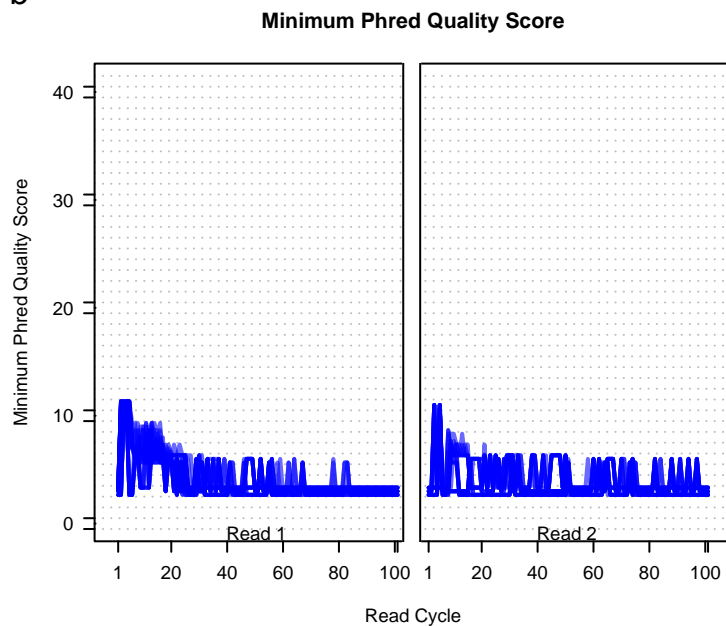


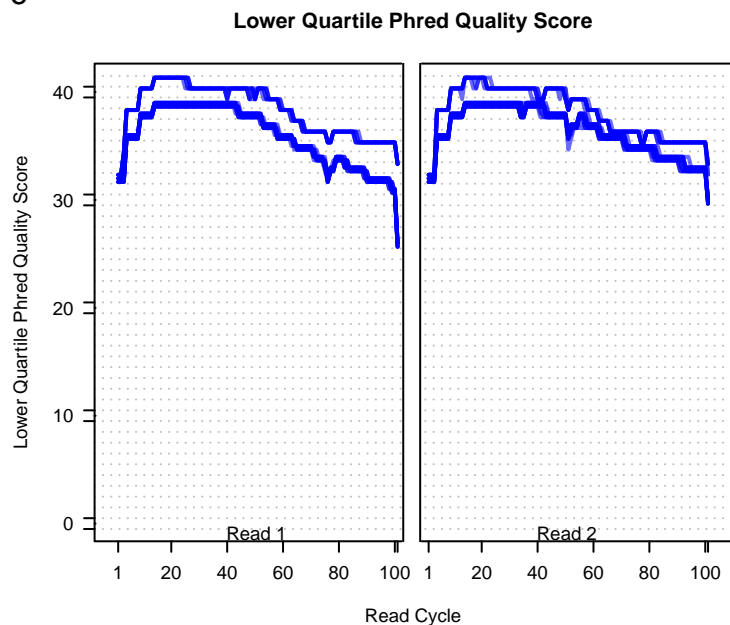
a

All Quality Control Summary Plots

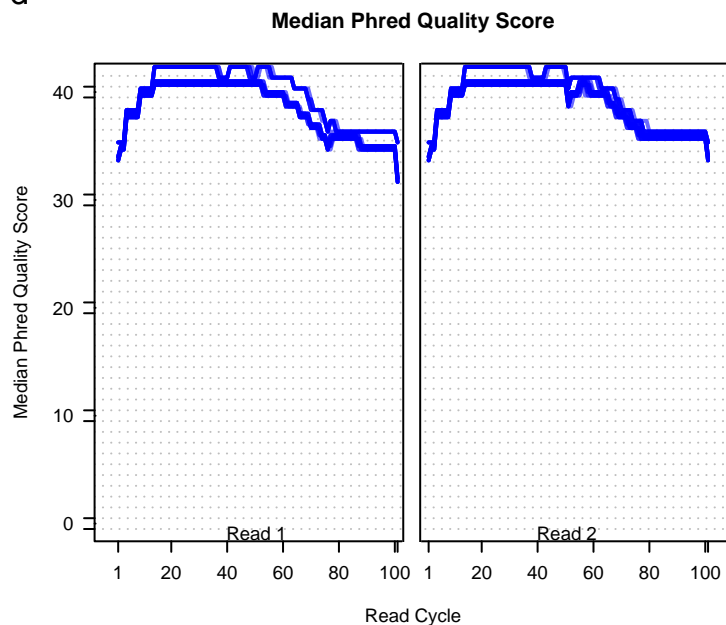
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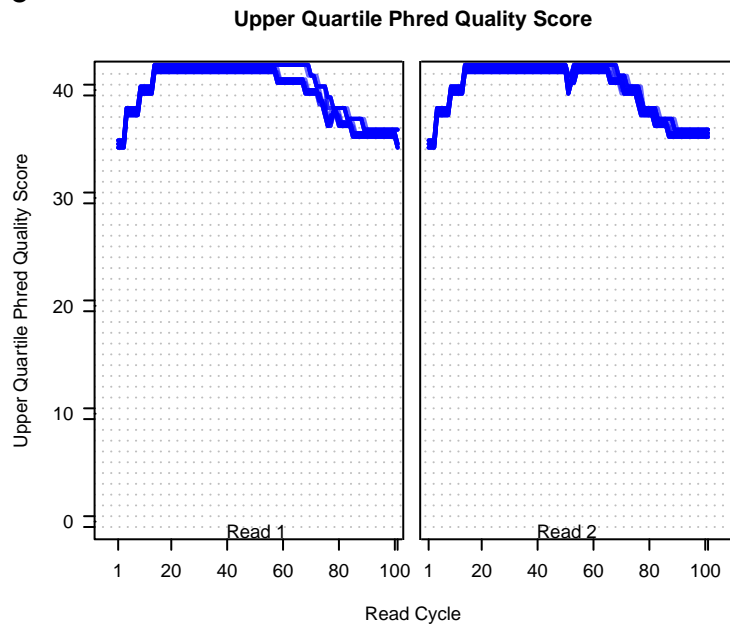
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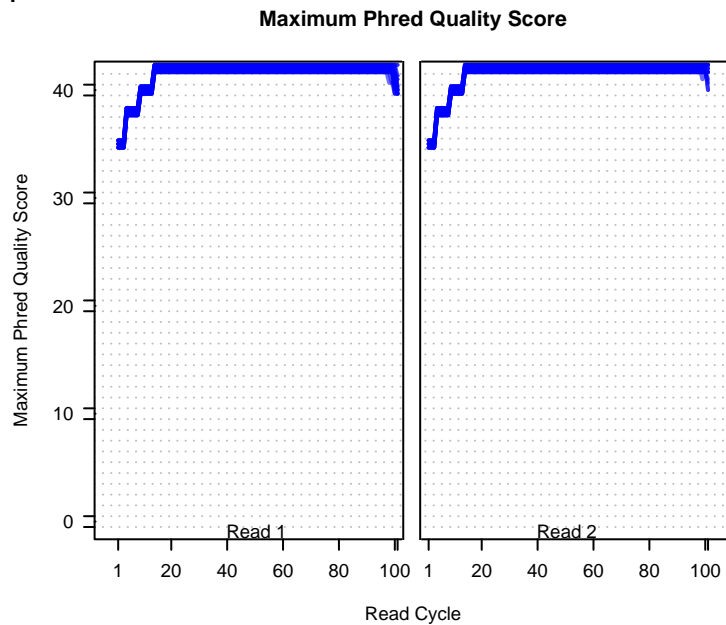
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e

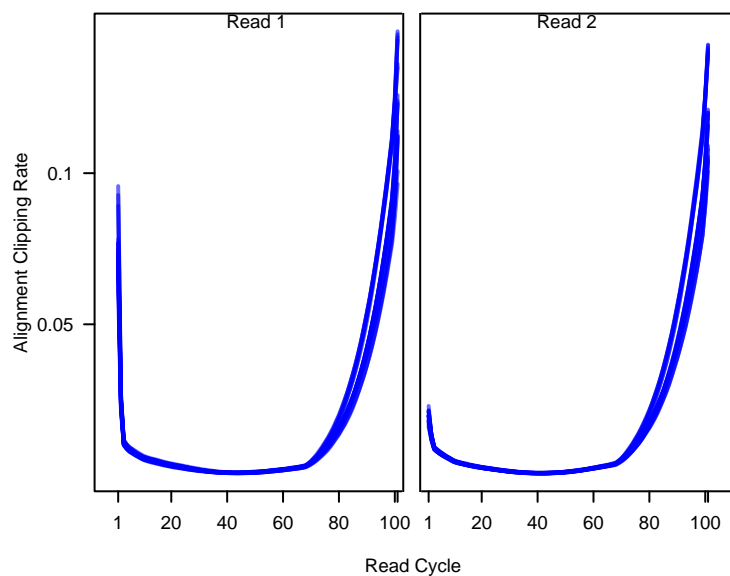


f



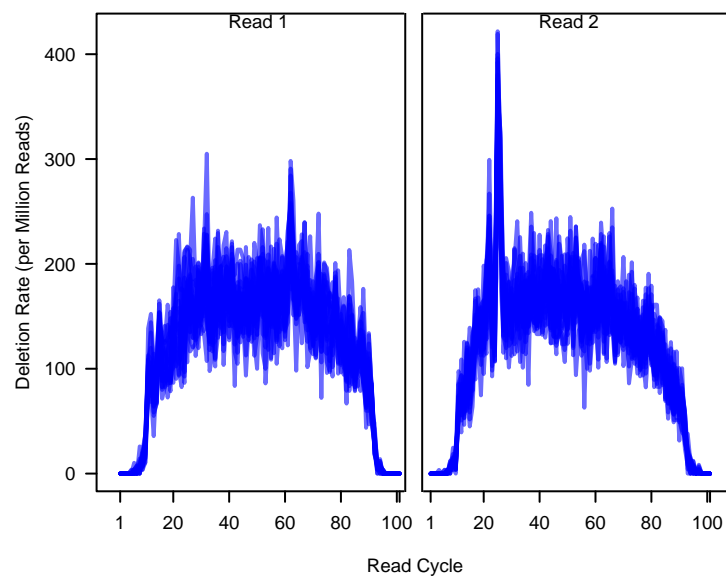
g

Alignment Clipping Rate, by read cycle



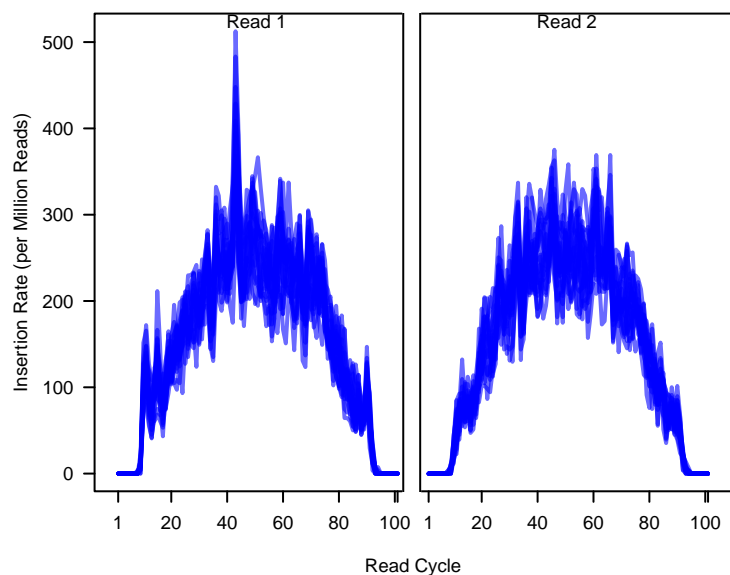
h

Deletion Rate, by read cycle



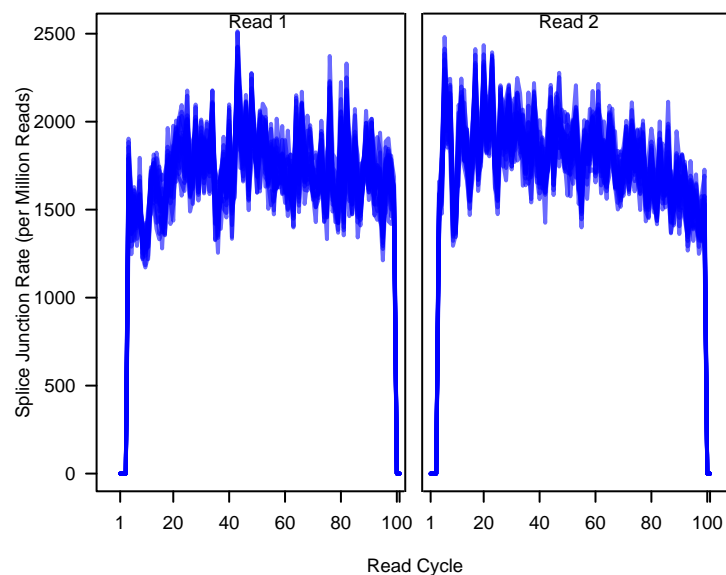
i

Insertion Rate, by read cycle



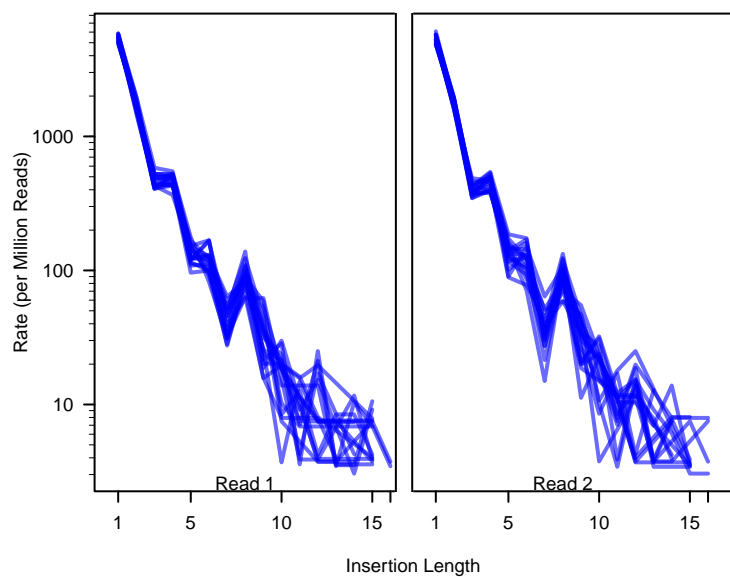
j

Splice Junction Rate, by read cycle



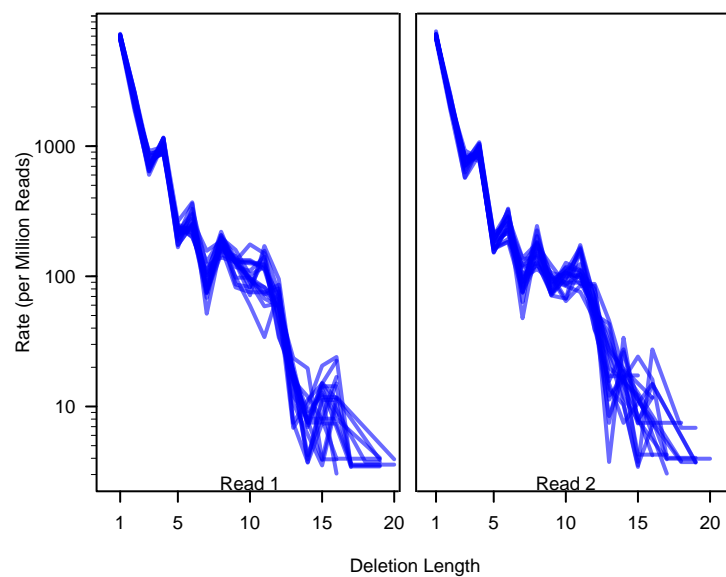
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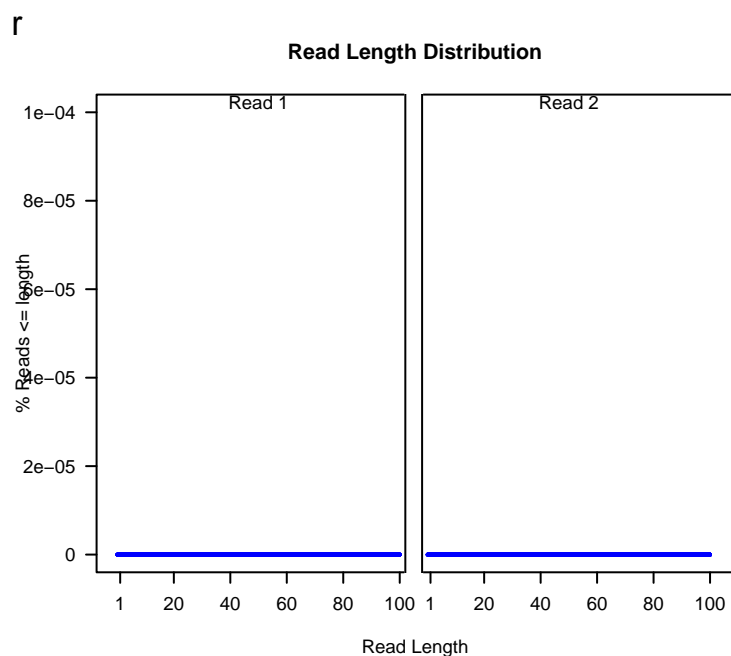
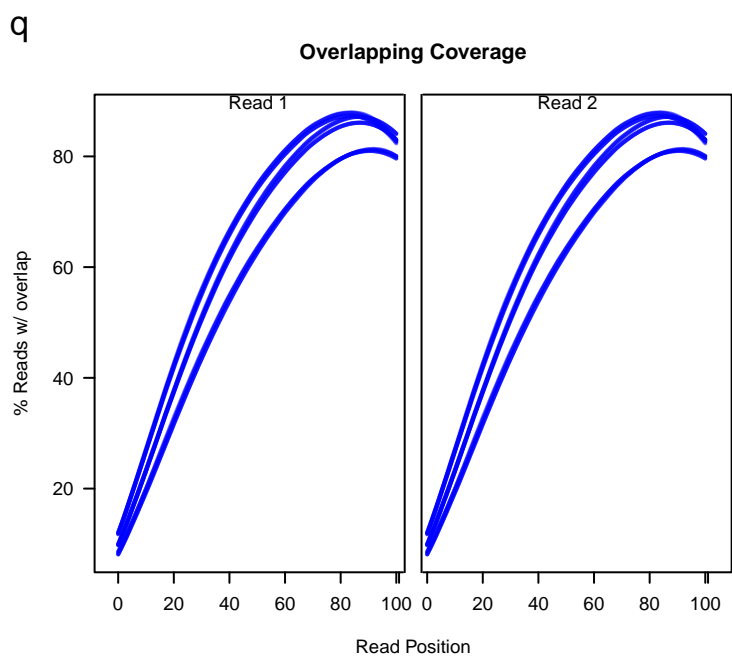
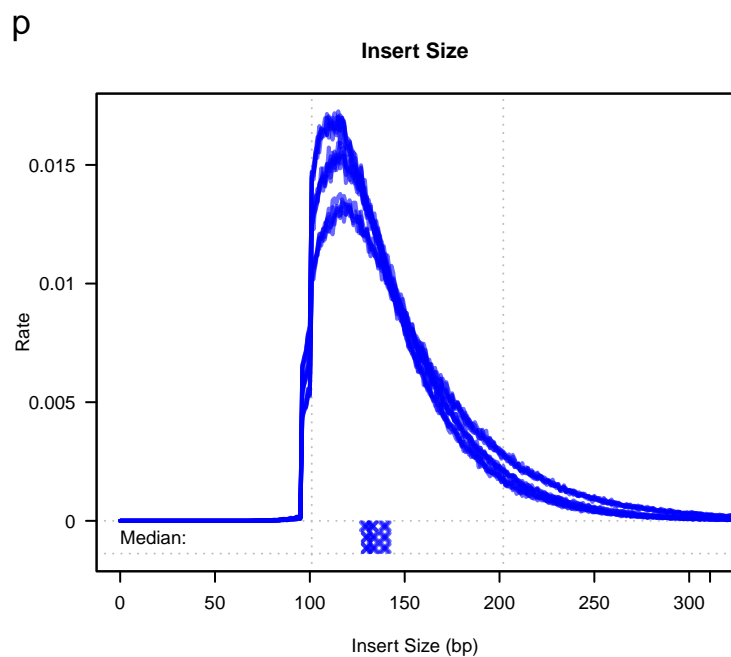
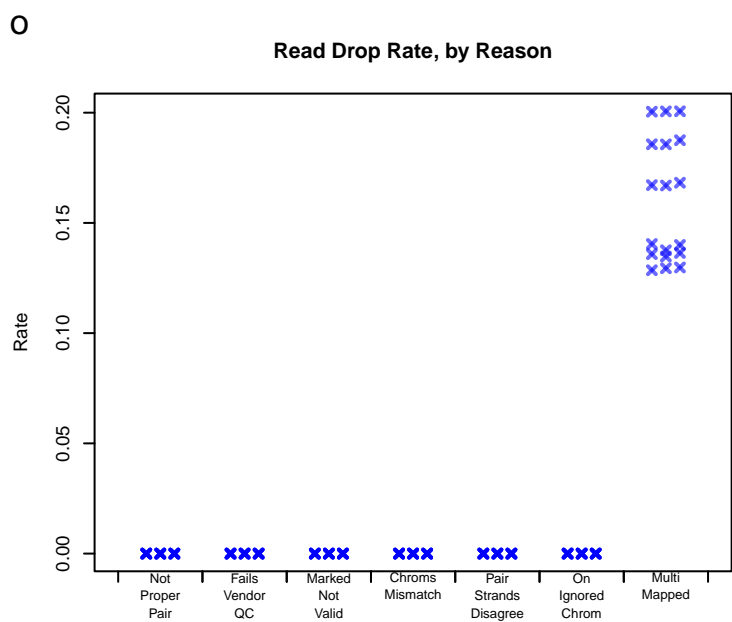
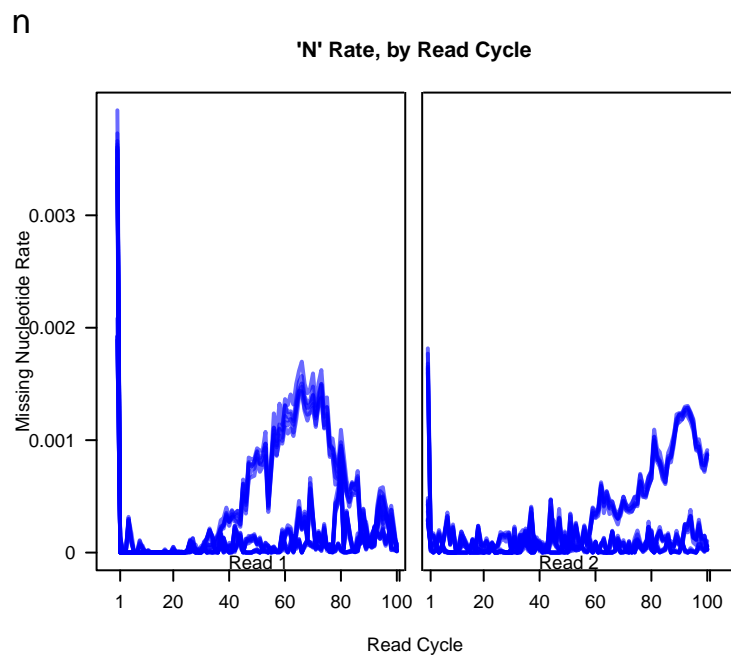
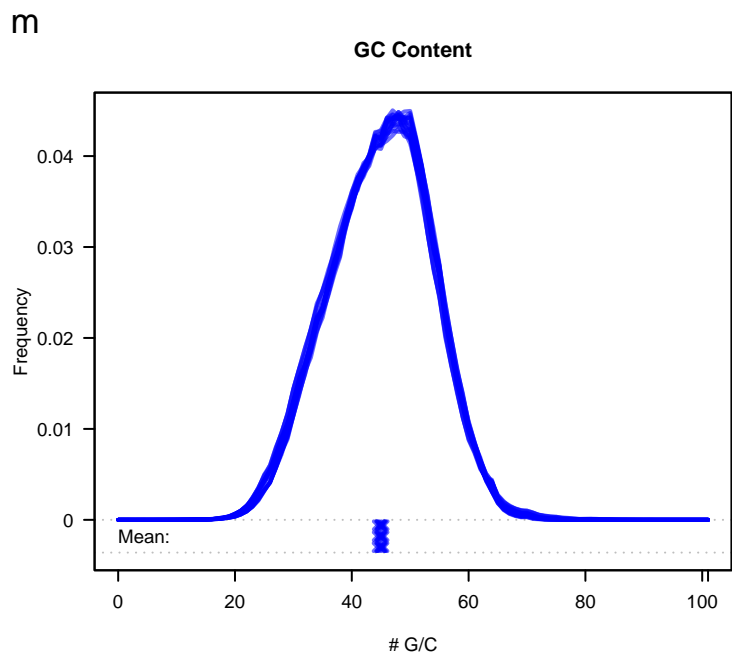
Insertion Length Distribution



l

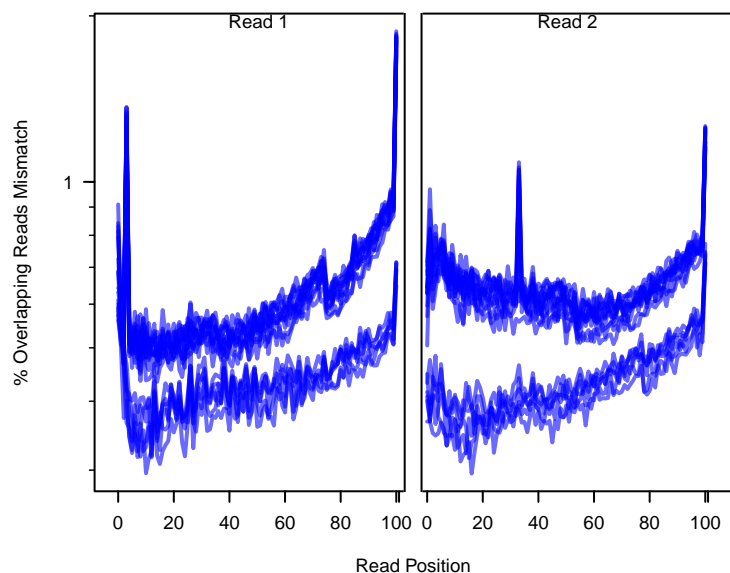
Deletion Length Distribution





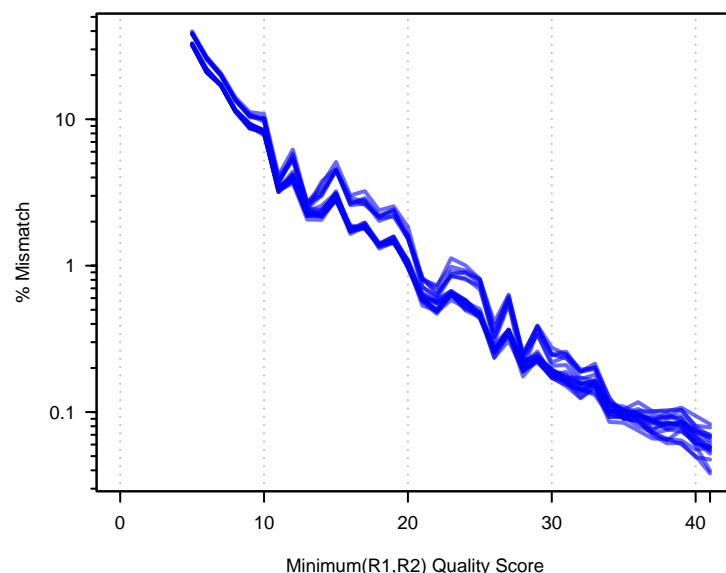
S

Overlap Mismatch by Read Cycle



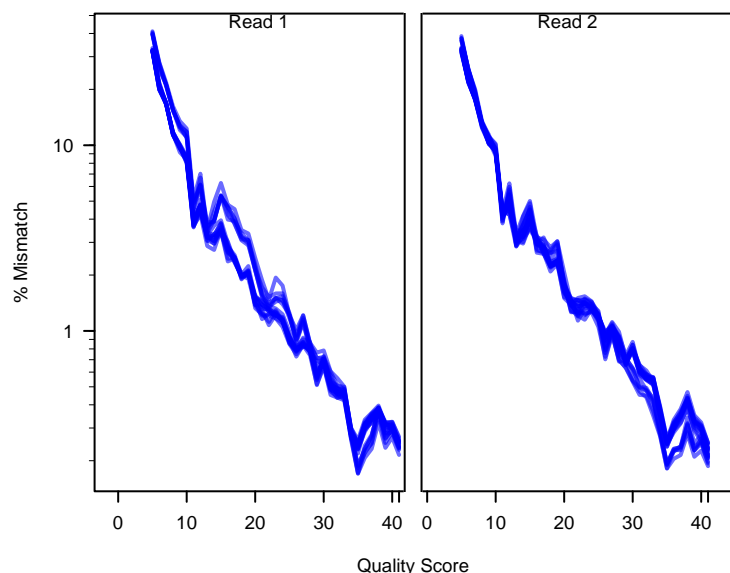
t

Overlapping Mismatch by Min Qual



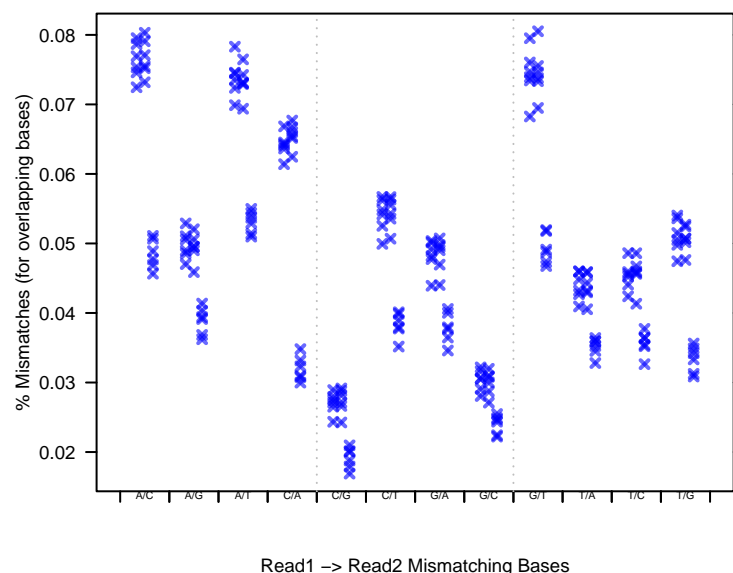
U

Overlap Mismatch by Read Qual



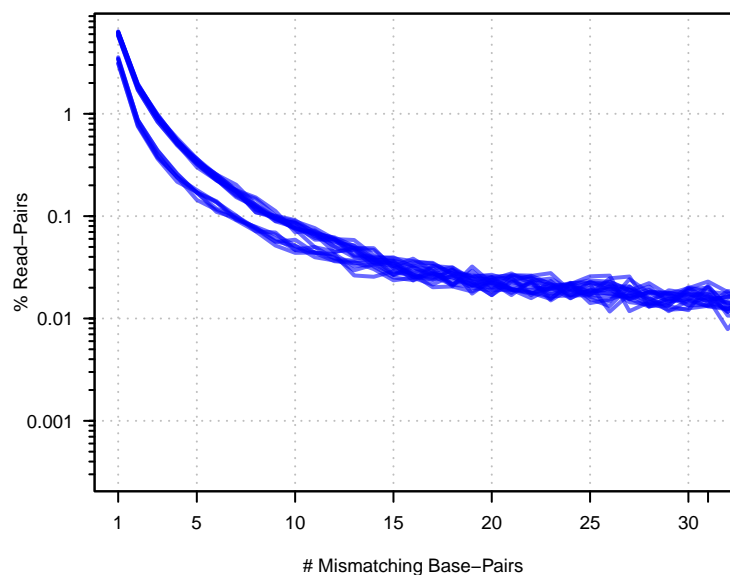
V

Overlap Mismatch Combinations



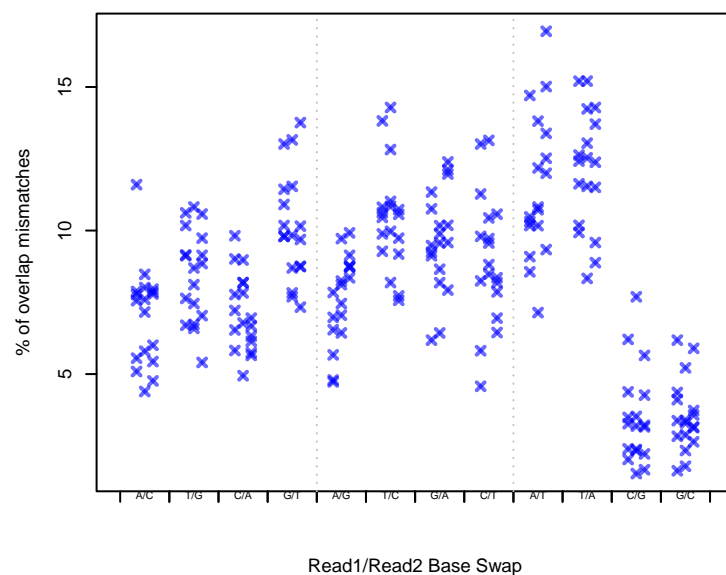
W

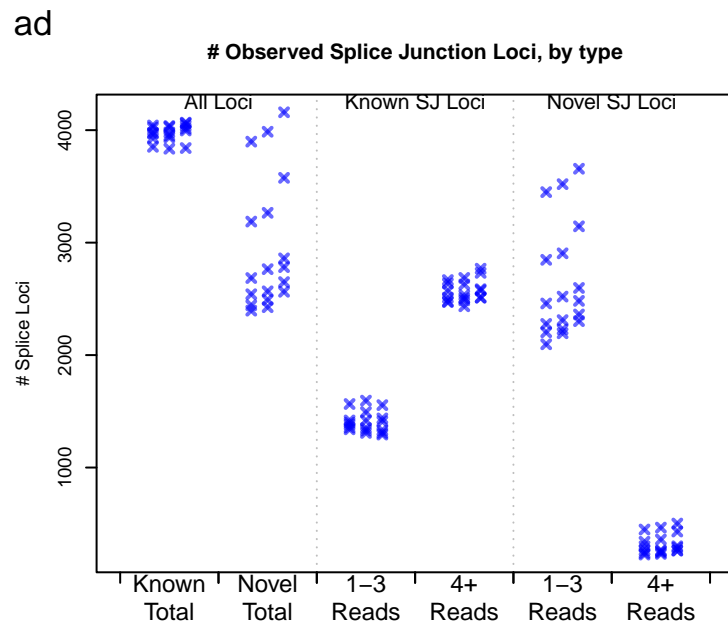
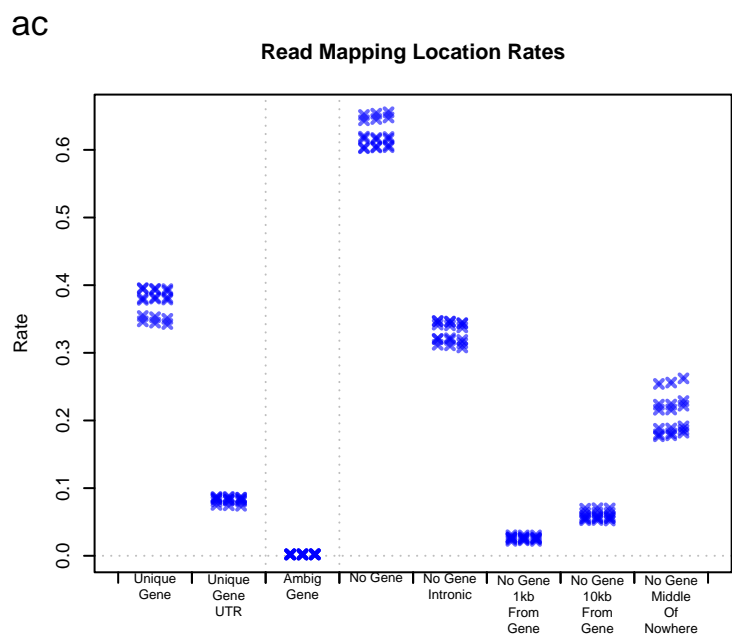
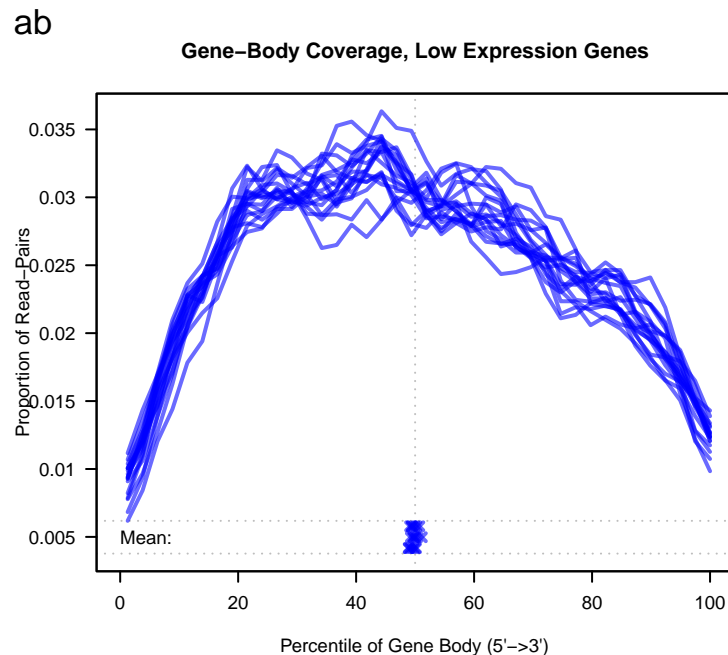
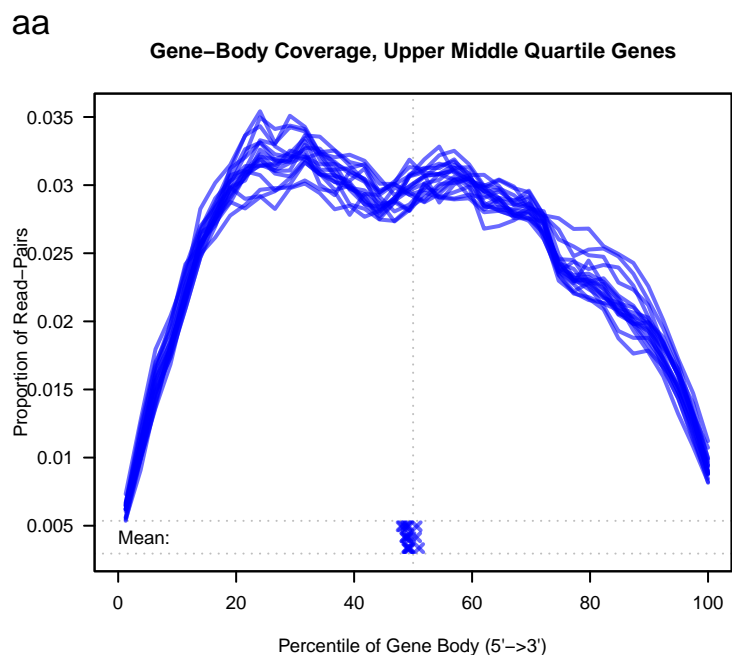
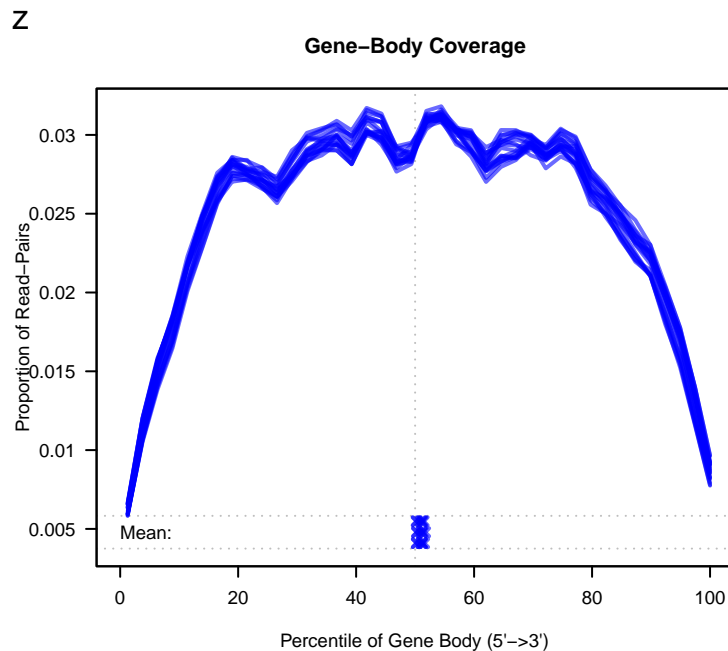
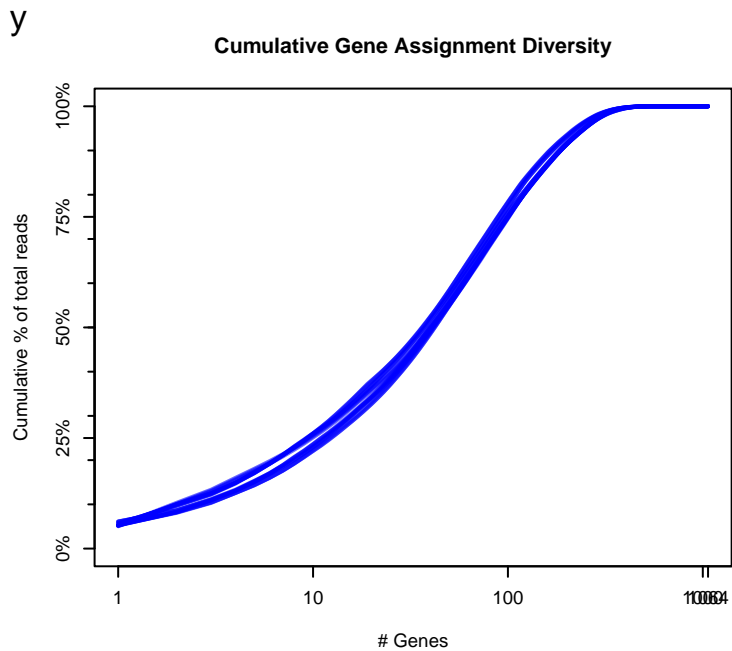
Overlap Mismatch Size Frequency



X

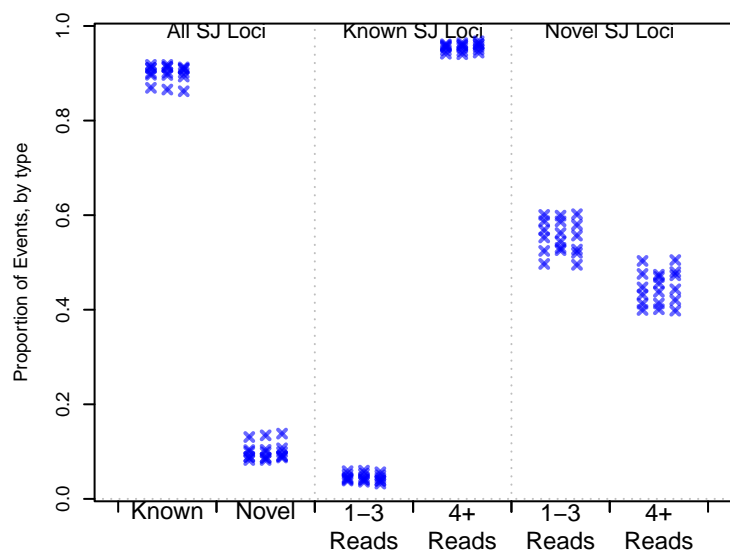
Overlap Mismatch Pairs At Phred == 41





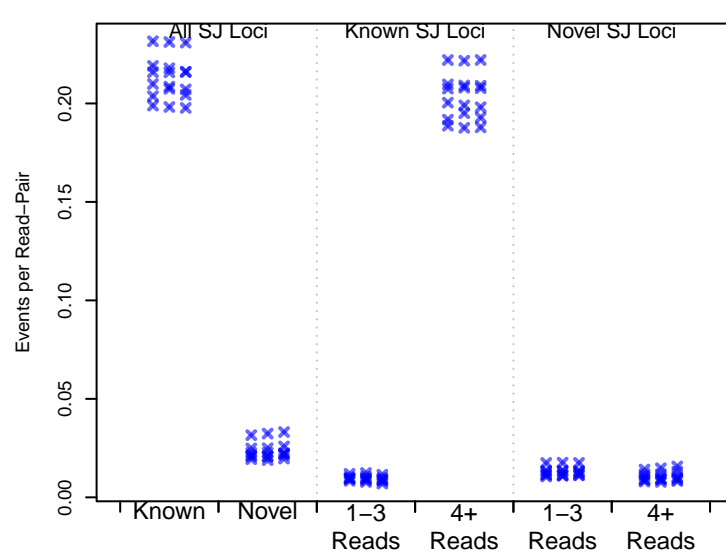
ae

Breakdown of Splice Junction Events, by type



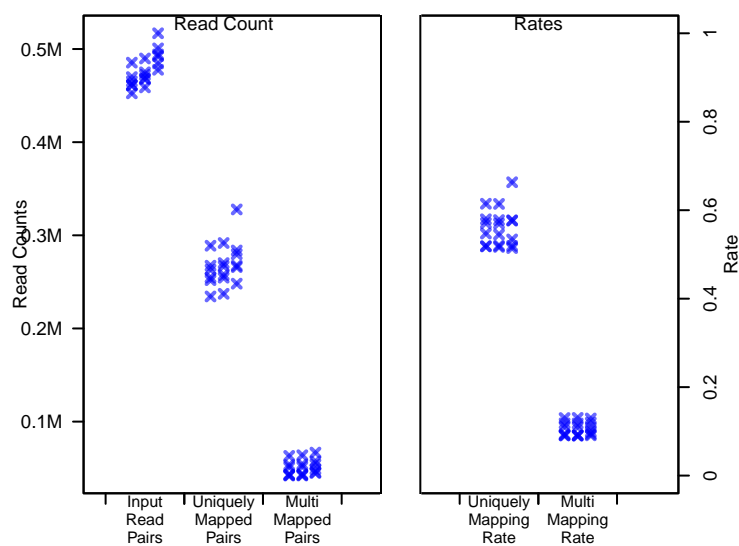
af

Splice Junction Event Rates per Read-Pair



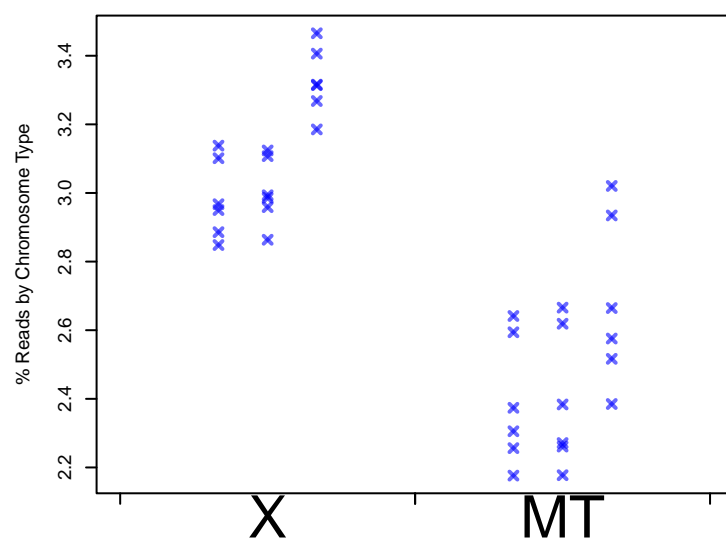
ag

Mapping Stats



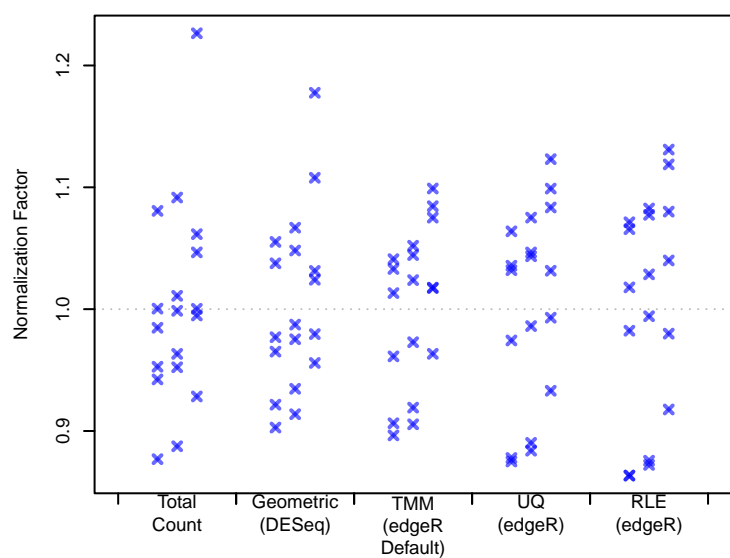
ah

Chromosome Distribution (Excluding Autosomes)



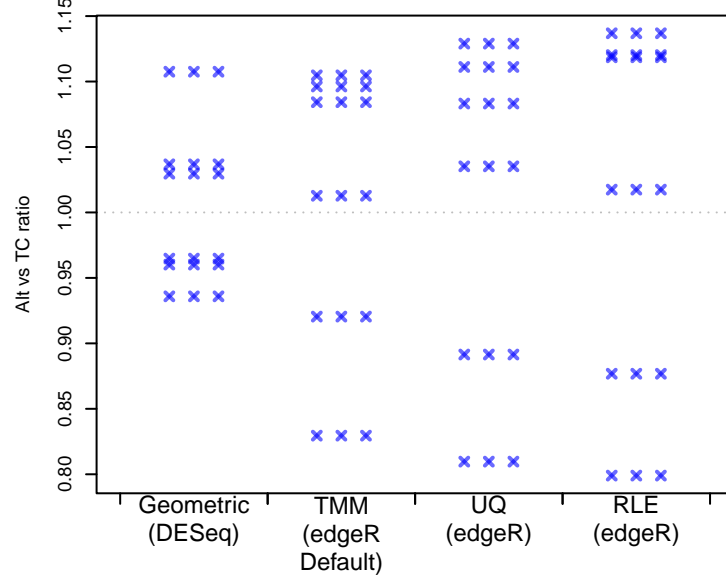
ai

Normalization Factors



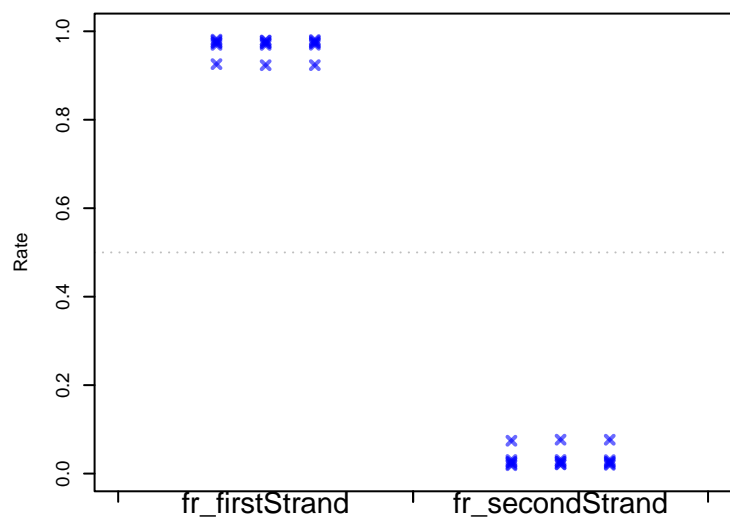
aj

Normalization Factors vs Total-Count Normalization



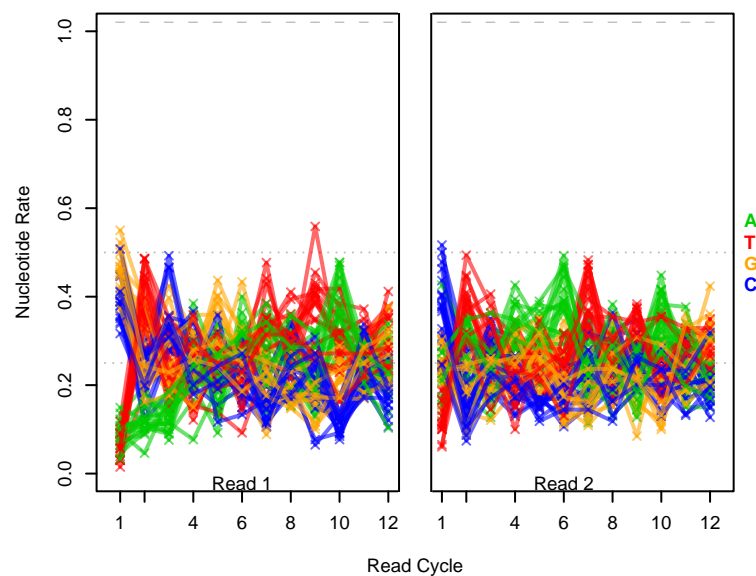
ak

Strandedness Test



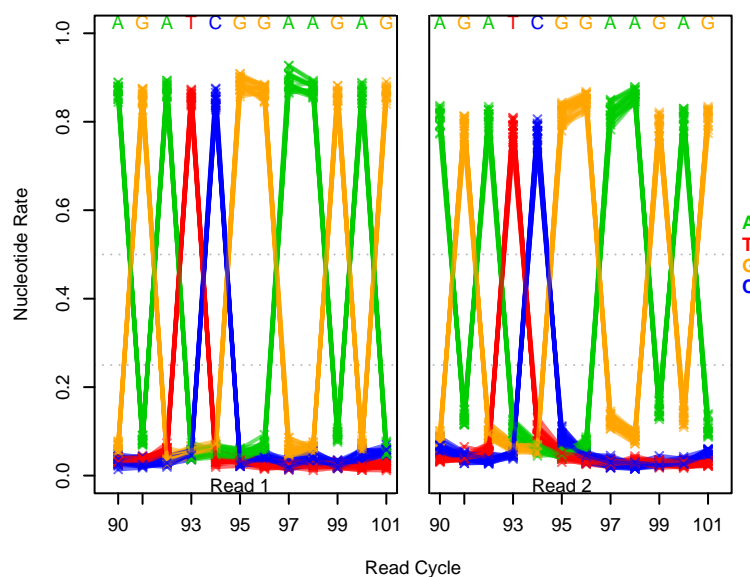
al

Nucleotide Rate by Cycle, Leading Clipped bases (12)



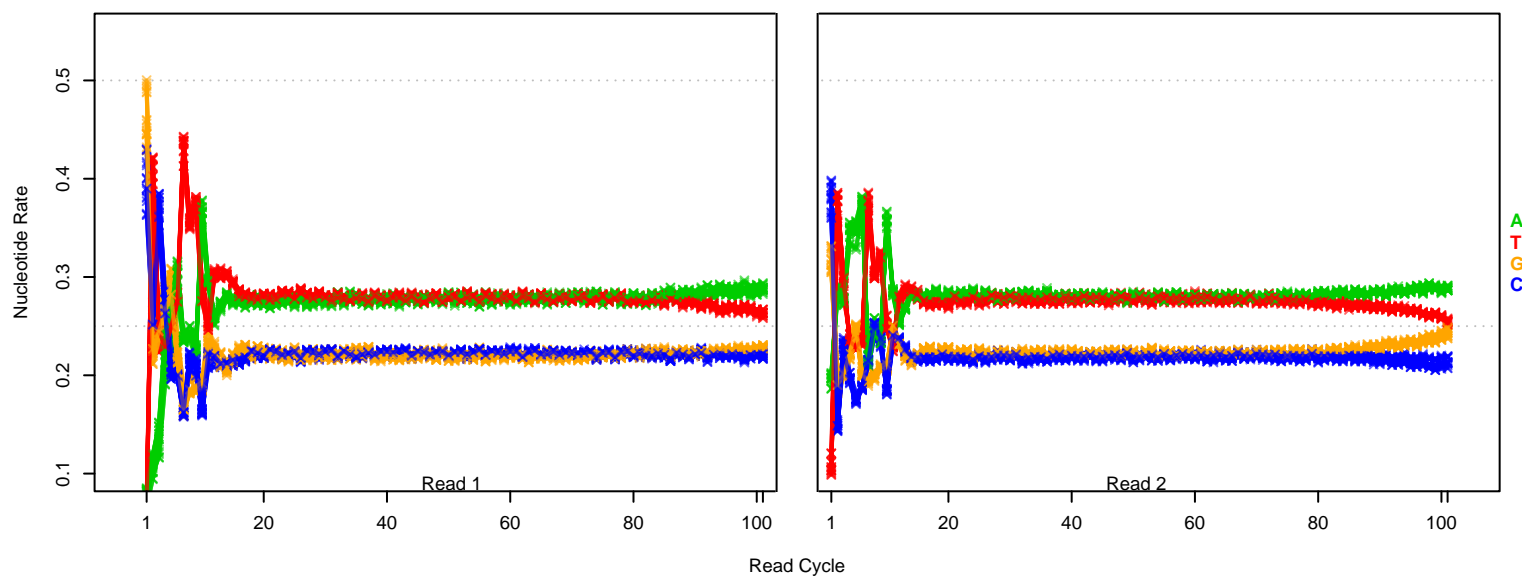
am

Nucleotide Rate by Cycle, Trailing Clipped bases (12)



an

Raw Nucleotide Rate by Cycle



Nucleotide Rate by Cycle, Aligned bases only

