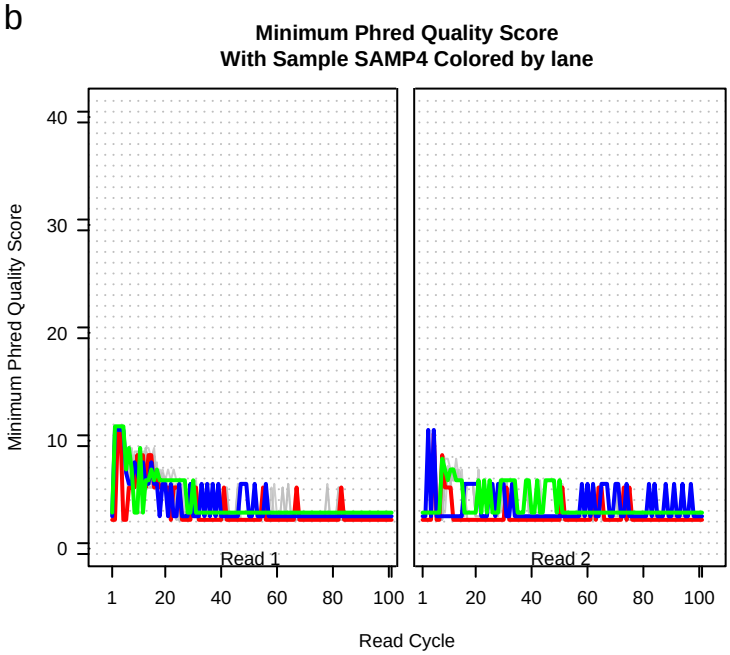
a

# Sample Highlight: SAMP4 Colored by Lane

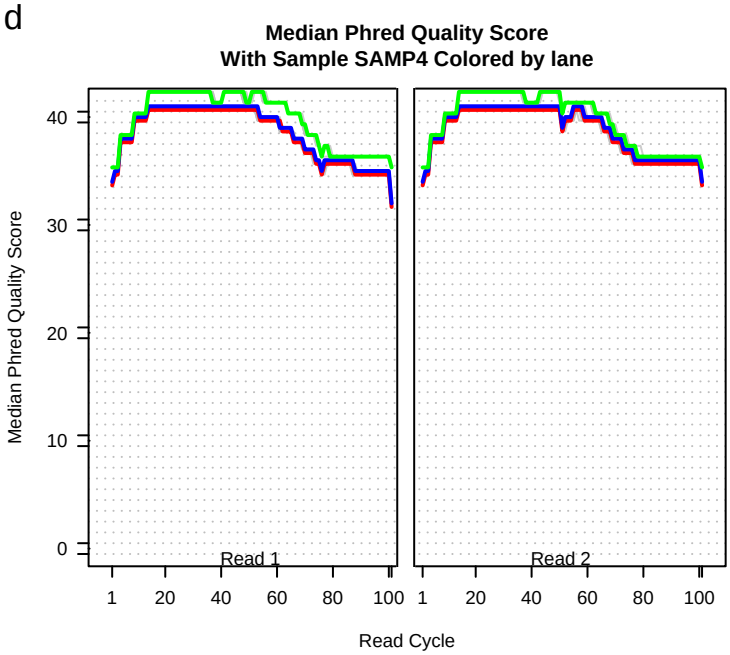
RG1
RG2
RG3
Other Samples

b

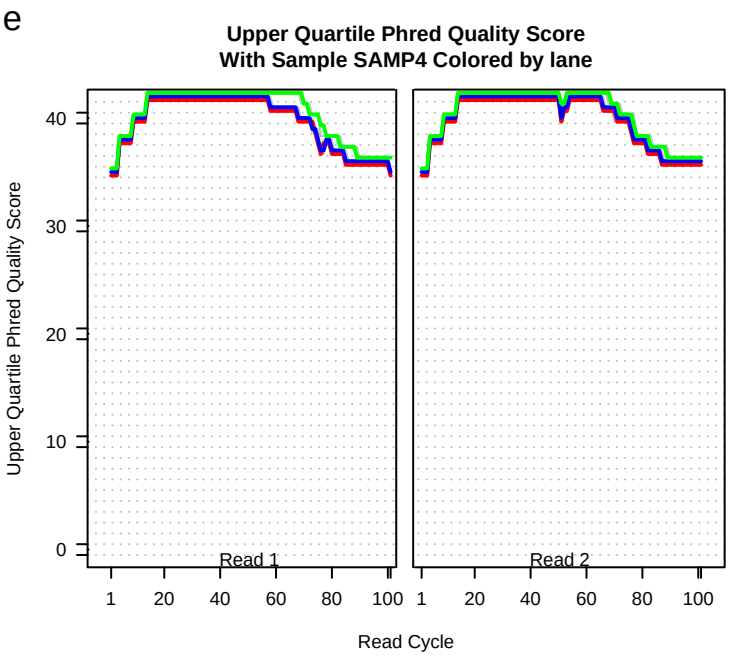



c

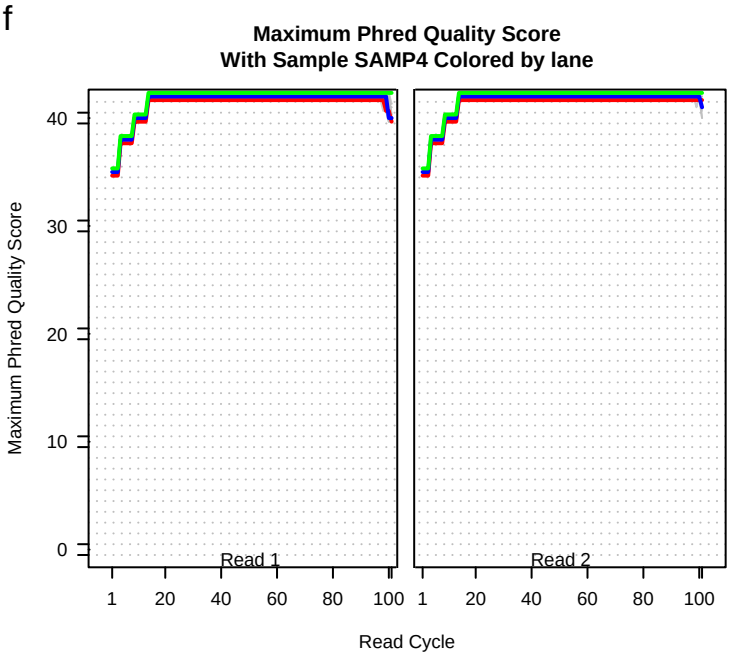
d



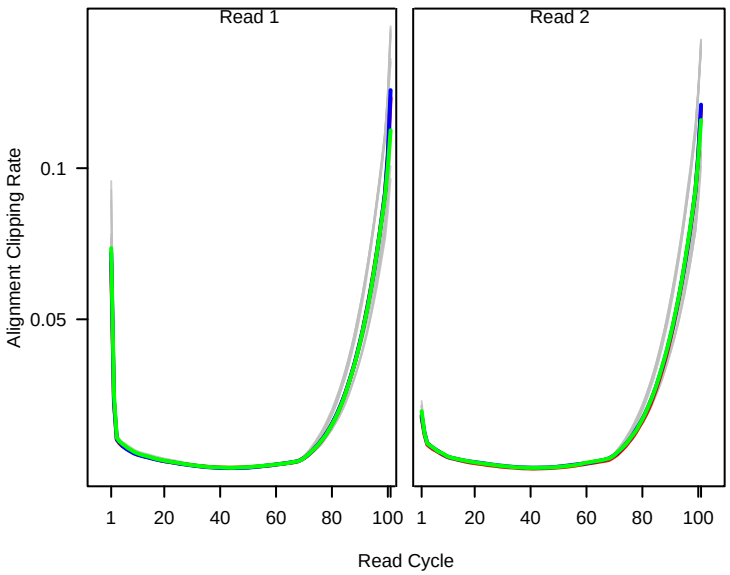

e



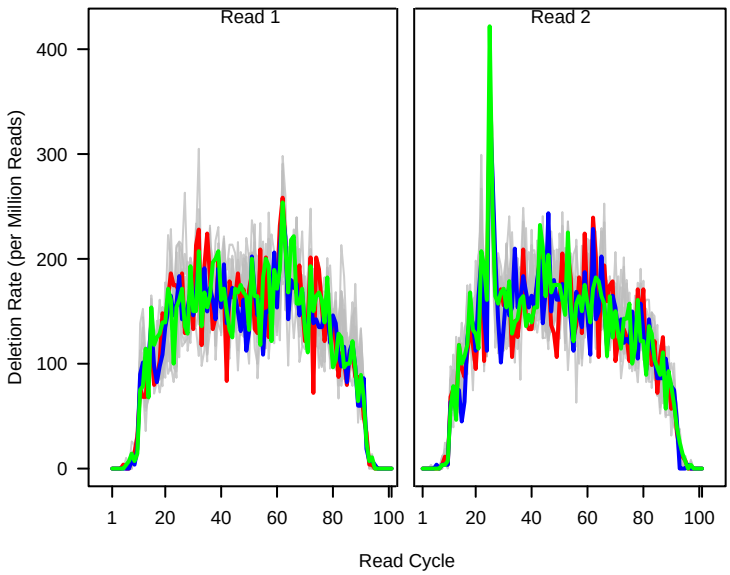

f



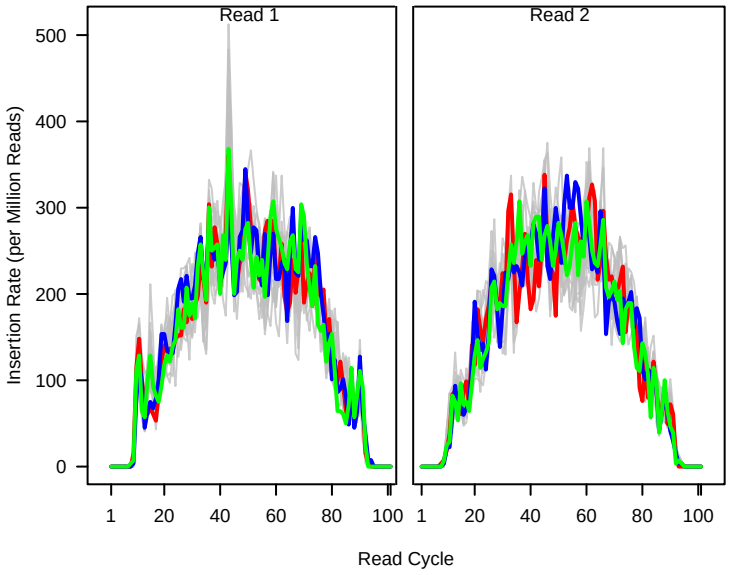
g


Alignment Clipping Rate, by read cycle
With Sample SAMP4 Colored by lane
Read 1
Read 2
Alignment Clipping Rate
0.1
0.05
1
20
40
60
80
100
Read Cycle

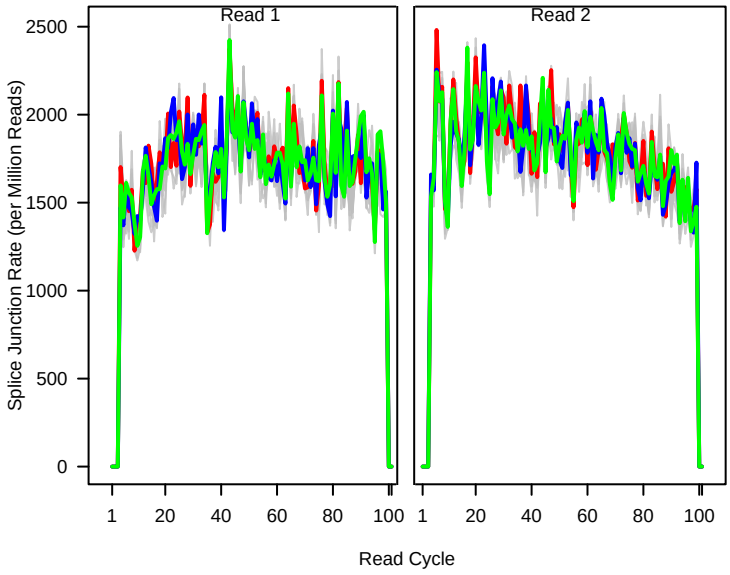
h


Deletion Rate, by read cycle
With Sample SAMP4 Colored by lane
Read 1
Read 2
Deletion Rate (per Million Reads)
400
300
200
100
0
1
20
40
60
80
100
Read Cycle

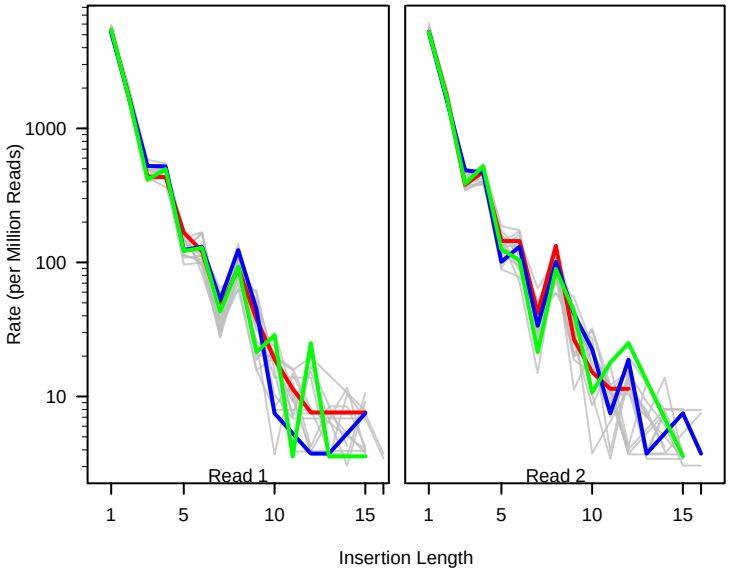
i


Insertion Rate, by read cycle
With Sample SAMP4 Colored by lane
Read 1
Read 2
Insertion Rate (per Million Reads)
500
400
300
200
100
0
1
20
40
60
80
100
Read Cycle

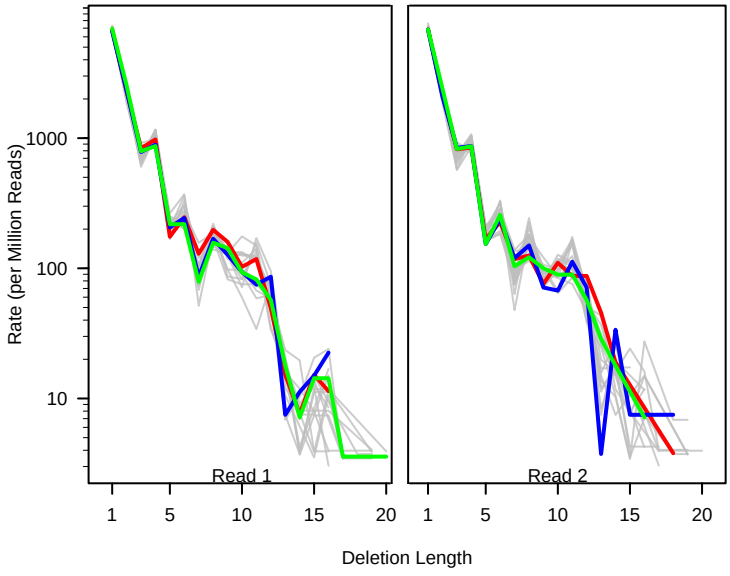
j


Splice Junction Rate, by read cycle
With Sample SAMP4 Colored by lane
Read 1
Read 2
Splice Junction Rate (per Million Reads)
2500
2000
1500
1000
500
0
1
20
40
60
80
100
Read Cycle

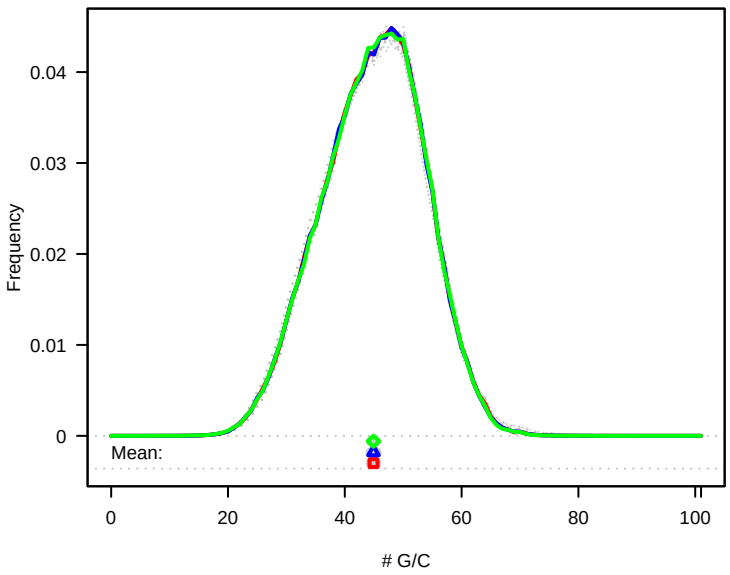
k


Insertion Length Distribution
With Sample SAMP4 Colored by lane
Read 1
Read 2
Rate (per Million Reads)
1000
100
10
1
5
10
15
Insertion Length

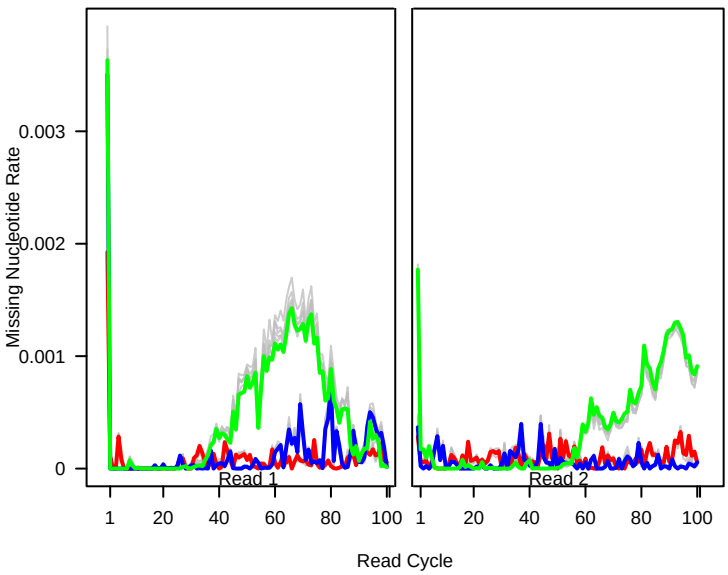
l


Deletion Length Distribution
With Sample SAMP4 Colored by lane
Read 1
Read 2
Rate (per Million Reads)
1000
100
10
1
5
10
15
20
Deletion Length

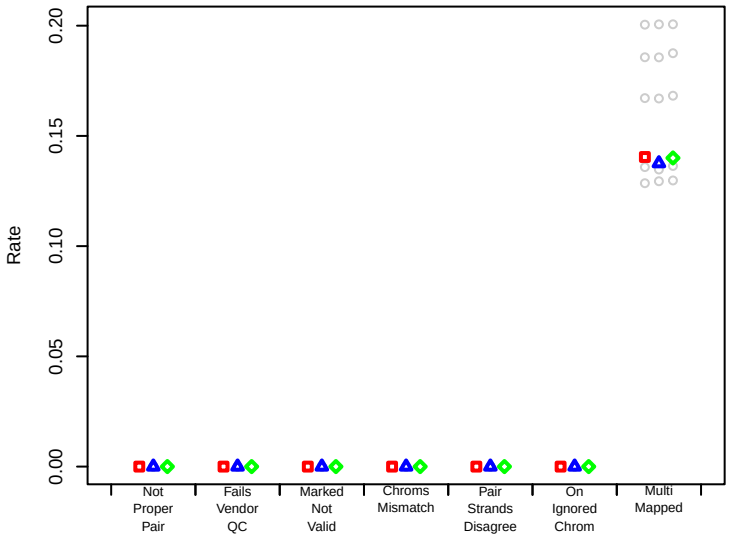
m


GC Content
With Sample SAMP4 Colored by lane
Frequency
0.04
0.03
0.02
0.01
0
Mean:
0
20
40
60
80
100
# G/C

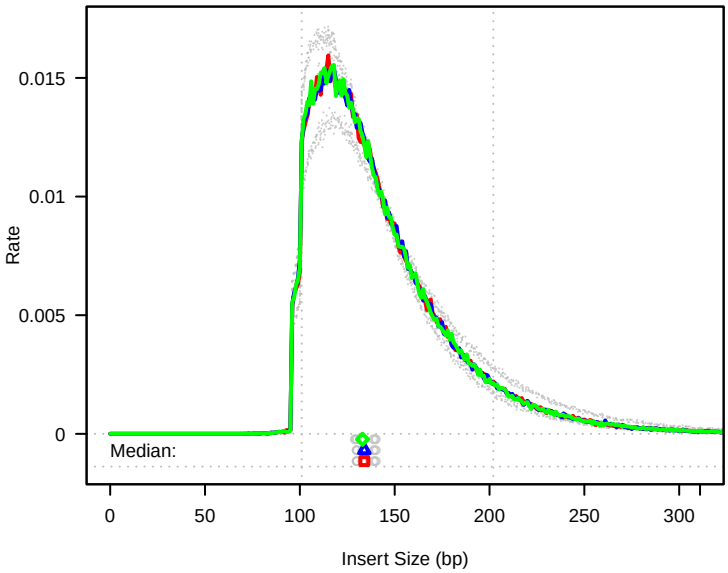
n


'N' Rate, by Read Cycle
With Sample SAMP4 Colored by lane
Missing Nucleotide Rate
0.003
0.002
0.001
0
Read 1
Read 2
1
20
40
60
80
100
Read Cycle

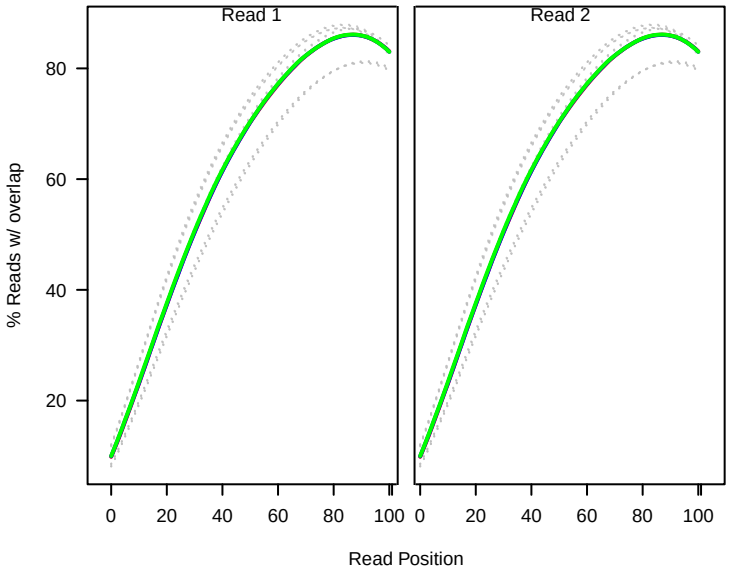
o


Read Drop Rate, by Reason
With Sample SAMP4 Colored by lane
Rate
0.20
0.15
0.10
0.05
0.00
Not Proper Pair
Fails Vendor QC
Marked Not Valid
Chroms Mismatch
Pair Strands Disagree
On Ignored Chrom
Multi Mapped

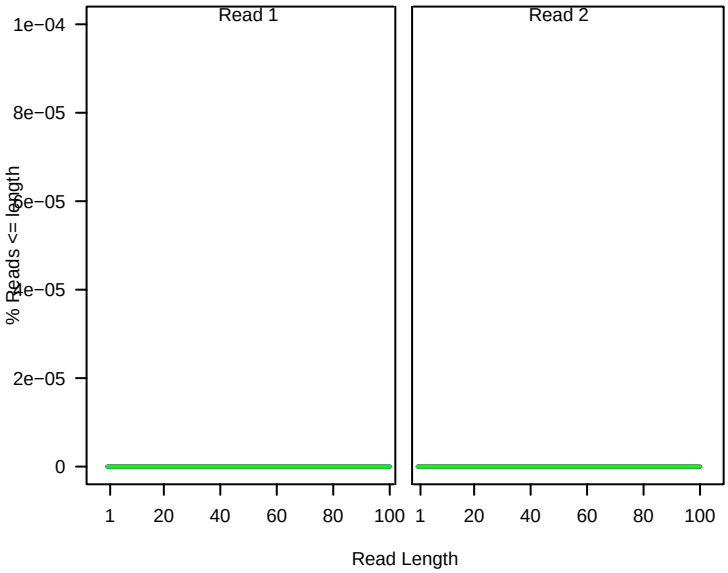
p


Insert Size
With Sample SAMP4 Colored by lane
Rate
0.015
0.01
0.005
0
Median:
0
50
100
150
200
250
300
Insert Size (bp)

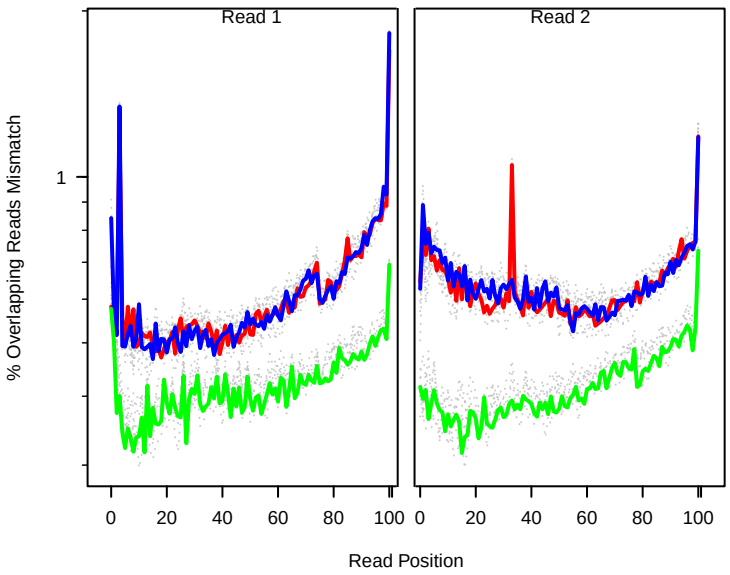
q


Overlapping Coverage
With Sample SAMP4 Colored by lane
Read 1
Read 2
% Reads w/ overlap
80
60
40
20
0
20
40
60
80
100
Read Position

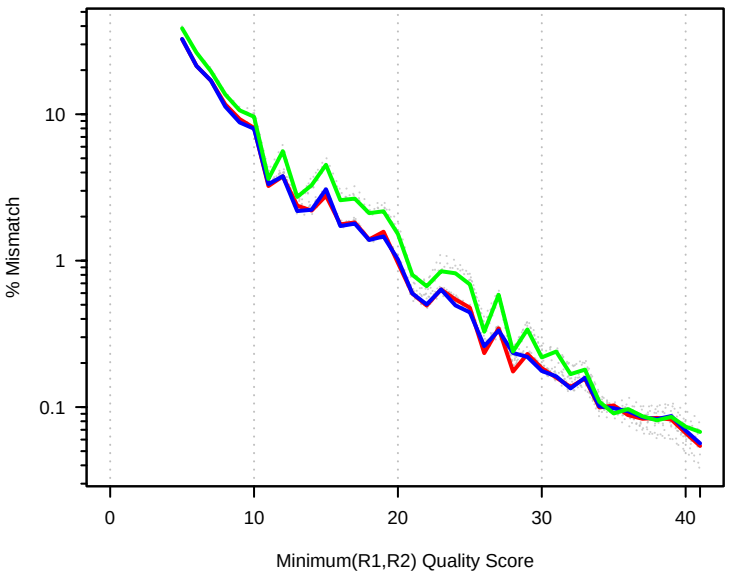
r


Read Length Distribution
With Sample SAMP4 Colored by lane
Read 1
Read 2
% Reads <= length
1e−04
8e−05
6e−05
4e−05
2e−05
0
1
20
40
60
80
100
Read Length

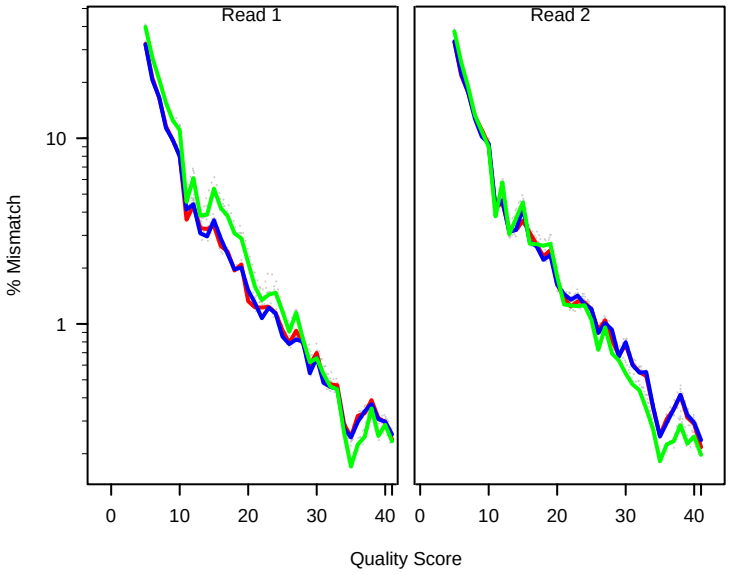
s


Overlap Mismatch by Read Cycle
With Sample SAMP4 Colored by lane
Read 1
Read 2
% Overlapping Reads Mismatch
1
0
20
40
60
80
100
Read Position

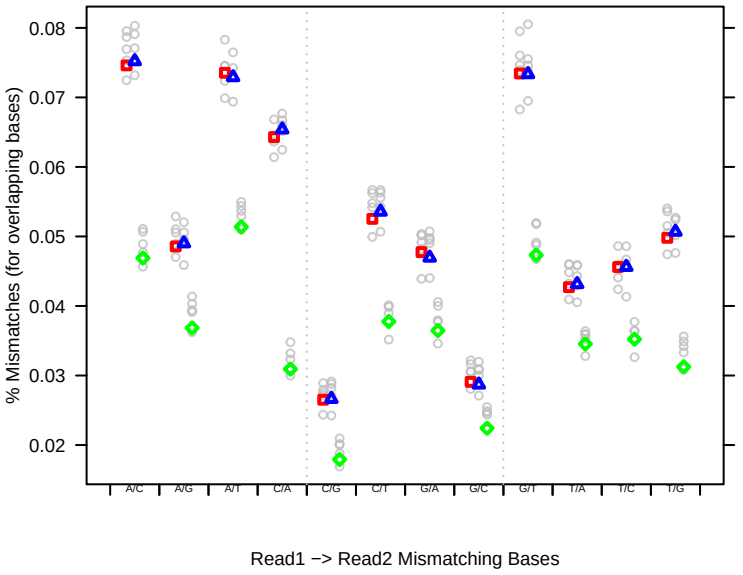
t


Overlapping Mismatch by Min Qual
With Sample SAMP4 Colored by lane
% Mismatch
10
1
0.1
0
10
20
30
40
Minimum(R1,R2) Quality Score

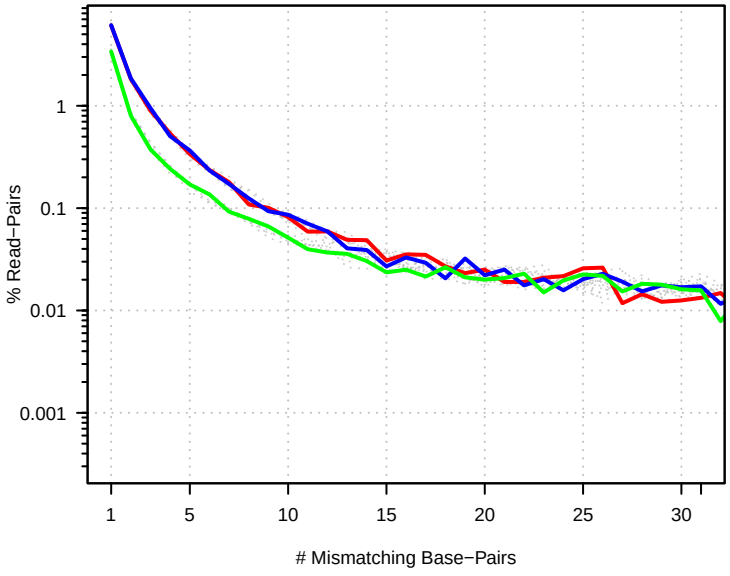
u


Overlap Mismatch by Read Qual
With Sample SAMP4 Colored by lane
Read 1
Read 2
% Mismatch
10
1
0
10
20
30
40
Quality Score

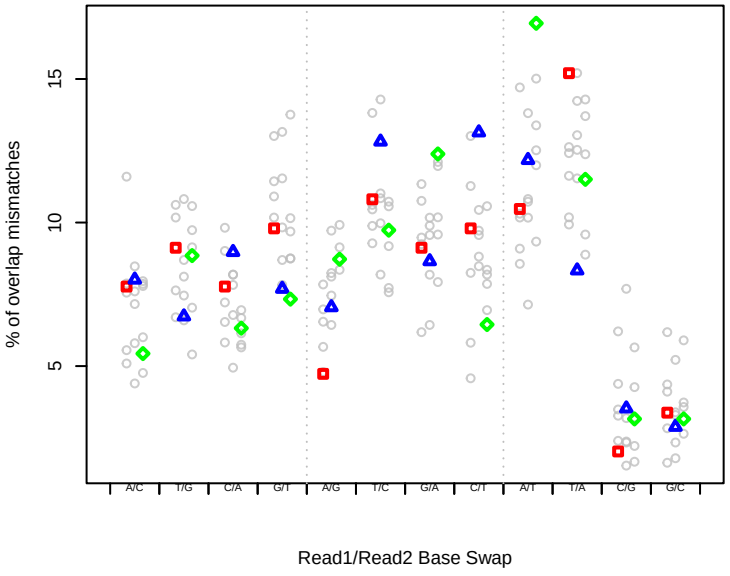
v


Overlap Mismatch Combinations
With Sample SAMP4 Colored by lane
% Mismatches (for overlapping bases)
0.08
0.07
0.06
0.05
0.04
0.03
0.02
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

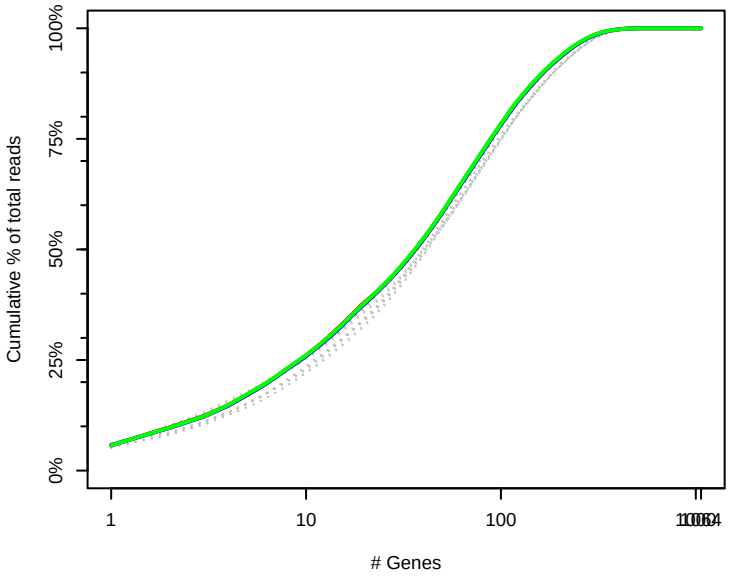
w


Overlap Mismatch Size Frequency
With Sample SAMP4 Colored by lane
% Read-Pairs
1
0.1
0.01
0.001
1
5
10
15
20
25
30
# Mismatching Base-Pairs

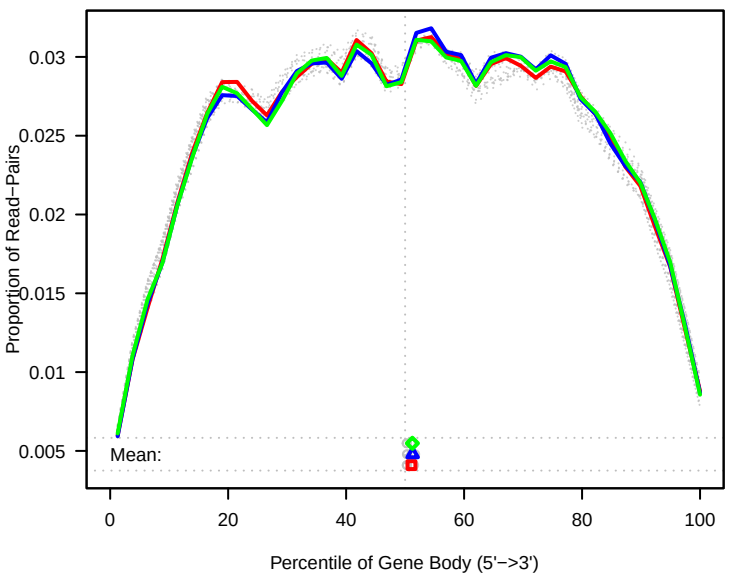
x


Overlap Mismatch Pairs At Phred == 41
With Sample SAMP4 Colored by lane
% of overlap mismatches
15
10
5
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

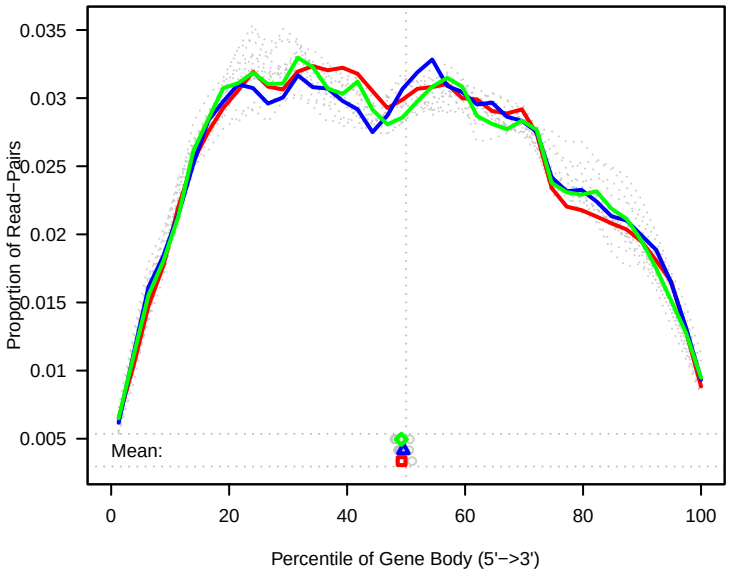
y


Cumulative Gene Assignment Diversity
With Sample SAMP4 Colored by lane
Cumulative % of total reads
0%
25%
50%
75%
100%
1
10
100
# Genes

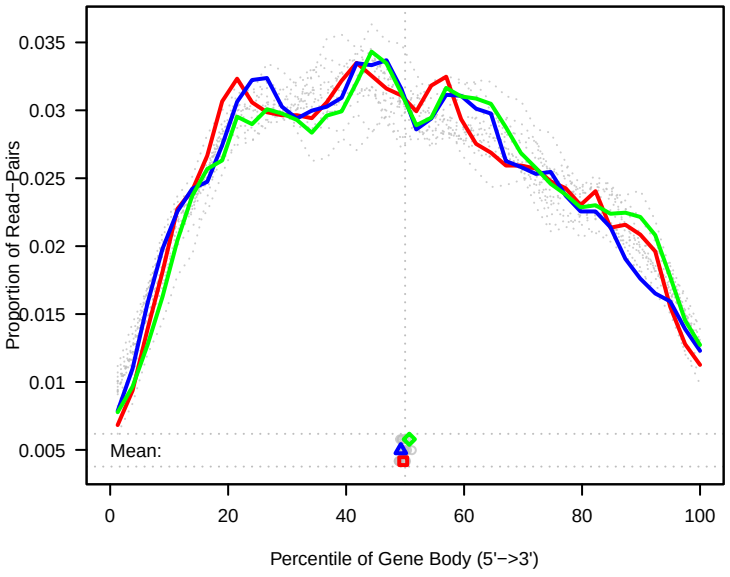
z


Gene−Body Coverage
With Sample SAMP4 Colored by lane
Proportion of Read−Pairs
0.005
0.01
0.015
0.02
0.025
0.03
Mean:
0
20
40
60
80
100
Percentile of Gene Body (5'−>3')

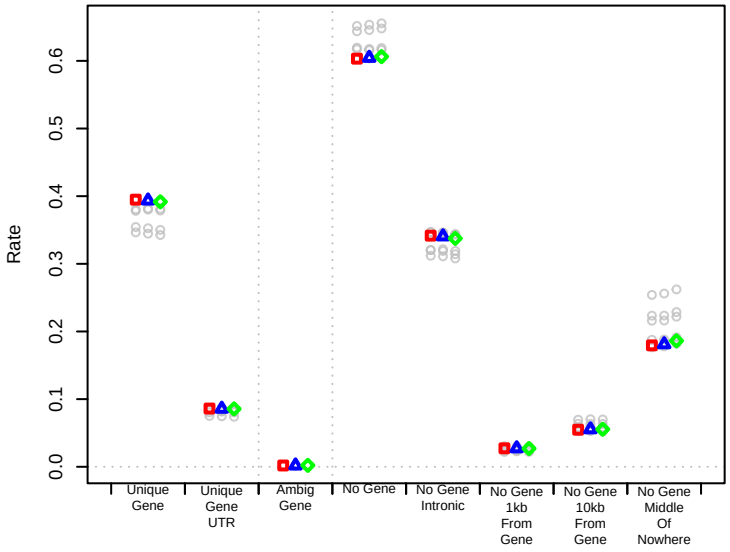
aa


Gene−Body Coverage, Upper Middle Quartile Genes
With Sample SAMP4 Colored by lane
Proportion of Read−Pairs
0.005
0.01
0.015
0.02
0.025
0.03
0.035
Mean:
0
20
40
60
80
100
Percentile of Gene Body (5'−>3')

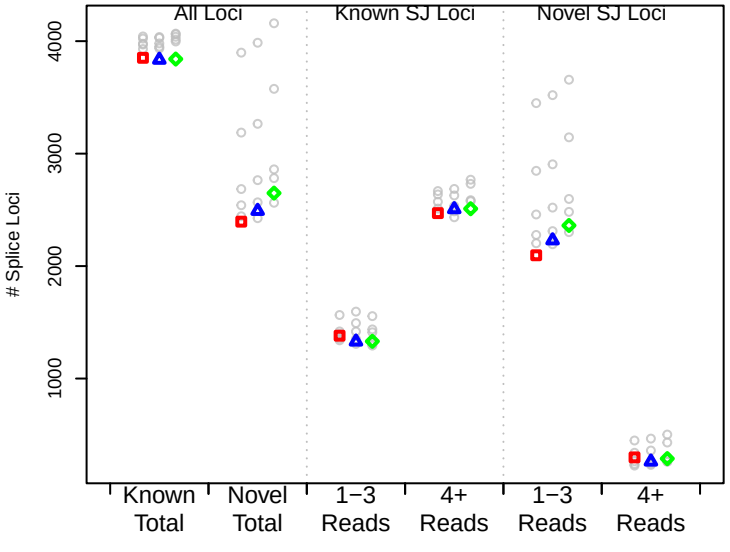
ab


Gene−Body Coverage, Low Expression Genes
With Sample SAMP4 Colored by lane
Proportion of Read−Pairs
0.005
0.01
0.015
0.02
0.025
0.03
0.035
Mean:
0
20
40
60
80
100
Percentile of Gene Body (5'−>3')

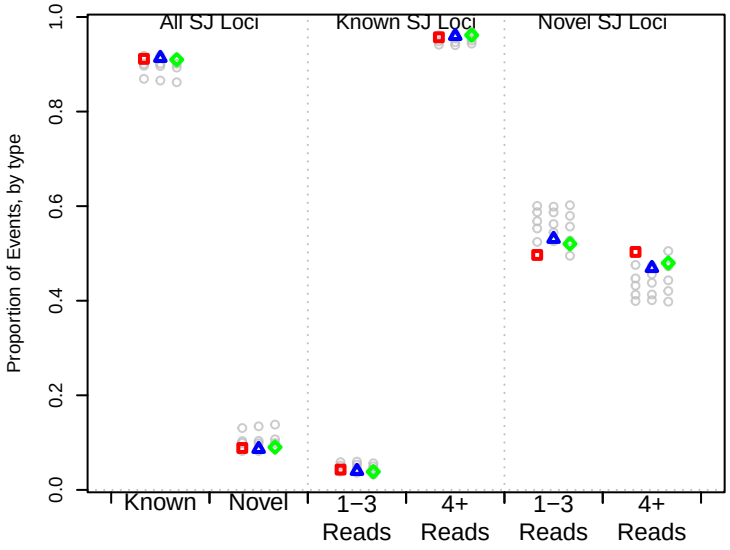
ac


Read Mapping Location Rates
With Sample SAMP4 Colored by lane
Rate
0.0
0.1
0.2
0.3
0.4
0.5
0.6
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

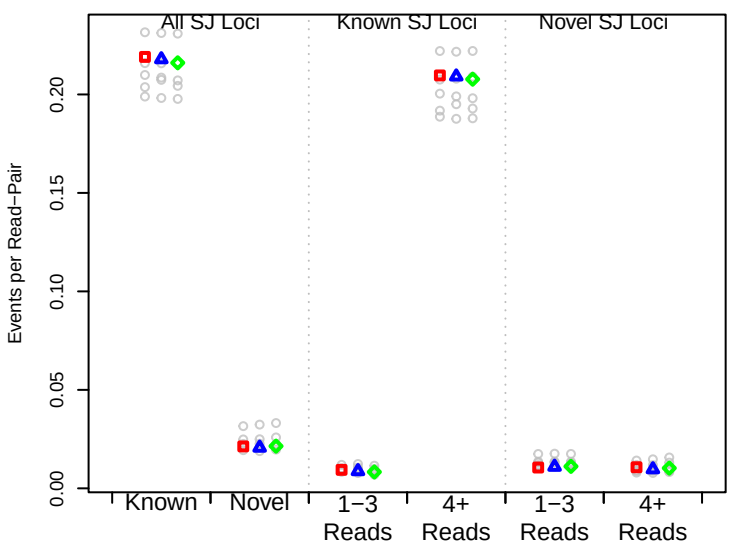
ad


# Observed Splice Junction Loci, by type
With Sample SAMP4 Colored by lane
All Loci
Known SJ Loci
Novel SJ Loci
# Splice Loci
1000
2000
3000
4000
Known Total
Novel Total
1−3 Reads
4+ Reads
1−3 Reads
4+ Reads

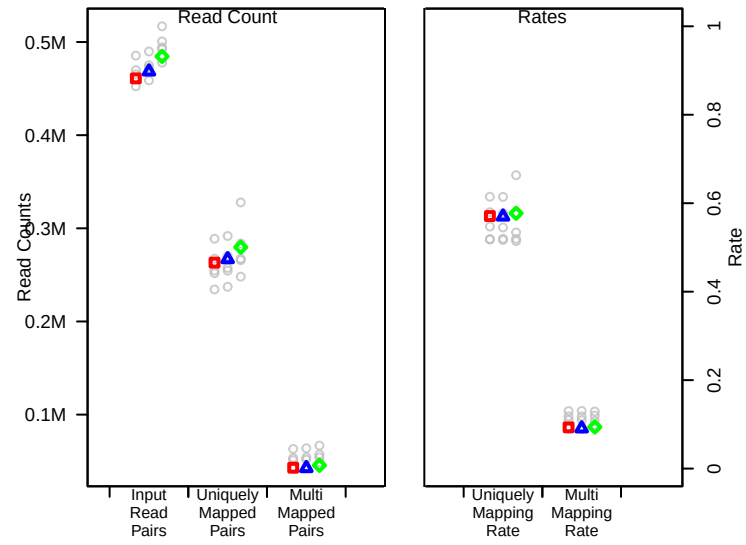
ae



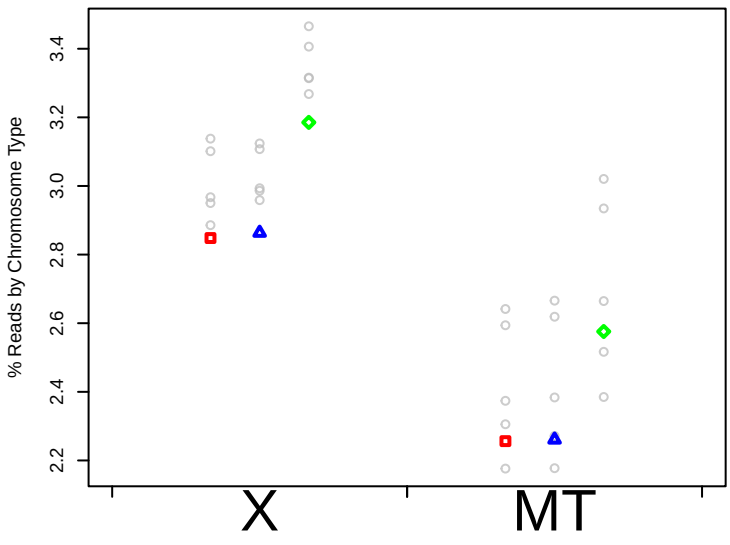

af



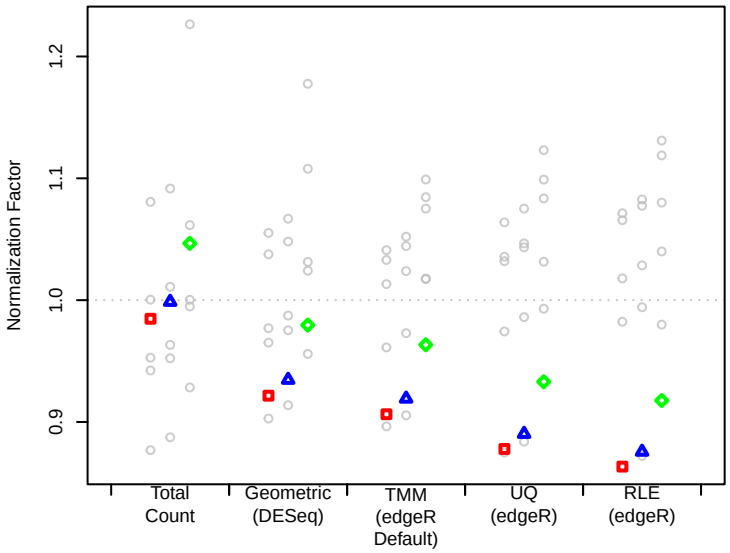

ag



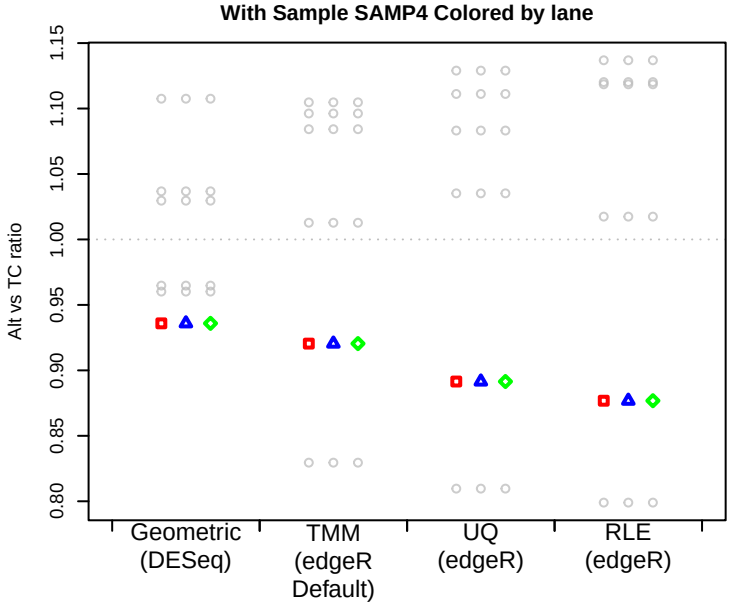

ah



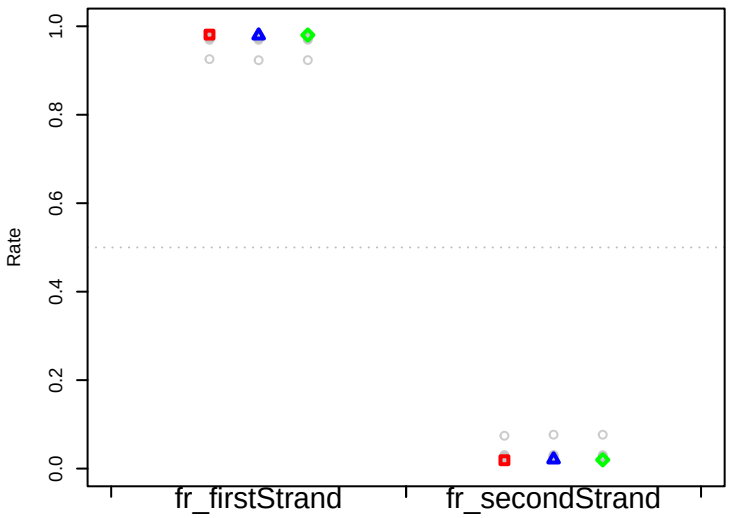

ai



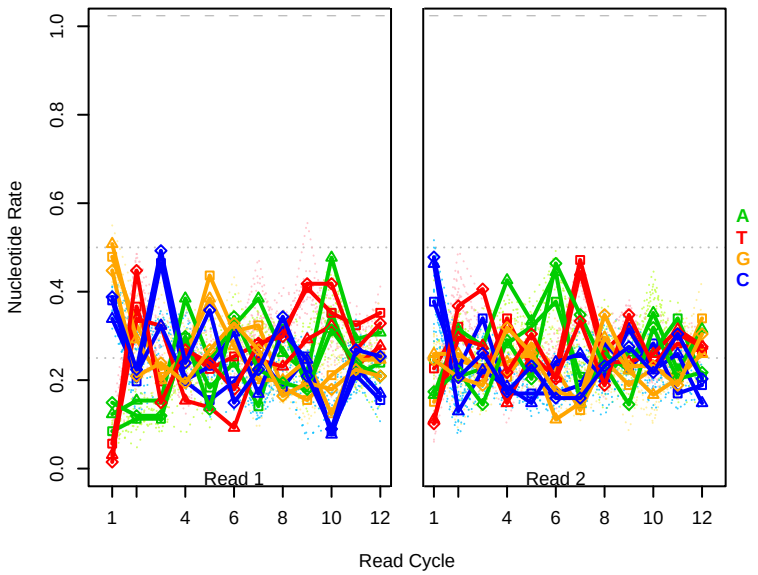

aj



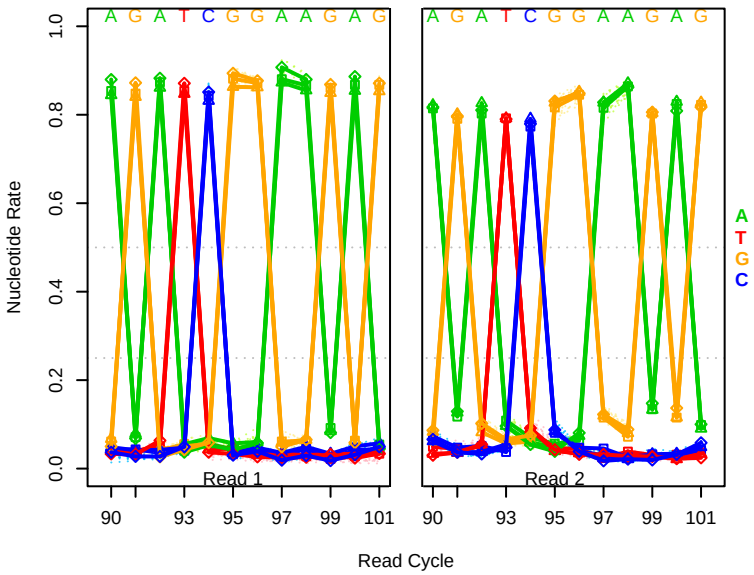
ak


Strandedness Test
With Sample SAMP4 Colored by lane
Rate
0.0
0.2
0.4
0.6
0.8
1.0
fr_firstStrand
fr_secondStrand

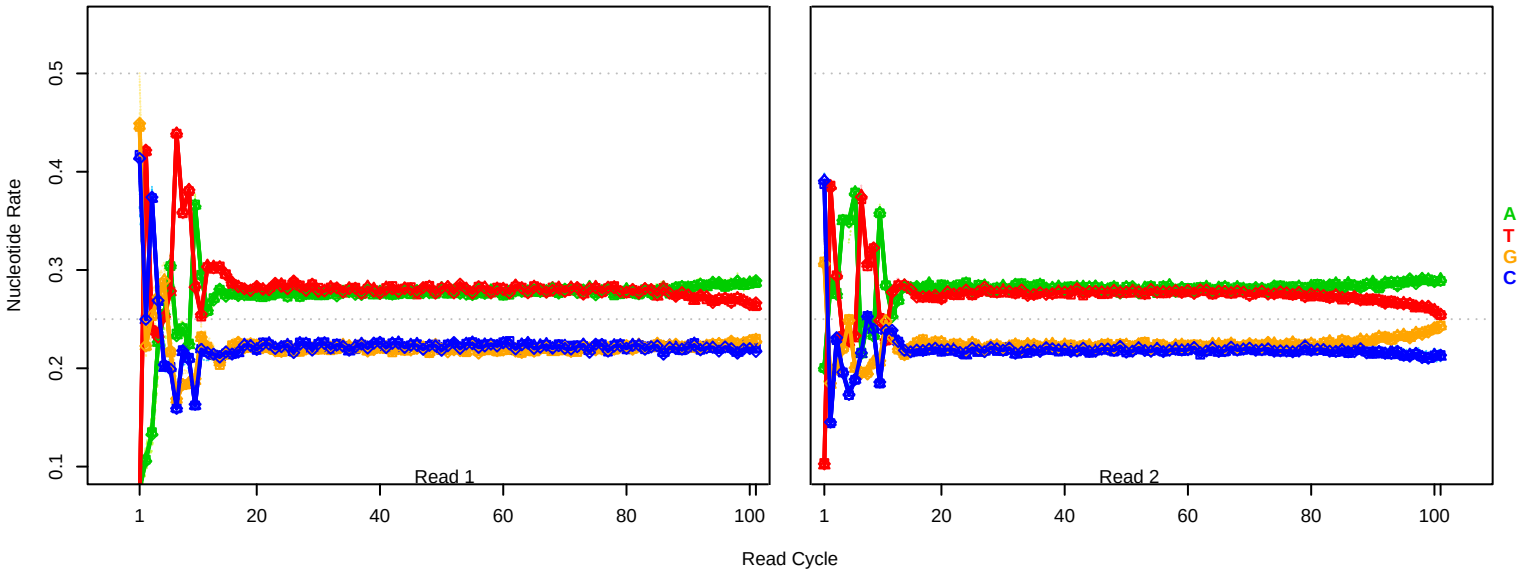
al


Nucleotide Rate by Cycle, Leading Clipped bases (12)
With Sample SAMP4 in Bold
Nucleotide Rate
0.0
0.2
0.4
0.6
0.8
1.0
Read 1
Read 2
1
4
6
8
10
12
Read Cycle
A
T
G
C

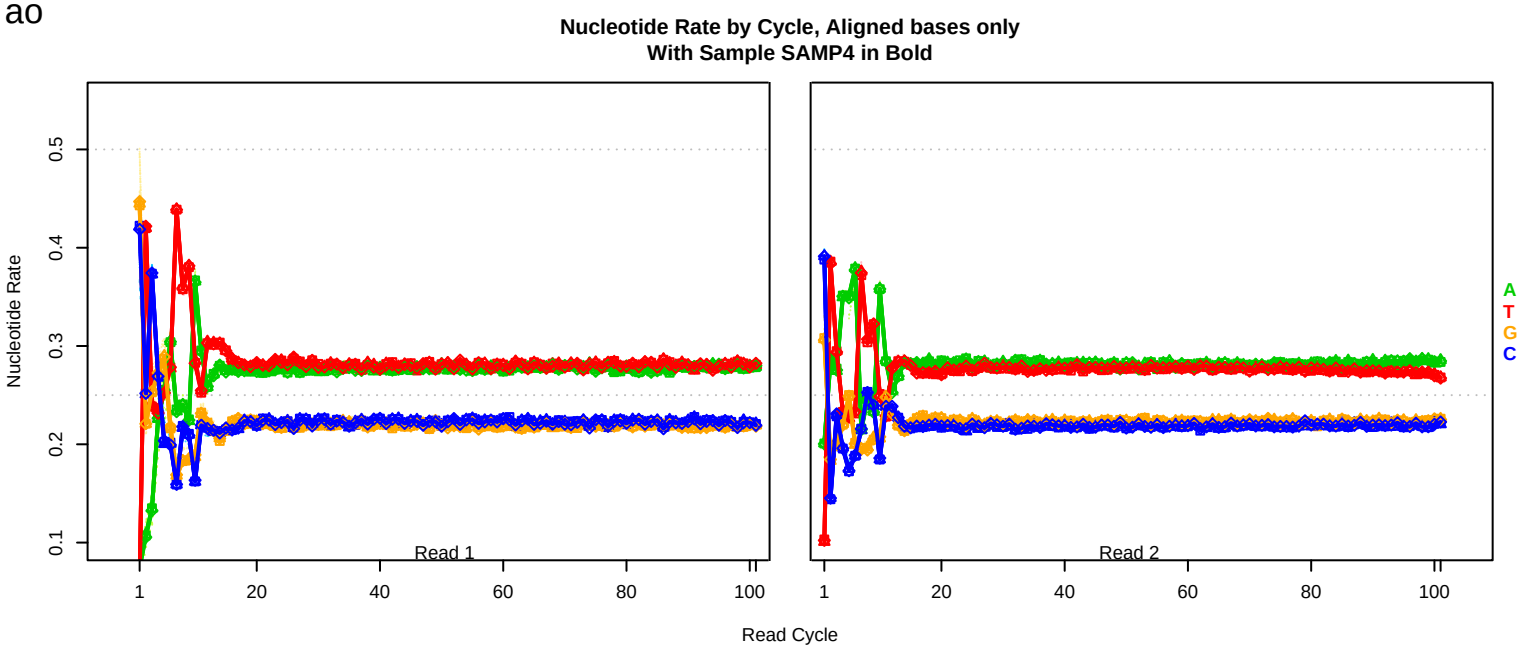
am


Nucleotide Rate by Cycle, Trailing Clipped bases (12)
With Sample SAMP4 in Bold
A G A T C G G A A G A G
Nucleotide Rate
0.0
0.2
0.4
0.6
0.8
1.0
Read 1
Read 2
90
93
95
97
99
101
Read Cycle
A
T
G
C

an


Raw Nucleotide Rate by Cycle
With Sample SAMP4 in Bold
Nucleotide Rate
0.1
0.2
0.3
0.4
0.5
Read 1
Read 2
1
20
40
60
80
100
Read Cycle
A
T
G
C

ao


Nucleotide Rate by Cycle, Aligned bases only
With Sample SAMP4 in Bold
Nucleotide Rate
0.1
0.2
0.3
0.4
0.5
Read 1
Read 2
1
20
40
60
80
100
Read Cycle
A
T
G
C