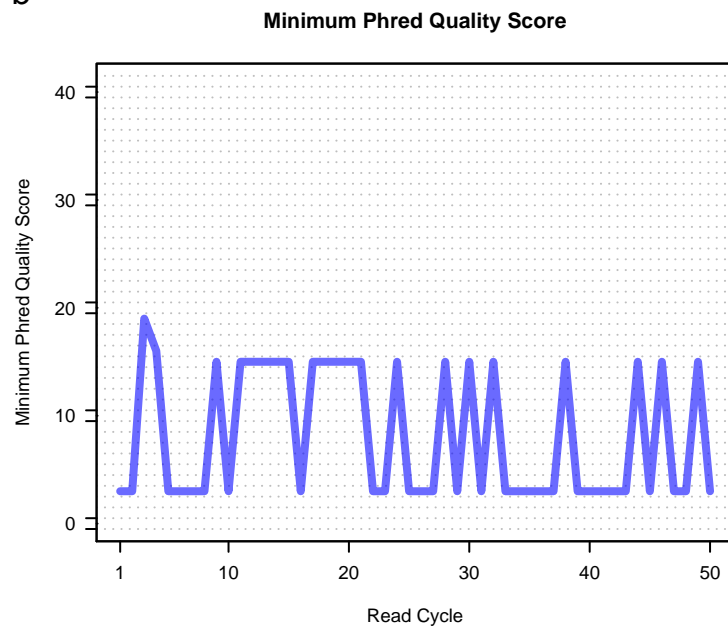


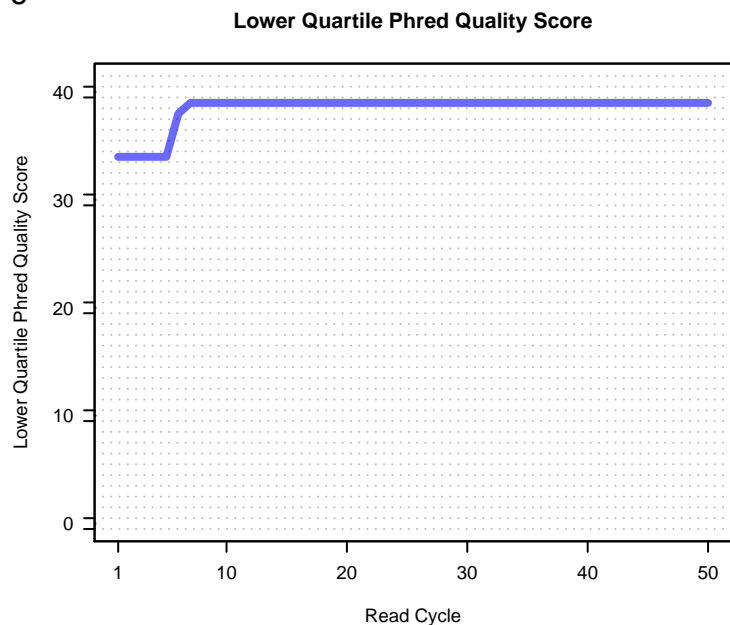
a

# All Quality Control Summary Plots

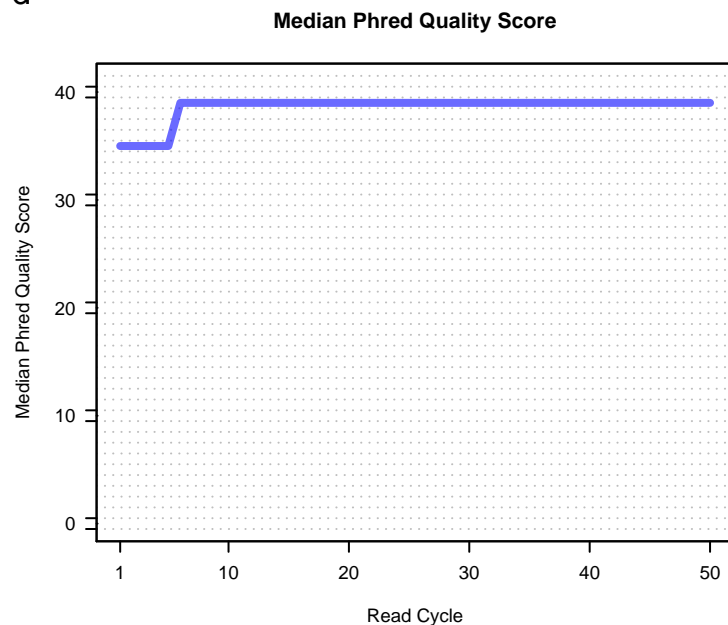
b



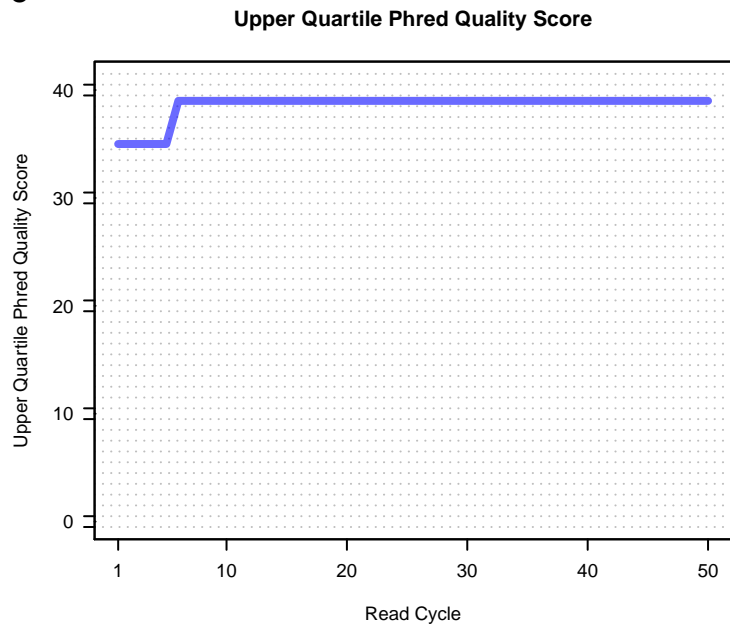
c



d



e

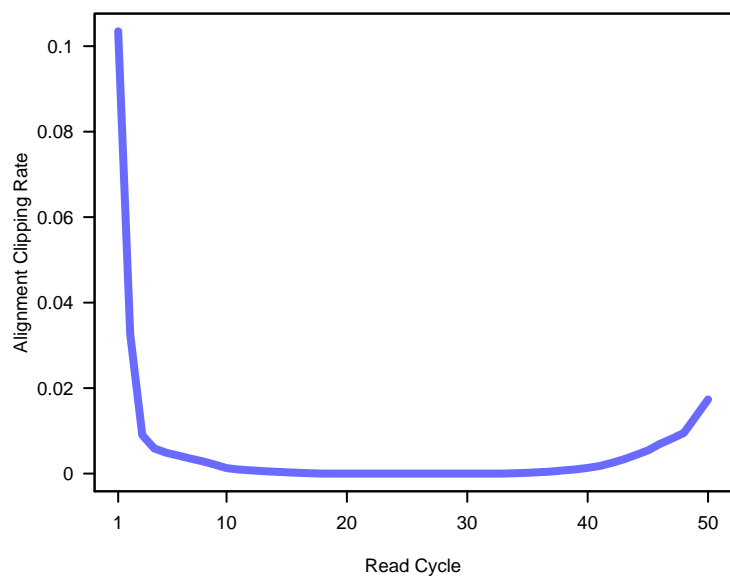


f



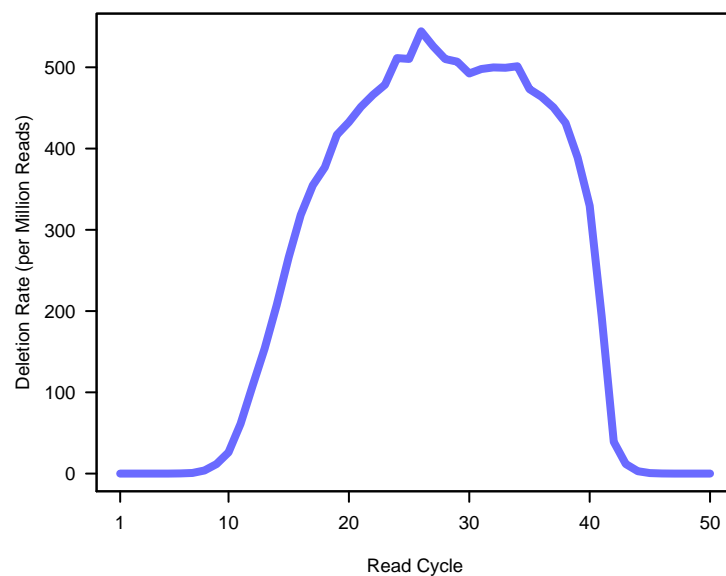
g

Alignment Clipping Rate, by read cycle



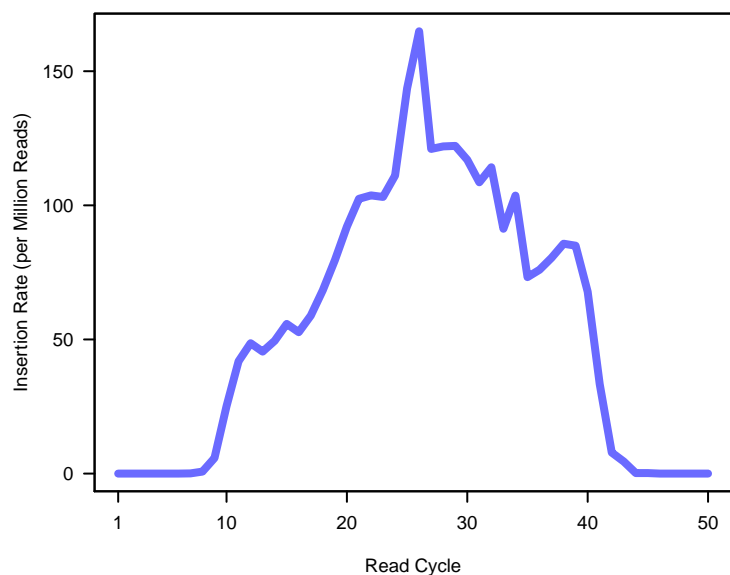
h

Deletion Rate, by read cycle



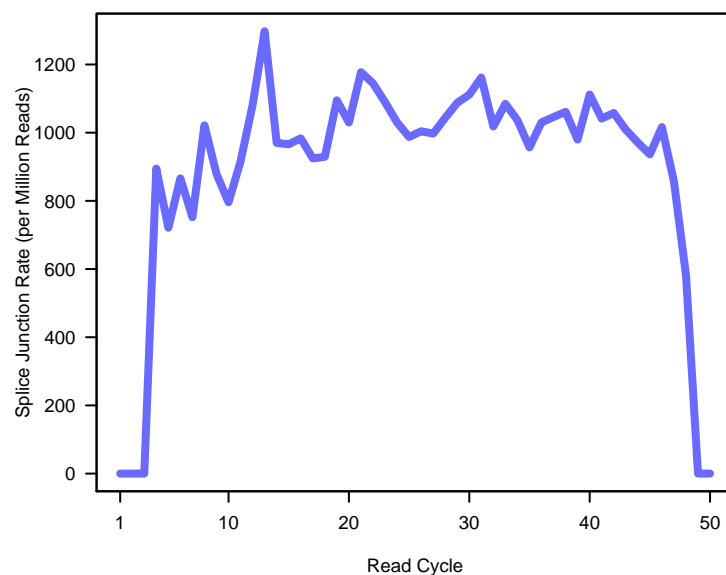
i

Insertion Rate, by read cycle



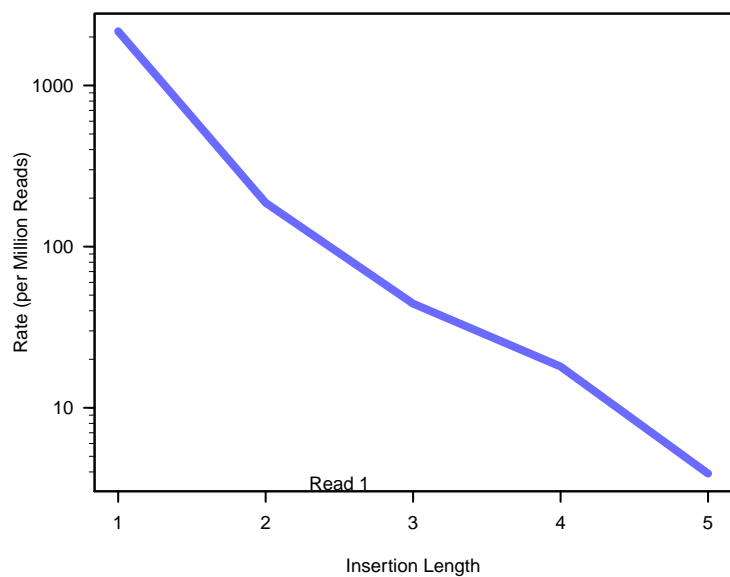
j

Splice Junction Rate, by read cycle



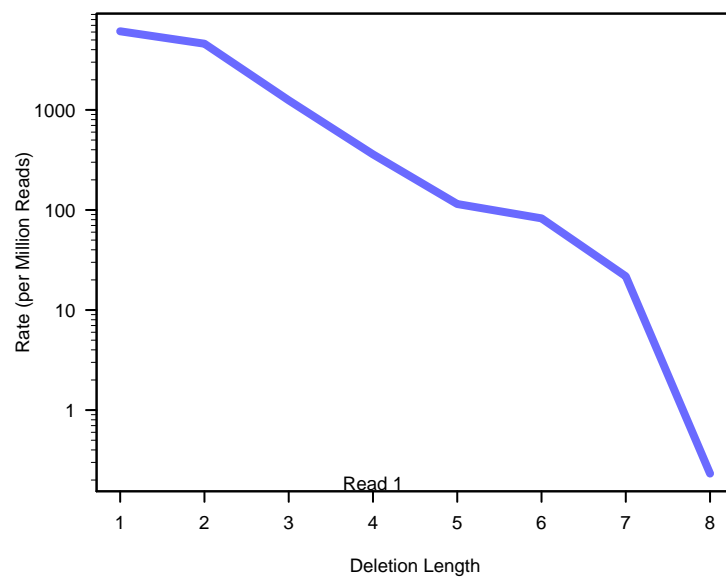
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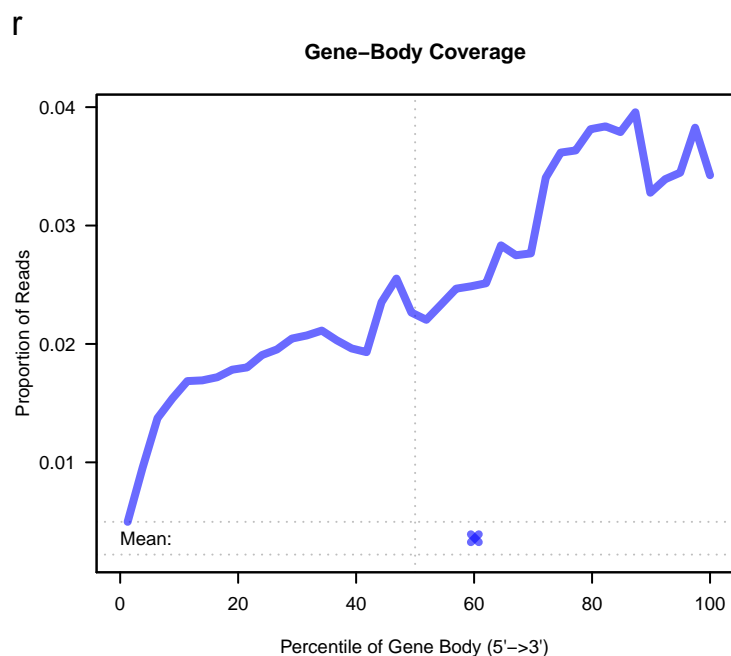
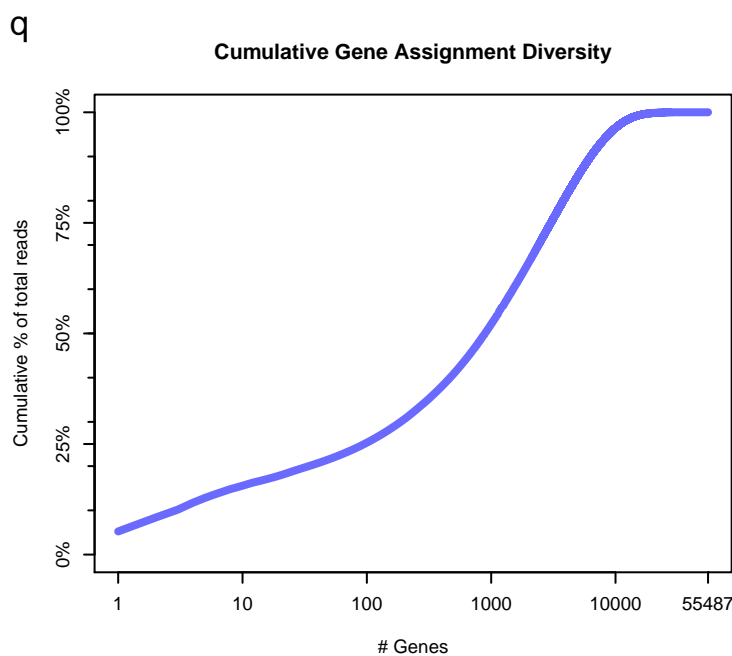
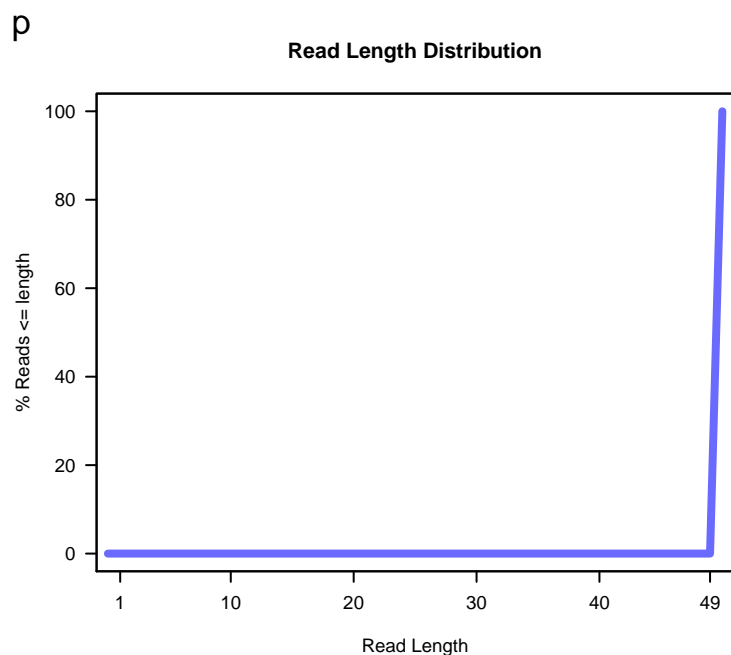
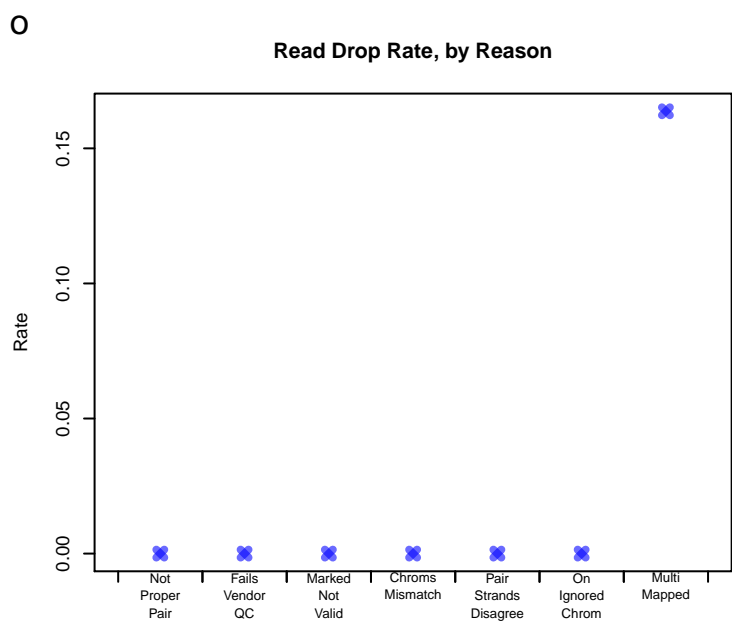
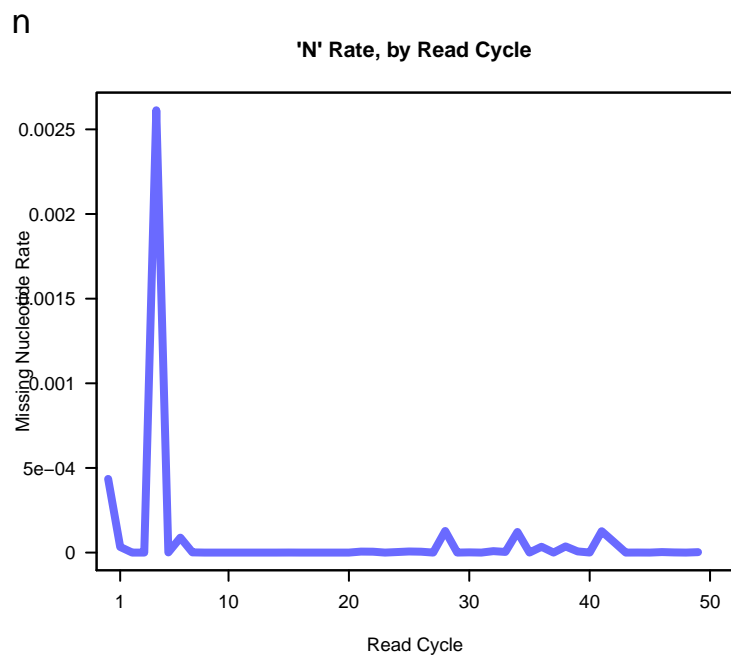
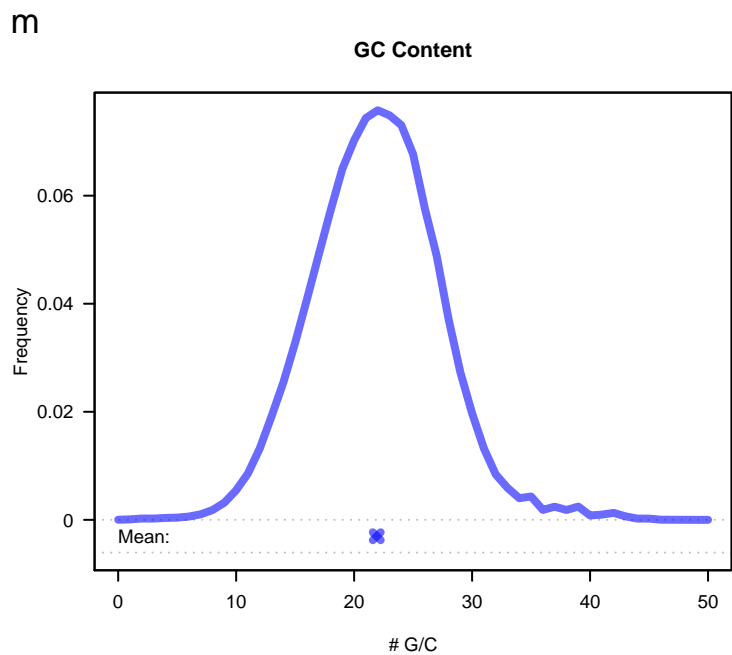
Insertion Length Distribution



l

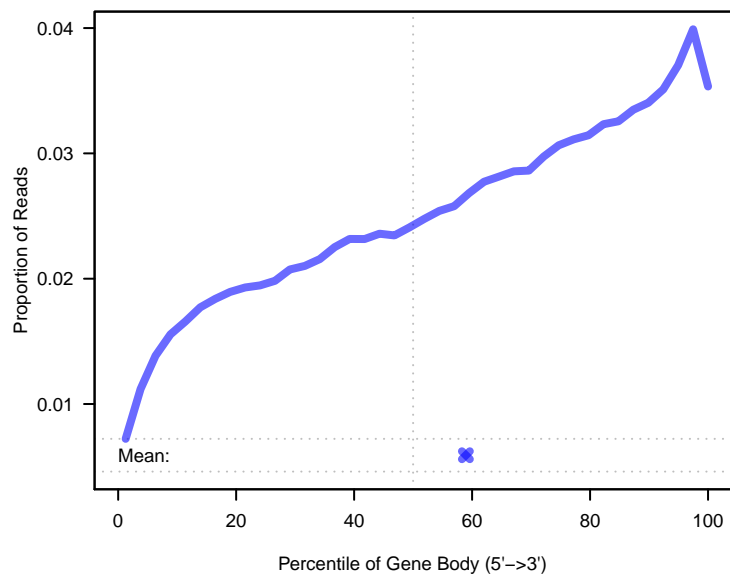
Deletion Length Distribution





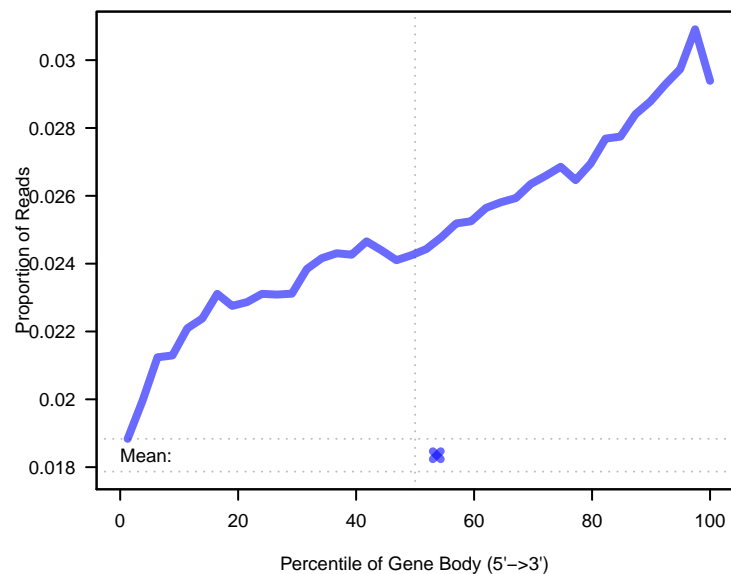
s

Gene-Body Coverage, Upper Middle Quartile Genes



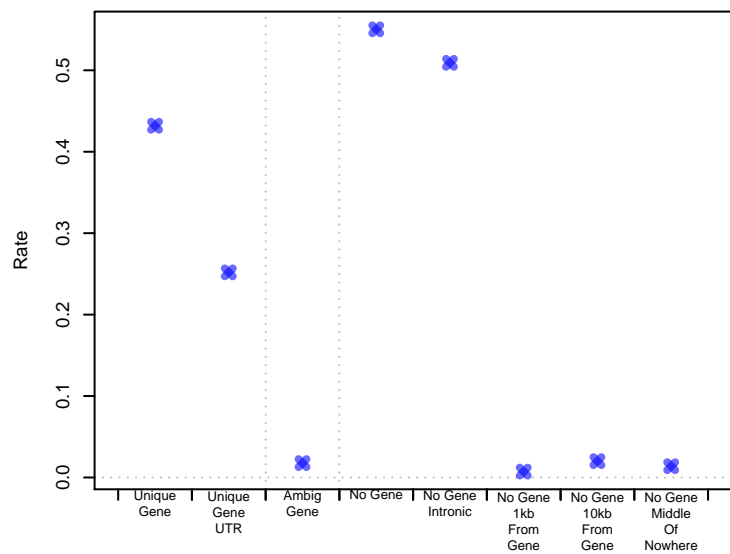
t

Gene-Body Coverage, Low Expression Genes



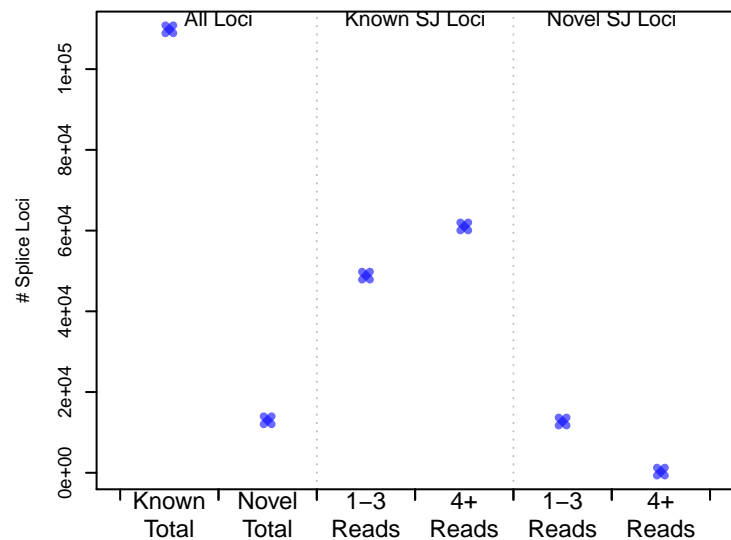
u

Read Mapping Location Rates



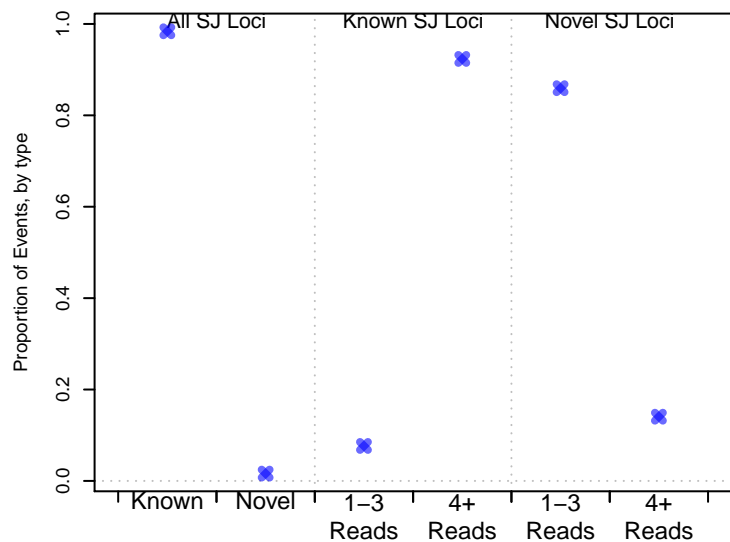
v

# Observed Splice Junction Loci, by type



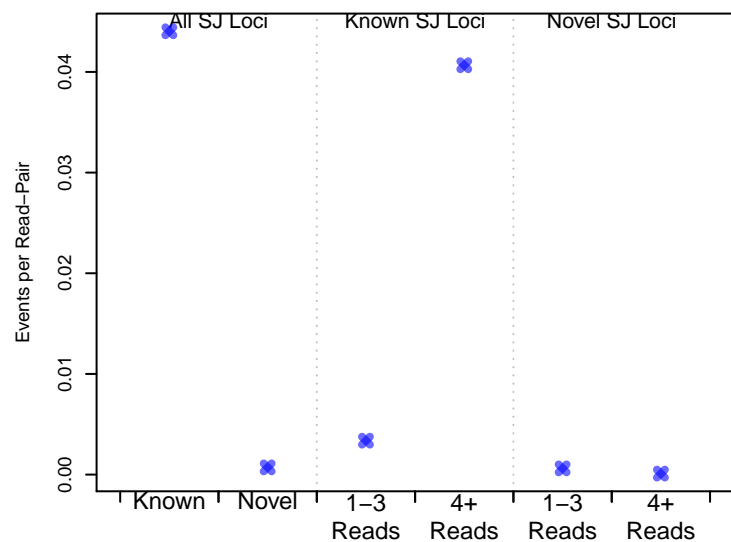
w

Breakdown of Splice Junction Events, by type



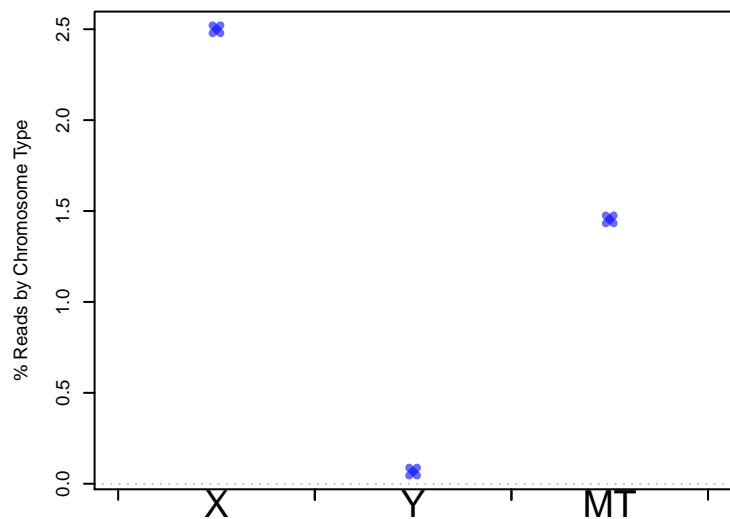
x

Splice Junction Event Rates per Read-Pair



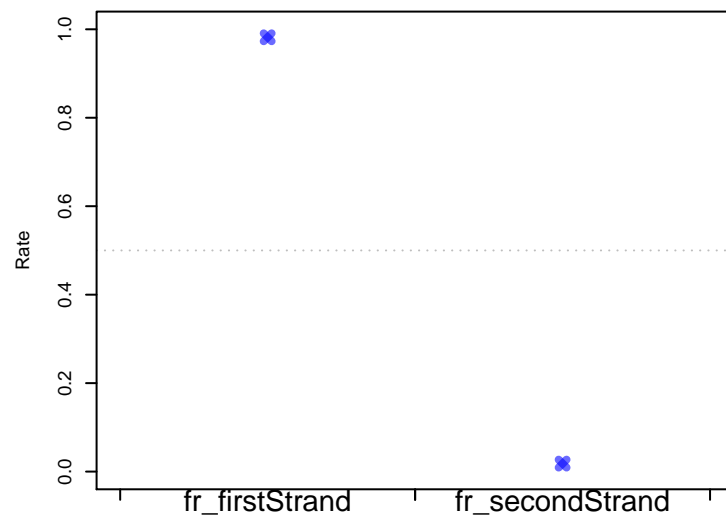
y

Chromosome Distribution (Excluding Autosomes)



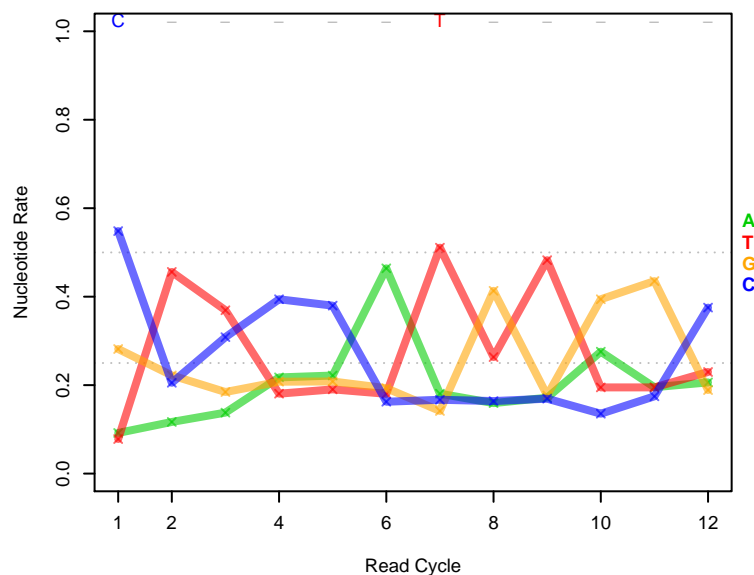
Z

Strandedness Test



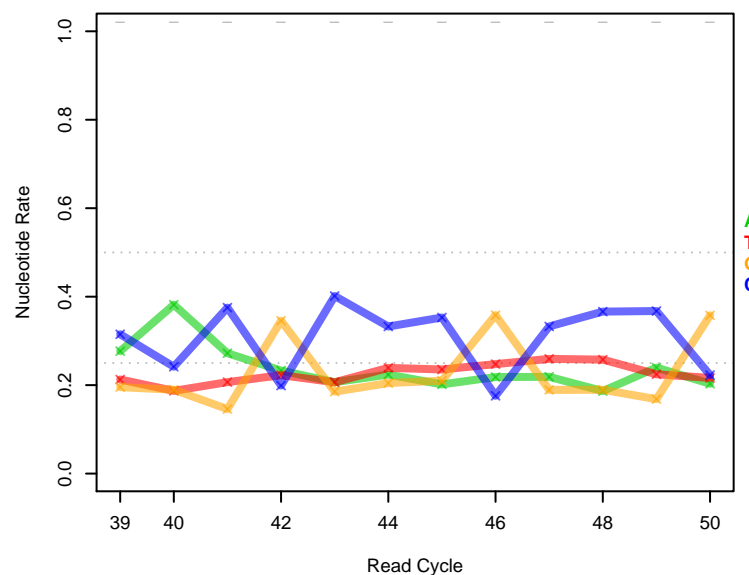
aa

Nucleotide Rate by Cycle, Leading Clipped bases (12)



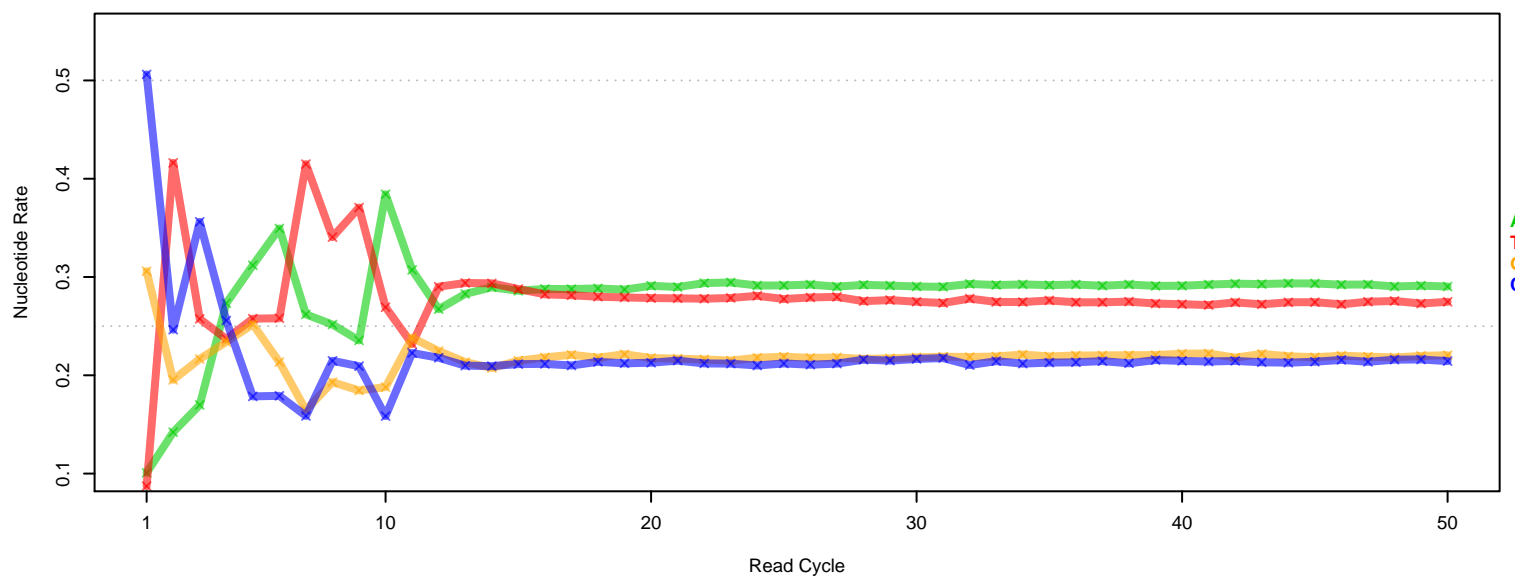
ab

Nucleotide Rate by Cycle, Trailing Clipped bases (12)



ac

Raw Nucleotide Rate by Cycle



Nucleotide Rate by Cycle, Aligned bases only

