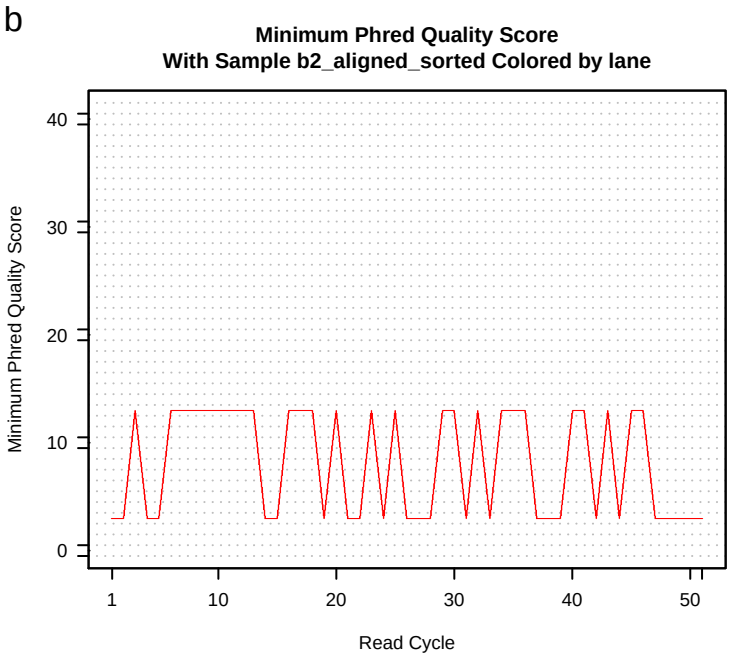
a

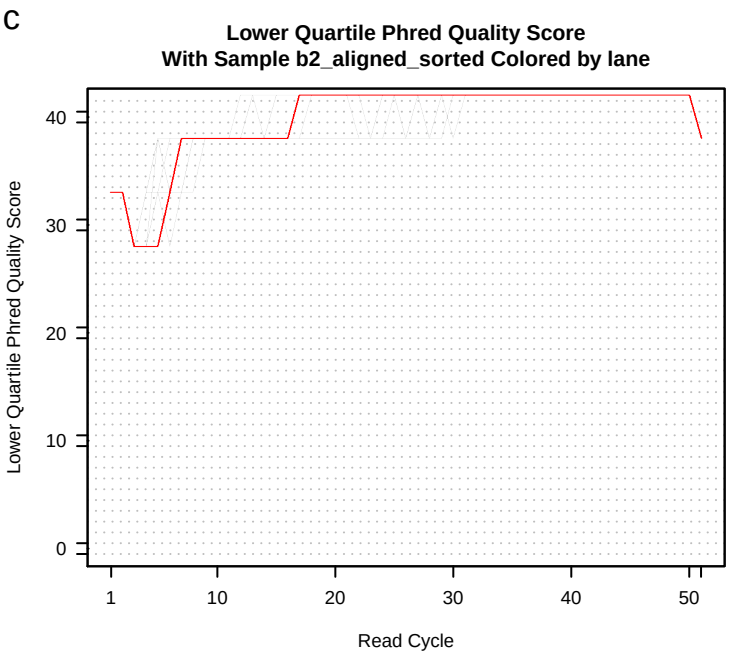
Sample Highlight:
b2_aligned_sorted
Colored by Lane

UNKNOWN
Other Samples

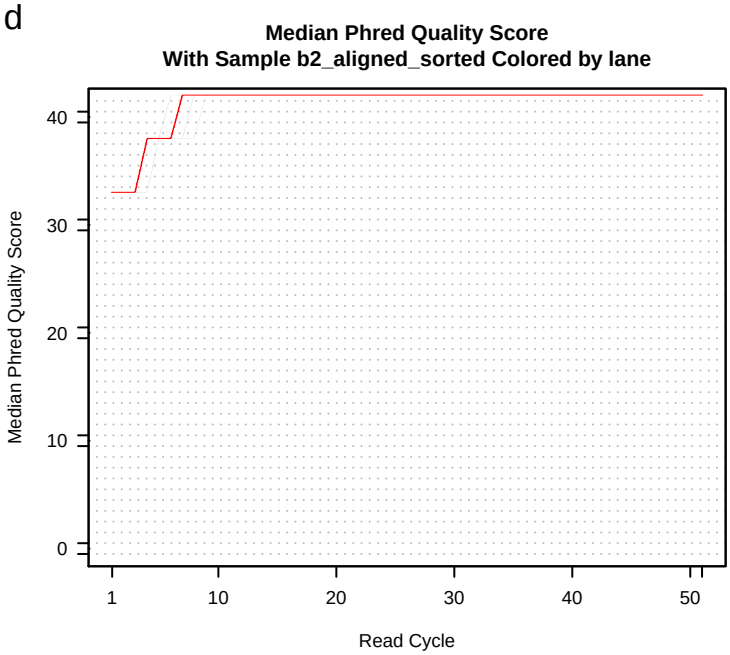
b



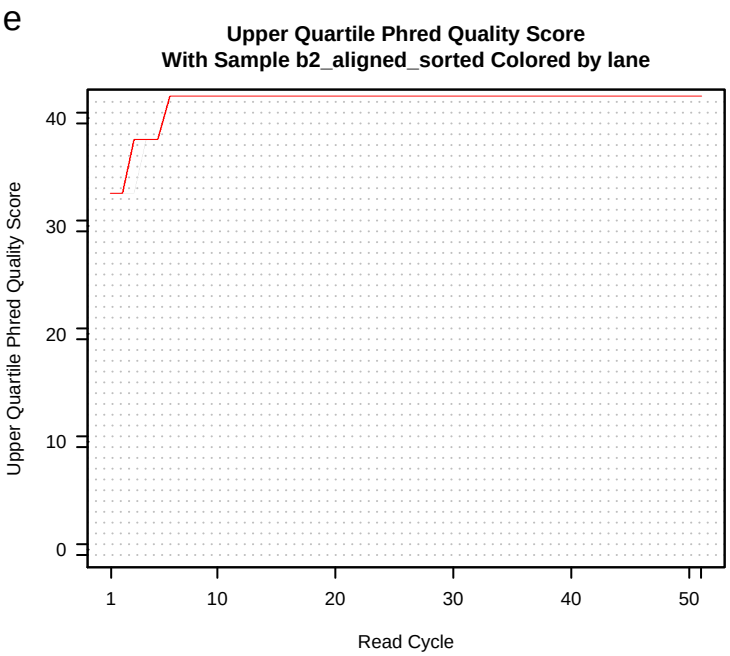

c



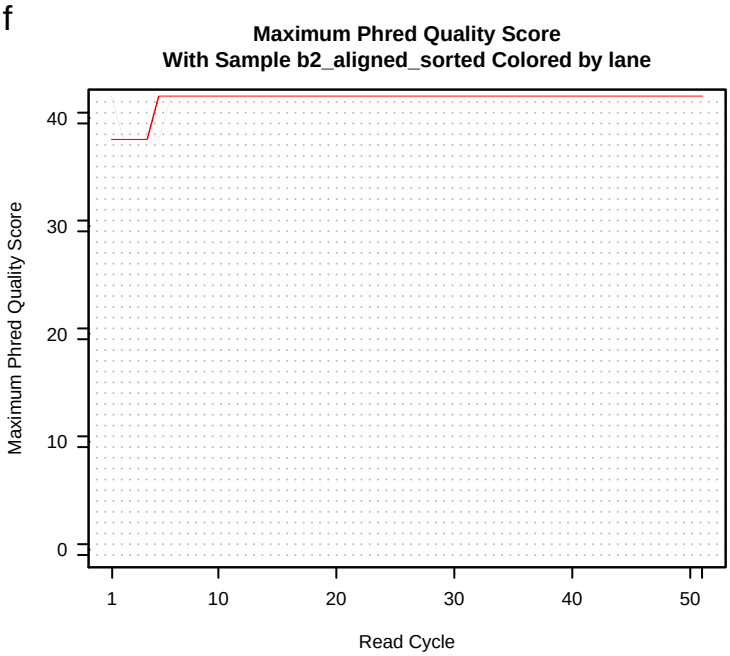

d



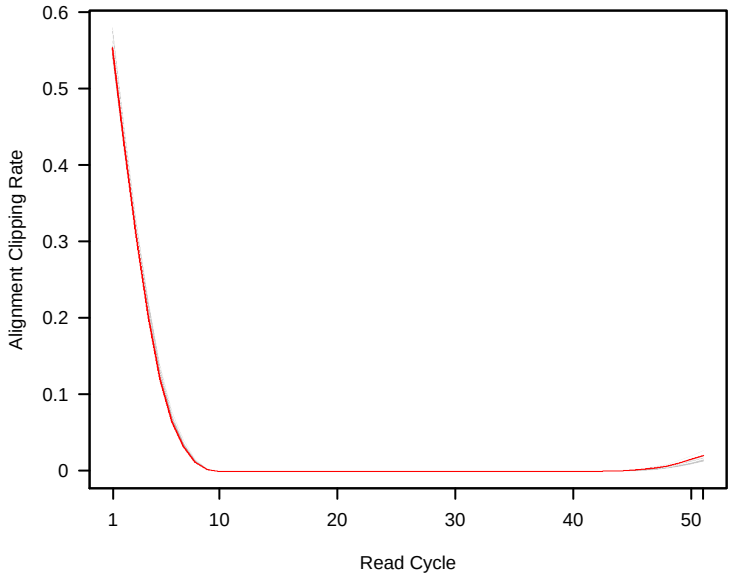

e



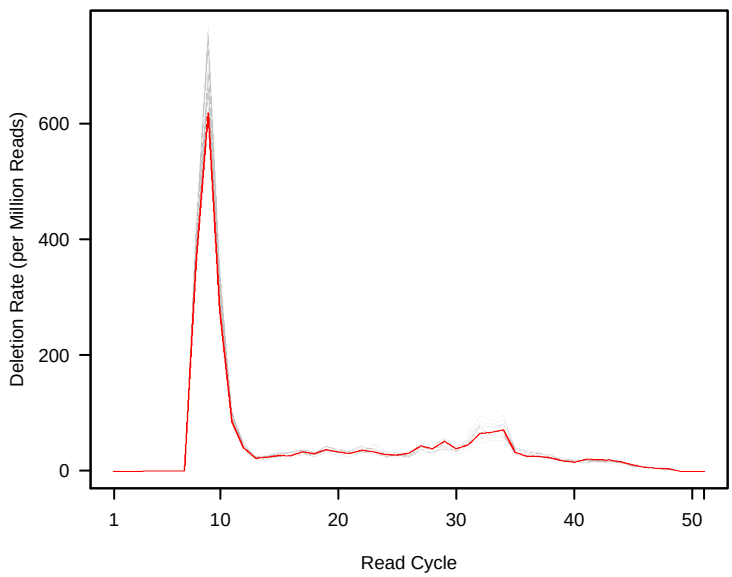

f



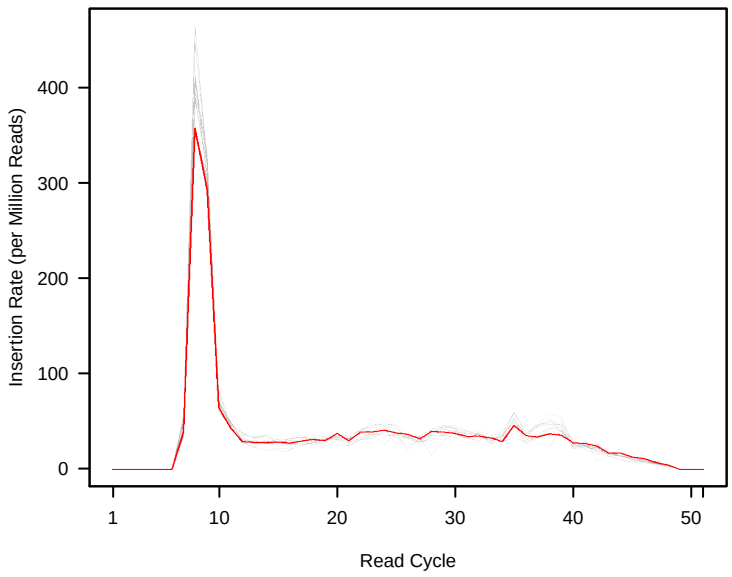
g


Alignment Clipping Rate, by read cycle
With Sample b2_aligned_sorted Colored by lane
Alignment Clipping Rate
0.6
0.5
0.4
0.3
0.2
0.1
0
1
10
20
30
40
50
Read Cycle

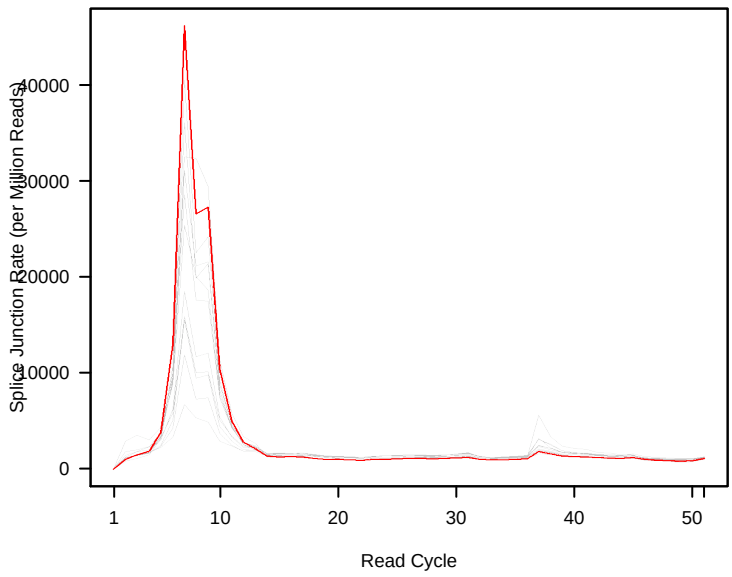
h


Deletion Rate, by read cycle
With Sample b2_aligned_sorted Colored by lane
Deletion Rate (per Million Reads)
600
400
200
0
1
10
20
30
40
50
Read Cycle

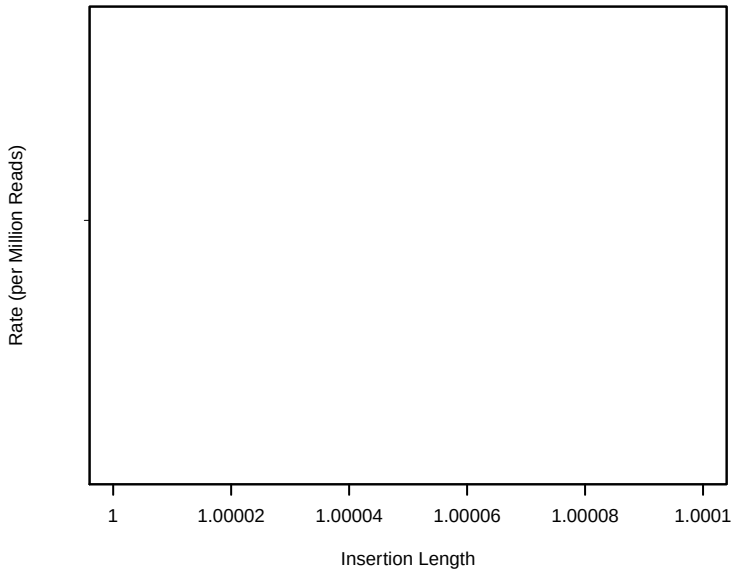
i


Insertion Rate, by read cycle
With Sample b2_aligned_sorted Colored by lane
Insertion Rate (per Million Reads)
400
300
200
100
0
1
10
20
30
40
50
Read Cycle

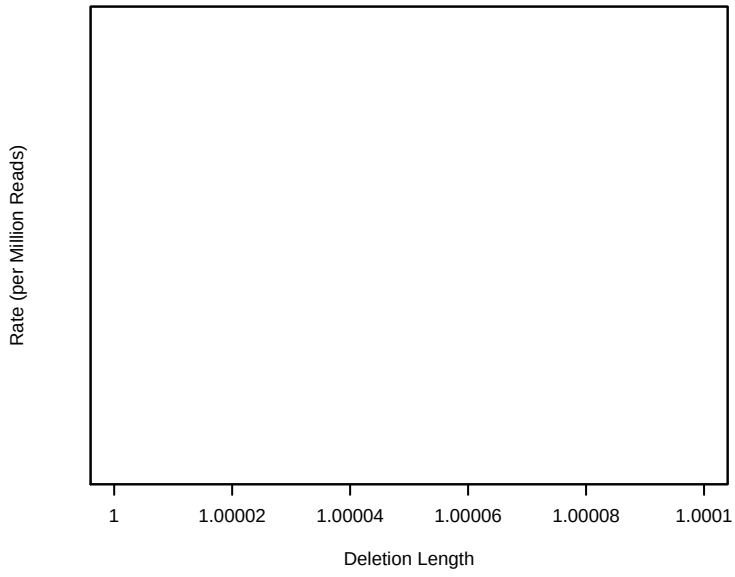
j


Splice Junction Rate, by read cycle
With Sample b2_aligned_sorted Colored by lane
Splice Junction Rate (per Million Reads)
40000
30000
20000
10000
0
1
10
20
30
40
50
Read Cycle

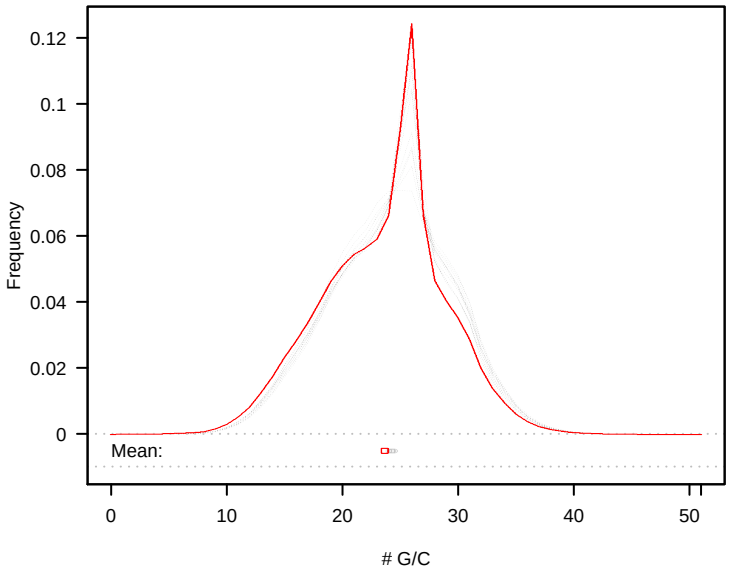
k


Insertion Length Distribution
With Sample b2_aligned_sorted Colored by lane
Rate (per Million Reads)
1
1.00002
1.00004
1.00006
1.00008
1.0001
Insertion Length

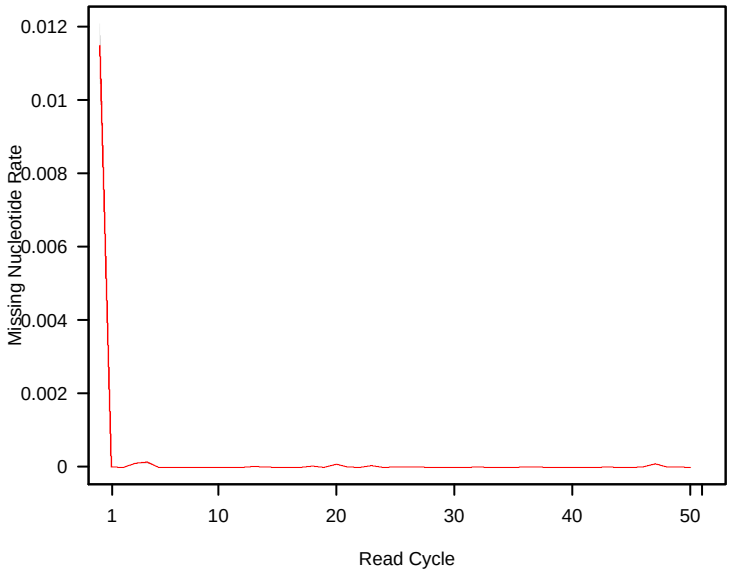
l


Deletion Length Distribution
With Sample b2_aligned_sorted Colored by lane
Rate (per Million Reads)
1
1.00002
1.00004
1.00006
1.00008
1.0001
Deletion Length

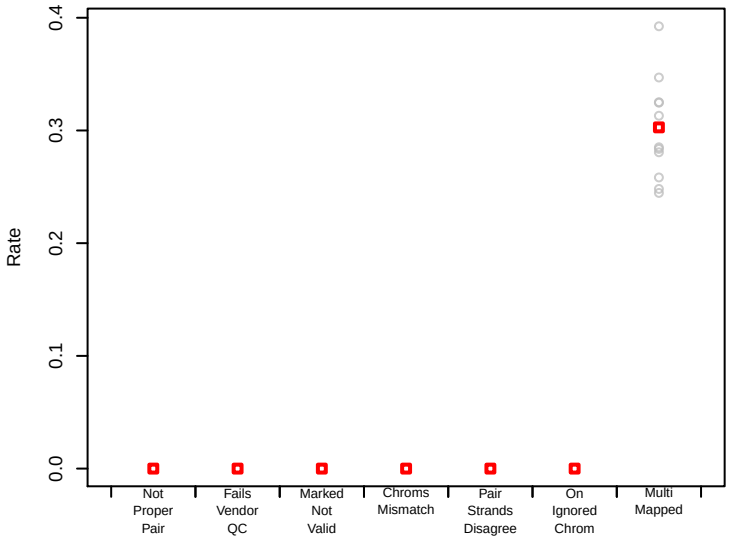
m


GC Content
With Sample b2_aligned_sorted Colored by lane
Frequency
0.12
0.1
0.08
0.06
0.04
0.02
0
Mean:
0
10
20
30
40
50
# G/C

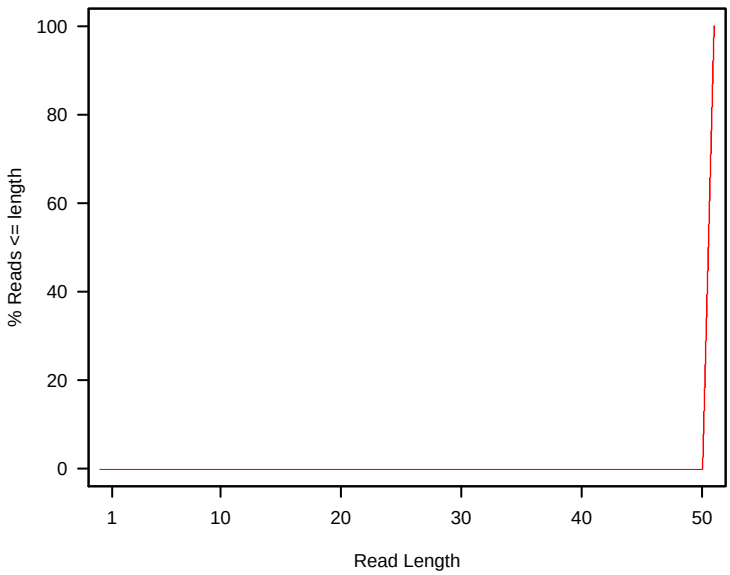
n


'N' Rate, by Read Cycle
With Sample b2_aligned_sorted Colored by lane
Missing Nucleotide Rate
0.012
0.01
0.008
0.006
0.004
0.002
0
1
10
20
30
40
50
Read Cycle

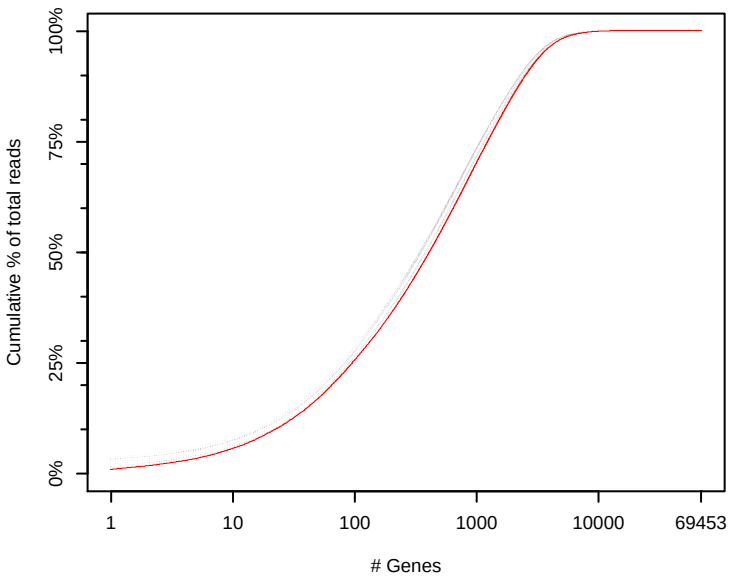
o


Read Drop Rate, by Reason
With Sample b2_aligned_sorted Colored by lane
Rate
0.4
0.3
0.2
0.1
0.0
Not Proper Pair
Fails Vendor QC
Marked Not Valid
Chroms Mismatch
Pair Strands Disagree
On Ignored Chrom
Multi Mapped

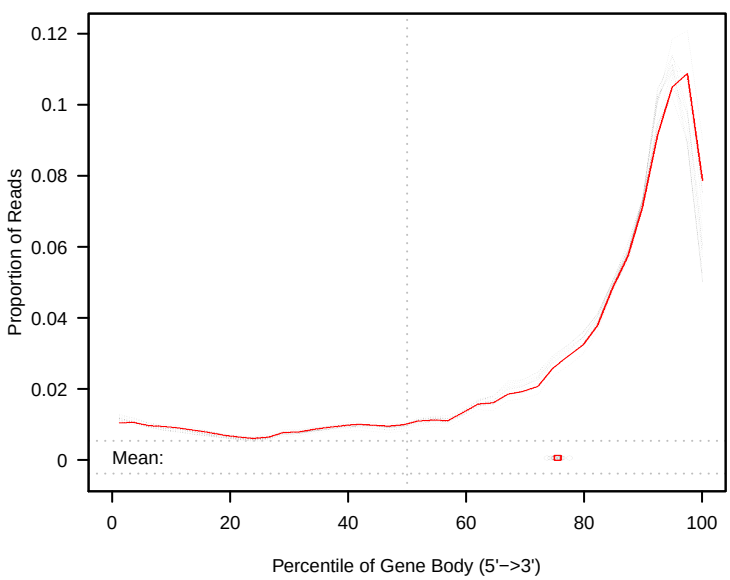
p


Read Length Distribution
With Sample b2_aligned_sorted Colored by lane
% Reads <= length
100
80
60
40
20
0
1
10
20
30
40
50
Read Length

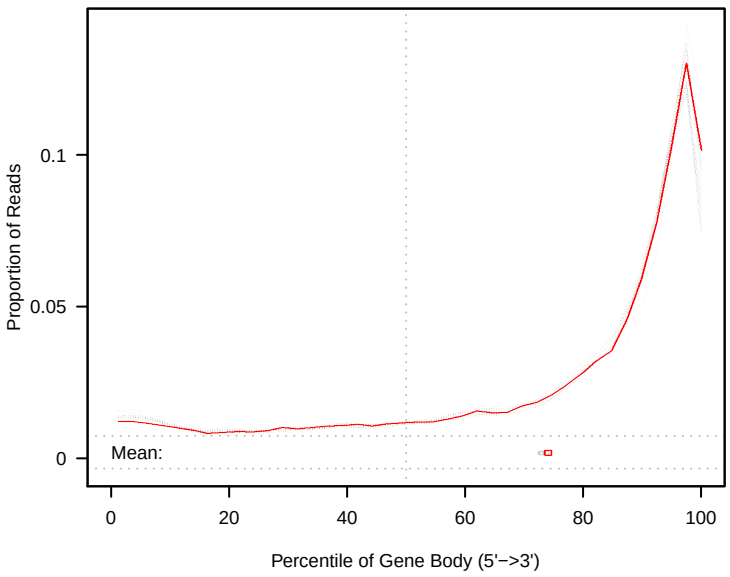
q


Cumulative Gene Assignment Diversity
With Sample b2_aligned_sorted Colored by lane
Cumulative % of total reads
100%
75%
50%
25%
0%
1
10
100
1000
10000
69453
# Genes

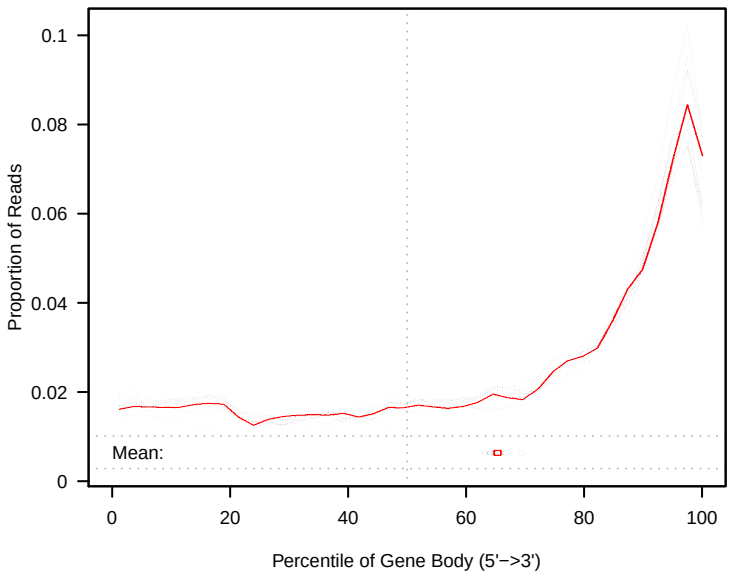
r


Gene−Body Coverage
With Sample b2_aligned_sorted Colored by lane
Proportion of Reads
0.12
0.1
0.08
0.06
0.04
0.02
0
Mean:
0
20
40
60
80
100
Percentile of Gene Body (5'−>3')

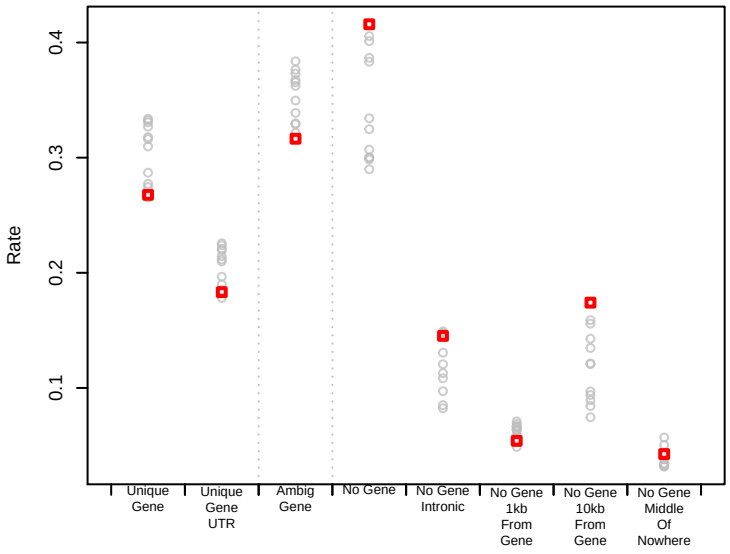
s


Gene−Body Coverage, Upper Middle Quartile Genes
With Sample b2_aligned_sorted Colored by lane
Proportion of Reads
0
0.05
0.1
Mean:
0
20
40
60
80
100
Percentile of Gene Body (5'−>3')

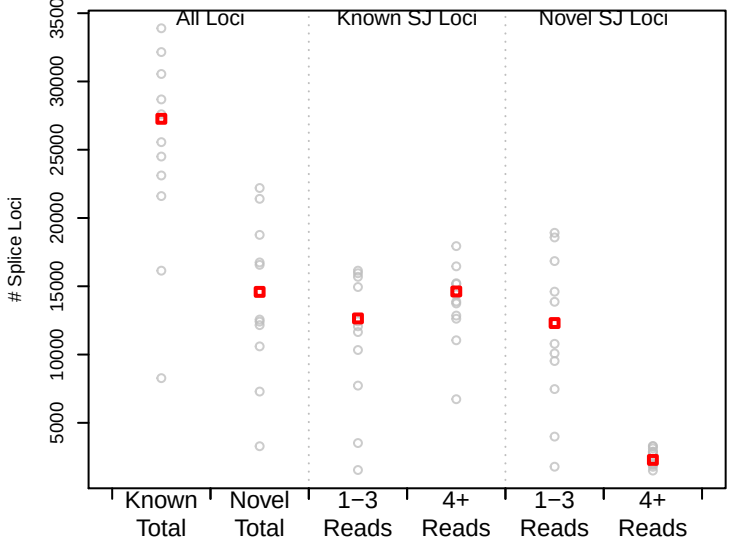
t


Gene−Body Coverage, Low Expression Genes
With Sample b2_aligned_sorted Colored by lane
Proportion of Reads
0
0.02
0.04
0.06
0.08
0.1
Mean:
0
20
40
60
80
100
Percentile of Gene Body (5'−>3')

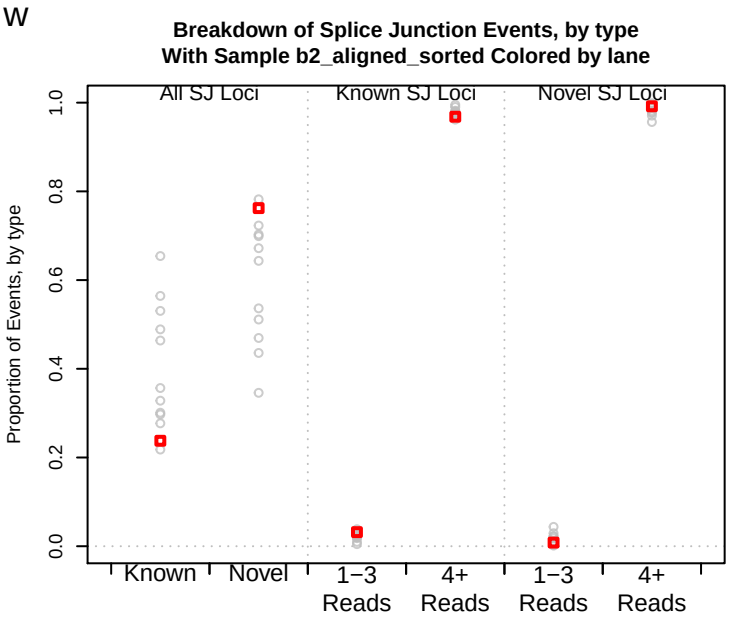
u


Read Mapping Location Rates
With Sample b2_aligned_sorted Colored by lane
Rate
0.1
0.2
0.3
0.4
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

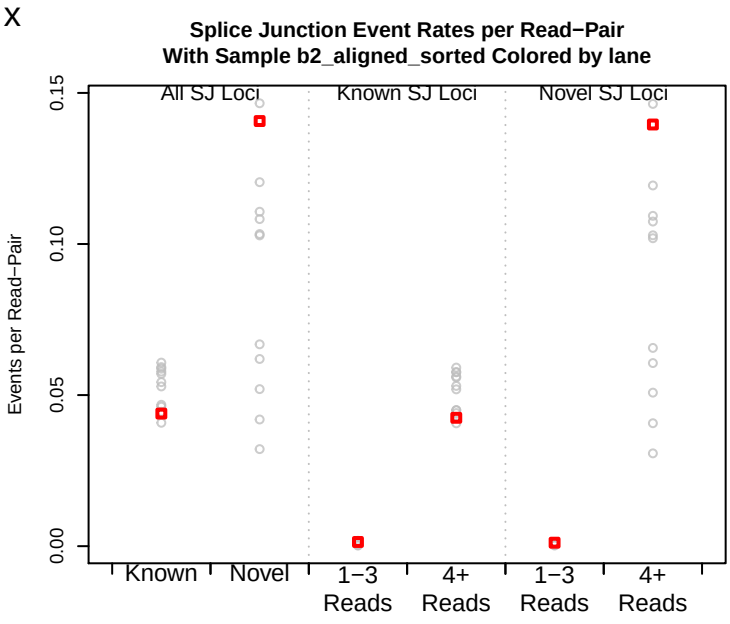
v


# Observed Splice Junction Loci, by type
With Sample b2_aligned_sorted Colored by lane
# Splice Loci
5000
10000
15000
20000
25000
30000
35000
All Loci
Known SJ Loci
Novel SJ Loci
Known Total
Novel Total
1−3 Reads
4+ Reads
1−3 Reads
4+ Reads

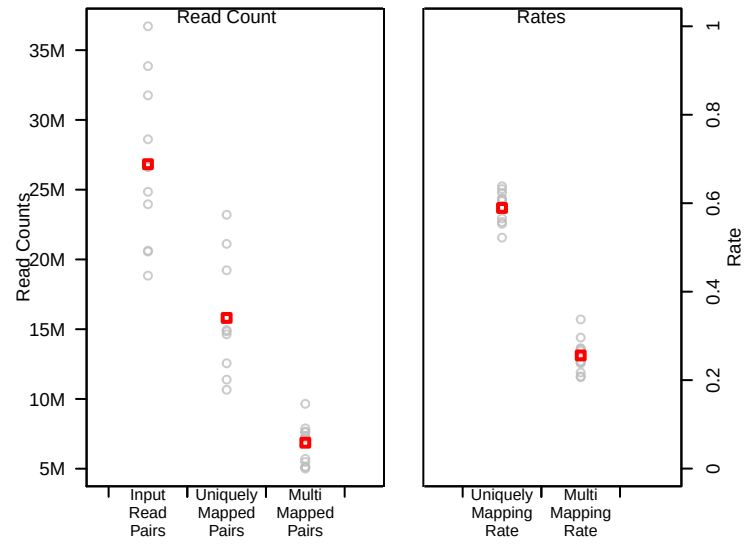
w


Breakdown of Splice Junction Events, by type
With Sample b2_aligned_sorted Colored by lane
Proportion of Events, by type
0.0
0.2
0.4
0.6
0.8
1.0
All SJ Loci
Known SJ Loci
Novel SJ Loci
Known
Novel
1−3 Reads
4+ Reads
1−3 Reads
4+ Reads

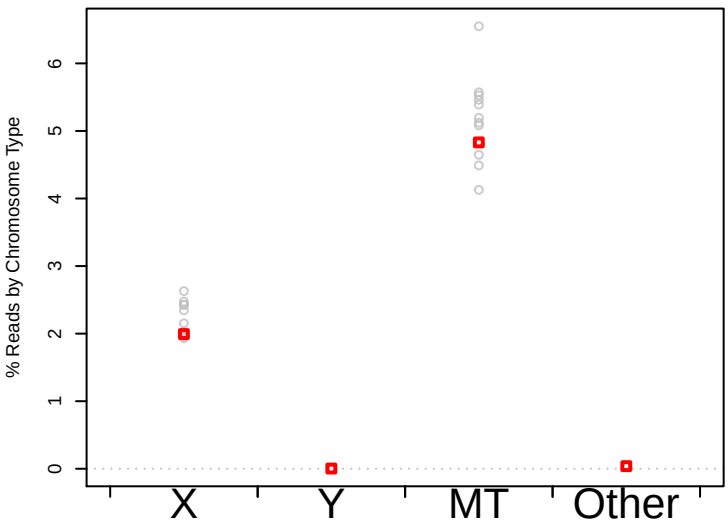
x


Splice Junction Event Rates per Read−Pair
With Sample b2_aligned_sorted Colored by lane
Events per Read−Pair
0.00
0.05
0.10
0.15
All SJ Loci
Known SJ Loci
Novel SJ Loci
Known
Novel
1−3 Reads
4+ Reads
1−3 Reads
4+ Reads

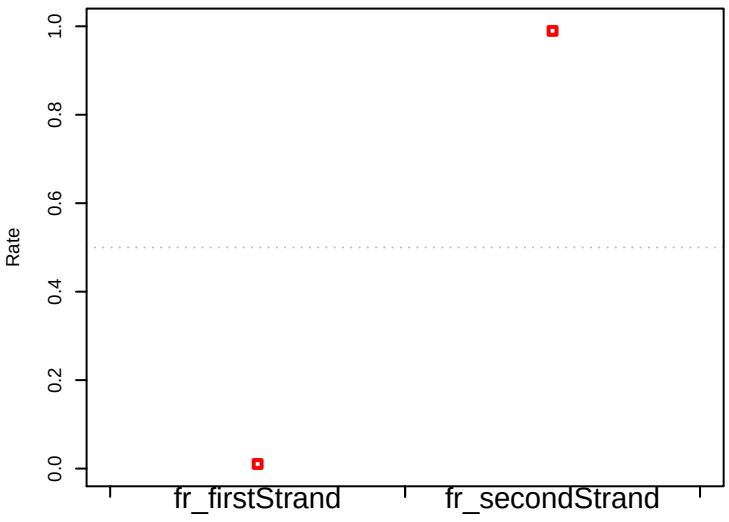
y


Mapping Stats
With Sample b2_aligned_sorted Colored by lane
Read Count
Rates
Read Counts
Rate
35M
30M
25M
20M
15M
10M
5M
0
0.2
0.4
0.6
0.8
1
Input Read Pairs
Uniquely Mapped Pairs
Multi Mapped Pairs
Uniquely Mapping Rate
Multi Mapping Rate

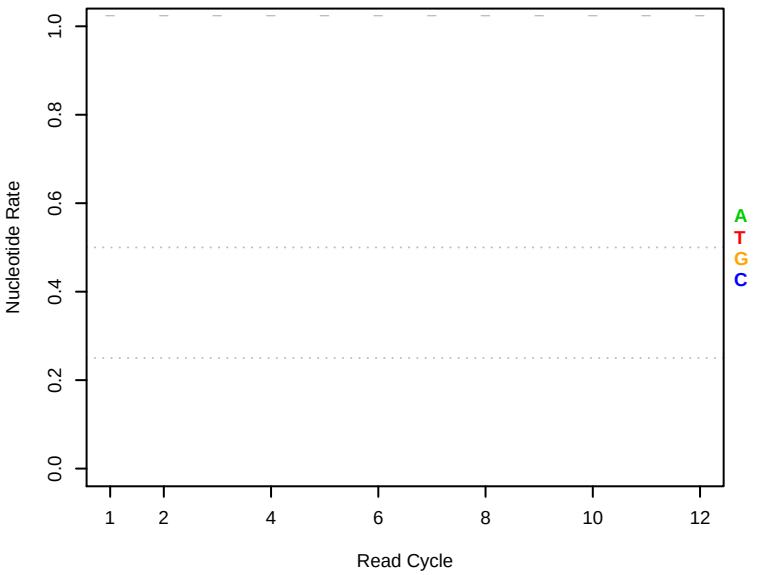
z


Chromosome Distribution (Excluding Autosomes)
With Sample b2_aligned_sorted Colored by lane
% Reads by Chromosome Type
0
1
2
3
4
5
6
X
Y
MT
Other

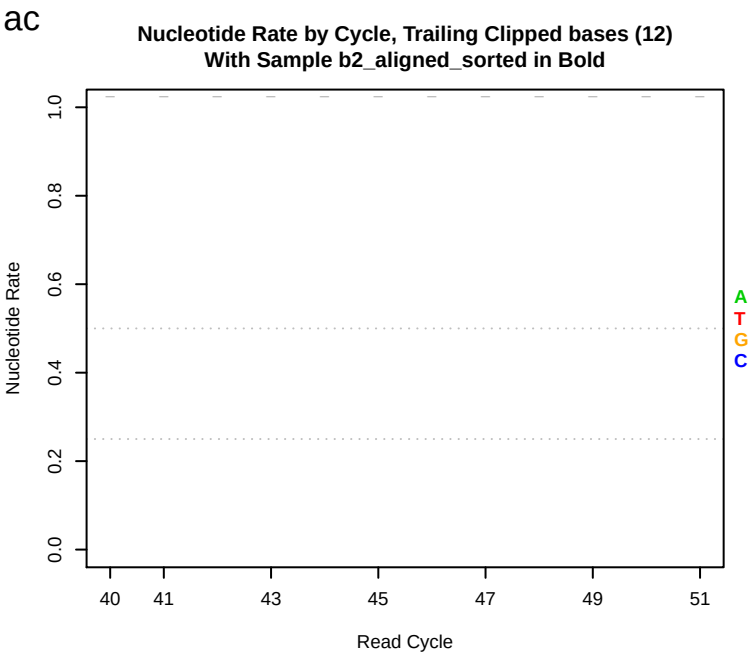
aa


Strandedness Test
With Sample b2_aligned_sorted Colored by lane
Rate
0.0
0.2
0.4
0.6
0.8
1.0
fr_firstStrand
fr_secondStrand

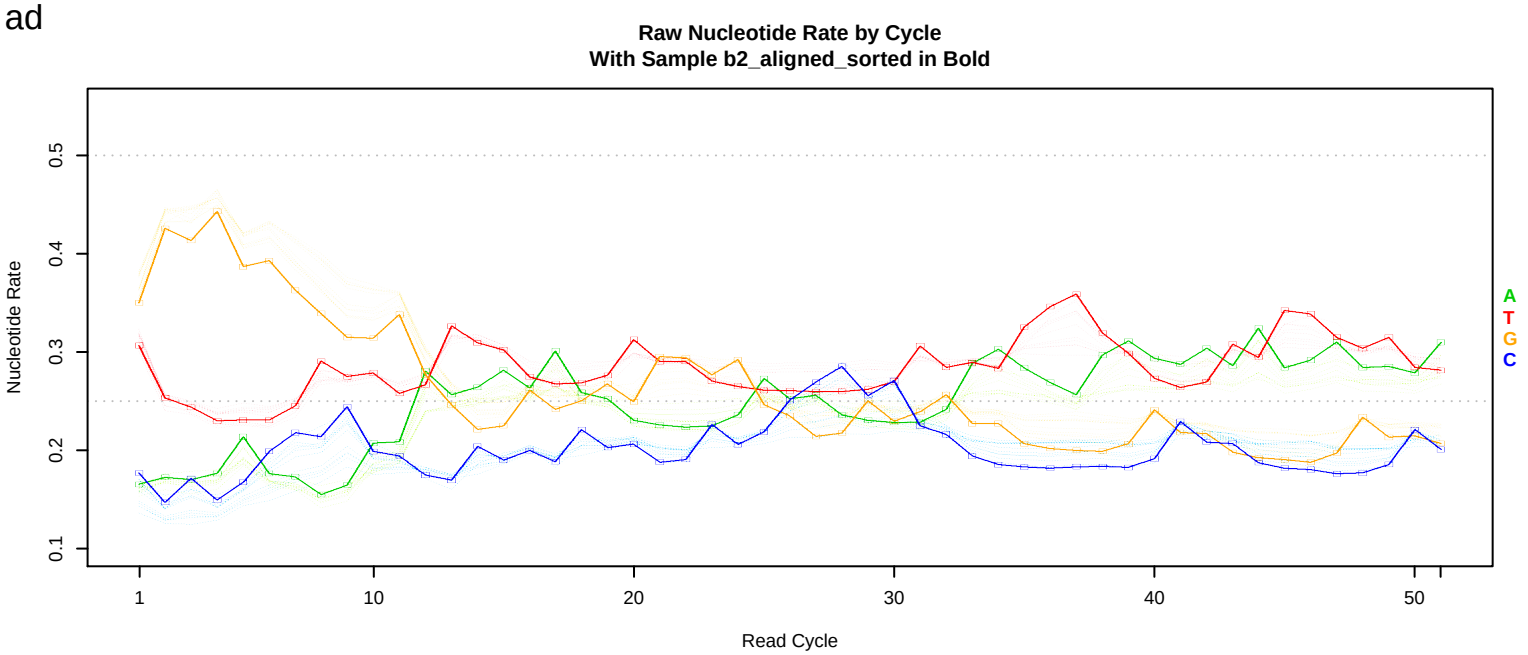
ab


Nucleotide Rate by Cycle, Leading Clipped bases (12)
With Sample b2_aligned_sorted in Bold
Nucleotide Rate
0.0
0.2
0.4
0.6
0.8
1.0
1
2
4
6
8
10
12
Read Cycle
A
T
G
C

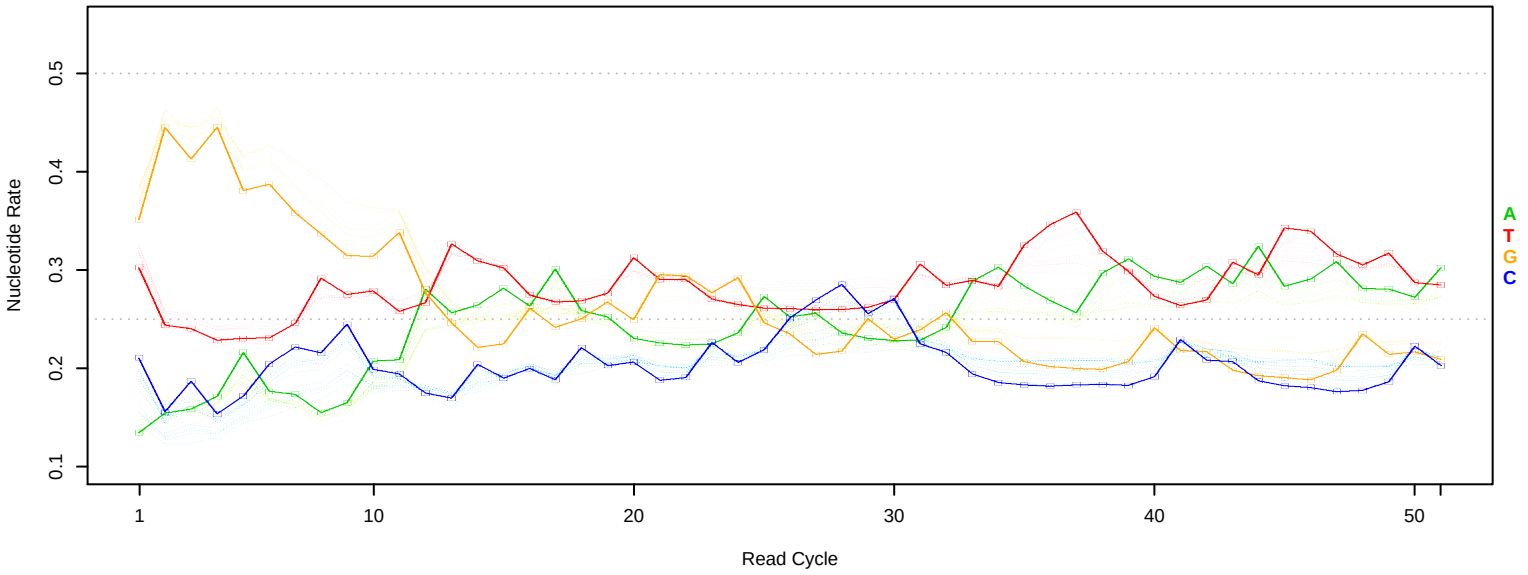
ac


Nucleotide Rate by Cycle, Trailing Clipped bases (12)
With Sample b2_aligned_sorted in Bold
Nucleotide Rate
0.0
0.2
0.4
0.6
0.8
1.0
40
41
43
45
47
49
51
Read Cycle
A
T
G
C

ad


Raw Nucleotide Rate by Cycle
With Sample b2_aligned_sorted in Bold
Nucleotide Rate
0.1
0.2
0.3
0.4
0.5
1
10
20
30
40
50
Read Cycle
A
T
G
C

ae


Nucleotide Rate by Cycle, Aligned bases only
With Sample b2_aligned_sorted in Bold
Nucleotide Rate
0.1
0.2
0.3
0.4
0.5
1
10
20
30
40
50
Read Cycle
A
T
G
C