

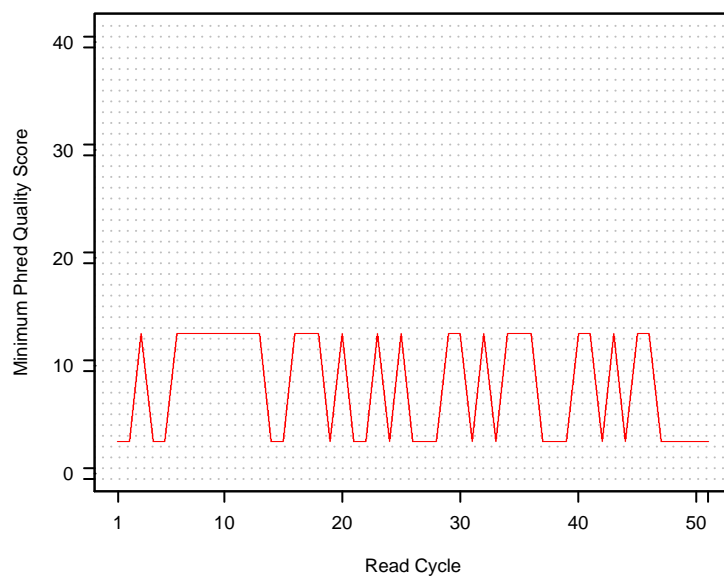
a

Sample Highlight:
e1_aligned_sorted
Colored by Lane



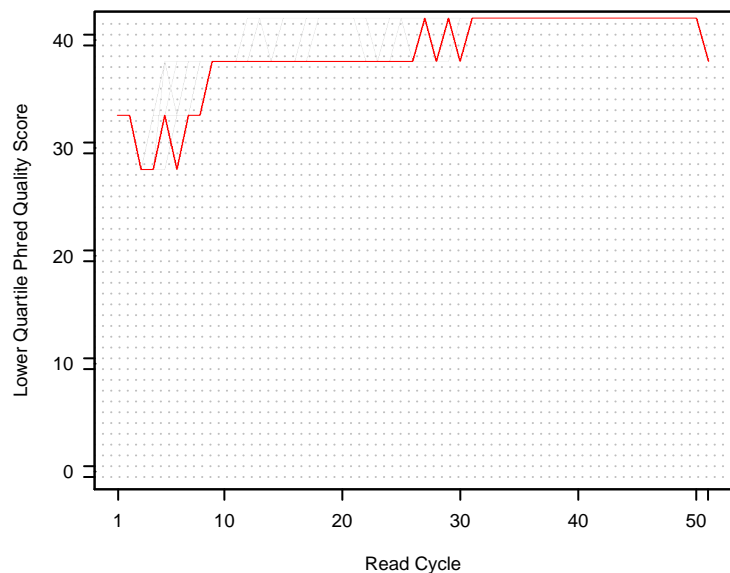
b

Minimum Phred Quality Score
With Sample e1_aligned_sorted Colored by lane



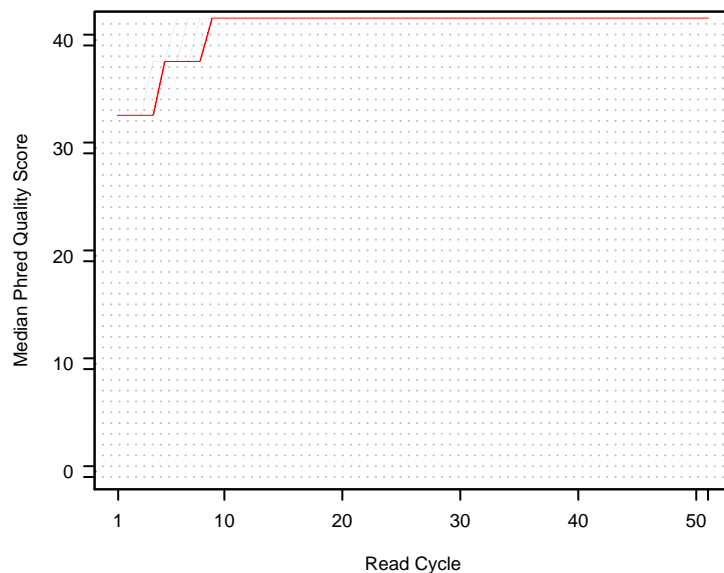
c

Lower Quartile Phred Quality Score
With Sample e1_aligned_sorted Colored by lane



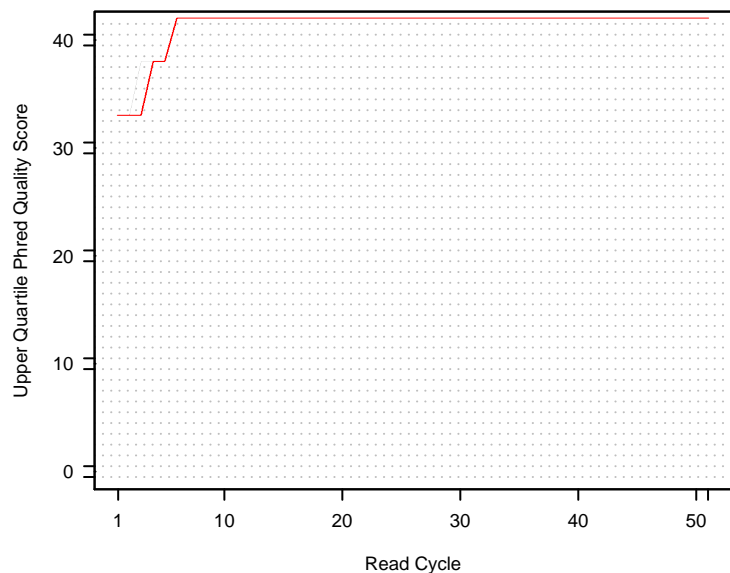
d

Median Phred Quality Score
With Sample e1_aligned_sorted Colored by lane



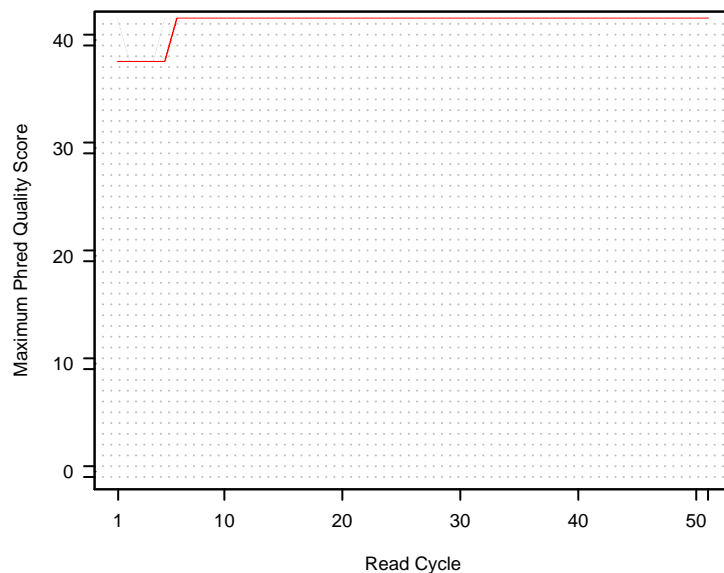
e

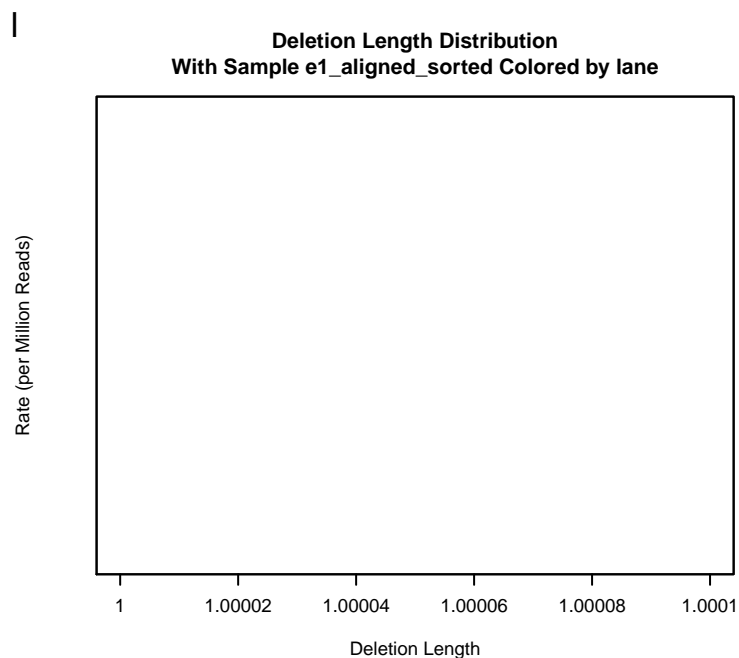
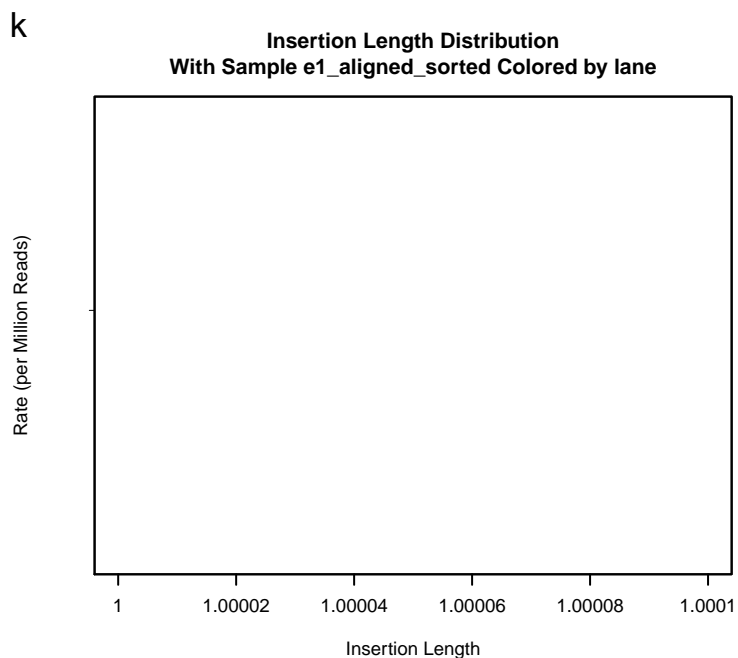
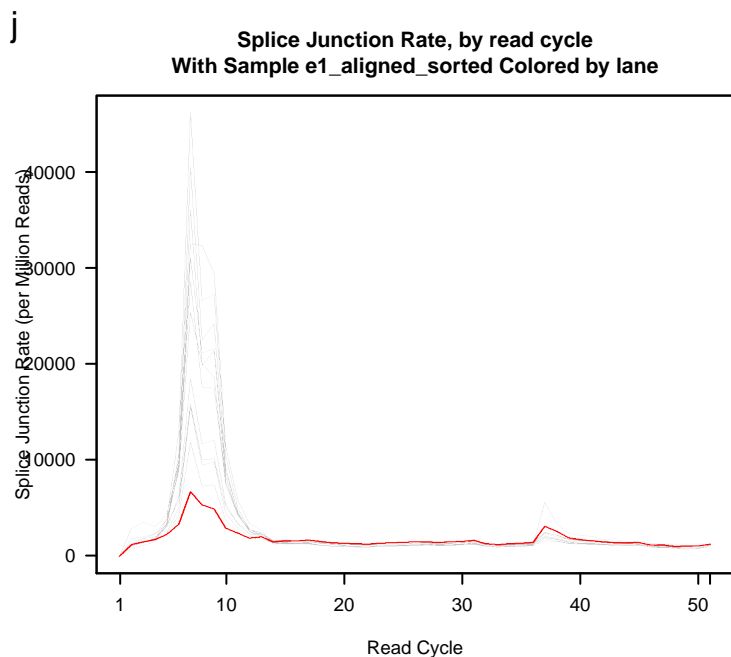
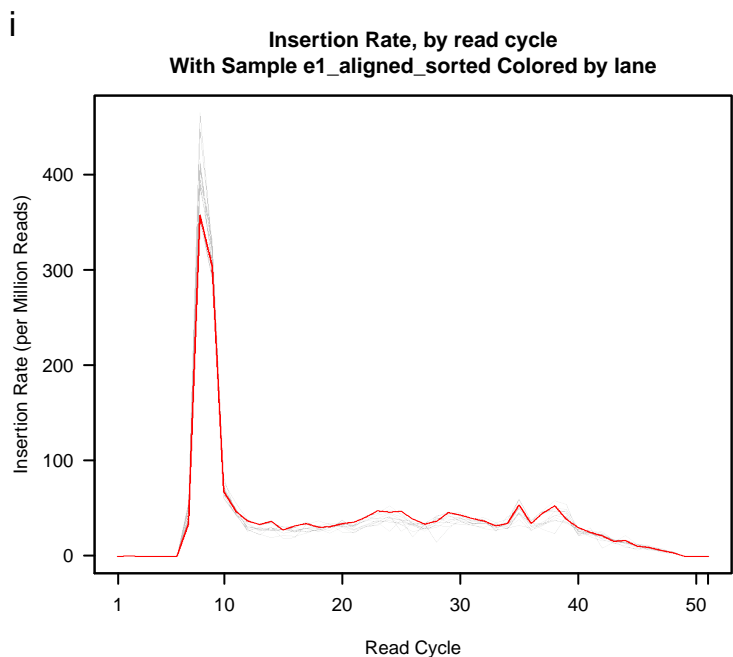
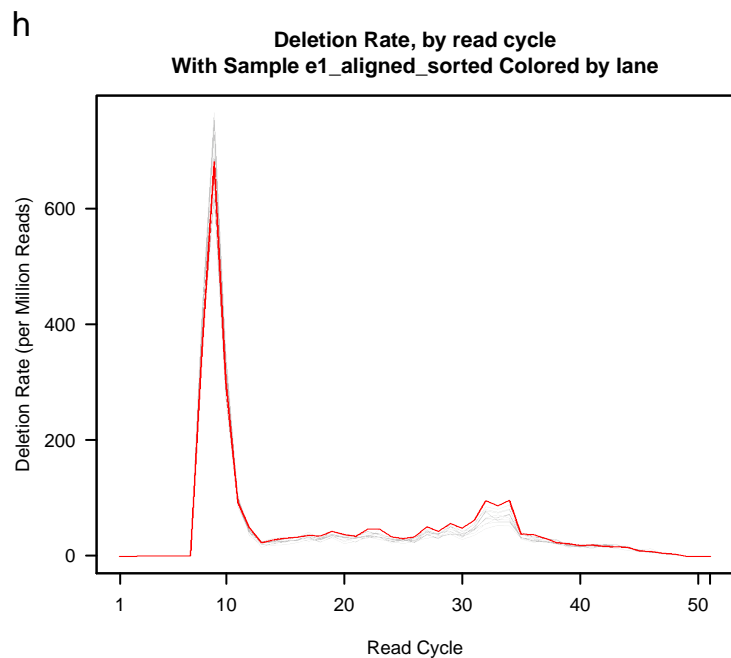
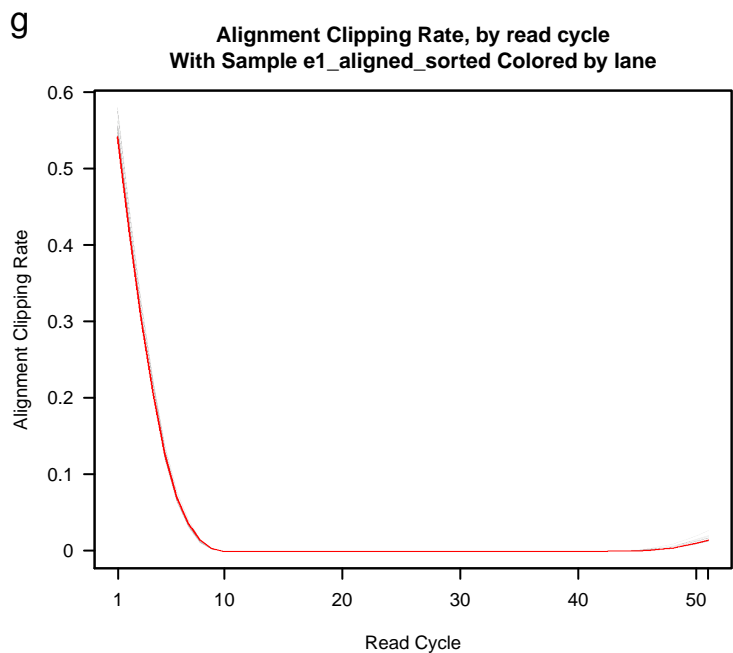
Upper Quartile Phred Quality Score
With Sample e1_aligned_sorted Colored by lane

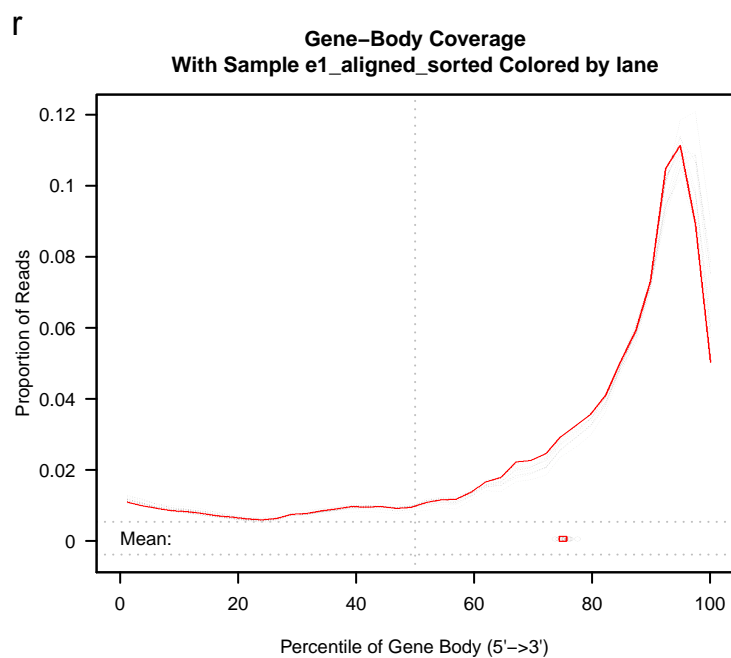
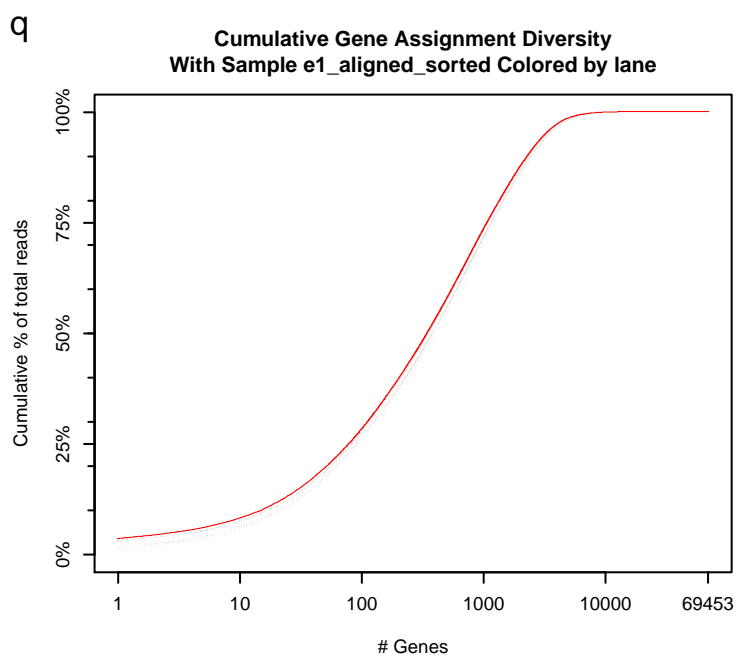
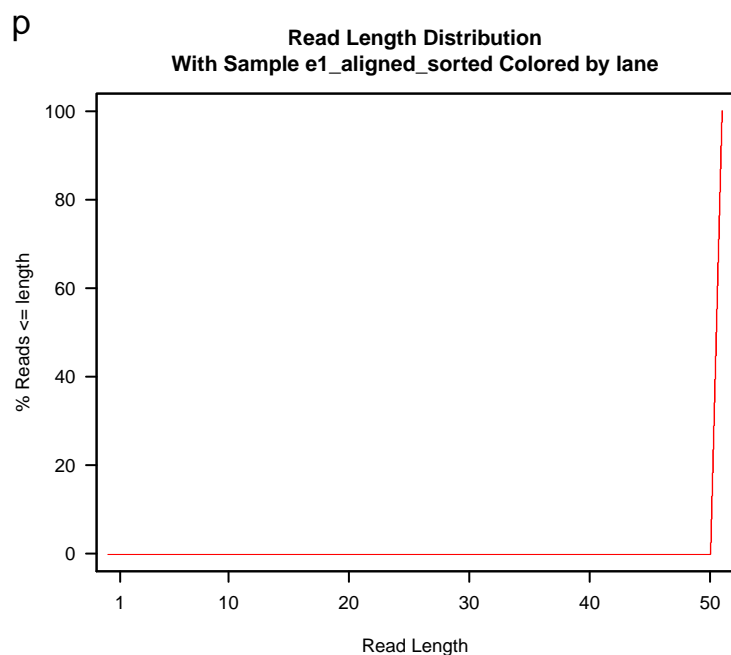
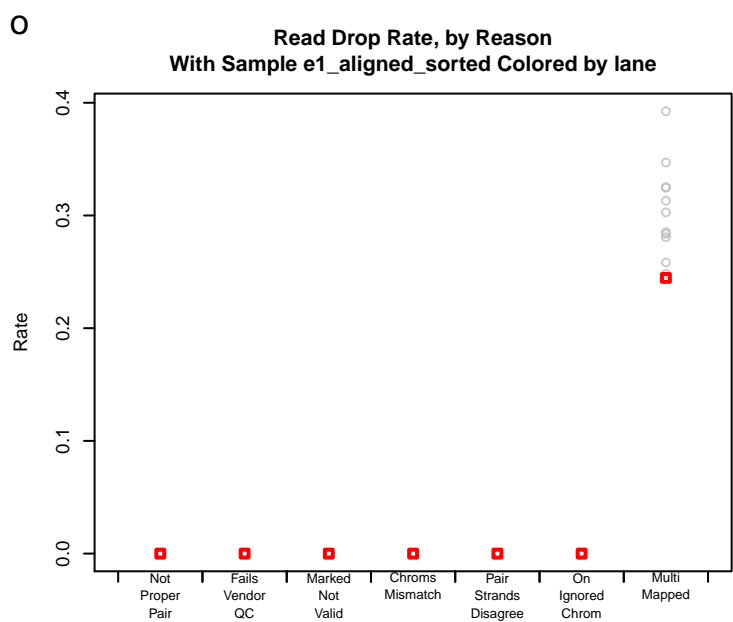
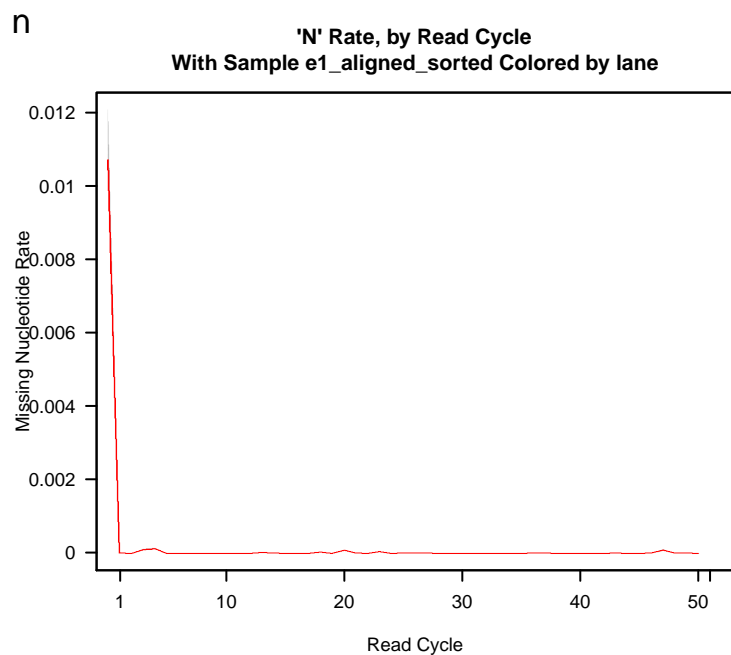
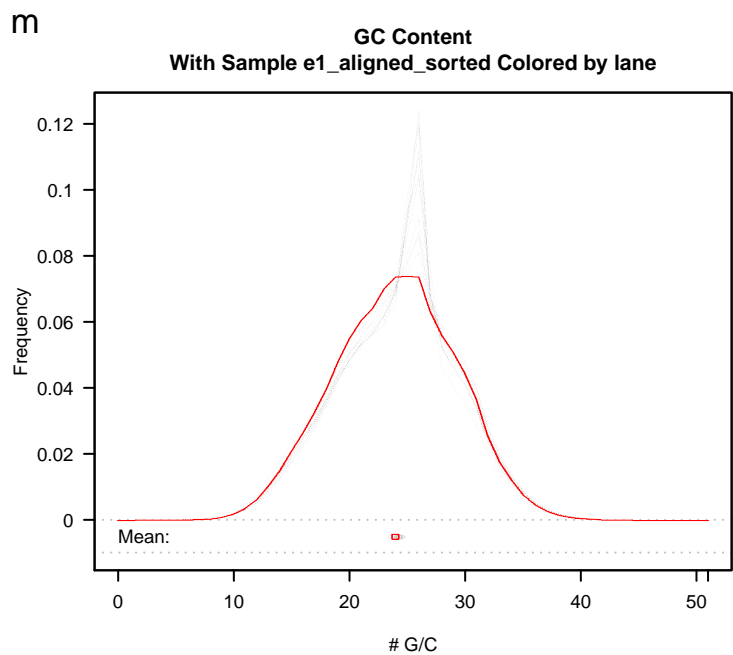


f

Maximum Phred Quality Score
With Sample e1_aligned_sorted Colored by lane

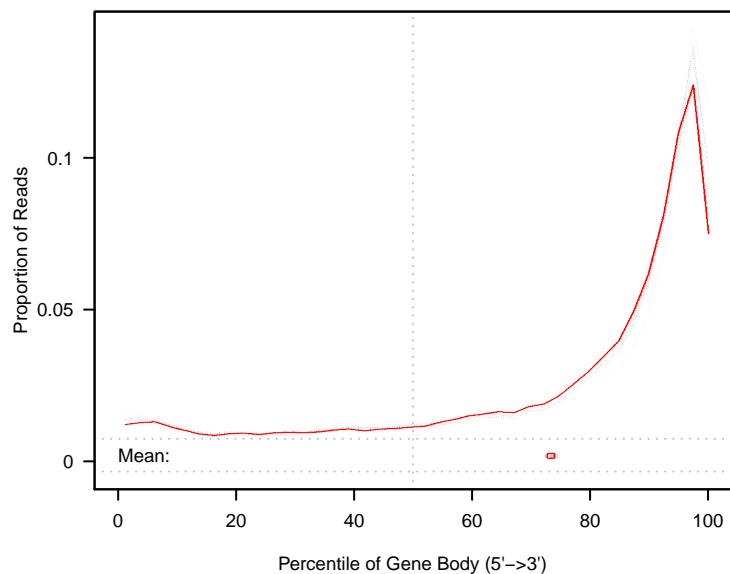






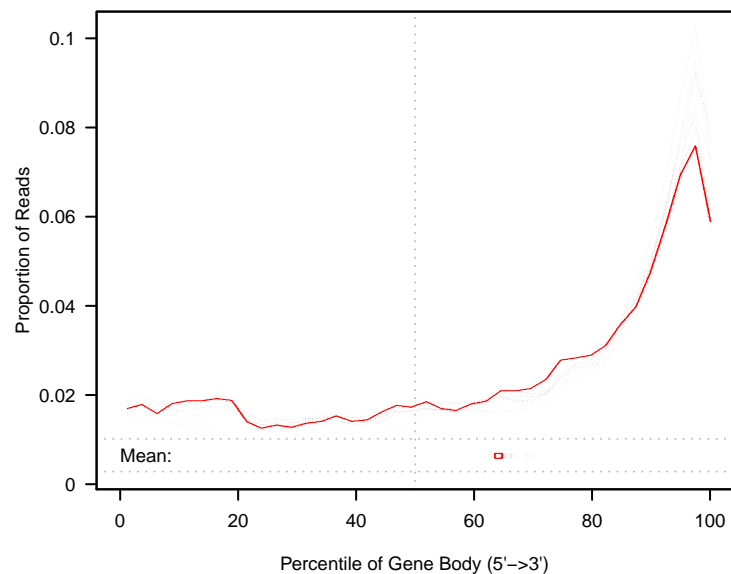
S

Gene-Body Coverage, Upper Middle Quartile Genes
With Sample e1_aligned_sorted Colored by lane



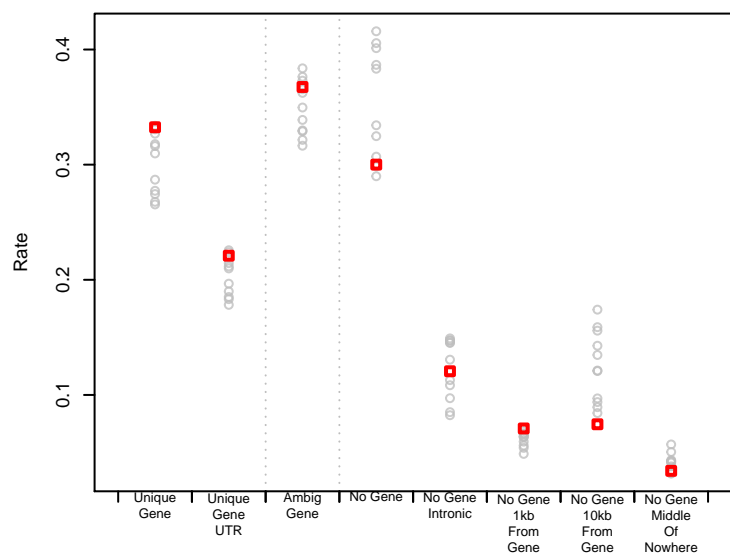
t

Gene-Body Coverage, Low Expression Genes
With Sample e1_aligned_sorted Colored by lane



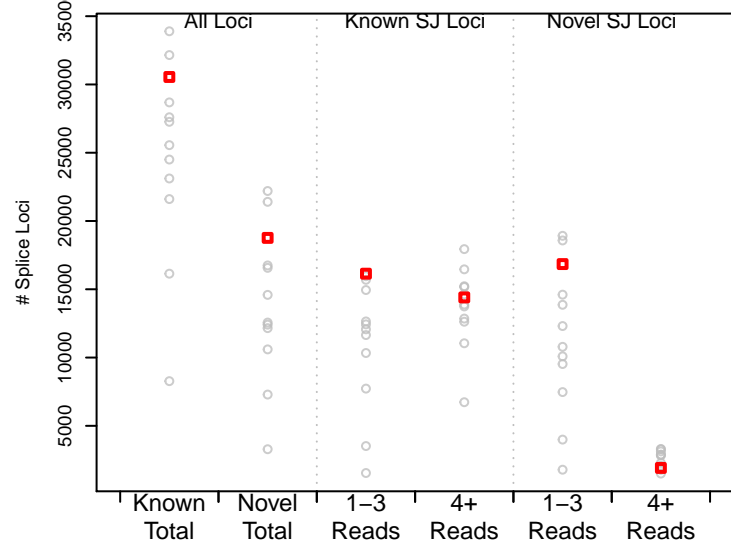
U

Read Mapping Location Rates
With Sample e1_aligned_sorted Colored by lane



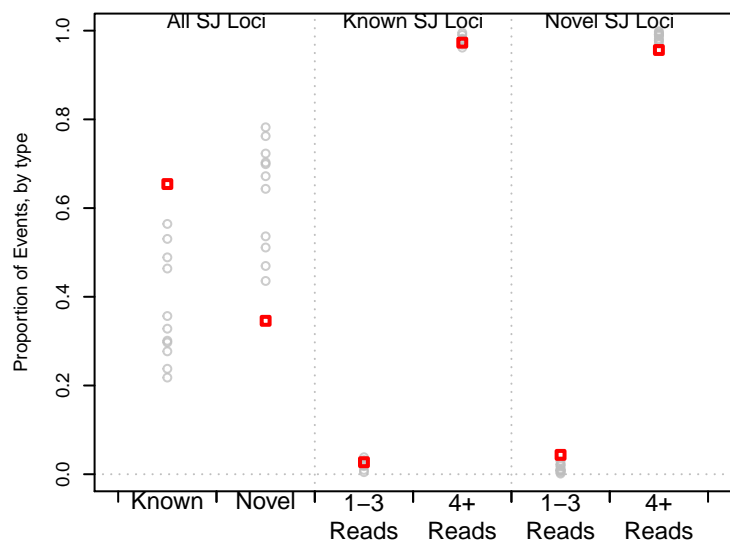
V

Observed Splice Junction Loci, by type
With Sample e1_aligned_sorted Colored by lane



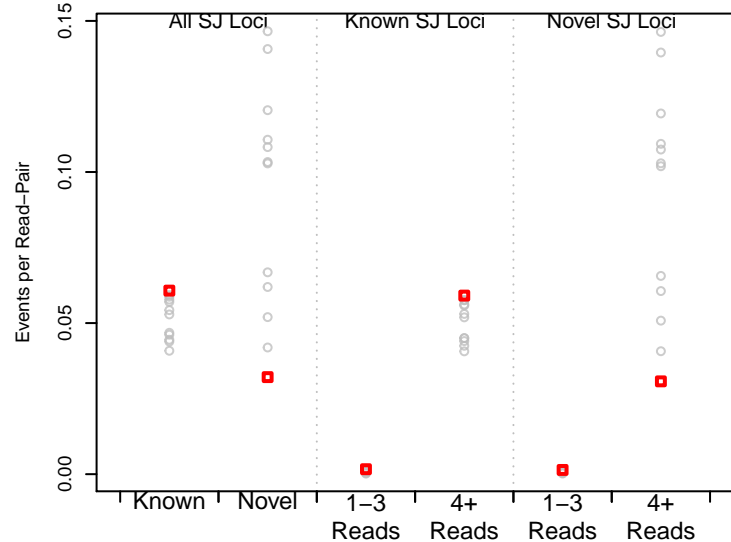
W

Breakdown of Splice Junction Events, by type
With Sample e1_aligned_sorted Colored by lane

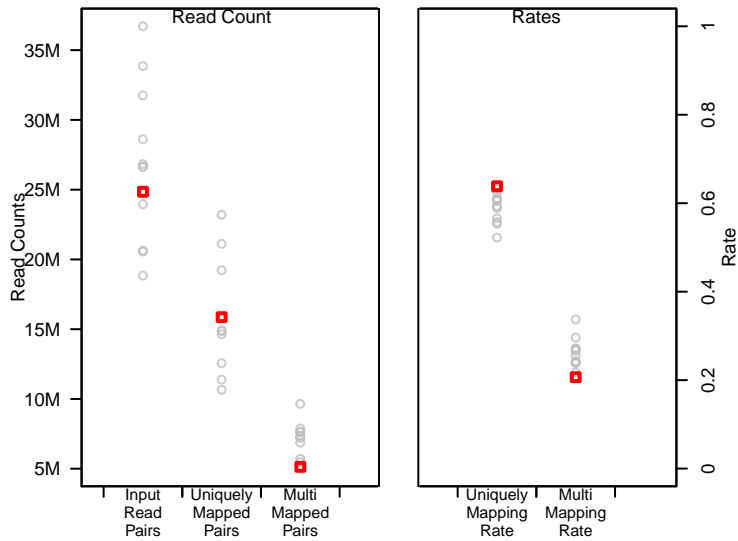


X

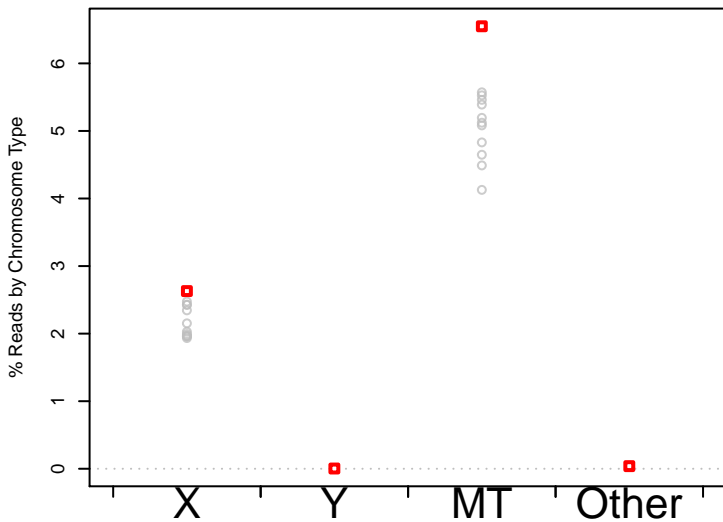
Splice Junction Event Rates per Read-Pair
With Sample e1_aligned_sorted Colored by lane



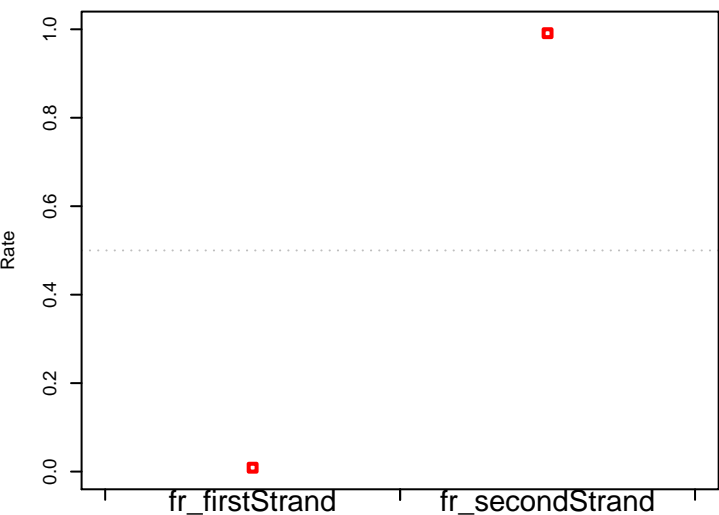
y Mapping Stats
With Sample e1_aligned_sorted Colored by lane



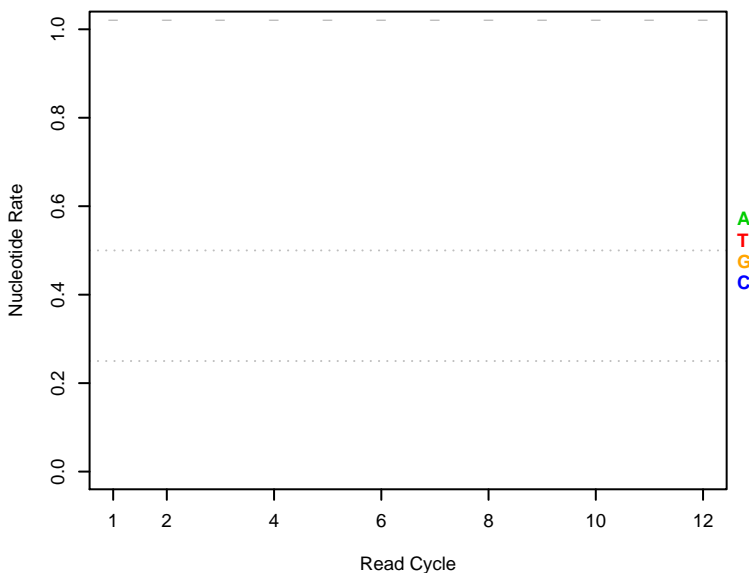
Z Chromosome Distribution (Excluding Autosomes)
With Sample e1_aligned_sorted Colored by lane



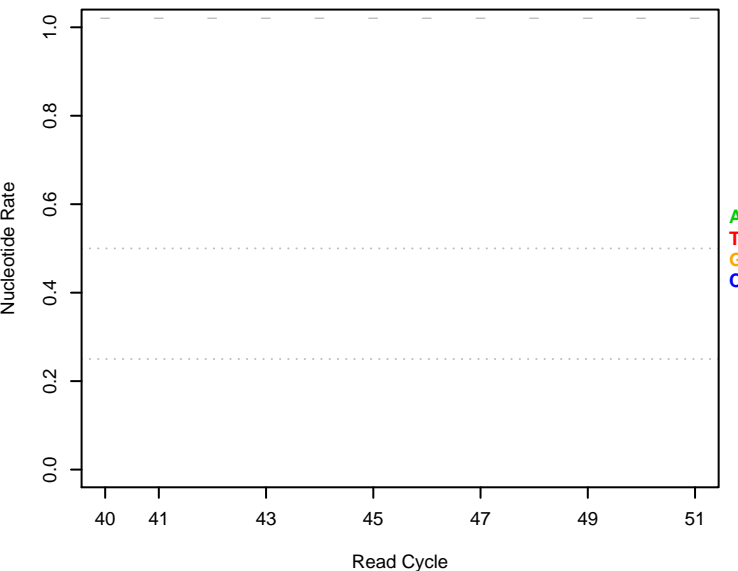
aa Strandedness Test
With Sample e1_aligned_sorted Colored by lane



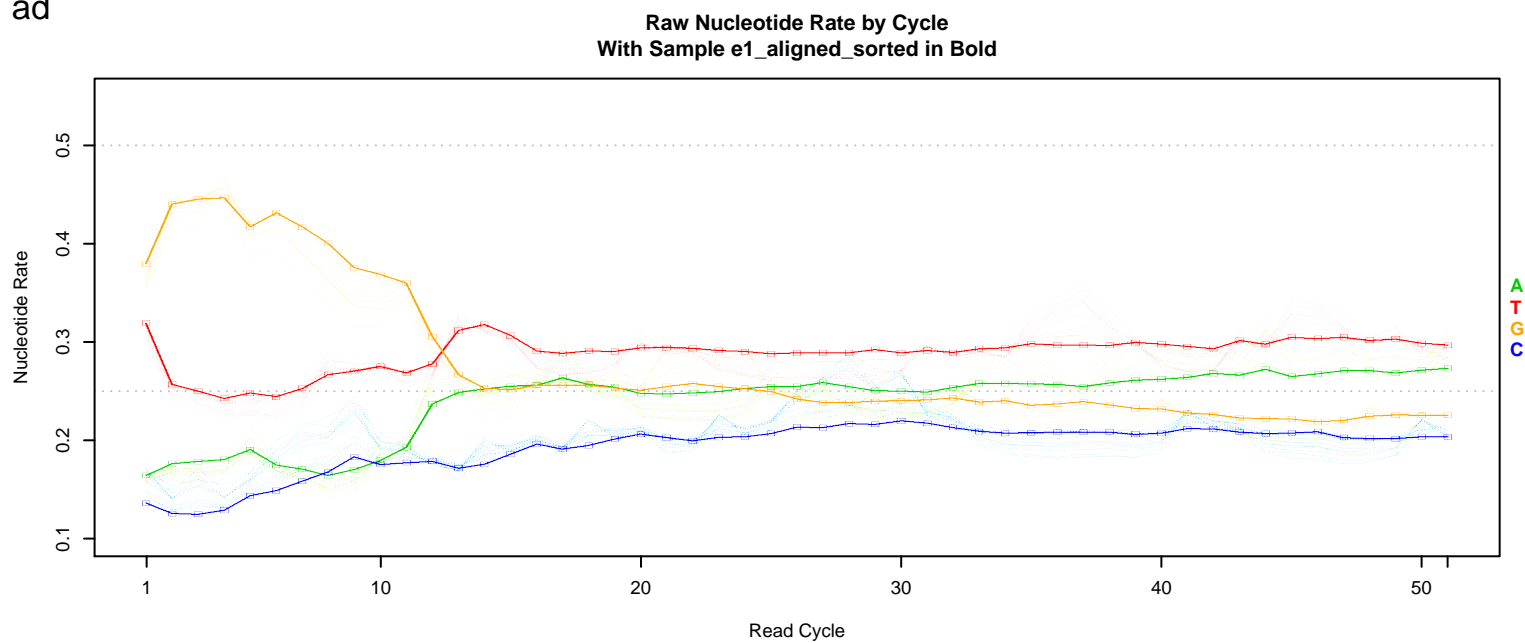
ab Nucleotide Rate by Cycle, Leading Clipped bases (12)
With Sample e1_aligned_sorted in Bold



ac Nucleotide Rate by Cycle, Trailing Clipped bases (12)
With Sample e1_aligned_sorted in Bold



ad



ae

