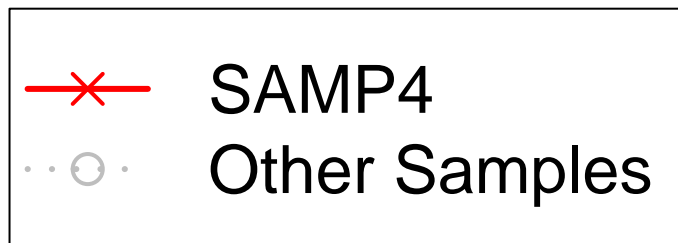


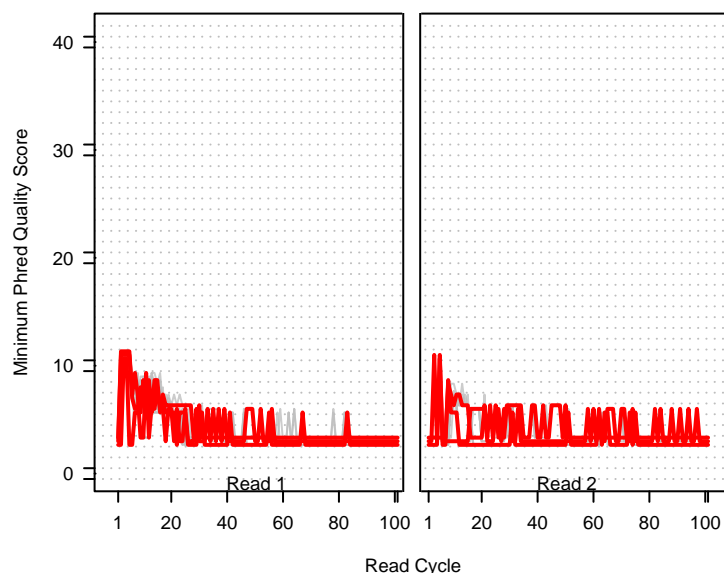
a

# Sample Highlight: SAMP4



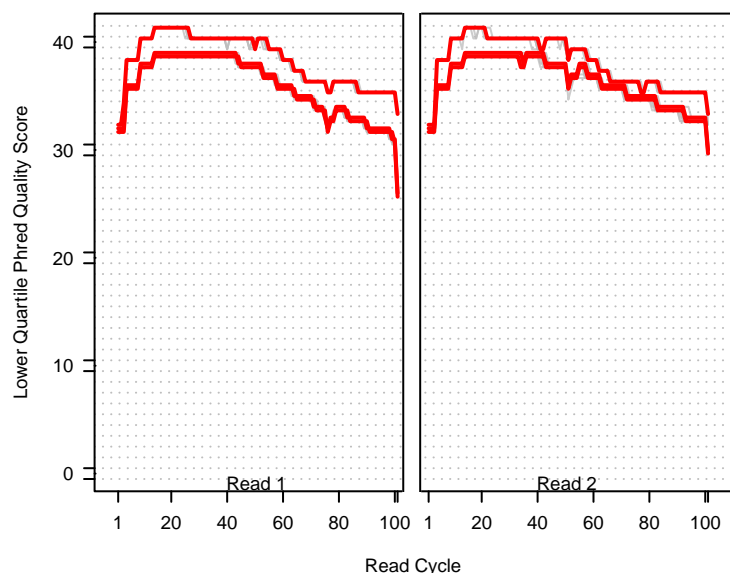
b

Minimum Phred Quality Score  
With Sample SAMP4 in red



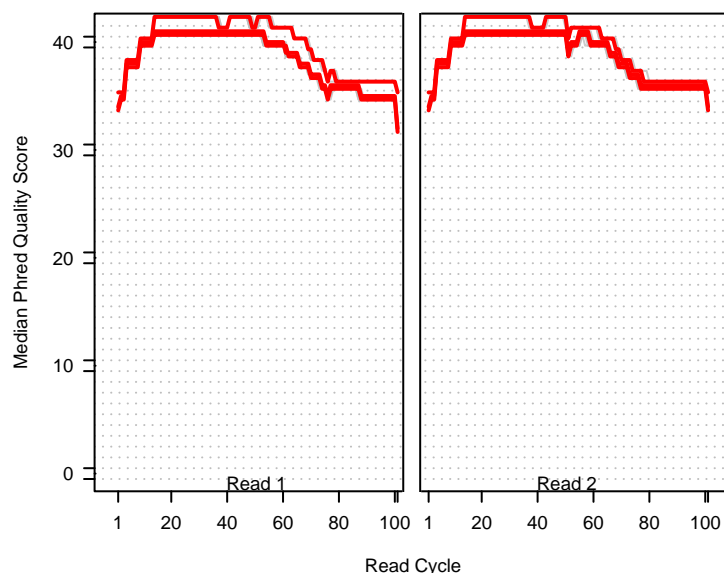
c

Lower Quartile Phred Quality Score  
With Sample SAMP4 in red



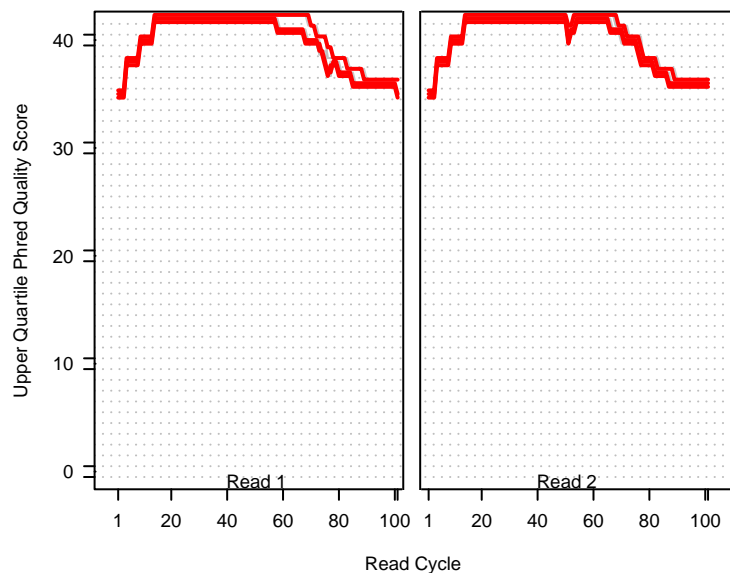
d

Median Phred Quality Score  
With Sample SAMP4 in red



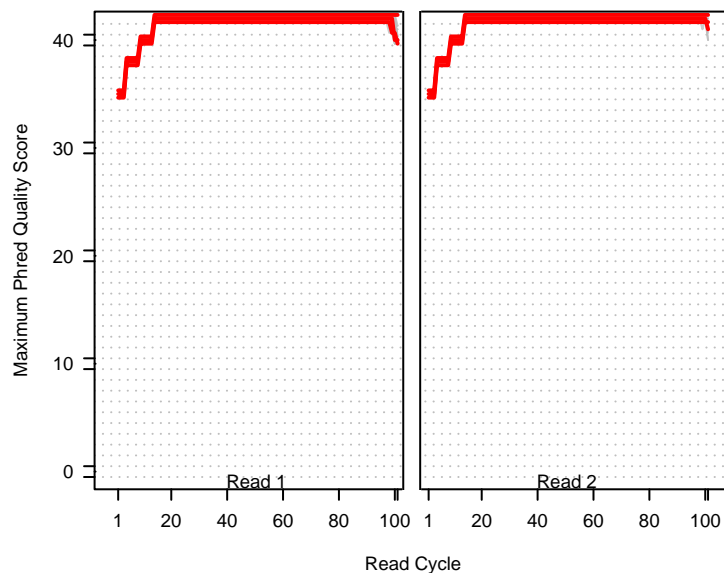
e

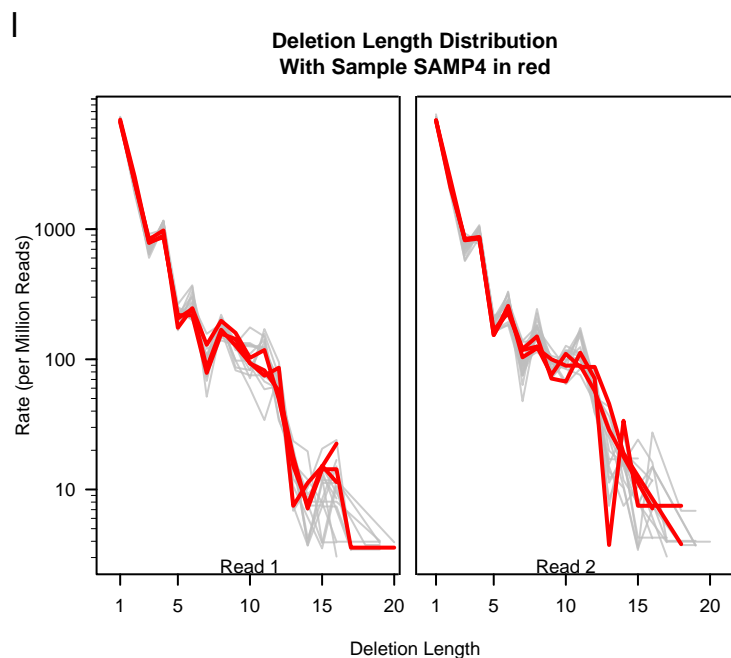
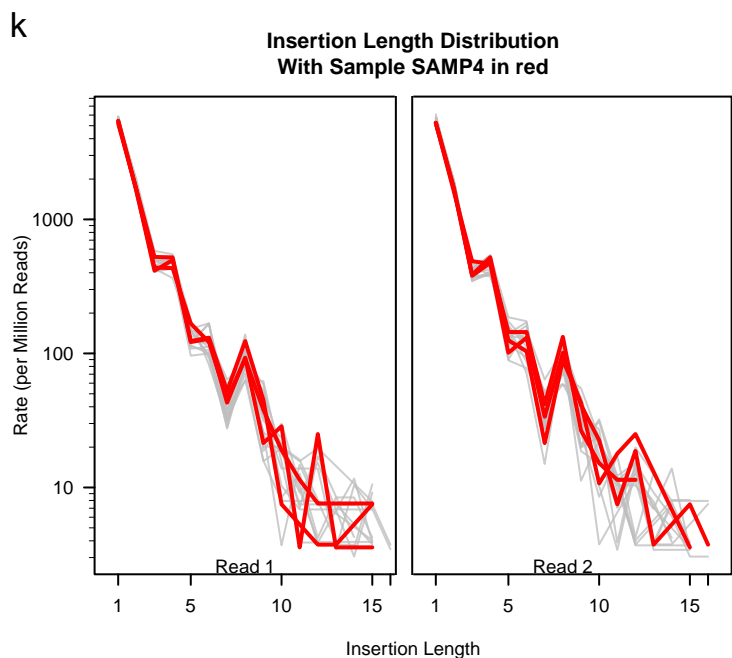
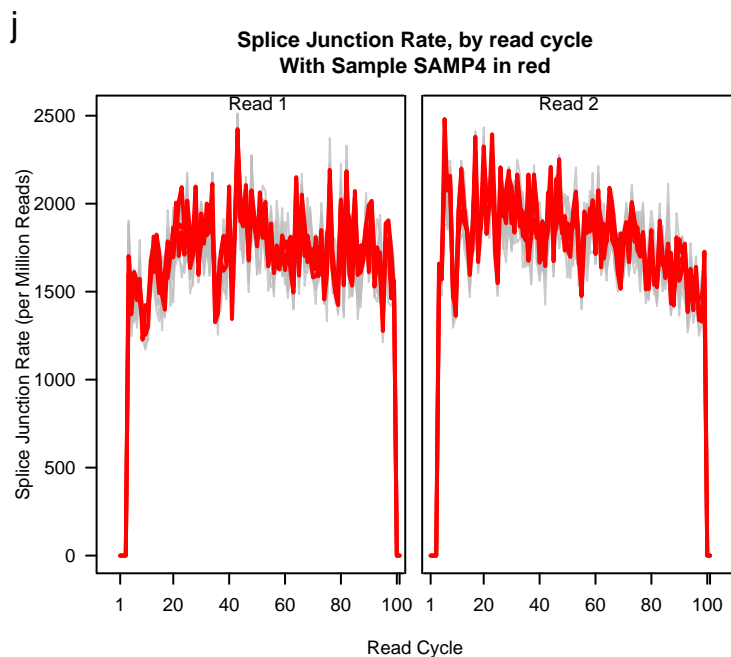
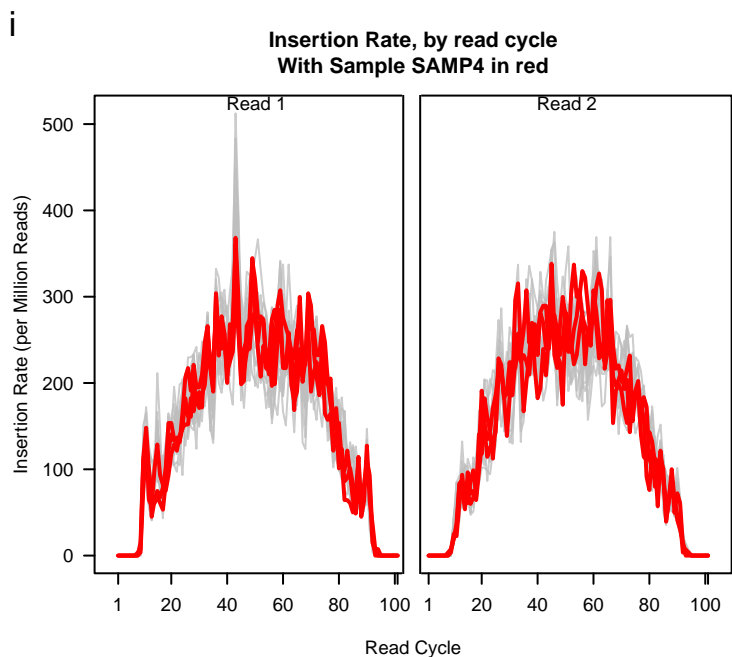
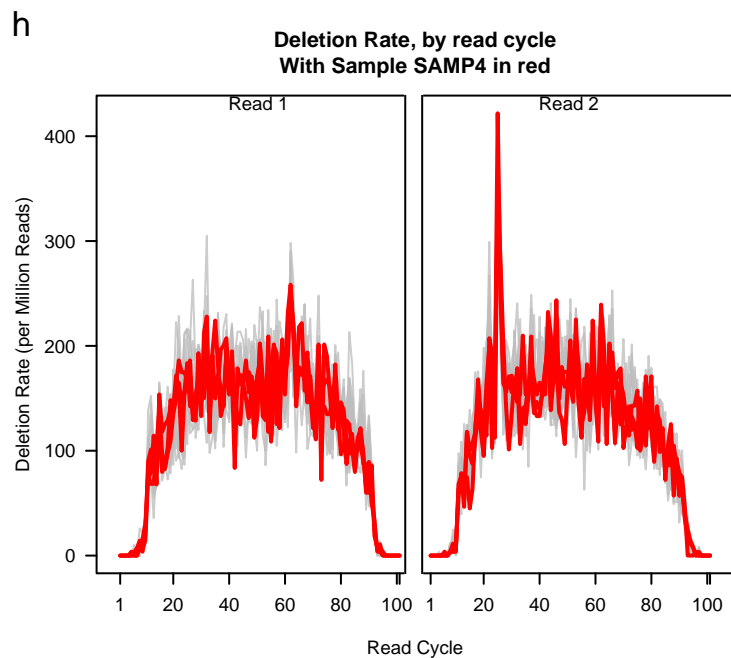
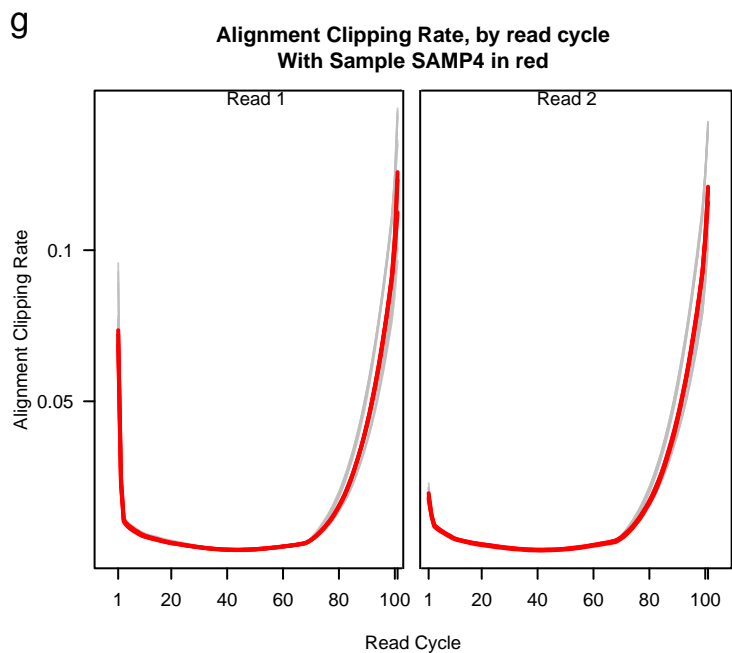
Upper Quartile Phred Quality Score  
With Sample SAMP4 in red

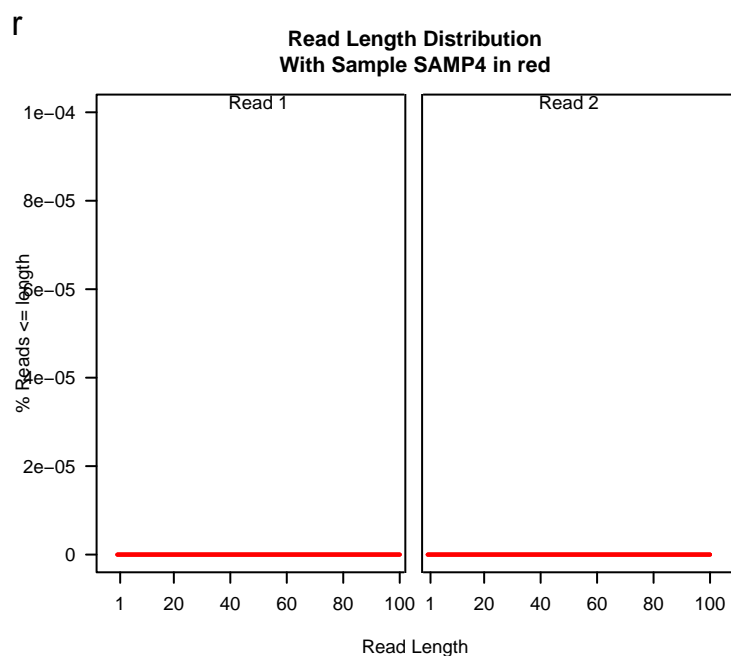
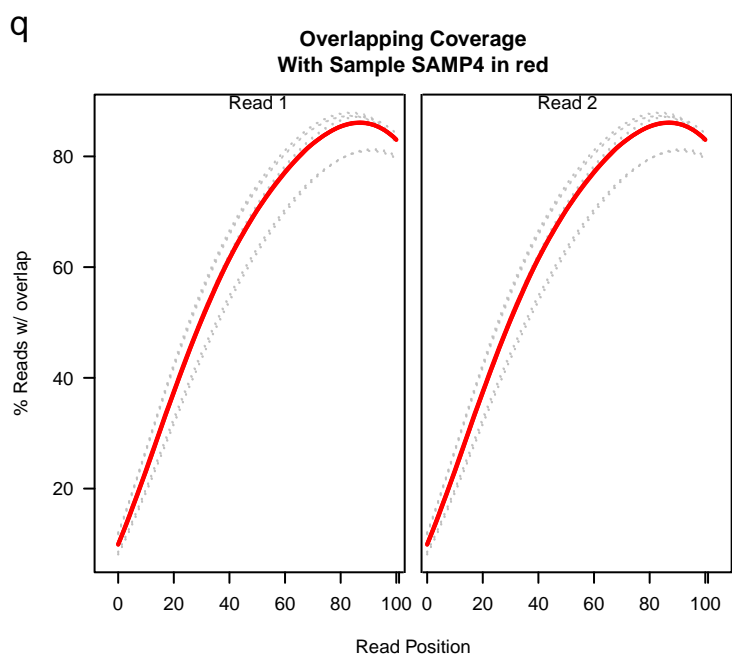
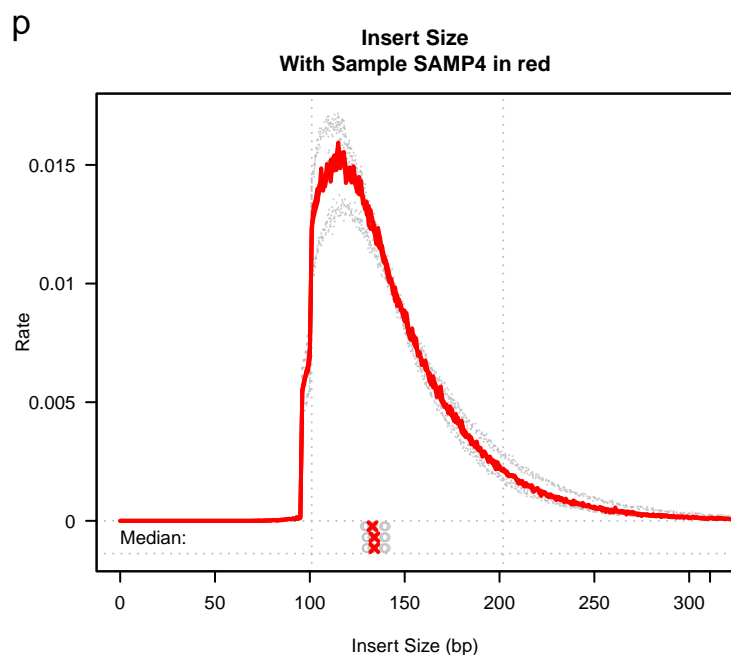
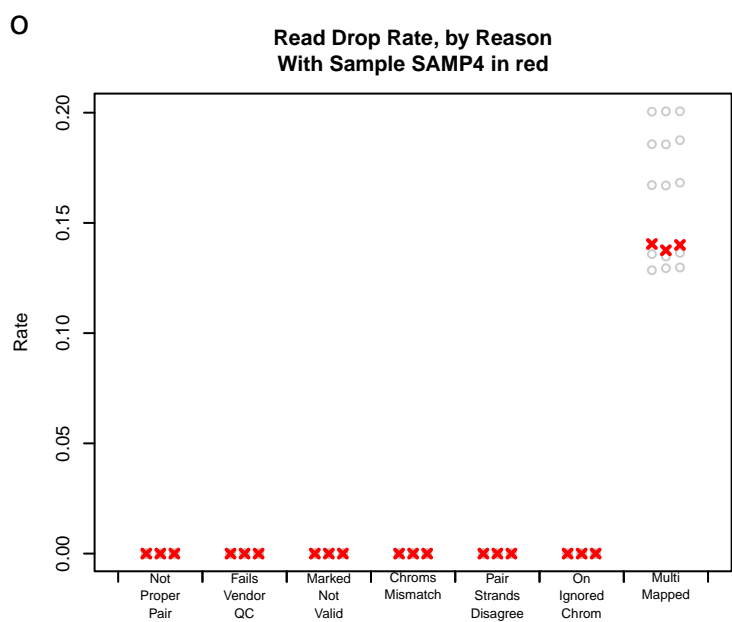
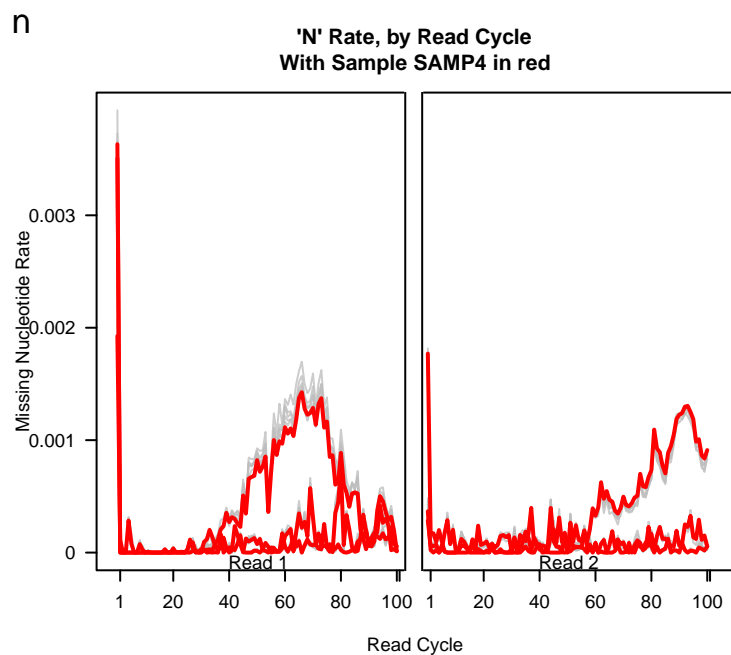
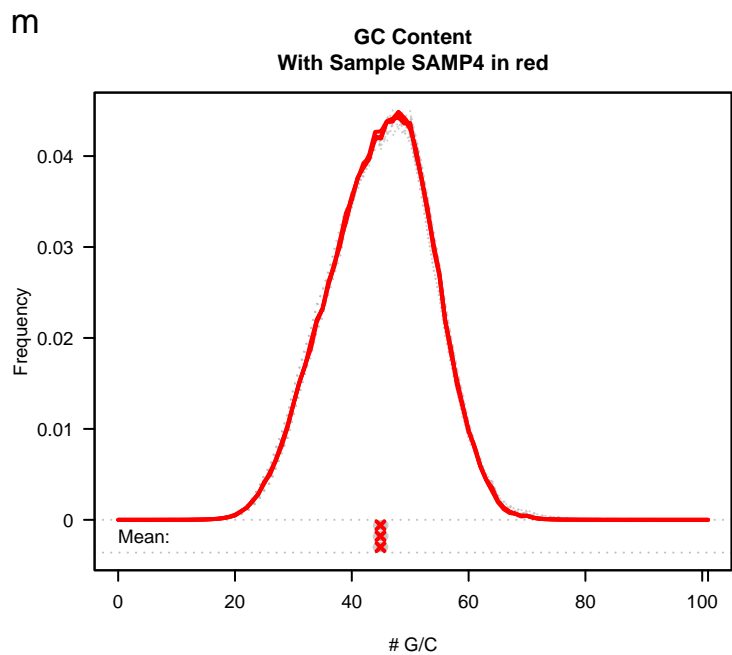


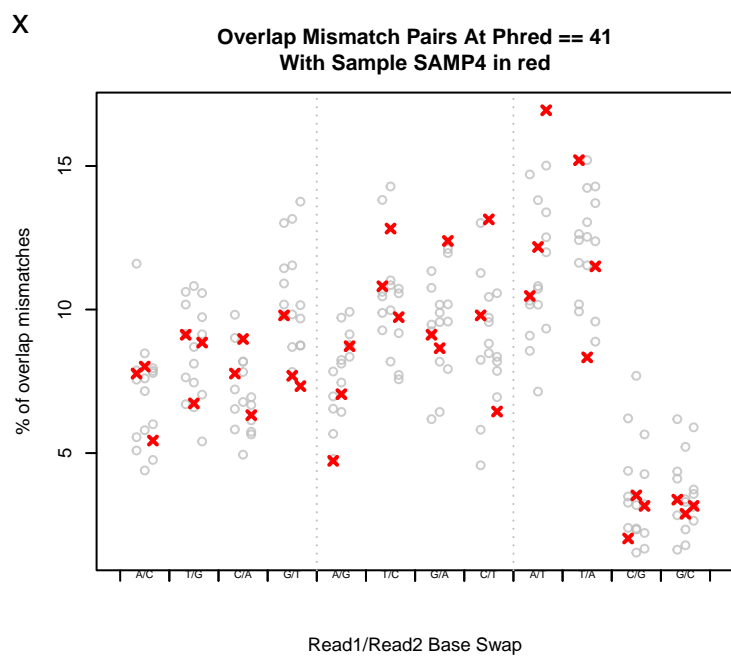
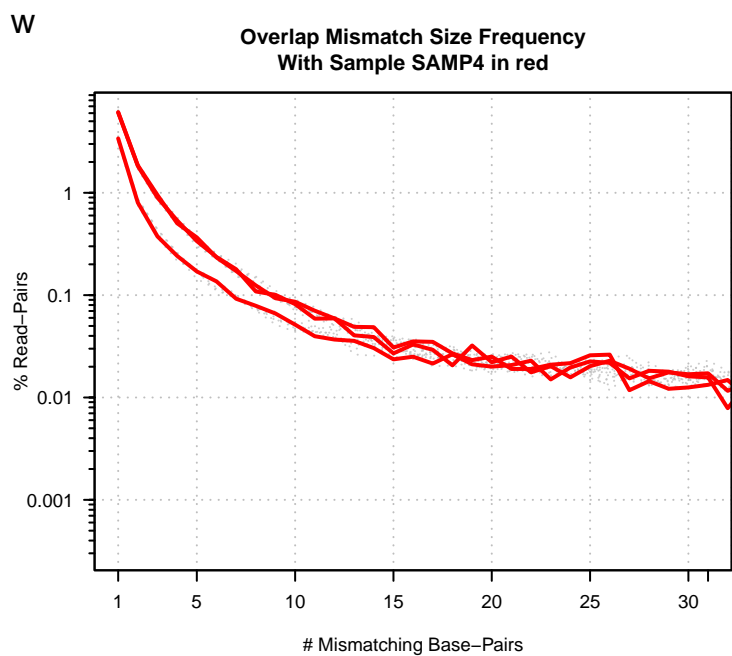
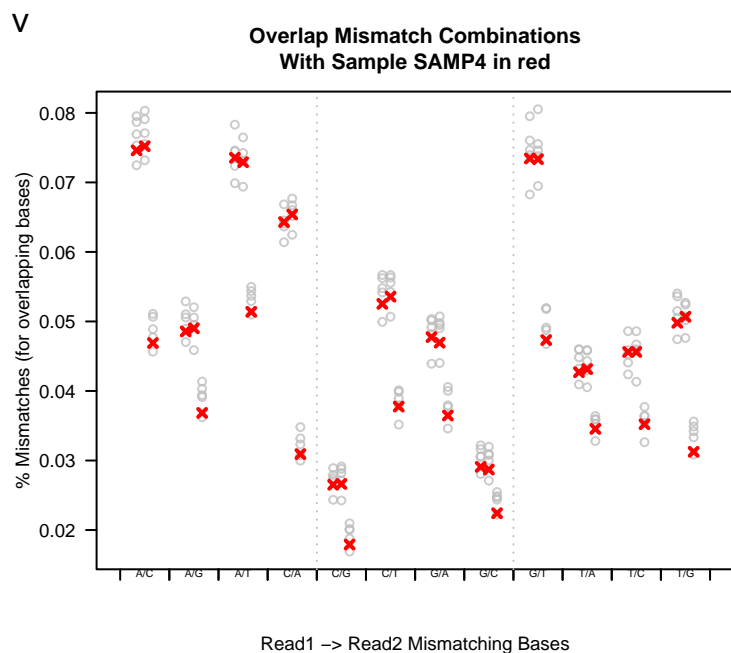
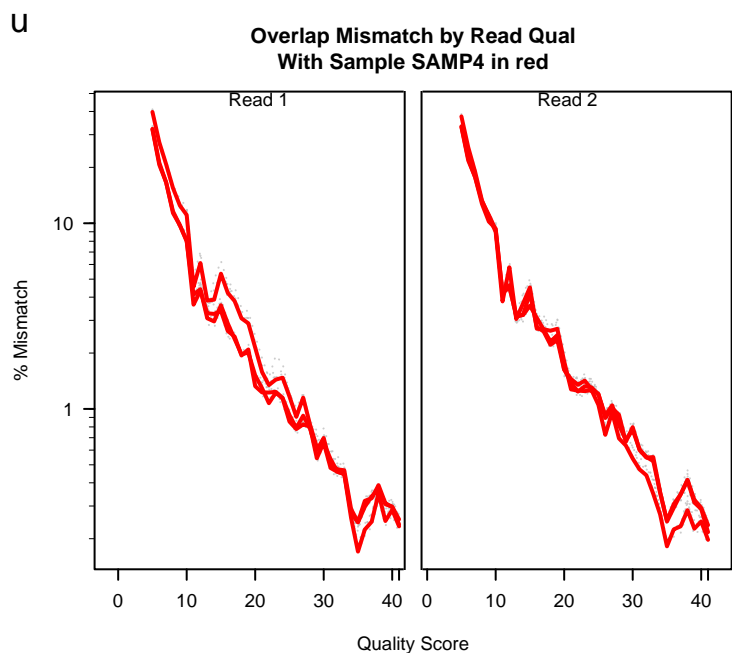
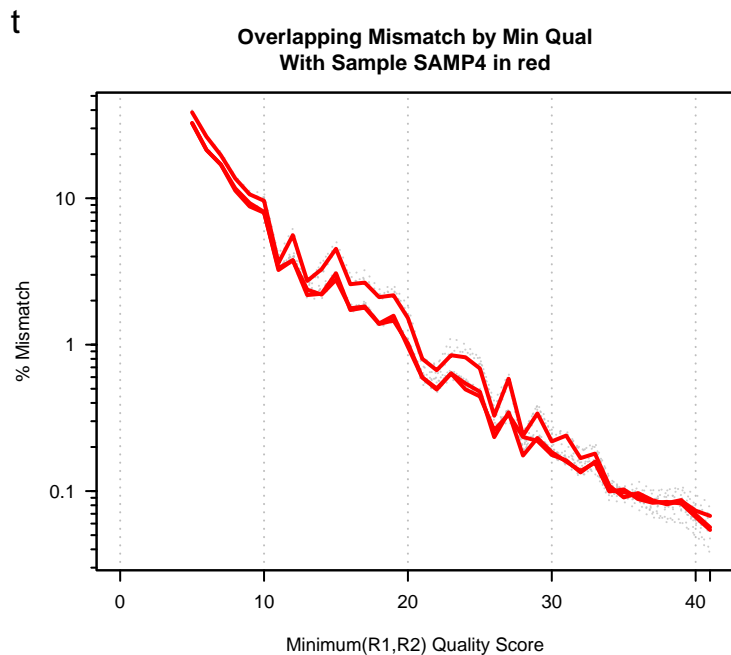
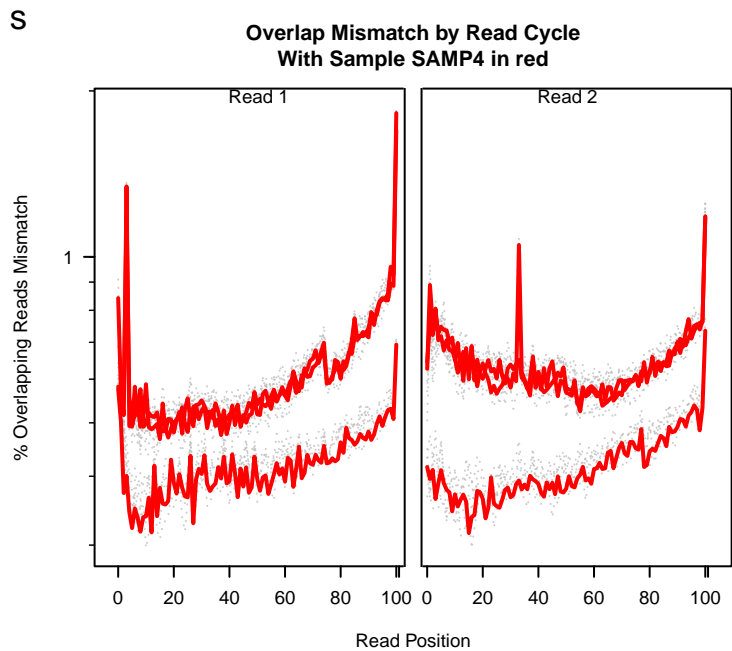
f

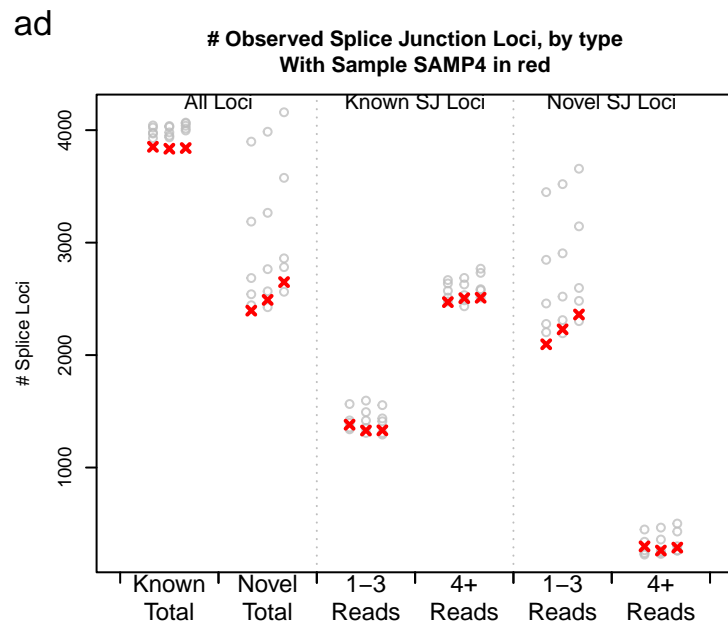
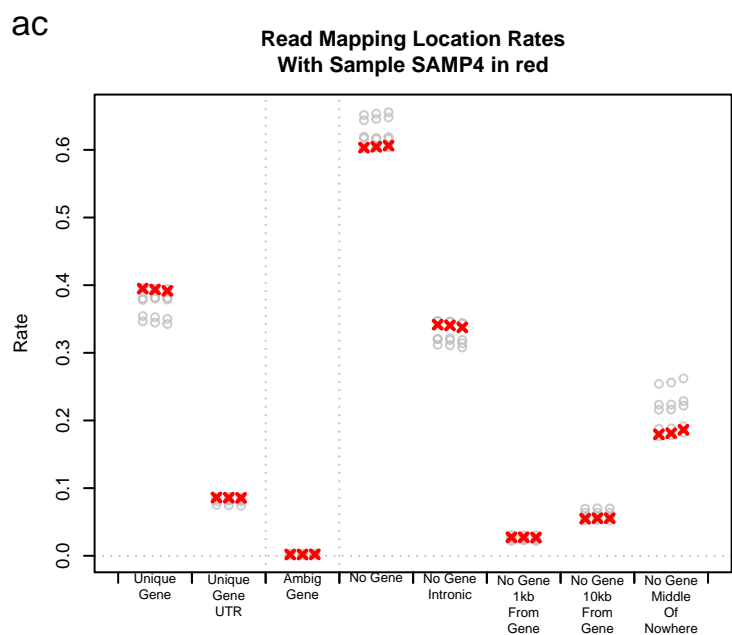
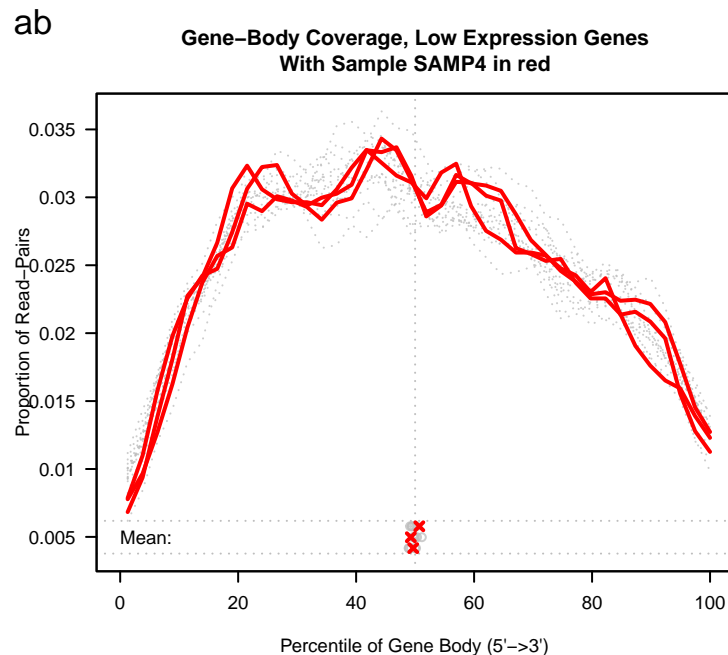
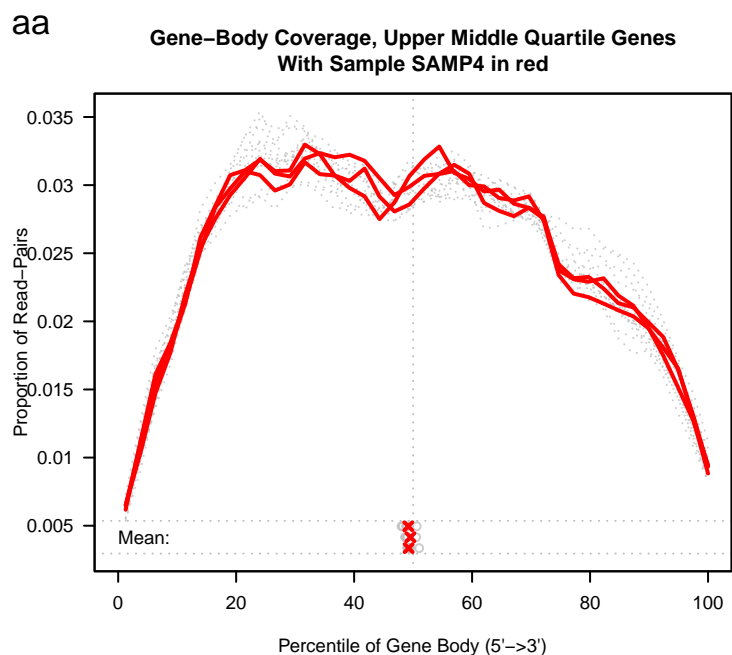
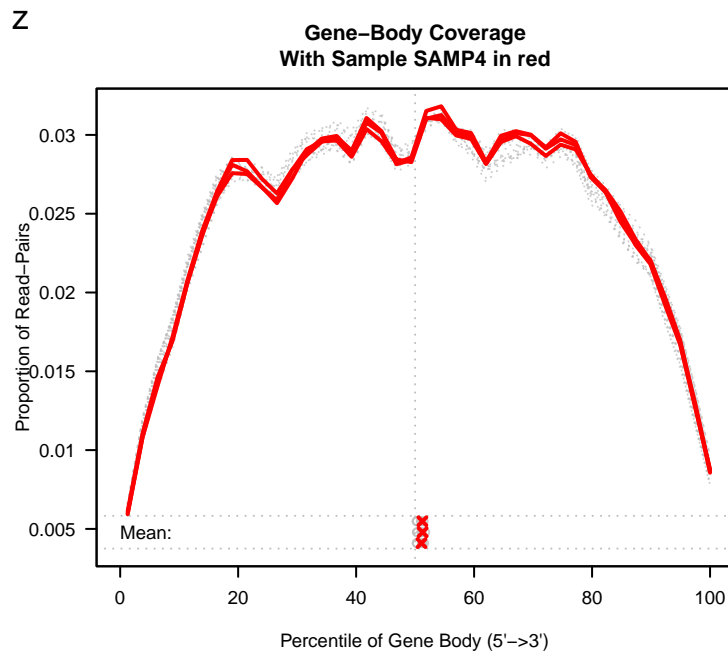
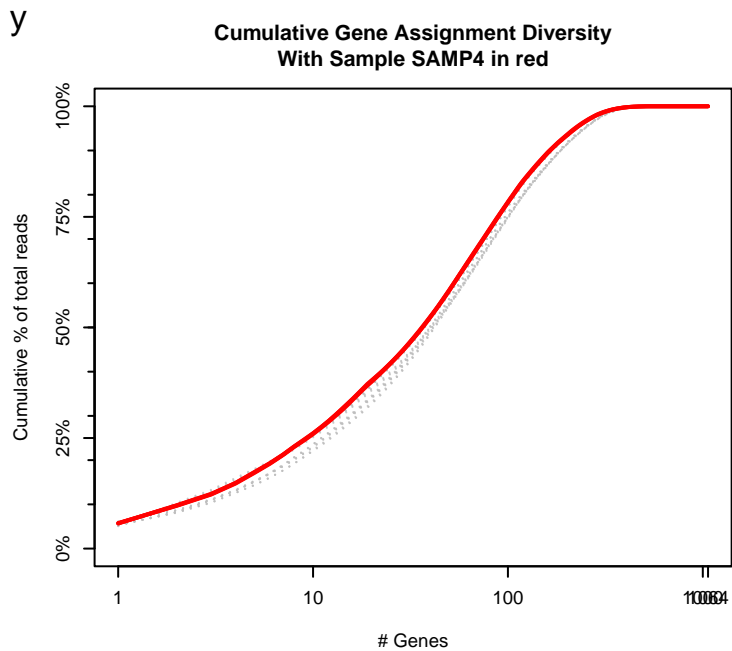
Maximum Phred Quality Score  
With Sample SAMP4 in red



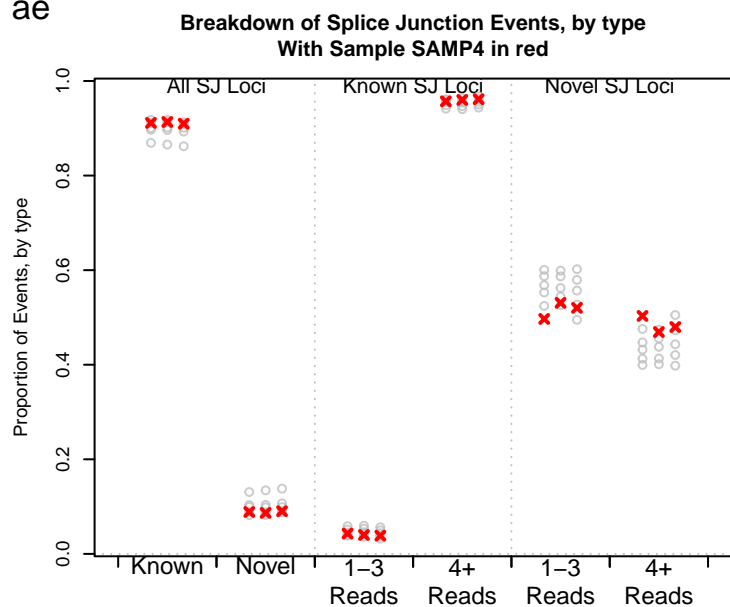




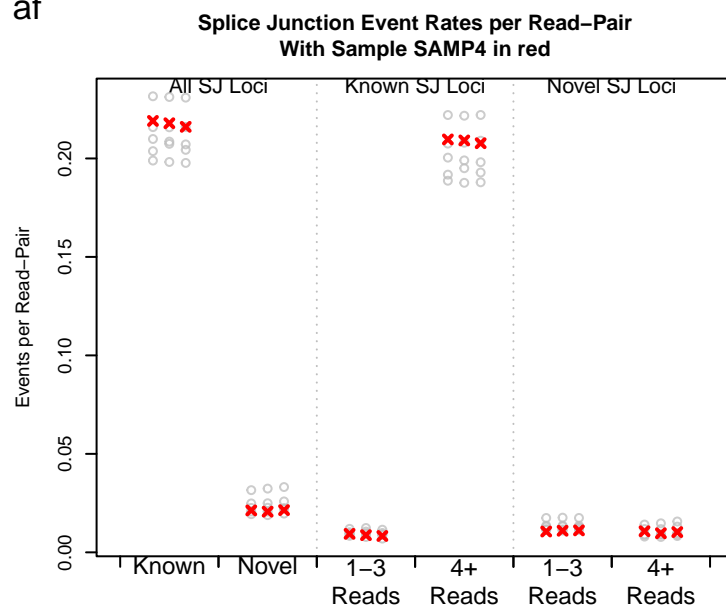




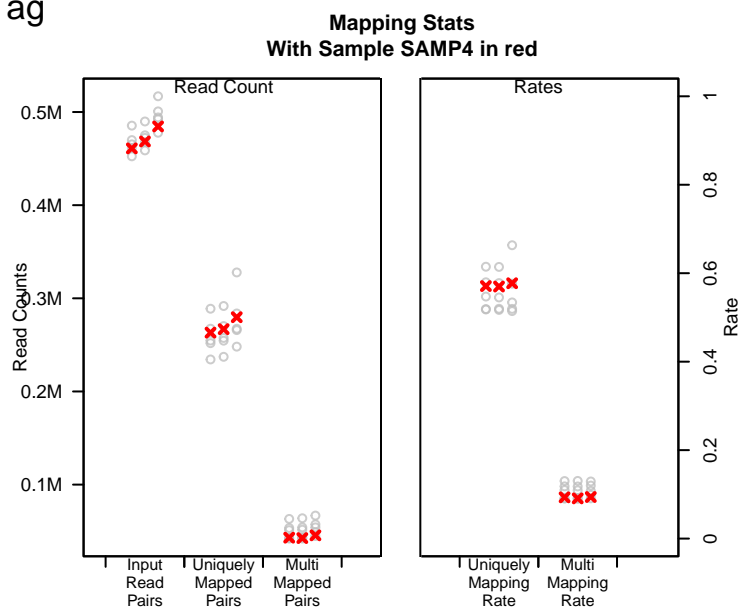
ae



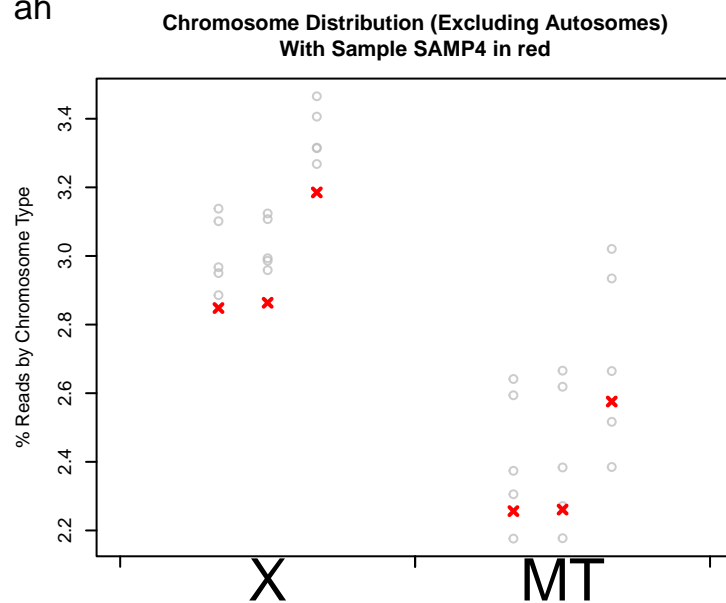
af



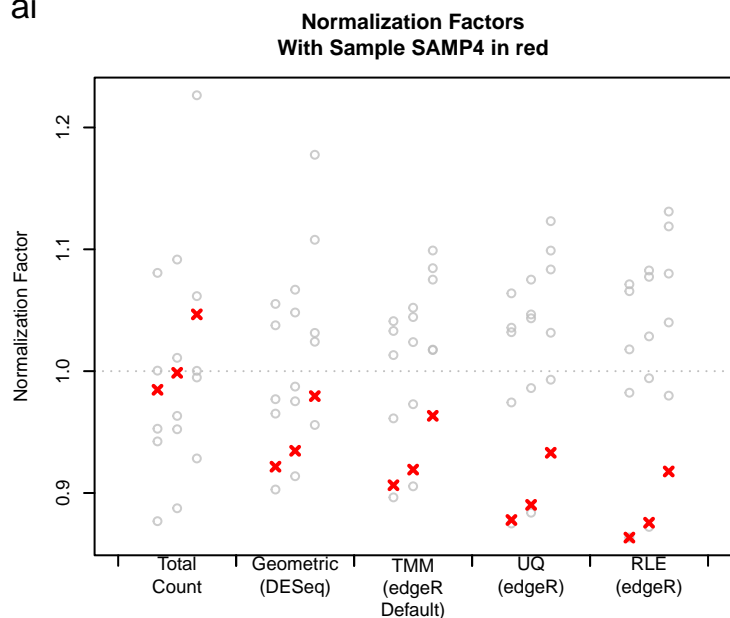
ag



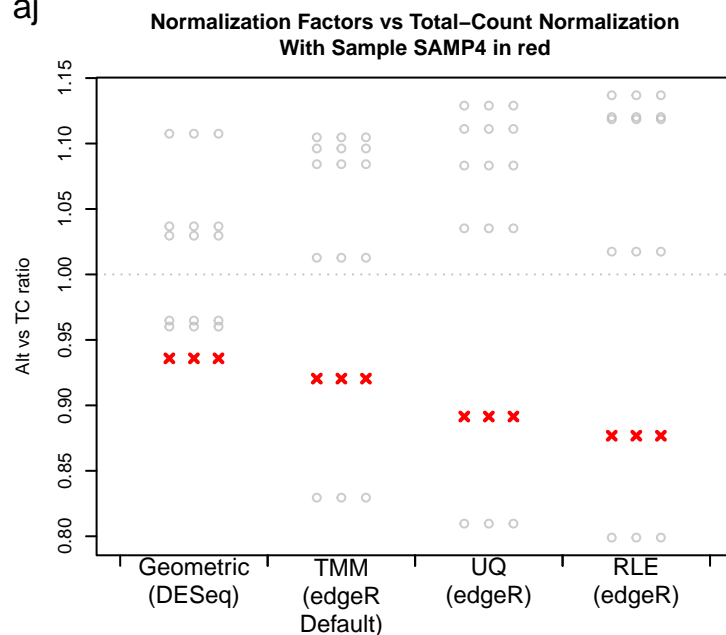
ah



ai

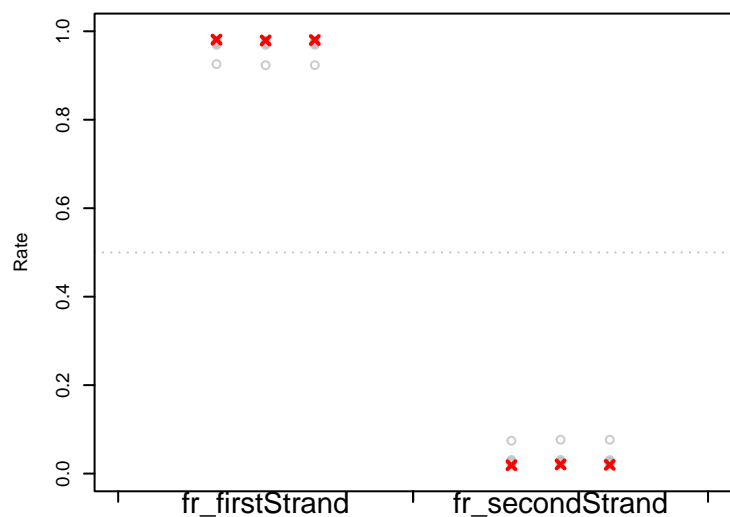


aj



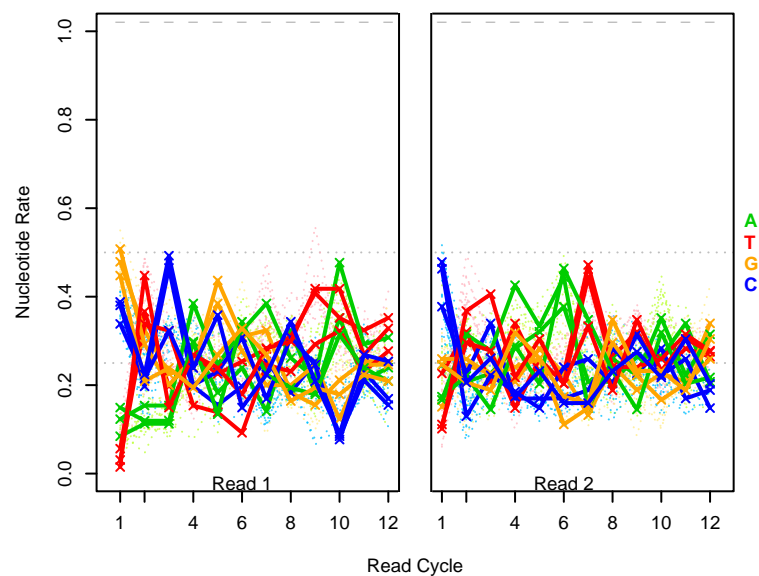
ak

**Strandedness Test**  
With Sample SAMP4 in red



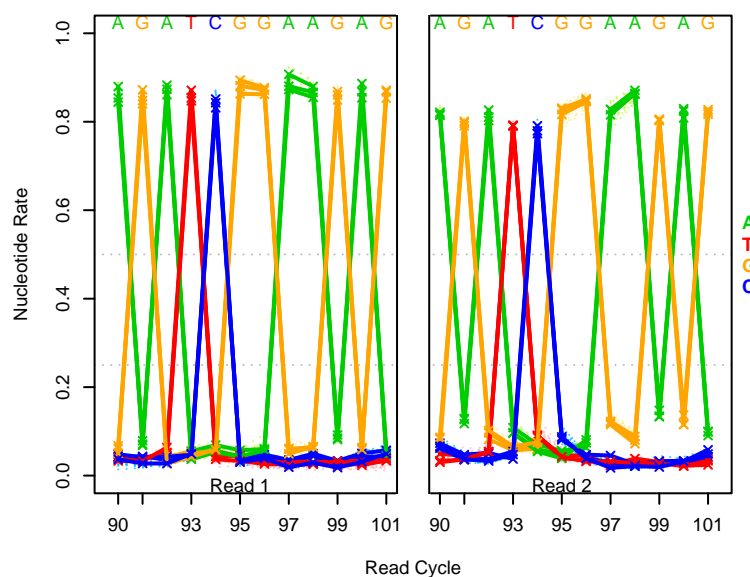
al

**Nucleotide Rate by Cycle, Leading Clipped bases (12)**  
With Sample SAMP4 in red



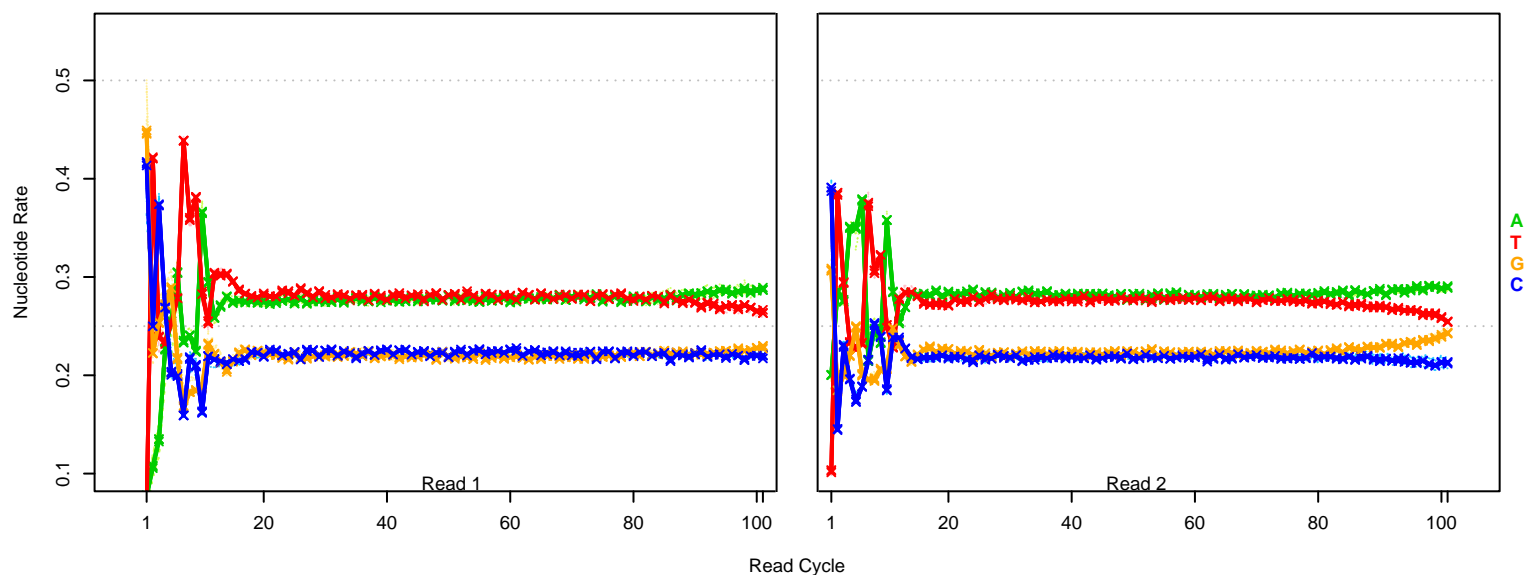
am

**Nucleotide Rate by Cycle, Trailing Clipped bases (12)**  
With Sample SAMP4 in red



an

**Raw Nucleotide Rate by Cycle**  
With Sample SAMP4 in red



ao

Nucleotide Rate by Cycle, Aligned bases only  
With Sample SAMP4 in red

