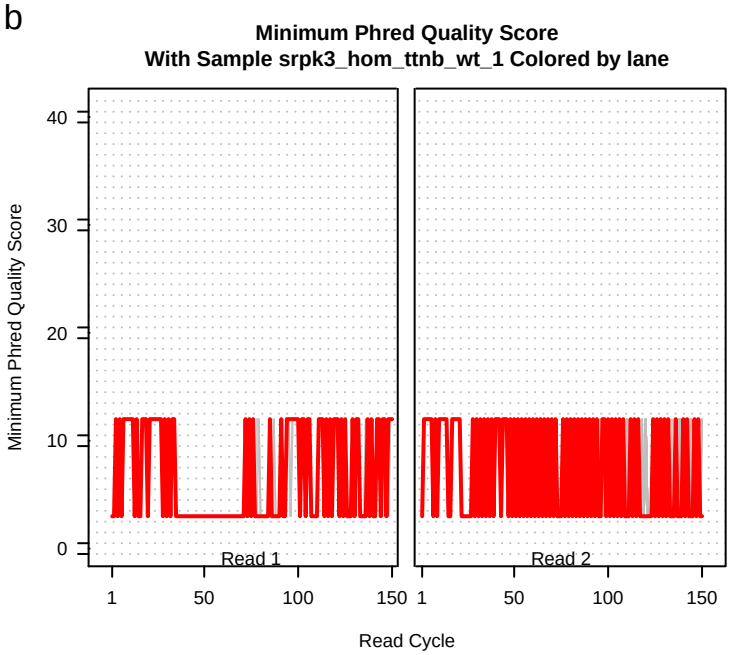
a

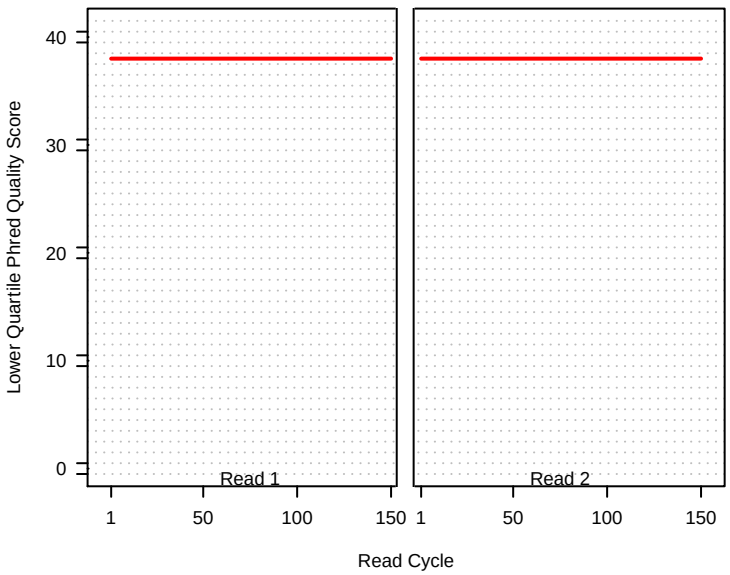
Sample Highlight:
srpk3_hom_ttnb_wt_1
Colored by Lane

UNKNOWN
Other Samples

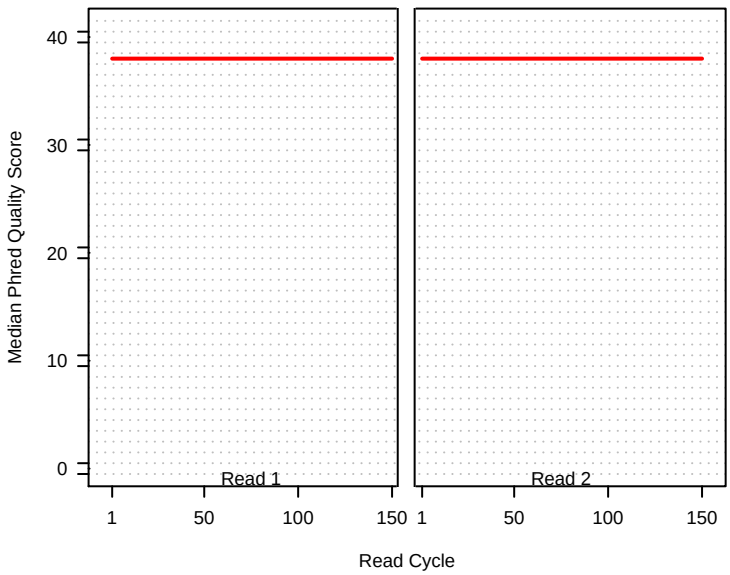
b



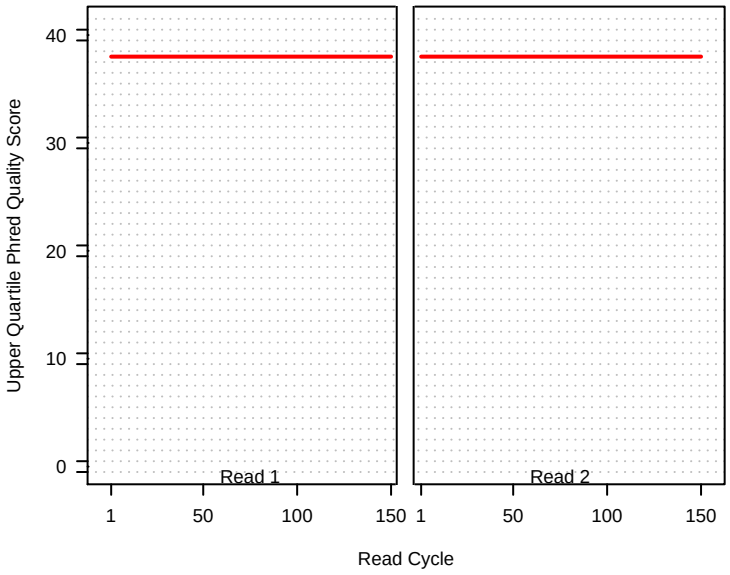
c



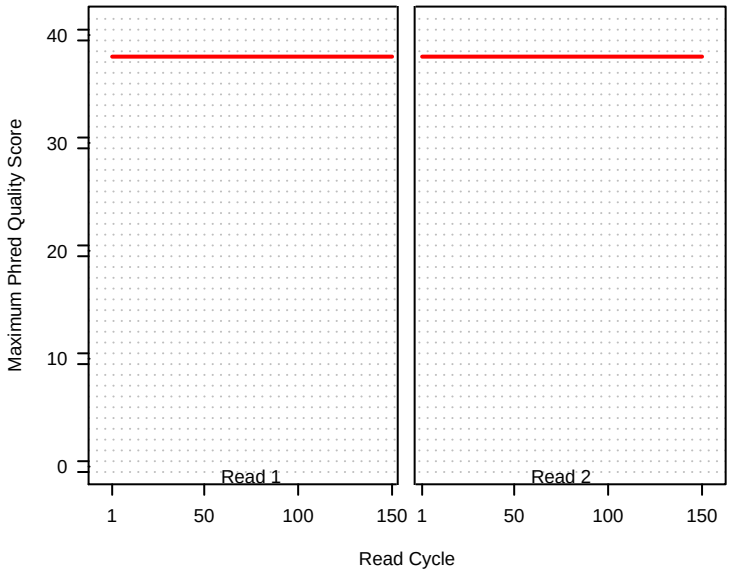
d



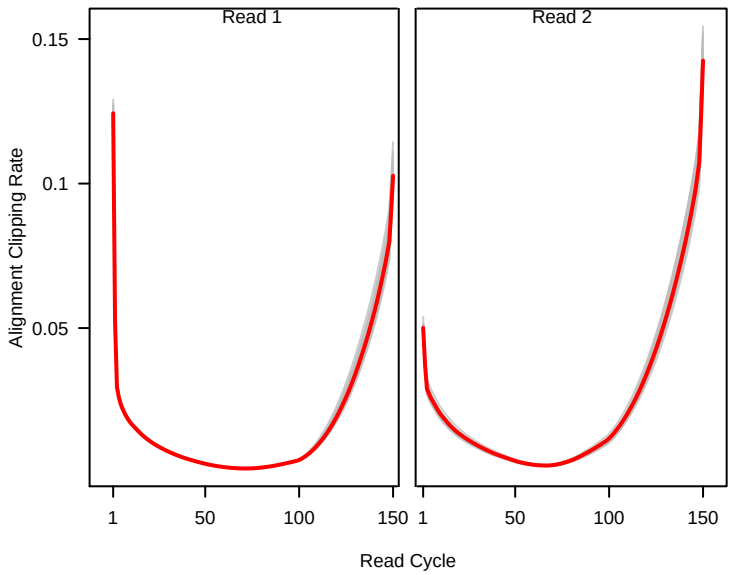
e



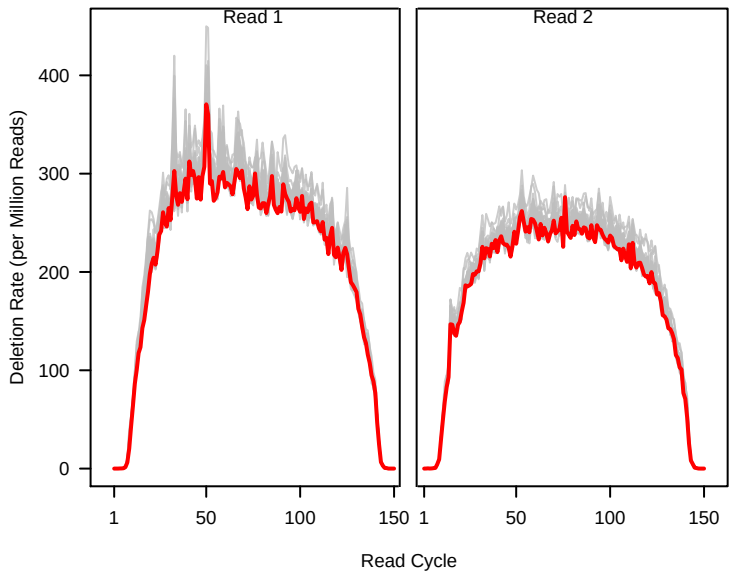
f



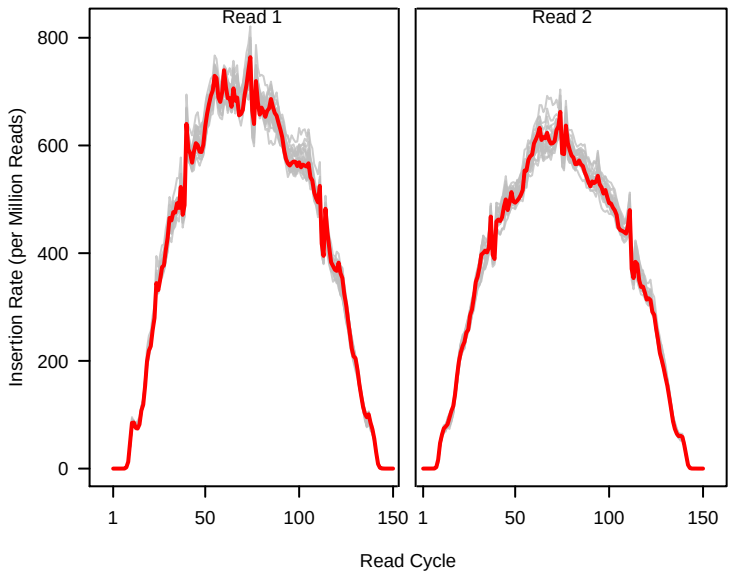
g


Alignment Clipping Rate, by read cycle
With Sample srpk3_hom_ttnb_wt_1 Colored by lane
Read 1
Read 2
Alignment Clipping Rate
0.15
0.1
0.05
1
50
100
150
Read Cycle

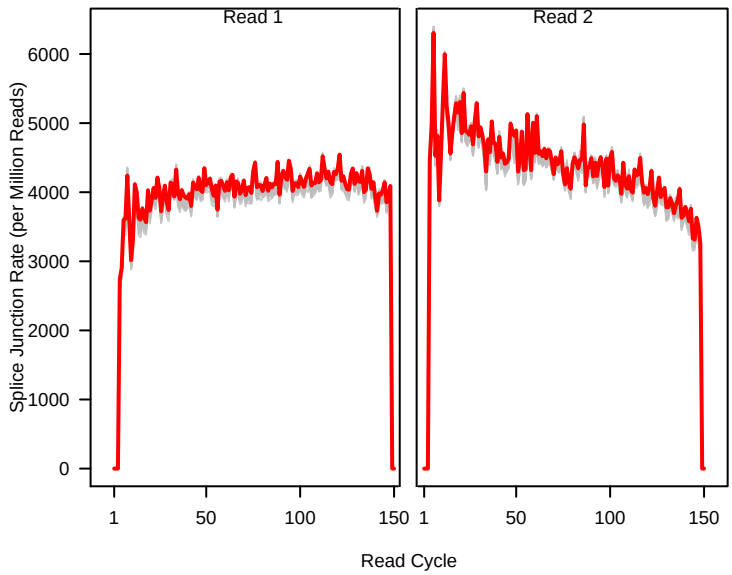
h


Deletion Rate, by read cycle
With Sample srpk3_hom_ttnb_wt_1 Colored by lane
Read 1
Read 2
Deletion Rate (per Million Reads)
400
300
200
100
0
1
50
100
150
Read Cycle

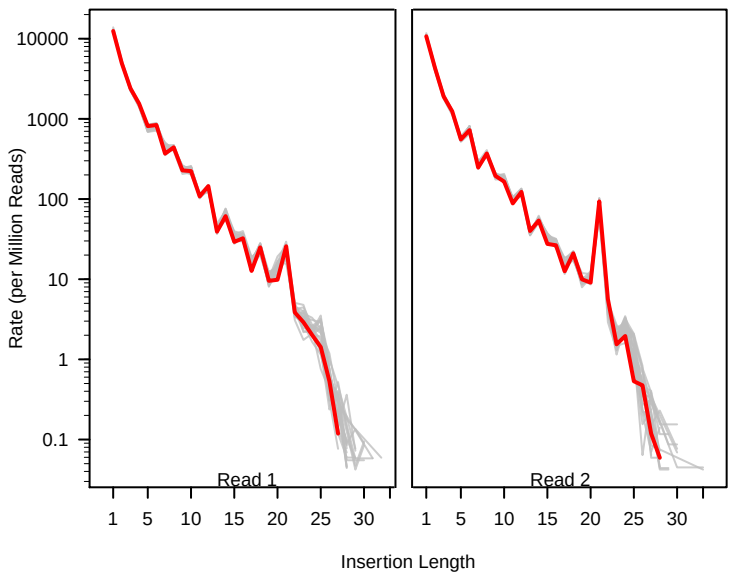
i


Insertion Rate, by read cycle
With Sample srpk3_hom_ttnb_wt_1 Colored by lane
Read 1
Read 2
Insertion Rate (per Million Reads)
800
600
400
200
0
1
50
100
150
Read Cycle

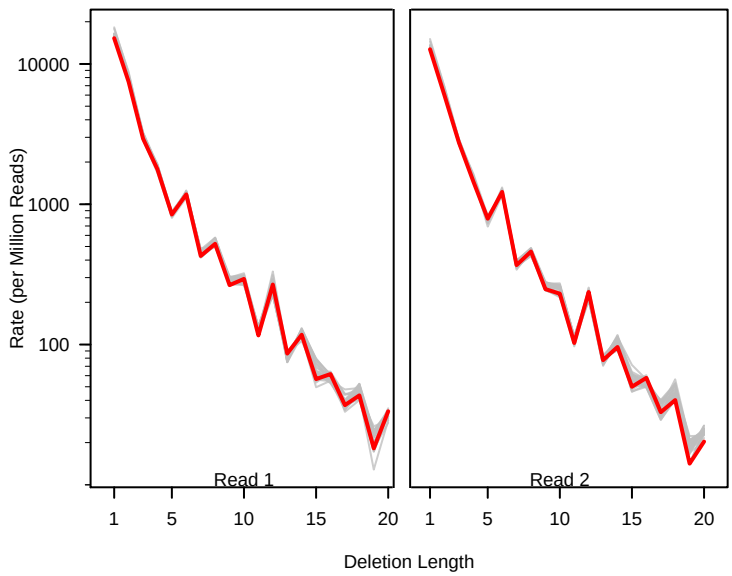
j


Splice Junction Rate, by read cycle
With Sample srpk3_hom_ttnb_wt_1 Colored by lane
Read 1
Read 2
Splice Junction Rate (per Million Reads)
6000
5000
4000
3000
2000
1000
0
1
50
100
150
Read Cycle

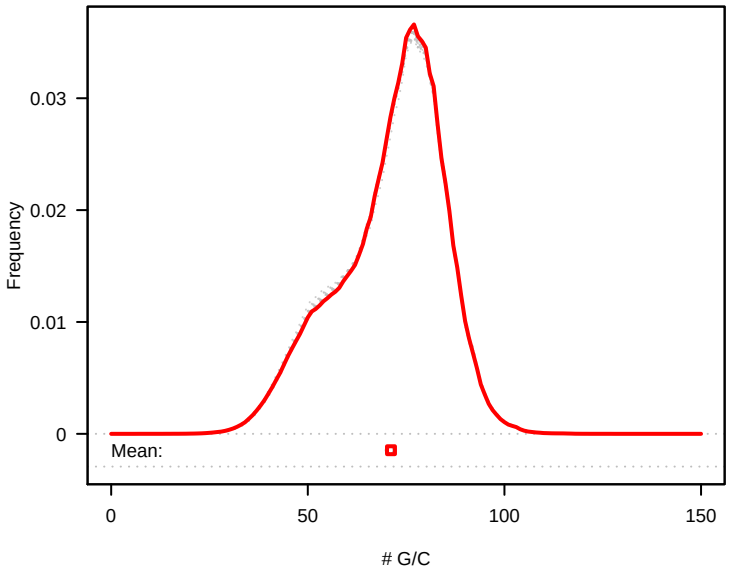
k


Insertion Length Distribution
With Sample srpk3_hom_ttnb_wt_1 Colored by lane
Read 1
Read 2
Rate (per Million Reads)
10000
1000
100
10
1
0.1
1
5
10
15
20
25
30
Insertion Length

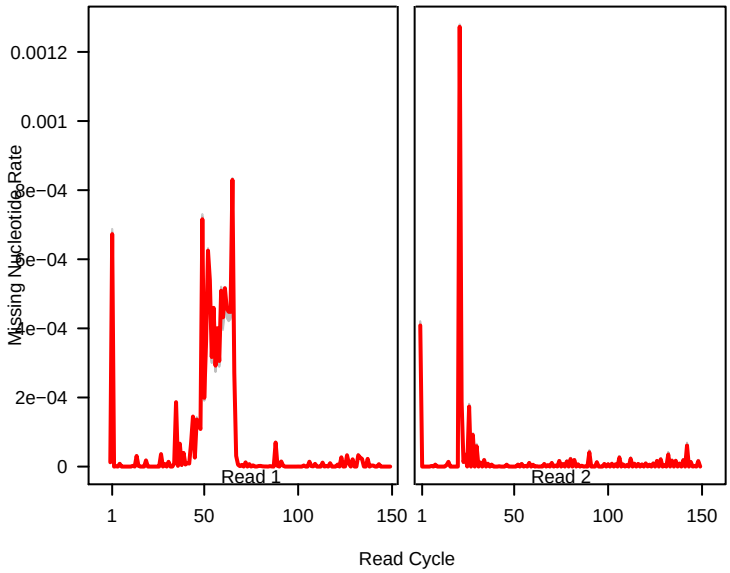
l


Deletion Length Distribution
With Sample srpk3_hom_ttnb_wt_1 Colored by lane
Read 1
Read 2
Rate (per Million Reads)
10000
1000
100
1
5
10
15
20
Deletion Length

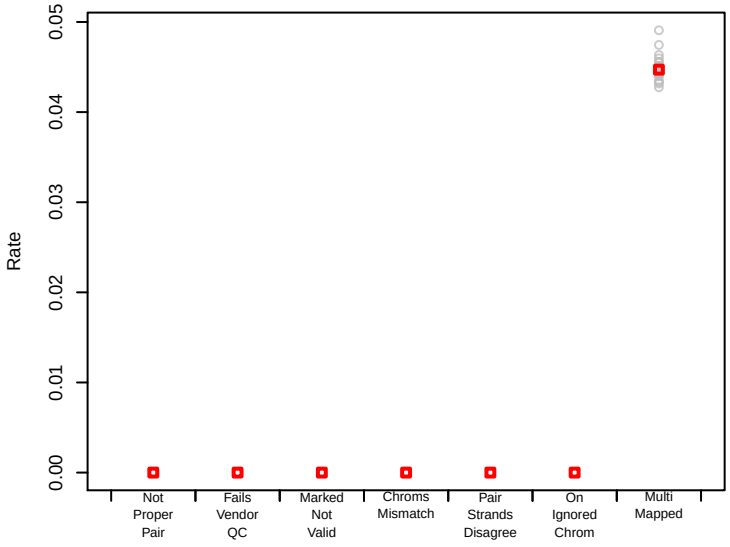
m


GC Content
With Sample srpk3_hom_ttnb_wt_1 Colored by lane
Frequency
0.03
0.02
0.01
0
Mean:
0
50
100
150
G/C

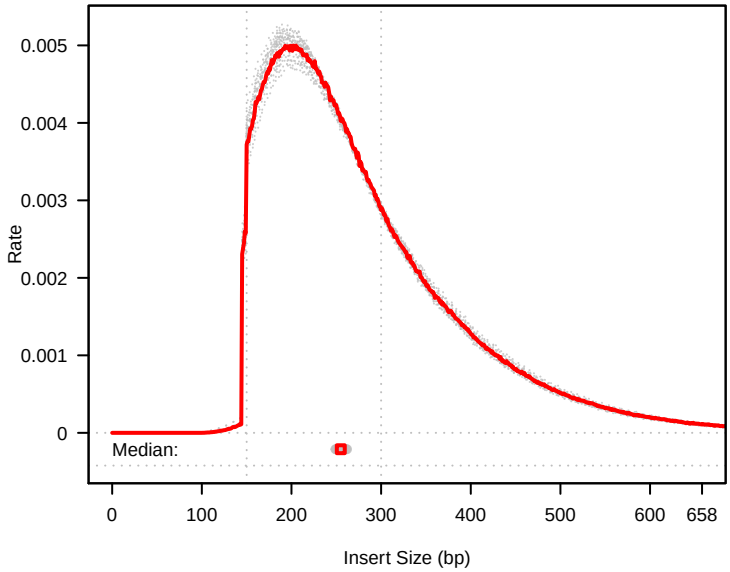
n


'N' Rate, by Read Cycle
With Sample srpk3_hom_ttnb_wt_1 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
Read Cycle

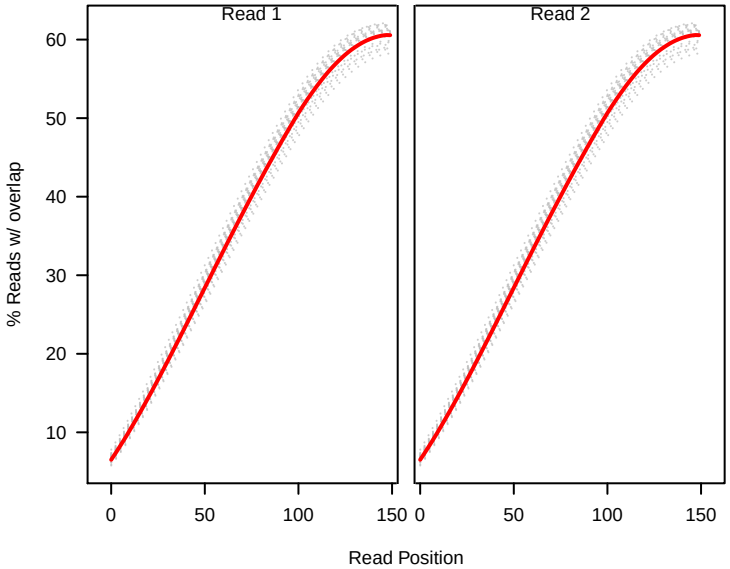
o


Read Drop Rate, by Reason
With Sample srpk3_hom_ttnb_wt_1 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

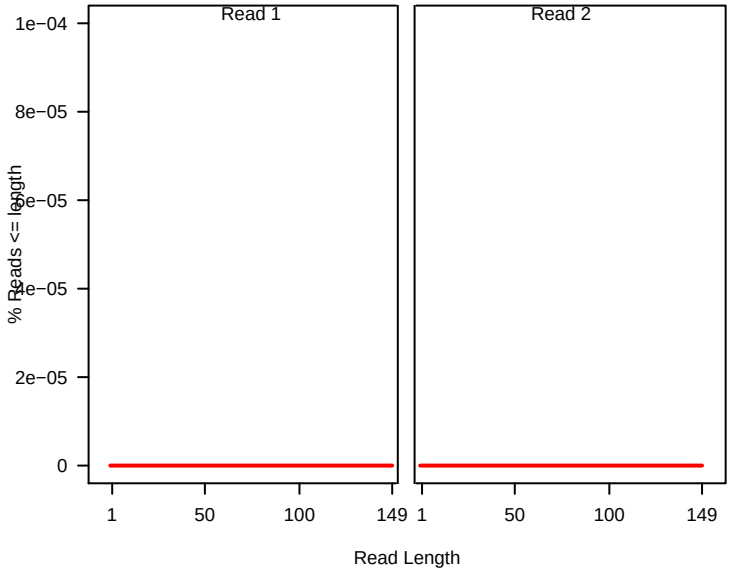
p


Insert Size
With Sample srpk3_hom_ttnb_wt_1 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)

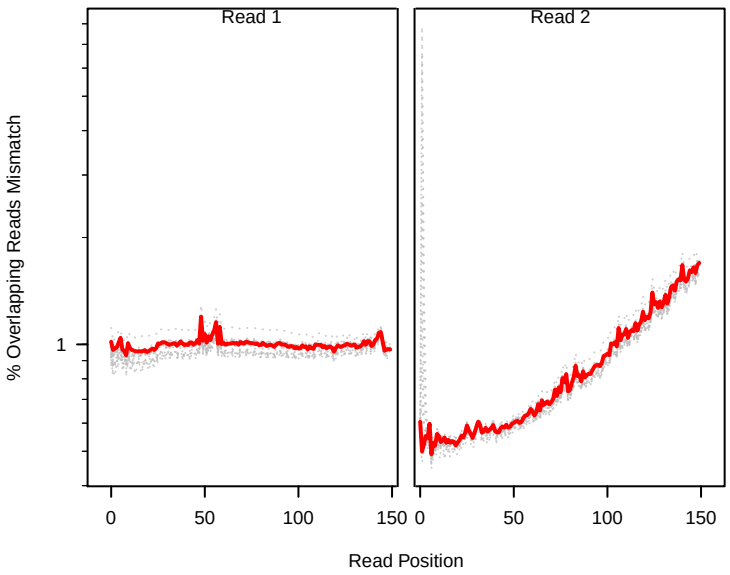
q


Overlapping Coverage
With Sample srpk3_hom_ttnb_wt_1 Colored by lane
Read 1
Read 2
% Reads w/ overlap
60
50
40
30
20
10
0
50
100
150
Read Position

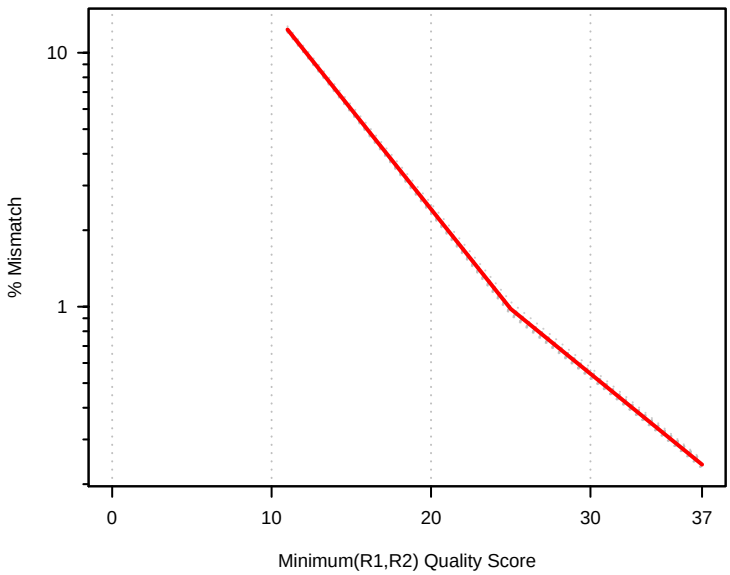
r


Read Length Distribution
With Sample srpk3_hom_ttnb_wt_1 Colored by lane
Read 1
Read 2
% Reads <= length
1e−04
8e−05
6e−05
4e−05
2e−05
0
1
50
100
149
Read Length

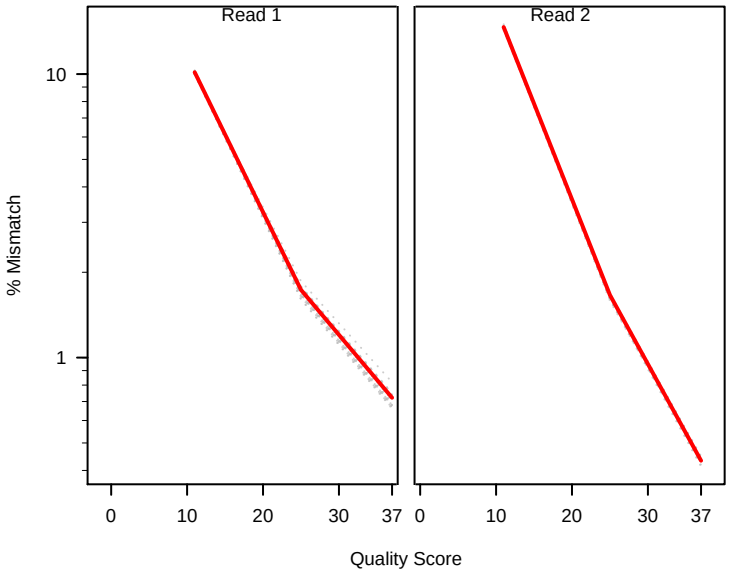
s


Overlap Mismatch by Read Cycle
With Sample srpk3_hom_ttnb_wt_1 Colored by lane
Read 1
Read 2
% Overlapping Reads Mismatch
1
0
50
100
150
Read Position

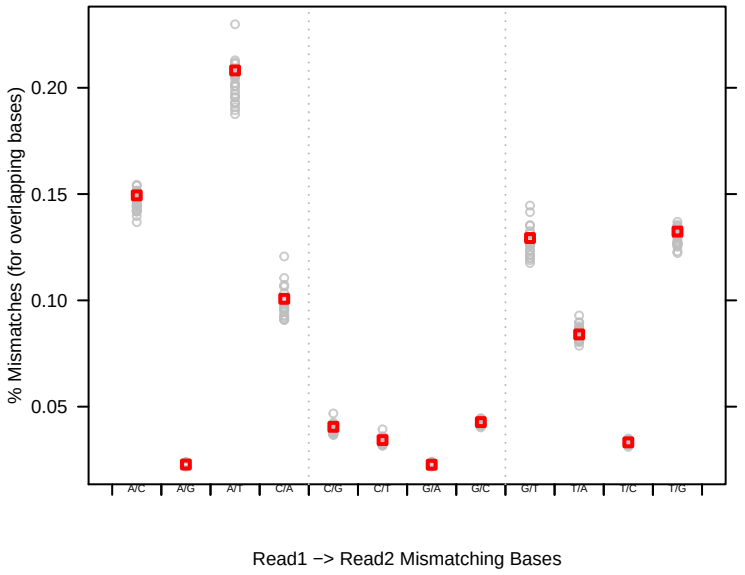
t


Overlapping Mismatch by Min Qual
With Sample srpk3_hom_ttnb_wt_1 Colored by lane
% Mismatch
10
1
0
10
20
30
37
Minimum(R1,R2) Quality Score

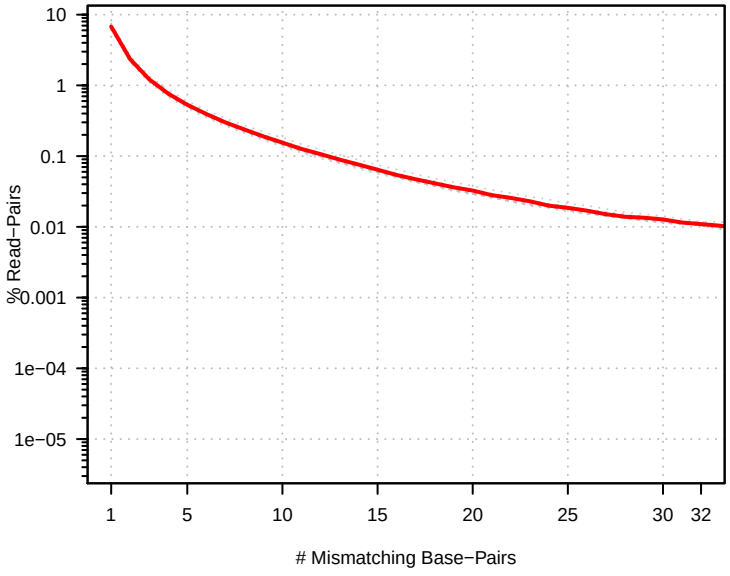
u


Overlap Mismatch by Read Qual
With Sample srpk3_hom_ttnb_wt_1 Colored by lane
Read 1
Read 2
% Mismatch
10
1
0
10
20
30
37
Quality Score

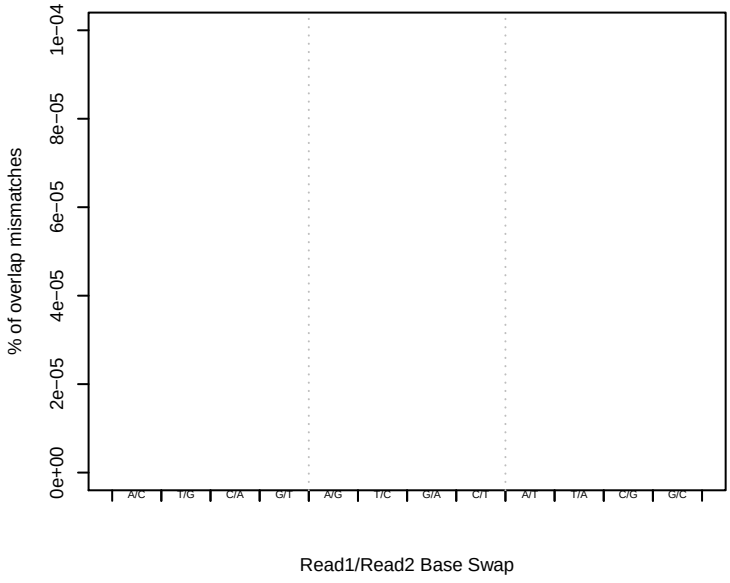
v


Overlap Mismatch Combinations
With Sample srpk3_hom_ttnb_wt_1 Colored by lane
% Mismatches (for overlapping bases)
0.20
0.15
0.10
0.05
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

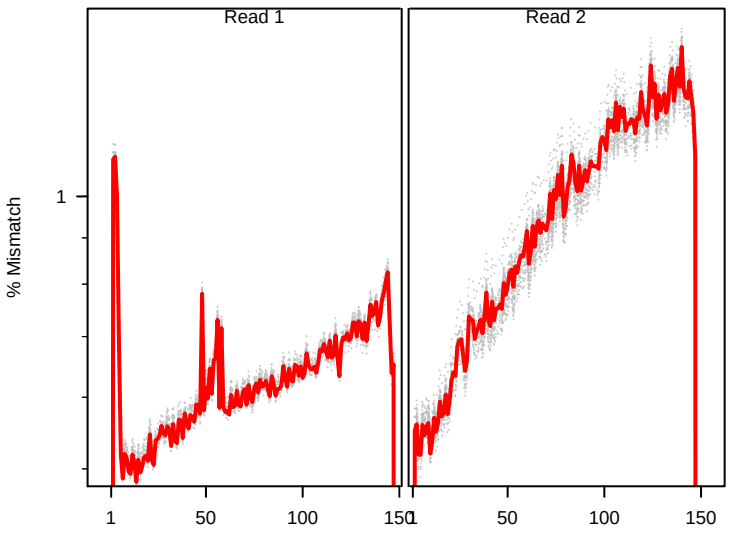
w


Overlap Mismatch Size Frequency
With Sample srpk3_hom_ttnb_wt_1 Colored by lane
% Read-Pairs
10
1
0.1
0.01
0.001
1e-04
1e-05
1
5
10
15
20
25
30
32
Mismatching Base-Pairs

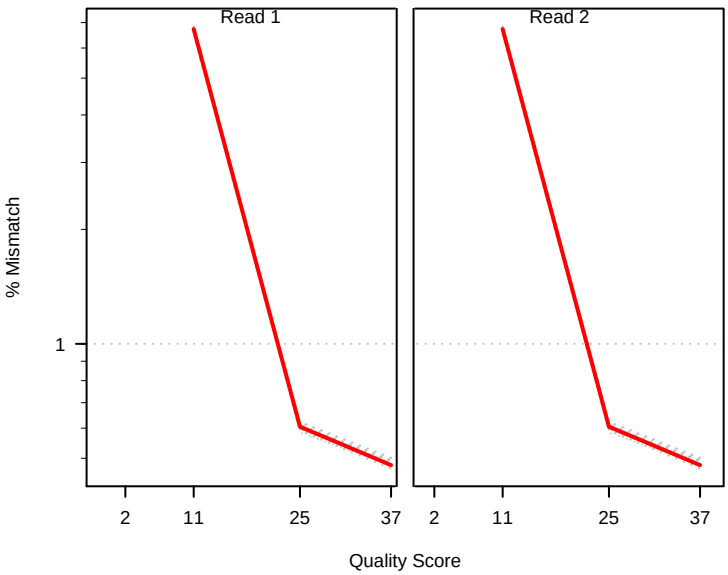
x


Overlap Mismatch Pairs At Phred == 41
With Sample srpk3_hom_ttnb_wt_1 Colored by lane
% of overlap mismatches
1e-04
8e-05
6e-05
4e-05
2e-05
0e+00
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

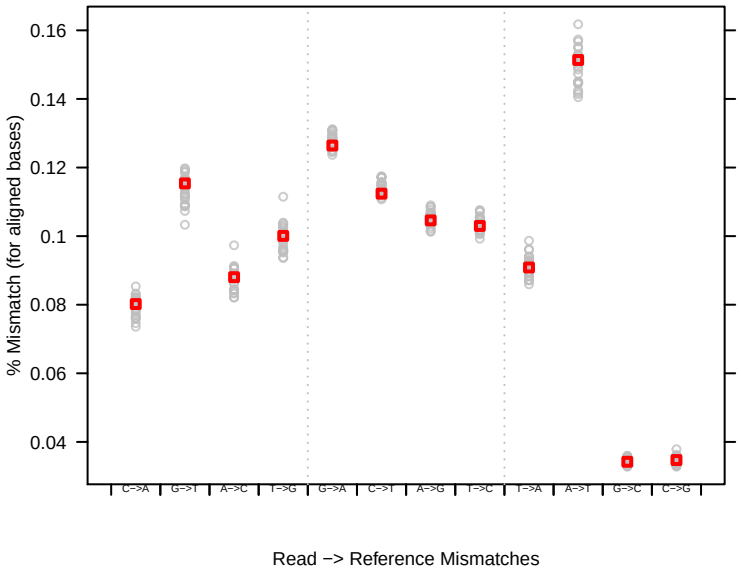
y


Reference Mismatch by Read Cycle
With Sample srpk3_hom_ttnb_wt_1 Colored by lane
Read 1
Read 2
% Mismatch
1
1
50
100
150
1
50
100
150

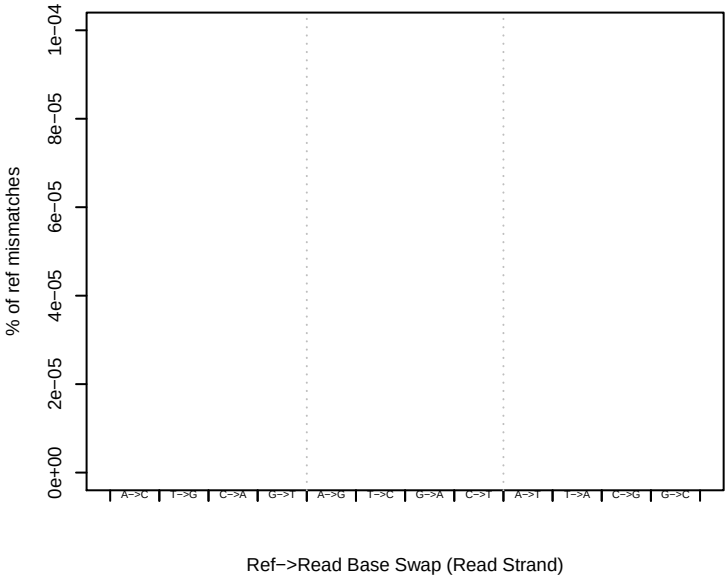
z


Reference Mismatch by Read Qual
With Sample srpk3_hom_ttnb_wt_1 Colored by lane
Read 1
Read 2
% Mismatch
1
2
11
25
37
2
11
25
37
Quality Score

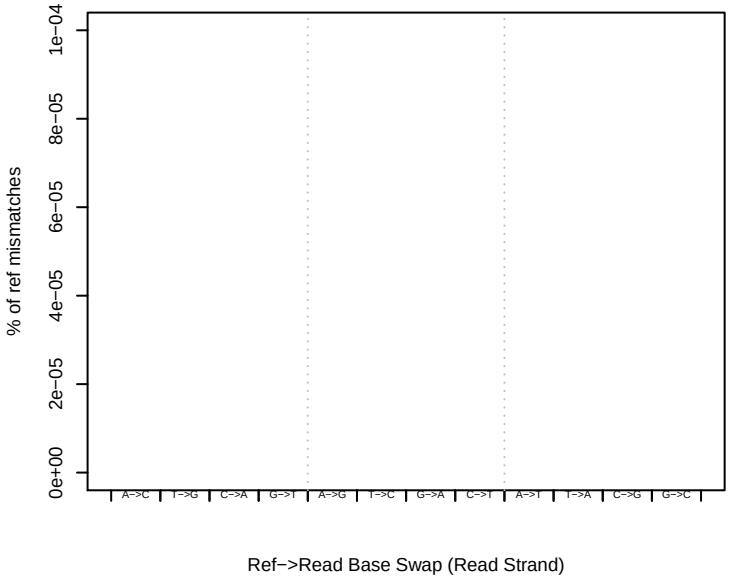
aa


Reference Mismatch Combinations
With Sample srpk3_hom_ttnb_wt_1 Colored by lane
% Mismatch (for aligned bases)
0.16
0.14
0.12
0.1
0.08
0.06
0.04
C->A
G->T
A->C
T->G
G->A
C->T
A->G
T->C
T->A
A->T
G->C
C->G
Read -> Reference Mismatches

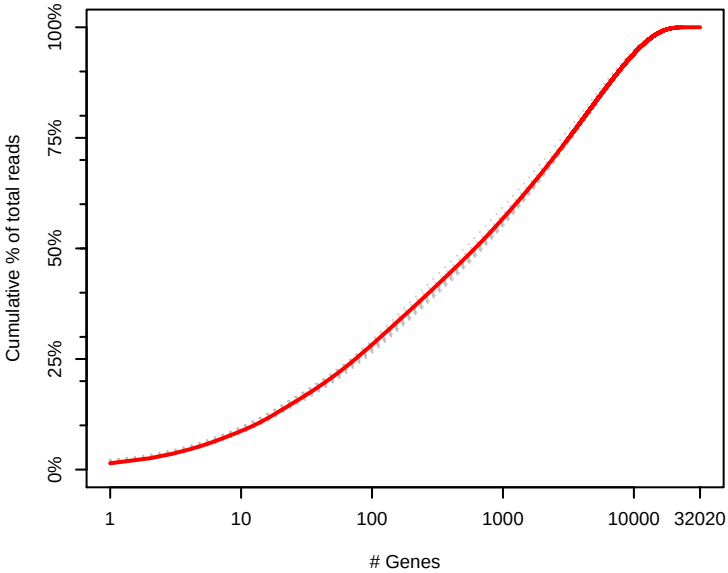
ab


R1 Ref Mismatches At Phred == 41
With Sample srpk3_hom_ttnb_wt_1 Colored by lane
% of ref mismatches
1e-04
8e-05
6e-05
4e-05
2e-05
0e+00
A->C
T->G
C->A
G->T
A->G
T->C
G->A
C->T
A->T
T->A
C->G
G->C
Ref->Read Base Swap (Read Strand)

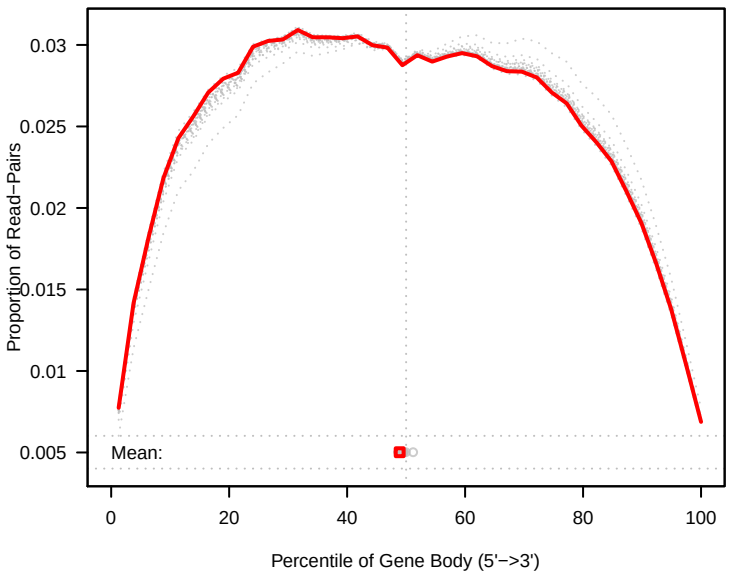
ac


R2 Ref Mismatches At Phred == 41
With Sample srpk3_hom_ttnb_wt_1 Colored by lane
% of ref mismatches
1e-04
8e-05
6e-05
4e-05
2e-05
0e+00
A->C
T->G
C->A
G->T
A->G
T->C
G->A
C->T
A->T
T->A
C->G
G->C
Ref->Read Base Swap (Read Strand)

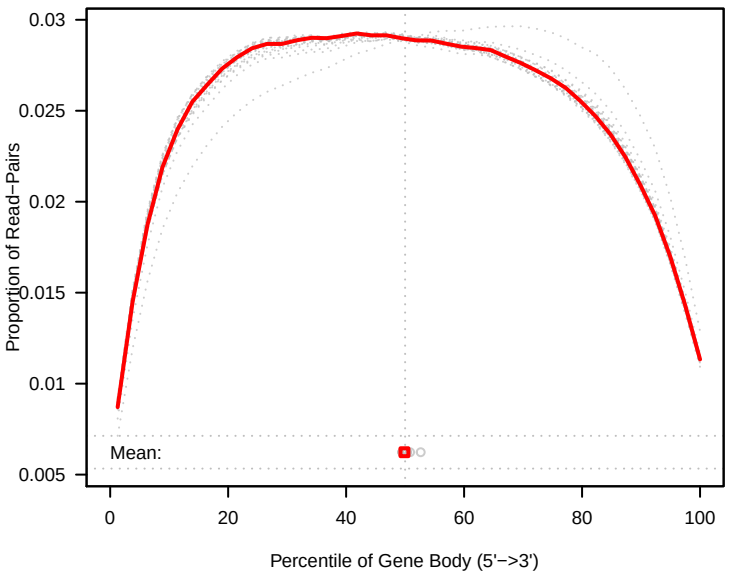
ad


Cumulative Gene Assignment Diversity
With Sample srpk3_hom_ttnb_wt_1 Colored by lane
Cumulative % of total reads
100%
75%
50%
25%
0%
1
10
100
1000
10000
32020
Genes

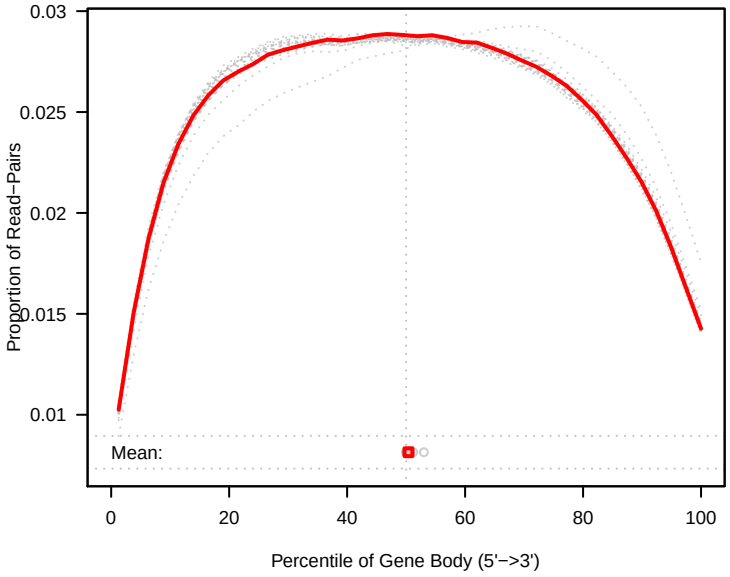
ae



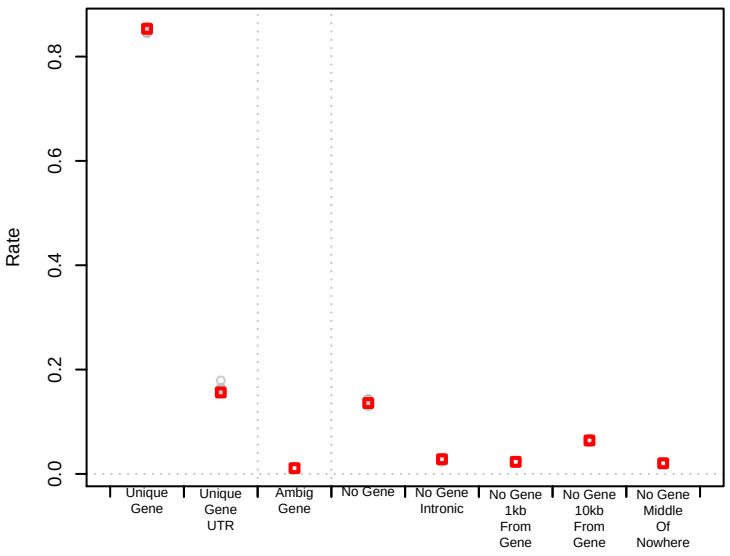
af



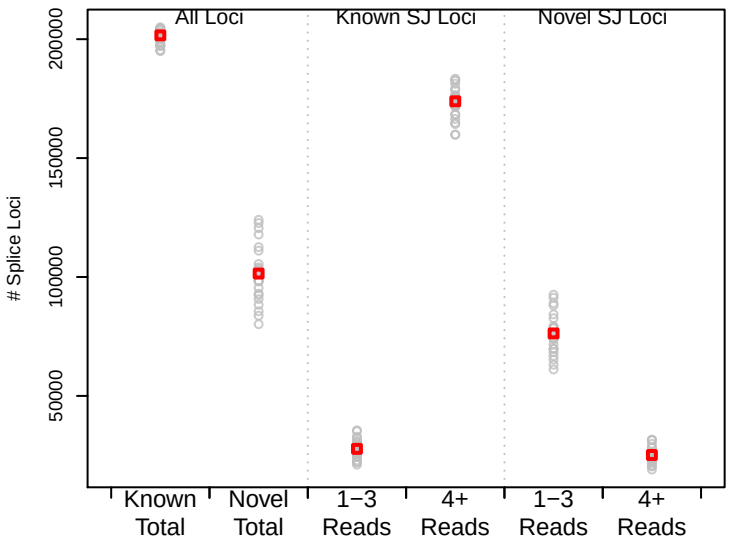
ag



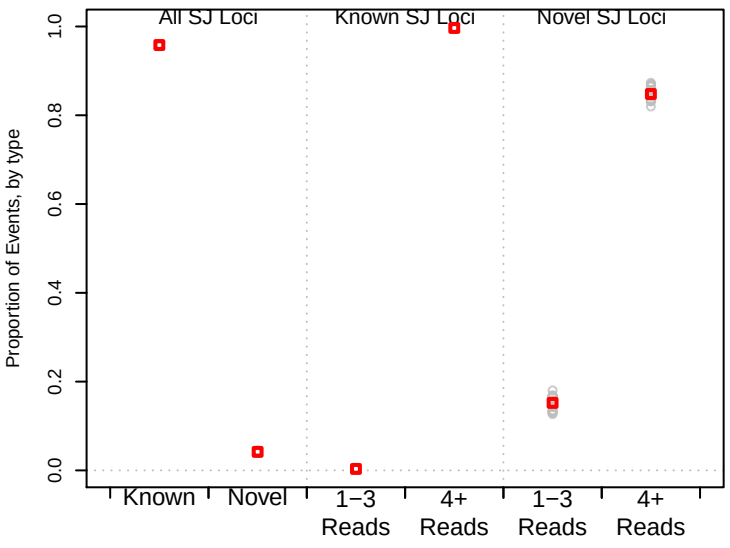
ah



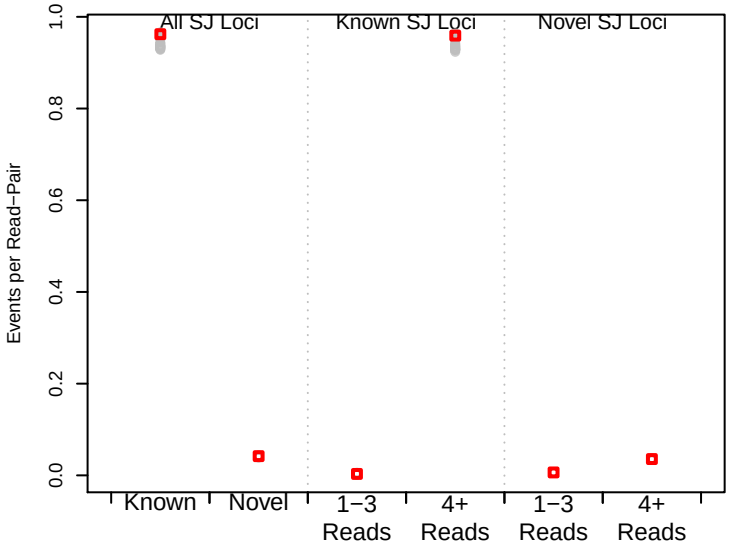
ai



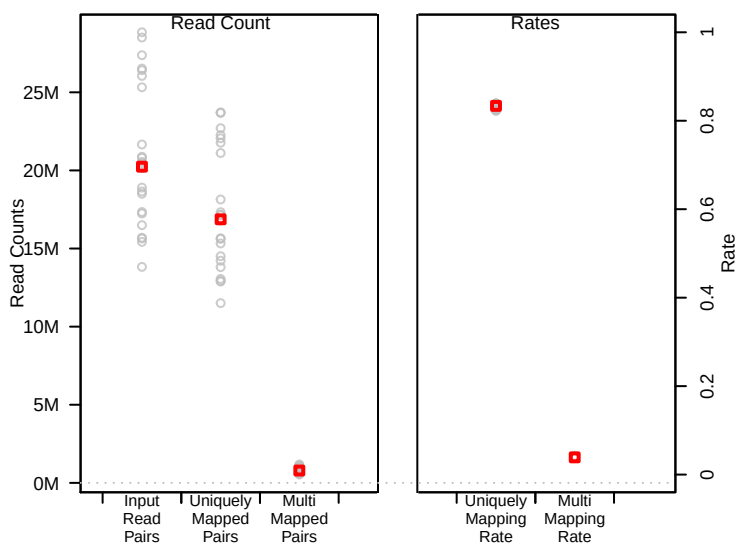
aj



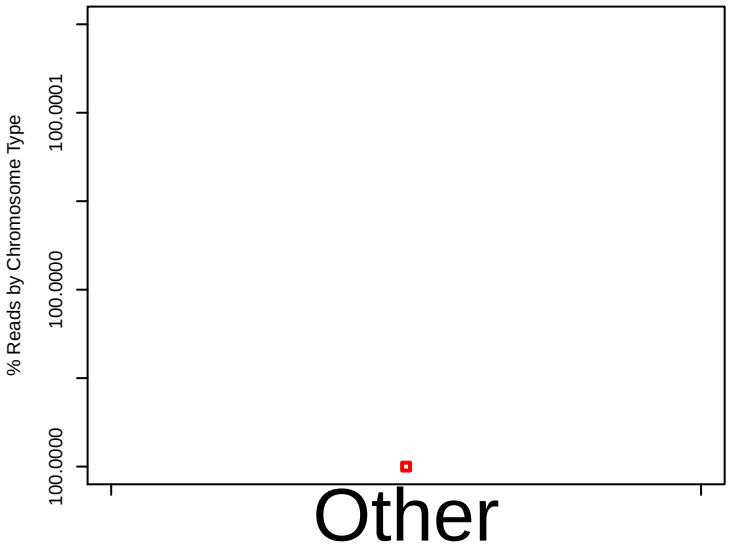
ak



al



am



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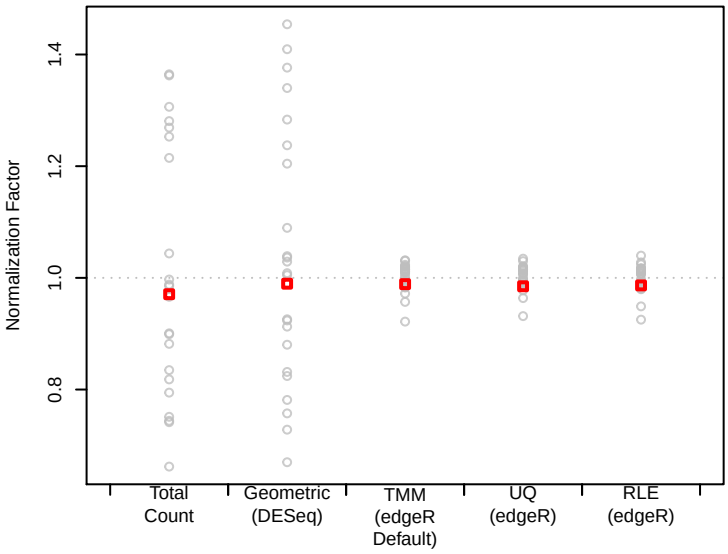

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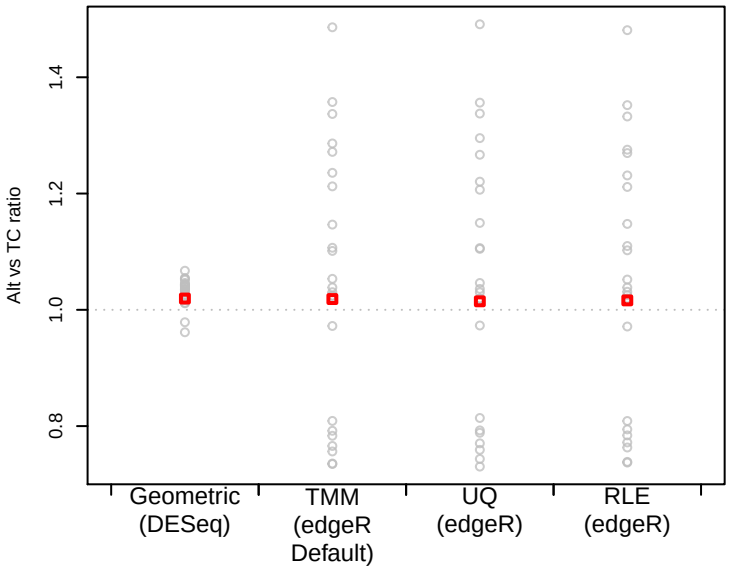

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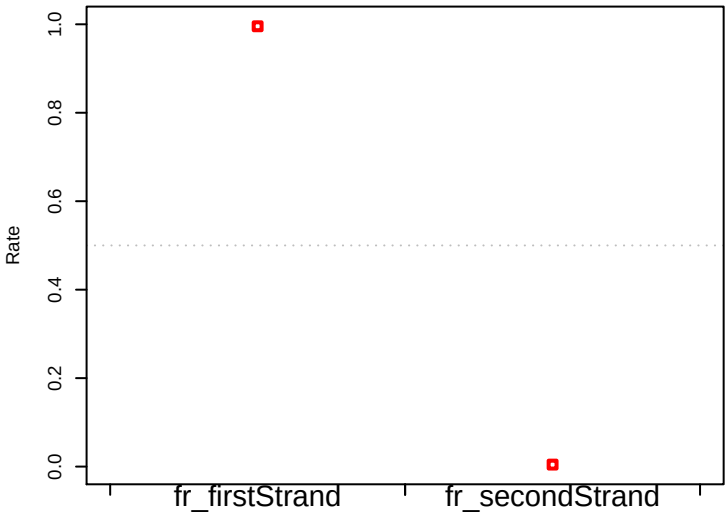

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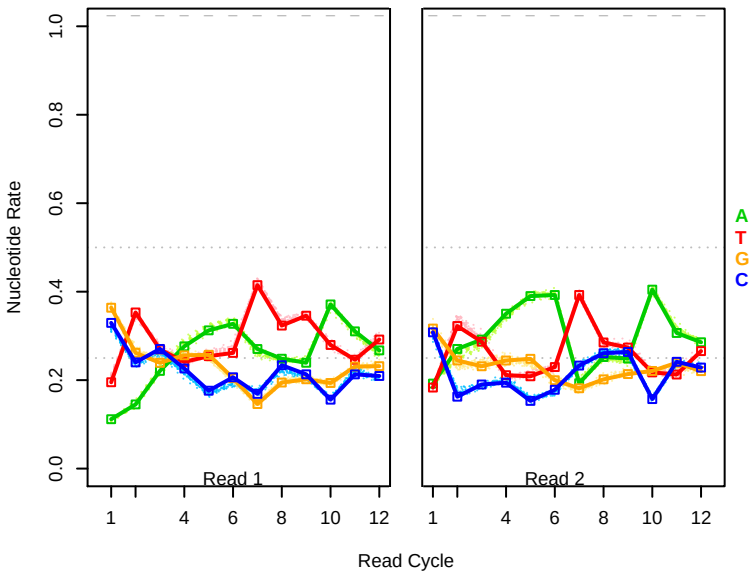
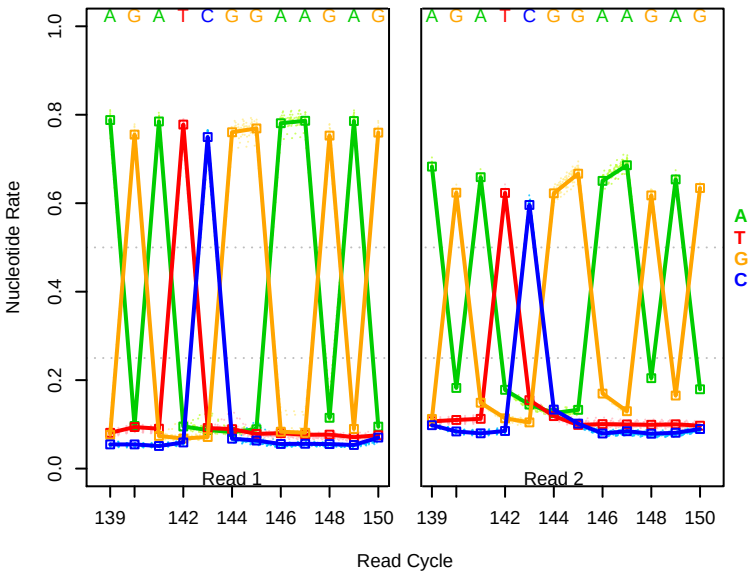
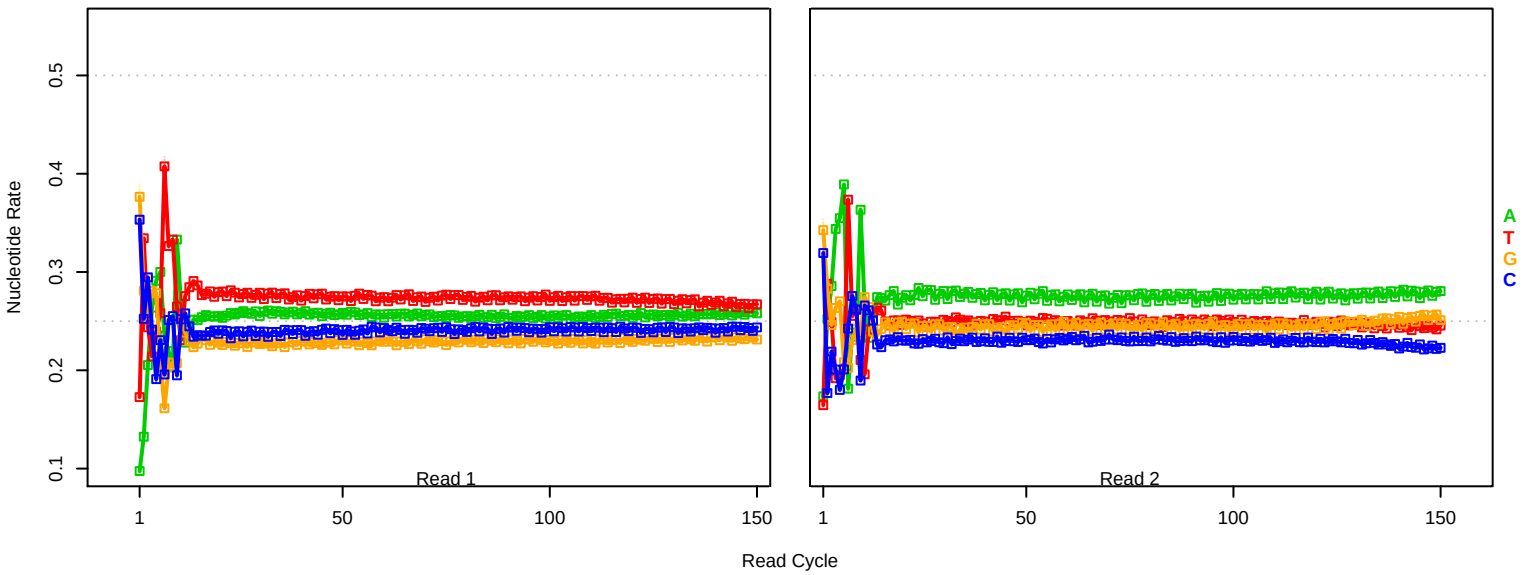

Nucleotide Rate by Cycle, Leading Clipped bases (12)
With Sample srpk3_hom_ttnb_wt_1 in Bold
Nucleotide Rate
Read 1
Read 2
Read Cycle
A
T
G
C

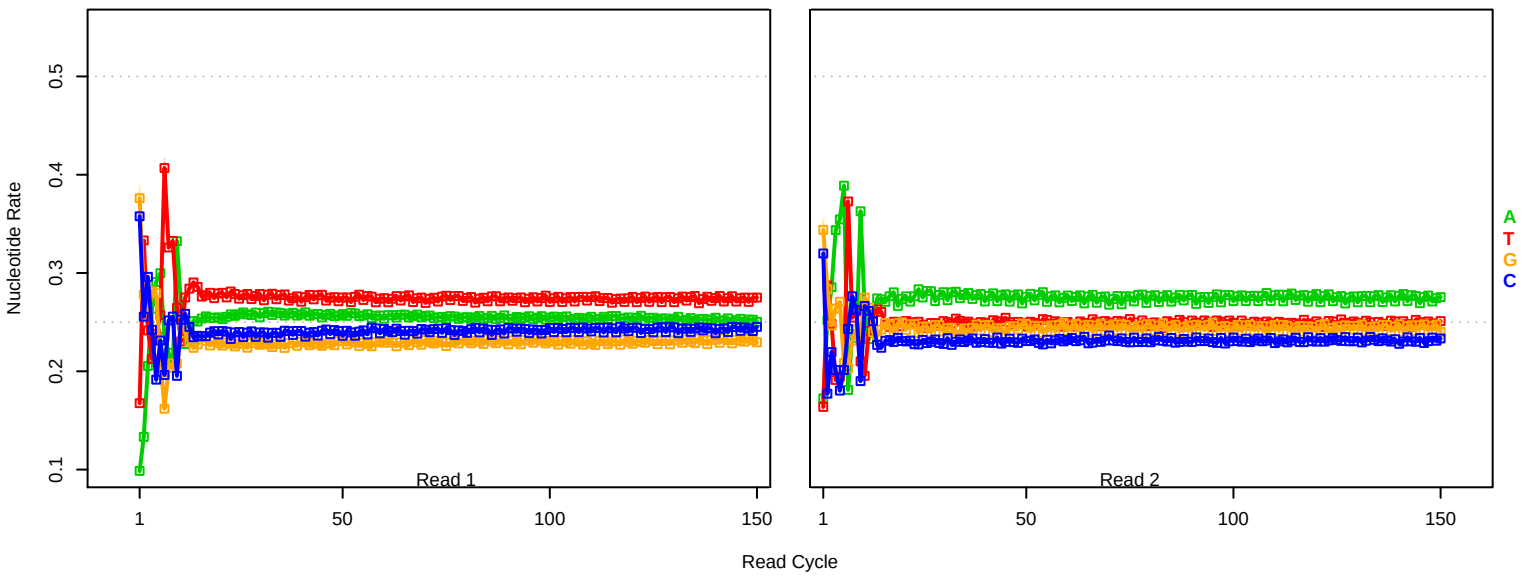
ar


Nucleotide Rate by Cycle, Trailing Clipped bases (12)
With Sample srpk3_hom_ttnb_wt_1 in Bold
A G A T C G G A A G A G
Nucleotide Rate
Read 1
Read 2
Read Cycle
A
T
G
C

as


Raw Nucleotide Rate by Cycle
With Sample srpk3_hom_ttnb_wt_1 in Bold
Nucleotide Rate
Read 1
Read 2
Read Cycle
A
T
G
C

at


Nucleotide Rate by Cycle, Aligned bases only
With Sample srpk3_hom_ttnb_wt_1 in Bold
Nucleotide Rate
Read 1
Read 2
Read Cycle
A
T
G
C