

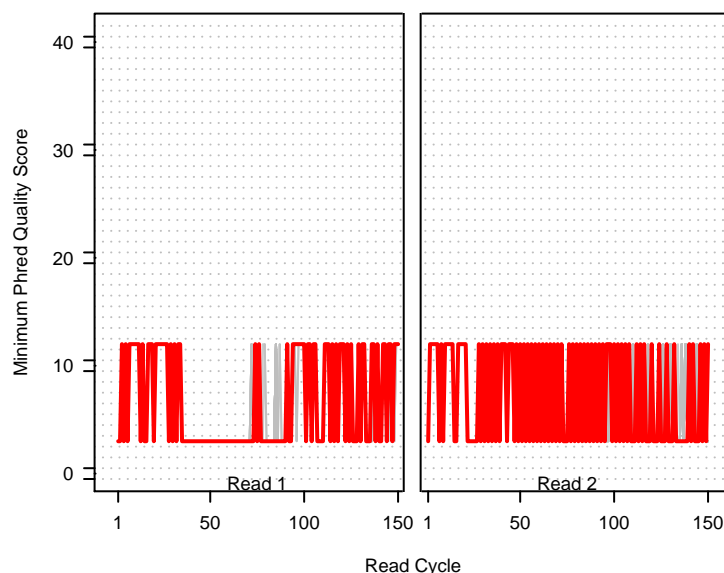
a

Sample Highlight:  
srpk3\_wt\_ttnb\_wt\_5  
Colored by Lane



b

Minimum Phred Quality Score  
With Sample srpk3\_wt\_ttnb\_wt\_5 Colored by lane



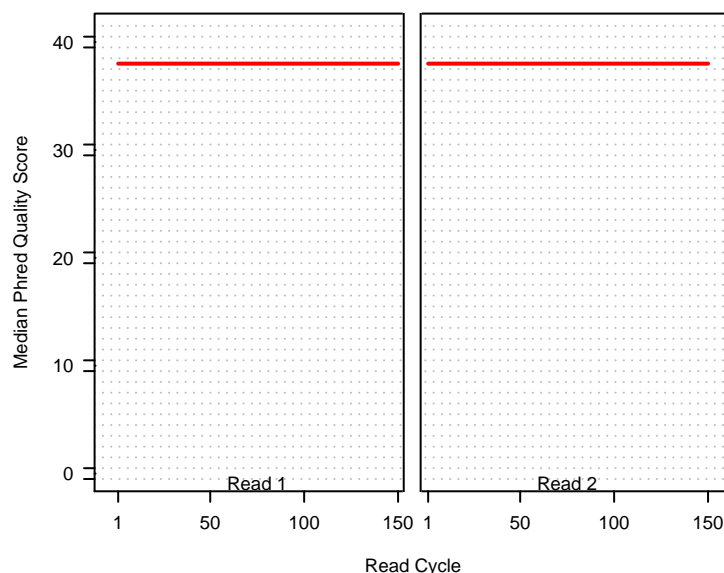
c

Lower Quartile Phred Quality Score  
With Sample srpk3\_wt\_ttnb\_wt\_5 Colored by lane



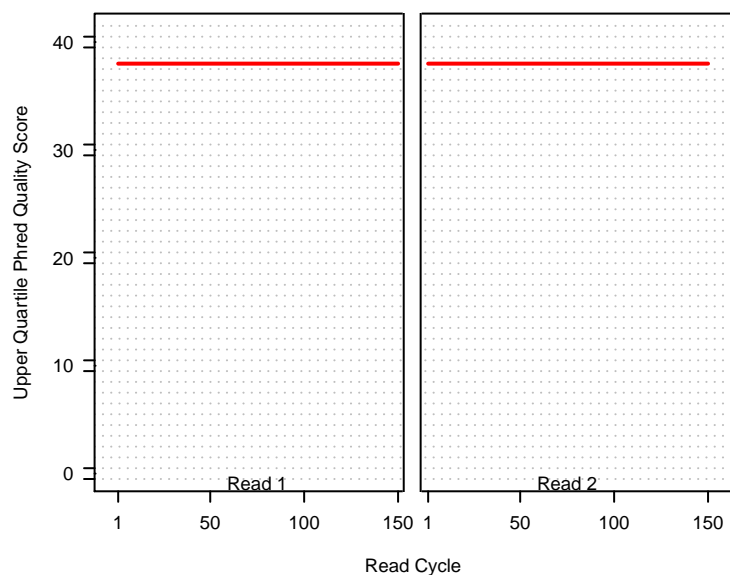
d

Median Phred Quality Score  
With Sample srpk3\_wt\_ttnb\_wt\_5 Colored by lane



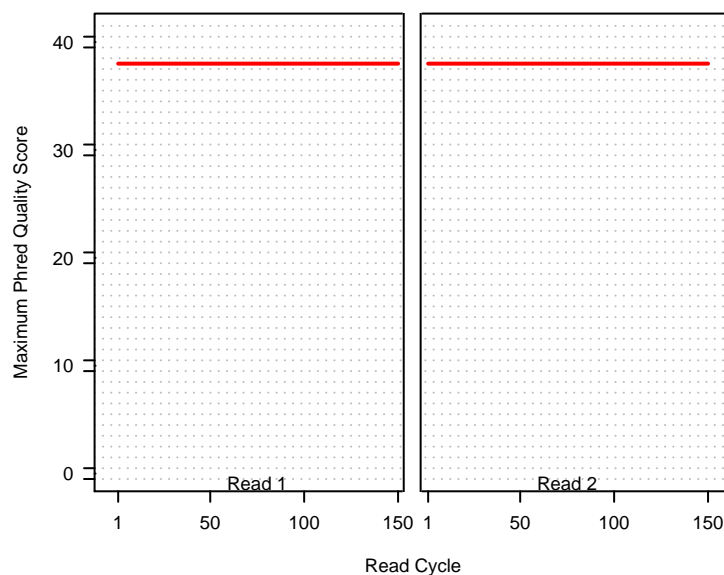
e

Upper Quartile Phred Quality Score  
With Sample srpk3\_wt\_ttnb\_wt\_5 Colored by lane



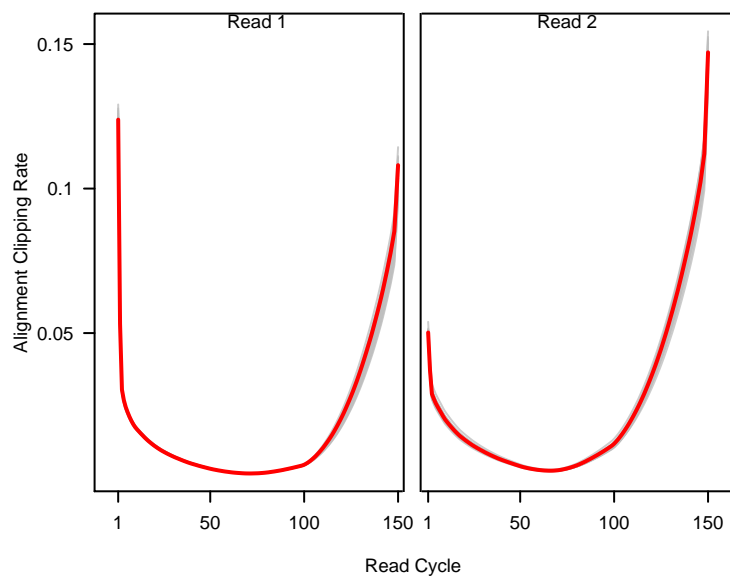
f

Maximum Phred Quality Score  
With Sample srpk3\_wt\_ttnb\_wt\_5 Colored by lane



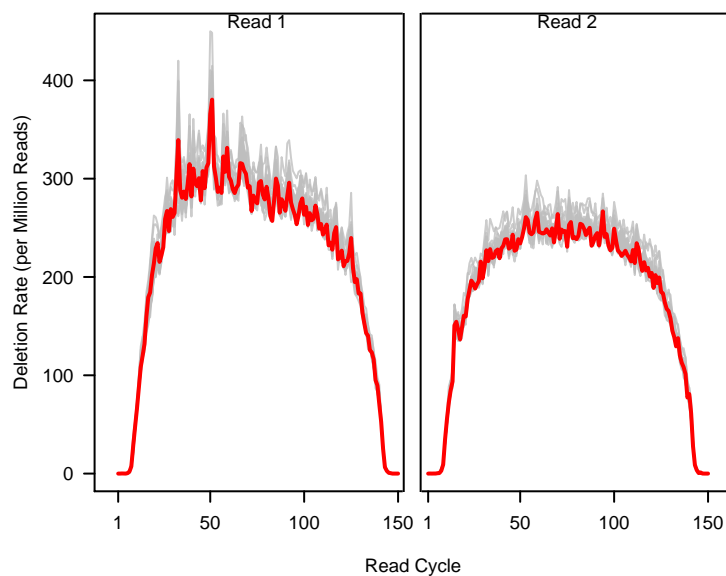
g

Alignment Clipping Rate, by read cycle  
With Sample srp3k3\_wt\_ttnb\_wt\_5 Colored by lane



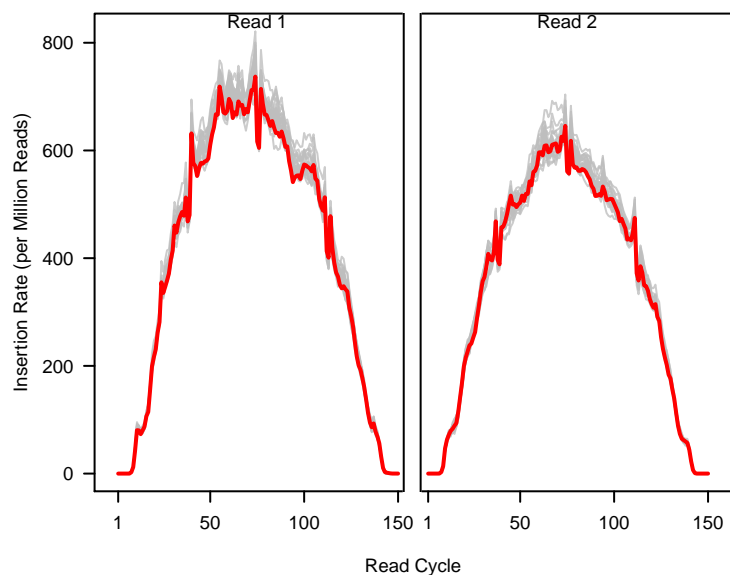
h

Deletion Rate, by read cycle  
With Sample srp3k3\_wt\_ttnb\_wt\_5 Colored by lane



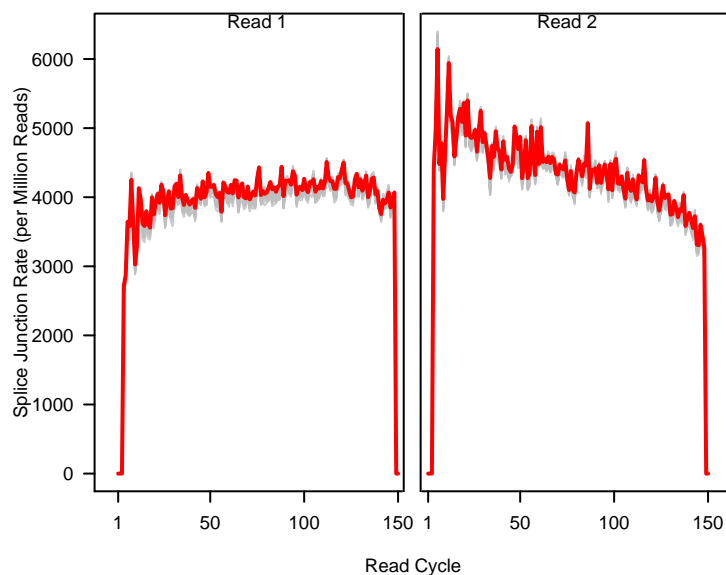
i

Insertion Rate, by read cycle  
With Sample srp3k3\_wt\_ttnb\_wt\_5 Colored by lane



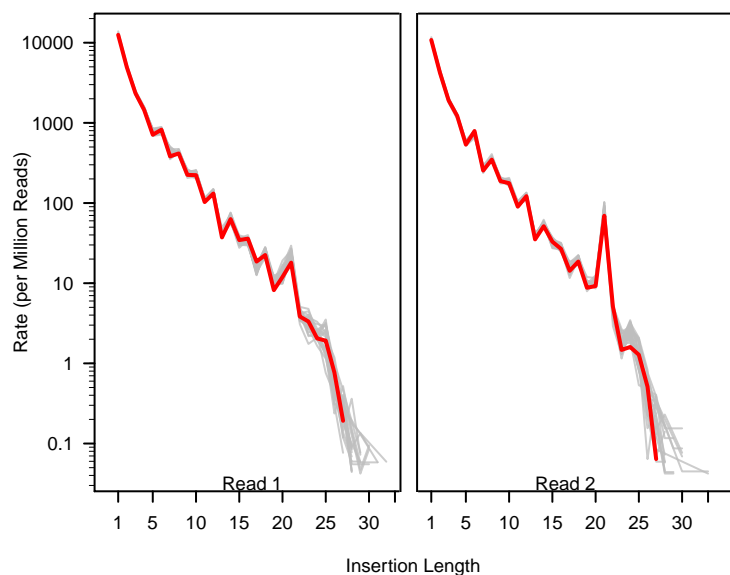
j

Splice Junction Rate, by read cycle  
With Sample srp3k3\_wt\_ttnb\_wt\_5 Colored by lane



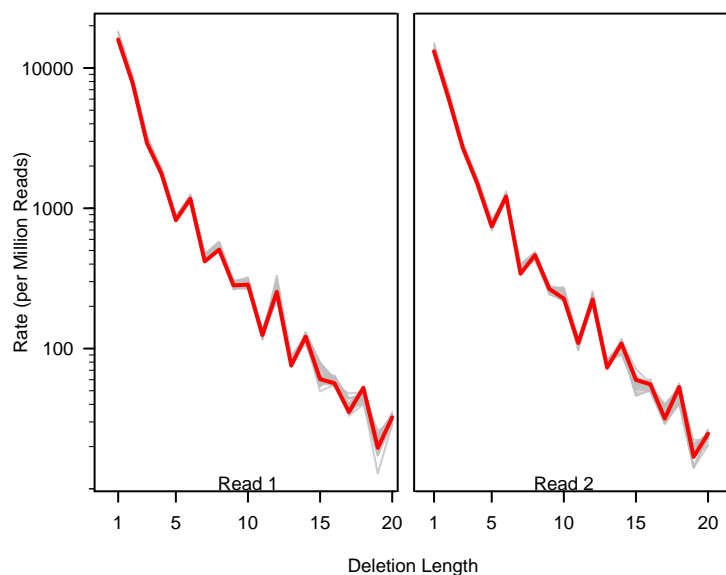
k

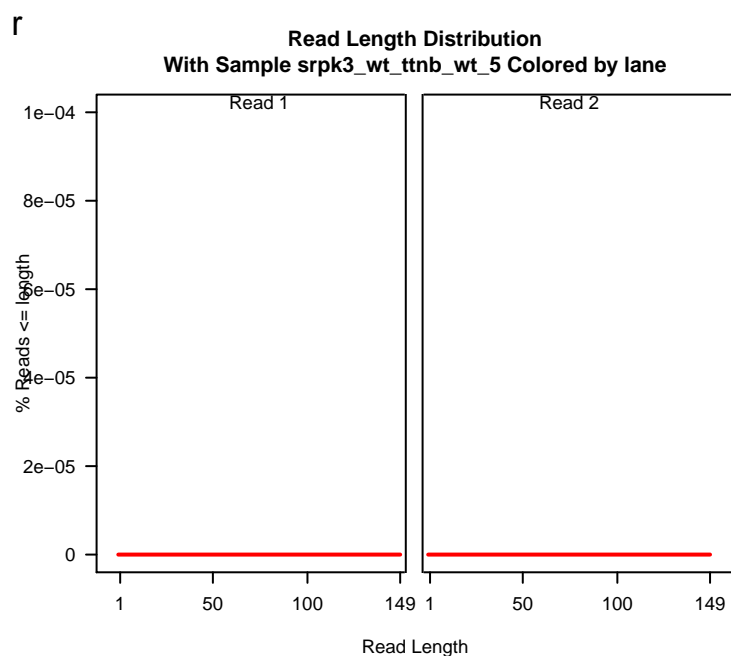
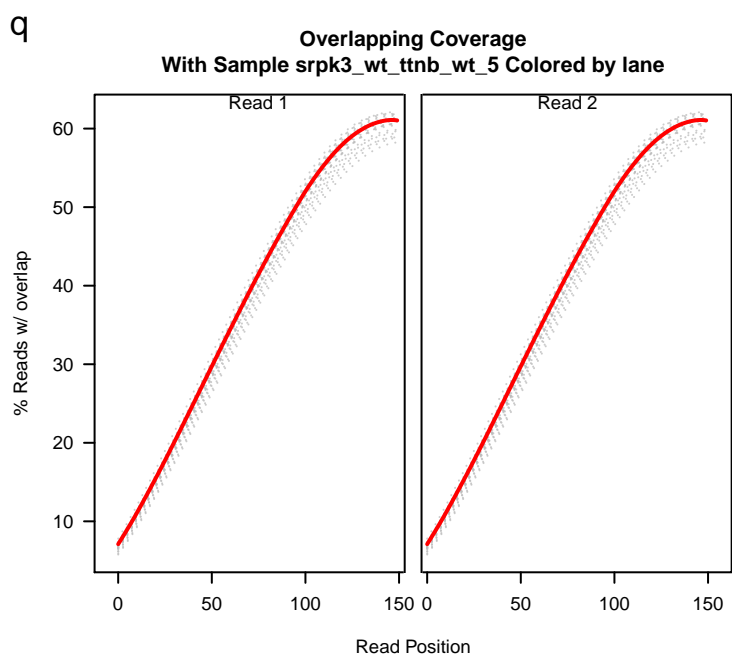
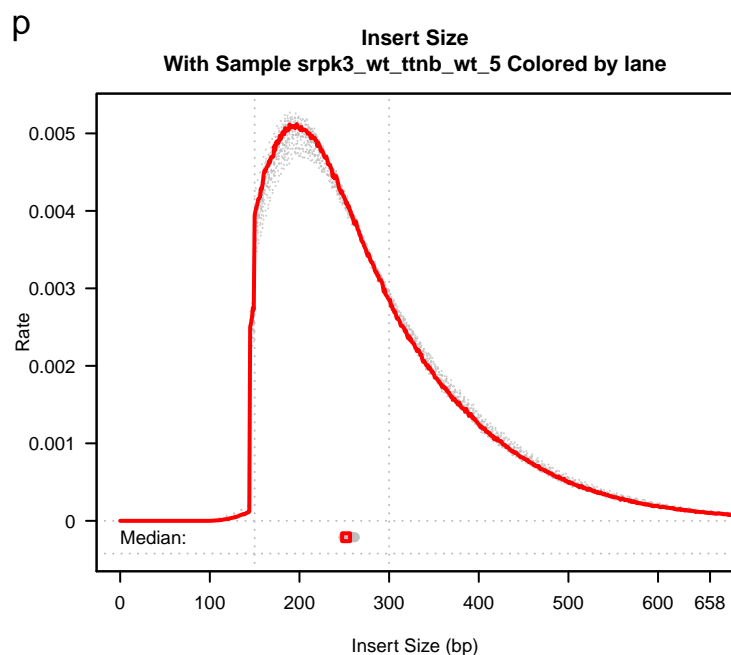
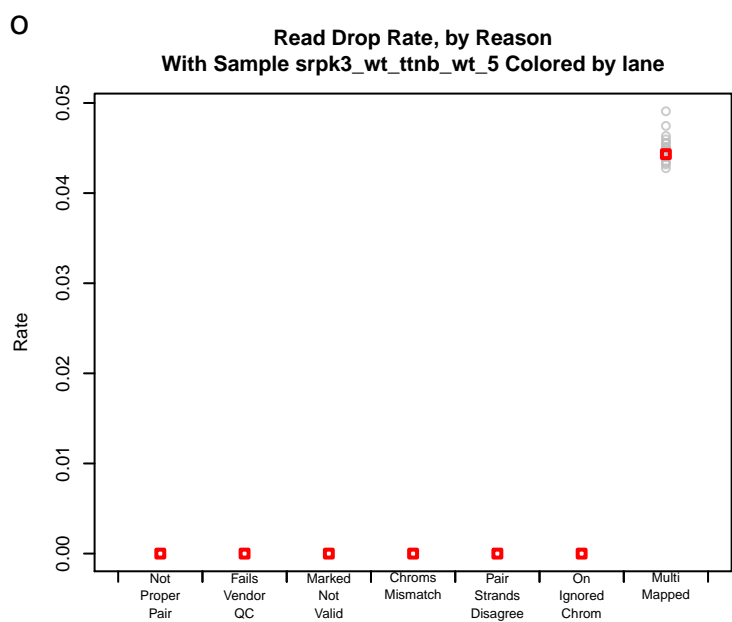
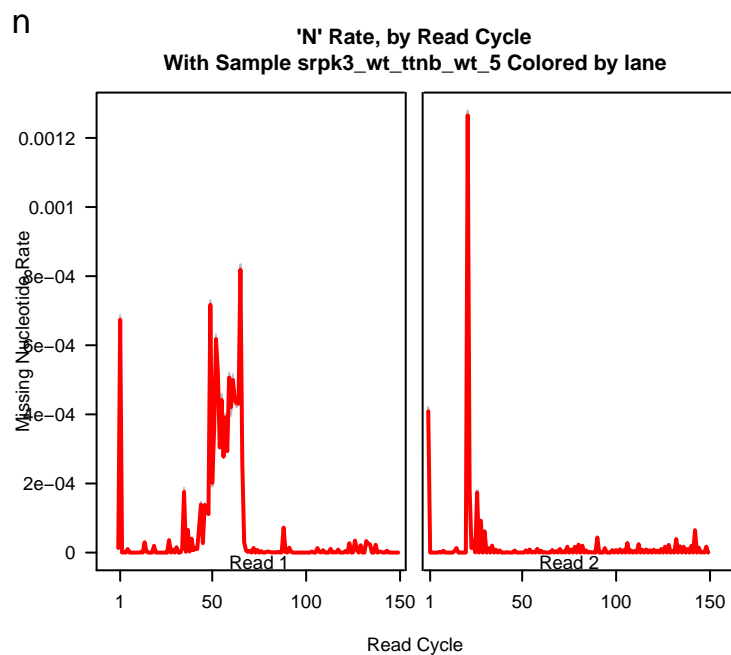
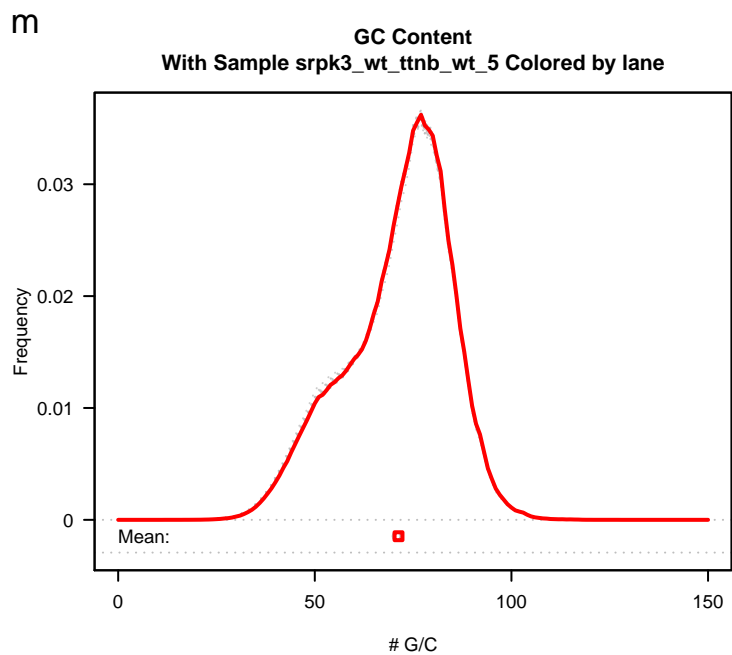
Insertion Length Distribution  
With Sample srp3k3\_wt\_ttnb\_wt\_5 Colored by lane



l

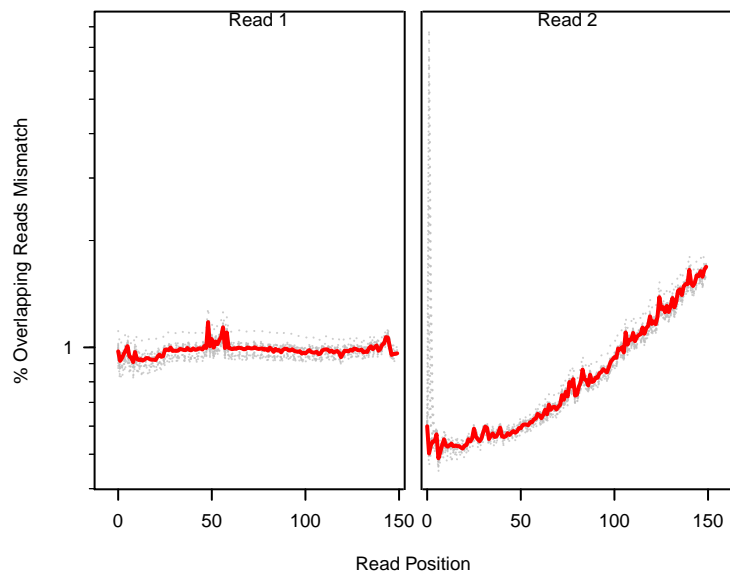
Deletion Length Distribution  
With Sample srp3k3\_wt\_ttnb\_wt\_5 Colored by lane





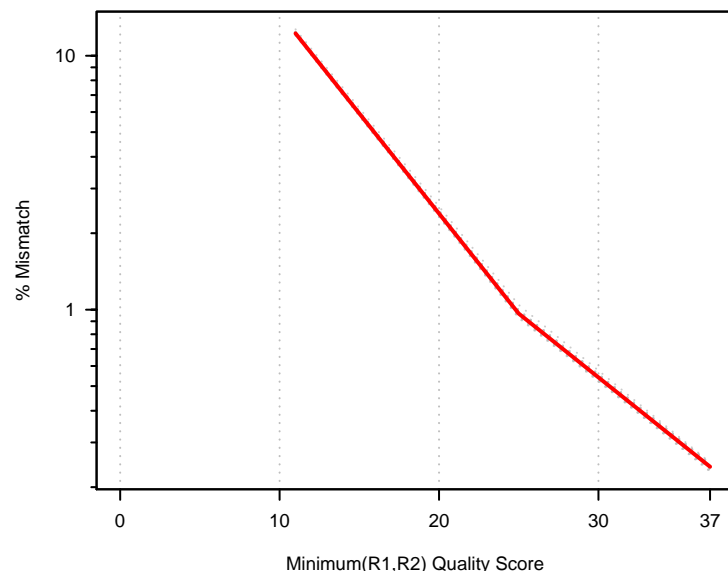
S

**Overlap Mismatch by Read Cycle**  
With Sample srpk3\_wt\_ttnb\_wt\_5 Colored by lane



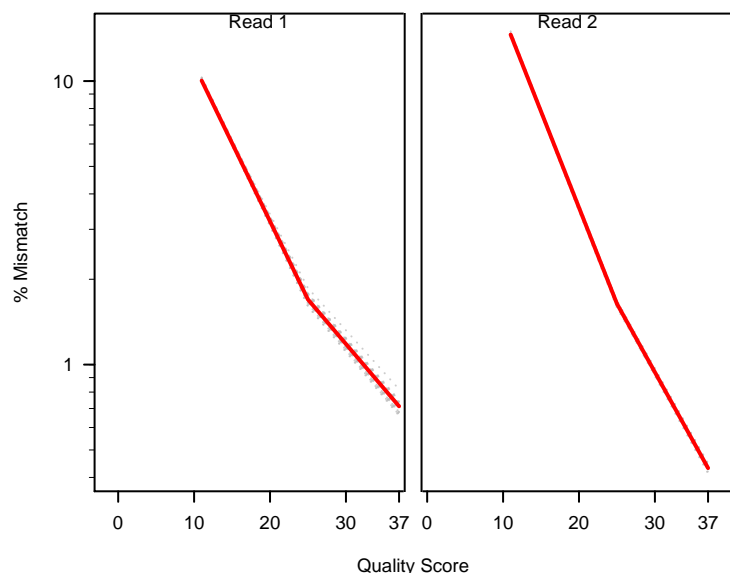
t

**Overlapping Mismatch by Min Qual**  
With Sample srpk3\_wt\_ttnb\_wt\_5 Colored by lane



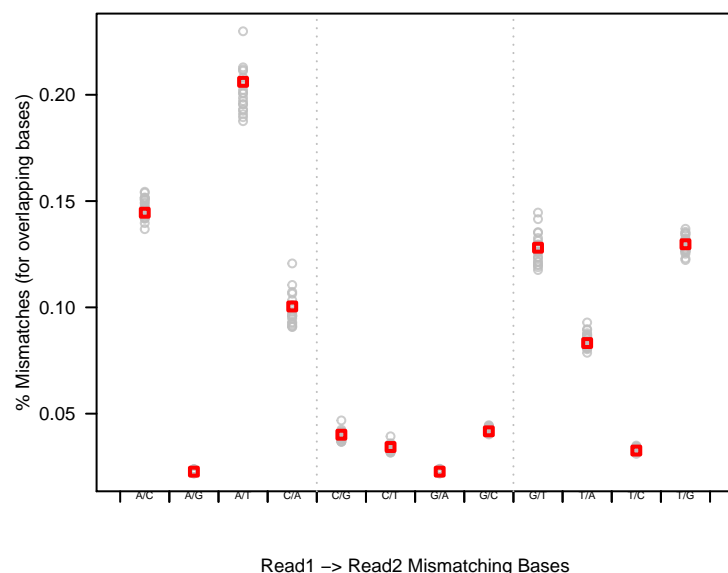
U

**Overlap Mismatch by Read Qual**  
With Sample srpk3\_wt\_ttnb\_wt\_5 Colored by lane



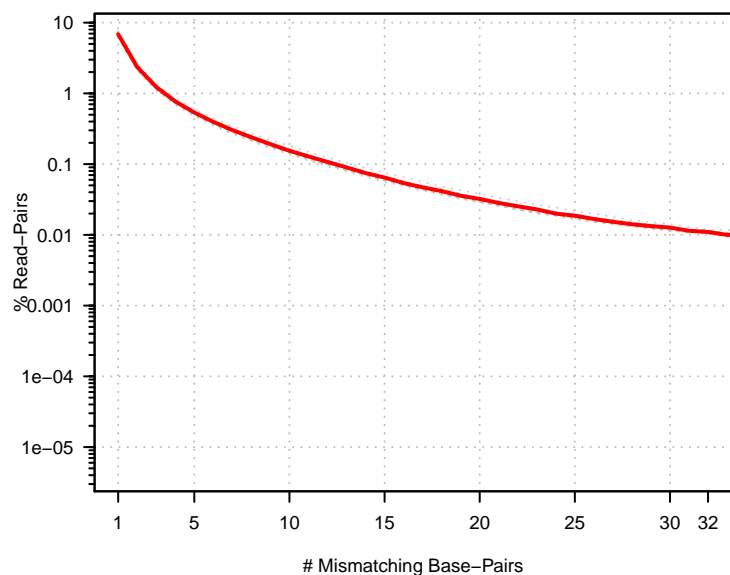
V

**Overlap Mismatch Combinations**  
With Sample srpk3\_wt\_ttnb\_wt\_5 Colored by lane



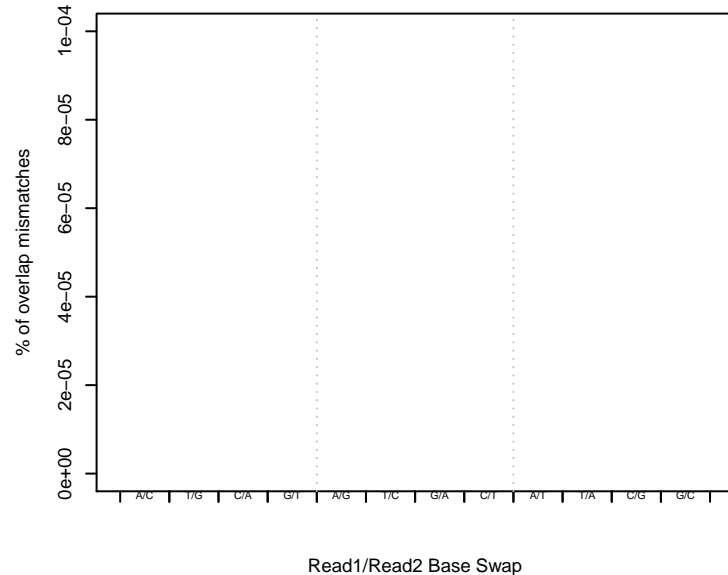
W

**Overlap Mismatch Size Frequency**  
With Sample srpk3\_wt\_ttnb\_wt\_5 Colored by lane



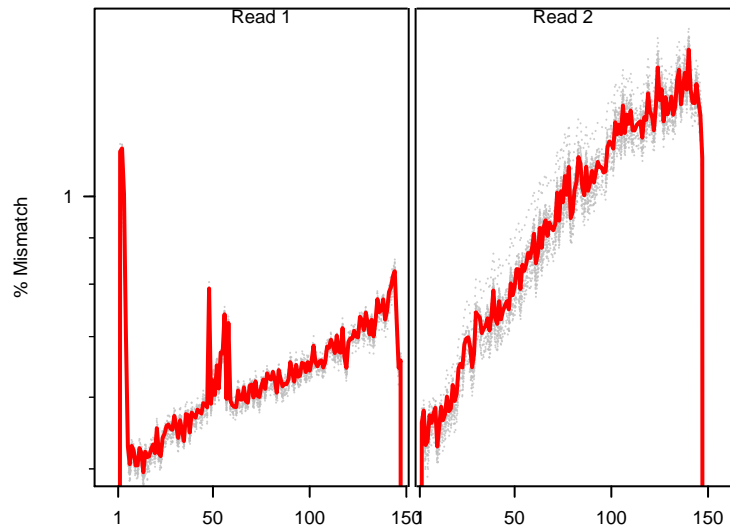
X

**Overlap Mismatch Pairs At Phred == 41**  
With Sample srpk3\_wt\_ttnb\_wt\_5 Colored by lane



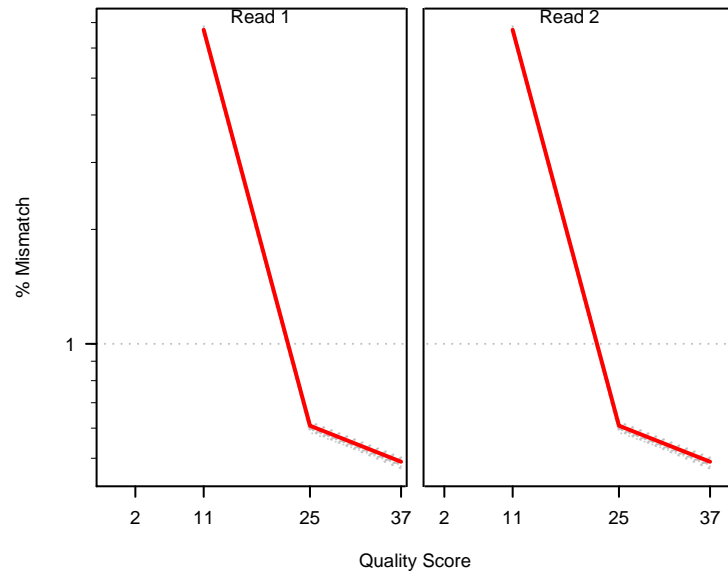
y

**Reference Mismatch by Read Cycle**  
With Sample srpk3\_wt\_ttnb\_wt\_5 Colored by lane



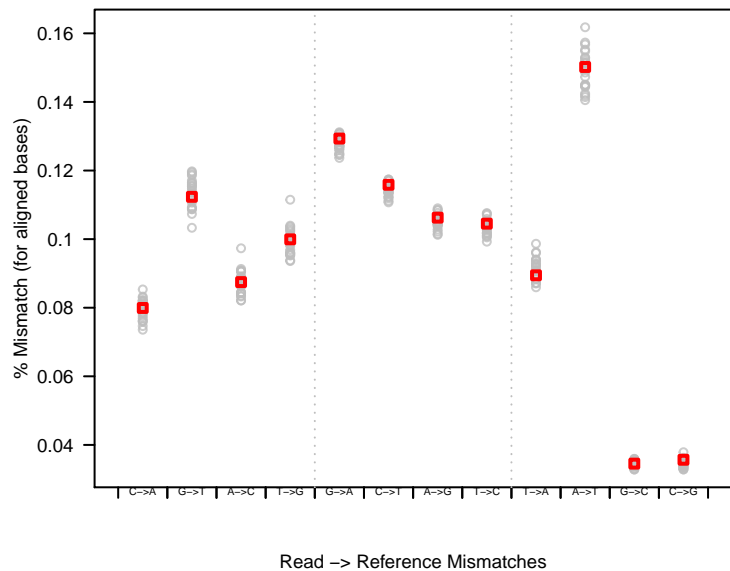
Z

**Reference Mismatch by Read Qual**  
With Sample srpk3\_wt\_ttnb\_wt\_5 Colored by lane



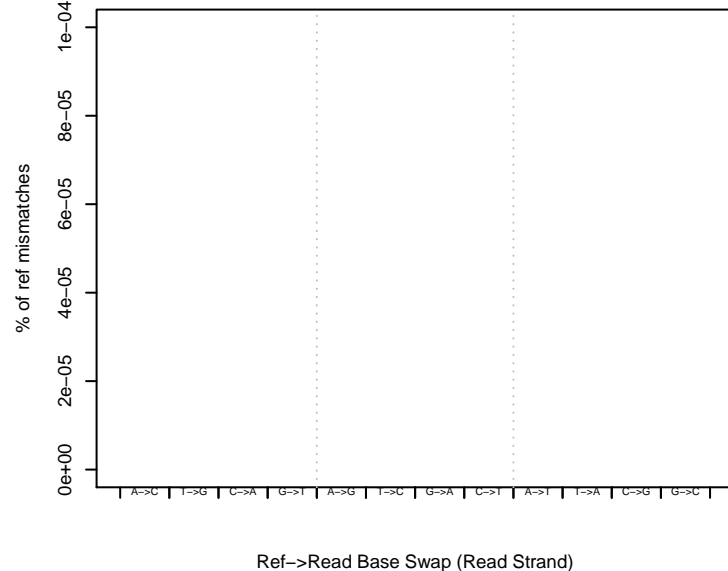
aa

**Reference Mismatch Combinations**  
With Sample srpk3\_wt\_ttnb\_wt\_5 Colored by lane



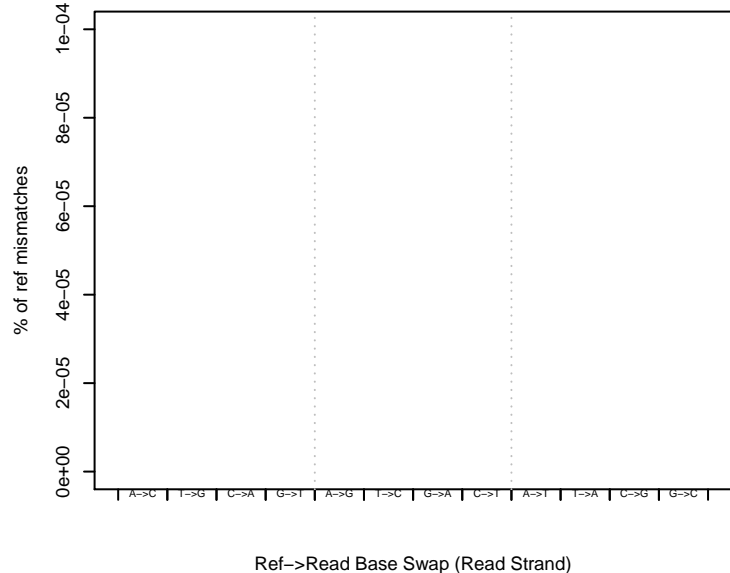
ab

**R1 Ref Mismatches At Phred == 41**  
With Sample srpk3\_wt\_ttnb\_wt\_5 Colored by lane



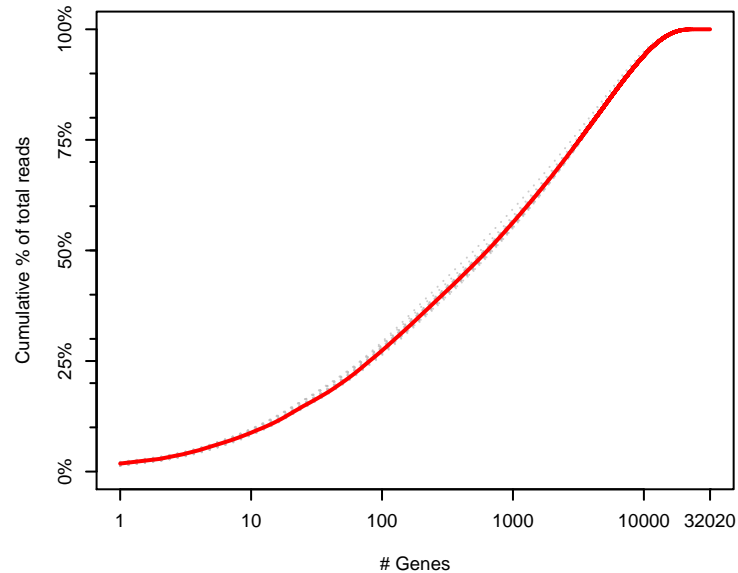
ac

**R2 Ref Mismatches At Phred == 41**  
With Sample srpk3\_wt\_ttnb\_wt\_5 Colored by lane



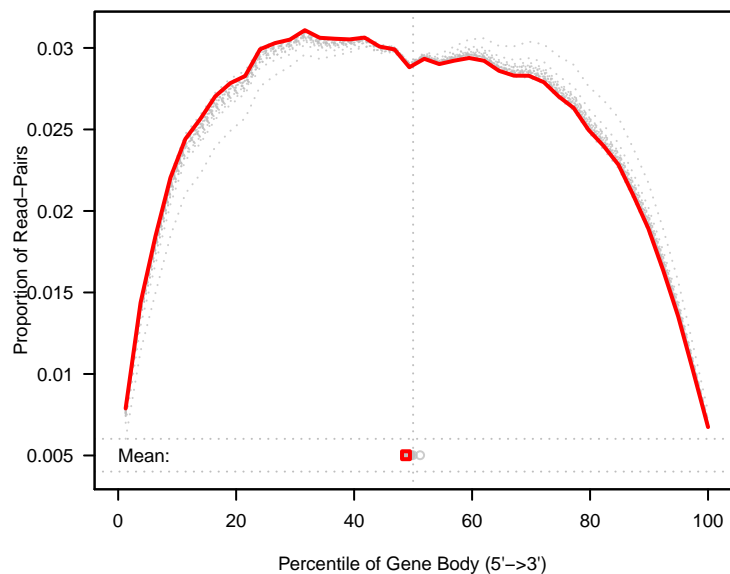
ad

**Cumulative Gene Assignment Diversity**  
With Sample srpk3\_wt\_ttnb\_wt\_5 Colored by lane



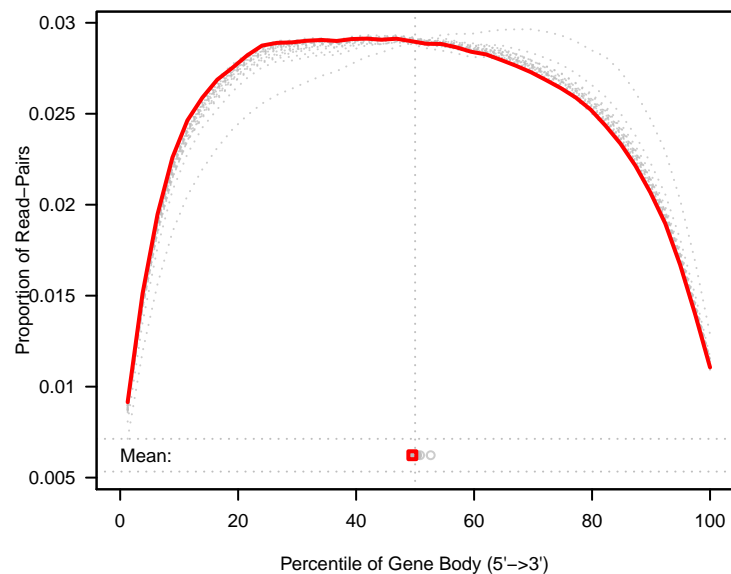
ae

**Gene-Body Coverage**  
With Sample srpk3\_wt\_ttnb\_wt\_5 Colored by lane



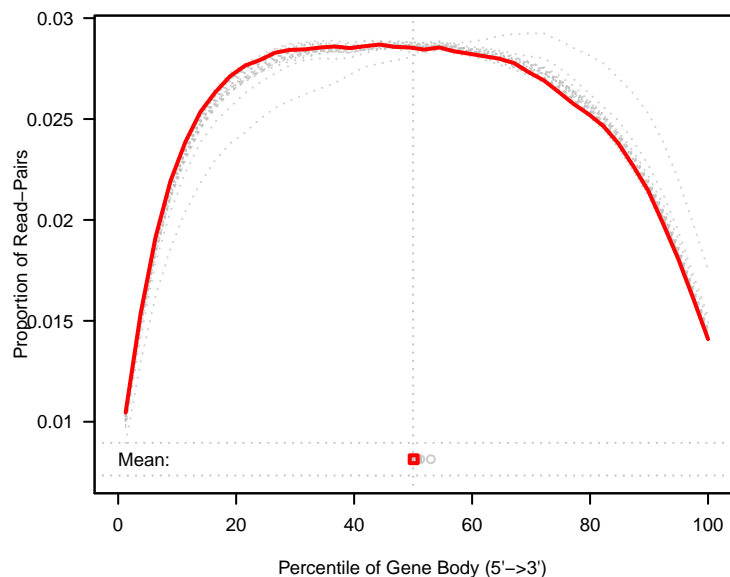
af

**Gene-Body Coverage, Upper Middle Quartile Genes**  
With Sample srpk3\_wt\_ttnb\_wt\_5 Colored by lane



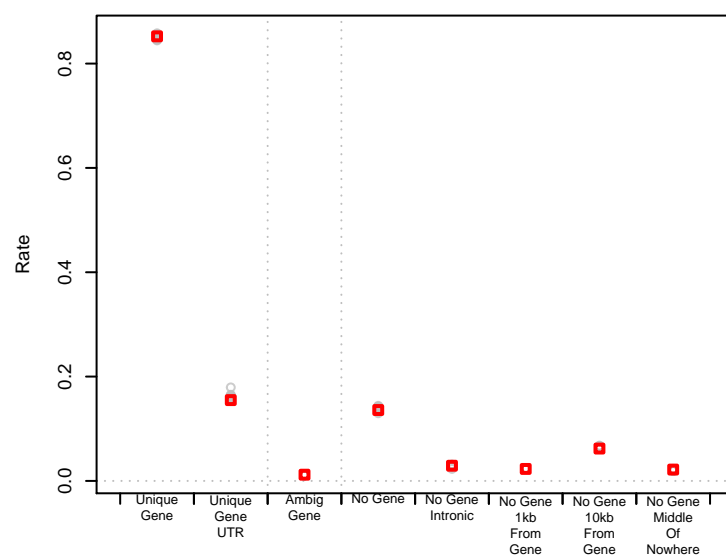
ag

**Gene-Body Coverage, Low Expression Genes**  
With Sample srpk3\_wt\_ttnb\_wt\_5 Colored by lane



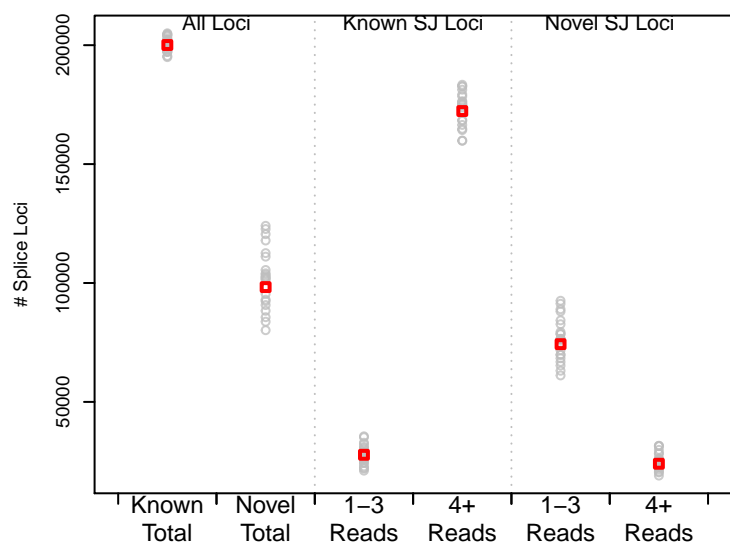
ah

**Read Mapping Location Rates**  
With Sample srpk3\_wt\_ttnb\_wt\_5 Colored by lane



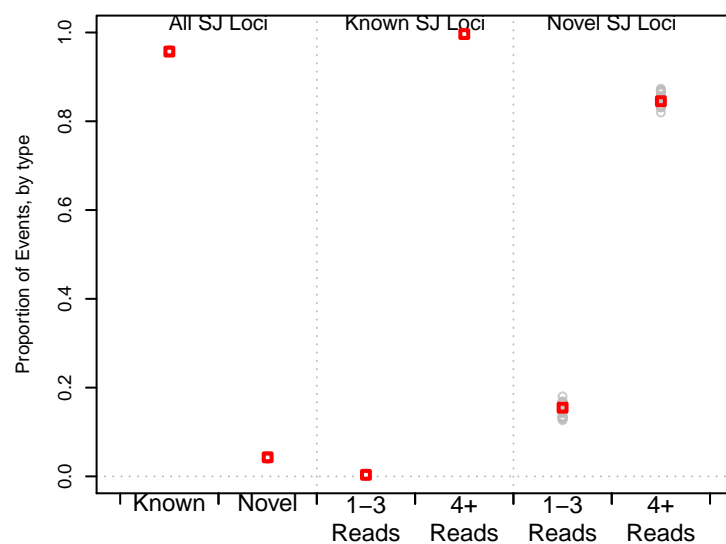
ai

**# Observed Splice Junction Loci, by type**  
With Sample srpk3\_wt\_ttnb\_wt\_5 Colored by lane

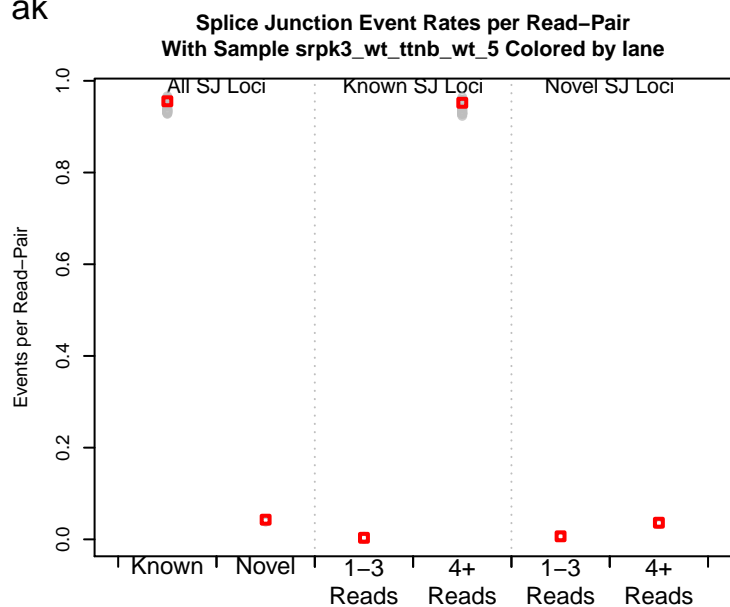


aj

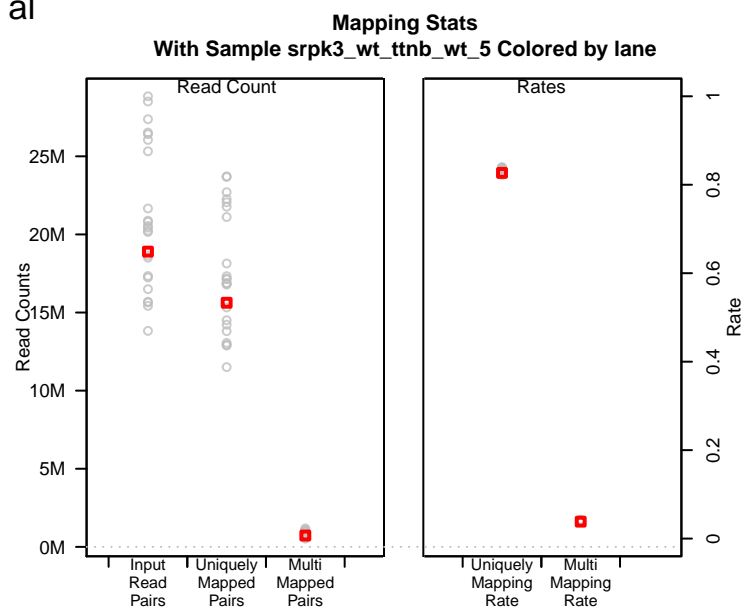
**Breakdown of Splice Junction Events, by type**  
With Sample srpk3\_wt\_ttnb\_wt\_5 Colored by lane



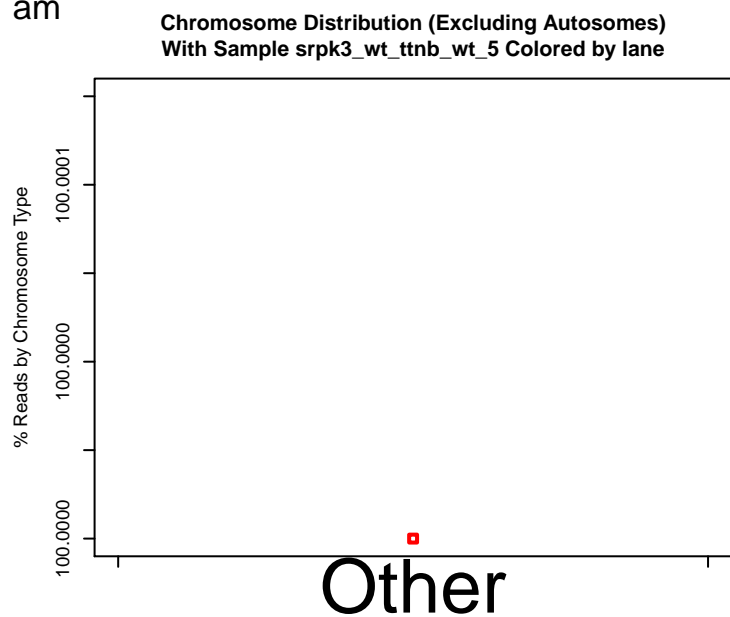
ak



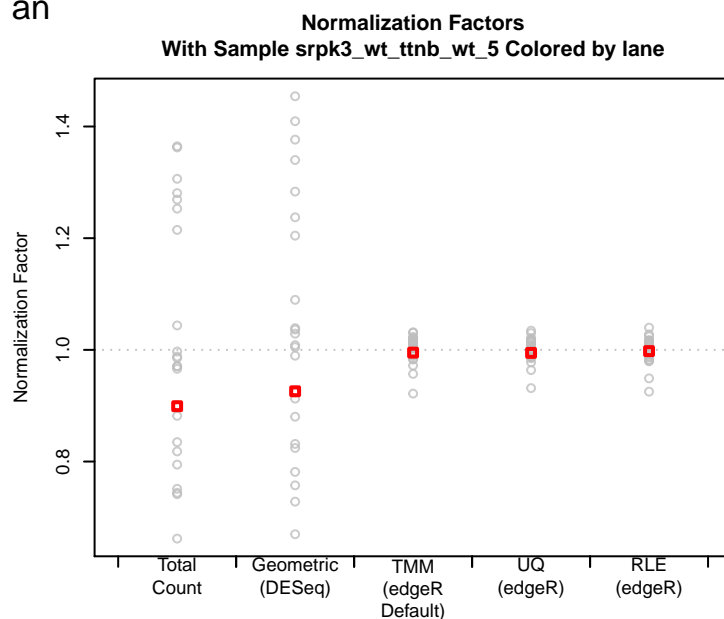
al



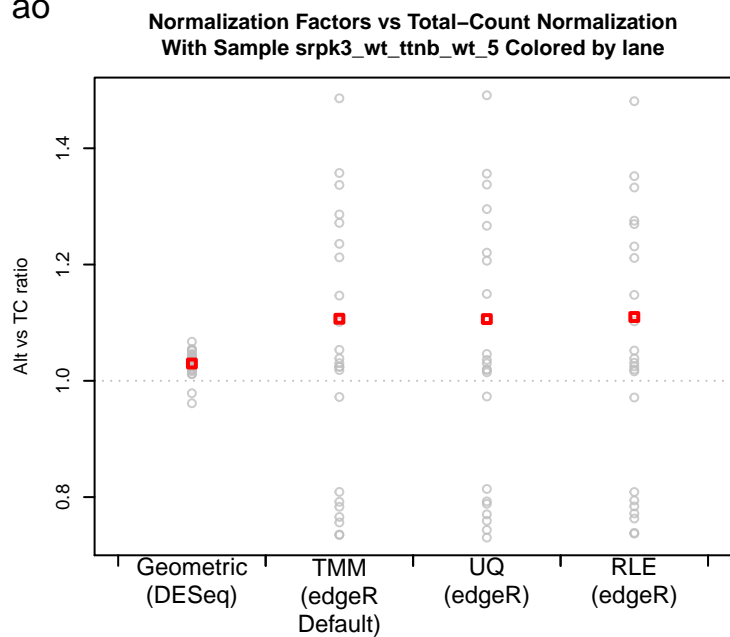
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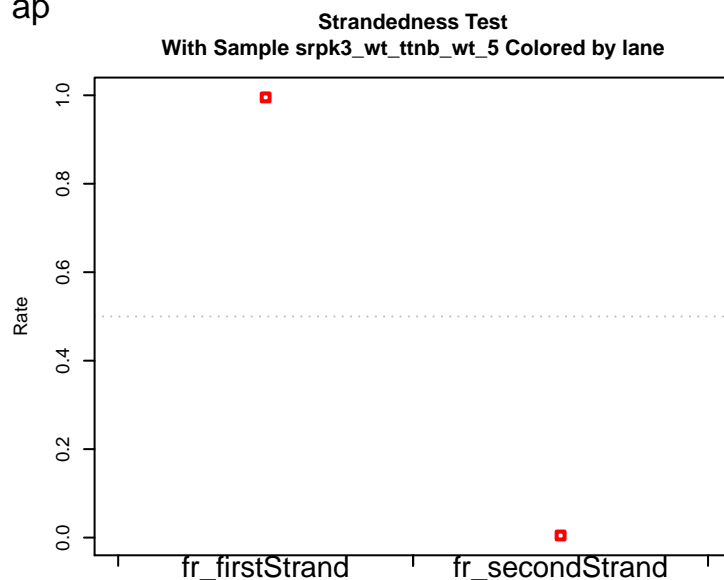
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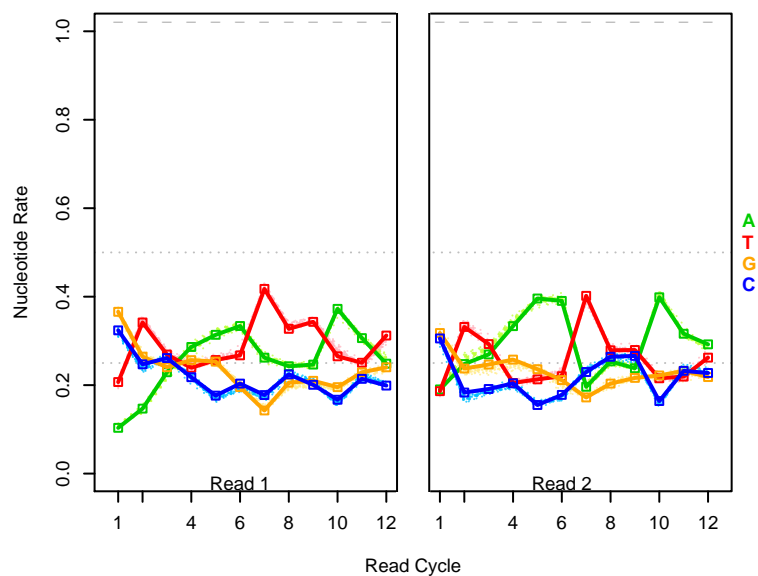


ap



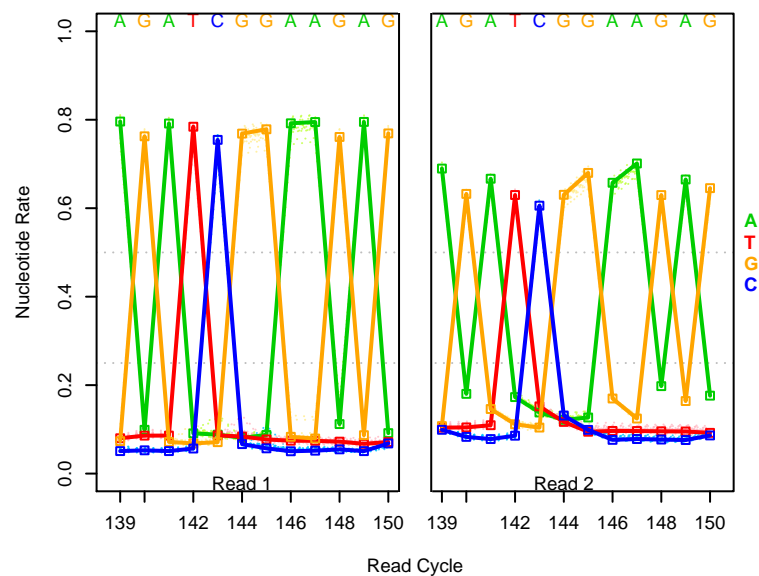
aq

Nucleotide Rate by Cycle, Leading Clipped bases (12)  
With Sample **srpk3\_wt\_ttnb\_wt\_5** in Bold



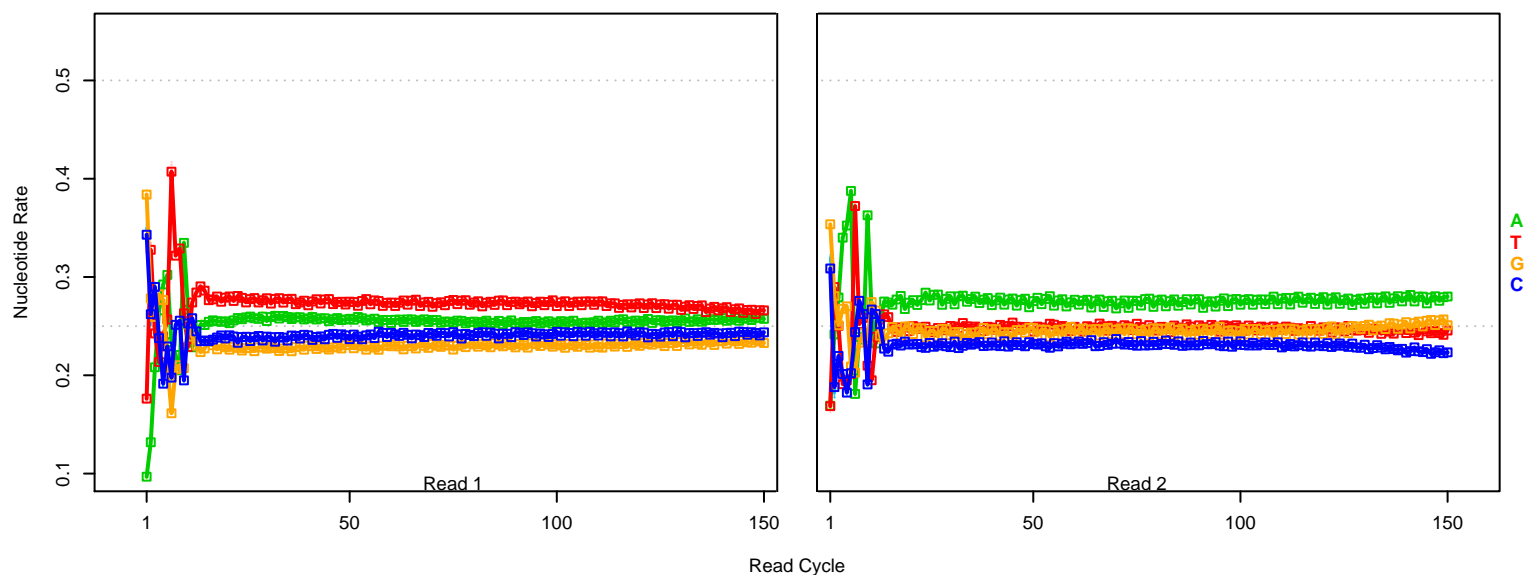
ar

Nucleotide Rate by Cycle, Trailing Clipped bases (12)  
With Sample **srpk3\_wt\_ttnb\_wt\_5** in Bold



as

Raw Nucleotide Rate by Cycle  
With Sample **srpk3\_wt\_ttnb\_wt\_5** in Bold



at

Nucleotide Rate by Cycle, Aligned bases only  
With Sample **srpk3\_wt\_ttnb\_wt\_5** in Bold

