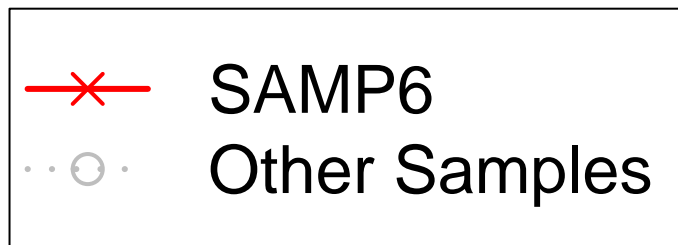
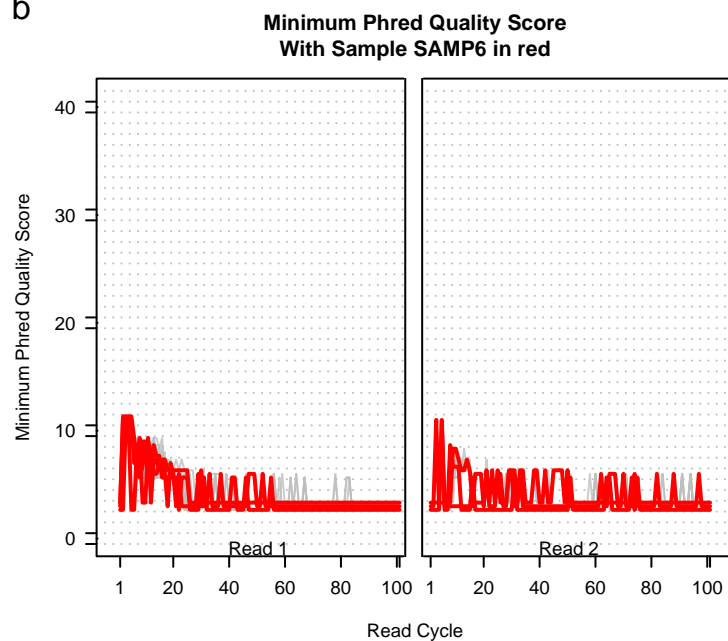


a

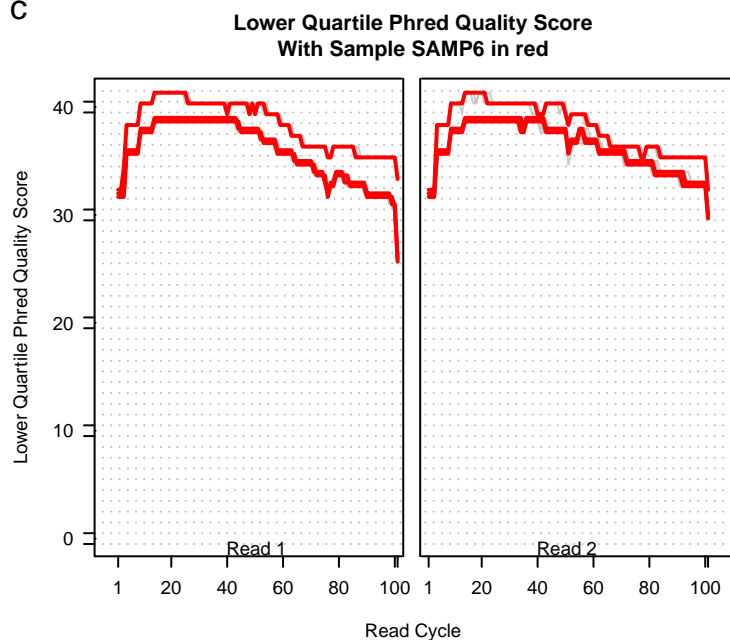
## Sample Highlight: SAMP6



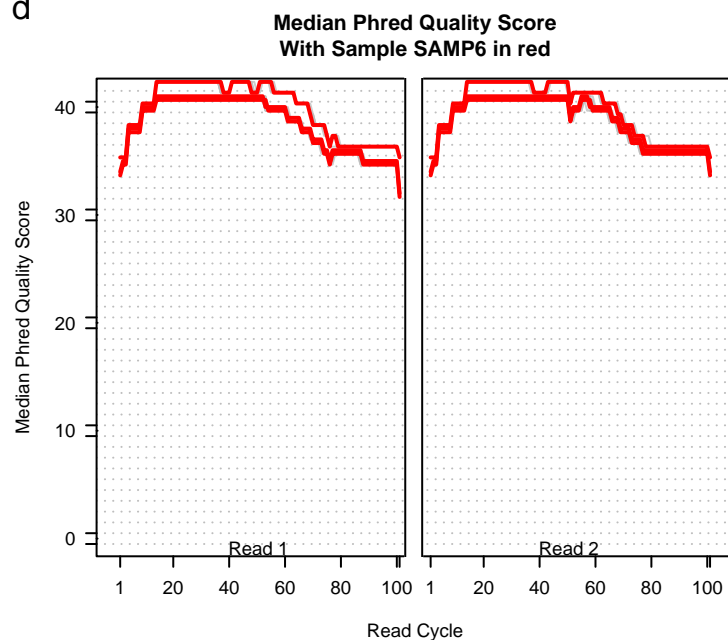
b



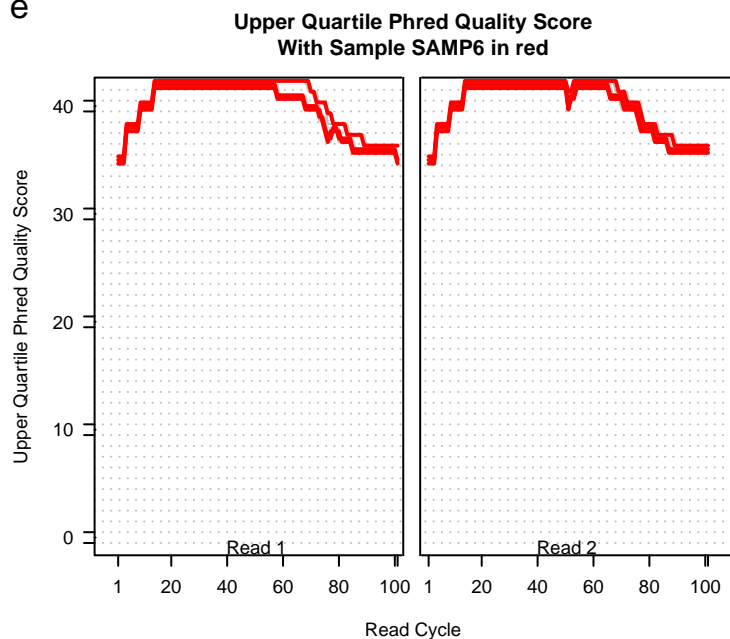
c



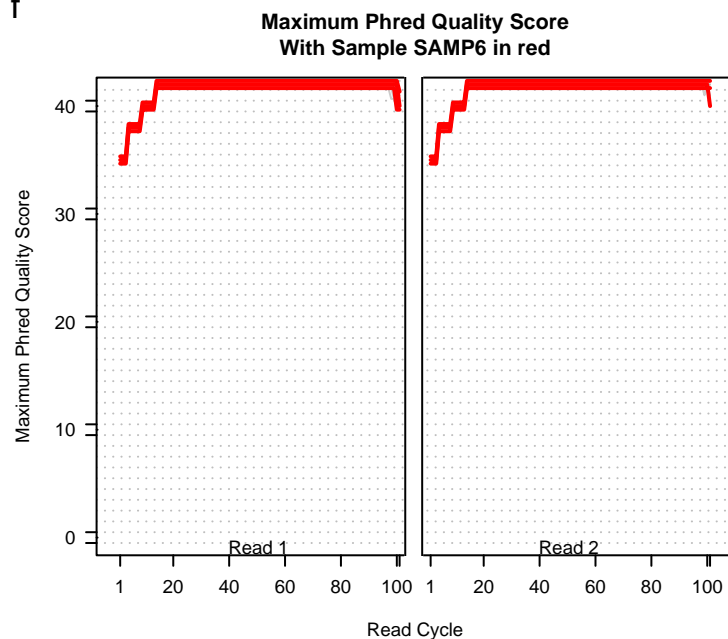
d

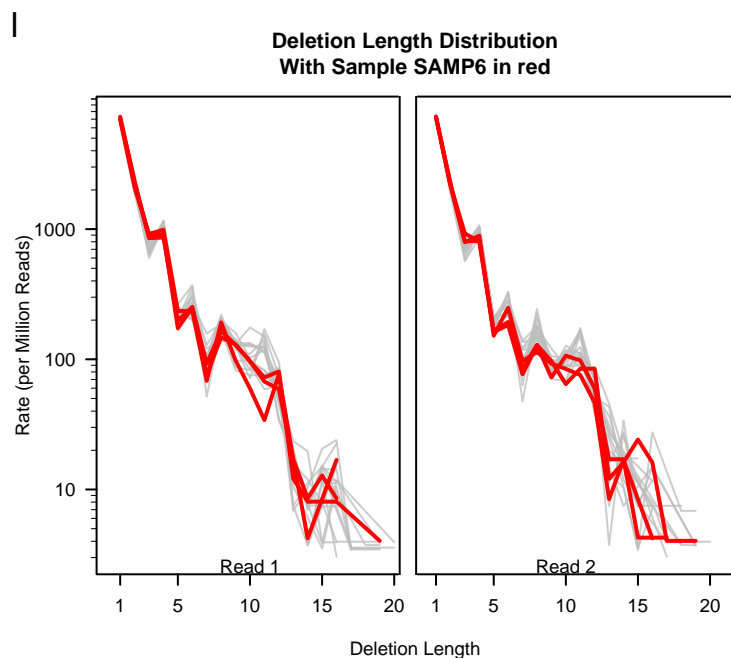
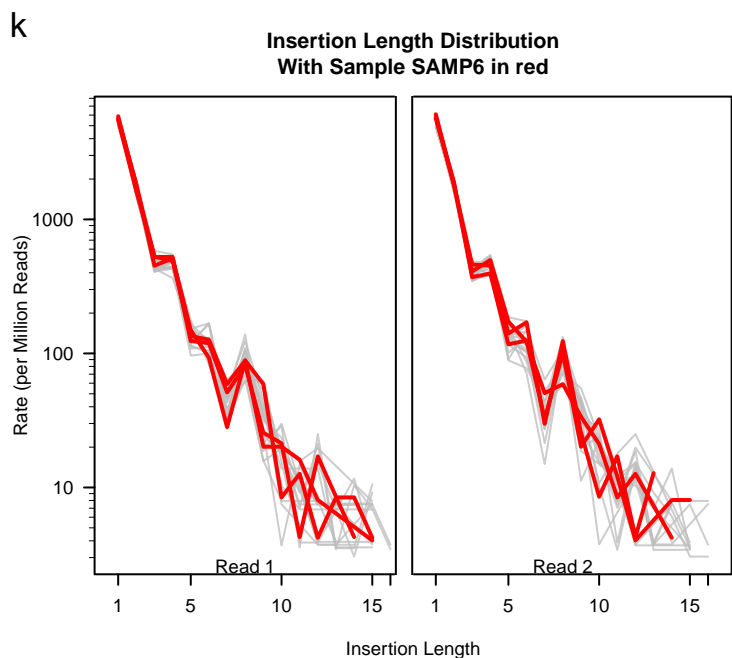
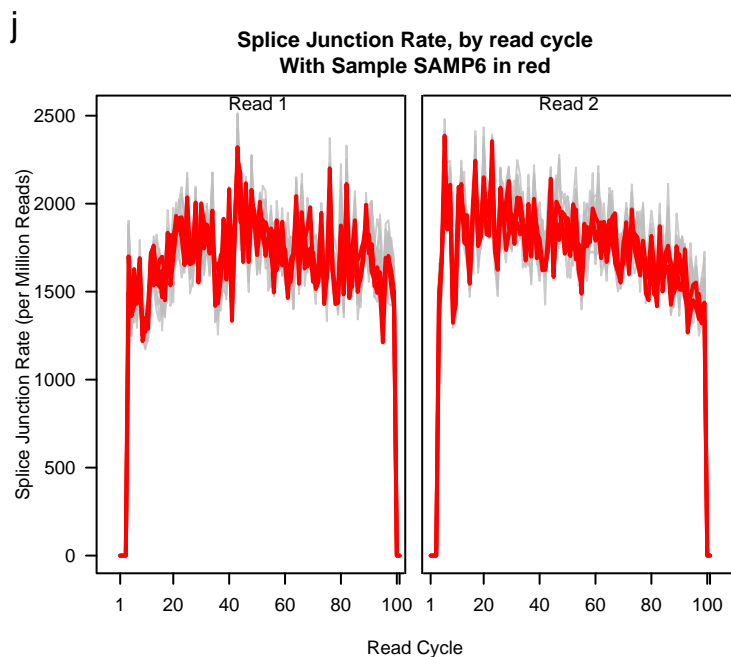
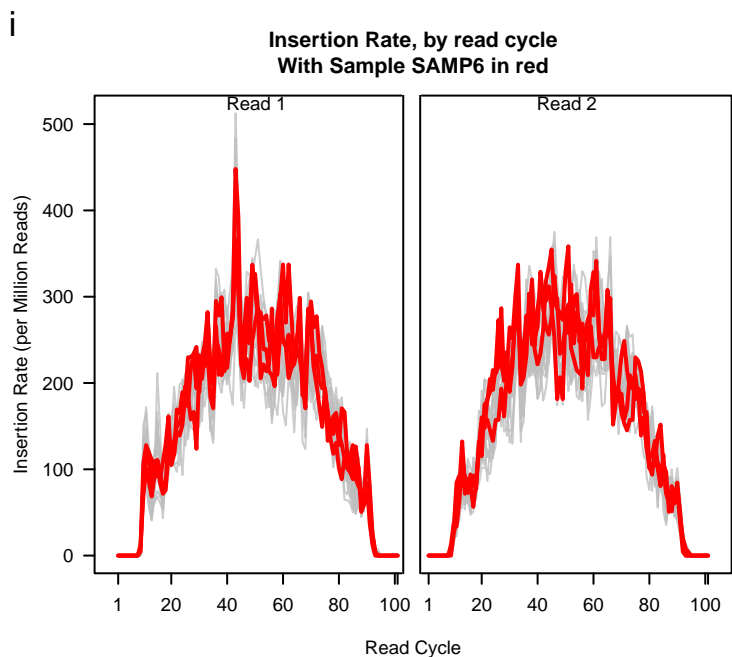
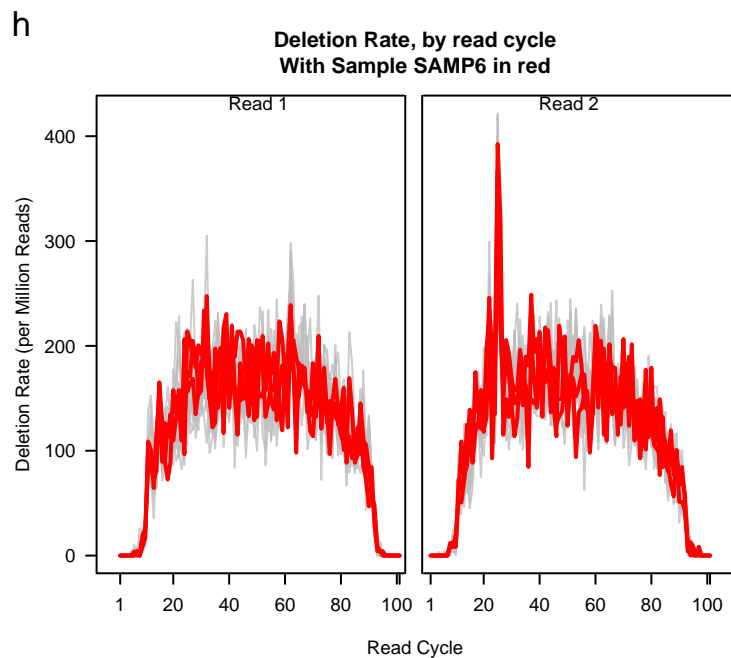
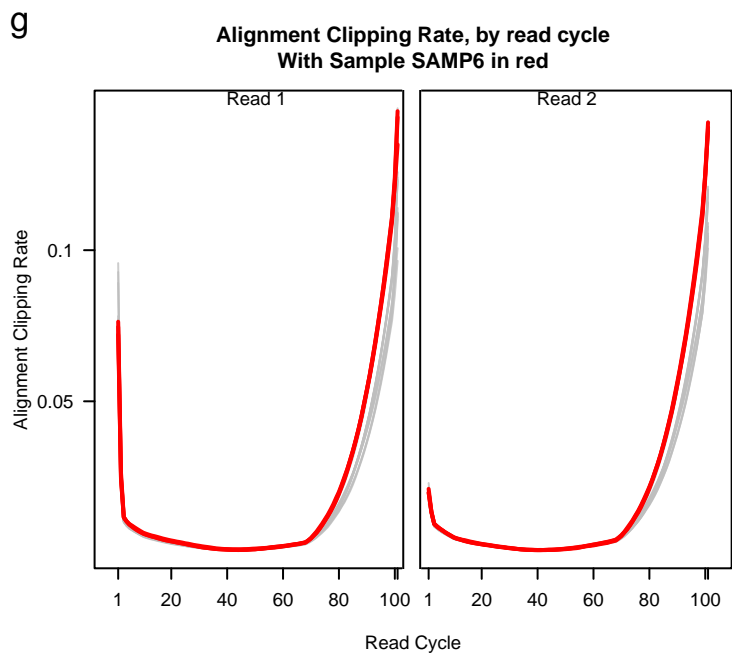


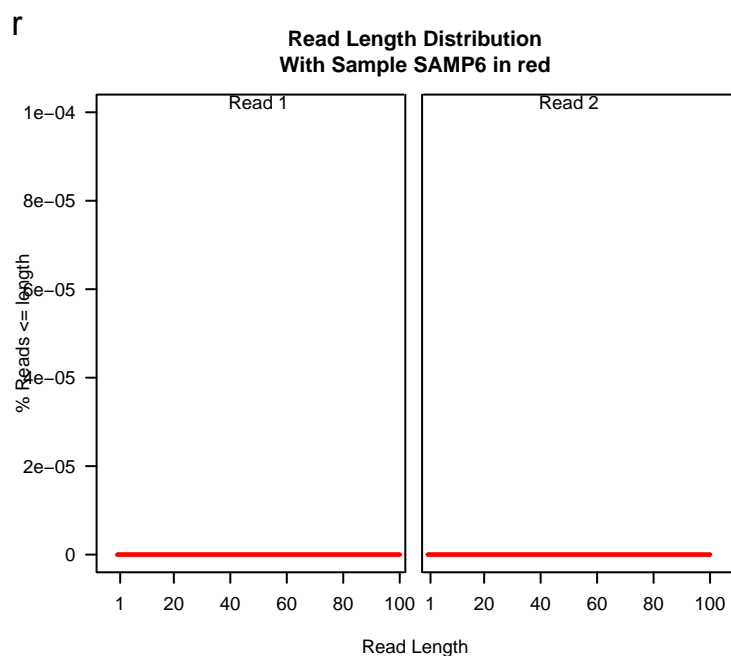
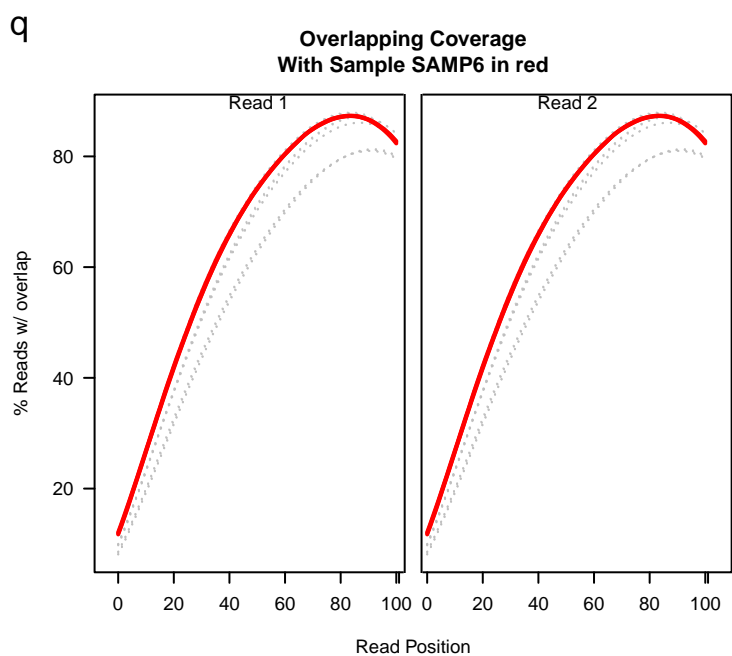
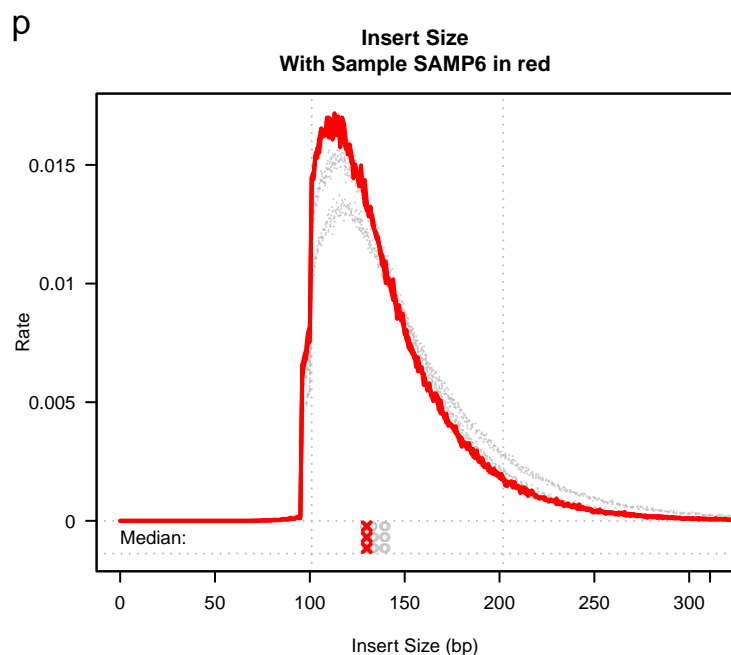
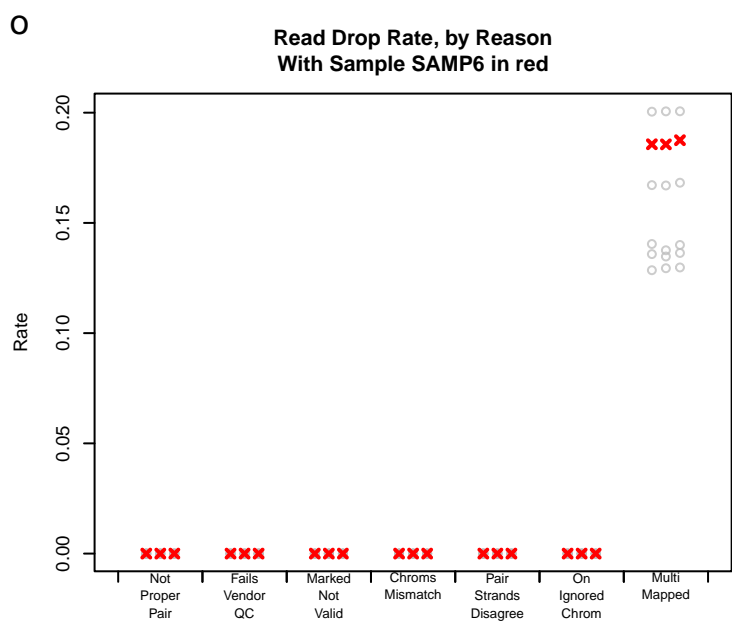
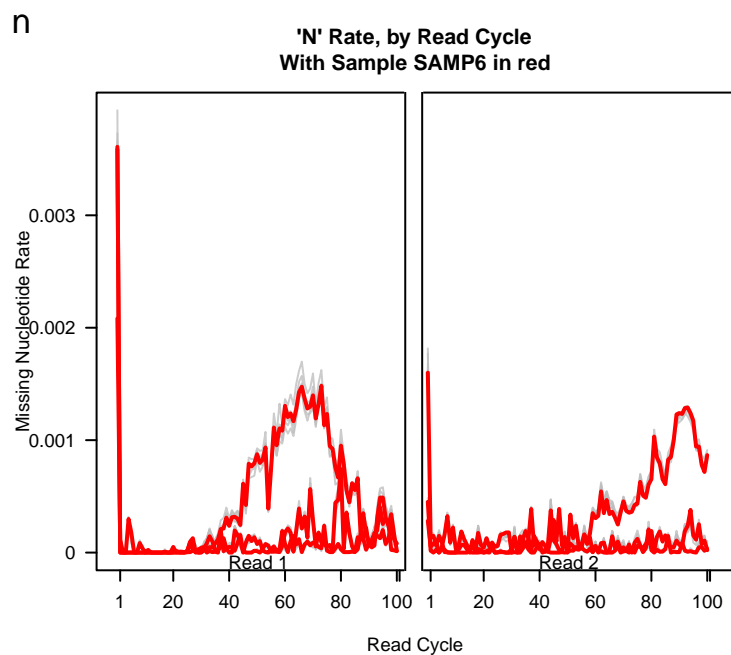
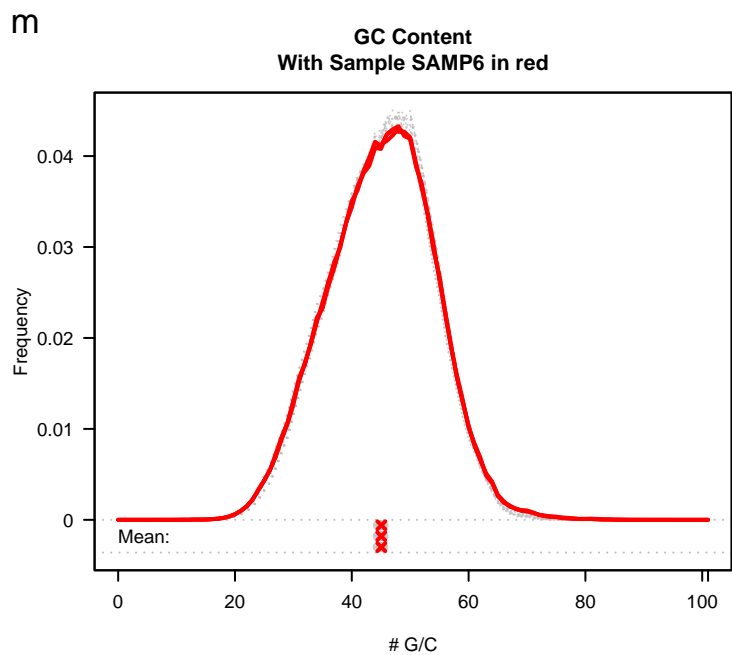
e

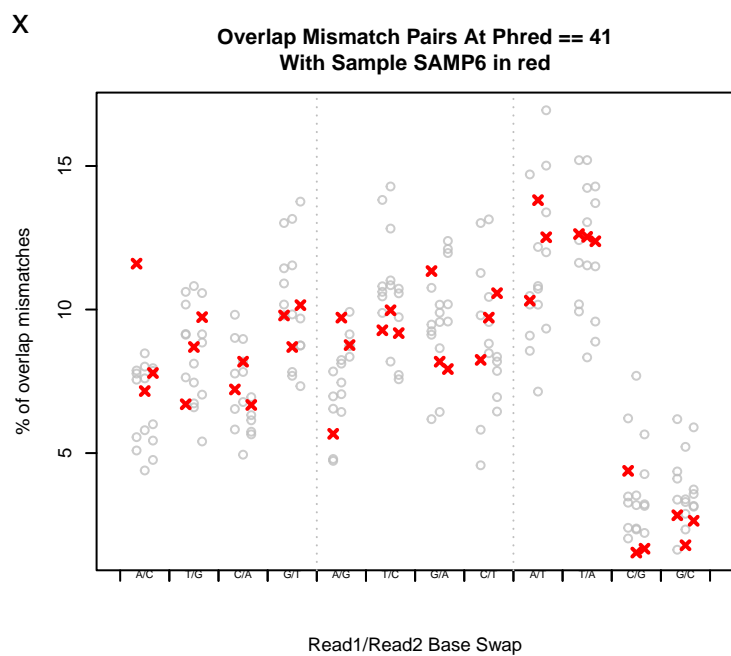
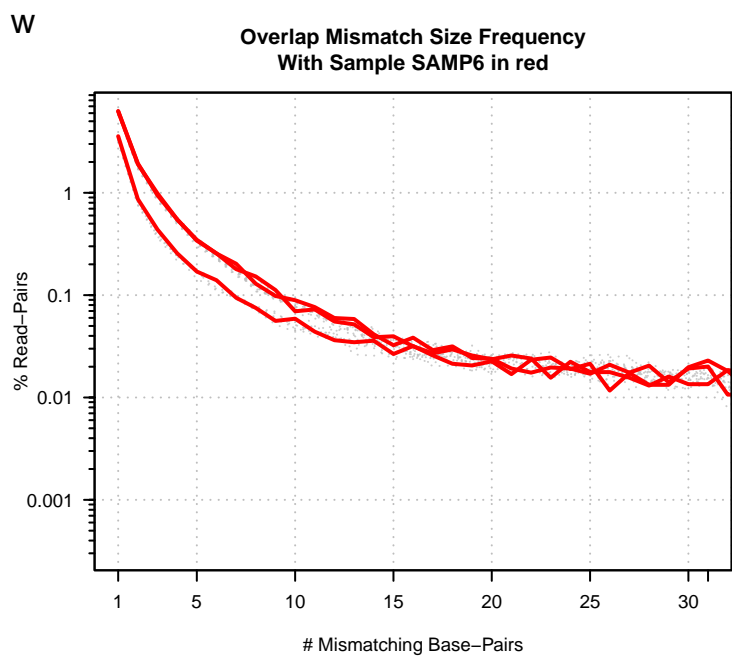
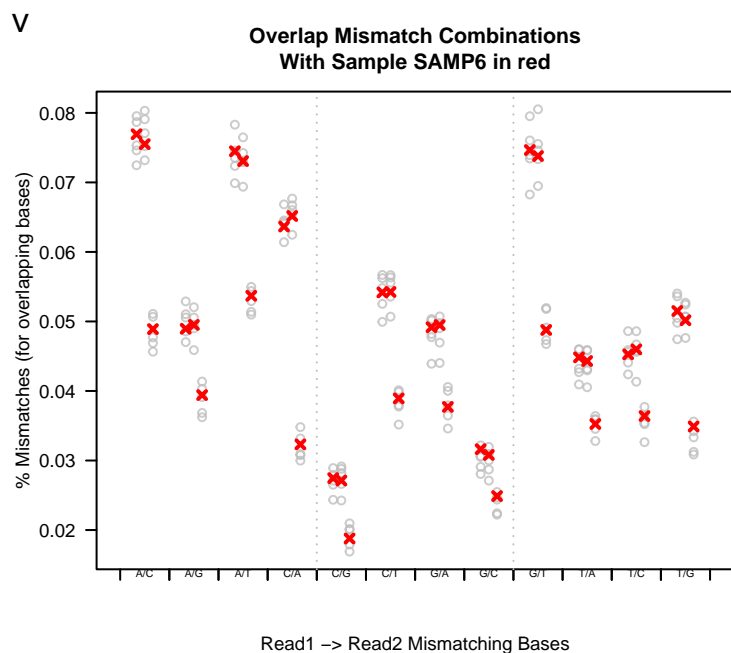
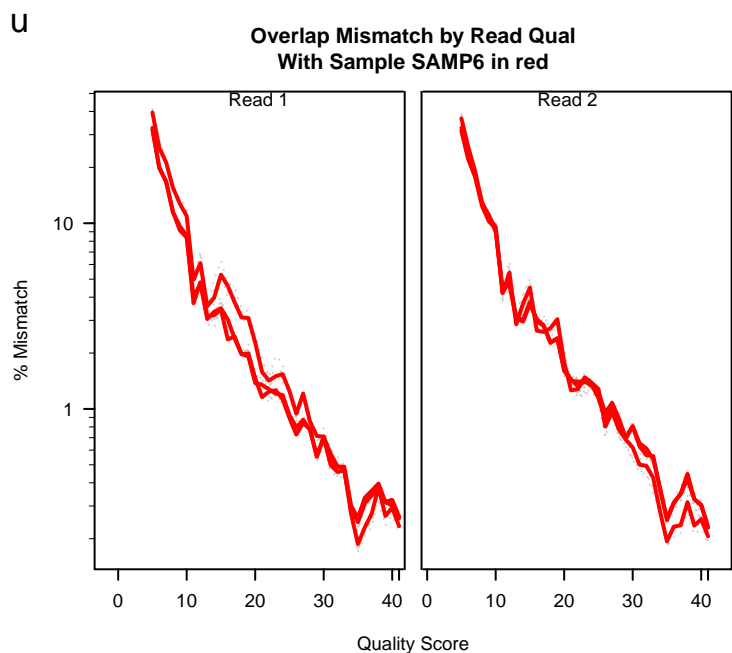
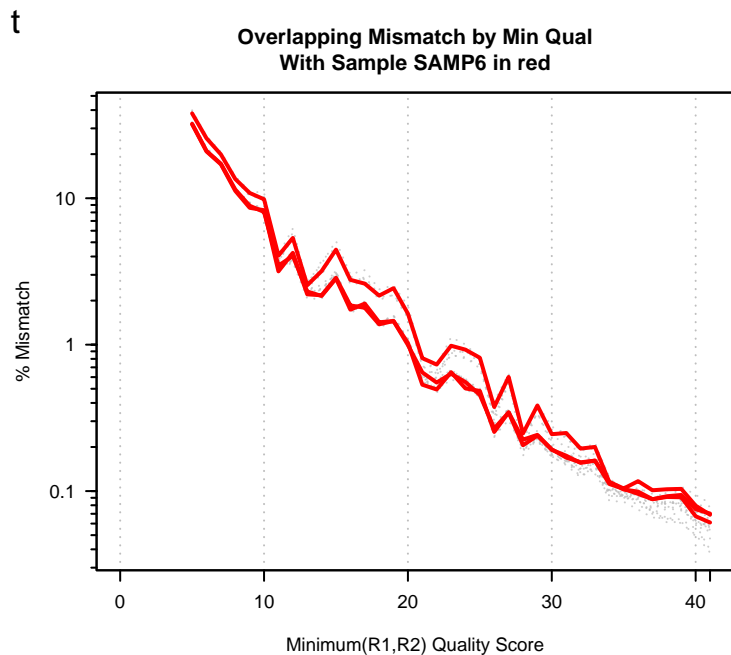
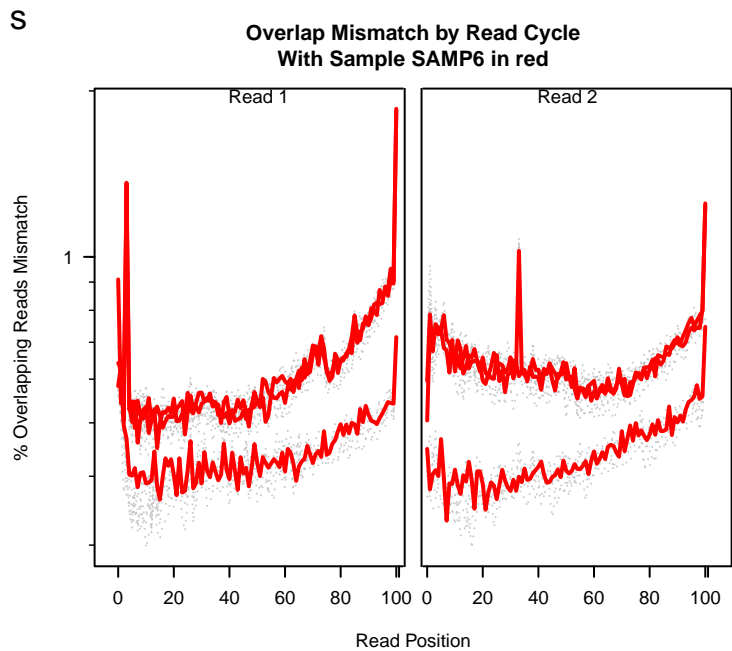


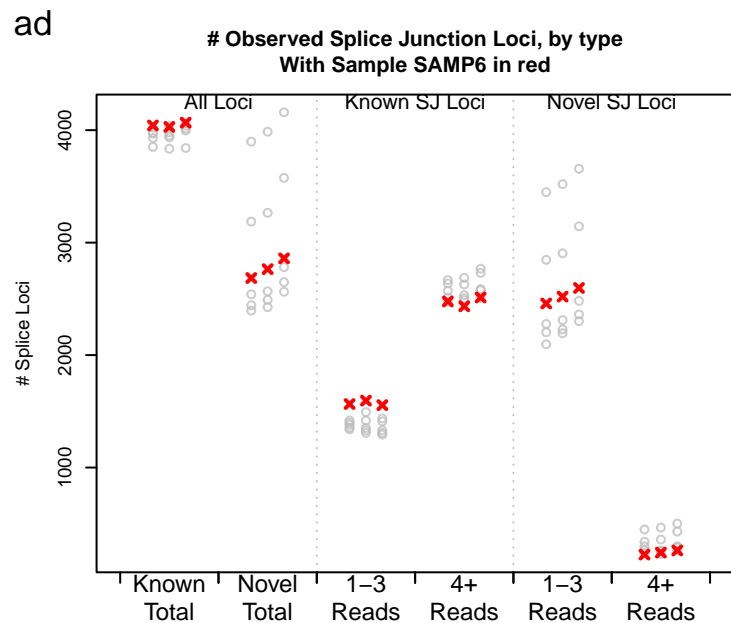
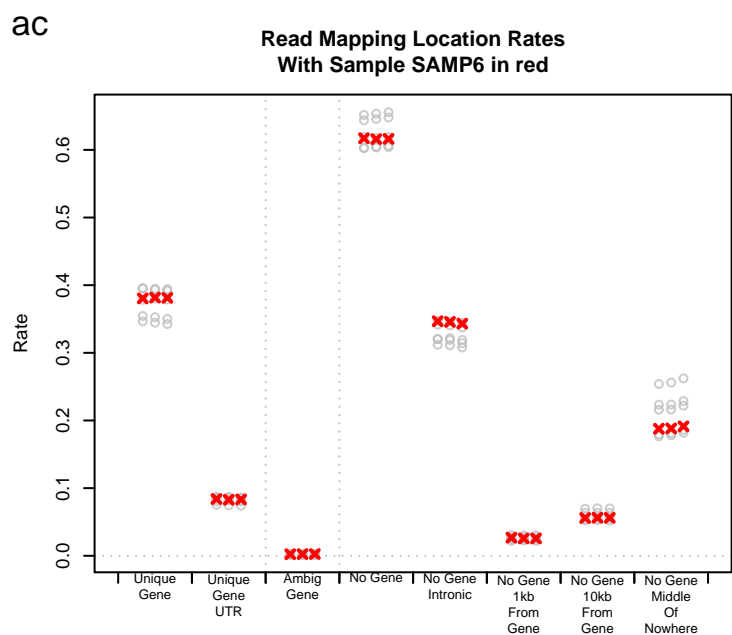
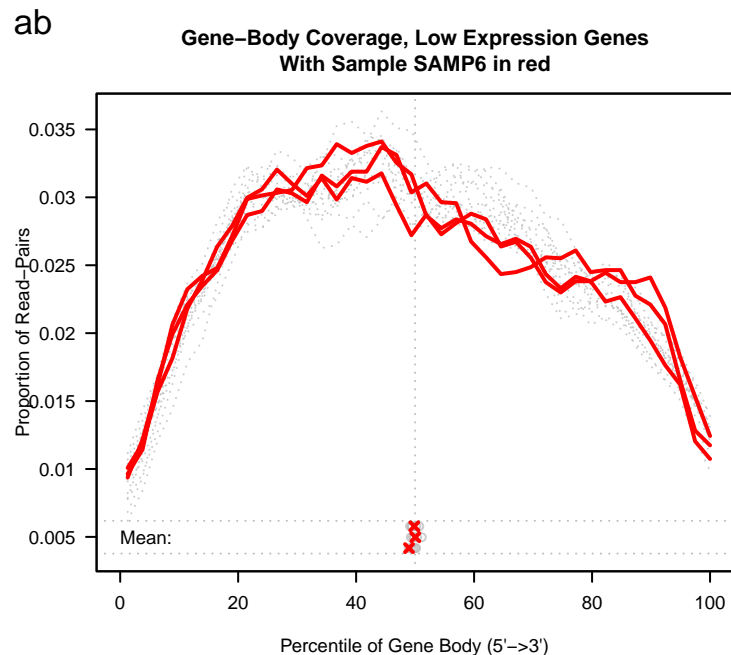
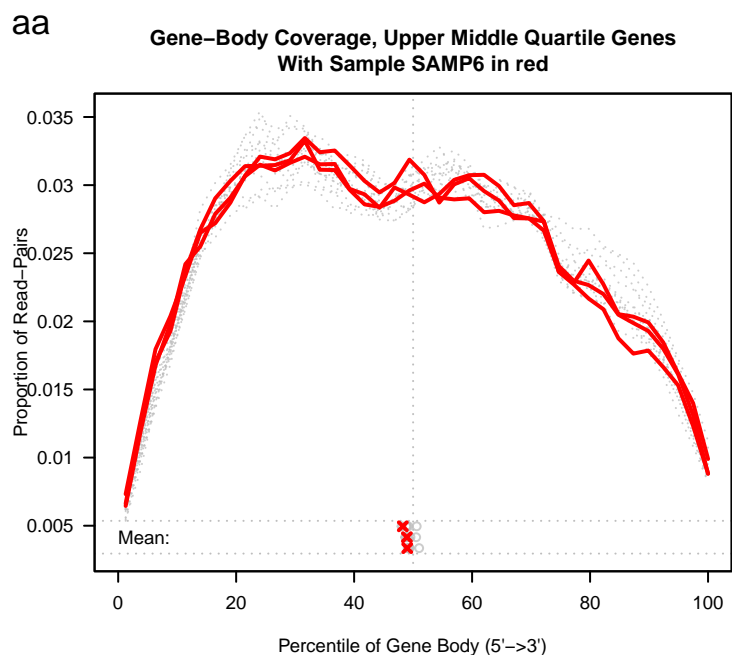
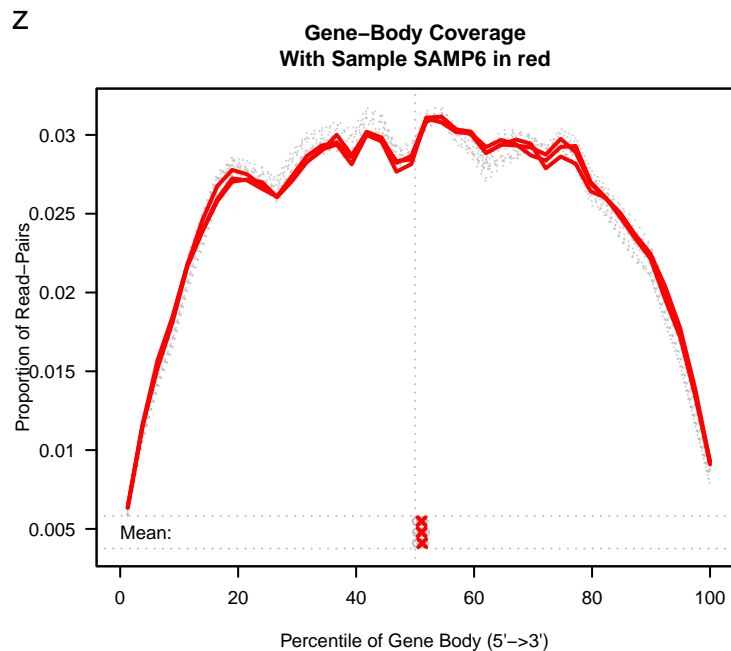
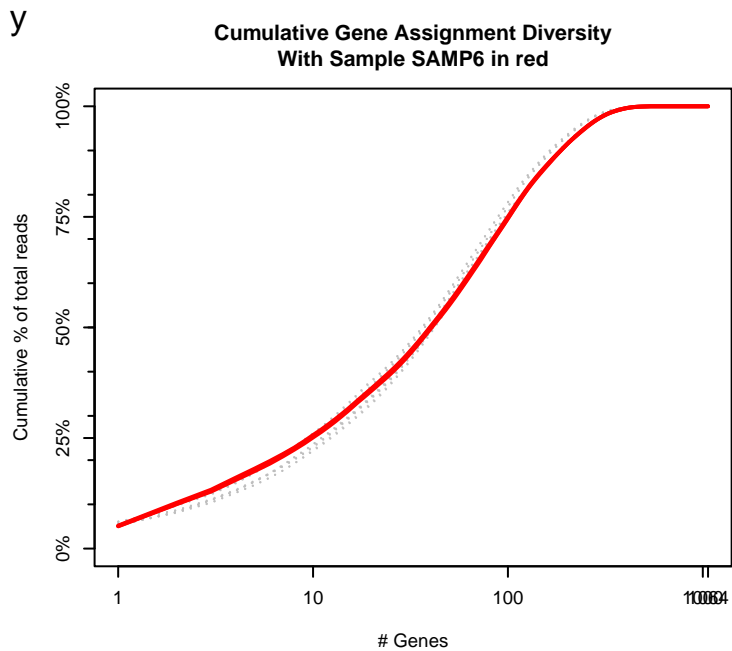
f



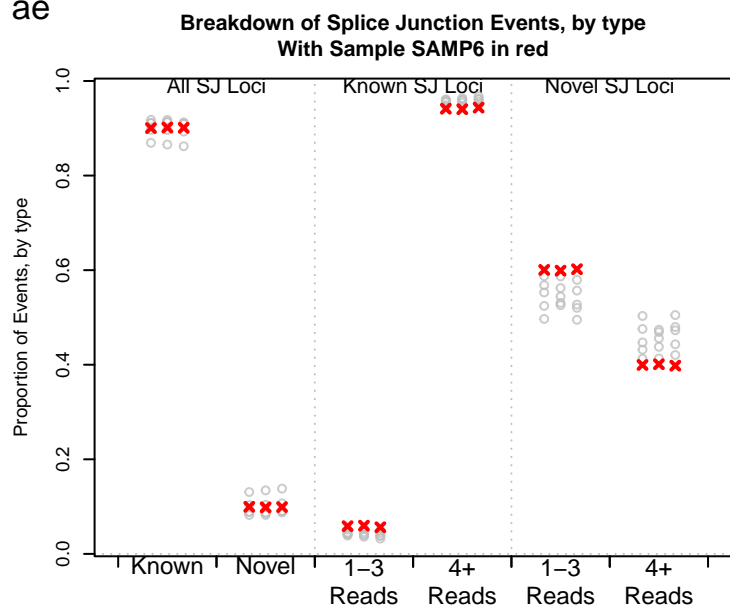




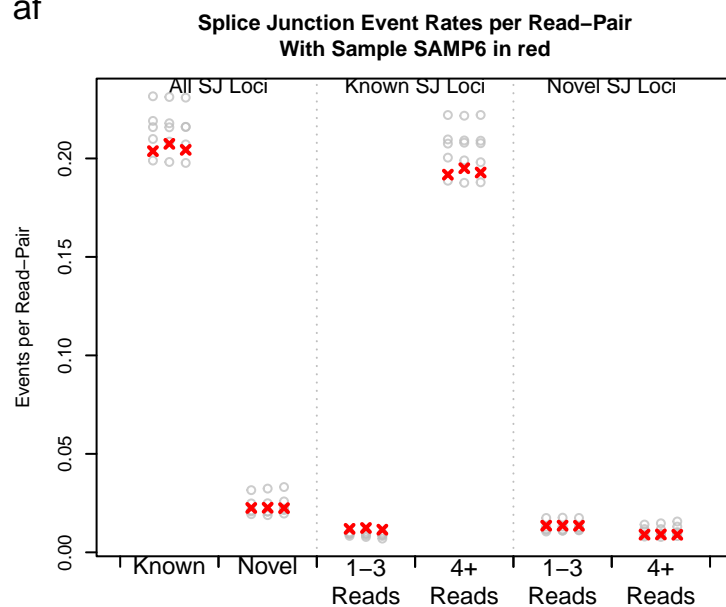




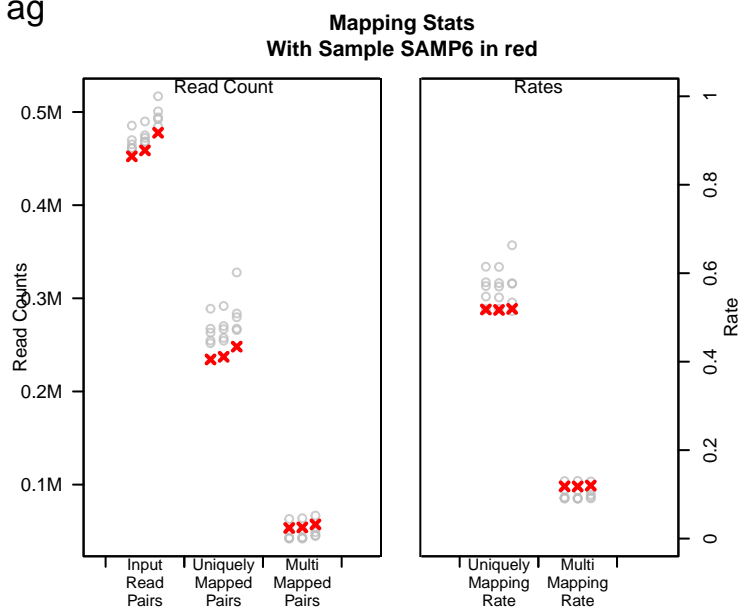
ae



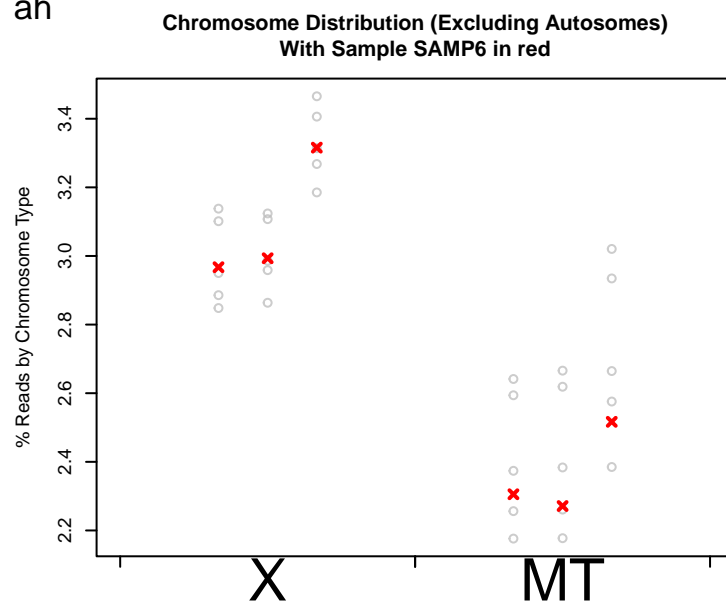
af



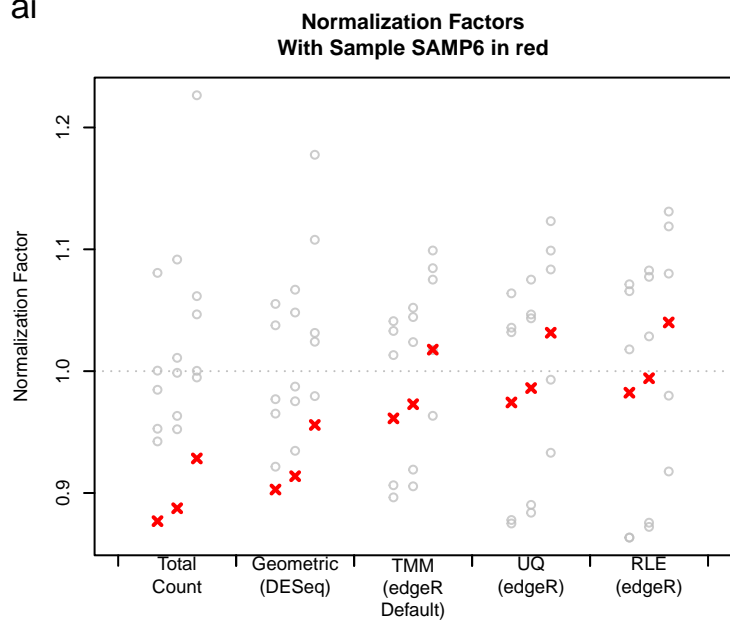
ag



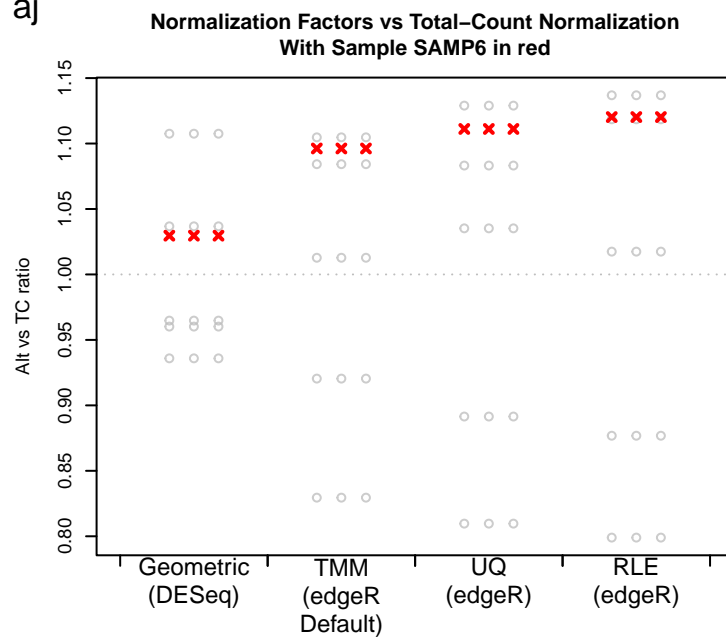
ah



ai

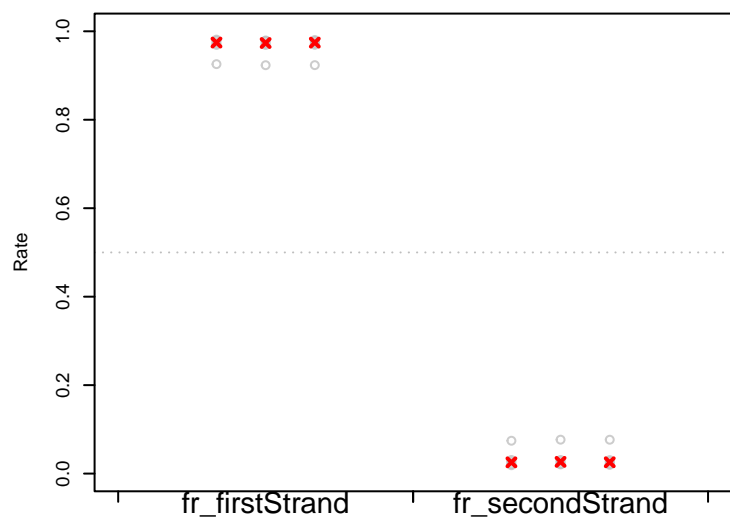


aj



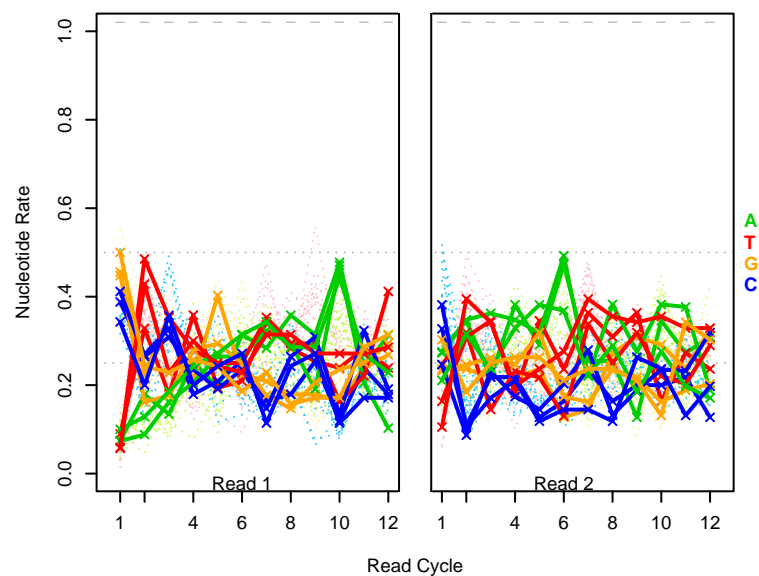
ak

**Strandedness Test**  
With Sample SAMP6 in red



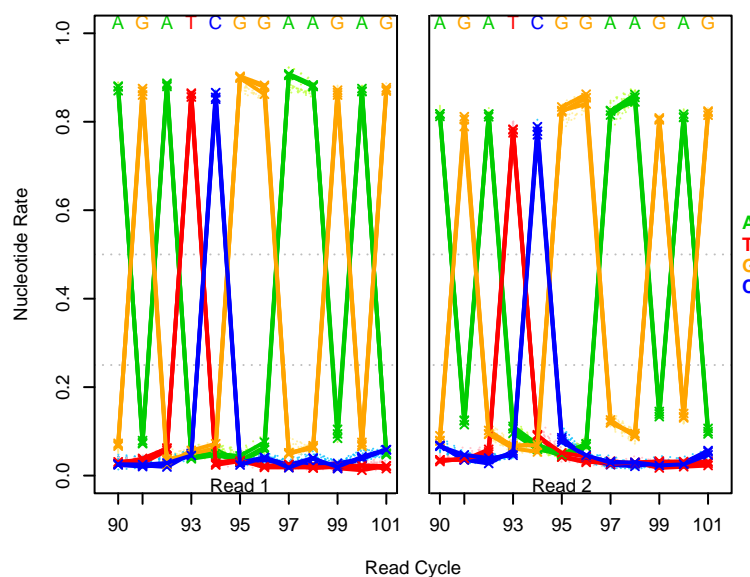
al

**Nucleotide Rate by Cycle, Leading Clipped bases (12)**  
With Sample SAMP6 in red



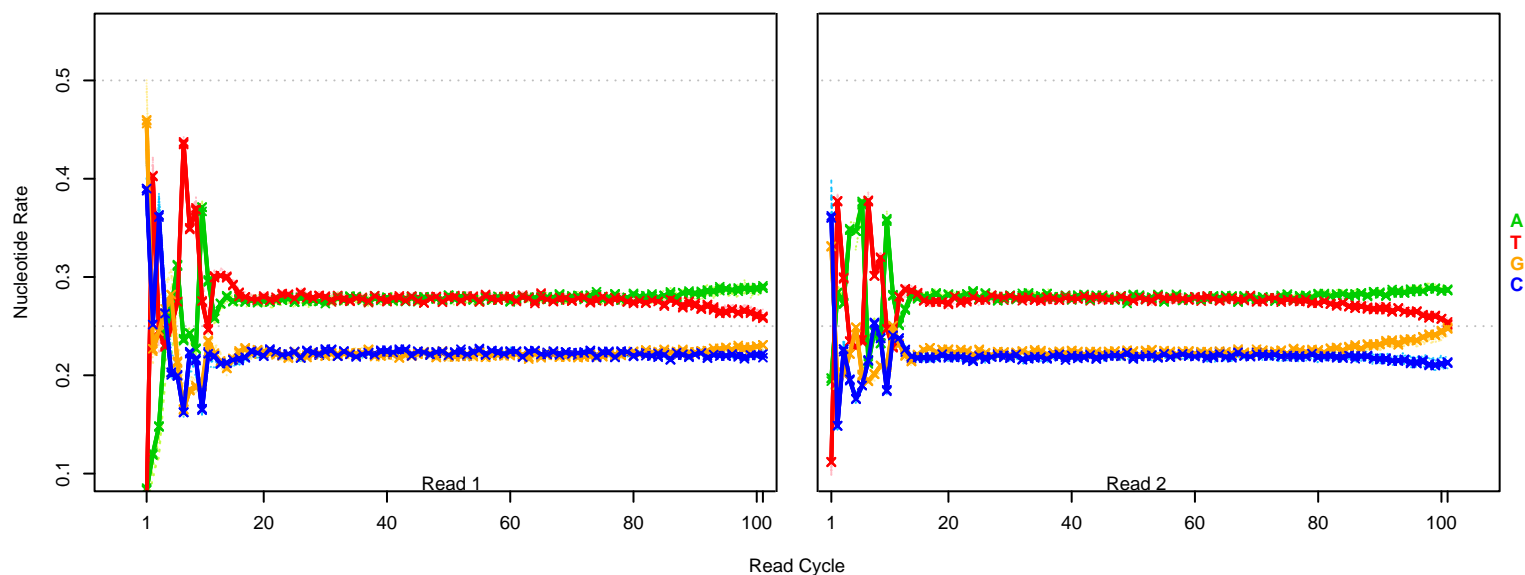
am

**Nucleotide Rate by Cycle, Trailing Clipped bases (12)**  
With Sample SAMP6 in red



an

**Raw Nucleotide Rate by Cycle**  
With Sample SAMP6 in red



ao

Nucleotide Rate by Cycle, Aligned bases only  
With Sample SAMP6 in red

