

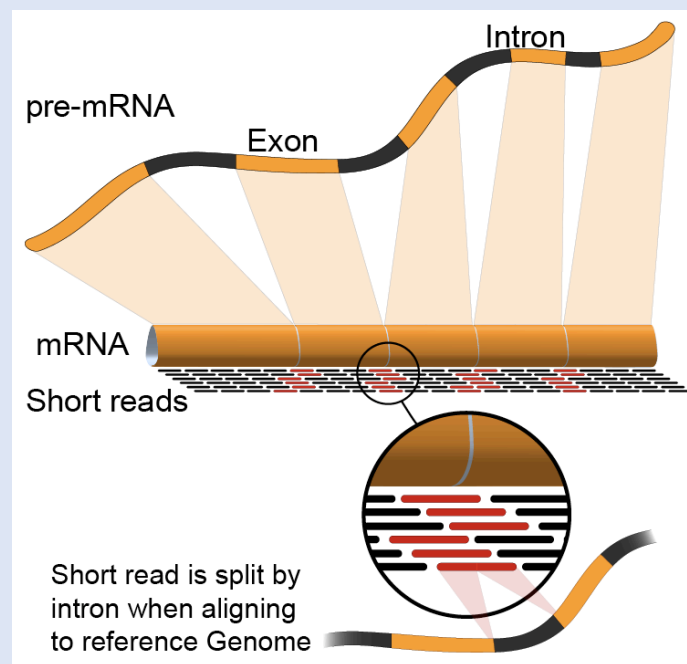


Cold  
Spring  
Harbor  
Laboratory

# RNA-Seq Module 2 Alignment QC

John Chamberlin, Kelsy Cotto, Felicia Gomez, Obi Griffith, Malachi Griffith,  
Simone Longo, Allegra Petti, Aaron Quinlan, Megan Richters, Huiming Xia  
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CSH Cold Spring Harbor Laboratory  
bioinformatics.ca

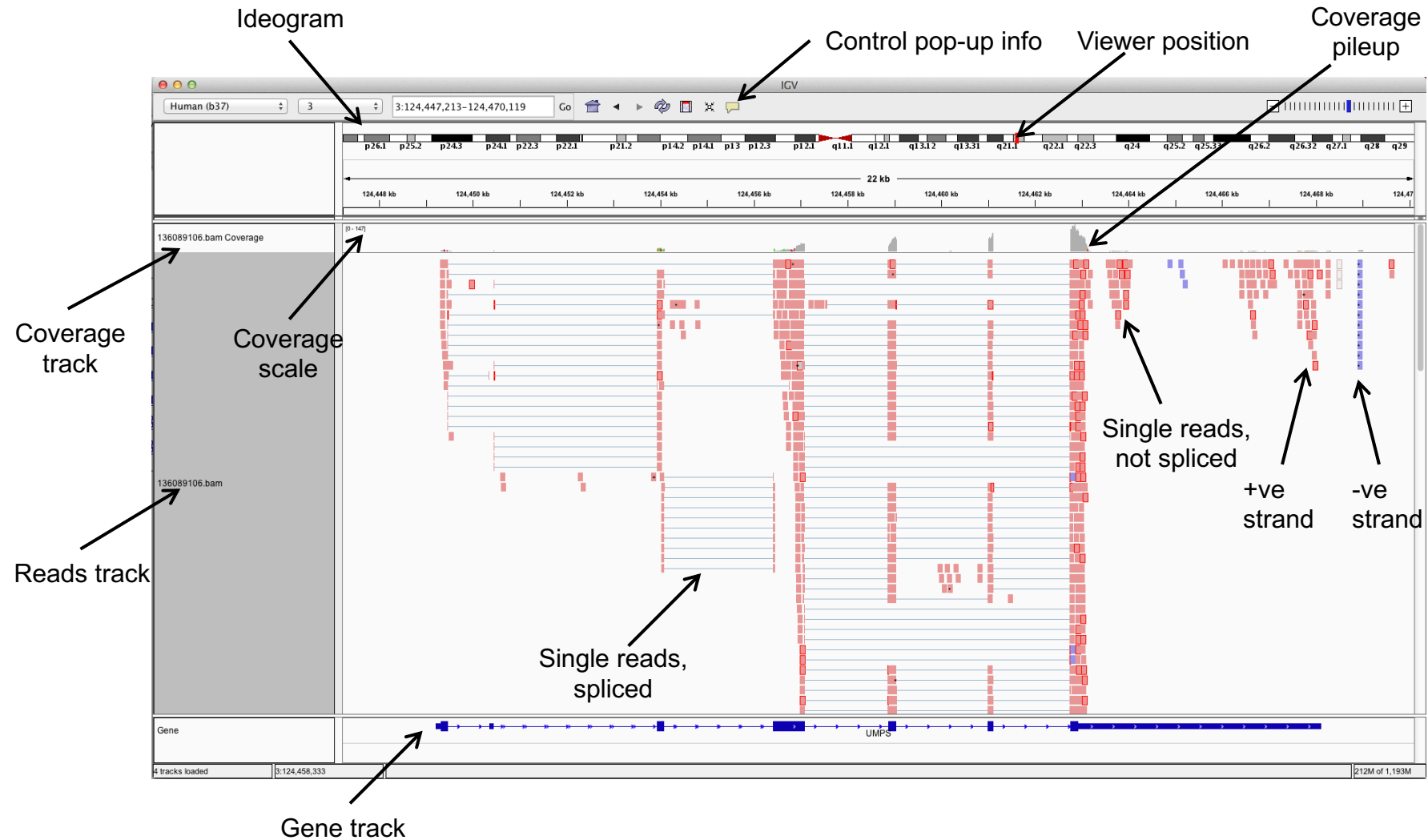


 Washington University in St. Louis  
SCHOOL OF MEDICINE

# Learning objectives of module 3

- Visualization of RNA-seq alignments in IGV
- Alignment QC Assessment
- BAM read counting and determination of variant allele expression status

# Visualization of RNA-seq alignments in IGV browser



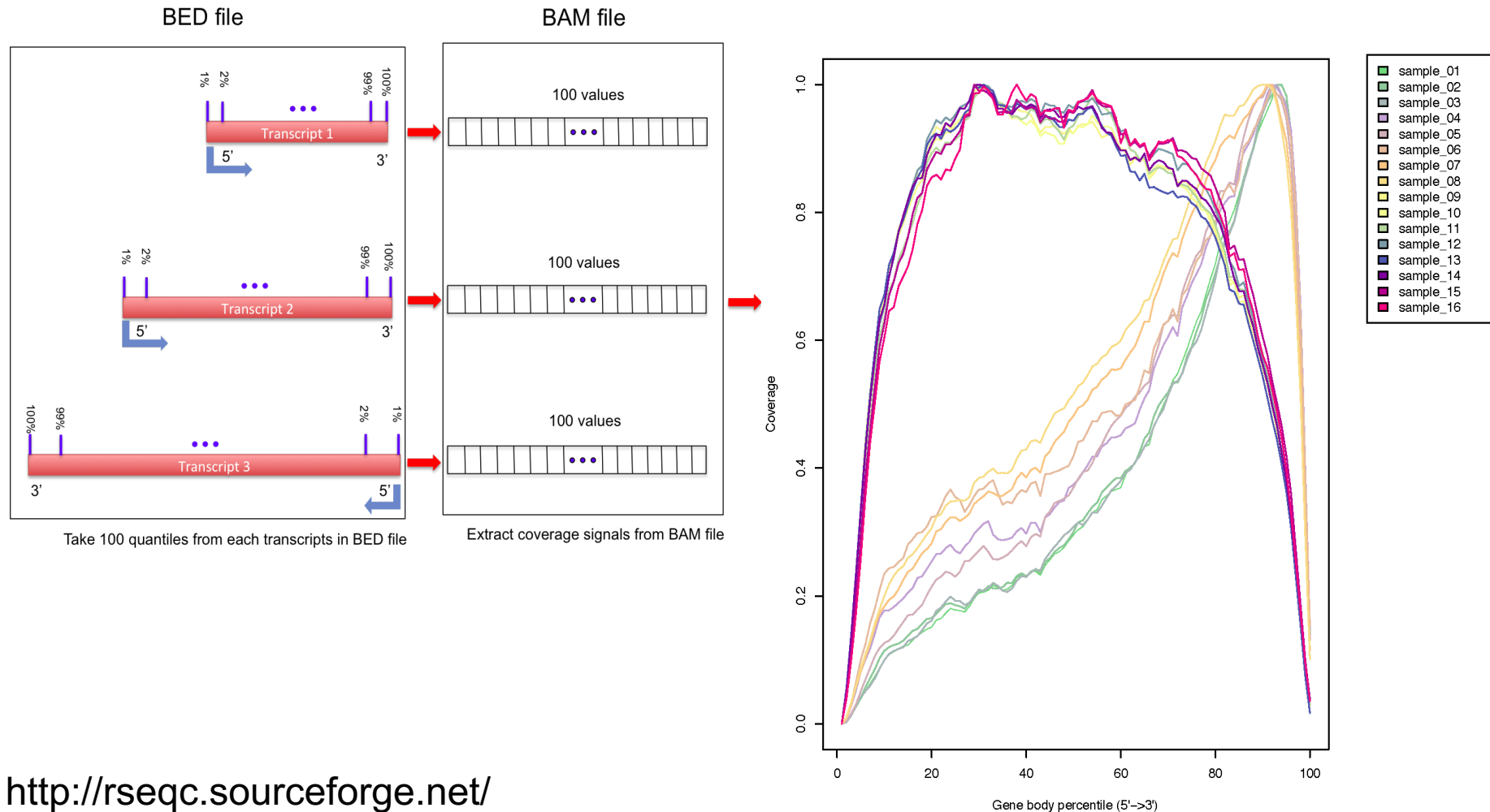
# Alternative viewers to IGV

- Alternative viewers to IGV
  - <http://www.biostars.org/p/12752/>
  - <http://www.biostars.org/p/71300/>
- Artemis, BamView, Chipster, gbrowse2, GenoViewer, MagicViewer, **Savant**, Tablet, tview

# Alignment QC Assessment

- 3' and 5' Bias
- Nucleotide Content
- Base/Read Quality
- PCR Artifact
- Sequencing Depth
- Base Distribution
- Insert Size Distribution

# Alignment QC: 3' & 5' Bias



# Alignment QC: Nucleotide Content

- **Random primers** are used to reverse transcribe RNA fragments into double-stranded complementary DNA (dscDNA)
- Causes certain patterns to be over represented at the beginning (5' end) of reads
- Deviation from expected  $A\% = C\% = G\% = T\% = 25\%$

Journal List > Nucleic Acids Res > v.38(12); 2010 Jul > PMC2896536

Nucleic Acids Research

Nucleic Acids Res. 2010 Jul; 38(12): e131.

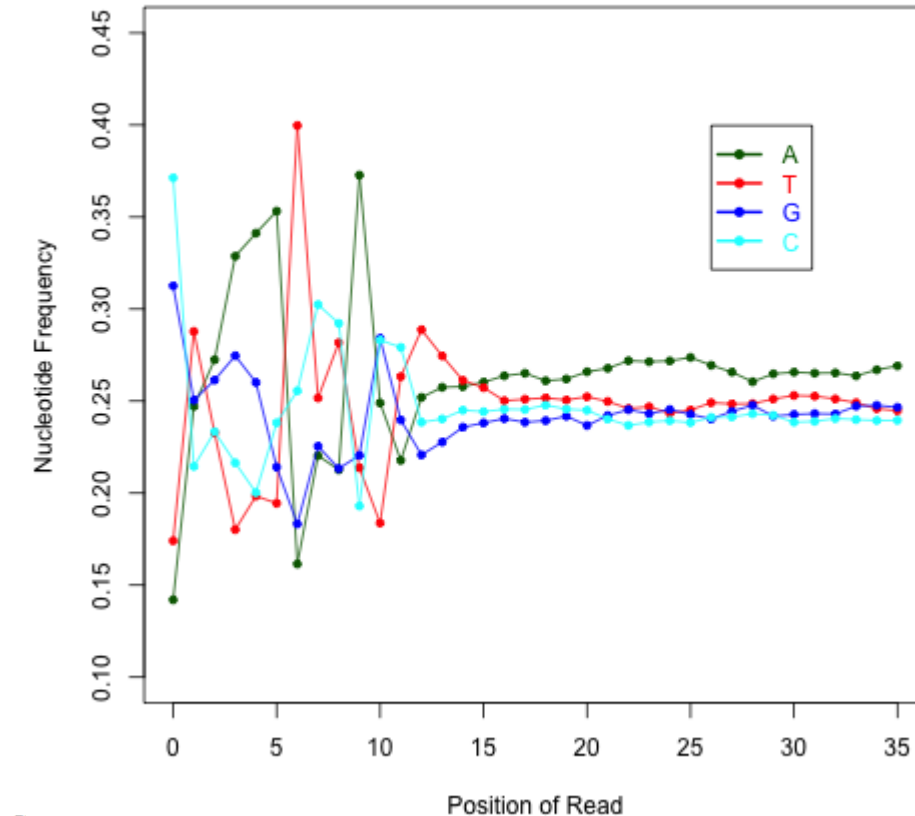
Published online 2010 Apr 14. doi: [10.1093/nar/gkq224](https://doi.org/10.1093/nar/gkq224)

## Biases in Illumina transcriptome sequencing caused by random hexamer priming

Kasper D. Hansen,<sup>1,\*</sup> Steven E. Brenner,<sup>2</sup> and Sandrine Dudoit<sup>1,3</sup>

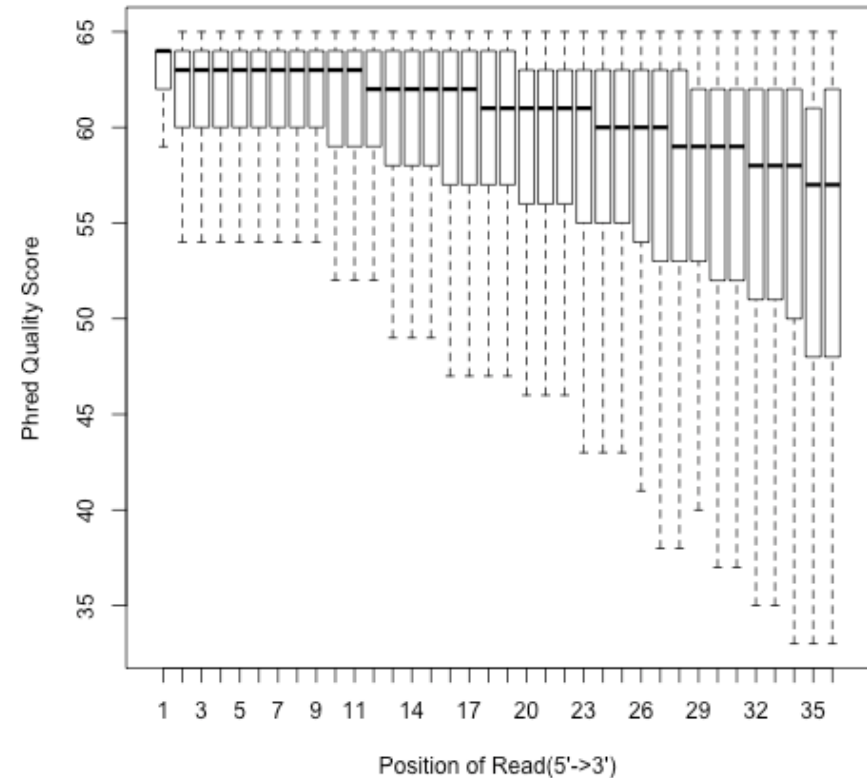
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# Alignment QC: Quality Distribution

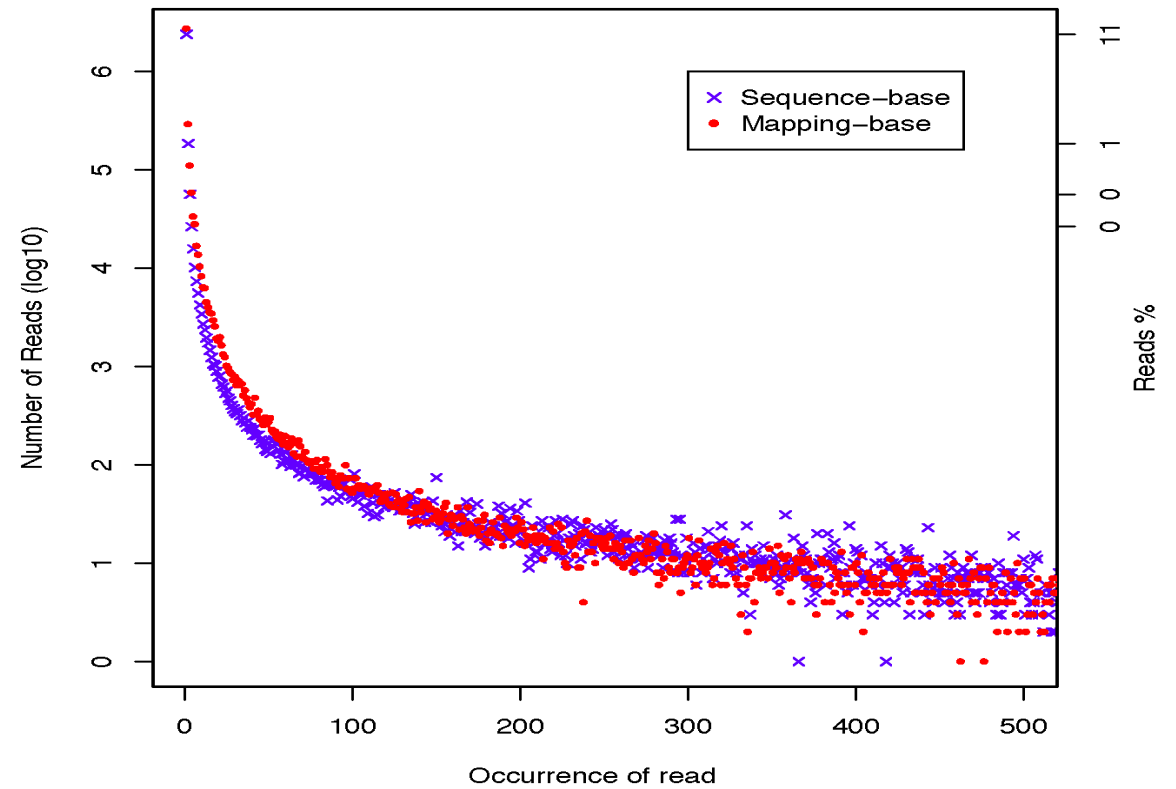
- Phred quality score is widely used to characterize the quality of base-calling
- Phred quality score =  $-10 \times \log_{10}(P)$ , here  $P$  is probability that base-calling is wrong
- Phred score of 30 means there is 1/1000 chance that the base-calling is wrong
- The quality of the bases tend to drop at the end of the read, a pattern observed in sequencing by synthesis techniques





# Alignment QC: PCR Duplication

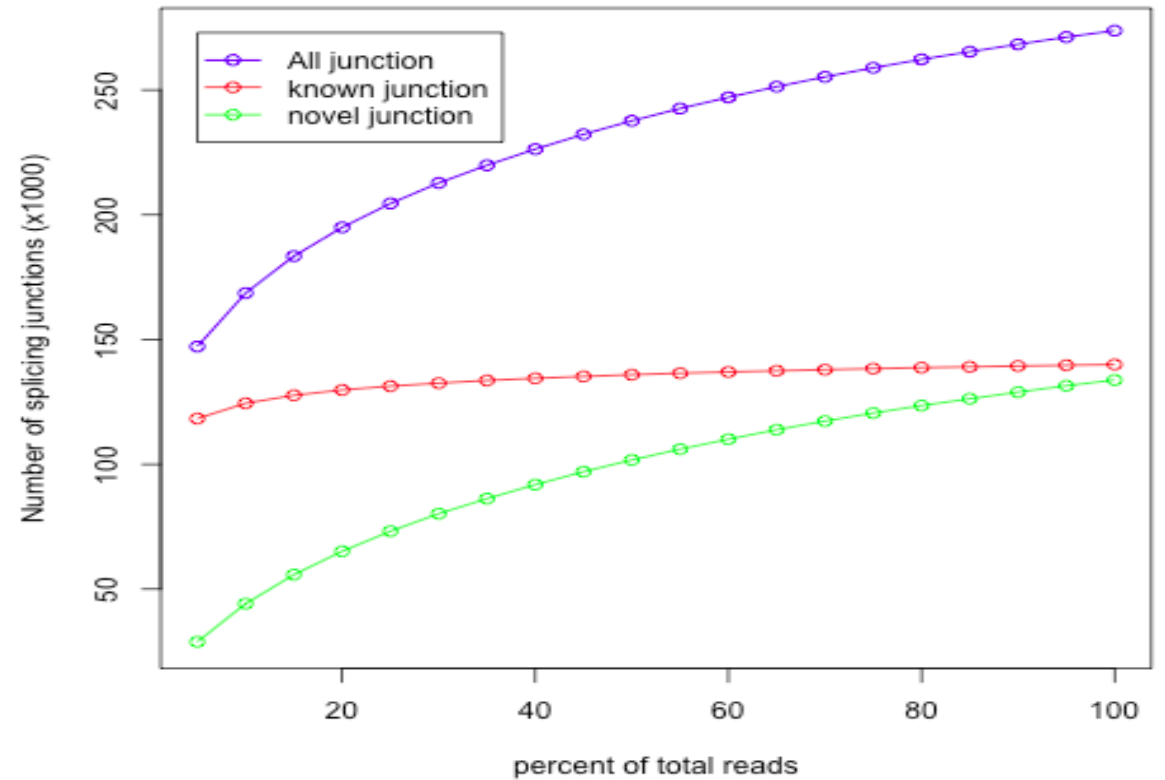
- Duplicate reads are reads that have the same start/end positions and same exact sequence
- In DNA-seq, reads/start point is used as a metric to assess PCR duplication rate
- In DNA-seq, duplicate reads are collapsed using tools such as picard
- How is RNA-seq different from DNA-seq?



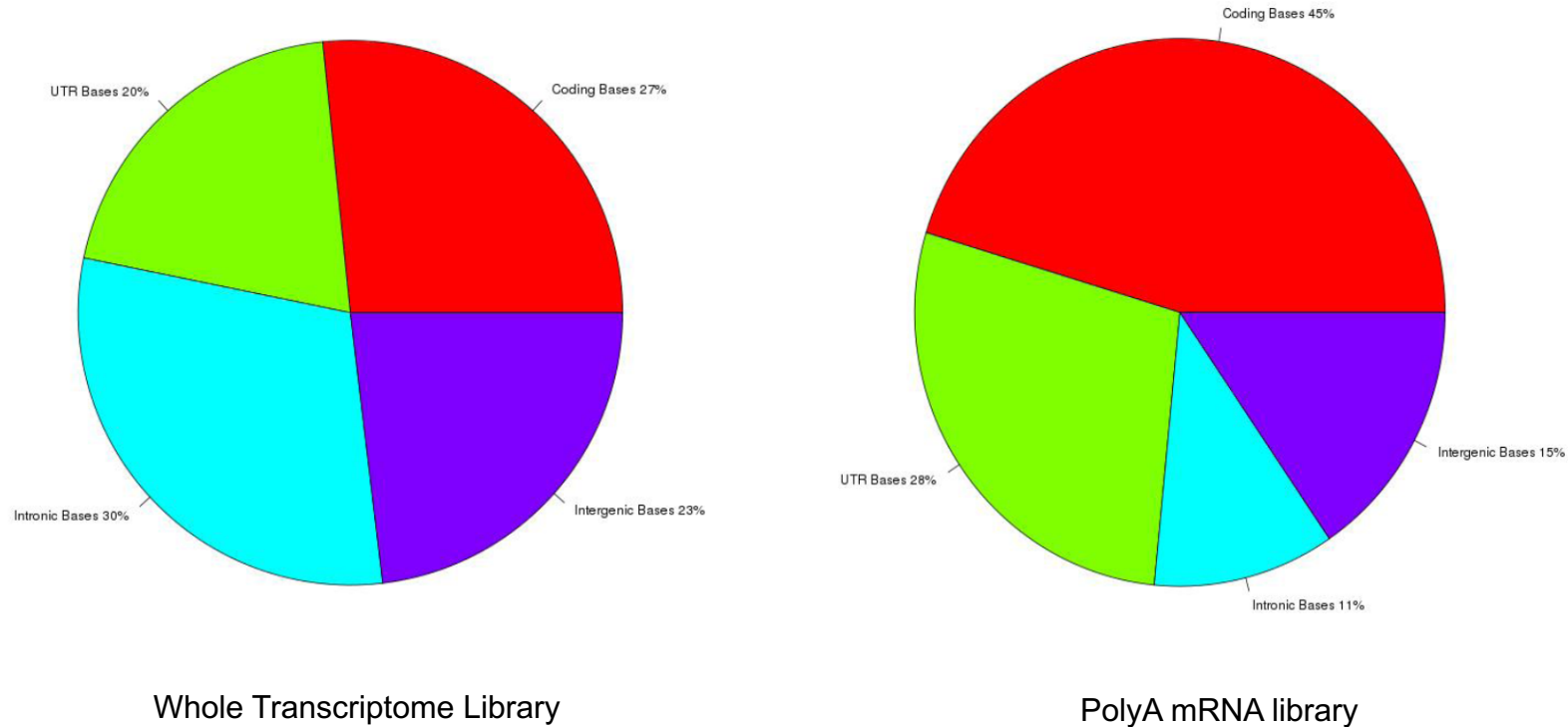
<http://rseqc.sourceforge.net/>

# Alignment QC: Sequencing Depth

- **Have we sequenced deep enough?**
- In DNA-seq, we can determine this by looking at the average coverage over the sequenced region. Is it above a certain threshold?
- In RNA-seq, this is a challenge due to the variability in gene abundance
- Use splice junctions detection rate as a way to identify desired sequencing depth
- Check for saturation by resampling 5%, 10%, 15%, ..., 95% of total alignments from aligned file, and then detect splice junctions from each subset and compare to reference gene model.
- This method ensures that you have sufficient coverage to perform alternative splicing analyses

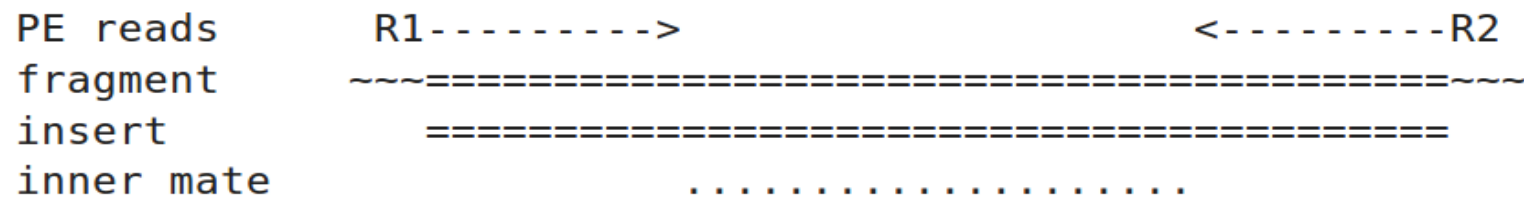
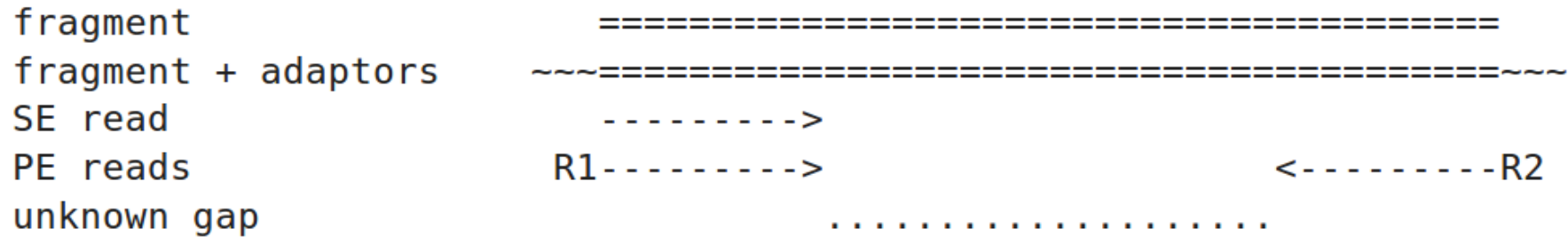


# Alignment QC: Base Distribution



- Your sequenced bases distribution will depend on the library preparation protocol selected

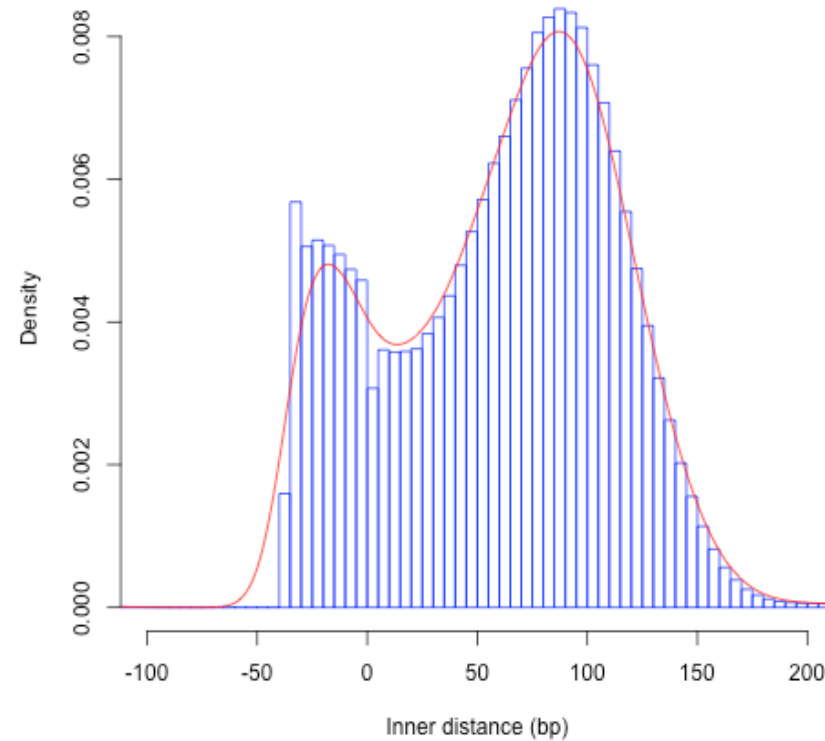
# Alignment QC: Insert Size



<http://thegenomefactory.blogspot.ca/2013/08/paired-end-read-confusion-library.html>

# Alignment QC: Insert Size

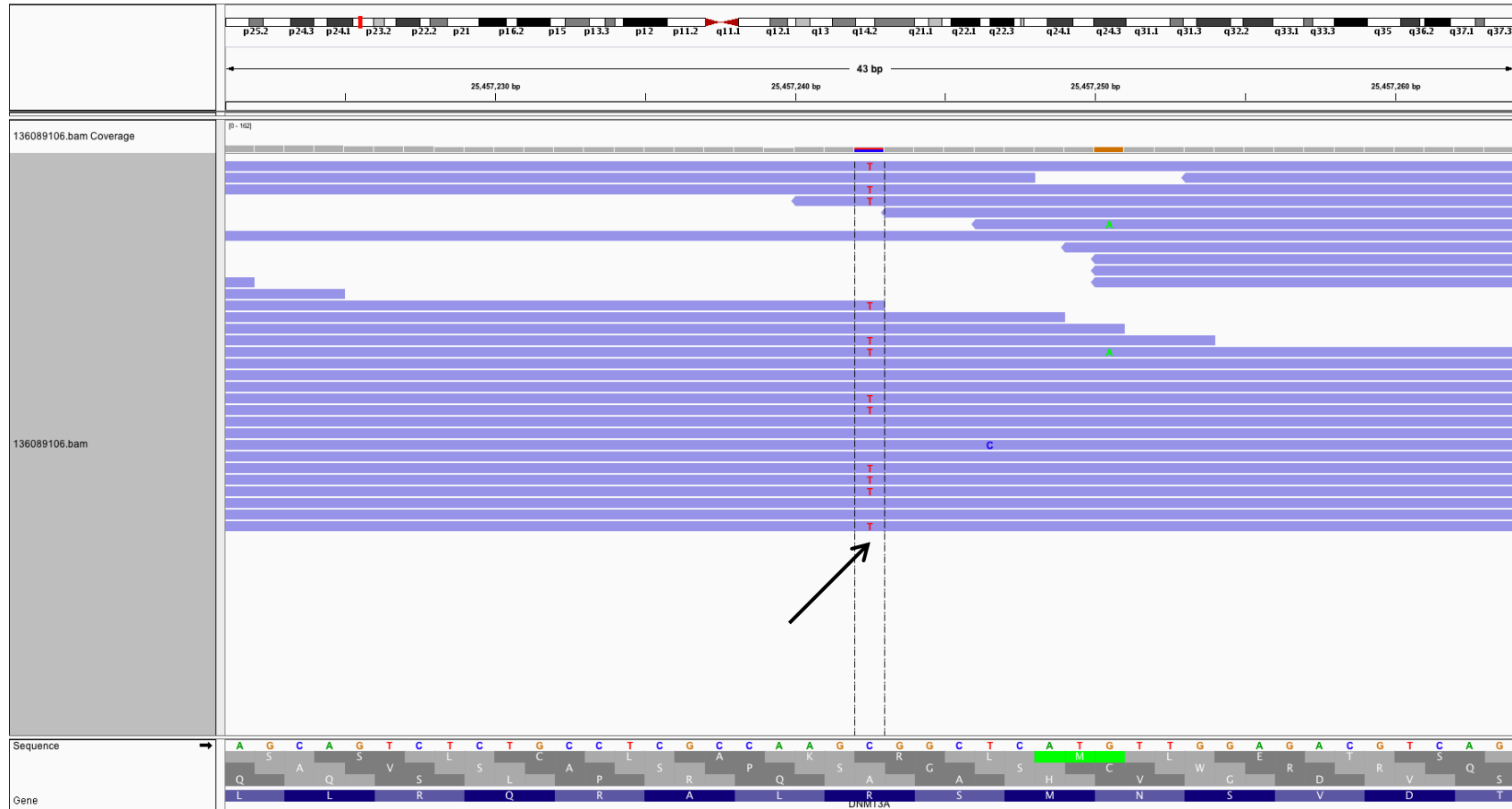
Mean=60;SD=52



Consistent with library size selection?

<http://rseqc.sourceforge.net>

# BAM read counting and variant allele expression status



- A variant C->T is observed in 12 of 25 reads covering this position. Variant allele frequency (VAF)  $12/25 = 48\%$ .
- Both alleles appear to be expressed equally (not always the case) -> heterozygous, no allele specific expression
- How can we determine variant read counts, depth of coverage, and VAF without manually viewing in IGV?

We are on a Coffee Break &  
Networking Session