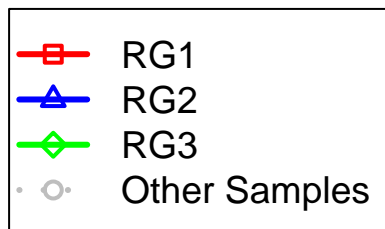
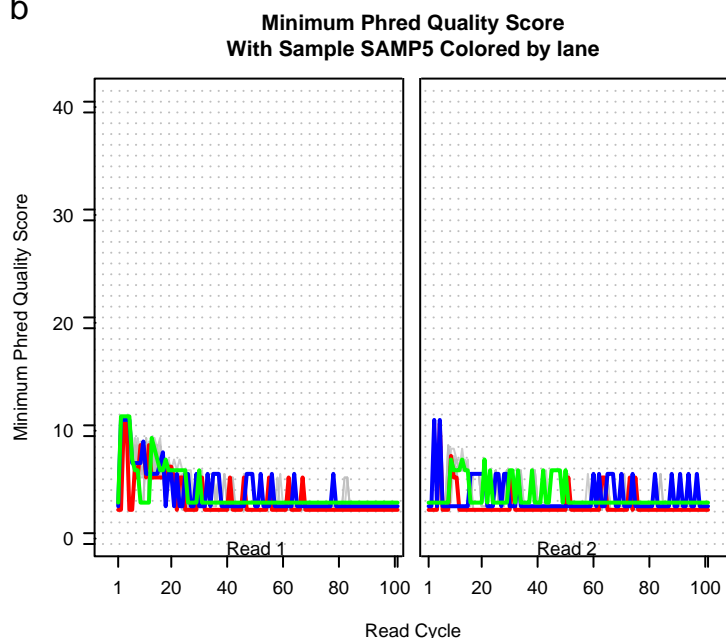


a

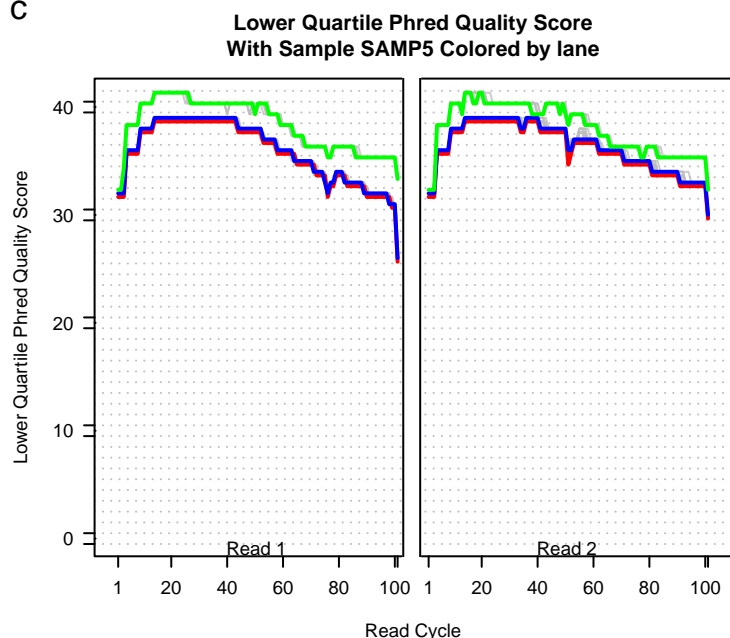
# Sample Highlight: SAMP5 Colored by Lane



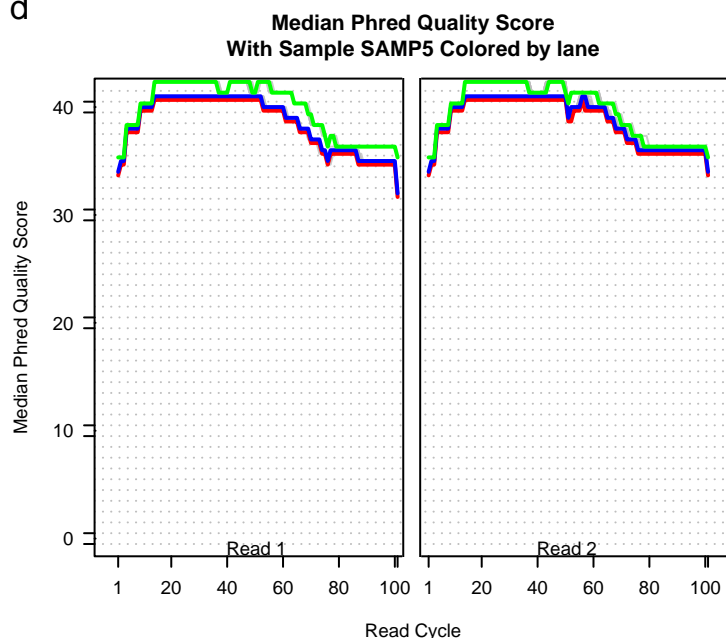
b



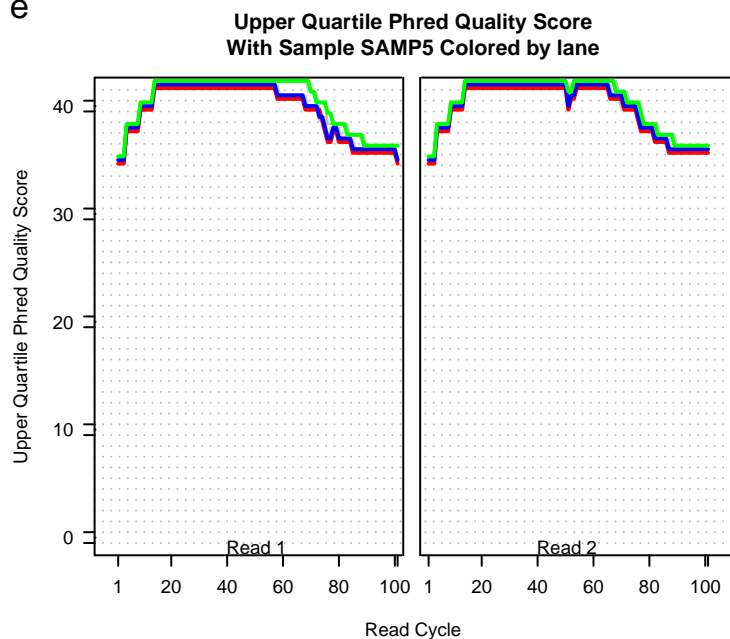
c



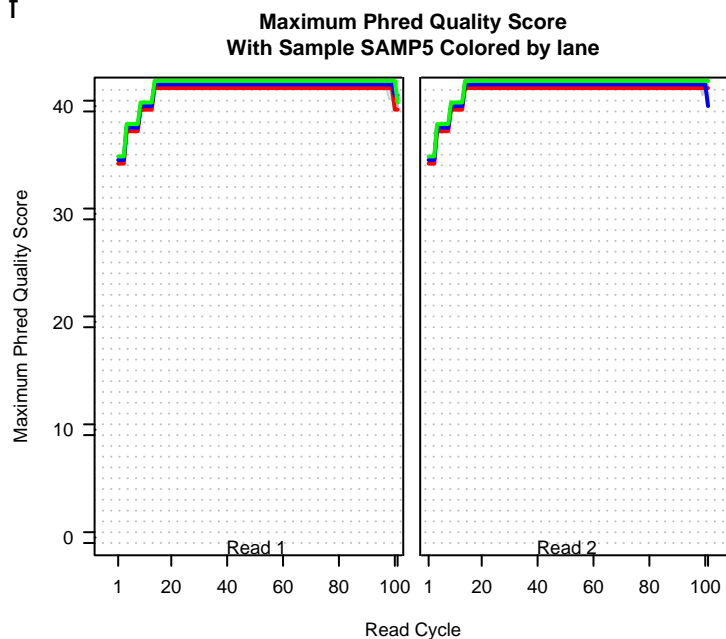
d

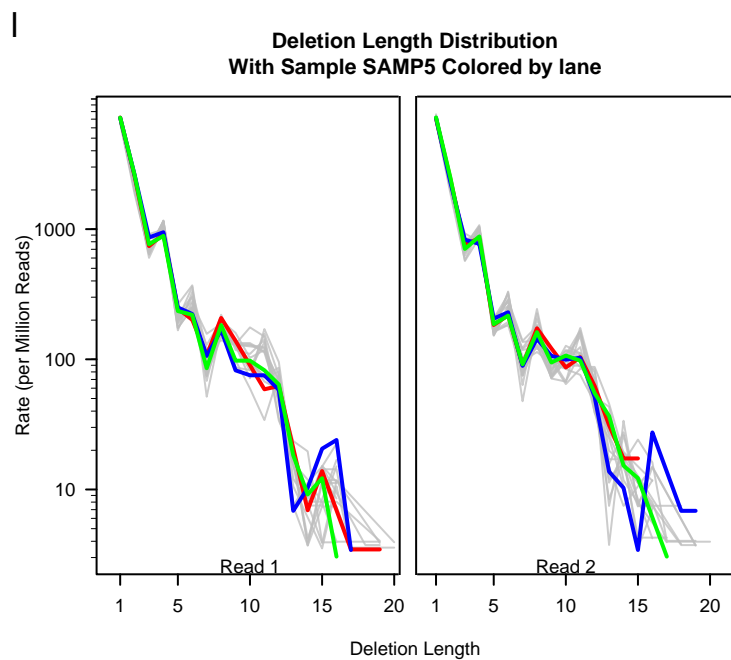
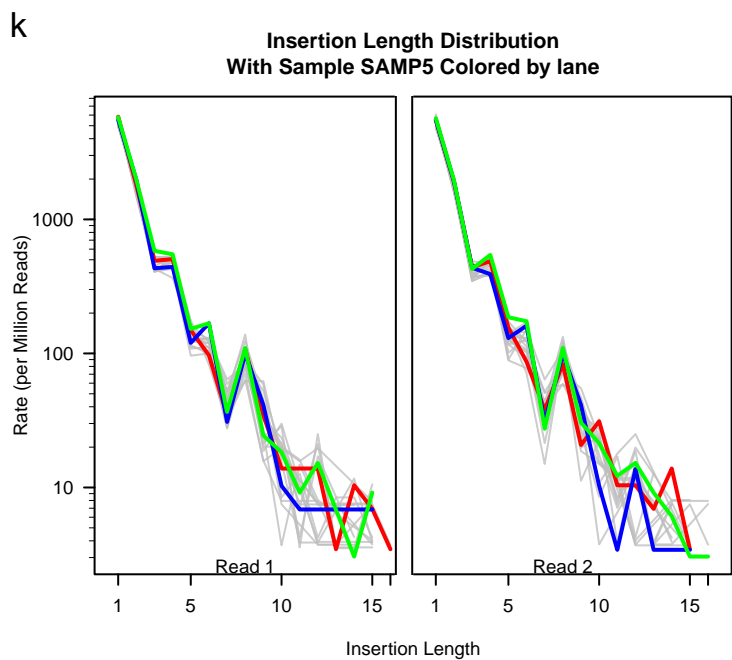
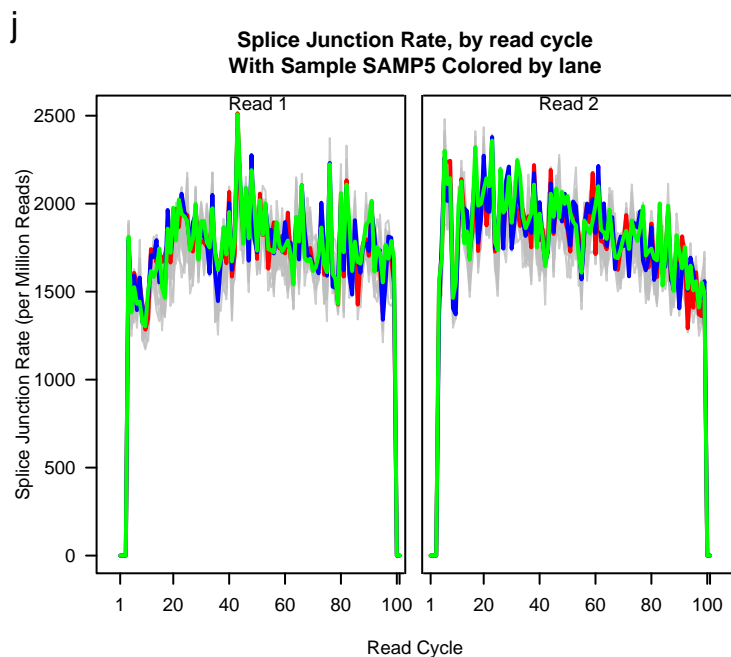
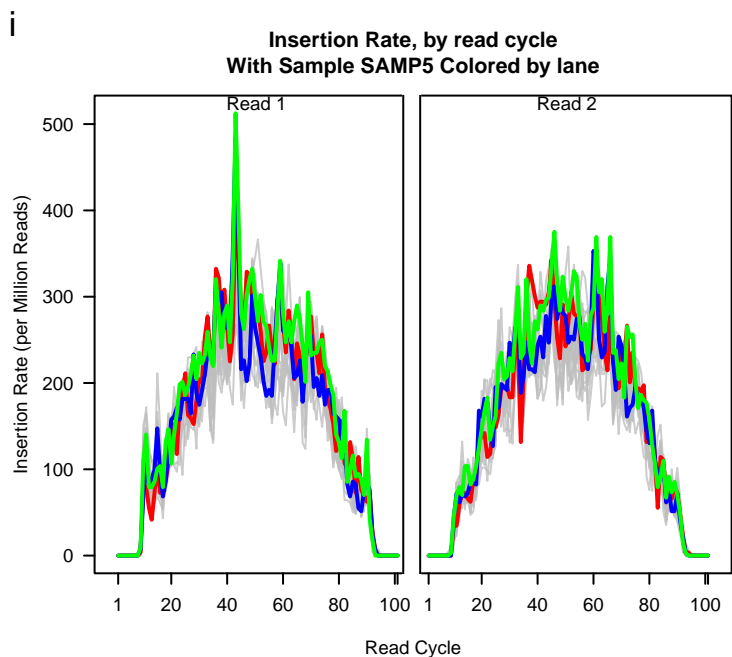
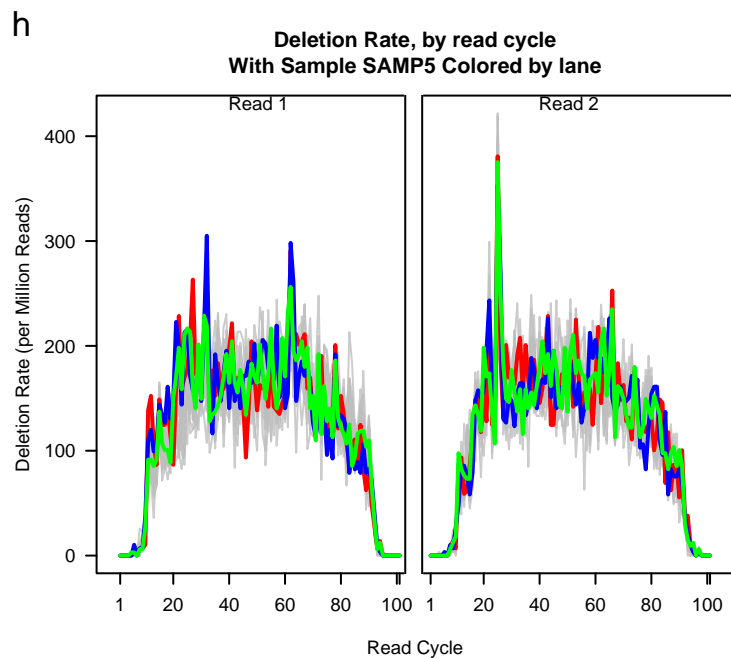
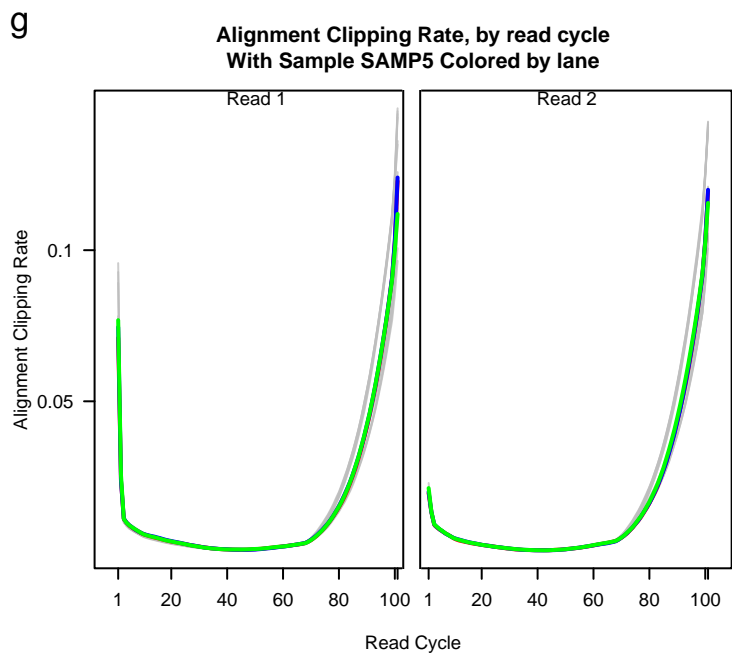


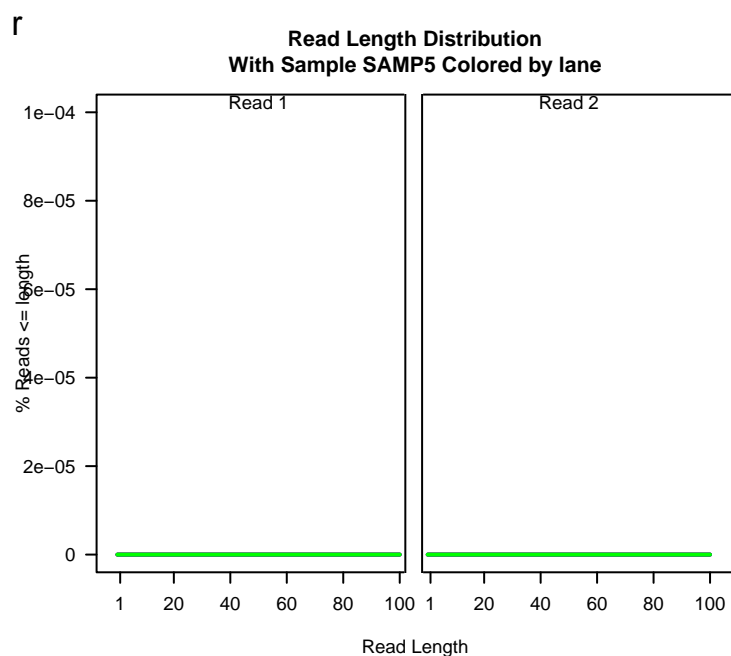
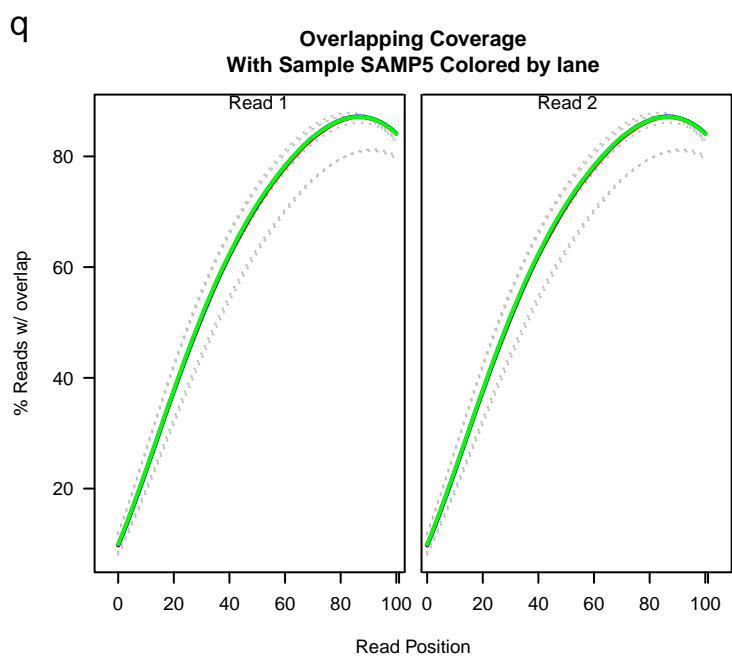
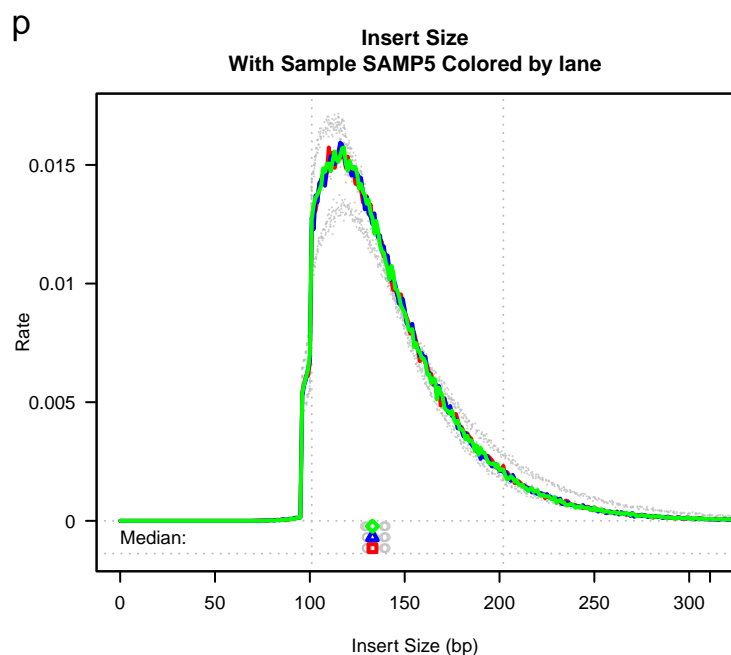
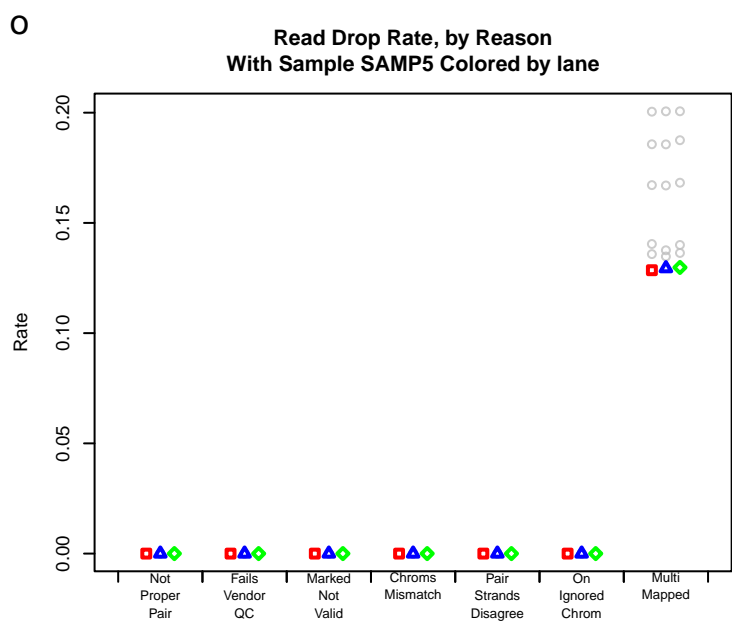
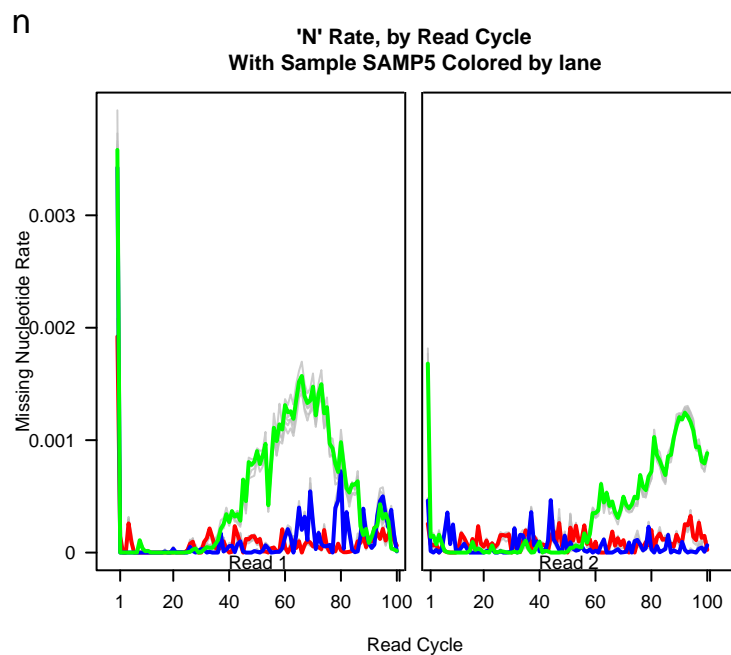
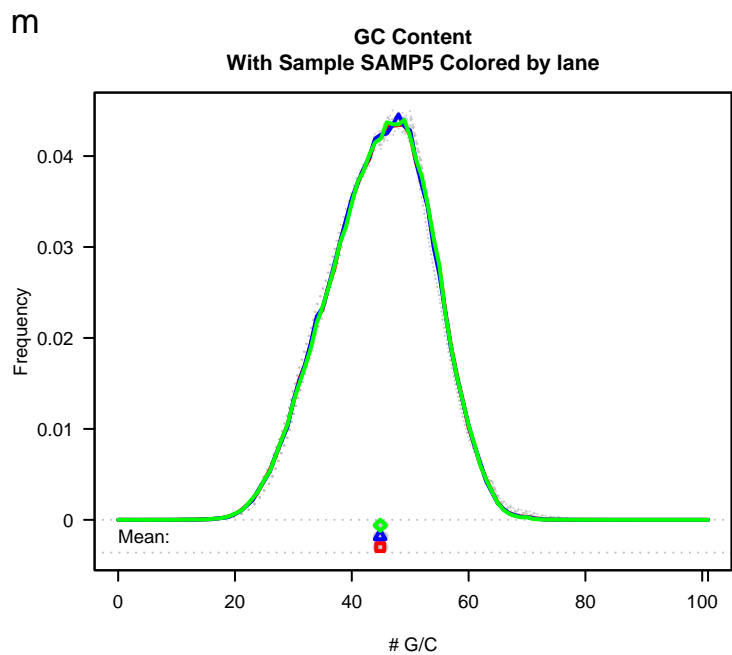
e

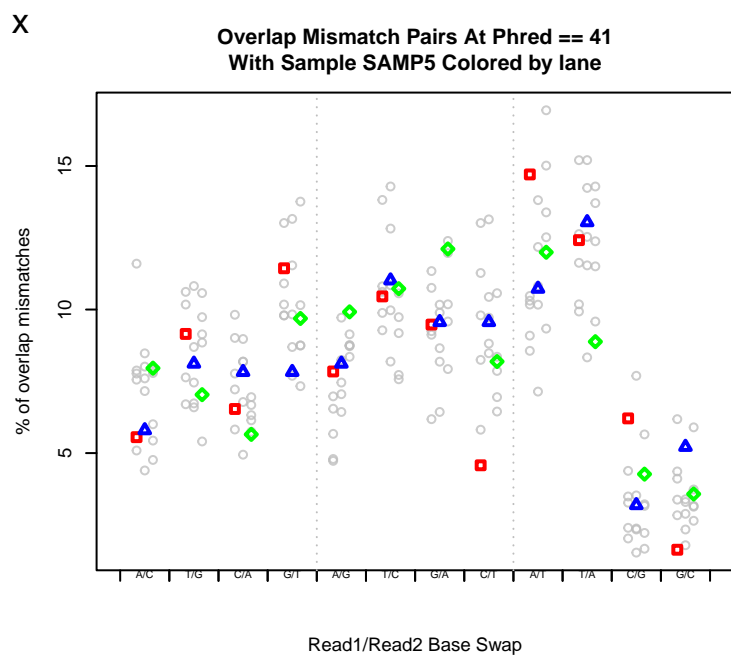
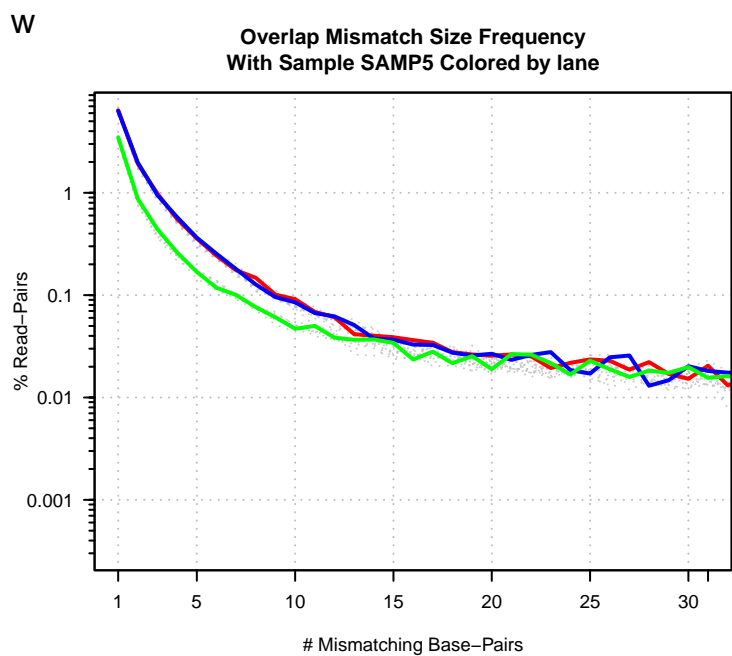
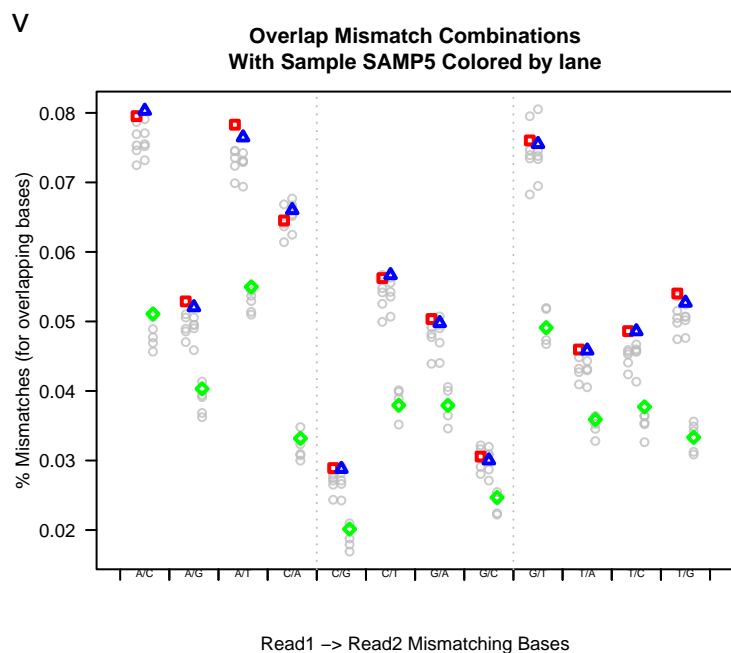
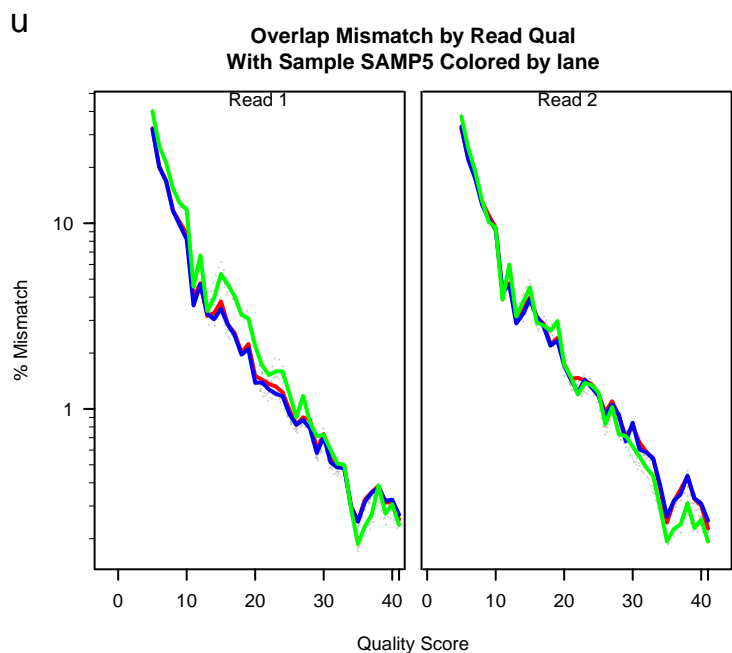
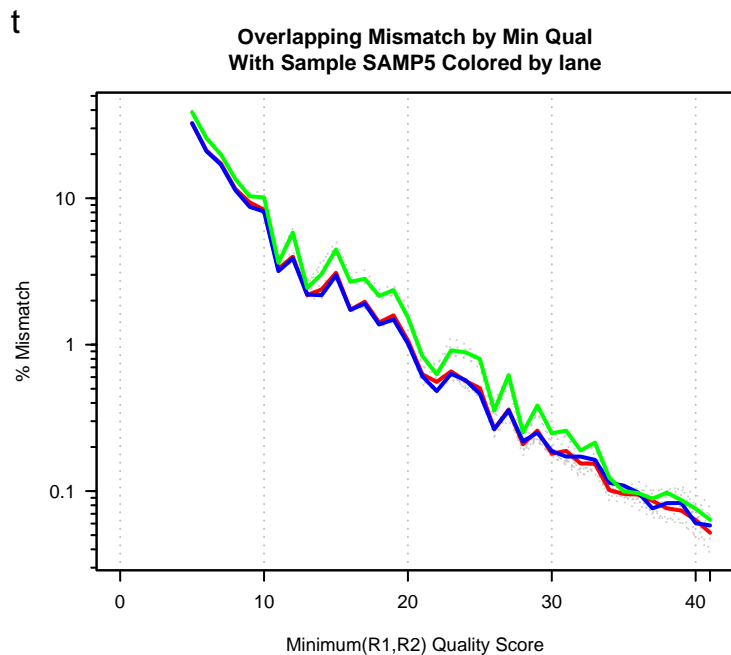
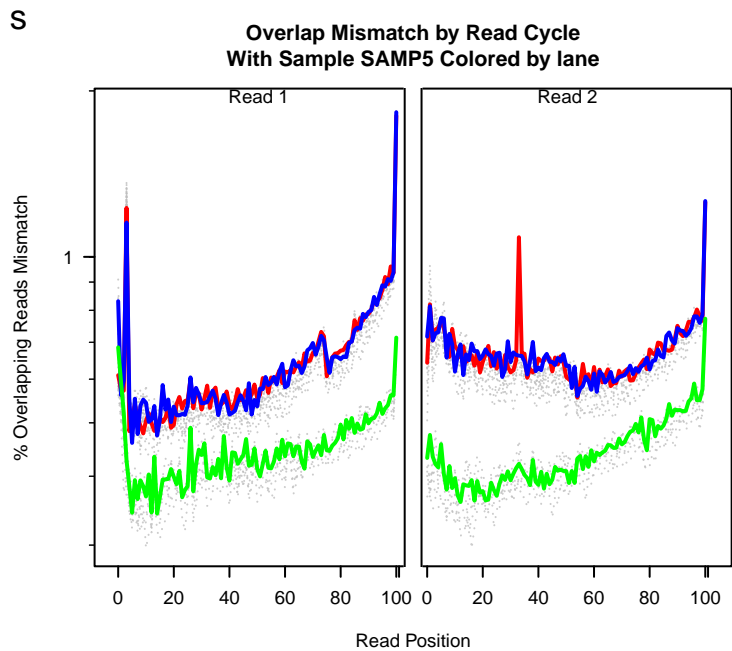


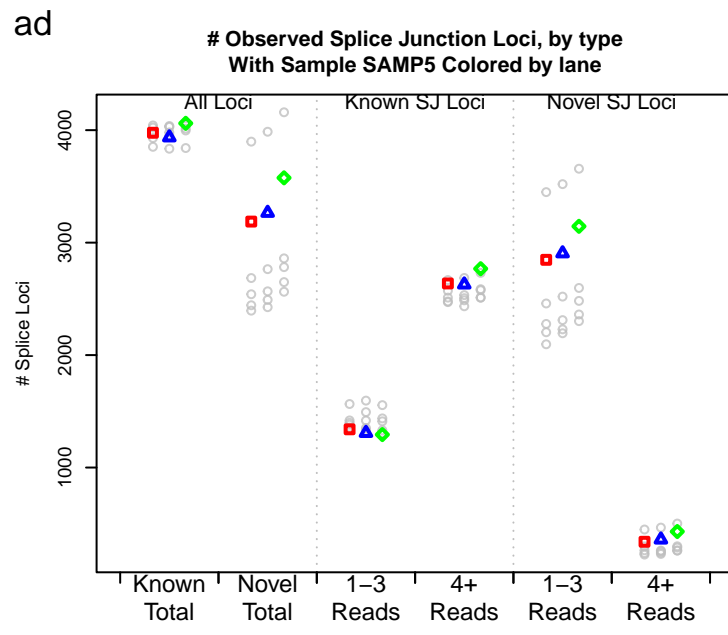
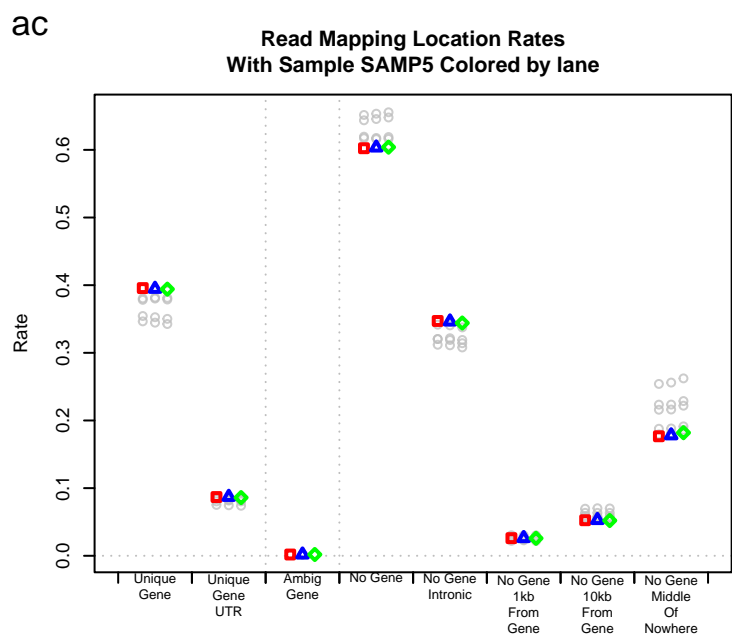
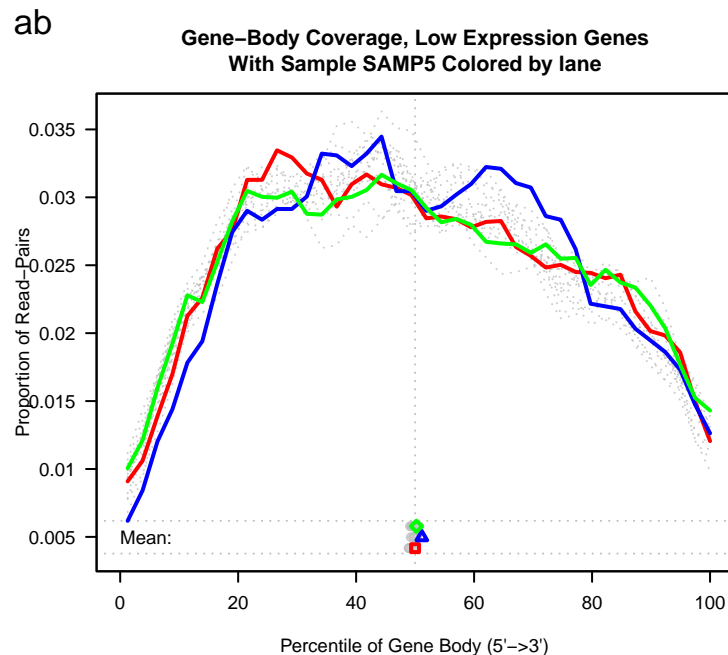
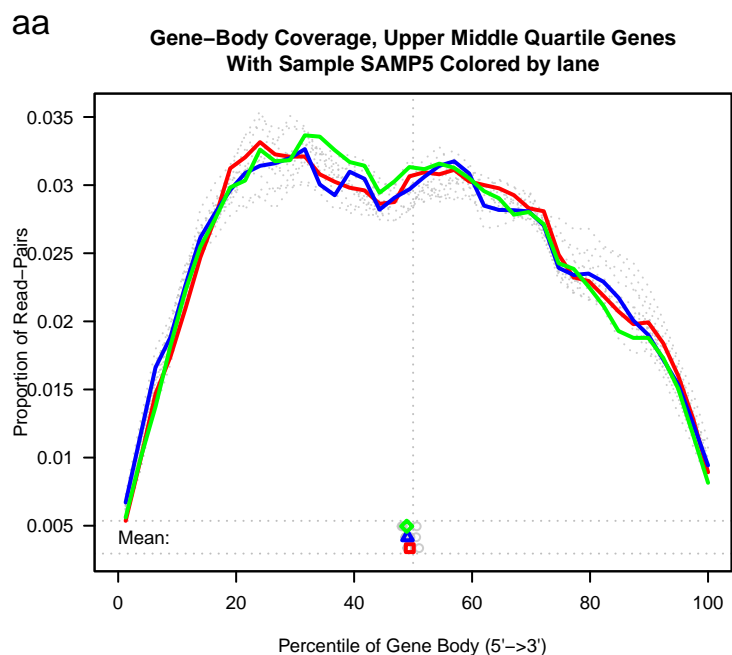
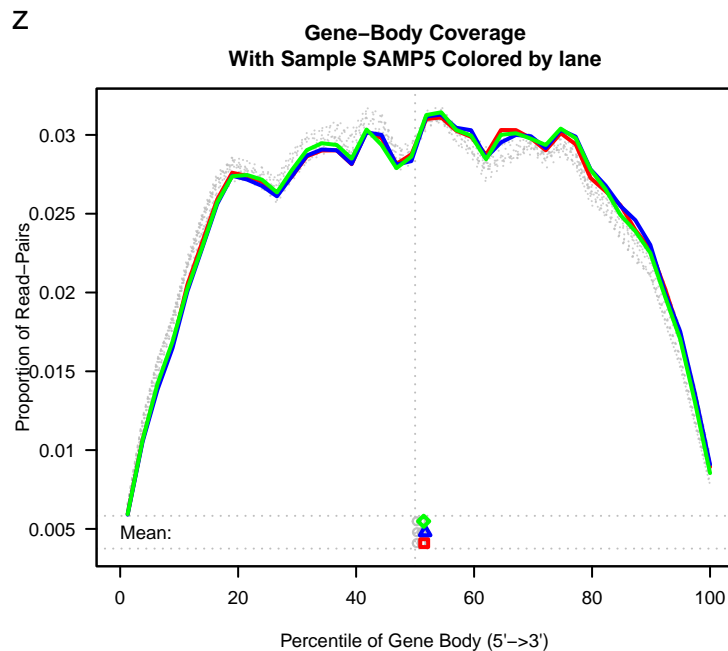
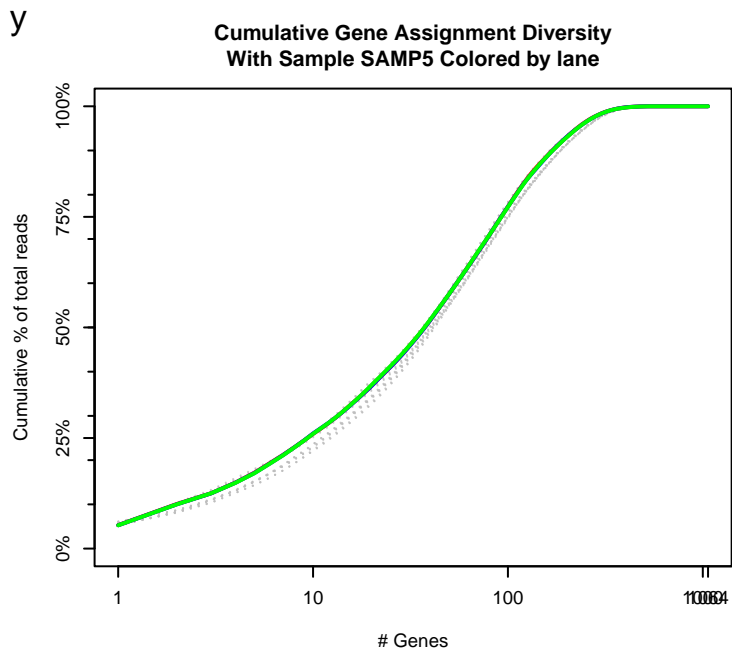
f



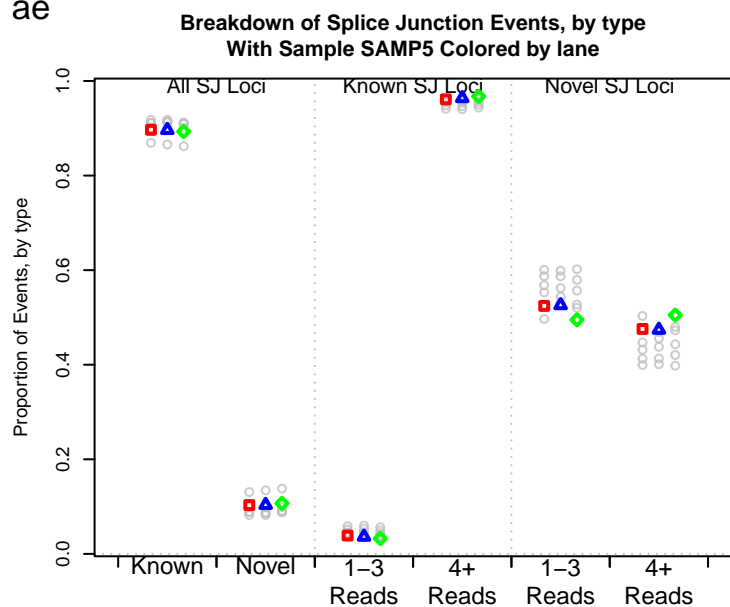




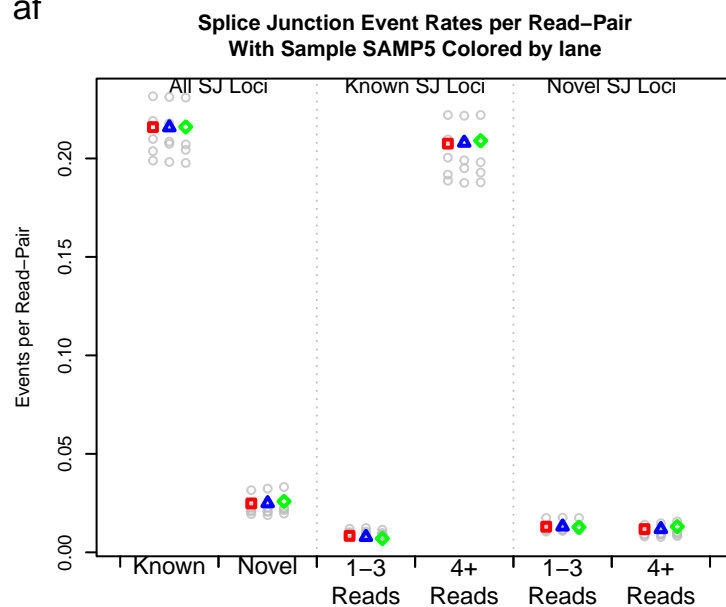




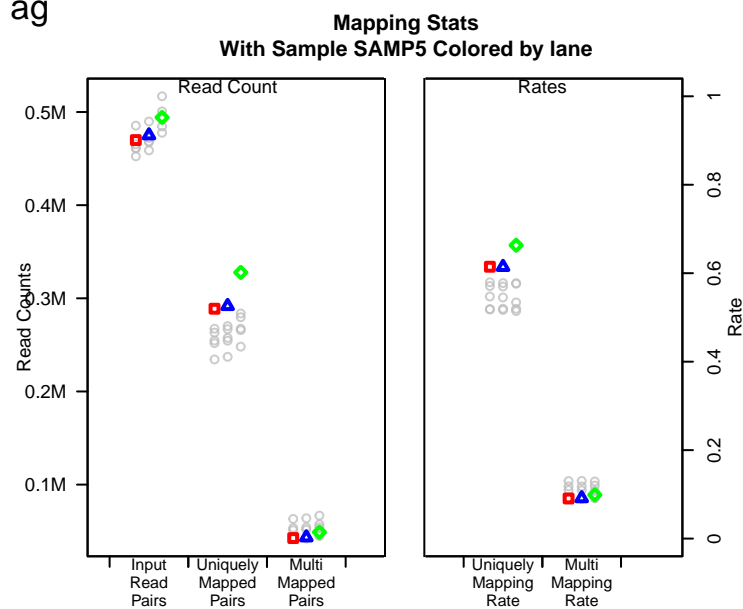
ae



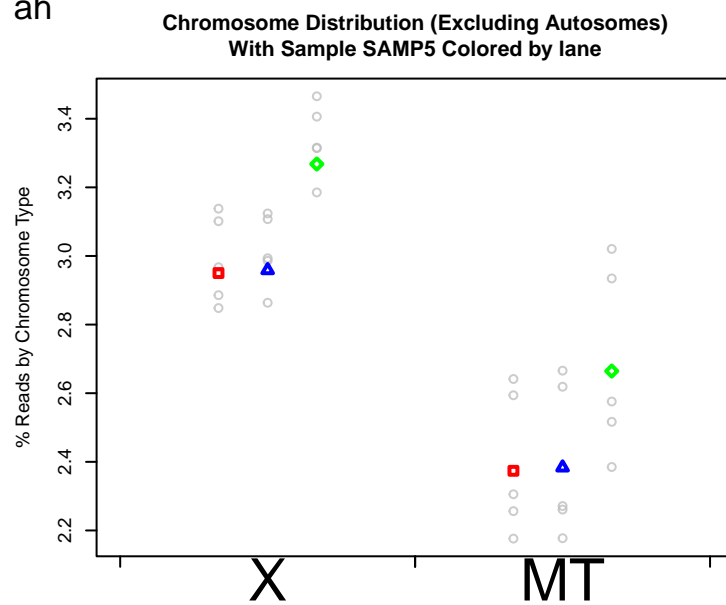
af



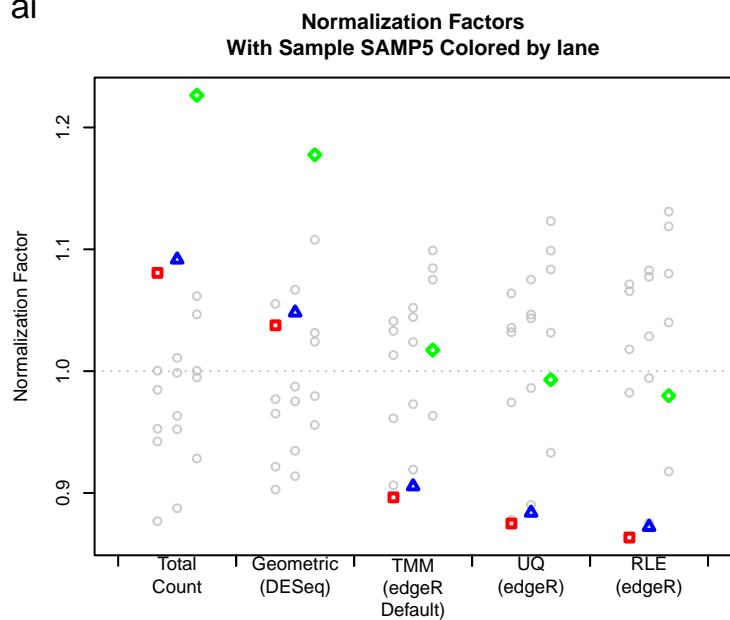
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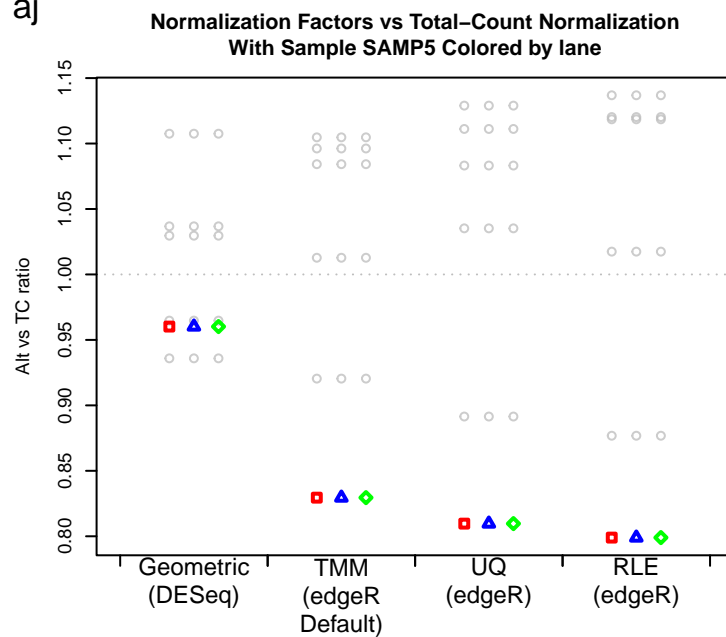
ah



ai

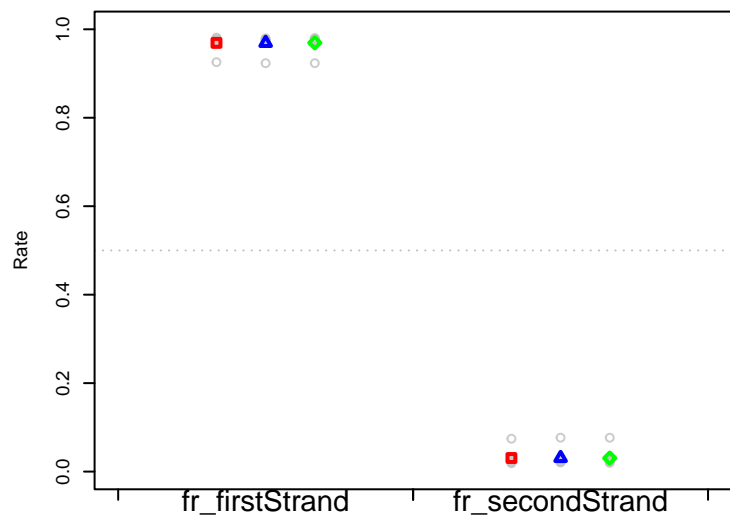


aj



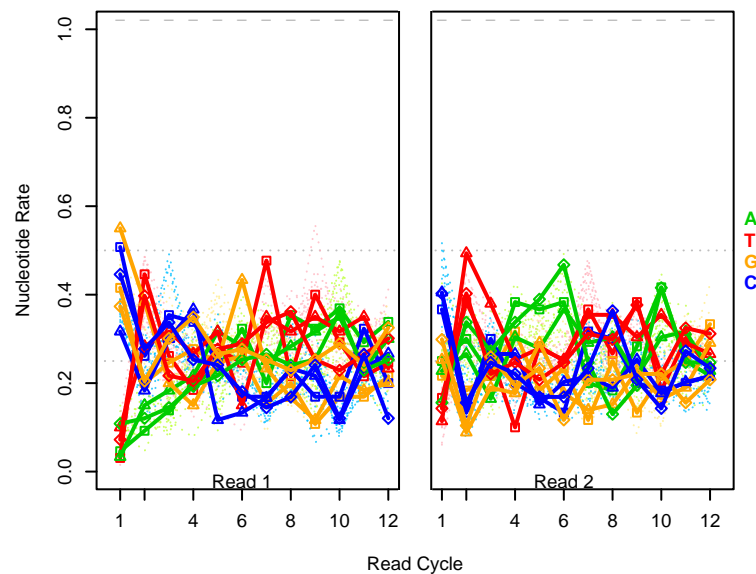
ak

Strandedness Test  
With Sample SAMP5 Colored by lane



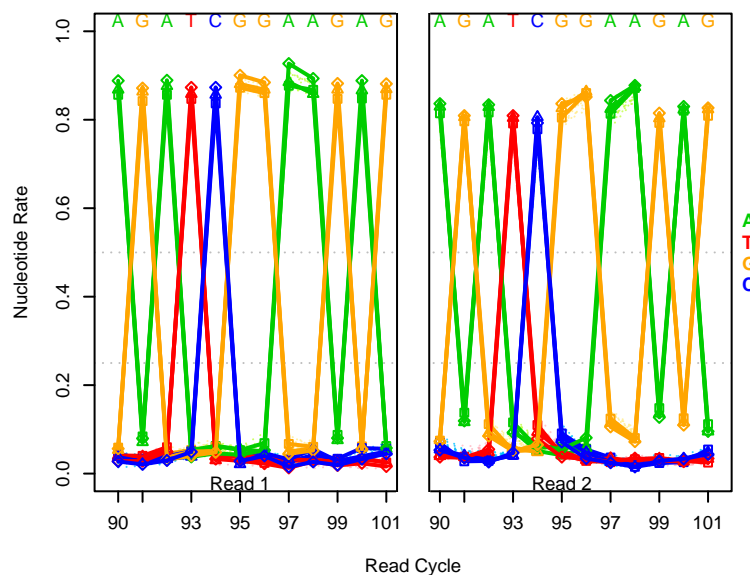
al

Nucleotide Rate by Cycle, Leading Clipped bases (12)  
With Sample SAMP5 in Bold



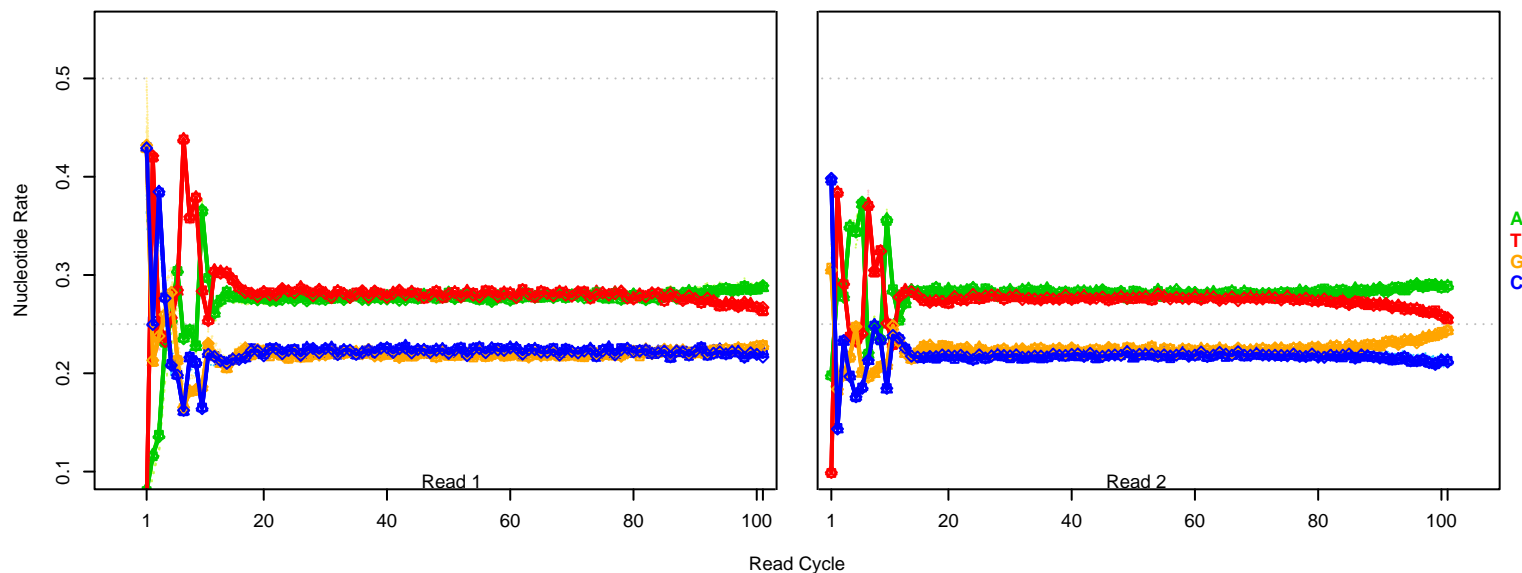
am

Nucleotide Rate by Cycle, Trailing Clipped bases (12)  
With Sample SAMP5 in Bold



an

Raw Nucleotide Rate by Cycle  
With Sample SAMP5 in Bold



ao

Nucleotide Rate by Cycle, Aligned bases only  
With Sample SAMP5 in Bold

