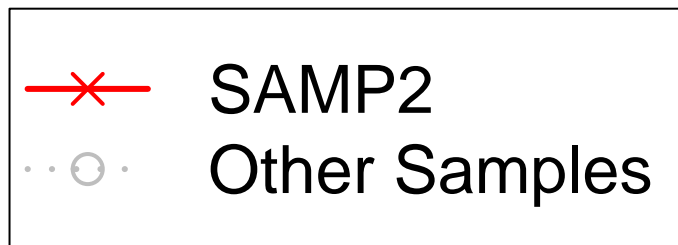
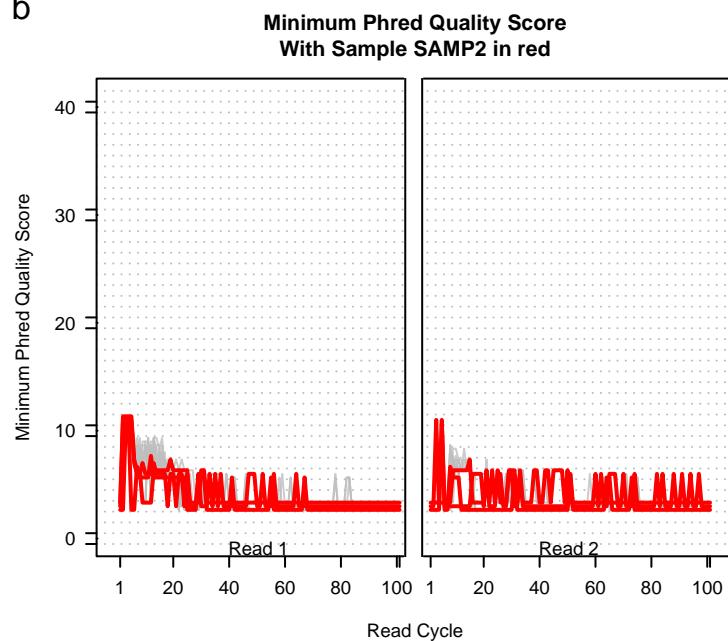


a

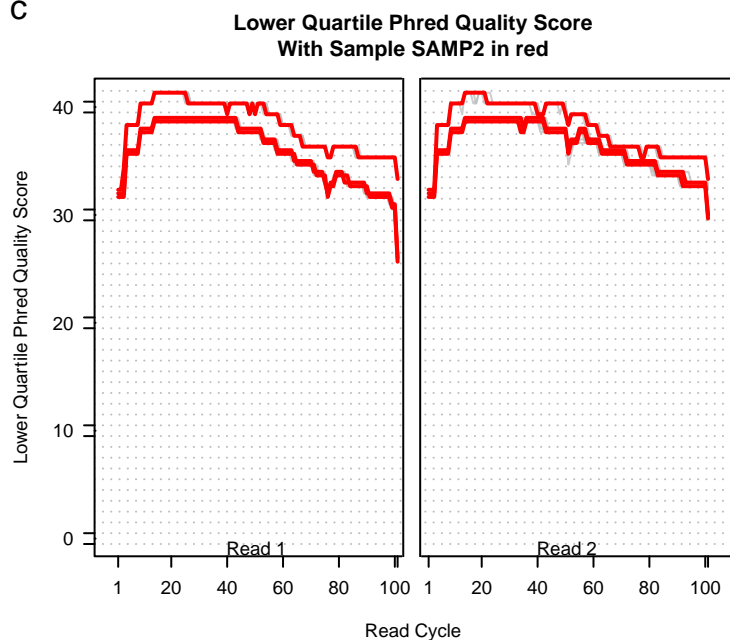
Sample Highlight: SAMP2



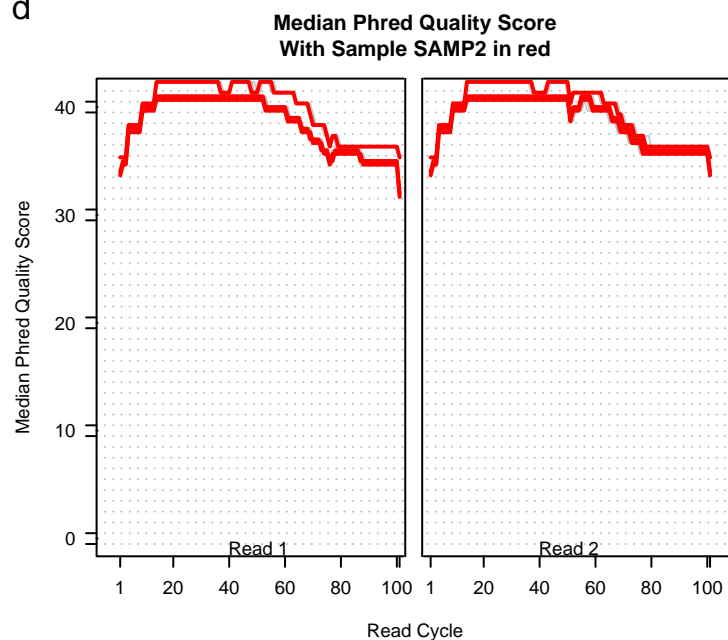
b



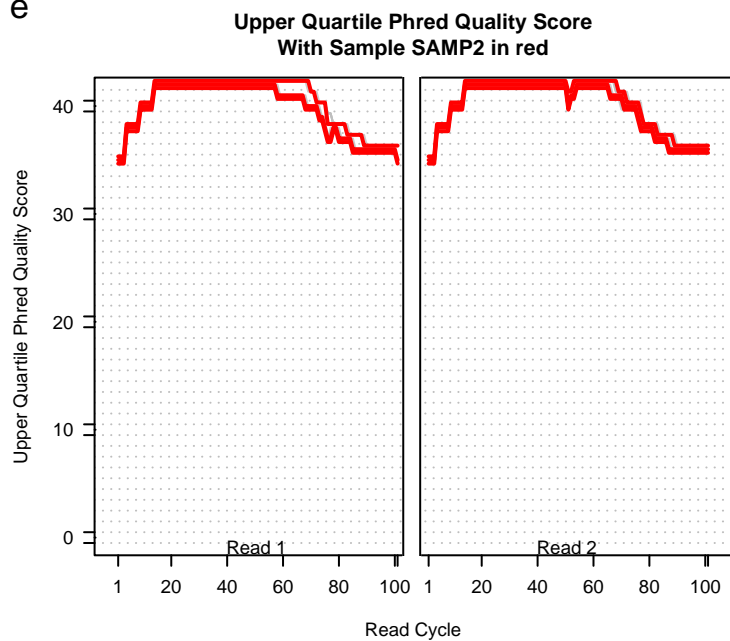
c



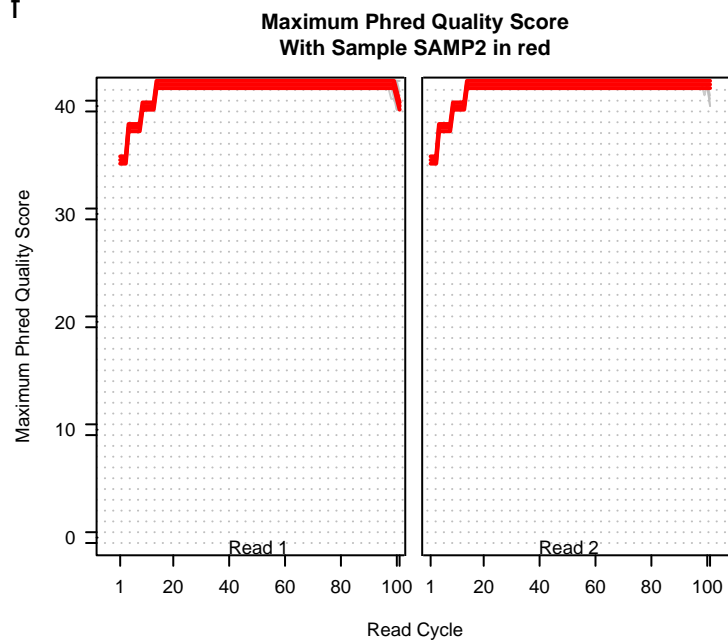
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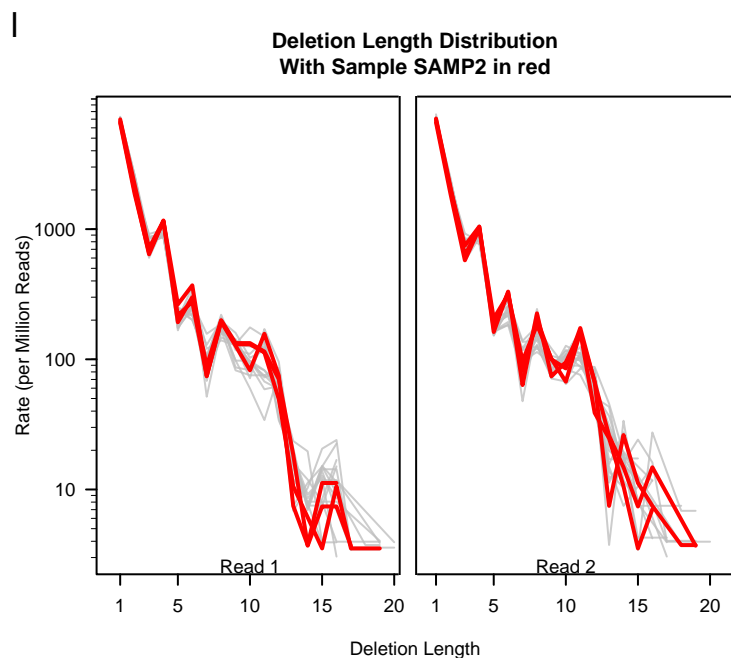
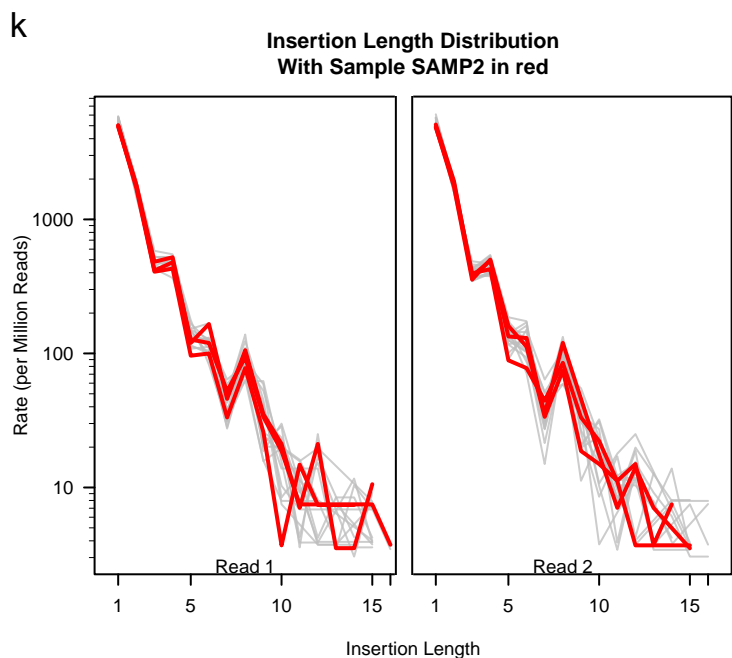
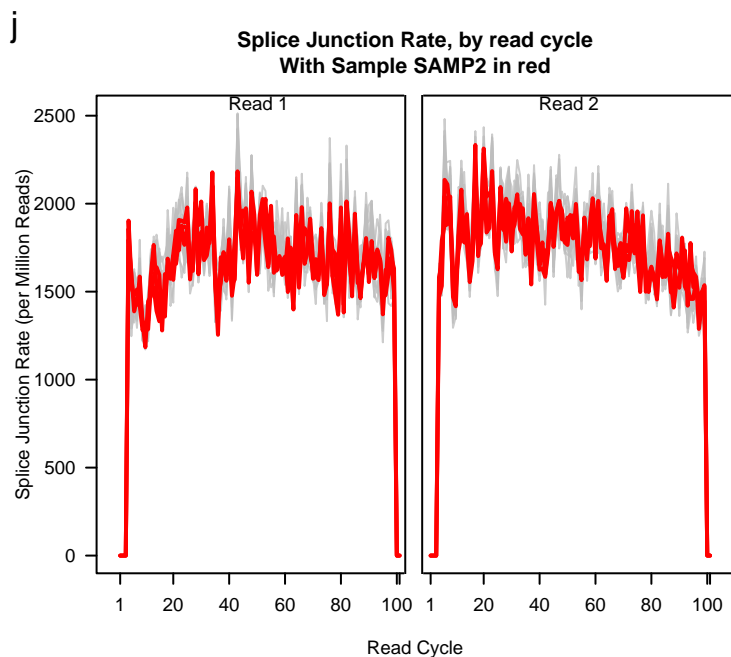
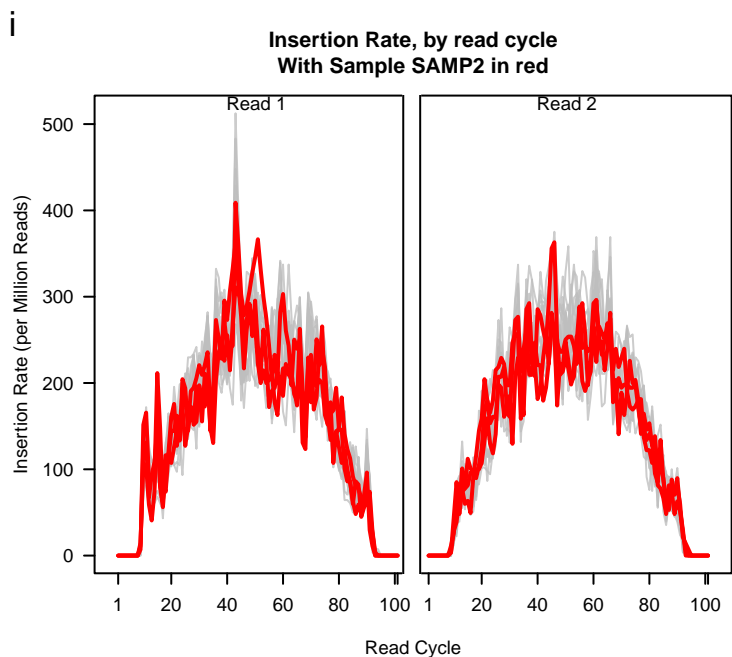
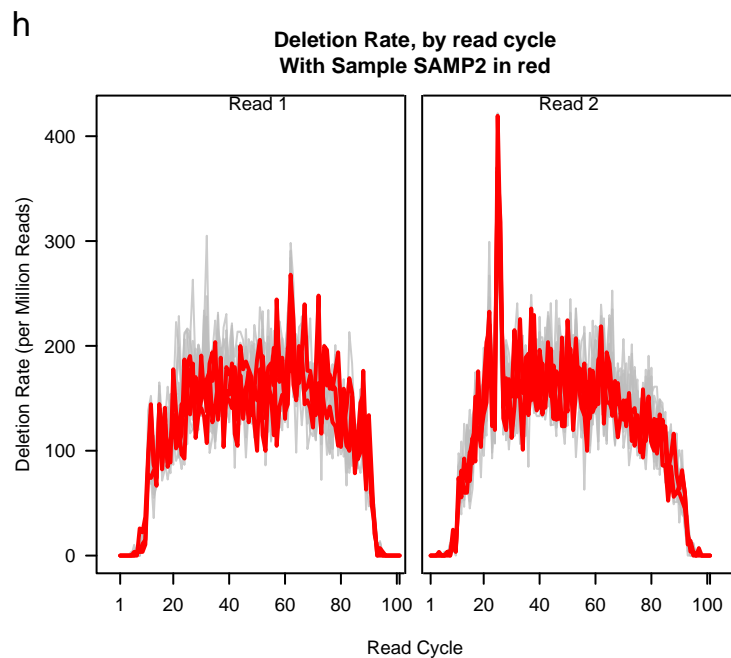
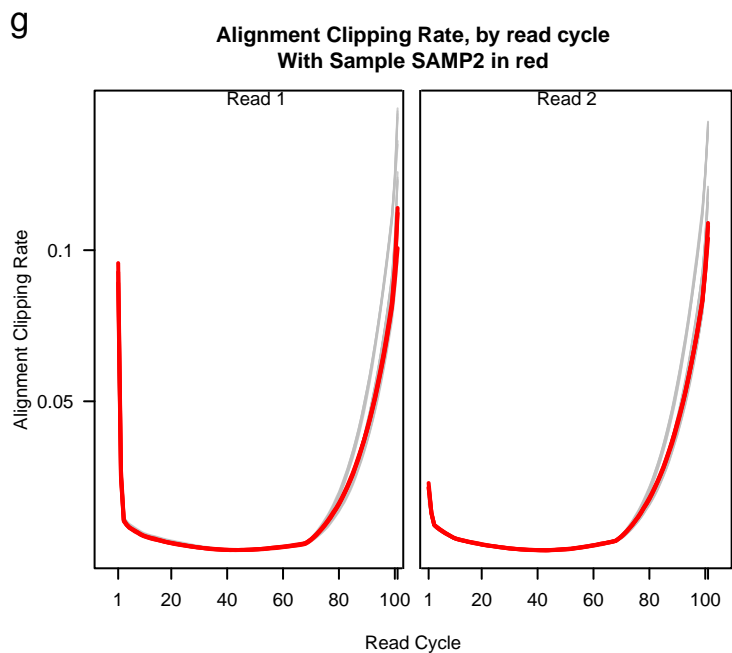


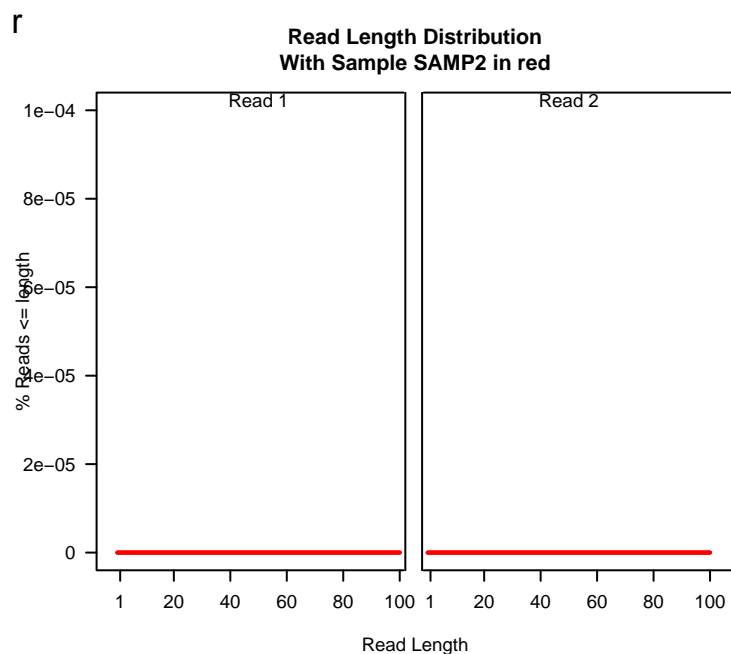
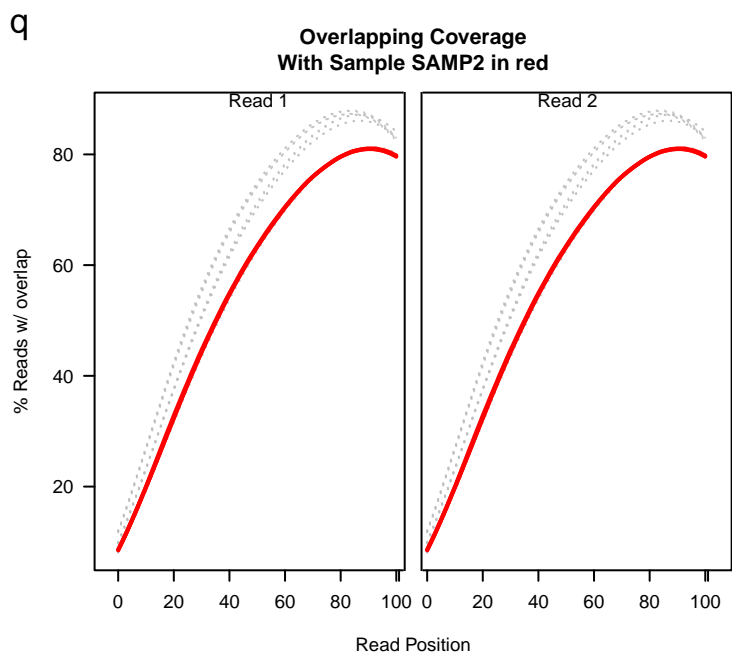
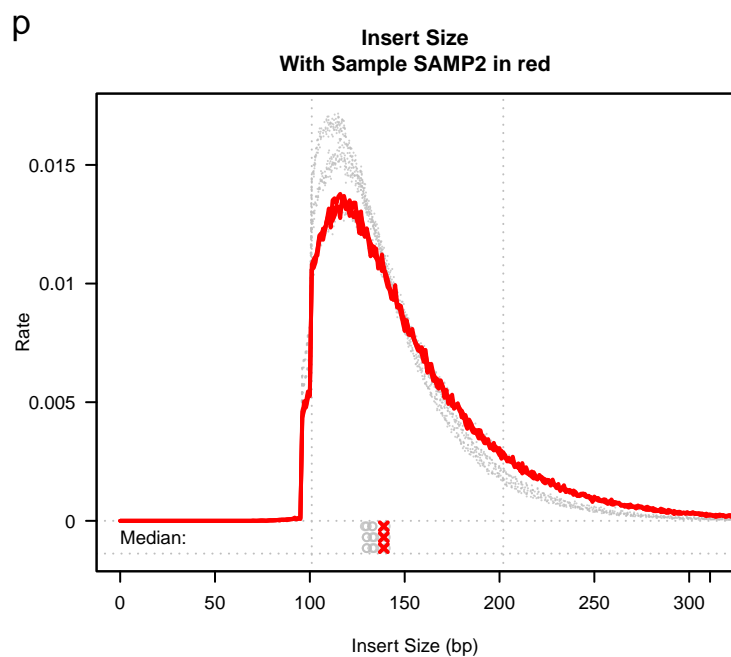
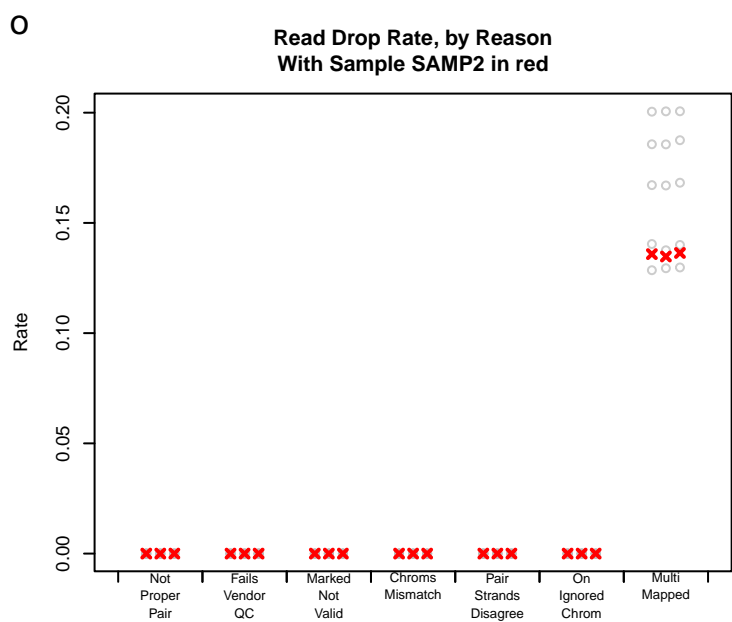
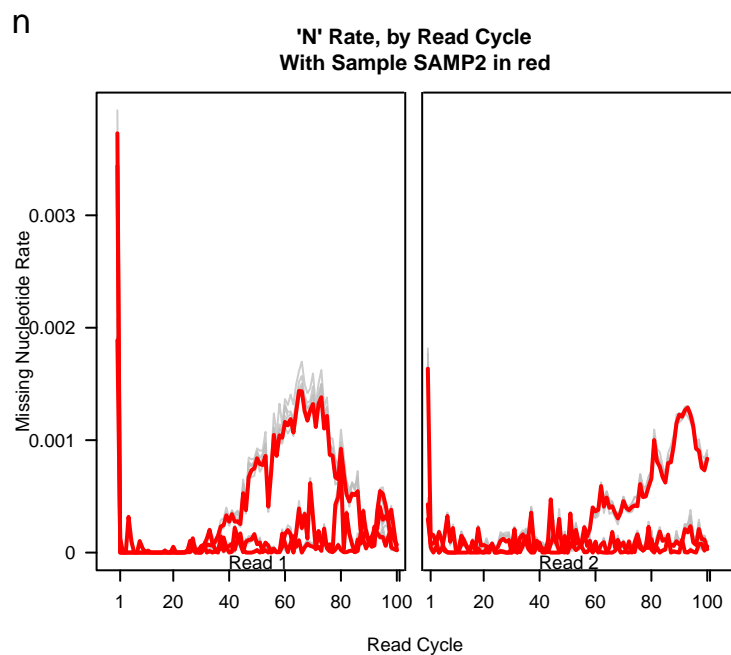
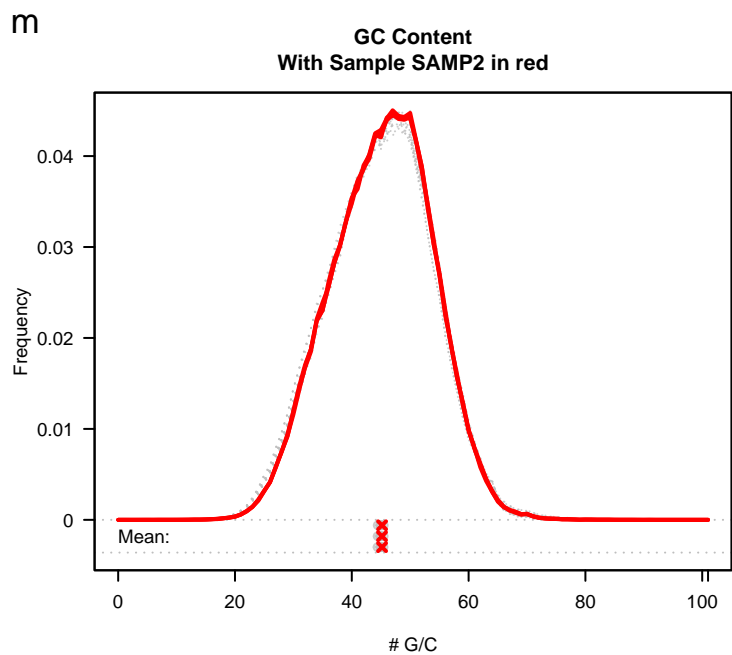
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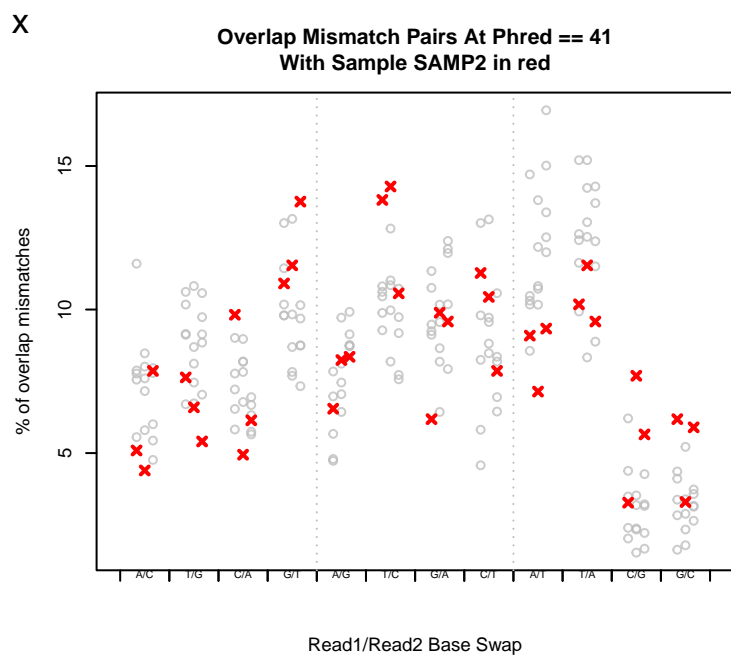
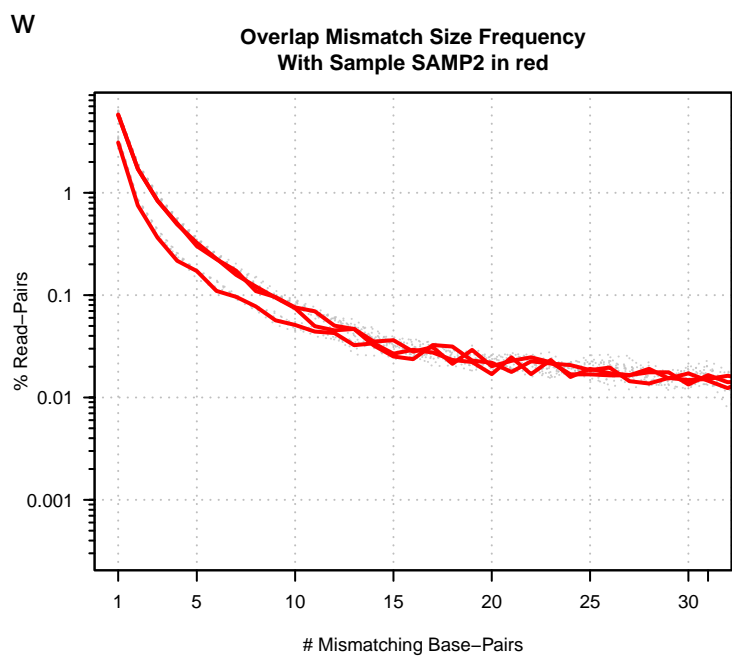
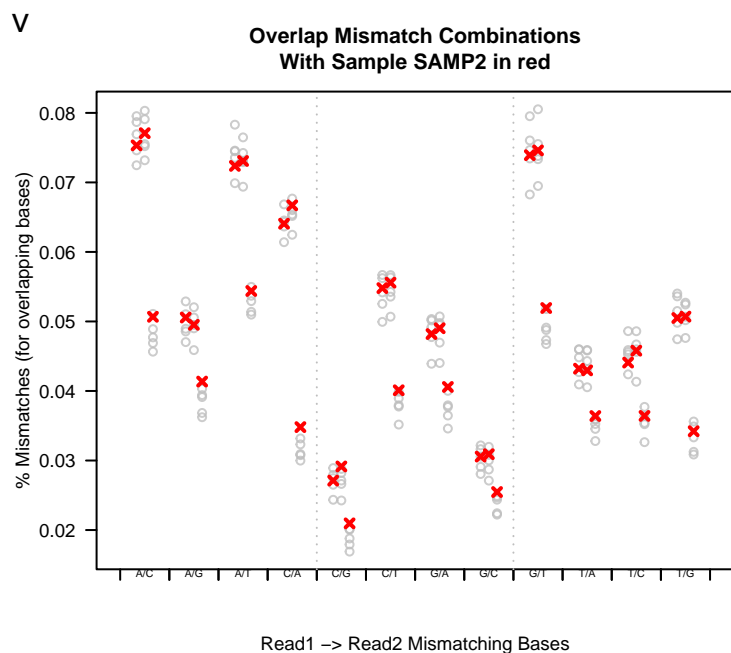
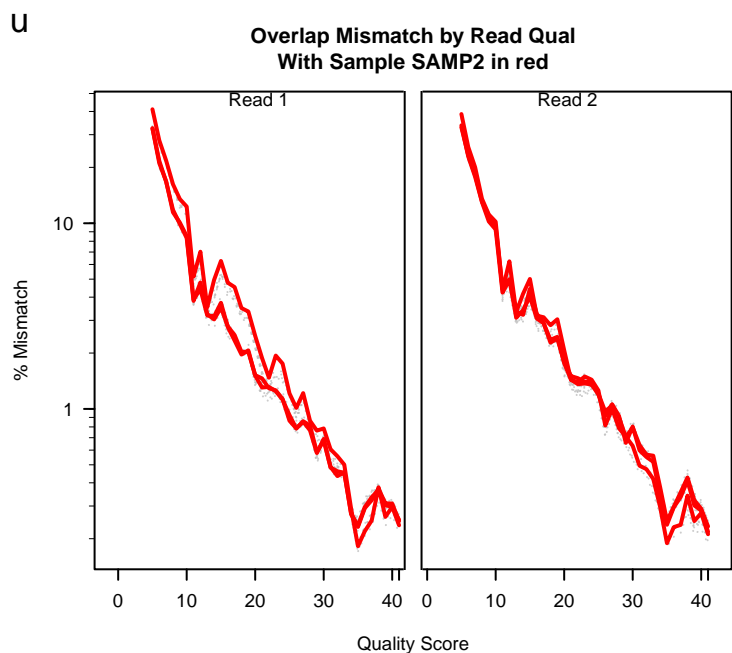
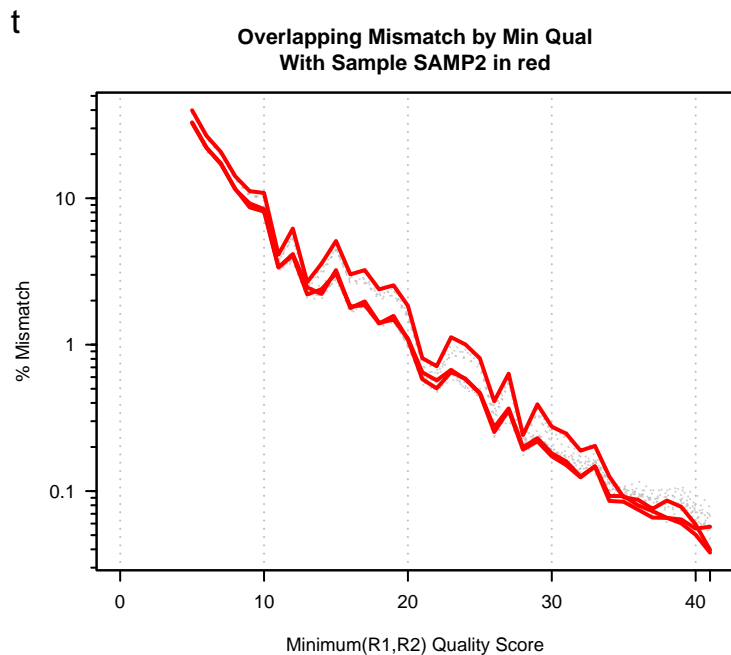
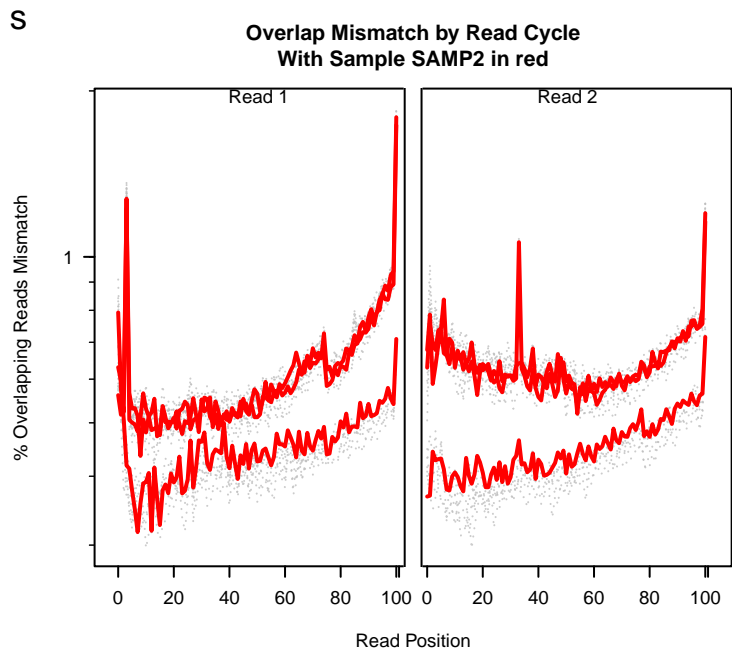


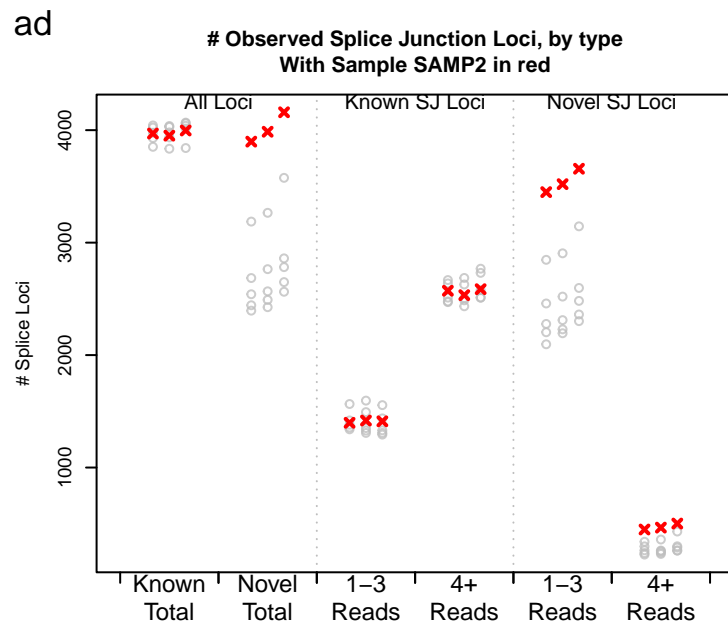
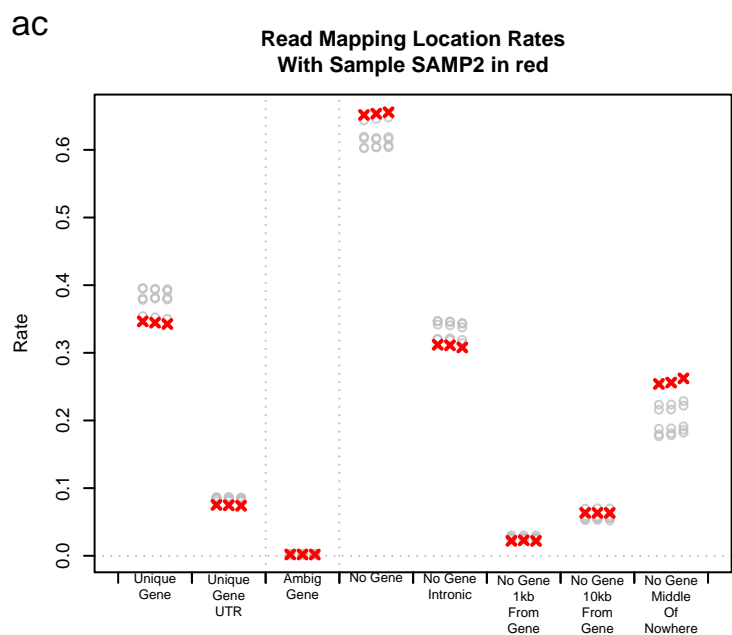
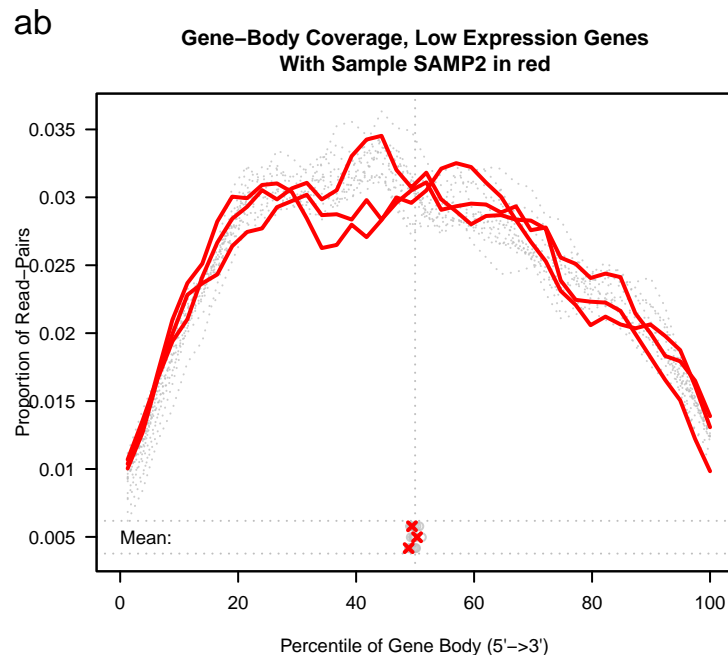
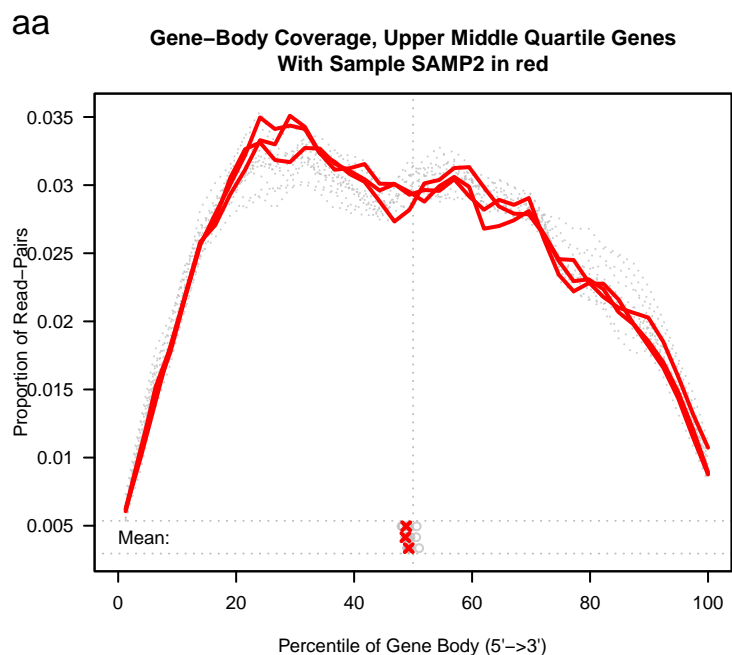
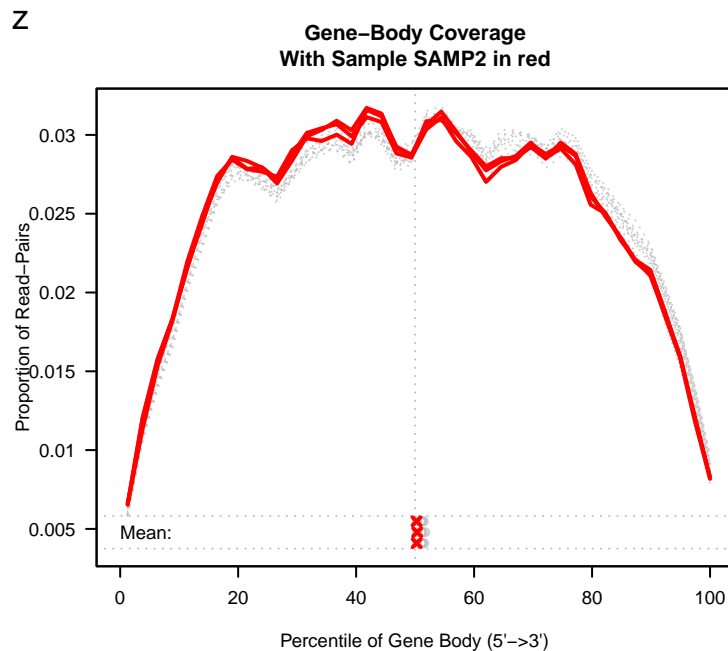
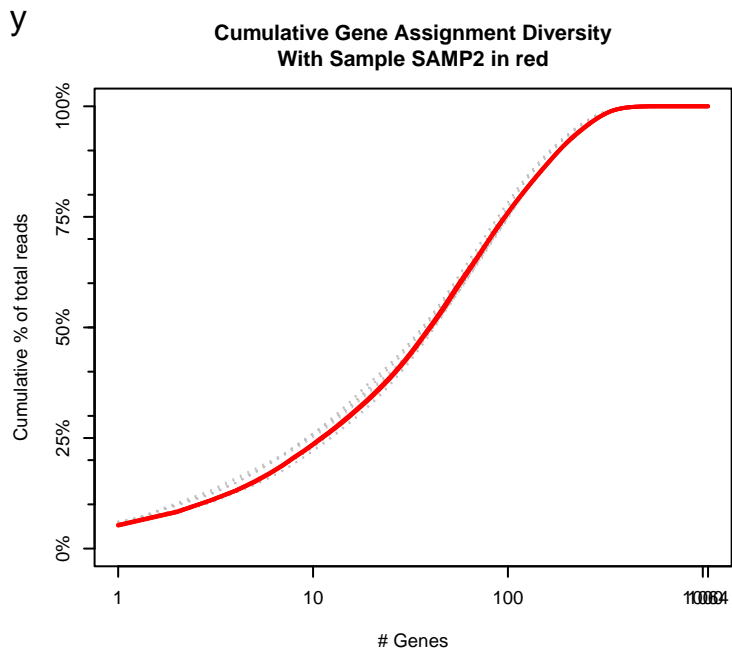
f



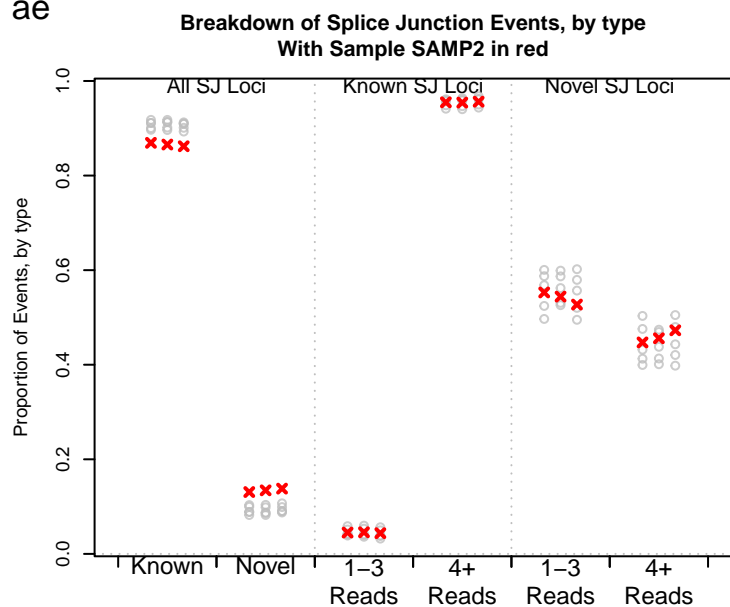




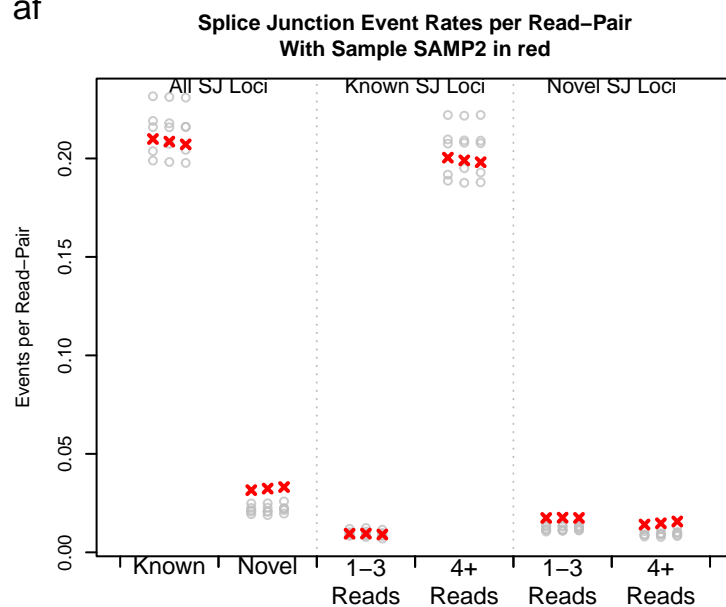




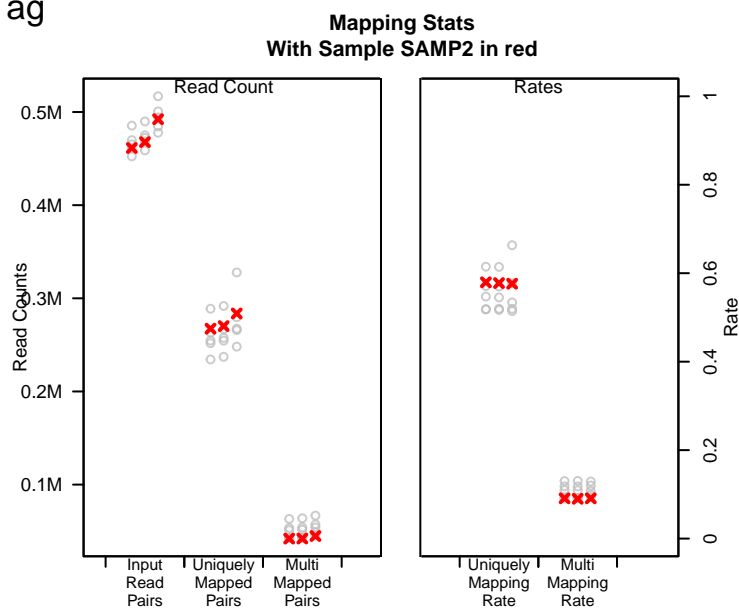
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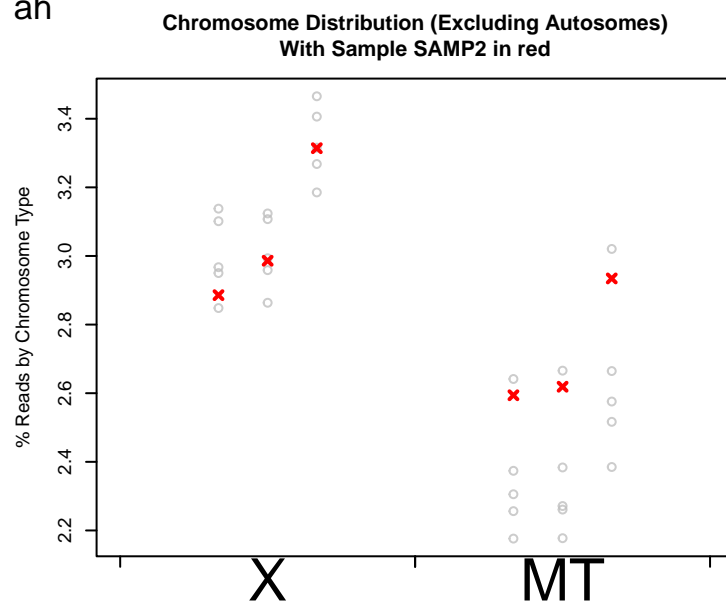
af



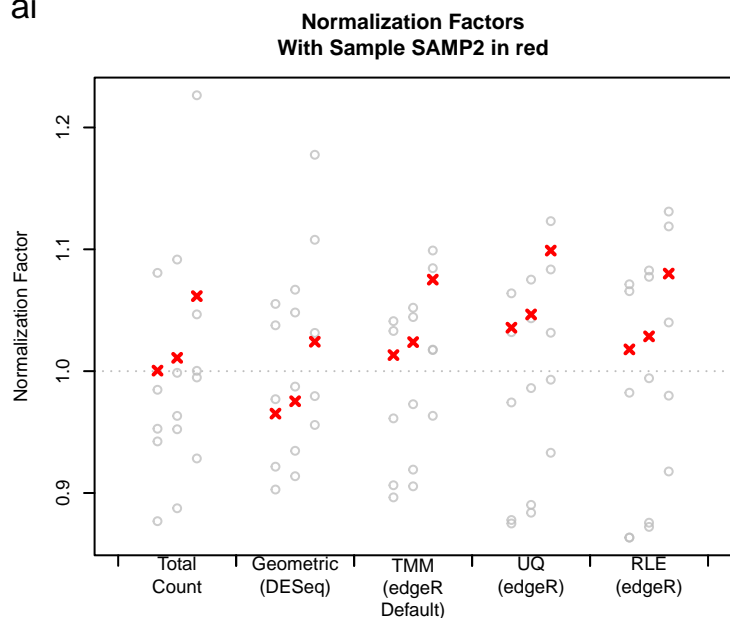
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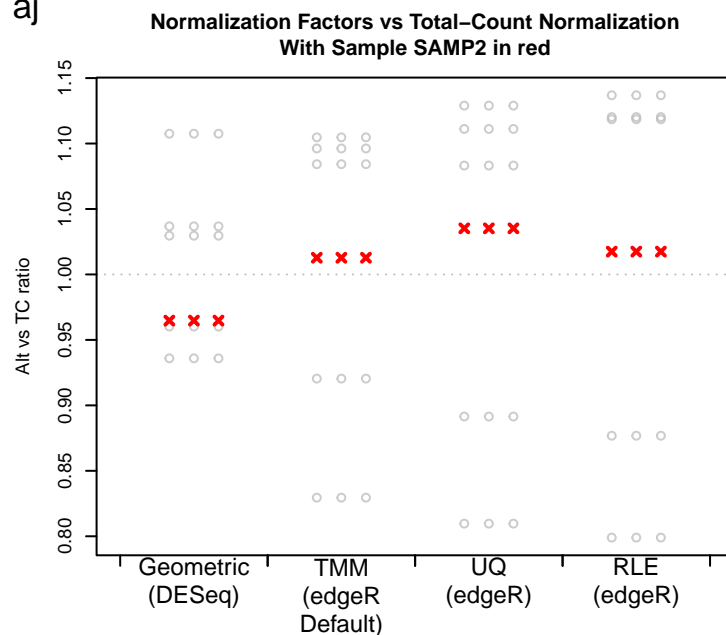
ah



ai

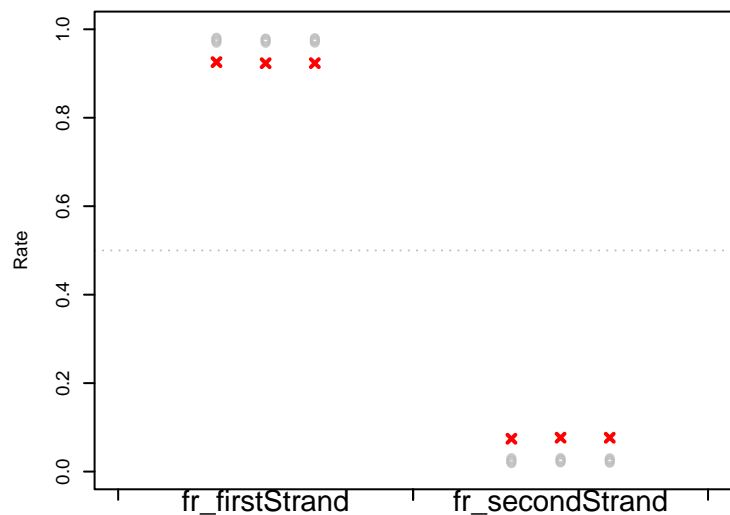


aj



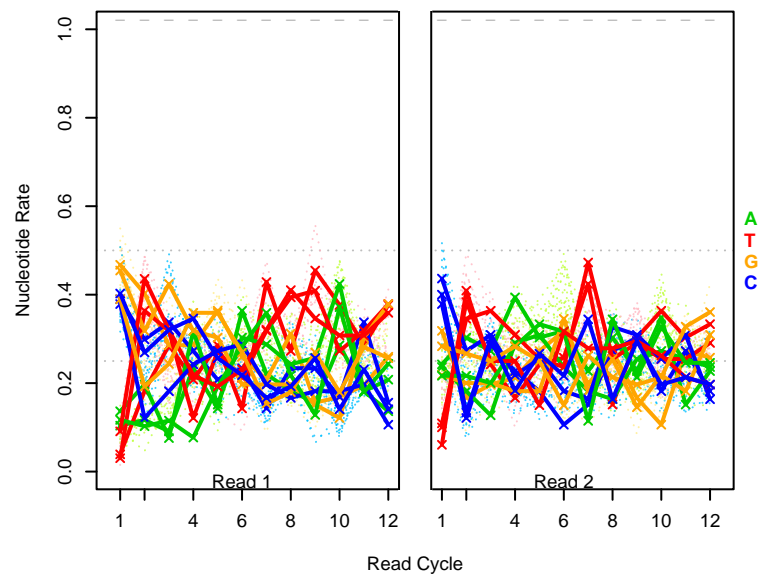
ak

Strandedness Test
With Sample SAMP2 in red



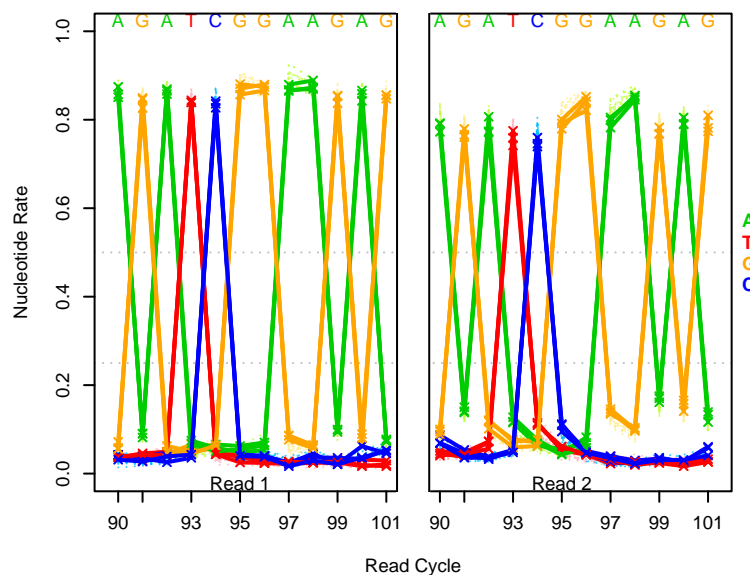
al

Nucleotide Rate by Cycle, Leading Clipped bases (12)
With Sample SAMP2 in red



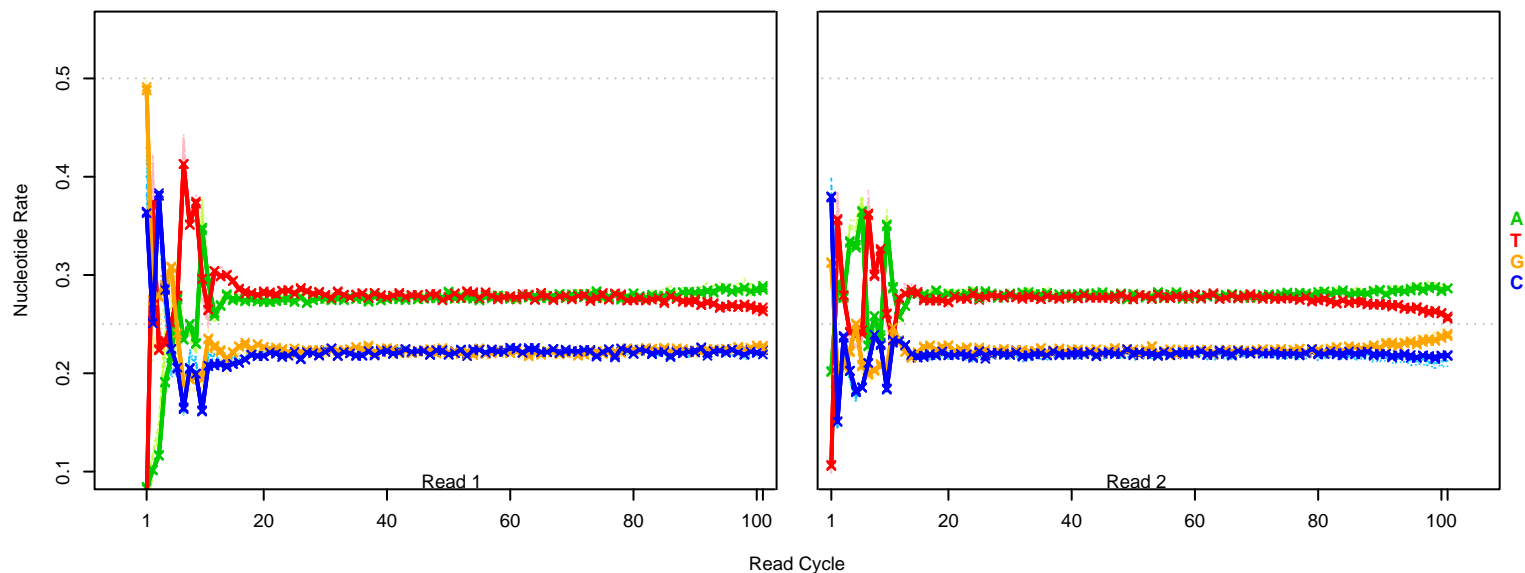
am

Nucleotide Rate by Cycle, Trailing Clipped bases (12)
With Sample SAMP2 in red



an

Raw Nucleotide Rate by Cycle
With Sample SAMP2 in red



ao

Nucleotide Rate by Cycle, Aligned bases only
With Sample SAMP2 in red

