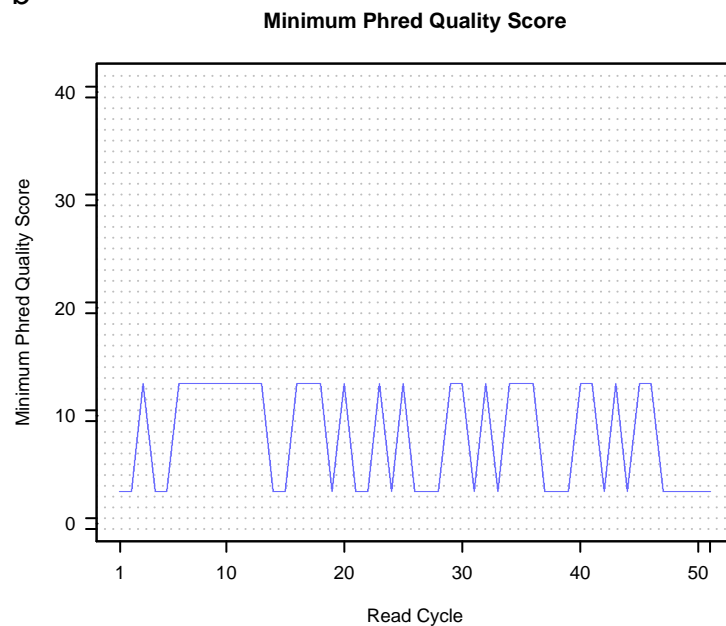


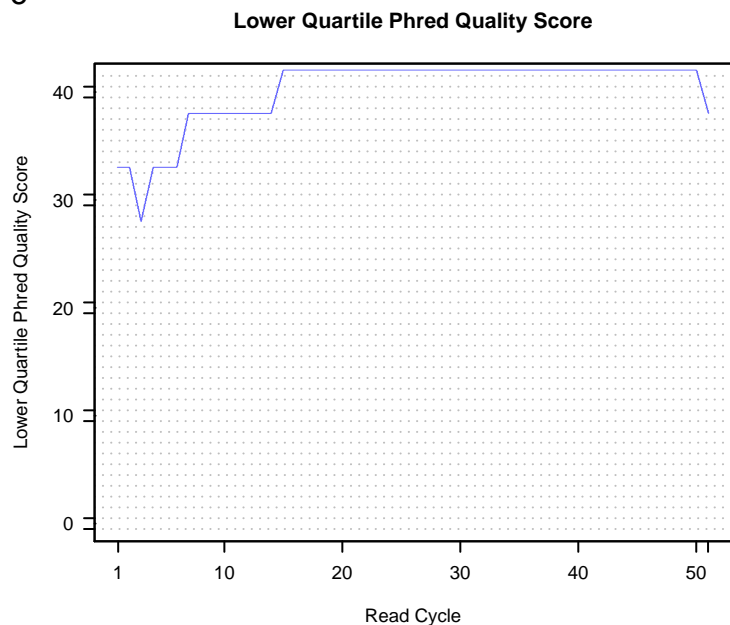
a

All Quality Control Summary Plots

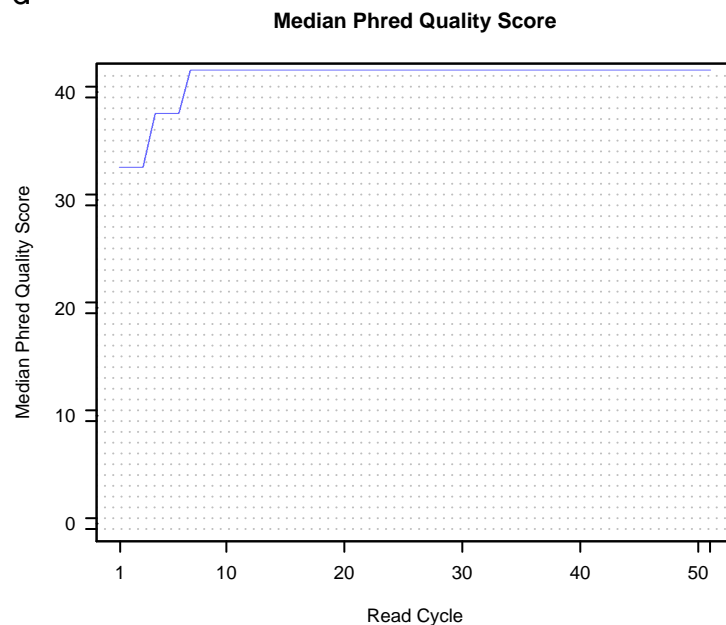
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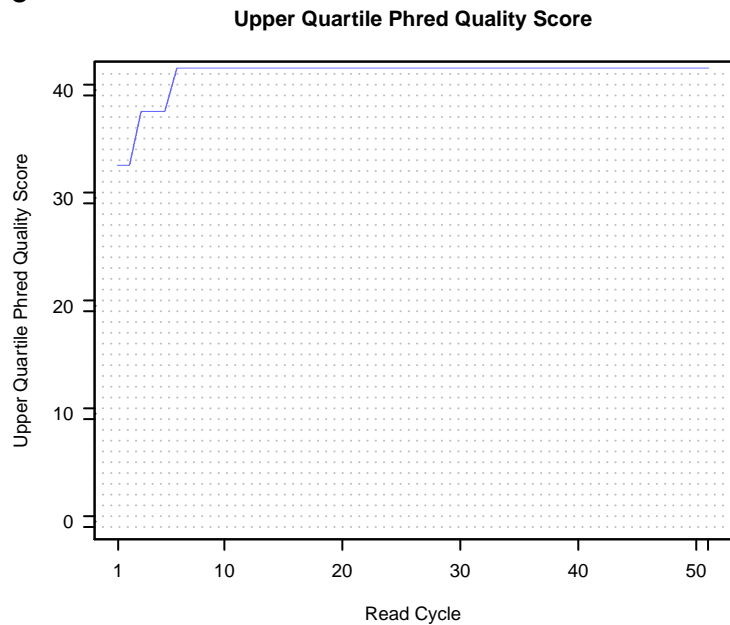
c



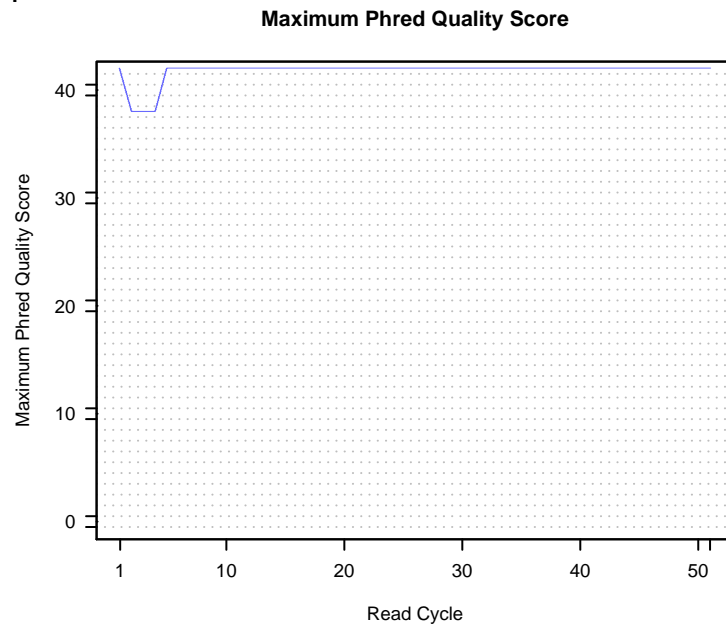
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e

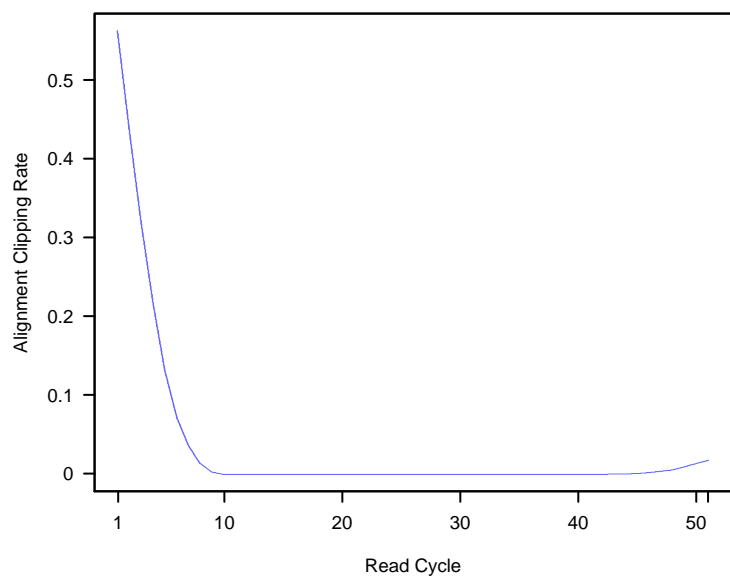


f



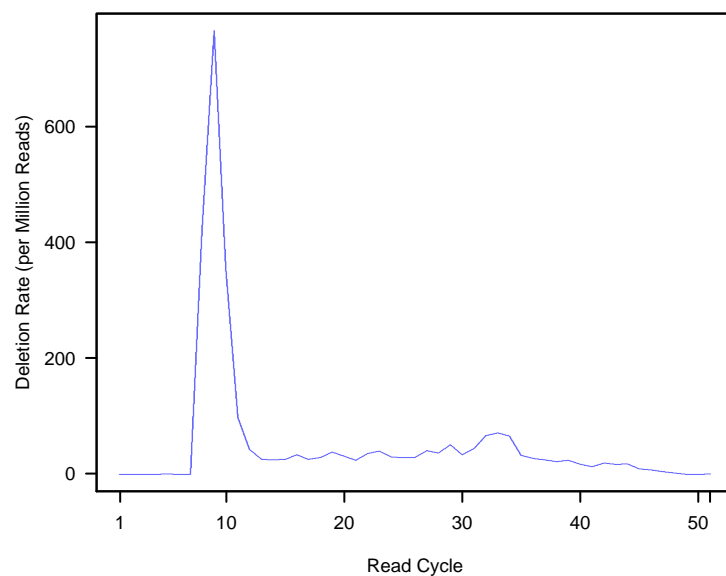
g

Alignment Clipping Rate, by read cycle



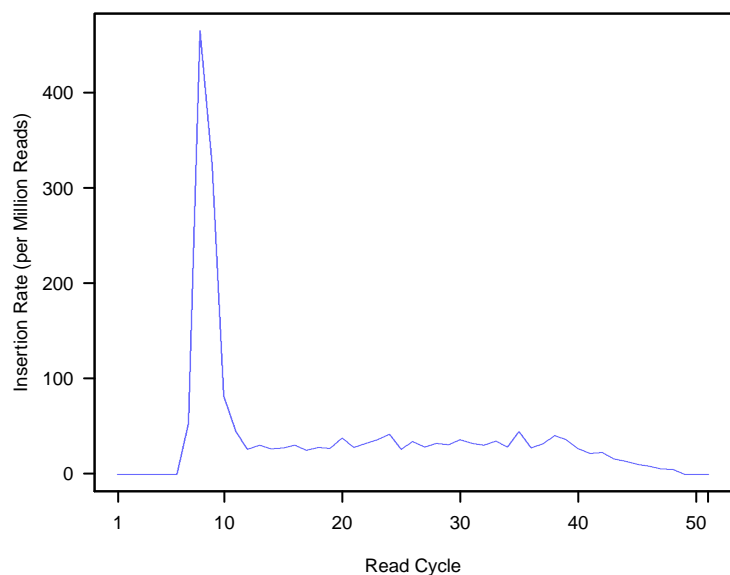
h

Deletion Rate, by read cycle



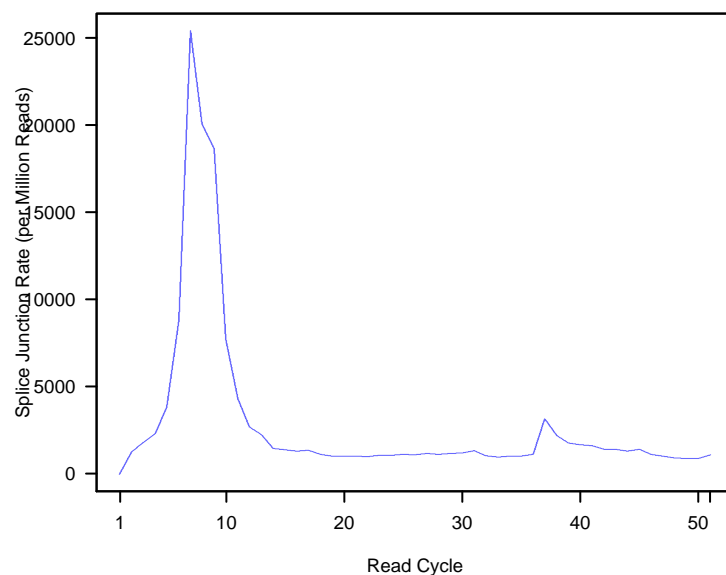
i

Insertion Rate, by read cycle



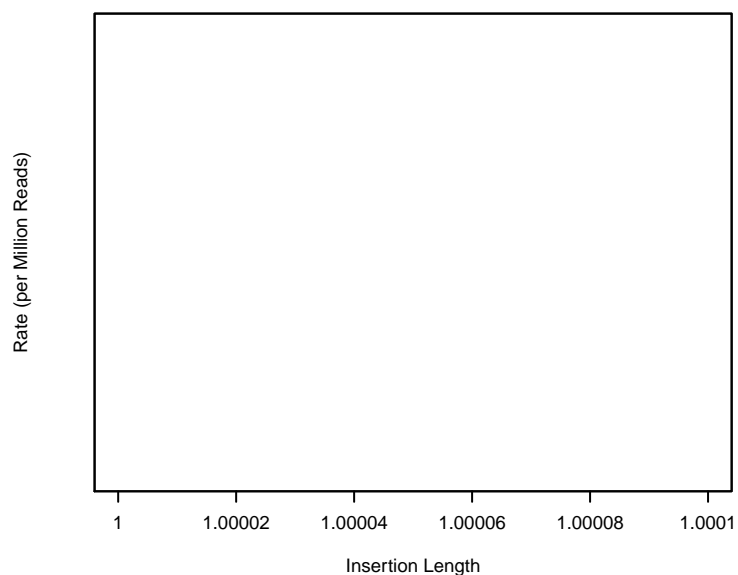
j

Splice Junction Rate, by read cycle



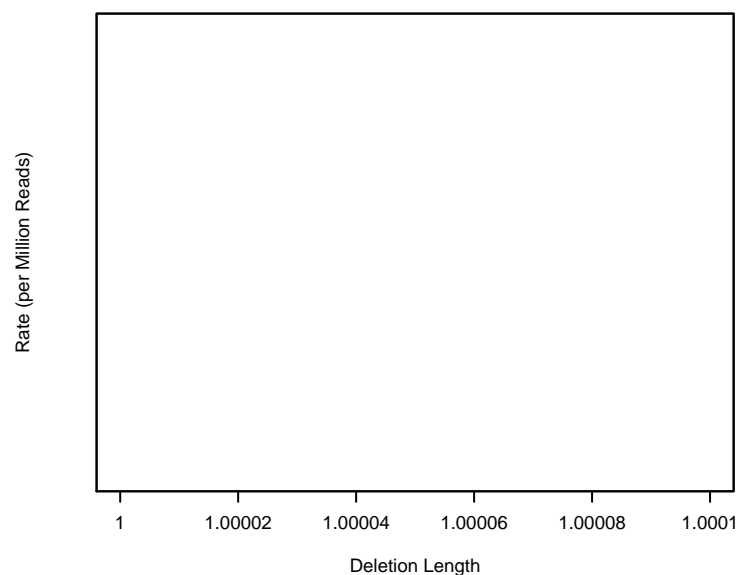
k

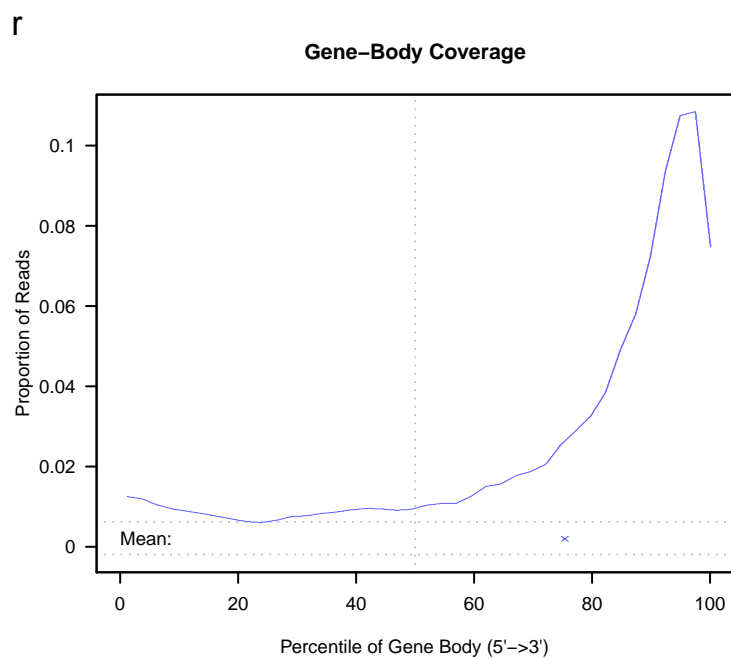
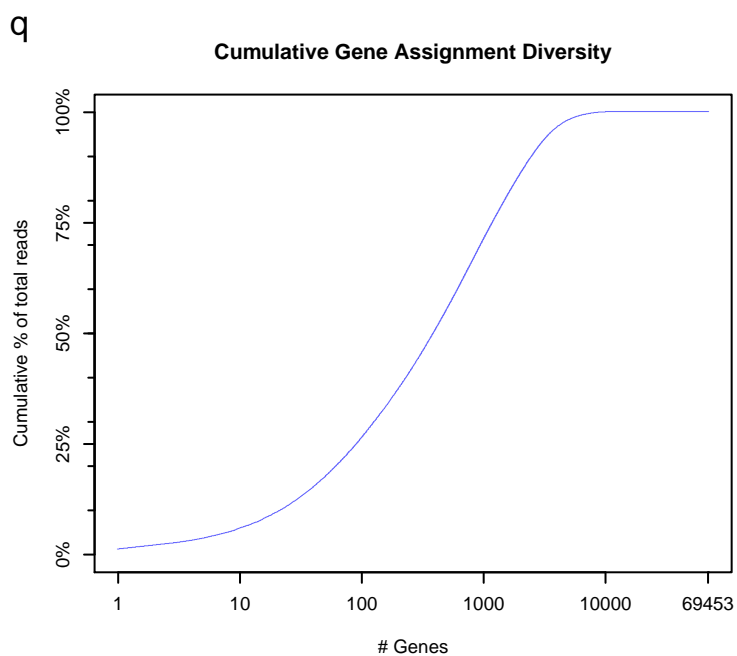
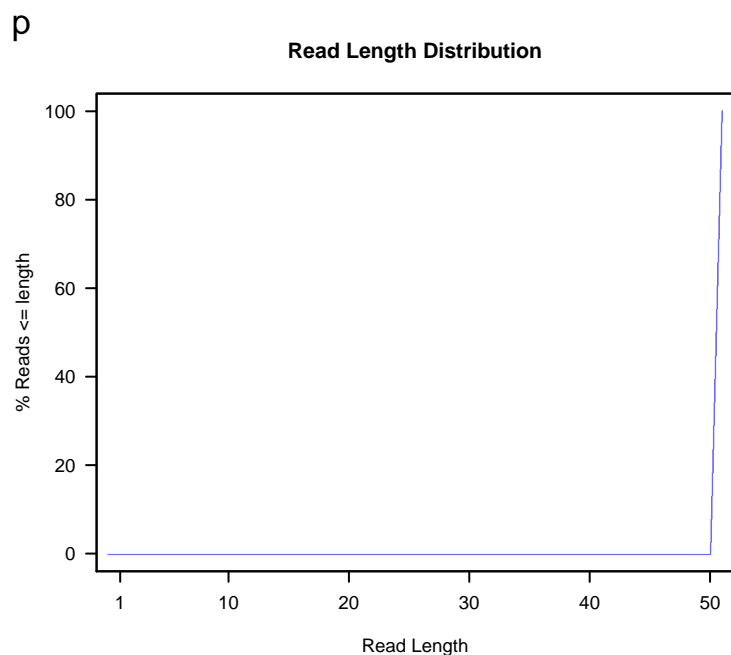
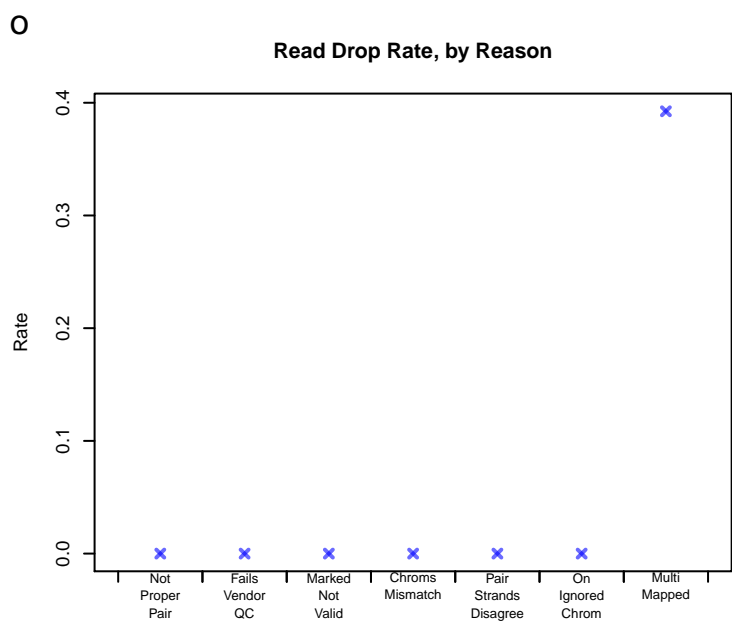
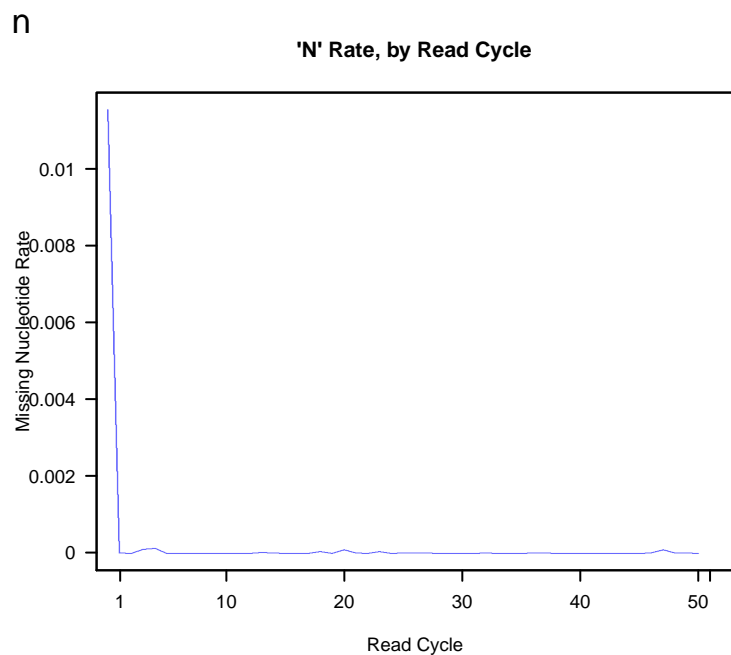
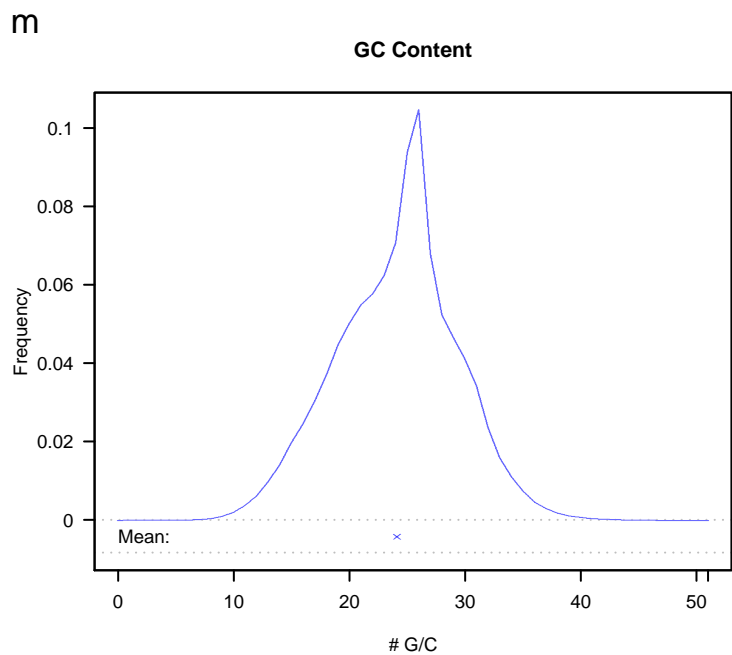
Insertion Length Distribution



l

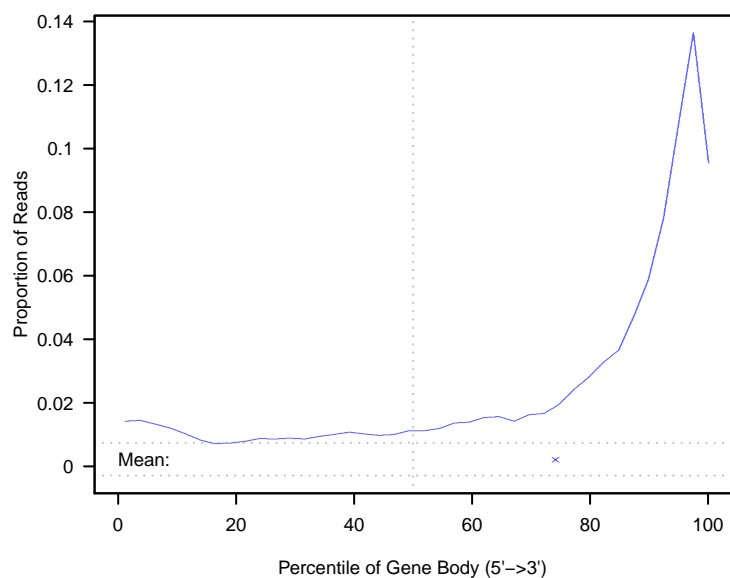
Deletion Length Distribution





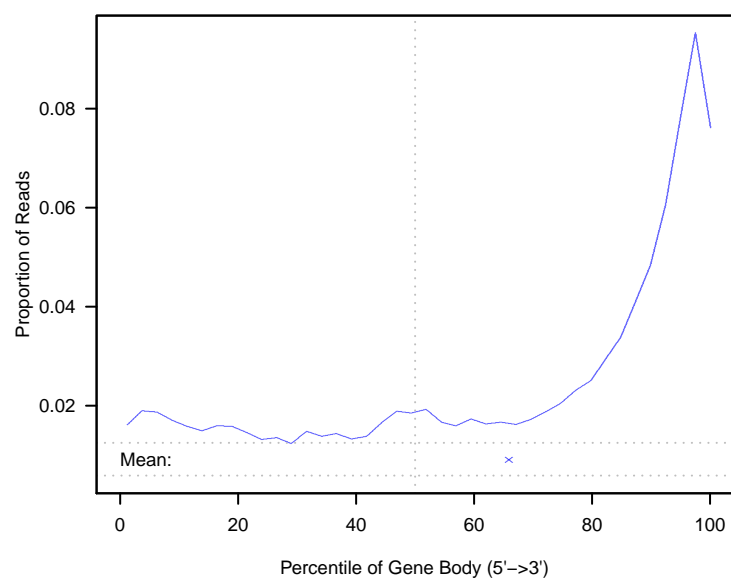
s

Gene-Body Coverage, Upper Middle Quartile Genes



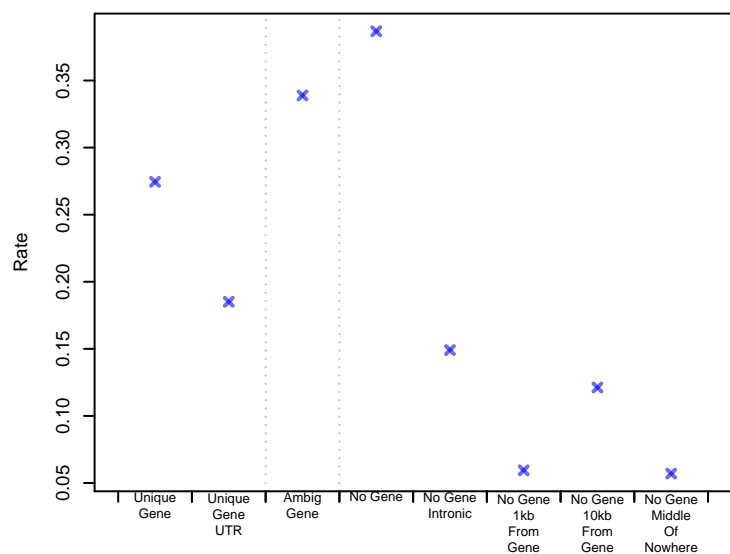
t

Gene-Body Coverage, Low Expression Genes



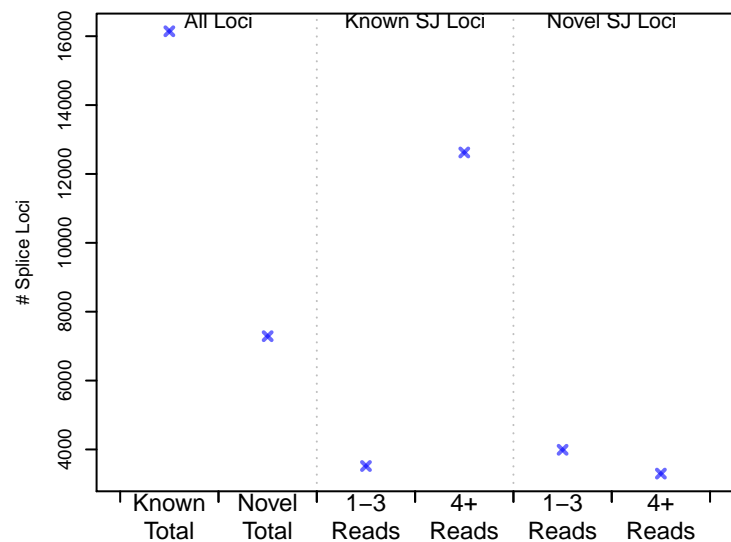
u

Read Mapping Location Rates



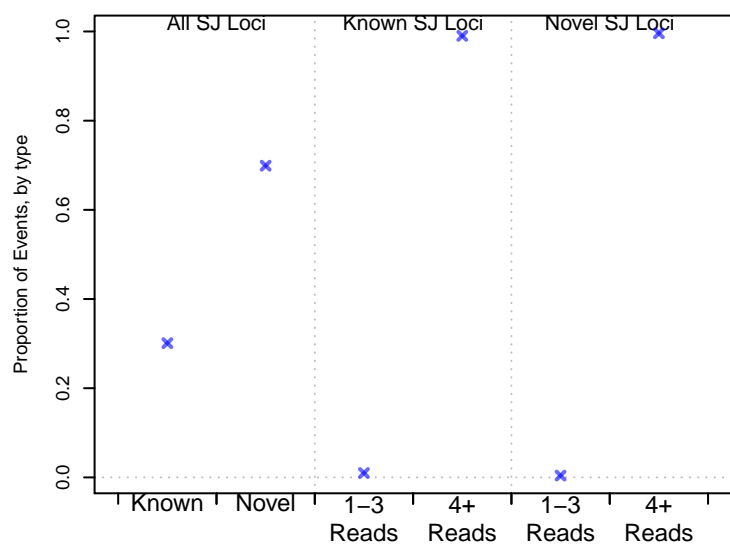
v

Observed Splice Junction Loci, by type



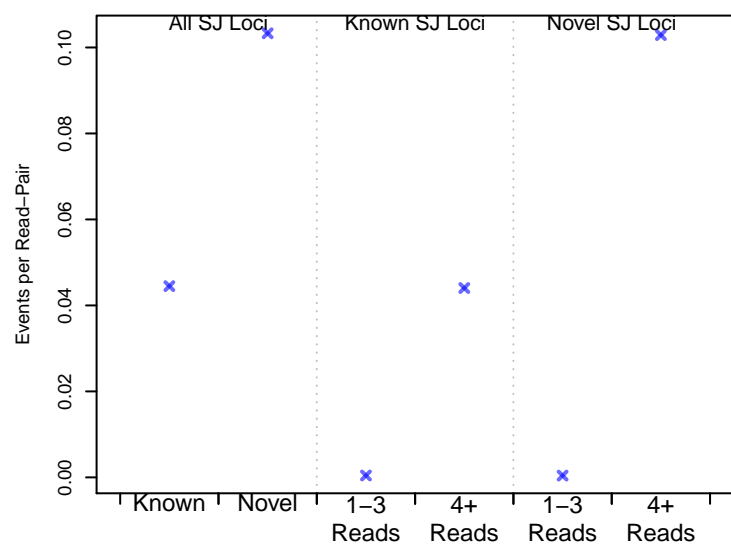
w

Breakdown of Splice Junction Events, by type

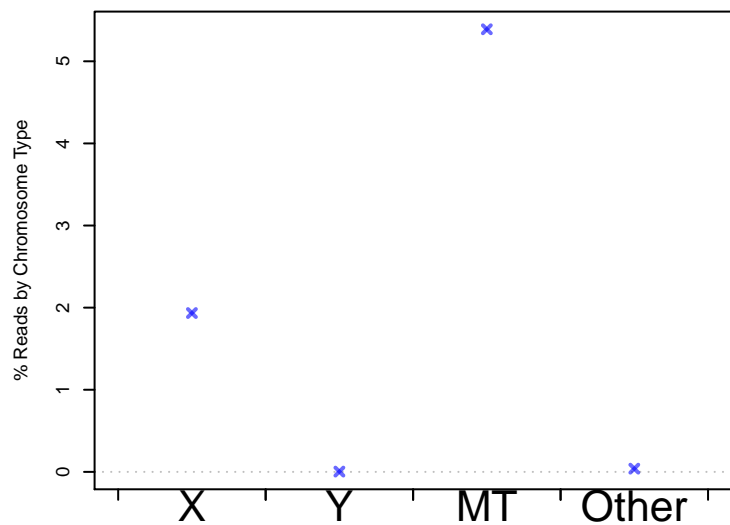


x

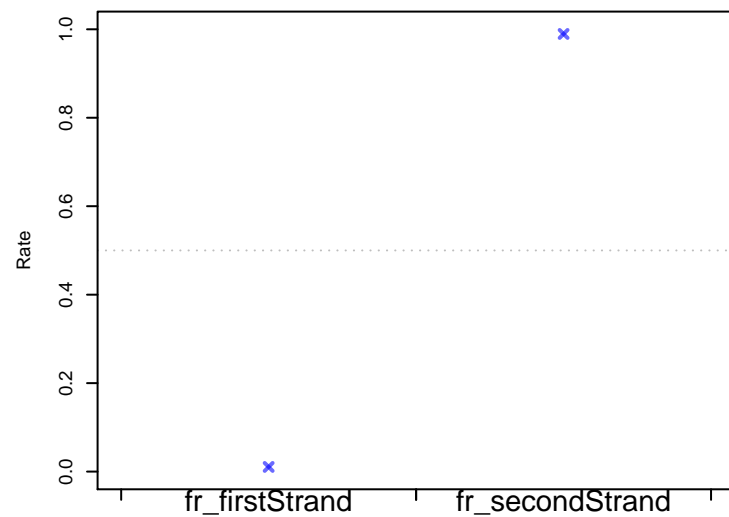
Splice Junction Event Rates per Read-Pair



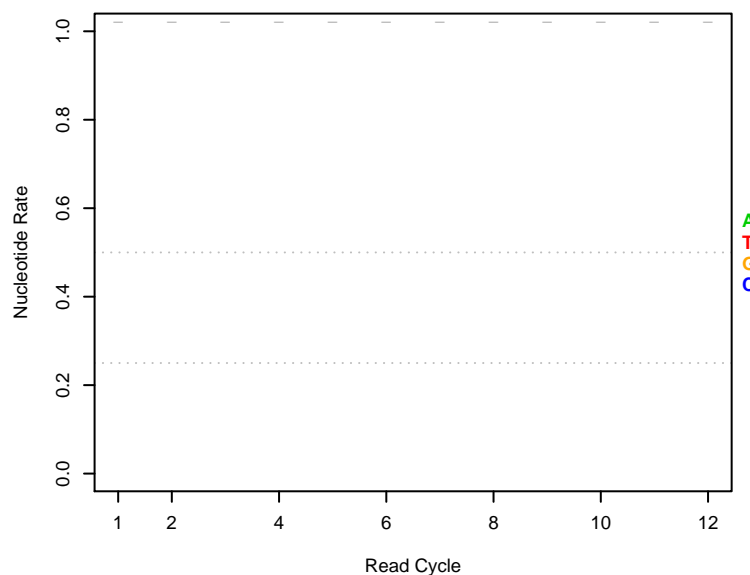
y **Chromosome Distribution (Excluding Autosomes)**



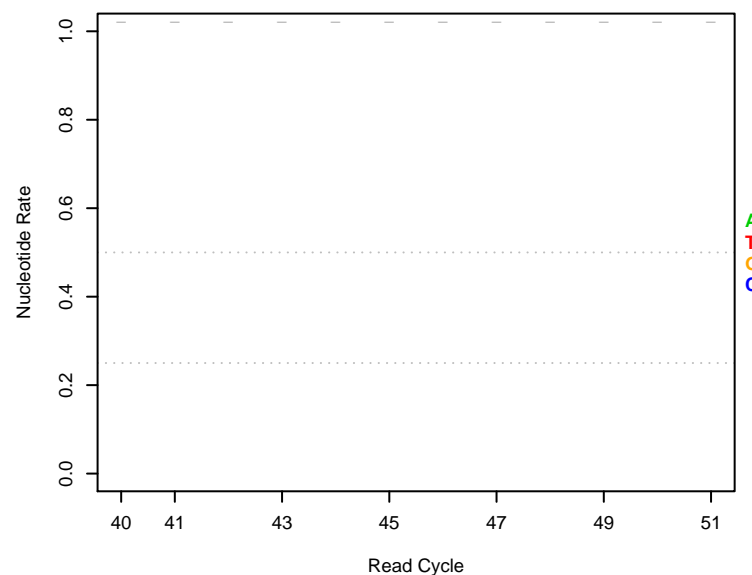
z **Strandedness Test**



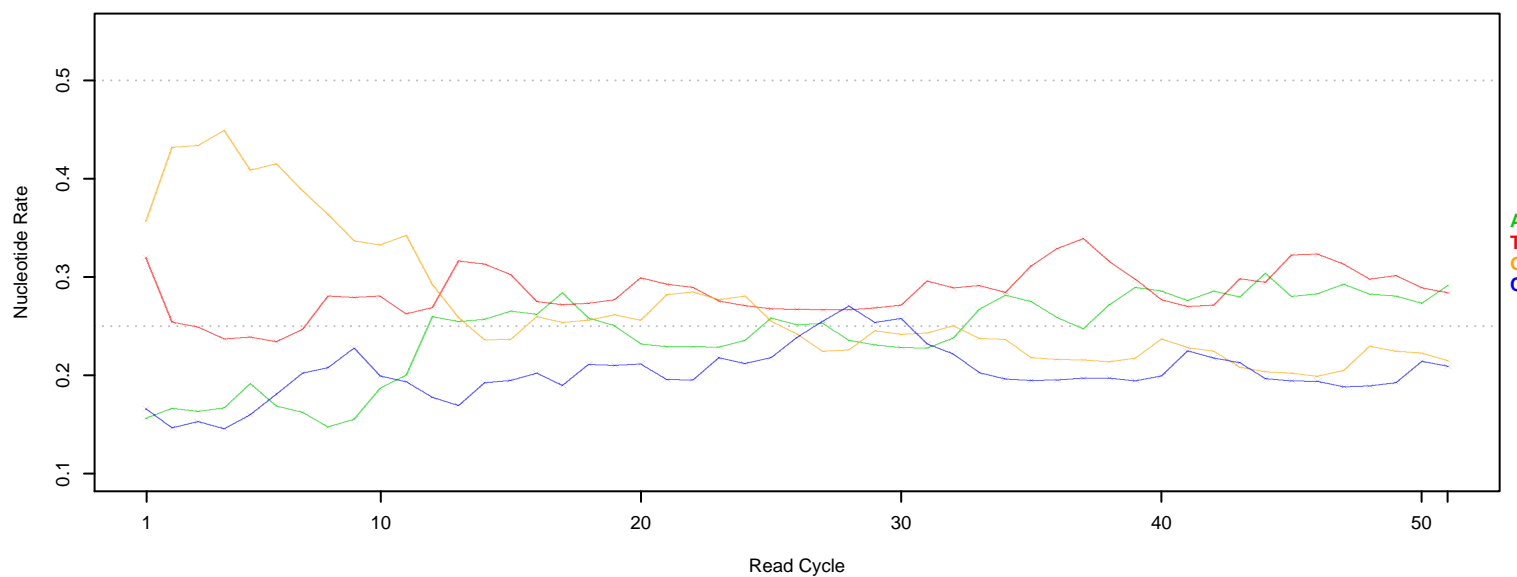
aa **Nucleotide Rate by Cycle, Leading Clipped bases (12)**



ab **Nucleotide Rate by Cycle, Trailing Clipped bases (12)**



ac **Raw Nucleotide Rate by Cycle**



Nucleotide Rate by Cycle, Aligned bases only

