

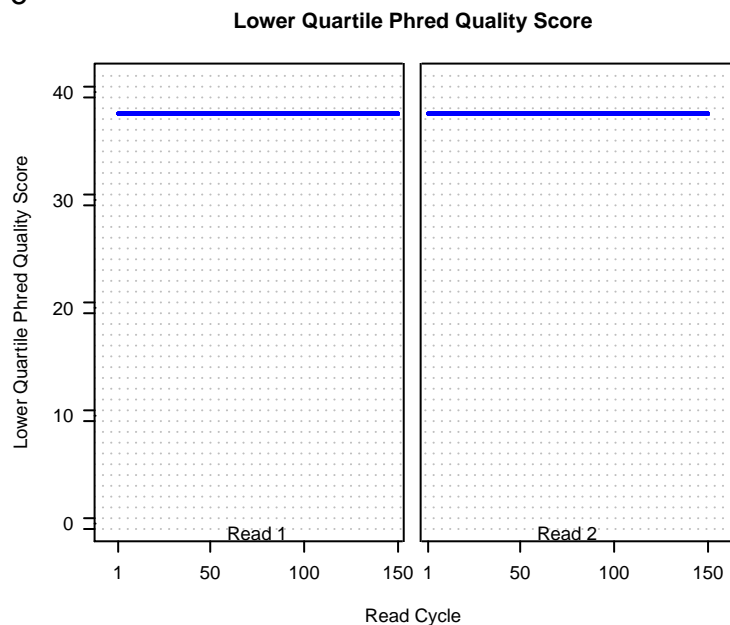
a

# All Quality Control Summary Plots

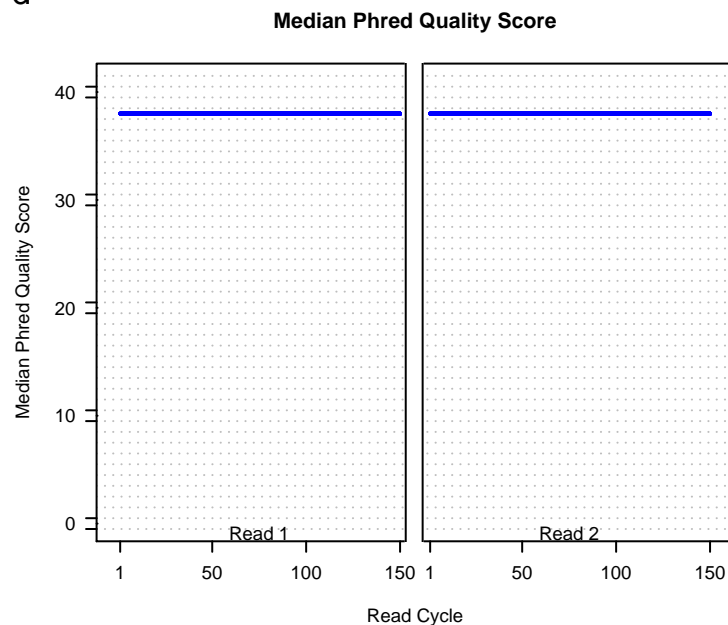
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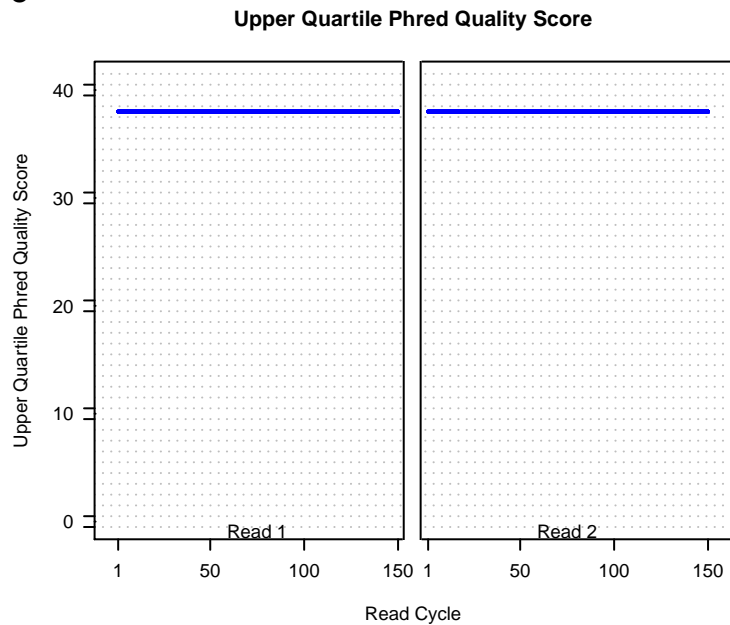
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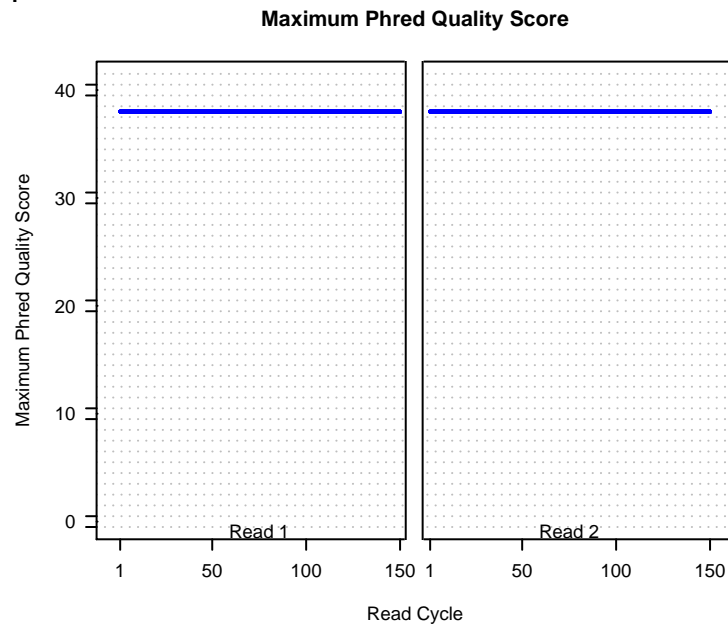
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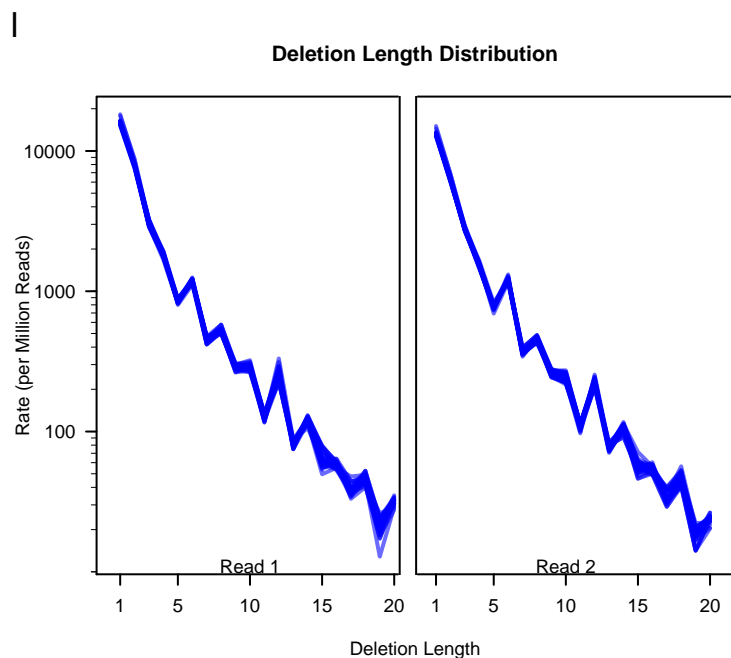
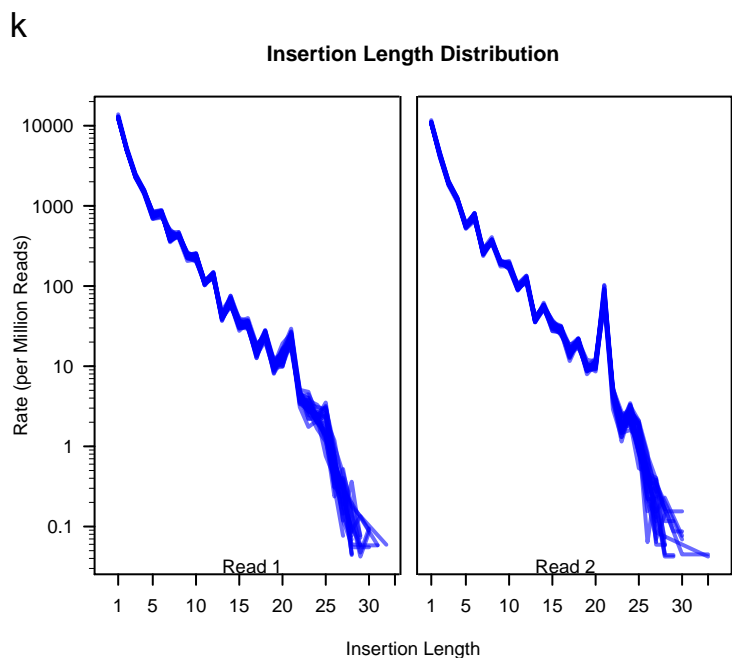
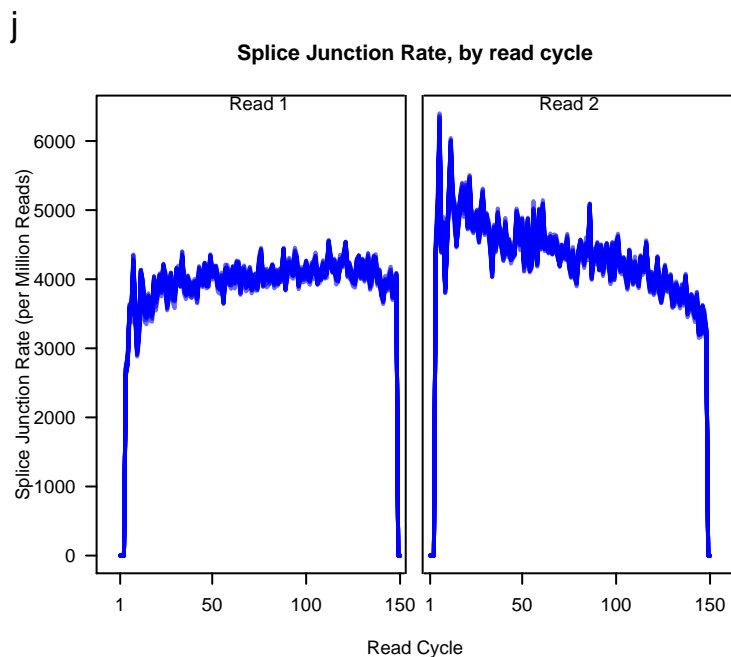
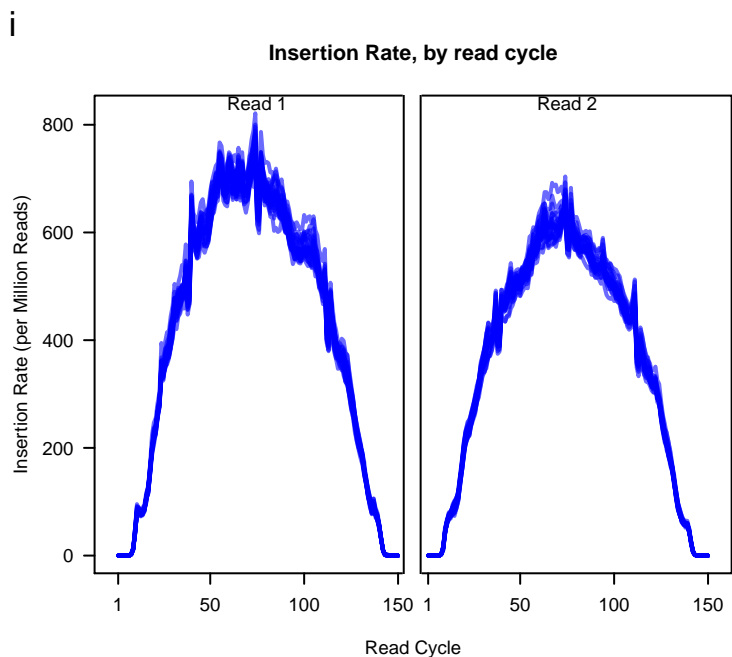
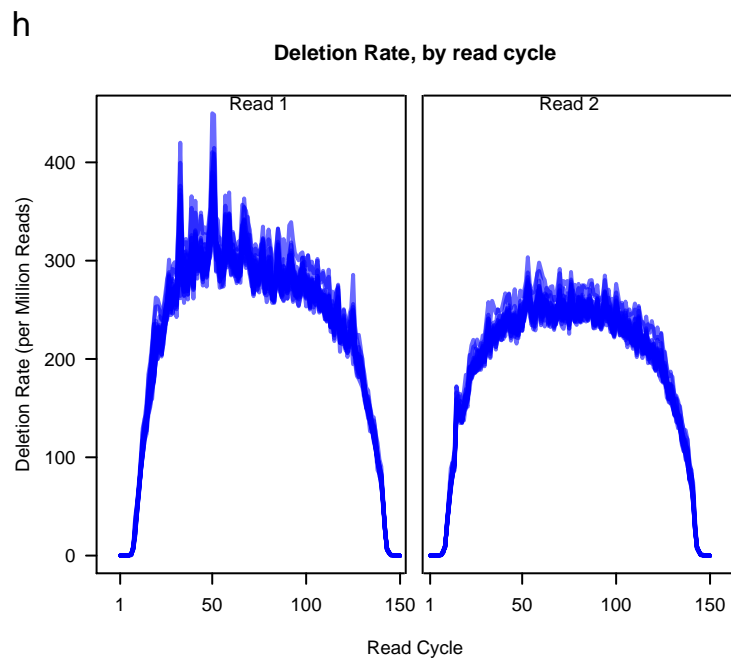
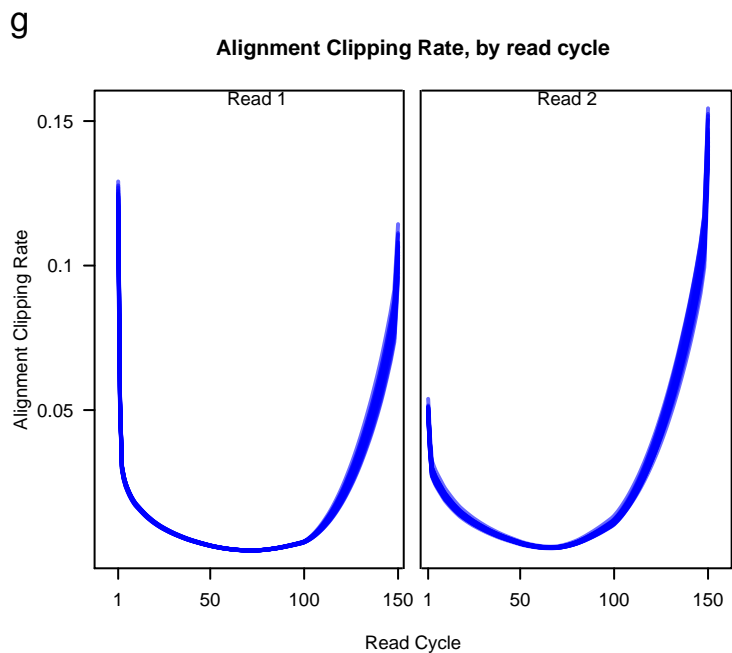


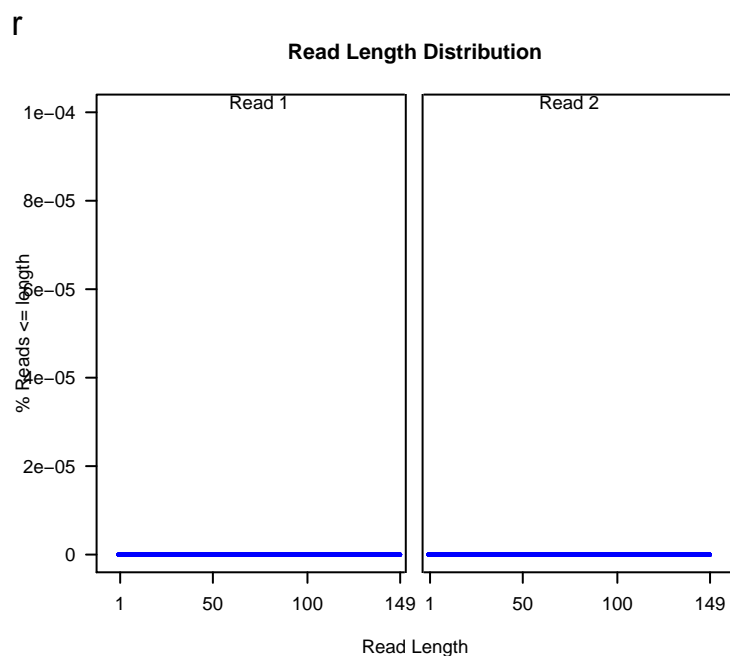
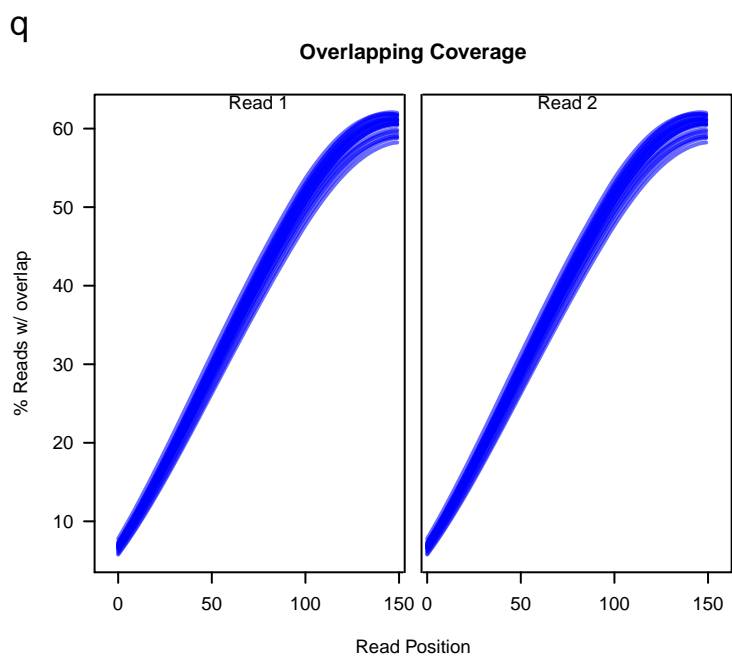
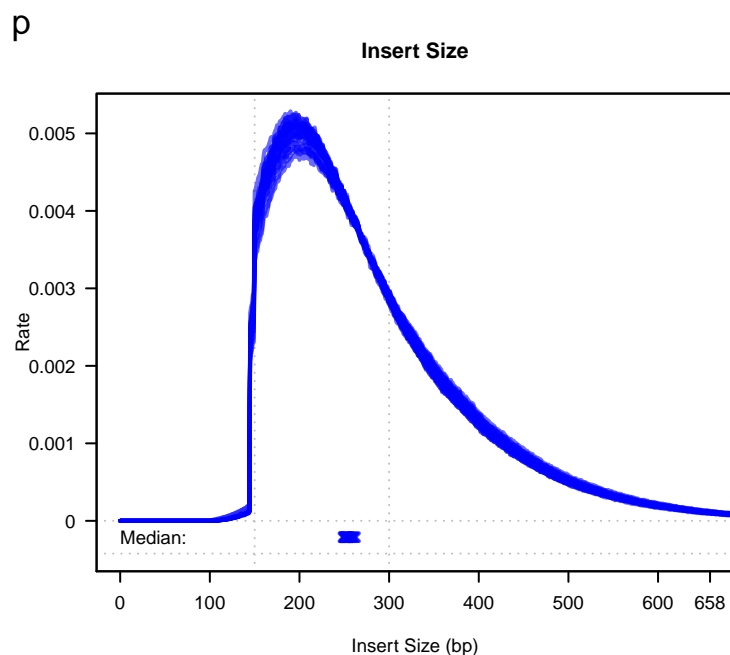
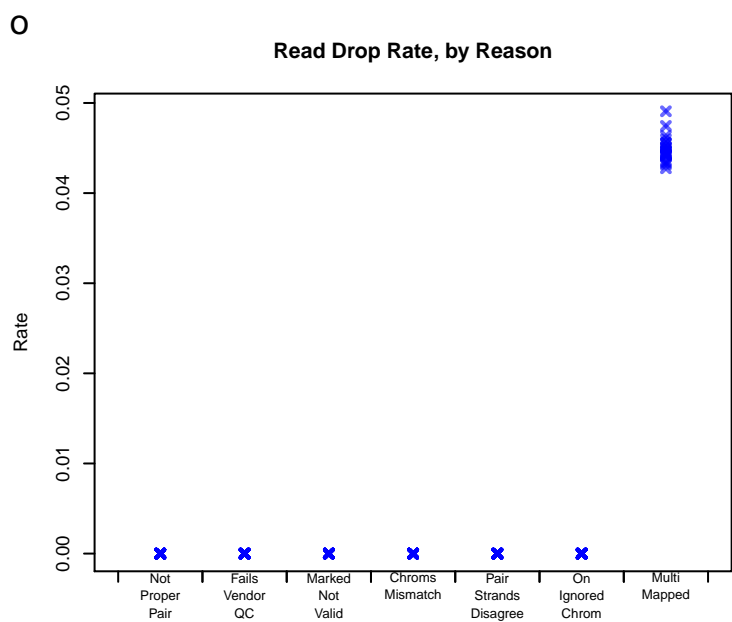
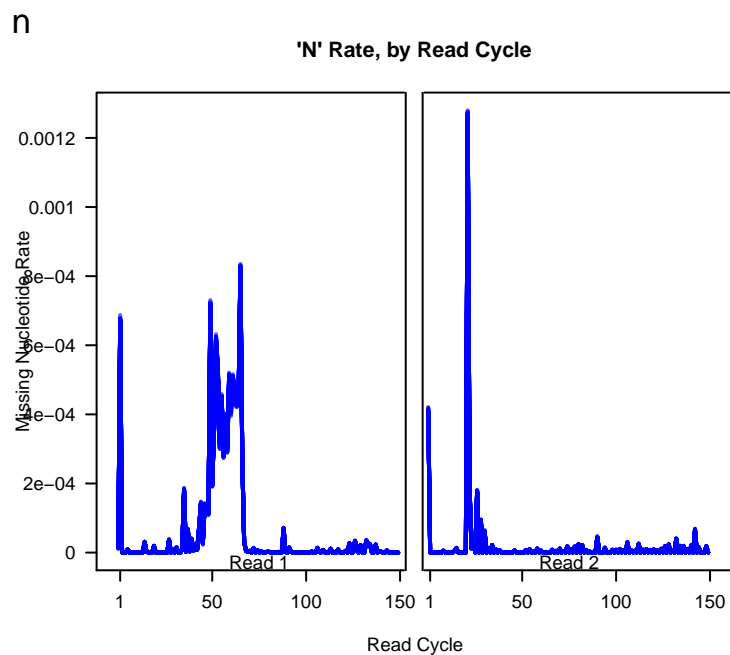
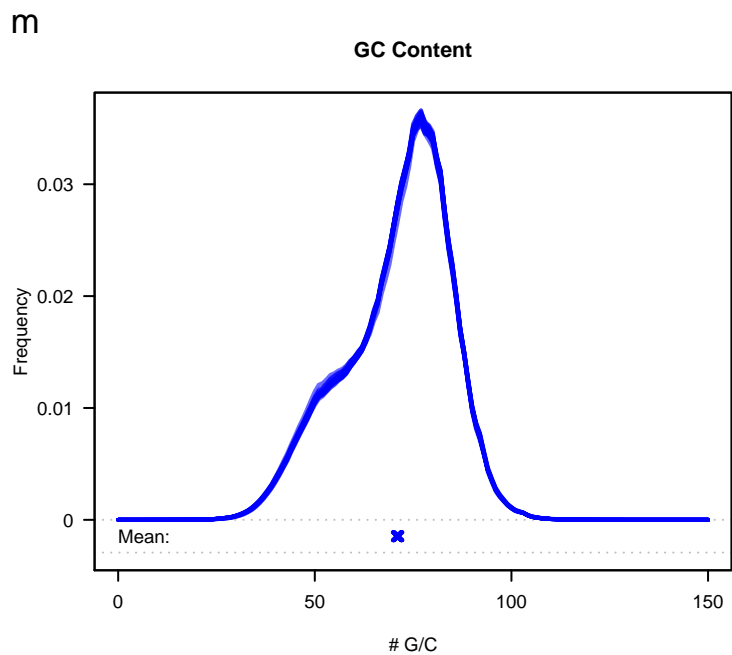
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f

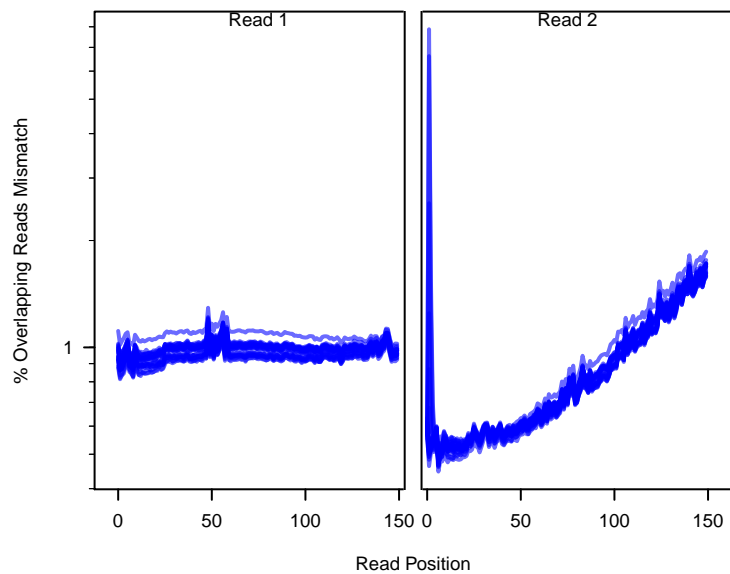






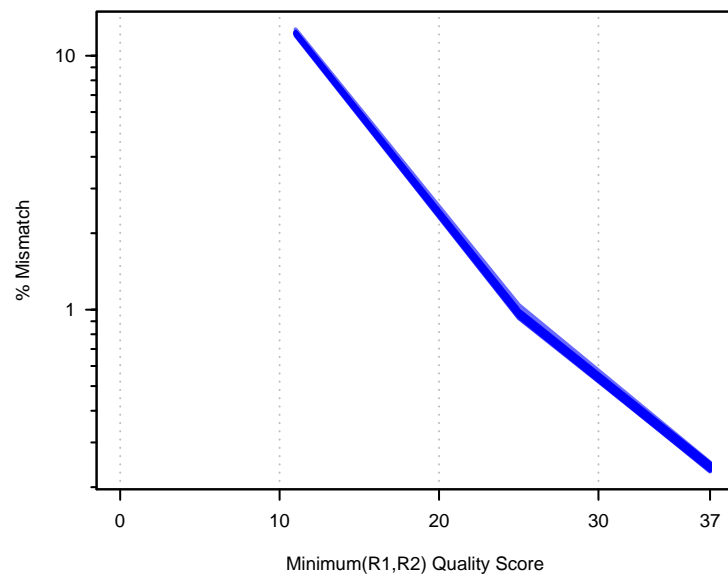
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Overlap Mismatch by Read Cycle



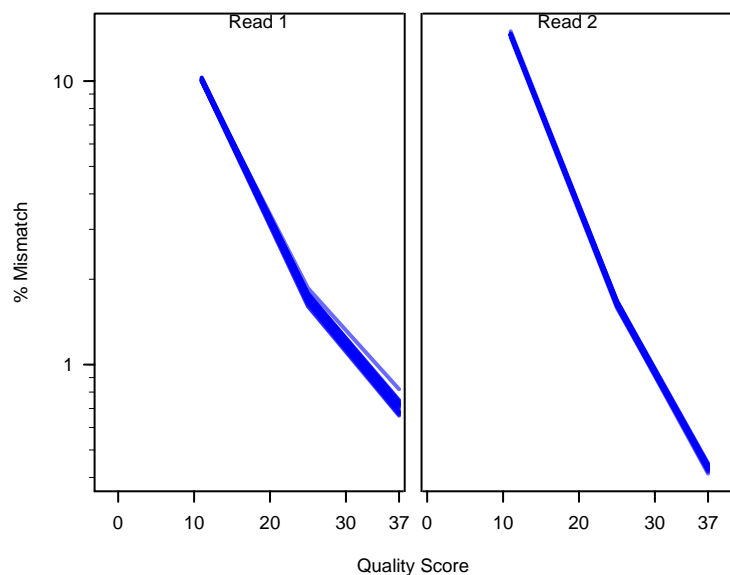
t

Overlapping Mismatch by Min Qual



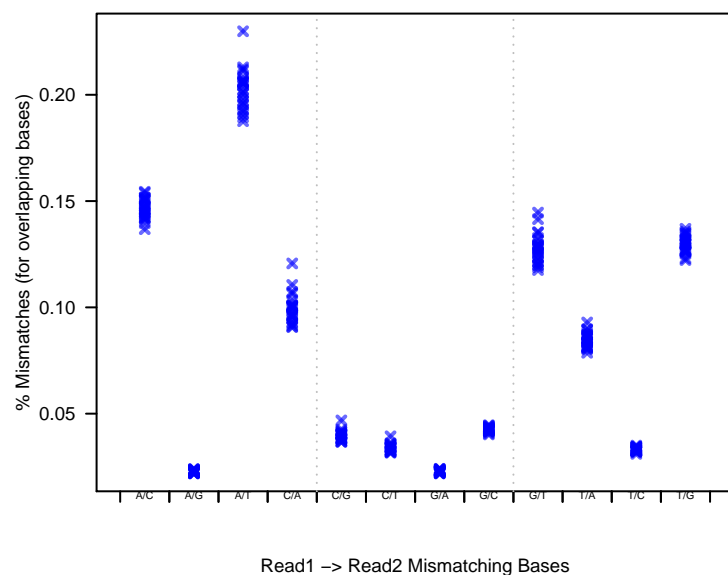
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Overlap Mismatch by Read Qual



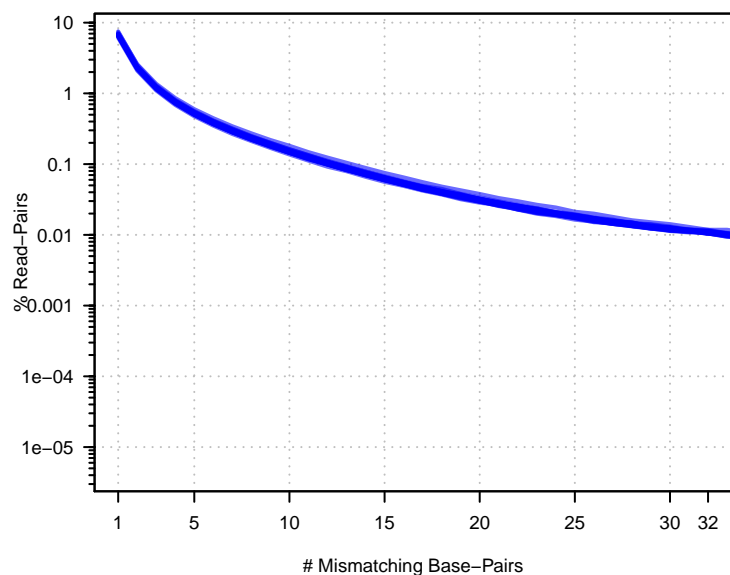
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Overlap Mismatch Combinations



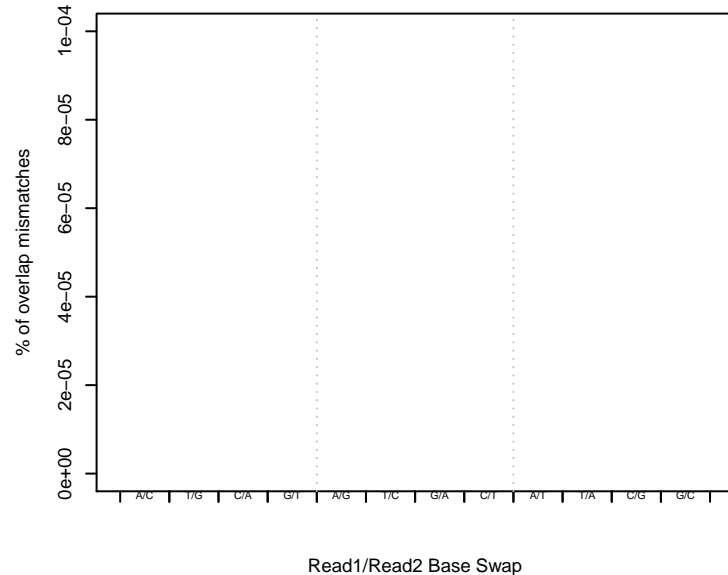
w

Overlap Mismatch Size Frequency



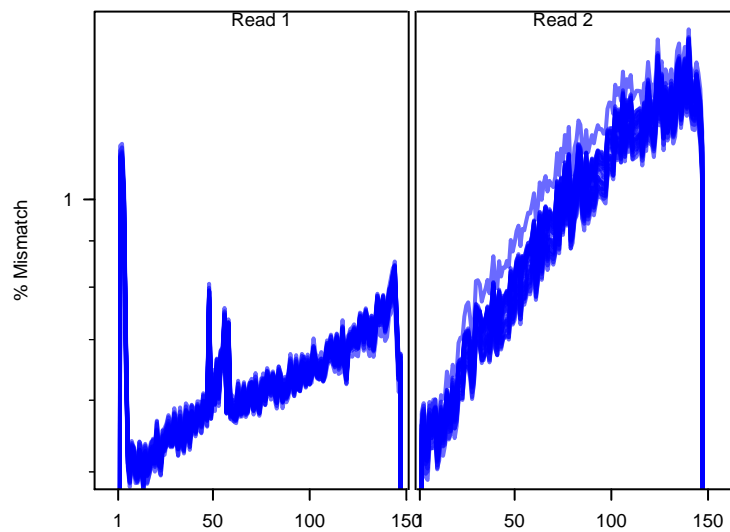
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Overlap Mismatch Pairs At Phred == 41



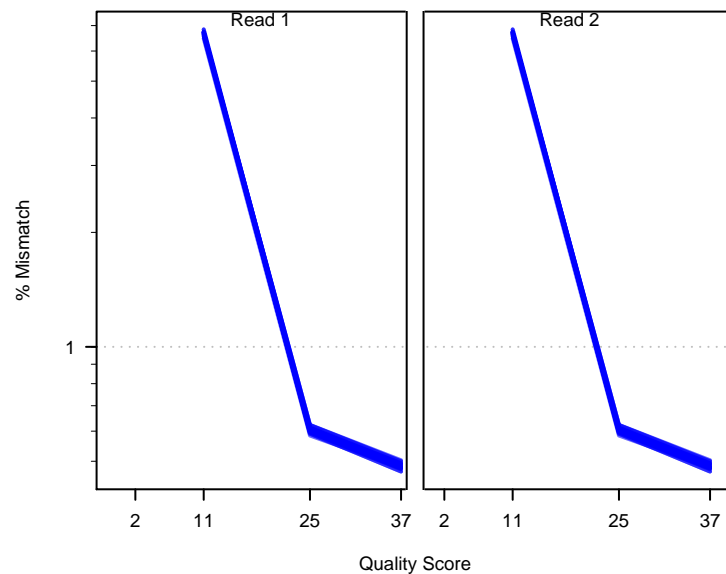
y

Reference Mismatch by Read Cycle



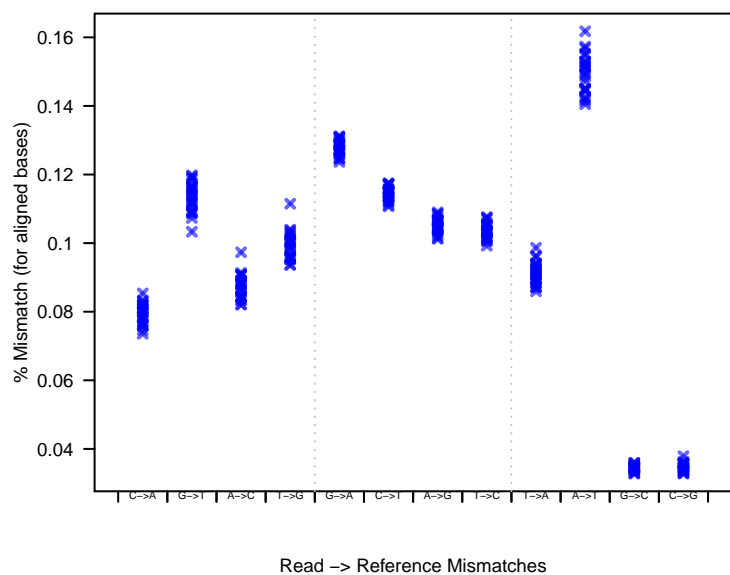
Z

Reference Mismatch by Read Qual



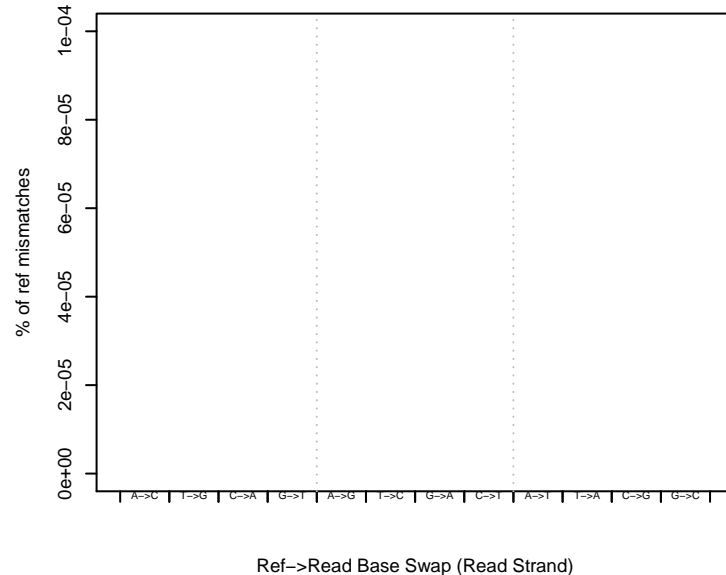
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Reference Mismatch Combinations



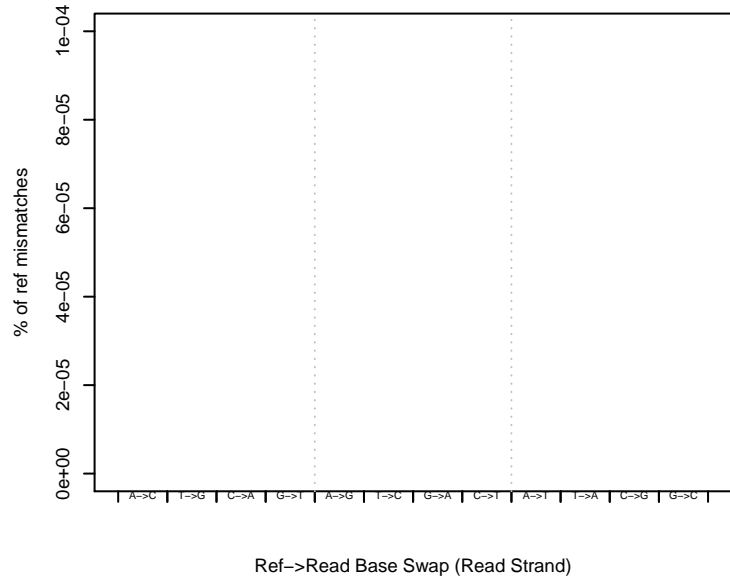
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R1 Ref Mismatches At Phred == 41



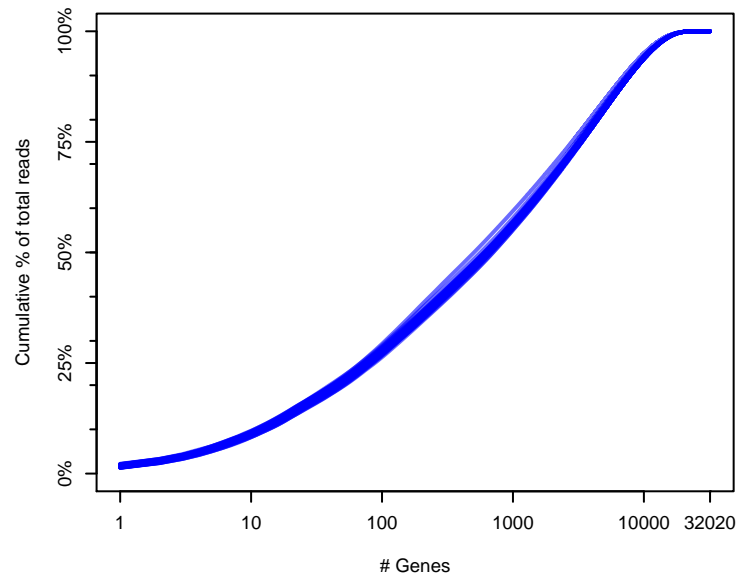
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R2 Ref Mismatches At Phred == 41



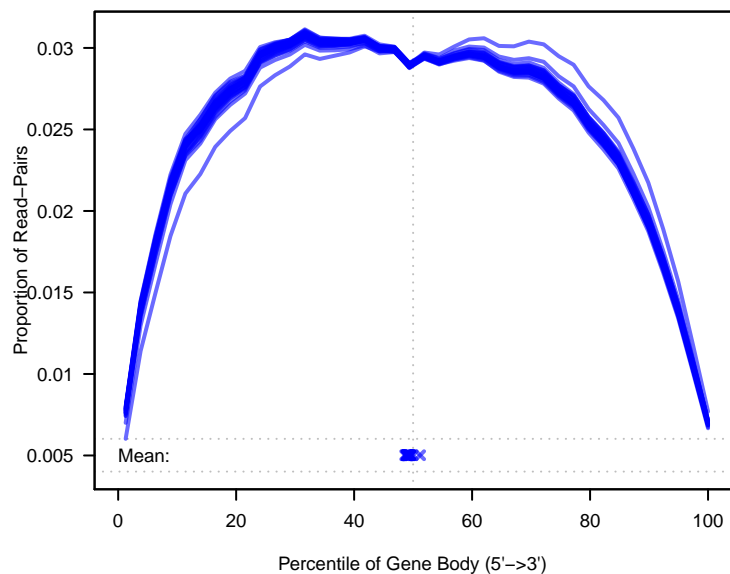
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Cumulative Gene Assignment Diversity



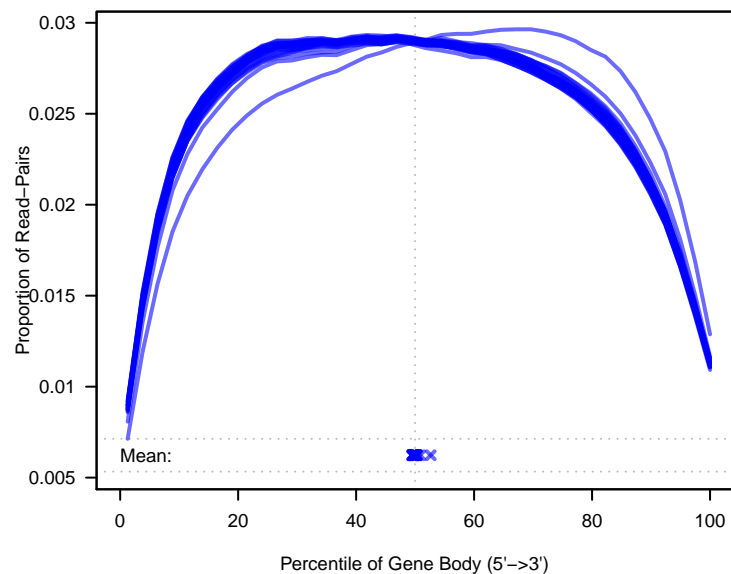
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Gene-Body Coverage



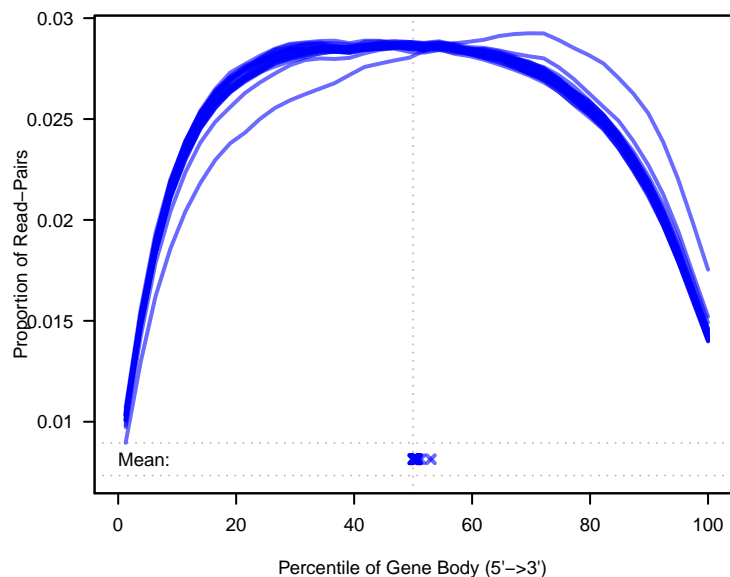
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Gene-Body Coverage, Upper Middle Quartile Genes



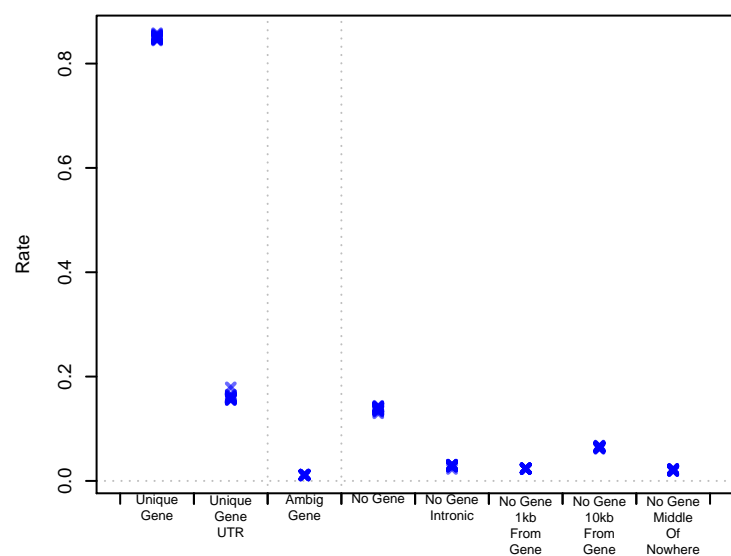
ag

Gene-Body Coverage, Low Expression Genes



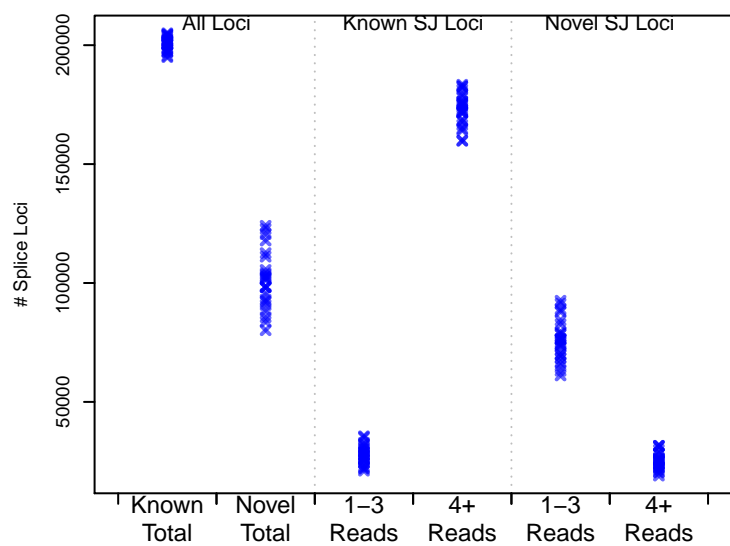
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Read Mapping Location Rates



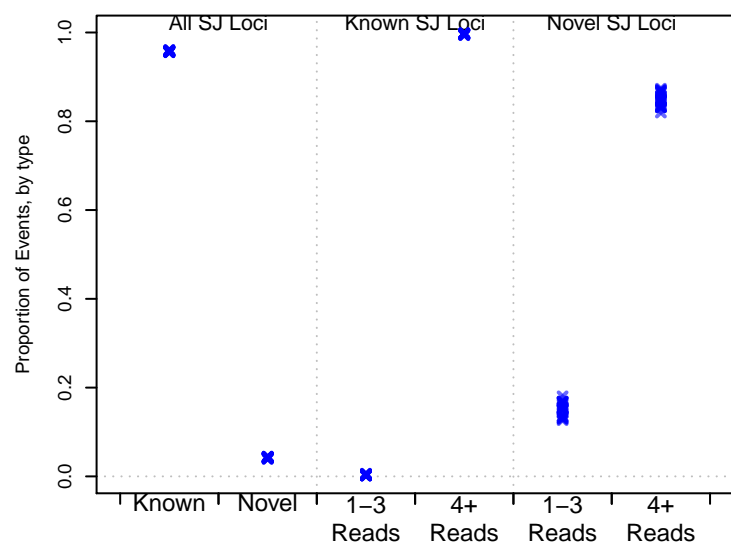
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# Observed Splice Junction Loci, by type

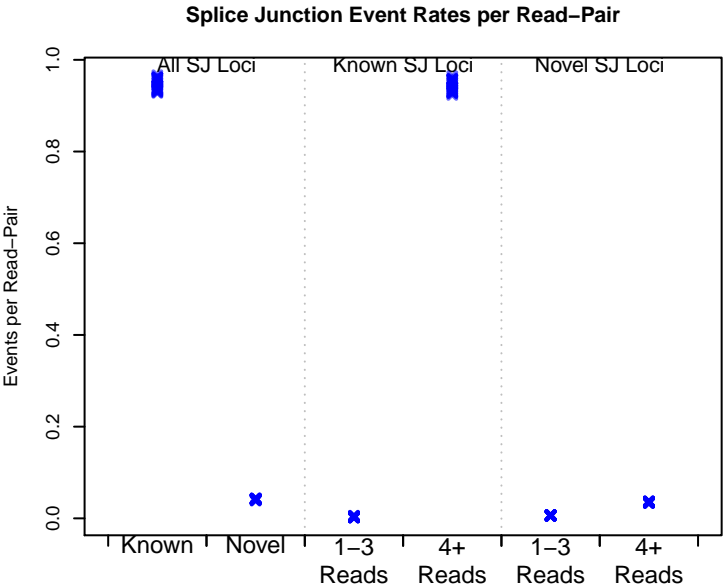


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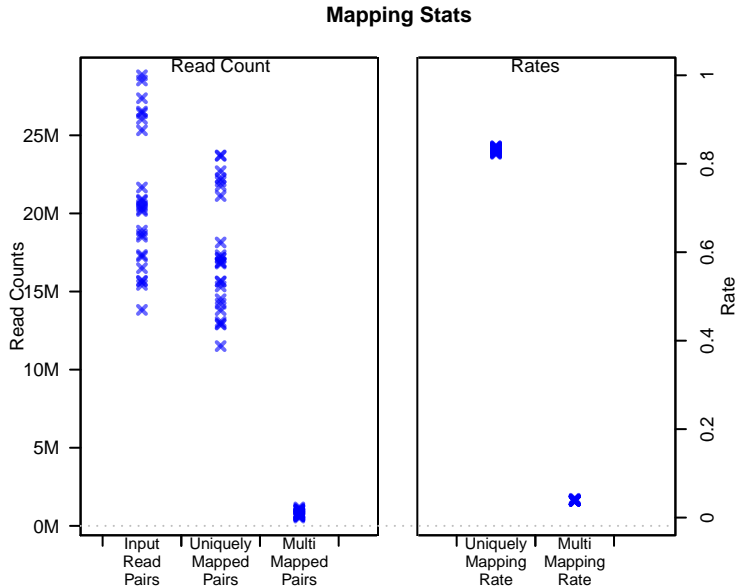
Breakdown of Splice Junction Events, by type



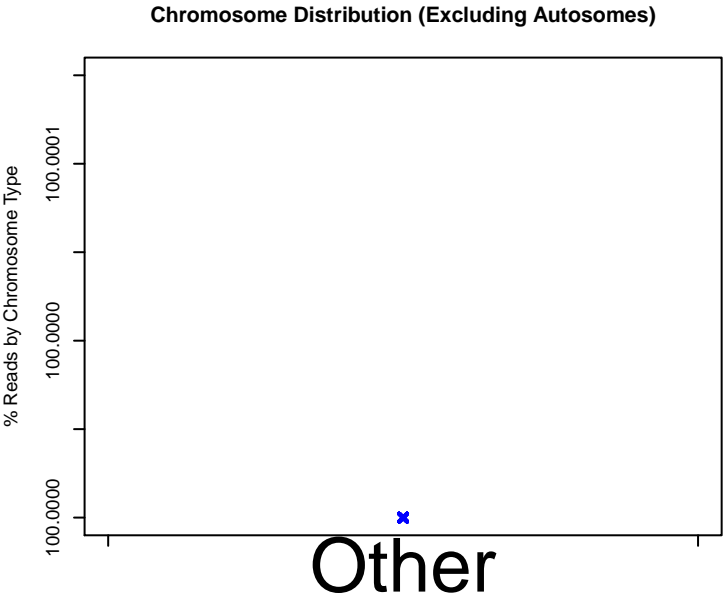
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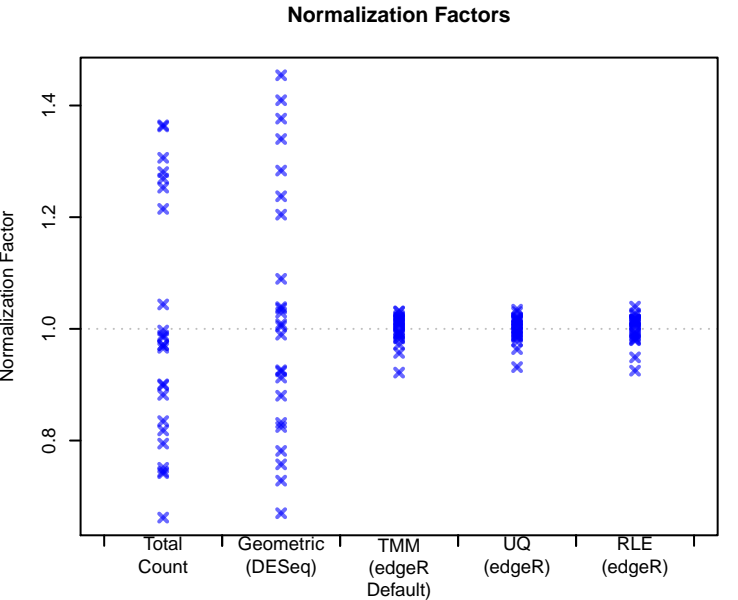
al



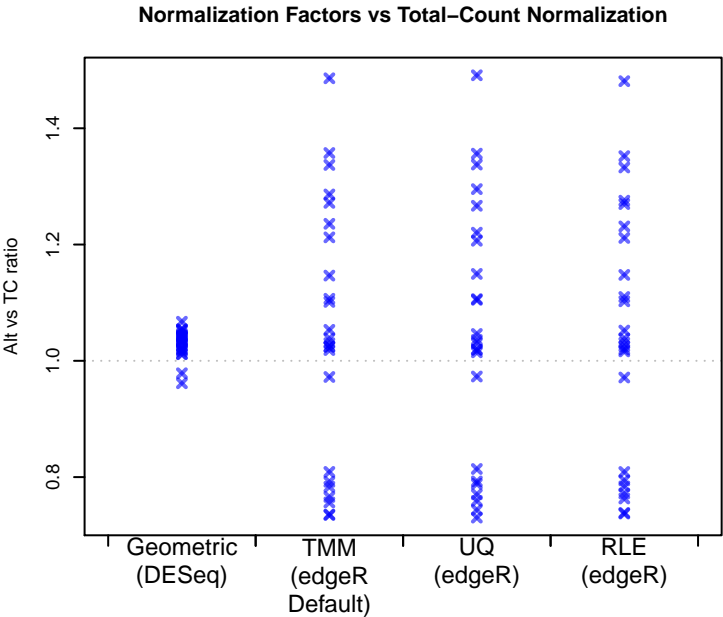
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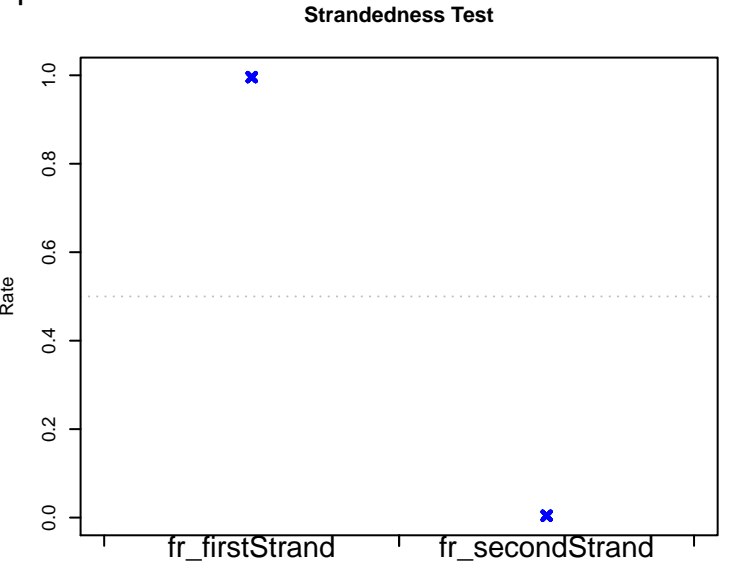
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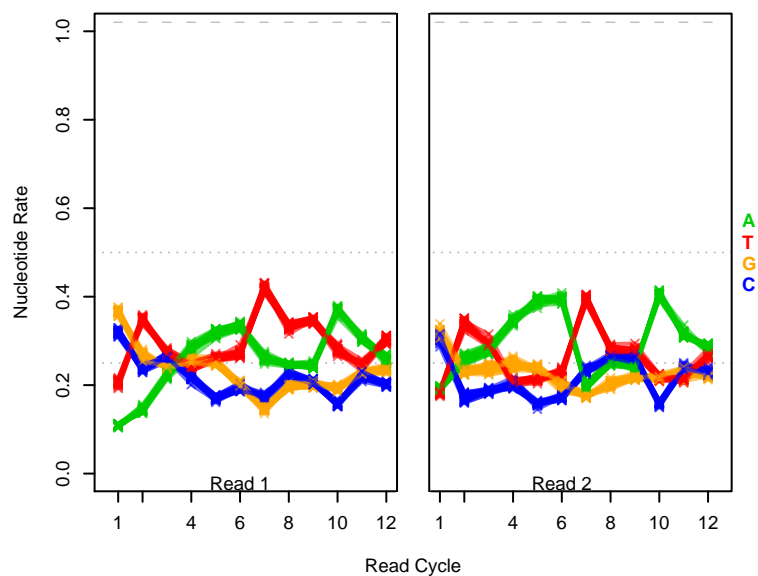


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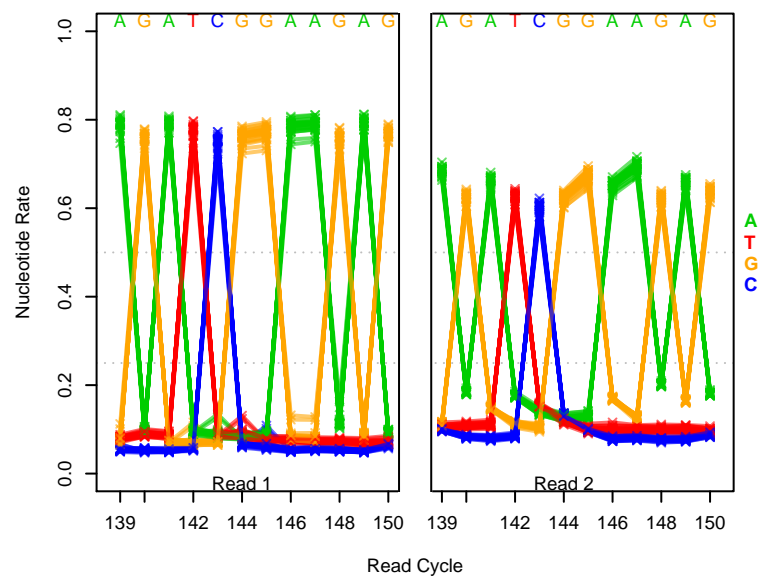
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Nucleotide Rate by Cycle, Leading Clipped bases (12)



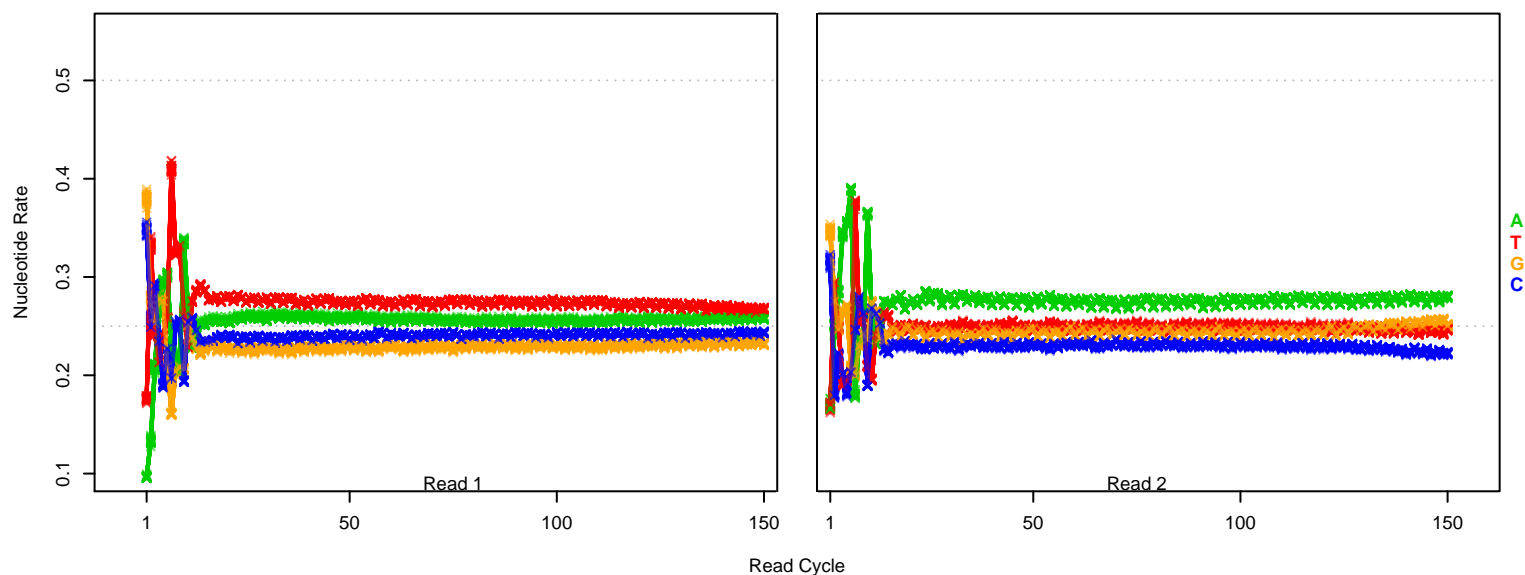
ar

Nucleotide Rate by Cycle, Trailing Clipped bases (12)



as

Raw Nucleotide Rate by Cycle



at

Nucleotide Rate by Cycle, Aligned bases only

