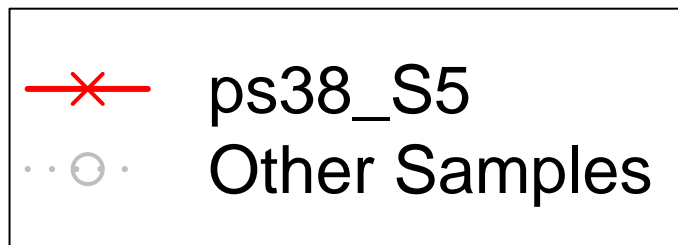


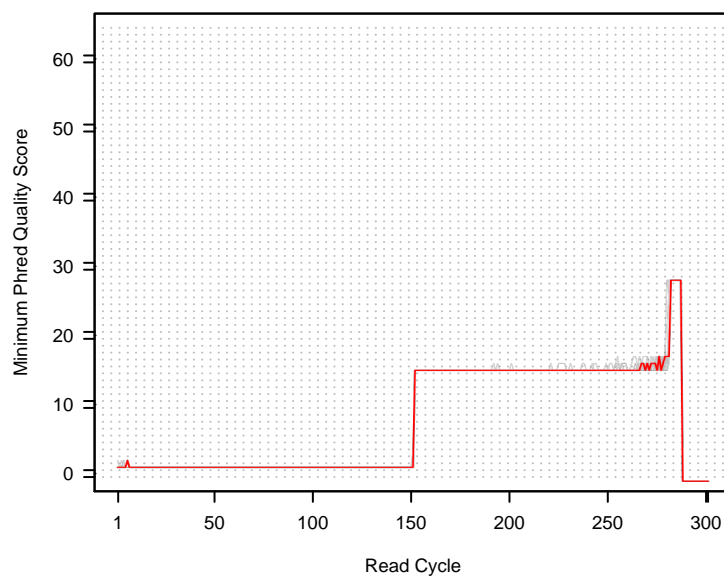
a

Sample Highlight: ps38_S5



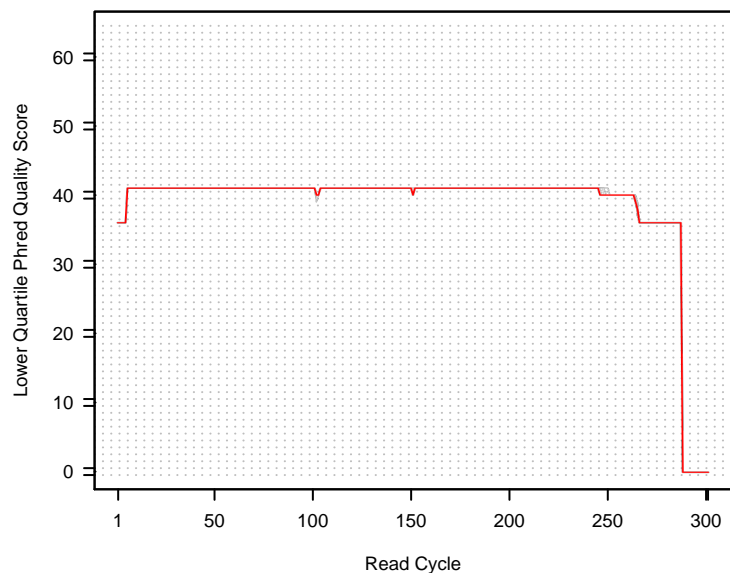
b

Minimum Phred Quality Score
With Sample ps38_S5 in red



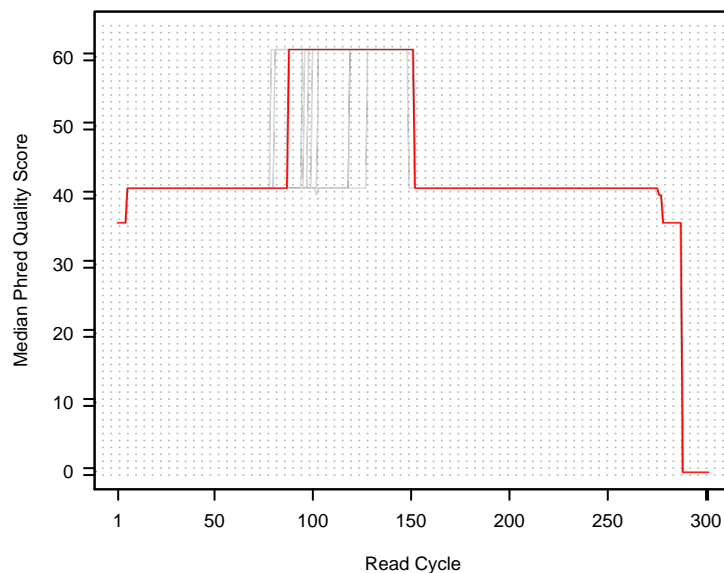
c

Lower Quartile Phred Quality Score
With Sample ps38_S5 in red



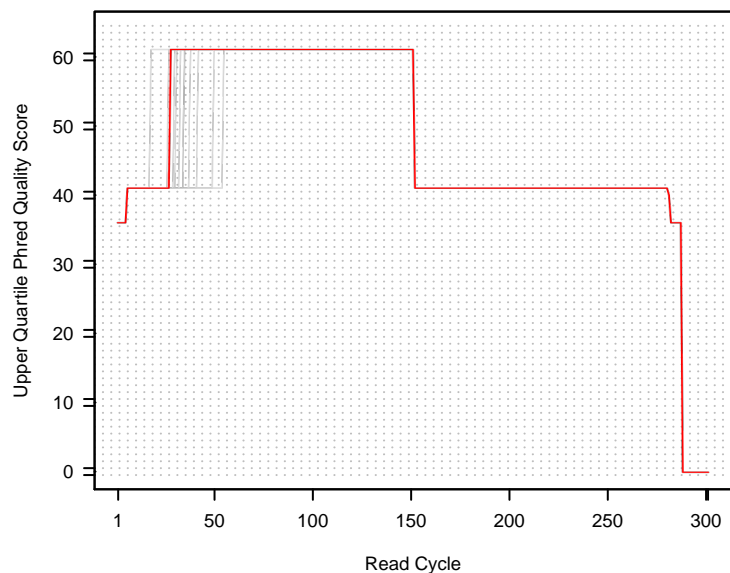
d

Median Phred Quality Score
With Sample ps38_S5 in red



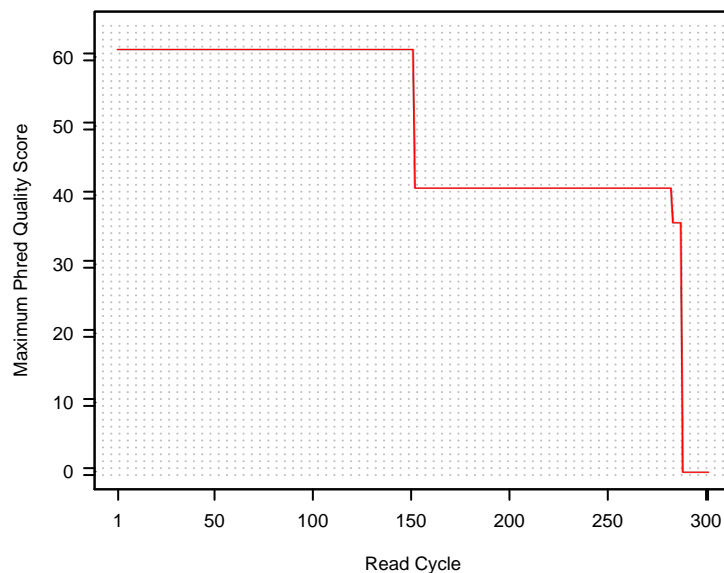
e

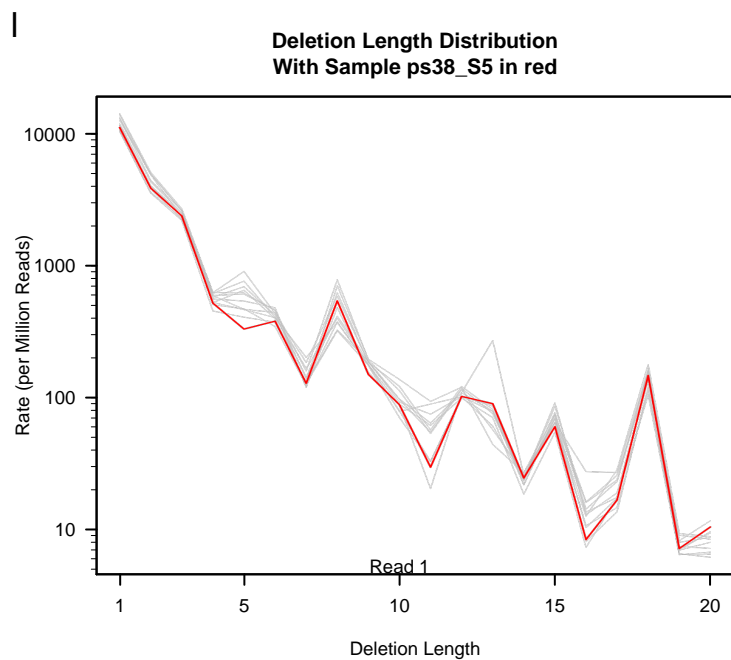
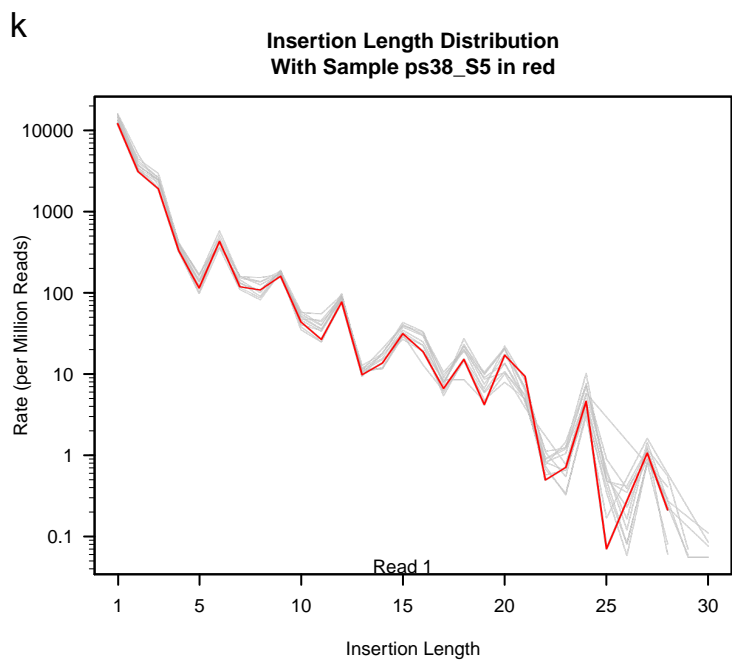
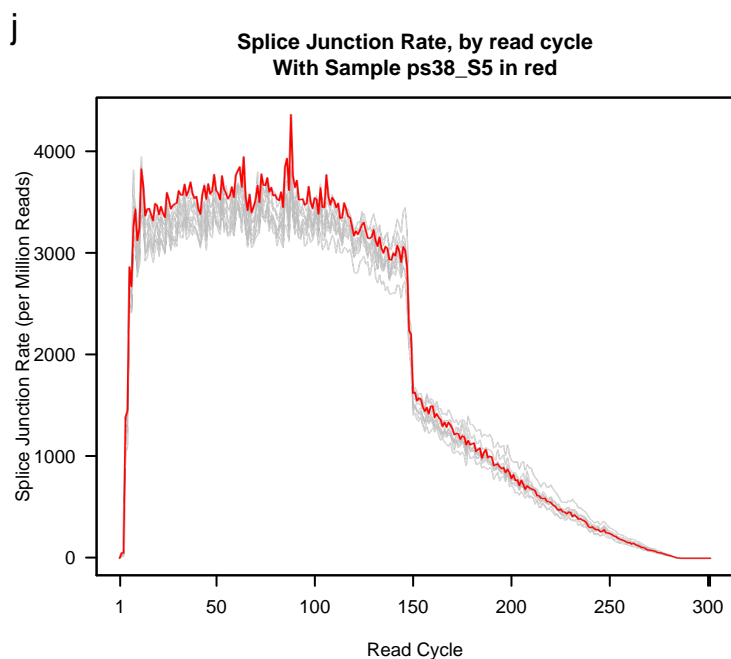
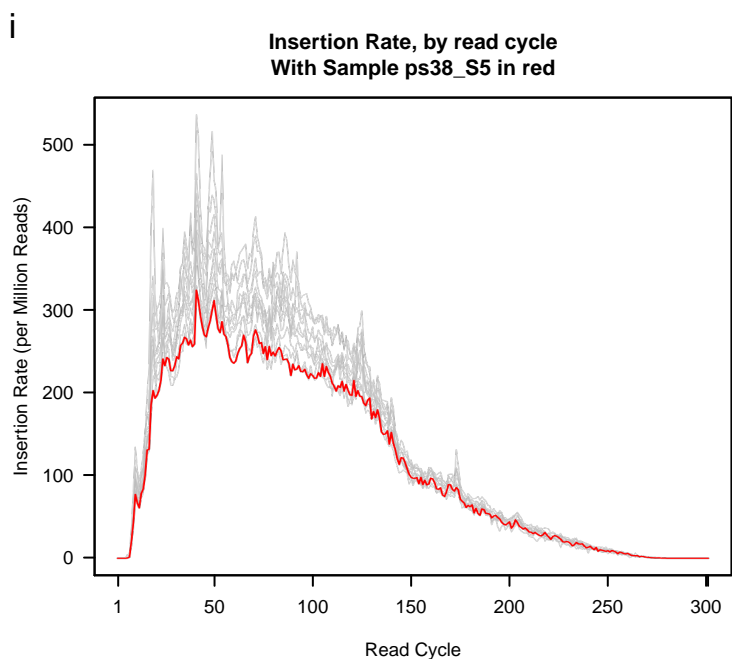
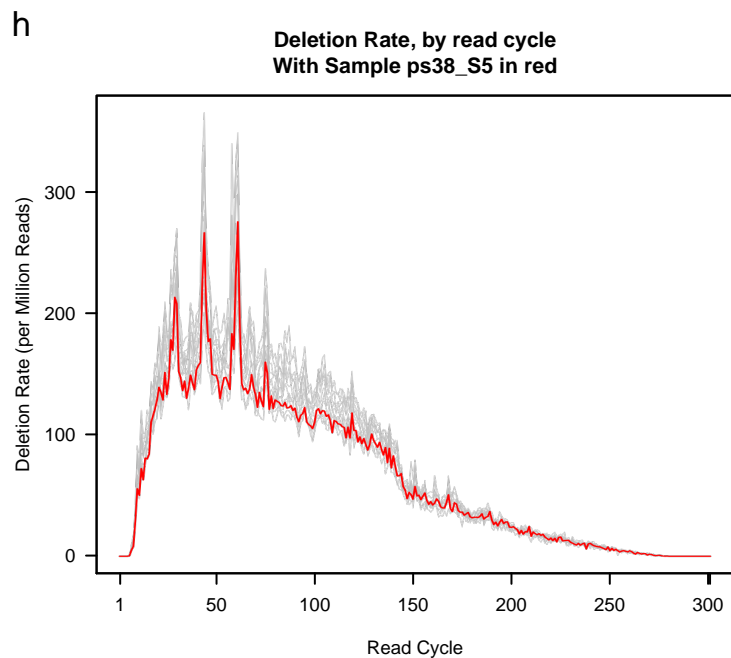
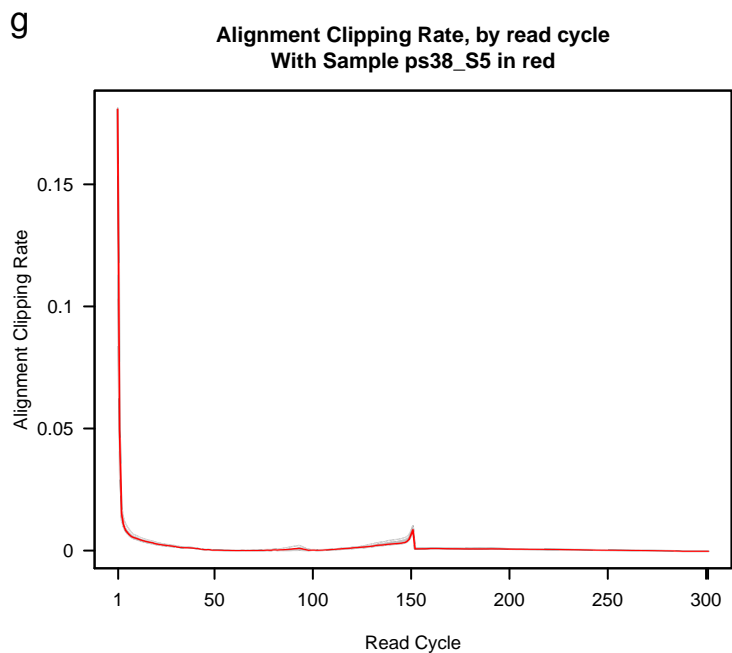
Upper Quartile Phred Quality Score
With Sample ps38_S5 in red

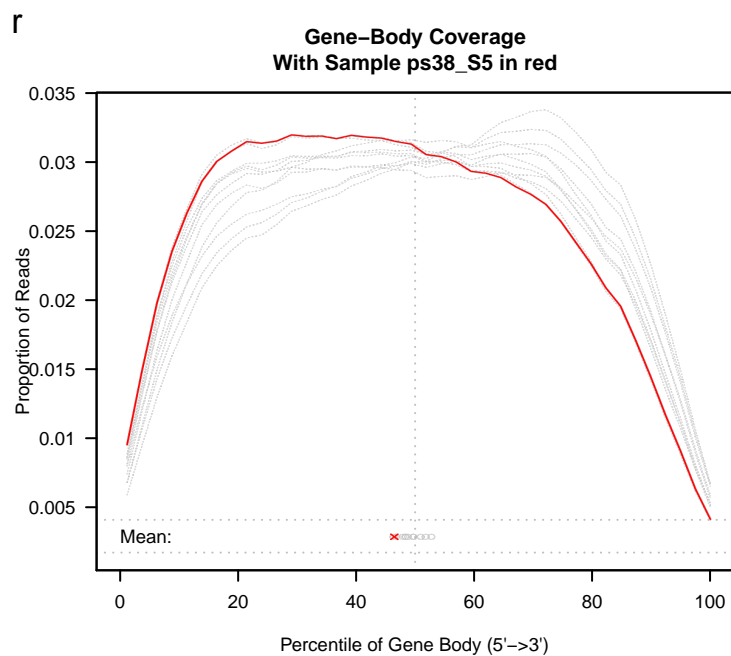
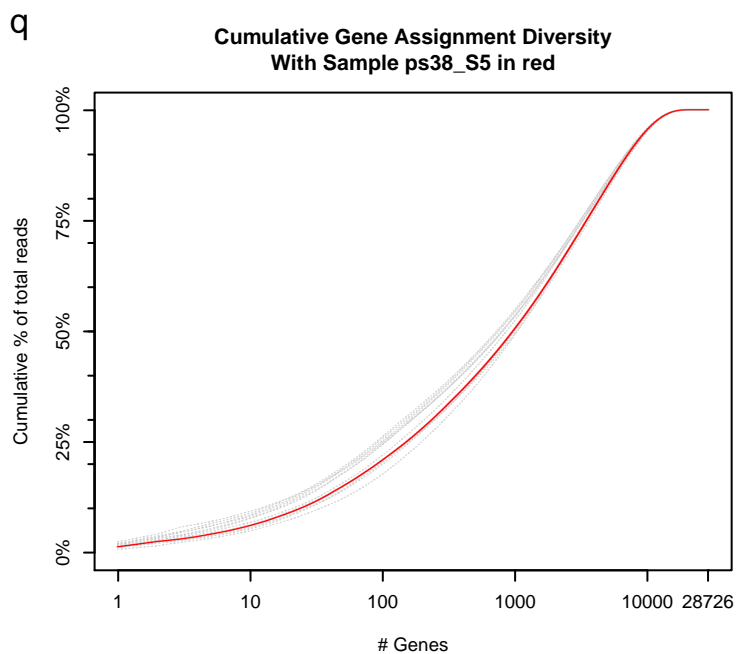
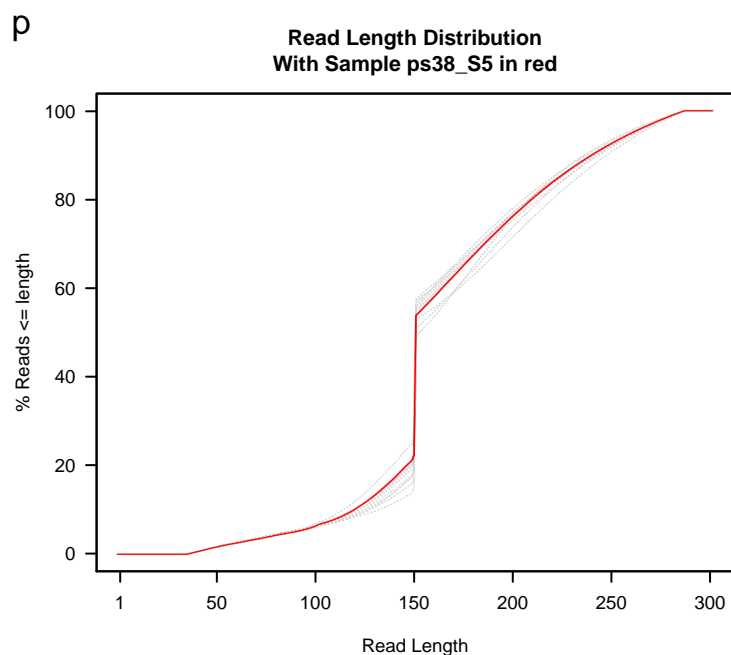
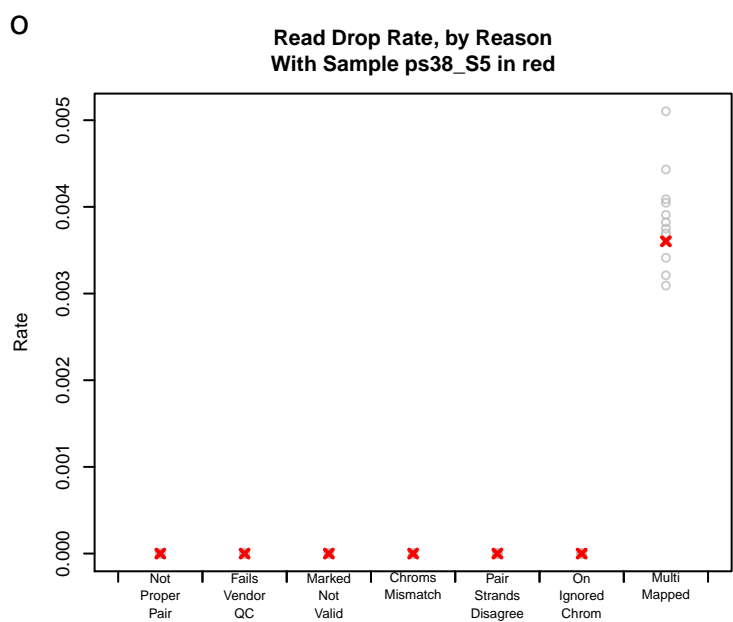
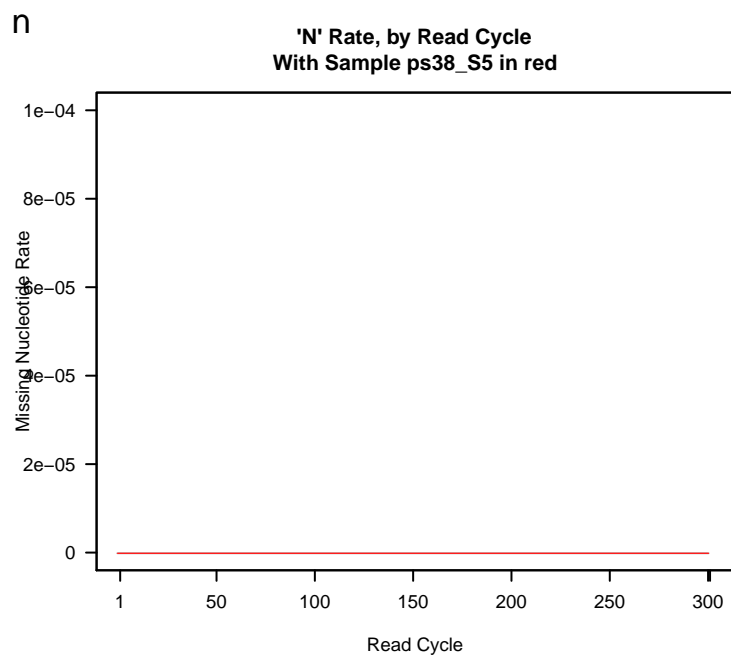
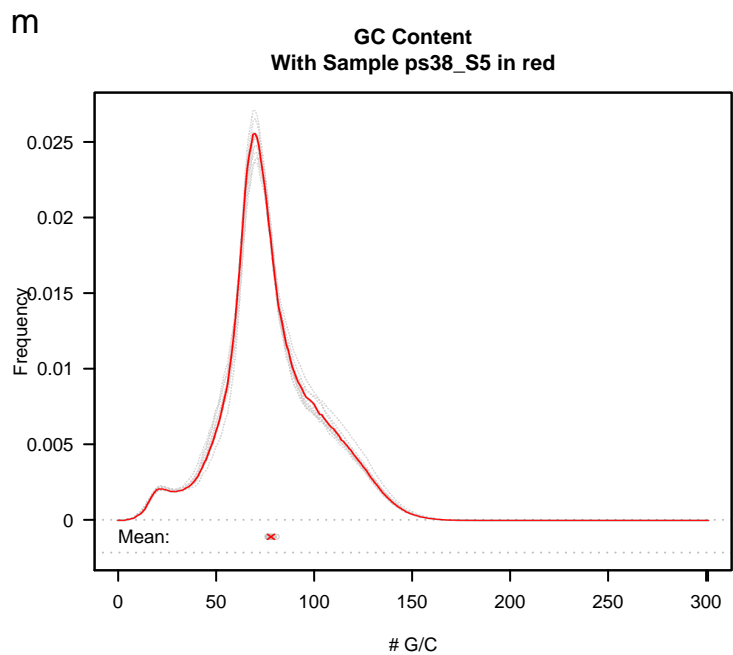


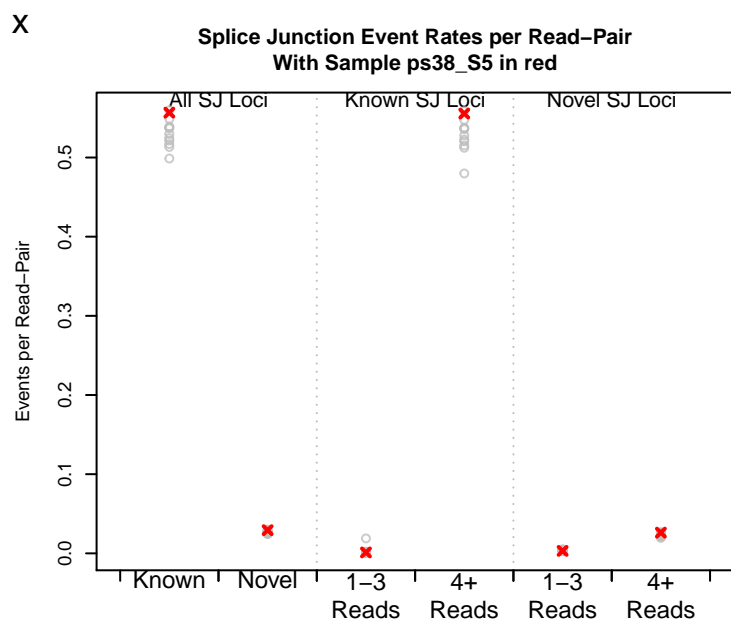
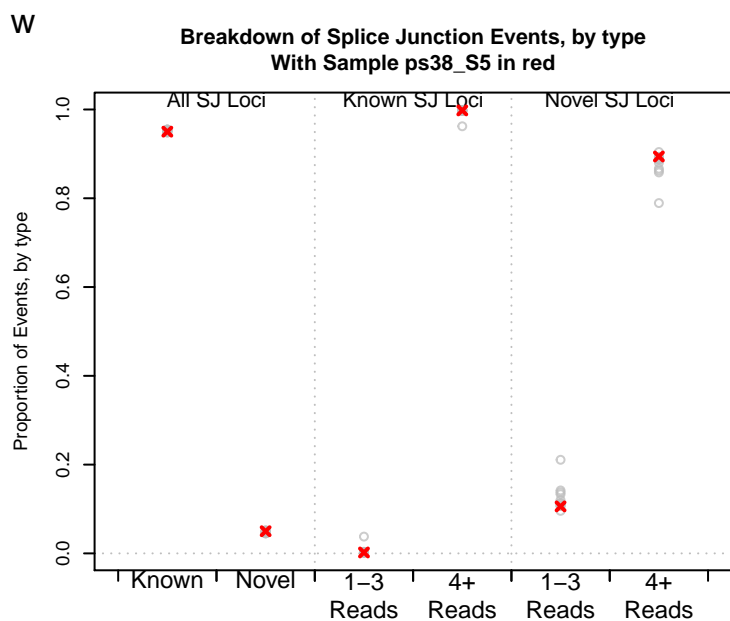
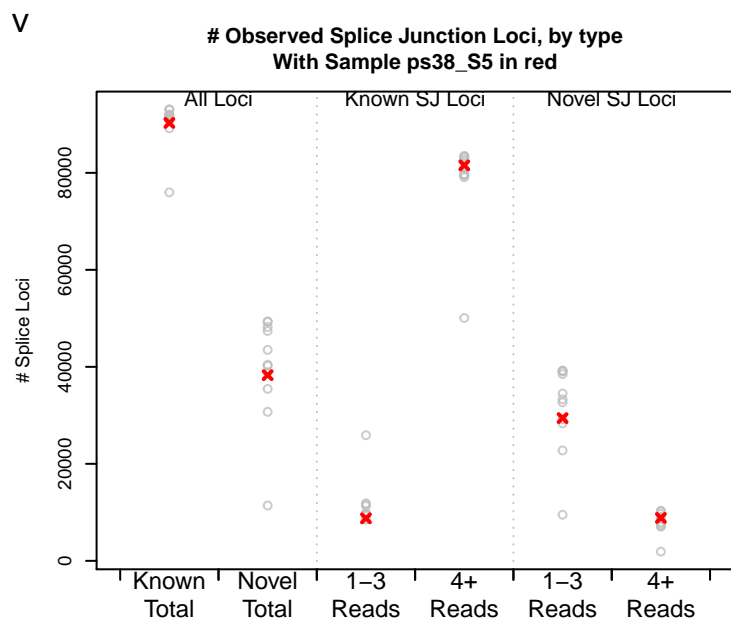
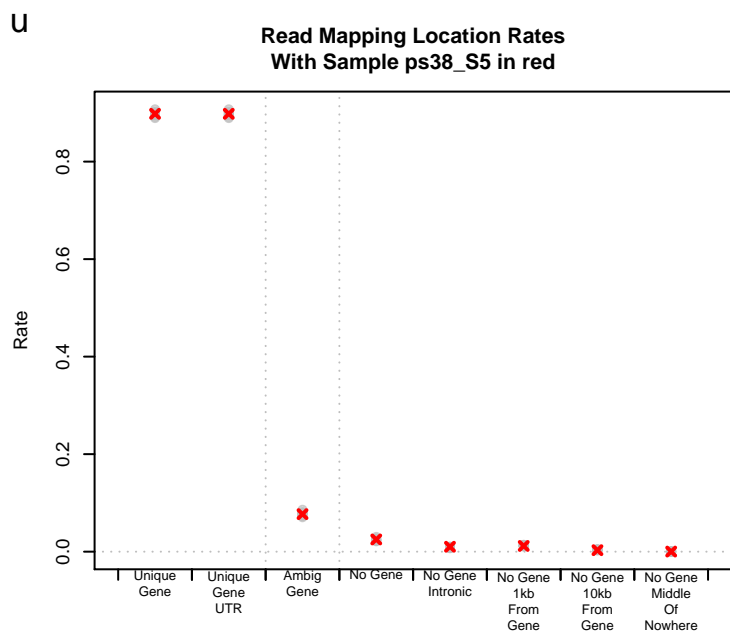
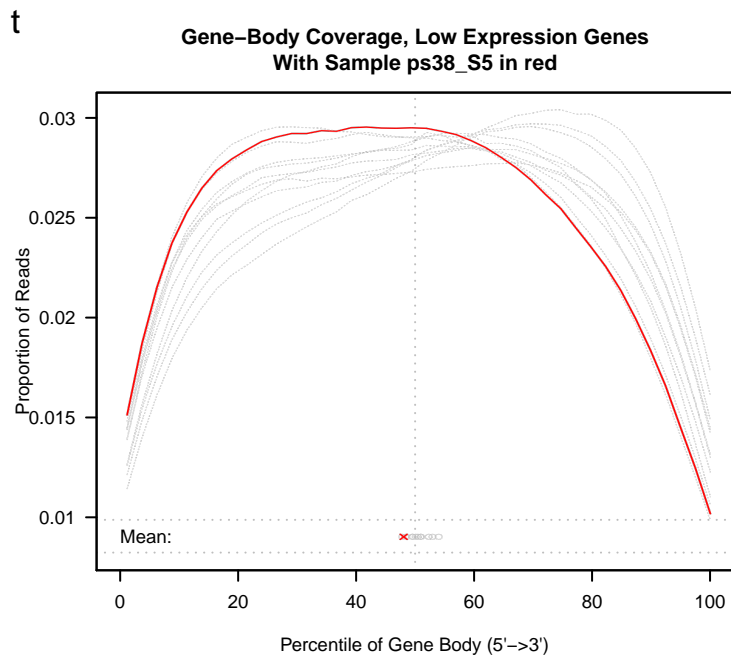
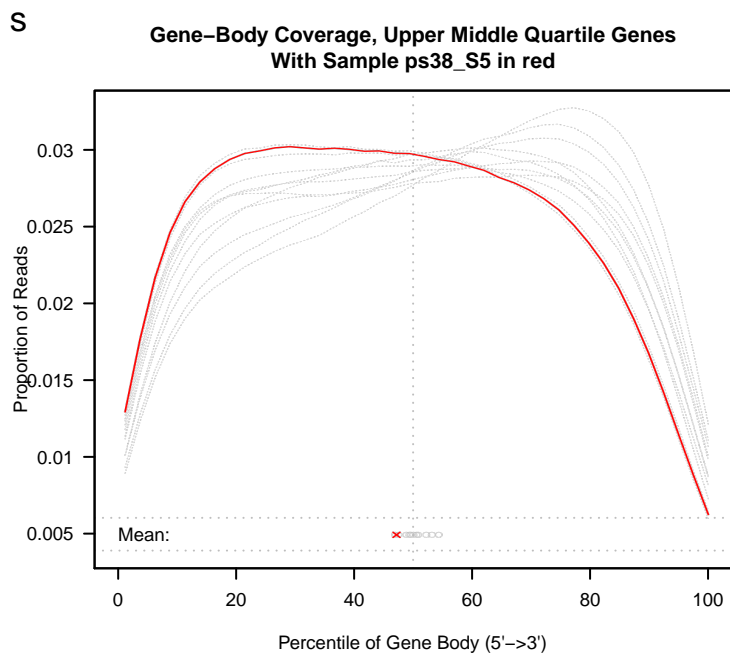
f

Maximum Phred Quality Score
With Sample ps38_S5 in red



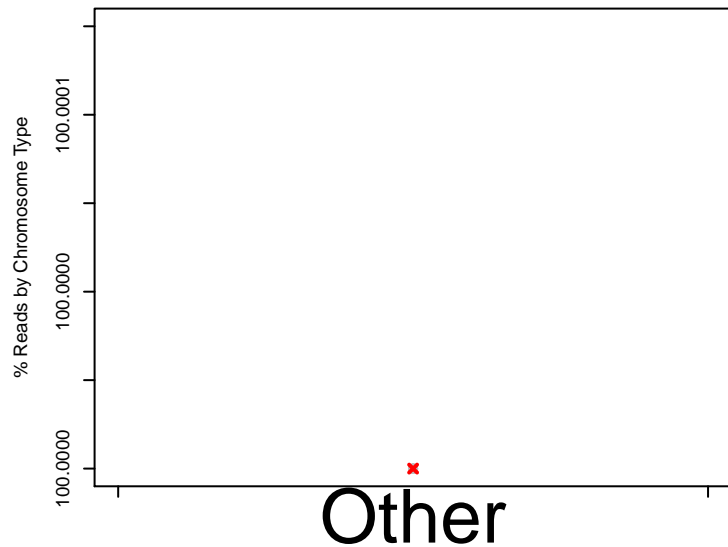






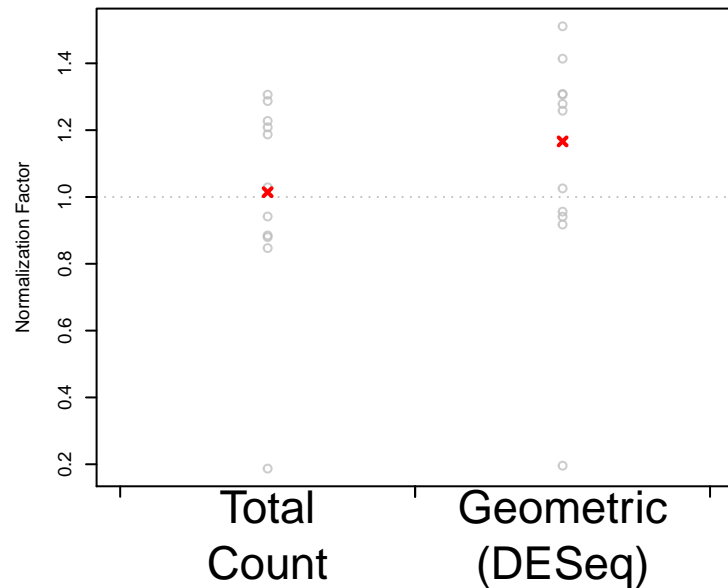
y

Chromosome Distribution (Excluding Autosomes)
With Sample ps38_S5 in red



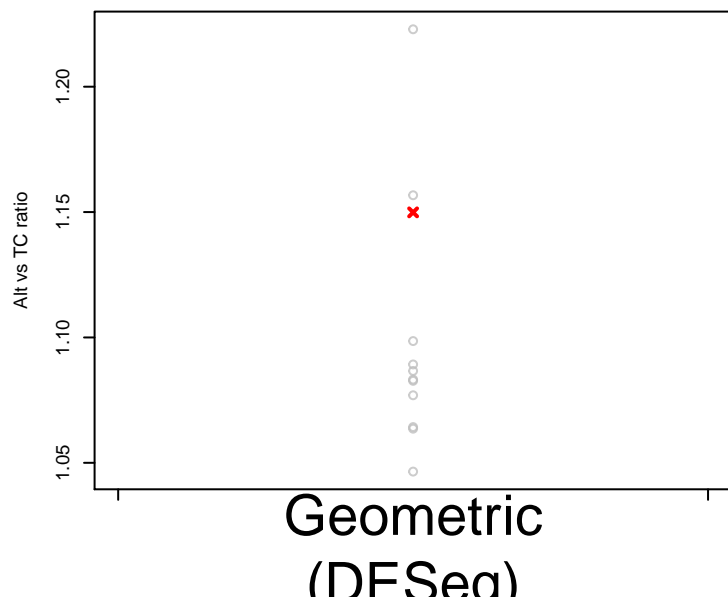
Z

Normalization Factors
With Sample ps38_S5 in red



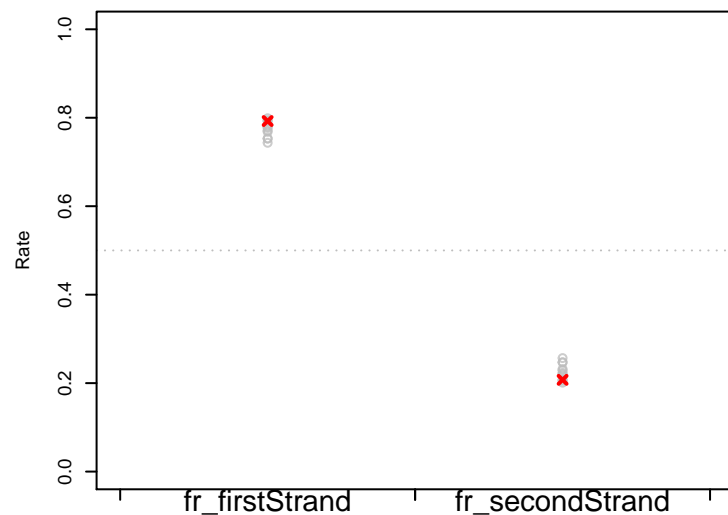
aa

Normalization Factors vs Total-Count Normalization
With Sample ps38_S5 in red



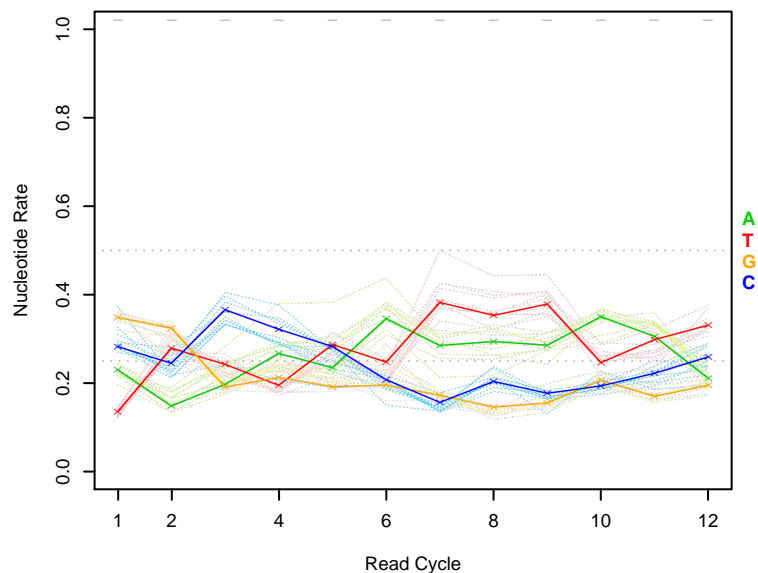
ab

Strandedness Test
With Sample ps38_S5 in red



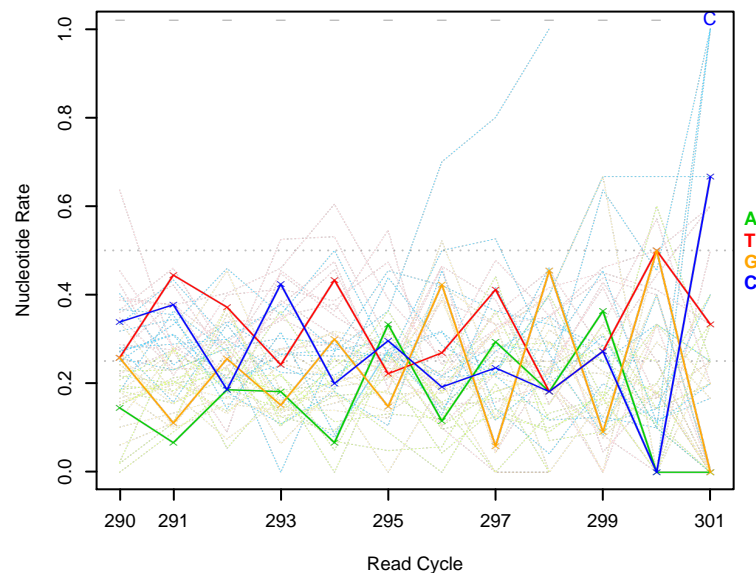
ac

Nucleotide Rate by Cycle, Leading Clipped bases (12)
With Sample ps38_S5 in red

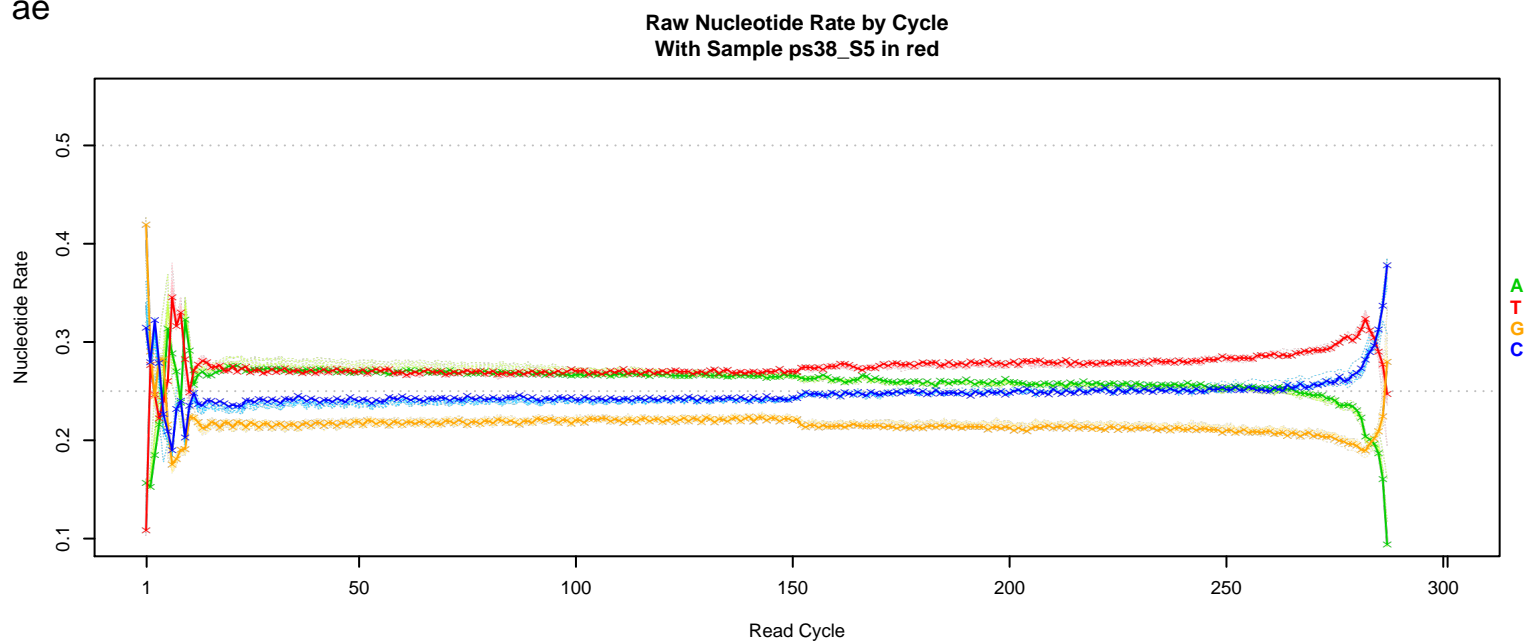


ad

Nucleotide Rate by Cycle, Trailing Clipped bases (12)
With Sample ps38_S5 in red



ae



af

