

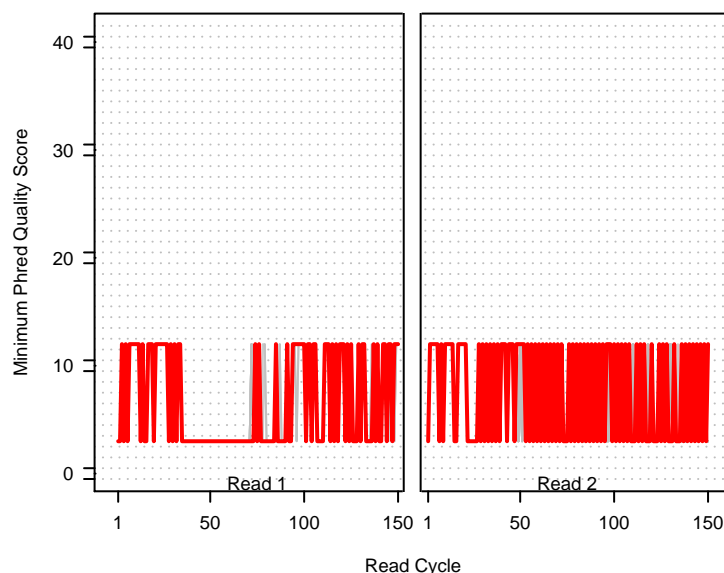
a

Sample Highlight:
srpk3_hom_ttnb_wt_5
Colored by Lane



b

Minimum Phred Quality Score
With Sample srpk3_hom_ttnb_wt_5 Colored by lane



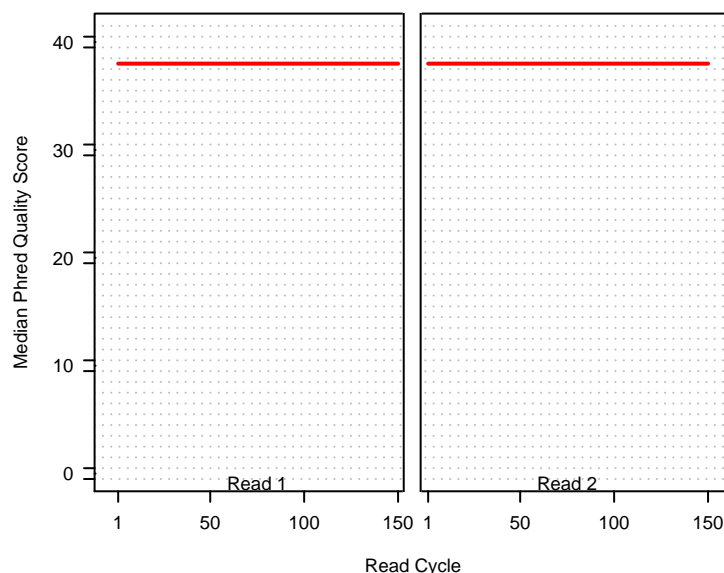
c

Lower Quartile Phred Quality Score
With Sample srpk3_hom_ttnb_wt_5 Colored by lane



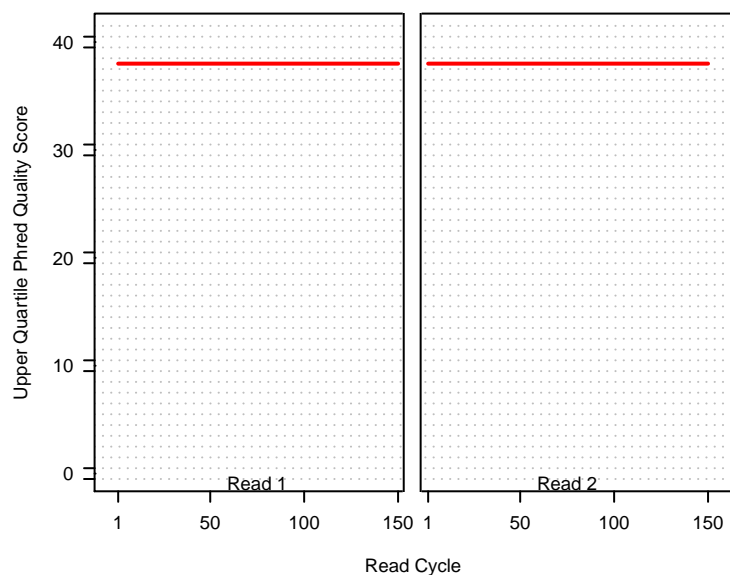
d

Median Phred Quality Score
With Sample srpk3_hom_ttnb_wt_5 Colored by lane



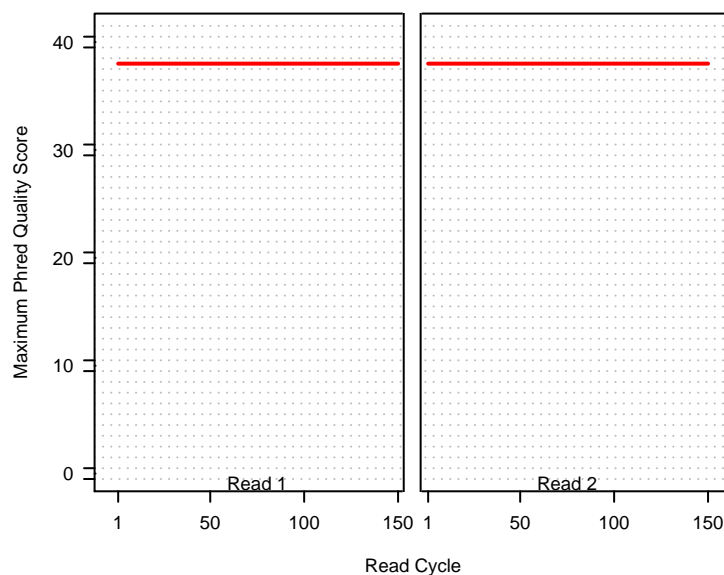
e

Upper Quartile Phred Quality Score
With Sample srpk3_hom_ttnb_wt_5 Colored by lane

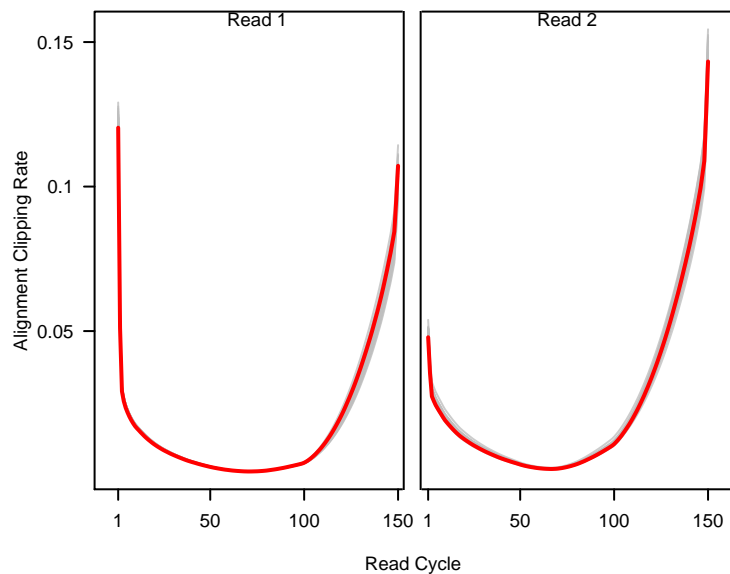


f

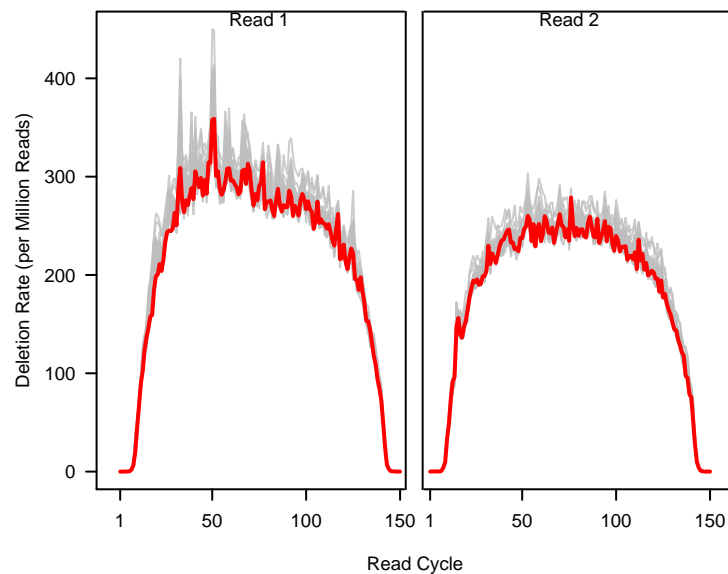
Maximum Phred Quality Score
With Sample srpk3_hom_ttnb_wt_5 Colored by lane



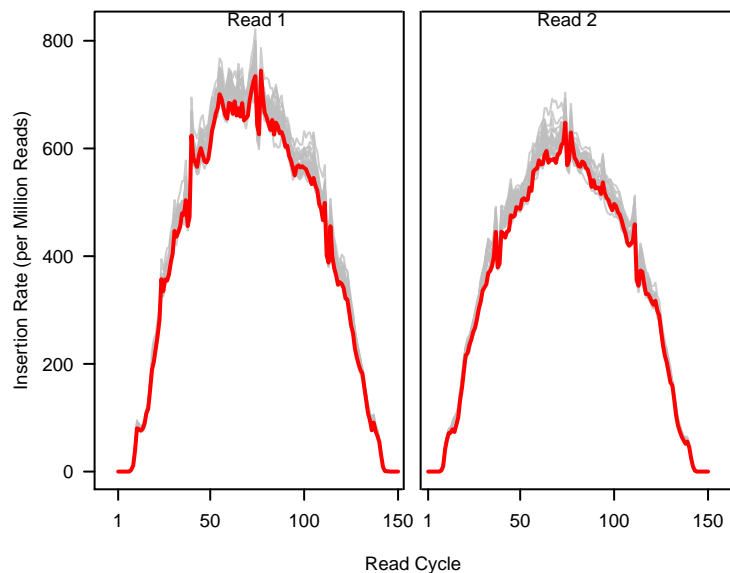
g Alignment Clipping Rate, by read cycle
With Sample srpk3_hom_ttnb_wt_5 Colored by lane



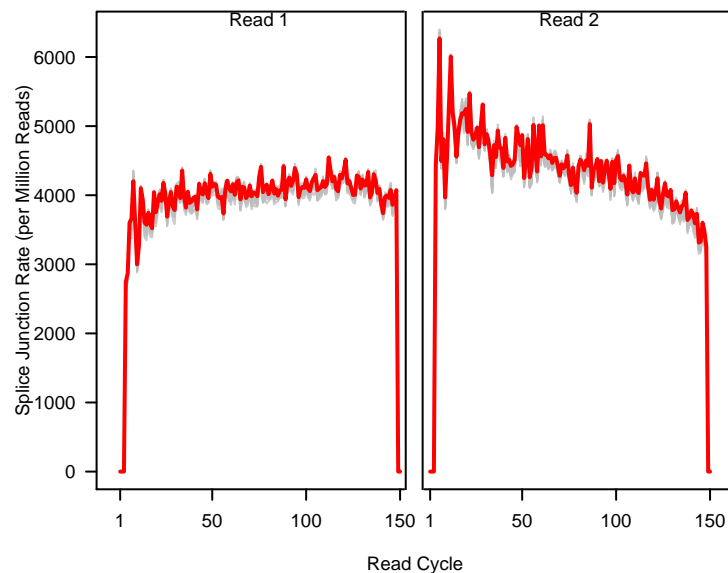
h Deletion Rate, by read cycle
With Sample srpk3_hom_ttnb_wt_5 Colored by lane



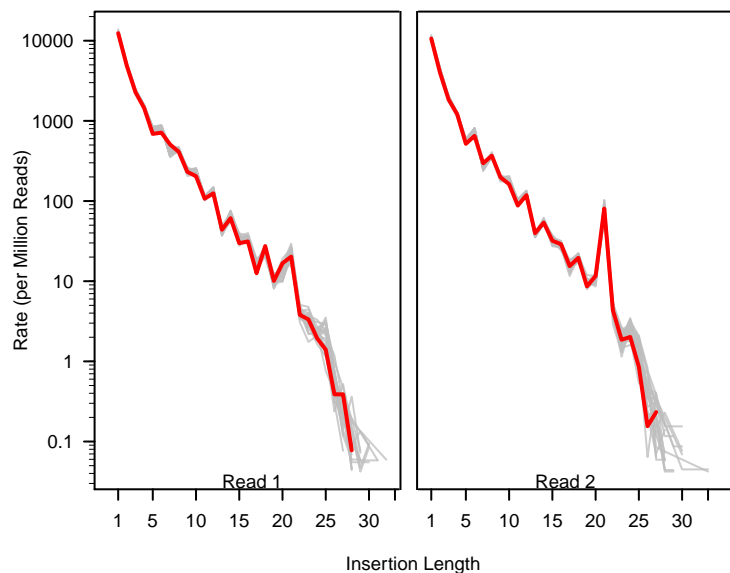
i Insertion Rate, by read cycle
With Sample srpk3_hom_ttnb_wt_5 Colored by lane



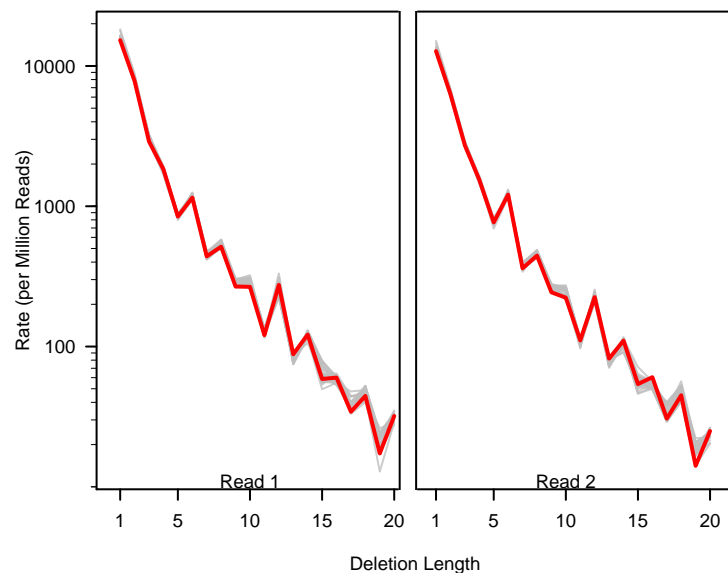
j Splice Junction Rate, by read cycle
With Sample srpk3_hom_ttnb_wt_5 Colored by lane

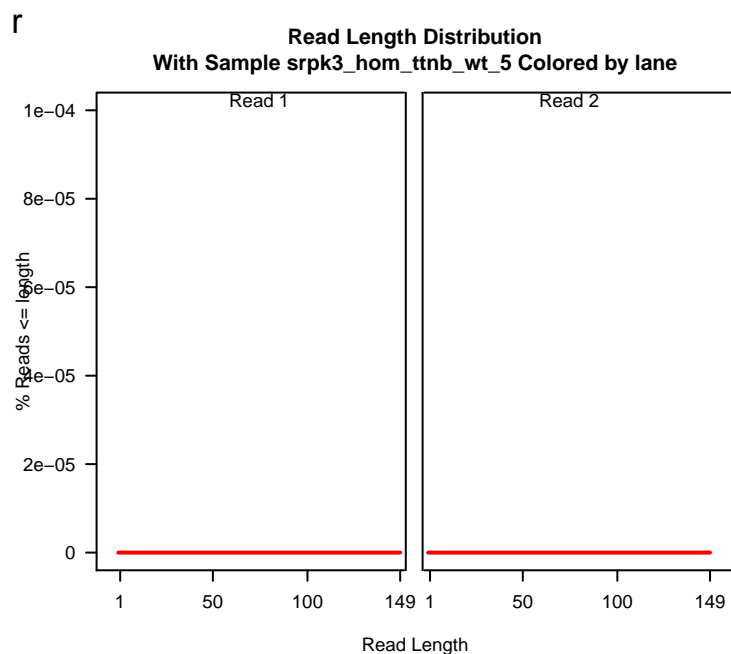
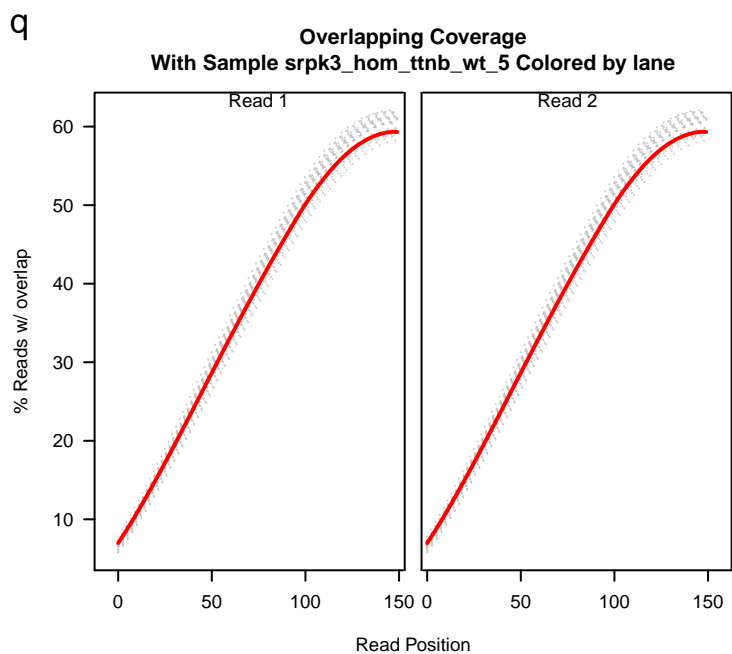
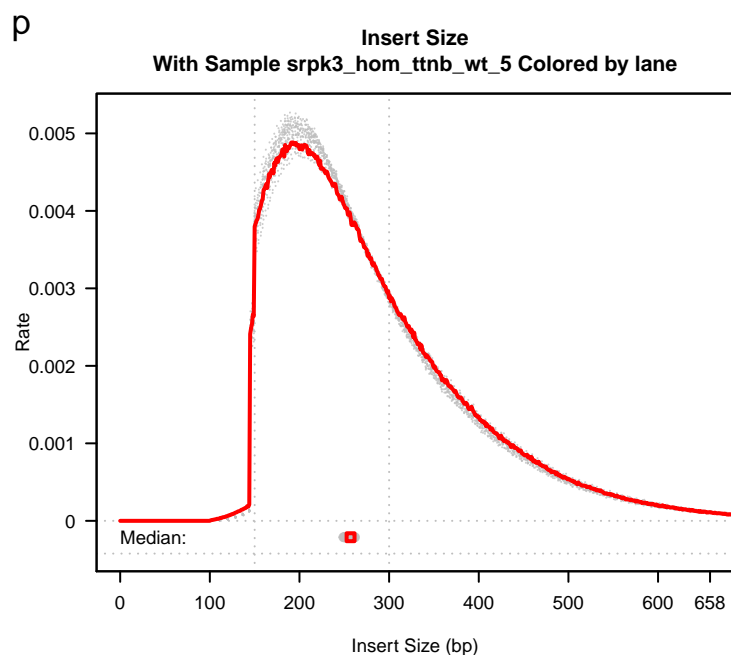
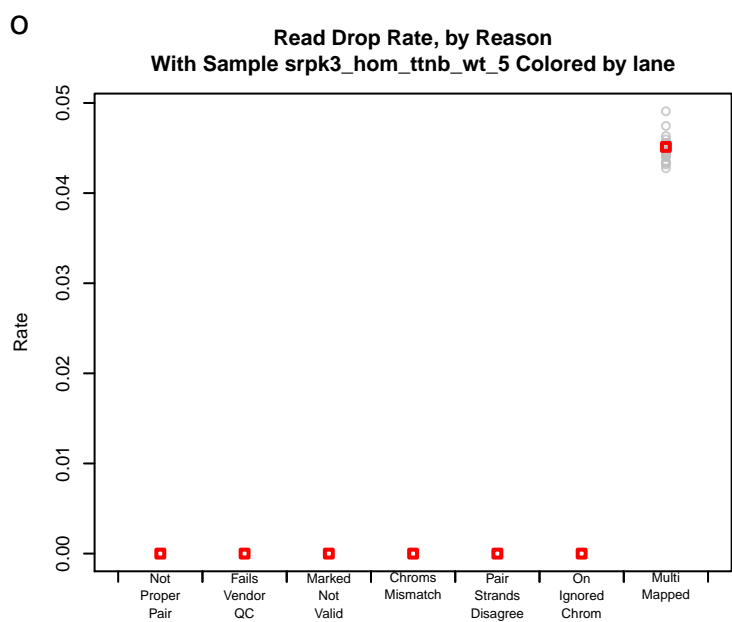
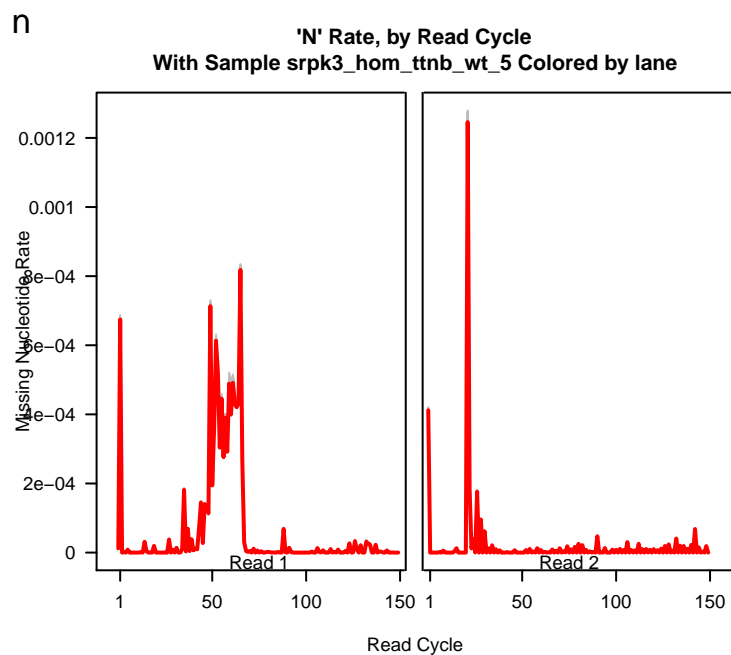
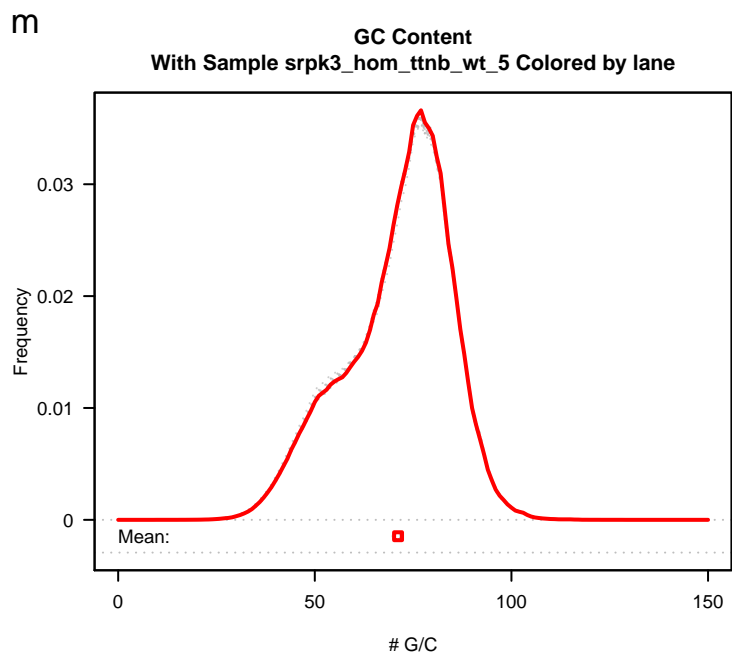


k Insertion Length Distribution
With Sample srpk3_hom_ttnb_wt_5 Colored by lane



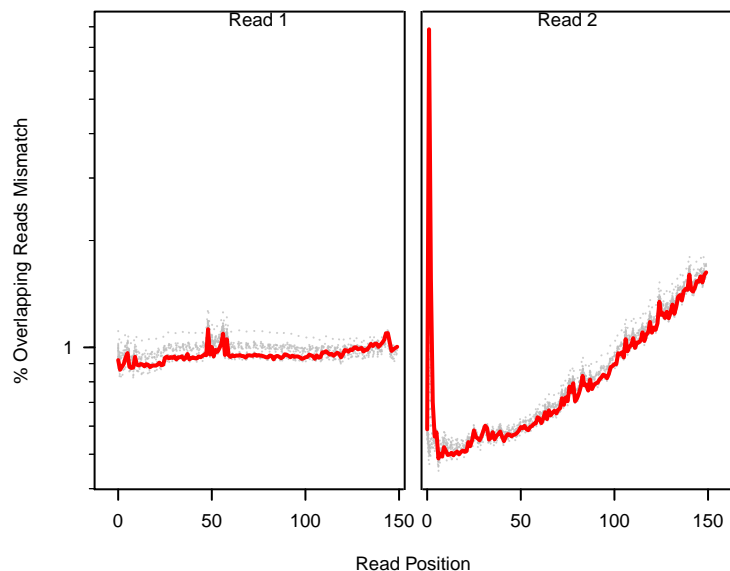
l Deletion Length Distribution
With Sample srpk3_hom_ttnb_wt_5 Colored by lane





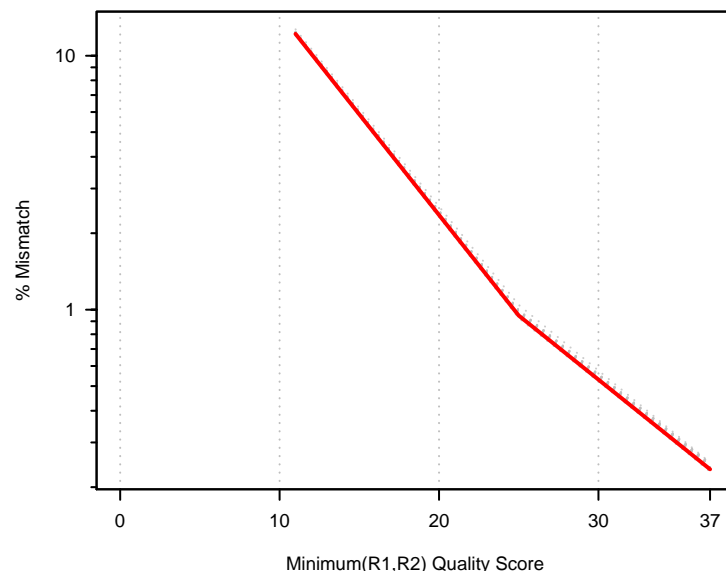
s

Overlap Mismatch by Read Cycle
With Sample *srpk3_hom_ttnb_wt_5* Colored by lane



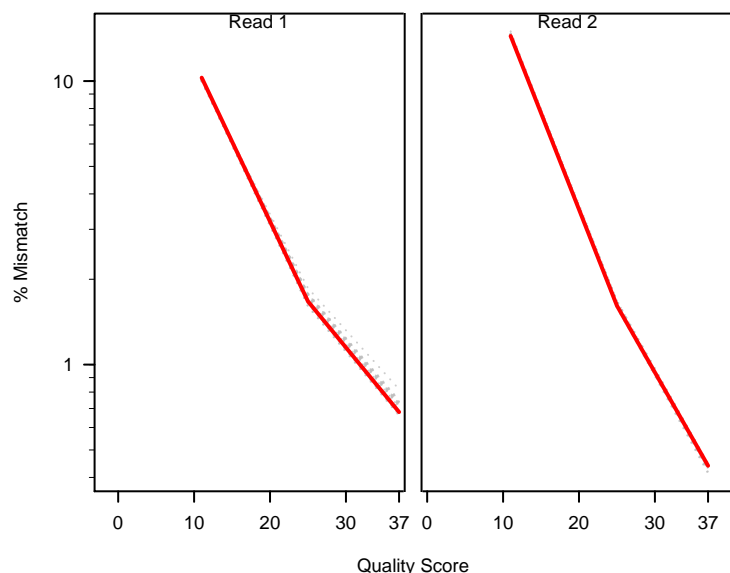
t

Overlapping Mismatch by Min Qual
With Sample *srpk3_hom_ttnb_wt_5* Colored by lane



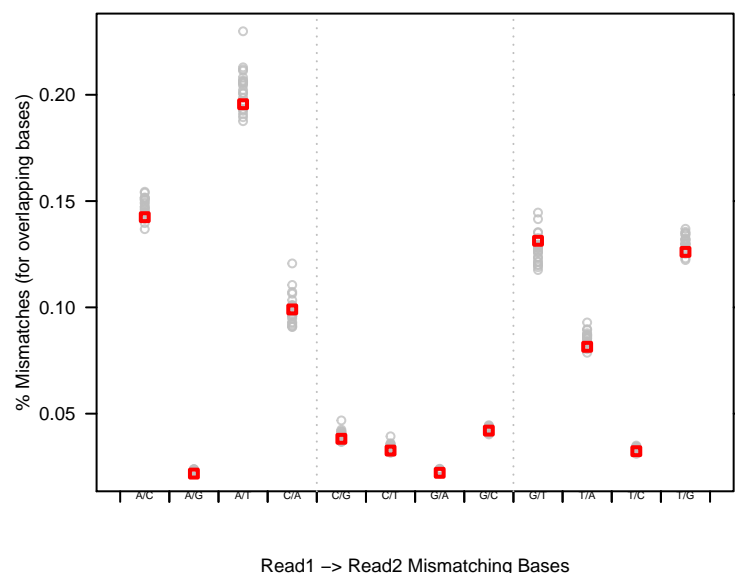
u

Overlap Mismatch by Read Qual
With Sample *srpk3_hom_ttnb_wt_5* Colored by lane



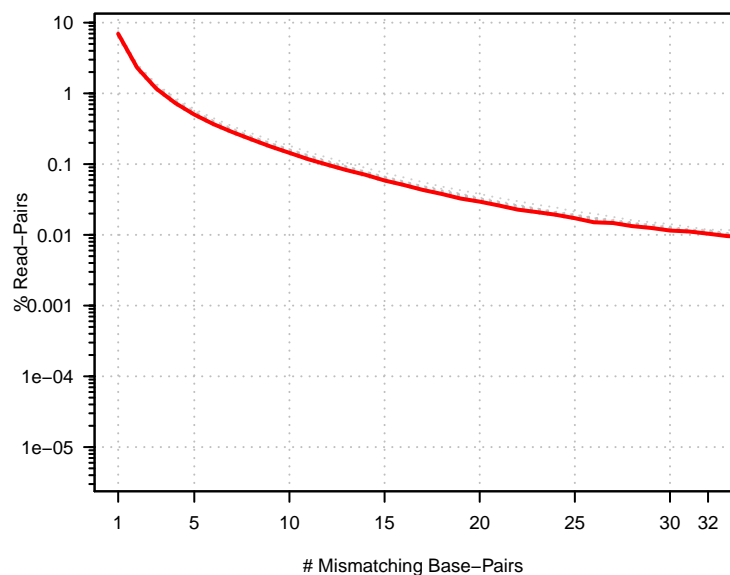
v

Overlap Mismatch Combinations
With Sample *srpk3_hom_ttnb_wt_5* Colored by lane



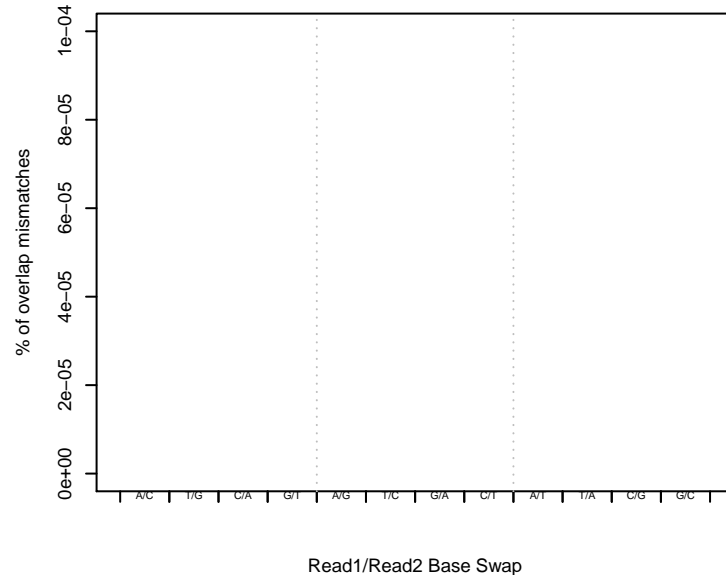
w

Overlap Mismatch Size Frequency
With Sample *srpk3_hom_ttnb_wt_5* Colored by lane



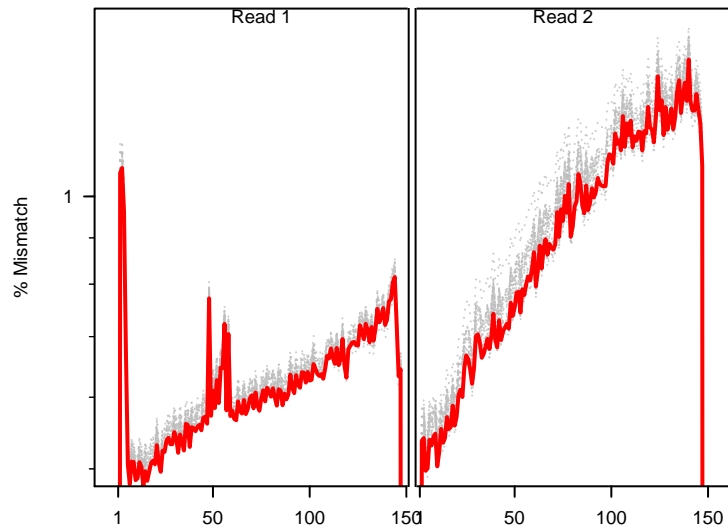
x

Overlap Mismatch Pairs At Phred == 41
With Sample *srpk3_hom_ttnb_wt_5* Colored by lane



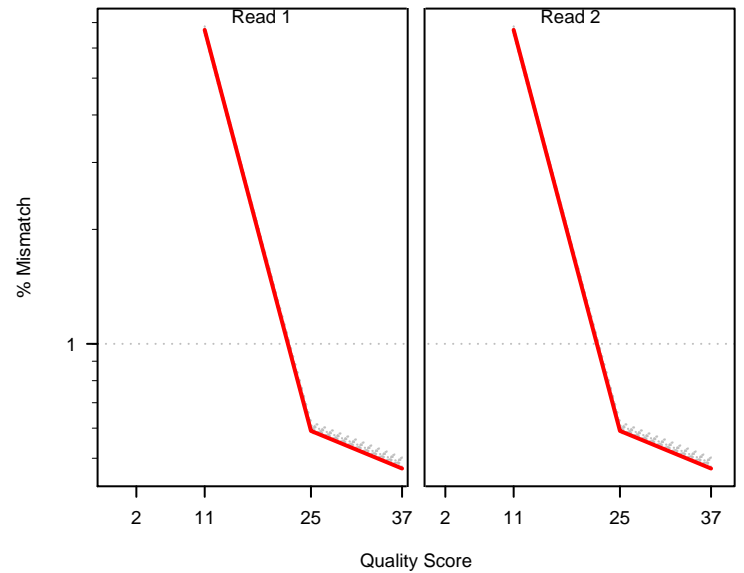
y

Reference Mismatch by Read Cycle
With Sample *srpk3_hom_ttnb_wt_5* Colored by lane



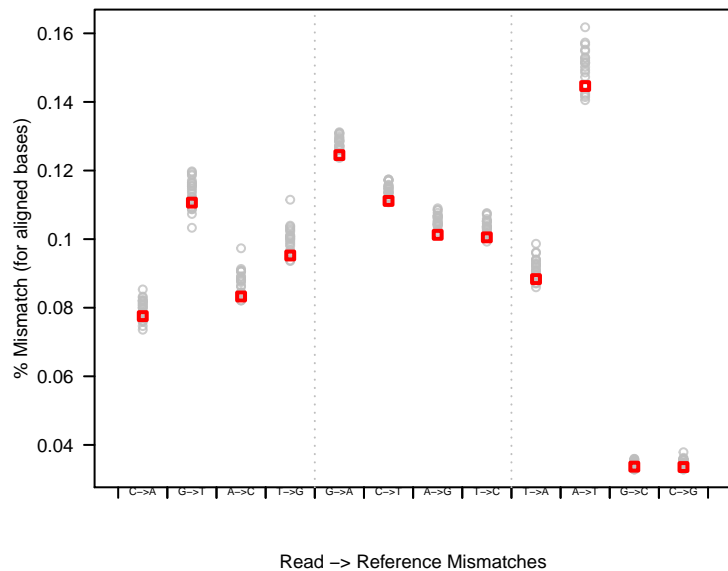
Z

Reference Mismatch by Read Qual
With Sample *srpk3_hom_ttnb_wt_5* Colored by lane



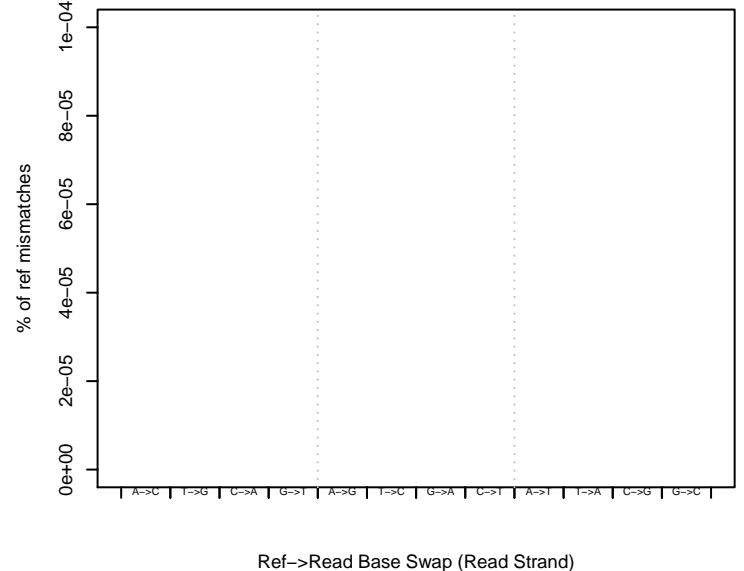
aa

Reference Mismatch Combinations
With Sample *srpk3_hom_ttnb_wt_5* Colored by lane



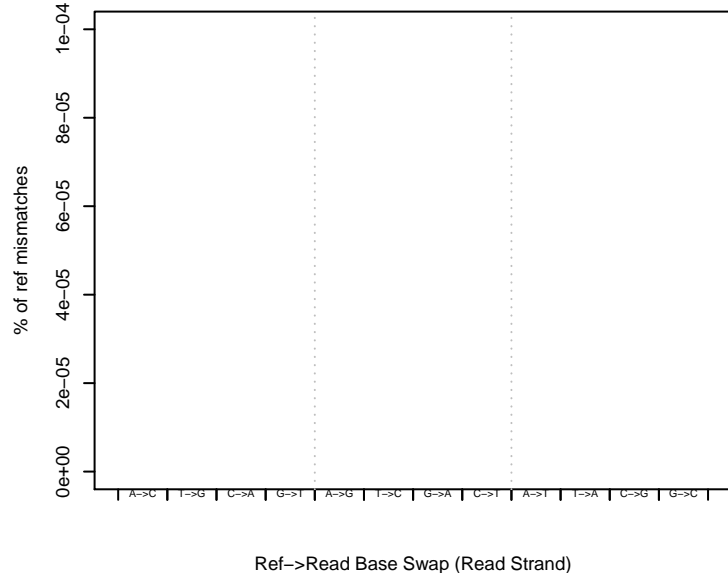
ab

R1 Ref Mismatches At Phred == 41
With Sample *srpk3_hom_ttnb_wt_5* Colored by lane



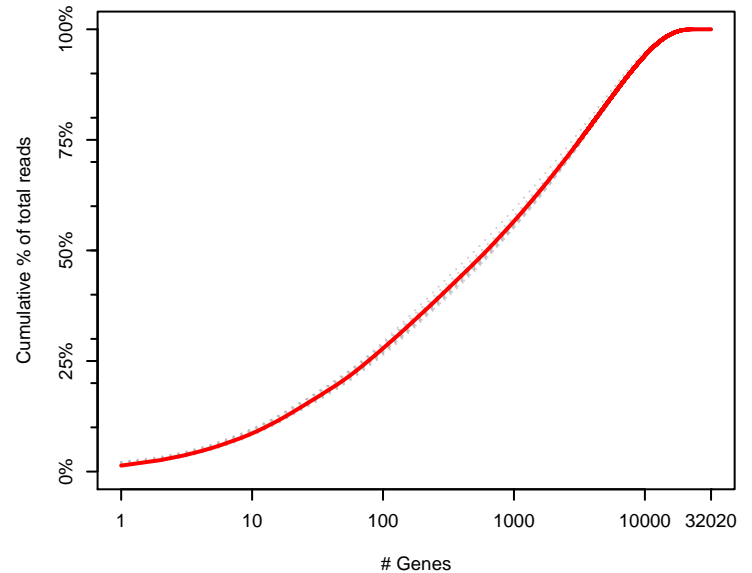
ac

R2 Ref Mismatches At Phred == 41
With Sample *srpk3_hom_ttnb_wt_5* Colored by lane



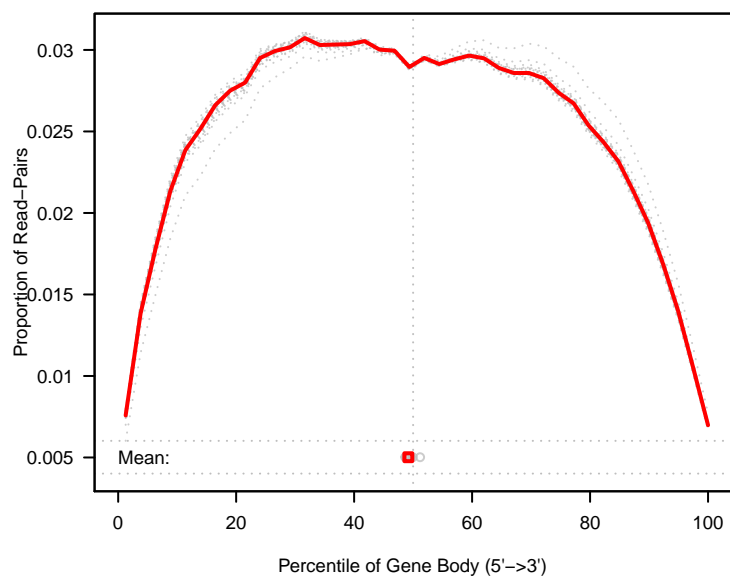
ad

Cumulative Gene Assignment Diversity
With Sample *srpk3_hom_ttnb_wt_5* Colored by lane



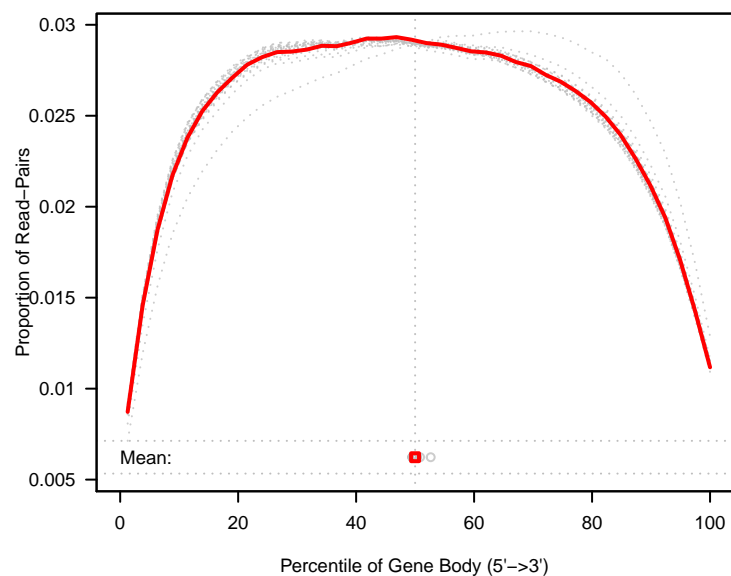
ae

Gene-Body Coverage
With Sample *srpk3_hom_ttnb_wt_5* Colored by lane



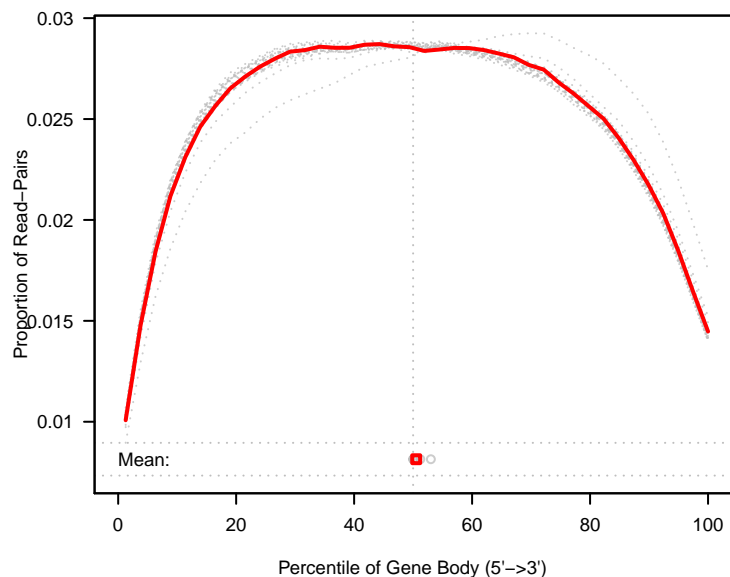
af

Gene-Body Coverage, Upper Middle Quartile Genes
With Sample *srpk3_hom_ttnb_wt_5* Colored by lane



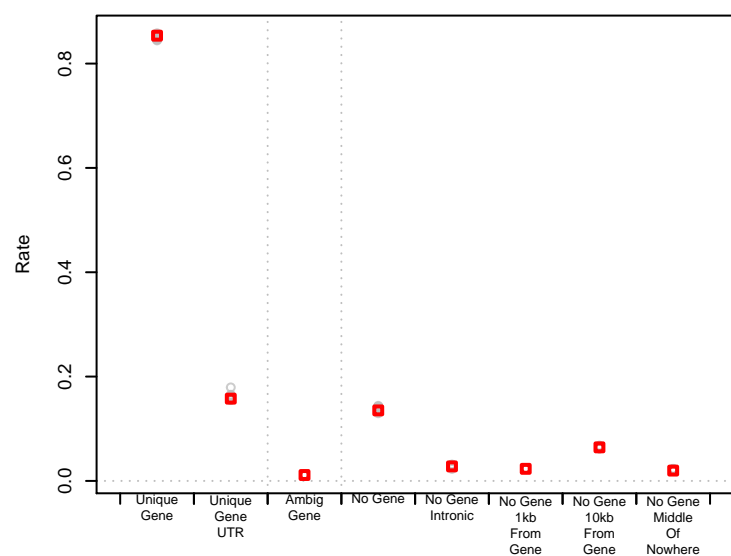
ag

Gene-Body Coverage, Low Expression Genes
With Sample *srpk3_hom_ttnb_wt_5* Colored by lane



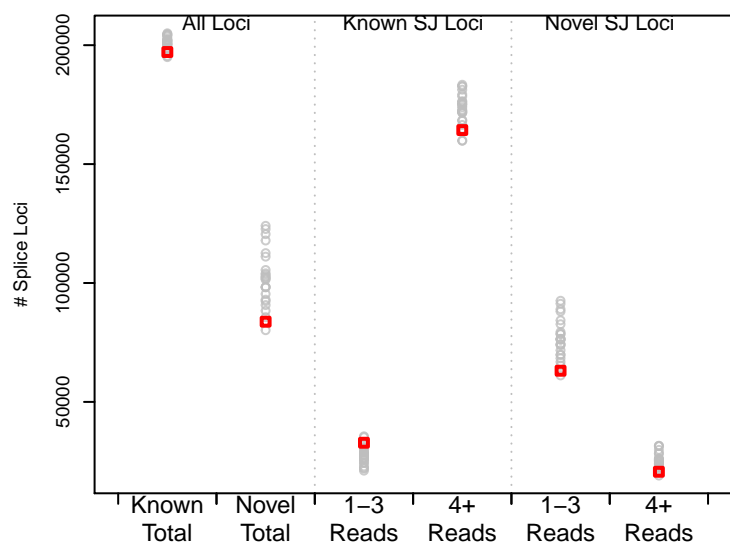
ah

Read Mapping Location Rates
With Sample *srpk3_hom_ttnb_wt_5* Colored by lane



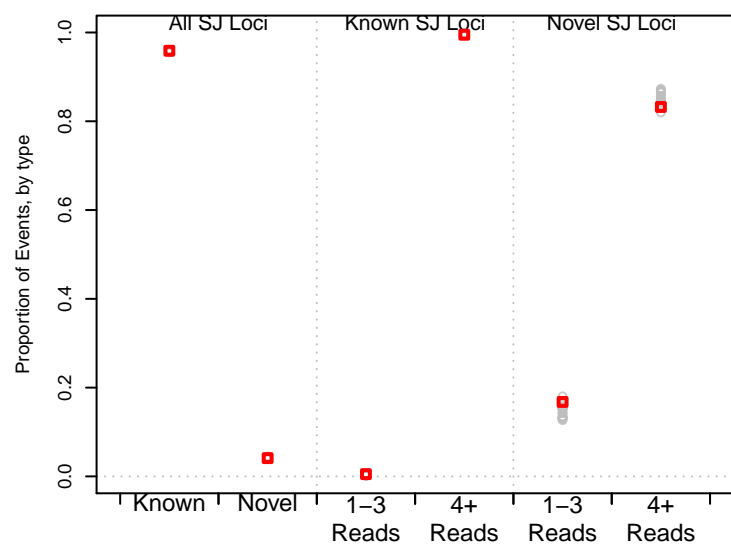
ai

Observed Splice Junction Loci, by type
With Sample *srpk3_hom_ttnb_wt_5* Colored by lane

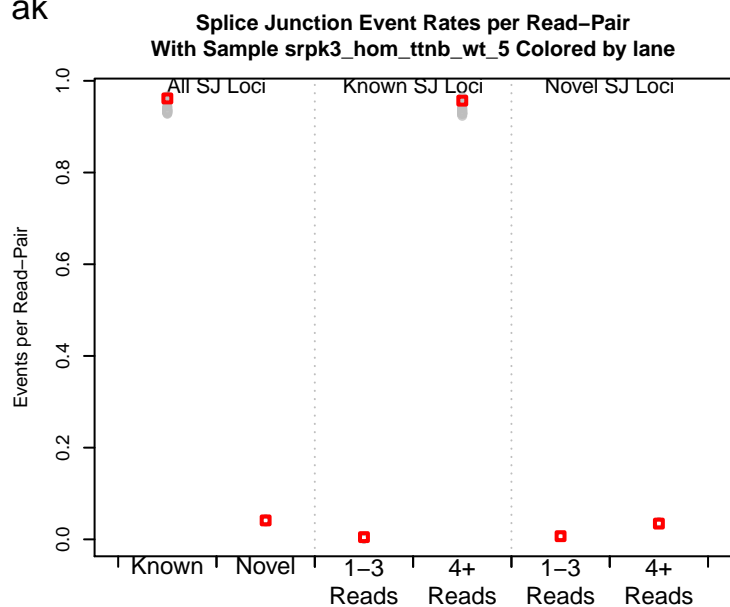


aj

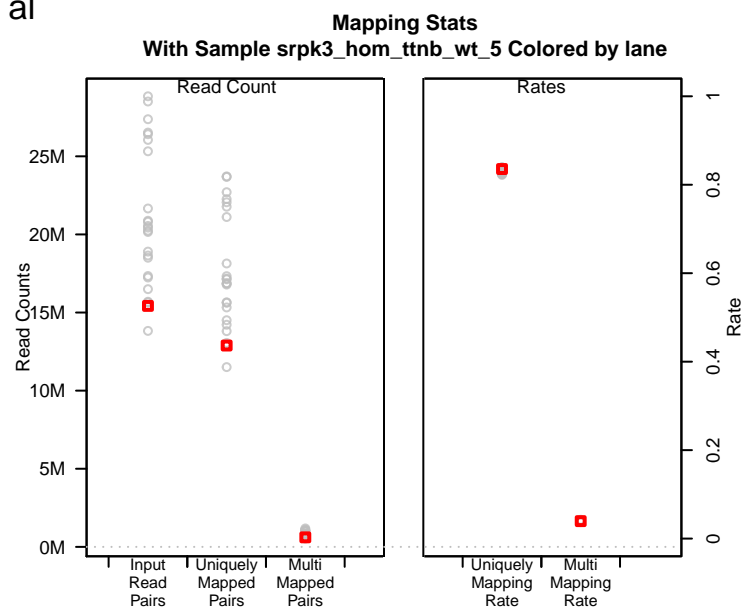
Breakdown of Splice Junction Events, by type
With Sample *srpk3_hom_ttnb_wt_5* Colored by lane



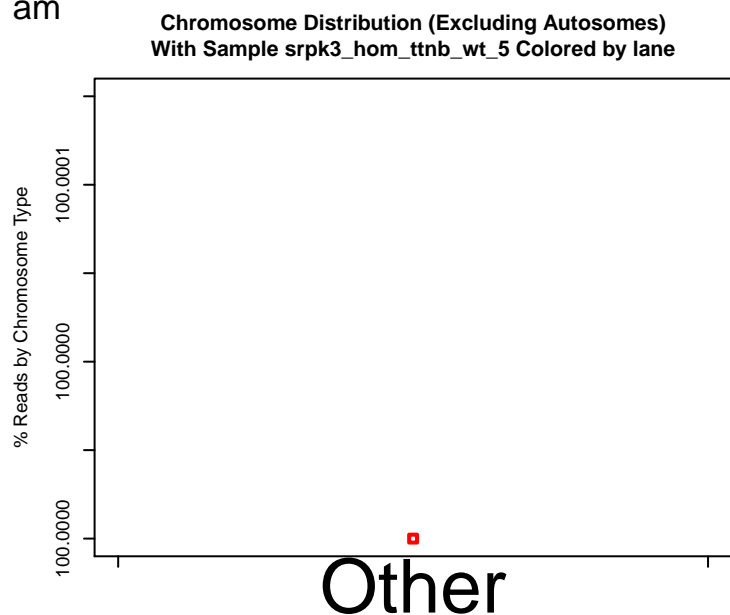
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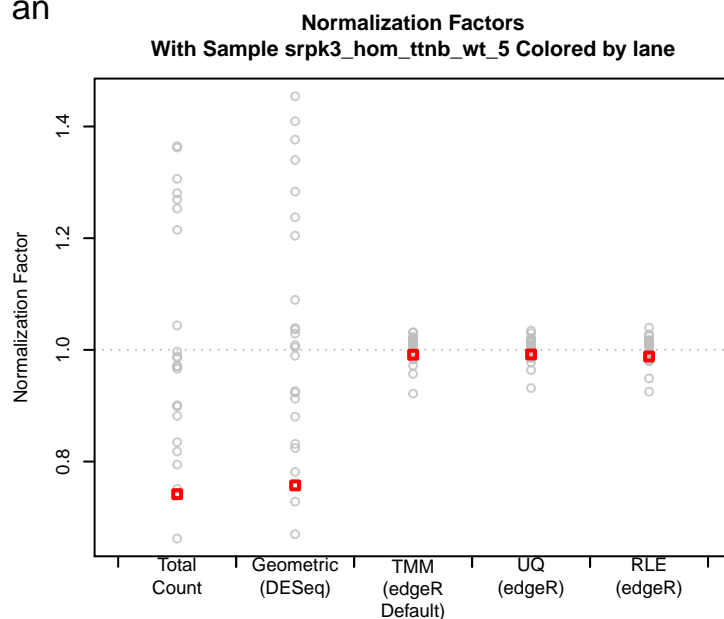
al



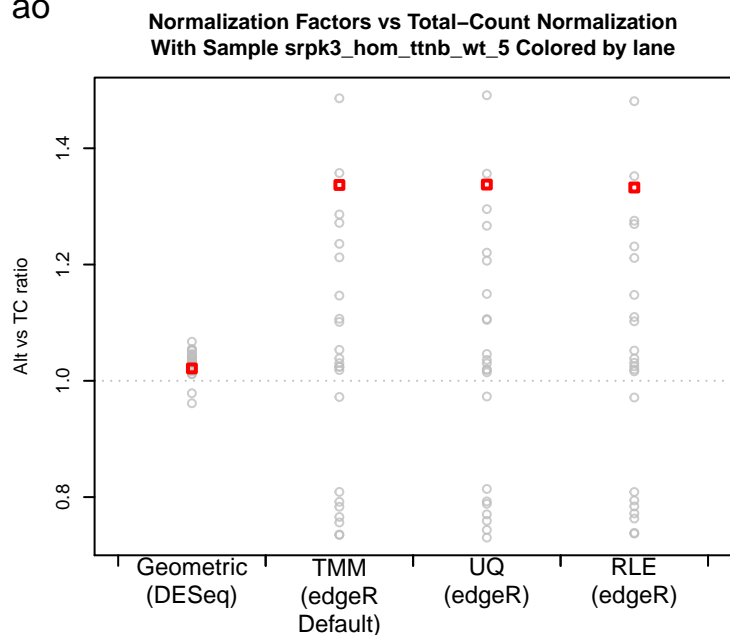
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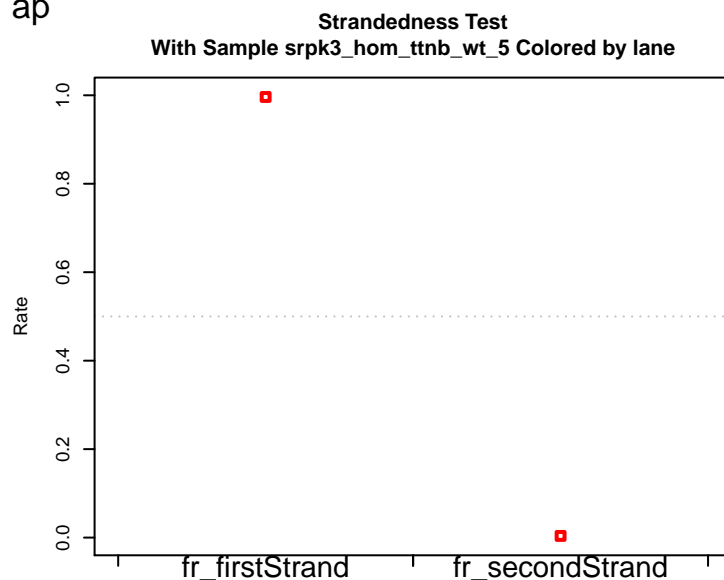
an



ao

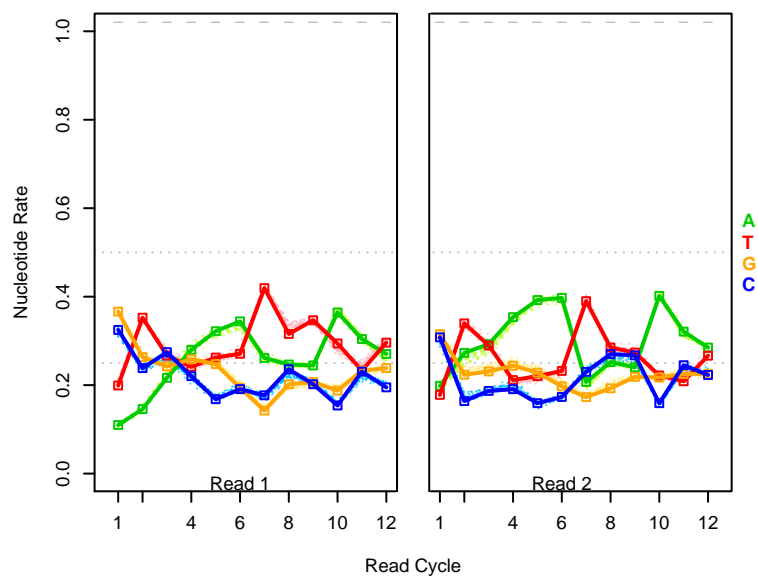


ap



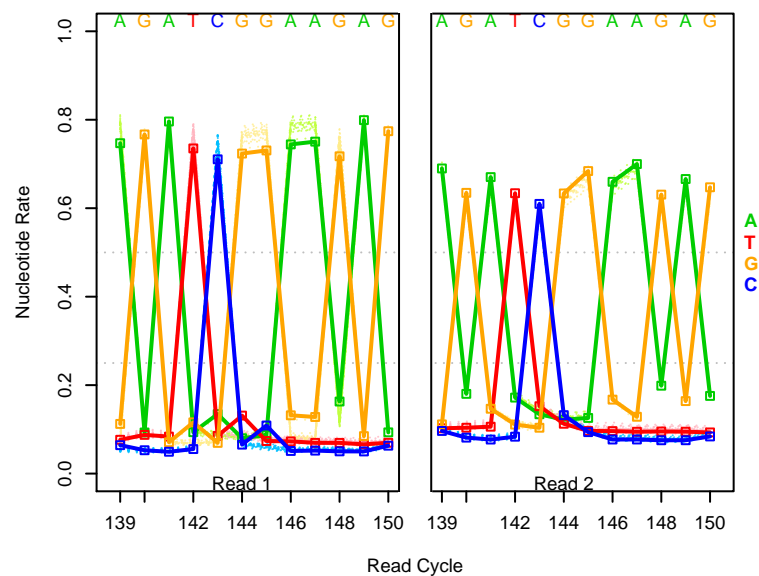
aq

Nucleotide Rate by Cycle, Leading Clipped bases (12)
With Sample **srpk3_hom_ttnb_wt_5** in Bold



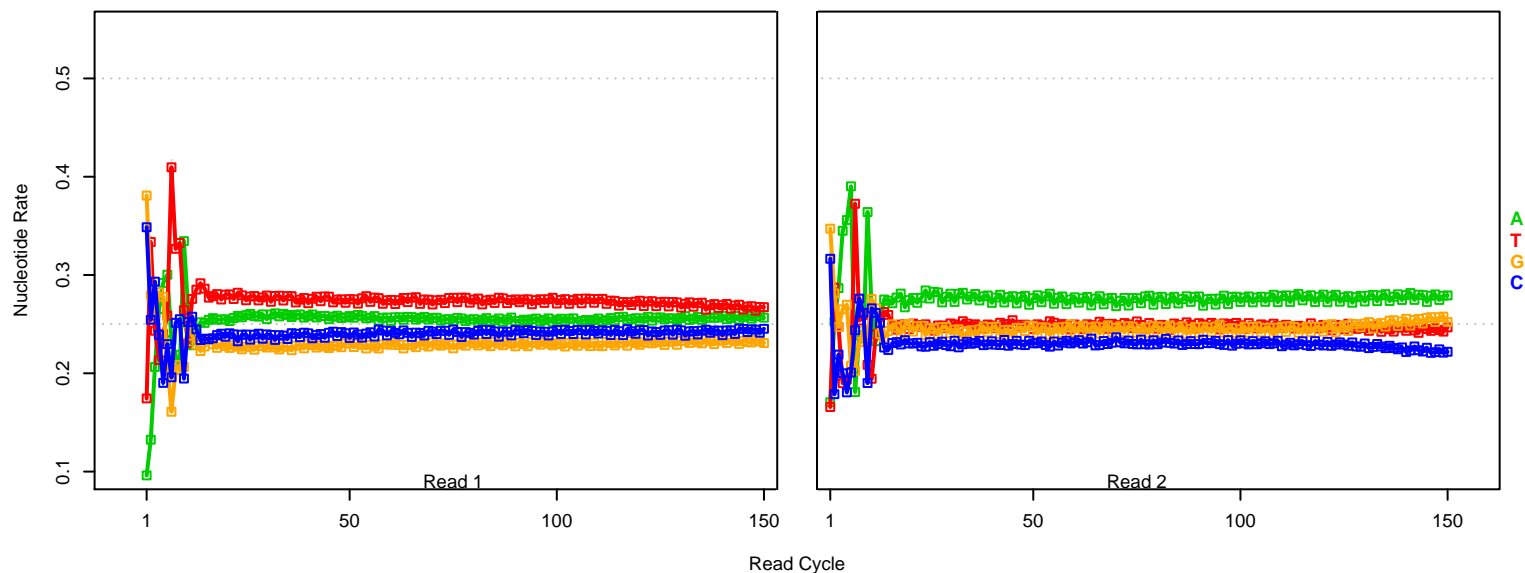
ar

Nucleotide Rate by Cycle, Trailing Clipped bases (12)
With Sample **srpk3_hom_ttnb_wt_5** in Bold



as

Raw Nucleotide Rate by Cycle
With Sample **srpk3_hom_ttnb_wt_5** in Bold



at

Nucleotide Rate by Cycle, Aligned bases only
With Sample **srpk3_hom_ttnb_wt_5** in Bold

