a

Sample Highlight:
srpk3_wt_ttnb_wt_3
Colored by Lane

□ — UNKNOWN
○ Other Samples

b

Minimum Phred Quality Score
With Sample srpk3_wt_ttnb_wt_3 Colored by lane
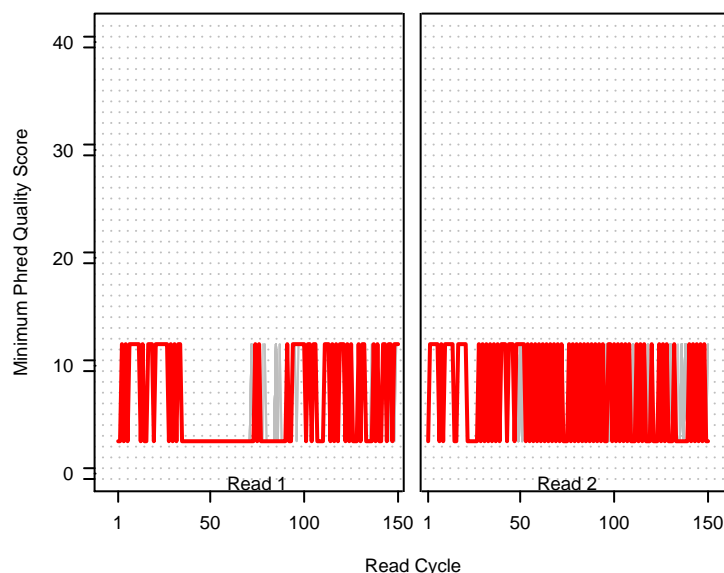
Read 1   Read 2

Read Cycle

Minimum Phred Quality Score

c

Lower Quartile Phred Quality Score
With Sample srpk3_wt_ttnb_wt_3 Colored by lane

Read 1   Read 2

Read Cycle

Lower Quartile Phred Quality Score

d

Median Phred Quality Score
With Sample srpk3_wt_ttnb_wt_3 Colored by lane

Read 1   Read 2

Read Cycle

Median Phred Quality Score

e

Upper Quartile Phred Quality Score
With Sample srpk3_wt_ttnb_wt_3 Colored by lane

Read 1   Read 2

Read Cycle

Upper Quartile Phred Quality Score

f

Maximum Phred Quality Score
With Sample srpk3_wt_ttnb_wt_3 Colored by lane

Read 1   Read 2
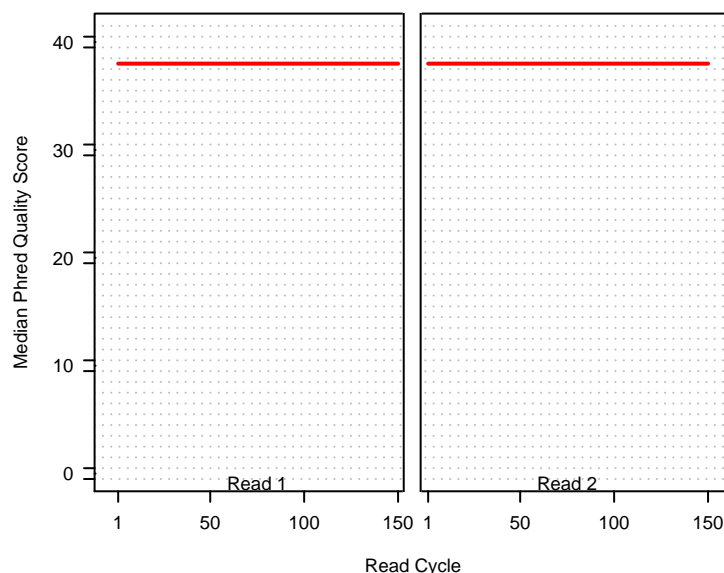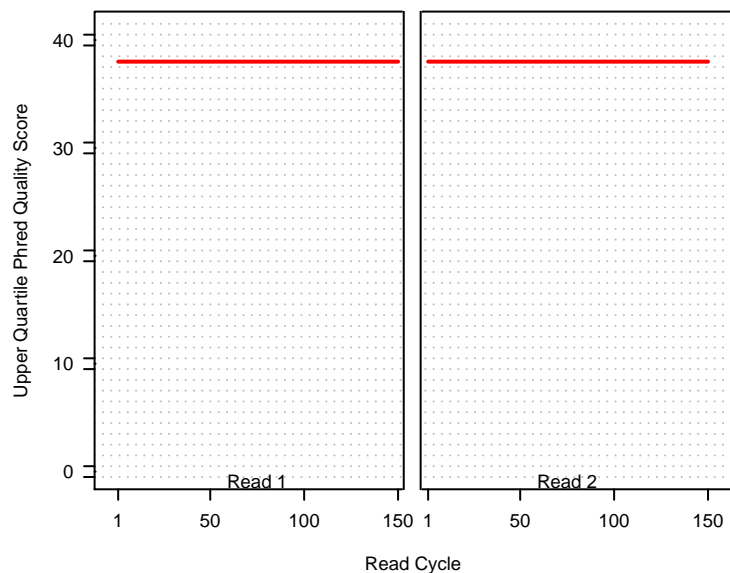
Read Cycle

Maximum Phred Quality Score
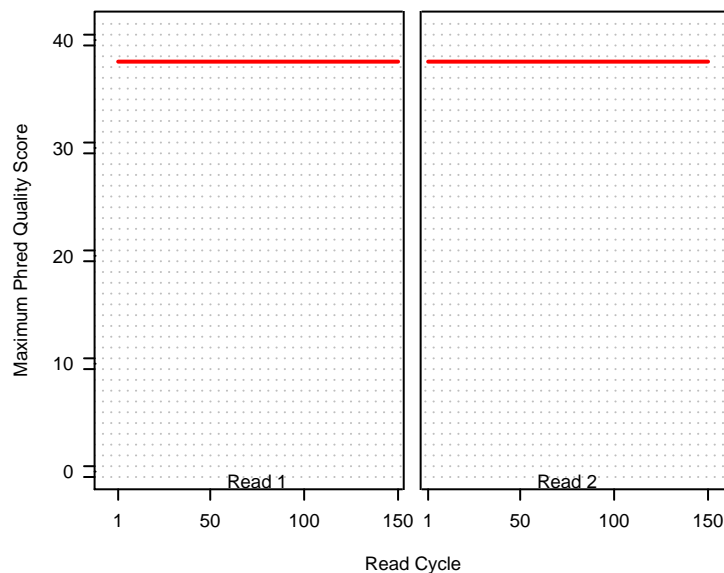
g **Alignment Clipping Rate, by read cycle**
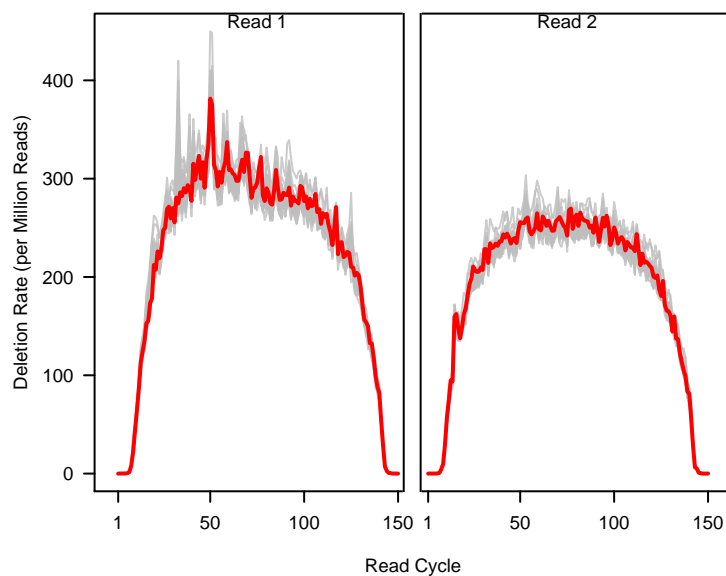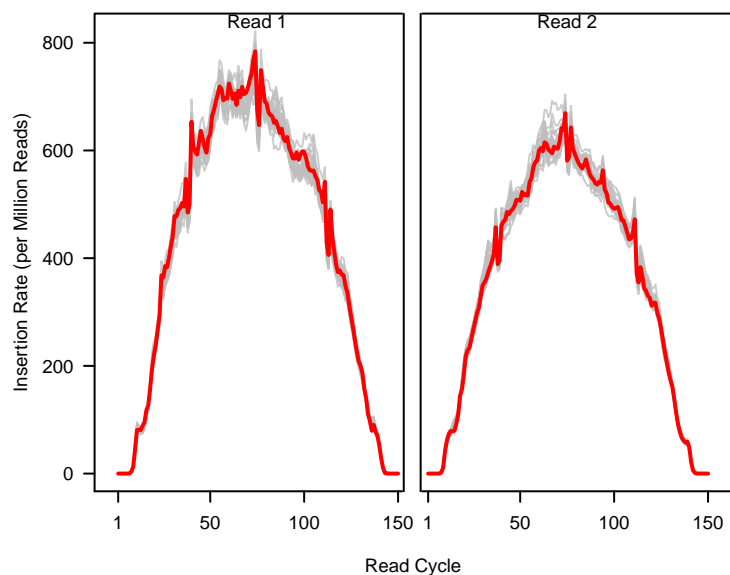**With Sample srpk3_wt_ttnb_wt_3 Colored by lane**
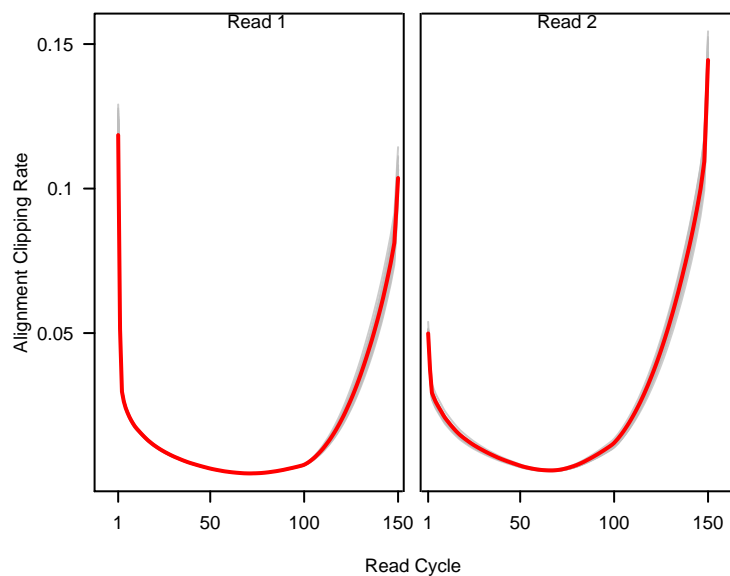
h **Deletion Rate, by read cycle**
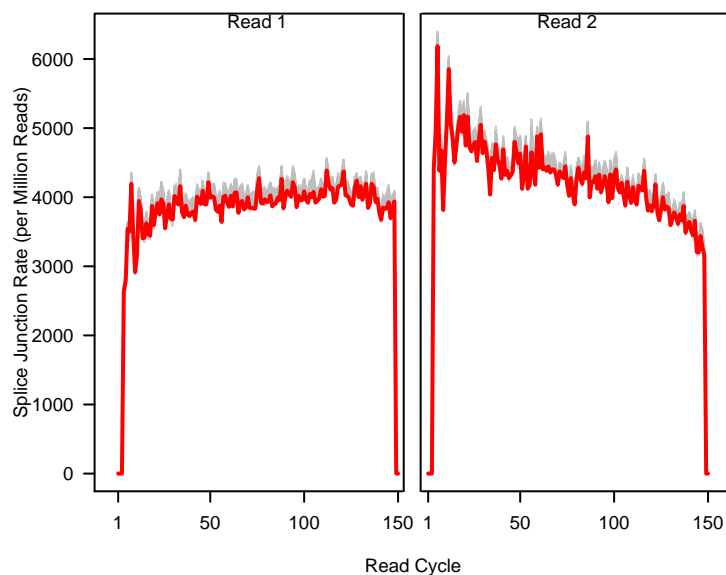**With Sample srpk3_wt_ttnb_wt_3 Colored by lane**

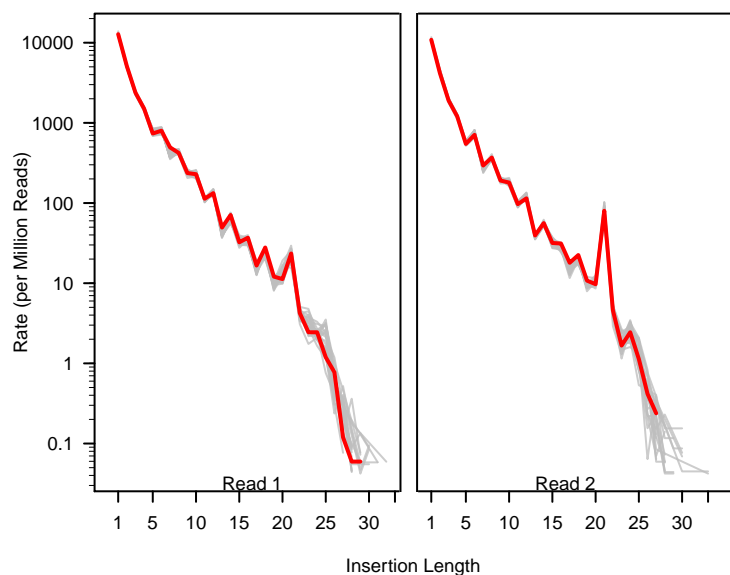i **Insertion Rate, by read cycle**
With Sample srpk3_wt_ttnb_wt_3 Colored by lane

j **Splice Junction Rate, by read cycle**
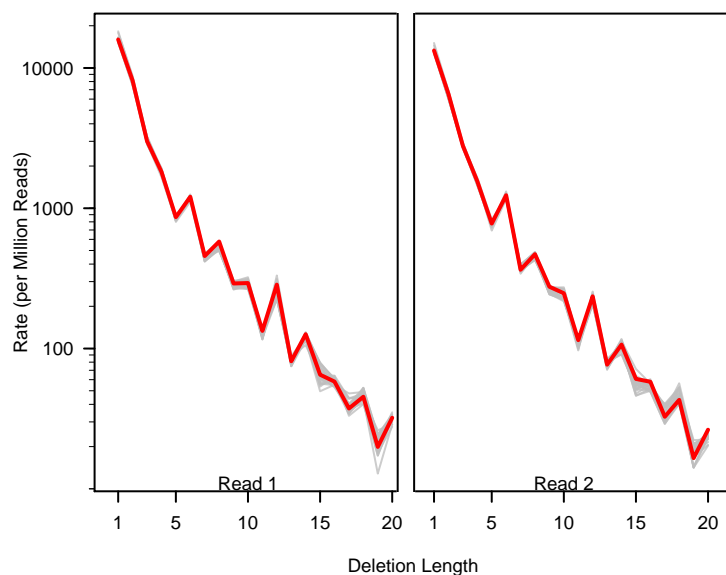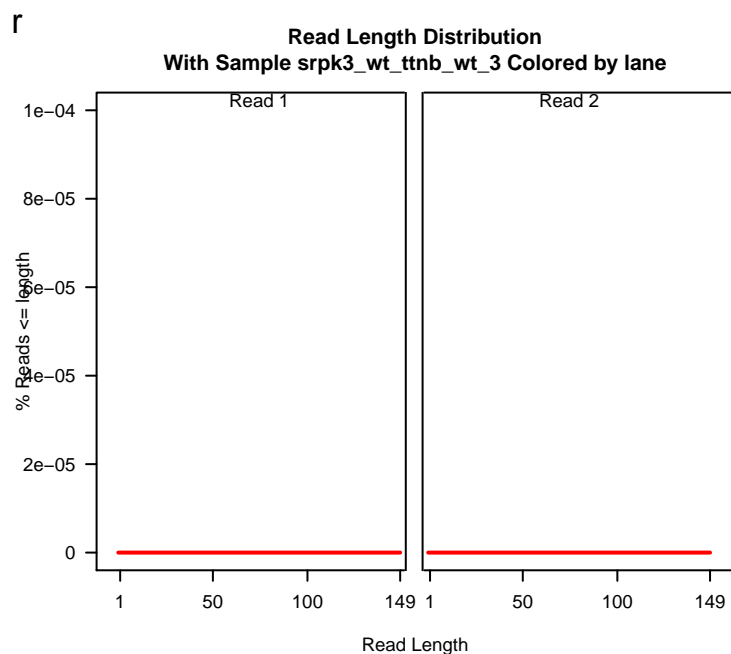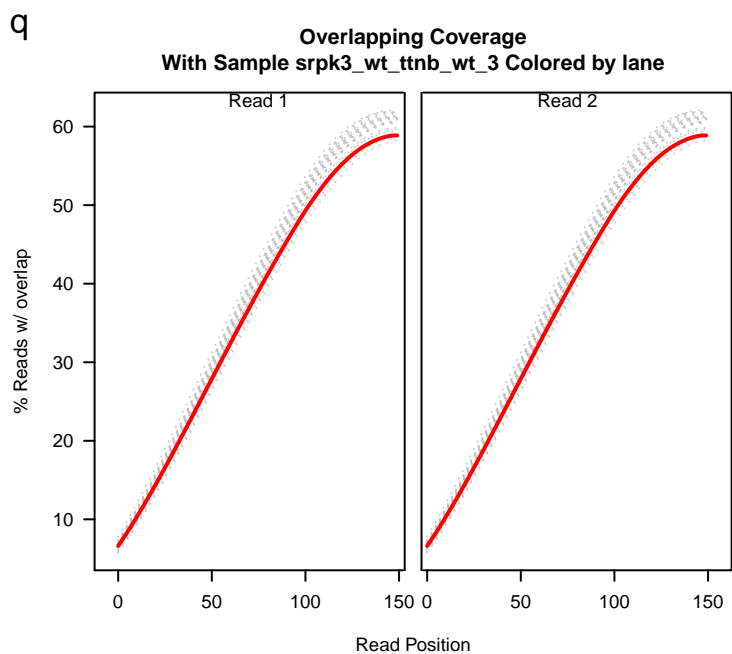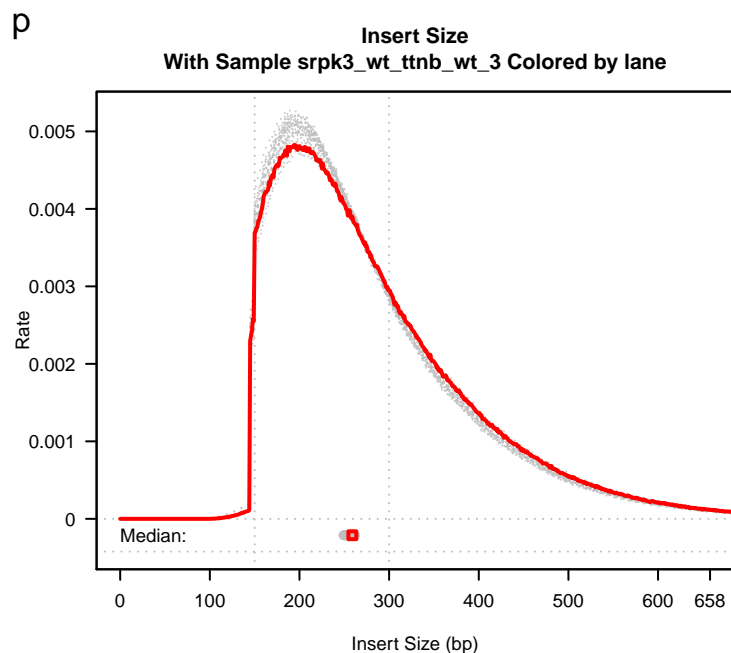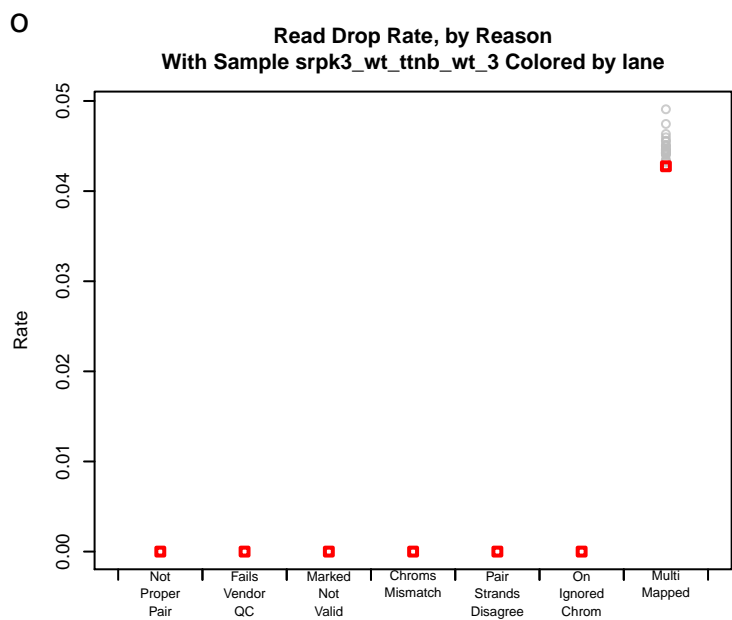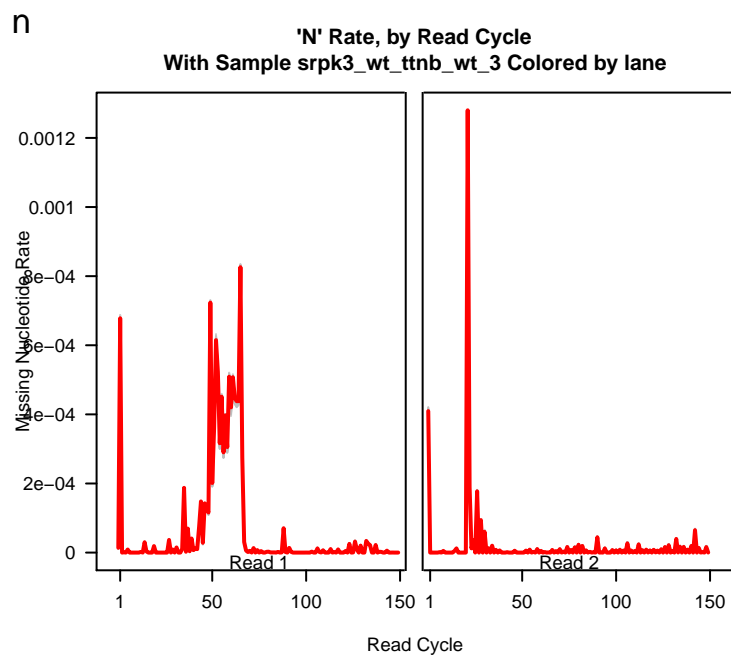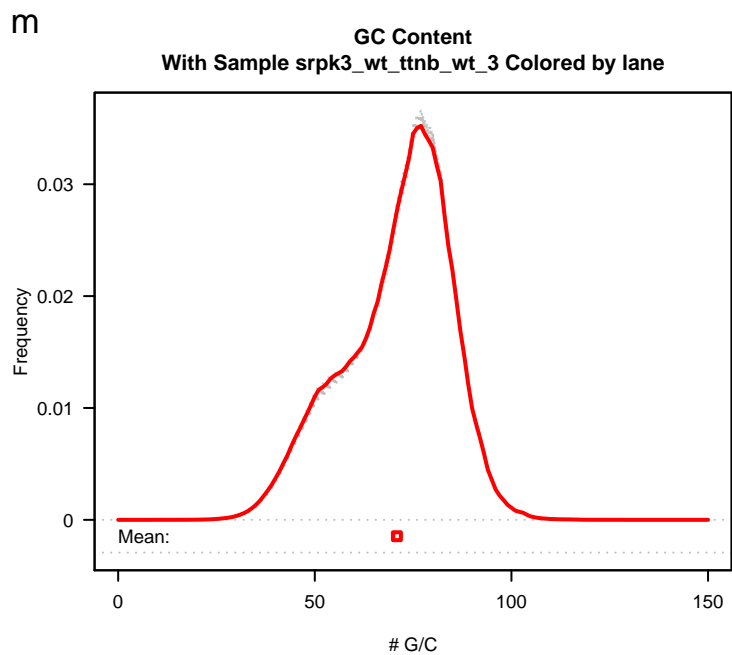**With Sample srpk3_wt_ttnb_wt_3 Colored by lane**

k **Insertion Length Distribution**
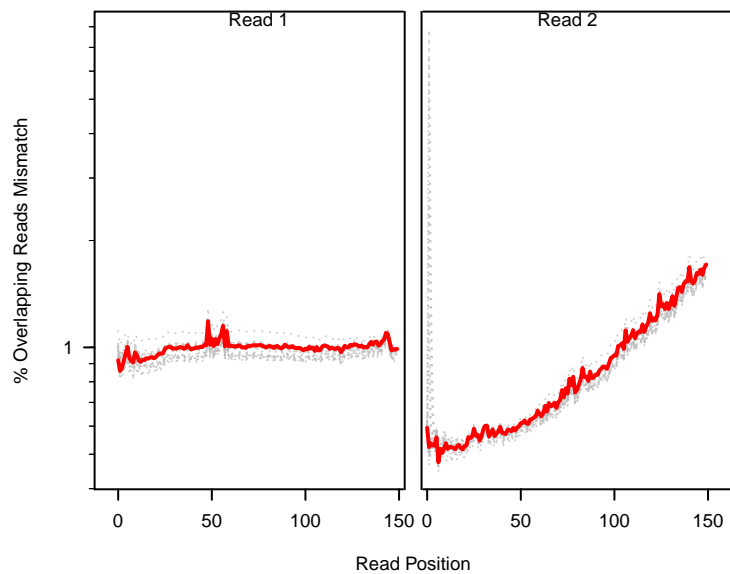**With Sample srpk3_wt_ttnb_wt_3 Colored by lane**

l **Deletion Length Distribution**
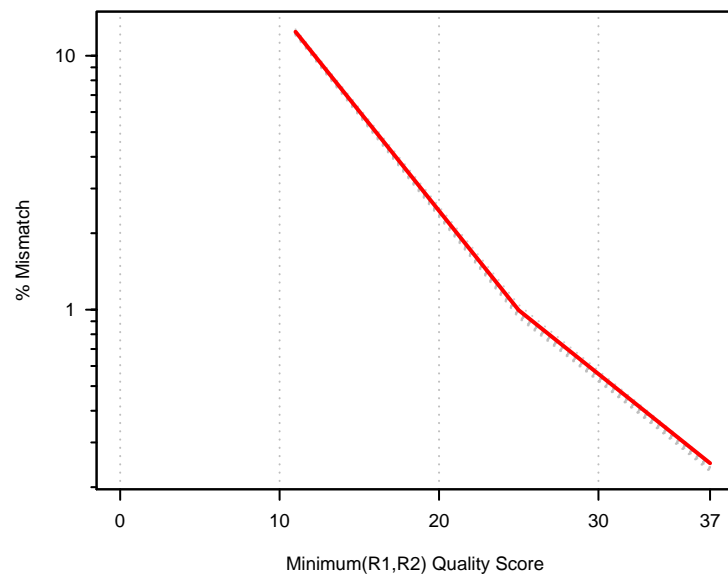**With Sample srpk3_wt_ttnb_wt_3 Colored by lane**

m

GC Content
With Sample srpk3_wt_ttnb_wt_3 Colored by lane

Frequency

0.03

0.02

0.01

0

Mean:

0   50   100   150

G/C

n

'N' Rate, by Read Cycle
With Sample srpk3_wt_ttnb_wt_3 Colored by lane

Missing Nucleotide Rate

0.0012

0.001

8e-04

6e-04

4e-04

2e-04

0

Read 1   Read 2

1   50   100   150   1   50   100   150

Read Cycle

o

Read Drop Rate, by Reason
With Sample srpk3_wt_ttnb_wt_3 Colored by lane

Rate

0.05

0.04

0.03

0.02

0.01

0.00

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_wt_3 Colored by lane

Rate

0.005

0.004

0.003

0.002

0.001

0

Median:

0   100   200   300   400   500   600 658

Insert Size (bp)

q

Overlapping Coverage
With Sample srpk3_wt_ttnb_wt_3 Colored by lane

% Reads w/ overlap

60

50

40

30

20

10

Read 1   Read 2

0   50   100   150   0   50   100   150

Read Position

r

Read Length Distribution
With Sample srpk3_wt_ttnb_wt_3 Colored by lane

% Reads <= length

1e-04

8e-05

6e-05

4e-05

2e-05

0

Read 1   Read 2

1   50   100   149   1   50   100   149

Read Length

s

Overlap Mismatch by Read Cycle
With Sample srpk3_wt_ttnb_wt_3 Colored by lane

Read 1 | Read 2

% Overlapping Reads Mismatch

Read Position

t

Overlapping Mismatch by Min Qual
With Sample srpk3_wt_ttnb_wt_3 Colored by lane

% Mismatch

Minimum(R1,R2) Quality Score

u

Overlap Mismatch by Read Qual
With Sample srpk3_wt_ttnb_wt_3 Colored by lane

Read 1 | Read 2

% Mismatch

Quality Score
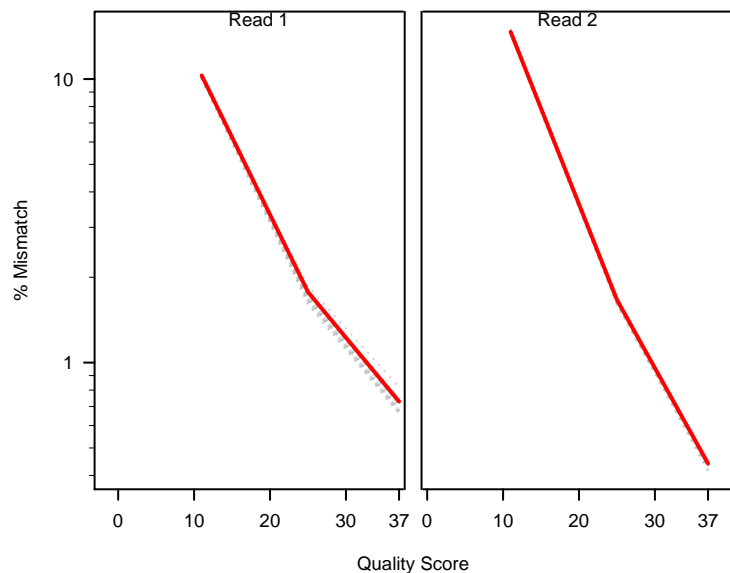
V

Overlap Mismatch Combinations
With Sample srpk3_wt_ttnb_wt_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
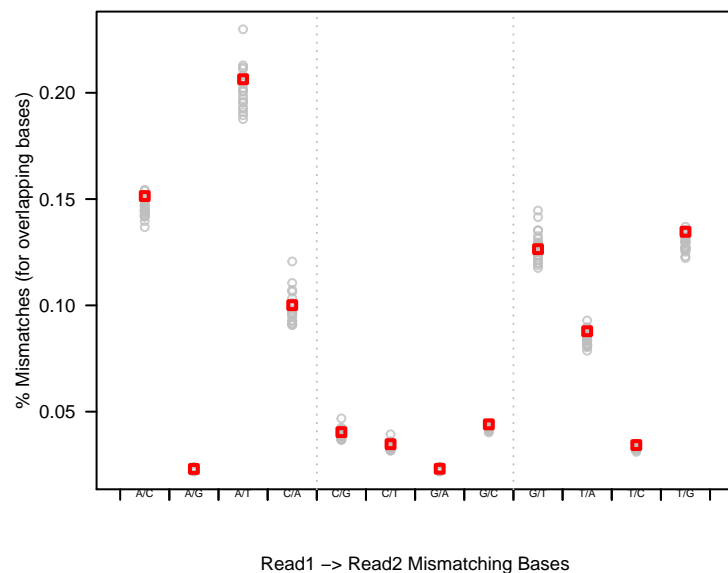
W

Overlap Mismatch Size Frequency
With Sample srpk3_wt_ttnb_wt_3 Colored by lane

% Read–Pairs

Mismatching Base–Pairs
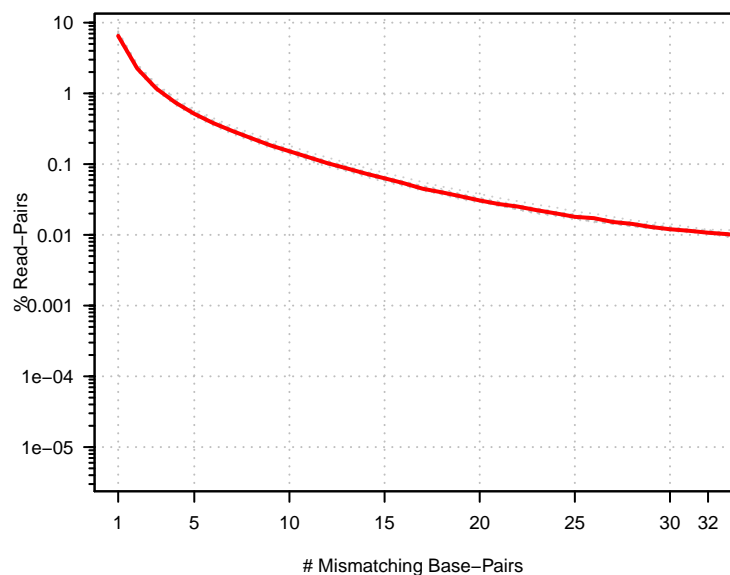
X

Overlap Mismatch Pairs At Phred == 41
With Sample srpk3_wt_ttnb_wt_3 Colored by lane
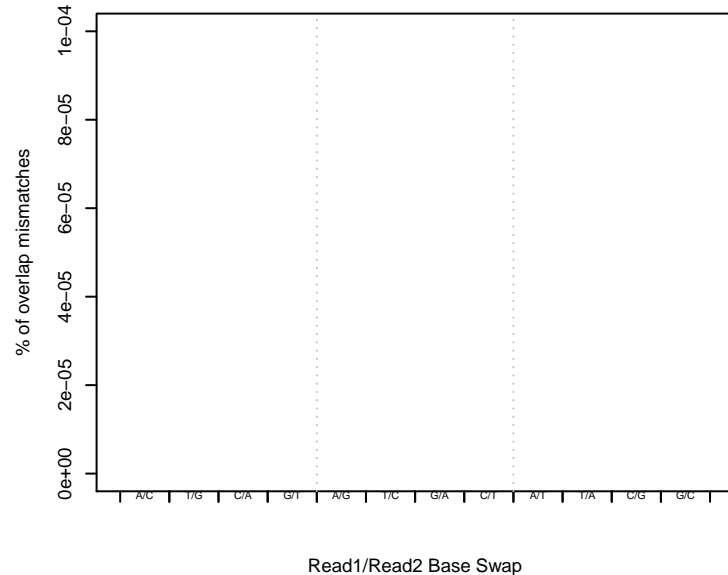
% of overlap mismatches

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_wt_3 Colored by lane

Read 1 — Read 2

% Mismatch

z

Reference Mismatch by Read Qual
With Sample srpk3_wt_ttnb_wt_3 Colored by lane

Read 1 — Read 2
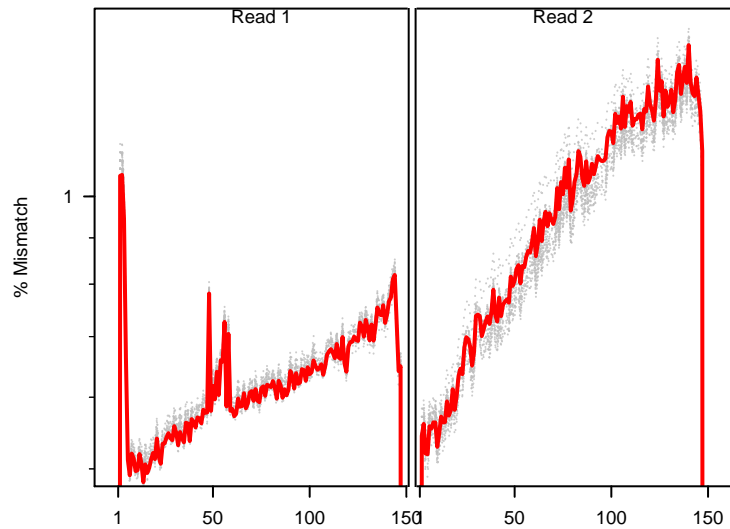
% Mismatch

Quality Score
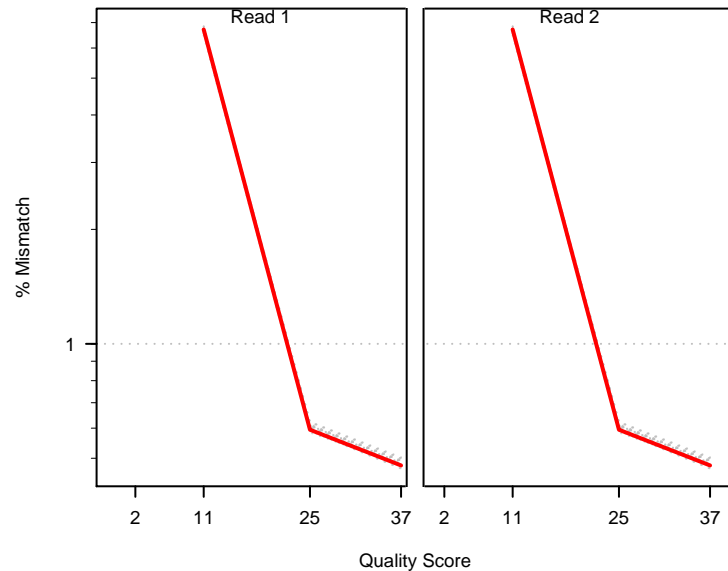
aa

Reference Mismatch Combinations
With Sample srpk3_wt_ttnb_wt_3 Colored by lane
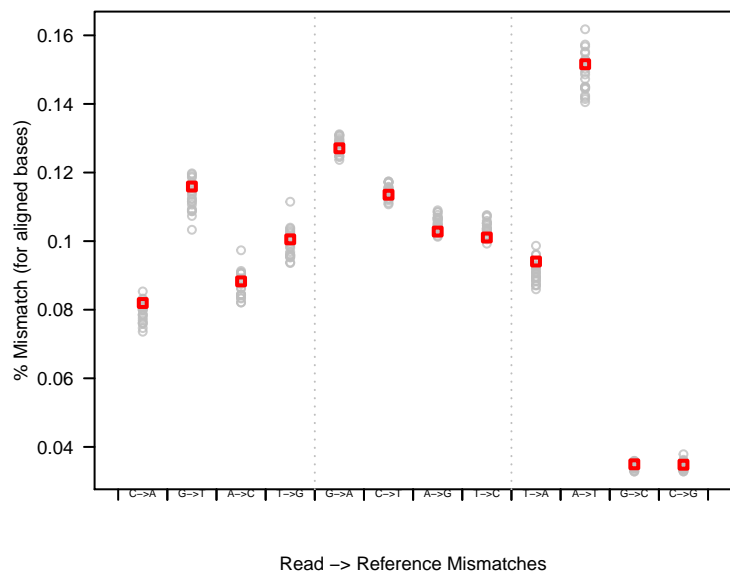
% Mismatch (for aligned bases)

Read –> Reference Mismatches

ab

R1 Ref Mismatches At Phred == 41
With Sample srpk3_wt_ttnb_wt_3 Colored by lane

% of ref mismatches

Ref–>Read Base Swap (Read Strand)

ac

R2 Ref Mismatches At Phred == 41
With Sample srpk3_wt_ttnb_wt_3 Colored by lane

% of ref mismatches

Ref–>Read Base Swap (Read Strand)
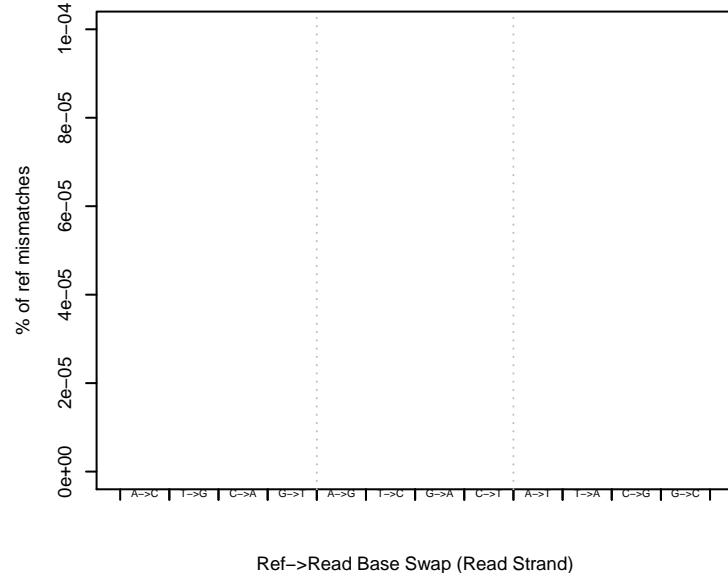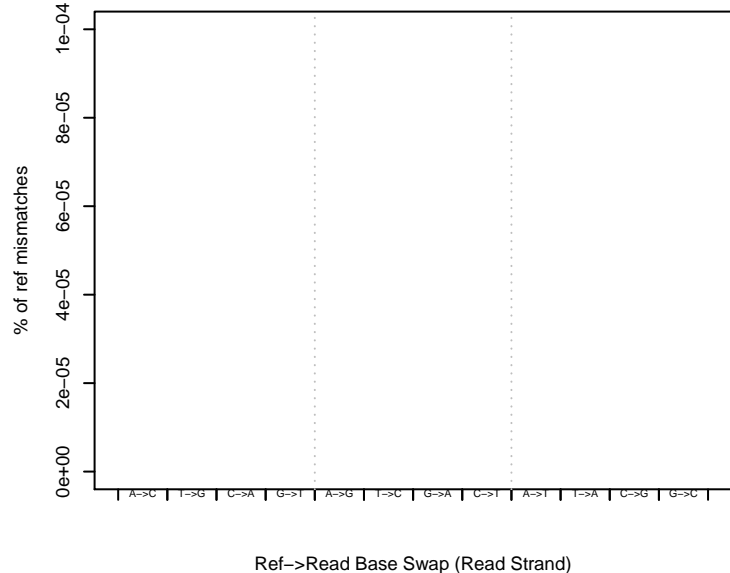
ad

Cumulative Gene Assignment Diversity
With Sample srpk3_wt_ttnb_wt_3 Colored by lane
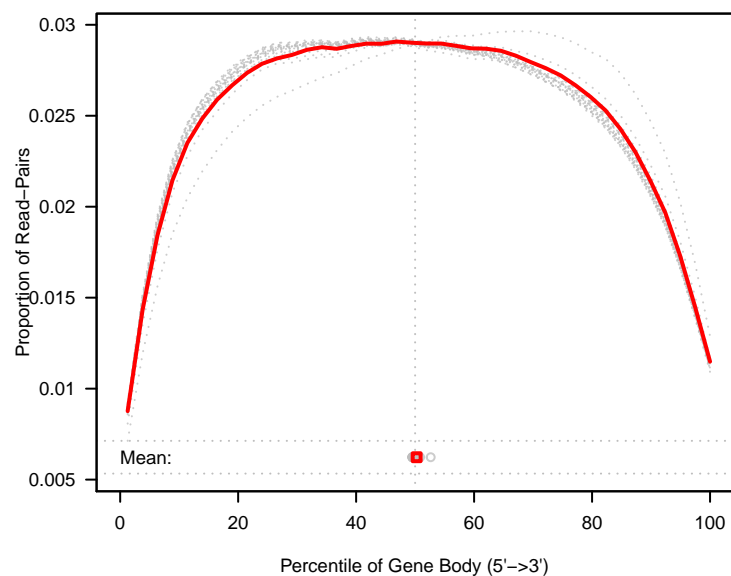
Cumulative % of total reads
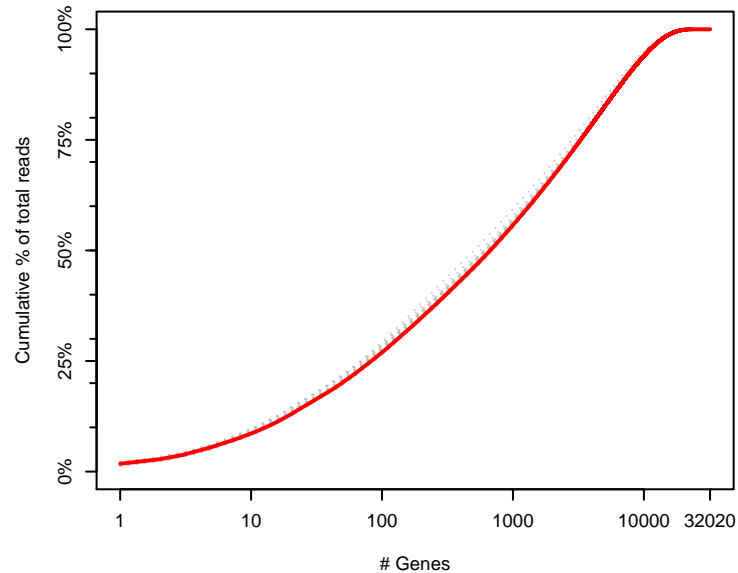
Genes

ae

Gene−Body Coverage
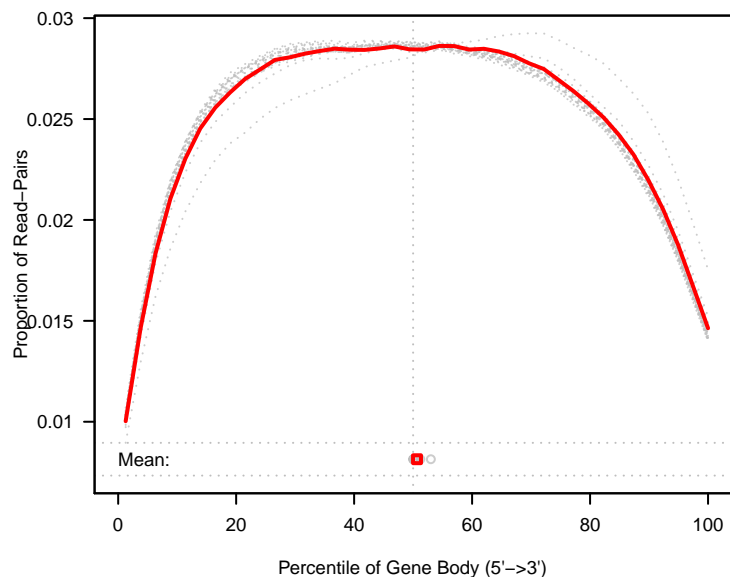**With Sample srpk3_wt_ttnb_wt_3 Colored by lane**
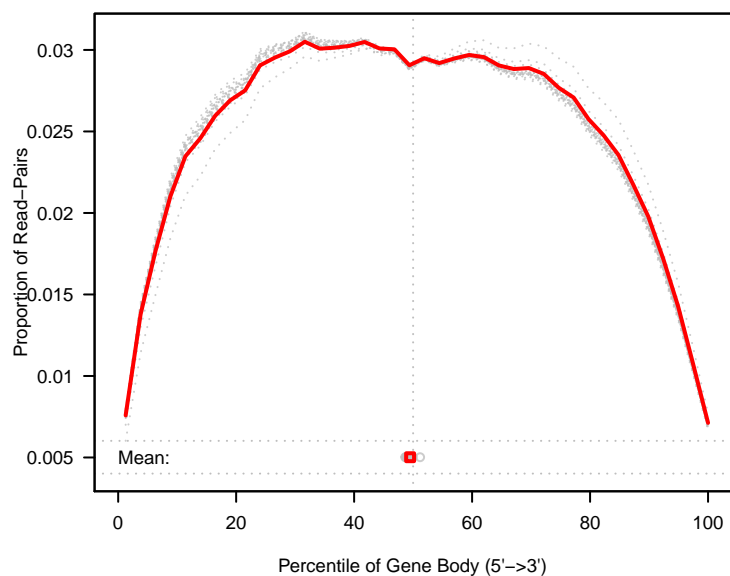
af

Gene−Body Coverage, Upper Middle Quartile Genes
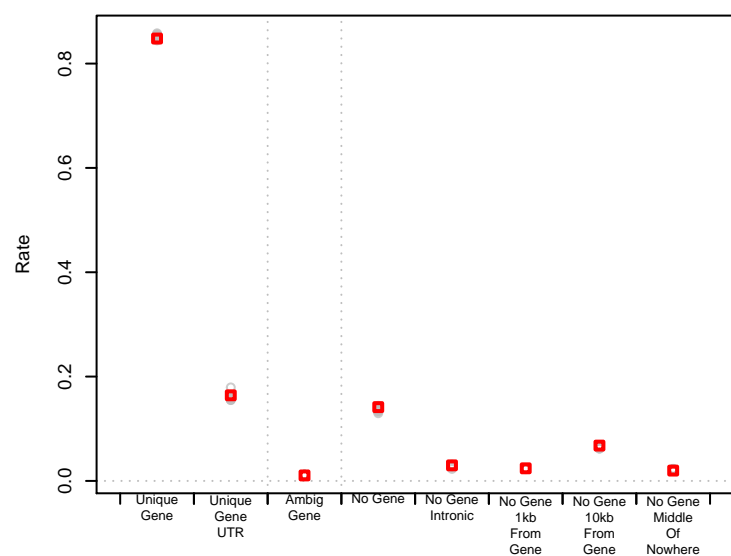**With Sample srpk3_wt_ttnb_wt_3 Colored by lane**

ag

Gene−Body Coverage, Low Expression Genes
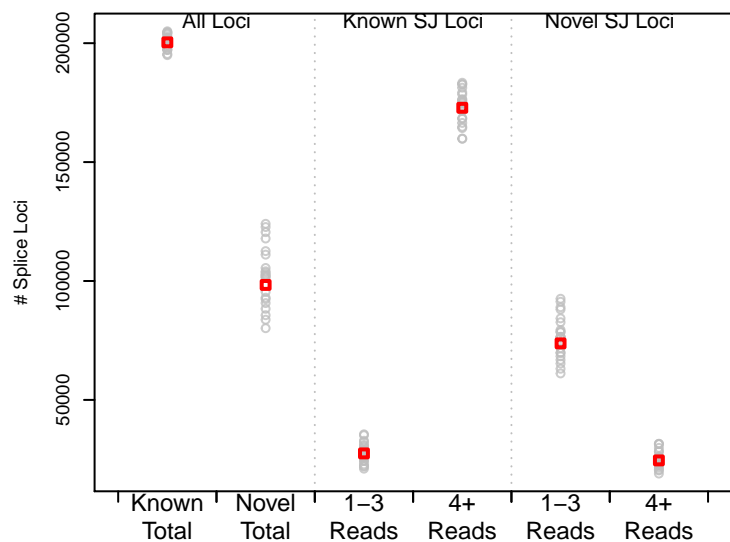**With Sample srpk3_wt_ttnb_wt_3 Colored by lane**

ah

Read Mapping Location Rates
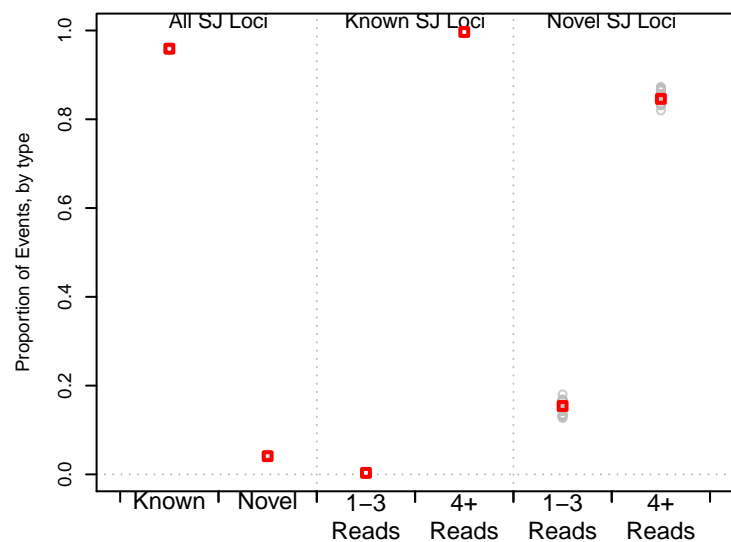**With Sample srpk3_wt_ttnb_wt_3 Colored by lane**

ai

 # Observed Splice Junction Loci, by type
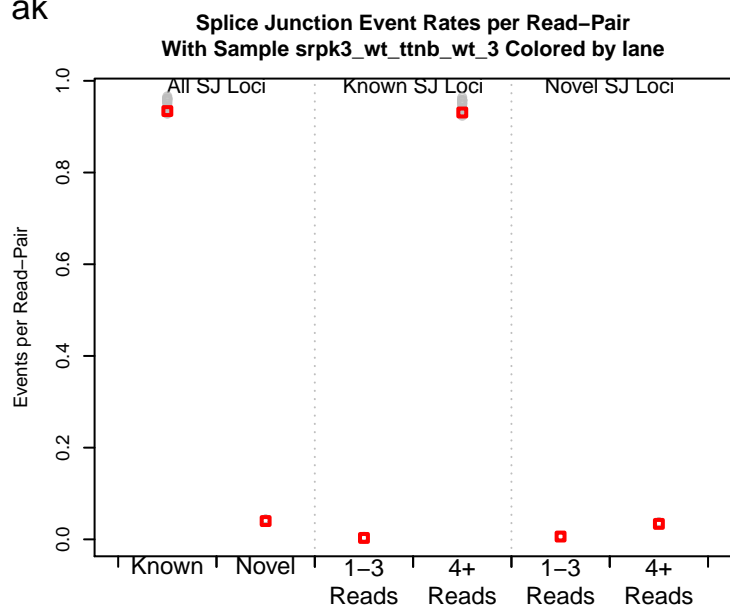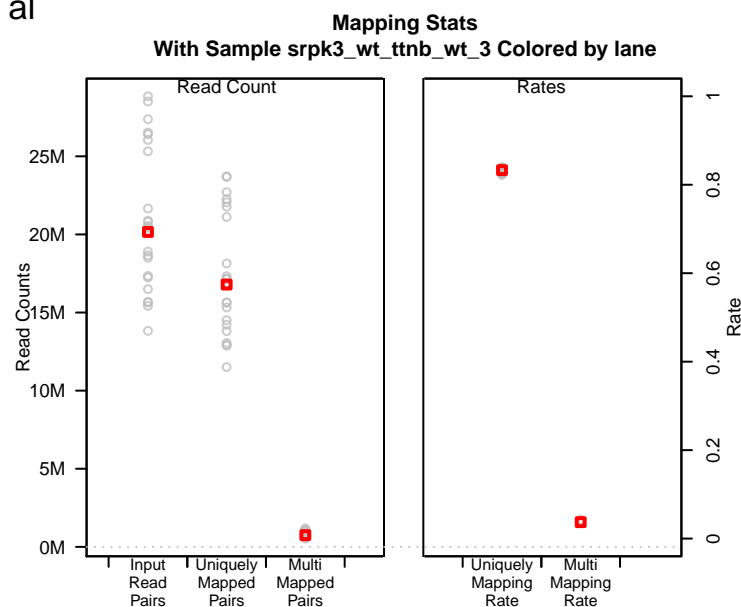**With Sample srpk3_wt_ttnb_wt_3 Colored by lane**

aj

Breakdown of Splice Junction Events, by type
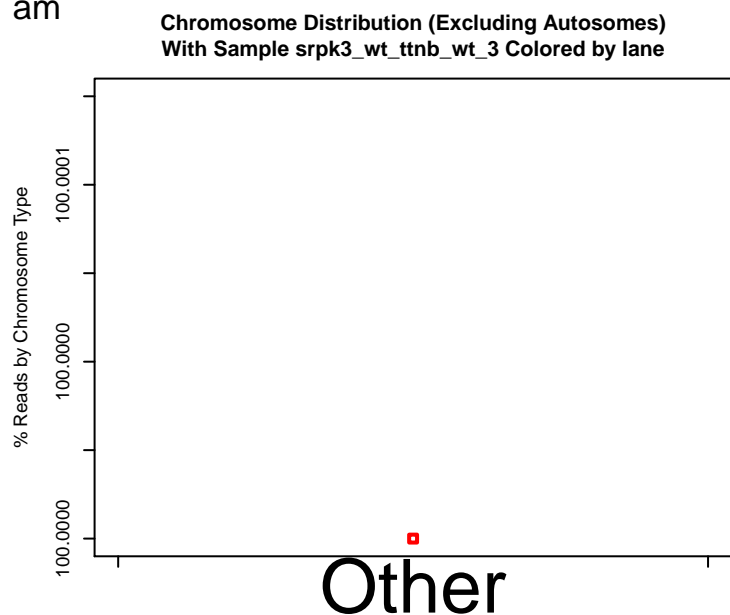**With Sample srpk3_wt_ttnb_wt_3 Colored by lane**

ak

Splice Junction Event Rates per Read–Pair
With Sample srpk3_wt_ttnb_wt_3 Colored by lane

al

Mapping Stats
With Sample srpk3_wt_ttnb_wt_3 Colored by lane

am

Chromosome Distribution (Excluding Autosomes)
With Sample srpk3_wt_ttnb_wt_3 Colored by lane

an

Normalization Factors
With Sample srpk3_wt_ttnb_wt_3 Colored by lane

ao

Normalization Factors vs Total–Count Normalization
With Sample srpk3_wt_ttnb_wt_3 Colored by lane

ap

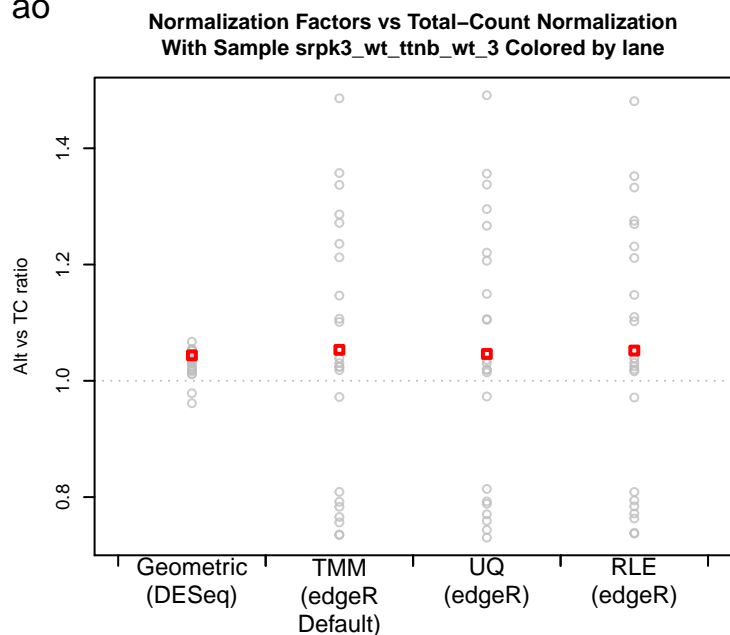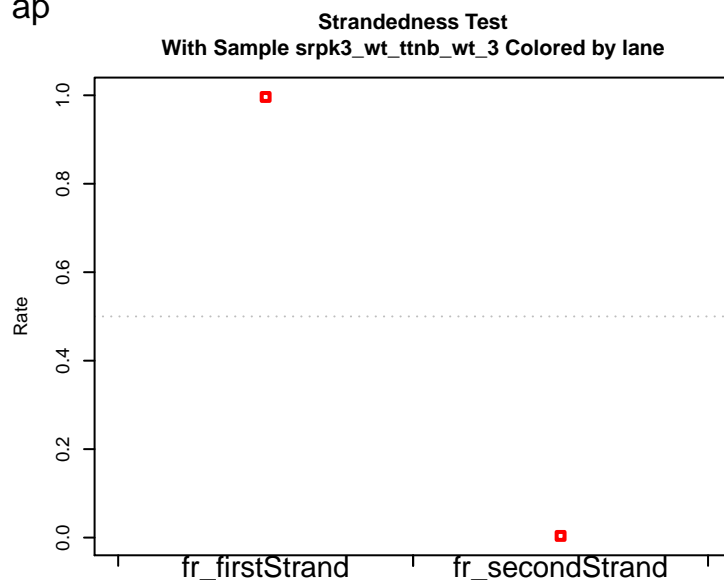## Strandedness Test
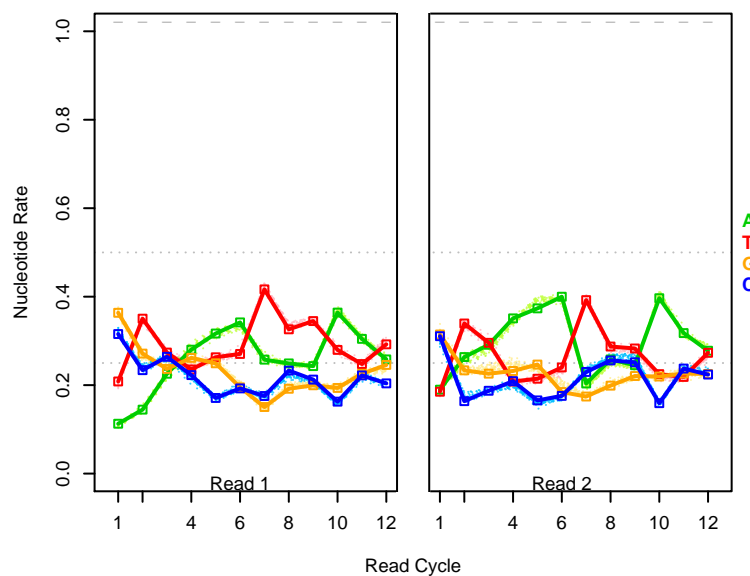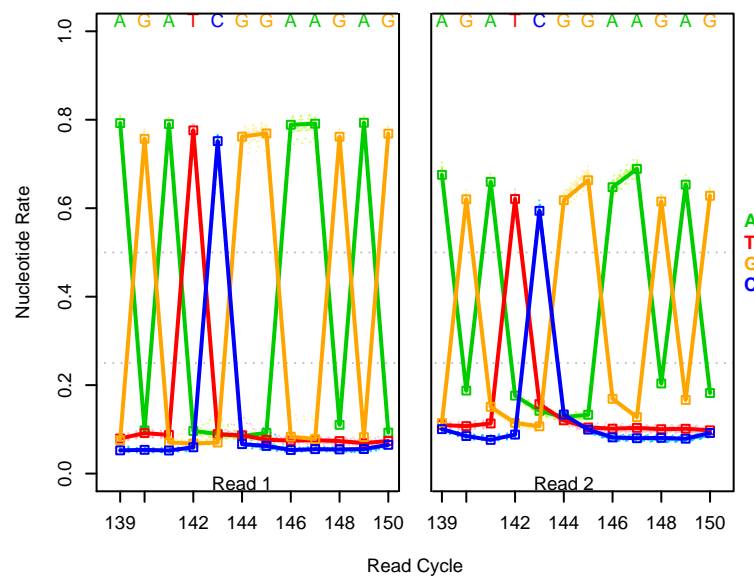## With Sample srpk3_wt_ttnb_wt_3 Colored by lane

aq

Nucleotide Rate by Cycle, Leading Clipped bases (12)
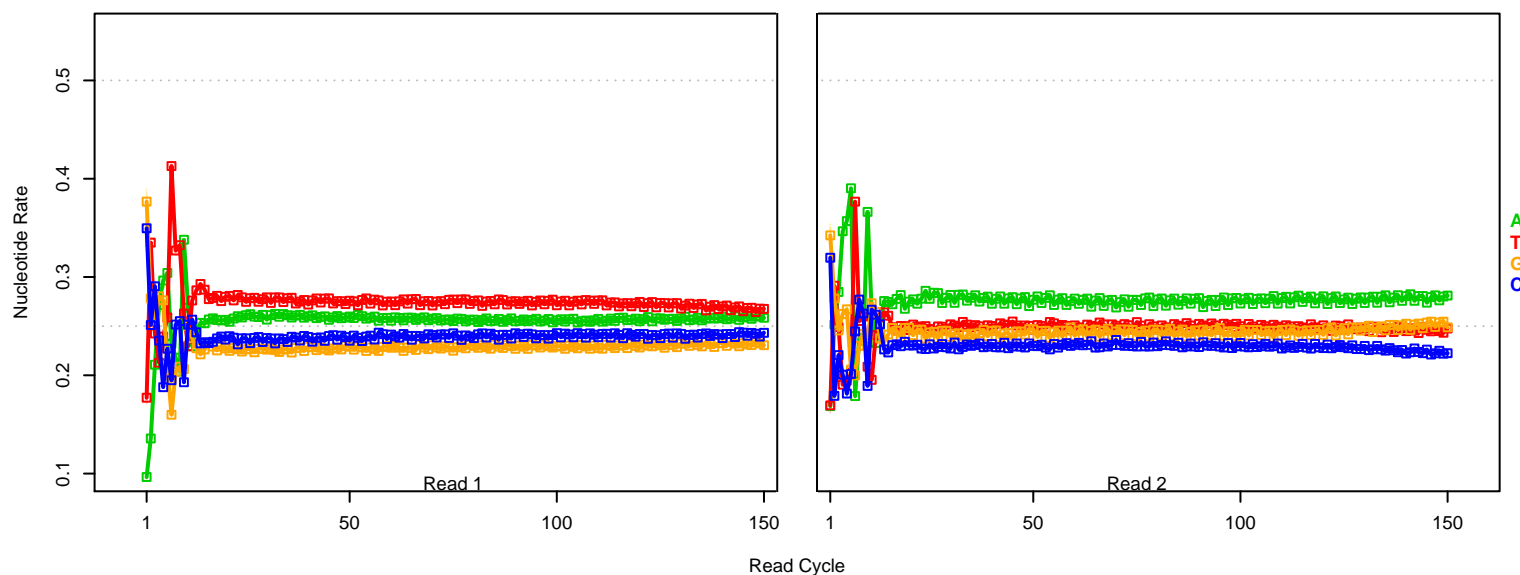**With Sample srpk3_wt_ttnb_wt_3 in Bold**

ar

Nucleotide Rate by Cycle, Trailing Clipped bases (12)
With Sample srpk3_wt_ttnb_wt_3 in Bold

as

Raw Nucleotide Rate by Cycle
With Sample srpk3_wt_ttnb_wt_3 in Bold

at

Nucleotide Rate by Cycle, Aligned bases only
With Sample srpk3_wt_ttnb_wt_3 in Bold