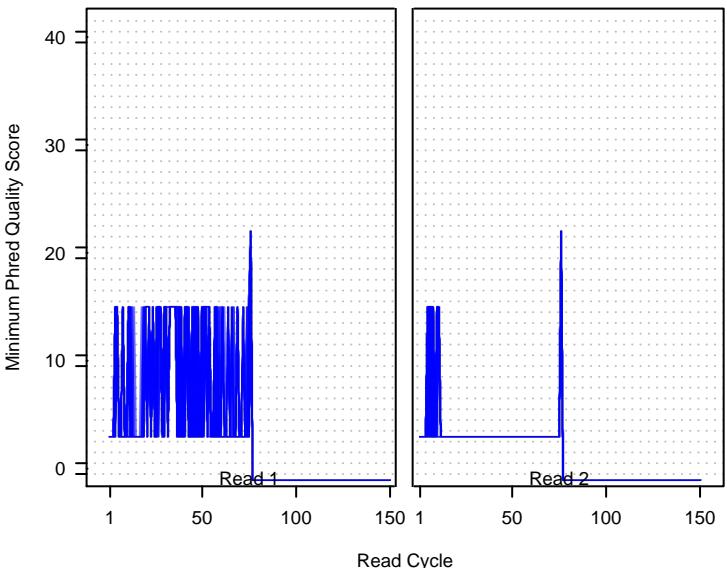


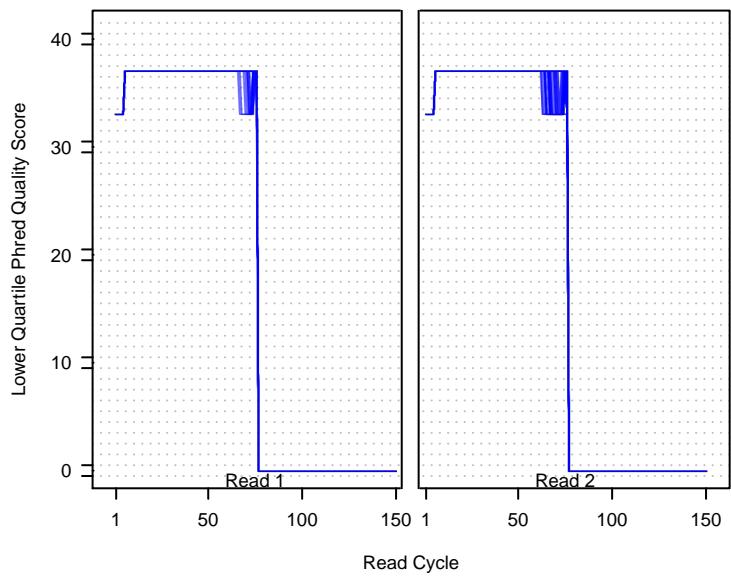
a

All Quality Control Summary Plots

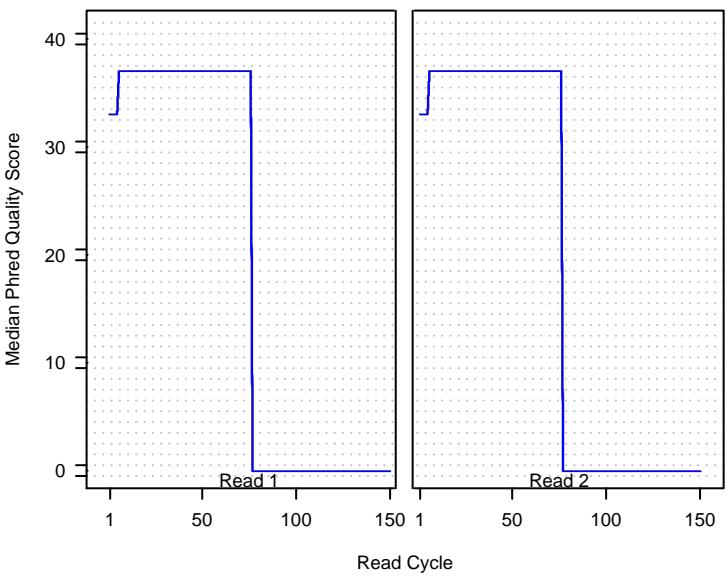
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Minimum Phred Quality Score

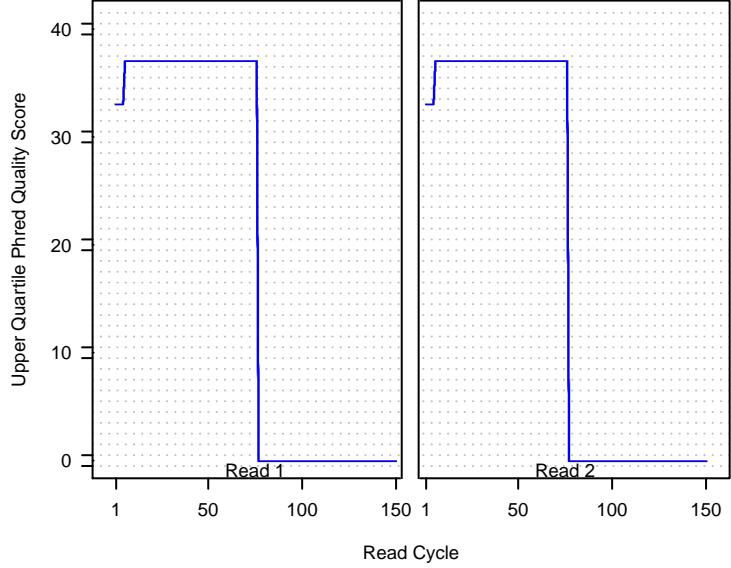
c

Lower Quartile Phred Quality Score

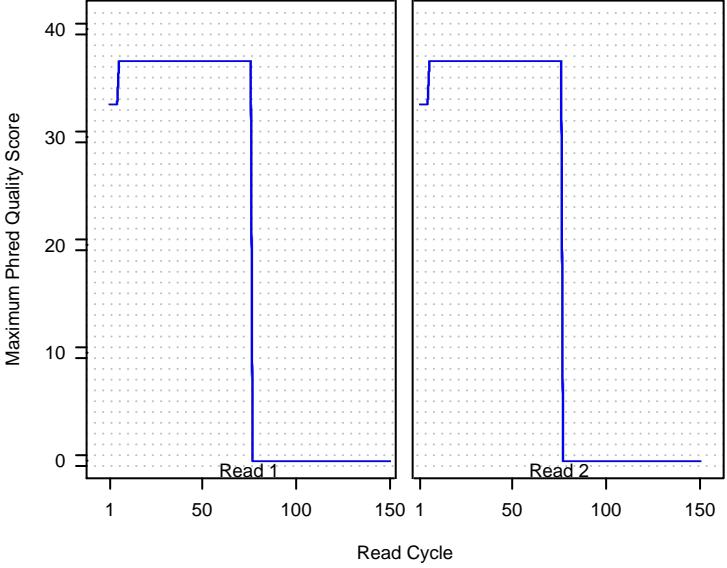
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Median Phred Quality Score

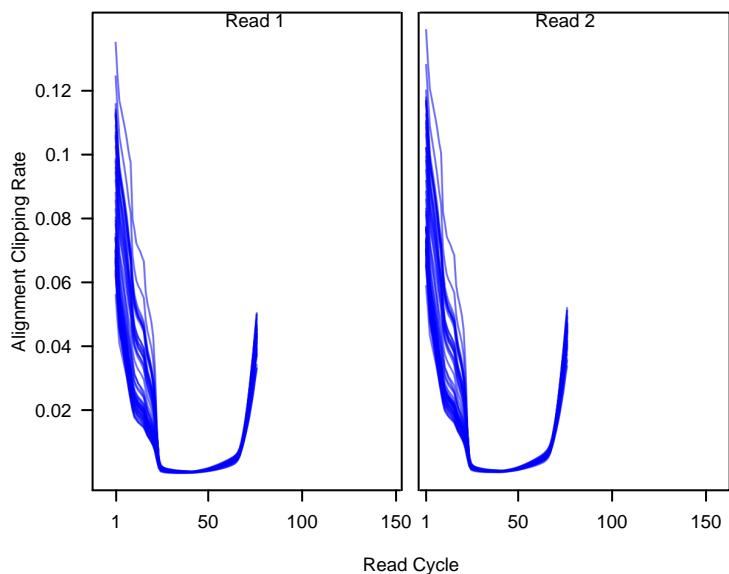
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Upper Quartile Phred Quality Score

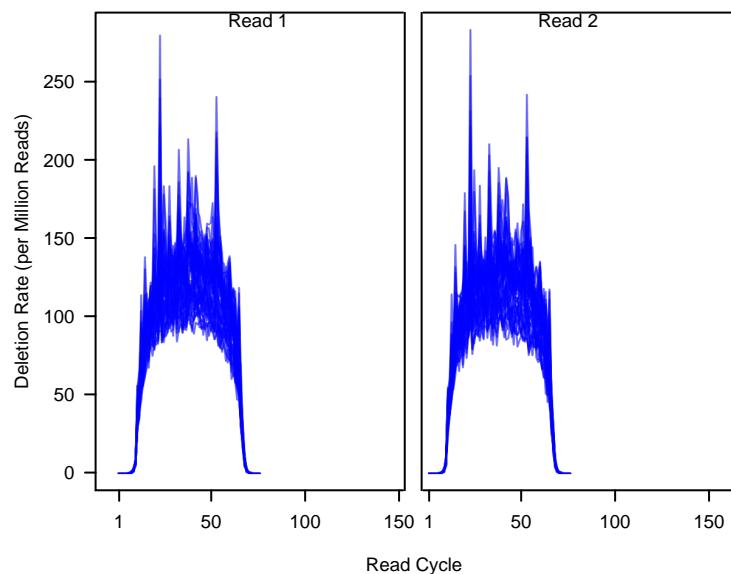
f

Maximum Phred Quality Score

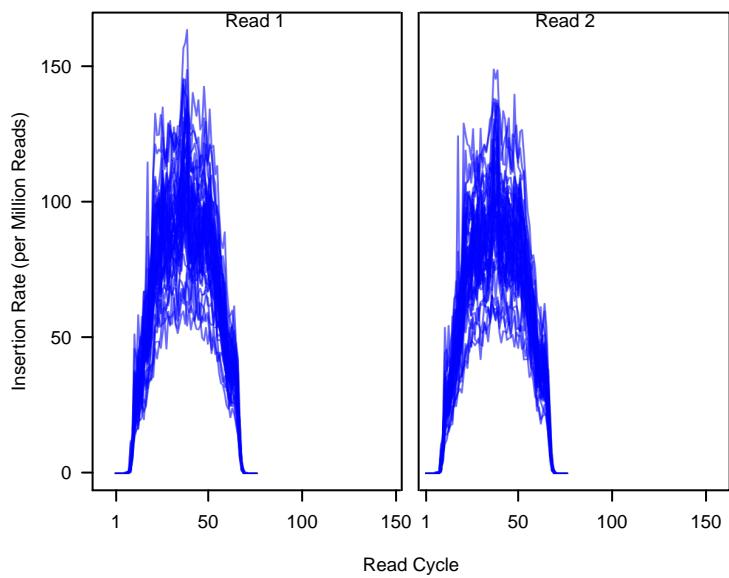
g

Alignment Clipping Rate, by read cycle

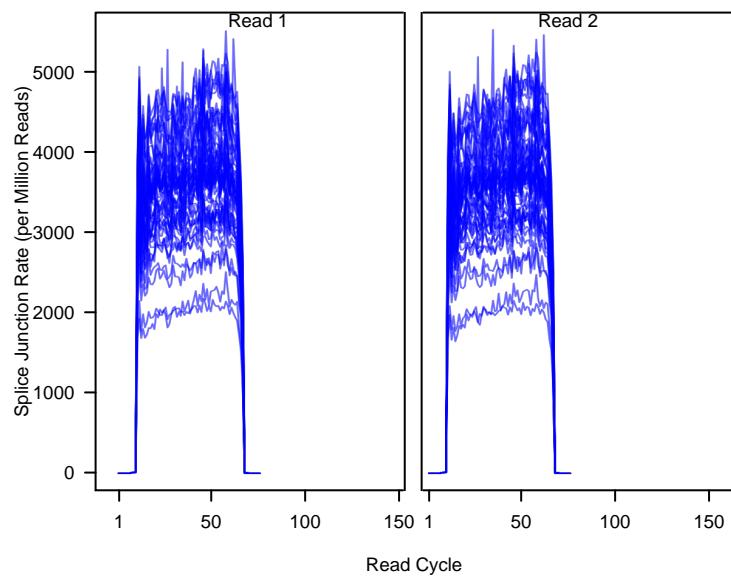
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Deletion Rate, by read cycle

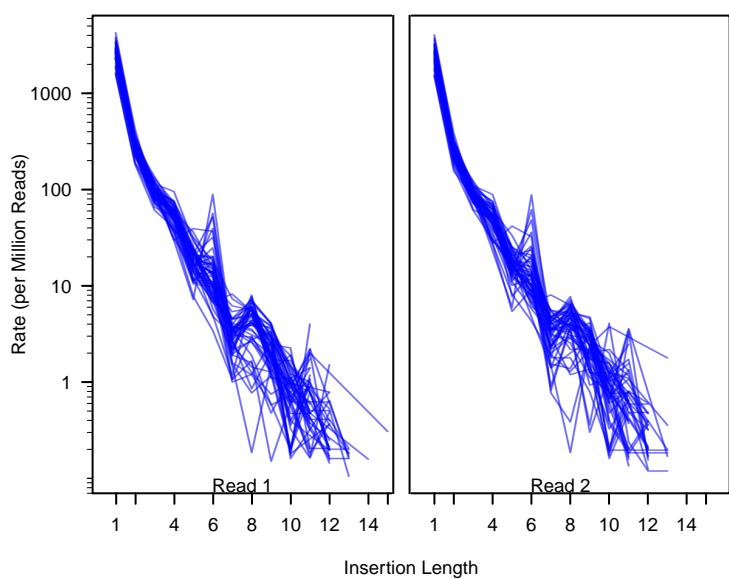
i

Insertion Rate, by read cycle

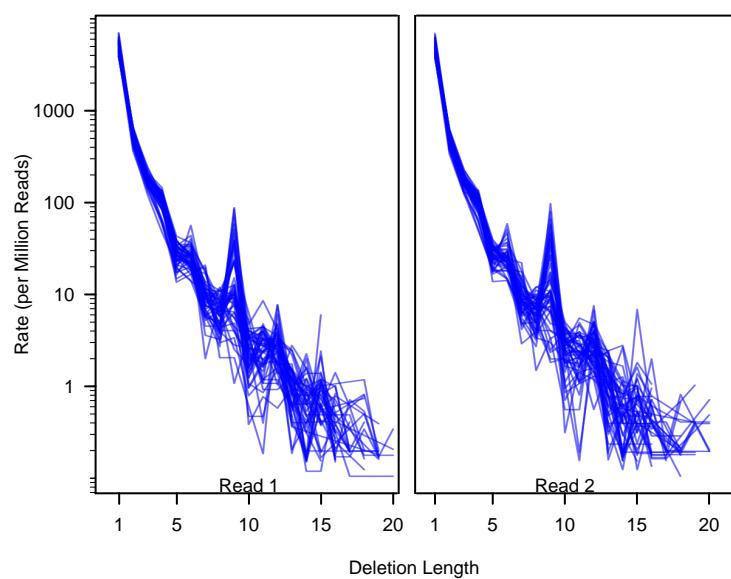
j

Splice Junction Rate, by read cycle

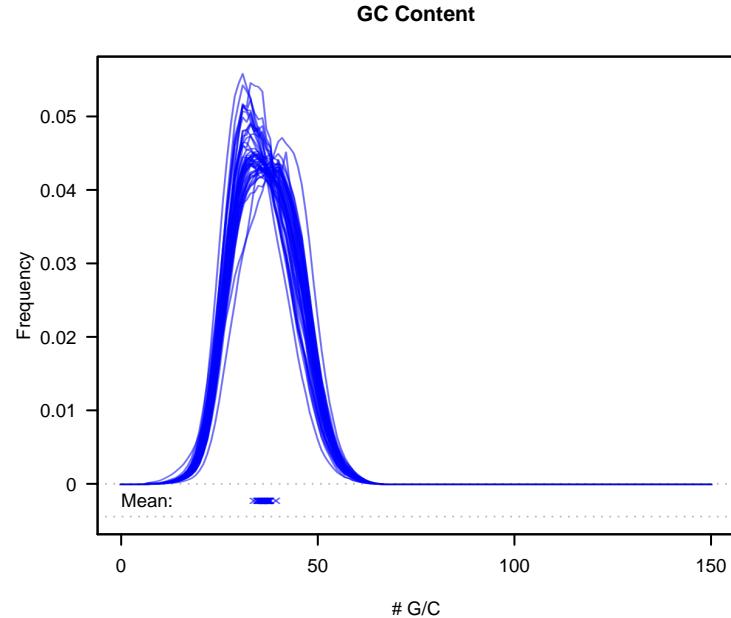
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Insertion Length Distribution

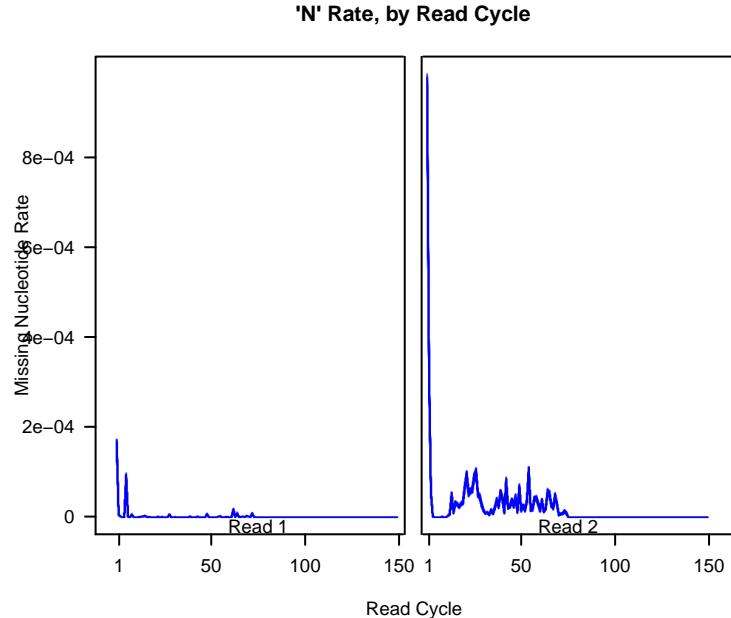
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Deletion Length Distribution

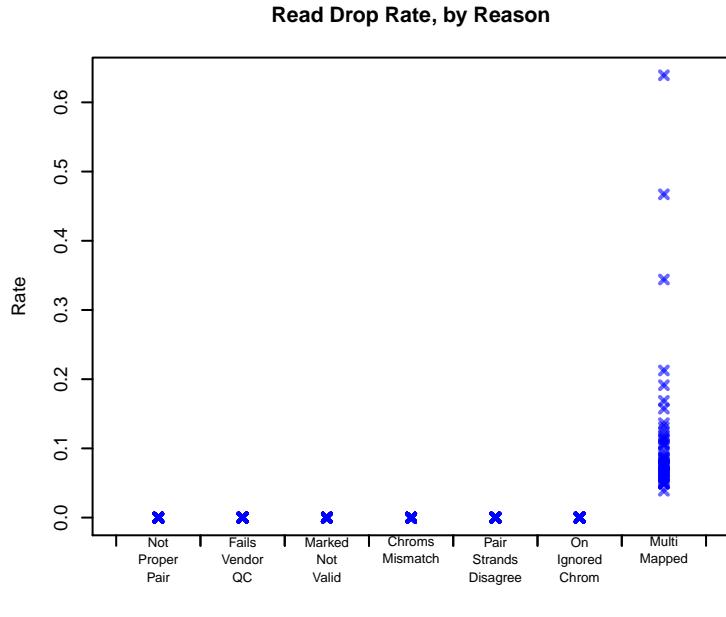
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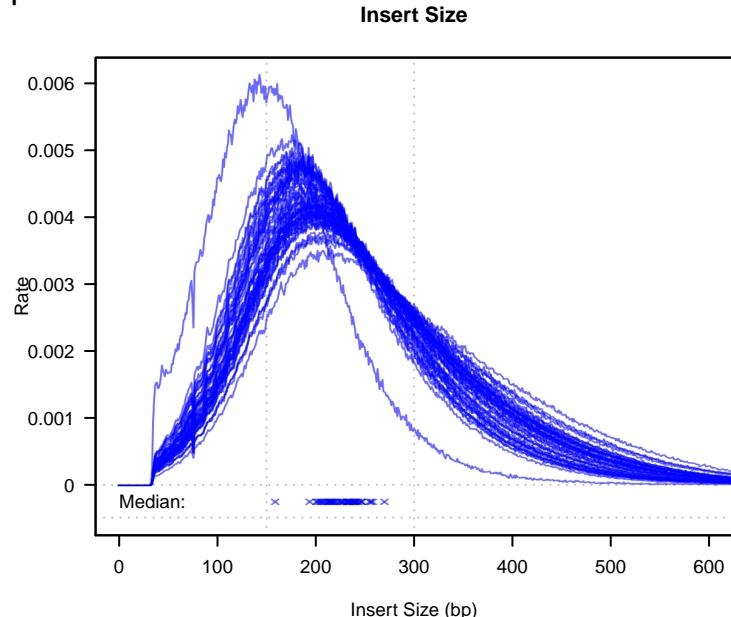
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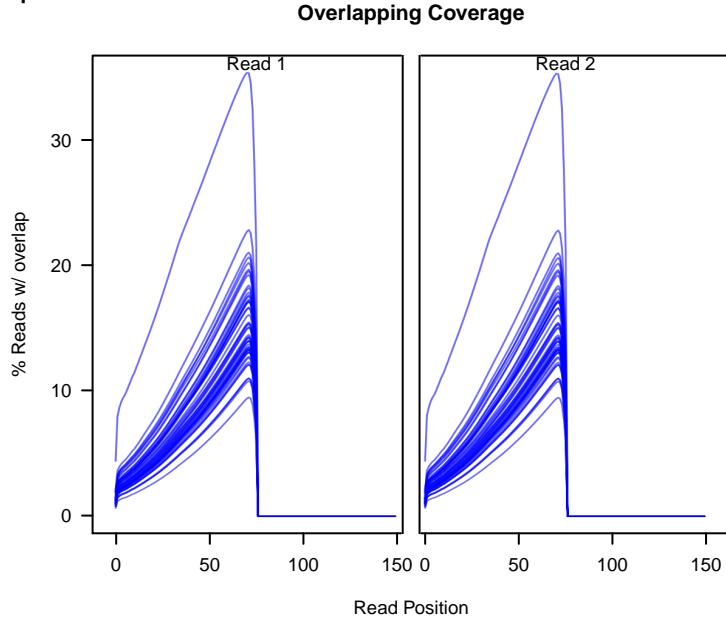
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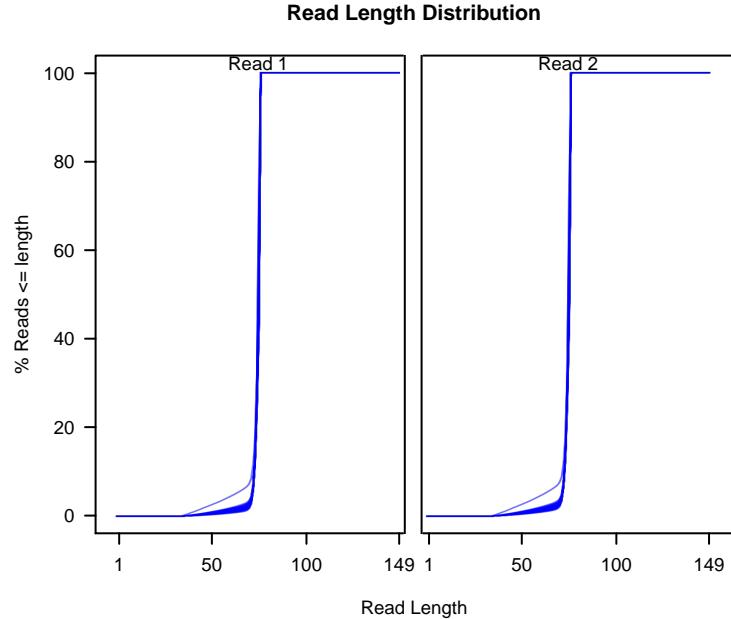
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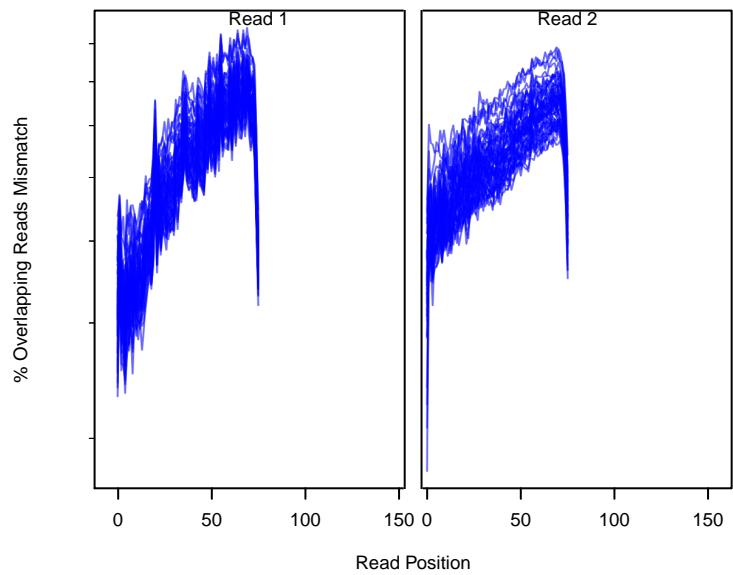
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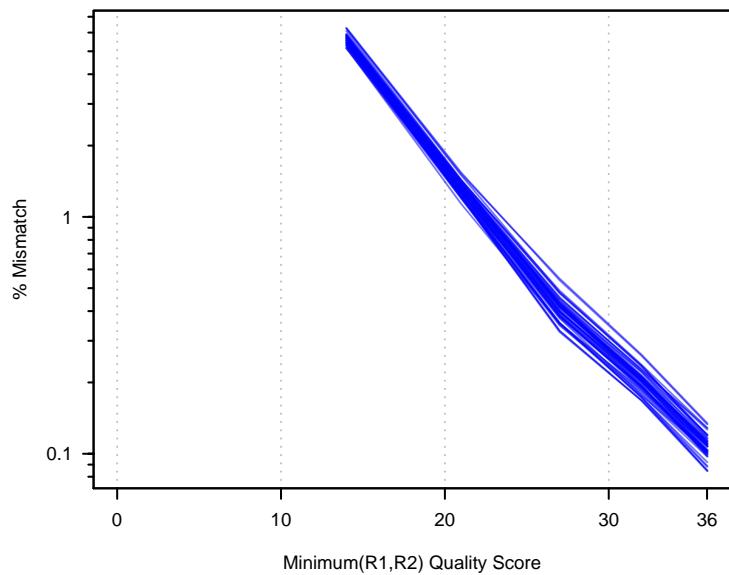
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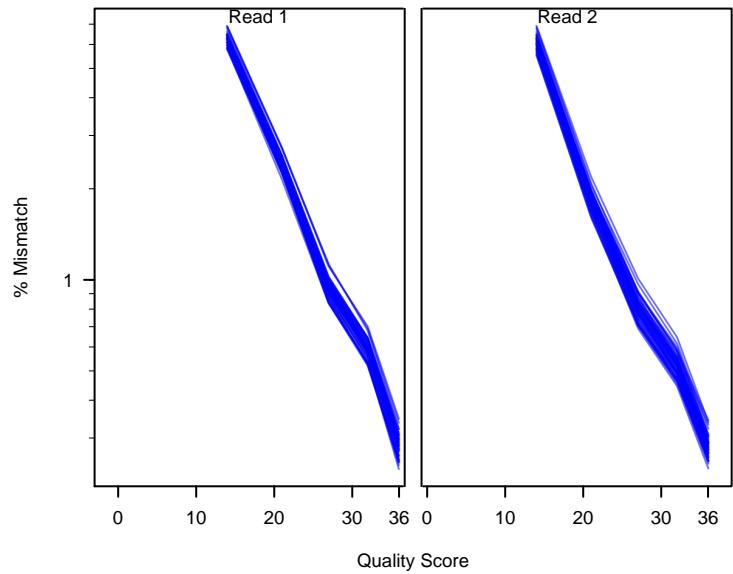
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Overlap Mismatch by Read Cycle

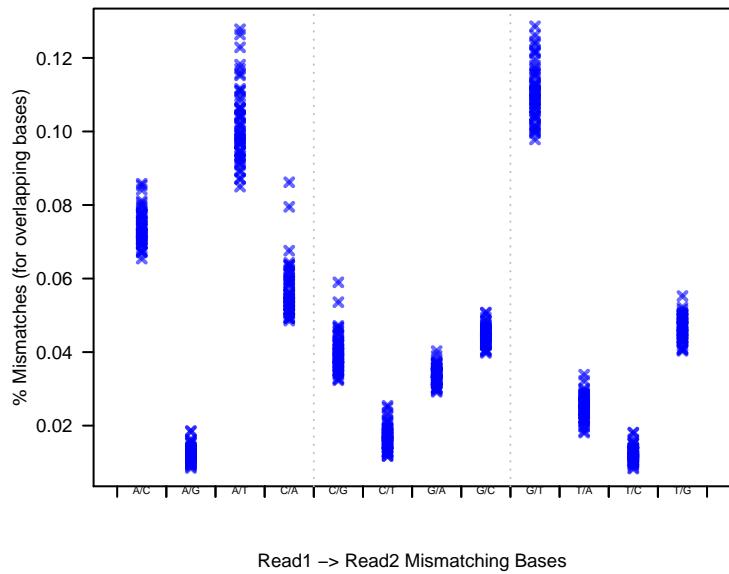
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Overlapping Mismatch by Min Qual

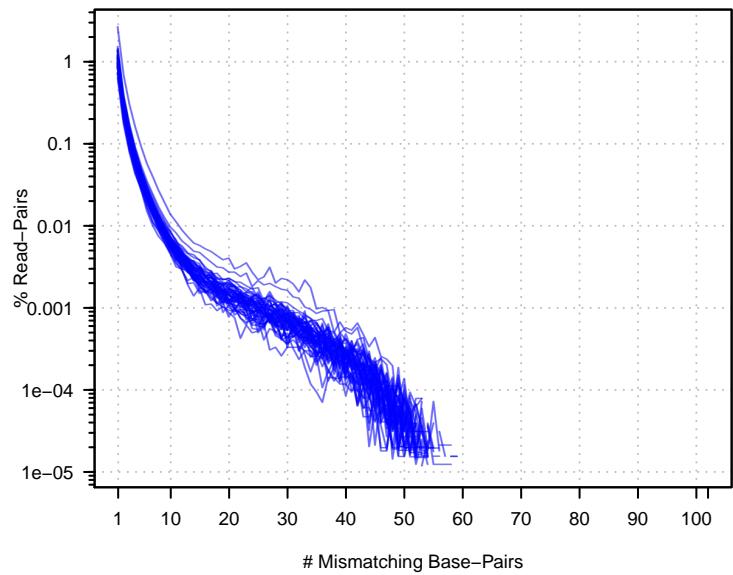
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Overlap Mismatch by Read Qual

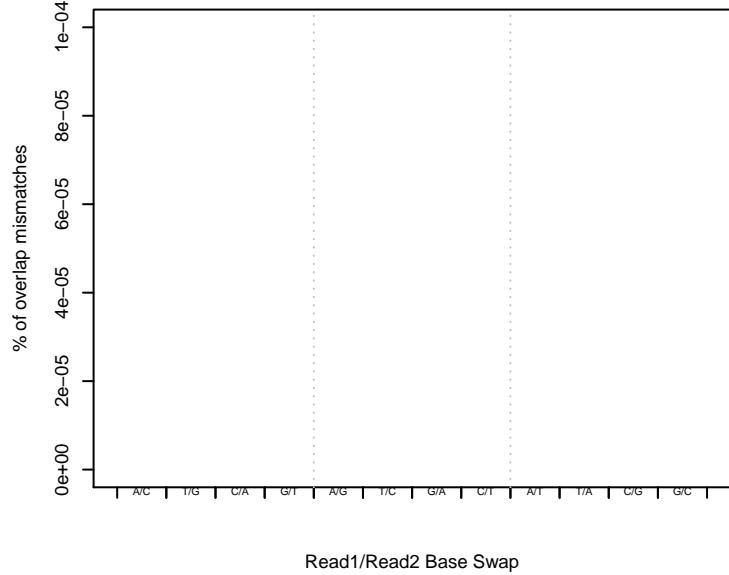
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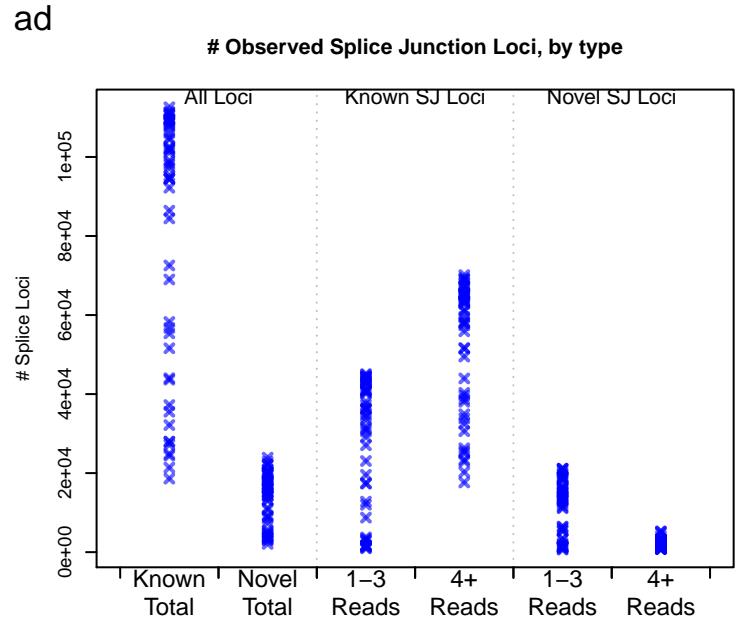
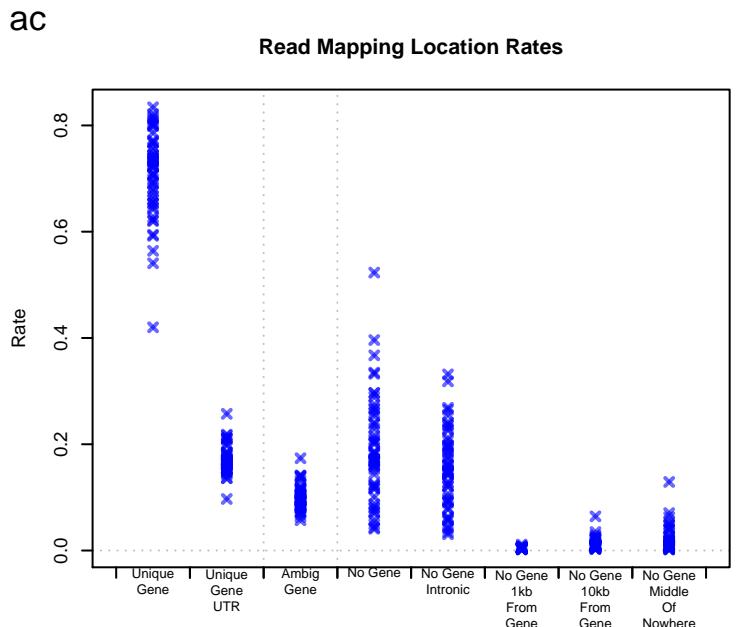
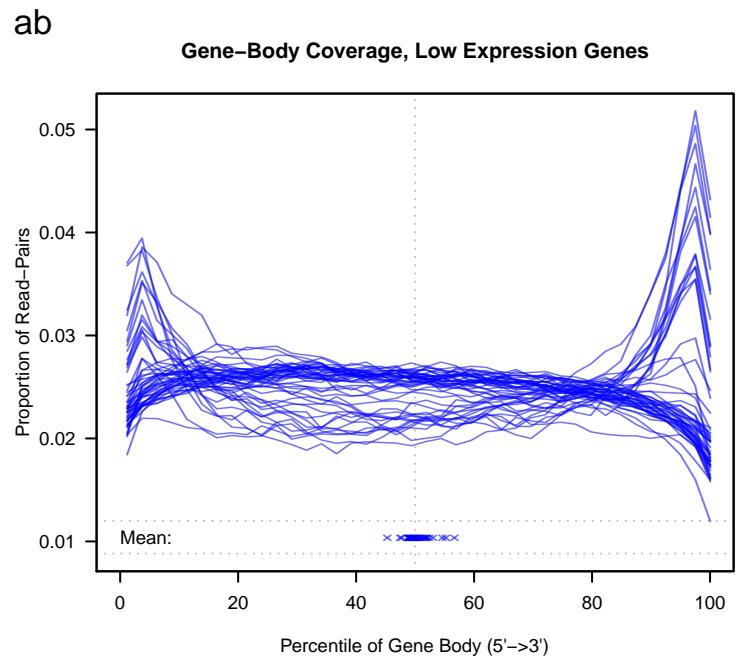
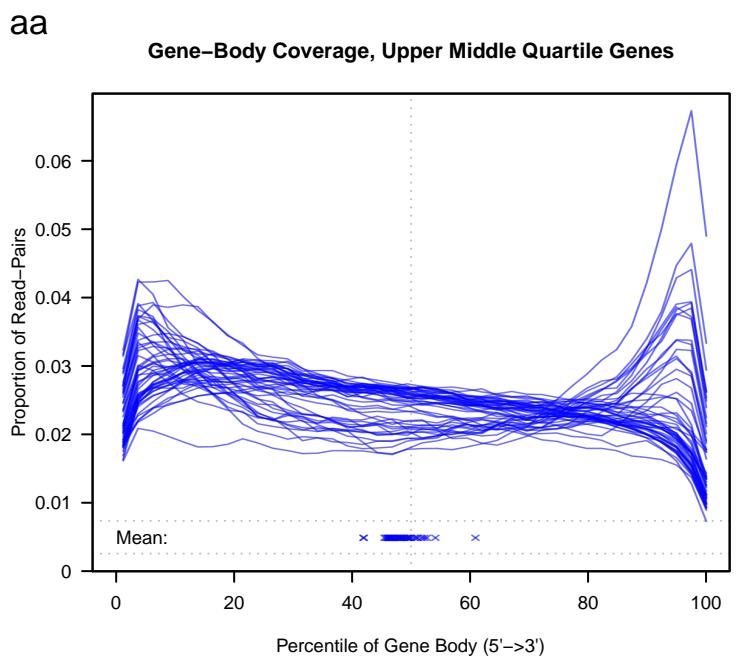
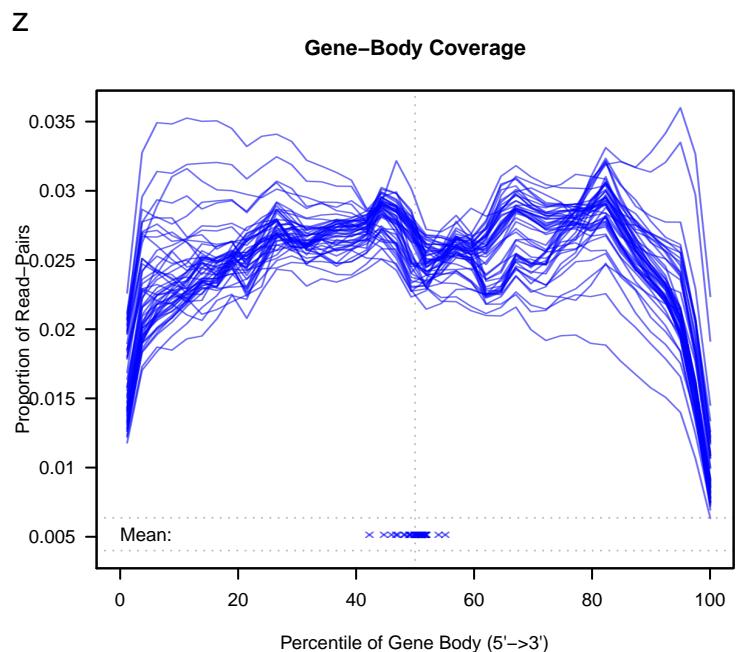
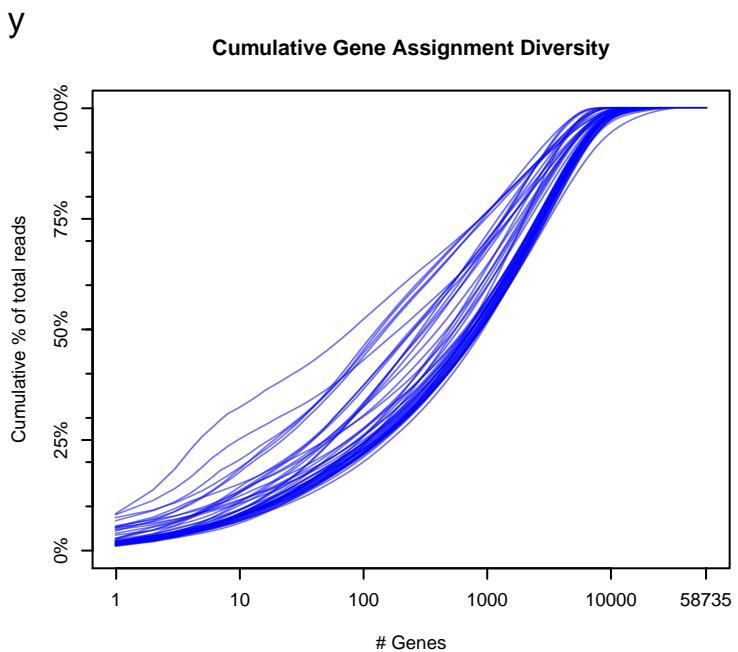
Overlap Mismatch Combinations

w

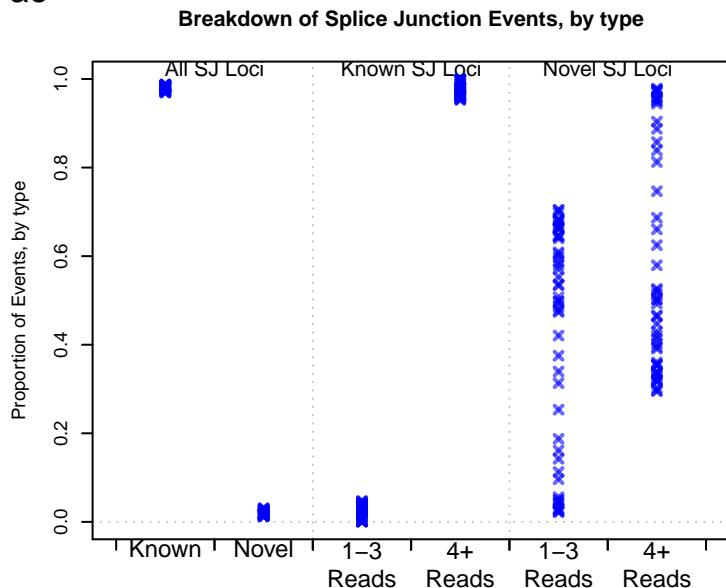
Overlap Mismatch Size Frequency

x

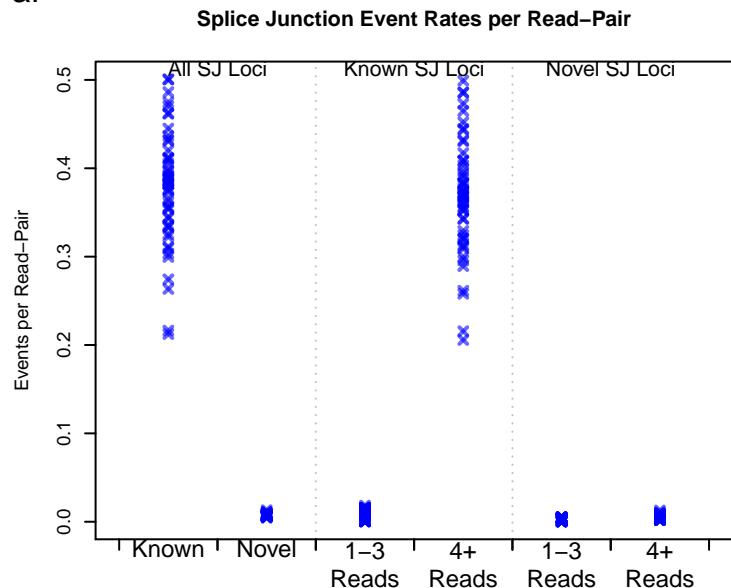
Overlap Mismatch Pairs At Phred == 41



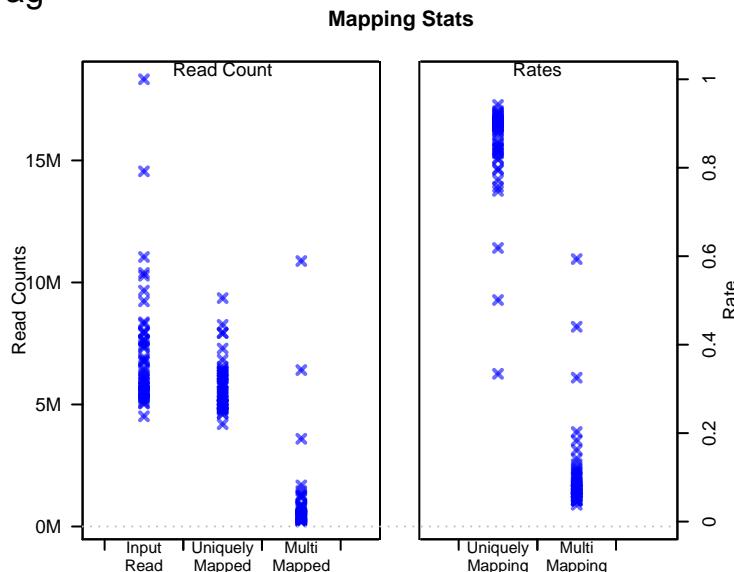
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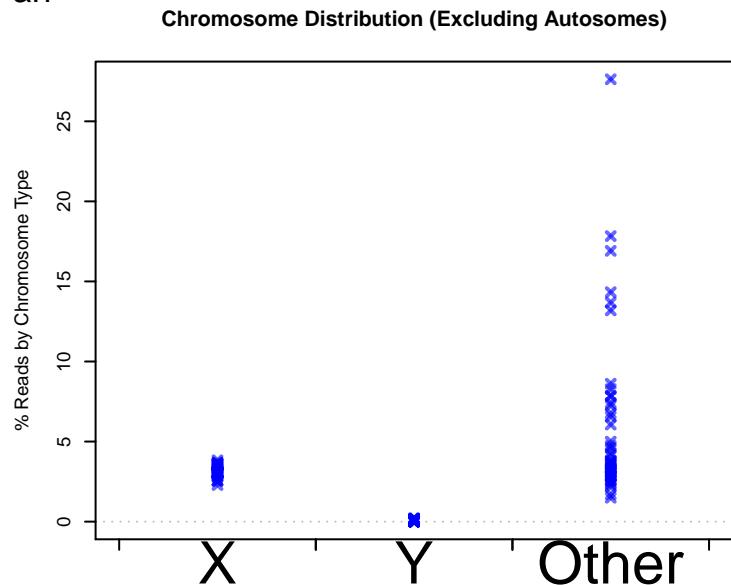
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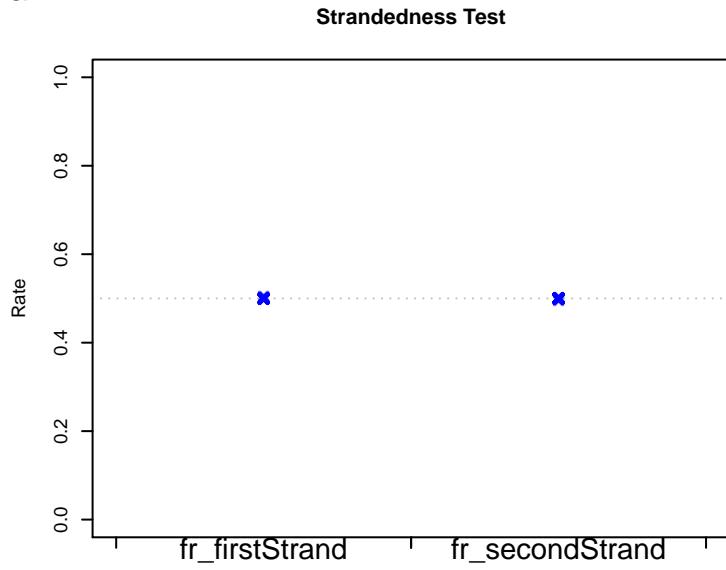
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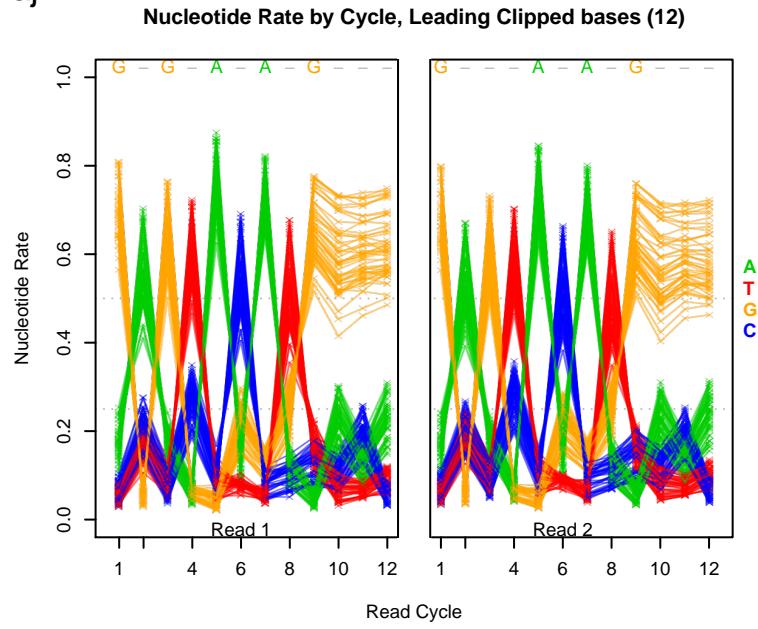
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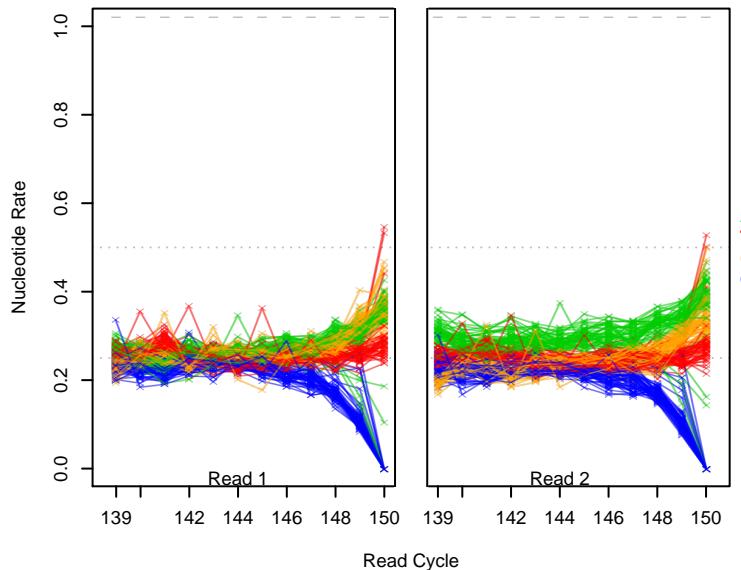


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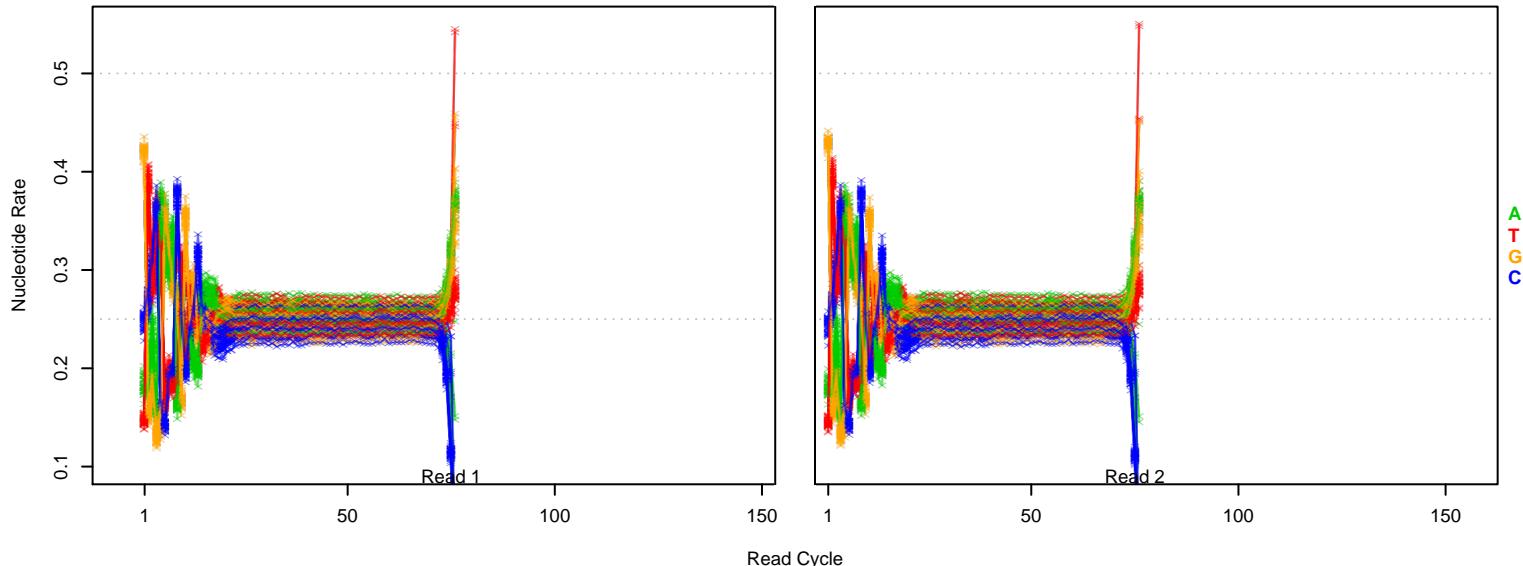
ak

Nucleotide Rate by Cycle, Trailing Clipped bases (12)



al

Raw Nucleotide Rate by Cycle



am

Nucleotide Rate by Cycle, Aligned bases only

