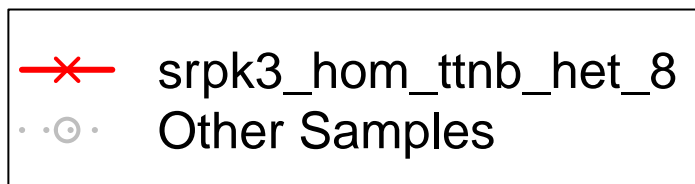


a

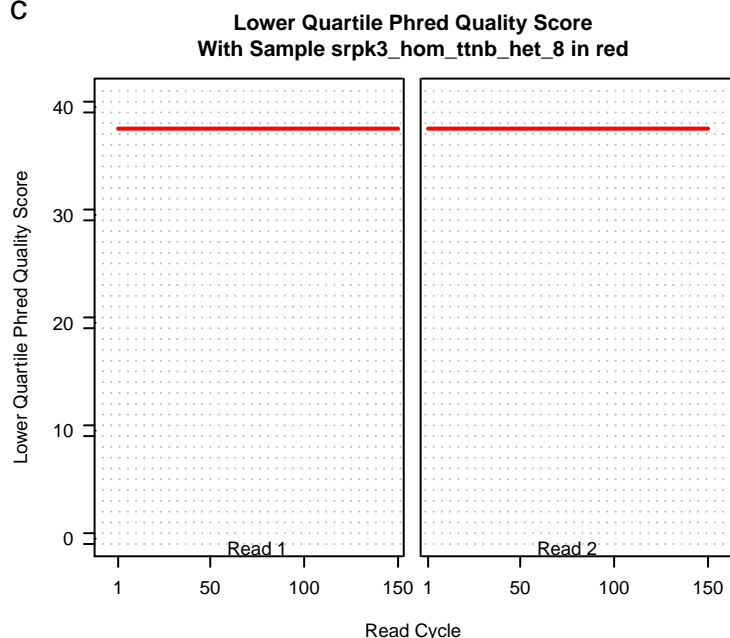
Sample Highlight:  
srpk3\_hom\_ttnb\_het\_8



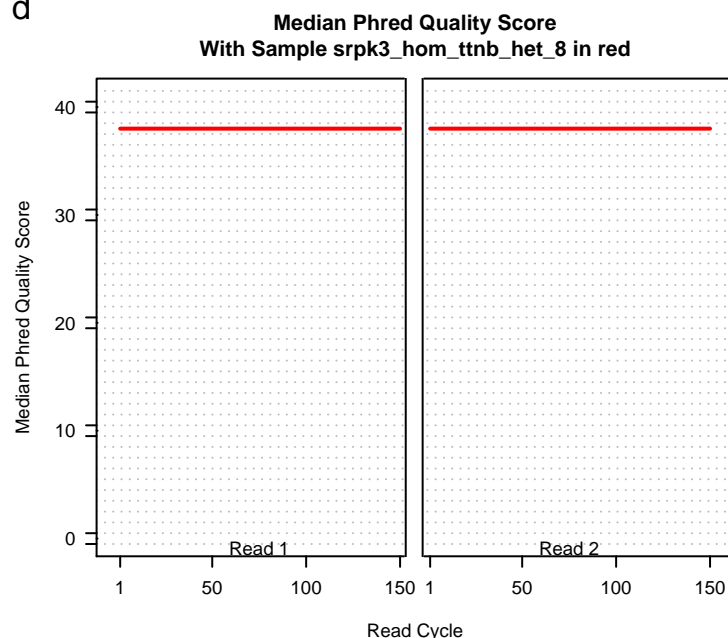
b



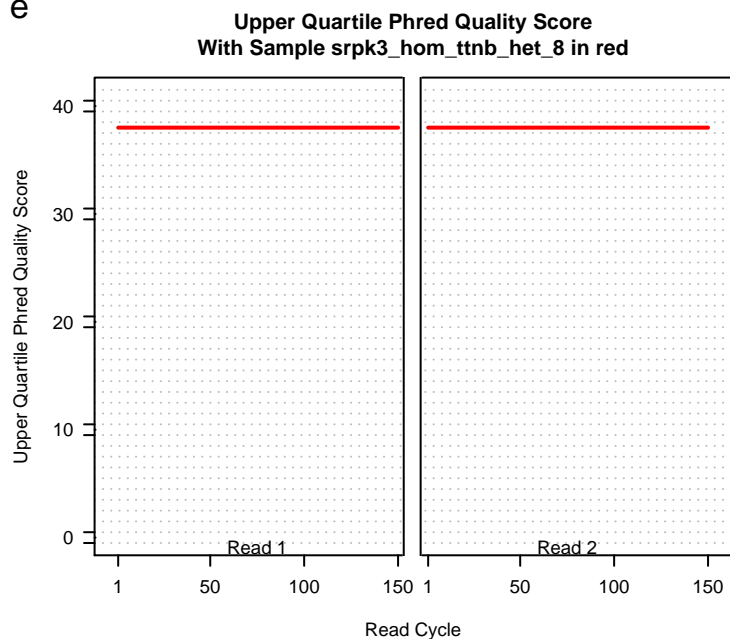
c



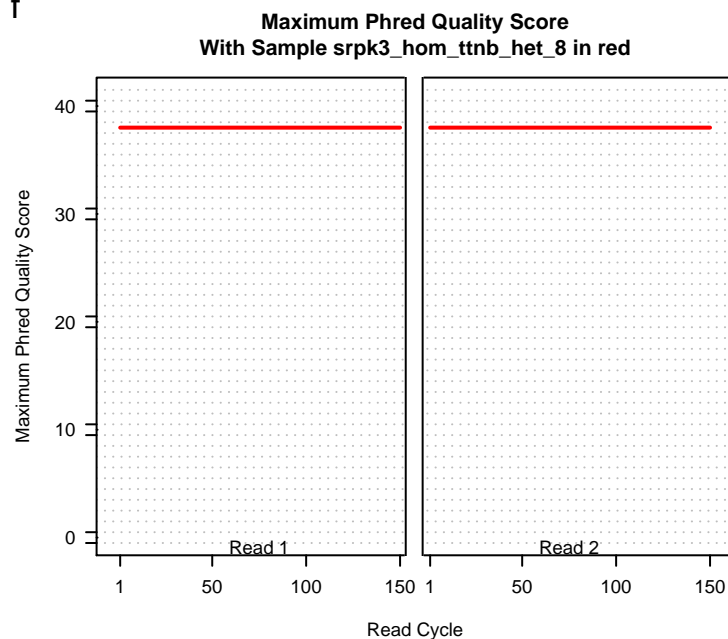
d

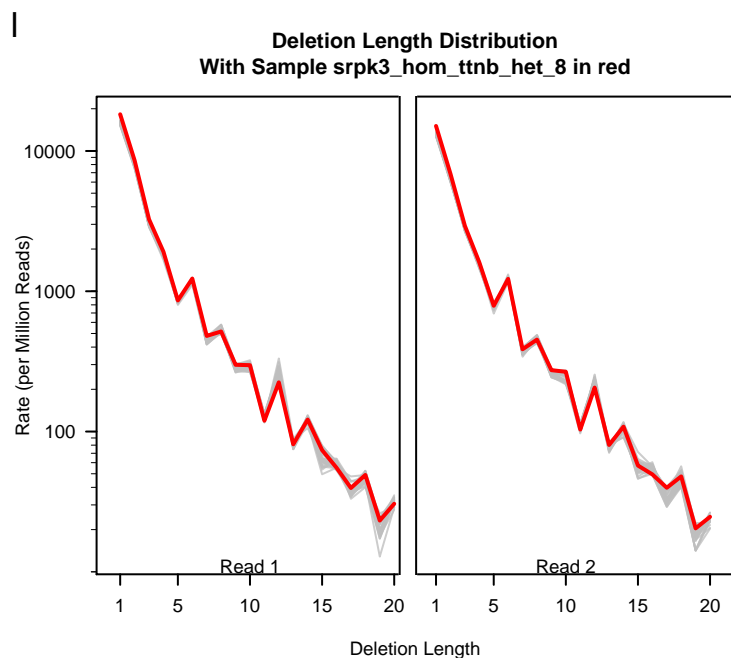
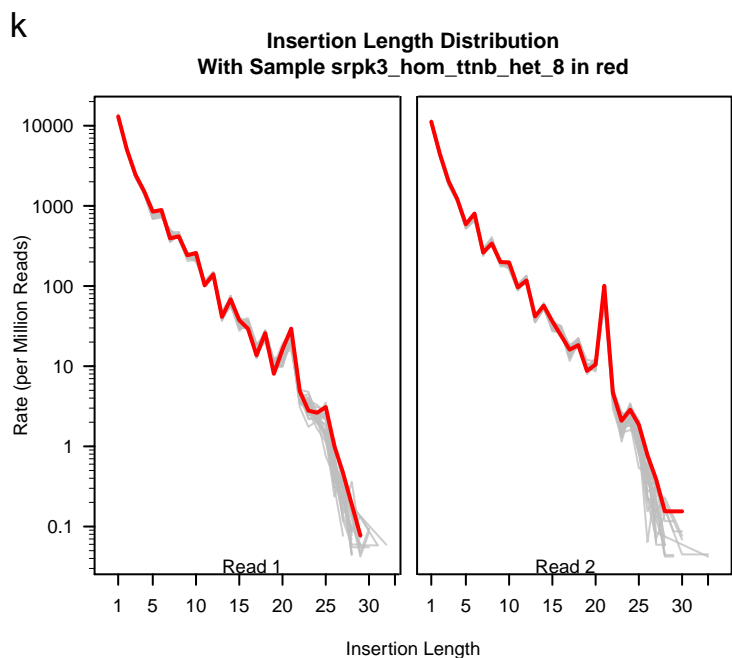
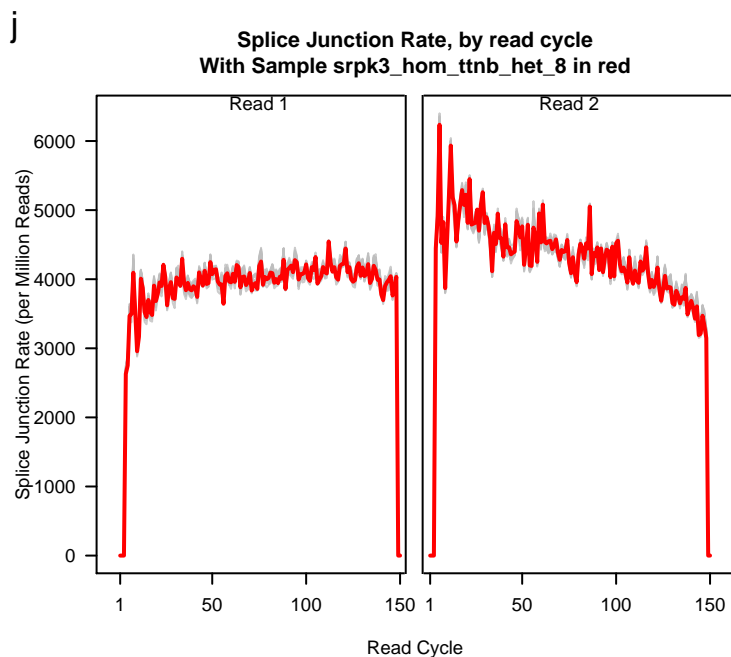
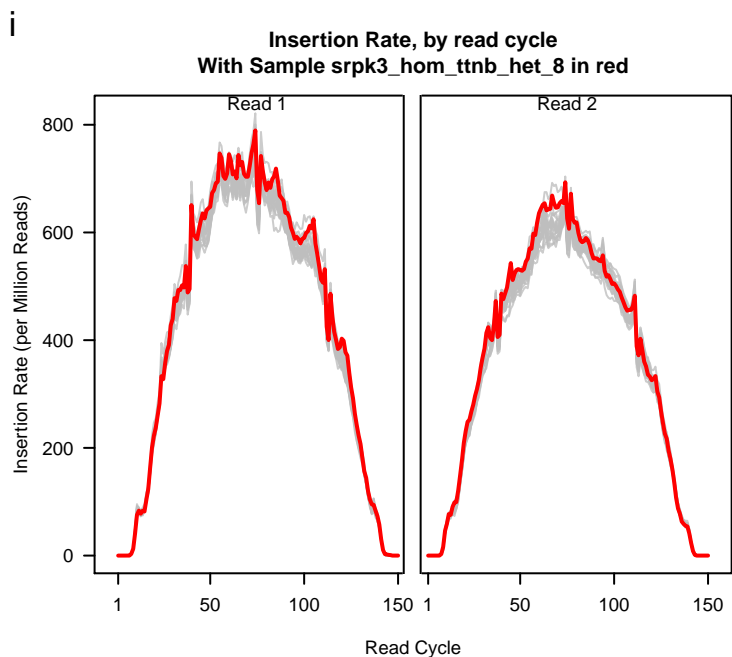
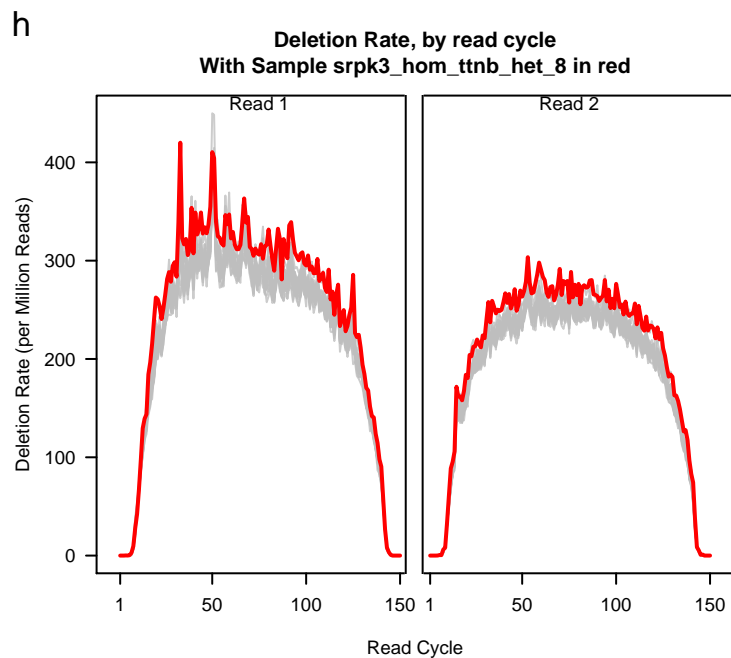
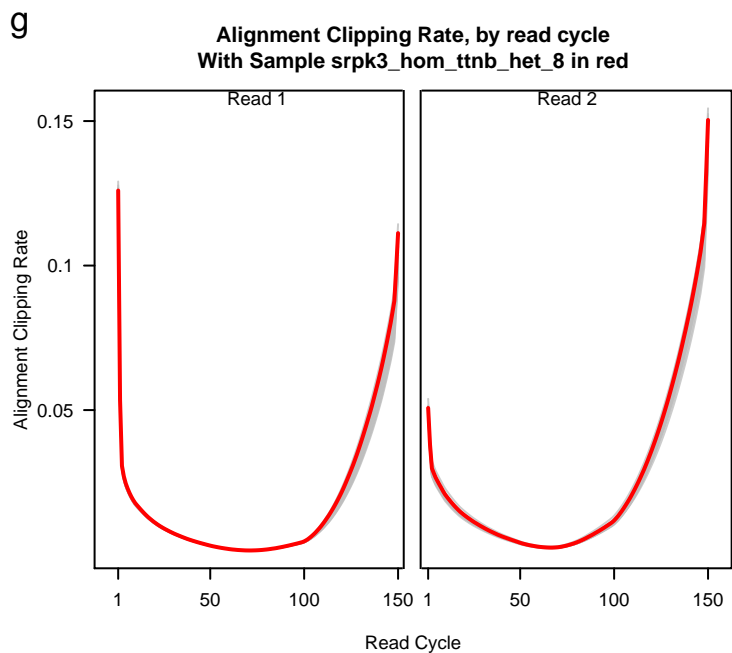


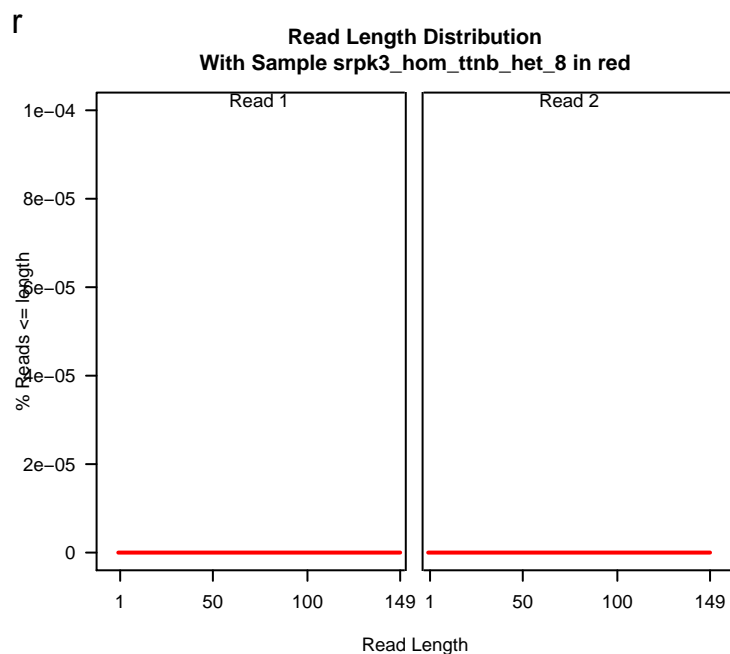
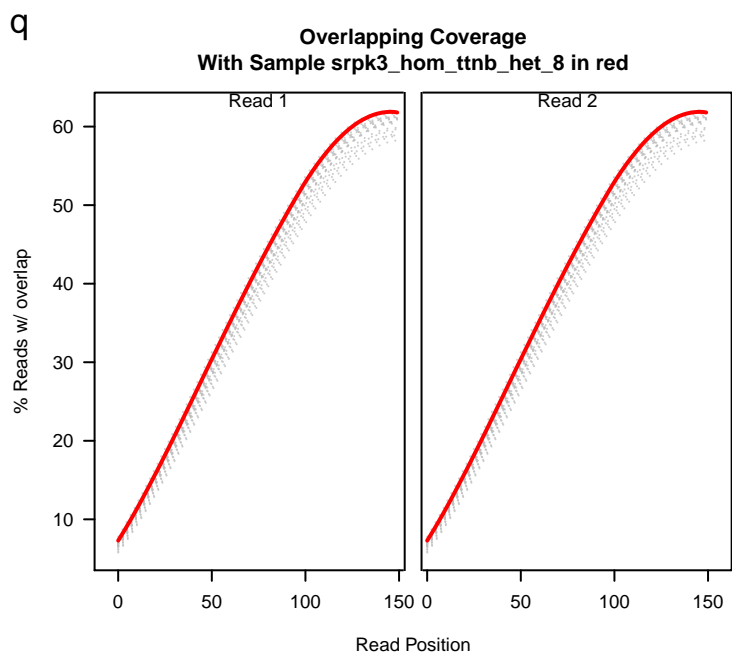
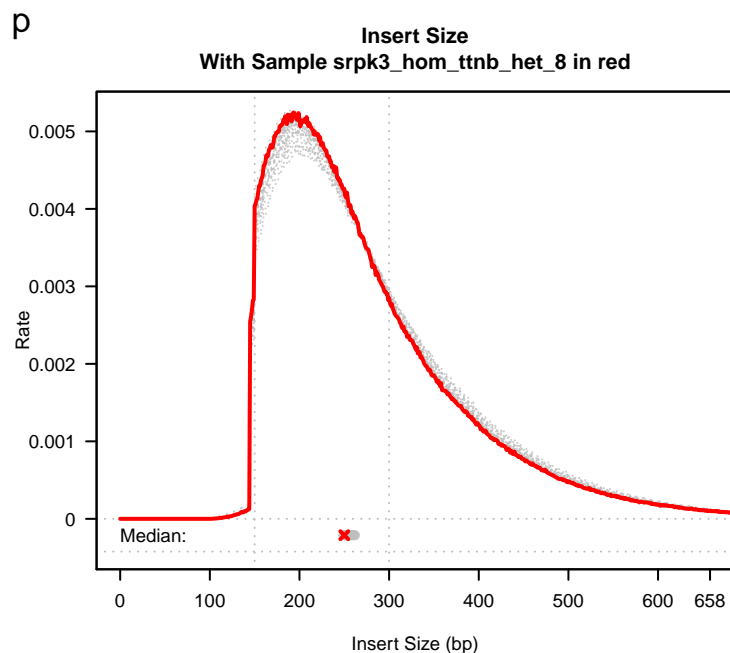
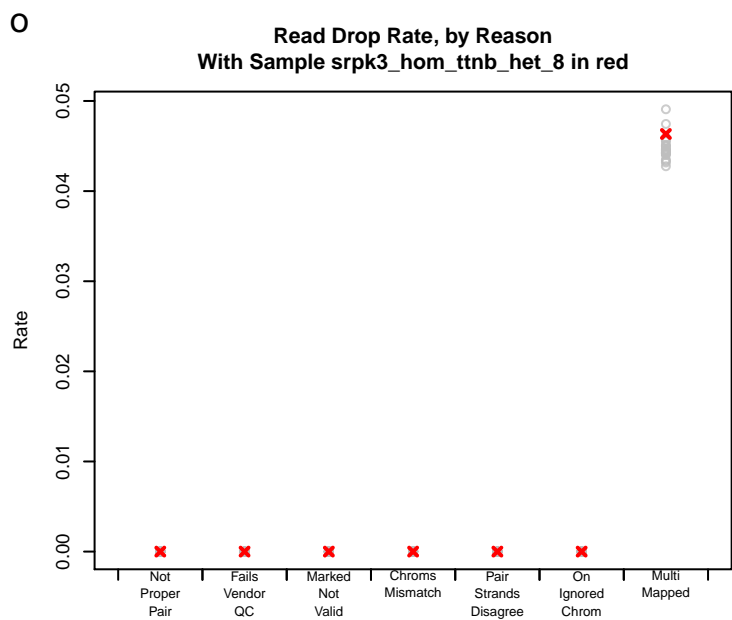
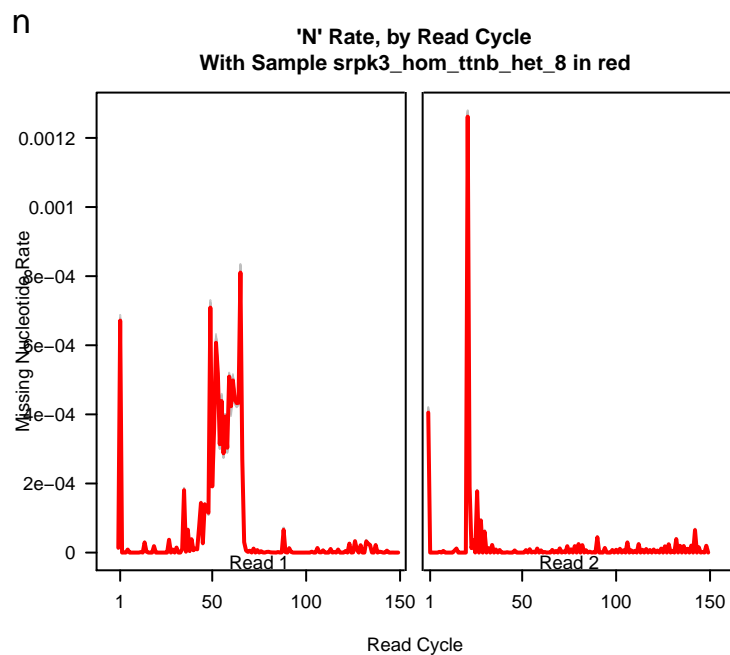
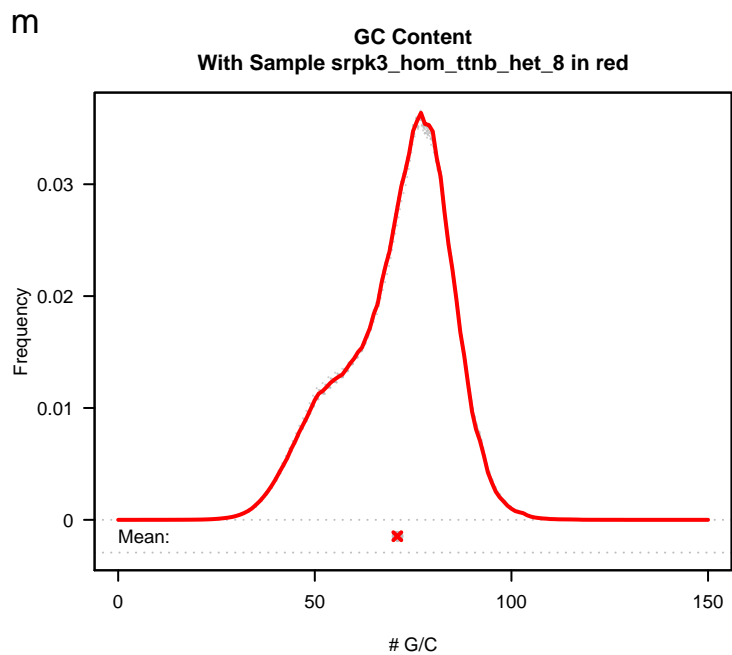
e

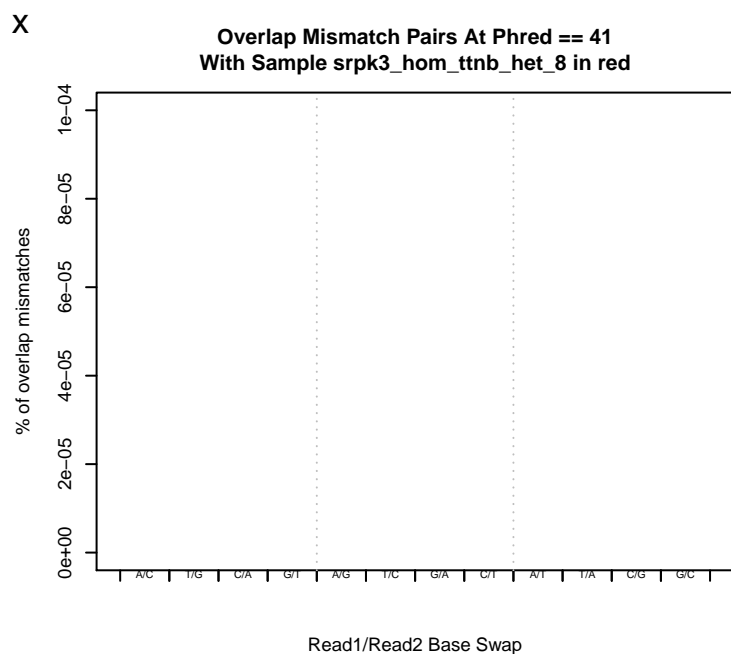
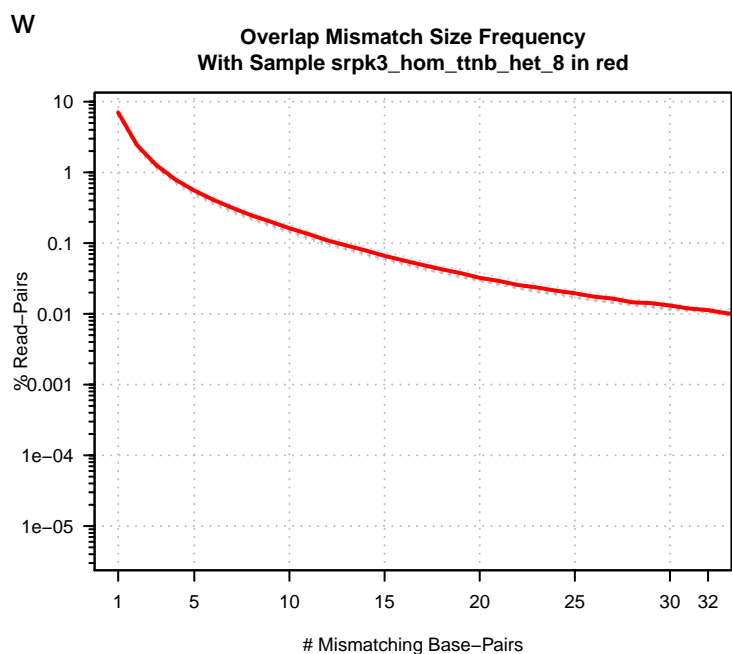
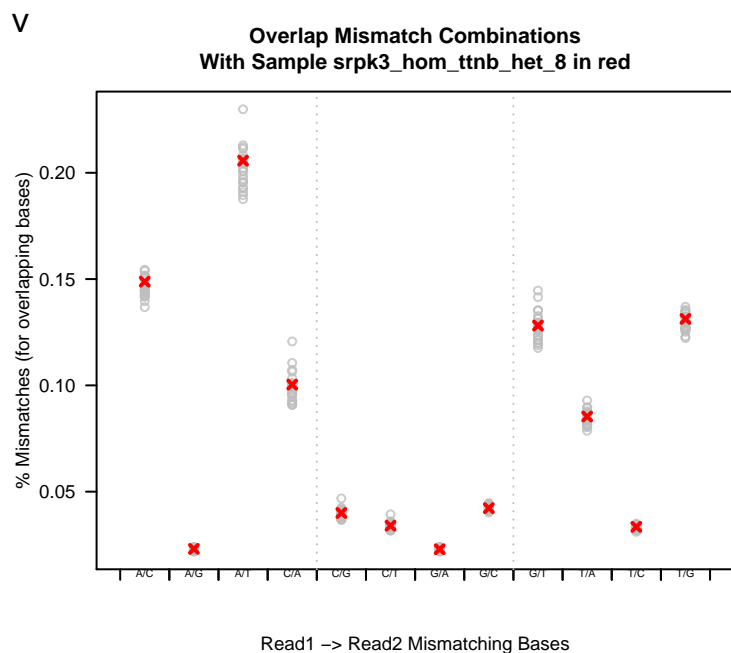
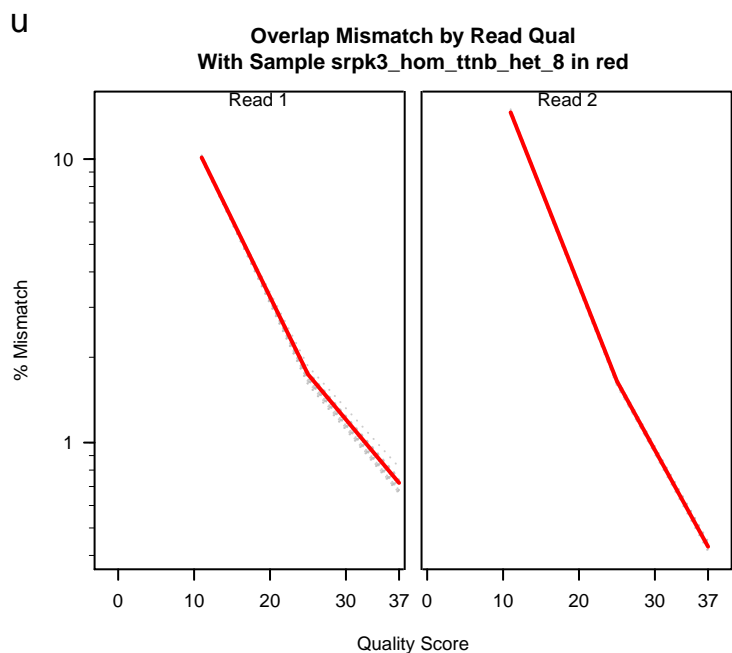
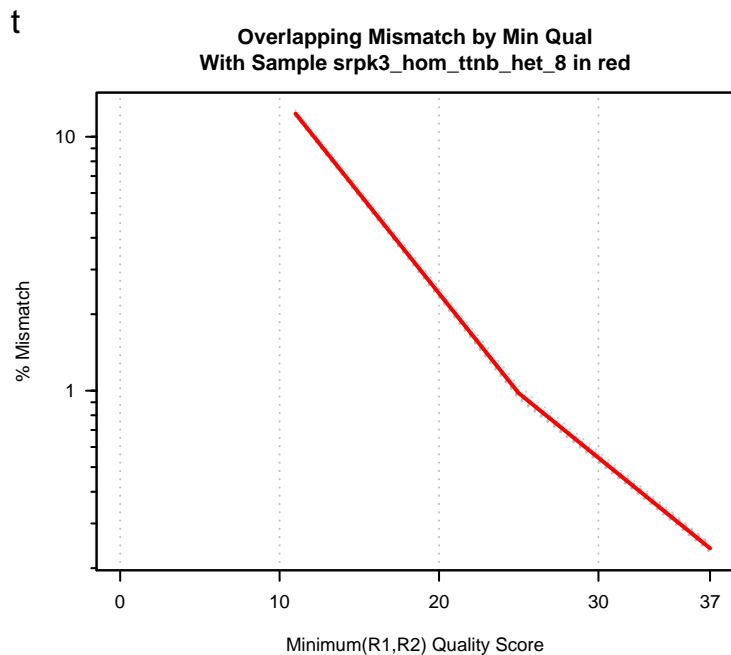
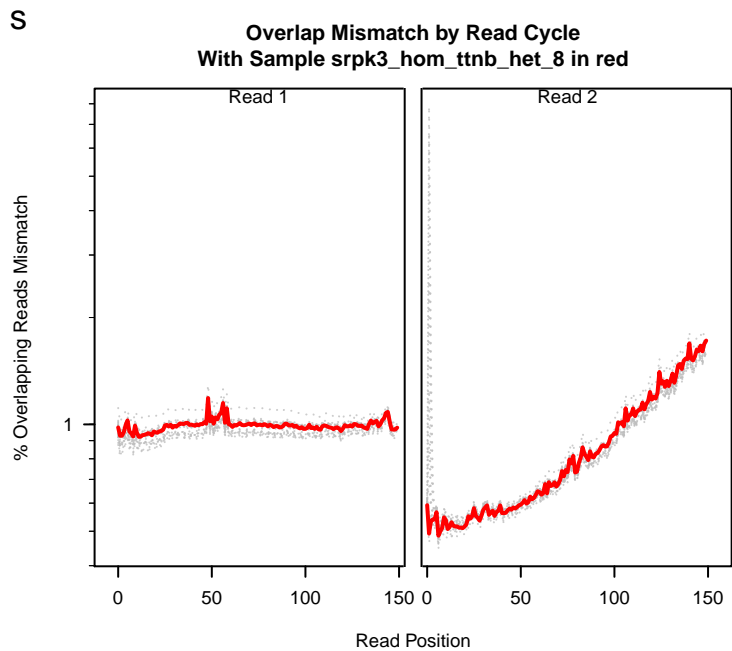


f



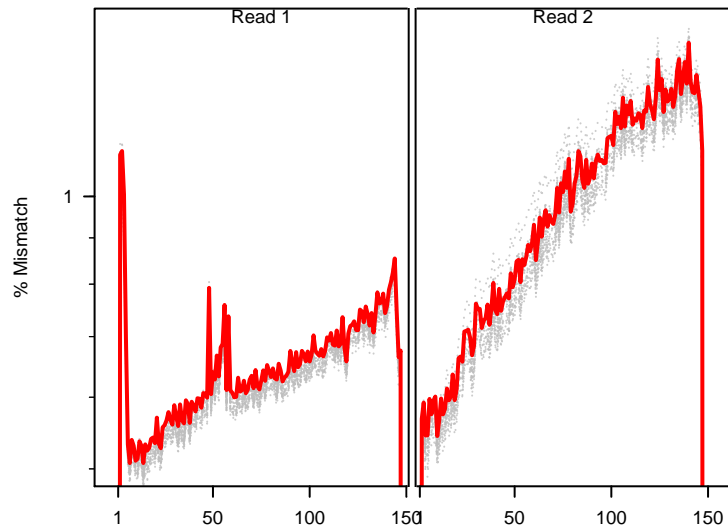






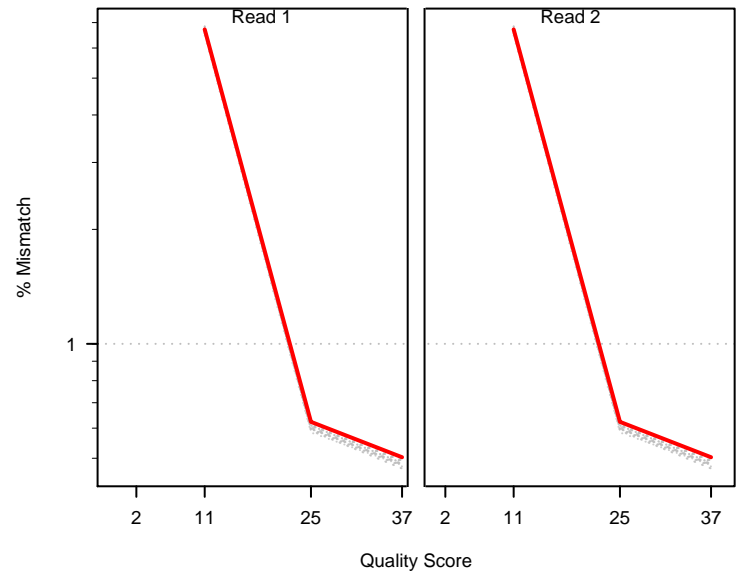
y

**Reference Mismatch by Read Cycle**  
With Sample srpk3\_hom\_ttnb\_het\_8 in red



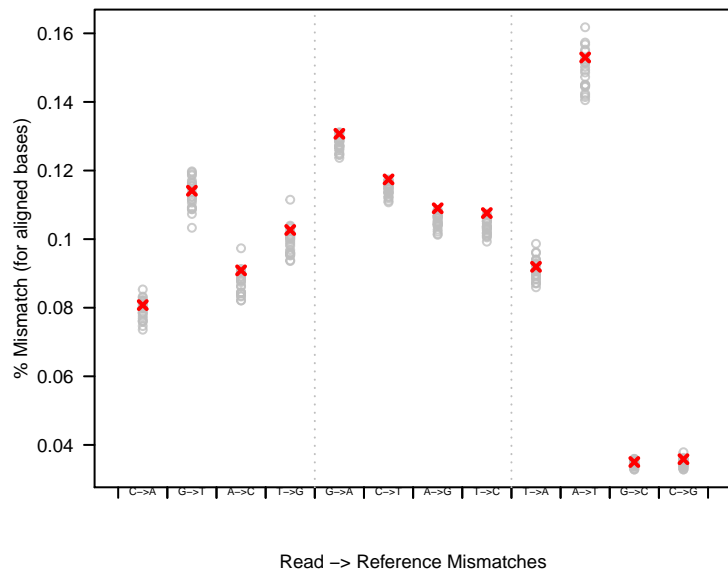
Z

**Reference Mismatch by Read Qual**  
With Sample srpk3\_hom\_ttnb\_het\_8 in red



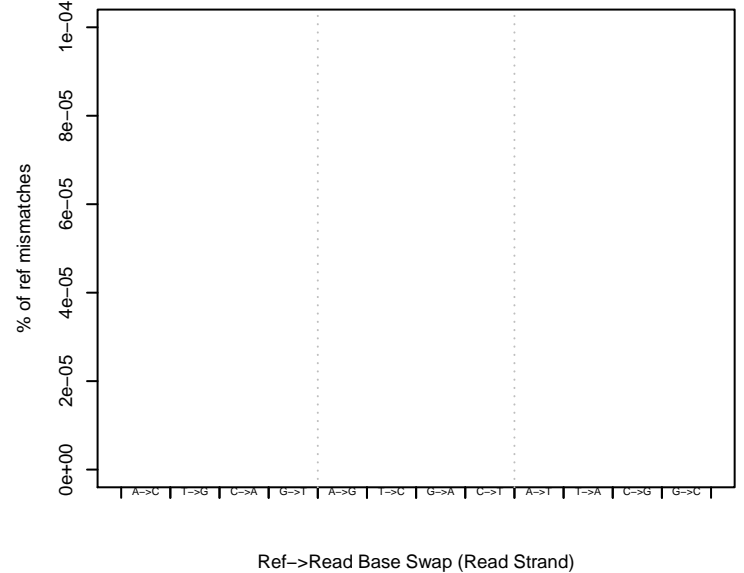
aa

**Reference Mismatch Combinations**  
With Sample srpk3\_hom\_ttnb\_het\_8 in red



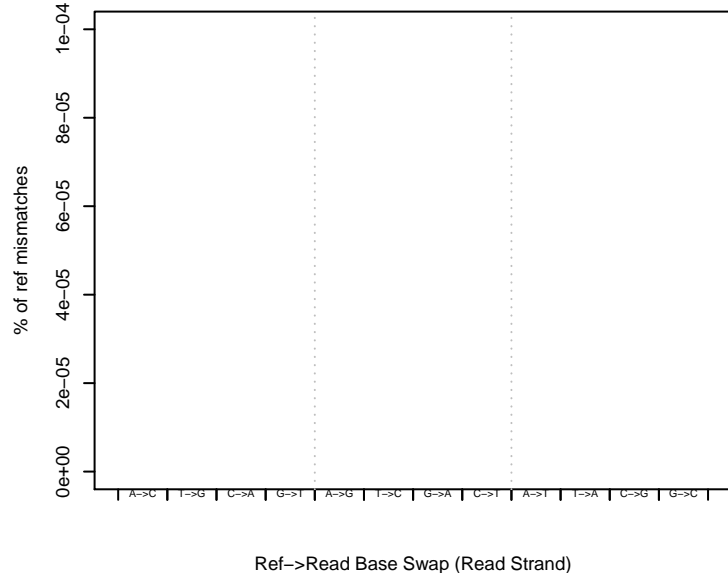
ab

**R1 Ref Mismatches At Phred == 41**  
With Sample srpk3\_hom\_ttnb\_het\_8 in red



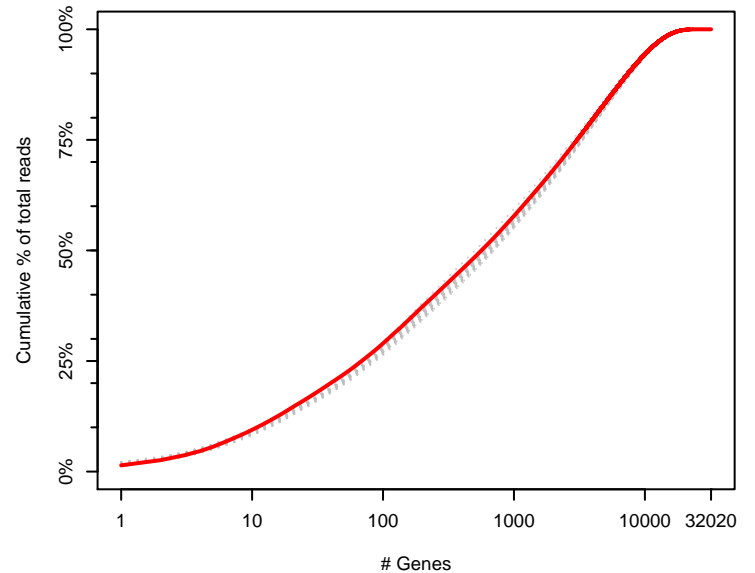
ac

**R2 Ref Mismatches At Phred == 41**  
With Sample srpk3\_hom\_ttnb\_het\_8 in red



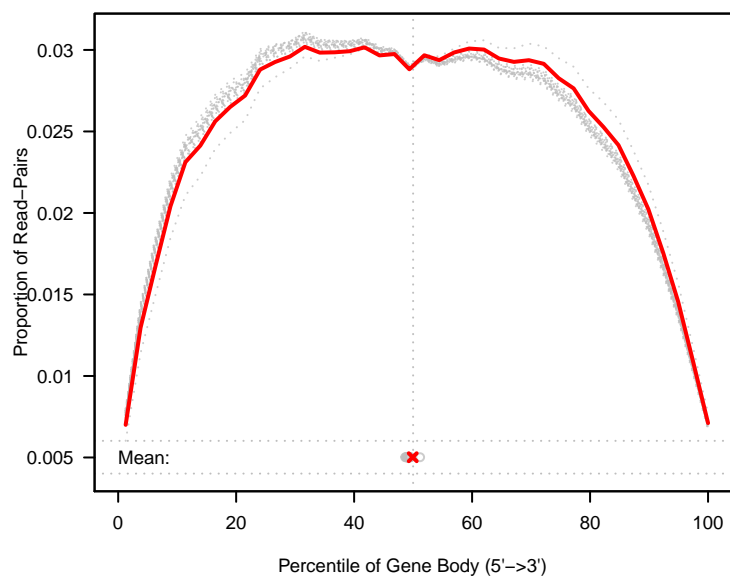
ad

**Cumulative Gene Assignment Diversity**  
With Sample srpk3\_hom\_ttnb\_het\_8 in red



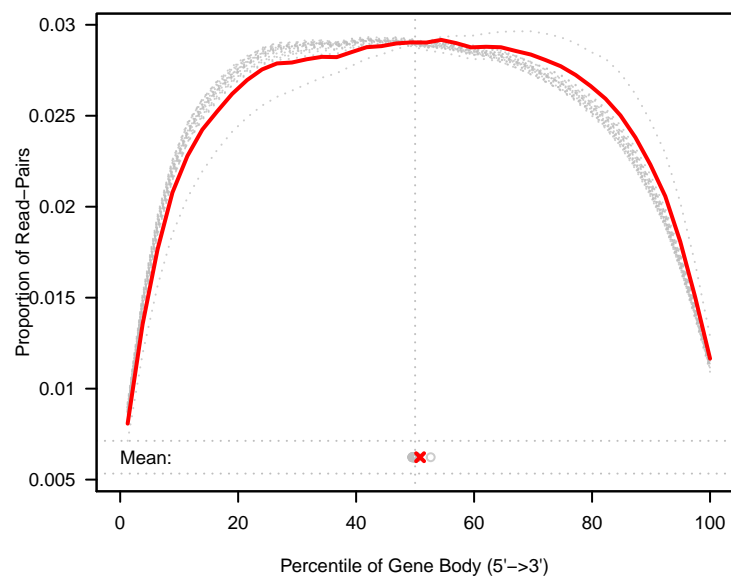
ae

**Gene–Body Coverage**  
With Sample *srpk3\_hom\_ttnb\_het\_8* in red



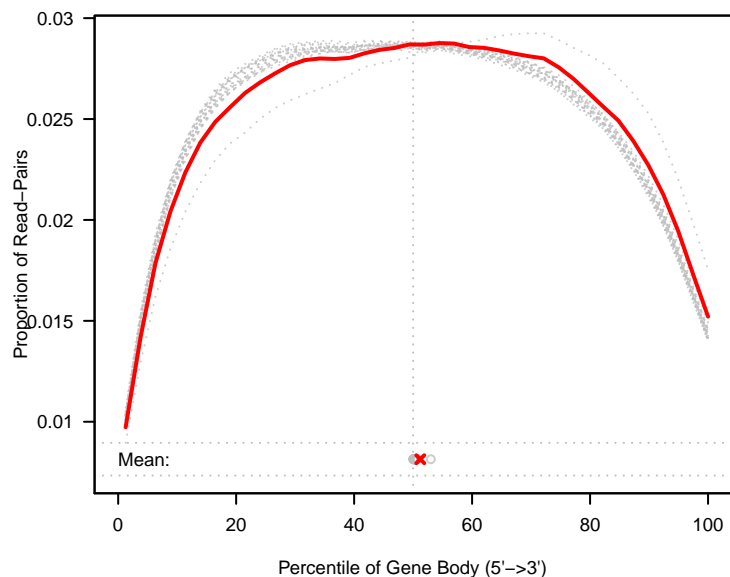
af

**Gene–Body Coverage, Upper Middle Quartile Genes**  
With Sample *srpk3\_hom\_ttnb\_het\_8* in red



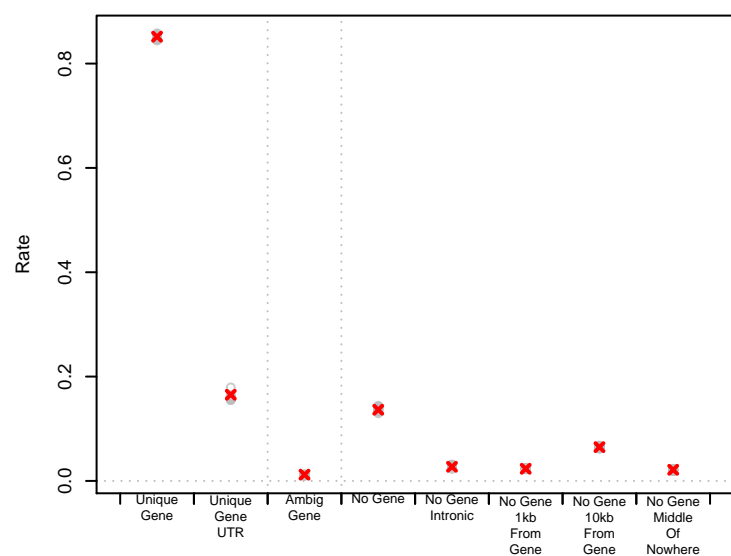
ag

**Gene–Body Coverage, Low Expression Genes**  
With Sample *srpk3\_hom\_ttnb\_het\_8* in red



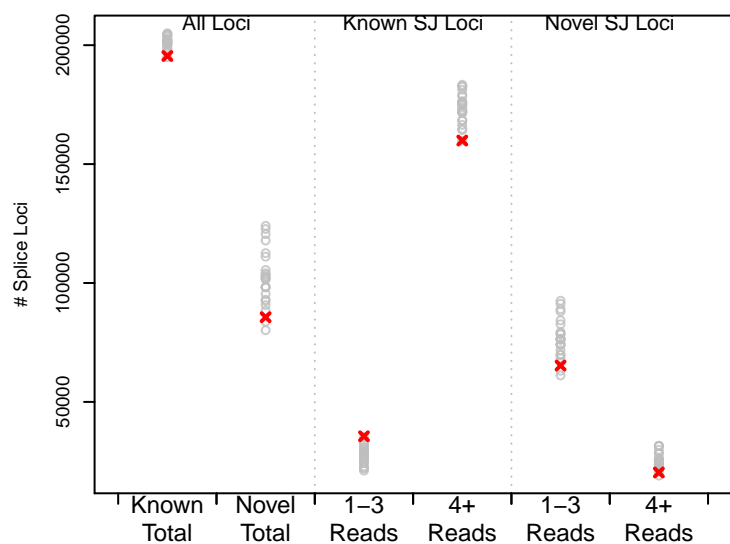
ah

**Read Mapping Location Rates**  
With Sample *srpk3\_hom\_ttnb\_het\_8* in red



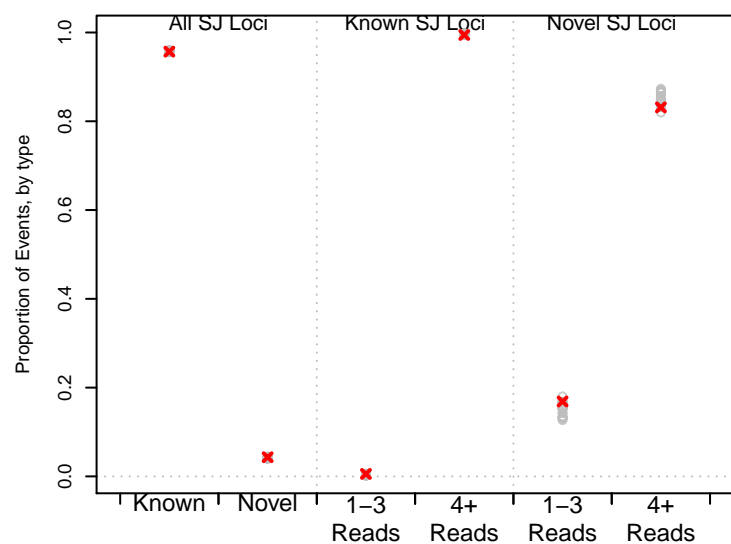
ai

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

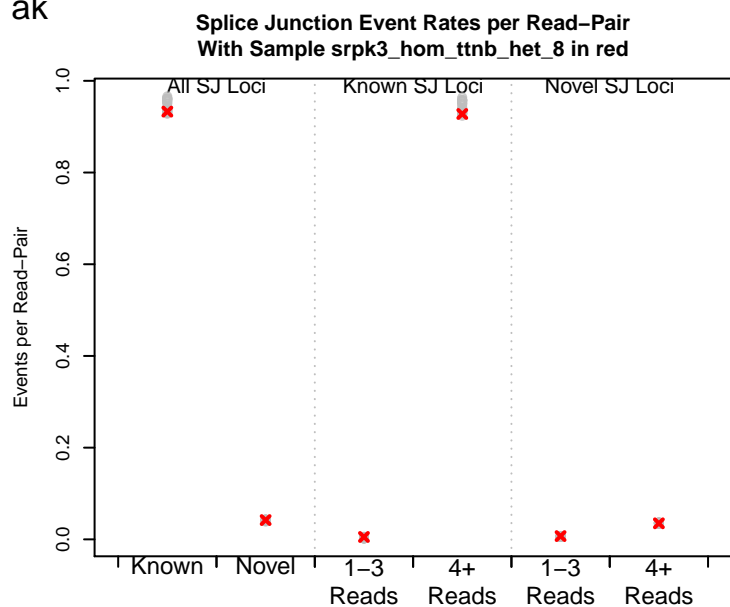


aj

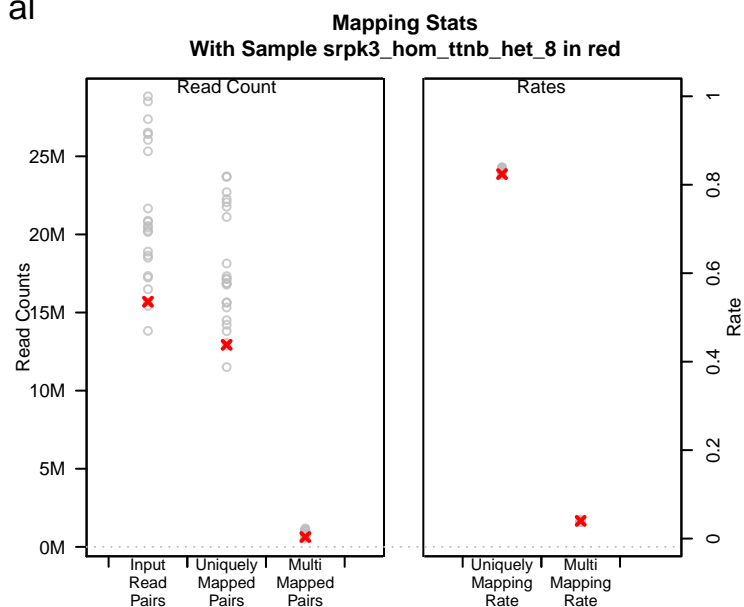
**Breakdown of Splice Junction Events, by type**  
With Sample *srpk3\_hom\_ttnb\_het\_8* in red



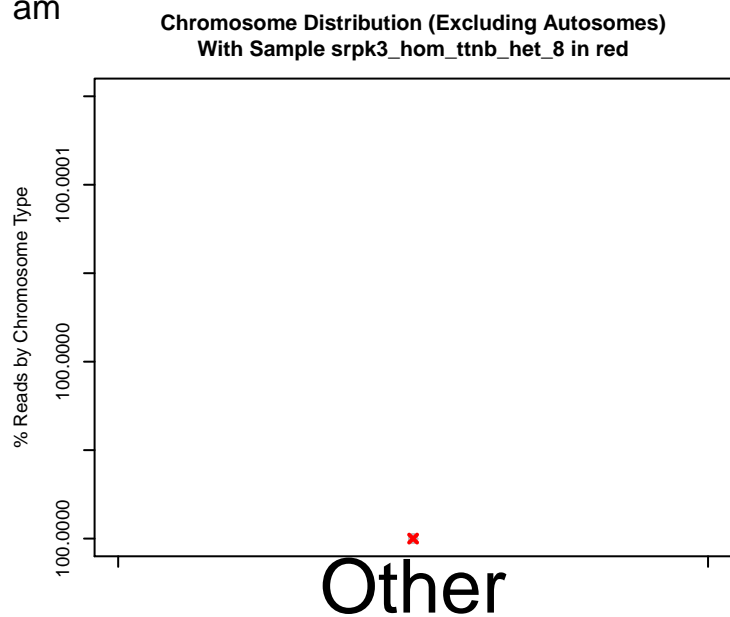
ak



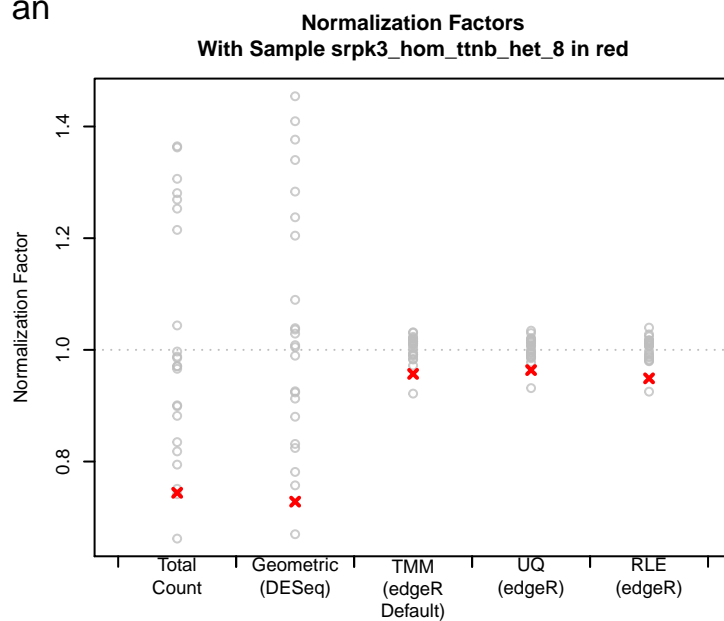
al



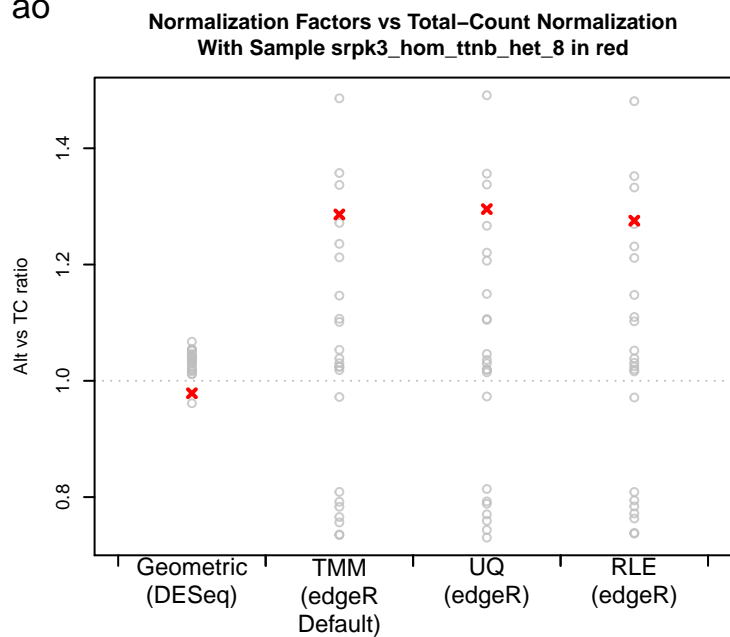
am



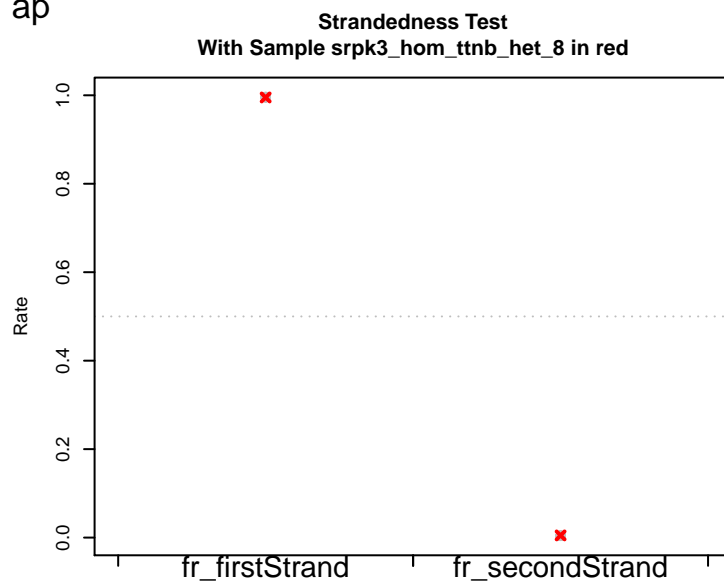
an



ao

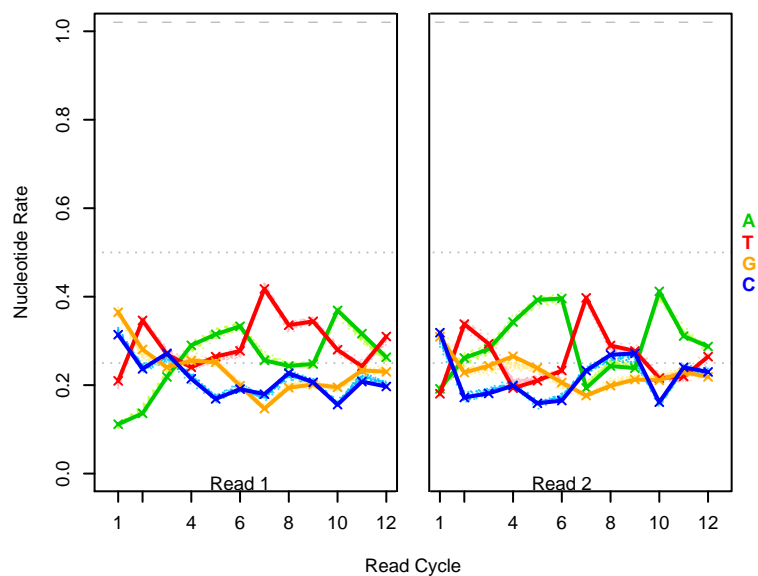


ap



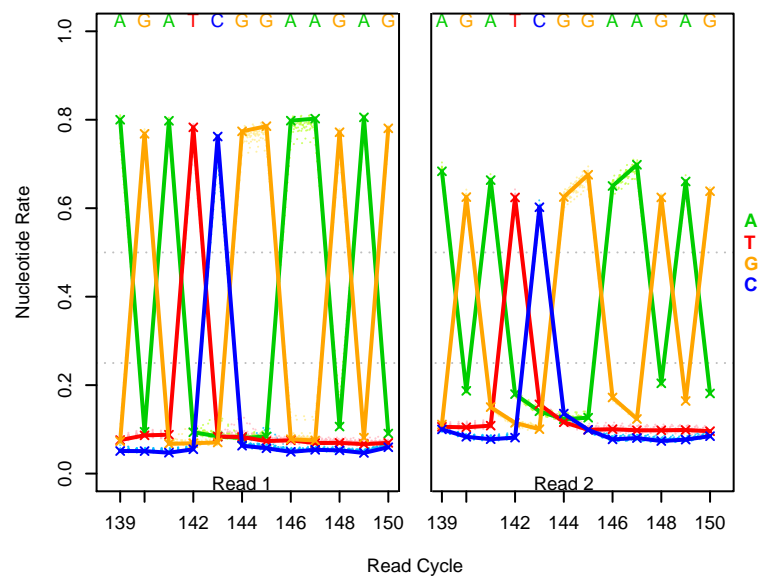
aq

Nucleotide Rate by Cycle, Leading Clipped bases (12)  
With Sample srp33\_hom\_ttnb\_het\_8 in red



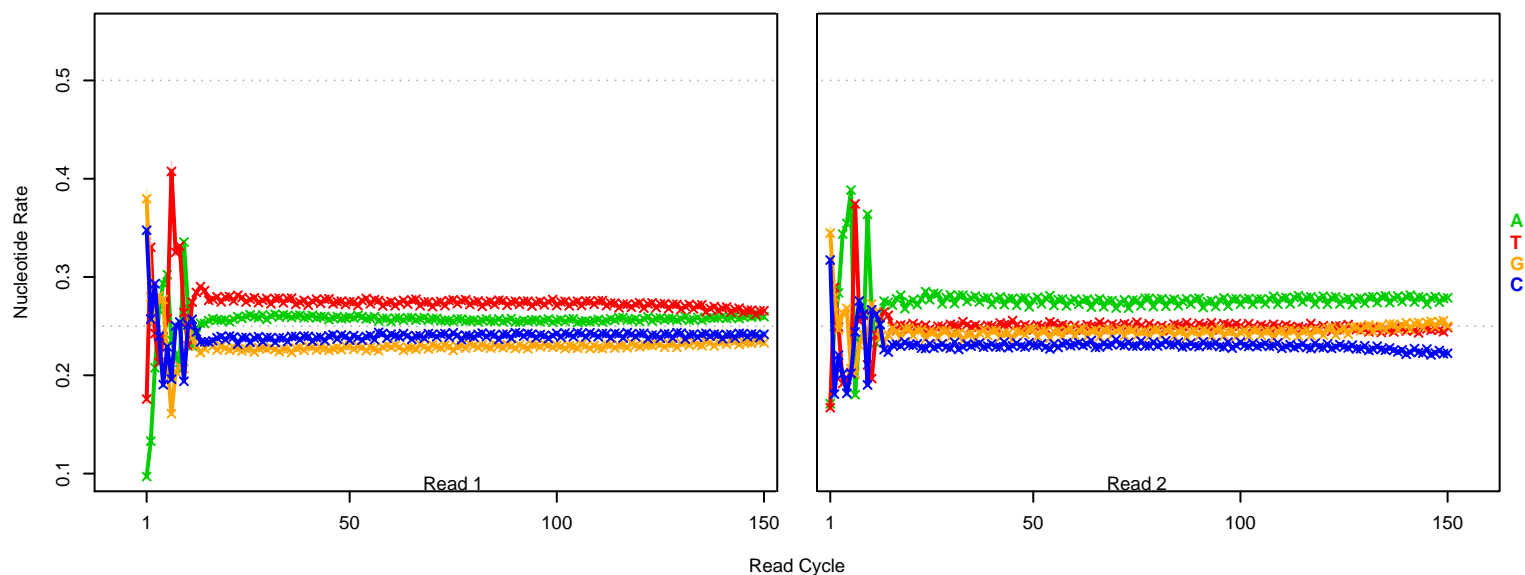
ar

Nucleotide Rate by Cycle, Trailing Clipped bases (12)  
With Sample srp33\_hom\_ttnb\_het\_8 in red



as

Raw Nucleotide Rate by Cycle  
With Sample srp33\_hom\_ttnb\_het\_8 in red



at

Nucleotide Rate by Cycle, Aligned bases only  
With Sample srp33\_hom\_ttnb\_het\_8 in red

