The Krumlov Trinity Transcriptomics Experience

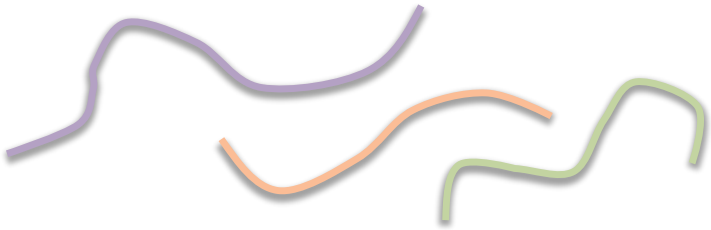
Brian Haas

Broad Institute

Workshop on Genomics, Cesky Krumlov, Jan 2019

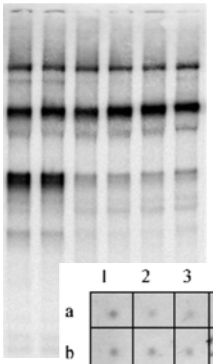
Biological Investigations Empowered by Transcriptomics

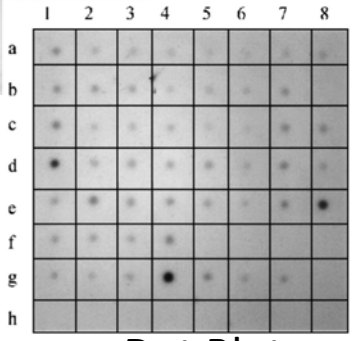
Extract RNA,
… some protocol for processing, ...



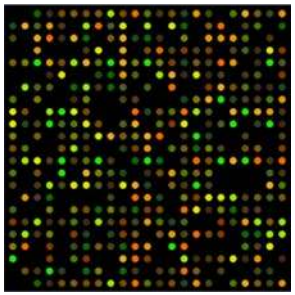
Analysis Method
(pick your favorite)

Northern

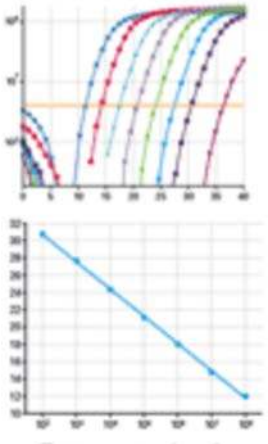




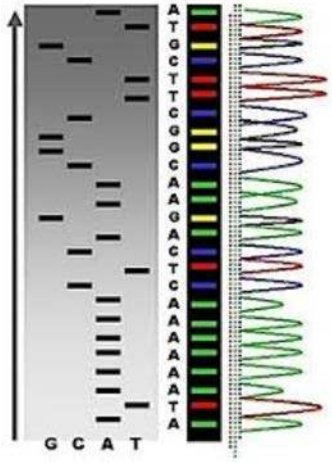
Dot Blot



Microarray



qRT-PCR



Sanger Sequencing

Other…

Minion

MinION

Historical Timeline of Transcriptomics (from 1970)

Reverse Transcription (1970)

Northern Blot
Sanger Sequencing
(1977)

Expressed Sequence Tags (1992)

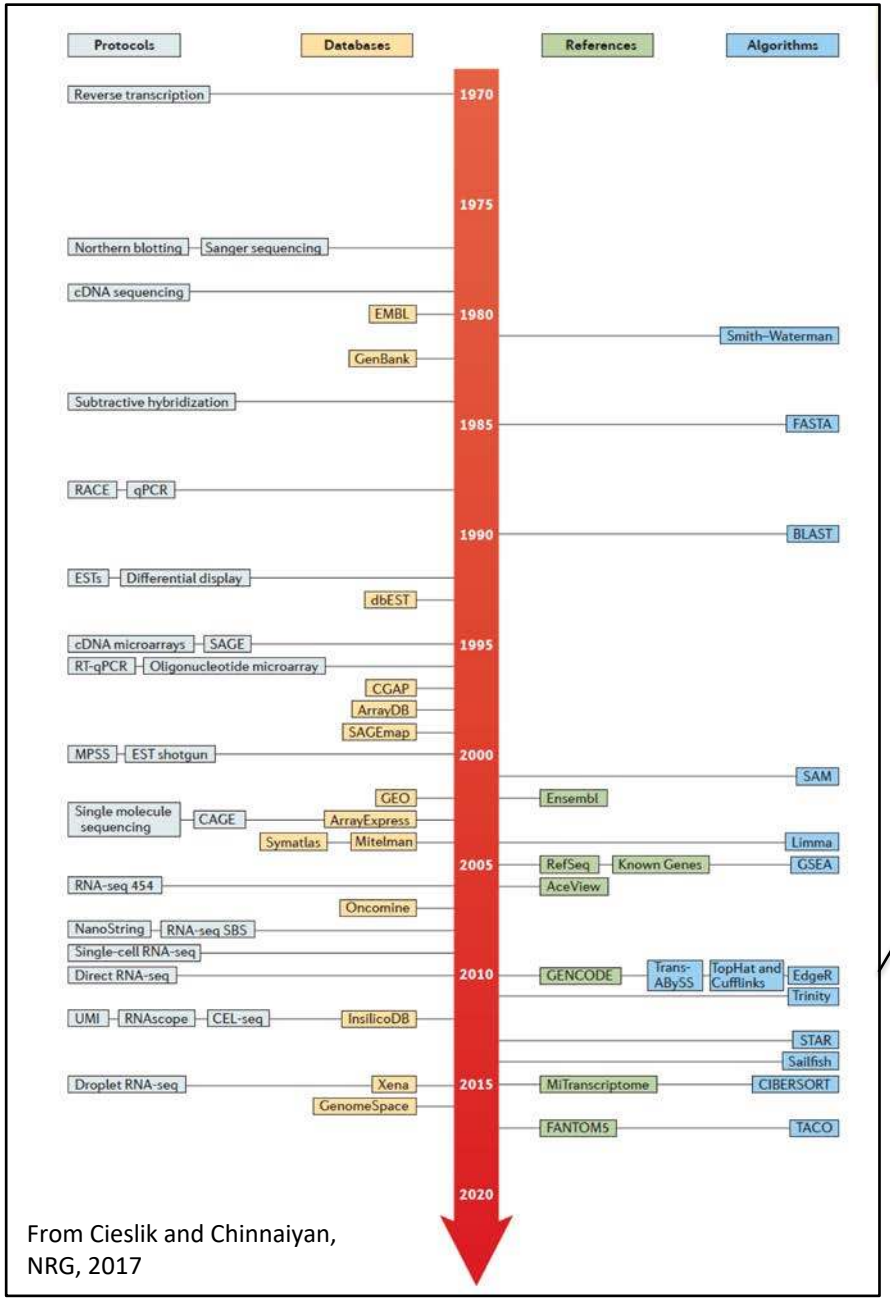
cDNA microarrays (1995)

RNA-Seq (2006-2008)

PacBio IsoSeq (2014)

Droplet single cell RNA-Seq (2015)

Direct RNA Seq Nanopore (2018)



From Cieslik and Chinnaiyan, NRG, 2017

Note: Just a small sampling of what's available.

Smith Waterman (1981)

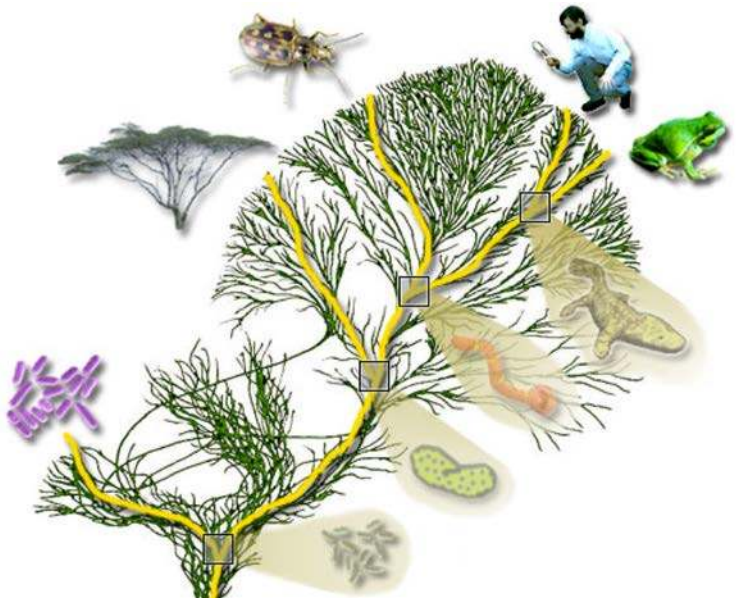
BLAST (1990)

Tophat/Cufflinks (2010)

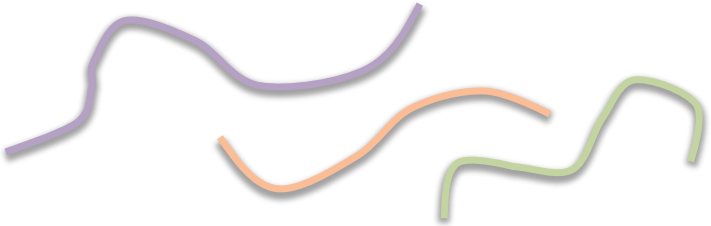
RSEM (2011)

Kallisto (2016)
Salmon (2017)

Modern Transcriptome Studies Empowered by RNA-seq



Extract RNA, convert to cDNA



Next-gen Sequencer
(pick your favorite)

Millions to Billions of Reads

Generating RNA-Seq: *How to Choose?*

Platform	Project Firefly 2018	MiniSeq	MiSeq	Next Seq 550	HiSeq 2500 RR	Hiseq 2500 V3	HiSeq 2500 V4	HiSeq 4000	HiSeq X	Nova Seq S1 2018	Nova Seq S2	Nova Seq S4	5500 XL	318 HiQ 520	Ion 530	Ion Proton P1	PGM HiQ 540	RS P6-C4	Sequel	R&D end 2018	Smidg ION RnD	Mini ION R9.5	Grid ION X5	Prome thION RnD	Prome thION theor etical	QiaGen Gene Reader	BGI SEQ 500	BGI SEQ 50	#
Reads: (M)	4	25	25	400	600	3000	4000	5000	6000	3300	6600	20000	1400	3-5	15-20	165	60-80	5.5	38.5	--	--	--	--	--	--	400	1600	1600	--
Read length: (paired-end*)	150*	150*	300*	150*	100*	100*	125*	150*	150*	150*	150*	150*	60	200 400	200 400	200	200	15K	12K	32K	--	--	--	--	--	--	100*	50	--
Run time: (d)	0.54	1	2	1.2	1.125	11	6	3.5	3	1.66	1.66	1.66	7	0.37	0.16	--	0.16	4.3	--	--	--	2	2	2	--	--	1	0.4	--
Yield: (Gb)	1	7.5	15	120	120	600	1000	1500	1800	1000	2000	6000	180	1.5	7	10	12	12	5	150	4	8	40	2400	11000	80	200	8	--
Rate: (Gb/d)	1.85	7.5	7.5	100	106.6	55	166	400	600	600	1200	3600	30	5.5	50	--	93.75	2.8	--	--	--	4	20	1200	5500	--	200	20	--
Reagents: ($K)	0.1	1.75	1	5	6.145	23.47	29.9	--	--	--	--	--	10.5	0.6	--	1	1.2	2.4	--	1	--	0.5	1.5	--	--	0.5	--	--	--
per-Gb: ($)	100	233	66	50	51.2	39.1	31.7	20.5	7.08	18	15	5.8	58.33	--	--	100	--	200	80	6.6	--	62.5	37.5	20	4.3	--	--	--	--
hg-30x: ($)	12000	28000	8000	5000	6144	4692	3804	2460	849.6	1800	1564	700	7000	--	--	12000	--	24000	9600	1000	--	7500	4500	2400	500	--	600	--	
Machine: ($)	30K	49.5K	99K	250K	740K	690K	690K	900K	1M	999K	999K	999K	595K	50K	65K	243K	242K	695K	350K	350K	--	--	125K	75K	75K	--	200K	--	--
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#curl "https://docs.google.com/spreadsheets/d/1GMMfhyLK0-q8Xklo3YxlWaZA5vVMuhU1kg41g4xLkXc/export?gid=4&format=csv" | grep -v '^#' | grep -v '^"' | column -t -s\, | less -S																													

*Not all shown at scale

Generating RNA-Seq: *How to Choose?*

Platform	Project Firefly 2018	MiniSeq	MiSeq	Next Seq 550	HiSeq 2500 RR	Hiseq 2500 V
Reads: (M)	4	25	25	400	600	300
Read length: (paired-end*)	150*	150*	300*	150*	100*	100
Run time: (d)	0.54	1	2	1.2	1.125	1
Yield: (Gb)	1	7.5	15	120	120	60
Rate: (Gb/d)	1.85	7.5	7.5	100	106.6	5
Reagents: ($K)	0.1	1.75	1	5	6.145	23.4
per-Gb: ($)	100	233	66	50	51.2	39.
hg-30x: ($)	12000	28000	8000	5000	6144	469
Machine: ($)	30K	49.5K	99K	250K	740K	690

#Page maintained by http://twitter.com/albertvilella http://t
#curl "https://docs.google.com/spreadsheets/d/1GMMfhyLK0-q

g	Mini ION R9.5	Grid ION X5	Prome thION RnD	Prome thION theor etical	QiaGen Gene Reader	BGI SEQ 500	BGI SEQ 50	#
--	--	--	--	--	400	1600	1600	--
--	--	--	--	--	--	100*	50	--
--	2	2	2	--	--	1	0.4	--
4	8	40	2400	11000	80	200	8	--
--	4	20	1200	5500	--	200	20	--
--	0.5	1.5	--	--	0.5	--	--	--
--	62.5	37.5	20	4.3	--	--	--	--
--	7500	4500	2400	500	--	600	--	
--	--	125K	75K	75K	--	200K	--	--

"What I especially like about this baby is this little drawer where I can keep my lunch."

Thx Joshua Levin, for the cartoon. ☺

Small to Large

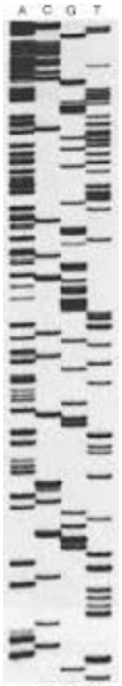
Each has pros/cons

Small to Less Large

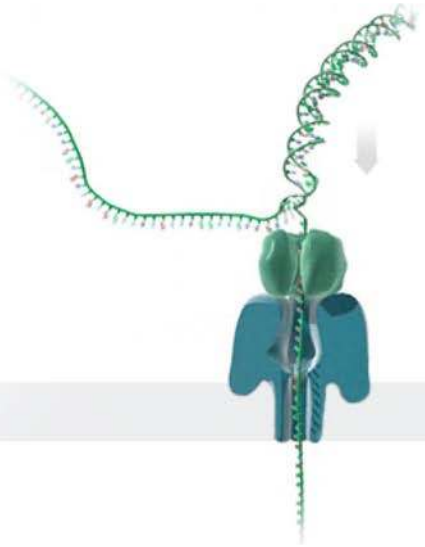
Each technology continues to advance

Personal Reflections… (and haunting memories)

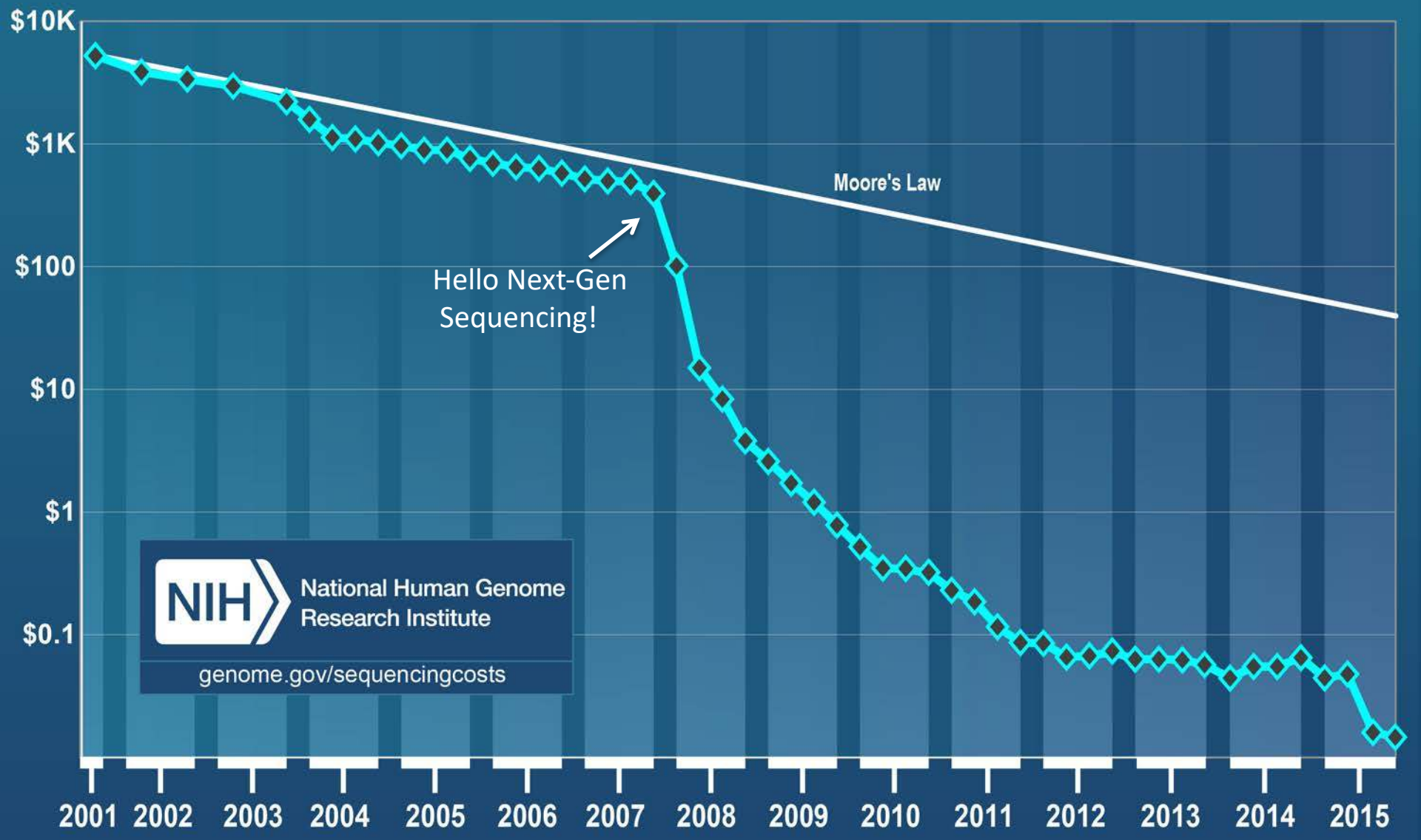
Circa 1995



Now



Cost per Raw Megabase of DNA Sequence



From https://www.genome.gov/sequencingcostsdata/

A Plethora of Biological Sequence Analyses Enabled by RNA-Seq

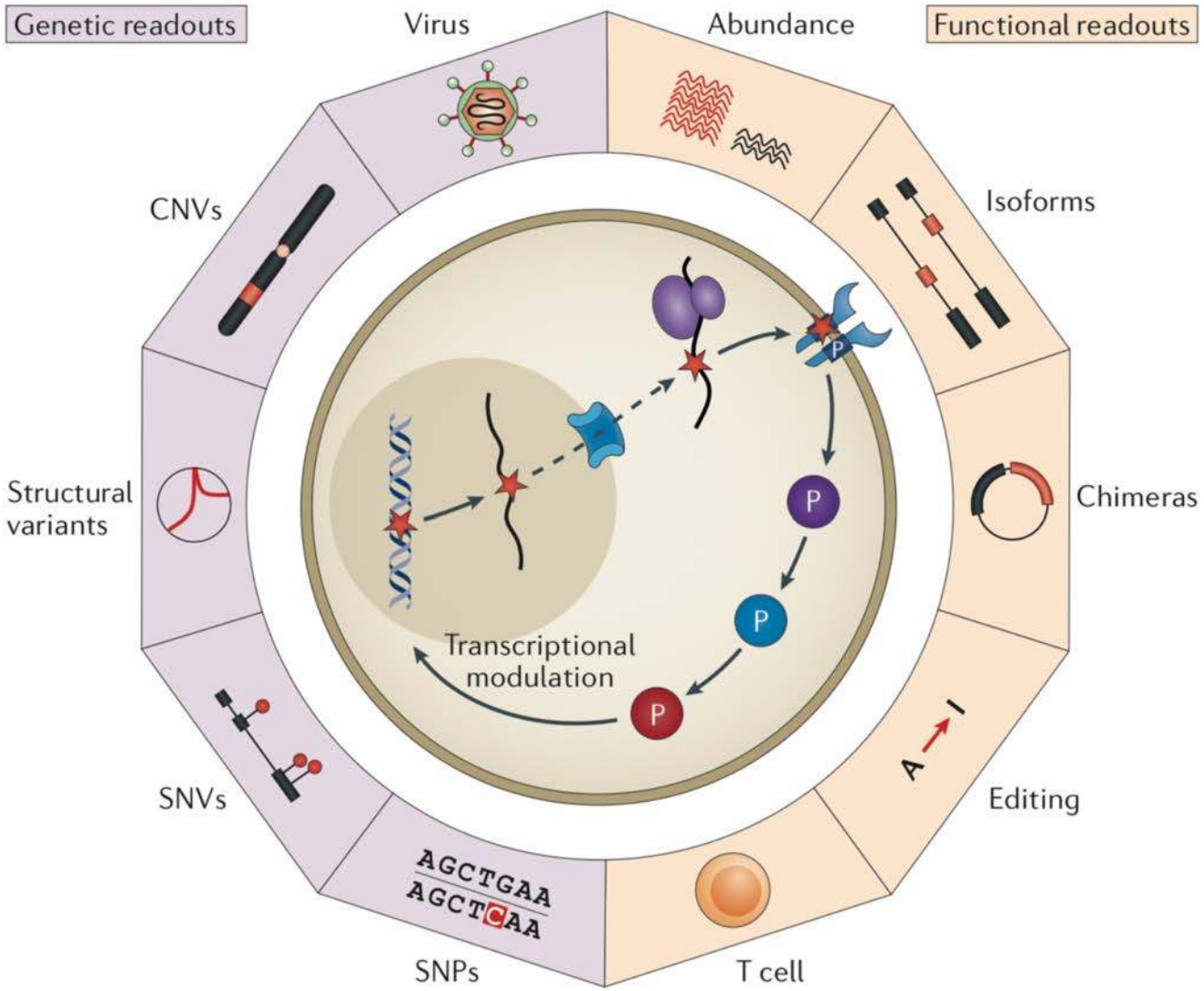
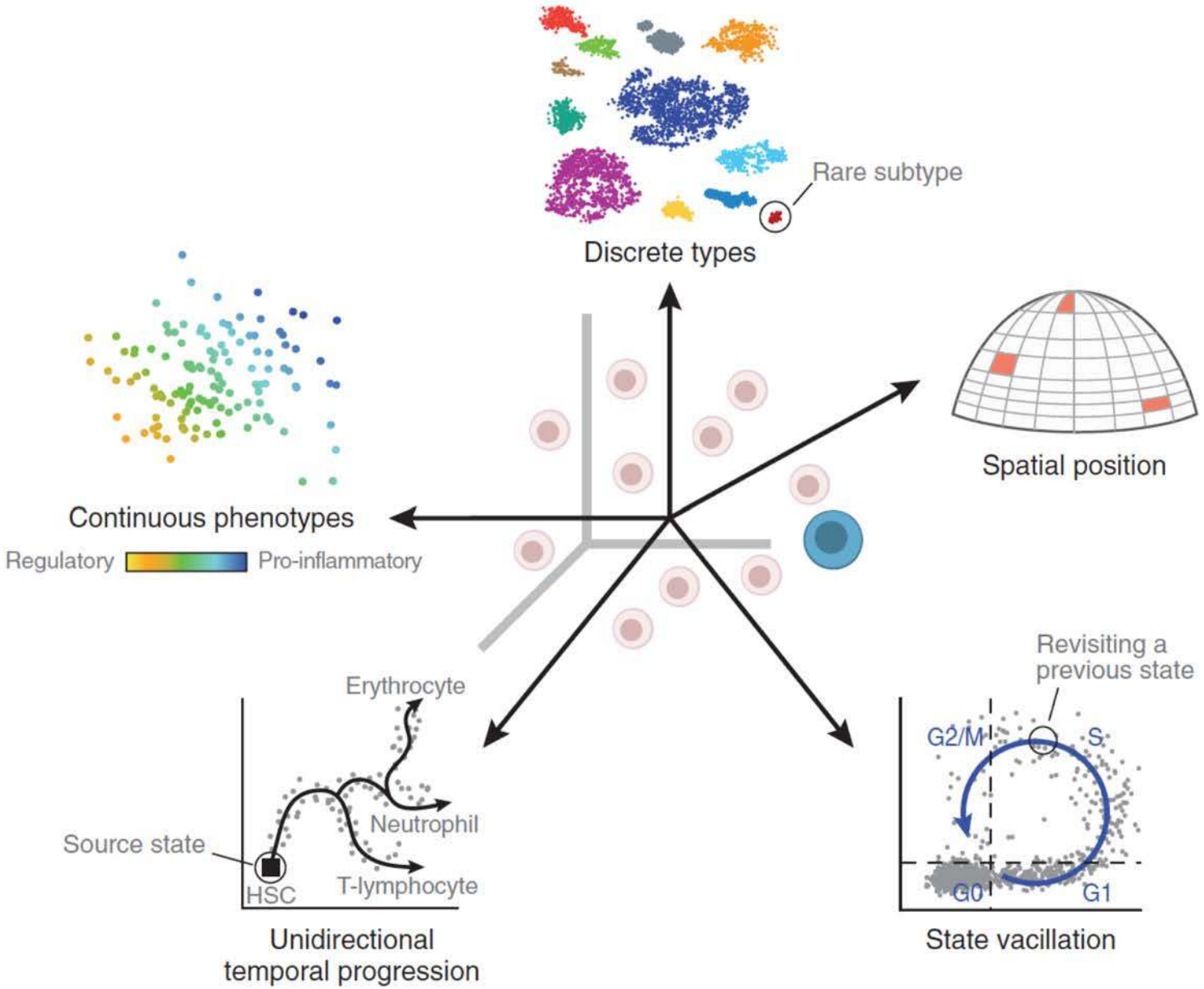


Figure 2 | **Transcriptome profiling for genetic causes and functional phenotypic readouts.**

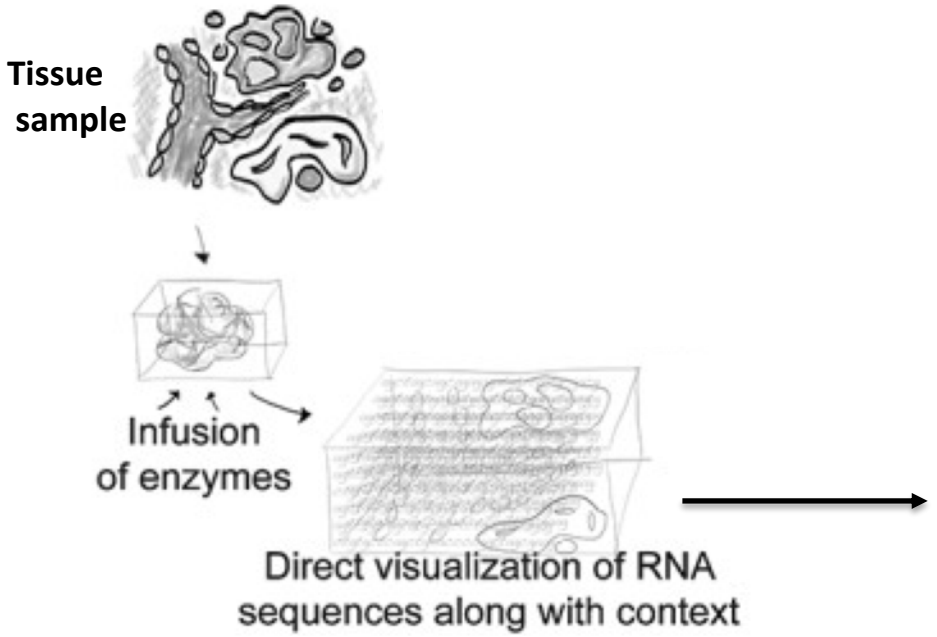
From Cieslik and Chinnaiyan, NRG, 2017

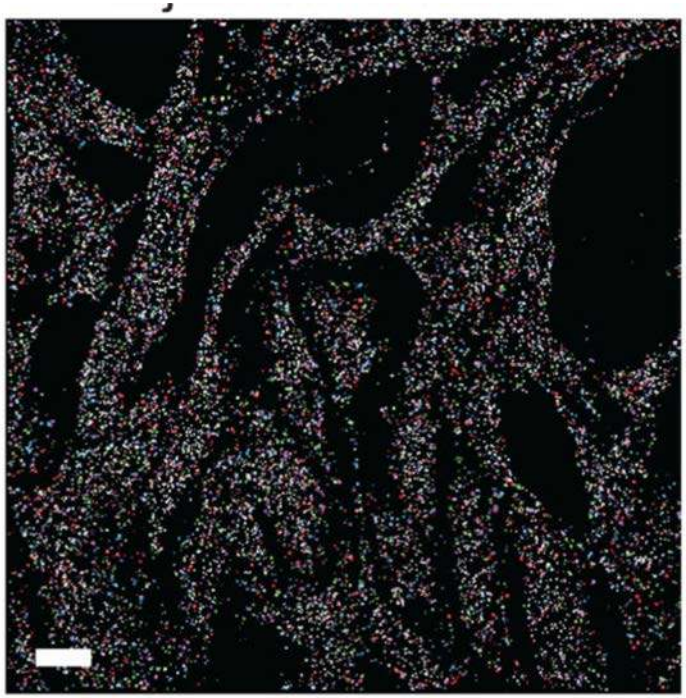
RNA-Seq is Empowering Discovery at Single Cell Resolution



Wagner, Regev, and Yosef. NBT 2016

Fluorescent in situ RNA sequencing (FISSEQ)





Fibroblasts, FISSEQ gene pixels

Adapted from:
JH Lee, 2017, PMC5315614
JH Lee, 2014, PMC4140943

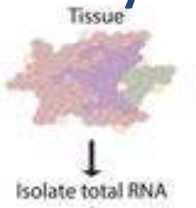
Transcriptomics Lecture Overview

- Overview of RNA-Seq
- Transcript reconstruction methods
- Trinity de novo assembly
- Transcriptome quality assessment

(coffee break)

- Expression quantitation
- Differential expression analysis
- Functional annotation
- Case study: salamander transcriptome

RNA-seq library fragmentation and size selection strategies that influence interpretation and analysis.



http://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1004393 Griffith et al., 2015

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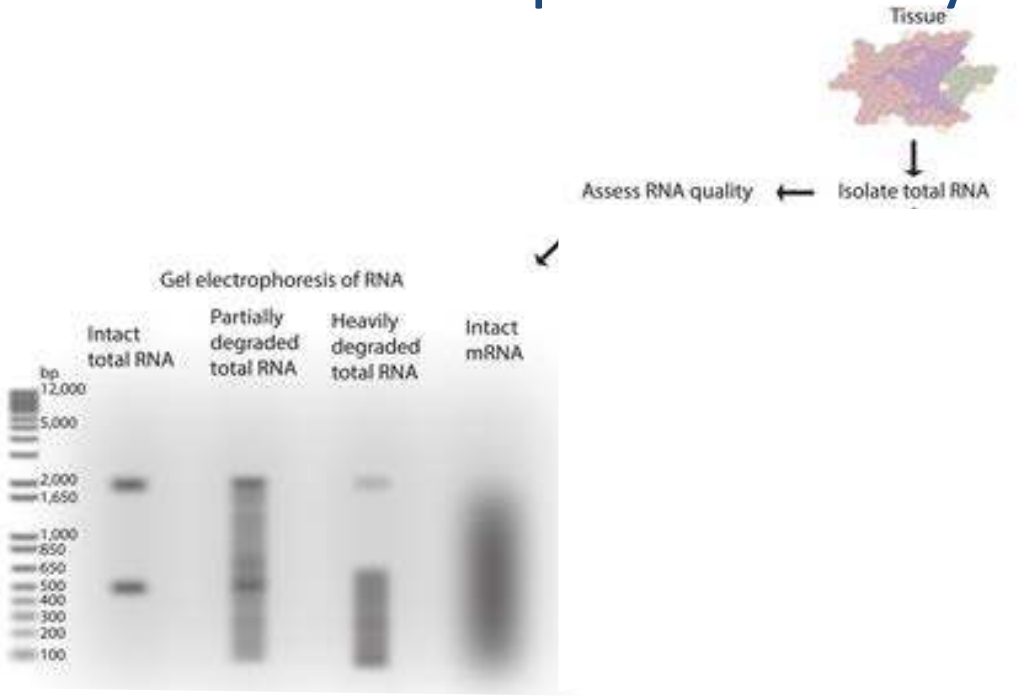

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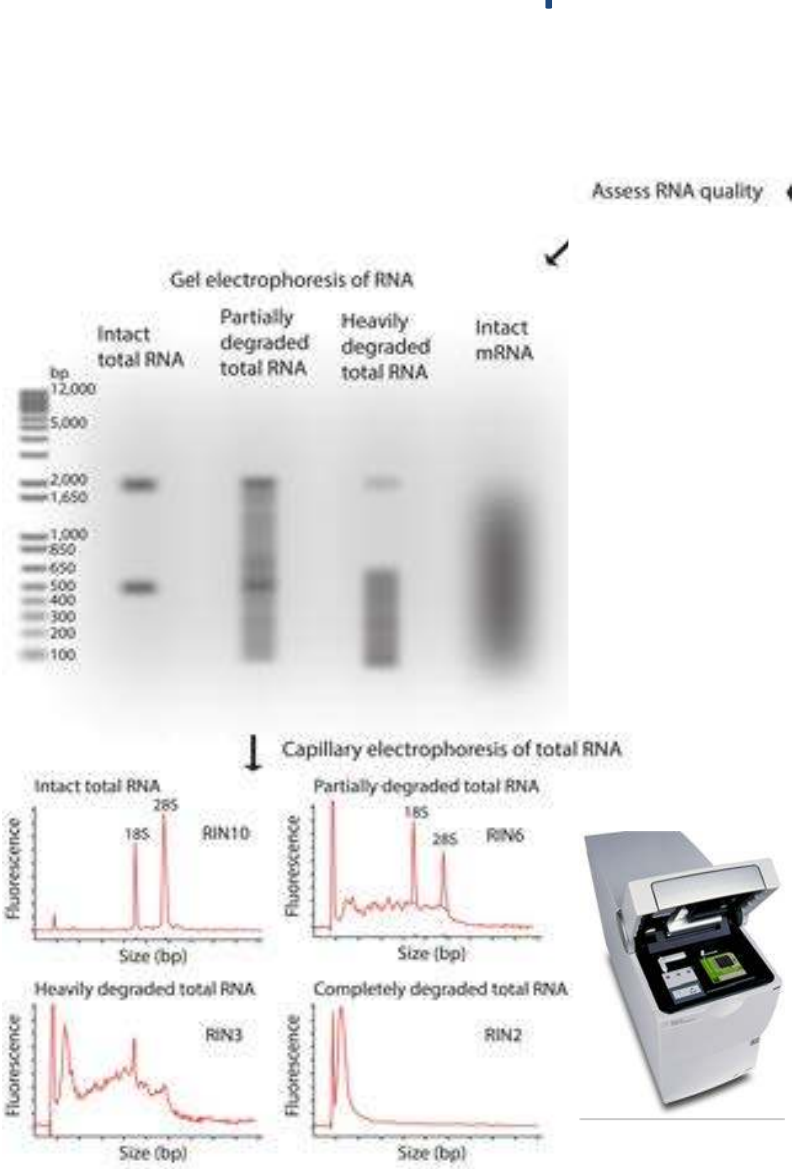

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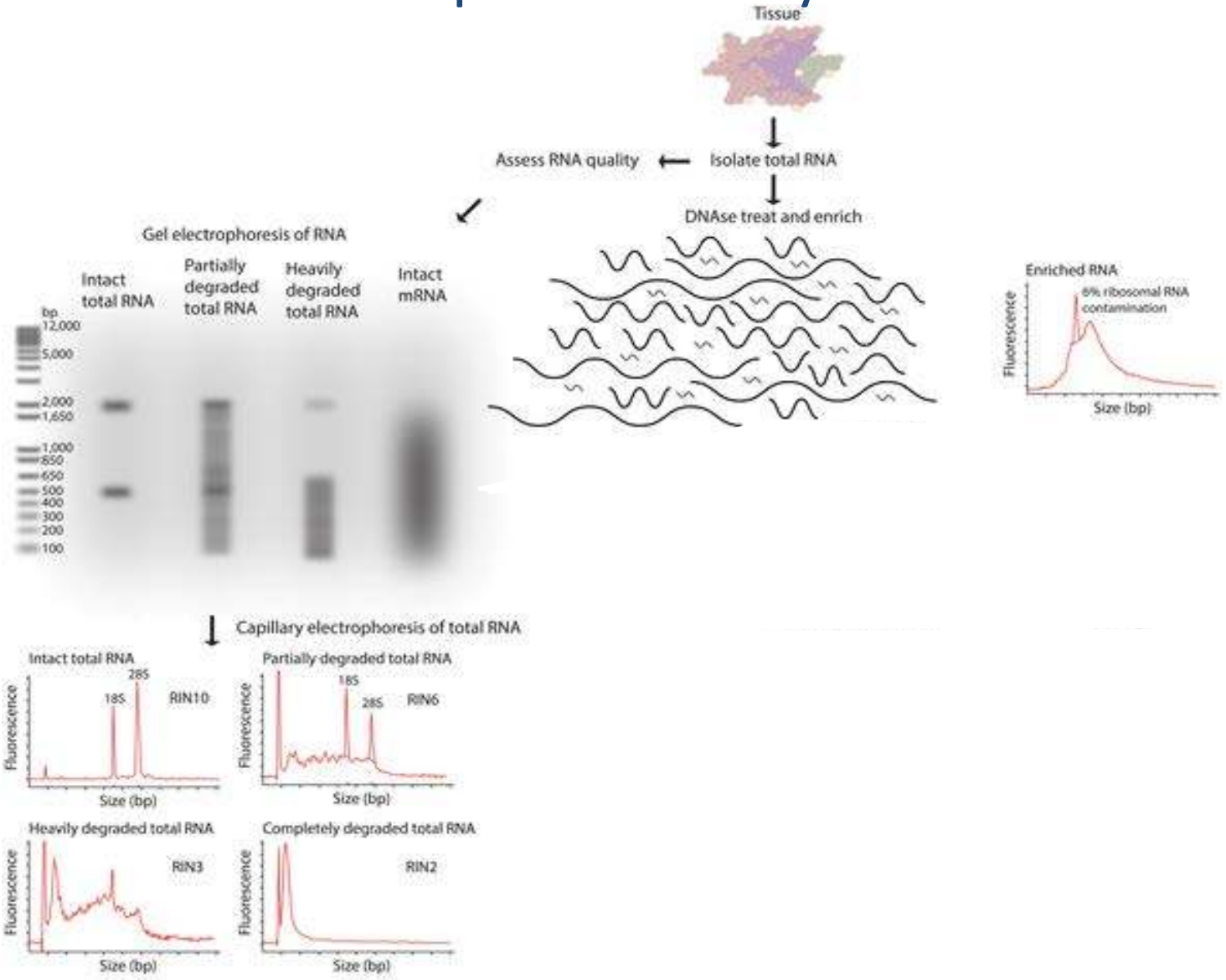

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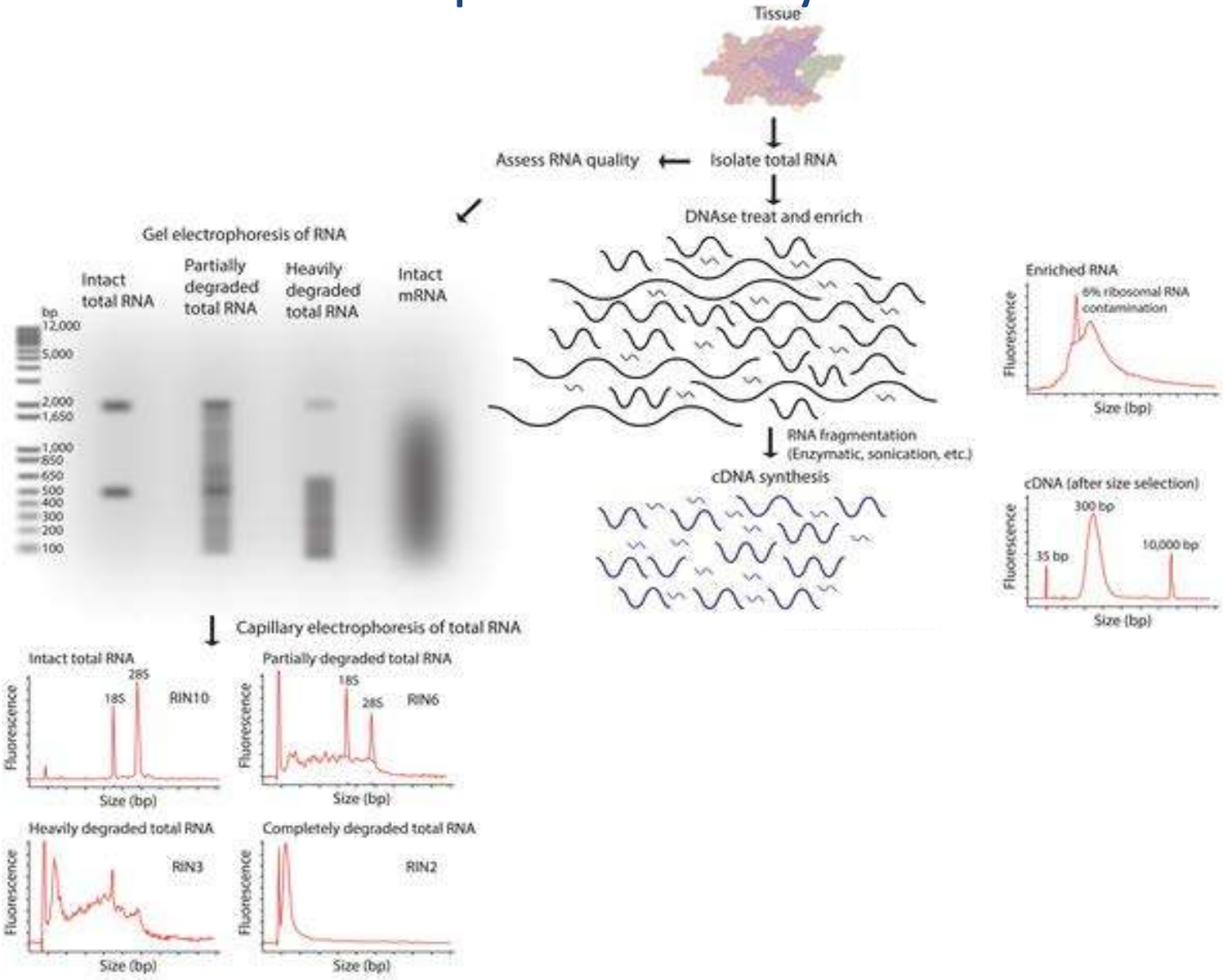

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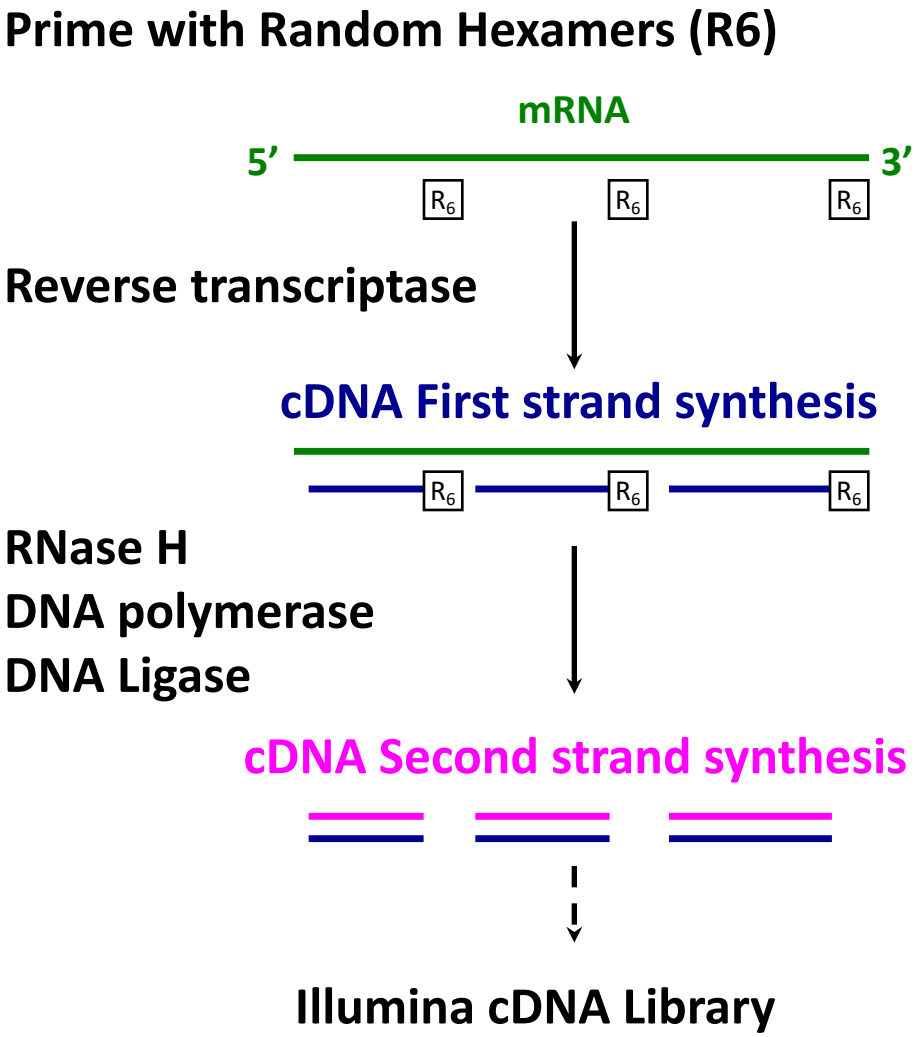
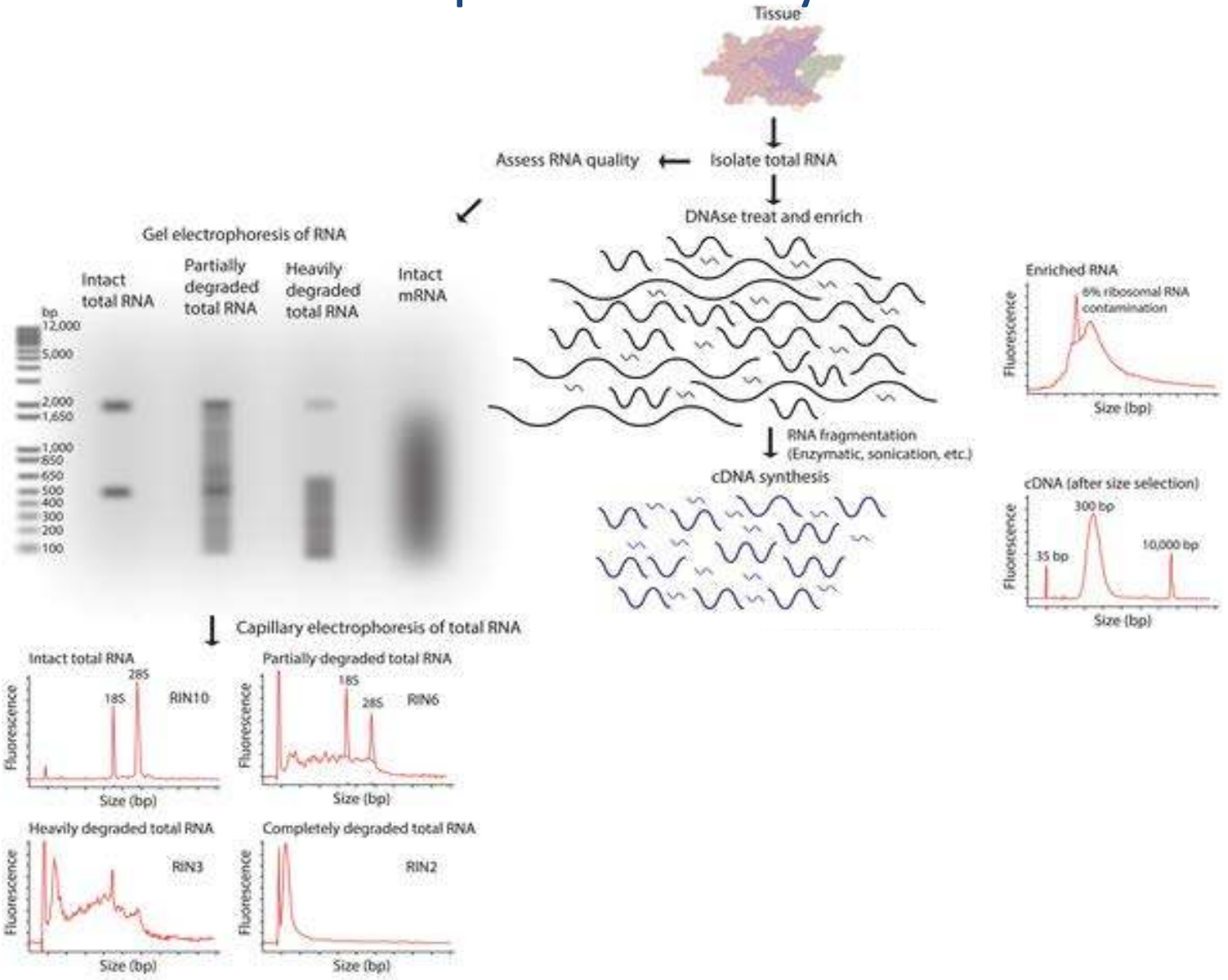
RNA-Seq: How do we make cDNA?



Slide courtesy of Joshua Levin, Broad Institute.

RNA-seq library fragmentation and size selection strategies that influence interpretation and analysis.



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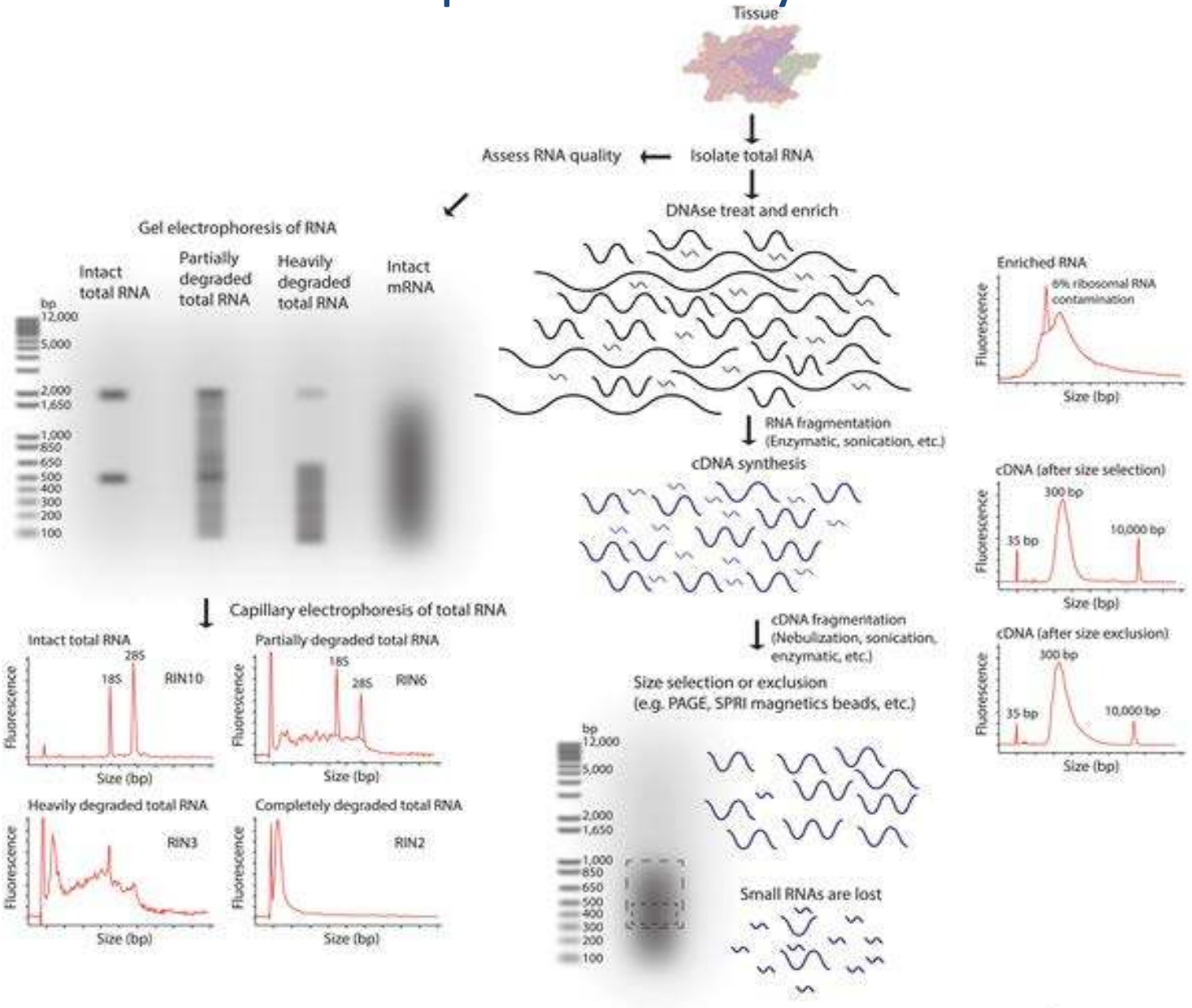

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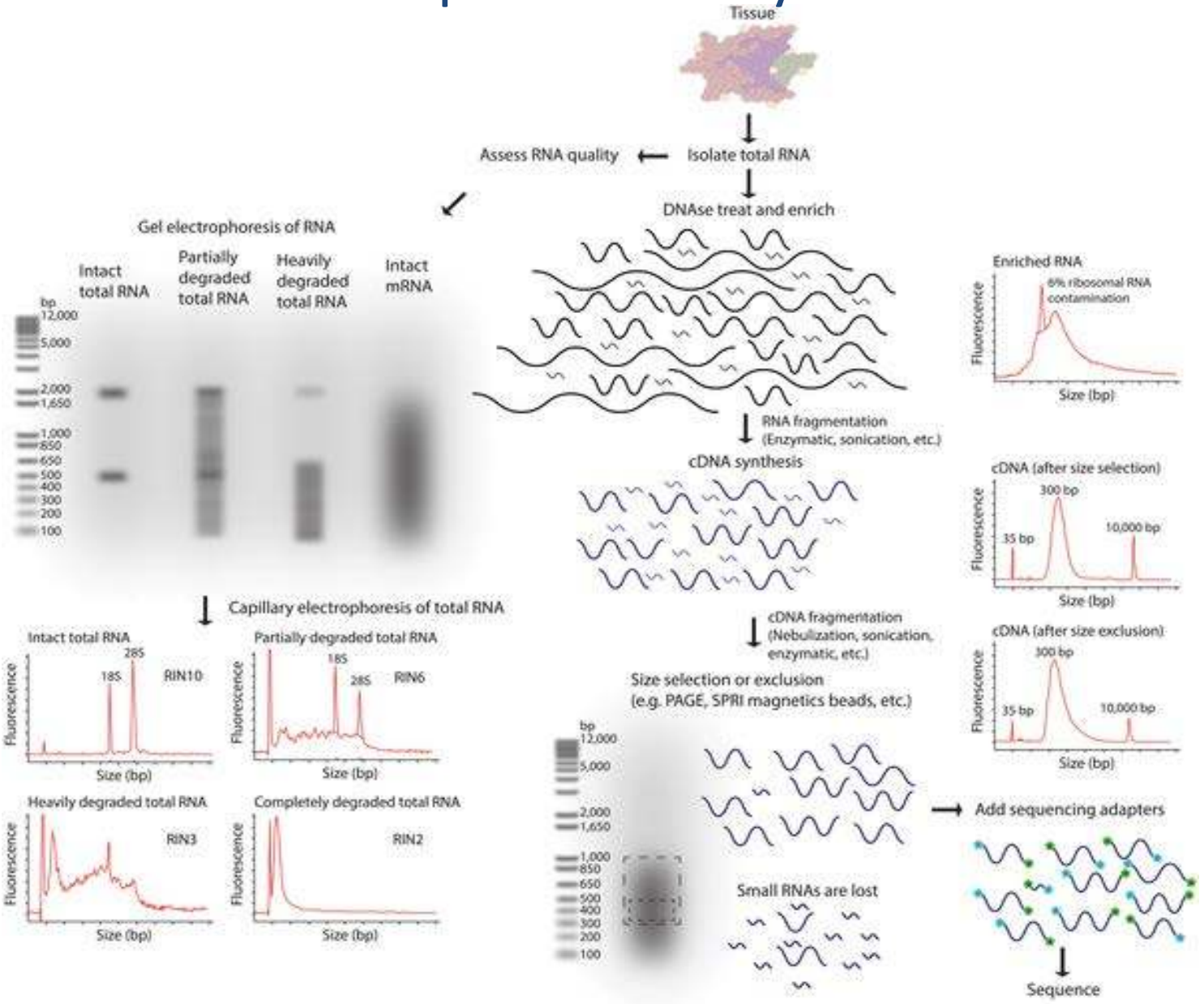

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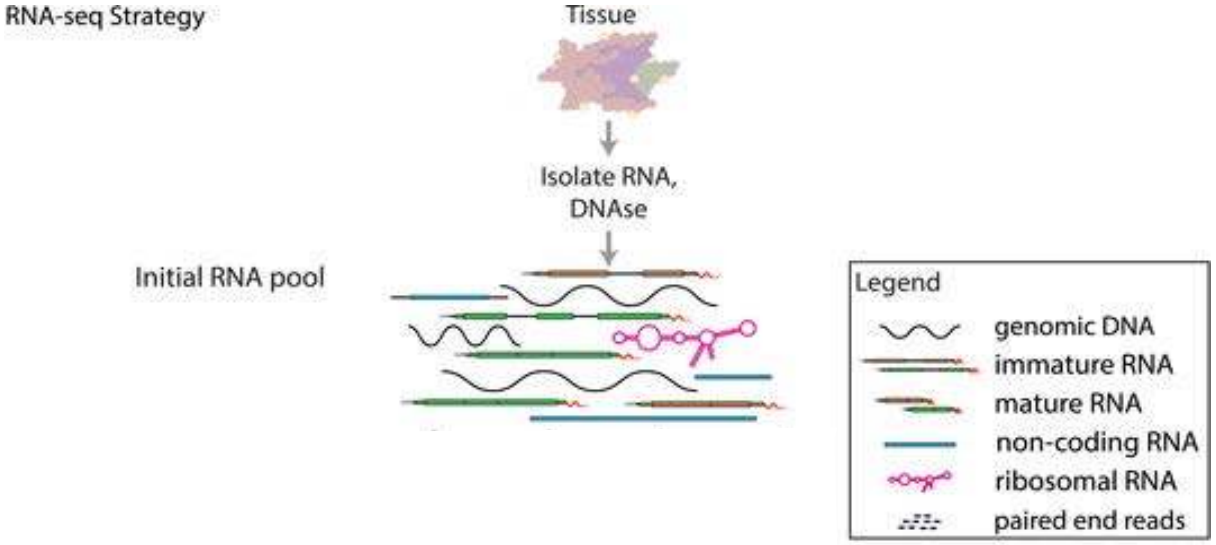
RNA-seq library enrichment strategies that influence interpretation and analysis.



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Griffith et al., 2015

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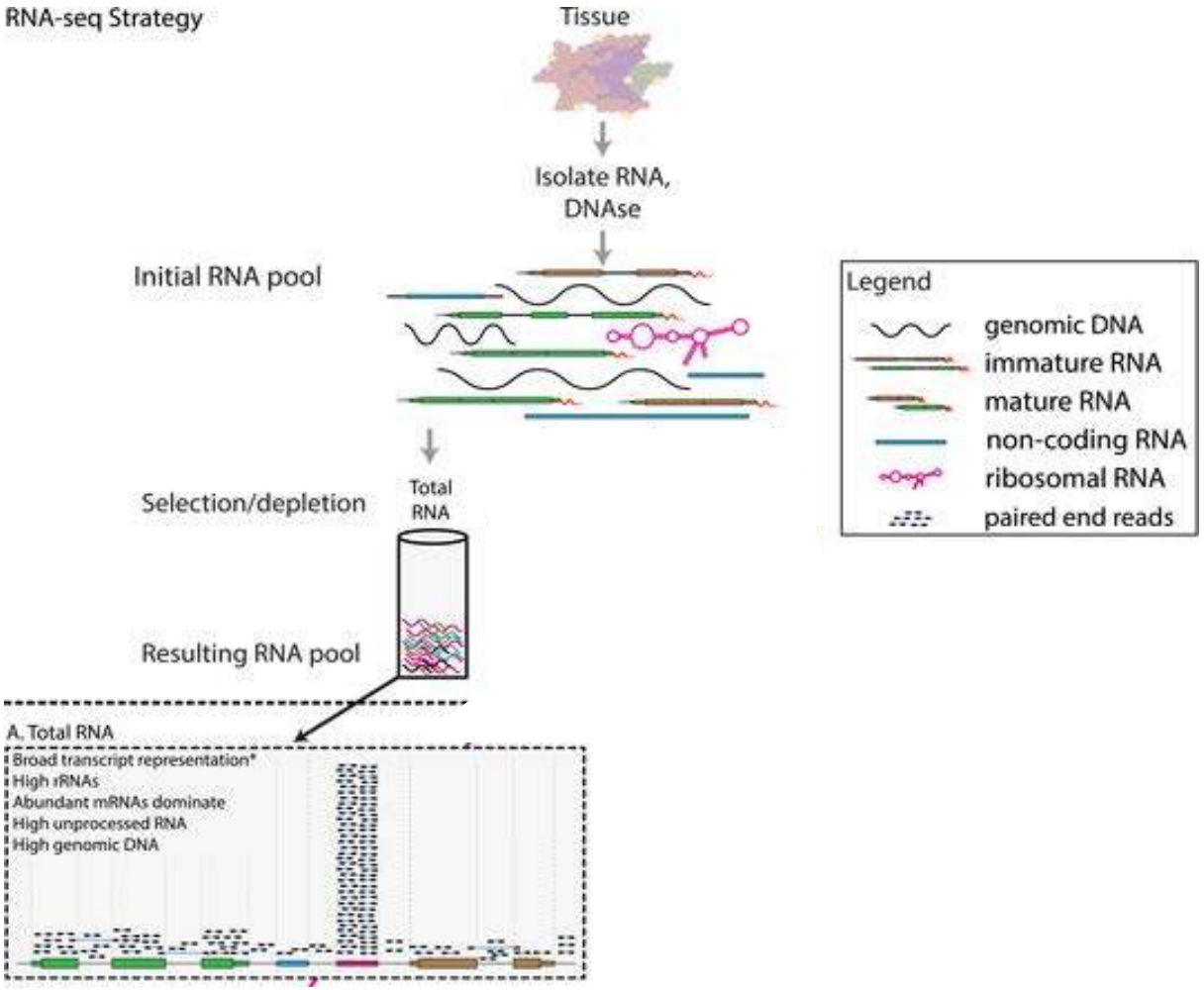

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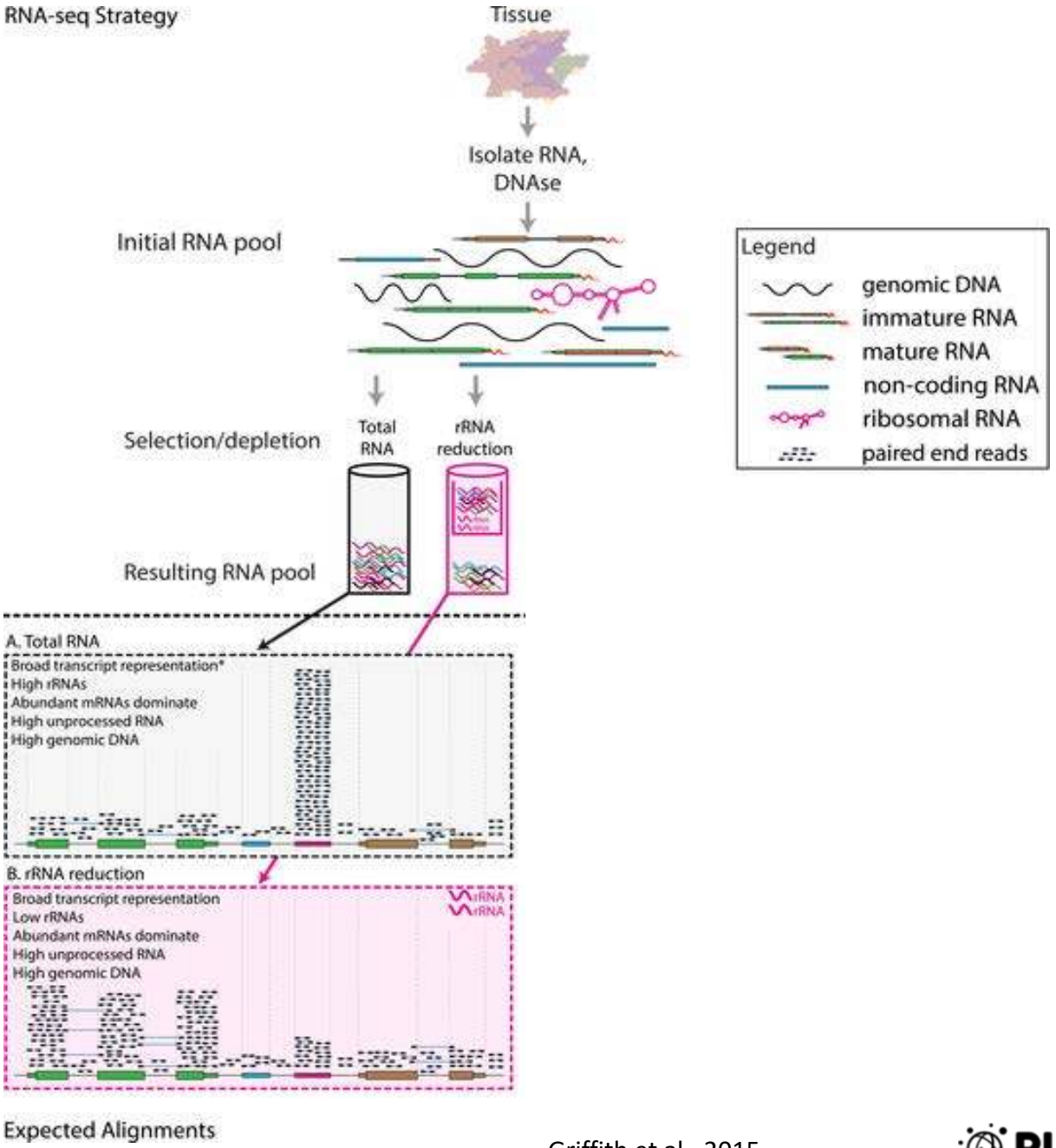

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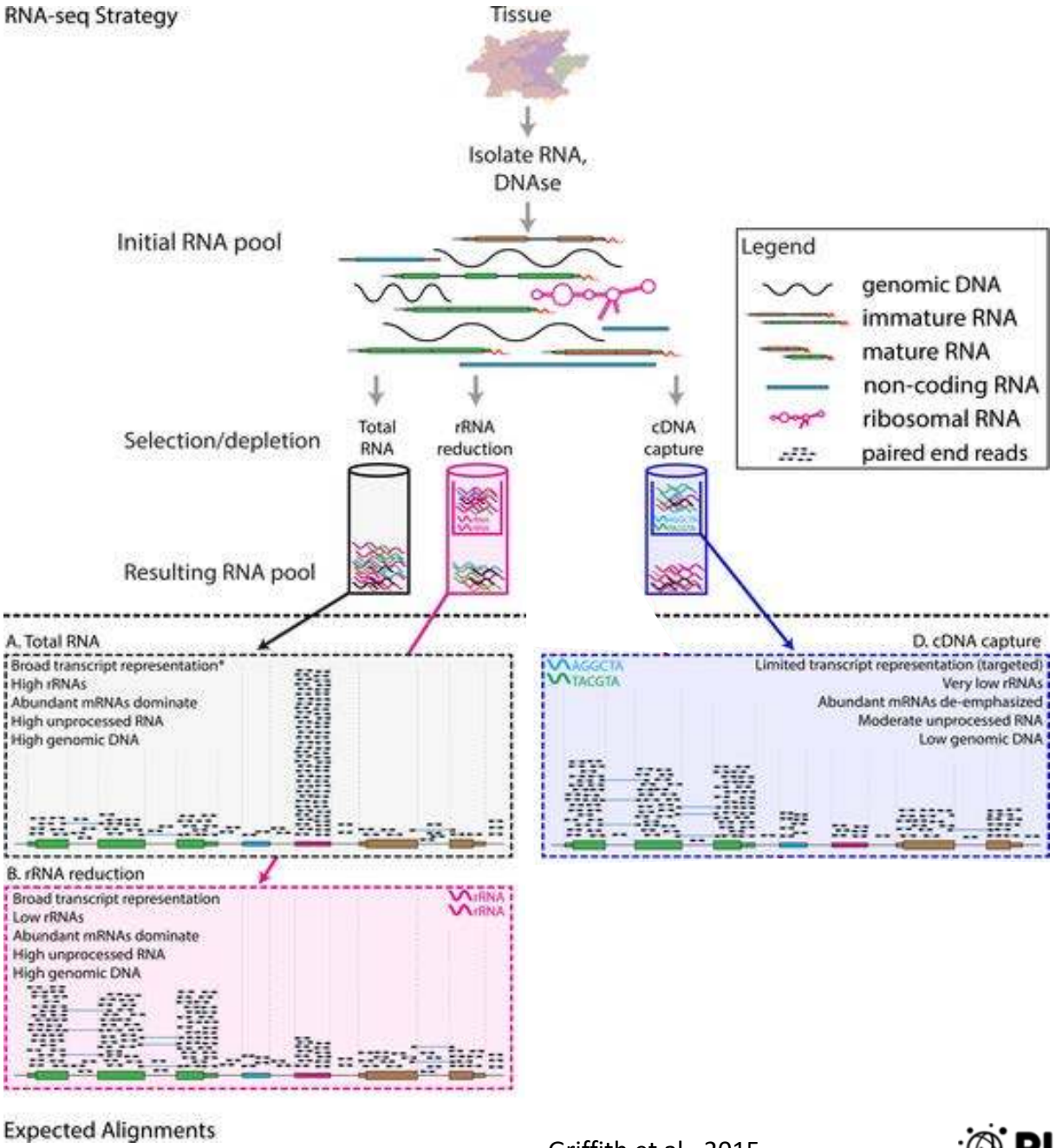

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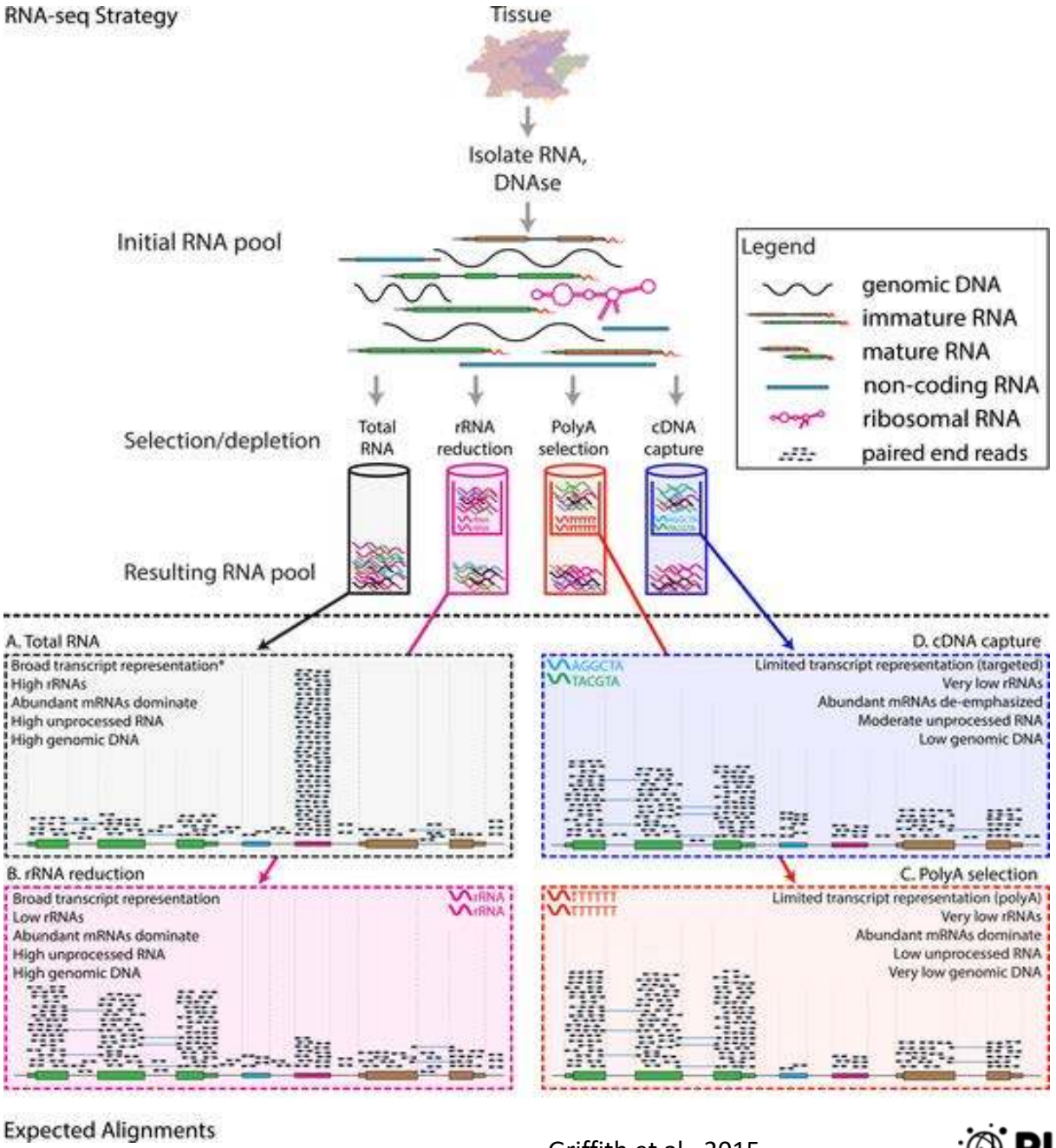

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Griffith et al., 2015

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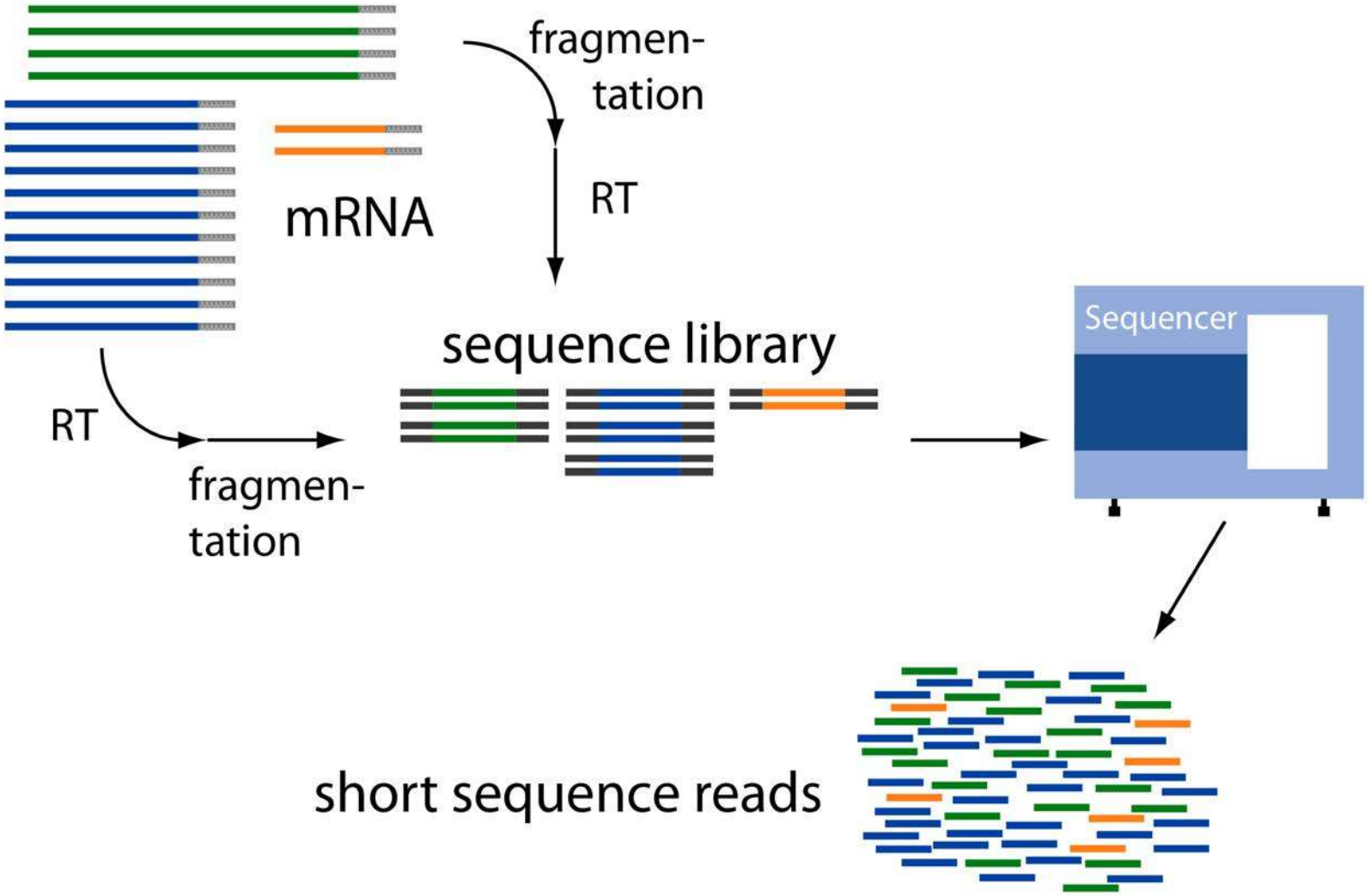
Overview of RNA-Seq



From: http://www2.fml.tuebingen.mpg.de/raetsch/members/research/transcriptomics.html

Common Data Formats for RNA-Seq

FASTA format:

```
>61DFRAAXX100204:1:100:10494:3070/1
AAACAACAGGGCACATTGTCACTCTTGTATTTGAAAAACACTTTCCGGCCAT
```

FASTQ format:

```
@61DFRAAXX100204:1:100:10494:3070/1
AAACAACAGGGCACATTGTCACTCTTGTATTTGAAAAACACTTTCCGGCCAT
+
ACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCBC?CCCCCCCCC@@CACCCCCA
```

Read

Quality values

AsciiEncodedQual(x) = -10 * log10(Pwrong(x)) + 33

AsciiEncodedQual (‘C’) = **64**

So, Pwrong(‘C’) = 10^((**64**-33/ (-10)) = 10^-3.4 = **0.0004**

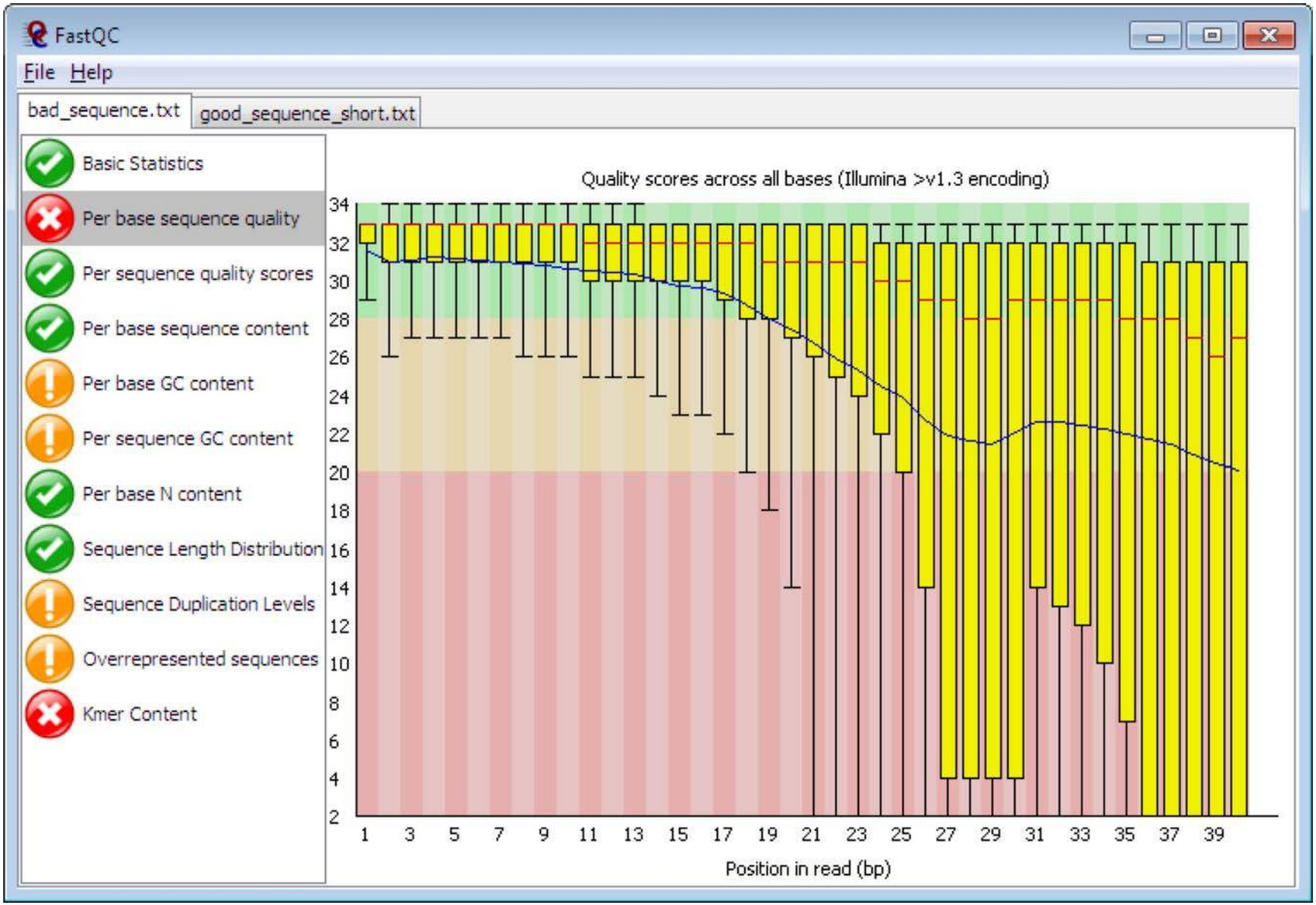
Paired-end Sequences

Two FastQ files, read name indicates left (/1) or right (/2) read of paired-end

```
@61DFRAAXX100204:1:100:10494:3070/1
AAACAACAGGGCACATTGTCACTCTTGTATTTGAAAAACACTTTCCGGCCAT
+
ACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCBC?CCCCCCCCC@@CACCCCCA
```

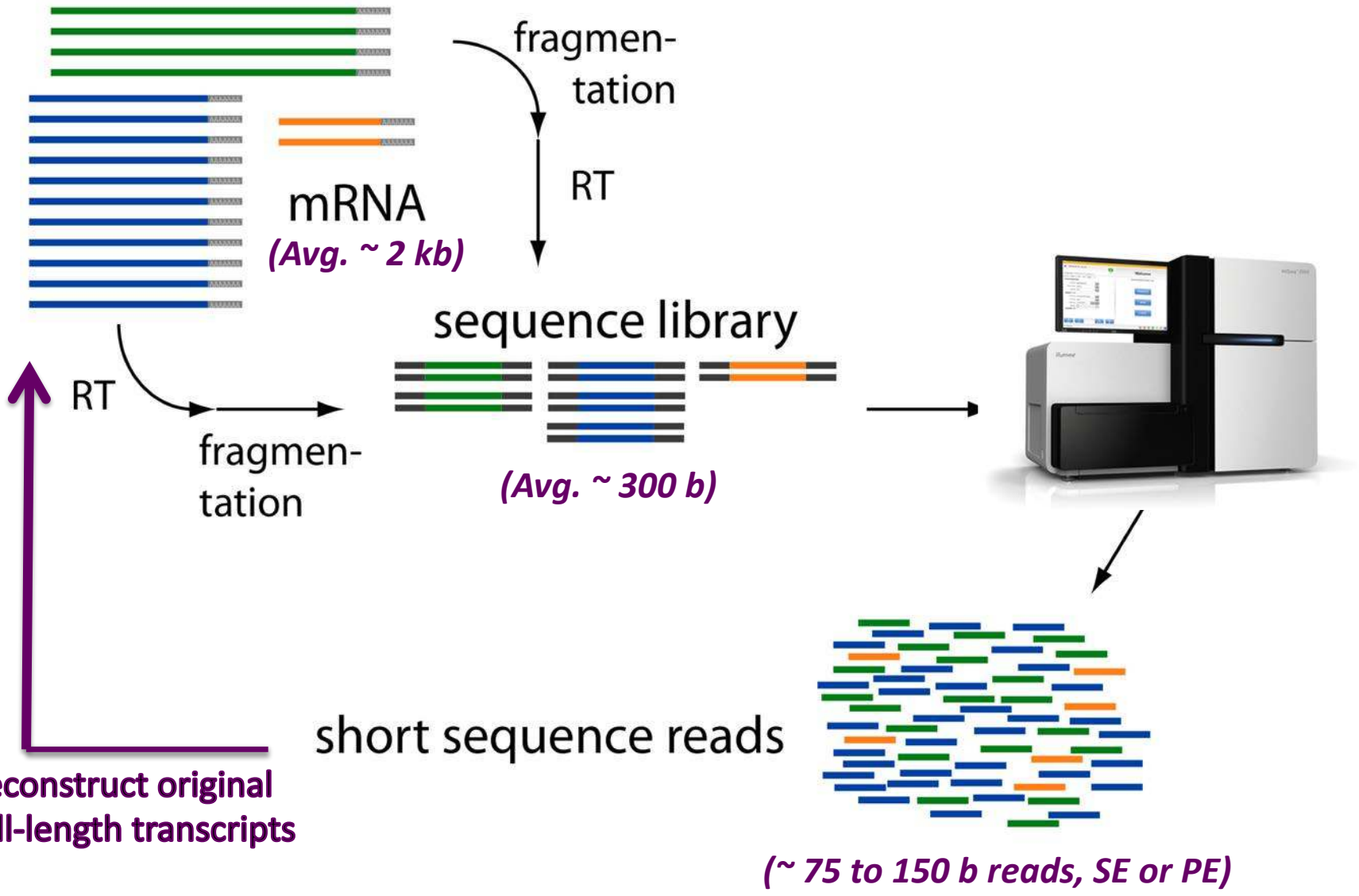
```
@61DFRAAXX100204:1:100:10494:3070/2
CTCAAATGGTTAATTCTCAGGCTGCAAATATTCGTTCAGGATGGAAGAACA
+
C<CCCCCCCACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCBCCCC
```

Read Quality Assessment



From: http://www.bioinformatics.babraham.ac.uk/projects/fastqc/

RNA-Seq Challenge: Transcript Reconstruction



Adapted from: http://www2.fml.tuebingen.mpg.de/raetsch/members/research/transcriptomics.html

Transcript Reconstruction from RNA-Seq Reads

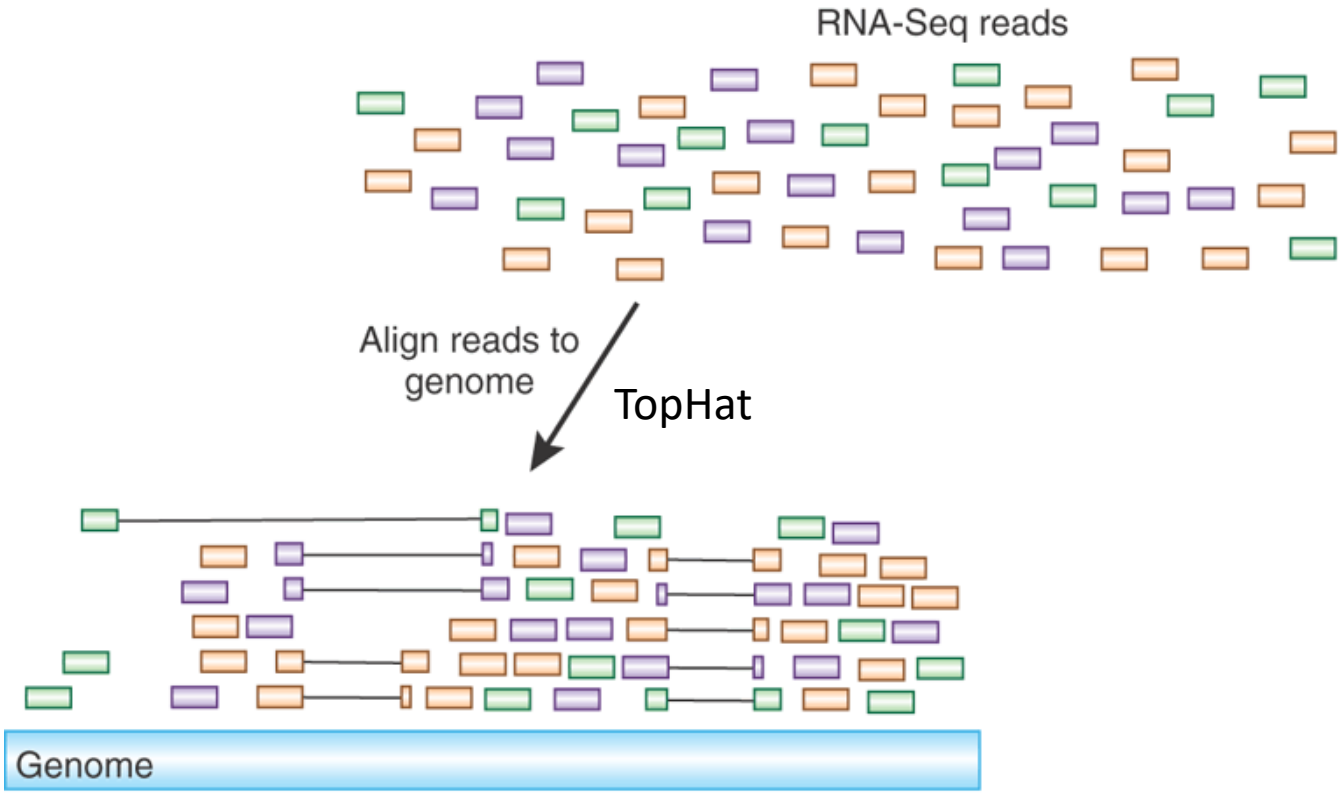
Advancing RNA-Seq analysis

Brian J Haas & Michael C Zody

Nature Biotech, 2010

New methods for analyzing RNA-Seq data enable *de novo* reconstruction of the transcriptome.

Transcript Reconstruction from RNA-Seq Reads



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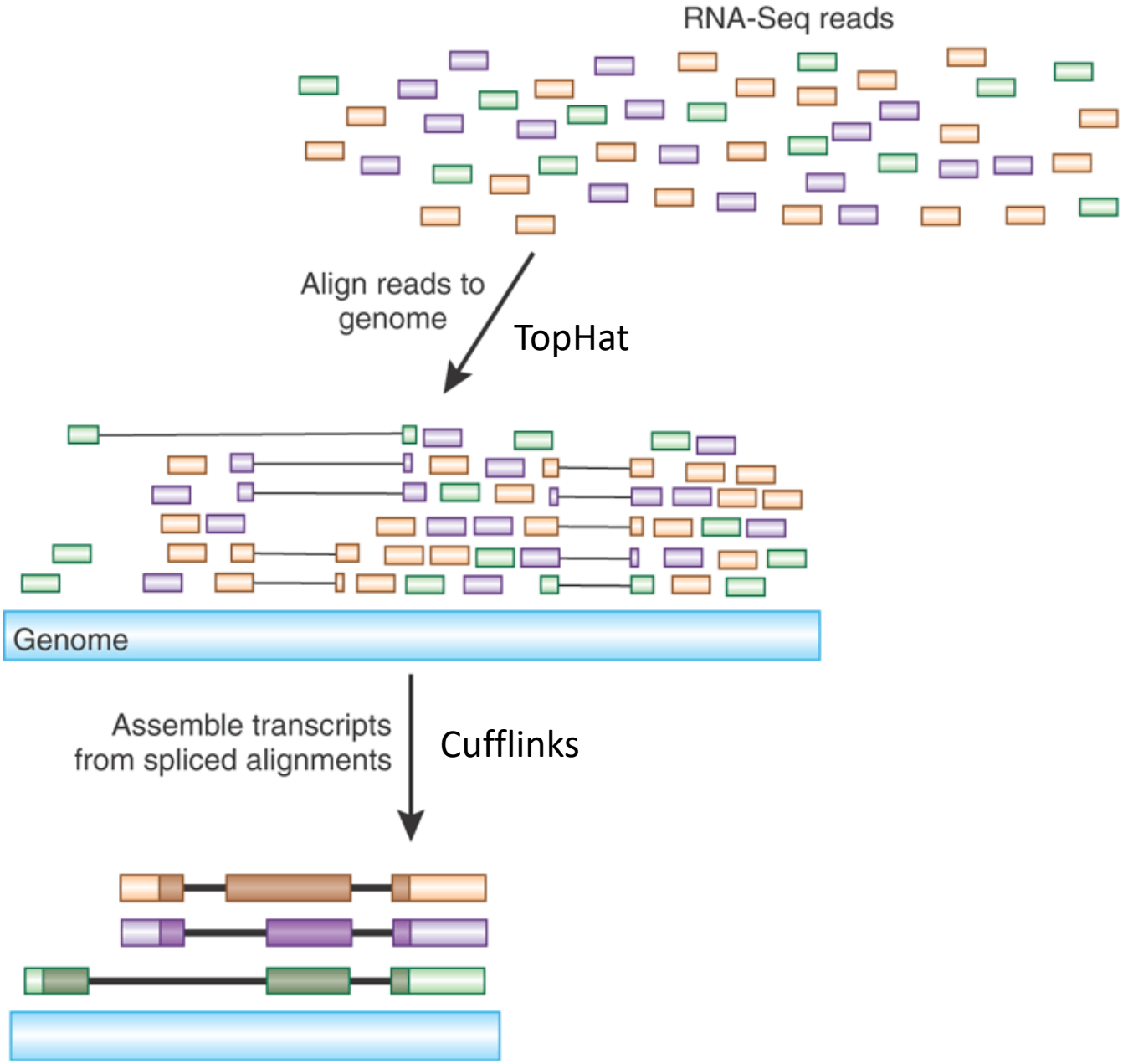

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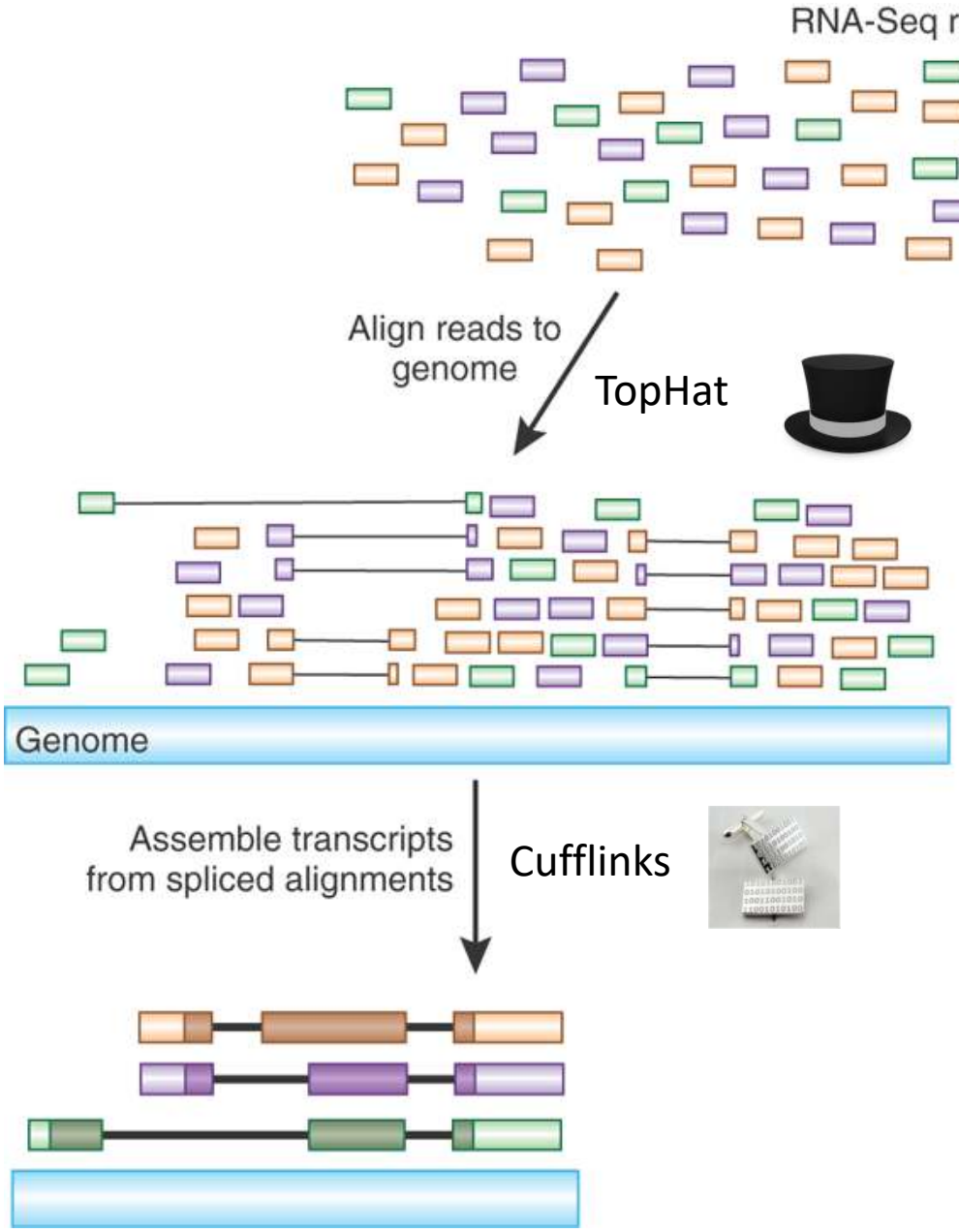

The Tuxedo Suite:

End-to-end **Genome**-based RNA-Seq Analysis Software Package

NATURE PROTOCOLS | PROTOCOL

Differential gene and transcript expression analysis of RNA-seq experiments with TopHat and Cufflinks

Cole Trapnell, Adam Roberts, Loyal Goff, Geo Pertea, Daehwan Kim, David R Kelley, Harold Pimentel, Steven L Salzberg, John L Rinn & Lior Pachter

Affiliations | Contributions | Corresponding author

Nature Protocols **7**, 562–578 (2012) | doi:10.1038/nprot.2012.016
Published online 01 March 2012

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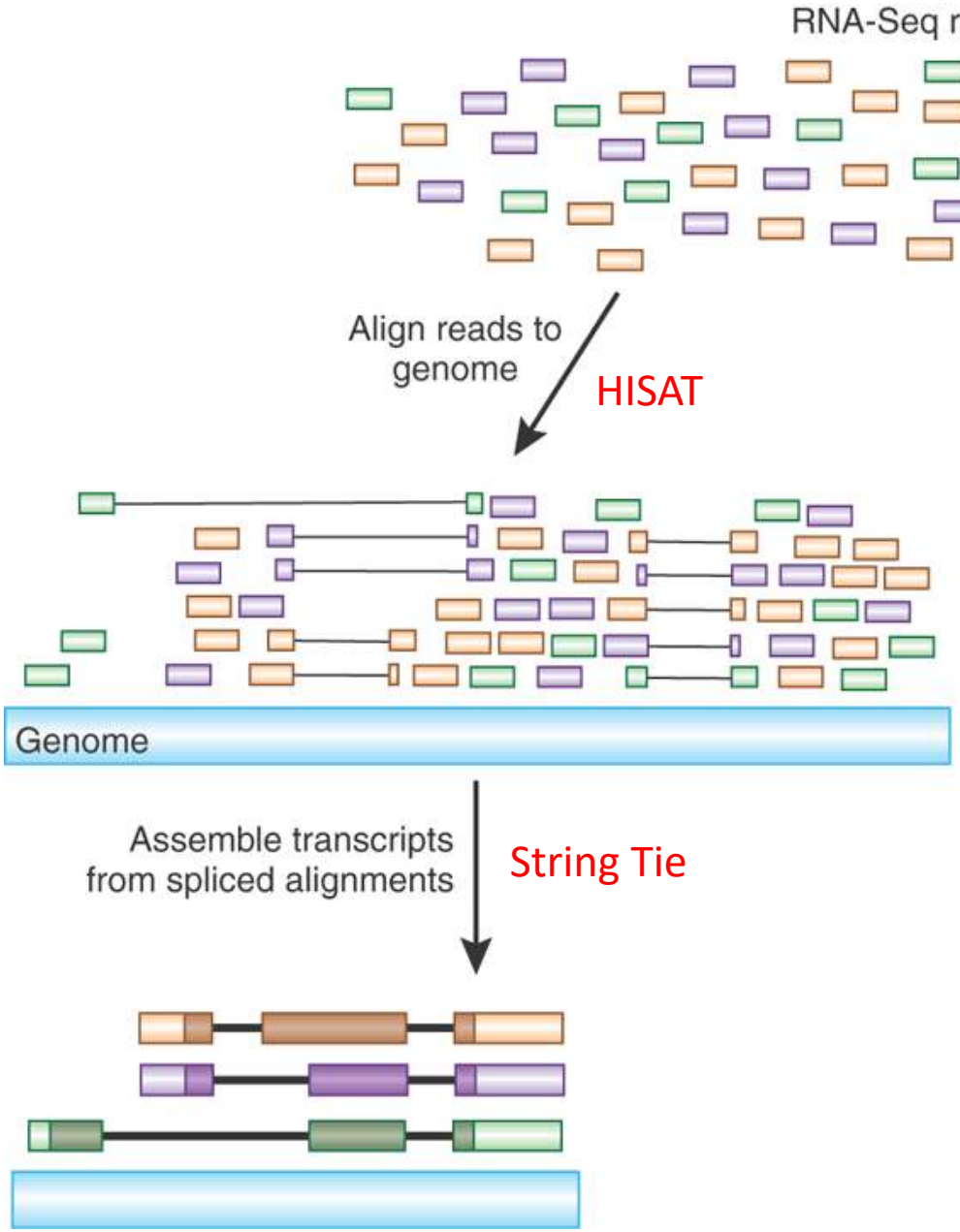

The "New Tuxedo" Suite:

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NATURE PROTOCOLS | PROTOCOL

Transcript-level expression analysis of RNA-seq experiments with HISAT, StringTie and Ballgown

Mihaela Pertea, Daehwan Kim, Geo M Pertea, Jeffrey T Leek & Steven L Salzberg

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Nature Protocols **11**, 1650–1667 (2016) | doi:10.1038/nprot.2016.095
Published online 11 August 2016

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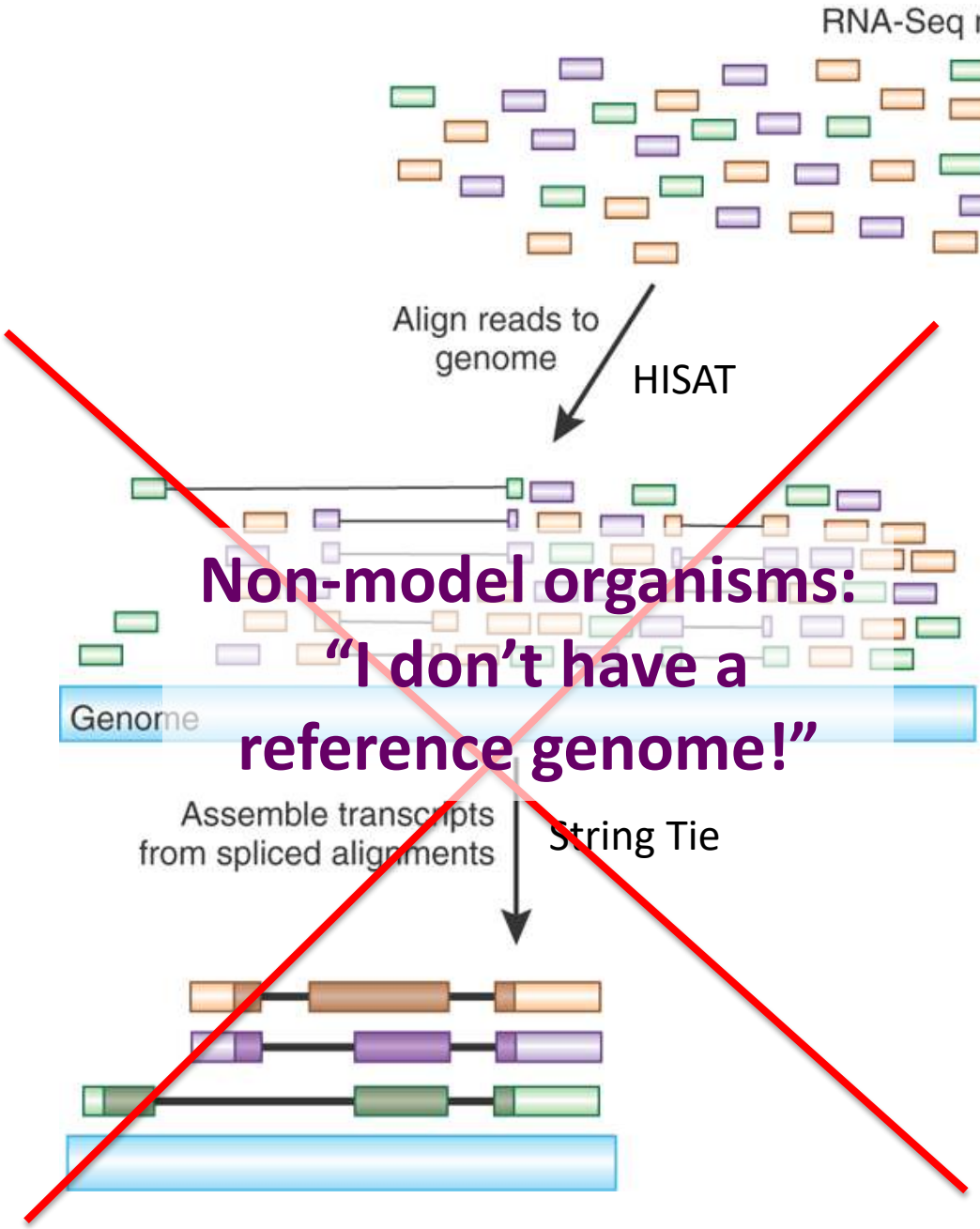

Non-model organisms: "I don't have a reference genome!"

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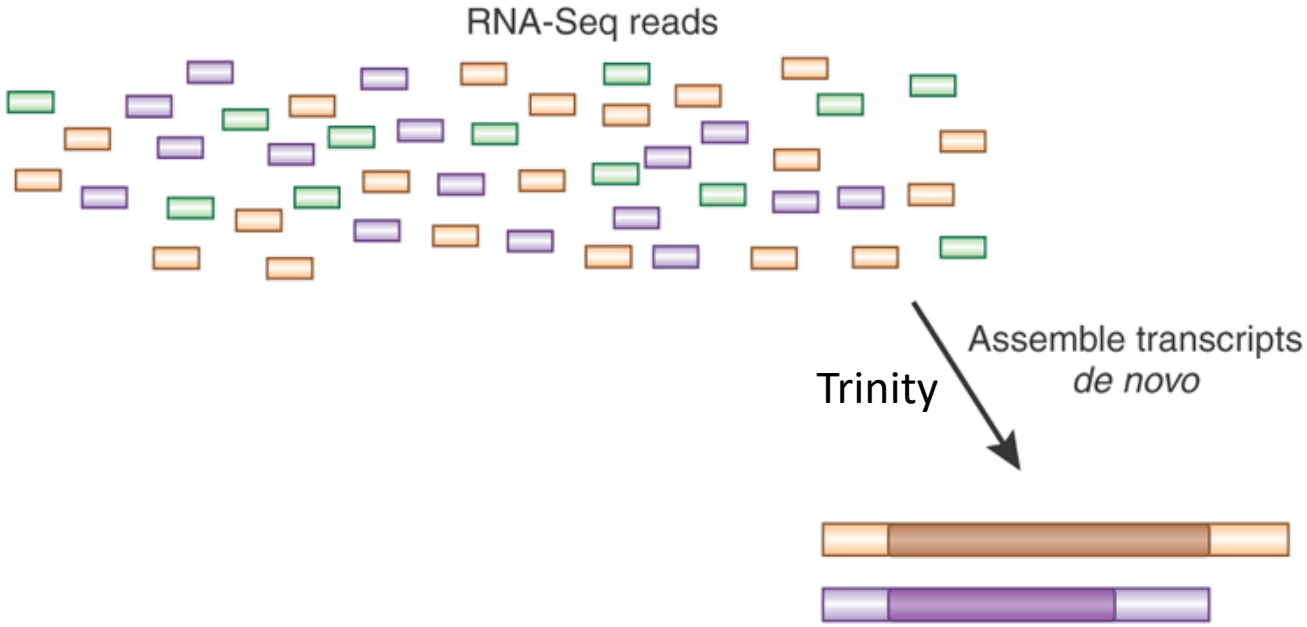

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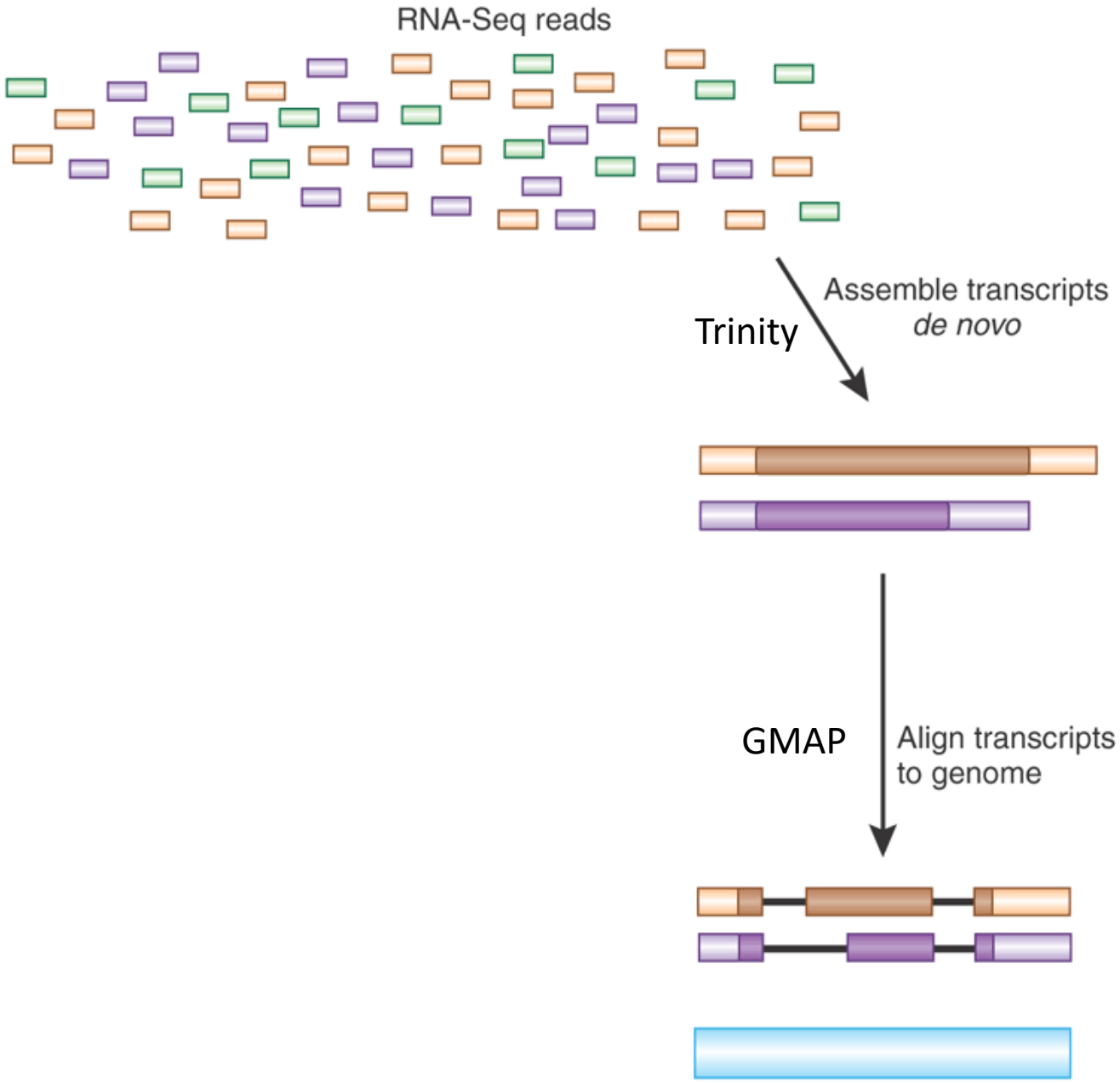

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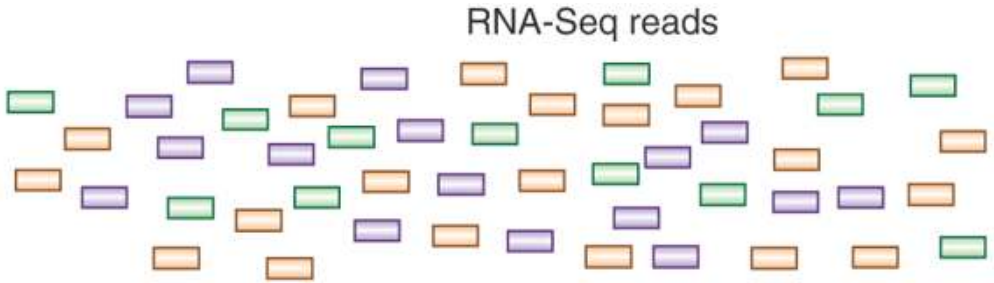


End-to-end **Transcriptome**-based
RNA-Seq Analysis
Software Package

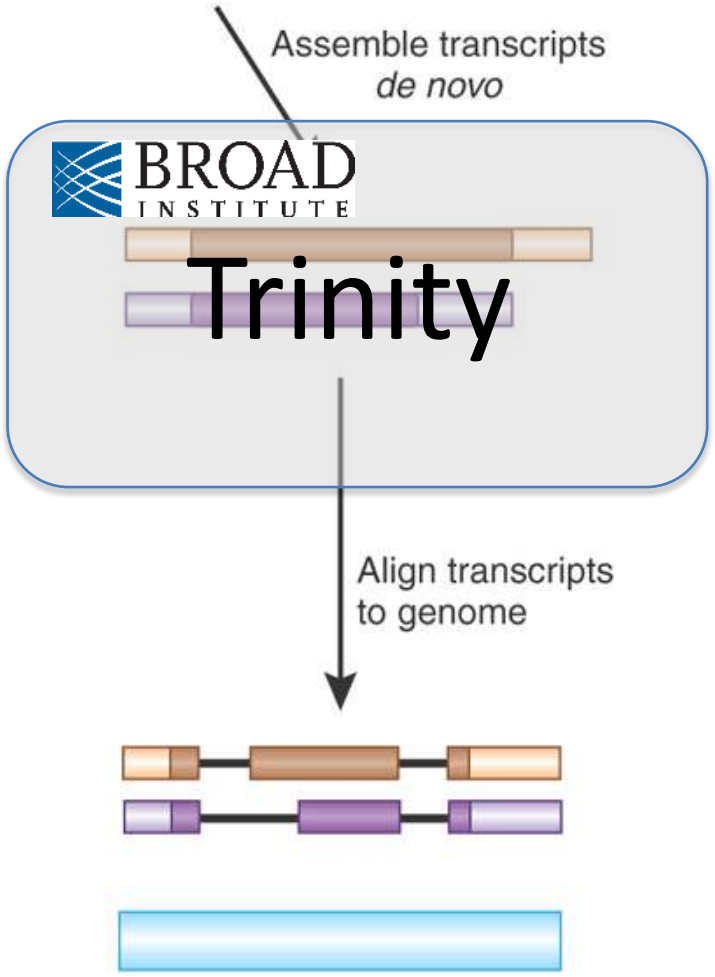
NATURE PROTOCOLS | PROTOCOL

De novo transcript sequence reconstruction from RNA-seq using the Trinity platform for reference generation and analysis

Brian J Haas, Alexie Papanicolaou, Moran Yassour, Manfred Grabherr, Philip D Blood, Joshua Bowden, Matthew Brian Couger, David Eccles, Bo Li, Matthias Lieber, Matthew D MacManes, Michael Ott, Joshua Orvis, Nathalie Pochet, Francesco Strozzi, Nathan Weeks, Rick Westerman, Thomas William, Colin N Dewey, Robert Henschel, Richard D LeDuc, Nir Friedman & Aviv Regev

Affiliations | Contributions | Corresponding authors

Nature Protocols **8**, 1494–1512 (2013) | doi:10.1038/nprot.2013.084
Published online 11 July 2013



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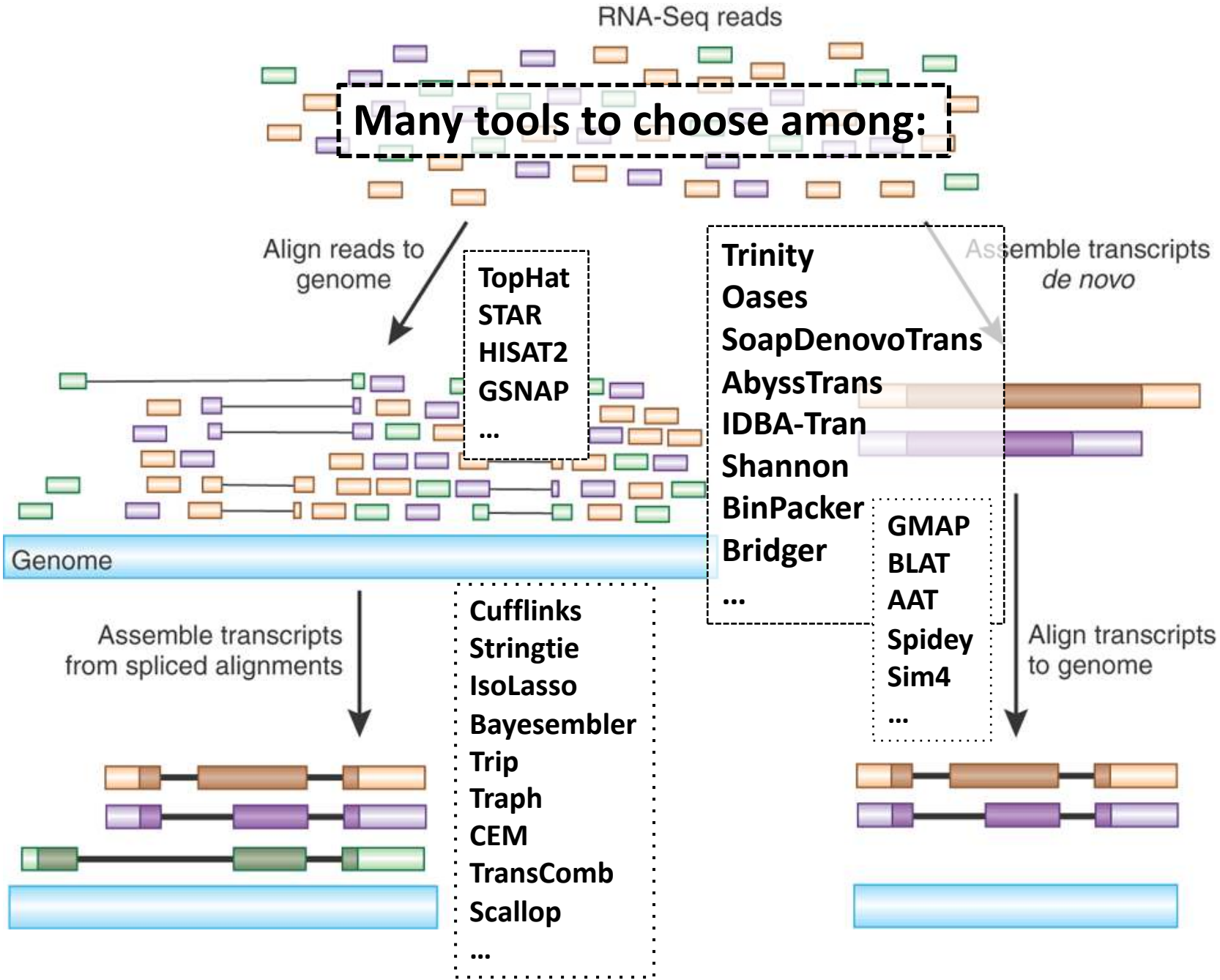

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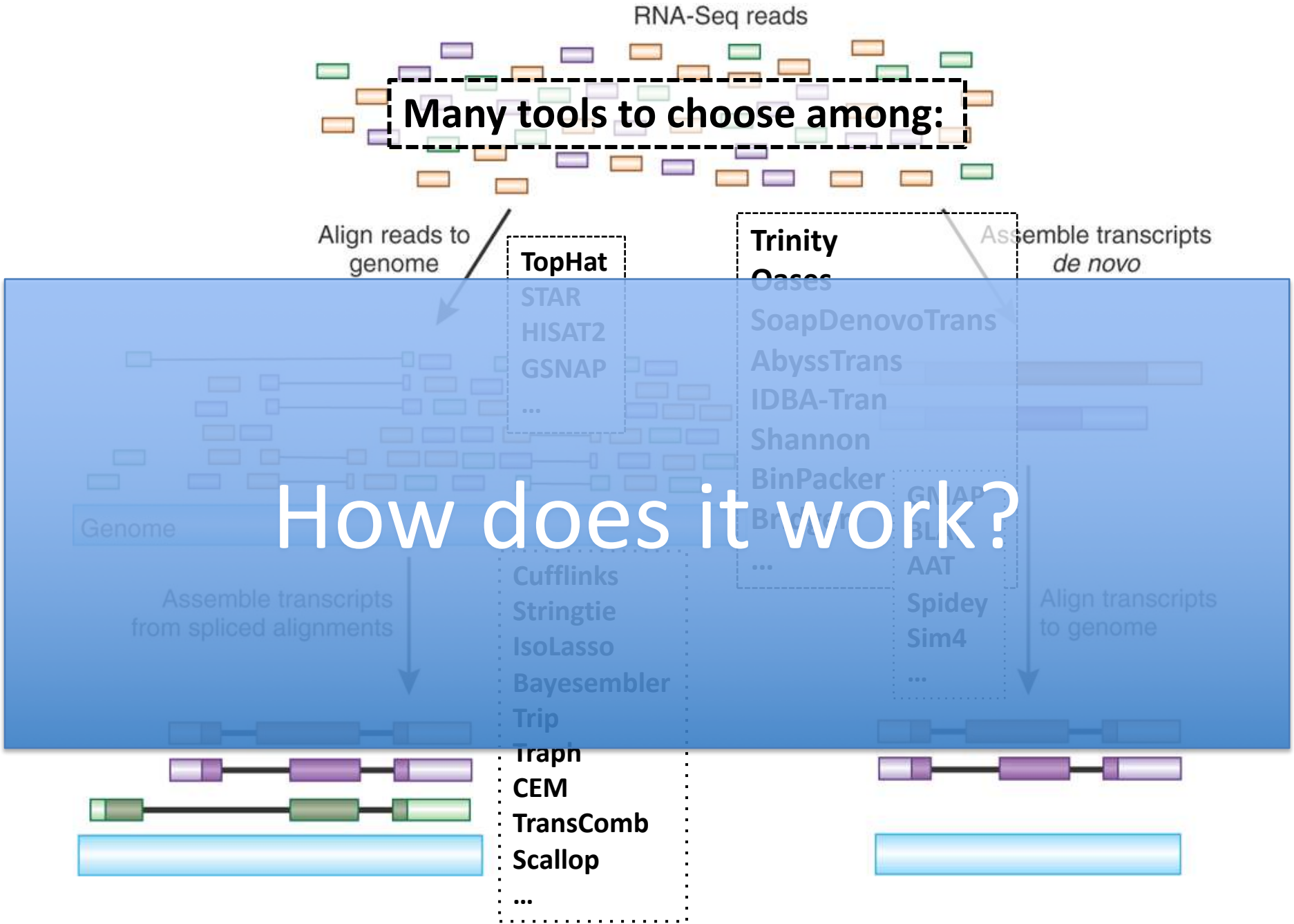
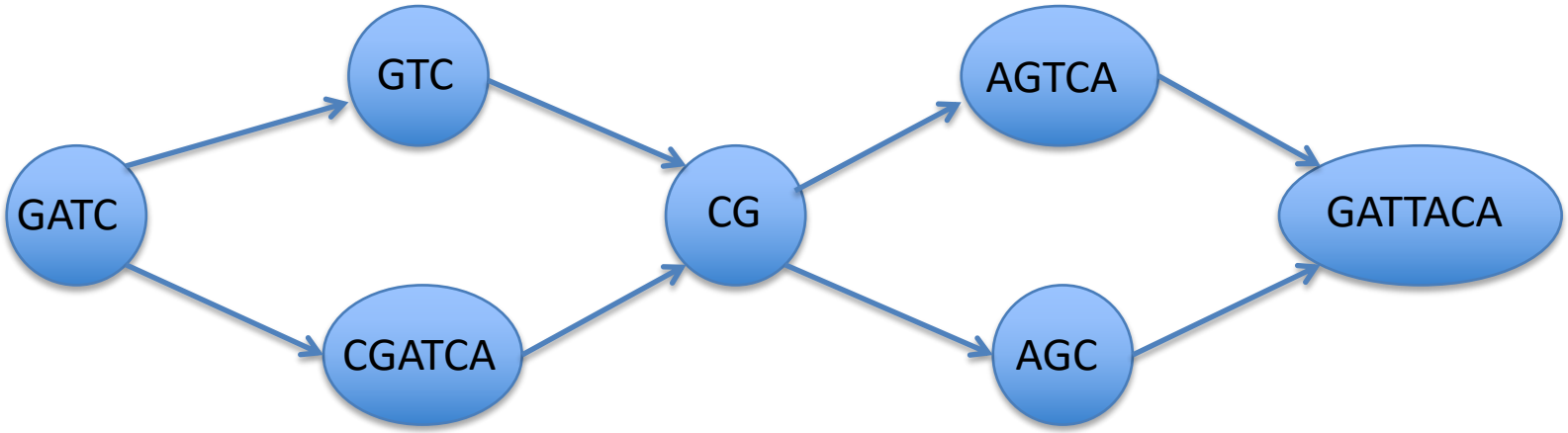


Graph Data Structures Commonly Used For Assembly

- Sequence
- Order
- Orientation (+, -)
- Overlap

Reads to Graph



Nodes = sequence (+/-)
Edges = order, overlap

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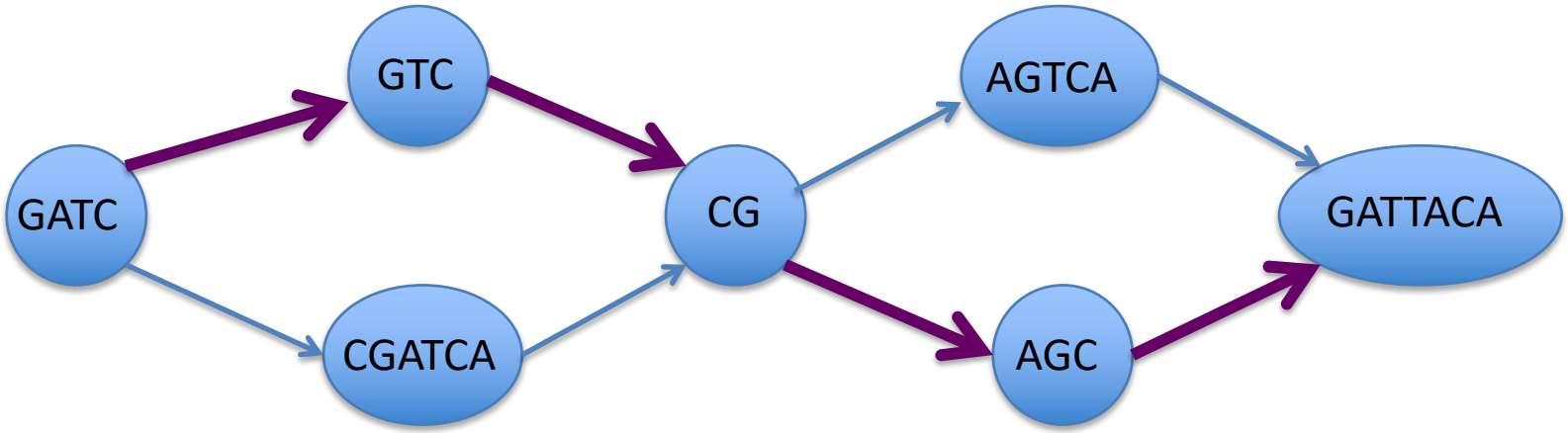
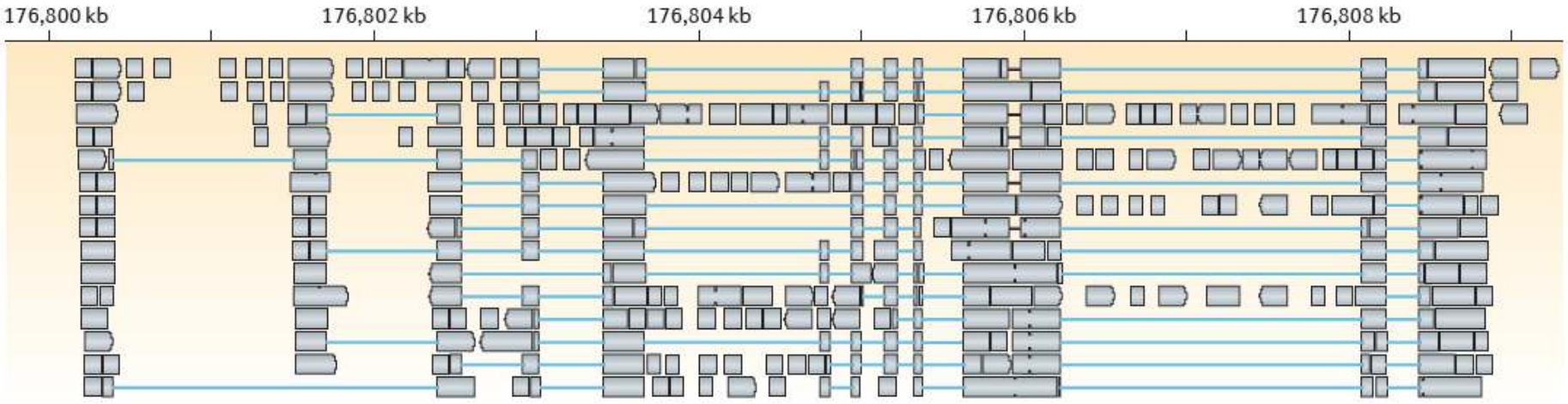


GATCGTCCGAGCGATTACA

Nodes = sequence (+/-)
Edges = order, overlap

Genome-Guided Transcript Reconstruction

Splice-align reads to the genome



From Martin & Wang. Nature Reviews in Genetics. 2011

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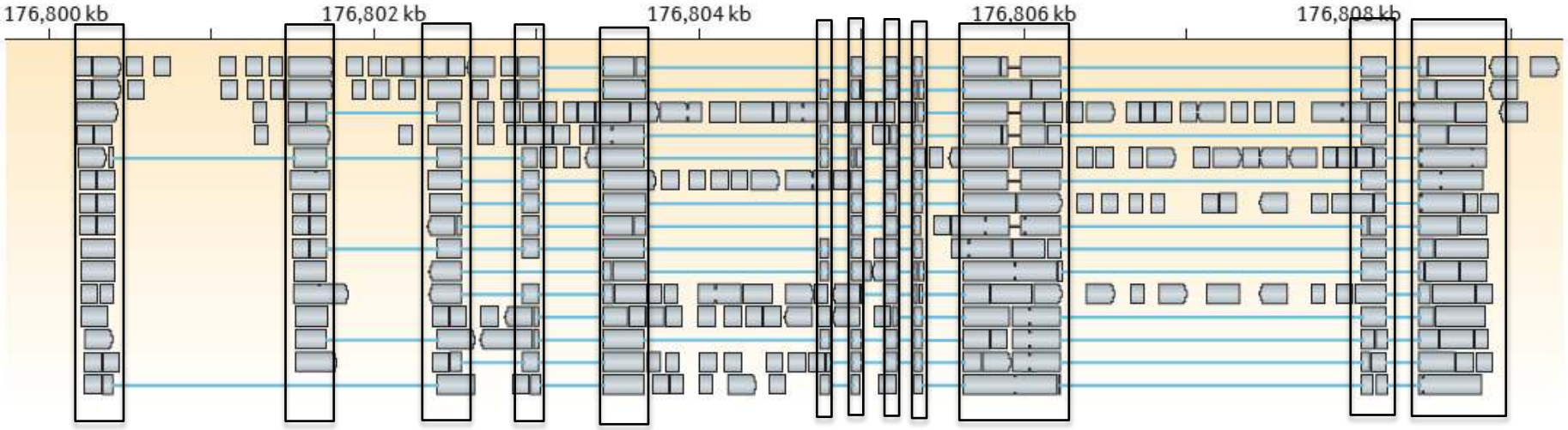


Alignment segment piles => exon regions

From Martin & Wang. Nature Reviews in Genetics. 2011

Genome-Guided Transcript Reconstruction

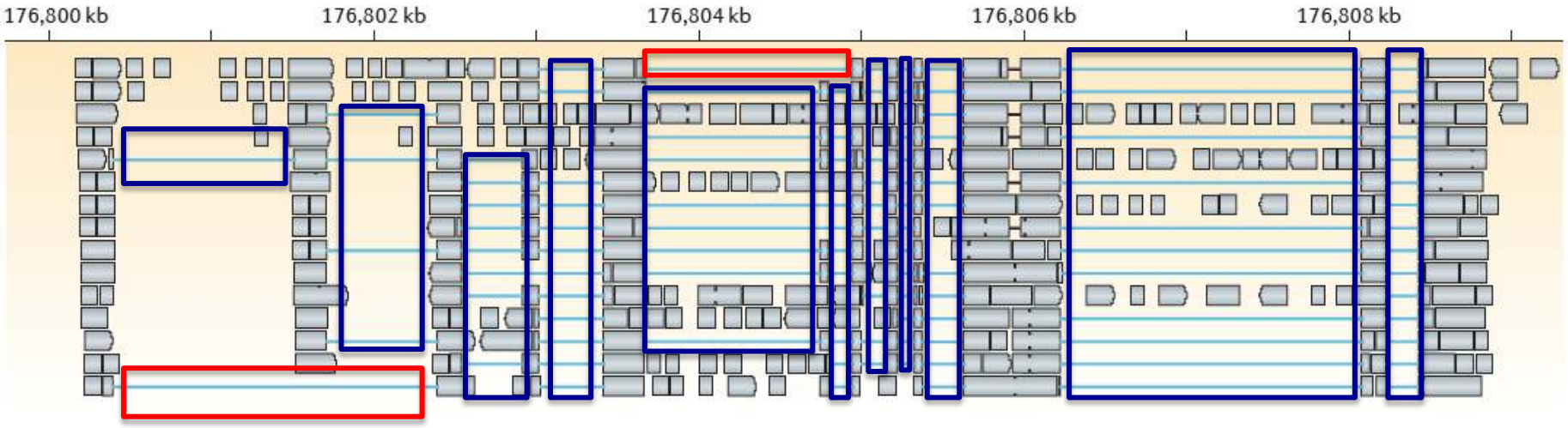
Splice-align reads to the genome

Large alignment gaps => introns

From Martin & Wang. Nature Reviews in Genetics. 2011

Genome-Guided Transcript Reconstruction

Splice-align reads to the genome

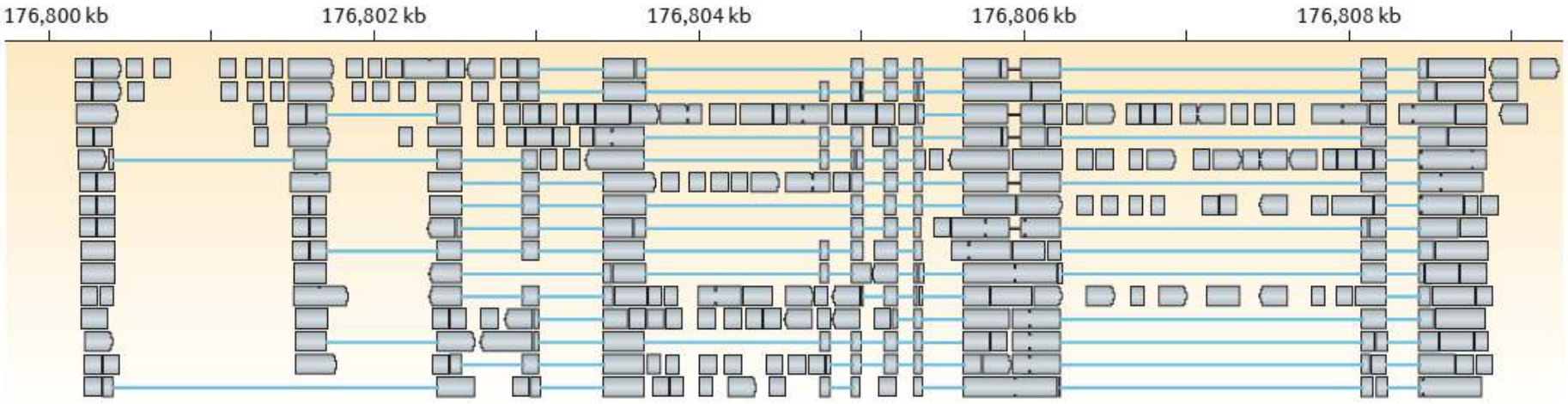


Overlapping but different introns = evidence of alternative splicing

From Martin & Wang. Nature Reviews in Genetics. 2011

Genome-Guided Transcript Reconstruction

Splice-align reads to the genome



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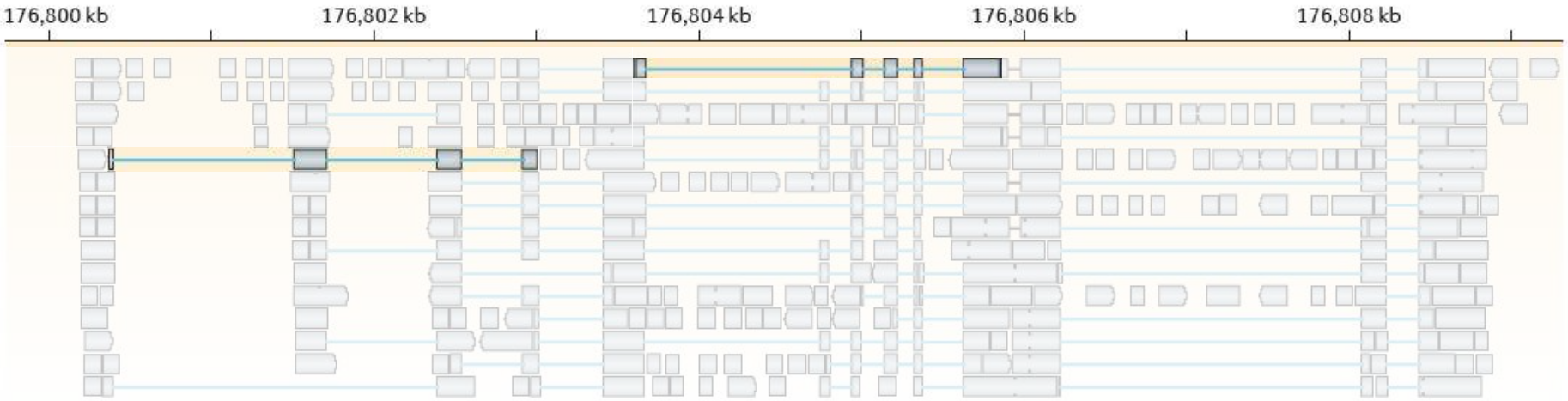
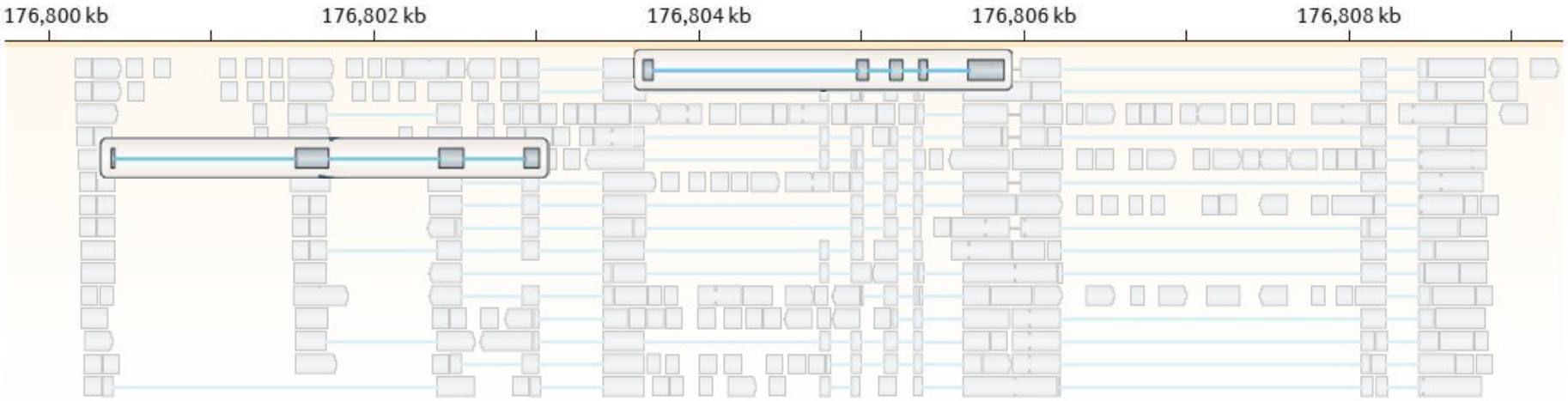


Individual reads can yield multiple exon and intron segments (splice patterns)

From Martin & Wang. Nature Reviews in Genetics. 2011

Genome-Guided Transcript Reconstruction

Splice-align reads to the genome



Nodes = unique splice patterns

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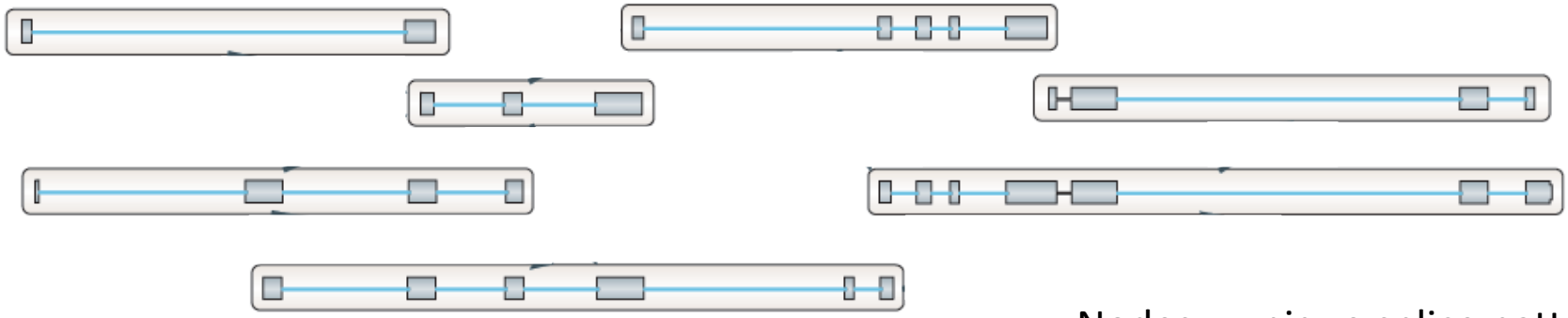
Genome-Guided Transcript Reconstruction

Splice-align reads to the genome

Construct graph from unique splice patterns of aligned reads.



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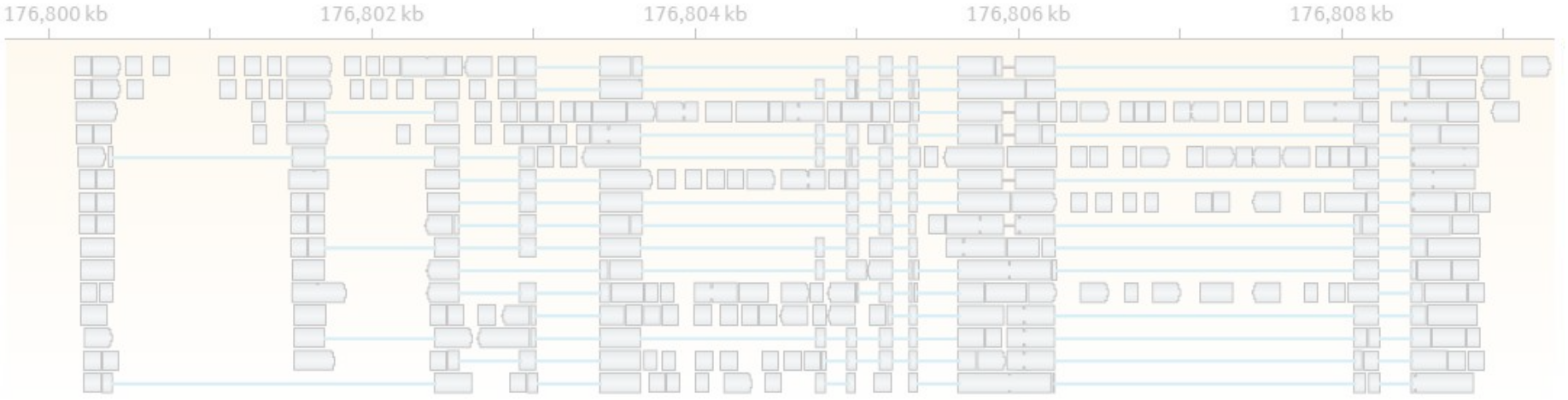
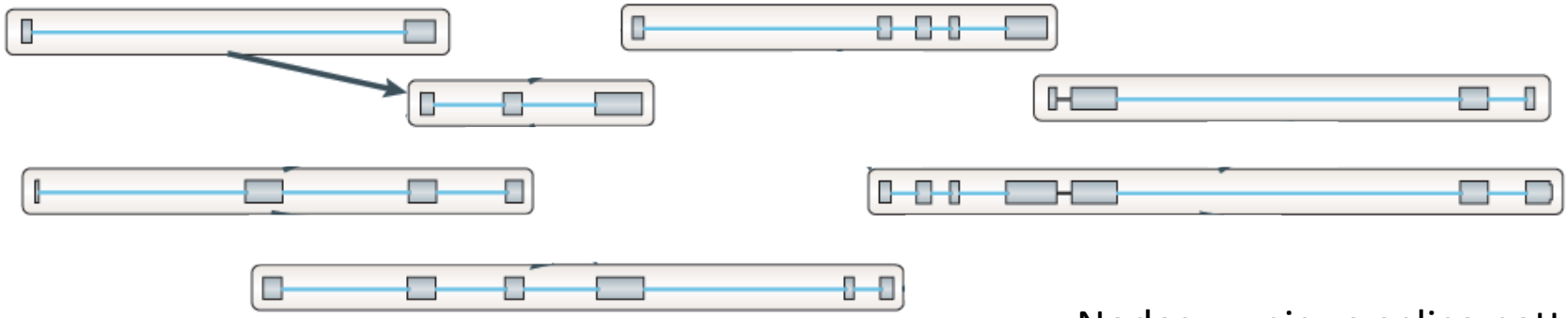


Construct graph from unique splice patterns of aligned reads.



Nodes = unique splice patterns
Edges = compatible patterns

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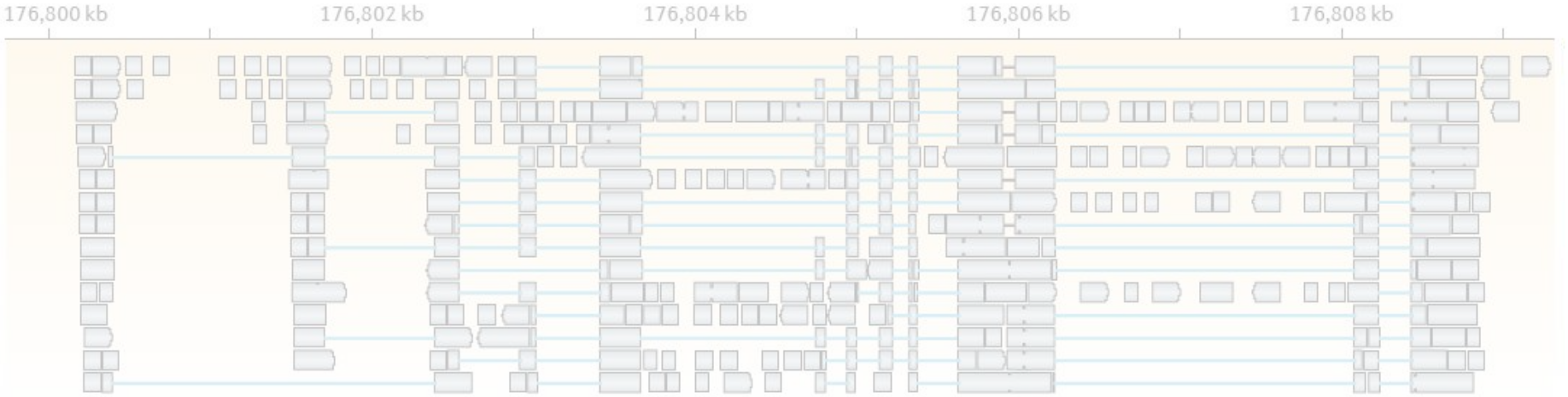
Genome-Guided Transcript Reconstruction

Splice-align reads to the genome



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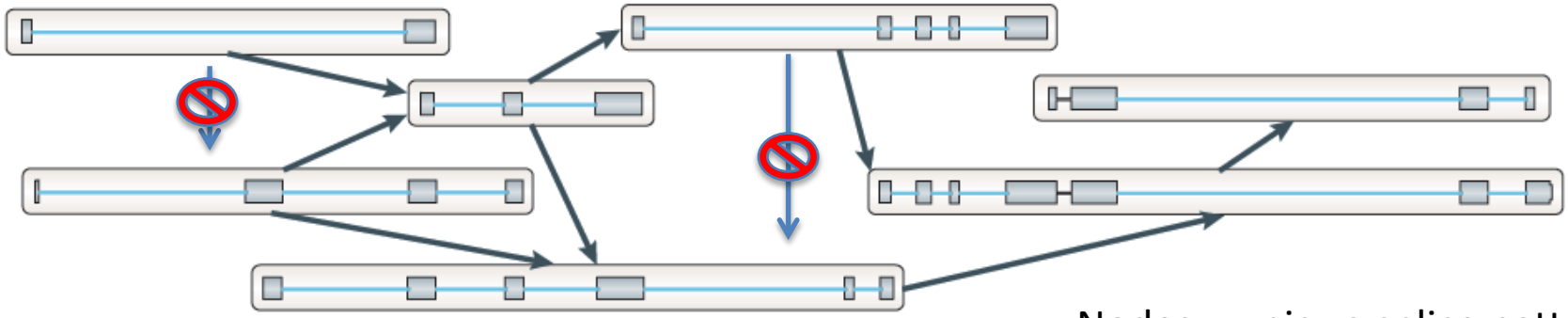

Nodes = unique splice patterns
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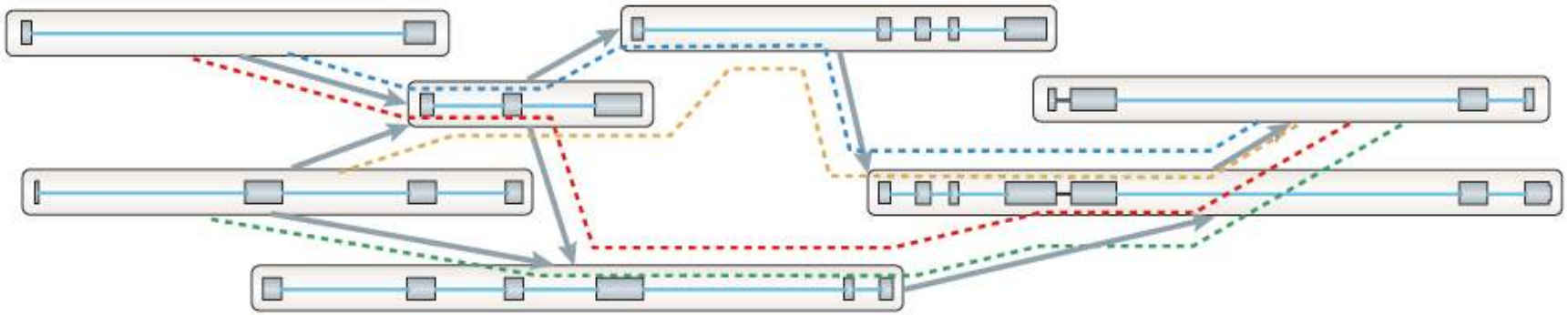
Genome-Guided Transcript Reconstruction

Traverse paths through the graph to assemble transcript isoforms



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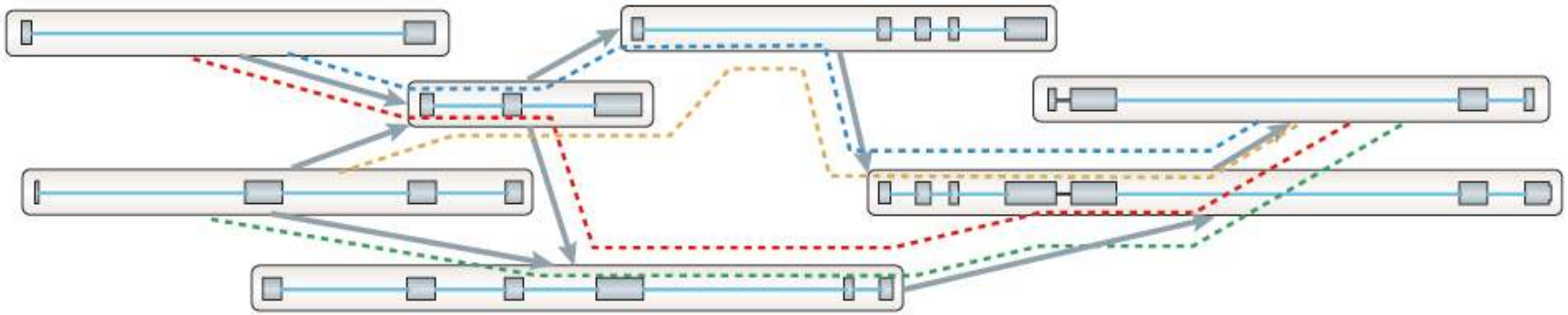
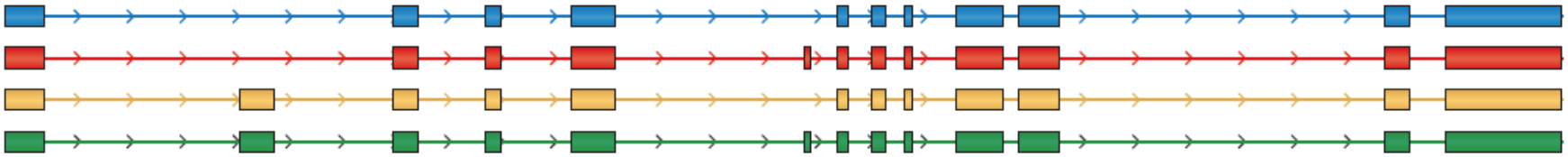


Reconstructed isoforms

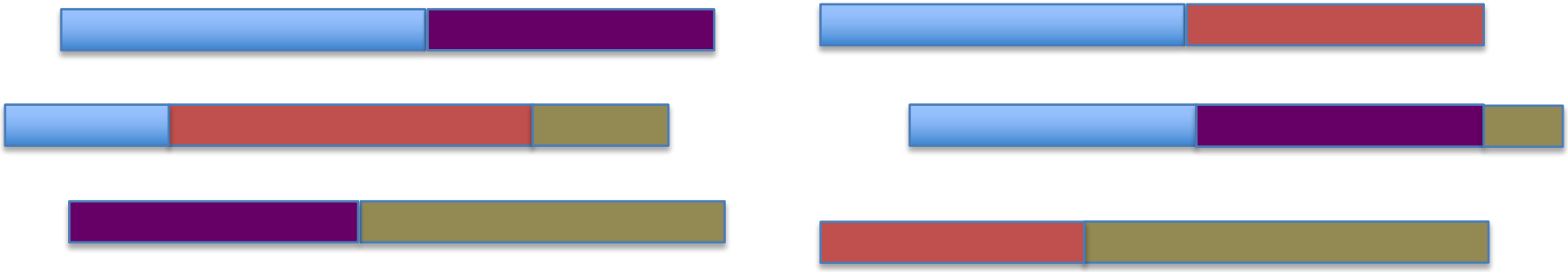


From Martin & Wang. Nature Reviews in Genetics. 2011

What if you don’t have a high quality reference genome sequence?

Genome-free de novo transcript reconstruction to the rescue.

Read Overlap Graph: Reads as nodes, overlaps as edges



Read Overlap Graph: Reads as nodes, overlaps as edges

Node = read
Edge = overlap

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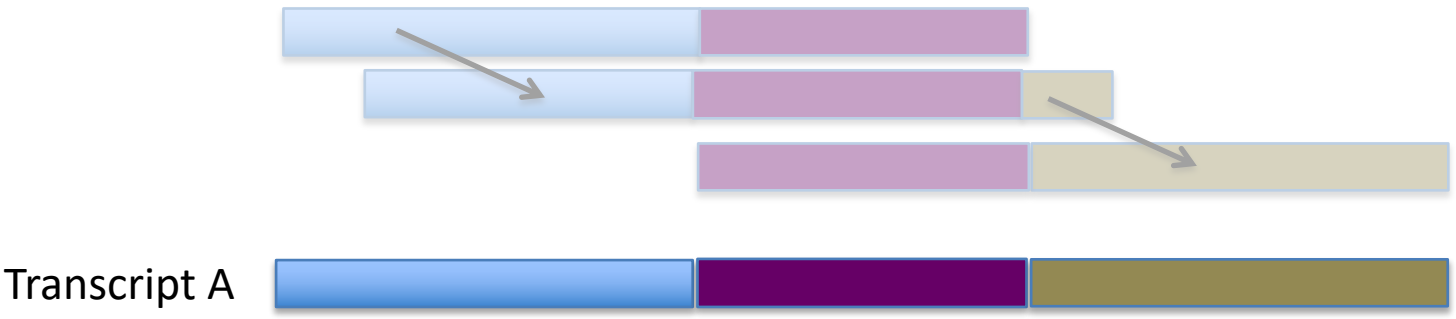
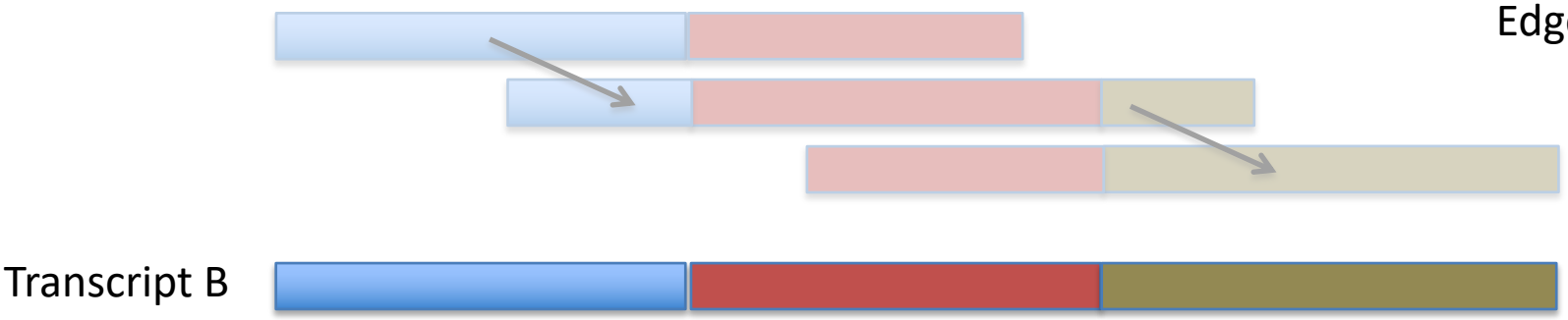
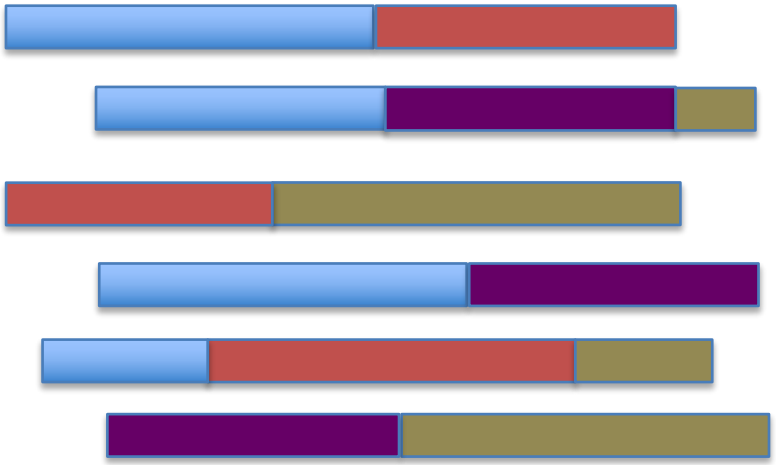


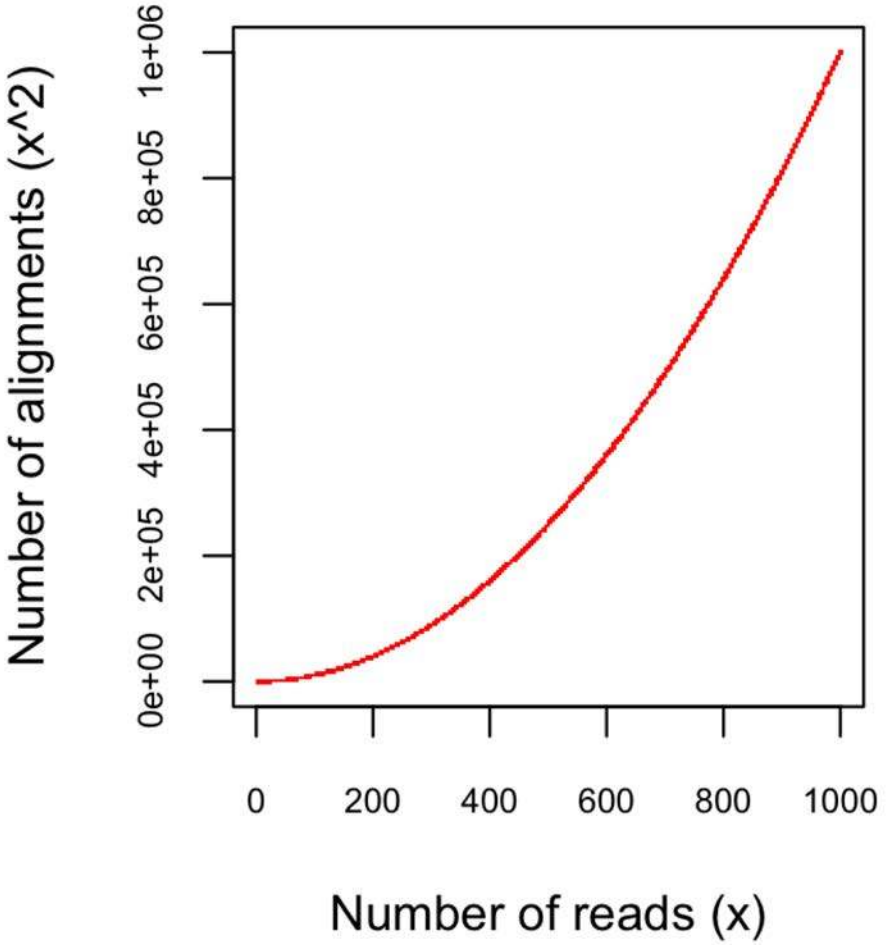
Generate consensus sequence where reads overlap

Node = read
Edge = overlap



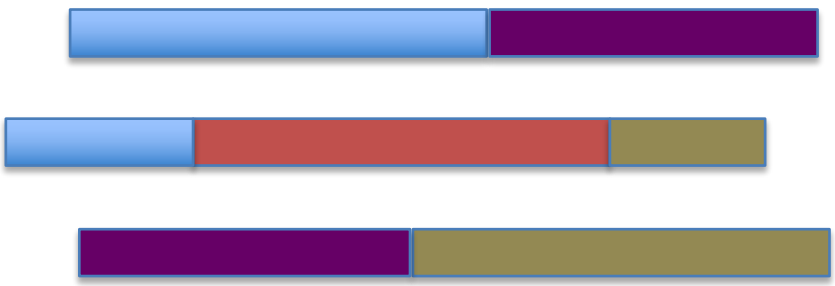
Finding pairwise overlaps between *n* reads involves ~ n^2 comparisons.



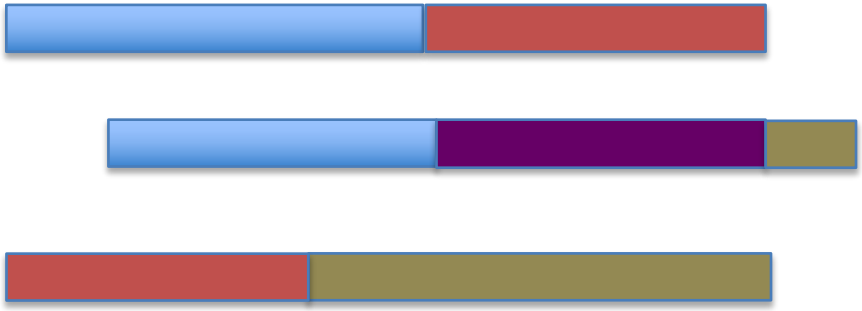


Impractical for typical RNA-Seq data (50M reads)

No genome to align to…



De novo assembly required

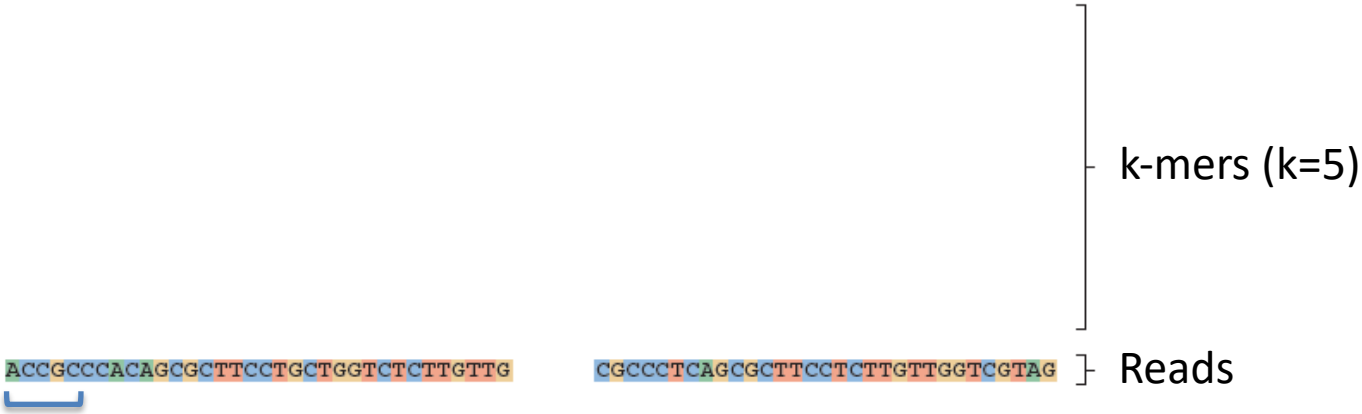


Want to avoid n^2 read alignments to define overlaps

Use a de Bruijn graph

Sequence Assembly via de Bruijn Graphs

Generate all substrings of length k from the reads



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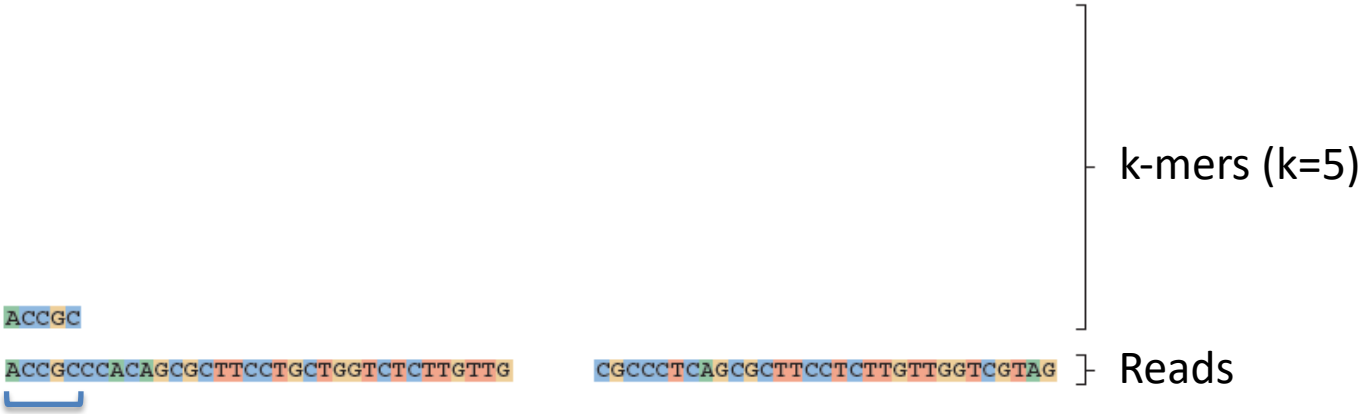

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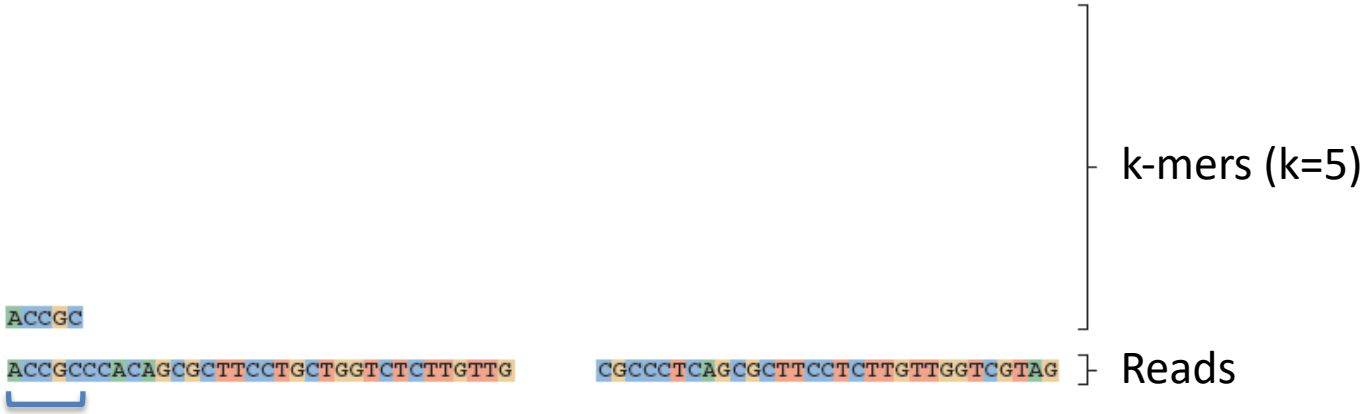

Construct the de Bruijn graph

Nodes = unique k-mers

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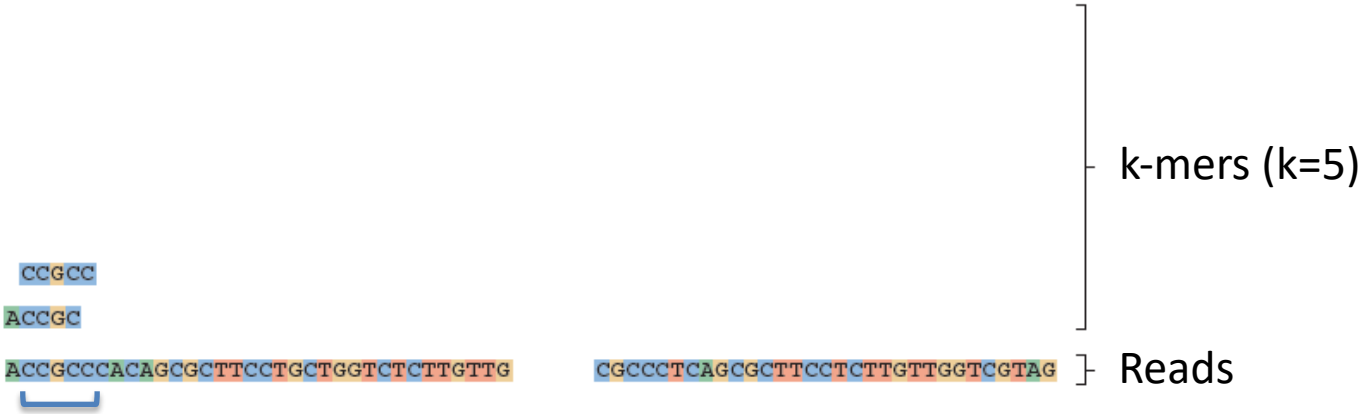

Construct the de Bruijn graph

Nodes = unique k-mers
Edges = overlap by (k-1)

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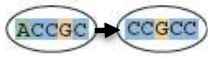

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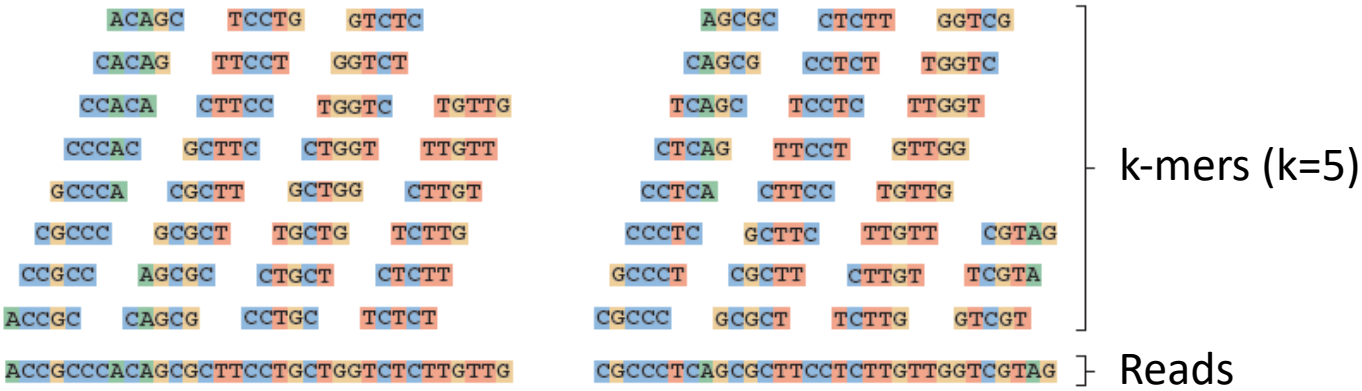

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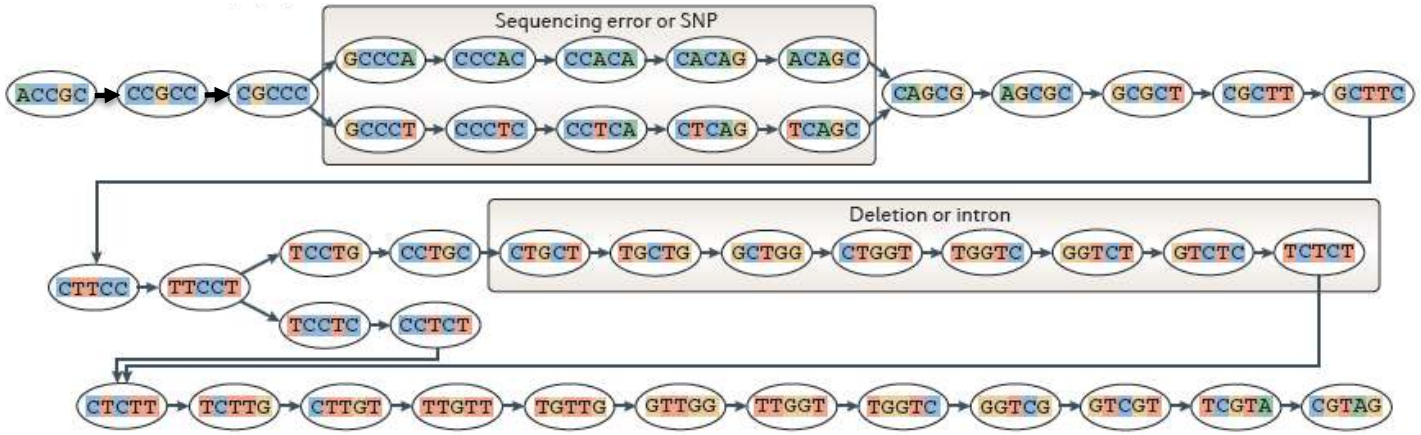

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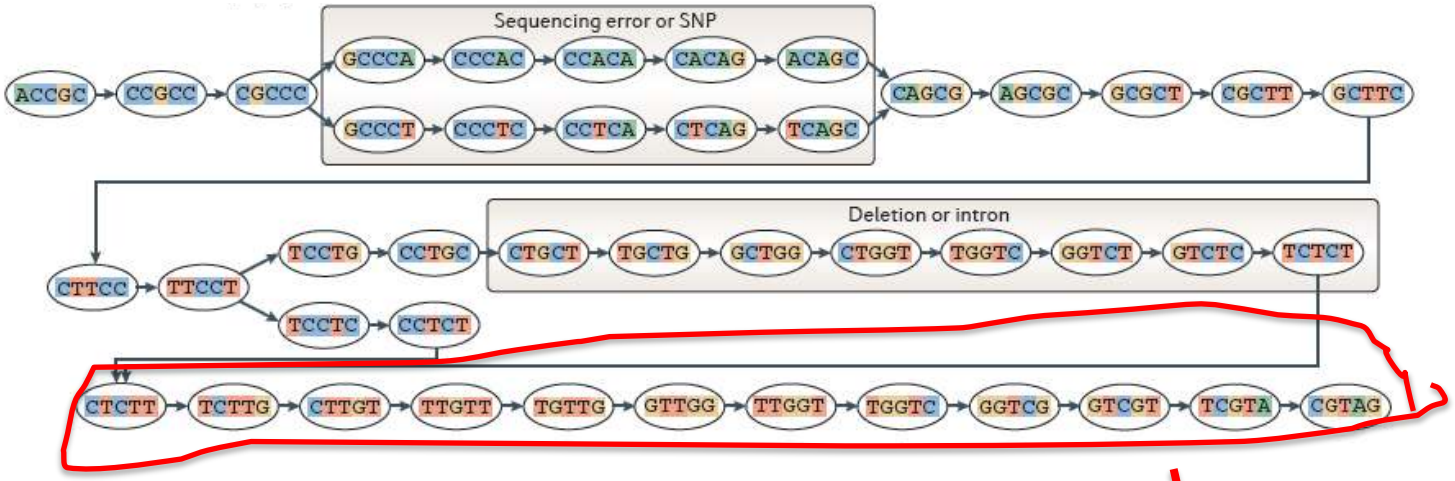
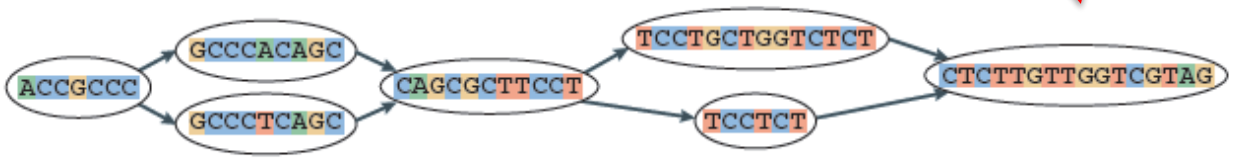


Collapse the de Bruijn graph



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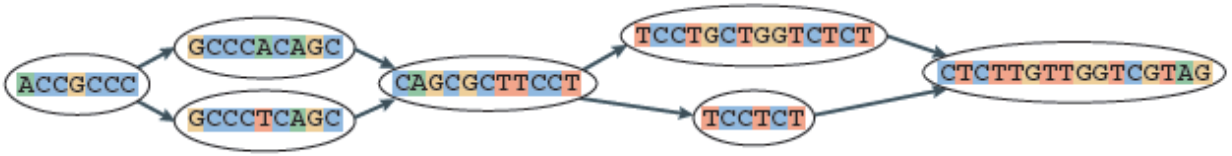
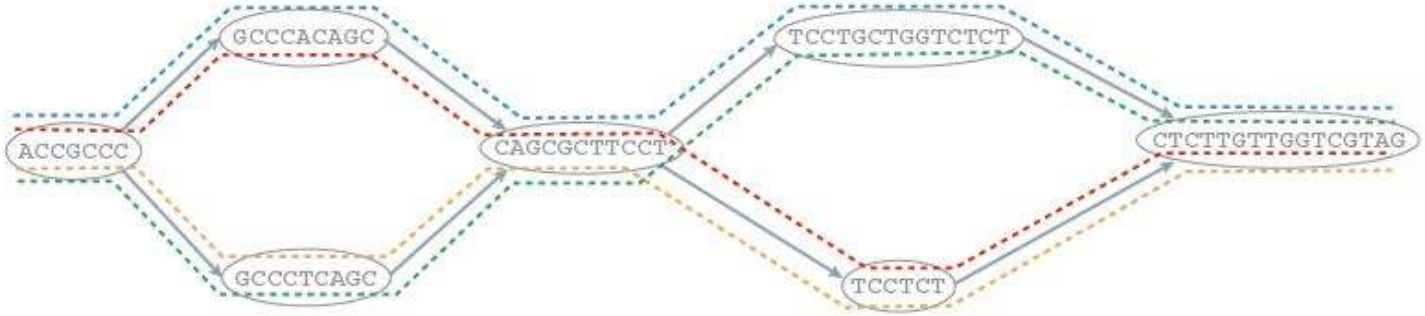


Traverse the graph



Assemble Transcript Isoforms

```
------ ACCGCCCACAGCGCTTCCTGCTGGTCTCTTGTTGGTCGTAG
------ ACCGCCCACAGCGCTTCCT--------CTTGTTGGTCGTAG
------ ACCGCCCTCAGCGCTTCCT--------CTTGTTGGTCGTAG
------ ACCGCCCTCAGCGCTTCCTGCTGGTCTCTTGTTGGTCGTAG
```

From Martin & Wang, Nat. Rev. Genet. 2011

Contrasting Genome and Transcriptome Assembly

Genome Assembly

- Uniform coverage
- Single contig per locus
- Double-stranded

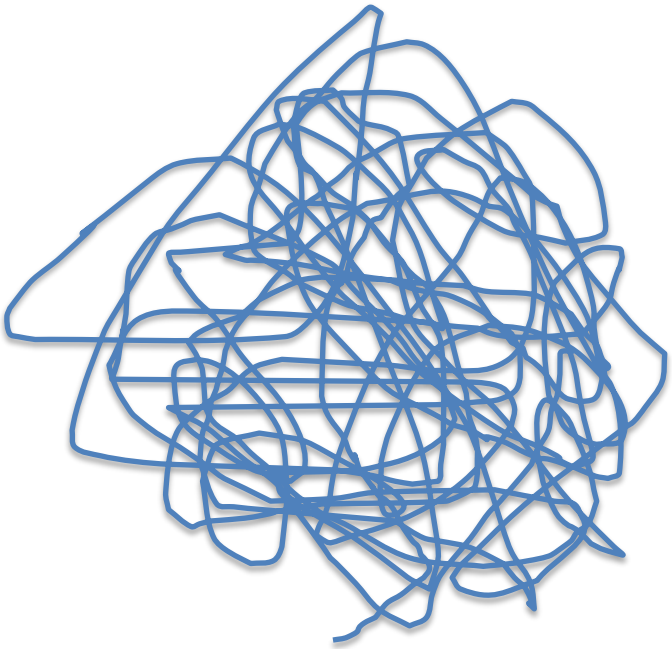
Transcriptome Assembly

- Exponentially distributed coverage levels
- Multiple contigs per locus (alt splicing)
- Strand-specific

Trinity Aggregates Isolated Transcript Graphs

Genome Assembly

Single Massive Graph



Entire chromosomes represented.

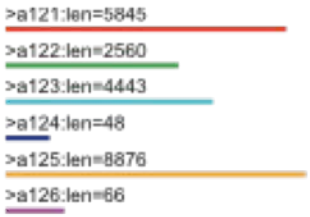
Trinity Transcriptome Assembly

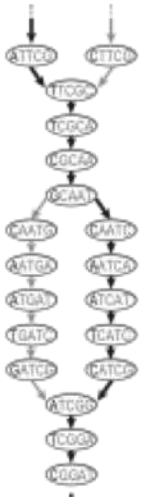
Many Thousands of Small Graphs

Ideally, one graph per expressed gene.

Trinity – How it works:

RNA-Seq reads → **Linear contigs** → **de-Bruijn graphs** → **Transcripts + Isoforms**





...CTTCGCAA...TGATCGGAT...
...ATTCGCAA...TCATCGGAT...

Thousands of disjoint graphs

Inchworm Algorithm

- Decompose all reads into overlapping Kmers => hashtable(kmer, count)

Read: **AATGTGAAAACTGGATTACATGCTGGTATGTC**…

AATGTGA

ATGTGAA Overlapping kmers of length (k)

TGTGAAA

…

Kmer Catalog (hashtable)

Kmer	Count among all reads
AATGTGA	4
ATGTGAA	2
TGTGAAA	1
GATTACA	9

Inchworm Algorithm

- Decompose all reads into overlapping Kmers => hashtable(kmer, count)
- Identify seed kmer as most abundant Kmer, ignoring low-complexity kmers.

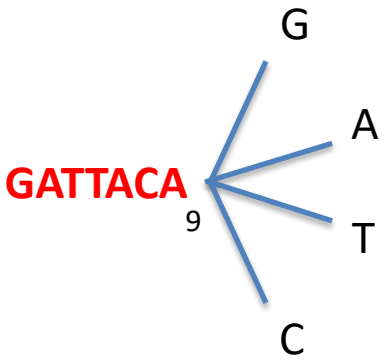
GATTACA
9

Kmer Catalog (hashtable)

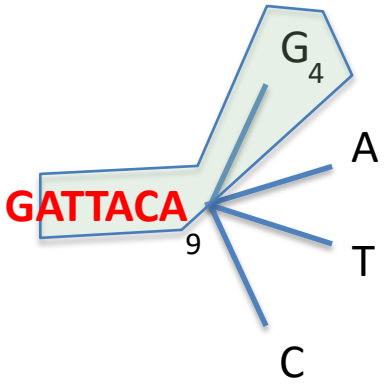
Kmer	Count among all reads
AATGTGA	4
ATGTGAA	2
TGTGAAA	1
GATTACA	9

Inchworm Algorithm

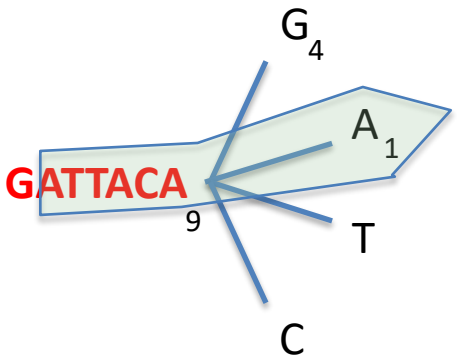
- Decompose all reads into overlapping Kmers => hashtable(kmer, count)
- Identify seed kmer as most abundant Kmer, ignoring low-complexity kmers.
- Extend kmer at 3’ end, guided by coverage.



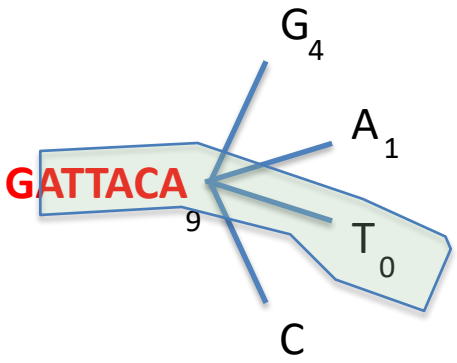
Inchworm Algorithm



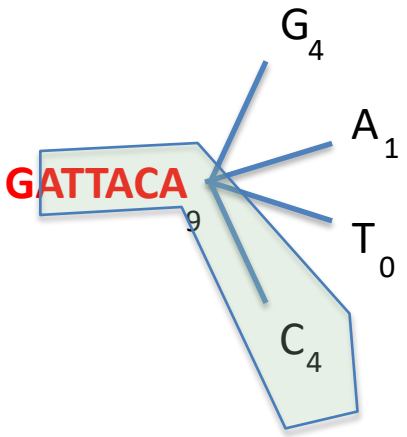
Inchworm Algorithm



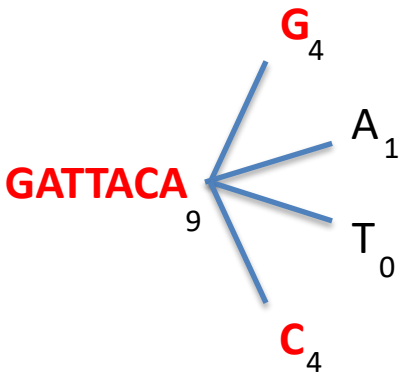
Inchworm Algorithm



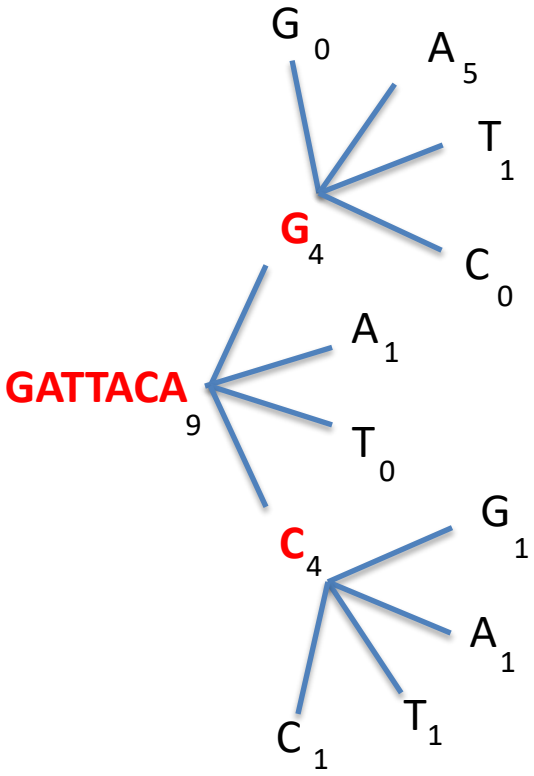
Inchworm Algorithm



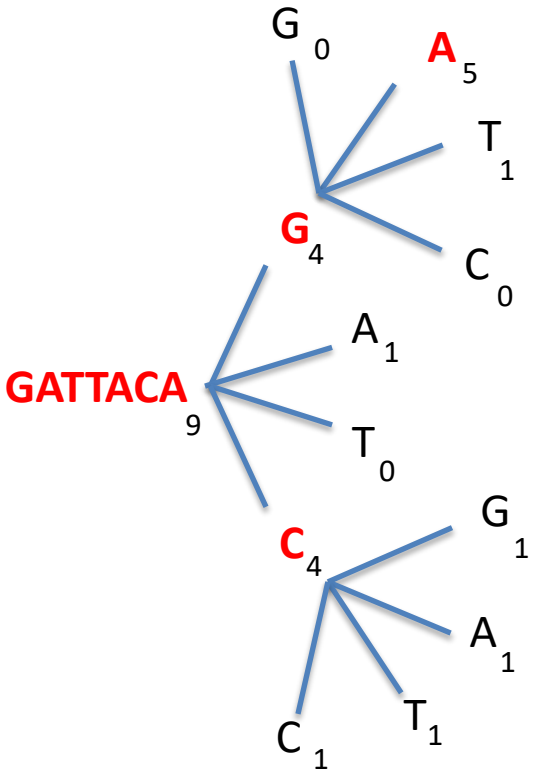
Inchworm Algorithm



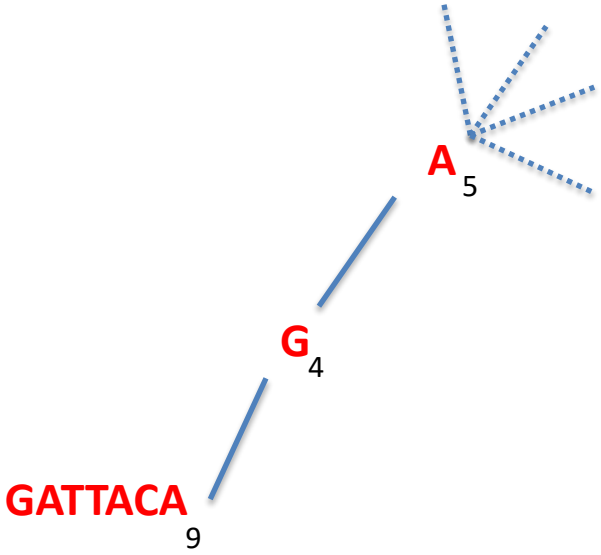
Inchworm Algorithm



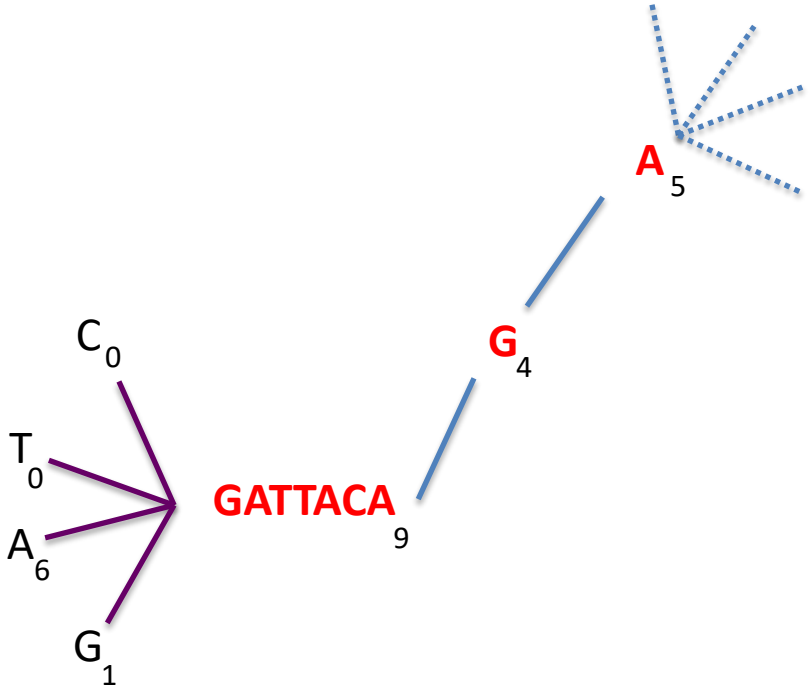
Inchworm Algorithm



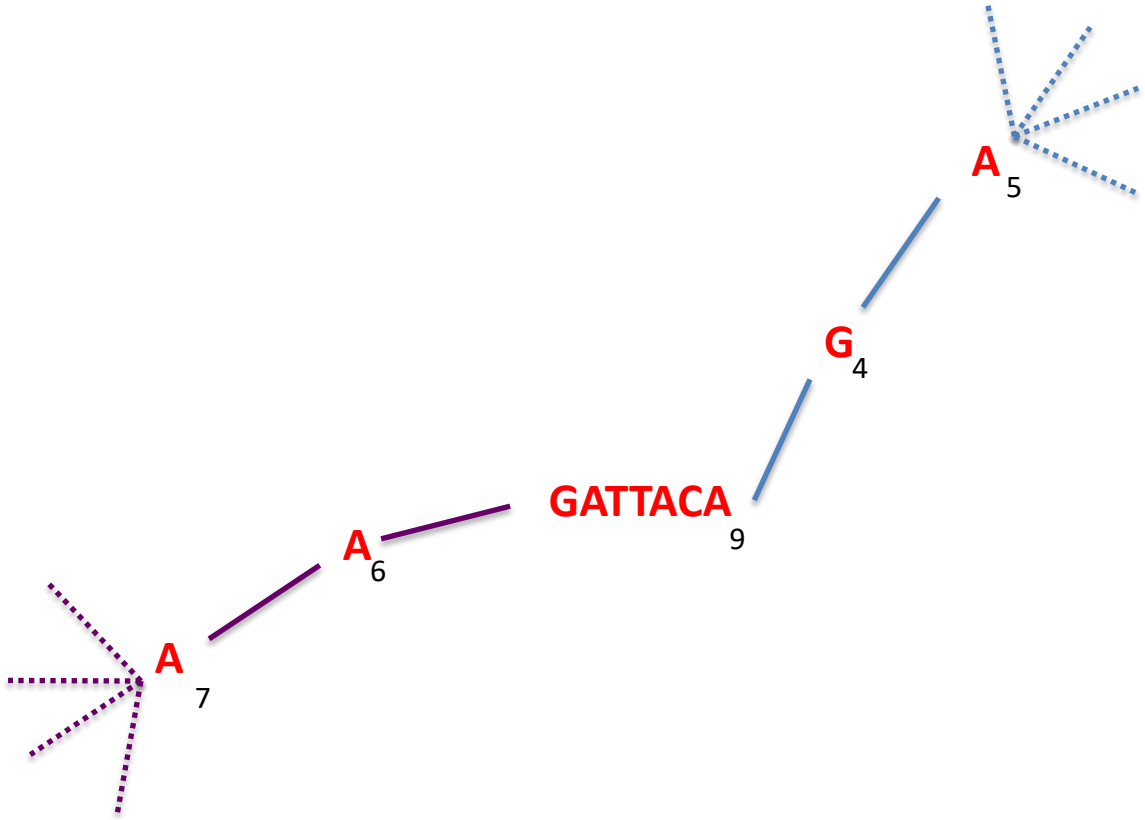
Inchworm Algorithm



Inchworm Algorithm



Inchworm Algorithm



Report contig: ….AAGATTACAGA….

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

Inchworm Contigs from Alt-Spliced Transcripts

Expressed isoforms

Isoform A

Isoform B

Inchworm Contigs from Alt-Spliced Transcripts

Expressed isoforms

Isoform A

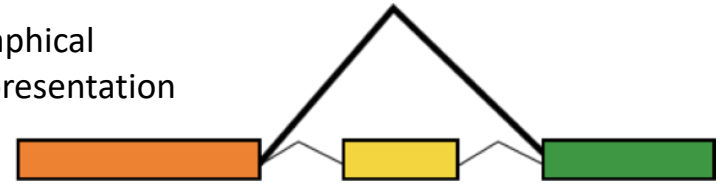
Isoform B

Expression

(low)

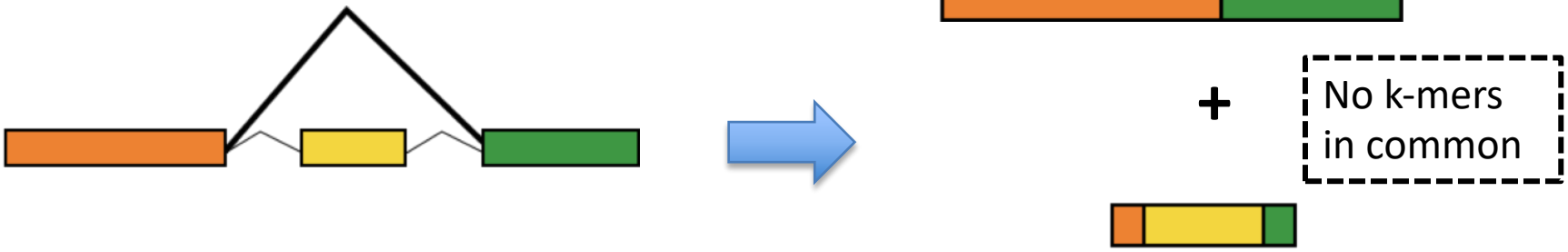
(high)

Graphical representation

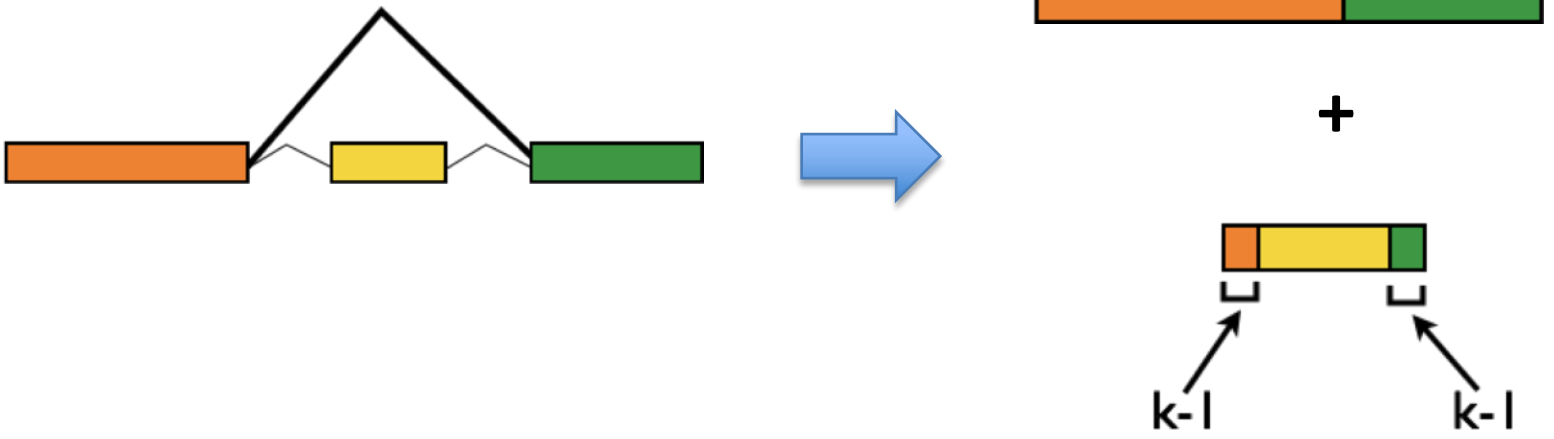


Inchworm Contigs from Alt-Spliced Transcripts

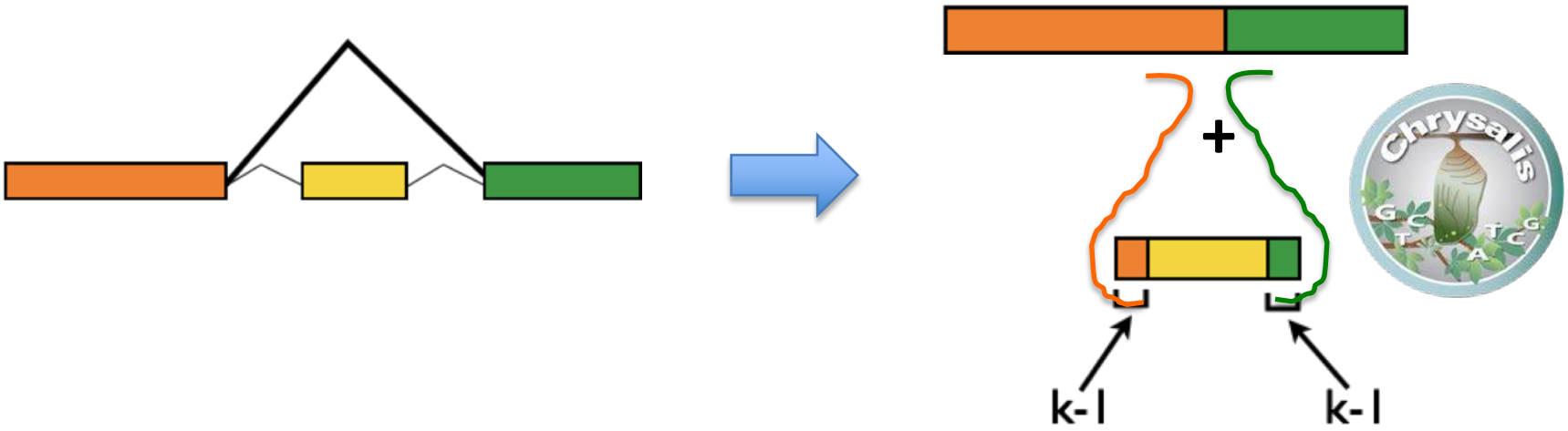
Inchworm Contigs from Alt-Spliced Transcripts



Inchworm Contigs from Alt-Spliced Transcripts



Chrysalis Re-groups Related Inchworm Contigs



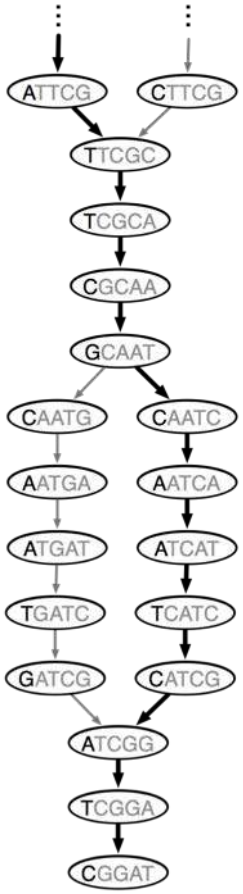
Chrysalis uses (k-1) overlaps and read support to link related Inchworm contigs

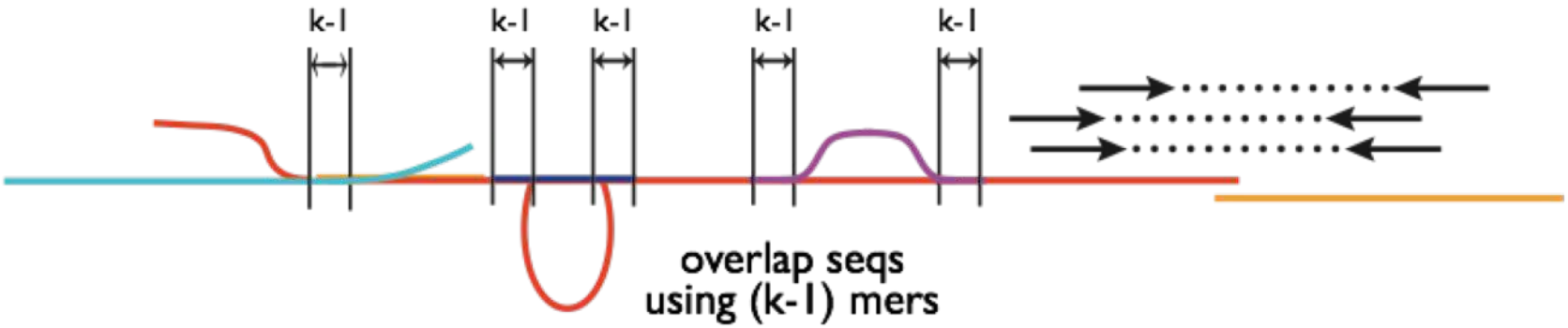
Chrysalis

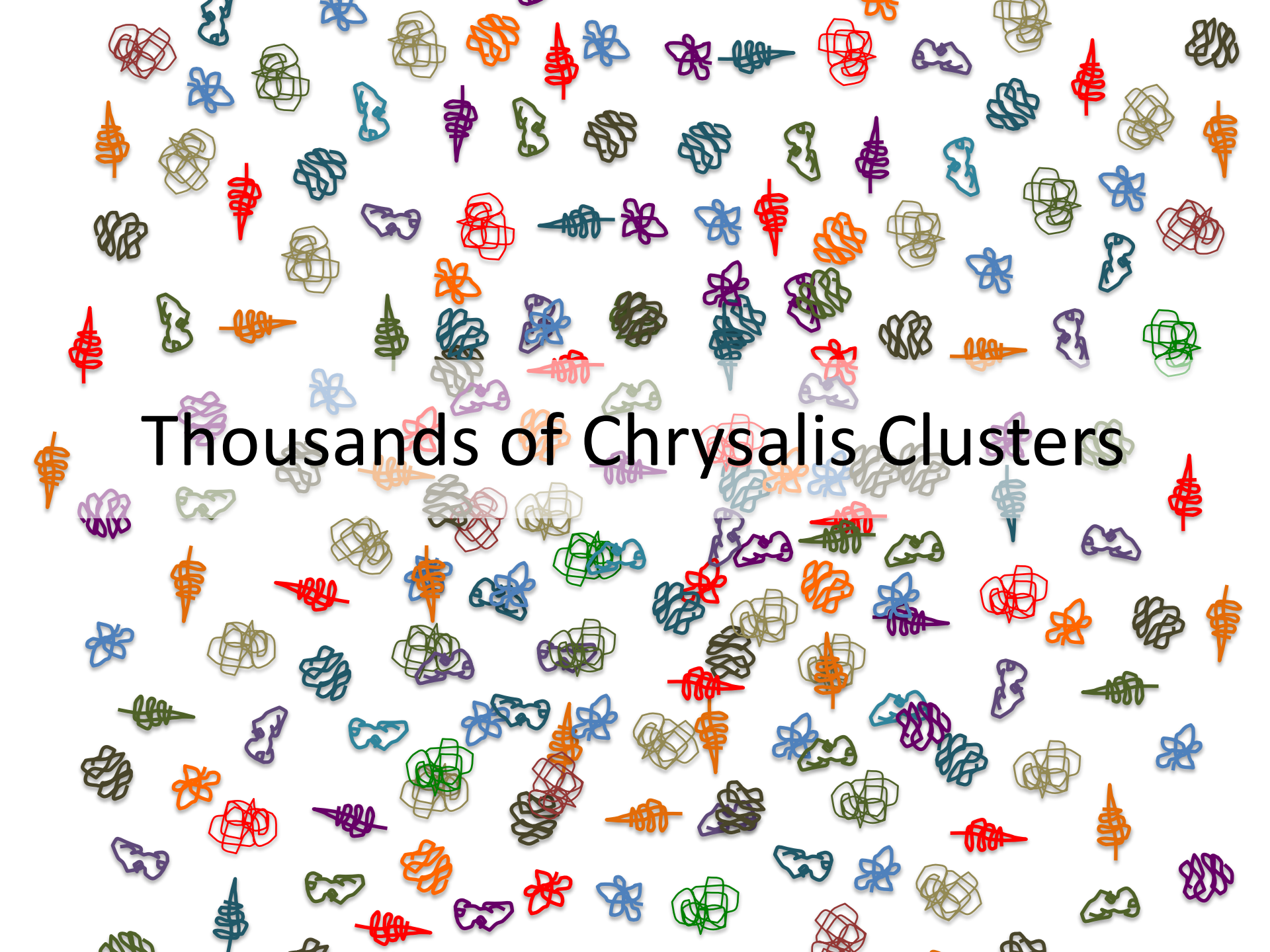
>a121:len=5845
>a122:len=2560
>a123:len=4443
>a124:len=48
>a125:len=8876
>a126:len=66

Integrate isoforms
via k-1 overlaps

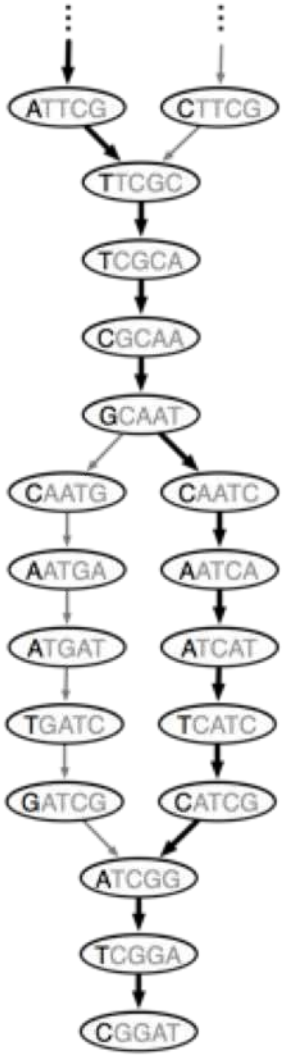
Build de Bruijn Graphs
(ideally, one per gene)





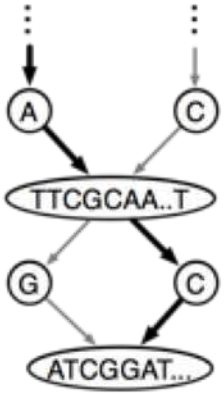

Thousands of Chrysalis Clusters

Butterfly



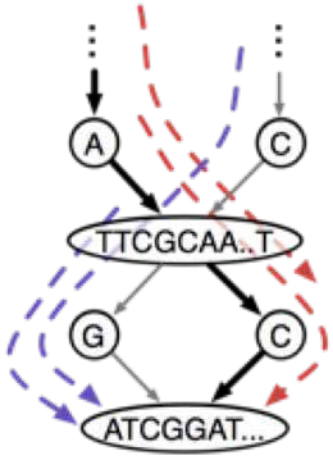
de Bruijn graph

compacting



compact graph

finding paths



compact graph with reads

extracting sequences

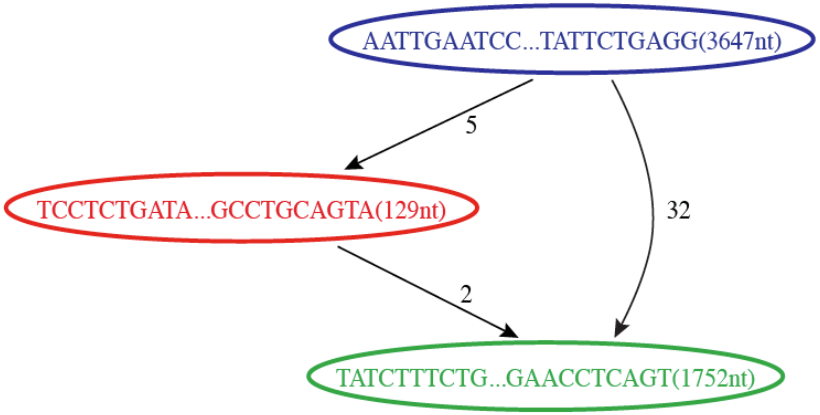
..CTTCGCAA..TGATCGGAT...

..ATTCGCAA..TCATCGGAT...

sequences (isoforms and paralogs)

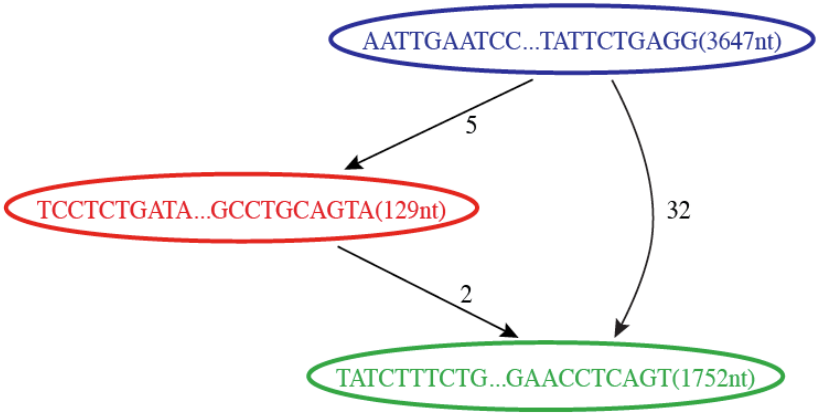
Butterfly Example 1:
Reconstruction of Alternatively Spliced Transcripts

Butterfly's Compacted Sequence Graph



Reconstruction of Alternatively Spliced Transcripts

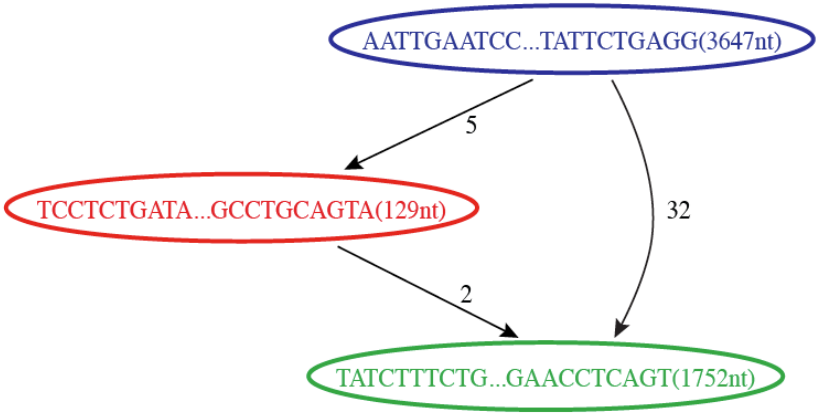
Butterfly's Compacted Sequence Graph



Reconstructed Transcripts

Reconstruction of Alternatively Spliced Transcripts

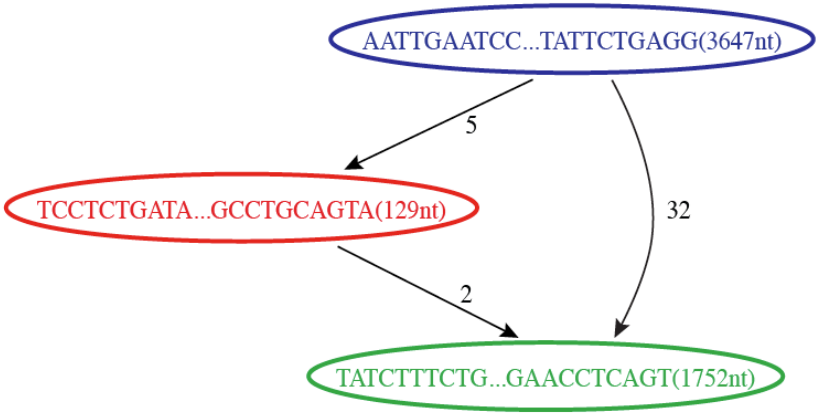
Butterfly's Compacted Sequence Graph



Reconstructed Transcripts

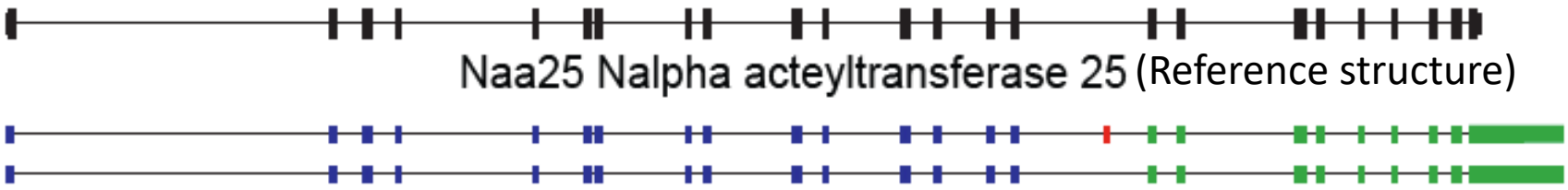
Reconstruction of Alternatively Spliced Transcripts

Butterfly's Compacted Sequence Graph

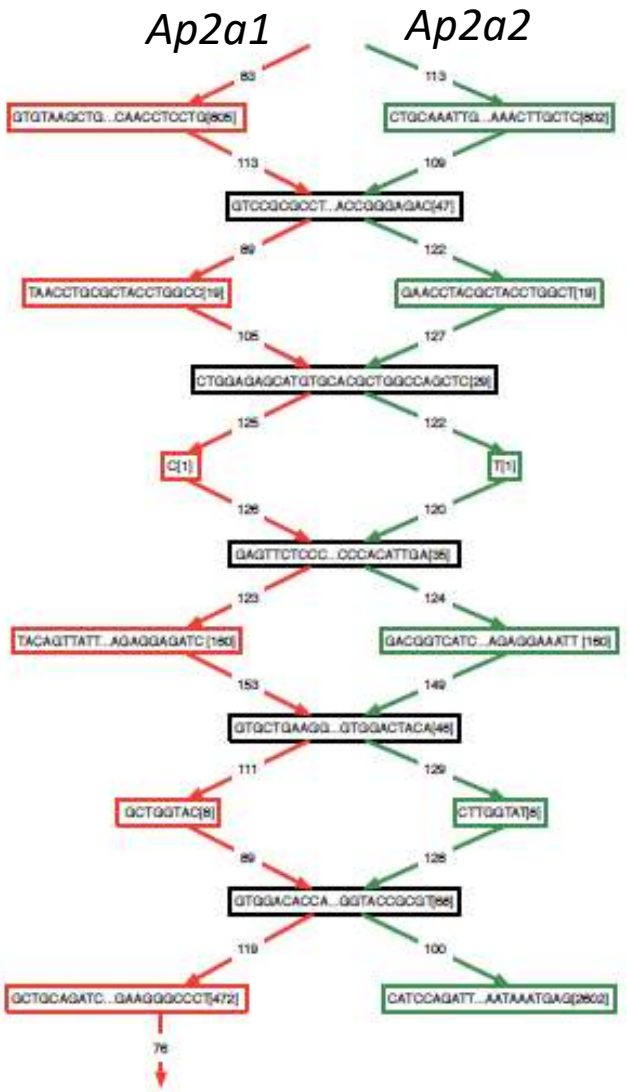


Reconstructed Transcripts

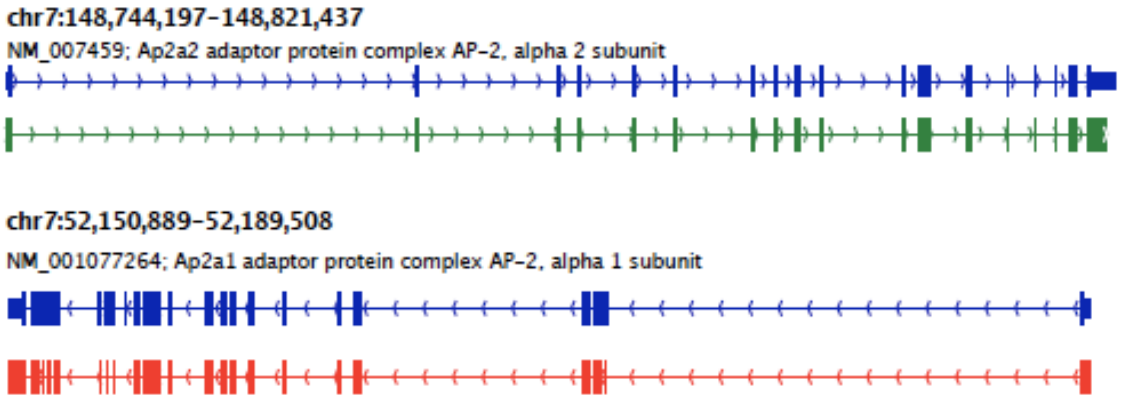
Aligned to Mouse Genome

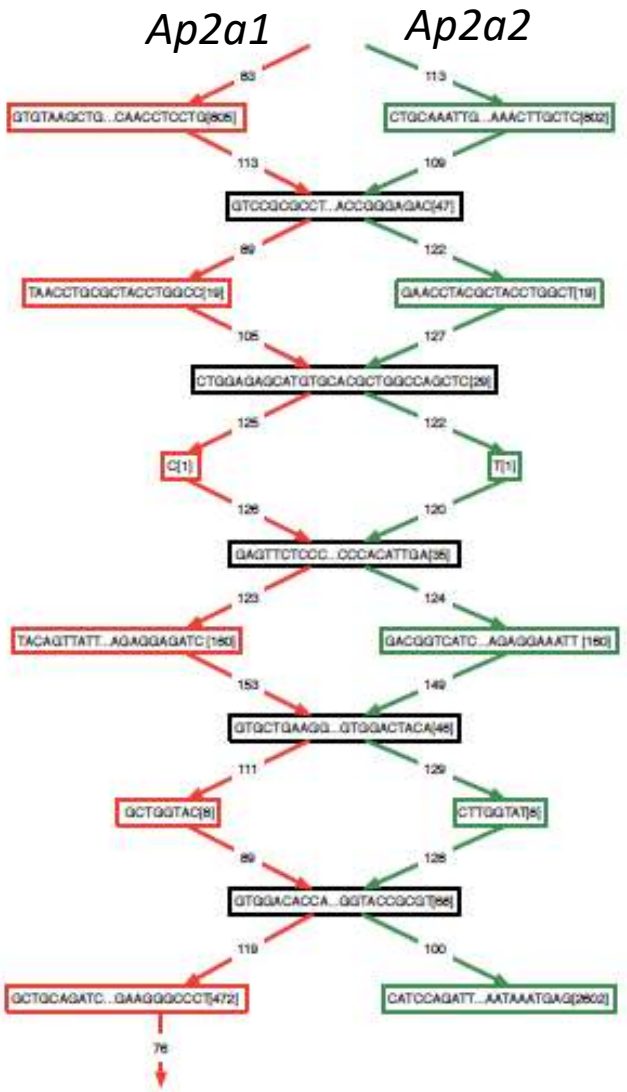


Butterfly Example 2:
Teasing Apart Transcripts of Paralogous Genes



Teasing Apart Transcripts of Paralogous Genes





Strand-specific RNA-Seq is Preferred

Computationally: fewer confounding graph structures in de novo assembly:

ex. Forward != reverse complement

(GGAA != TTCC)

Biologically: separate sense vs. antisense transcription

NATURE METHODS | VOL.7 NO.9 | SEPTEMBER 2010 |

BROAD INSTITUTE

Comprehensive comparative analysis of strand-specific RNA sequencing methods

Joshua Z Levin[1,6], Moran Yassour[1–3,6], Xian Adiconis[1], Chad Nusbaum[1], Dawn Anne Thompson[1], Nir Friedman[3,4], Andreas Gnirke[1] & Aviv Regev[1,2,5]

Strand-specific, massively parallel cDNA sequencing (RNA-seq) is a powerful tool for transcript discovery, genome annotation

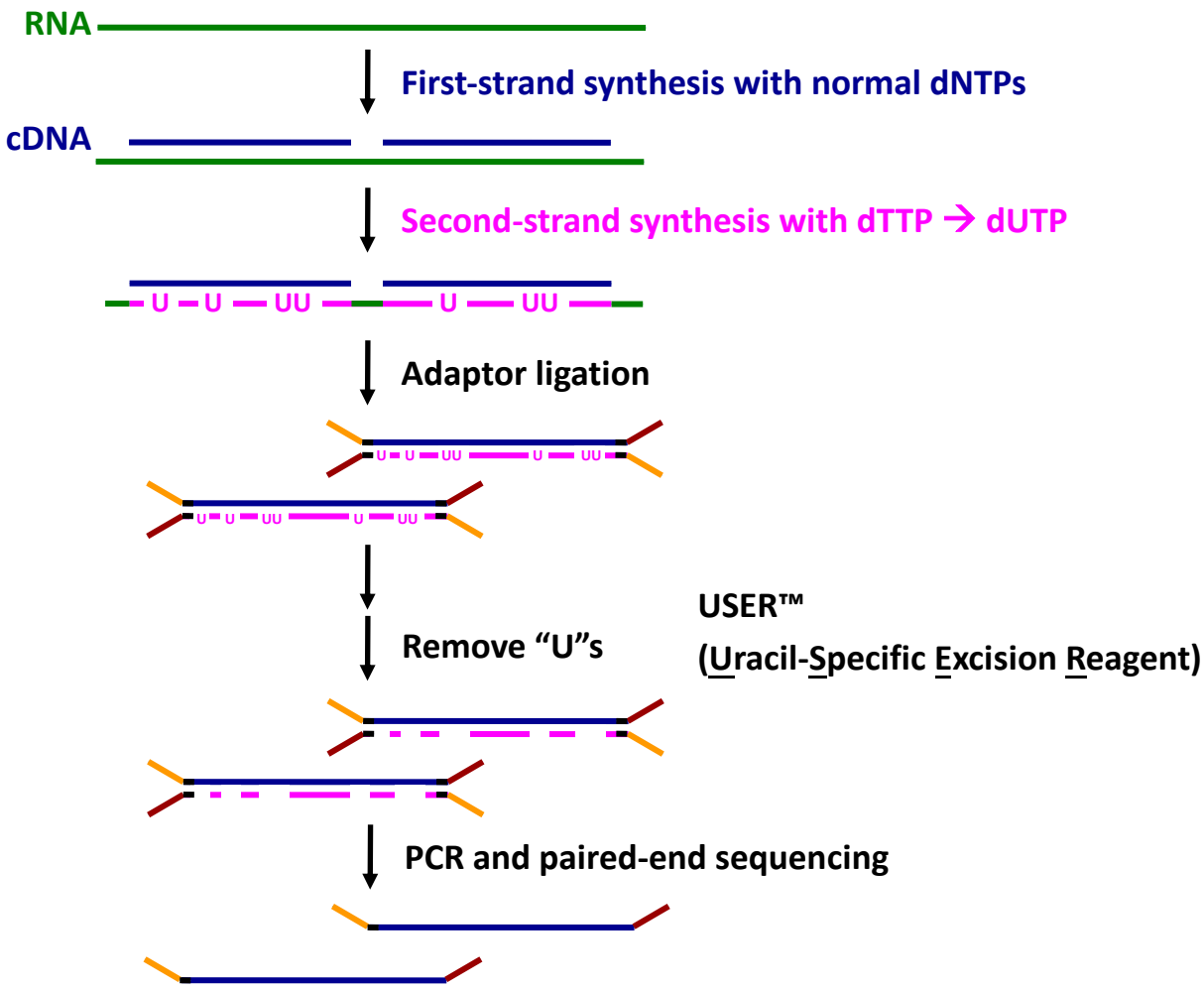
'dUTP second strand marking' identified as the leading protocol

computational pipeline to compare library quality metrics from any RNA-seq method. Using the well-annotated *Saccharomyces cerevisiae* transcriptome as a benchmark, we compared seven library-construction protocols, including both published and

Nevertheless, direct information on the originating strand can substantially enhance the value of an RNA-seq experiment. For

boundaries of adjacent genes transcribed on opposite strands and resolve the correct expression levels of coding or noncoding overlapping transcripts. These tasks are particularly challenging in small microbial genomes, prokaryotic and eukaryotic, in which

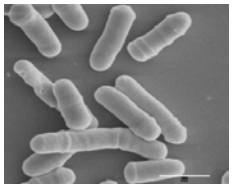
dUTP 2nd Strand Method: Our Favorite



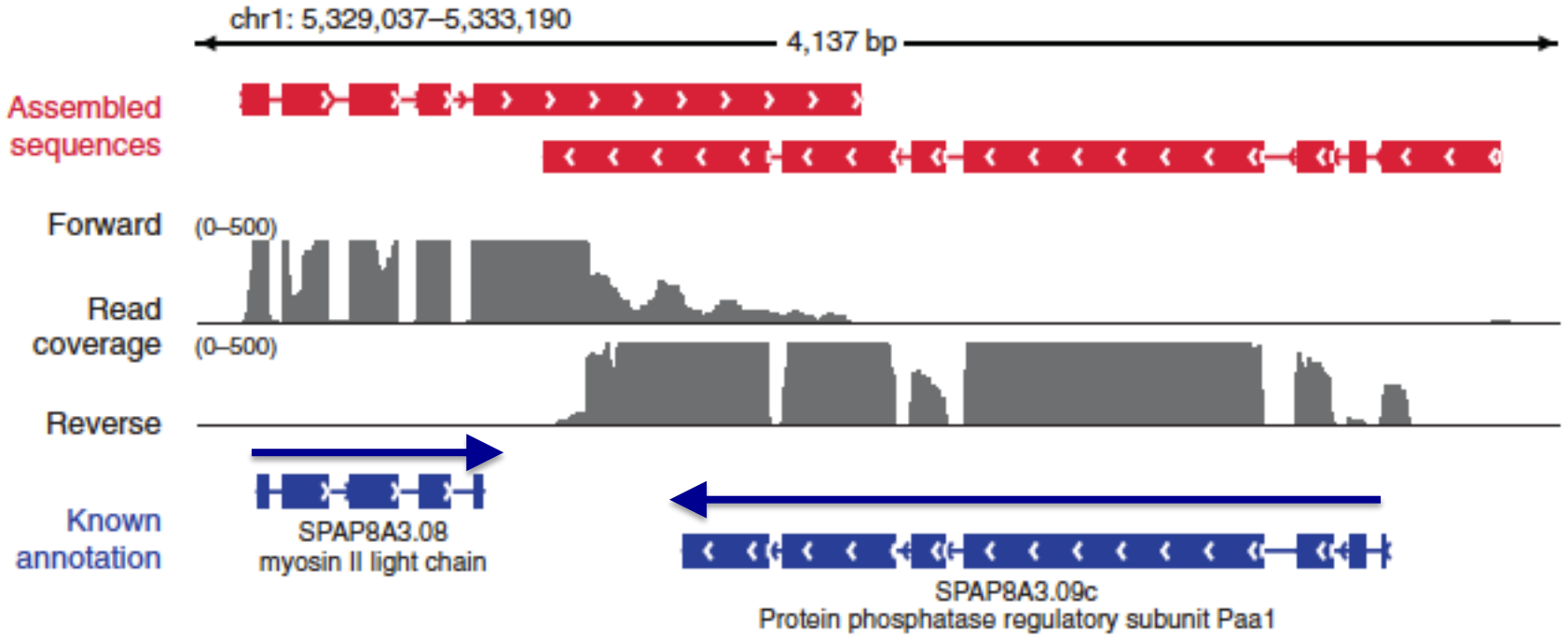
Modified from Parkhomchuk *et al.* (2009) *Nucleic Acids Res.* 37:e123

Slide courtesy of Joshua Levin, Broad Institute.

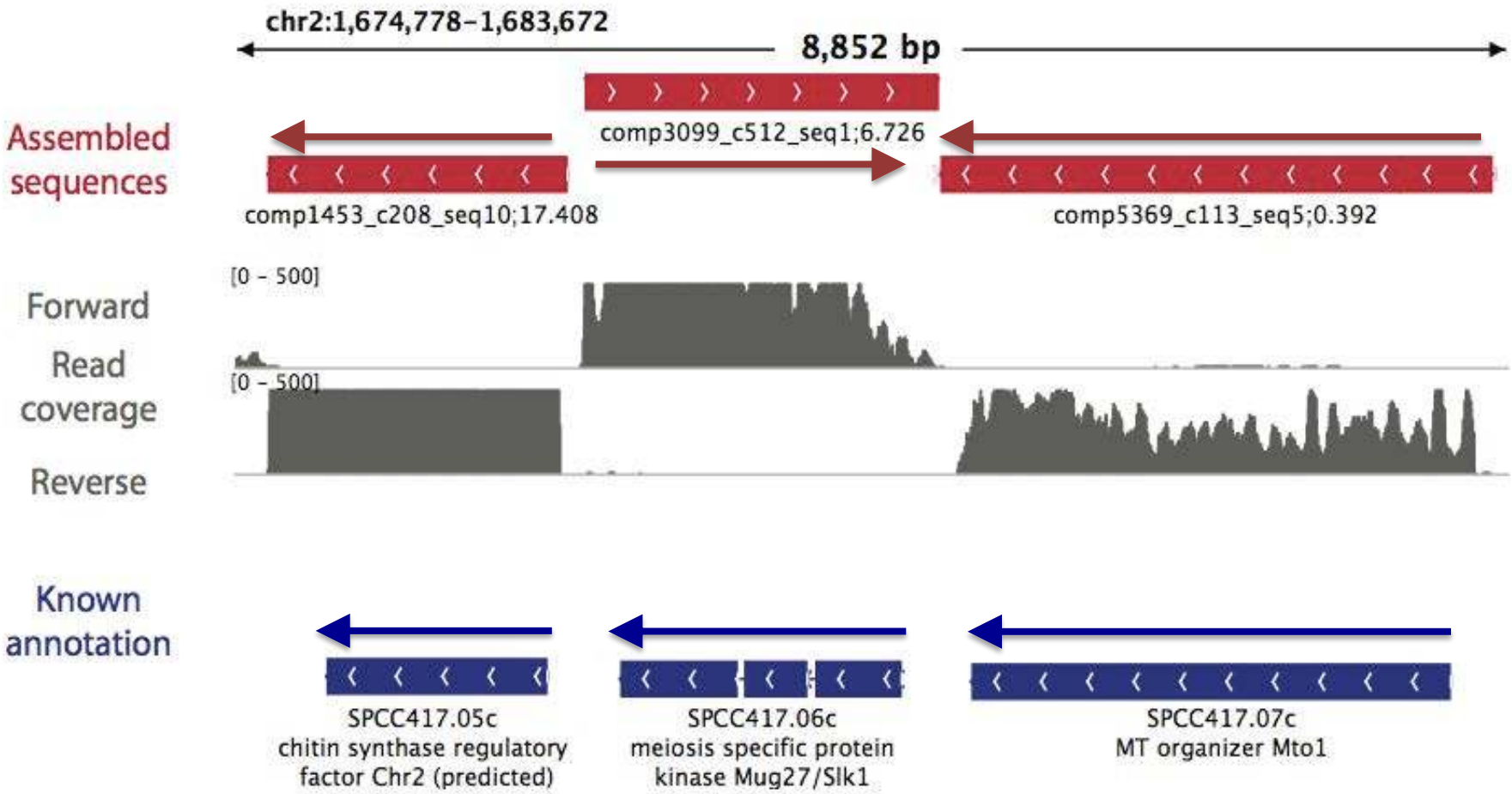
Overlapping UTRs from Opposite Strands

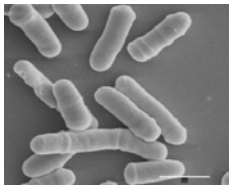


Schizosacharomyces pombe
(fission yeast)



Antisense-dominated Transcription





nature protocols

Transcriptome Assembly is Just the End of the Beginning…

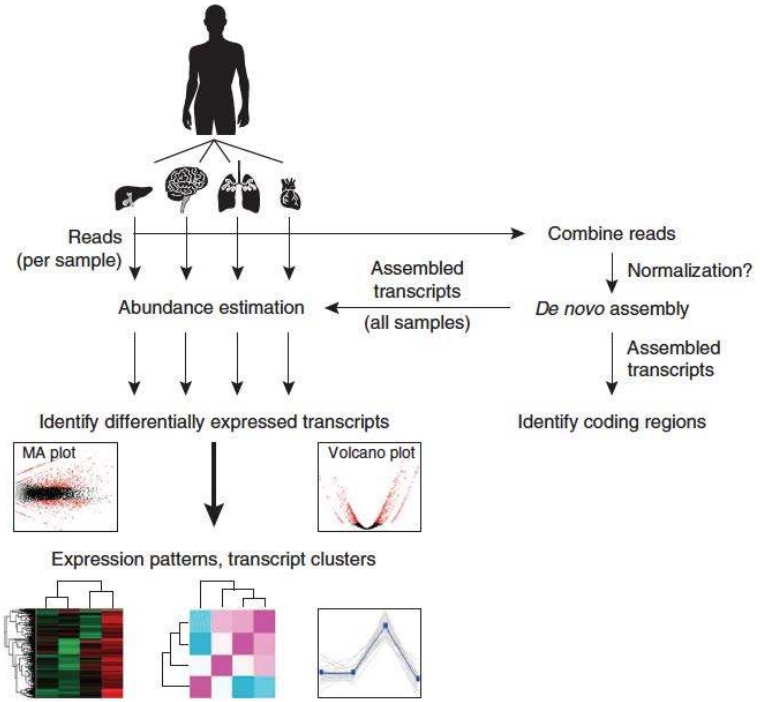
NATURE PROTOCOLS | PROTOCOL

De novo transcript sequence reconstruction from RNA-seq using the Trinity platform for reference generation and analysis

Brian J Haas, Alexie Papanicolaou, Moran Yassour, Manfred Grabherr, Philip D Blood, Joshua Bowden, Matthew Brian Couger, David Eccles, Bo Li, Matthias Lieber, Matthew D MacManes, Michael Ott, Joshua Orvis, Nathalie Pochet, Francesco Strozzi, Nathan Weeks, Rick Westerman, Thomas William, Colin N Dewey, Robert Henschel, Richard D LeDuc, Nir Friedman & Aviv Regev

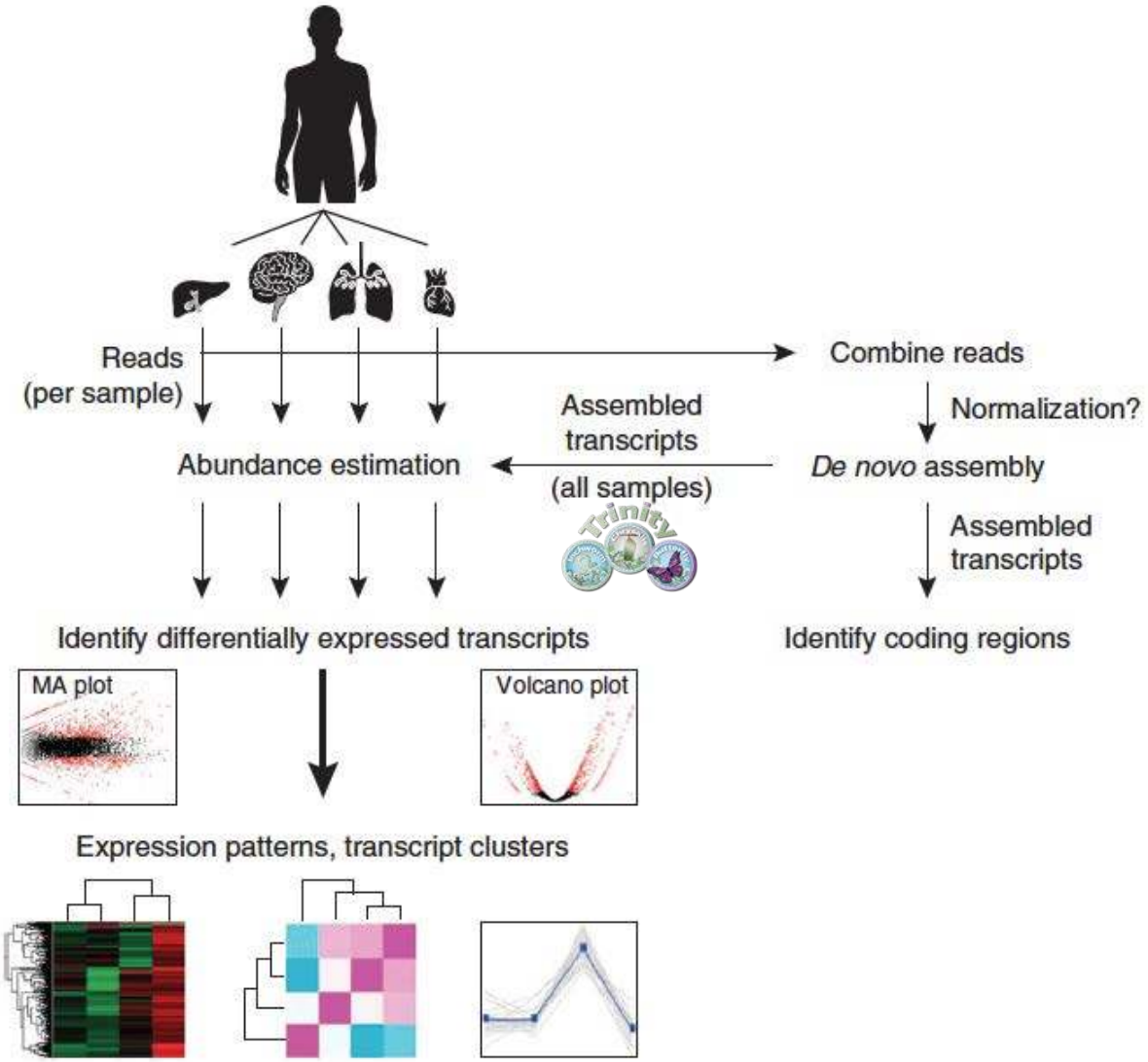
Affiliations | Contributions | Corresponding authors

Nature Protocols **8**, 1494–1512 (2013) | doi:10.1038/nprot.2013.084
Published online 11 July 2013



Trinity Framework for De novo Transcriptome Assembly and Analysis

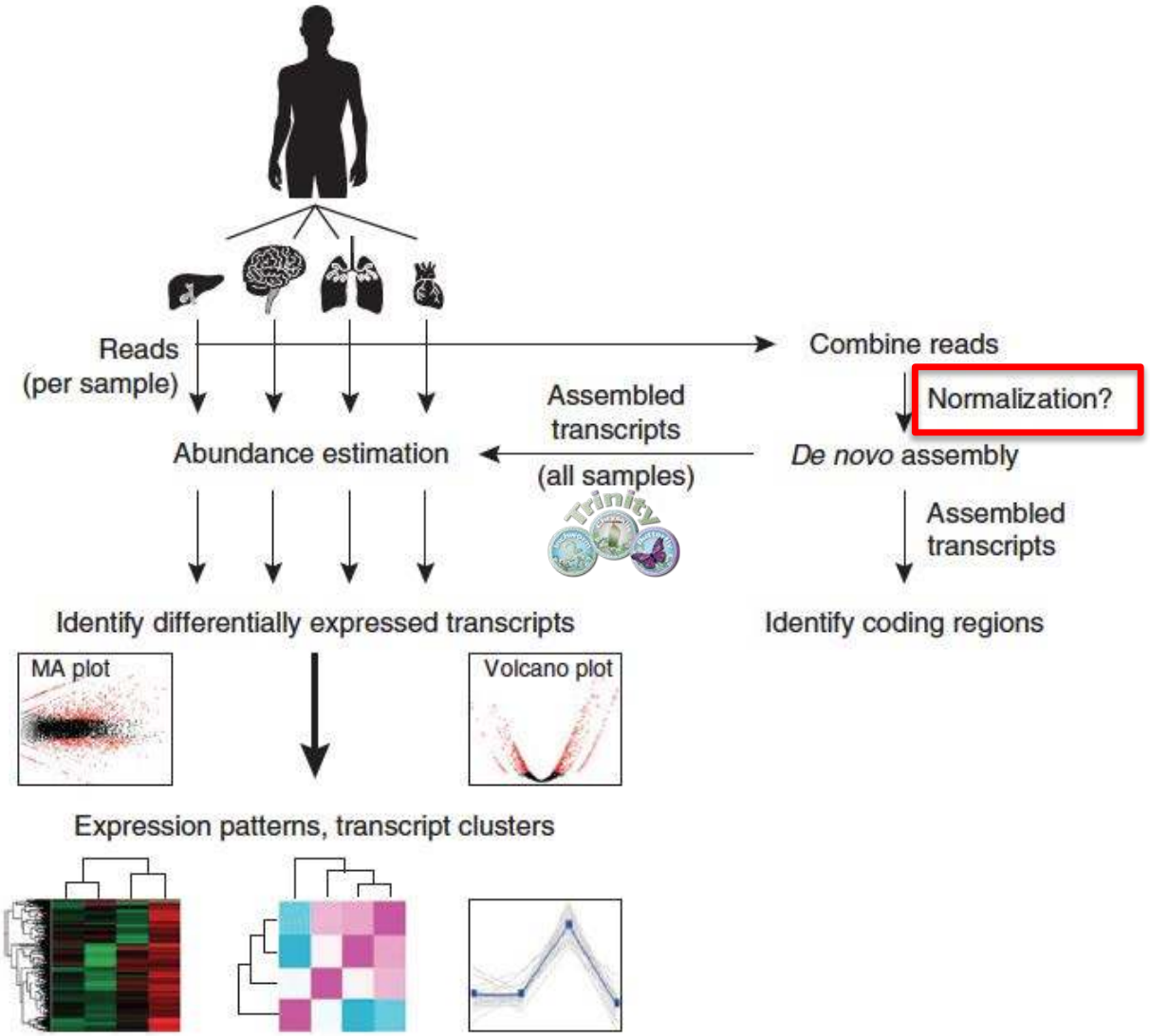
(focus of the transcriptomics lab)



Bioconductor,
& Trinity

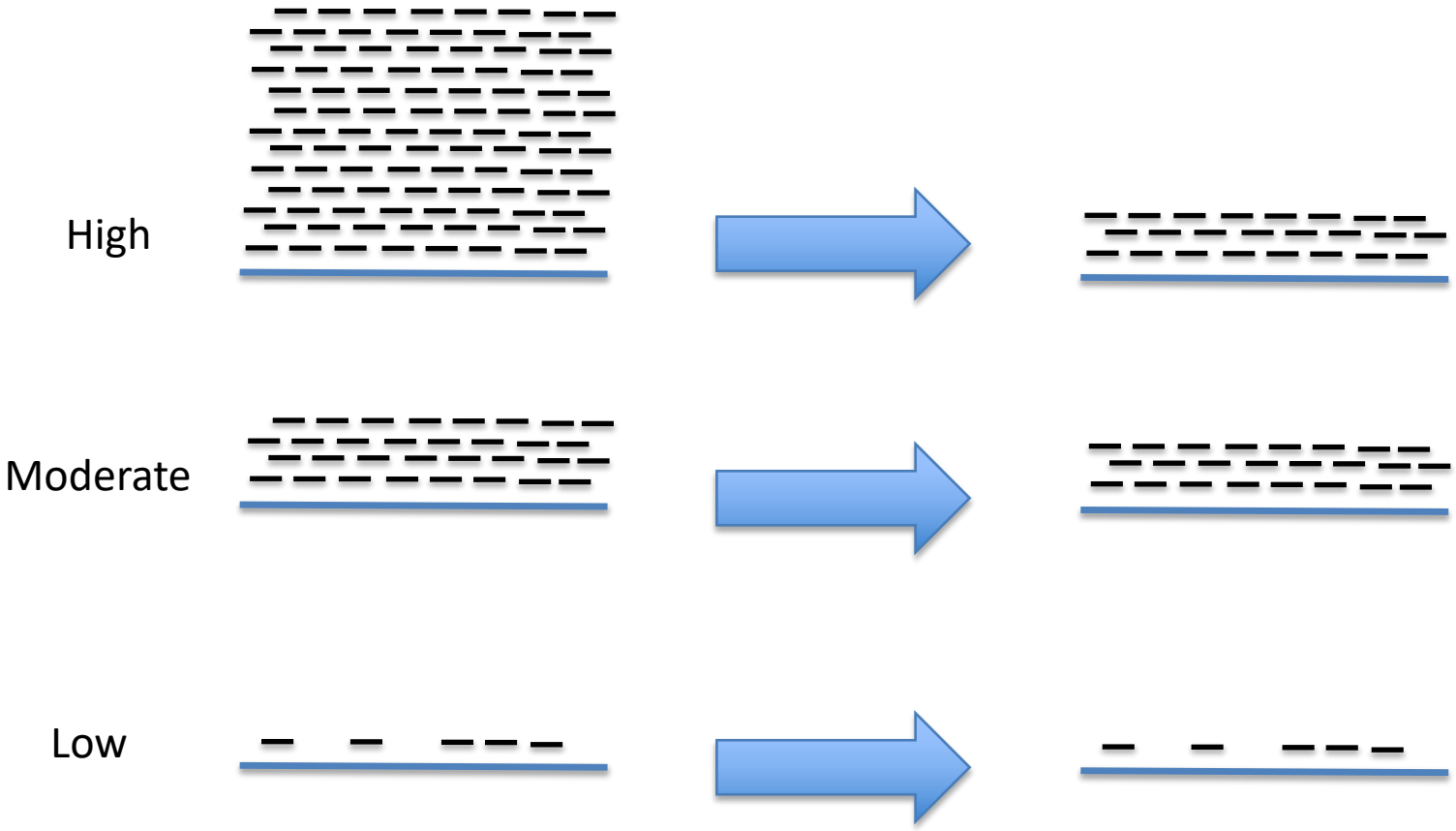
Trinity Framework for De novo Transcriptome Assembly and Analysis

(focus of the transcriptomics lab)

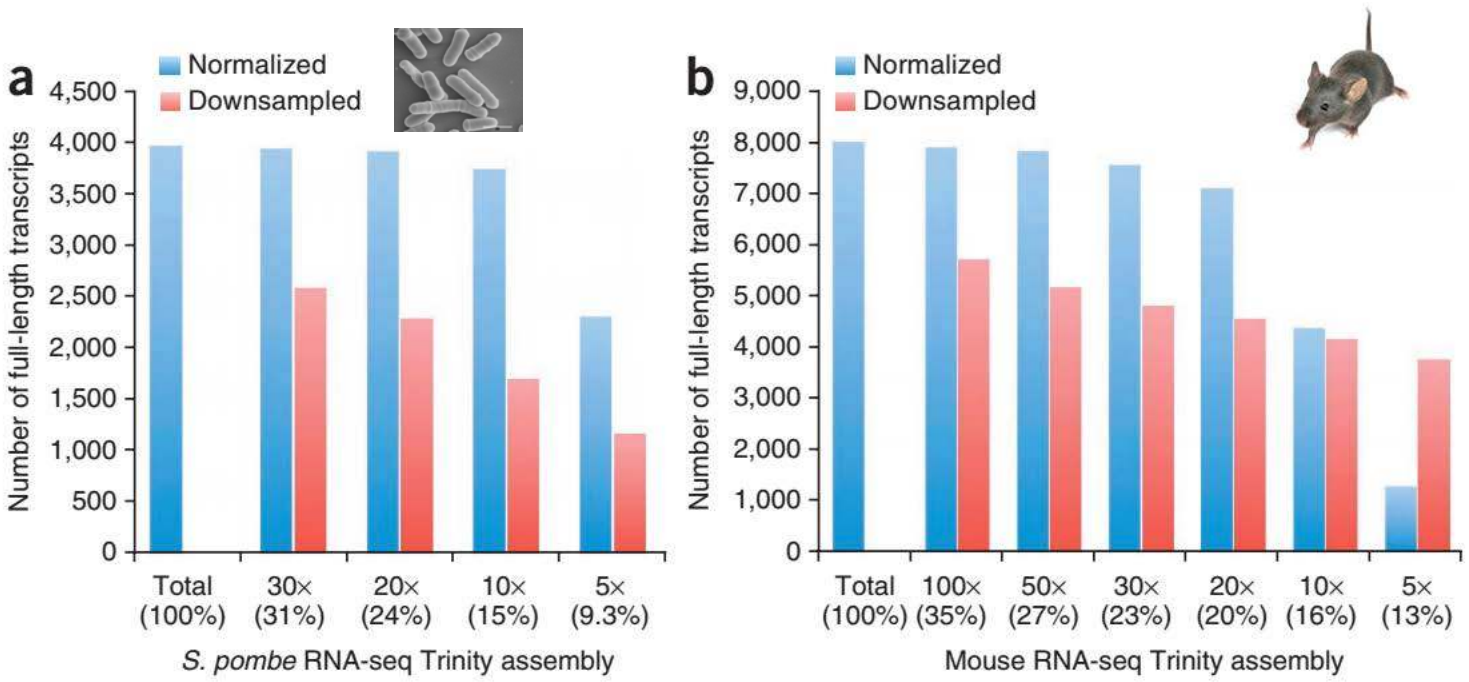


Bioconductor,
& Trinity

In silico normalization of reads



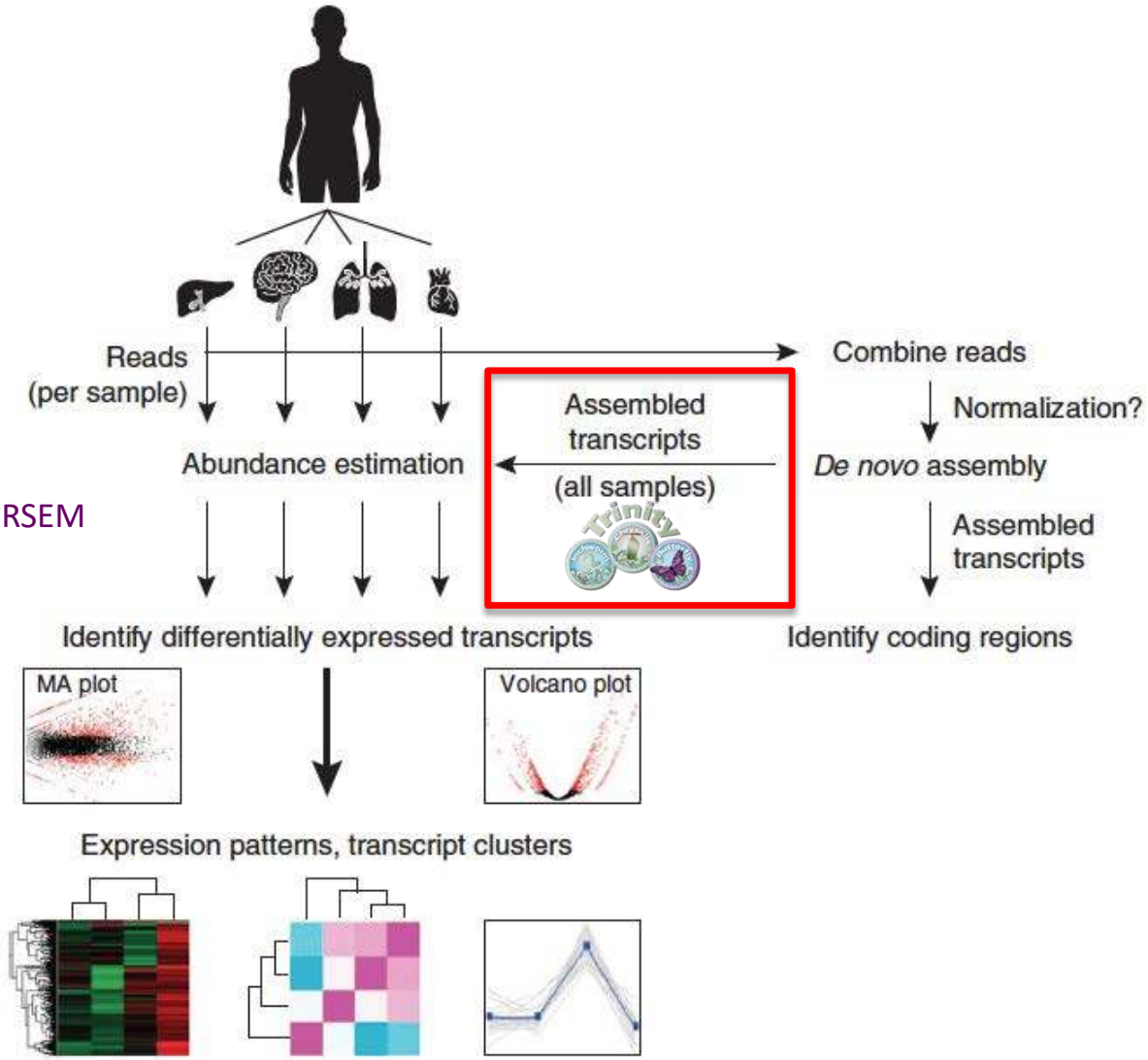
Impact of Normalization on *De novo* Full-length Transcript Reconstruction



Largely retain full-length reconstruction, but use less RAM and assemble much faster.

Haas et al., 2013

Trinity Framework for De novo Transcriptome Assembly and Analysis



Bowtie & RSEM

Bioconductor,
& Trinity

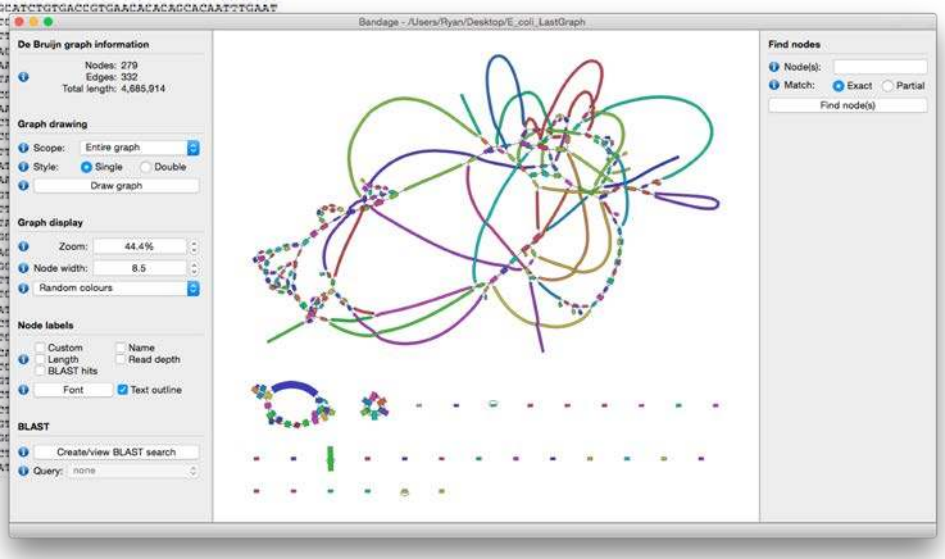
Trinity output: A multi-fasta file

>comp0_c0_seq1 len=5528 path=[1:0-3646 10775:3647-3775 3648:3776-5527]

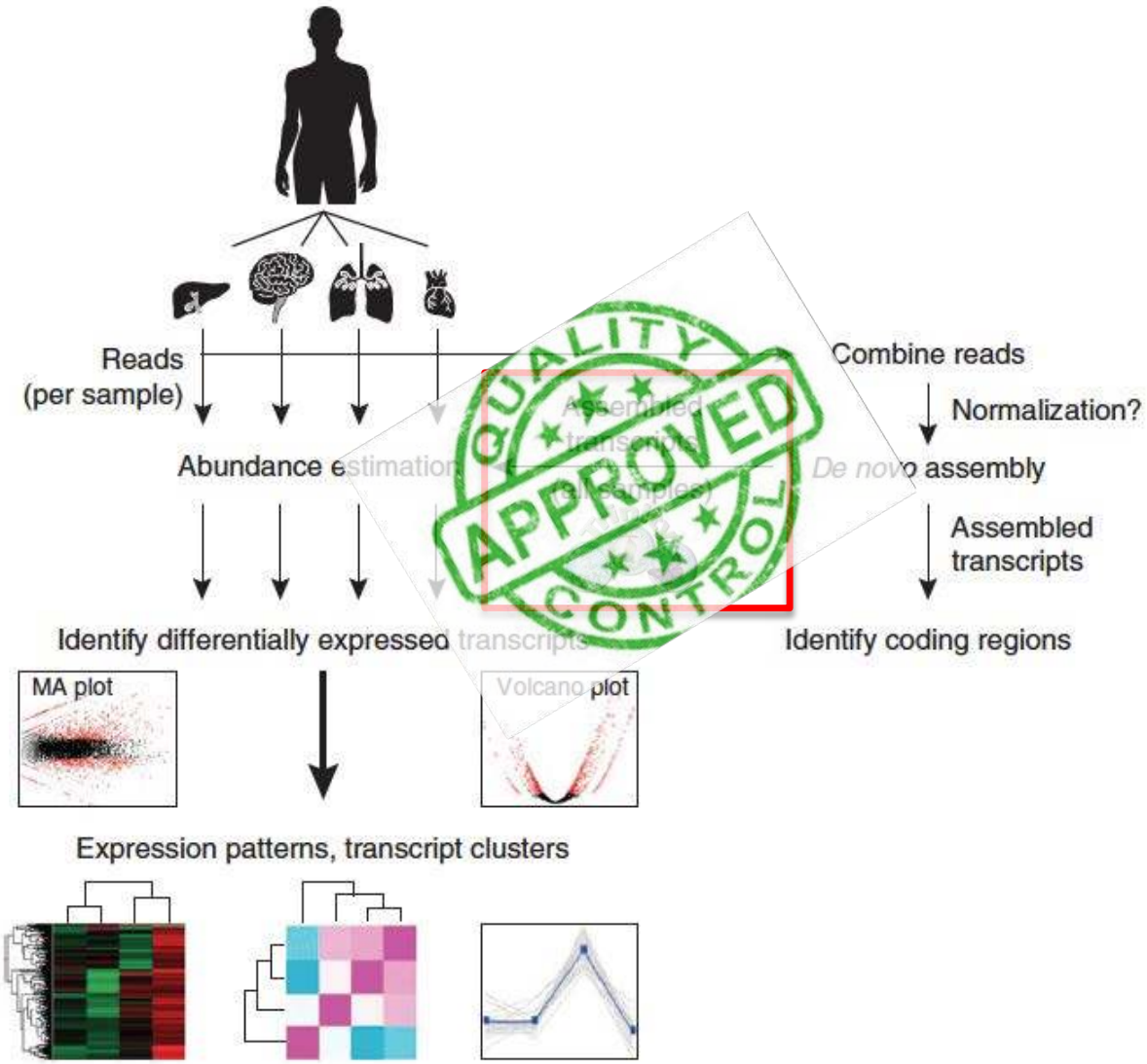
>comp0_c0_seq2 len=5399 path=[1:0-3646 3648:3647-5398]

Can visualize using Bandage

https://rrwick.github.io/Bandage/

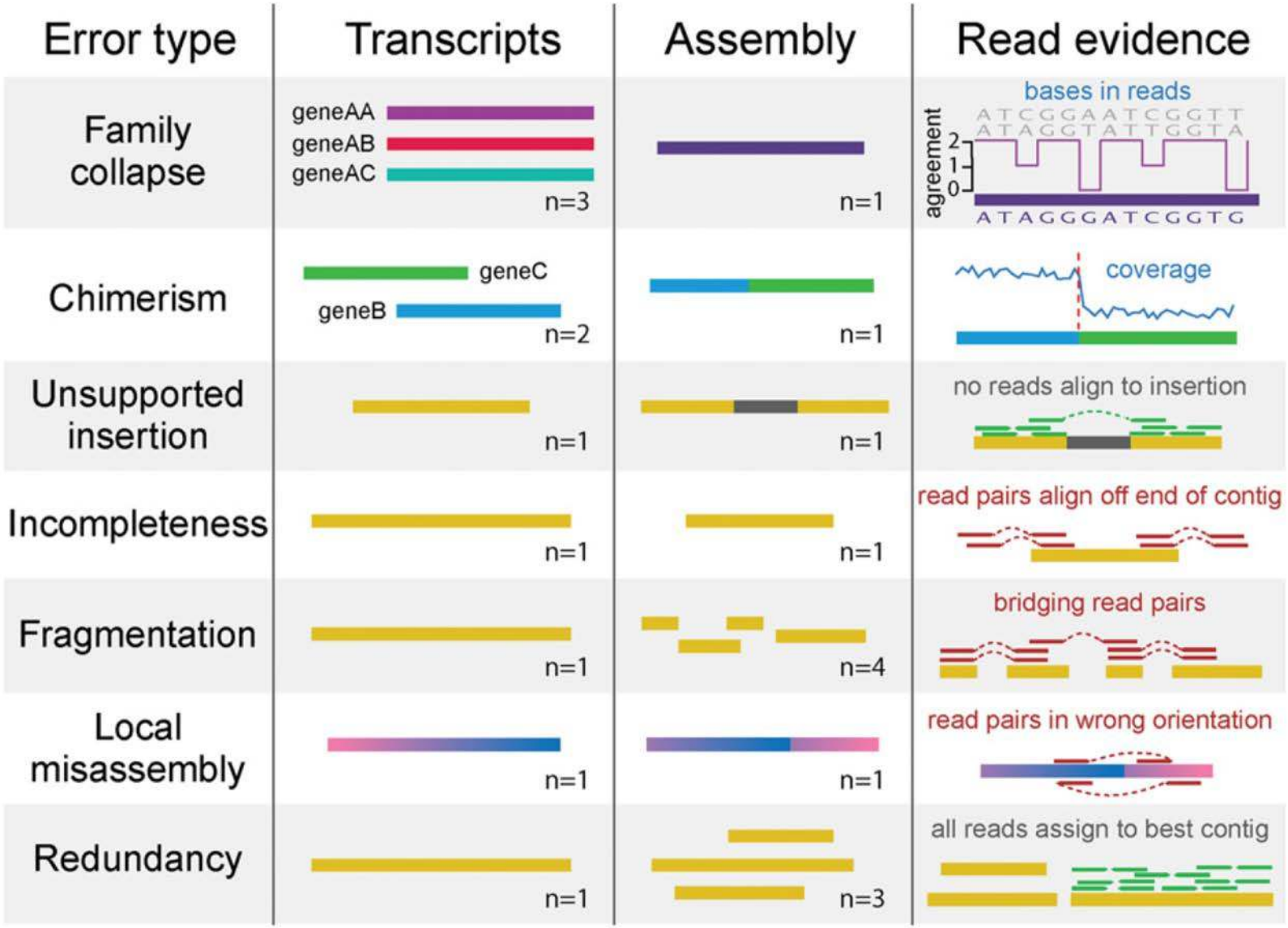


Evaluating the quality of your transcriptome assembly



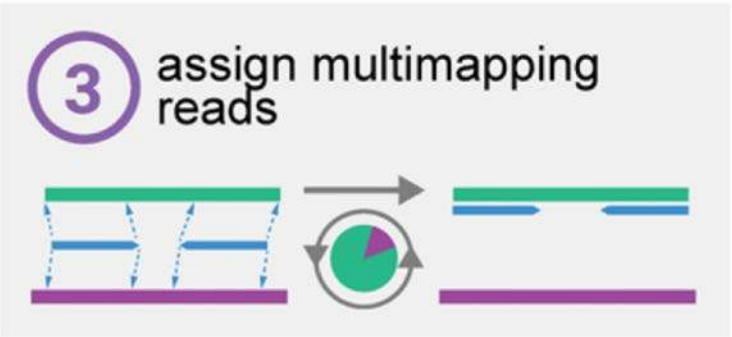
Bioconductor,
& Trinity

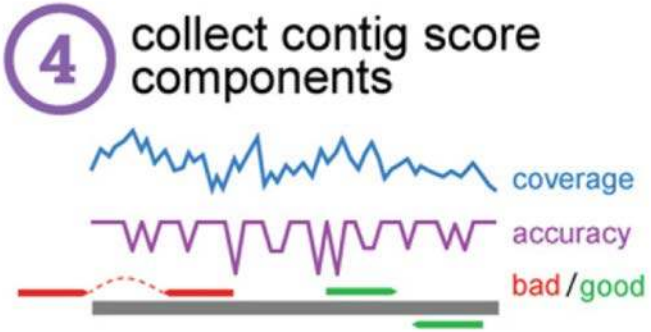
De novo Transcriptome Assembly is Prone to Certain Types of Errors

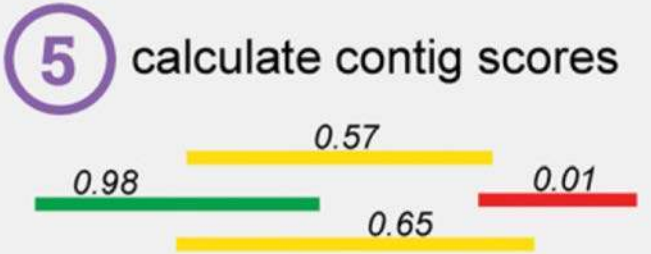


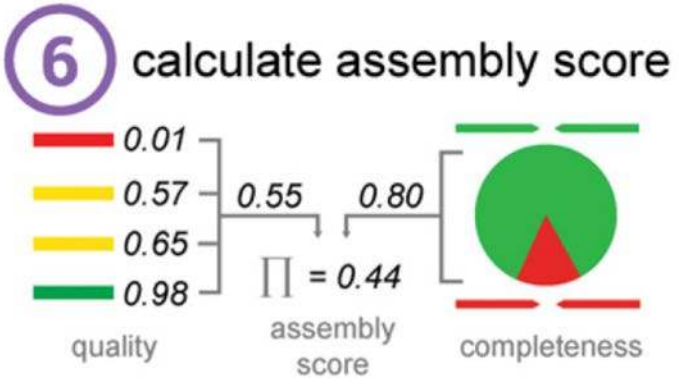
Smith-Unna et al. Genome Research, 2016

TransRate









Smith-Unna et al. Genome Research, 2016

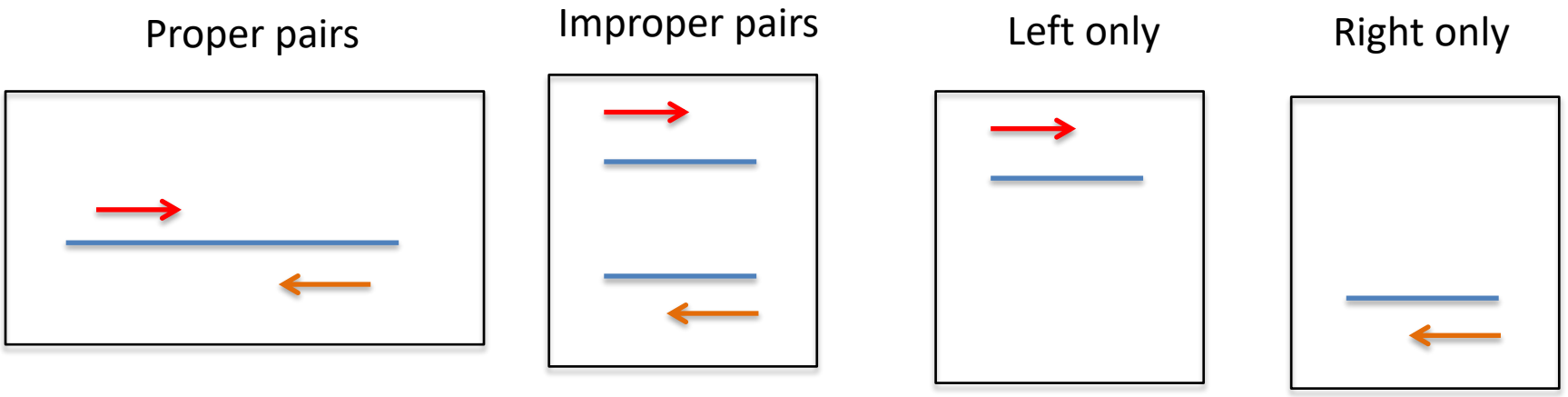
Simple Quantitative and Qualitative Assembly Metrics

Read representation by assembly

Align reads to the assembled transcripts using Bowtie.
A typical 'good' assembly has ~80 % reads mapping to the assembly and ~80% are properly paired.

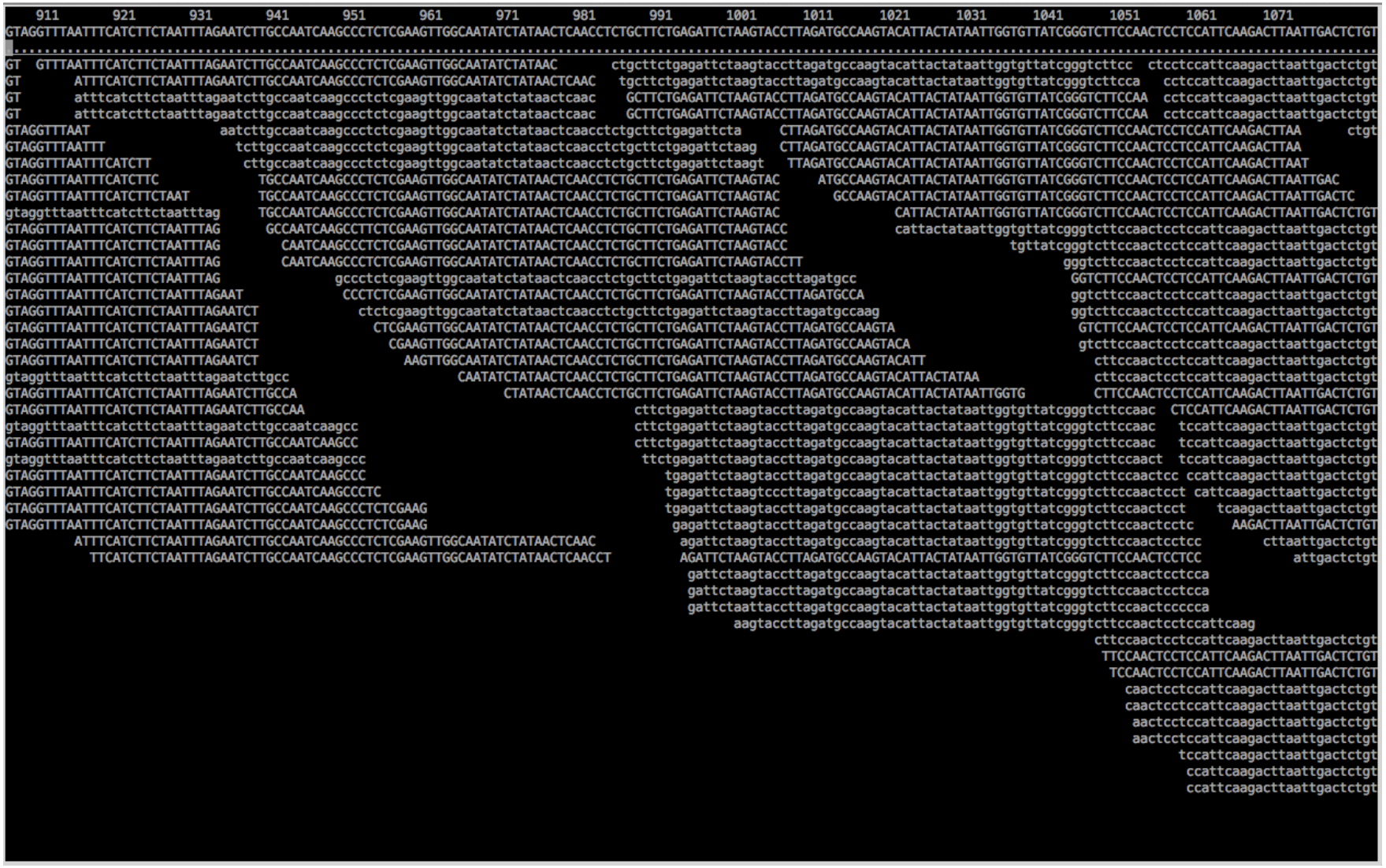
Given read pair: 

Possible mapping contexts in the Trinity assembly are reported:



Assembled transcript contig is only as good as its read support.

% samtools tview alignments.bam target.fasta



IGV

www.broadinstitute.org/igv/

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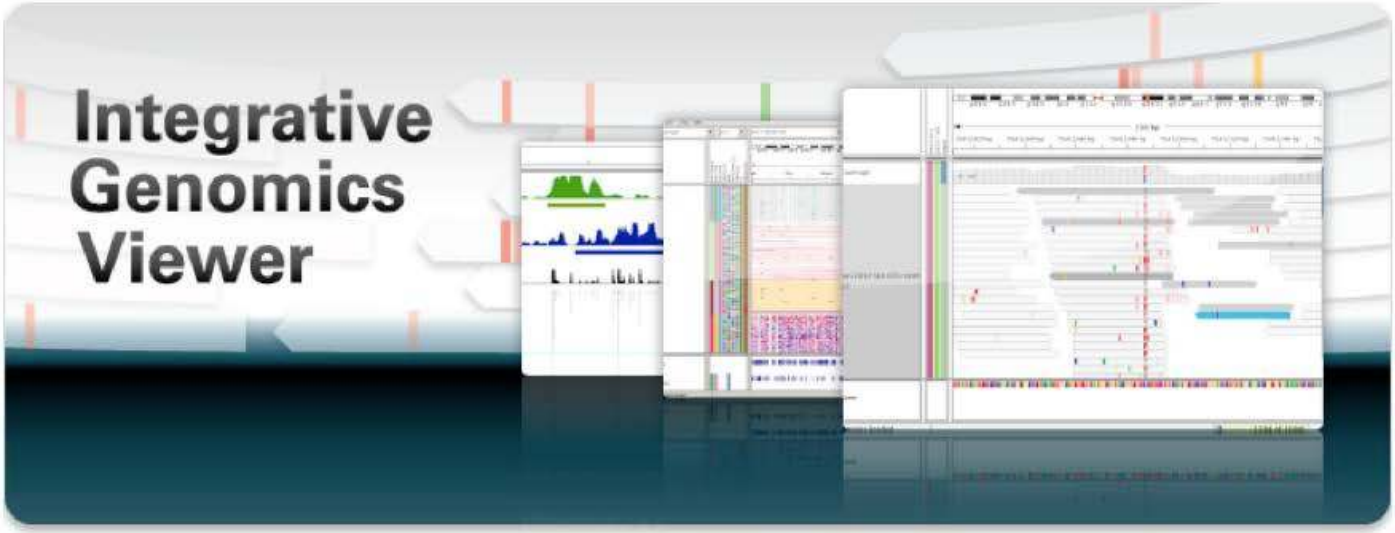


What's New

July 3, 2012. Soybean (Glycine max) and Rat (rn5) genomes have been updated.

April 20, 2012. IGV 2.1 has been released. See the release notes for more details.

April 19, 2012. See our new IGV paper in Briefings in Bioinformatics.

Overview

Citing IGV

To cite your use of IGV in your publication:

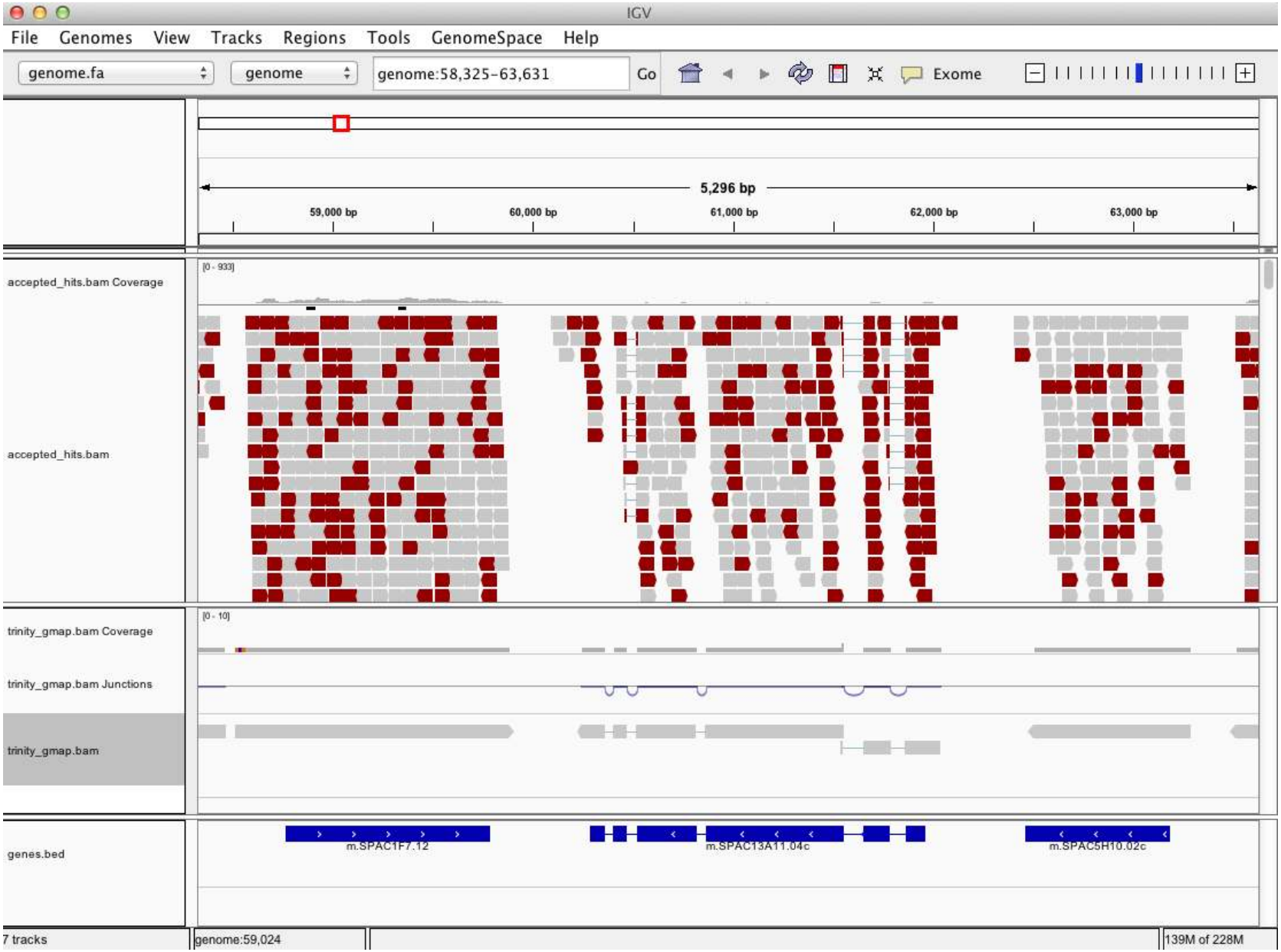
James T. Robinson, Helga Thorvaldsdóttir, Wendy Winckler, Mitchell Guttman, Eric S. Lander, Gad Getz, Jill P. Mesirov. **Integrative Genomics Viewer**. Nature Biotechnology 29, 24–26 (2011), or

Helga Thorvaldsdottir, James T. Robinson, Jill P. Mesirov. **Integrative Genomics Viewer (IGV): high-performance genomics data visualization and exploration.**

Can Examine Transcript Read Support Using IGV

Can align Trinity transcripts to genome scaffolds to examine intron/exon structures

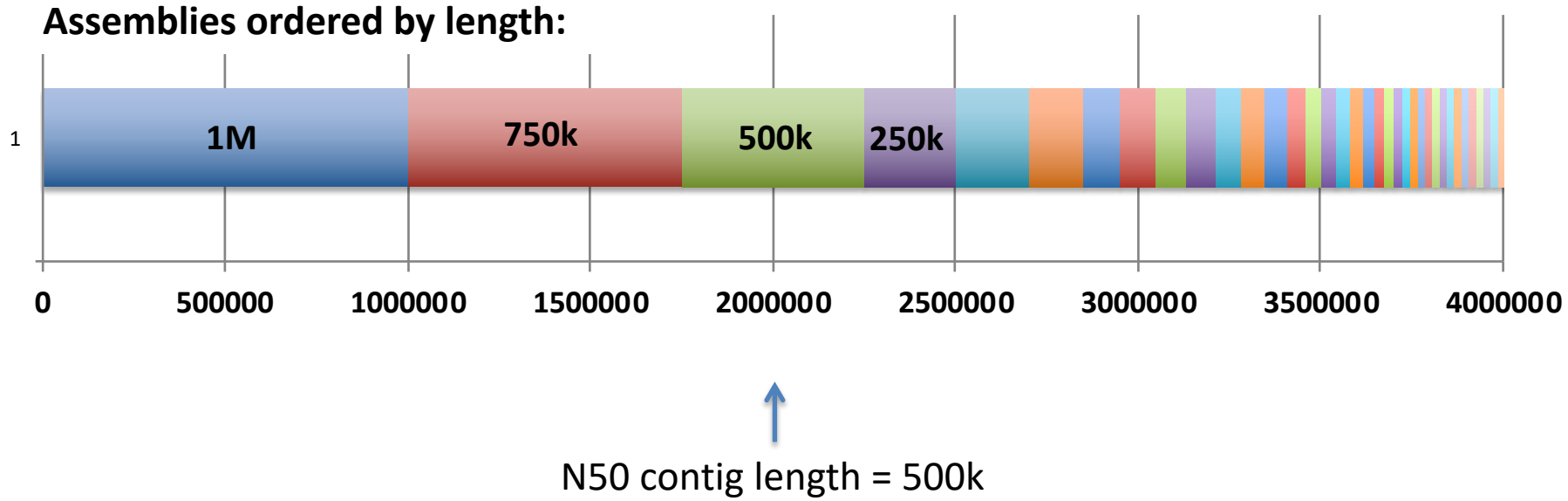
(Trinity transcripts aligned to the genome using GMAP)



The Contig N50 statistic

"At least half of assembled bases are in contigs that are at least ***N50*** bases in length"

In genome assemblies – used often to judge 'which assembly is better'



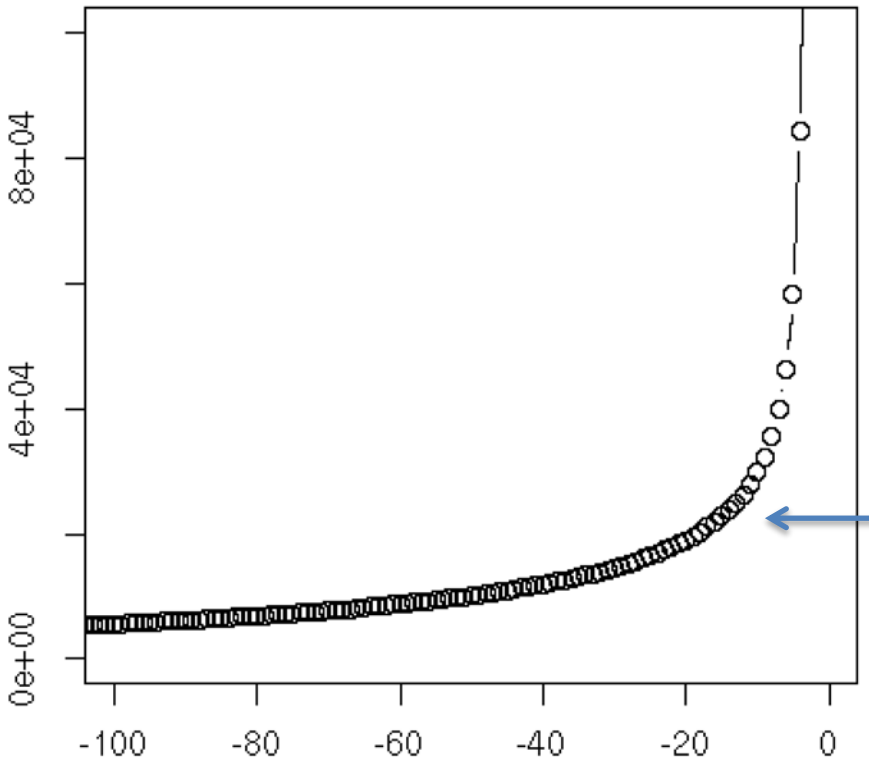
Often, most assembled transcripts are *very* lowly expressed

(How many ‘transcripts & genes’ are there really?)

1.4 million Trinity transcript contigs

N50 ~ 500 bases

Cumulative # of Transcripts

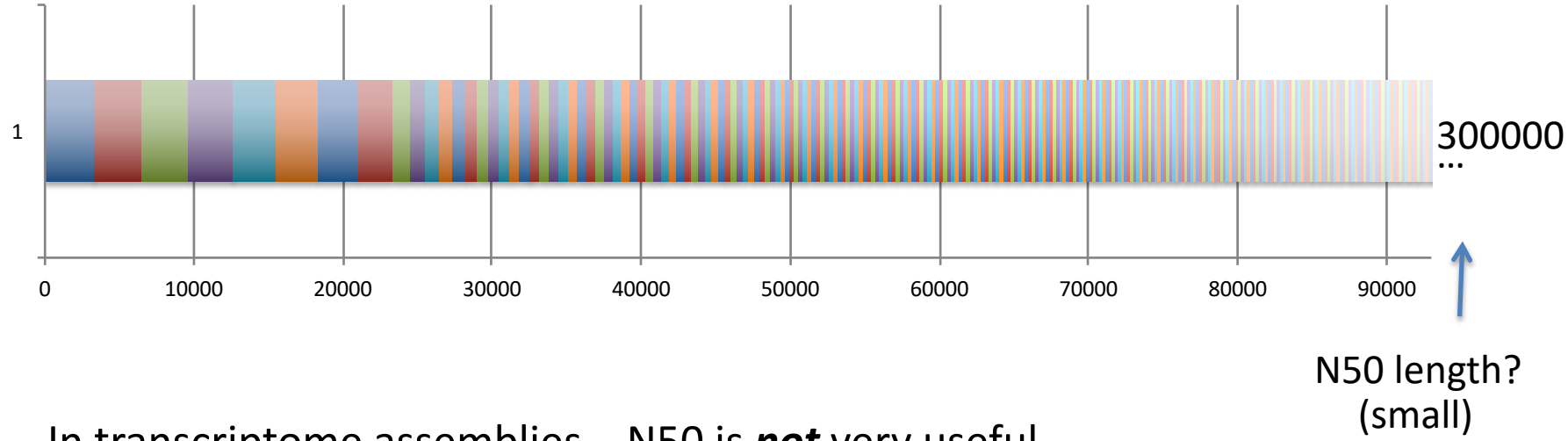


20k transcripts

Expression

* Salamander transcriptome

N50 Calculation for *Transcriptome* Assemblies??



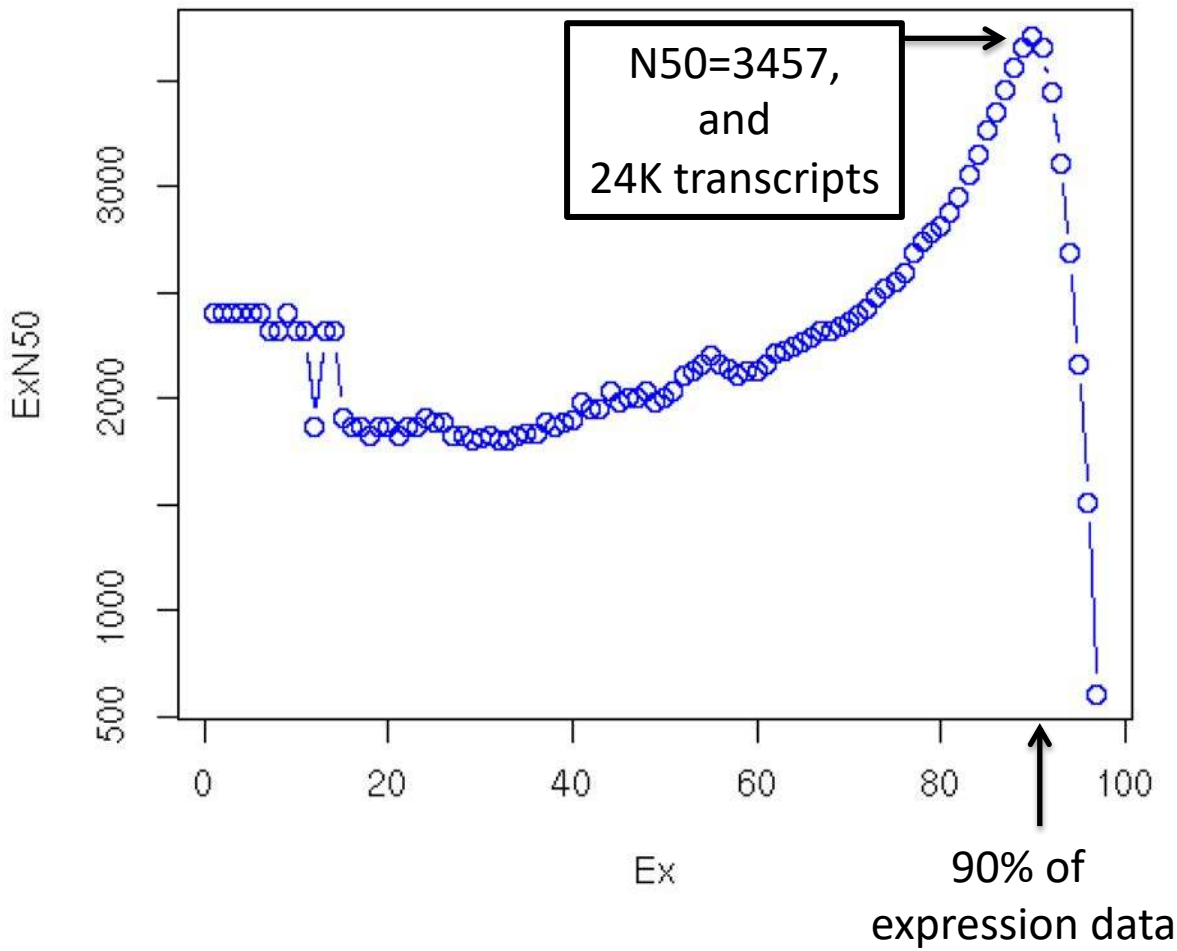
In transcriptome assemblies – N50 is ***not*** very useful.

- Overzealous isoform annotation for long transcripts drives higher N50
- Very sensitive reconstruction for short lowly expressed transcripts drives lower N50

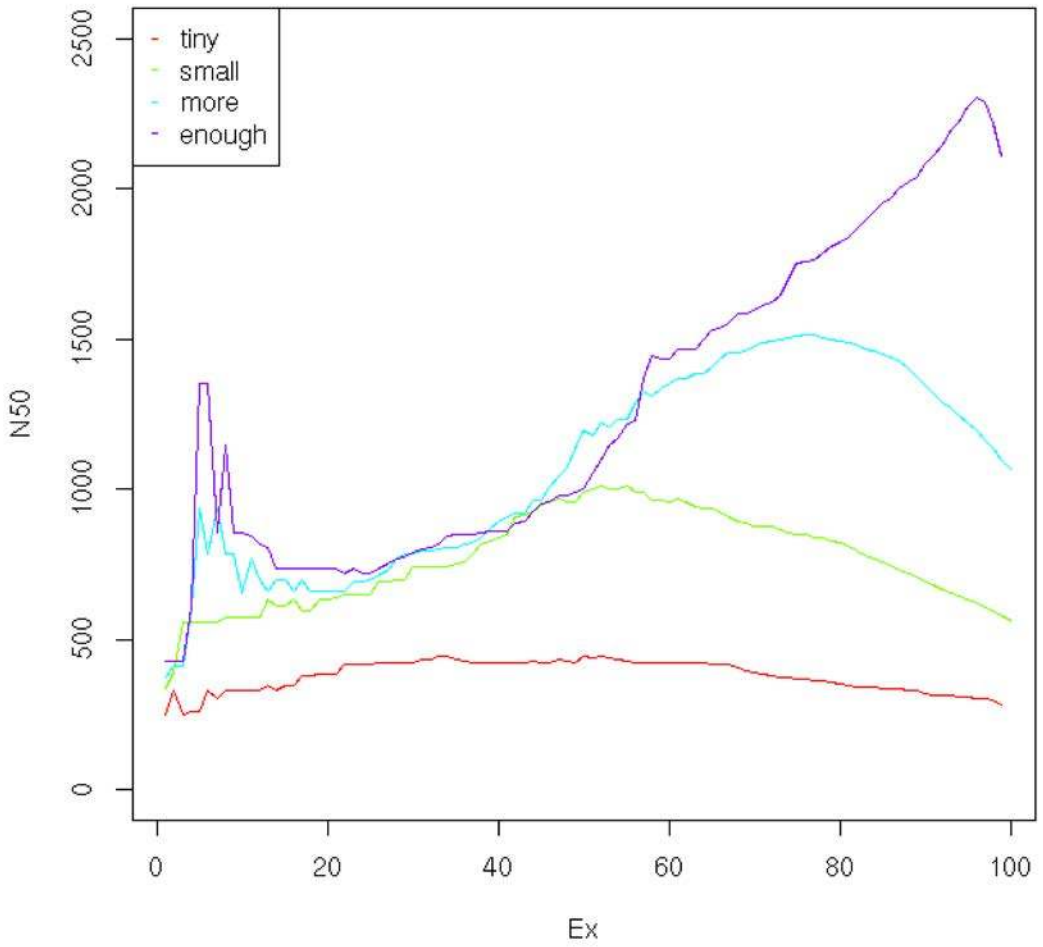
Expression-informed N50 Calculation for Transcriptome Assemblies (ExN50)

Compute N50 Based on the Top-most Highly Expressed Transcripts

- Sort contigs by expression value, descendingly.
- Compute N50 given minimum % total expression data thresholds => ExN50



ExN50 Profiles for Different Trinity Assemblies Using Different Read Depths



Millions of Reads

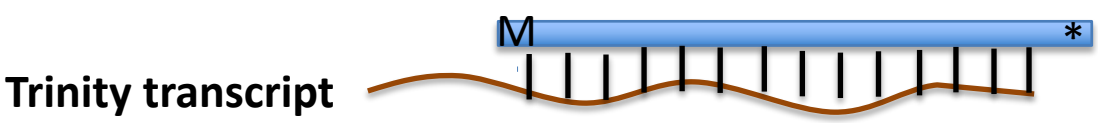
Thousands of Reads

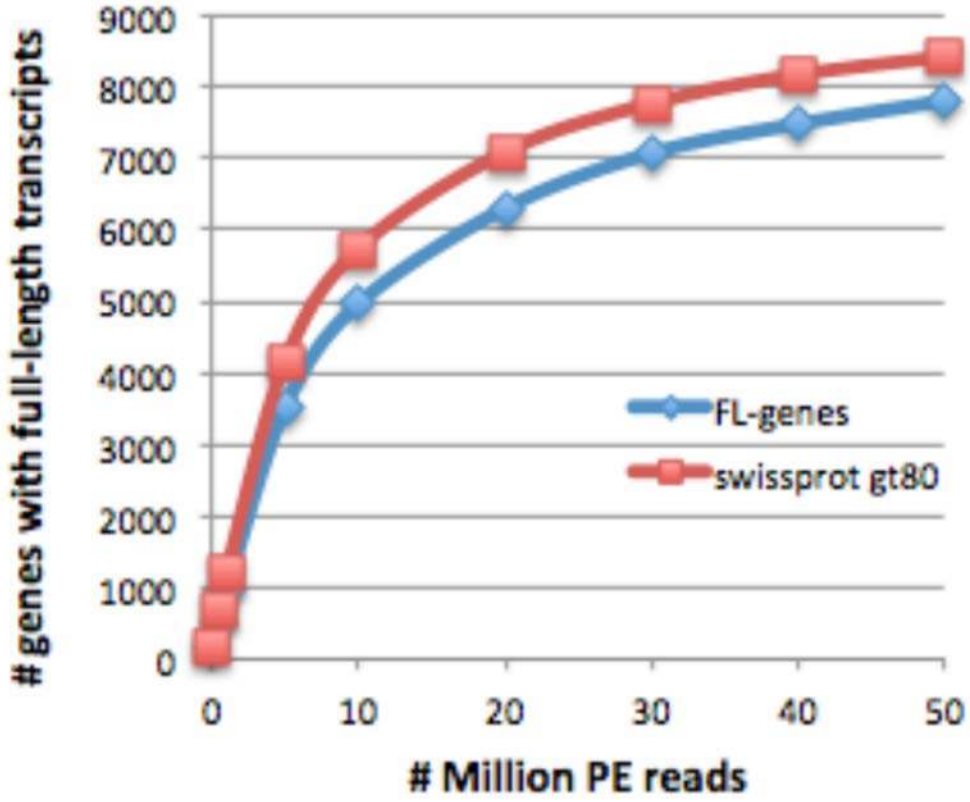
Note shift in ExN50 profiles as you assemble more and more reads.

* Candida transcriptome

Evaluating the quality of your transcriptome assembly

Full-length Transcript Detection via BLASTX





Have you sequenced deeply enough?

* Mouse transcriptome

Haas et al. Nat. Protoc. 2013

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CEGG Home | OrthoDB *v9* | BUSCO *v2*

BUSCO v2

Assessing genome assembly and annotation completeness with **B**enchmarking **U**niversal **S**ingle-**C**opy **O**rthologs

About BUSCO

BUSCO *v2* provides quantitative measures for the assessment of genome assembly, gene set, and transcriptome completeness, based on evolutionarily-informed expectations of gene content from near-universal single-copy orthologs selected from OrthoDB *v9*.

BUSCO assessments are implemented in open-source software, with a large selection of lineage-specific sets of Benchmarking Universal Single-Copy Orthologs. These conserved orthologs are ideal candidates for large-scale phylogenomics studies, and the annotated BUSCO gene models built during genome assessments provide a comprehensive gene predictor training set for use as part of genome annotation pipelines.

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Zdobnov's Computational Evolutionary Genomics group

CEGG Home | OrthoDB *v9* | BUSCO *v2*

Assessing genome assembly and annotation completeness with Benchmarking Universal Single-Copy Orthologs

#Summarized BUSCO benchmarking for file: Trinity.fasta
#BUSCO was run in mode: trans

Summarized benchmarks in BUSCO notation:
C:88%[D:53%],F:4.5%,M:7.3%,n:3023

Representing:

1045	Complete Single-copy BUSCOs
1617	Complete Duplicated BUSCOs
139	Fragmented BUSCOs
222	Missing BUSCOs
3023	Total BUSCO groups searched

Detonate: Which assembly is better?

"RSEM-EVAL [sic] uses a novel probabilistic model-based method to compute the joint probability of both an assembly and the RNA-Seq data as an evaluation score."

$$\text{score}_{\text{RSEM-EVAL}}(A) = \log P(A, D)$$

"the RSEM-EVAL score of an assembly is defined as the log joint probability of the assembly A and the reads D used to construct it"

$$\begin{aligned}\log P(A, D) &= \log \int_{\Lambda} P(D|A, \Lambda) P(A|\Lambda) P(\Lambda) d\Lambda \\ &\approx \underbrace{\log P(D|A, \Lambda_{\text{MLE}})}_{\text{likelihood}} + \underbrace{\log P(A|\Lambda_{\text{MLE}})}_{\text{assembly prior}} \\ &\quad - \underbrace{\frac{1}{2}(M+1)\log N}_{\text{BIC penalty}},\end{aligned}$$

Li et al. **Evaluation of de novo transcriptome assemblies from RNA-Seq data**, Genome Biology 2014

Detonate: Which assembly is better?

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$$\approx \underbrace{\log P(D|A,\Lambda_{\text{MLE}})}_{\text{likelihood}} + \underbrace{\log P(A|\Lambda_{\text{MLE}})}_{\text{assembly prior}}$$
$$\underbrace{-\frac{1}{2}(M+1)\log N,}_{\text{BIC penalty}}$$

Bigger Score = Better Assembly

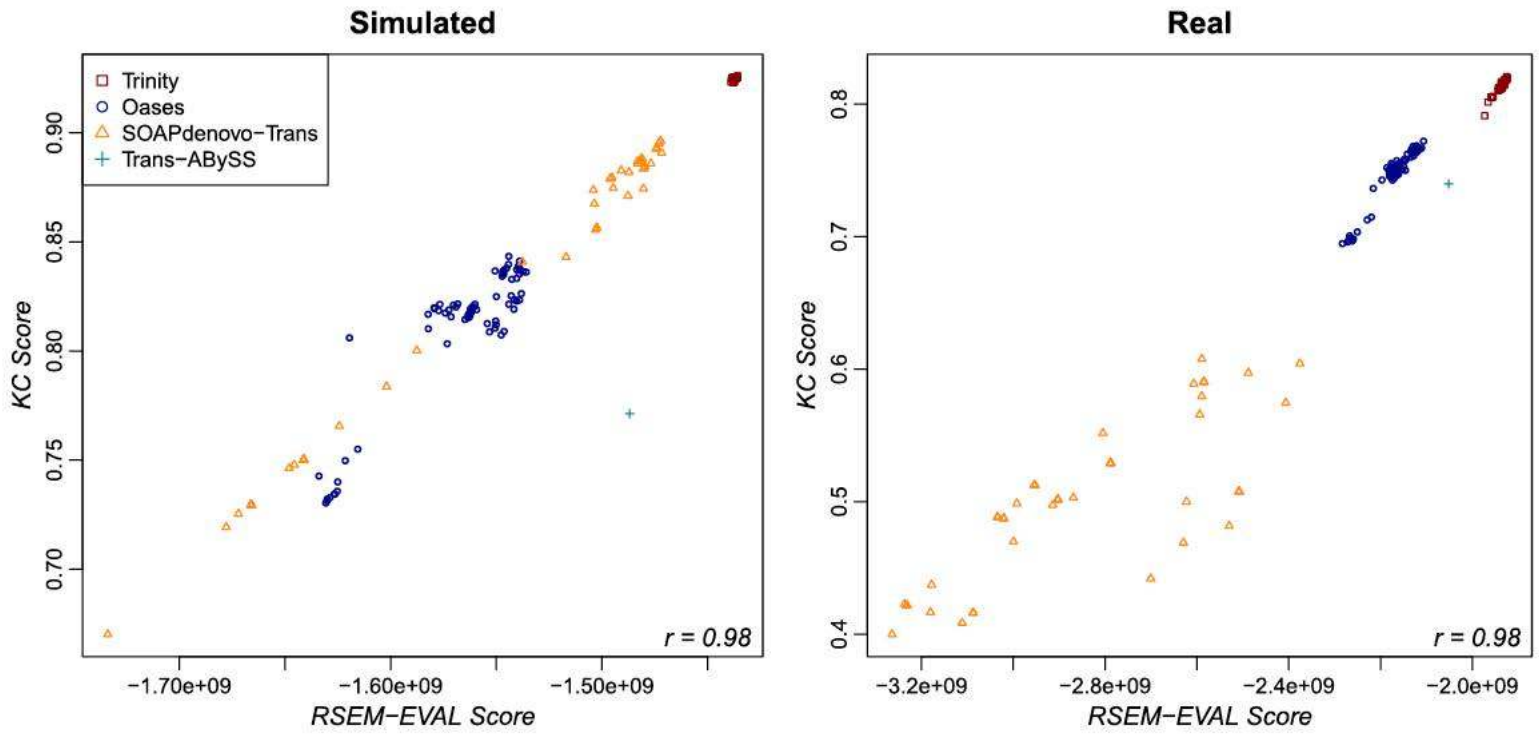
Li et al. **Evaluation of de novo transcriptome assemblies from RNA-Seq data**, Genome Biology 2014

Detonate: Which assembly is better?

"RSEM-EVAL [sic] uses a novel probabilistic model-based method to compute the joint probability of both an assembly and the RNA-Seq data as an evaluation score."

Yay Trinity!!

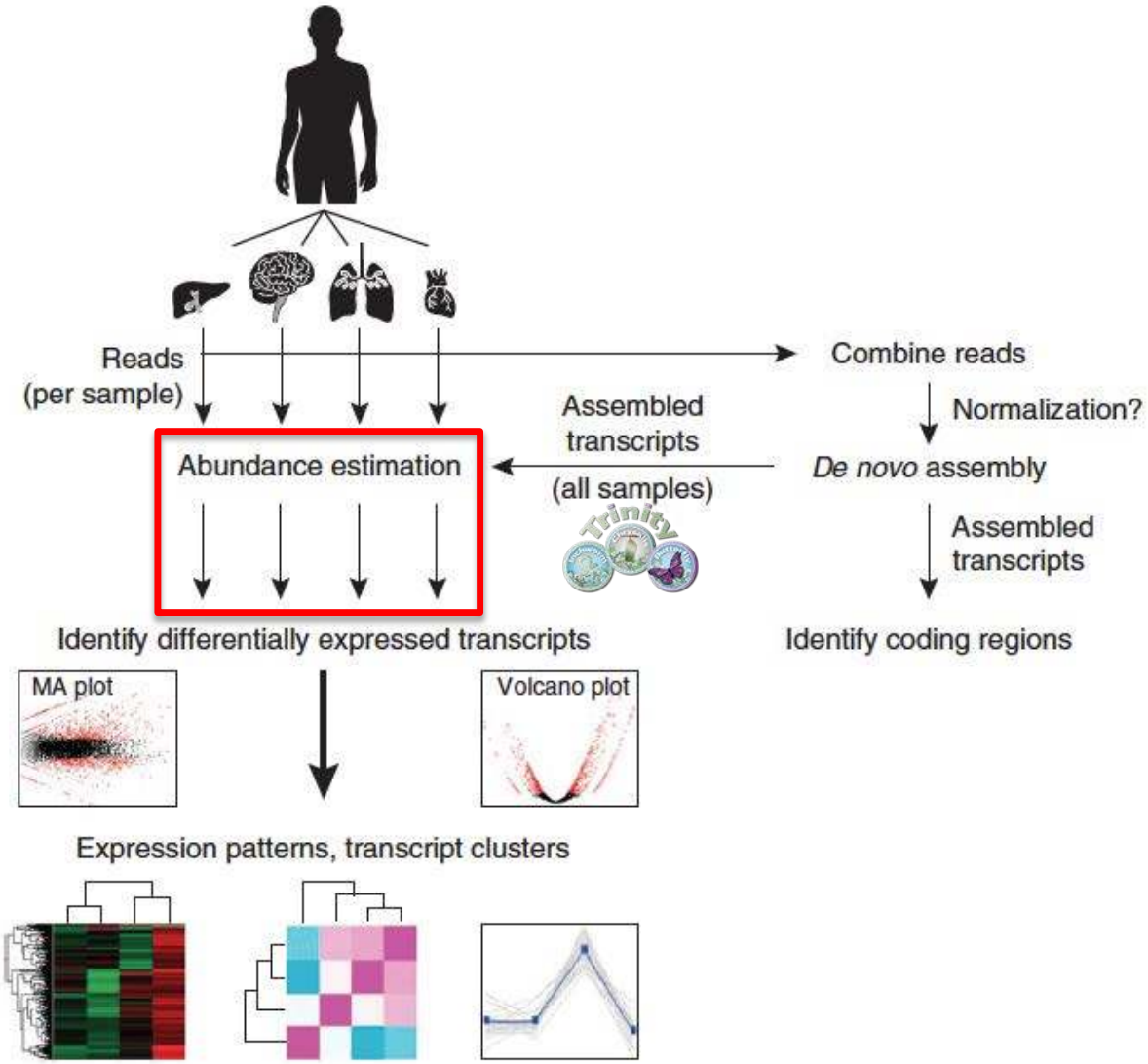
Ref Genome –based metric



RSEM-EVAL Genome-free metric

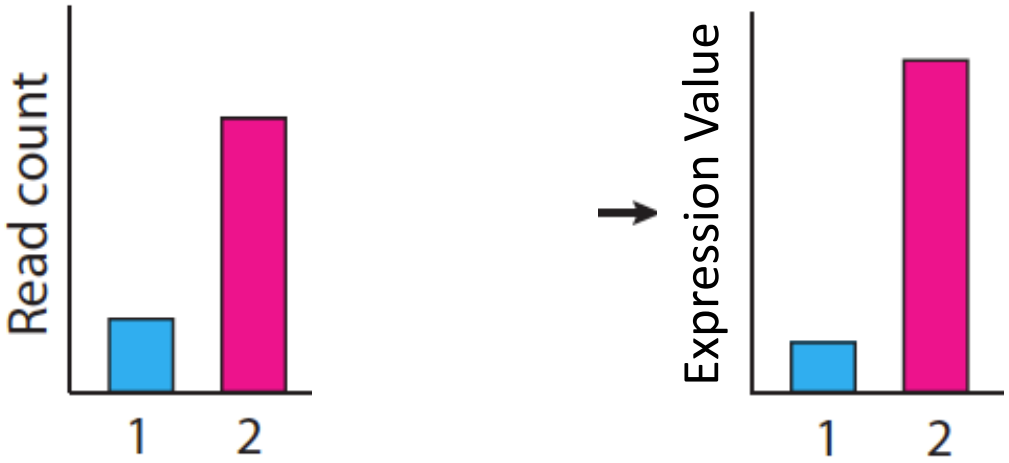
Li et al. **Evaluation of de novo transcriptome assemblies from RNA-Seq data**, Genome Biology 2014

Abundance Estimation
(Aka. Computing Expression Values)



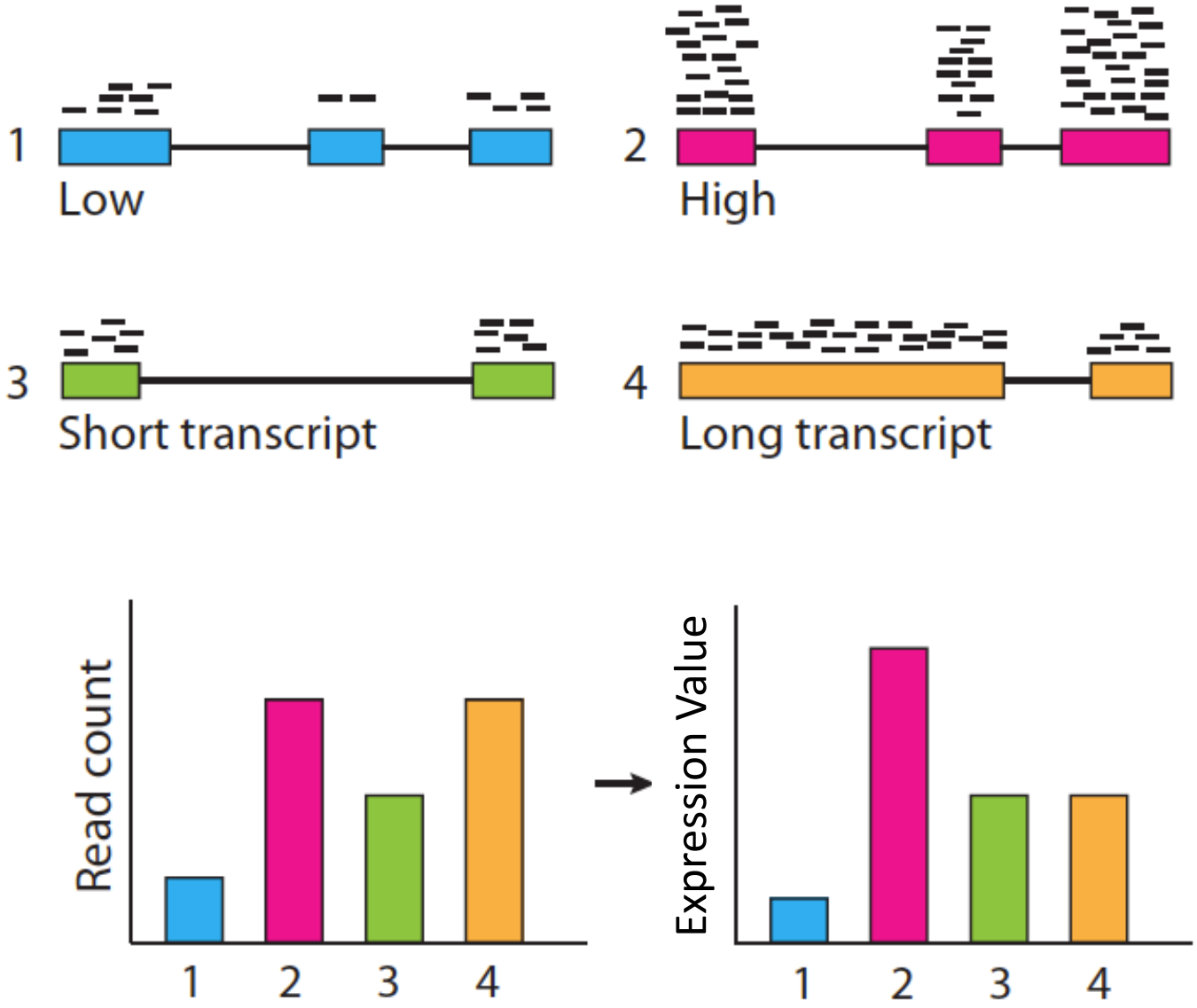
Bioconductor,
& Trinity

Calculating expression of genes and transcripts



Slide courtesy of Cole Trapnell

Calculating expression of genes and transcripts



Slide courtesy of Cole Trapnell

Normalized Expression Values

- Transcript-mapped read counts are normalized for both length of the transcript and total depth of sequencing.

- Reported as: Number of RNA-Seq **F**ragments
  Per **K**ilobase of transcript
  per total **M**illion fragments mapped

FPKM

RPKM (reads per kb per M) used with Single-end RNA-Seq reads
FPKM used with Paired-end RNA-Seq reads.

Transcripts per Million (TPM)

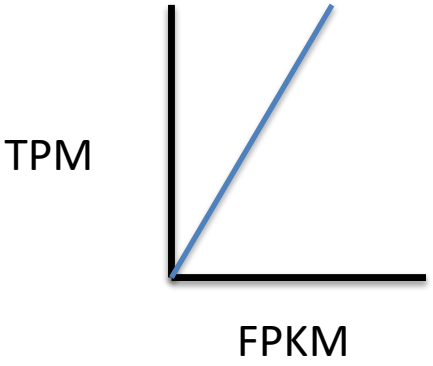
$$TPM_i = \frac{FPKM_i}{\sum_j FPKM} * 1e6$$

Preferred metric for measuring expression

- Better reflects transcript concentration in the sample.
- Nicely sums to 1 million

Linear relationship between TPM and FPKM values.

Both are valid metrics, but best to be consistent.



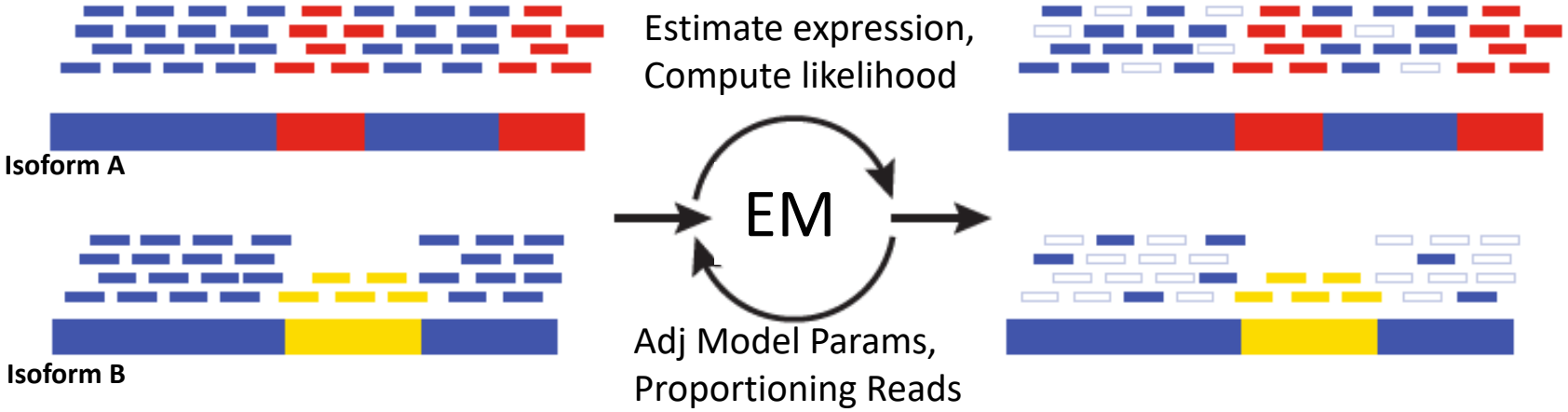
Multiply-mapped Reads Confound Abundance Estimation

Isoform A

Isoform B

Blue = multiply-mapped reads
Red, Yellow = uniquely-mapped reads

Multiply-mapped Reads Confound Abundance Estimation



Blue = multiply-mapped reads
Red, Yellow = uniquely-mapped reads

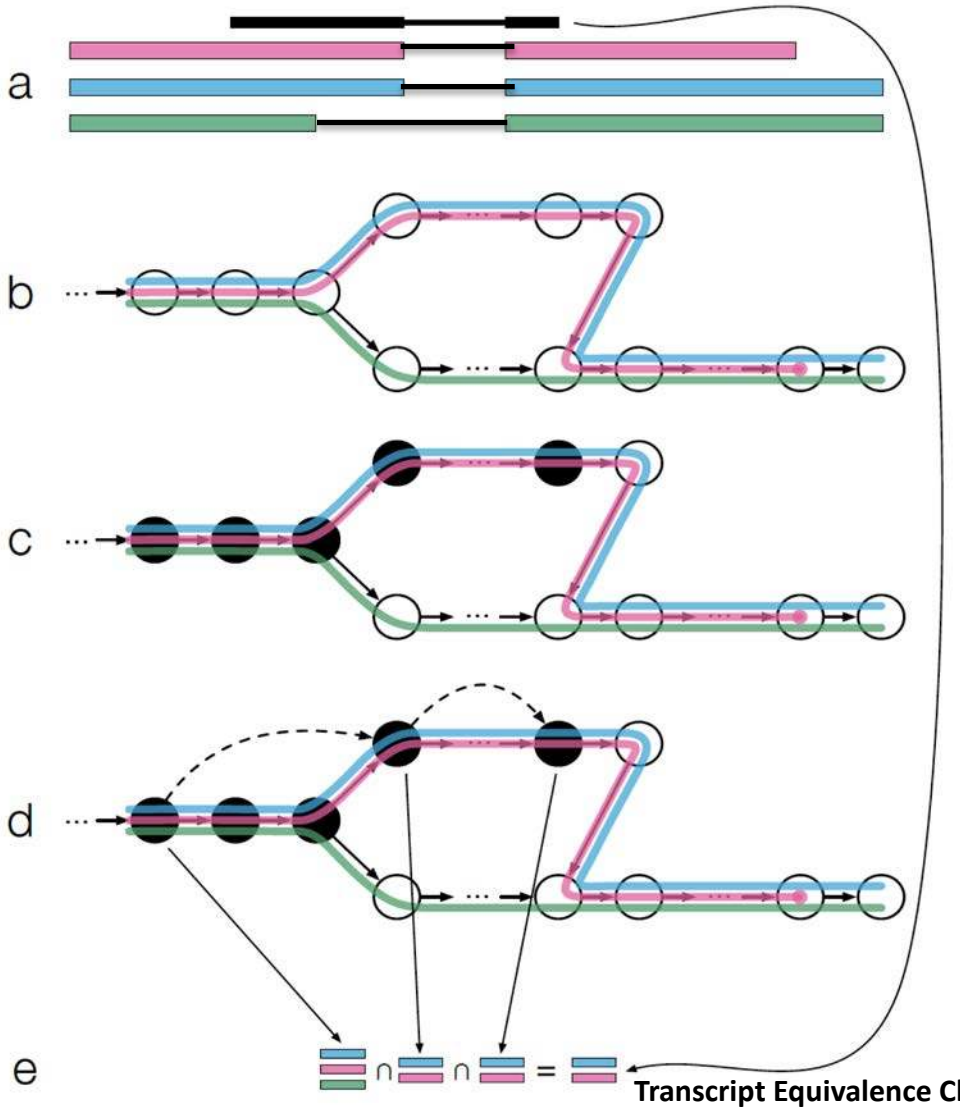
Use Expectation Maximization (EM) to find the most likely assignment of reads to transcripts.

Performed by:

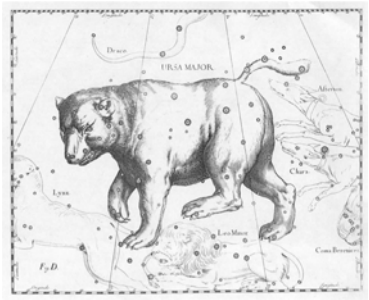
- Cufflinks, String Tie (Tuxedo)
- RSEM, eXpress (genome-free)
- Kallisto, Salmon (alignment-free)

Fast Abundance Estimation Using Pseudo-alignments and Equivalence Classes

(Kallisto software, Bray et al., NBT 2016)

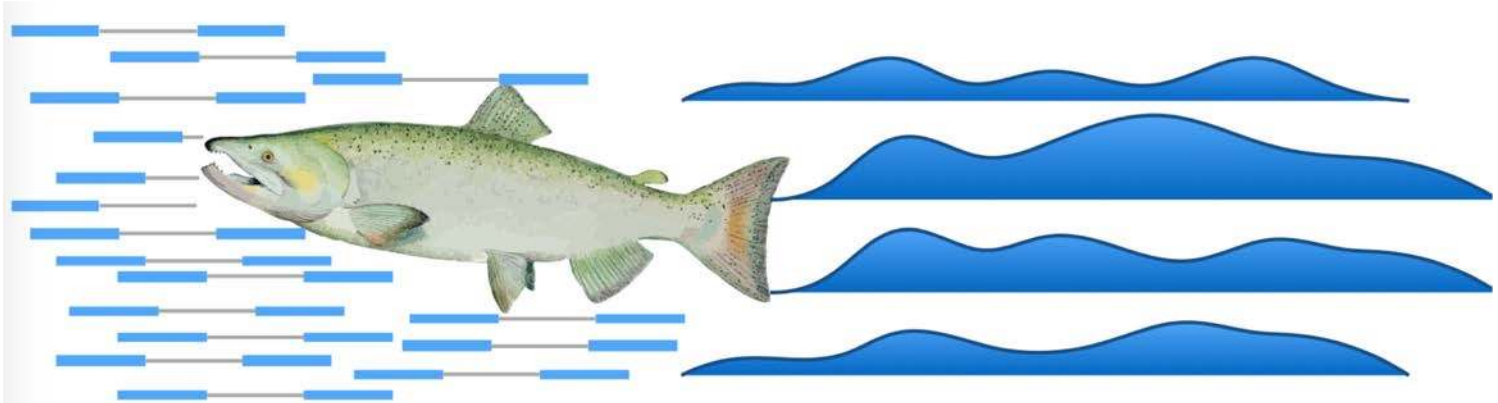


Transcript Equivalence Class
aka Transcript Compatibility Class



https://pachterlab.github.io/kallisto/

Adapted from Fig 1 from Bray et al.



Salmon —*Don't count . . . quantify!*

Uses a suffix array instead of the de Bruijn graph

nature methods

Altmetric: 210 Citations: 42 More detail »

Brief Communication

Salmon provides fast and bias-aware quantification of transcript expression

Rob Patro, Geet Duggal, Michael I Love, Rafael A Irizarry & Carl Kingsford

Nature Methods **14**, 417–419 (2017)
doi:10.1038/nmeth.4197
Download Citation

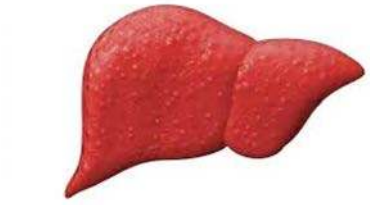
Received: 29 August 2016
Accepted: 22 January 2017
Published online: 06 March 2017

https://combine-lab.github.io/salmon/

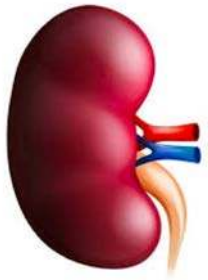
Comparing RNA-Seq Samples

Some Cross-sample Normalization May Be Required

eg.

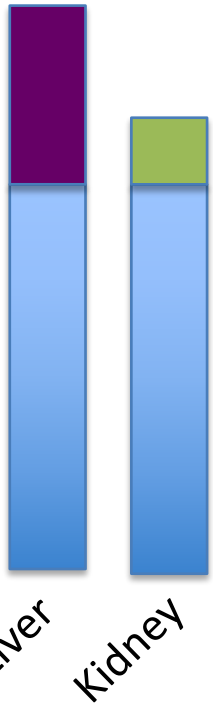


Vs.

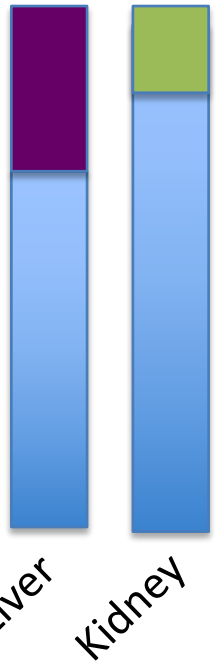


Why cross-sample normalization is important

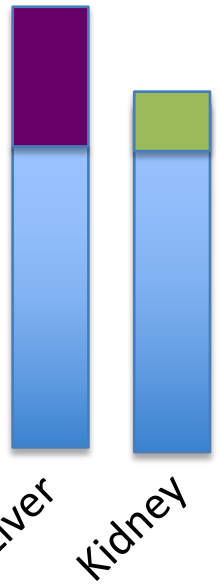
Absolute RNA quantities per cell



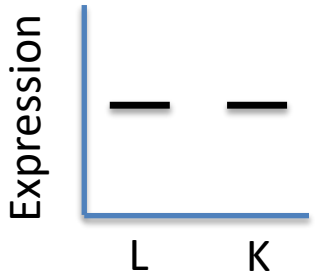
Measured relative abundance via RNA-Seq

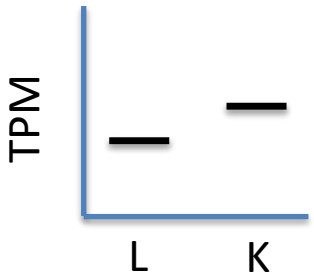


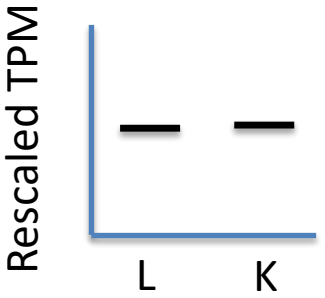
Cross-sample normalized (rescaled) relative abundance



eg. Some housekeeping gene's expression level:







Cross-sample Normalization Required
Otherwise, housekeeping genes look diff expressed due to sample composition differences

Subset of genes highly expressed in liver

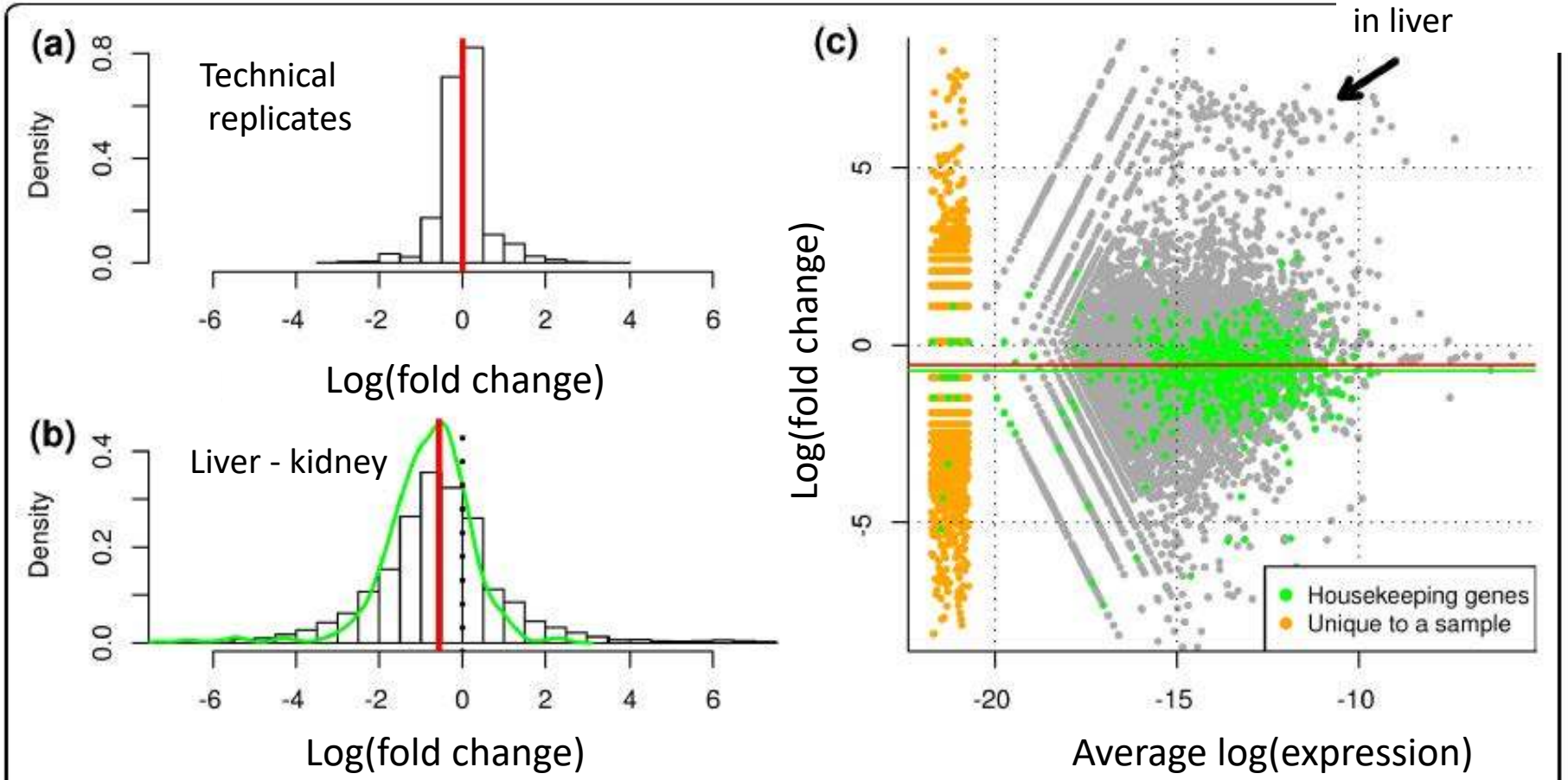
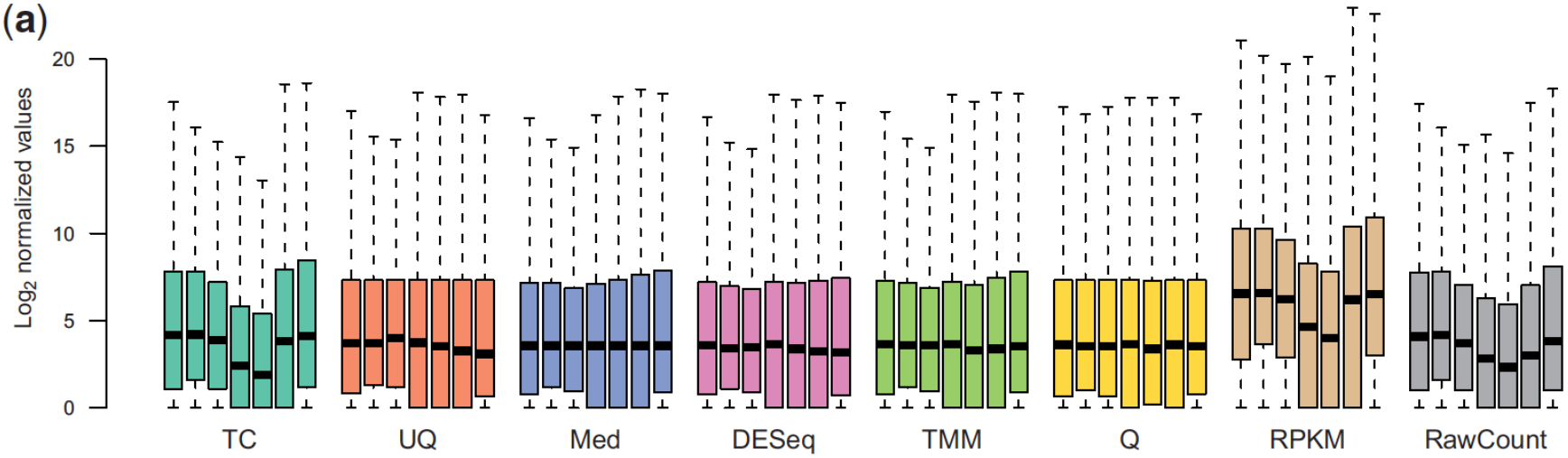


Figure 1 Normalization is required for RNA-seq data. Data from [6] comparing log ratios of **(a)** technical replicates and **(b)** liver versus kidney expression levels, after adjusting for the total number of reads in each sample. The green line shows the smoothed distribution of log-fold-changes of the housekeeping genes. **(c)** An M versus A plot comparing liver and kidney shows a clear offset from zero. Green points indicate 545 housekeeping genes, while the green line signifies the median log-ratio of the housekeeping genes. The red line shows the estimated TMM normalization factor. The smear of orange points highlights the genes that were observed in only one of the liver or kidney [illegible] the overall bias in log-fold-changes.

Adapted from: Robinson and Oshlack, Genome Biology, 2010

Normalization methods for Illumina high-throughput RNA sequencing data analysis.



From “A comprehensive evaluation of normalization methods for Illumina high throughput RNA sequencing data analysis” Brief Bioinform. 2013 Nov;14(6):671-83
http://www.ncbi.nlm.nih.gov/pubmed/22988256

Differential Expression Analysis

Thx, Charlotte Soneson! ☺

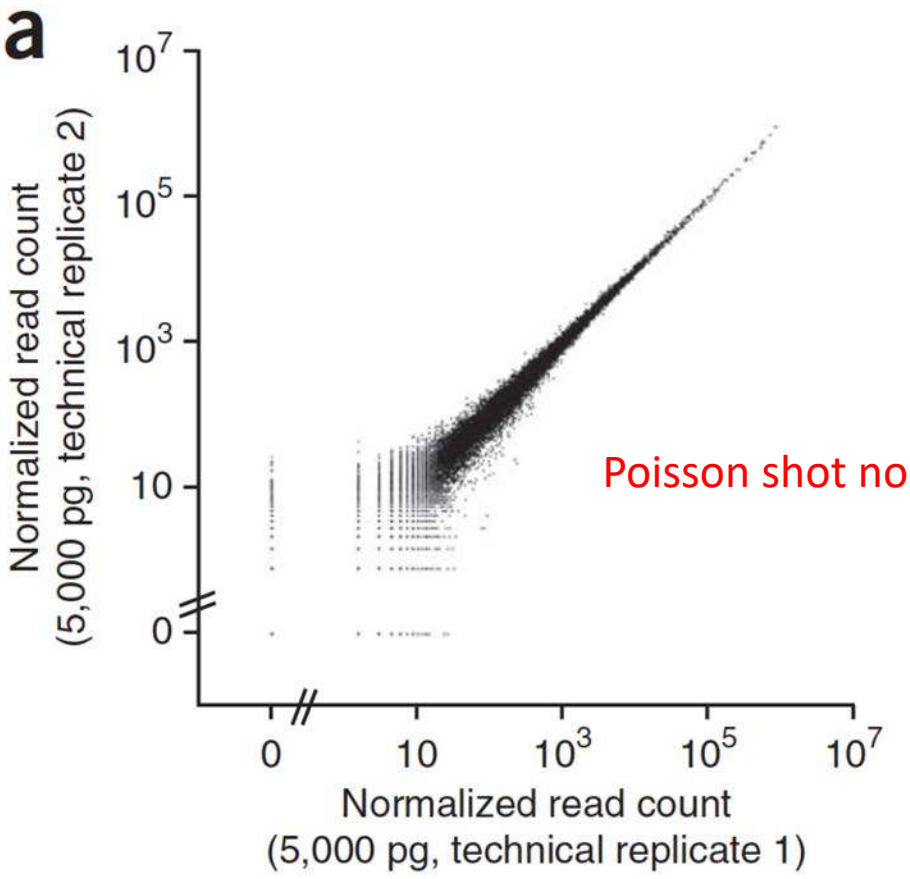
Differential Expression Analysis Involves

- Counting reads mapped to features
- Statistical significance testing

Beware of small counts leading to notable fold changes

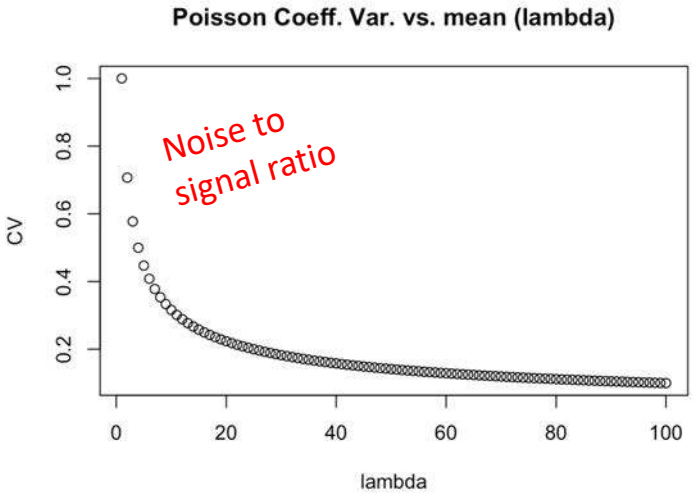
	Sample_A	**Sample_B**	**Fold_Change**	**Significant?**
Gene A	1	2	2-fold	No
Gene B	100	200	2-fold	Yes

Variation Observed Between Technical Replicates



Variation observed is well described by models of random sampling (Poisson Distribution)

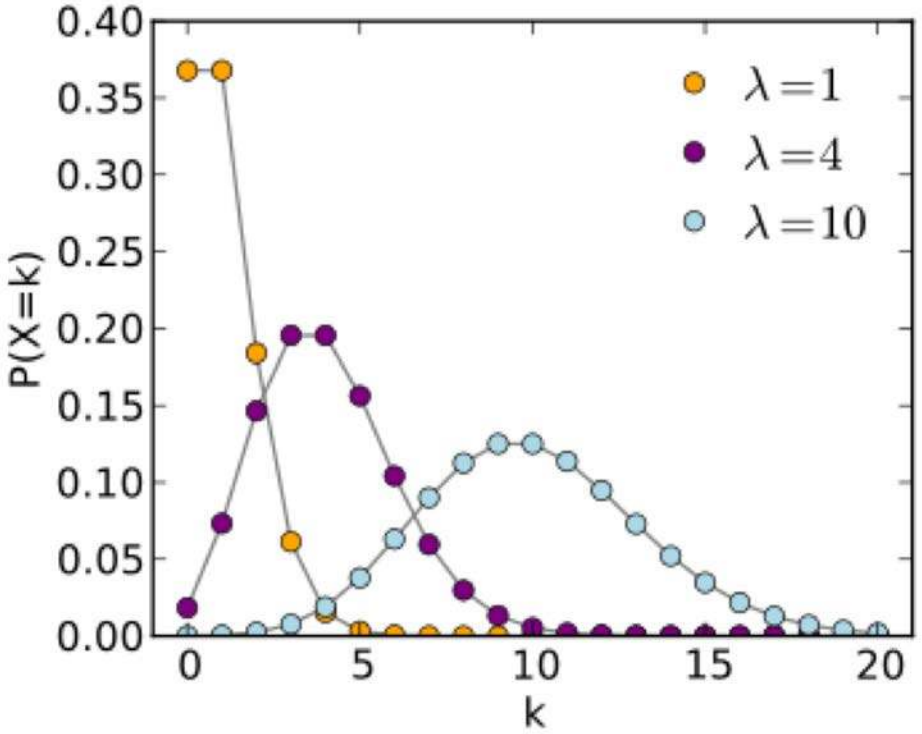
Poisson shot noise is high for small counts.



* plot from Brennecke, et al. Nature Methods, 2013

Observed RNA-Seq Counts Result from Random Sampling of the Population of Reads

Technical variation in RNA-Seq counts per feature is well modeled by the Poisson distribution



Mean # fragments

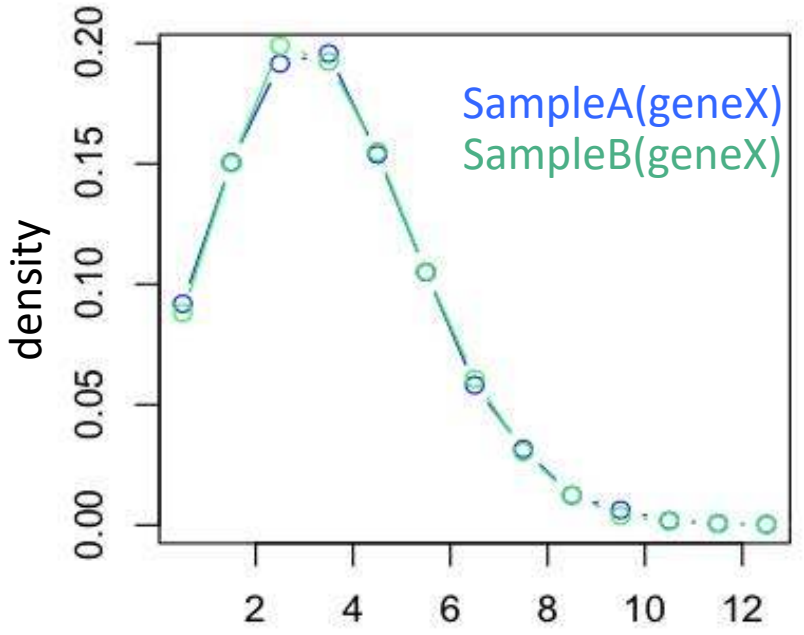
(observed read counts)

See: http://en.wikipedia.org/wiki/Poisson_distribution

Example: One gene*not* differentially expressed

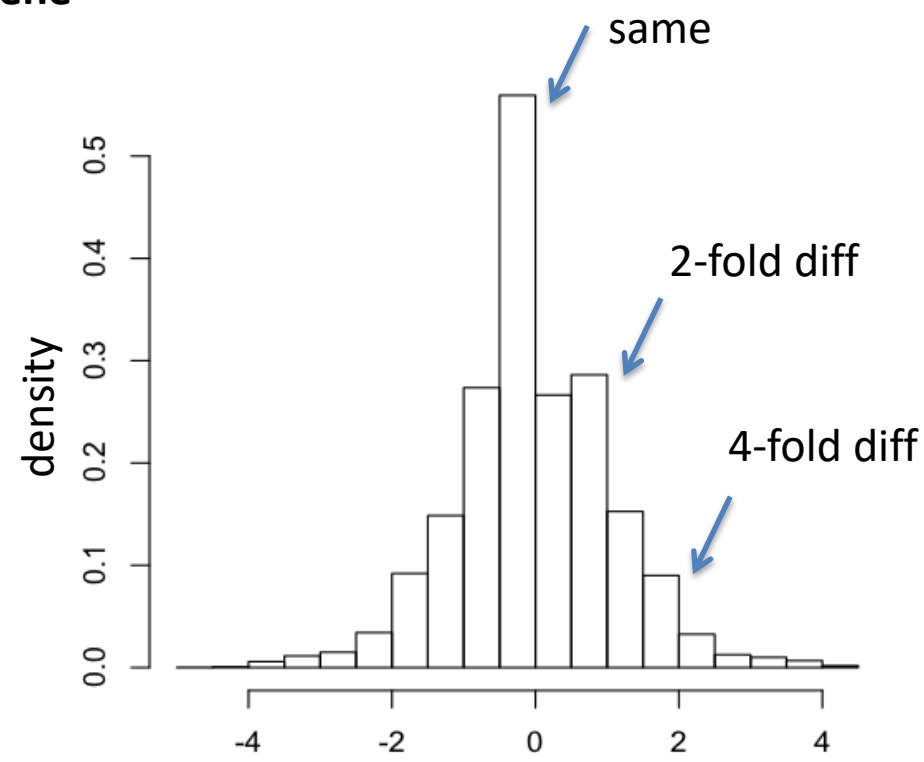
Example: SampleA(gene) = SampleB(gene) = 4 reads

Distribution of observed counts for single gene (under Poisson model)



(k) number of reads observed

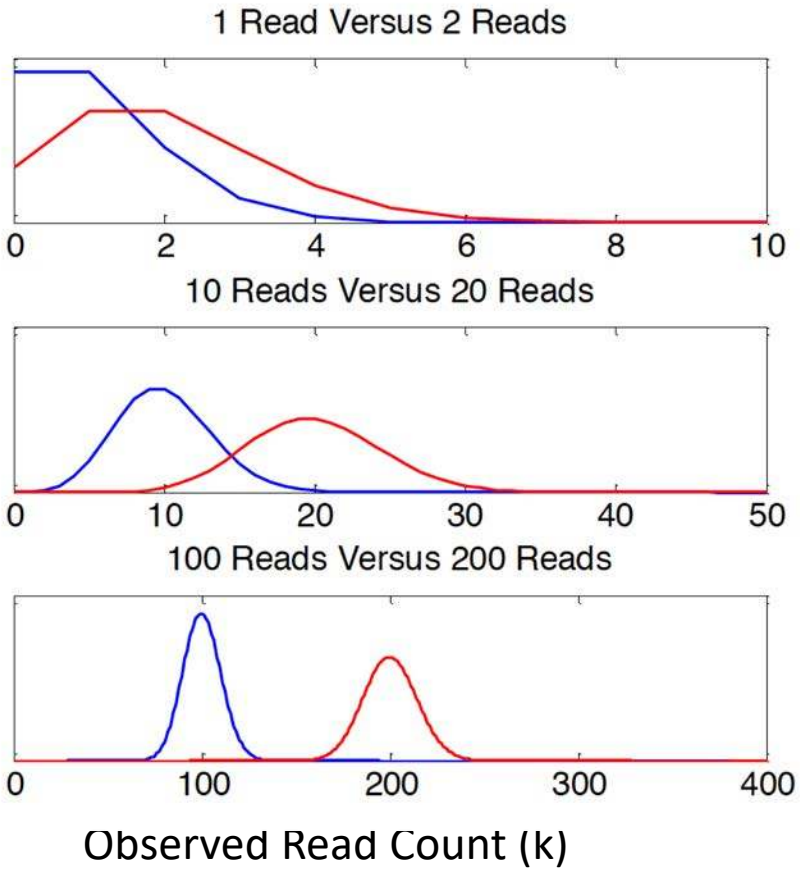
Dist. of $\log_2$(fold change) values



x = $\log_2$(SampleA/SampleB)

Sequencing Depth Matters

Poisson distributions for counts based on **2-fold** expression differences



No confidence in 2-fold difference. Likely observed by chance.

High confidence in 2-fold difference. Unlikely observed by chance.

From: http://gkno2.tumblr.com/post/24629975632/thinking-about-rna-seq-experimental-design-for
and from supplementary text of Busby et al., Bioinformatics, 2013

Greater Depth = More Statistical Power

Example: Single gene, reads sampled at different sequencing depths

Reads per sample	Sample A Number of reads	Sample B Number of reads	P-value (Fishers Exact Test)
100,000	1	2	1
1,000,000	10	20	0.099
10,000,000	100	200	**8.0e-09**

Technical vs. Biological Replicates

RNA-Seq Technical replicates aren't essential

(Technical variation is well-modeled by the Poisson distribution)

"We find that the Illumina sequencing data are highly replicable, with relatively little technical variation, and thus, for many purposes, it may suffice **to sequence each mRNA sample only once**" *Marioni et al., Genome Research, 2008*

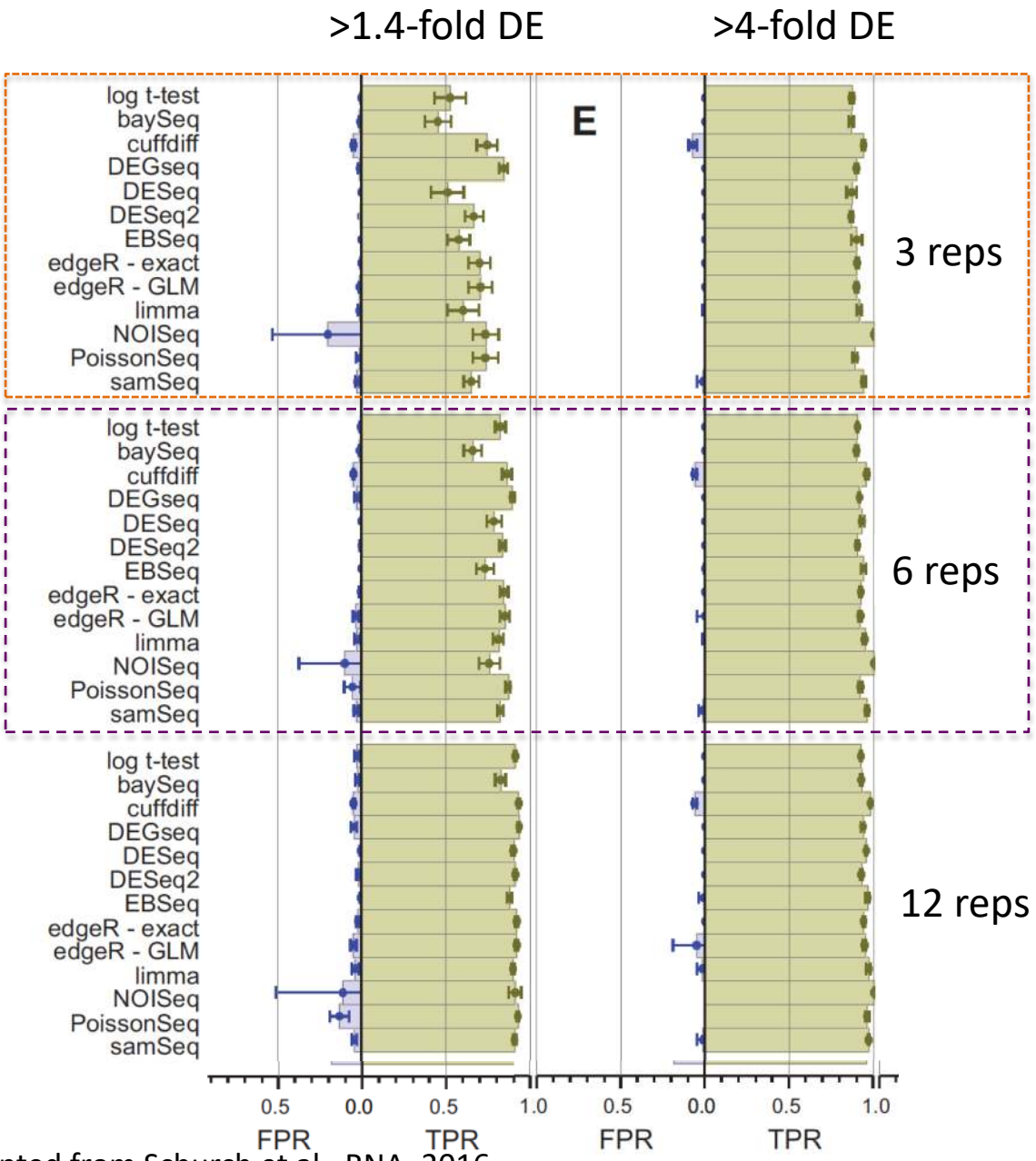
However, biological replicates *ARE* essential

total_variance = technical_variance + biological_variance

(Total variance well-modeled by negative binomial distribution)

"… **at least six biological replicates should be used**, rising to at least 12 when it is important to identify SDE genes for all fold changes." *Schurch et al., RNA, 2016*

DE Accuracy Improves with Higher Biological Replication



At a minimum, do 3 bio replicates

Respectable goal

*Figure taken and adapted from Schurch et al., RNA, 2016

Tools for DE analysis with RNA-Seq

edgeR
ShrinkSeq
DESeq
baySeq
Vsf
Limma/Voom
mmdiff
cuffdiff

ROTS
TSPM
DESeq2
EBSeq
NBPSeq
SAMseq
NoiSeq
Sleuth

(italicized not in R/Bioconductor but stand-alone)

See: http://www.biomedcentral.com/1471-2105/14/91
A comparison of methods for differential expression analysis of RNA-seq data
Soneson & Delorenzi, 2013

Typical output from DE analysis

	logFC	logCPM	PValue	FDR
TRINITY_DN876_c0_g1_i1	-7.15049572793027	10.6197708379285	0	0
TRINITY_DN6470_c0_g1_i1	-7.26777912190146	7.03987604865422	1.687485656951e-287	6.46813252309319e-284
TRINITY_DN5186_c0_g1_i1	-7.85623682454322	9.18570464327063	1.17049180235068e-278	2.99099671894011e-275
TRINITY_DN768_c0_g1_i1	7.72884741150304	9.7514619195169	4.32504881419265e-272	8.28895605240022e-269
TRINITY_DN70_c0_g1_i1	-12.7646078189688	7.86482982471445	3.92853491279431e-253	6.02322972829624e-250
TRINITY_DN1587_c0_g1_i1	-5.89392061881667	9.07366563894607	6.32919557933429e-243	8.08660221852944e-240
TRINITY_DN3236_c0_g1_i1	-7.27029815068473	8.02209568234202	3.64955175271959e-235	3.99678053376405e-232
TRINITY_DN4631_c0_g1_i1	-7.45310693639574	6.91664918183241	4.30540921272851e-229	4.1256583780971e-226
TRINITY_DN5082_c0_g5_i1	-5.33154406167545	10.6977538760467	2.74243356676259e-225	2.33594396920022e-222
TRINITY_DN1789_c0_g3_i1	10.2032564835076	7.32607652700285	1.44273728647186e-213	1.10600240380933e-210
TRINITY_DN4204_c0_g1_i1	4.81030233739325	9.88844409410644	9.27180216086162e-205	6.46160321501501e-202
TRINITY_DN799_c0_g1_i1	-4.22044475626154	6.9937398638711	1.24746518421083e-197	7.96922341846683e-195
TRINITY_DN196_c0_g2_i1	4.60597918494257	9.86878463857276	1.9819997623131e-192	1.16877001368402e-189
TRINITY_DN5041_c0_g1_i1	-4.27126549355785	9.70894399883	1.8930437900069e-185	1.03657669244235e-182
TRINITY_DN1619_c0_g1_i1	-4.47156415953777	9.22535948721718	1.76766063029526e-181	9.03392426122899e-179
TRINITY_DN899_c0_g1_i1	-4.90914328409143	7.93768691394594	1.11054513767547e-180	5.32089939088761e-178
TRINITY_DN324_c0_g2_i1	4.87160837667488	6.84850312231775	2.20092562166991e-179	9.92487989160089e-177
TRINITY_DN3241_c0_g1_i1	-4.77760618069256	7.94111259715689	1.60585457735621e-173	6.83915621667372e-171
TRINITY_DN4379_c0_g1_i1	3.85133572453294	7.23712813663389	3.48140532848425e-164	1.4046554341137e-161
TRINITY_DN1919_c0_g1_i1	4.05998814332136	6.95937301668582	1.8588621194715e-161	7.12501850393425e-159
TRINITY_DN2504_c0_g1_i1	-6.92417817059644	6.20370039359785	2.42022459856956e-160	8.83497227268296e-158

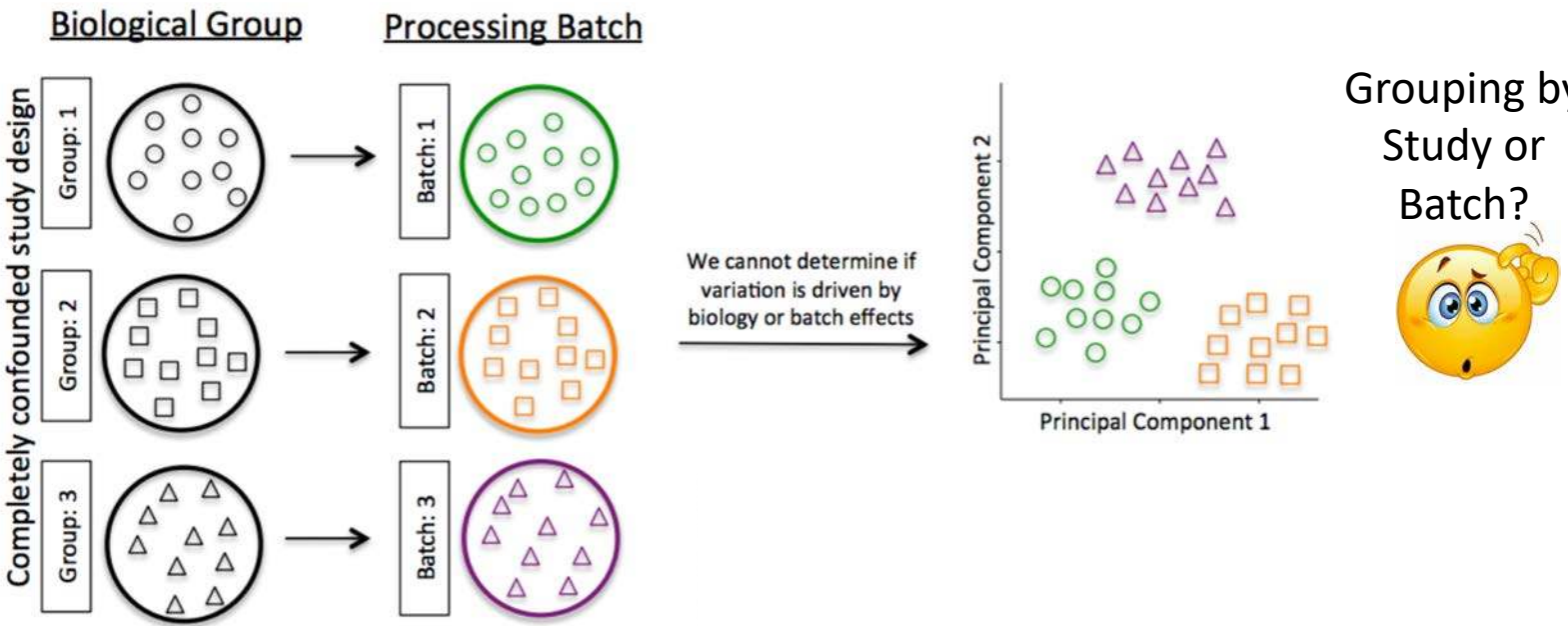
…

Up vs. Down regulated

Avg. expression level

Significance

Avoid Batch Effects

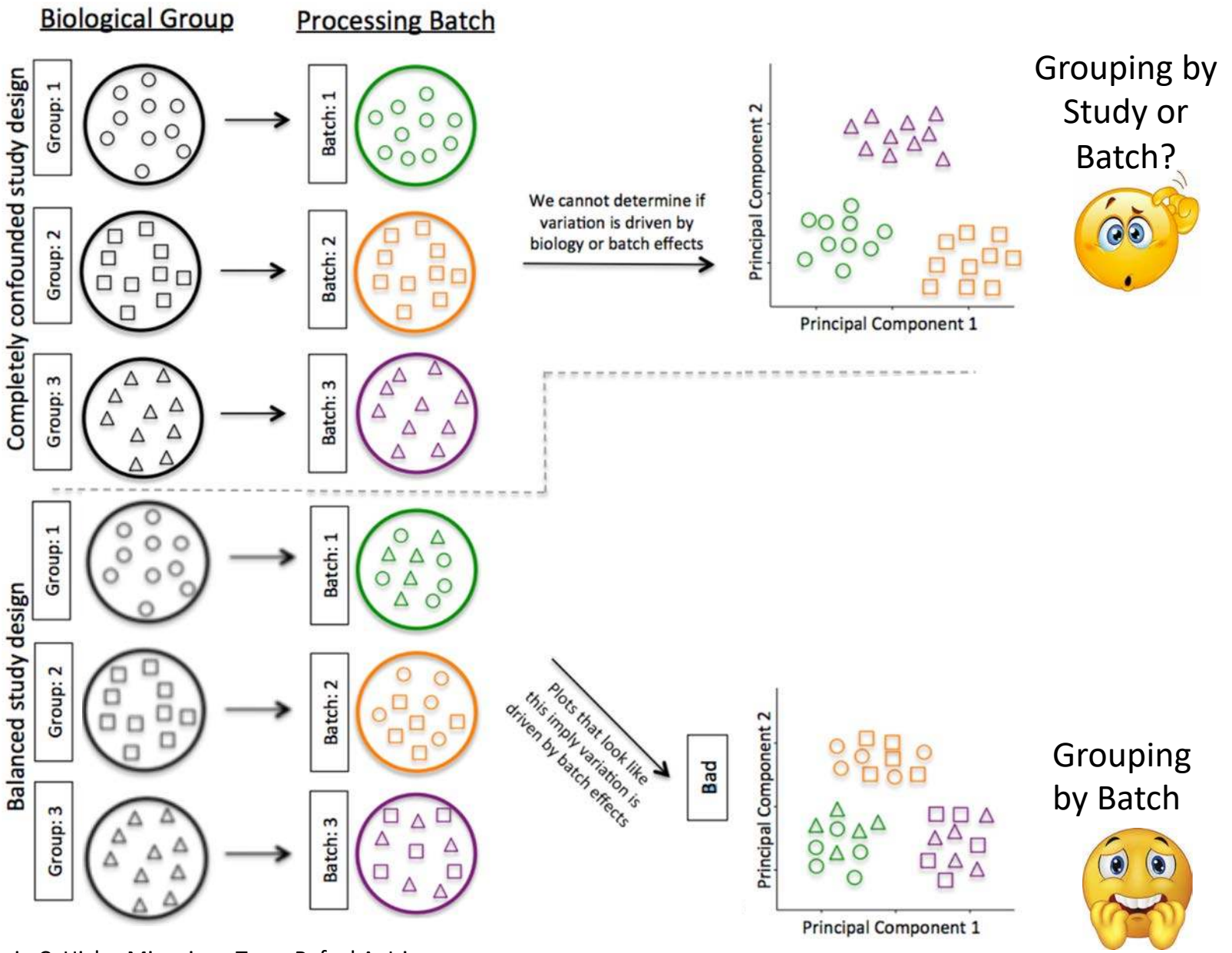


Batch variable types:

- Times and dates
- Technician processing the samples
- Sequencing machine, or flow cell lane (Illumina)

Adapted from: Stephanie C. Hicks, Mingxiang Teng, Rafael A. Irizarry.
https://www.biorxiv.org/content/early/2015/09/04/025528
On the widespread and critical impact of systematic bias and batch effects in single-cell RNA-Seq data.

Avoid Batch Effects



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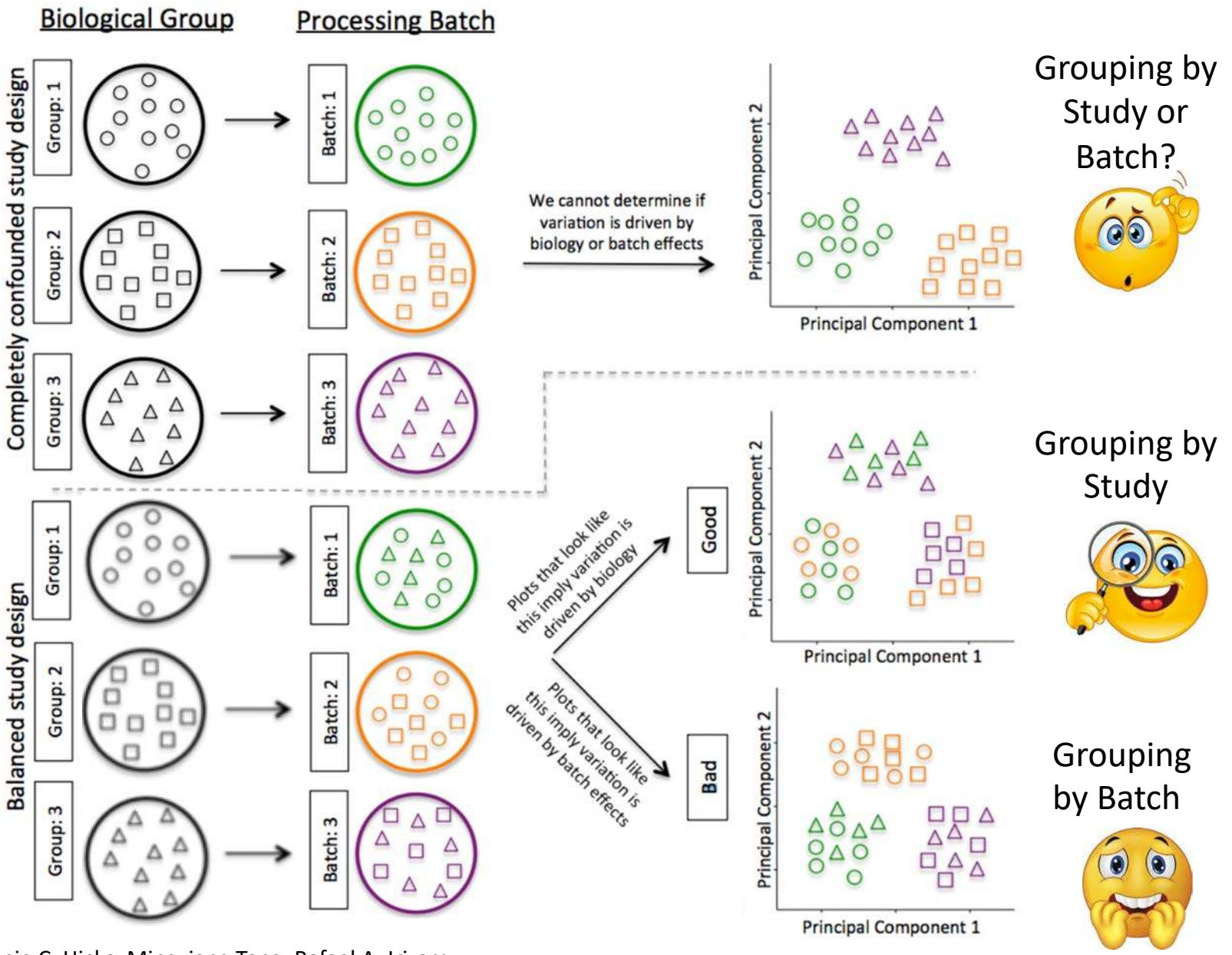
https://www.biorxiv.org/content/early/2015/09/04/025528
On the widespread and critical impact of systematic bias and batch effects in single-cell RNA-Seq data.

(Explore Batch Removal Techniques)

Avoid Batch Effects



Adapted from: Stephanie C. Hicks, Mingxiang Teng, Rafael A. Irizarry.
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On the widespread and critical impact of systematic bias and batch effects in single-cell RNA-Seq data.

(Explore Batch Removal Techniques)

Mouse and human tissue expression more similar within than between species. *?!?!?*

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PNAS

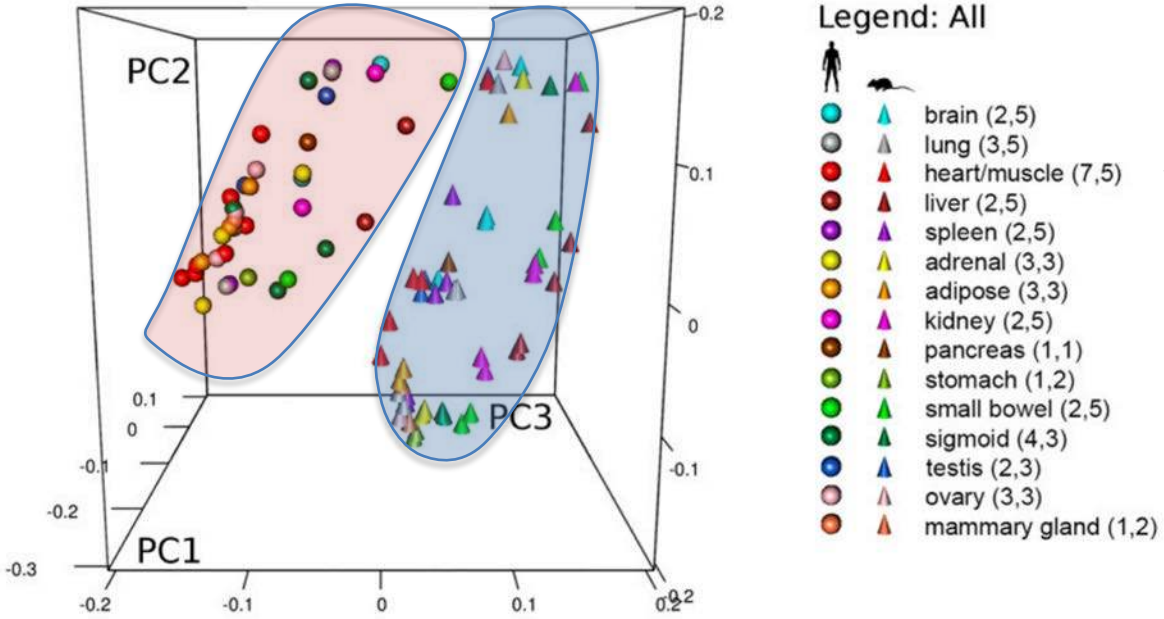
Proceedings of the National Academy of Sciences of the United States of America

Proc Natl Acad Sci U S A. 2014 Dec 2; 111(48): 17224–17229.
Published online 2014 Nov 20. doi: 10.1073/pnas.1413624111
Genetics

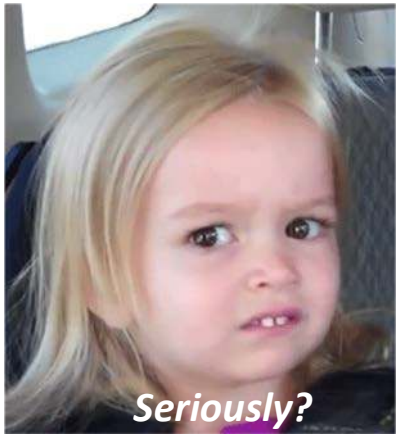
PMCID: PMC4260565
PMID: 25413365

Comparison of the transcriptional landscapes between human and mouse tissues

Shin Lin,[a,b,1] Yiing Lin,[c,1] Joseph R. Nery,[d] Mark A. Urich,[d] Alessandra Breschi,[e,f] Carrie A. Davis,[g] Alexander Dobin,[g] Christopher Zaleski,[g] Michael A. Beer,[h] William C. Chapman,[c] Thomas R. Gingeras,[g,i] Joseph R. Ecker,[d,j,2] and Michael P. Snyder[a,2]



"… our results indicate that for the human–mouse comparison, tissues appear more similar to one another within the same species than to the comparable organs of other species …"



~6 months later

RESEARCH ARTICLE

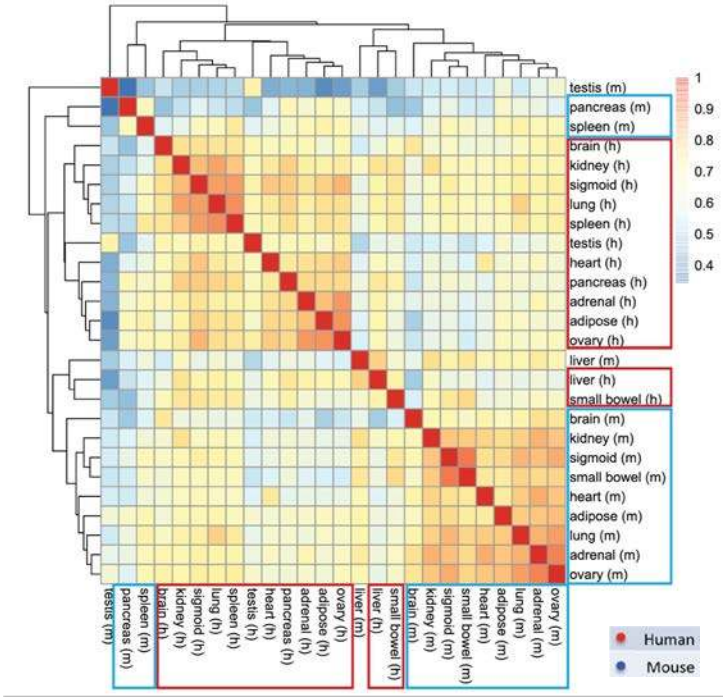
A reanalysis of mouse ENCODE comparative gene expression data [version 1; referees: 3 approved, 1 approved with reservations]

Yoav Gilad, Orna Mizrahi-Man
Department of Human Genetics, University of Chicago, Chicago, IL, 60637, USA

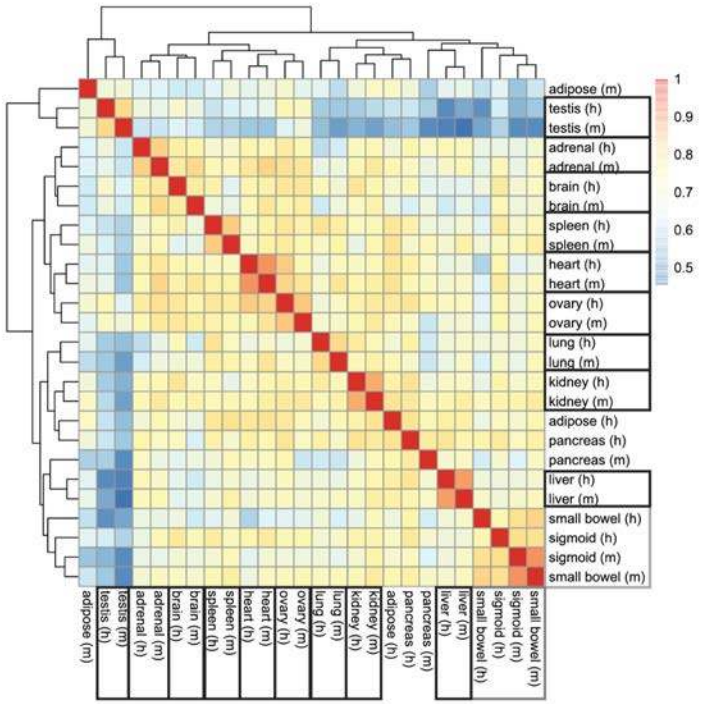
Grouping of samples by Sequencing Batch

D87PMJN1 (run 253, flow cell D2GUAACXX, lane 7)	D87PMJN1 (run 253, flow cell D2GUAACXX , lane 8)	D4LHBFN1 (run 276, flow cell C2HKJACXX , lane 4)	MONK (run 312, flow cell C2GR3ACXX , lane 6)	HWI-ST373 (run 375, flow cell C3172ACXX , lane 7)
heart	adipose	adipose	heart	brain
kidney	adrenal	adrenal	kidney	pancreas
liver	sigmoid colon	sigmoid colon	liver	brain
small bowel	lung	lung	small bowel	spleen
spleen	ovary	ovary	testis	Human
testis		pancreas		Mouse

Yes, tissue expression patterns within species more similar than between species, but doesn't make sense and maybe due to a batch effect?



Post Batch Correction:
Tissue patterns more similar than by species

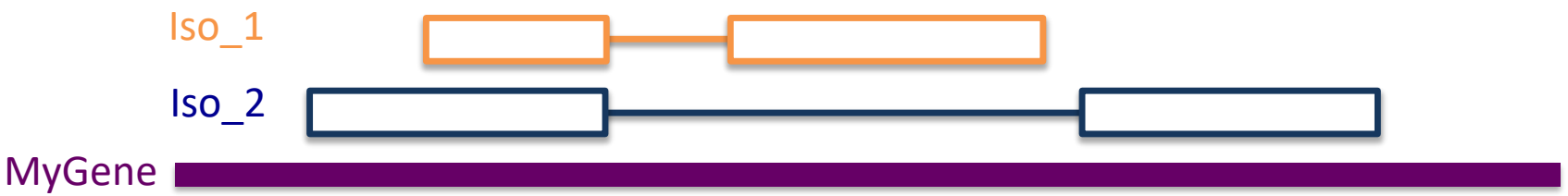


Flavors of Differential Expression Analyses

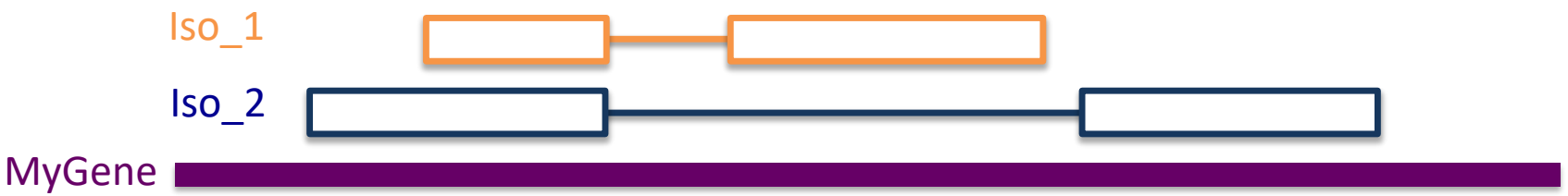
- Transcripts:
  - Differential Transcript Expression (DTE)
  - Differential Transcript Usage (DTU)
  - Differential Exon Usage (DEU)
- Gene:
  - Differential Gene Expression (DGE)
  - Gene Differential Expression (GDE)

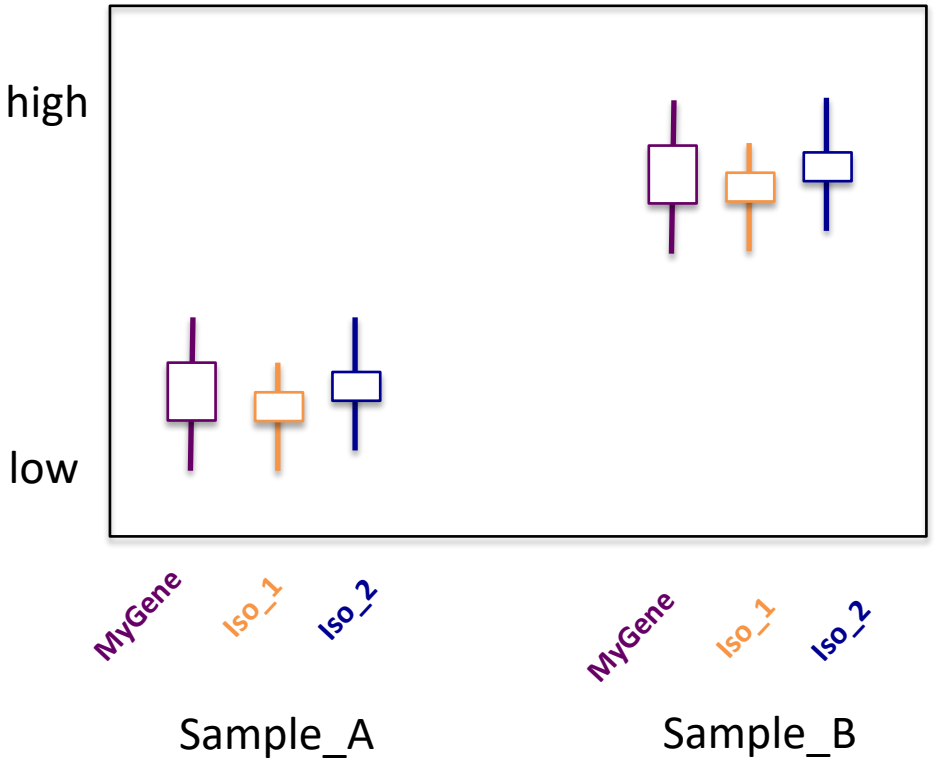
?

Differential Gene Expression (DGE) and Differential Transcript Expression (DTE) (Example 1)



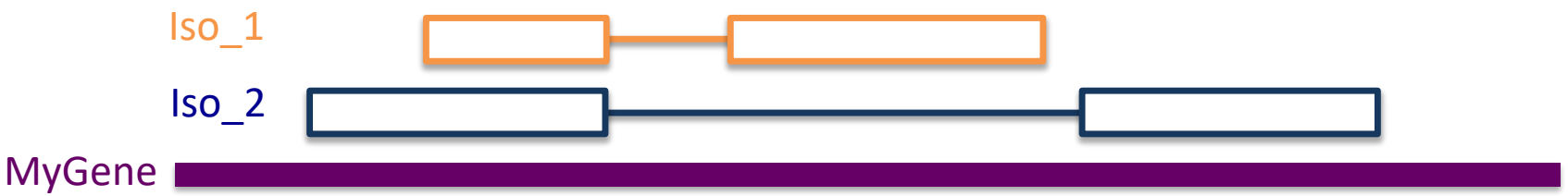
Differential Gene Expression (DGE) and Differential Transcript Expression (DTE) (Example 1)

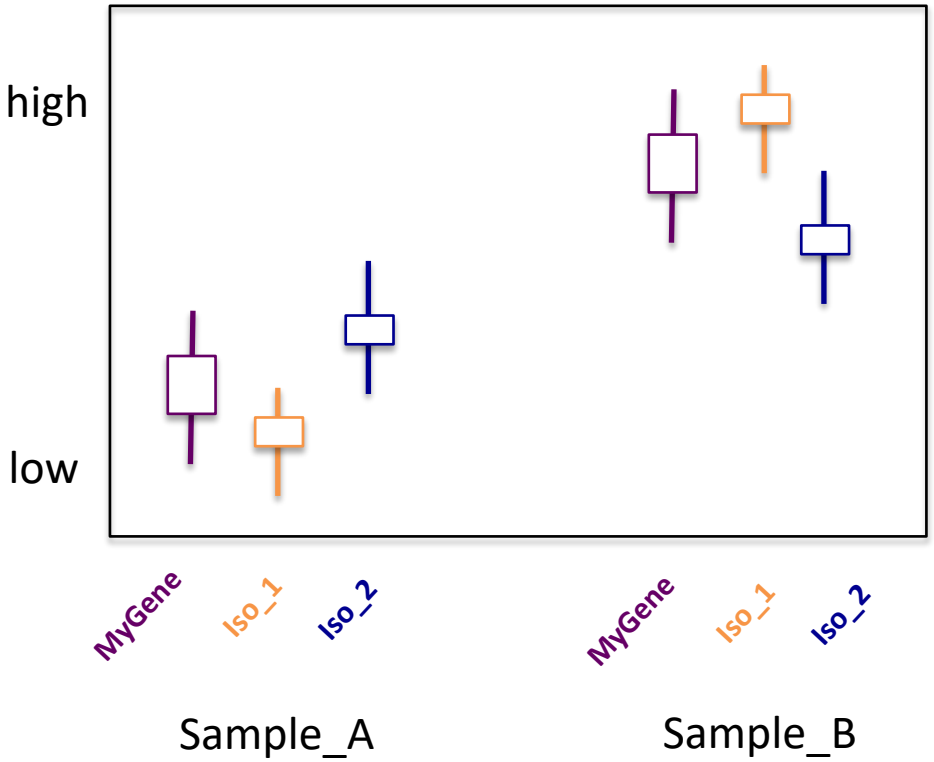




Feature	Diff Expressed?
MyGene	Yes
Iso_1	Yes
Iso_2	Yes
Diff. Transcript Usage ? (eg. Isoform switching)	No

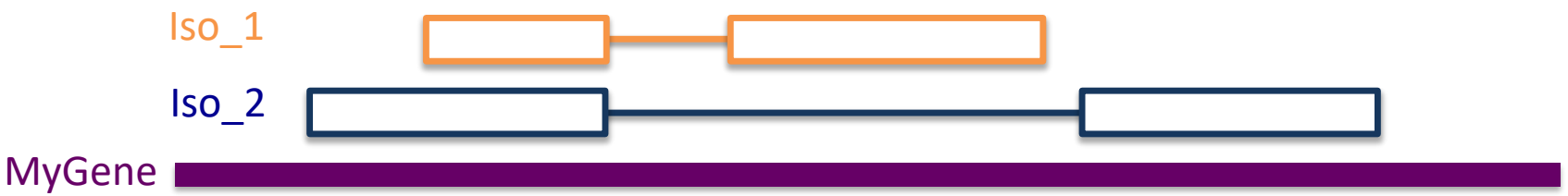
Differential Gene Expression (DGE) and Differential Transcript Expression (DTE) (Example 2)

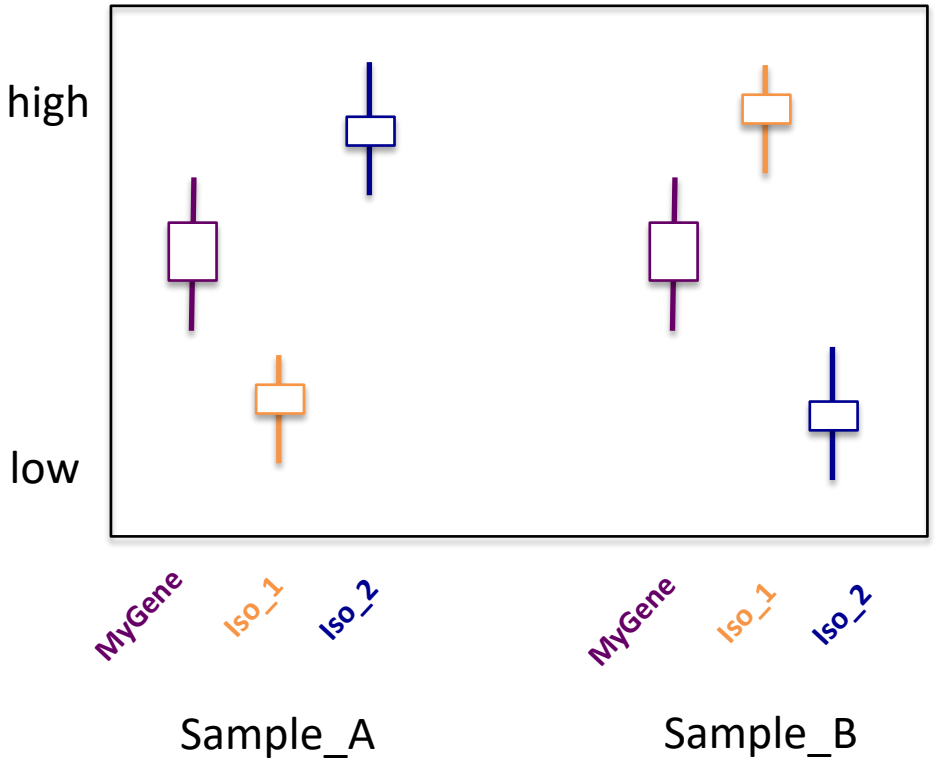




Feature	Diff Expressed?
MyGene	Yes
Iso_1	Yes
Iso_2	Yes
Diff. Transcript Usage ? (eg. Isoform switching)	Yes

Differential Gene Expression (DGE) and Differential Transcript Expression (DTE) (Example 3)



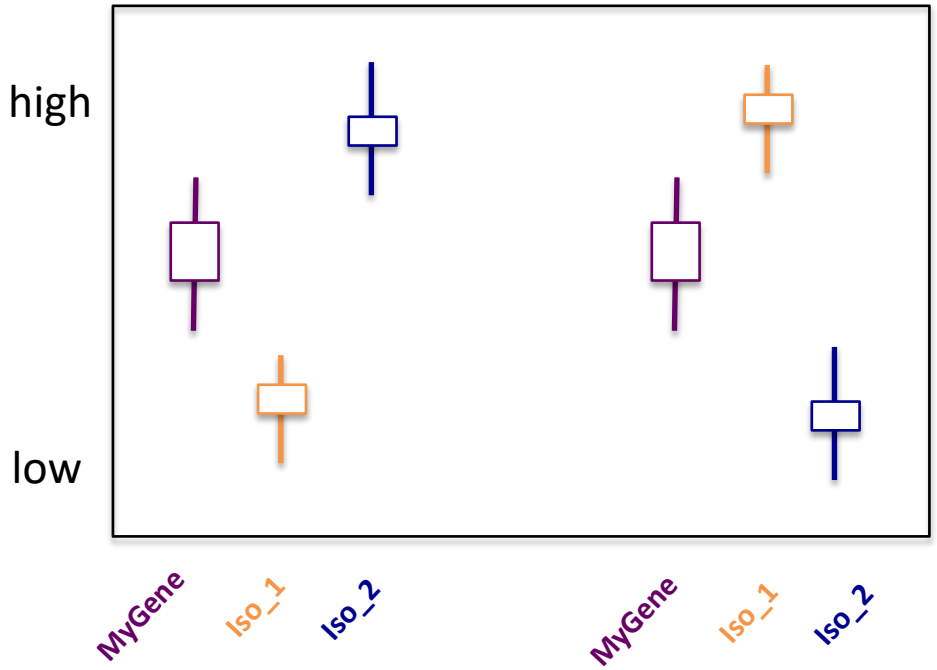


Feature	Diff Expressed?
MyGene	No
Iso_1	Yes
Iso_2	Yes
Diff. Transcript Usage ? (eg. Isoform switching)	Yes

Differential Gene Expression (DGE) and Differential Transcript Expression (DTE) (Example 3)

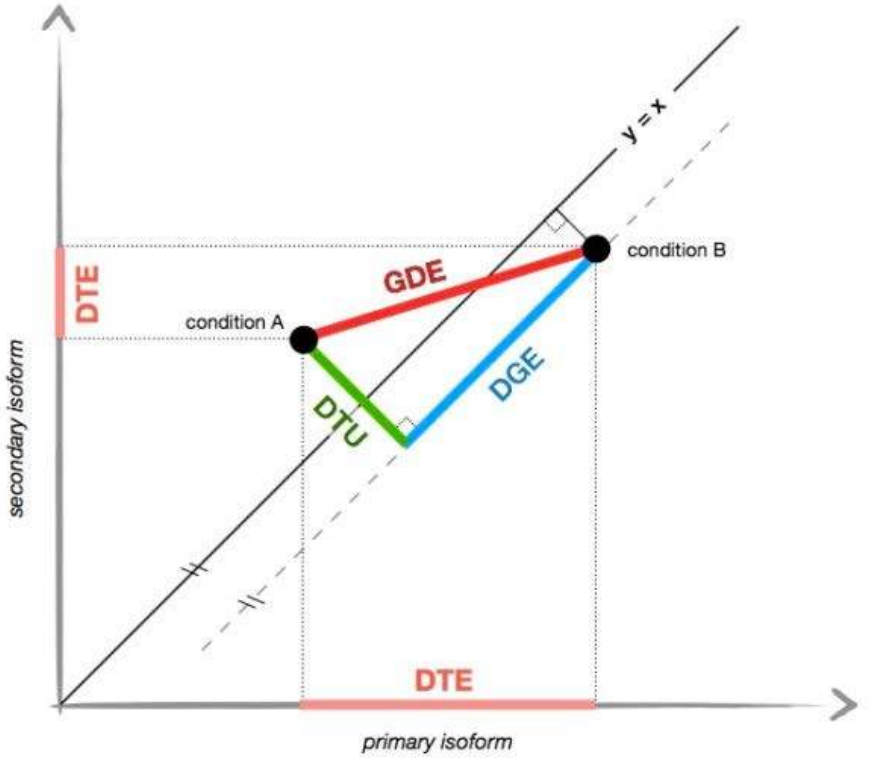
From Gene-level view (DGE): not apparent
From Transcript-level view (GDE): Yes, gene should be acknowledged as having changed.

Prevailing viewpoint:
DTE or DTU -> Gene Diff Expressed (GDE)



Feature	Diff Expressed?
MyGene	No?
Iso_1	Yes
Iso_2	Yes
Diff. Transcript Usage ? (eg. Isoform switching)	Yes

Clarifying view: (DTE or DTU or DGE) as special cases of Gene Differential Expression (DGE)

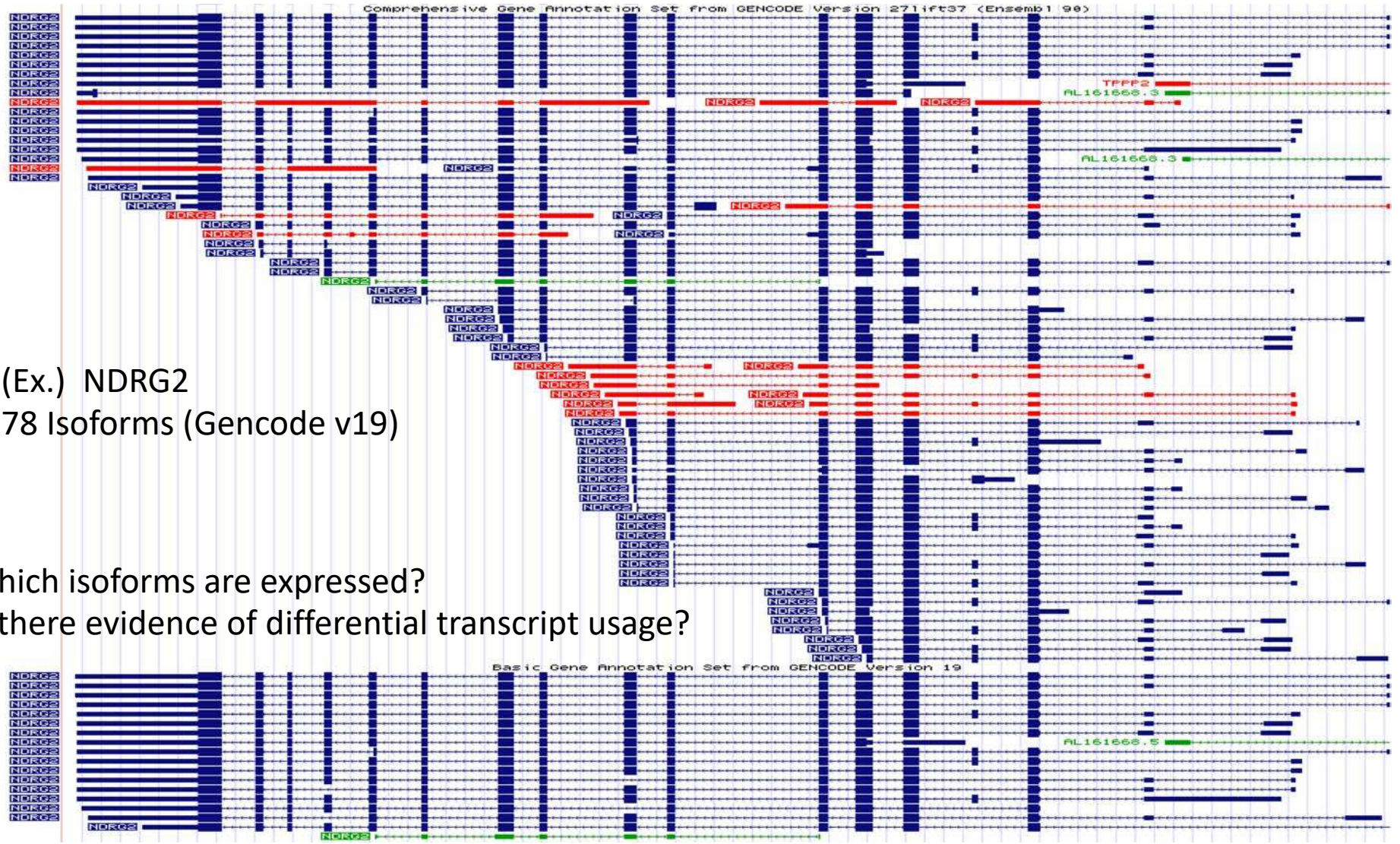


DTE: differential transcript expression
DTU: differential transcript usage
DGE: differential gene expression (gene-level analysis)
GDE: gene differential expression (transcript-level analysis)

Ntranos, Yi, et al., 2018 – see supp.

[See Lior Pachter's blog post: https://liorpachter.wordpress.com/2019/01/07/fast-and-accurate-gene-differential-expression-by-testing-transcript-compatibility-counts/](https://liorpachter.wordpress.com/2019/01/07/fast-and-accurate-gene-differential-expression-by-testing-transcript-compatibility-counts/)

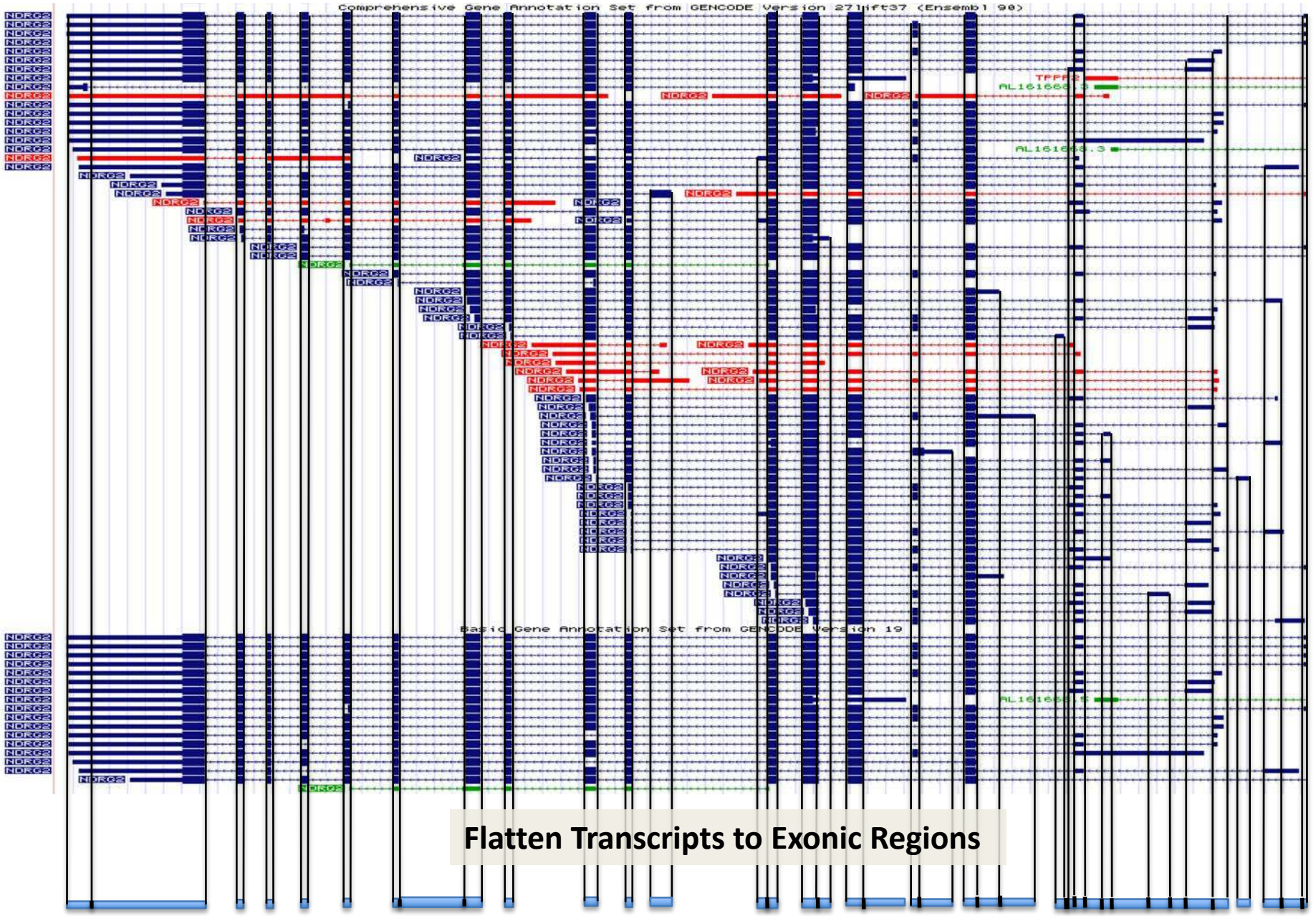
High Confidence Differential Transcript Expression is Difficult to Attain With Many Candidate Isoforms



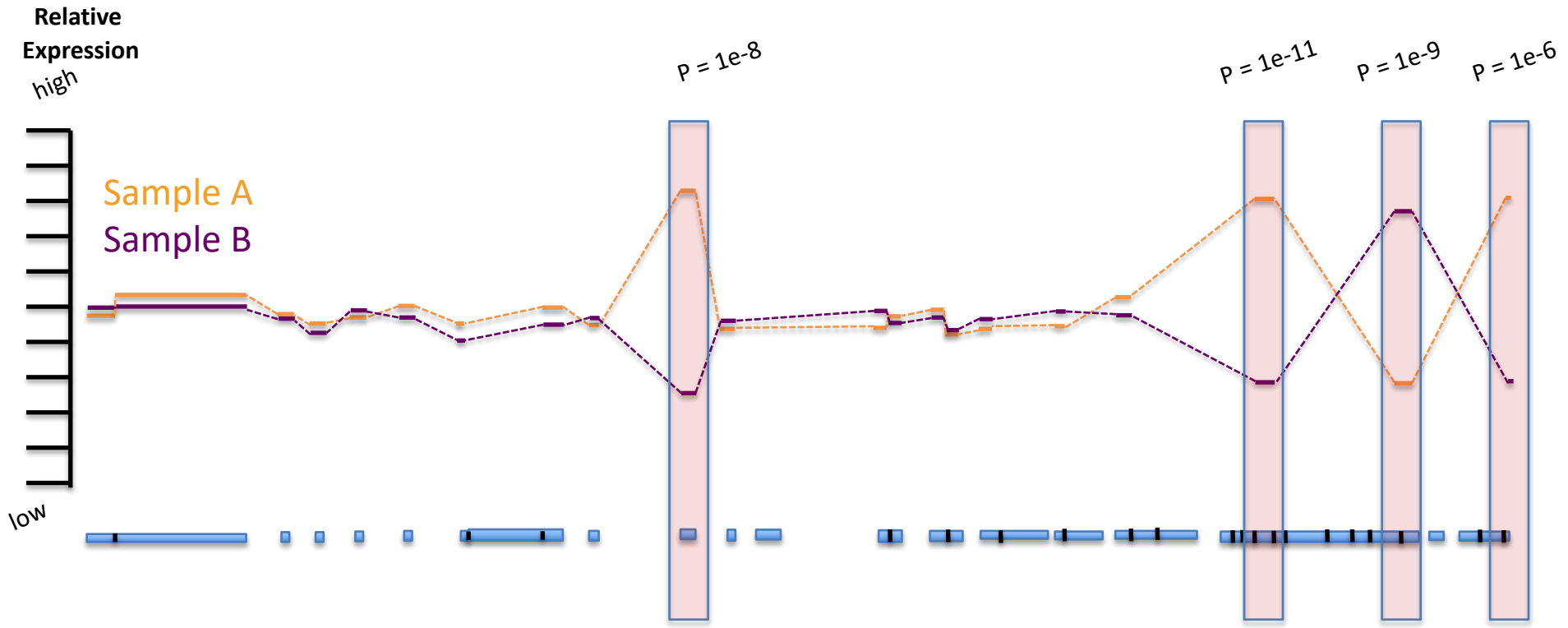
(Ex.) NDRG2
78 Isoforms (Gencode v19)

Which isoforms are expressed?
Is there evidence of differential transcript usage?

Measure Differential Transcript Usage (DTU) via Differential Exon Usage (DEU)



Measure Differential Transcript Usage (DTU) via Differential Exon Usage (DEU)



GENOME RESEARCH
CSHL Press | Journal Home | Subscriptions | eTOC Alerts | BioSupplyNet

Genome Res. 2012 Oct; 22(10): 2008–2017. PMCID: PMC3460195
doi: 10.1101/gr.133744.111

Detecting differential usage of exons from RNA-seq data

Simon Anders,[1,2] Alejandro Reyes,[1] and Wolfgang Huber

Averaged Replicates

Each Replicate

Flattened gene structure:

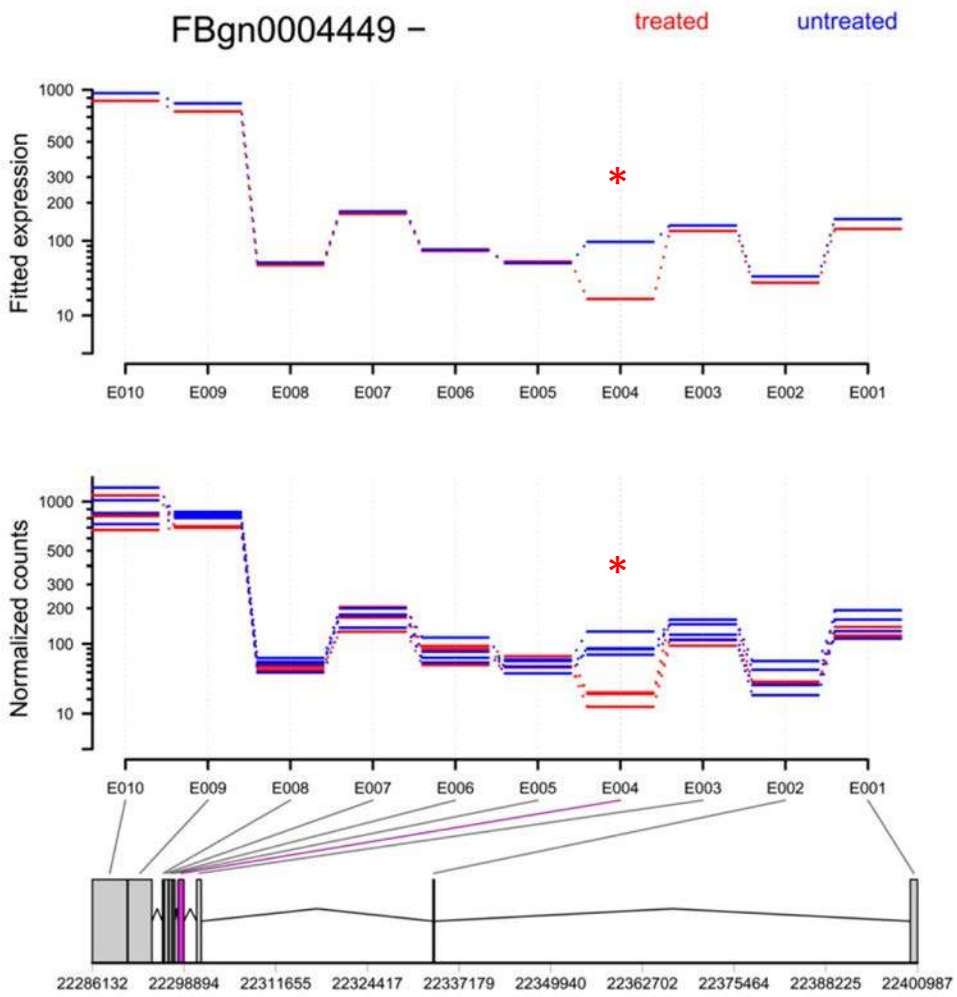
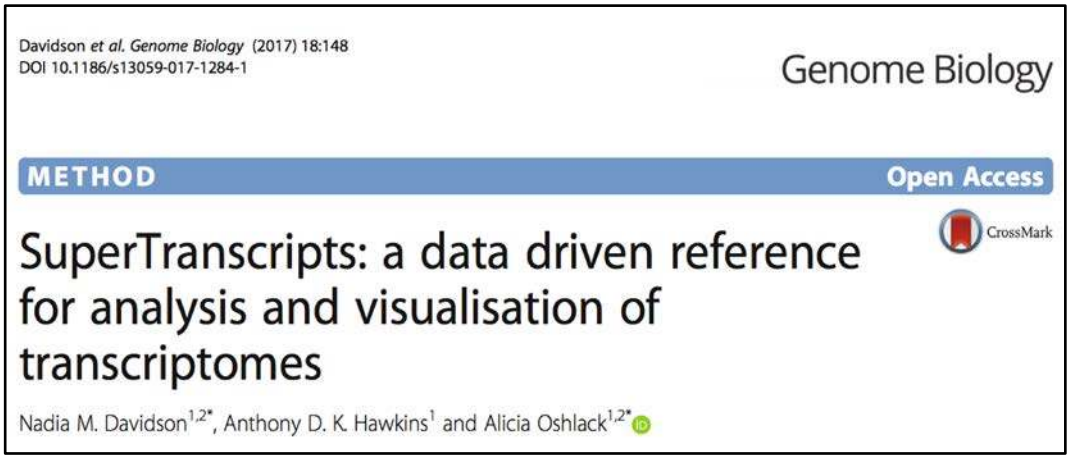


Figure 3. The treatment of knocking down the splicing factor *pasilla* affects the fourth exon (counting bin E004) of the gene *Ten-m* (CG5723). (*Top* panel) Fitted values according to the linear model; (*middle* panel) normalized counts for each sample; (*bottom* panel) flattened gene model. (Red) Data for knockdown samples; (blue) control.

Enabling Differential Transcript Usage Analysis for De novo Transcriptome Assemblies



Davidson *et al. Genome Biology* (2017) 18:148
DOI 10.1186/s13059-017-1284-1

Genome Biology

METHOD

Open Access

SuperTranscripts: a data driven reference for analysis and visualisation of transcriptomes

Nadia M. Davidson[1,2*], Anthony D. K. Hawkins[1] and Alicia Oshlack[1,2*]

Enabling Differential Transcript Usage Analysis for De novo Transcriptome Assemblies

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Genome Biology

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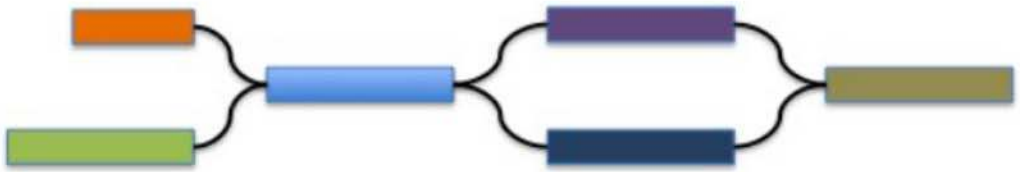
Nadia M. Davidson[1,2*], Anthony D. K. Hawkins[1] and Alicia Oshlack[1,2*]

Transcript splice graph:



Similar method and protocols now integrated into Trinity:
https://github.com/trinityrnaseq/trinityrnaseq/wiki/SuperTranscripts

Enabling Differential Transcript Usage Analysis for De novo Transcriptome Assemblies

Davidson *et al. Genome Biology* (2017) 18:148
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Genome Biology

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Nadia M. Davidson[1,2*], Anthony D. K. Hawkins[1] and Alicia Oshlack[1,2*]

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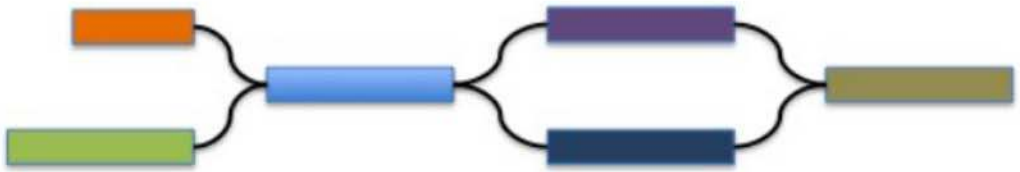


Linearize graph via topological sorting
or graph multiple alignment

SuperTranscript:

DEXseq for DTU,
GATK for Variant Detection

Similar method and protocols now integrated into Trinity:
https://github.com/trinityrnaseq/trinityrnaseq/wiki/SuperTranscripts

Further Pushing the Envelope with RNA-Seq Analysis

Audoux *et al. Genome Biology* (2017) 18:243
DOI 10.1186/s13059-017-1372-2

Genome Biology

METHOD Open Access

DE-kupl: exhaustive capture of biological variation in RNA-seq data through *k*-mer decomposition

Jérôme Audoux[1], Nicolas Philippe[2,3], Rayan Chikhi[4], Mikaël Salson[4], Mélina Gallopin[5], Marc Gabriel[5,6], Jérémy Le Coz[5], Emilie Drouineau[5], Thérèse Commes[1,2] and Daniel Gautheret[5,6*]

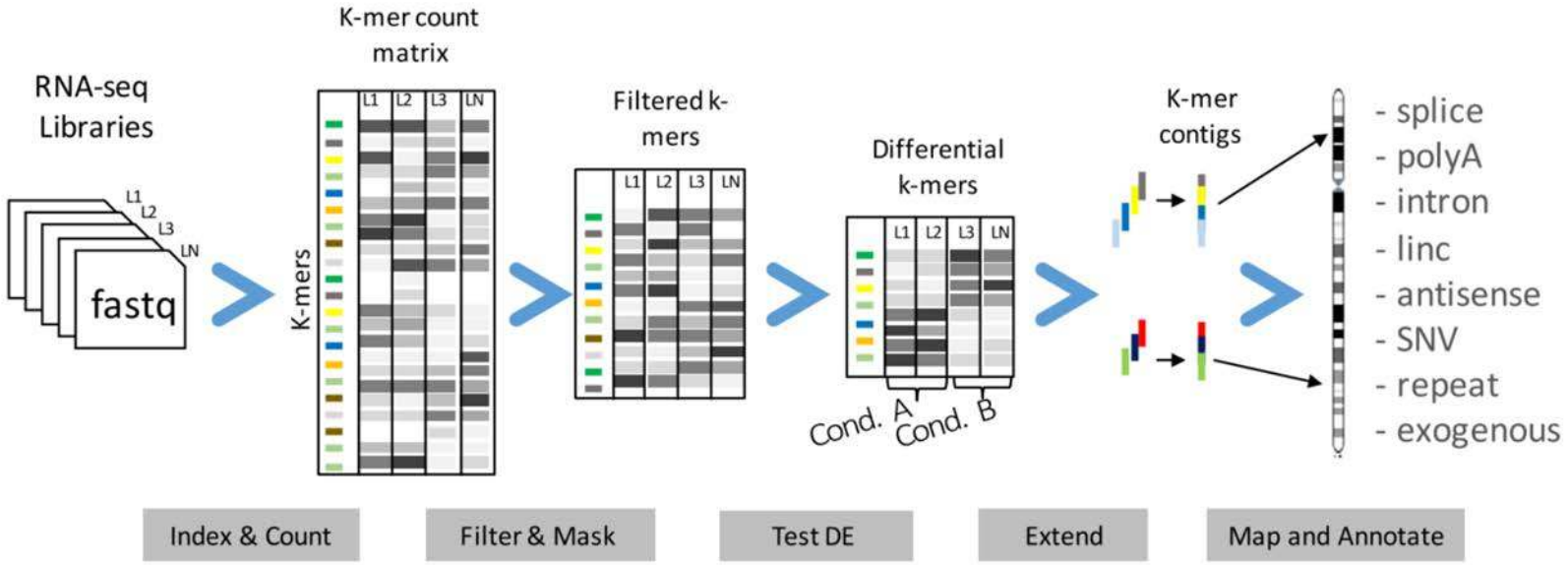


Fig. 4 The DE-kupl pipeline for the discovery and analysis of differentially expressed *k*-mers. First, Jellyfish is applied to count *k*-mers in all libraries. *k*-mers counts are then joined into a count matrix and filtered for low recurrence and matching to the reference transcriptome. Normalization factors are computed from raw *k*-mer counts and the differential expression procedure is applied. Finally, overlapping differentially expressed *k*-mers are extended into contigs and annotated based on their alignment to the reference and overlap with annotated genes

Instead of Gene, Transcript, or Exon Counts (or expression levels…
Can we use the newly defined Transcript Equivalence Classes for DE?

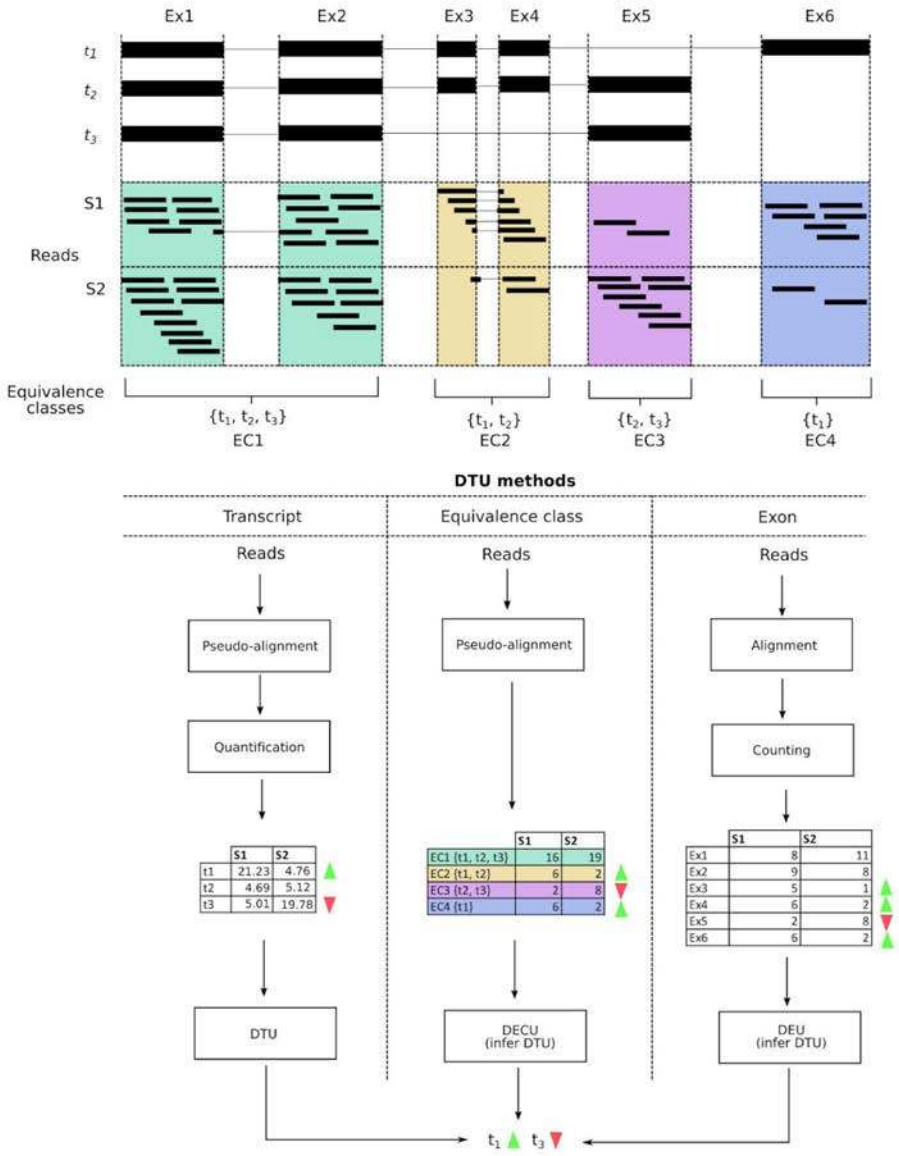


Fig. from Marek Cmero, Nadia M Davidson, Alicia Oshlack bioRxiv, Dec. 2018

Again, see Lior Pachter's blog post: https://liorpachter.wordpress.com/2019/01/07/fast-and-accurate-gene-differential-expression-by-testing-transcript-compatibility-counts/

Which feature to choose for DE analysis?

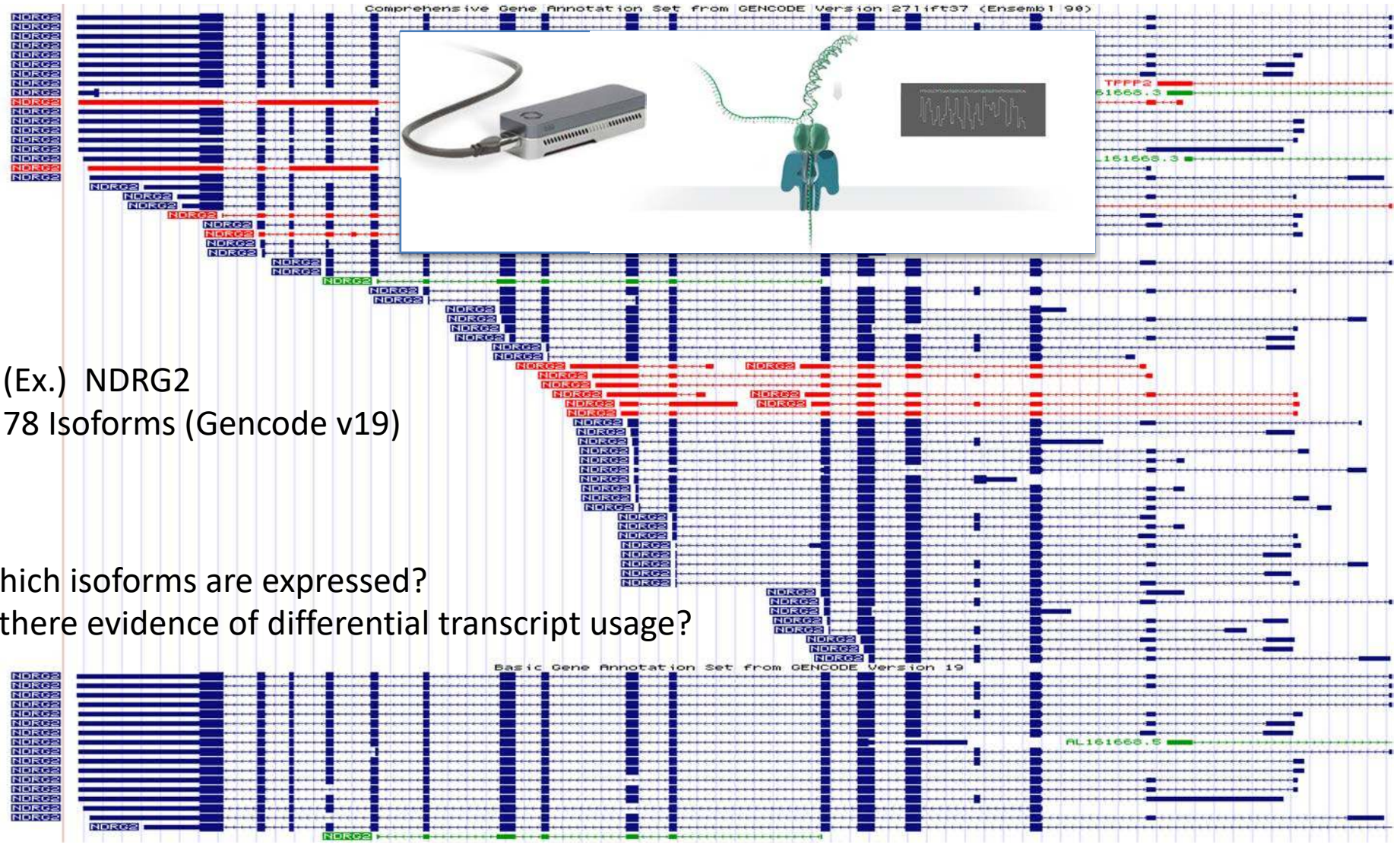
Feature	Pro	Con
Gene	Simplest, easily interpretable	Can hide evidence for DTU (iso switching)
Transcript	Illuminates the biological targets of interest.	Read mapping uncertainty among many isoforms confounding identification.
Exon	Detect evidence of DTU leveraging many isoform structures, and pinpoint exonic regions of interest.	May not easily identify specific isoforms of interest in shared exon situations.
Equivalence Class	Very Fast, not requiring read alignment nor sophisticated abundance estimation.	Biological interpretability can be challenging.

Routine

Semi-specialized

Burgeoning

Too complex… don’t guess from short reads, use long reads.



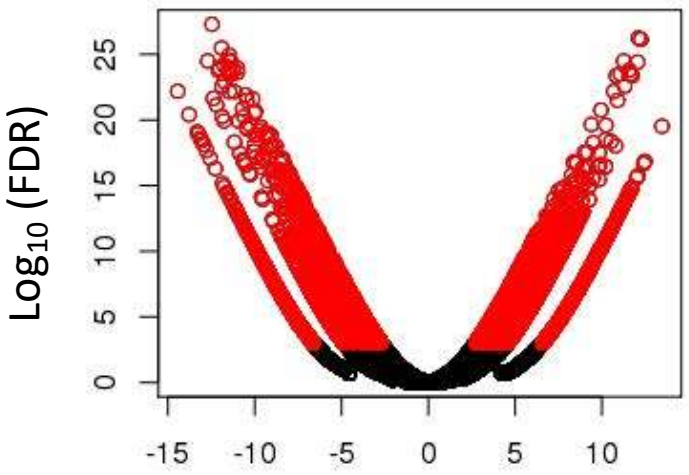
(Ex.) NDRG2
78 Isoforms (Gencode v19)

Which isoforms are expressed?
Is there evidence of differential transcript usage?

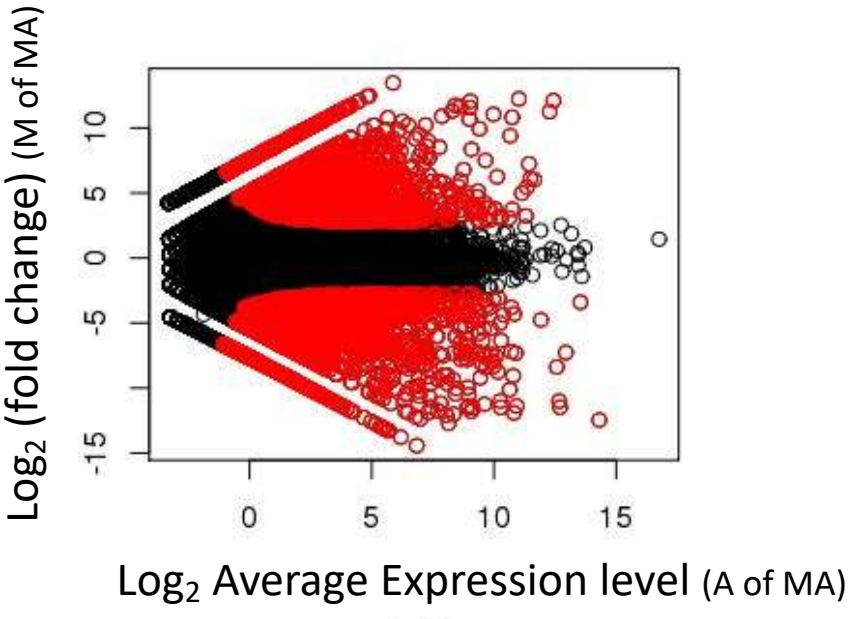
Visualization of DE results and Expression Profiling

Plotting Pairwise Differential Expression Data

Volcano plot
(fold change vs. significance)

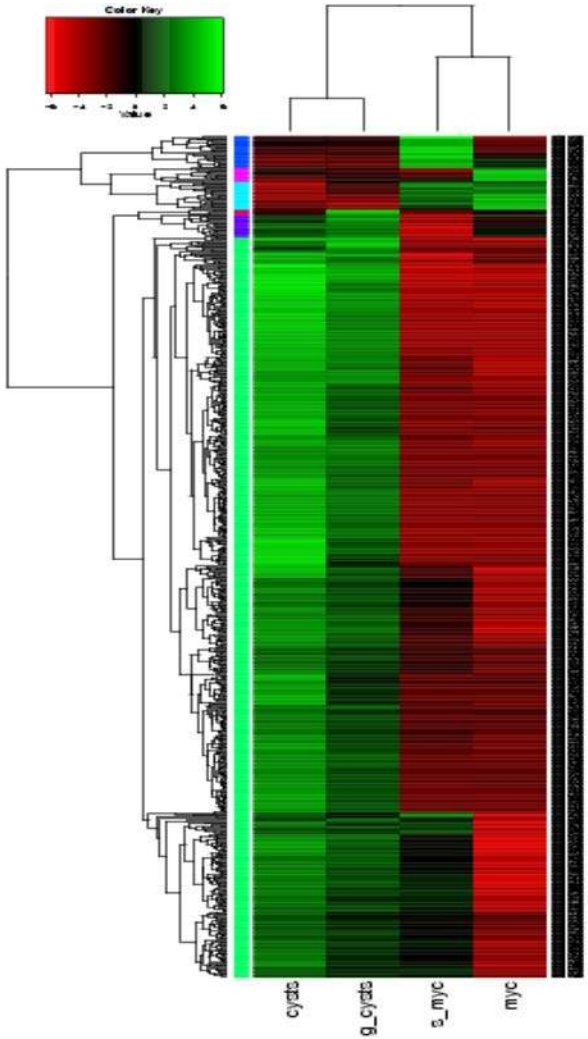


MA plot
(abundance vs. fold change)



Significantly differently expressed transcripts have FDR <= 0.001
(shown in red)

Comparing Multiple Samples



Heatmaps provide an effective tool for navigating differential expression across multiple samples.

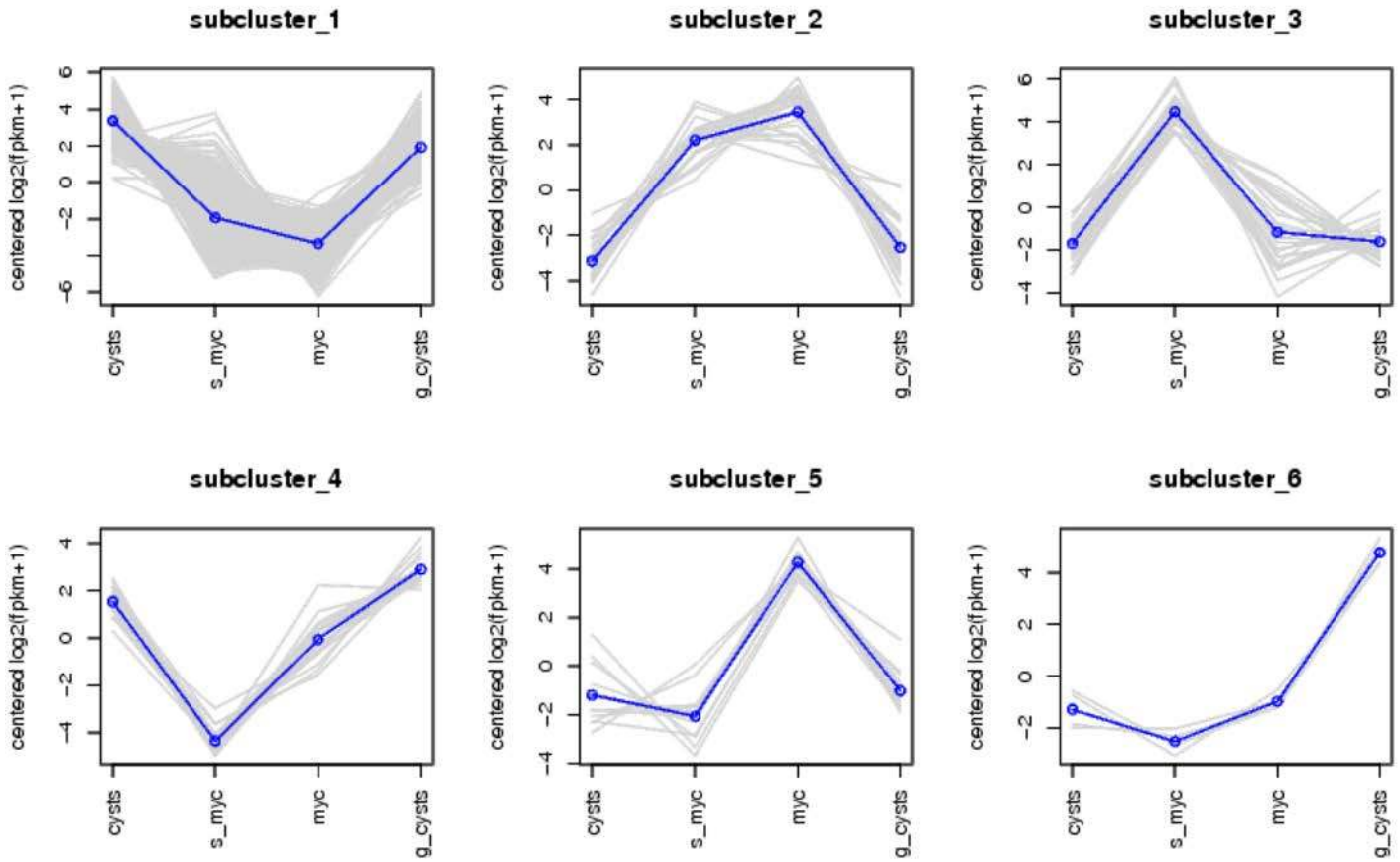
Clustering can be performed across both axes:

-cluster transcripts with similar expression patters.

-cluster samples according to similar expression values among transcripts.

Examining Patterns of Expression Across Samples

Can extract clusters of transcripts and examine them separately.



Transcript Functional Annotation

GGAGCTGGAGGCCCCCAGGCAACTACACCGTCCACGTACCCAGAGGGGCTGGGCCCTCCC
ACCAGAGACCACGCCCTGGTGTGCCTTAGGGGCCCTGGTTTGTTAGTCTCTGAGTGTGCA
GTTGCTGCACATGGGGCCCTGGCGCTTGCTGCACCAACTTCCTGTTGGGCCCGTGGTCCT
TGGAGGCATGCAGTTCAGCAGACAGTGACTCAGCCATCCACCCAACATGCGGAACGTGTC
TCTTCTGCAGGTCCCGGTCCACAGCAGGATTCCCCCTCTGTGAAAAGGCACGCTGATCTG
TCTGGA TCGAC
TCTCCC TCCCA
AAAGAC CCTGG
GGCTTG CCTAA
TGACCT TGCTG
GAAAAG CAGCC
TTGTCA TTCCA
GGAAGCACATAATTGAAGGACTGAAAGCGTCCCTGGAGCGGCTGCAGCTGGAGTACGTGG
ATGTGGTTTTTGCCAACCGCCCAGACCCCAACACGCCCATGGAAGAGACCGTGCGGGCCA
TGACCCATGTCATCAACCAGGGGATGGCCATGTACTGGGGCACATCACGCTGGAGCTCCA
TGGAGATCATGGAGGCCTACTCGGTGGCTCGGCAGTTCAACCTGATCCCGCCCATCTGCG
AGCAAGCGGAATATCACATGTTCCAGAGGGAGAAGGTGGAGGTCCAGCTGCCAGAGCTGT
TCCACAAGATAGGAGTAGGTGCCATGACCTGGTCCCCTCTGGCGTGCGGCATCGTCTCAG
GGAAGTATGACAGCGGGATCCCACCCTACTCCAGAGCCTCCCTGAAGGGCTACCAGTGGT
TGAAGGACAAGATCCTGAGTGAGGAGGGTCGCCGCCAGCAGGCCAAGCTGAAGGAACTGC
AGGCCATTGCCGAACGCCTGGGCTGCACCCTACCCCAGCTGGCCATAGCCTGGTGCCTGA
GGAATGAGGGTGTCAGCTCCGTGCTTCTGGGTGCTTCCAATGCAGAACAACTTATGGAGA

Can we gather hints of biological function from sequence?

Methods used to predict function from sequence

- Sequence homology

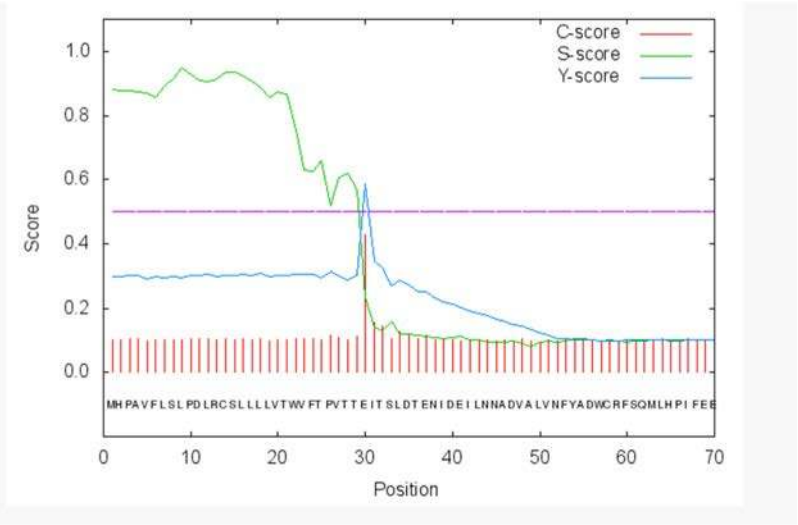
Searching protein database for sequence similarity

```
Query           THVHRPYNEHKSLSGTARYMSINTHLGREQSRRDDLESMGHVFMYFLRGSLPW--QGLKA
                T    P +  K   GT  Y S + HLG    RR DLE +G      L   LPW  Q L A
Database Match  TGDFKP-DPKKMHNGTIEYTSRDAHLG-VPTRRADLEILGYNLIEWLGAELPWVTQKLLA
```

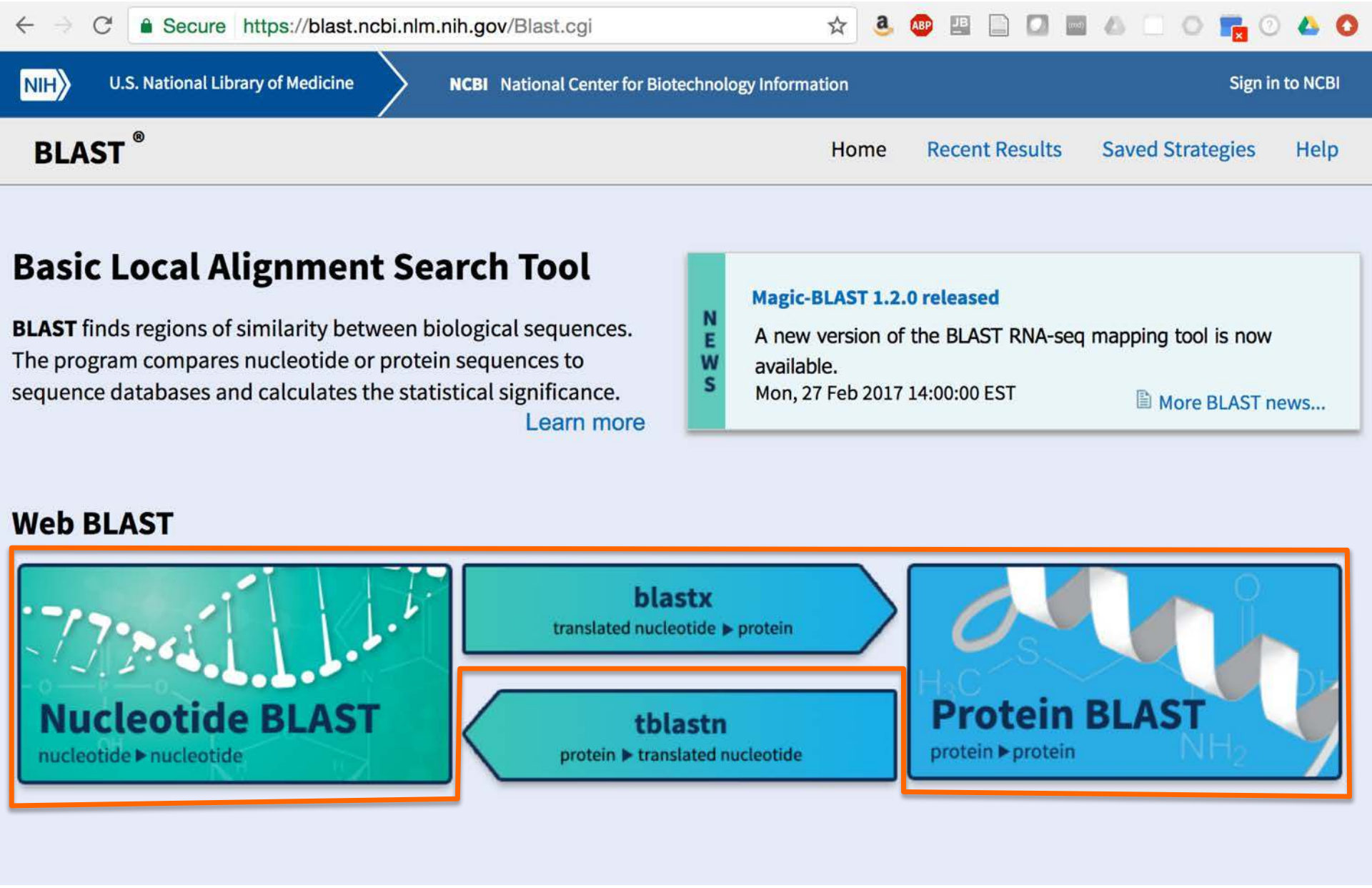
- Sequence composition

Predict functions of sequence using machine learning methods for pattern recognition.

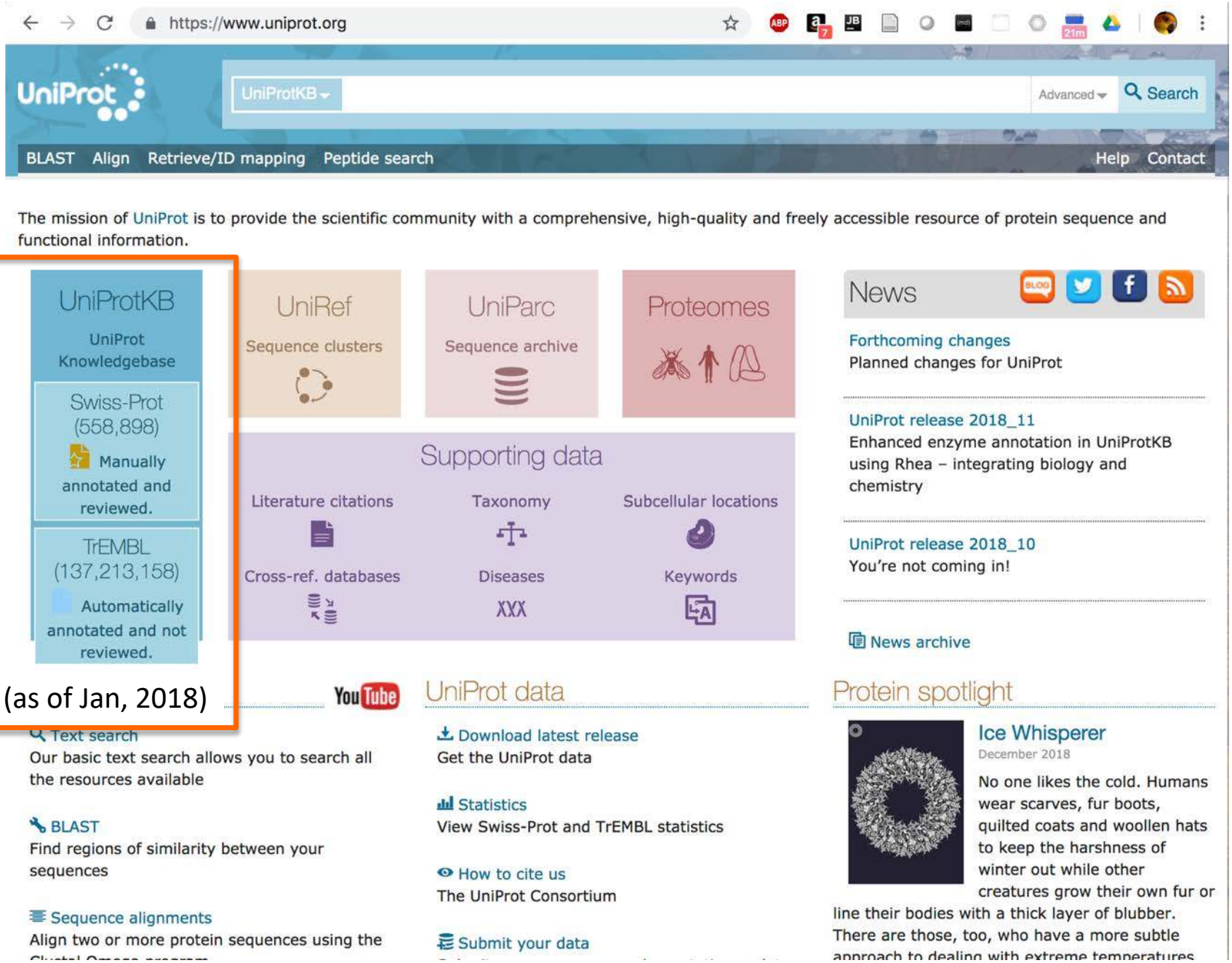
- Neural Networks
- Hidden Markov Models



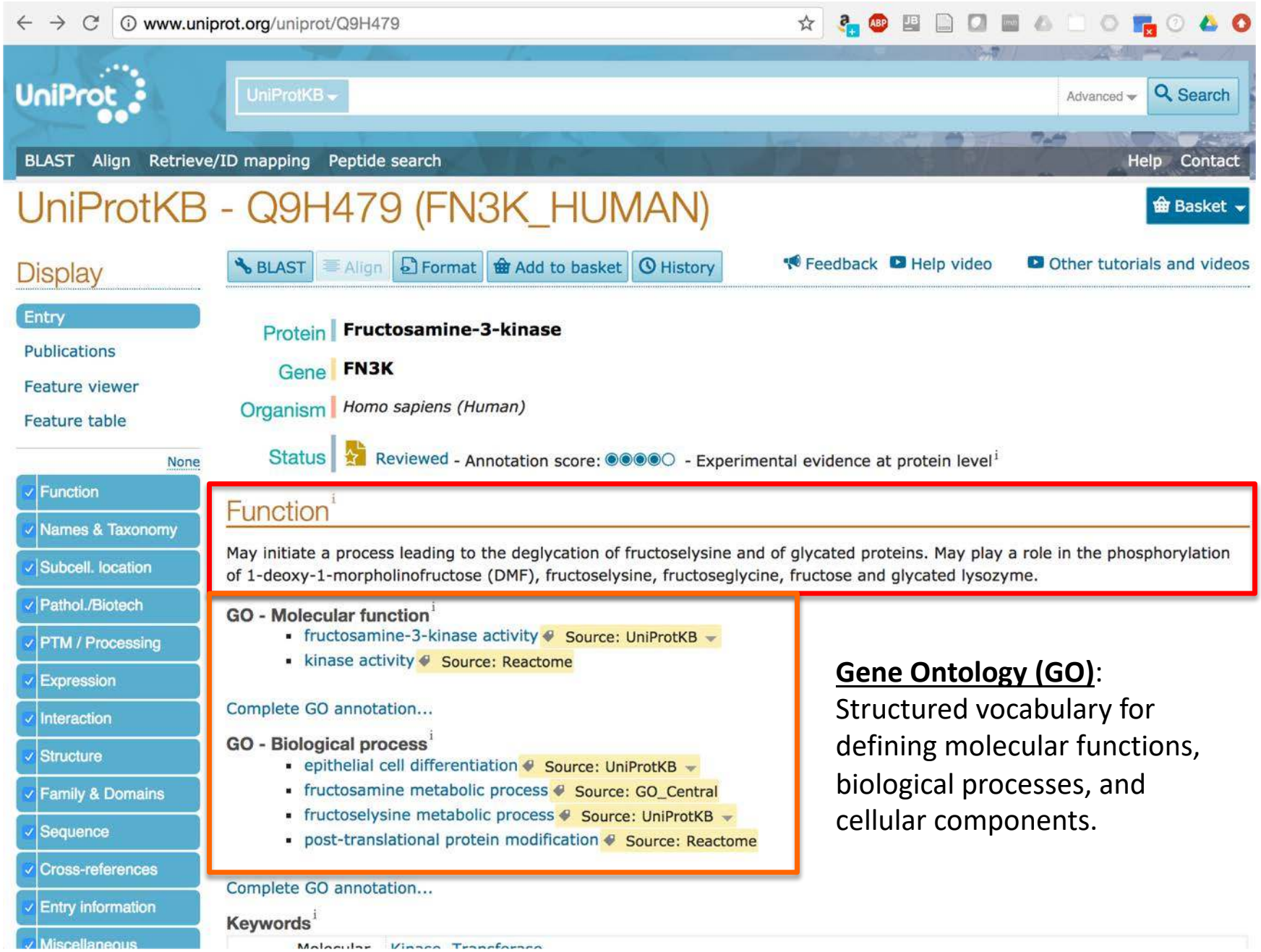
Use BLAST to search for sequence similarity to known proteins



The Swiss-Prot database is a valuable source of proteins with known functions



Example of a Swiss-Prot Record



Gene Ontology (GO):
Structured vocabulary for defining molecular functions, biological processes, and cellular components.

No significant sequence similarity… What else?

GGAGCTGGAGGCCCCCAGGCAACTACACCGTCCACGTACCCAGAGGGGCTGGGCCCTCCC
ACCAGAGACCACGCCCTGGTGTGCCTTAGGGGCCCTGGTTTGTTAGTCTCTGAGTGTGCA
GTTGCTGCACATGGGGCCCTGGCGCTTGCTGCACCAACTTCCTGTTGGGCCCGTGGTCCT
TGGAGGCATGCAGTTCAGCAGACAGTGACTCAGCCATCCACCCAACATGCGGAACGTGTC
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TGACCCATGTCATCAACCAGGGGATGGCCATGTACTGGGGCACATCACGCTGGAGCTCCA
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GGAAGTATGACAGCGGGATCCCACCCTACTCCAGAGCCTCCCTGAAGGGCTACCAGTGGT
TGAAGGACAAGATCCTGAGTGAGGAGGGTCGCCGCCAGCAGGCCAAGCTGAAGGAACTGC
AGGCCATTGCCGAACGCCTGGGCTGCACCCTACCCCAGCTGGCCATAGCCTGGTGCCTGA
GGAATGAGGGTGTCAGCTCCGTGCTTCTGGGTGCTTCCAATGCAGAACAACTTATGGAGA

Is there an ORF for a potential Coding Region?

GGAGCTGGAGGCCCCCAGGCAACTACACCGTCCACGTACCCAGAGGGGCTGGGCCCTCCC
ACCAGAGACCACGCCCTGGTGTGCCTTAGGGGCCCTGGTTTGTTAGTCTCTGAGTGTGCA
GTTGCTGCACATGGGGCCCTGGCGCTTGCTGCACCAACTTCCTGTTGGGCCCGTGGTCCT
TGGAGGCATGCAGTTCAGCAGACAGTGACTCAGCCATCCACCCAACATGCGGAACGTGTC
TCTTCTGCAGGTCCCGGTCCACAGCAGGATTCCCCCTCTGTGAAAAGGCACGCTGATCTG
TCTGGATAAGTGTGGCCGGCCCCATGTATCCGGAATCAACCACGGGGTCCCCAGCTCGAC
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GGCTTGGAACATGGGTGACCTTCGGGGGCCAGATCACGGATGAGATGGCAGAGCACCTAA
TGACCTTGGCCTACGATAATGGCATCAACCTGTTCGATACGGCGGAGGTCTACGCTGCTG
GAAAAGCTGAAGTGGTATTAGGGAACATCATTAAGAAGAAGGGATGGAGACGGTCCAGCC
TTGTCATCACCACCAAGATCTTCTGGGGTGGAAAAGCGGAGACTGAGAGAGGCCTTTCCA
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TGACCCATGTCATCAACCAGGGGATGGCCATGTACTGGGGCACATCACGCTGGAGCTCCA
TGGAGATCATGGAGGCCTACTCGGTGGCTCGGCAGTTCAACCTGATCCCGCCCATCTGCG
AGCAAGCGGAATATCACATGTTCCAGAGGGAGAAGGTGGAGGTCCAGCTGCCAGAGCTGT
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GGAAGTATGACAGCGGGATCCCACCCTACTCCAGAGCCTCCCTGAAGGGCTACCAGTGGT
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AGGCCATTGCCGAACGCCTGGGCTGCACCCTACCCCAGCTGGCCATAGCCTGGTGCCTGA
GGAATGAGGGTGTCAGCTCCGTGCTTCTGGGTGCTTCCAATGCAGAACAACTTATGGAGA

Is there an ORF for a potential Coding Region?

GGAGCTGGAGGCCCCCAGGCAACTACACCGTCCACGTACCCAGAGGGGCTGGGCCCTCCC
ACCAGAGACCACGCCCTGGTGTGCCTTAGGGGCCCTGGTTTGTTAGTCTCTGAGTGTGCA
GTTGCTGCAC**ATGGGGCCCTGGCGCTTGCTGCACCAACTTCCTGTTGGGCCCGTGGTCCT**
TGGAGGCATGCAGTTCAGCAGACAGTGACTCAGCCATCCACCCAACATGCGGAACGTGTC
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TCTGGATAAGTGTGGCCGGCCCCATGTATCCGGAATCAACCACGGGGTCCCCAGCTCGAC
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AGGCCATTGCCGAACGCCTGGGCTGCACCCTACCCCAGCTGGCCATAGCCTGGTGCCTGA
GGAATGAGGGTGTCAGCTCCGTGCTTCTGGGTGCTTCCAATGCAGAACAACTTATGGAGA

Find all ORFs using ORFfinder

Secure https://www.ncbi.nlm.nih.gov/orffinder/

NCBI Resources How To Sign in to NCBI

ORFfinder PubMed Search

Open Reading Frame Finder

ORF finder searches for open reading frames (ORFs) in the DNA sequence you enter. The program returns the range of each ORF, along with its protein translation. Use ORF finder to search newly sequenced DNA for potential protein encoding segments, verify predicted protein using newly developed SMART BLAST or regular BLASTP.

This web version of the ORF finder is limited to the subrange of the query sequence up to 50 kb long. Stand-alone version, which doesn't have query sequence length limitation, is available for Linux x64.

Examples (click to set values, then click Submit button) :

- NC_011604 Salmonella enterica plasmid pWES-1; genetic code: 11; 'ATG' and alternative initiation codons; minimal ORF length: 300 nt
- NM_000059; genetic code: 1; start codon: 'ATG only'; minimal ORF length: 150 nt

Enter Query Sequence

Enter accession number, gi, or nucleotide sequence in FASTA format:

```
GGAGCTGGAGGCCCCCAGGCAACTACACCGTCCACGTACCCAGAGGGGCTGGGCCCTCCC
ACCAGAGACCACGCCCTGGTGTGCCTTAGGGGCCCTGGTTTGTTAGTCTCTGAGTGTGCA
GTTGCTGCACATGGGGCCCTGGCGCTTGCTGCACCAACTTCCTGTTGGGCCCGTGGTCCT
TGGAGGCATGCAGTTCAGCAGACAGTGACTCAGCCATCCACCCAACATGCGGAACGTGTC
TCTTCTGCAGGTCCCGGTCCACAGCAGGATTCCCCCTCTGTGAAAAGGCACGCTGATCTG
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```
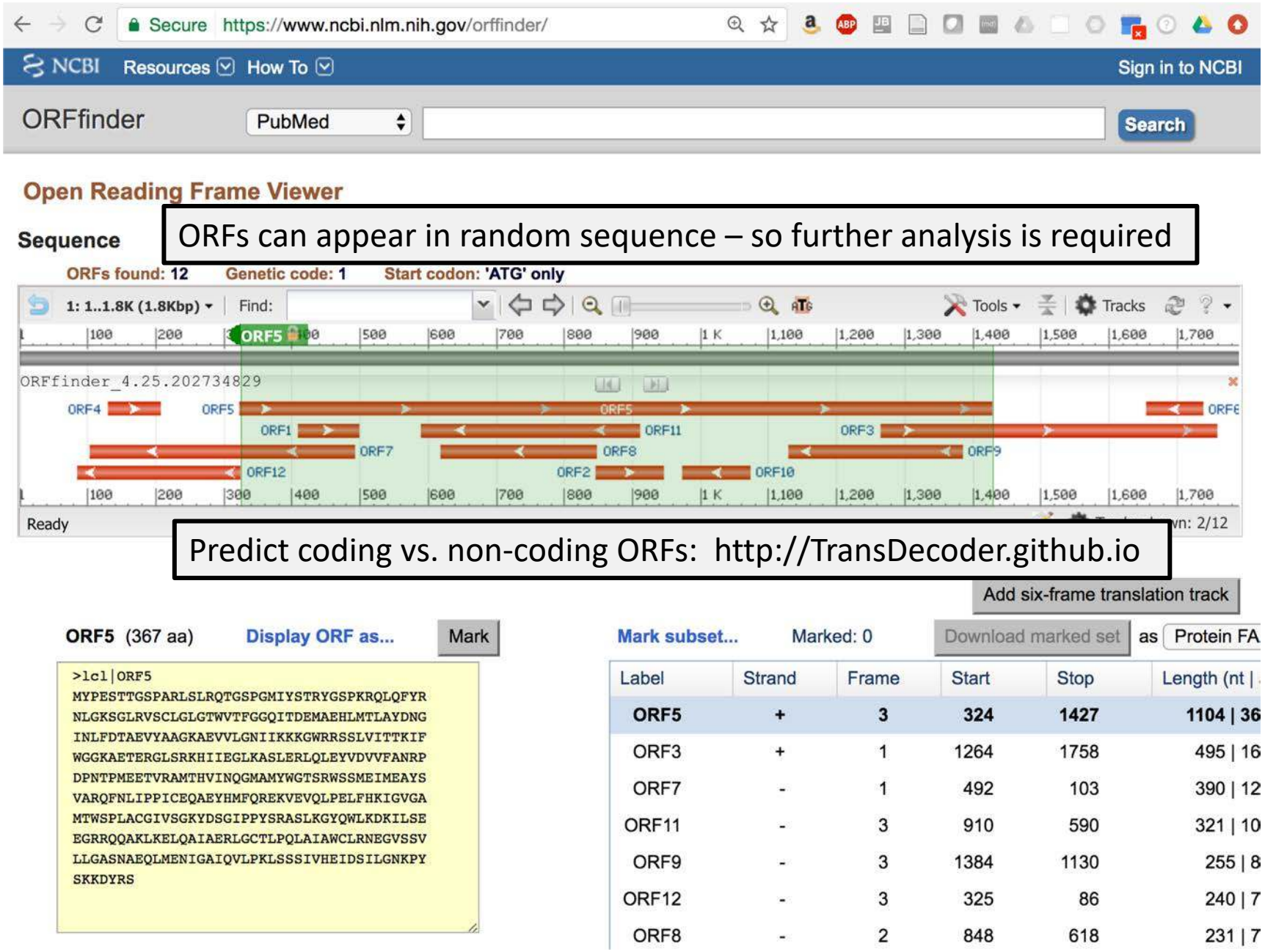
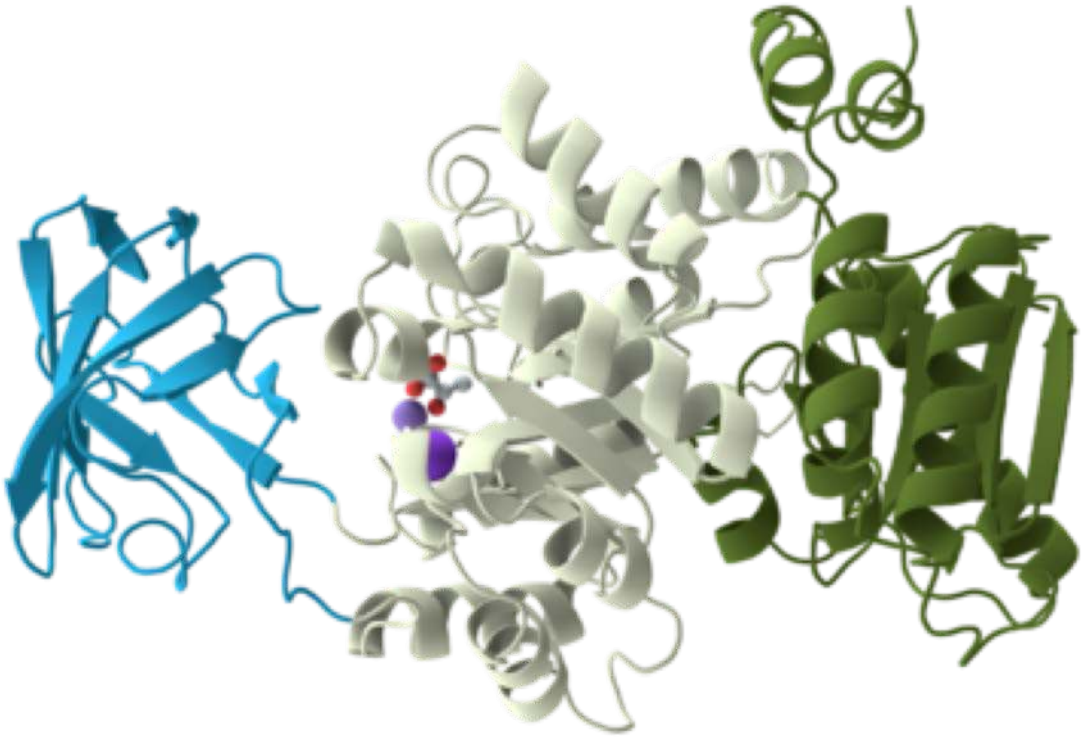

From: To:

ORFfinder finds all open reading frames and provides translations



Can we recognize functional domains in putative coding regions?

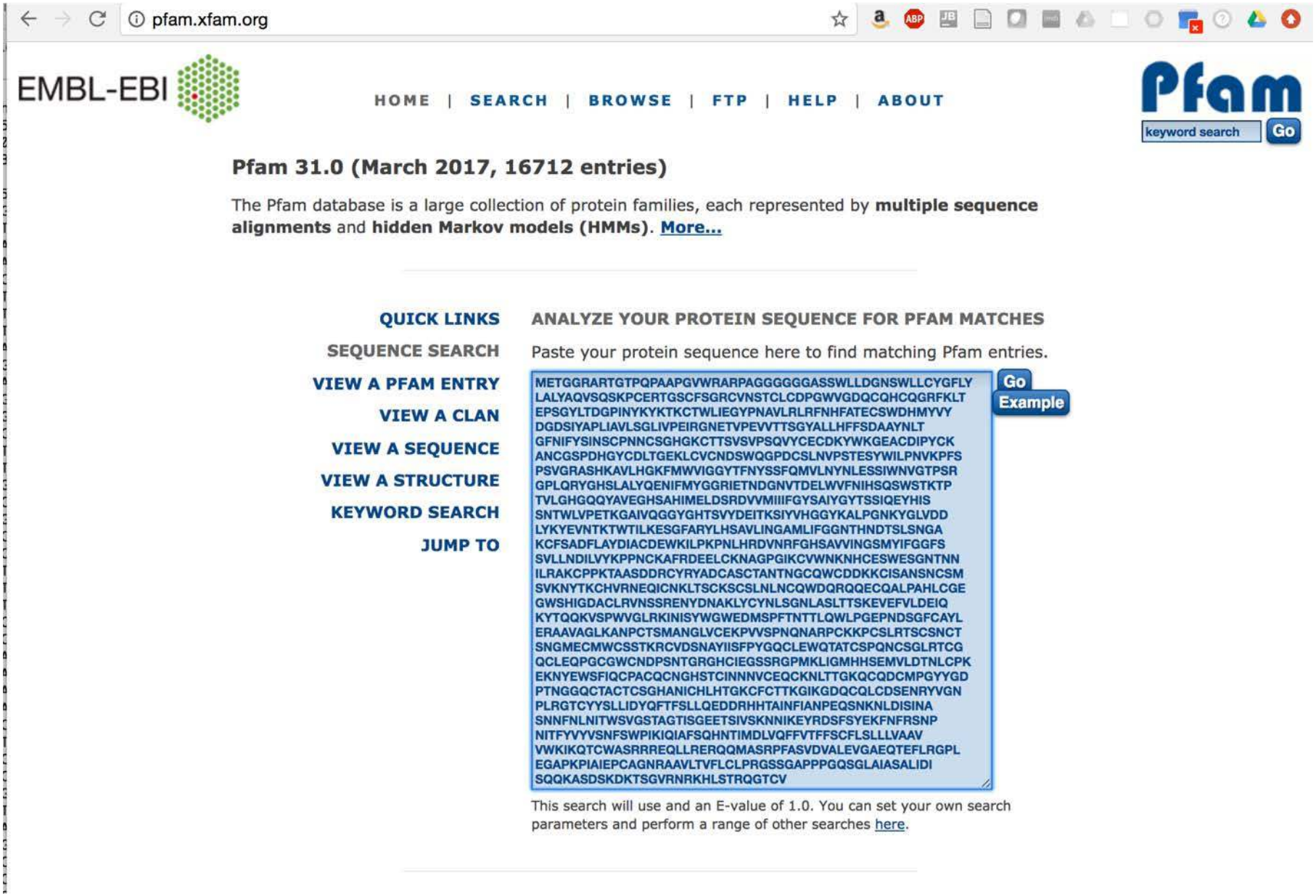


Hints at substrate binding or catalytic activity

DNA, RNA, calcium, phoshate, etc.

Glycoslase, methylase, kinase, nuclease, lipase, protease, etc.

Search the Pfam library of HMMs to identify potential functional domains



Example Pfam report illustrating modular domain architecture

pfam.xfam.org/search/sequence

EMBL-EBI

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Pfam keyword search Go

Sequence search results

Show the detailed description of this results page.

We found **9** Pfam-A matches to your search sequence (**all** significant)

Show the search options and sequence that you submitted.

Return to the search form to look for Pfam domains on a new sequence.

Significant Pfam-A Matches

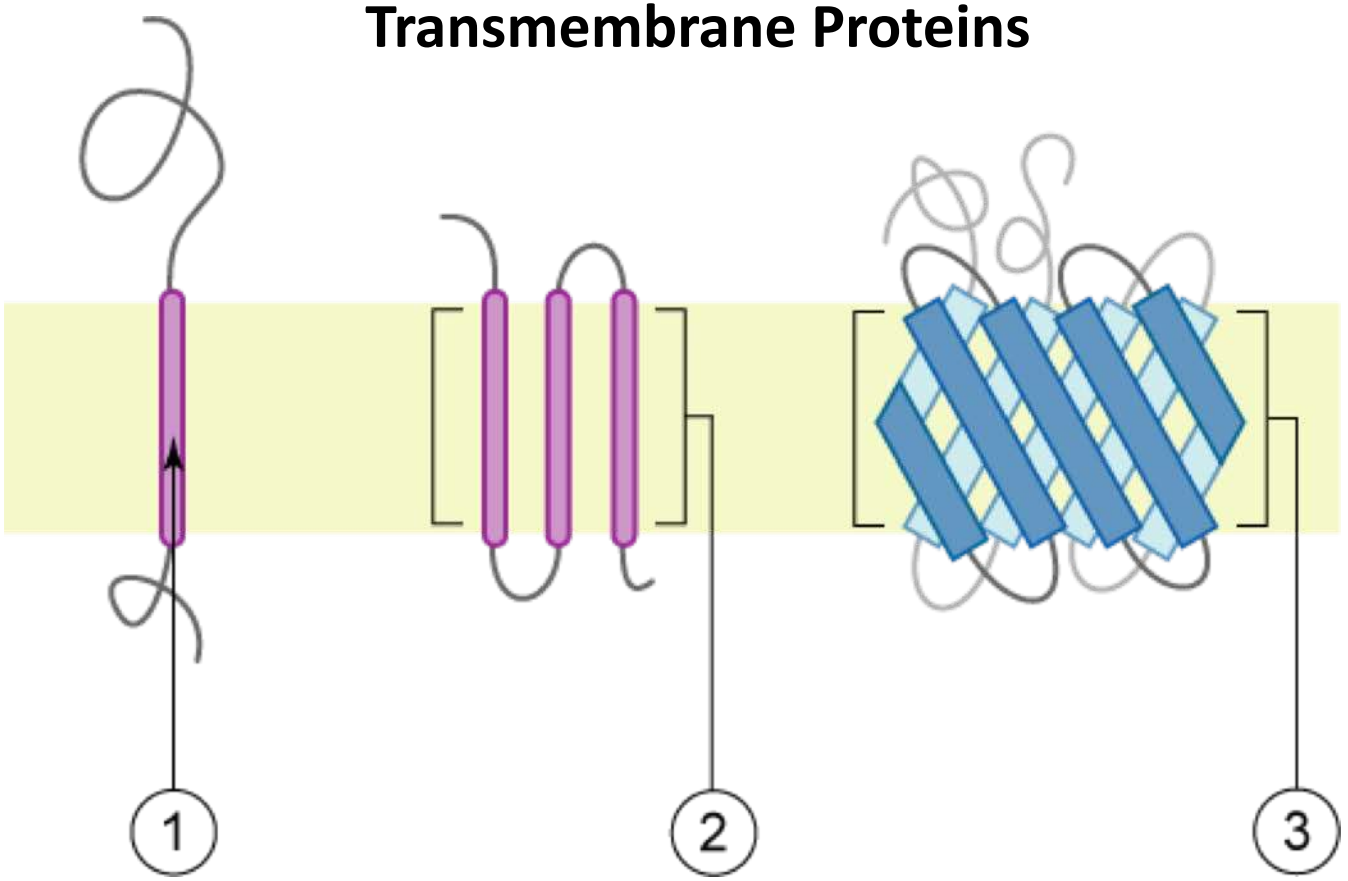
Show or hide all alignments.

Family	Description	Entry type	Clan	Envelope		Alignment		HMM		HMM length	Bit score	E-value	Predicted active sites	Show/hide alignment
				Start	End	Start	End	From	To					
CUB	CUB domain	Domain	CL0164	93	206	93	206	1	110	110	42.2	7.7e-11	n/a	Show
EGF_2	EGF-like domain	Domain	CL0001	249	280	249	280	1	32	32	22.5	0.0001	n/a	Show
Kelch_5	Kelch motif	Repeat	CL0186	351	393	352	392	**2**	**41**	42	33.7	2.2e-08	n/a	Show
Kelch_4	Galactose oxidase, central domain	Repeat	CL0186	466	518	468	514	**3**	**44**	49	20.6	0.0003	n/a	Show
Kelch_1	Kelch motif	Repeat	CL0186	520	574	520	573	1	**45**	46	20.0	0.00033	n/a	Show
Kelch_5	Kelch motif	Repeat	CL0186	579	614	581	613	**5**	**40**	42	25.3	9.7e-06	n/a	Show
Lectin_C	Lectin C-type domain	Domain	CL0056	765	874	766	874	**2**	108	108	70.2	2e-19	n/a	Show
PSI	Plexin repeat	Family	CL0630	889	939	890	938	**2**	**50**	51	27.8	2.5e-06	n/a	Show
PSI	Plexin repeat	Family	CL0630	942	1012	942	1012	1	51	51	50.0	2.9e-13	n/a	Show

Comments or questions on the site? Send a mail to **pfam-help@ebi.ac.uk**.

European Molecular Biology Laboratory

Transmembrane Proteins



Single transmembrane α-helix (bitopic membrane protein)

Polytopic transmembrane α-helical protein

Polytopic transmembrane β-sheet protein

From: https://en.wikipedia.org/wiki/Transmembrane_protein

Using TMHMM to identify putative transmembrane proteins

www.cbs.dtu.dk/services/TMHMM/

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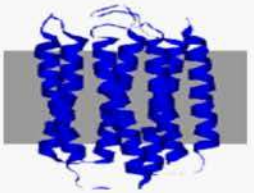
TMHMM Server v. 2.0

Prediction of transmembrane helices in proteins



Instructions

SUBMISSION

Submission of a local file in FASTA format (HTML 3.0 or higher)

Choose File | No file chosen

OR by pasting sequence(s) in FASTA format:

```
MEILCEDNTSLSSIPNSLMQVDGDSGLYRNDFNSRDANSSDASNWTIDGENRTNLSFEG
YLPPTCLSILHLQEKNWSALLTAVVIILTIAGNILVIMAVSLEKKLQNATNYFLMSLAIADMLL
GFLVMPVSMLTILYGYRWPLPSKLCAVWIYLDVLFSTASIMHLCAISLDRYVAIQNPIHHSR
FNSRTKAFLKIIAVWTISVGVSMPIPVFGLQDDSKVFKQGSCLLADDNFVLIGSFVAFFIPLTI
MVITYFLTIKSLQKEATLCVSDLSTRAKLASFSFL
```

Output format:

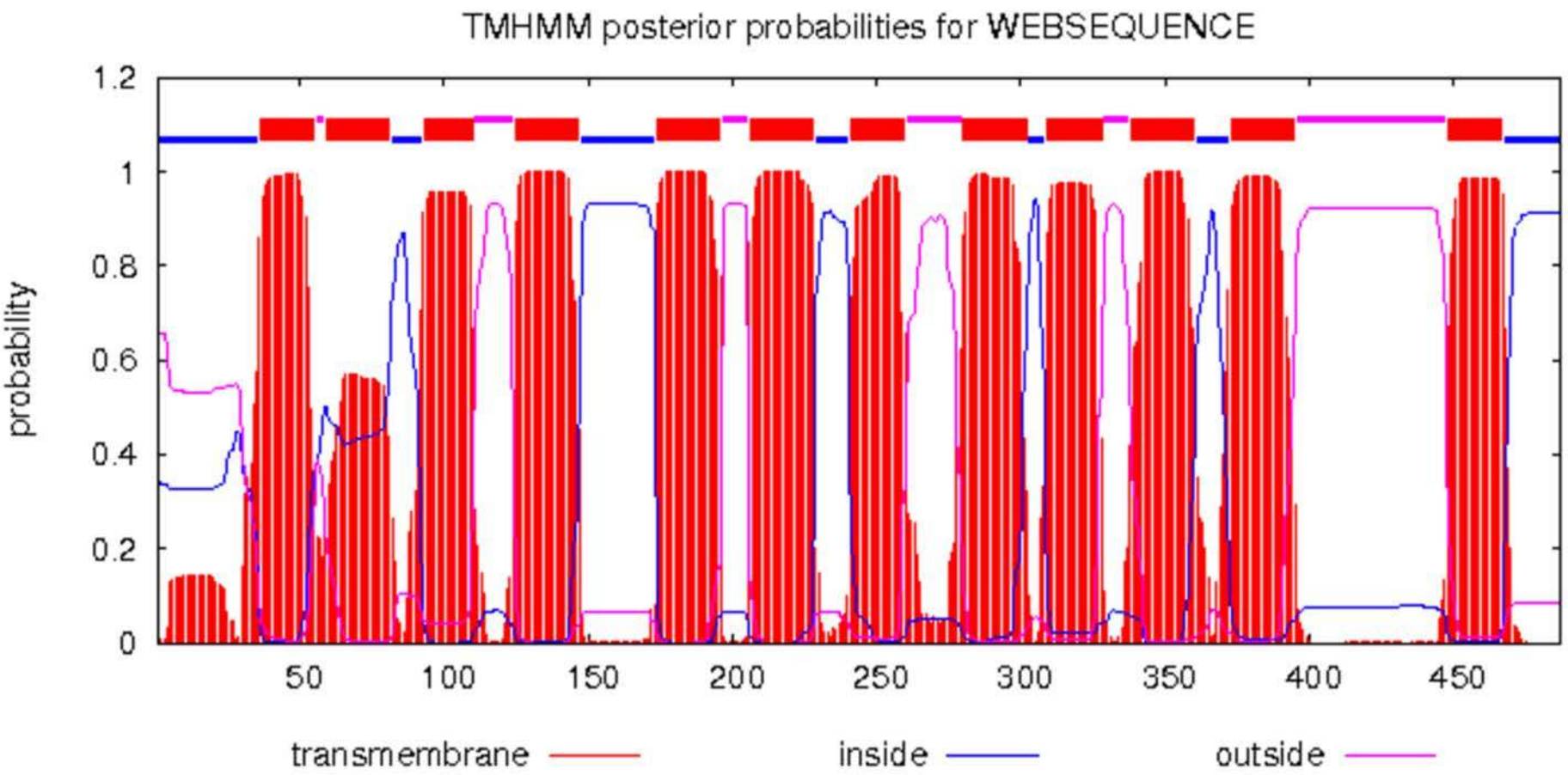
- (•) Extensive, with graphics
- ( ) Extensive, no graphics
- ( ) One line per protein

Other options:

- [ ] Use old model (version 1)

Submit | Clear

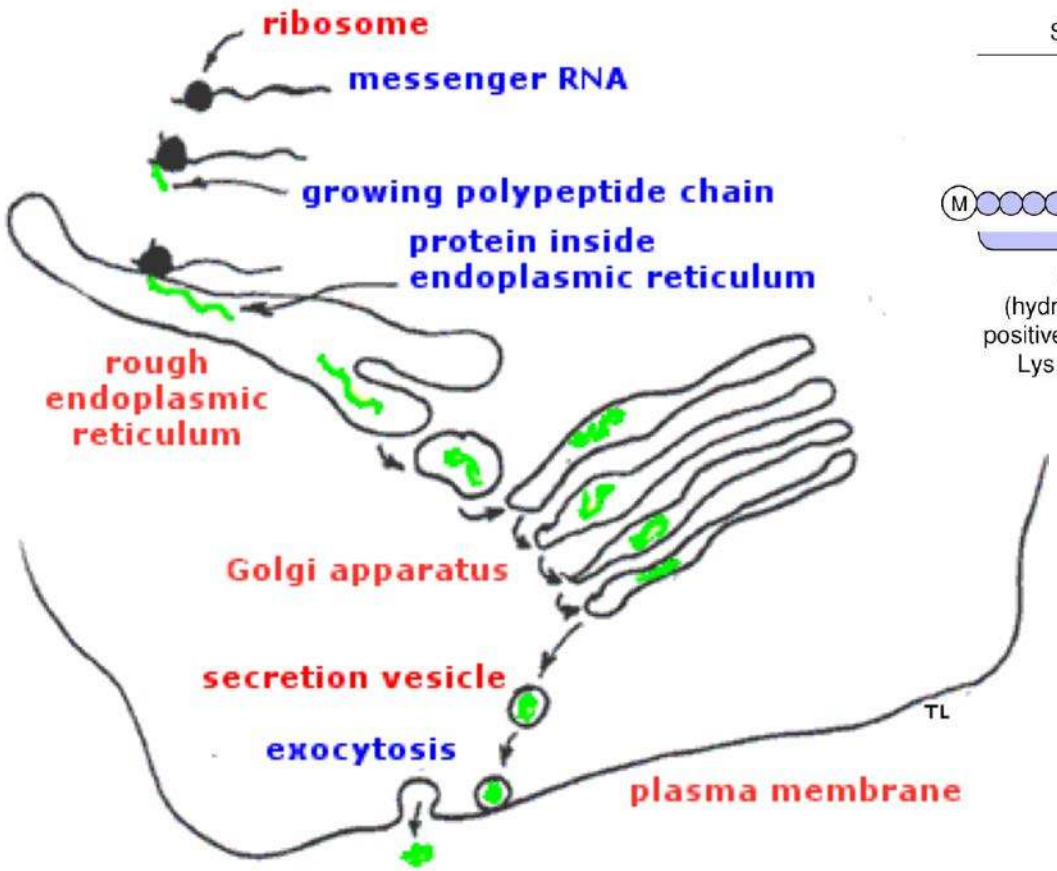
Trans-membrane Domains via TmHMM



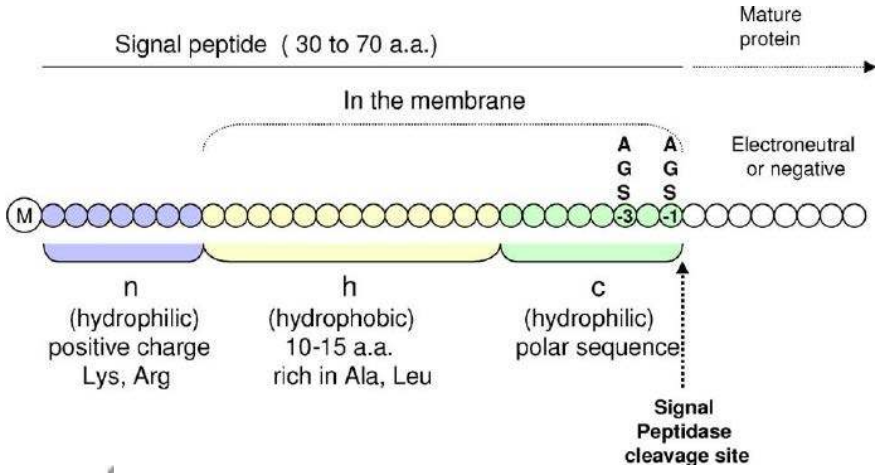
Topology=i36-55o59-81i93-110o125-147i174-196o206-228i241-260o280-302i309-328o338-360i373-395o448-467i

http://www.cbs.dtu.dk/services/TMHMM/

Predicting Secreted Proteins

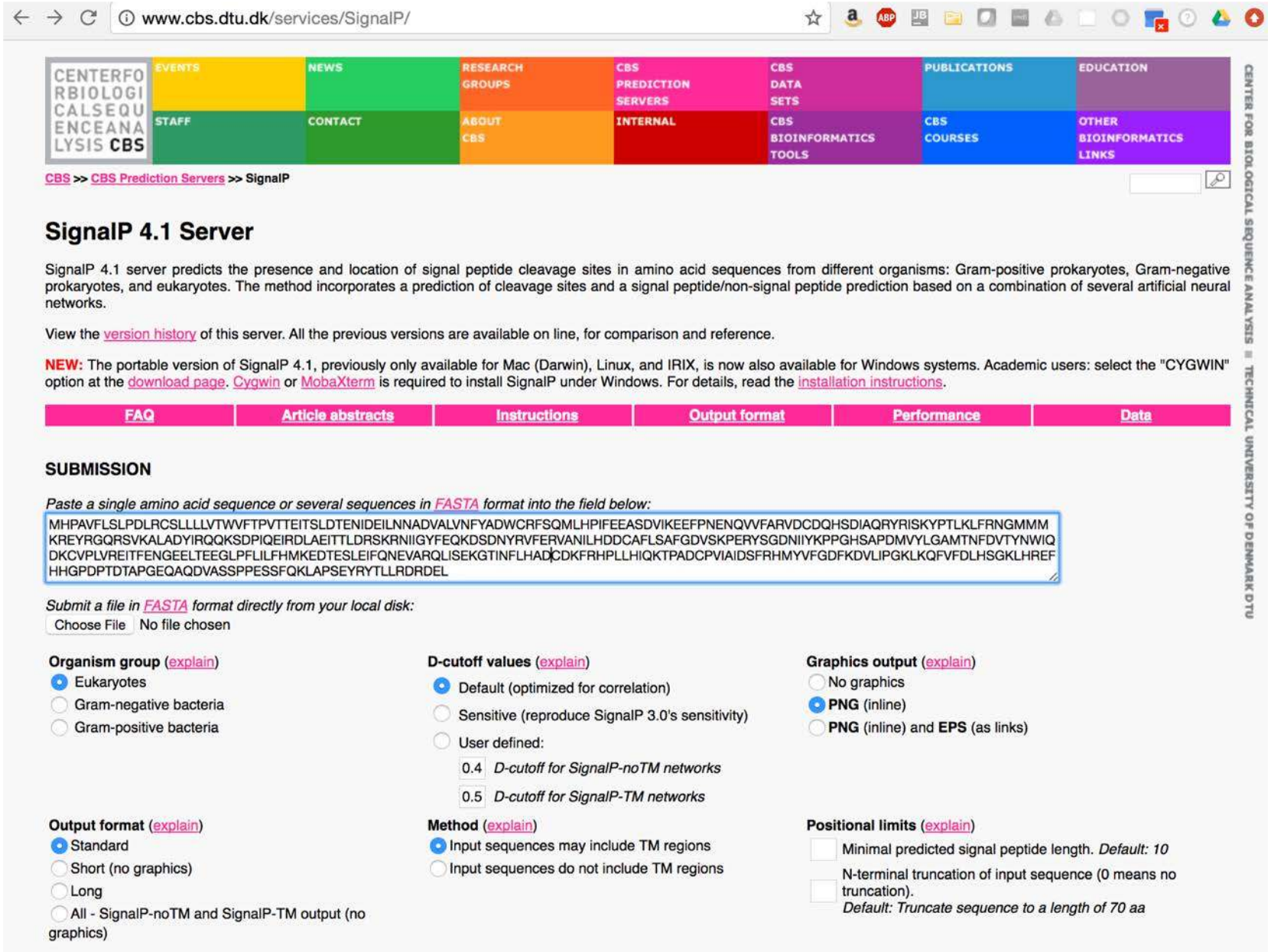


(from: https://courses.washington.edu/conj/cell/secretion.htm)



(from: Vaccine 23(15):1770-8)

SignalP: Prediction of N-terminal signal peptides
(predict secreted proteins)



Example SignalP predicted signal peptide

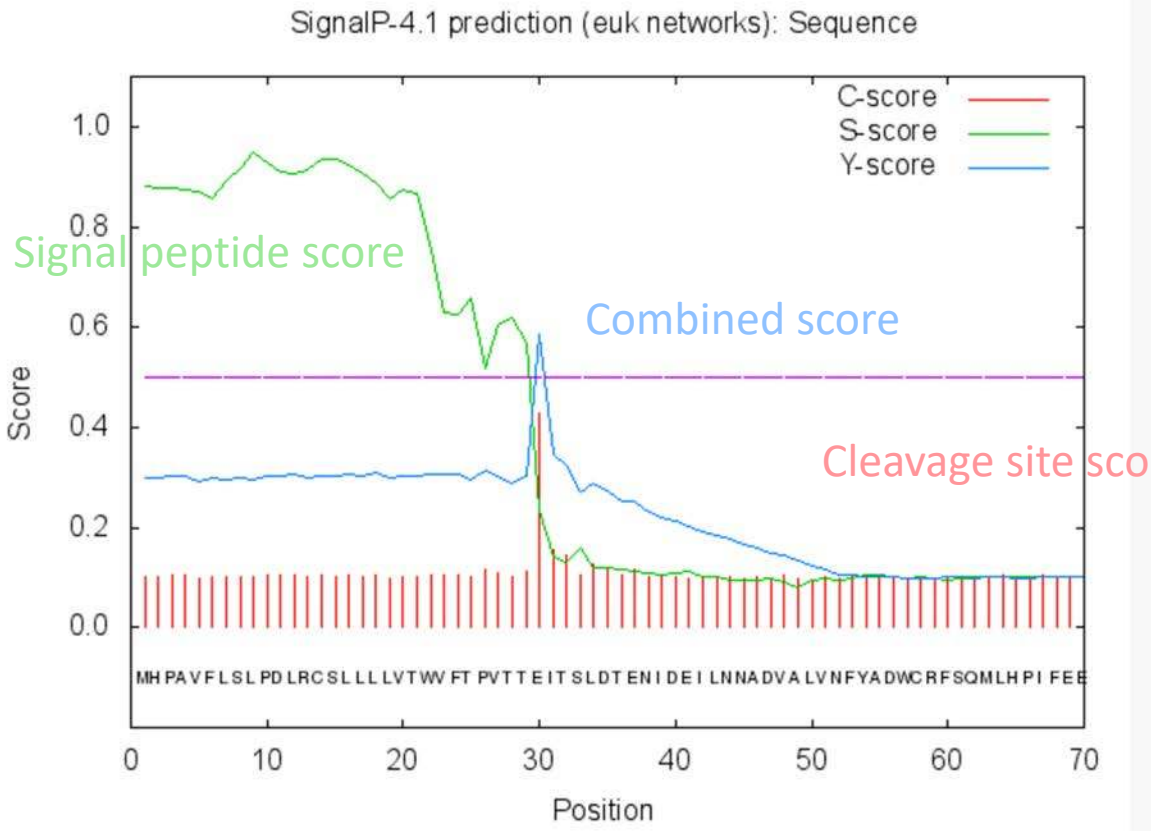
www.cbs.dtu.dk/cgi-bin/webface2.fcgi?jobid=58FFF29C00005F854B357EEA&w...

CENTERFO RBIOLOGI CALSEQU ENCEANA LYSIS CBS

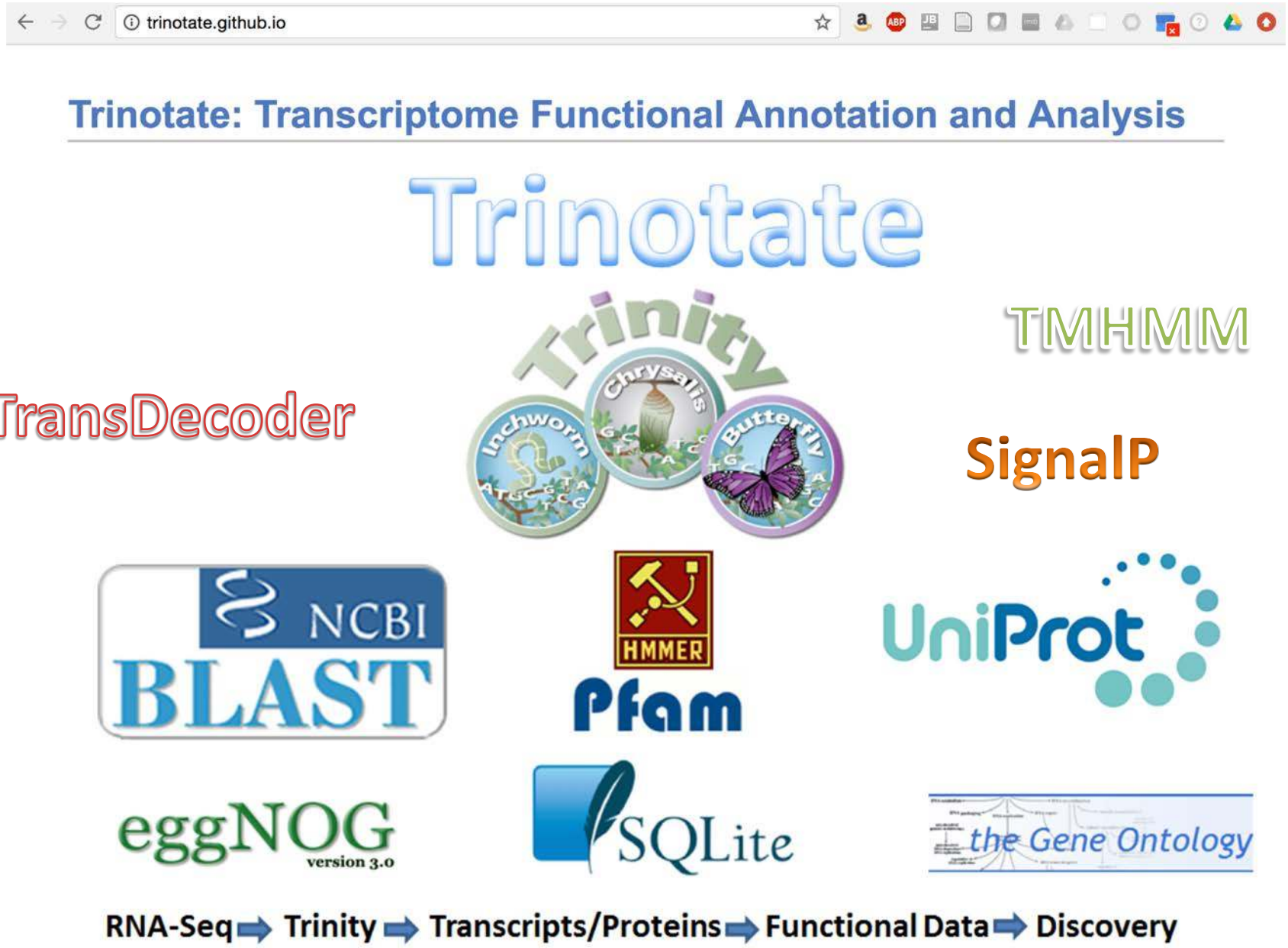
SignalP 4.1 Server - prediction results

Technical University of Denmark

```
# SignalP-4.1 euk predictions
>Sequence
```



Transcriptome-scale functional annotation using Trinotate



GoSeq for Functional Enrichment Testing

SwissProt

(GO assignments included in records)

Pfam

(Pfam2GO)

Trinotate Gene Ontology Assignments

METHOD | OPEN ACCESS

Gene ontology analysis for RNA-seq: accounting for selection bias

Matthew D Young, Matthew J Wakefield, Gordon K Smyth and Alicia Oshlack

Genome Biology 2010 11:R14 | DOI: 10.1186/gb-2010-11-2-r14

Gene ontology functional enrichment

	(+) Differentially Expressed	(-) Not Differentially Expressed	Totals
+ Gene Ontology	50	200	250
- Gene Ontology	1950	17800	19750
Totals	2000	18000	20000

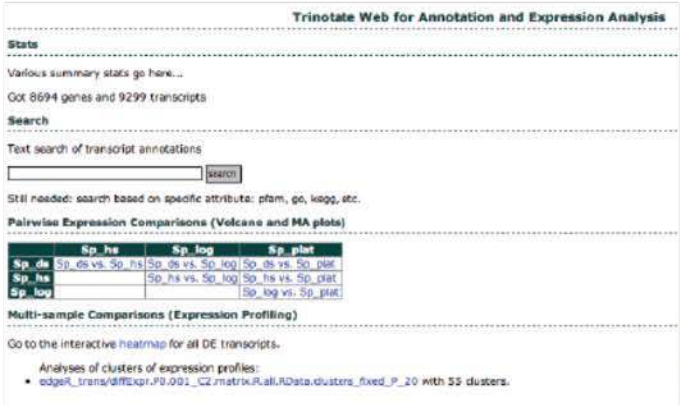
	drawn	not drawn	total
green marbles	k	$K - k$	K
red marbles	$n - k$	$N + k - n - K$	$N - K$
total	n	$N - n$	N

The probability of drawing exactly k green marbles can be calculated by the formula

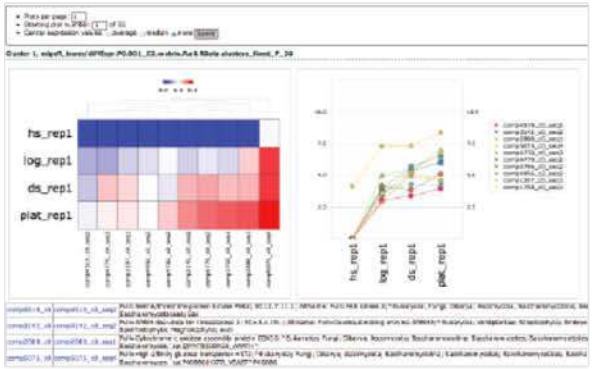
$$P(X = k) = f(k; N, K, n) = \frac{\binom{K}{k}\binom{N-K}{n-k}}{\binom{N}{n}}.$$

Trinotate Web for Interactive Analysis

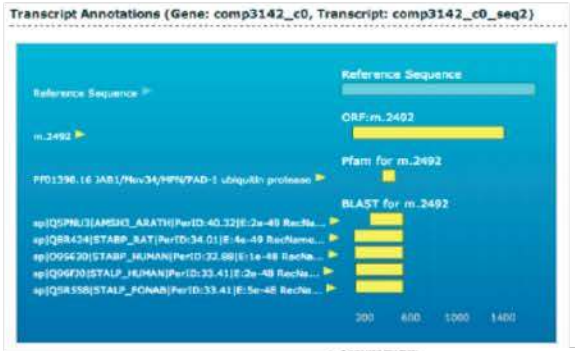
TrinotateWeb Entry Point

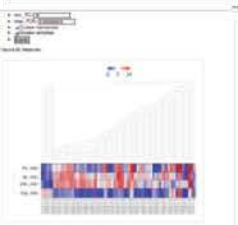


Clustered Expression Profiles

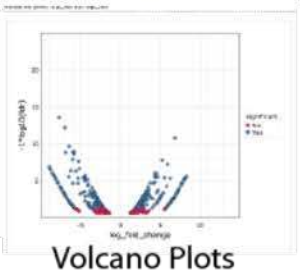


Transcript/Protein Annotation Report
Blast Hits, Pfam Domains, etc.

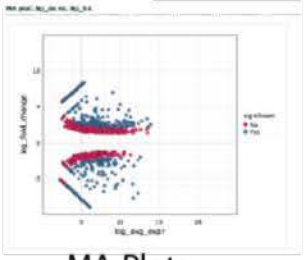




Heatmaps

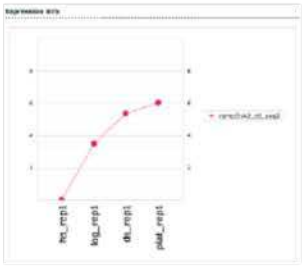


Volcano Plots



MA-Plots

Very Early Release and
Just Scratching the Surface



Individual Transcript
Expression Profiles

Transcript and
Protein Sequences

Deciphering the Cell Circuitry of Limb Regeneration Via Single Cell Transcriptome Studies

Work done in collaboration with Jessica Whited's lab

BWH

BRMC

Brigham Regenerative Medicine Center

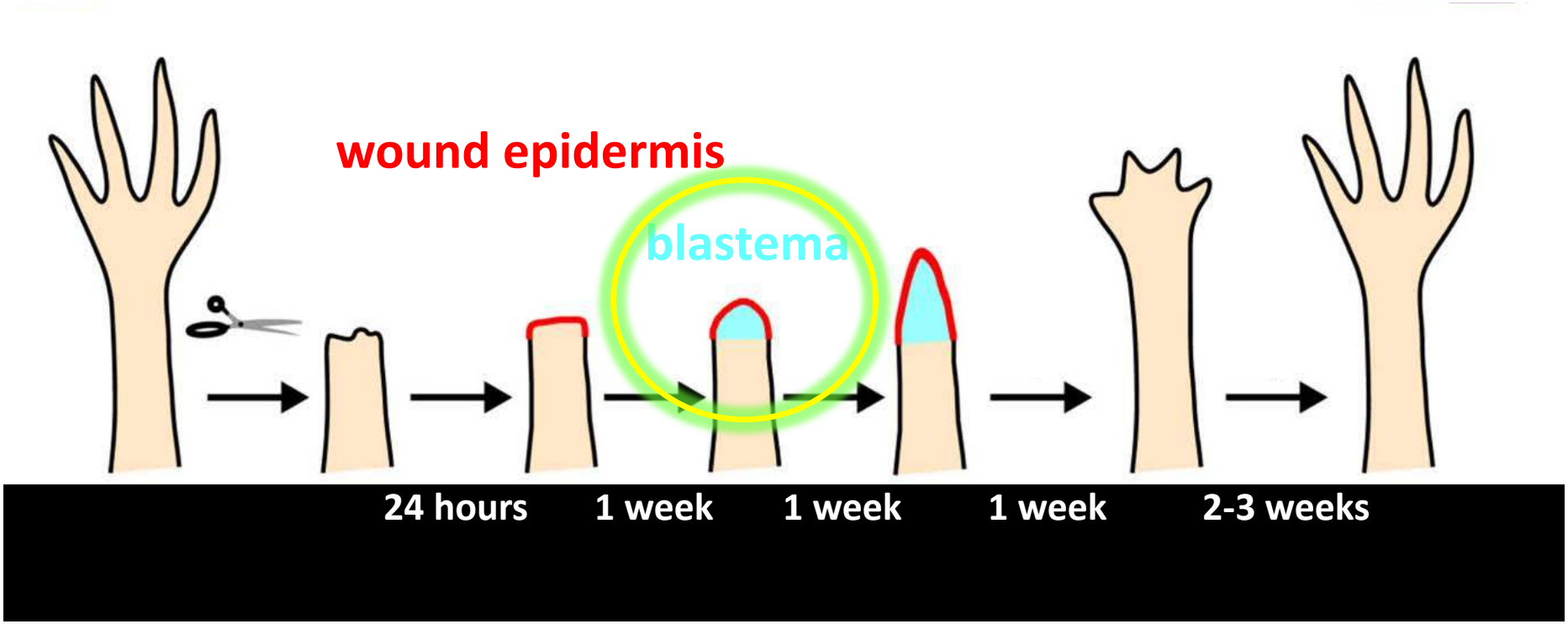
Axolotl (*Ambystoma mexicanum*) Transcriptomics

Axolotl "water monster”, aka Mexican salamander or Mexican walking fish.

- Model for vertebrate studies of tissue regeneration
- Short generation time
- Can fully regenerate a severed limb in just weeks.
- Genome estimated at ~30 Gb (not yet sequenced)

Google Anonymous Axolotl Icon

Key morphological steps during limb regeneration



BWH BRMC Brigham Regenerative Medicine Center

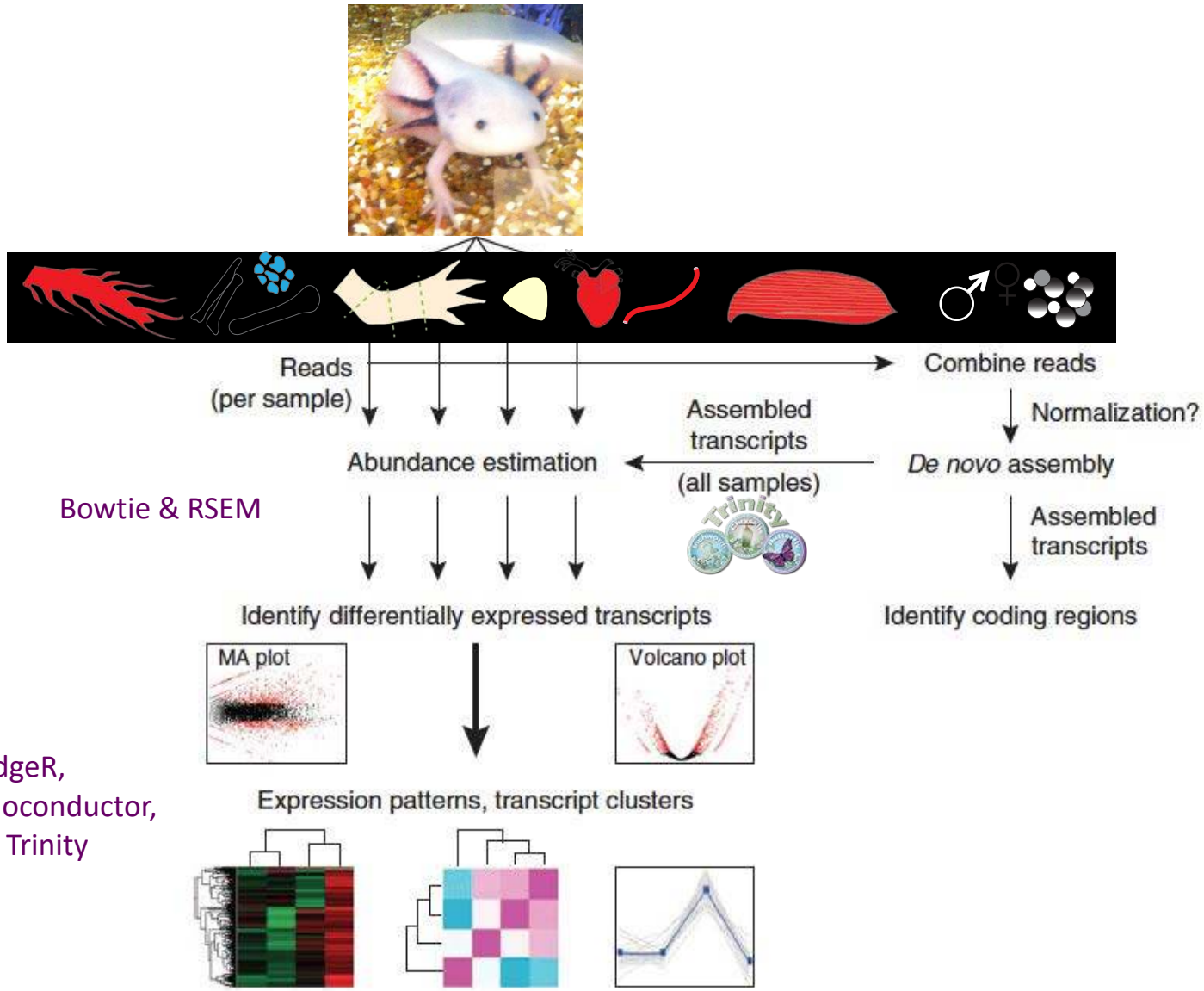
Jessica Whited, Mark Mannucci, Ari Haberberg

1. Building a reference Axolotl transcriptome

limb tissues and select other tissues with biological replicates

1.3 billion of
100 bp paired-end
Illumina reads

Framework for De novo Transcriptome Assembly and Analysis



Bowtie & RSEM

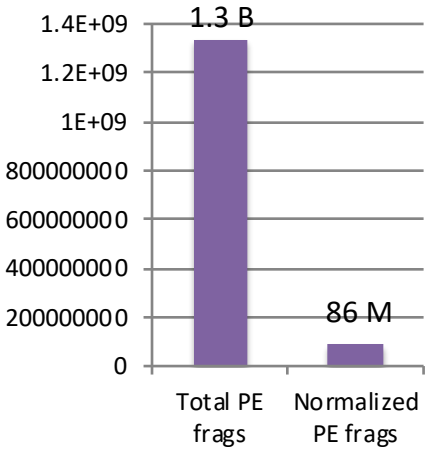
EdgeR,
Bioconductor,
& Trinity

1.3 Billion
Total Reads

86 Million
Normalized Reads

Axolotl Transcriptome De novo Assembly Statistics And Quality Assessment

In silico Normalization

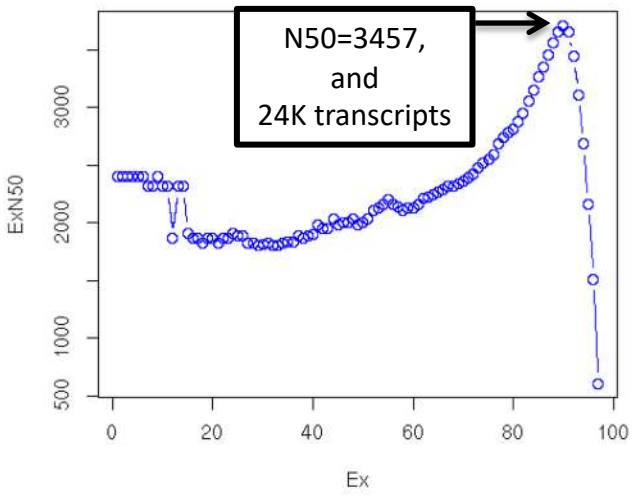


Counts of Transcripts

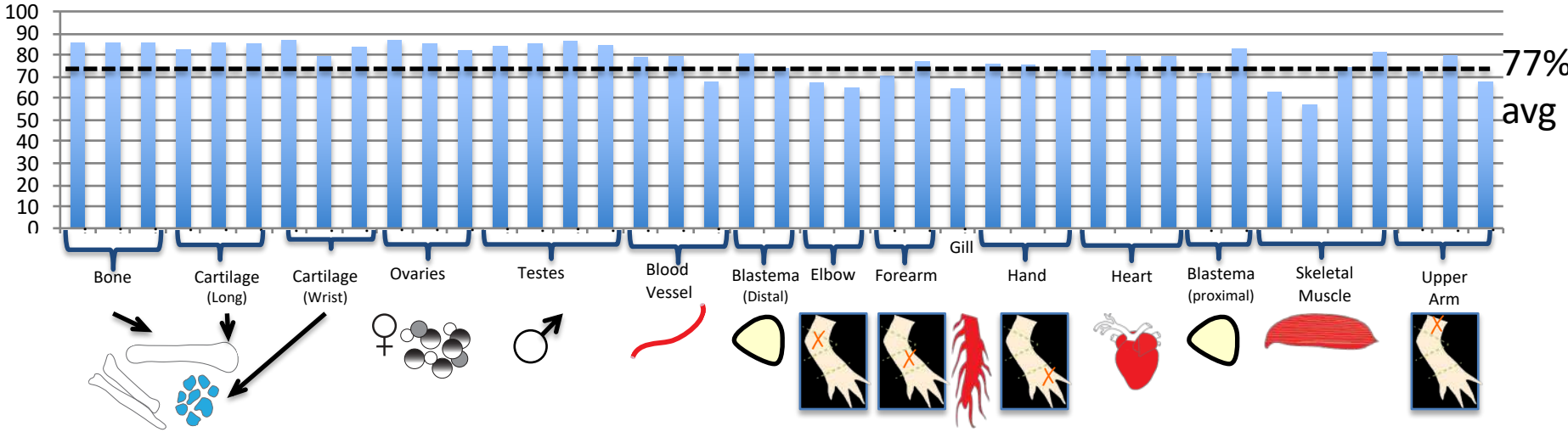
Trinity contigs (transcripts)	**1,554,055**
Trinity components (genes)	**1,388,798**

Min. length 200 bases

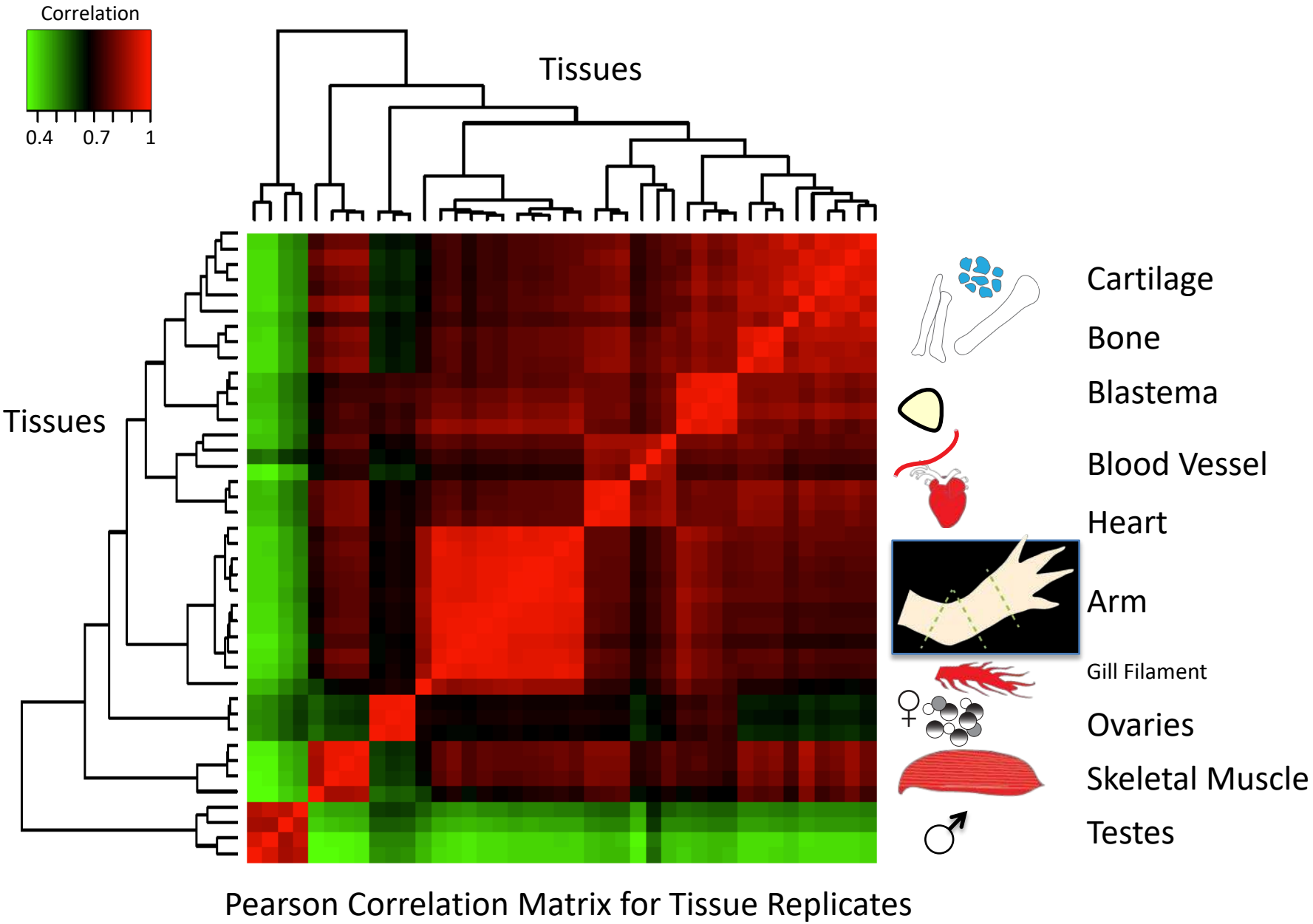
ExN50 looks good!



Percent of Non-normalized Fragments Mapping as Properly Paired to Transcriptome

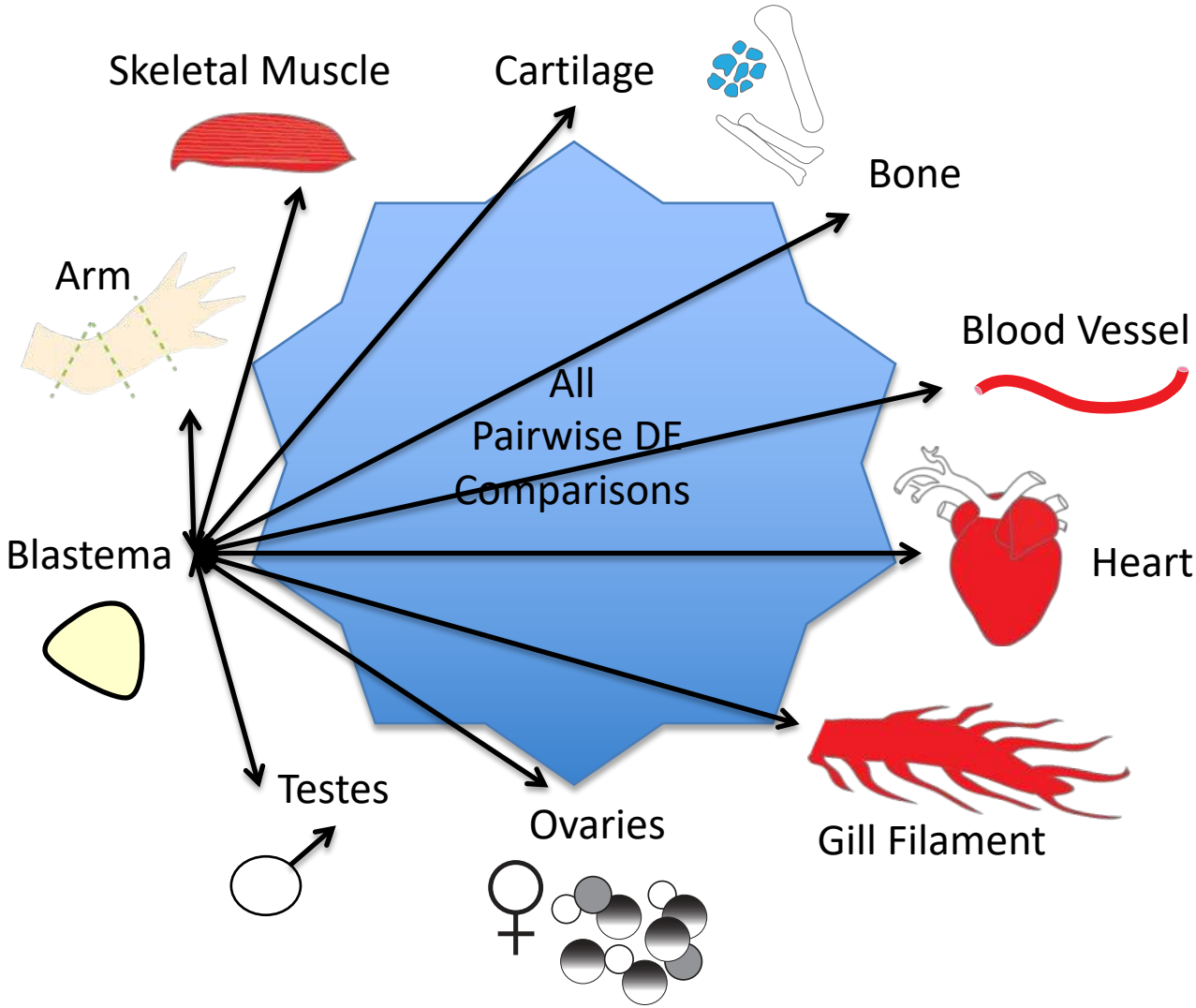


Biological Replicates Cluster According to Sample



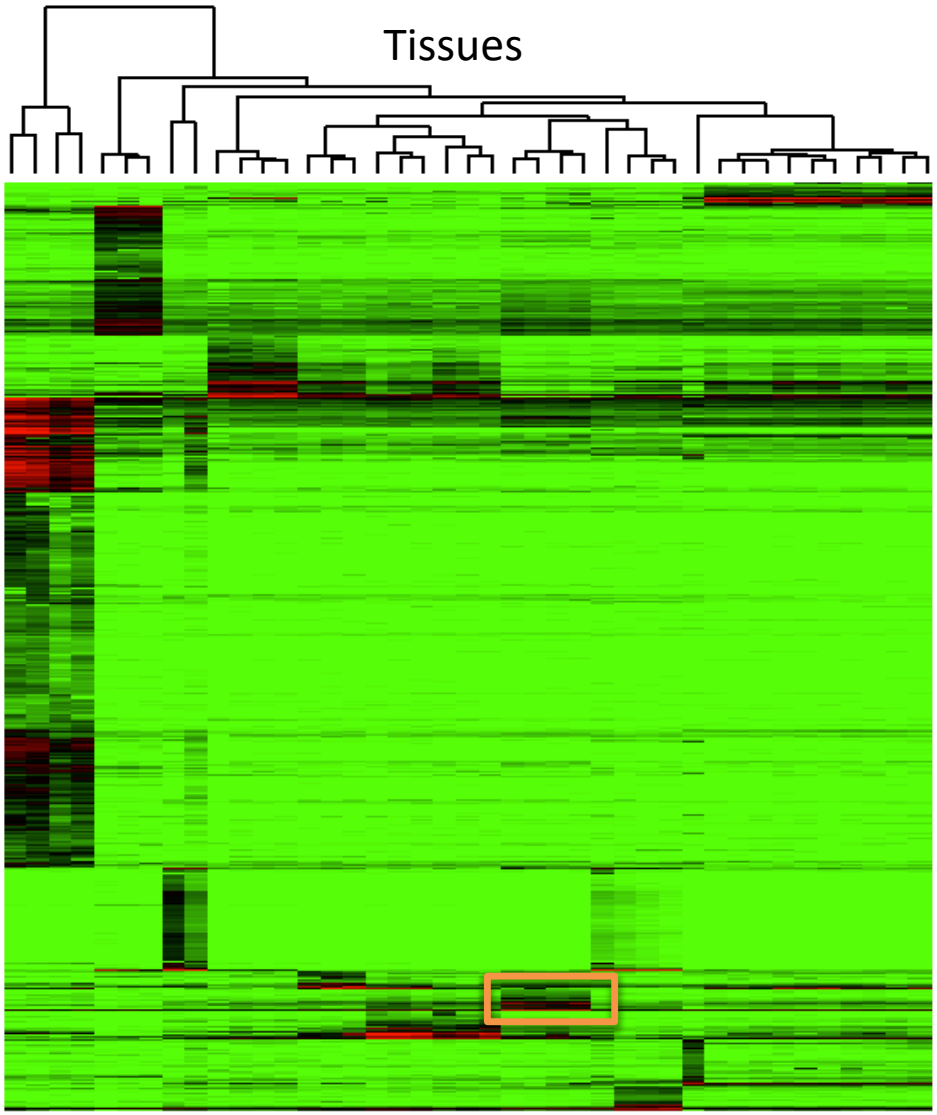
Pearson Correlation Matrix for Tissue Replicates

2. Identification of Tissue-enriched Expression



EdgeR, min 4-fold change, FDR <= 1e-3

Identification of Tissue-enriched Gene Expression



Arm (193), GO: thick ascending limb development [8.8e-5]

Ovaries (1225)

Skeletal Muscle (539)

Testes (4113), GO: spermatogenesis [2.5e-14]

Blood Vessel (939)

Bone (272), GO: myeloid leukocyte differentiation [2.2e-3]

Blastema (202): limb morphogenesis [2.5e-5]

Cartilage (255), GO: collagen fibril organization [4.5e-10]

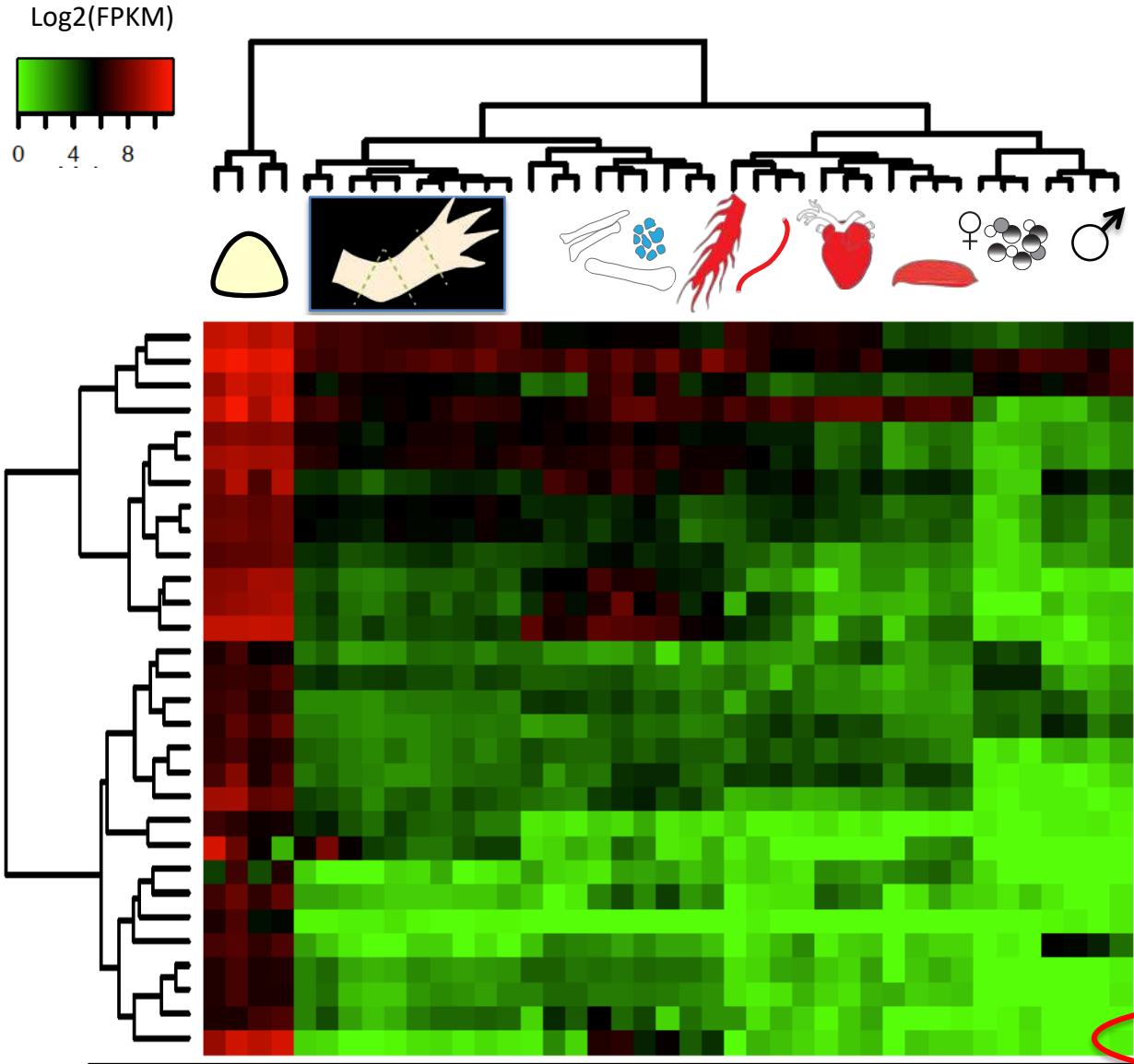
Gill Filament (765)

Heart (238),
GO: vascular process in circulatory system [2.6e-3]

EdgeR, min 4-fold change, FDR <= 1e-3

Functional enrichment using GO-Seq

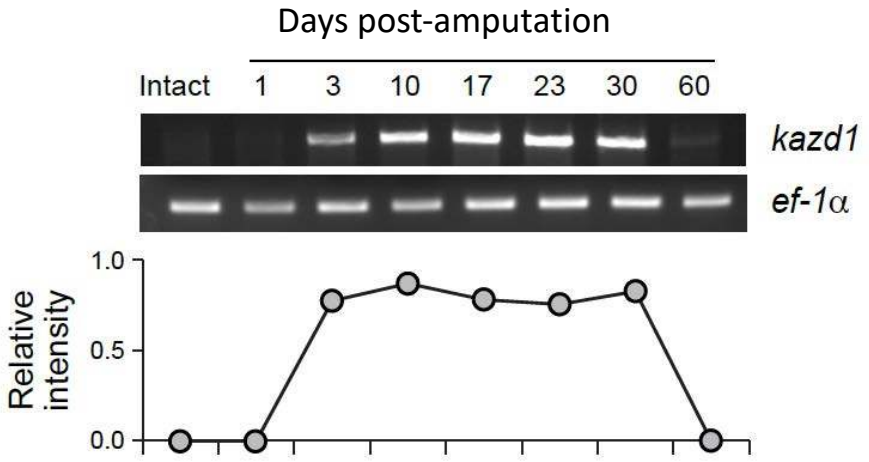
Most Highly Expressed Blastema-enriched Genes



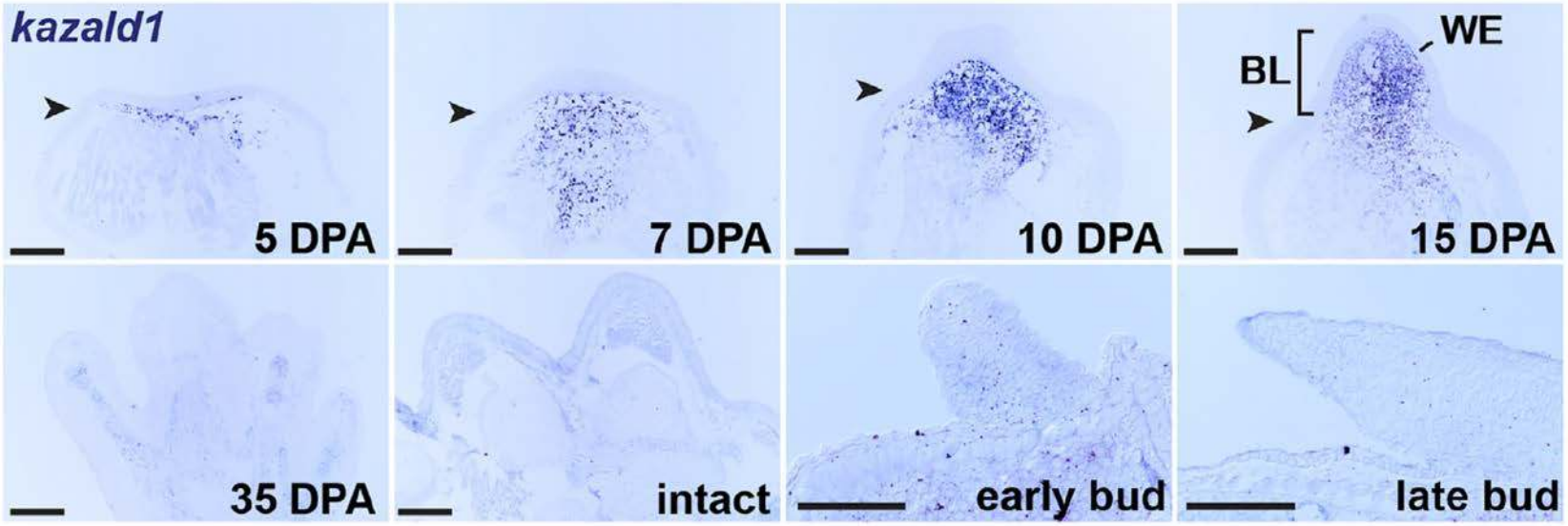
Color key: Regulator Signaling Structure and Extracellular Matrix

Functional Characterization of Blastema-enriched KAZD1

RT-PCR Timecourse of Kazald1 Expression



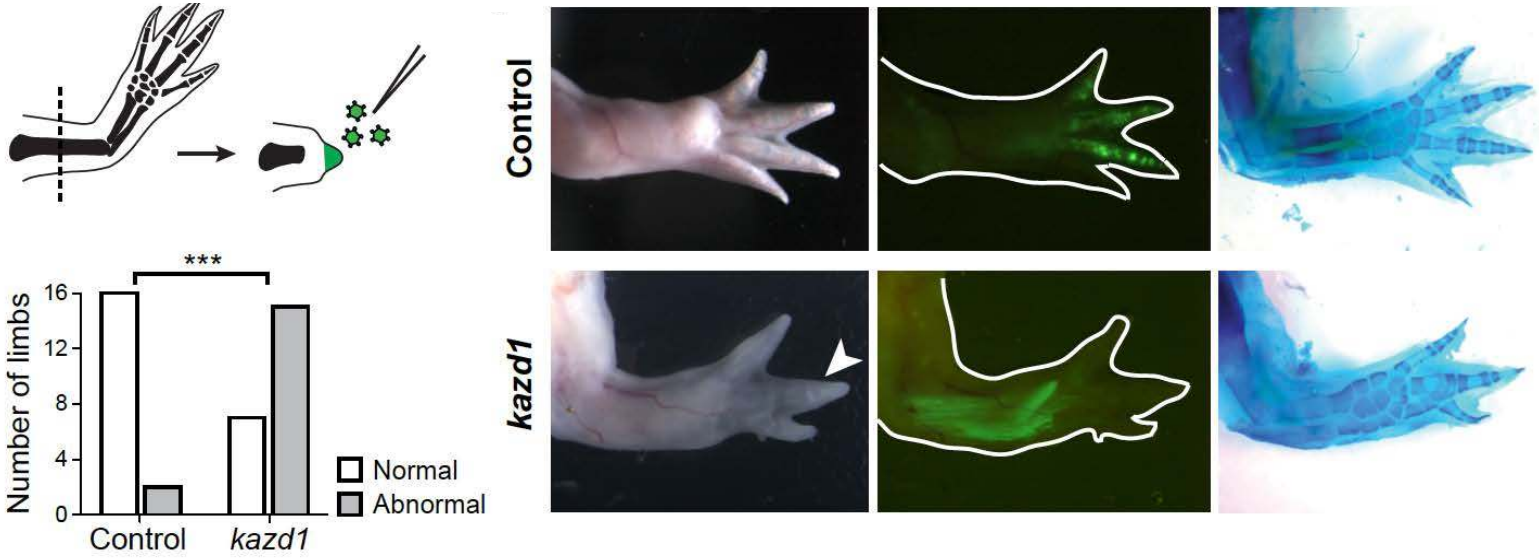
In situ hybridization of kazald1 over course of regeneration



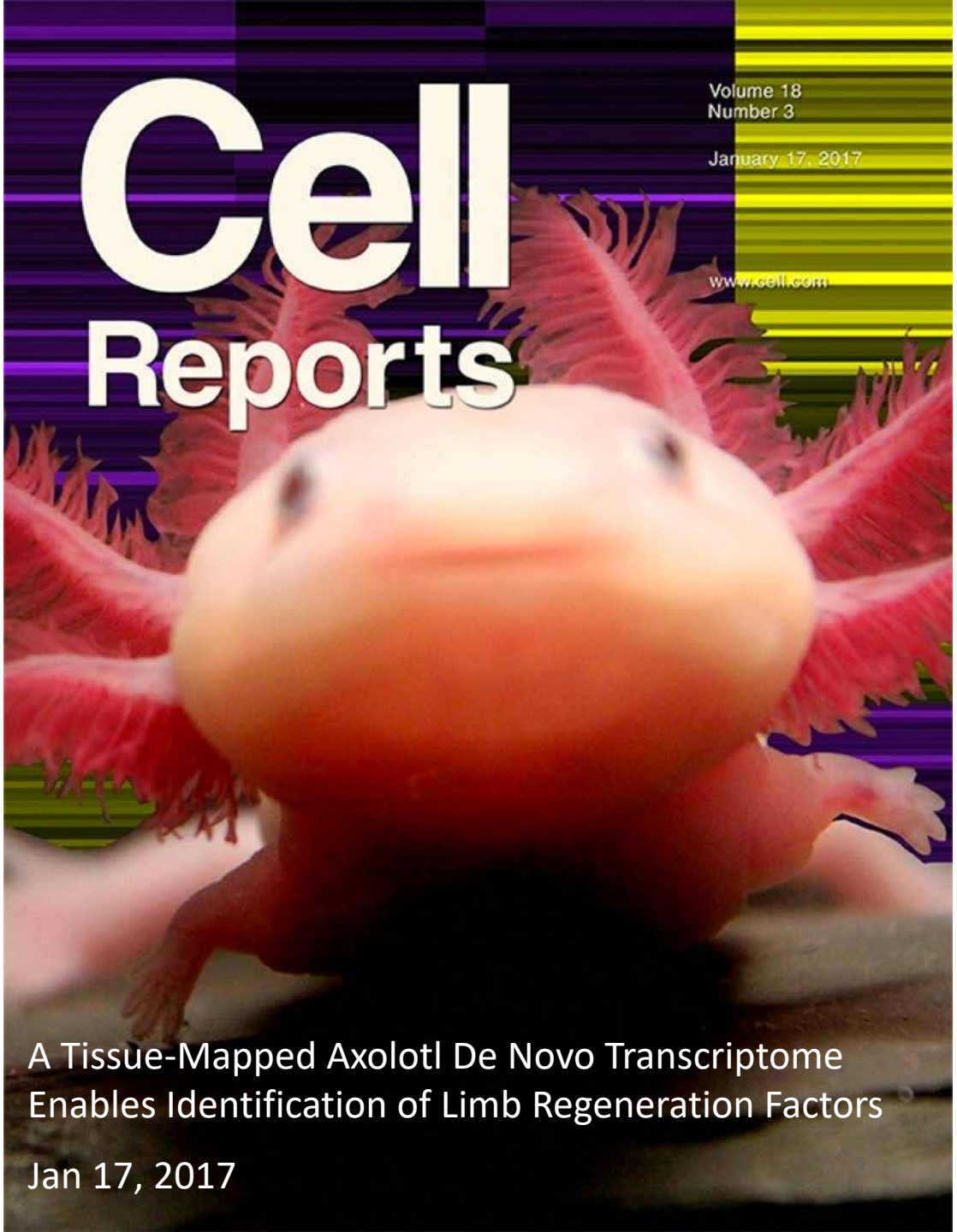
Work by Jessica Whited's group, Cell Reports, 2017

Morpholino Knockdown of Kazald1 Expression

Viral-based Delivered Over-expression of KAZD1 Leads to Regeneration Defects



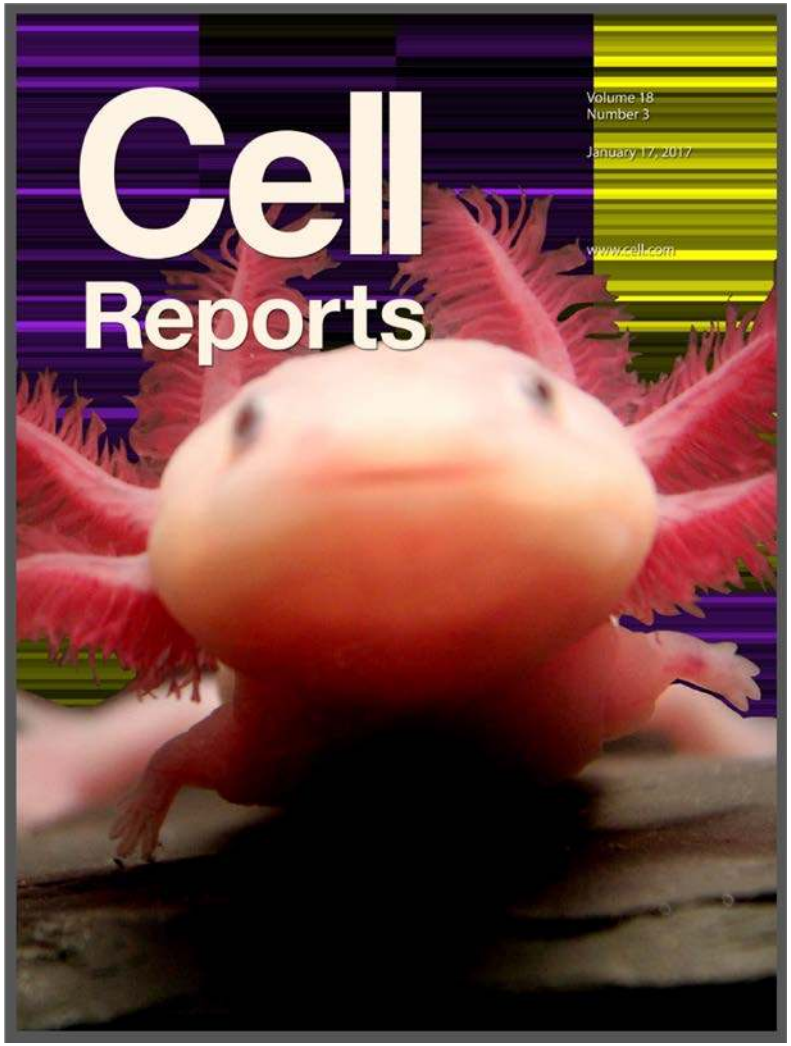
Work by Jessica Whited's group, Cell Reports, 2017



A Tissue-Mapped Axolotl De Novo Transcriptome Enables Identification of Limb Regeneration Factors

Jan 17, 2017

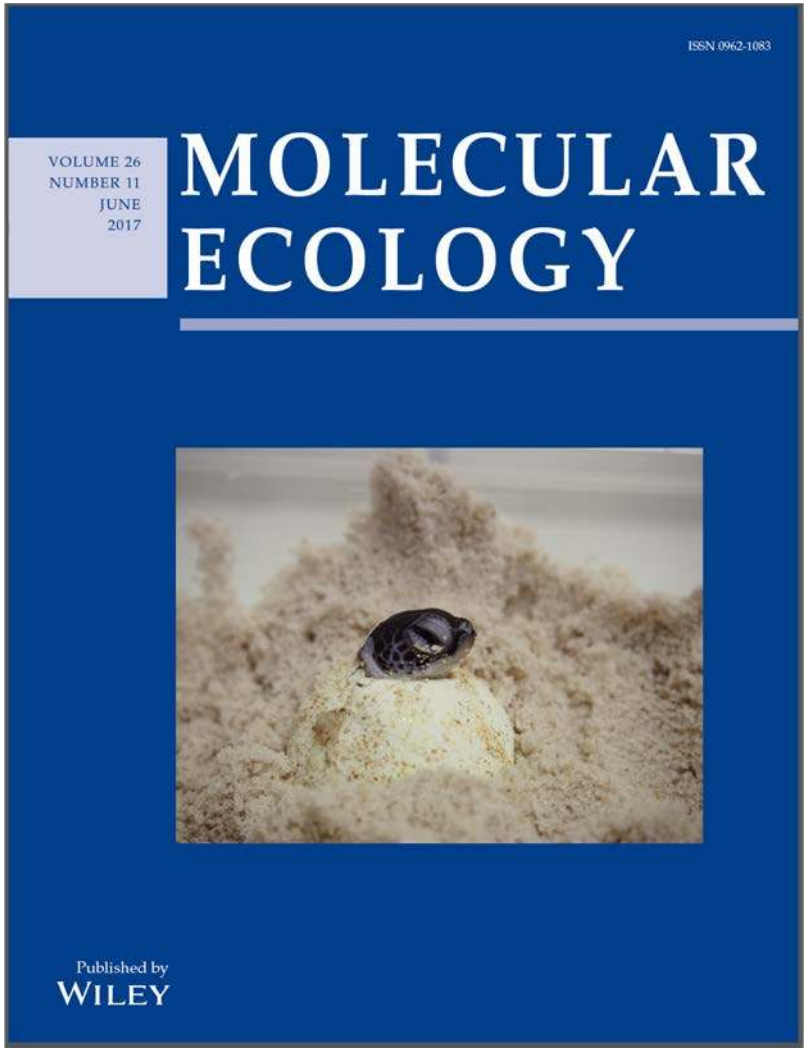
Example Applications of the Trinity RNA-Seq Protocol



Resource

A Tissue-Mapped Axolotl De Novo Transcriptome Enables Identification of Limb Regeneration Factors

Donald M. Bryant[1,6], Kimberly Johnson[1,6], Tia DiTommaso[1], Timothy Tickle[2], Matthew Brian Couger[3], Duygu Payzin-Dogru[1], Tae J. Lee[1], Nicholas D. Leigh[1], Tzu-Hsing Kuo[1], Francis G. Davis[1], Joel Bateman[1], Sevara Bryant[1], Anna R. Guzikowski[1], Stephanie L. Tsai[4], Steven Coyne[1], William W. Ye[1], Robert M. Freeman Jr.[5], Leonid Peshkin[5], Clifford J. Tabin[4], Aviv Regev[2], Brian J. Haas[2], , , Jessica L. Whited[1,7],



Original Article

Loggerhead sea turtle embryos (*Caretta caretta*) regulate expression of stress response and developmental genes when exposed to a biologically realistic heat stress

Blair P. Bentley, Brian J. Haas, Jamie N. Tedeschi, Oliver Berry

Summary of Key Points

- RNA-Seq is a versatile method for transcriptome analysis enabling quantification and novel transcript discovery.
- Expression quantification is based on sampling and counting reads derived from transcripts
- Fold changes based on few read counts lack statistical significance.
- Trinity assembly and supported downstream computational analysis tools facilitate transcriptome studies.
- The Trinity framework can empower transcriptome studies for organisms lacking reference genome sequences (ex. Axolotl) or suboptimal references (ex. cancer).

Summary of Current Trends

- Quantification without read alignment (pseudalignment – kallisto, salmon).
- Differential expression w/o expression estimation (transcript equivalence classes)
- Leverage longer reads (no assembly required?) (pacbio, nanopore)

Acknowledgements

BROAD INSTITUTE

Current and Former Trinity Contributors

Aviv Regev
* Brian Haas
Moran Yassour
Manfred Grabherr
Asma Bankapur
Tim Tickle
Christophe Georgescu
Vrushali Fangal
Maxwell Brown

igv

Jill Mesirov
James Robinson

Trinotate & TrinoateWeb
Brian Couger
Leonardo Gonzalez

BWH BRMC Brigham Regenerative Medicine Center

Salamander limb regeneration
Jessica Whited
Nick Leigh
Kim Johnson
Donald Bryant
Tia DiTommaso
Tae Lee
Anna Guzikowski

Trinity is funded by:

ITCR Informatics Technology for Cancer Research

NIH NATIONAL CANCER INSTITUTE

Transcriptomics Lab

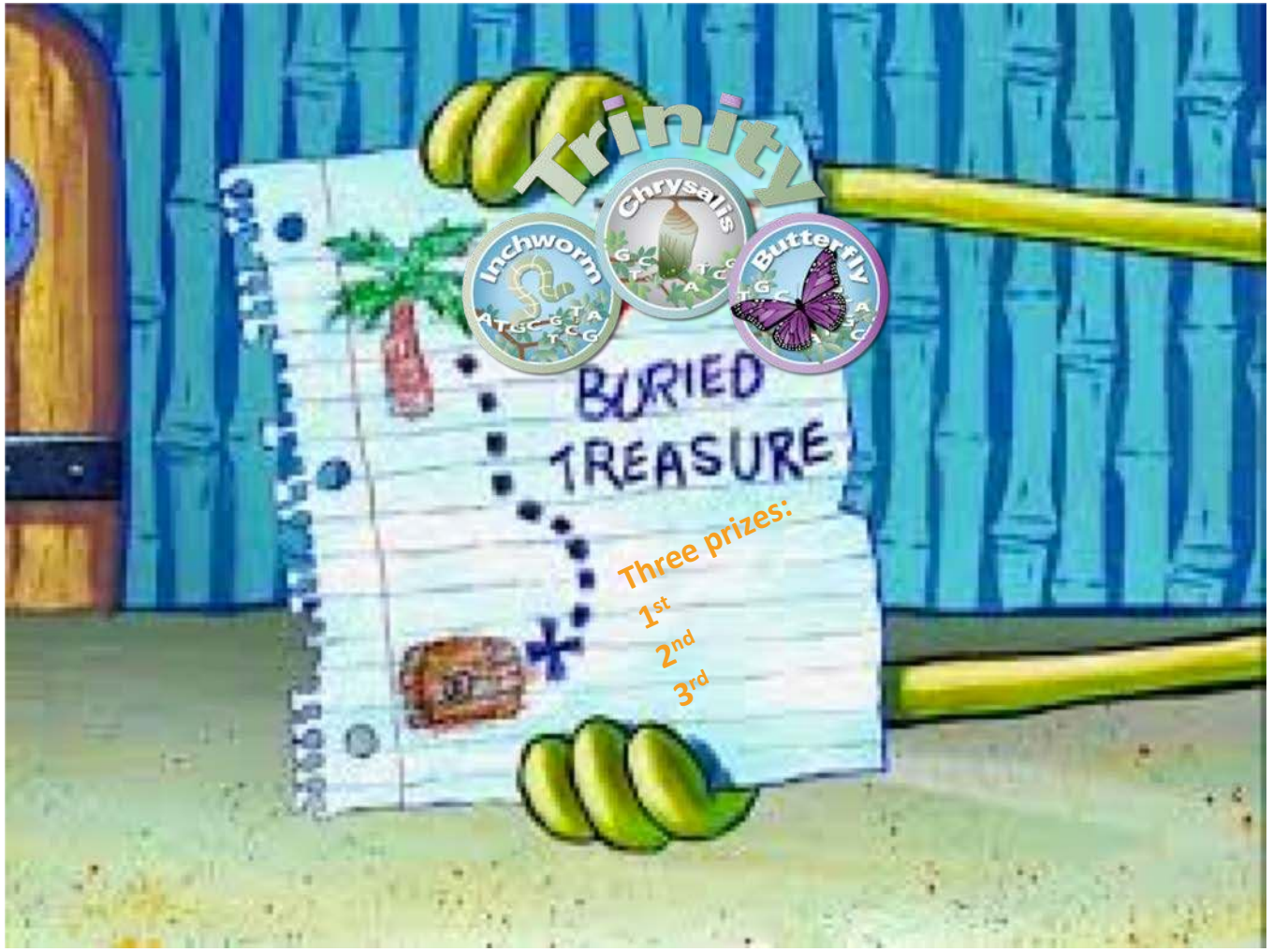
(Krumlov Prelate, 2-5pm)

De novo RNA-Seq Assembly, Annotation, and Analysis Using Trinity and Trinotate

The following details the steps involved in:

- Generating a Trinity de novo RNA-Seq assembly
- Evaluating the quality of the assembly
- Quantifying transcript expression levels
- Identifying differentially expressed (DE) transcripts
- Functionally annotating transcripts using Trinotate and predicting coding regions using TransDecoder
- Examining functional enrichments for DE transcripts using GOseq
- Interactively Exploring annotations and expression data via TrinotateWeb

Trinity Treasure Hunt!!! ☺



Will provide link to the challenge via slack – stay tuned, will start ~ 8pm

Slack channel: #transcriptomicslab