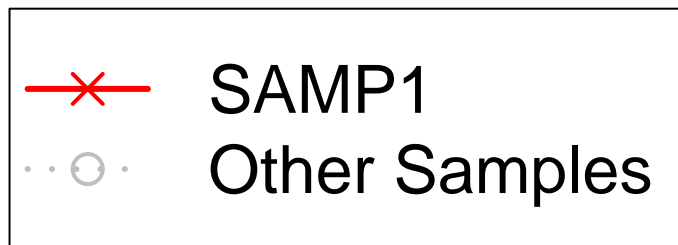
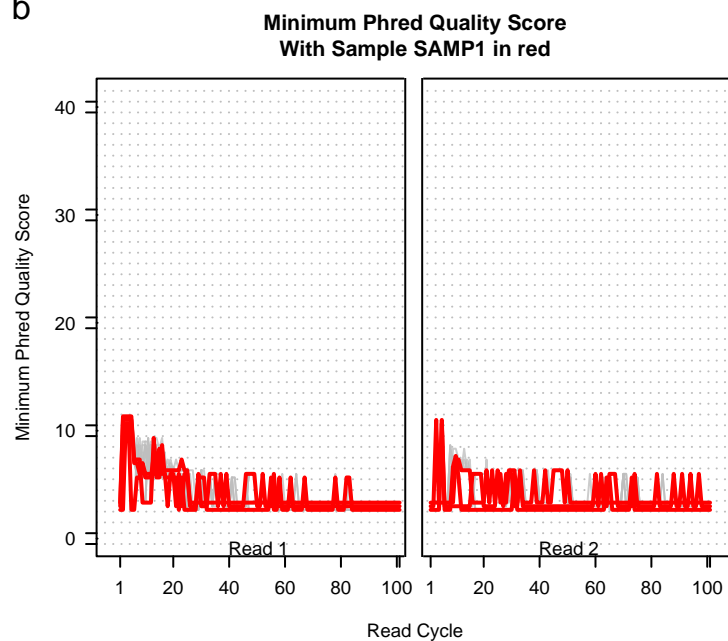


a

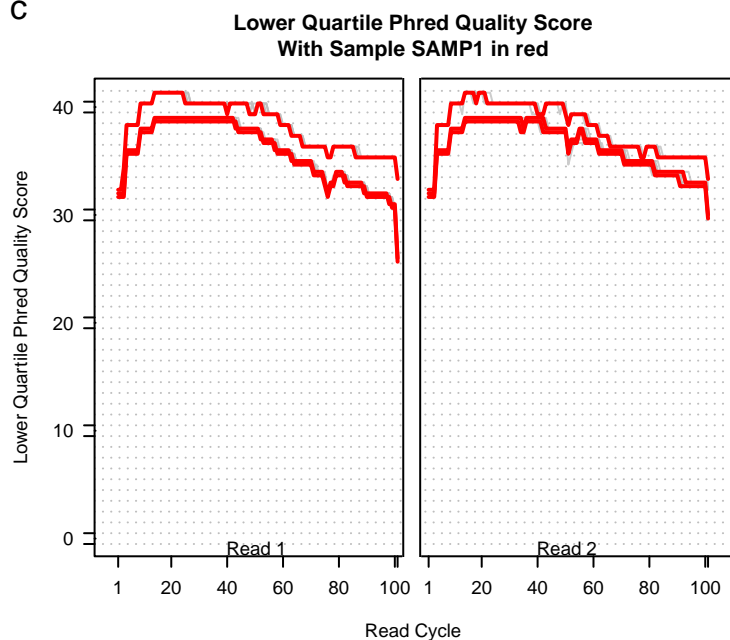
# Sample Highlight: SAMP1



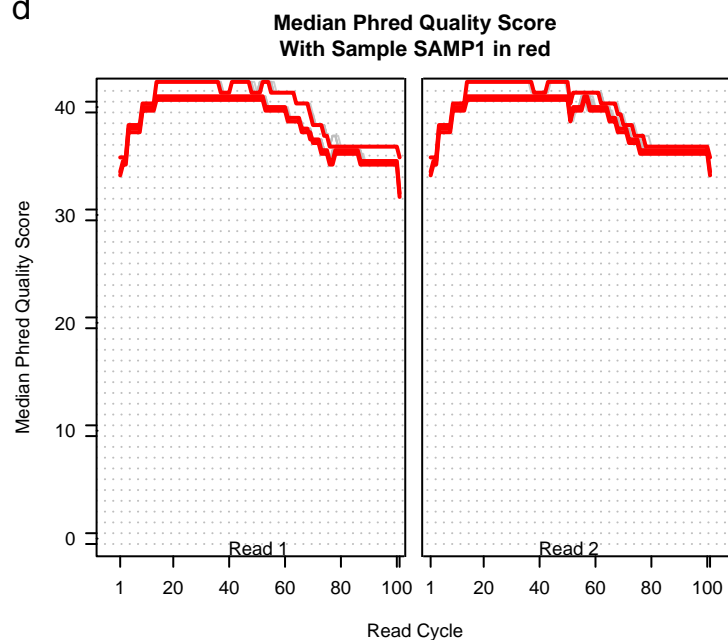
b



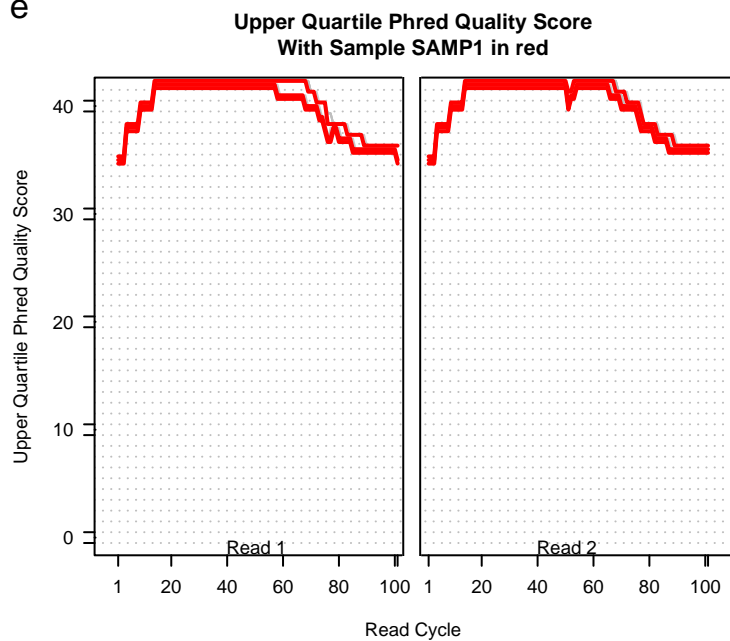
c



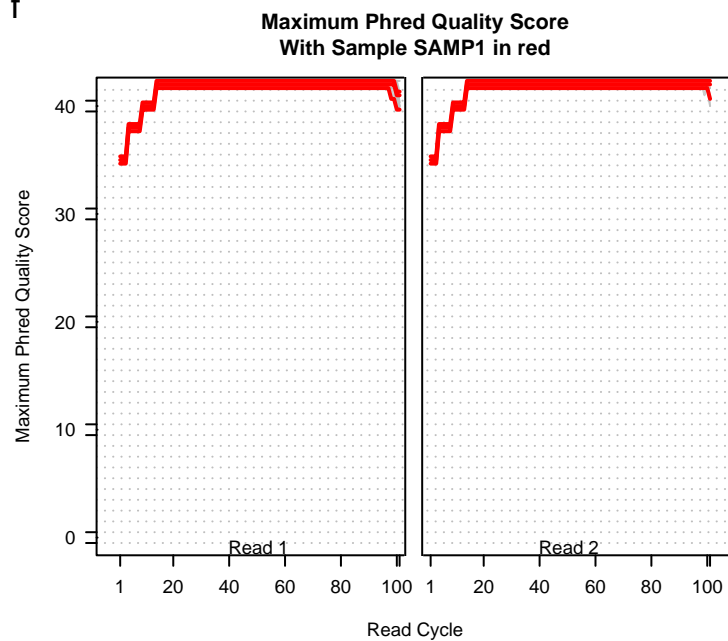
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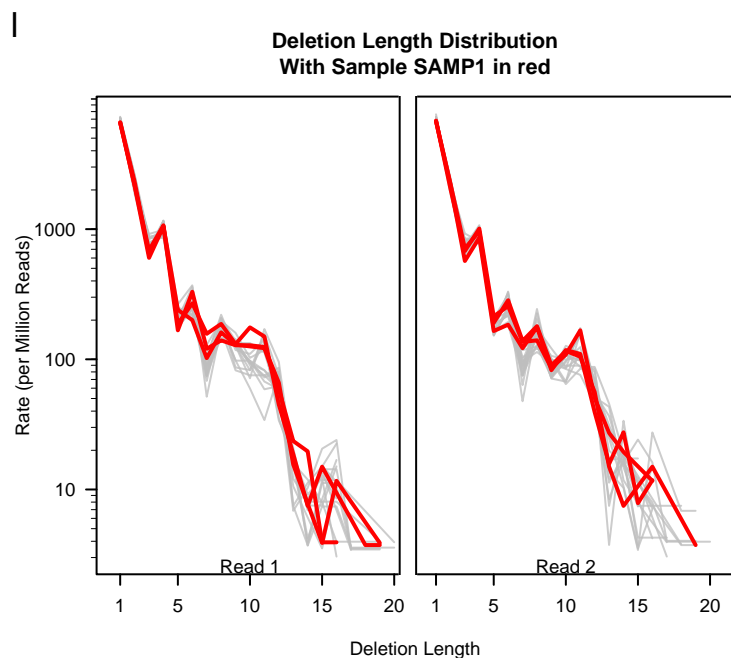
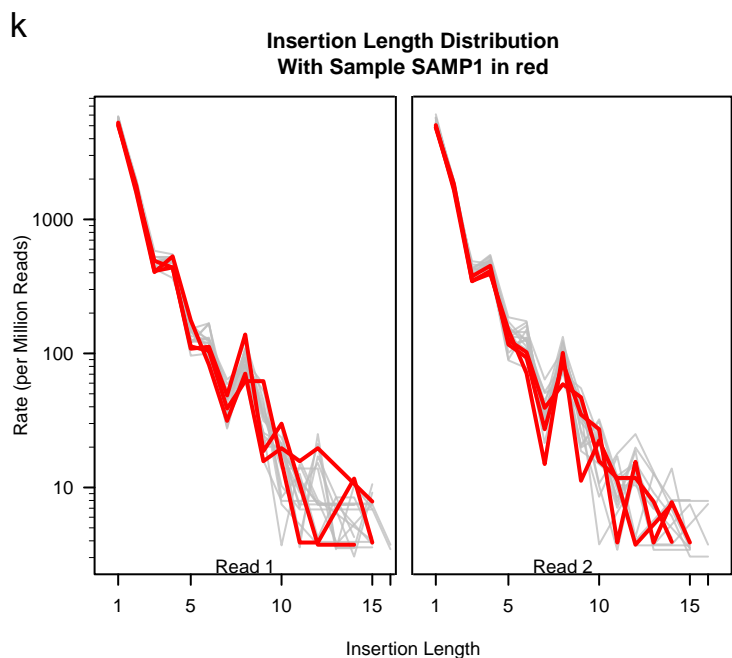
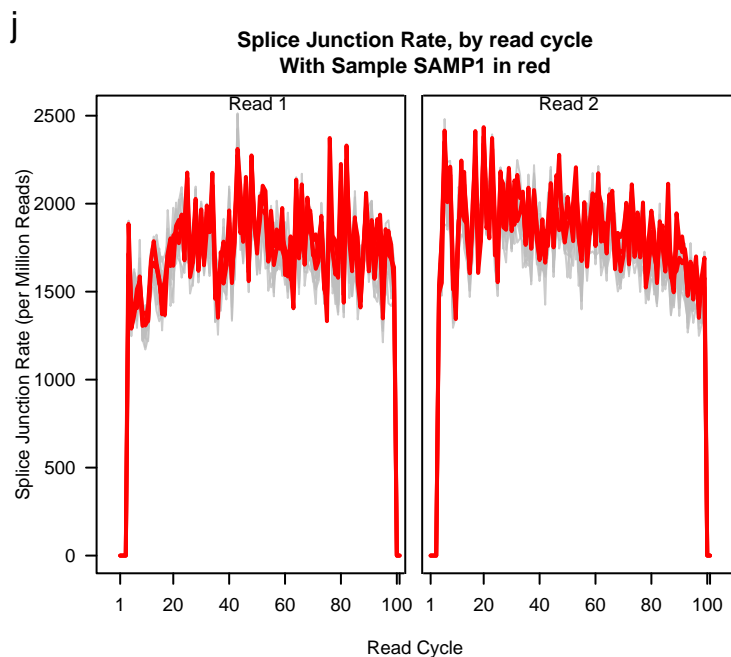
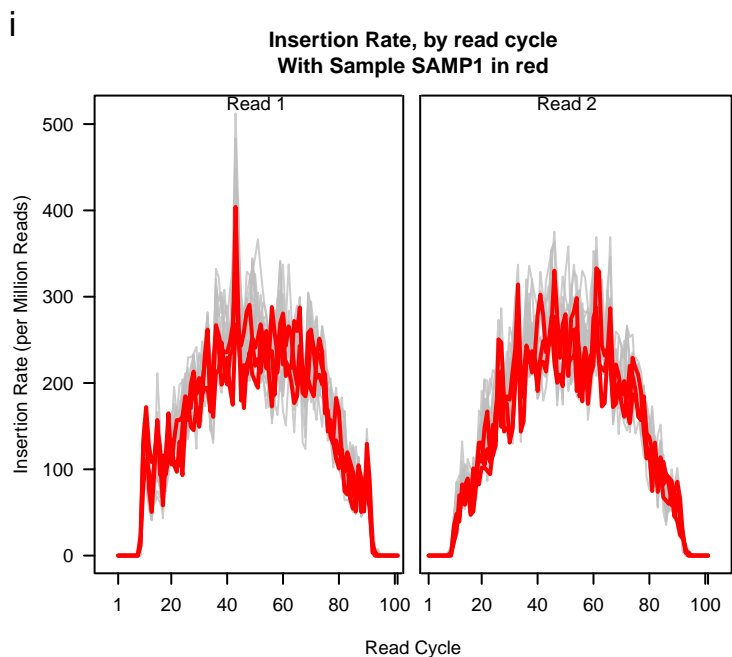
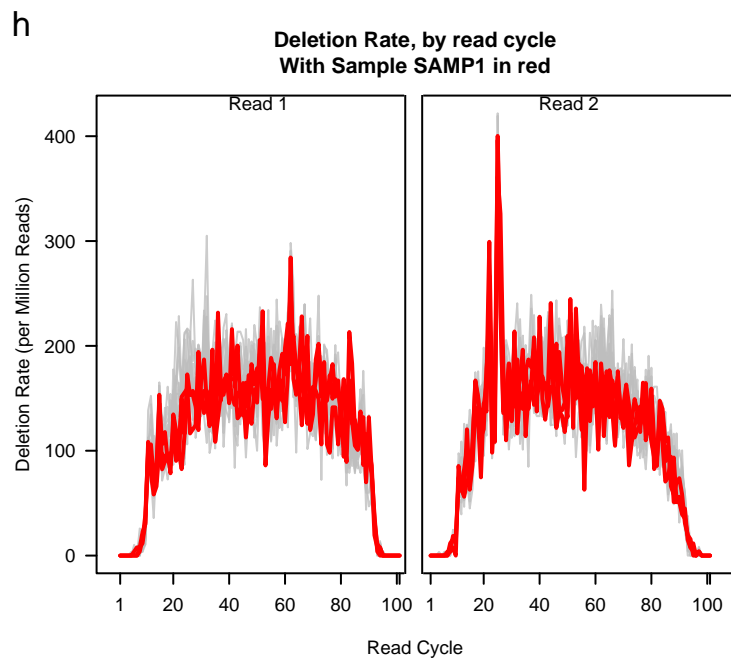
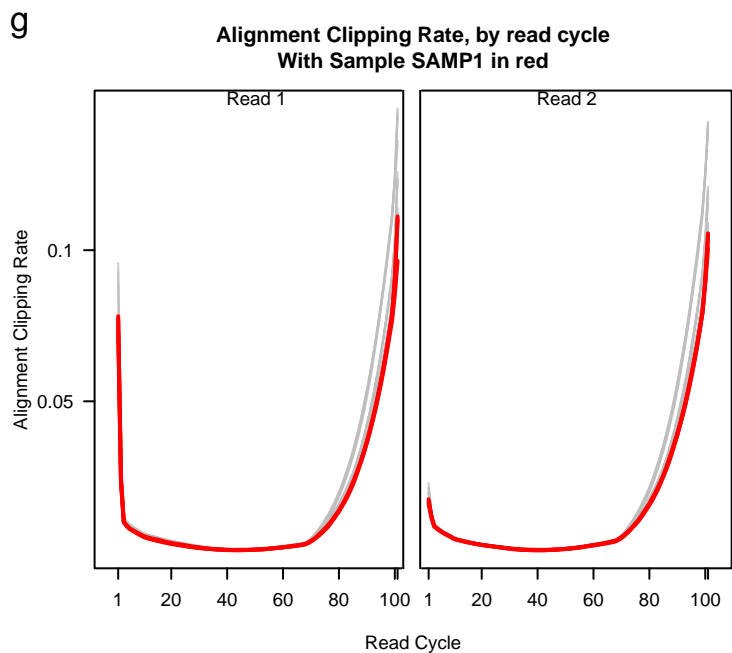


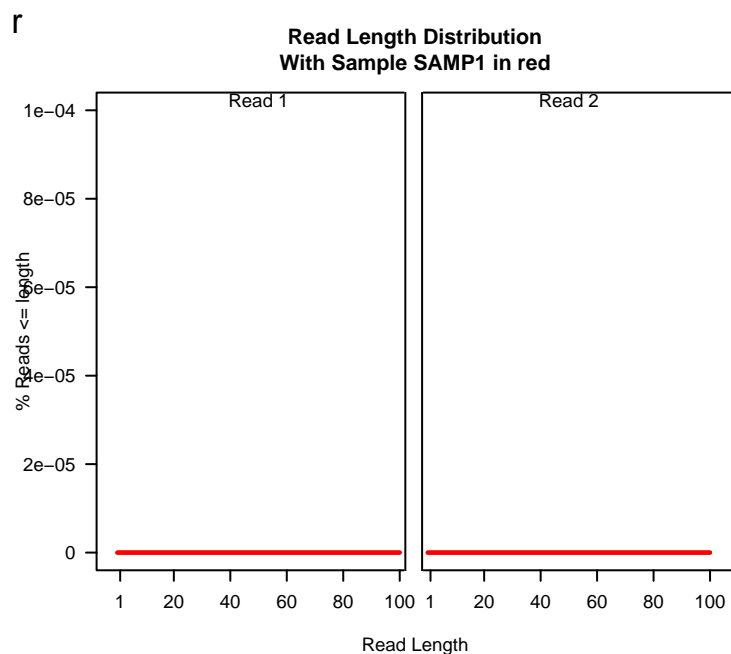
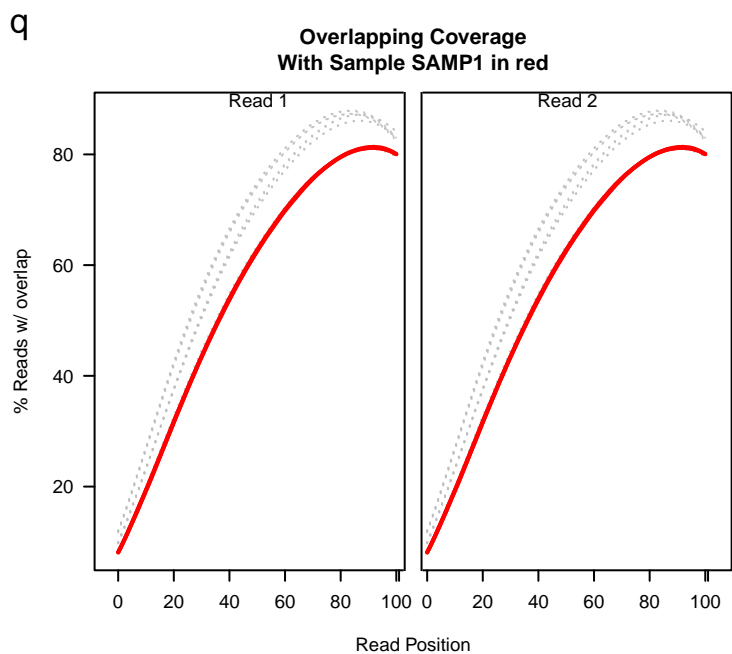
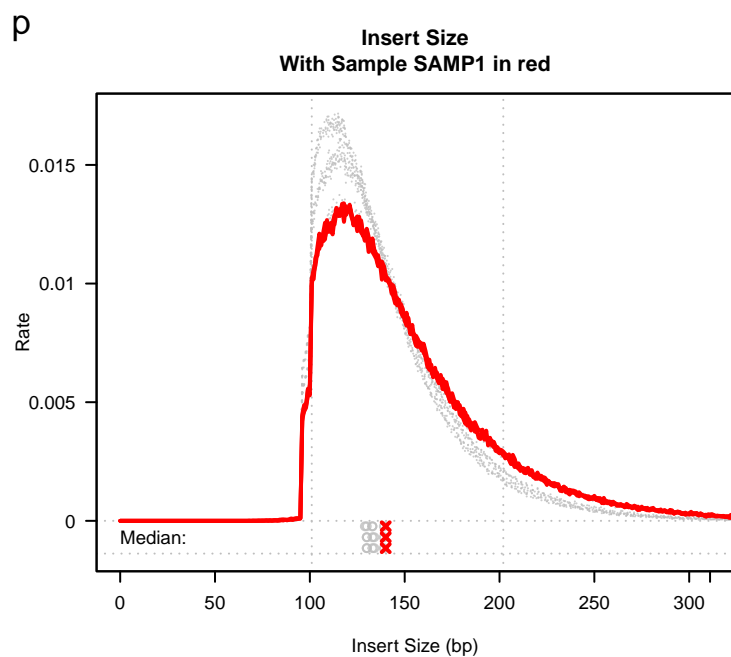
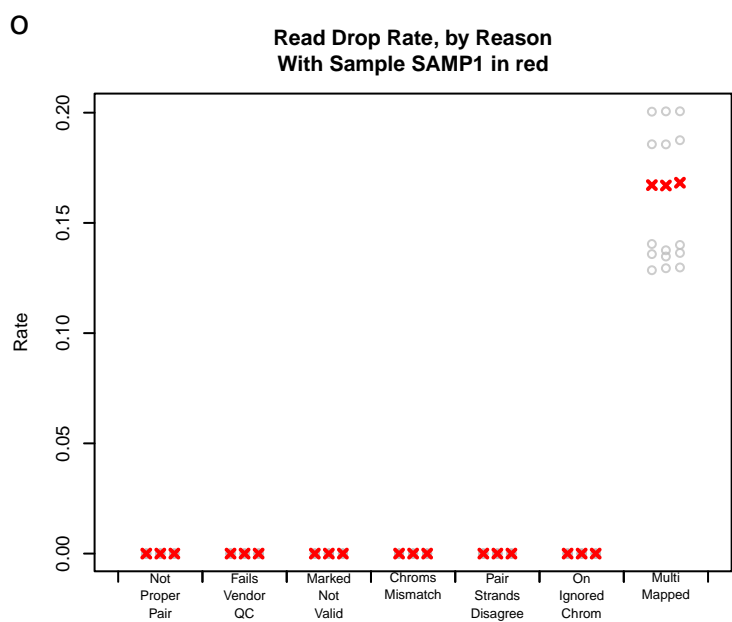
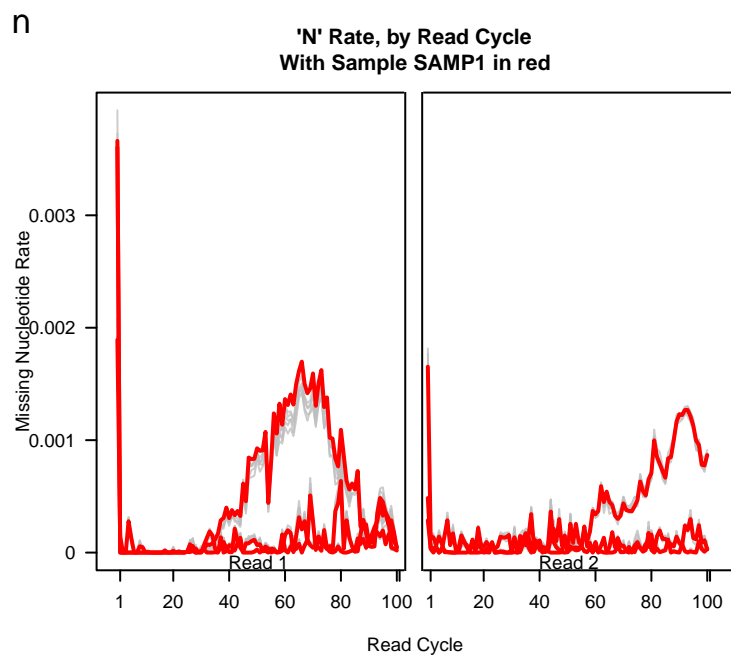
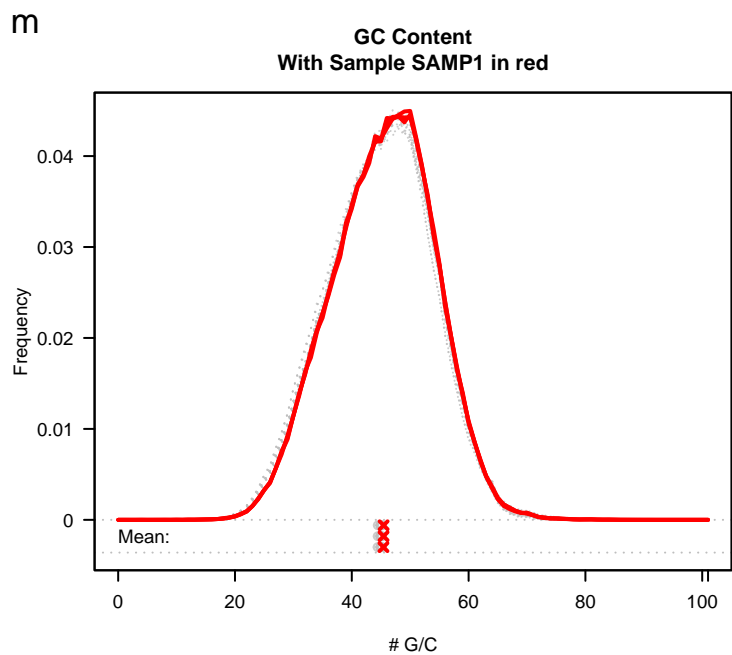
e

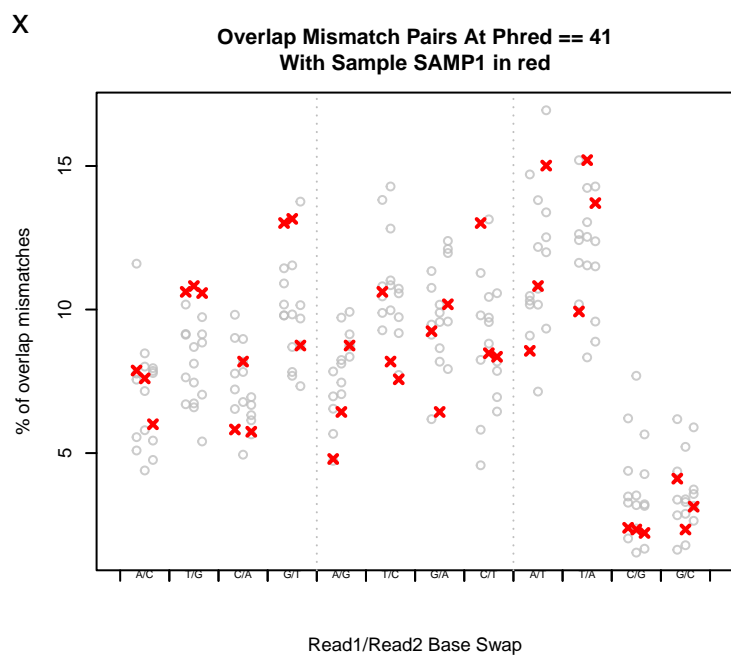
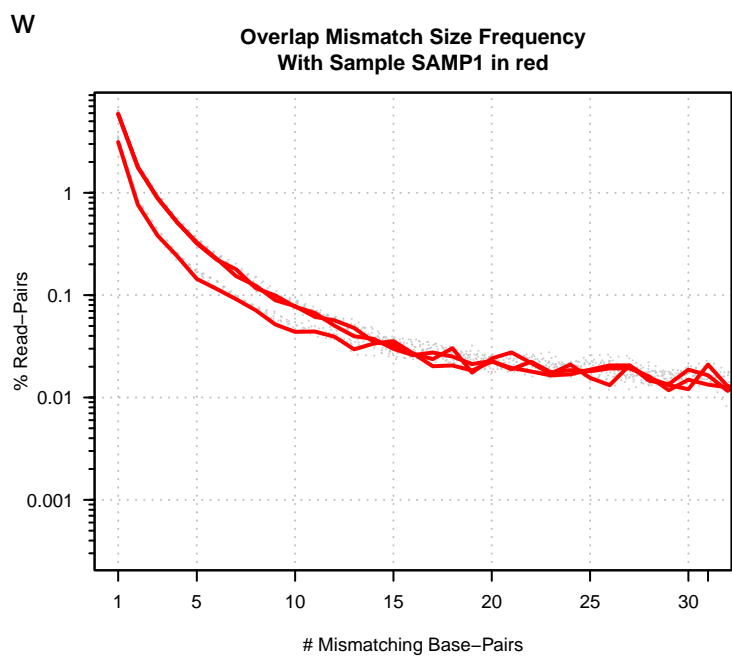
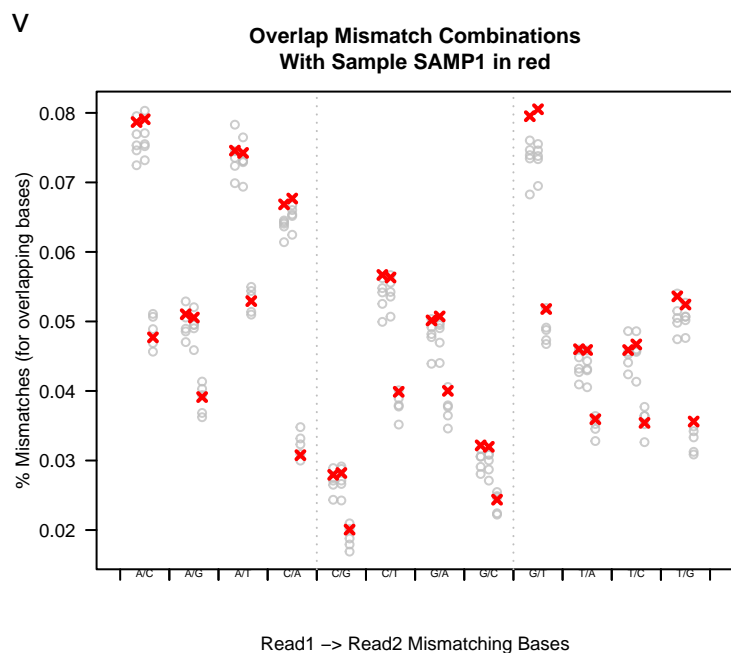
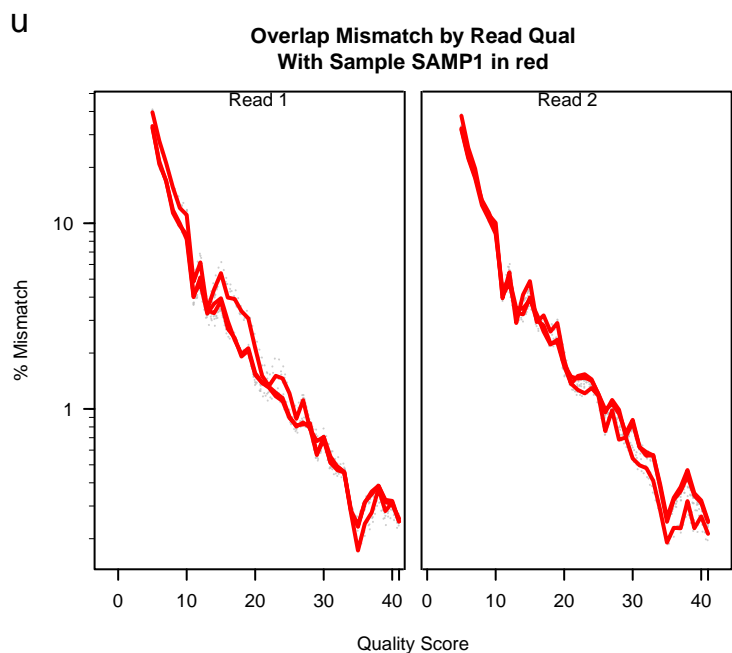
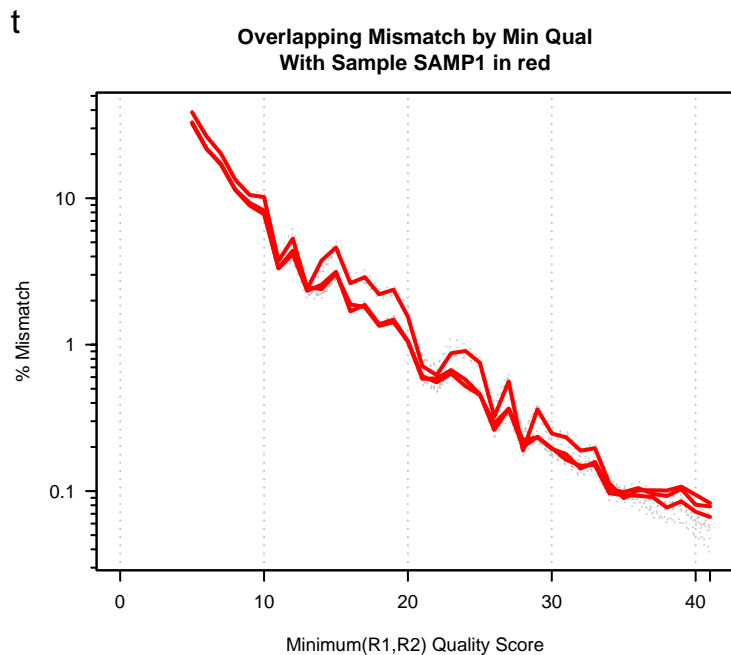
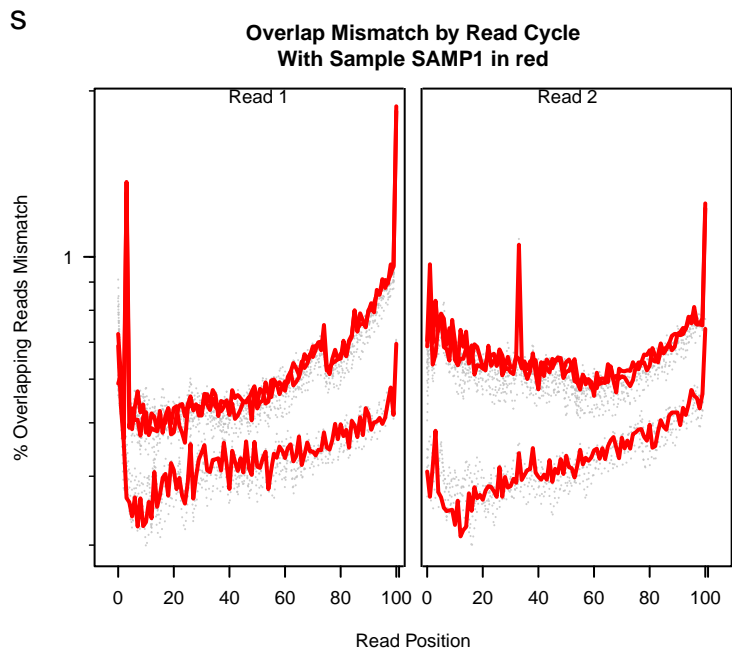


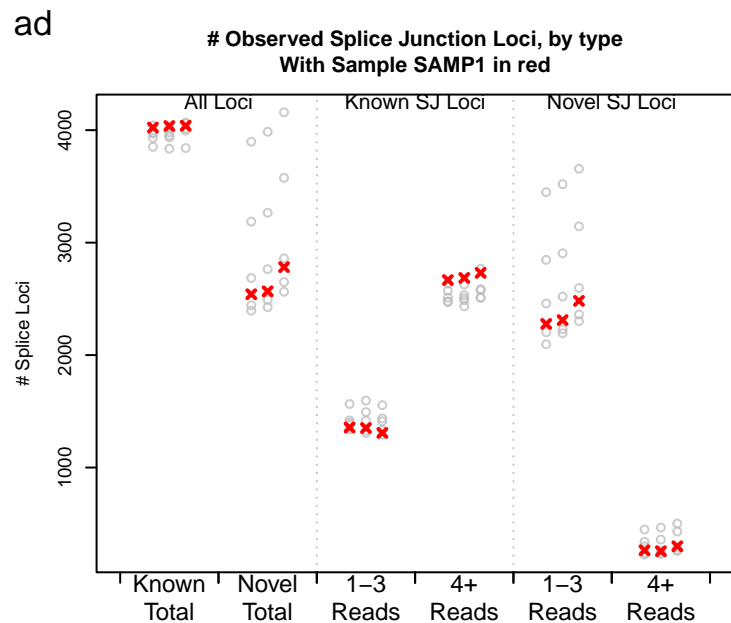
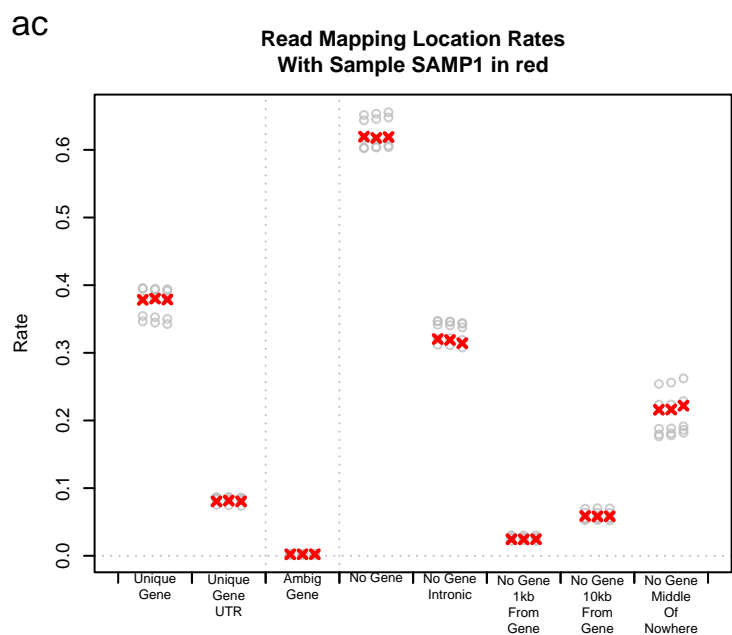
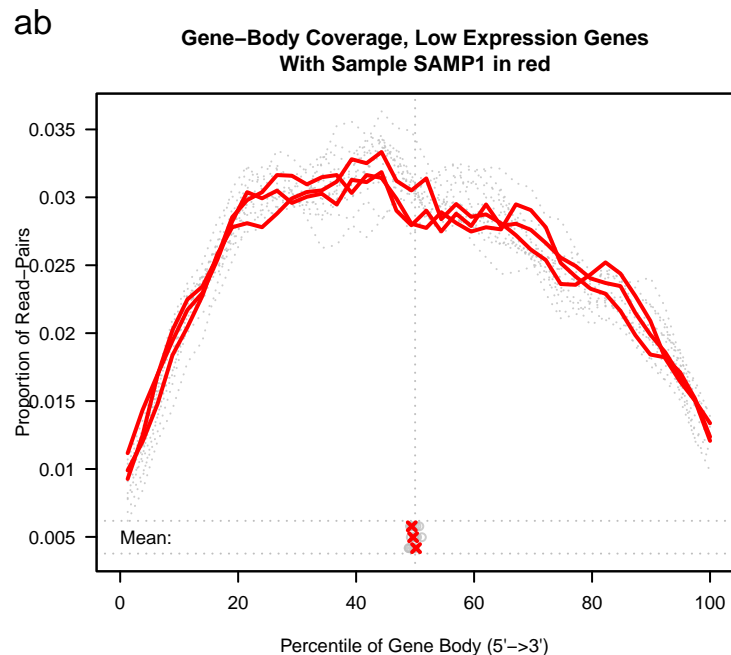
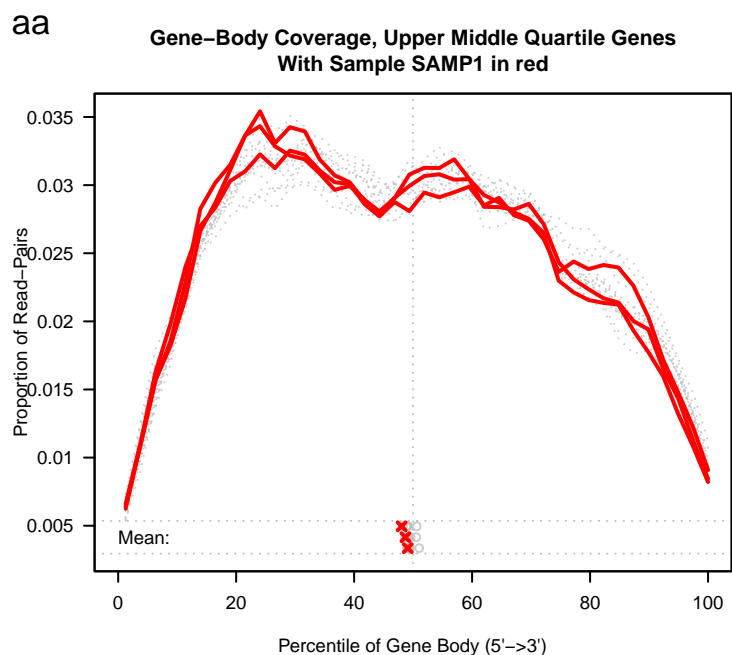
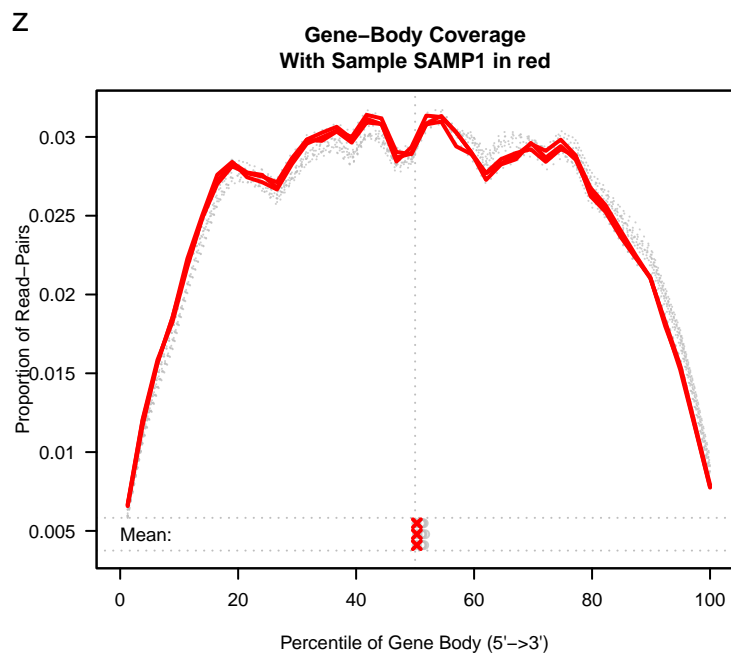
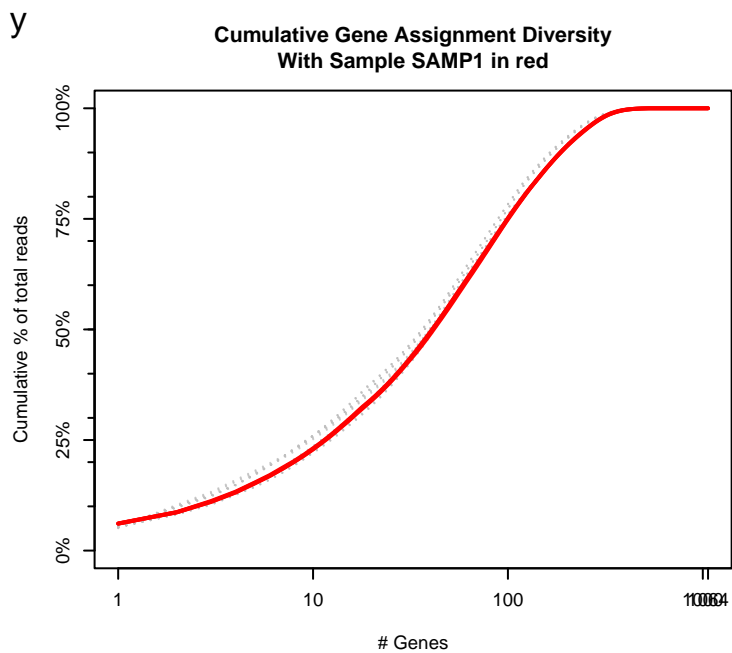
f



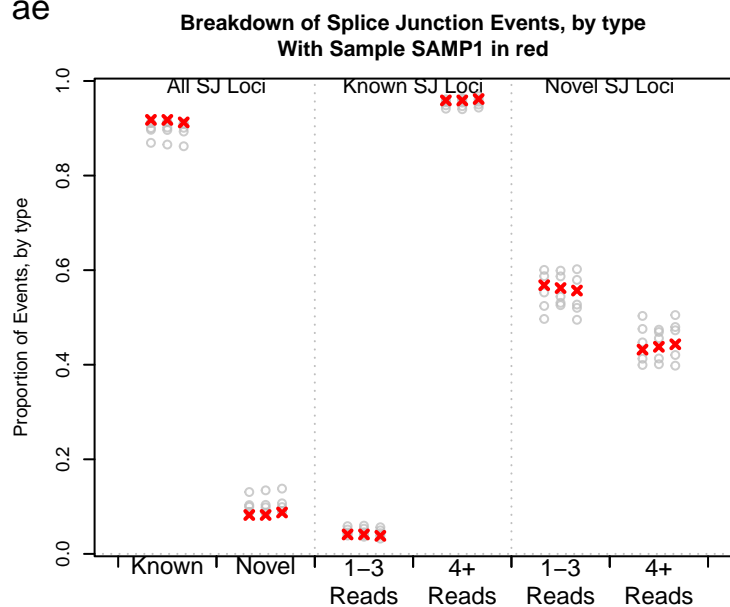




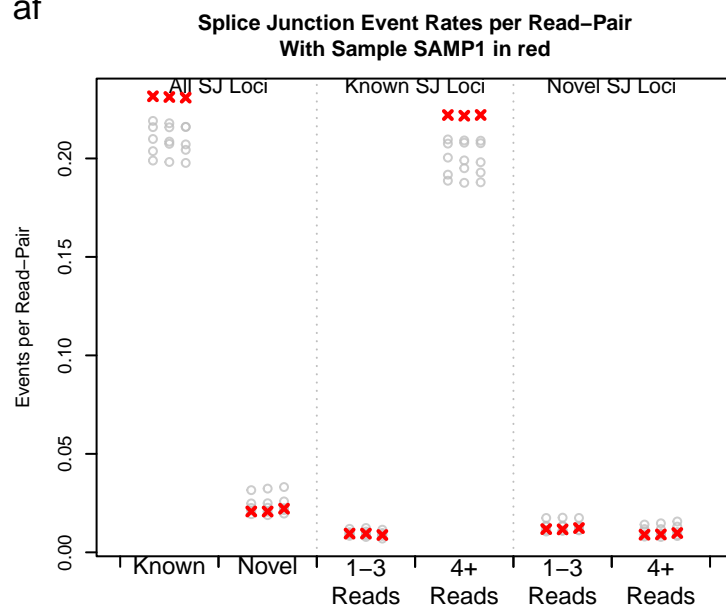




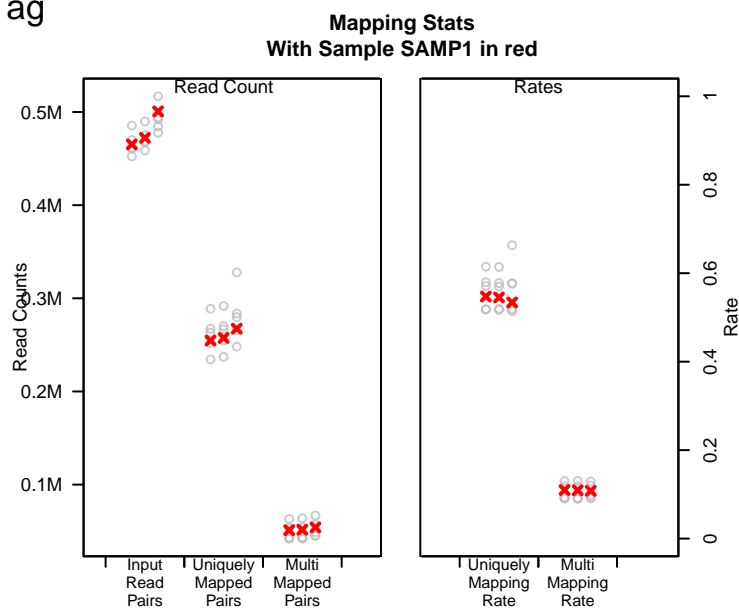
ae



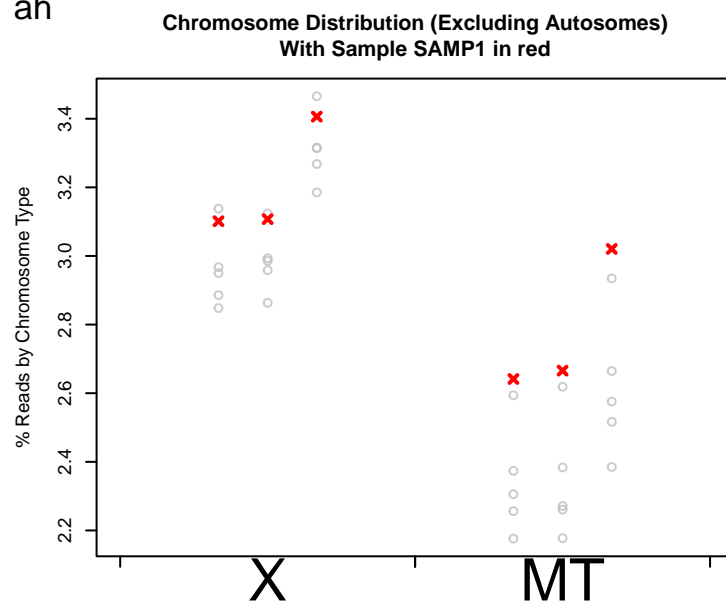
af



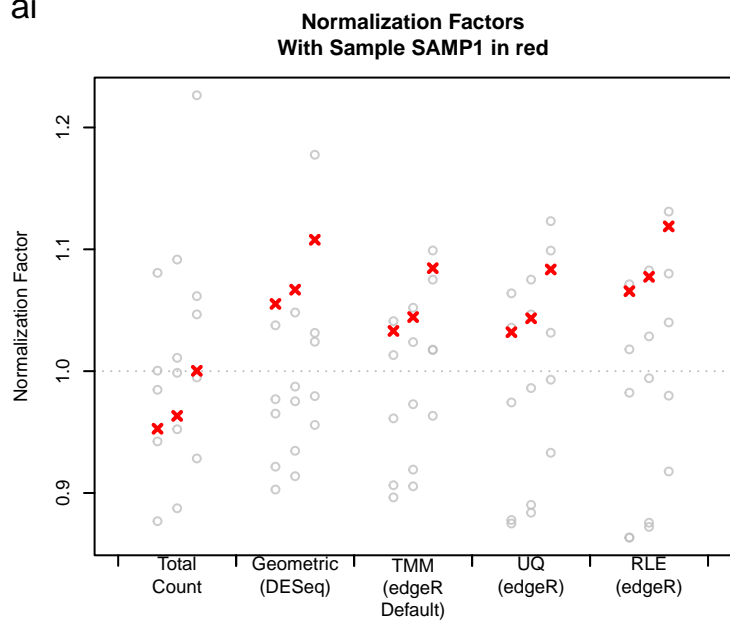
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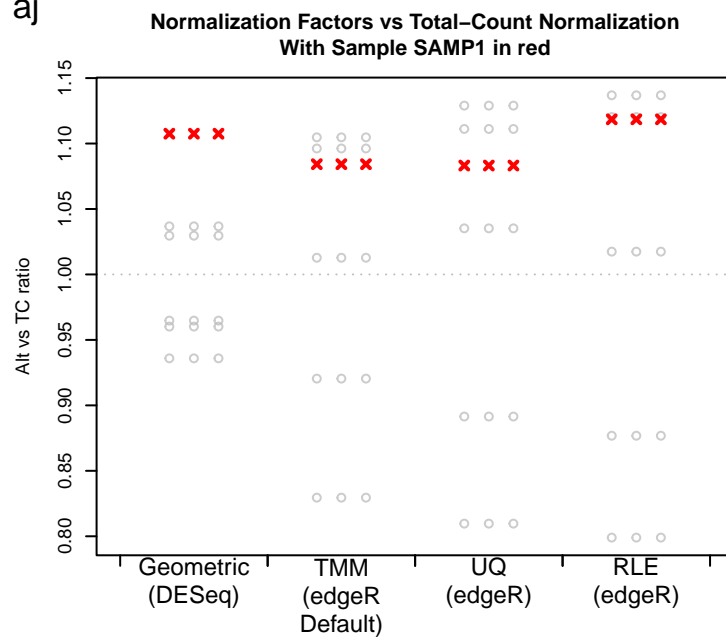
ah



ai

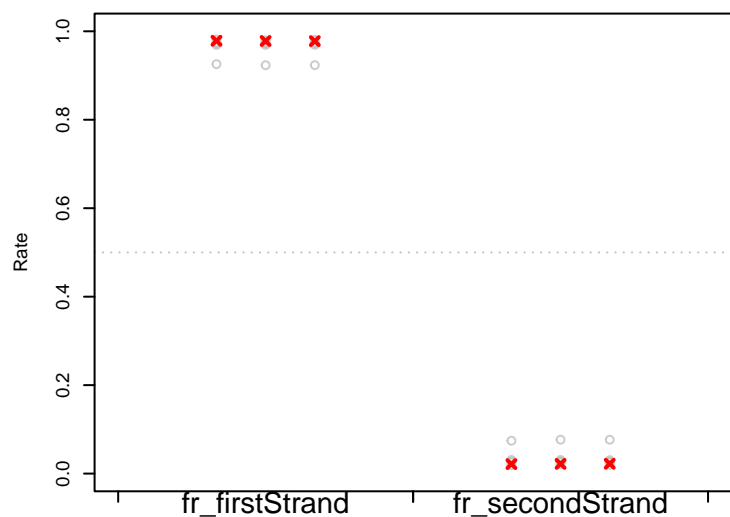


aj



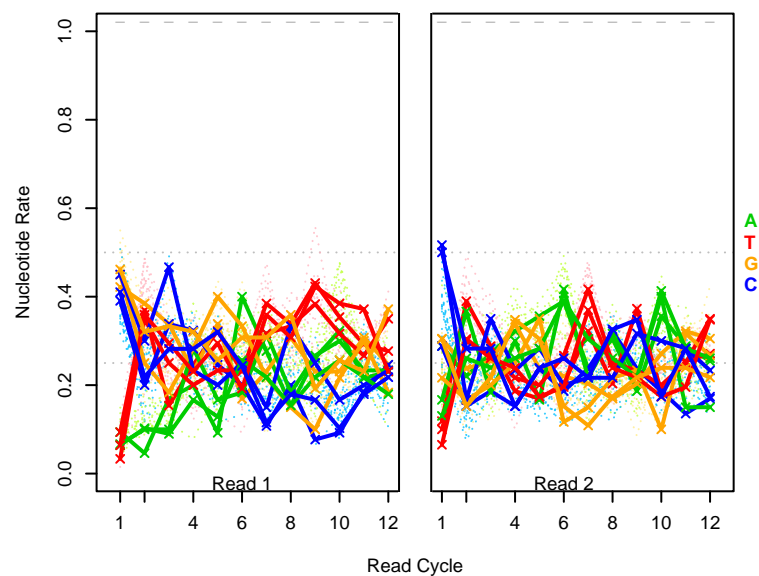
ak

**Strandedness Test**  
With Sample SAMP1 in red



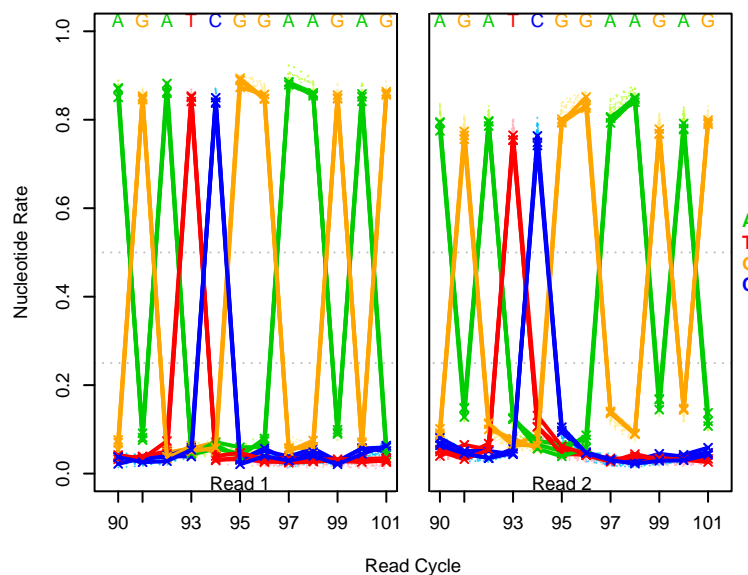
al

**Nucleotide Rate by Cycle, Leading Clipped bases (12)**  
With Sample SAMP1 in red



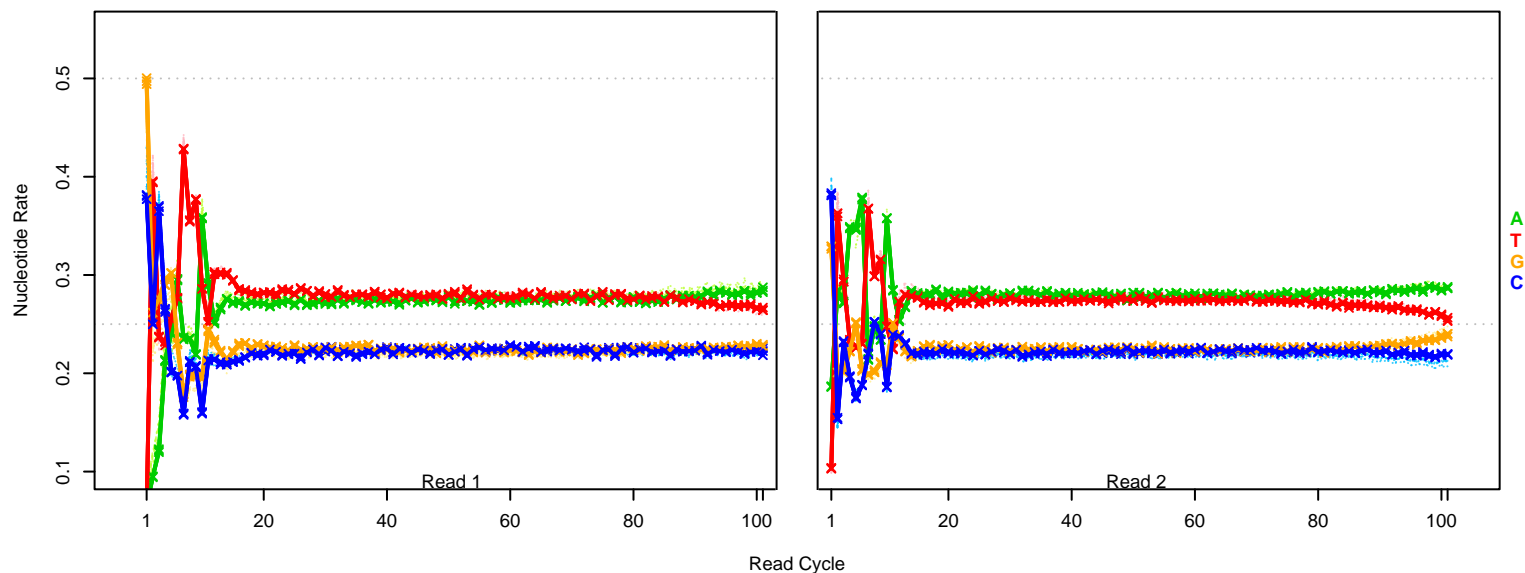
am

**Nucleotide Rate by Cycle, Trailing Clipped bases (12)**  
With Sample SAMP1 in red



an

**Raw Nucleotide Rate by Cycle**  
With Sample SAMP1 in red



ao

Nucleotide Rate by Cycle, Aligned bases only  
With Sample SAMP1 in red

