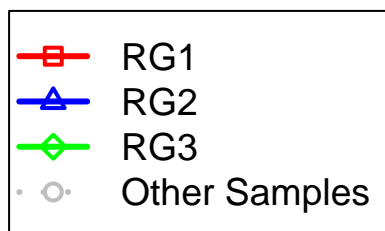
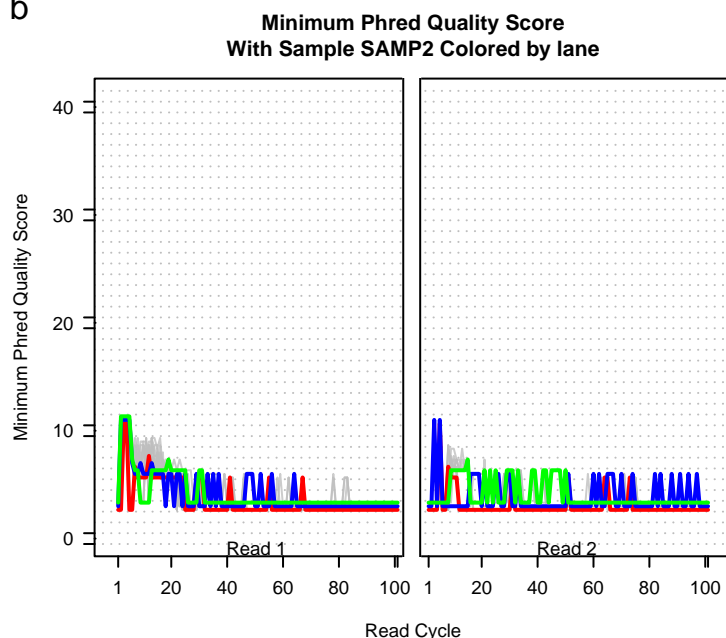


a

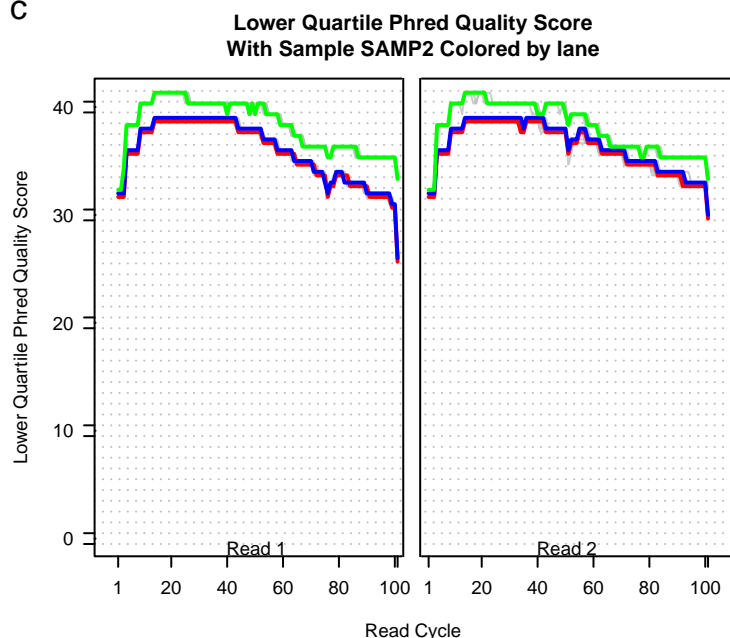
Sample Highlight: SAMP2 Colored by Lane



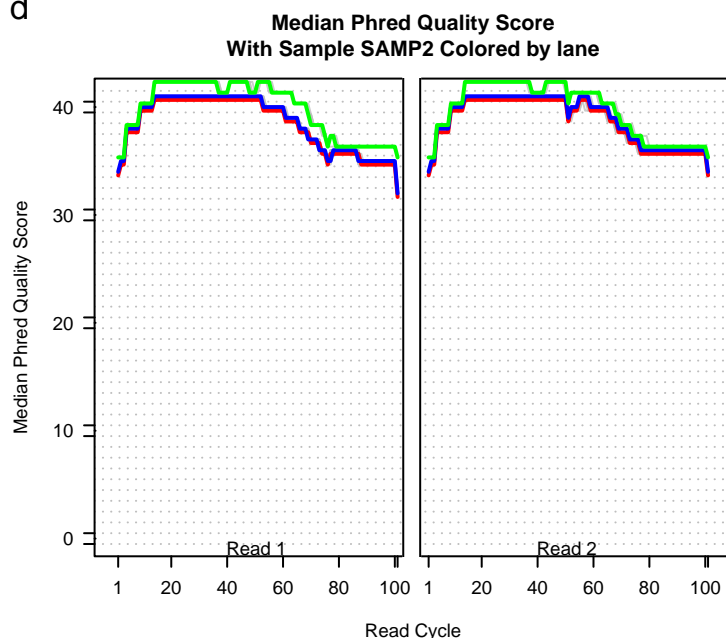
b



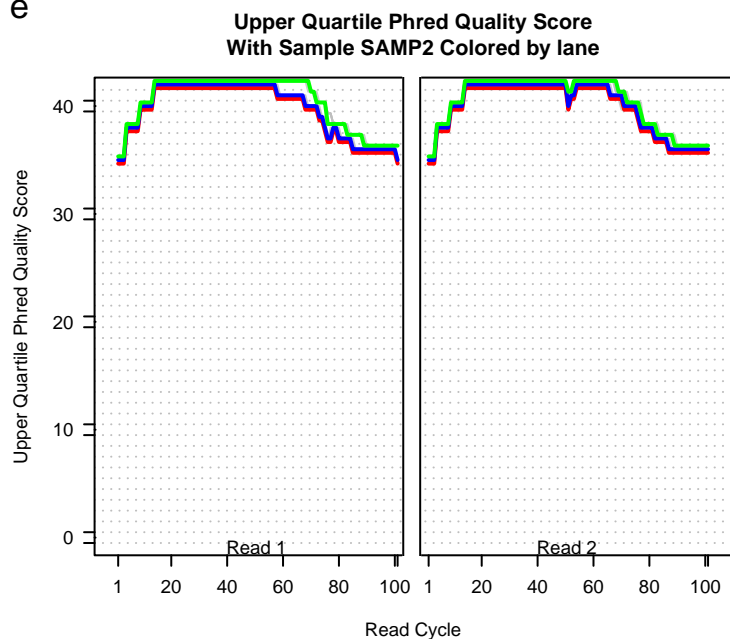
c



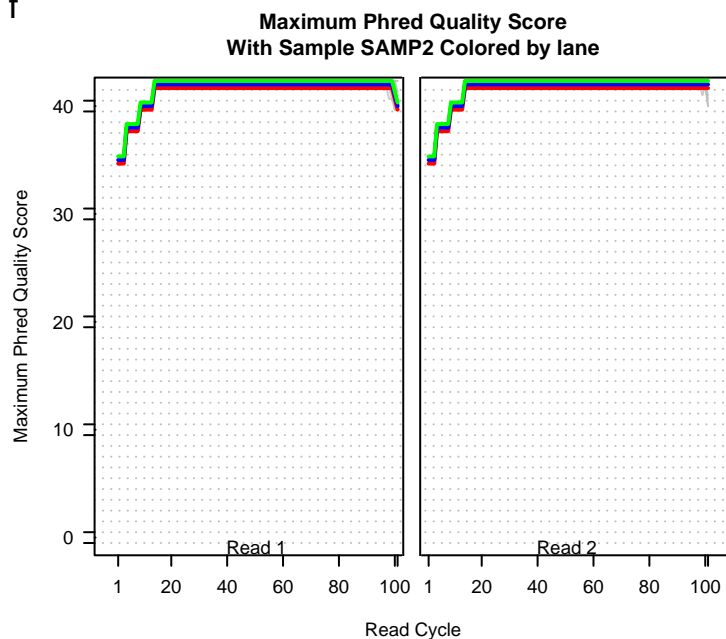
d

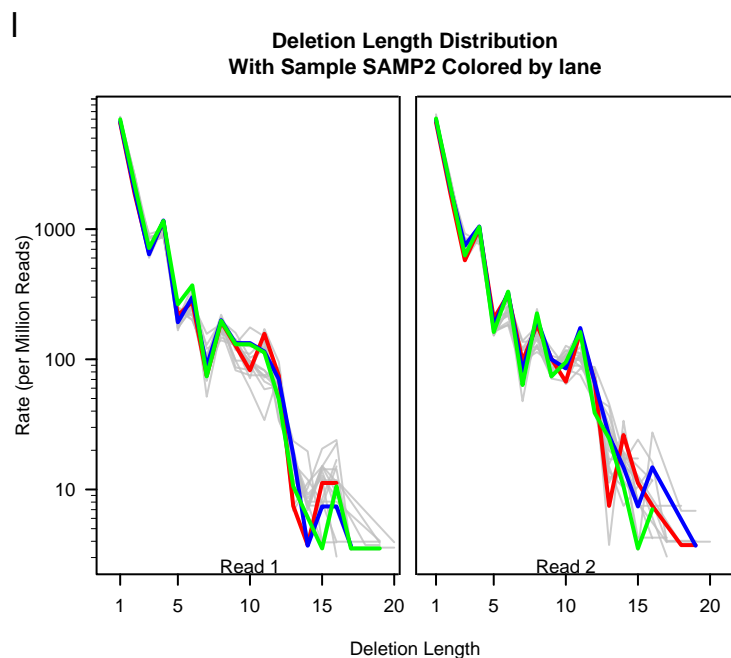
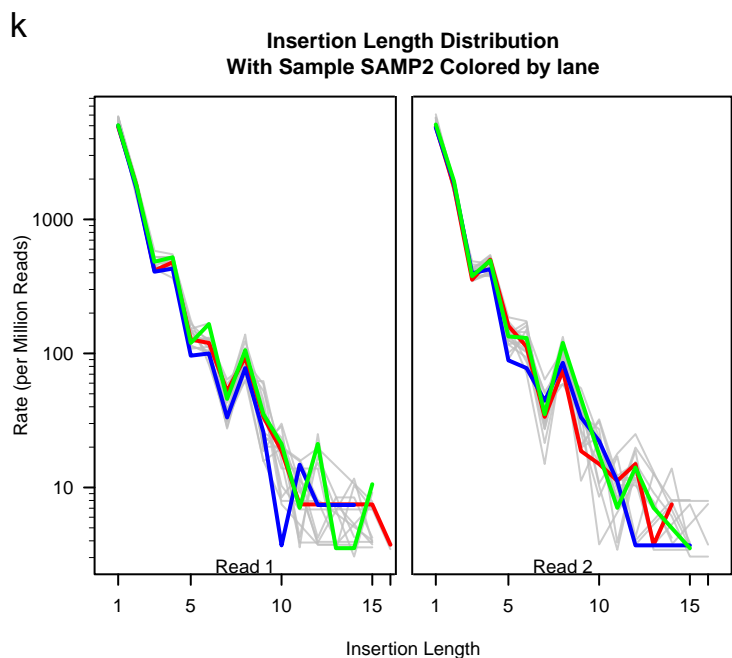
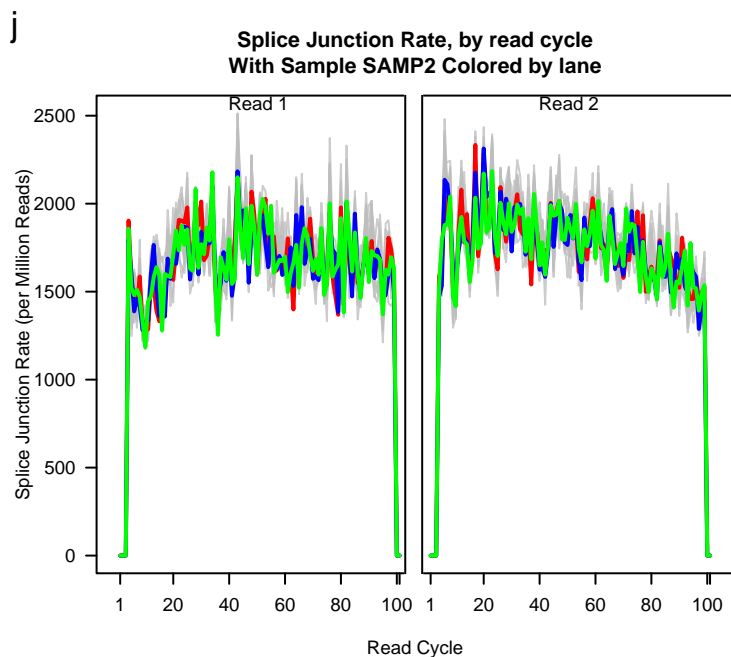
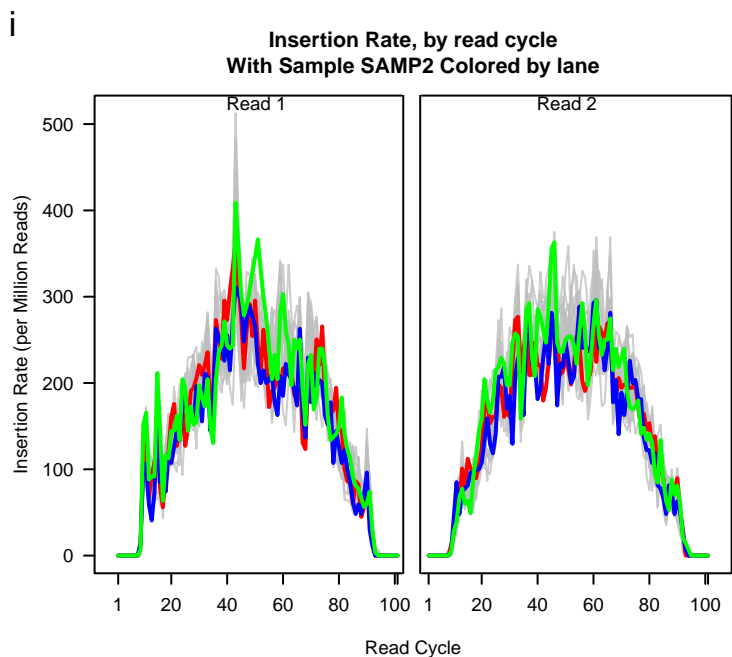
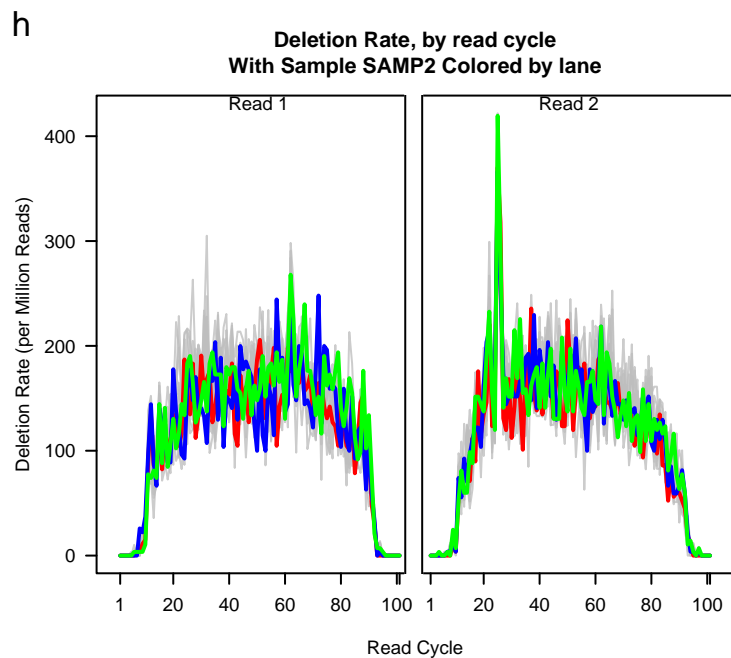
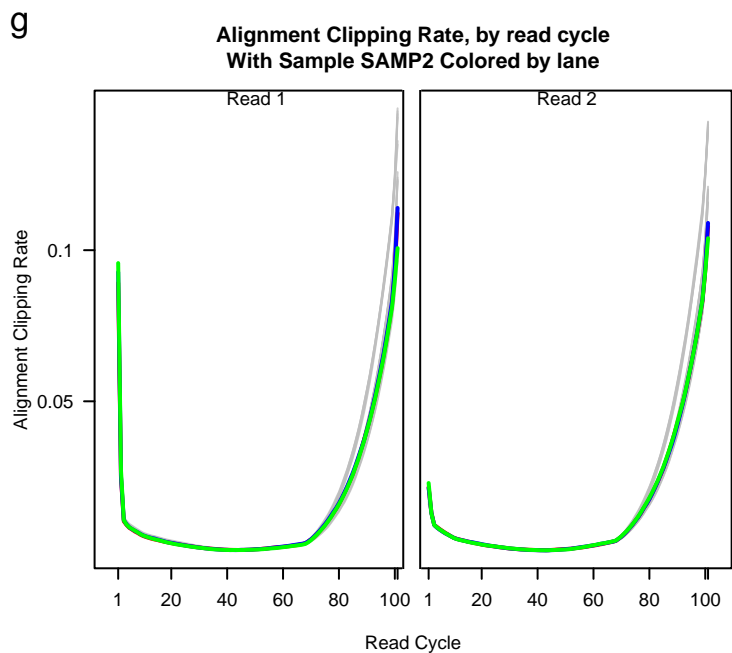


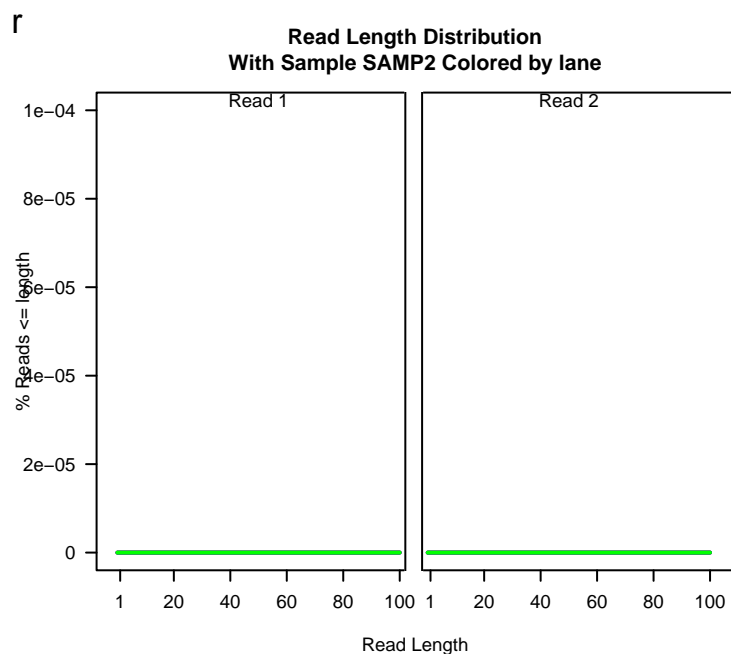
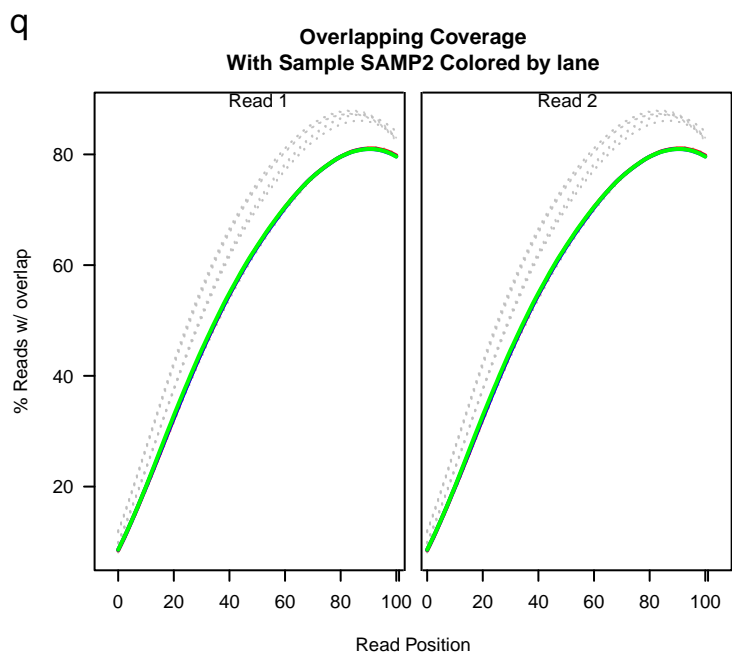
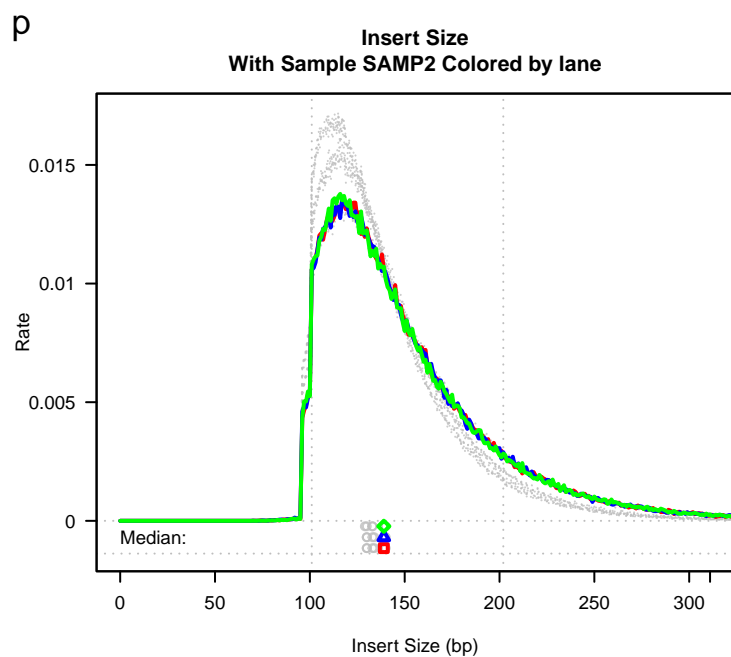
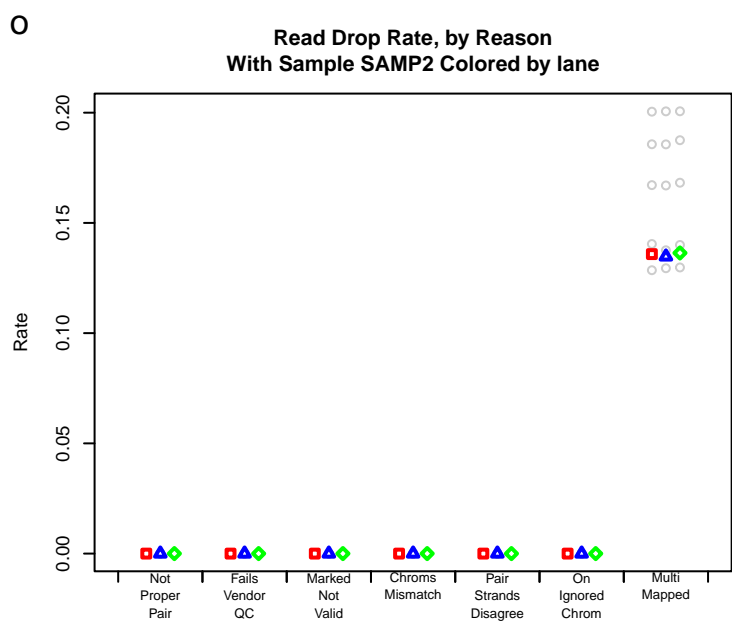
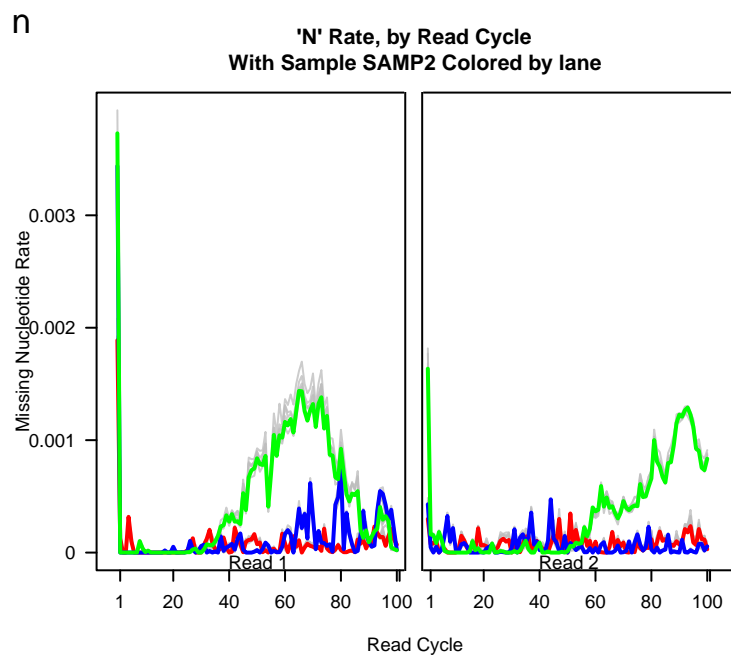
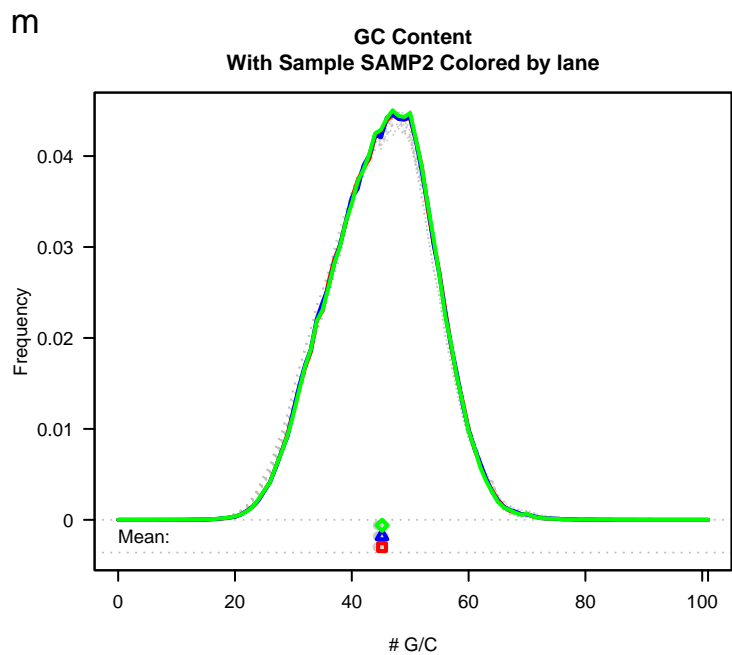
e

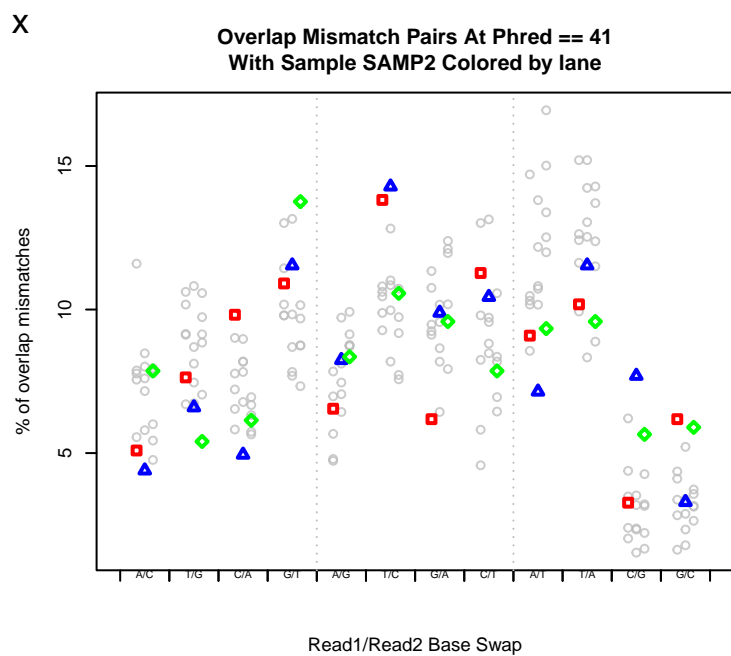
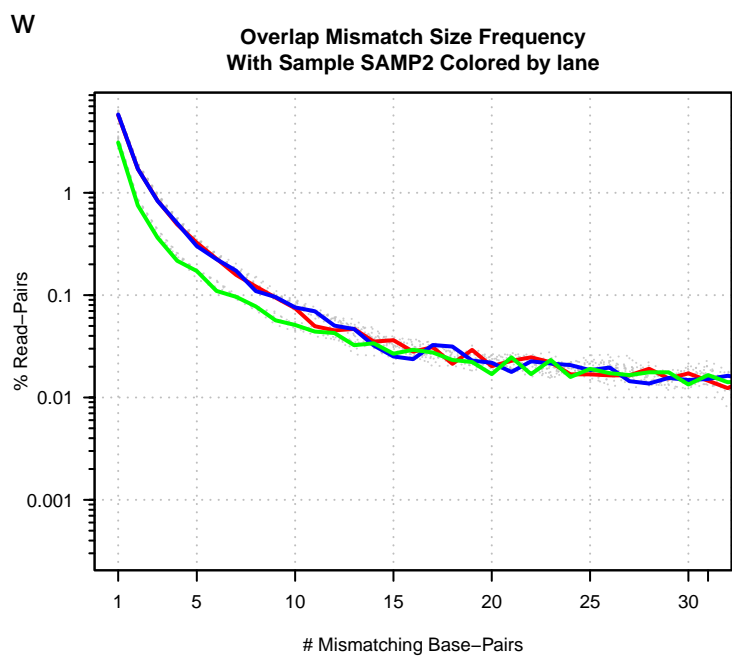
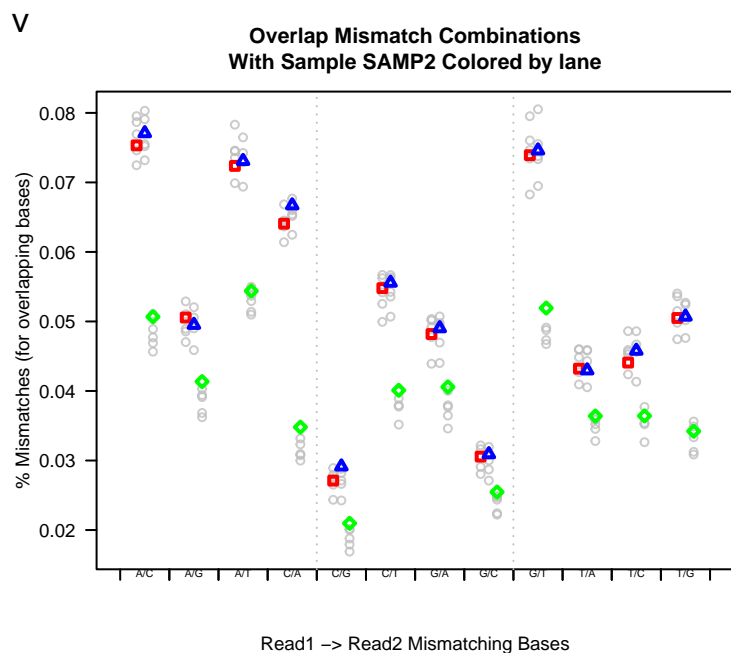
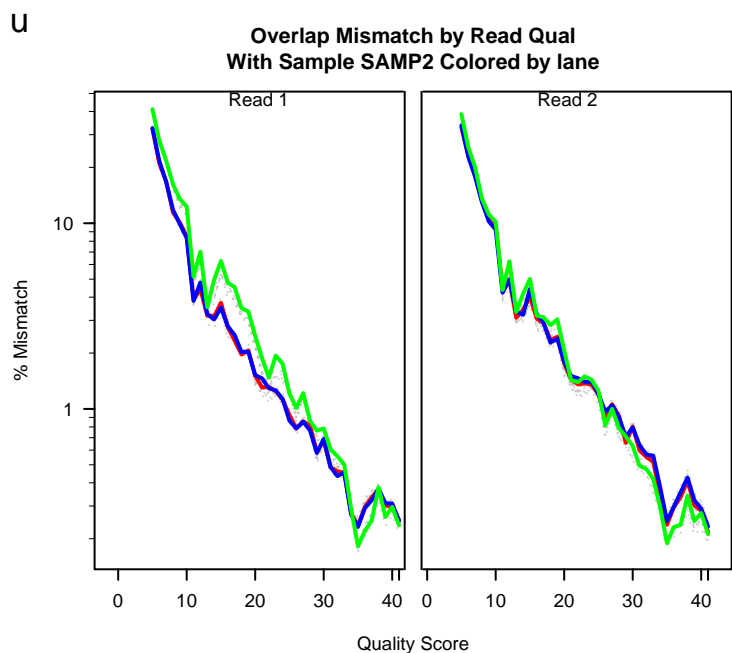
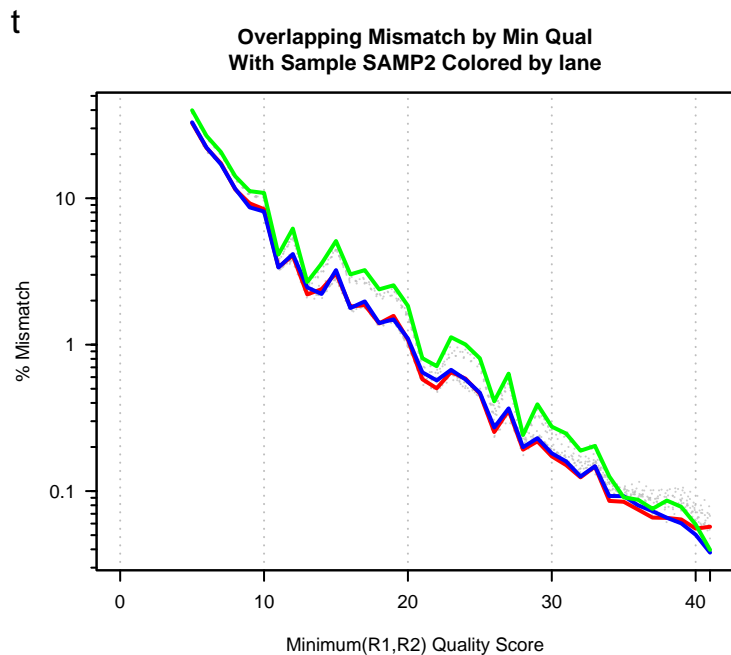
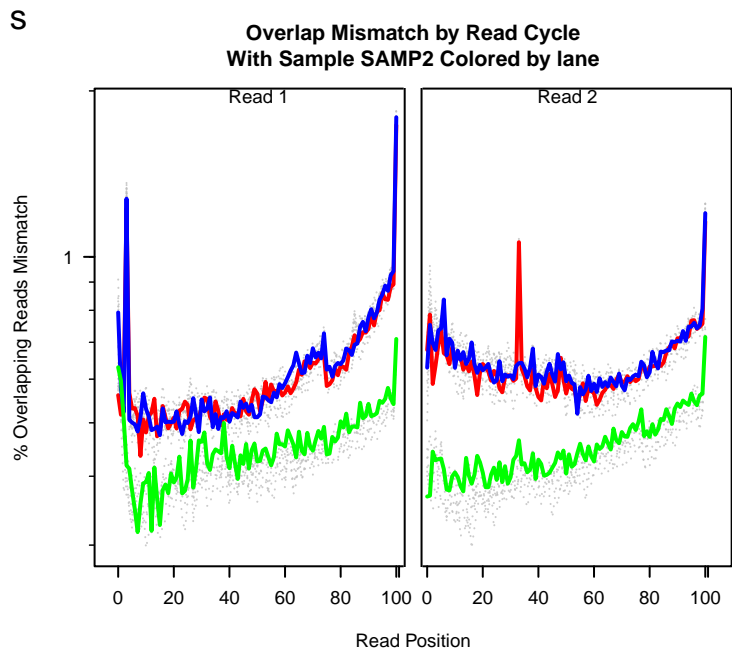


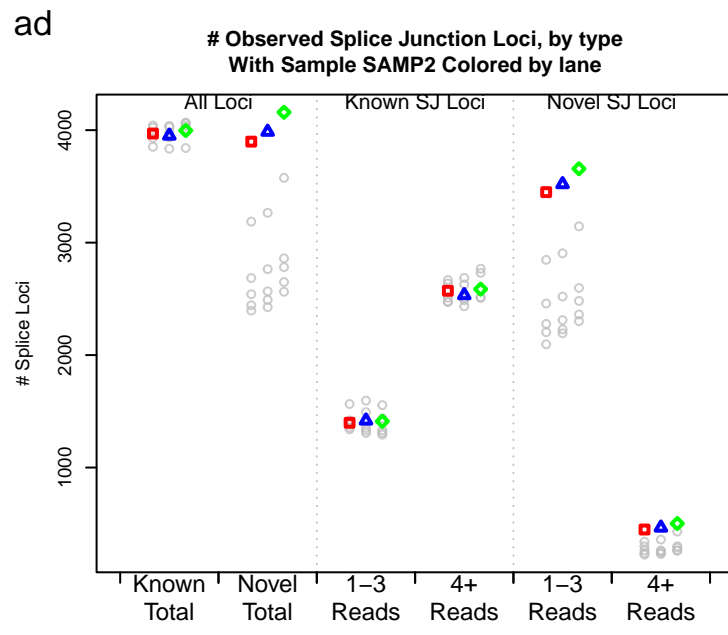
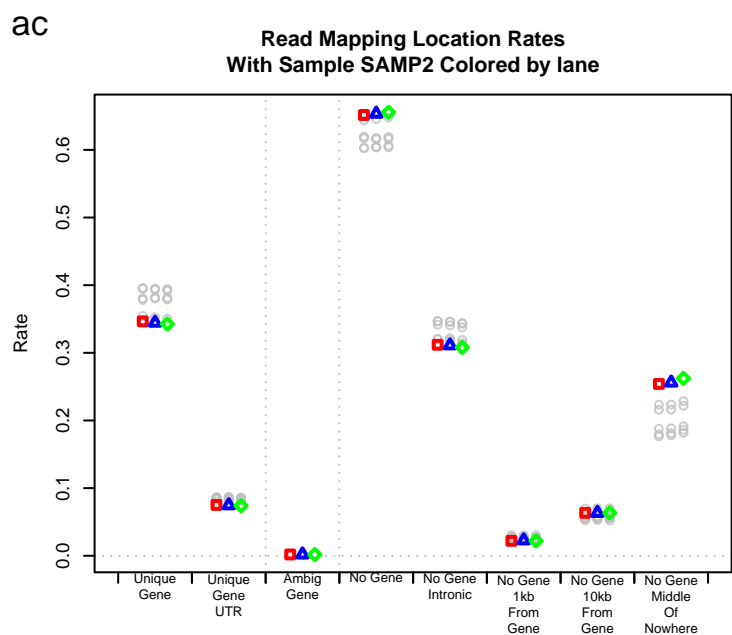
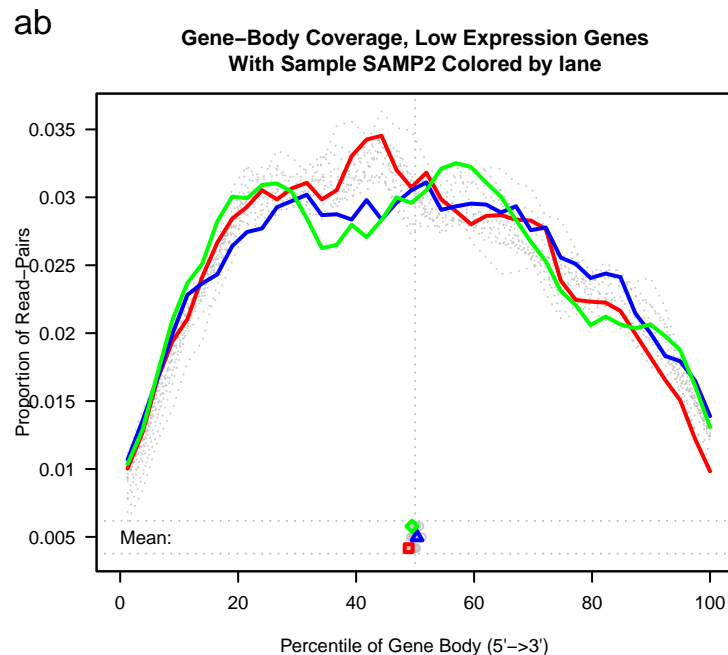
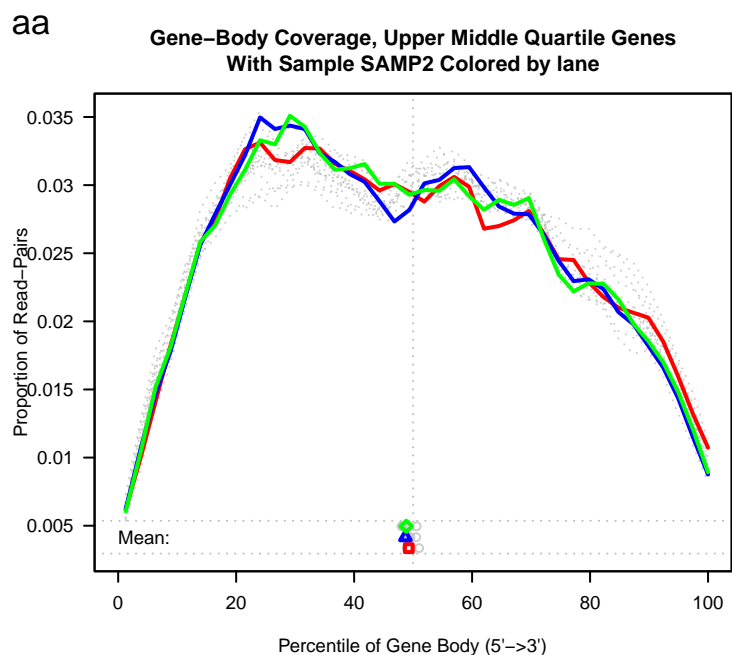
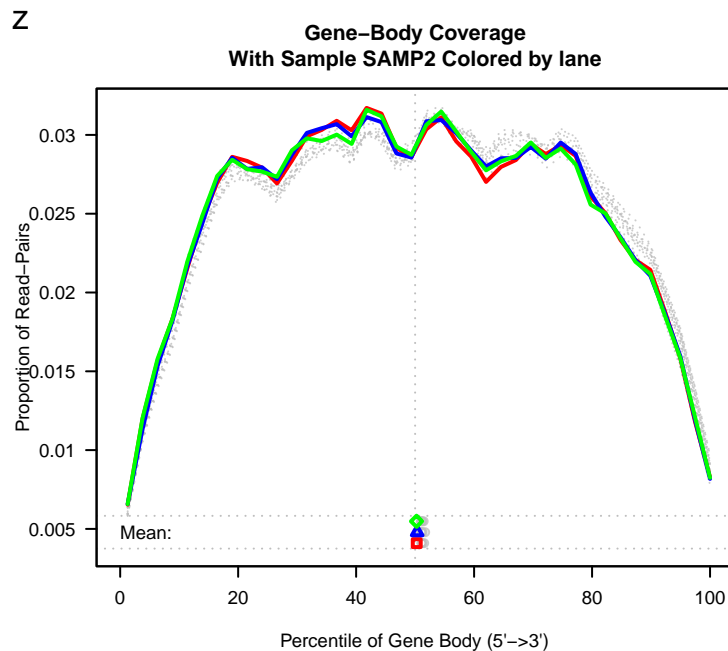
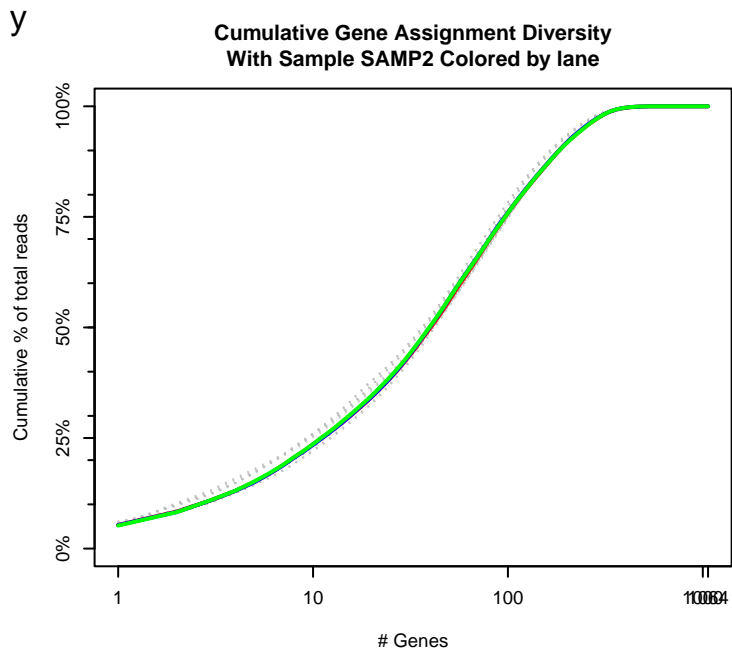
f



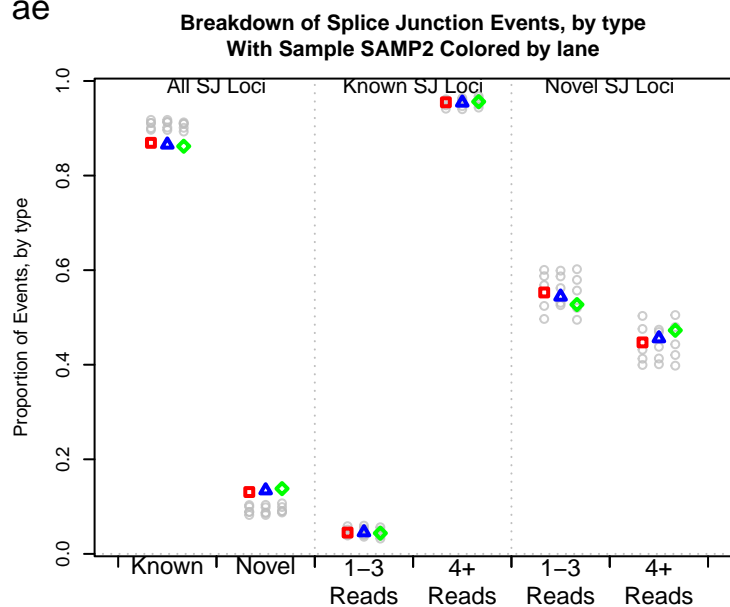




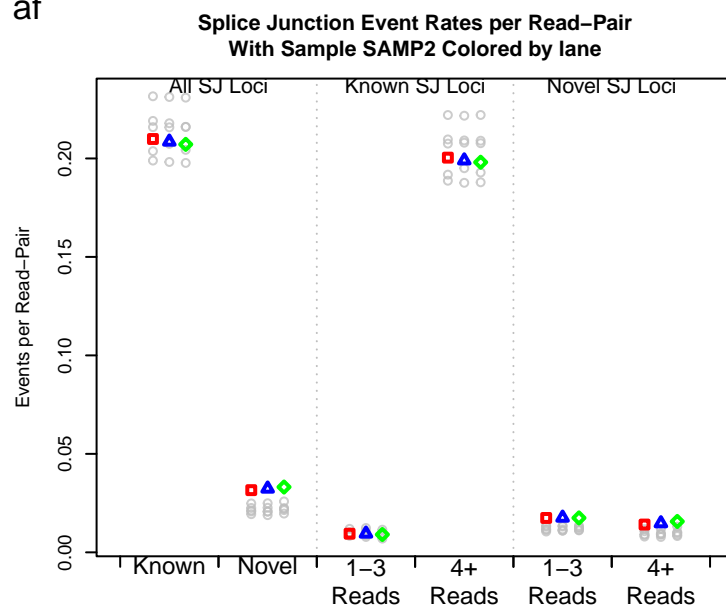




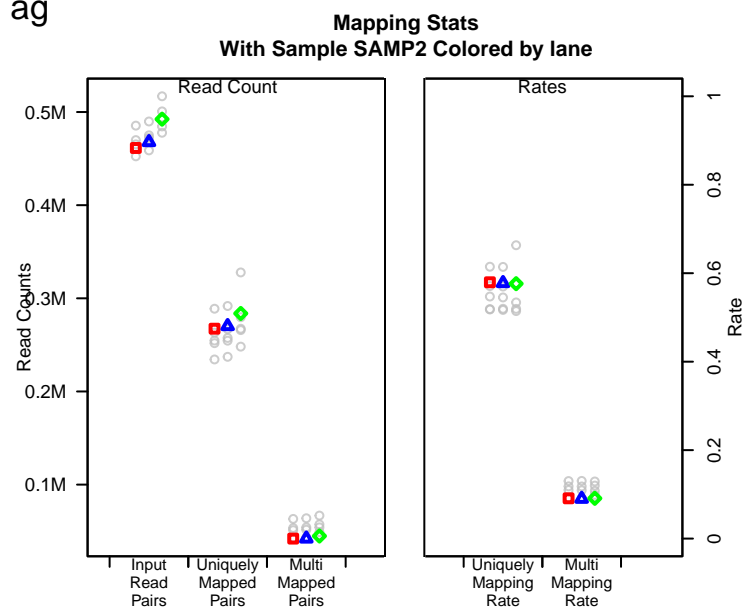
ae



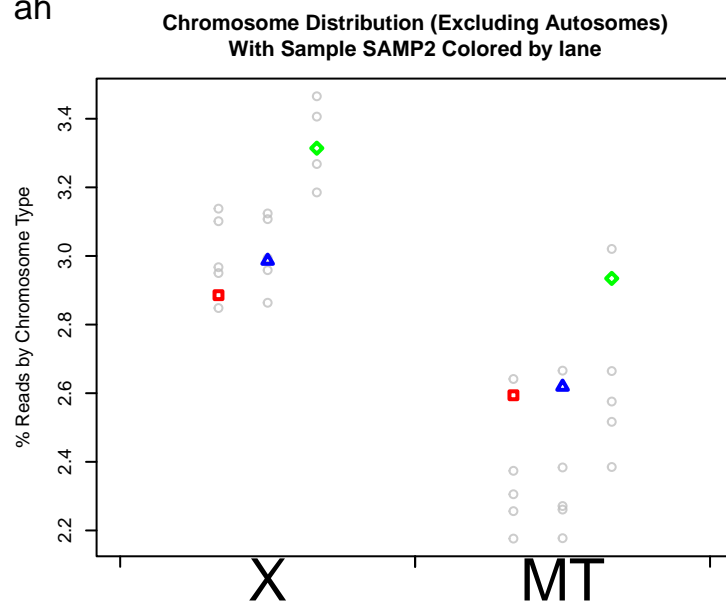
af



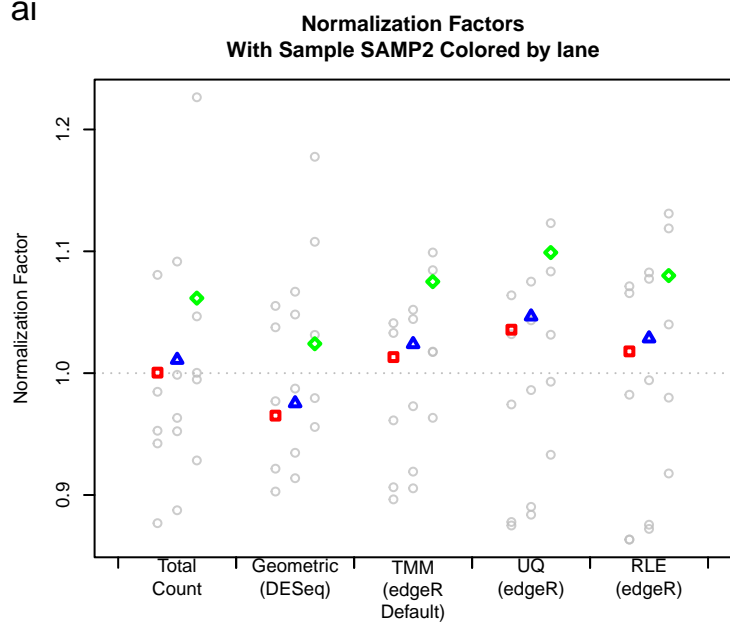
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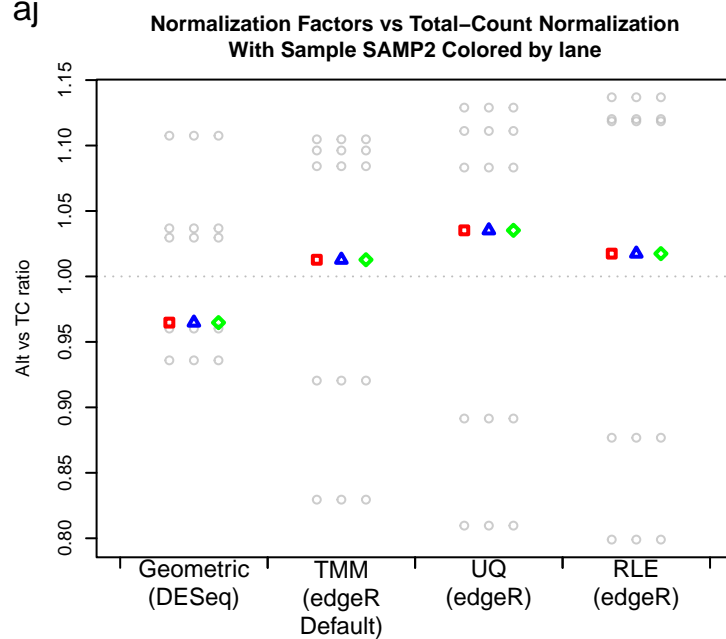
ah



ai

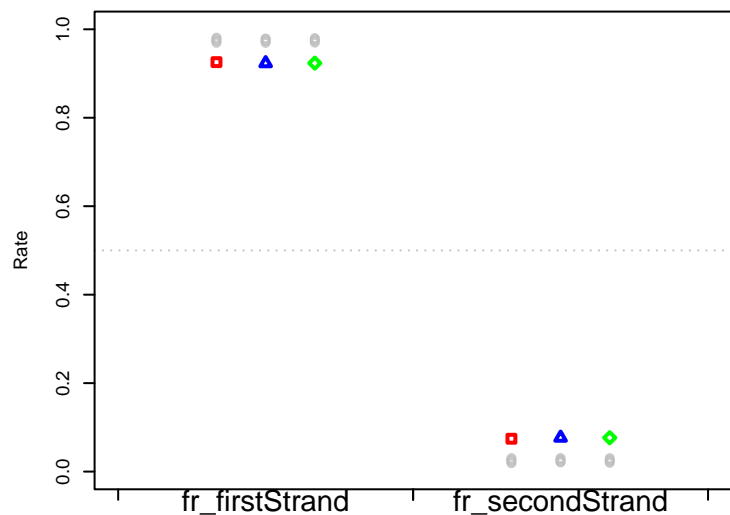


aj



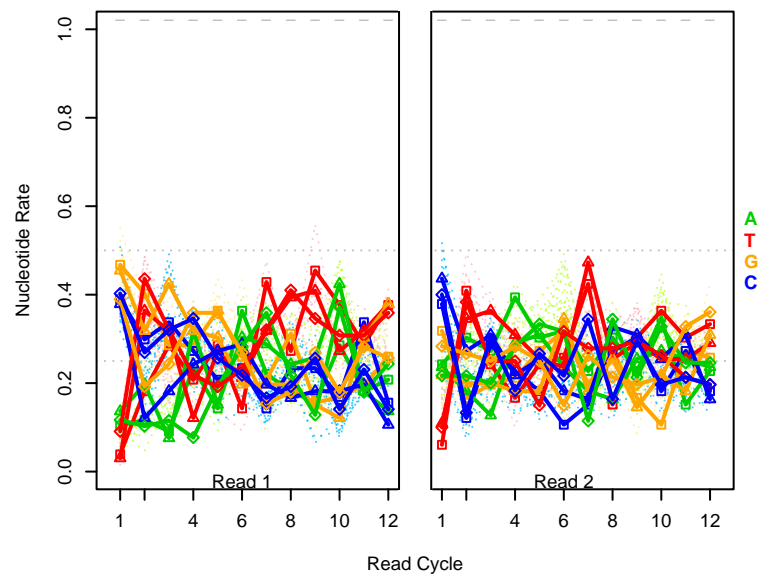
ak

Strandedness Test
With Sample SAMP2 Colored by lane



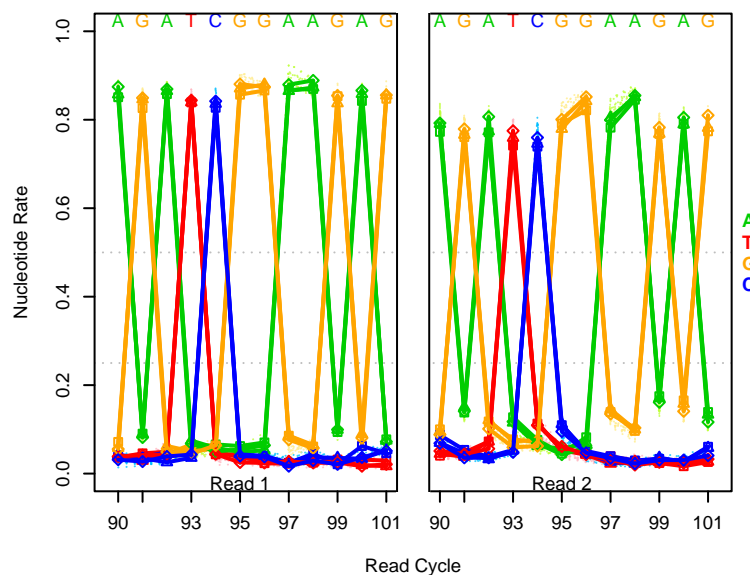
al

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



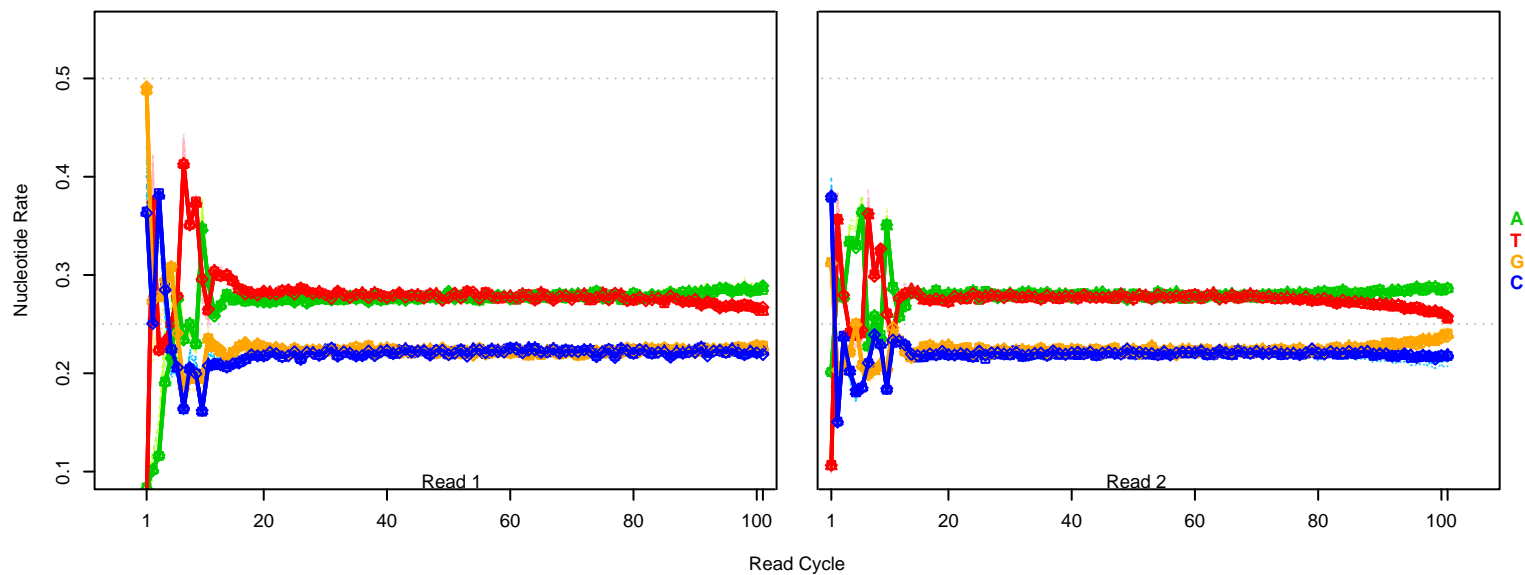
am

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



an

Raw Nucleotide Rate by Cycle
With Sample SAMP2 in Bold



ao

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

