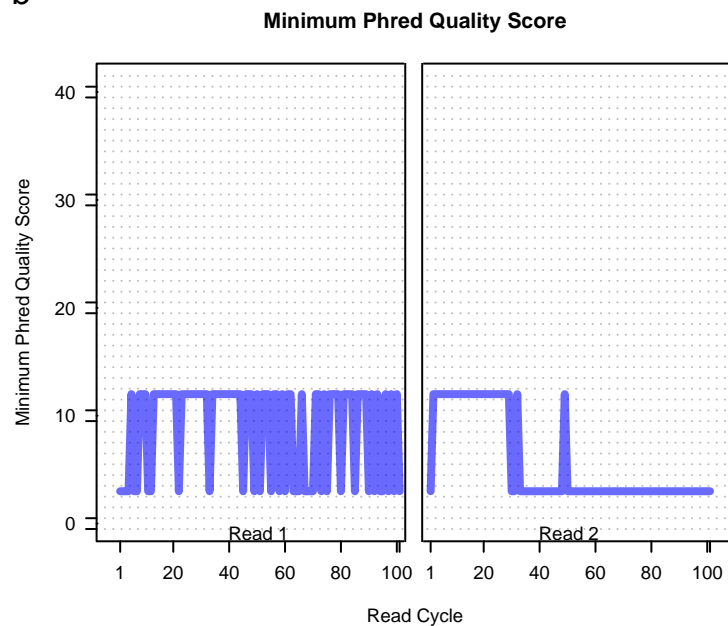


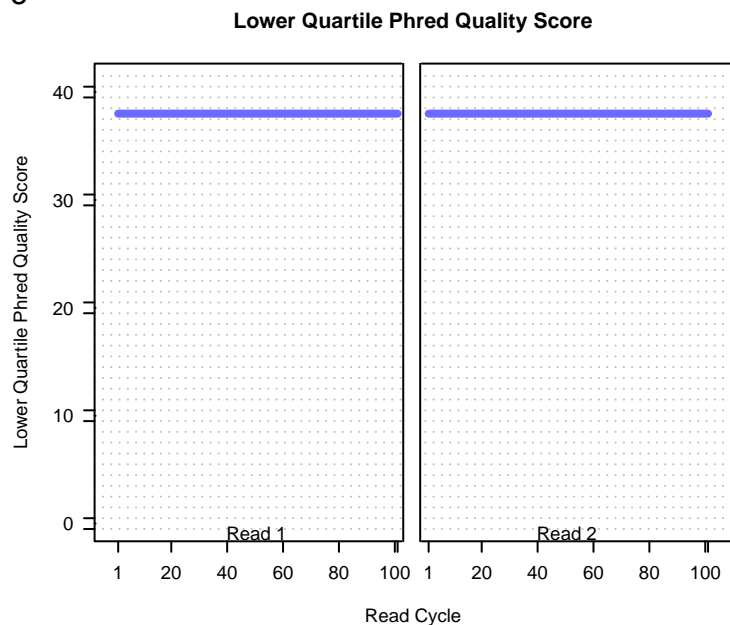
a

All Quality Control Summary Plots

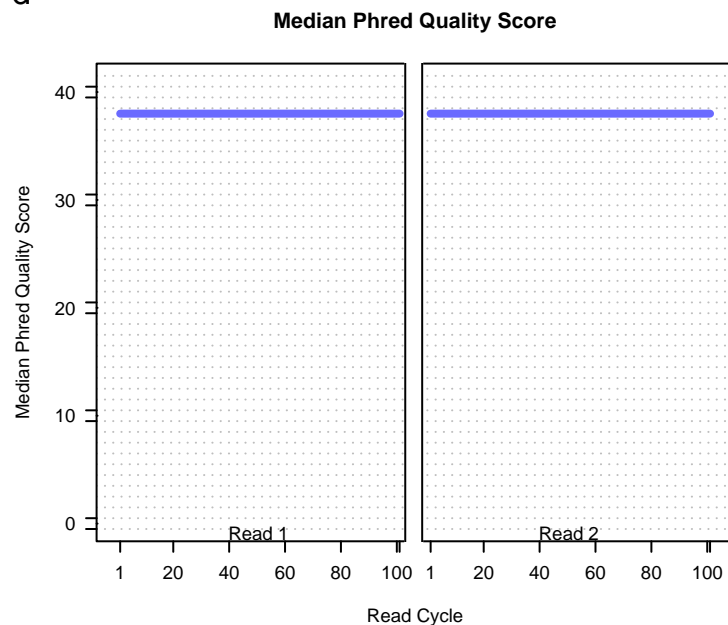
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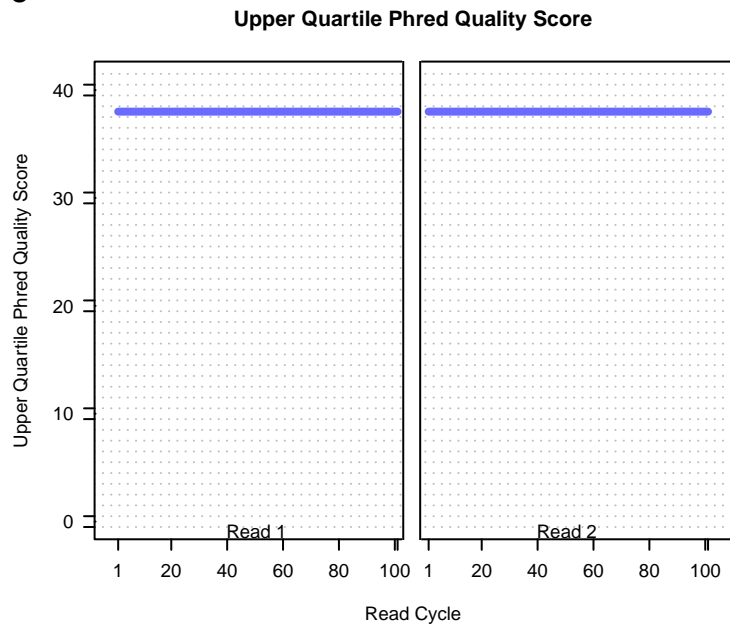
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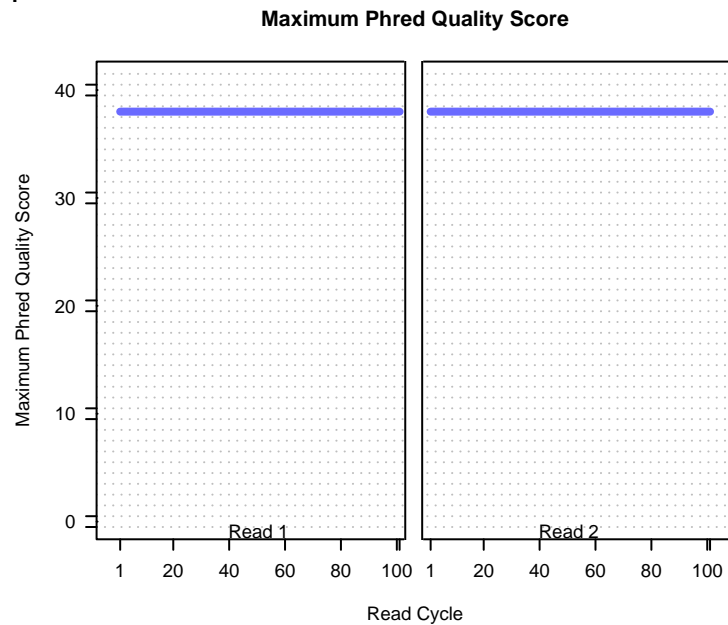
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e

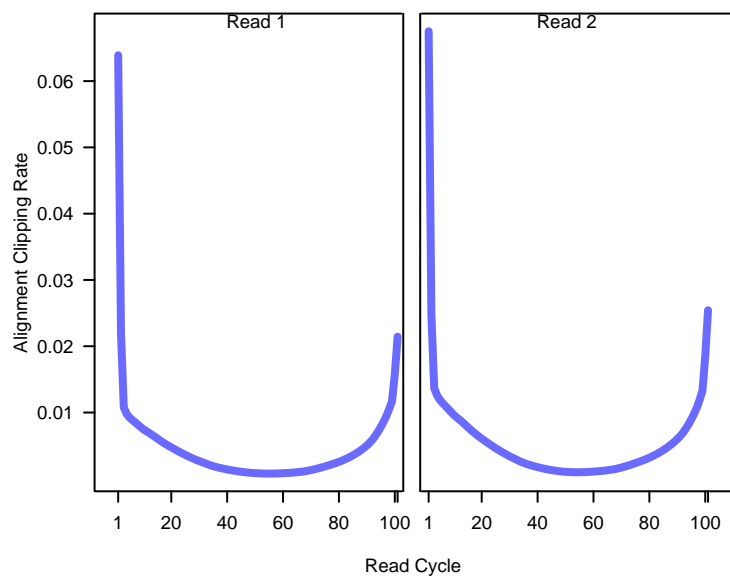


f



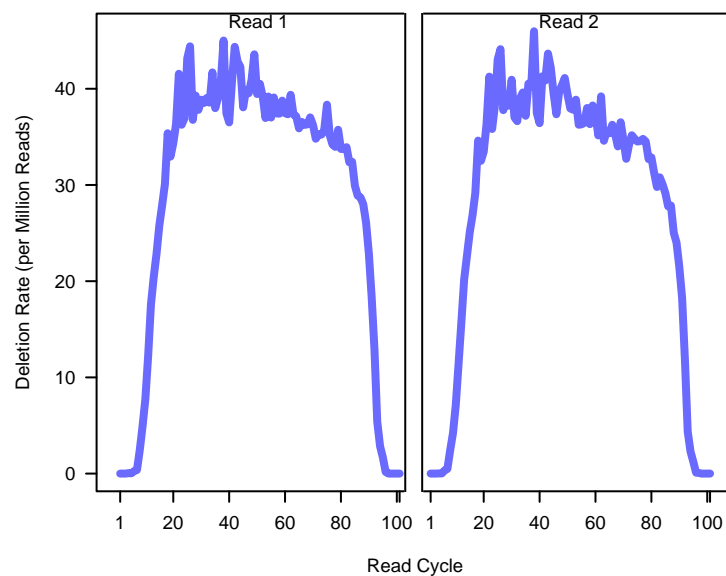
g

Alignment Clipping Rate, by read cycle



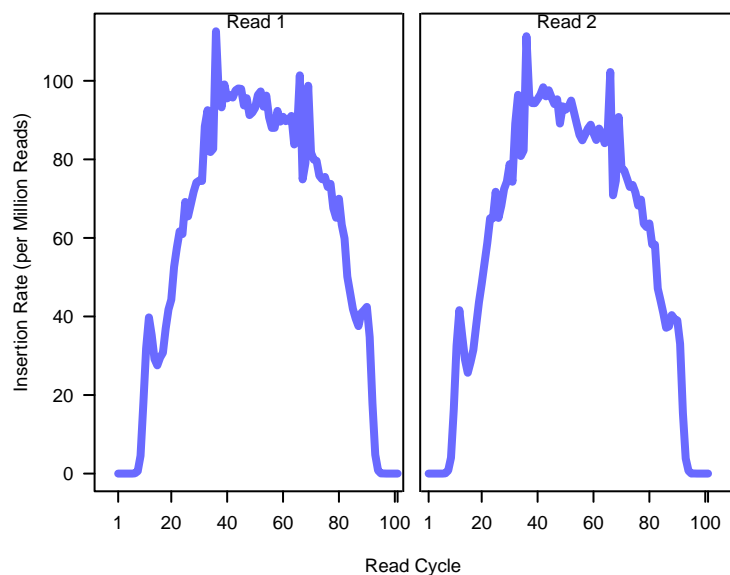
h

Deletion Rate, by read cycle



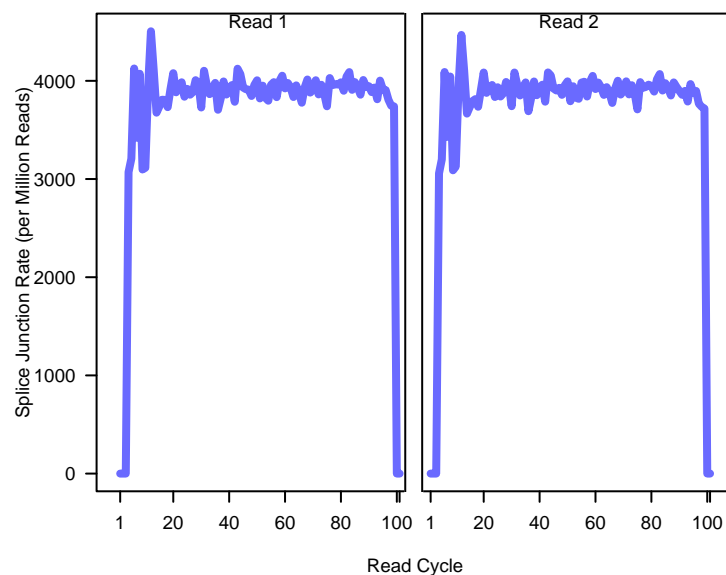
i

Insertion Rate, by read cycle



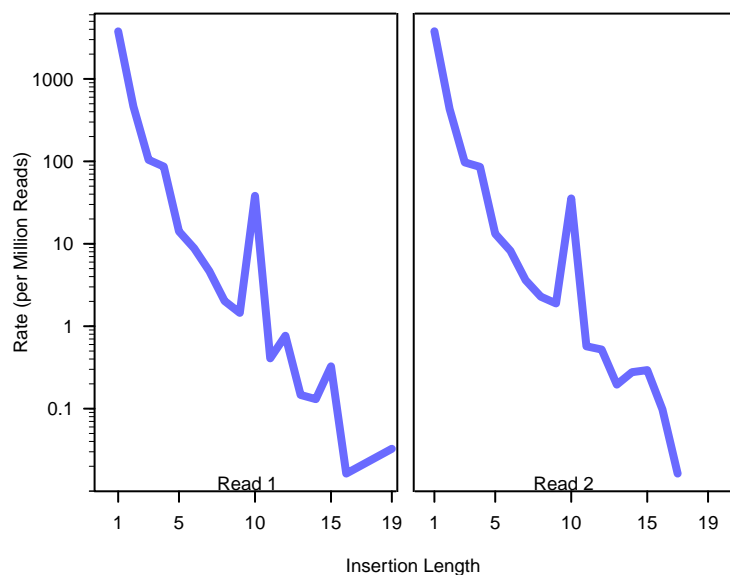
j

Splice Junction Rate, by read cycle



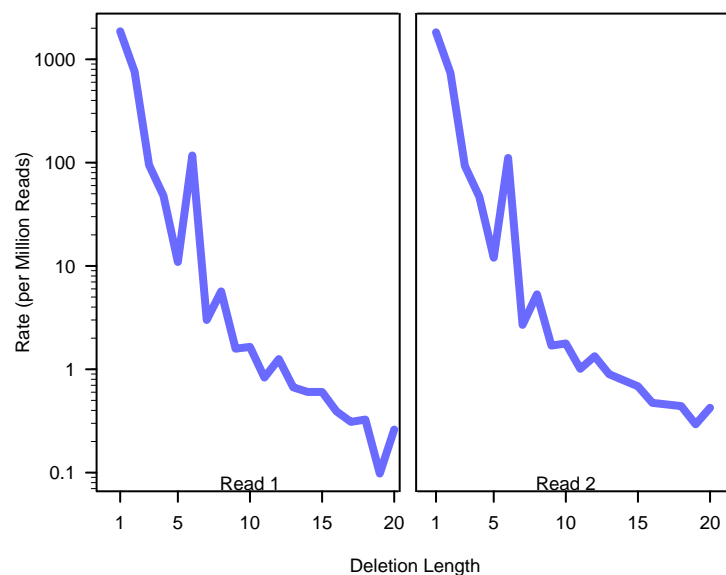
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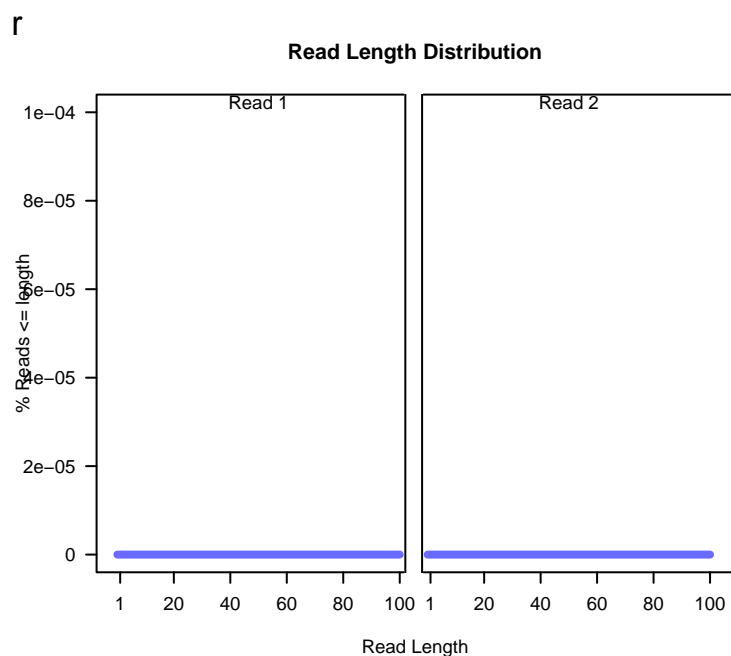
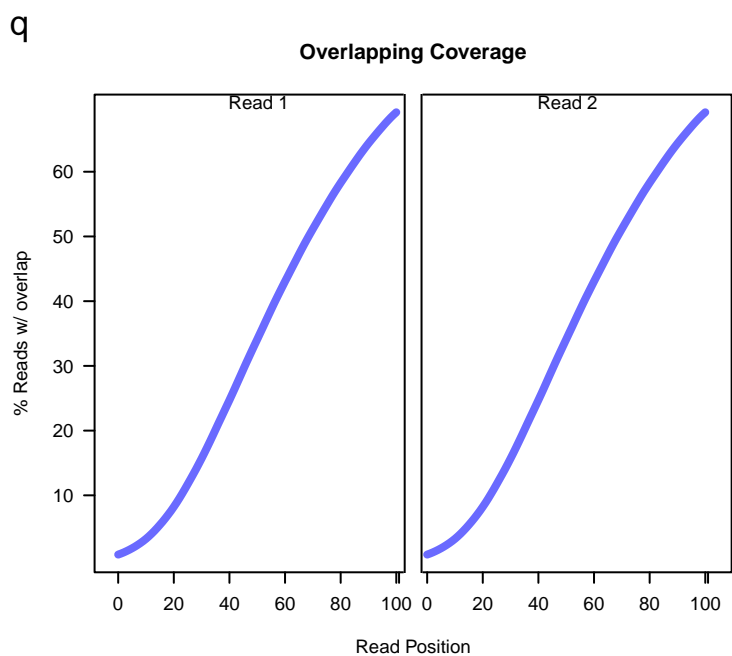
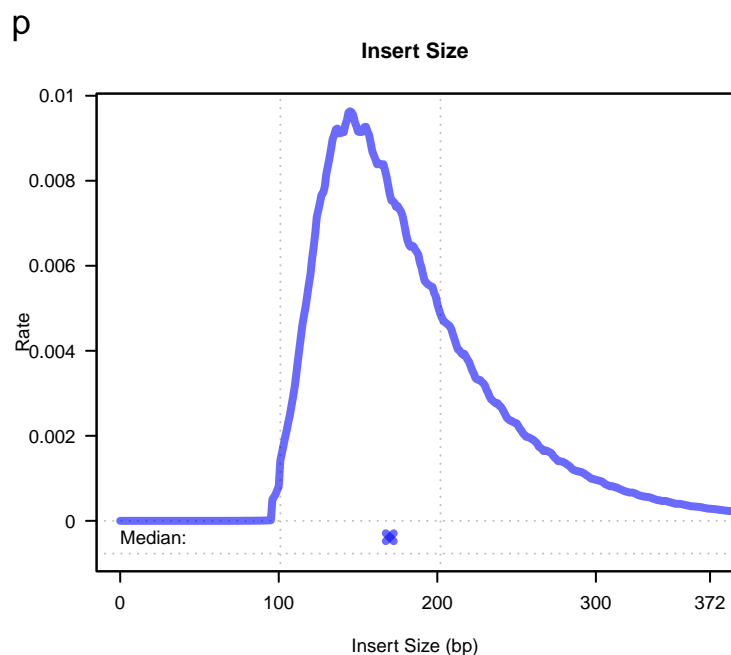
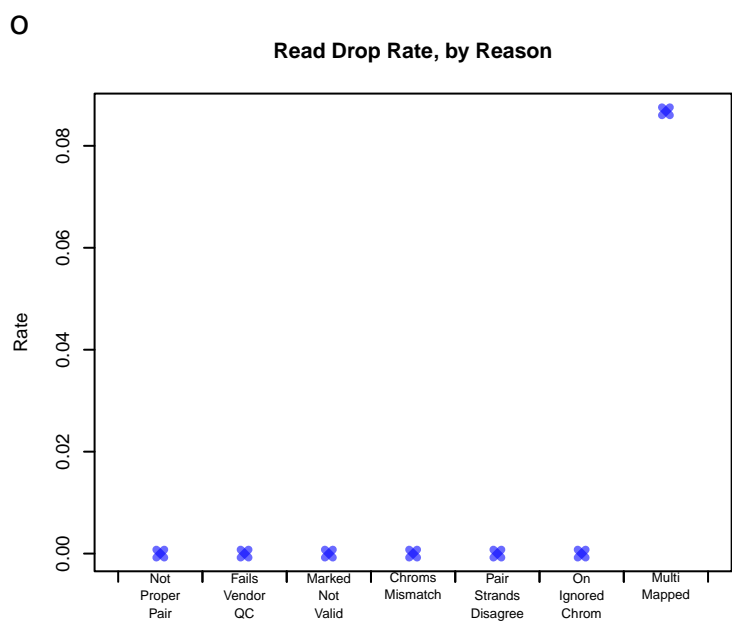
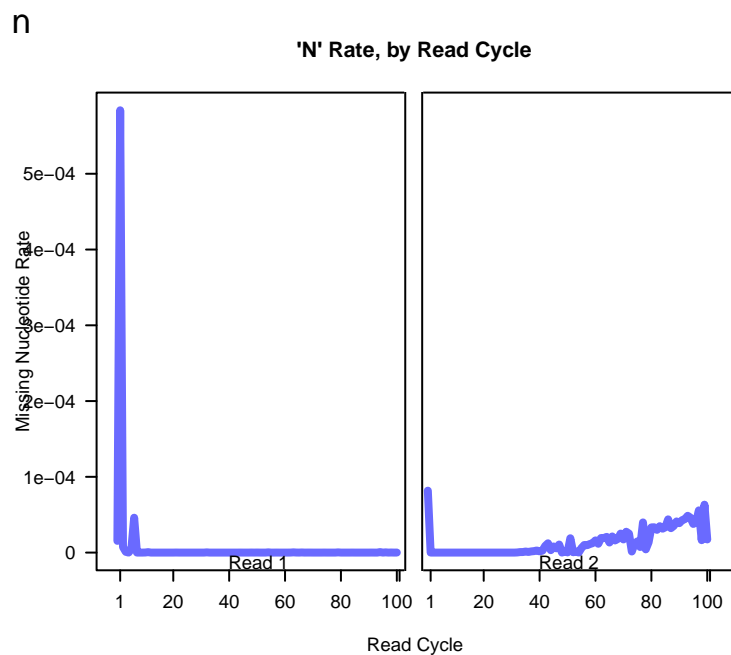
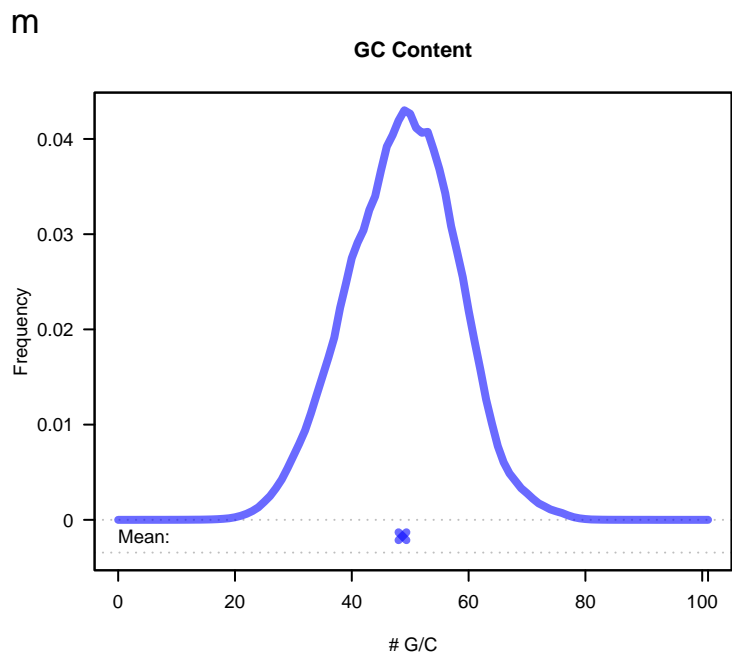
Insertion Length Distribution



l

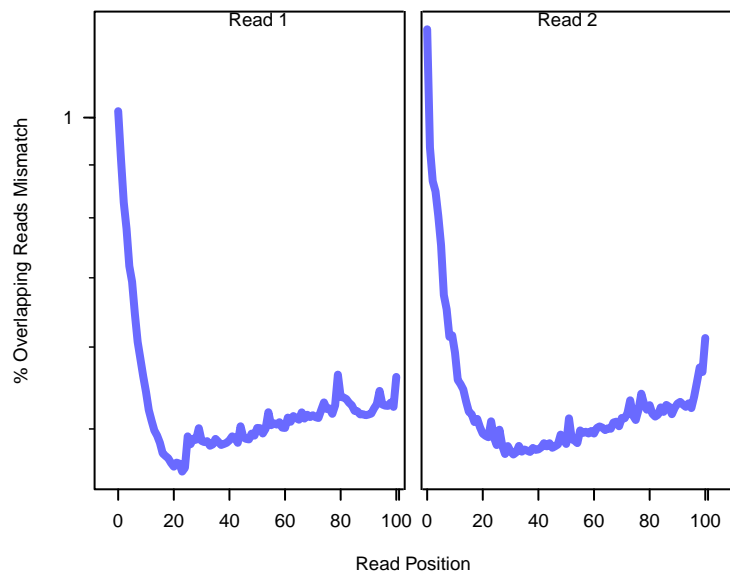
Deletion Length Distribution





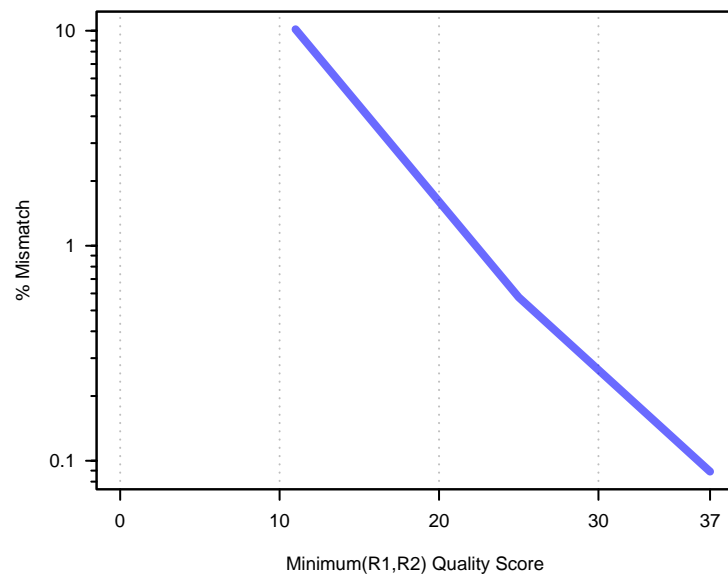
s

Overlap Mismatch by Read Cycle



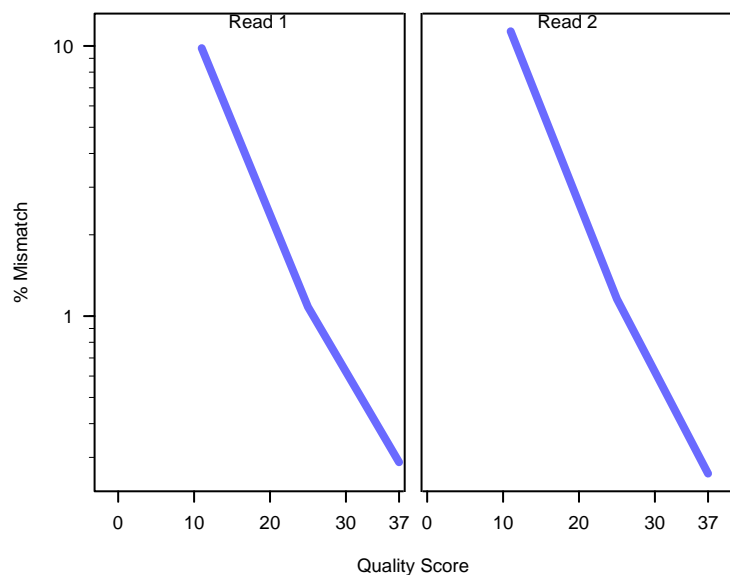
t

Overlapping Mismatch by Min Qual



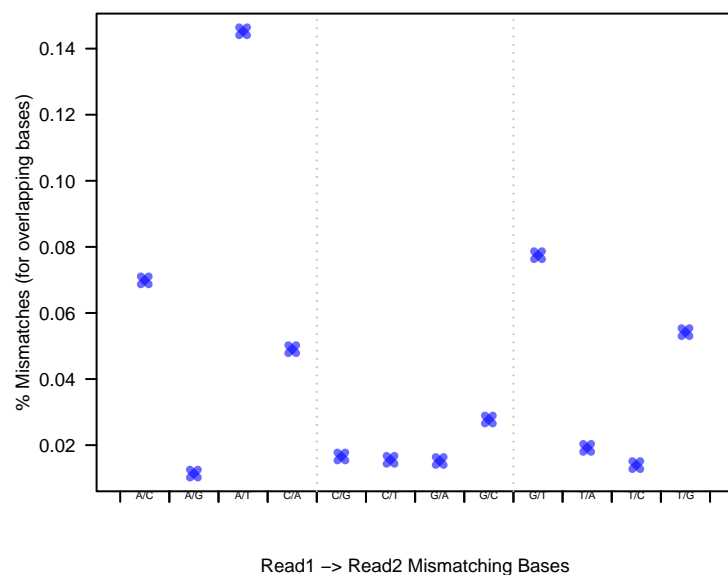
u

Overlap Mismatch by Read Qual



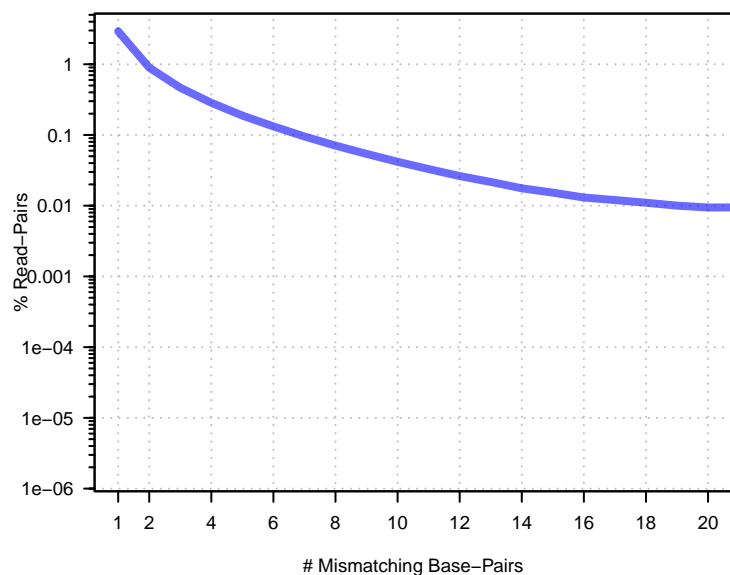
v

Overlap Mismatch Combinations



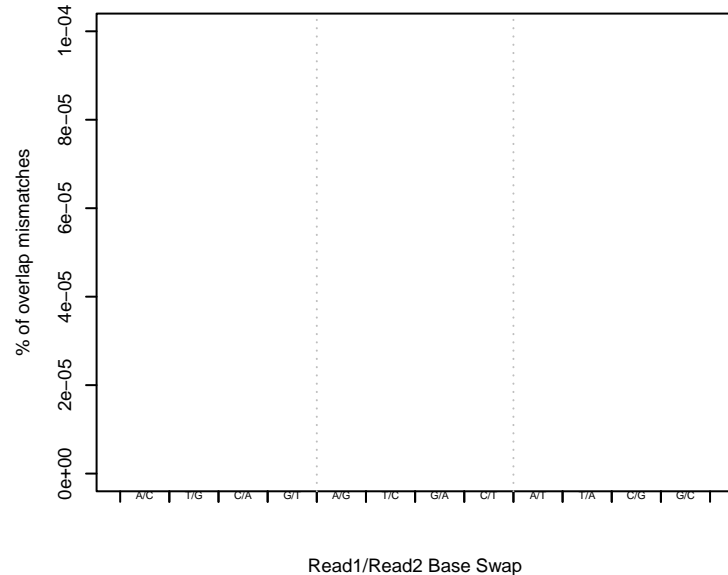
w

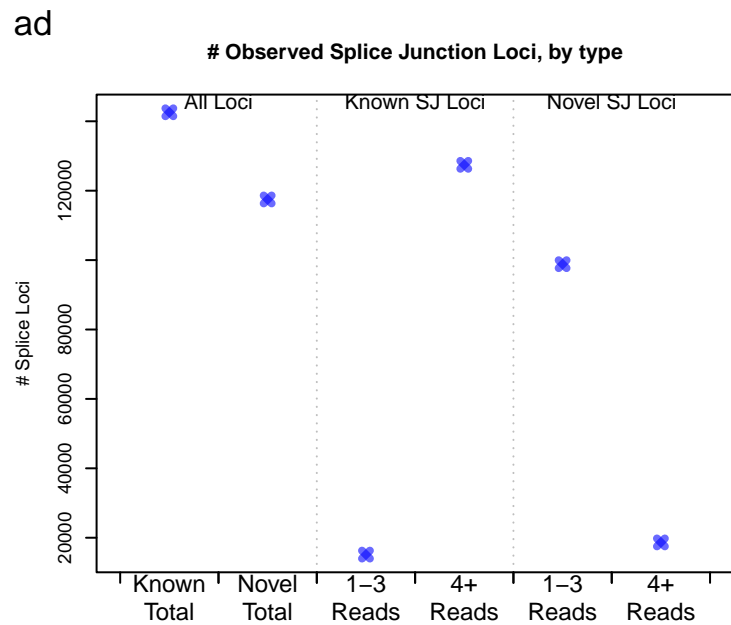
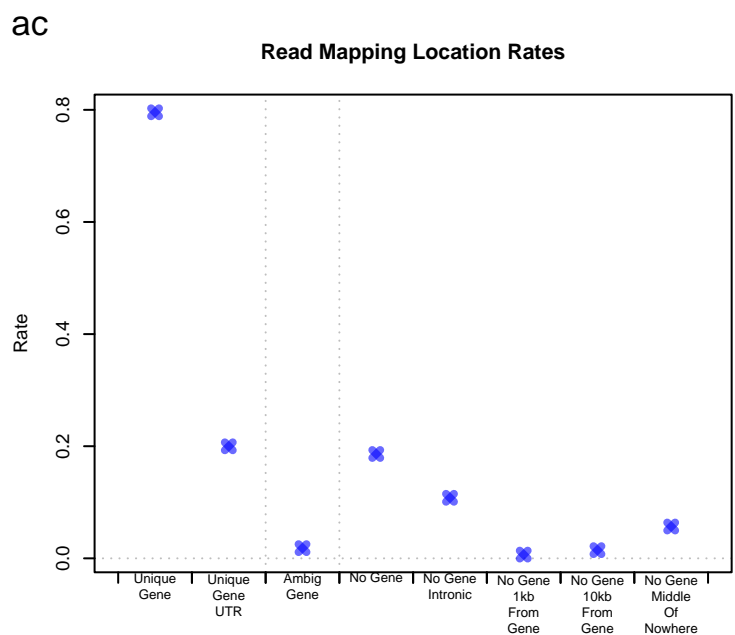
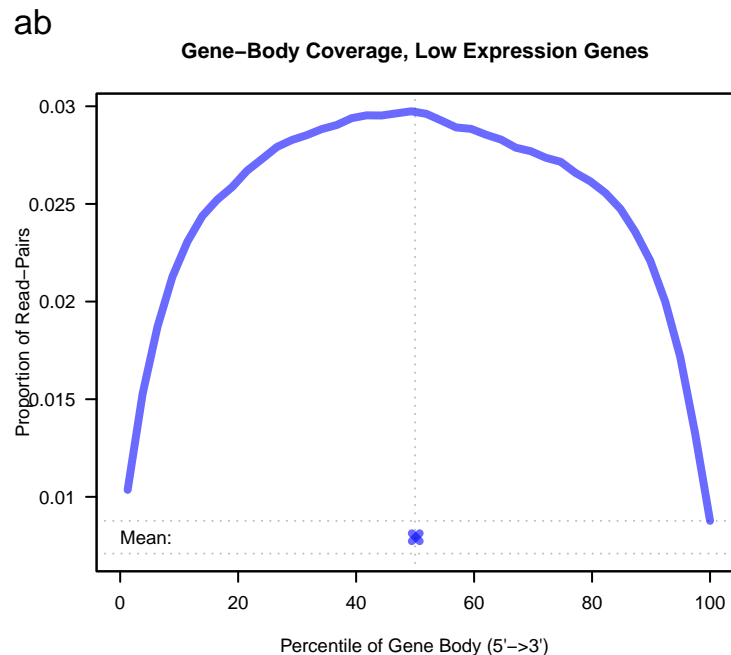
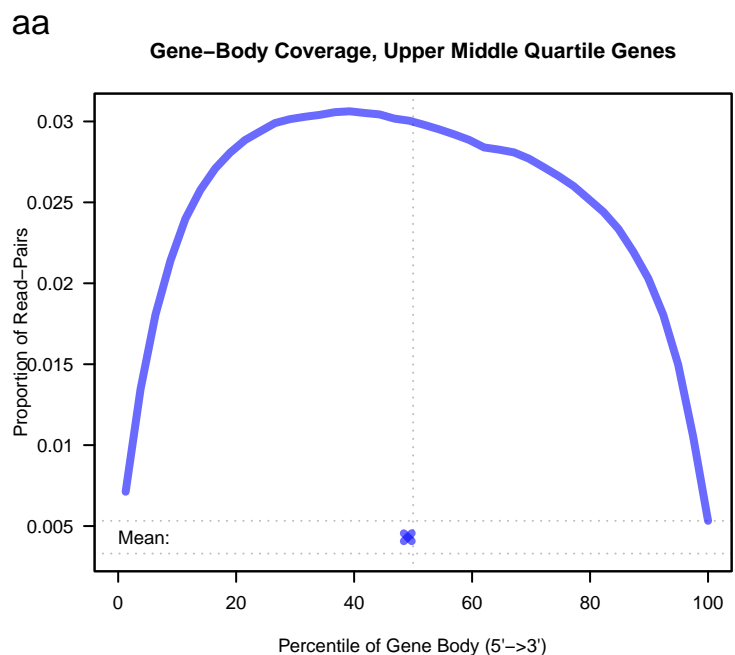
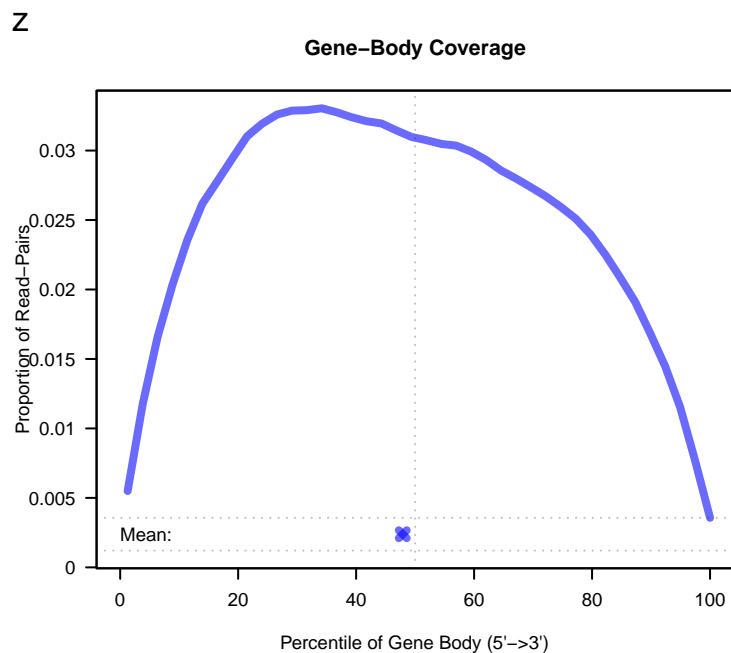
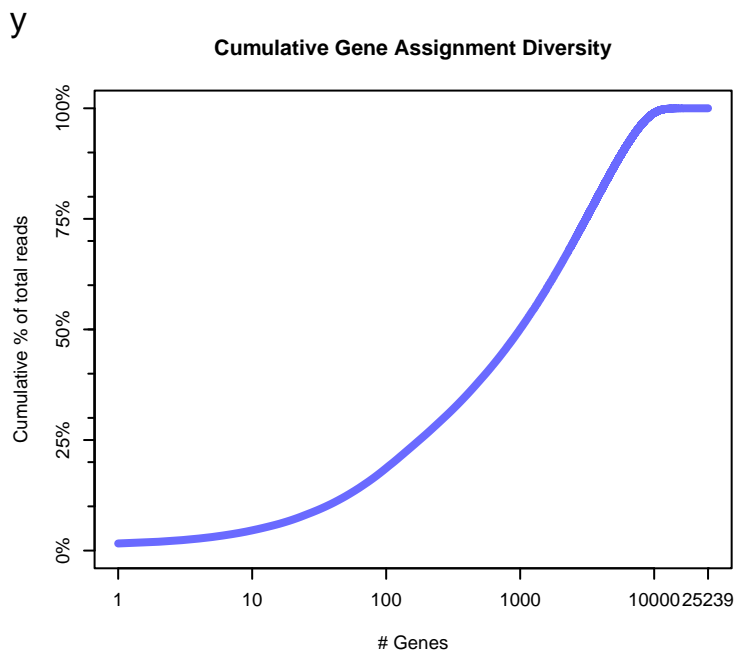
Overlap Mismatch Size Frequency



x

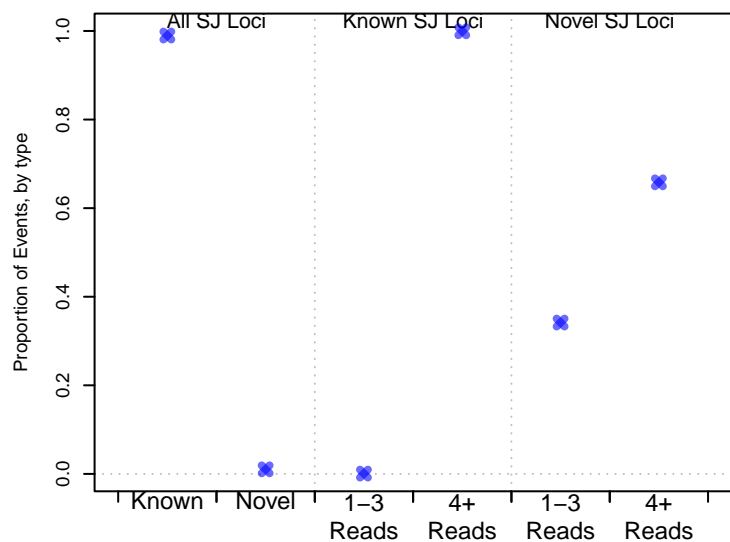
Overlap Mismatch Pairs At Phred == 41





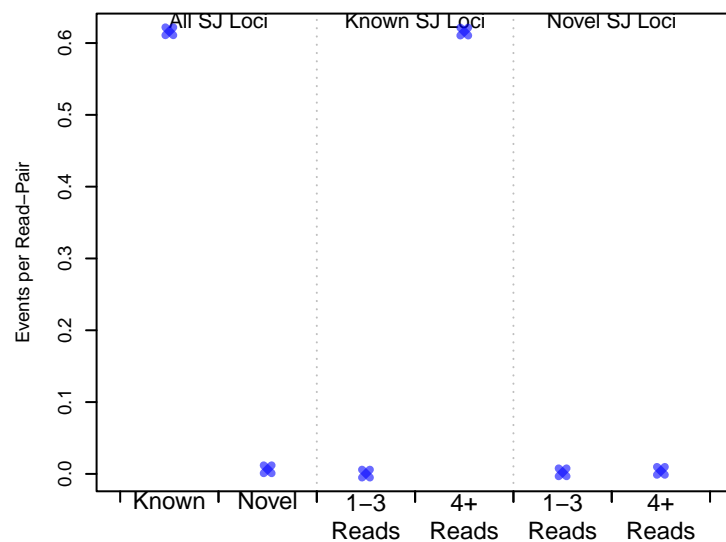
ae

Breakdown of Splice Junction Events, by type



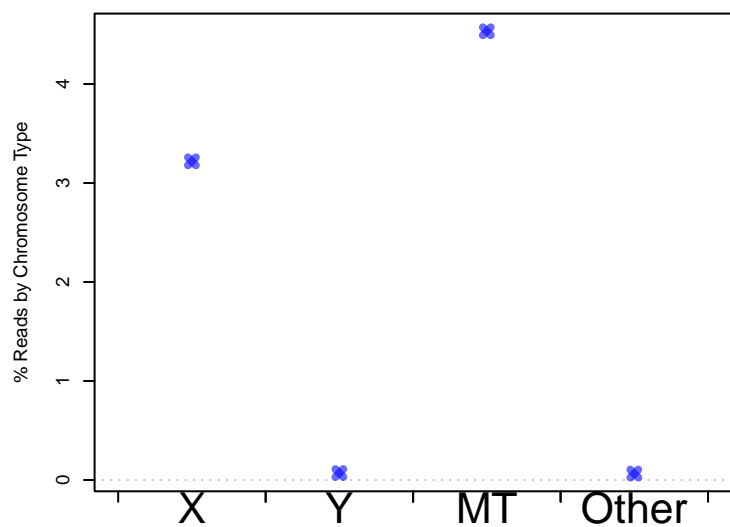
af

Splice Junction Event Rates per Read-Pair



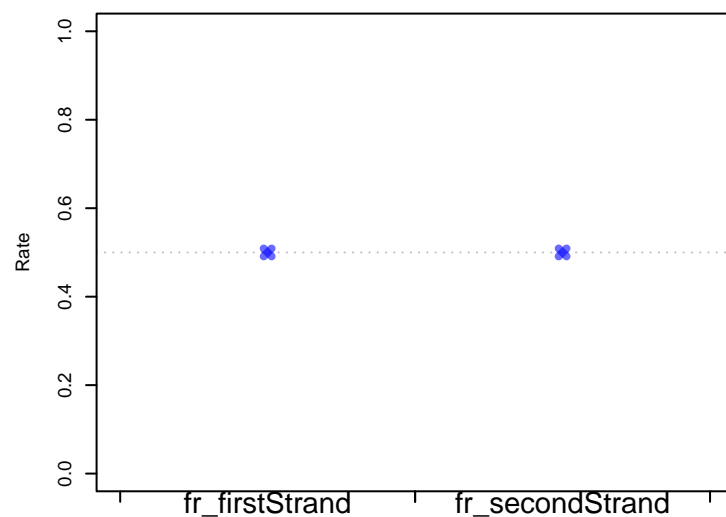
ag

Chromosome Distribution (Excluding Autosomes)



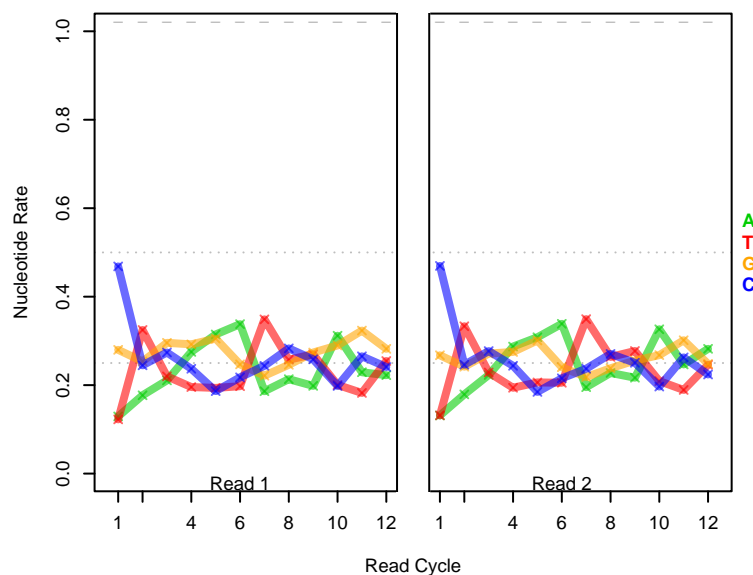
ah

Strandedness Test



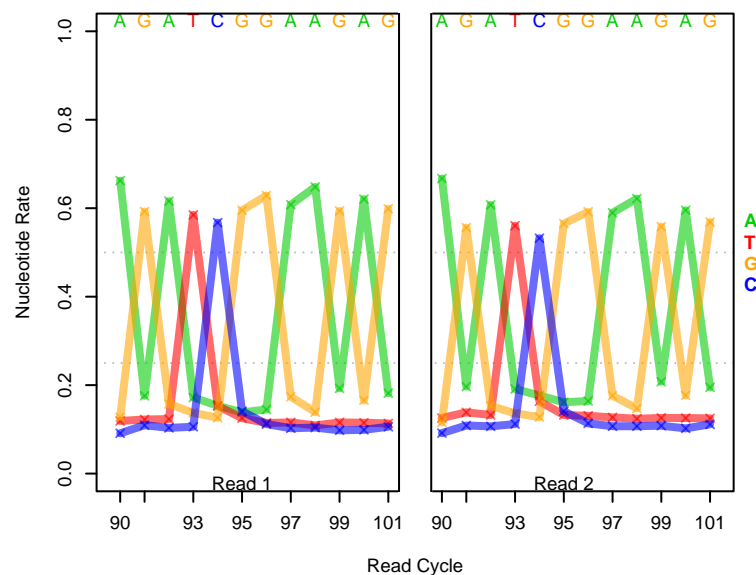
ai

Nucleotide Rate by Cycle, Leading Clipped bases (12)

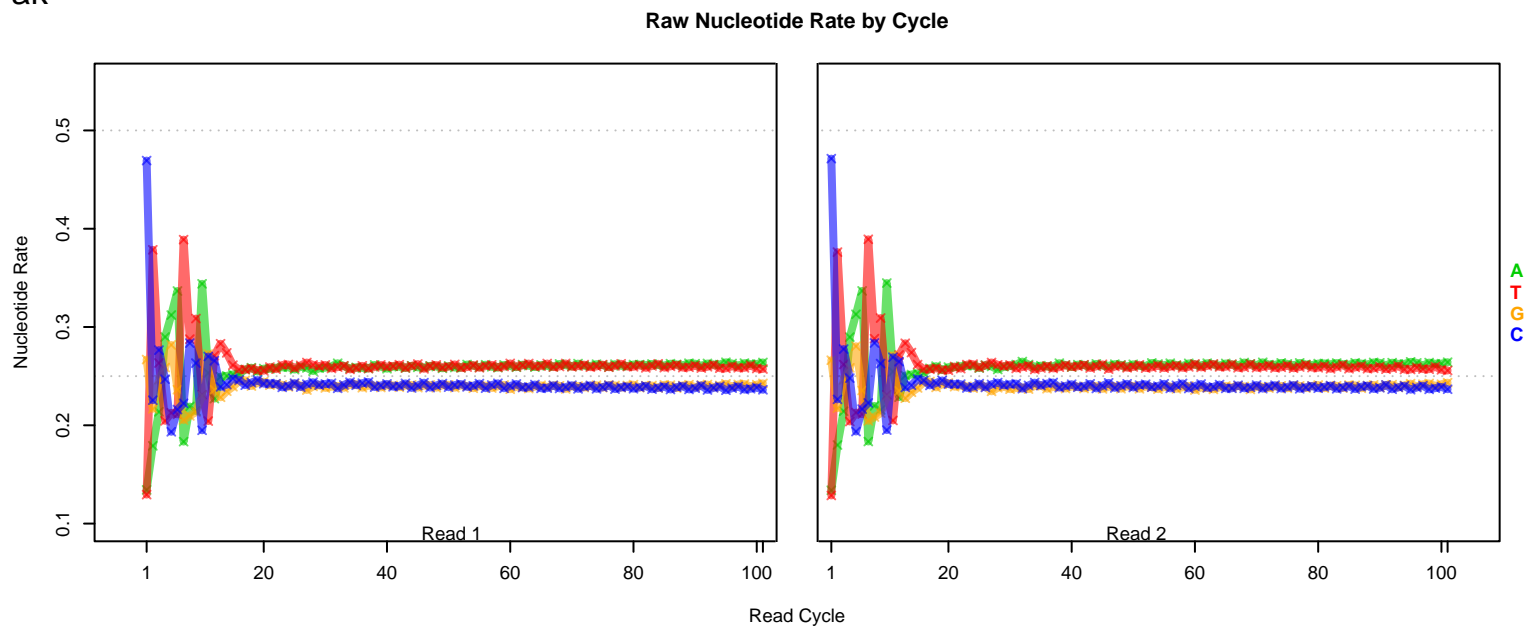


aj

Nucleotide Rate by Cycle, Trailing Clipped bases (12)



ak



al

