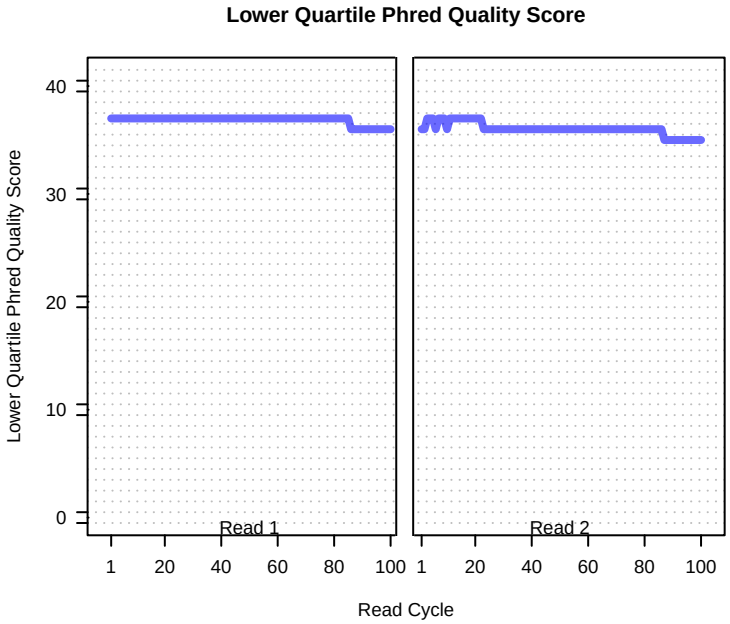
a

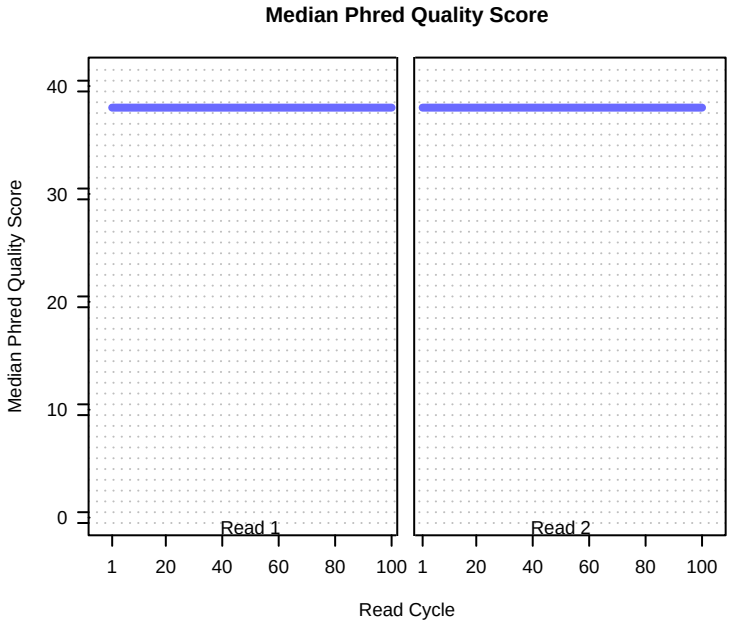
# All Quality Control Summary Plots

b

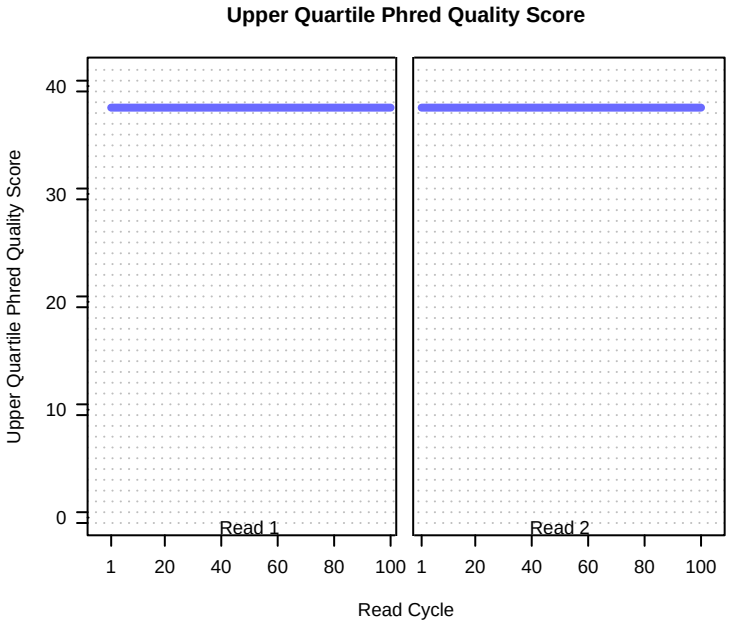
c



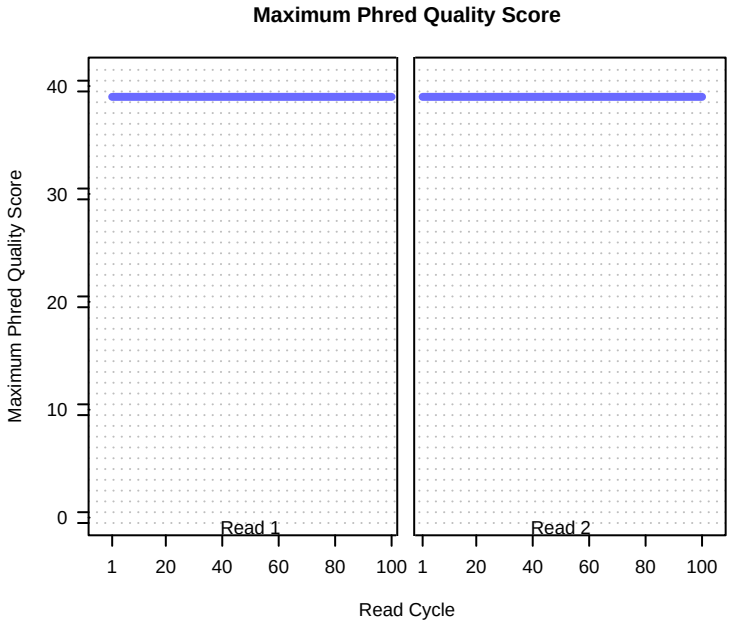

d



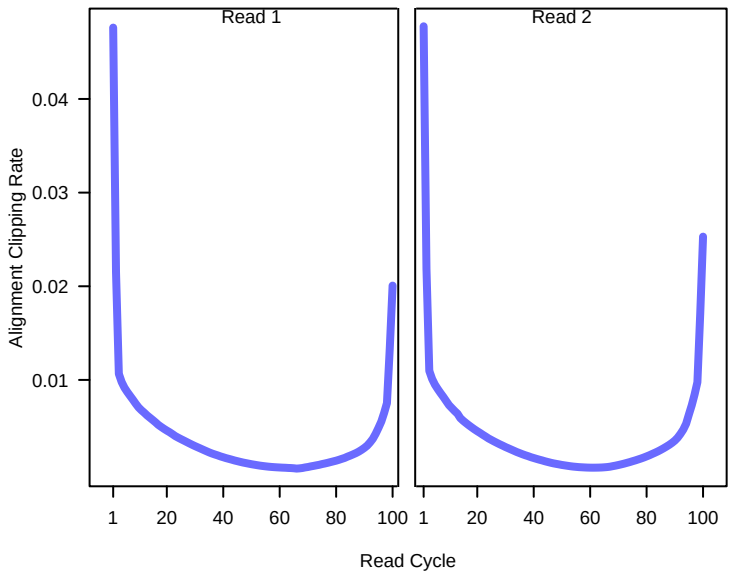

e



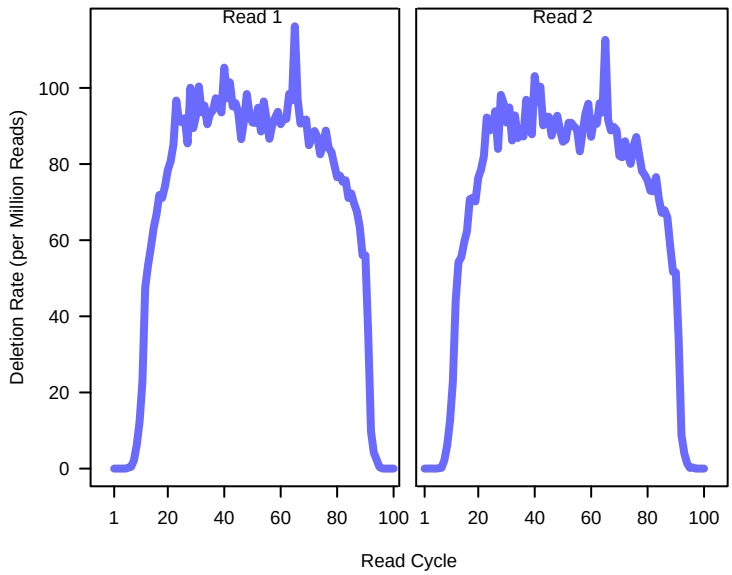

f



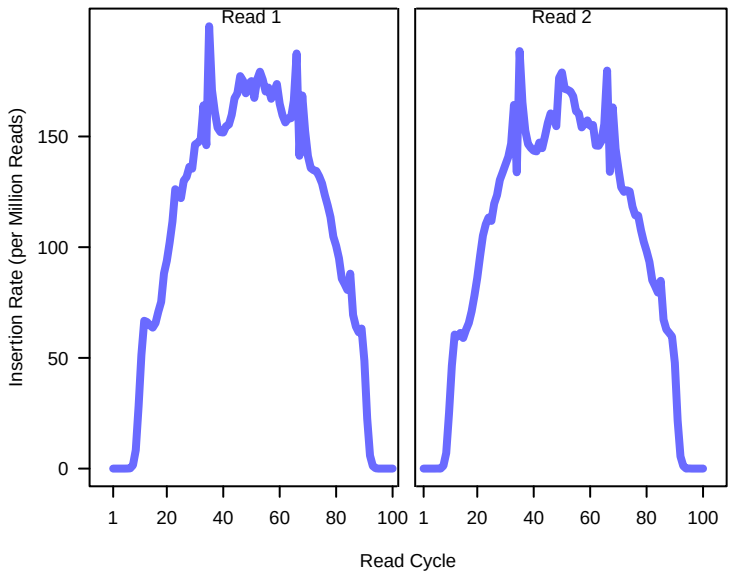
g


Alignment Clipping Rate, by read cycle
Read 1
Read 2
Alignment Clipping Rate
0.04
0.03
0.02
0.01
1
20
40
60
80
100
Read Cycle

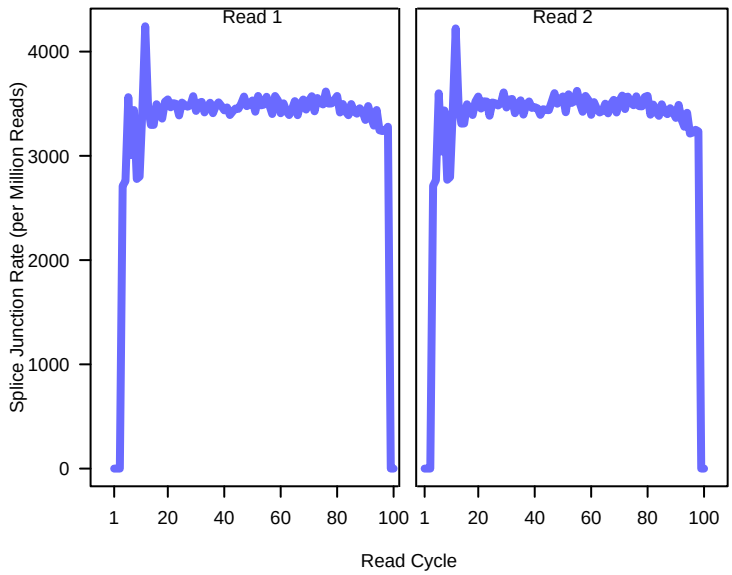
h


Deletion Rate, by read cycle
Read 1
Read 2
Deletion Rate (per Million Reads)
100
80
60
40
20
0
1
20
40
60
80
100
Read Cycle

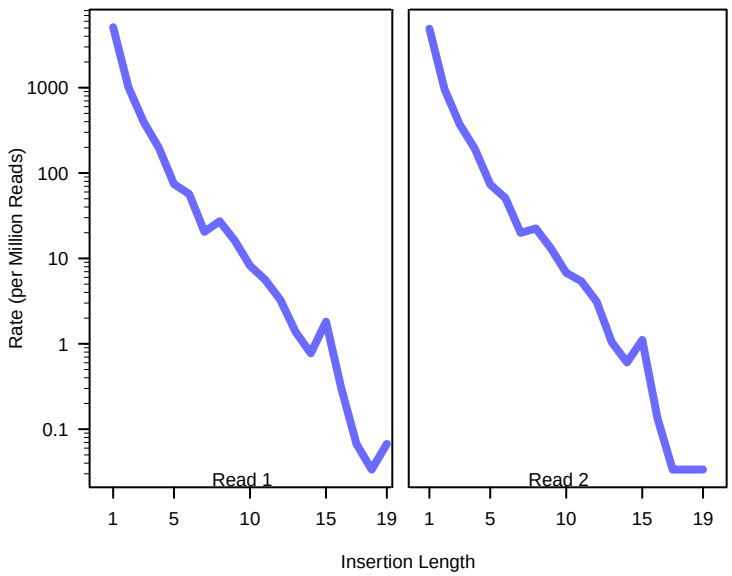
i


Insertion Rate, by read cycle
Read 1
Read 2
Insertion Rate (per Million Reads)
150
100
50
0
1
20
40
60
80
100
Read Cycle

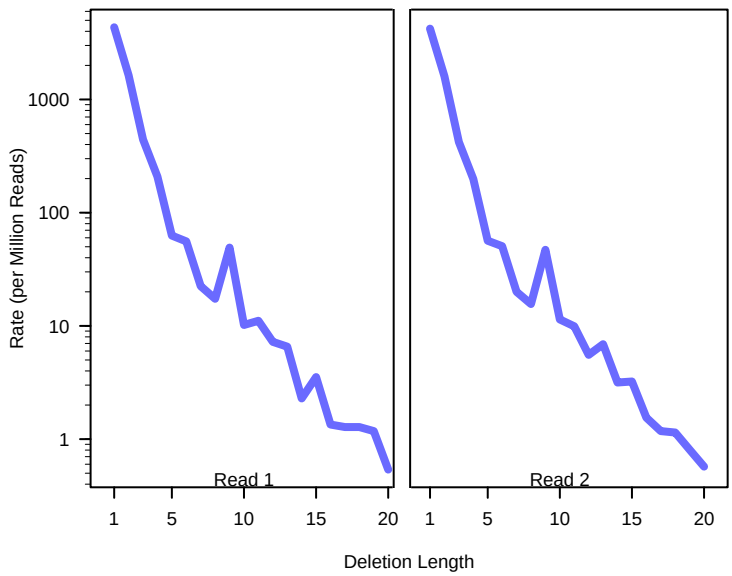
j


Splice Junction Rate, by read cycle
Read 1
Read 2
Splice Junction Rate (per Million Reads)
4000
3000
2000
1000
0
1
20
40
60
80
100
Read Cycle

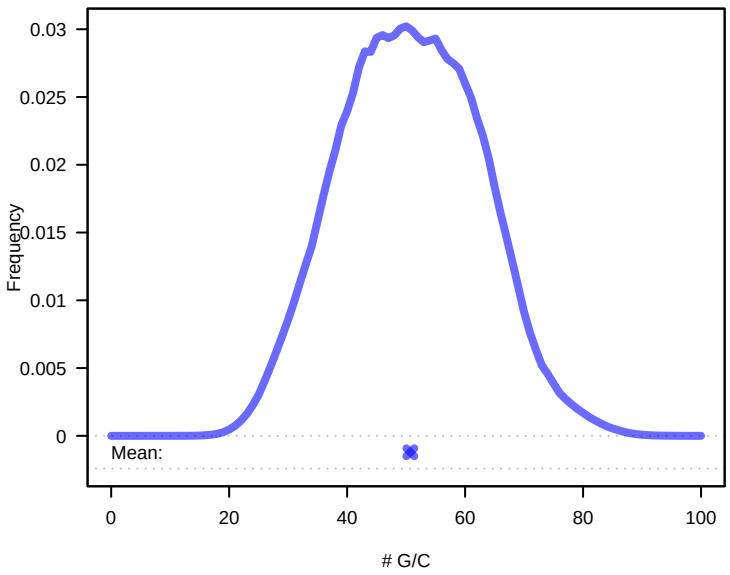
k


Insertion Length Distribution
Read 1
Read 2
Rate (per Million Reads)
1000
100
10
1
0.1
1
5
10
15
19
Insertion Length

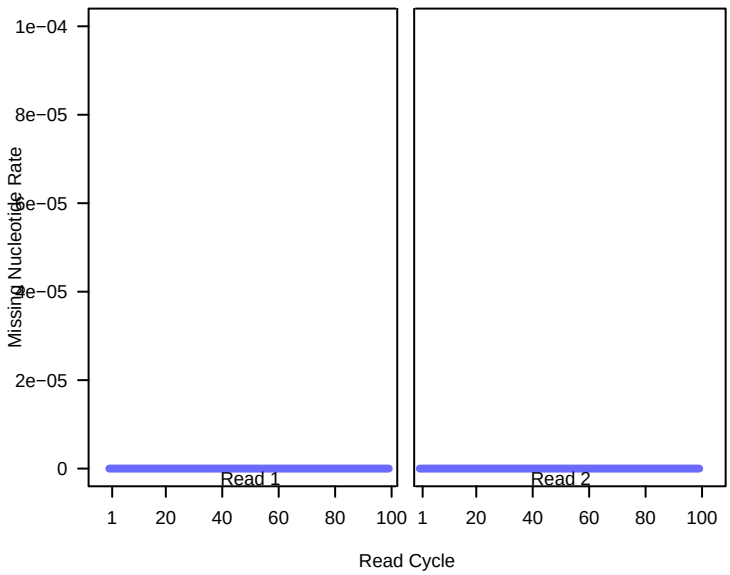
l


Deletion Length Distribution
Read 1
Read 2
Rate (per Million Reads)
1000
100
10
1
1
5
10
15
20
Deletion Length

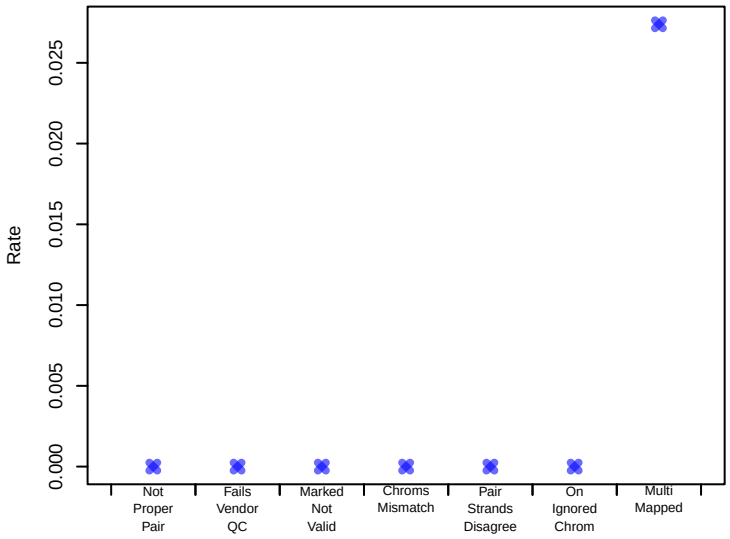
m


GC Content
Frequency
0.03
0.025
0.02
0.015
0.01
0.005
0
Mean:
0
20
40
60
80
100
# G/C

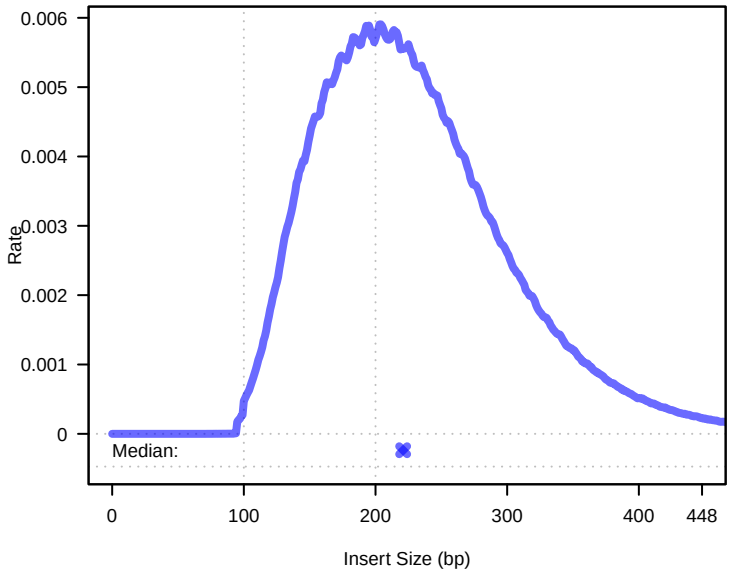
n


'N' Rate, by Read Cycle
Missing Nucleotide Rate
1e−04
8e−05
6e−05
4e−05
2e−05
0
Read 1
Read 2
1
20
40
60
80
100
Read Cycle

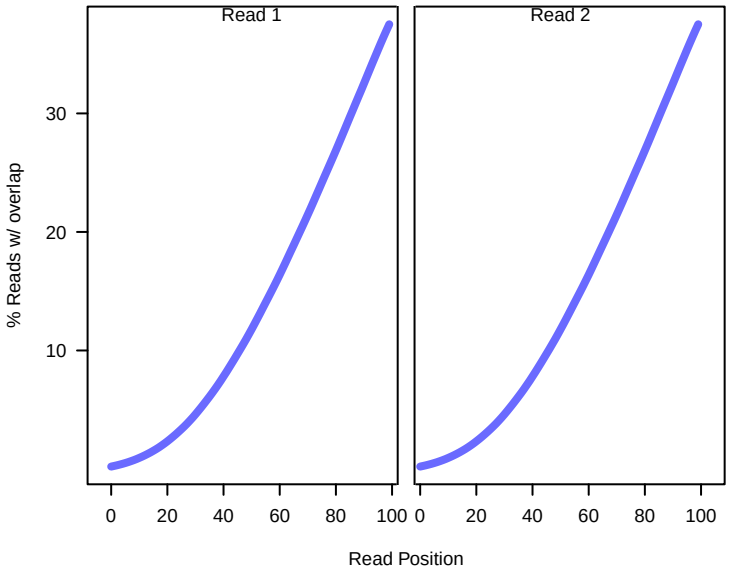
o


Read Drop Rate, by Reason
Rate
0.025
0.020
0.015
0.010
0.005
0.000
Not Proper Pair
Fails Vendor QC
Marked Not Valid
Chroms Mismatch
Pair Strands Disagree
On Ignored Chrom
Multi Mapped

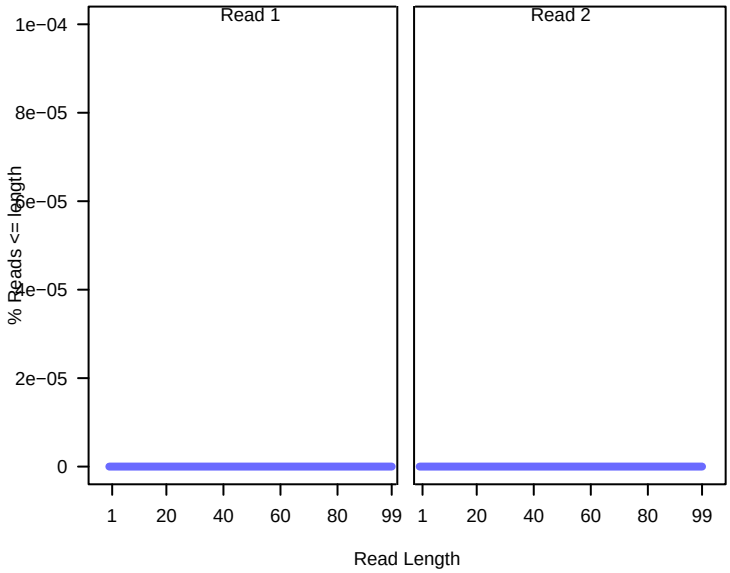
p


Insert Size
Rate
0.006
0.005
0.004
0.003
0.002
0.001
0
Median:
0
100
200
300
400
448
Insert Size (bp)

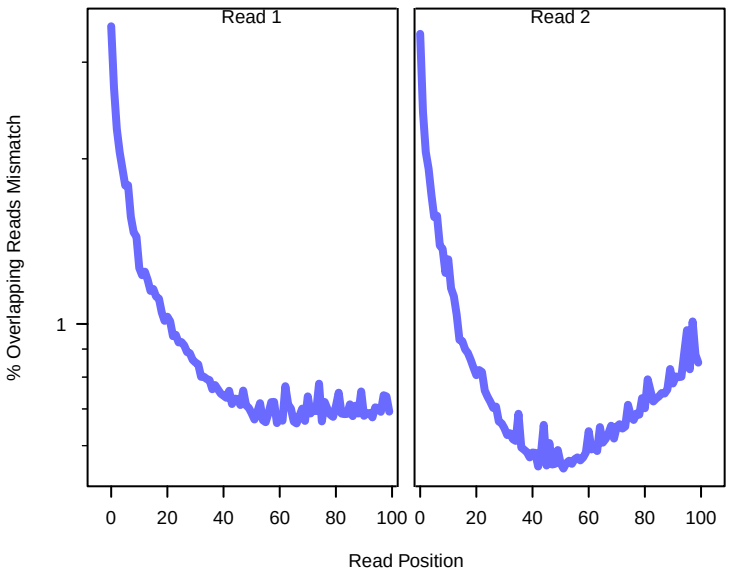
q


Overlapping Coverage
Read 1
Read 2
% Reads w/ overlap
30
20
10
0
20
40
60
80
100
Read Position

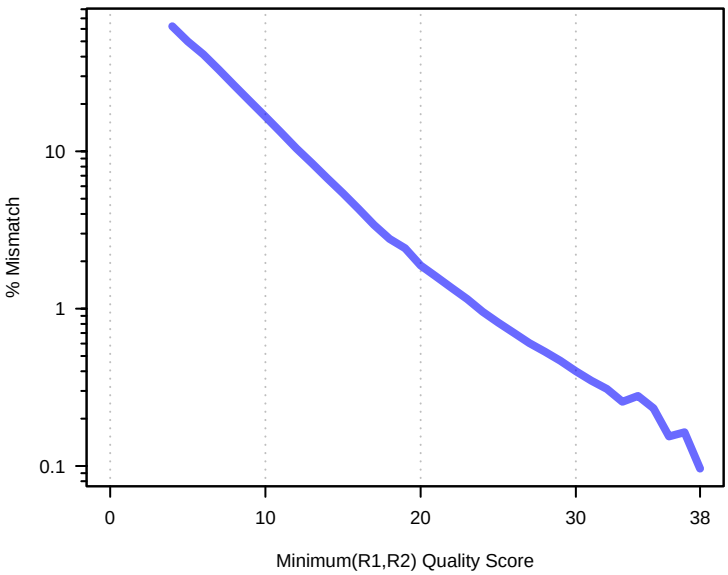
r


Read Length Distribution
Read 1
Read 2
% Reads <= length
1e−04
8e−05
6e−05
4e−05
2e−05
0
1
20
40
60
80
99
Read Length

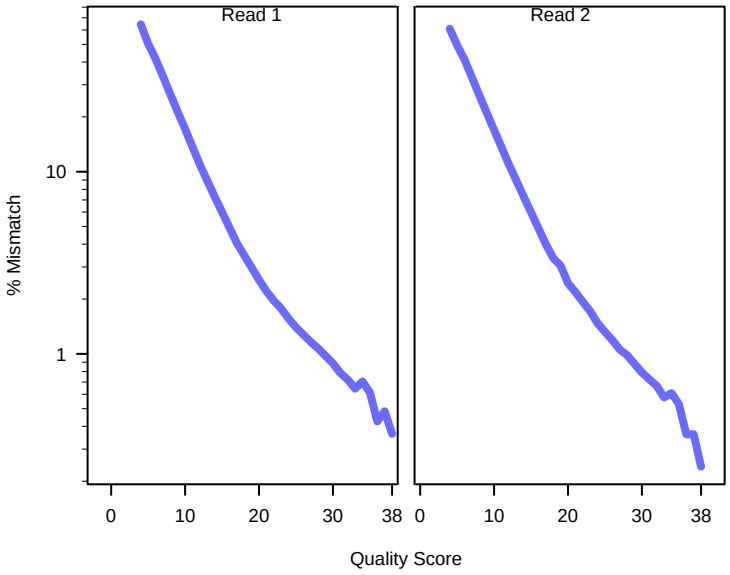
s


Overlap Mismatch by Read Cycle
Read 1
Read 2
% Overlapping Reads Mismatch
1
0
20
40
60
80
100
Read Position

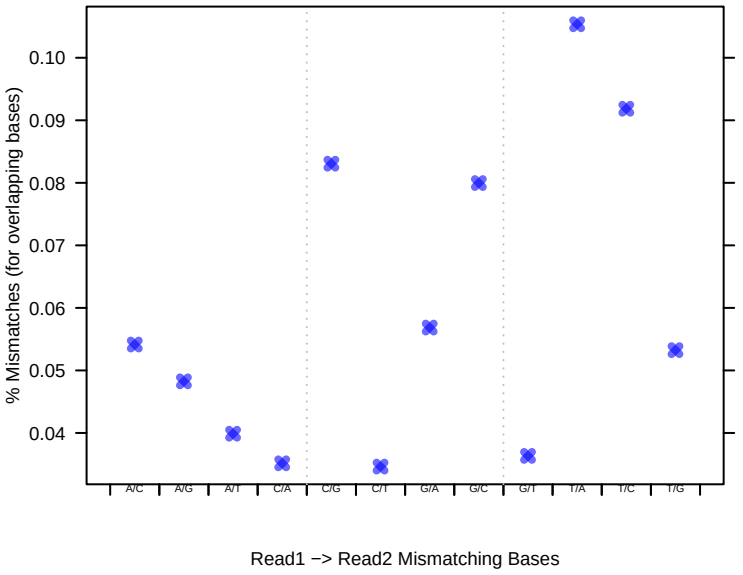
t


Overlapping Mismatch by Min Qual
% Mismatch
10
1
0.1
0
10
20
30
38
Minimum(R1,R2) Quality Score

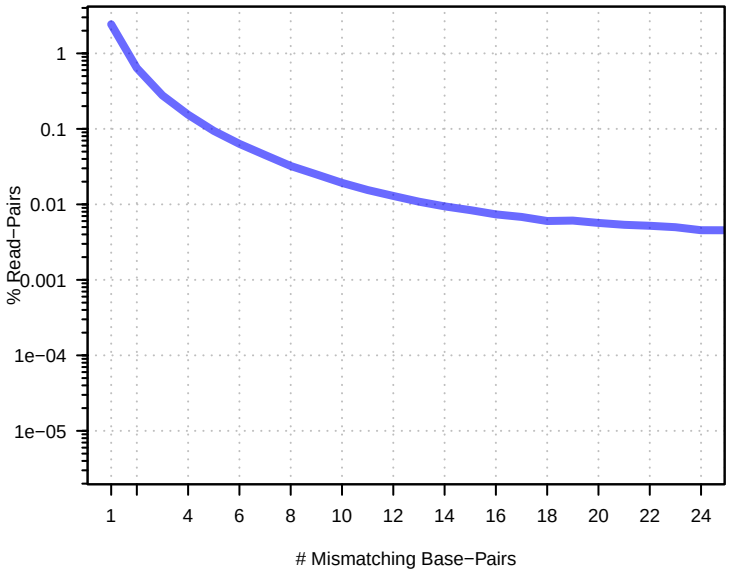
u


Overlap Mismatch by Read Qual
Read 1
Read 2
% Mismatch
10
1
0
10
20
30
38
Quality Score

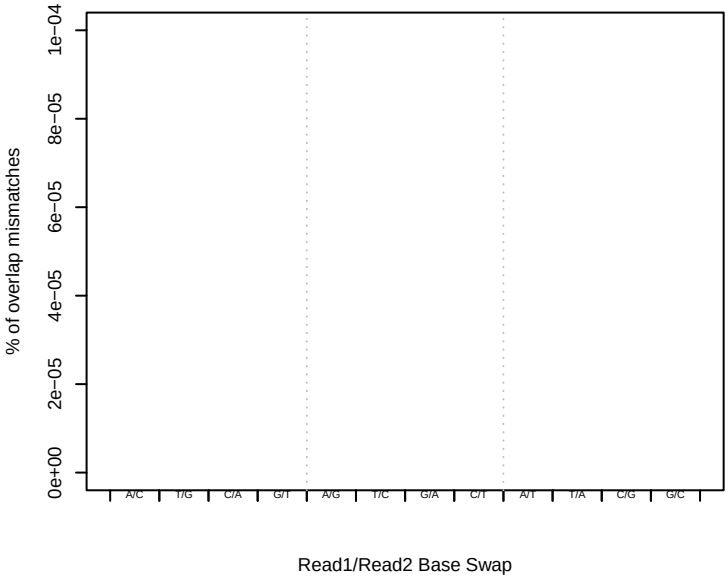
v


Overlap Mismatch Combinations
% Mismatches (for overlapping bases)
0.10
0.09
0.08
0.07
0.06
0.05
0.04
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

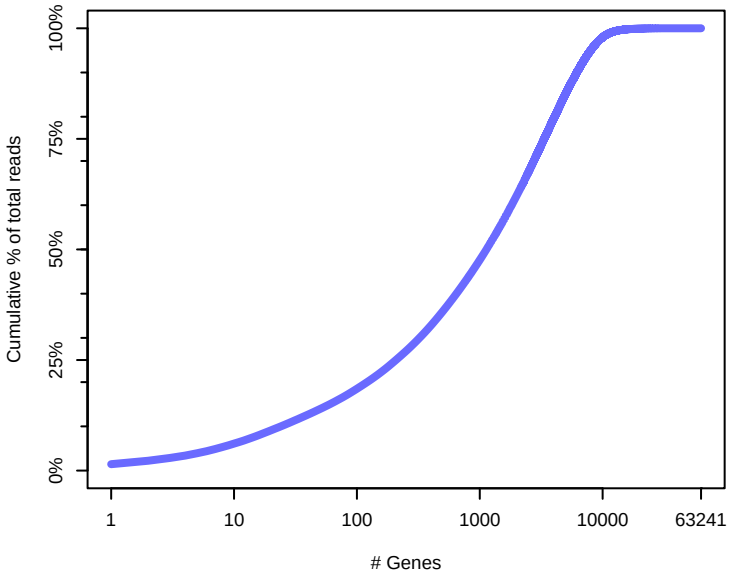
w


Overlap Mismatch Size Frequency
% Read-Pairs
1
0.1
0.01
0.001
1e-04
1e-05
1
4
6
8
10
12
14
16
18
20
22
24
# Mismatching Base-Pairs

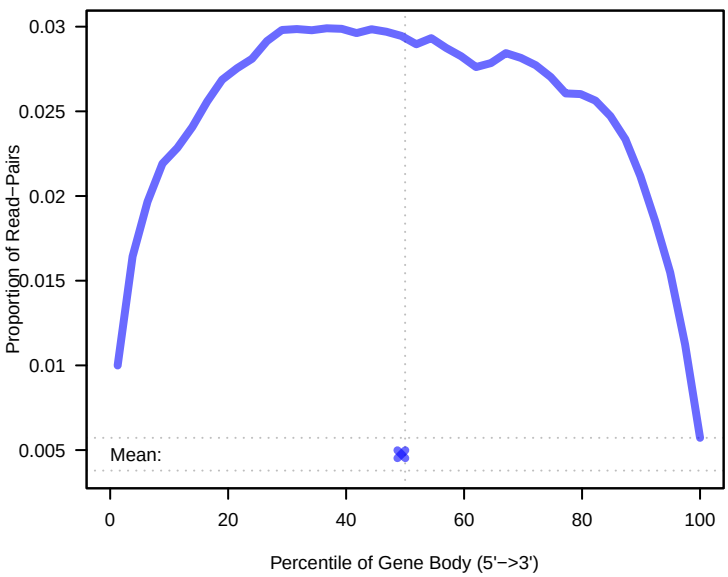
x


Overlap Mismatch Pairs At Phred == 41
% of overlap mismatches
0e+00
2e-05
4e-05
6e-05
8e-05
1e-04
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

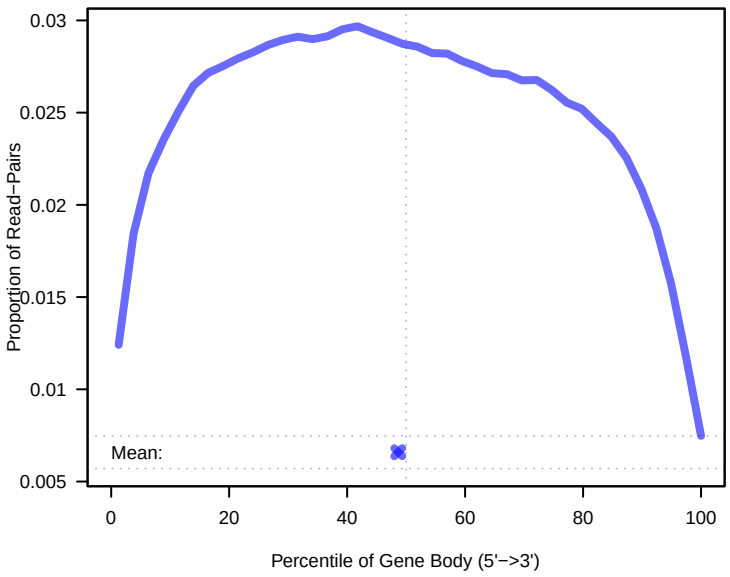
y


Cumulative Gene Assignment Diversity
Cumulative % of total reads
0%
25%
50%
75%
100%
1
10
100
1000
10000
63241
# Genes

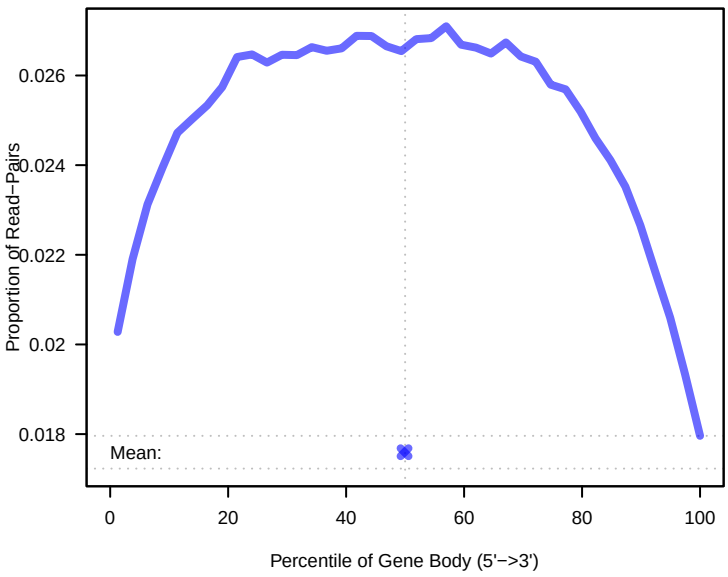
z


Gene−Body Coverage
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')

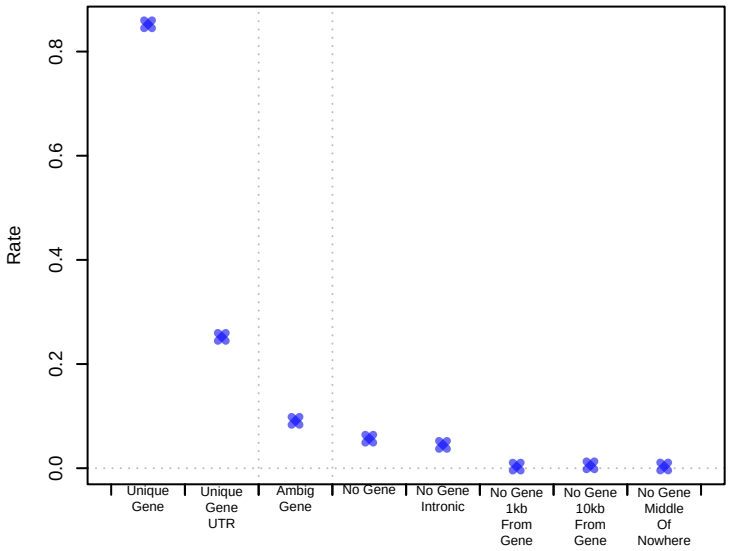
aa


Gene−Body Coverage, Upper Middle Quartile Genes
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')

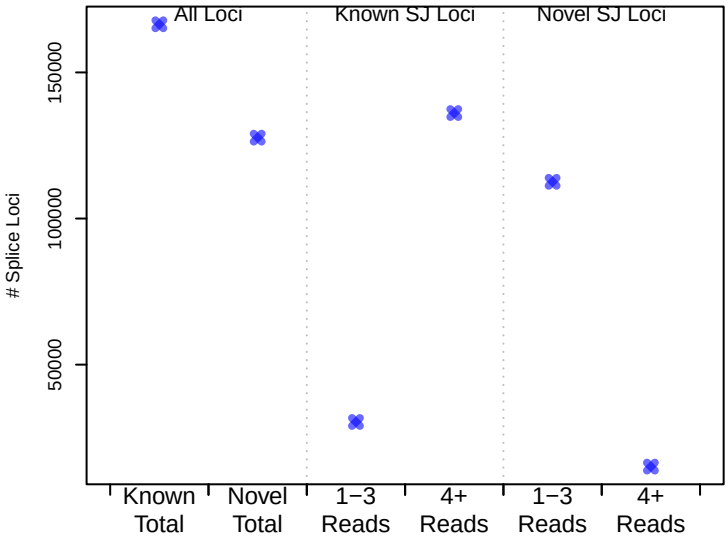
ab


Gene−Body Coverage, Low Expression Genes
Proportion of Read−Pairs
0.018
0.02
0.022
0.024
0.026
Mean:
0
20
40
60
80
100
Percentile of Gene Body (5'−>3')

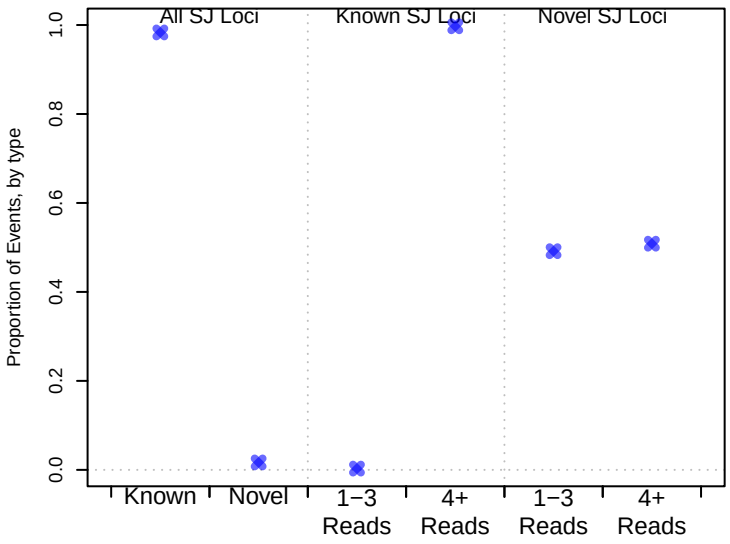
ac


Read Mapping Location Rates
Rate
0.0
0.2
0.4
0.6
0.8
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

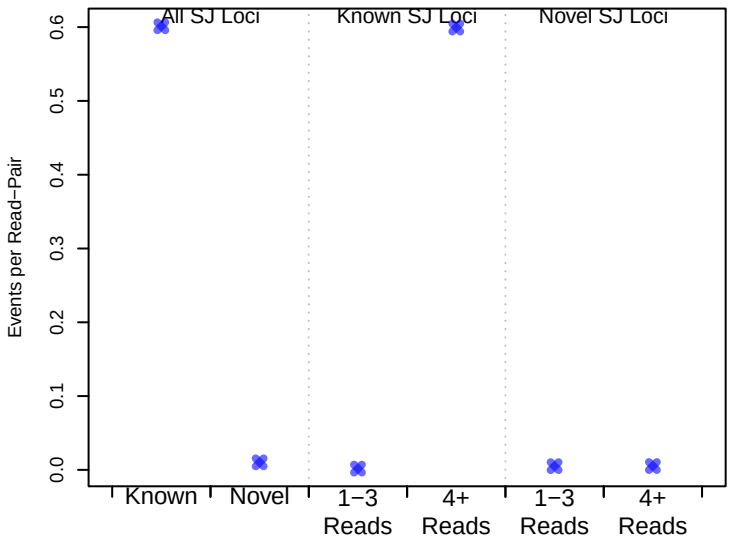
ad


# Observed Splice Junction Loci, by type
# Splice Loci
50000
100000
150000
All Loci
Known SJ Loci
Novel SJ Loci
Known Total
Novel Total
1−3 Reads
4+ Reads
1−3 Reads
4+ Reads

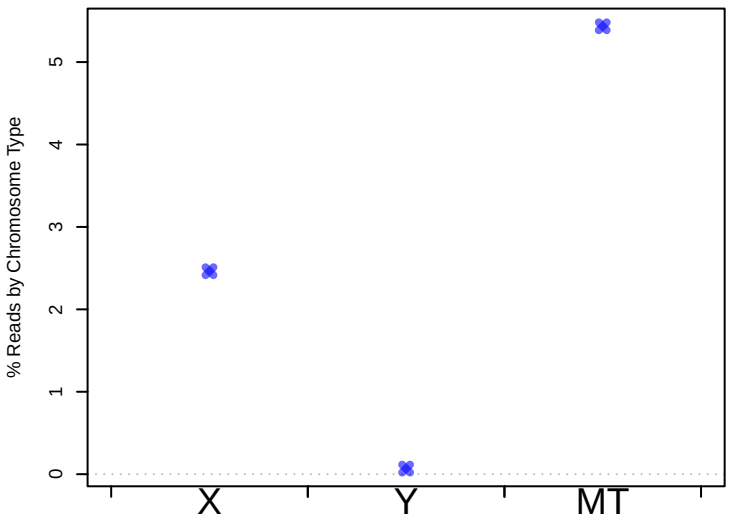
ae



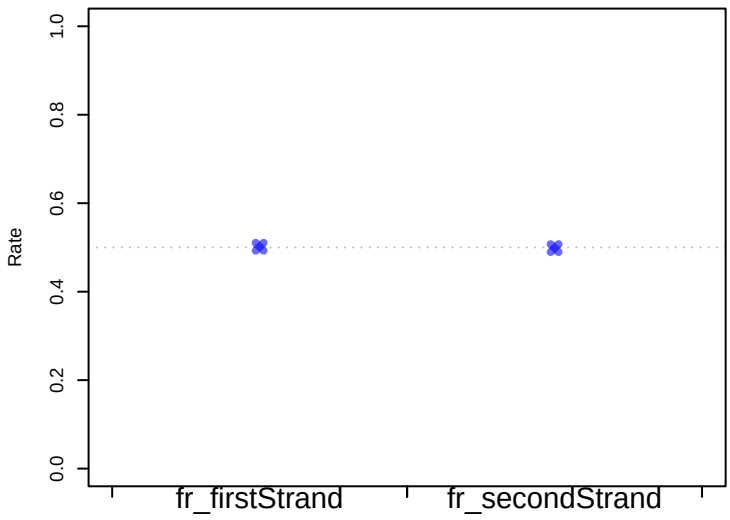

af



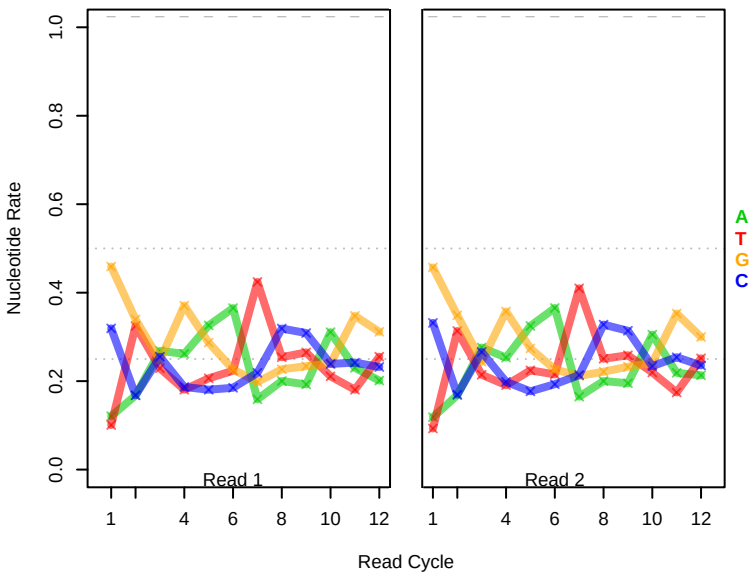

ag



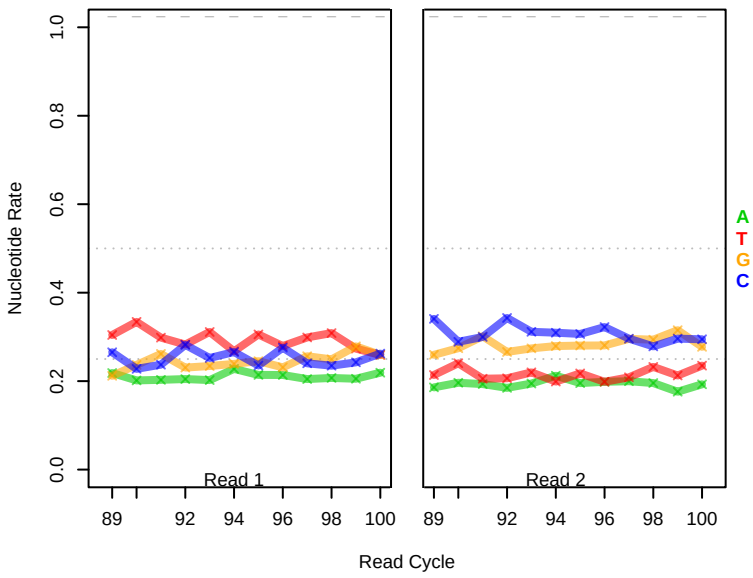

ah



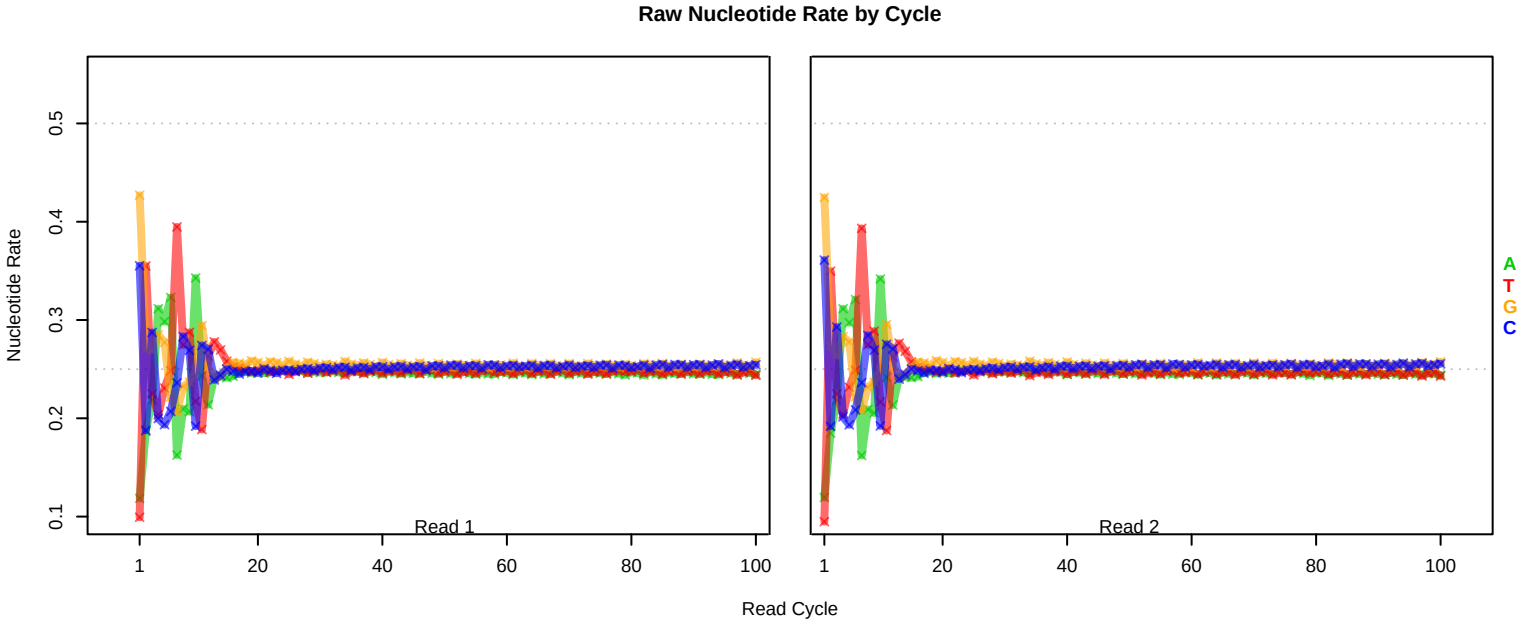

ai



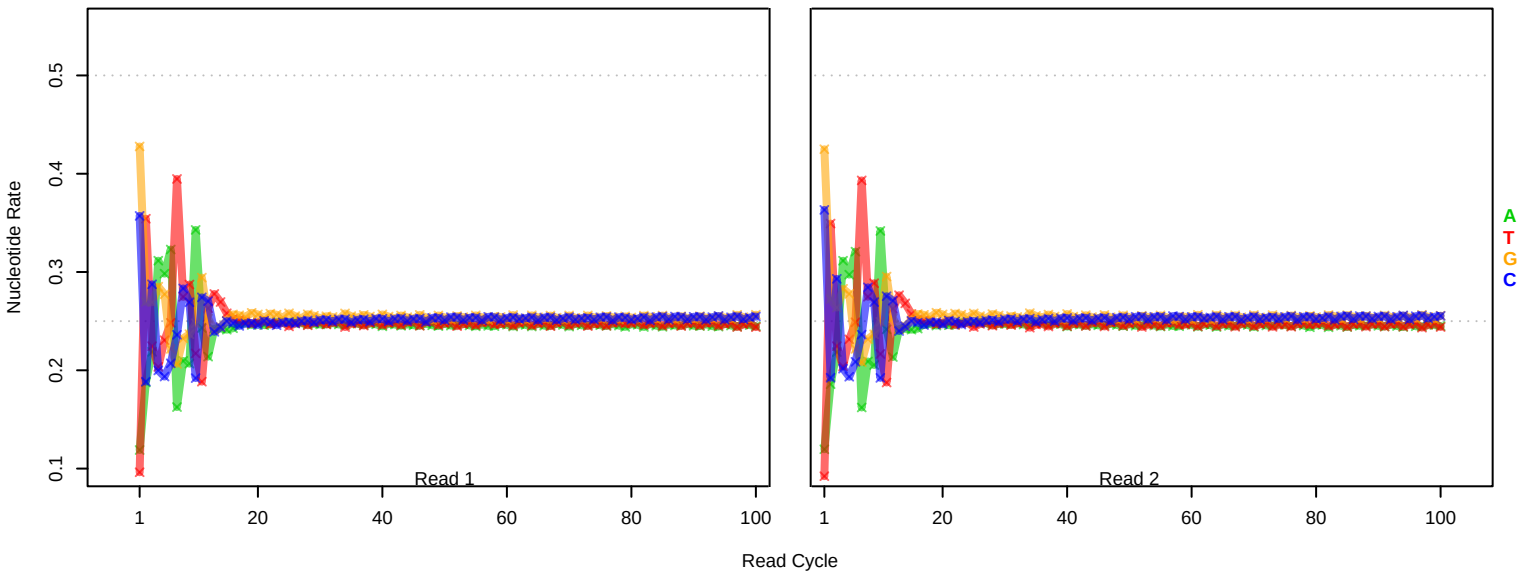

aj



ak


Raw Nucleotide Rate by Cycle
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

al


Nucleotide Rate by Cycle, Aligned bases only
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