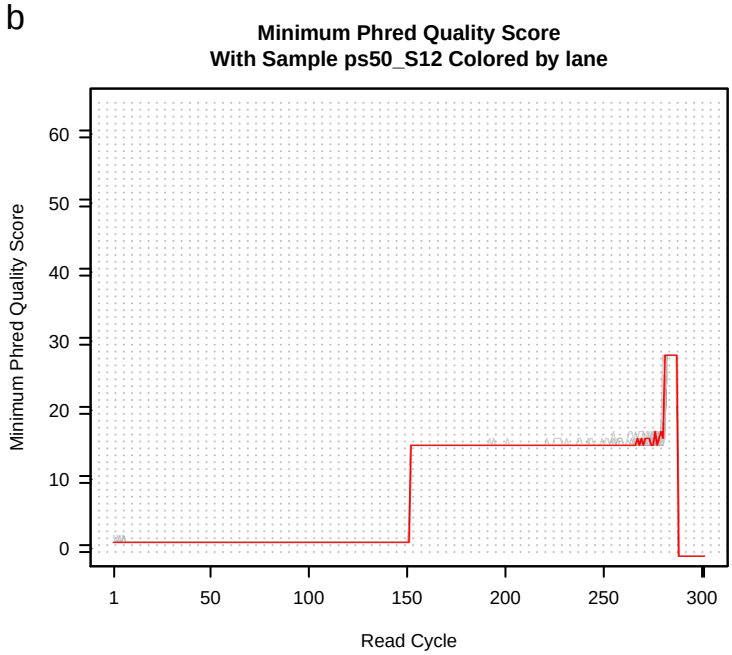
a

Sample Highlight:
ps50_S12
Colored by Lane

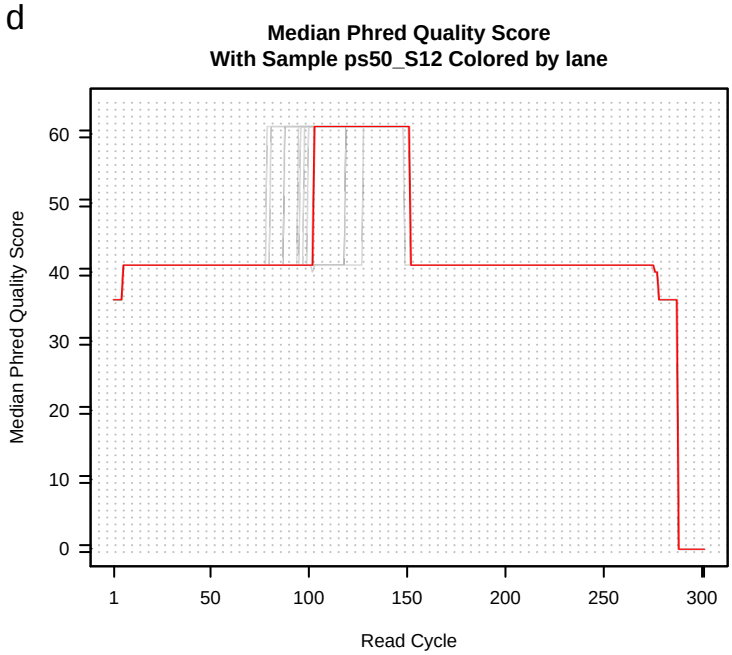
UNKNOWN
Other Samples

b



c

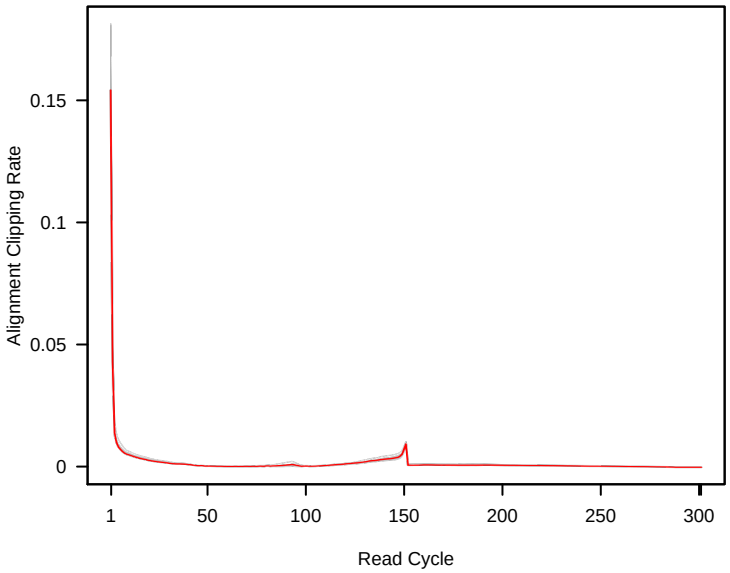
d



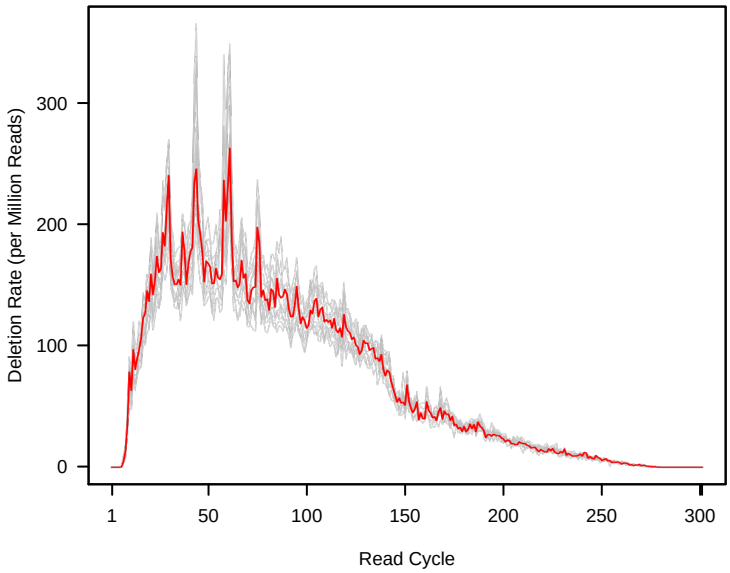
e

f

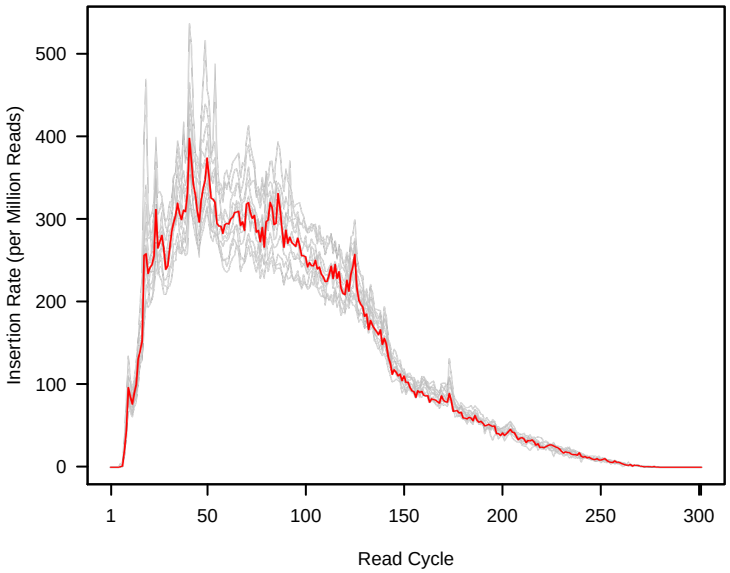
g


Alignment Clipping Rate, by read cycle
With Sample ps50_S12 Colored by lane
Alignment Clipping Rate
0.15
0.1
0.05
0
1
50
100
150
200
250
300
Read Cycle

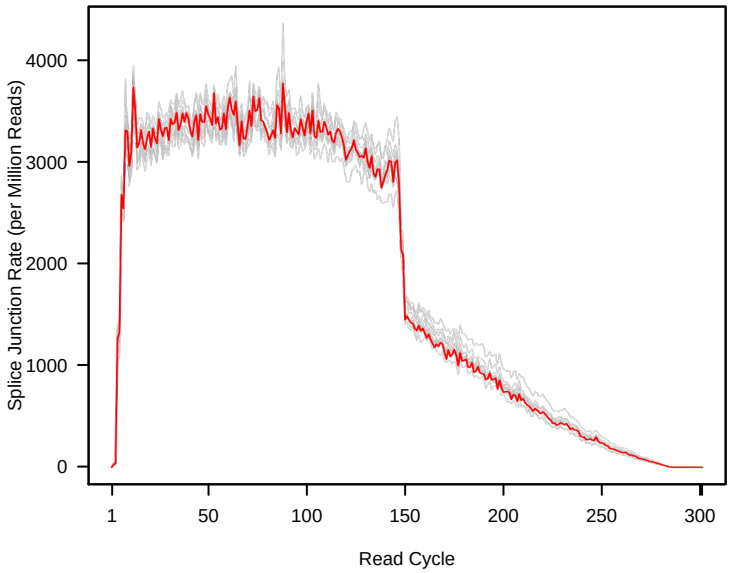
h


Deletion Rate, by read cycle
With Sample ps50_S12 Colored by lane
Deletion Rate (per Million Reads)
300
200
100
0
1
50
100
150
200
250
300
Read Cycle

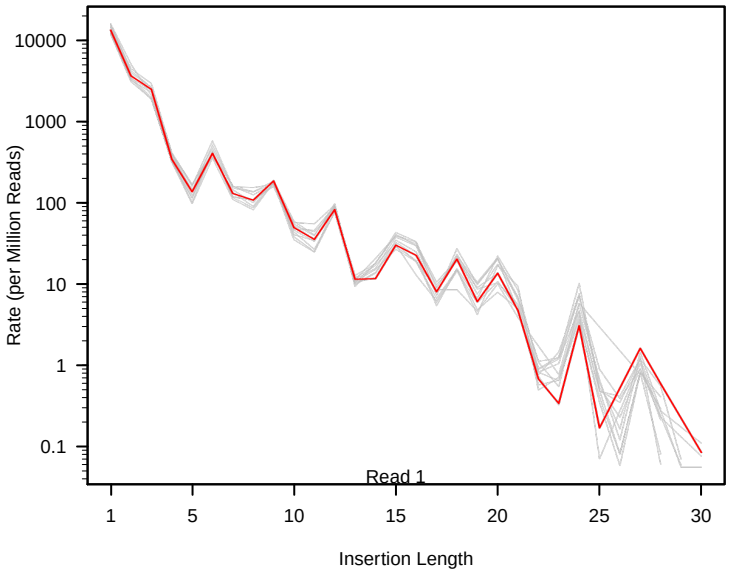
i


Insertion Rate, by read cycle
With Sample ps50_S12 Colored by lane
Insertion Rate (per Million Reads)
500
400
300
200
100
0
1
50
100
150
200
250
300
Read Cycle

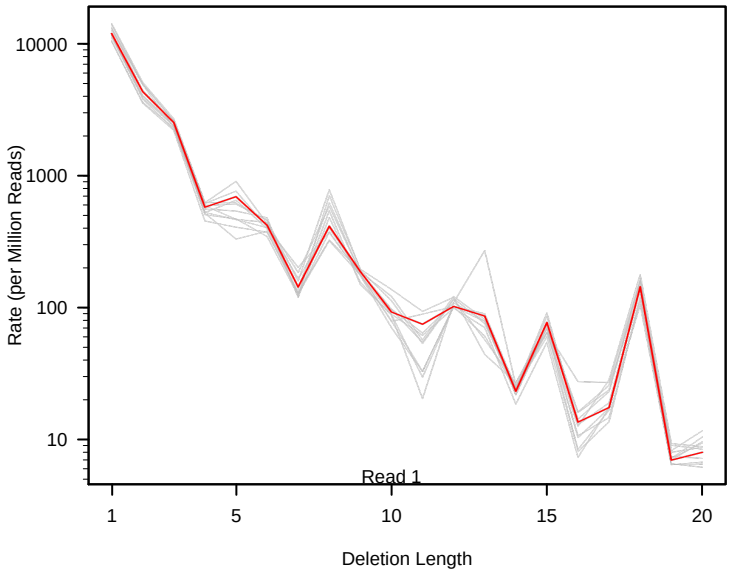
j


Splice Junction Rate, by read cycle
With Sample ps50_S12 Colored by lane
Splice Junction Rate (per Million Reads)
4000
3000
2000
1000
0
1
50
100
150
200
250
300
Read Cycle

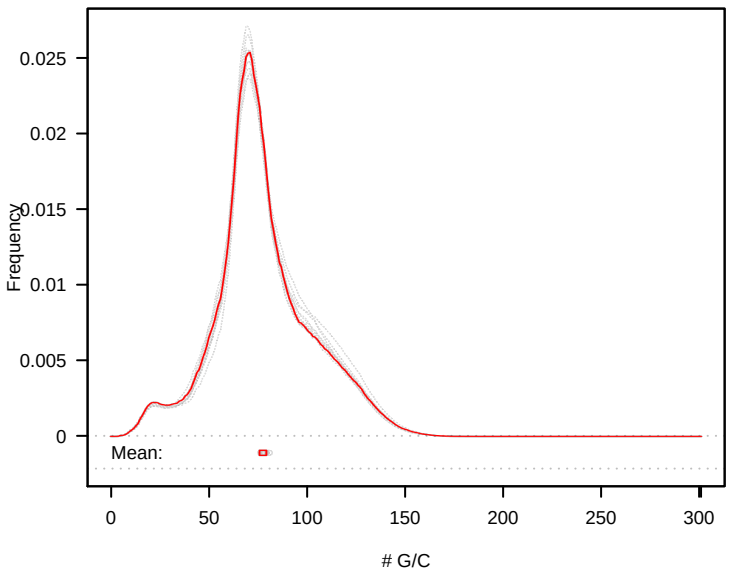
k


Insertion Length Distribution
With Sample ps50_S12 Colored by lane
Rate (per Million Reads)
10000
1000
100
10
1
0.1
Read 1
1
5
10
15
20
25
30
Insertion Length

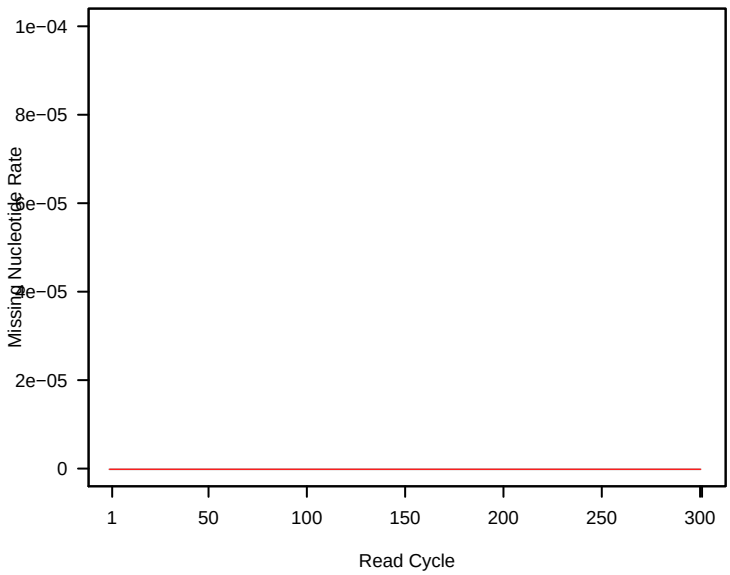
l


Deletion Length Distribution
With Sample ps50_S12 Colored by lane
Rate (per Million Reads)
10000
1000
100
10
Read 1
1
5
10
15
20
Deletion Length

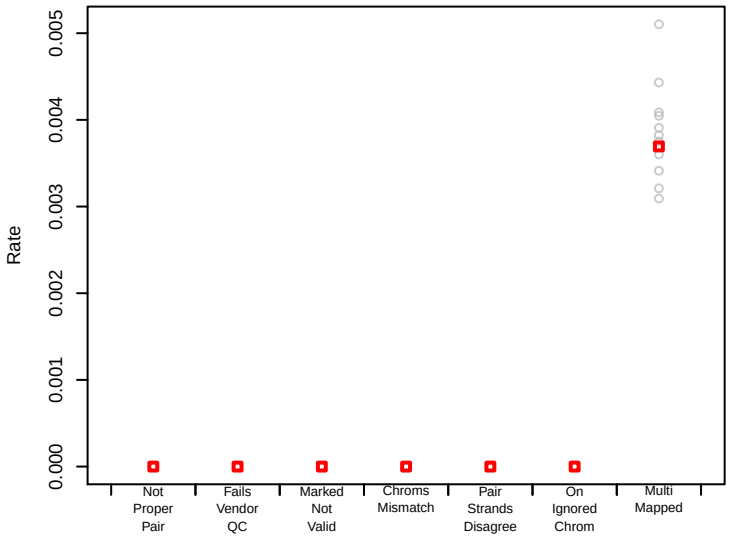
m


GC Content
With Sample ps50_S12 Colored by lane
Frequency
0.025
0.02
0.015
0.01
0.005
0
Mean:
0
50
100
150
200
250
300
G/C

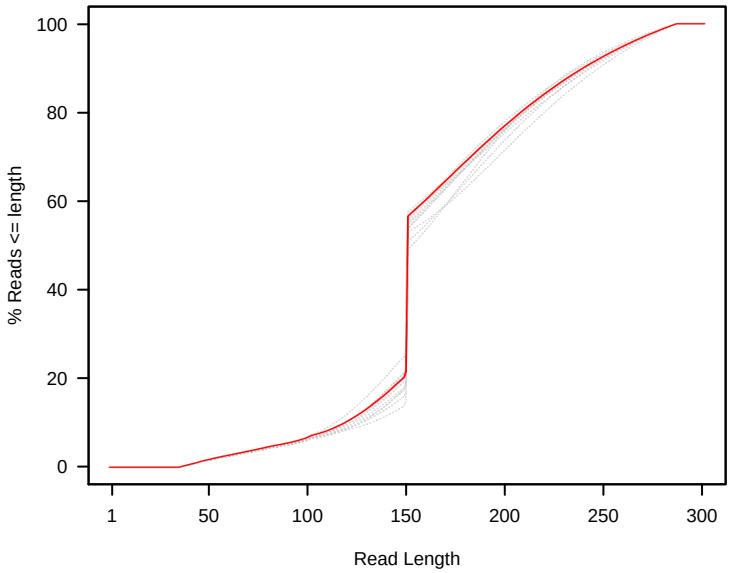
n


'N' Rate, by Read Cycle
With Sample ps50_S12 Colored by lane
Missing Nucleotide Rate
1e−04
8e−05
6e−05
4e−05
2e−05
0
1
50
100
150
200
250
300
Read Cycle

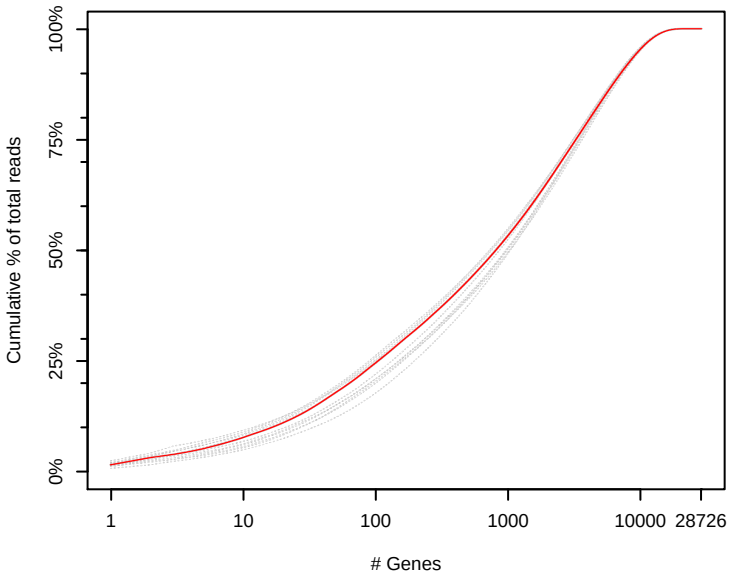
o


Read Drop Rate, by Reason
With Sample ps50_S12 Colored by lane
Rate
0.005
0.004
0.003
0.002
0.001
0.000
Not Proper Pair
Fails Vendor QC
Marked Not Valid
Chroms Mismatch
Pair Strands Disagree
On Ignored Chrom
Multi Mapped

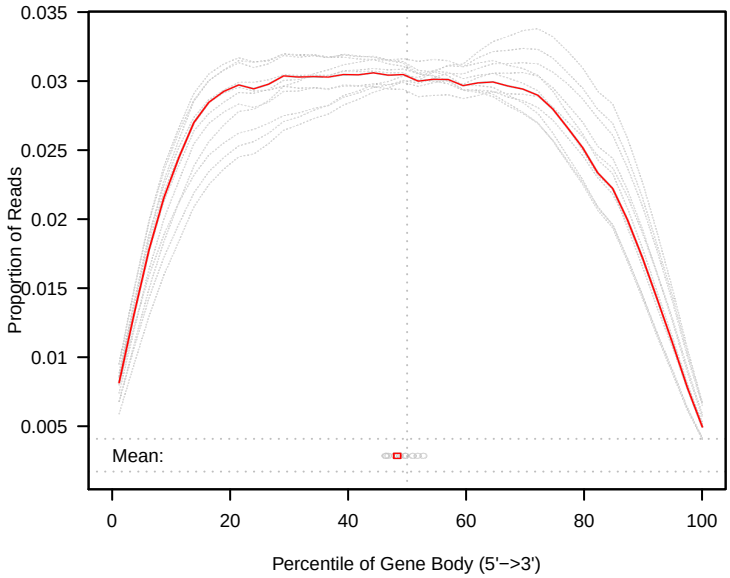
p


Read Length Distribution
With Sample ps50_S12 Colored by lane
% Reads <= length
100
80
60
40
20
0
1
50
100
150
200
250
300
Read Length

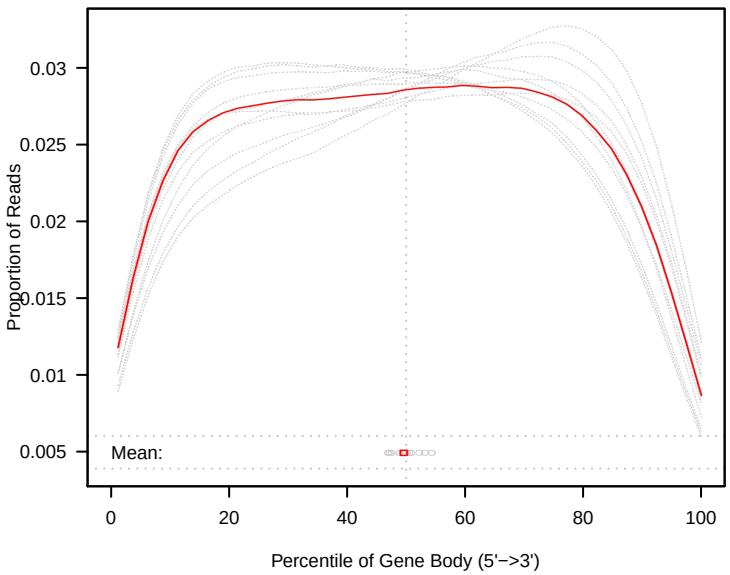
q


Cumulative Gene Assignment Diversity
With Sample ps50_S12 Colored by lane
Cumulative % of total reads
100%
75%
50%
25%
0%
1
10
100
1000
10000
28726
Genes

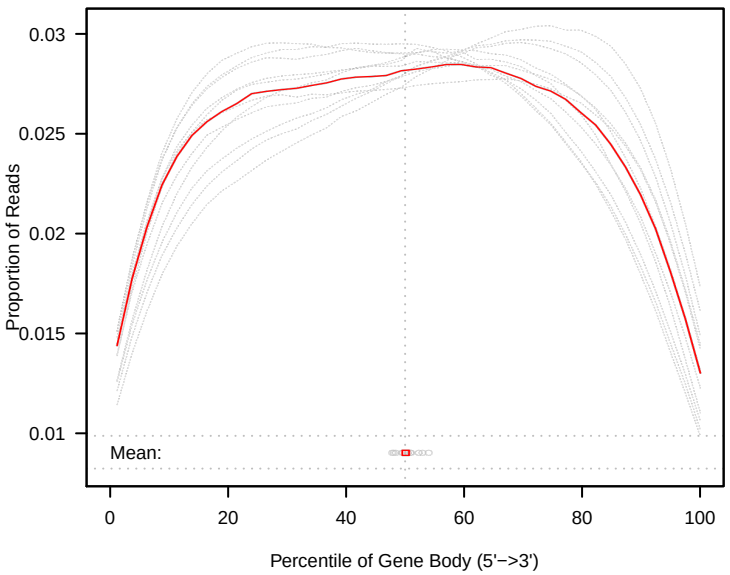
r


Gene−Body Coverage
With Sample ps50_S12 Colored by lane
Proportion of Reads
0.035
0.03
0.025
0.02
0.015
0.01
0.005
Mean:
0
20
40
60
80
100
Percentile of Gene Body (5'−>3')

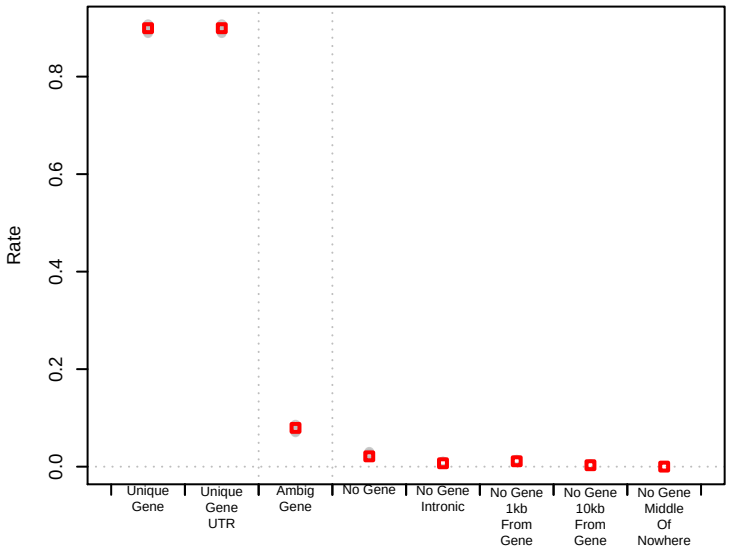
s


Gene−Body Coverage, Upper Middle Quartile Genes
With Sample ps50_S12 Colored by lane
Proportion of Reads
0.03
0.025
0.02
0.015
0.01
0.005
Mean:
0
20
40
60
80
100
Percentile of Gene Body (5'−>3')

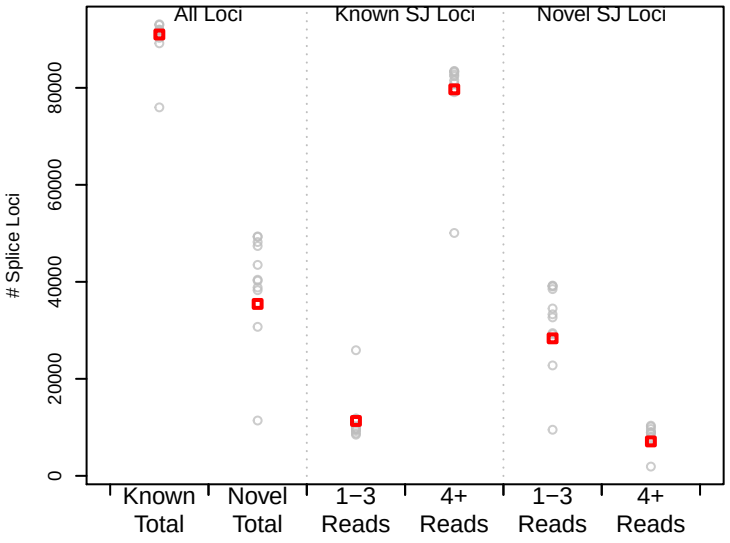
t


Gene−Body Coverage, Low Expression Genes
With Sample ps50_S12 Colored by lane
Proportion of Reads
0.03
0.025
0.02
0.015
0.01
Mean:
0
20
40
60
80
100
Percentile of Gene Body (5'−>3')

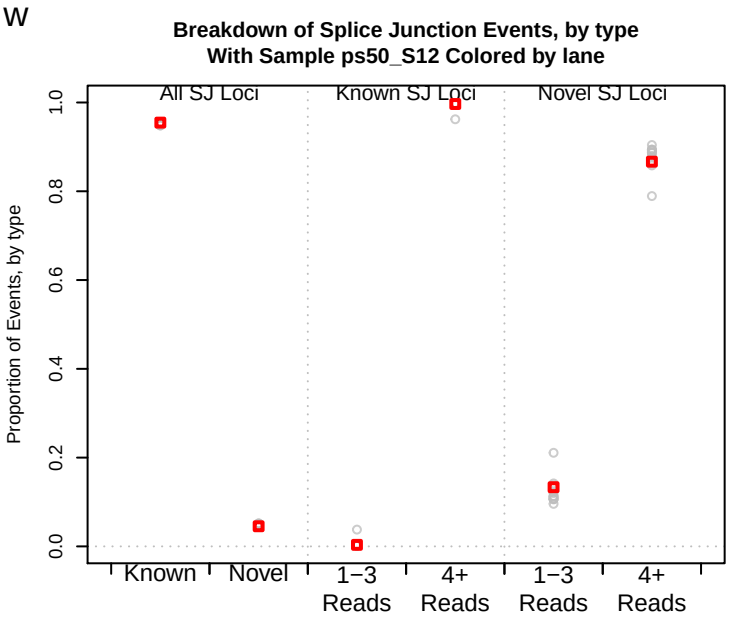
u


Read Mapping Location Rates
With Sample ps50_S12 Colored by lane
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

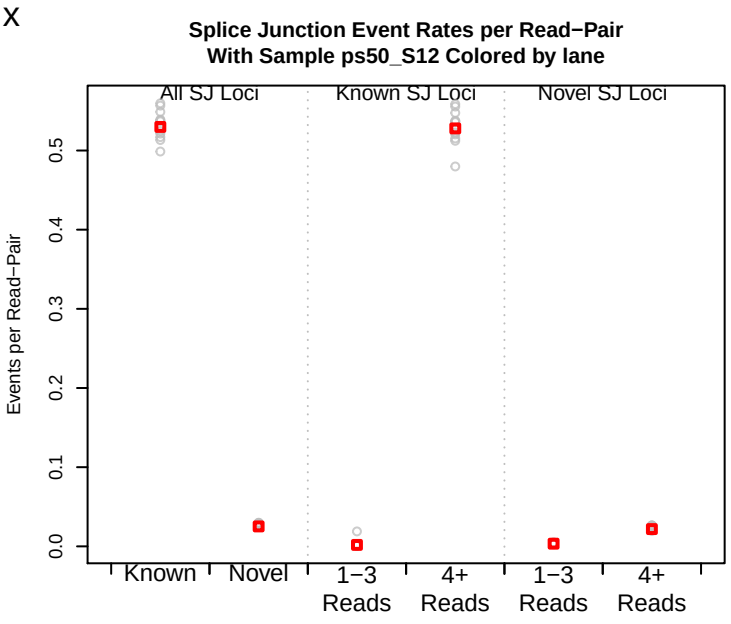
v


Observed Splice Junction Loci, by type
With Sample ps50_S12 Colored by lane
Splice Loci
0
20000
40000
60000
80000
All Loci
Known SJ Loci
Novel SJ Loci
Known Total
Novel Total
1−3 Reads
4+ Reads
1−3 Reads
4+ Reads

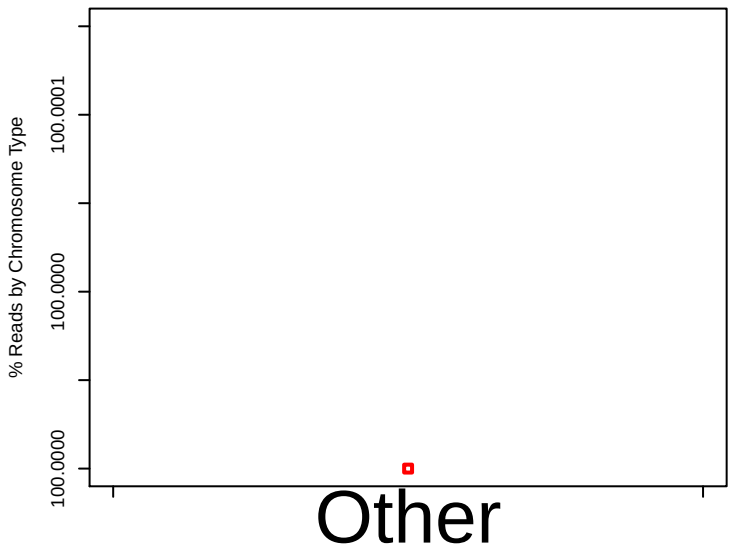
w


Breakdown of Splice Junction Events, by type
With Sample ps50_S12 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

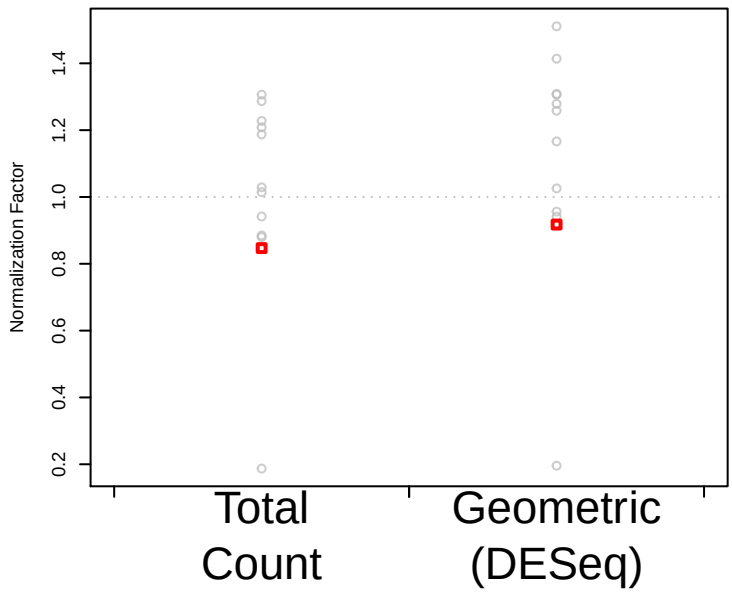
x


Splice Junction Event Rates per Read−Pair
With Sample ps50_S12 Colored by lane
Events per Read−Pair
0.0
0.1
0.2
0.3
0.4
0.5
All SJ Loci
Known SJ Loci
Novel SJ Loci
Known
Novel
1−3 Reads
4+ Reads
1−3 Reads
4+ Reads

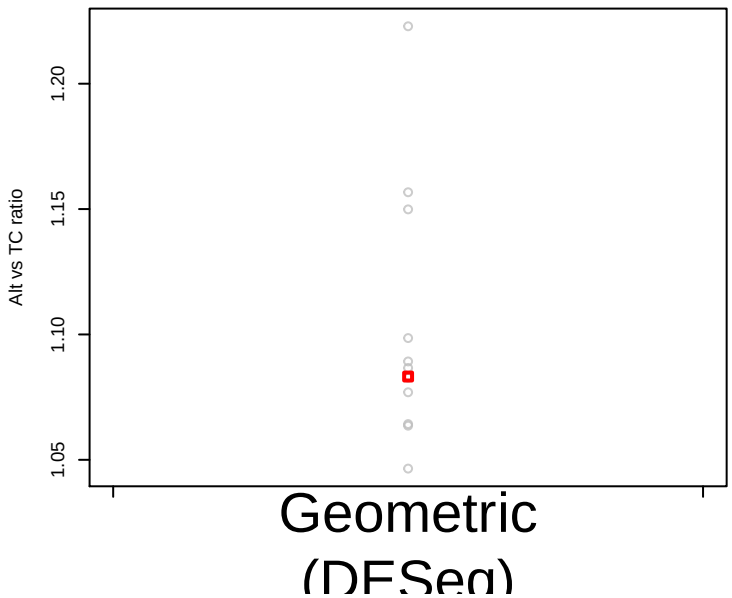
y


Chromosome Distribution (Excluding Autosomes)
With Sample ps50_S12 Colored by lane
% Reads by Chromosome Type
100.0001
100.0000
100.0000
Other

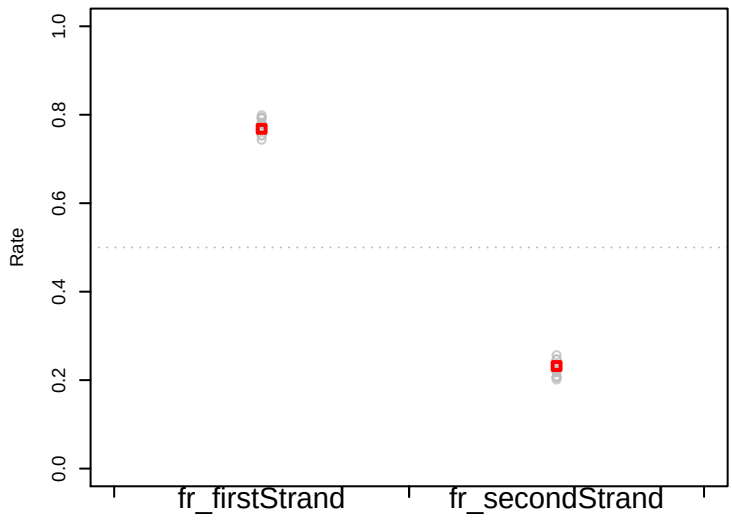
z


Normalization Factors
With Sample ps50_S12 Colored by lane
Normalization Factor
0.2
0.4
0.6
0.8
1.0
1.2
1.4
Total Count
Geometric (DESeq)

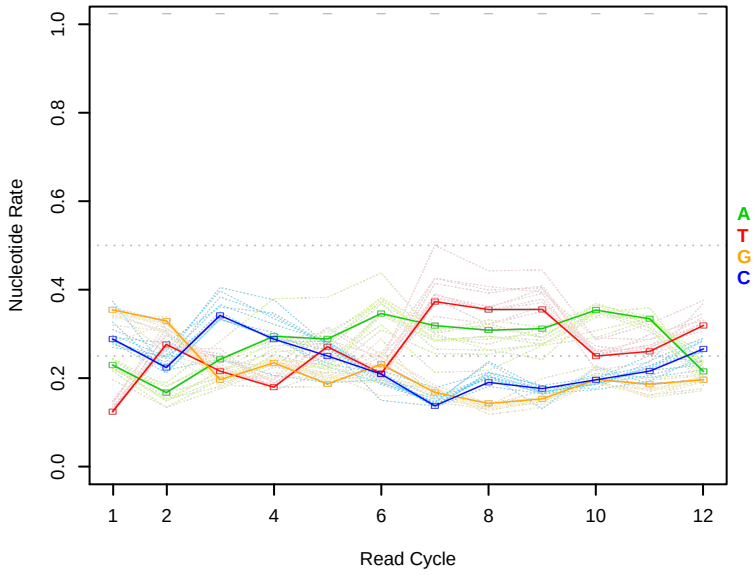
aa


Normalization Factors vs Total−Count Normalization
With Sample ps50_S12 Colored by lane
Alt vs TC ratio
1.05
1.10
1.15
1.20
Geometric (DESeq)

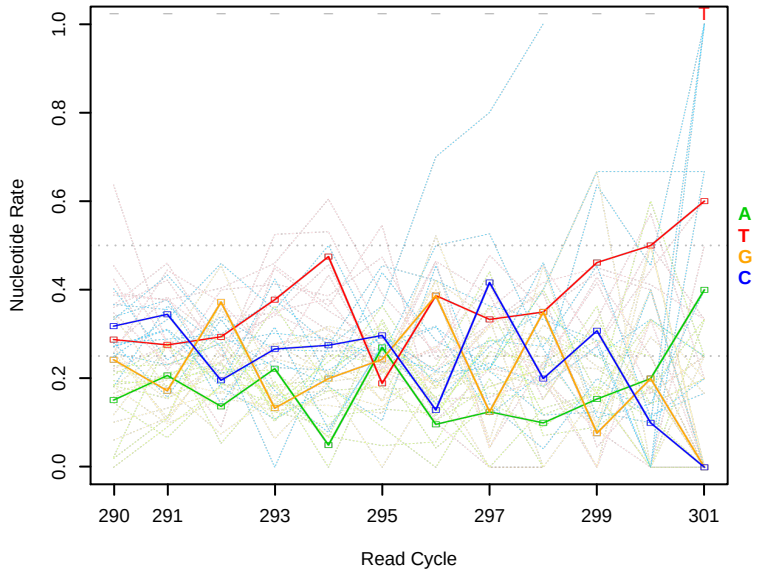
ab


Strandedness Test
With Sample ps50_S12 Colored by lane
Rate
0.0
0.2
0.4
0.6
0.8
1.0
fr_firstStrand
fr_secondStrand

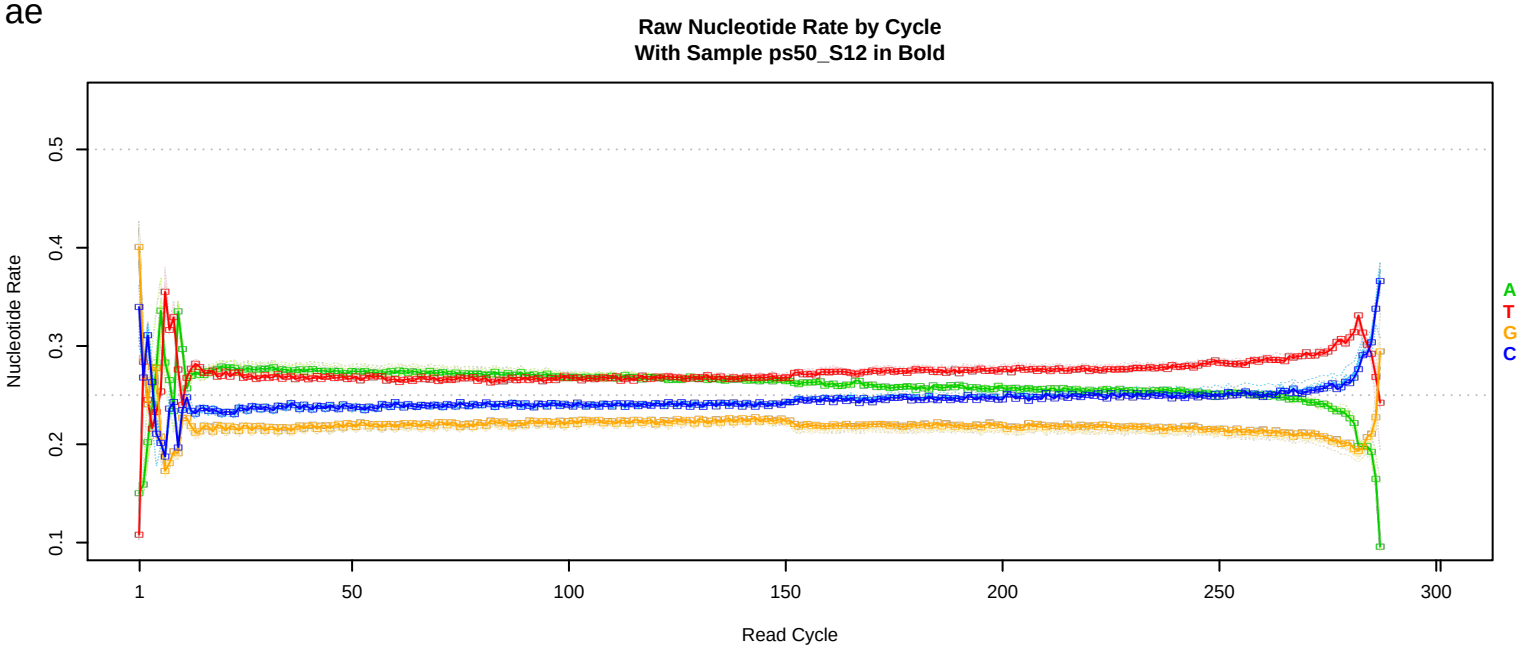
ac


Nucleotide Rate by Cycle, Leading Clipped bases (12)
With Sample ps50_S12 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

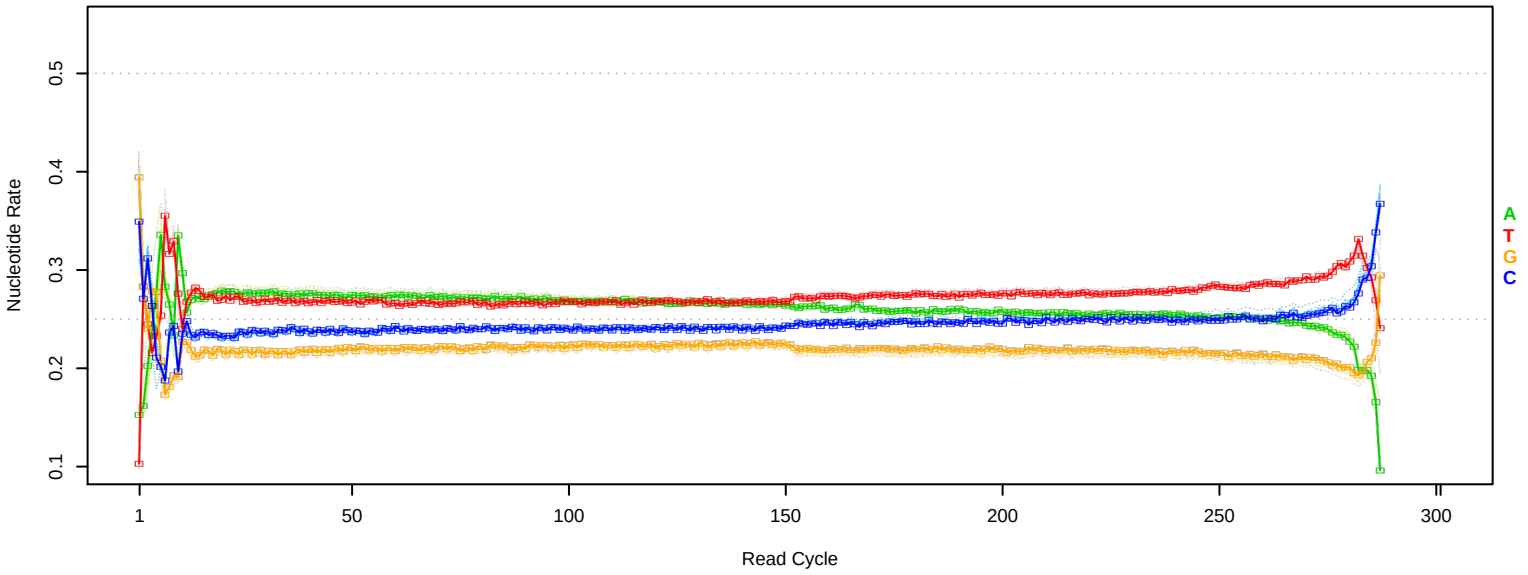
ad


Nucleotide Rate by Cycle, Trailing Clipped bases (12)
With Sample ps50_S12 in Bold
Nucleotide Rate
0.0
0.2
0.4
0.6
0.8
1.0
290
291
293
295
297
299
301
Read Cycle
A
T
G
C

ae


Raw Nucleotide Rate by Cycle
With Sample ps50_S12 in Bold
Nucleotide Rate
0.1
0.2
0.3
0.4
0.5
1
50
100
150
200
250
300
Read Cycle
A
T
G
C

af


Nucleotide Rate by Cycle, Aligned bases only
With Sample ps50_S12 in Bold
Nucleotide Rate
0.1
0.2
0.3
0.4
0.5
1
50
100
150
200
250
300
Read Cycle
A
T
G
C