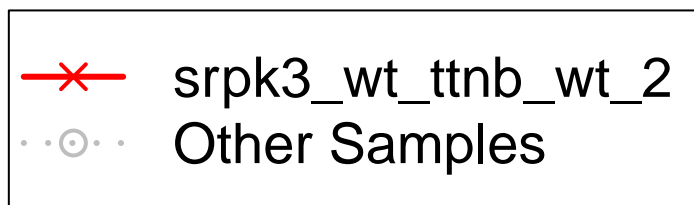


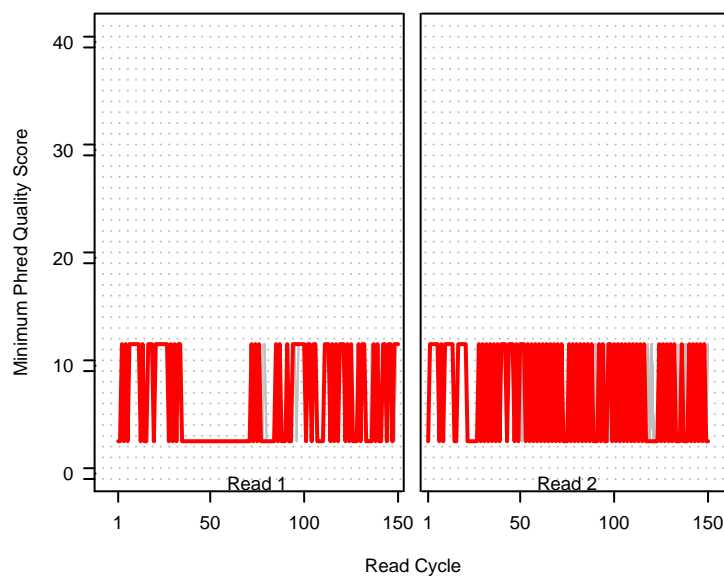
a

Sample Highlight:  
srpk3\_wt\_ttnb\_wt\_2



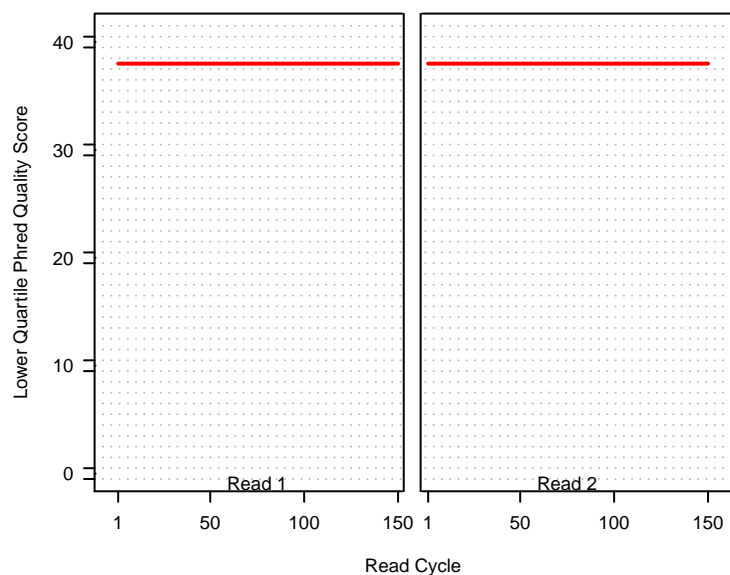
b

Minimum Phred Quality Score  
With Sample srpk3\_wt\_ttnb\_wt\_2 in red



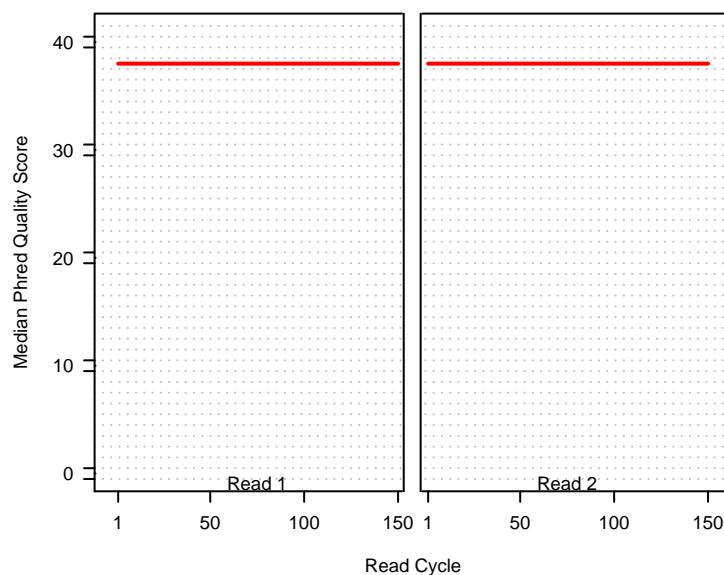
c

Lower Quartile Phred Quality Score  
With Sample srpk3\_wt\_ttnb\_wt\_2 in red



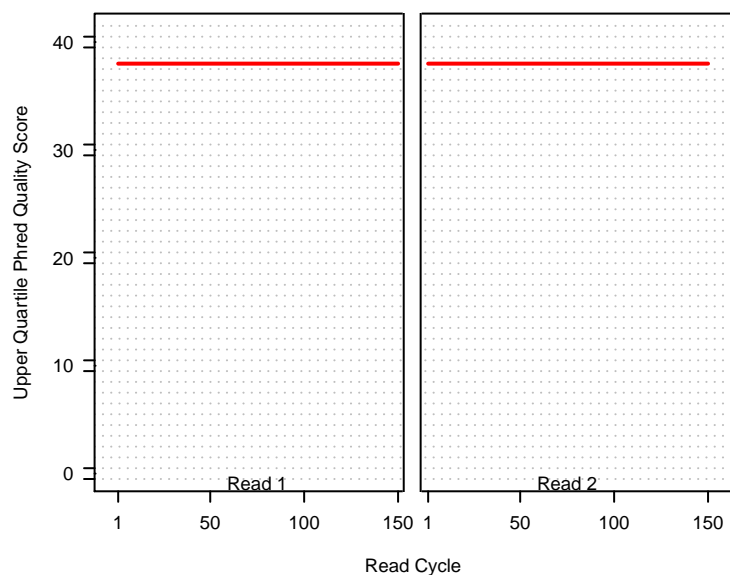
d

Median Phred Quality Score  
With Sample srpk3\_wt\_ttnb\_wt\_2 in red



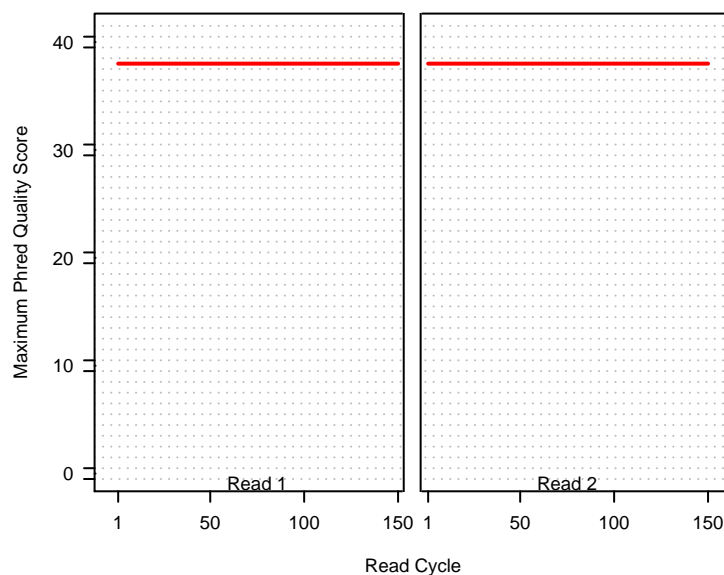
e

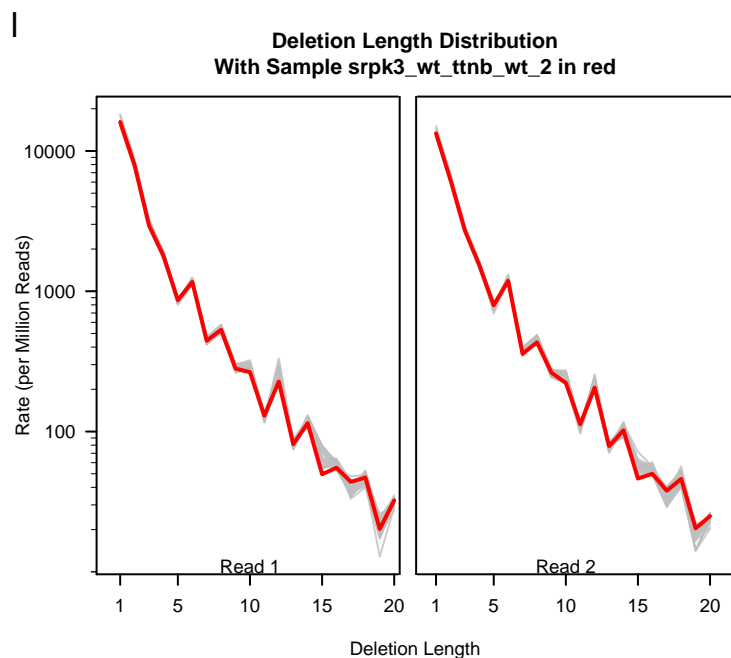
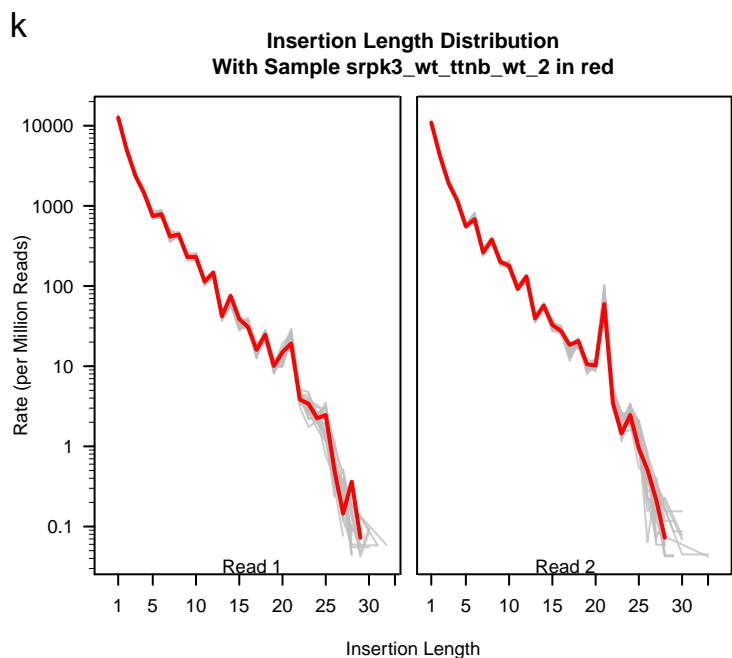
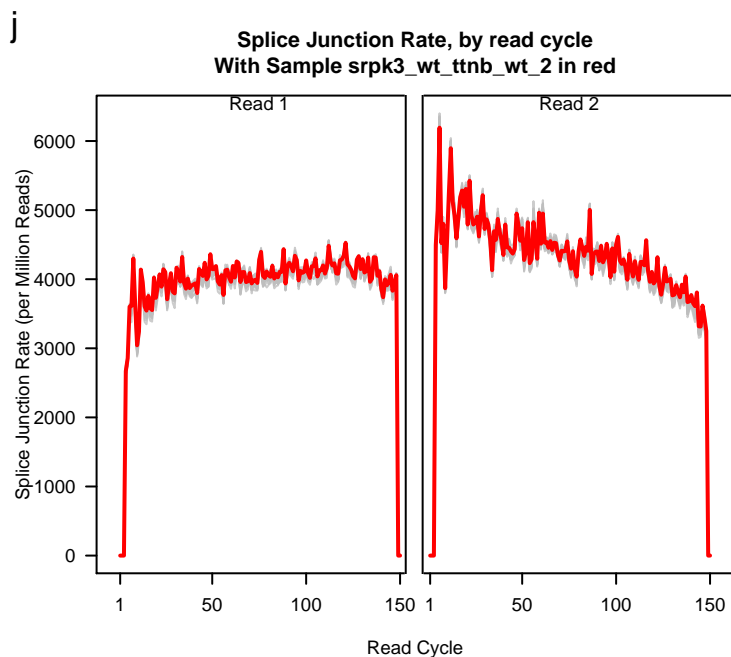
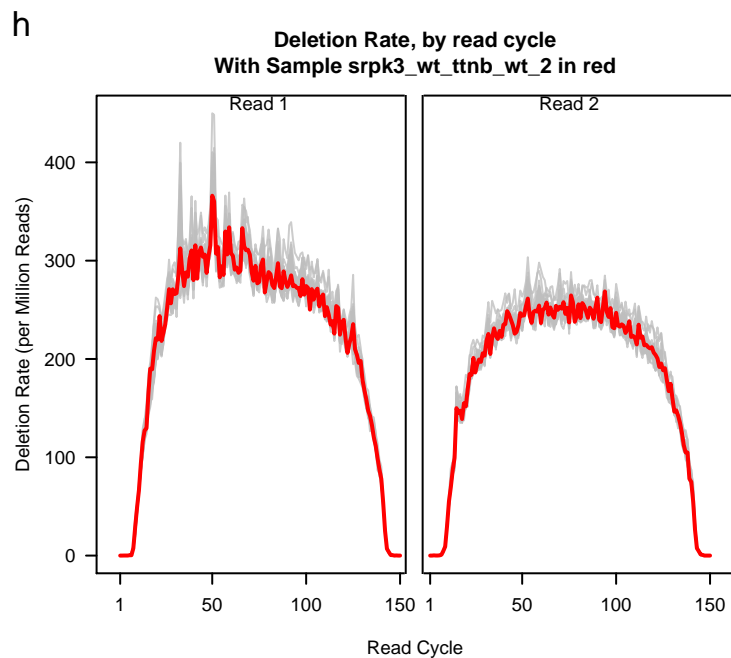
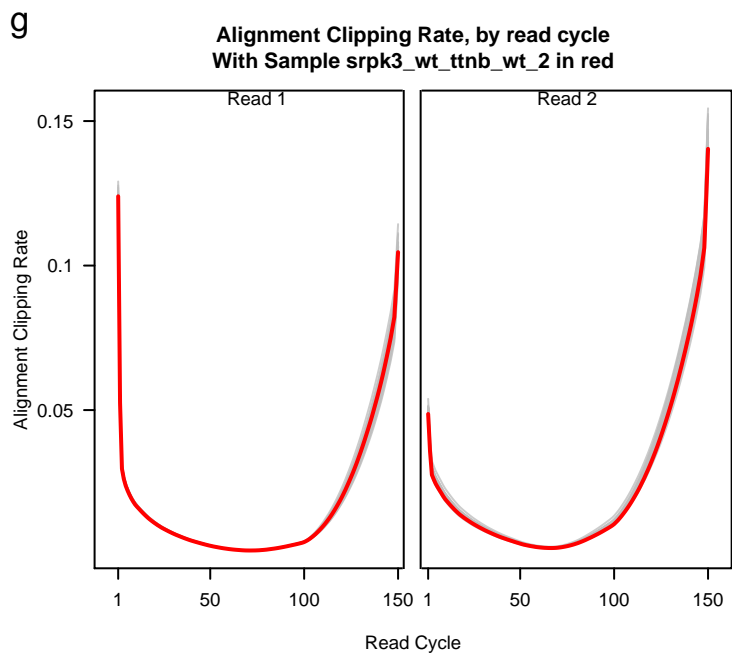
Upper Quartile Phred Quality Score  
With Sample srpk3\_wt\_ttnb\_wt\_2 in red

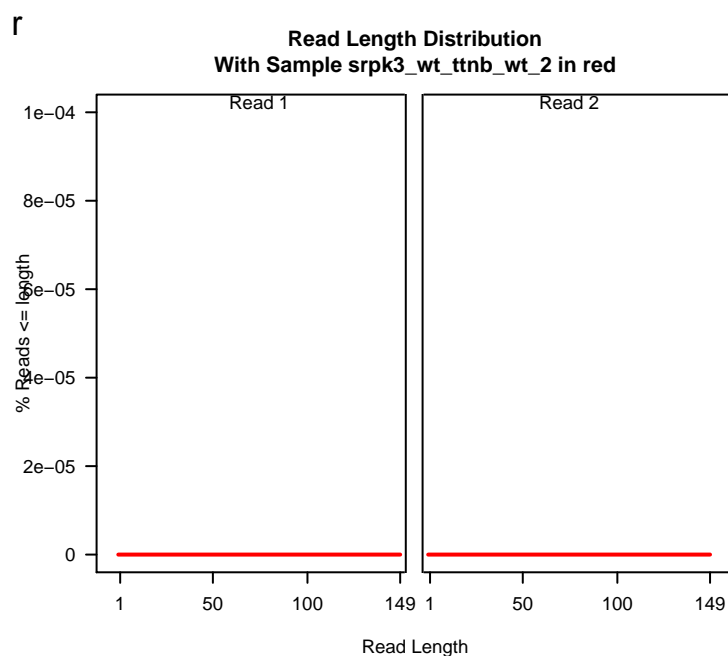
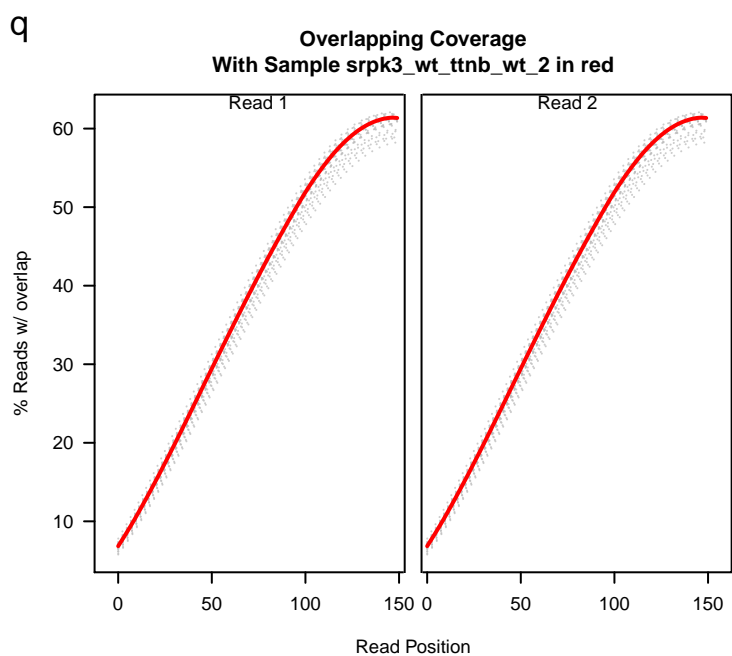
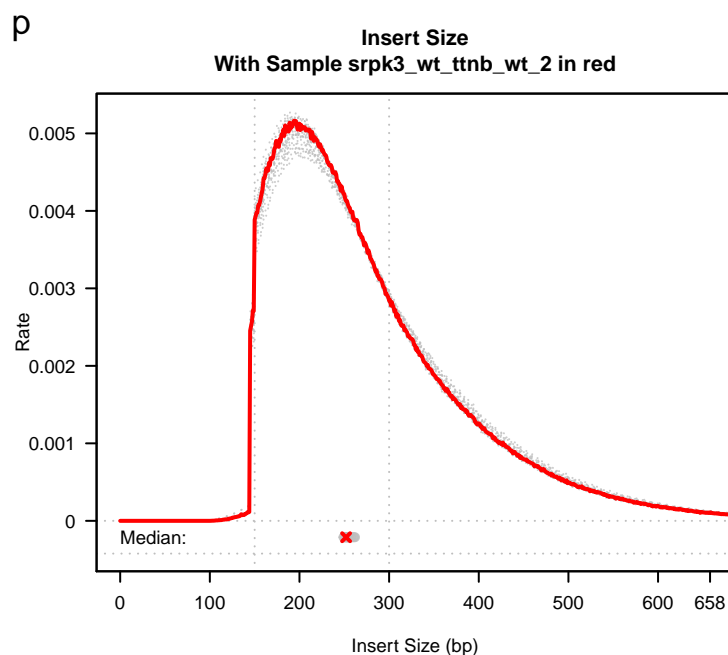
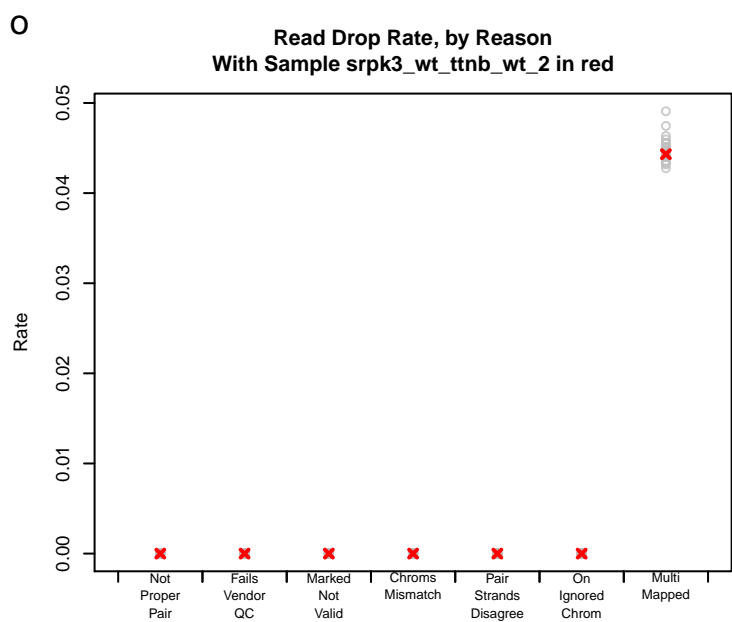
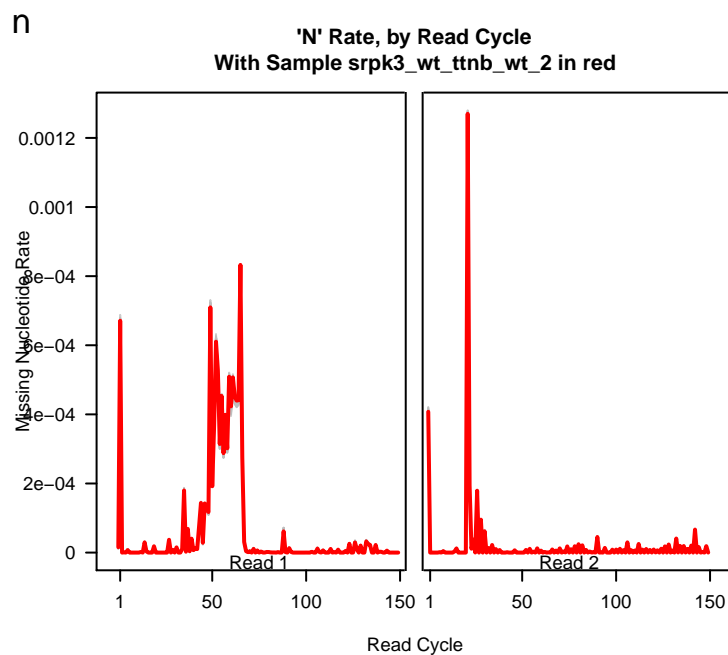
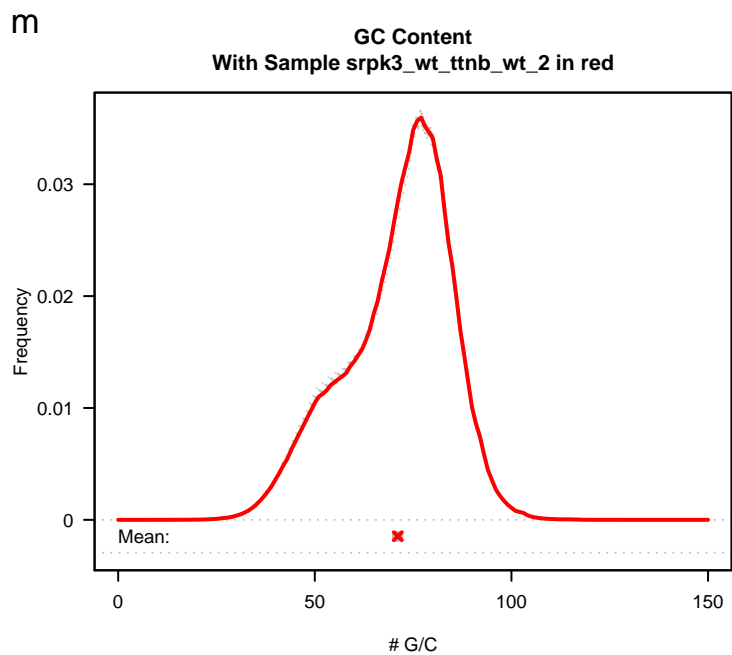


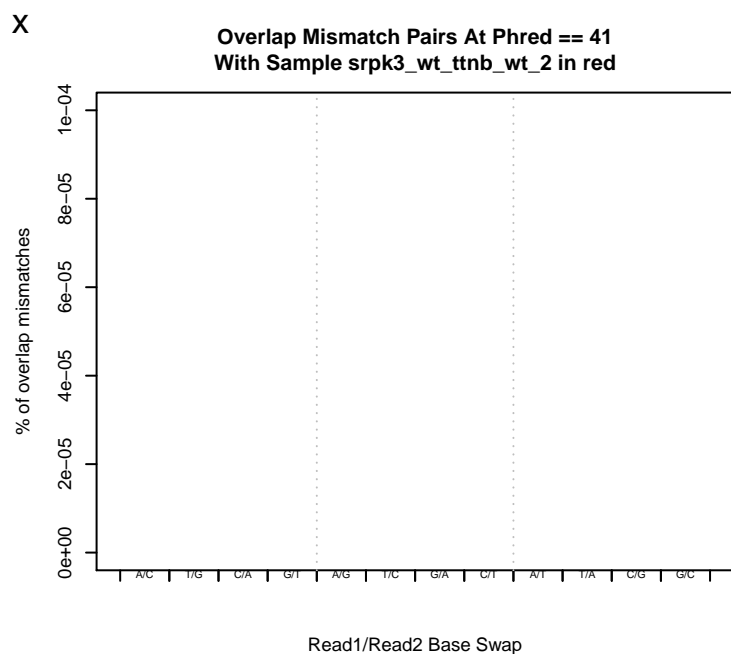
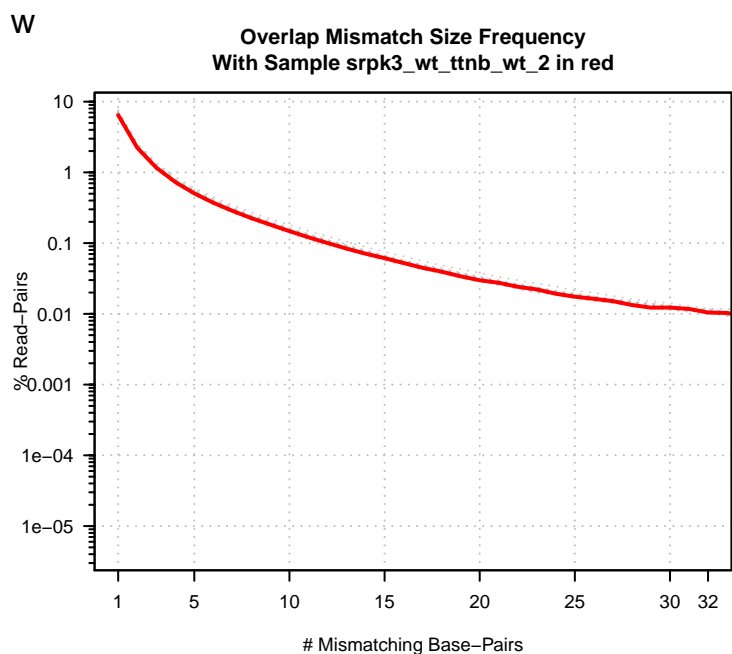
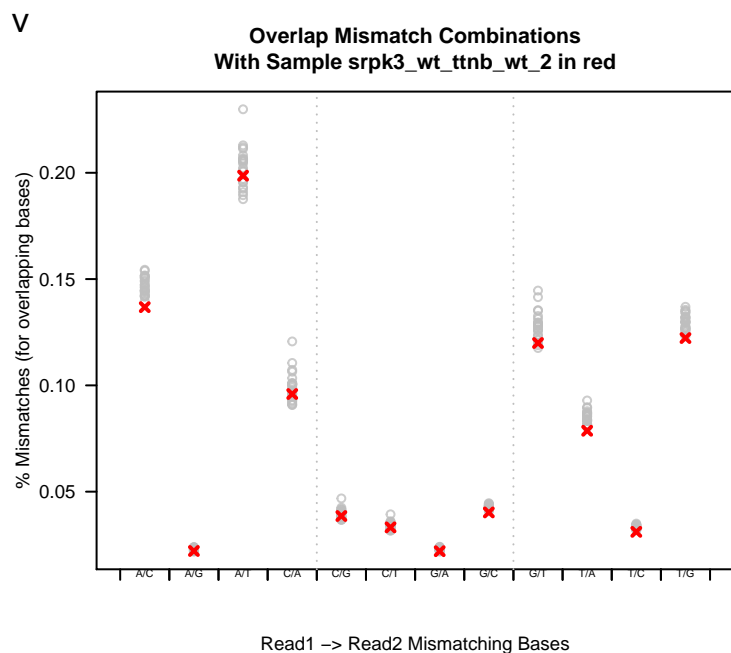
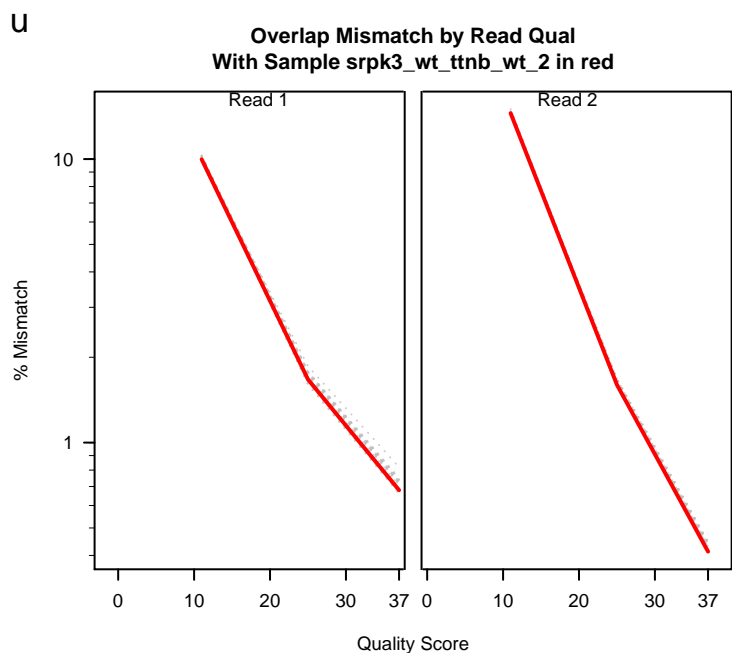
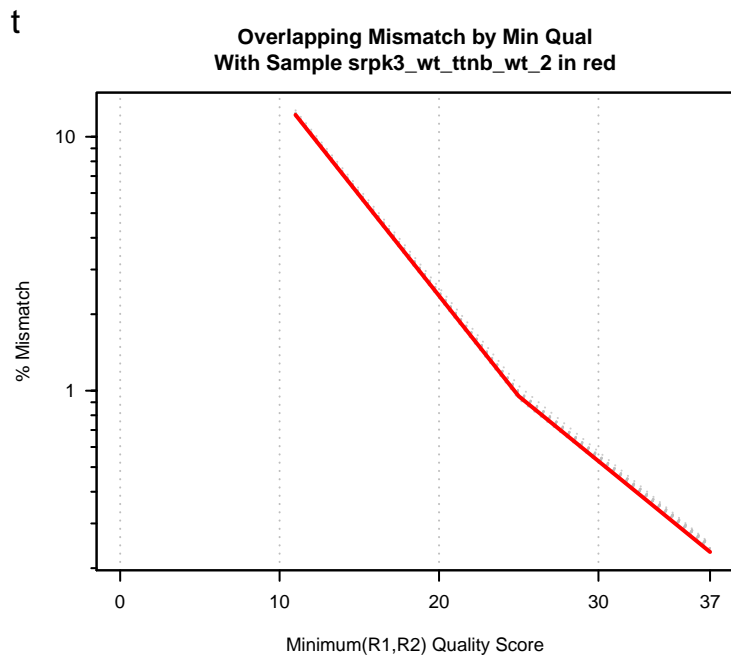
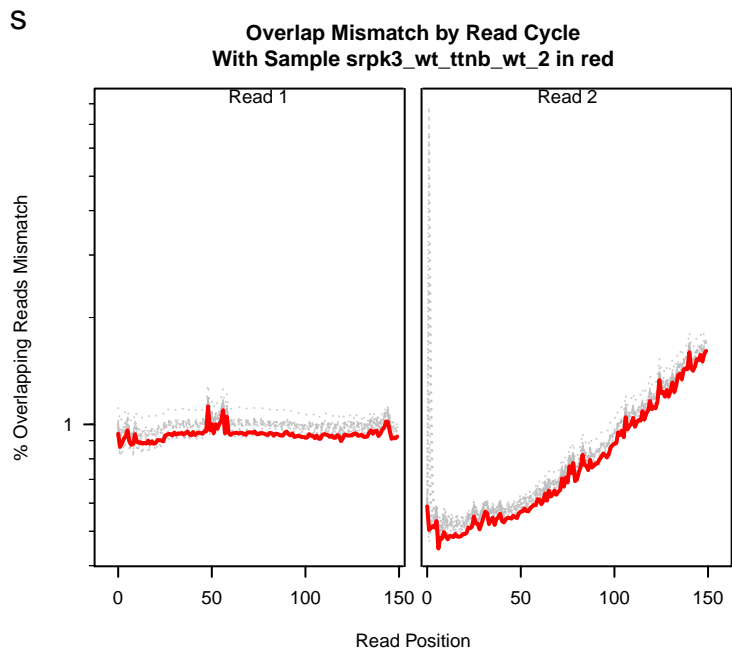
f

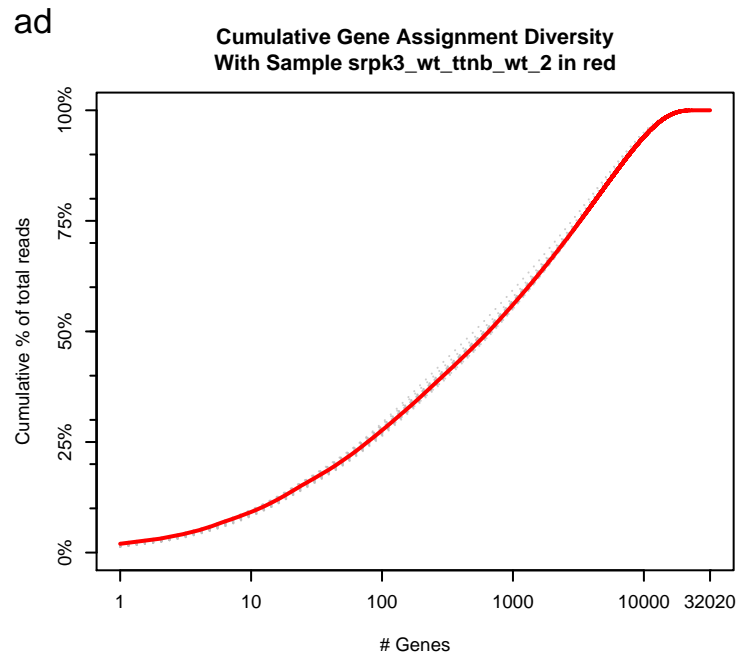
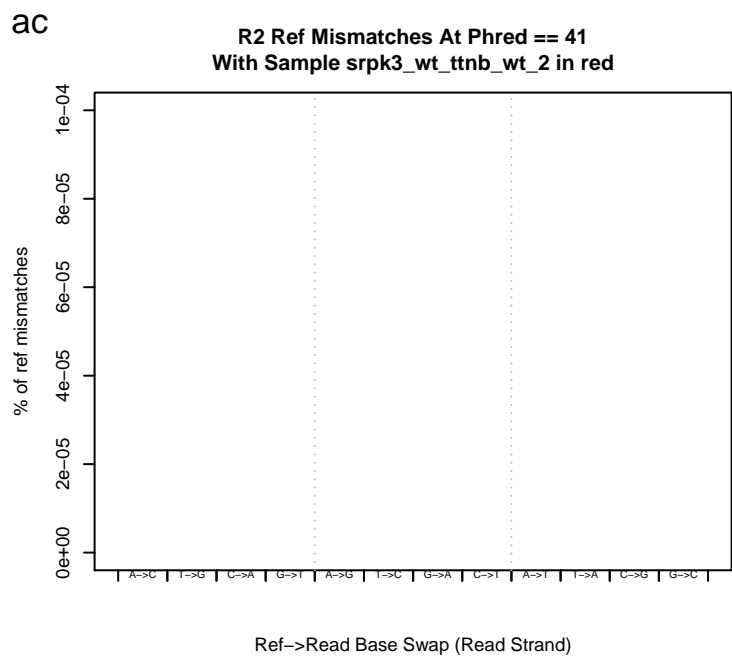
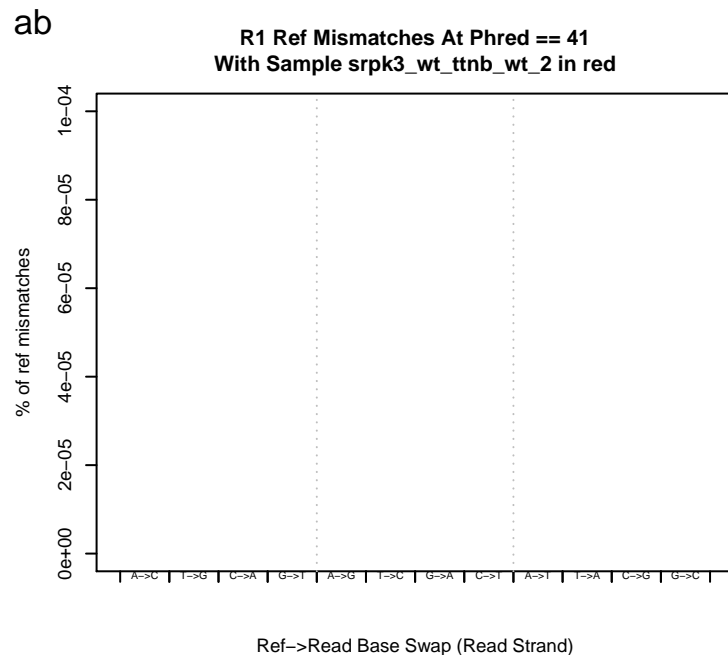
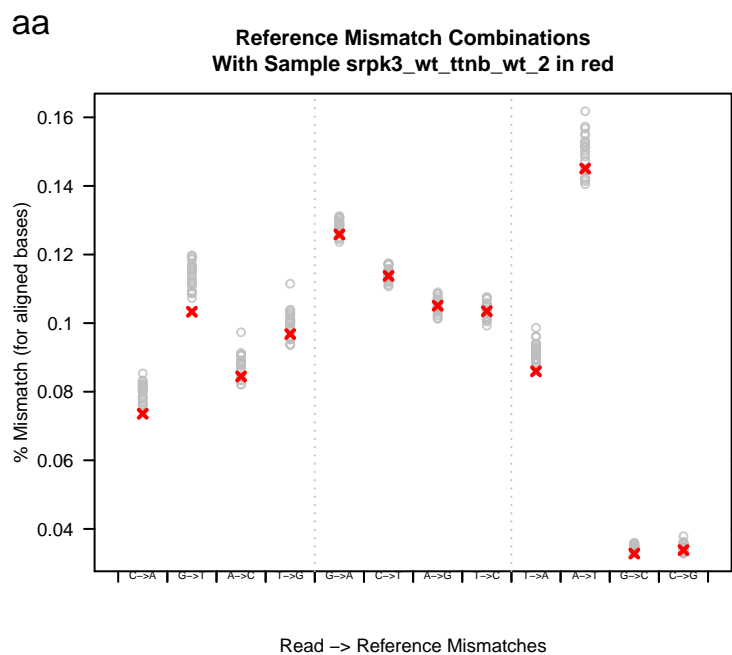
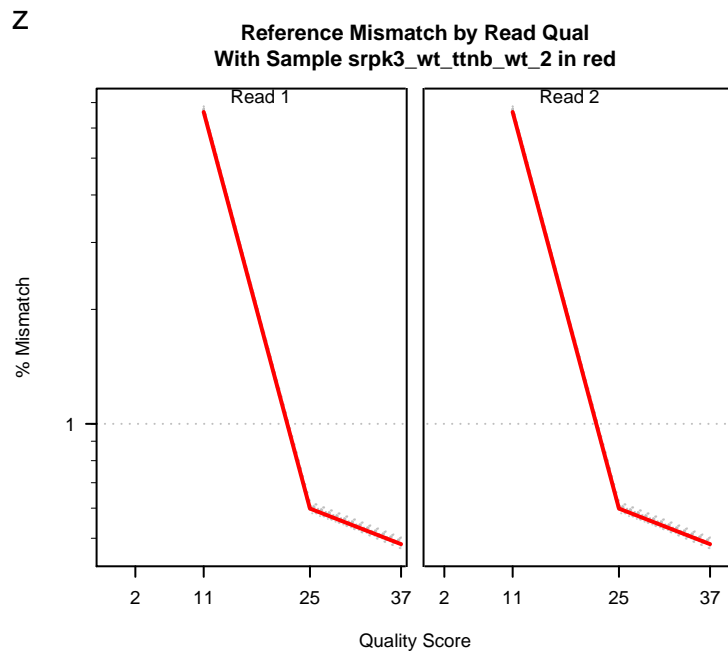
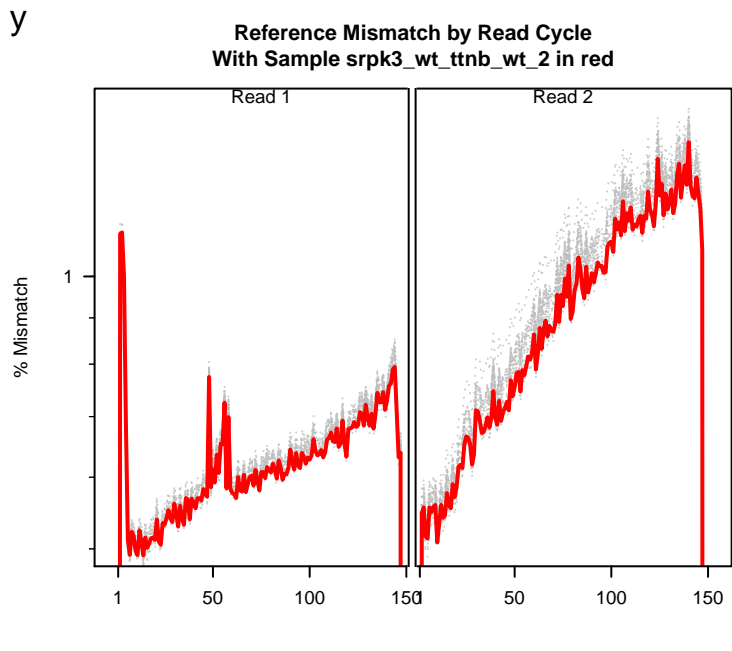
Maximum Phred Quality Score  
With Sample srpk3\_wt\_ttnb\_wt\_2 in red





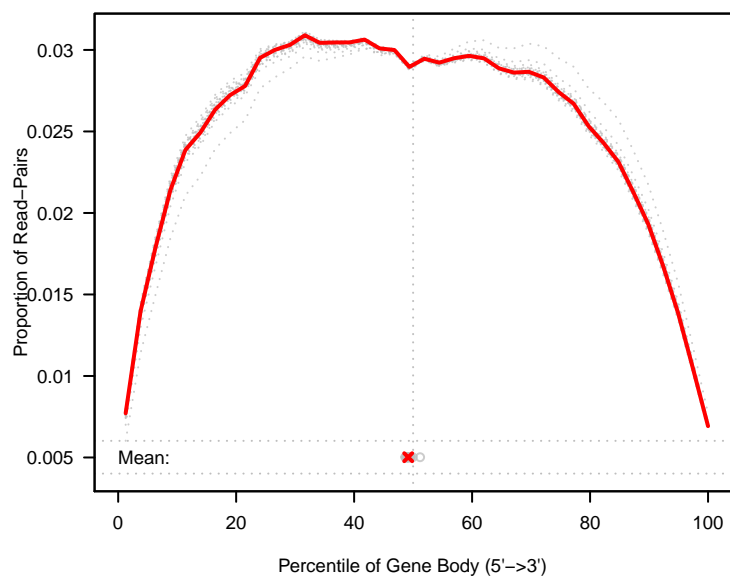






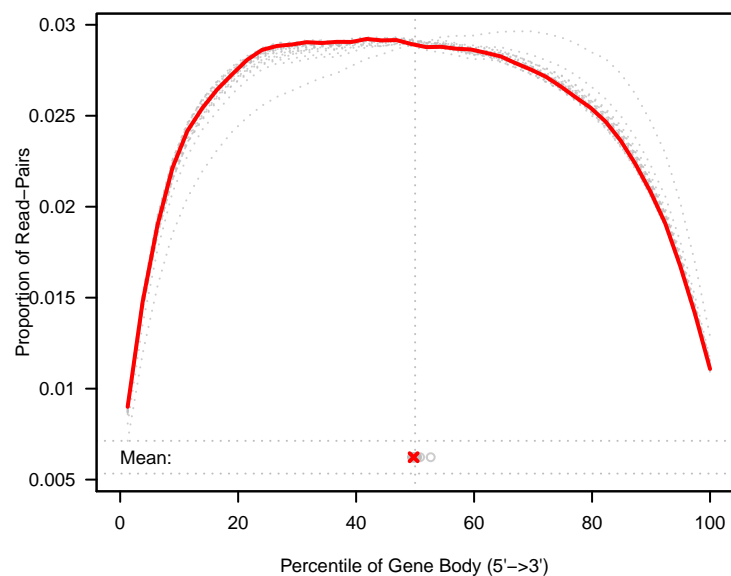
ae

**Gene-Body Coverage**  
With Sample `srpk3_wt_ttnb_wt_2` in red



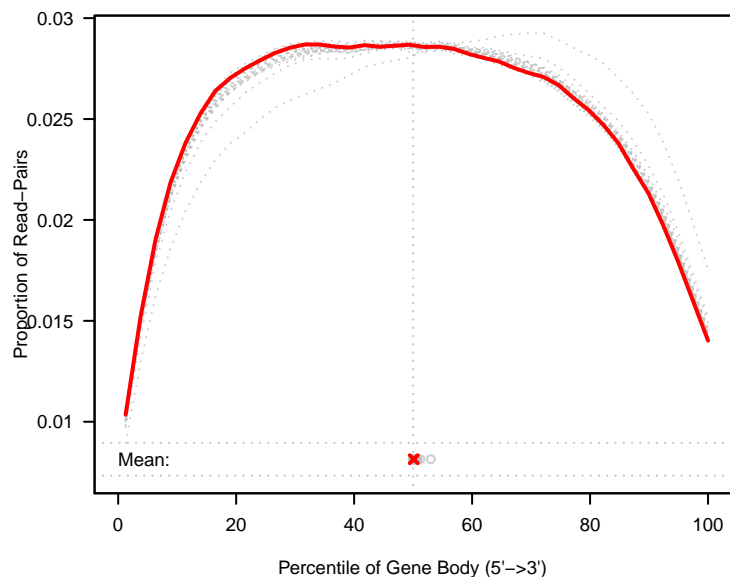
af

**Gene-Body Coverage, Upper Middle Quartile Genes**  
With Sample `srpk3_wt_ttnb_wt_2` in red



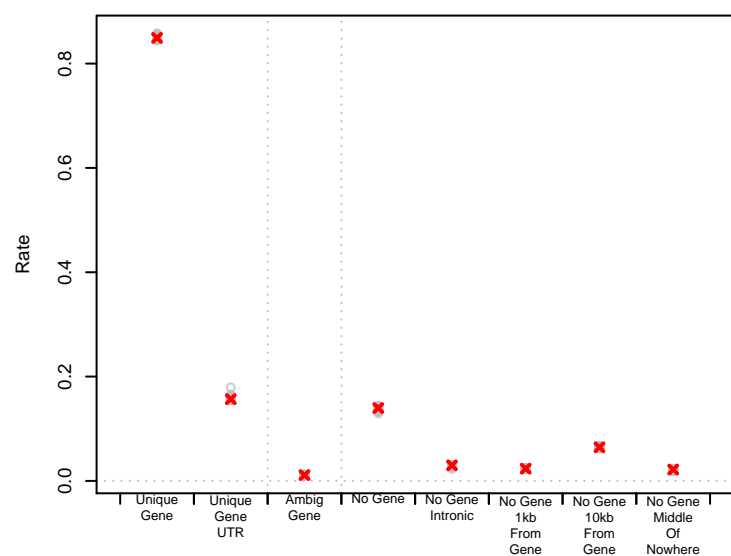
ag

**Gene-Body Coverage, Low Expression Genes**  
With Sample `srpk3_wt_ttnb_wt_2` in red



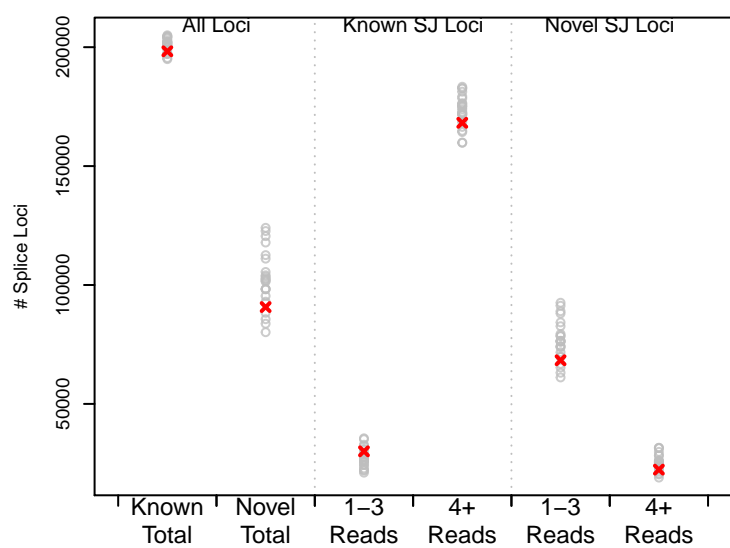
ah

**Read Mapping Location Rates**  
With Sample `srpk3_wt_ttnb_wt_2` in red



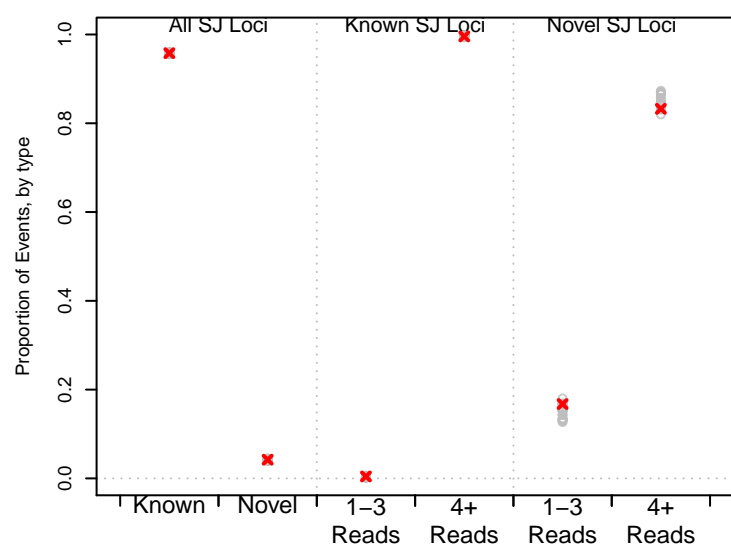
ai

**# Observed Splice Junction Loci, by type**  
With Sample `srpk3_wt_ttnb_wt_2` in red

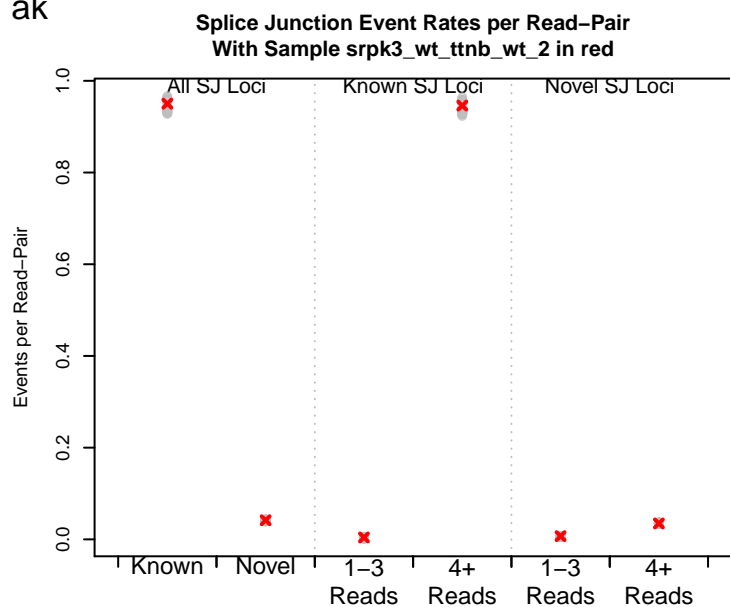


aj

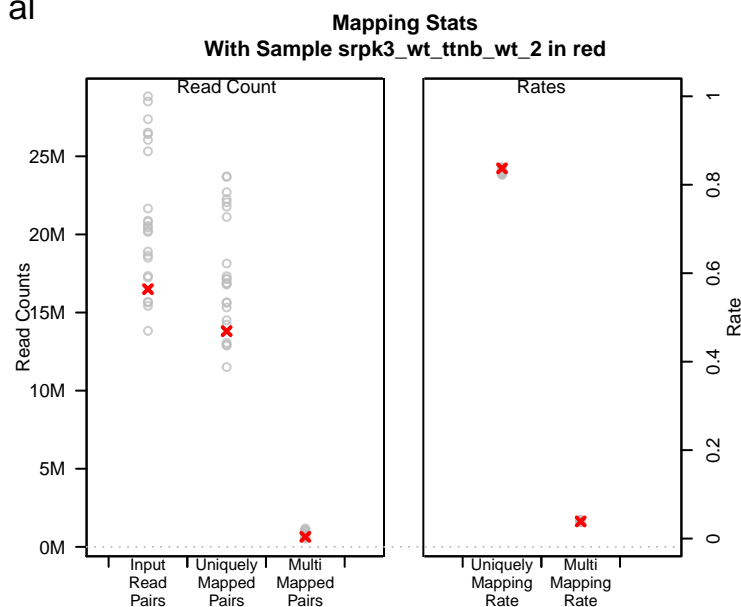
**Breakdown of Splice Junction Events, by type**  
With Sample `srpk3_wt_ttnb_wt_2` in red



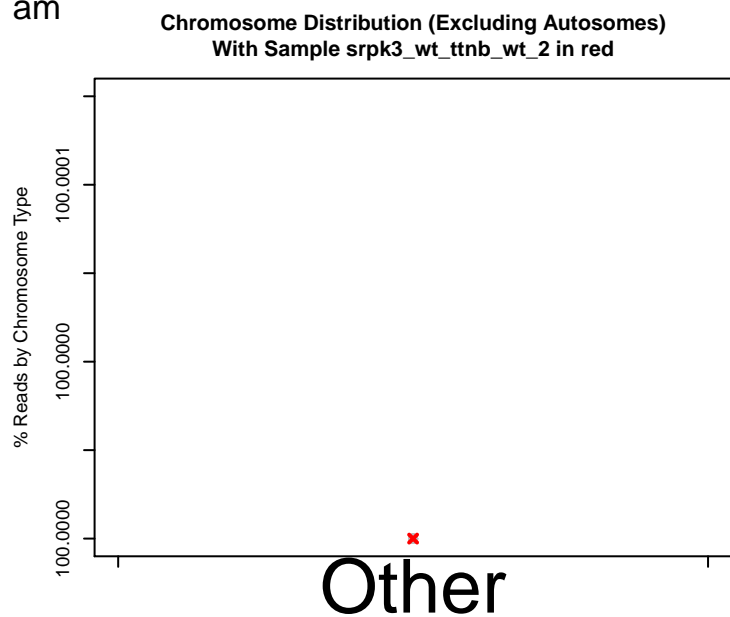
ak



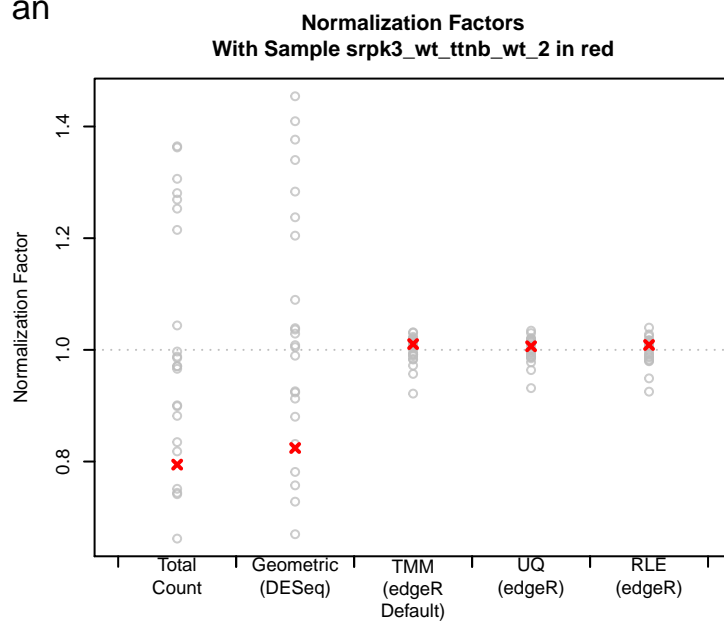
al



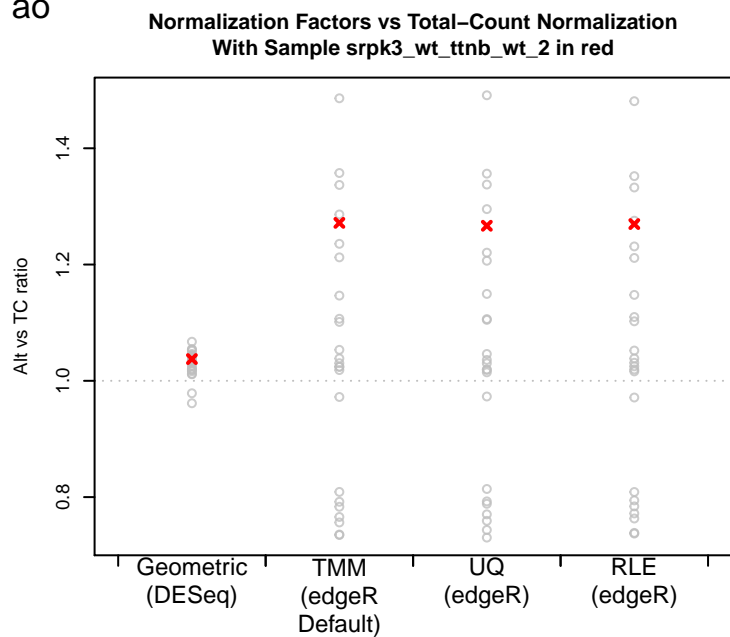
am



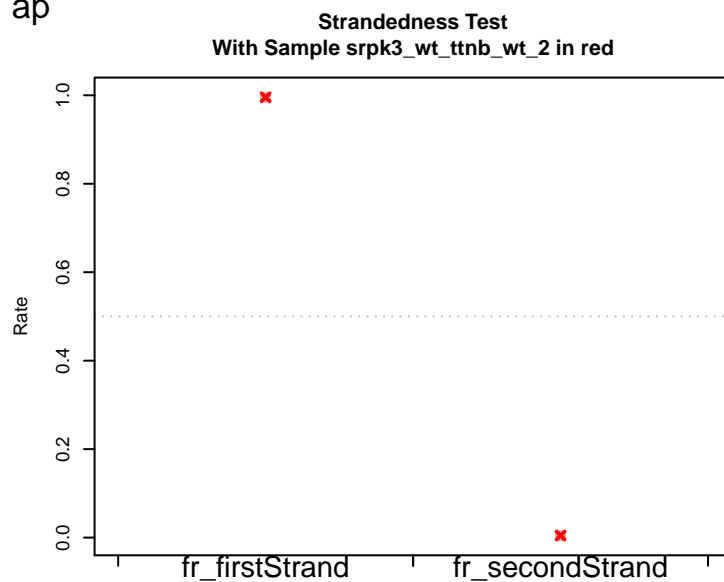
an



ao

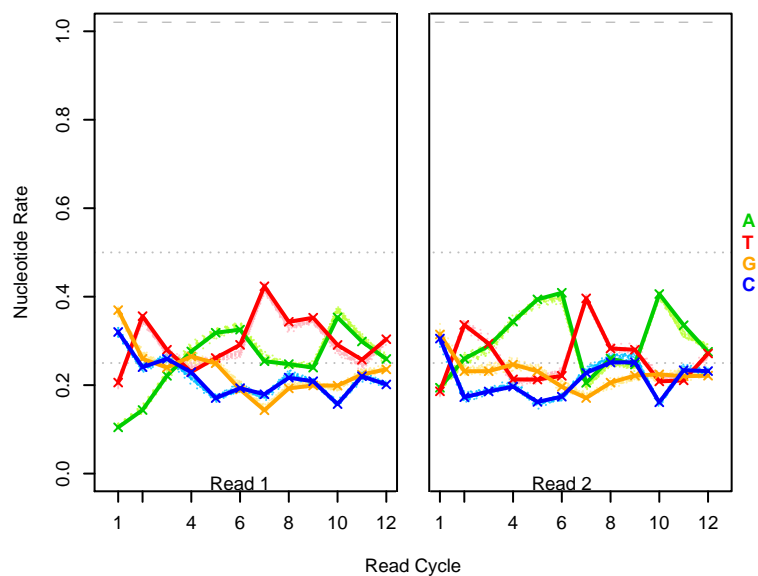


ap



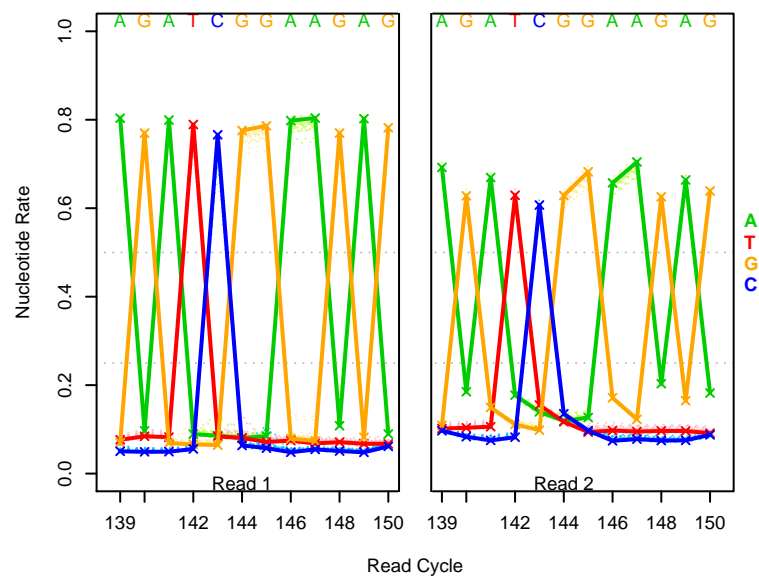
aq

**Nucleotide Rate by Cycle, Leading Clipped bases (12)**  
With Sample srpk3\_wt\_ttnb\_wt\_2 in red



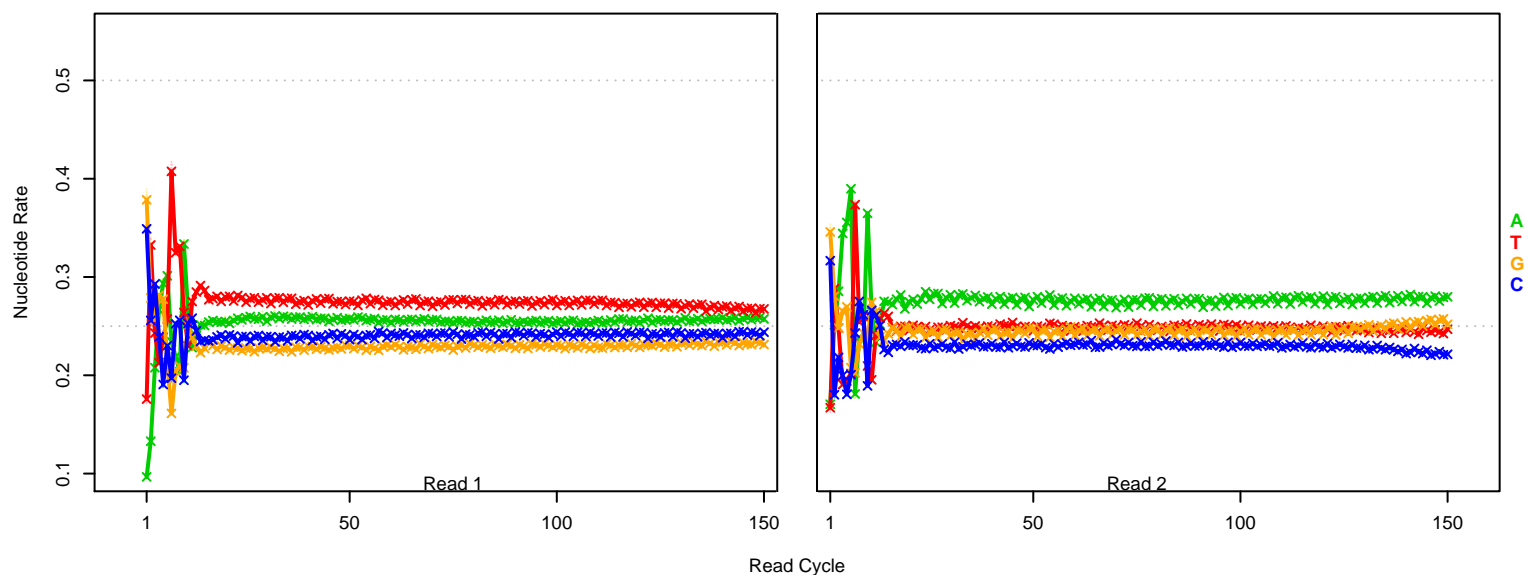
ar

**Nucleotide Rate by Cycle, Trailing Clipped bases (12)**  
With Sample srpk3\_wt\_ttnb\_wt\_2 in red



as

**Raw Nucleotide Rate by Cycle**  
With Sample srpk3\_wt\_ttnb\_wt\_2 in red



at

**Nucleotide Rate by Cycle, Aligned bases only**  
With Sample srpk3\_wt\_ttnb\_wt\_2 in red

