a

Sample Highlight:
srpk3_hom_ttnb_het_1
Colored by Lane

☐ — UNKNOWN
⊙ ⋯ Other Samples

b

Minimum Phred Quality Score
With Sample srpk3_hom_ttnb_het_1 Colored by lane
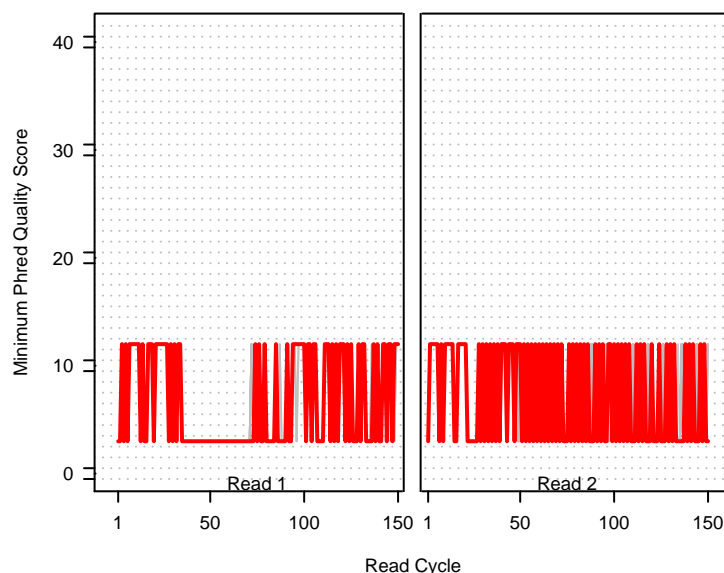
Minimum Phred Quality Score

Read 1 | Read 2

Read Cycle

c

Lower Quartile Phred Quality Score
With Sample srpk3_hom_ttnb_het_1 Colored by lane

Lower Quartile Phred Quality Score

Read 1 | Read 2

Read Cycle

d

Median Phred Quality Score
With Sample srpk3_hom_ttnb_het_1 Colored by lane

Median Phred Quality Score

Read 1 | Read 2

Read Cycle

e

Upper Quartile Phred Quality Score
With Sample srpk3_hom_ttnb_het_1 Colored by lane

Upper Quartile Phred Quality Score

Read 1 | Read 2

Read Cycle

f

Maximum Phred Quality Score
With Sample srpk3_hom_ttnb_het_1 Colored by lane

Maximum Phred Quality Score

Read 1 | Read 2
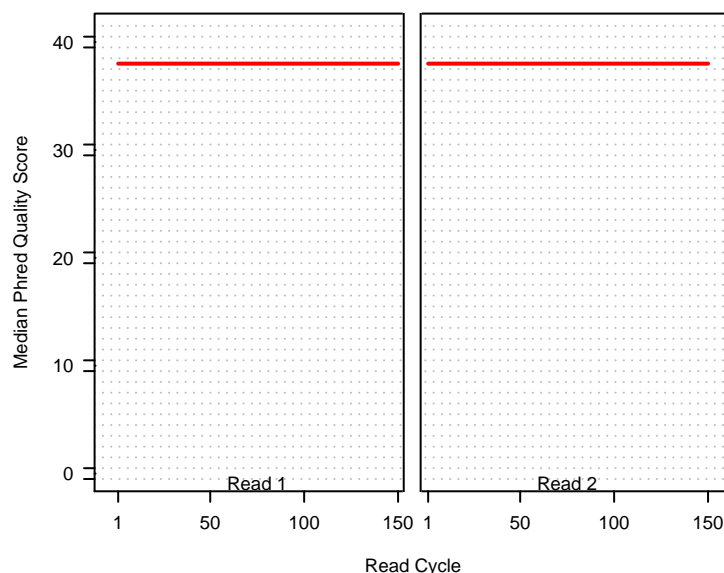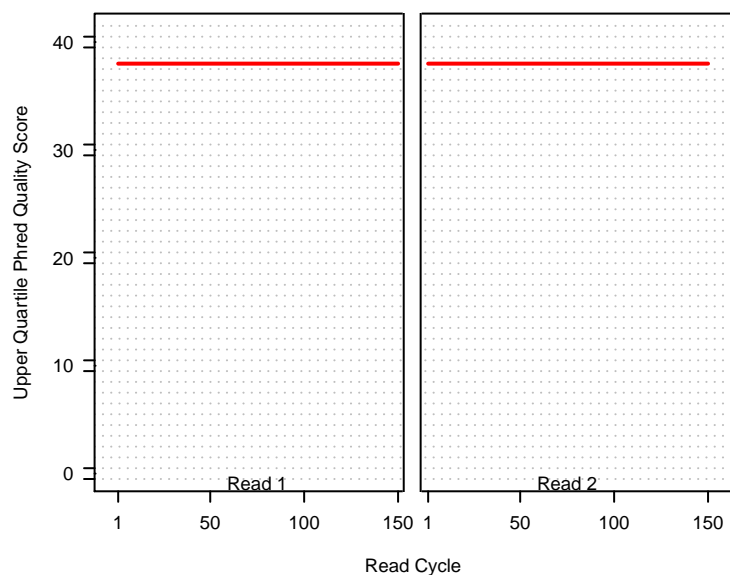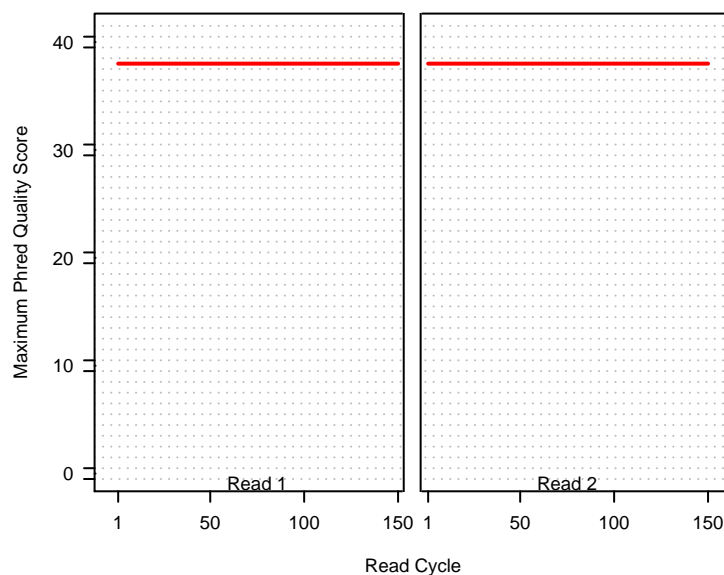
Read Cycle

g **Alignment Clipping Rate, by read cycle**
With Sample srpk3_hom_ttnb_het_1 Colored by lane
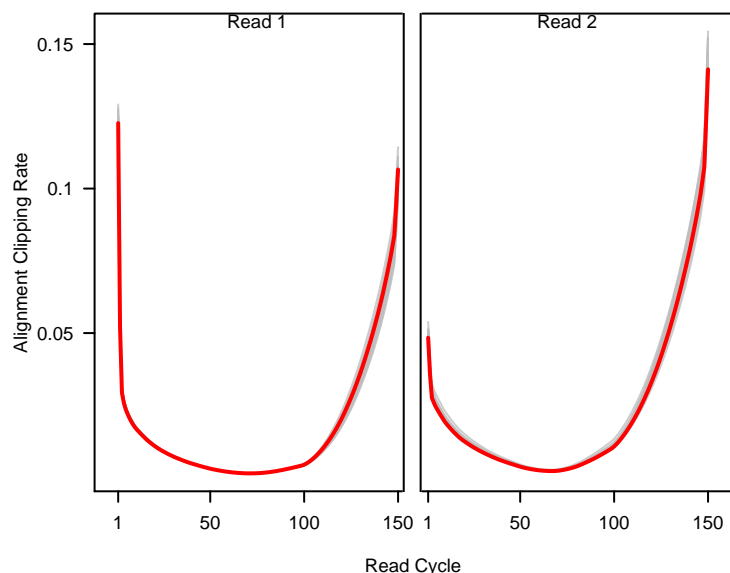
h **Deletion Rate, by read cycle**
With Sample srpk3_hom_ttnb_het_1 Colored by lane

i **Insertion Rate, by read cycle**
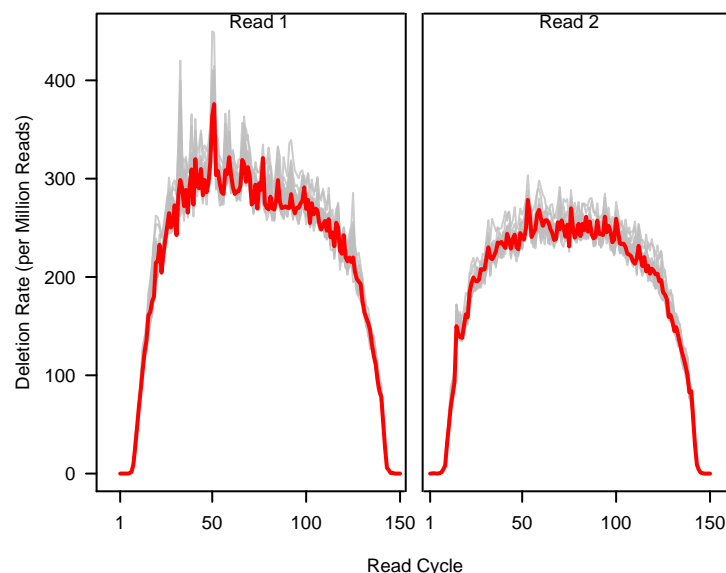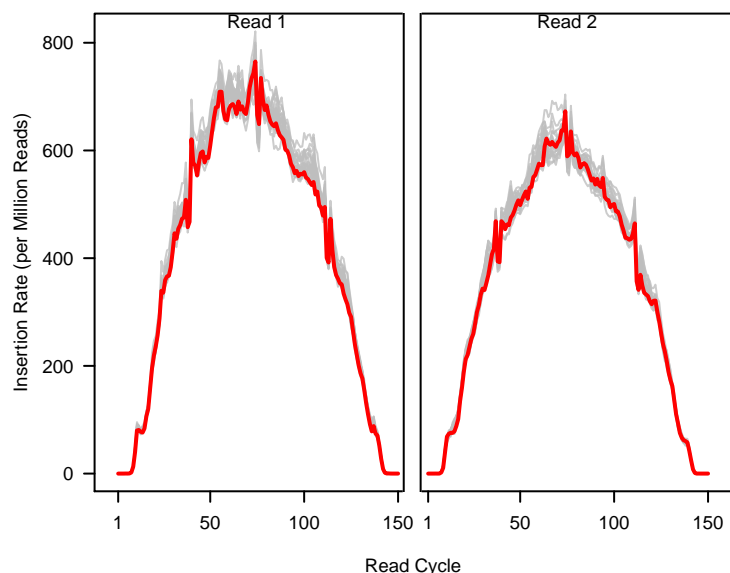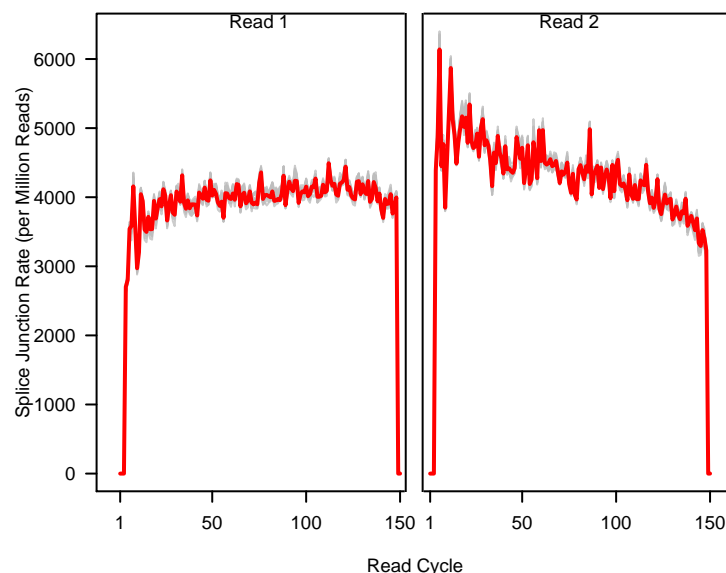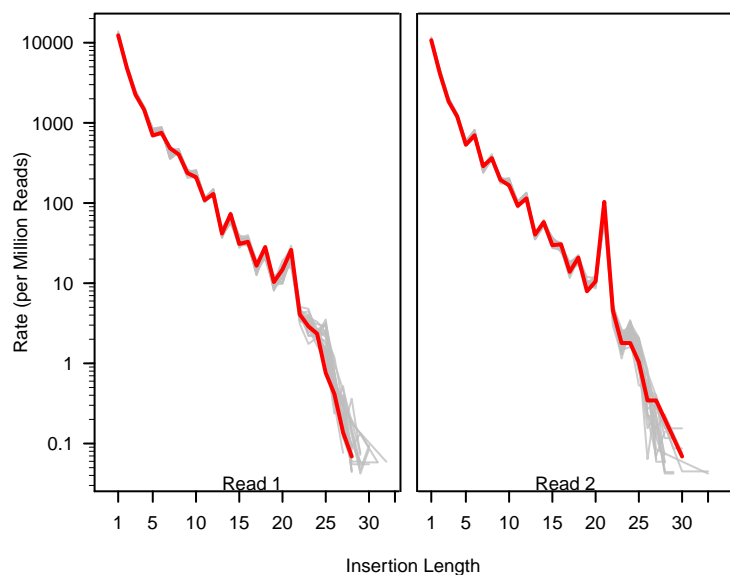With Sample srpk3_hom_ttnb_het_1 Colored by lane

j **Splice Junction Rate, by read cycle**
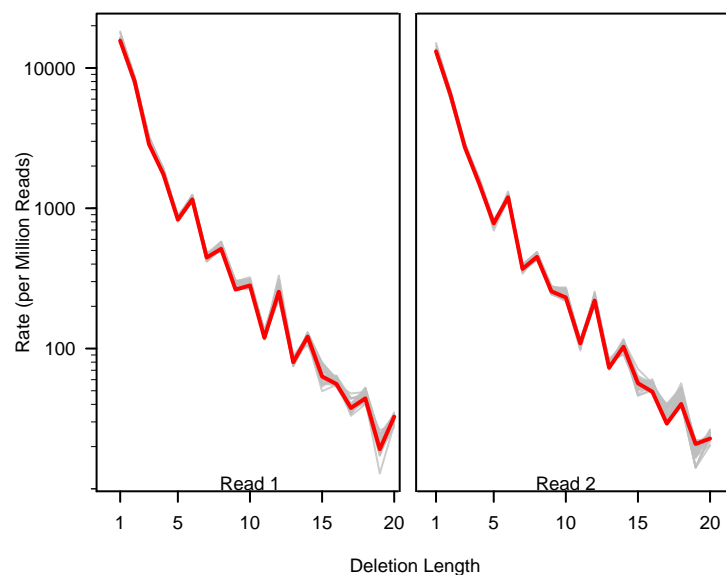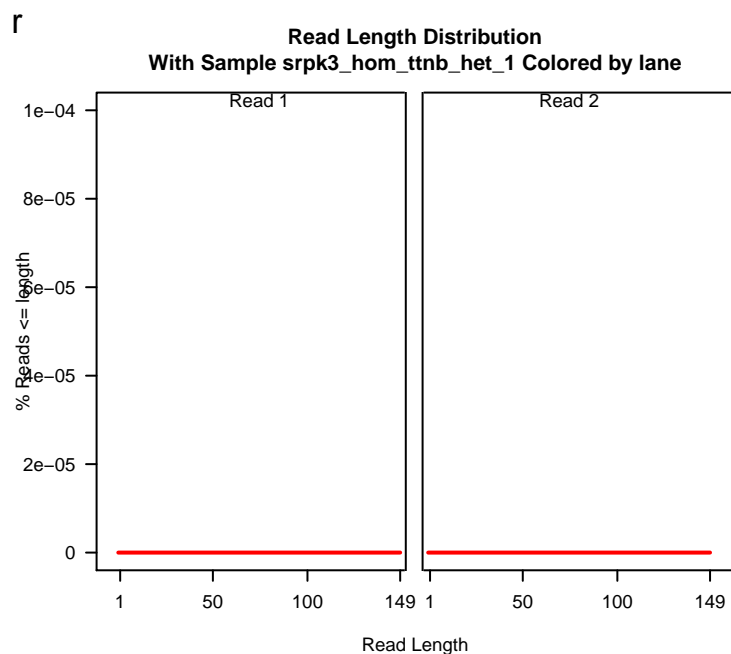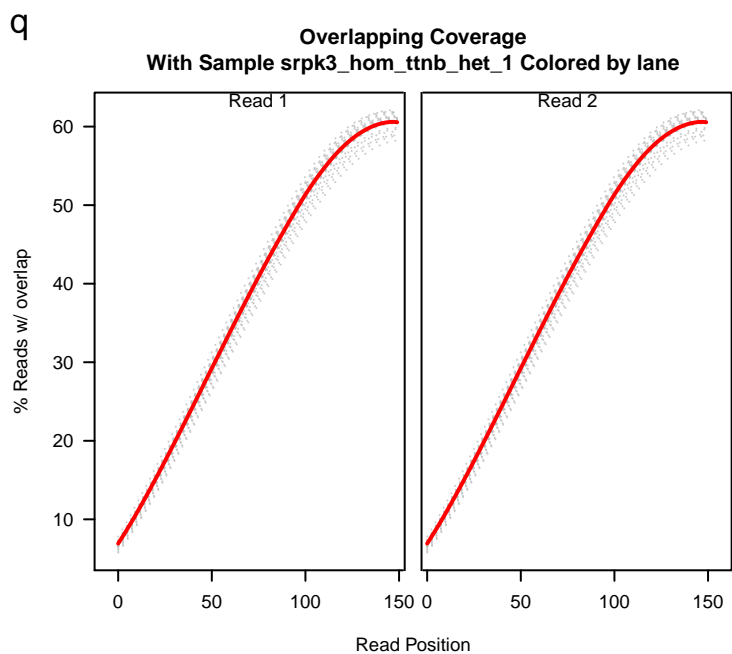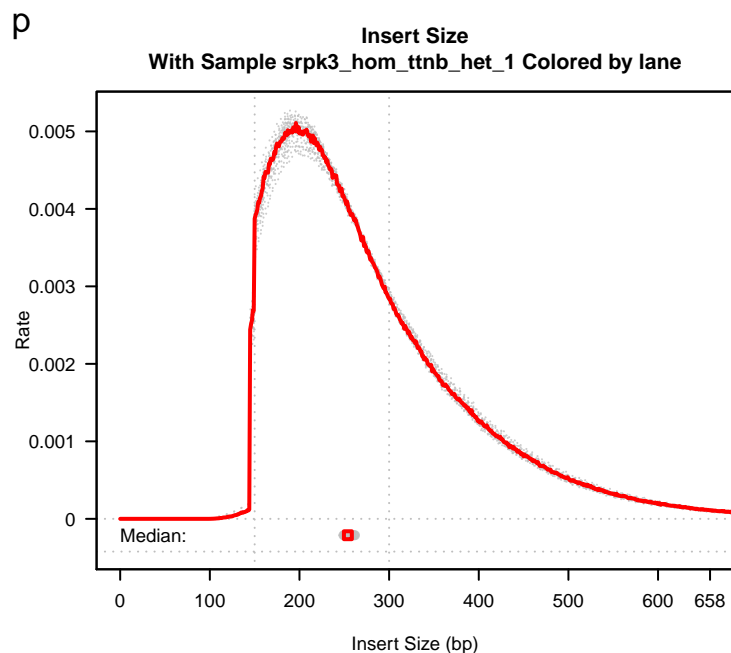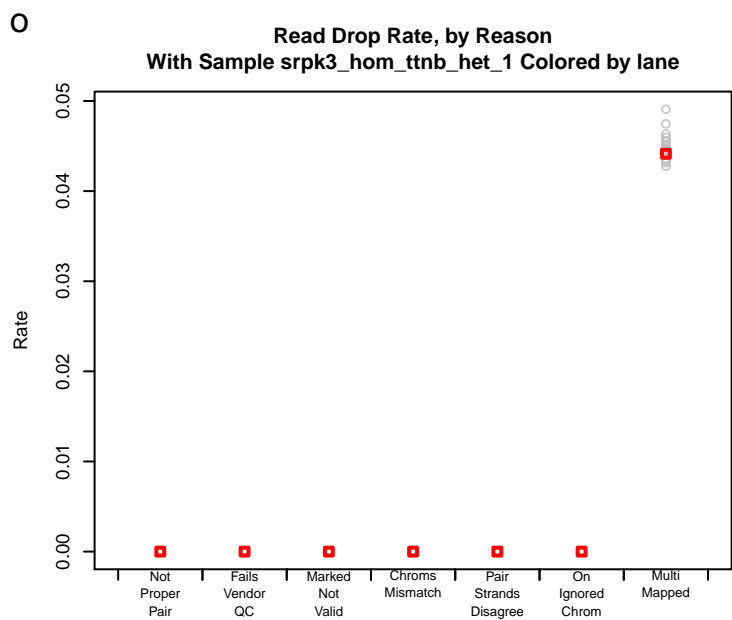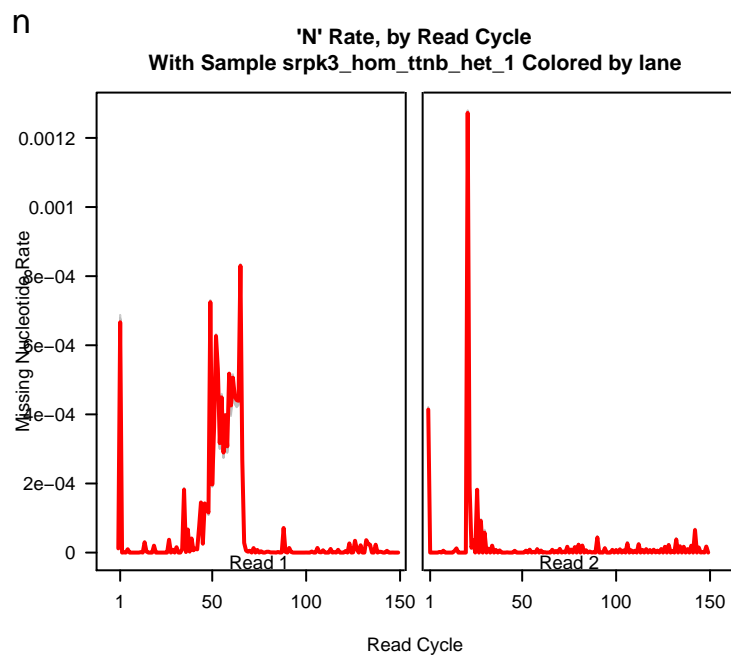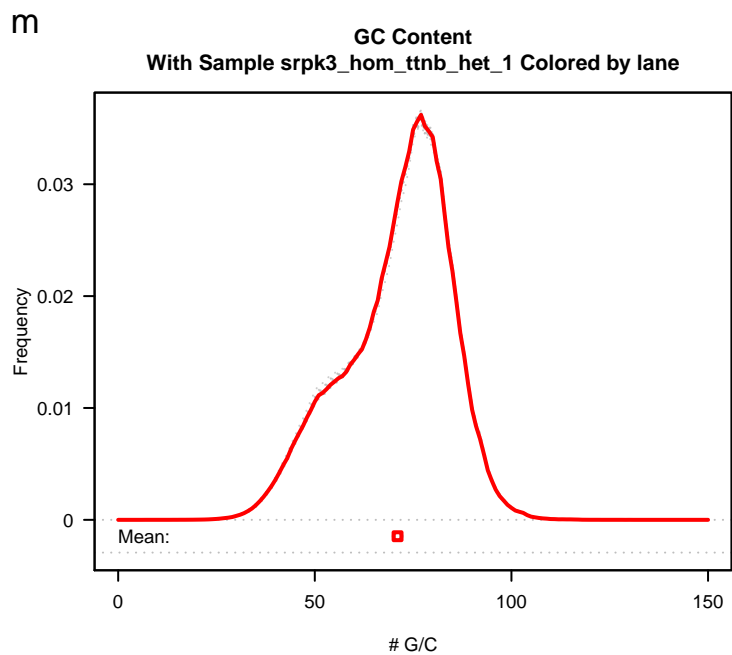With Sample srpk3_hom_ttnb_het_1 Colored by lane

k **Insertion Length Distribution**
With Sample srpk3_hom_ttnb_het_1 Colored by lane

l **Deletion Length Distribution**
With Sample srpk3_hom_ttnb_het_1 Colored by lane

m

GC Content
With Sample srpk3_hom_ttnb_het_1 Colored by lane

n

'N' Rate, by Read Cycle
With Sample srpk3_hom_ttnb_het_1 Colored by lane

o

Read Drop Rate, by Reason
With Sample srpk3_hom_ttnb_het_1 Colored by lane

p

Insert Size
With Sample srpk3_hom_ttnb_het_1 Colored by lane

q

Overlapping Coverage
With Sample srpk3_hom_ttnb_het_1 Colored by lane

r

Read Length Distribution
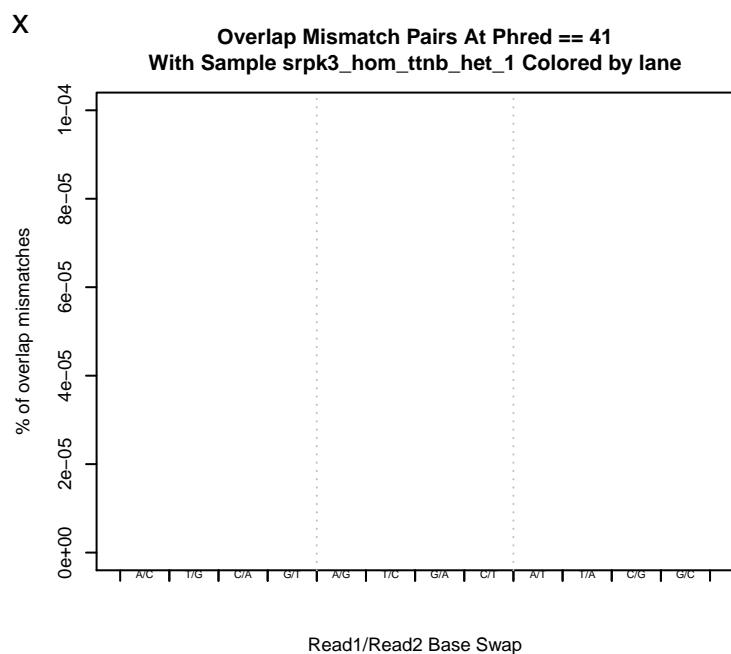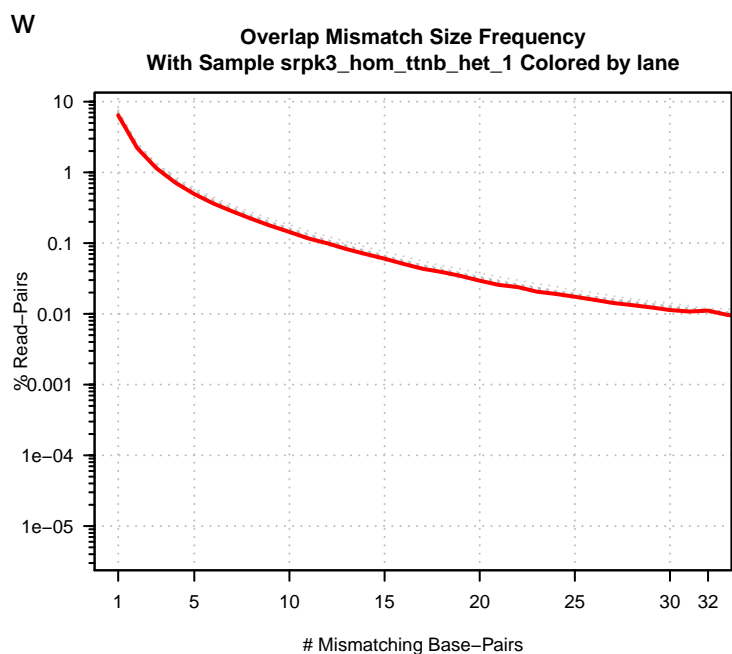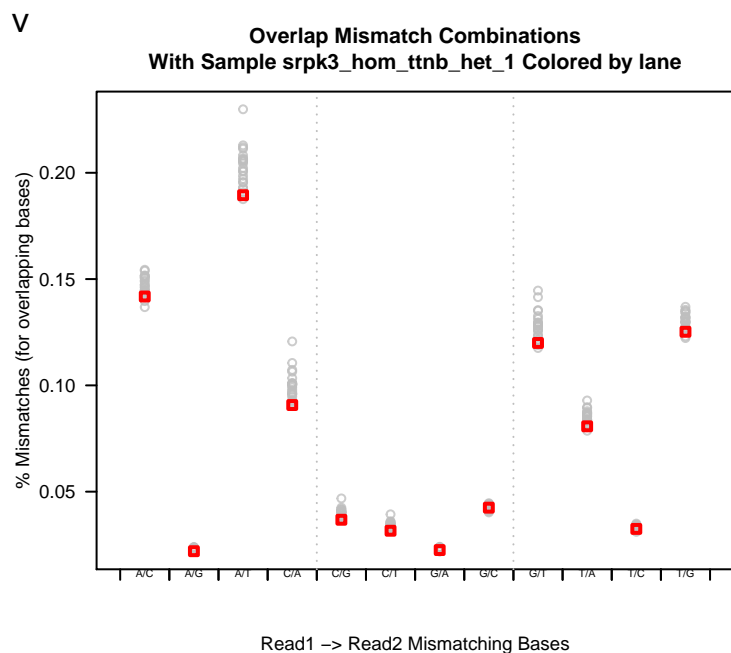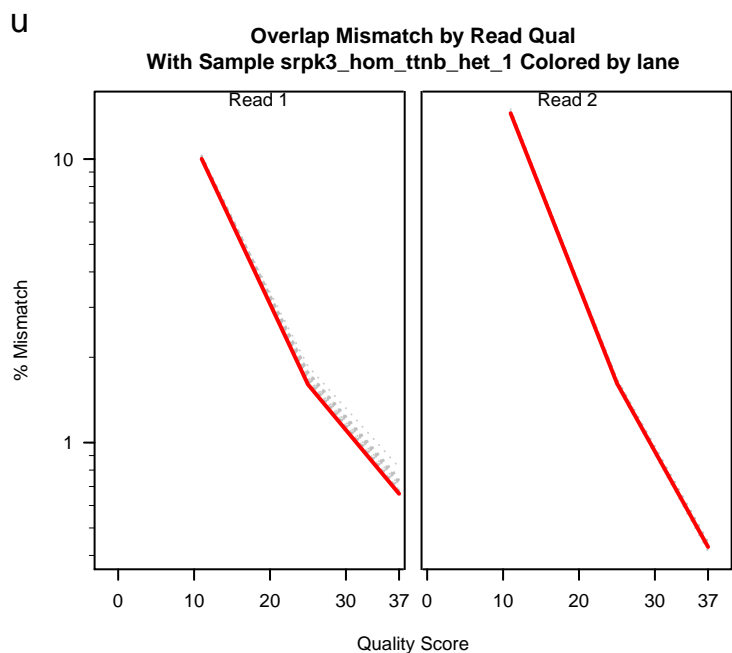**With Sample srpk3_hom_ttnb_het_1 Colored by lane**

s — Overlap Mismatch by Read Cycle
With Sample srpk3_hom_ttnb_het_1 Colored by lane

t — Overlapping Mismatch by Min Qual
With Sample srpk3_hom_ttnb_het_1 Colored by lane

u — Overlap Mismatch by Read Qual
With Sample srpk3_hom_ttnb_het_1 Colored by lane

V — Overlap Mismatch Combinations
With Sample srpk3_hom_ttnb_het_1 Colored by lane

W — Overlap Mismatch Size Frequency
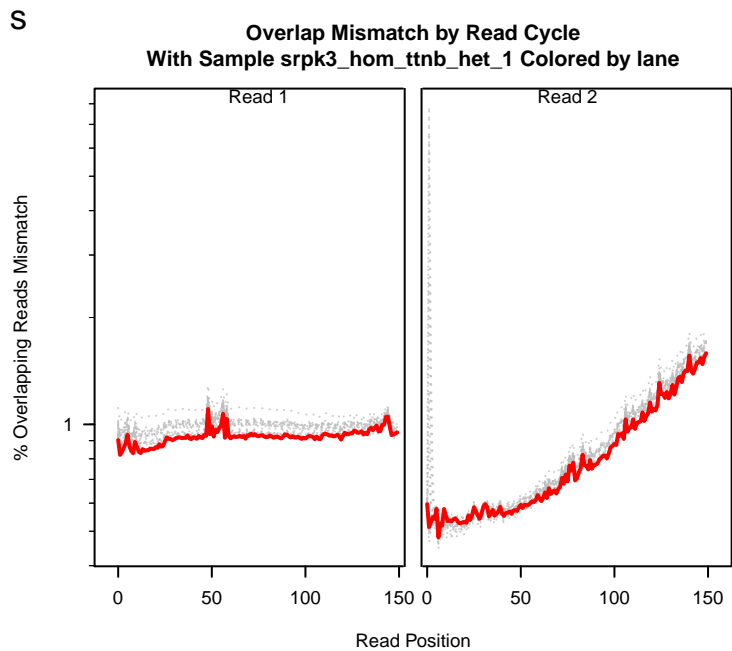With Sample srpk3_hom_ttnb_het_1 Colored by lane

X — Overlap Mismatch Pairs At Phred == 41
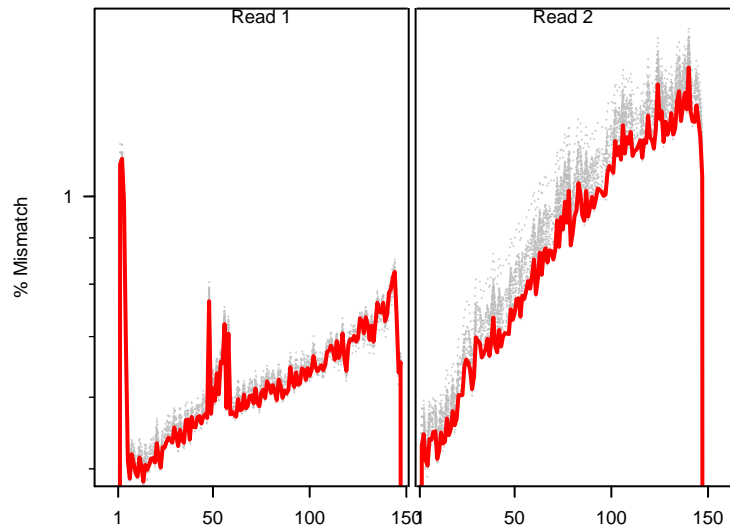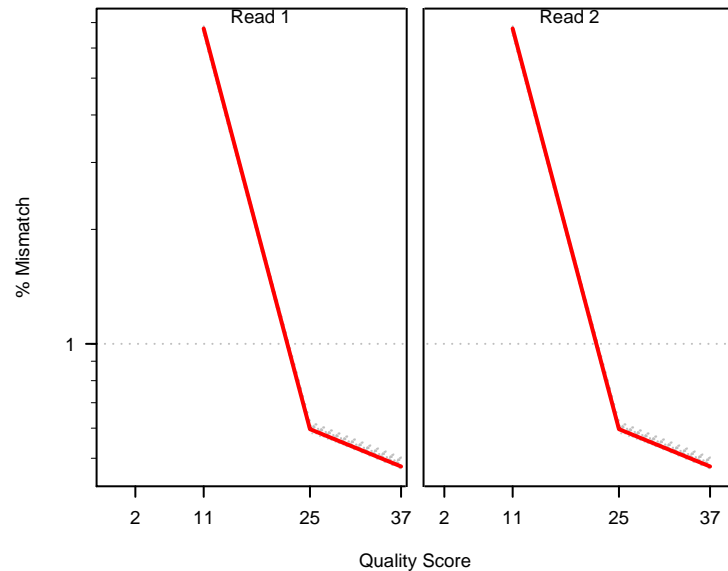With Sample srpk3_hom_ttnb_het_1 Colored by lane

y

Reference Mismatch by Read Cycle
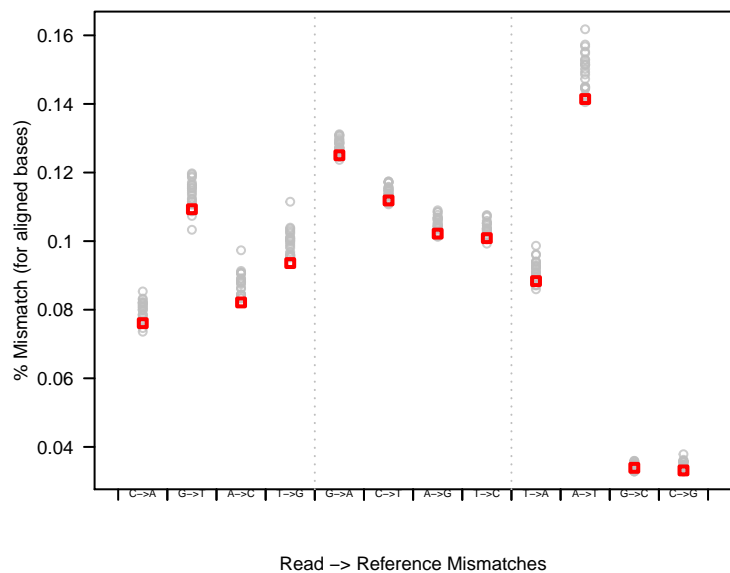**With Sample srpk3_hom_ttnb_het_1 Colored by lane**

z

Reference Mismatch by Read Qual
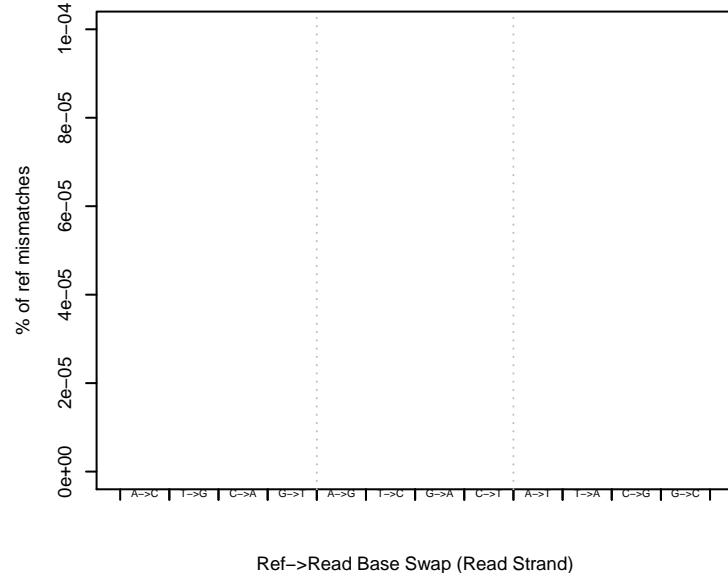**With Sample srpk3_hom_ttnb_het_1 Colored by lane**

aa

Reference Mismatch Combinations
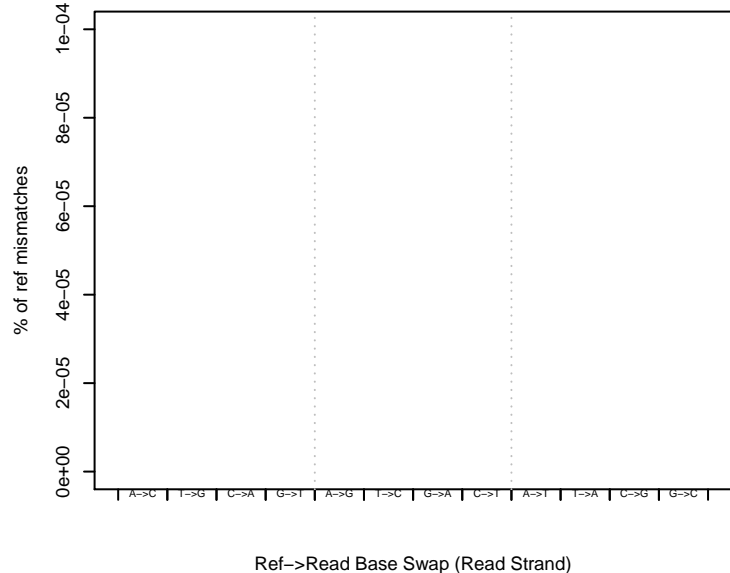**With Sample srpk3_hom_ttnb_het_1 Colored by lane**

ab

R1 Ref Mismatches At Phred == 41
With Sample srpk3_hom_ttnb_het_1 Colored by lane
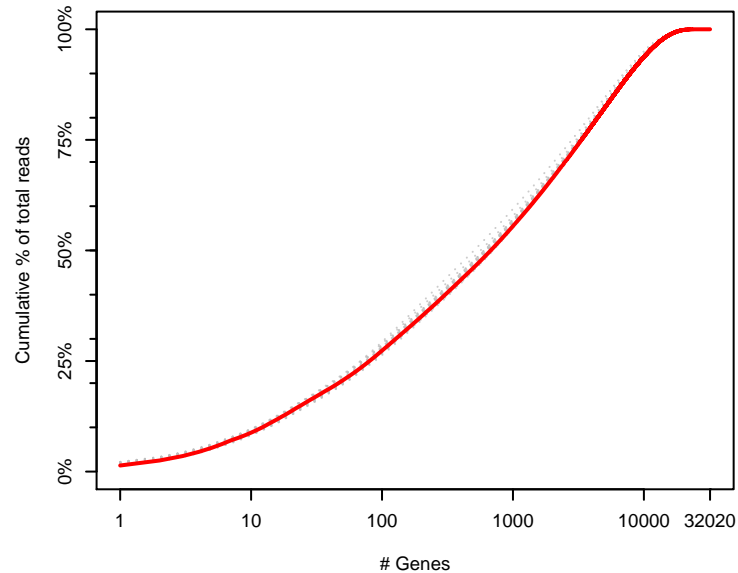

ac

R2 Ref Mismatches At Phred == 41
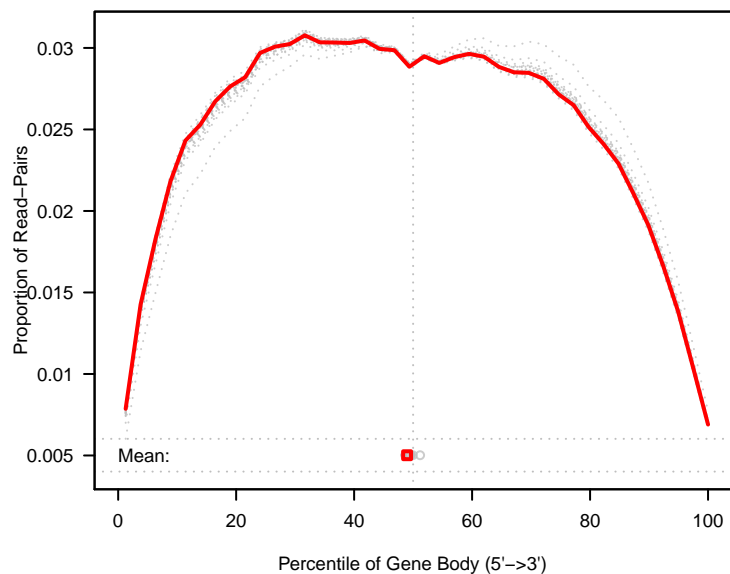**With Sample srpk3_hom_ttnb_het_1 Colored by lane**

ad

Cumulative Gene Assignment Diversity
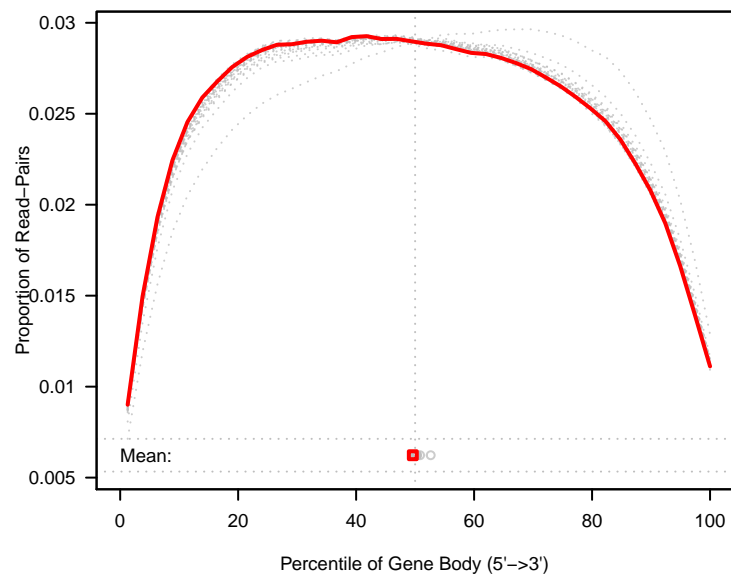**With Sample srpk3_hom_ttnb_het_1 Colored by lane**

ae

Gene–Body Coverage
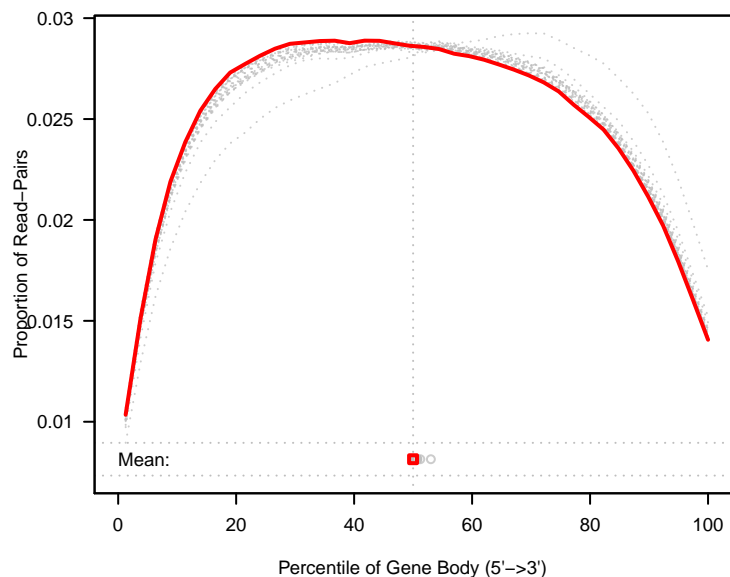**With Sample srpk3_hom_ttnb_het_1 Colored by lane**

Proportion of Read-Pairs

Mean:

Percentile of Gene Body (5'->3')

af

Gene–Body Coverage, Upper Middle Quartile Genes
With Sample srpk3_hom_ttnb_het_1 Colored by lane

Proportion of Read-Pairs

Mean:

Percentile of Gene Body (5'->3')

ag

Gene–Body Coverage, Low Expression Genes
With Sample srpk3_hom_ttnb_het_1 Colored by lane

Proportion of Read-Pairs

Mean:

Percentile of Gene Body (5'->3')

ah

Read Mapping Location Rates
With Sample srpk3_hom_ttnb_het_1 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
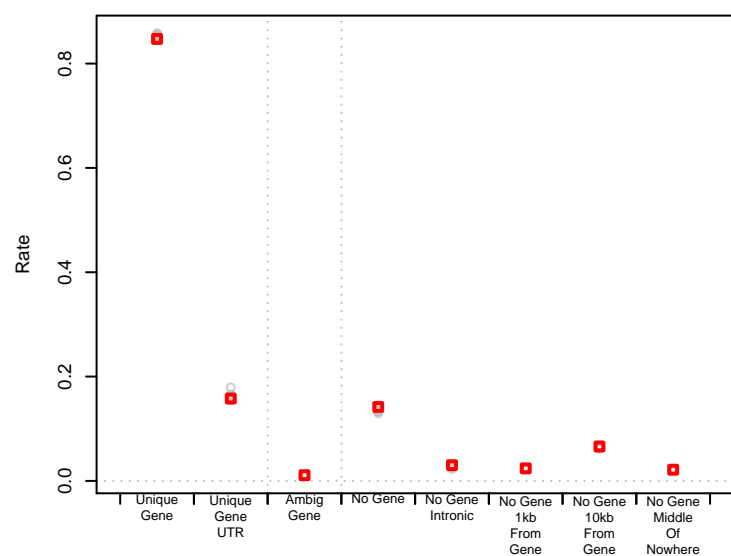
ai

 # Observed Splice Junction Loci, by type
With Sample srpk3_hom_ttnb_het_1 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
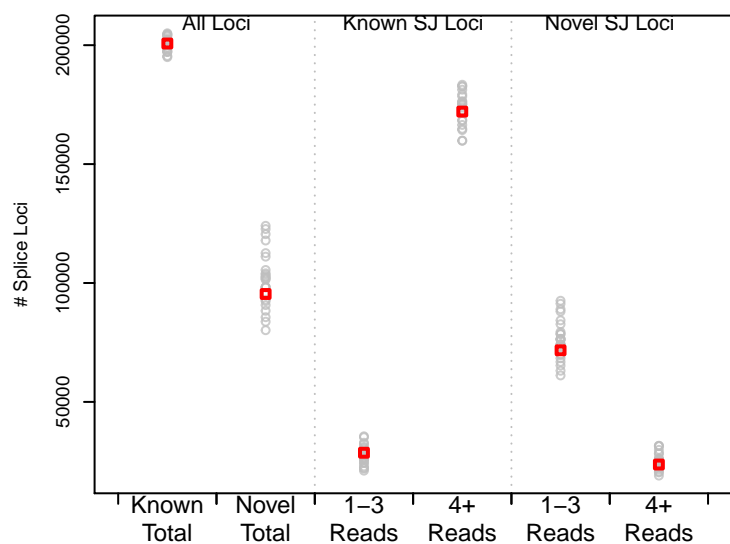
aj

Breakdown of Splice Junction Events, by type
With Sample srpk3_hom_ttnb_het_1 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_hom_ttnb_het_1 Colored by lane

al

Mapping Stats
With Sample srpk3_hom_ttnb_het_1 Colored by lane

am

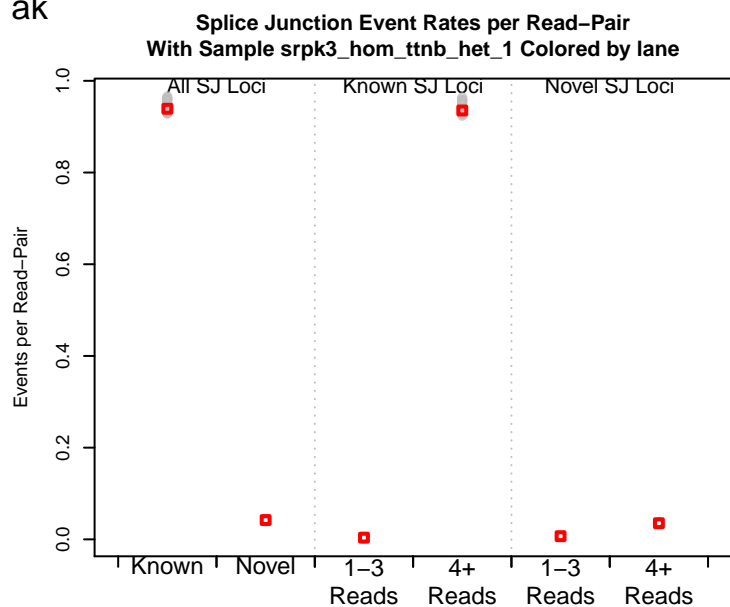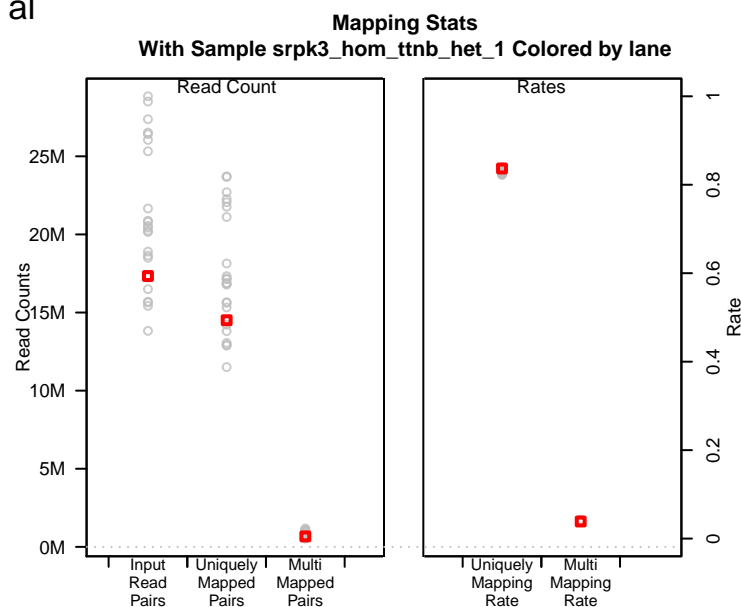**Chromosome Distribution (Excluding Autosomes)**
With Sample srpk3_hom_ttnb_het_1 Colored by lane

an

Normalization Factors
With Sample srpk3_hom_ttnb_het_1 Colored by lane

ao

Normalization Factors vs Total−Count Normalization
With Sample srpk3_hom_ttnb_het_1 Colored by lane

ap

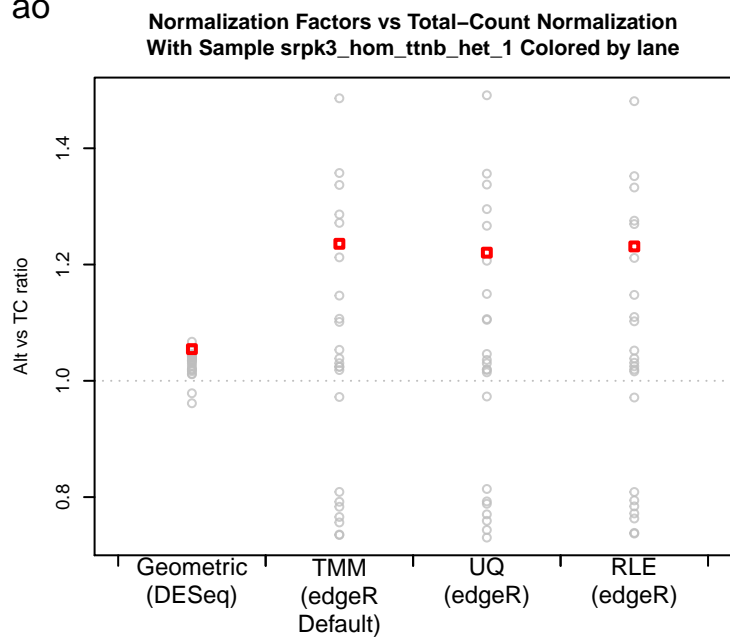**Strandedness Test**
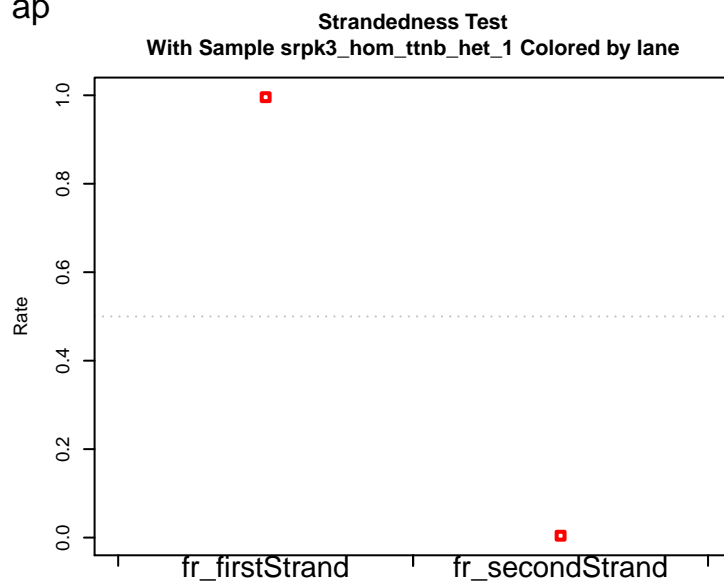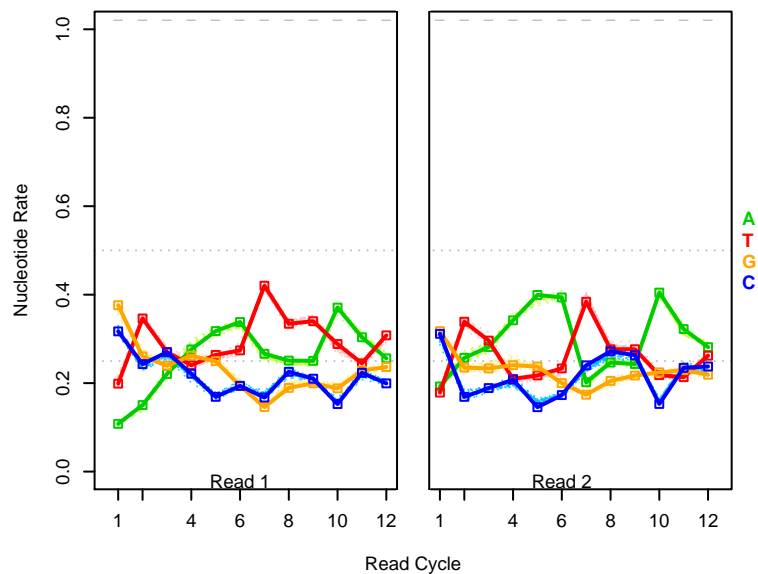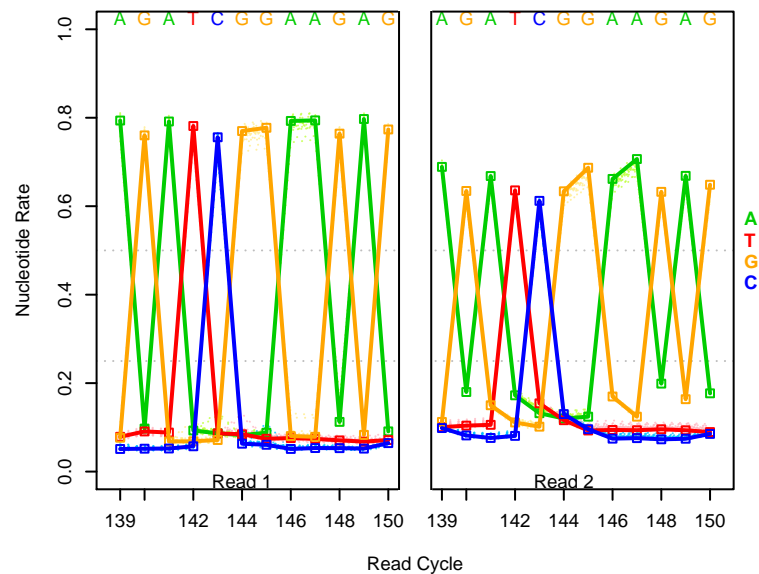**With Sample srpk3_hom_ttnb_het_1 Colored by lane**

aq

Nucleotide Rate by Cycle, Leading Clipped bases (12)
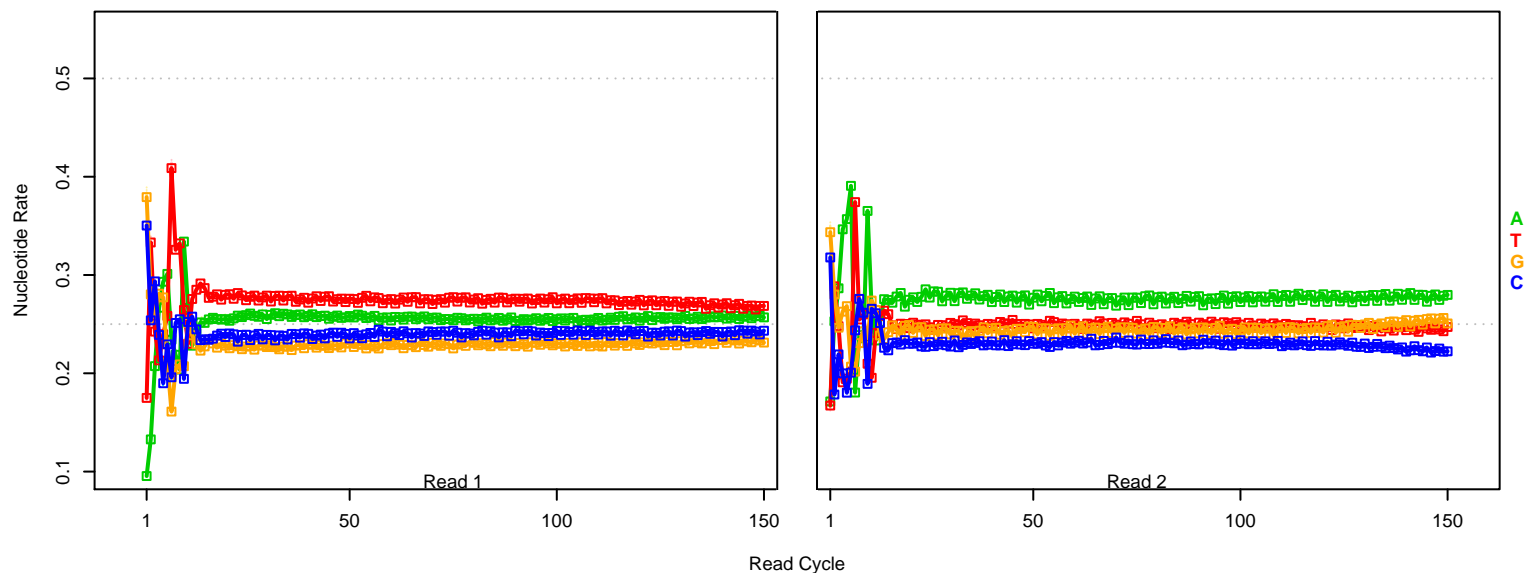**With Sample srpk3_hom_ttnb_het_1 in Bold**

ar

Nucleotide Rate by Cycle, Trailing Clipped bases (12)
With Sample srpk3_hom_ttnb_het_1 in Bold

as

Raw Nucleotide Rate by Cycle
With Sample srpk3_hom_ttnb_het_1 in Bold

at

Nucleotide Rate by Cycle, Aligned bases only
With Sample srpk3_hom_ttnb_het_1 in Bold