

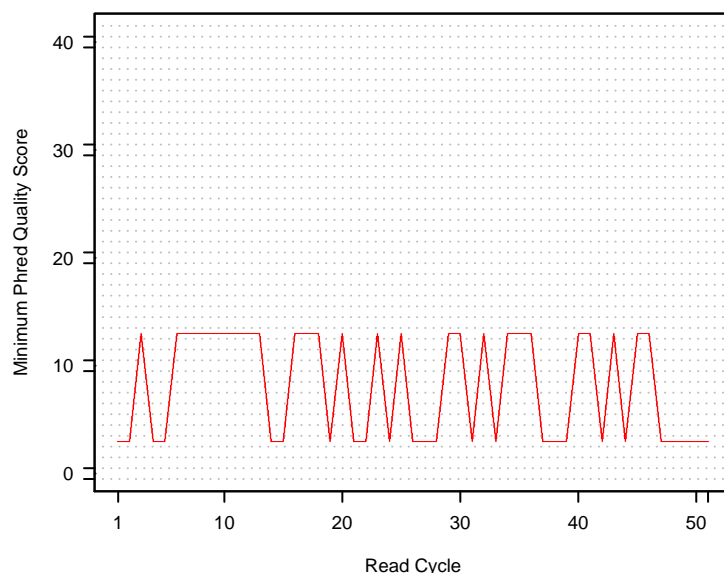
a

Sample Highlight:  
e2\_aligned\_sorted  
Colored by Lane



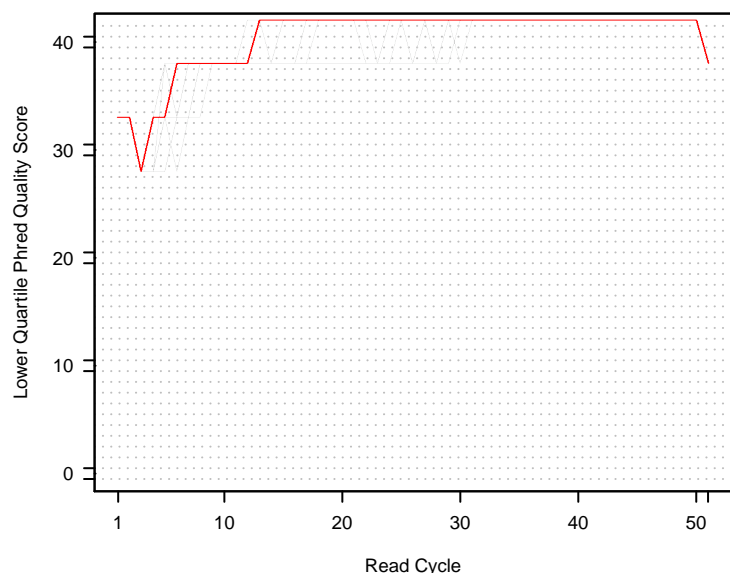
b

Minimum Phred Quality Score  
With Sample e2\_aligned\_sorted Colored by lane



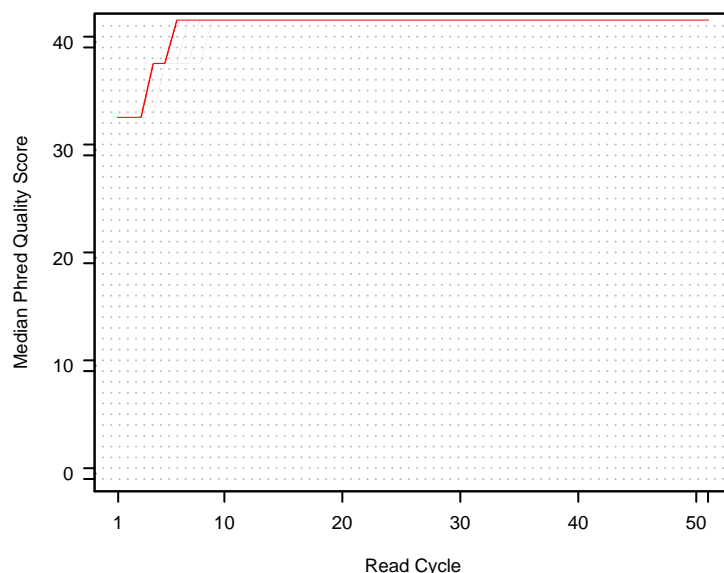
c

Lower Quartile Phred Quality Score  
With Sample e2\_aligned\_sorted Colored by lane



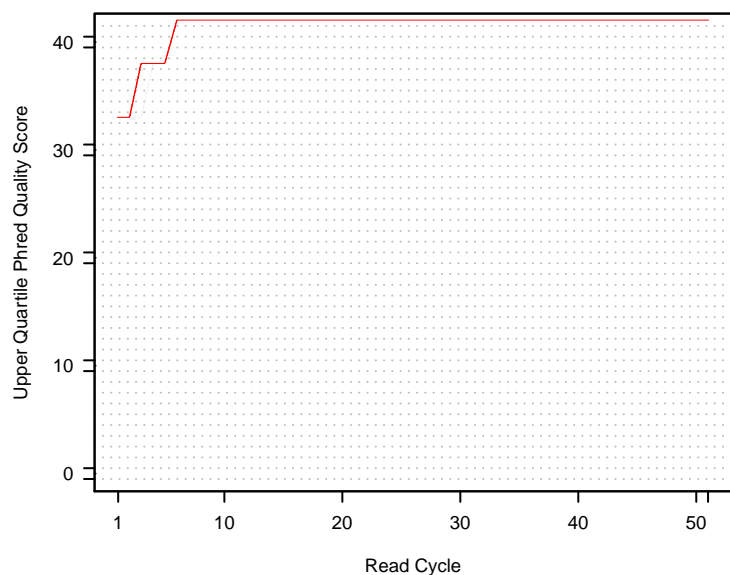
d

Median Phred Quality Score  
With Sample e2\_aligned\_sorted Colored by lane



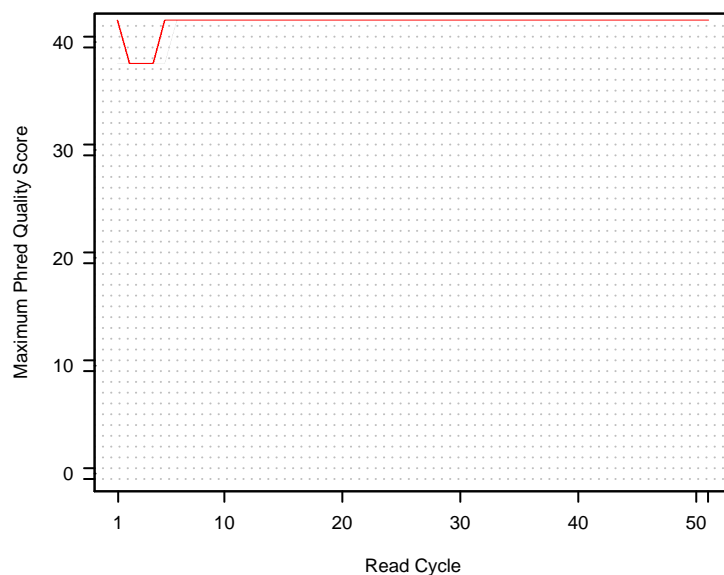
e

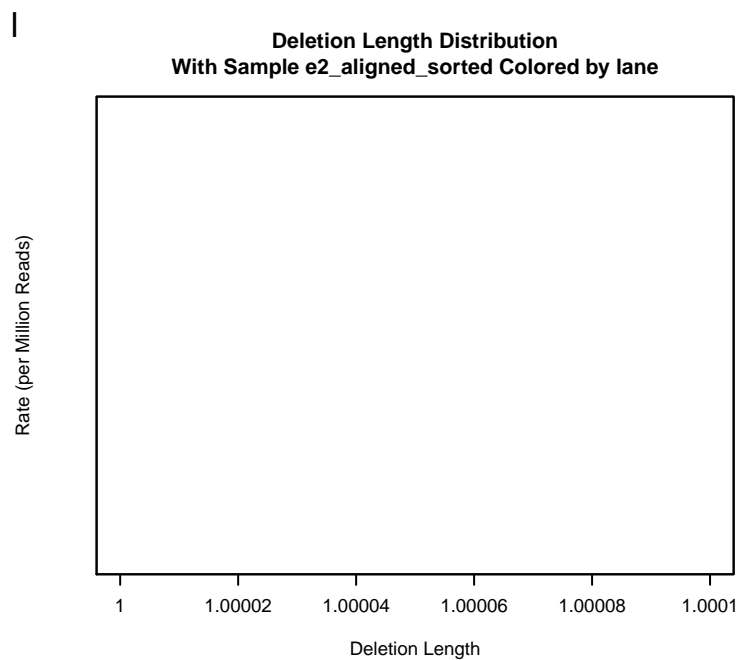
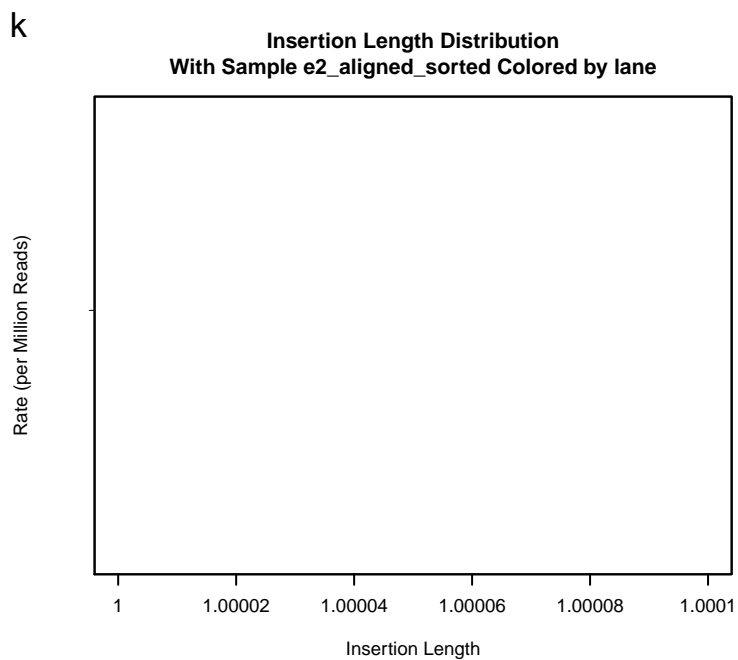
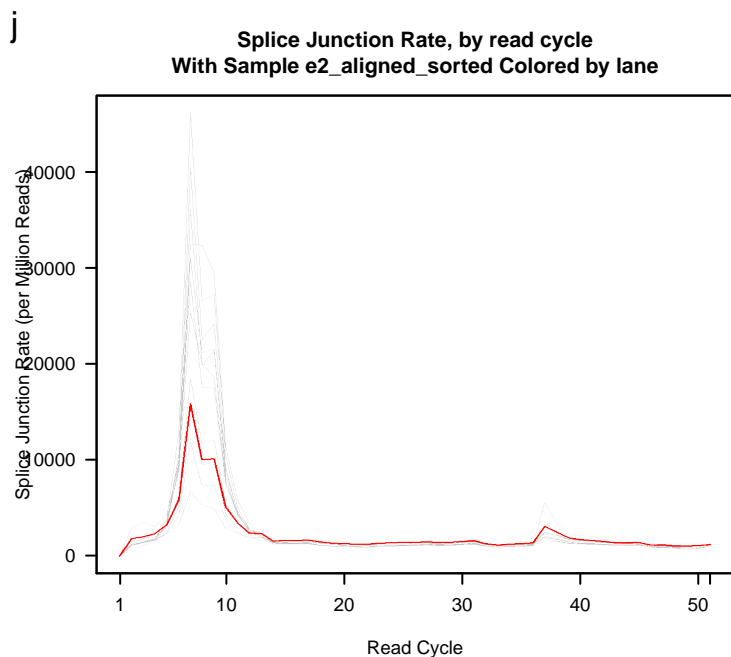
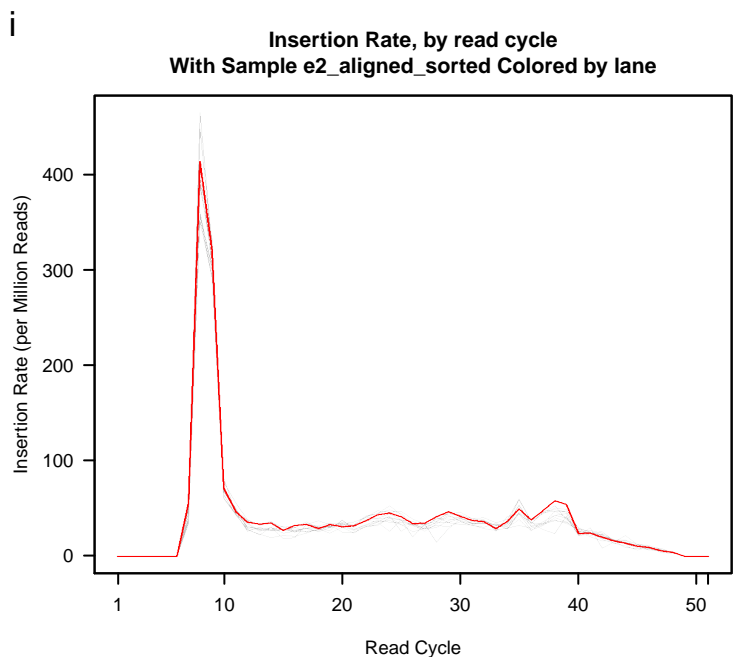
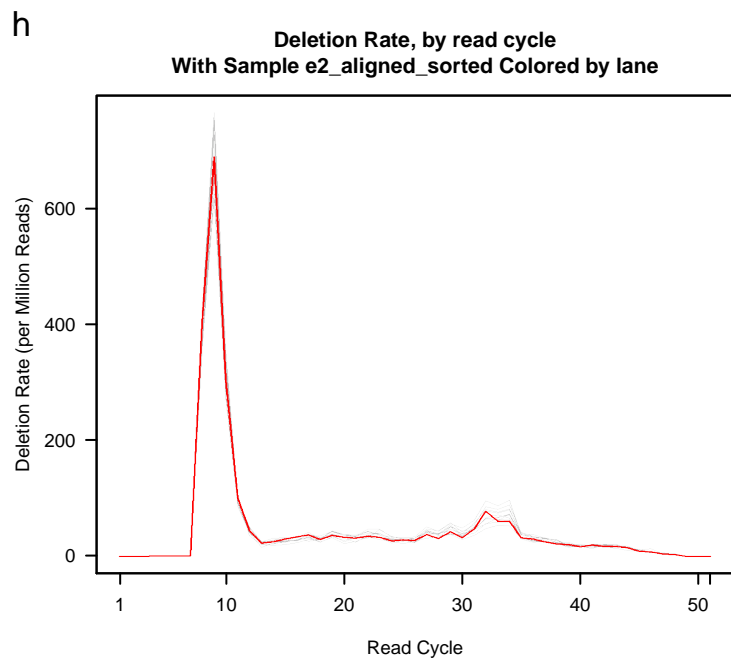
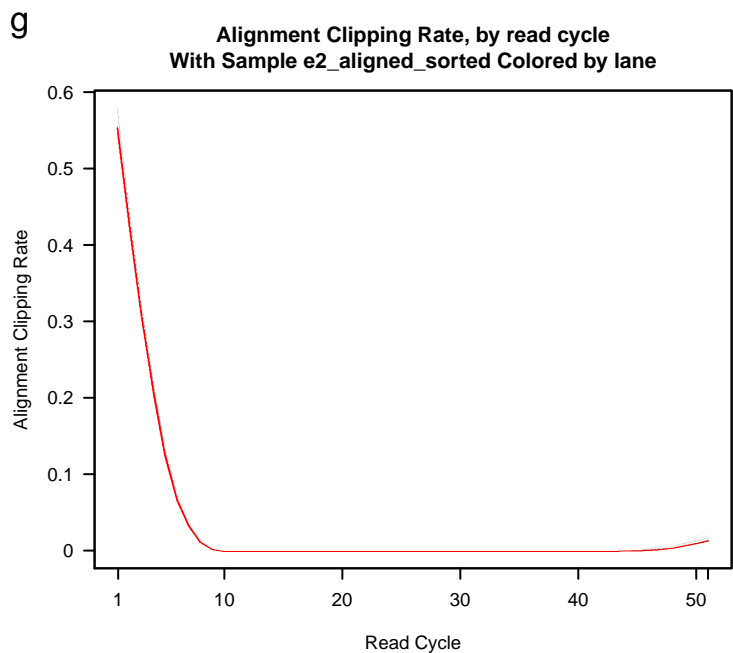
Upper Quartile Phred Quality Score  
With Sample e2\_aligned\_sorted Colored by lane

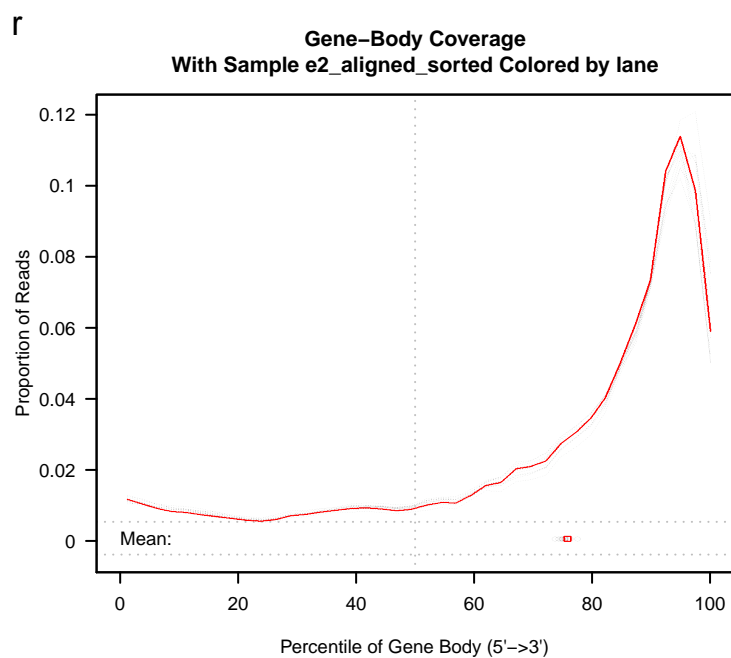
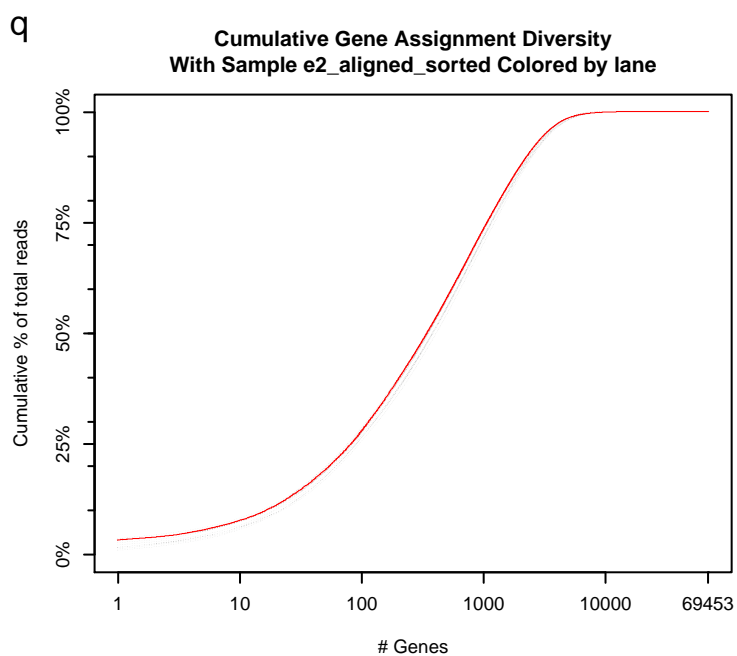
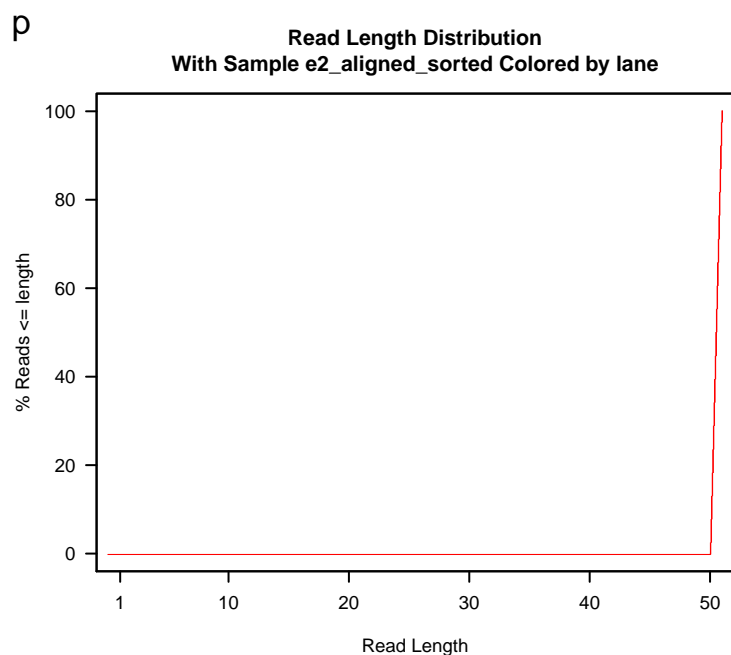
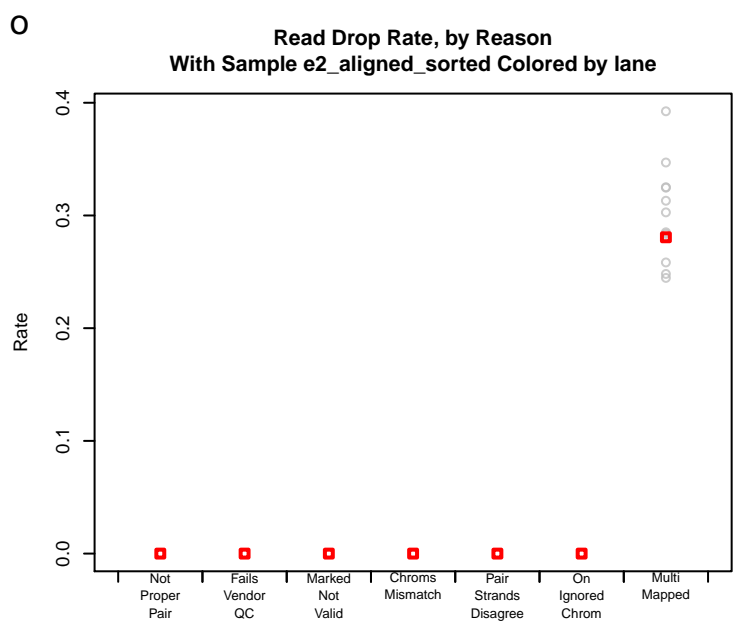
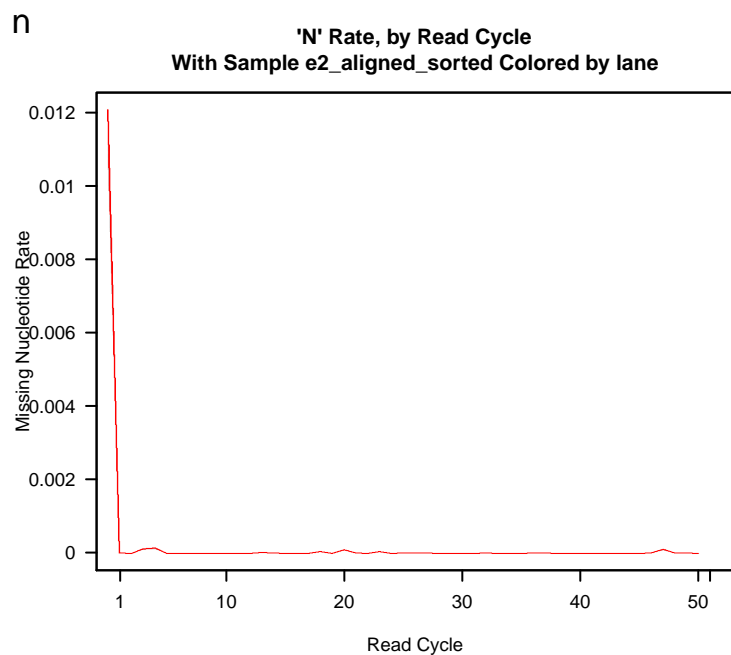
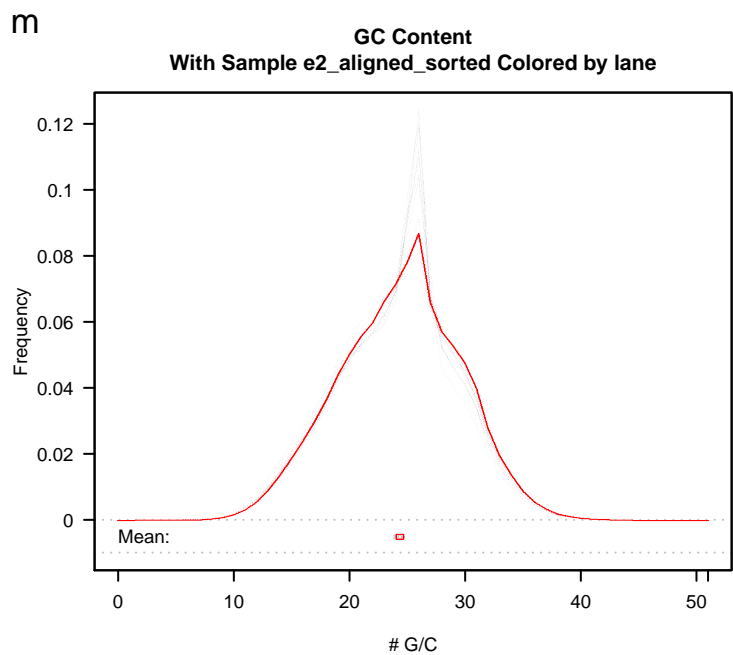


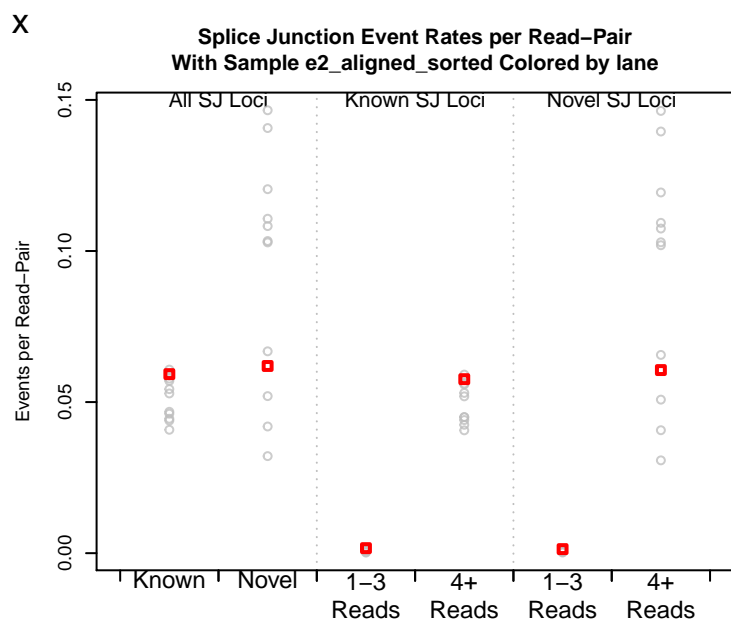
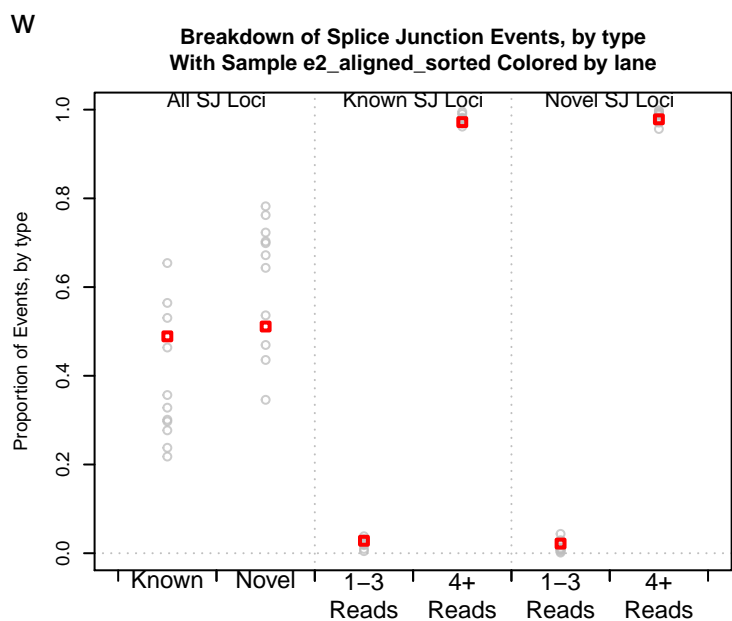
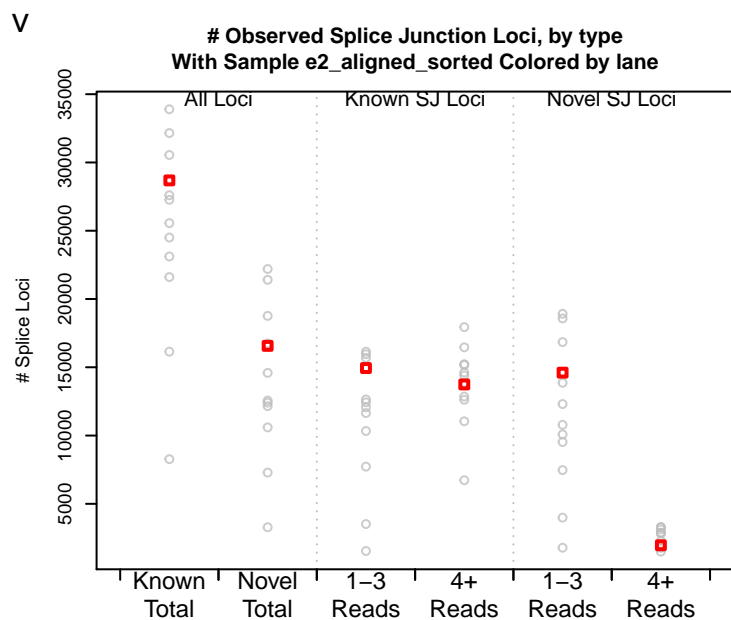
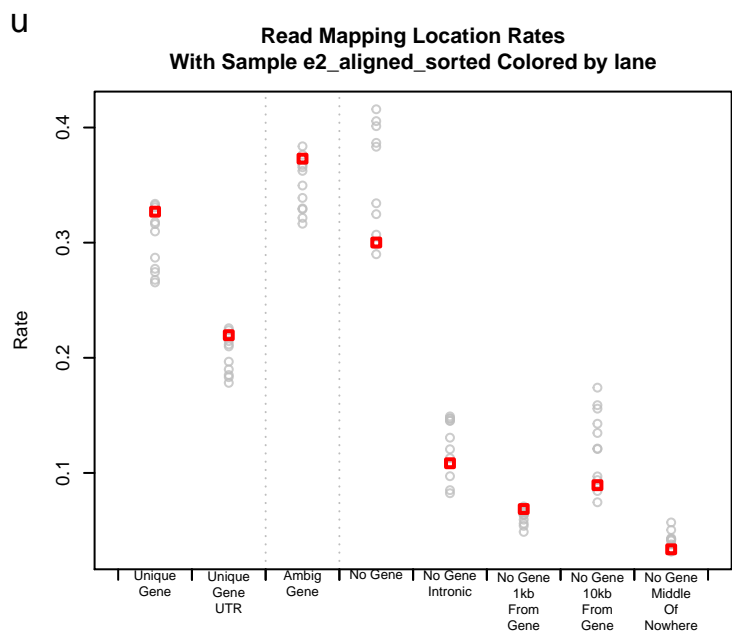
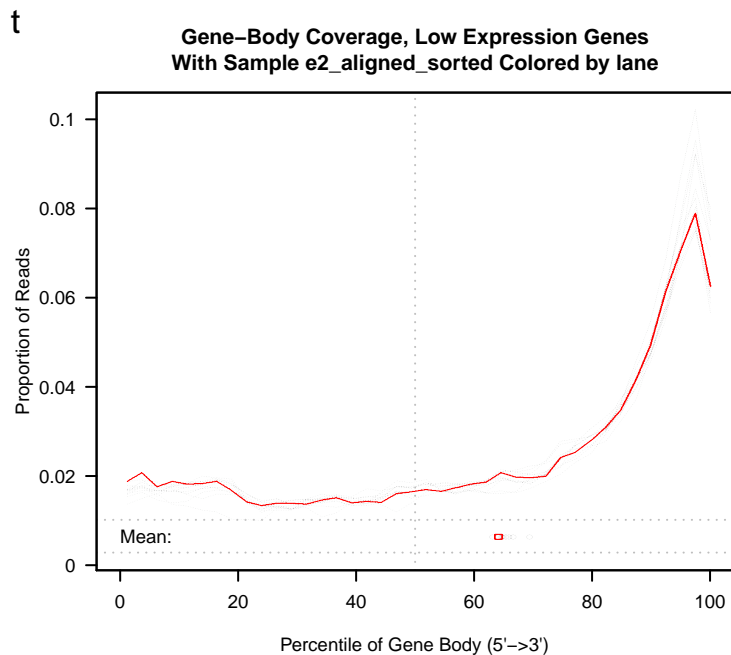
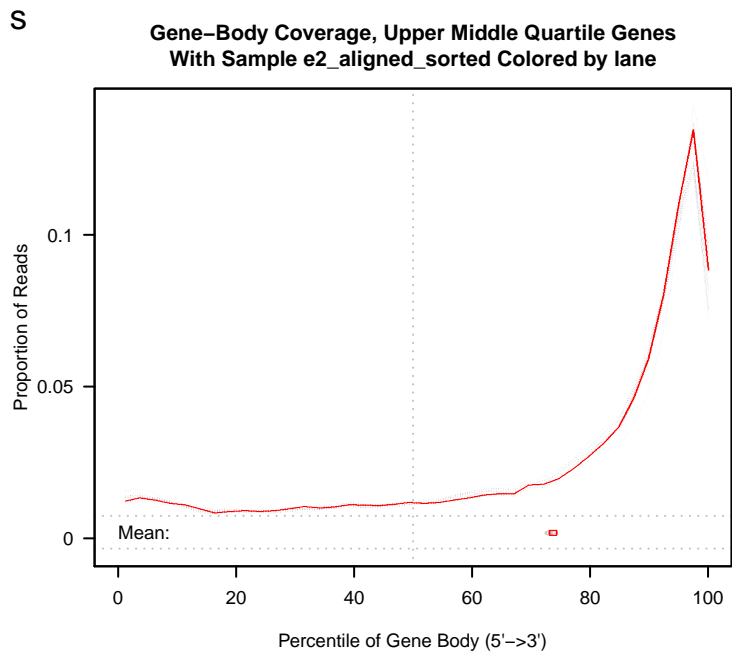
f

Maximum Phred Quality Score  
With Sample e2\_aligned\_sorted Colored by lane

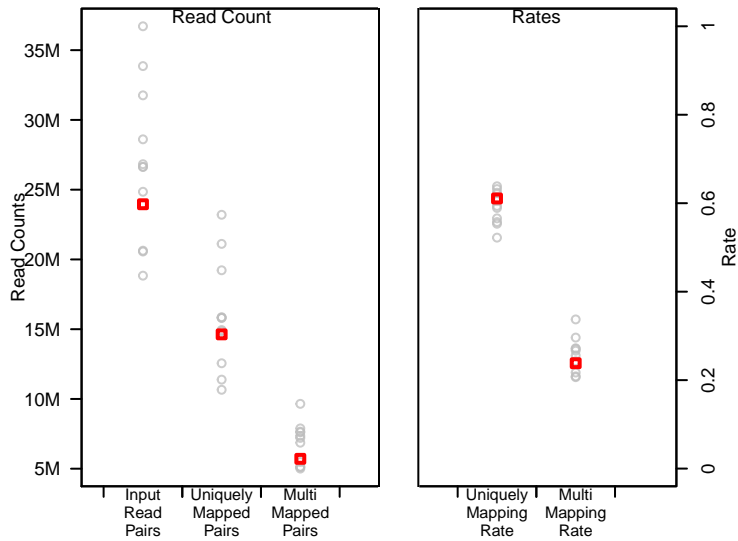




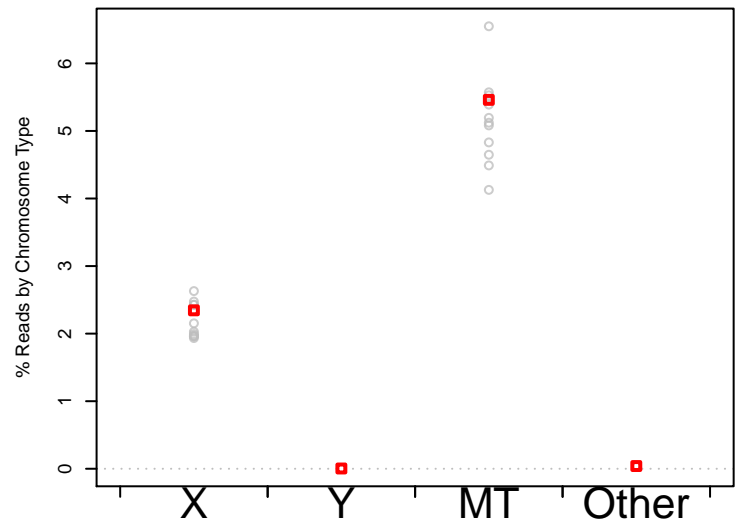




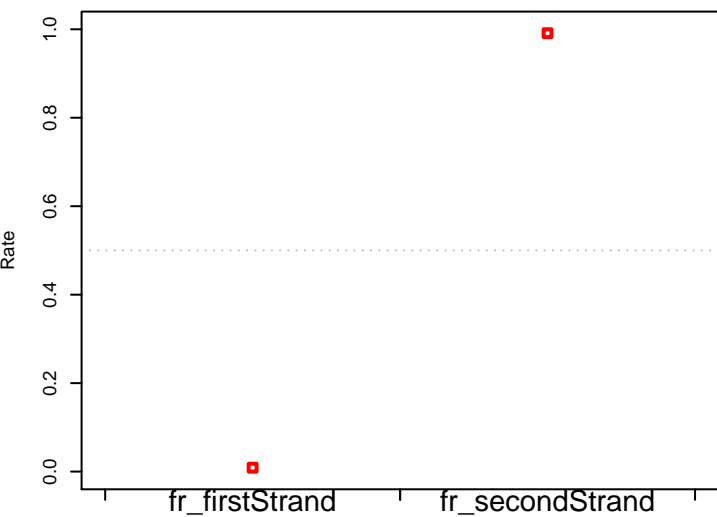
y Mapping Stats  
With Sample e2\_aligned\_sorted Colored by lane



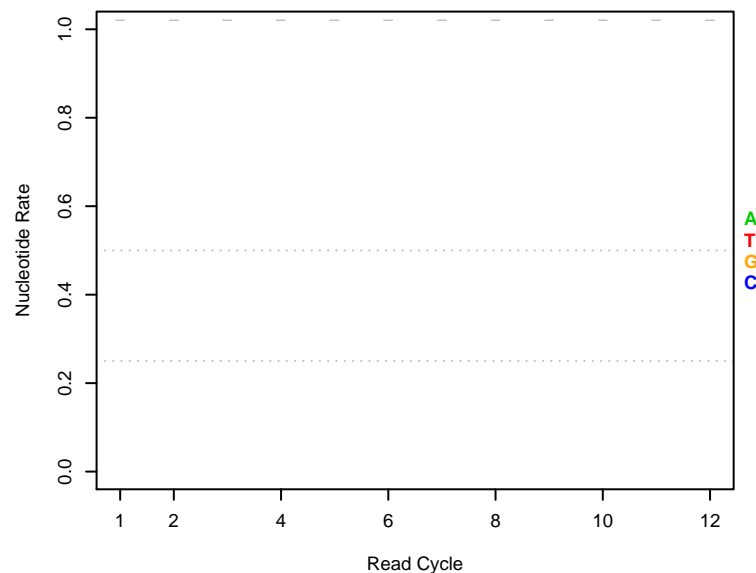
Z Chromosome Distribution (Excluding Autosomes)  
With Sample e2\_aligned\_sorted Colored by lane



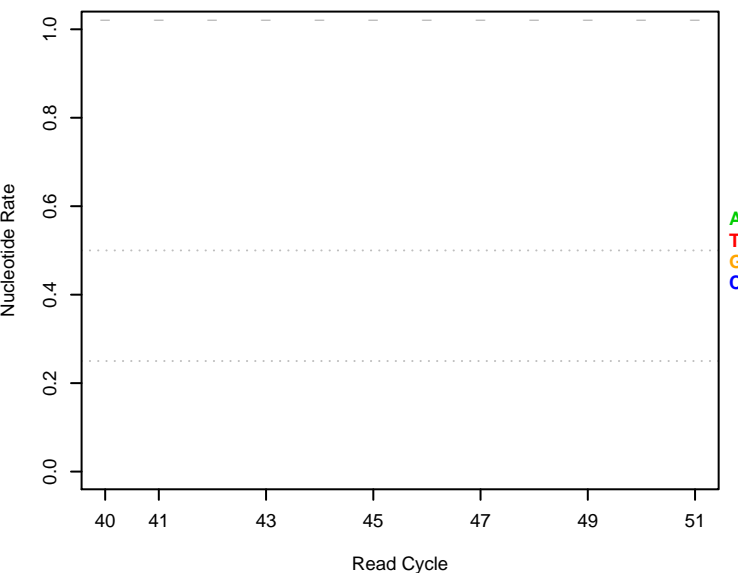
aa Strandedness Test  
With Sample e2\_aligned\_sorted Colored by lane



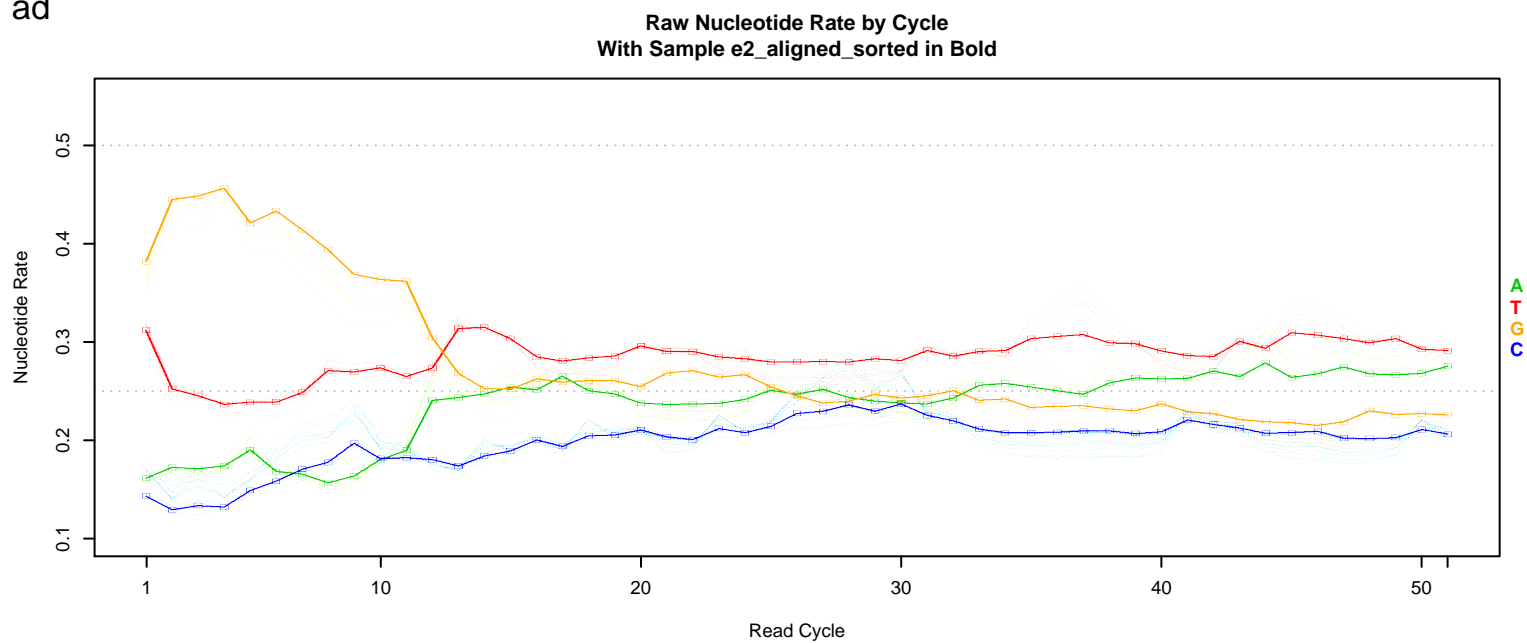
ab Nucleotide Rate by Cycle, Leading Clipped bases (12)  
With Sample e2\_aligned\_sorted in Bold



ac Nucleotide Rate by Cycle, Trailing Clipped bases (12)  
With Sample e2\_aligned\_sorted in Bold



ad



ae

