a

Sample Highlight:
srpk3_wt_ttnb_het_3
Colored by Lane

— □ — UNKNOWN
· · ○ · · Other Samples

b

Minimum Phred Quality Score
With Sample srpk3_wt_ttnb_het_3 Colored by lane
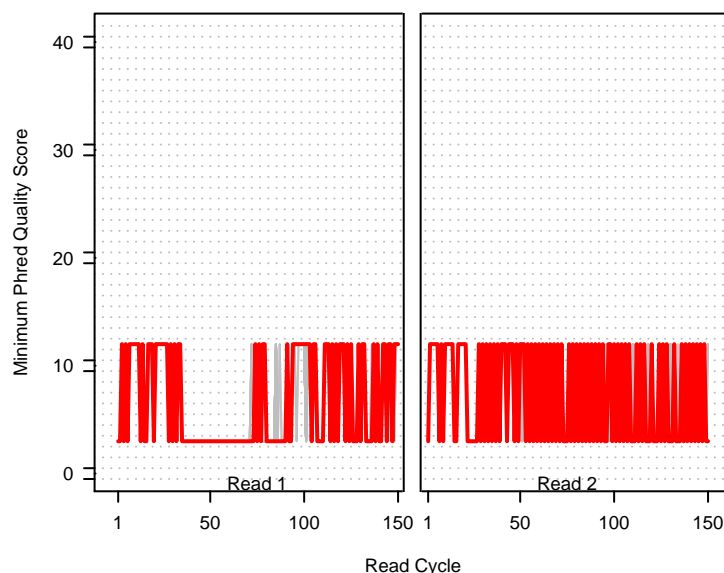
Minimum Phred Quality Score

Read 1   Read 2

Read Cycle

c

Lower Quartile Phred Quality Score
With Sample srpk3_wt_ttnb_het_3 Colored by lane

Lower Quartile Phred Quality Score

Read 1   Read 2

Read Cycle

d

Median Phred Quality Score
With Sample srpk3_wt_ttnb_het_3 Colored by lane

Median Phred Quality Score

Read 1   Read 2

Read Cycle

e

Upper Quartile Phred Quality Score
With Sample srpk3_wt_ttnb_het_3 Colored by lane

Upper Quartile Phred Quality Score

Read 1   Read 2

Read Cycle

f

Maximum Phred Quality Score
With Sample srpk3_wt_ttnb_het_3 Colored by lane

Maximum Phred Quality Score

Read 1   Read 2
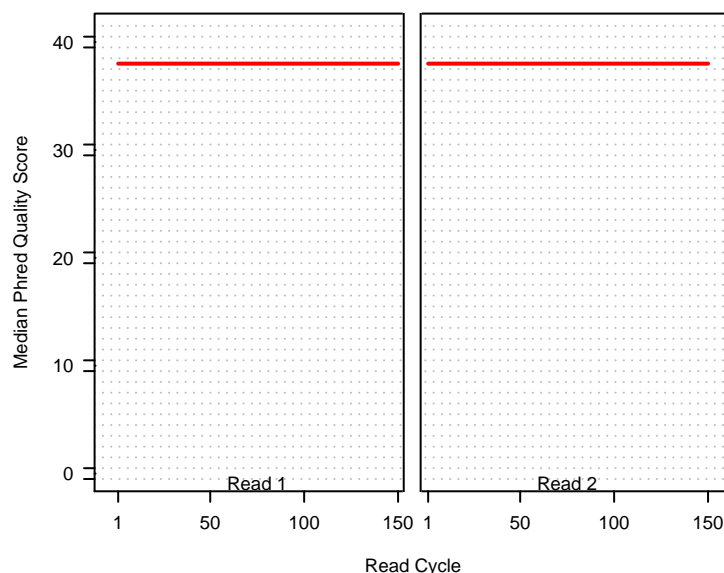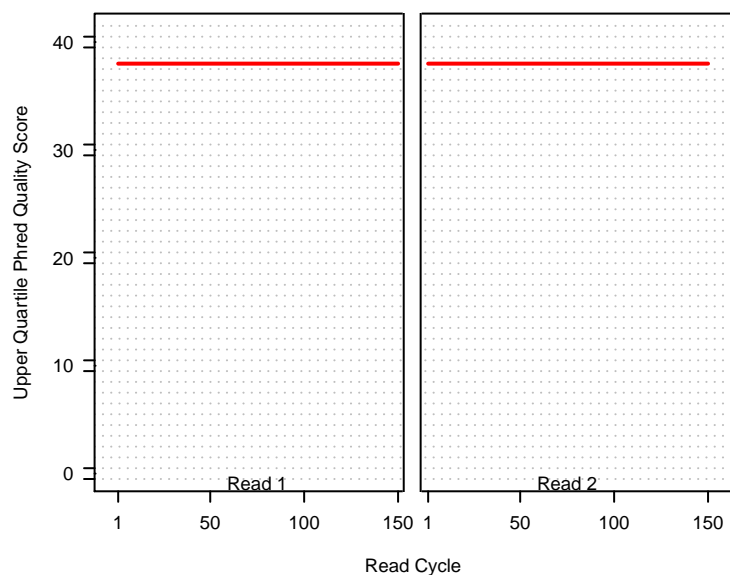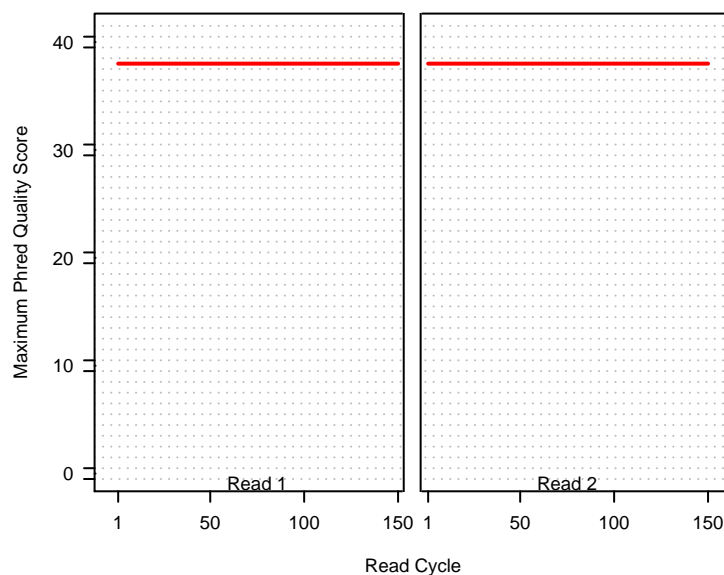
Read Cycle

g Alignment Clipping Rate, by read cycle
With Sample srpk3_wt_ttnb_het_3 Colored by lane
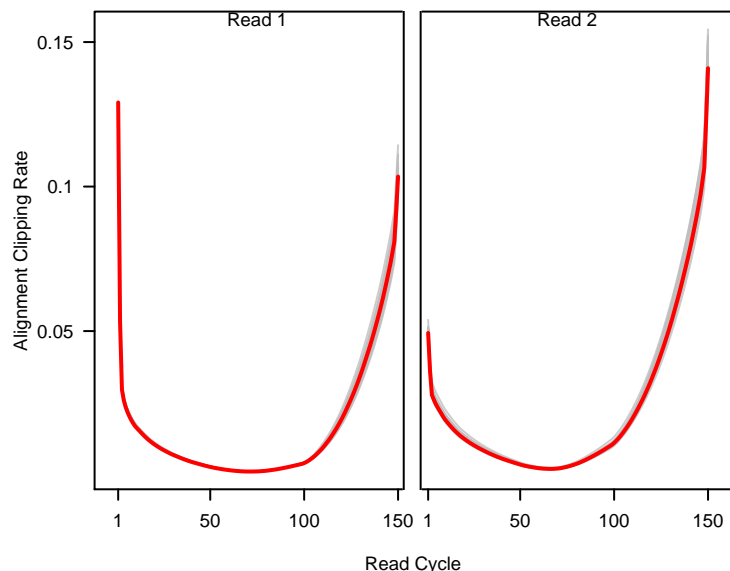
h Deletion Rate, by read cycle
With Sample srpk3_wt_ttnb_het_3 Colored by lane

i Insertion Rate, by read cycle
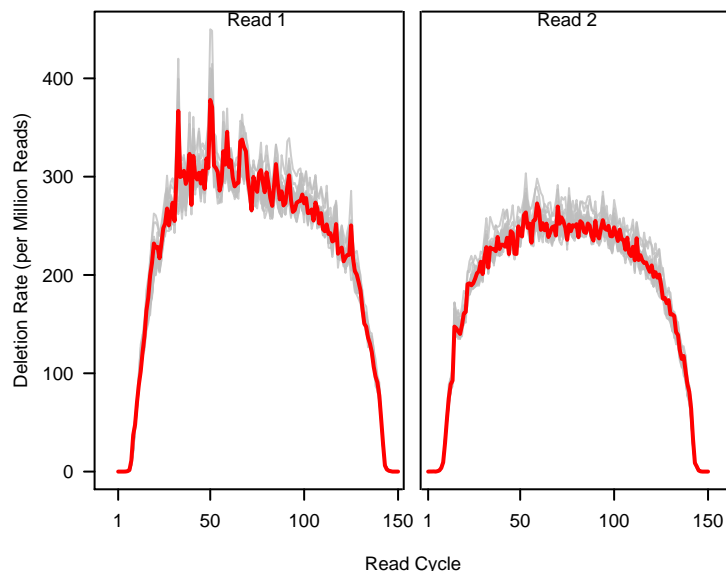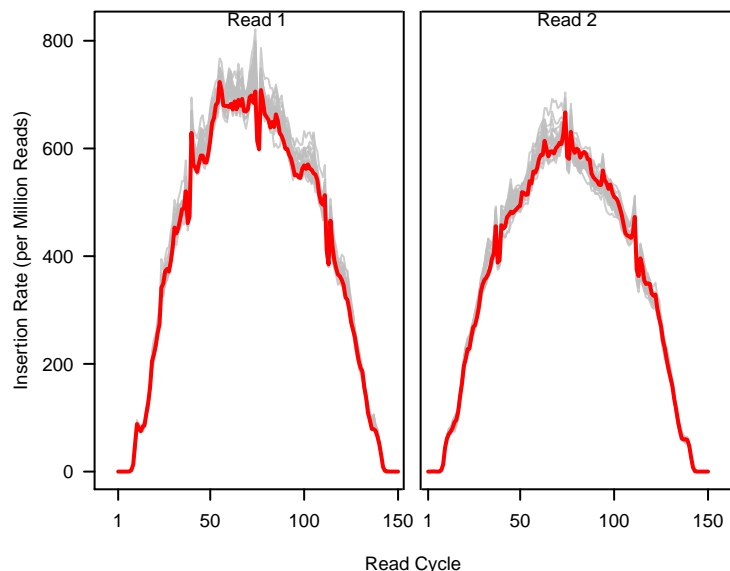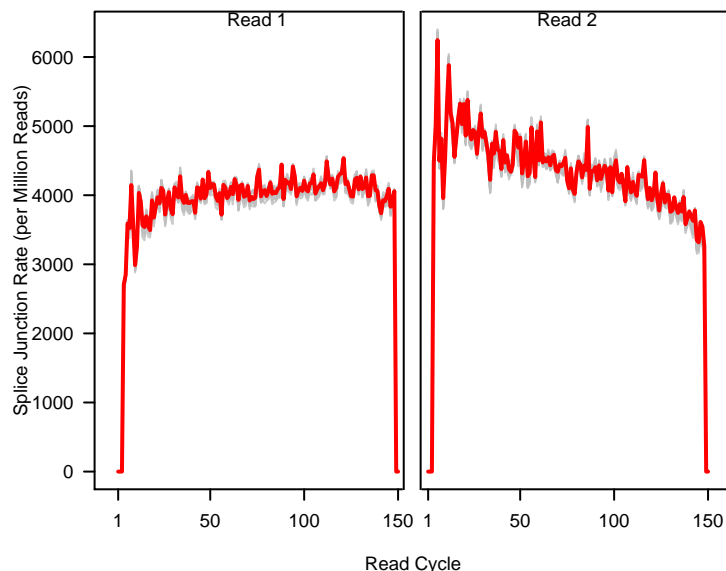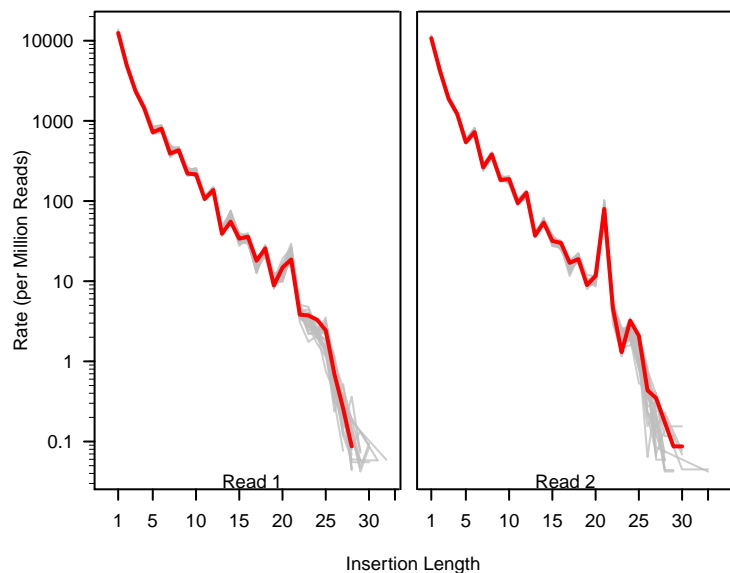With Sample srpk3_wt_ttnb_het_3 Colored by lane

j Splice Junction Rate, by read cycle
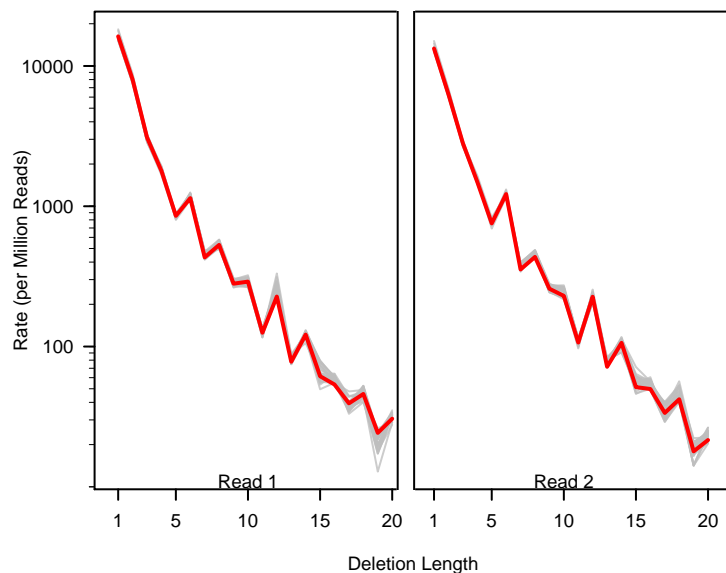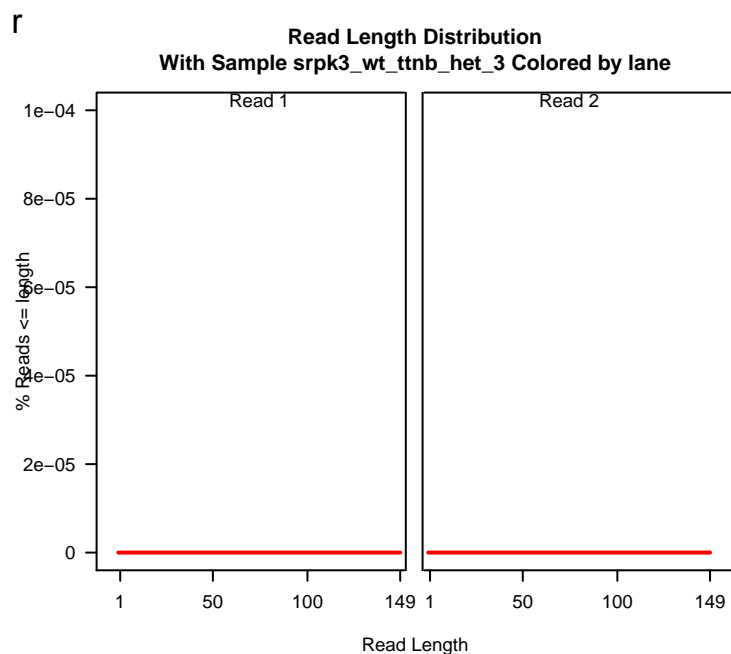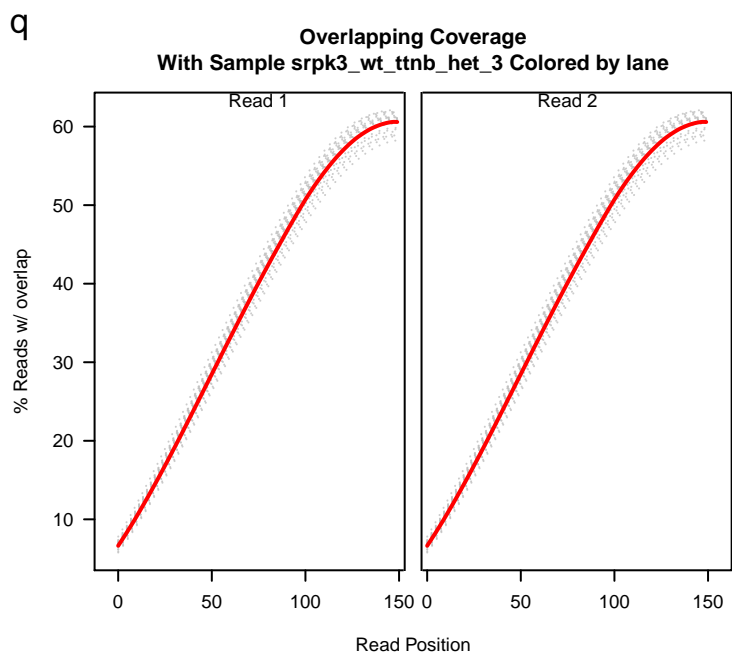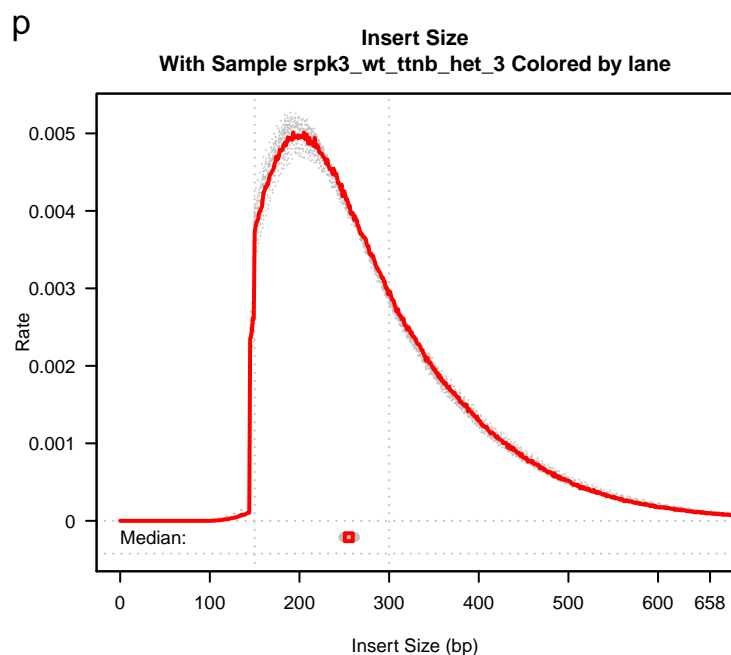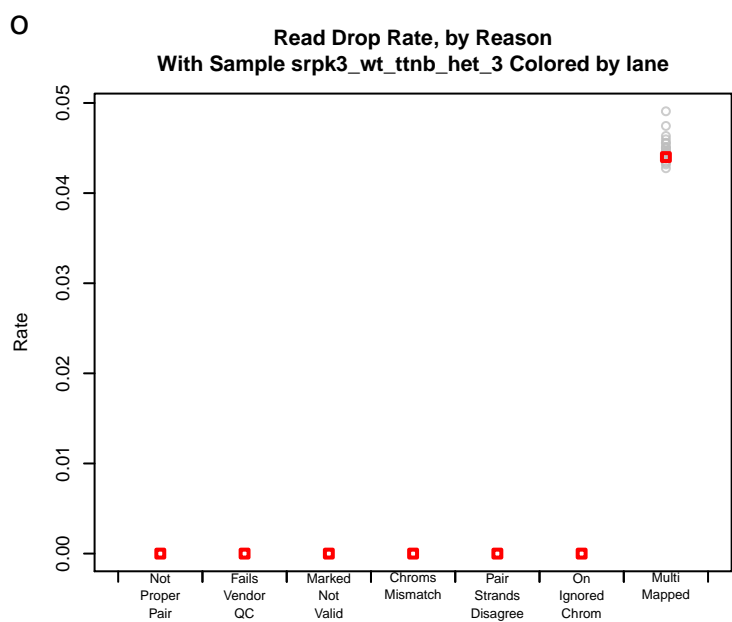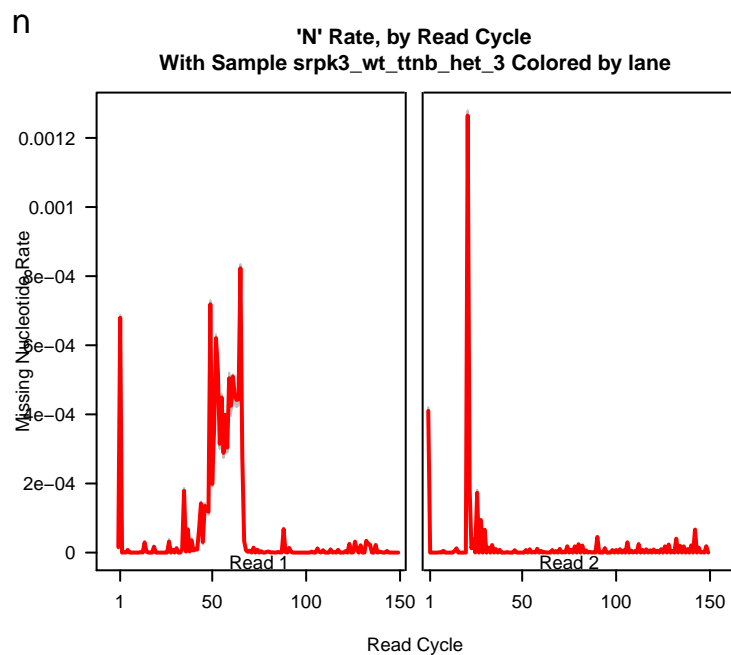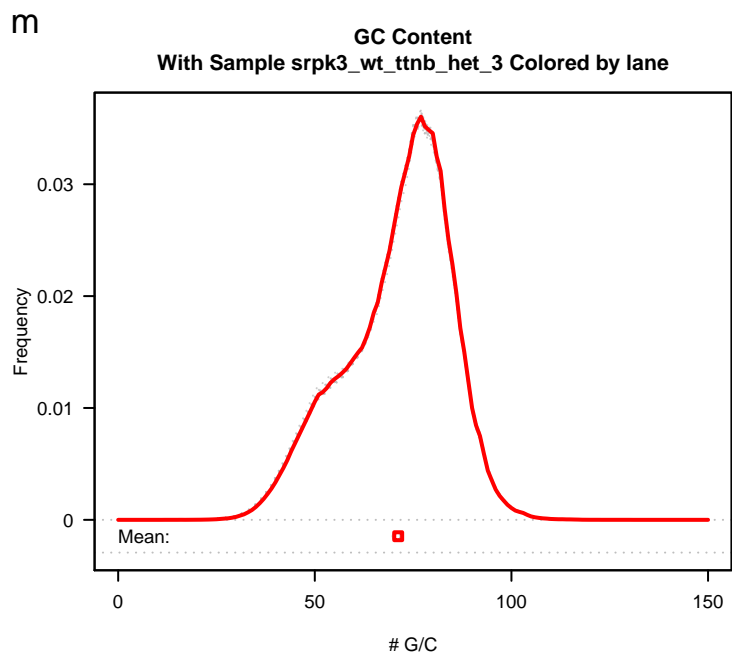With Sample srpk3_wt_ttnb_het_3 Colored by lane

k Insertion Length Distribution
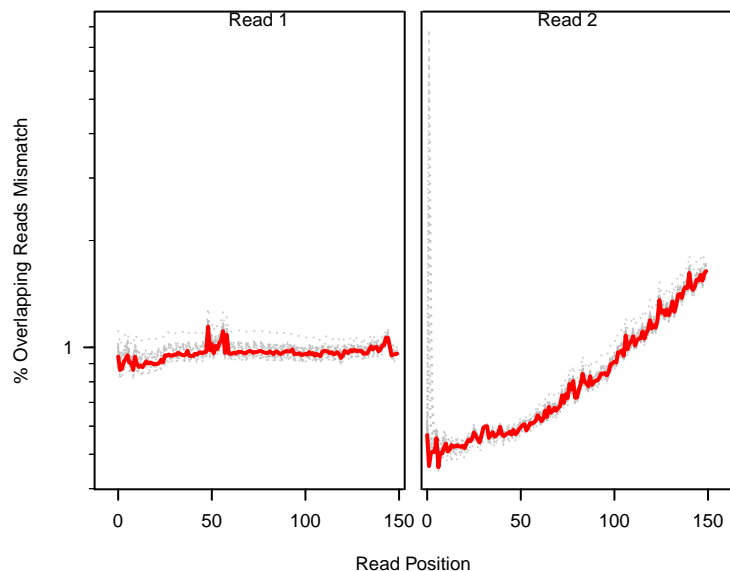With Sample srpk3_wt_ttnb_het_3 Colored by lane

l Deletion Length Distribution
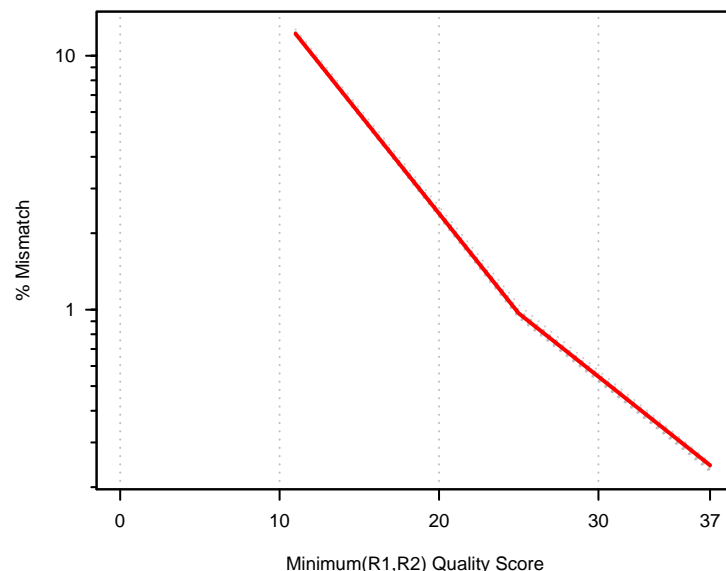With Sample srpk3_wt_ttnb_het_3 Colored by lane

m

GC Content
With Sample srpk3_wt_ttnb_het_3 Colored by lane

Frequency

Mean:

G/C

n

'N' Rate, by Read Cycle
With Sample srpk3_wt_ttnb_het_3 Colored by lane

Missing Nucleotide Rate

Read 1   Read 2

Read Cycle

o

Read Drop Rate, by Reason
With Sample srpk3_wt_ttnb_het_3 Colored by lane

Rate

Not Proper Pair | Fails Vendor QC | Marked Not Valid | Chroms Mismatch | Pair Strands Disagree | On Ignored Chrom | Multi Mapped

p

Insert Size
With Sample srpk3_wt_ttnb_het_3 Colored by lane

Rate

Median:

Insert Size (bp)

q

Overlapping Coverage
With Sample srpk3_wt_ttnb_het_3 Colored by lane

% Reads w/ overlap

Read 1   Read 2

Read Position

r

Read Length Distribution
With Sample srpk3_wt_ttnb_het_3 Colored by lane

% Reads <= length

Read 1   Read 2

Read Length

s

Overlap Mismatch by Read Cycle
With Sample srpk3_wt_ttnb_het_3 Colored by lane

Read 1   Read 2

% Overlapping Reads Mismatch

Read Position

t

Overlapping Mismatch by Min Qual
With Sample srpk3_wt_ttnb_het_3 Colored by lane

% Mismatch

Minimum(R1,R2) Quality Score

u

Overlap Mismatch by Read Qual
With Sample srpk3_wt_ttnb_het_3 Colored by lane

Read 1   Read 2

% Mismatch

Quality Score
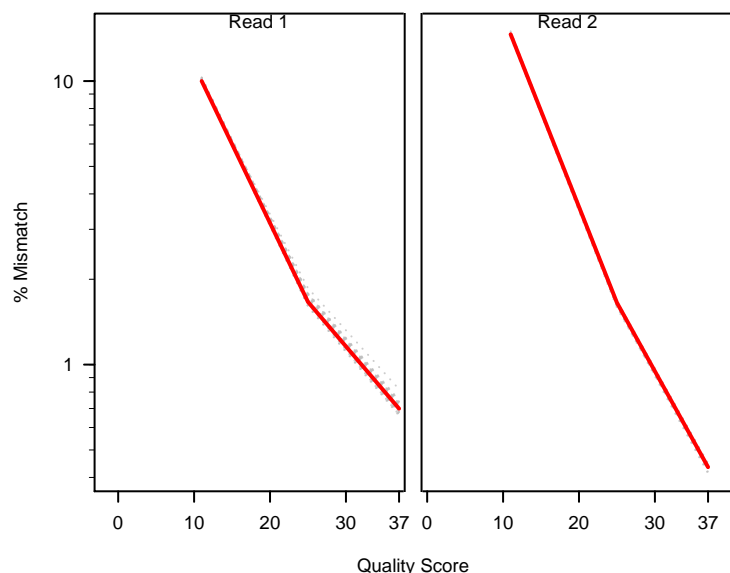
V

Overlap Mismatch Combinations
With Sample srpk3_wt_ttnb_het_3 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_wt_ttnb_het_3 Colored by lane

% Read−Pairs

Mismatching Base−Pairs
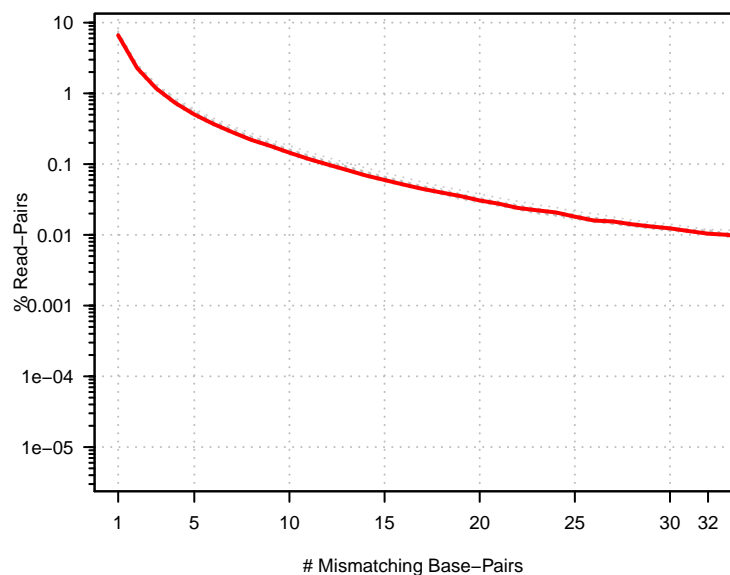
X

Overlap Mismatch Pairs At Phred == 41
With Sample srpk3_wt_ttnb_het_3 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_wt_ttnb_het_3 Colored by lane
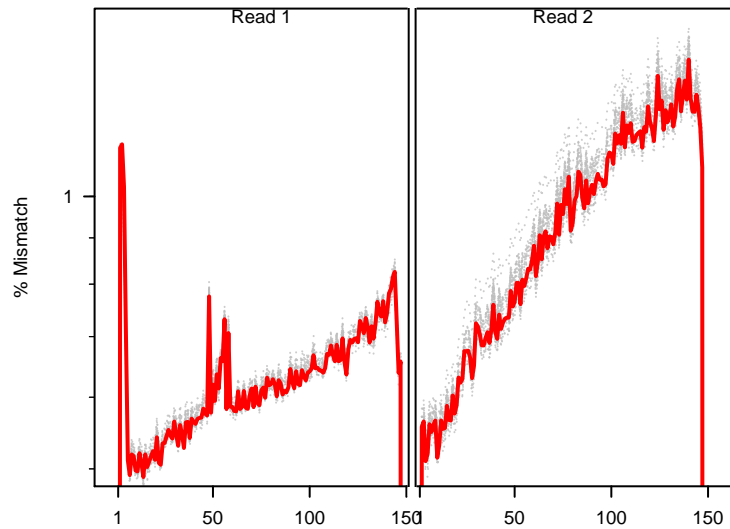
z

Reference Mismatch by Read Qual
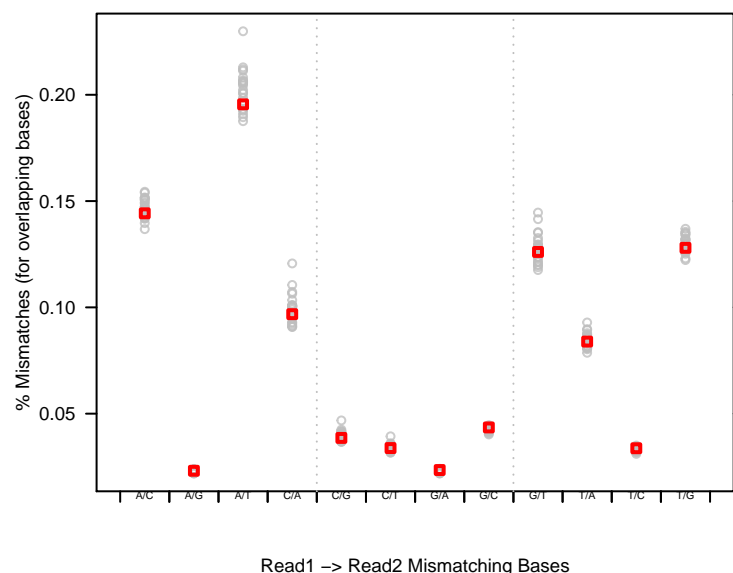### With Sample srpk3_wt_ttnb_het_3 Colored by lane

aa

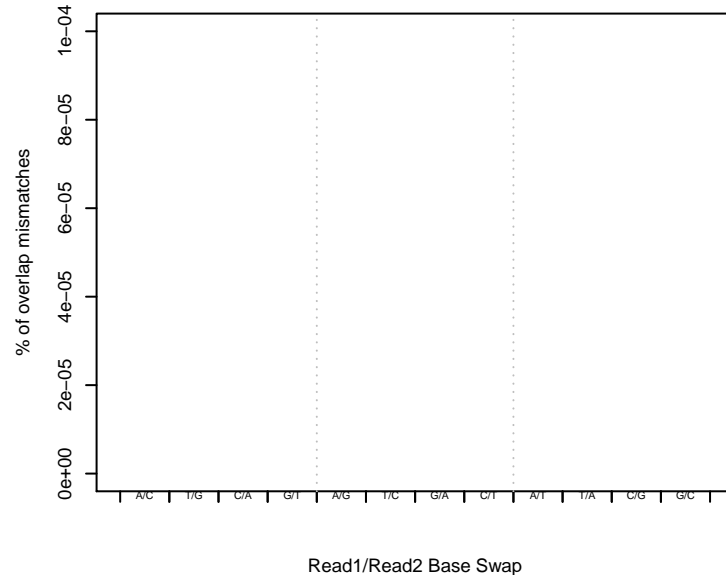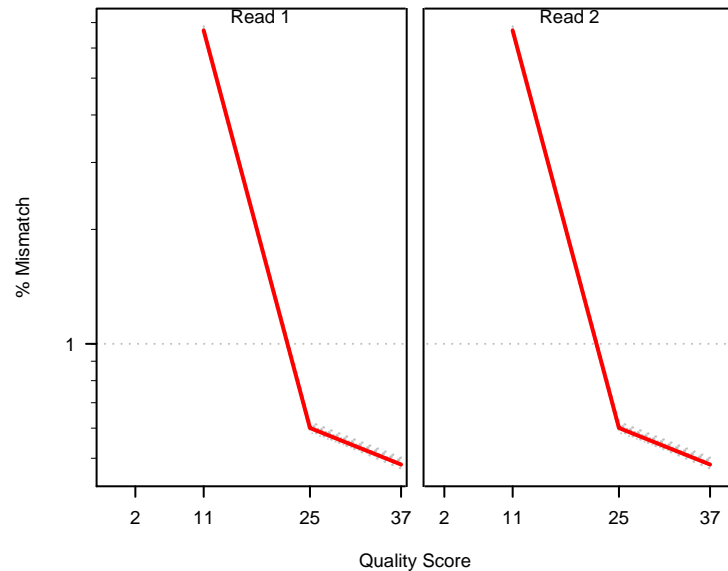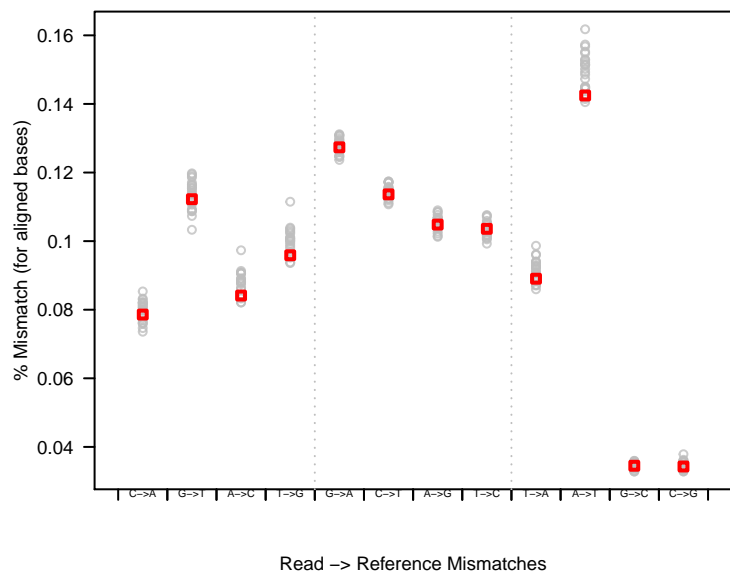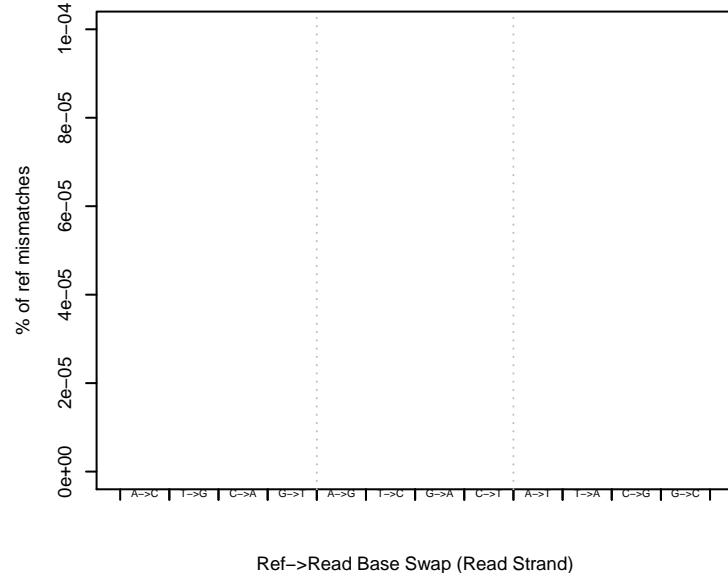## Reference Mismatch Combinations
With Sample srpk3_wt_ttnb_het_3 Colored by lane
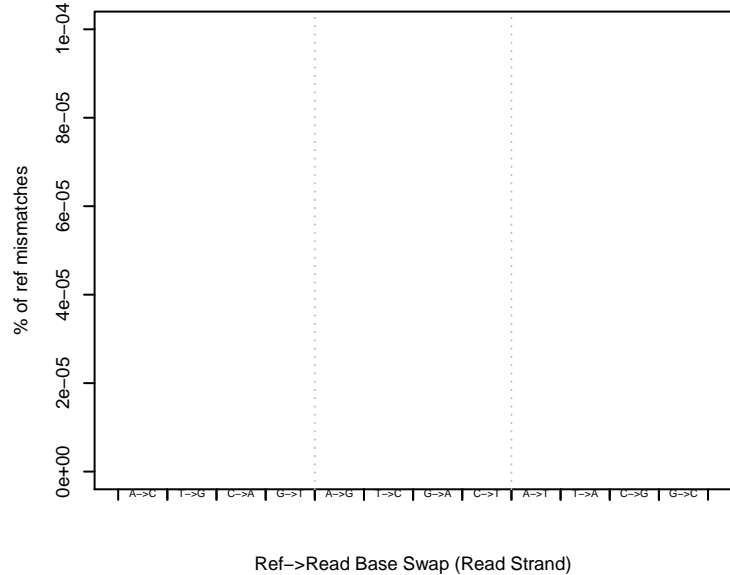

ab

R1 Ref Mismatches At Phred == 41
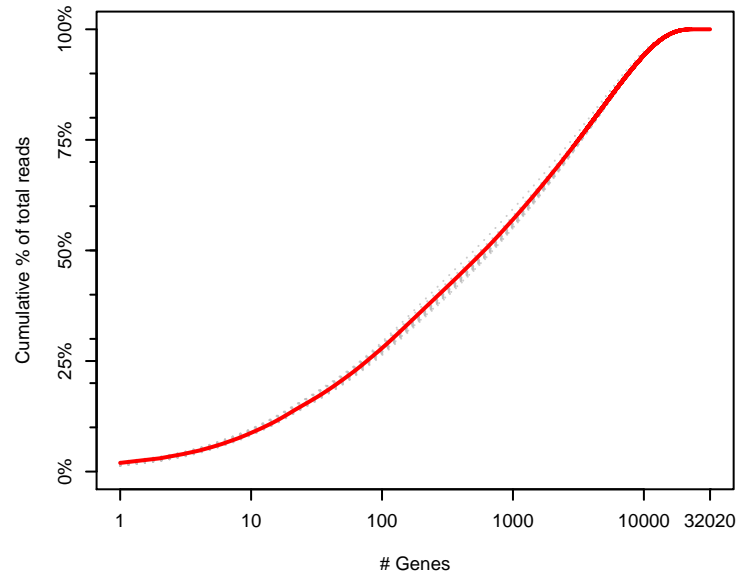### With Sample srpk3_wt_ttnb_het_3 Colored by lane

ac

R2 Ref Mismatches At Phred == 41
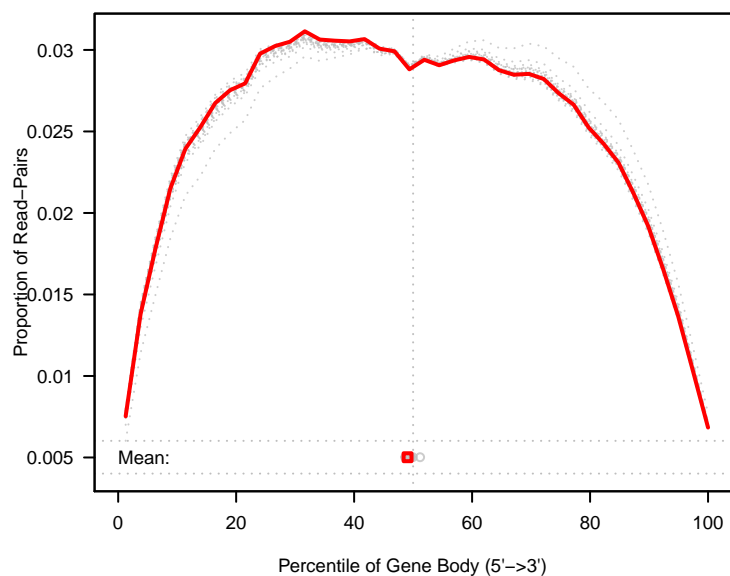### With Sample srpk3_wt_ttnb_het_3 Colored by lane

ad

Cumulative Gene Assignment Diversity
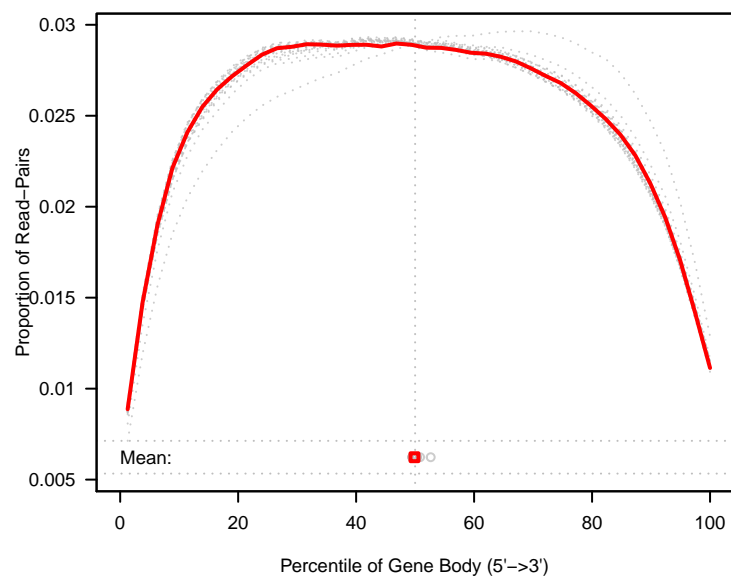### With Sample srpk3_wt_ttnb_het_3 Colored by lane

ae

Gene−Body Coverage
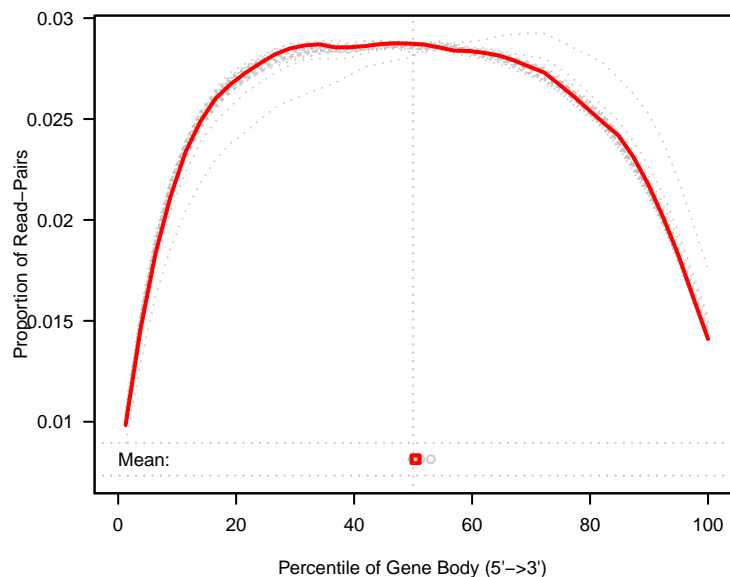**With Sample srpk3_wt_ttnb_het_3 Colored by lane**

Proportion of Read-Pairs

Percentile of Gene Body (5'−>3')

Mean:

af

Gene−Body Coverage, Upper Middle Quartile Genes
With Sample srpk3_wt_ttnb_het_3 Colored by lane

Proportion of Read-Pairs

Percentile of Gene Body (5'−>3')

Mean:

ag

Gene−Body Coverage, Low Expression Genes
With Sample srpk3_wt_ttnb_het_3 Colored by lane

Proportion of Read-Pairs

Percentile of Gene Body (5'−>3')

Mean:

ah

Read Mapping Location Rates
With Sample srpk3_wt_ttnb_het_3 Colored by lane

Rate

Unique Gene | Unique Gene UTR | Ambig Gene | No Gene | No Gene Intronic | No Gene 1kb From Gene | No Gene 10kb From Gene | No Gene Middle Of Nowhere
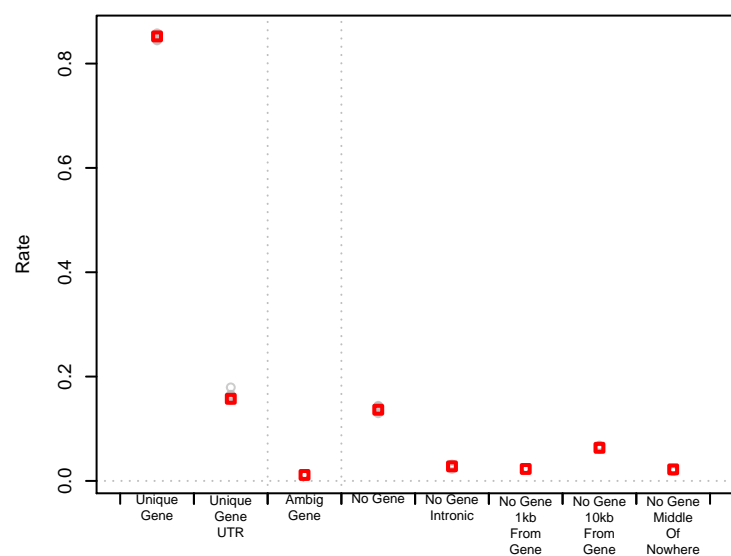
ai

 # Observed Splice Junction Loci, by type
With Sample srpk3_wt_ttnb_het_3 Colored by lane

Splice Loci

All Loci | Known SJ Loci | Novel SJ Loci

Known Total | Novel Total | 1−3 Reads | 4+ Reads | 1−3 Reads | 4+ Reads
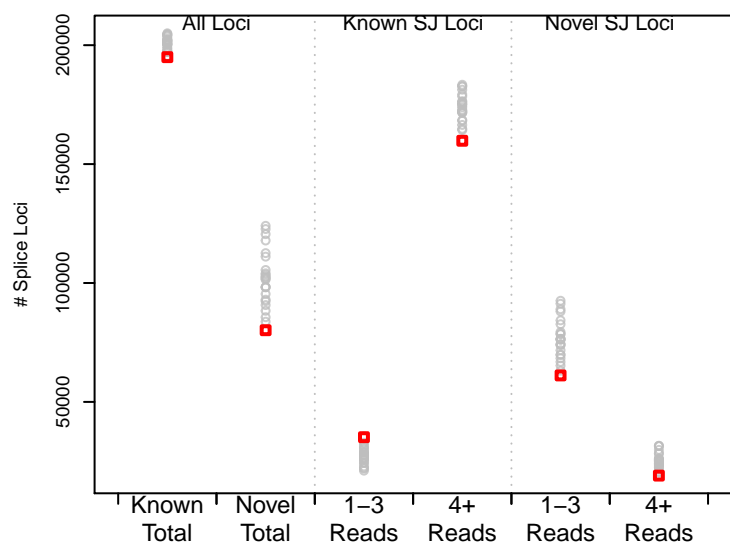
aj

Breakdown of Splice Junction Events, by type
With Sample srpk3_wt_ttnb_het_3 Colored by lane

Proportion of Events, by type

All SJ Loci | Known SJ Loci | Novel SJ Loci

Known | Novel | 1−3 Reads | 4+ Reads | 1−3 Reads | 4+ Reads

ak — Splice Junction Event Rates per Read−Pair
With Sample srpk3_wt_ttnb_het_3 Colored by lane

al — Mapping Stats
With Sample srpk3_wt_ttnb_het_3 Colored by lane

am — Chromosome Distribution (Excluding Autosomes)
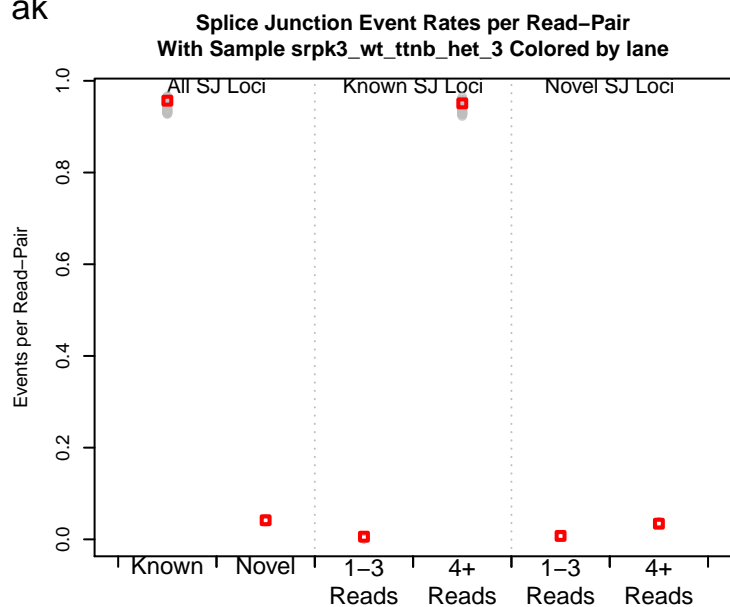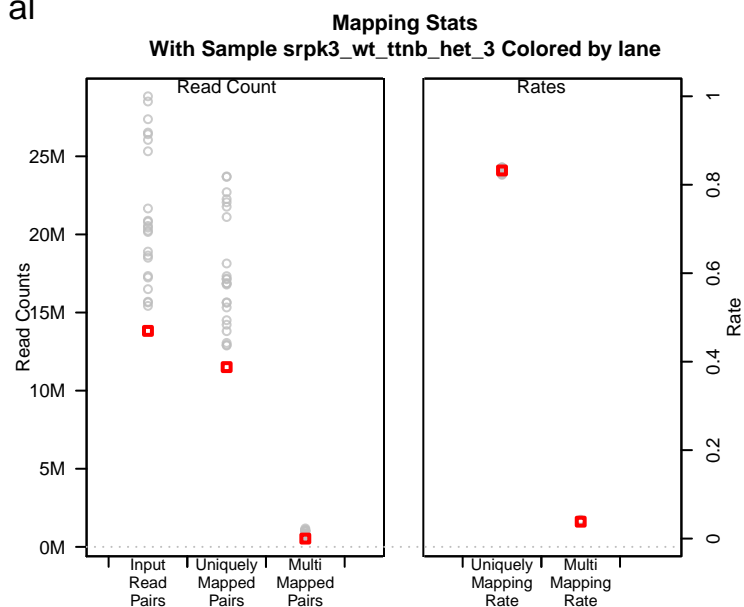With Sample srpk3_wt_ttnb_het_3 Colored by lane

an — Normalization Factors
With Sample srpk3_wt_ttnb_het_3 Colored by lane

ao — Normalization Factors vs Total−Count Normalization
With Sample srpk3_wt_ttnb_het_3 Colored by lane

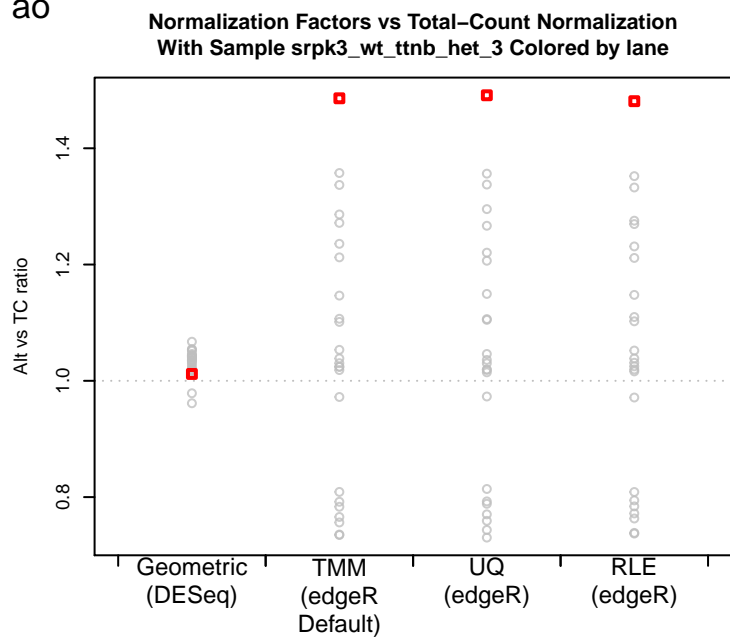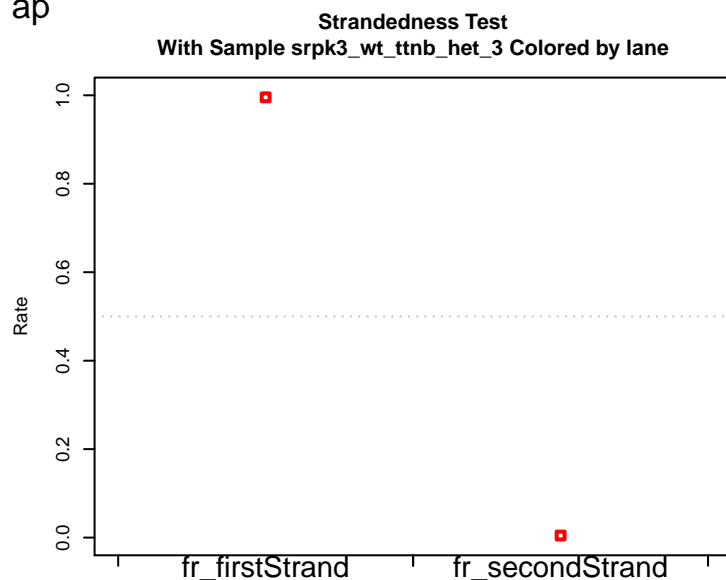**ap** — Strandedness Test
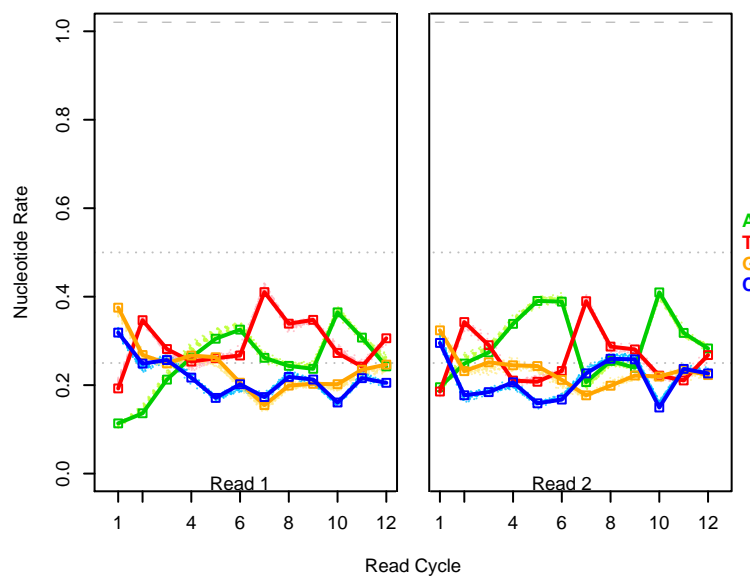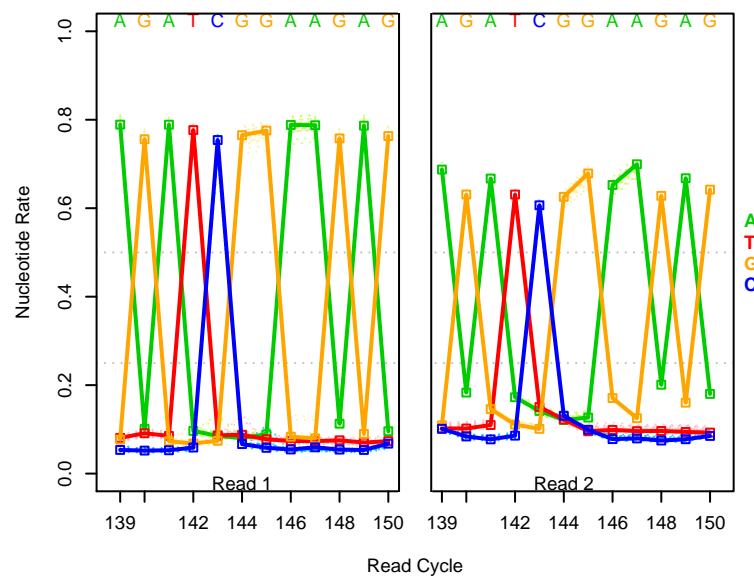With Sample srpk3_wt_ttnb_het_3 Colored by lane

aq

Nucleotide Rate by Cycle, Leading Clipped bases (12)
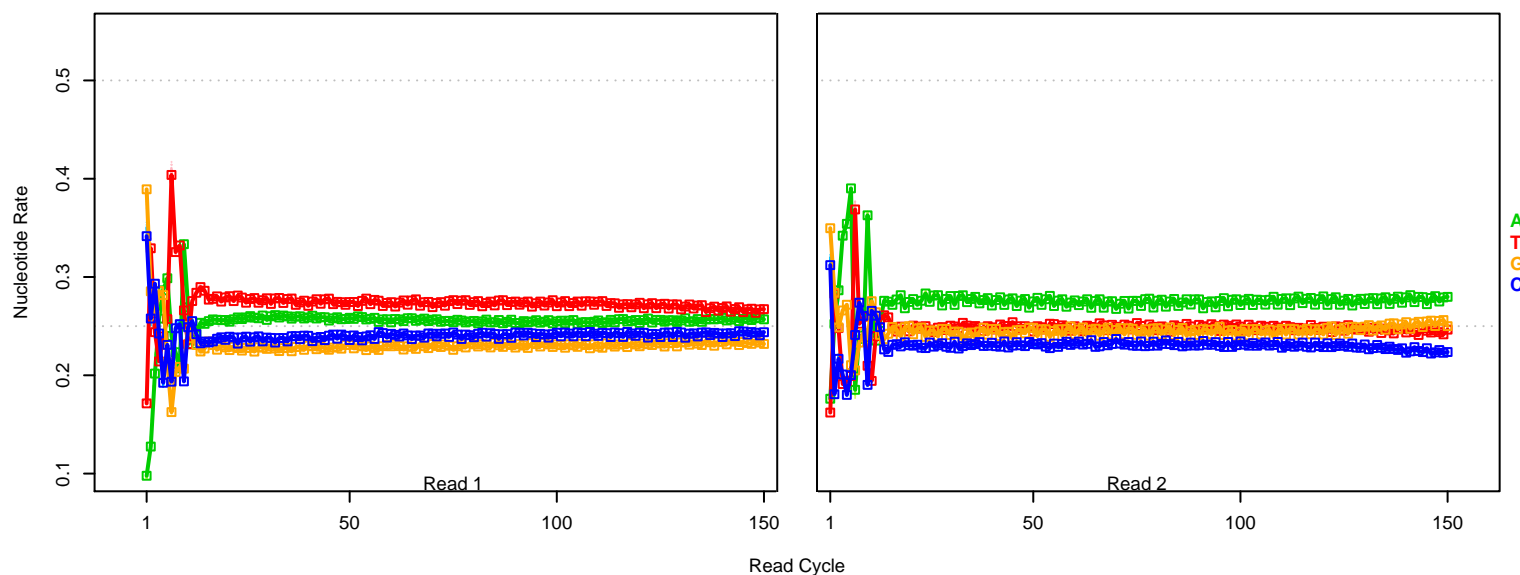With Sample srpk3_wt_ttnb_het_3 in Bold

ar

Nucleotide Rate by Cycle, Trailing Clipped bases (12)
With Sample srpk3_wt_ttnb_het_3 in Bold

as

Raw Nucleotide Rate by Cycle
With Sample srpk3_wt_ttnb_het_3 in Bold

at

Nucleotide Rate by Cycle, Aligned bases only
With Sample srpk3_wt_ttnb_het_3 in Bold