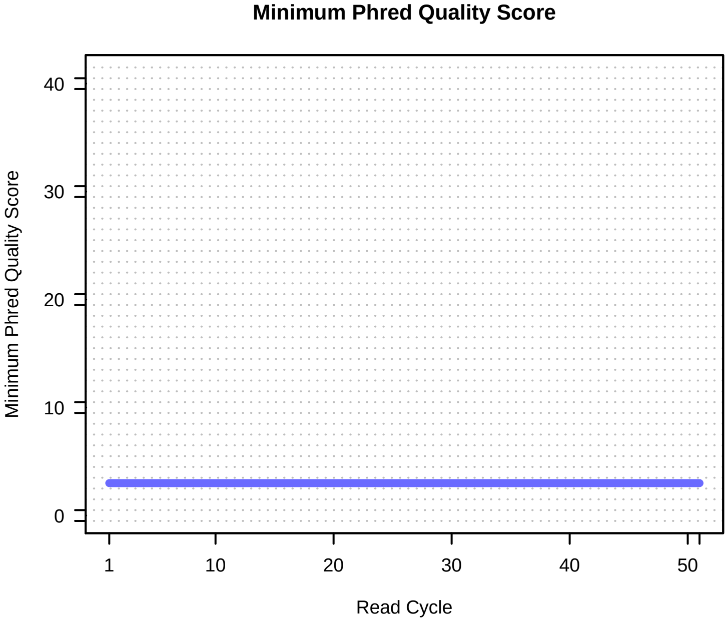
a

All
Quality Control
Summary Plots

b



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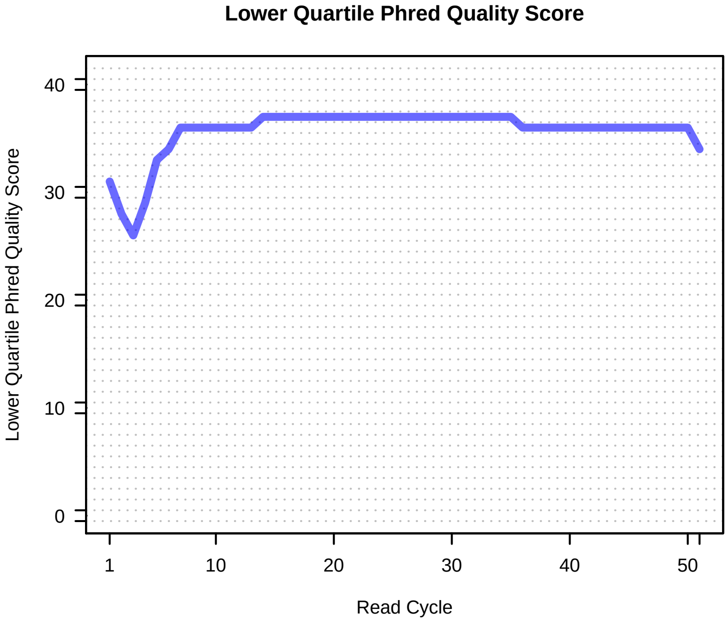

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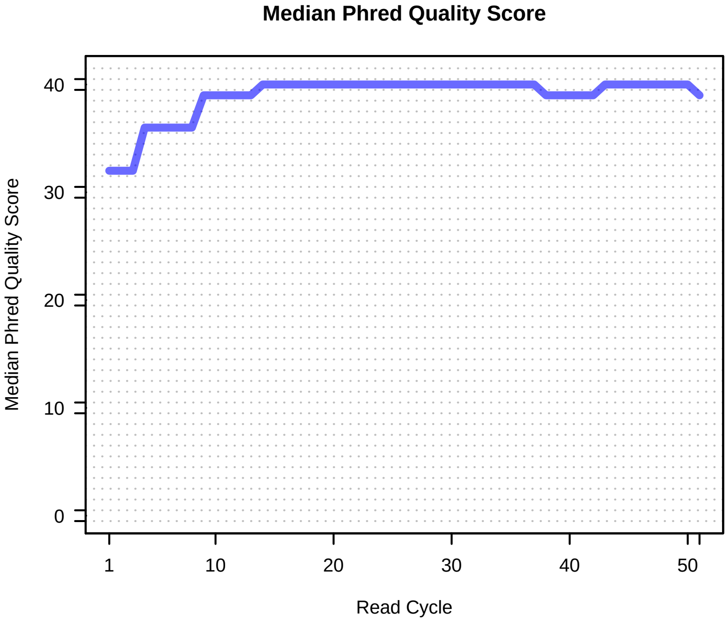

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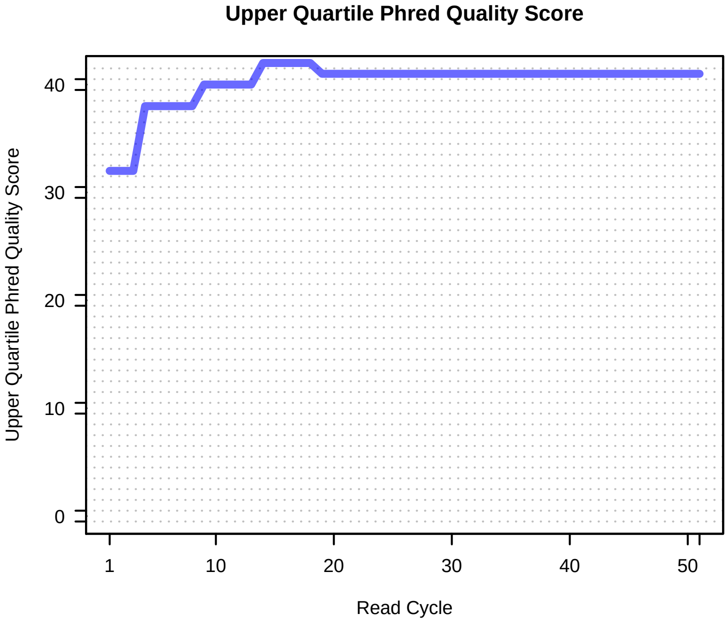

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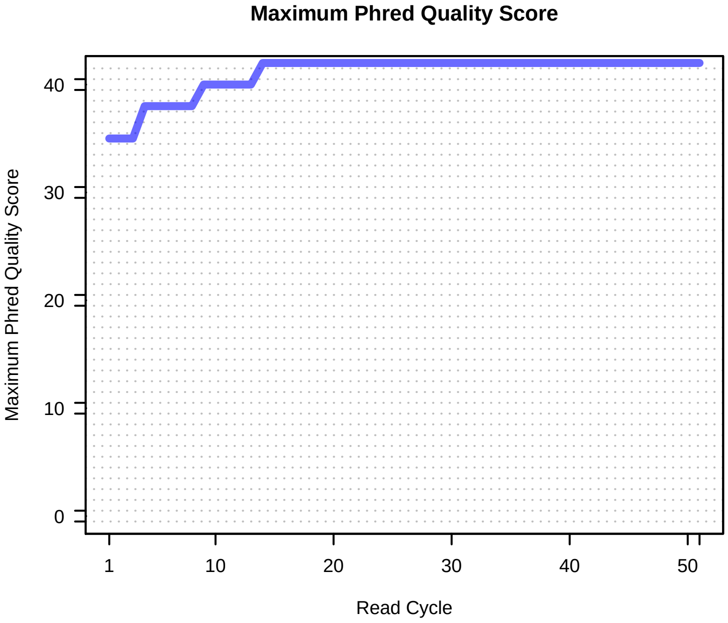

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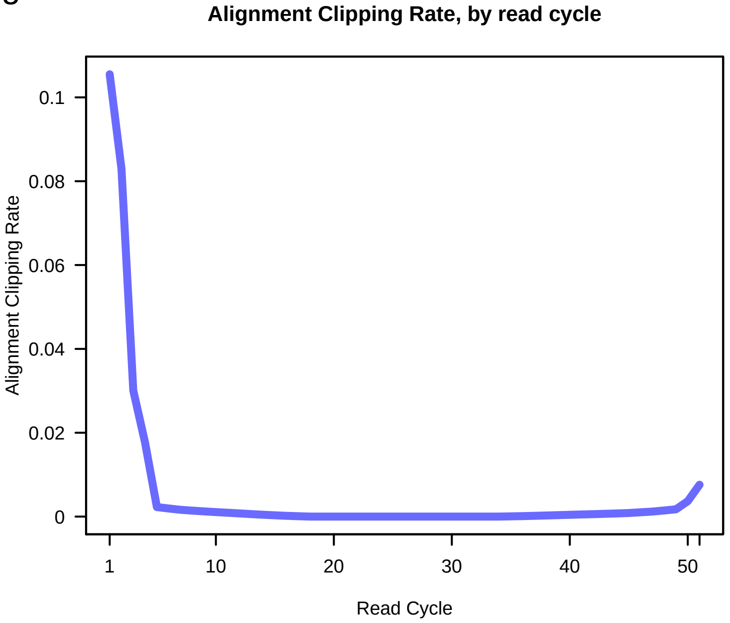
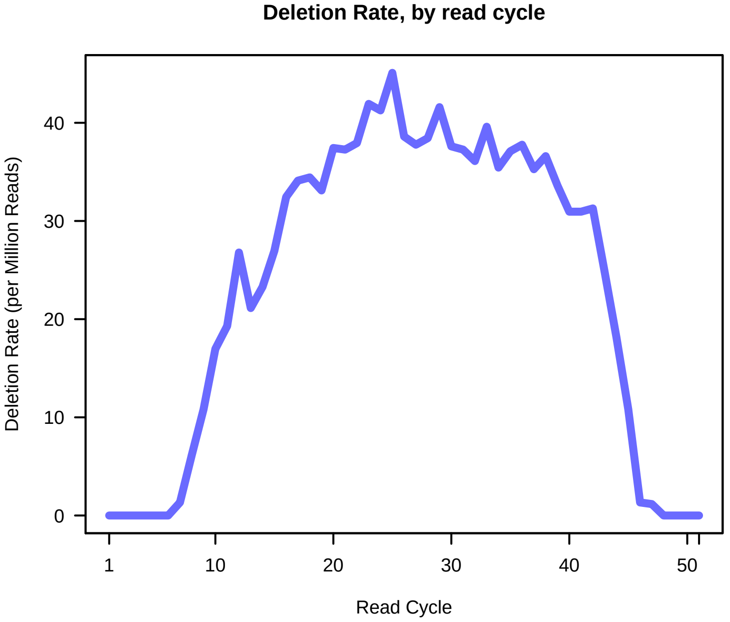
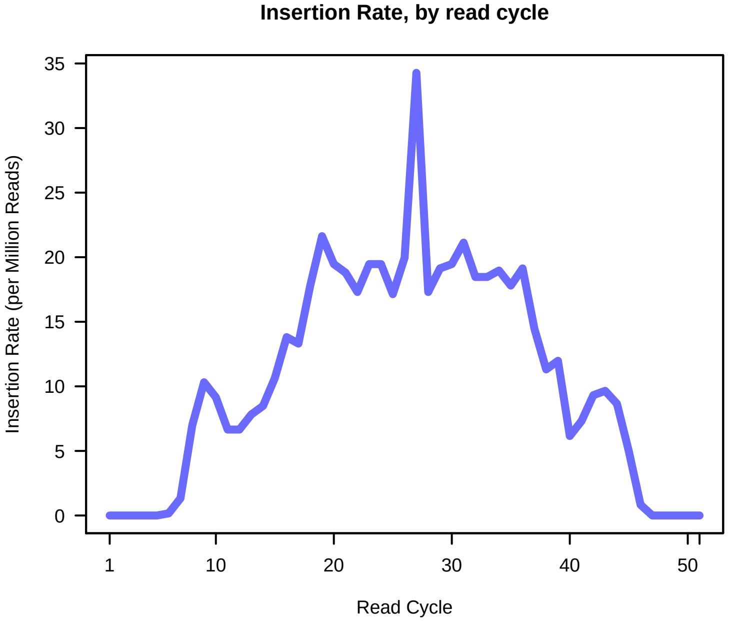

Alignment Clipping Rate, by read cycle

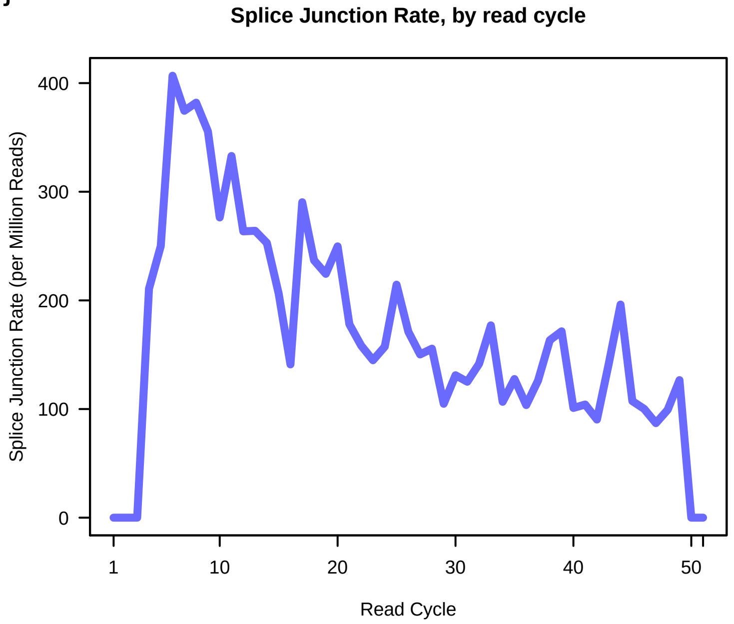
h


Deletion Rate, by read cycle

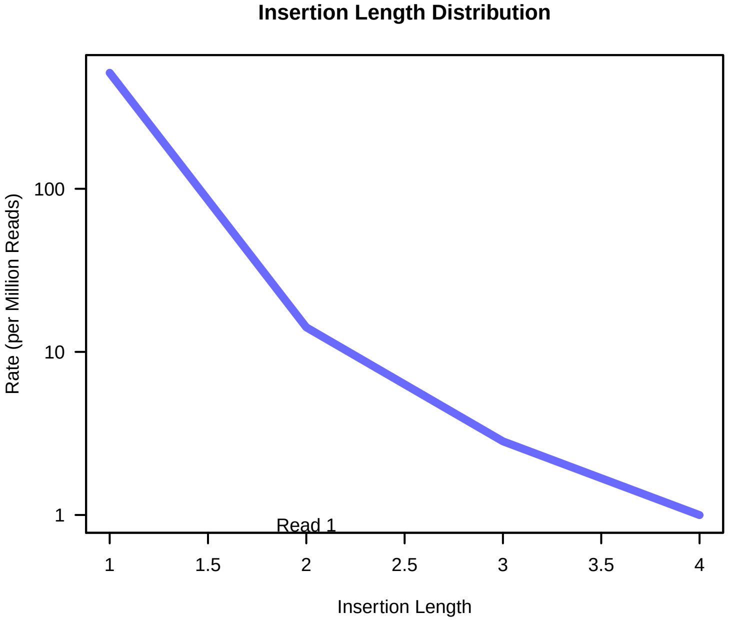
i


Insertion Rate, by read cycle

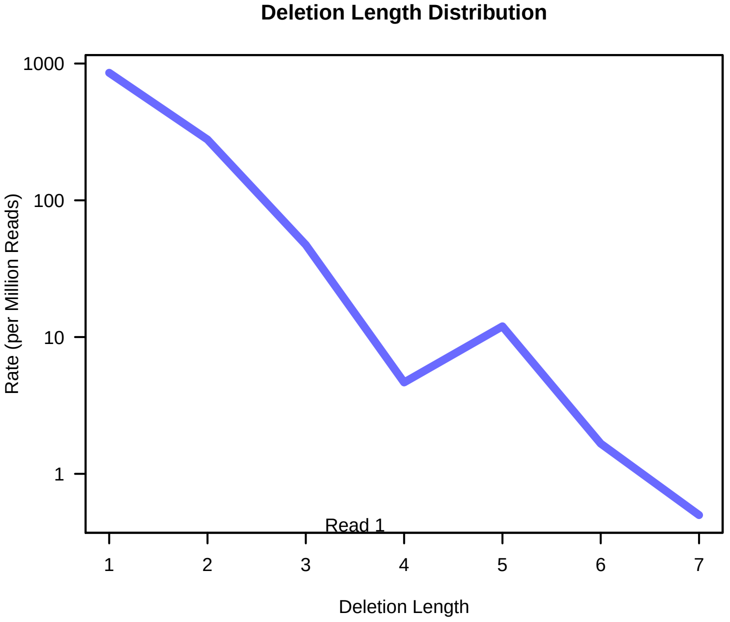
j


Splice Junction Rate, by read cycle

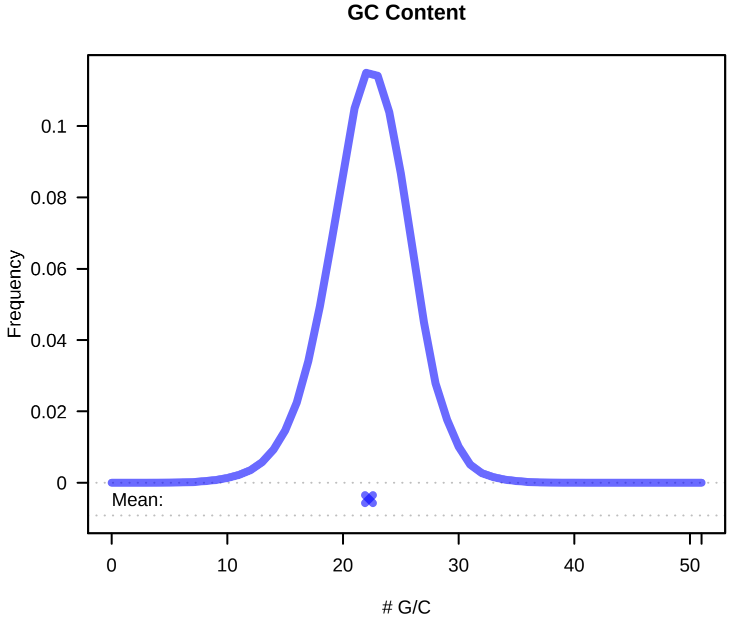
k


Insertion Length Distribution

l


Deletion Length Distribution

m



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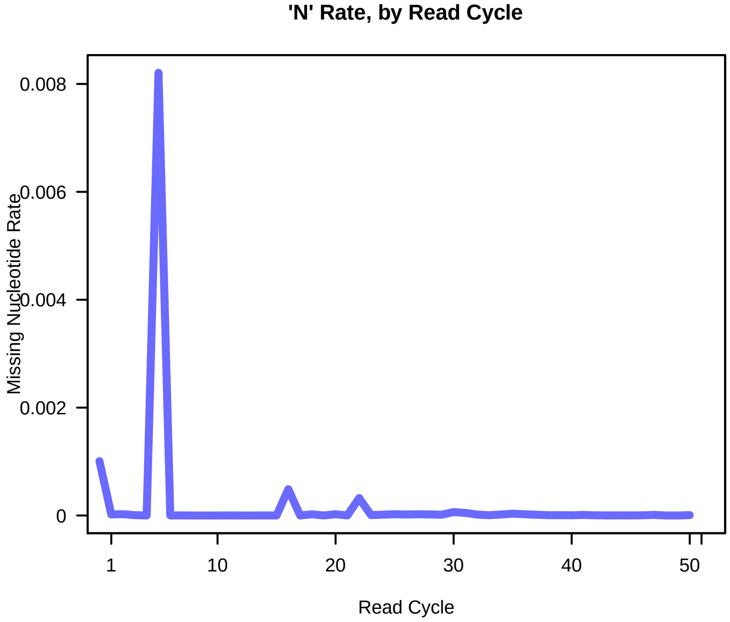

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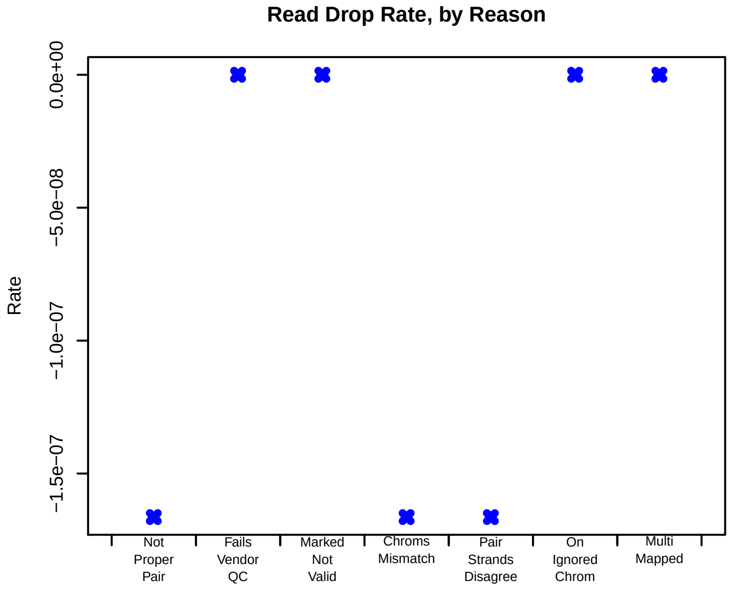
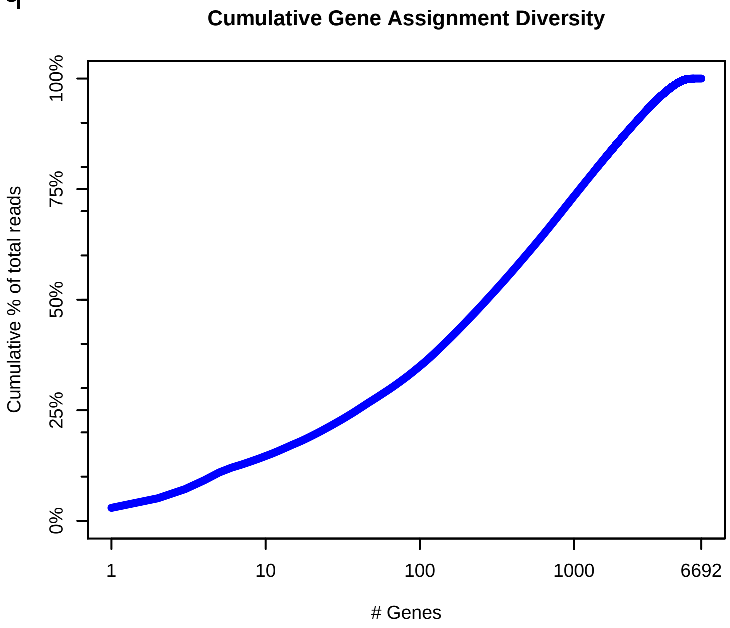


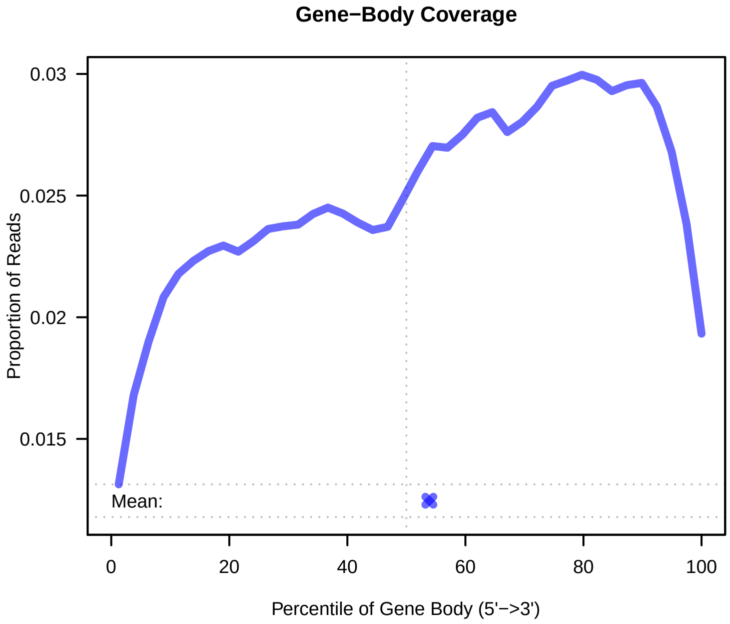
p

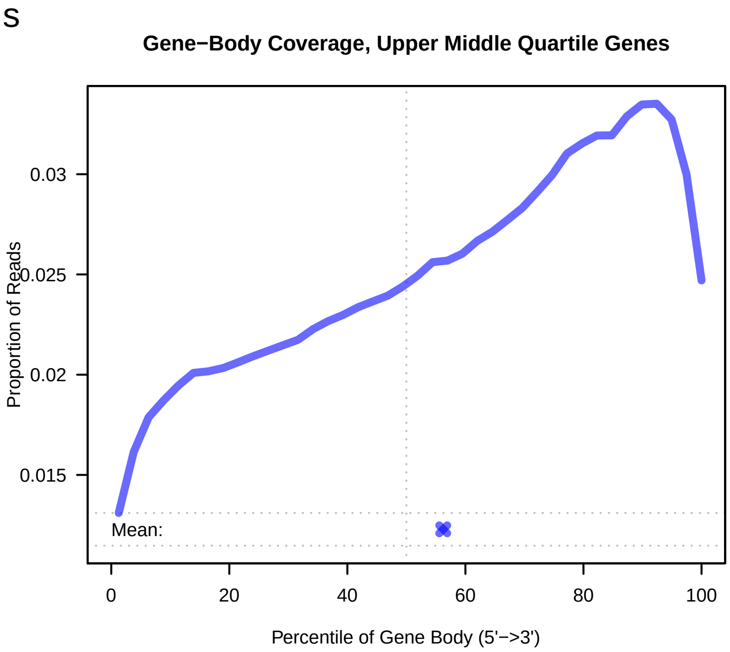
Insert Size Not Applicable
in Single−End Mode!
Skipping...

q

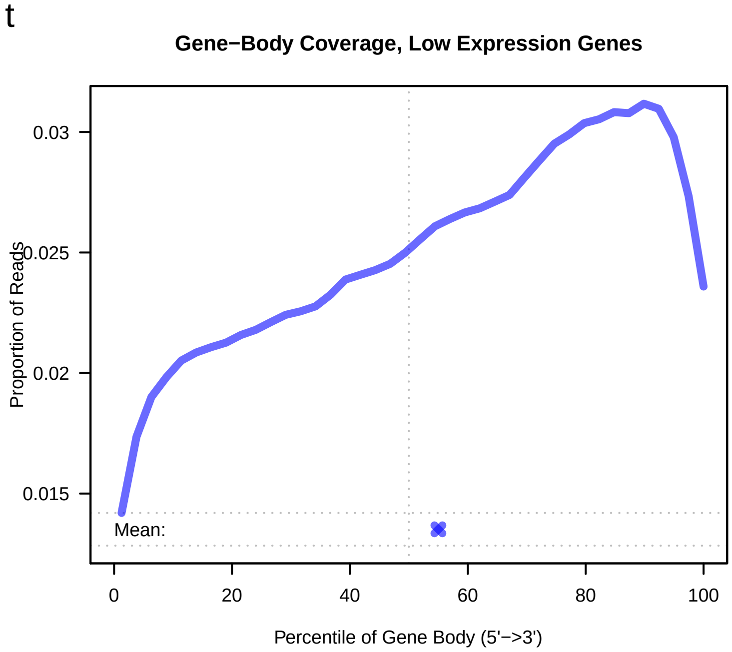


r

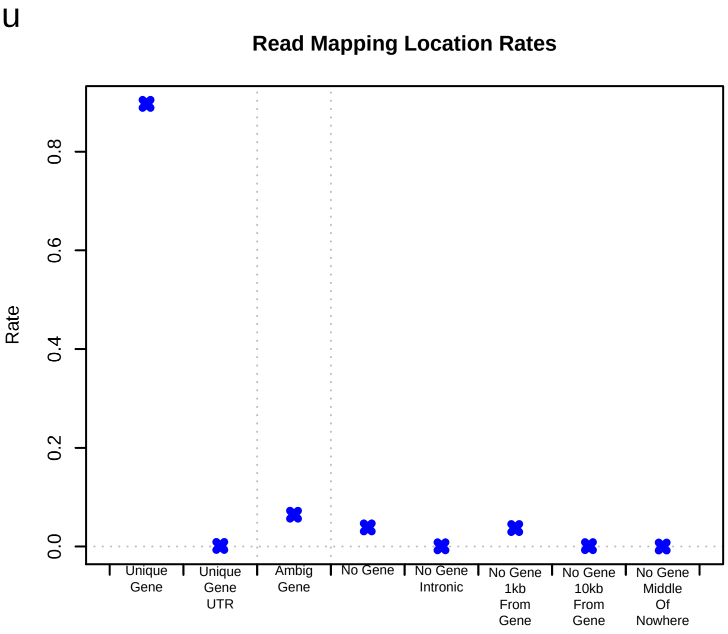




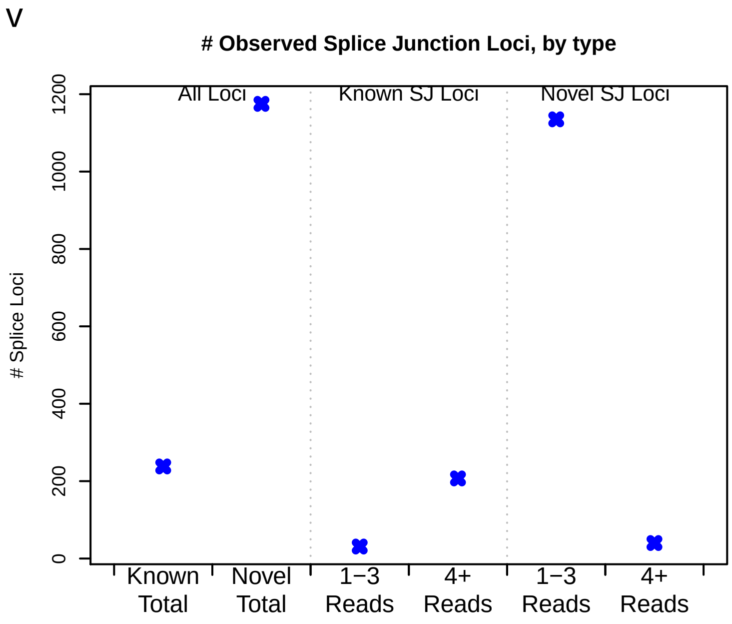
Gene−Body Coverage, Upper Middle Quartile Genes



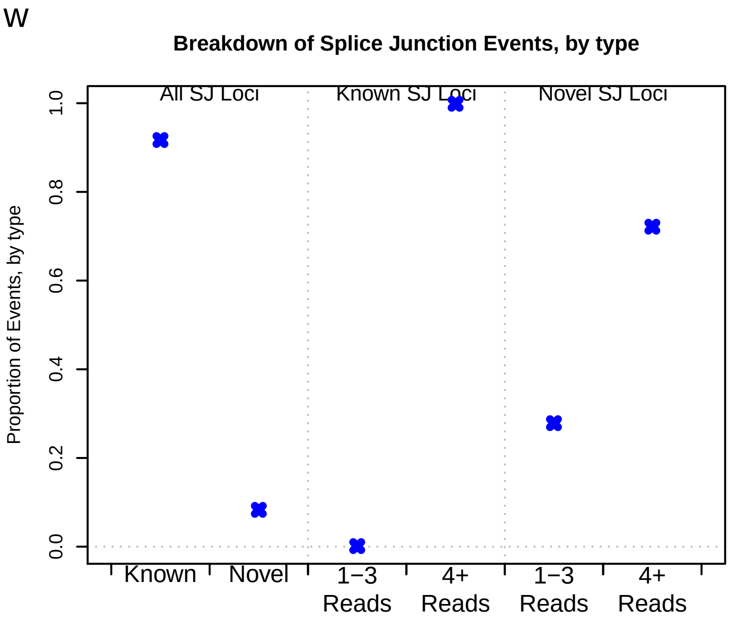
Gene−Body Coverage, Low Expression Genes



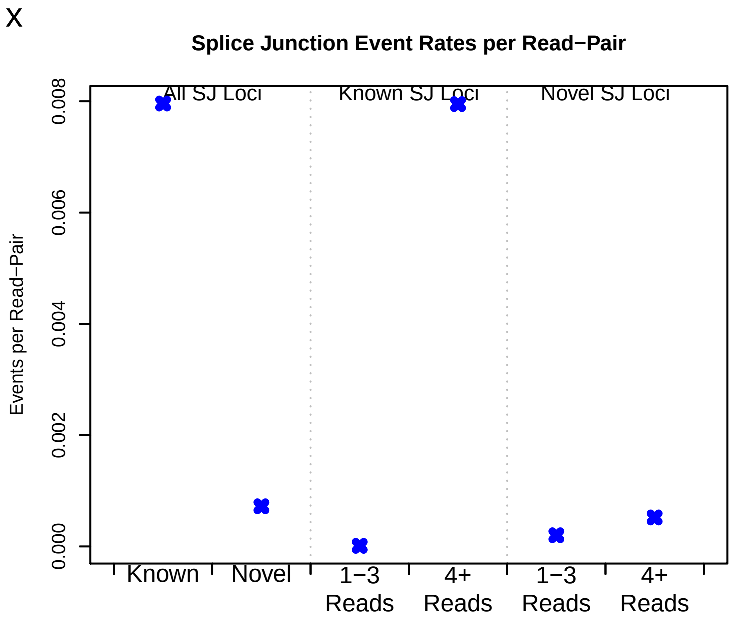
Read Mapping Location Rates



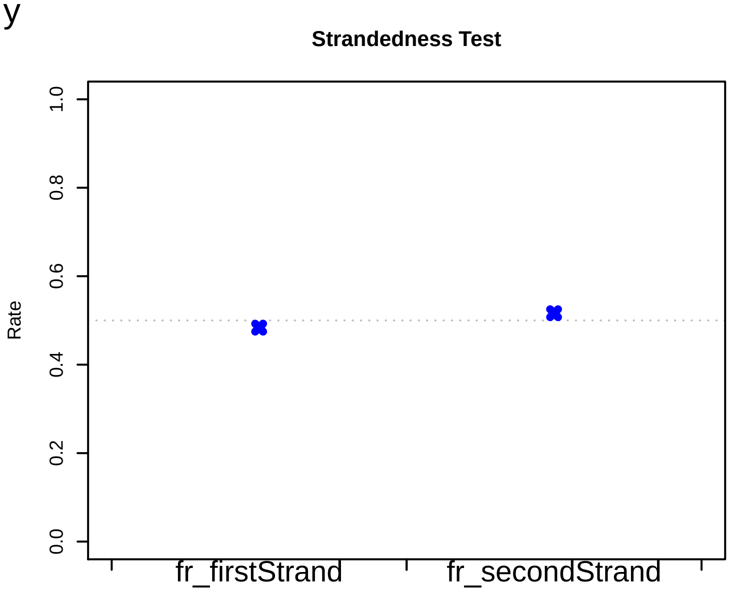
Observed Splice Junction Loci, by type



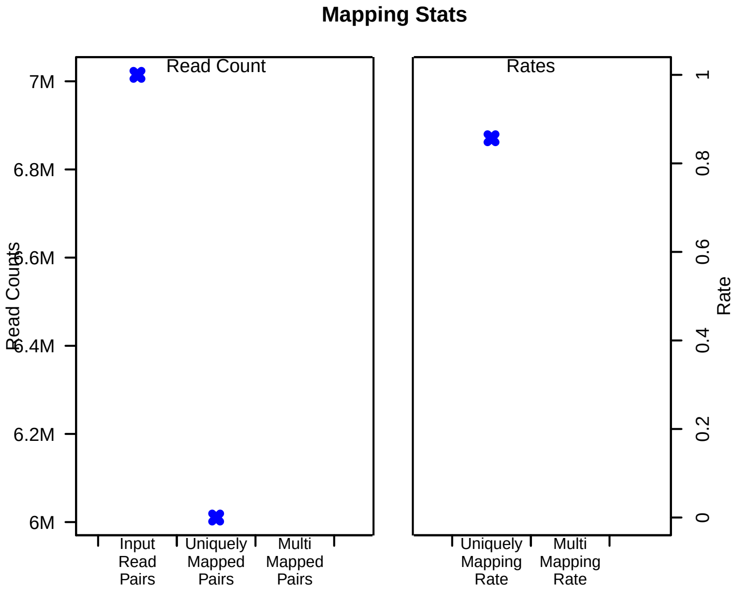
Breakdown of Splice Junction Events, by type



Splice Junction Event Rates per Read−Pair y



z



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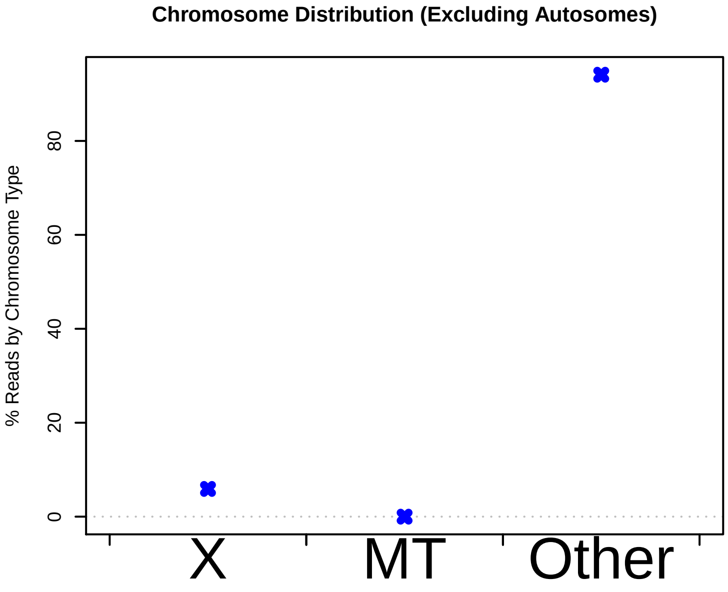


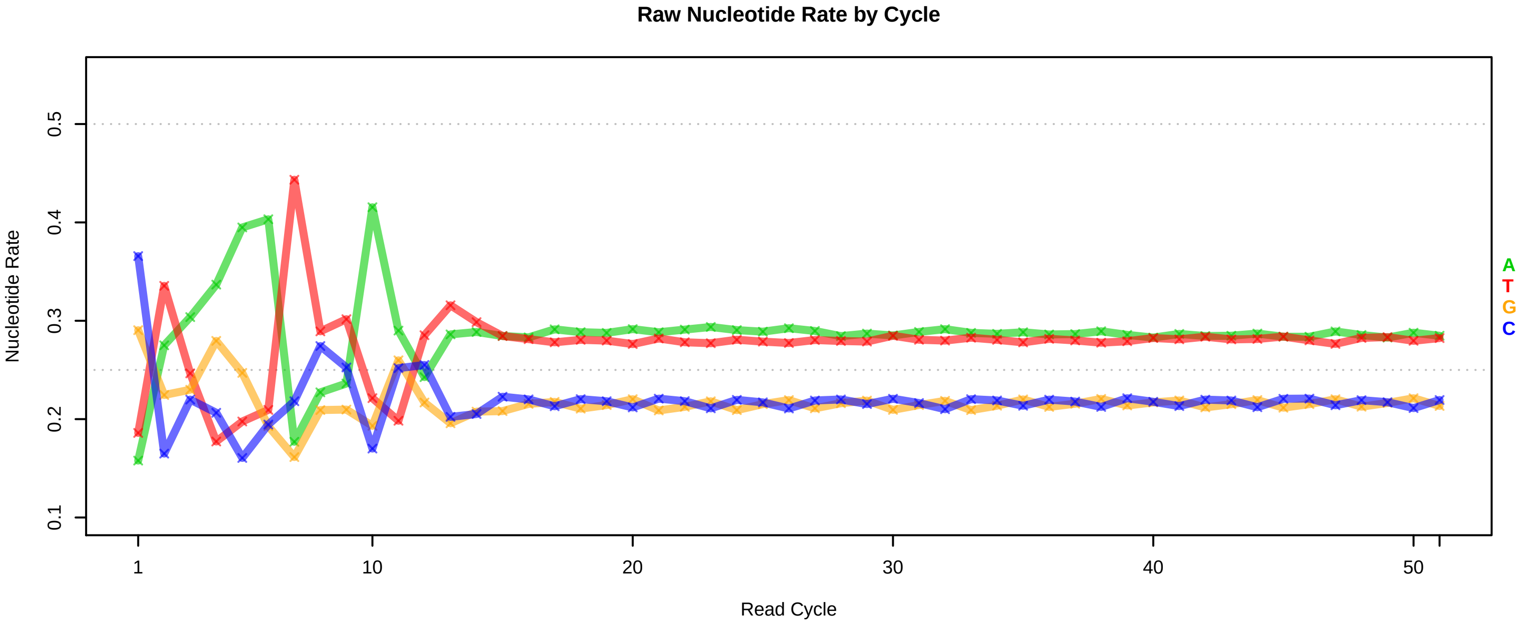
ab

Normalization Factors
Data Not Found
Skipping...

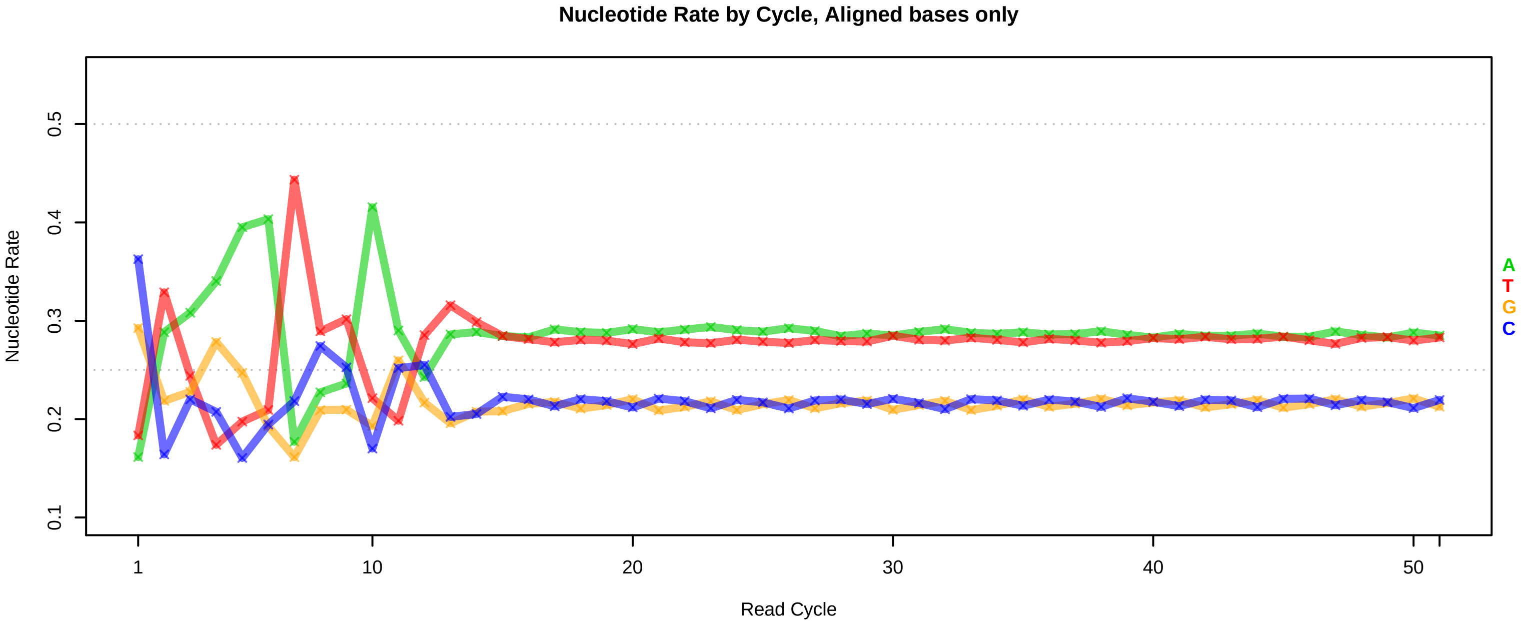
ac

Normalization Factors
Data Not Found
Skipping...

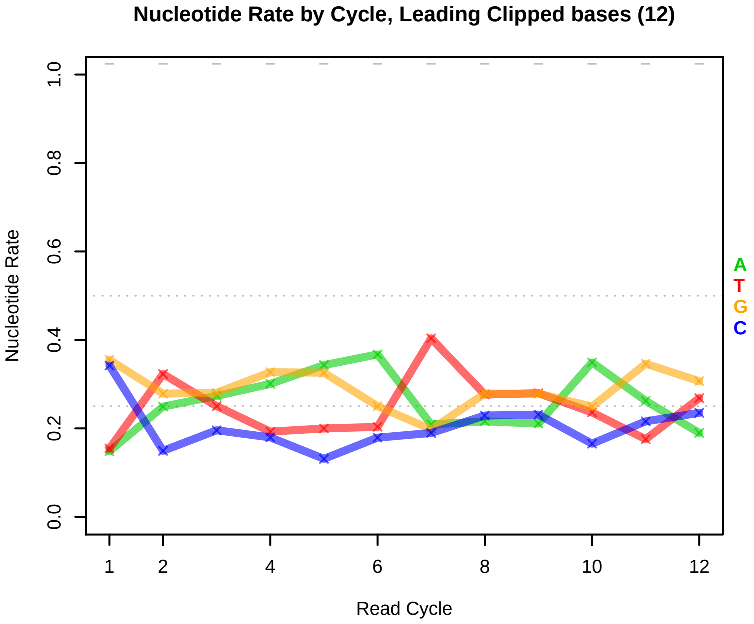
ad


Raw Nucleotide Rate by Cycle

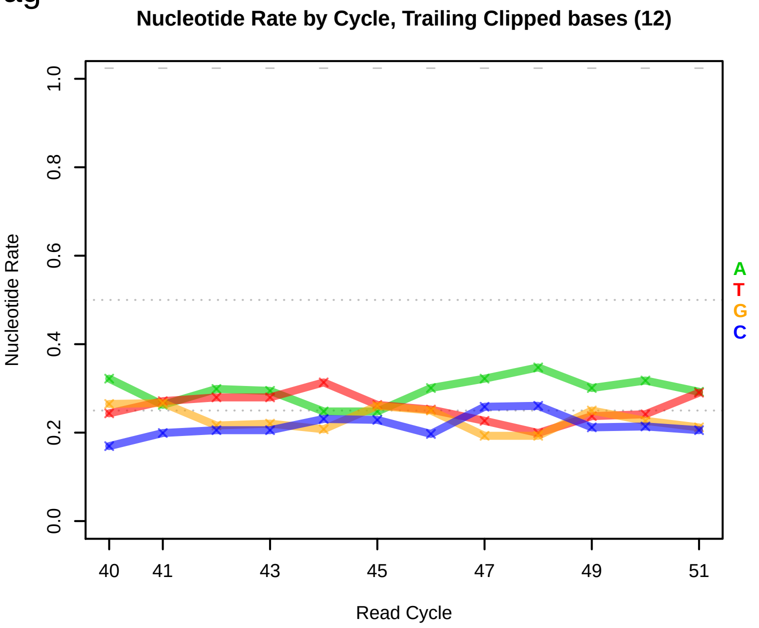
ae


Nucleotide Rate by Cycle, Aligned bases only

af


Nucleotide Rate by Cycle, Leading Clipped bases (12)

ag


Nucleotide Rate by Cycle, Trailing Clipped bases (12)