

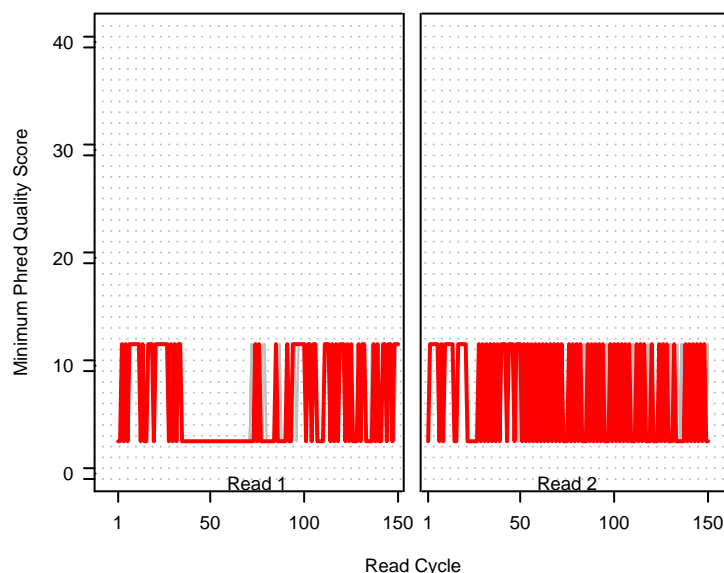
a

Sample Highlight:  
srpk3\_hom\_ttnb\_het\_8  
Colored by Lane



b

Minimum Phred Quality Score  
With Sample srpk3\_hom\_ttnb\_het\_8 Colored by lane



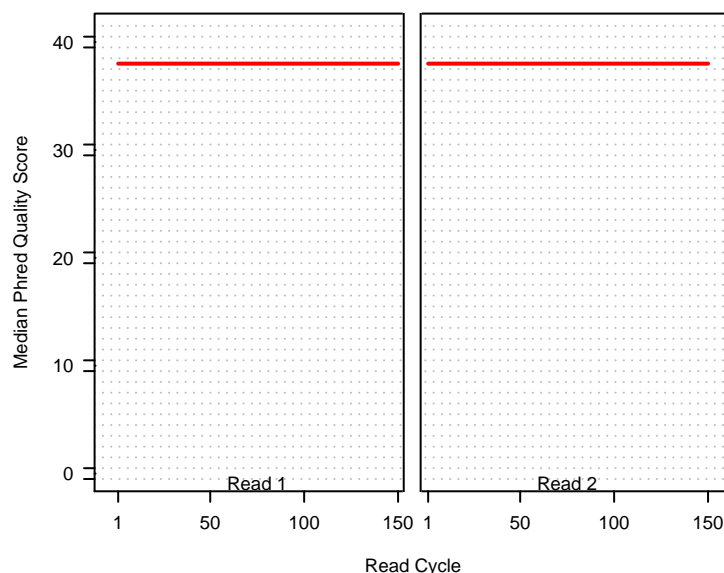
c

Lower Quartile Phred Quality Score  
With Sample srpk3\_hom\_ttnb\_het\_8 Colored by lane



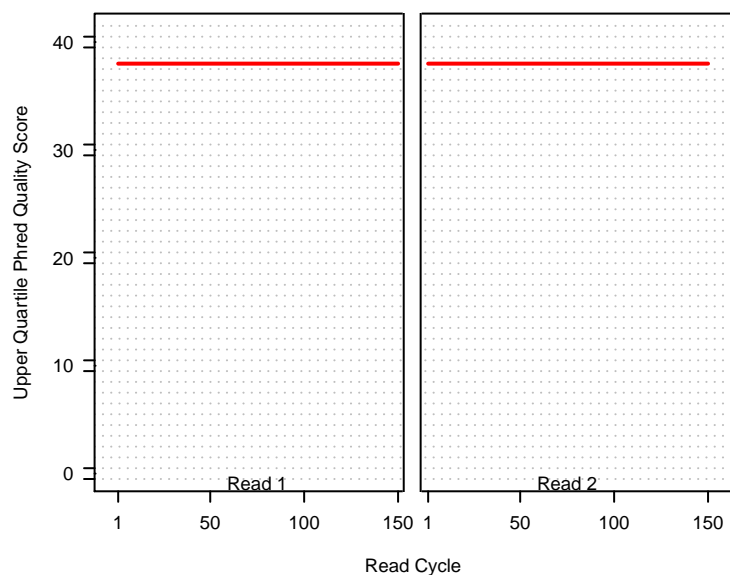
d

Median Phred Quality Score  
With Sample srpk3\_hom\_ttnb\_het\_8 Colored by lane



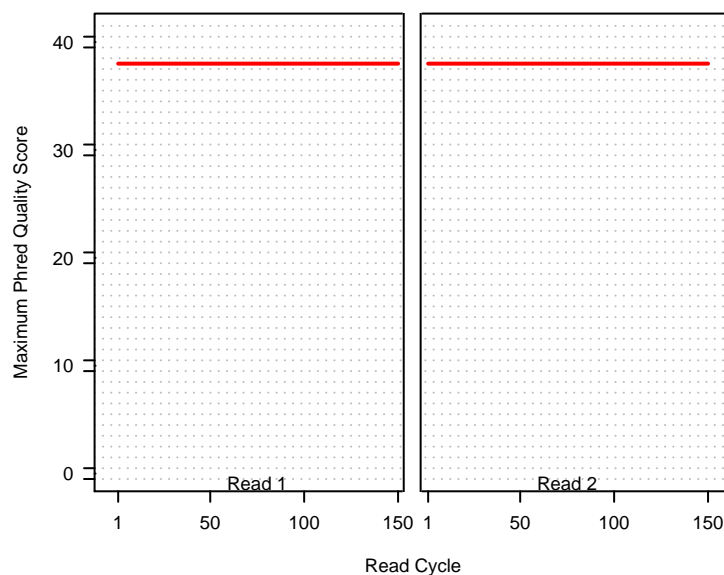
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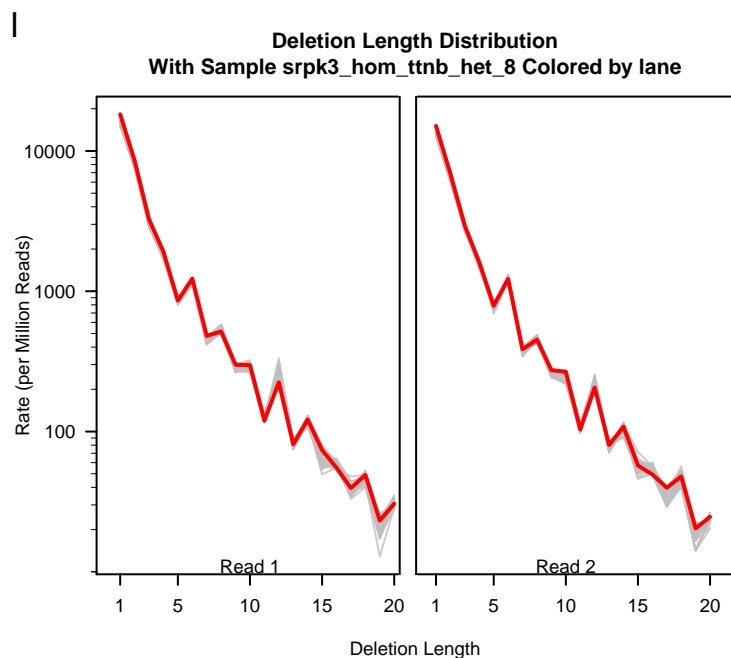
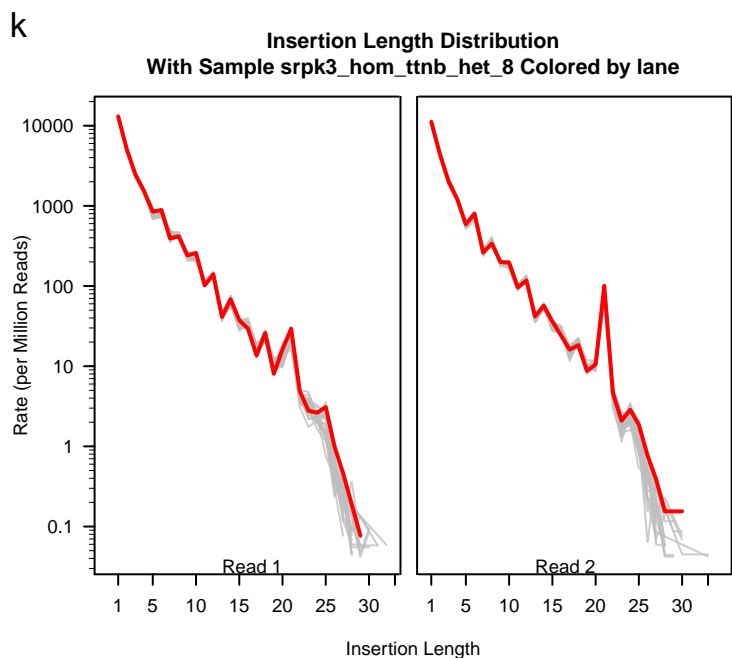
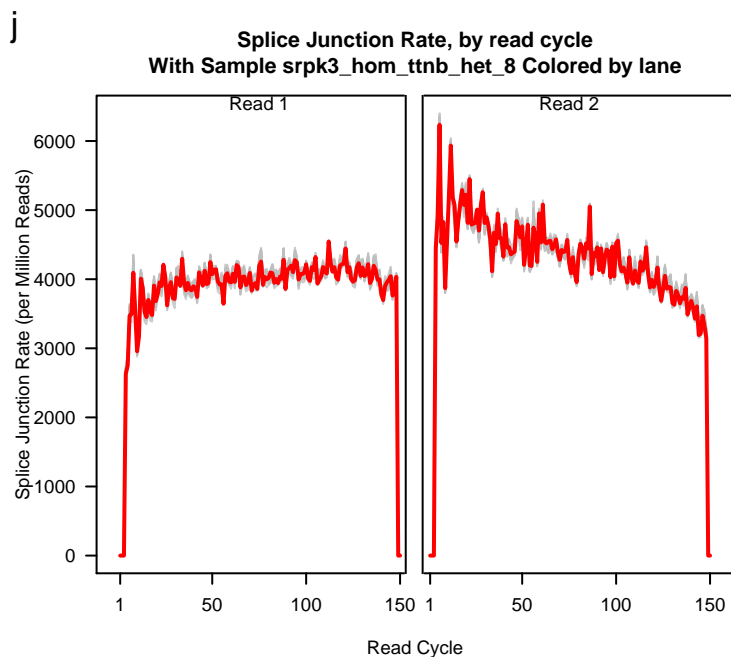
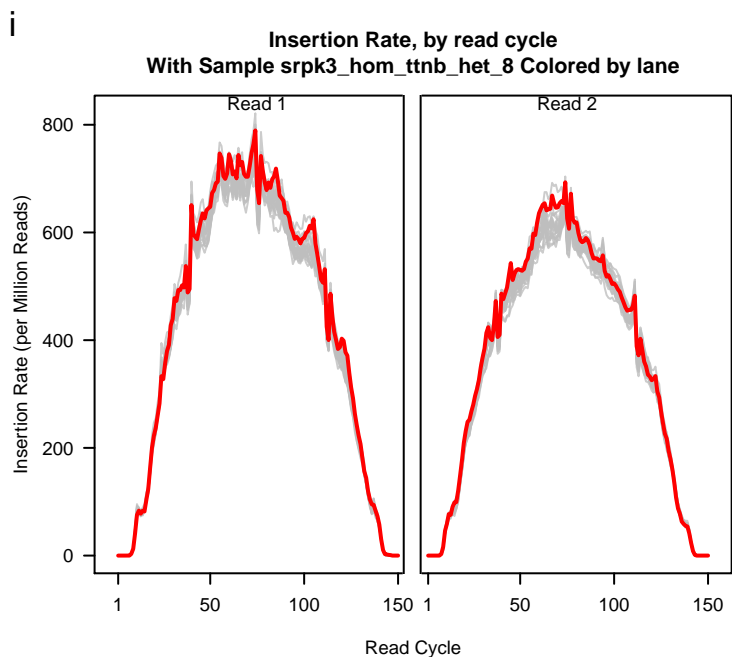
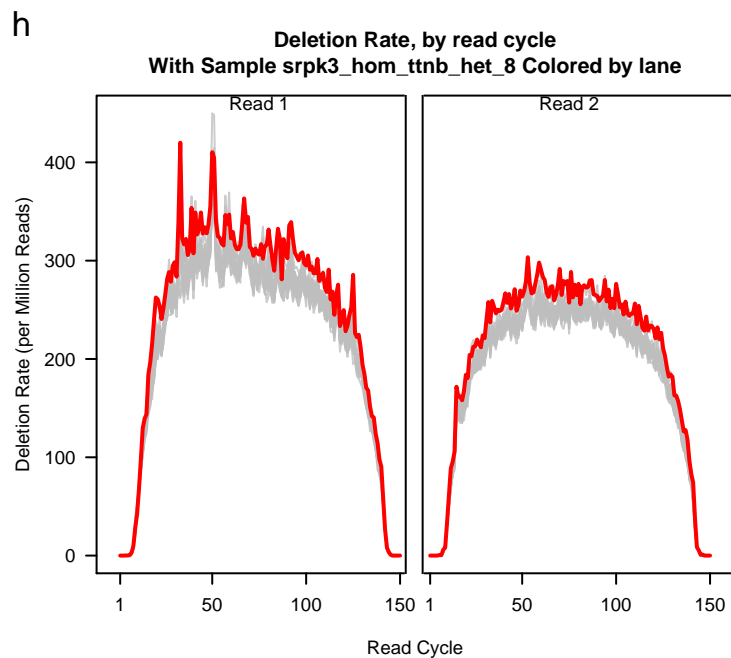
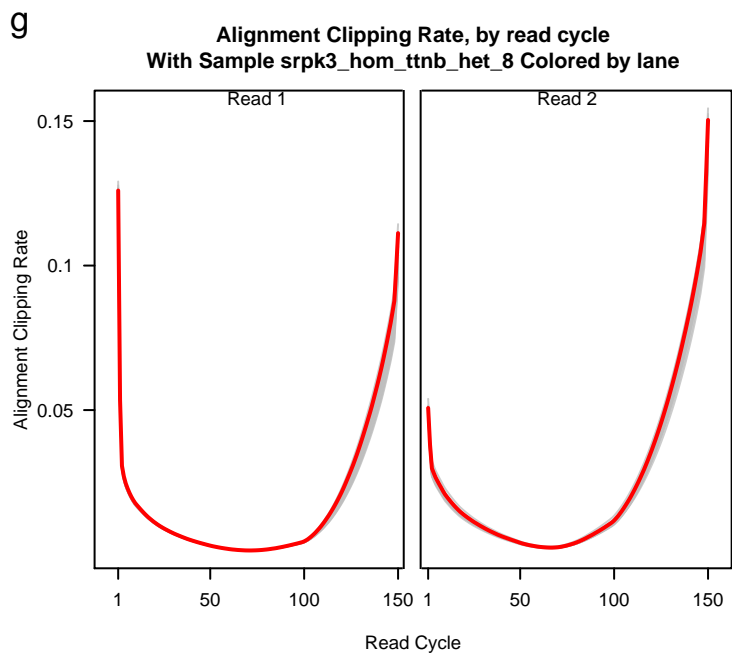
Upper Quartile Phred Quality Score  
With Sample srpk3\_hom\_ttnb\_het\_8 Colored by lane

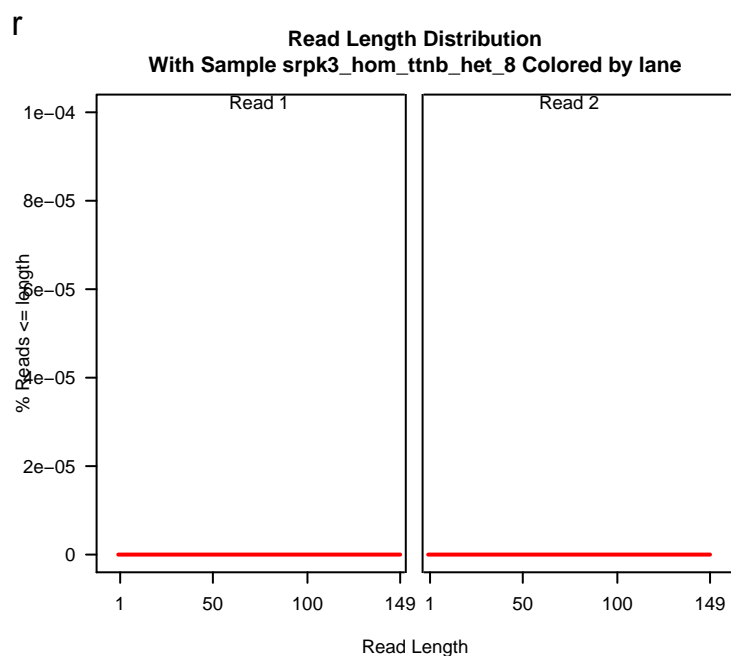
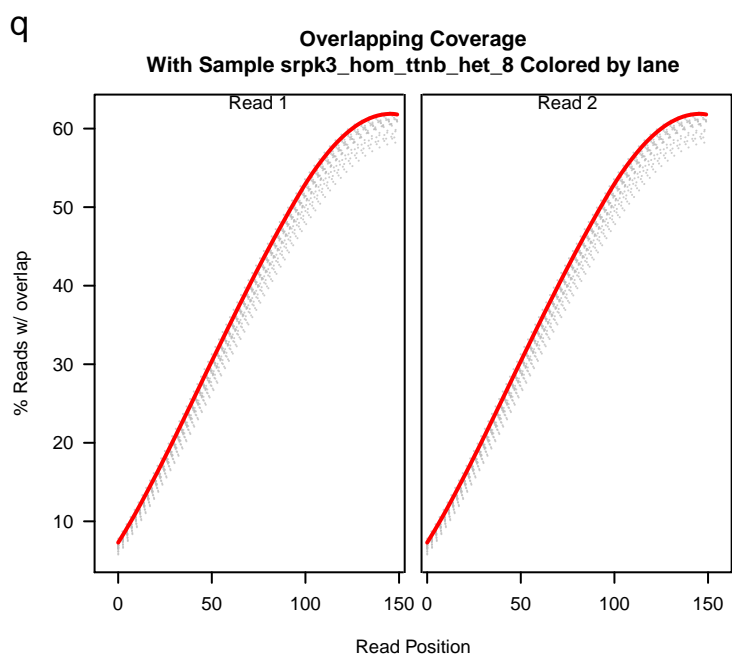
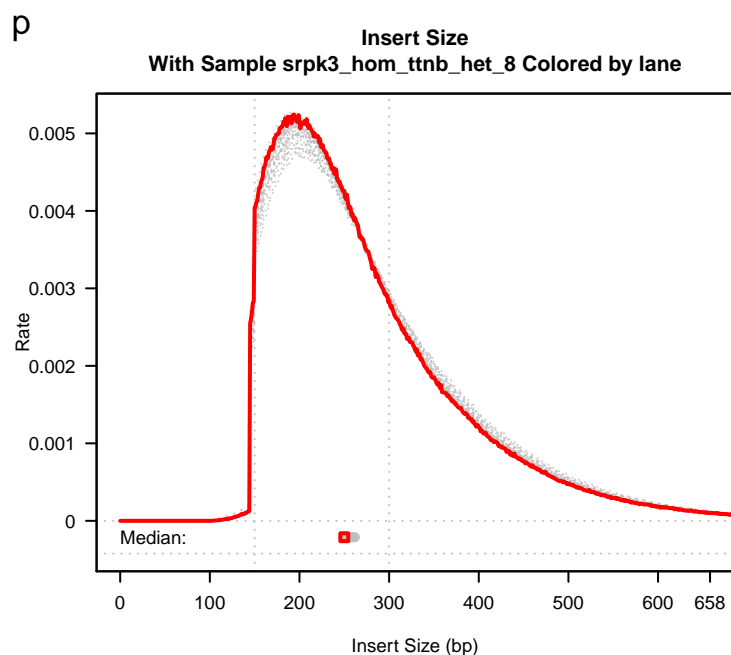
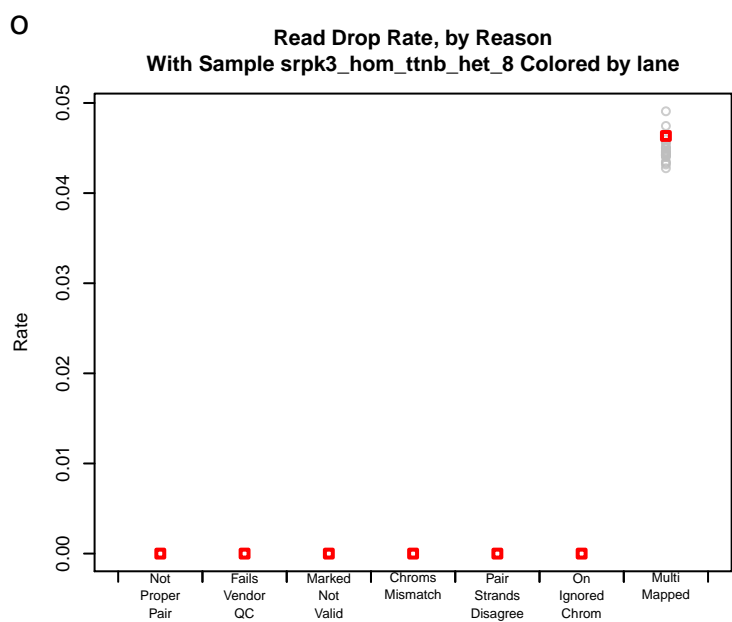
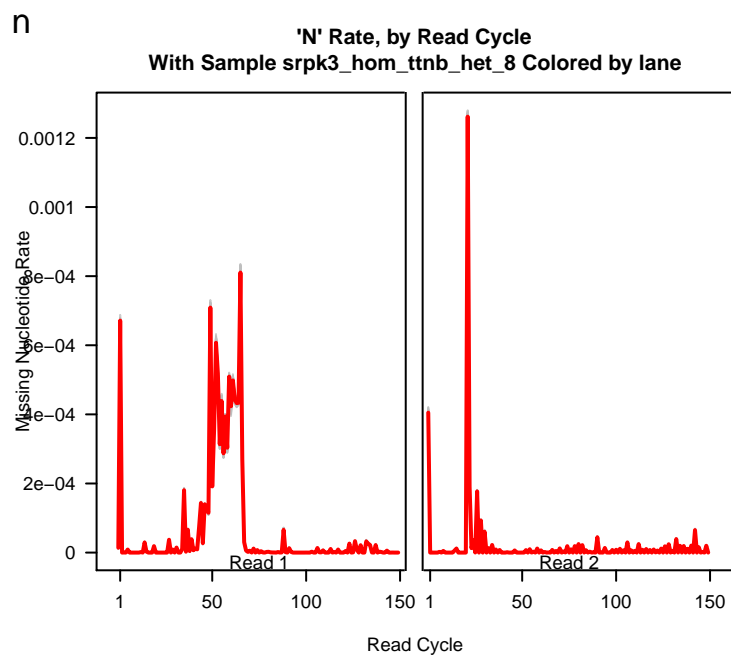
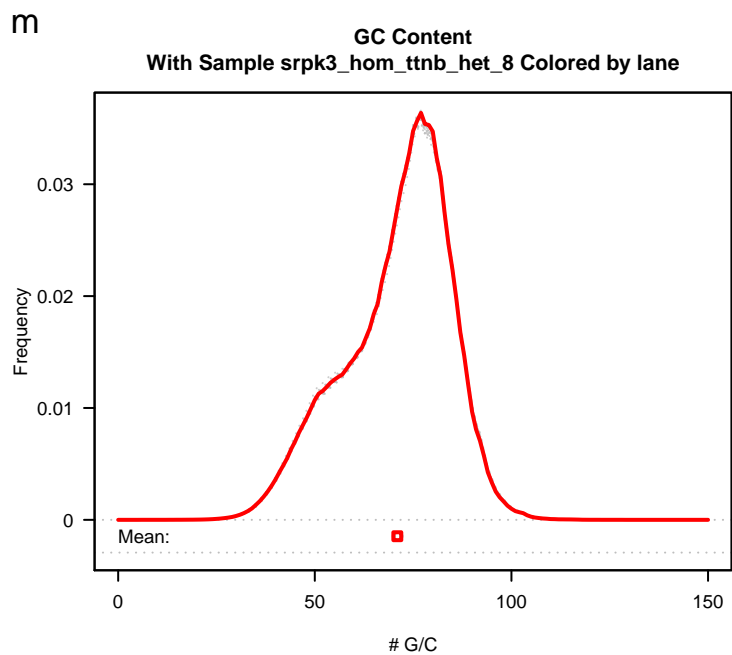


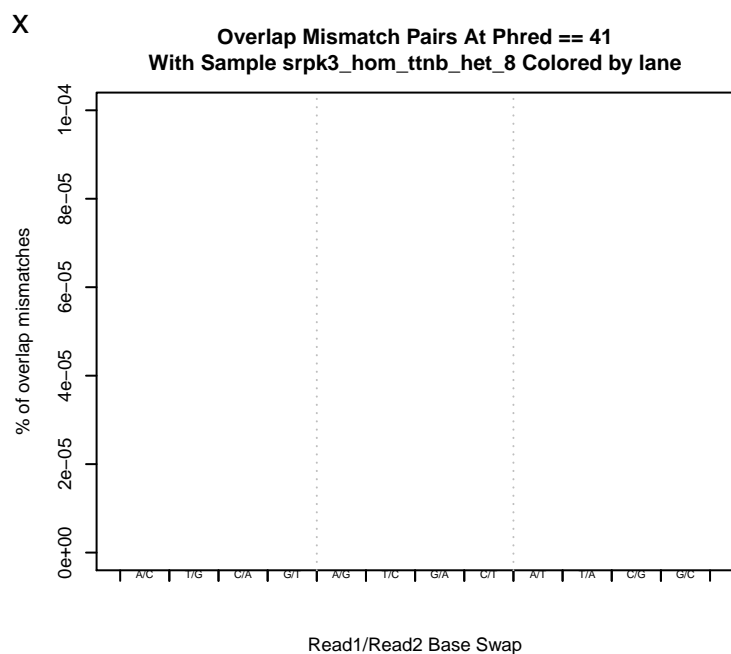
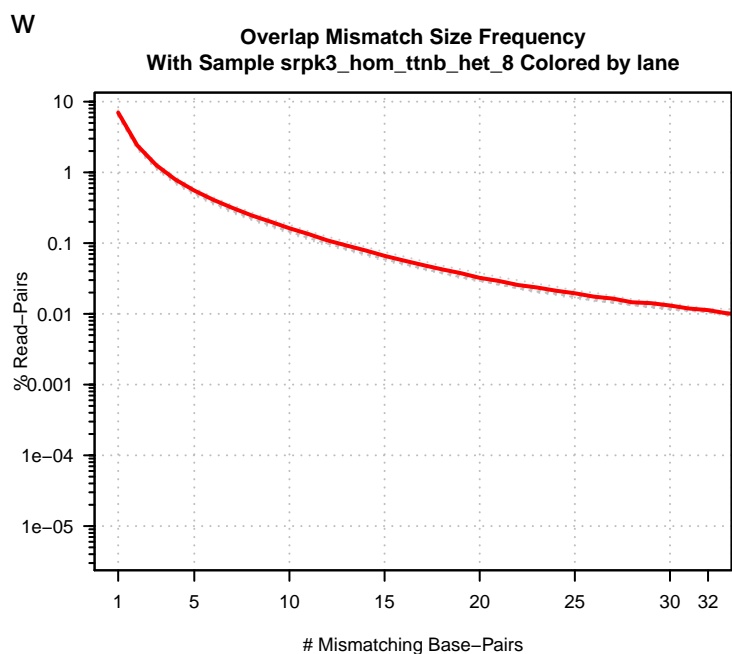
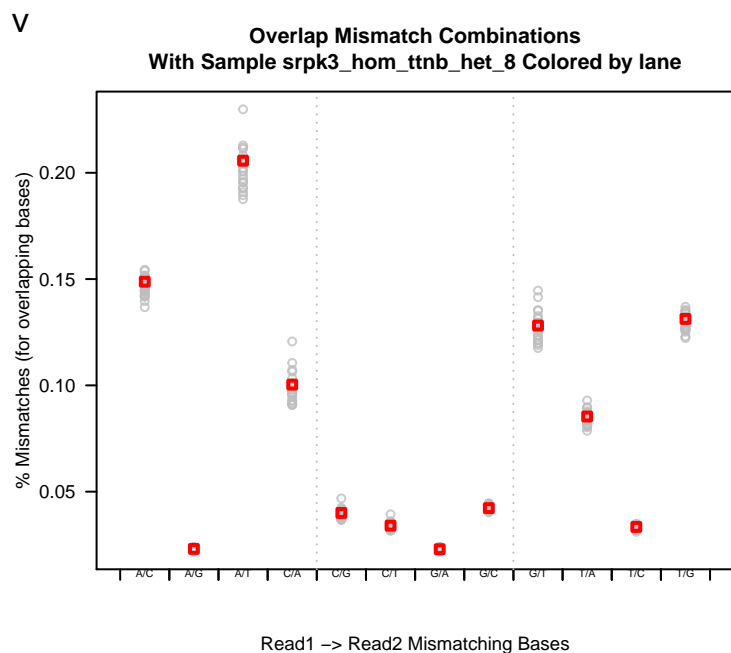
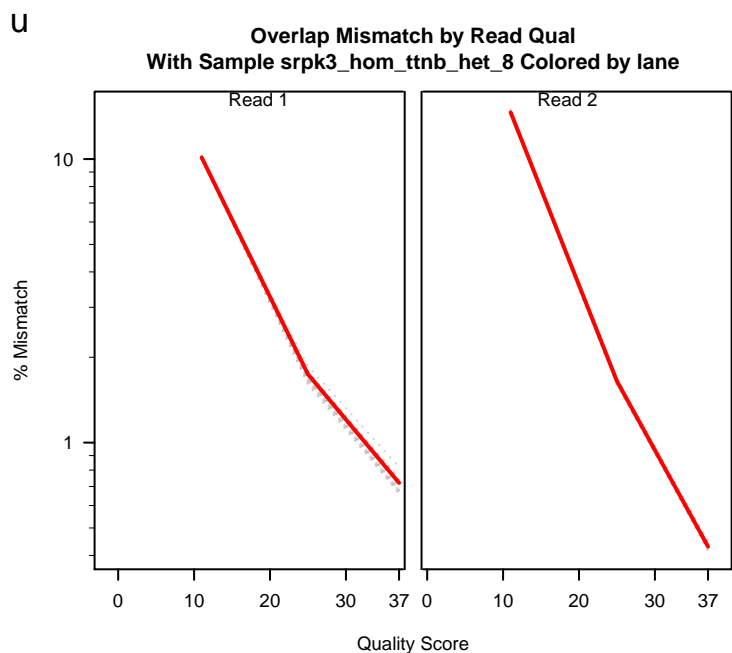
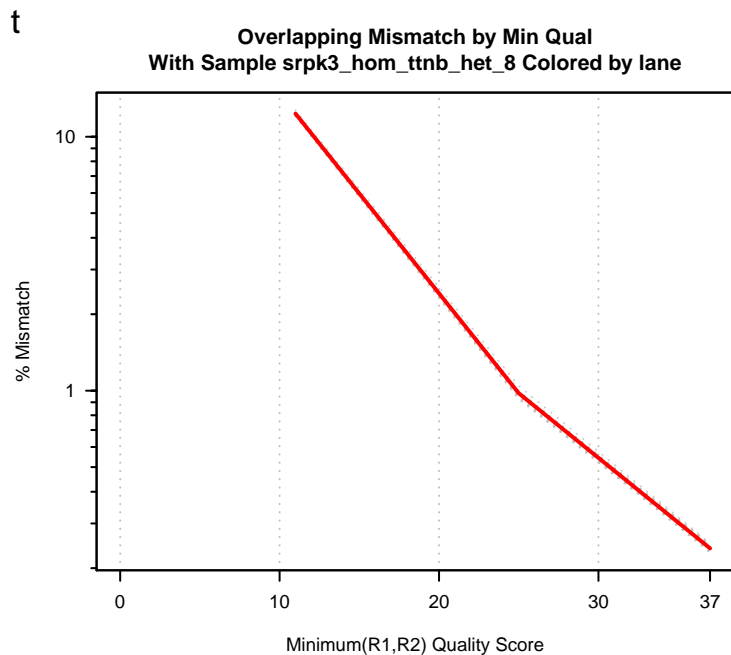
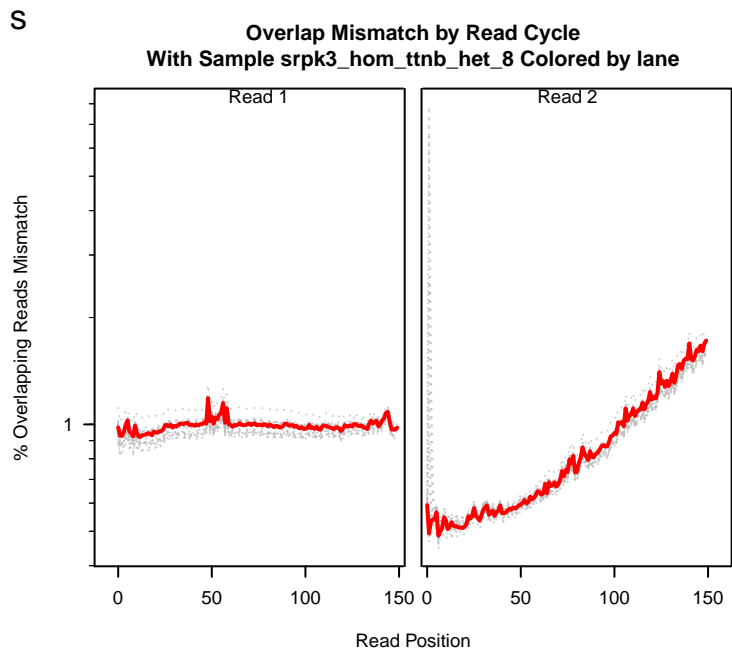
f

Maximum Phred Quality Score  
With Sample srpk3\_hom\_ttnb\_het\_8 Colored by lane



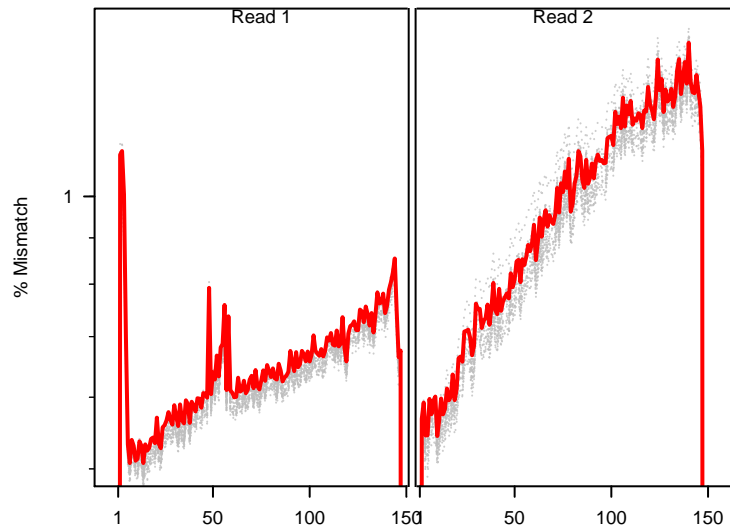






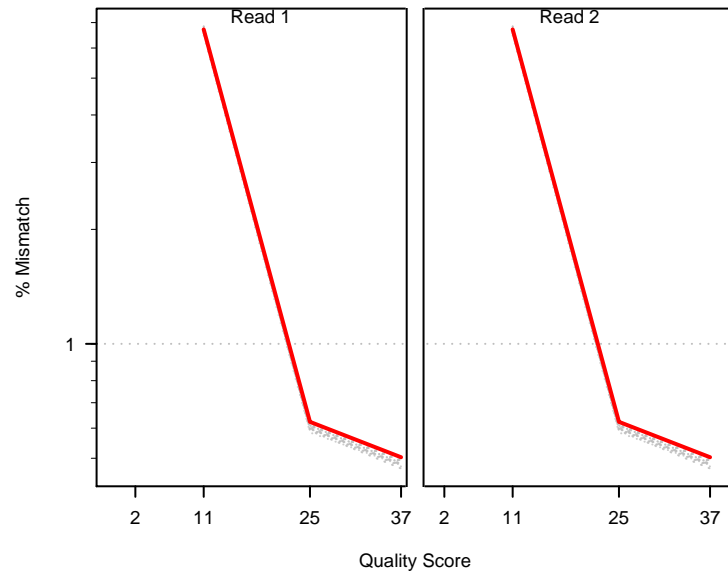
y

**Reference Mismatch by Read Cycle**  
With Sample *srpk3\_hom\_ttnb\_het\_8* Colored by lane



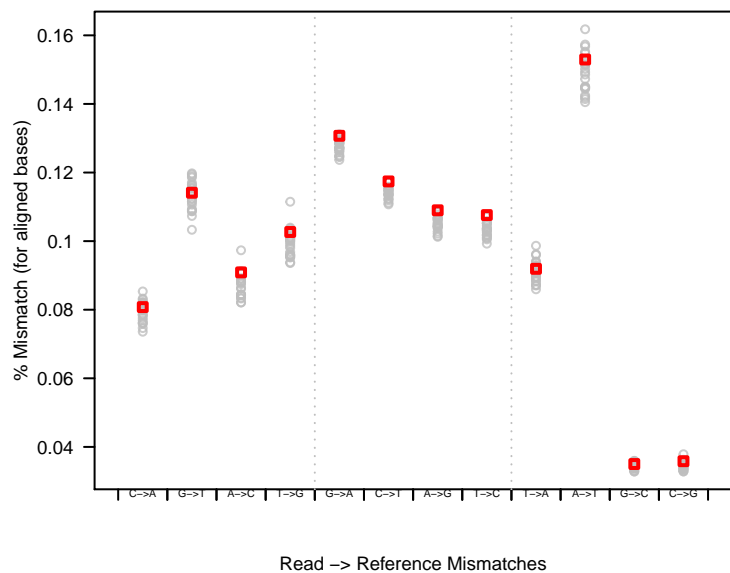
Z

**Reference Mismatch by Read Qual**  
With Sample *srpk3\_hom\_ttnb\_het\_8* Colored by lane



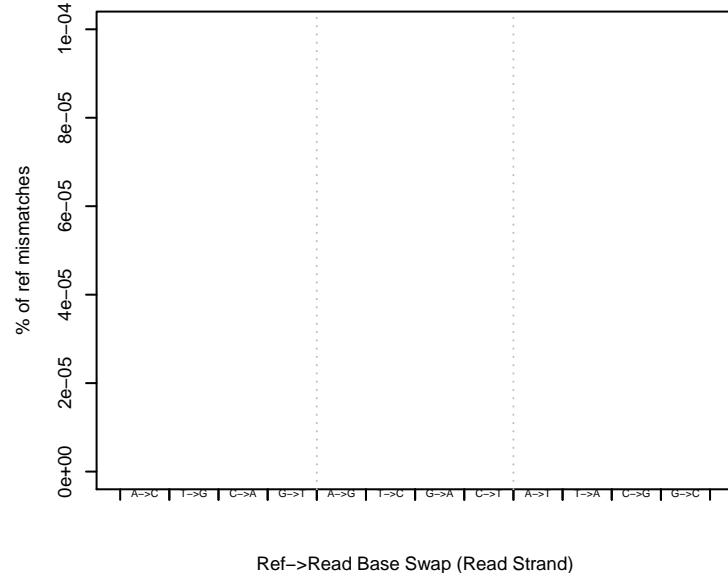
aa

**Reference Mismatch Combinations**  
With Sample *srpk3\_hom\_ttnb\_het\_8* Colored by lane



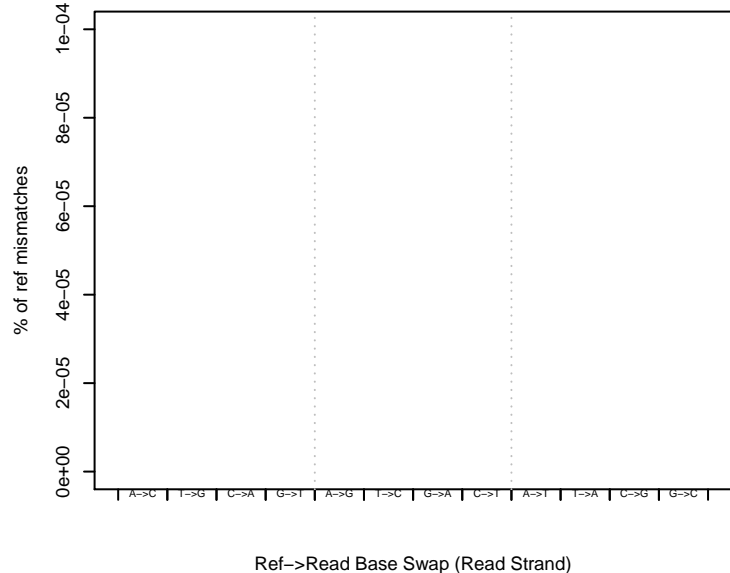
ab

**R1 Ref Mismatches At Phred == 41**  
With Sample *srpk3\_hom\_ttnb\_het\_8* Colored by lane



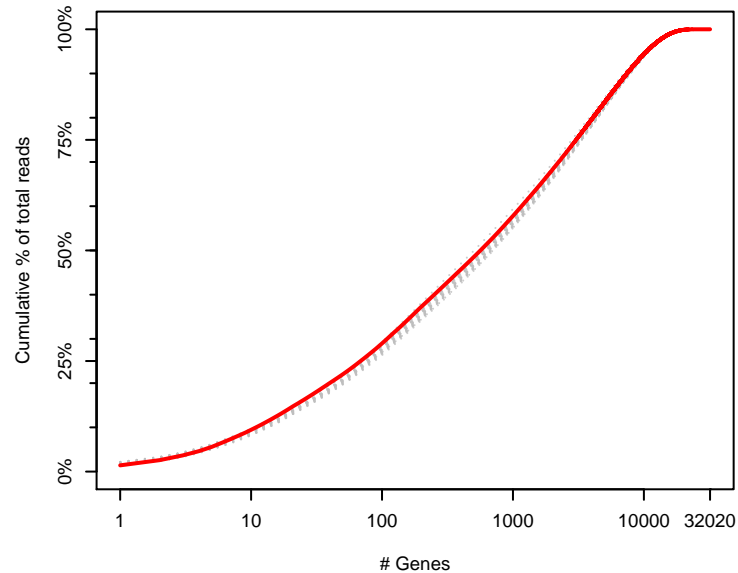
ac

**R2 Ref Mismatches At Phred == 41**  
With Sample *srpk3\_hom\_ttnb\_het\_8* Colored by lane



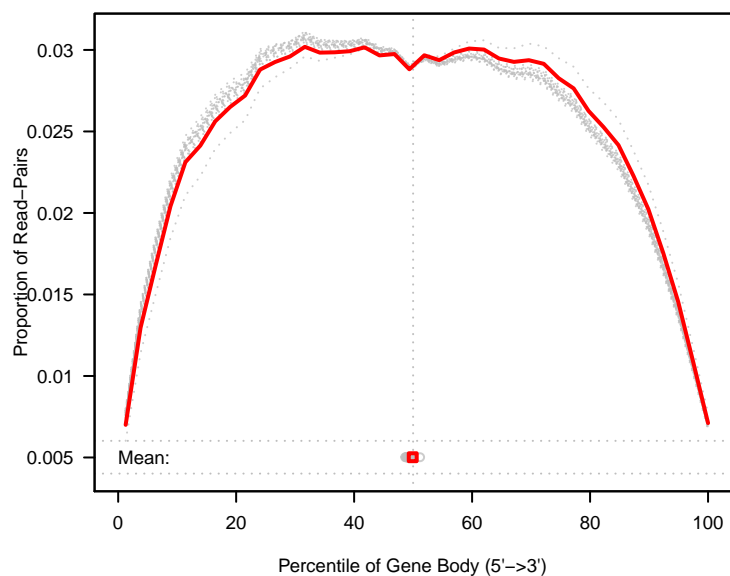
ad

**Cumulative Gene Assignment Diversity**  
With Sample *srpk3\_hom\_ttnb\_het\_8* Colored by lane



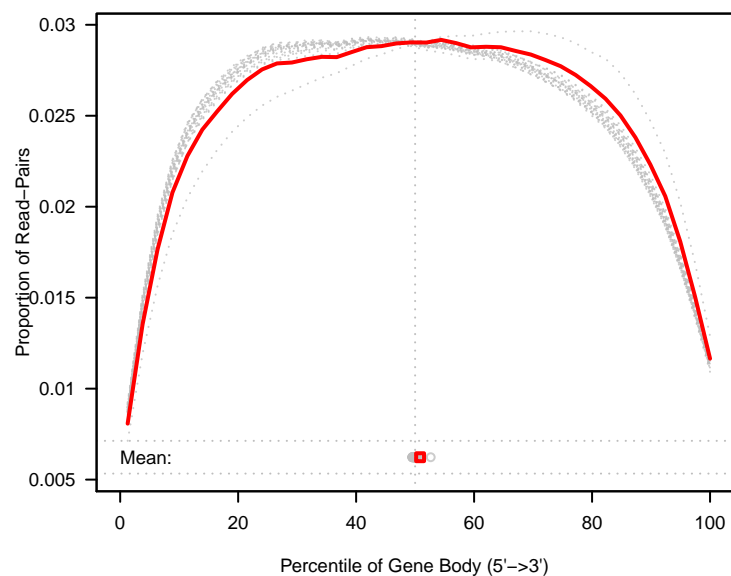
ae

**Gene–Body Coverage**  
With Sample *srpk3\_hom\_ttnb\_het\_8* Colored by lane



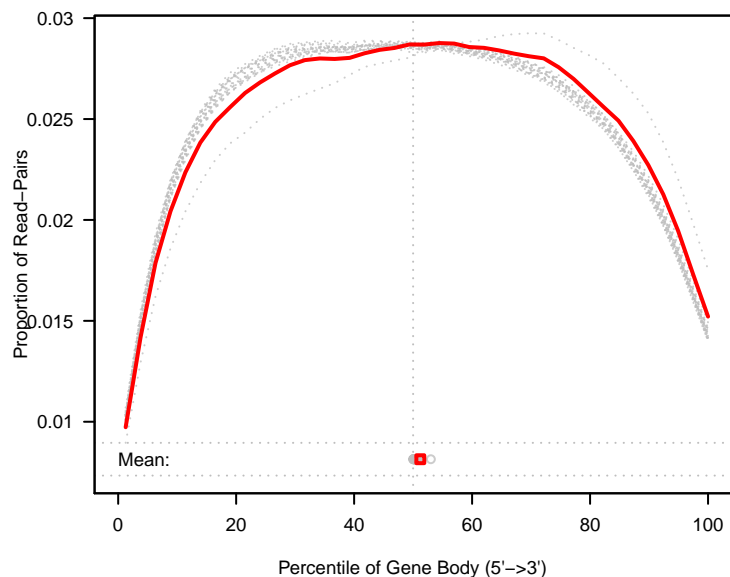
af

**Gene–Body Coverage, Upper Middle Quartile Genes**  
With Sample *srpk3\_hom\_ttnb\_het\_8* Colored by lane



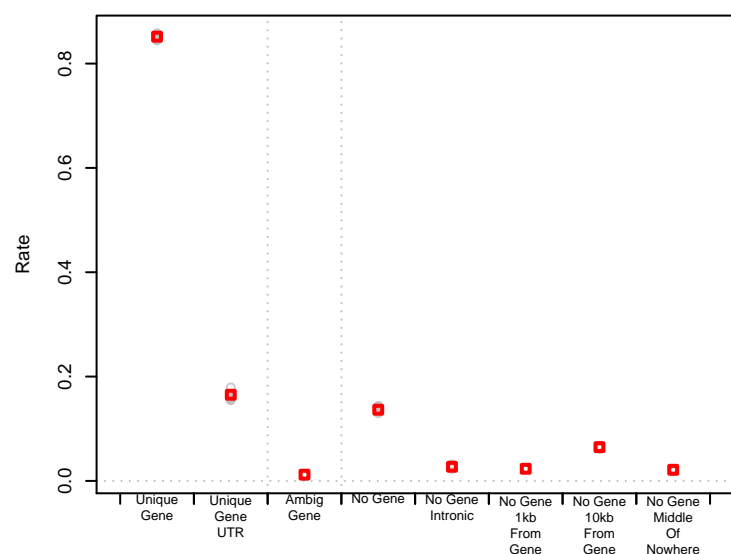
ag

**Gene–Body Coverage, Low Expression Genes**  
With Sample *srpk3\_hom\_ttnb\_het\_8* Colored by lane



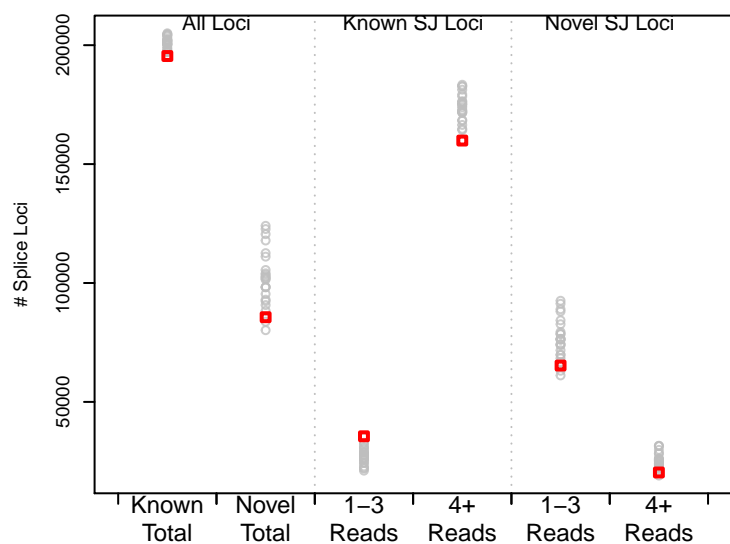
ah

**Read Mapping Location Rates**  
With Sample *srpk3\_hom\_ttnb\_het\_8* Colored by lane



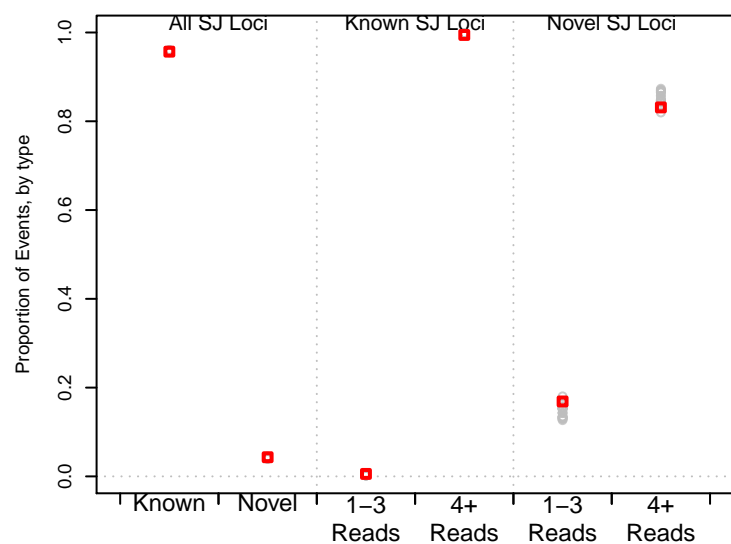
ai

**# Observed Splice Junction Loci, by type**  
With Sample *srpk3\_hom\_ttnb\_het\_8* Colored by lane

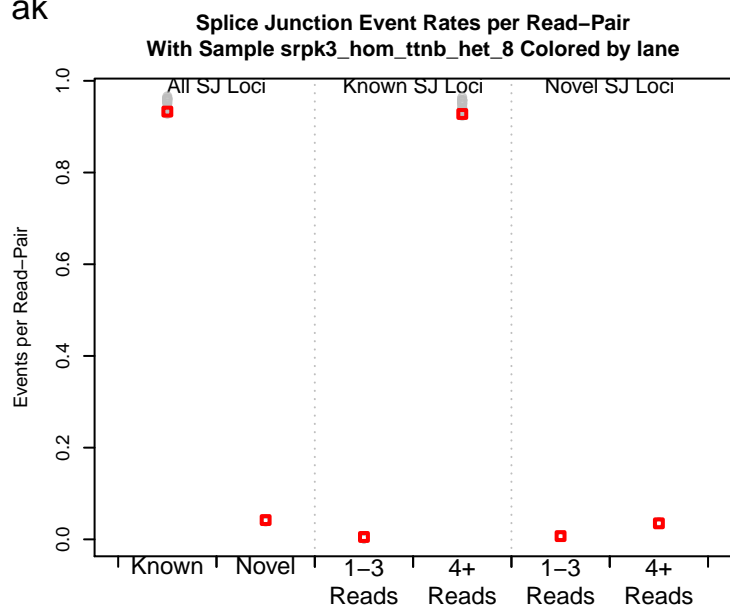


aj

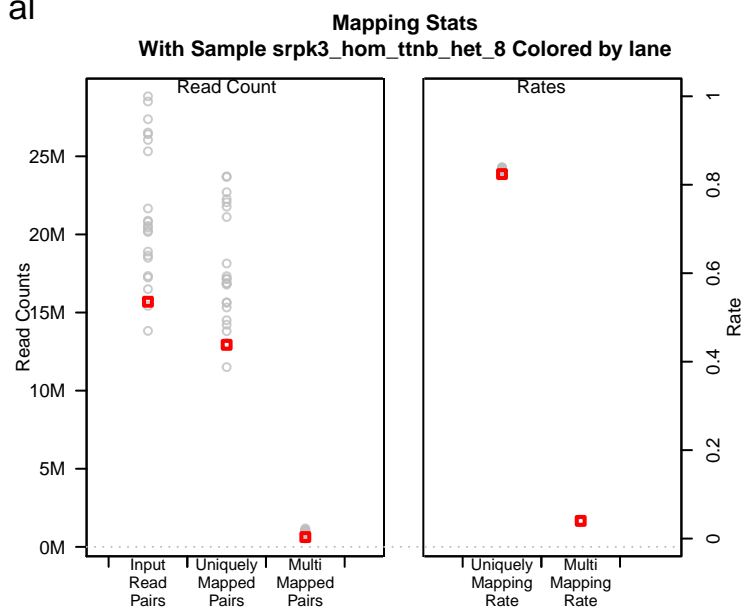
**Breakdown of Splice Junction Events, by type**  
With Sample *srpk3\_hom\_ttnb\_het\_8* Colored by lane



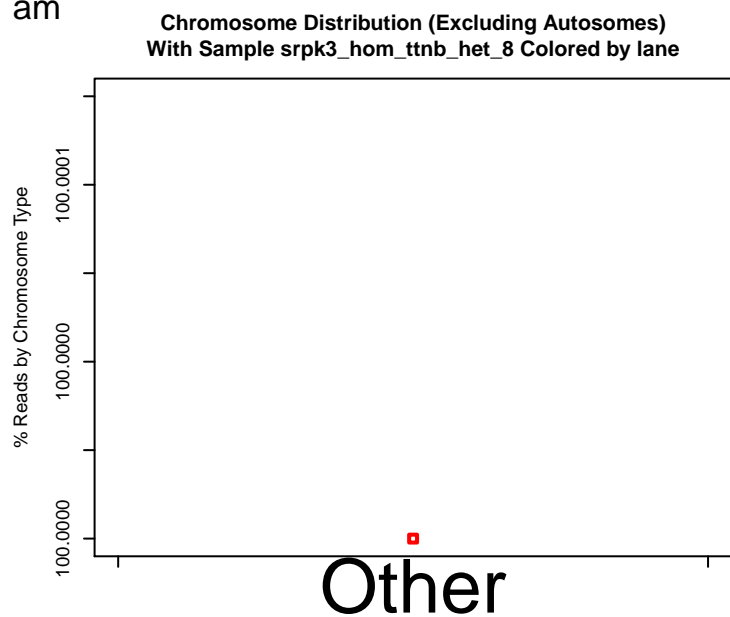
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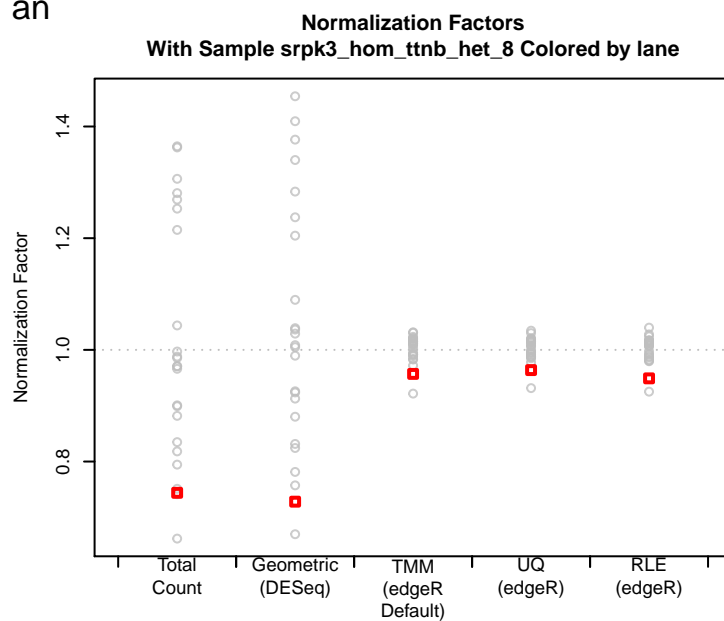
al



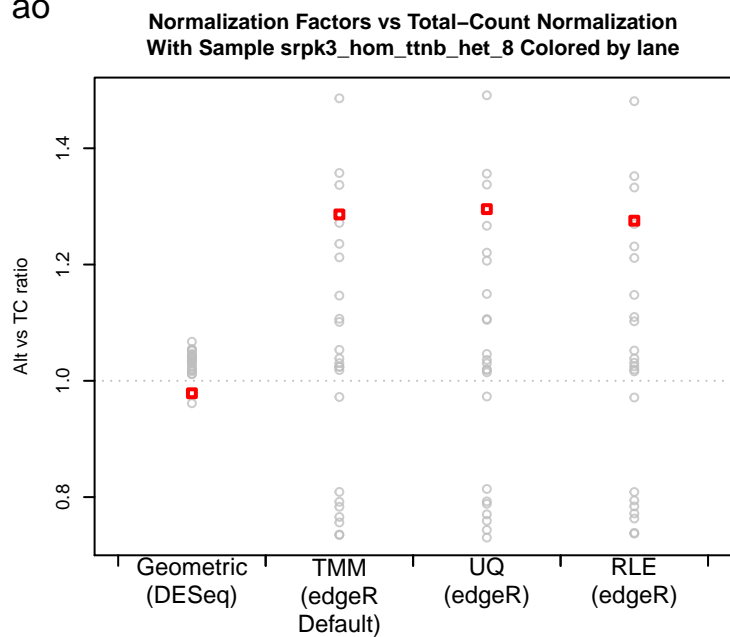
am



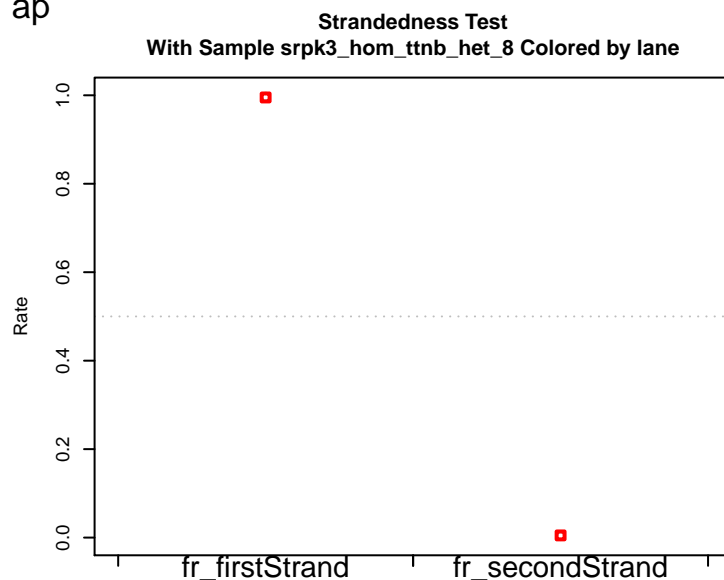
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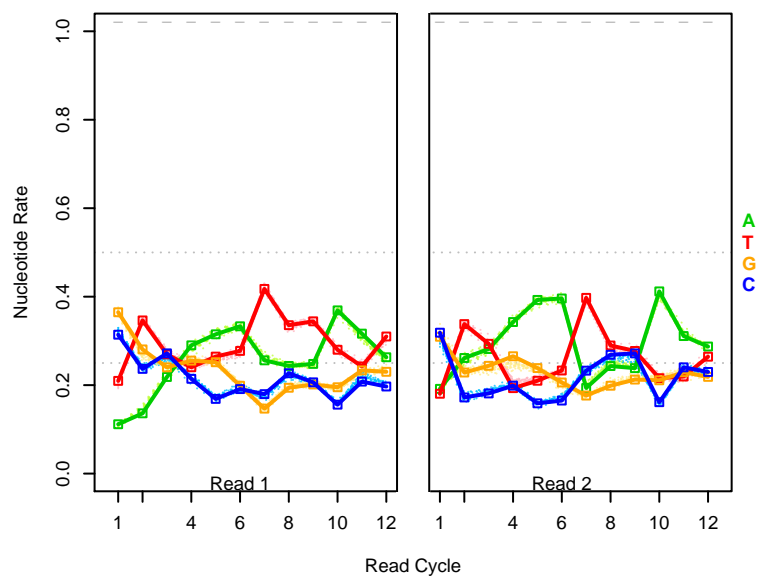


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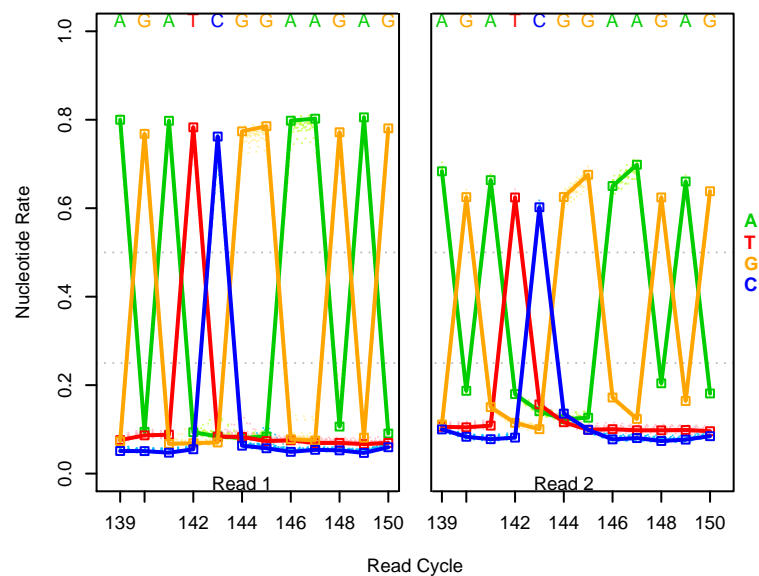
aq

Nucleotide Rate by Cycle, Leading Clipped bases (12)  
With Sample **srpk3\_hom\_ttnb\_het\_8** in Bold



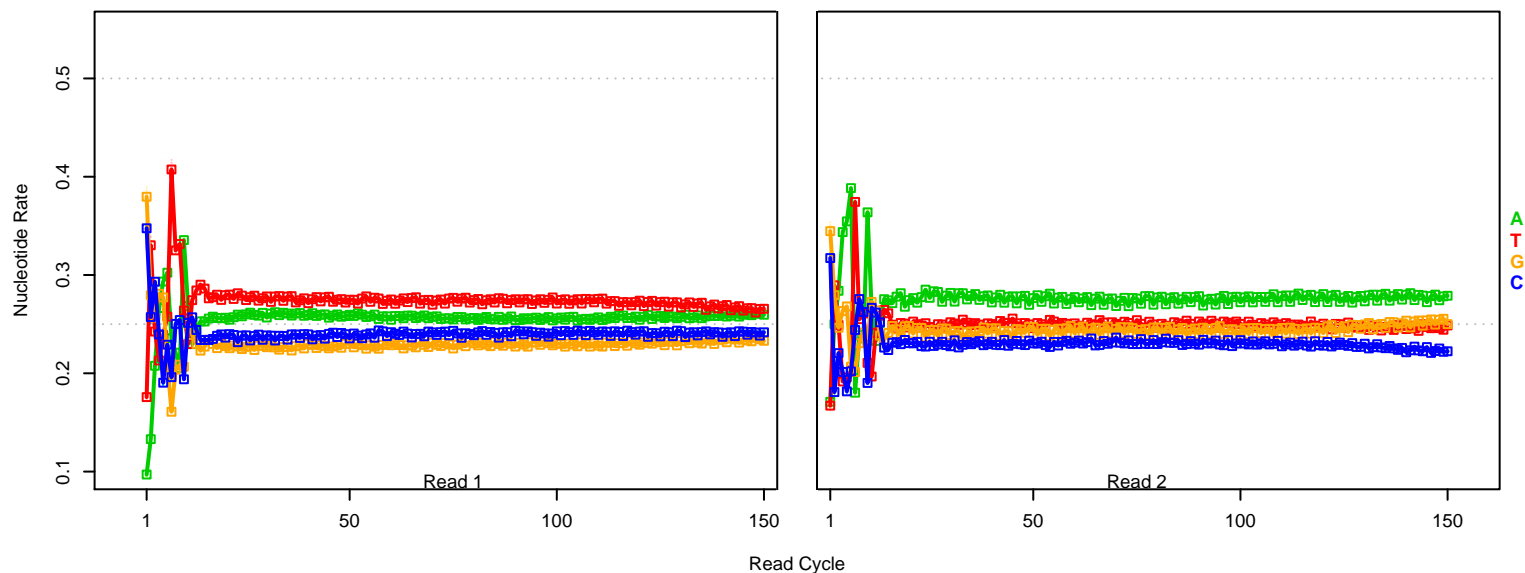
ar

Nucleotide Rate by Cycle, Trailing Clipped bases (12)  
With Sample **srpk3\_hom\_ttnb\_het\_8** in Bold



as

Raw Nucleotide Rate by Cycle  
With Sample **srpk3\_hom\_ttnb\_het\_8** in Bold



at

Nucleotide Rate by Cycle, Aligned bases only  
With Sample **srpk3\_hom\_ttnb\_het\_8** in Bold

