a

Sample Highlight:
srpk3_hom_ttnb_wt_4
Colored by Lane

■ UNKNOWN
○ Other Samples

b

Minimum Phred Quality Score
With Sample srpk3_hom_ttnb_wt_4 Colored by lane
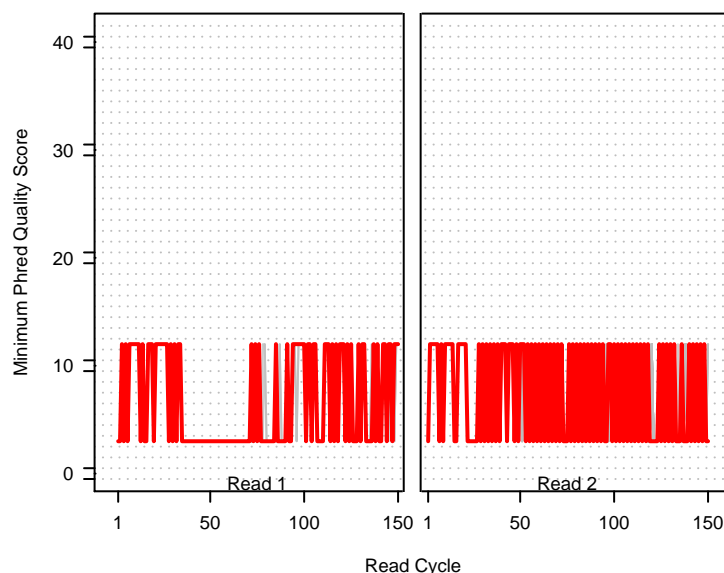
Minimum Phred Quality Score

Read 1   Read 2

Read Cycle

c

Lower Quartile Phred Quality Score
With Sample srpk3_hom_ttnb_wt_4 Colored by lane

Lower Quartile Phred Quality Score

Read 1   Read 2

Read Cycle

d

Median Phred Quality Score
With Sample srpk3_hom_ttnb_wt_4 Colored by lane

Median Phred Quality Score

Read 1   Read 2

Read Cycle

e

Upper Quartile Phred Quality Score
With Sample srpk3_hom_ttnb_wt_4 Colored by lane

Upper Quartile Phred Quality Score

Read 1   Read 2

Read Cycle

f

Maximum Phred Quality Score
With Sample srpk3_hom_ttnb_wt_4 Colored by lane

Maximum Phred Quality Score

Read 1   Read 2
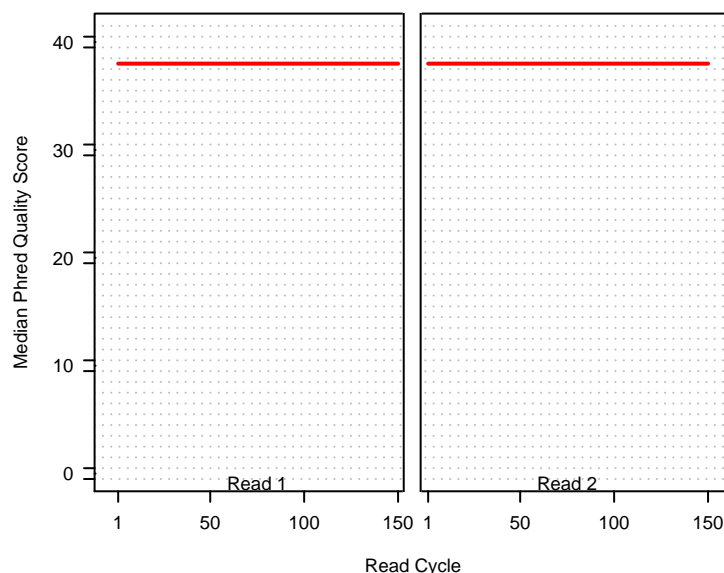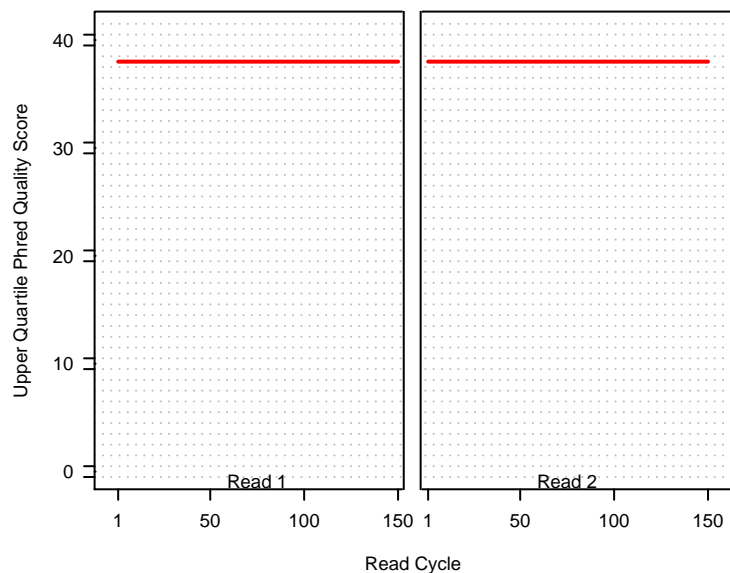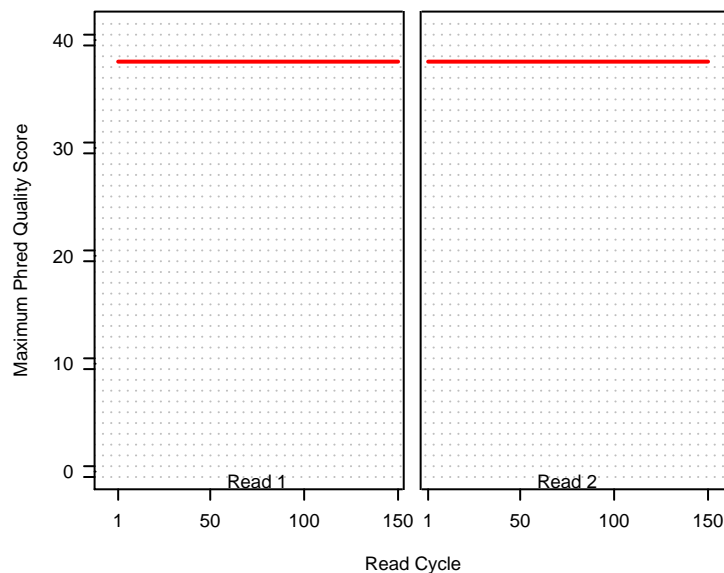
Read Cycle

g Alignment Clipping Rate, by read cycle
With Sample srpk3_hom_ttnb_wt_4 Colored by lane
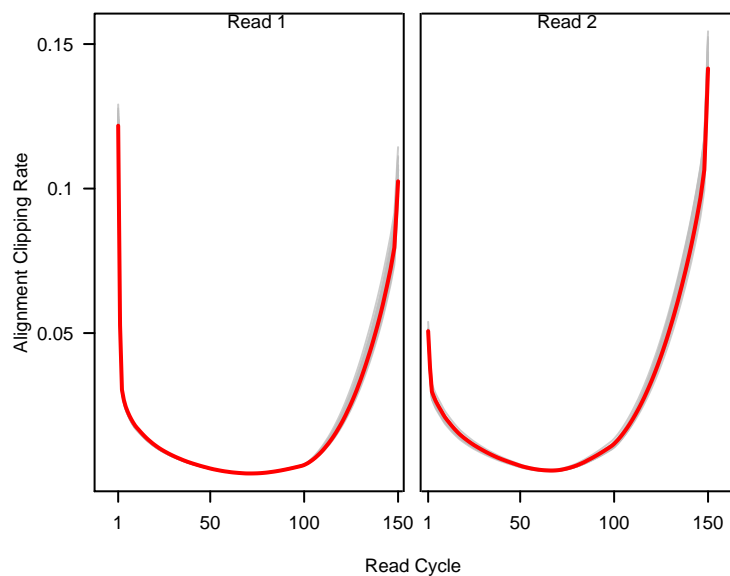
h Deletion Rate, by read cycle
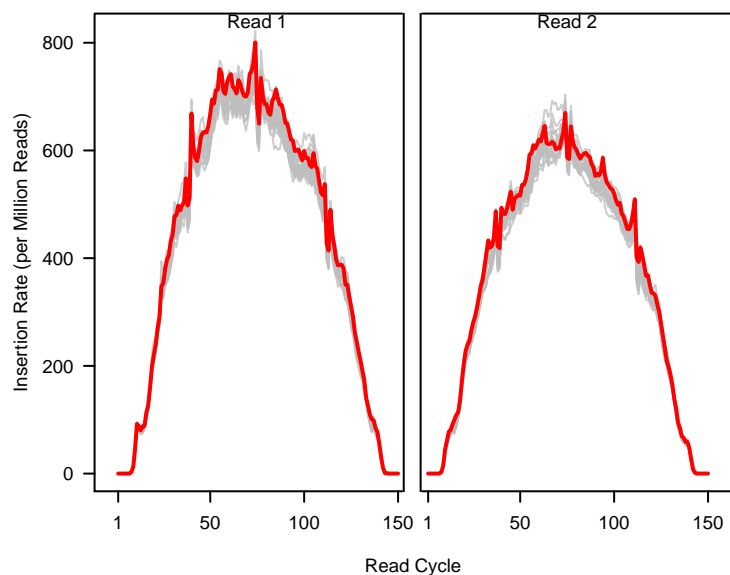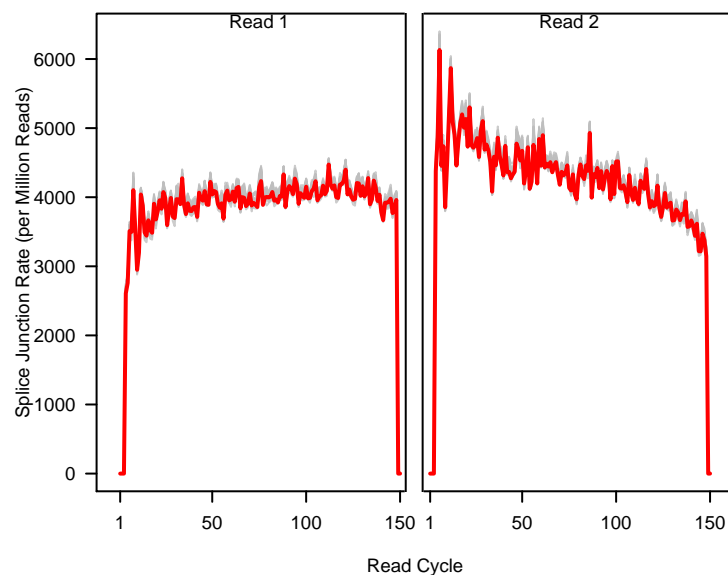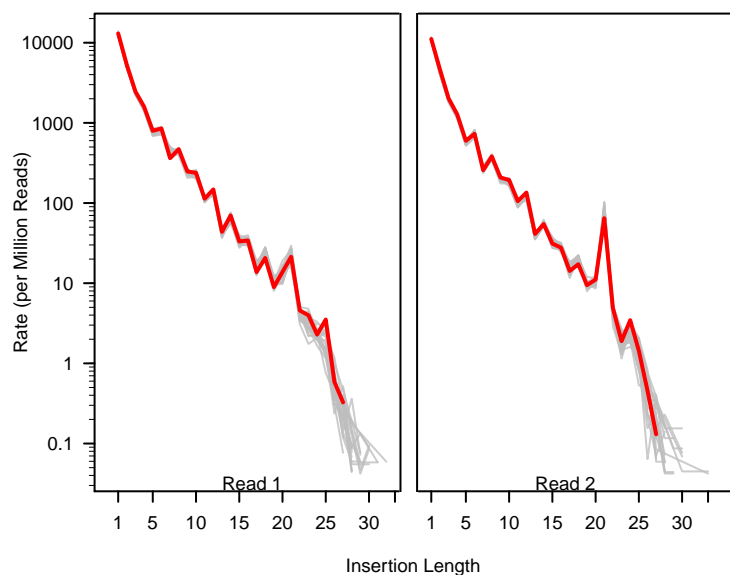With Sample srpk3_hom_ttnb_wt_4 Colored by lane
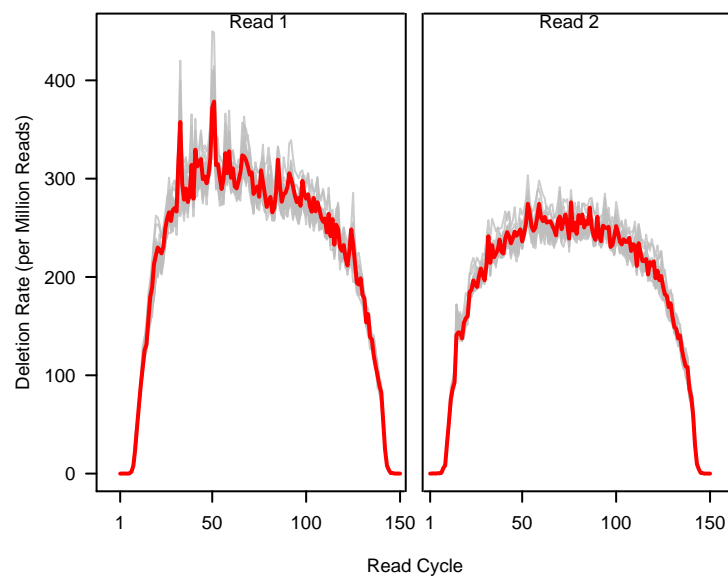
i Insertion Rate, by read cycle
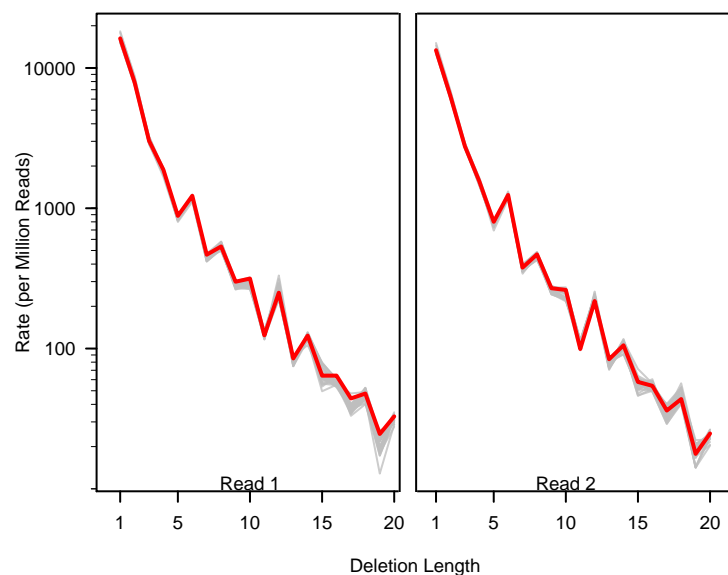With Sample srpk3_hom_ttnb_wt_4 Colored by lane

j Splice Junction Rate, by read cycle
With Sample srpk3_hom_ttnb_wt_4 Colored by lane

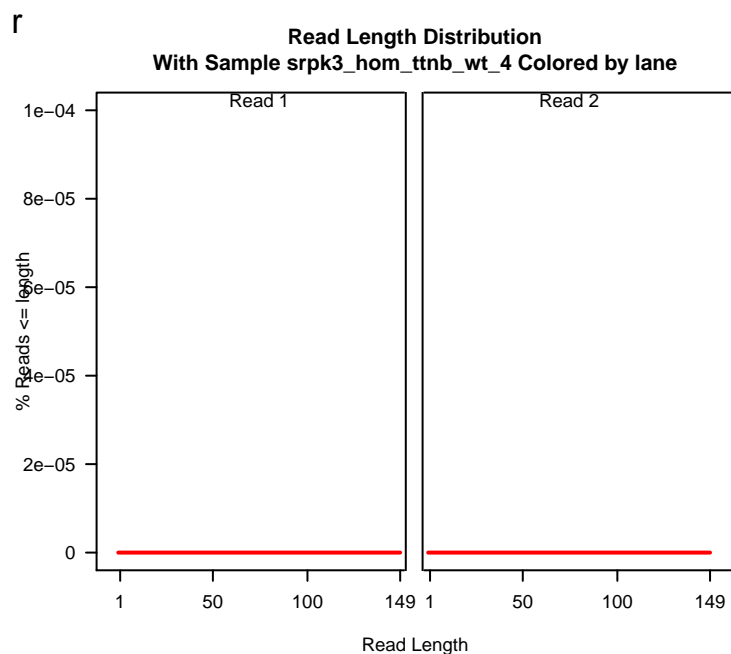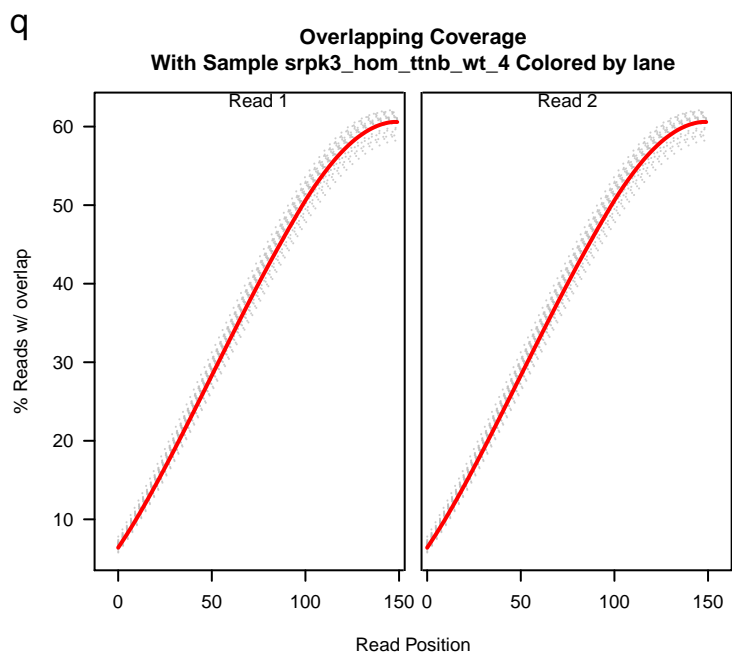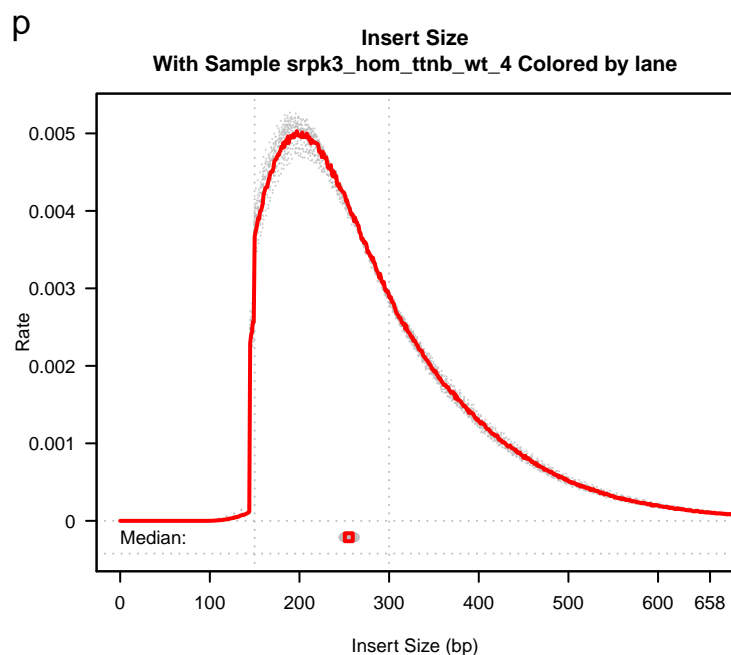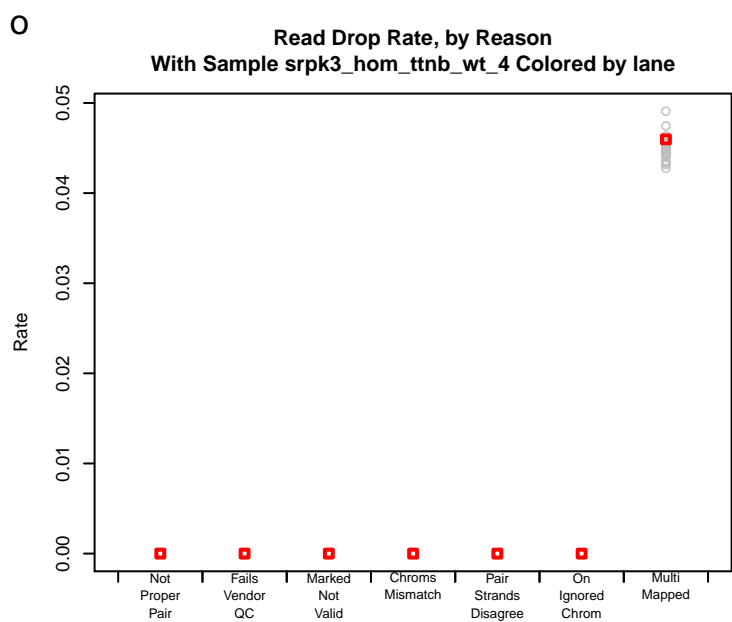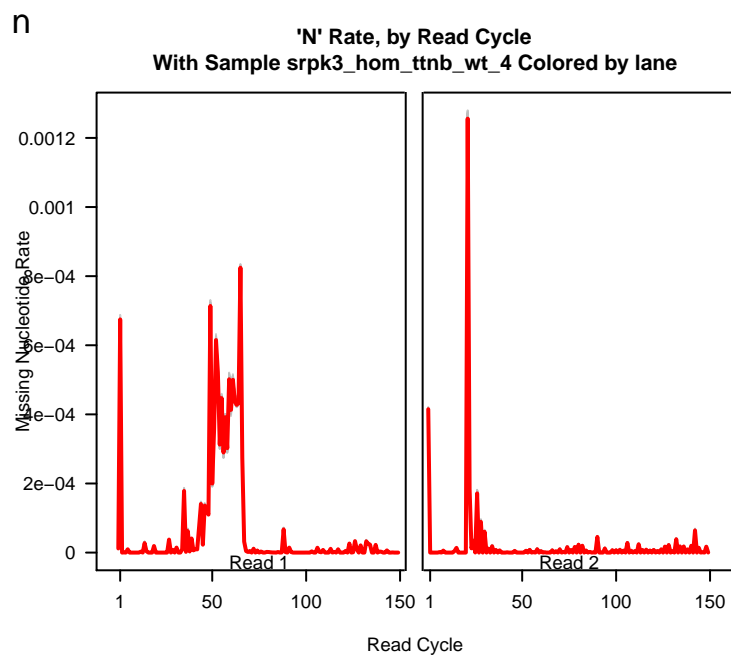**k** Insertion Length Distribution
With Sample srpk3_hom_ttnb_wt_4 Colored by lane

l Deletion Length Distribution
With Sample srpk3_hom_ttnb_wt_4 Colored by lane
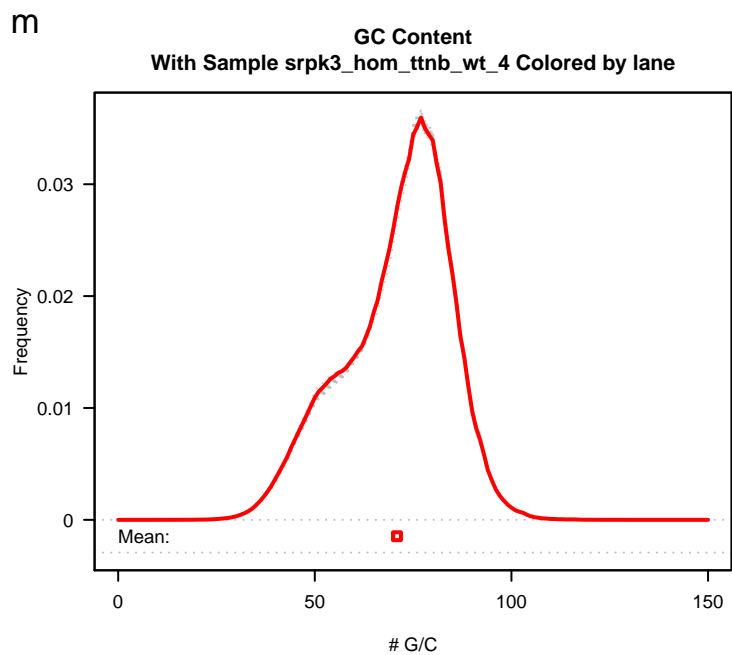
m GC Content
With Sample srpk3_hom_ttnb_wt_4 Colored by lane

n 'N' Rate, by Read Cycle
With Sample srpk3_hom_ttnb_wt_4 Colored by lane

o Read Drop Rate, by Reason
With Sample srpk3_hom_ttnb_wt_4 Colored by lane

p Insert Size
With Sample srpk3_hom_ttnb_wt_4 Colored by lane

q Overlapping Coverage
With Sample srpk3_hom_ttnb_wt_4 Colored by lane
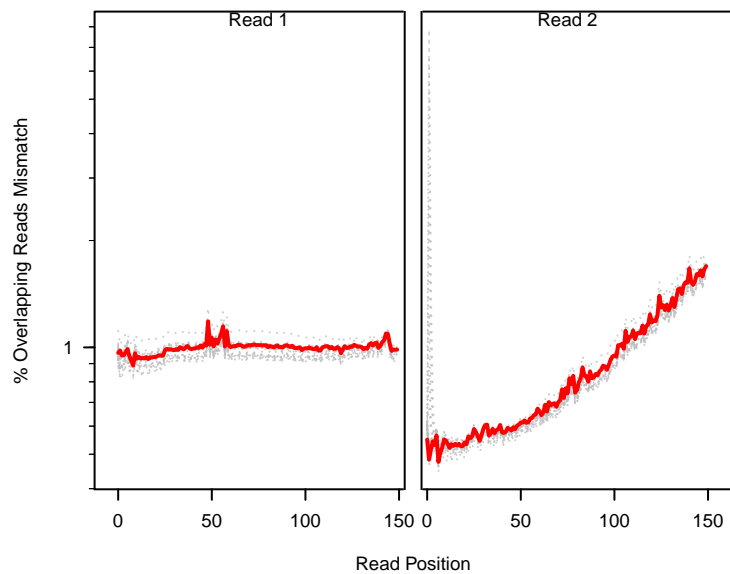
r Read Length Distribution
With Sample srpk3_hom_ttnb_wt_4 Colored by lane

s

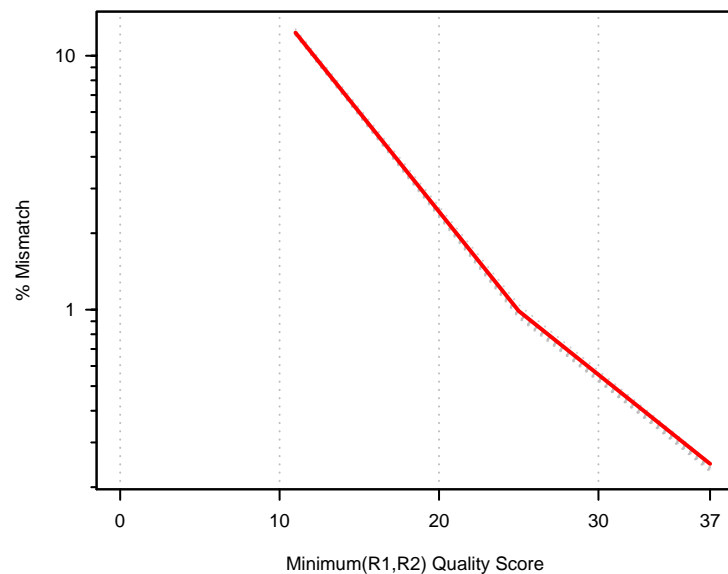## Overlap Mismatch by Read Cycle
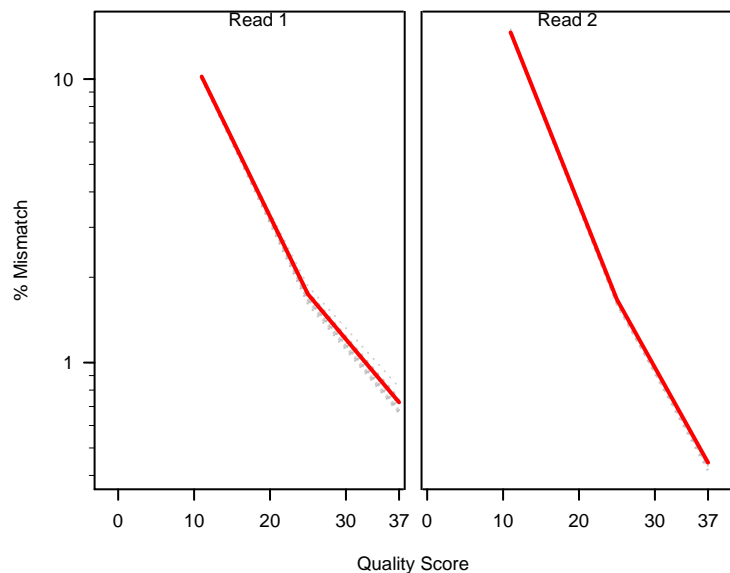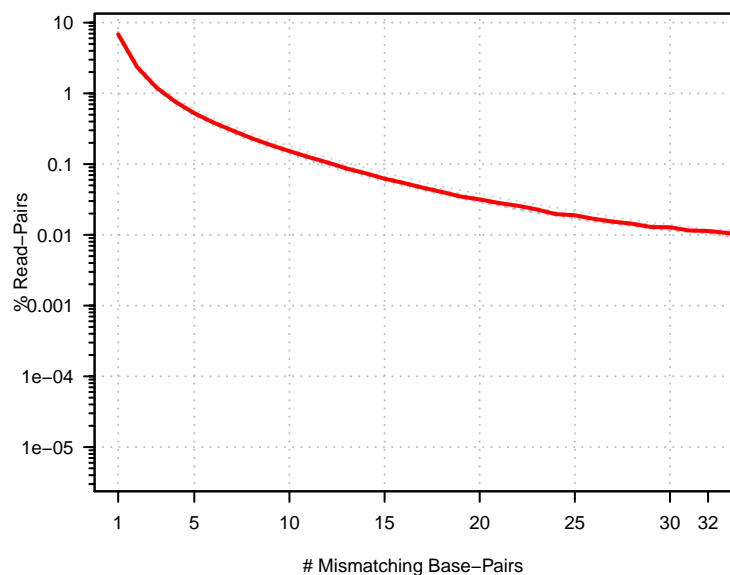## With Sample srpk3_hom_ttnb_wt_4 Colored by lane

Read 1 | Read 2

% Overlapping Reads Mismatch

Read Position

t

Overlapping Mismatch by Min Qual
With Sample srpk3_hom_ttnb_wt_4 Colored by lane

% Mismatch

Minimum(R1,R2) Quality Score

u

Overlap Mismatch by Read Qual
With Sample srpk3_hom_ttnb_wt_4 Colored by lane

Read 1 | Read 2

% Mismatch

Quality Score

V

Overlap Mismatch Combinations
With Sample srpk3_hom_ttnb_wt_4 Colored by lane

% Mismatches (for overlapping bases)

A/C A/G A/T C/A C/G C/T G/A G/C G/T T/A T/C T/G

Read1 –> Read2 Mismatching Bases
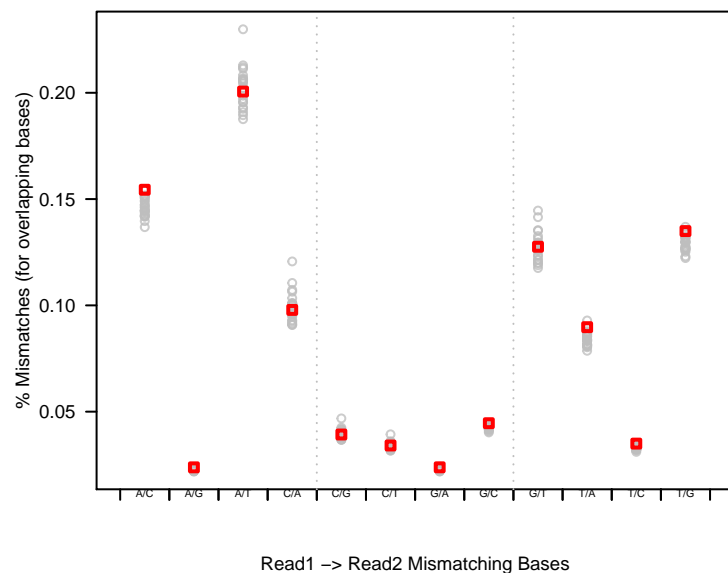
W

Overlap Mismatch Size Frequency
With Sample srpk3_hom_ttnb_wt_4 Colored by lane

% Read–Pairs

Mismatching Base–Pairs

X

Overlap Mismatch Pairs At Phred == 41
With Sample srpk3_hom_ttnb_wt_4 Colored by lane
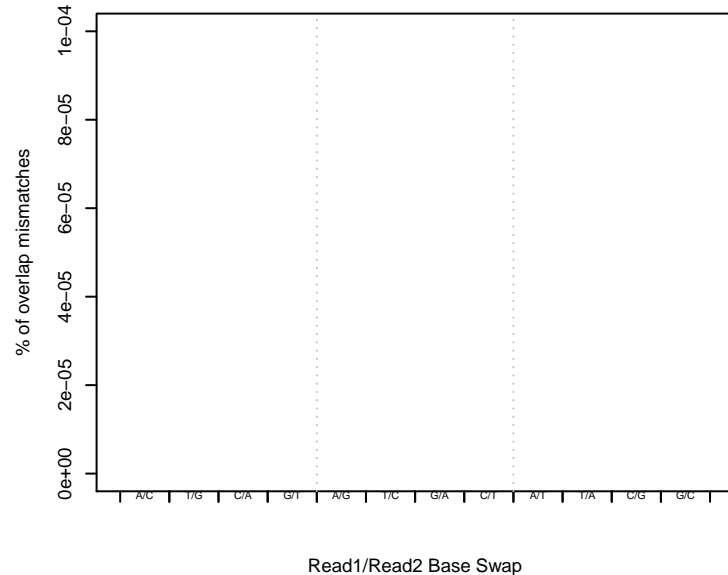
% of overlap mismatches

A/C T/G C/A G/T A/G T/C G/A C/T A/T T/A C/G G/C

Read1/Read2 Base Swap

y

Reference Mismatch by Read Cycle
With Sample srpk3_hom_ttnb_wt_4 Colored by lane

Read 1   Read 2

% Mismatch

z

Reference Mismatch by Read Qual
With Sample srpk3_hom_ttnb_wt_4 Colored by lane

Read 1   Read 2
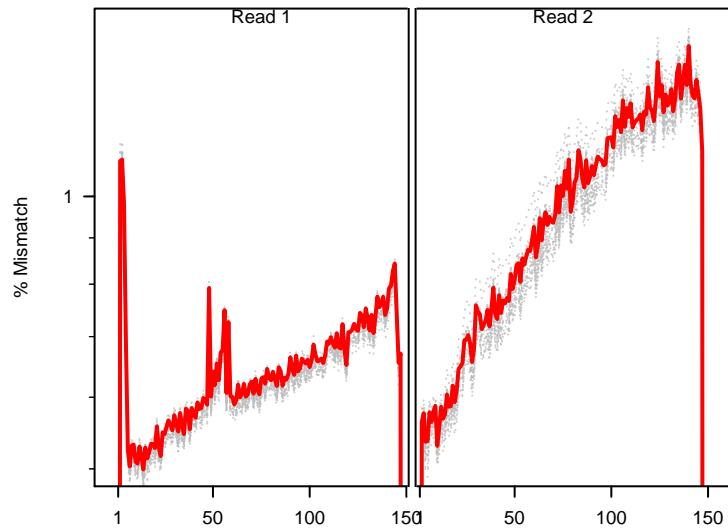
% Mismatch

Quality Score
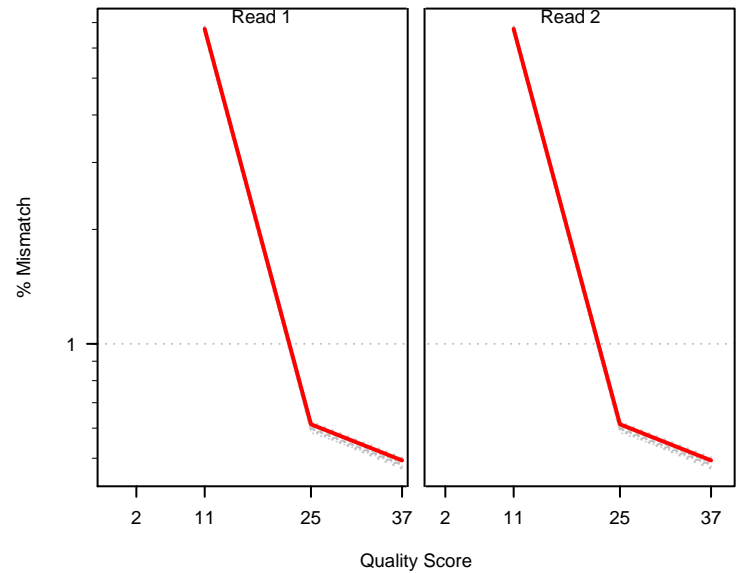
aa

Reference Mismatch Combinations
With Sample srpk3_hom_ttnb_wt_4 Colored by lane
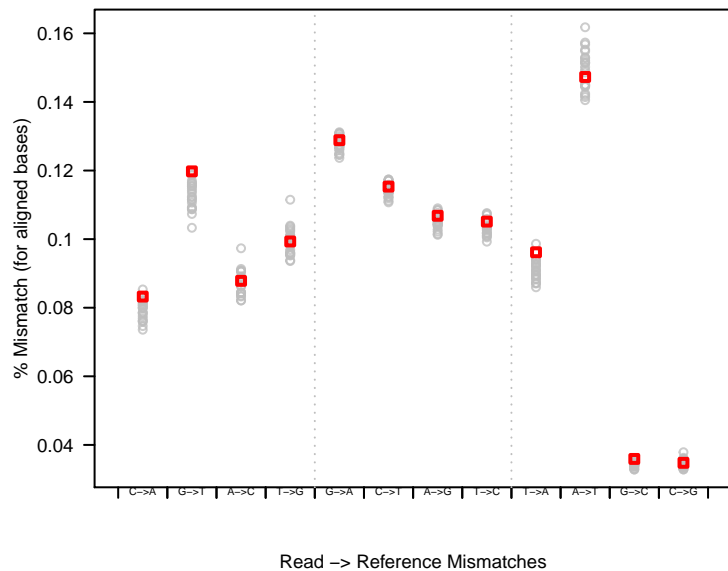
% Mismatch (for aligned bases)

Read –> Reference Mismatches

ab

R1 Ref Mismatches At Phred == 41
With Sample srpk3_hom_ttnb_wt_4 Colored by lane

% of ref mismatches

Ref–>Read Base Swap (Read Strand)

ac

R2 Ref Mismatches At Phred == 41
With Sample srpk3_hom_ttnb_wt_4 Colored by lane

% of ref mismatches

Ref–>Read Base Swap (Read Strand)
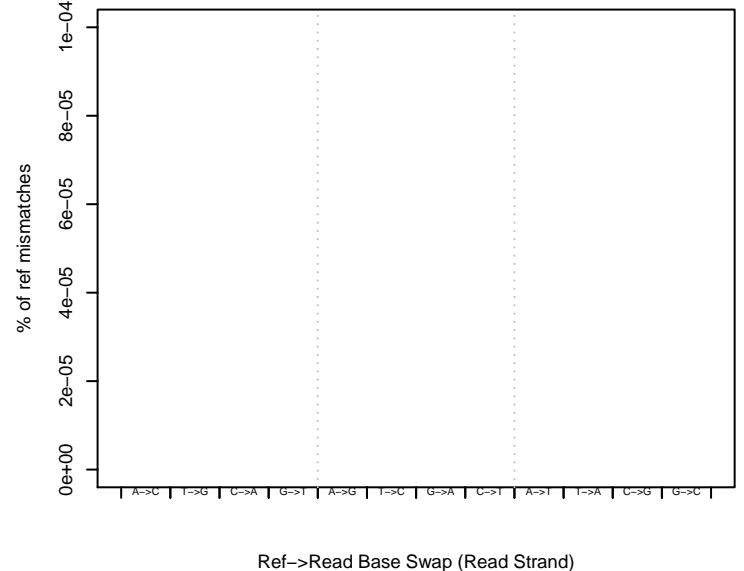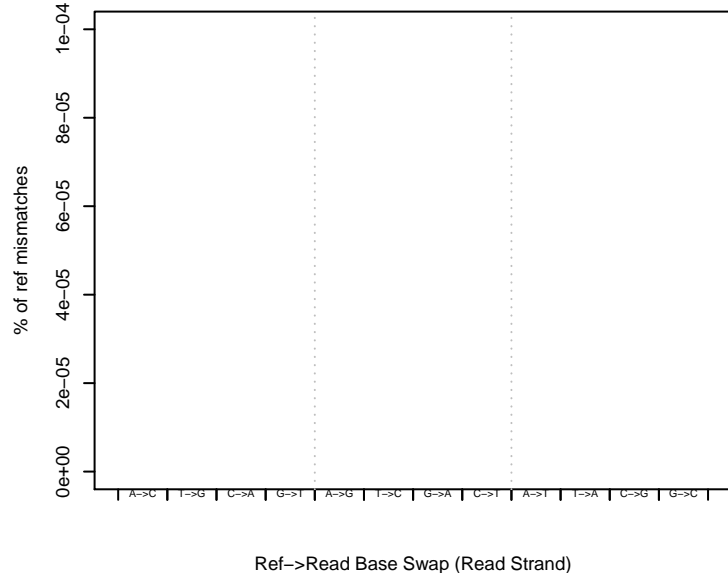
ad

Cumulative Gene Assignment Diversity
With Sample srpk3_hom_ttnb_wt_4 Colored by lane

Cumulative % of total reads
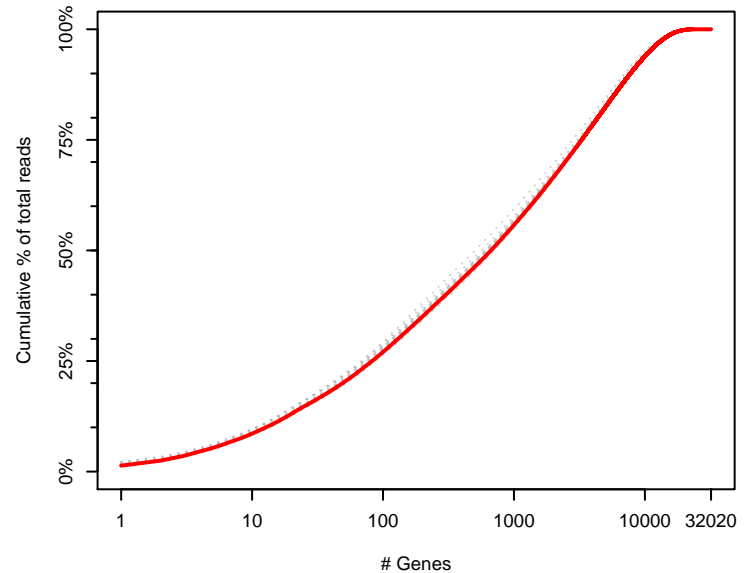
Genes

ae — Gene–Body Coverage
With Sample srpk3_hom_ttnb_wt_4 Colored by lane
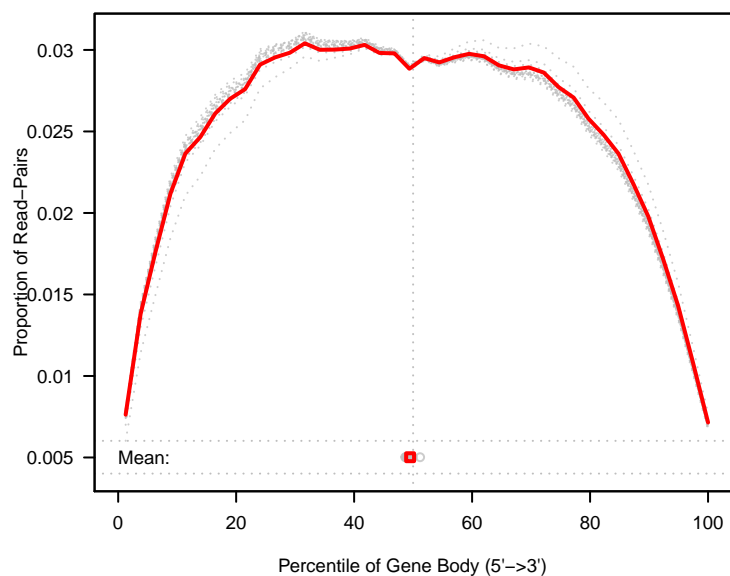
af — Gene–Body Coverage, Upper Middle Quartile Genes
With Sample srpk3_hom_ttnb_wt_4 Colored by lane

ag — Gene–Body Coverage, Low Expression Genes
With Sample srpk3_hom_ttnb_wt_4 Colored by lane

ah — Read Mapping Location Rates
With Sample srpk3_hom_ttnb_wt_4 Colored by lane

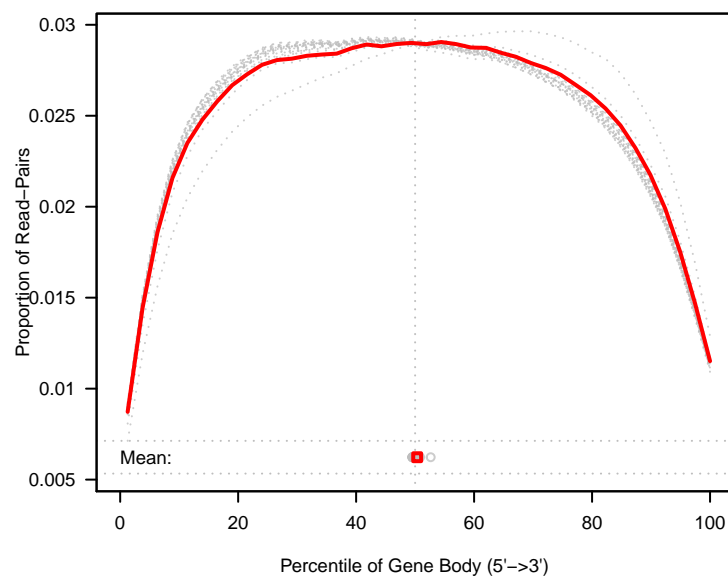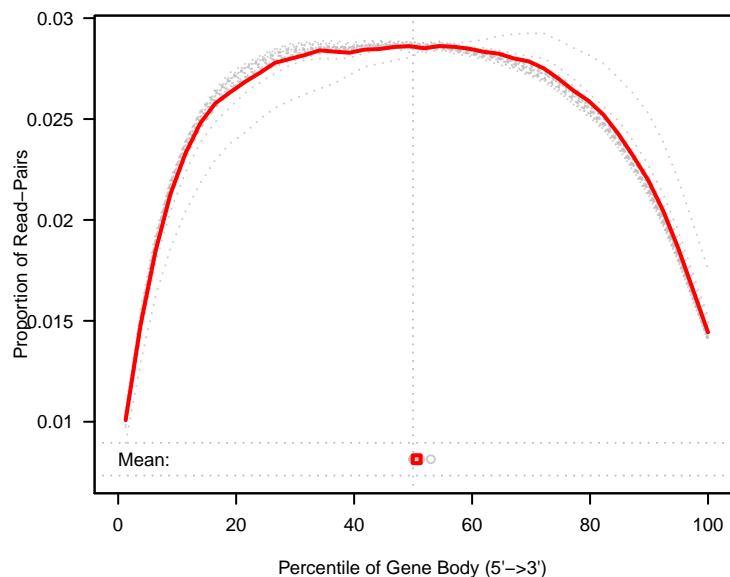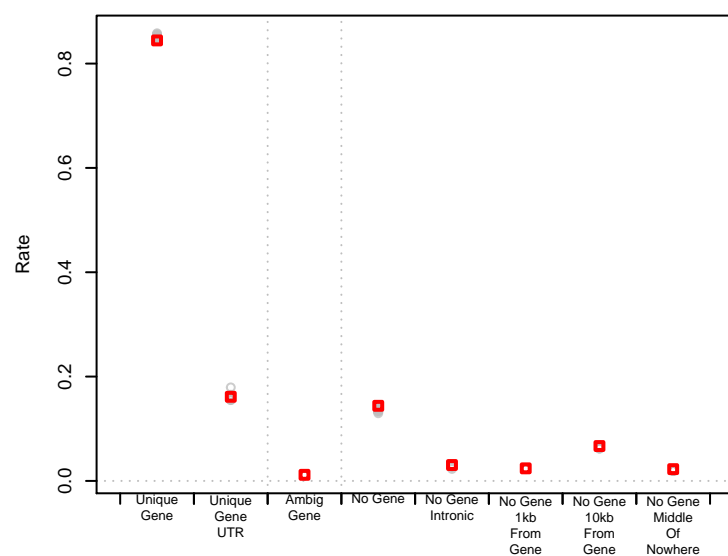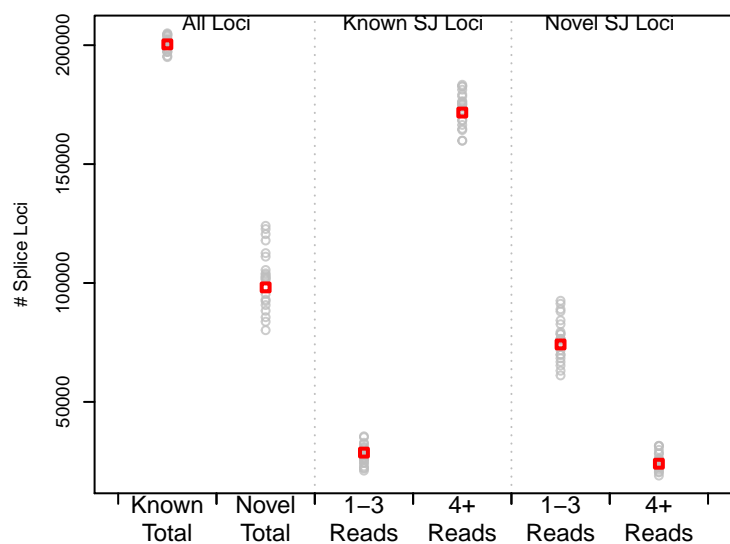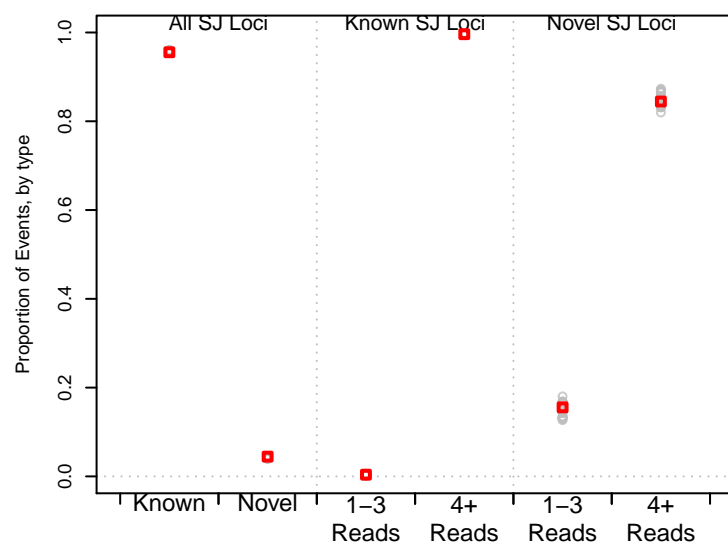**ai** — # Observed Splice Junction Loci, by type
With Sample srpk3_hom_ttnb_wt_4 Colored by lane

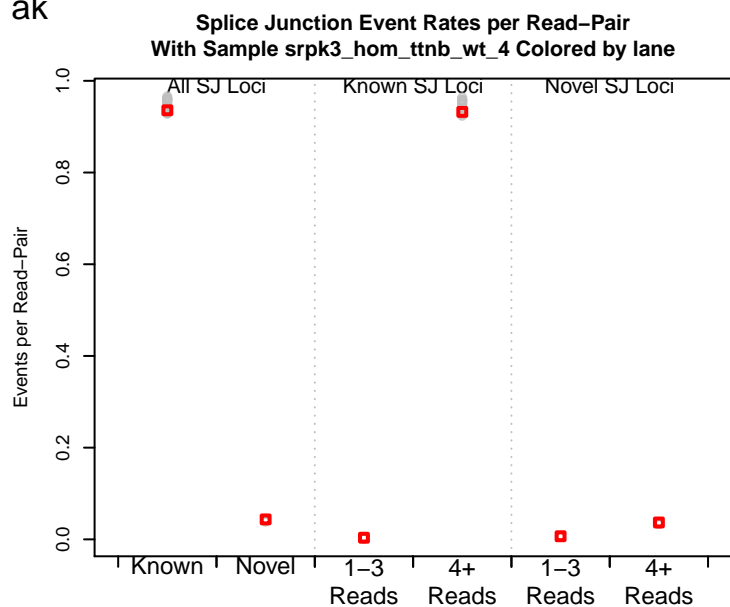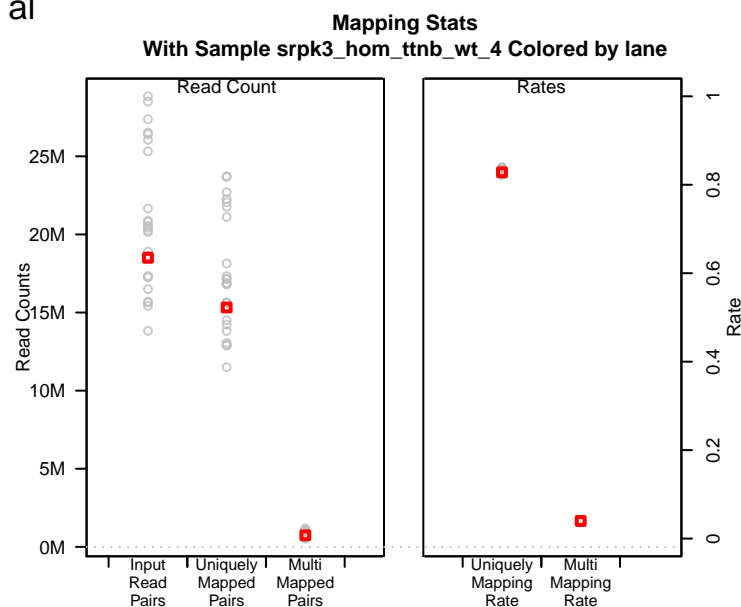**aj** — Breakdown of Splice Junction Events, by type
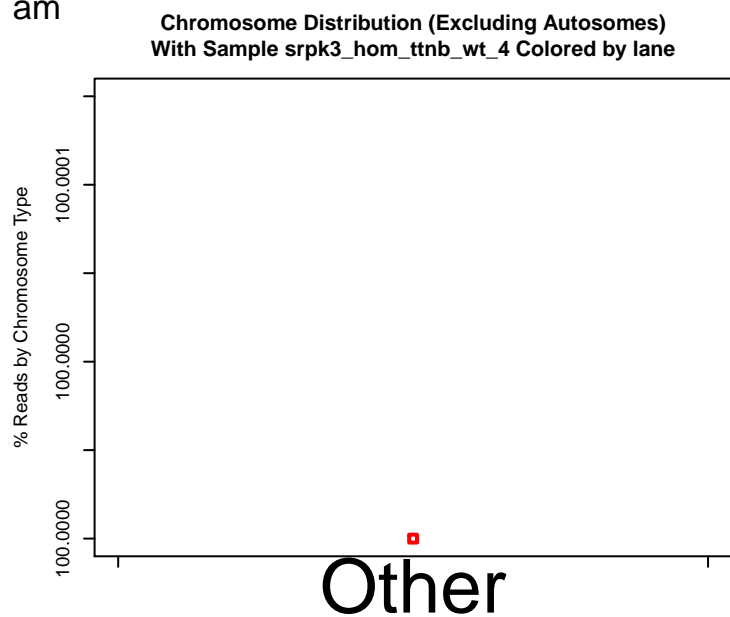With Sample srpk3_hom_ttnb_wt_4 Colored by lane

ak

Splice Junction Event Rates per Read-Pair
With Sample srpk3_hom_ttnb_wt_4 Colored by lane

Events per Read-Pair

All SJ Loci   Known SJ Loci   Novel SJ Loci

Known   Novel   1-3 Reads   4+ Reads   1-3 Reads   4+ Reads

al

Mapping Stats
With Sample srpk3_hom_ttnb_wt_4 Colored by lane

Read Count   Rates

Read Counts   Rate

Input Read Pairs   Uniquely Mapped Pairs   Multi Mapped Pairs   Uniquely Mapping Rate   Multi Mapping Rate

am

Chromosome Distribution (Excluding Autosomes)
With Sample srpk3_hom_ttnb_wt_4 Colored by lane

% Reads by Chromosome Type

Other

an

Normalization Factors
With Sample srpk3_hom_ttnb_wt_4 Colored by lane

Normalization Factor

Total Count   Geometric (DESeq)   TMM (edgeR Default)   UQ (edgeR)   RLE (edgeR)

ao

Normalization Factors vs Total-Count Normalization
With Sample srpk3_hom_ttnb_wt_4 Colored by lane

Alt vs TC ratio

Geometric (DESeq)   TMM (edgeR Default)   UQ (edgeR)   RLE (edgeR)

ap

Strandedness Test
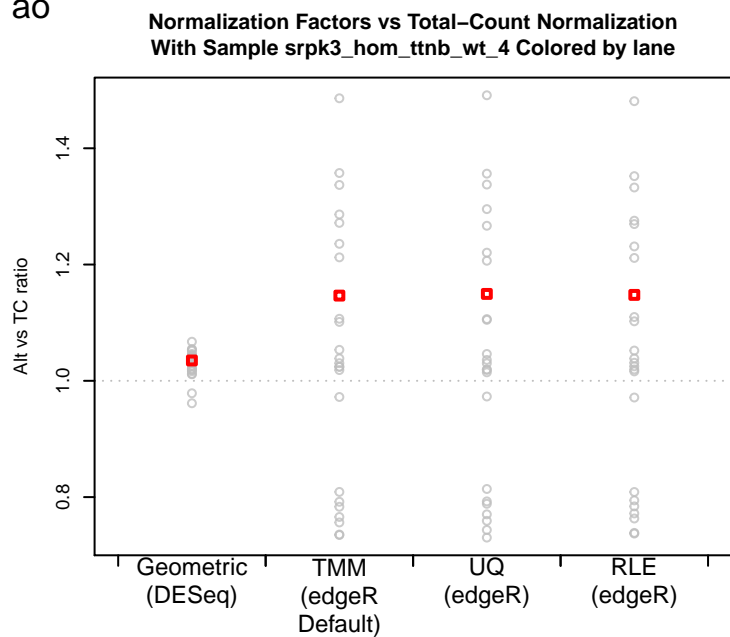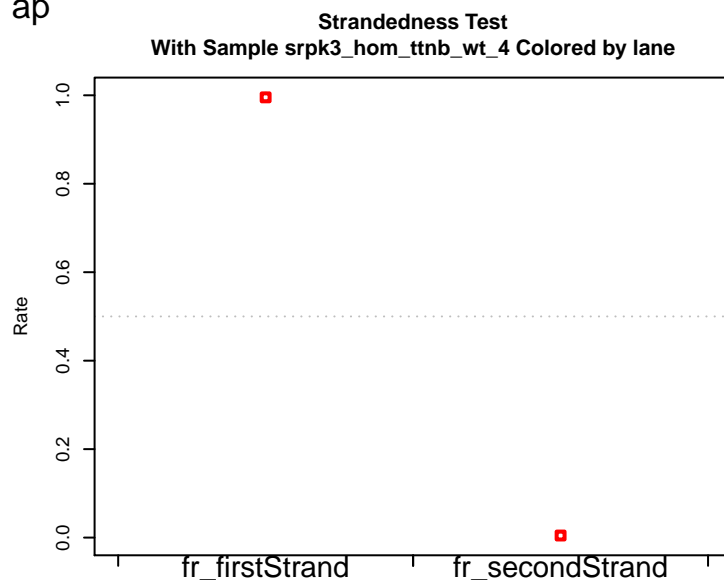**With Sample srpk3_hom_ttnb_wt_4 Colored by lane**
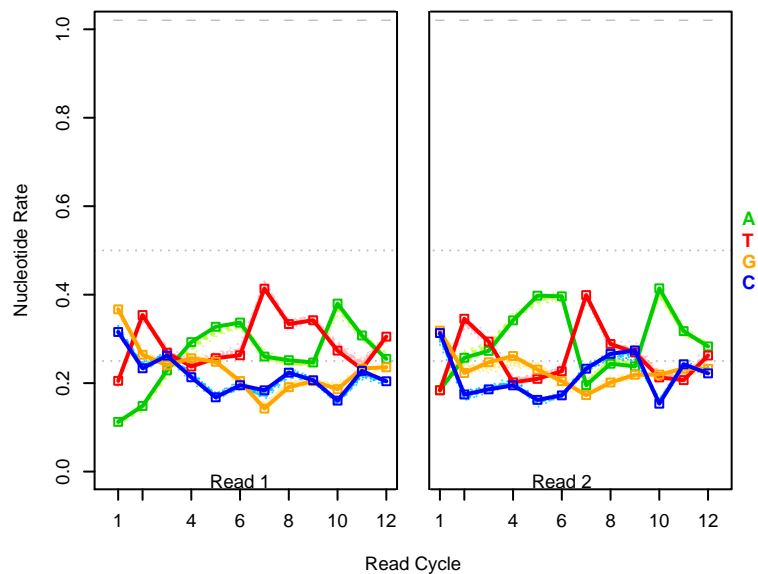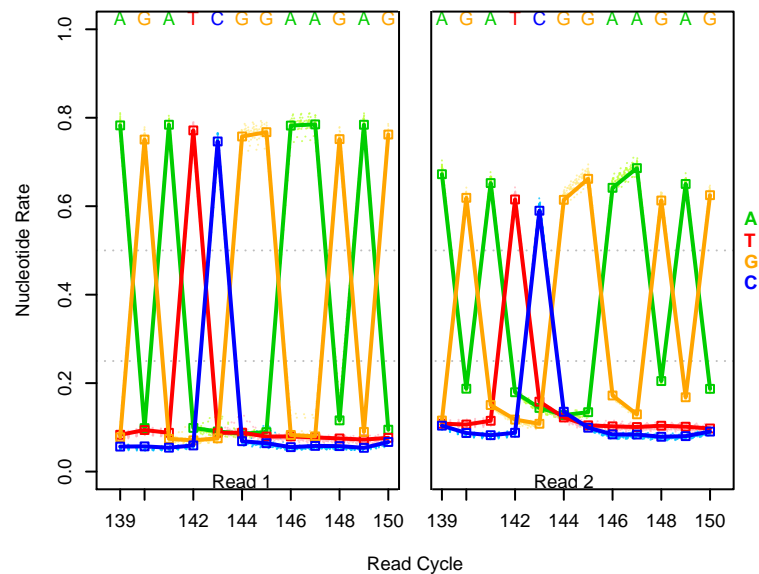
Rate

fr_firstStrand   fr_secondStrand

aq

Nucleotide Rate by Cycle, Leading Clipped bases (12)
With Sample srpk3_hom_ttnb_wt_4 in Bold

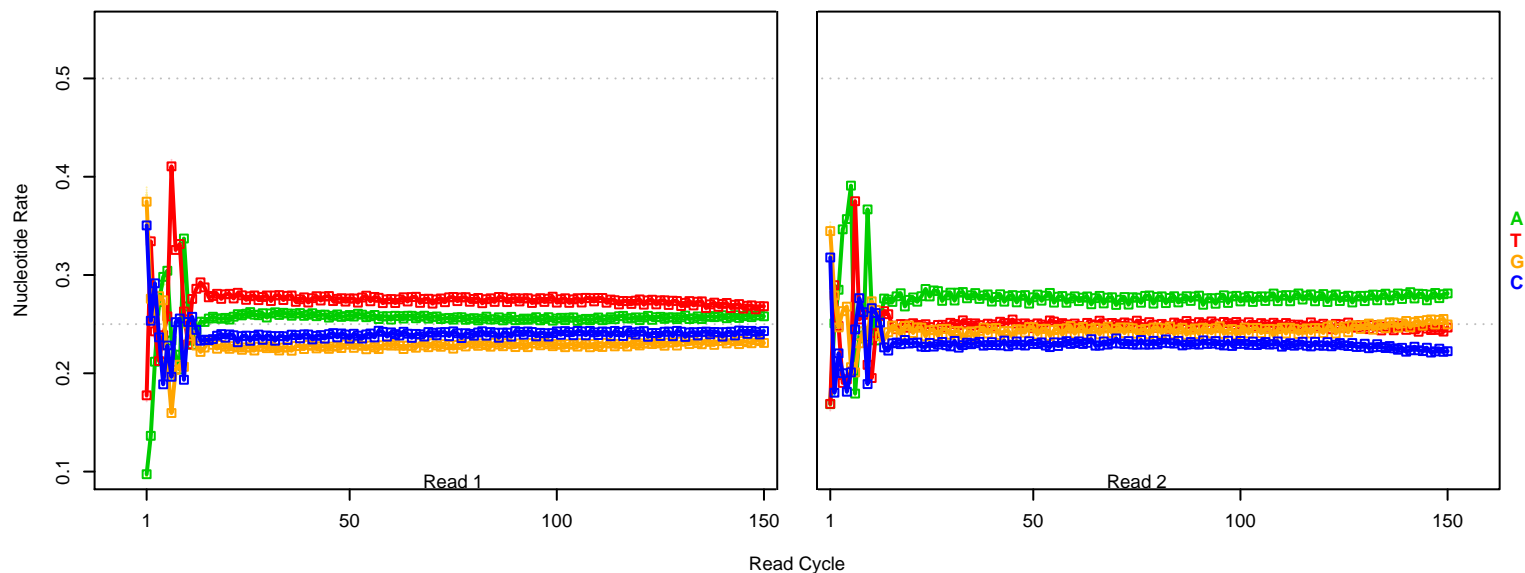**ar**

Nucleotide Rate by Cycle, Trailing Clipped bases (12)
With Sample srpk3_hom_ttnb_wt_4 in Bold

as

Raw Nucleotide Rate by Cycle
With Sample srpk3_hom_ttnb_wt_4 in Bold

at

Nucleotide Rate by Cycle, Aligned bases only
With Sample srpk3_hom_ttnb_wt_4 in Bold