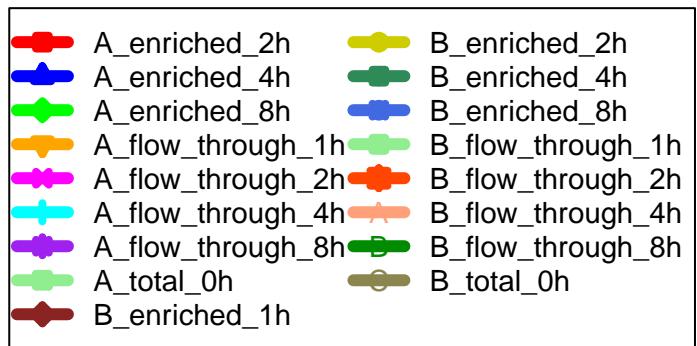


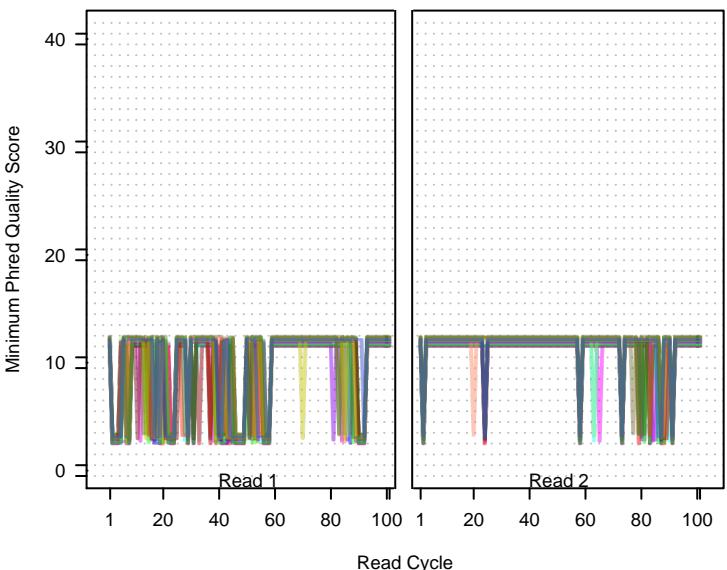
a

Summary Plots, By Sample



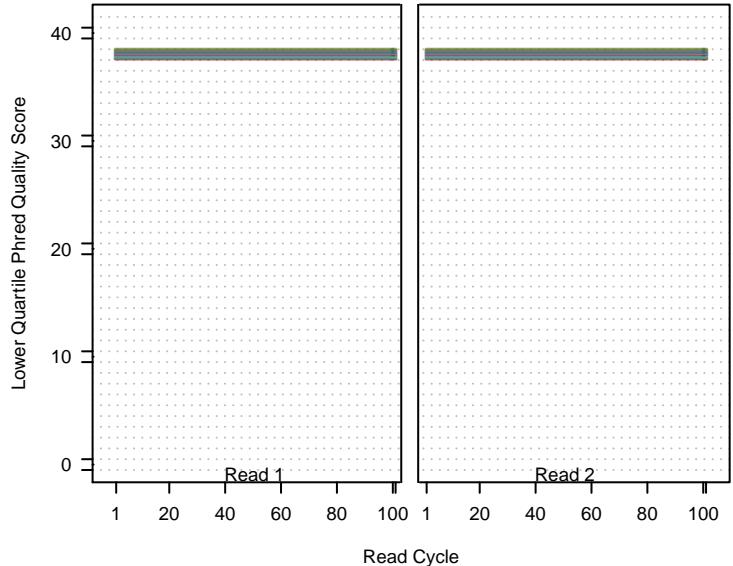
b

Minimum Phred Quality Score
Colored by Sample



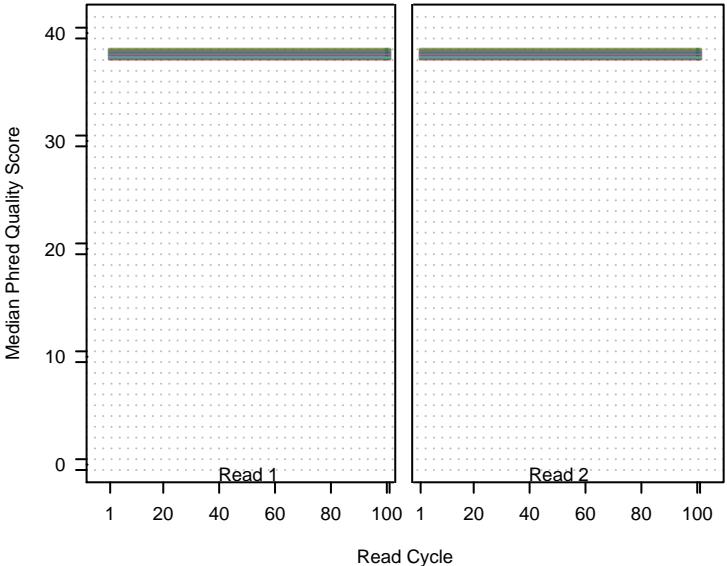
c

Lower Quartile Phred Quality Score
Colored by Sample



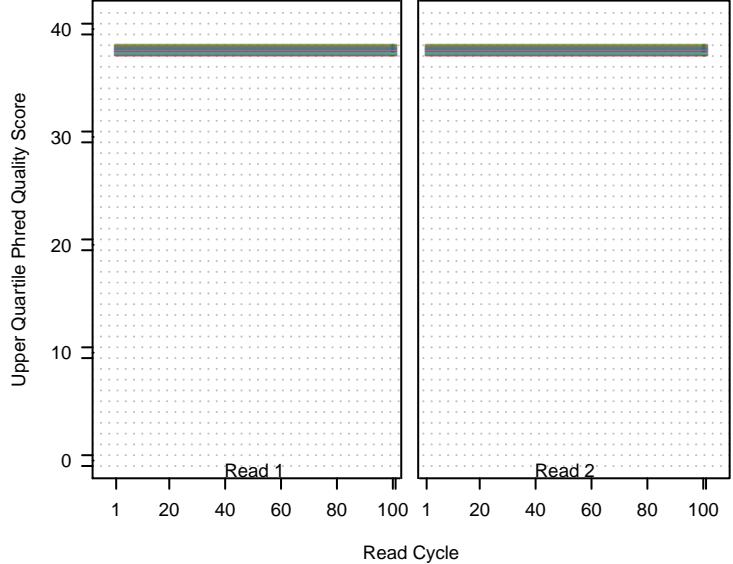
d

Median Phred Quality Score
Colored by Sample



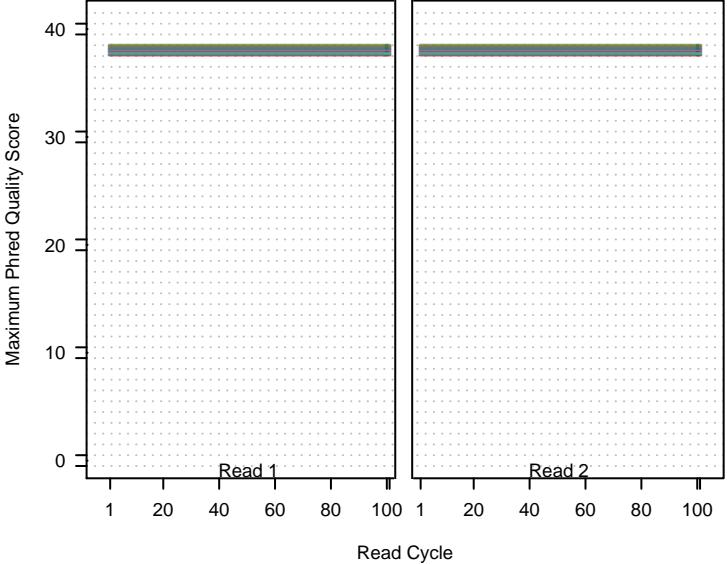
e

Upper Quartile Phred Quality Score
Colored by Sample



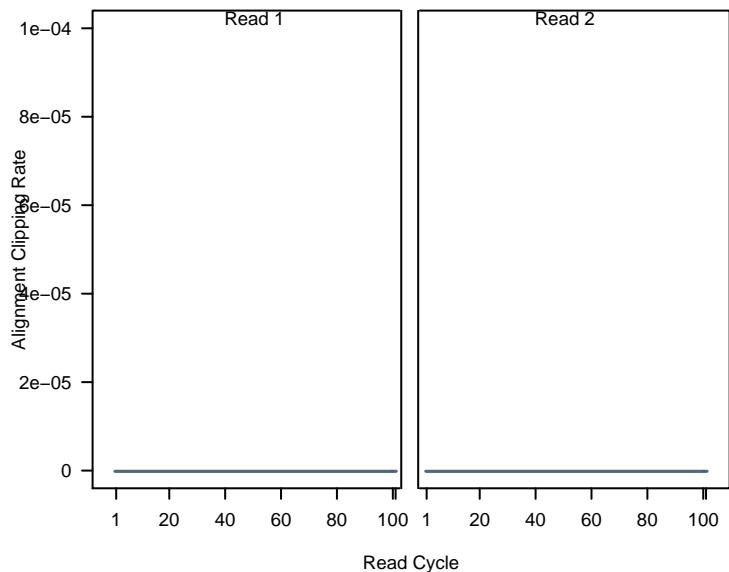
f

Maximum Phred Quality Score
Colored by Sample



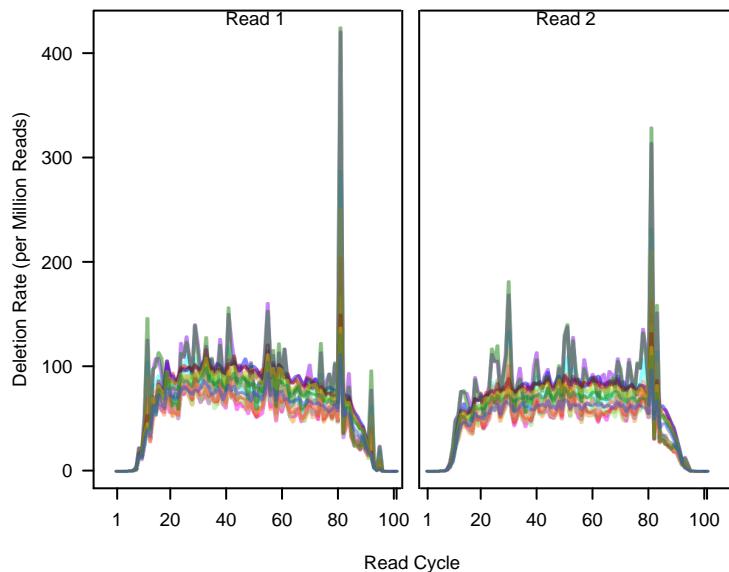
g

**Alignment Clipping Rate, by read cycle
Colored by Sample**



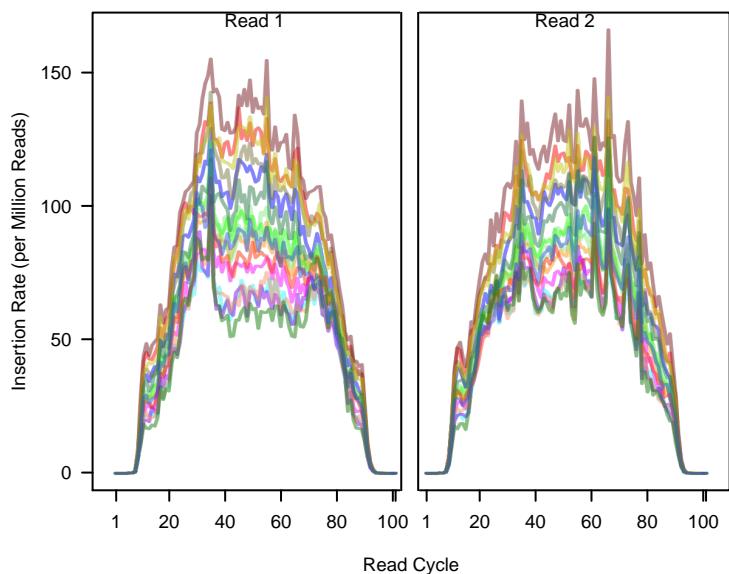
h

**Deletion Rate, by read cycle
Colored by Sample**



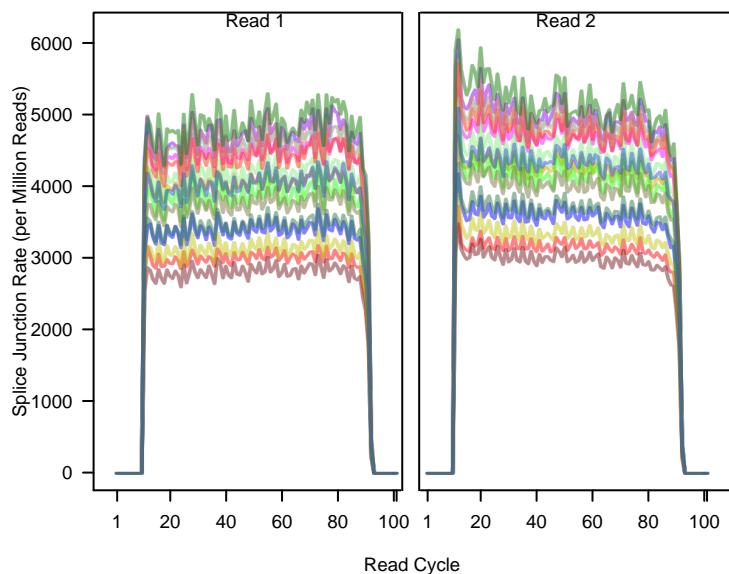
i

**Insertion Rate, by read cycle
Colored by Sample**



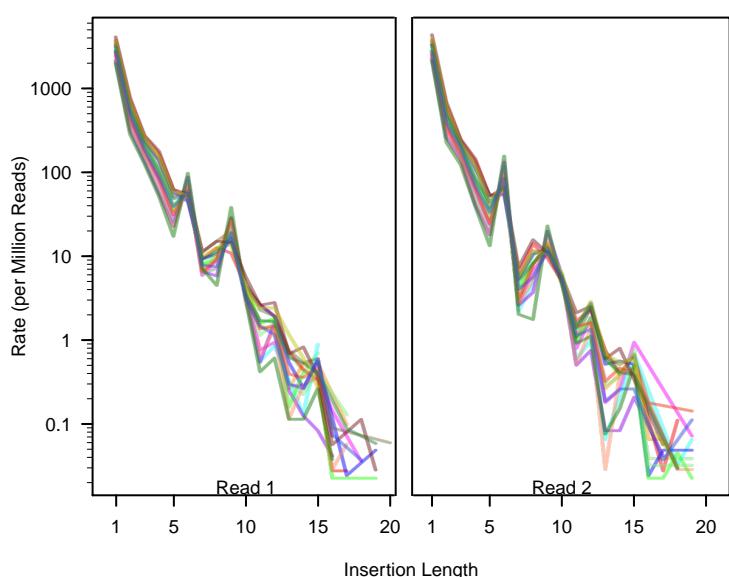
j

**Splice Junction Rate, by read cycle
Colored by Sample**



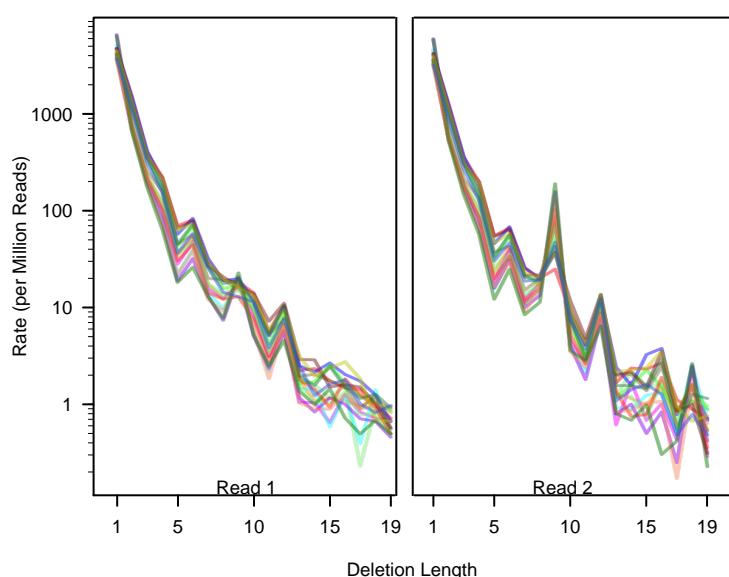
k

**Insertion Length Distribution
Colored by Sample**

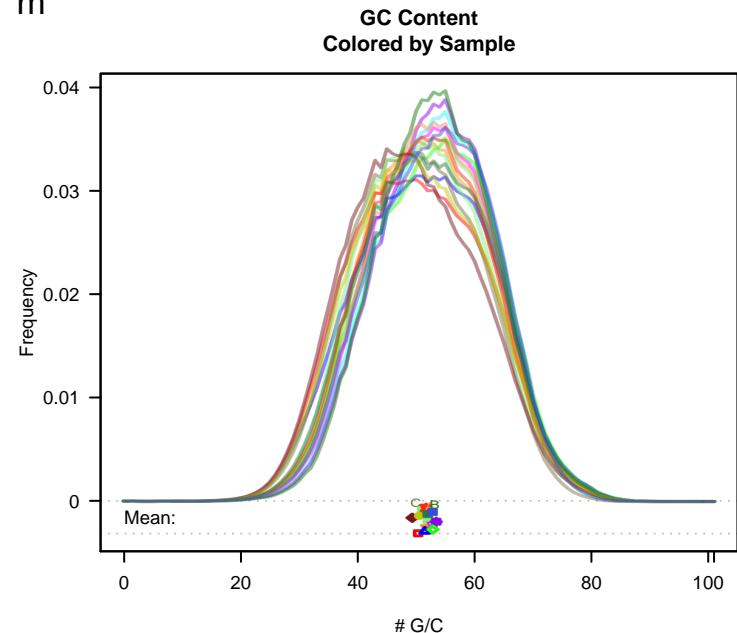


l

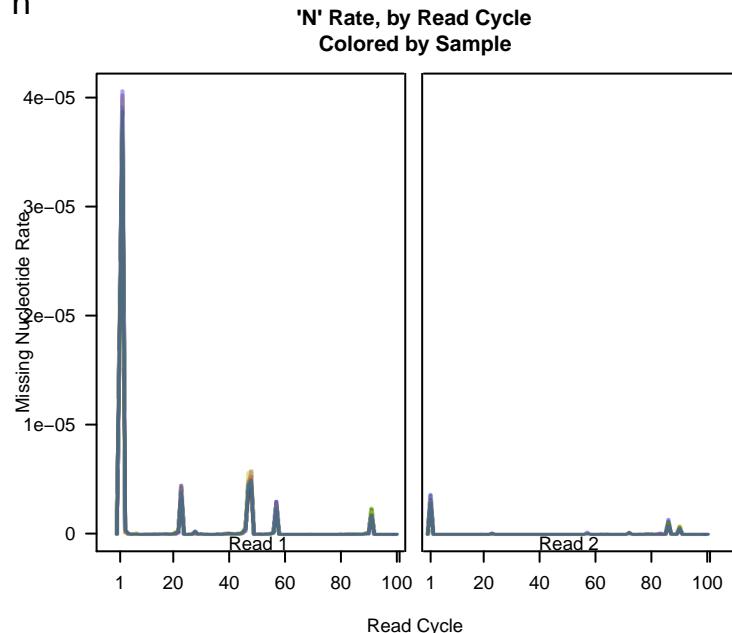
**Deletion Length Distribution
Colored by Sample**



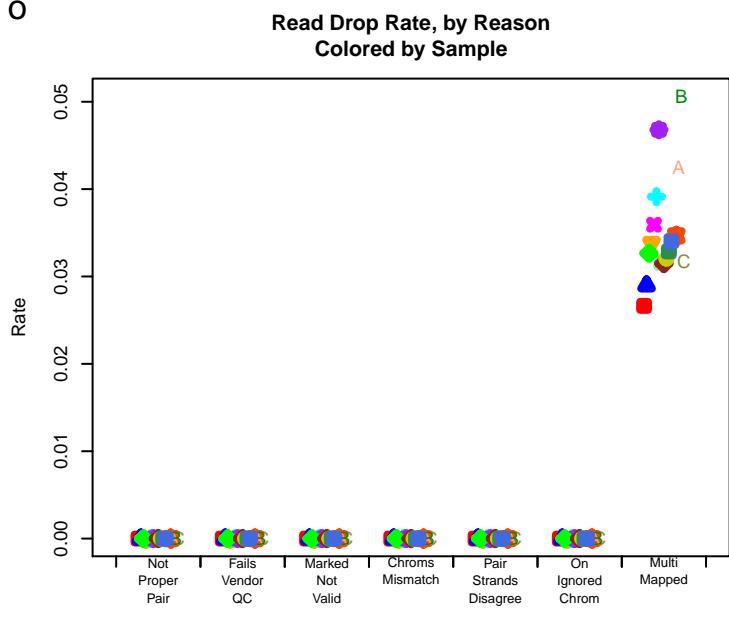
m



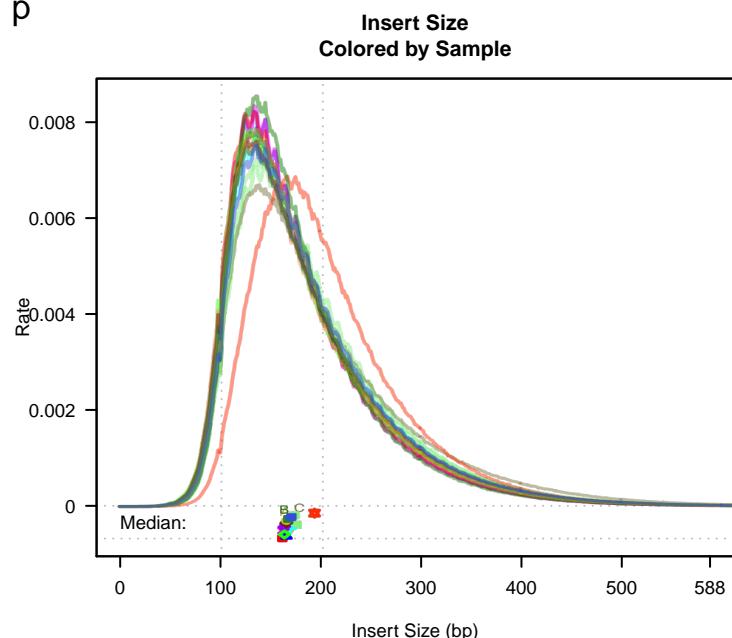
n



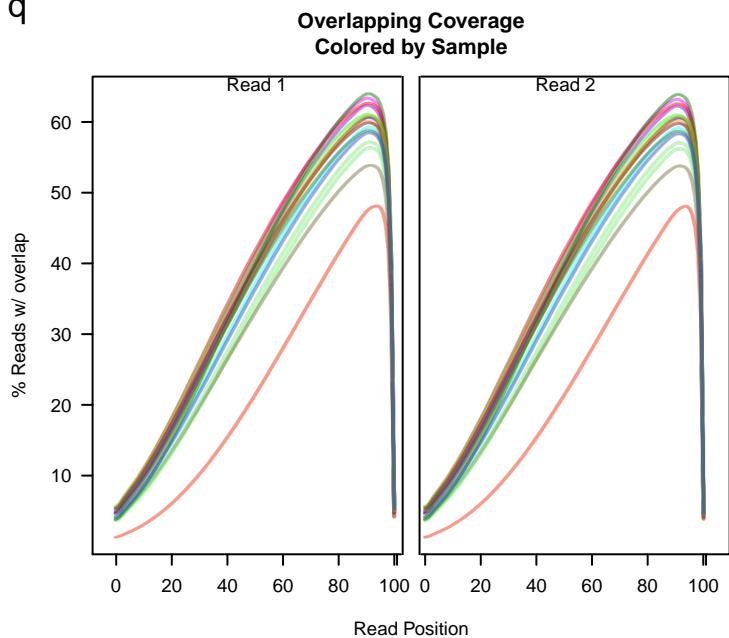
o



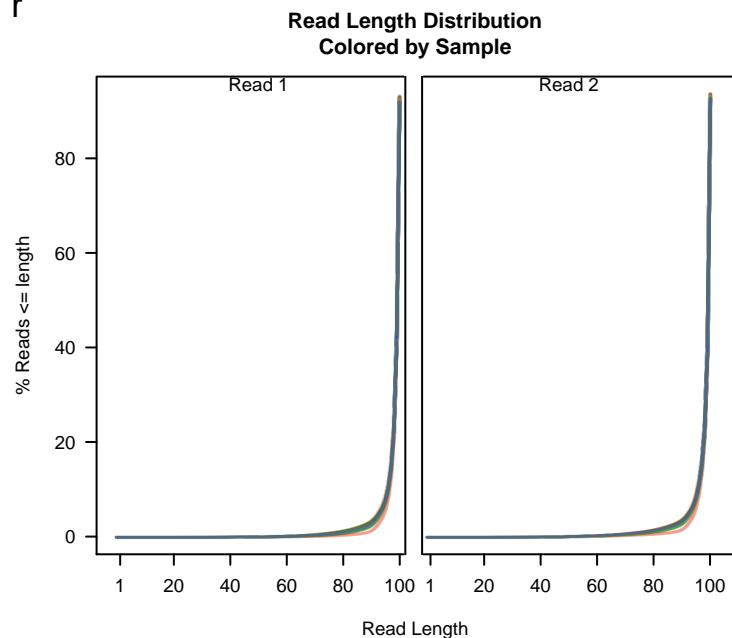
p



q

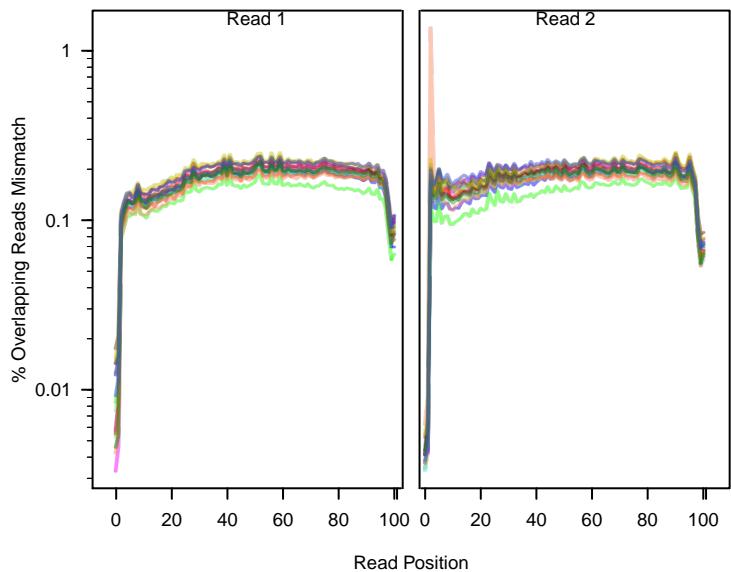


r



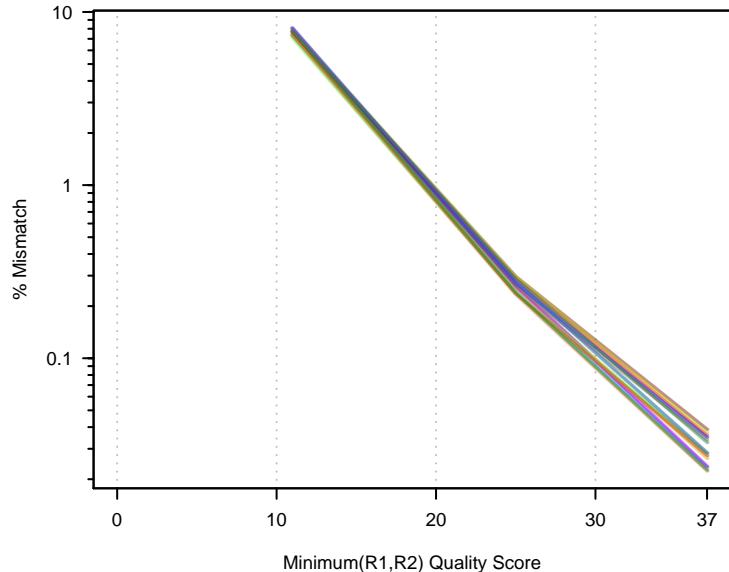
S

**Overlap Mismatch by Read Cycle
Colored by Sample**



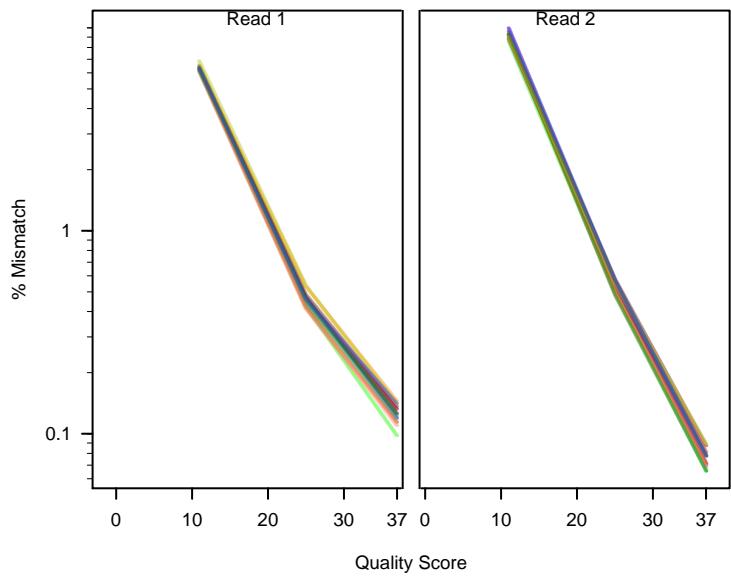
t

**Overlapping Mismatch by Min Qual
Colored by Sample**



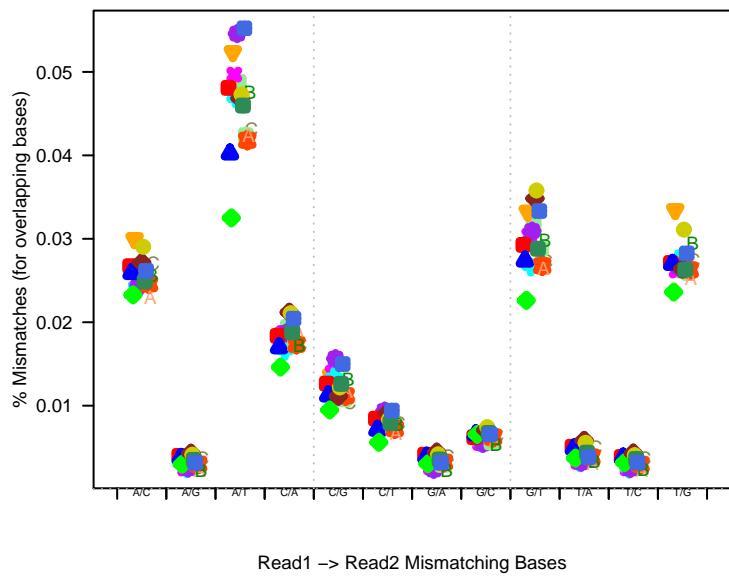
U

**Overlap Mismatch by Read Qual
Colored by Sample**



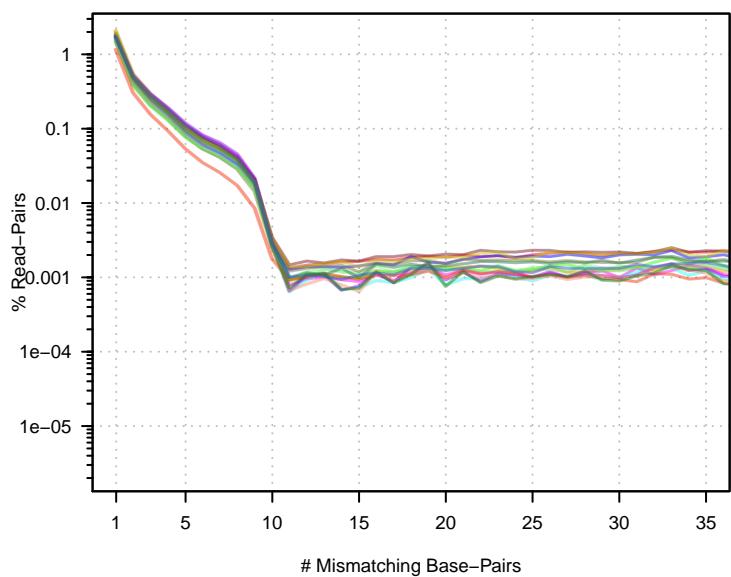
V

**Overlap Mismatch Combinations
Colored by Sample**



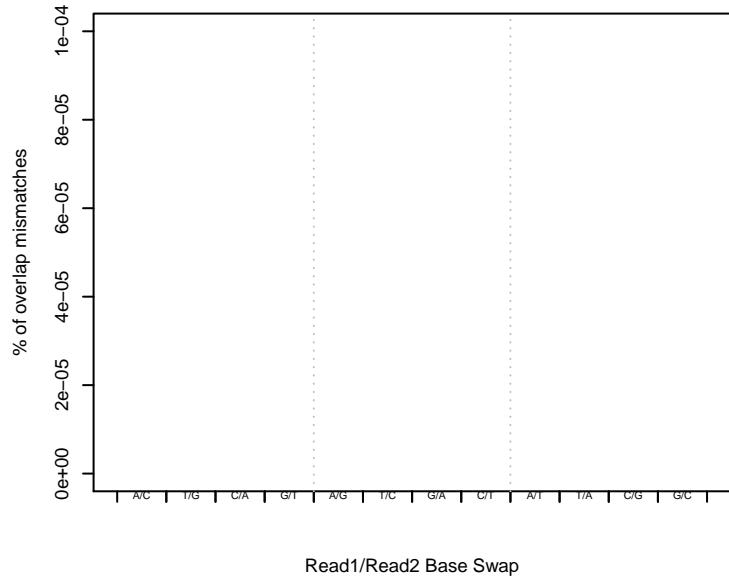
W

**Overlap Mismatch Size Frequency
Colored by Sample**



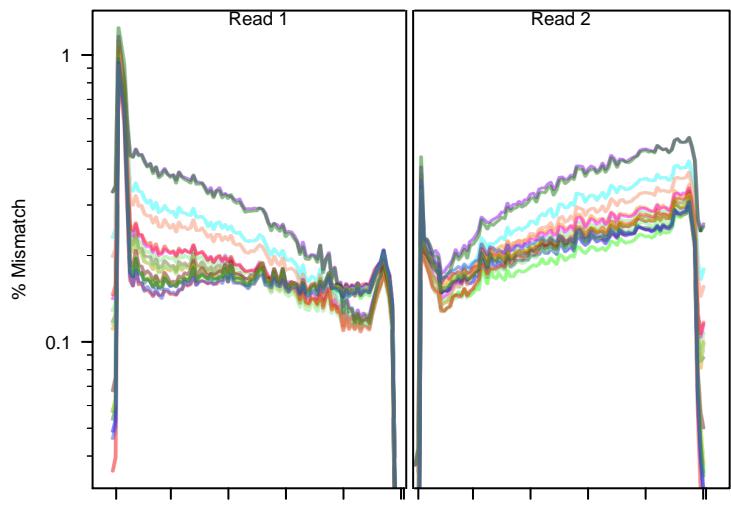
X

**Overlap Mismatch Pairs At Phred == 41
Colored by Sample**



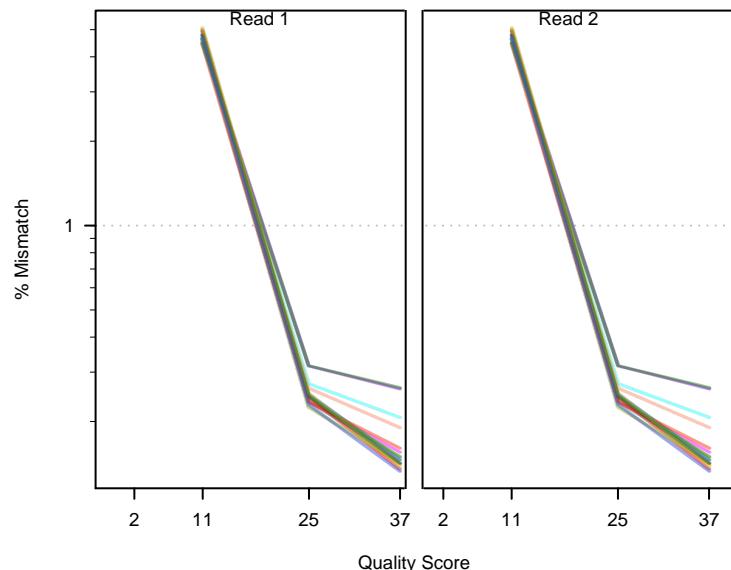
y

**Reference Mismatch by Read Cycle
Colored by Sample**



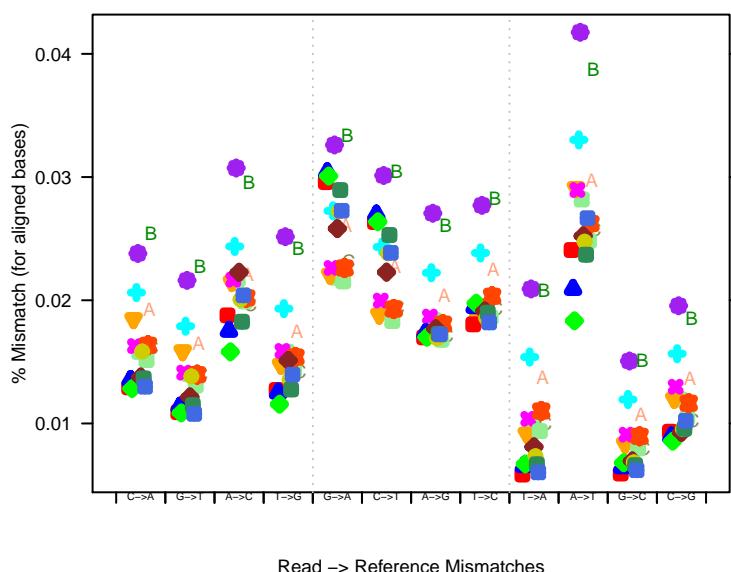
Z

**Reference Mismatch by Read Qual
Colored by Sample**



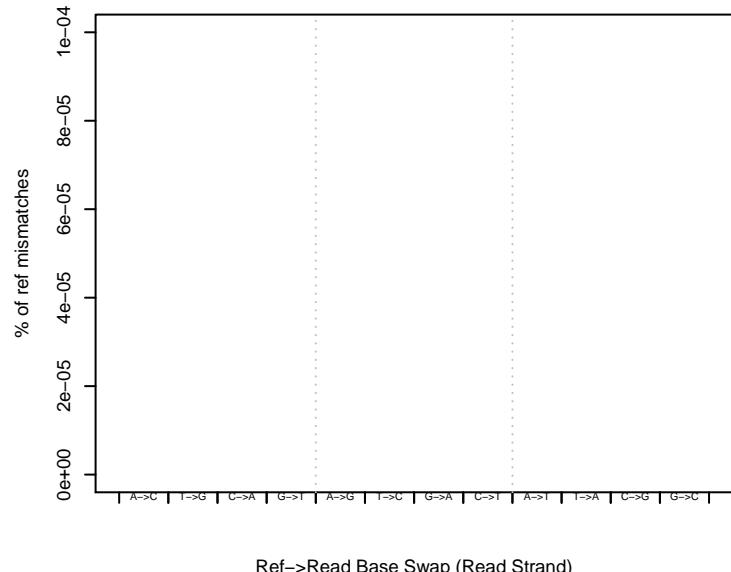
aa

**Reference Mismatch Combinations
Colored by Sample**



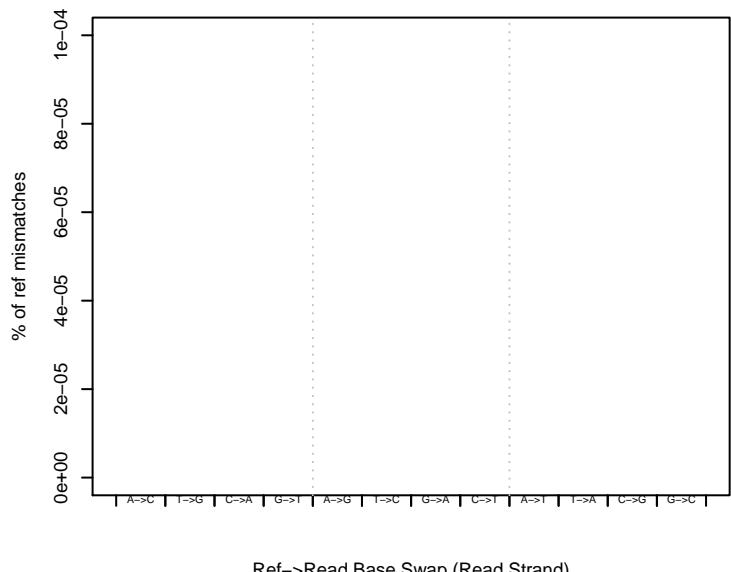
ab

**R1 Ref Mismatches At Phred == 41
Colored by Sample**



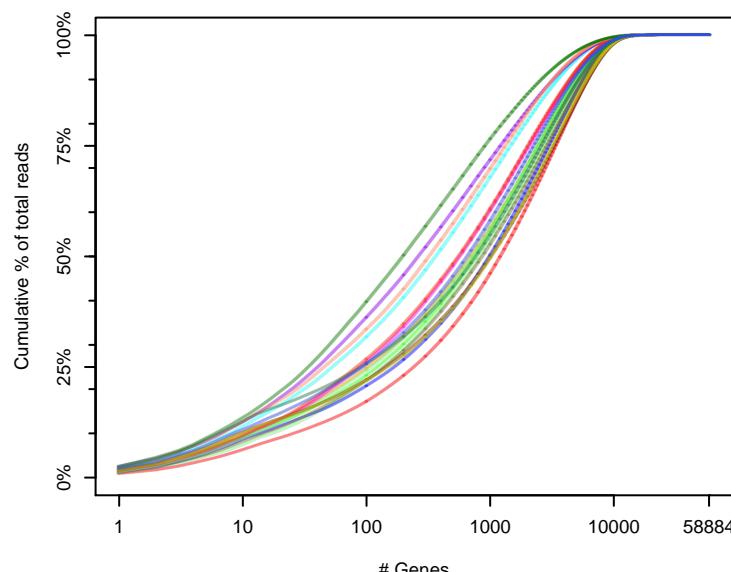
ac

**R2 Ref Mismatches At Phred == 41
Colored by Sample**

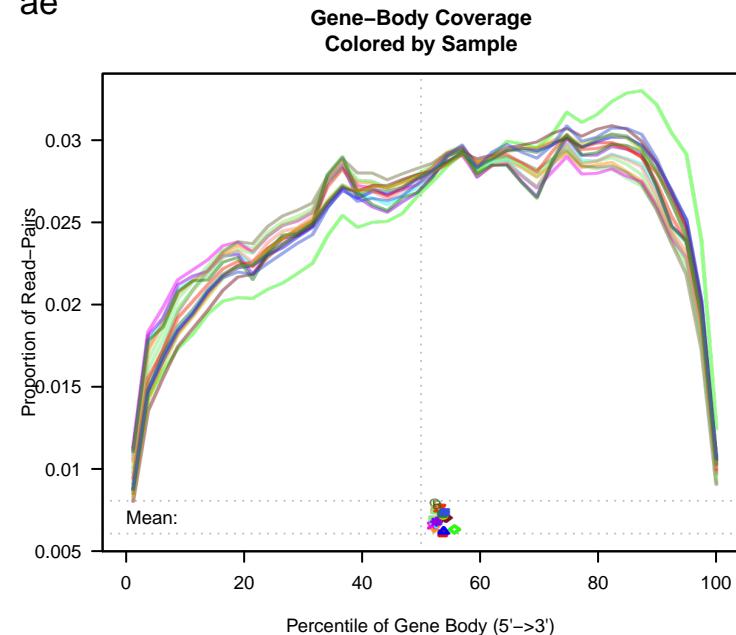


ad

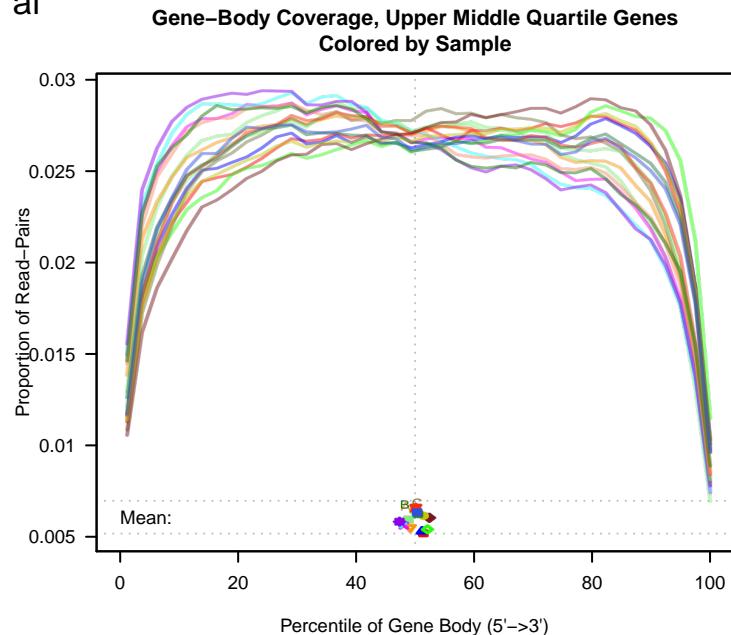
**Cumulative Gene Assignment Diversity
Colored by Sample**



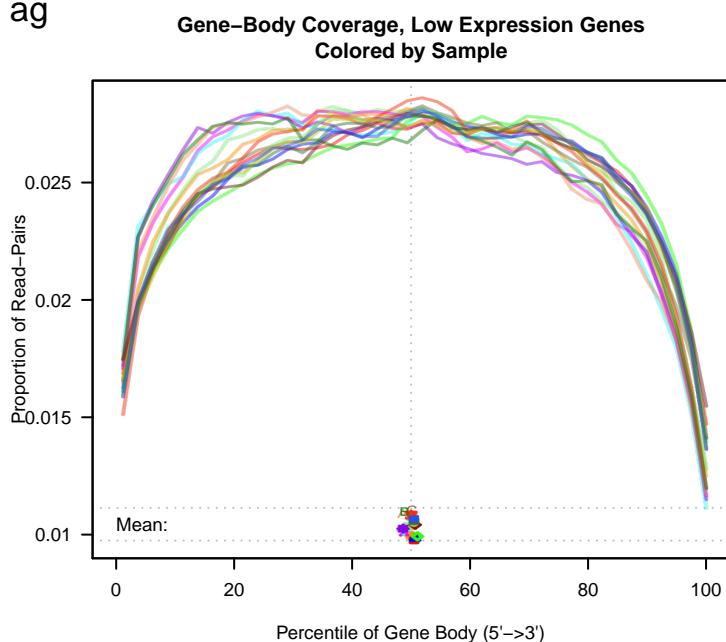
ae



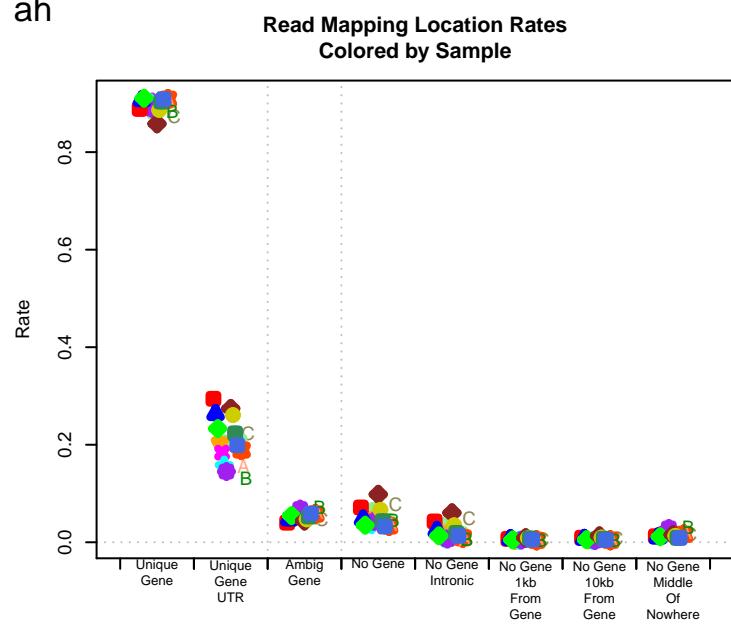
af



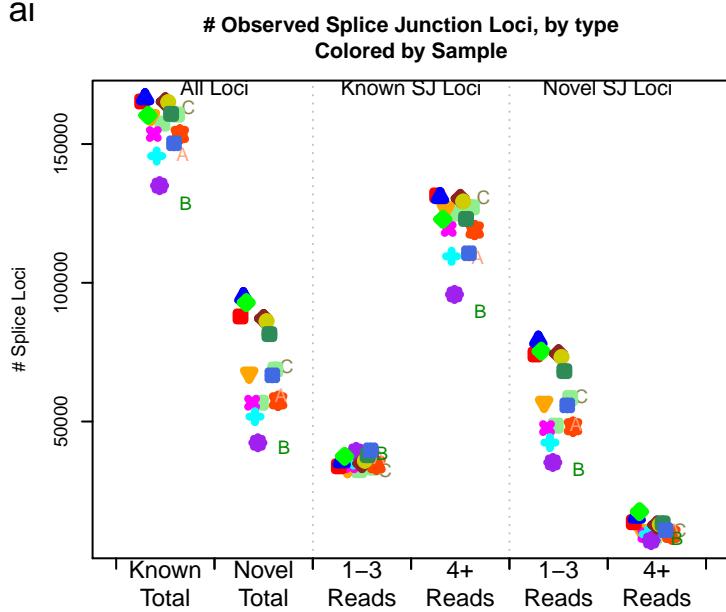
ag



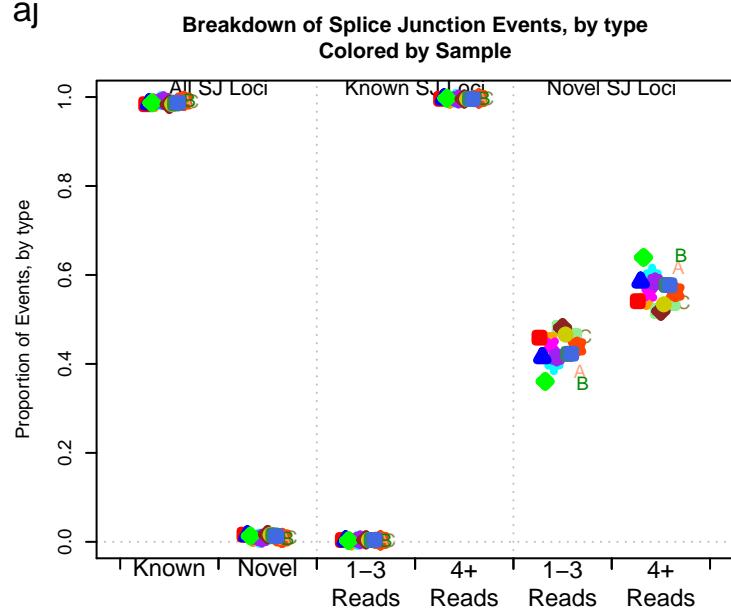
ah



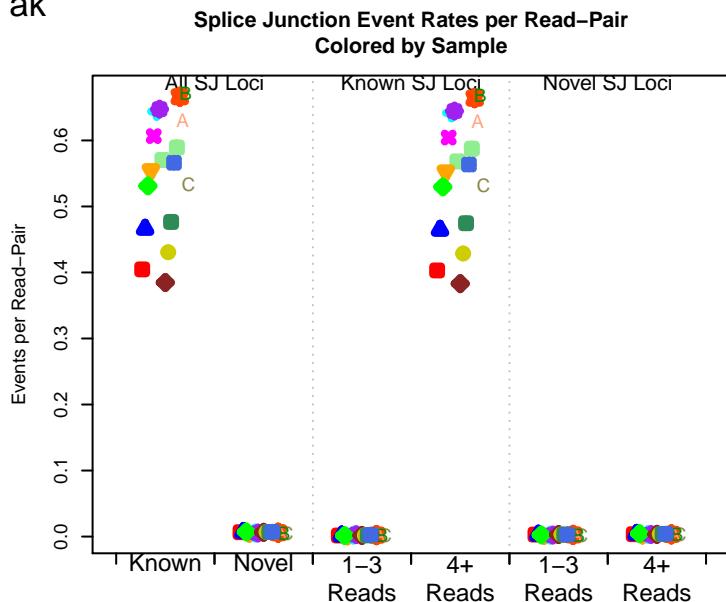
ai



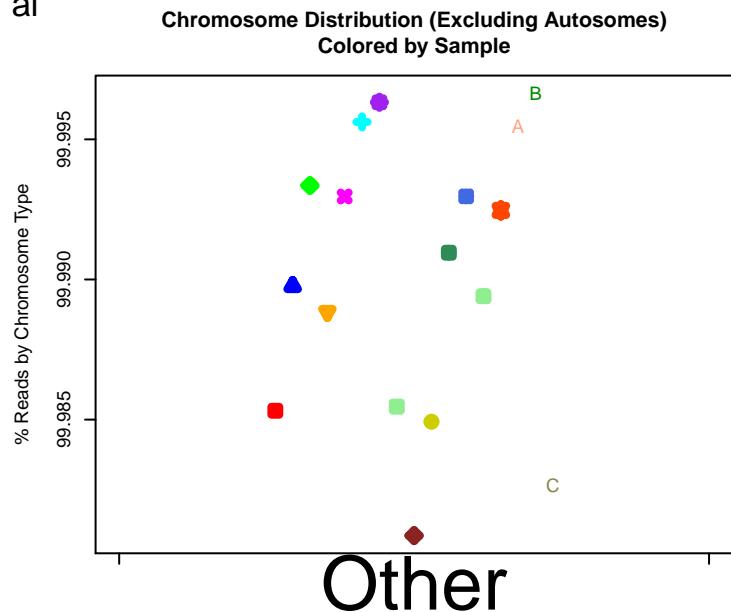
aj



ak

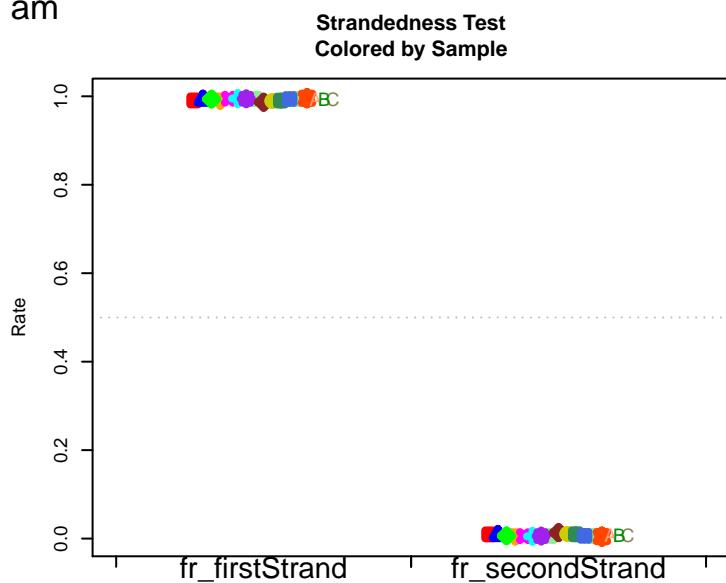


al

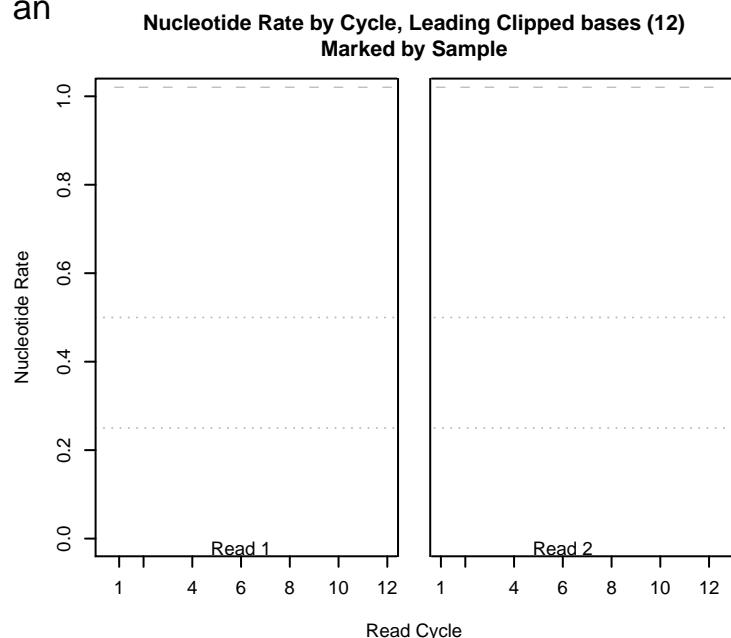


Other

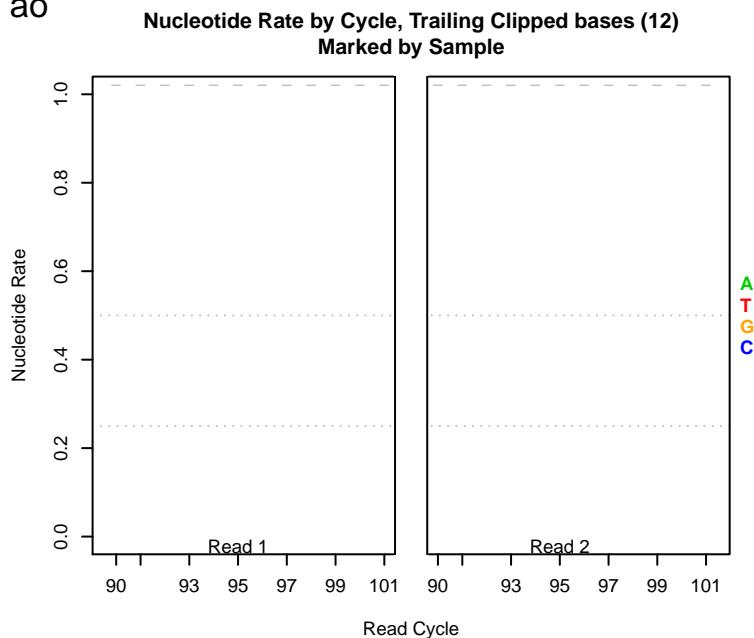
am



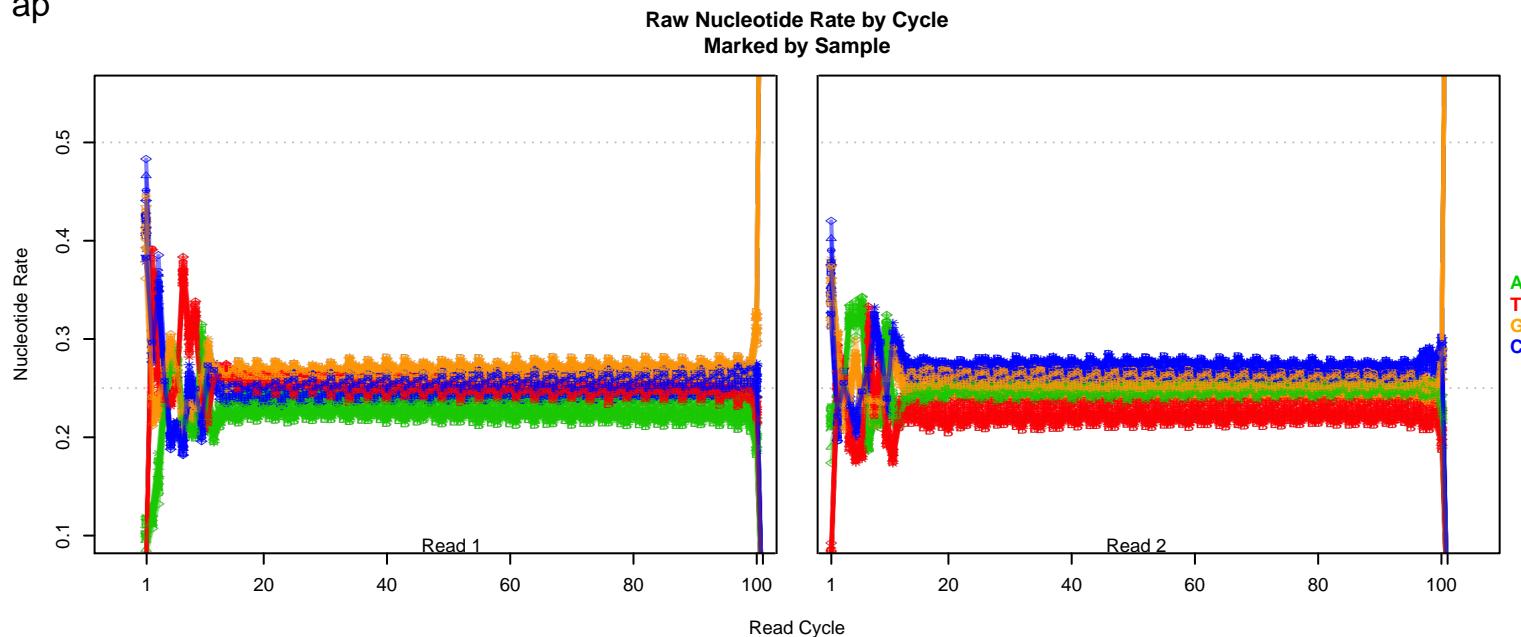
an



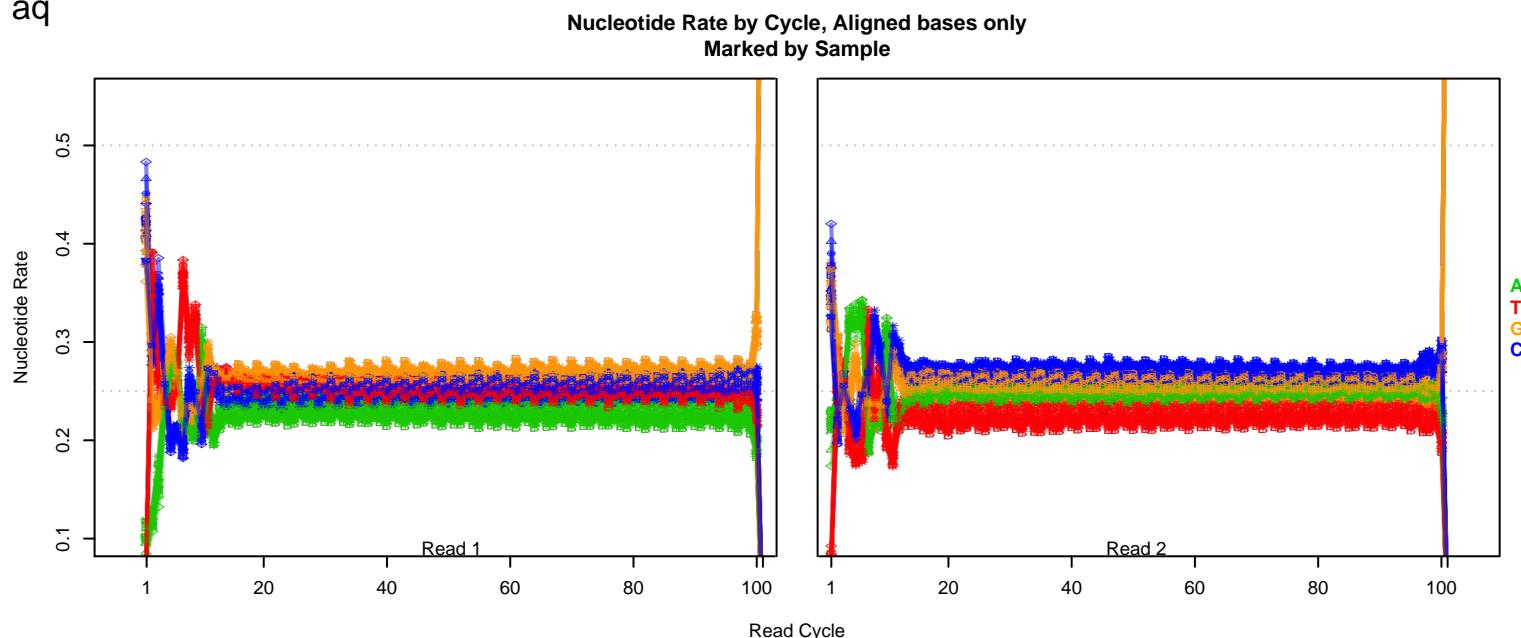
ao



ap

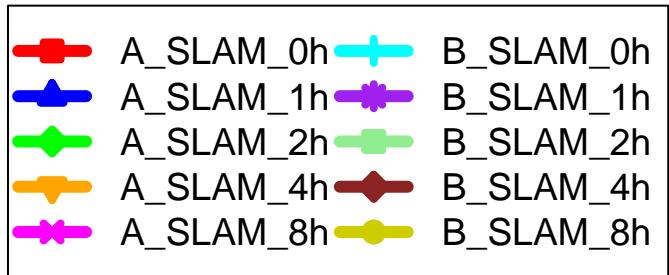


aq



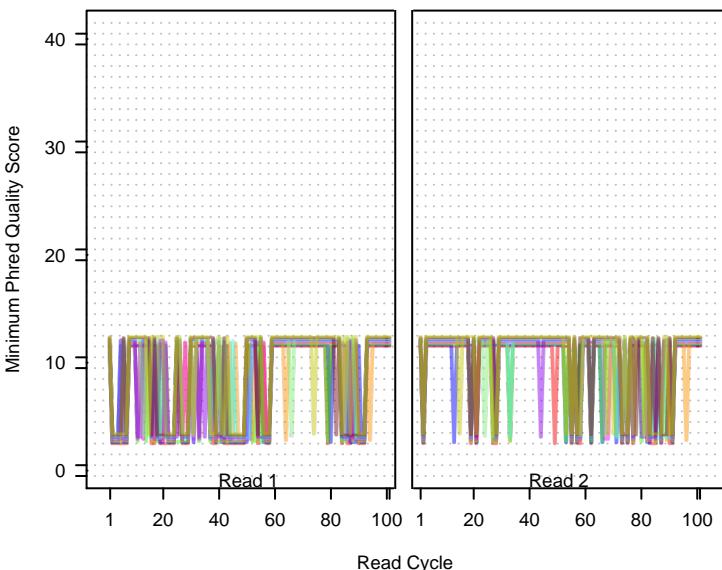
a

Summary Plots, By Sample



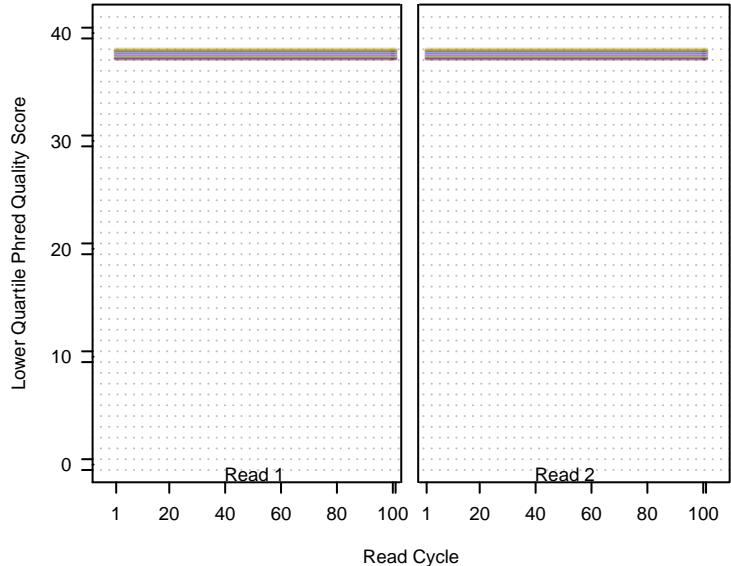
b

Minimum Phred Quality Score
Colored by Sample



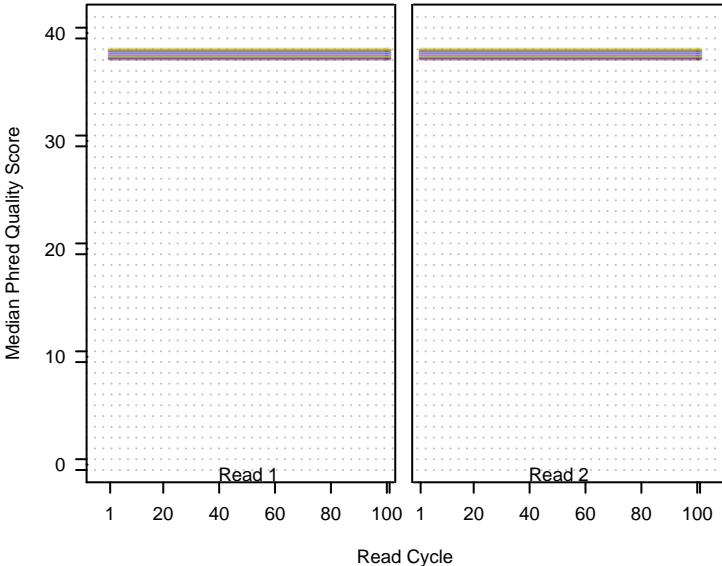
c

Lower Quartile Phred Quality Score
Colored by Sample



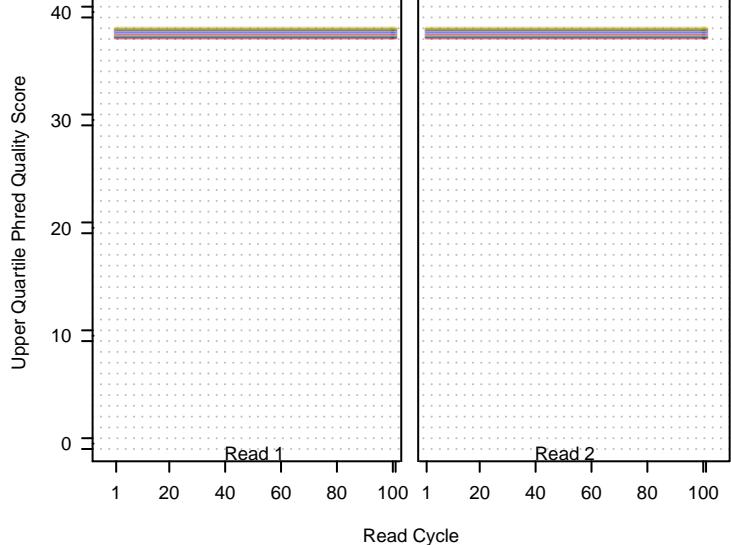
d

Median Phred Quality Score
Colored by Sample



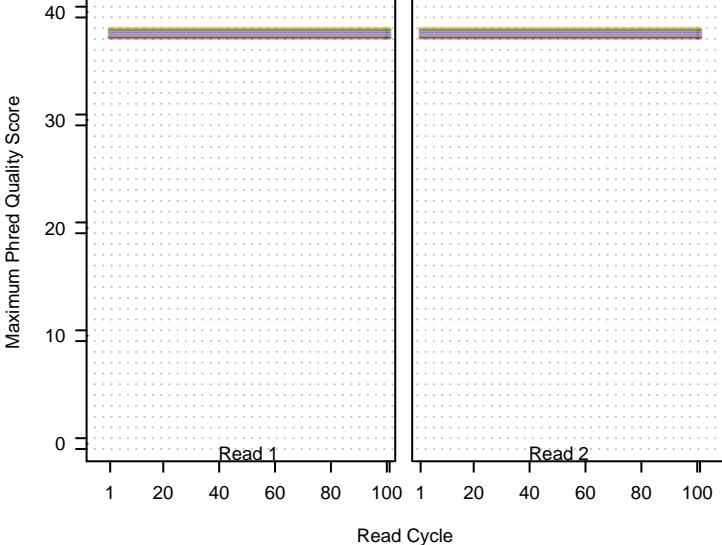
e

Upper Quartile Phred Quality Score
Colored by Sample



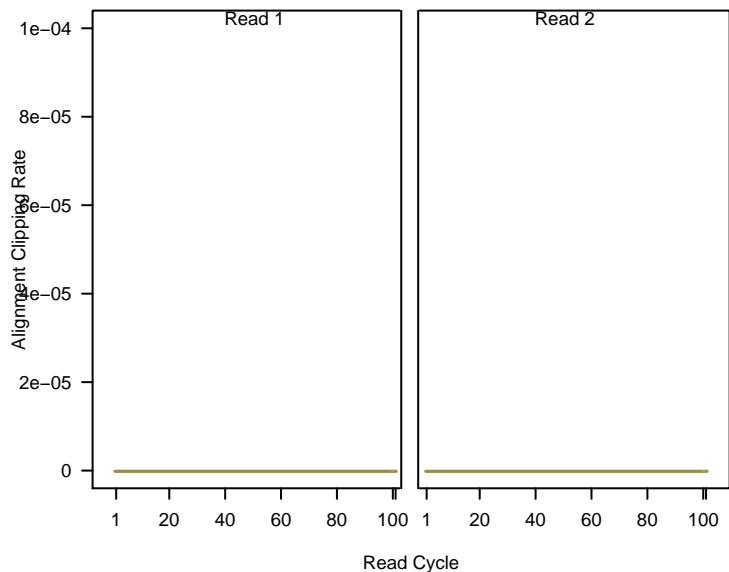
f

Maximum Phred Quality Score
Colored by Sample



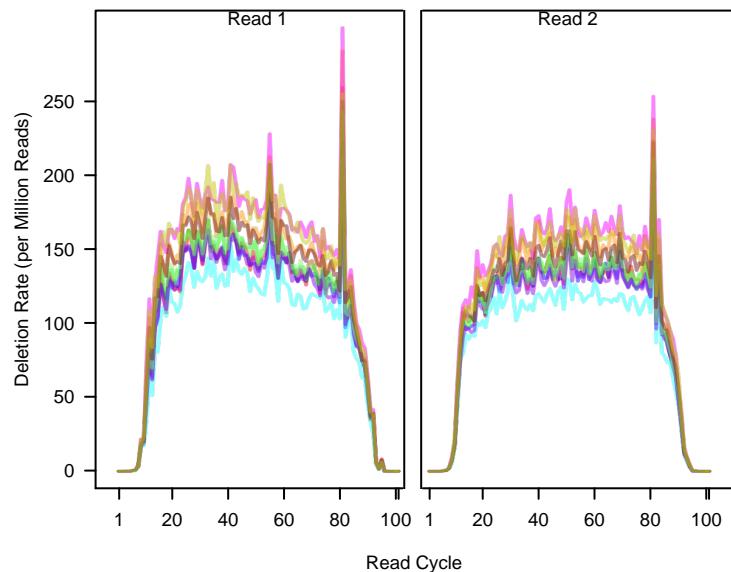
g

**Alignment Clipping Rate, by read cycle
Colored by Sample**



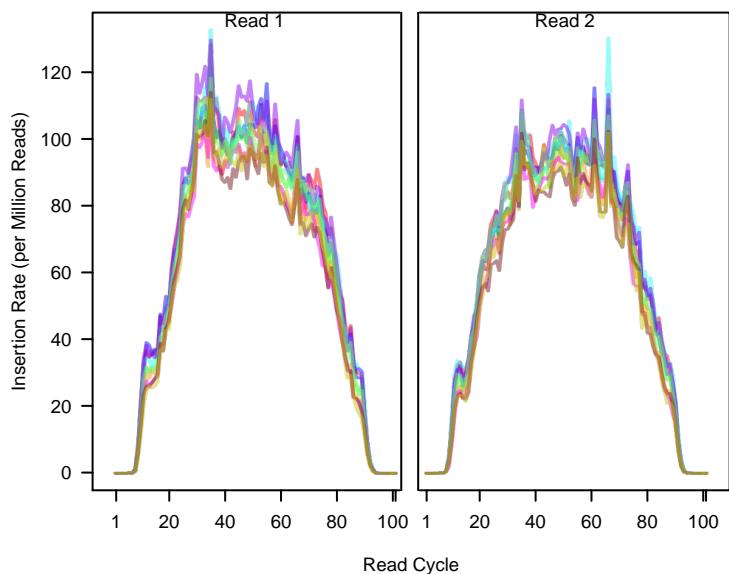
h

**Deletion Rate, by read cycle
Colored by Sample**



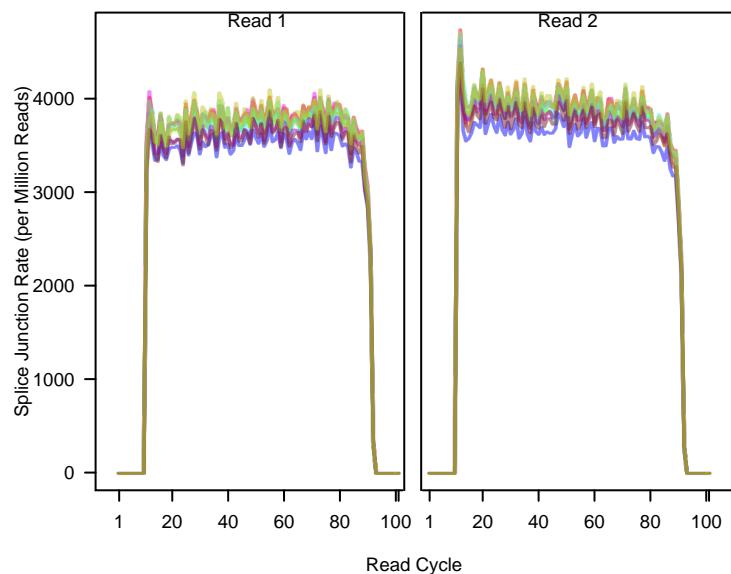
i

**Insertion Rate, by read cycle
Colored by Sample**



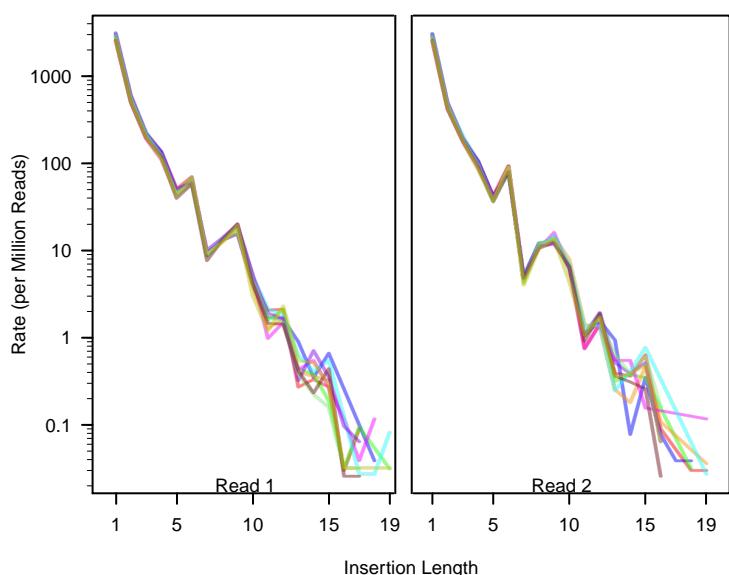
j

**Splice Junction Rate, by read cycle
Colored by Sample**



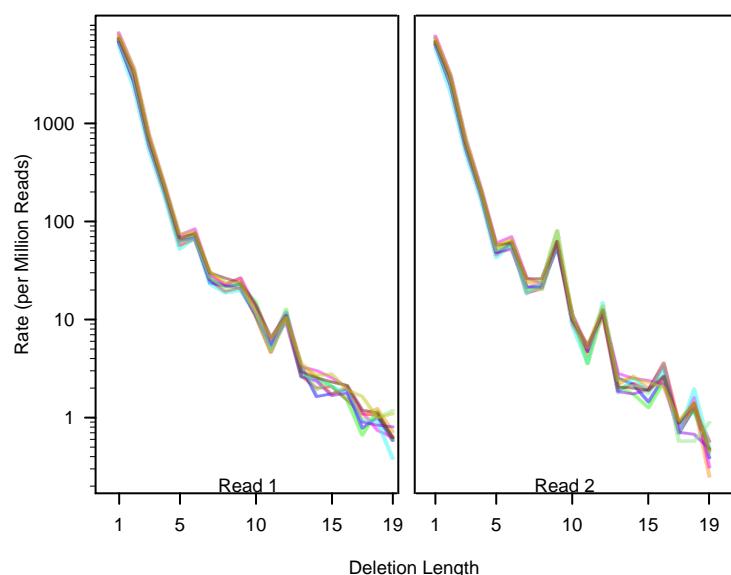
k

**Insertion Length Distribution
Colored by Sample**

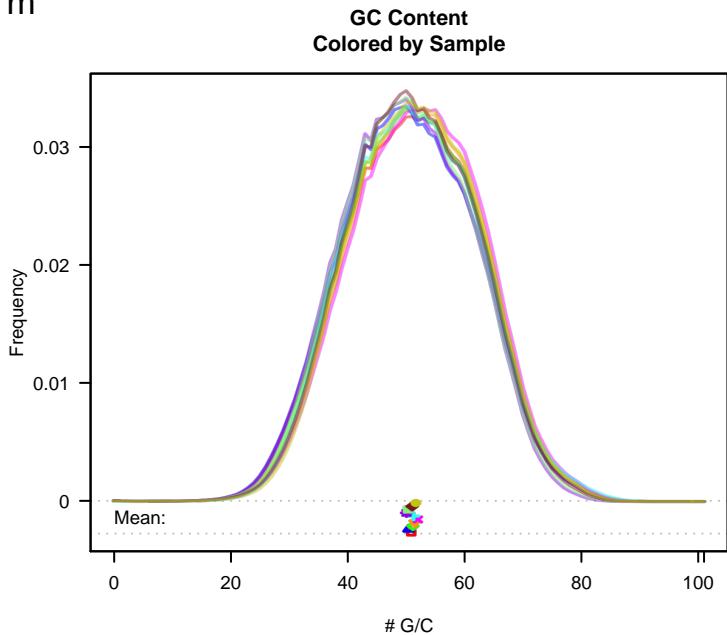


l

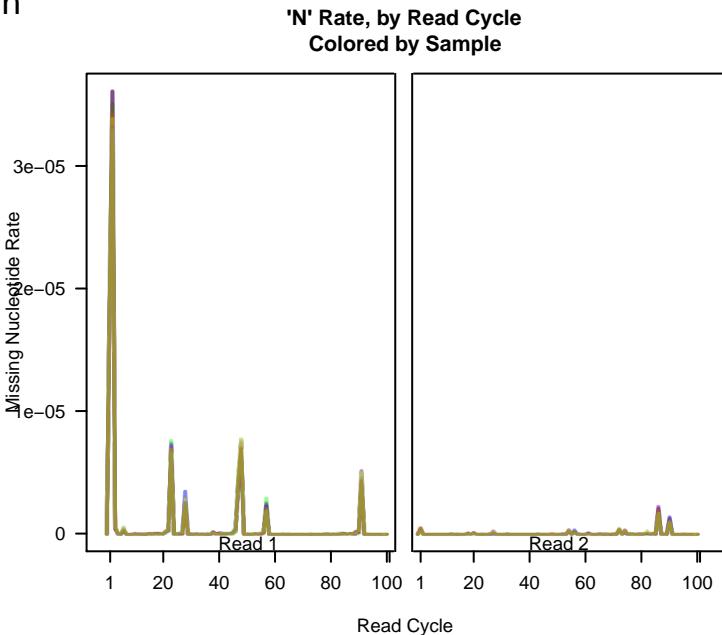
**Deletion Length Distribution
Colored by Sample**



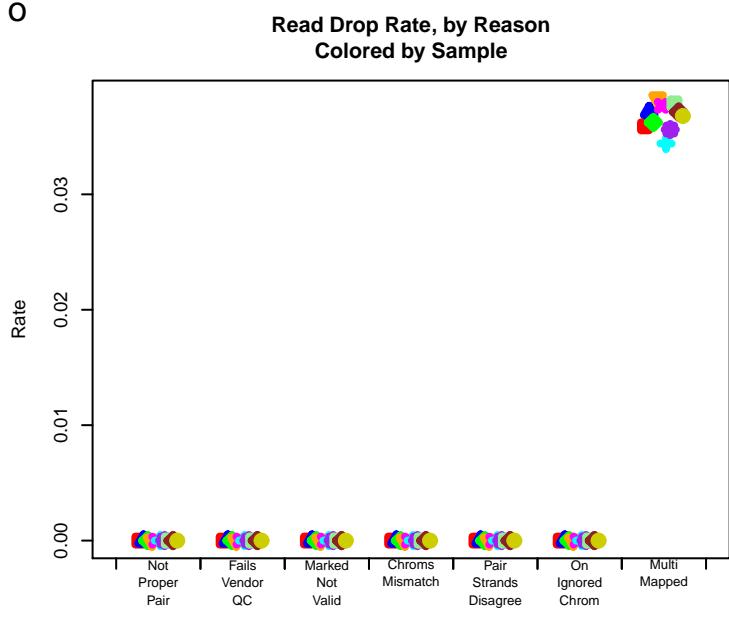
m



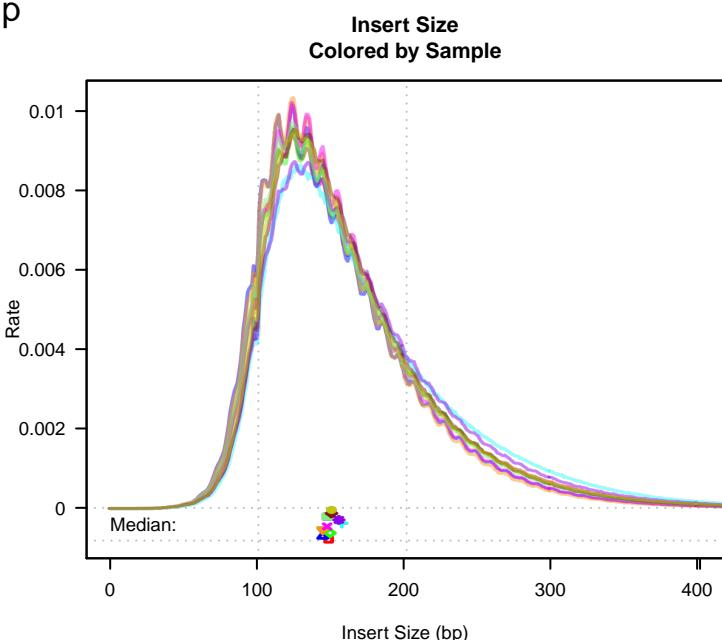
n



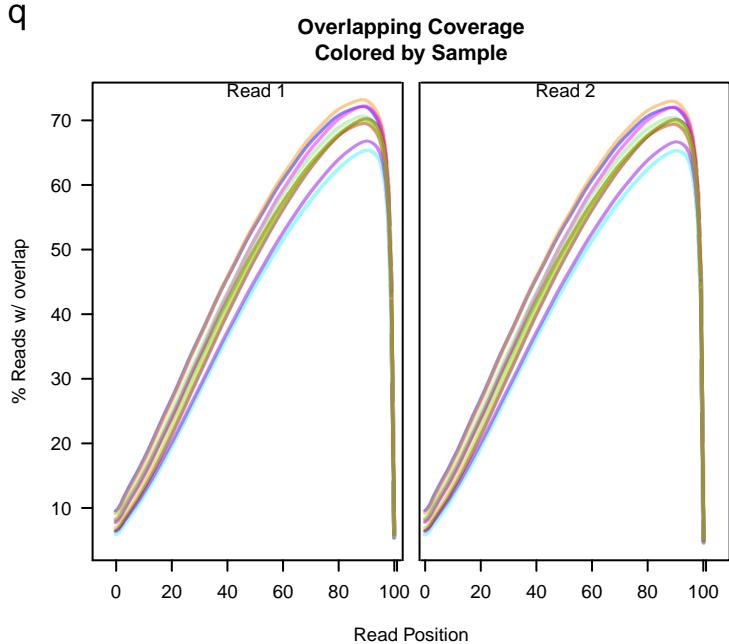
o



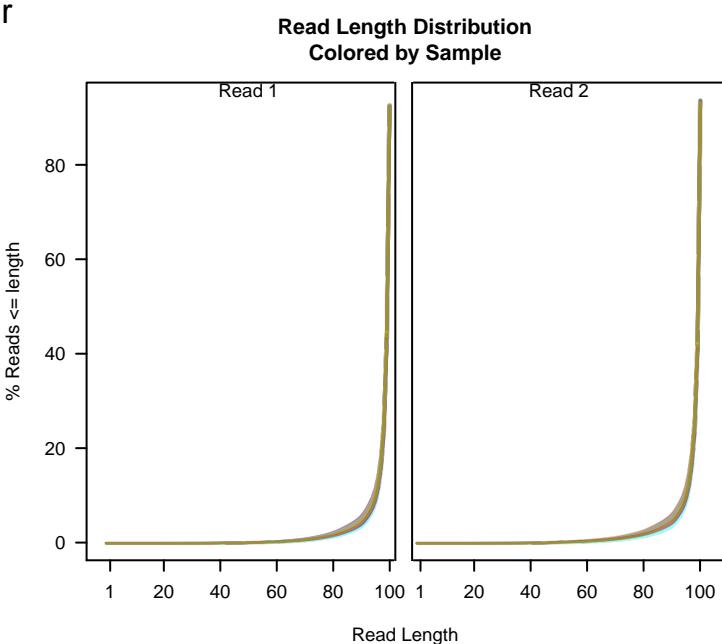
p



q

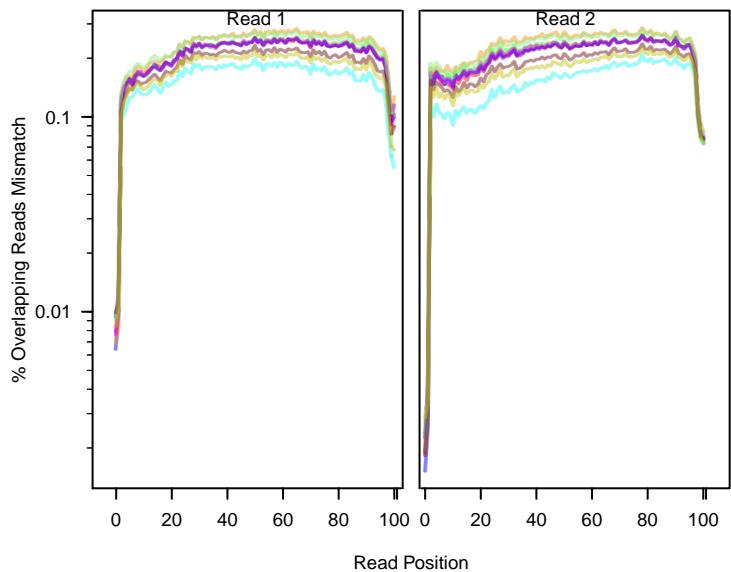


r



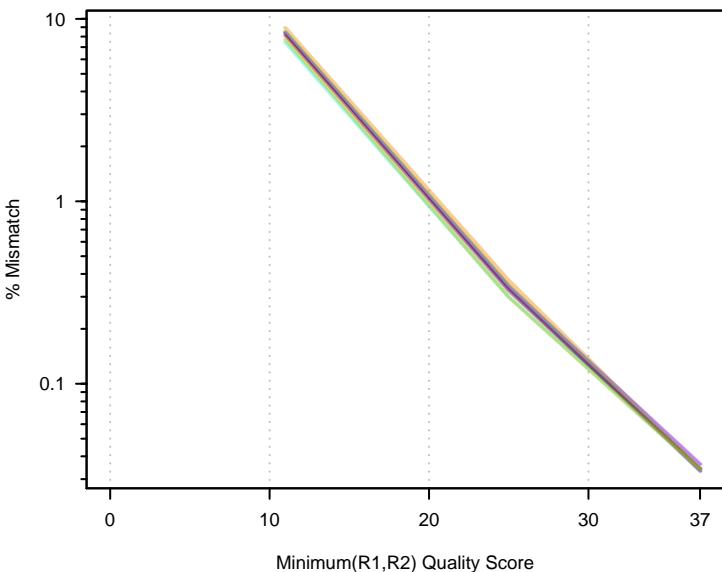
S

**Overlap Mismatch by Read Cycle
Colored by Sample**



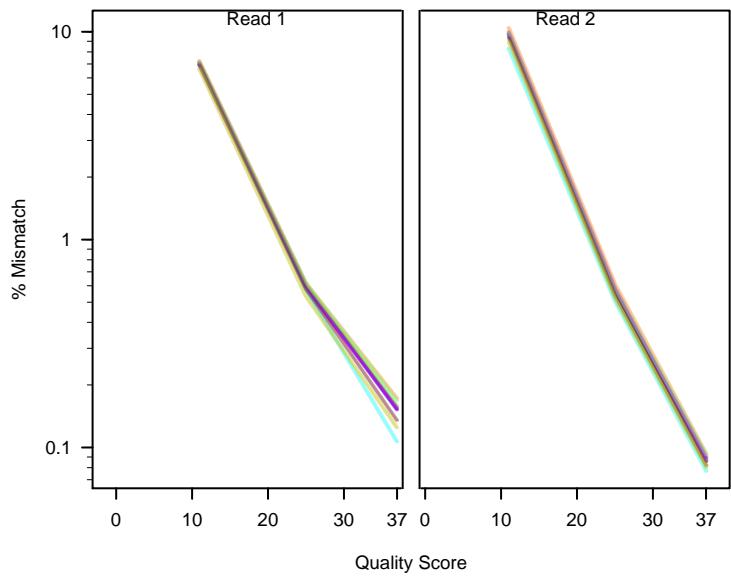
t

**Overlapping Mismatch by Min Qual
Colored by Sample**



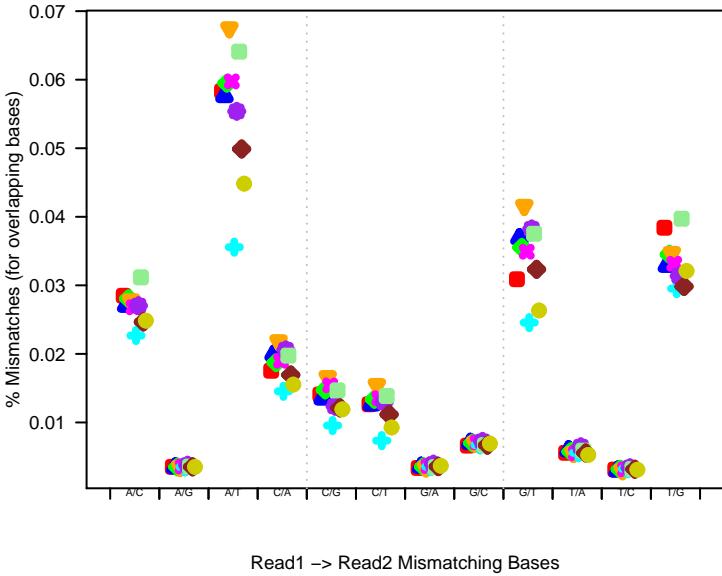
U

**Overlap Mismatch by Read Qual
Colored by Sample**



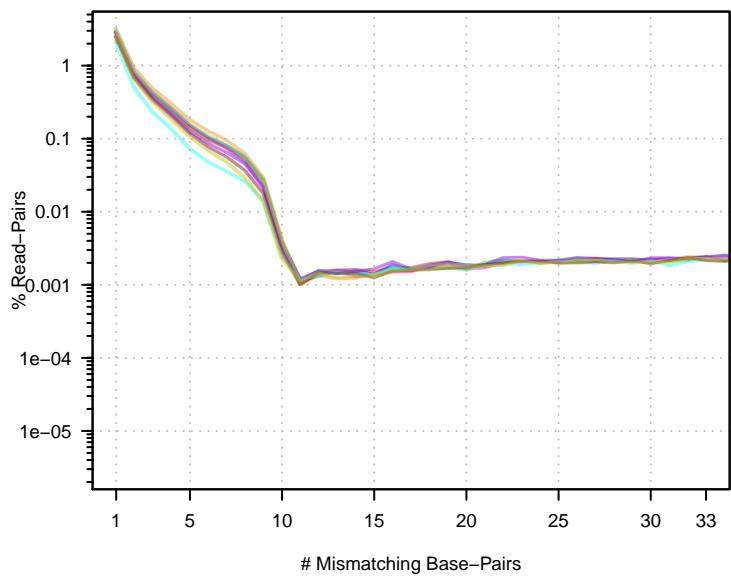
V

**Overlap Mismatch Combinations
Colored by Sample**



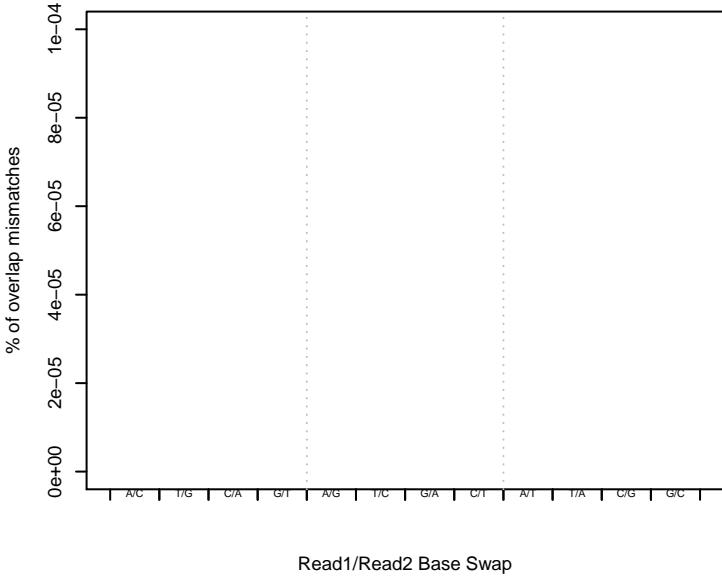
W

**Overlap Mismatch Size Frequency
Colored by Sample**



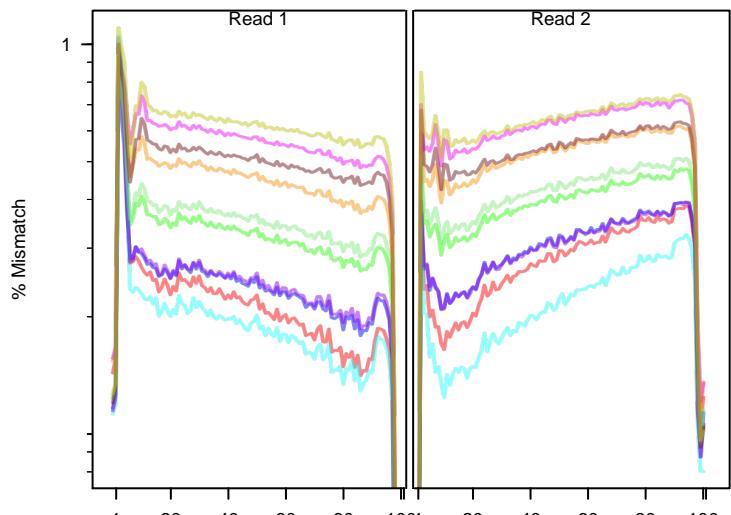
X

**Overlap Mismatch Pairs At Phred == 41
Colored by Sample**



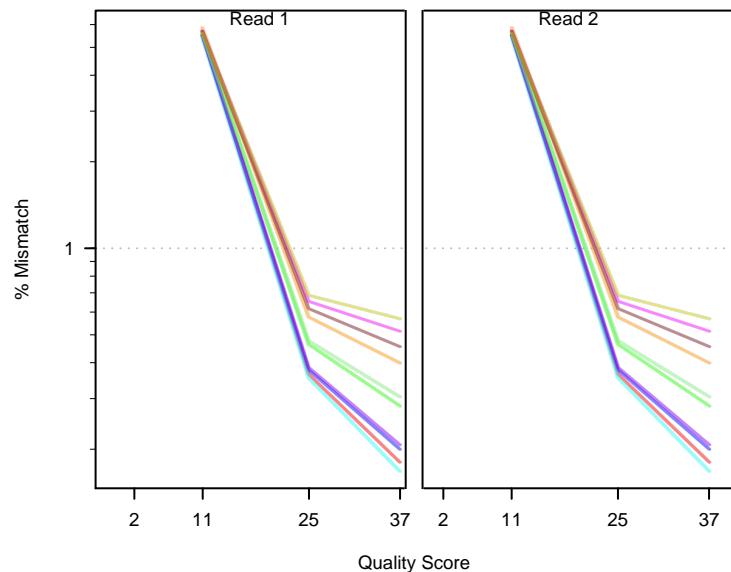
y

**Reference Mismatch by Read Cycle
Colored by Sample**



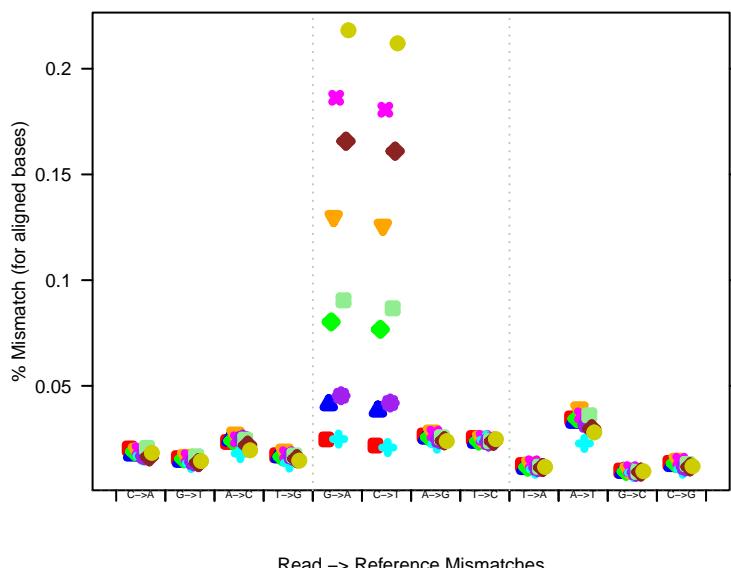
Z

**Reference Mismatch by Read Qual
Colored by Sample**



aa

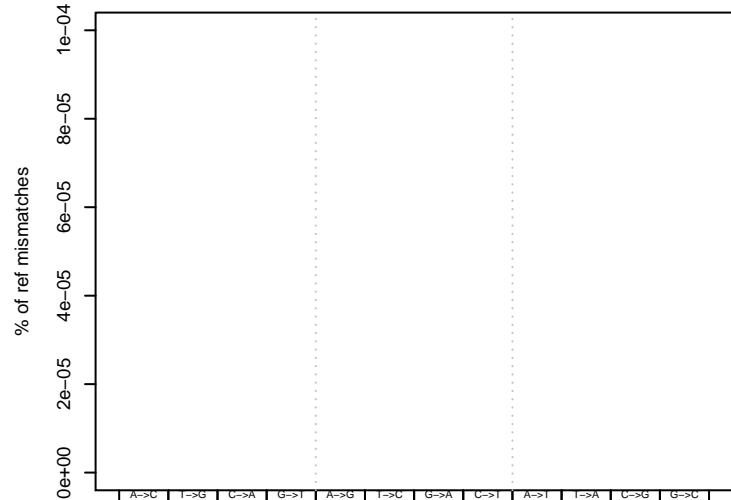
**Reference Mismatch Combinations
Colored by Sample**



Read → Reference Mismatches

ab

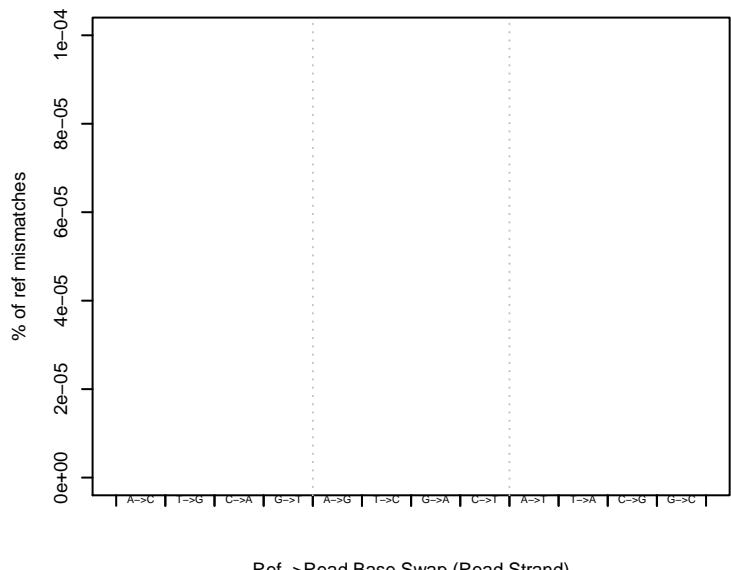
**R1 Ref Mismatches At Phred == 41
Colored by Sample**



Ref→Read Base Swap (Read Strand)

ac

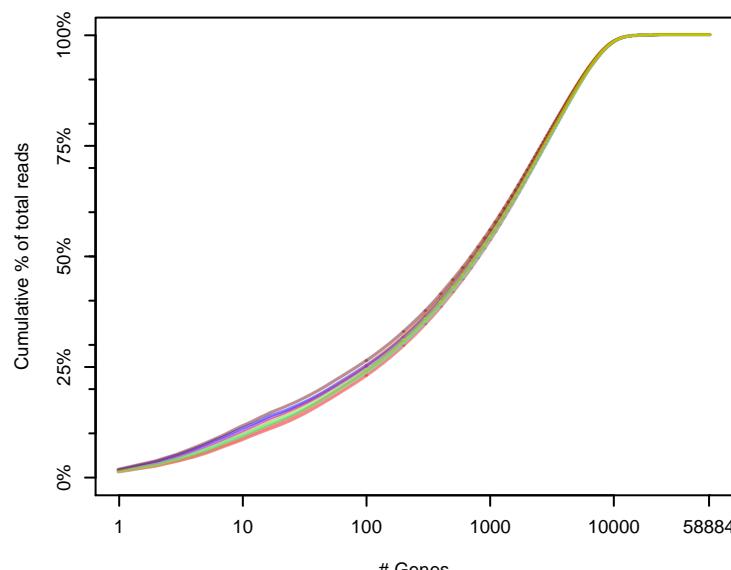
**R2 Ref Mismatches At Phred == 41
Colored by Sample**



Ref→Read Base Swap (Read Strand)

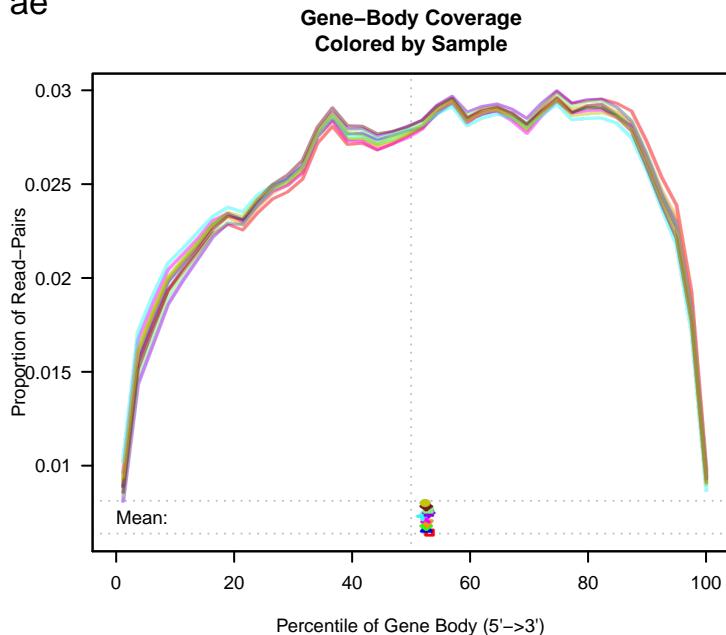
ad

**Cumulative Gene Assignment Diversity
Colored by Sample**

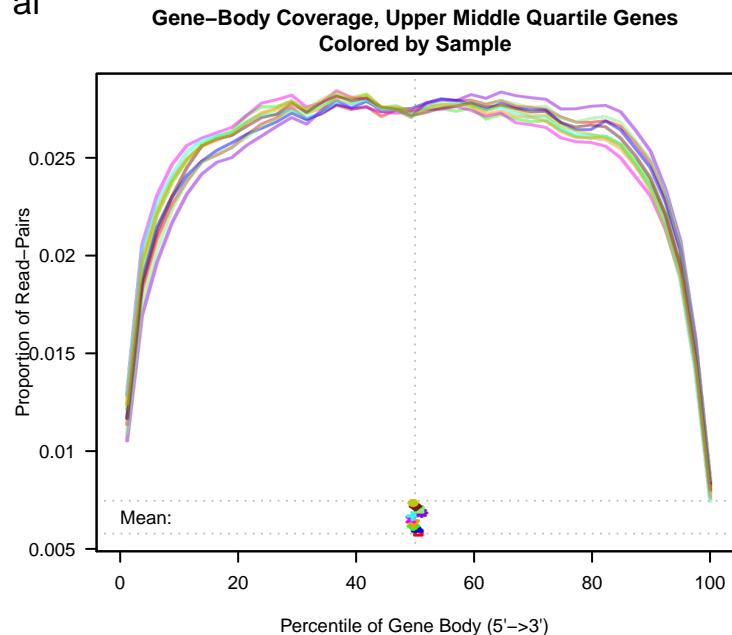


Genes

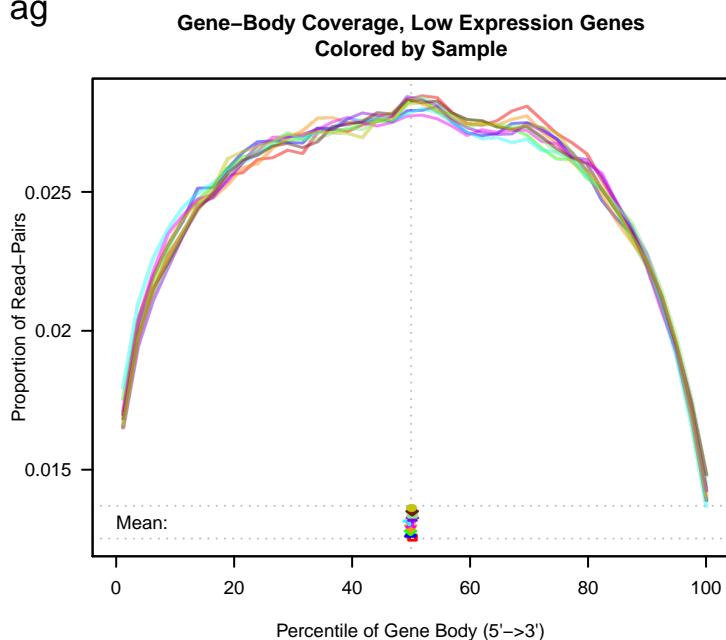
ae



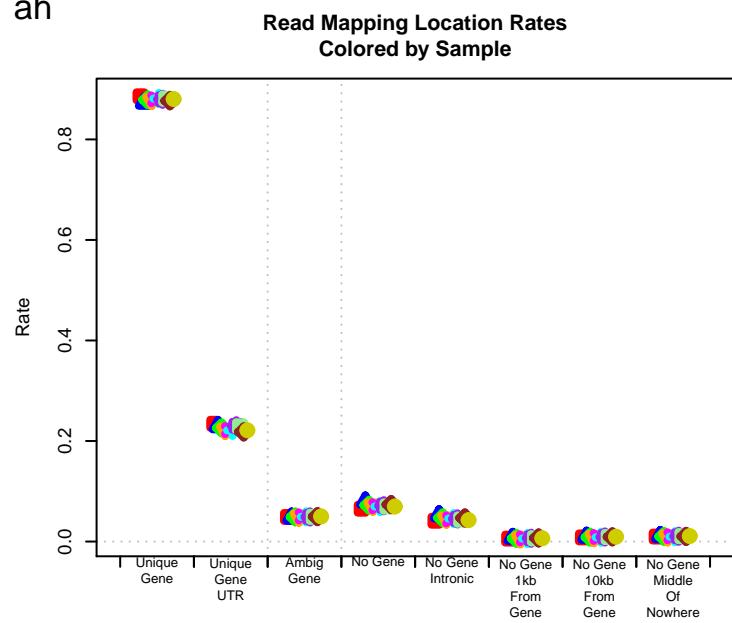
af



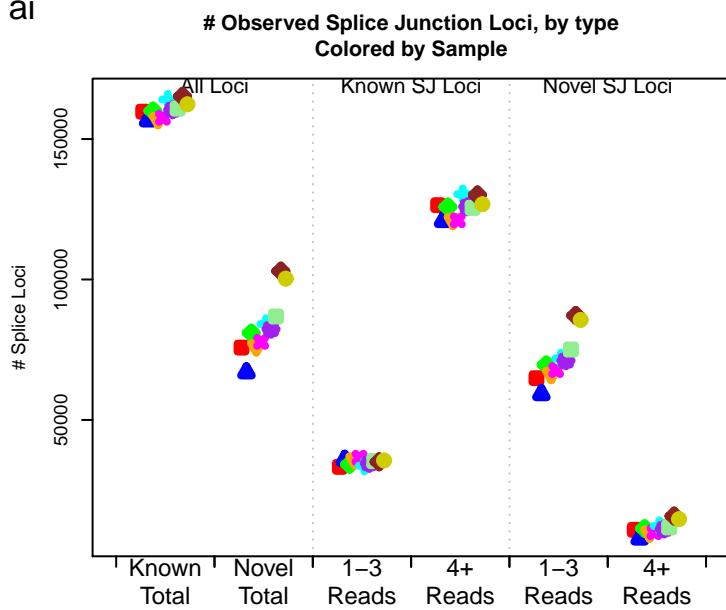
ag



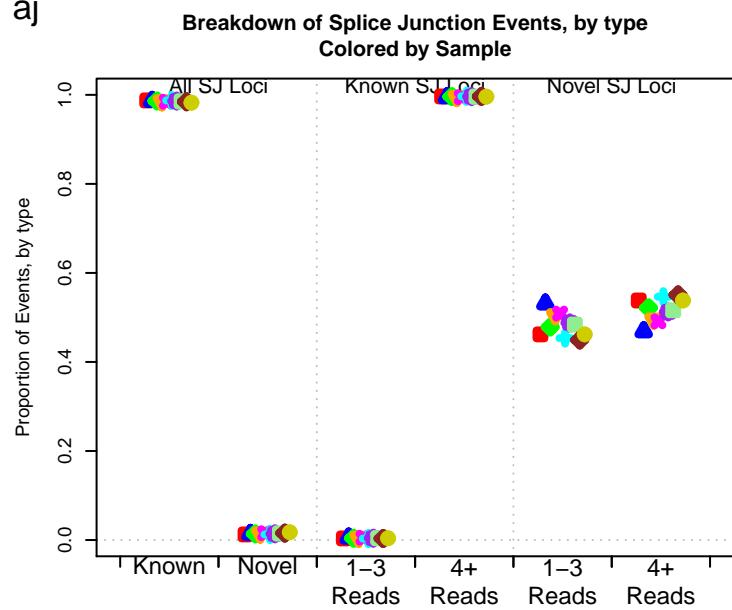
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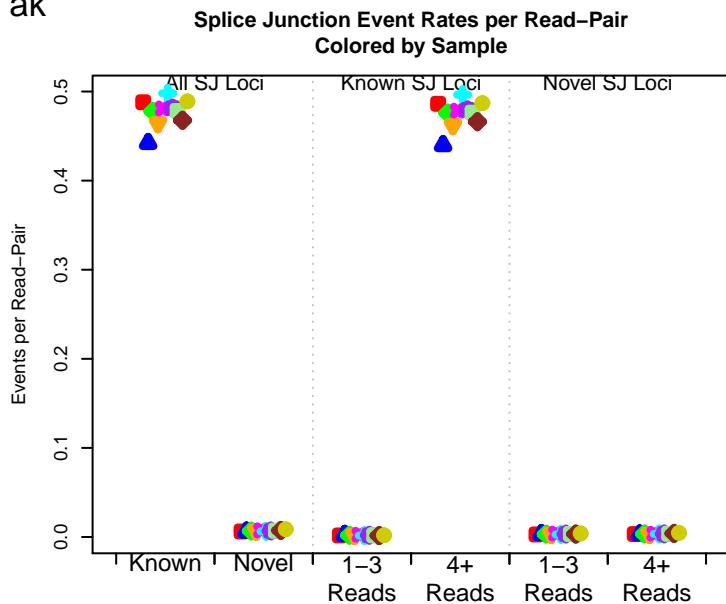
ai



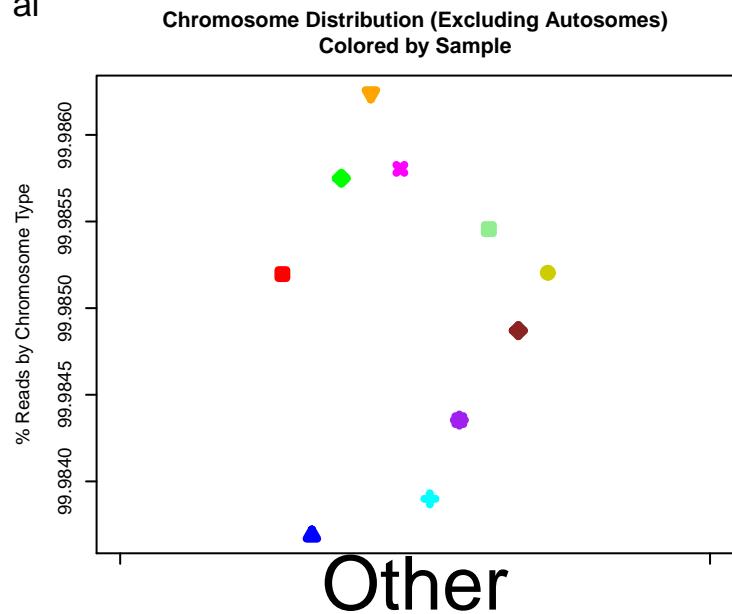
aj



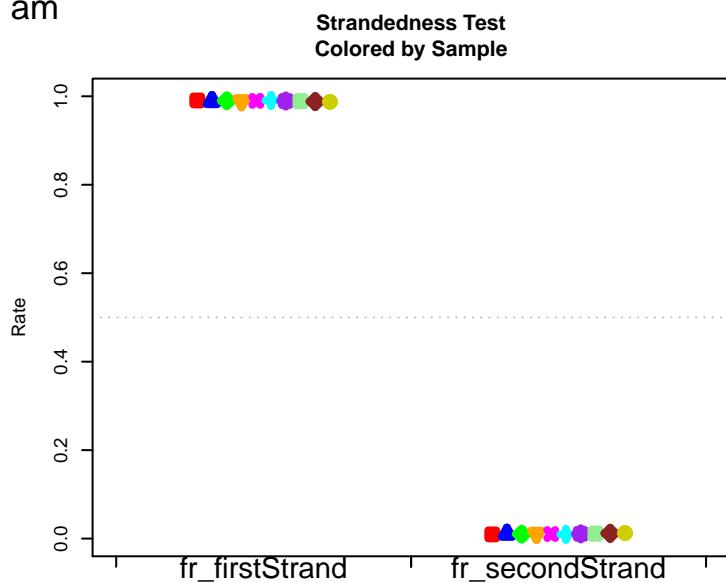
ak



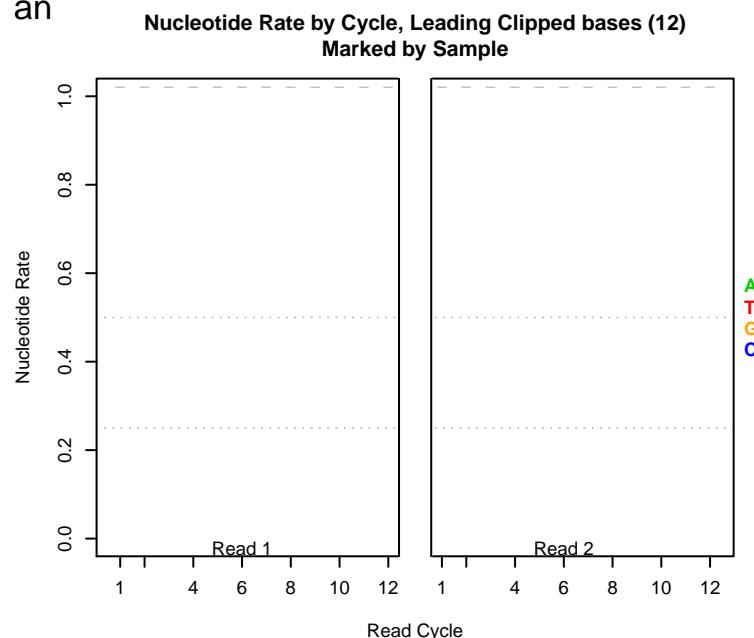
al



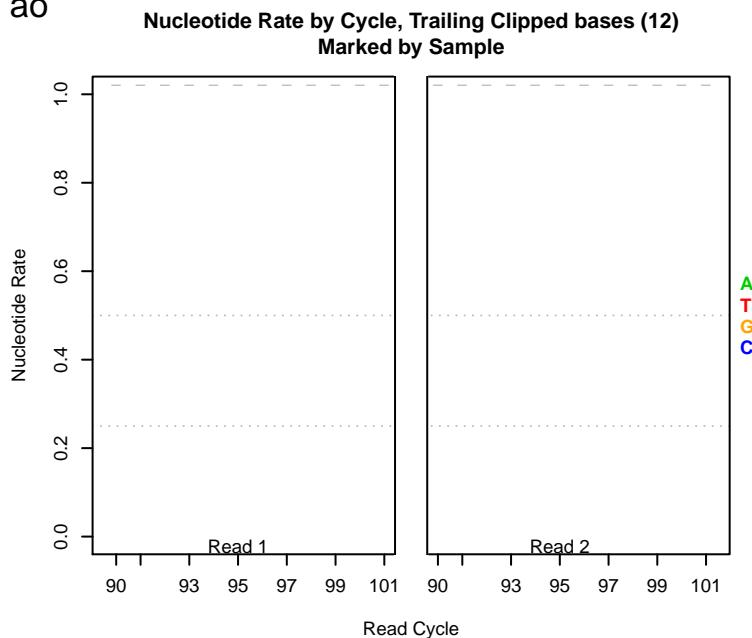
am



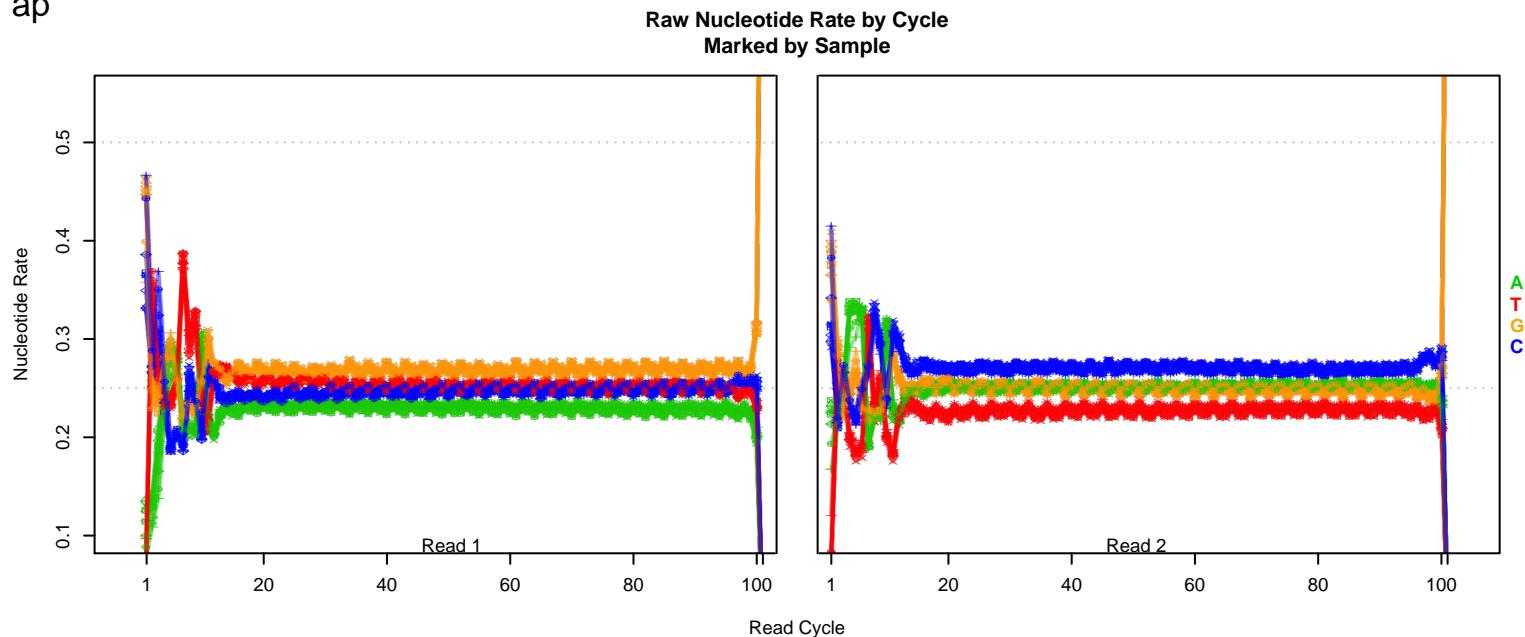
an



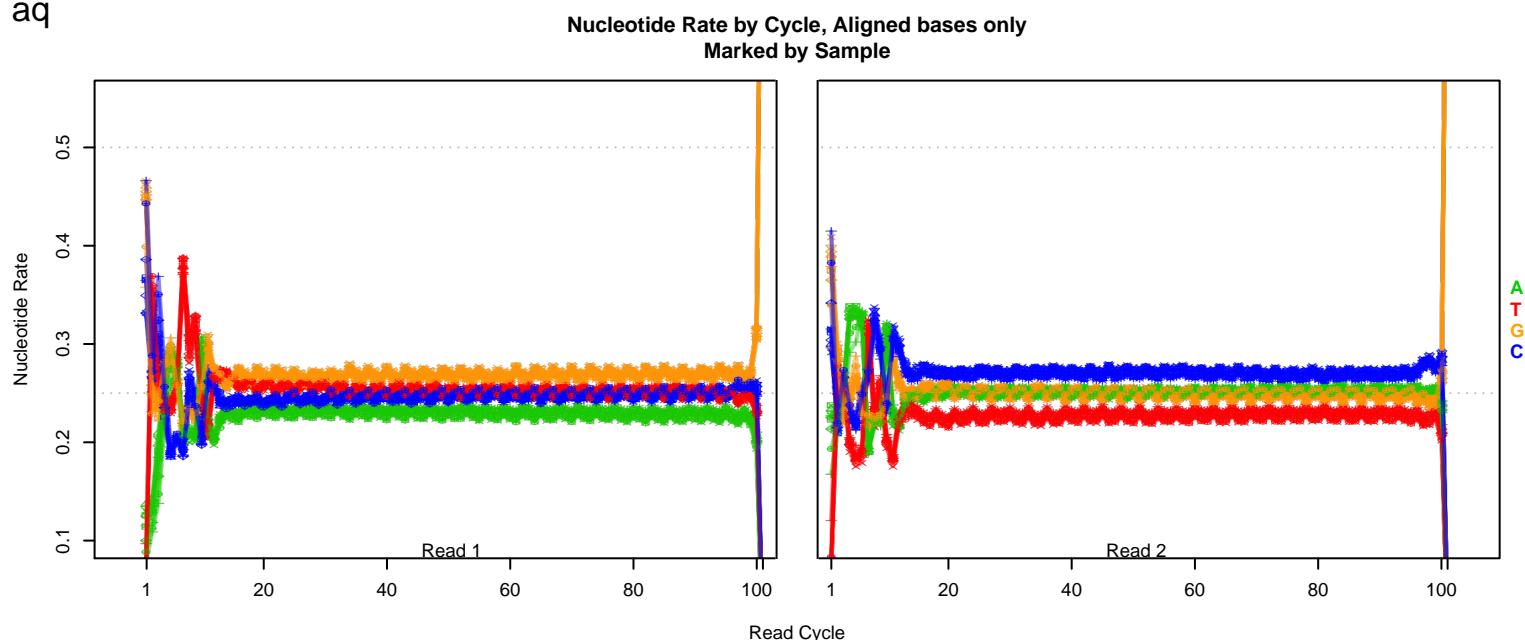
ao



ap

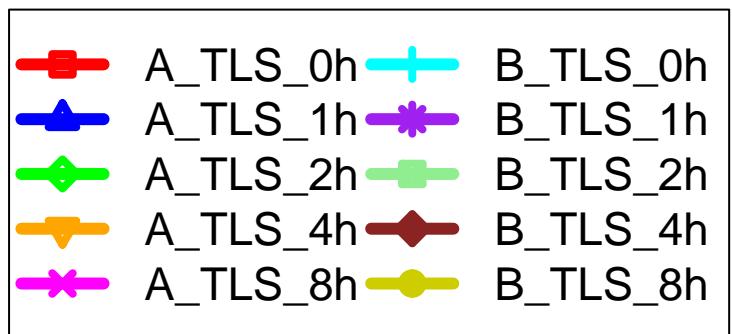


aq



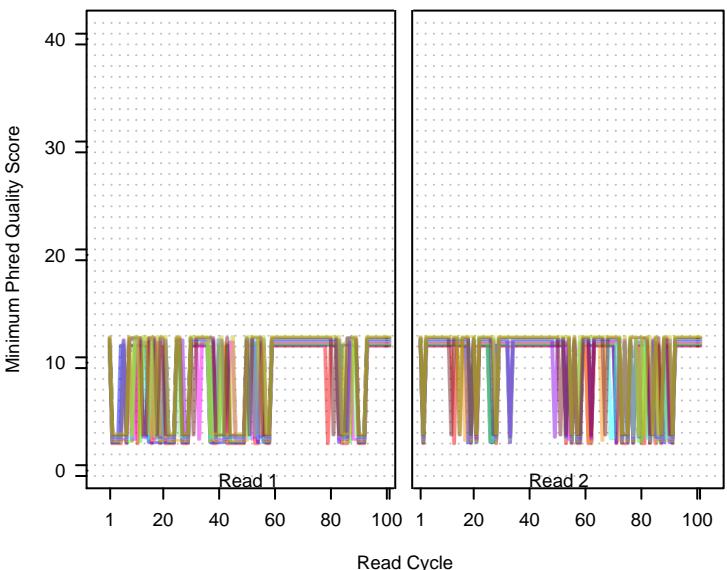
a

Summary Plots, By Sample



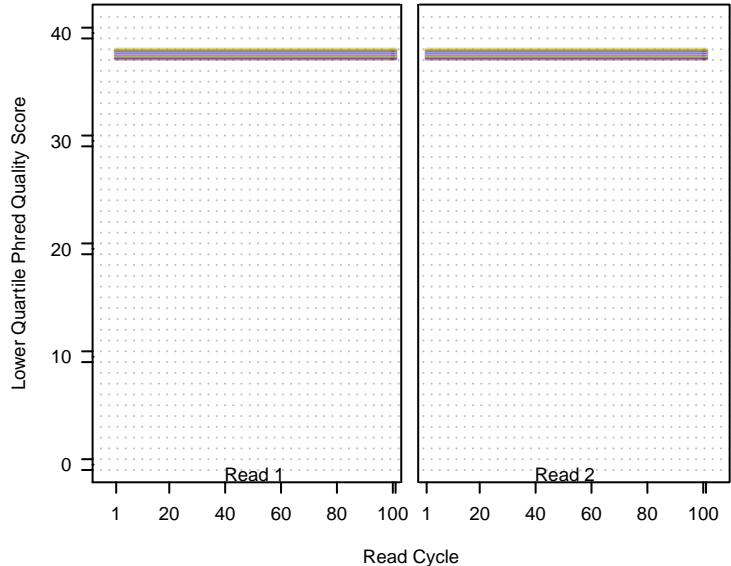
b

Minimum Phred Quality Score
Colored by Sample



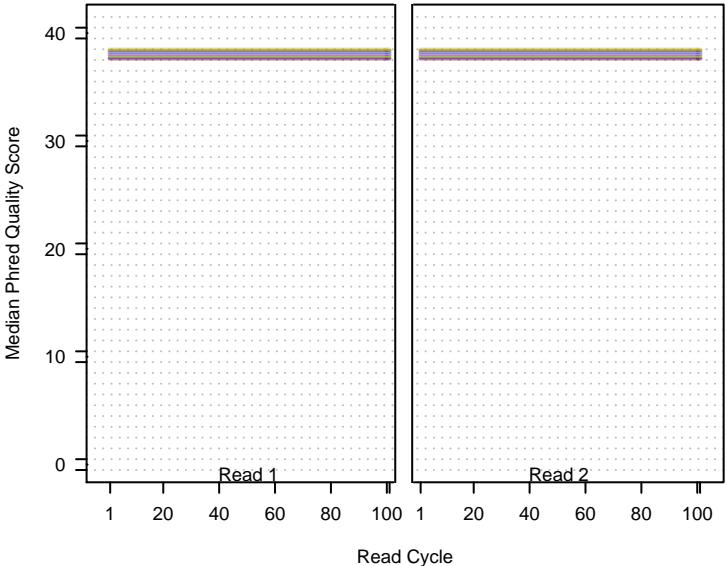
c

Lower Quartile Phred Quality Score
Colored by Sample



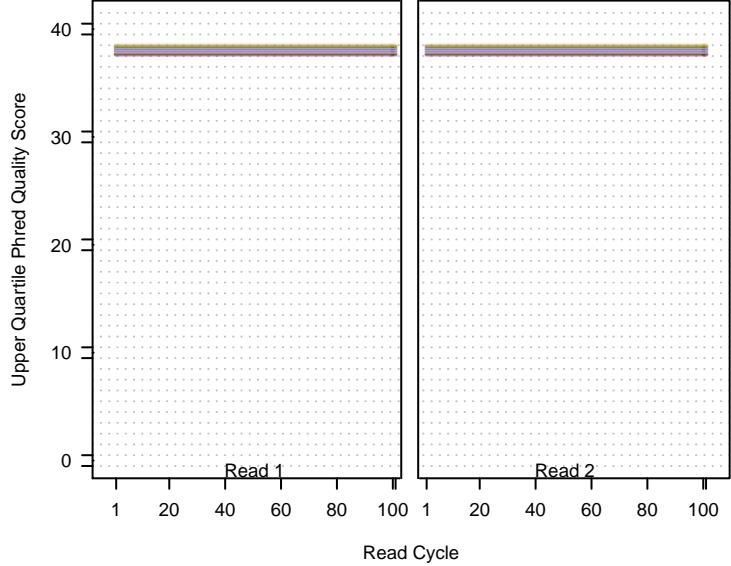
d

Median Phred Quality Score
Colored by Sample



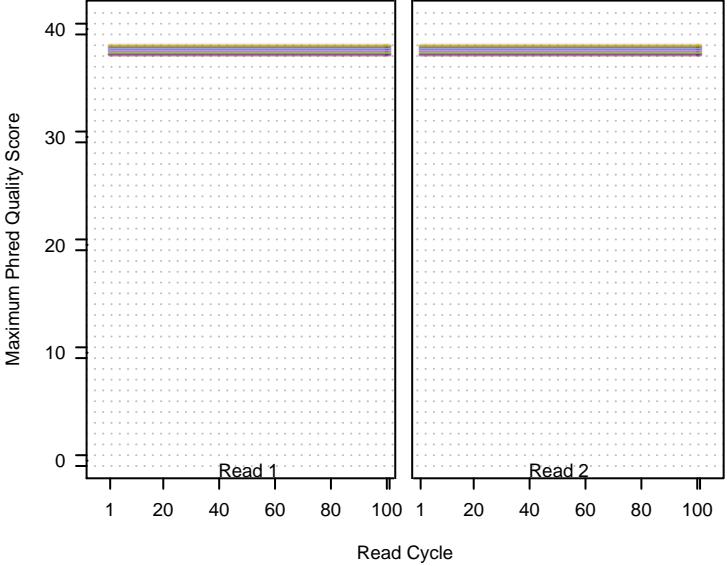
e

Upper Quartile Phred Quality Score
Colored by Sample



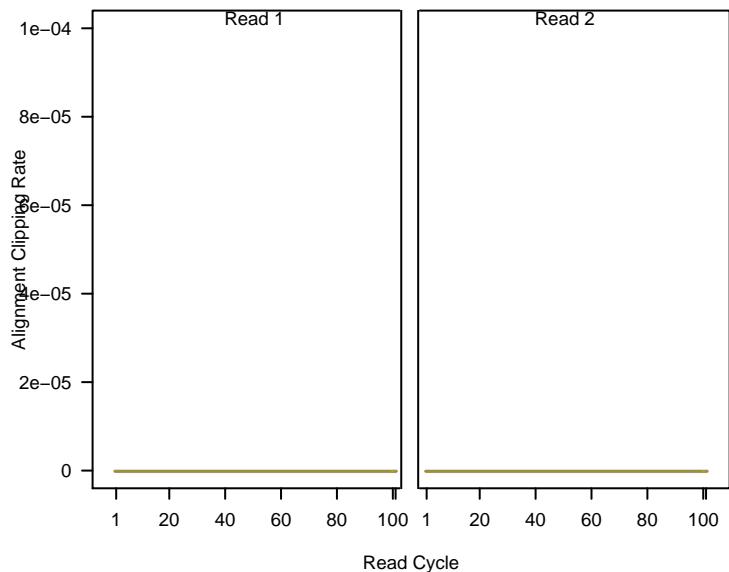
f

Maximum Phred Quality Score
Colored by Sample



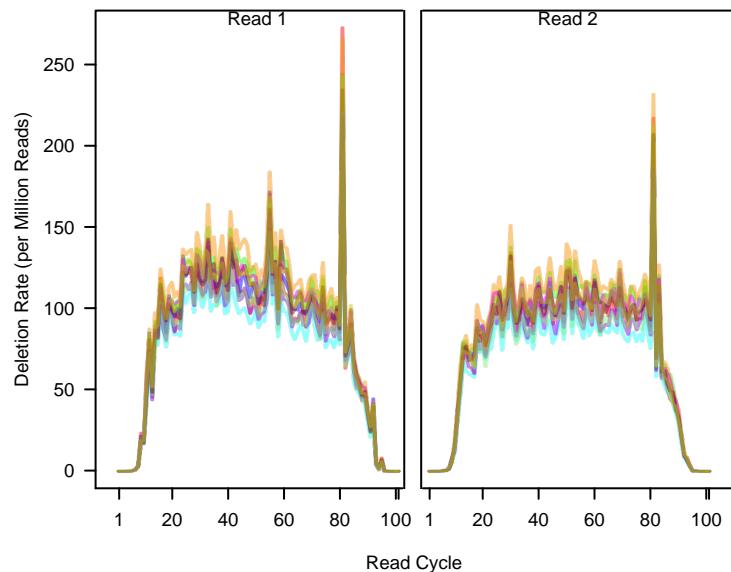
g

**Alignment Clipping Rate, by read cycle
Colored by Sample**



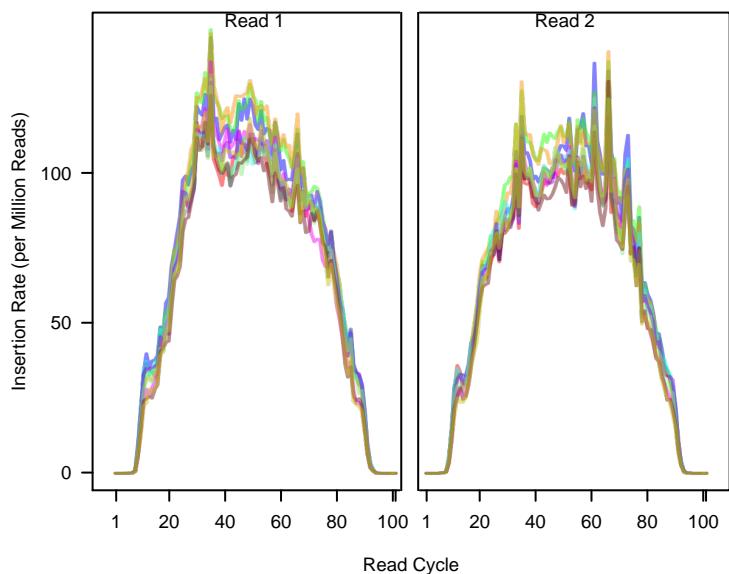
h

**Deletion Rate, by read cycle
Colored by Sample**



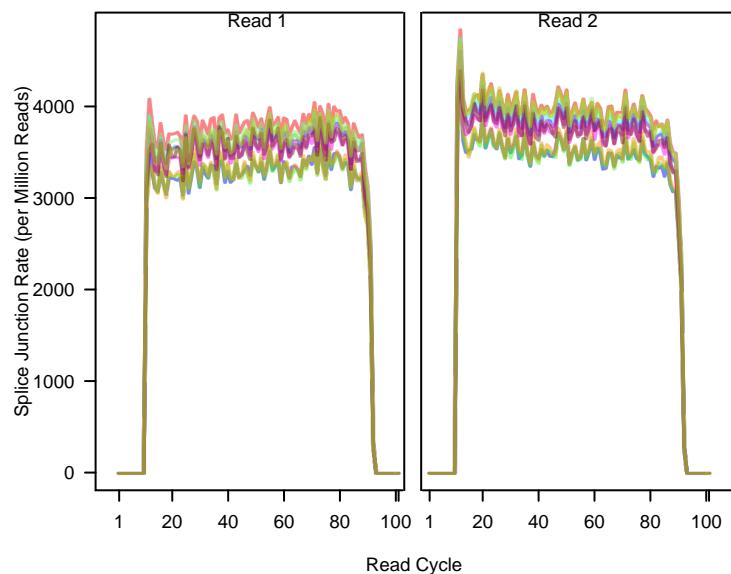
i

**Insertion Rate, by read cycle
Colored by Sample**



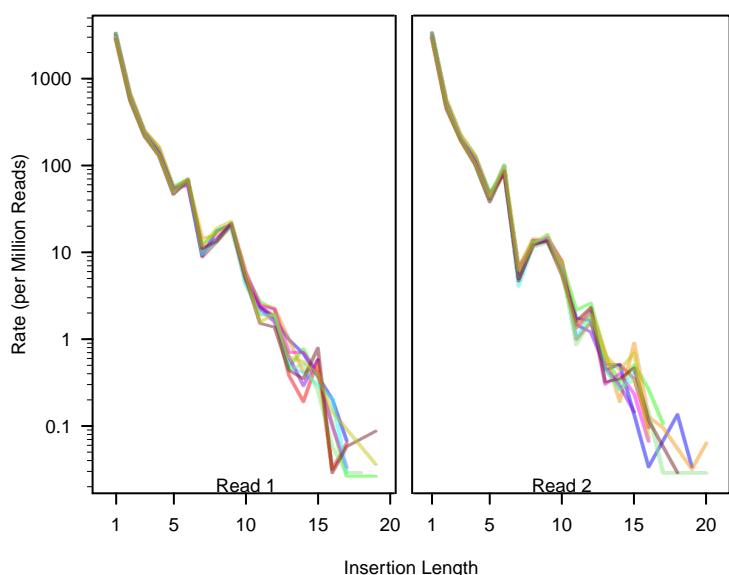
j

**Splice Junction Rate, by read cycle
Colored by Sample**



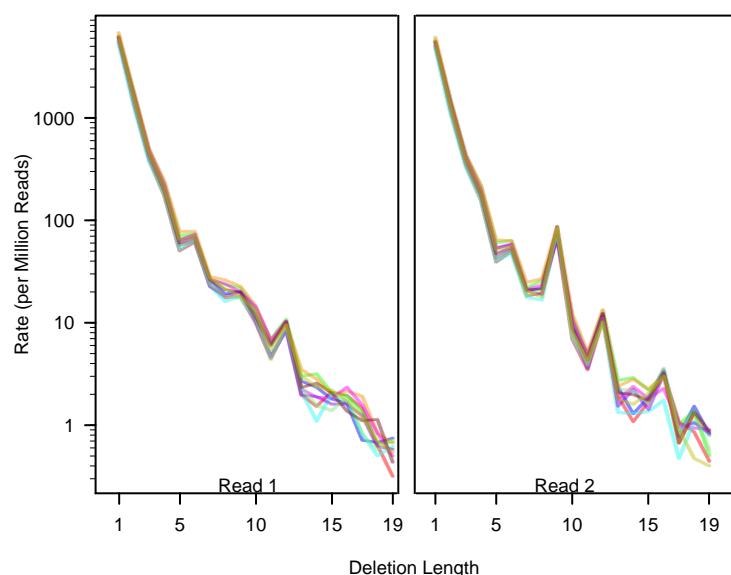
k

**Insertion Length Distribution
Colored by Sample**

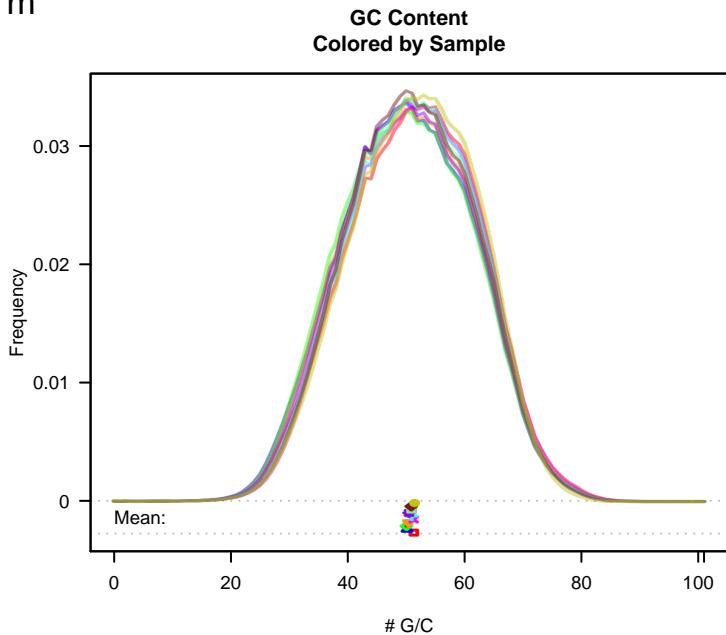


l

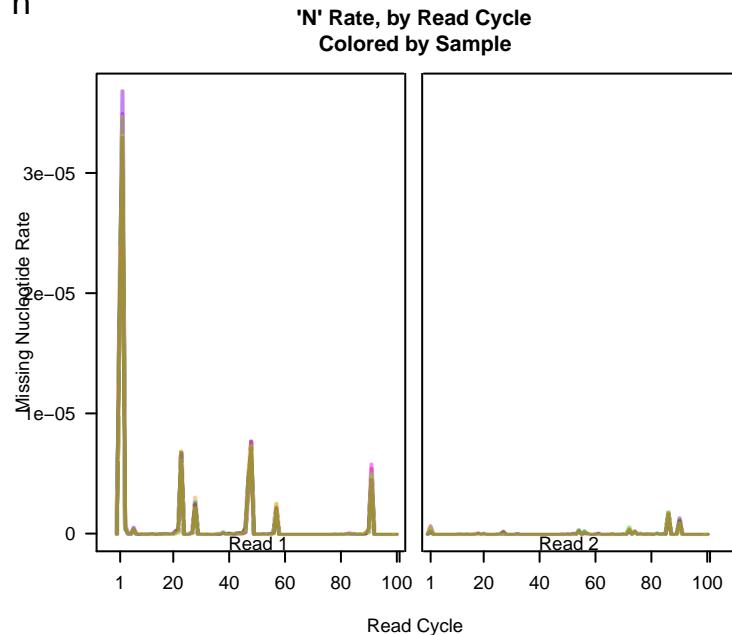
**Deletion Length Distribution
Colored by Sample**



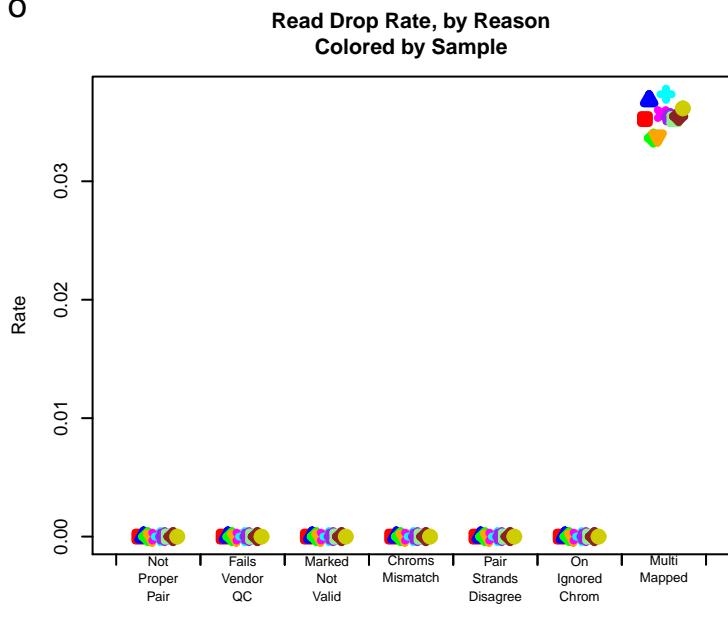
m



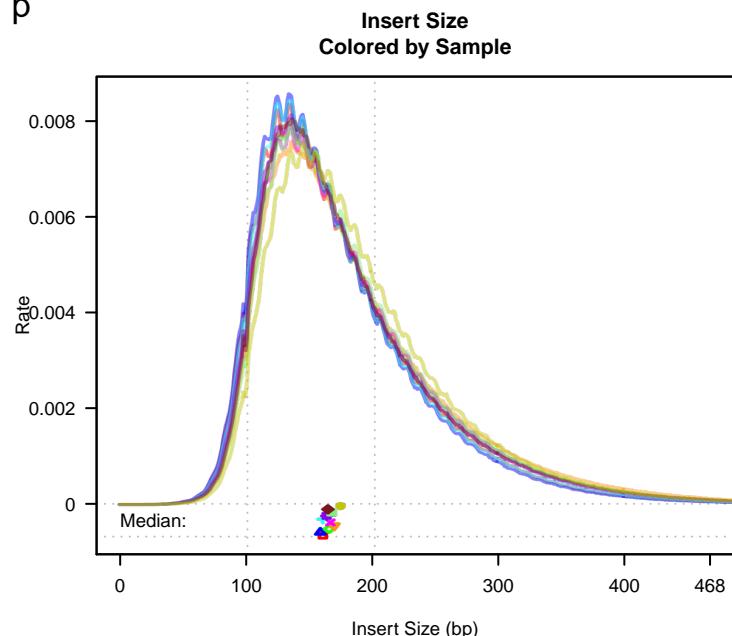
n



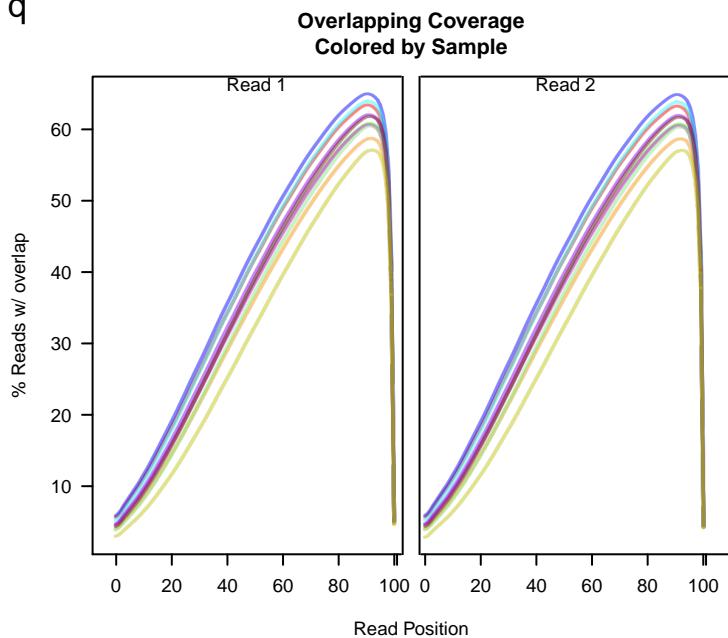
o



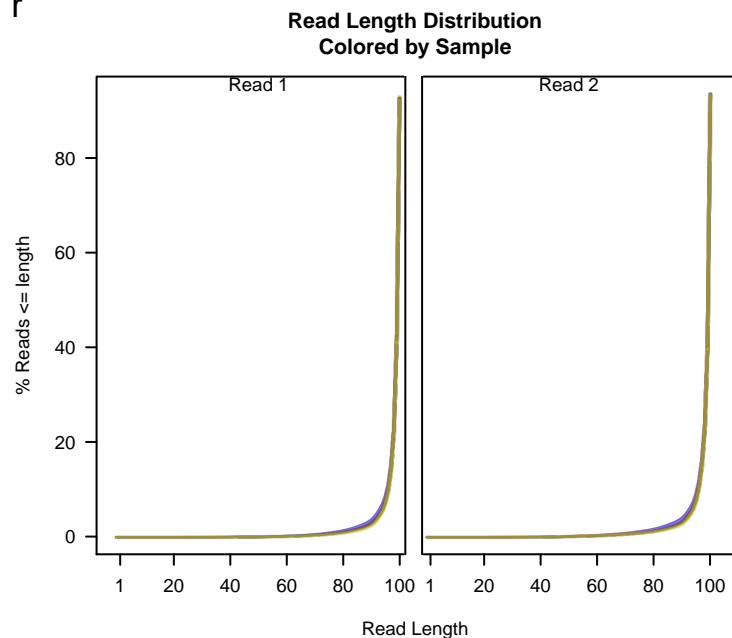
p



q

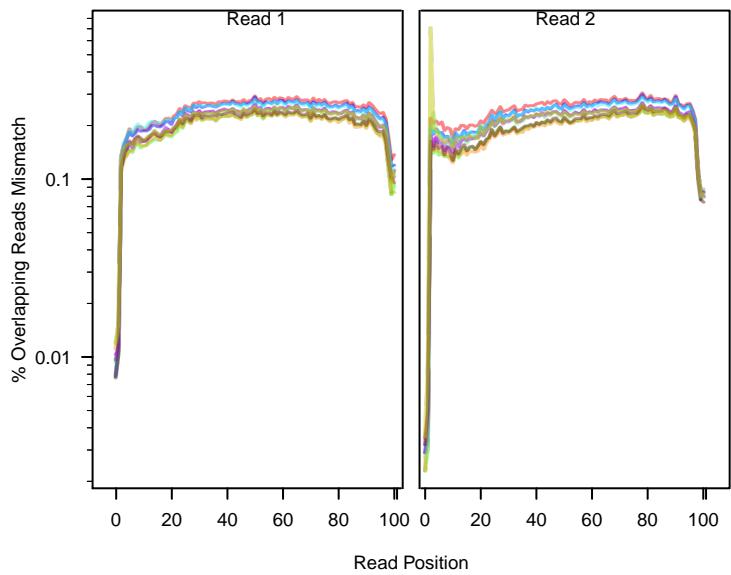


r



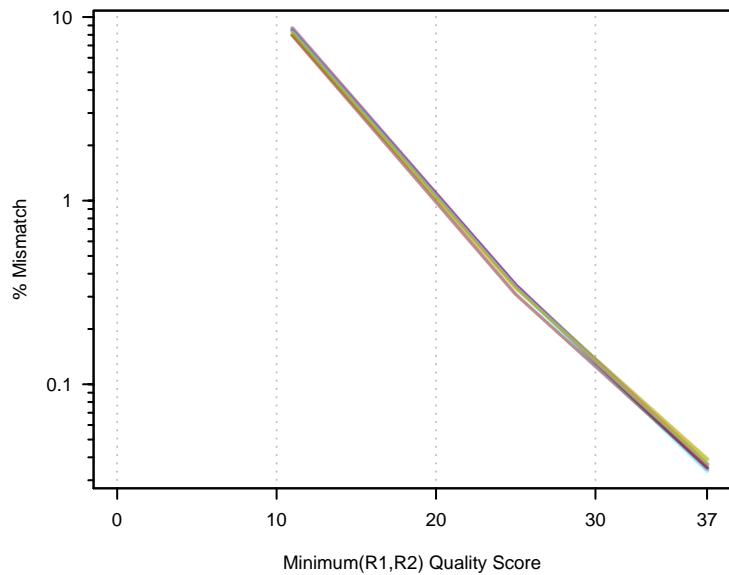
S

**Overlap Mismatch by Read Cycle
Colored by Sample**



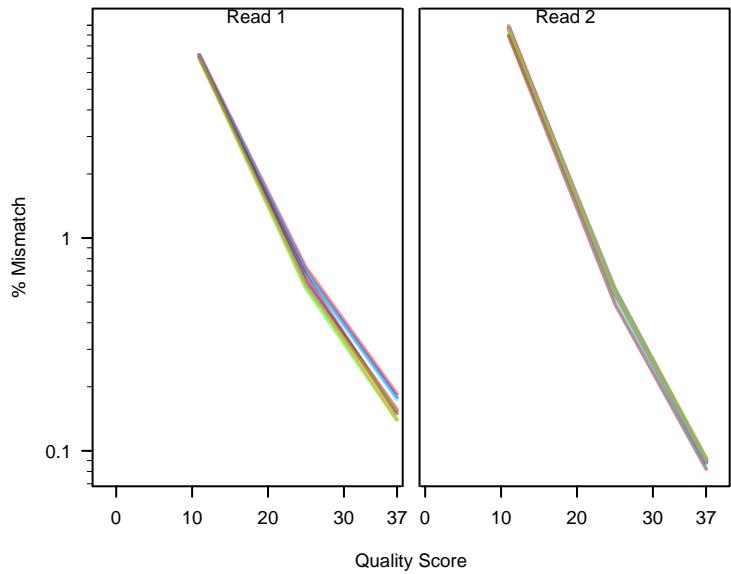
t

**Overlapping Mismatch by Min Qual
Colored by Sample**



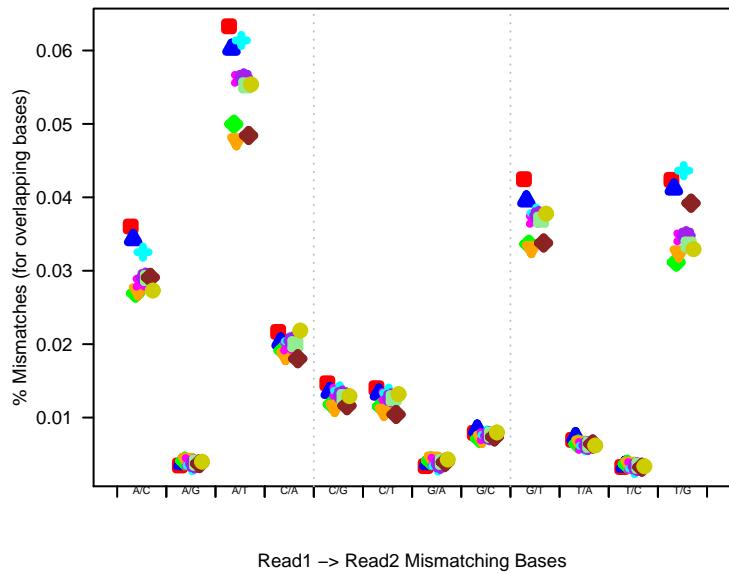
U

**Overlap Mismatch by Read Qual
Colored by Sample**



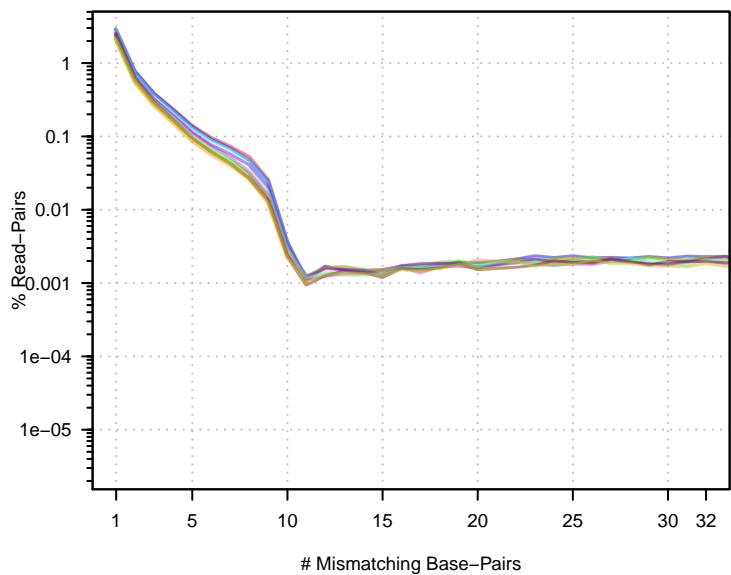
V

**Overlap Mismatch Combinations
Colored by Sample**



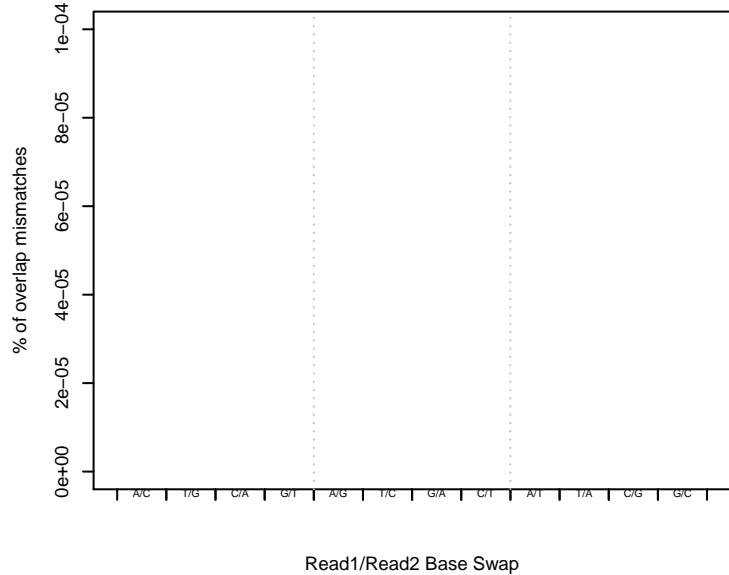
W

**Overlap Mismatch Size Frequency
Colored by Sample**



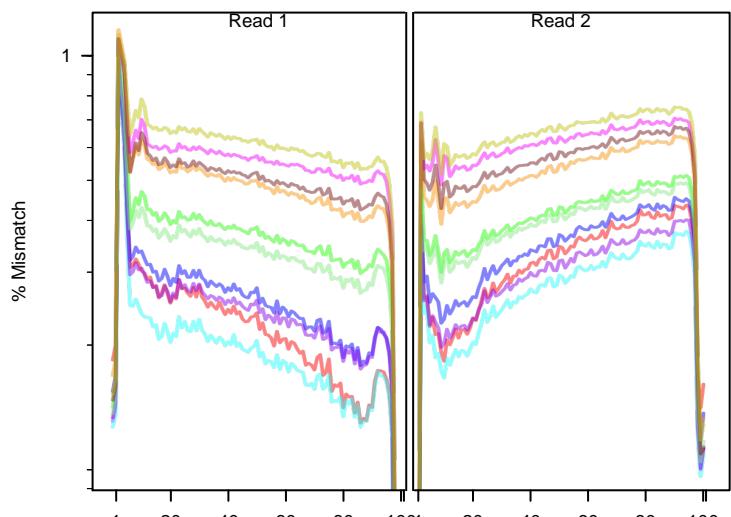
X

**Overlap Mismatch Pairs At Phred == 41
Colored by Sample**



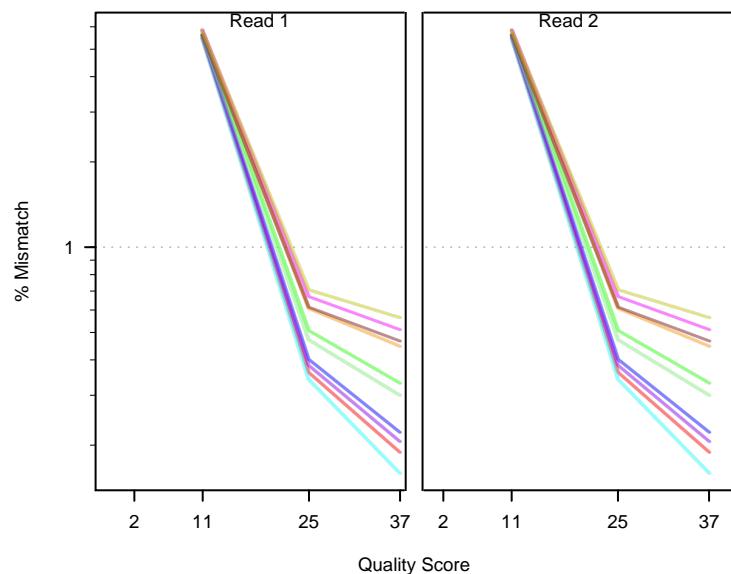
y

**Reference Mismatch by Read Cycle
Colored by Sample**



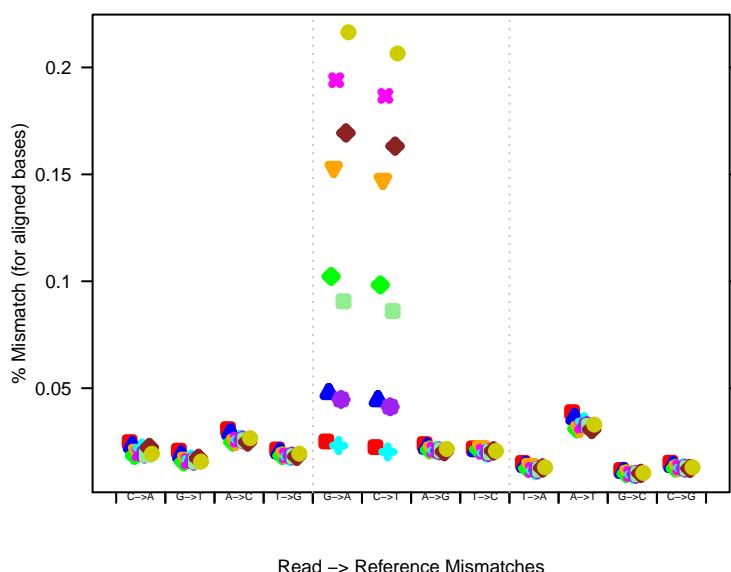
Z

**Reference Mismatch by Read Qual
Colored by Sample**



aa

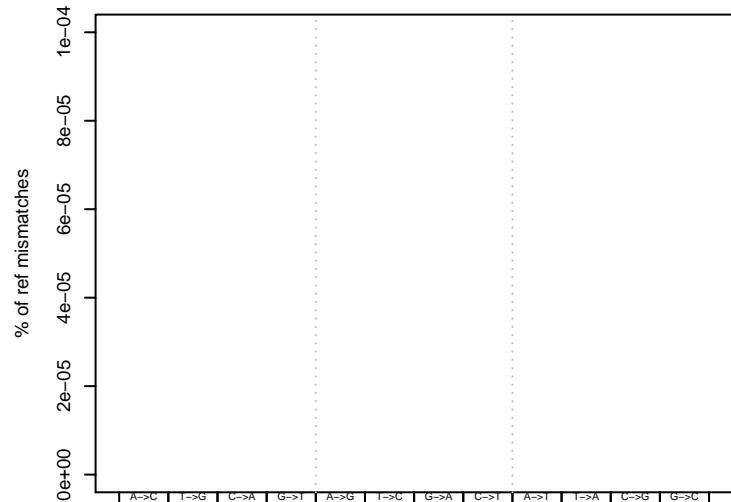
**Reference Mismatch Combinations
Colored by Sample**



Read → Reference Mismatches

ab

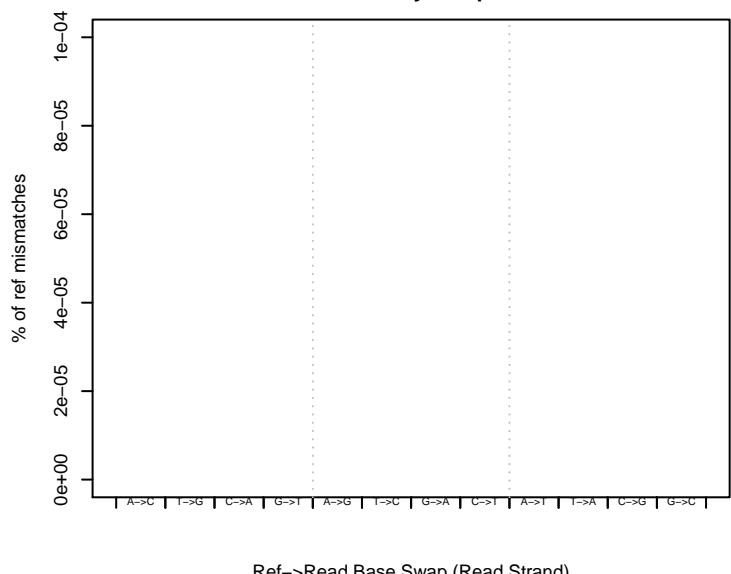
**R1 Ref Mismatches At Phred == 41
Colored by Sample**



Ref->Read Base Swap (Read Strand)

ac

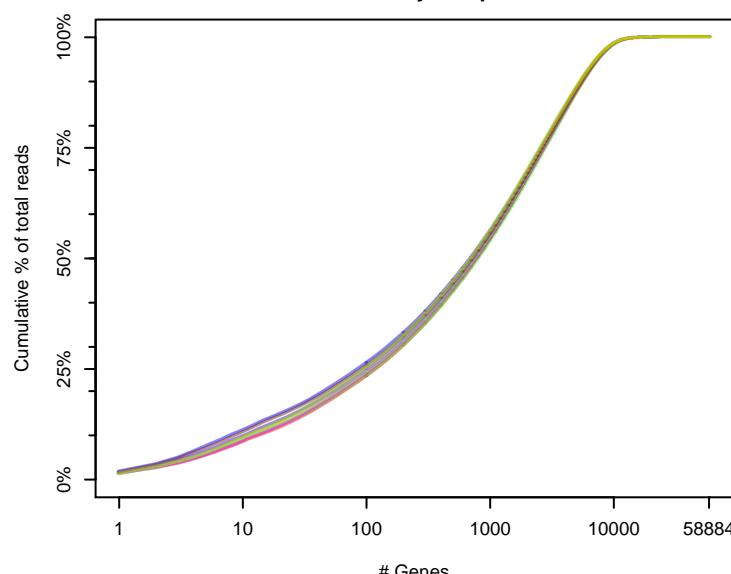
**R2 Ref Mismatches At Phred == 41
Colored by Sample**



Ref->Read Base Swap (Read Strand)

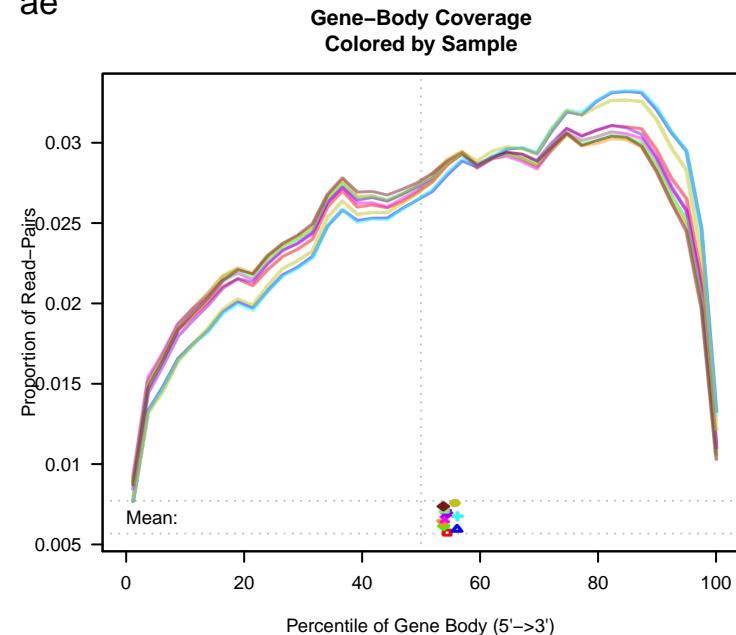
ad

**Cumulative Gene Assignment Diversity
Colored by Sample**

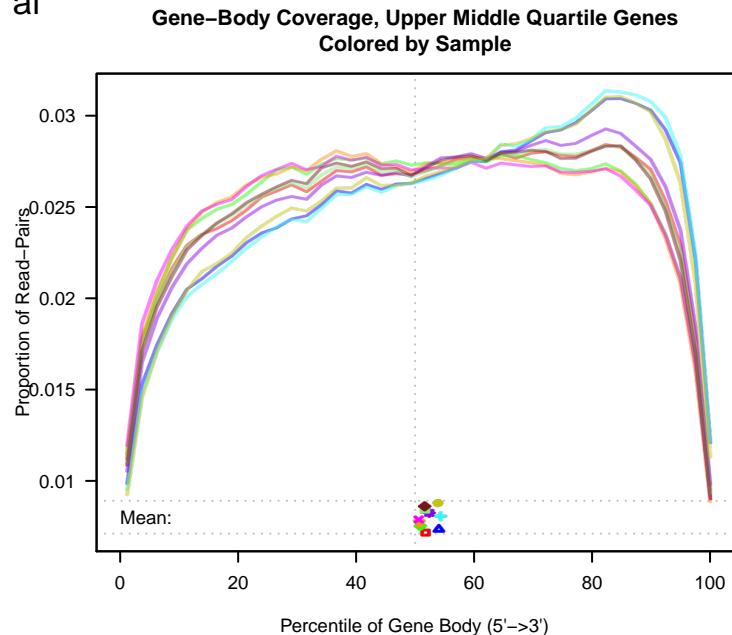


Genes

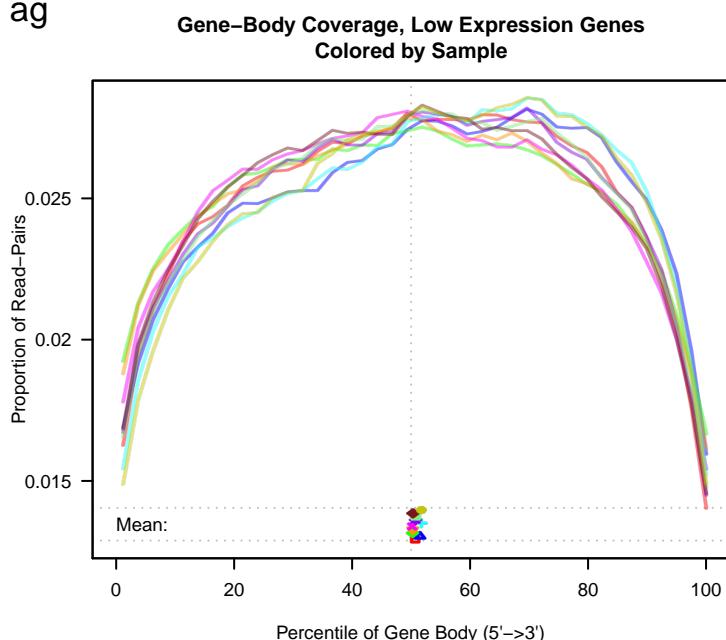
ae



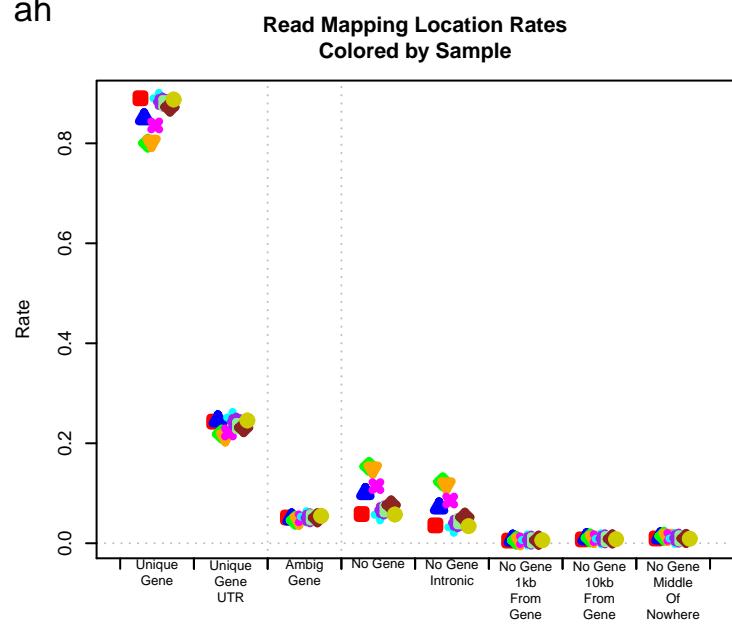
af



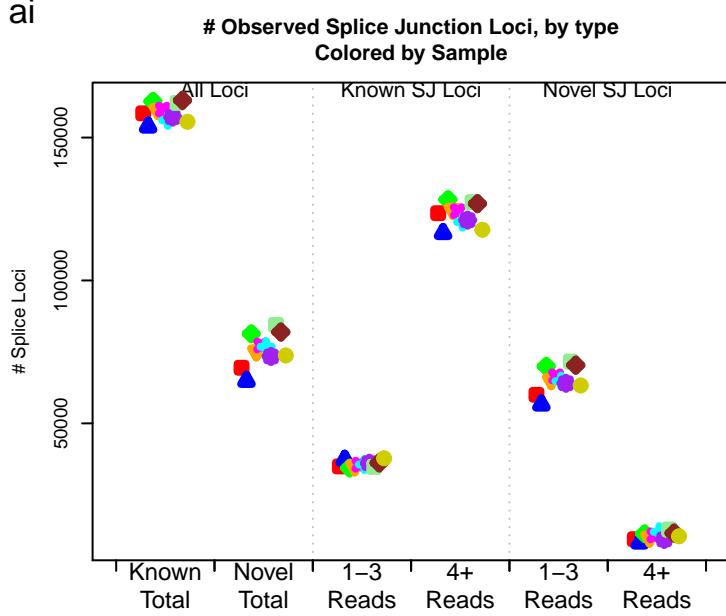
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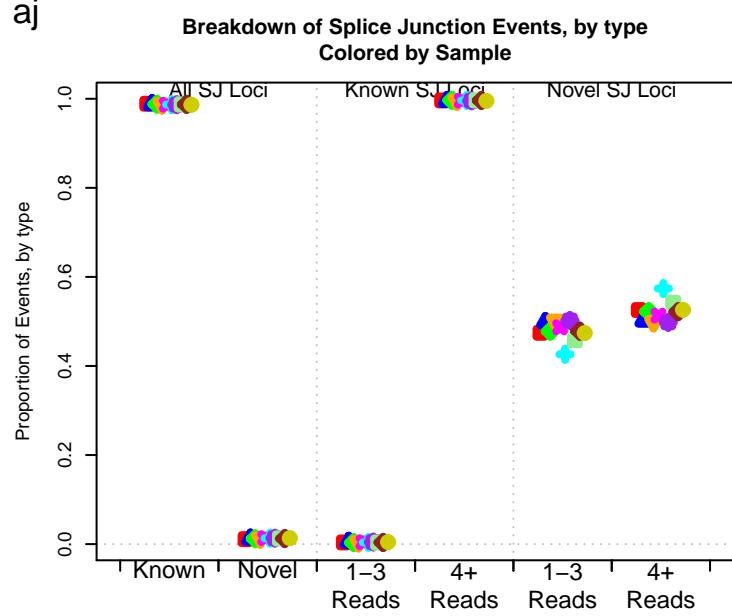
ah



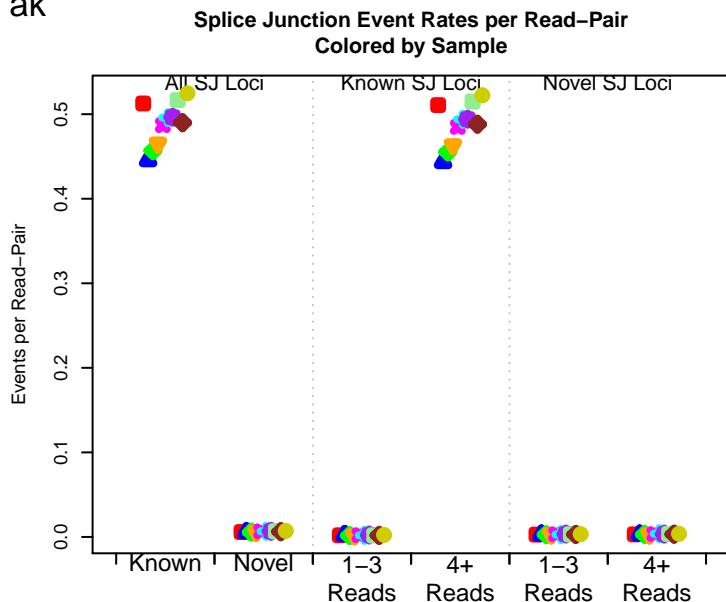
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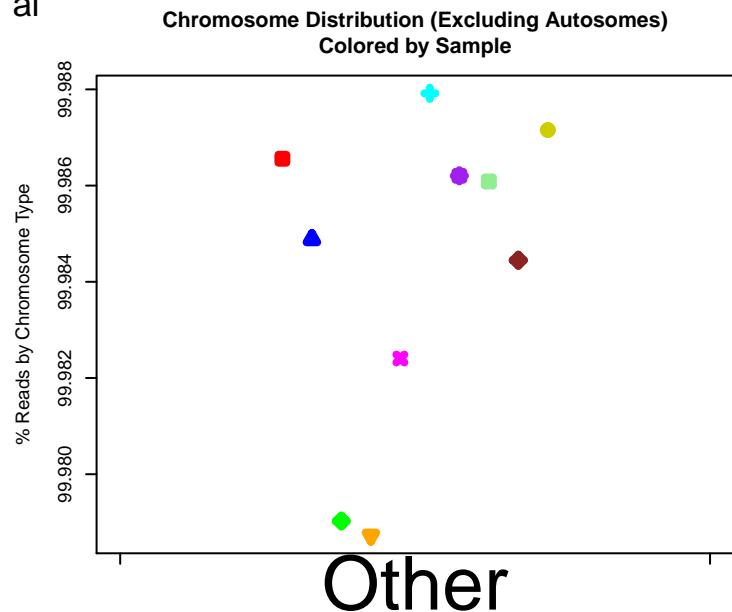
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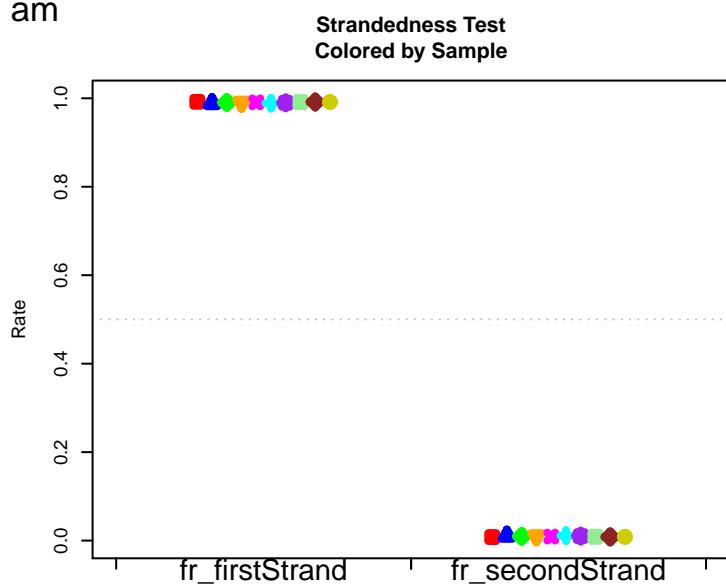
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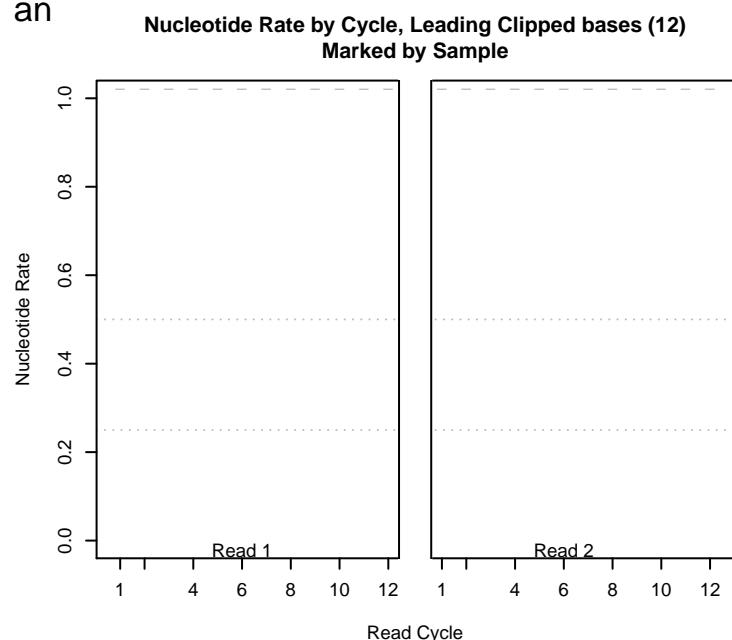
al



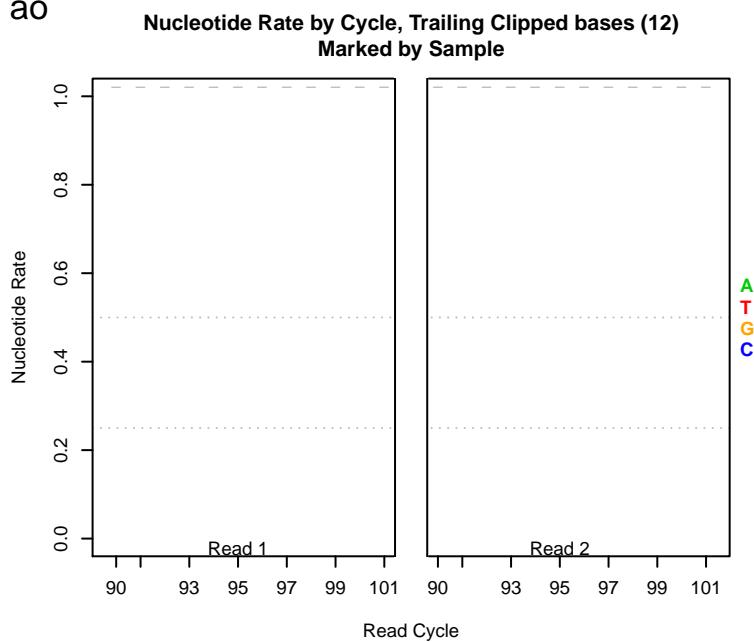
am



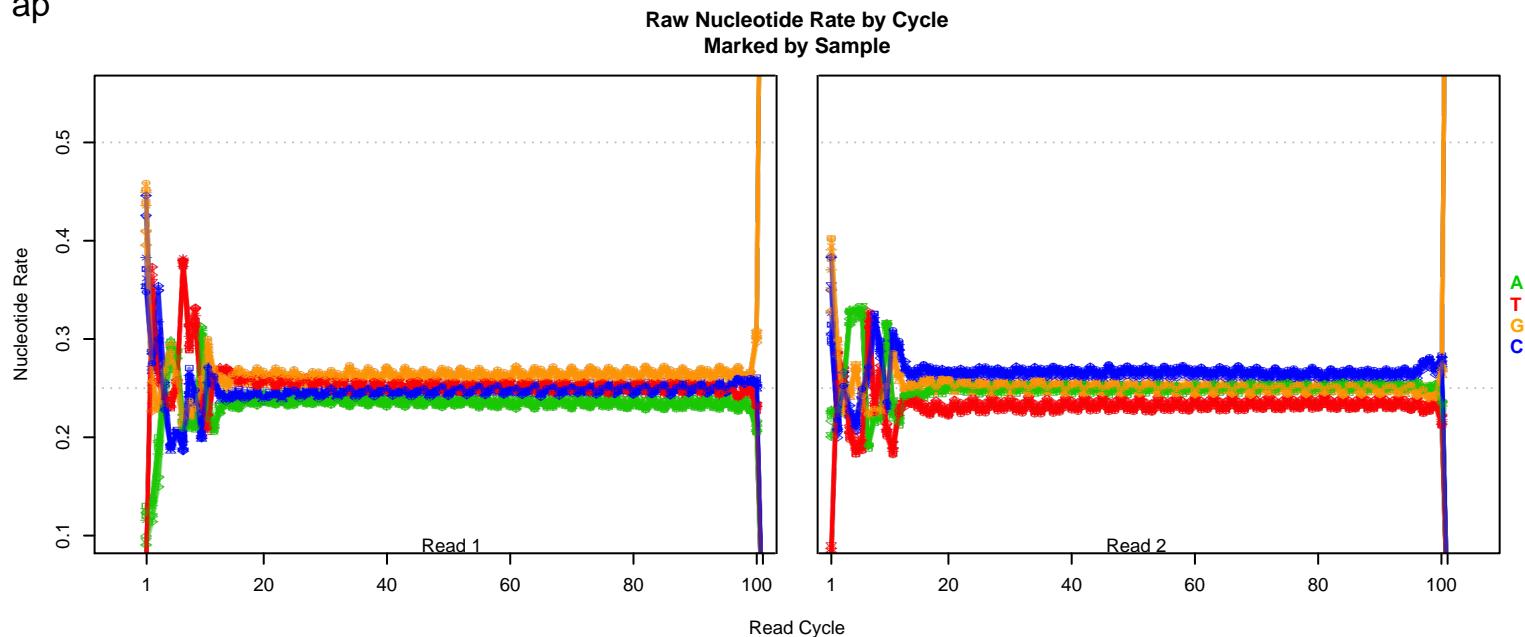
an



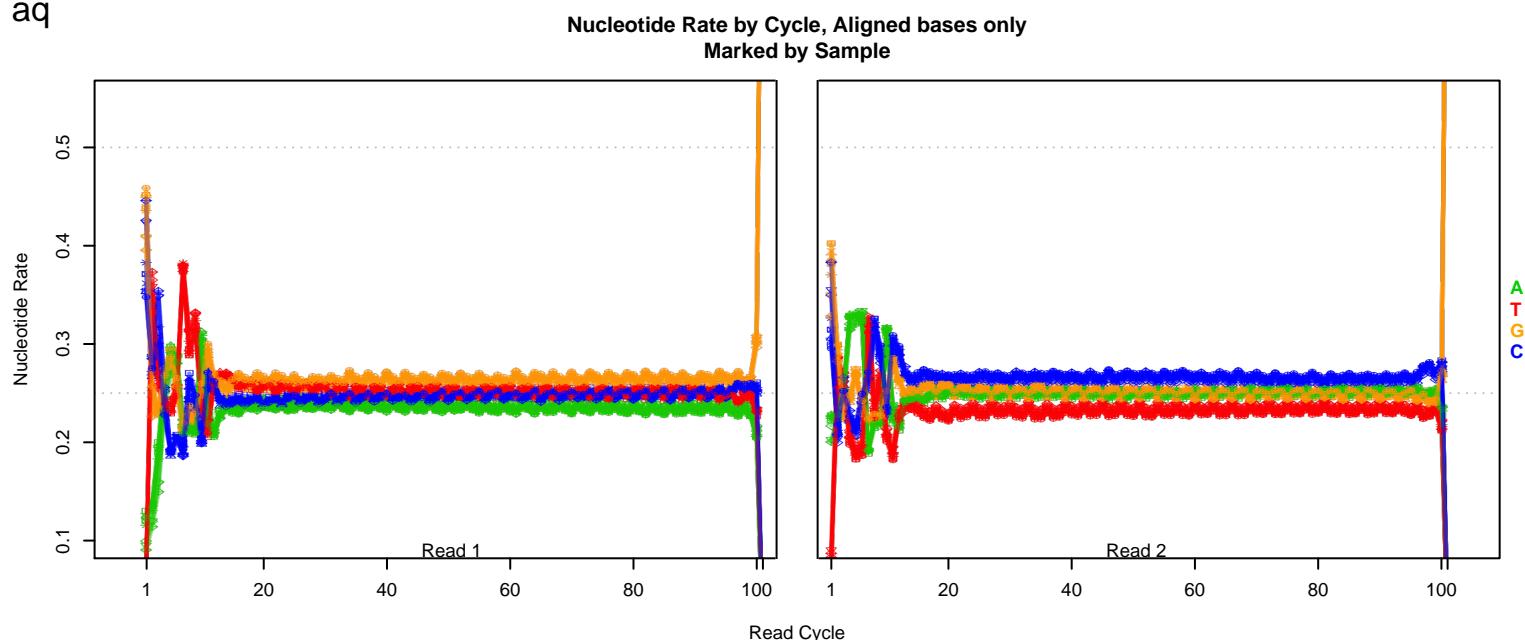
ao



ap

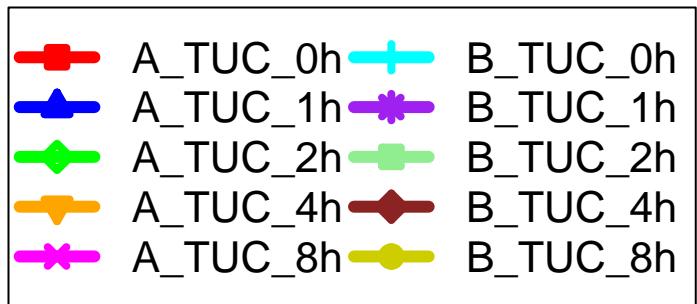


aq



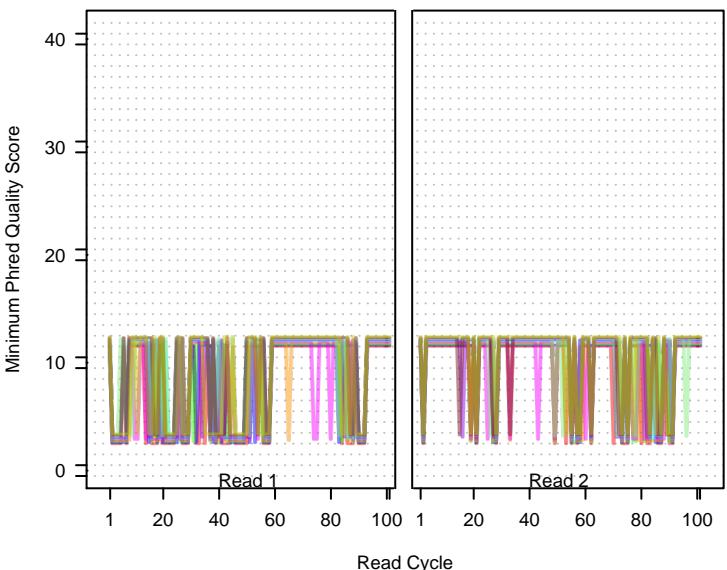
a

Summary Plots, By Sample



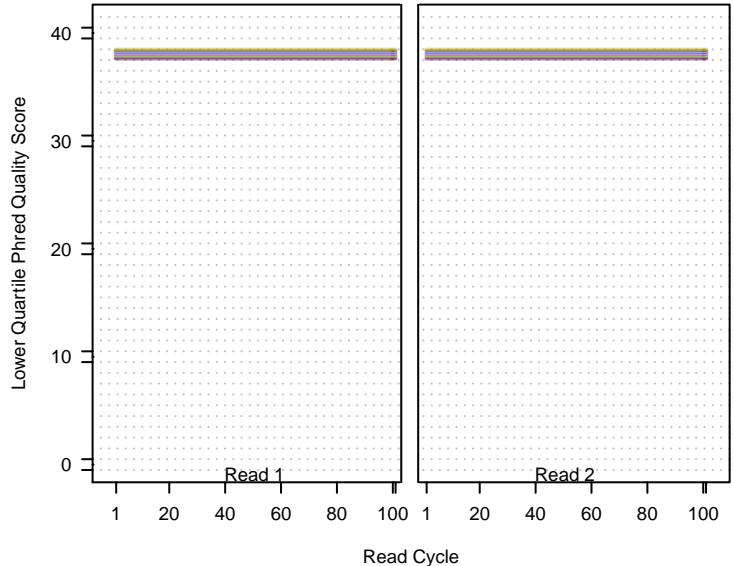
b

Minimum Phred Quality Score
Colored by Sample



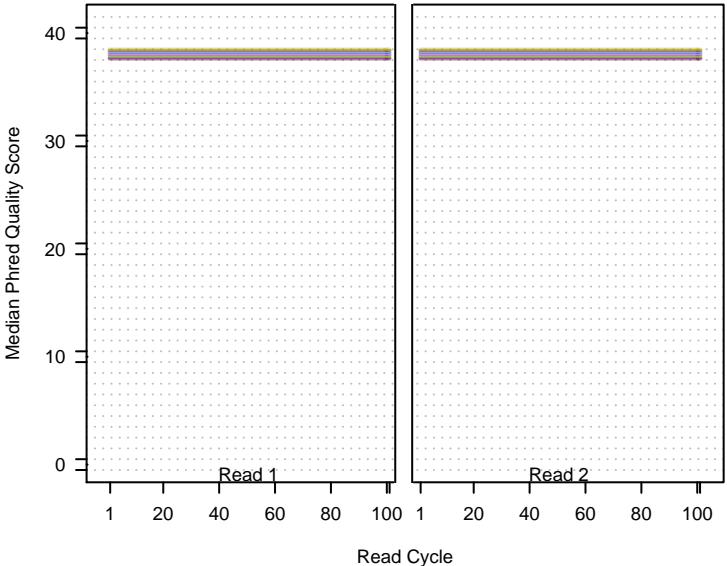
c

Lower Quartile Phred Quality Score
Colored by Sample



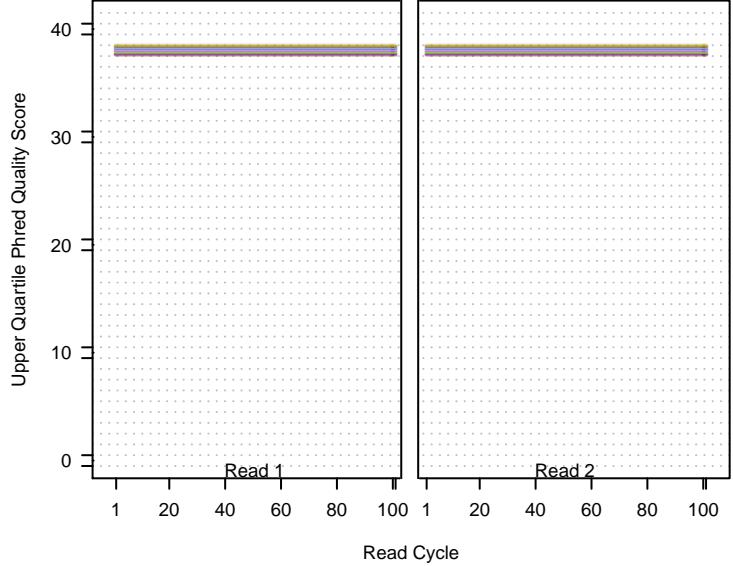
d

Median Phred Quality Score
Colored by Sample



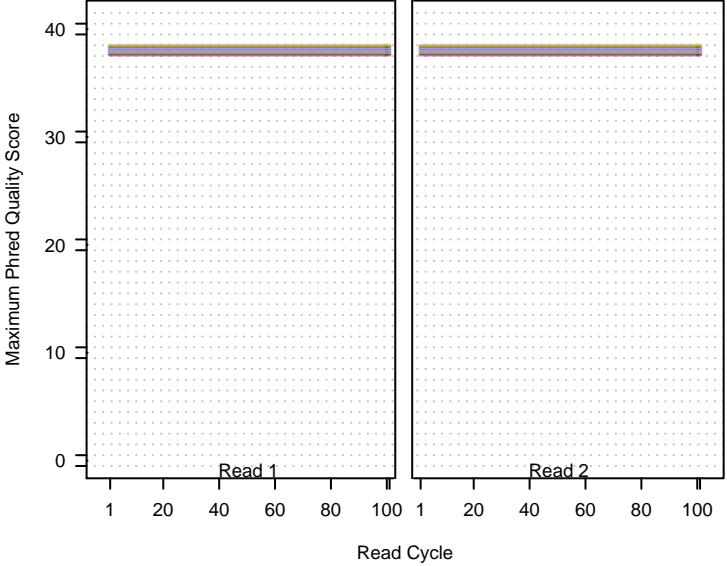
e

Upper Quartile Phred Quality Score
Colored by Sample



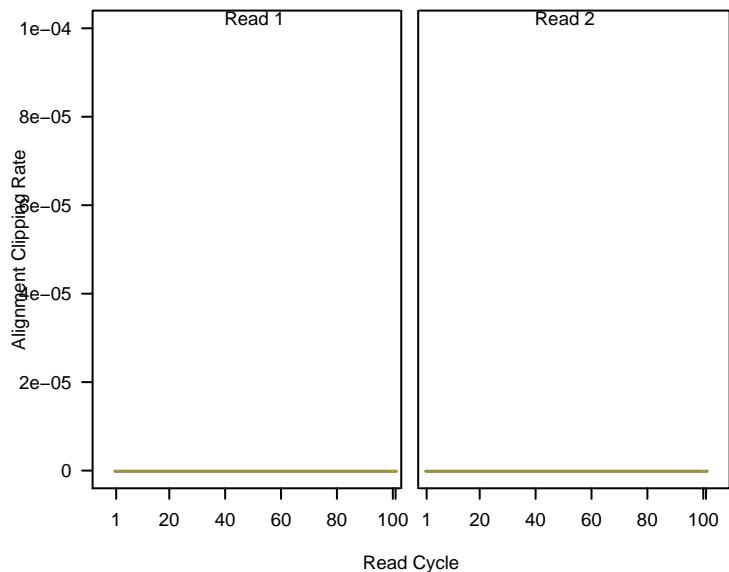
f

Maximum Phred Quality Score
Colored by Sample



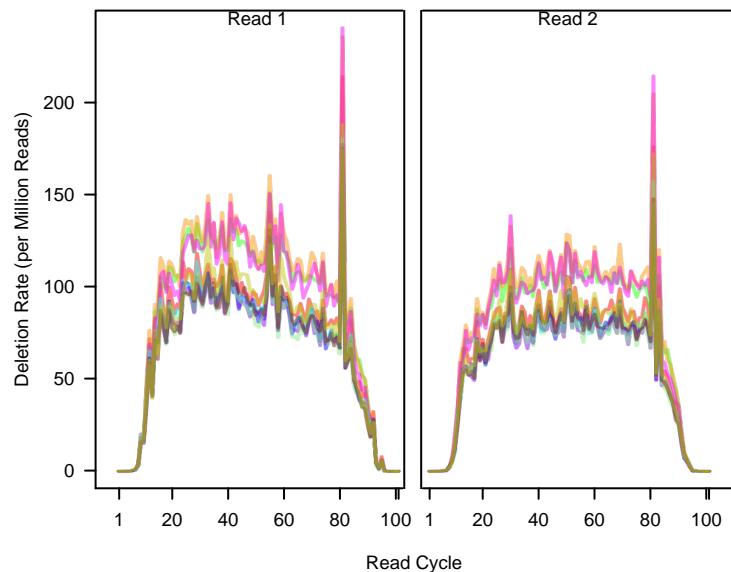
g

**Alignment Clipping Rate, by read cycle
Colored by Sample**



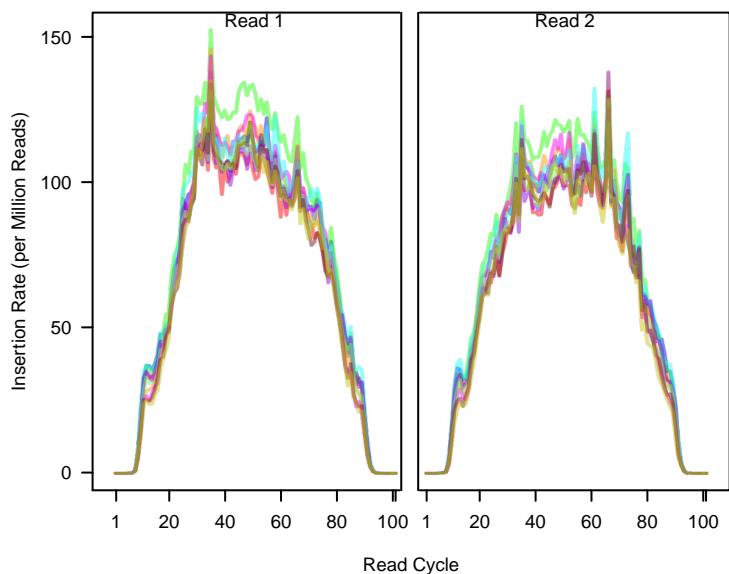
h

**Deletion Rate, by read cycle
Colored by Sample**



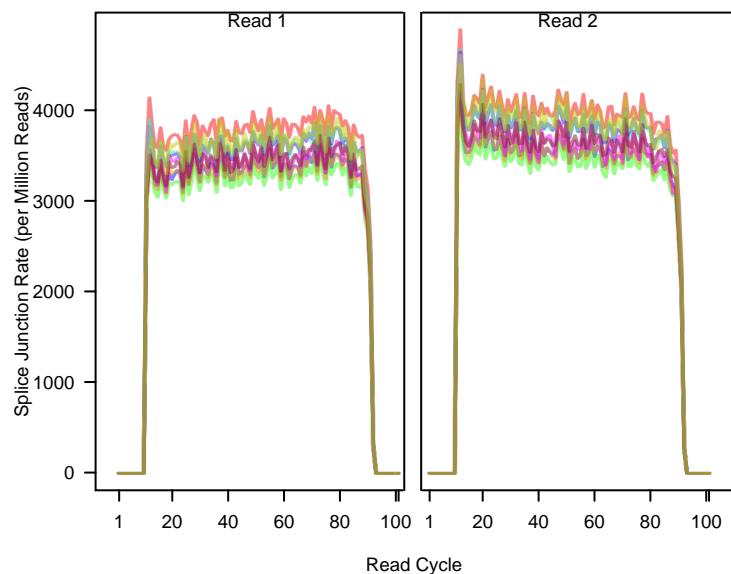
i

**Insertion Rate, by read cycle
Colored by Sample**



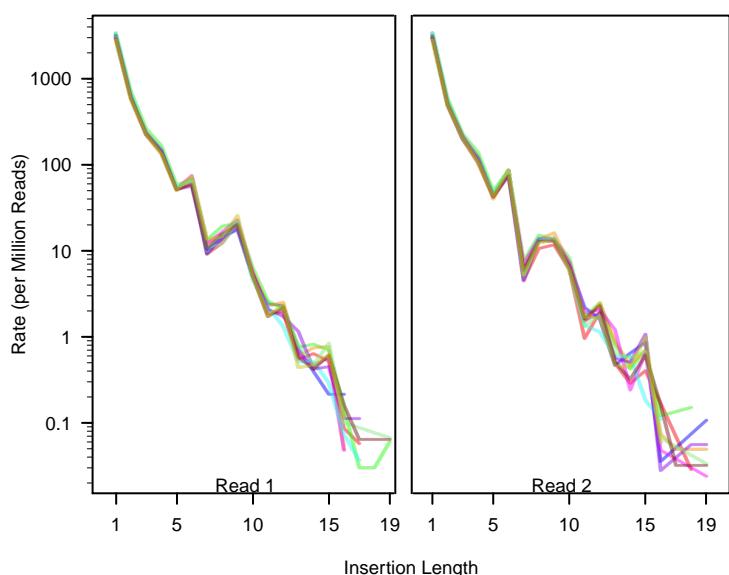
j

**Splice Junction Rate, by read cycle
Colored by Sample**



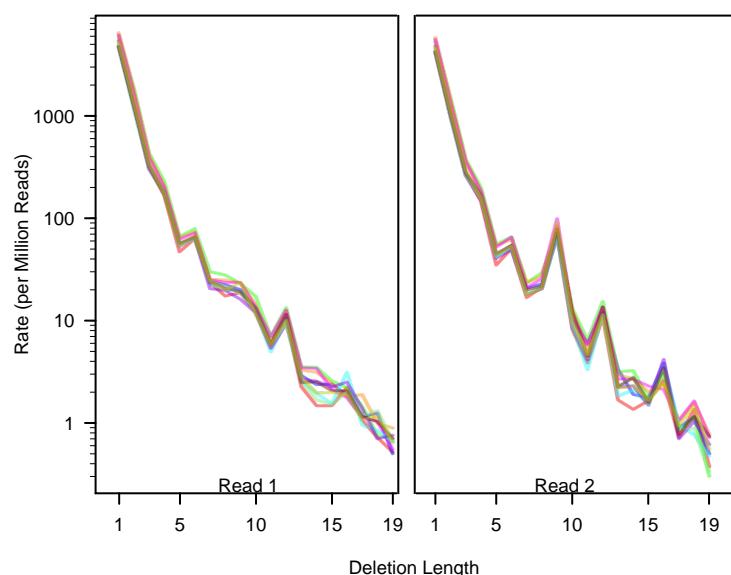
k

**Insertion Length Distribution
Colored by Sample**

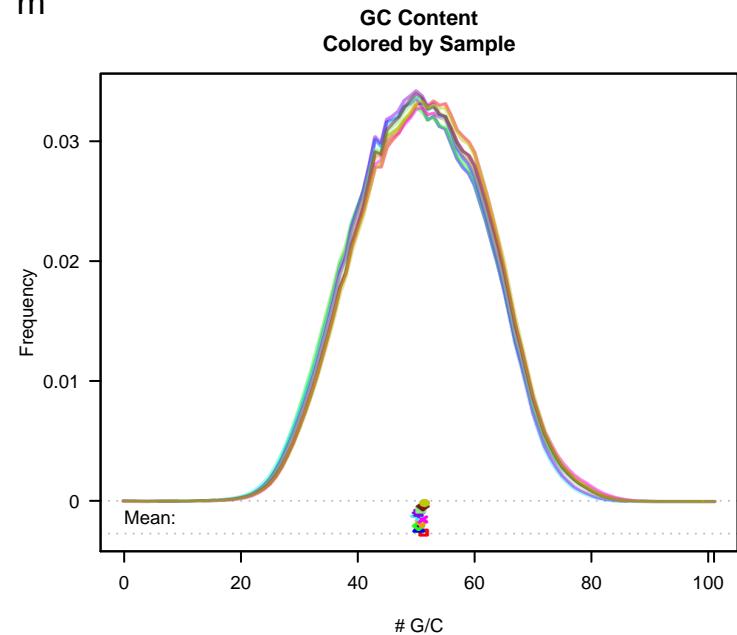


l

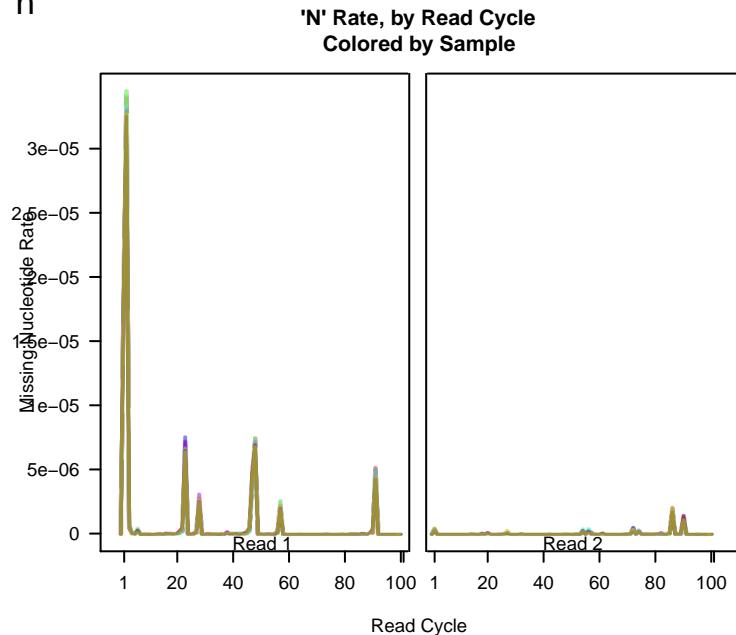
**Deletion Length Distribution
Colored by Sample**



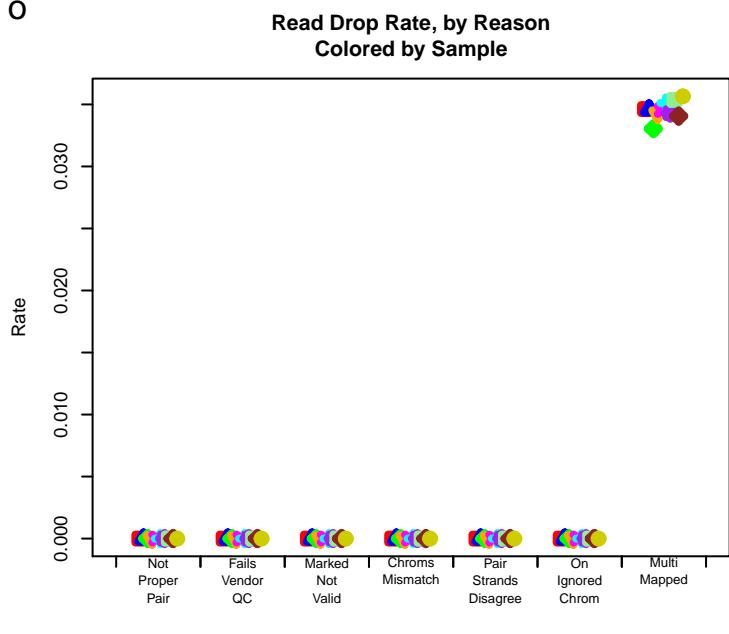
m



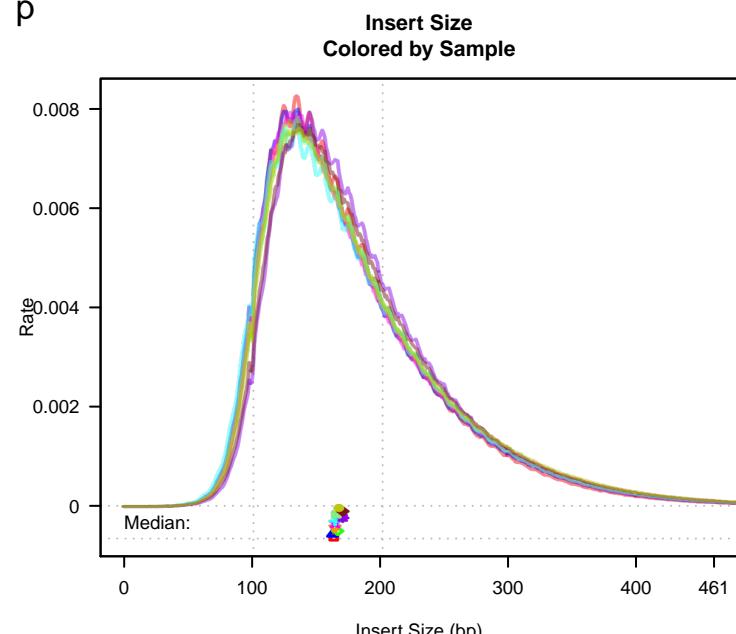
n



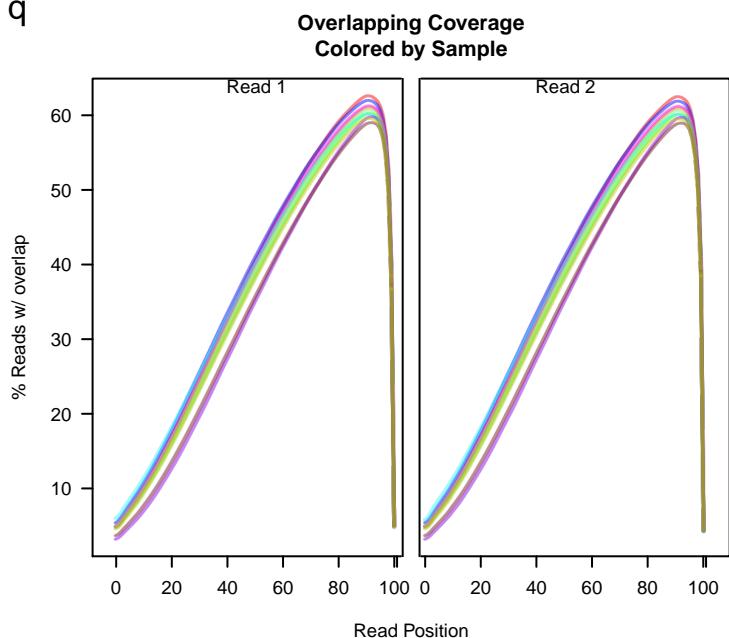
o



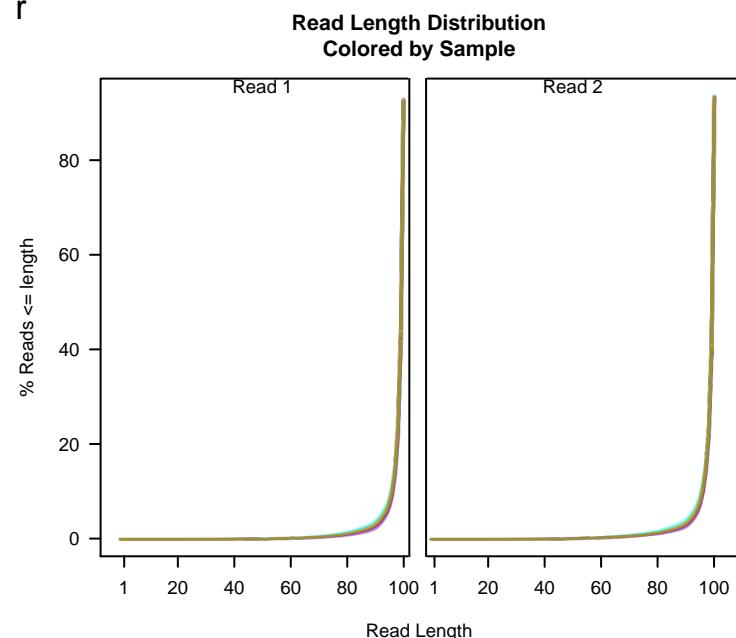
p



q

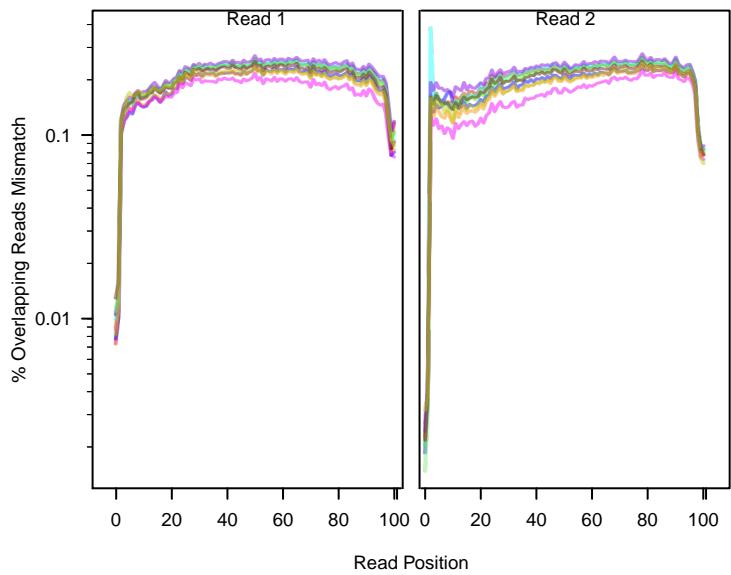


r



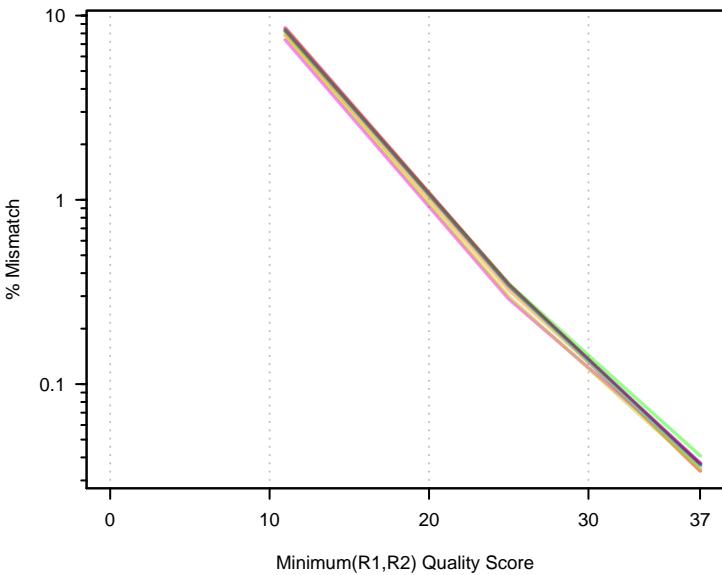
S

**Overlap Mismatch by Read Cycle
Colored by Sample**



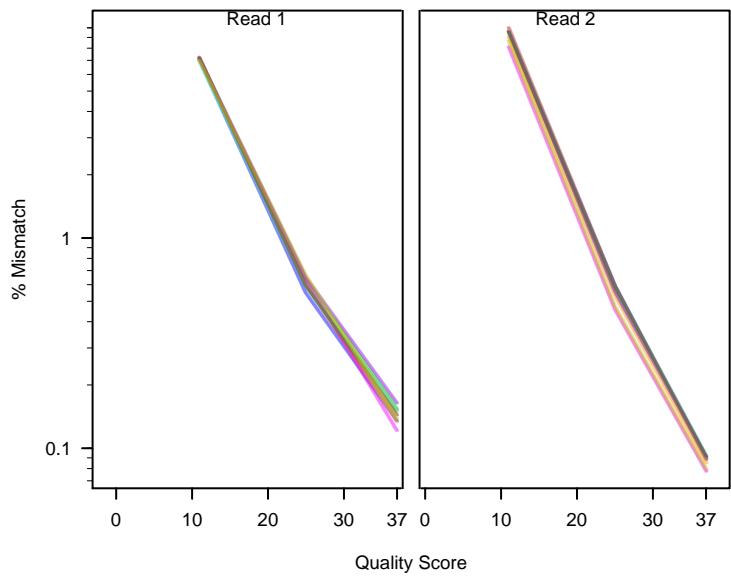
t

**Overlapping Mismatch by Min Qual
Colored by Sample**



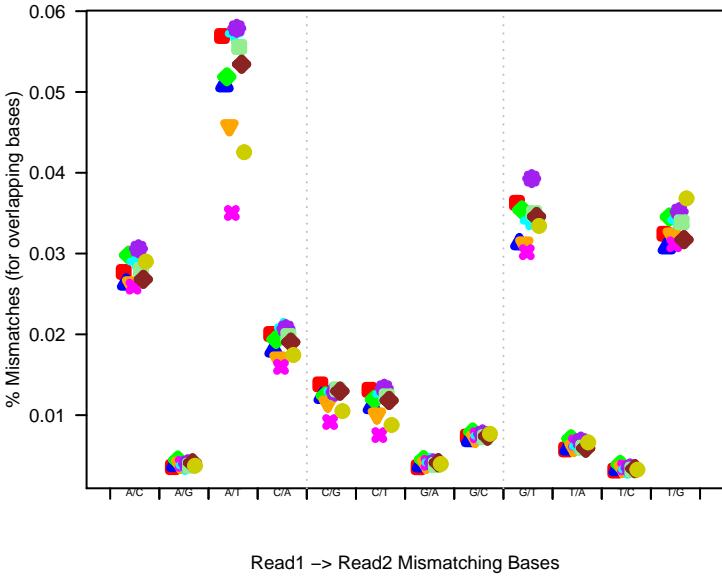
U

**Overlap Mismatch by Read Qual
Colored by Sample**



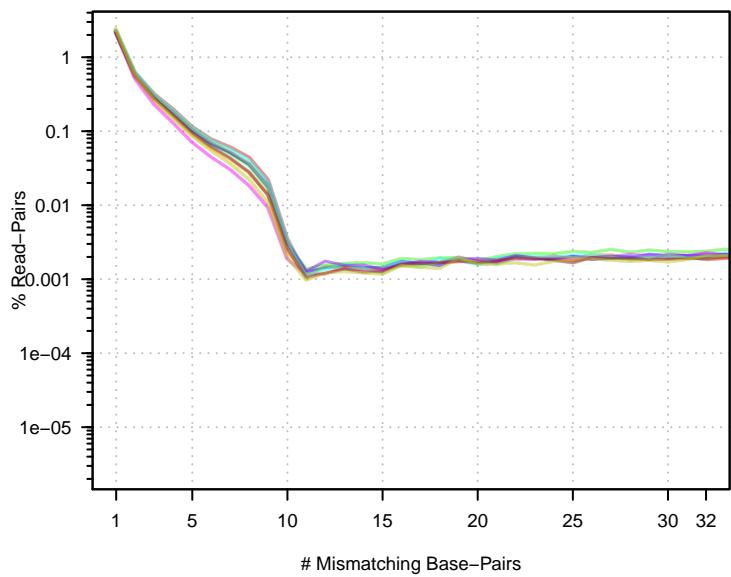
V

**Overlap Mismatch Combinations
Colored by Sample**



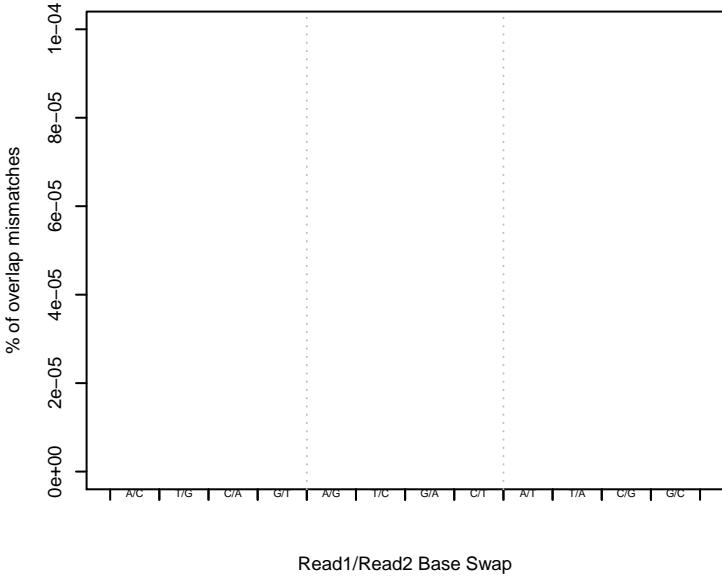
W

**Overlap Mismatch Size Frequency
Colored by Sample**



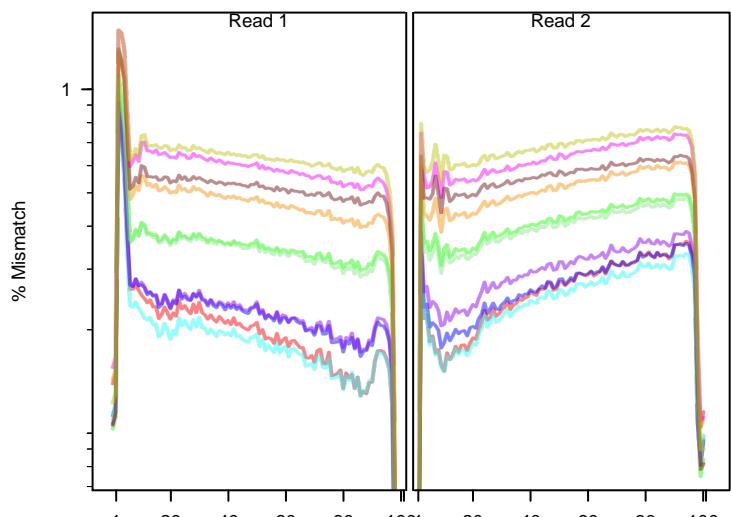
X

**Overlap Mismatch Pairs At Phred == 41
Colored by Sample**



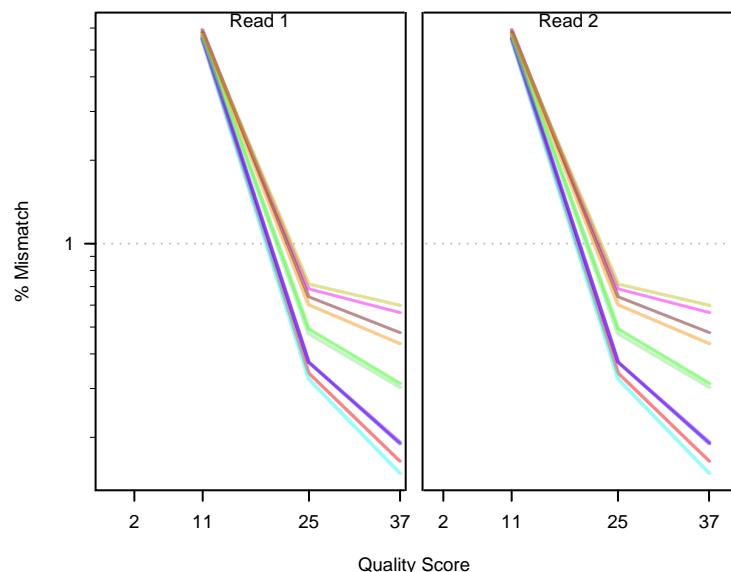
y

**Reference Mismatch by Read Cycle
Colored by Sample**



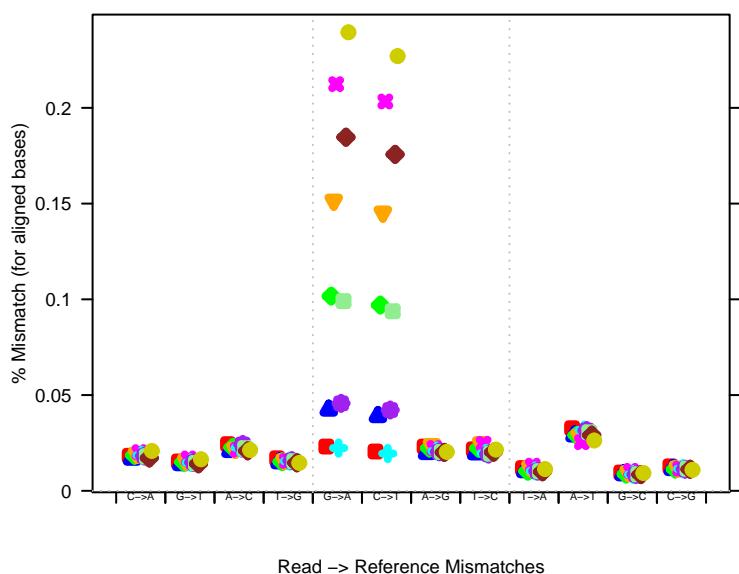
Z

**Reference Mismatch by Read Qual
Colored by Sample**



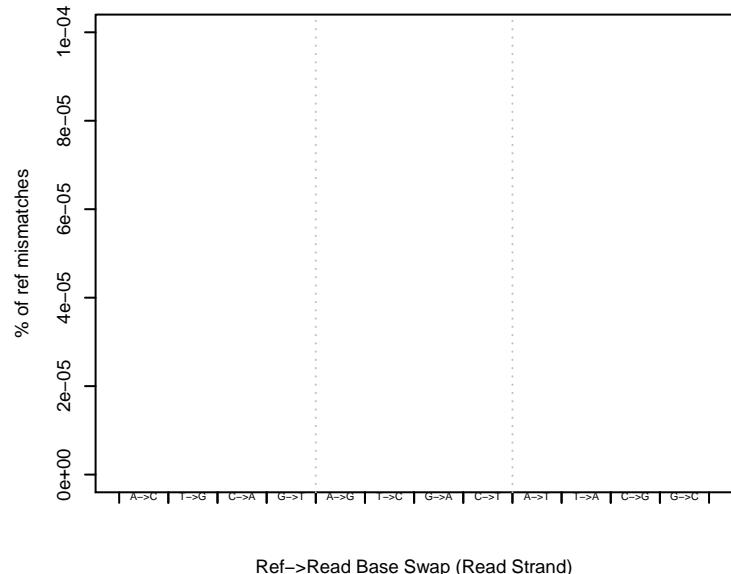
aa

**Reference Mismatch Combinations
Colored by Sample**



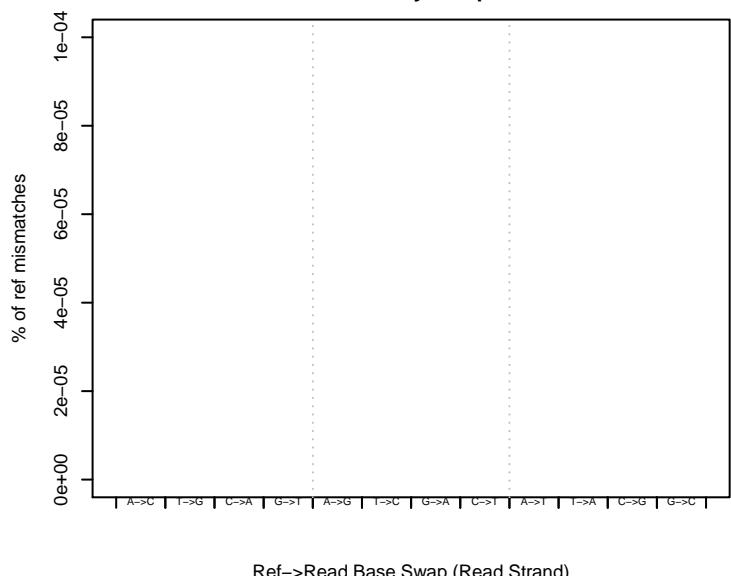
ab

**R1 Ref Mismatches At Phred == 41
Colored by Sample**



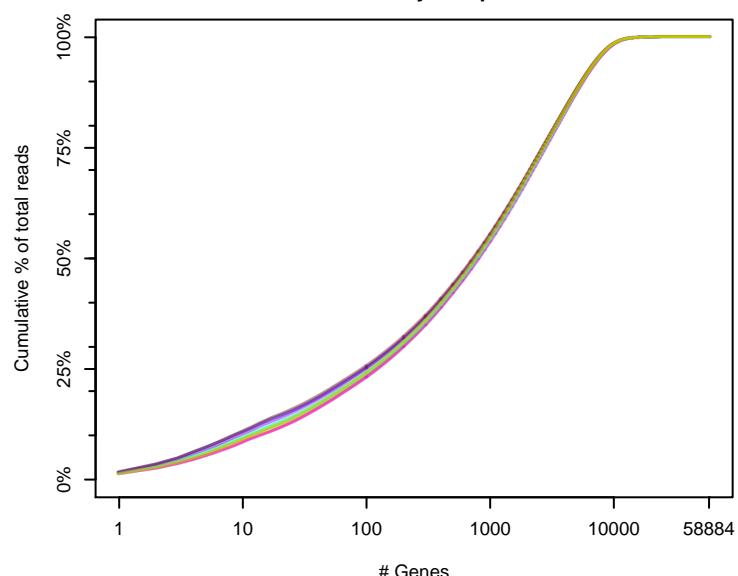
ac

**R2 Ref Mismatches At Phred == 41
Colored by Sample**

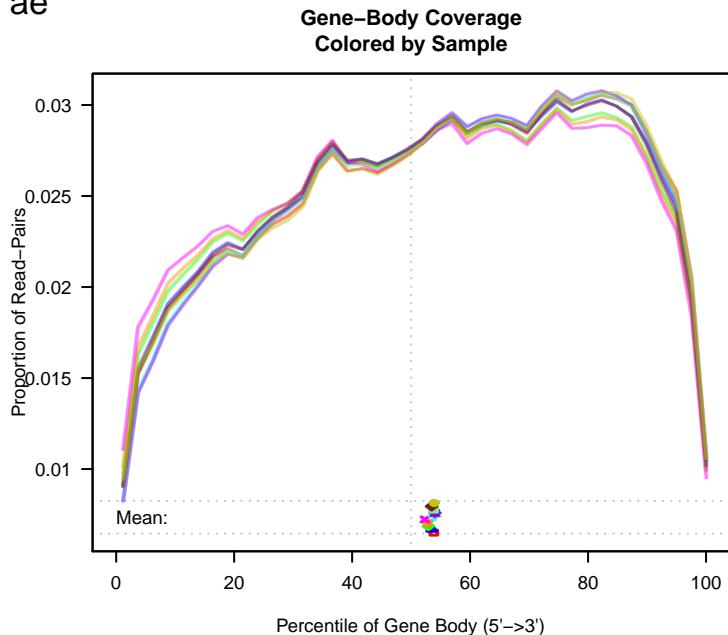


ad

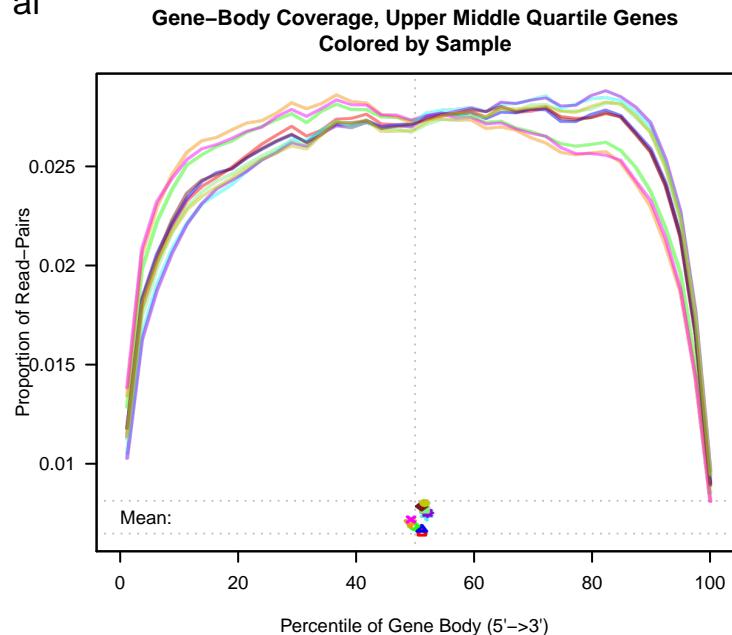
**Cumulative Gene Assignment Diversity
Colored by Sample**



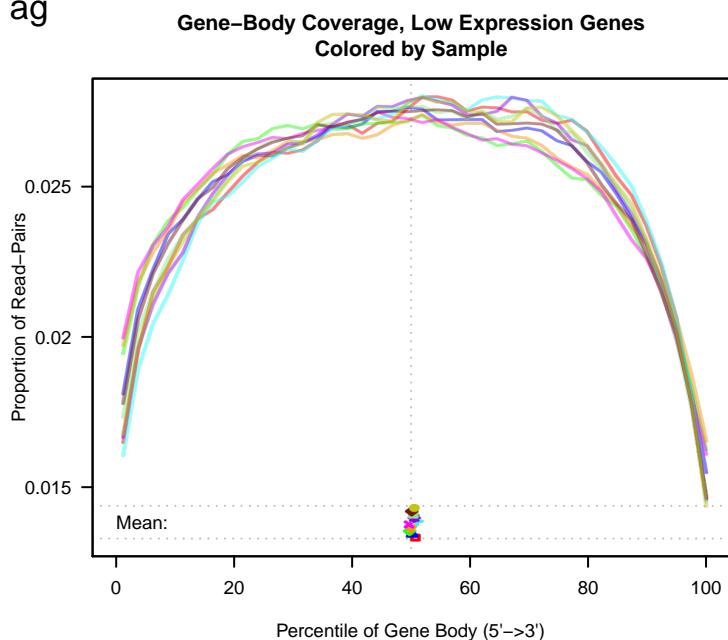
ae



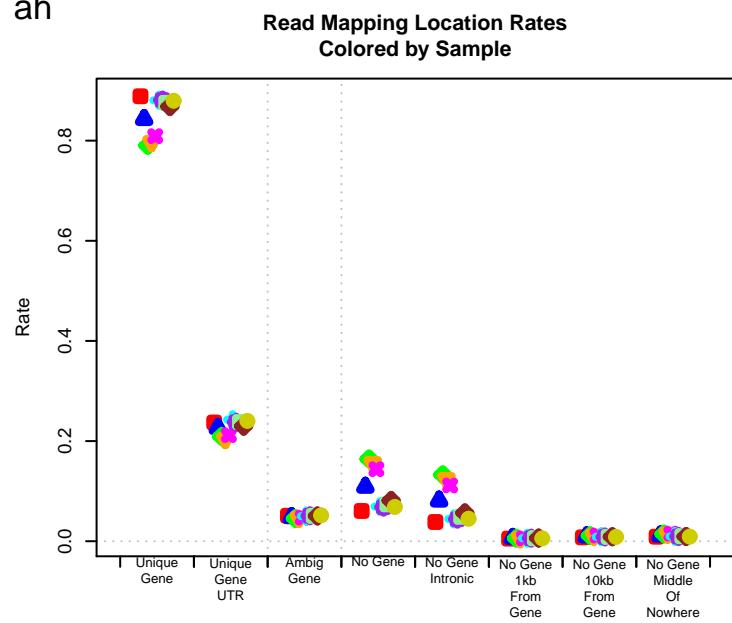
af



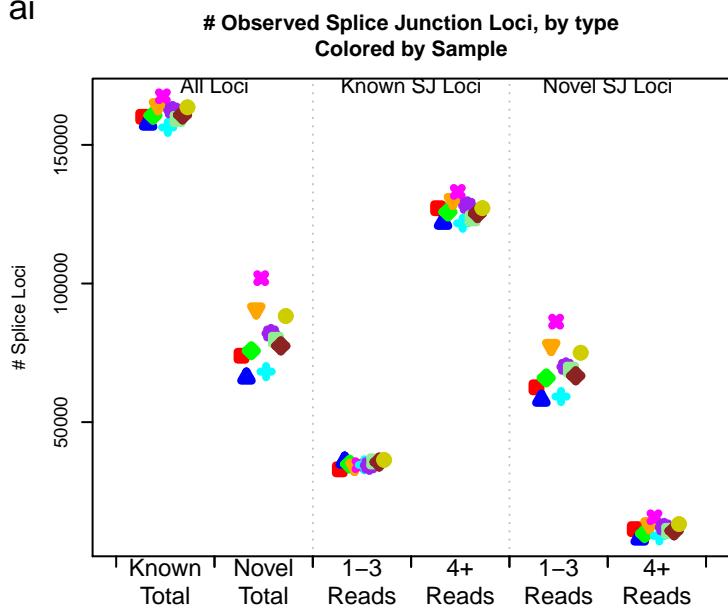
ag



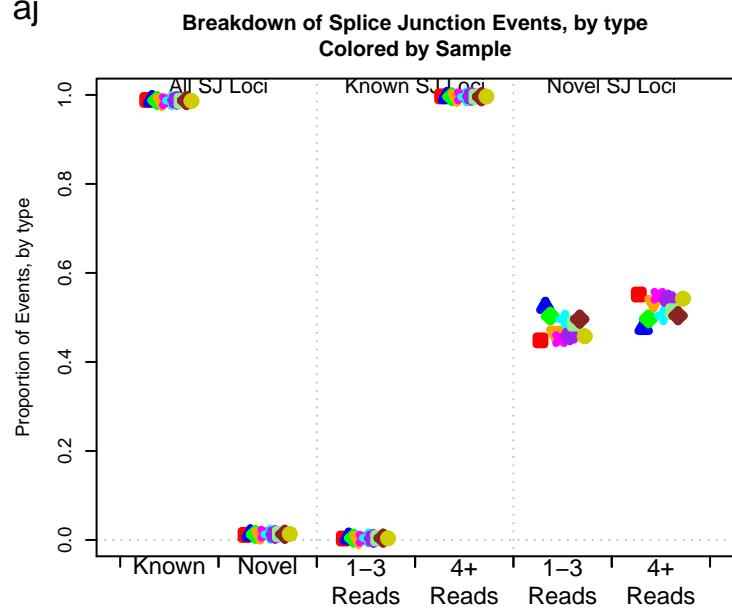
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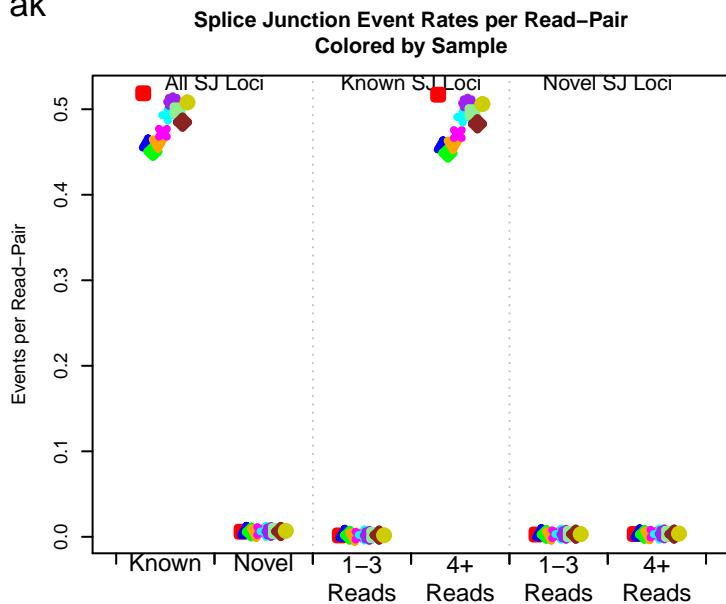
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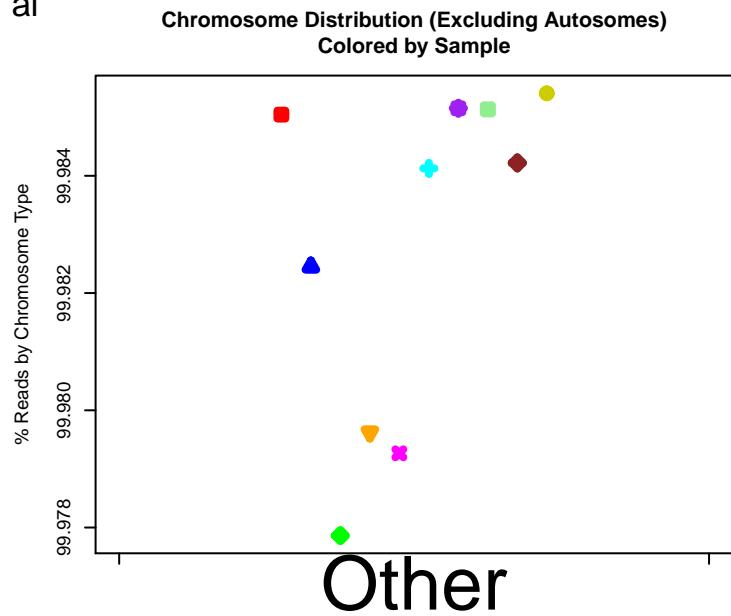
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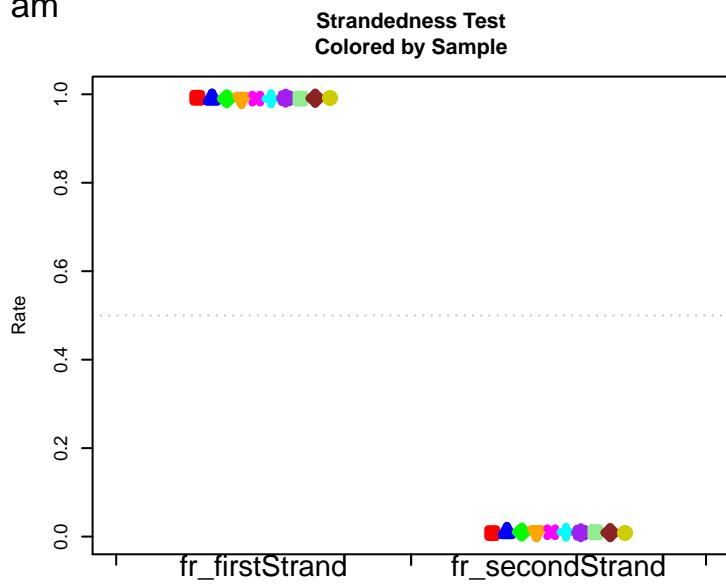


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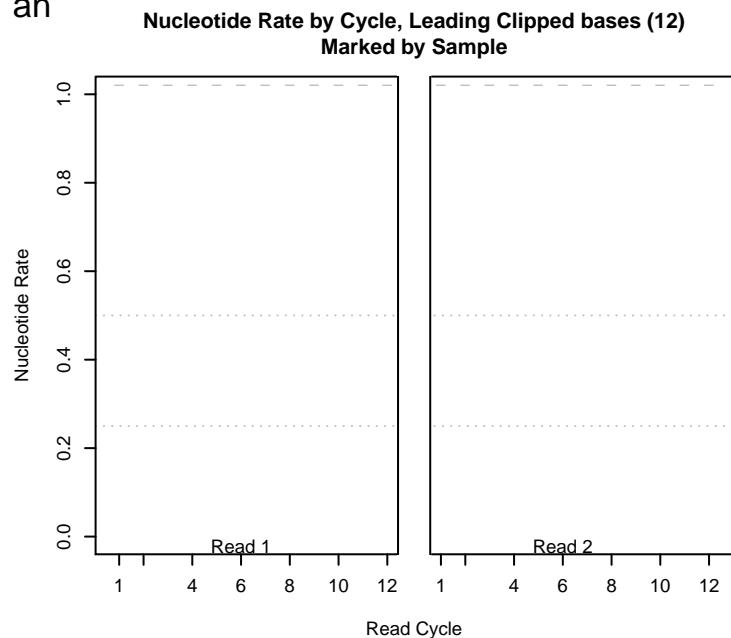


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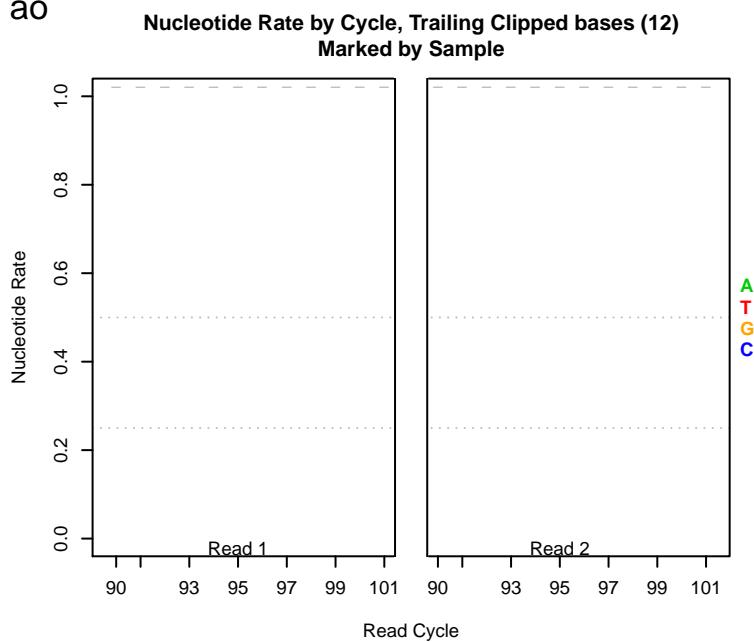
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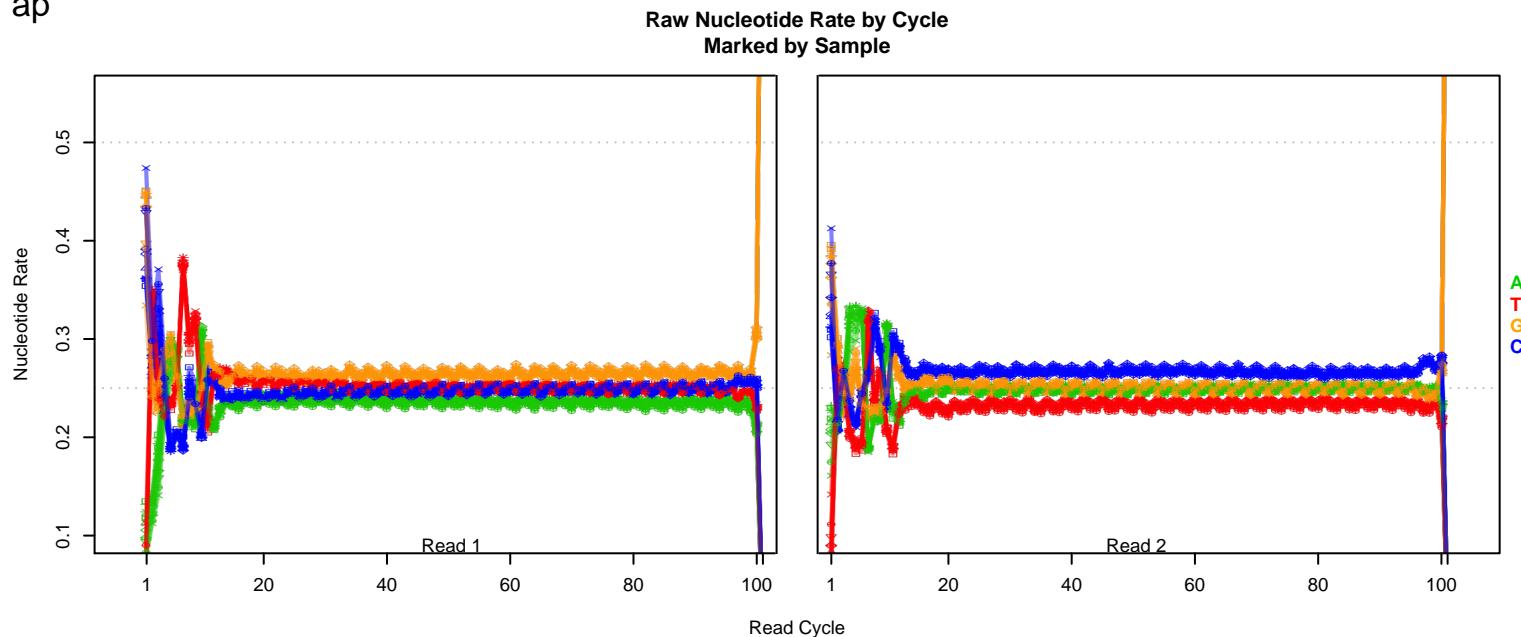
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