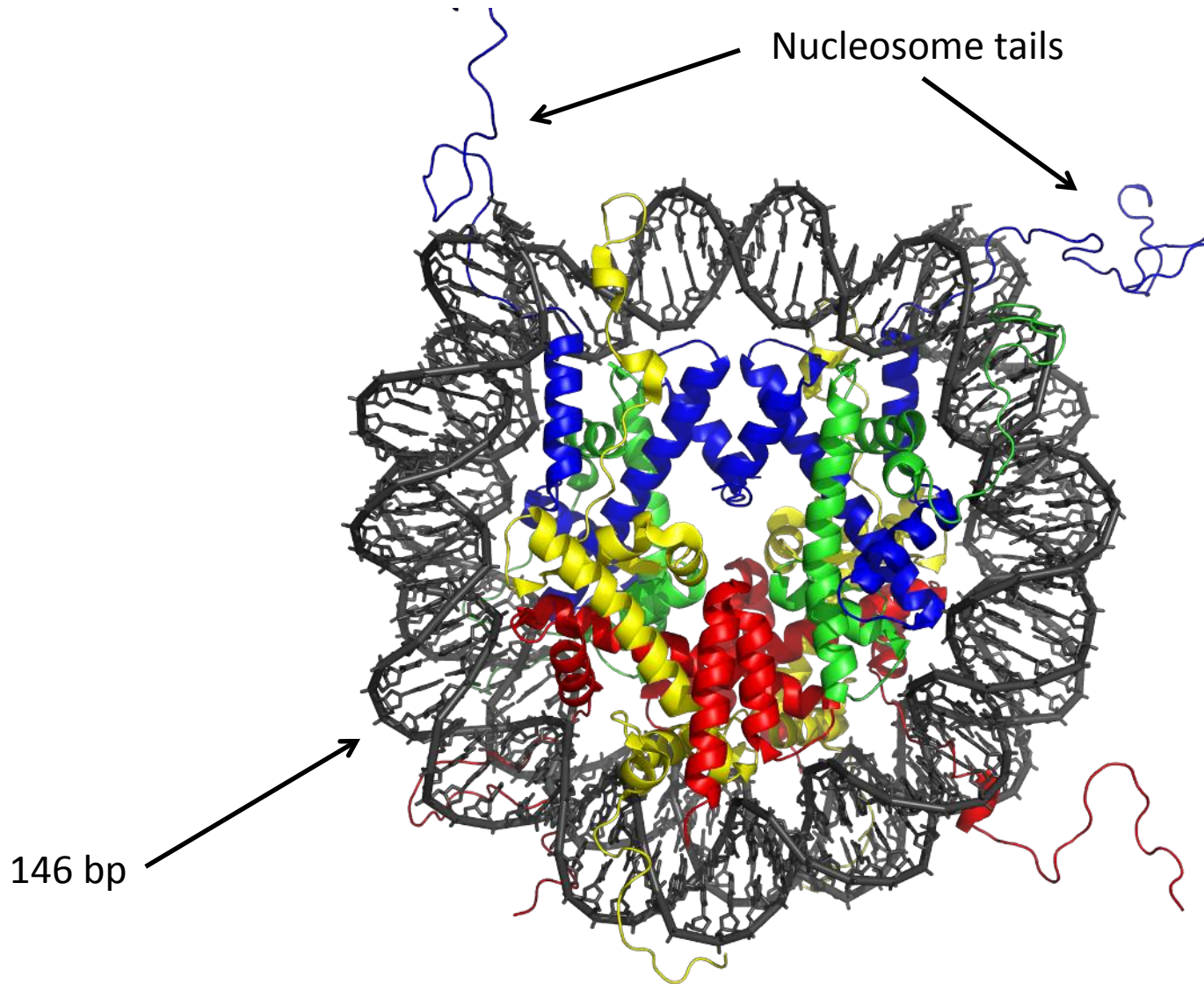
Transcription factor regulation

See <http://vimeo.com/30034882>

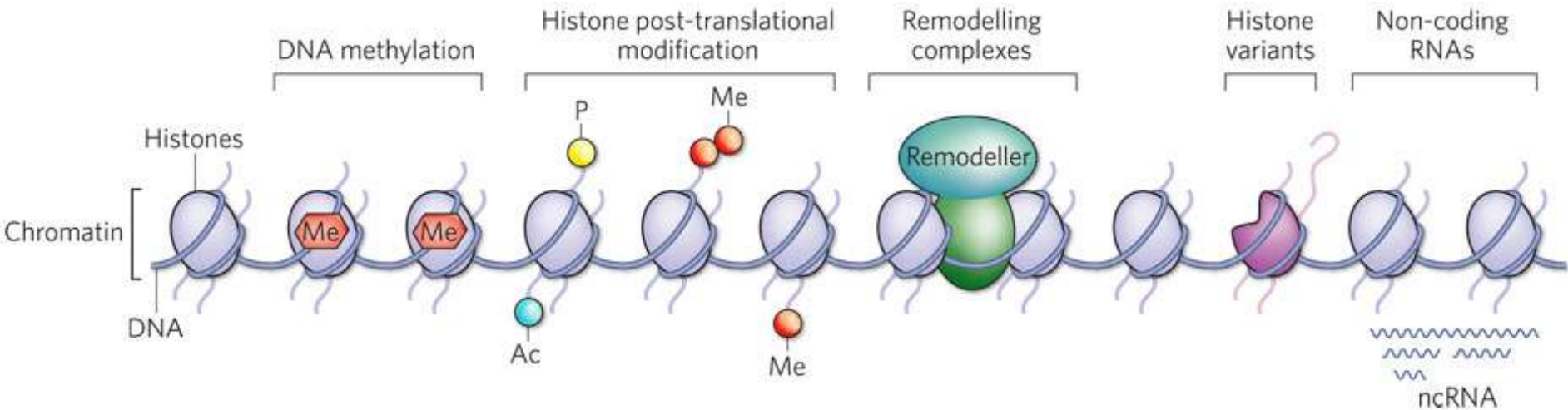
DNA is not naked



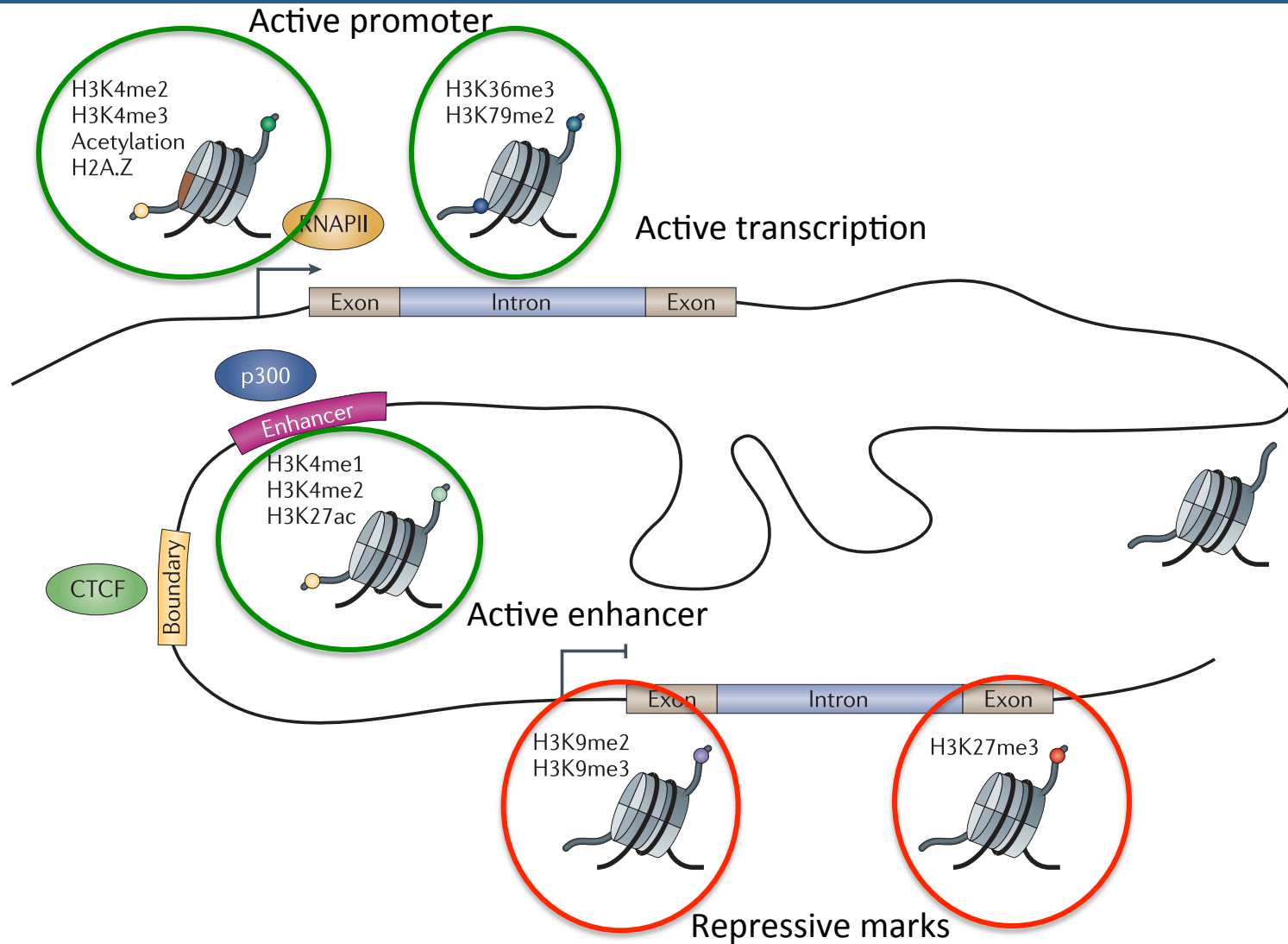
Nucleosomes interact with nuclear factors through tails



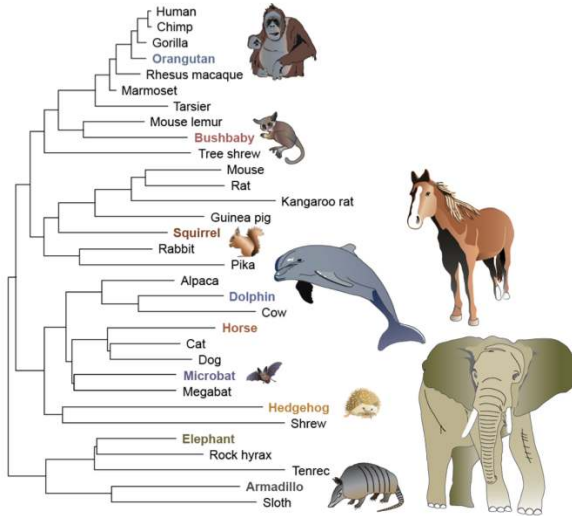
Cell identity is determined by its epigenetic state



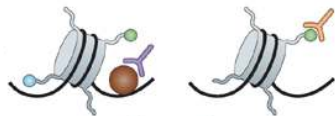
Which controls the genome functional elements



We seek to map and functionally characterize elements



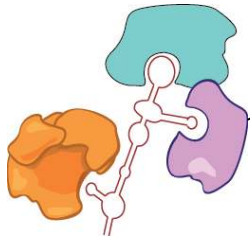
Estimate the “functional genome” by finding what is under selection



ChIP



RNA



RNA-Protein interactions

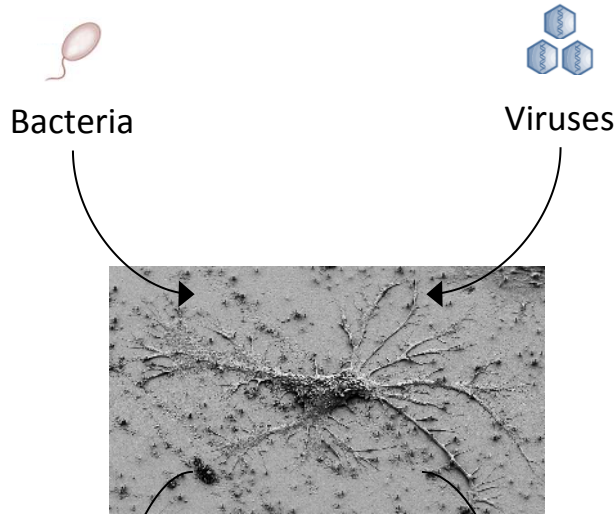


- Develop informatics tools for new methods
- Develop models of transcriptional regulation
- Develop models of epigenetic interactions
- Evolution of large non-coding RNAs

We want to ultimately understand the cell circuits of the cell

For example: wiring of innate immune cells

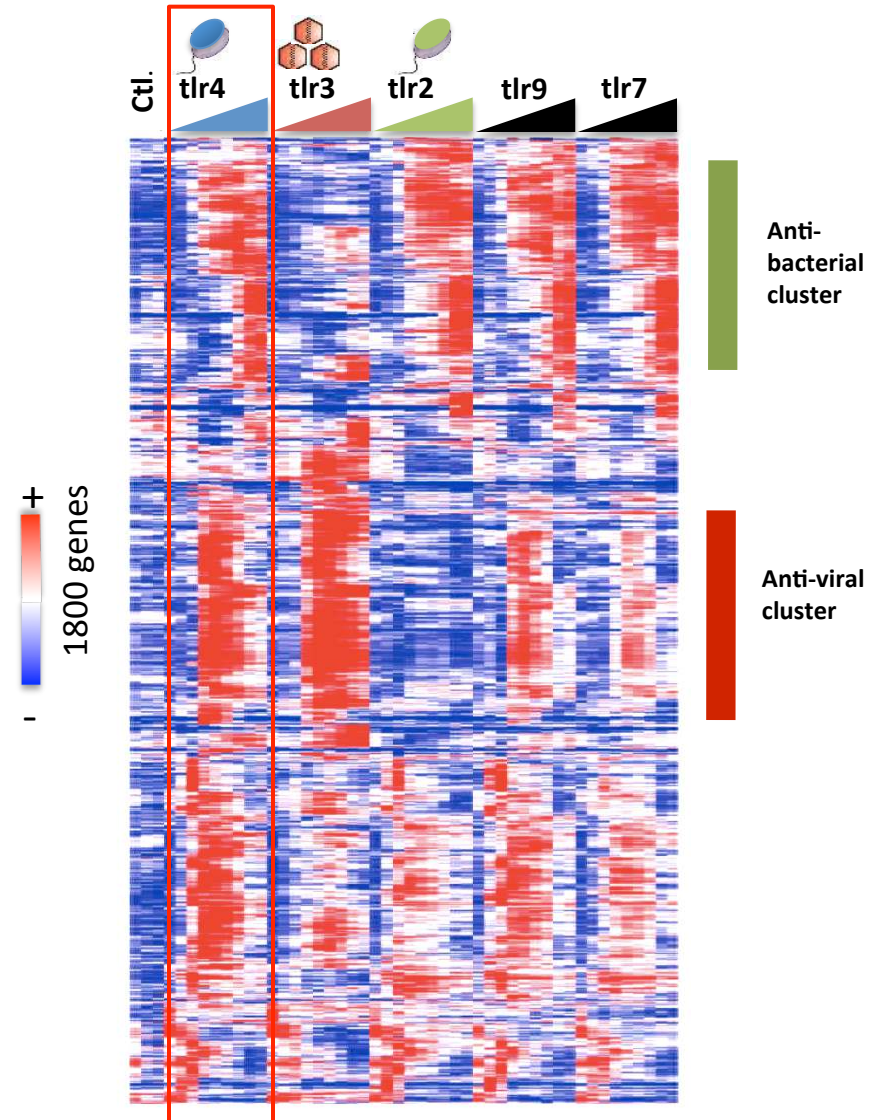
Input



Output

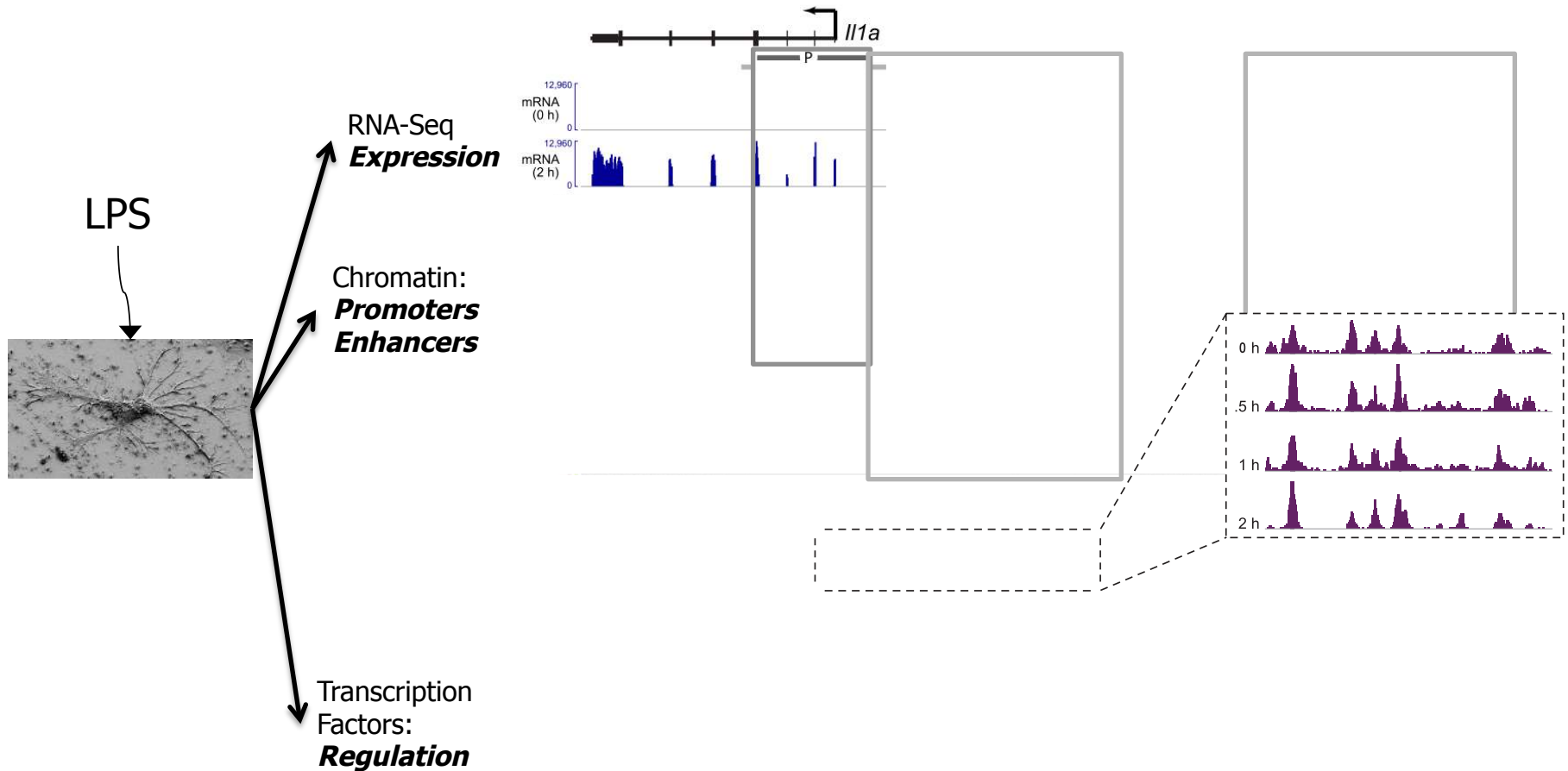
Anti-bacterial
program
(inflammation)

Anti-viral
program
(interferon)



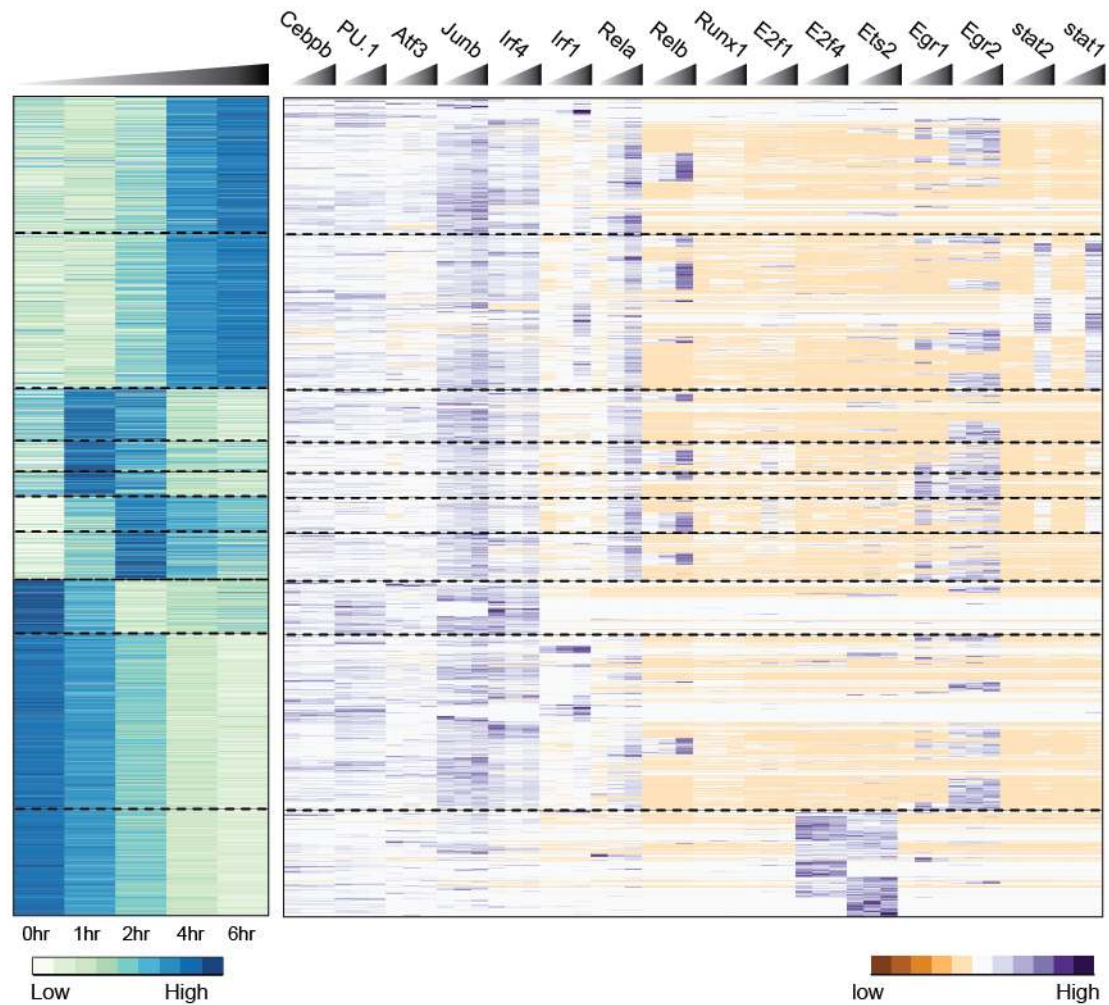
How is this response controlled?

Chip-Seq + RNA-Seq to map and relate components



Sequencing libraries allow us to map output, state and the circuit of the cell

Into specific functional sets



Late inflammation

Anti-viral genes

No enrichment
Early inflammation

Sequencing: applications

Counting applications

- Profiling
 - microRNAs
 - Immunogenomics
 - Transcriptomics
 - Epigenomics
 - Map histone modifications
 - Map DNA methylation
 - 3D genome conformation
 - Nucleic acid Interactions
- Cancer genomics
 - Map translocations, CNVs, structural changes
 - Profile somatic mutations
 - Genome assembly
 - Ancient DNA (Neanderthal)
 - Pathogen discovery
 - Metagenomics

Polymorphism/mutation discovery

- Bacteria
- Genome dynamics
- Exon (and other target) sequencing
- Disease gene sequencing
- Variation and association studies
- Genetics and gene discovery



Sequencing libraries to probe the genome

- RNA-Seq
 - Transcriptional output
 - Annotation
 - miRNA
 - Ribosomal profiling
- ChIP-Seq
 - Nucleosome positioning
 - Open/closed chromatin
 - Transcription factor binding
- CLIP-Seq
 - Protein-RNA interactions
- Hi-C
 - 3D genome conformation

RNA-Seq libraries I: “Standard” full-length

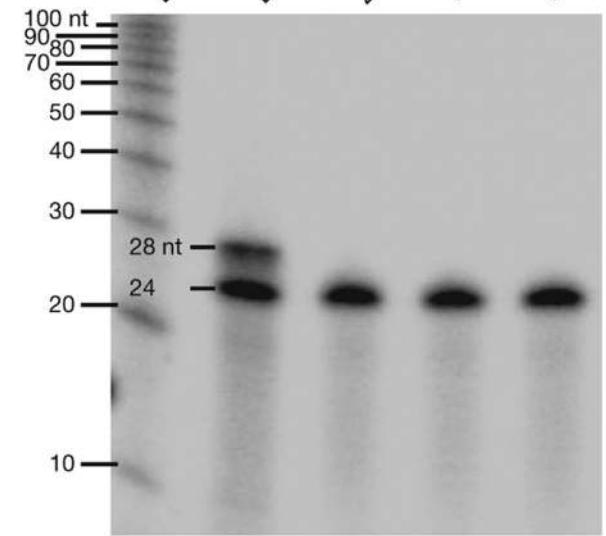
- “Source: intact, **high qual.** RNA (polyA selected or ribosomal depleted)
- RNA → cDNA → sequence
- Uses:
 - Annotation. Requires high depth, paired-end sequencing. ~50 mill
 - Gene expression. Requires low depth, single end sequence, ~ 5-10 mill
 - Differential Gene expression. Requires ~ 5-10 mill, at least 3 replicates, single end

RNA-Seq libraries II: End-sequence libraries

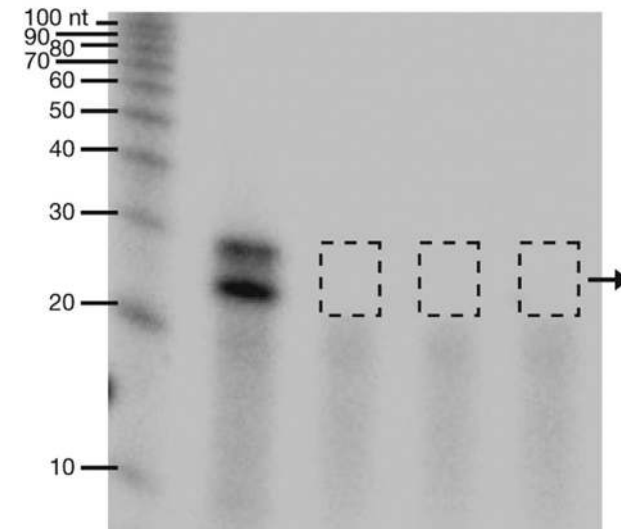
- Target the start or end of transcripts.
- Source: End-enriched RNA
 - Fragmented then selected
 - Fragmented then enzymatically purified
- Uses:
 - Annotation of transcriptional start sites
 - Annotation of 3' UTRs
 - Quantification and gene expression
 - Depth required 3-8 mill reads
 - Low quality RNA samples

RNA-Seq libraries III: Small RNA libraries

- Source: size selected RNA
- Uses: miRNA, piRNA annotation and quantification
 - Short single end 30-50 bp reads
 - Depth: 5-10 mill reads



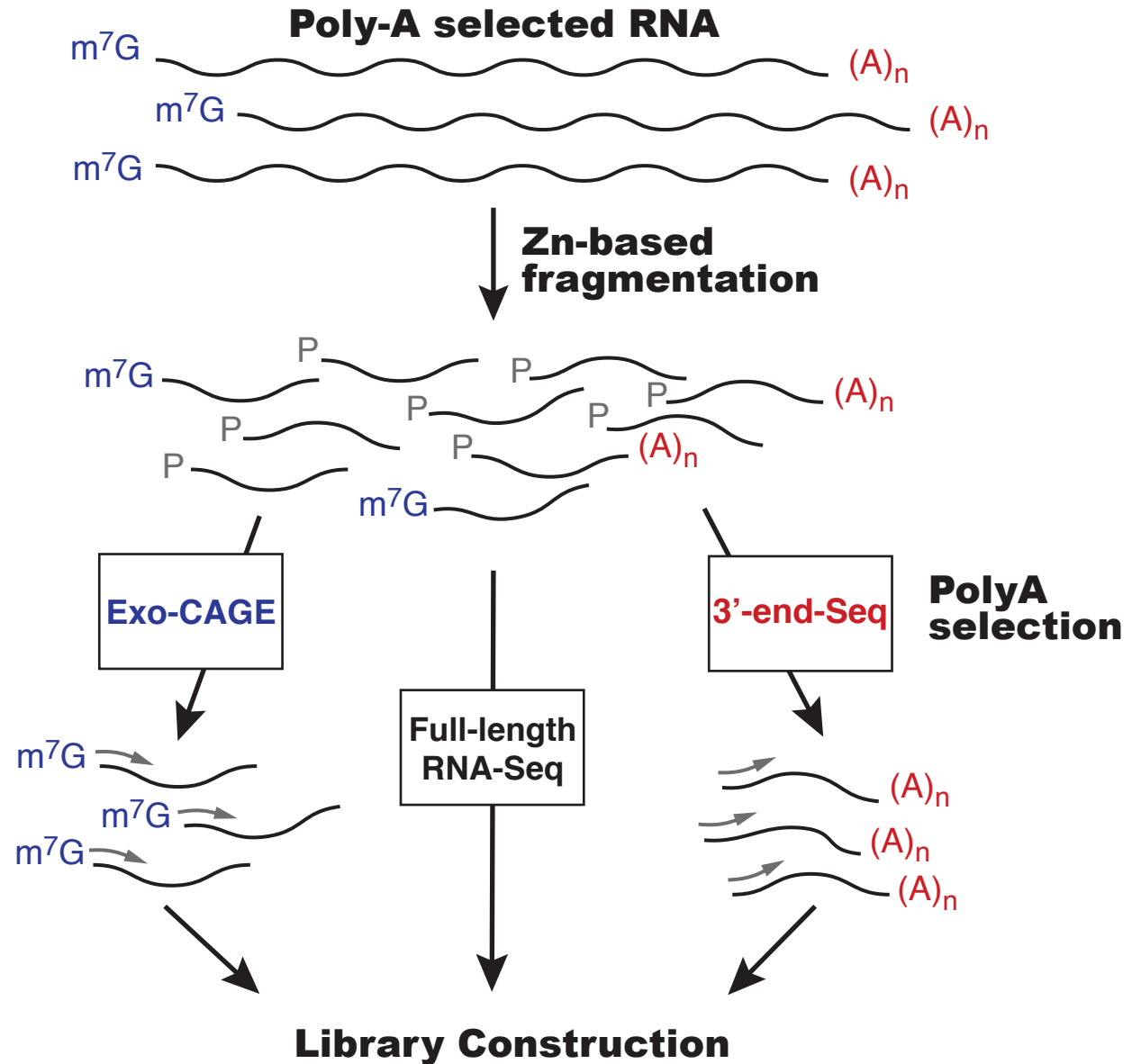
↓ Size-select small RN
to clone and sequen



When you need both annotation and quantification

- Attempt three replicates per condition
- Pool libraries to obtain ~15 mill reads per replicate
- Sequence using paired ends
- Analysis:
 - Merge replicate alignments for annotation
 - Split alignments for differential expression analysis

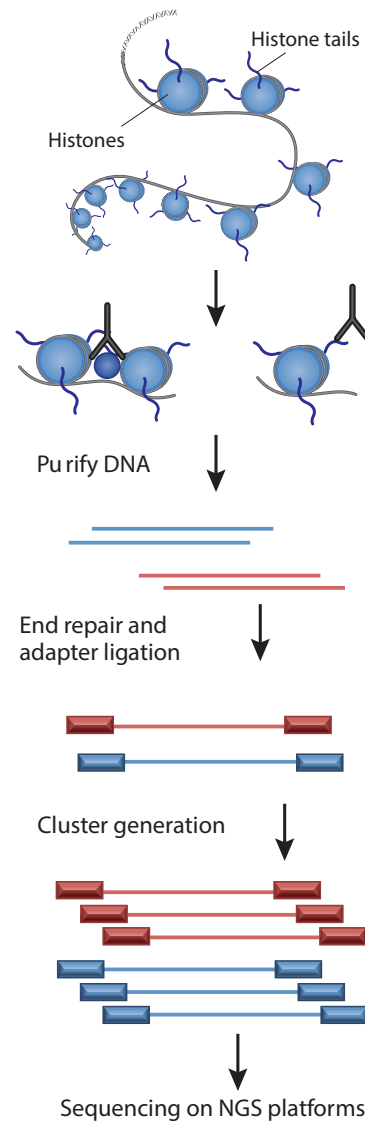
RNA-Seq libraries: Summary



ChIP-Seq libraries:

- Crosslinked, immunoprecipitated DNA
- DNA → sequence
- Uses:
 - Mapping nucleosomes (huge depth required)
 - Mapping histones with specific tails
 - Mapping transcription factor sites
 - Requires ~ 5-10 mill, at least 2-3 replicates, single end

ChIP-Seq protocol



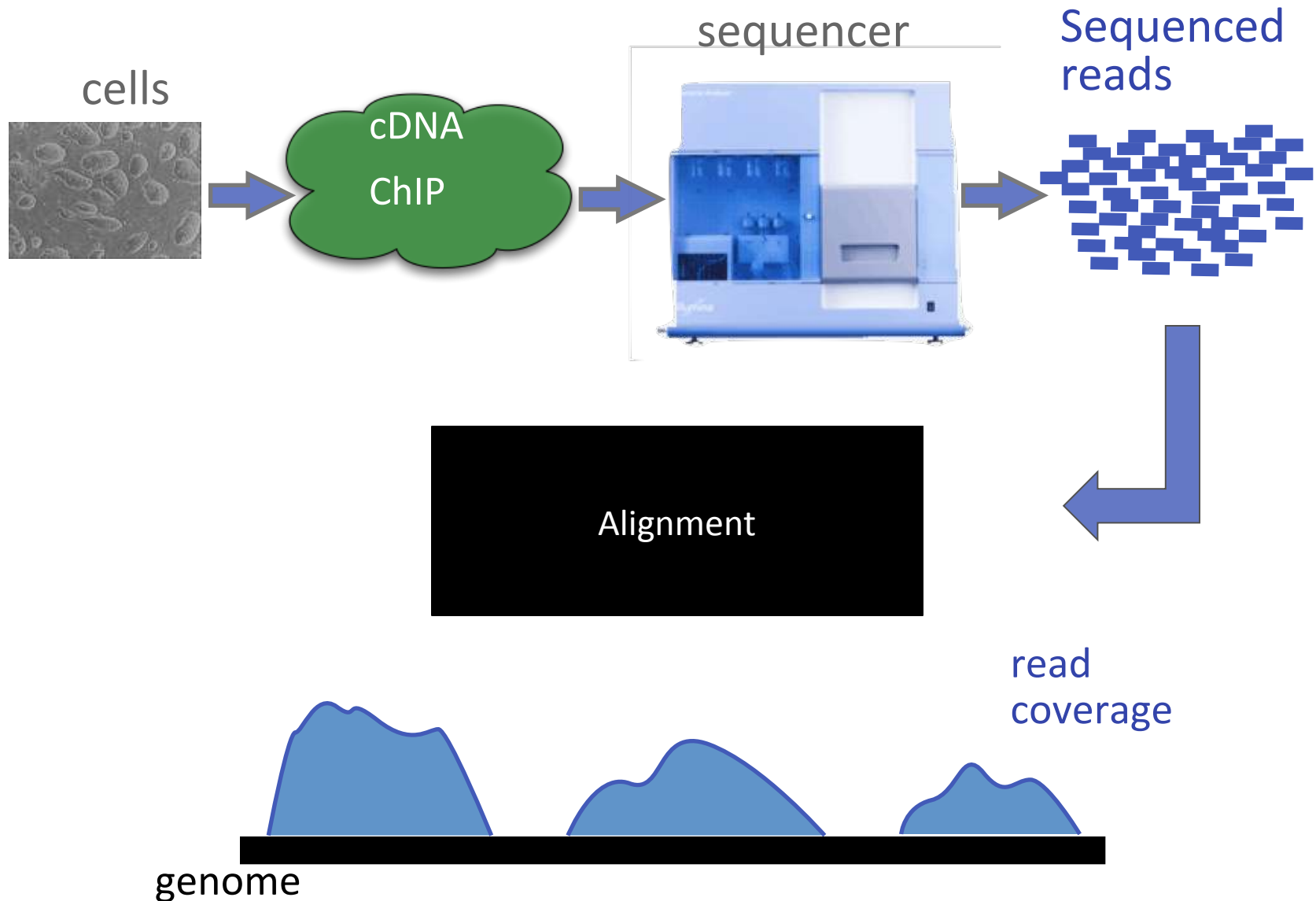
CLIP-Seq libraries and ribosome footprinting:

- Crosslinked, immunoprecipitated **RNA**
 - RNA → cDNA → sequence
 - Uses:
 - Mapping RNA/protein interactions
 - Find miRNA regulated transcripts
 - Mapping translation rates
 - Annotate ORFs
-
- The diagram uses curly braces to group the 'Uses' list items. A brace on the right side groups the first two items ('Mapping RNA/protein interactions' and 'Find miRNA regulated transcripts') and is labeled 'CLIP-Seq'. Another brace on the right side groups the last two items ('Mapping translation rates' and 'Annotate ORFs') and is labeled 'Ribosomal profiling'.

Analysis of counting data requires 3 broad tasks

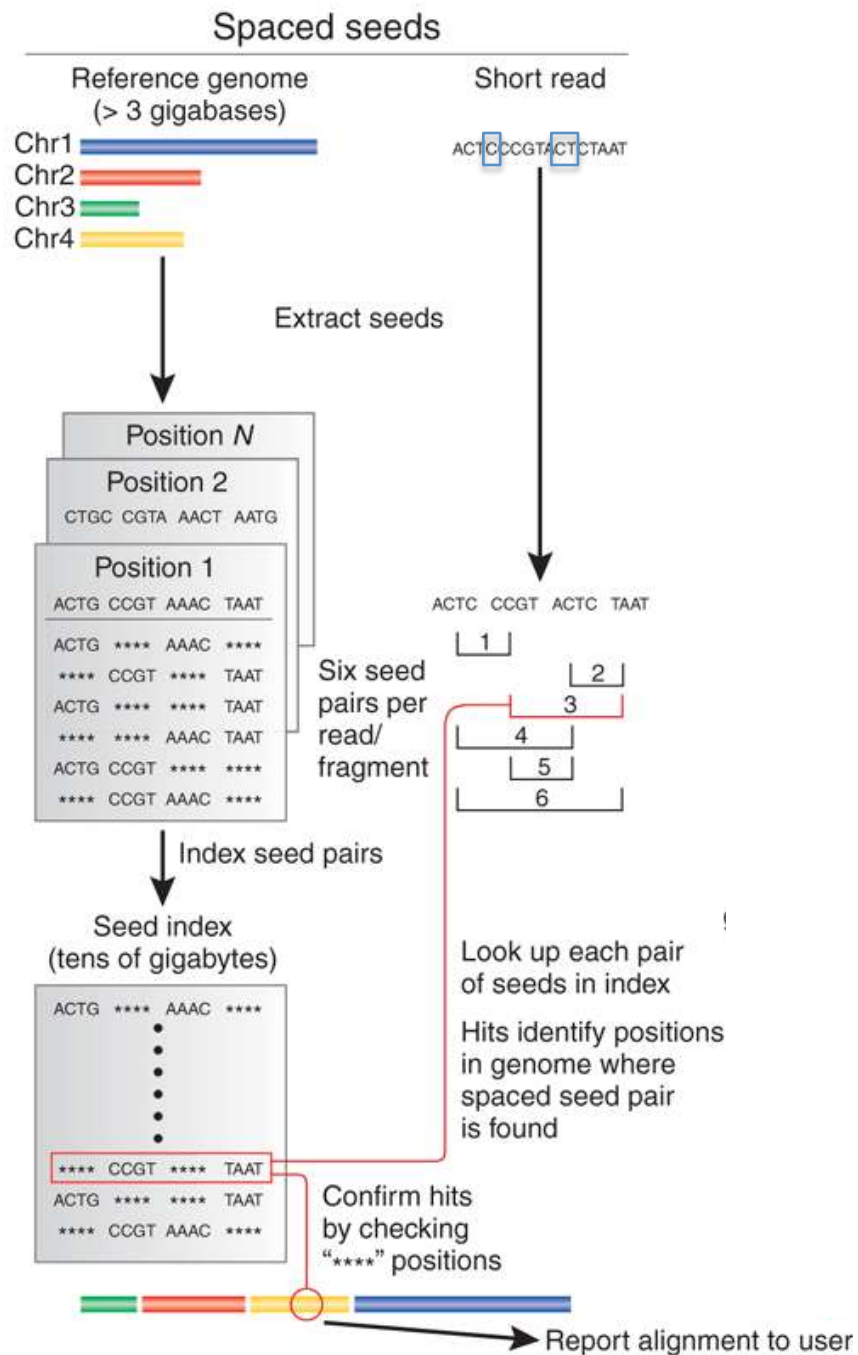
- Read mapping (alignment): Placing short reads in the genome
- Reconstruction: Finding the regions that originated the reads
- Quantification:
 - Assigning scores to regions
 - Finding regions that are differentially represented between two or more samples.

Once sequenced the problem becomes computational



Analysis of counting data requires 3 broad tasks

- Read mapping (alignment): Placing short reads in the genome
- Reconstruction: Finding the regions that originated the reads
- Quantification:
 - Assigning scores to regions
 - Finding regions that are differentially represented between two or more samples.



Spaced seed alignment – Hashing the genome

G:

accgattgactgaatgg

 ccttaaggggtcctagttgcgagacacatgctg

accgtgggattg

aatg

Store spaced seed positions

accg	attg	****	****	→	0
accg	****	actg	****	→	0
accg	****	****	aatg	→	0,45
****	attg	actg	****	→	0
****	attg	****	aatg	→	0
****	****	actg	aatg	→	0

ccga	ttga	****	****	→	1
ccga	****	ctga	****	→	1
ccga	****	****	atgg	→	1
****	ttga	ctga	****	→	1
****	ttga	****	atgg	→	1
****	****	ctga	atgg	→	1

Spaced seed alignment – Mapping reads

G: accgattgactgaatggccttaaggggtcctagttgcgagacacatgctgaccgtgggattgaatg.....

accg	attg	****	****	→	0
accg	****	actg	****	→	0
accg	****	****	aatg	→	0,45
****	attg	actg	****	→	0
****	attg	****	aatg	→	0
****	****	actg	aatg	→	0

×

×

✓

×

×

×

q: accg at^ag acc^cg aatg

accgattgactgaatg

accgtgggattgaatg

2 mismatches

5 mismatches

ccga	ttga	****	****	→	1
ccga	****	ctga	****	→	1
ccga	****	****	atgg	→	1
****	ttga	ctga	****	→	1
****	ttga	****	atgg	→	1
****	****	ctga	atgg	→	1

×

×

×

×

×

×

Report position 0

But, how confidence are we in the placement?

$$q_{MS} = -10 \log_{10} P(\text{read is wrongly mapped})$$

Mapping quality

What does $q_{MS} = -10 \log_{10} P(\text{read is wrongly mapped})$ mean?

Lets compute the probability the read originated at genome position i

q : accg atag accg aatg

q_s : 30 40 25 30 30 20 10 20 40 30 20 30 40 40 30 25

$q_s[k] = -10 \log_{10} P(\text{sequencing error at base } k)$, the PHRED score. Equivalently:

$$P(\text{sequencing error at base } k) = 10^{-\frac{q_s[k]}{10}}$$

So the probability that a read originates from a given genome position i is:

$$P(q | G, i) = \prod_{j \text{ match}} P(q_j \text{ good call}) \prod_{j \text{ mismatch}} P(q_j \text{ bad call}) \approx \prod_{j \text{ mismatch}} P(q_j \text{ bad call})$$

In our example

$$P(q | G, 0) = [(1 - 10^{-3})^6 (1 - 10^{-4})^4 (1 - 10^{-2.5})^2 (1 - 10^{-2})^2] [10^{-1} 10^{-2}] = [0.97] * [0.001] \approx 0.001$$

Mapping quality

What we want to estimate is $q_{MS} = -10 \log_{10} P(\text{read is wrongly mapped})$

That is, the posterior probability, the probability that the region starting at i was sequenced *given* that we observed the read q :

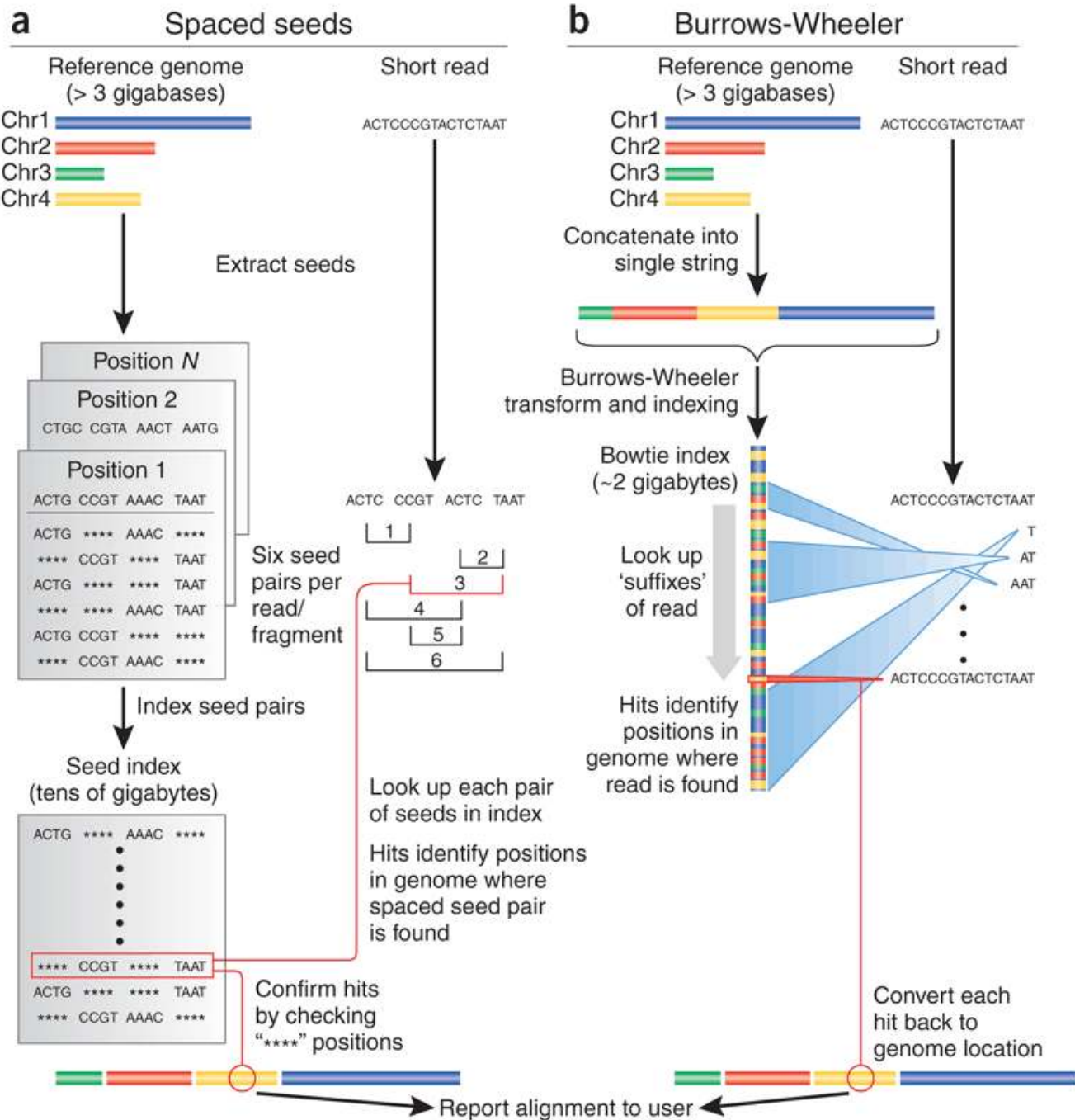
$$P(i | G, q) = \frac{P(q | G, i)P(i | G)}{P(q | G)} = \frac{P(q | G, i)P(i | G)}{\sum_j P(q | G, j)}$$

Fortunately, there are efficient ways to approximate this probability (see Li, H *genome Research* 2008, for example)

$$q_{MS} = -10 \log_{10} (1 - P(i | G, q))$$

Considerations

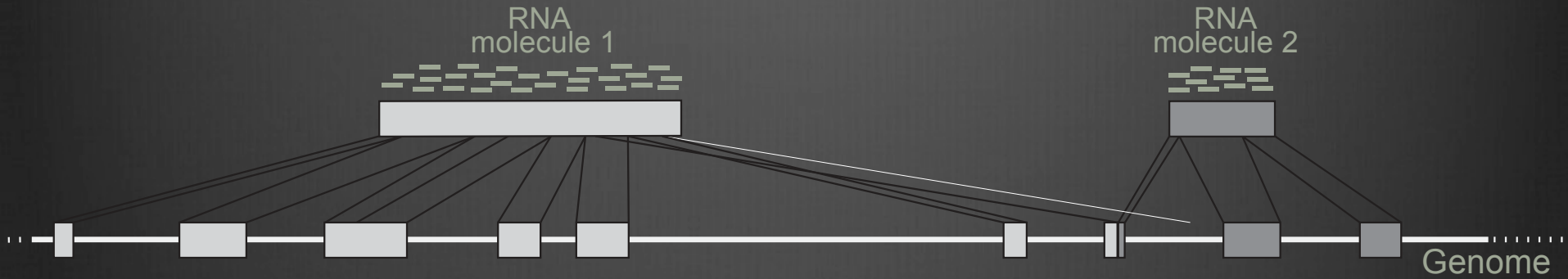
- Trade-off between sensitivity, speed and memory
 - Smaller seeds allow for greater mismatches at the cost of more tries
 - Smaller seeds result in a smaller tables (table size is at most 4^k), larger seeds increase speed (less tries, but more seeds)



Considerations

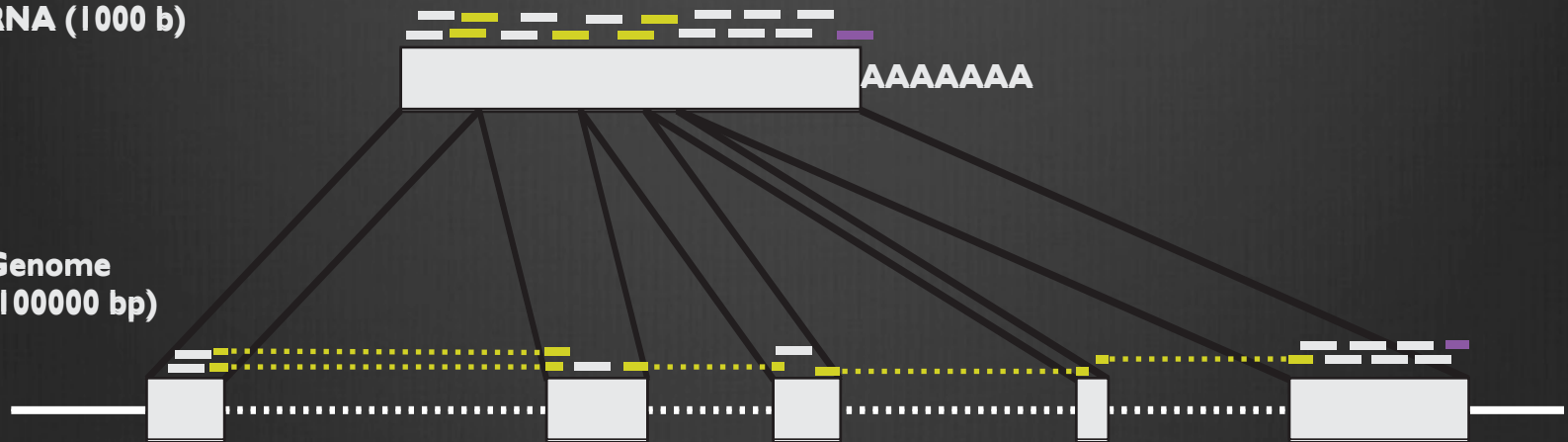
- BWT-based algorithms rely on perfect matches for speed
- When dealing with mismatches, algorithms “backtrack” when the alignment extension fails.
- Backtracking is expensive
- As read length increases novel algorithms are required

RNA-Seq Read mapping



RNA (1000 b)

Genome (100000 bp)



Short read mapping software for ChIP-Seq

Seed-extend

	Short indels	Use base qual
Maq	No	YES
RMAP	Yes	YES
SeqMap	Yes	NO
SHRiMP	Yes	NO

BWT

	Use Base qual
BWA	YES
Bowtie	NO
Stampy*	YES
Bowtie2*	(NO)

***Stampy is a hybrid approach which first uses BWA to map reads then uses seed-extend only to reads not mapped by BWA**

***Bowtie2 breaks reads into smaller pieces and maps these “seeds” using a BWT genome.**

Mapping RNA-Seq reads: Seed-extend spliced alignment (e.g. GSNAP)



Mapping RNA-Seq reads: Exon-first spliced alignment (e.g. TopHat)



Short read mapping software for RNA-Seq

Seed-extend

	Short indels	Use base qual
GSNAP	Yes	?
QPALMA	Yes	NO
BLAT	Yes	NO

Exon-first

	Use base qual
STAR	NO
TopHat	NO

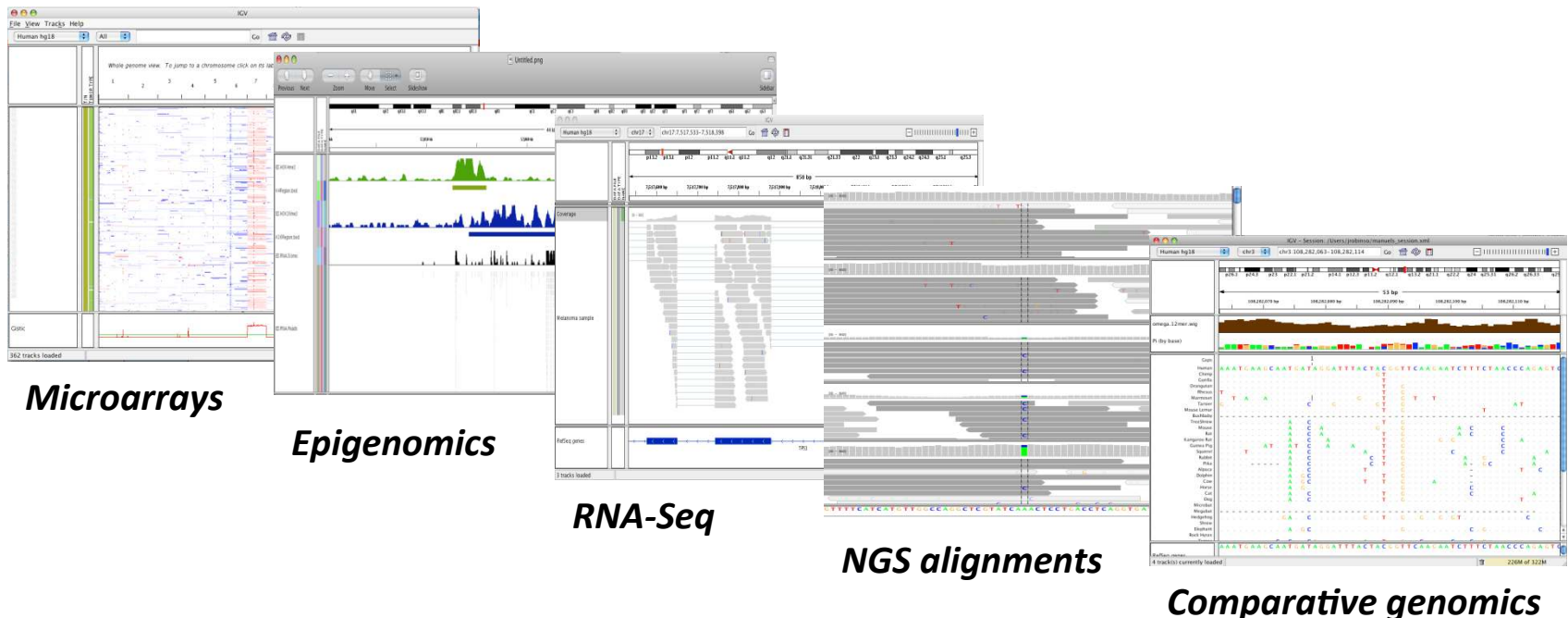
Exon-first alignments will map contiguous first at the expense of spliced hits

IGV: Integrative Genomics Viewer



A desktop application

for the visualization and interactive exploration
of genomic data



Microarrays

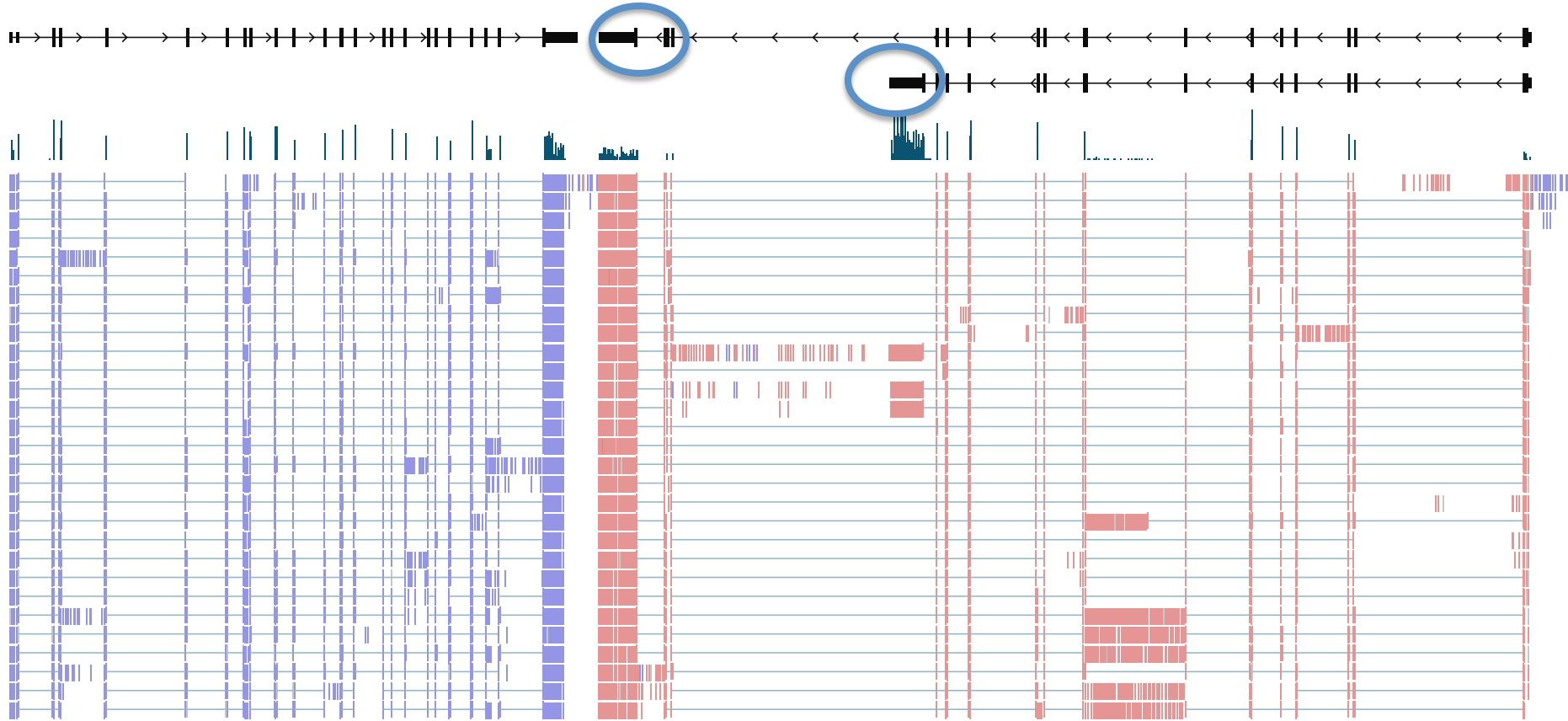
Epigenomics

RNA-Seq

NGS alignments

Comparative genomics

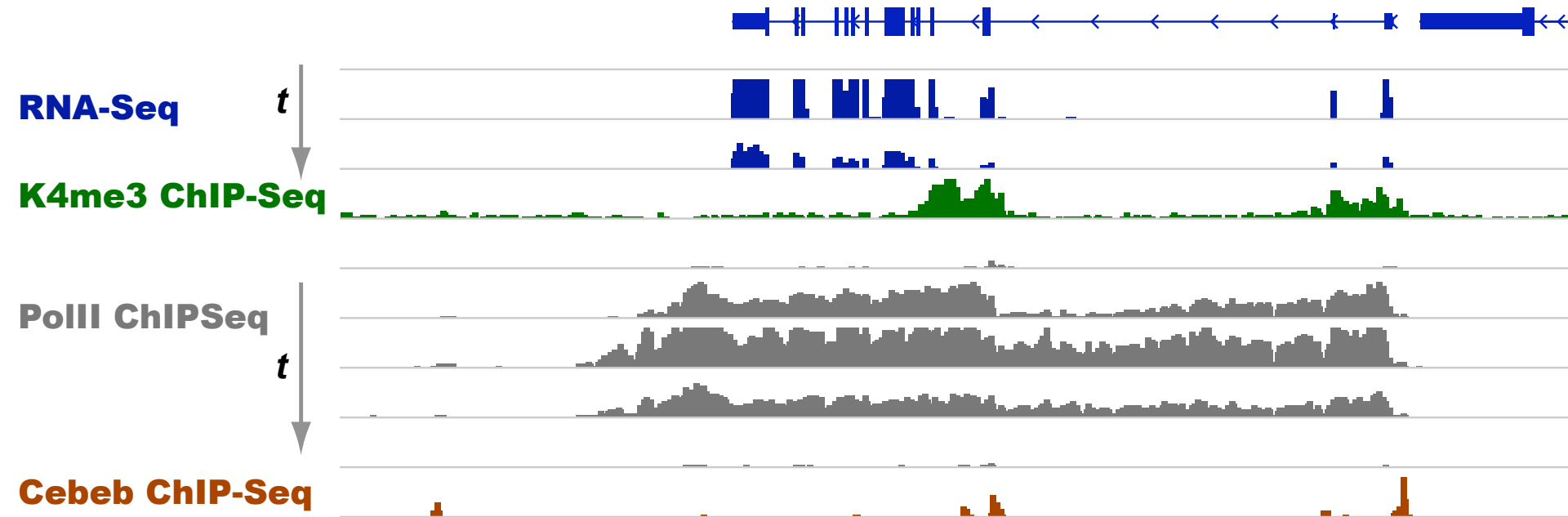
Visualizing read alignments with IGV — RNASeq



Strand specific library!

Gap between reads spanning exons

Visualizing read alignments with IGV — zooming out



Mapping longer reads



MiSeq “Bench” sequencer

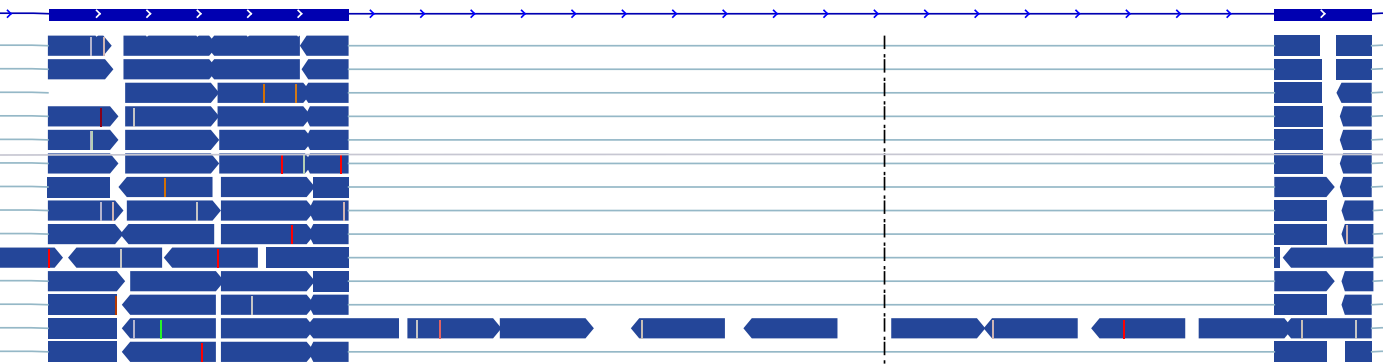
~15 Million 2x250 base reads.

Ideal for **deep annotation of Targeted RNA**

Large number of expected mismatches

Given sequencing errors (>1.5%) + SNPs

expect many reads with >4 mismatches



Short (76b) reads



Long (250b) reads

Longer, reads mapping cannot be done with standard BWT based aligners

How do “short” read aligners responded to read increase?

- Break reads into seeds (e.g. 16nt every 10nt)
- Use BWT or HashTable to find candidate positions
- Prioritize candidates
- Extend top candidates using classical alignment techniques.

Aligner	Technique
TopHat2 (Bowtie2)	BWT
GSNAP	Hash Table
STAR	Suffix (similar to BWT)

Analysis of counting data requires 3 broad tasks

- Read mapping (alignment): Placing short reads in the genome
- Reconstruction: Finding the regions that originated the reads
- Quantification:
 - Assigning scores to regions
 - Finding regions that are differentially represented between two or more samples.

What does significance means?

- RNA-Seq: The gene is expressed
- ChIP-Seq: Factor binds the region
- CLIP-Seq: Protein binds RNA region
- Ribosomal footprinting:
 - Transcript is translated
 - Ribosomes stalling at region

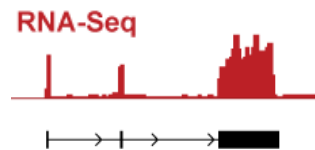
How do we find peaks?



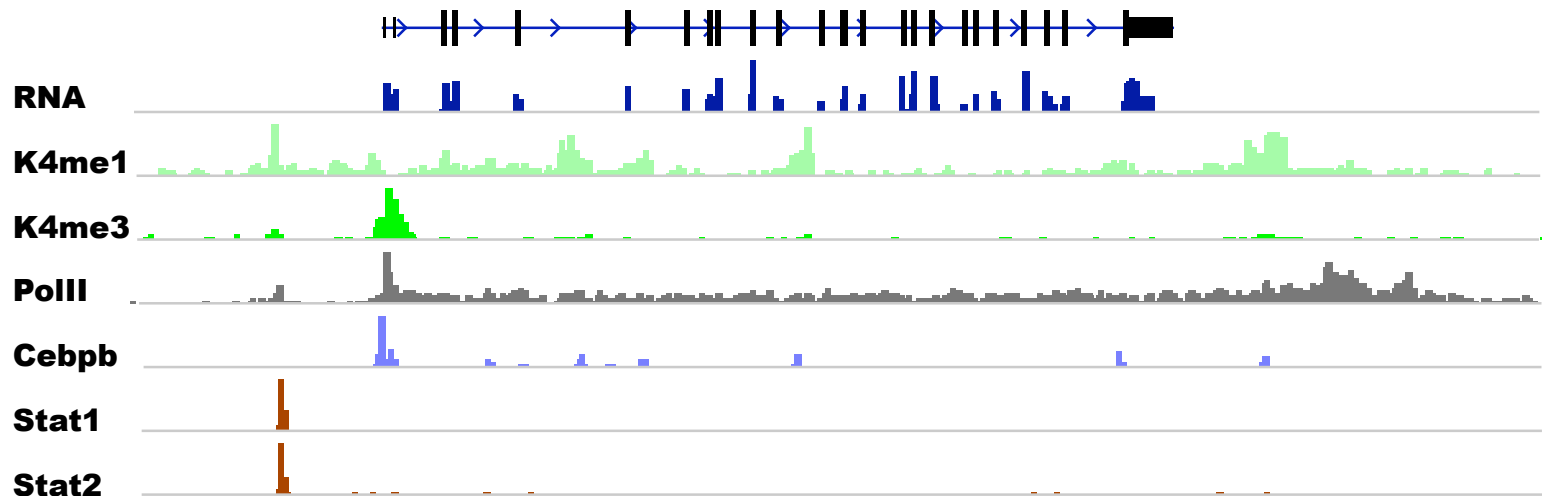
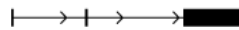
Short modification



Long modification

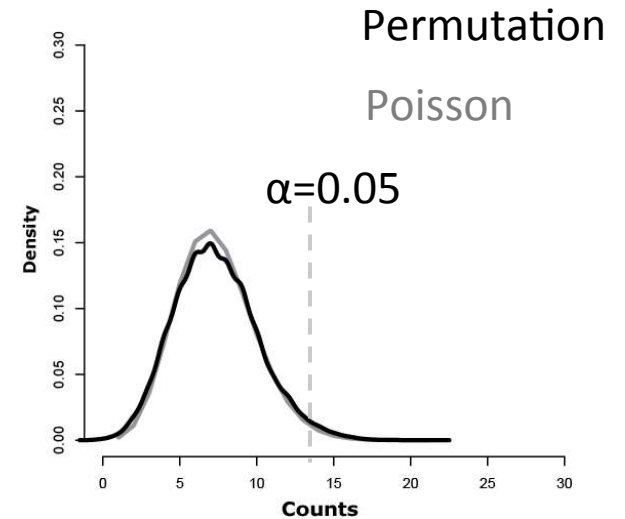
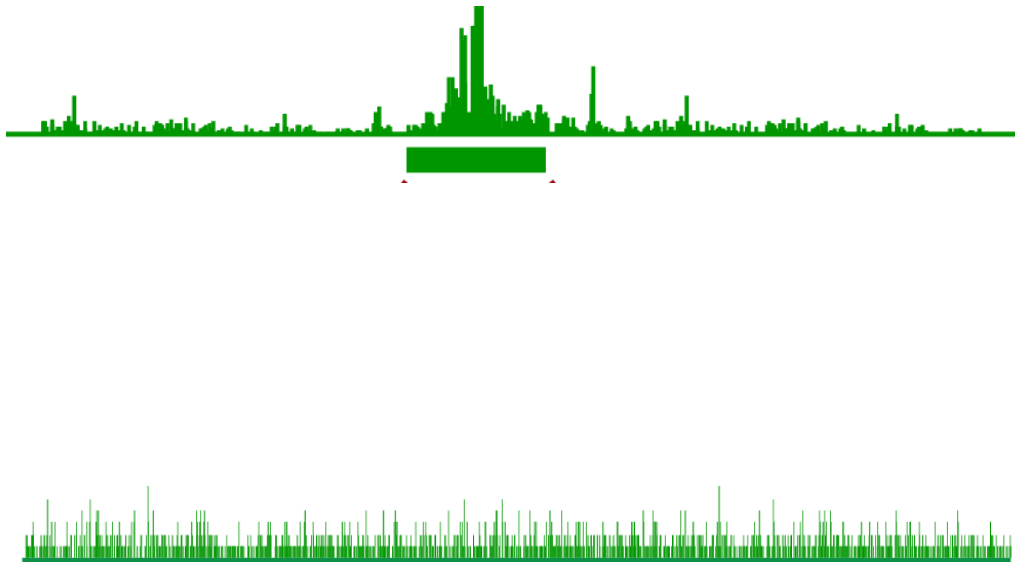


Discontinuous data



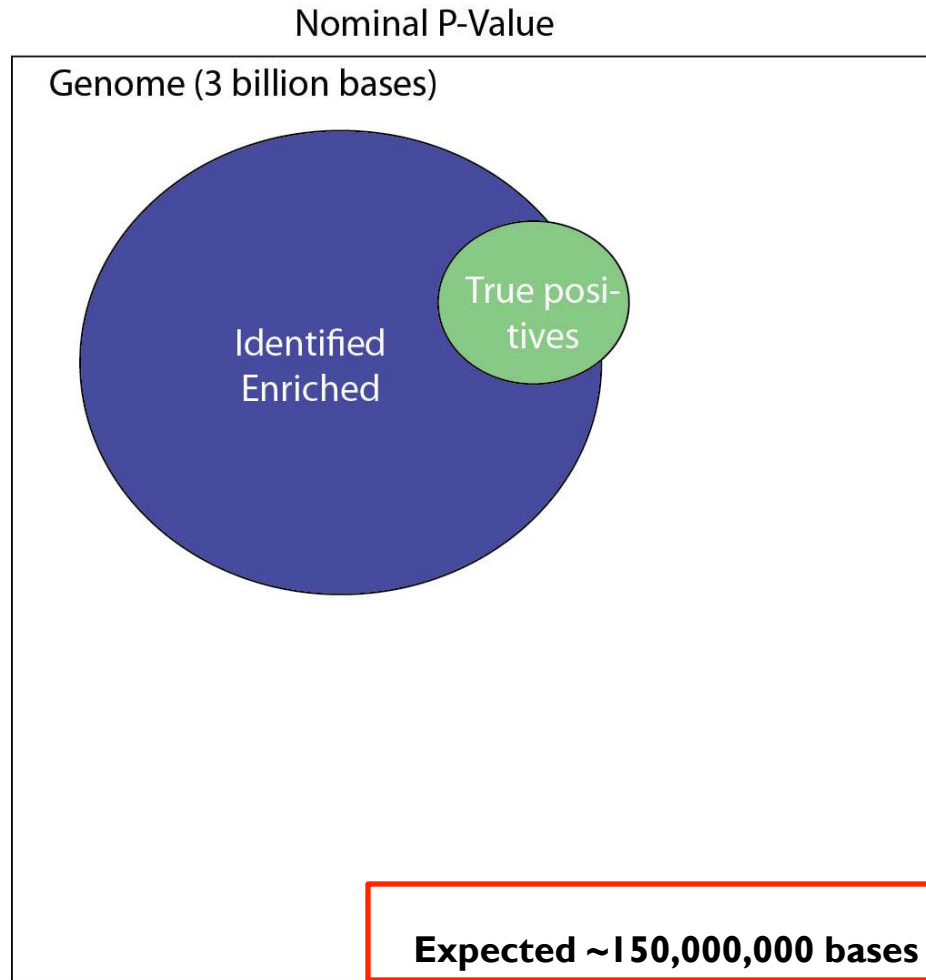
Scripture is a method to solve this general question

Our approach



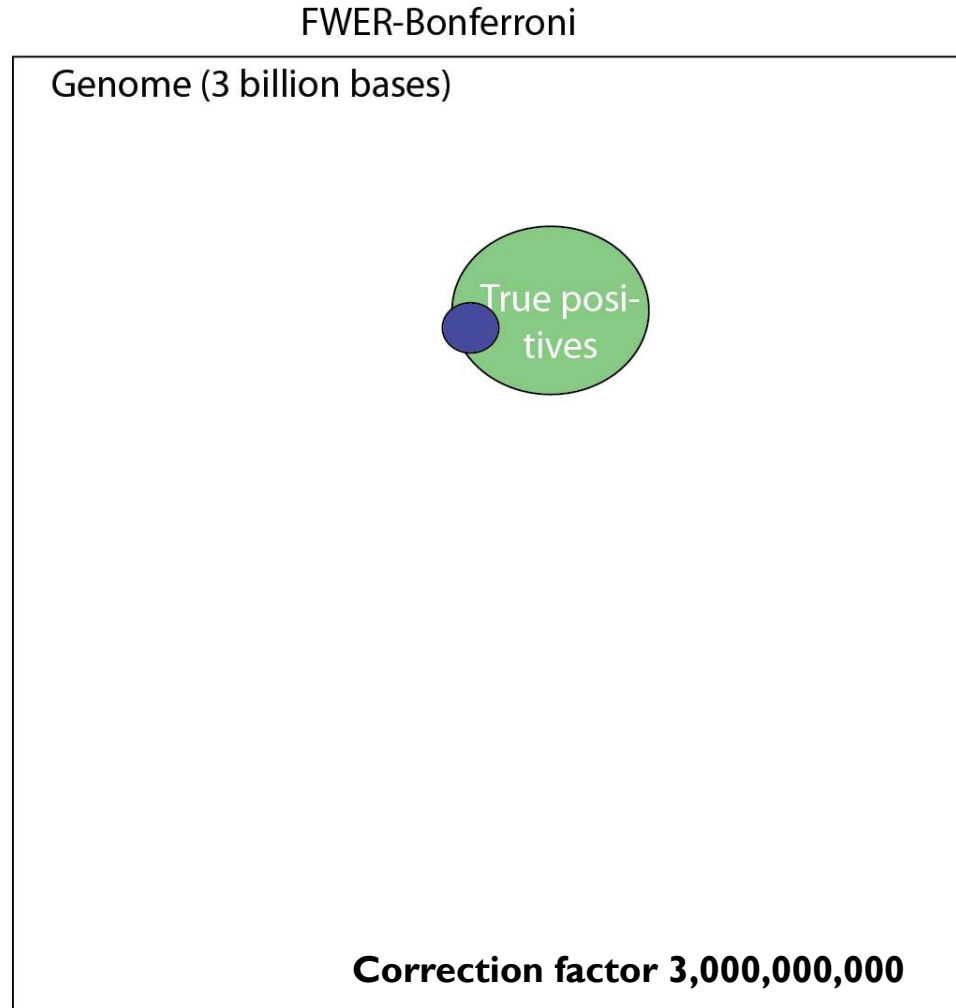
We have an efficient way to compute read count p-values ...

The genome is big, many things happen by chance



We need to correct for multiple hypothesis testing

Bonferroni correction is way to conservative

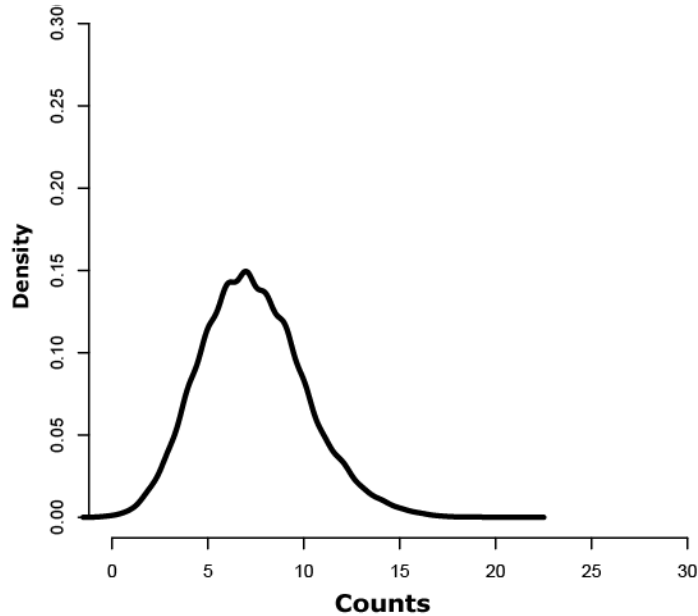


Bonferroni corrects the number of hits but misses many true hits because its too conservative – How do we get more power?

Controlling FWER

Max Count distribution

$$\alpha=0.05 \quad \alpha_{\text{FWER}}=0.05$$



Count distribution (Poisson)

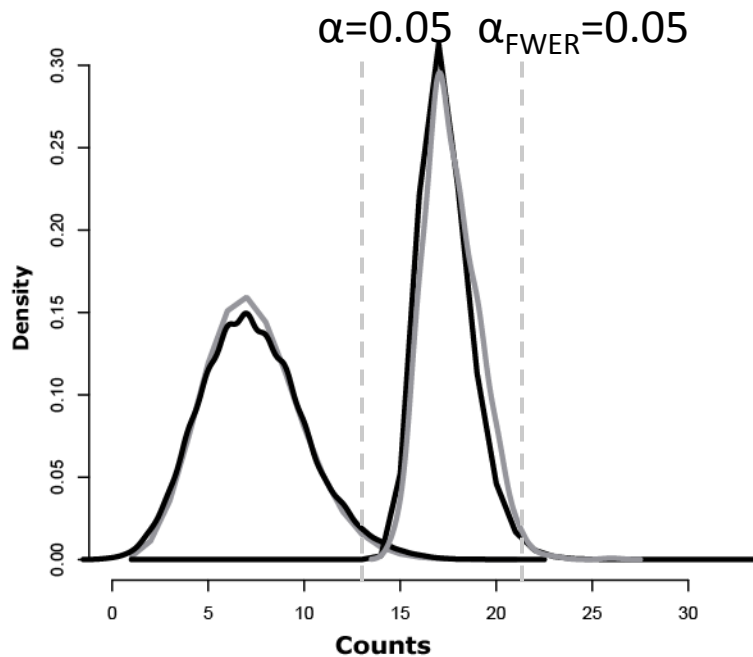
Given a region of size w and an observed read count n . What is the probability that one or more of the 3×10^9 regions of size w has read count $\geq n$ under the null distribution?

We could go back to our permutations and compute an FWER: **max of the genome-wide distributions of same sized region**) $\rightarrow$ but really really really slow!!!

Scan distribution, an old problem

- Is the observed number of read counts over our region of interest high?
- Given a set of Geiger counts across a region find clusters of high radioactivity
- Are there time intervals where assembly line errors are high?

Scan distribution



Thankfully, the ***Scan Distribution*** computes a closed form for this distribution.

ACCOUNTS for dependency of overlapping windows thus more powerful!

Poisson distribution

Scan distribution for a Poisson process

The probability of observing k reads on a window of size w in a genome of size L given a total of N reads can be approximated by (Alm 1983):

$$P(k|\lambda w, N, L) \approx 1 - F_p(k-1|\lambda w)e^{-\frac{k-w\lambda}{k}\lambda(T-w)}P(k-1|\lambda w)$$

where

$P(k-1|\lambda w)$ is the Poisson probability of observing $k-1$ counts given an expected count of λw

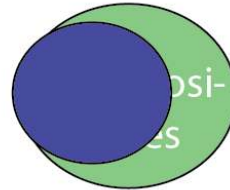
and

$F_p(k-1|\lambda w)$ is the Poisson probability of observing $k-1$ or fewer counts given an expectation of λw reads

The scan distribution gives a computationally very efficient way to estimate the FWER

FWER-Scan Statistics

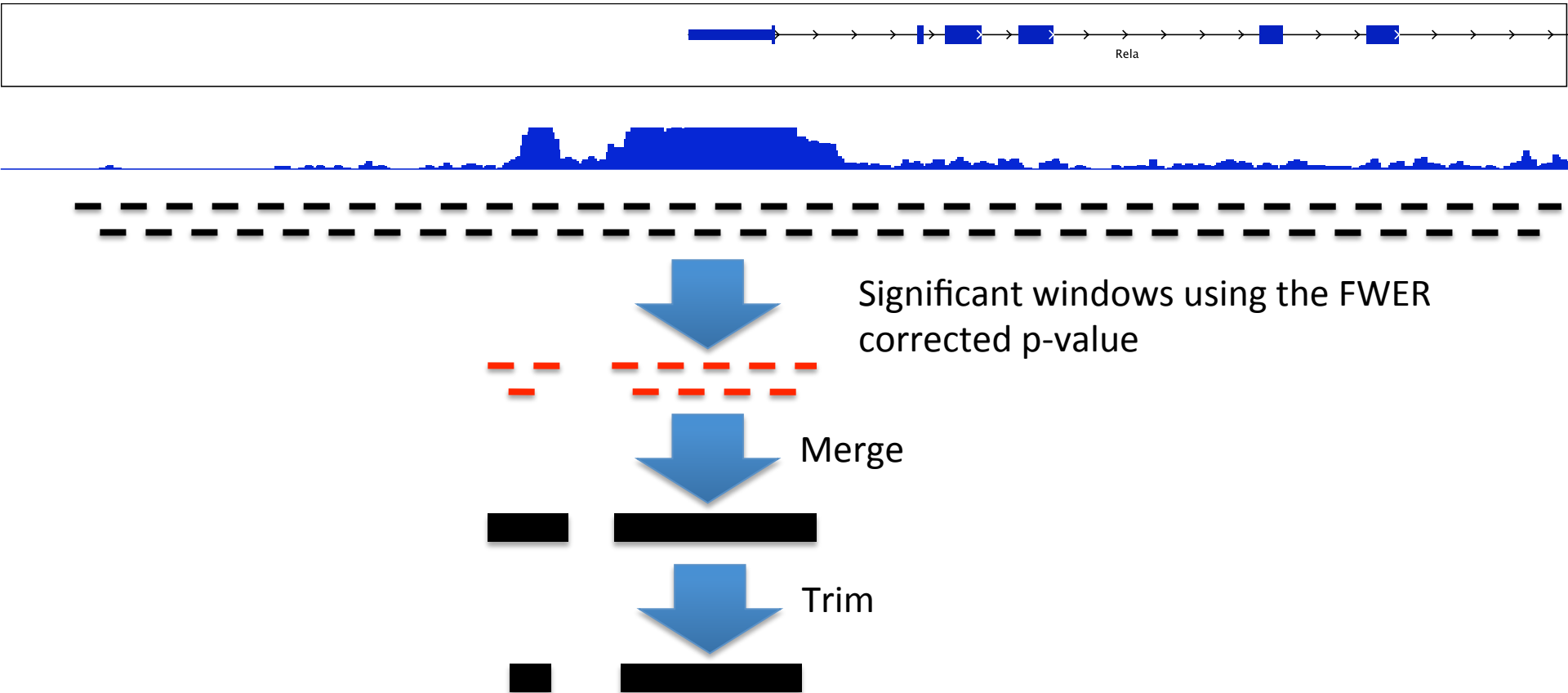
Genome (3 billion bases)



By utilizing the dependency of overlapping windows we have greater power, while still controlling the same genome-wide false positive rate.

Segmentation method for contiguous regions

Example : PolII ChIP

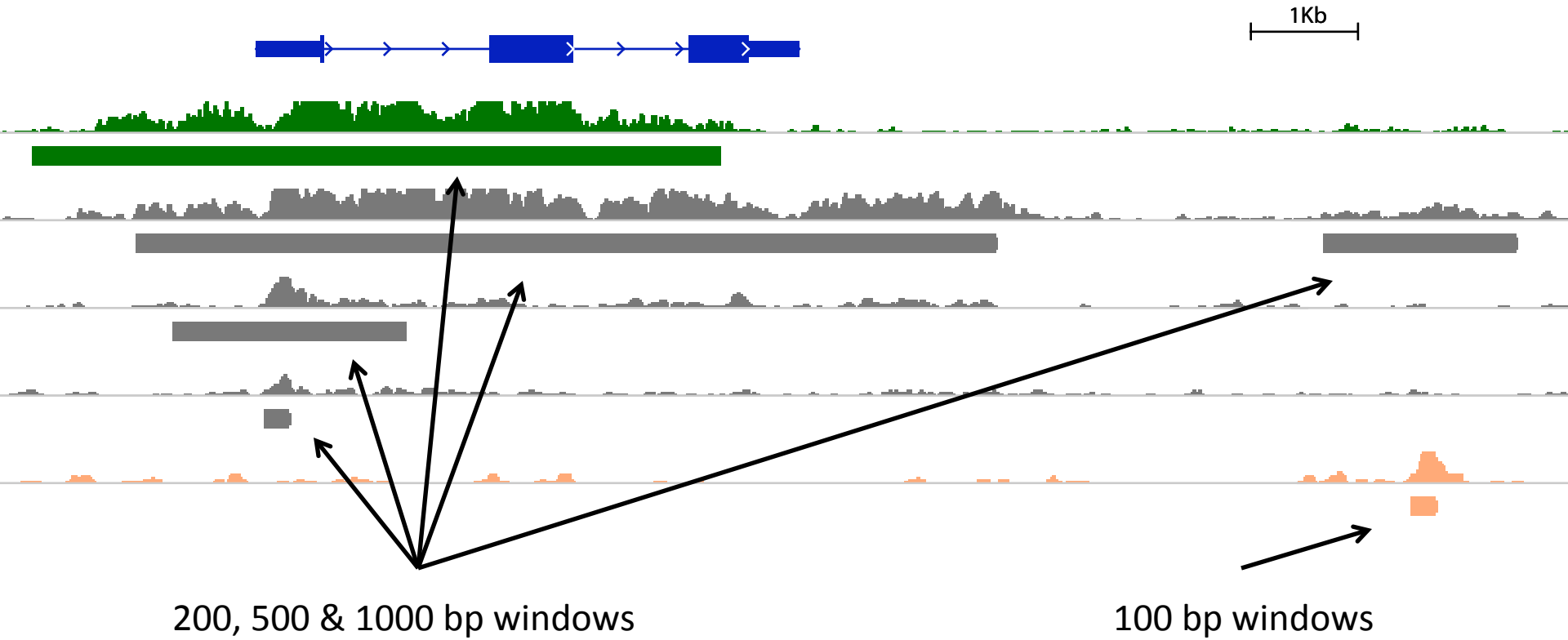


But, which window?

We use multiple windows

- Small windows detect small punctuate regions.
- Longer windows can detect regions of moderate enrichment over long spans.
- In practice we scan different windows, finding significant ones in each scan.
- In practice, it helps to use some prior information in picking the windows although globally it might be ok.

Applying Scripture to a variety of ChIP-Seq data



Can we identify enriched regions across different data types?

H3K4me3



Short modification



H3K36me3

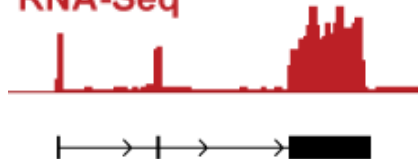


Long modification



Using chromatin signatures we discovered hundreds of putative genes.
What is their structure?

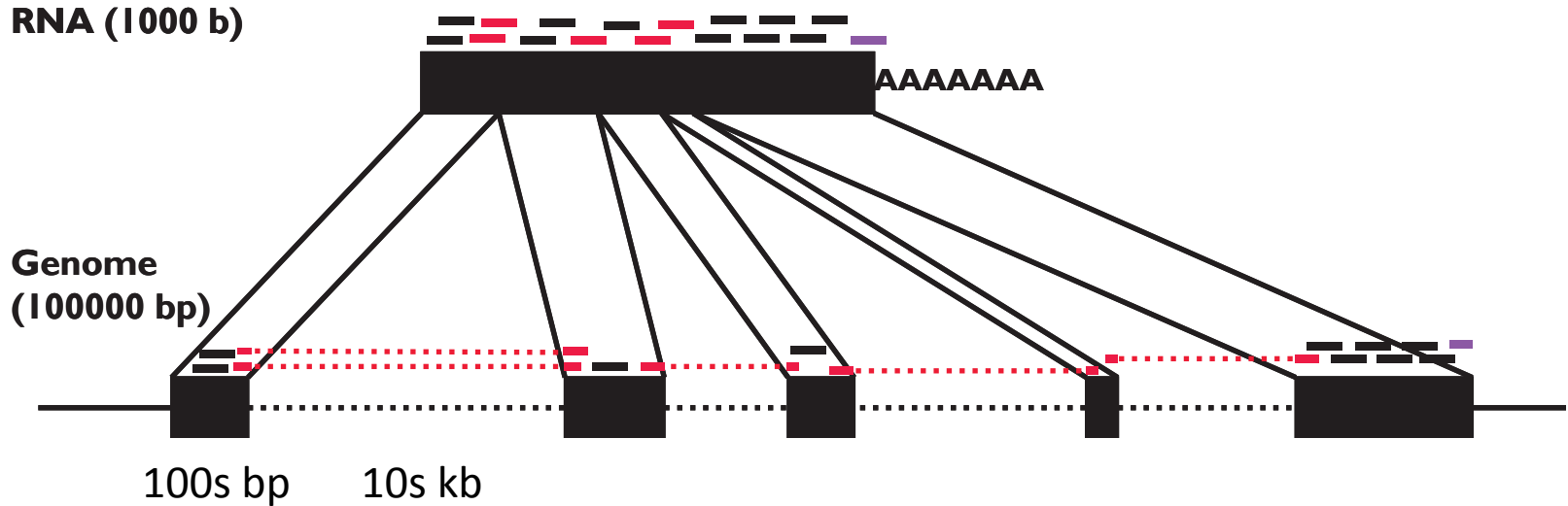
RNA-Seq



Discontinuous data: RNA-Seq to find gene structures for this gene-like regions

Scripture for RNA-Seq:
Extending segmentation to discontinuous regions

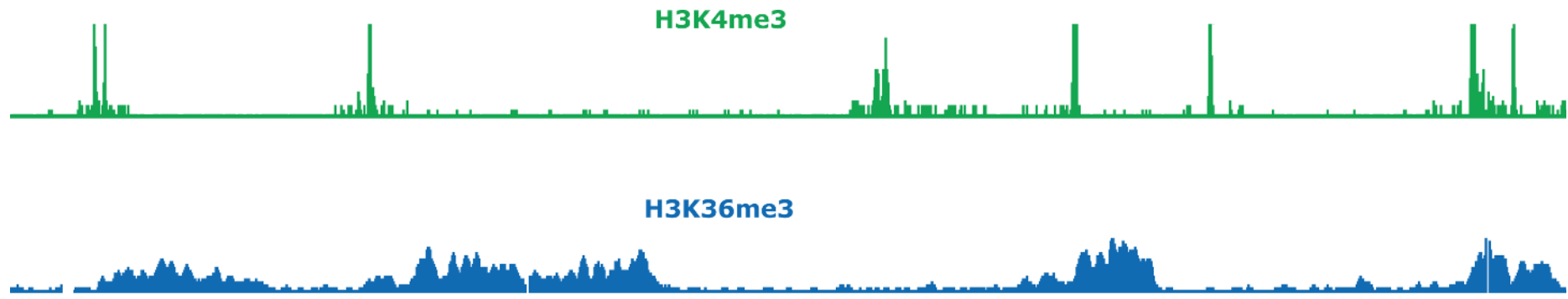
The transcript reconstruction problem as a segmentation problem



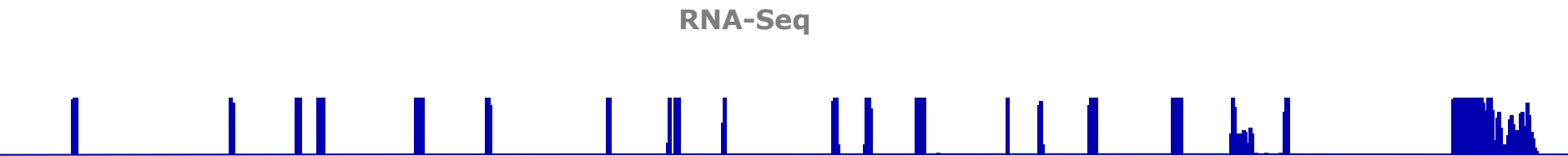
Challenges:

- Genes exist at many different expression levels, spanning several orders of magnitude.
- Reads originate from both mature mRNA (exons) and immature mRNA (introns) and it can be problematic to distinguish between them.
- Reads are short and genes can have many isoforms making it challenging to determine which isoform produced each read.

Scripture: A statistical genome-guided transcriptome reconstruction

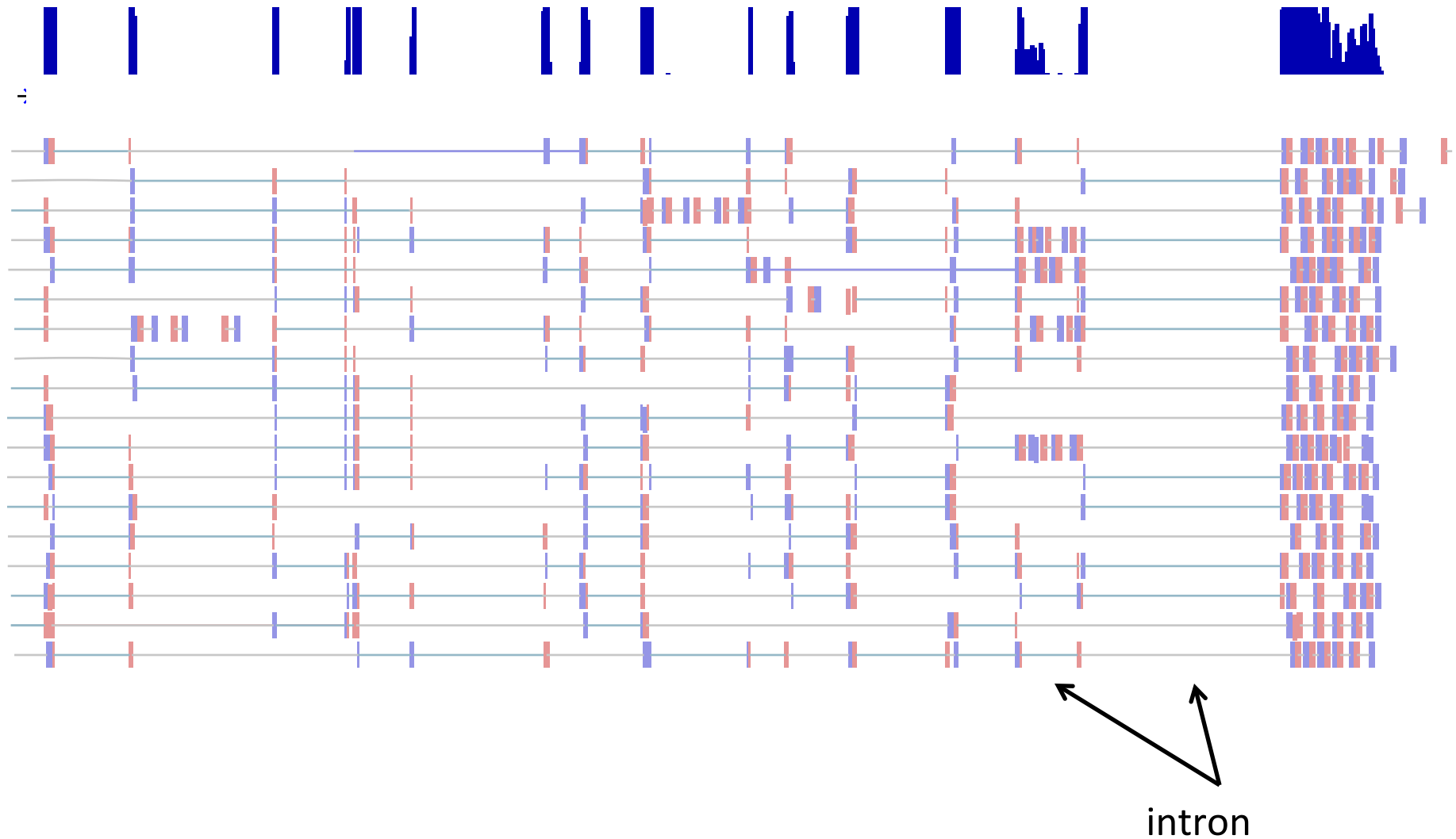


Statistical segmentation of chromatin modifications uses continuity of segments to increase power for interval detection



If we know the connectivity of fragments, we can increase our power to detect transcripts

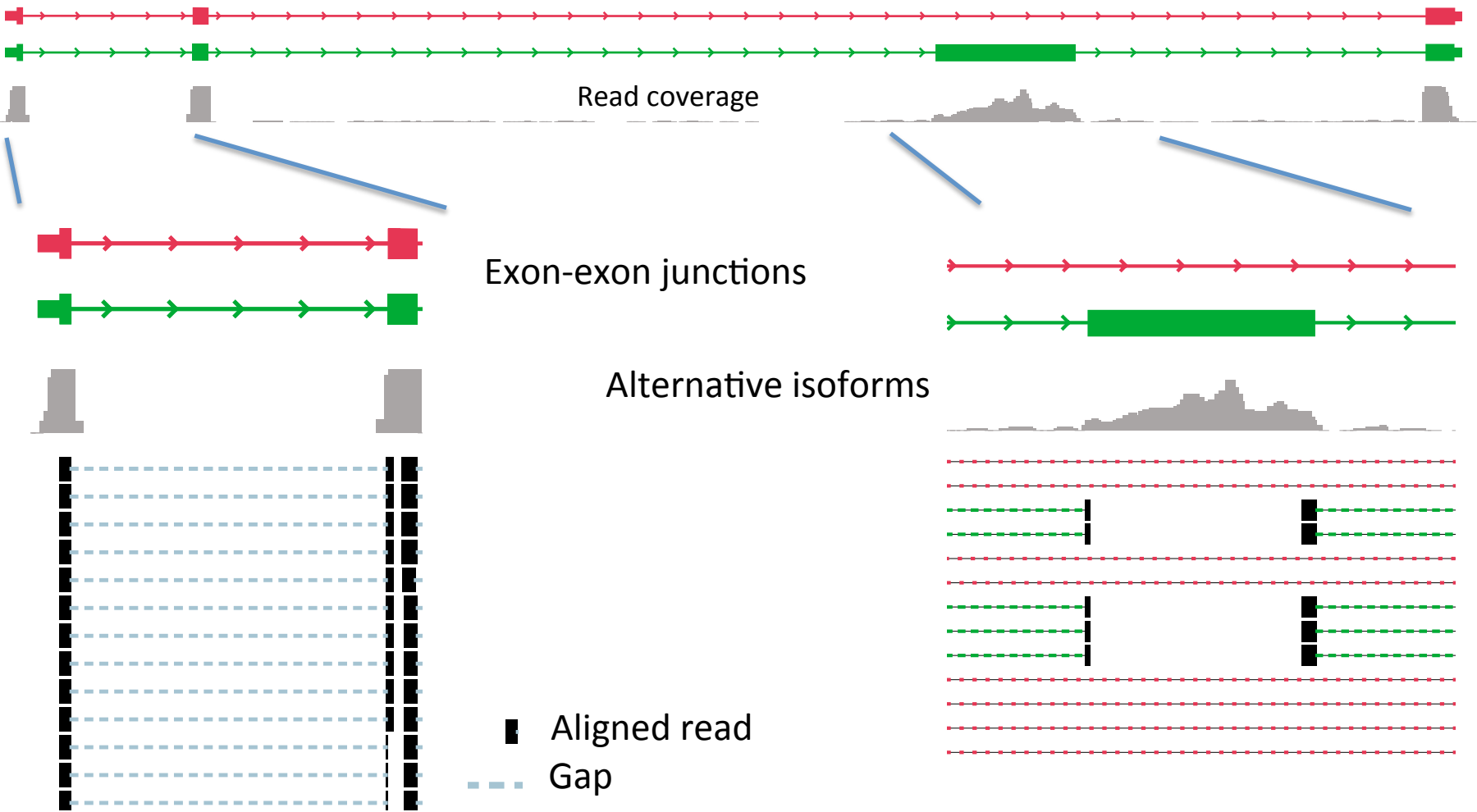
Longer (76) reads provide increased number of junction reads



Exon junction spanning reads provide the connectivity information.

The power of spliced alignments

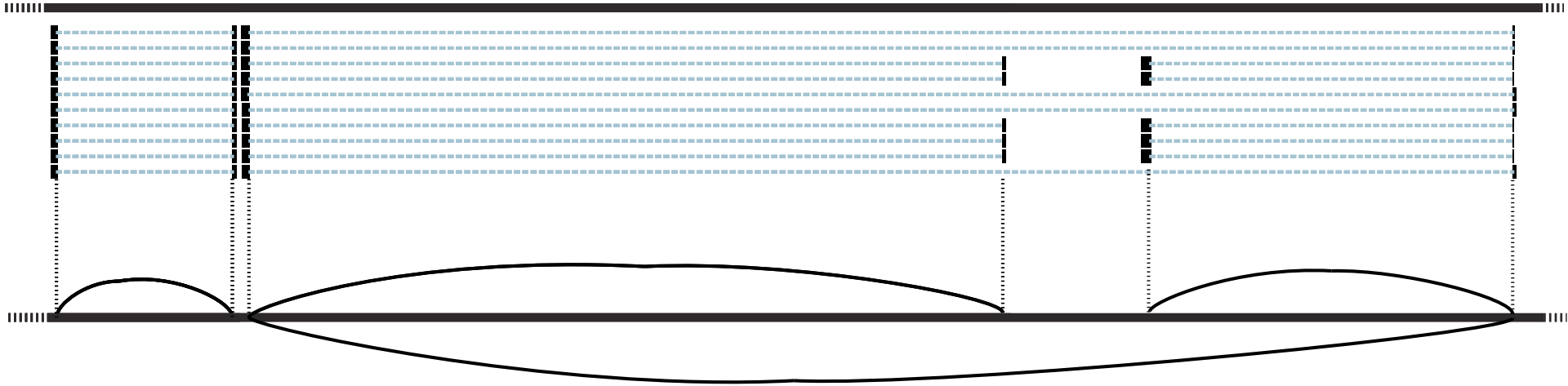
Protein coding gene with 2 isoforms



Statistical reconstruction of the transcriptome

Step 1: Align Reads to the genome allowing gaps flanked by splice sites

genome

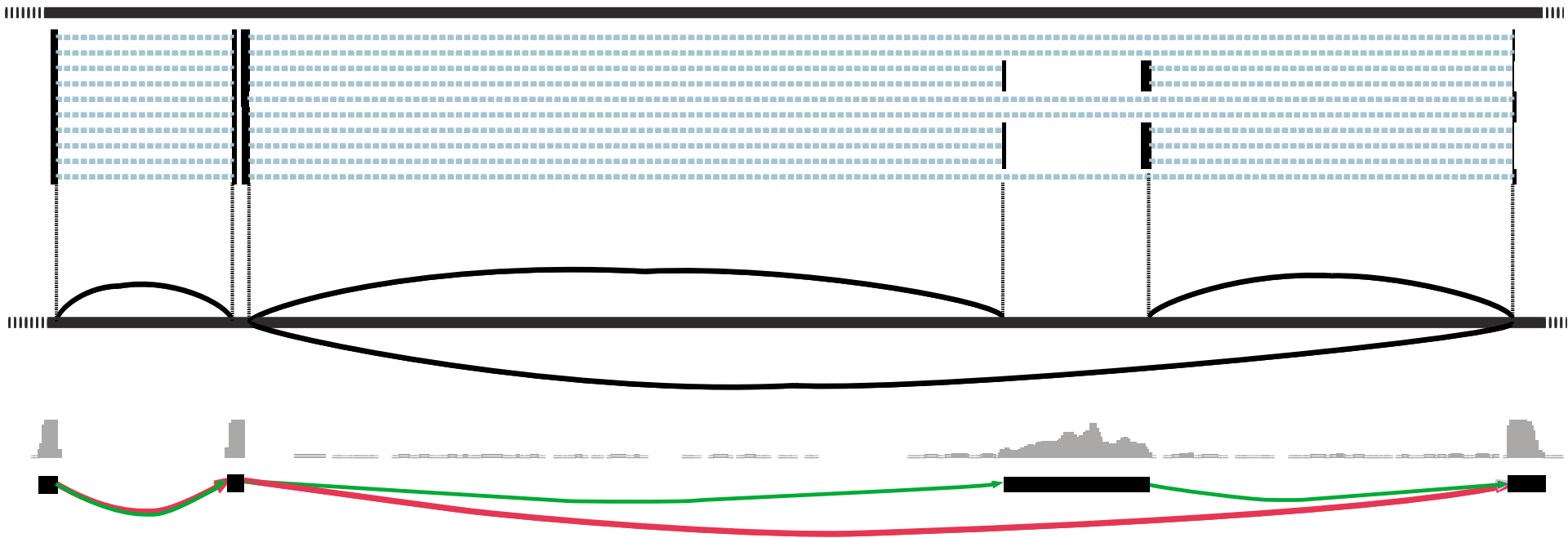


Step 2: Build an oriented connectivity graph using every spliced alignment and orienting edges using the flanking splicing motifs

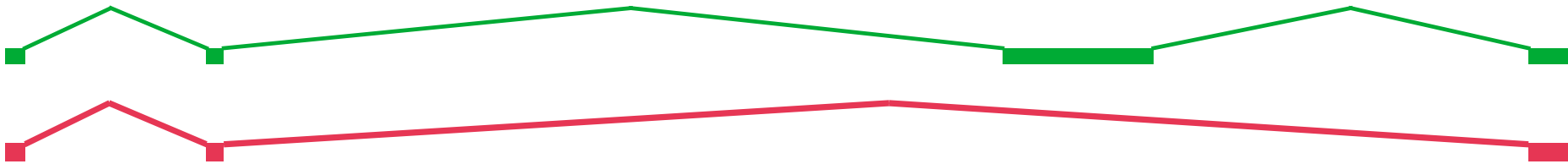
The “connectivity graph” connects all bases that are directly connected within the transcriptome

Statistical reconstruction of the transcriptome

Step 3: Identify “segments” across the graph



Step 4: Find significant segments



Can we identify enriched regions across different data types?

H3K4me3



Short modification



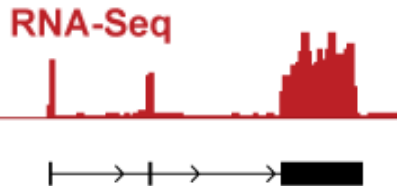
H3K36me3



Long modification



RNA-Seq

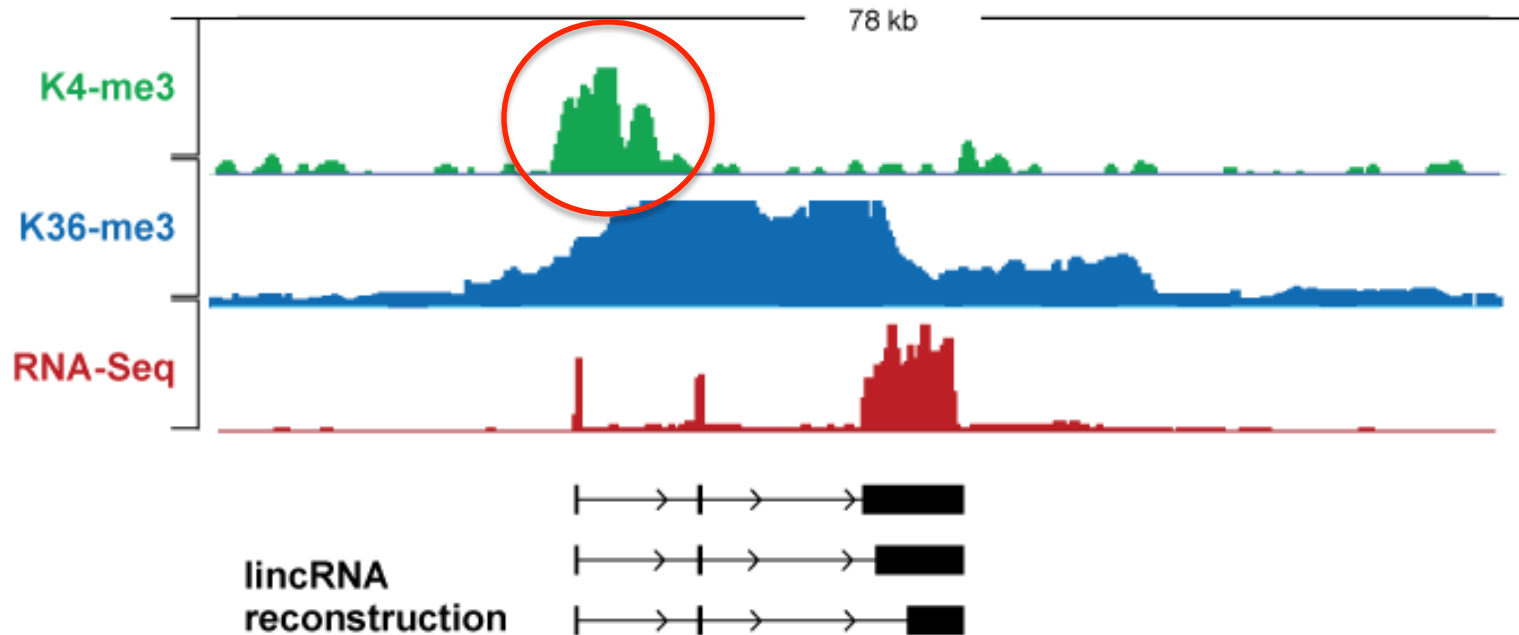


Discontinuous data



Are we really sure reconstructions are complete?

RNA-Seq data is incomplete for comprehensive annotation



Library construction can help provide more information. More on this later

Applying scripture: Annotating the mouse transcriptome

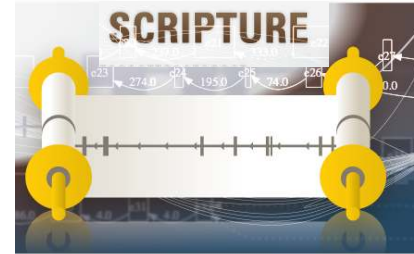
Reconstructing the mouse transcriptome (45M paired reads)



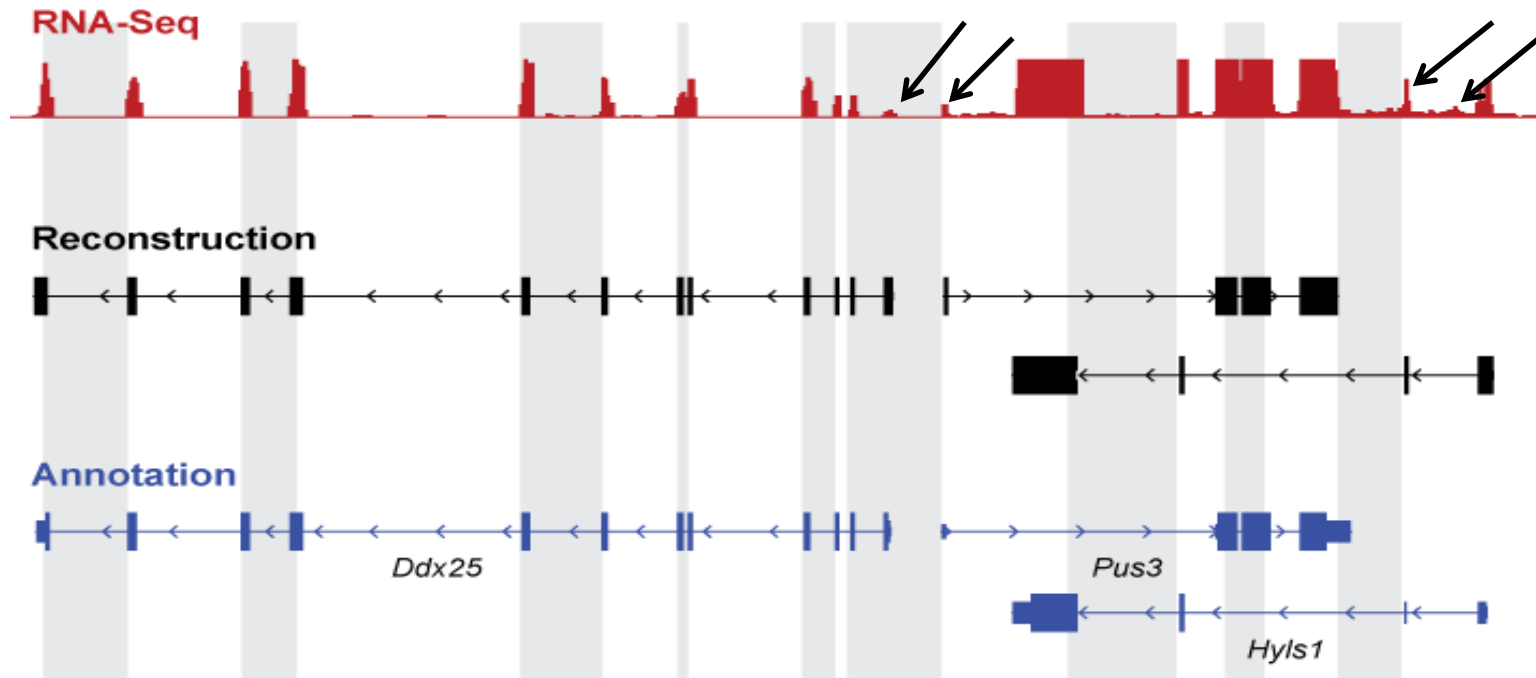
Mouse Cell
Types



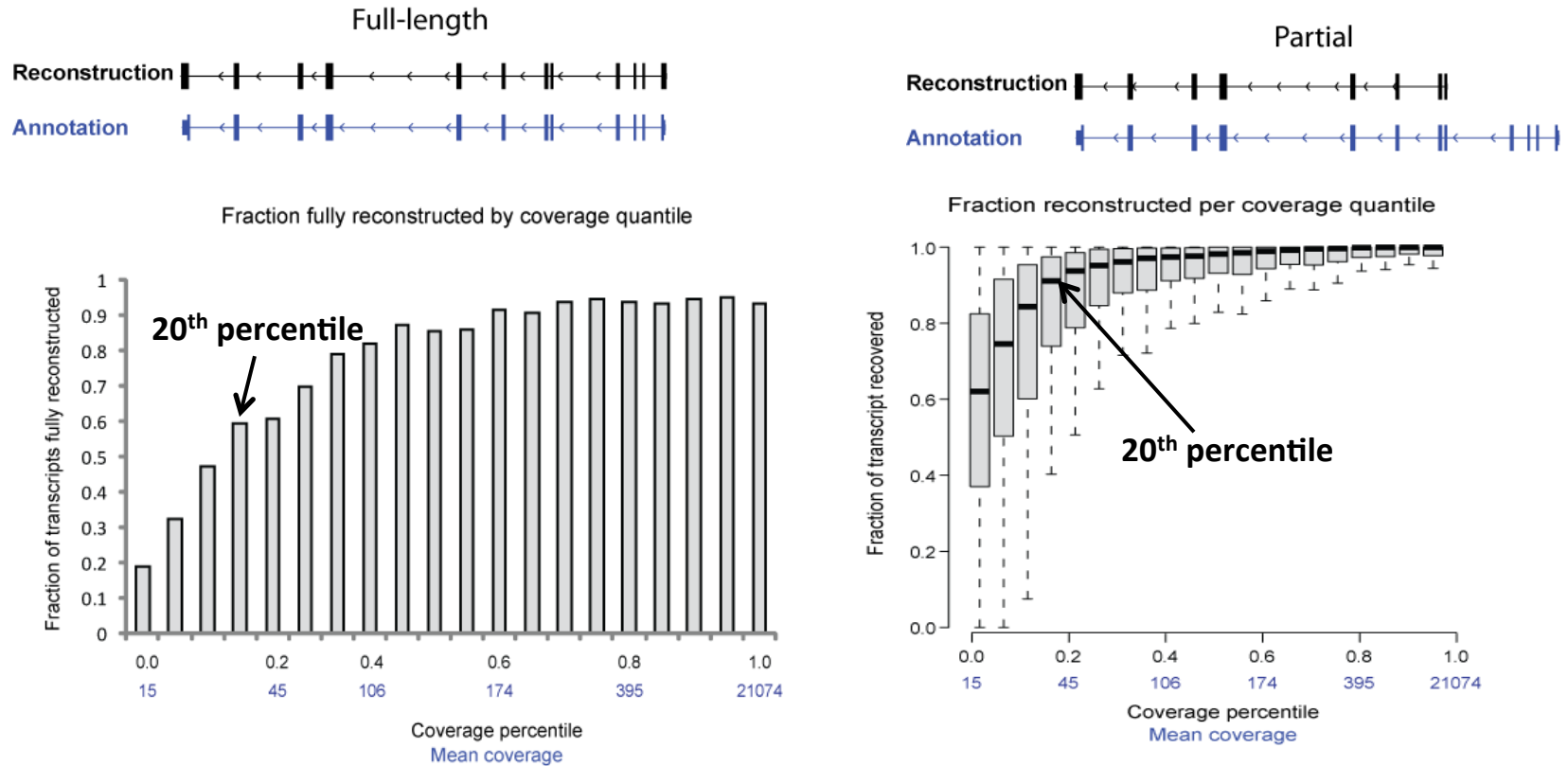
Sequence



Reconstruct

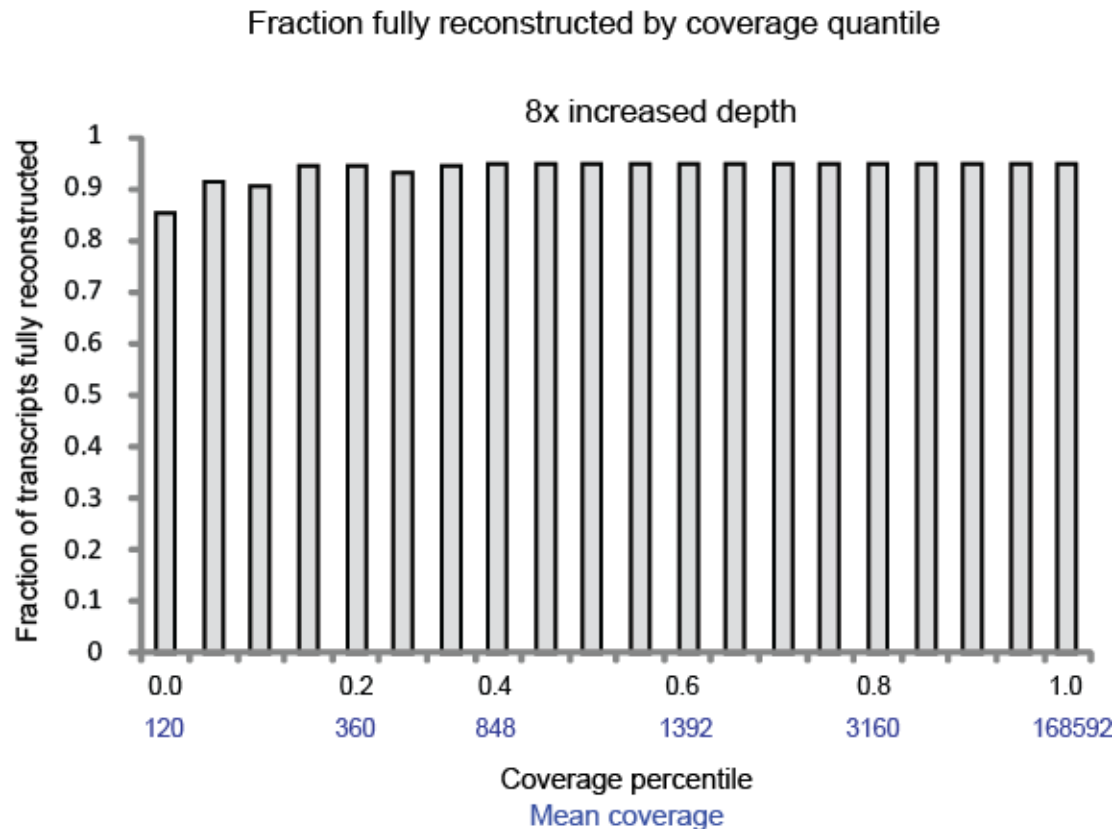


Sensitivity across expression levels



**Even at low expression (20th percentile), we have:
average coverage of transcript is ~95% and 60% have full coverage**

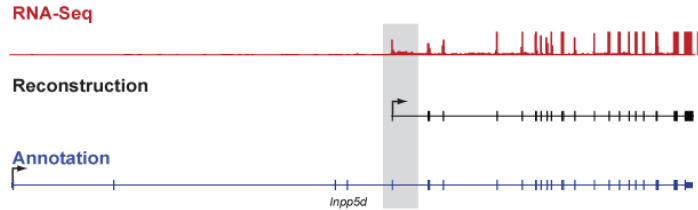
Sensitivity at low expression levels improves with depth



As coverage increases we are able to fully reconstruct a larger percentage of known protein-coding genes

Novel variation in protein-coding genes

Novel 5' Start Sites



ES cells

3 cell types

1,804

3,137

1,310

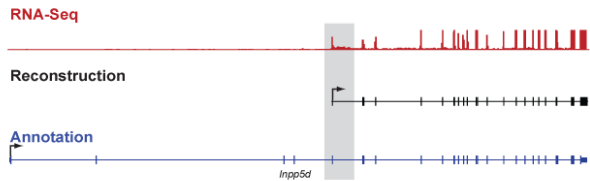
2,477

588

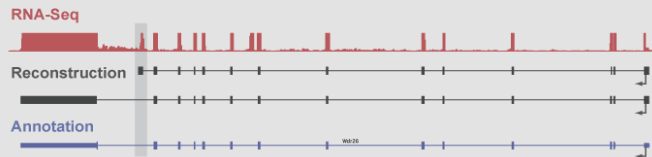
903

Novel variation in protein-coding genes

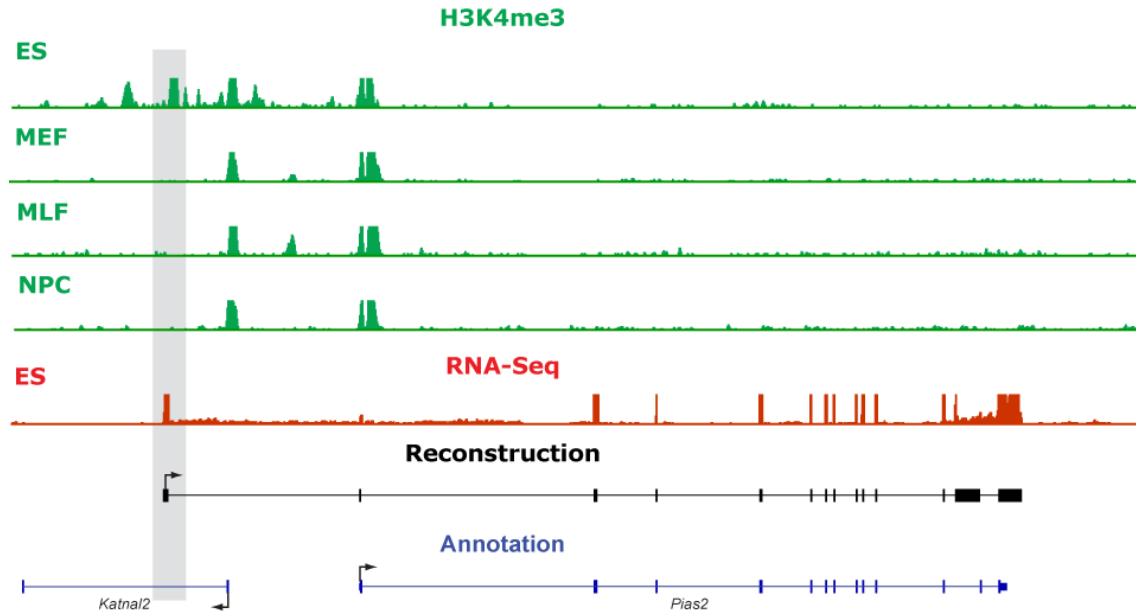
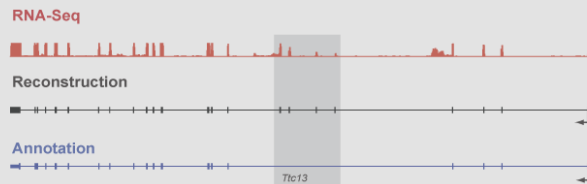
Novel 5' Start Sites



Novel 3' End



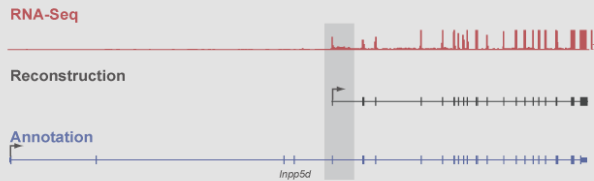
Novel Coding Exons



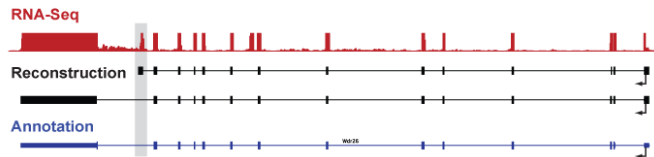
~85% overlap K4me3

Novel variation in protein-coding genes

Novel 5' Start Sites

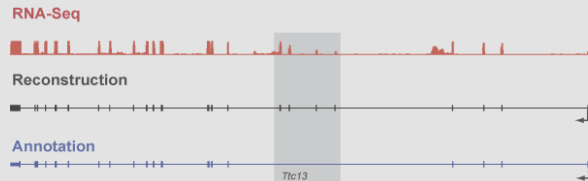


Novel 3' End



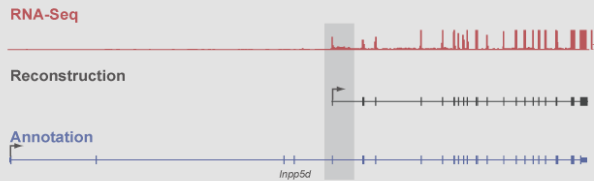
**~50% contain polyA motif
Compared to ~6% for random**

Novel Coding Exons

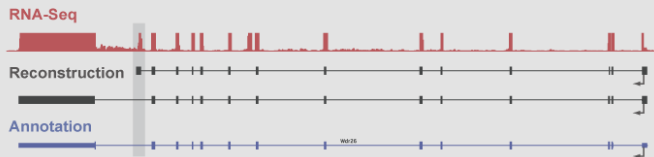


Novel variation in protein-coding genes

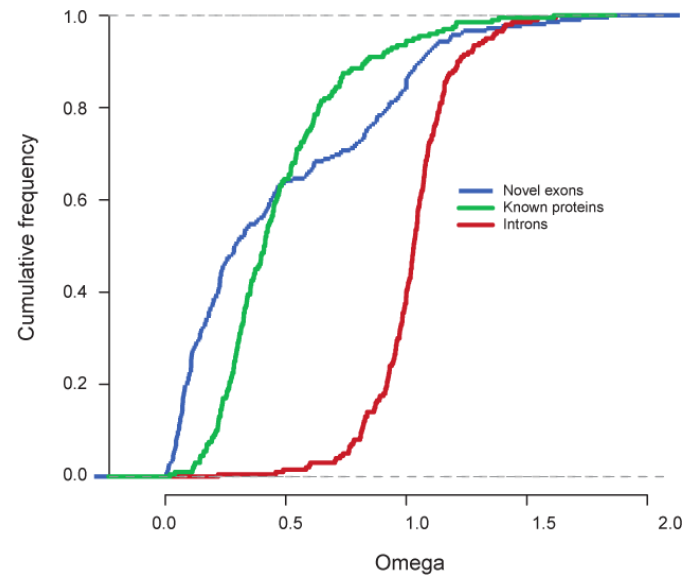
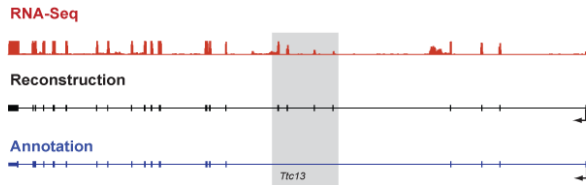
Novel 5' Start Sites



Novel 3' End



Novel Coding Exons



~80% retain ORF

What about novel genes?

Class 1: Overlapping ncRNA



Class 2: Large Intergenic ncRNA (lincRNA)

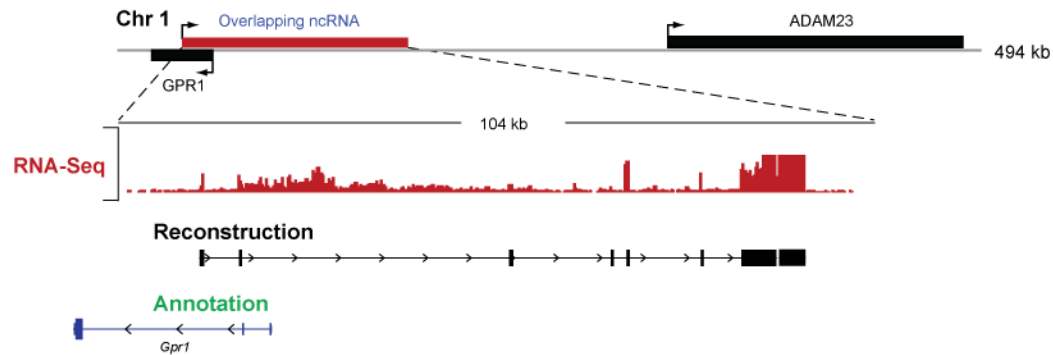


Class 3: Novel protein-coding genes



Class I: Overlapping ncRNA

Overlapping ncRNA



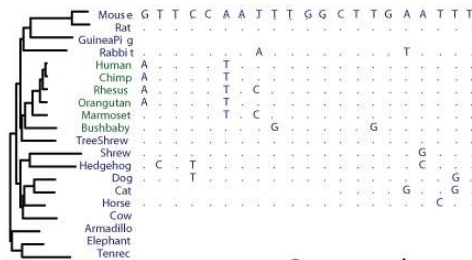
ES cells

3 cell types

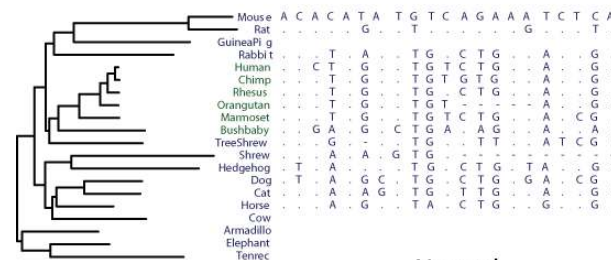
201

446

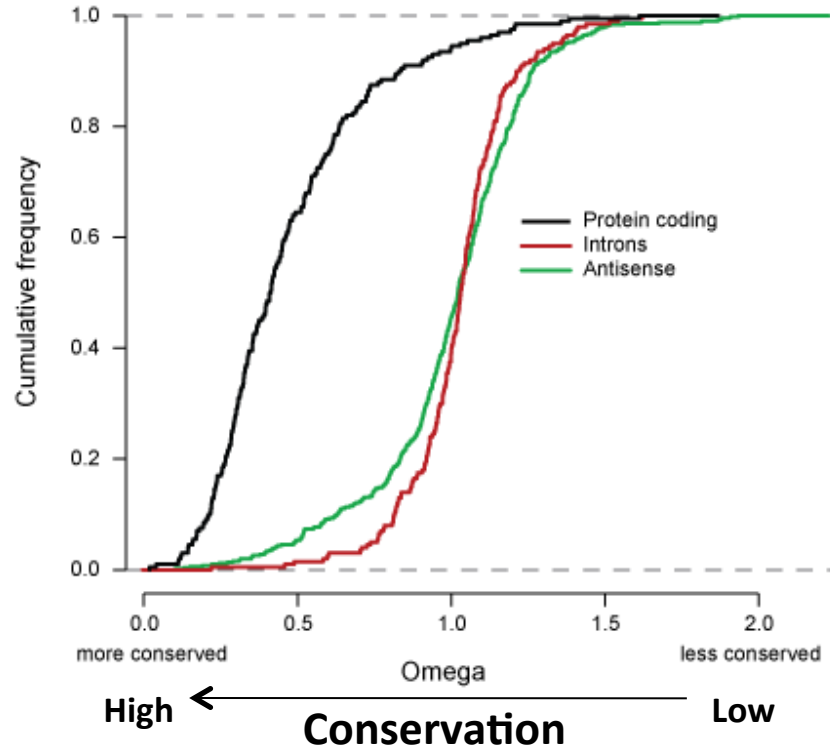
Overlapping ncRNAs: low evolutionary conservation



Conserved



Neutral



SiPhy – (Garber et al. Bioinformatics, 2009)

Overlapping ncRNAs show little evolutionary conservation

RNA (non-protein coding) Genes

Class 1: Overlapping ncRNA



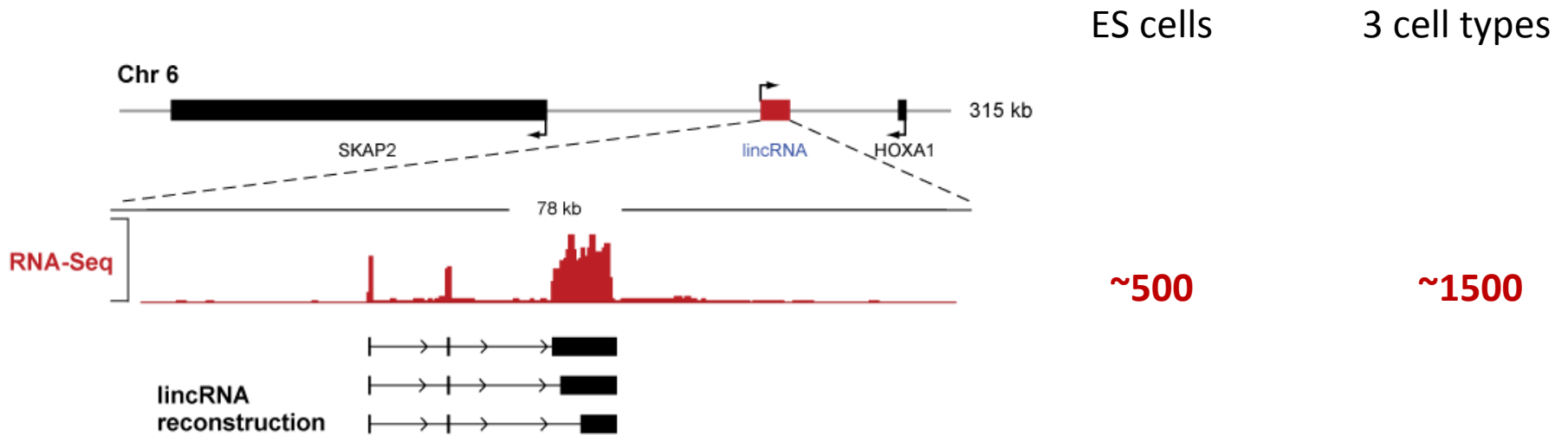
Class 2: Large Intergenic ncRNA (lincRNA)



Class 3: Novel protein-coding genes

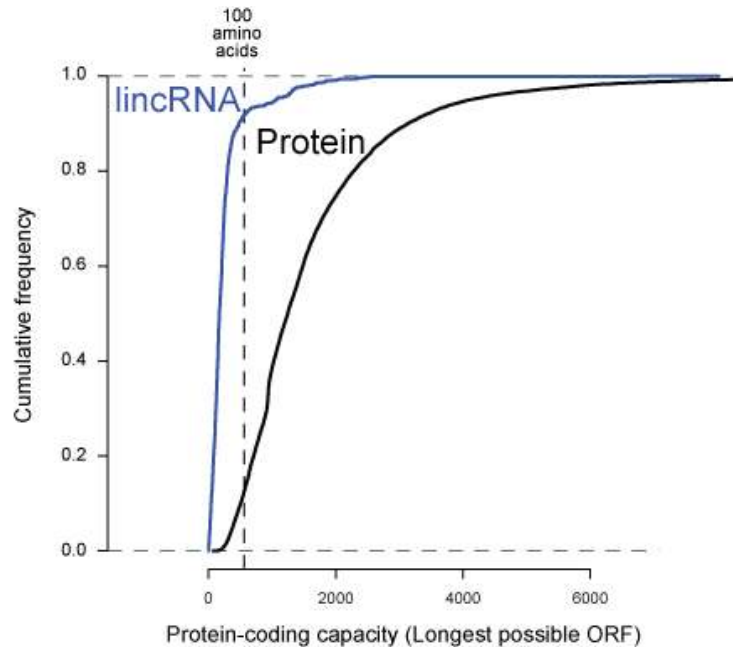


Class 2: Intergenic ncRNA (lincRNA)

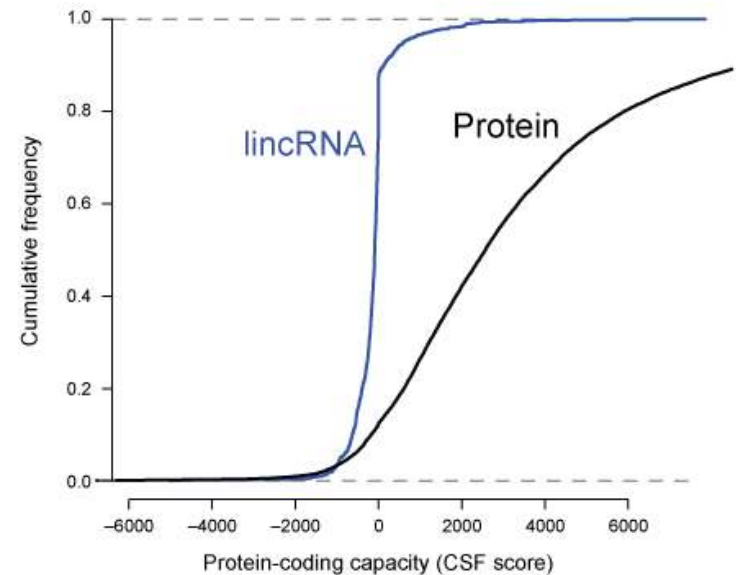


lincRNAs: How do we know they are non-coding?

ORF Length

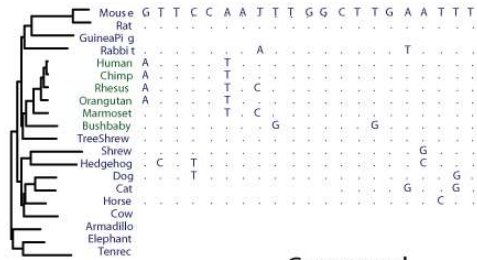


CSF (ORF Conservation)

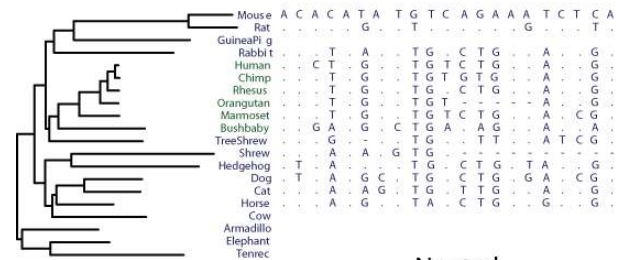


>95% do not encode proteins

lincRNAs: under constraint



Conserved



Neutral

High ← Conservation → Low

What about novel coding genes?

Class 1: Overlapping ncRNA



Class 2: Large Intergenic ncRNA (lincRNA)

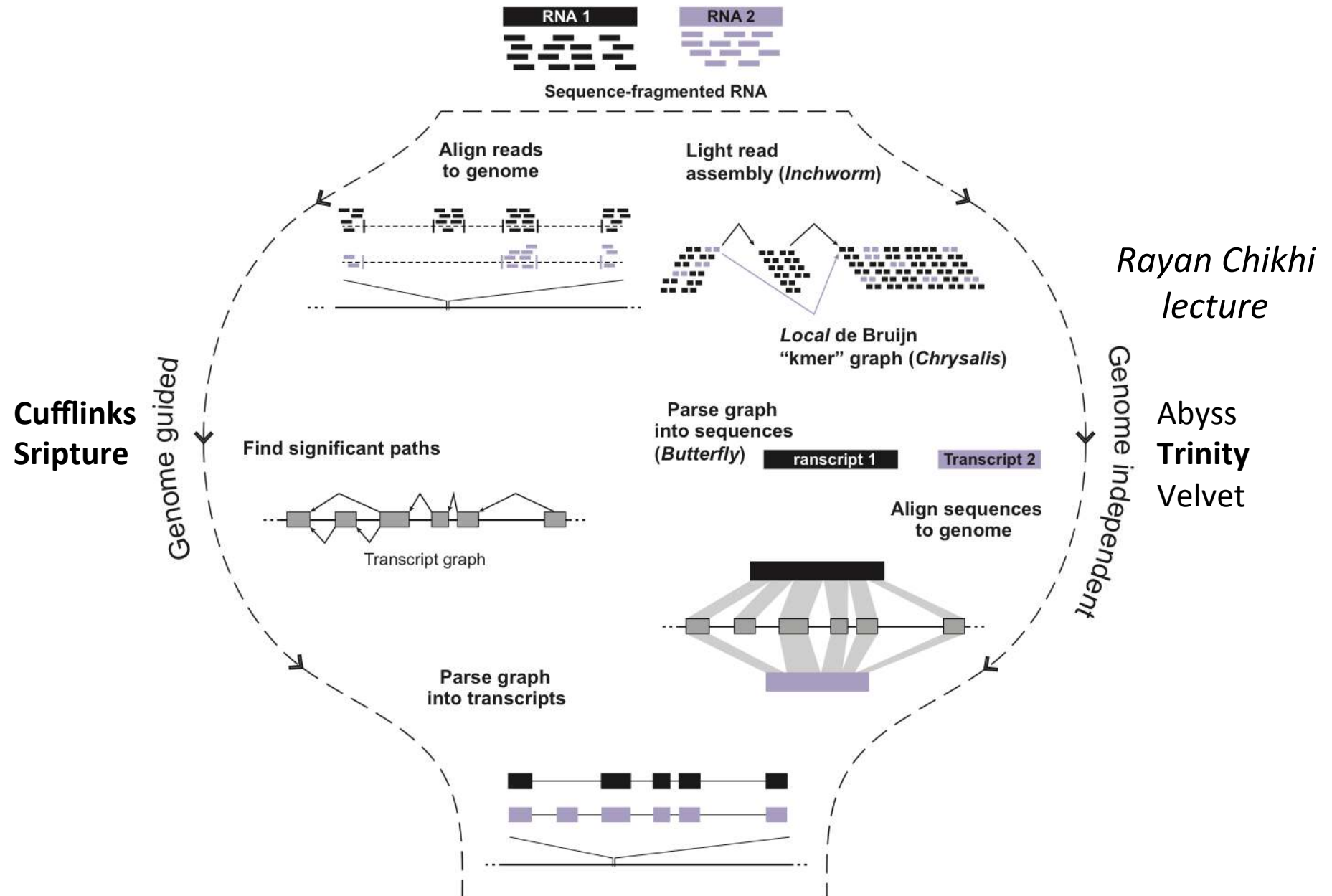


Class 3: Novel protein-coding genes



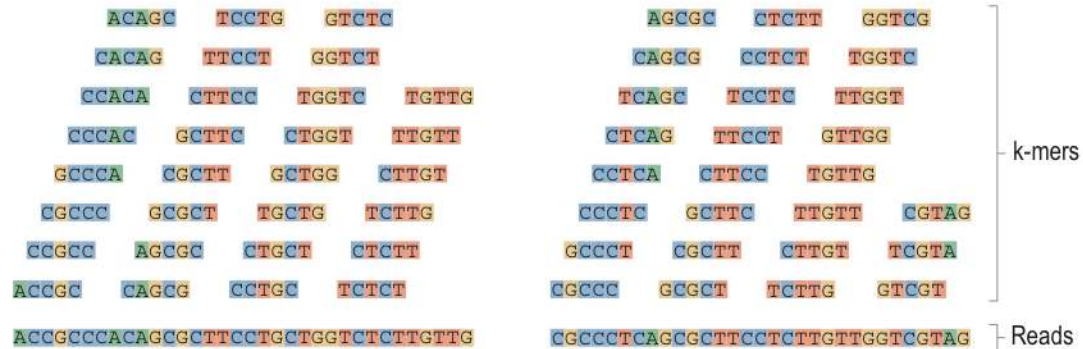
~40 novel protein-coding genes

If there is no reference genome!
Genome independent methods



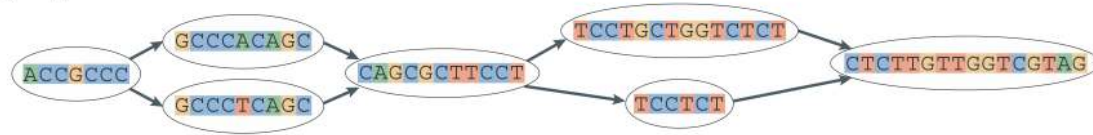
Assembly approach

1) Extract all substring of length k from reads



Assembly approach

3) Collapse graph



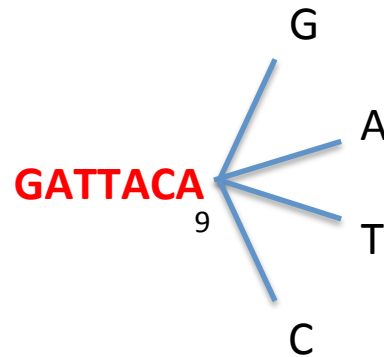
But this challenging already with DNA and RNA has many different challenges

The Trinity approach: Localize

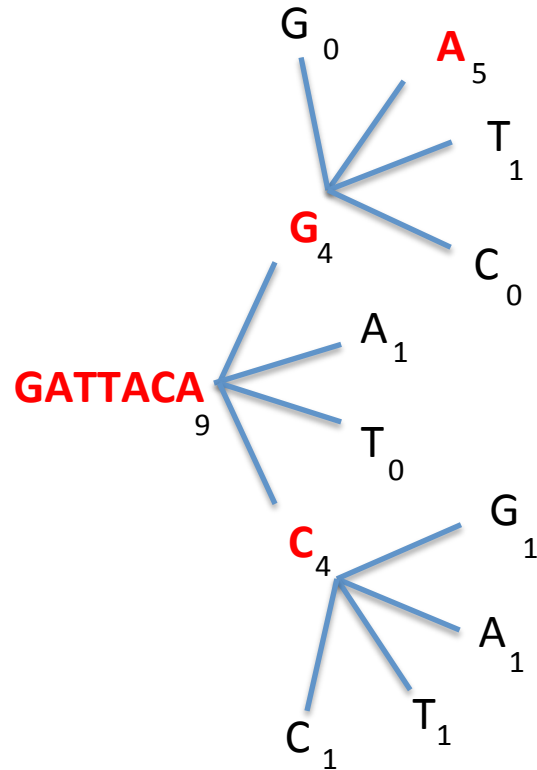
Decompose all reads into overlapping Kmers (25-mers)

Identify seed kmer as most abundant Kmer, ignoring low-complexity kmers.

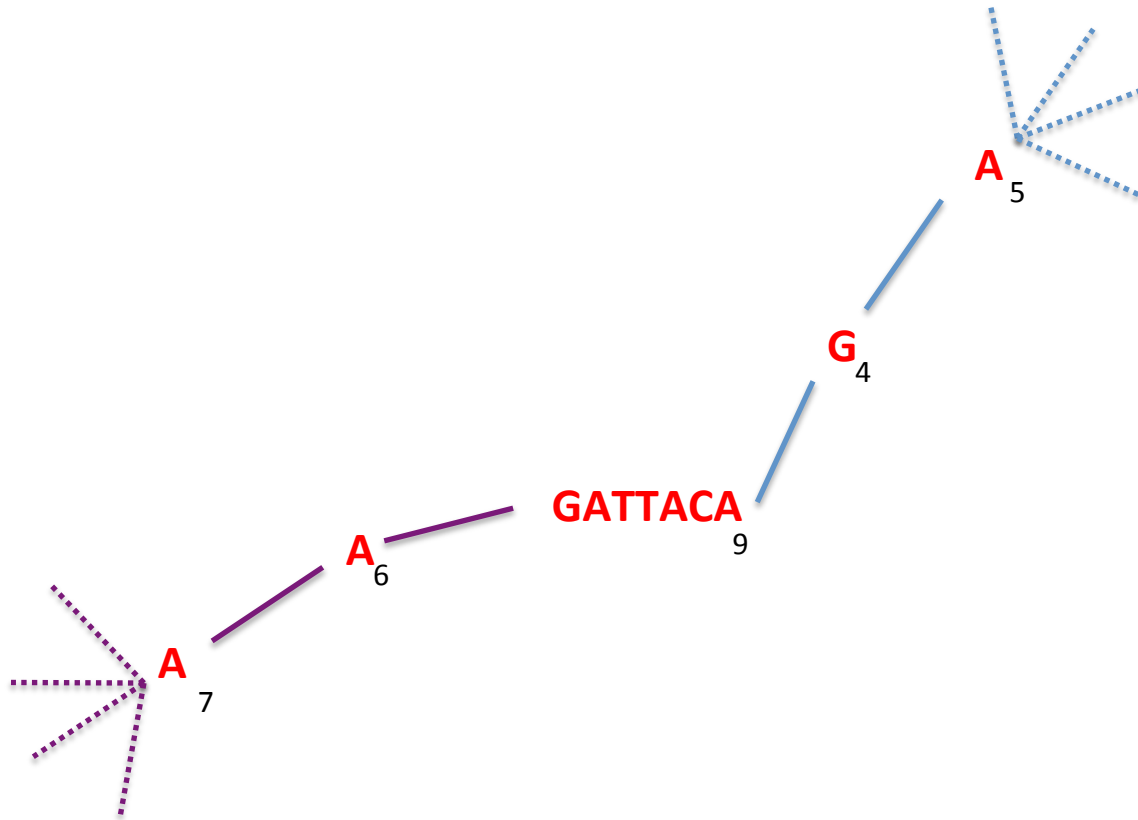
Extend kmer at 3' end, guided by coverage.



The Trinity approach: Localize



The Trinity approach: Localize



Report contig: **....AAGATTACAGA....**

Remove assembled kmers from catalog, then repeat the entire process.

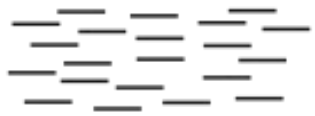
Trinity approach: Assemble



RNA-Seq
reads



Group similar contigs



key: localize the assembly problem

Pros and cons of each approach

- Transcript assembly methods are the obvious choice for organisms without a reference sequence.
- Genome-guided approaches are ideal for annotating high-quality genomes and expanding the catalog of expressed transcripts and comparing transcriptomes of different cell types or conditions.
- Hybrid approaches for lesser quality or transcriptomes that underwent major rearrangements, such as in cancer cell.
- More than 1000 fold variability in expression levels makes assembly a harder problem for transcriptome assembly compared with regular genome assembly.
- Genome guided methods are very sensitive to alignment artifacts.

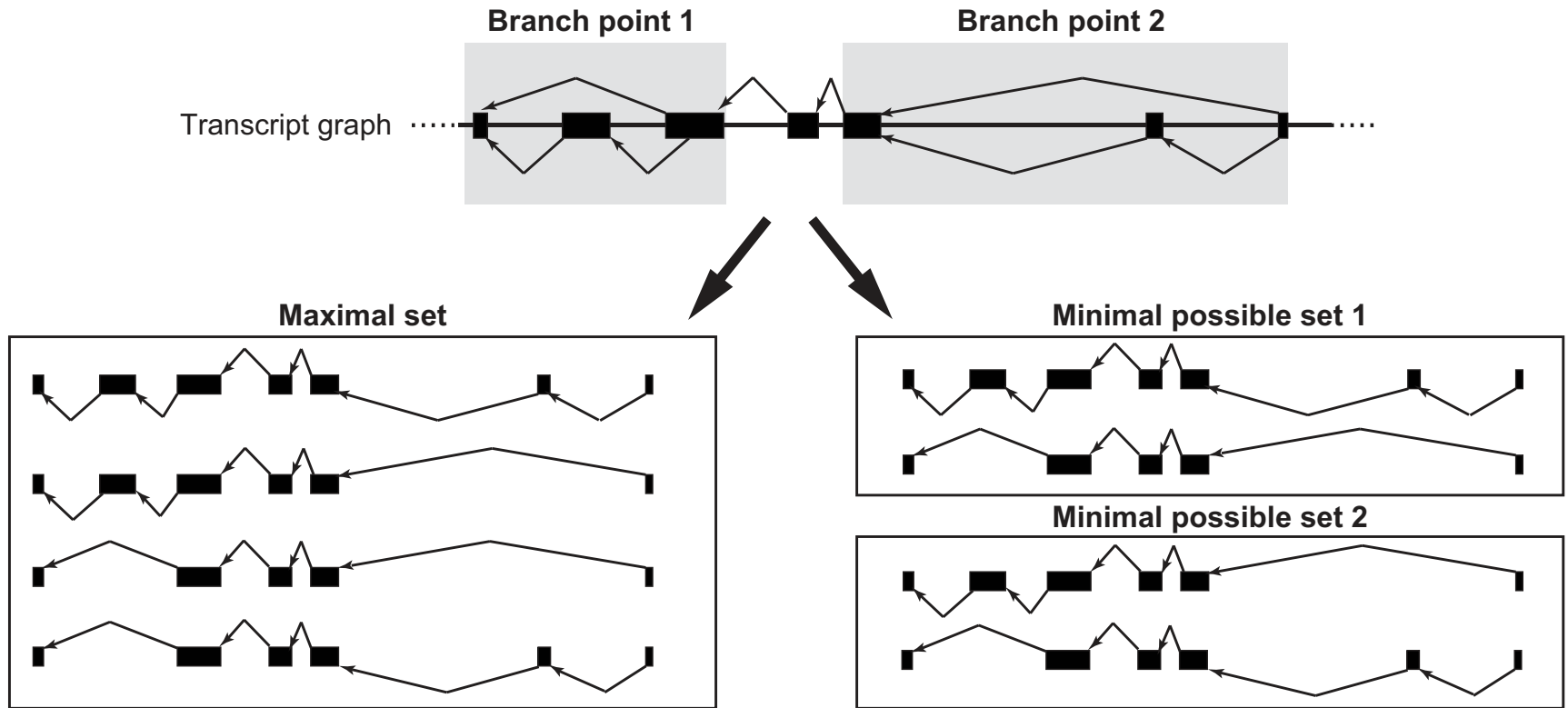
RNA-Seq transcript reconstruction software

Assembly	Genome Guided
Oasis (velvet)	Cufflinks
Trans-ABYSS	Scripture
Trinity	

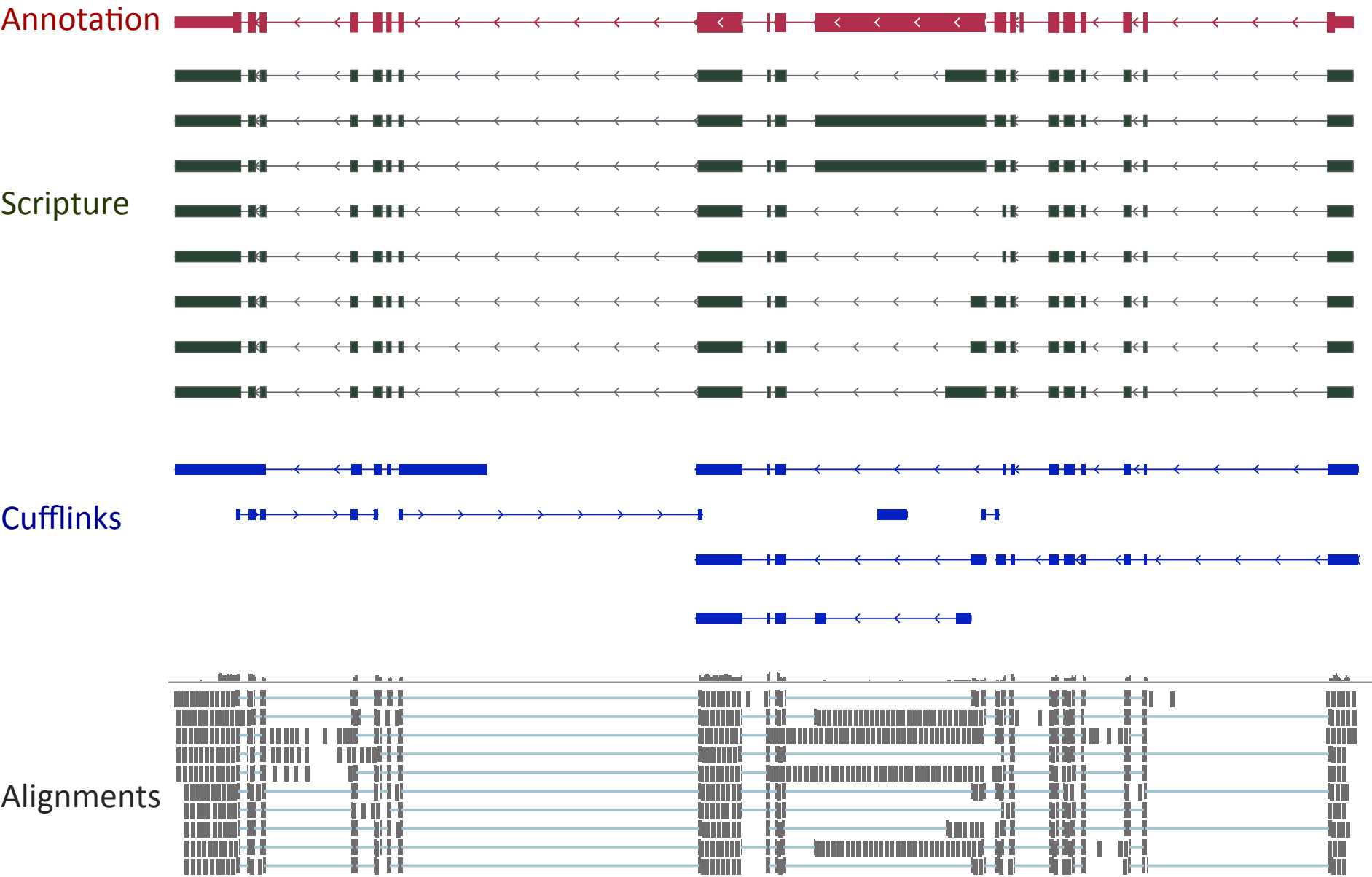
Differences between Cufflinks and Scripture

- Scripture was designed with annotation in mind. It reports all possible transcripts that are *significantly expressed* given the aligned data (*Maximum sensitivity*).
- Cufflinks was designed with quantification in mind. It limits reported isoforms to the minimal number that explains the data (*Maximum precision*).

Maximum sensitivity vs. maximal precision



Differences between Cufflinks and Scripture - Example

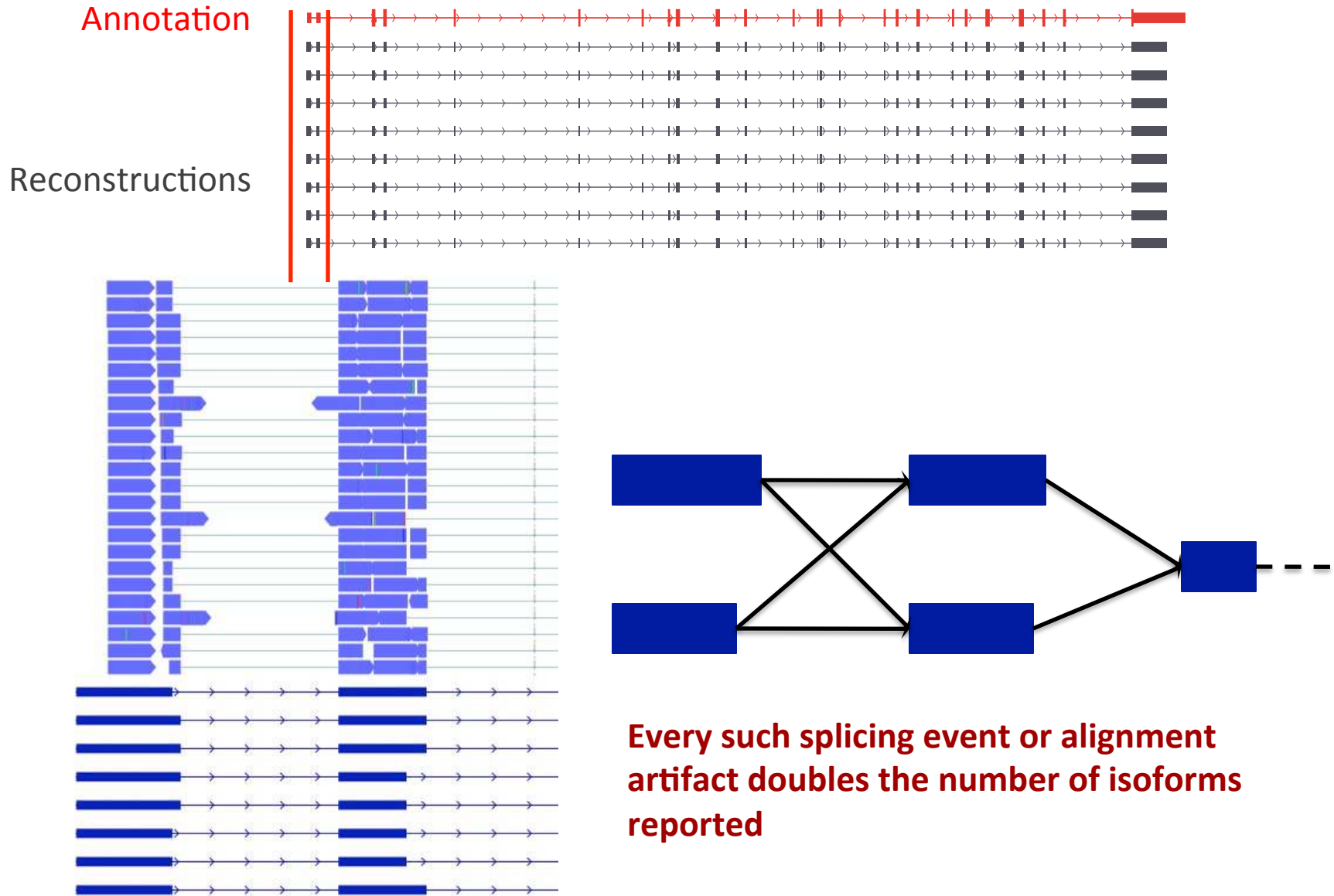


Comparing reconstructions

	CPU Hours	Total Memory	Genes fully reconstructed	Mean isoforms per reconstruction	Mean fragments per known annotation	Number of fragments predicted
Cufflinks	10	1.4 G	5,994	1.2	1.4	159,856
Scripture	16	3.5 G	6,221	1.6	1.3	61,922
Trans- Abyss	650	120 G ⁴	3,330	4.7	2.6	3,117,238

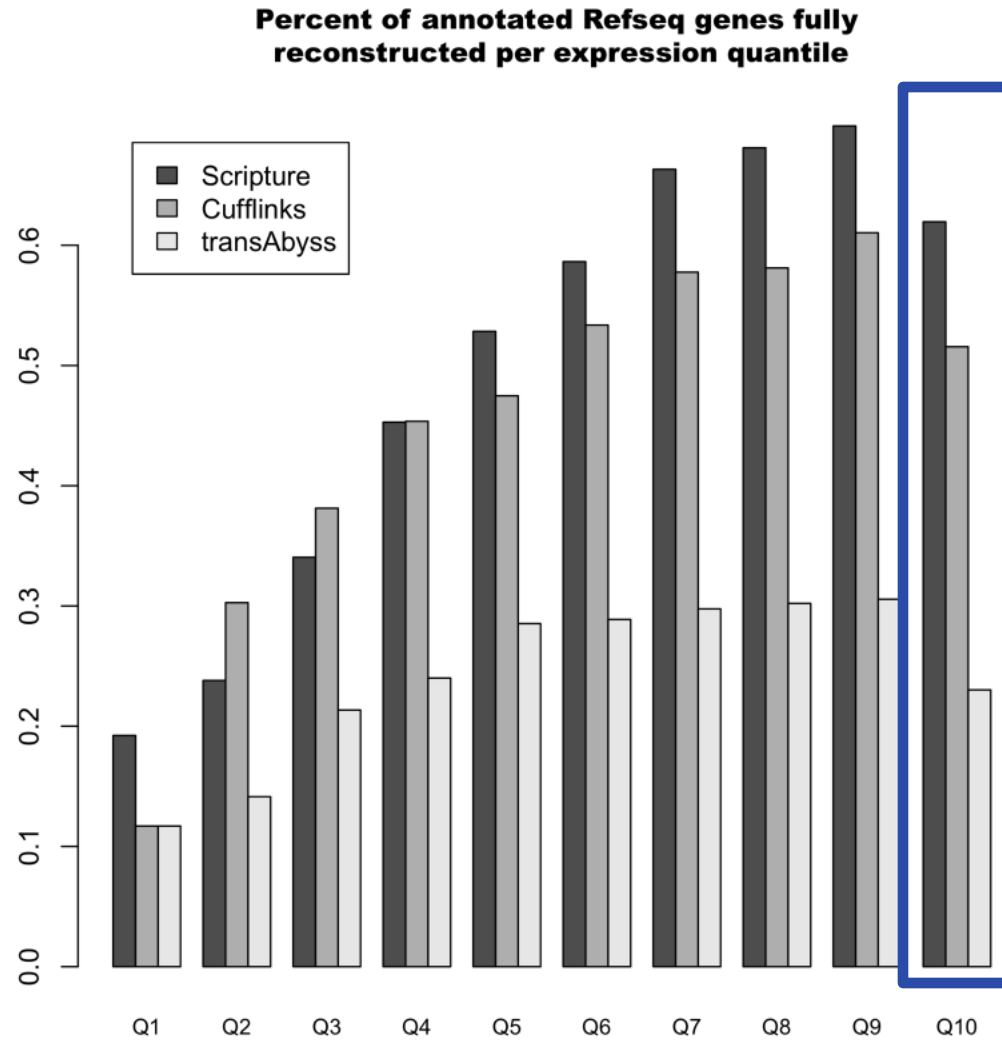
Many of the bogus locus and isoforms are due to alignment artifacts

Why so many isoforms



Longer reads (already possible) will reduce the uncertainty and possibilities

Reconstruction comparison



Too much of a good thing is not handled well by most reconstruction methods

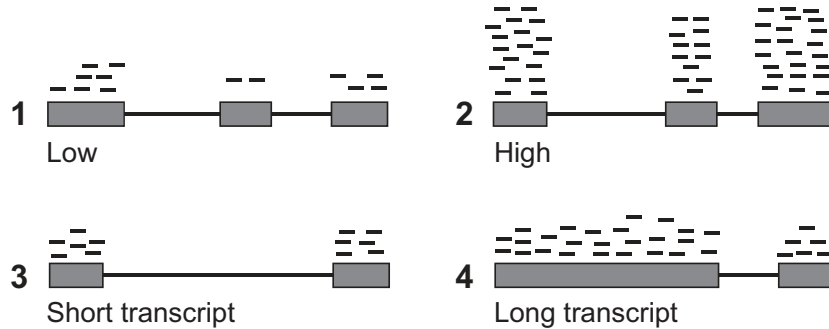
Analysis of counting data requires 3 broad tasks

- Read mapping (alignment): Placing short reads in the genome
- Reconstruction: Finding the regions that originated the reads
- Quantification:
 - Assigning scores to regions
 - Finding regions that are differentially represented between two or more samples.

RNA-Seq quantification

- Is a given gene (or isoform) expressed?
- Is expression gene A $>$ gene B?
- Is expression of gene A isoform $a_1 >$ gene A isoform a_2 ?
- Given two samples is expression of gene A in sample 1 $>$ gene A in sample 2?

Quantification: only one isoform



$$RPKM = 10^9 \frac{\#reads}{length \times TotalReads}$$

Reads per kilobase of exonic
sequence per million mapped reads
(Mortazavi et al Nature methods 2008)

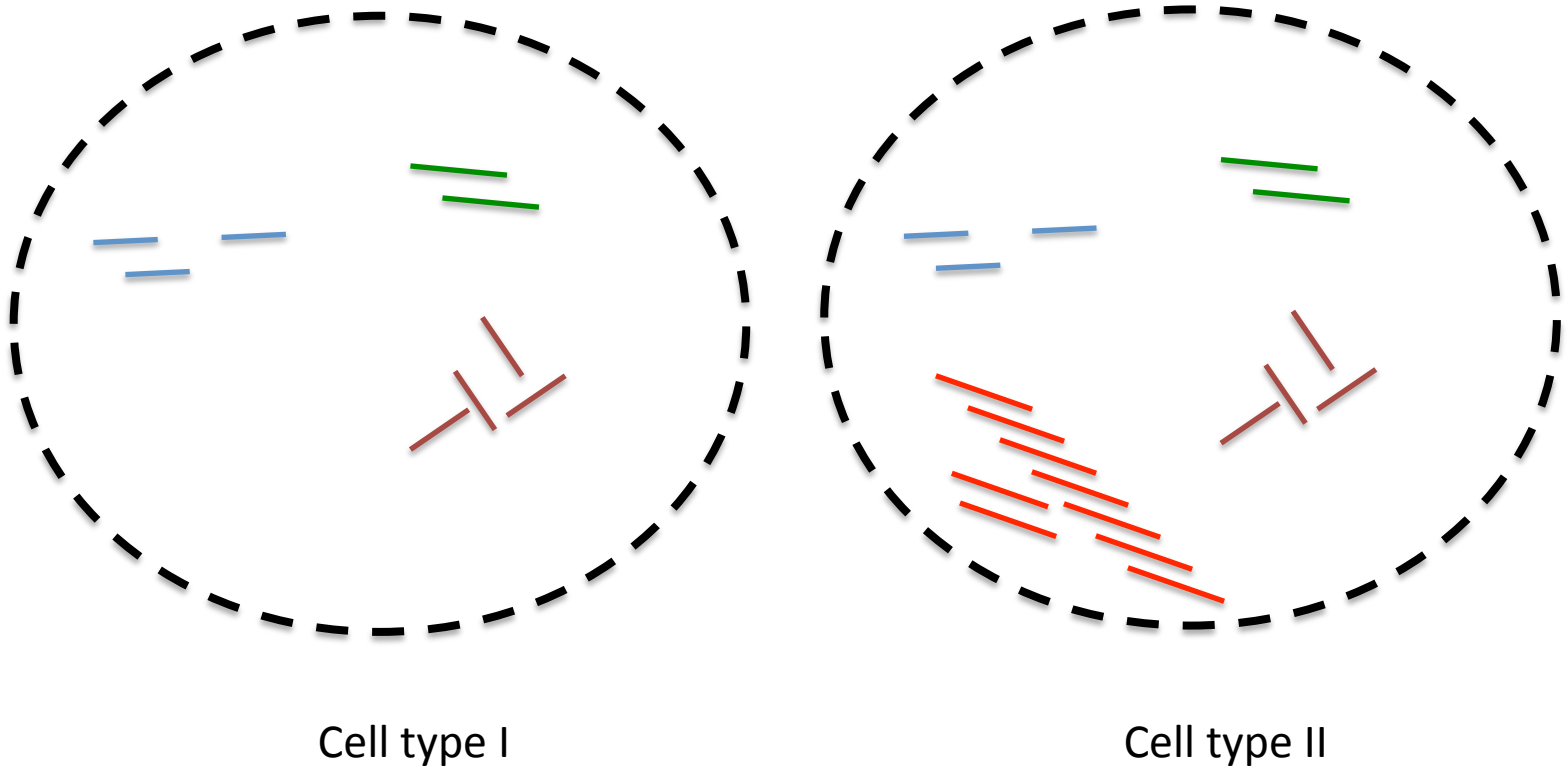
- Fragmentation of transcripts results in length bias: longer transcripts have higher counts
- Different experiments have different yields. Normalization is key for cross lane comparisons

Complexity increases when multiple isoforms exist

Normalization depends on the application

- To compare within a sequence run (lane), RPKM accounts for length bias.
- RPKM is not optimal for cross experiment comparisons.
 - Different samples may have different compositions.

Step 2: Different RNA compositions



Normalizing by total reads does not work well for samples with very different RNA composition

Step2: More robust normalization

Counts for gene i in experiment j

$$s_j = \text{median}_i \frac{k_{ij}}{\left(\prod_{v=1}^m k_{iv} \right)^{1/m}}$$

Geometric mean for that gene over ALL experiments

i runs through all n genes

j through all m samples

k_{ij} is the observed counts for gene i in sample j

s_j is the normalization constant

Lets do an experiment (and do a short R practice)

```
> s1 = c(100, 200, 300, 400, 10)
```

```
> s2 = c(50, 100, 150, 200, 500)
```

```
> norm = sum(s2)/sum(s1)
```

```
> plot(s2, s1*norm, log="xy")
```

```
> abline(a = 0, b = 1)
```

```
> g = sqrt(s1 * s2)
```

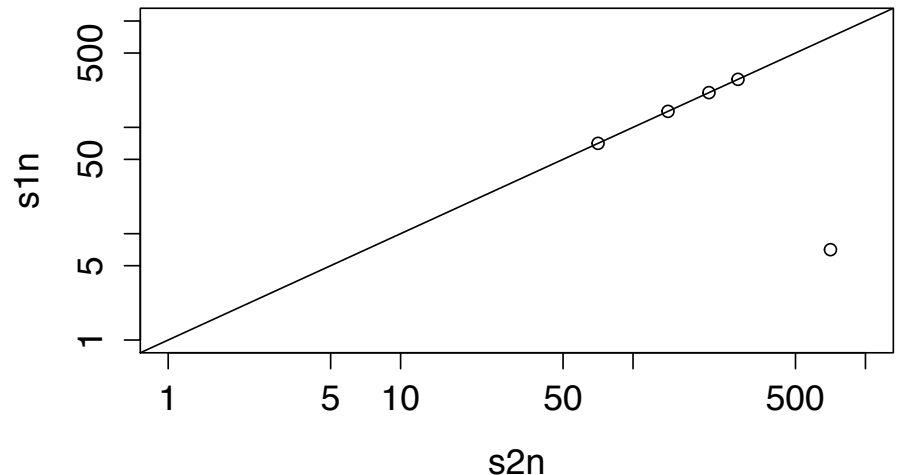
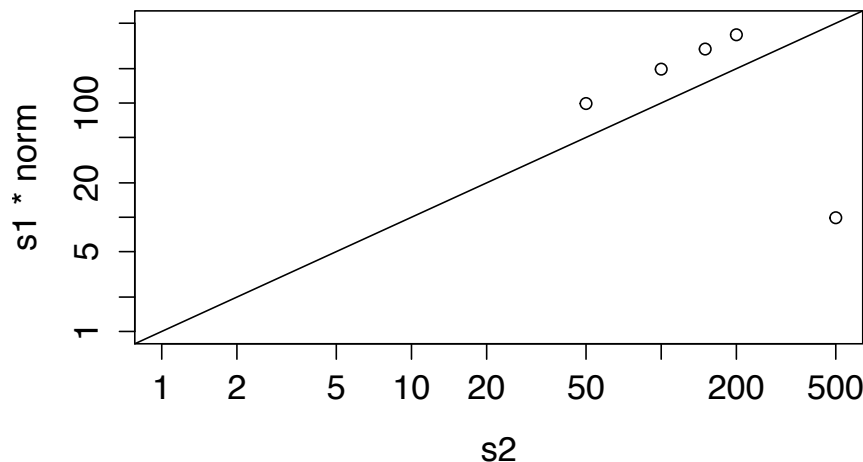
```
> s1n = s1/median(s1/g); s2n = s2/median(s2/g)
```

```
> plot(s2n, s1n, log="xy")
```

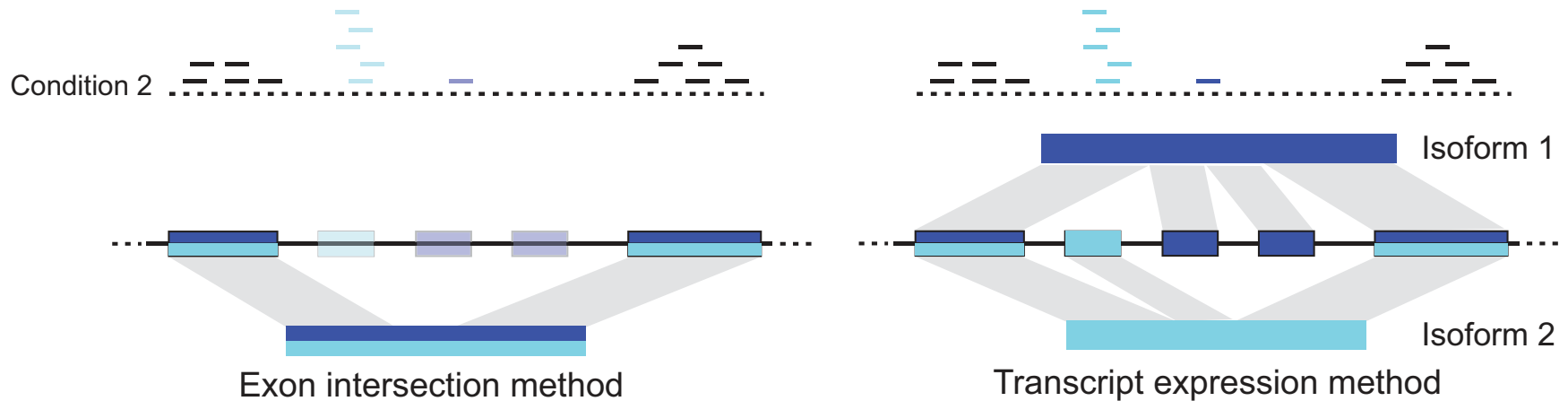
```
> abline(a = 0, b = 1)
```

Similar read number,
one transcript many fold changed

Size normalization results in 2-fold
changes in *all* transcripts



But, how to compute counts for complex gene structures?



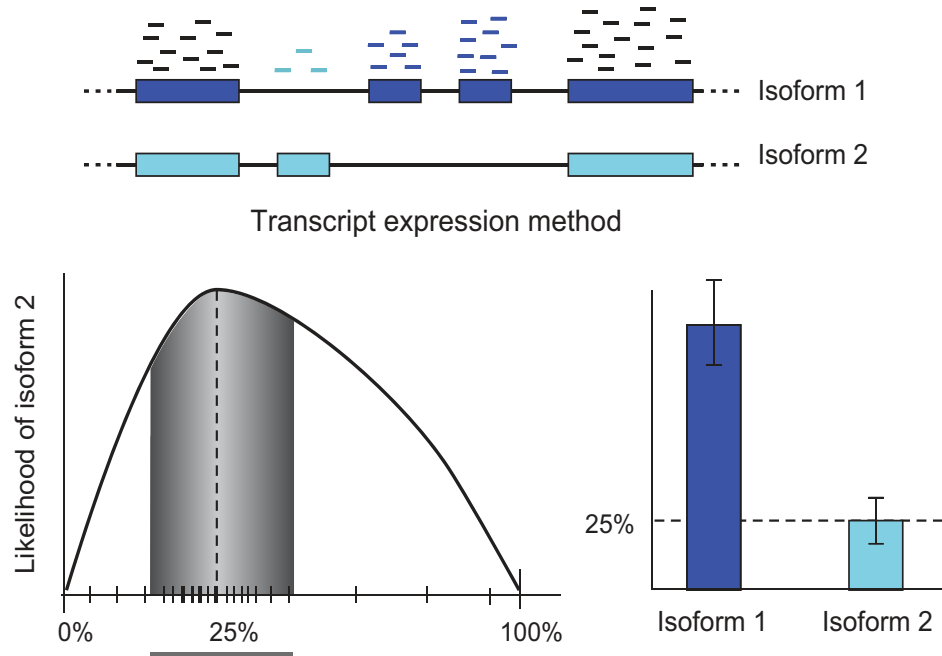
Three popular options:

Exon *intersection* model: Score constituent exons

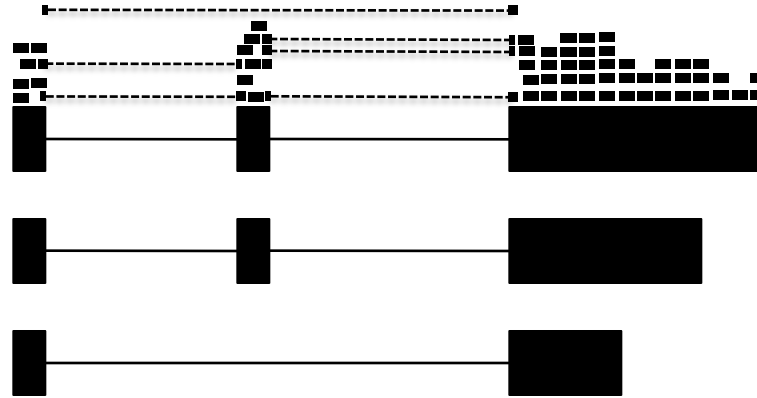
Exon *union* model: Score the the “merged” transcript

Transcript expression model: Assign reads uniquely to different isoforms. *Not a trivial problem!*

Quantification: read assignment method



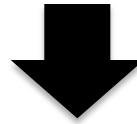
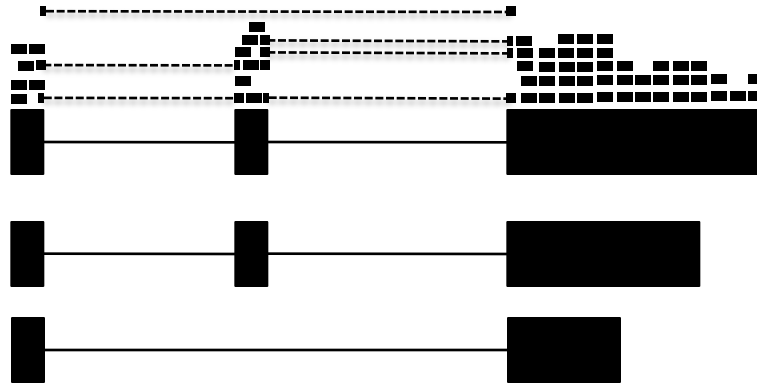
Quantification with multiple isoforms



How do we define the gene expression?

How do we compute the expression of each isoform?

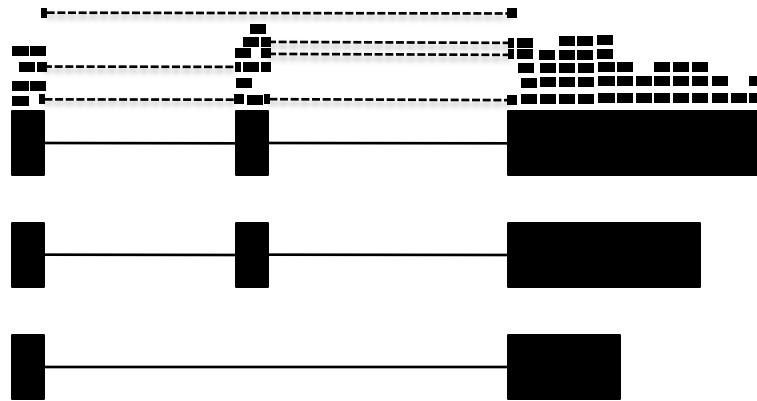
Computing gene expression



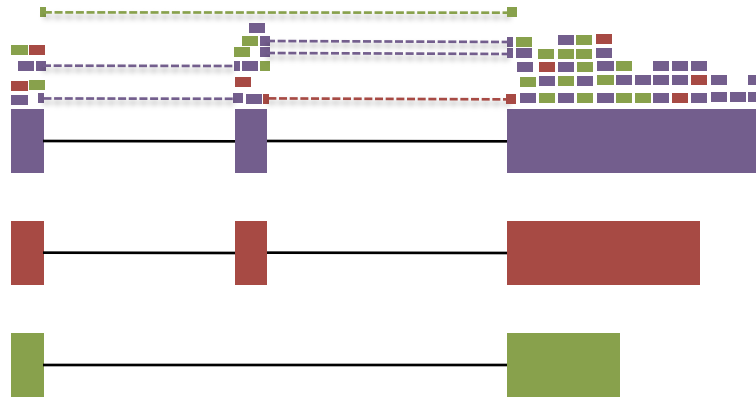
Idea1: RPKM of the
constitutive reads
(Neuma, Alexa-Seq,
Scripture)



Computing gene expression — isoform deconvolution



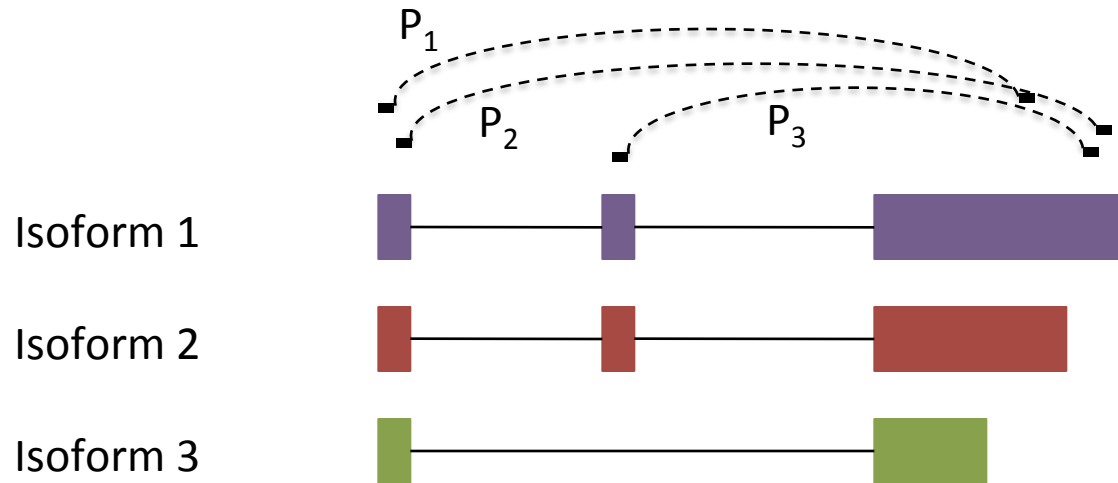
Computing gene expression — isoform deconvolution



If we knew the origin of the reads we could compute each isoform's expression. The gene's expression would be the sum of the expression of all its isoforms.

$$E = \text{RPKM}_1 + \text{RPKM}_2 + \text{RPKM}_3$$

Paired-end reads are easier to associate to isoforms

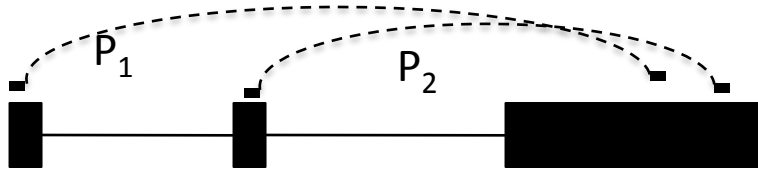


Paired ends increase isoform deconvolution confidence

- P₁ originates from isoform 1 or 2 but not 3.
- P₂ and P₃ originate from isoform 1

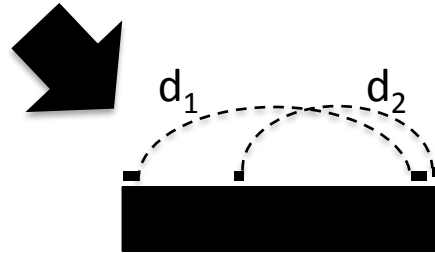
Do paired-end reads also help identifying reads originating in isoform 3?

We can estimate the insert size distribution

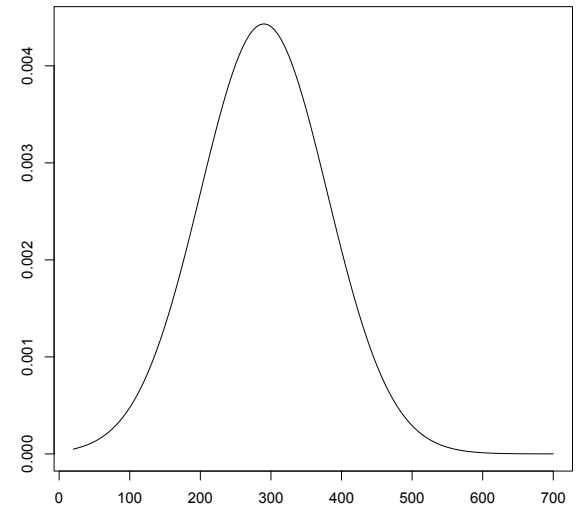


Get all single isoform reconstructions

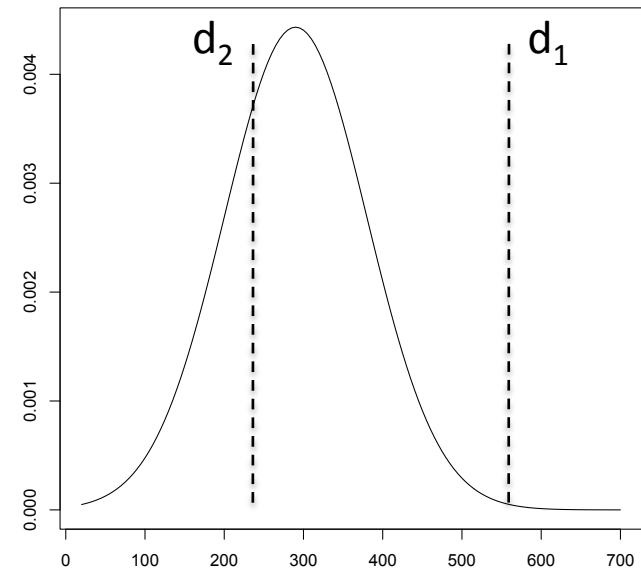
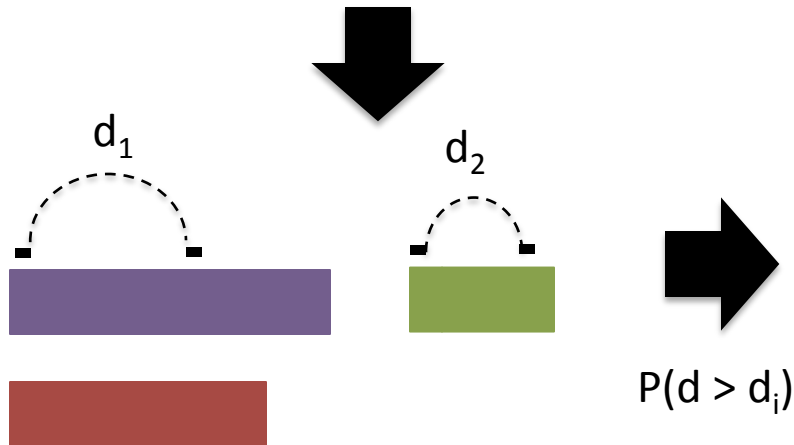
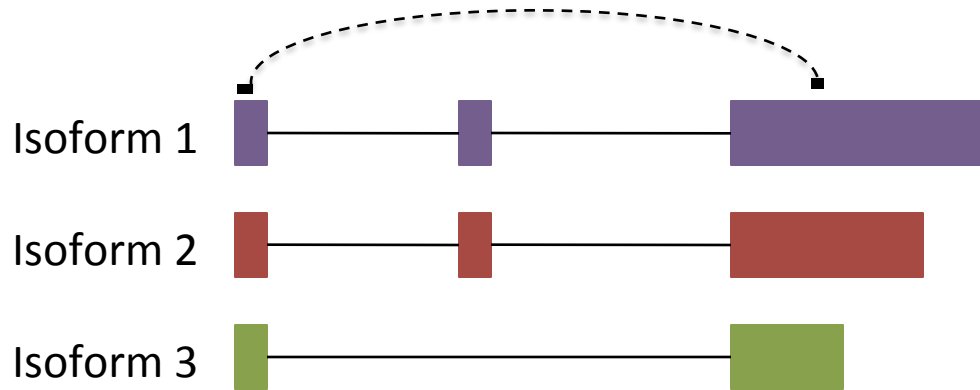
Splice and compute insert distance



Estimate insert size empirical distribution



... and use it for probabilistic read assignment



For methods such as MISO, Cufflinks and RSEM, it is critical to have paired-end data

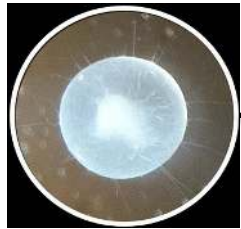
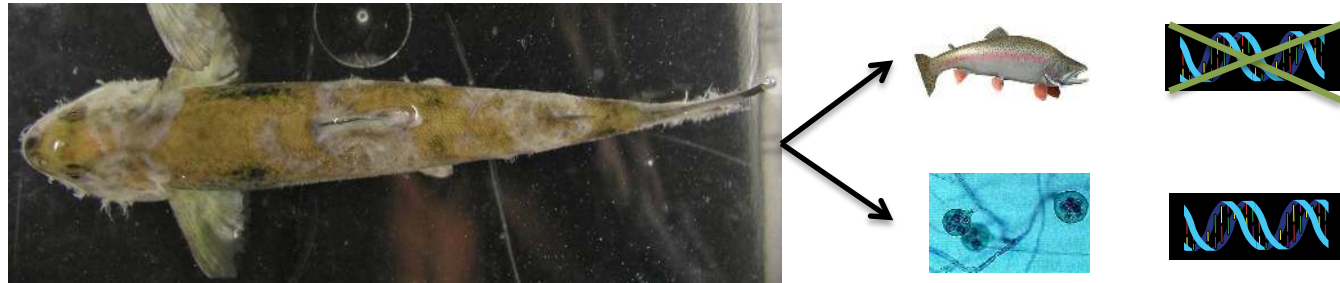
RNA-Seq quantification summary

- Counts must be estimated from ambiguous read/transcript assignment.
 - Using simplified gene models (intersection)
 - Probabilistic read assignment
- Counts must be normalized
 - RPKM is sufficient for intra-library comparisons
 - More sophisticated normalizations to account for differences in library composition for inter-library comparisons.

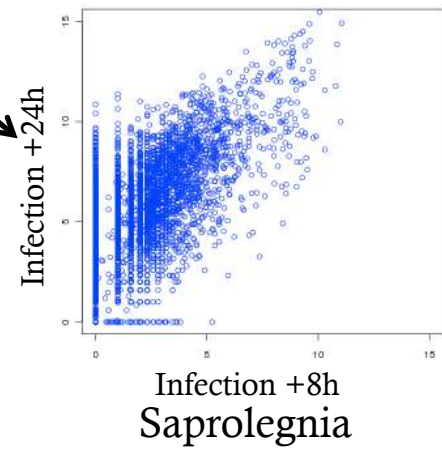
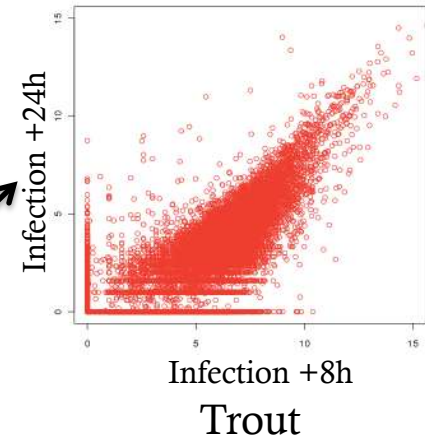
Programs to measure transcript expression

Implemented method	
Alexa-seq	Gene expression using intersection model
ERANGE	Gene expression using union model
Scripture	Gene expression using intersection model
Cufflinks	Transcript deconvolution by solving the maximum likelihood problem
MISO	Transcript deconvolution by solving the maximum likelihood problem
RSEM	Transcript deconvolution by solving the maximum likelihood problem

Advantages of RSEM, DESeq



Infected fish cells



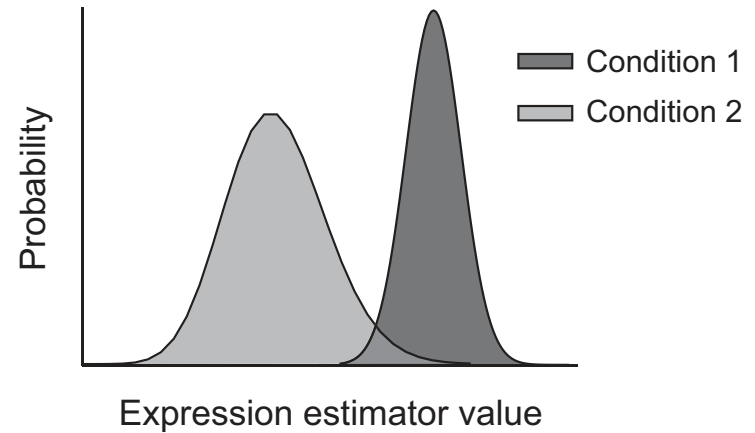
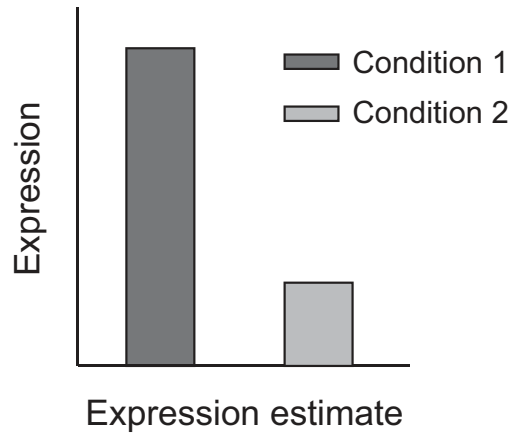
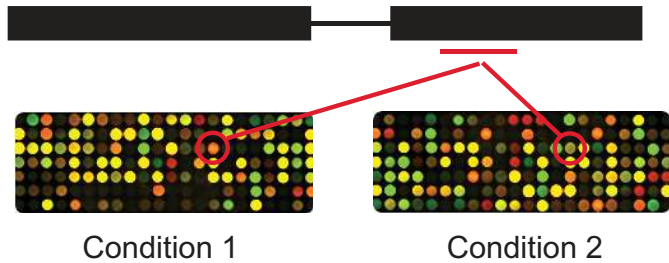
Analysis of counting data requires 3 broad tasks

- Read mapping (alignment): Placing short reads in the genome
- Reconstruction: Finding the regions that originated the reads
- Quantification:
 - Assigning scores to regions
 - Finding regions that are differentially represented between two or more samples.

Differential Gene Expression Questions

- Finding genes that have different expression between two or more conditions.
- Find gene with isoforms expressed at different levels between two or more conditions.
 - Find differentially used slicing events
 - Find alternatively used transcription start sites
 - Find alternatively used 3' UTRs

Differential gene expression using RNA-Seq



•(Normalized) read counts $\leftrightarrow$ Hybridization intensity

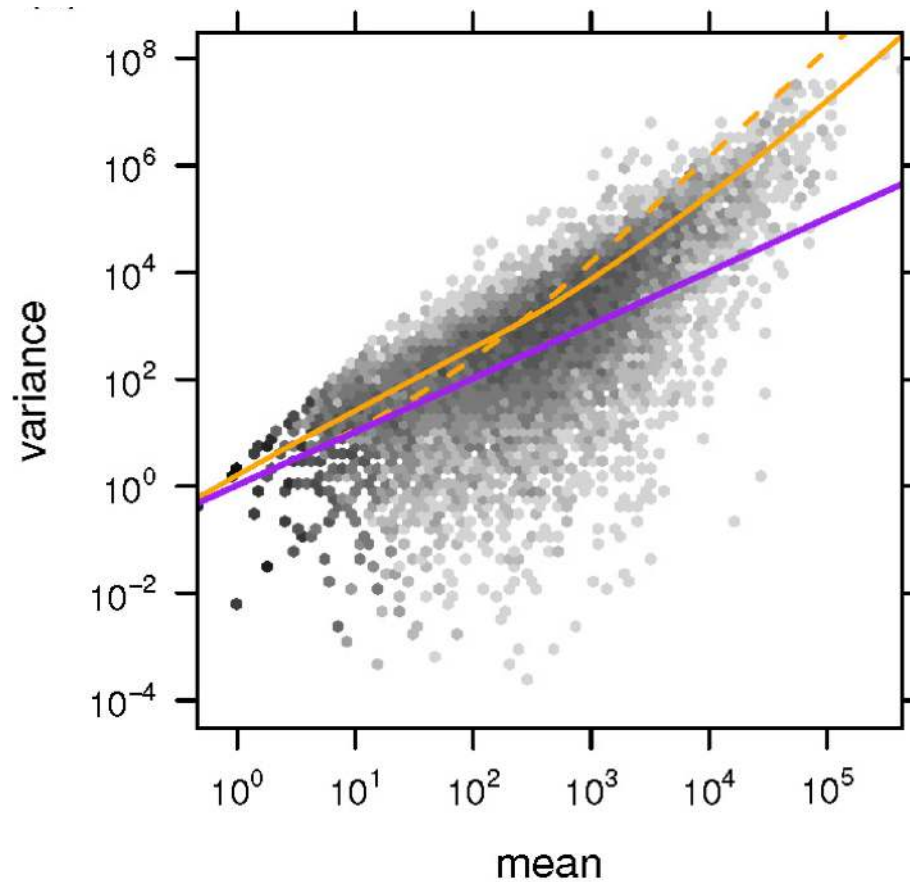
Differential analysis strategies

- Use read counts
 - Standard Fisher exact test

	Condition A	Condition B
Gene A reads	n_a	n_b
Rest of reads	N_a	N_b

- Model read counts (Poisson, negative binomial) and test whether models are distinct
- Use empirical approaches that do not rely on parametric assumptions (more on this later)

Poisson model does not work



Adapted from Anders, 2010

Biological variance does not follow a Poisson model

Using a parametric model (DESeq, Cufflinks)

Because of overdispersion DESeq and Cufflinks uses a Negative binomial to model read counts

$$K_{g,s} \sim \mathcal{N}(K_{g,s}, \sigma_{g,s}); \quad \sigma_{g,s} = K_{g,s} + \nu_{g,s}$$

Given observed counts for two samples in replicates

$$k_{g,s_1} \dots k_{g,s_n}; \quad k_{g,t_1} \dots k_{g,t_m}$$

DESeq tests the null hypothesis that all counts are sampled from the same distribution

$$P\left(\sum_i k_{g,s_i} + \sum_j k_{g,t_j} \mid \mu_s = \mu_t\right)$$

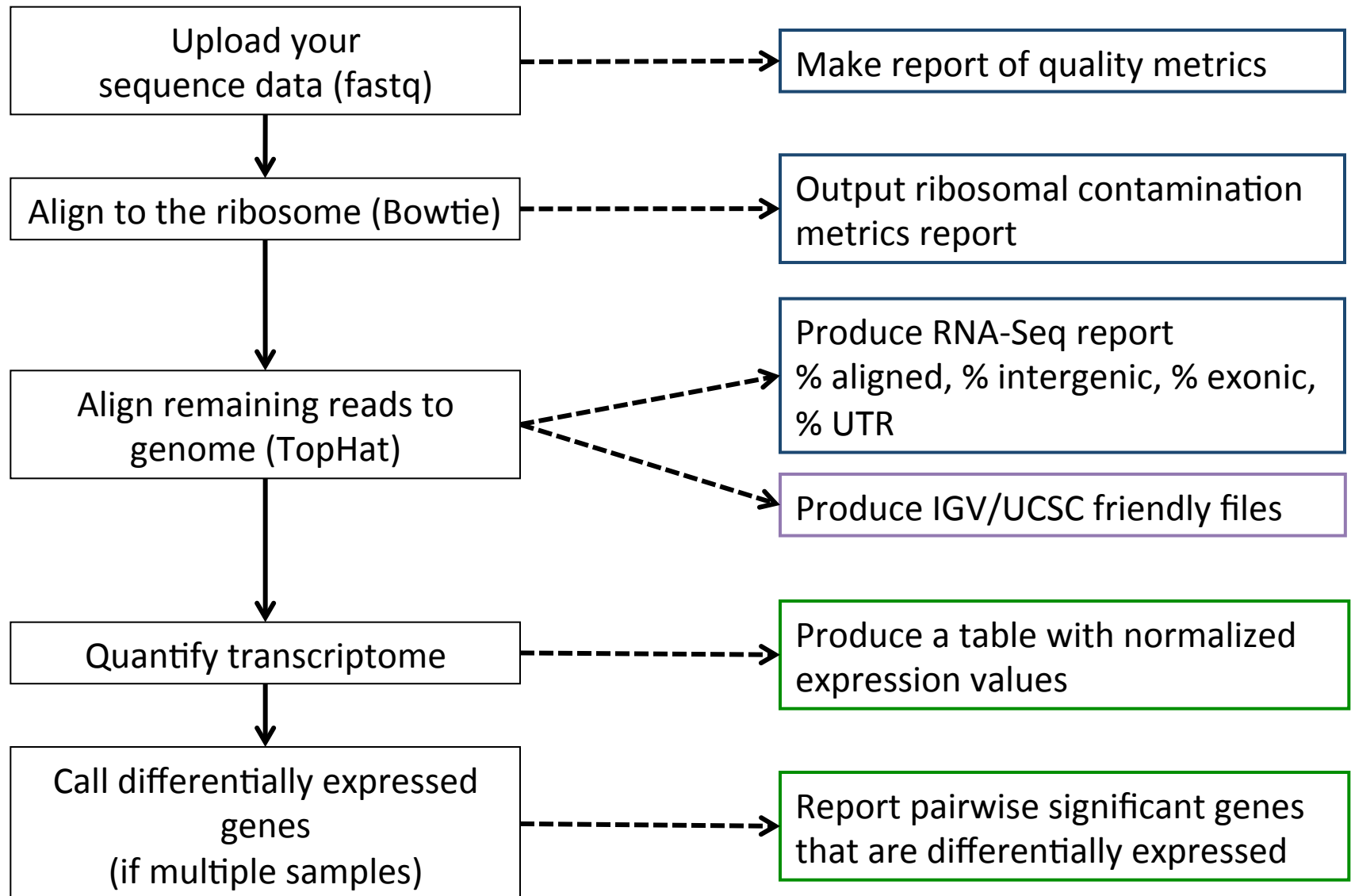
RNA-Seq differential expression software

	Underlying model	Notes
DegSeq	Normal. Mean and variance estimated from replicates	Works directly from reference transcriptome and read alignment
EdgeR	Negative Binomial	Gene read counts table
DESeq	Negative Binomial	Gene read counts table
Cufflinks	Poisson Negative Binomial	Works directly from the alignments
Myrna	Empirical	Sequence reads and reference transcriptome

The quest for inexpensive expression assays

- Goal: Routinely profile hundreds of samples
- Why?
 - Human variability in health and disease
 - Perturbation studies
 - Clinical applications of expression profiling
- Current costs
 - Affy ~\$300-\$400/sample
 - Illumina bead arrays \$150/sample
 - RNA-Seq (20 mill reads) ~\$400-\$500/sample (\$350 in sequencing)
- RNA-Seq disadvantages
 - Complex analysis
 - Length bias

Our typical pipeline (e.g. RNA-Seq)



Final considerations on quantification

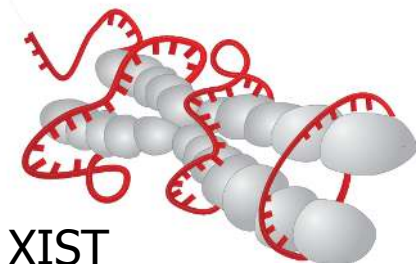
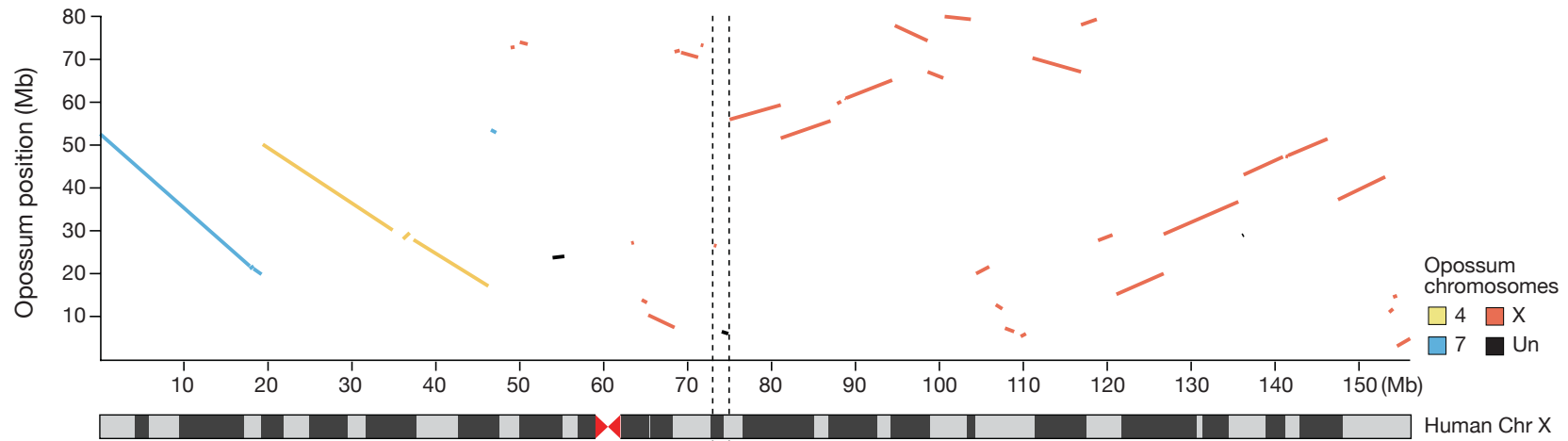
- Using different libraries:
 - Targeting the 3' end
 - Targeting 5' end
- What depth do we really need?

Final considerations: The steps of Sequencing analysis

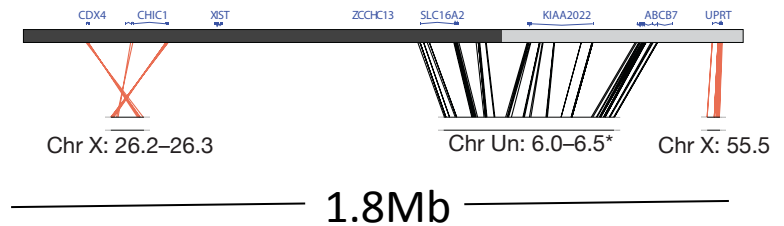
- Filter reads (fastq file) by removing adapter, splitting barcodes.
 - Evaluate overall quality, look for drop in quality at ends. Trim reads if ends are of low quality
- Alignment to the genome
 - Use transcriptome if available
 - Filter out likely PCR duplicates (reads that align to the same place in the genome)
 - Evaluate ribosomal contamination
 - What percent of reads aligned
- Reconstruct(?)
- Quantify
 - Normalize according to application

A Vignette: Large non-coding RNA,
are they an evolutionary playground?

Lincs are placental specific



XIST



XIST does not seem to exist in the marsupial genome, it is likely a placental innovation

lincRNAs play key roles in biological processes

The Noncoding RNA *Taurine Upregulated Gene 1*
Is Required for Differentiation
of the Murine Retina

Long Noncoding RNA as Modular Scaffold of Histone Modification Complexes

lincRNAs act in the circuitry controlling
pluripotency and differentiation

Rsx is a metatherian RNA with *Xist*-like properties in
X-chromosome inactivation

lncRNA-dependent mechanisms of androgen-
receptor-regulated gene activation programs

Circadian changes in long noncoding RNAs in the
pineal gland

A Long Noncoding RNA Mediates Both
Activation and Repression of Immune
Response Genes

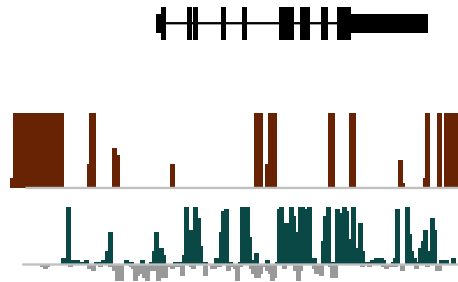
Play important roles in a variety of
biological process

- Development
- Cancer
- Immunity
- Differentiation
- Circadian cycle

Morten Møller^f,
Comparative Sequencing

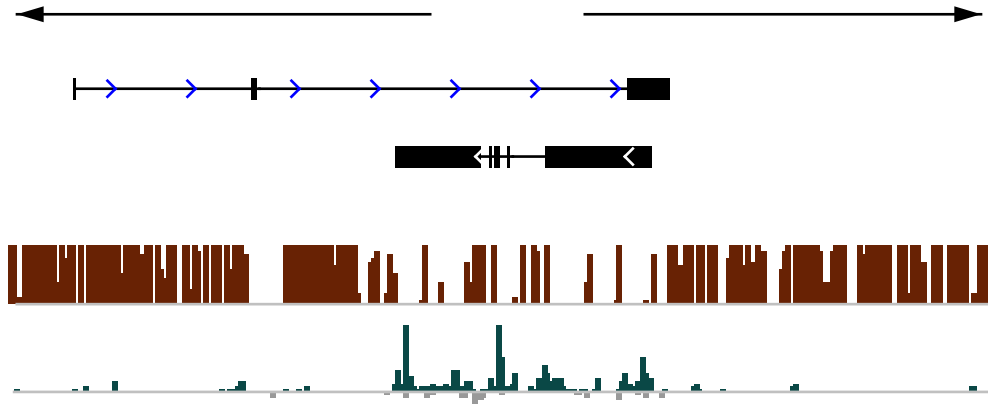
Susan Carpenter,^{1,2} Maninjay Atianand,¹ Daniel Aiello,¹ Emiliano P. Ricci,³
Pallavi Gandhi,¹ Lisa L. Hall,⁴ Meg Byron,⁴ Brian Monks,¹ Meabh Henry-Bezy,¹
Jeanne B. Lawrence,⁴ Luke A. J. O'Neill,² Melissa J. Moore,³ Daniel R.
Caffrey,^{1*†} Katherine A. Fitzgerald^{1*†}

lincRNA are an evolutionary puzzle



Intergenic

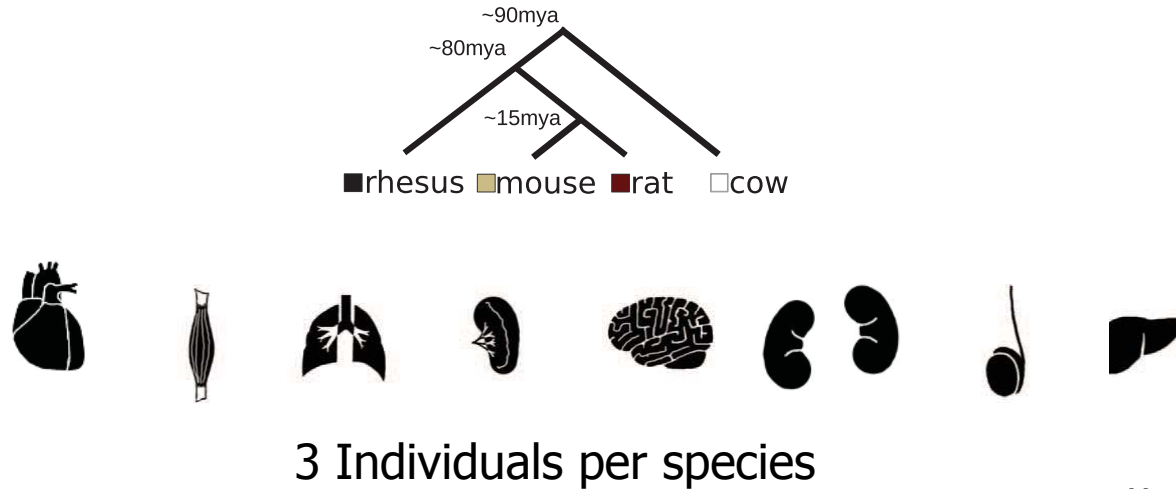
lincRNA



Using expression to assess conservation

- Hypothesis 1: lincRNAs are under “patchy” constraint or a rapidly evolving (Xist?)
 - Sequence conservation would be underestimating lincRNA conservation
 - Evidence of syntenic **conserved expression**
- Hypothesis 2: lincRNAs are young and many are transcriptional noise
 - **Expression is species specific**
 - Sequence conservation not informative
- Hypothesis 3: lincRNAs are easily replaceable by functional orthologs (linc-cox2?)
 - Sequence conservation not informative
 - Syntenic conserved expression not informative

Evolutionary profiling RNA-Seq dataset



Merkin et al. Science 2012

ARTICLE

doi:10.1038/nature10532

The evolution of gene expression levels in mammalian organs

Human
+
Chimp

David Brawand^{1,2*}, Magali Soumillon^{1,2*}, Anamaria Necșulea^{1,2*}, Philippe Julien^{1,2}, Gábor Csárdi^{2,3}, Patrick Harrigan⁴, Manuela Weier¹, Angélica Liechti¹, Ayinuer Aximu-Petri⁵, Martin Kircher⁵, Frank W. Albert^{5†}, Ulrich Zeller⁶, Philipp Khaitovich⁷, Frank Grützner⁸, Sven Bergmann^{2,3}, Rasmus Nielsen^{4,9}, Svante Pääbo⁵ & Henrik Kaessmann^{1,2}

A human centric approach

All GENCODE long noncoding transcripts

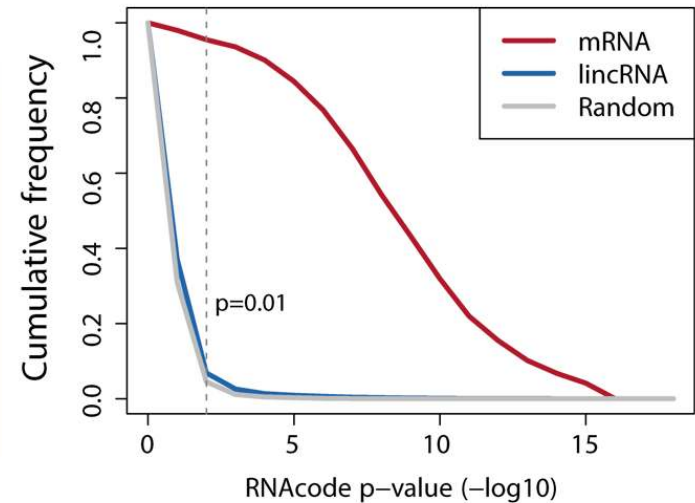
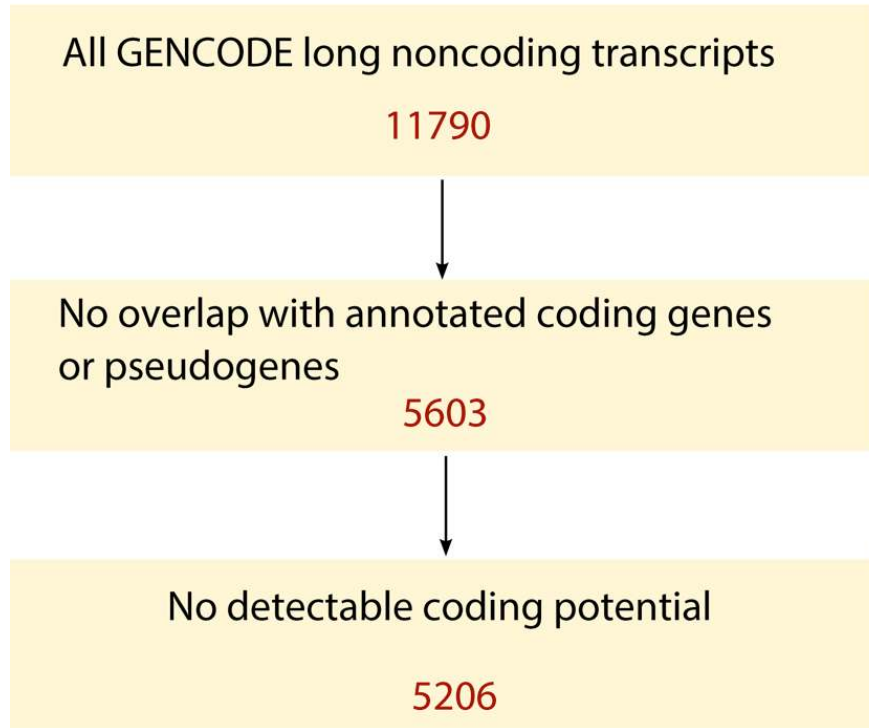
11790



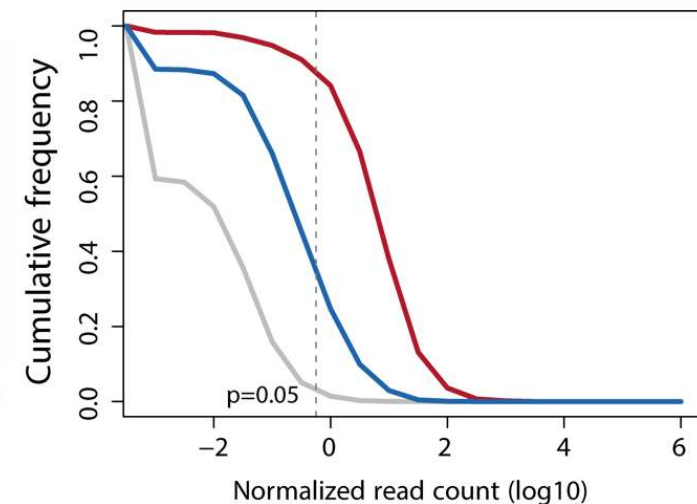
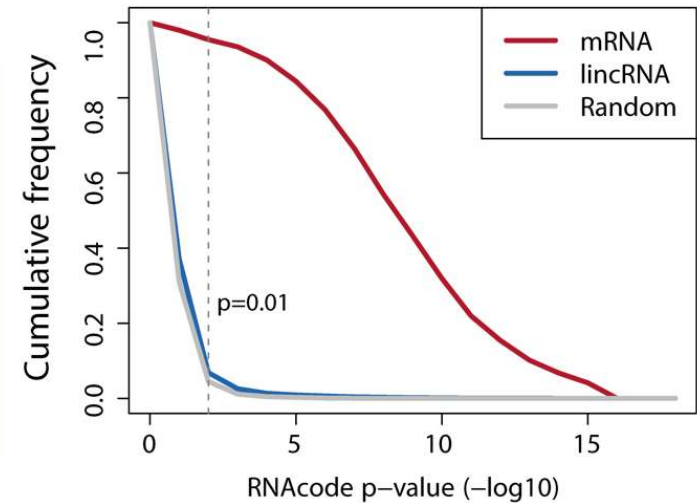
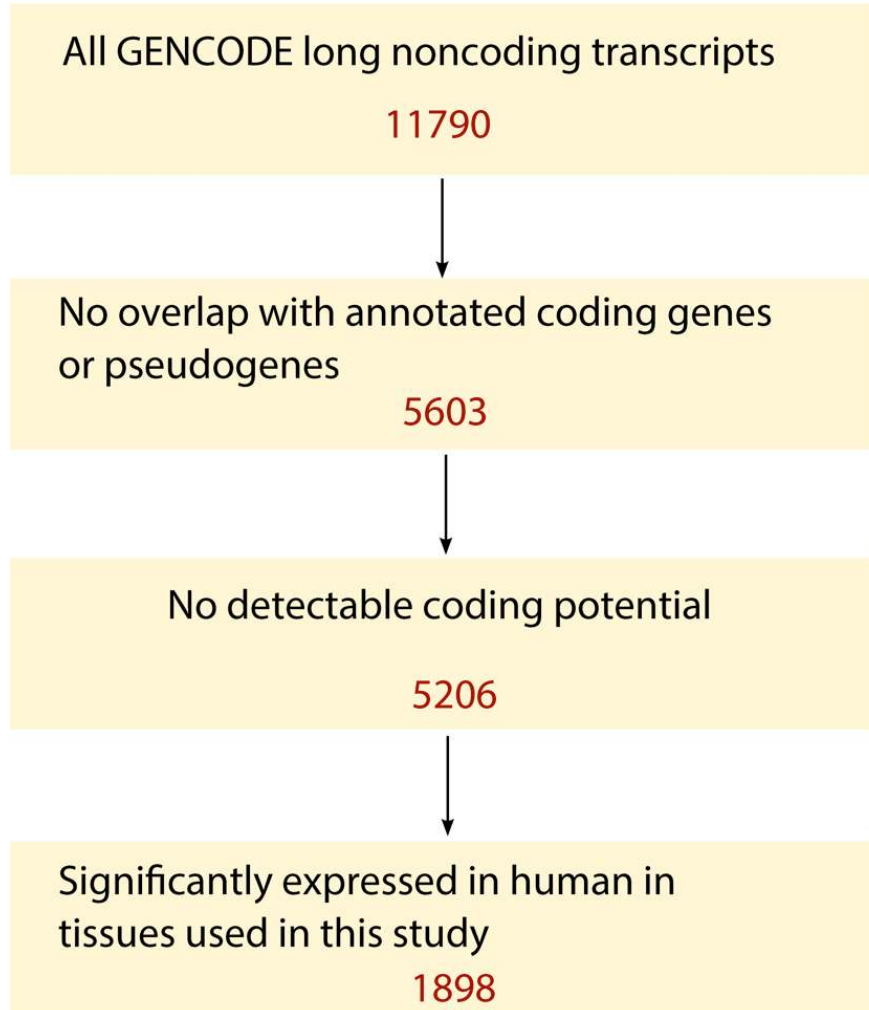
No overlap with annotated coding genes
or pseudogenes

5603

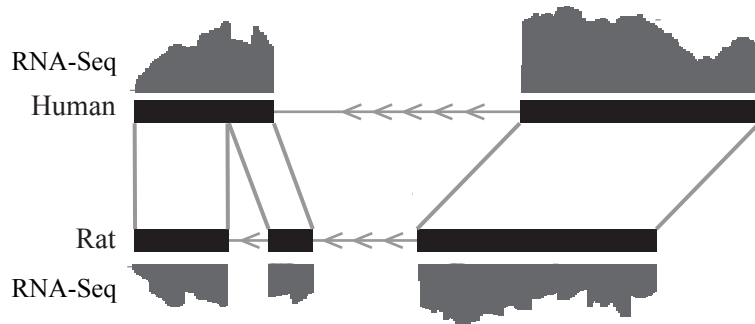
A human centric approach



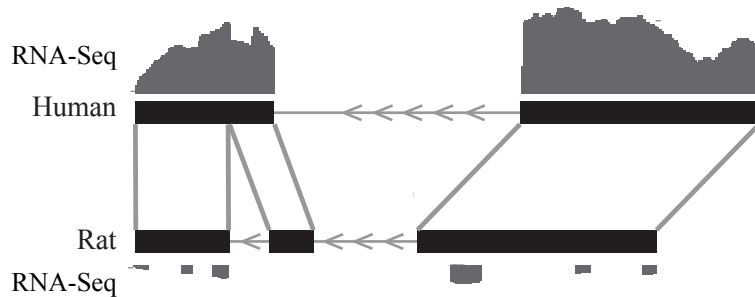
A human centric approach



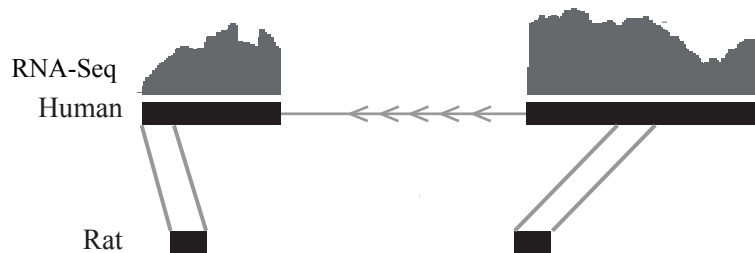
Assessing orthologous expression



Can find orthologous loci with significant expression

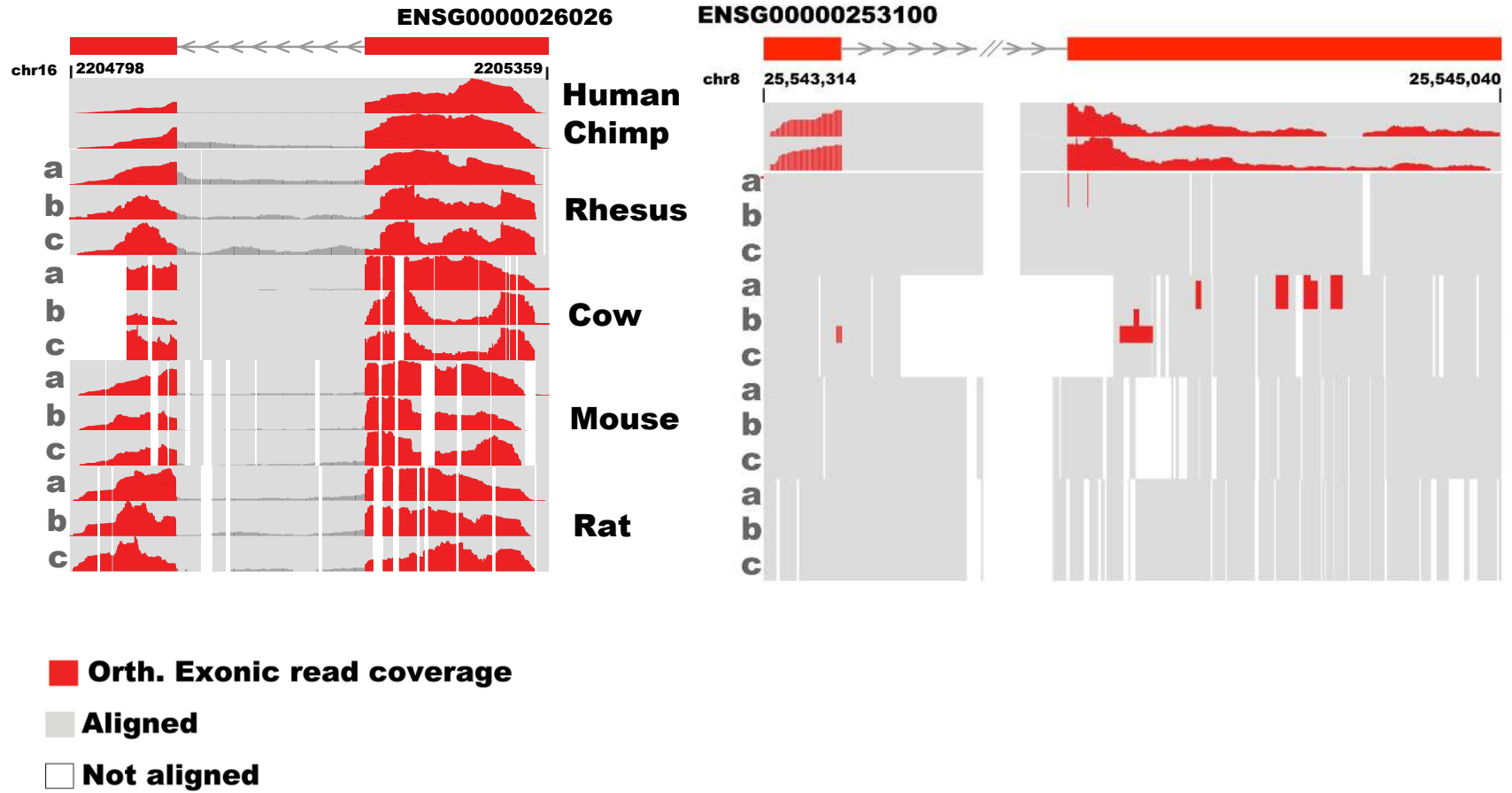


Can find orthologous loci but without significant expression

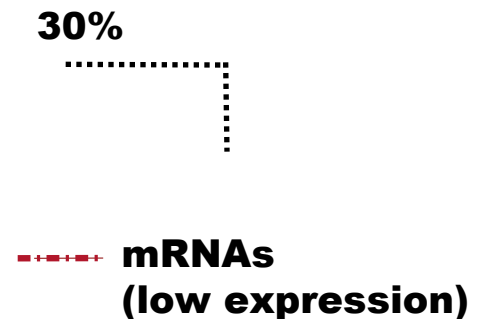
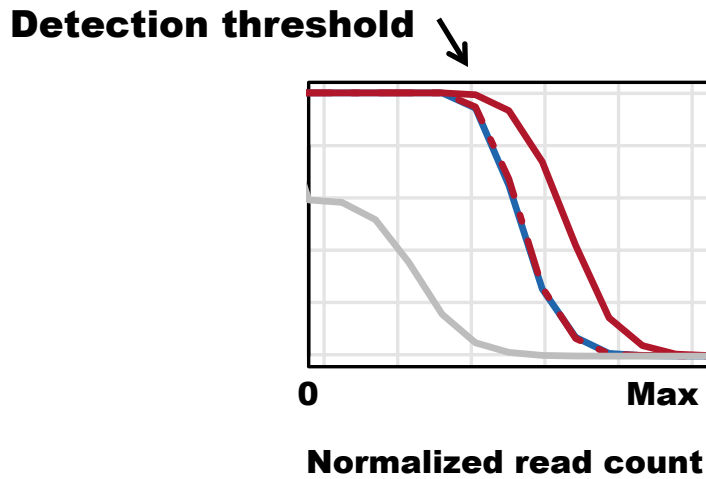
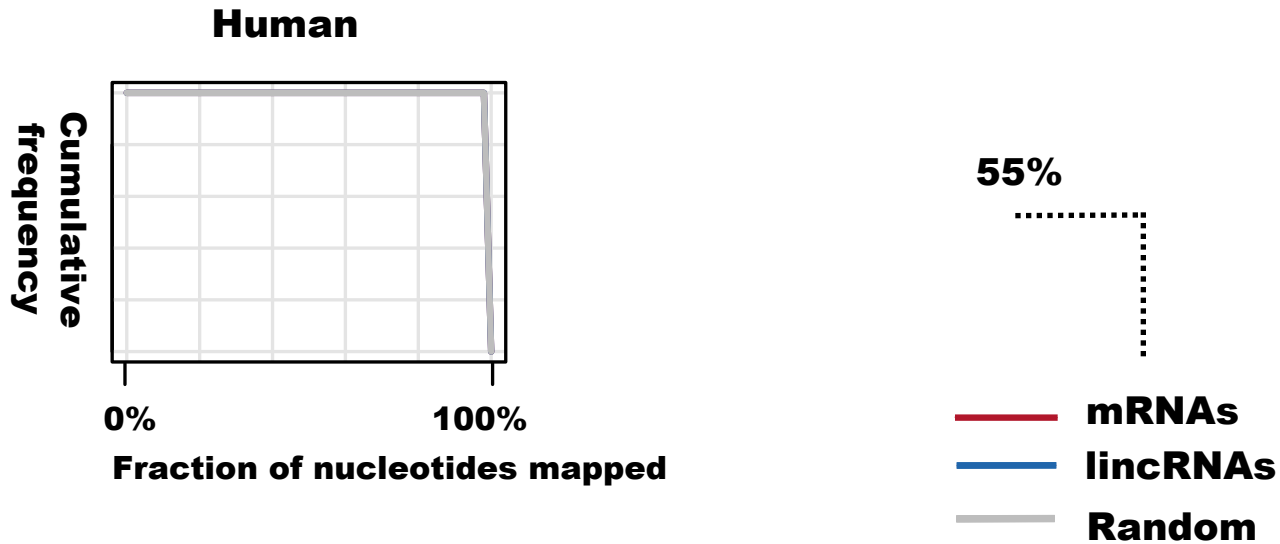


Cannot find orthologous loci

How many are lost or gained?

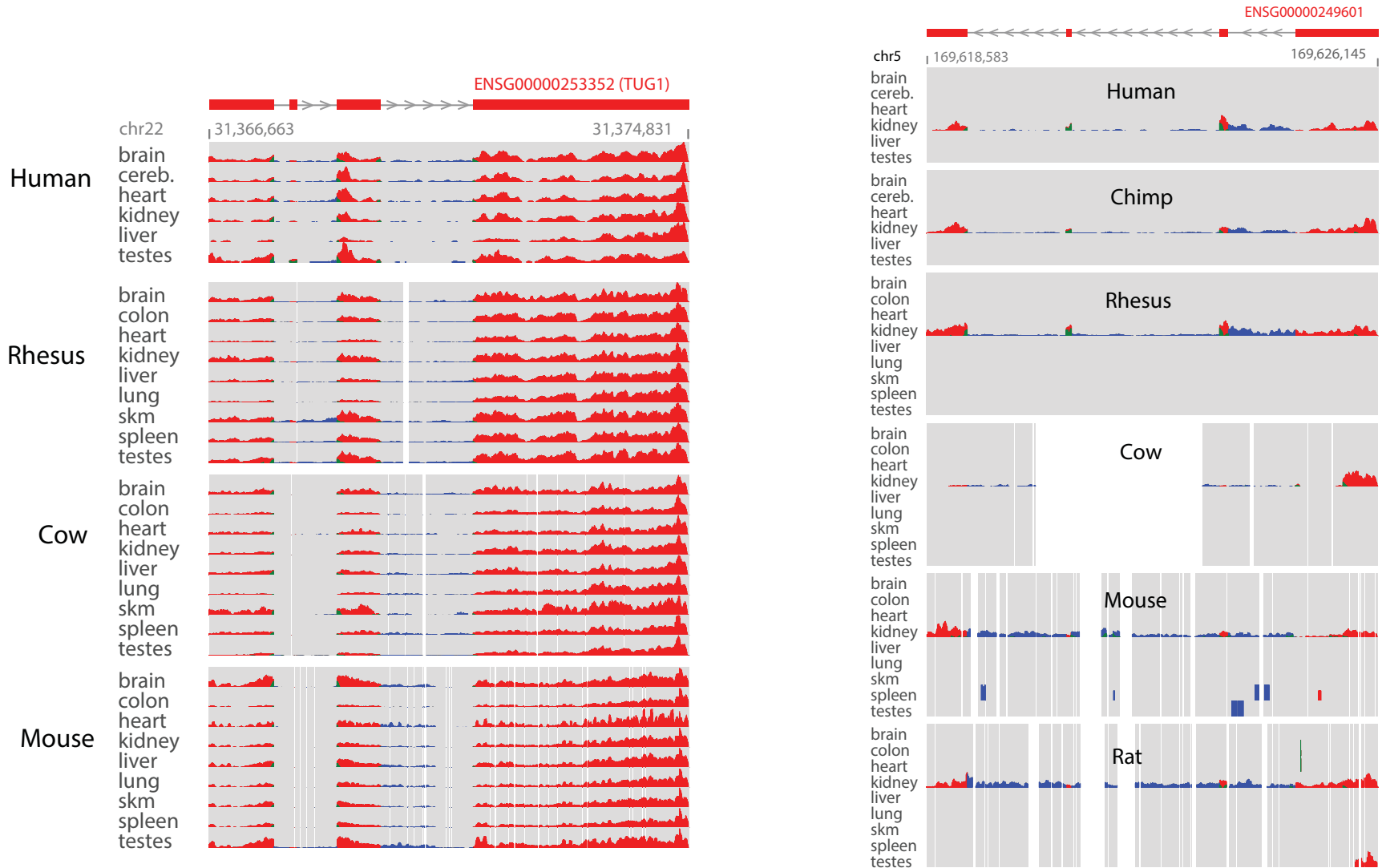


Conservation of Expression decays rapidly

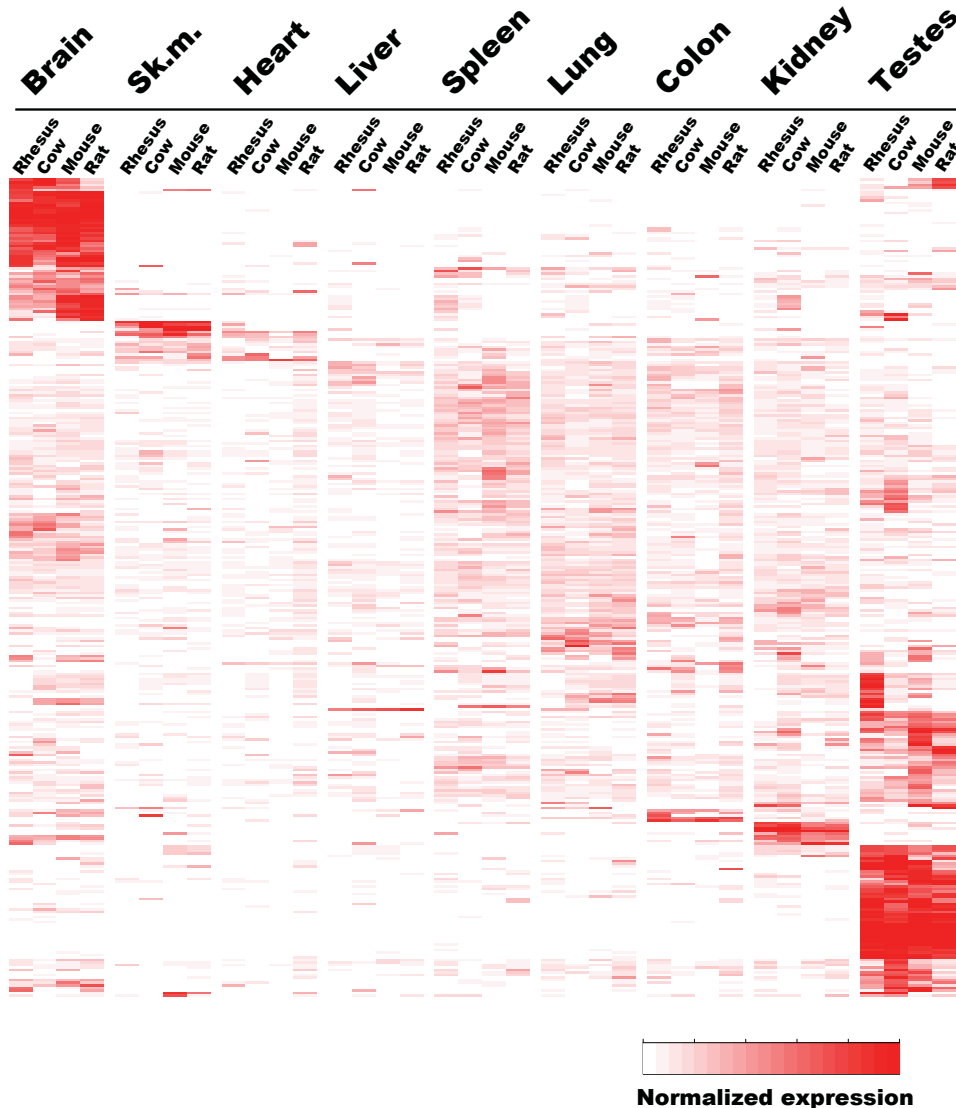


lincRNAs are lost much faster than predicted by their sequence conservation

Orothologous lincRNAs preserve their tissue specificity



Orthologous lincRNAs preserve their tissue specificity

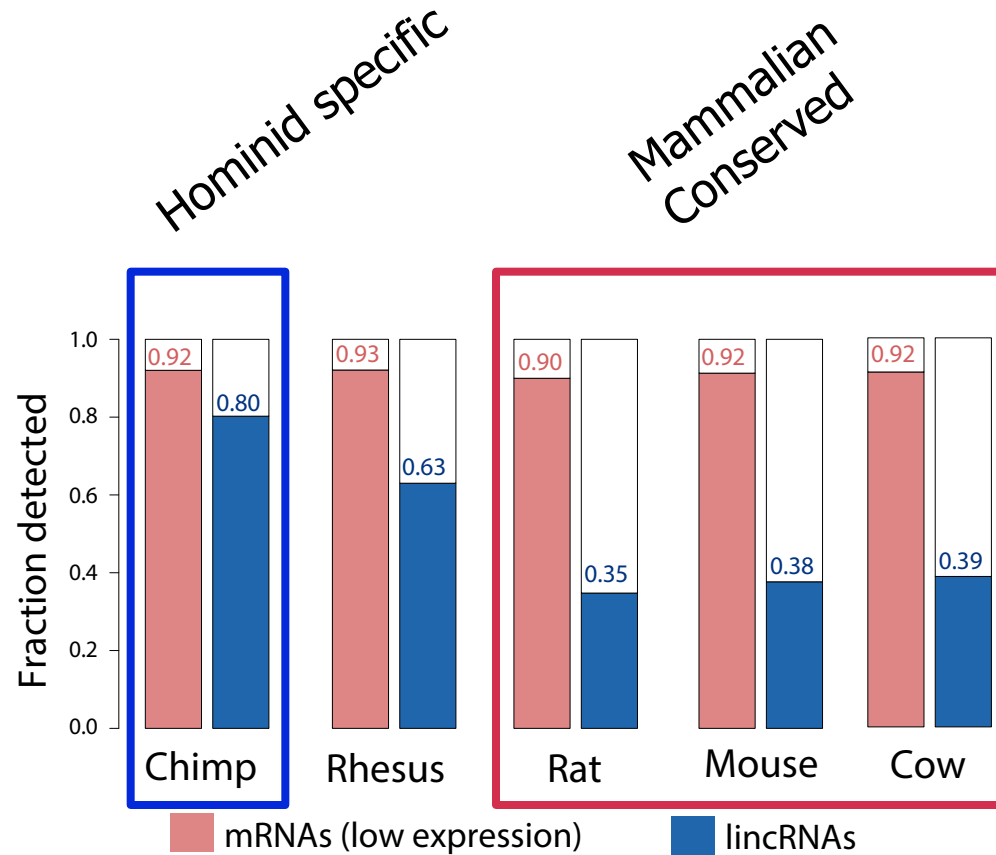


Rhesus	Cow	Mouse	Rat	
1.00	0.53	0.50	0.45	Rhesus
	1.00	0.52	0.46	Cow
		1.00	0.66	Mouse
			1.00	Rat
lncRNAs				

Rhesus	Mouse	Rat	Cow	
1.00	0.53	0.53	0.54	Rhesus
	1.00	0.54	0.54	Cow
		1.00	0.72	Mouse
			1.00	Rat
mRNAs				

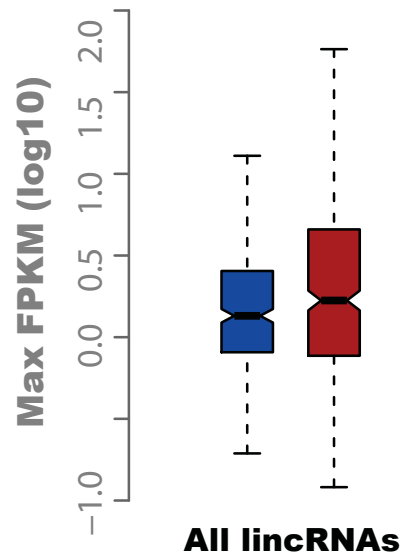
Conserved lincRNAs have conserved regulation

Young vs conserved lincRNAs



Similarly expressed yet more tissue specific

Expression level



 **Hominid-specific lincRNAs**

 **Mammalian-conserved lincRNAs**

XIST like counterpart

LETTER

doi:10.1038/nature11171

***Rsx* is a metatherian RNA with *Xist*-like properties in X-chromosome inactivation**

Jennifer Grant¹, Shantha K. Mahadevaiah¹, Pavel Khil², Mahesh N. Sangrithi¹, Hélène Royo¹, Janine Duckworth³, John R. McCarrey⁴, John L. VandeBerg⁵, Marilyn B. Renfree⁶, Willie Taylor¹, Greg Elgar¹, R. Daniel Camerini-Otero², Mike J. Gilchrist¹ & James M. A. Turner¹

- Female Specific
- Large non-coding (> 20Kb)
- Coats the Xi
- Inactive in Germline cells
- Contains tandem repeats
- Capable of inactivating autosomes

Grant al. *Nature* 2012

Is *Rsx* a functional ortholog of XIST

Key observations

- lincRNAs have a very rapid rate of gain and loss
- Rapid gain/loss makes the XIST/RSX model where lincRNAs may be easily replaced appealing until ... proven wrong or a more reasonable model arises
- Repetitive sequence could be a driving force in the genesis of lincRNAs
- Gene structure seems to be preserved only when junctions may play a functional role and turnover very rapidly when they not.
- There are certainly different classes of lincRNAs with different evolutionary signatures.

Thanks



Stephan Washietl (MIT)



Jenny Chen (MIT/
Broad)



Manolis Kellis (MIT)

Garber lab

Xiaopeng Zhu



Shaked Affik



Jenny Chen



Sabah Kadri



Postdocs invited!

Bioinformatics core

A. Kucukural Heannady Shulha



Garberlab.umassmed.edu