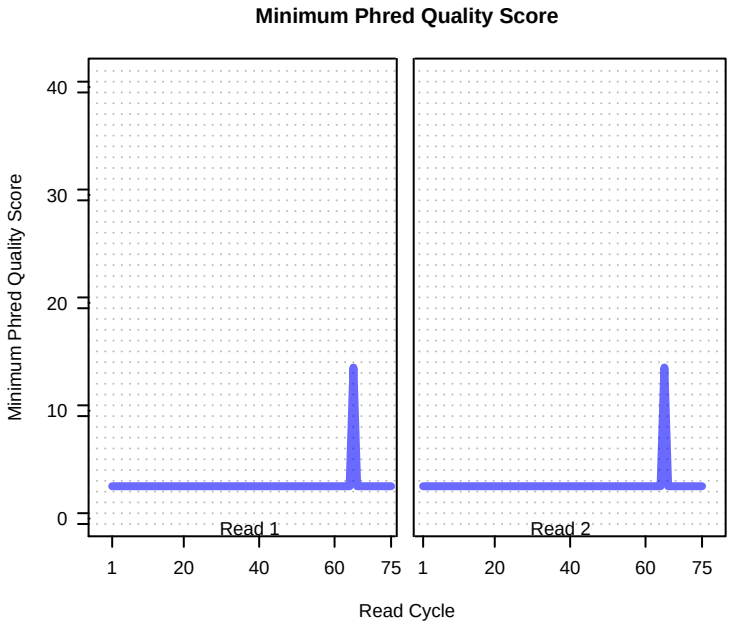
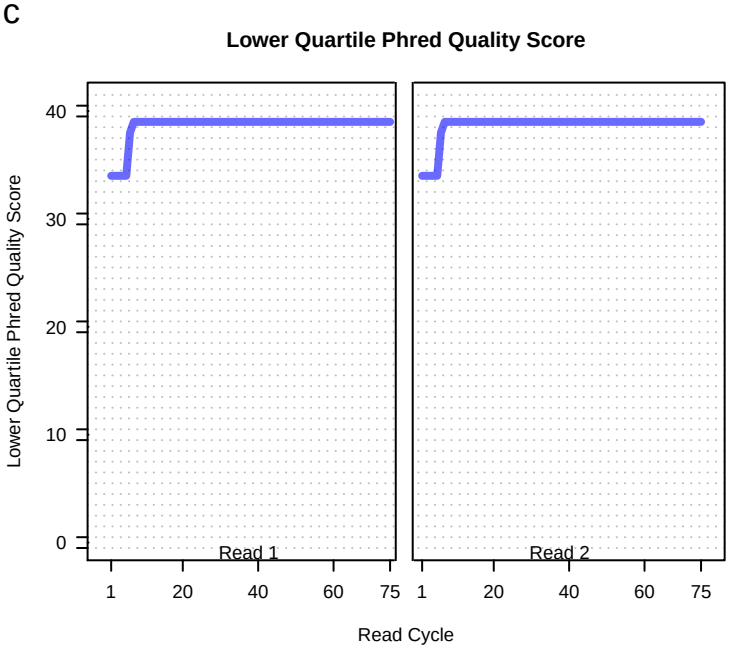
a

All Quality Control Summary Plots

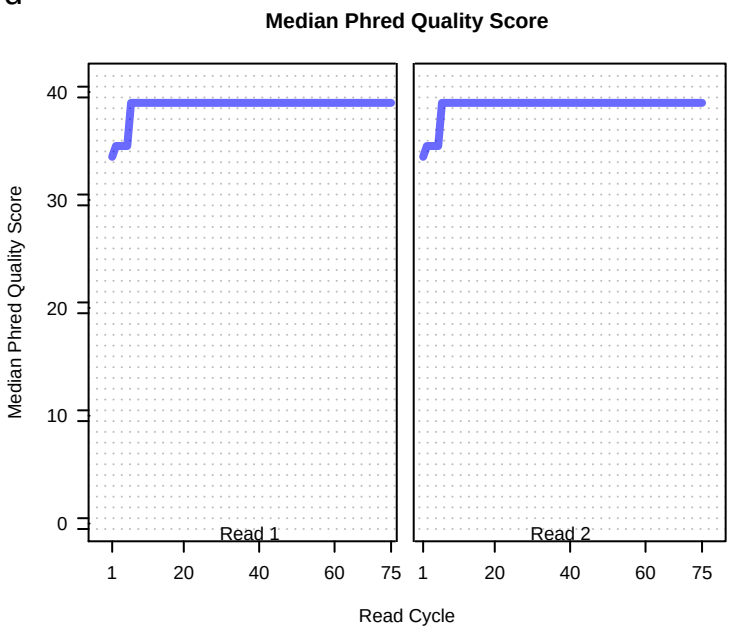
b



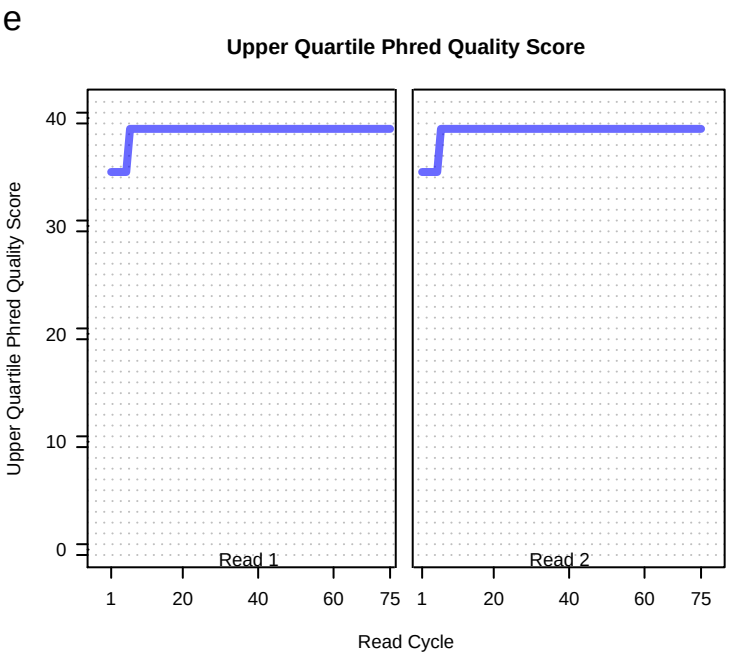
c



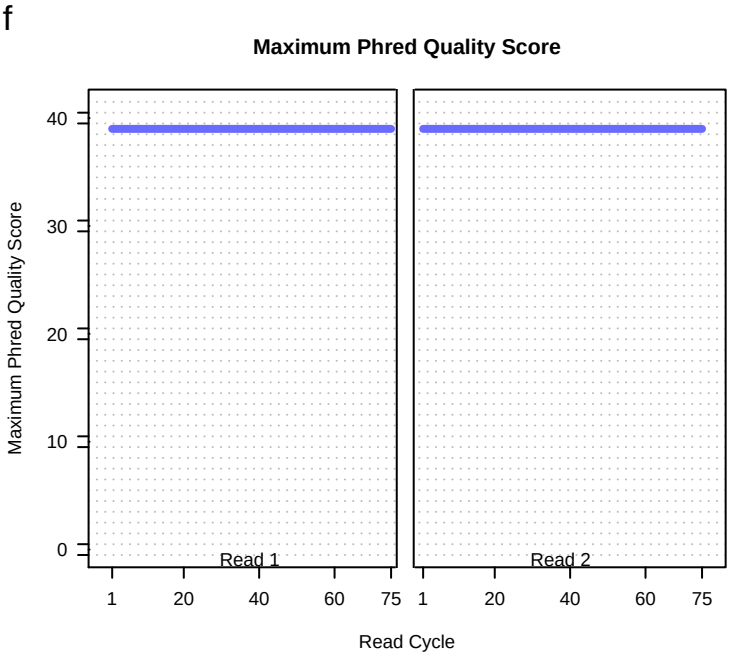
d



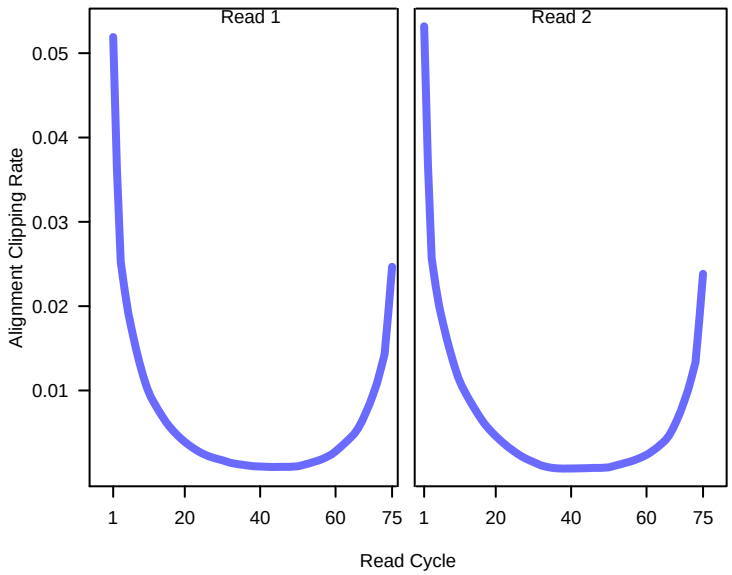
e



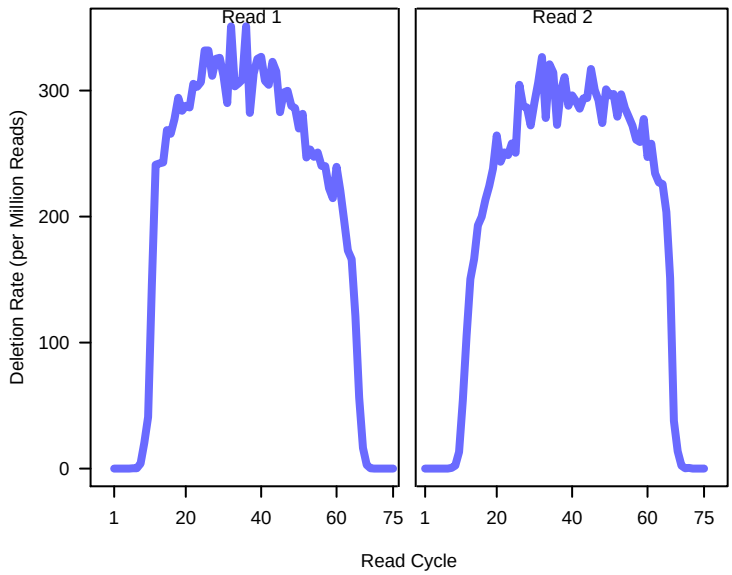
f



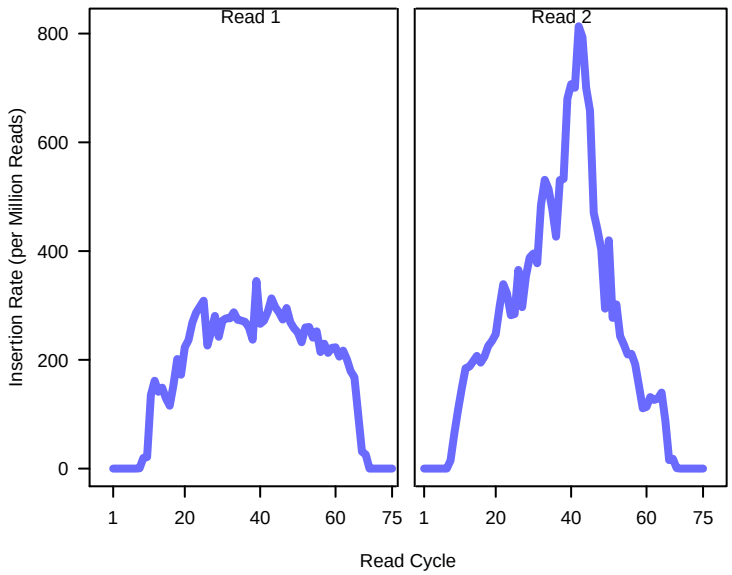
g


Alignment Clipping Rate, by read cycle
Read 1
Read 2
Alignment Clipping Rate
0.05
0.04
0.03
0.02
0.01
1
20
40
60
75
Read Cycle

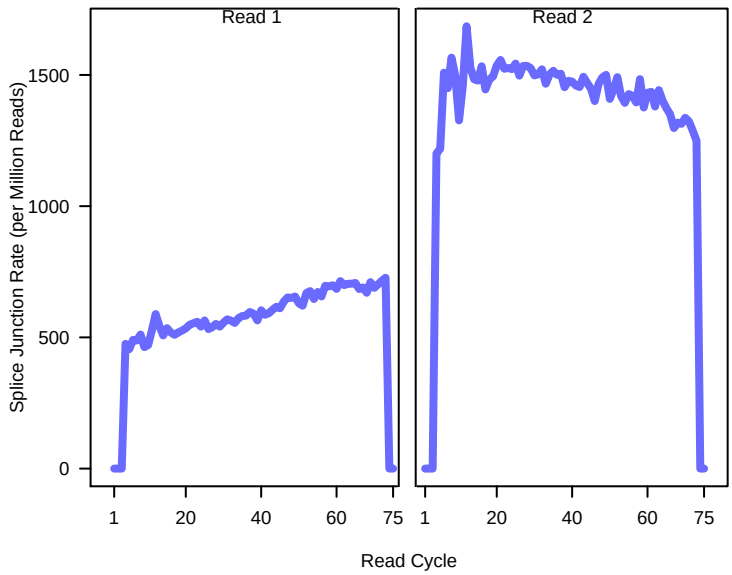
h


Deletion Rate, by read cycle
Read 1
Read 2
Deletion Rate (per Million Reads)
300
200
100
0
1
20
40
60
75
Read Cycle

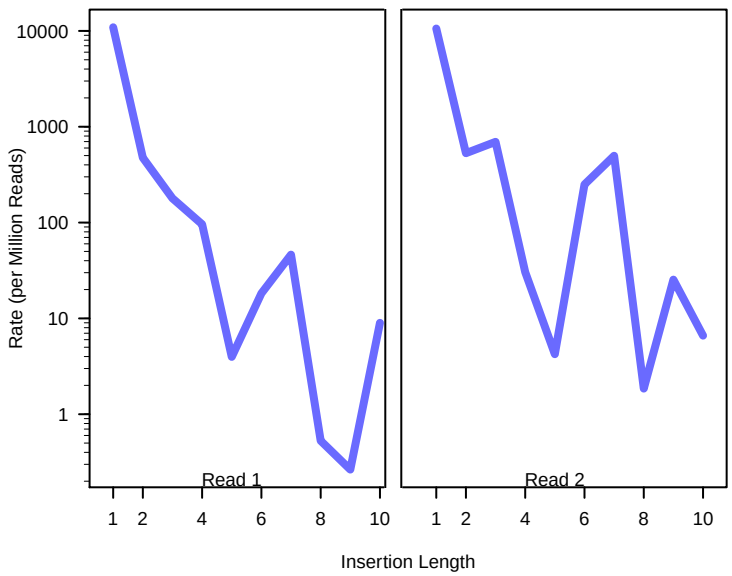
i


Insertion Rate, by read cycle
Read 1
Read 2
Insertion Rate (per Million Reads)
800
600
400
200
0
1
20
40
60
75
Read Cycle

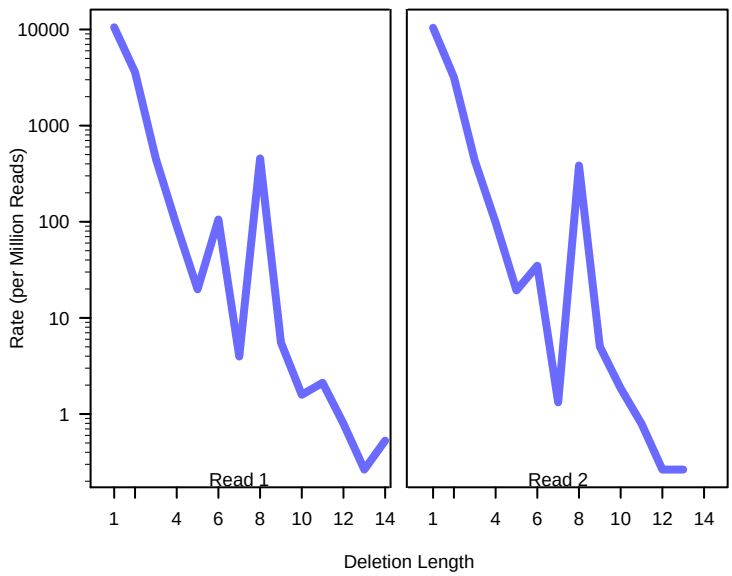
j


Splice Junction Rate, by read cycle
Read 1
Read 2
Splice Junction Rate (per Million Reads)
1500
1000
500
0
1
20
40
60
75
Read Cycle

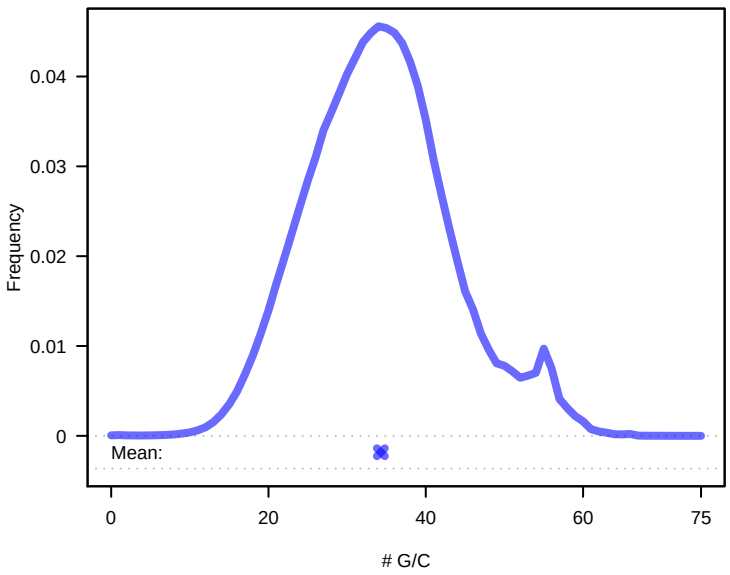
k


Insertion Length Distribution
Read 1
Read 2
Rate (per Million Reads)
10000
1000
100
10
1
1
2
4
6
8
10
Insertion Length

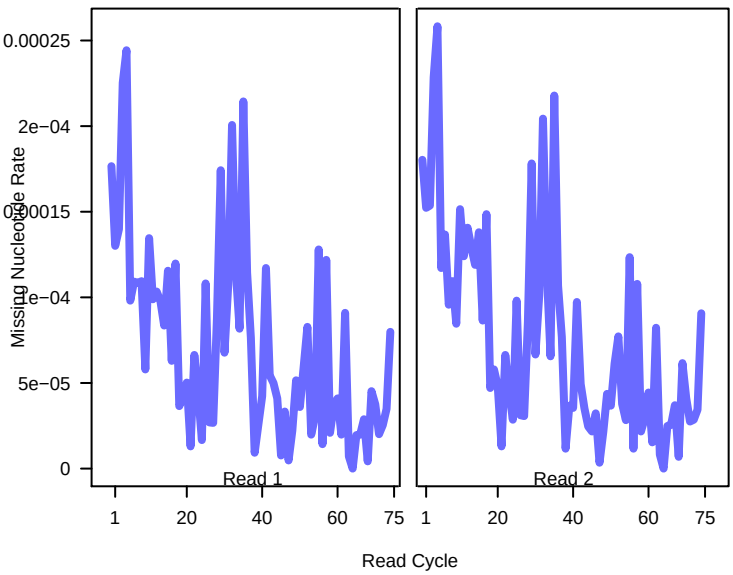
l


Deletion Length Distribution
Read 1
Read 2
Rate (per Million Reads)
10000
1000
100
10
1
1
4
6
8
10
12
14
Deletion Length

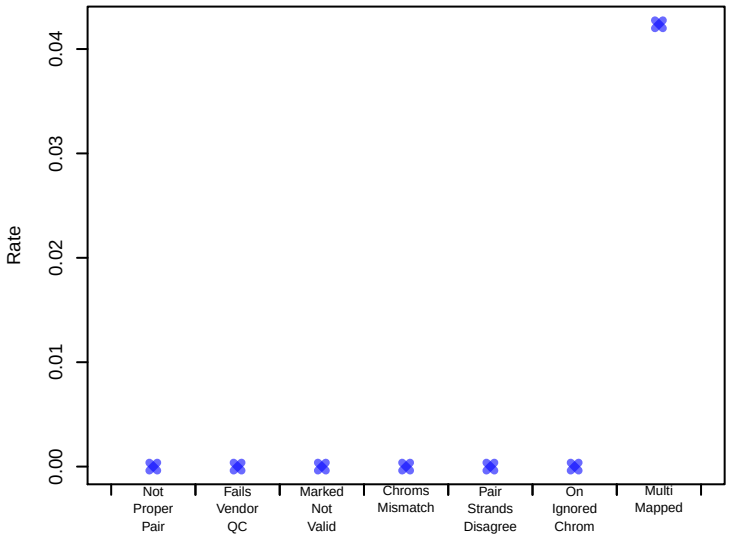
m


GC Content
Frequency
0.04
0.03
0.02
0.01
0
Mean:
0
20
40
60
75
G/C

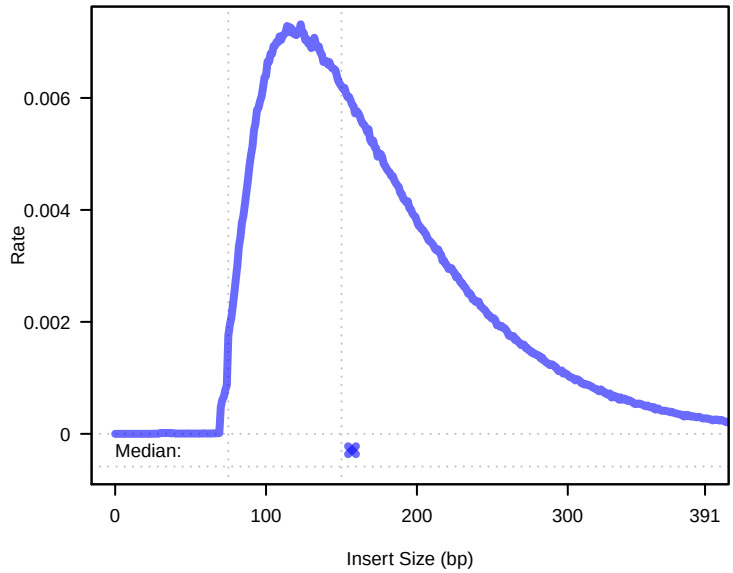
n


'N' Rate, by Read Cycle
Missing Nucleotide Rate
0.00025
2e−04
0.00015
1e−04
5e−05
0
Read 1
Read 2
1
20
40
60
75
Read Cycle

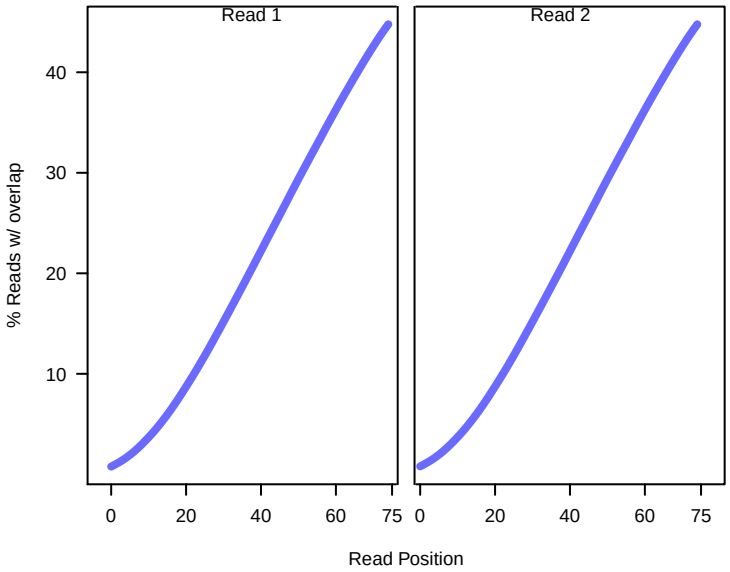
o


Read Drop Rate, by Reason
Rate
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

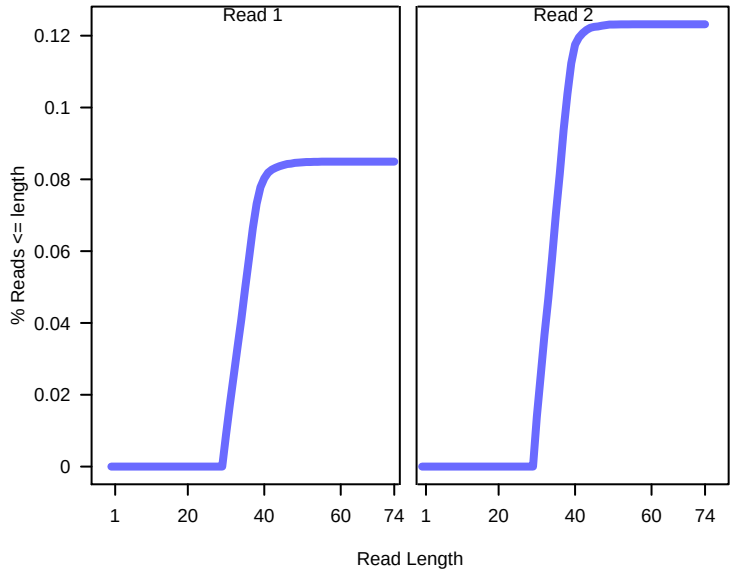
p


Insert Size
Rate
0.006
0.004
0.002
0
Median:
0
100
200
300
391
Insert Size (bp)

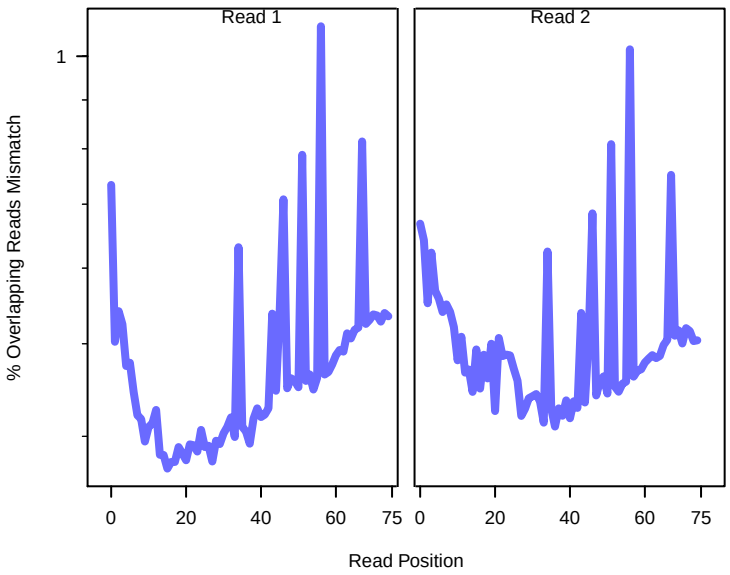
q


Overlapping Coverage
Read 1
Read 2
% Reads w/ overlap
40
30
20
10
0
20
40
60
75
Read Position

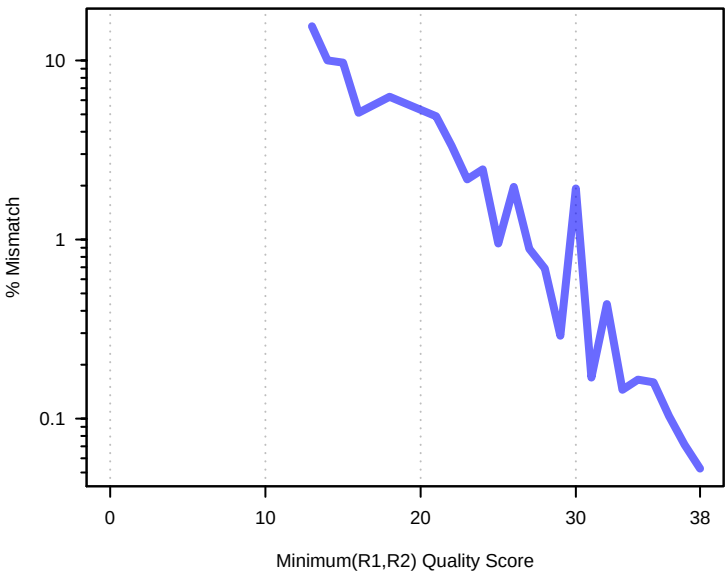
r


Read Length Distribution
Read 1
Read 2
% Reads <= length
0.12
0.1
0.08
0.06
0.04
0.02
0
1
20
40
60
74
Read Length

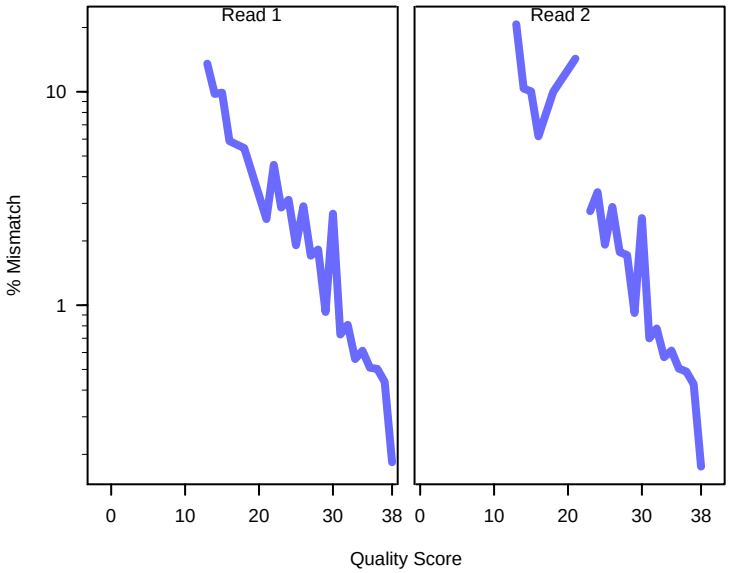
s


Overlap Mismatch by Read Cycle
Read 1
Read 2
% Overlapping Reads Mismatch
1
0
20
40
60
75
Read Position

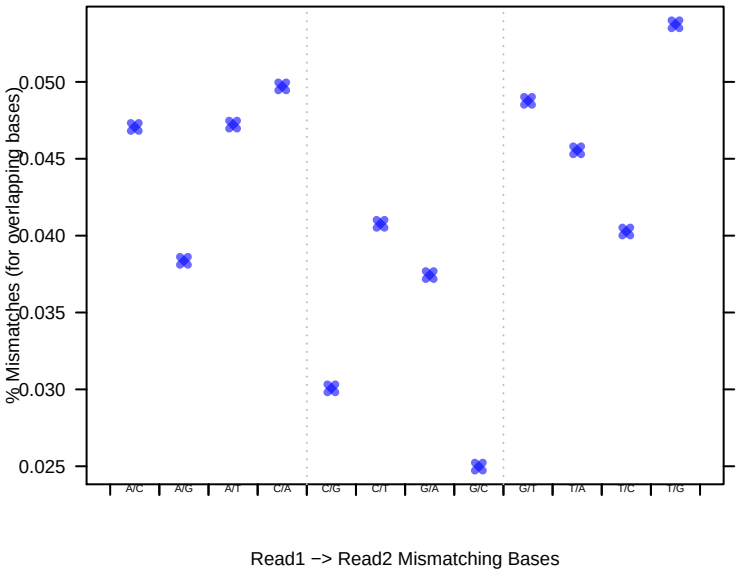
t


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

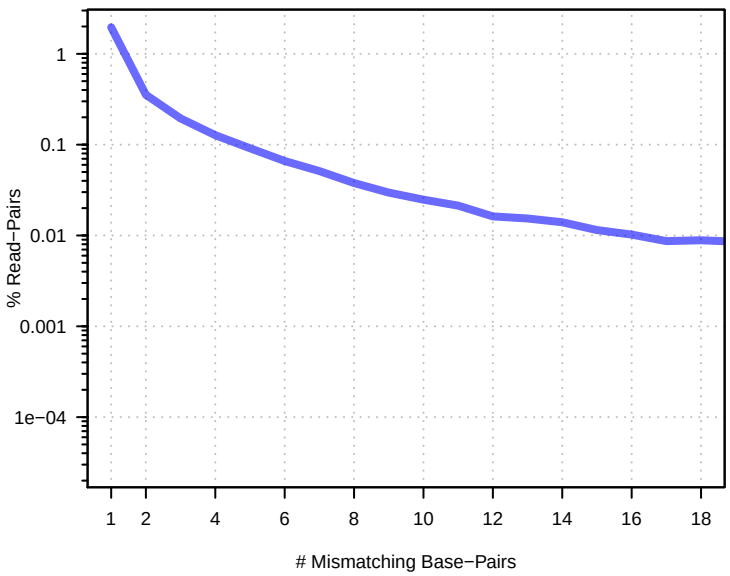
u


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

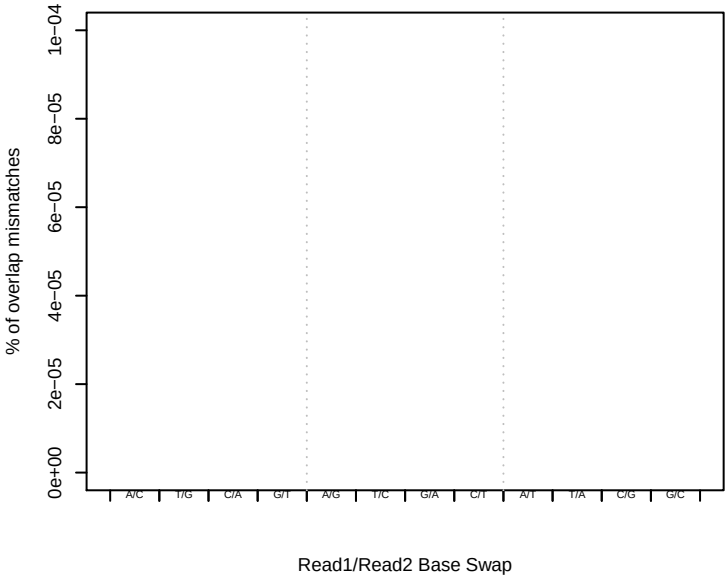
v


Overlap Mismatch Combinations
% Mismatches (for overlapping bases)
0.050
0.045
0.040
0.035
0.030
0.025
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

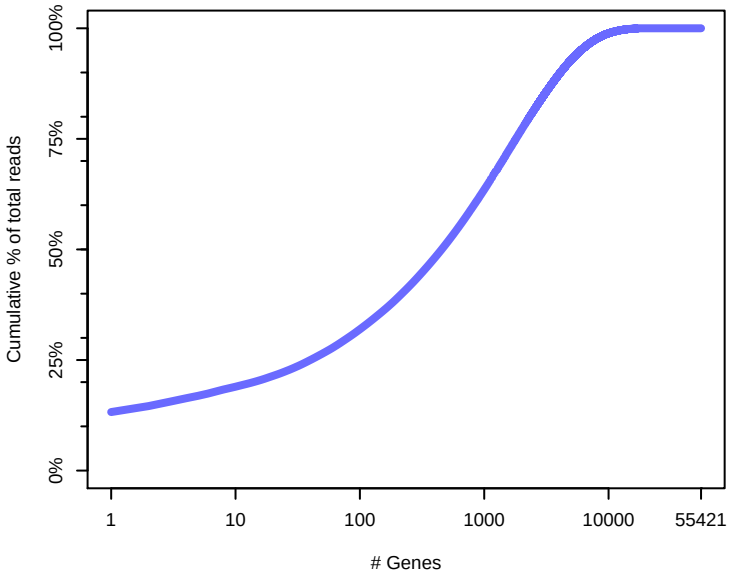
w


Overlap Mismatch Size Frequency
% Read−Pairs
1
0.1
0.01
0.001
1e−04
1
2
4
6
8
10
12
14
16
18
Mismatching Base−Pairs

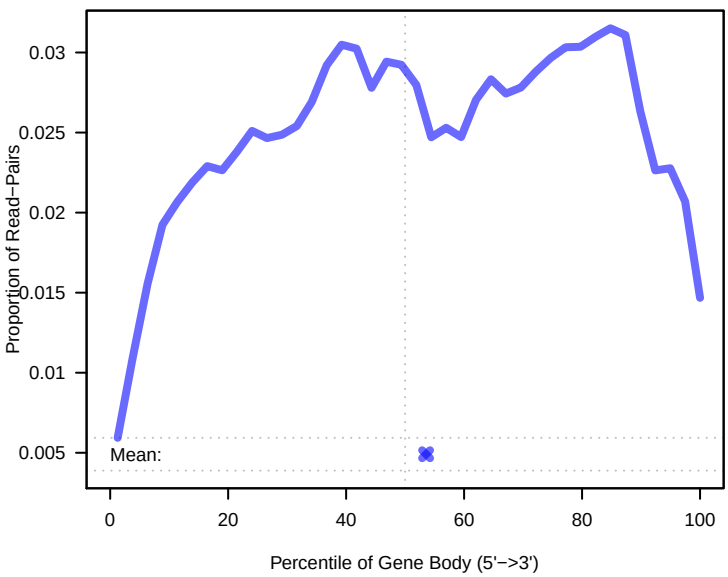
x


Overlap Mismatch Pairs At Phred == 41
% 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

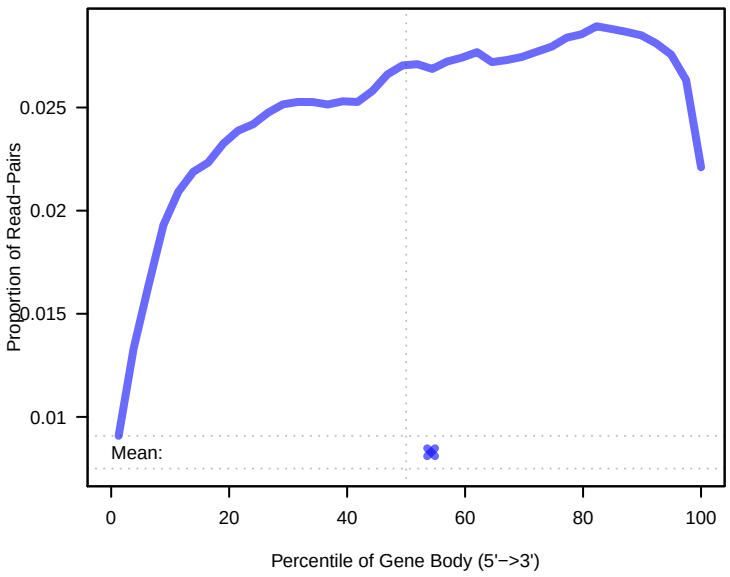
y


Cumulative Gene Assignment Diversity
Cumulative % of total reads
0%
25%
50%
75%
100%
1
10
100
1000
10000
55421
Genes

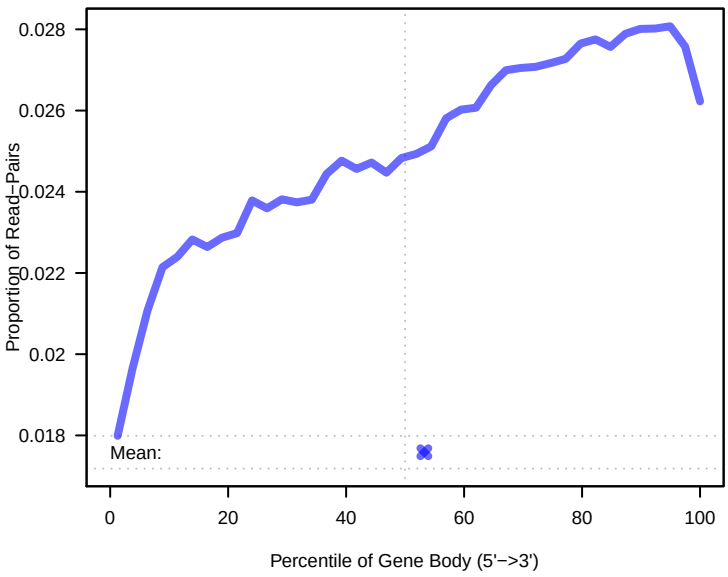
z


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')

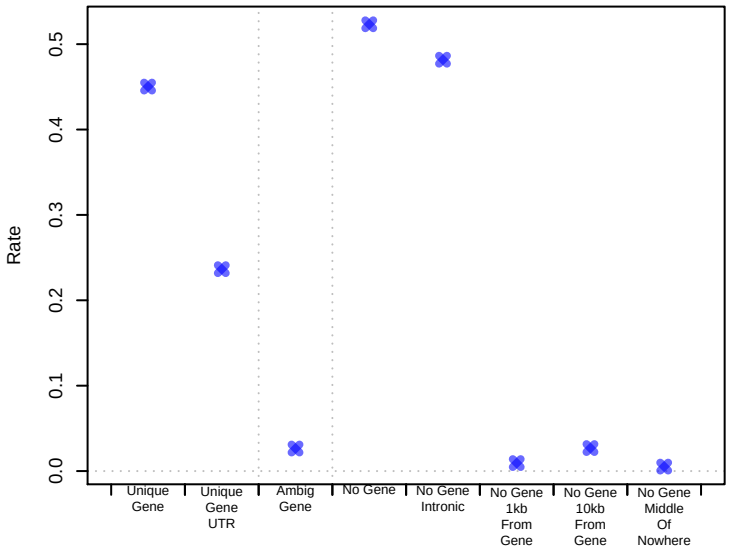
aa


Gene−Body Coverage, Upper Middle Quartile Genes
Proportion of Read−Pairs
0.01
0.015
0.02
0.025
Mean:
0
20
40
60
80
100
Percentile of Gene Body (5'−>3')

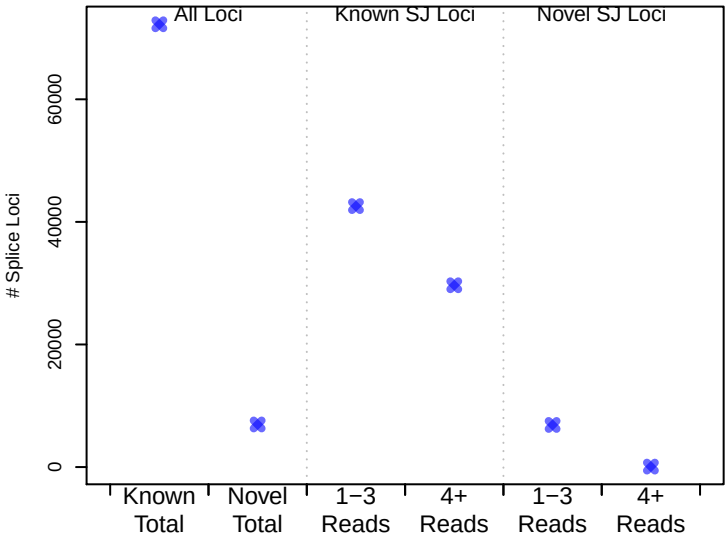
ab


Gene−Body Coverage, Low Expression Genes
Proportion of Read−Pairs
0.018
0.02
0.022
0.024
0.026
0.028
Mean:
0
20
40
60
80
100
Percentile of Gene Body (5'−>3')

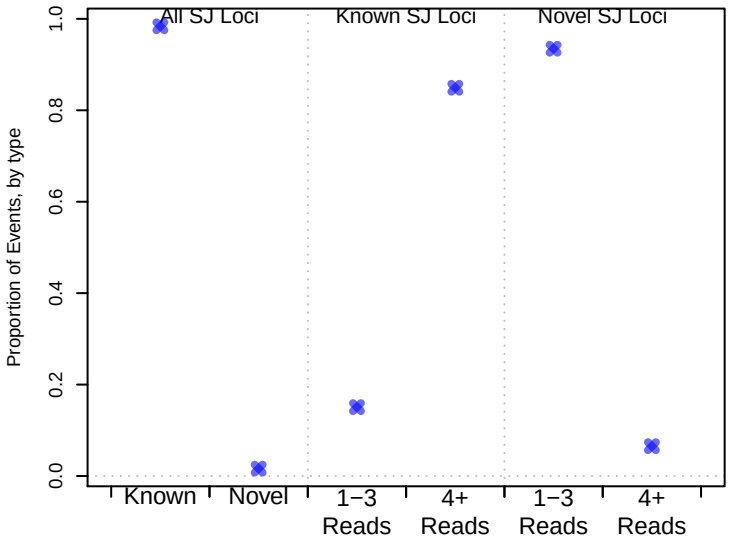
ac


Read Mapping Location Rates
Rate
0.0
0.1
0.2
0.3
0.4
0.5
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

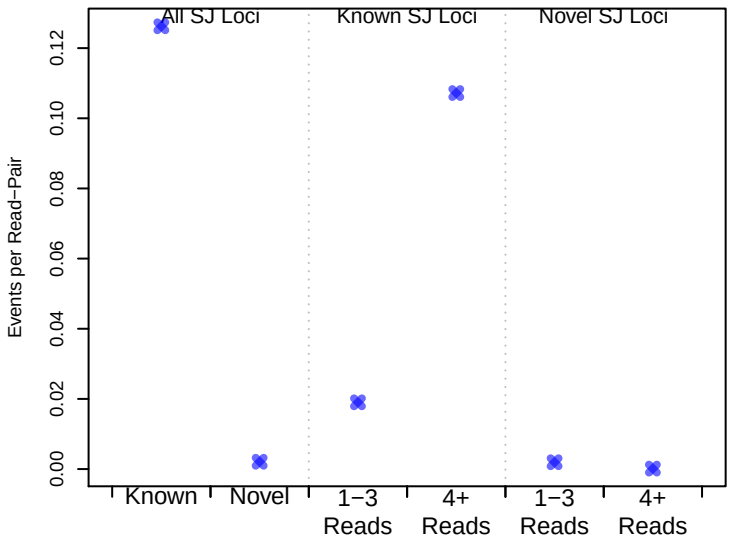
ad


Observed Splice Junction Loci, by type
Splice Loci
0
20000
40000
60000
All Loci
Known SJ Loci
Novel SJ Loci
Known Total
Novel Total
1−3 Reads
4+ Reads
1−3 Reads
4+ Reads

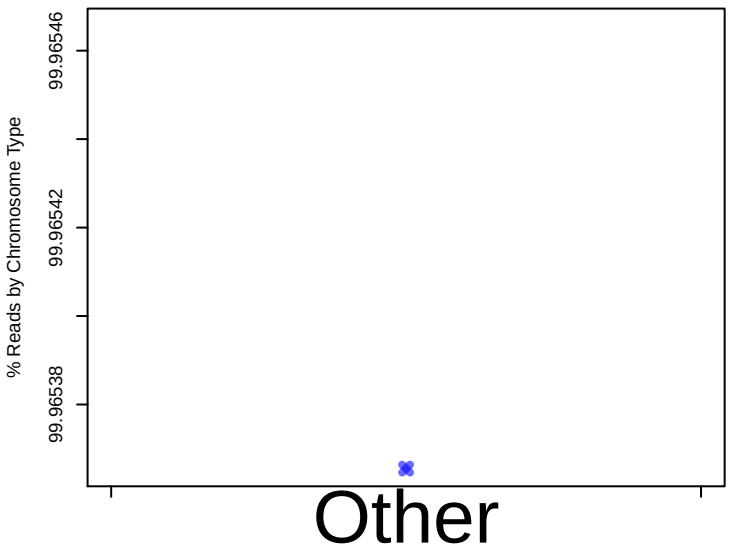
ae



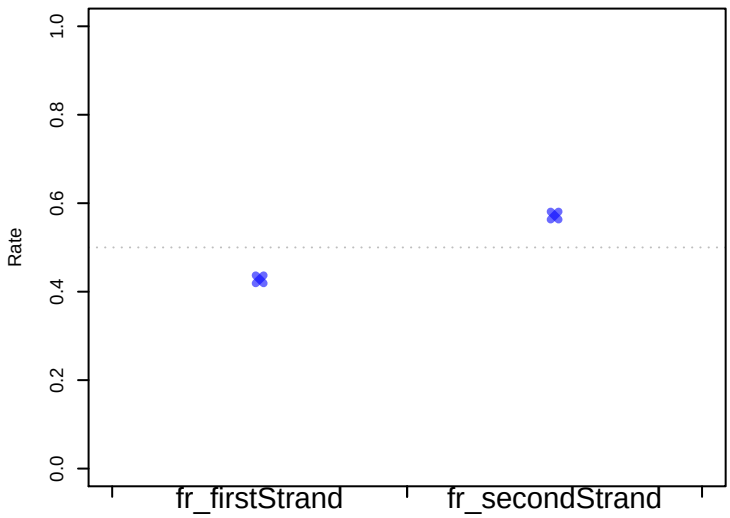
af



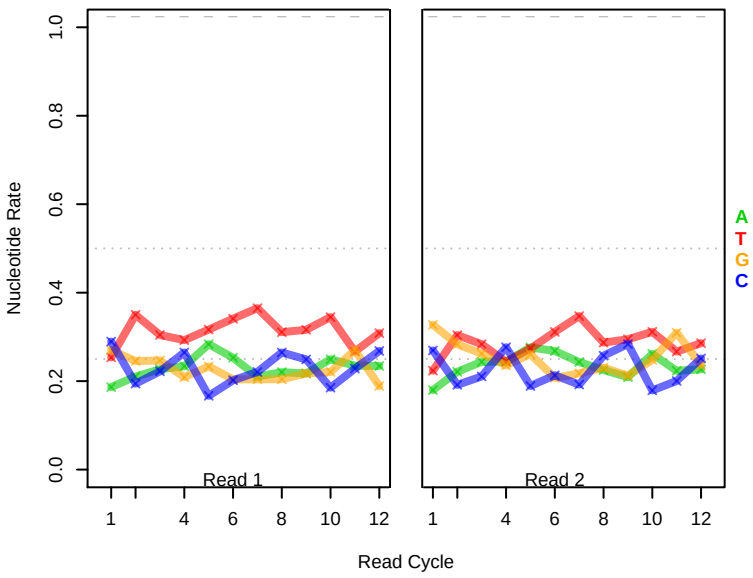
ag



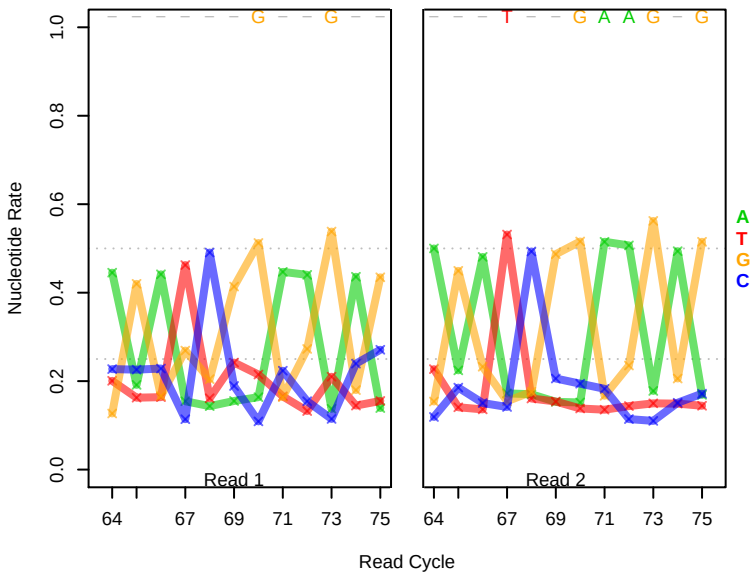
ah



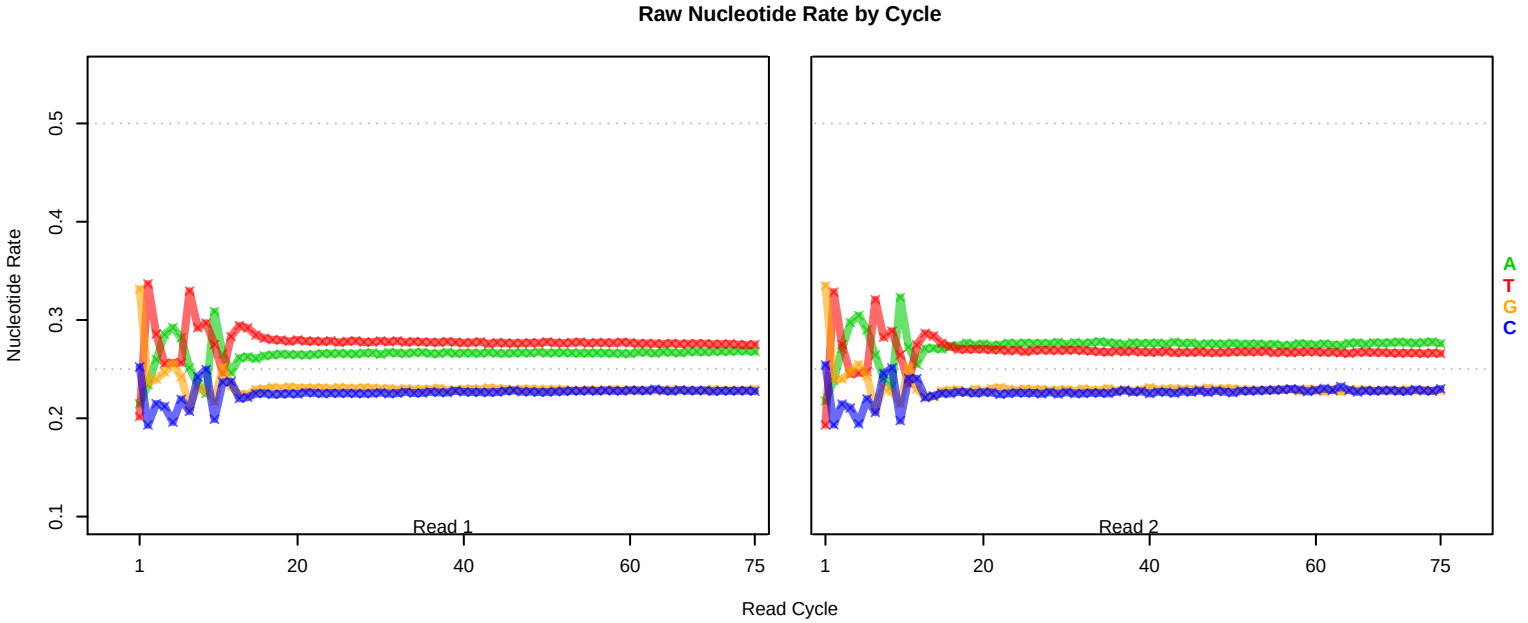
ai



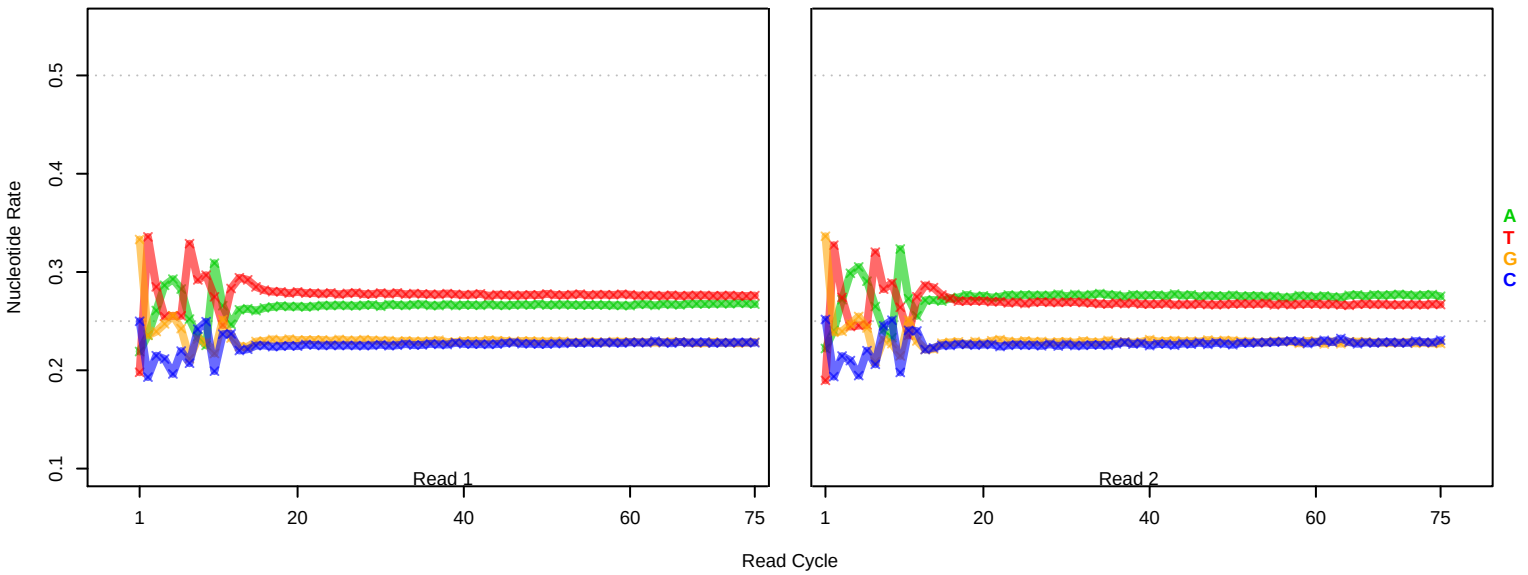
aj



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
75
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
75
Read Cycle
A
T
G
C